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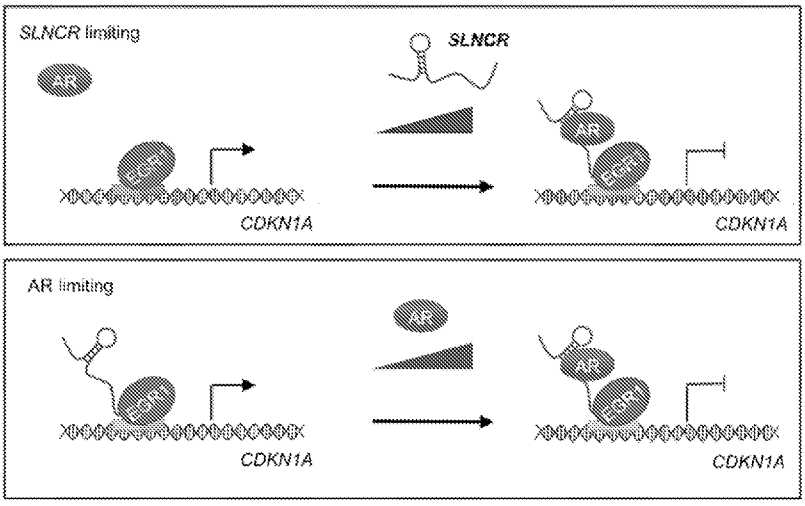
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(54) **Title:** COMPOSITIONS AND METHODS FOR TREATING AR-AND/OR LNCRNA-MEDIATED DISEASES

FIG. 26



(57) **Abstract:** The present invention is based, at least in part, on the discovery that androgen receptor (AR) interacts with long non-coding RNA (lncRNA) in a sequence-specific manner, and that single-stranded nucleic acids designed to sterically block the interaction between AR and such lncRNA without significantly altering the expression of AR and/or lnc RNA can be applied to effectively modulate the activity of AR or lncRNA.

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COMPOSITIONS AND METHODS FOR TREATING AR- AND/OR LNCRNA-MEDIATED DISEASES

Cross-Reference to Related Applications

This application claims the benefit of U.S. Provisional Application No. 62/557,997, filed on September 13, 2017; and U.S. Provisional Application No. 62/699,960, filed on July 18, 2018; the entire contents of each applications are incorporated herein in their entirety by this reference.

Statement of Rights

This invention was made with government support under grant numbers 5R01CA185151-04, R01CA140986, R35GM122532, 1ZIABC011585, T32AI007386, T32CA009156, and 4R01DK102165-04, awarded by the National Institutes of Health. The U.S. government has certain rights in the present invention.

Background of the Invention

Long non-coding RNAs (lncRNAs) are spliced, capped, and generally polyadenylated transcripts of >200 nucleotides. Many lncRNAs have been demonstrated to play critical roles in tissue physiology, disease processes, immune regulation and cancer. Remarkably, despite their established importance, the fundamental mechanism of action of lncRNAs has been poorly studied; only a few of the predicted >90,000 human lncRNAs have been well characterized. Despite this, it is believed that many lncRNAs function through direct interactions with protein partners, acting to scaffold the formation of ribonucleoprotein (RNP) complexes required for regulation of critical cellular processes. Well-characterized examples of scaffolding lncRNAs include XIST, which regulates X-chromosome inactivation through association with histone modification complexes, and *HOTAIR*, an oncogenic lncRNA that coordinates gene expression patterns partially through interactions with the polycomb repressive complex (Hajjari, M. and A. Salavaty, Cancer Biol Med, 2015. 12(1): p. 1-9; Cerase, A., *et al.*, Genome Biol, 2015. 16: p. 166).

Scaffolding lncRNAs may also bind and regulate the activity of transcription factors. For example, the lncRNAs *SLNCR1* and *HOTAIR*, and possibly *SRA1* and *PCGEM1*, bind to the androgen receptor (AR) protein to modulate its downstream transcriptional activity (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37; Zhang, A., *et*

al., Cell Rep, 2015. 13(1): p. 209-21; Agoulnik, I.U. and N.L. Weigel, Steroids, 2009. 74(8): p. 669-74; Prensner, J.R., *et al.*, Oncotarget, 2014. 5(6): p. 1434-8; Yang, L., *et al.*, Nature, 2013. 500(7464): p. 598-602). Interestingly, in contrast to canonical AR activation, in which an androgenic ligand, such as dihydrotestosterone (DHT), binds to AR to elicit nuclear localization and protein dimerization in a head-to-tail formation, lncRNA-mediated AR function occurs in an androgen-independent manner (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37; Zhang, A., *et al.*, Cell Rep, 2015. 13(1): p. 209-21; Yang, L., *et al.*, Nature, 2013. 500(7464): p. 598-602). In this way, RNA-driven AR function is fine-tuned to modulate expression of only a subset of genes, as opposed to global, androgen-driven AR activation. Although AR has been implicated in multiple cancers, including prostate, bladder, kidney, lung, liver, pancreatic, thyroid, and breast cancers, the fundamental mechanisms of AR activation in many of these cancers is not well-established (Chang, C., *et al.*, Oncogene, 2014. 33: p. 3225-3234; Kanda, T., *et al.*, World J Gastroenterol, 2014. 20: p. 9229-9236; Stanley, J.A., *et al.*, J Steroid Biochem Mol Biol, 2012. 130: p. 105-124). RNA-driven AR function is believed to function largely in an oncogenic manner (Zhang, A., *et al.*, Cell Rep, 2015. 13(1): p. 209-21; Yang, L., *et al.*, Nature, 2013. 500(7464): p. 598-602). For example, it has been revealed that *SLNCR1* increases AR occupancy at the promoter of the gene encoding the matrix metalloproteinase MMP9, increasing MMP9-mediated melanoma invasion (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Thus, understanding of lncRNA-driven, androgen-independent regulation of AR activity, including RNA-mediated activation, may explain many unresolved questions regarding AR's oncogenic or tumor suppressive functions and is an intriguing and clinically-relevant area of research.

In addition to AR, *SLNCR1* also binds to the transcription factor brain-specific homeobox protein 3a (Brn3a), and all three components are required for increased melanoma invasion (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). A highly conserved region of *SLNCR1* (*SLNCR1*^{cons}), spanning nucleotides (nts) 372-672, is necessary and sufficient to mediate increased melanoma invasion. The scaffolding model for lncRNA function posits that lncRNAs bind multiple protein partners concurrently. In agreement with this model, Brn3a and AR bind to adjacent sequences on *SLNCR1*^{cons}, with Brn3a binding to *SLNCR1*$^{462\text{-}572}$, while AR binds to *SLNCR1*$^{568\text{-}637}$.

The predicted or confirmed AR-binding lncRNAs (*SLNCR1*, *HOTAIR*, *SRA1* and *PCGEM1*) contain a highly conserved region of approximately 28 nts (Schmidt, K., *et al.*,

Cell Rep, 2016. 15(9): p. 2025-37). This conserved sequence is located within the segment of *SLNCR1*, *HOTAIR*, and *PCGEM1* required for AR-lncRNA association (*SLNCR1*$^{568-637}$, *HOTAIR*$^{1-360}$, and *PCGEM*$^{421-480}$), indicating that AR interacts with RNA in a sequence-specific manner (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37; Yang, L., *et al.*, Nature, 2013. 500(7464): p. 598-602; Zhang, A., *et al.*, Cell Rep, 2015. 13(1): p. 209-21). Moreover, *HOTAIR* and *PCGEM1* mediate ligand-independent AR transcriptional activity, indicating that these interactions may play an important role in AR-driven, androgen-independent cancers (Yang, L., *et al.*, Nature, 2013. 500(7464): p. 598-602; Zhang, A., *et al.*, Cell Rep, 2015. 13(1): p. 209-21).

The world-wide incidence of melanoma has been on the rise for the past 30 years. In the United States, there are ~73,000 new cases diagnosed and ~10,000 deaths annually attributed to melanoma (Siegel, R.L., Miller, K.D., and A. Jemal, CA: a cancer journal for clinicians, 2015. 65: p. 5-29). Of these deaths, approximately two-thirds will occur in males, the result of a well-established sex bias disfavoring males in melanoma etiology (Bidoli, E., *et al.,* BMC Cancer, 2012. 12: p. 443; de Vries, E., *et al.,* Annals of oncology : official journal of the European Society for Medical Oncology / ESMO, 2007. 18: p. 1110-1116; Fisher, D.E., and A.C. Geller, JAMA Dermatology, 2013. 149: p. 903-904; Geller, A.C., *et al.,* JAMA, 2002. 288: p. 1719-1720; Joosse, A., *et al.,* The Journal of Investigative Dermatology, 2011. 131: p. 719-726; Schwartz, J.L., *et al.,* Cancer, 2002. 95: p. 1562-1568; Swetter, S.M., *et al.,* Archives of Dermatology, 2009. 145: p. 488-490). In addition to a significant survival advantage compared to males (38%), females demonstrate fewer metastases, a longer delay before relapse, and higher curable rates, strongly indicating a biological basis for the observed sex bias (Gamba, C.S., *et al.,* JAMA Dermatology, 2013. 149: 912-920; Joosse, A., *et al.,* Journal of Clinical Oncology : Official Journal of the American Society of Clinical Oncology, 2012. 30: p. 2240-2247; Joosse, A., *et al.,* The Journal of Investigative Dermatology, 2011. 131: p. 719-726).

AR regulates tumorigenesis in many human cancers, including prostate, breast, kidney, lung, bladder and liver (Chang, C., *et al.,* Oncogene, 2014. 33: p. 3225-3234). AR may function as a tumor suppressor or oncogene, likely dependent on cellular context and the presence or absence of AR-modulating factors. For example, AR activity in prostate cancer cells may be modulated by RNAs, including the lncRNA *HOTAIR* (Zhang, A., *et al.*, Cell Rep, 2015. 13(1): p. 209-21), or by proteins, such as the transcriptional repressor RE1-Silencing Transcription Factor (REST, also called Neuron-Restrictive Silencer Factor,

NRSF) (Svensson, C., *et al.*, Nucleic Acids Res, 2014. 42(2): p. 999-1015). Early studies suggested that AR has oncogenic functions in melanoma, and that differences in AR function or expression might explain the observed melanoma gender differences (de Vries, E., *et al.,* Annals of oncology : official journal of the European Society for Medical Oncology / ESMO, 2008. 19: p. 583-589; Joosse, A., *et al.,* The Journal of Investigative Dermatology, 2011. 131: p. 719-726; Li, W.Q., *et al.,* Journal of Clinical Oncology : Official Journal of the American Society of Clinical Oncology, 2013. 31: p. 4394-4399; Micheli, A., *et al.,* European Journal of Cancer, 2009. 45: p. 1017-1027; Morvillo, V., *et al.,* Pigment Cell Res, 1995. 8: p. 135-141; Morvillo, V., *et al.,* Melanoma Research, 2002. 12: p. 529-538; Spanogle, J.P., *et al.,* Journal of the American Academy of Dermatology, 2010. 62: p. 757-767). In direct support of an oncogenic function for AR, AR was shown recently to increase melanoma invasion through transcriptional upregulation of the matrix metalloproteinase MMP9 (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Interestingly, this regulation occurs independently of canonical AR activation, in which an androgen (such as testosterone) binds to the receptor to elicit downstream transcriptional patterns. Instead, AR-mediated invasion requires a novel lncRNA *SLNCR,* specifically the abundant *SLNCR1* isoform that directly binds to and recruits AR to the *MMP9* promoter.

LncRNAs are transcripts of >200 nucleotides that lack an open-reading frame and exhibit cell-type and tissue-specific expression. LncRNAs are important regulators of tissue physiology and disease processes, and may function as either oncogenes or tumor suppressors (Li, J., Xuan, Z., and C. Liu, International Journal of Molecular Sciences, 2013. 14: p. 18790-18808; Serviss, J.T., Johnsson, P., and D. Grander, Frontiers in Genetics, 2014. 5: p. 234). While the fundamental mechanism of many lncRNA remains unknown, many (like *SLNCR*) function through direct interactions with proteins. Using a highly-sensitive technique developed for the identification of RNA-associated transcription factors called RATA (RNA-associated transcription factor array), *SLNCR* was shown to bind to multiple transcription factors, possibly regulating their downstream transcriptional activities (Schmidt K, *et al.,* J Biol Methods, 2017. 4(1): p. e67; Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). In addition to AR and Brn3a, both of which are required for *SLNCR1*-mediated regulation of *MMP9*, early growth response 1 (EGR1) was identified as a candidate *SLNCR1*-interacting transcription factor (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37).

EGR1 is a zinc-finger transcription factor implicated in many human cancers, likely functioning as a tumor suppressor. In prostate cancer, EGR1 is a critical regulator of AR function (Yang, S.Z., and S.A. Abdulkadir, Journal of Biological Chemistry, 2003. 278(41): p. 39906-11). In melanoma, EGR1 has been implicated in apoptosis, cell growth, and fibronectin matrix synthesis (Ahmed, M.M., *et al.,* The Journal of Biological Chemistry, 1996. 271: p. 29231-29237; Gaggioli, C., *et al.,* Oncogene, 2005. 24: p. 1423-1433; Muthukkumar, S., *et al.,* Mol Cell Biol, 1995. 15: 6262-6272; Sells, S.F., *et al.,* Mol Cell Biol, 1995. 15: p. 682-692). Other roles for EGR1 in melanomagenesis, including biological consequences of possible physical interactions with *SLNCR* and/or AR have not been described.

Currently, it is nearly impossible to predict lncRNA function from sequence analysis alone because so little is known about the role of lncRNA sequence and structural motifs relative to interactions with other proteins and nucleic acids. This general lack of understanding of the mechanisms of lncRNA activity hinders the development and potential therapeutic impact of modalities and strategies that target lncRNAs. Thus, there is a critical need for studies of the fundamental biology of lncRNAs and identification of functional lncRNA motifs. Establishing sequence and/or structural parameters to enable prediction of lncRNA-protein binding activity will significantly advance our ability to identify and characterize functional lncRNAs, and to design novel lncRNA-targeting therapeutics.

Summary of the Invention

The present invention is based, at least in part, on the discovery that AR interacts with lnc RNA in a sequence-specific manner, and that single-stranded nucleic acids designed to sterically block the interaction between AR and such lncRNA without significantly altering the expression of AR and/or lncRNA can be applied to effectively modulate the activity of AR or lncRNA.

The present invention is also based, at least in part, on the discovery that the N-terminal, regulatory domain (NTD) of AR (AR NTD) interacts with an unstructured, pyrimidine-rich RNA in a sequence-specific manner. A novel AR-binding motif in HOXA11AS-203 is described herein such that this lncRNA also functions in complex with AR. In-cell SHAPE reveals that *SLNCR1*'s AR-binding motifs are found in a region of high structural flexibility, and that *SLNCR1*'s AR binding motifs display in-cell protections consistent with protein binding. Mutational analysis confirms that *SLNCR1*'s AR-binding

motifs are required for *SLNCR1*- and AR-mediated melanoma invasion. Furthermore, designed single-stranded oligos to sterically block the interaction of AR and *SLNCR1* show that these oligos negate *SLNCR1*-mediated melanoma invasion. It is revealed herein how characterizing lncRNA structure and protein interactions enables identification of novel lncRNA function and supports design of novel lncRNA-targeting therapeutics.

The present invention is further based, at least in part, on the discovery that AR directly binds many *SLNCR*-regulated genes in a ligand-independent manner in cancer cells. It is discovered herein that *SLNCR* directly recruits AR to EGR1-bound chromatin. AR and *SLNCR* act as a transcriptional switch, reversing EGR1-mediated upregulation of the $p21^{Waf1/Cip1}$ tumor suppressor gene. These results indicate that *SLNCR*, AR and EGR1 form a novel regulatory triad that regulates cancer proliferation. These data demonstrate that a comprehensive evaluation of AR function in melanoma is critical to understanding the mechanistic underpinnings of the melanoma sex bias.

In one aspect, a single-stranded nucleic acid that binds to androgen receptor (AR) or a long non-coding RNA (lncRNA), and blocks interaction between AR and the lncRNA, wherein the single-stranded nucleic acid does not significantly reduce the expression of AR or the lncRNA, is provided.

Numerous embodiments are further provided that can be applied to any aspect of the present invention and/or combined with any other embodiment described herein. For example, in one embodiment, the single-stranded nuclei acid binds to AR to block the interaction of AR with the lncRNA. In another embodiment, the single-stranded nucleic acid localizes at least partially to the nucleus. For example, the single-stranded nucleic acid localizes to the nucleus. In still another embodiment, the single-stranded nucleic acid is at least 11 nucleotides (nt) in length (e.g., 17 nt in length). In yet another embodiment, the single-stranded nucleic acid dose not comprise a high level of secondary structure. In another embodiment, the single-stranded nucleic acid comprises at least one UCUCCU or UCUCCA motif. In still another embodiment, the single-stranded nucleic acid comprises two or more motifs selected from the group consisting of UCUCCU and UCUCCA motifs. The single-stranded nucleic acid may further comprise an internal sequence between these motifs. Such internal sequence may be 9 nt in length. In yet another embodiment, the single-stranded nucleic acid is at least 20 nt in length, and the pyrimidine content within a 17-20 nt region of the single-stranded nucleic acid that comprises the UCUCCU or UCUCCA motif is at least 65% (e.g., more than 75%). In another embodiment, the

lncRNA is selected from the group of SLNCR, HOXA11-AS-203, SRA1, HOTAIR, and PCGEM1. For example, the the lncRNA is SLNCR. In still another embodiment, the single-stranded nucleic acid is selected from the group of MIMIC 1 (SEQ ID NO: 23), MIMIC 2 (SEQ ID NO: 24), MUT L (SEQ ID NO:4), MUT R (SEQ ID NO:5), MUT I (SEQ ID NO:8), MUT PT (SEQ ID NO:7), WT-17 ((SEQ ID NO:9), WT-20 (SEQ ID NO:10), SRA1 (SEQ ID NO:20), and WT-11 (SEQ ID NO:17).

In one embodiment, the single-stranded nucleic acid binds to the lncRNA to block the interaction of AR with the lncRNA. In another embodiment, the nucleic acid contains at least one AGGAGA or UGGAGA motif. In still another embodiment, if the lncRNA contains two consecutive motifs selected from the group consisting of UCUCCU and UCUCCA motifs, the single-stranded nucleic acid binds to both motifs simultaneously with an appropriate internal sequence between the sequences that bind to the two motifs. In yet another embodiment, the lncRNA is selected from the group of SLNCR, HOXA11-AS-203, SRA1, HOTAIR, and PCGEM1. For example, the the lncRNA is SLNCR. In another embodiment, the single-stranded nucleic acid localizes at least partially to the nucleus. In still another embodiment, the single-stranded nucleic acid is at least 20 nt in length (e.g., 28 nt in length). In yet another embodiment, the single-stranded nucleic acid dose not comprise a high level of secondary structure. In another embodiment, the single-stranded nucleic acid comprises an AGGAGA motif and a UGGAGA motif. In still another embodiment, the single-stranded nucleic acid comprises a GGAGA motif and a UGGAGA motif. In yet another embodiment, the single-stranded nucleic acid comprises an AGGAGA motif and a UGGAG motif. In another embodiment, the single-stranded nucleic acid comprises a GGAGA motif and a UGGAG motif. In still another embodiment, the two motifs are linked by an internal sequence. Such internal sequence may be 9 nt in length. In yet another embodiment, the internal sequence has more than 75% (e.g., 100%) sequence identity to the sequence AGACCAGGG. In another embodiment, the single-stranded nucleic acid is at least 30 nt in length, and the purine content within a 30 nt region of the single-stranded nucleic acid that comprises the AGGAGA or UGGAGA motif is at least 65% (e.g., more than 75%). In still another embodiment, the single-stranded nucleic acid is ANTISENSE 1 (SEQ ID NO: 25) or ANTISENSE 2 (SEQ ID NO: 26).

In one embodiment, the single-stranded nucleic acid comprises at least one chemical modification. In another embodiment, the single-stranded nucleic acid penetrates the cellular membrane of a cell in the absence of a delivery vehicle. In still another

embodiment, the chemical modification extends the half-life of the single-stranded nucleic acid in a cell. For example, the chemical modificaiton may be any chemical modificaiton of nucleic acid known in the art, such as one selected from the group consisting of a FANA chemical modification, a fluorinated nucleoside, a DNA nucleotide, a 2′-O-methylated nucleoside, a phosphorothioate bond and a cholesterol moiety. In certain embodiment, the nucleic acid comprises a FANA chemical modification.

In one embodiment, a pharmaceutical composition comprising the single-stranded nucleic acid and a pharmaceutically acceptable agent selected from the group consisting of excipients, diluents, and carriers, is provided. In another embodiment, the pharmaceutical composition comprises the single-stranded nucleic acid at a purity of at least 75%. In still another embodiment, the pharmaceutical composition further comprises a nuclear receptor targeting drug. The nuclear receptor targeting drugs, described herein, may be luteinizing hormone-releasing hormone (LHRH) analogs, androgen receptor inhibitors, anti-androgens, hormone blocking drugs, nuclear receptor agonists, nuclear receptor antagonists, selective receptor modulators, selective androgen receptor modulators (SARMs), selective estrogen receptor modulators (SERMs), selective progesterone receptor modulators (SPRMs), selective glucocorticoid receptor agonists (SEGRAs), or selective glucocorticoid receptor modulators (SEGRMs). For example, the nuclear receptor target drug may be selected from the group consisting of leuprolide (Lupron®, Eligard®), goserelin (Zoladex®), triptorelin (Trelstar®), histrelin (Vantas®), degarelix (Firmagon®), bicalutamide (Casode®), enzalutamide (Xtandi®), flutamide (Eulexin®), nilutamide (Nilandron®), ketoconazole (Nizoral®), abiraterone (Zytiga®), dexamethasone, megestrol acetate (Megace®), medroxyprogesterone acetate (MPA), ethisterone, norethindrone acetate, norethisterone, norethynodrel, ethynodiol diacetate, norethindrone, norgestimate, norgestrel, levonorgestrel, medroxyprogesterone acetate, desogestrel, etonogestrel, drospirenone, norelgestromin, desogestrel, etonogestrel, gestodene, dienogest, drospirenone, elcometrine, nomegestrol acetate, trimegestone, tanaproget, BMS948, mifepristone, 4-hydroxytamoxifen, CINPA1, Cyproterone acetate (Androcur®, Cyprostat®, Siterone®), chlormadinone acetate (Clordion®, Gestafortin®, Lormin®, Non-Ovlon®, Normenon®, Verton®), 17-hydroxyprogesterone (17-OHP), THC, clotrimazole, PK11195 [1-(2-chlorophenyl)-N-methyl-N-(1-methylpropyl)-3-isoquinolinecarboxamide], meclizine, androstanol, CITCO [6-(4-chlorophenyl)imidazo [2,1-b][1,3] thiazole-5-carbaldehyde O-(3,4-dichlorobenzyl) oxime], zearalenone (ZEN), T0901317, S07662, enobosarm, BMS-

564,929, LGD-4033, AC-262,356, JNJ-28330835, LGD-2226, LGD-3303, S-40503, S-23, clomifene, femarelle, ormeloxifene, raloxifene, tamoxifen, toremifene, lasofoxifene, ospemifene, afimoxifene, arzoxifene, bazedoxifene, gulvestrant (Faslodex®, ICI-182780), CDB-4124, asoprisnil, proellex, mapracorat (BOL-303242-X, ZK 245186), fosdagrocorat (PF-04171327), ZK 216348, and 55D1E1.

In one embodiment, a vector comprising the single-stranded nucleic acid is provided. The vector may be an expression vector. In another embodiment, a host cell transfected with such expression vector is provided. In still another embodiment, a method of producing a single-stranded nucleic acid comprising culturing the host cell in an appropriate culture medium to, thereby, produce the single-stranded nucleic acid, is provided. The host cell could be a bacterial cell or a eukaryotic cell. In yet another embodiment, a method of producing a single-stranded nucleic acid comprising transcribing the vector *in vitro* under an appropriate reaction condition, and isolating the single-stranded nucleic acid from the reaction mixture, is provided.

In another aspect, a method of treating a subject afflicted with an AR- and/or lncRNA-mediated disease is provided, the method comprising administering to the subject a therapeutically effective amount of a single-stranded nucleic acid that binds to androgen receptor (AR) or a long non-coding RNA (lncRNA), and blocks interaction between AR and the lncRNA, wherein the single-stranded nucleic acid does not significantly reduce the expression of AR or the lncRNA.

As described above, numerous embodiments are further provided that can be applied to any aspect of the present invention and/or combined with any other embodiment described herein. For example, in one embodiment, the AR- and/or lncRNA-mediated disease is androgen-independent. In another embodiment, the AR- and/or lncRNA-mediated disease is selected from the group of cancer, inflammatory disease, metabolic diseases, spontaneous abortion, alopecia, Alzheimer disease, androgen-insensitivity syndrome, heart disease (e.g., artiosclerosis, coronary artery disease, and cardiomyopathy), azoospermia, cholelithiasis, cognition disorders, cryptorchidism, depressive disorder, diabetes mellitus, diabetic retinopathy, sex development disorders, bone fractures, hyperglycemia, hypertension, hypospadias, hypertrophy, hyperandrogenism, infertility, klinefelter syndrome, liver cirrhosis, liver disease, lupus, migraine disorder, Menkes Kinky Hair Syndrome, muscular atrophy, nerve degeneration, obesity, oligospermia, osteoarthritis, osteoporosis, Paget Disease, Polycystic Ovary Syndrome, Primary Ovarian Insuffiency,

Schizophrenia, spinal fractures, thrombocytosis, thyroid diseases, Tourette syndrome, Turner syndrome, and autoimmune disease. The cancer, described herein, may be, e.g., melanoma, lung adenocarcinoma, lung squamous cell carcinoma, cervical cancer, ovarian cancer, uterine cancer, pancreatic cancer, colorectal cancer, lower grade glioma, glioblastoma multiforme, breast cancer, endometrial cancer, prostate cancer, testicular cancer, thyroid cancer, osteosarcoma, esophageal cancer, liver cancer or bladder cancer. For example, the cancer is melanoma. The inflammatory disease, described herein, may be, e.g., acne vulgaris, asthma, and rheumatoid arthritis. The autoimmune disease described herein, may be, e.g., lupus, type I diabetes, and multiple sclerosis. In still another embodiment, the single-stranded nucleic acid inhibits the growth and/or metastasis the cancer.

In still another aspect, a method of inhibiting proliferation or invasion of cancer cells is provided, the method comprising contacting the cancer cells with a single-stranded nucleic acid that binds to androgen receptor (AR) or a long non-coding RNA (lncRNA), and blocks interaction between AR and the lncRNA, wherein the single-stranded nucleic acid does not significantly reduce the expression of AR or the lncRNA.

As described above, numerous embodiments are further provided that can be applied to any aspect of the present invention and/or combined with any other embodiment described herein. For example, in one embodiment, the single-stranded nucleic acid is administered in a pharmaceutically acceptable formulation. In another embodiment, the lncRNA is selected from the group of SLNCR, HOXA11-AS-203, SRA1, HOTAIR and PCGEM1. For example, the lncRNA is SLNCR. In still another embodiment, the single-stranded nucleic acid is selected from the group consisting of MIMIC 1, MIMIC 2, ANTISENSE 1, and ANTISENSE 2. In yet another embodiment, the single-stranded nucleic acid inhibits a SLNCR-regulated gene. The SLNCR-regulated gene, described herein, may be, e.g., MMP9, p21, CXCL2, JUN, STAT3, IL24, or MCAM. In another embodiment, the method further comprises admisnistering a nuclear receptor targeting drug. The nuclear receptor targeting drugs, described herein, may be luteinizing hormone-releasing hormone (LHRH) analogs, androgen receptor inhibitors, anti-androgens, hormone blocking drugs, nuclear receptor agonists, nuclear receptor antagonists, selective receptor modulators, selective androgen receptor modulators (SARMs), selective estrogen receptor modulators (SERMs), selective progesterone receptor modulators (SPRMs), selective glucocorticoid receptor agonists (SEGRAs), or selective glucocorticoid receptor modulators

(SEGRMs). For example, the nuclear receptor target drug may be selected from the group consisting of leuprolide (Lupron®, Eligard®), goserelin (Zoladex®), triptorelin (Trelstar®), histrelin (Vantas®), degarelix (Firmagon®), bicalutamide (Casode®), enzalutamide (Xtandi®), flutamide (Eulexin®), nilutamide (Nilandron®), ketoconazole (Nizoral®), abiraterone (Zytiga®), dexamethasone, megestrol acetate (Megace®), medroxyprogesterone acetate (MPA), ethisterone, norethindrone acetate, norethisterone, norethynodrel, ethynodiol diacetate, norethindrone, norgestimate, norgestrel, levonorgestrel, medroxyprogesterone acetate, desogestrel, etonogestrel, drospirenone, norelgestromin, desogestrel, etonogestrel, gestodene, dienogest, drospirenone, elcometrine, nomegestrol acetate, trimegestone, tanaproget, BMS948, mifepristone, 4-hydroxytamoxifen, CINPA1, Cyproterone acetate (Androcur®, Cyprostat®, Siterone®), chlormadinone acetate (Clordion®, Gestafortin®, Lormin®, Non-Ovlon®, Normenon®, Verton®), 17-hydroxyprogesterone (17-OHP), THC, clotrimazole, PK11195 [1-(2-chlorophenyl)-N-methyl-N-(1-methylpropyl)-3-isoquinolinecarboxamide], meclizine, androstanol, CITCO [6-(4-chlorophenyl)imidazo [2,1-b][1,3] thiazole-5-carbaldehyde O-(3,4-dichlorobenzyl) oxime], zearalenone (ZEN), T0901317, S07662, enobosarm, BMS-564,929, LGD-4033, AC-262,356, JNJ-28330835, LGD-2226, LGD-3303, S-40503, S-23, clomifene, femarelle, ormeloxifene, raloxifene, tamoxifen, toremifene, lasofoxifene, ospemifene, afimoxifene, arzoxifene, bazedoxifene, gulvestrant (Faslodex®, ICI-182780), CDB-4124, asoprisnil, proellex, mapracorat (BOL-303242-X, ZK 245186), fosdagrocorat (PF-04171327), ZK 216348, and 55D1E1. In still another embodiment, the subject is a mammal (e.g., human). In yet another embodiment, the mammal is an animal model of an AR- and/or lncRNA-mediated disease.

In yet another aspect, a cell-based method for identifying a single-stranded nucleic acid that binds to AR or a lncRNA and blocks interaction between AR and the lncRNA is provided, the method comprising: a) contacting a cell expressing AR and/or lncRNA with a test single-stranded nucleic acid that binds to AR or the lncRNA; and b) determining that the single-stranded nucleic acid blocks interaction between AR and the lncRNA, wherein the single-stranded nucleic acid does not significantly reduce the expression of AR or the lncRNA, optionally further determining that the single-stranded nucleic acid treats an AR- and/or lncRNA-mediated disease.

As described above, numerous embodiments are further provided that can be applied to any aspect of the present invention and/or combined with any other embodiment

described herein. For example, in one embodiment, the said cells are isolated from an animal model of an AR- and/or lncRNA-mediated disease, or a human patient afflicted with the AR- and/or lncRNA-mediated disease. In another embodiment, the step of contacting occurs *in vivo*, *ex vivo*, or *in vitro*. In still another embodiment, the method further comprisies determining the ability of the test single-stranded nucleic acid to bind to either AR or lncRNA before or after determining the effect of the test single-stranded nucleic acid on the interaction between AR and the lncRNA. In yet another embodiment, the method further comprises determining the effect of the test single-stranded nucleic acid on the level of expression of AR or lncRNA before or after determining the effect of the test single-stranded nucleic acid on the interaction between AR and the lncRNA. In another embodiment, the method further comprises determining the activity of AR or lncRNA in the disease cell. The activity of AR or lncRNA may be assessed by determining the magnitude of cellular proliferation, cell death, cellular migration, replication, induction of angiogenesis, cellular invasion/metastasis, immune response, immune evasion, or transcription of AR- or lncRNA-regulated genes.

In another aspect, an *in vitro* cell-free method for identifying a single-stranded nucleic acid that binds to AR or a lncRNA and blocks interaction between AR and the lncRNA is provided, the method comprising a) contacting a mixture of AR protein and lncRNA with a test single-stranded nucleic acid that binds to AR or the lncRNA; and b) determining that the single-stranded nucleic acid blocks interaction between AR and the lncRNA, wherein the single-stranded nucleic acid does not significantly reduce the expression of AR or the lncRNA, optionally further determining that the single-stranded nucleic acid treats an AR- and/or lncRNA-mediated disease.

As described above, numerous embodiments are further provided that can be applied to any aspect of the present invention and/or combined with any other embodiment described herein. For example, in one embodiment, in one embodiment, the method further comprises determining the ability of the test single-stranded nucleic acid to bind to either AR or lncRNA before or after determining the effect of the test single-stranded nucleic acid on the interaction between AR and the lncRNA. In another embodiment, the lncRNA is a full-length RNA, or functional variants or fragments thereof. In still another embodiment, AR is a full-length protein, or functional variants or fragments thereof. In yet another embodiment, AR is an N-terminal region of AR protein having the amino acid sequence of SEQ ID NO: 27.

Brief Description of Figures

FIG. 1A – FIG. 1C show REMSA-based identification of minimal requirements for AR-*SLNCR1* interaction. FIG. 1A shows sequences of biotinylated probes used in these assays. The highly-predicted secondary structure of WT-41 is shown below. For REMSA results shown in FIG. 1B – FIG. 1C, the indicated probes (from FIG. 1A) were incubated with increasing concentrations of either full-length AR (FIG. 1B) or a truncated protein corresponding to AR's N-terminal region (FIG. 1C), resolved on a 5% TBE gel and probed using Streptavidin-HRP following transfer to a negatively charged membrane. The lines indicate either unbound labeled probe or the slower migrating RNA/protein complexes.

FIG. 2A – FIG. 2C show that AR's N-terminus specifically binds to biotinylated probes corresponding to WT-41, WT-28, and WT-20 as comfirmed by competition assays. FIG. 2A shows schematic of AR's protein domains. NTD = N-terminal domain, DBD = DNA binding domain, and LBD = ligand binding domain. The recombinant N-terminal AR protein used in these studies (amino acids 2-556) is denoted. For REMSA results shown in FIG. 2B – FIG. 2C, probes were incubated with 600 nM of recombinant (FIG. 2B) full-length AR protein, or (FIG. 2C) N-terminal AR protein. Where indicated, 10 μM of unlabeled RNA competitor corresponding to WT-41 was added prior to addition of biotinylated probes. REMSAs were completed as in FIG. 1A-FIG. 1C.

FIG. 3A – FIG. 3G show that AR binds to single-stranded RNA in a sequence specific manner. Sequences of biotinylated probes used in these assays are shown in FIG. 3A and FIG. 3C. Nucleotides that are mutated compared to wild-type *SLNCR1* are highlighted in red, bonded font. The predicted AR binding motifs are highlighted in the grey boxes. The yellow box denotes the non-endogenous AR binding motif in MUT PT. FIG. 3B and FIG. 3E show REMSA of the indicated probes incubated with 600 nM of recombinant N-terminal AR, as in FIG. 1B and FIG. 1C. FIG. 3D shows highly-predicted secondary structure of stem-loop probe with the non-endogenous nucleotides denoted by the red bar in (FIG. 3C). FIG. 3F shows the measurement of binding affinity by surface plasmon resonance (SPR) of the indicated concentrations of either WT-41 (left panel) or WT-20 (right panel) to full-length recombinant AR. RU, resonance units. FIG. 3G shows the consensus motif identified among AR-binding RNA sequences.

FIG. 4A – FIG. 4O show that AR does not bind promiscuously to pyrimidine-rich RNAs, and that AR and Brn3a binding sites reside within an unstructured region of *SLNCR1 in vivo*. FIG. 4A-4O further show the SHAPE-guided modeling of the *SLNCR1*

RNA structure. Sequences of biotinylated probes used in these assays are shown in FIG. 4A. FIG. 4B shows REMSA of the indicated probes incubated with 600 nM of recombinant N-terminal AR., as in FIG. 1B and FIG. 1C. FIG. 4C-4E show the normalized SHAPE reactivity profiles for WM1976 cell *SLNCR1*$^{403\text{-}780}$ RNA from (FIG. 4C) cell-free extracted nuclear RNA, (FIG. 4D) in-cell total cellular RNA, and (FIG. 4E) cell-free extracted cytoplasmic RNA. Colored bars with associated errors represent SHAPE reactivities (see scale). Purple and dark blue rectangles mark Brn3a and AR interaction sites, respectively. Grey and light blue rectangles represent sites of significant in-cell SHAPE and DMS protection, respectively. Grey bars below zero indicate residues with high background (and are thus classified as no-data). No data are collected for 5′ and 3′ nucleotides where RT and PCR primers bind. FIG. 4F-4H show the SHAPE-guided modeling reveals *SLNCR1*$^{403\text{-}780}$ has limited stable RNA structure. FIG. 4F shows the SHAPE profile for U1 snRNA. Colored arcs represent SHAPE-modeled base pairs with associated pairing probability. Entropy values (bottom) are local 50 nucleotide windowed medians. The horizontal dotted line marks the low entropy threshold 0.03. Purple shading indicates regions where windowed-median SHAPE and entropy values both fall below predetermined thresholds (0.4 SHAPE, 0.03 entropy) and grey shading marks expanded motif boundaries. FIG. 4G shows the comparison of increases in mutation rates (proportional to SHAPE reactivities) for *SLNCR1*$^{403\text{-}780}$ and U1 snRNA from nuclear extracts. On the X-axis, 5NIA, DMSO, and Denatured refer to the nucleotide mutation rates observed after MaP RT and sequencing of 5NIA treated, untreated, and denaturing control sample RNA, respectively. FIG. 4H shows the SHAPE profile for *SLNCR1*$^{403\text{-}780}$ lncRNA. SHAPE reactivities and Shannon entropies are plotted on the same scale as in panel A. Vertical dashed lines highlight a region of especially high SHAPE reactivity and high entropy. FIG. 4I-4J show that SHAPE-MaP accurately models structure and protein-binding of U1 snRNA. FIG. 4I-4J show the normalized SHAPE reactivity profiles for U1 small nuclear RNA from (FIG. 4I) cell-free extracted nuclear RNA (WM1976 cells) or (FIG. 4J) in-cell total RNA. Colored bars with associated errors represent SHAPE reactivities (see scale). 70K, U1A, and Sm protein interaction sites on U1, backed by crystal structure data, are highlighted above. Grey rectangles above 0 represent sites of significant in-cell SHAPE protection. Grey bars below zero indicate residues with high background (and are thus classified as no-data). No data are collected for 5′ and 3′ nts where RT and PCR primers bind. FIG. 4K shows the colored arcplot of modeled base-pairs with labeled probabilities (bottom) aligned to the modeled

minimum free energy secondary structure (top). All correct duplexes are observed in the model (black), and only one extra duplex is predicted (grey) where normally U1 RNA is engaged by proteins *in vivo*. FIG. 4L shows the comparison of SHAPE-MaP and DMS-MaP mutation rates. Differences in mutation rates of *SLNCR1*$^{403\text{-}720}$ between treated and untreated cell-free (nucleus) and in-cell SHAPE and DMS-MaP experiments on WM1976 cells are shown. Mutation rate differences have been averaged over a 10 nucleotide window and 5NIA rates were scaled up by the DMS/5NIA median ratio for ease of comparison. FIG. 4M-4O show the minimum free energy and alternative models of *SLNCR1*$^{403\text{-}780}$. FIG. 4M shows the colored arcplot of modeled base-pairs with labeled probabilities (bottom) aligned to the modeled minimum free energy secondary structure (top) of *SLNCR1*$^{403\text{-}780}$. Low SHAPE, low entropy regions relative to the global SLNCR403-780 median, which do not conform to the thresholds described in the text, are highlighted in purple, and grey shading marks expanded motif boundaries. Secondary structure projections of the (FIG. 4N) minimum free energy model and (FIG. 4O) arcplot-supported alternative structures are represented with associated SHAPE reactivities and in-cell reagent protections. SS1 and SS2 denote low SHAPE, low Shannon regions 1 and 2 that are maintained in both models. All expanded low SHAPE, low entropy structures are shaded gray.

FIG. 5A – FIG. 5C show that mutation of *SLNCR1*'s AR binding motif negates *SLNCR1*-mediated invasion. FIG. 5A shows schematic of the *SLNCR1* sequences expressed in (FIG. 5B), zoomed in on the region containing site-directed mutations within the AR binding motif. FIG. 5B shows matrigel invasion assays of A375 cells transfected with either an empty vector or a vector expressing the indicated *SLNCR1* sequence. *SLNCR1*^{cons} corresponds to *SLNCR1* nts 372-672. Invasion is calculated as the percent of invading cells compared to mobile cells as counted in 8 fields of view. Top panels show representative images of the indicated invading and mobile cells. Quantification from 3 independent replicates, represented as mean ± SD, is shown at the bottom. FIG. 5C shows that the *SLNCR1* expression vectors express similar levels of S*LNCR1*. RT-qPCR data is represented as the fold change compared to A375 vector control, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the Student's t-test: * p-value < 0.05, ** p-value < 0.005, ns = not significant.

FIG. 6A – FIG. 6D show that AR directly binds to a sequence corresponding to lncRNA HOXA11-AS1-203, and possibly *SRA1*. Sequences of probes corresponding to the regions of the indicated lncRNAs predicted to bind to AR are shown in FIG. 6A. FIG. 6B shows REMSA of the indicated probes incubated with 600 nM of recombinant N-terminal AR, as in FIG. 1B and FIG. 1C. FIG. 6C shows schematic of the genomic loci of HOXA11 gene (blue) and its cognate antisense RNAs (green). The HOXA11AS transcript variant 203 contains the AR binding sequence and is highlighted in red. Transcript variants are based on Ensembl genome assembly: GRCh38.p10 (GCA_000001405.25). FIG. 6D shows sequence of HOXA11AS-203 variant, with the sequence corresponding to the probe used in (FIG. 6A; highlighted in yellow).

FIG. 7A – FIG. 7B show that AR's N-terminal region likely directly binds to *SRA1* and HOXA11AS-203. For REMSA shown in FIG. 7A, the biotinylated probe corresponding to a region of *SRA1* (FIG. 6A) was incubated with 600 nM of recombinant N-terminal AR protein. In lane 3, 10 μM of unlabeled RNA competitor corresponding to WT-41 was added prior to addition of biotinylated probes. REMSA was completed as in FIG. 1B and FIG. 1C. FIG. 7B shows that HOXA11AS-203 is expressed in AR-expressing tissues. Expression of *HOXA11AS-203* was quantified using RT-qPCR with isoform specific primers, represented as the fold change compared to skeletal muscle expression, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. *AR* mRNA expression is represented as the average RPKM from GTEx RNA-seq, as presented in The Human Protein Atlas.

FIG. 8 shows that FANA-modified oligos are gymnotically delivered to melanoma short-term cultures. The indicated melanoma short term cultures were seeded in a 24-well plate, and Alexa-labeled scrambled FANA-modified oligos were added 24 hours later at the indicated concentrations. Cells were incubated for 4 days, and Alexa 647 signal was quantified using FACs.

FIG. 9A – FIG. 9C show that sterically-blocking the AR-*SLNCR1* interaction negates or prevents *SLNCR1*-mediated melanoma invasion. FIG. 9A – FIG. 9B show that steric-blocking FANA-modified oligos block the interaction of AR and SLNCR1. RNA electromobility shift assay (REMSA) using a biotinylated RNA probe corresponding to the region of SLNCR1 that binds to AR (UAUUUUUCCCUCUCCACCCU). RNA binding reactions were assembled in REMSA binding buffer (Thermo Scientific) with 0.5 nM of biotinylated RNA probe, 2 μg of yeast tRNA, 600 nM of N-terminal AR protein

(corresponding to amino acids 2-556) where indicated, and 10 μM of the indicated FANA-modified oligos where indicated. FANA-oligos were designed to either bind to AR (AR binders, or MIMIC), or are the reverse compliment (ANTISENSE) to SLNCR1 and bind to the lncRNA. Reactions were incubated at room temperature for 25 minutes, 5x loading buffer was added, and samples were resolved on a 5% TBE gel in 0.5X TBE buffer. Following electrophoresis, the gel was transferred to Amersham Hybond-N+ membrane (GE Healthcare), crosslinked, and probed using the LightShift® Chemiluminescent RNA EMSA Kit (Thermo Scientific). dsRNA = double stranded RNA, formed upon addition of the reverse compliment FANA oligos. FIG. 9C shows that FANA-modified oligos block *SLNCR1*-mediated melanoma invasion. Matrigel invasion assays of A375 cells transfected with either an empty vector or a vector expression *SLNCR1*. The indicated FANA-modified oligos were added 24 hours post-transfection, at a final concentration of 500 nM. Invasion is calculated as the percent of invading cells compared to mobile cells as counted in 8 fields of view. Top panels show representative images of the indicated invading and mobile cells. Quantification from 3 independent replicates, represented as mean ± SD, is shown at the bottom. Significance compared to the vector and scramble only control was calculated using the Student's t-test: * p-value < 0.05, ** p-value < 0.005, *** p-value < 0.0005, ns = not significant.

FIG. 10A – FIG. 10D show that sterically-blocking the AR-*SLNCR1* interaction negates *SLNCR1*-mediated *MMP9* upregulation. Relative (FIG. 10A) *SLNCR1* or (FIG. 10B) *MMP9* expression in A375 cells transfected with either an empty or *SLNCR1*-expressing plasmid, and following addition of the indicated FANA-modified oligos. RT-qPCR data is represented as the fold change compared to A375 vector and scramble control, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. Significance in FIG. 10B was calculated using the Student's t-test compared to vector/scramble only control: * p-value < 0.05, n.s. = not significant. FIG. 10C-10D show that mutation of *SLNCR1*'s AR motifs 1 and 2 negates *SLNCR1*-mediated *MMP9* upregulation. Relative (FIG. 10C) *SLNCR1* or (FIG. 10D) *MMP9* expression in A375 cells transfected with plasmids expressing either wild-type or mutant *SLNCR1*-expressing plasmids. RT-qPCR data is represented as the fold change compared to A375 vector control, normalized to GAPDH. Error bars represent standard deviations calculated from 3 reactions. Significance in FIG. 10D was calculated using the Student's t-test compared to vector only control: ** p-value < 0.005, **** p-value < 0.001, n.s. = not significant.

FIG. 11 shows that AR's N-terminal region likely requires at least 11 nucleotides for RNA binding. For REMSA shown in FIG. 11, either 11 nucleotide (WT-11) or 10 nucleotide (WT-10) biotinylated probes corresponding to a region of *SLNCR1* was incubated with 600 nM of recombinant N-terminal AR protein. REMSA was completed as in FIG. 1B and FIG. 1C.

FIG. 12A – FIG. 12L show that *SLNCR* is expressed in a gender- and stage-specific manner, regulates melanoma cell proliferation, and increase melanoma invasion. FIG. 12A shows box plots of *SLNCR* expression from 150 TCGA melanomas categorized by patient gender and stage of melanoma. Data are represented as mean ± SEM. Significance was calculated using the one-way analysis variance (ANOVA). FIG. 12B shows box plots of *SLNCR* expression from male (left panel) or female (right panel) melanomas pre- and post-lymph node metastasis. Data are represented as mean ± SEM. Significance was calculated using the two-tailed Student's t-test: * p-value < 0.05, ** p-value < 0.005, n.s. = not significance. FIG. 12C shows Kaplan-Meier survival analysis high- or low-*SLNCR* expressing TCGA male or female melanomas, defined by the median *SLNCR* expression (RPKM = 14.1). FIG. 12D shows representing expression of *AR* mRNA in male or female melanomas exhibiting low (left panel) or high (right panel) expression of *SLNCR*. FIG. 12E shows Heat map of differentially expressed genes upon knockdown of *SLNCR* in the MSTC WM1976. The shading represents the log2 fold change compared to scramble siRNA control. Genes are clustered with Euclidean distance and average linkage clustering. FIG. 12F shows Gene Ontology biological process enriched in differential expressed genes represented in (FIG. 12E). FIG. 12G shows that the indicated MSTCs were seeded in 96-well plates, transfected with the indicated siRNAs and cell proliferation was quantified at the indicated time points using WST-1 proliferation reagent. Each assay was repeated 2-3 times, and shown is one representative assay. Error bars represent the mean ± SD of 3 technical replicates. Significance was calculated using the two-way analysis variance (ANOVA), with the Dunnett test for multiple comparison testing. * p-value < 0.05, ** p-value < 0.005, *** p-value < 0.0005, **** p < 0.0001. FIG. 12H shows the Tukey box plots of *SLNCR* expression in TCGA melanomas (n=172) exhibiting low (≤1) or high (>1) primary mitotic growth rates. Significance was calculated using a Mann-Whitney test: * p < 0.05. FIG. 12I-12L show that *SLNCR1*, but not *SLNCR2* nor *SLNCR3*, increase melanoma invasion. FIG. 12I shows schematic of the exons (numbered) of the 3 *SLNCR* isoforms previously identified in melanomas (not drawn to scale). Denoted is the sequence

required for AR binding, and the regions targeted by the siRNAs used in this study. FIG. 12J shows quantification from 3 independent replicates, represented as mean ± SD, of matrigel invasion assays of A375 cells transfected with the indicated empty or *SLNCR*-expressing plasmid. Invasion is calculated as the percent of invading cells compared to mobile cells as counted in 8 fields of view. FIG. 12K shows relative *MMP9* (left) or *SLNCR* (right) expression in A375 cells transfected with the indicated empty or *SLNCR*-expressing plasmid. RT-qPCR data is represented as the fold change compared to scramble control, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the two-tailed Student's t-test: ** $p < 0.005$. FIG. 12L shows RNA immunoprecipitations from HEK293T cells transfected with GFP-tagged AR, using α-AR antibody or a matched IgG nonspecific control. Left panel shows the western blot analysis of input or bound proteins following IP with either IgG or α-AR (AR) antibodies. Right panel shows the relative enrichment of the indicated transcript measured via RT-qPCR compared to IgG nonspecific control.

FIG. 13A – FIG. 13F. FIG. 13A shows box plot of *SLNCR* expression from pre- and post-metastatic melanomas. Data are represented as mean ± SEM. Significance was calculated using the two-tailed Student's t-test: n.s. = not significance. FIG. 13B shows box plot of relative AR protein expression, determined via reverse phase protein array (RPPA), in male and female TCGA melanomas. Data are represented as mean ± SEM. Significance was calculated using the two-tailed Student's t-test: * p-value < 0.05. FIG. 13C-13F show that siRNA-mediated knockdown of *SLNCR* does not affect melanoma apoptosis. FIG. 13C shows relative *SLNCR* expression in the indicated cells transfected with either scramble or *SLNCR*-targeting siRNAs. RT-qPCR data is represented as the fold change compared to scramble control, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the two-tailed Student's t-test: * p-value < 0.05, ** p-value < 0.005, *** p-value < 0.0005, n.s. = not significance. FIG. 13D shows the populations of apoptotic cells in A375, WM1976, and WM858 cells transfected with either scramble or *SLNCR*-targeting siRNAs by FACS. Specifically, FIG. 13D shows representative scatter plots of annexin V and 7-AAD staining, as measured via fluorescence-activated cell sorting (FACS) analysis, of the indicated melanoma cells transfected with the indicated siRNAs. Cells are classified as "viable" (Q4, bottom left), "apoptotic" (Q1, top left), or "necrotic" (Q4, top right). FIG. 13E shows the Scatter plot of the log2 fold change of genes significantly dysregulated ($p < 0.01$) upon knockdown of

both *SLNCR1* and *SLNCR* (all isoforms). Genes that are dysregulated in an opposing manner by *SLNCR1* versus *SLNCR* are labeled and denoted in red. Pearson's correlation (r) was calculated using GraphPad Prism. FIG. 13F shows the scatter plot of primary melanoma mitotic growth rate versus Log2 *SLNCR* expression for 172 melanomas from the TCGA (mitotic growth rate was available for only 172 melanomas).

FIG. 14A – FIG. 14B show that *SLNCR* and AR cooperatively regulate melanoma proliferation in a hormone-independent manner. The indicated cells were either transfected with the indicated siRNAs (FIG. 14A) or FANA-modified oligos were added to cell media (FIG. 14B) 24 hours after cells were seeded in 96-well plates. Cell proliferation was quantified using WST-1 reagent, as in FIG. 12B. Error bars represent the mean ± SD of 3 technical replicates. Significance was calculated using the two-way analysis of variance (ANOVA), with the Dunnett test for multiple comparison testing, n.s. = not significant, **** = $p < 0.0001$.

FIG. 15A – FIG. 15D show that AR increases melanoma cell proliferation. FIG. 15A shows that vehicle-control or the indicated concentration of flutamide was added twenty-four hours after the indicated cells were seeded in 96-well plates. Cell proliferation was quantified using WST-1 reagent, as in FIG. 12B. FIG. 15B shows relative *AR* expression in the indicated cells transfected with either scramble or *SLNCR*-targeting siRNAs. FIG. 15C shows western blot of A375 cell lysates following transfection with the indicated siRNAs. Left panel: representative blot probed with α-AR and α-GAPDH antibodies. Right panel: quantification from three independent replicates, normalized to GAPDH. FIG. 15 D shows relative *SLNCR* expression in the indicated cells following addition of the indicated FANA-modified oligos. RT-qPCR data ((FIG. 15A) and (FIG. 15C)) is represented as the fold change compared to scramble control, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the Student's t-test: * p-value < 0.05, ** p-value < 0.005, *** p-value < 0.0005.

FIG. 16A – FIG. 16C show that AR is bound at the promoters of a number of *SLNCR*-regulated genes. Left panel of FIG. 16A shows Venn diagram representing the number of active genes (*i.e.* AR bound genes) in A375 cells transfected with either an empty or *SLNCR*-expressing plasmid. Right panel of FIG. 16A shows plot of tag densities for vector or *SLNCR1*-expressing cells. FIG. 16B shows Venn diagram representing AR active genes (as determined via AR ChIP-Seq of either vector or *SLNCR*-expressing cells),

SLNCR differentially expressed (DE) genes (as determined via RNA-seq), and the genes that are both AR-bound and *SLNCR*-regulated. FIG. 16C shows the Integrated Genome Viewer plots displaying AR ChIP-seq read intensities from vector control (light blue, top track), *SLNCR1*-expressing cells (dark blue, middle track) or input control (grey, bottom track) corresponding to the indicated genomic loci. Numbers on the top left indicate plot height for tracks (significant enrichment, Binomial Test $p<0.0001$).

FIG. 17A – FIG. 17C show that *SLNCR* and AR regulate many overlapping genes, including genes implicated in melanoma proliferation. FIG. 17A shows relative expression of the indicated genes from indicated cells transfected with either scramble, *SLNCR*-, or AR-targeting siRNAs. RT-qPCR data is represented as the fold change compared to scramble control, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the Student's t-test: * p-value < 0.05, ** p-value < 0.005, *** p-value < 0.0005. FIG. 17B shows scatterplots of *SLNCR* expression and expression of the indicated genes from TCGA patient melanomas (n = 150). Nonparametric two-tailed Spearman correlation coefficients and significances are shown. FIG. 17C shows heat map of *SLNCR*-regulated genes (as in FIG. 12A) that are also AR-bound. The shading represents the log2 fold change compared to scramble siRNA control. Genes are clustered with Euclidean distance and average linkage clustering. Red arrows depict genes that are implicated in cell proliferation.

FIG. 18A – FIG. 18H show that *SLNCR* and AR inhibit expression of *CDKN1A*/p21 independently of p53. FIG. 18A and 18B show that the knockdown of *SLNCR* or AR increase *CDKN1A* levels. FIG. 18A, 18B and 18E show relative expression of the indicated genes from indicated cells transfected with either scramble, *SLNCR*-, or AR-targeting siRNAs. RNA was isolated 72 hours post transfection with 10 nM of the indicated siRNAs. RT-qPCR data is represented as the fold change compared to scramble control, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the Student's t-test: * p-value < 0.05, ** p-value < 0.005, *** p-value < 0.0005. FIG. 18C, 18D and 18F show in western blot data that knockdown of *SLNCR* or AR increase p21 protein levels independently of p53. 72 hours post-transfection of the indicated cells with 10 nM of the indicated siRNAs, lysate was prepared using M-PER Mammalian Protein Extraction Reagent (Thermo Scientific), according to manufacturer's instructions. Samples were separated on BioRad Any kD™ Mini-PROTEAN® TGX™ Precast Protein Gels and transferred to LF-PVDF using the

mixed MW protocol on the BioRad Transblot Turbo. The following antibodies were used: Cell Signaling P21 Waf1/Cip1 (12D1) at 1:1000, Cell Signaling GAPDH (14C10) at 1:5000, LICOR secondary at 1:10,000. Protein normalization is represented as a fold change of p21 levels, normalized to GAPDH levels, and was performed using ImageJ software. Bars represent mean ±SD from 3 independent biological replicates. FIG. 18E shows that AR and *SLNCR* inhibit *CDKN1A* expression independently of p53. Relative expression of the indicated transcripts 72 hours post-transfection of the p53-deficient SK-MEL-28 melanoma cell line with 10 nM of either scramble or *SLNCR* or AR targeting siRNAs, as in FIG. 18A and 18B. FIG. 18F shows that AR and *SLNCR* inhibit p21 expression independently of p53. Same as in FIG. 18C and 18D, using p53-deficient SK-MEL-28 melanoma cell line. Significance was calculated using the Student's t-test: * $p < 0.05$, ** $p < 0.005$, *** $p < 0.0005$. FIG. 18G shows knockdown of *CDKN1A* in A375 cells. Left panel shows relative *CDKN1A* expression following transfection of the indicated siRNAs, represented as the fold change compared to scramble control, normalized to GAPDH. Middle panel shows western blot of A375 cell lysates following transfection with the indicated siRNAs probed with α-p21 and α-GAPDH antibodies. Right panel shows quantification from three independent replicates, normalized to GAPDH. FIG. 18H shows cell proliferation quantified using WST-1 reagent following transfection with the indicated siRNAs. Significance was calculated using the two-way analysis of variance (ANOVA), with the Dunnett test for multiple comparison testing, **** $p < 0.0001$. RT-qPCR data are represented as the fold change compared to scramble control, normalized to GAPDH. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the Student's t-test: * $p < 0.05$, ** $p < 0.005$, *** $p < 0.0005$.

FIG. 19A – FIG. 19D show *SLNCR* and AR do not directly regulate expression of *TP53*. FIG.19A and 19B show relative expression of *TP53* from indicated cells transfected with either scramble, *SLNCR*-, or AR-targeting siRNAs. RNA was isolated 72 hours post transfection with 10 nM of the indicated siRNAs. RT-qPCR data is represented as the fold change compared to scramble control, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the Student's t-test and was determined to not be significant: no indication indicates difference was not significant, ** p-value < 0.005. FIG. 19C shows that knockdown of *SLNCR* or AR in A375 melanoma cells does not affect p53 expression. FIG. 19C shows western blots of the indicated cells transfected with the indicated siRNAs were performed as in FIG. 18C,

18D, and 18F. Santa Cruz p53 (DO-1) sc-126 was used at 1:200. Protein levels were quantified using ImageJ, and are presented as a fold change of p21 levels, normalized to GAPDH levels. Bars represent mean ±SD from 3 independent biological replicates. FIG. 19D shows that knockdown of *SLNCR* does not affect *AR* expression. Relative expression of *AR* 72 hours post-transfection of the indicated cells with 10 nM of either scramble or *SLNCR* targeting siRNAs is shown. RT-qPCR data are represented as the fold change compared to scramble control, normalized to GAPDH. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the Student's t-test and is only indicated where determined to be significant: ** $p < 0.005$.

FIG. 20A – FIG. 20D. FIG. 20A shows that *SLNCR* regulates cell cycle progression, and *SLNCR* knockdown induces G2 cell cycle arrest. Indicated cells were seeded in a 96-well plate, transfected with 10 nM of the indicated siRNAs, and incubated in a humidified chamber for 72 hours. Cells were then fixed in cold 70% ethanol for 2 hours, incubate in LifeTech PI/RNaseA solution for 30 minutes at 37 °C, and analyzed on FACs machine Fortessa X-20. Cell populations were analyzed using FlowJo software, and significance was calculated using GraphPad Prism software. Top panel: Cell populations of one representative analysis in WM858 cells. Bottom panel: Bars represent the average percent of total cells in the indicated stage of the cell cycle, and error bars represent SD from 3 independent replicates. Significance was calculated using the two-tailed Student's t-test via GraphPad Prism, n.s. = not significant, * p-value < 0.05. FIG. 20B and FIG. 20C show that *SLNCR* regulates activity of multiple transcription factors. For FIG. 20B, FWM1976 cells were seeded in 6-well dishes, transfected with either scramble or si-*SLNCR* (1) siRNAs, and 48 or 72 hours post transfections cells were fractionated using NE-PER fractionation kit. Approximately 10 µg of the nuclear fraction for input directly in Signosis' Transcription Factor Activation Array I. The ratio of relative luminescence units (RLUs) corresponding to the indicated transcription factor signals of si-*SLNCR* (1) versus scramble control. Bars represent mean ± SD from 2 independent biological replicates. FIG. 20C shows that transcription factor network enriched among genes that are significantly dysregulated upon *SLNCR* knockdown in WM1976, that are not bound by AR as determined via AR ChIP-seq. Analysis was performed by MetaCore (Thompson Reuters), against a set of genes normally expressed in human tissue. FIG. 20D shows the transcription factor activity in WM1976 nuclear lysate following transfection with either scramble or si-*SLNCR* (1) siRNA measured by Signosis' Transcription Factor Activation

Array I. The raw relative luminescence units (RLUs) are shown for all transcription factor probes included in the array.

FIG. 21A – FIG. 21B show that *SLNCR* does not regulate cell cycle in A375 cells, and AR does not regulate cell cycle progression in multiple melanoma cells. Cell cycle analysis of the indicated cells transfected with 10 nM of the indicated siRNAs was performed as done in FIG. 20A.

FIG. 22A – FIG. 22H show that AR-bound, *SLNCR*-regulated genes contain an enriched motif with high similarity to the *SLNCR*-bound transcription factor EGR1, and that co-binding of *SLNCR*-associated transcription factors EGR1 and AR is enriched on *SLNCR*-regulated genes. FIG. 22A shows that TOMTOM analysis of AR ChIP-seq peaks found within 10,000 basepairs of *SLNCR*-regulated genes (as determined via RNA-seq) identified a significant enrichment of a motif (bottom) resembling the EGR1 DNA binding motif (top) (p-value 2.24e-05). FIG. 22B shows that that EGR1 is significantly enriched in *SLNCR1* immunoprecipitate. FIG. 22B shows western blot analysis of total A375 lysate ('Input') or immunoprecipitate enriched following incubation with in vitro transcribed, biotinylated full-length *SLNCR1* ('Bound'). AR and the S6 Ribosomal Protein serve as positive controls, while GAPDH serves as a negative control. Western bot was performed as in FIG. 18C, 18D, and 18F. Cell Signaling Egr1 (44D5) was used at 1:1000, and Cell Signaling S6 Ribosomal Protein (5G10) was used at 1:1000. For REMSA results shown in FIG. 22C shows that EGR1 directly binds to *SLNCR1*. FIG. 22C, in vitro transcribed, biotinylated full length *SLNCR1* was incubated with the indicated concentration of recombinant EGR1 corresponding to amino acids 282-433 (Aviva Systems Biology, catalogue number OPCD02876). Where indicated, 10 μM of unlabeled RNA competitor corresponding to full length *SLNCR1* was added prior to addition of biotinylated *SLNCR1*. REMSAs were completed as in FIG. 1A-FIG. 1C. For FIG. 22D, TOMTOM analysis identified a significant enrichment of a motif in EGR1 ChIP-seq peaks (bottom) showing significant similarity to the consensus EGR1 DNA binding motif (top panel). FIG. 22E is a venn diagram representating the genes significantly differentially expressed upon *SLNCR* knockdown (*SLNCR* DE genes or *SLNCR* DEGs) in WM1976 cells (pink), and genes bound by either AR (blue) or EGR1 (green) within 10,000 bp of the annotated gene in A375 cells (Fisher Exact $p<0.0001$). FIG. 22F shows RNA immunoprecipitations from A375 cells using α-EGR1 antibody or a matched IgG nonspecific control. Left panel shows western blot analysis of input and either bound or flow-through (F.T.) samples following

immunoprecipitation with the indicated antibody. Right panel shows relative enrichment of *SLNCR* measured via RT-qPCR compared to input after normalization to the indicated transcript. FIG. 22G shows the Integrated Genome Viewer plot displaying AR (blue) and EGR1 (green) ChIP-seq read intensities for the indicated transcripts. AR ChIP-seq reads are from the sample ectopically expressing *SLNCR1*. Numbers on the top left indicate plot height for each track. FIG. 22H shows the Integrated Genome Viewer plot displaying EGR1 ChIP-seq read intensities for the indicated transcripts. Numbers on the left indicate plot height.

FIG. 23A – FIG. 23C show that the majority of EGR1 bound genes are also bound by AR, and that AR and EGR1 cobind EGR1 consensus DNA motifs in melanoma cells. FIG. 23A shows that the REST motif (top) is significantly enriched in AR ChIP-seq peaks both in the presence (*SLNCR1*) or absence (vector) of ectopic *SLNCR1* in A375 cells, as determined via TOMTOM analysis. The Venn diagram in FIG. 23B represents the degree of overlap between total sequences bound by AR or EGR1 (active regions) as determined via ChIP-seq in A375 cells. Specifically, the Venn diagram represents the total regions bound by either AR in A375 cells transfected with vector (light blue) or *SLNCR1*-expressing plasmid (blue), or bound by EGR1 (green). AR ChIP-seq was performed both in the presence (*SLNCR1*) or absence (vector) of ectopic *SLNCR1*. FIG. 23C is the same as in FIG. 23B, but combining all AR bound regions from both ChIP-seq experiments (vector and *SLNCR1*), and limiting the analysis to only DNA sequences found within 10,000 bp of an annotated gene. Specifically, the Venn diagram represents the genes bound by either AR (blue) or EGR1 (green) within 10,000 bp of an annotated gene in A375 cells.

FIG. 24A – FIG. 24D show that EGR1 increases expression of p21, and the EGR1 DNA binding site is required for AR and *SLNCR*-mediated repression of p21. FIG. 24A-24C show that knockdown of EGR1 decreases *CDKN1A* levels independent of p53. FIG. 24A and 24B show that relative expression of *EGR1* or *CDKN1A* from indicated cells transfected with either scramble, EGR1-targeting siRNAs. RNA was isolated 72 hours post transfection with 10 nM of the indicated siRNAs. RT-qPCR data is represented as the fold change compared to scramble control, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the Student's t-test: * p-value < 0.05, ** p-value < 0.005 and *** p-value < 0.0005. FIG. 24C shows western blots of the indicated cells transfected with the indicated siRNAs were performed as in FIG. 18C, 18D, and 18F. Specifically, the left panel shows the

representative western blot analysis of A375 (top) or SK-MEL-28 (bottom) cell lysates probed for EGR1, GAPDH, or p21 levels. Middle and right panels show the protein levels that were quantified using ImageJ, and are presented as relative expression of the indicated protein, normalized to GAPDH levels. Bars represent mean ±SD from 3 independent biological replicates. FIG. 24D shows that the mutation of the EGR1 DNA binding site negates AR- and *SLNCR*-mediated *CDKN1A* regulation. FIG. 24D shows the schematic of the promoter region of *CDKN1A* cloned upstream of a luciferase reporter. The wild-type EGR1 binding was mutated as shown below, and both the wild-type and mutant sequences of EGR/AR binding site are shown below, with mutated bases in red. Mutation of the EGR1 binding site prevents AR- and *SLNCR*-mediated regulation of p21. A375 cells were transfected with a p21-firefly (FL) reporter plasmid, a CMV-RL (renilla luciferase) control, and the indicated siRNAs. Specifically, A375 cells were transfected with the indicated siRNAs, and 24 hours later were subsequently transfected with the wildtype (top panel) or mutant (bottom panel) *CDKN1A* firefly (FL) reporter plasmid and a CMV-RL (renilla luciferase) control. Luciferase activity was measured 24 hours post-transfection. Relative FL activity was calculated as a fold-change compared to vector and scramble only control cells, after normalization to RL activity. Shown is one representative assay from at least fourindependent biological replicates. Error bars represent standard deviation from three technical replicates. Significance was calculated using the Student's t-test: * p-value < 0.05, ** p-value < 0.005, *** p-value < 0.0005, ns = not significant.

FIG. 25A – FIG. 25E show that AR and *SLNCR*-mediated regulation of p21 does not require p53 or androgens, and AR and p21 show gender-specific expression. FIG. 25A shows that EGR1 does not regulate *TP53* expression. Knockdown of EGR1 does not affect TP53 levels. Relative expression of TP53 72 hours post-transfection of either A375 (left) or SK-MEL-28 (right) cells with 10 nM of either scramble or EGR1-targeting siRNAs. RT-qPCR of the indicated cells transfected with scramble or EGR1 targeting siRNAs. RNA was isolated 72 hours post transfection with 20 nM of the indicated siRNAs. RT-qPCR data is represented as the fold change compared to scramble control, normalized to *GAPDH*. Error bars represent standard deviations calculated from 3 reactions. Significance was calculated using the Student's t-test and was determined to not be significant. FIG. 25B and 25C present results from luciferase assays, as in FIG. 24D. FIG. 25B shows that AR and *SLNCR*-mediated regulation of the *CDKN1A* does not require the presence of androgens (i.e. effects are observed even when cells are hormone-derpived:

grown in phenol-red free media containing charcoal stripped FBS). Same as in FIG. 22C, using A375 cells grown in hormone-starved conditions. Significance was calculated using the Student's t-test: * $p < 0.05$, ** $p < 0.005$, *** $p < 0.0005$, ns = not significant. FIG. 25C are one representative assay where knockdown of *SLNCR* or AR increases expression from the *CDKN1A* promoter (replicating results seen at the endogenous promoter). The discrepancy seen in these assays (i.e. either increased expression, seen here, or decreased expression, seen in FIG. 24D) likely result from altered stoichiometry of the transcription factors, lncRNA, and DNA due to variations in transfection between individual experiments. FIG. 25D showst hat female p-53 deficient melanomas express significantly higher levels of p21 than males. P21 protein expression was taken from The Cancer Genome Atlas (TCGA), from only p-53 deficient (i.e. p53 mutant) melanomas as determined via RNA-seq. Significance was calculated using Student's t-test. FIG. 25E shows gender specific expression of AR and p21. Box plot of relative p21 (left) and AR (right) expression, but for only p53-deficient melanomas, is shown. Significance was calculated using the Student's t-test: * $p < 0.05$.

FIG. 26. shows a model for AR- and *SLNCR*-mediated, EGR1-dependent but p53-independent regulation of p21. In the absence of either *SLNCR* (top panel) or AR (bottom panel), EGR1 binds to its cognate DNA binding site in the *CDKN1A* promoter and increases expression. Once *SLNCR* and AR levels exceed the required threshold, *SLNCR* recruits AR to EGR1-bound chromatin to repress gene expression.

For any figure showing a bar histogram, curve, or other data associated with a legend, the bars, curve, or other data presented from left to right for each indication correspond directly and in order to the boxes from top to bottom of the legend.

Detailed Description of the present invention

The present invention is based, at least in part, on the discovery that the N-terminal, regulatory domain of AR interacts with single-stranded, pyrimidine rich RNA in a sequence-specific manner, and that single-stranded nucleic acids designed to sterically block the interaction of AR and such RNA without significantly altering the expression of AR and/or RNA (*e.g.*, 2'-deoxy-2'-fluoro-D-arabinonuleic acid (2'-FANA)-modified single-stranded nucleic acids that bind AR or SLNCR to modulate SLNCR-mediated melanoma invasion).

I. Definitions

The articles "a" and "an" are used herein to refer to one or to more than one (*i.e.,* to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

Unless otherwise specified herein, the terms "antibody" and "antibodies" broadly encompass naturally-occurring forms of antibodies (*e.g.,* IgG, IgA, IgM, IgE) and recombinant antibodies such as single-chain antibodies, chimeric and humanized antibodies and multi-specific antibodies, as well as fragments and derivatives of all of the foregoing, which fragments and derivatives have at least an antigenic binding site. Antibody derivatives may comprise a protein or chemical moiety conjugated to an antibody.

The term "antibody" as used herein also includes an "antigen-binding portion" of an antibody (or simply "antibody portion"). The term "antigen-binding portion", as used herein, refers to one or more fragments of an antibody that retain the ability to specifically bind to an antigen. It has been shown that the antigen-binding function of an antibody can be performed by fragments of a full-length antibody. Examples of binding fragments encompassed within the term "antigen-binding portion" of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward *et al.*, (1989) *Nature* 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR). Furthermore, although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent polypeptides (known as single chain Fv (scFv); see *e.g.,* Bird *et al.* (1988) *Science* 242:423-426; and Huston *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883; and Osbourn *et al.* 1998, Nature Biotechnology 16: 778). Such single chain antibodies are also intended to be encompassed within the term "antigen-binding portion" of an antibody. Any VH and VL sequences of specific scFv can be linked to human immunoglobulin constant region cDNA or genomic sequences, in order to generate expression vectors encoding complete IgG polypeptides or other isotypes. VH and VL can also be used in the generation of Fab , Fv or other fragments of immunoglobulins using either protein chemistry or recombinant DNA

technology. Other forms of single chain antibodies, such as diabodies are also encompassed. Diabodies are bivalent, bispecific antibodies in which VH and VL domains are expressed on a single polypeptide chain, but using a linker that is too short to allow for pairing between the two domains on the same chain, thereby forcing the domains to pair with complementary domains of another chain and creating two antigen binding sites (see *e.g.,* Holliger, P., *et al.* (1993) *Proc. Natl. Acad. Sci. USA* 90:6444-6448; Poljak, R. J., *et al.* (1994) *Structure* 2:1121-1123).

Still further, an antibody or antigen-binding portion thereof may be part of larger immunoadhesion polypeptides, formed by covalent or noncovalent association of the antibody or antibody portion with one or more other proteins or peptides. Examples of such immunoadhesion polypeptides include use of the streptavidin core region to make a tetrameric scFv polypeptide (Kipriyanov, S.M., *et al.* (1995) *Human Antibodies and Hybridomas* 6:93-101) and use of a cysteine residue, a marker peptide and a C-terminal polyhistidine tag to make bivalent and biotinylated scFv polypeptides (Kipriyanov, S.M., *et al.* (1994) *Mol. Immunol.* 31:1047-1058). Antibody portions, such as Fab and $F(ab')_2$ fragments, can be prepared from whole antibodies using conventional techniques, such as papain or pepsin digestion, respectively, of whole antibodies. Moreover, antibodies, antibody portions and immunoadhesion polypeptides can be obtained using standard recombinant DNA techniques, as described herein.

Antibodies may be polyclonal or monoclonal; xenogeneic, allogeneic, or syngeneic; or modified forms thereof (*e.g.,* humanized, chimeric, etc.). Antibodies may also be fully human. The terms "monoclonal antibodies" and "monoclonal antibody composition", as used herein, refer to a population of antibody polypeptides that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of an antigen, whereas the term "polyclonal antibodies" and "polyclonal antibody composition" refer to a population of antibody polypeptides that contain multiple species of antigen binding sites capable of interacting with a particular antigen. A monoclonal antibody composition typically displays a single binding affinity for a particular antigen with which it immunoreacts.

The term "antisense" nucleic acid polypeptide comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.,* complementary to the coding strand of a double-stranded cDNA polypeptide, complementary to an mRNA

sequence or complementary to the coding strand of a gene. Accordingly, an antisense nucleic acid polypeptide can hydrogen bond to a sense nucleic acid polypeptide.

The term "body fluid" refers to fluids that are excreted or secreted from the body as well as fluids that are normally not (*e.g.,* amniotic fluid, aqueous humor, bile, blood and blood plasma, cerebrospinal fluid, cerumen and earwax, cowper's fluid or pre-ejaculatory fluid, chyle, chyme, stool, female ejaculate, interstitial fluid, intracellular fluid, lymph, menses, breast milk, mucus, pleural fluid, peritoneal fluid, pus, saliva, sebum, semen, serum, sweat, synovial fluid, tears, urine, vaginal lubrication, vitreous humor, vomit). In a preferred embodiment, body fluids are restricted to blood-related fluids, including whole blood, serum, plasma, and the like.

The terms "cancer" or "tumor" or "hyperproliferative disorder" refer to the presence of cells possessing characteristics typical of cancer-causing cells, such as uncontrolled proliferation, immortality, metastatic potential, rapid growth and proliferation rate, and certain characteristic morphological features. Cancer is generally associated with uncontrolled cell growth, invasion of such cells to adjacent tissues, and the spread of such cells to other organs of the body by vascular and lymphatic menas. Cancer invasion occurs when cancer cells intrude on and cross the normal boundaries of adjacent tissue, which can be measured by assaying cancer cell migration, enzymatic destruction of basement membranes by cancer cells, and the like. In some embodiments, a particular stage of cancer is relevant and such stages can include the time period before and/or after angiogenesis, cellular invasion, and/or metastasis. Cancer cells are often in the form of a solid tumor, but such cells may exist alone within an animal, or may be a non-tumorigenic cancer cell, such as a leukemia cell. Cancers include, but are not limited to, B cell cancer, *e.g.,* multiple myeloma, Waldenström's macroglobulinemia, the heavy chain diseases, such as, for example, alpha chain disease, gamma chain disease, and mu chain disease, benign monoclonal gammopathy, and immunocytic amyloidosis, melanomas, breast cancer, lung cancer, bronchus cancer, colorectal cancer, prostate cancer, pancreatic cancer, stomach cancer, ovarian cancer, urinary bladder cancer, brain or central nervous system cancer, peripheral nervous system cancer, esophageal cancer, cervical cancer, uterine or endometrial cancer, cancer of the oral cavity or pharynx, liver cancer, kidney cancer, testicular cancer, biliary tract cancer, small bowel or appendix cancer, salivary gland cancer, thyroid gland cancer, adrenal gland cancer, osteosarcoma, chondrosarcoma, cancer of hematological tissues, and the like. Other non-limiting examples of types of cancers

applicable to the methods encompassed by the present invention include human sarcomas and carcinomas, *e.g.,* fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, colorectal cancer, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, liver cancer, choriocarcinoma, seminoma, embryonal carcinoma, Wilms' tumor, cervical cancer, bone cancer, brain tumor, testicular cancer, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, melanoma, neuroblastoma, retinoblastoma; leukemias, *e.g.,* acute lymphocytic leukemia and acute myelocytic leukemia (myeloblastic, promyelocytic, myelomonocytic, monocytic and erythroleukemia); chronic leukemia (chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia); and polycythemia vera, lymphoma (Hodgkin's disease and non-Hodgkin's disease), multiple myeloma, Waldenstrom's macroglobulinemia, and heavy chain disease. In some embodiments, the cancer whose phenotype is determined by the method of the present invention is an epithelial cancer such as, but not limited to, bladder cancer, breast cancer, cervical cancer, colon cancer, gynecologic cancers, renal cancer, laryngeal cancer, lung cancer, oral cancer, head and neck cancer, ovarian cancer, pancreatic cancer, prostate cancer, or skin cancer. In other embodiments, the cancer is breast cancer, prostate cancer, lung cancer, or colon cancer. In still other embodiments, the epithelial cancer is non-small-cell lung cancer, nonpapillary renal cell carcinoma, cervical carcinoma, ovarian carcinoma (*e.g.,* serous ovarian carcinoma), or breast carcinoma. The epithelial cancers may be characterized in various other ways including, but not limited to, serous, endometrioid, mucinous, clear cell, brenner, or undifferentiated. In some embodiments, the present invention is used in the treatment, diagnosis, and/or prognosis melanoma and its subtypes.

The term “classifying” includes “to associate” or “to categorize” a sample with a disease state. In certain instances, “classifying” is based on statistical evidence, empirical evidence, or both. In certain embodiments, the methods and systems of classifying use of a

so-called training set of samples having known disease states. Once established, the training data set serves as a basis, model, or template against which the features of an unknown sample are compared, in order to classify the unknown disease state of the sample. In certain instances, classifying the sample is akin to diagnosing the disease state of the sample. In certain other instances, classifying the sample is akin to differentiating the disease state of the sample from another disease state.

The term "coding region" refers to regions of a nucleotide sequence comprising codons which are translated into amino acid residues, whereas the term "noncoding region" refers to regions of a nucleotide sequence that are not translated into amino acids (*e.g.,* 5' and 3' untranslated regions).

The term "complementary" refers to the broad concept of sequence complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of a second nucleic acid region which is antiparallel to the first region if the residue is thymine or uracil. Similarly, it is known that a cytosine residue of a first nucleic acid strand is capable of base pairing with a residue of a second nucleic acid strand which is antiparallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the two regions are arranged in an antiparallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an antiparallel fashion, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion. More preferably, all nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion.

The term "control" refers to any reference standard suitable to provide a comparison to the expression products in the test sample. In one embodiment, the control comprises obtaining a "control sample" from which expression product levels are detected and compared to the expression product levels from the test sample. Such a control sample may comprise any suitable sample, including but not limited to a sample from a control cancer patient (can be stored sample or previous sample measurement) with a known outcome;

normal tissue or cells isolated from a subject, such as a normal patient or the cancer patient, cultured primary cells/tissues isolated from a subject such as a normal subject or the cancer patient, adjacent normal cells/tissues obtained from the same organ or body location of the cancer patient, a tissue or cell sample isolated from a normal subject, or a primary cells/tissues obtained from a depository. In another preferred embodiment, the control may comprise a reference standard expression product level from any suitable source, including but not limited to housekeeping genes, an expression product level range from normal tissue (or other previously analyzed control sample), a previously determined expression product level range within a test sample from a group of patients, or a set of patients with a certain outcome (for example, survival for one, two, three, four years, etc.) or receiving a certain treatment. It will be understood by those of skill in the art that such control samples and reference standard expression product levels can be used in combination as controls in the methods of the present invention. In one embodiment, the control may comprise normal or non-cancerous cell/tissue sample. In another preferred embodiment, the control may comprise an expression level for a set of patients, such as a set of cancer patients, or for a set of cancer patients receiving a certain treatment, or for a set of patients with one outcome versus another outcome. In the former case, the specific expression product level of each patient can be assigned to a percentile level of expression, or expressed as either higher or lower than the mean or average of the reference standard expression level. In another preferred embodiment, the control may comprise normal cells, cells from patients treated with combination chemotherapy and cells from patients having benign cancer. In another embodiment, the control may also comprise a measured value for example, average level of expression of a particular gene in a population compared to the level of expression of a housekeeping gene in the same population. Such a population may comprise normal subjects, cancer patients who have not undergone any treatment (*i.e.,* treatment naive), cancer patients undergoing therapy, or patients having benign cancer. In another preferred embodiment, the control comprises a ratio transformation of expression product levels, including but not limited to determining a ratio of expression product levels of two genes in the test sample and comparing it to any suitable ratio of the same two genes in a reference standard; determining expression product levels of the two or more genes in the test sample and determining a difference in expression product levels in any suitable control; and determining expression product levels of the two or more genes in the test sample, normalizing their expression to expression of housekeeping genes in the test sample, and

comparing to any suitable control. In particularly preferred embodiments, the control comprises a control sample which is the same lineage and/or type as the test sample. In another embodiment, the control may comprise expression product levels grouped as percentiles within or based on a set of patient samples, such as all patients with cancer. In one embodiment a control expression product level is established wherein higher or lower levels of expression product relative to, for instance, a particular percentile, are used as the basis for predicting outcome. In another preferred embodiment, a control expression product level is established using expression product levels from cancer control patients with a known outcome, and the expression product levels from the test sample are compared to the control expression product level as the basis for predicting outcome. As demonstrated by the data below, the methods of the present invention are not limited to use of a specific cut-point in comparing the level of expression product in the test sample to the control.

As used herein, the term "costimulate" with reference to activated immune cells includes the ability of a costimulatory molecule to provide a second, non-activating receptor mediated signal (a "costimulatory signal") that induces proliferation or effector function. For example, a costimulatory signal can result in cytokine secretion, *e.g.,* in a T cell that has received a T cell-receptor-mediated signal. Immune cells that have received a cell-receptor mediated signal, *e.g.,* via an activating receptor are referred to herein as "activated immune cells."

The term "diagnosing cancer" includes the use of the methods, systems, and code of the present invention to determine the presence or absence of a cancer or subtype thereof in an individual. The term also includes methods, systems, and code for assessing the level of disease activity in an individual. Diagnosis can be performed directly by the agent providing therapeutic treatment. Alternatively, a person providing therapeutic agent can request the diagnostic assay to be performed. The diagnostician and/or the therapeutic interventionist can interpret the diagnostic assay results to determine a therapeutic strategy. Similarly, such alternative processes can apply to other assays, such as prognostic assays.

A molecule is "fixed" or "affixed" to a substrate if it is covalently or non-covalently associated with the substrate such the substrate can be rinsed with a fluid (*e.g.,* standard saline citrate, pH 7.4) without a substantial fraction of the molecule dissociating from the substrate.

The term "gene expression data" or "gene expression level" as used herein refers to information regarding the relative or absolute level of expression of a gene or set of genes in a cell or group of cells. The level of expression of a gene may be determined based on the level of RNA, such as mRNA, encoded by the gene. Alternatively, the level of expression may be determined based on the level of a polypeptide or fragment thereof encoded by the gene. Gene expression data may be acquired for an individual cell, or for a group of cells such as a tumor or biopsy sample. Gene expression data and gene expression levels can be stored on computer readable media, *e.g.,* the computer readable medium used in conjunction with a microarray or chip reading device. Such gene expression data can be manipulated to generate gene expression signatures.

The term "gene expression signature" or "signature" as used herein refers to a group of coordinately expressed genes. The genes making up this signature may be expressed in a specific cell lineage, stage of differentiation, or during a particular biological response. The genes can reflect biological aspects of the tumors in which they are expressed, such as the cell of origin of the cancer, the nature of the non-malignant cells in the biopsy, and the oncogenic mechanisms responsible for the cancer.

The term "homologous" or "homology" as used herein, refers to nucleotide sequence similarity between two regions of the same nucleic acid strand or between regions of two different nucleic acid strands. When a nucleotide residue position in both regions is occupied by the same nucleotide residue, then the regions are homologous at that position. A first region is homologous to a second region if at least one nucleotide residue position of each region is occupied by the same residue. Homology between two regions is expressed in terms of the proportion of nucleotide residue positions of the two regions that are occupied by the same nucleotide residue. By way of example, a region having the nucleotide sequence 5'-ATTGCC-3' and a region having the nucleotide sequence 5'-TATGGC-3' share 50% homology. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residue positions of each of the portions are occupied by the same nucleotide residue. More preferably, all nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.

The term "host cell" is intended to refer to a cell into which a nucleic acid of the present invention, such as a recombinant expression vector of the present invention, has

been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It should be understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

The term "humanized antibody," as used herein, is intended to include antibodies made by a non-human cell having variable and constant regions which have been altered to more closely resemble antibodies that would be made by a human cell, for example, by altering the non-human antibody amino acid sequence to incorporate amino acids found in human germline immunoglobulin sequences. Humanized antibodies may include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.,* mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*), for example in the CDRs.

The term "humanized antibody", as used herein, also includes antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

As used herein, the term "immune cell" refers to cells that play a role in the immune response. Immune cells are of hematopoietic origin, and include lymphocytes, such as B cells and T cells; natural killer cells; myeloid cells, such as monocytes, macrophages, eosinophils, mast cells, basophils, and granulocytes.

As used herein, the term "immune response" includes T cell mediated and/or B cell mediated immune responses. Exemplary immune responses include T cell responses, *e.g.,* cytokine production and cellular cytotoxicity. In addition, the term immune response includes immune responses that are indirectly effected by T cell activation, *e.g.,* antibody production (humoral responses) and activation of cytokine responsive cells, *e.g.,* macrophages.

The term "immunotherapeutic agent" can include any molecule, peptide, antibody or other agent which can stimulate a host immune system to generate an immune response to a tumor or cancer in the subject. Various immunotherapeutic agents are useful in the compositions and methods described herein. Numerous anti-cancer agents in the immunotherapeutic agent class are well-known in the art and include, without limitation, antibodies that block or inhibit the function of PD-1, PD-L1, PD-L2, CTLA4, and the like.

As used herein, the term "inhibit" includes the decrease, limitation, or blockage, of, for example a particular action, function, or interaction. For example, cancer is "inhibited" if at least one symptom of the cancer, such as hyperproliferative growth, is alleviated, terminated, slowed, or prevented. As used herein, cancer is also "inhibited" if recurrence or metastasis the cancer is reduced, slowed, delayed, or prevented.

As used herein, the term "inhibitory signal" refers to a signal transmitted via an inhibitory receptor (*e.g.,* CTLA-4 or PD-1) for a polypeptide on an immune cell. Such a signal antagonizes a signal via an activating receptor (*e.g.,* via a TCR, CD3, BCR, or Fc polypeptide) and can result in, *e.g.,* inhibition of second messenger generation; an inhibition of proliferation; an inhibition of effector function in the immune cell, *e.g.,* reduced phagocytosis, reduced antibody production, reduced cellular cytotoxicity, the failure of the immune cell to produce mediators, (such as cytokines (*e.g.,* IL-2) and/or mediators of allergic responses); or the development of anergy.

As used herein, the term "interaction," when referring to an interaction between two molecules, refers to the physical contact (*e.g.,* binding) of the molecules with one another. Generally, such an interaction results in an activity (which produces a biological effect) of one or both of said molecules. The activity may be a direct activity of one or both of the molecules. Alternatively, one or both molecules in the interaction may be prevented from binding their ligand, and thus be held inactive with respect to ligand binding activity (*e.g.,* binding its ligand and triggering or inhibiting an immune response). To inhibit such an interaction results in the disruption of the activity of one or more molecules involved in the interaction. To enhance such an interaction is to prolong or increase the likelihood of said physical contact, and prolong or increase the likelihood of said activity.

An "isolated antibody," as used herein, is intended to refer to an antibody that is substantially free of other antibodies having different antigenic specificities. Moreover, an isolated antibody may be substantially free of other cellular material and/or chemicals.

As used herein, an "isolated protein" refers to a protein that is substantially free of other proteins, cellular material, separation medium, and culture medium when isolated from cells or produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the antibody, polypeptide, peptide or fusion protein is derived, or substantially free from chemical precursors or other chemicals

when chemically synthesized. The language "substantially free of cellular material" includes preparations, in which compositions of the present invention are separated from cellular components of the cells from which they are isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of having less than about 30%, 20%, 10%, or 5% (by dry weight) of cellular material. When an antibody, polypeptide, peptide or fusion protein or fragment thereof, *e.g.,* a biologically active fragment thereof, is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.,* culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

A "kit" is any manufacture (*e.g.,* a package or container) comprising at least one reagent, *e.g.,* a probe, for specifically detecting or modulating the expression of a marker of the present invention. The kit may be promoted, distributed, or sold as a unit for performing the methods of the present invention.

The term "melanoma" generally refers to cancers derived from melanocytes. Although melanocytes are predominantly located in skin, they are also found in other parts of the body, including the eye and bowel. Although cutaneous melanoma is most common, melanoma can originate from any melanocyte in the body. Though melanoma is less than five percent of the skin cancers, it is the seventh most common malignancy in the U.S. and is responsible for most of the skin cancer related deaths. The incidence has increased dramatically in the last several decades due to altered sun exposure habits of the population. Several hereditary risk factors are also known. Other important risk factors are the number of pigment nevi, the number dysplastic nevi, and skin type. An increased risk is coupled to many nevi, both benign and dysplastic, and fair skin. Familial history of malignant melanomas is a risk factor, and approximately 8-12% of malignant melanoma cases are familial. Additional details are well-known, such as described in US Pat. Publs. 2012-0269764 and 2013-0237445.

Malignant melanomas are clinically recognized based on the ABCD(E) system, where A stands for asymmetry, B for border irregularity, C for color variation, D for diameter >5 mm, and E for evolving. Further, an excision biopsy can be performed in order to corroborate a diagnosis using microscopic evaluation. Infiltrative malignant melanoma is traditionally divided into four principal histopathological subgroups: superficial spreading melanoma (SSM), nodular malignant melanoma (NMM), lentigo maligna

melanoma (LMM), and acral lentiginous melanoma (ALM). Other rare types also exists, such as desmoplastic malignant melanoma. A substantial subset of malignant melanomas appear to arise from melanocytic nevi and features of dysplastic nevi are often found in the vicinity of infiltrative melanomas. Melanoma is thought to arise through stages of progression from normal melanocytes or nevus cells through a dysplastic nevus stage and further to an in situ stage before becoming invasive. Some of the subtypes evolve through different phases of tumor progression, which are called radial growth phase (RGP) and vertical growth phase (VGP).

Malignant melanomas are staged according to the American Joint Committee on Cancer (AJCC) TNM-classification system, where Clark level is considered in T-classification. The T stage describes the local extent of the primary tumor, *i.e.*, how far the tumor has invaded and imposed growth into surrounding tissues, whereas the N stage and M stage describe how the tumor has developed metastases, with the N stage describing spread of tumor to lymph nodes and the M stage describing growth of tumor in other distant organs. Early stages include: T0-1, N0, M0, representing localized tumors with negative lymph nodes. More advanced stages include: T2-4, N0, M0, localized tumors with more widespread growth and T1-4, N1-3, M0, tumors that have metastasized to lymph nodes and T1-4, N1-3, M1, tumors with a metastasis detected in a distant organ.

Stages I and II represent no metastatic disease and for stage I (T1a/b-2a,N0,M0) prognosis is very good. The 5-year survival for stage I disease is 90-95%, for stage II (T2b-4-b,N0,M0) the corresponding survival rate ranges from 80 to 45%. Stages III (T1a-4-b,N1a-3,M0) and IV (T(aII),N(aII),M1a-c) represent spread disease, and for these stages 5-year survival rates range from 70 to 24%, and from 19 to 7%, respectively. "Clark's level" is a measure of the layers of skin involved in a melanoma and is a melanoma prognostic factor. For example, level I involves the epidermis. Level II involves the epidermis and upper dermis. Level III involves the epidermis, upper dermis, and lower dermis. Level IV involves the epidermis, upper dermis, lower dermis, and subcutis. When the primary tumor has a thickness of >1 mm, ulceration, or Clark level IV-V, sentinel node biopsy (SNB) is typically performed. SNB is performed by identifying the first draining lymph node/s (*i.e.*, the SN) from the tumour. This is normally done by injection of radiolabelled colloid particles in the area around the tumour, followed by injection of Vital Blue dye. Rather than dissection of all regional lymph nodes, which was the earlier standard procedure, only

the sentinel nodes are generally removed and carefully examined. Following complete lymph node dissection is only performed in confirmed positive cases.

In addition to staging and diagnosis, factors like T-stage, Clark level, SNB status, Breslow's depth, ulceration, and the like can be used as endpoints and/or surrogates for analyses according to the present invention. For example, patients who are diagnosed at an advanced stage with metastases generally have a poor prognosis. For patients diagnosed with a localized disease, the thickness of the tumor measured in mm (Breslow) and ulceration can be endpoints for prognosis. Breslow's depth is determined by using an ocular micrometer at a right angle to the skin. The depth from the granular layer of the epidermis to the deepest point of invasion to which tumor cells have invaded the skin is directly measured. Clark level is important for thin lesions (<1 mm). Other prognostic factors include age, anatomic site of the primary tumor and gender. The sentinel node (SN) status can also be a prognostic factor, especially since the 5-year survival of SN-negative patients has been shown to be as high as 90%. Similarly, overall survival (OS) can be used as a standard primary endpoint. OS takes in to account time to death, irrespective of cause, *e.g.* if the death is due to cancer or not. Loss to follow-up is censored and regional recurrence, distant metastases, second primary malignant melanomas and second other primary cancers are ignored. Other surrogate endpoints for survival can be used, as described further herein, such as disease-free survival (DFS), which includes time to any event related to the same cancer, *i.e.* all cancer recurrences and deaths from the same cancer are events.

In addition to endpoints, certain diagnostic and prognostic markers can be analyzed in conjunction with the methods described herein. For example, lactate dehydrogenase (LDH) can be measured as a marker for disease progression. Patients with distant metastases and elevated LDH levels belong to stage IV M1c. Another serum biomarker of interest is S100B. High S100B levels are associated with disease progression, and a decrease in the S100B level is an indicator of treatment response. Melanoma-inhibiting activity (MIA) is yet another serum biomarker that has been evaluated regarding its prognostic value. Studies have shown that elevated MIA levels are rare in stage I and II disease, whereas in stage III or IV, elevation in MIA levels can be seen in 60-100% of cases. Additional useful biomarkers include RGS1 (associated with reduced relapse-free survival (RFS)), osteopontin (associated with both reduced RFS and disease-specific survival (DSS), and predictive of SLN metastases), HER3 (associated with reduced

survival), and NCOA3 (associated with poor RFS and DSS, and predictive of SLN metastases). In addition, HMB-45, Ki-67 (MIB1), MITF and MART-1/Melan-A or combinations of any described marker may be used for staining (Ivan & Prieto, 2010, Future Oncol. 6(7), 1163-1175; Linos *et al.*, 2011, Biomarkers Med. 5(3) 333-360). In a literature review Rothberg *et al.* report that melanoma cell adhesion molecule (MCAM)/MUC18, matrix metalloproteinase-2, Ki-67, proliferating cell nuclear antigen (PCNA) and p16/INK4A are predictive of either all-cause mortality or melanoma specific mortality (Rothberg *et al.*, 2009 J. Nat. Canc. Inst. 101(7) 452-474).

Currently, the typical primary treatment of malignant melanoma is radical surgery. Even though survival rates are high after excision of the primary tumour, melanomas tend to metastasize relatively early, and for patients with metastatic melanoma the prognosis is poor, with a 5-year survival rate of less than 10%. Radical removal of distant metastases with surgery can be an option and systemic chemotherapy can be applied, but response rates are normally low (in most cases less than 20%), and most treatment regiments fail to prolong overall survival. The first FDA-approved chemotherapeutic agent for treatment of metastatic melanoma was dacarbazine (DTIC), which can give response rates of approximately 20%, but where less than 5% may be complete responses. Temozolamid is an analog of DTIC that has the advantage of oral administration, and which have been shown to give a similar response as DTIC. Other chemotherapeutic agents, for example different nitrosureas, cisplatin, carboplatin, and vinca alkaloids, have been used, but without any increase in response rates. Since chemotherapy is an inefficient treatment method, immunotherapy agents have also been proposed. Most studied are interferon-alpha and interleukin-2. As single agents they have not been shown to give a better response than conventional treatment, but in combination with chemotherapeutic agents higher response rates have been reported. For patients with resected stage IIB or III melanoma, some studies have shown that adjuvant interferon alfa has led to longer disease free survival. For first- or second-line stage III and IV melanoma systemic treatments include: carboplatin, cisplatin, dacarbazine, interferon alfa, high-dose interleukin-2, paclitaxel, temozolomide, vinblastine or combinations thereof (NCCN Guidelines, ME-D, MS-9-13). Recently, the FDA approved Zelboraf™ (vemurafenib, also known as INN, PLX4032, RG7204 or R05185426) for unresectable or metastatic melanoma with the BRAF V600E mutation (Bollag *et al.* (2010) *Nature* 467:596-599 and Chapman *et al.* (2011) *New Eng. J. Med.* 364:2507-2516). Another recently approved drug for unresectable or metastatic melanoma

is Yervoy®(ipilimumab) an antibody which binds to cytotoxic T-lymphocyte-associated antigen 4 (CTLA-4) (Hodi *et al.* (2010) *New Eng. J. Med.* 363:711-723). Others recently reported that patients with KIT receptor activating mutations or over-expression responded to Gleevac® (imatinib mesylate) (Carvajal *et al.* (2011) *JAMA* 305:2327-2334). In addition, radiation treatment may be given as an adjuvant after removal of lymphatic metastases, but malignant melanomas are relatively radioresistant. Radiation treatment might also be used as palliative treatment. Melanoma oncologists have also noted that BRAF mutations are common in both primary and metastatic melanomas and that these mutations are reported to be present in 50-70% of all melanomas. This has led to an interest in B-raf inhibitors, such as sorafenib, as therapeutic agents.

The term "modulate" includes up-regulation and down-regulation, *e.g.,* enhancing or inhibiting a response.

The "normal" or "control" level of expression of AR or lncRNA is the level of expression of the AR or lncRNA in cells of a subject, *e.g.,* a human patient, not afflicted with an AR- and/or lncRNA-mediated disease. An "over-expression" or "significantly higher level of expression" of AR or lncRNA refers to an expression level in a test sample that is greater than the standard error of the assay employed to assess expression, and is preferably at least 1.1, 1.2, 1.3, 1.4, 1.5, 1.6. 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 10.5, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 times or more higher than the expression activity or level of the AR or lncRNA in a control sample (*e.g.,* sample from a healthy subject not having the AR- and/or lncRNA-mediated disease) and preferably, the average expression level of AR or lncRNA in several control samples. A "significantly lower level of expression" of AR or lncRNA refers to an expression level in a test sample that is at least 1.1, 1.2, 1.3, 1.4, 1.5, 1.6. 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 10.5, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 times or more lower than the expression level of the AR or lncRNA in a control sample (*e.g.,* sample from a healthy subject not having the AR- and/or lncRNA-mediated disease) and preferably, the average expression level of the AR or lncRNA in several control samples.

The term "nuclear receptor target drugs" refers to a agents that inhibit the expression and/or activity of nuclear receptors involved in regulating gene expression of gene sets. Nuclear receptors target drugs are well-known in the art and include, without limitation, luteinizing hormone-releasing hormone (LHRH) analogs, androgen receptor

inhibitors, anti-androgens, hormone blocking drugs, nuclear receptor agonists, nuclear receptor antagonists, selective receptor modulators, selective androgen receptor modulators (SARMs), selective estrogen receptor modulators (SERMs), selective progesterone receptor modulators (SPRMs), selective glucocorticoid receptor agonists (SEGRAs), and selective glucocorticoid receptor modulators (SEGRMs). Specific agents are also well-known in the art and include, without limitation, leuprolide (Lupron®, Eligard®), goserelin (Zoladex®), triptorelin (Trelstar®), histrelin (Vantas®), degarelix (Firmagon®), bicalutamide (Casode®), enzalutamide (Xtandi®), flutamide (Eulexin®), nilutamide (Nilandron®), ketoconazole (Nizoral®), abiraterone (Zytiga®), dexamethasone, megestrol acetate (Megace®), medroxyprogesterone acetate (MPA), ethisterone, norethindrone acetate, norethisterone, norethynodrel, ethynodiol diacetate, norethindrone, norgestimate, norgestrel, levonorgestrel, medroxyprogesterone acetate, desogestrel, etonogestrel, drospirenone, norelgestromin, desogestrel, etonogestrel, gestodene, dienogest, drospirenone, elcometrine, nomegestrol acetate, trimegestone, tanaproget, BMS948, mifepristone, 4-hydroxytamoxifen, CINPA1, Cyproterone acetate (Androcur®, Cyprostat®, Siterone®), chlormadinone acetate (Clordion®, Gestafortin®, Lormin®, Non-Ovlon®, Normenon®, Verton®), 17-hydroxyprogesterone (17-OHP), THC, clotrimazole, PK11195 [1-(2-chlorophenyl)-*N*-methyl-*N*-(1-methylpropyl)-3-isoquinolinecarboxamide], meclizine, androstanol, CITCO [6-(4-chlorophenyl)imidazo [2,1-*b*][1,3] thiazole-5-carbaldehyde *O*-(3,4-dichlorobenzyl) oxime], zearalenone (ZEN), T0901317, S07662, enobosarm, BMS-564,929, LGD-4033, AC-262,356, JNJ-28330835, LGD-2226, LGD-3303, S-40503, S-23, clomifene, femarelle, ormeloxifene, raloxifene, tamoxifen, toremifene, lasofoxifene, ospemifene, afimoxifene, arzoxifene, bazedoxifene, gulvestrant (Faslodex®, ICI-182780), CDB-4124, asoprisnil, proellex, mapracorat (BOL-303242-X, ZK 245186), fosdagrocorat (PF-04171327), ZK 216348, and 55D1E1. Additional exemplary agents include antibodies, small molecules, peptides, peptidomimetics, natural ligands, and derivatives of natural ligands, that can either bind and/or inactivate or inhibit immune checkpoint proteins, or fragments thereof; as well as RNA interference, antisense, nucleic acid aptamers, etc. that can downregulate the expression and/or activity of nuclear receptor targets, or fragments thereof.

The term “pre-malignant lesions” as described herein refers to a lesion that, while not cancerous, has potential for becoming cancerous. It also includes the term “pre-malignant disorders” or “potentially malignant disorders.” In particular this refers to a

benign, morphologically and/or histologically altered tissue that has a greater than normal risk of malignant transformation, and a disease or a patient's habit that does not necessarily alter the clinical appearance of local tissue but is associated with a greater than normal risk of precancerous lesion or cancer development in that tissue (leukoplakia, erythroplakia, erytroleukoplakia lichen planus (lichenoid reaction) and any lesion or an area which histological examination showed atypia of cells or dysplasia.

The term "probe" refers to any molecule which is capable of selectively binding to a specifically intended target molecule, for example, a nucleotide transcript or protein encoded by or corresponding to a marker. Probes can be either synthesized by one skilled in the art, or derived from appropriate biological preparations. For purposes of detection of the target molecule, probes may be specifically designed to be labeled, as described herein. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

The term "prognosis" includes a prediction of the probable course and outcome of cancer or the likelihood of recovery from the disease. In some embodiments, the use of statistical algorithms provides a prognosis cancer in an individual. For example, the prognosis can be surgery, development of a clinical subtype of melanoma, development of one or more clinical factors, development of intestinal cancer, or recovery from the disease. In some embodiments, the term "good prognosis" indicates that the expected or likely outcome after treatment of melanoma is good. The term "poor prognosis" indicates that the expected or likely outcome after treatment of melanoma is not good.

The term "resistance" refers to an acquired or natural resistance of a cancer sample or a mammal to a cancer therapy (*i.e.*, being nonresponsive to or having reduced or limited response to the therapeutic treatment), such as having a reduced response to a therapeutic treatment by 25% or more, for example, 30%, 40%, 50%, 60%, 70%, 80%, or more, to 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 15-fold, 20-fold or more. The reduction in response can be measured by comparing with the same cancer sample or mammal before the resistance is acquired, or by comparing with a different cancer sample or a mammal who is known to have no resistance to the therapeutic treatment. A typical acquired resistance to chemotherapy is called "multidrug resistance." The multidrug resistance can be mediated by P-glycoprotein or can be mediated by other mechanisms, or it can occur when a mammal is infected with a multi-drug-resistant microorganism or a combination of microorganisms. The determination of resistance to a therapeutic treatment is routine in the art and within the

skill of an ordinarily skilled clinician, for example, can be measured by cell proliferative assays and cell death assays as described herein as "sensitizing." In some embodiments, the term "reverses resistance" means that the use of a second agent in combination with a primary cancer therapy (*e.g.*, chemotherapeutic or radiation therapy) is able to produce a significant decrease in tumor volume at a level of statistical significance (*e.g.*, $p<0.05$) when compared to tumor volume of untreated tumor in the circumstance where the primary cancer therapy (*e.g.*, chemotherapeutic or radiation therapy) alone is unable to produce a statistically significant decrease in tumor volume compared to tumor volume of untreated tumor. This generally applies to tumor volume measurements made at a time when the untreated tumor is growing log rhythmically.

The term "sensitize" means to alter cancer cells or tumor cells in a way that allows for more effective treatment of the associated cancer with a cancer therapy (*e.g.*, chemotherapeutic or radiation therapy. In some embodiments, normal cells are not affected to an extent that causes the normal cells to be unduly injured by the cancer therapy (*e.g.*, chemotherapy or radiation therapy). An increased sensitivity or a reduced sensitivity to a therapeutic treatment is measured according to a known method in the art for the particular treatment and methods described herein below, including, but not limited to, cell proliferative assays (Tanigawa N, Kern D H, Kikasa Y, Morton D L, Cancer Res 1982; 42: 2159-2164), cell death assays (Weisenthal L M, Shoemaker R H, Marsden J A, Dill P L, Baker J A, Moran E M, Cancer Res 1984; 94: 161-173; Weisenthal L M, Lippman M E, Cancer Treat Rep 1985; 69: 615-632; Weisenthal L M, In: Kaspers G J L, Pieters R, Twentyman P R, Weisenthal L M, Veerman A J P, eds. Drug Resistance in Leukemia and Lymphoma. Langhorne, P A: Harwood Academic Publishers, 1993: 415-432; Weisenthal L M, Contrib Gynecol Obstet 1994; 19: 82-90). The sensitivity or resistance may also be measured in animal by measuring the tumor size reduction over a period of time, for example, 6 month for human and 4-6 weeks for mouse. A composition or a method sensitizes response to a therapeutic treatment if the increase in treatment sensitivity or the reduction in resistance is 25% or more, for example, 30%, 40%, 50%, 60%, 70%, 80%, or more, to 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 15-fold, 20-fold or more, compared to treatment sensitivity or resistance in the absence of such composition or method. The determination of sensitivity or resistance to a therapeutic treatment is routine in the art and within the skill of an ordinarily skilled clinician. It is to be understood that any method described herein for enhancing the efficacy of a cancer therapy can be equally applied to

methods for sensitizing hyperproliferative or otherwise cancerous cells (*e.g.*, resistant cells) to the cancer therapy.

The term "SLNCR," unless otherwise specified, refers to the known SLNCR (SLNCR1) lncRNA, as well as its isoforms, such as SLNCR2 (SLNCR4A) and SLNCR3 (SLNCR4B), and biologically active fragments thereof. SLNCR1, also known as LINC00673 in the art, is a 2,257 nucleotide sequence associated with Ref Seq Gene ID NR_036488.1 and Entrez Gene ID 100499467. It is located immediately downstream of another lncRNA known as LINC00511 on human chromosome 17. SLNCR2 (SLNCR4A) and SLNCR3 (SLNCR4B) are isoforms described herein. SLNCR and its isoforms act as a scaffold to bring together one or more transcription factors and associated co-activators and/or co-repressors for translocation to the nucleus and activation and/or repression of gene expression. In cancer cells, such as melanoma cells, SLNCR and its isoforms mediate one or more of the following functions: 1) expression or activity of MMP9; 2) downregulation of naturally-occurring SLNCR isoforms; 3) modulation of the expression of one or more genes listed in Figures 7, 14, 16, 17,19, and 31; 4) the expression of PLA2G4C, CT45A6, EGR2, RP11-820L6.1, EGR1, ATF3, VCX3A, SPCS2, FABP5, MAGEA2B, RPL41P1, RPS17, HNRNPA1P10, TXNIP, RPL21P75, EIF3CL, RPL7, CT45A3, GTF2IP1, CDK7, HIST1H1C, CT45A1, BTG2, RPS27, RP11-3P17.3, FDCSP, CITED4, IL34, and PD-L1; 5) cellular proliferation; 6) cell death; 7) cellular migration; 8) genomic replication; 9) angiogenesis induction; 10) cellular invasion; 11) cancer metastasis; 12) binding to one or more protein transcription factors (TF) selected from the group consisting of SRC-1/NCOA-1 (*e.g.*, REFSEQ: NP_671766.1, NP_671756.1, and NP_003734.3); PXR/NR1I2 (*e.g.*, REFSEQ: NP_003880.3, NP_071285.1, and NP_148934.1); PAX5 (*e.g.*, REFSEQ: NP_001267476.1, NP_001267477.1, NP_001267480.1, NP_001267482.1, NP_001267483.1, NP_001267484.1, NP_001267485.1, NP_001267479.1, NP_001267478.1, NP_057953.1, and NP_001267481.1); EGR-1 (*e.g.*, REFSEQ: NP_001955.1); AR (*e.g.*, REFSEQ: NP_000035); E2F-1 (*e.g.*, REFSEQ: NP_005216.1); CAR/NR1I3 (*e.g.*, REFSEQ: NP_001070950.1, NP_001070949.1, NP_001070949.1, NP_001070947.1, NP_001070945.1, NP_001070946.1, NP_001070944.1, NP_001070942.1, NP_001070941.1, NP_001070940.1, and NP_001070939.1); PBX1 (*e.g.*, REFSEQ: NP_001191892.1, NP_001191890.1, and NP_002576.1); ATF2 (*e.g.*, REFSEQ: NP_001243021.1, NP_001243019.1, NP_001871.2, NP_001243023.1, NP_001243022.1,

and NP_001243020.1); C/EBP (*e.g.*, REFSEQ: NP_001272758, NP_001272807, NP_001239225, NP_005186, NP_005751, and NP_001796); BRN-3/POU4F1 (*e.g.*, REFSEQ: NP_006228.3); HNF4 (*e.g.*, REFSEQ: NP_000448 and NP_004124); NF-kB (*e.g.*, REFSEQ: NP_001158884, NP_001138610, NP_001070962, NP_006500, and NP_001278675); AP2 (*e.g.*, REFSEQ: NP_001027451, NP_003212.2, NP_001025177.1, NP_001273.1, NP_003213.1, NP_758438.2, and NP_848643.2); OCT4/POU5F1 (*e.g.*, REFSEQ: NP_001272916.1, NP_001272915.1, NP_001167002.1, NP_976034.4, NP_002692.2), SP1(REFSEQ: NP_001238754.1, NP_003100.1, and NP_612482.2); STAT5 (*e.g.*, REFSEQ: NP_001275649.1, NP_001275648.1, NP_001275647.1, NP_003143.2, and NP_036580.2); p53 (*e.g.*, REFSEQ: NP_001119584.1, NP_000537.3, NP_001263626.1, NP_001263690.1, NP_001263689.1, NP_001119590.1, NP_001119587.1, NP_001119586.1, NP_001119585.1, NP_001263628.1, NP_001263627.1, NP_001263625.1, NP_001263624.1, NP_001119589.1, and NP_001119588.1); TFIID (*e.g.*, REFSEQ: NP_001165556.1, NP_001273003.1, NP_003175.1, NP_114129.1, NP_003176.1, NP_001280654.1, NP_008882.1, NP_001177344.1, NP_005633.1, NP_612639.1, NP_001015892.1, NP_057059.1, NP_006275.1, NP_001257417.1, NP_001128690.1, NP_005636.1, and NP_003478.1); SLIRP (*e.g.*, REFSEQ: NP_112487.1, NP_001254792.1, NP_001254793.1); STAT3 (*e.g.*, REFSEQ: NP_003141.2, NP_644805.1, NP_998827.1); REST (*e.g.*, REFSEQ: NP_005603.3, NP_001180437.1, including isoforms of REST, such as REST4 (*e.g.*, REFSEQ: AEJ31941.1 and UniProt: L0B3Z2, A0A087X1C2, L0B1S6, and A0A087X1C2)); and DAX1 (*e.g.*, REFSEQ: NP_000466.2), optionally wherein the SLNCR-TF complex can translocate to the nucleus; 13) regulation of immune response and/or immune evasion; and 14) modulation of one or more genes listed in Tables S5 and S6 affected by SLNCR overexpression. It has been determined herein that certain SLNCR structural features common or different among the SLNCR isoforms are related to SLNCR function. For example, a highly conserved approximately 301 nucleotide sequence common to the SLNCR 1-3 isoforms (referred to as "SLNCR cons" herein) is sufficient for cancer cell invasion. Similarly, a portion or all of an approximately 111 nucleotide sequence common to the SLNCR 1-3 isoforms (referred to as "SLNCR delta cons" herein) is required for cancer cell invasion. The representative SLNCR sequences, as well as annotations of structural domains and biologically active fragments associated with SLNCR function are shown in WO 2017/007941.

The term "synergistic effect" refers to the combined effect of two or more anticancer agents or chemotherapy drugs can be greater than the sum of the separate effects of the anticancer agents or chemotherapy drugs alone.

The term "subject" refers to any healthy animal, mammal or human, or any animal, mammal or human afflicted with a condition of interest (*e.g.*, cancer). The term "subject" is interchangeable with "patient." In some embodiments, a subject does not have any cancer other than melanoma. In other embodiments, the subject has melanoma but does not have one or more other cancers of interest. For example, in some embodiments, a subject does not have renal cell carcinoma, head or neck cancer, and/or lung cancer.

The language "substantially free of chemical precursors or other chemicals" includes preparations of antibody, polypeptide, peptide or fusion protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of antibody, polypeptide, peptide or fusion protein having less than about 30% (by dry weight) of chemical precursors or non-antibody, polypeptide, peptide or fusion protein chemicals, more preferably less than about 20% chemical precursors or non-antibody, polypeptide, peptide or fusion protein chemicals, still more preferably less than about 10% chemical precursors or non-antibody, polypeptide, peptide or fusion protein chemicals, and most preferably less than about 5% chemical precursors or non- antibody, polypeptide, peptide or fusion protein chemicals.

The term "substantially pure cell population" refers to a population of cells having a specified cell marker characteristic and differentiation potential that is at least about 50%, preferably at least about 75-80%, more preferably at least about 85-90%, and most preferably at least about 95% of the cells making up the total cell population. Thus, a "substantially pure cell population" refers to a population of cells that contain fewer than about 50%, preferably fewer than about 20-25%, more preferably fewer than about 10-15%, and most preferably fewer than about 5% of cells that do not display a specified marker characteristic and differentiation potential under designated assay conditions.

As used herein, the term "survival" includes all of the following: survival until mortality, also known as overall survival (wherein said mortality may be either irrespective of cause or tumor related); "recurrence-free survival" (wherein the term recurrence shall include both localized and distant recurrence); metastasis free survival; disease free survival (wherein the term disease shall include cancer and diseases associated therewith). The

length of said survival may be calculated by reference to a defined start point (*e.g.*, time of diagnosis or start of treatment) and end point (*e.g.*, death, recurrence or metastasis). In addition, criteria for efficacy of treatment can be expanded to include response to chemotherapy, probability of survival, probability of metastasis within a given time period, and probability of tumor recurrence.

A "transcribed polynucleotide" or "nucleotide transcript" is a polynucleotide (*e.g.*, an mRNA, hnRNA, cDNA, mature miRNA, pre-miRNA, pri-miRNA, miRNA*, piwiRNA, anti-miRNA, or a miRNA binding site, or a variant thereof or an analog of such RNA or cDNA) which is complementary to or homologous with all or a portion of a mature mRNA made by transcription of a marker of the present invention and normal post-transcriptional processing (*e.g.*, splicing), if any, of the RNA transcript, and reverse transcription of the RNA transcript. In some embodiments, transcribed polynucleotides are "long non-coding RNAs" or "lcRNAs" that are defined as transcribed polynucleotides that do not naturally encode a translated protein. lcRNAs are generally sequences longer than about 100 nucleotides and can be as long as up to tens of kilobases, although the length definition is a matter of convenience for distinguishing traditionally small nucleic acids like microRNAs, siRNAs, and piwi-associated RNAs. lcRNAs may be located separate from protein coding genes (long intergenic ncRNAs or lincRNAs), or reside near or within protein coding genes (Guttman *et al.* (2009) *Nature* 458:223-227; Katayama *et al.* (2005) *Science* 309:1564-1566; Kim *et al.* (2010) *Nature* 465:182-187; De Santa *et al.* (2010) *PLoS Biol.* 8:e1000384).

As used herein, the term "vector" refers to a nucleic acid capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments may be ligated. Another type of vector is a viral vector, wherein additional DNA segments may be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors" or simply "expression vectors." In general, expression vectors of utility in recombinant DNA techniques are often

in the form of plasmids. In the present specification, "plasmid" and "vector" may be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

As used herein, the term "unresponsiveness" includes refractivity of immune cells to stimulation, *e.g.*, stimulation via an activating receptor or a cytokine. Unresponsiveness can occur, *e.g.*, because of exposure to immunosuppressants or exposure to high doses of antigen. As used herein, the term "anergy" or "tolerance" includes refractivity to activating receptor-mediated stimulation. Such refractivity is generally antigen-specific and persists after exposure to the tolerizing antigen has ceased. For example, anergy in T cells (as opposed to unresponsiveness) is characterized by lack of cytokine production, *e.g.*, IL-2. T cell anergy occurs when T cells are exposed to antigen and receive a first signal (a T cell receptor or CD-3 mediated signal) in the absence of a second signal (a costimulatory signal). Under these conditions, reexposure of the cells to the same antigen (even if reexposure occurs in the presence of a costimulatory polypeptide) results in failure to produce cytokines and, thus, failure to proliferate. Anergic T cells can, however, proliferate if cultured with cytokines (*e.g.*, IL-2). For example, T cell anergy can also be observed by the lack of IL-2 production by T lymphocytes as measured by ELISA or by a proliferation assay using an indicator cell line. Alternatively, a reporter gene construct can be used. For example, anergic T cells fail to initiate IL-2 gene transcription induced by a heterologous promoter under the control of the 5' IL-2 gene enhancer or by a multimer of the AP1 sequence that can be found within the enhancer (Kang *et al.* (1992) *Science* 257:1134).

As used herein, the term "high level of secondary structure" refers to a strong hairpin structure which is predicted to form within a given single-stranded nucleic acid sequence, as predicted by RNAStructure (Reuter *et al.* (2010) BMC Bioinformatics 11:129) or similar RNA secondary structure prediction software programs. In some embodiments, the single-stranded nucleic acid sequence has less than or equal to 30%, 29%, 28%, 27%, 26%, 25%, 24%, 23%, 22%, 21%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or less, or any range in between inclusive (*e.g.*, 5-15%), of the nucleotides base pair with each other. In other embodiments, the single-stranded nucleic acid sequence has a sequence within which the nucleotides form fewer than or equal to 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13,

12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 base pairs, or any range in between inclusive (*e.g.*, 5-15 base pairs), with each other.

"AR- and/or lncRNA-mediated disease" refers to disease or condition associated with an aberrant expression or activity of AR and/or an lncRNA. The AR- and/or lncRNA-mediated diseases include, but are not limited to, cancer (e.g., melanoma, lung adenocarcinoma, lung squamous cell carcinoma, cervical cancer, ovarian cancer, uterine cancer, pancreatic cancer, colorectal cancer, lower grade glioma, glioblastoma multiforme, breast cancer, endometrial cancer, prostate cancer, testicular cancer, thyroid cancer, osteosarcoma, esophageal cancer, liver cancer or bladder cancer), inflammatory disease (e.g., acne vulgaris, asthma, or rheumatoid arthritis), metabolic diseases, spontaneous abortion, alopecia, Alzheimer disease, androgen-insensitivity syndrome, heart disease (e.g., artiosclerosis, coronary artery disease, or cardiomyopathy), azoospermia, cholelithiasis, cognition disorders, cryptorchidism, depressive disorder, diabetes mellitus, diabetic retinopathy, sex development disorders, bone fractures, hyperglycemia, hypertension, hypospadias, hypertrophy, hyperandrogenism, infertility, klinefelter syndrome, liver cirrhosis, liver disease, lupus, migraine disorder, Menkes Kinky Hair Syndrome, muscular atrophy, nerve degeneration, obesity, oligospermia, osteoarthritis, osteoporosis, Paget Disease, Polycystic Ovary Syndrome, Primary Ovarian Insuffiency, Schizophrenia, spinal fractures, thrombocytosis, thyroid diseases, Tourette syndrome, Turner syndrome, and autoimmune disease (e.g., lupus, type I diabetes, or multiple sclerosis).

There is a known and definite correspondence between the amino acid sequence of a particular protein and the nucleotide sequences that can code for the protein, as defined by the genetic code (shown below). Likewise, there is a known and definite correspondence between the nucleotide sequence of a particular nucleic acid and the amino acid sequence encoded by that nucleic acid, as defined by the genetic code.

GENETIC CODE	
Alanine (Ala, A)	GCA, GCC, GCG, GCT
Arginine (Arg, R)	AGA, ACG, CGA, CGC, CGG, CGT
Asparagine (Asn, N)	AAC, AAT
Aspartic acid (Asp, D)	GAC, GAT
Cysteine (Cys, C)	TGC, TGT
Glutamic acid (Glu, E)	GAA, GAG

Glutamine (Gln, Q)	CAA, CAG
Glycine (Gly, G)	GGA, GGC, GGG, GGT
Histidine (His, H)	CAC, CAT
Isoleucine (Ile, I)	ATA, ATC, ATT
Leucine (Leu, L)	CTA, CTC, CTG, CTT, TTA, TTG
Lysine (Lys, K)	AAA, AAG
Methionine (Met, M)	ATG
Phenylalanine (Phe, F)	TTC, TTT
Proline (Pro, P)	CCA, CCC, CCG, CCT
Serine (Ser, S)	AGC, AGT, TCA, TCC, TCG, TCT
Threonine (Thr, T)	ACA, ACC, ACG, ACT
Tryptophan (Trp, W)	TGG
Tyrosine (Tyr, Y)	TAC, TAT
Valine (Val, V)	GTA, GTC, GTG, GTT
Termination signal (end)	TAA, TAG, TGA

An important and well-known feature of the genetic code is its redundancy, whereby, for most of the amino acids used to make proteins, more than one coding nucleotide triplet may be employed (illustrated above). Therefore, a number of different nucleotide sequences may code for a given amino acid sequence. Such nucleotide sequences are considered functionally equivalent since they result in the production of the same amino acid sequence in all organisms (although certain organisms may translate some sequences more efficiently than they do others). Moreover, occasionally, a methylated variant of a purine or pyrimidine may be found in a given nucleotide sequence. Such methylations do not affect the coding relationship between the trinucleotide codon and the corresponding amino acid.

In view of the foregoing, the nucleotide sequence of a DNA or RNA coding for a fusion protein or polypeptide of the present invention (or any portion thereof) can be used to derive the fusion protein or polypeptide amino acid sequence, using the genetic code to translate the DNA or RNA into an amino acid sequence. Likewise, for a fusion protein or polypeptide amino acid sequence, corresponding nucleotide sequences that can encode the fusion protein or polypeptide can be deduced from the genetic code (which, because of its redundancy, will produce multiple nucleic acid sequences for any given amino acid sequence). Thus, description and/or disclosure herein of a nucleotide sequence which

encodes a fusion protein or polypeptide should be considered to also include description and/or disclosure of the amino acid sequence encoded by the nucleotide sequence. Similarly, description and/or disclosure of a fusion protein or polypeptide amino acid sequence herein should be considered to also include description and/or disclosure of all possible nucleotide sequences that can encode the amino acid sequence.

Finally, exemplary single-stranded nucleic acid sequences as well as the nucleic acid and protein sequences of the N-terminal region of AR encompassed within the scope of compositions-of-matter and methods of the present invention are shown below.

Table 1: single-stranded oligos tested for androgen receptor binding

WT-41: CUGGAGGUAUUUUUCCCUCUCCACCCUGGUCUUCUCCUGUA (SEQ ID NO: 1)

WT-28: UUCCCUCUCCACCCUGGUCUUCUCCUGU (SEQ ID NO: 2)

WT-20: UAUUUUUCCCUCUCCACCCU (SEQ ID NO: 3)

MUT L: AUCGCUCUCAACCCUGGUCUUCUCCUGU (SEQ ID NO: 4)

MUT R: UUCCCUCUCCACCCUGGUAGUCUCAGGU (SEQ ID NO: 5)

MUT FL: AUCGCUCUCAACCCUGGUAGUCUCAGGU (SEQ ID NO: 6)

MUT PT: UCCUUUCCUCACCCUGGUCUUCUUCCGU (SEQ ID NO: 7)

MUT I: UUCCCUCUCCAGCAUGGUCUUCUCCUGU (SEQ ID NO: 8)

WT-17: UAUUUUUCCCUCUCCAC (SEQ ID NO: 9)

MUT-20: UAUUUUUCCCUCUCCACCCU (SEQ ID NO: 10)

Stem-loop: UGGAGGUAUUUUUCCCUCUCCAC (SEQ ID NO: 11)

REP-UC: UCUCUCUCUCUCUCUCUCUC (SEQ ID NO: 12)

REP-UUUC: UUCUUUCUUUCUUUCUUUCU (SEQ ID NO: 13)

REP-CCCU: CCCUCCCUCCCUCCCUCCCU (SEQ ID NO: 14)

UCUCCA: CCCUCUCCAUCUCCACUC (SEQ ID NO: 15)

UCUCCU: CCCUCUCCUUCUCCUCUC (SEQ ID NO: 16)

WT-11: UUCCCUCUCCA (SEQ ID NO: 17)

WT-10: CUUCUCCUGU (SEQ ID NO: 18)

HOTAIR: UUCCAGCCUCCAGGCCCUGCCUUCUGCCUGC (SEQ ID NO: 19)

SRA1: UCCCCGCAUCAGAGACUUCUCCUGG (SEQ ID NO: 20)

PCGEM1: UUACAAGACACAGGCCUACUCCUAG (SEQ ID NO: 21)

HOXA11-AS1: CCUUUUGUUUUUCCCUCUCCAGG (SEQ ID NO: 22)

Table 2: FANA-modified oligos that block the interaction of AR and SLNCR1

MIMIC 1: UUCCCUCTCCACCCUGGTCTUCUCCUGU (SEQ ID NO: 23)

MIMIC 2: CCUCUCCACCCTGGUCUUCUC (SEQ ID NO: 24)

ANTISENSE 1: ACAGGAGAAGACCAGGGUGGAGAGGGAA (SEQ ID NO: 25)

ANTISENSE 2: GGAGAAGACCAGGGUGGAGAG (SEQ ID NO: 26)

Table 3:

N-terminal region of AR Amino Acid sequence (SEQ ID NO: 27)

MEVQLGLGRVYPRPPSKTYRGAFQNLFQSVREVIQNPGPRHPEAASAAPPGASLLL
LQQQQQQQQQQQQQQQQQQQQETSPRQQQQQQGEDGSPQAHRRGPTGYLVLD
EEQQPSQPQSALECHPERGCVPEPGAAVAASKGLPQQLPAPPDEDDSAAPSTLSLLG
PTFPGLSSCSADLKDILSEASTMQLLQQQQQEAVSEGSSSGRAREASGAPTSSKDNY
LGGTSTISDNAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLGVPPAVR
PTPCAPLAECKGSLLDDSAGKSTEDTAEYSPFKGGYTKGLEGESLGCSGSAAAGSS
GTLELPSTLSLYKSGALDEAAAYQSRDYYNFPLALAGPPPPPPPPHPHARIKLENPL
DYGSAWAAAAAQCRYGDLASLHGAGAAGPGSGSPSAAASSSWHTLFTAEEGQLY
GPCGGGGGGGGGGGGGGGGGGGGGGGGEAGAVAPYGYTRPPQGLAGQESDFTA
PDVWYPGGMVSRVPYPSPTCVKSEMGPWMDSYSGPYGDMRLETARDHVLPIDYY
FPPQ

N-terminal region of AR cDNA sequence (SEQ ID NO: 28)

ATGGAAGTGCAGTTAGGGCTGGGAAGGGTCTACCCTCGGCCGCCGTCCAAGAC
CTACCGAGGAGCTTTCCAGAATCTGTTCCAGAGCGTGCGCGAAGTGATCCAGA
ACCCGGGCCCCAGGCACCCAGAGGCCGCGAGCGCAGCACCTCCCGGCGCCAGT
TTGCTGCTGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
GCAGCAGCAGCAGCAGCAGCAGCAAGAGACTAGCCCCAGGCAGCAGCAG
CAGCAGCAGGGTGAGGATGGTTCTCCCCAAGCCCATCGTAGAGGCCCCACAGG
CTACCTGGTCCTGGATGAGGAACAGCAACCTTCACAGCCGCAGTCGGCCCTGG
AGTGCCACCCCGAGAGAGGTTGCGTCCCAGAGCCTGGAGCCGCCGTGGCCGCC
AGCAAGGGGCTGCCGCAGCAGCTGCCAGCACCTCCGGACGAGGATGACTCAGC
TGCCCCATCCACGTTGTCCCTGCTGGGCCCCACTTTCCCCGGCTTAAGCAGCTG
CTCCGCTGACCTTAAAGACATCCTGAGCGAGGCCAGCACCATGCAACTCCTTCA

GCAACAGCAGCAGGAAGCAGTATCCGAAGGCAGCAGCAGCGGGAGAGCGAGG
GAGGCCTCGGGGGCTCCCACTTCCTCCAAGGACAATTACTTAGGGGGCACTTCG
ACCATTTCTGACAACGCCAAGGAGTTGTGTAAGGCAGTGTCGGTGTCCATGGGC
CTGGGTGTGGAGGCGTTGGAGCATCTGAGTCCAGGGGAACAGCTTCGGGGGGA
TTGCATGTACGCCCCACTTTTGGGAGTTCCACCCGCTGTGCGTCCCACTCCTTGT
GCCCCATTGGCCGAATGCAAAGGTTCTCTGCTAGACGACAGCGCAGGCAAGAG
CACTGAAGATACTGCTGAGTATTCCCCTTTCAAGGGAGGTTACACCAAAGGGCT
AGAAGGCGAGAGCCTAGGCTGCTCTGGCAGCGCTGCAGCAGGGAGCTCCGGGA
CACTTGAACTGCCGTCTACCCTGTCTCTCTACAAGTCCGGAGCACTGGACGAGG
CAGCTGCGTACCAGAGTCGCGACTACTACAACTTTCCACTGGCTCTGGCCGGAC
CGCCGCCCCCTCCGCCGCCTCCCCATCCCCACGCTCGCATCAAGCTGGAGAACC
CGCTGGACTACGGCAGCGCCTGGGCGGCTGCGGCGGCGCAGTGCCGCTATGGG
GACCTGGCGAGCCTGCATGGCGCGGGTGCAGCGGGACCCGGTTCTGGGTCACC
CTCAGCCGCCGCTTCCTCATCCTGGCACACTCTCTTCACAGCCGAAGAAGGCCA
GTTGTATGGACCGTGTGGTGGTGGTGGGGGTGGTGGCGGCGGCGGCGGCGGCG
GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGAGGCGGGAGCTGTAGCCCC
CTACGGCTACACTCGGCCCCCTCAGGGGCTGGCGGGCCAGGAAAGCGACTTCA
CCGCACCTGATGTGTGGTACCCTGGCGGCATGGTGAGCAGAGTGCCCTATCCCA
GTCCCACTTGTGTCAAAAGCGAAATGGGCCCCTGGATGGATAGCTACTCCGGA
CCTTACGGGGACATGCGTTTGGAGACTGCCAGGGACCATGTTTTGCCCATTGAC
TATTACTTTCCACCCCAGAA

II. Nucleic Acids that block AR-lncRNA interaction, Related Agents, and Compositions

Novel agents and compositions of the present invention are provided herein. Such agents and compositions can bind to AR or lncRNA, and block the interaction between AR and lncRNA. In some embodiments, such agents and compositions do not significantly reduce the expression level of AR or lncRNA. Such agents and compositions can also be used for the prevention and treatment of cancers, such as melanoma, as well as conditions in which AR or lncRNA is associated or aberrantly expressed (*e.g.*, inflammatory disease and autoimmune disease). Exemplary agents include single-stranded nucleic acids that either (i) reverse complement to lncRNA's AR binding seqeunce, which bind to lncRNA to generate double stranded RNA incapable of AR binding, or (ii) mimics of the lncRNA AR binding sequence, which bind directly to AR to preclude lncRNA binding. In some

embodiments, the single-stranded nucleic acid is a RNA molecule. In some other embodiments, the single-stranded nucleic acid is a RNA/DNA chimera.

a. Single-Stranded Nucleic Acids

In some embodiments, the single-stranded nucleic acid binds to AR to preclude lncRNA binding. The single-stranded nucleic acid may localize in both cytoplasm and nucleus, or at least partially to the nucleus. The single-stranded nucleic acid can be at least 11 nucleotides in length, and are less than about 1000, 900, 800, 700, 600, 500, 400, 300, 200, 100, 50, 40, 30, 25, 24, 23, 22, 21,20, 19, 18, 17, 16, 15, 14, 13, or 12 nucleotides in length. In a preferred embodiment, the single-stranded nucleic acid is 17 nucleotides in length. The single-stranded nucleic acid may be longer than 17 nucleotides, but may not comprise a high level of secondary structure. The single-stranded nucleic acid comprises at least one UCUCCU or UCUCCA motif, *e.g.*, the single-stranded nucleic acid may contain one, two, three, or more such motifs. If two or more such motifs are present in the single-stranded nucleic acids, they may not be consecutive. An internal sequence with optimal length between any two of such motifs may be required. In certain embodiments, the internal seqeunce is 9 nucleotides in length. In some embodiments, the single-stranded nucleic acid is at least 20 nucleotides in length, and contain at least 65%, preferably >75% (e.g, >80%, >85%, >90%, or >95%), pyrimidine (U/T and C) content within the about 17-20 nucleotide region containing the UCUCCU or UCUCCA motif.

In some other embodiments, the single-stranded nucleic acid binds to lncRNA to generate double-stranded RNA incapable of AR-binding. Such single-stranded nucleic acid may contain at least one AGGAGA or UGGAGA motif, for example, it may contain one, two, three or more of such motifs. If the lncRNA contains consecutive UCUCCU or UCUCCA motifs, the single-stranded nucleic acid may bind to both motifs simultaneously, with the appropriate internal sequence to facilitate specific and high affinity interaction.

In some embodiments, lncRNA includes SLNCR, HOXA11-AS-203, SRA1, PCGEM1, and HOTAIR. In certain embodiments, the lncRNA is SLNCR, and the single-stranded nucleic acid binds to SLNCR to generate double-stranded RNA incapable of AR-binding. Such single-stranded nucleic acid may exhibit at least partial nuclear localization. It may be at least 20 nucleotides long, and are less than about 1000, 900, 800, 700, 600, 500, 400, 300, 200, 100, 50, 40, 35, 30, 29, 28, 27, 26, 25, 24, 23, 22, or 21 nucleotides in length. In a preferred embodiment, the single-stranded nucleic acid is 28 nucleotides in length. The single-stranded nucleic acid may be longer than 28 nucleotides, but may not

comprise a high level of secondary structure. In some embodiments, the single-stranded nucleic acid may contain two intact AGGAGA or UGGAGA motifs (*e.g.*, an AGGAGA motif followed by a UGGAGA motif). In some other embodiments, the first A in the AGGAGA motif, or the last A in the UGGAGA motif, may be lacking. The two AGGAGA or UGGAGA motifs are linked by an internal seqeunce. In certain embodiment, the internal sequence is 9 nucleotides in length, and may have more than 75% homogloy (*e.g.*, more than 80%, 85%, 90%, 95%, 99% homology) to the sequence AGACCAGGG. In certain preferred embodiment, the internal sequence has 100% homology to the sequence AGACCAGGG. In some embodiments, the single-stranded nucleic acid is at least 30 nucleotides long, and may contain at least 65% purine (G and A), preferably >75% (*e.g.*, >80%, >85%, >90%, >95%, >99%), within the about 30 nucleotides surrounding the AGGAGA or UGGAGA motifs.

Also provided herein are compositions comprising one or more nucleic acids comprising or capable of expressing at least 1, 2, 3, 4, 5, 10, 20 or more singled-strande nucleic acids that block the AR-lncRNA interaction. In some embodiments, a composition may comprise a library of nucleic acids comprising or capable of expressing said singled-strande nucleic acids, or pools of said singled-stranded nucleic acids. A pool of nucleic acids may comprise about 2-5, 5-10, 10-20, 10-30 or more nucleic acids comprising or capable of expressing said singled-stranded nucleic acids.

In one embodiment, binding may be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interactions in the major groove of the double helix.

b. Chemical Modifications, Production, and Delivery of Nucleic Acids

Singled-stranded nucleic acids of the methods and compositions presented herein can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of cellular nucleic acids (*e.g.,* small RNAs, mRNA, lncRNA, and/or genomic DNA). Alternatively, the expression plasmid can produce RNA which encodes mRNA, miRNA, pre-miRNA, pri-miRNA, miRNA*, piwiRNA, anti-miRNA, or a miRNA binding site, or a variant thereof. For example, selection of plasmids suitable for expressing the miRNAs, methods for inserting nucleic acid sequences into the plasmid, and methods of delivering the recombinant plasmid to the cells of interest are within the skill in the art. See, for example, Zeng *et al.* (2002), Molecular Cell 9:1327-1333; Tuschl (2002), Nat. Biotechnol, 20:446-448;

Brummelkamp *et al.* (2002), Science 296:550-553; Miyagishi *et al.* (2002), Nat. Biotechnol. 20:497-500; Paddison *et al.* (2002), Genes Dev. 16:948-958; Lee *et al.* (2002), Nat. Biotechnol. 20:500-505; and Paul *et al.* (2002), Nat. Biotechnol. 20:505-508, the entire disclosures of which are herein incorporated by reference.

Alternatively, singled-stranded nucleic acids are oligonucleotide probes that are generated *ex vivo* and which, when introduced into the cell, results in hybridization with cellular nucleic acids (*e.g.*, lncRNA) or binding to AR. Such oligonucleotide probes are preferably modified oligonucleotides that are resistant to endogenous nucleases, *e.g.*, exonucleases and/or endonucleases, and are therefore stable *in vivo*. Exemplary nucleic acid molecules for use as singled-stranded nucleic acids are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol *et al.* (1988) BioTechniques 6:958-976; and Stein *et al.* (1988) Cancer Res 48:2659-2668.

Singled-stranded nucleic acids can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof. Singled-stranded nucleic acids can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc., and may include other appended groups such as peptides (*e.g.,* for targeting host cell receptors), or agents facilitating transport across the cell membrane (see, *e.g.,* Letsinger *et al.* (1989) Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre *et al.* (1987) Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810, published December 15, 1988) or the blood-brain barrier (see, *e.g.,* PCT Publication No. W089/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, *e.g.,* Krol *et al.* (1988) BioTechniques 6:958-976) or intercalating agents. (See, *e.g.,* Zon (1988), Pharm. Res. 5:539-549). To this end, singled-stranded nucleic acids may be conjugated to another molecule, *e.g.,* a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

Singled-stranded nucleic acids may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxytiethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine,

2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Singled-stranded nucleic acids may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

In certain embodiments, a compound comprises a singled-stranded nucleic acid conjugated to one or more moieties which enhance the activity, cellular distribution or cellular uptake of the resulting nucleic acid. In certain such embodiments, the moiety is a cholesterol moiety (*e.g.,* antagomirs) or a lipid moiety or liposome conjugate. Additional moieties for conjugation include carbohydrates, phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. In certain embodiments, a conjugate group is attached directly to the singled-stranded nucleic acid. In certain embodiments, a conjugate group is attached to the singled-stranded nucleic acid by a linking moiety selected from amino, hydroxyl, carboxylic acid, thiol, unsaturations (*e.g.,* double or triple bonds), 8-amino-3,6-dioxaoctanoic acid (ADO), succinimidyl 4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC), 6-aminohexanoic acid (AHEX or AHA), substituted C1-C10 alkyl, substituted or unsubstituted C2-C10 alkenyl, and substituted or unsubstituted C2-C10 alkynyl. In certain such embodiments, a substituent group is selected from hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl, nitro, thiol, thioalkoxy, halogen, alkyl, aryl, alkenyl and alkynyl.

In certain such embodiments, the compound comprises the singled-stranded nucleic acid having one or more stabilizing groups that are attached to one or both termini of the singled-stranded nucleic acid to enhance properties such as, for example, nuclease stability. Included in stabilizing groups are cap structures. These terminal modifications protect the singled-stranded nucleic acid from exonuclease degradation, and can help in delivery and/or localization within a cell. The cap can be present at the 5'-terminus (5'-cap), or at the 3'-terminus (3'-cap), or can be present on both termini. Cap structures include, for example, inverted deoxy abasic caps.

Suitable cap structures include a 4',5'-methylene nucleotide, a 1-(beta-D-erythrofuranosyl) nucleotide, a 4'-thio nucleotide, a carbocyclic nucleotide, a 1,5-anhydrohexitol nucleotide, an L-nucleotide, an alpha-nucleotide, a modified base nucleotide, a phosphorodithioate linkage, a threo-pentofuranosyl nucleotide, an acyclic 3',4'-seco nucleotide, an acyclic 3,4-dihydroxybutyl nucleotide, an acyclic 3,5-dihydroxypentyl nucleotide, a 3'-3'-inverted nucleotide moiety, a 3'-3'-inverted abasic moiety, a 3'-2'-inverted nucleotide moiety, a 3'-2'-inverted abasic moiety, a 1,4-butanediol phosphate, a 3'-phosphoramidate, a hexylphosphate, an aminohexyl phosphate, a 3'-phosphate, a 3'-phosphorothioate, a phosphorodithioate, a bridging methylphosphonate moiety, and a non-bridging methylphosphonate moiety 5'-amino-alkyl phosphate, a 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate, a 6-aminohexyl phosphate, a 1,2-aminododecyl phosphate, a hydroxypropyl phosphate, a 5'-5'-inverted nucleotide moiety, a 5'-5'-inverted abasic moiety, a 5'-phosphoramidate, a 5'-phosphorothioate, a 5'-amino, a bridging and/or non-bridging 5'-phosphoramidate, a phosphorothioate, and a 5'-mercapto moiety.

It is to be understood that additional well-known nucleic acid architecture or chemistry can be applied. Different modifications can be placed at different positions to prevent the singled-stranded nucleic acid from activating RNase H and/or being capable of recruiting the RNAi machinery. In another embodiment, they may be placed such as to allow RNase H activation and/or recruitment of the RNAi machinery. The modifications can be non-natural bases, *e.g.* universal bases. It may be modifications on the backbone sugar or phosphate, *e.g.*, 2′-O-modifications including LNA or phosphorothioate linkages. As used herein, it makes no difference whether the modifications are present on the nucleotide before incorporation into the oligonucleotide or whether the oligonucleotide is modified after synthesis.

Preferred modifications are those that increase the affinity of the singled-stranded nucleic acid for complementary sequences of lncRNAs, *i.e.* increases the tm (melting temperature) of the singled-stranded nucleic acid base paired to a complementary sequence. Such modifications include 2′-O-flouro, 2′-O-methyl, 2′-O-methoxyethyl. The use of LNA (locked nucleic acid) units, phosphoramidate, PNA (peptide nucleic acid) units or INA (intercalating nucleic acid) units is preferred. For shorter singled-stranded nucleic acids, it is preferred that a higher percentage of affinity increasing modifications are present. If the singled-stranded nucleic acid is less than 12 or 10 units long, it may be composed entirely

of LNA units. A wide range of other non-natural units may also be build into the singled-stranded nucleic acid, *e.g.*, morpholino, 2′-deoxy-2′-fluoro-arabinonucleic acid (FANA) and arabinonucleic acid (ANA). In a preferred embodiment, the fraction of units modified at either the base or sugar relatively to the units not modified at either the base or sugar is selected from the group consisting of less than less than 99%, 95%, less than 90%, less than 85% or less than 75%, less than 70%, less than 65%, less than 60%, less than 50%, less than 45%, less than 40%, less than 35%, less than 30%, less than 25%, less than 20%, less than 15%, less than 10%, and less than 5%, less than 1%, more than 99%, more than 95%, more than 90%, more than 85% or more than 75%, more than 70%, more than 65%, more than 60%, more than 50%, more than 45%, more than 40%, more than 35%, more than 30%, more than 25%, more than 20%, more than 15%, more than 10%, and more than 5% and more than 1%.

Singled-stranded nucleic acids can also contain a neutral peptide-like backbone. Such molecules are termed peptide nucleic acid (PNA)-oligomers and are described, *e.g.,* in Perry-O'Keefe *et al.* (1996) Proc. Natl. Acad. Sci. U.S.A. 93:14670 and in Eglom *et al.* (1993) Nature 365:566. One advantage of PNA oligomers is their capability to bind to complementary DNA essentially independently from the ionic strength of the medium due to the neutral backbone of the DNA. In yet another embodiment, singled-stranded nucleic acids comprise at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In a further embodiment, singled-stranded nucleic acids are α-anomeric oligonucleotides. An α-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual b-units, the strands run parallel to each other (Gautier *et al.* (1987) Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-0-methylribonucleotide (Inoue *et al.* (1987) Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) FEBS Lett. 215:327-330).

Singled-stranded nucleic acids of the methods and compositions presented herein may be synthesized by standard methods known in the art, *e.g.,* by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein *et al.* (1988) Nucl. Acids Res. 16:3209, methylphosphonate oligonucleotides can

be prepared by use of controlled pore glass polymer supports (Sarin *et al.* (1988) Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc. For example, an isolated miRNA can be chemically synthesized or recombinantly produced using methods known in the art. In some instances, miRNA are chemically synthesized using appropriately protected ribonucleoside phosphoramidites and a conventional DNA/RNA synthesizer. Commercial suppliers of synthetic RNA molecules or synthesis reagents include, *e.g.,* Proligo (Hamburg, Germany), Dharmacon Research (Lafayette, Colo., USA), Pierce Chemical (part of Perbio Science, Rockford, Ill., USA), Glen Research (Sterling, Va., USA), ChemGenes (Ashland, Mass., USA), Cruachem (Glasgow, UK), and Exiqon (Vedbaek, Denmark).

Singled-stranded nucleic acids can be delivered to cells *in vivo*. A number of methods have been developed for delivering singled-stranded nucleic acids to cells; *e.g.,* singled-stranded nucleic acids can be injected directly into the tissue site, or modified singled-stranded nucleic acids, designed to target the desired cells (*e.g.,* singled-stranded nucleic acids linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systematically. Alternatively, singled-strand nucleic acids can be FANA-modified and gymnotically delivered to desired cells (*e.g.*, short-term melanoma cell cultures).

Singled-stranded nucleic acids of the methods and compositions presented herein may be prepared by any method known in the art for the synthesis DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well-known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Moreover, various well-known modifications to nucleic acid molecules may be introduced as a means of increasing intracellular stability and half-life. One of skill in the art will readily understand that polypeptides, small nucleic acids, and antisense oligonucleotides can be further linked to another peptide or polypeptide (*e.g.,* a heterologous peptide), *e.g.,* that serves as a means of protein detection. Non-limiting

examples of label peptide or polypeptide moieties useful for detection in the invention include, without limitation, suitable enzymes such as horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; epitope tags, such as FLAG, MYC, HA, or HIS tags; fluorophores such as green fluorescent protein; dyes; radioisotopes; digoxygenin; biotin; antibodies; polymers; as well as others known in the art, for example, in Principles of Fluorescence Spectroscopy, Joseph R. Lakowicz (Editor), Plenum Pub Corp, 2nd edition (July 1999).

c. Combinatory Therapy

Singled-stranded nucleic acids can be incorporated into pharmaceutical compositions and administered to a subject *in vivo*. The compositions may contain a single such molecule or agent or any combination of agents described herein. Based on the genetic pathway analyses described herein, it is believed that such combinations of agents is especially effective in diagnosing, prognosing, preventing, and treating melanoma. Thus, "single active agents" described herein can be combined with other pharmacologically active compounds ("second active agents") known in the art according to the methods and compositions provided herein. It is believed that certain combinations work synergistically in the treatment of particular types of melanoma. Second active agents can be large molecules (*e.g.,* proteins) or small molecules (*e.g.,* synthetic inorganic, organometallic, or organic molecules).

Examples of large molecule active agents include, but are not limited to, hematopoietic growth factors, cytokines, and monoclonal and polyclonal antibodies. Typical large molecule active agents are biological molecules, such as naturally occurring or artificially made proteins. Proteins that are particularly useful in this invention include proteins that stimulate the survival and/or proliferation of hematopoietic precursor cells and immunologically active poietic cells *in vitro* or *in vivo*. Others stimulate the division and differentiation of committed erythroid progenitors in cells *in vitro* or *in vivo*. Particular proteins include, but are not limited to: interleukins, such as IL-2 (including recombinant IL-II ("rIL2") and canarypox IL-2), IL-10, IL-12, and IL-18; interferons, such as interferon alfa-2a, interferon alfa-2b, interferon alpha-n1, interferon alpha-n3, interferon beta-Ia, and interferon gamma-Ib; GM-CF and GM-CSF; and EPO.

Particular proteins that can be used in the methods and compositions provided herein include, but are not limited to: filgrastim, which is sold in the United States under the trade name Neupogen® (Amgen, Thousand Oaks, Calif.); sargramostim, which is sold

in the United States under the trade name Leukine® (Immunex, Seattle, Wash.); and recombinant EPO, which is sold in the United States under the trade name Epogen® (Amgen, Thousand Oaks, Calif.). Recombinant and mutated forms of GM-CSF can be prepared as described in U.S. Pat. Nos. 5,391,485; 5,393,870; and 5,229,496; all of which are incorporated herein by reference. Recombinant and mutated forms of G-CSF can be prepared as described in U.S. Pat. Nos. 4,810,643; 4,999,291; 5,528,823; and 5,580,755; all of which are incorporated herein by reference.

When antibodies are used, the therapy is called immunotherapy. Antibodies that can be used in combination with the methods described herein include monoclonal and polyclonal antibodies. Examples of antibodies include, but are not limited to, ipilimumab (Yervoy®), trastuzumab (Herceptin®), rituximab (Rituxan®), bevacizumab (Avastin®), pertuzumab (Omnitarg®), tositumomab (Bexxar®), edrecolomab (Panorex®), and G250. Compounds of the present invention can also be combined with, or used in combination with, anti-TNF-α antibodies. Large molecule active agents may be administered in the form of anti-cancer vaccines. For example, vaccines that secrete, or cause the secretion of, cytokines such as IL-2, G-CSF, and GM-CSF can be used in the methods, pharmaceutical compositions, and kits provided herein. See, *e.g.*, Emens, L. A., *et al.*, Curr. Opinion Mol. Ther. 3(1):77-84 (2001).

Second active agents that are small molecules can also be used to in combination as provided herein. Examples of small molecule second active agents include, but are not limited to, anti-cancer agents, antibiotics, immunosuppressive agents, and steroids.

In some embodiments, well-known "combination chemotherapy" regimens can be used. In one embodiment, the combination chemotherapy comprises a combination of two or more of cyclophosphamide, hydroxydaunorubicin (also known as doxorubicin or adriamycin), oncovorin (vincristine), and prednisone. In another preferred embodiment, the combination chemotherapy comprises a combination of cyclophsophamide, oncovorin, prednisone, and one or more chemotherapeutics selected from the group consisting of anthracycline, hydroxydaunorubicin, epirubicin, and motixantrone.

Examples of other anti-cancer agents include, but are not limited to: acivicin; aclarubicin; acodazole hydrochloride; acronine; adozelesin; aldesleukin; altretamine; ambomycin; ametantrone acetate; amsacrine; anastrozole; anthramycin; asparaginase; asperlin; azacitidine; azetepa; azotomycin; batimastat; benzodepa; bicalutamide; bisantrene hydrochloride; bisnafide dimesylate; bizelesin; bleomycin sulfate; brequinar sodium;

bropirimine; busulfan; cactinomycin; calusterone; caracemide; carbetimer; carboplatin; carmustine; carubicin hydrochloride; carzelesin; cedefingol; celecoxib (COX-2 inhibitor); chlorambucil; cirolemycin; cisplatin; cladribine; crisnatol mesylate; cyclophosphamide; cytarabine; dacarbazine; dactinomycin; daunorubicin hydrochloride; decitabine; dexormaplatin; dezaguanine; dezaguanine mesylate; diaziquone; docetaxel; doxorubicin; doxorubicin hydrochloride; droloxifene; droloxifene citrate; dromostanolone propionate; duazomycin; edatrexate; eflornithine hydrochloride; elsamitrucin; enloplatin; enpromate; epipropidine; epirubicin hydrochloride; erbulozole; esorubicin hydrochloride; estramustine; estramustine phosphate sodium; etanidazole; etoposide; etoposide phosphate; etoprine; fadrozole hydrochloride; fazarabine; fenretinide; floxuridine; fludarabine phosphate; fluorouracil; fluorocitabine; fosquidone; fostriecin sodium; gemcitabine; gemcitabine hydrochloride; hydroxyurea; idarubicin hydrochloride; ifosfamide; ilmofosine; iproplatin; irinotecan; irinotecan hydrochloride; lanreotide acetate; letrozole; leuprolide acetate; liarozole hydrochloride; lometrexol sodium; lomustine; losoxantrone hydrochloride; masoprocol; maytansine; mechlorethamine hydrochloride; megestrol acetate; melengestrol acetate; melphalan; menogaril; mercaptopurine; methotrexate; methotrexate sodium; metoprine; meturedepa; mitindomide; mitocarcin; mitocromin; mitogillin; mitomalcin; mitomycin; mitosper; mitotane; mitoxantrone hydrochloride; mycophenolic acid; nocodazole; nogalamycin; ormaplatin; oxisuran; paclitaxel; pegaspargase; peliomycin; pentamustine; peplomycin sulfate; perfosfamide; pipobroman; piposulfan; piroxantrone hydrochloride; plicamycin; plomestane; porfimer sodium; porfiromycin; prednimustine; procarbazine hydrochloride; puromycin; puromycin hydrochloride; pyrazofurin; riboprine; safingol; safingol hydrochloride; semustine; simtrazene; sparfosate sodium; sparsomycin; spirogermanium hydrochloride; spiromustine; spiroplatin; streptonigrin; streptozocin; sulofenur; talisomycin; tecogalan sodium; taxotere; tegafur; teloxantrone hydrochloride; temoporfin; teniposide; teroxirone; testolactone; thiamiprine; thioguanine; thiotepa; tiazofurin; tirapazamine; toremifene citrate; trestolone acetate; triciribine phosphate; trimetrexate; trimetrexate glucuronate; triptorelin; tubulozole hydrochloride; uracil mustard; uredepa; vapreotide; verteporfin; vinblastine sulfate; vincristine sulfate; vindesine; vindesine sulfate; vinepidine sulfate; vinglycinate sulfate; vinleurosine sulfate; vinorelbine tartrate; vinrosidine sulfate; vinzolidine sulfate; vorozole; zeniplatin; zinostatin; and zorubicin hydrochloride.

Other anti-cancer drugs include, but are not limited to: 20-epi-1,25 dihydroxyvitamin D3; 5-ethynyluracil; abiraterone; aclarubicin; acylfulvene; adecypenol; adozelesin; aldesleukin; ALL-TK antagonists; altretamine; ambamustine; amidox; amifostine; aminolevulinic acid; amrubicin; amsacrine; anagrelide; anastrozole; andrographolide; angiogenesis inhibitors; antagonist D; antagonist G; antarelix; anti-dorsalizing morphogenetic protein-1; antiandrogen, prostatic carcinoma; antiestrogen; antineoplaston; antisense oligonucleotides; aphidicolin glycinate; apoptosis gene modulators; apoptosis regulators; apurinic acid; ara-CDP-DL-PTBA; arginine deaminase; asulacrine; atamestane; atrimustine; axinastatin 1; axinastatin 2; axinastatin 3; azasetron; azatoxin; azatyrosine; baccatin III derivatives; balanol; batimastat; BCR/ABL antagonists; benzochlorins; benzoylstaurosporine; beta lactam derivatives; beta-alethine; betaclamycin B; betulinic acid; bFGF inhibitor; bicalutamide; bisantrene; bisaziridinylspermine; bisnafide; bistratene A; bizelesin; breflate; bropirimine; budotitane; buthionine sulfoximine; calcipotriol; calphostin C; camptothecin derivatives; capecitabine; carboxamide-amino-triazole; carboxyamidotriazole; CaRest M3; CARN 700; cartilage derived inhibitor; carzelesin; casein kinase inhibitors (ICOS); castanospermine; cecropin B; cetrorelix; chlorins; chloroquinoxaline sulfonamide; cicaprost; cis-porphyrin; cladribine; clomifene analogues; clotrimazole; collismycin A; collismycin B; combretastatin A4; combretastatin analogue; conagenin; crambescidin 816; crisnatol; cryptophycin 8; cryptophycin A derivatives; curacin A; cyclopentanthraquinones; cycloplatam; cyclosporin A; cypemycin; cytarabine ocfosfate; cytolytic factor; cytostatin; dacliximab; decitabine; dehydrodidemnin B; deslorelin; dexamethasone; dexifosfamide; dexrazoxane; dexverapamil; diaziquone; didemnin B; didox; diethylnorspermine; dihydro-5-azacytidine; dihydrotaxol, 9-; dioxamycin; diphenyl spiromustine; docetaxel; docosanol; dolasetron; doxifluridine; doxorubicin; droloxifene; dronabinol; duocarmycin SA; ebselen; ecomustine; edelfosine; edrecolomab; eflornithine; elemene; emitefur; epirubicin; epristeride; estramustine analogue; estrogen agonists; estrogen antagonists; etanidazole; etoposide phosphate; exemestane; fadrozole; fazarabine; fenretinide; filgrastim; finasteride; flavopiridol; flezelastine; fluasterone; fludarabine; fluorodaunorunicin hydrochloride; forfenimex; formestane; fostriecin; fotemustine; gadolinium texaphyrin; gallium nitrate; galocitabine; ganirelix; gelatinase inhibitors; gemcitabine; glutathione inhibitors; hepsulfam; heregulin; hexamethylene bisacetamide; hypericin; ibandronic acid; idarubicin; idoxifene; idramantone; ilmofosine; ilomastat; imatinib (*e.g.*, Gleevec®), imiquimod;

immunostimulant peptides; insulin-like growth factor-1 receptor inhibitor; interferon agonists; interferons; interleukins; iobenguane; iododoxorubicin; ipomeanol, 4-; iroplact; irsogladine; isobengazole; isohomohalicondrin B; itasetron; jasplakinolide; kahalalide F; lamellarin-N triacetate; lanreotide; leinamycin; lenograstim; lentinan sulfate; leptolstatin; letrozole; leukemia inhibiting factor; leukocyte alpha interferon; leuprolide+estrogen+progesterone; leuprorelin; levamisole; liarozole; linear polyamine analogue; lipophilic disaccharide peptide; lipophilic platinum compounds; lissoclinamide 7; lobaplatin; lombricine; lometrexol; lonidamine; losoxantrone; loxoribine; lurtotecan; lutetium texaphyrin; lysofylline; lytic peptides; maitansine; mannostatin A; marimastat; masoprocol; maspin; matrilysin inhibitors; matrix metalloproteinase inhibitors; menogaril; merbarone; meterelin; methioninase; metoclopramide; MIF inhibitor; mifepristone; miltefosine; mirimostim; mitoguazone; mitolactol; mitomycin analogues; mitonafide; mitotoxin fibroblast growth factor-saporin; mitoxantrone; mofarotene; molgramostim; Erbitux, human chorionic gonadotrophin; monophosphoryl lipid A+myobacterium cell wall sk; mopidamol; mustard anticancer agent; mycaperoxide B; mycobacterial cell wall extract; myriaporone; N-acetyldinaline; N-substituted benzamides; nafarelin; nagrestip; naloxone+pentazocine; napavin; naphterpin; nartograstim; nedaplatin; nemorubicin; neridronic acid; nilutamide; nisamycin; nitric oxide modulators; nitroxide antioxidant; nitrullyn; oblimersen (Genasense®); O6-benzylguanine; octreotide; okicenone; oligonucleotides; onapristone; ondansetron; ondansetron; oracin; oral cytokine inducer; ormaplatin; osaterone; oxaliplatin; oxaunomycin; paclitaxel; paclitaxel analogues; paclitaxel derivatives; palauamine; palmitoylrhizoxin; pamidronic acid; panaxytriol; panomifene; parabactin; pazelliptine; pegaspargase; peldesine; pentosan polysulfate sodium; pentostatin; pentrozole; perflubron; perfosfamide; perillyl alcohol; phenazinomycin; phenylacetate; phosphatase inhibitors; picibanil; pilocarpine hydrochloride; pirarubicin; piritrexim; placetin A; placetin B; plasminogen activator inhibitor; platinum complex; platinum compounds; platinum-triamine complex; porfimer sodium; porfiromycin; prednisone; propyl bis-acridone; prostaglandin J2; proteasome inhibitors; protein A-based immune modulator; protein kinase C inhibitor; protein kinase C inhibitors, microalgal; protein tyrosine phosphatase inhibitors; purine nucleoside phosphorylase inhibitors; purpurins; pyrazoloacridine; pyridoxylated hemoglobin polyoxyethylene conjugate; raf antagonists; raltitrexed; ramosetron; ras farnesyl protein transferase inhibitors; ras inhibitors; ras-GAP inhibitor; retelliptine demethylated; rhenium

Re 186 etidronate; rhizoxin; ribozymes; RII retinamide; rohitukine; romurtide; roquinimex; rubiginone B1; ruboxyl; safingol; saintopin; SarCNU; sarcophytol A; sargramostim; Sdi 1 mimetics; semustine; senescence derived inhibitor 1; sense oligonucleotides; signal transduction inhibitors; sizofuran; sobuzoxane; sodium borocaptate; sodium phenylacetate; solverol; somatomedin binding protein; sonermin; sparfosic acid; spicamycin D; spiromustine; splenopentin; spongistatin 1; squalamine; stipiamide; stromelysin inhibitors; sulfinosine; superactive vasoactive intestinal peptide antagonist; suradista; suramin; swainsonine; tallimustine; tamoxifen methiodide; tauromustine; tazarotene; tecogalan sodium; tegafur; tellurapyrylium; telomerase inhibitors; temoporfin; teniposide; tetrachlorodecaoxide; tetrazomine; thaliblastine; thiocoraline; thrombopoietin; thrombopoietin mimetic; thymalfasin; thymopoietin receptor agonist; thymotrinan; thyroid stimulating hormone; tin ethyl etiopurpurin; tirapazamine; titanocene bichloride; topsentin; toremifene; translation inhibitors; tretinoin; triacetyluridine; triciribine; trimetrexate; triptorelin; tropisetron; turosteride; tyrosine kinase inhibitors; tyrphostins; UBC inhibitors; ubenimex; urogenital sinus-derived growth inhibitory factor; urokinase receptor antagonists; vapreotide; variolin B; velaresol; veramine; verdins; verteporfin; vinorelbine; vinxaltine; vitaxin; vorozole; zanoterone; zeniplatin; zilascorb; and zinostatin stimalamer. Specific second active agents include, but are not limited to, chlorambucil, fludarabine, dexamethasone (Decadron®), hydrocortisone, methylprednisolone, cilostamide, doxorubicin (Doxil®), forskolin, rituximab, cyclosporin A, cisplatin, vincristine, PDE7 inhibitors such as BRL-50481 and IR-202, dual PDE4/7 inhibitors such as IR-284, cilostazol, meribendan, milrinone, vesnarionone, enoximone and pimobendan, Syk inhibitors such as fostamatinib disodium (R406/R788), R343, R-112 and Excellair® (ZaBeCor Pharmaceuticals, Bala Cynwyd, Pa.).

Moreover, singled-stranded nucleic acids in combination with nuclear receptor inhibitors are described herein.

d. Vectors and Host Cells

In some embodiments, vectors and/or host cells are further provided. In one aspect of the present invention pertains to the use of vectors, preferably expression vectors, containing a nucleic acid encoding RNAs that block AR-lncRNA interaction. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated.

Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors." In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions. In one embodiment, adenoviral vectors comprising a nucleic acid encoding RNAs that block AR-lncRNA interaction are used.

The recombinant expression vectors of the present invention comprise a nucleic acid of the present invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of RNA desired, *etc.*

The recombinant expression vectors of the present invention can be designed for expression of the desired nucleic acid in prokaryotic or eukaryotic cells. For example, a single-stranded nucleic acid can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*. Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89). Examples of suitable yeast expression vectors include pYepSec1 (Baldari, *et al.*, (1987) *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Examples of suitable baculovirus expression vectors useful for insect cell hosts include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39). Examples of suitable mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195).

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters such as in melanoma cancer cells are well-known in the art (see, for example, Pleshkan *et al.* (2011) *Acta Nat.* 3:13-21).

Another aspect of the present invention pertains to host cells into which a recombinant expression vector of the present invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, single-stranded nucleic acids can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or

mammalian cells (such as Fao hepatoma cells, primary hepatocytes, Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

A cell culture includes host cells, media and other byproducts. Suitable media for cell culture are well-known in the art.

III. Methods of Selecting Agents and Compositions

Another aspect of the present invention relates to methods of selecting agents (*e.g.*, single-stranded nucleic acids) which bind to AR or lncRNA, and block AR-lncRNA interaction. Such methods can use screening assays, including cell-based and non-cell based assays.

In one embodiment, the invention relates to assays for screening candidate or test compounds which bind to AR or lncRNA, and block AR-lncRNA interaction. Such compounds include, without limitation, single-stranded nucleic acids.

In one embodiment, an assay is a cell-based assay, comprising contacting a cell with a test single-stranded nucleic acid and determining the ability of the test single-stranded nucleic acid to block the interaction between AR (either full-lentgh or N-terminal region of AR) and lncRNA as measured by direct binding or by measuring a parameter of cancer.

For example, in a direct binding assay, the lncRNA, AR protein, or a fragment(s) thereof (*e.g.*, N-terminal region of AR), can be coupled with a radioisotope or enzymatic label such that binding of the lncRNA or a fragment(s) thereof to AR protein or a fragment(s) thereof (*e.g.*, N-terminal region of AR) can be determined by detecting the labeled molecule in a complex. For example, the lncRNA, AR protein, or a fragment(s) thereof, can be labeled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting.

Alternatively, AR protein or a fragment(s) thereof (*e.g.*, N-terminal region of AR) can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. AR protein, or a fragment(s) thereof (*e.g.*, N-terminal region of AR) can also be detected directly with a specific anti-AR antibody. LncRNA or a fragment(s) thereof can be biotinylated, and the labed RNA probes can then be detected with streptavidin-HRP and chemiluminescent.

It is also within the scope of this invention to determine the ability of a single-stranded nucleic acid to block the interactions beween a lncRNA or a fragment thereof, and AR protein or a fragment(s) thereof (*e.g.*, N-terminal region of AR), without the labeling of any of the interactants (*e.g.,* using a microphysiometer as described in McConnell, H. M. *et al.* (1992) *Science* 257:1906-1912). As used herein, a "microphysiometer" (*e.g.,* Cytosensor) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between compound and receptor.

In a preferred embodiment, determining the ability of a single-stranded nucleic acid to block the interaction betweem a lncRNA or a fragment thereof, and AR protein or a fragment(s) thereof (*e.g.*, N-terminal region of AR), can be accomplished by determining the activity of one or more members of the set of interacting molecules. For example, the activity of AR or lncRNA can be determined by detecting the induction of a reporter gene (comprising a target-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker), or detecting a cellular response regulated by AR or lncRNA, (*e.g.,* modulations of biological pathways identified herein, such as cell proliferation, cell invasion, and/or transcription of AR- and/or lncRNA-regulated genes).

In yet another embodiment, an assay of the present invention is a cell-free assay in which a lncRNA or a fragment(s) thereof, and AR protein or a fragment(s) thereof (*e.g.*, N-terminal region of AR protein), are contacted with a test single-stranded nucleic acid, and the ability of the test single-stranded nucleic acid to block the interaction between the lncRNA or a fragment(s) thereof, and AR protein or a fragment(s) thereof (*e.g.*, N-terminal region of AR protein), is determined. Blocking of the interaction between the lncRNA or a fragment(s) thereof, and AR protein or a fragment(s) thereof (*e.g.*, N-terminal region of AR protein), can be determined either directly or indirectly as described above. Determining

the ability of the single-stranded nucleic acid to block the interaction between the lncRNA or a fragment(s) thereof, and AR protein or a fragment(s) thereof (*e.g.*, N-terminal region of AR protein) can also be accomplished using a technology such as real-time Biomolecular Interaction Analysis (BIA) (Sjolander, S. and Urbaniczky, C. (1991) *Anal. Chem.* 63:2338-2345 and Szabo *et al.* (1995) *Curr. Opin. Struct. Biol.* 5:699-705). As used herein, "BIA" is a technology for studying biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BIAcore). Changes in the optical phenomenon of surface plasmon resonance (SPR) can be used as an indication of real-time reactions between biological polypeptides. AR protein or a fragment thereof (*e.g.*, N-termial of AR protein) can be immobilized on a BIAcore chip, and lncRNA or a fragment thereof can be tested for binding to the immobilized AR protein or fragment thereof. An example of using the BIA technology is described by Fitz *et al.* (1997) *Oncogene* 15:613.

The cell-free assays of the present invention are amenable to use of both soluble and/or membrane-bound forms of AR proteins. In the case of cell-free assays in which a membrane-bound form of AR protein is used it may be desirable to utilize a solubilizing agent such that the membrane-bound form of the AR protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)$_n$, 3-[(3-cholamidopropyl)dimethylamminio]-1-propane sulfonate (CHAPS), 3-[(3-cholamidopropyl)dimethylamminio]-2-hydroxy-1-propane sulfonate (CHAPSO), or N-dodecyl=N,N-dimethyl-3-ammonio-1-propane sulfonate.

In one or more embodiments of the above described assay methods, it may be desirable to immobilize either the lncRNA or a fragment(s) thereof, or AR protein or a fragment(s) thereof, to facilitate separation of complexed from uncomplexed forms of the reactants, as well as to accommodate automation of the assay. In one embodiment, a fusion protein can be provided which adds a domain that allows one or both of the proteins to be bound to a matrix. For example, glutathione-S-transferase-base fusion proteins, can be adsorbed onto glutathione Sepharose® beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then combined with lncRNA in the presence or absence of the test single-stranded nucleic acid, and the mixture incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove

any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of binding or activity determined using standard techniques.

In an alternative embodiment, determining the ability of the test single-stranded nucleic acid to modulate the interaction between lncRNA or a fragment thereof, and AR protein or a fragment thereof (*e.g.*, the N-terminal region of AR), can be accomplished by determining the ability of the test single-stranded nucleic acid to modulate the activity of a gene, *e.g.,* nucleic acid, or gene product, *e.g.,* polypeptide, that functions downstream of the interaction. For example, cellular proliferation or invasion can be determined by monitoring cell number count, cellular movement, matrigel assays, induction of proliferation- and/or invasion-related gene expression, and the like, as described further herein.

In another aspect, the invention pertains to a combination of two or more of the assays described herein. For example, a modulating agent can be identified using a cell-based or a cell-free assay, and the ability of the agent to modulate the interaction between lncRNA and AR protein or a fragment thereof can be confirmed *in vivo*, *e.g.,* in an animal such as an animal model for cellular transformation and/or tumorigenesis.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

V. Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) an AR- and/or lncRNA-medidated disease.

1. Prophylactic Methods

In one aspect, the present invention provides a method for preventing in a subject, a disease or condition associated with an aberrant expression or activity of AR and/or a

lncRNA, by administering to the subject an agent (e.g, a single-stranded nucleic acid) which binds to AR or the lncRNA, and blocks AR-lncRNA interaction. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the AR and/or lncRNA expression or activity aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression.

2. Therapeutic Methods

Another aspect of the present invention pertains to methods for treating a subject affliated with a disease or condition associated with an aberrant expression or activity of AR and/or a lncRNA, by administering to the subject an agent (e.g, a single-stranded nucleic acid) which binds to AR or the lncRNA, and blocks AR-lncRNA interaction. The disease or condition associated with an aberrant expression or activity of AR and/or a lncRNA include cancer, such as melanoma, as well as inflammatory and autoimmune diseases. Accordingly, the interaction between lncRNA or a fragment thereof and AR protein or a fragment(s) thereof can be modulated in order to modulate cancer growth and/or metastasis, as well as the immune response.

Modulatory methods of the present invention involve contacting a cell with a single-stranded nucleic acid of the present invention, that binds to AR or a lncRNA and block the interaction between AR and the lncRNA within the cell. An agent that blocks the interaction between AR and a lncRNA can be an agent as described herein.

These modulatory methods can be performed *in vitro* (*e.g.,* by contacting the cell with the agent) or, alternatively, by contacting an agent with cells *in vivo* (*e.g.,* by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a condition or disorder that would benefit from blocking the interaction between AR and a lncRNA, *e.g.,* a disorder characterized by unwanted, insufficient, or aberrant expression or activity of AR and/or lncRNA. In one embodiment, the method involves administering an agent (*e.g.,* an agent identified by a screening assay described herein), or combination of agents that blocks the interaction between AR and a lncRNA.

In addition, these modulatory agents can also be administered in combination therapy with, *e.g.,* chemotherapeutic agents, hormones, antiangiogens, radiolabelled, compounds, or with surgery, cryotherapy, and/or radiotherapy. The preceding treatment methods can be administered in conjunction with other forms of conventional therapy (*e.g.,* standard-of-care treatments for cancer well-known to the skilled artisan), either

consecutively with, pre- or post-conventional therapy. For example, these modulatory agents can be administered with a therapeutically effective dose of chemotherapeutic agent. In another embodiment, these modulatory agents are administered in conjunction with chemotherapy to enhance the activity and efficacy of the chemotherapeutic agent. The Physicians' Desk Reference (PDR) discloses dosages of chemotherapeutic agents that have been used in the treatment of various cancers. The dosing regimen and dosages of these aforementioned chemotherapeutic drugs that are therapeutically effective will depend on the particular melanoma, being treated, the extent of the disease and other factors familiar to the physician of skill in the art and can be determined by the physician.

IV. Pharmaceutical Compositions

In another aspect, the present invention provides pharmaceutically acceptable compositions which comprise a therapeutically-effective amount of a single-stranded nucleic acid that binds to AR or lncRNA, and blocks the interaction between AR and the lncRNA, formulated together with one or more pharmaceutically acceptable carriers (additives) and/or diluents. As described in detail below, the pharmaceutical compositions of the present invention may be specially formulated for administration in solid or liquid form, including those adapted for the following: (1) oral administration, for example, drenches (aqueous or non-aqueous solutions or suspensions), tablets, boluses, powders, granules, pastes; (2) parenteral administration, for example, by subcutaneous, intramuscular or intravenous injection as, for example, a sterile solution or suspension; (3) topical application, for example, as a cream, ointment or spray applied to the skin; (4) intravaginally or intrarectally, for example, as a pessary, cream or foam; or (5) aerosol, for example, as an aqueous aerosol, liposomal preparation or solid particles containing the compound.

The phrase "therapeutically-effective amount" as used herein means that amount of a single-stranded nucleic acid that binds to AR or lncRNA, and blocks the interaction between AR and the lncRNA, which is effective for producing some desired therapeutic effect, *e.g.,* cancer treatment, at a reasonable benefit/risk ratio.

The phrase "pharmaceutically acceptable" is employed herein to refer to those agents, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

The phrase "pharmaceutically-acceptable carrier" as used herein means a pharmaceutically-acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, solvent or encapsulating material, involved in carrying or transporting the subject chemical from one organ, or portion of the body, to another organ, or portion of the body. Each carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the subject. Some examples of materials which can serve as pharmaceutically-acceptable carriers include: (1) sugars, such as lactose, glucose and sucrose; (2) starches, such as corn starch and potato starch; (3) cellulose, and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; (4) powdered tragacanth; (5) malt; (6) gelatin; (7) talc; (8) excipients, such as cocoa butter and suppository waxes; (9) oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; (10) glycols, such as propylene glycol; (11) polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; (12) esters, such as ethyl oleate and ethyl laurate; (13) agar; (14) buffering agents, such as magnesium hydroxide and aluminum hydroxide; (15) alginic acid; (16) pyrogen-free water; (17) isotonic saline; (18) Ringer's solution; (19) ethyl alcohol; (20) phosphate buffer solutions; and (21) other non-toxic compatible substances employed in pharmaceutical formulations.

Formulations useful in the methods of the present invention include those suitable for oral, nasal, topical (including buccal and sublingual), rectal, vaginal, aerosol and/or parenteral administration. The formulations may conveniently be presented in unit dosage form and may be prepared by any methods well-known in the art of pharmacy. The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will vary depending upon the host being treated, the particular mode of administration. The amount of active ingredient, which can be combined with a carrier material to produce a single dosage form will generally be that amount of the compound which produces a therapeutic effect. Generally, out of one hundred per cent, this amount will range from about 1% to about 99% of active ingredient, preferably from about 5% to about 70%, most preferably from about 10% to about 30%.

Formulations suitable for oral administration may be in the form of capsules, cachets, pills, tablets, lozenges (using a flavored basis, usually sucrose and acacia or tragacanth), powders, granules, or as a solution or a suspension in an aqueous or non-aqueous liquid, or as an oil-in-water or water-in-oil liquid emulsion, or as an elixir or syrup,

or as pastilles (using an inert base, such as gelatin and glycerin, or sucrose and acacia) and/or as mouth washes and the like, each containing a predetermined amount of an agent as an active ingredient. A compound may also be administered as a bolus, electuary or paste.

In solid dosage forms for oral administration (capsules, tablets, pills, dragees, powders, granules and the like), the active ingredient is mixed with one or more pharmaceutically-acceptable carriers, such as sodium citrate or dicalcium phosphate, and/or any of the following: (1) fillers or extenders, such as starches, lactose, sucrose, glucose, mannitol, and/or silicic acid; (2) binders, such as, for example, carboxymethylcellulose, alginates, gelatin, polyvinyl pyrrolidone, sucrose and/or acacia; (3) humectants, such as glycerol; (4) disintegrating agents, such as agar-agar, calcium carbonate, potato or tapioca starch, alginic acid, certain silicates, and sodium carbonate; (5) solution retarding agents, such as paraffin; (6) absorption accelerators, such as quaternary ammonium compounds; (7) wetting agents, such as, for example, acetyl alcohol and glycerol monostearate; (8) absorbents, such as kaolin and bentonite clay; (9) lubricants, such a talc, calcium stearate, magnesium stearate, solid polyethylene glycols, sodium lauryl sulfate, and mixtures thereof; and (10) coloring agents. In the case of capsules, tablets and pills, the pharmaceutical compositions may also comprise buffering agents. Solid compositions of a similar type may also be employed as fillers in soft and hard-filled gelatin capsules using such excipients as lactose or milk sugars, as well as high molecular weight polyethylene glycols and the like.

A tablet may be made by compression or molding, optionally with one or more accessory ingredients. Compressed tablets may be prepared using binder (for example, gelatin or hydroxypropylmethyl cellulose), lubricant, inert diluent, preservative, disintegrant (for example, sodium starch glycolate or cross-linked sodium carboxymethyl cellulose), surface-active or dispersing agent. Molded tablets may be made by molding in a suitable machine a mixture of the powdered peptide or peptidomimetic moistened with an inert liquid diluent.

Tablets, and other solid dosage forms, such as dragees, capsules, pills and granules, may optionally be scored or prepared with coatings and shells, such as enteric coatings and other coatings well-known in the pharmaceutical-formulating art. They may also be formulated so as to provide slow or controlled release of the active ingredient therein using, for example, hydroxypropylmethyl cellulose in varying proportions to provide the desired

release profile, other polymer matrices, liposomes and/or microspheres. They may be sterilized by, for example, filtration through a bacteria-retaining filter, or by incorporating sterilizing agents in the form of sterile solid compositions, which can be dissolved in sterile water, or some other sterile injectable medium immediately before use. These compositions may also optionally contain opacifying agents and may be of a composition that they release the active ingredient(s) only, or preferentially, in a certain portion of the gastrointestinal tract, optionally, in a delayed manner. Examples of embedding compositions, which can be used include polymeric substances and waxes. The active ingredient can also be in micro-encapsulated form, if appropriate, with one or more of the above-described excipients.

Liquid dosage forms for oral administration include pharmaceutically acceptable emulsions, microemulsions, solutions, suspensions, syrups and elixirs. In addition to the active ingredient, the liquid dosage forms may contain inert diluents commonly used in the art, such as, for example, water or other solvents, solubilizing agents and emulsifiers, such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, oils (in particular, cottonseed, groundnut, corn, germ, olive, castor and sesame oils), glycerol, tetrahydrofuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof.

Besides inert diluents, the oral compositions can also include adjuvants such as wetting agents, emulsifying and suspending agents, sweetening, flavoring, coloring, perfuming and preservative agents.

Suspensions, in addition to the active agent may contain suspending agents as, for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonite, agar-agar and tragacanth, and mixtures thereof.

Formulations for rectal or vaginal administration may be presented as a suppository, which may be prepared by mixing one or more therapeutic agents with one or more suitable nonirritating excipients or carriers comprising, for example, cocoa butter, polyethylene glycol, a suppository wax or a salicylate, and which is solid at room temperature, but liquid at body temperature and, therefore, will melt in the rectum or vaginal cavity and release the active agent.

Formulations which are suitable for vaginal administration also include pessaries, tampons, creams, gels, pastes, foams or spray formulations containing such carriers as are known in the art to be appropriate.

Dosage forms for the topical or transdermal administration of a single-stranded nucleic acid that binds to AR or lncRNA and blocks the interaction between AR and the lncRNA, include powders, sprays, ointments, pastes, creams, lotions, gels, solutions, patches and inhalants. The active component may be mixed under sterile conditions with a pharmaceutically-acceptable carrier, and with any preservatives, buffers, or propellants which may be required.

The ointments, pastes, creams and gels may contain, in addition to a therapeutic agent, excipients, such as animal and vegetable fats, oils, waxes, paraffins, starch, tragacanth, cellulose derivatives, polyethylene glycols, silicones, bentonites, silicic acid, talc and zinc oxide, or mixtures thereof.

Powders and sprays can contain, in addition to a single-stranded nucleic acid that binds to AR or lncRNA and blocks the interaction between AR and the lncRNA, excipients such as lactose, talc, silicic acid, aluminum hydroxide, calcium silicates and polyamide powder, or mixtures of these substances. Sprays can additionally contain customary propellants, such as chlorofluorohydrocarbons and volatile unsubstituted hydrocarbons, such as butane and propane.

The single-stranded nucleic acid that binds to AR or lncRNA and blocks the interaction between AR and the lncRNA, can be alternatively administered by aerosol. This is accomplished by preparing an aqueous aerosol, liposomal preparation or solid particles containing the compound. A nonaqueous (*e.g.,* fluorocarbon propellant) suspension could be used. Sonic nebulizers are preferred because they minimize exposing the agent to shear, which can result in degradation of the compound.

Ordinarily, an aqueous aerosol is made by formulating an aqueous solution or suspension of the agent together with conventional pharmaceutically acceptable carriers and stabilizers. The carriers and stabilizers vary with the requirements of the particular compound, but typically include nonionic surfactants (Tweens, Pluronics, or polyethylene glycol), innocuous proteins like serum albumin, sorbitan esters, oleic acid, lecithin, amino acids such as glycine, buffers, salts, sugars or sugar alcohols. Aerosols generally are prepared from isotonic solutions.

Transdermal patches have the added advantage of providing controlled delivery of a therapeutic agent to the body. Such dosage forms can be made by dissolving or dispersing the agent in the proper medium. Absorption enhancers can also be used to increase the flux of the peptidomimetic across the skin. The rate of such flux can be controlled by either providing a rate controlling membrane or dispersing the peptidomimetic in a polymer matrix or gel.

Ophthalmic formulations, eye ointments, powders, solutions and the like, are also contemplated as being within the scope of this invention.

Pharmaceutical compositions of this invention suitable for parenteral administration comprise one or more therapeutic agents in combination with one or more pharmaceutically-acceptable sterile isotonic aqueous or nonaqueous solutions, dispersions, suspensions or emulsions, or sterile powders which may be reconstituted into sterile injectable solutions or dispersions just prior to use, which may contain antioxidants, buffers, bacteriostats, solutes which render the formulation isotonic with the blood of the intended recipient or suspending or thickening agents.

Examples of suitable aqueous and nonaqueous carriers which may be employed in the pharmaceutical compositions of the present invention include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants.

These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of the action of microorganisms may be ensured by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the like. It may also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents which delay absorption such as aluminum monostearate and gelatin.

In some cases, in order to prolong the effect of a drug, it is desirable to slow the absorption of the drug from subcutaneous or intramuscular injection. This may be accomplished by the use of a liquid suspension of crystalline or amorphous material having

poor water solubility. The rate of absorption of the drug then depends upon its rate of dissolution, which, in turn, may depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally-administered drug form is accomplished by dissolving or suspending the drug in an oil vehicle.

Injectable depot forms are made by forming microencapsule matrices of a single-stranded nucleic acid that binds to AR or lncRNA and blocks the interaction between AR and the lncRNA, in biodegradable polymers such as polylactide-polyglycolide. Depending on the ratio of drug to polymer, and the nature of the particular polymer employed, the rate of drug release can be controlled. Examples of other biodegradable polymers include poly(orthoesters) and poly(anhydrides). Depot injectable formulations are also prepared by entrapping the drug in liposomes or microemulsions, which are compatible with body tissue.

When the agents of the present invention are administered as pharmaceuticals, to humans and animals, they can be given per se or as a pharmaceutical composition containing, for example, 0.1 to 99.5% (more preferably, 0.5 to 90%) of active ingredient in combination with a pharmaceutically acceptable carrier.

Actual dosage levels of the active ingredients in the pharmaceutical compositions of this invention may be determined by the methods of the present invention so as to obtain an amount of the active ingredient, which is effective to achieve the desired therapeutic response for a particular subject, composition, and mode of administration, without being toxic to the subject.

The nucleic acid molecules of the present invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or by stereotactic injection (see *e.g.,* Chen *et al.* (1994) Proc. Natl. Acad. Sci. USA 91:3054 3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.,* retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

V. Administration of Agents

The prevention, and/or treatment modulating agents of the present invention are administered to subjects in a biologically compatible form suitable for pharmaceutical administration *in vivo*. By "biologically compatible form suitable for administration *in vivo*" is meant a form of the nucleic acid to be administered in which any toxic effects are outweighed by the therapeutic effects of the nucleic acid. The term "subject" is intended to include living organisms, *e.g.*, mammals. Examples of subjects include humans, dogs, cats, mice, rats, and transgenic species thereof. Administration of an agent as described herein can be in any pharmacological form including a therapeutically active amount of an agent alone or in combination with a pharmaceutically acceptable carrier.

Administration of a therapeutically active amount of the therapeutic composition of the present invention is defined as an amount effective, at dosages and for periods of time necessary, to achieve the desired result. For example, a therapeutically active amount of a single-stranded nucleic acid may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the nucleic acid to elicit a desired response in the individual. Dosage regimens can be adjusted to provide the optimum therapeutic response. For example, several divided doses can be administered daily or the dose can be proportionally reduced as indicated by the exigencies of the therapeutic situation.

It will also be appreciated that the effective dosage of the therapeutic composition of the present invention used for treatment may increase or decrease over the course of a particular treatment. Changes in dosage may result from the results of diagnostic assays. In addition, the therapeutic composition of the present invention can also be administered in combination therapy with, *e.g.*, chemotherapeutic agents, hormones, antiangiogens, radiolabelled, compounds, or with surgery, cryotherapy, and/or radiotherapy. A therapeutic composition of the present invention can also be administered in conjunction with other forms of conventional therapy, either consecutively with, pre- or post-conventional therapy. For example, the therapeutic composition of the present invention can be administered with a therapeutically effective dose of chemotherapeutic agent. In another embodiment, the therapeutic composition of the present invention can be administered in conjunction with chemotherapy to enhance the activity and efficacy of the chemotherapeutic agent. The Physicians' Desk Reference (PDR) discloses dosages of chemotherapeutic agents that have been used in the treatment of various cancers. The dosing regimen and dosages of these

aforementioned chemotherapeutic drugs that are therapeutically effective will depend on the particular cancer, *e.g.*, melanoma, being treated, the extent of the disease and other factors familiar to the physician of skill in the art and can be determined by the physician. In another embodiment, the therapeutic composition of the present invention can be administered in conjunction with one or more nuclear receptor targeting drugs.

The agents of the present invention described herein can be administered in a convenient manner such as by injection (subcutaneous, intravenous, etc.), oral administration, inhalation, transdermal application, or rectal administration. Depending on the route of administration, the active compound can be coated in a material to protect the compound from the action of enzymes, acids and other natural conditions which may inactivate the compound. For example, for administration of agents, by other than parenteral administration, it may be desirable to coat the agent with, or co-administer the agent with, a material to prevent its inactivation.

An agent can be administered to an individual in an appropriate carrier, diluent or adjuvant, co-administered with enzyme inhibitors or in an appropriate carrier such as liposomes. Pharmaceutically acceptable diluents include saline and aqueous buffer solutions. Adjuvant is used in its broadest sense and includes any immune stimulating compound such as interferon. Adjuvants contemplated herein include resorcinols, non-ionic surfactants such as polyoxyethylene oleyl ether and n-hexadecyl polyethylene ether. Enzyme inhibitors include pancreatic trypsin inhibitor, diisopropylfluorophosphate (DEEP) and trasylol. Liposomes include water-in-oil-in-water emulsions as well as conventional liposomes (Sterna *et al.* (1984) *J. Neuroimmunol.* 7:27).

The agent may also be administered parenterally or intraperitoneally. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof, and in oils. Under ordinary conditions of storage and use, these preparations may contain a preservative to prevent the growth of microorganisms.

Pharmaceutical compositions of agents suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. In all cases the composition will preferably be sterile and must be fluid to the extent that easy syringeability exists. It will preferably be stable under the conditions of manufacture and storage and preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example,

water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it is preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating an agent of the pbresent invention (*e.g.,* a single-stranded nucleic acid) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the agent plus any additional desired ingredient from a previously sterile-filtered solution thereof.

When the agent is suitably protected, as described above, the agent can be orally administered, for example, with an inert diluent or an assimilable edible carrier. As used herein "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like. The use of such media and agents for pharmaceutically active substances is well-known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the therapeutic compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. "Dosage unit form", as used herein, refers to physically discrete units suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required

pharmaceutical carrier. The specification for the dosage unit forms of the present invention are dictated by, and directly dependent on, (a) the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

In addition, the agents of the present invention described herein can be administered using nanoparticle-based composition and delivery methods well-known to the skilled artisan. For example, nanoparticle-based delivery for improved nucleic acid (*e.g.,* small RNAs) therapeutics are well-known in the art (*Expert Opinion on Biological Therapy* 7:1811-1822).

Exemplification

This invention is further illustrated by the following examples, which should not be construed as limiting.

Example 1: Materials and Methods for Examples 2-6 and 14-17

Reagents

Biotinylated and unmodified RNA probes were purchased from Integrated DNA Technologies. Full-length, recombinant AR protein containing an N-terminus DDDK tag was purchased from Abcam (ab82609). N-terminal recombinant AR protein containing an N-terminal 6x HIS tag was purchased from RayBiotech (RB-14-0003P). Steric-blocking 2'-FANA modified oligos were gifts from AUM LifeTech. The plasmid expressing full-length *SLNCR1* was previously described (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Site-directed mutagenesis was used to obtain all *SLNCR1* mutant plasmids described herein, using oligo sequences listed in Table 4.

RNA electrophoretic mobility shift assays

REMSAs were performed using Thermo Fisher Scientific LightShift Chemiluminescent RNA EMSA (REMSA) Kit, according to manufacturer's instructions. Briefly, 20 µl binding reactions were assembled in low-adhesion tubes in 1X binding buffer (10mM HEPES pH 7.3, 20 mM KCl, 1 mM $MgCl_2$, 1 mM DTT), with 2 µg of yeast tRNA, the indicated amount of either recombinant full-length or N-terminal recombinant protein, 0.5 nM final concentration of the biotinylated RNA probe, and 10 µM of unlabeled competitor RNA (if applicable). Reactions were incubated at room temperature for 20 minutes, at which time 5 µl of loading dye was added, and 20 µl was electrophoresed on Bio-Rad's 5% Mini-PROTEAN® TBE Gel, 10 well, 30 µl (Cat number #4565013). RNA

and protein/RNA complexes were transferred to GE Healthcare Amersham Hybond –N+ Membrane in 0.5x TBE at 400 mA for 30 minutes in 0.5X TBE on Bio-Rad's Trans Blot Turbo Transfer System. Detection was performed as described, using Bio-Rad's ChemiDoc™ XRS+ System. MEME analysis (at World Wide Web address of www.meme-suite.org) was performed using the normal motif discovery mode, searching for any number of motif repetitions using 0-order background model of sequences within the input sequences WT-41, WT-28, WT-20, WT-17, MUT R, MUT L, MUT PT, MUT I, HOXA11-AS1.

Plasmid construction

The plasmid expressing full-length *SLNCR1* was previously described (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Site-directed mutagenesis was used to obtain all *SLNCR1* mutant plasmids described here, using oligo sequences listed in Table 4.

Table 4. Oligos used in this study

Sequence	Name	Type
CT***TC***CCACCCTGGTCTTCTCCTGTAA	*SLNCR1*$^{\text{AR MUT 1}}$ Forward	SDM
GG***GA***AGGGAAAAATACCTCCAGCTTGGC	*SLNCR1*$^{\text{AR MUT 1}}$ Reverse	SDM
T***AG***TCTC***AG***GTAACGTGTGGCCGCCTTTTC	*SLNCR1*$^{\text{AR MUT 2}}$ Forward	SDM
C***CT***GAGA***CT***ACCAGGGTGGAGAGGGAAAAATACC	*SLNCR1*$^{\text{AR MUT 2}}$ Reverse	SDM
C***CT***GAGA***CT***ACCAGGGTGG***GA***AGGGAAAAATACC	*SLNCR1*$^{\text{AR MUT 1 and 2}}$ Forward	SDM
CT***TC***CCACCCTGGT***AG***TCTC***AG***GTAA	*SLNCR1*$^{\text{AR MUT 1 and 2}}$ Reverse	SDM
GAGAACGTGGTGGAATCAGA	*SLNCR* Forward	qPCR
TCCCATCCTCTTTCTTGTCC	*SLNCR* Reverse	qPCR
CGAACTTTGACAGCGACAAG	*MMP9* Forward	qPCR
CACTGAGGAATGATCTAAGCCC	*MMP9* Reverse	qPCR
GAAGGTGAAGGTCGGAGT	*GAPDH* Forward	qPCR
GAAGATGGTGATGGGATTTC	*GAPDH* Reverse	qPCR
CTTTAGAGGCGCTGACATCC	*HOXA11AS-203* Forward	qPCR
AGAAATGGAACTCGGACTTGG	*HOXA11AS-203* Reverse	qPCR

* SDM = site-directed mutagenesis primers. Mutations from wild-type *SLNCR1* are highlighted in bolded font. The *SLNCR1*$^{\text{AR MUT 1 and 2}}$ expressing plasmids was generated through PCR amplification of *SLNCR1*$^{\text{AR MUT 2}}$ using the indicated plasmids.

Cell Culture

A375 cells were purchased from ATCC. WM1976 cells were from the collection of the Wistar Institute (Philadelphia, PA). Cells were were cultured as adherent cells in DMEM (Dulbecco's modified eagle medium, Invitrogen) without glutamine supplemented with 10% fetal bovine serum (FBS). Lipofectamine® 2000 (Life Technologies) was used for all plasmid transfections.

Surface Plasmon Resonance

SPR experiments were performed on a Biacore 3000. Full length AR protein (Abcam) was dialyzed against 10 mM NaOAc pH 5 and subsequently coupled to a CM5 chip (GE) using EDC/NHS coupling. The system was equilibrated to running buffer (10mM HEPES pH 7.3, 20 mM KCl, 1 mM $MgCl_2$, 1 mM DTT) and RNA (IDT) was subsequently injected (30 uL/min flow rate, one minute injection followed by 5-15 minutes dissociation).

Denatured control RNA SHAPE probing

WM1976 cells were grown in 6-well plates (2 wells per experiment) to ~80% confluency. Media was aspirated, cells were washed once in PBS, and total RNA was extracted using 1 mL TRIzol reagent (Thermo Fisher) per well. Total RNA (15 µL) was combined with 5 µL of 10x denaturing buffer [500 mM HEPES pH 8, 40 mM EDTA] and 25 µL of formamide, and the mixture was incubated at 95 °C for 1 minute. 5 µL of 10x SHAPE reagent [250 mM 5-nitroisatoic anhydride (5NIA)] was added to the denatured RNA and incubation at 95 °C continued for 1 min. Denatured modified RNA was purified using a 1.8x ratio of Agencourt RNA Clean XP beads (Beckman Coulter) and eluted in 88 µL of nuclease-free water.

In-cell SHAPE probing

WM1976 cells were grown in 6-well plates (4 wells per experiment) to ~80% confluency. Cells were washed once in PBS before adding to each well 900 µL of PBS. To two wells, 100 µL of 10x SHAPE reagent [250 mM 5-nitroisatoic anhydride (5NIA)] was added while 100 µL of neat DMSO were added to each of the remaining two wells. Plates were mixed concurrently with reagent addition and then incubated at 37 °C for 10 minutes. Media was aspirated, cells were washed once in PBS, and total RNA was extracted using 1 mL TRIzol reagent (Thermo Fisher) per well. Resulting pellets were resuspended in 88 µL of water per 2 wells.

In-cell DMS probing

WM1976 cells were grown in 6-well plates (4 wells per experiment) to ~80% confluency. Cells were washed once in PBS before adding to each well 900 µL of DMS Folding Buffer [300 mM Bicine pH 8, 100 mM NaCl, 5 mM $MgCl_2$]. To two wells, 100 µL of 10x DMS reagent [1:5 dimethyl sulfate (DMS): ethanol] was added while 100 µL of neat ethanol were added to each of the remaining two wells. Plates were mixed concurrently with reagent addition and then incubated at 37 °C for 6 minutes. DMS was quenched with 200 µL of beta-mercaptoethanol and cells were placed on ice for 5 minutes.

Excess buffer was removed, cells were washed once in PBS, and total RNA was extracted using 1 mL TRIzol reagent (Thermo Fisher) per well. Resulting pellets were resuspended in 88 µL of water per two wells.

Cell-Free RNA extraction and protein digestion

WM1976 cells were grown in two 10 cm dishes to ~80% confluency. Both plates were washed once in PBS before scraping and lysis in 2.5 mL of ice-cold cytoplasmic lysis buffer [40 mM Tris pH 8, 175 mM NaCl, 6 mM $MgCl_2$, 1 mM $CaCl_2$, 256 mM Sucrose, 0.5% Triton-X 100, 0.5 Units/µL RNasin (Promega), 0.45 Units/µl DNase I (Roche)]. Cells were lysed for 5 minutes on ice with intermittent mixing. Cell nuclei were pelleted at 3000 x g for 5 minutes at 4 °C (nuclear fraction), and the resulting supernatant (cytoplasmic fraction) was transferred to a new tube. A volume of 2.5 mL of proteinase K buffer [40 mM Tris pH 8, 200 mM NaCl, 1.5% Sodium Dodecyl Sulfate, and 0.5 mg/mL Proteinase K] was added to the nuclear pellets. The supernatant (cytoplasmic fraction) volume was increased to 5 mL to include a final concentration of 200 mM NaCl, 1.5% Sodium Dodecyl Sulfate, and 0.5 mg/mL Proteinase K (Thermo Fisher). Proteins were digested for 45 minutes at 23 °C with intermittent mixing.

RNA separation and buffer exchange

Nucleic acids were extracted twice with 1 volume of Phenol Chloroform Isoamyl Alcohol (25:24:1) that was pre-equilibrated with either 1.1x SHAPE Folding Buffer [110 mM HEPES pH 8, 110 mM NaCl, 5.5 mM $MgCl_2$] or 1.1x DMS Folding Buffer [330 mM Bicine pH 8, 110 mM NaCl, 5.5 mM $MgCl_2$]. Excess Phenol was removed through two subsequent 1 volume chloroform extractions. The final aqueous layer was buffer exchanged into 1.1x SHAPE Folding Buffer or 1.1x DMS Folding Buffer using PD-10 Desalting Columns (GE Healthcare Life Sciences). The resulting RNA solution (3.5 mL nuclear/7 mL cytoplasmic) was incubated at 37 °C for 20 minutes before being split into two equal volumes for control and probe treatment samples.

5NIA SHAPE probing of extracted RNA

A $1/10^{th}$ volume of 10x SHAPE reagent [250 mM 5-nitroisatoic anhydride (5NIA)] in DMSO was added to one sample of RNA while neat DMSO was added to the other. Samples were incubated at 37 °C for 10 minutes.

DMS probing of extracted RNA

A 1/10 volume of 10x DMS Solution [1:5 Dimethyl Sulfate (DMS):Ethanol] was added to one sample of RNA while neat ethanol was added to the other. Samples were

incubated at 37 °C for 6 minutes. DMS was quenched with 1/5 volume of beta-mercaptoethanol and immediately placed on ice for 5 minutes.

Precipitation of probe-reacted RNA

Cell-free RNA was precipitated with 1/10 volume of 2 M NH_4OAc and 1 volume of isopropanol. RNA was pelleted at 10,000 x g for 10 minutes at 4 °C. After 1 wash in 75% ethanol, the resulting pellet was dried and then resuspended in 88 µL of water.

DNase Treatment of cell-derived RNAs

To 88 µL of in-cell or cell-free RNA samples, 10 µL of 10x TURBO DNase buffer and 4 Units of TURBO DNase (Thermo Fisher) were added and the mixture was incubated at 37 °C for 1 hour. Following this incubation, 2 more Units of TURBO DNase were added and incubation continued at 37 °C for another 1 hour. RNA was purified using a 1.8x ratio of Agencourt RNAClean XP magnetic beads (Beckman Coulter) and eluted into 20-30 µL of nuclease-free water.

SLNCR MaP

From each sample of RNA from WM1976 in-cell and cell-free probing experiments, 1-3 µg were subjected to mutational profiling (MaP) reverse transcription (Siegfried, N.A., *et al.,* Nature Methods, 2014. 11: p. 959-965; Smola, M.J., *et al.,* Nat Protoc, 2015. 10: p. 1643-1669) using a primer specific to *SLNCR*. The cDNA generated was buffer exchanged over Illustra microspin G-50 columns (GE Healthcare). Output cDNA (5 µL) was used as a template for 50 µL PCR reactions (Q5 Hot-start polymerase, NEB) with primers made to amplify nt 403-780 of *SLNCR1* and add adapter sequences [1x Q5 reaction buffer, 250 nM each primer, 200 µM dNTPs, 3% DMSO, 0.02 Units/µL Q5 Hot-start polymerase]. PCR proceeded in a touchdown format: 98 °C for 2 minutes, 20 cycles of [98 °C for 10 s , 68 °C (decreasing by 1 °C each cycle until reaching 63 °C) for 30 s , 72 °C 30 s], and 72 °C for 2 min. Step 1 PCR products were purified using a 0.8x ratio of Agencourt AMPure XP beads (Beckman Coulter) and eluted in 20 µL of nuclease-free water. Purified PCR products (3 ng) were used as a template in 50 µL of PCR meant to add multiplex indices and remaining sequence necessary for Illumina sequencing [1xQ5 reaction buffer, 500 nM each index primer, 200 µM dNTPs, 3% DMSO, 0.02 Units/µL Q5 Hot-start polymerase]. Step 2 PCR proceeded as follows: 98 °C for 2 minutes, 10 cycles of [98 °C for 10 s , 66 °C for 30 s , 72 °C 20 s], and 72 °C for 2 min. Step 2 PCR products were purified using a 0.8x ratio of Agencourt AMPure XP beads (Beckman Coulter) and eluted in 20 µL of nuclease-free water.

SLNCR Conserved Region RT primer: 5′-GGATCAGTCCTTCCCATCC

SLNCR step 1 amp F: 5′-

GACTGGAGTTCAGACGTGTGCTCTTCCGATCTNNNNNACCTCCGCGAGTCTGG

SLNCR step 1 amp R: 5′-

CCCTACACGACGCTCTTCCGATCTNNNNNGGATCAGTCCTTCCCATCC

Truseq LT step 2 with index F: 5′-CAAGCAGAAGACGGCATACGAG-(index)$_8$-GT**GACTGGAGTTCAGAC**

Truseq LT Universal Adapter R: 5′-

AATGATACGGCGACCACCGAGATCTACACTCTTT**CCCTACACGACGCTCTTCC GATCT**

U1 snRNA MaP

The procedure for U1 snRNA MaP RT was similar to that of *SLNCR* MaP with minor modifications: (1) U1-specific primers were used for RT and step 1 PCR, (2) During step 1 PCR, the touchdown protocol began with an annealing temperature of 72 °C and only decreased to 64 °C, and (3) Step 1 PCR included 500 nM of each primer, no DMSO, and only 25 µL of total volume.

U1 RT primer: 5′-CAGGGGAAAGCGCGAA

U1 step 1 F: 5′-

GACTGGAGTTCAGACGTGTGCTCTTCCGATCTNNNNNATACTTACCTGGCA

U1 step 1 R: 5′-

CCCTACACGACGCTCTTCCGATCTNNNNNCAGGGGAAAGCGCGAA

Sequencing and profile generation

Purified *SLNCR* amplicons were pooled and sequenced on an Illumina Miseq instrument, outputting 2 x 300 paired end datasets. For U1 libraries, 2x 150 paired end datasets were generated instead. Reverse transcription of *SLNCR* yielded three products, corresponding to 3 alternatively spliced forms of *SLNCR* (*SLNCR1*: 2257 nucleotides, *SLNCR2*: 2522 nucleotides, newly observed isoform *SLNCR4*: 2160 nucleotides). Data from these isoforms were separated before alignment by fragment lengths after merging paired reads. SLNCR1-specific merged reads were then aligned to the *SLNCR1*/LINC00673 sequence (NCBI Reference NR_036488.1) using the ShapeMapper2 software (Busan, S., and K.M. Weeks, RNA, 2018. 24(2): p. 143-148; Smola, M.J., *et al.*, Nat Protoc, 2015. 10: p. 1643-1669) with the command shapemapper --target [TARGET].fa --modified --U [MERGED-TREATED-READS].fastq --untreated --U [MERGED-

UNTREATED-READS].fastq --denatured --U [MERGED-DENATURED-READS].fastq. When aligning DMS reads, the denatured control was excluded. U1 reads were similarly aligned to the U1 snRNA sequence (NCBI Reference NR_004430.2).

Discovery of in-cell SHAPE protections with deltaSHAPE

In-cell SHAPE and DMS protection sites were identified through comparison of in-cell and cell-free reactivities using the deltaSHAPE program with default settings (Smola, M.J., *et al.,* Biochemistry, 2015. 54: p. 6867-6875; Smola, M.J., *et al.,* Proc. Nat. Acad. of Sci. of the U. S. A., 2016. 113: p. 10322-10327). In-cell data were scaled such that the 95th percentile reactivity matched the average of cell-free 95th percentile reactivities. Significant nucleotide protections were identified in both nuclear and cytoplasmic fractions with the criteria of being centered in window of 5 nucleotides that contains 3 nucleotides with positive smoothed deltaSHAPE values (cell-free minus in-cell), positive Z-factors, and Z-scores above 1. Additional regions with smoothed deltaSHAPE values above 1 and Z-factors above 0.5 were also considered to account for skewing of Z-score by highly reactive sites.

RNA structure modeling with SuperFold

Base-pairing probabilities, Shannon entropy, and arcplot base-pairing projections were generated by the SuperFold analysis pipeline (Smola, M.J., *et al.,* Nat Protoc, 2015. 10: p. 1643-1669). For FIG. 4F-4H, *SLNCR1*$^{403-780}$ data were scaled to the U1 normalization factor created by the boxplot approach (Hajdin, C.E., *et al.*, Proc. Nat. Acad. of Sci. of the U. S. A., 2013. 110: p. 5498-5503), where reactivities above the larger of the 90th percentile and 1.5 x the interquartile range are first removed as outliers and the top 10% of remaining reactivities are averaged (the normalization factor). The original *SLNCR1* data were divided by this U1 normalization factor to obtain U1-scaled reactivity profiles. Low SHAPE, low entropy regions were identified by two methods: [1] as nucleotides where the 50 nucleotide window-median SHAPE and entropy values fall below 0.4 and 0.03, respectively (FIG. 4F-4H), and [2] nucleotides where the 50 nucleotide window-median SHAPE and entropy values fall below the global medians (FIG. 4M-4O). Regions separated by 5 or fewer nucleotides were combined and only regions spanning at least 30 nucleotides were retained before expanding to include overlapping base-pair arcs. RNA secondary structure representations of *SLNCR*1 were generated from ShapeMapper and SuperFold outputs using VARNA (Darty, K., *et al.*, Bioinformatics, 2009. 25: p. 1974-1975).

Invasion Assays

A375 cells were seeded at 25 x 10^4 cells in a 6-well plate and transfected with 2,500ng of the indicated plasmid 24 hours later. For assays using FANA-modified oligos, media was changed 7-8 hours post-transfection to media containing 1 μM final concentration of the indicated oligo. Approximately 28 hours post-transfection, 2.5 x 10^4 cells in serum-free media were plated in either BD BioCoat™ matrigel inserts or uncoated control inserts (Corning), placed into DMEM with 30% FBS (fetal bovine serum), and incubated for 16 hours. Cells that did not migrate or invade were removed using a cotton tipped swap, chambers were rinsed twice with PBS, and stained using Fisher HealthCare™ PROTOCOL™ Hema 3™ Fixative and Solutions. Cells were imaged on 20x magnification in 8 fields of view for 3 independent replicates. All statistical analyses were performed using GraphPad Prism version 7.01 for Windows (GraphPad Software, La Jolla California USA).

RNA extraction and quantification

RNA was isolated using Qiagen RNeasy® Mini Kit and treated with DNase. cDNA was generated using Bio-Rad's iScript™ cDNA synthesis kit and quantified as previously described (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). For tissue specific expression analysis, cDNA was generated from Human Total RNA Master Panel II (Clontech). *AR* mRNA expression was taken from the Genotype-Tissue Expression (GTEx) Project was supported by the Common Fund of the Office of the Director of the National Institutes of Health, and by NCI, NHGRI, NHLBI, NIDA, NIMH, and NINDS (Consortium, G.T., Science, 2015. 348(6235): p. 648-60). The GTEx data used for the analyses described in this manuscript were obtained from The Human Protein Atlas available at World Wide Web address of www.proteinatlas.org (Uhlen, M., *et al.*, Science, 2015. 347(6220): p. 1260419).

Example 2: The N-terminal region of AR binds to single-stranded RNA in a sequence-specific manner

Previously, RNA immunoprecipitation assays were used to identify an approximately 100 nucleotide (nt) region of *SLNCR1* required for interaction with AR (nts 568-673) (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). To further characterize the interaction of AR with *SLNCR1*, RNA electrophoretic mobility shift assays (REMSA) were used. Increasing concentration of the full-length AR protein significantly retards the migration of a 41 nt single-stranded biotinylated RNA probe corresponding to wild-type

SLNCR1 nucleotides 597-637 (WT-41), indicating that AR binds this RNA sequence, and that that this RNA sequence is sufficient for AR binding (FIG. 1A-1B). At higher AR concentrations (>200 nM), a second shift was observed, possibly resulting from AR protein dimerization or binding of multiple proteins on a single RNA probe.

AR is comprised of discreet protein domains, including a C-terminal ligand binding domain, a flexible hinge region, a DNA-binding domain, and an NTD required for interactions with many protein and RNA co-factors, including the lncRNAs *SRA1* and *PCGEM1* (FIG. 1A) (Lanz, R.B., *et al.*, Cell, 1999. 97: p. 17-27; Yang, L., *et al.*, Nature, 2013. 500(7464): p. 598-602). The lncRNA *PCGEM1* binds to the N-terminal regulatory region of AR (Yang, L., *et al.*, Nature, 2013. 500(7464): p. 598-602). To test if the *SLNCR1* sequence WT-41 also binds to the N-terminal region of AR, REMSA using a truncated version of AR (amino acids 2-566), spanning the N-terminal region (FIG. 2A) were repeated. Indeed, the truncated version of AR (amino acids 2-566) spanning AR NTD also binds and slows migration of WT-41, indicating that *SLNCR1* binds to and interacts with the N-terminus of AR (FIG. 1A and FIG. 1C). Even at high concentrations, the N-terminal AR does not result in a secondary downward shift of the RNA probe as is observed with full-length AR, possible due to the inability of the truncated protein to dimerize. Thus, the N-terminal protein was used for the majority of the subsequent experiments.

RNA-binding proteins may bind RNA in a sequence- and/or structure-specific manner. Since the 5' end of WT-41 is highly predicted to form a stable stem-loop structure, while the 3' end is likely unstructured, whether AR binds to shorter sequence *SLNCR1* fragments WT-28 and WT-20 was tested (FIG. 1A). These shorter UC-rich sequences are unlikely to form any stable secondary structures. N-terminal AR significantly reduces migration of both WT-28 and WT-20, indicating that AR binds to single-stranded pyrimidine-rich RNAs (FIG. 1C). Thus, REMSAs revealed that AR NTD also binds shorter UC-rich *SLNCR1* sequences WT-28 and WT-20 (FIG. 1C). Addition of unlabeled probes corresponding to WT-41 successfully outcompetes binding of labeled WT-41, WT-28, or WT-20 to either full-length or N-terminal AR, confirming that that the observed mobility shifts result from specific RNA binding (FIG. 2B, FIG. 2C, and FIG. 4C). Combined, these data show that the AR NTD is sufficient for binding to short sequences of pyrimidine-rich RNA.

To investigate if AR binds RNA in a sequence specific-manner, REMSA was used to test the effects of various mutations of WT-28 on AR binding. Mutations in either the

left, 5' end of WT-28 (MUT L, containing 3 base changes), or the right, 3' end of the RNA (MUT R, containing 4 base changes), do not abolish AR-binding (FIG. 3A and FIG. 3B). A slightly altered migration pattern of MUT L was noted, however, indicating modified AR binding compared to WT-28 or MUT R. Interestingly, combining MUT L and MUT R mutations (MUT full-length, or MUT FL) completely abolishes AR binding. This result indicates that either (i) AR binds to pyrimidine-rich RNA in a non-sequence specific manner, and combining MUT L and MUT R (consisting of pyrimidine – to – purine mutations) into a single sequence drops the total pyrimidine percentage below the threshold required for AR binding, or (ii) WT-28 contains two AR binding motifs, only one of which is mutated in MUT L and MUT R. Inconsistent with pyrimidine-rich sequence binding, AR does not bind 20 nts probes consisting of UC, UUUC or CCCU repeats (REP-UC, REP-UUUC, or REP-CCCU, respectively, FIG. 4A and FIG. 4B). Consistent with sequence-specific binding of two AR-binding motifs, a UCUCCU/A motif is present on both the 5' and 3' end of WT-28 (FIG. 3A). Thus, a series of experiments was designed to test if AR specifically recognized the UCUCCU/A motif. First, a probe containing 7 pyrimidine mutations (U to C or C to U) across the total length of WT-28 was generated. In addition, this probe was designed so that while the endogenous motifs were mutated, a single, non-endogenous motif (UCUCCU) just upstream but partially overlapping with motif 1 (MUT shifted motif, MUT PT) was generated. MUT PT's migration pattern upon AR binding is similar to MUT L, which contains only one UCUCCU motif, indicateing that AR binding to both probes is comparably altered compared to WT-28. Second, mutation of the sequence internal to these two motifs (MUT internal, MUT I) does not alter AR binding (FIG. 3A and 3B). Third, probes corresponding to the *SLNCR1* sequence shifted slightly upstream of WT-28, and importantly containing only motif UCUCCA motif (WT-17 and WT-20), are bound by AR (FIG. 3C and 3E). Finally, mutating 2 nts of this motif in the absence of any additional motifs, abolished AR binding (WT-20 versus MUT-20, FIG. 3C and 3E), thus confirming that AR binding requires at least one intact UCUCCU/A motif. It was determined that AR does not bind 18 nt probes containing two repeats of these motifs (either UCUCCU or UCUCCA, FIG. 4A), indicateing that AR is unable to bind to two consecutive motifs. Consistent with previous data, introduction of non-endogenous nucleotides at the 3' end of WT-17 to induce a stable stem-loop structure abolished binding (FIGS. 3C, 3D and 3E), confirming specific binding to single-stranded RNAs.

Collectively, these data reveal that AR binds to single-stranded, pyrimidine-rich RNA containing at least one UCUCCU/A motif.

RNA-binding proteins may bind RNA in a sequence- and/or structure-specific manner. A series of mutational analyses was used to probe the potential sequence requirements of the AR/RNA interaction, identifying a set of wild-type and mutated RNAs that retain the ability to bind AR NTD (FIG. 3A-3E and 3G). Motif enrichment analysis (multiple EM for motif elicitation, MEME) of this set of tested RNAs identified a significantly enriched (E-value = 1.3×10^{-13}) 9 nt motif CYUYUCCWS (Y = pyrimidine [C or U], W = weak [A or U] and S = strong [C or G]) required for AR-RNA binding, indicating that AR NTD binds to RNA in a sequence-specific manner (FIG. 3G) (Bailey, T.L., *et al.*, Nucleic Acids Research, 2009. 37: p. W202-208). *SLNCR1* contains 2 of these motifs (nts 612-620 and nts 627-635, motif 1 and motif 2), located in close proximity to each other. Both motifs are contained within WT-41 and WT-28 (FIG. 2A and 3G).

Several lines of evidence indicate that only one motif is required for interaction with AR. First, WT-20 contains only one motif and is still bound by AR NTD (FIG. 1C). Second, mutations in either motif 1 (MUT L [left], containing 3 base changes), or motif 2 of WT-28 (MUT R [right], containing 4 base changes) do not abolish AR-binding when the other motif is present (FIG. 3B and 3C). The altered migration pattern of MUT L, however, indicates that AR engages each motif in a unique way. Third, combining MUT L and MUT R mutations (MUT full-length, or MUT FL) completely abolished AR binding (FIG. 3A-3B). Fourth, and perhaps most importantly, mutating 2 nts of the single motif in WT-20 abolished AR binding (WT-20 versus MUT-20, FIG. 3B and 3D). Fifth, truncation of WT-20 to a 17 nt probe ending at the 3' end of motif 1 (WT-17) retains AR binding (FIG. 3D). Together, these data show that a single CYUYUCCWS motif is sufficient for specific recognition by AR NTD.

Considering that the CYUYUCCWS motif identified above is a short pyrimidine-rich sequence, it was determined if pyrimidine-rich sequences that do not contain this motif also confer AR binding. AR does not bind 20 nt probes consisting of UC, UUUC or CCCU repeats (REP-UC, REP-UUUC, or REP-CCCU, respectively) or to 18 nt probes containing two sequential repeats of a UCUCCA motif (FIG. 4A-4B). Further, *SLNCR1* contains a near consensus motif approximately 100 nts upstream (nts 547-555, CUUCUCCAU) of motifs 1 and 2 that falls outside of the $SLNCR1^{568\text{-}637}$ region previously identified to be required for AR (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). REMSA confirms

that AR NTD does not bind a 15-nt probe corresponding to this upstream motif, indicating that a U in position 9 is not accepted. Mutations between motifs 1 and 2 that do not alter either CYUYUCCWS motif do not affect AR binding (FIG. 3A-3B). A probe containing 7 pyrimidine transitions (U to C or C to U) across WT-28 (MUT-pyrimidine transitions, or MUT PT) that disrupt both of the original motifs 1 and 2 but introduce a new CYUYUCCWS consensus motif (CCUUUCCUC) retains AR binding (FIG. 3A-3B). These data further indicate that AR specifically binds the CYUYUCCWS motif.

To test whether RNA structure interferes with AR binding, AR-RNA binding was compared in the presence or absence of secondary structure (FIG. 1A and 3D-3F). Introduction of non-endogenous nucleotides at the 5′ end of WT-17 that induce a stable stem-loop structure encompassing 6 nts of motif 1 abolished AR NTD binding (FIG. 3D-3E). Surface plasmon resonance (SPR) using full-length protein confirms that AR has a ~3 fold higher affinity for WT-20 (K_D = 251 nM), which contains an unstructured motif 1 alone, than WT-41 (K_D = 741 nM), which includes motif 1 in a stem-loop and an unstructured motif 2 (FIG. 3F). Together, these data reveal that AR NTD binds pyrimidine-rich RNA containing at least one loosely-structured CYUYUCCWS motif.

In agreement with previous work indicating that *SLNCR1*- and AR-mediated phenotypes occur in the absence of androgens (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37), data presented herein indicate that an AR monomer can bind to *SLNCR1* in the absence of protein dimerization. Specifically, (1) AR binds RNA independently of androgens *in vitro* (FIG. 1B); (2) AR NTD, which is incapable of forming head-to-tail dimers, binds RNA *in vitro* (FIG. 3B); and (3) only one AR binding motif is required for AR/RNA interaction (FIG. 3A-3G). Thus, it was considered if AR has differential affinity to motif 1 versus motif 2. Although WT-41 contains both AR binding motifs, only motif 2 is likely accessible for AR binding, as motif 1 forms a highly-stable stem-loop structure occluded from AR binding (FIG. 1A). Considering that AR displayed a ~3-fold higher affinity for WT-20 (containing only motif 1: CCUCUCCAC) compared to WT-41 (where only motif 2 is accessible: CUUCUCCUG), AR has a higher affinity for motif 1 compared to motif 2 (FIG. 3F).

Example 3: *SLNCR1*'s AR binding motif is required for *SLNCR1*- and AR-mediated melanoma invasion

To test if the *in vitro* REMSA results recapitulate AR-*SLNCR1* interactions in the cell, whether mutations in the AR binding motif identified above affect known AR-

SLNCR1-mediated phenotypic changes was investigated. Ectopic expression of *SLNCR1* significantly increases the invasiveness, as quantified by matrigel invasion assays, of A375 melanoma cells in an AR-dependent manner through transcriptional upregulation of the matrix metalloproteinase MMP9 [3]. Moreover, ectopic expression of a highly conserved, ~300 nt sequence of *SLNCR1* containing the AR-binding sequence is sufficient to induce increased melanoma invasion. Thus, A375 invasion was quantified after expression of wild-type, full-length *SLNCR1*, *SLNCR1*^{cons}, or *SLNCR1* harboring site-directed mutations in the AR binding motif 1, motif 2, or both motif 1 and 2 (*SLNCR*$^{AR\ MUT\ 1}$, *SLNCR1*$^{AR\ MUT\ 2}$, or *SLNCR1*$^{AR\ MUT\ 1\ and\ 2}$, respectively). Consistent with our *in vitro* data, mutation of either motif 1 or motif 2 slightly negated *SLNCR1*'s ability to increase melanoma invasion, while mutation of both completely abolished *SLNCR1*-mediated invasion (FIGs. 5A and 5B). Importantly, and in agreement with results from invasion assays, although all *SLNCR1* mutants are expressed at similar levels, *MMP9* levels are significantly increased only with expression of either full-length or the conserved sequence of *SLNCR1* (FIG. 5C).

Example 4: Sequence based identification of novel AR-interacting lncRNA HOXA11-AS-203

Previously, a region of sequence similarity between multiple lncRNAs predicted or shown to bind to AR was identified, including *HOTAIR*, *SRA1*, and *PCGEM1*, that overlaps with the WT-28 *SLNCR1* sequence (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Of these lncRNAs, only *SRA1* contains an intact potential AR-binding motif (motif 2-UCUCCU). Indeed, AR does result in a slight, but reproducible, shift of the *SRA1* probe that is successfully competed away by unlabeled WT-41 probe (FIG. 6A and 7A), indicating that *SRA1* directly binds AR, though further work is required to confirm this interaction. In contrast, probes corresponding to the conserved region of *HOTAIR* or *PCGEM1*, which do not contain a UCUCCU/A motif, do not bind N-terminal AR in the REMSA assay (FIGs. 6A and 6B). The conditions used in the assay do not account for additional protein or RNA factors, nor do they enable mammalian-specific post-translational modifications of AR, that may be required for mediating these interactions *in vivo*. Indeed, the AR-*PCGEM1* interaction requires both protein- and AR-modifications, as discussed later. These results further confirm that, in a minimal *in vitro* system, AR requires the presence of at least one UCUCCU/A motif for RNA binding.

The ability to predict lncRNA binding partners, and more generally function, from sequence analysis alone remains largely uninvestigated. A region of sequence similarity between multiple lncRNAs predicted or shown to bind to AR, including *HOTAIR*, *SRA1*, and *PCGEM1*, that overlaps with the WT-28 *SLNCR1* sequence was previously identified (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Of these lncRNAs, only *SRA1* contains an intact potential AR-binding motif (CUUCUCCUG). Indeed, in REMSA, addition of AR results in a slight, but reproducible, shift of the *SRA1* probe that is successfully competed away by unlabeled WT-41 probe (FIG. 6A and 7A), indicating that *SRA1* directly binds AR.

In contrast, probes corresponding to the conserved region of *HOTAIR* or *PCGEM1*, which do not contain a CYUYUCCWS motif, do not bind AR NTD in REMSA assays (FIG. 6A-6B). The conditions used in REMSA assays do not account for additional protein or RNA factors, nor do they enable mammalian-specific post-translational modifications of AR, that may be required for mediating these interactions *in vivo*. Indeed, the AR-*PCGEM1* interaction requires both protein- and AR-modifications, as discussed later. These results further confirm that, in a minimal *in vitro* system, AR requires the presence of at least one CYUYUCCWS motif for RNA binding. Thus, nucleotide BLAST search (available on the World Wide Web at blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastSearch) was used to identify additional non-coding RNAs containing either a containing a consensus or near-consensus AR binding motif, corresponding to the sequences of WT-28 or WT-20. A 1,169 nt transcript expressed divergently from the HOXA11 gene, lncRNA HOXA11-AS-203 (Ensembl transcript ENST00000520395, gene ENSG00000240990), contains a region of high similarity to WT-20 (FIG. 6C and 6D). A probe corresponding to 23 nt of the HOXA11-AS-203 sequence is significantly shifted upon incubation with the N-terminal AR, indicating that the N-terminal region of AR directly binds to this sequence. Moreover, RT-qPCR profiling of a panel of human tissues reveals that this lncRNA isoform is expressed in AR-expressing tissues, including the prostate, uterus, and testis (FIG. 7B), indicating that this interaction may occur *in vivo*. HOXA11-AS-203 and AR are co-expressed in several human tissues, including the prostate, uterus, and testis, indicating that this interaction occurs *in vivo* (FIG. 7B). These data demonstrate that the AR-binding RNA motif identified herein may be predictive of the ability of a lncRNA to bind to AR; these data indicate that perturbing AR binding to lncRNAs can block AR-dependent functions of

lncRNAs in multiple tissues. These data demonstrate that the presence of the AR-binding RNA motif identified here may be predictive of a lncRNA's ability to bind to AR.

Example 5: Inhibiting the AR-*SLNCR1* interaction using 2'-FANA-modified oligonucleotides negates *SLNCR1*-mediated melanoma invasion

To develop candidate novel therapeutics inhibiting the *SLNCR1*- and AR-mediated invasion, and to assess the therapeutic potential of inhibiting the *SLNCR1*-AR interaction short (21-28 nucleotide) oligos were designed that are either (i) reverse complement or antisense to *SLNCR1*'s AR binding sequence, which bind to *SLNCR1* to generate double stranded RNA incapable of AR binding (ANTISENSE 1 and ANTISENSE 2), or (ii) mimics of the *SLNCR1* AR binding sequence, which bind directly to AR to preclude or inhibit *SLNCR* binding (MIMIC 1 and MIMIC 2, FIG. 9A). These oligonucleotides are composed of 2′-deoxy-2′-fluoro-D-arabinonucleic acid (2′-FANA) and unmodified DNA nucleotides specifically arranged to enhance intracellular stability of the oligonucleotide without eliciting RNase H mediated cleavage and therefore downregulation of *SLNCR1* (FIG. 10A) (Ferrari, N., *et al.*, Ann N Y Acad Sci, 2006. 1082: p. 91-102). Importantly, these probes are designed to block both CYUYUCCWS motifs present in *SLNCR1*. Both *SLNCR1*- and AR-binding FANA modified oligonucleotides are capable of sterically blocking the AR- *SLNCR1* interaction *in vitro* (FIG. 9B). Addition of ANTISENSE oligonucleotides upwardly shifts the biotinylated probe, confirming the formation of dsRNA. Gymnotic delivery (*i.e.* delivery of naked oligos independent of any agents) of 2′-deoxy-2′-fluoro-D-arabinonucleic acid (2′-FANA) modified oligos to A375 melanoma cells (FIG. 8) significantly reduces *SLNCR1*-mediated melanoma invasion, without affecting *SLNCR1* expression (FIGs. 9C and 10A). Consistently, while ectopic expression of *SLNCR1* significantly increases *MMP9* mRNA as previously shown, addition of the oligo blockers attenuates this increase (FIG. 10B). In the presence of MIMIC 2, a reproducible trend, though not significant, for increased *MMP9* levels was observed, indicating that this oligo does not block the *SLNCR1*-AR interaction as well in cells. MIMIC 1 and ANTISENSE 1 negate *SLNCR1*-mediated *MMP9* upregulation more efficiently than MIMIC 2 and ANTISENSE 2, which are truncated by 7 nts. Collectively, these data demonstrate that single-stranded AR- or *SLNCR1*-targeting oligonucleotides can be used to block the interaction of AR and *SLNCR1*, attenuating *SLNCR1*-mediated melanoma invasion.

Example 6: Minimal RNA sequence length required for AR binding

To determine the minimal RNA sequence length required for AR N-terminal domain binding, REMSA was used to check for AR binding to shorter biotinylated probes corresponding to wild-type *SLNCR*. AR binds to 11 nucleotide long sequence containing a UCUCCA motif (WT-11, FIG. 11). AR does not bind to a 10 nucleotide sequence containing an UCUCCU sequence (WT-10). Thus, AR requires at least 11 nucleotides for efficient RNA binding.

Example 7: Materials and Methods for Examples 8-12 and 18-19

Cell Culture

MSTCs (WM1976 (p53 wild-type) and WM858 ($BRAF^{V600E}$, $p53^{MUT}$)) are from the Wistar Institute collection, A375 ($BRAF^{V600E}$, p53 wild-type, $CDKN2A^{E61*}$) and SK-MEL-28 ($BRAF^{V600E}$, $EGFR^{P753S}$, $P53^{L145R}$) cells were purchased from ATCC. Unless otherwise indicated, cells were grown in DMEM (Invitrogen) without glutamine supplemented with 10% fetal bovine serum (FBS). All siRNAs were transfected using RNAiMAX® (Thermo Fisher). *AR* and *SLNCR* targeting siRNAs were used at 10 nM final concentration. *EGR1* targeting siRNA was used at 20 nM. Hormone-deprived cells were cultured in phenol-red free DMEM without glutamine (Invitrogen) with 5% charcoal-stripped FBS (Sigma-Aldrich). For knockdown and flutamide proliferation assays, cells were seeded at 0.4×10^4 cells/well in a 96-well plate. For assays using FANA-modified oligos (AUM Technologies), cells were seeded at 0.3×10^4 cells/well in a 96-well plate. Cells were treated with FANA-oligos, flutamide, or transfected with the indicated siRNAs 24 hours post seeding, and proliferation was measured using a 1:10 dilution of WST-1 proliferation reagent (Roche) at the indicated time points. Cells were incubated for one hour at 37°C, and absorbance at 450 nM was measured. For cell cycle analyses, cells were harvested and washed 72 hours post-transfection, fixed in cold 70% ethanol for 2 hours, and incubated in LifeTech PI/RNaseA solution for 30 minutes at 37 degrees. For analysis of apoptosis, cells were seeded at 30×10^4 cells/well in 6-well plate, harvested 72 hours post-transfection, and stained using Biolegends Pacific Blue™ Annexin V Apoptosis Kit with 7-AAD. Cells were analyzed on a Fortessa X-20 and populations were identified and quantified using FlowJo software. For luciferase assays, A375 cells were seeded in 96-well plates at 0.75×10^4 cells per well, transfected 24 hours later with the indicated siRNAs. Fifty micrograms of either wild-type or mutated *CDKN1A* reporter plasmid and 50 µg of a pCMV-renilla

luciferase control vector were transfected Lipofectamine® 2000 (Life Technologies) 24 hours post-transfection of siRNAs. Luciferase activity was measured another 24 hours later using Promega Dual-Glo® Luciferase Assay system. The *CDKN1A* reporter plasmid was generated by replacing the MMTV promoter in pGL4.36 vector (Promega) using Gibson Cloning (Gibson, D.G., *et al.,* Nature Methods, 2009. 6: p. 343-345). Sequences for all siRNAs and oligos used in this study can be found in Table 17. For transcription factor activation arrays, WM1976 cells were seeded in 6-well tissue culture treated dishes, transfected 24 hours later with either scramble or si-*SLNCR* (1) siRNA, and were harvested and fractionated using the Thermo Scientific NE-PER Nuclear and Cytoplasmic Extraction Kit, according to the manufacturer's instructions, 3 days after transfection. Ten micrograms of nuclear lysate was used directly as input into the Signosis TF Activation Profiling Plate Array I. For AR ChIP-seq, A375 cells were cultured in phenol-red-free DMEM without glutamine (Invitrogen), supplemented with 5% charcoal-stripped FBS, and transfected with the indicated plasmid 24 hr post-seeding. For EGR1 ChIP-seq, A375 cells were cultured in DMEM without glutamine (Invitrogen), supplemented with 10% FBS, and grown to ~80% confluency. Cells were crosslinked in 1% formaldehyde for 15 min 48 hr post-transfection, and the reaction was quenched by addition of 0.125 M glycine. ChIP-seq was performed by Active Motif.

Table 5: siRNA sequences

siEGR1 target sequence: CAGGACAATTGAAATTTGCTA

siSLNCR (1) target sequence: TTAGGTCAAATAGGATCTAAA

siSLNCR (2): AAAGACGTTTACACCGAGAAA

siAR (1): CAGGAATTCCTGTGCATGAAA

siAR (2): CACGGGAAGTTTAGAGAGCTA

siAR (3): CTGCTACTCTTCAGCATTATT

RNA immunoprecipitation and chromatin immunoprecipitation and sequencing.

AR and EGR1 RIP assays were performed as previously described with minor modifications (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). For EGR1 RIP, IgG or α-EGR1 antibody was added to A375 cell lysate at a final concentration of 0.5 µg and rotated at 4°C for 2 hours. Lysate was then incubated with Protein A Dynabeads® (Life Technologies) (25 µl slurry) for 1 hour at 4°C and samples were processed as described. Fold enrichment of SLNCR was calculated as the fold enrichment in the IgG or EGR1 IP

compared to input control after normalization to the indicated mRNA transcript (18S, GAPDH, ACTIN).

For AR ChIP-seq, A375 cells were cultured in phenol-red-free DMEM without glutamine (Invitrogen), supplemented with 5% charcoal-stripped FBS, and transfected with the indicated plasmid 24 hour post-seeding. For EGR1 ChIP-seq, A375 cells were cultured in DMEM without glutamine (Invitrogen), supplemented with 10% FBS, and grown to ~80% confluency. Cells were crosslinked in 1% formaldehyde for 15 min 48 hour post-transfection, and the reaction was quenched by addition of 0.125 M glycine. ChIP-seq was performed by Active Motif using Santa Cruz AR (H-280), or Cell Signaling EGR1 (44D5). After chromatin isolation and fractionation, 75-nt reads were generated by Illumina sequencing (using NextSeq 500), and were mapped to human reference genome (hg19) using the BWA algorithm with default settings. The 3' ends of aligned reads were extended in silico using Active Motif software to a length of 150-200 bp. Fragment density was determined based on the number of reads corresponding to 32-nucleotide genomic bins. Peak calling, to identify intervals with local enrichment in reads, was performed using MACS (Zhang, Y., *et al.,* Genome Biol, 2008. 9: p. R137). MACS default cutoff p-value is $1e^{-7}$ for narrow peaks and $1e^{-1}$ for broad peaks. Peak filtering was performed by removing false ChIP-Seq peaks as defined within the ENCODE blacklist. Active regions were defined by the start coordinate of the most upstream interval and the downstream coordinate of the most downstream interval. Active genes are defined as any active region present within 10,000 bps upstream or downstream of an annotated gene.

RNA-sequencing and analysis

Total RNA was isolated from WM1976 transfected with either scramble, si-SLNCR (1) or si-SLNCR (2) siRNAs, in duplicate, using Trizol. Sequencing cDNA libraries were prepared from 1ug of total RNA using the Illumina TruSeq RNA sample preparation kit (v2). Libraries were pooled and sequenced on the Illumina HiSeq 2500 platform. Normalized read counts (FPKM) were generated in Cufflinks v2.1.1 (available on the World Wide Web at cole-trapnell-lab.github.io/cufflinks/) by mapping onto the hg19 build of the human transcriptome (available on the World Wide Web at support.illumina.com/sequencing/sequencing_software/igenome.html). Raw FASTQ sequence was mapped using Bowtie (Langmead, B., et al., Genome Biol, 2009. 10(3): p. R25), and differentially expressed genes were identified using CuffDiff (available on the World Wide Web at cufflinks.cbcb.umd.edu/), comparing duplicate scramble controls

against duplicate conditions of both SLNCR-specific knockdowns. Values represented in the heatmaps were generated by CuffDiff comparison of duplicate scramble controls versus duplicates of only one siRNA duplicate. GeneOntology Enrichment Analysis was performed in MetaCore (Thompson Reuters), against a control background set of genes expressed in skin cells.

Gene expression of AR- and *SLNCR*-target genes was accessed using cBioPortal (Cerami, E., *et al.,* Cancer Discov, 2012. 2: p. 401-404; Gao, J., *et al.,* Sci Signal, 2013. 6: p. pl1). All statistics (including T-tests, ANOVAs, and correlations) were calculated using GraphPad Prism version 7.00 for Windows, GraphPad Software, La Jolla California USA (on the World Wide Web at www.graphpad.com). Bonferroni correction for multiple hypothesis testing was performed by defining the significance threshold as the critical p=0.05 divided by the total number of comparisons. BAM files from RNA-seq and ChIP-seq were visualized using the Integrated Genome Viewer (on the World Wide Web at broadinstitute.org/igv/) (Robinson, J.T., *et al.,* Nat Biotechnol, 2011. 29(1):24-6; Thorvaldsdottir, H., Robinson, J.T., and J.P. Mesirov, Brief Bioinform, 2013. 14(2):178-92).

Apoptosis assay

Cells were seeded at 30 x 10^4 cells/well in 6-well plate. Transfected with 10nM final or indicated siRNAs using RNAiMAX 24 post-seeding. 72 hours post-transfection, cells were prepped for FACs using Biolegends Pacific Blue™ Annexin V Apoptosis Kit with 7-AAD.

TF activation array

WM1976 cells were seeded in 6-well tissue culture treated dishes, transfected 24 hours later with either scramble or si-SLNCR (1) siRNAs, and 48 hours post transfections cells were harvested and fractionated using NE-PER fractionation kit. Approximately 10 µg of the nuclear fraction for input directly in Signosis' Transcription Factor Activation Array I. Alternatively, cells transfected with siRNA were harvested and fractionated using the Thermo Scientific NE-PER Nuclear and Cytoplasmic Extraction Kit, according to the manufacturer's instructions, 3 days after transfection. Ten micrograms of nuclear lysate was used directly as input into the Signosis TF Activation Profiling Plate Array I.

Cell cycle analysis

Fixed in cold 70% ethanol for 2 hours. Incubate in LifeTech PI/RNaseA solution for 30 minutes at 37 degrees. Ran on FACs machine Fortessa X-20, analyzed using FlowJo software.

Protein extraction and analysis

Unless otherwise indicated, lysate was prepared using M-PER Mammalian Protein Extraction Reagent (Thermo Scientific), according to manufacturer's instructions. Samples were separated on BioRad Any kD™ Mini-PROTEAN® TGX™ Precast Protein Gels and transferred to LF-PVDF using the mixed MW protocol on the BioRad Transblot Turbo. The following antibodies were used: Santa Cruz p53 (DO-1) sc-126 at 1:200, AR (M-20) sc-816 at 1:200, Cell Signaling P21 Waf1/Cip1 (12D1) at 1:1000, Cell Signaling Egr1 (44D5) at 1:1000, Cell Signaling S6 Ribosomal Protein (5G10) at 1:1000, and Cell Signaling GAPDH (14C10) at 1:5000. Santa Cruz AR (H-280) was used for AR ChIP-PCR.

72 hours post-transfection of the indicated cells with 10 nM of the indicated siRNAs, lysate was prepared using M-PER Mammalian Protein Extraction Reagent (Thermo Scientific), according to manufacturer's instructions. Samples were separated on BioRad Any kD™ Mini-PROTEAN® TGX™ Precast Protein Gels and transferred to LF-PVDF using the mixed MW protocol on the BioRad Transblot Turbo. The following antibodies were used: Santa Cruz p53 (DO-1) sc-126 at 1:200, AR (M-20) sc-816 at 1:200, Cell Signaling P21 Waf1/Cip1 (12D1) at 1:1000, Cell Signaling Egr1 (44D5) at 1:1000, Cell Signaling GAPDH (14C10) at 1:5000.

RNA electrophoretic mobility shift assays

REMSAs were performed using Thermo Fisher Scientific LightShift Chemiluminescent RNA EMSA (REMSA) Kit, according to manufacturer's instructions. Briefly, 20 µl binding reactions were assembled in low-adhesion tubes in 1X binding buffer (10mM HEPES pH 7.3, 20 mM KCl, 1 mM MgCl2, 1 mM DTT), with 2 µg of yeast tRNA, the indicated amount of recombinant EGR1 corresponding to amino acids 282-433 (Aviva Systems Biology, catalogue number OPCD02876), 0.5 nM final concentration of the biotinylated SLNCR1, and 10 µM of unlabeled SLNCR1 where indicated. Reactions were incubated at room temperature for 20 minutes, 5 µl of loading dye was added, and 20 µl was electrophoresed on Bio-Rad's 5% Mini-PROTEAN® TBE Gel, 10 well, 30 µl. RNA and protein/RNA complexes were transferred to GE Healthcare Amersham Hybond –N+ Membrane in 0.5x TBE at 400 mA for 30 minutes in 0.5X TBE on Bio-Rad's Trans Blot

Turbo Transfer System. Detection was performed according to LightShift REMSA kit, using Bio-Rad's ChemiDoc™ XRS+ System.

TCGA informatics and statistical analyses

GeneOntology Enrichment Analysis was performed in MetaCore (Thompson Reuters), against a control background set of genes expressed in skin cells. Gene expression of AR- and *SLNCR*-target genes, p21 protein levels, and p53 mutational status were accessed using cBioPortal (Cerami, E., *et al.,* Cancer Discov, 2012. 2: p. 401-404; Gao, J., *et al.,* Sci Signal, 2013. 6: p. pl1). SLNCR RNA expression values were derived from normalized read coverage across the SLNCR genomic range. Raw RNA-Seq data for cutaneous melanoma (SKCM) was downloaded from the NCI Genomic Data Commons (GDC). The RNA-Seq data was in the format of BAM files representing an alignment, using the STAR aligner, of raw reads to hg38. Human gene models were downloaded from RefSeq on November 3rd, 2017, and the SLNCR ranges were defined from the range of LINC00673. For each patient, the total number of reads aligning the SLNCR genomic region was obtained by parsing the output of samtools flagstat and SLNCR-specific counts were normalized by the total number of reads aligning to hg38. The expression values for non-SLNCR genes were obtained by downloading a results table from Xenabrowser (on the World Wide Web at https://toil.xenahubs.net/download/tcga_rsem_isoform_tpm.gz). TPM expression values were computed from a reanalysis of the TCGA dataset under the TOIL framework using RSEM. Hierarchical multiple regression analysis was performed using R v3.2.2, where the model estimates and p-values, based on the t-statistic, were calculated using the 'lm' function. *SLNCR* and *EGR1* mRNA expression values were log2 transformed to account for non-normal distributions. Expression of AR, p53 and p21 protein was accessed from Level 4 cross-batch normalized data in The Cancer Proteome Atlas (Li, J., *et al.,* Nature Methods, 2013. 10: p. 1046-1047). All continuous variables were converted to z-scores in order to improve interpretability of the model output. To determine the set of parameters present in the final model, standard reduction techniques were used, including iterative removal of the least significant parameter along with evaluation of the Akaike's information criterion (AIC) and ANOVA comparisons of model fit. P53-deficient melanomas were defined as (i) primary melanomas or metastases of known melanoma origin, (ii) patients with no prior treatment, and (iii) harboring nonfunctional p53 mutations, as defined by the TP53 database (p53.fr) (Leroy, B., *et al.,* Hum Mutat, 2014. 35: p. 756-765). Patients containing R248W or Y220C gain of function

p53 mutations were excluded based on reported regulation of p21 (Di Fiore, R., *et al.,* Bone, 2014. 60: p. 198-212; Song, H., Hollstein, M., and Y. Xu, Nature Cell Biol, 2007. 9: p. 573-580; Xu, J., *et al.,* Cell Death Dis, 2014. 5: p. e1108). Bonferroni correction for multiple hypothesis testing was performed by defining the significance threshold as the critical P-value (0.05) divided by the total number of comparisons. BAM files from RNA-seq and ChIP-seq were visualized using the Integrated Genome Viewer (on the World Wide Web at broadinstitute.org/igv/) (Robinson, J.T., *et al.,* Nat Biotechnol, 2011. 29(1):24-6; Thorvaldsdottir, H., Robinson, J.T., and J.P. Mesirov, Brief Bioinform, 2013. 14(2):178-92).

Statistics

T-tests, ANOVAs, and correlations were calculated using GraphPad Prism version 7.00 for Windows, GraphPad Software, La Jolla California USA (on the World Wide Web at www.graphpad.com). In proliferation assays error bars represent the mean ± SD of 3 technical replicates. Significance was calculated using the two-way analysis of variance (ANOVA), with the Dunnett test for multiple comparison testing. For binding enrichments, statistical significance was calculated using a either a Binomial test (two-sided) by comparing the observed versus expected probabilities under independence or using a Fisher Exact test of the co-bound targets, using GraphPad Prism software. In cell cycle assays, cell populations were analyzed using FlowJo software, and significance was calculated using GraphPad Prism software. Bars represent the average percent of total cells in the indicated stage of the cell cycle, and error bars represent SD from 3 independent replicates. RT-qPCR data is represented as the fold change compared to scramble control, normalized to GAPDH. Error bars represent standard deviations calculated from 3 reactions. Protein levels were quantified using ImageJ, and are presented as a fold change normalized to GAPDH levels. Bars represent mean ± SD from 3 independent biological replicates. Significance for RNA and protein quantification was calculated using the Student's t-test. Significance was calculated using a two-tailed Student's t-test. Transcription Factor Activation Array is represented by relative luminescence mean ± SD from 2 independent biological replicates.

Example 8: AR and *SLNCR* exhibit sex-specific differences in human melanomas

Previous work revealed that *SLNCR* directly binds AR, recruiting it to specific genomic locations to modulate AR transcriptional activity (Schmidt, K., *et al.*, Cell Rep,

2016. 15(9): p. 2025-37). Since AR has been implicated as a potential oncogene in melanoma, and *SLNCR* (but not AR) expression is associated with worse overall melanoma survival (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37), it indicates that *SLNCR* imparts oncogenic functions to AR. If true, this functional relationship may explain why (i) AR expression is not associated with melanoma survival, and (ii) canonical AR functionality alone is unable to account for the observed melanoma gender bias. To first determine if *SLNCR* demonstrates sex-specific expression or effects, *SLNCR* expression was interrogated from 150 sequenced melanomas from The Cancer Genome Atlas (TCGA). An analysis variance model (ANOVA) reveals a significant gender-specific effect of *SLNCR* expression related to stage of melanoma (p-value = 0.0384, FIG. 12A). Specifically, *SLNCR* expression is higher in females prior to local dissemination (Stages I and II). In agreement with these results, *SLNCR* expression is significantly higher in females prior to lymph node metastasis (NX/N0 versus N1/N2/N3, FIG. 12B). Notably, however, expression in males, or in total melanoma patients, is not significantly altered upon metastasis, possibly a consequence of lower expression in pre-metastatic males compared to females (FIGs. 12A, 12B and 13A). Taken together, these results reveal that *SLNCR* expression is gender- and stage-specific.

Male melanomas express significantly higher levels of AR than female melanomas (p-value = 0.046, FIG. 13B). Thus, if *SLNCR* mediates AR's oncogenic functions, *SLNCR* expression would likely be associated with gender-specific melanoma survival. Intriguingly, while high *SLNCR* expression (RPKM > 14.1) is associated with worse melanoma survival total melanoma patients (log-rank p-value = 0.043, (Schmidt, K., *et al.*, Cell Rep, 2016. **15**(9): p. 2025-37)) and females (log rank p-value = 0.048, FIG. 1C), this association is not as significant in males (log-rank p-value = 0.17). Moreover, males exhibited a slight trend of worse survival than females at low levels of *SLNCR* (p-value = 0.18, FIG. 12B). Said another way, males appear to be hyper-sensitized to low levels of *SLNCR* compared to females. It is believed that low-*SLNCR* male melanomas express higher levels of *AR* than low-*SLNCR* female melanomas, rendering the low levels of *SLNCR* capable of inducing oncogenic effects of AR. Consistent with the observations, male low-*SLNCR* melanomas express significantly higher levels of *AR* (p = 0.02, two-tailed) than low-*SLNCR* female melanomas. Among high-*SLNCR* melanomas, where no gender-specific effects are observed, similar levels of *AR* are expressed in males and females. Collectively, these data indicate that there is a functional relationship between

SLNCR and AR with possible implications for the melanoma gender bias, warranting further investigation.

Example 9: The lncRNA *SLNCR* and ligand-independent AR increase melanoma cell proliferation

While previous work focused on the most prevalent *SLNCR* isoform, *SLNCR1*, the role of all *SLNCR* isoforms in AR functionality and melanoma etiology were fully characterized here. To account for possible overlapping functions between the multiple *SLNCR* isoforms, siRNAs were designed to knockdown of all *SLNCR* isoforms, resulting in ~60-80% knockdown of *SLNCR* in two patient-derived melanoma short-term cultures (MSTCs), WM1976 and WM858 (FIG. 13A). Importantly, MSTCs have undergone minimal passages outside of the patient and provide an accurate genetic model of melanoma (Lin, W.M., *et al.*, Cancer Res, 2008. 68(3): p. 664-73). Using RNA-sequencing (RNA-seq), melanoma cells were transcriptionally profiled before and after siRNA-mediated knockdown of *SLNCR* in WM1976, the MSTC which expresses higher levels of *SLNCR* (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Following siRNA-mediated depletion of *SLNCR*, 222 genes are significantly dysregulated (p-value < 0.01, FIG. 12E, Table 6A and Table 6B). Specifically, 131 genes are significantly upregulated compared to a scramble siRNA control, while knockdown of *SLNCR* decreases expression of 91 genes. Gene Ontology (GO) Enrichment analysis these differentially expressed (DE) genes (MetaCore) identifies a significant enrichment of genes involved in multiple cancer-relevant processes, including cell adhesion/motility, apoptosis, differentiation, response to stress and proliferation (FIG. 12F). Indeed, roles for *SLNCR1* were previously identified in melanoma invasion and motility (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). The possible roles for *SLNCR* in melanoma proliferation were particularly interesteing, as *SLNCR* has been implicated in proliferation of lung cancer and other cancers. Consistent with a role in regulation of cell proliferation, knockdown of *SLNCR* significantly decreases proliferation of both MSTCs compared to a scramble siRNA control (p-value < 0.0001, FIG. 12G). Proliferation of the melanoma cell line A375 is also significantly reduced upon knockdown of *SLNCR*, albeit to a lesser extent than observed in the MSTCs, possibly due to (i) lower endogenous levels of *SLNCR* in these cells (Schmidt, K., *et al.*, Cell Rep, 2016. **15**(9): p. 2025-37), (ii) lower efficiency of *SLNCR* depletion (FIG. 13C) and/or (iii) the faster proliferative rate of A375 cells, which shortens the observable duration of

knockdown. Importantly, knockdown of *SLNCR* does not significantly alter the number of apoptotic cells in either MSTC, or in A375 melanoma cells (FIG. 13D). Collectively, these experiments indicate that *SLNCR* increases melanoma proliferation.

GO Enrichment analysis of the 222 DEGs upon *SLNCR* knockdown identifies significant enrichment of genes involved in multiple cancer-relevant processes, including cell adhesion/motility, apoptosis, differentiation, response to stress and proliferation (FIG. 12F). Possible roles for *SLNCR* in melanoma proliferation is of particular interest, as *SLNCR* has been implicated in proliferation of pancreatic, gastric, and non-small-cell lung cancers (Huang, M., *et al.,* Mol Ther, 2017. 25: p. 1014-1026; Lu, W., *et al.,* Molecular Cancer, 2017. 16: p. 118; Shi, X., *et al.,* Oncotarget, 2016. 7: p. 25558-25575; Zheng, J., *et al.,* Nature Genetics, 2016. 48: 747-757). Consistent with enrichment of cell proliferation genes identified with GO analysis (~22%, or 49 out of 222 DEGs, $p = 2.54 \times 10^{-48}$, FIG. 12F), interrogation of The Cancer Genome Atlas (TCGA) data reveals that *SLNCR* expression is significantly correlated with the mitotic growth rate of primary melanomas (Spearman $r = 0.20$, $p = 0.0083$, FIG. 13F), with slow-growing melanomas expressing significantly lower levels of *SLNCR* (mitotic growth rate ≤ 1 versus >1 mitosis/mm^2, $p = 0.014$, FIG. 12H). *SLNCR* knockdown significantly decreased proliferation of both MSTCs compared to a scramble siRNA control ($p < 0.0001$, FIG. 12G). Proliferation of the melanoma cell line A375 is slightly reduced upon *SLNCR* knockdown ($p<0.0001$) likely due to lower endogenous levels of *SLNCR* which limits the fold depletion and range of knockdown-related phenotypes (FIG. 12G) (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Importantly, knockdown of *SLNCR* did not alter the percentage of apoptotic cells in either MSTC, or in A375 melanoma cells (FIG. 13D). Collectively, these experiments indicate that *SLNCR* increases melanoma proliferation. Because depleting *SLNCR1* alone did not affect cell growth, *SLNCR* isoforms likely share an overlapping role in regulation of melanoma proliferation, with *SLNCR2* and *SLNCR3* able to functionally compensate in the absence of *SLNCR1* (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37).

Previous work revealed that *SLNCR* directly binds AR, recruiting it to specific genomic locations to modulate AR transcriptional activity (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Consistent with previous studies implicating AR in melanoma cell growth and proliferation (Morvillo, V., *et al.,* Melanoma Research, 2002. 12: p. 529-538; Morvillo, V., *et al.,* Pigment Cell Res, 1995. 8: p. 135-141), the anti-androgen

flutamide significantly decreases melanoma cell proliferation (FIG. 15A, $p<0.0001$, FIG. 15A). While this indicates an androgen-dependent role for AR in melanoma proliferation, *SLNCR* and AR interact even in the absence of canonical ligand-induced AR activation (*i.e.*, in hormone-deprived cells, Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). While standard cell culture conditions use fetal bovine serum which contains exogenous hormones, it is unknown if these standard cell culture conditions accurately reflect the natural hormone state of the melanoma tumor microenvironment. To test if AR regulates melanoma proliferation in the absence of androgen, cell proliferation of hormone-deprived cells (cells grown in phenol-red free media supplemented with charcoal stripped media) was quantified before and after depletion of AR. Two AR-targeting siRNAs result in ~60-90% knockdown of *AR* in all 3 hormone-deprived melanoma cells (FIG. 15B and 15C). Knockdown of AR significantly decreases proliferation of hormone-deprived melanoma cells ($p<0.0001$, FIG. 14A), confirming that AR regulates melanoma proliferation in an androgen-independent manner (FIG. 14A). To confirm that *SLNCR* and AR cooperatively regulate melanoma cell growth and proliferation, short single-stranded RNA oligos were designed to sterically block the interaction of *SLNCR* and AR. These oligos block the interaction either by direct binding to AR, mimicking the sequence region of SLNCR responsible for mediating this interaction (MIMIC 1 or MIMIC 2) and dominantly repress AR-binding *SLNCR*, or are the reverse complement to the *SLNCR* sequence required for AR binding, generating dsRNA that is unable to bind AR (ANTISENSE 1 or ANTISENSE 2). The antisense oligonucleotides are specifically designed to bind to *SLNCR* without eliciting RNase H-mediated degradation of *SLNCR*. Gymnotic delivery (i.e. delivery without the use of transfection reagents) of either AR- or *SLNCR*-binding 2′-deoxy-2′-fluoro-D-arabinonucleic acid (2′-FANA) modified oligonucleotides significantly decreases melanoma proliferation (FIG. 14B) without decreasing *SLNCR* expression (FIG. 14B and 15D). Moreover, these oligos contain FANA modifications, enabling reagent-free gymnotic uptake into the cells. Steric blocking oligonucleotides occasionally upregulate *SLNCR* expression 2-3 fold, possibly resulting from a feedback loop regulating *SLNCR* expression that is initiated upon inhibition of *SLNCR* function. Decreased cell proliferation upon inhibition of the *SLNCR*-AR interaction, despite increased *SLNCR* expression, further indicates that *SLNCR* and AR cooperatively regulate melanoma proliferation. Thus, these steric blocking oligos confirm that *SLNCR* and AR cooperatively regulate melanoma cell growth and represent a possible novel melanoma therapeutic.

Example 10: *SLNCR* and AR cooperatively regulate expression of a subset of melanoma genes

To gain mechanistic insights into the molecular pathways regulating AR- and *SLNCR*-mediated cell proliferation, AR chromatin immunoprecipitation and massively parallel sequencing (ChIP-seq) was used to identify genomic loci bound by ligand-free AR (i.e., hormone-deprived cells). Because AR expression in the MSTCs is below the level detectable by western blot and are therefore technically challenging, AR ChIP-seq was performed from A375 melanoma cells, which express detectable levels of AR (FIG. 15B). To identify loci bound specifically by androgen-independent AR, ChIP-seq was performed from hormone-deprived cells. Moreover, to confirm the sensitivity of ChIP-seq to detect potentially subtle lncRNA-induced changes in AR function, AR binding sites were identified in cells transfected with either an empty or *SLNCR1*-expressing vector, previously shown to affect AR occupancy at least 1 target gene (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Because *SLNCR1* regulates AR occupancy at at least one genomic region (Schmidt, K., *et al.,* Cell Rep, 2016. 15(9): p. 2025-37), cells were transfected with either an empty or *SLNCR1*-expressing vector, representing either endogenous *SLNCR* levels or *SLNCR1*-overexpression conditions. AR ChIP-seq identified a total of 9,974 AR binding regions (referred to as 'active regions', 5,717 for the empty vector and 8,239 for the *SLNCR1*-expressing vector) in hormone-deprived A375 melanoma cells (Table 7). AR ChIP-seq identified a total of 5,717 AR binding regions in hormone-deprived A375 melanoma cells with only endogenous *SLNCR1* levels (listed under 1_A375_pNL7_minus_lncRNA) (Table 7). Consistent with lncRNA-regulated AR function, *SLNCR1* expression increased the number of AR active regions to 8,239, identifying a total of 4,257 unique AR binding sites (listed under 2_A375_pNL97_plus_lncRNA::1 Peak Value on the table 7) (FIG. 16A). The majority of the binding events in both the vector and *SLNCR*-expressing cells occurred within 10,000 bases pairs of annotated genes (as defined by NCBI, 78.66% and 79.13%, respectively, as shown in Tables 8 and 14), hereafter referred to as 'active genes,' indicating that AR regulates gene expression even in the absence of canonical androgen signaling. Table 7 contains active regions identified for both the vector control (pNL7 minus lncRNA), as well as the SLNCR expression condition (pNL97 plus lncRNA), and all the statistics is shown in Table 8. Moreover, *SLNCR1* overexpression significantly increased tag density at

transcriptional start sites (FIG. 16A). Several previously identified AR-target genes, including C15orf40, POLR2A, and WDR70 (Wang, B.D., *et al.*, Prostate Cancer, 2013. 2013: p. 763569; Massie, C.E., *et al.*, EMBO Rep, 2007. 8(9): p. 871-8), display strong (average peak intensities ~60-110) and clear AR ChIP-seq peaks, consistent with direct AR binding and confirming the accuracy of the AR ChIP-seq analysis. Moreover, AR ChIP-seq analysis also identified known ligand-independent AR targets, including NR6A1 (Average peak ~40) MIPEP (average peak ~175), and WWOX (average peak ~40) (Lin, B., et al., PLoS One, 2009. 4(8): p. e6589; Massie, C.E., et al., EMBO Rep, 2007. 8(9): p. 871-8; Wang, B.D., et al., Prostate Cancer, 2013. 2013: p. 763569).

Several lines of evidence indicate that *SLNCR1* regulates AR chromatin occupancy. *SLNCR1* overexpression (i) increased the number of AR active regions (from 5,717 to 8,239 active regions, with 4,257 unique sites), without increasing expression or altering localization of AR (FIG. 16A) (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37), (ii) increased tag density at transcriptional start sites (FIG. 16A), (iii) increased AR occupancy at 101 of 112 sites with altered AR binding as identified by differential binding analysis (using model-based analysis of ChIP-seq, MACS; Tables 9A and 9B); and (iv) dysregulated 9 (9.2%) of the possible 98 associated genes (included in our RNA-seq analysis) exhibiting differential AR binding ($p<0.05$) (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37). Collectively, these data indicate that *SLNCR1* recruits AR to particular genomic loci. Because AR binds multiple *SLNCR1*- and *SLNCR*-regulated genes even in the absence of ectopically expressed *SLNCR1* (Table 8), all identified AR-bound genes were considered in subsequent analyses.

To identify candidate AR- and *SLNCR*-regulated genes, genes that are both AR-bound (active region within 10,000 bp of gene annotation) as determined by AR ChIP-seq (Tables 8 and 9), and *SLNCR*-regulated, as determined by RNA-seq (Tables 6A and 6B) were searched. Interestingly, consistent with a functional relationship between *SLNCR* and AR, almost half of *SLNCR*-regulated genes are directly bound by AR. For example, 25.3% of genes (9,139 out of 36,074 NCBI-defined genes) were bound by AR but 43.2% of *SLNCR*-regulated genes (96/222) were bound by AR (Binomial Test $p<0.0001$,FIG. 16B and Table 10), indicating that AR directly regulates a large number of *SLNCR* transcriptional targets. Additionally, 45.5% of genes (50/110) dysregulated by *SLNCR1* overexpression were bound by AR (Binomial Test $p=0.0001$) and 43.8% (53/121) of genes dysregulated by *SLNCR1* knockdown were bound by AR (Binomial Test $p=0.0003$), further

confirming that AR-binding is enriched on *SLNCR*- and *SLNCR1*-regulated genes (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37). Consistent with *SLNCR* and AR cooperatively regulating melanoma cell proliferation, AR-binding is enriched among the *SLNCR*-regulated proliferative genes (~37%, 18/49, FIG. 17C). Interestingly, 53 AR-bound genes are significantly upregulated upon *SLNCR* knockdown, while 43 genes are significantly downregulated, indicating that the directional regulation of cooperative AR/*SLNCR* function depends on genomic context.

Many of the AR-bound, *SLNCR*-regulated genes are known or believed to play important roles in melanoma etiology, including the Gro oncogene and chemokine ligand CXCL2 (log2 fold change -2.0), the JUN oncogene (log2 fold change 0.9), the STAT3 transcription factor (Log2 fold change -0.9), the interleukin IL24 (log2 fold change 2.5), and the melanoma cell adhesion molecule MCAM (log2 fold change 1.2). To validate that the analysis faithfully identified AR- and *SLNCR*-regulated genes, RT-qPCR was used to quantify levels of *JUN*, *CXCL2*, and *STAT3* before and after siRNA-mediated knockdown of either *SLNCR* or AR. RT-qPCR of several AR-bound, *SLNCR*-regulated genes (*JUN*, *CXCL2*, and *STAT3*) before and after siRNA-mediated knockdown of either *SLNCR* or *AR* confirms that *SLNCR* and AR regulate expression of these target genes in both WM1976 and A375 cells (FIG. 17A). In agreement with RNA-seq, knockdown of *SLNCR* significantly increases levels of *JUN* (1.5 – 2.5 fold), while significantly decreasing levels of *CXCL2* and *STAT3* (0.75 – 0.5 fold) in both WM1976 and A375 cells. Knockdown of *AR* recapitulates increased *JUN* levels (1.5 – 2.5 fold), while decreased *STAT3* levels are observed in A375 cells only (0.5 fold), possibly due to lower levels of AR (and therefore a weakened phenotype) in WM1976 cells. Interestingly, contrary to decreased levels upon *SLNCR* knockdown, *AR* knockdown significantly increases levels of *CXCL2* (1.25 – 1.75 fold), revealing that *SLNCR* and AR may regulate expression of target genes in an opposing manner. Integrative analysis of *SLNCR* RNA-seq and AR ChIP-seq dataset reveals that AR-binding is enriched on *SLNCR*-regulated genes, and indicate that AR and *SLNCR* similarly regulate expression of many of these target genes both *in vitro* and *in vivo*.

To confirm *SLNCR*- regulated expression of several of these candidate target genes *in vivo*, expression correlations from The Cancer Genome Atlas (TCGA) was interrogated. As expected, *SLNCR* expression is positively correlated with expression of *STAT3* (Spearman correlation coefficients of $r = 0.22$, p-value < 0.01). *SLNCR* expression is also correlated with *TMEM59* and *FAM46A* expression (Spearman correlation coefficients r =

0.49, p-value < 0.0001 and r = 0.29, p-value < 0.001, respectively), genes which are significantly decreased upon *SLNCR* depletion (Log2 fold change -0.79 and -0.7, respectively), while *SLNCR* expression is negatively correlated with mRNA levels of ZYX (Spearman correlation coefficient of -0.43), a gene which is significantly upregulated with *SLNCR* knockdown (Log2 fold change 0.8). Analysis of TCGA expression data reveals that AR is significantly correlated with expression of over half of *SLNCR*-regulated genes (148/222), 66 of which are also bound by AR based on our ChIP-seq analysis (Table 6D). Correcting for multiple hypothesis testing (Bonferroni correction) maintained significance of AR correlation with 92 *SLNCR*-regulated genes, 43 of which are bound by AR. There is a significant concordance between target gene correlations with *SLNCR* and AR expression (Spearman r = 0.2, p = 0.003 overall), further confirming that *SLNCR* and AR cooperatively regulate expression of many of these target genes, *in vivo*. Collectively, integration of *SLNCR* RNA-seq and AR ChIP-seq analyses identifies many *SLNCR*-regulated, AR-bound genes, many of which are implicated in melanoma growth and progression.

Example 11: *SLNCR* and AR cooperatively inhibit expression of the cyclin-dependent kinase inhibitor p21 in a p53-independent manner

The mechanism of AR- and *SLNCR*-mediated regulation of one representative gene was examined. Because *SLNCR* and AR cooperatively increase melanoma cell proliferation, AR-bound and *SLNCR*-regulated genes implicated in melanoma cell growth were searched for. Out of the 222 *SLNCR*-regulated genes, 49 (~22%) are implicated in cell proliferation. Moreover, 18 of these 49 proliferative genes (~37%) are directly bound by ligand-independent AR, indicateing that AR and *SLNCR* increase cell proliferation through regulation of multiple genes (FIG. 17C). Of these, the *SLNCR*-mediated regulation of *CKDN1A*, the gene encoding the tumor suppressive cyclin dependent kinase (CDK) inhibitor 1A ($p21^{Cip1/Waf1}$), was particularly interesting, for several reasons: (i) p21 is an important regulator of cell cycle progression and anti-proliferative pathways, inducing G1 or G2 cell cycle arrest (Gire, V., and V. Dulic, Cell Cycle, 2015. 14: p. 297-304; Giuliano, S., et al., Pigment Cell Melanoma Res, 2011. 24: p. 295-308; Yanagi, T., et al., The Journal of Biological Chemistry, 2003. 278: p. 39906-39911), (ii) its expression is commonly dysregulated in multiple tumors , including melanoma (Abbas, T., and A. Dutta, Nat Rev Cancer, 2009. 9: p. 400-414; Jiang, H., et al., Oncogene, 1995. 10: p. 1855-1864; Vidal, M.J., et al., Melanoma Research, 1995. 5: p. 243-250), (iii) while expression is tightly

correlation to wildtype p53 activity, p53-independent regulation remains unknown and (iv) it is known to be transcriptionally regulated by other non-coding RNAs (Dimitrova, N., et al., Molecular Cell, 2014. 54: p. 777-790; Leveille, N., et al., Nature Communications, 2015. 6: p. 6520; Morris, K.V., et al., PLoS Genetics, 2008. 4: p. e1000258). Additionally, (v) p21 inhibits melanoma proliferation, as depletion of p21 increases proliferation of A375 cells (FIG. 18G and 18H, $p<0.0001$) (Yanagi, T., et al., The Journal of Biological Chemistry, 2003. 278: p. 39906-39911). In agreement with the RNA-seq analysis, knockdown of *SLNCR* in WM1976, as well as A375 cells, results in a significant upregulation of *CDKN1A* mRNA or p21 mRNA (~1.5-2.5 fold increase, FIG. 18A). To test if AR also inhibits expression of *CDKN1A*, mRNA levels were quantified following knockdown of AR and observed a similar increase in *CDKN1A* (i.e., p21 mRNA) levels (~1.3-2.5 fold increase, FIG. 18B). Furthermore, increased p21 mRNA levels upon knockdown of either AR or *SLNCR* correspond to an increase in p21 protein levels (~1.4-3 fold increase, FIG. 18C and 18D). Thus, *SLNCR* and AR transcriptionally repress p21 expression.

Expression of p21 may be regulated by the related tumor suppressor protein p53, or through less well-characterized p53-independent mechanisms. Neither p53 mRNA (*TP53*) nor protein are significantly altered upon knockdown of AR or *SLNCR* in WM1976 or A375 ($p53^{WT}$) cells, indicating that p21 is regulated in a p53 independent manner (FIG. 19A - FIG. 19C). Moreover, knockdown of SLNCR or AR significantly upregulates p21 mRNA and protein levels in the p53 mutant ($p53^{L145R}$, inactive) primary malignant melanoma cell line SK-MEL-28 (~1.5-4 fold increase in both mRNA and protein, FIGs. 18E and F), confirming p53-independent regulation. Thus, the data indicates that AR and *SLNCR* directly inhibit expression of p21 in a p53-independent manner.

In addition to cell proliferation, p21 regulates many additional cellular processes. Since SLNCR regulates p21 expression, whether SLNCR knockdown mimics p21-induced melanoma phenotypes was investigated herein. First, p21 inhibits CDK activity, leading to G1 or G2 cell cycle arrest. Consistently, knockdown of *SLNCR* induces G2 cell cycle arrest in WM858 ($p53^{MUT}$) cells and WM1976 ($p53^{WT}$) cells, observed as a significant increase in the percent G2/M cells while the percent of G1/G0decreased (FIG. 20A) (Gire, V., and V. Dulic, Cell Cycle, 2015. 14: p. 297-304; Giuliano, S., et al., Pigment Cell Melanoma Res, 2011. 24: p. 295-308; Yanagi, T., et al., The Journal of Biological Chemistry, 2003. 278: p. 39906-39911). Knockdown of *SLNCR* does not significantly alter A375 cell cycle

progression (FIG. 19A), likely due to lower overall levels of *SLNCR* in these cells. Knockdown of AR does not affect cell cycle progression in any of these cells (FIG. 21B), possibly due to pleotropic effects of the transcription factor. These data demonstrate that *SLNCR* depletion phenocopies p21 induction of G2/M melanoma cell cycle arrest.

In addition to inducing cell cycle arrest, p21 also regulates activity of multiple transcription factors (Abbas, T., and A. Dutta, Nat Rev Cancer, 2009. 9: p. 400-414). Thus, nuclear transcription factor activity in WM1976 cells was quantified before and after depletion of SLNCR. Therefore, nuclear transcription factor binding to specific DNA motifs in WM1976 cells before and after depletion of *SLNCR* was quantified (FIG. 20B and 20D). *SLNCR* knockdown reduced DNA binding of two transcription factors bound to and regulated by SLNCR1 *(*AR and Brn3a) by 60%, as measured by transcription factor activation array. Knockdown of *SLNCR* significantly reduces AR and BRN3a activity (~60%), transcription factors bound and regulated by SLNCR1. *SLNCR* knockdown also decreased DNA binding by other candidate *SLNCR*-interacting proteins, including EGR-1 (70%), E2F-1 (30%), ATF2 (70%), and the ATF2-containing Activator Protein 1 (API) transcription factor heterodimer (~60%) (Schmidt, K., *et al.*, Cell Rep, 2016. **15**(9): p. 2025-37). Decreased DNA binding by AR occurred independently of altered *AR* expression or localization (FIG. 19D) (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37). *SLNCR* knockdown also alters activity and DNA binding of known p21 targets, decreasing activity of the estrogen receptor (ER) and C/EBP (both ~40% reduced activity) (Fritah, A., *et al.*, Mol Cell Biol, 2005. 25(6): p. 2419-30; Harris, T.E., *et al.*, J Biol Chem, 2001. 276(31): p. 29200-9), and significantly increasing SMAD activity (~2.7 fold) and DNA binding by SMAD (~270%) (Dai, M., *et al.*, Breast Cancer Res, 2012. 14(5): p. R127). Moreover, E2F-1 is both a candidate *SLNCR* interactor (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37) and known to be directly inhibited by p21 (Dimri, G.P., *et al.*, Mol Cell Biol, 1996. 16(6): p. 2987-97; Teplyuk, N.M., *et al.*, Oncotarget, 2015. 6(6): p. 3770-83; Isaeva, A.R. and V.I. Mitev, J Dermatol Sci, 2009. 55(2): p. 134-6; Jung, Y.S., Y. Qian, and X. Chen, Cell Signal, 2010. 22(7): p. 1003-12) and is consistently downregulated upon knockdown of *SLNCR* (30%). This data confirms that SLNCR both directly (through protein-RNA interactions) and indirectly (through p21-mediated regulation) affects and regulates activity of multiple transcription factors. Collectively, *SLNCR* knockdown phenocopies p21-mediated cell cycle arrest and transcription factor

regulation, indicating that *SLNCR* knockdown induces a biologically-relevant upregulation of p21.

Because *SLNCR* knockdown dysregulated the activity of multiple transcription factors (FIG. 20B), it is next investigated if altered transcription factor activity might explain SLNCR-regulated transcriptional networks, and transcriptional effects of *SLNCR* not directly attributed to AR binding. Importantly, since AR is a known mediator of SLNCR-regulation, the analysis was limited to the 126 *SLNCR*-regulated genes not bound by AR (FIG. 16B). Indeed, when limiting the analysis to the 126 *SLNCR*-regulated genes not bound by AR (FIG. 16B), a significant enrichment of *SLNCR*-regulated transcription factor networks was observed, as identified by the transcription factor activation array (FIG. 20B), including ER, AR, C/EBP, EGR1 and E2F1 (FIG. 20C). Interestingly, *SLNCR* knockdown also significantly alters expression of many genes in the CREB1 and STAT3 networks, *i.e.,* STAT3-regulated genes, a transcription factor whose expression is regulated by both *SLNCR* and AR (Table 10 and FIG. 17A). *STAT3* was previously identified as being AR-bound and *SLNCR*-regulated (Table 10), indicating that *SLNCR* directly regulates STAT3 expression. Enrichment of genes in the CREB1 network may be artifact resulting from a high degree of overlap between transcription factor targets. However, depletion of *SLNCR* does not appear to affect STAT3 activity (FIG. 20D), warranting further investigation into the nature of STAT3 regulation. Collectively, these studies indicate that, in addition to cooperative transcriptional regulation of AR-bound genes, *SLNCR* regulates expression of additional non-AR bound genes through modulation of transcription factor activity, possibly through inhibition of p21. Moreover, SLNCR knockdown mimics known p21-induced phenotypes, including cell cycle arrest and altered transcription factor activity. Thus, SLNCR-mediated regulation of p21 expression results in biologically-meaningful phenotypic changes.

Example 12: *SLNCR* binds EGR1 and recruits AR to EGR-bound loci

To investigate how *SLNCR* and AR mechanistically regulate target gene expression, AR ChIP-seq data was interrogated to identify either known or novel motifs present and enriched in AR-bound genes (AR ChIP-seq datasets). MEME and TOMTOM analysis (Bailey, T.L., et al., Nucleic Acids Research, 2009. 37: p. W202-208) of AR ChIP-seq peaks identifies an enrichment of a conserved motif similar to the DNA binding motif of RE1-Silencing Transcription Factor (REST, or Neuron-Restrictive Silencer Factor, NRSF), a transcriptional repressor known to mediate AR activity in prostate cancer ($(p=1e^{-191}$,

FIG. 23A) (Svensson, C., *et al.*, Nucleic Acids Res, 2014. 42(2): p. 999-1015). However, the REST motif was not enriched in AR binding sites among *SLNCR*-regulated genes. Instead, the DNA binding site of the EGR1 transcription factor was enriched ($p=2.24e^{-05}$, FIG. 22A). Limiting the analysis to only AR ChIP-seq peaks found near or within *SLNCR*-regulated genes identifies a unique conserved motif highly similar to the EGR1 DNA binding motif (p-value 2.24e-05, FIG. 22A), indicating that AR binds to *SLNCR*-regulated genes through a distinct mechanism, perhaps in cooperation with EGR1.

Both previous (Schmidt, K., *et al.*, Cell Rep, 2016. 15(9): p. 2025-37) results and results described herein (FIG. 20A-20C) indicate that EGR1 and *SLNCR* directly and/or functionally interact. In further support of a direct physical interaction, incubation of biotinylated, full length SLNCR1 with A375 melanoma cell lysate followed by streptavidin pulldown significantly enriches EGR1 and AR (FIG. 22B), as well as the RNA binding ribosomal protein Rps6 (FIG. 22A). This interaction was independently validated using RNA immunoprecipitation (RIP) assays, which enriched *SLNCR* (~4-10 fold) in RNAs immunoprecipitating with EGR1 (FIG. 22F). These data confirm that endogenous levels of *SLNCR* and EGR1 interact in A375 cells.

To distinguish between direct interaction of *SLNCR* and EGR1 versus an indirect interaction mediated by secondarily-associated macromolecules, RNA electrophoretic mobility shift assays (REMSA) was performed. As shown by REMSA, recombinant EGR1 protein (corresponding to amino acids 282-433) significantly alters the mobility of full length, *in vitro* transcribed biotinylated *SLNCR1* in a protein concentration dependent manner (FIG. 22B-22C). Interestingly, EGR1 binding significantly increases RNA mobility (sub-shifted complex),, as opposed to more commonly observed RNA retardation (super-shifted complex), possibly a result of altered (likely relaxed) RNA secondary structure upon protein binding. Unlabeled *SLNCR1* is able to compete for EGR1 binding, observed as a loss of increased mobility (*i.e.* upward shift), confirming a direct and specific EGR1-*SLNCR1* interaction. Collectively, these data further confirm that endogenous *SLNCR* and EGR1 directly interact *in vitro* and at endogenous levels in melanoma cells.

Given that *SLNCR1* binds to EGR1, and the EGR1 motif is significantly enriched in AR-bound, *SLNCR*-regulated genes, it is hypothesized that AR colocalizes and binds to a subset of *SLNCR*-regulated genes in cooperation with EGR1. Thus, EGR1 ChIP-seq was first used to determine global EGR1 binding sites in A375 cells, identifying a total of 16,789 active regions (Table 11). Interestingly, despite a relatively small overlap (18.5%)

between EGR1 and AR bound regions overall (FIG. 23B), the majority (4,091 out of 6,960, or 58.8%) of EGR1 active genes (i.e. active regions that are located within 10,000 bp of an annotated gene, Table 12) overlap with AR active genes. A higher proportional overlap between AR and EGR1 binding-sites within gene regions indicates a functional relationship between the two transcription factors. EGR1 binds a total of 8,373 active regions (Table 11), corresponding to a total of 6,960 active genes (Table 12). Consistent with expected genomic occupancy, EGR1 ChIP-seq analysis identified many known EGR1-regulated genes, including *CCDC28B*, *ATAD2*, and the promoter of *EGR1* itself (FIG. 22H) (Arora, S., et al., Genome Biol, 2008. 9: p. R166; Kubosaki, A., et al., Genome Biol, 2009. 10: p. R41; Subbaramaiah, K., et al., The Journal of Biological Chemistry, 2004. 279: p. 12647-12658). Unlike AR, EGR1 appears to bind its known DNA binding sequence in A375 cells, as a sequence resembling this motif is the most significantly enriched in EGR1 ChIP-seq peaks ($p < 1x10^{-5}$, FIG. 22D).

Surprisingly, a significant overlap between AR and EGR1 binding sites was observed. Additionally, AR and EGR1 frequently co-bound at *SLNCR*-regulated genes. Although AR and EGR1 bound only 25.3% (9,139 of 36,074) and 19.3% (6,960 of 36,074) of all genes, respectively, AR bound to 58.8% of EGR1-bound genes (4,091 out of 6,960 total EGR1 active genes, Binomial Test $p<0.0001$, FIG. 23C). It is important to note that co-bound genes were identified through a stringent analysis of overlapping ChIP-seq reads. This was accomplished by directly integrating AR- and EGR1- ChIP-seq reads (spanning an average of only 747 bps) rather than extrapolating binding events occurring within 10,000 bps of an annotated gene. EGR1 bound to 31% of *SLNCR*-regulated genes (68 out of 222 genes, Binomial Test, $p=0.0003$) and 46% of *SLNCR*-regulated, AR-bound genes (44 out of 96 genes Tables 13A and 13B, Fisher Exact $p<0.0001$, FIG. 22E). Consistent with cooperative transcription factor binding, AR and EGR1 ChIP-seq peak read intensities overlapped within many of the 44 *SLNCR*-regulated, AR- and EGR-bound genes, including *PSAT1*, *SHF*, *SLC36A11*, and *SSU72*, and the divergently-transcribed, *SLNCR*-regulated gene pair *NAA50* and *ATP6V1A* (FIG. 22G). Collectively, these data reveal that AR and EGR binding sites overlap more frequently than would be expected by chance, and that these sites are enriched among *SLNCR*-regulated genes. Because AR and EGR1 binding occurs at known or predicted EGR1 DNA binding motif, these data indicate that EGR1 is required for regulation of at least a subset of AR- and *SLNCR*-regulated genes.

If a functional interaction exists between SLNCR, AR and EGR1 that dictates binding of these transcription factors to chromatin, a higher frequency of EGR1 at SLNCR-regulated AR-bound genes would be expected. Thus, the identification of SLNCR-regulated genes with the AR and EGR1 ChIP-seq data were integrated. Interestingly, while EGR1 binds to roughly a third of SLNCR-regulated genes (68 out of 222 total, ~31%), EGR1 is bound to a higher proportion of SLNCR-regulated, AR-bound genes (44 out of 96 AR-bound, SLNCR-regulated genes, ~46%, Table 13A and Table 13B). Briefly, Table 13A contains expression data for all SLNCR-regulated genes, as identified via RNA-seq. The last 3 columns contain information on whether a ChIP-peak was identified for AR with endogenous SLNCR (pNL7_minus_lncRNA, column L), AR with ectopic SLNCR expression (pNL97_plus_lncRNA, column M), or EGR (column N). A '1' denotes the presence of a peak, while '0' denotes absence of a peak. Moreover, in contrast to the ~58.8% of all EGR1 active genes that overlap with AR genes, the percentage of overlap increases to 64.7% (44 out of 68 genes) when limited to only SLNCR-regulated genes. Collectively, these data indicates that EGR1 is involved in AR- and SLNCR-mediated gene regulation of at least a subset of SLNCR-regulated genes.Since SLNCR binds to both AR and EGR1, AR and EGR1 co-bind EGR1 motifs within *SLNCR*-regulated genes, and EGR1 occupancy is proportionally higher at SLNCR-regulated and AR-bound genes, SLNCR might recruit AR to EGR1-occupied genomic regions. If true, SLNCR- and AR-based regulation of target would require EGR1. Specifically, EGR1 should regulate expression of these genes, and *SLNCR*- and AR-based regulation would require an intact EGR1 DNA binding site. In support of EGR1-mediated regulation, EGR1 expression is significantly correlated with expression of over half of *SLNCR*-regulated genes (65.3%, 145/222), while significant correlation is maintained for 71 of these genes after correcting for multiple hypothesis testing (Bonferroni correction, $p < 0.00023$, Table 6D). To first test if EGR1 regulates p21, p21 mRNA and protein expression was quantified following siRNA-mediated knock down of EGR1. EGR1 positively regulates expression of p21 because EGR1 knockdown decreased p21 mRNA and protein levels (FIG. 24B-24C). Contrary to results seen upon knockdown of AR or SLNCR, knockdown of EGR1 significantly decreases p21 mRNA and protein levels (FIG. 14A and 14B). Moreover, EGR1 regulates p21 independent of p53, because EGR1 knockdown in the p53-mutant SK-MEL-28 cells decreased p21 levels (FIG. 24B-24C and 25A). Decreased p21 levels occurs independently of p53, as this decrease is seen in the p53 mutant SK-MEL-28 cells (FIGs.

14A, 14B and 15A). Thus, EGR1 increases CDKN1A/p21 expression, acting in opposition to AR and SLNCR. In other words, in contrast to *SLNCR* and AR which repress p21, EGR1 activates p21 expression in a p53-independent manner.

It is next tested if AR- and *SLNCR*-mediated *CDKN1A* regulation requires EGR1 binding to the CDKN1A loci. To test whether *SLNCR*- and AR-mediated p21 regulation requires an intact EGR1 binding site, a firefly luciferase reporter construct containing 4663 nucleotides (nts) of the *CDKN1A* promoter, spanning from the first transcription start site to 2966 nts upstream of the translation start codon and containing the AR- and EGR1-bound consensus EGR1 DNA binding site, was generated (FIG. 24). Surprisingly, and contrary to increased endogenous mRNA and protein levels, knockdown of *SLNCR* or AR significantly decreases luciferase activity and the expression of the ectopic *CDKN1A* luciferase reporter in A375. This discrepancy is likely due to inherent differences between genomic DNA and ectopically-expressed plasmid DNA and is discussed in more detail later. Consistent with ligand-independent AR activation, *SLNCR* and AR knockdown also decreased expression of the *CDKN1A* reporter even in the absence of exogenous hormones (FIG. 25B). Most importantly, however, mutation of the EGR1 binding site negates the ability of AR or *SLNCR* to regulate expression from the *CDKNA* promoter. These data strongly indicate that AR and *SLNCR* associate with the *CDKN1A* promoter through the EGR1 binding site and EGR1 DNA binding site is required for *SLNCR*- and AR-based regulation of *CDKN1A*.

Example 13: P53-deficient female melanomas express higher levels of p21 than male melanomas

Given that SLNCR mediates ligand-independent AR function in melanoma, and the gender-specific expression of both AR and SLNCR, TCGA data for gender-specific expression of p21 was interrogated. Due to the likelihood that p53-dependent mechanisms of p21 regulation are likely dominant pathways of regulation, the analysis was limited to p53-deficient melanomas (as determined via RNA-seq). Consistent with the model that SLNCR-mediates AR repression of CDKN1A, females express significantly higher levels of p21 than males (FIG. 25D).

Example 14: AR and Brn3a binding sites reside within an unstructured region of SLNCR1, in vivo

The *in vitro* data presented herein indicate that AR preferentially binds to unstructured, single-strand RNA in a sequence-specific manner. However, REMSA combined with sequence and structural prediction analyses do not accurately predict how an RNA sequence folds in the context of an entire transcript within a cell. Indeed, proteins and other cellular macromolecules can lead to changes in RNA structure that cannot be accurately predicted by *in silico*-only calculations of RNA in solution. Therefore, it was sought to experimentally determine if *SLNCR1*'s AR-binding motifs are (1) accessible to protein interactions and (2) predicted to be bound by protein, *in vivo*. Specifically, the secondary structure of *SLNCR1* was modeled using measurements of RNA flexibility within patient-derived melanoma cells.

To understand the local RNA structure and nucleotide accessibility of *SLNCR1* AR-binding motifs, *in vivo*, SHAPE and mutational profiling (MaP) was performed. SHAPE-MaP provides experimental evidence for RNA secondary structures at nucleotide resolution, including in living cells (Siegfried, N.A., et al., Nature Methods, 2014. 11: p. 959-965; Smola, M.J., et al., Nat Protoc, 2015. 10: p. 1643-1669). The SHAPE-MaP approach was applied using the melanoma short-term culture (MSTC) WM1976, whose invasion potential can be disrupted through siRNA-mediated depletion of *SLNCR1* (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37). Importantly, MSTCs have undergone limited passages outside of the patient and therefore closely reflect the genetics and relative expression patterns of the tumor, *in situ*.

The structure of *SLNCR1* was probed using the SHAPE reagent 5-nitroisatoic anhydride (5NIA) and the methylating agent dimethyl sulfate (DMS). 5NIA has an extended half-life in solution (100 seconds), enabling superior structure probing in certain cell lines. DMS methylates nucleotide bases at a higher rate than 5NIA acylates nucleotide sugars, but DMS reacts most strongly with only adenosine and cytosine. Using 5NIA and DMS, the nucleotide flexibilities of *SLNCR1* was probed both within WM1976 cells (in-cell) and after gentle extraction of the RNA from WM1976 cells into a protein-free environment (cell-free). The SHAPE reactivities of cell-extracted RNA (cell-free) can be used to model RNA in its native cellular structure, and in-cell SHAPE reactivities both provide further evidence in support of structured motifs and also identify RNA sequences whose structure changes in the presence of proteins. To discern whether *SLNCR1* modifications or protein-mediated folding events lead to different stable RNA conformations in the nucleus, where the *SLNCR*-AR complex can regulate transcription,

versus in the cytoplasm, extracted RNA (cell-free) was separated into nuclear and cytoplasmic fractions before treatment with 5NIA or DMS. Sites of SHAPE and DMS modification within in-cell and cell-free RNAs were encoded as non-template-encoded nucleotides or deletions in the cDNA generated during reverse transcription, which can then be detected by massively parallel sequencing (Homan, P.J., et al., Proc. Nat. Acad. of Sci. of the U. S. A., 2014. 111: p. 13858-13863; Siegfried, N.A., et al., Nature Methods, 2014. 11: p. 959-965; Smola, M.J., et al., Nat Protoc, 2015. 10: p. 1643-1669). Using a gene-specific reverse transcription primer and gene-specific PCR amplification primers, single-nucleotide resolution structural information on nts 403-780 of *SLNCR1* (*SLNCR1*$^{403\text{-}780}$) was obtained. This region encompasses most of *SLNCR1*^{cons} (nts 372-672), including the Brn3a binding region (*SLNCR1*$^{462\text{-}572}$) and both AR binding motifs, required for mediating melanoma invasion. The frequency of observed sequence changes in synthesized cDNAs were converted into SHAPE or DMS reactivity values for each nucleotide (Siegfried, N.A., et al., Nature Methods, 2014. 11: p. 959-965; Smola, M.J., et al., Nat Protoc, 2015. 10: p. 1643-1669).

Generally high SHAPE reactivity was observed across *SLNCR1*$^{403\text{-}780}$ in cell-free RNA (FIG. 18A and 18C), indicating some level of flexibility within the region and a lack of a single, well-defined structure, even in the absence of cellular components. To calibrate the reactivity scale, SHAPE reactivities were also collected for the highly structured U1 small nuclear RNA (snRNA) (FIG. 17-18 and 22A). While a similar range of SHAPE reactivities was observed for both *SLNCR1* and U1 snRNA, reactive nucleotides were more widespread and diffuse in *SLNCR1*$^{403\text{-}780}$ with fewer regions of dense lowly or highly reactive nucleotides that define the U1 snRNA (FIG. 17C, 18A, 18C, 22A, and 22B). The average SHAPE reactivity in *SLNCR1* is highest across nts 495-570, which overlap the *SLNCR1* region that is necessary for interaction with Brn3a (*SLNCR1*$^{462\text{-}572}$) (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37). The SHAPE reactivity profiles of *SLNCR1* when extracted from the nucleus and the cytoplasm are nearly identical, indicating that events in either compartment do not induce stable changes to the structure of this region of *SLNCR1* (FIG. 18A and 18C). When RNAs were treated with 5NIA in-cell, the reactivity profile largely resembled the cell-free profiles, with regions of average to low SHAPE reactivity flanking a more highly-reactive conserved region (FIG. 18B). DMS modification patterns for both extracted and in-cell *SLNCR1* were broadly comparable to our 5NIA data despite the differences in modification mechanism (FIG. 19 and 20). Together, these data indicate

that the *SLNCR1*$^{403\text{-}780}$ RNA lacks extensive stable secondary structure, especially within the Brn3a-binding region (*SLNCR1*$^{462\text{-}572}$). The in-cell data presented herein indicate that the cellular environment does not impose any wide-ranging structural shifts in *SLNCR*$^{403\text{-}780}$, and further confirm the presence of a large flexible region accessible to single-stranded RNA-binding proteins.

Example 15: Proteins bind multiple regions of SLNCR1^{cons}, including AR motifs, in vivo

Comparison of cell-free and in-cell SHAPE and DMS profiles enables discovery of nucleotides that are protected in living cells, often indicative of protein binding to these regions of RNA (Smola, M.J., et al., Biochemistry, 2015. 54: p. 6867-6875; Smola, M.J., et al., Proc. Nat. Acad. of Sci. of the U. S. A., 2016. 113: p. 10322-10327). For example, loops in the U1 snRNA engaged by the 70K, U1A, and Sm proteins are highly reactive to SHAPE in the cell-free state but become lowly reactive in-cell (FIG. 17 and 18) (Kondo, Y., et al., Elife, 2015. 4; Pomeranz Krummel, D.A., et al., Nature, 2009. 458: p. 475-480). Many in-cell protections from SHAPE and DMS reactivity throughout *SLNCR1*$^{403\text{-}780}$ was observed, consistent with interactions with RNA-binding proteins (FIG. 18). Two of the three largest decreases in in-cell SHAPE reactivity were observed within the Brn3a-interacting region (*SLNCR1*$^{462\text{-}572}$). One statistically significant protection (Z-factor = 0.59, Z-score = 1.21) was observed at the 5′ end of the first AR motif and another adjacent to the 3′ end of the second motif (Z-factor = 0.60, Z-score = 1.20), indicating that these motifs are protein-bound *in vivo*. Agreement between the two probing reagents was observed: all DMS protection sites are within 5 nucleotides of an in-cell SHAPE protection (FIG. 18). Importantly, DMS probing corroborated the in-cell SHAPE protection of the first AR motif, further confirming that this motif is indeed protein-bound in cells. Moreover, stronger observed in-cell protection at motif 1 is consistent with the data presented herein showing that AR binds the *SLNCR1* motif 1 with higher affinity than motif 2 (FIG. 12G).

Example 16: SHAPE-guided modeling of SLNCR^{cons} reveals a high-flexibility region flanked by limited RNA structure

It was next sought to better understand the structural context of the Brn3a-binding region and the AR motifs that are critical for AR-mediated function. To do this, the *SLNCR1* 5NIA data were further analyzed using the SuperFold SHAPE analysis pipeline,

which enables modeling of RNA structures using measured SHAPE reactivities (Smola, M.J., et al., Nat Protoc, 2015. 10: p. 1643-1669). In SHAPE-driven models of RNA structure, regions of high SHAPE reactivity are modeled as mostly unpaired, regions of low SHAPE reactivity are modeled as paired, and the resulting base-pairing probabilities can be used to generate a minimum free energy model that represents the dominant RNA structure conformation. As a control, 5NIA SHAPE data and SuperFold were used to model the U1 snRNA extracted from WM1976 cells and recovered the correct four-stem structure (FIG. 22A and 18G). The reactivities for the U1 snRNA and *SLNCR*$^{403\text{-}780}$ were placed on the same SHAPE reactivity scale (see Methods). Compared to U1, the distribution of SHAPE reactivities in *SLNCR*$^{403\text{-}780}$ is strongly shifted to the right, indicating that this region of *SLNCR1* is much more reactive and thus less structured than the U1 snRNA (FIG. 22B). Shannon entropies were also computed for both RNAs, which is a measure of structural well-determinedness and RNA conformational diversity: high Shannon entropy corresponds to an absence of a well-defined structure and many potential RNA states. *SLNCR1*$^{403\text{-}780}$ global median entropy (0.19) is much greater than that of the highly structured U1 snRNA (0.01), indicative of a lack of well-defined structure within the lncRNA region (FIG. 22A and 22F). The Brn3a-binding region (*SLNCR1*$^{462\text{-}572}$) has both high SHAPE reactivity and high entropy, indicating a highly-flexible region that samples many conformations. The AR motifs themselves are moderately reactive when compared to the rest of *SLNCR*$^{403\text{-}780}$, but have differing levels of entropy between them. *SLNCR1* AR motif 1 has moderately low SHAPE reactivity (0.32) but high entropy (0.44), indicating that the motif samples multiple base-pairing states but is unlikely to exist in a stable conformation. AR motif 2 is both lowly reactive (0.32) and has low entropy (0.07), indicating that this motif potentially persists in a partially base-paired state.

One strategy to detect well-defined structure motifs is to identify regions of both low SHAPE reactivity and low Shannon entropy (Siegfried, N.A., et al., Nature Methods, 2014. 11: p. 959-965). Setting thresholds of median SHAPE < 0.4 (likely to be base-paired) and median entropy < 0.03 (base-pairing probability > 93%) identifies a low SHAPE, low entropy region within U1 snRNA that, when expanded to include intersecting helices (See Methods), includes the entirety of U1 in a well-defined structure motif (FIG. 18B), as expected for this RNA with a well-defined functional structure. Applying the same thresholds to *SLNCR*$^{403\text{-}780}$ reveals no low SHAPE, low entropy regions (FIG. 22F). Relaxing these thresholds or looking for regions with reactivities and entropies below the

global medians enable modeling of potential secondary structures (FIG. 22 and 23), but the relative high reactivity and entropy of *SLNCR1*$^{403\text{-}780}$ indicate that these structures do not persist stably *in vivo*. Together, the REMSA and SHAPE data presented herein confirm a model wherein *SLNCR1*^{cons} is unstructured, enabling interaction with AR, *in vivo*.

Example 17: AR binding to its cognate motif is required for SLNCR1-mediated melanoma invasion

To assess the consequences of AR binding to it cognate elements *in vivo*, the two identified AR binding motifs were mutated and tested for *SLNCR1*-mediated melanoma invasion. Ectopic expression of *SLNCR1* or *SLNCR1*^{cons} significantly increased the invasion of A375 melanoma cells, as quantified by matrigel invasion assays (FIG. 24). Importantly, expression of *SLNCR1* harboring site-directed mutations in the AR binding motifs 1 or 2 (*SLNCR1*$^{AR\ MUT1}$ or *SLNCR1*$^{AR\ MUT2}$, respectively) enabled *SLNCR1*-mediated melanoma invasion, though diminished when compared to wildtype. However, mutation of both motifs (*SLNCR1*$^{AR\ MUT\ 1+2}$) abolished *SLNCR1*-mediated invasion (FIG. 24). The additive suppression of the invasion phenotype indicates that both motifs contribute to *SLNCR1*- and AR-mediated melanoma invasion, and is consistent with *in vitro* REMSA results indicating that AR binding requires the presence of at least one CYUYUCCWS motif (FIG. 14A).

Because *SLNCR1*-mediated invasion occurs through transcriptional upregulation of *MMP9*, *SLNCR1* and *MMP9* levels were quantified upon expression of the three AR mutant *SLNCR1* constructs. *MMP9* levels are significantly increased with expression of *SLNCR1*, but not changed upon expression of *SLNCR1*$^{AR\ MUT1}$ or *SLNCR1*$^{AR\ MUT\ 1\ and\ 2}$ (~3-fold increase, FIG. 25). Interestingly, mutation of AR motif 2 attenuated (but did not abolish) *SLNCR1*-mediated invasion while *MMP9* levels significantly increased upon expression of *SLNCR1*$^{AR\ MUT\ 2}$ (~4-fold increase, FIG. 24B and 25B). The discrepancy of increased *MMP9* levels but not increased melanoma invasion with expression of *SLNCR1*$^{AR\ MUT\ 2}$ may be due to differences in the kinetics of *MMP9* upregulation in the presence or absence of *SLNCR1*'s higher affinity AR binding motif 1.

The work presented herein identifies a novel sequence-specific lncRNA motif responsible for mediating protein binding and thereby lncRNA function. This work demonstrates that AR NTD binds with high affinity to unstructured, pyrimidine-rich RNA in a sequence-specific manner. This work further demonstrates that the AR-RNA

interactions observed herein occur in an androgen-independent manner. Moreover, AR NTD, which lacks the ligand-binding domain, is sufficient for RNA binding. The observation that lncRNAs regulate AR activity independently of androgens has important implications for the study of AR in the context of human cancers. For example, multiple AR-driven cancers show only limited response to anti-androgen therapies, indicating androgen-independent mechanisms for multiple AR-driven cancers (Morvillo, V., et al., Pigment Cell Res, 1995. 8: p. 135-141; Morvillo, V., et al., Melanoma Research, 2002. 12: p. 529-538; Rose, C., et al., Eur J Cancer Clin Oncol, 1985. 21: p. 1171-1174). Increasing our understanding of novel RNA-mediated AR function may help reconcile these inconsistencies and explain the failure of anti-androgens in the treatment of these tumors. AR is capable of binding *SLNCR1* independently of canonical androgen-mediated AR activation and dimerization, which is normally necessary for AR target recognition (Brinkmann, A.O., et al., J Steroid Biochem Mol Biol, 1999. 69: p. 307-313). It is intriguing that *SLNCR1* contains two AR binding motifs in close proximity (spanning 24 nts). AR appears to interact independently and uniquely with each site, as evidenced by altered REMSA migration patterns and phenotypic differences upon mutation of either motif 1 or motif 2 (FIG. 3G and 9B). In-cell protections and phenotypic data indicate that motif 1 is predominantly involved in AR binding (FIG. 4C, 5B and 10D), possibly due to the higher affinity of AR to this sequence (FIG. 1 and 3F). The second, low affinity binding site may either (1) accommodate or anchor AR dimers following canonical activation, or (2) independently bind a second AR monomer, forcing proximal dimerization and possibly initiating cooperative activity. It is noted that high concentrations of full-length AR, but not AR NTD, resulted in a secondary sub-shift of the WT-41 probe, indicating a change in protein:RNA stoichiometry (FIG. 1B and 1C). Because AR NTD is unable to form head-to-tail dimers, this indicates that, at high protein concentrations, dimerized AR may bind *SLNCR1*. Forced dimerization of AR is not required for transcriptional upregulation of MMP9 and increased invasion, as mutation of AR binding motif 2 does not abolish activity (FIG. 5 and 10). However, it is possible that binding of two AR monomers, particularly in cells expressing high AR, may elicit a unique transcriptional response.

The results presented herein indicate that AR binds RNA independently of its DNA-binding domain. AR may also bind actively transcribed lncRNAs, recruiting AR *in cis* to particular genomic regions independently of DNA encoded AR response elements (AREs).

The proximal recruitment of AR to these regions may be sufficient to elicit AR-mediated transcriptional regulation of the lncRNA or other neighboring genes. In this way, AR may regulate expression of many non-ARE containing genes. Indeed, many lncRNAs are expressed divergently or antisense to protein-coding genes, and expression of many of these lncRNAs have been linked to transcriptional changes in expression of cognate mRNA. In addition to AR, many other transcription factors also bind RNA independently of canonical DNA interactions (Long, Y., et al., Sci Adv, 2017. 3: p. eaao2110). Identification of RNA-binding transcription factors and elucidation of their RNA sequence- or structure-requirements is critical to fully appreciate the complexities of regulated gene expression.

Identification of protein-associated lncRNA motifs is critical to establish methods for predicting lncRNA function from sequence analysis alone, as indicated herein by identification of a novel, AR-binding sequence in the HOXA11AS-203 lncRNA (FIG. 6). It is observed herein that AR NTD directly binds *SLNCR1*, but not *PCGEM1* or *HOTAIR*, independently of additional protein cofactors. This selective binding is consistent with previous work revealing that the AR-*PCGEM1* interaction requires binding of the lncRNA *PRNCR1* to AR's carboxyl-terminus, recruitment of DOT1L, and methylation at AR K349 (Yang, L., et al., Nature, 2013. 500(7464): p. 598-602). The results presented herein also indicate that AR NTD binds *SRA1* (FIG. 7A). The AR-*SRA1* interaction appears weaker and/or more transient compared to the AR-*SLNCR1* interaction (FIG. 7A), possibly due to the presence of only one CYUYUCCWS motif found within a non-pyrimidine-rich sequence, compared to the two motifs found in *SLNCR1*'s highly pyrimidine-rich sequence.

Many lncRNAs, including *SLNCR1*, are likely composed of varying combinations of discrete domains that impart functional specificity through assembly of associated proteins, RNA and DNA (Guttman, M., and J.L. Rinn, Nature, 2012. 482: p. 339-346). These lncRNA domains might impart function through a variety of means, for example: (1) by acting as allosteric regulators, assuming complex secondary and tertiary structures that present a unique surface for interaction and impart new or enhanced activities on associated macromolecules (Shamovsky, I., et al., Nature, 2006. 440: p. 556-560; Wang, X., et al., Nature, 2008. 454: p. 126-130); (2) by acting as sponges that compete for binding to factors and thus inhibit their effects (Lee, S., et al., Cell, 2016. 164: p. 69-80); or (3) by providing protein-specific landing platforms to scaffold formation of higher order complexes, thereby coordinating the activities of multiple associated proteins through induced proximity (Cerase, A., et al., Genome Biol, 2015. 16: p. 166). *SLNCR1*$^{403\text{-}780}$ behaves most like option

3, serving as a flexible scaffold for AR and Brn3 to coordinate their transcriptional activities. The high-affinity AR-binding motif 1, which exists at the junction of the highly flexible Brn3a-binding domain and a lower SHAPE and entropy 3′ region, may be more accessible than AR-binding motif 2, which resides within the lower SHAPE and entropy region (FIG. 4H). Ultimately, binding of Brn3a to the flexible scaffold may enhance recognition of downstream AR-binding motifs, and recognition of AR motif 1 might increase the accessibility of motif 2. In other cancer cell lines, *SLNCR1* interacts with epigenetic regulators EZH2, DNMT1, LSD1, though it is unknown if these interactions occur in the melanomas used in this study (Ba, M.C., et al., Oncotarget, 2017. 8: p. 95542-95553; Huang, M., et al., Mol Ther, 2017. 25: p. 1014-1026; Ma, C., et al., Oncotarget, 2017. 8: p. 32696-32705; Shi, X., et al., Oncotarget, 2016. 7: p. 25558-25575). Given that the most significant SHAPE protection in-cell within $SLNCR1^{403\text{-}780}$ lies adjacent to the Brn3a and AR interacting domains (nts 672-678), it is likely that additional yet unidentified factors associate with *SLNCR1* and guide ribonucleoprotein complex assembly.

Proteins that are scaffolded by lncRNAs may bind RNA structural elements, as suggested for *HOTAIR* and *SRA1*, and sequence motifs, as shown here for *SLNCR1* (Guo, X., et al., Briefings in Functional Genomics, 2016. 15: p. 38-46). Identification of short RNA sequences or groups of RNA sequences predicted to have similar interactors may reveal sequence and/or structural requirements predictive of lncRNA biology. This high resolution functional information is necessary to improve our ability to predict lncRNA function from sequence analysis and secondary structure predictions, ultimately leading to the determination of the mechanisms of uncharacterized lncRNAs. The work presented herein demonstrates that identification and characterization of protein-lncRNA interactions enables prediction of novel lncRNA interactions which could function similarly in orthologous pathways.

Given their critical role in the regulation of complex gene expression patterns and their implication in many human cancers, lncRNAs are rapidly emerging as an attractive class of novel pharmacological targets. Despite several hurdles early in the development of oligonucleotide therapeutics, particularly surrounding oligonucleotide delivery and stability, several oligonucleotide-based therapeutics have since been approved (Juliano, R.L., Nucleic Acids Research, 2016. 44: p. 6518-6548; Lundin, K.E., et al., Hum Gene Ther, 2015. 26: p. 475-485; Stein, C.A., and D. Castanotto, Mol Ther, 2017. 25: p. 1069-1075). It is demonstrated for the first time herein that chemically stable oligonucleotides

that block the AR-*SLNCR1* interaction inhibit *SLNCR1*-mediated melanoma invasion, indicating that disrupting this interaction has potential therapeutic relevance. Thus, characterizing lncRNA-protein interactions presents a novel avenue for the design and implementation of lncRNA-targeting therapies. In addition to oligonucleotide-based approaches, whose systemic delivery strategies are currently limited by accumulation in the liver, small molecules could also be used to selectively inhibit the AR-*SLNCR1* interaction. Importantly, the *SLNCR1* structural information generated here is critical to enable identification of small molecules that bind to *SLNCR1* and selectively inhibit AR binding Connelly, C.M., et al., Cell Chem Biol, 2016. 23: p. 1077-1090).

Example 18: *SLNCR* isoforms exhibit both unique and overlapping functions

Melanomas express at least 3 isoforms of *SLNCR*, *SLNCR1-3* (FIG. 12I). *SLNCR1* is the shortest and most prevalent isoform, while *SLNCR2* and *SLNCR3* differ only in the inclusion of an additional exon of varying length. It was previously demonstrated that *SLNCR1* binds to AR and recruits it to the MMP9 promoter, and that *SLNCR1* and AR are required for transcriptionally upregulating *MMP9* expression and promoting melanoma invasion (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37). Surprisingly, unlike *SLNCR1*, neither *SLNCR2* nor *SLNCR3* upregulate *MMP9* nor increase melanoma invasion, indicating that *SLNCR* isoforms have at least partially unique functions (FIG. 12J and 12K). Isoform-specific functions cannot be explained by differences in AR binding, as all 3 isoforms contain the RNA region required for AR binding and consistently bind AR *in vivo* (FIG. 12I and 12L). Thus, all three *SLNCR* isoforms likely regulate AR activity.

To investigate the role for isoform-overlapping *SLNCR* function in melanoma development, siRNAs were designed to knockdown all *SLNCR* isoforms (hereafter '*SLNCR*' refers to '*SLNCR1-3*') (FIG. 12I). These siRNAs knocked down *SLNCR* by ~60-80% in two patient-derived melanoma short-term cultures (MSTCs), WM1976 and WM858, and by 50-70% in the immortalized malignant melanoma cell line A375 (FIG. 13C). Importantly, MSTCs have undergone minimal passages outside of the patient and provide an accurate genetic model of melanoma (Lin, W.M., et al., Cancer Res, 2008. 68(3): p. 664-73). WM1976 and WM858 exhibit moderate to high levels of *SLNCR* expression, and are amenable to genetic studies requiring transfection of DNA or RNA (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37). Using RNA-sequencing (RNA-seq), melanoma cells were transcriptionally profiled before and after siRNA-mediated

knockdown of *SLNCR* in WM1976, the MSTC expressing highest levels of *SLNCR*. Depletion of *SLNCR* significantly dysregulated 222 genes compared to a scramble siRNA control, upregulating 131 genes and downregulating 91 genes ($p < 0.01$, FIG. 12E, Tables 6A-6C).

Analysis of the full melanoma dataset from The Cancer Genome Atlas (TCGA) revealed that *SLNCR* expression is significantly correlated with expression of 120 candidate target genes ($p < 0.05$, Table 6D) (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37). Moreover, expression of *SLNCR* and 62 of these target genes is significantly correlated even when correcting for multiple hypothesis testing (Bonferroni correction, $p < 0.00023$), strongly indicating that the RNA-seq analysis faithfully identified many *SLNCR*-regulated genes.

Next, *SLNCR* differentially-expressed genes (DEGs) identified herein were compared to isoform-specific *SLNCR1* DEGs identified previously (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37). Of the 222 *SLNCR* DEGs, 41 genes (18.5%) were also dysregulated upon knockdown of *SLNCR1* (Tables 6A-6C, $p < 0.01$ in both RNA-seq experiments). Moreover, the majority (35 out of 41) of *SLNCR* and *SLNCR1* DEGs displayed concordant dysregulation (Pearson $r = 0.27$, $p < 0.0001$, FIG. 13E), reflecting that *SLNCR1* and *SLNCR* similarly regulate these genes.

Importantly, 6 DEGs are discordantly regulated upon *SLNCR* or *SLNCR1* knockdown, supporting the conclusion that *SLNCR* isoforms have unique functions. Two of these discordantly regulated genes, fibronection (*FN1*) and integrin subunit beta-1 (*ITGB1*), regulate cell-matrix adhesion (Gene Ontology [GO] Enrichment analysis, GO category 0007161, $p = 1.02 \times 10^{-06}$, false discovery rate $= 1.58 \times 10^{-02}$), while another two of these genes, transmembrane protein 45A (TMEM45A) and Ras-related protein RAB31, have been implicated in cancer invasion and cell adhesion (Grismayer, B., et al., Molecular Cancer, 2012. 11: p. 62; Guo, J., et al., Oncology Reports, 2015. 33: p. 3124-3130). Combined with the findings that (i) *SLNCR1*, but not *SLNCR2* or *SLNCR3*, increase melanoma invasion (FIG. 12), and (ii) knockdown of *SLNCR1,* but not *SLNCR*, significantly decreases *MMP9* (Tables 6A-6C), it is concluded herein that *SLNCR* isoforms uniquely regulate melanoma invasion. Because knockdown of *SLNCR* or *SLNCR1* only similarly dysregulates the majority of DEGs, and all three *SLNCR* isoforms bind AR, isoform-overlapping regulation of AR was focused in the Examples presented herein.

Example 19: Implications of *SLNCR*-mediated AR activity and the melanoma gender bias

The results presented herein indicate that *SLNCR*-mediated repression of p21 requires AR and EGR1. AR has previously been implicated in the melanoma gender bias, in which men suffer more frequent and severe melanomas than females (Joosse, A., et al., The Journal of Investigative Dermatology, 2011. 131: p. 719-726; Micheli, A., et al., European Journal of Cancer, 2009. 45: p. 1017-1027; Siegel, R.L., Miller, K.D., and A. Jemal, CA: a cancer journal for clinicians, 2015. 65: p. 5-29; Spanogle, J.P., et al., Journal of the American Academy of Dermatology, 2010. 62: p. 757-767). More recent studies have confirmed oncogenic AR activity in melanoma (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37; Wang, Y., et al., Oncogene, 2017. 36: p. 1644-1654). Combined with the fact that primary male melanomas express higher AR protein than female melanomas ($p = 0.046$, FIG. 13B), it is believed that oncogenic AR activity contributes to the observed gender differences.

To explore potential contributions of *SLNCR*-mediated AR activity to these gender differences, TCGA was interrogated to determine if p21 is expressed in a gender-specific manner. To avoid confounding the analysis with p53-dependent regulation of p21, the analysis was limited to p53-deficient melanomas (Table 15). Consistent with the model that *SLNCR* and AR cooperatively repress *CDKN1A* expression, and the fact that males express higher levels of AR, male p53-deficient melanomas express significantly lower levels of p21 than females ($p = 0.045$, FIG. 25E). The gender-specific expression of a known melanoma tumor suppressor lends credence to the hypothesis that transcriptional regulation by *SLNCR* and AR contributes to the melanoma gender bias.

Despite the long-held belief that AR contributes to melanomagenesis, there has been little progress in determining the role of AR in melanoma etiology. Moreover, the interpretation that AR acts as a melanoma oncogene has been confounded by the fact that AR expression is not associated with worse overall melanoma survival. It is comprehensively interrogated herein the role of AR in melanoma gene regulation, identifying many AR-regulated tumor suppressors and oncogenes. This work indicates that *SLNCR* imparts androgen-independent oncogenic activity to AR, including repression of p21. The work presented herein highlights the importance of *SLNCR* in mediating AR's oncogenic effects in melanoma, particularly in the context of the melanoma gender bias.

Collectively, the data presented herein is consistent with a model in which *SLNCR* recruits AR to chromatin-bound EGR1 to inhibit EGR1-mediated transcriptional activation of p21 (FIG. 26). Under normal physiological conditions, EGR1 binds directly to an EGR1 consensus motif located within the *CDKN1A* promoter, increasing p21 expression. During melanomagenesis, *SLNCR* recruits AR to chromatin-bound EGR1 to inhibit EGR1 transcriptional activation of p21.

To further explore the relationship between p21 and known regulatory proteins and RNAs (identified here and elsewhere), possible associations between *SLNCR*, AR, EGR1, p53 and gender with p21 expression within the TCGA melanoma dataset (using available protein expression for AR, p53 and p21, n = 354) were investigated. Using hierarchical multiple regression it was identified herein a model containing a significant three-way interaction between *EGR1* mRNA, AR and p53 expression associated with p21 expression (estimate [95% CI] = 0.12 [0.03, 0.21], p = 0.008, Table 16). This finding is in line with data indicating that EGR1 and p53 upregulate p21 (FIG. 22 and 23), and that AR and p53 are transcriptionally and functionally linked (Table 8). The regression model also identified a borderline nonsignificant three-way interaction between EGR1, AR, and *SLNCR* (estimate [95% CI] = -0.12 [-0.25, 0.001], p = 0.052) and a significant two-way interaction between SLNCR and EGR1 (estimate [95% CI] = -0.10 (-0.19, -0.01), p = 0.024), indicating an inverse association between *SLNCR* and p21 expression dependent on the levels of EGR1 and AR. This is consistent with the mechanism demonstrated herein that EGR1 is required for *SLNCR*-mediated repression of p21. Considering the data presented herein indicating that (i) *SLNCR* binds EGR1 and AR (FIG. 22) (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37), (ii) *SLNCR* or AR knockdown increased p21 expression (FIG. 18 and 20), (iii) AR and EGR1 bind to an EGR1 DNA binding site in the p21 promoter, and (iv) the EGR1 binding site is required for *SLNCR* and AR-mediated p21 regulation (FIG. 24D), identification of this possible interaction further confirms the conclusion that *SLNCR*-mediated repression of p21 requires AR and EGR1.

SLNCR- and AR-regulated gene expression appears to be gene-specific, as *SLNCR*-mediated recruitment of AR may either increase or decrease gene expression (FIG. 17A). Intriguingly, *SLNCR* and AR can have opposing effects on a single loci, as seen with *CXCL2* (FIG. 17A).

The observations described herein provide the first global characterization of a role for AR in melanoma biology and confirm that AR binds to many melanoma-relevant genes.

Remarkably, AR is associated with these regions even in the absence of canonical hormone-mediated activation, indicating that traditional anti-androgen therapies are unlikely to inhibit oncogenic activities of AR. Instead, *SLNCR* likely recruits AR to many loci. It is important to note that *SLNCR*, but not AR, expression is associated with shorter overall melanoma survival (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37) and may be required for mediating gender-specific differences in AR activity. Collectively, the data presented herein demonstrates *SLNCR*-mediated AR function as a novel, oncogenic pathway, resulting in gender-specific differences in target gene expression. Moreover, this work is further proof that non-coding RNAs are critical regulators of human gene expression. Detailed mechanistic studies of the fundamental actions of lncRNAs and identification of their associated protein partners is critical to the design and implementation of new therapeutics.

Table 6A. Differential expression of transcripts upon siRNA knockdown of *SLNCR* in WM1976

Table 6A lists all transcripts that show differential expression upon siRNA knockdown of *SLNCR* in WM1976.

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Table 6A

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000023445	ENSG00000023445	BIRC3	11:102188214-102210134	OK	4.13371	1.08253	-1.93303	-2.26856	5.00E-05	0.0312848
ENSG00000026751	ENSG00000026751	SLAMF7	1:160709036-160724611	OK	5.97929	38.2066	2.67578	4.41381	5.00E-05	0.0312848
ENSG00000064300	ENSG00000064300	NGFR	17:47572654-47661189	OK	1.67048	6.8959	2.04548	3.34679	5.00E-05	0.0312848
ENSG00000076706	ENSG00000076706	MCAM	11:119179240-119192231	OK	100.539	234.556	1.22218	1.86587	5.00E-05	0.0312848
ENSG00000081041	ENSG00000081041	CXCL2	4:74962751-74965010	OK	14.0676	3.5472	-1.98762	-3.14041	5.00E-05	0.0312848
ENSG00000112655	ENSG00000112655	PTK7	6:43044005-43129457	OK	3.15858	7.91906	1.32605	1.94636	5.00E-05	0.0312848
ENSG00000116199	ENSG00000116199	FAM20B	1:178994938-179045697	OK	29.2921	11.4249	-1.35833	-2.51375	5.00E-05	0.0312848
ENSG00000121644	ENSG00000121644	DESI2	1:244816236-244872335	OK	12.0807	23.1934	0.941009	2.09924	5.00E-05	0.0312848
ENSG00000128564	ENSG00000128564	VGF	7:100805789-100808874	OK	0.73792	10.7728	3.86778	5.79161	5.00E-05	0.0312848
ENSG00000135046	ENSG00000135046	ANXA1	9:75766672-75785309	OK	25.4681	77.6662	1.6086	3.5394	5.00E-05	0.0312848
ENSG00000135218	ENSG00000135218	CD36	7:79959507-80308593	OK	1.65152	5.07246	1.61889	1.65931	5.00E-05	0.0312848
ENSG00000136999	ENSG00000136999	NOV	8:120428545-120474590	OK	25.789	62.1996	1.27015	2.45775	5.00E-05	0.0312848
ENSG00000141934	ENSG00000141934	PPAP2C	19:281039-291393	OK	12.3733	31.2973	1.33881	2.66514	5.00E-05	0.0312848
ENSG00000142627	ENSG00000142627	EPHA2	1:16450831-16483824	OK	5.75231	16.7272	1.53998	3.01115	5.00E-05	0.0312848
ENSG00000142949	ENSG00000142949	PTPRF	1:43990857-44089343	OK	7.42886	15.4218	1.05376	2.3162	5.00E-05	0.0312848
ENSG00000146674	ENSG00000146674	IGFBP3	7:45951948-45961473	OK	131.778	64.7348	-1.02549	-2.3814	5.00E-05	0.0312848
ENSG00000162892	ENSG00000162892	IL24	1:207070787-207077484	OK	3.22045	18.364	2.51155	3.6908	5.00E-05	0.0312848
ENSG00000163739	ENSG00000163739	CXCL1	4:74735109-74736959	OK	193.549	79.2914	-1.28746	-3.10424	5.00E-05	0.0312848
ENSG00000187135	ENSG00000187135	VSTM2B	19:29777917-30055386	OK	19.8708	42.1179	1.08379	2.39601	5.00E-05	0.0312848
ENSG00000188725	ENSG00000188725	SMIM15	5:60453535-60560756	OK	14.5261	47.955	1.72303	2.43568	5.00E-05	0.0312848
ENSG00000188783	ENSG00000188783	PRELP	1:203444955-203460480	OK	4.36771	1.01705	-2.10248	-3.80575	5.00E-05	0.0312848
ENSG00000221869	ENSG00000221869	CEBPD	8:48649470-48651648	OK	18.1426	6.8175	-1.41207	-2.88943	5.00E-05	0.0312848
ENSG00000227036	ENSG00000227036	LINC00511	17:70319263-70636611	OK	66.6256	14.7663	-2.17377	-3.78493	5.00E-05	0.0312848
ENSG00000080546	ENSG00000080546	SESN1	6:109307639-109416022	OK	7.60393	16.1685	1.08837	2.24271	0.0001	0.0513964
ENSG00000135318	ENSG00000135318	NT5E	6:86159808-86205500	OK	0.401159	2.60483	2.69894	2.43235	0.0001	0.0513964
ENSG00000139734	ENSG00000139734	DIAPH3	13:60239716-60738121	OK	11.8944	5.3762	-1.14562	-2.45815	0.0001	0.0513964
ENSG00000203837	ENSG00000203837	PNLIPRP3	10:118187378-118237469	OK	0.909978	3.17066	1.80088	2.63668	0.0001	0.0513964
ENSG00000236529	ENSG00000236529	RP13-254B10.1	7:65305198-65305583	OK	0.671322	0	#NAME?	#NAME?	0.0001	0.0513964
ENSG00000116741	ENSG00000116741	RGS2	1:192778168-192781403	OK	18.3603	38.3176	1.06142	2.24773	0.00015	0.0654136
ENSG00000121769	ENSG00000121769	FABP3	1:31838471-31849697	OK	6.3945	19.6954	1.62296	2.52296	0.00015	0.0654136
ENSG00000131409	ENSG00000131409	LRRC4B	19:51020148-51071302	OK	0.715032	2.73315	1.93448	2.2952	0.00015	0.0654136
ENSG00000139629	ENSG00000139629	GALNT6	12:51745030-51902980	OK	1.31767	4.66084	1.8226	1.24603	0.00015	0.0654136
ENSG00000143479	ENSG00000143479	DYRK3	1:206807993-206857764	OK	13.5467	26.9437	0.992011	2.21373	0.00015	0.0654136
ENSG00000005884	ENSG00000005884	ITGA3	17:48133331-48167845	OK	49.5687	99.2248	1.00127	1.51567	0.0002	0.0777892
ENSG00000114019	ENSG00000114019	AMOTL2	3:134070693-134094321	OK	8.38079	16.4089	0.969322	2.19786	0.0002	0.0777892
ENSG00000124762	ENSG00000124762	CDKN1A	6:36644304-36655116	OK	118.389	234.584	0.986566	2.20357	0.0002	0.0777892
ENSG00000131016	ENSG00000131016	AKAP12	6:151561133-151679692	OK	27.5808	14.525	-0.925125	-2.2599	0.0002	0.0777892
ENSG00000006327	ENSG00000006327	TNFRSF12A	16:3064712-3072384	OK	49.7551	96.5548	0.956506	1.66362	0.00025	0.0856607
ENSG00000100522	ENSG00000100522	GNPNAT1	14:53241911-53258386	OK	8.64083	20.4092	1.23998	1.74834	0.00025	0.0856607
ENSG00000108387	ENSG00000108387	SEPT9	17:56597197-56769416	OK	94.4412	44.0601	-1.09994	-2.23588	0.00025	0.0856607
ENSG00000118193	ENSG00000118193	KIF14	1:200520627-200589862	OK	9.48301	4.76494	-0.992889	-2.27274	0.00025	0.0856607
ENSG00000204291	ENSG00000204291	COL15A1	9:101705460-101833069	OK	6.55412	2.72614	-1.26554	-1.8544	0.00025	0.0856607
ENSG00000112237	ENSG00000112237	CCNC	6:99990255-100016972	OK	18.1063	37.9683	1.0683	1.93005	0.00035	0.114474
ENSG00000116717	ENSG00000116717	GADD45A	1:68150743-68154021	OK	15.2303	31.2765	1.03814	2.22335	0.00035	0.114474
ENSG00000143320	ENSG00000143320	CRABP2	1:156669397-156675608	OK	6.97026	17.5389	1.33127	2.28463	0.0004	0.125139
ENSG00000253276	ENSG00000253276	CCDC71L	7:106012696-106410653	OK	5.963	11.894	0.996121	2.21128	0.0004	0.125139
ENSG00000170385	ENSG00000170385	SLC30A1	1:211744909-211752084	OK	8.72539	16.164	0.889494	2.11712	0.0005	0.153096
ENSG00000088451	ENSG00000088451	TGDS	13:95226307-95248511	OK	20.6139	10.2359	-1.00998	-2.11989	0.00055	0.155197
ENSG00000114573	ENSG00000114573	ATP6V1A	3:113465718-113530903	OK	21.2949	38.5301	0.855479	2.10447	0.00055	0.155197
ENSG00000184584	ENSG00000184584	TMEM173	5:138855118-138862520	OK	7.01309	15.6661	1.15952	2.03032	0.00055	0.155197
ENSG00000244486	ENSG00000244486	SCARF2	22:20778873-20850170	OK	8.94016	22.4294	1.32702	1.99562	0.00055	0.155197
ENSG00000110492	ENSG00000110492	MDK	11:46402305-46405375	OK	25.2382	52.2038	1.04855	2.20429	0.0006	0.156993
ENSG00000127418	ENSG00000127418	FGFRL1	4:1003723-1020685	OK	1.00723	2.80924	1.47979	1.88378	0.0006	0.156993
ENSG00000132170	ENSG00000132170	PPARG	3:12328866-12475855	OK	1.75238	4.59908	1.39203	1.94601	0.0006	0.156993
ENSG00000221890	ENSG00000221890	NPTXR	22:39214456-39239987	OK	0.217667	0.758341	1.80073	2.44749	0.0006	0.156993
ENSG00000146285	ENSG00000146285	SCML4	6:108025307-108145521	OK	9.4712	4.09559	-1.20948	-2.09148	0.00065	0.167038
ENSG00000106733	ENSG00000106733	NMRK1	9:77675488-77703133	OK	8.84129	3.04853	-1.53615	-2.27211	0.0007	0.173684
ENSG00000128283	ENSG00000128283	CDC42EP1	22:37956453-37965412	OK	4.01718	8.27091	1.04186	1.93046	0.0007	0.173684
ENSG00000072571	ENSG00000072571	HMMR	5:162887208-162921064	OK	13.5653	5.79204	-1.22777	-1.83021	0.00085	0.20053
ENSG00000150093	ENSG00000150093	ITGB1	10:33189246-33371030	OK	52.4046	94.7021	0.853703	1.44068	0.00085	0.20053
ENSG00000166341	ENSG00000166341	DCHS1	11:6642555-6677085	OK	0.285433	0.767141	1.42634	2.1675	0.00085	0.20053
ENSG00000130150	ENSG00000130150	MOSPD2	X:14891562-14940449	OK	13.5226	6.65653	-1.02253	-2.0274	0.0009	0.202373
ENSG00000131196	ENSG00000131196	NFATC1	18:77155855-77289325	OK	1.75474	4.12983	1.23483	1.71553	0.0009	0.202373
ENSG00000213390	ENSG00000213390	ARHGAP19	10:98757794-99052413	OK	6.99423	3.24805	-1.10659	-1.79453	0.0009	0.202373
ENSG00000136244	ENSG00000136244	IL6	7:22765013-22771621	OK	5.02845	1.51731	-1.7286	-1.91983	0.00095	0.207143
ENSG00000177606	ENSG00000177606	JUN	1:59246464-59249785	OK	10.4766	19.5204	0.897808	2.04886	0.00095	0.207143
ENSG00000113657	ENSG00000113657	DPYSL3	5:146770373-146889619	OK	15.4293	8.06641	-0.935674	-1.79598	0.001	0.211632
ENSG00000164172	ENSG00000164172	MOCS2	5:52391508-52410956	OK	56.145	29.8509	-0.911381	-2.00531	0.001	0.211632
ENSG00000100906	ENSG00000100906	NFKBIA	14:35870716-35873955	OK	55.9969	31.104	-0.848248	-1.8809	0.00105	0.212825
ENSG00000146072	ENSG00000146072	TNFRSF21	6:47199267-47277641	OK	50.0336	28.3262	-0.820761	-2.0503	0.00105	0.212825

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000242265	ENSG00000242265	PEG10	7:94285636-94299007	OK	21.1897	12.0467	-0.814728	-1.92451	0.00105	0.212825
ENSG00000115232	ENSG00000115232	ITGA4	2:182321928-182400914	OK	13.1927	6.96395	-0.921764	-1.90872	0.0011	0.219863
ENSG00000066032	ENSG00000066032	CTNNA2	2:79384131-80875905	OK	21.563	11.5223	-0.904134	-1.40629	0.00115	0.223644
ENSG00000160867	ENSG00000160867	FGFR4	5:176513886-176525145	OK	3.89227	8.17217	1.07011	1.50145	0.00115	0.223644
ENSG00000110092	ENSG00000110092	CCND1	11:69455854-69490184	OK	192.129	360.135	0.906462	1.4578	0.00125	0.236694
ENSG00000169499	ENSG00000169499	PLEKHA2	8:38758752-38831428	OK	22.9374	11.1184	-1.04475	-1.28826	0.00125	0.236694
ENSG00000072163	ENSG00000072163	LIMS2	2:128395955-128439360	OK	1.45637	3.70447	1.34689	1.78381	0.0013	0.242965
ENSG00000161638	ENSG00000161638	ITGA5	12:54747444-54891472	OK	1.09852	3.7346	1.76539	1.3458	0.00135	0.249075
ENSG00000168610	ENSG00000168610	STAT3	17:40465341-40540586	OK	30.2507	16.4808	-0.876182	-1.70382	0.00145	0.257617
ENSG00000176845	ENSG00000176845	METRNL	17:81037566-81052864	OK	2.55424	7.14771	1.48459	1.93361	0.00145	0.257617
ENSG00000188452	ENSG00000188452	CERKL	2:182401402-182545603	OK	3.54	1.71127	-1.04869	-1.6834	0.00145	0.257617
ENSG00000184500	ENSG00000184500	PROS1	3:93591880-93692910	OK	41.7949	74.3832	0.831652	1.81377	0.0015	0.26325
ENSG00000112977	ENSG00000112977	DAP	5:10679341-10770406	OK	45.0937	24.9333	-0.854849	-1.89643	0.00155	0.26774
ENSG00000012660	ENSG00000012660	ELOVL5	6:53132195-53213947	OK	81.5122	42.2344	-0.948598	-1.88364	0.0016	0.26774
ENSG00000186205	ENSG00000186205	1-Mar	1:220960100-220987735	OK	0.475762	1.67109	1.81248	1.25238	0.0016	0.26774
ENSG00000271267	ENSG00000271267	RP11-29H23.7	1:155535840-155536097	OK	1.14862	0	#NAME?	#NAME?	0.0016	0.26774
ENSG00000105011	ENSG00000105011	ASF1B	19:14229917-14247768	OK	16.3743	7.03868	-1.21806	-2.0438	0.00185	0.302538
ENSG00000134594	ENSG00000134594	RAB33A	X:129305622-129318844	OK	1.32442	3.86526	1.5452	2.15278	0.00185	0.302538
ENSG00000106780	ENSG00000106780	MEGF9	9:123363090-123476748	OK	19.3849	11.2286	-0.787752	-1.91703	0.002	0.316286
ENSG00000108691	ENSG00000108691	CCL2	17:32581899-32584222	OK	5.60181	1.72269	-1.70123	-2.04687	0.002	0.316286
ENSG00000197540	ENSG00000197540	GZMM	19:544033-549919	OK	0.813084	2.82344	1.79598	2.03735	0.002	0.316286
ENSG00000184371	ENSG00000184371	CSF1	1:110452863-110473614	OK	2.64526	5.59344	1.08033	1.60331	0.00205	0.320669
ENSG00000169551	ENSG00000169551	CT55	X:134290460-134305322	OK	2.36382	5.62545	1.25085	2.00336	0.0021	0.324958
ENSG00000114739	ENSG00000114739	ACVR2B	3:38492517-38534633	OK	3.47377	1.64035	-1.0825	-1.68698	0.0022	0.330406
ENSG00000159216	ENSG00000159216	RUNX1	21:36160097-37376965	OK	6.31318	2.92037	-1.11221	-1.39277	0.0022	0.330406
ENSG00000122966	ENSG00000122966	CIT	12:120123594-120315095	OK	35.6414	17.4359	-1.03149	-1.06929	0.00225	0.330406
ENSG00000135842	ENSG00000135842	FAM129A	1:184759857-184943682	OK	26.9178	45.3861	0.753693	1.69486	0.00225	0.330406
ENSG00000166845	ENSG00000166845	C18orf54	18:51850727-51911588	OK	4.08815	1.83818	-1.15317	-1.52171	0.00225	0.330406
ENSG00000073712	ENSG00000073712	FERMT2	14:53323985-53419153	OK	6.82605	12.2169	0.839753	1.70744	0.0023	0.334336
ENSG00000160075	ENSG00000160075	SSU72	1:1477052-1510249	OK	48.2648	82.4522	0.772586	1.84461	0.00235	0.338189
ENSG00000044524	ENSG00000044524	EPHA3	3:89156673-89531284	OK	5.83338	3.05215	-0.934503	-1.87533	0.0024	0.338612
ENSG00000159840	ENSG00000159840	ZYX	7:143078172-143220542	OK	16.9019	29.9165	0.823754	1.77001	0.0024	0.338612
ENSG00000125355	ENSG00000125355	TMEM255A	X:119392504-119445411	OK	15.0477	28.5983	0.926389	1.34158	0.00245	0.339019
ENSG00000179817	ENSG00000179817	MRGPRX4	11:18161732-18211168	OK	0.271425	1.63545	2.59106	2.50602	0.00245	0.339019
ENSG00000116209	ENSG00000116209	TMEM59	1:54497346-54519177	OK	127.508	73.7472	-0.789927	-1.81063	0.00255	0.346199
ENSG00000139350	ENSG00000139350	NEDD1	12:97301000-97347129	OK	14.3328	7.72155	-0.892359	-1.55055	0.00255	0.346199
ENSG00000172731	ENSG00000172731	LRRC20	10:72058728-72142382	OK	9.39818	4.15292	-1.17826	-1.84486	0.0026	0.349688
ENSG00000123643	ENSG00000123643	SLC36A1	5:150816606-150871942	OK	4.6104	8.95246	0.957393	1.41949	0.00265	0.353112
ENSG00000075618	ENSG00000075618	FSCN1	7:5632438-5646286	OK	1.59735	3.43963	1.10657	1.65237	0.00275	0.356534
ENSG00000174705	ENSG00000174705	SH3PXD2B	5:171752184-171881527	OK	4.98931	8.89785	0.834616	1.24287	0.00275	0.356534
ENSG00000198087	ENSG00000198087	CD2AP	6:47445524-47594999	OK	27.8033	16.6359	-0.740957	-1.67872	0.00275	0.356534
ENSG00000130600	ENSG00000130600	H19	11:2016405-2022700	OK	7.79369	17.2386	1.14527	1.65485	0.0028	0.359775
ENSG00000135069	ENSG00000135069	PSAT1	9:80912058-80945009	OK	29.4253	51.3665	0.80377	1.84882	0.00285	0.362608
ENSG00000233461	ENSG00000233461	RP11-295G20.2	1:231658133-231664302	OK	241.367	135.24	-0.8357	-1.84518	0.0029	0.362608
ENSG00000118513	ENSG00000118513	MYB	6:135502452-135540311	OK	3.20516	1.59044	-1.01097	-1.43408	0.00295	0.362608
ENSG00000106404	ENSG00000106404	CLDN15	7:100875372-100882101	OK	2.12577	0.756299	-1.49095	-1.63333	0.003	0.362608
ENSG00000170442	ENSG00000170442	KRT86	12:52626303-52702947	OK	0.093486	0.85226	3.18847	1.37006	0.003	0.362608
ENSG00000170264	ENSG00000170264	FAM161A	2:62051988-62081278	OK	15.1729	8.13648	-0.899016	-1.55989	0.00305	0.362608
ENSG00000183668	ENSG00000183668	PSG9	19:43715942-43773682	OK	1.11182	4.3564	1.97022	2.06532	0.00305	0.362608
ENSG00000205213	ENSG00000205213	LGR4	11:27387507-27503980	OK	3.23452	5.88105	0.862522	1.5531	0.00305	0.362608
ENSG00000180921	ENSG00000180921	FAM83H	8:144806102-144815971	OK	2.74058	5.12344	0.902631	1.85085	0.0031	0.362608
ENSG00000236719	ENSG00000236719	OVAAL	1:180528111-180535654	OK	0.464653	1.75045	1.9135	2.17005	0.0031	0.362608
ENSG00000031691	ENSG00000031691	CENPQ	6:49431090-49460820	OK	14.246	7.31419	-0.961787	-1.89876	0.00315	0.362608
ENSG00000151718	ENSG00000151718	WWC2	4:184020445-184241930	OK	3.3601	6.60421	0.974883	1.54712	0.00315	0.362608
ENSG00000163430	ENSG00000163430	FSTL1	3:120111139-120170100	OK	42.0042	19.0439	-1.1412	-1.49289	0.00315	0.362608
ENSG00000123240	ENSG00000123240	OPTN	10:12938626-13180291	OK	40.9391	23.2796	-0.814413	-1.41941	0.0032	0.362608
ENSG00000152291	ENSG00000152291	TGOLN2	2:85545146-85555548	OK	58.9807	34.646	-0.767556	-1.78771	0.0032	0.362608
ENSG00000160588	ENSG00000160588	MPZL3	11:118097408-118123065	OK	0.166065	0.691753	2.05851	1.36449	0.00325	0.36531
ENSG00000070669	ENSG00000070669	ASNS	7:97481429-97501854	OK	10.5099	18.9779	0.852571	1.71265	0.0033	0.36531
ENSG00000167608	ENSG00000167608	TMC4	19:54663845-54676944	OK	0.165663	0.836146	2.3355	0.675342	0.0033	0.36531
ENSG00000138119	ENSG00000138119	MYOF	10:95066185-95242074	OK	9.61062	17.1202	0.833	1.43307	0.0035	0.3731
ENSG00000138798	ENSG00000138798	EGF	4:110834039-110933422	OK	1.73343	3.53428	1.02778	1.16683	0.0035	0.3731
ENSG00000146670	ENSG00000146670	CDCA5	11:64833771-64851636	OK	28.692	16.7239	-0.778741	-1.65933	0.0035	0.3731
ENSG00000151025	ENSG00000151025	GPR158	10:25401986-25891155	OK	17.3546	7.85686	-1.14329	-1.83734	0.0035	0.3731
ENSG00000250343	ENSG00000250343	CTC-255N20.1	5:146559766-146614422	OK	3.23806	0.993385	-1.7047	-1.9836	0.0035	0.3731
ENSG00000117305	ENSG00000117305	HMGCL	1:24128374-24165110	OK	14.48	7.36592	-0.97512	-1.7663	0.00365	0.385846
ENSG00000115414	ENSG00000115414	FN1	2:216225162-216300895	OK	233.939	129.157	-0.857003	-1.4106	0.0037	0.385846
ENSG00000158764	ENSG00000158764	ITLN2	1:160901528-160924589	OK	8.68181	19.0695	1.1352	1.83255	0.0037	0.385846
ENSG00000158050	ENSG00000158050	DUSP2	2:96808904-96811179	OK	2.29522	4.98394	1.11866	1.81251	0.00385	0.395752
ENSG00000174307	ENSG00000174307	PHLDA3	1:201434619-201438365	OK	66.2584	110.097	0.732594	1.755	0.00385	0.395753

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000165304	ENSG00000165304	MELK	9:36572858-36677678	OK	20.7899	11.5941	-0.842489	-1.72809	0.0039	0.398049
ENSG00000170915	ENSG00000170915	PAQR8	6:52226218-52272575	OK	7.05365	3.89604	-0.856361	-1.81448	0.00395	0.39975
ENSG00000049449	ENSG00000049449	RCN1	11:31806339-32127301	OK	51.2029	89.2247	0.801218	1.56985	0.004	0.39975
ENSG00000138606	ENSG00000138606	SHF	15:45384847-45493373	OK	1.38259	3.94601	1.51302	1.64378	0.004	0.39975
ENSG00000156475	ENSG00000156475	PPP2R2B	5:145942788-146464347	OK	2.64995	1.05274	-1.33182	-1.14104	0.00405	0.401956
ENSG00000111057	ENSG00000111057	KRT18	12:53290976-53346686	OK	5.10018	10.1964	0.999441	1.73926	0.00415	0.409059
ENSG00000181458	ENSG00000181458	TMEM45A	3:100211462-100296288	OK	2.61078	0.895709	-1.54338	-1.59436	0.00425	0.413255
ENSG00000198682	ENSG00000198682	PAPSS2	10:89367741-89507462	OK	2.78637	6.08011	1.12571	1.47623	0.00425	0.413255
ENSG00000165195	ENSG00000165195	PIGA	X:15337572-15353676	OK	22.0951	11.5056	-0.941392	-1.57152	0.0043	0.415311
ENSG00000140044	ENSG00000140044	JDP2	14:75890385-75940814	OK	2.09781	5.19138	1.30723	1.70211	0.00445	0.424106
ENSG00000151725	ENSG00000151725	CENPU	4:185570766-185655287	OK	25.8647	13.2643	-0.963431	-1.77309	0.00445	0.424106
ENSG00000231925	ENSG00000231925	TAPBP	6:33267470-33282164	OK	28.0034	15.7022	-0.834637	-1.73379	0.00455	0.430783
ENSG00000178726	ENSG00000178726	THBD	20:23026269-23030378	OK	0.206776	0.680587	1.71871	2.01187	0.0046	0.43173
ENSG00000125148	ENSG00000125148	MT2A	16:56642110-56643409	OK	50.8286	27.0803	-0.908396	-1.80864	0.00465	0.43173
ENSG00000257390	ENSG00000257390	RP11-762I7.5	12:56137063-56236750	OK	0	1.9829	inf	#NAME?	0.00465	0.43173
ENSG00000237289	ENSG00000237289	CKMT1B	15:43885251-44010458	OK	0.310184	1.06677	1.78206	0.738184	0.0047	0.433575
ENSG00000136274	ENSG00000136274	NACAD	7:45120036-45128513	OK	0.281946	1.08894	1.94943	1.1403	0.0048	0.43998
ENSG00000118785	ENSG00000118785	SPP1	4:88896818-88904562	OK	74.2821	44.3676	-0.743508	-1.65602	0.005	0.452547
ENSG00000184363	ENSG00000184363	PKP3	11:392613-404908	OK	0.135499	0.656222	2.27591	0.513756	0.005	0.452547
ENSG00000181315	ENSG00000181315	ZNF322	6:26634610-26659980	OK	5.2553	2.29499	-1.19528	-1.44822	0.00515	0.46321
ENSG00000172819	ENSG00000172819	RARG	12:53604353-53626764	OK	18.7399	10.4549	-0.841934	-1.50363	0.0052	0.464802
ENSG00000163808	ENSG00000163808	KIF15	3:44803208-44914868	OK	10.1628	5.12214	-0.988477	-1.44087	0.00525	0.466375
ENSG00000170961	ENSG00000170961	HAS2	8:122624355-122656933	OK	17.852	10.6641	-0.74332	-1.71857	0.0053	0.467076
ENSG00000159167	ENSG00000159167	STC1	8:23699427-23712320	OK	11.5631	5.22023	-1.14735	-1.69133	0.0054	0.467076
ENSG00000166831	ENSG00000166831	RBPMS2	15:65032090-65067786	OK	1.40517	3.19285	1.18411	1.74456	0.0054	0.467076
ENSG00000170017	ENSG00000170017	ALCAM	3:105085752-105295744	OK	13.1829	22.8556	0.793874	1.60366	0.0054	0.467076
ENSG00000139645	ENSG00000139645	ANKRD52	12:56623832-56652175	OK	29.0711	17.9548	-0.695213	-1.40279	0.00545	0.467076
ENSG00000056998	ENSG00000056998	GYG2	X:2746828-2800859	OK	60.914	35.0509	-0.797324	-1.54683	0.00555	0.467076
ENSG00000102034	ENSG00000102034	ELF4	X:129198848-129244691	OK	1.69674	3.33841	0.976396	1.67715	0.00555	0.467076
ENSG00000158006	ENSG00000158006	PAFAH2	1:26286257-26324648	OK	5.65278	2.46761	-1.19584	-1.35907	0.00555	0.467076
ENSG00000164627	ENSG00000164627	KIF6	6:39297765-39693181	OK	8.20587	4.03378	-1.02453	-1.73798	0.00555	0.467076
ENSG00000069424	ENSG00000069424	KCNAB2	1:5922870-6161253	OK	14.8258	29.5563	0.995352	1.49034	0.00585	0.485182
ENSG00000144837	ENSG00000144837	PLA1A	3:119316688-119348658	OK	24.0294	14.0899	-0.770135	-1.67452	0.00585	0.485182
ENSG00000112773	ENSG00000112773	FAM46A	6:82201155-82462491	OK	13.8034	8.48817	-0.701499	-1.63757	0.0059	0.485182
ENSG00000175602	ENSG00000175602	CCDC85B	11:65657874-65659105	OK	27.6634	47.5076	0.780179	1.70618	0.0059	0.485182
ENSG00000165475	ENSG00000165475	CRYL1	13:20977805-21099996	OK	56.4969	34.0208	-0.731754	-1.68359	0.006	0.490602
ENSG00000118420	ENSG00000118420	UBE3D	6:83602116-83775560	OK	3.02825	6.54309	1.11149	1.93949	0.00615	0.500026
ENSG00000115461	ENSG00000115461	IGFBP5	2:217536827-217858802	OK	3.6735	1.24197	-1.56452	-1.32071	0.00625	0.502479
ENSG00000172247	ENSG00000172247	C1QTNF4	11:47611215-47616211	OK	0.193578	1.28168	2.72704	1.17078	0.00625	0.502479
ENSG00000168461	ENSG00000168461	RAB31	18:9708161-9862548	OK	6.26355	11.0572	0.81993	1.17191	0.00635	0.50635
ENSG00000167693	ENSG00000167693	NXN	17:702552-883010	OK	0.811196	2.38063	1.55322	1.26365	0.00645	0.50635
ENSG00000100417	ENSG00000100417	PMM1	22:41956766-41985894	OK	38.2446	22.7522	-0.749252	-1.64924	0.0065	0.50635
ENSG00000137752	ENSG00000137752	CASP1	11:104896169-104972158	OK	1.51173	3.5718	1.24045	1.09761	0.0065	0.50635
ENSG00000143437	ENSG00000143437	ARNT	1:150782180-150849244	OK	26.4835	14.6511	-0.85408	-1.35707	0.0065	0.50635
ENSG00000136816	ENSG00000136816	TOR1B	9:132565431-132573560	OK	15.6206	9.07792	-0.783017	-1.44047	0.00655	0.50635
ENSG00000129946	ENSG00000129946	SHC2	19:416582-460996	OK	5.11101	10.1368	0.987918	1.65694	0.0066	0.50635
ENSG00000147650	ENSG00000147650	LRP12	8:105501458-105601252	OK	32.5455	61.4048	0.915894	1.61471	0.0066	0.50635
ENSG00000104332	ENSG00000104332	SFRP1	8:41119480-41167016	OK	1.42489	2.87921	1.01482	1.74322	0.00665	0.50635
ENSG00000155111	ENSG00000155111	CDK19	6:110931180-111137161	OK	5.16057	2.77353	-0.895808	-1.10818	0.00665	0.50635
ENSG00000230836	ENSG00000230836	AC104135.4	2:75167384-75169797	OK	8.00754	14.7379	0.880096	1.68063	0.00675	0.511259
ENSG00000203805	ENSG00000203805	PPAPDC1A	10:122216465-122349367	OK	5.33478	11.9924	1.16862	1.66146	0.007	0.525966
ENSG00000121579	ENSG00000121579	NAA50	3:113435306-113465147	OK	37.0055	71.9164	0.958582	1.64276	0.00705	0.525966
ENSG00000073670	ENSG00000073670	ADAM11	17:42836398-42859214	OK	4.03268	7.9687	0.982605	1.59961	0.0071	0.525966
ENSG00000133636	ENSG00000133636	NTS	12:86268072-86276770	OK	1.45476	0.434451	-1.74351	-1.66134	0.00715	0.525966
ENSG00000204516	ENSG00000204516	MICB	6:31462657-31478901	OK	2.74406	5.42895	0.984358	1.56391	0.00715	0.525966
ENSG00000115956	ENSG00000115956	PLEK	2:68588345-68624585	OK	0.163438	0.751818	2.20164	1.59759	0.0072	0.525965
ENSG00000166710	ENSG00000166710	B2M	15:45003674-45011075	OK	0.456503	1.68041	1.88012	0.978707	0.0072	0.525966
ENSG00000135048	ENSG00000135048	TMEM2	9:74298281-74431606	OK	15.5166	27.5806	0.829844	1.33739	0.0073	0.530577
ENSG00000163734	ENSG00000163734	CXCL3	4:74902305-74904524	OK	2.06829	0.74806	-1.46721	-1.58927	0.00755	0.544137
ENSG00000244694	ENSG00000244694	PTCHD4	6:47845763-48036425	OK	6.34424	10.9158	0.782898	1.62782	0.0076	0.544137
ENSG00000261087	ENSG00000261087	KB-1460A1.5	8:102179032-102181857	OK	0.388269	1.01224	1.38242	1.75909	0.0076	0.544137
ENSG00000144355	ENSG00000144355	DLX1	2:172949467-172954405	OK	5.60562	2.73048	-1.03772	-1.56543	0.0078	0.555692
ENSG00000136048	ENSG00000136048	DRAM1	12:102271128-102405908	OK	4.98693	8.73904	0.809324	1.28224	0.0079	0.560044
ENSG00000185875	ENSG00000185875	THNSL1	10:25305586-25315593	OK	1.7592	0.848754	-1.0515	-1.66905	0.00795	0.560826
ENSG00000090621	ENSG00000090621	PABPC4	1:40026487-40042462	OK	49.7917	83.6748	0.748888	1.30039	0.008	0.5616
ENSG00000065809	ENSG00000065809	FAM107B	10:14560555-14816896	OK	1.10846	2.54432	1.19872	0.868112	0.00805	0.562367
ENSG00000131374	ENSG00000131374	TBC1D5	3:17198653-18959184	OK	26.6305	15.2557	-0.803731	-0.875512	0.00815	0.566602
ENSG00000130203	ENSG00000130203	APOE	19:45409010-45412650	OK	251.199	414.985	0.72423	1.62993	0.0083	0.568787
ENSG00000172183	ENSG00000172183	ISG20	15:89179383-89199714	OK	1.37799	4.51629	1.71257	1.48651	0.0083	0.568787
ENSG00000186654	ENSG00000186654	PRR5	22:45064592-45258665	OK	3.83389	7.50062	0.9682	1.59202	0.0083	0.568787
ENSG00000107281	ENSG00000107281	NPDC1	9:139933921-139940655	OK	0.539845	1.57573	1.5454	1.12091	0.00845	0.576322
ENSG00000113758	ENSG00000113758	DBN1	5:176883608-176901402	OK	24.7406	41.949	0.761756	1.48535	0.00855	0.580392
ENSG00000179627	ENSG00000179627	ZBTB42	14:105266932-105271049	OK	1.37187	2.72406	0.989613	1.62455	0.00865	0.581692
ENSG00000184990	ENSG00000184990	SIVA1	14:105219436-105234831	OK	97.069	56.3659	-0.784188	-1.6355	0.00865	0.581692
ENSG00000011566	ENSG00000011566	MAP4K3	2:39476406-39945103	OK	11.8812	19.2447	0.695783	1.12394	0.0087	0.582333
ENSG00000104783	ENSG00000104783	KCNN4	19:44270684-44285409	OK	0.348731	1.35945	1.96283	1.09381	0.00905	0.602956
ENSG00000130513	ENSG00000130513	GDF15	19:18485540-18499986	OK	1046.11	1778.98	0.766015	1.60183	0.0091	0.603494

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000108924	ENSG00000108924	HLF	17:53342372-53402426	OK	0.287422	0.928197	1.69126	0.731493	0.00925	0.606107
ENSG00000185909	ENSG00000185909	KLHDC8B	3:49209043-49213917	OK	16.2449	29.4712	0.859313	1.54404	0.0093	0.606107
ENSG00000101197	ENSG00000101197	BIRC7	20:61867234-61871859	OK	163.212	263.676	0.692021	1.54672	0.00935	0.606107
ENSG00000118640	ENSG00000118640	VAMP8	2:85788684-85809154	OK	0.464121	1.68446	1.85971	1.50169	0.00935	0.606107
ENSG00000147434	ENSG00000147434	CHRNA6	8:42607762-42651535	OK	0.37526	1.15333	1.61985	1.07815	0.00935	0.606107
ENSG00000133816	ENSG00000133816	MICAL2	11:12115542-12285334	OK	5.11434	9.6951	0.922706	1.10154	0.00945	0.60712
ENSG00000168843	ENSG00000168843	FSTL5	4:162300104-163085187	OK	1.98116	0.951795	-1.05762	-1.40385	0.00945	0.60712
ENSG00000163735	ENSG00000163735	CXCL5	4:74861358-74864496	OK	1.6759	0.745335	-1.16897	-1.63257	0.00965	0.617214
ENSG00000174371	ENSG00000174371	EXO1	1:242011268-242058450	OK	19.123	10.5998	-0.85128	-1.29699	0.0098	0.624035
ENSG00000110852	ENSG00000110852	CLEC2B	12:10005582-10022735	OK	0.435409	1.24056	1.51055	1.38266	0.01005	0.637135
ENSG00000107020	ENSG00000107020	PLGRKT	9:5357972-5437878	OK	43.1027	25.3877	-0.76365	-1.51456	0.01025	0.646964
ENSG00000196074	ENSG00000196074	SYCP2	20:58438617-58508710	OK	8.00259	3.29014	-1.28232	-1.31517	0.0103	0.647281
ENSG00000166165	ENSG00000166165	CKB	14:103985995-103989448	OK	98.1496	169.77	0.790531	1.5428	0.01035	0.647595
ENSG00000104833	ENSG00000104833	TUBB4A	19:6494329-6502859	OK	34.8695	53.843	0.626792	1.44818	0.0104	0.647906
ENSG00000197249	ENSG00000197249	SERPINA1	14:94843083-94857030	OK	0.929621	1.99145	1.0991	0.992985	0.0105	0.651317
ENSG00000167994	ENSG00000167994	RAB3IL1	11:61664772-61687741	OK	10.0734	16.51	0.71279	1.43754	0.01055	0.65161
ENSG00000158516	ENSG00000158516	CPA2	7:129906666-129929638	OK	1.9283	3.98401	1.04689	1.51623	0.0106	0.6519
ENSG00000243759	ENSG00000243759	ST13P15	3:142984063-143567373	OK	2.83287	6.63084	1.22693	1.64794	0.0107	0.65525
ENSG00000225259	ENSG00000225259	ST13P6	8:134420248-134421471	OK	30.1269	58.8382	0.965699	1.55557	0.0108	0.658571
ENSG00000092529	ENSG00000092529	CAPN3	15:42500610-42704516	OK	203.418	104.612	-0.959395	-1.66342	0.011	0.667937
ENSG00000225106	ENSG00000225106	RP11-429E11.2	20:59827481-60515673	OK	3.93337	8.63266	1.13404	1.66042	0.01105	0.668154
ENSG00000151233	ENSG00000151233	GXYLT1	12:42475646-42538681	OK	9.27249	4.7871	-0.953805	-1.56478	0.0111	0.668369
ENSG00000094975	ENSG00000094975	SUCO	1:172501488-172580971	OK	17.1123	10.8215	-0.661127	-1.38034	0.01115	0.668582
ENSG00000089356	ENSG00000089356	FXYD3	19:35606731-35615228	OK	275.662	168.838	-0.707259	-1.57482	0.0113	0.671976
ENSG00000169306	ENSG00000169306	IL1RAPL1	X:28605515-29974840	OK	0.350947	0.912804	1.37905	1.64358	0.0113	0.671976
ENSG00000204941	ENSG00000204941	PSG5	19:43670407-43690688	OK	0.235515	0.796622	1.75808	0.797573	0.01135	0.672172
ENSG00000120889	ENSG00000120889	TNFRSF10B	8:22545171-22941132	OK	49.0853	82.117	0.742389	1.4432	0.0116	0.6786
ENSG00000184489	ENSG00000184489	PTP4A3	8:142400038-142441620	OK	4.36358	8.35602	0.937304	1.50819	0.0116	0.6786
ENSG00000235750	ENSG00000235750	KIAA0040	1:175126122-175162135	OK	0.435964	1.15848	1.40995	1.16659	0.0116	0.6786
ENSG00000117632	ENSG00000117632	STMN1	1:26210671-26233482	OK	361.458	223.773	-0.691795	-1.56371	0.0117	0.679093
ENSG00000004700	ENSG00000004700	RECQL	12:21590548-21654603	OK	33.2392	18.5152	-0.844179	-1.33891	0.01175	0.679093
ENSG00000136158	ENSG00000136158	SPRY2	13:80910110-80915086	OK	38.7162	59.7058	0.624933	1.52645	0.01175	0.679093
ENSG00000119314	ENSG00000119314	PTBP3	9:114980714-115095947	OK	15.6994	10.0734	-0.640166	-1.31742	0.01185	0.682133
ENSG00000119946	ENSG00000119946	CNNM1	10:101088855-101154087	OK	0.941088	1.88041	0.998642	1.27957	0.01195	0.685149
ENSG00000186185	ENSG00000186185	KIF18B	17:43002076-43025082	OK	15.6335	8.63521	-0.856337	-1.30099	0.01215	0.693852
ENSG00000130707	ENSG00000130707	ASS1	9:133320315-133376661	OK	0.363974	1.12979	1.63414	0.811171	0.01235	0.69972
ENSG00000175592	ENSG00000175592	FOSL1	11:65659519-65668044	OK	21.7287	36.1543	0.734568	1.54972	0.01235	0.69972
ENSG00000118276	ENSG00000118276	B4GALT6	18:29202209-29266786	OK	12.7686	7.08165	-0.85044	-1.5354	0.0124	0.699798
ENSG00000157600	ENSG00000157600	TMEM164	X:109245858-109425962	OK	14.7471	23.9912	0.702067	0.717176	0.01245	0.699875
ENSG00000133121	ENSG00000133121	STARD13	13:33677271-33924767	OK	4.44993	2.52613	-0.816854	-1.19584	0.0128	0.714015
ENSG00000178773	ENSG00000178773	CPNE7	16:89642175-89663654	OK	1.1222	3.23929	1.52935	1.13512	0.01285	0.714015
ENSG00000107581	ENSG00000107581	EIF3A	10:120794355-120840316	OK	96.3331	62.2733	-0.629417	-1.52179	0.0129	0.714015
ENSG00000112183	ENSG00000112183	RBM24	6:17281576-17294106	OK	2.92175	5.86513	1.00533	1.43946	0.0129	0.714015
ENSG00000087077	ENSG00000087077	TRIP6	7:100464759-100471076	OK	75.775	115.477	0.607807	1.41166	0.013	0.714057
ENSG00000169297	ENSG00000169297	NR0B1	X:30322322-30327715	OK	0.688699	1.67546	1.28261	1.35531	0.013	0.714057
ENSG00000100290	ENSG00000100290	BIK	22:43506753-43525718	OK	12.654	22.9222	0.857149	1.55269	0.0131	0.716814
ENSG00000140262	ENSG00000140262	TCF12	15:57210820-57591479	OK	8.99281	14.8301	0.721685	1.05965	0.0134	0.727575
ENSG00000119138	ENSG00000119138	KLF9	9:72999502-73029540	OK	8.89157	5.57031	-0.67468	-1.51853	0.01345	0.727575
ENSG00000006652	ENSG00000006652	IFRD1	7:112063022-112131117	OK	46.0832	73.4588	0.672695	1.46331	0.01355	0.727575
ENSG00000163811	ENSG00000163811	WDR43	2:29117508-29171088	OK	29.1928	50.5925	0.793314	1.31731	0.01355	0.727575
ENSG00000228110	ENSG00000228110	ST13P19	1:210438980-210440587	OK	2.49985	5.19356	1.05488	1.49215	0.01355	0.727575
ENSG00000163956	ENSG00000163956	LRPAP1	4:3508102-3534286	OK	138.615	83.1354	-0.737547	-1.51724	0.0136	0.727575
ENSG00000151743	ENSG00000151743	AMN1	12:31800093-31882108	OK	14.5583	7.48526	-0.959721	-1.41243	0.0138	0.735422
ENSG00000146592	ENSG00000146592	CREB5	7:28338939-28865511	OK	1.68809	4.64838	1.46133	1.10157	0.01385	0.735422
ENSG00000221930	ENSG00000221930	FAM45B	X:129611042-129658231	OK	21.3401	11.9799	-0.83295	-1.56446	0.0139	0.735422
ENSG00000110042	ENSG00000110042	DTX4	11:58938902-58980424	OK	4.8861	2.68768	-0.862319	-1.19602	0.01405	0.740407
ENSG00000158246	ENSG00000158246	FAM46B	1:27331510-27339327	OK	0.426816	1.05278	1.30252	1.57704	0.01415	0.740407
ENSG00000163785	ENSG00000163785	RYK	3:133784146-133969689	OK	19.4315	33.4477	0.783511	1.2212	0.0142	0.740407
ENSG00000269378	ENSG00000269378	ITGB1P1	19:14729928-14889353	OK	54.9608	96.6331	0.814115	1.53498	0.0142	0.740407
ENSG00000101856	ENSG00000101856	PGRMC1	X:118370215-118378429	OK	37.4333	57.0183	0.607103	1.4869	0.01445	0.748021
ENSG00000124098	ENSG00000124098	FAM210B	20:54933970-54943719	OK	122.7	79.7994	-0.620684	-1.37222	0.01445	0.748021
ENSG00000145431	ENSG00000145431	PDGFC	4:157681605-157892546	OK	0.866679	2.07429	1.25905	1.24281	0.01465	0.755527
ENSG00000105974	ENSG00000105974	CAV1	7:116164838-116201233	OK	121.654	72.2	-0.752713	-1.46435	0.0147	0.755528
ENSG00000119285	ENSG00000119285	HEATR1	1:236681299-236767804	OK	10.0495	17.5042	0.800579	1.13108	0.015	0.764522
ENSG00000056558	ENSG00000056558	TRAF1	9:123664670-123691451	OK	0.864421	1.65375	0.935932	1.54048	0.01505	0.764522
ENSG00000145391	ENSG00000145391	SETD7	4:140417094-140527853	OK	4.20357	6.87353	0.709438	1.20405	0.0151	0.764522
ENSG00000118596	ENSG00000118596	SLC16A7	12:59989847-60176395	OK	10.8285	4.98995	-1.11773	-1.31184	0.0152	0.764522
ENSG00000250588	ENSG00000250588	IQCJ-SCHIP1	3:158680023-159615155	OK	5.30388	11.0387	1.05746	1.49849	0.0152	0.764522
ENSG00000117724	ENSG00000117724	CENPF	1:214776537-214837931	OK	45.2638	21.9837	-1.04192	-1.27031	0.01525	0.764522
ENSG00000110031	ENSG00000110031	LPXN	11:58294343-58345693	OK	28.9292	45.2484	0.645341	1.39311	0.0153	0.764522
ENSG00000166851	ENSG00000166851	PLK1	16:23688976-23724821	OK	60.1761	39.5828	-0.604318	-1.35604	0.0153	0.764522
ENSG00000141542	ENSG00000141542	RAB40B	17:80612848-80656604	OK	2.77703	5.69819	1.03696	1.26441	0.0154	0.76621
ENSG00000101003	ENSG00000101003	GINS1	20:25388362-25433264	OK	12.8111	7.16943	-0.837466	-1.24166	0.01545	0.76621
ENSG00000122952	ENSG00000122952	ZWINT	10:58116988-58121036	OK	43.4329	25.9479	-0.743169	-1.46699	0.01555	0.76621

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000171017	ENSG00000171017	LRRC8E	19:7953389-7968427	OK	0.342964	1.03126	1.58828	0.992771	0.01555	0.76621
ENSG00000176438	ENSG00000176438	SYNE3	14:95883830-95942173	OK	2.99049	5.20579	0.799733	1.50814	0.0156	0.76621
ENSG00000164778	ENSG00000164778	EN2	7:155250823-155257526	OK	3.61342	6.1096	0.757714	1.46073	0.0157	0.768499
ENSG00000183762	ENSG00000183762	KREMEN1	22:29469065-29564321	OK	18.063	11.8961	-0.602556	-1.26783	0.01585	0.772317
ENSG00000138778	ENSG00000138778	CENPE	4:104026962-104119566	OK	4.5532	2.56613	-0.827288	-1.055	0.016	0.772317
ENSG00000196116	ENSG00000196116	TDRD7	9:100174231-100258407	OK	25.0626	37.7044	0.589194	1.35872	0.016	0.772317
ENSG00000196368	ENSG00000196368	NUDT11	X:51232862-51239448	OK	0.464092	1.09607	1.23985	1.5657	0.01605	0.772317
ENSG00000101210	ENSG00000101210	EEF1A2	20:62119365-62130505	OK	4.08733	7.48272	0.872402	1.4889	0.0161	0.772317
ENSG00000148411	ENSG00000148411	NACC2	9:138898382-138987131	OK	10.7802	16.3189	0.598153	1.41312	0.0161	0.772317
ENSG00000156509	ENSG00000156509	FBXO43	8:101145587-101158028	OK	1.211	0.545655	-1.15014	-1.54446	0.0163	0.779115
ENSG00000198208	ENSG00000198208	RPS6KL1	14:75370656-75390099	OK	1.56636	3.44265	1.13611	1.16276	0.01635	0.779115
ENSG00000165240	ENSG00000165240	ATP7A	X:77166193-77305892	OK	5.76214	3.41786	-0.753511	-1.51244	0.01645	0.78109
ENSG00000197601	ENSG00000197601	FAR1	11:13690216-13753893	OK	19.3359	10.4693	-0.885124	-1.35633	0.0165	0.78109
ENSG00000085831	ENSG00000085831	TTC39A	1:51752929-51810788	OK	35.1066	55.3921	0.657938	1.43409	0.0166	0.782019
ENSG00000185567	ENSG00000185567	AHNAK2	14:105403580-105444694	OK	13.8009	25.1694	0.866902	1.4136	0.01665	0.782019
ENSG00000130829	ENSG00000130829	DUSP9	X:152907945-152916781	OK	0.474999	1.12779	1.2475	1.32873	0.01675	0.782019
ENSG00000132541	ENSG00000132541	HRSP12	8:99114571-99129469	OK	14.6099	8.18762	-0.835435	-1.45412	0.0168	0.782019
ENSG00000188157	ENSG00000188157	AGRN	1:955502-991496	OK	33.8156	53.9396	0.673657	0.78737	0.0168	0.782019
ENSG00000012124	ENSG00000012124	CD22	19:35810163-35838258	OK	4.12925	2.08927	-0.982881	-0.900585	0.0169	0.782019
ENSG00000119541	ENSG00000119541	VPS4B	18:61056422-61089716	OK	13.7146	26.6244	0.95703	1.4531	0.0169	0.782019
ENSG00000176624	ENSG00000176624	MEX3C	18:48700919-48744674	OK	40.4489	73.1127	0.854022	1.40862	0.017	0.784125
ENSG00000077009	ENSG00000077009	NMRK2	19:3933100-3942414	OK	14.6896	25.3503	0.787207	1.46408	0.01715	0.787646
ENSG00000158022	ENSG00000158022	TRIM63	1:26377794-26394927	OK	48.8977	73.6195	0.590319	1.44592	0.0172	0.787646
ENSG00000183615	ENSG00000183615	FAM167B	1:32712833-32714457	OK	64.0276	99.028	0.629142	1.46422	0.0173	0.787646
ENSG00000103269	ENSG00000103269	RHBDL1	16:725665-728268	OK	0.527754	1.27994	1.27814	1.39811	0.01735	0.787646
ENSG00000136982	ENSG00000136982	DSCC1	8:120846215-120868250	OK	11.7729	7.21735	-0.705931	-1.42538	0.01735	0.787646
ENSG00000164109	ENSG00000164109	MAD2L1	4:120976762-121337921	OK	40.0223	23.2029	-0.7865	-1.44129	0.01745	0.789695
ENSG00000250903	ENSG00000250903	GMDS-AS1	6:2245981-2482256	OK	4.52009	1.85591	-1.28422	-1.29878	0.01755	0.791281
ENSG00000140682	ENSG00000140682	TGFB1I1	16:31482905-31489281	OK	0.981781	2.22544	1.18062	1.006	0.0176	0.791281
ENSG00000115170	ENSG00000115170	ACVR1	2:158592957-158732374	OK	26.5474	40.3299	0.603279	1.26666	0.01765	0.791281
ENSG00000113739	ENSG00000113739	STC2	5:172741715-172756506	OK	0.361763	1.19553	1.72453	1.07146	0.01795	0.802231
ENSG00000070808	ENSG00000070808	CAMK2A	5:149569519-149669854	OK	0.26648	0.779882	1.54923	0.884105	0.01805	0.803682
ENSG00000137501	ENSG00000137501	SYTL2	11:85405266-85522184	OK	11.9708	19.587	0.710371	1.12206	0.0181	0.803682
ENSG00000138166	ENSG00000138166	DUSP5	10:112257595-112271302	OK	3.0091	5.2711	0.808774	1.45232	0.01815	0.803682
ENSG00000187193	ENSG00000187193	MT1X	16:56716335-56721964	OK	10.8637	4.85788	-1.16112	-1.49881	0.0183	0.807838
ENSG00000153914	ENSG00000153914	SREK1	5:65435798-65479443	OK	27.2012	16.3619	-0.733332	-1.08881	0.01845	0.811969
ENSG00000105849	ENSG00000105849	TWISTNB	7:19735084-19748710	OK	15.0331	22.6397	0.590718	1.17202	0.0186	0.815348
ENSG00000121653	ENSG00000121653	MAPK8IP1	11:45907201-45928016	OK	2.44838	4.31631	0.817971	1.34683	0.0187	0.815348
ENSG00000102879	ENSG00000102879	CORO1A	16:30194147-30200397	OK	0.955577	2.29416	1.26352	0.894076	0.01875	0.815348
ENSG00000226950	ENSG00000226950	DANCR	4:53578596-53586998	OK	64.3671	97.725	0.602405	1.38209	0.01885	0.815348
ENSG00000104756	ENSG00000104756	KCTD9	8:25285365-25315992	OK	36.6718	18.4505	-0.991013	-1.17812	0.0189	0.815348
ENSG00000181649	ENSG00000181649	PHLDA2	11:2949502-2950685	OK	63.3425	95.4629	0.591766	1.40951	0.0189	0.815348
ENSG00000128298	ENSG00000128298	BAIAP2L2	22:38480895-38506677	OK	3.611	7.25502	1.00658	1.4333	0.019	0.815348
ENSG00000174021	ENSG00000174021	GNG5	1:84964007-85040163	OK	57.2201	95.2732	0.735547	1.47813	0.0191	0.815348
ENSG00000197766	ENSG00000197766	CFD	19:859452-863453	OK	0.776561	2.01422	1.37505	1.4076	0.0191	0.815348
ENSG00000081189	ENSG00000081189	MEF2C	5:87803362-88762215	OK	4.79117	8.17371	0.770612	1.06078	0.01915	0.815348
ENSG00000197622	ENSG00000197622	CDC42SE1	1:151020215-151042801	OK	86.4061	56.0822	-0.623589	-1.38807	0.01915	0.815348
ENSG00000100380	ENSG00000100380	ST13	22:41220538-41253026	OK	119.909	208.782	0.800059	1.39905	0.0193	0.819311
ENSG00000165238	ENSG00000165238	WNK2	9:95947197-96108696	OK	0.390808	1.31339	1.74877	0.902634	0.0195	0.820866
ENSG00000122574	ENSG00000122574	WIPF3	7:29846101-29956682	OK	2.13286	3.68816	0.790116	1.46586	0.01965	0.820866
ENSG00000134109	ENSG00000134109	EDEM1	3:5229226-5261642	OK	16.2155	24.2216	0.578918	0.891459	0.01965	0.820866
ENSG00000187951	ENSG00000187951	ARHGAP11B	15:30909160-31065196	OK	5.76882	2.73452	-1.07699	-1.1521	0.01965	0.820866
ENSG00000077713	ENSG00000077713	SLC25A43	X:118533022-118588441	OK	12.0243	7.44399	-0.691802	-1.38578	0.0198	0.820866
ENSG00000144746	ENSG00000144746	ARL6IP5	3:69134094-69155217	OK	59.8462	88.3148	0.561396	1.39285	0.0198	0.820866
ENSG00000077152	ENSG00000077152	UBE2T	1:202300784-202311108	OK	53.9194	34.5209	-0.643333	-1.42332	0.01985	0.820866
ENSG00000077232	ENSG00000077232	DNAJC10	2:183580998-183659191	OK	49.9378	31.6434	-0.658225	-1.24258	0.01985	0.820866
ENSG00000147813	ENSG00000147813	NAPRT1	8:144655659-144660819	OK	9.49097	16.4313	0.791816	1.312	0.01985	0.820866
ENSG00000106278	ENSG00000106278	PTPRZ1	7:121513142-121702090	OK	30.5088	19.2727	-0.662665	-1.17086	0.01995	0.822637
ENSG00000158373	ENSG00000158373	HIST1H2BD	6:26158348-26171577	OK	21.747	36.7859	0.758341	1.42648	0.02005	0.824399
ENSG00000126705	ENSG00000126705	AHDC1	1:27860545-27930942	OK	2.47784	3.99626	0.689569	1.26699	0.02035	0.833056
ENSG00000137845	ENSG00000137845	ADAM10	15:58887402-59042177	OK	29.1987	18.3617	-0.669208	-1.23963	0.02045	0.833056
ENSG00000105520	ENSG00000105520	DKFZP761J1410	19:11466061-11476374	OK	16.1413	24.4502	0.599089	1.27153	0.0205	0.833056
ENSG00000127022	ENSG00000127022	CANX	5:179105583-179157926	OK	165.665	254.44	0.61906	1.20704	0.0205	0.833056
ENSG00000087842	ENSG00000087842	PIR	X:15402920-15574652	OK	155.745	104.77	-0.571963	-1.38708	0.02055	0.833056
ENSG00000054793	ENSG00000054793	ATP9A	20:50213052-50385173	OK	15.0526	22.3607	0.570948	1.39074	0.02065	0.833479
ENSG00000154146	ENSG00000154146	NRGN	11:124609741-124617106	OK	1.5781	0.623538	-1.33964	-1.47944	0.02075	0.833479
ENSG00000258417	ENSG00000258417	OC90	8:133036466-133123406	OK	3.94233	2.0338	-0.954869	-1.42803	0.02075	0.833479
ENSG00000130766	ENSG00000130766	SESN2	1:28586037-28609002	OK	5.49569	8.81597	0.681817	1.43923	0.0208	0.833479
ENSG00000122042	ENSG00000122042	UBL3	13:30338507-30424821	OK	72.2293	107.64	0.575561	1.40176	0.02085	0.833479
ENSG00000189410	ENSG00000189410	SH2D5	1:21046224-21059330	OK	0.887574	1.99341	1.1673	0.985153	0.0211	0.841136
ENSG00000198830	ENSG00000198830	HMGN2	1:26798940-26802463	OK	197.376	131.94	-0.581058	-1.30836	0.0212	0.842788
ENSG00000152229	ENSG00000152229	PSTPIP2	18:43563501-43652238	OK	0.308026	0.755648	1.29466	0.945395	0.0213	0.844431
ENSG00000111266	ENSG00000111266	DUSP16	12:12628828-12715317	OK	10.7145	16.3457	0.609346	1.19995	0.0214	0.846064
ENSG00000137337	ENSG00000137337	MDC1	6:30667583-30685666	OK	14.6163	9.2823	-0.655023	-0.9056	0.0215	0.846644
ENSG00000164114	ENSG00000164114	MAP9	4:156197840-156302498	OK	5.73555	2.83882	-1.01464	-1.24249	0.0216	0.846644
ENSG00000196754	ENSG00000196754	S100A2	1:153533583-153540366	OK	2.81934	6.52262	1.21009	1.39356	0.02165	0.846644

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000247498	ENSG00000247498	RP11-392P7.6	12:13080659-13193613	OK	0.153561	0.671009	2.12752	0.288729	0.02165	0.846644
ENSG00000180828	ENSG00000180828	BHLHE22	8:65486862-65496181	OK	0.910178	0.403572	-1.17332	-1.48589	0.02215	0.861921
ENSG00000004660	ENSG00000004660	CAMKK1	17:3763608-3798185	OK	1.52057	2.71529	0.836495	1.42192	0.02225	0.861921
ENSG00000124641	ENSG00000124641	MED20	6:41873091-41888877	OK	24.52	14.9095	-0.717724	-1.35318	0.0223	0.861921
ENSG00000136280	ENSG00000136280	CCM2	7:45039073-45116068	OK	28.2196	18.3554	-0.620496	-1.31118	0.02235	0.861921
ENSG00000188290	ENSG00000188290	HES4	1:934341-935552	OK	0.448996	1.27011	1.50018	1.3502	0.02235	0.861921
ENSG00000205978	ENSG00000205978	NYNRIN	14:24867991-24888494	OK	0.197053	0.78685	1.9975	1.23486	0.0224	0.861921
ENSG00000223573	ENSG00000223573	TINCR	19:5558177-5568045	OK	0.668715	1.72422	1.36648	1.22442	0.0226	0.866905
ENSG00000151929	ENSG00000151929	BAG3	10:121410881-121437331	OK	14.3332	22.2164	0.632262	1.38918	0.02265	0.866905
ENSG00000047410	ENSG00000047410	TPR	1:186265404-186344825	OK	24.4462	15.47	-0.660135	-0.7504	0.0228	0.870331
ENSG00000109832	ENSG00000109832	DDX25	11:125773141-125808811	OK	0.351062	0.917051	1.38528	0.873366	0.0229	0.871434
ENSG00000150756	ENSG00000150756	FAM173B	5:10226441-10250027	OK	15.8172	8.65944	-0.869149	-1.39488	0.02295	0.871434
ENSG00000158292	ENSG00000158292	GPR153	1:6307405-6321035	OK	6.1405	9.70983	0.661089	1.41115	0.02305	0.872525
ENSG00000103479	ENSG00000103479	RBL2	16:53467888-53538323	OK	13.5907	8.62739	-0.655618	-1.08003	0.0231	0.872525
ENSG00000112290	ENSG00000112290	WASF1	6:110421021-110501207	OK	2.71323	4.81918	0.828774	1.27066	0.0232	0.873605
ENSG00000272373	ENSG00000272373	ZNF33B	10:43069632-43134016	OK	0.116482	1.02146	3.13244	0.514733	0.02325	0.873605
ENSG00000183161	ENSG00000183161	FANCF	11:22644078-22834601	OK	5.98539	10.1388	0.760365	1.39645	0.02335	0.874674
ENSG00000138592	ENSG00000138592	USP8	15:50716576-50838905	OK	14.3837	9.07222	-0.664905	-1.02303	0.0234	0.874674
ENSG00000003056	ENSG00000003056	M6PR	12:9066491-9102551	OK	136.048	208.569	0.616408	1.13859	0.0235	0.876136
ENSG00000091409	ENSG00000091409	ITGA6	2:173292081-173489823	OK	33.7577	54.906	0.701748	1.13057	0.0236	0.877591
ENSG00000106789	ENSG00000106789	CORO2A	9:100883256-100954922	OK	0.774341	1.38563	0.8395	1.38928	0.0237	0.877851
ENSG00000253522	ENSG00000253522	MIR146A	5:159895274-159914433	OK	79.7864	54.418	-0.552057	-1.35663	0.0238	0.877851
ENSG00000255717	ENSG00000255717	SNHG1	11:62619459-62623386	OK	73.0563	113.24	0.6323	1.38349	0.02395	0.877851
ENSG00000136731	ENSG00000136731	UGGT1	2:128848773-128953251	OK	28.2806	18.7075	-0.596196	-0.898766	0.02415	0.877851
ENSG00000197969	ENSG00000197969	VPS13A	9:79791671-80036457	OK	7.63193	4.70976	-0.696393	-0.744943	0.02415	0.877851
ENSG00000060140	ENSG00000060140	STYK1	12:10771537-10826917	OK	0.250252	0.965387	1.94772	0.743114	0.0242	0.877851
ENSG00000162600	ENSG00000162600	OMA1	1:57394882-59012474	OK	9.63213	5.5214	-0.802822	-1.16251	0.02425	0.877851
ENSG00000202538	ENSG00000202538	RNU4-2	12:120729565-120729706	OK	0	6.78845	inf	#NAME?	0.02425	0.877851
ENSG00000217801	ENSG00000217801	RP11-465B22.3	1:995113-1004735	OK	4.60663	10.6251	1.20569	1.46268	0.02425	0.877851
ENSG00000139187	ENSG00000139187	KLRG1	12:9102639-9163356	OK	1.2605	0.414465	-1.60468	-1.02589	0.0243	0.877851
ENSG00000139329	ENSG00000139329	LUM	12:91496405-91505608	OK	216.482	134.302	-0.688767	-1.37252	0.0243	0.877851
ENSG00000015133	ENSG00000015133	CCDC88C	14:91737666-91884188	OK	0.477267	1.09068	1.19236	0.72185	0.02435	0.877851
ENSG00000132481	ENSG00000132481	TRIM47	17:73870241-73875627	OK	3.87584	6.81697	0.814622	1.22535	0.0244	0.877851
ENSG00000035499	ENSG00000035499	DEPDC1B	5:59892738-59996017	OK	21.2673	13.8184	-0.622044	-1.34255	0.0247	0.881227
ENSG00000077150	ENSG00000077150	NFKB2	10:104153866-104162281	OK	23.0612	15.1955	-0.601826	-1.14236	0.0247	0.881227
ENSG00000111261	ENSG00000111261	MANSC1	12:12482197-12503475	OK	1.32117	2.63906	0.998205	1.33653	0.0247	0.881227
ENSG00000127329	ENSG00000127329	PTPRB	12:70861859-71031220	OK	0.858122	1.65007	0.943275	1.08609	0.02475	0.881227
ENSG00000115204	ENSG00000115204	MPV17	2:27532359-27548547	OK	59.6274	38.9452	-0.614529	-1.33302	0.0248	0.881227
ENSG00000065923	ENSG00000065923	SLC9A7	X:46464752-46618490	OK	0.31969	1.01275	1.66353	0.904247	0.02495	0.884373
ENSG00000112981	ENSG00000112981	NME5	5:137450865-137475132	OK	3.48128	1.71673	-1.01995	-1.16864	0.02505	0.885736
ENSG00000124795	ENSG00000124795	DEK	6:18224098-18265054	OK	110.756	72.6844	-0.607664	-1.20383	0.02525	0.890619
ENSG00000072195	ENSG00000072195	SPEG	2:220299567-220403494	OK	0.327925	0.846604	1.36832	0.284604	0.0254	0.89372
ENSG00000175455	ENSG00000175455	CCDC14	3:123616151-123680564	OK	22.6237	14.7179	-0.620257	-0.96431	0.02555	0.893775
ENSG00000142794	ENSG00000142794	NBPF3	1:21766620-21811498	OK	7.9335	4.63603	-0.775068	-1.2275	0.0256	0.893775
ENSG00000197122	ENSG00000197122	SRC	20:35973087-36034453	OK	11.5415	17.9495	0.637119	0.946977	0.0256	0.893775
ENSG00000141232	ENSG00000141232	TOB1	17:48939583-48987593	OK	34.2146	53.5818	0.647129	1.37705	0.02565	0.893775
ENSG00000023902	ENSG00000023902	PLEKHO1	1:150121372-150136916	OK	12.8462	21.6761	0.754757	1.33379	0.02585	0.894298
ENSG00000180488	ENSG00000180488	FAM73A	1:78245308-78344106	OK	4.03973	8.38153	1.05296	1.31648	0.02585	0.894298
ENSG00000006638	ENSG00000006638	TBXA2R	19:3594503-3606838	OK	3.72922	6.33385	0.764209	1.2532	0.02595	0.894298
ENSG00000065054	ENSG00000065054	SLC9A3R2	16:2075356-2089027	OK	4.82677	8.68288	0.847116	1.37433	0.026	0.894298
ENSG00000115884	ENSG00000115884	SDC1	2:20400557-20425194	OK	10.5568	16.7309	0.664337	1.30993	0.026	0.894298
ENSG00000204396	ENSG00000204396	VWA7	6:31733366-31745108	OK	0.192848	0.804752	2.06108	0.981253	0.02605	0.894298
ENSG00000131711	ENSG00000131711	MAP1B	5:71403060-71505395	OK	2.75866	4.25998	0.62688	1.25602	0.0261	0.894298
ENSG00000124942	ENSG00000124942	AHNAK	11:62201015-62323707	OK	25.1899	36.8926	0.550485	0.790905	0.02625	0.89688
ENSG00000118402	ENSG00000118402	ELOVL4	6:80624528-80657297	OK	1.93914	3.35002	0.788753	1.37773	0.0263	0.89688
ENSG00000232053	ENSG00000232053	AC009784.3	7:135777672-136122174	OK	0.289632	1.10059	1.92598	1.0534	0.02645	0.899863
ENSG00000104341	ENSG00000104341	LAPTM4B	8:98787284-98865241	OK	104.035	165.354	0.668486	1.32653	0.02675	0.907923
ENSG00000101928	ENSG00000101928	MOSPD1	X:134021655-134049297	OK	15.2539	25.4286	0.737279	1.27908	0.02685	0.909173
ENSG00000087510	ENSG00000087510	TFAP2C	20:55204357-55214339	OK	2.71394	4.67254	0.783816	1.34804	0.027	0.90997
ENSG00000184640	ENSG00000184640	9-Sep	17:75253818-75496678	OK	248.485	157.307	-0.659572	-1.03208	0.027	0.90997
ENSG00000145725	ENSG00000145725	PPIP5K2	5:102421703-102548500	OK	21.5872	12.3866	-0.801391	-1.0733	0.0272	0.914568
ENSG00000165891	ENSG00000165891	E2F7	12:77415026-77459360	OK	16.3373	11.0328	-0.566372	-1.07141	0.0275	0.915492
ENSG00000150938	ENSG00000150938	CRIM1	2:36583068-36873230	OK	2.39992	4.91631	1.03459	0.935383	0.02755	0.915492
ENSG00000021300	ENSG00000021300	PLEKHB1	11:73357222-73373864	OK	10.2737	6.69999	-0.61673	-1.13955	0.02765	0.915492
ENSG00000100504	ENSG00000100504	PYGL	14:51314839-51411454	OK	88.5677	59.5292	-0.573182	-1.26912	0.02765	0.915492
ENSG00000145386	ENSG00000145386	CCNA2	4:122722471-122745087	OK	26.4147	15.6015	-0.759656	-1.38053	0.02765	0.915492
ENSG00000250182	ENSG00000250182	EEF1A1P13	5:14652046-14653438	OK	63.315	93.5165	0.562673	1.34805	0.02765	0.915492
ENSG00000253738	ENSG00000253738	GS1-251I9.4	8:92072136-92082417	OK	10.7296	6.6274	-0.69508	-1.37003	0.0277	0.915492
ENSG00000111670	ENSG00000111670	GNPTAB	12:102139274-102224716	OK	89.8167	61.5707	-0.544741	-0.895588	0.02775	0.915492
ENSG00000164211	ENSG00000164211	STARD4	5:110831730-111353006	OK	16.016	9.67263	-0.727536	-1.24285	0.0278	0.915492
ENSG00000147475	ENSG00000147475	ERLIN2	8:37592278-37616619	OK	28.214	16.3037	-0.791209	-1.19598	0.028	0.919973

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000254389	ENSG00000254389	RHPN1-AS1	8:144448800-144450718	OK	0.36495	1.36344	1.90148	1.13386	0.0281	0.921155
ENSG00000119397	ENSG00000119397	CNTRL	9:123837140-123939888	OK	5.2132	3.0967	-0.751434	-1.13601	0.0283	0.925136
ENSG00000133805	ENSG00000133805	AMPD3	11:10329859-10529126	OK	0.825039	0.296667	-1.47562	-0.441668	0.02835	0.925136
ENSG00000146021	ENSG00000146021	KLHL3	5:136953188-137071779	OK	0.635634	0.291075	-1.1268	-0.577626	0.0286	0.929485
ENSG00000176204	ENSG00000176204	LRRTM4	2:76974844-77820445	OK	2.93729	1.68407	-0.802538	-1.26181	0.02875	0.929485
ENSG00000145247	ENSG00000145247	OCIAD2	4:48887035-48908954	OK	0.773258	2.12968	1.46162	0.793115	0.02885	0.929485
ENSG00000071073	ENSG00000071073	MGAT4A	2:99235568-99347589	OK	9.25278	4.62643	-0.999989	-1.18835	0.0289	0.929485
ENSG00000159459	ENSG00000159459	UBR1	15:43235094-43398311	OK	3.24778	5.38587	0.729727	0.917297	0.02895	0.929485
ENSG00000108379	ENSG00000108379	WNT3	17:44839871-44910520	OK	0.303628	0.672969	1.14823	0.914476	0.029	0.929485
ENSG00000197444	ENSG00000197444	OGDHL	10:50942688-50970425	OK	0.501628	1.01334	1.01443	1.06443	0.029	0.929485
ENSG00000253368	ENSG00000253368	TRNP1	1:27320197-27327389	OK	5.11894	9.28852	0.859605	1.33085	0.029	0.929486
ENSG00000069869	ENSG00000069869	NEDD4	15:56119119-56285944	OK	1.25583	2.32997	0.891674	0.84098	0.02915	0.932217
ENSG00000187514	ENSG00000187514	PTMA	2:232571516-232578251	OK	849.964	570.339	-0.575582	-1.31996	0.02945	0.937309
ENSG00000205693	ENSG00000205693	MANSC4	12:27915670-27924209	OK	0.2523	0.888904	1.81689	1.42696	0.0295	0.937309
ENSG00000084710	ENSG00000084710	EFR3B	2:25264998-25378243	OK	4.22033	2.47554	-0.76961	-1.33801	0.02965	0.937309
ENSG00000132669	ENSG00000132669	RIN2	20:19867164-19983101	OK	0.85786	1.66407	0.955898	1.02141	0.02965	0.937309
ENSG00000007968	ENSG00000007968	E2F2	1:23832921-23857712	OK	1.50925	0.814466	-0.889902	-1.2045	0.0297	0.937309
ENSG00000143228	ENSG00000143228	NUF2	1:163080910-163325554	OK	57.3881	39.3141	-0.545705	-1.15714	0.0297	0.937309
ENSG00000148950	ENSG00000148950	IMMP1L	11:31453947-31531192	OK	27.5918	13.1159	-1.07293	-1.53922	0.0298	0.937453
ENSG00000091136	ENSG00000091136	LAMB1	7:107531414-107643700	OK	29.2855	51.2549	0.807504	0.706174	0.0299	0.937453
ENSG00000261452	ENSG00000261452	RP11-509E16.1	2:25380062-25382006	OK	5.29109	3.00834	-0.814594	-1.34766	0.0299	0.937453
ENSG00000165914	ENSG00000165914	TTC7B	14:91006931-91282823	OK	40.0834	26.458	-0.599302	-0.934232	0.03	0.938543
ENSG00000257267	ENSG00000257267	ZNF271	18:32870245-32890730	OK	11.3854	6.87211	-0.728364	-1.34495	0.0301	0.939153
ENSG00000134853	ENSG00000134853	PDGFRA	4:54243809-55164414	OK	0.209643	0.89822	2.09913	0.417568	0.03015	0.939153
ENSG00000148400	ENSG00000148400	NOTCH1	9:139388895-139440314	OK	3.44932	5.33693	0.629698	1.08246	0.03025	0.940233
ENSG00000108830	ENSG00000108830	RND2	17:41177257-41184057	OK	0.234642	0.840828	1.84135	1.26336	0.03035	0.940831
ENSG00000254087	ENSG00000254087	LYN	8:56792371-56923940	OK	2.88891	5.19688	0.847117	1.17874	0.0304	0.940831
ENSG00000177054	ENSG00000177054	ZDHHC13	11:19138645-19197969	OK	3.78256	6.19901	0.712674	1.21814	0.03065	0.946533
ENSG00000133169	ENSG00000133169	BEX1	X:102317578-102319168	OK	0.403147	1.25876	1.64263	1.46774	0.03075	0.9471
ENSG00000109814	ENSG00000109814	UGDH	4:39500374-39640710	OK	29.3794	16.4897	-0.833235	-1.21888	0.0308	0.9471
ENSG00000223612	ENSG00000223612	RP11-289I10.2	1:148193171-148193875	OK	1.78202	3.68113	1.04664	1.27446	0.03115	0.95181
ENSG00000107679	ENSG00000107679	PLEKHA1	10:124134211-124191867	OK	14.6076	9.29409	-0.652329	-1.24612	0.0313	0.95181
ENSG00000185614	ENSG00000185614	FAM212A	3:49840686-49842463	OK	3.16625	5.88803	0.895009	1.34404	0.0313	0.95181
ENSG00000143171	ENSG00000143171	RXRG	1:165370158-165414433	OK	28.4303	19.1164	-0.57262	-1.24986	0.03135	0.95181
ENSG00000160325	ENSG00000160325	CACFD1	9:136325088-136335970	OK	3.97567	6.57222	0.725183	1.11577	0.03135	0.95181
ENSG00000257529	ENSG00000257529	RPL36A-HNRNPH2	X:100645811-100669121	OK	0.785997	0	#NAME?	#NAME?	0.03135	0.95181
ENSG00000007312	ENSG00000007312	CD79B	17:62006099-62009714	OK	0.813124	2.13097	1.38996	1.14942	0.03145	0.951858
ENSG00000243317	ENSG00000243317	C7orf73	7:135347243-135433594	OK	60.7763	41.0988	-0.564415	-1.28458	0.0315	0.951858
ENSG00000260534	ENSG00000260534	RP11-1006G14.4	15:72882031-72884186	OK	0.291294	0.676276	1.21514	1.34768	0.03155	0.951858
ENSG00000154065	ENSG00000154065	ANKRD29	18:21178889-21242849	OK	1.08165	2.66634	1.30163	1.26462	0.0317	0.953926
ENSG00000100162	ENSG00000100162	CENPM	22:42334724-42343168	OK	26.8805	16.9599	-0.664436	-1.3129	0.03185	0.953926
ENSG00000145506	ENSG00000145506	NKD2	5:1008943-1039058	OK	0.168403	0.704126	2.06392	0.513638	0.03185	0.953926
ENSG00000135636	ENSG00000135636	DYSF	2:71680851-71913898	OK	0.335756	0.834098	1.3128	0.60465	0.0319	0.953926
ENSG00000180739	ENSG00000180739	S1PR5	19:10623622-10628607	OK	0.620818	1.29177	1.05711	1.22331	0.03195	0.953926
ENSG00000224818	ENSG00000224818	RP11-134G8.8	1:201433510-201434274	OK	2.84872	5.91594	1.05429	1.34859	0.0323	0.96238
ENSG00000172086	ENSG00000172086	KRCC1	2:88326723-88355248	OK	4.48952	2.56813	-0.805842	-1.28413	0.03245	0.964851
ENSG00000070404	ENSG00000070404	FSTL3	19:676391-683385	OK	3.1638	5.77632	0.86849	1.1779	0.03255	0.965829
ENSG00000092853	ENSG00000092853	CLSPN	1:36185818-36235568	OK	6.23774	3.40341	-0.874041	-1.22387	0.03265	0.966803
ENSG00000228889	ENSG00000228889	UBAC2-AS1	13:99848630-99852964	OK	0.841862	1.69458	1.00927	1.3212	0.0328	0.96925
ENSG00000066027	ENSG00000066027	PPP2R5A	1:212458878-212535200	OK	26.407	37.9521	0.523257	1.26304	0.03295	0.970658
ENSG00000196576	ENSG00000196576	PLXNB2	22:50713407-50746056	OK	31.5814	45.5403	0.528068	0.895209	0.033	0.970658
ENSG00000162645	ENSG00000162645	GBP2	1:89571814-89641723	OK	2.84686	1.01894	-1.48231	-1.29805	0.03305	0.970658
ENSG00000179855	ENSG00000179855	GIPC3	19:3585550-3593539	OK	5.08971	7.77566	0.611381	1.29946	0.03315	0.971612
ENSG00000088832	ENSG00000088832	FKBP1A	20:1290618-1373806	OK	165.419	249.551	0.593209	1.27539	0.0334	0.97695
ENSG00000120693	ENSG00000120693	SMAD9	13:37418967-37494902	OK	4.74371	3.0159	-0.653428	-1.26937	0.0336	0.980806
ENSG00000120833	ENSG00000120833	SOCS2	12:93936238-93977263	OK	6.60823	11.7018	0.824393	1.27586	0.034	0.98249
ENSG00000165480	ENSG00000165480	SKA3	13:21727733-21750741	OK	13.4449	8.07787	-0.735014	-1.21104	0.034	0.98249
ENSG00000223891	ENSG00000223891	OSER1-AS1	20:42839599-42854667	OK	12.8256	7.55355	-0.763801	-1.29829	0.03415	0.98249
ENSG00000137285	ENSG00000137285	TUBB2B	6:3224494-3457256	OK	21.0863	40.0334	0.924896	1.44684	0.03425	0.98249
ENSG00000135823	ENSG00000135823	STX6	1:180882289-180992047	OK	15.9935	23.9737	0.583971	1.16731	0.0343	0.98249
ENSG00000136247	ENSG00000136247	ZDHHC4	7:6617064-6629005	OK	32.4811	20.7997	-0.643038	-1.3138	0.0343	0.98249
ENSG00000067560	ENSG00000067560	RHOA	3:49396577-49453908	OK	161.217	235.796	0.548534	1.27333	0.03435	0.98249
ENSG00000123496	ENSG00000123496	IL13RA2	X:114238537-114254540	OK	46.9483	68.2484	0.539721	1.28508	0.0344	0.98249
ENSG00000051180	ENSG00000051180	RAD51	15:40978921-41024354	OK	6.00488	2.69269	-1.15709	-1.20451	0.03455	0.98249
ENSG00000099840	ENSG00000099840	IZUMO4	19:2071036-2099592	OK	0.183046	0.764288	2.06191	0.40392	0.03455	0.98249
ENSG00000105379	ENSG00000105379	ETFB	19:51848422-51872257	OK	55.3377	36.2959	-0.608455	-1.29362	0.03455	0.98249
ENSG00000138182	ENSG00000138182	KIF20B	10:91461366-91534700	OK	6.46978	4.14872	-0.641051	-1.27468	0.0347	0.98249
ENSG00000115556	ENSG00000115556	PLCD4	2:219472487-219501907	OK	1.11313	2.25505	1.01854	0.864441	0.03475	0.98249
ENSG00000139438	ENSG00000139438	FAM222A	12:110152032-110211313	OK	4.10404	6.57346	0.679609	1.18801	0.03475	0.98249
ENSG00000143457	ENSG00000143457	GOLPH3L	1:150618700-150669630	OK	17.015	10.2175	-0.735761	-1.26165	0.03475	0.98249

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226742	ENSG00000226742	HSBP1L1	18:77724560-77730822	OK	24.678	38.9969	0.660132	1.3068	0.03475	0.98249
ENSG00000266578	ENSG00000266578	RP11-838N2.5	18:3284142-3327290	OK	1.11	0.349376	-1.66771	-1.41274	0.035	0.987618
ENSG00000124126	ENSG00000124126	PREX1	20:47240789-47444420	OK	1.91686	3.00947	0.650765	1.22366	0.03535	0.990604
ENSG00000164187	ENSG00000164187	LMBRD2	5:36098513-36152063	OK	4.59175	2.6545	-0.790602	-0.677148	0.03535	0.990604
ENSG00000161677	ENSG00000161677	JOSD2	19:51009254-51014610	OK	31.1192	19.2885	-0.690065	-1.21148	0.0354	0.990604
ENSG00000156802	ENSG00000156802	ATAD2	8:124332089-124428590	OK	13.9627	9.52595	-0.551645	-1.24683	0.03545	0.990604
ENSG00000188013	ENSG00000188013	MEIS3P2	17:20487070-20494493	OK	1.39387	2.79413	1.0033	1.32966	0.03545	0.990604
ENSG00000070087	ENSG00000070087	PFN2	3:149478891-149942977	OK	142.434	214.61	0.591426	1.11995	0.03555	0.990947
ENSG00000175155	ENSG00000175155	YPEL2	17:57409049-57480664	OK	7.01466	4.40261	-0.672015	-0.939487	0.0356	0.990947
ENSG00000180730	ENSG00000180730	SHISA2	13:26618734-26625169	OK	4.60667	2.75114	-0.743693	-1.29393	0.03585	0.99406
ENSG00000224397	ENSG00000224397	RP11-290F20.3	20:48884022-48896332	OK	21.9758	11.8842	-0.886872	-1.2488	0.03585	0.99406
ENSG00000177679	ENSG00000177679	SRRM3	7:75831215-75916605	OK	3.62785	5.84753	0.688713	1.25189	0.03625	0.9998
ENSG00000123989	ENSG00000123989	CHPF	2:220403668-220415317	OK	27.6189	41.7107	0.594761	1.2702	0.03635	0.9998
ENSG00000185896	ENSG00000185896	LAMP1	13:113951555-113977987	OK	97.6325	143.264	0.553239	1.28652	0.03645	0.9998
ENSG00000162444	ENSG00000162444	RBP7	1:10057263-10076078	OK	0.565111	1.63741	1.53481	1.25801	0.0365	0.9998
ENSG00000112319	ENSG00000112319	EYA4	6:133561735-134216691	OK	9.42222	14.3827	0.6102	1.16546	0.0366	0.9998
ENSG00000126752	ENSG00000126752	SSX1	X:48114751-48126879	OK	7.73116	4.58408	-0.754053	-1.28328	0.0367	0.9998
ENSG00000144357	ENSG00000144357	UBR3	2:170683967-170940641	OK	6.25178	9.28044	0.569926	1.02446	0.03695	0.9998
ENSG00000237506	ENSG00000237506	RPSAP15	X:86958276-86959307	OK	59.8153	86.9658	0.539933	1.27751	0.03695	0.9998
ENSG00000119681	ENSG00000119681	LTBP2	14:74964872-75079306	OK	0.485346	0.958214	0.981333	0.776934	0.0373	0.9998
ENSG00000260807	ENSG00000260807	RP11-161M6.2	16:903633-1031663	OK	0.161188	0.774684	2.26487	0.575263	0.03755	0.9998
ENSG00000228623	ENSG00000228623	ZNF883	9:115759494-115774507	OK	0.281504	0.632632	1.16821	1.29698	0.03765	0.9998
ENSG00000103540	ENSG00000103540	CCP110	16:19535132-19564730	OK	7.64842	4.97493	-0.620485	-0.988985	0.03775	0.9998
ENSG00000198959	ENSG00000198959	TGM2	20:36756862-36794980	OK	10.8479	16.6099	0.614624	1.28835	0.03775	0.9998
ENSG00000165244	ENSG00000165244	ZNF367	9:99148222-99180611	OK	4.67186	7.18998	0.62199	1.24278	0.03805	0.9998
ENSG00000030419	ENSG00000030419	IKZF2	2:213446080-214017151	OK	0.908933	0.466497	-0.962307	-0.641765	0.0382	0.9998
ENSG00000143067	ENSG00000143067	ZNF697	1:120162044-120190396	OK	21.6976	14.8957	-0.542643	-1.29296	0.03835	0.9998
ENSG00000146247	ENSG00000146247	PHIP	6:79577188-79787953	OK	7.19266	4.83088	-0.57424	-1.2806	0.0384	0.9998
ENSG00000132970	ENSG00000132970	WASF3	13:27131839-27263085	OK	3.38391	5.1313	0.600632	1.23827	0.0385	0.9998
ENSG00000231584	ENSG00000231584	FAHD2CP	2:96676298-96705199	OK	17.1891	10.6136	-0.695574	-1.25756	0.03855	0.9998
ENSG00000163069	ENSG00000163069	SGCB	4:52886871-52904648	OK	11.908	19.2296	0.691397	1.08219	0.03885	0.9998
ENSG00000179431	ENSG00000179431	FJX1	11:35639734-35642419	OK	1.93489	3.61496	0.901731	1.21302	0.0392	0.9998
ENSG00000196584	ENSG00000196584	XRCC2	7:152341863-152373250	OK	6.28742	3.90351	-0.687698	-1.25575	0.0394	0.9998
ENSG00000233117	ENSG00000233117	LINC00702	10:4243332-4286104	OK	0.495964	2.28948	2.20671	1.30346	0.03955	0.9998
ENSG00000270123	ENSG00000270123	VTRNA2-1	5:135416159-135416286	OK	23.0757	0	#NAME?	#NAME?	0.03955	0.9998
ENSG00000172660	ENSG00000172660	TAF15	17:34136458-34195895	OK	46.3098	30.3144	-0.611314	-1.16736	0.0398	0.9998
ENSG00000196843	ENSG00000196843	ARID5A	2:97202479-97218375	OK	3.06959	5.19317	0.758569	1.25601	0.03995	0.9998
ENSG00000107798	ENSG00000107798	LIPA	10:90973325-91174314	OK	54.7449	36.8906	-0.56947	-1.2199	0.04015	0.9998
ENSG00000182827	ENSG00000182827	ACBD3	1:226332379-226374431	OK	23.1538	33.6683	0.540141	0.834917	0.0402	0.9998
ENSG00000152127	ENSG00000152127	MGAT5	2:134877553-135212192	OK	47.5054	31.9464	-0.572438	-0.611724	0.04025	0.9998
ENSG00000182718	ENSG00000182718	ANXA2	15:60639332-60695082	OK	350.665	492.66	0.490498	1.17413	0.0403	0.9998
ENSG00000062725	ENSG00000062725	APPBP2	17:58520519-58603580	OK	24.2543	14.2742	-0.764834	-0.969732	0.04035	0.9998
ENSG00000236453	ENSG00000236453	AC003092.1	7:93652144-93695973	OK	1.40105	3.13734	1.16303	1.33068	0.0405	0.9998
ENSG00000164089	ENSG00000164089	ETNPPL	4:109663195-109684210	OK	9.16094	5.82447	-0.65337	-1.03289	0.04055	0.9998
ENSG00000108639	ENSG00000108639	SYNGR2	17:76164638-76169608	OK	39.5822	59.5538	0.589343	1.2846	0.04065	0.9998
ENSG00000135469	ENSG00000135469	COQ10A	12:56660641-56664750	OK	10.5183	16.6093	0.659082	1.25298	0.0407	0.9998
ENSG00000177084	ENSG00000177084	POLE	12:133200347-133263951	OK	11.3952	7.7131	-0.563039	-0.558894	0.0407	0.9998
ENSG00000079337	ENSG00000079337	RAPGEF3	12:48099867-48231681	OK	2.22413	5.2277	1.23294	0.869569	0.0408	0.9998
ENSG00000172379	ENSG00000172379	ARNT2	15:80696691-80890278	OK	18.2301	12.5296	-0.540979	-1.19749	0.04085	0.9998
ENSG00000008283	ENSG00000008283	CYB561	17:61509664-61523739	OK	6.10319	9.21906	0.595057	0.9637	0.04105	0.9998
ENSG00000101972	ENSG00000101972	STAG2	X:123093082-124097666	OK	25.255	16.7295	-0.594179	-0.841523	0.04105	0.9998
ENSG00000165923	ENSG00000165923	AGBL2	11:47681142-47736941	OK	1.08974	0.407667	-1.41852	-0.755938	0.0411	0.9998
ENSG00000085840	ENSG00000085840	ORC1	1:52838500-52870131	OK	3.94331	2.43713	-0.694224	-1.26635	0.04115	0.9998
ENSG00000083312	ENSG00000083312	TNPO1	5:72090231-72212560	OK	73.6212	109.468	0.572322	0.78143	0.04125	0.9998
ENSG00000173457	ENSG00000173457	PPP1R14B	11:64011955-64016966	OK	136.948	198.254	0.53372	1.25395	0.04125	0.9998
ENSG00000116663	ENSG00000116663	FBXO6	1:11724180-11734411	OK	15.2989	22.8666	0.579813	1.20971	0.04145	0.9998
ENSG00000100311	ENSG00000100311	PDGFB	22:39619363-39640756	OK	0.242057	0.711421	1.55536	0.88024	0.0415	0.9998
ENSG00000103855	ENSG00000103855	CD276	15:73976306-74006859	OK	28.8911	41.9926	0.539512	1.11784	0.0415	0.9998
ENSG00000154945	ENSG00000154945	ANKRD40	17:48770550-48785285	OK	29.3102	20.7618	-0.497469	-1.19798	0.0416	0.9998
ENSG00000010318	ENSG00000010318	PHF7	3:52444672-52457657	OK	4.62329	2.16085	-1.09732	-1.17273	0.04165	0.9998
ENSG00000205309	ENSG00000205309	NT5M	17:17206648-17250977	OK	2.95868	1.60955	-0.878302	-1.12713	0.04165	0.9998
ENSG00000169826	ENSG00000169826	CSGALNACT2	10:43633933-43680756	OK	1.91833	3.08988	0.687704	1.23952	0.0417	0.9998
ENSG00000160752	ENSG00000160752	FDPS	1:155278538-155300905	OK	467.603	304.055	-0.62095	-1.25153	0.04195	0.9998
ENSG00000090104	ENSG00000090104	RGS1	1:192544856-192549161	OK	41.4985	62.5187	0.59123	1.22438	0.042	0.9998
ENSG00000112759	ENSG00000112759	SLC29A1	6:44187241-44201888	OK	21.2184	31.3798	0.564522	1.30127	0.04205	0.9998
ENSG00000176208	ENSG00000176208	ATAD5	17:29158987-29222887	OK	2.19669	1.31446	-0.740861	-1.27608	0.04205	0.9998
ENSG00000138795	ENSG00000138795	LEF1	4:108968700-109177992	OK	49.3926	32.2771	-0.613782	-1.07572	0.0422	0.9998
ENSG00000123612	ENSG00000123612	ACVR1C	2:158383278-158485517	OK	1.41507	2.89122	1.0308	1.27501	0.0423	0.9998
ENSG00000178878	ENSG00000178878	APOLD1	12:12878850-12982915	OK	50.3874	32.3895	-0.637537	-1.24731	0.04235	0.9998
ENSG00000224184	ENSG00000224184	AC096559.1	2:11988747-12718474	OK	4.33454	2.03119	-1.09355	-1.14014	0.04235	0.9998
ENSG00000171365	ENSG00000171365	CLCN5	X:49687224-49863892	OK	8.84502	4.47033	-0.984485	-0.832621	0.0425	0.9998
ENSG00000136738	ENSG00000136738	STAM	10:17686123-17757913	OK	13.0222	19.0608	0.549639	1.12454	0.04255	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000177885	ENSG00000177885	GRB2	17:73314156-73401790	OK	50.2281	89.0447	0.826034	1.22082	0.04265	0.9998
ENSG00000149679	ENSG00000149679	CABLES2	20:60963687-60982341	OK	8.53626	4.52797	-0.914741	-1.21626	0.04285	0.9998
ENSG00000188906	ENSG00000188906	LRRK2	12:40579810-40763087	OK	4.73765	2.8441	-0.736201	-1.11947	0.04285	0.9998
ENSG00000196409	ENSG00000196409	ZNF658	9:40760699-40836415	OK	0.90256	0.460824	-0.969809	-1.17128	0.043	0.9998
ENSG00000136492	ENSG00000136492	BRIP1	17:59758626-59940882	OK	6.99852	4.72233	-0.567552	-1.02391	0.04305	0.9998
ENSG00000184879	ENSG00000184879	RP11-7G23.8	9:45733440-45734896	OK	1.34494	0	#NAME?	#NAME?	0.04305	0.9998
ENSG00000157680	ENSG00000157680	DGKI	7:137065782-137531838	OK	1.26061	2.5599	1.02197	0.858538	0.0432	0.9998
ENSG00000179941	ENSG00000179941	BBS10	12:76738253-76742222	OK	3.38703	2.08909	-0.697149	-1.25432	0.0432	0.9998
ENSG00000085563	ENSG00000085563	ABCB1	7:87133174-87461611	OK	0.600815	1.41592	1.23675	0.881288	0.04325	0.9998
ENSG00000163297	ENSG00000163297	ANTXR2	4:80822302-81046608	OK	4.72432	8.57632	0.860252	1.19733	0.04325	0.9998
ENSG00000100697	ENSG00000100697	DICER1	14:95552564-95646263	OK	19.4292	13.1299	-0.56537	-0.763794	0.0433	0.9998
ENSG00000163347	ENSG00000163347	CLDN1	3:190023489-190040264	OK	8.99603	13.5514	0.591078	0.937856	0.04345	0.9998
ENSG00000092929	ENSG00000092929	UNC13D	17:73823305-73840798	OK	0.417426	1.03894	1.31552	0.525418	0.0435	0.9998
ENSG00000149948	ENSG00000149948	HMGA2	12:66151799-66360075	OK	7.21432	11.3172	0.649582	0.958417	0.0436	0.9998
ENSG00000102158	ENSG00000102158	MAGT1	X:77081860-77151090	OK	22.0106	15.371	-0.517988	-1.20091	0.0437	0.9998
ENSG00000164023	ENSG00000164023	SGMS2	4:108745718-108899955	OK	1.30092	3.19424	1.29594	0.578052	0.0437	0.9998
ENSG00000108551	ENSG00000108551	RASD1	17:17397750-17399709	OK	10.2406	16.4769	0.686139	1.23682	0.0438	0.9998
ENSG00000186522	ENSG00000186522	10-Sep	2:110300558-110371783	OK	33.0203	22.9202	-0.526731	-1.06465	0.04395	0.9998
ENSG00000126787	ENSG00000126787	DLGAP5	14:55614829-55658396	OK	27.9606	19.5851	-0.513634	-1.09748	0.0444	0.9998
ENSG00000008735	ENSG00000008735	MAPK8IP2	22:51007289-51052409	OK	8.56472	15.3285	0.839739	1.25821	0.04455	0.9998
ENSG00000189057	ENSG00000189057	FAM111B	11:58874657-58894883	OK	4.17877	2.56143	-0.706125	-1.08786	0.04465	0.9998
ENSG00000068383	ENSG00000068383	INPP5A	10:134351323-134598269	OK	5.94854	10.1947	0.777206	1.15439	0.0447	0.9998
ENSG00000159184	ENSG00000159184	HOXB13	17:46800529-46806540	OK	2.65407	4.27362	0.687253	1.23998	0.0447	0.9998
ENSG00000207501	ENSG00000207501	RNVU1-14	1:148241464-148241628	OK	3.78844	0	#NAME?	#NAME?	0.04485	0.9998
ENSG00000100271	ENSG00000100271	TTLL1	22:43434590-43485434	OK	4.57942	2.70346	-0.760354	-1.18302	0.0451	0.9998
ENSG00000131080	ENSG00000131080	EDA2R	X:65815478-65859108	OK	8.15752	12.0985	0.568627	1.12267	0.0455	0.9998
ENSG00000149798	ENSG00000149798	CDC42EP2	11:65082288-65089900	OK	0.968457	1.74888	0.852673	1.18491	0.04555	0.9998
ENSG00000094804	ENSG00000094804	CDC6	17:38443884-38459171	OK	30.3859	18.4193	-0.722187	-1.14321	0.04565	0.9998
ENSG00000063587	ENSG00000063587	ZNF275	X:152599612-152625568	OK	1.31698	2.08122	0.660198	1.17345	0.04575	0.9998
ENSG00000151239	ENSG00000151239	TWF1	12:44187525-44200178	OK	80.8351	56.6181	-0.513718	-1.00137	0.046	0.9998
ENSG00000175294	ENSG00000175294	CATSPER1	11:65784222-65793988	OK	0.153568	0.877662	2.51479	1.42381	0.046	0.9998
ENSG00000234323	ENSG00000234323	RP11-308N19.1	9:109040672-109367076	OK	12.4676	7.94451	-0.650147	-1.21575	0.04615	0.9998
ENSG00000168028	ENSG00000168028	RPSA	3:39448179-39454033	OK	909.407	1326.37	0.544486	1.20245	0.0462	0.9998
ENSG00000139182	ENSG00000139182	CLSTN3	12:7281674-7311541	OK	4.55818	8.67031	0.927627	1.06319	0.0463	0.9998
ENSG00000137460	ENSG00000137460	FHDC1	4:153857503-153900848	OK	1.82702	1.11891	-0.707393	-1.2224	0.04635	0.9998
ENSG00000115290	ENSG00000115290	GRB14	2:165349321-165478358	OK	0.765247	2.03082	1.40806	1.07741	0.04655	0.9998
ENSG00000135476	ENSG00000135476	ESPL1	12:53662082-53687427	OK	17.561	12.2441	-0.520286	-0.898114	0.04655	0.9998
ENSG00000198919	ENSG00000198919	DZIP3	3:108308528-108413693	OK	7.46493	5.06667	-0.559092	-1.16744	0.04665	0.9998
ENSG00000183856	ENSG00000183856	IQGAP3	1:156495196-156542396	OK	21.719	15.1669	-0.518033	-0.850132	0.0468	0.9998
ENSG00000156521	ENSG00000156521	TYSND1	10:71897736-71906432	OK	11.0748	16.0445	0.534793	1.20648	0.04685	0.9998
ENSG00000115902	ENSG00000115902	SLC1A4	2:65215610-65250999	OK	40.5634	28.789	-0.494661	-1.06194	0.047	0.9998
ENSG00000138172	ENSG00000138172	CALHM2	10:105206542-105222452	OK	4.01428	6.69508	0.737959	1.19915	0.04705	0.9998
ENSG00000270164	ENSG00000270164	AC006129.4	19:42041544-42043266	OK	5.35471	12.0618	1.17156	1.3154	0.0471	0.9998
ENSG00000164266	ENSG00000164266	SPINK1	5:147204130-147211349	OK	0.636325	2.11502	1.73283	1.32028	0.0478	0.9998
ENSG00000018510	ENSG00000018510	AGPS	2:178092322-178408564	OK	8.45723	15.4897	0.87305	0.879363	0.0479	0.9998
ENSG00000231924	ENSG00000231924	PSG1	19:43370615-43383974	OK	0.29967	0.655995	1.13031	0.66737	0.04795	0.9998
ENSG00000072864	ENSG00000072864	NDE1	16:15737123-15950890	OK	42.8532	27.6593	-0.631635	-1.18162	0.04805	0.9998
ENSG00000143153	ENSG00000143153	ATP1B1	1:169074934-169337205	OK	5.53778	10.4067	0.910134	1.19284	0.0481	0.9998
ENSG00000116205	ENSG00000116205	TCEANC2	1:54519259-54578192	OK	3.46579	2.13795	-0.696957	-1.14591	0.04815	0.9998
ENSG00000144749	ENSG00000144749	LRIG1	3:66119284-66551687	OK	0.597168	1.60228	1.42392	0.766366	0.04825	0.9998
ENSG00000069702	ENSG00000069702	TGFBR3	1:92145901-92371892	OK	4.25952	6.44802	0.598165	1.04401	0.0483	0.9998
ENSG00000150551	ENSG00000150551	LYPD1	2:133174146-133429152	OK	4.03655	7.07841	0.810301	1.20285	0.04845	0.9998
ENSG00000179362	ENSG00000179362	HMGN2P46	15:45722726-45878488	OK	0.802207	0.134898	-2.57211	-0.540572	0.04845	0.9998
ENSG00000011426	ENSG00000011426	ANLN	7:36363829-36493400	OK	49.7352	35.3923	-0.490831	-0.962927	0.04855	0.9998
ENSG00000085491	ENSG00000085491	SLC25A24	1:108676657-108744113	OK	13.6982	9.27622	-0.562376	-1.20226	0.04855	0.9998
ENSG00000100167	ENSG00000100167	3-Sep	22:42372275-42394225	OK	2.17635	3.39779	0.642687	1.03844	0.04865	0.9998
ENSG00000100558	ENSG00000100558	PLEK2	14:67853699-67878917	OK	1.35569	2.52179	0.895418	1.04369	0.0487	0.9998
ENSG00000147854	ENSG00000147854	UHRF2	9:6413150-6507054	OK	20.3391	13.8446	-0.554929	-1.03499	0.04895	0.9998
ENSG00000182220	ENSG00000182220	ATP6AP2	X:40440145-40465889	OK	87.8883	62.4525	-0.492911	-1.1045	0.04915	0.9998
ENSG00000249855	ENSG00000249855	EEF1A1P19	5:43484060-43525412	OK	62.9307	92.1595	0.550369	1.21835	0.0492	0.9998
ENSG00000102781	ENSG00000102781	KATNAL1	13:30776766-30881621	OK	11.9644	7.23437	-0.725812	-1.07974	0.04925	0.9998
ENSG00000119042	ENSG00000119042	SATB2	2:200134222-200341658	OK	1.64419	2.67573	0.702557	1.05594	0.04925	0.9998
ENSG00000248309	ENSG00000248309	MEF2C-AS1	5:87803362-88762215	OK	0.39994	1.13826	1.50897	0.312326	0.04945	0.9998
ENSG00000047644	ENSG00000047644	WWC3	X:9983601-10112518	OK	9.51736	6.68485	-0.509665	-0.993784	0.04955	0.9998
ENSG00000181690	ENSG00000181690	PLAG1	8:57073462-57123883	OK	0.443982	0.972818	1.13167	1.0623	0.0496	0.9998
ENSG00000196943	ENSG00000196943	NOP9	14:24769067-24787242	OK	8.79083	12.8142	0.543674	1.17566	0.0497	0.9998
ENSG00000237310	ENSG00000237310	GS1-124K5.4	7:65958692-65960461	OK	5.26369	2.52823	-1.05795	-1.24519	0.04975	0.9998
ENSG00000033100	ENSG00000033100	CHPF2	7:150929574-150974982	OK	15.6499	24.5107	0.64726	1.1494	0.04985	0.9998
ENSG00000111602	ENSG00000111602	TIMELESS	12:56810902-56843187	OK	23.5845	16.7753	-0.491496	-1.13714	0.0499	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000255591	ENSG00000255591	AL590762.1	X:70503041-70521018	OK	0	6.54858	inf	#NAME?	0.04995	0.9998
ENSG00000141458	ENSG00000141458	NPC1	18:21083472-21166862	OK	31.7882	46.6883	0.55457	0.864881	0.05	0.9998
ENSG00000163535	ENSG00000163535	SGOL2	2:201353674-201448505	OK	10.5205	6.47886	-0.69939	-1.08761	0.05	0.9998
ENSG00000181104	ENSG00000181104	F2R	5:75699073-76031606	OK	17.065	24.963	0.548749	1.03804	0.0502	0.9998
ENSG00000243244	ENSG00000243244	STON1	2:48756521-49003654	OK	0.91874	0.48351	-0.926113	-1.06537	0.05025	0.9998
ENSG00000173598	ENSG00000173598	NUDT4	12:93771658-93797024	OK	82.7636	116.176	0.489237	1.16668	0.0504	0.9998
ENSG00000164746	ENSG00000164746	C7orf57	7:48075107-48100901	OK	1.02391	0.472975	-1.11426	-0.956505	0.0505	0.9998
ENSG00000089505	ENSG00000089505	CMTM1	16:66586465-66613040	OK	1.48542	0.496865	-1.57994	-0.305558	0.0506	0.9998
ENSG00000107438	ENSG00000107438	PDLIM1	10:96997328-97050781	OK	8.05079	12.2936	0.61071	1.16611	0.0506	0.9998
ENSG00000167632	ENSG00000167632	TRAPPC9	8:140742585-141468678	OK	9.45418	6.20316	-0.60795	-0.819563	0.0507	0.9998
ENSG00000126550	ENSG00000126550	HTN1	4:70916118-70924562	OK	38.4205	59.3502	0.627378	1.20214	0.0508	0.9998
ENSG00000154640	ENSG00000154640	BTG3	21:18965970-18985265	OK	49.8429	33.5312	-0.571882	-1.18107	0.0508	0.9998
ENSG00000156976	ENSG00000156976	EIF4A2	3:186499568-186524847	OK	366.781	539.079	0.555576	1.13455	0.05105	0.9998
ENSG00000149260	ENSG00000149260	CAPN5	11:76777978-76837201	OK	5.59022	8.56933	0.616279	1.05216	0.0511	0.9998
ENSG00000204792	ENSG00000204792	AC104135.3	2:75145274-75165545	OK	12.9984	23.6453	0.863214	1.16719	0.05115	0.9998
ENSG00000087086	ENSG00000087086	FTL	19:49468557-49470135	OK	3474.18	5369.48	0.628111	1.16963	0.0512	0.9998
ENSG00000112742	ENSG00000112742	TTK	6:80713603-80752244	OK	15.973	11.2499	-0.505725	-1.06878	0.05125	0.9998
ENSG00000164715	ENSG00000164715	LMTK2	7:97736196-97838945	OK	4.84352	3.33718	-0.537425	-1.15757	0.0513	0.9998
ENSG00000115226	ENSG00000115226	FNDC4	2:27714749-27718112	OK	1.74533	3.3221	0.928598	1.22176	0.05135	0.9998
ENSG00000024422	ENSG00000024422	EHD2	19:48110780-48246391	OK	2.95299	5.1139	0.792247	1.10566	0.0514	0.9998
ENSG00000013810	ENSG00000013810	TACC3	4:1723226-1746898	OK	21.5316	14.5604	-0.564408	-0.978551	0.0515	0.9998
ENSG00000221829	ENSG00000221829	FANCG	9:35073831-35080013	OK	20.6902	13.7997	-0.584314	-0.879083	0.05165	0.9998
ENSG00000134996	ENSG00000134996	OSTF1	9:77703458-77762181	OK	36.3705	24.7352	-0.556204	-1.19218	0.0517	0.9998
ENSG00000237821	ENSG00000237821	AC083873.4	7:132854173-132855272	OK	1.6254	3.02356	0.895458	1.22025	0.05175	0.9998
ENSG00000171004	ENSG00000171004	HS6ST2	X:131760043-132095423	OK	1.77672	3.10789	0.806722	1.17275	0.05215	0.9998
ENSG00000038274	ENSG00000038274	MAT2B	5:162930119-162946342	OK	29.0382	20.3724	-0.511333	-1.17697	0.0526	0.9998
ENSG00000138160	ENSG00000138160	KIF11	10:94353042-94415150	OK	17.4354	12.3772	-0.494333	-1.17253	0.0526	0.9998
ENSG00000144354	ENSG00000144354	CDCA7	2:174202946-174233725	OK	5.90212	3.67115	-0.685001	-1.17689	0.0526	0.9998
ENSG00000134160	ENSG00000134160	TRPM1	15:31293263-31453476	OK	67.9321	46.2271	-0.555355	-1.13702	0.05265	0.9998
ENSG00000102032	ENSG00000102032	RENBP	X:153200715-153210232	OK	25.3291	36.5245	0.528067	1.08461	0.05275	0.9998
ENSG00000198252	ENSG00000198252	STYX	14:53196897-53241716	OK	5.87767	3.98242	-0.561599	-1.18249	0.05275	0.9998
ENSG00000154822	ENSG00000154822	PLCL2	3:16844158-17132086	OK	0.881408	1.54289	0.807753	1.15773	0.0529	0.9998
ENSG00000215781	ENSG00000215781	AC011043.1	GL000195.1:43716-74342	OK	6.9451	4.36197	-0.671015	-1.16266	0.05325	0.9998
ENSG00000178999	ENSG00000178999	AURKB	17:8108055-8113918	OK	74.6678	52.7435	-0.501492	-1.0744	0.0533	0.9998
ENSG00000101096	ENSG00000101096	NFATC2	20:50003493-50179370	OK	13.9384	8.8768	-0.65095	-1.17411	0.05335	0.9998
ENSG00000198420	ENSG00000198420	FAM115A	7:143548467-143599291	OK	20.1594	12.7157	-0.664834	-0.924911	0.0534	0.9998
ENSG00000119508	ENSG00000119508	NR4A3	9:102584136-102629173	OK	9.89349	14.2288	0.524265	1.19395	0.0537	0.9998
ENSG00000226608	ENSG00000226608	FTLP3	20:4004551-4005091	OK	12.3033	20.3617	0.726807	1.12247	0.05375	0.9998
ENSG00000167700	ENSG00000167700	MFSD3	8:145734456-145736596	OK	15.2635	22.3331	0.549099	1.17701	0.0538	0.9998
ENSG00000155324	ENSG00000155324	GRAMD3	5:125695823-125832186	OK	4.43594	7.14407	0.687506	0.987635	0.05385	0.9998
ENSG00000049323	ENSG00000049323	LTBP1	2:33172038-33624576	OK	1.10636	1.95404	0.820644	0.779026	0.0539	0.9998
ENSG00000196440	ENSG00000196440	ARMCX4	X:100673274-100788446	OK	0.731436	1.56005	1.09279	0.812127	0.0539	0.9998
ENSG00000174501	ENSG00000174501	ANKRD36C	2:96514586-96657541	OK	2.02965	1.10434	-0.878052	-1.19048	0.05395	0.9998
ENSG00000105339	ENSG00000105339	DENND3	8:142127376-142205907	OK	1.40382	2.5966	0.887271	0.74702	0.0542	0.9998
ENSG00000196663	ENSG00000196663	TECPR2	14:102829299-102968818	OK	2.46883	4.5464	0.880898	0.833533	0.0542	0.9998
ENSG00000027075	ENSG00000027075	PRKCH	14:61654276-62125414	OK	9.83788	6.90052	-0.511641	-0.794021	0.0543	0.9998
ENSG00000126561	ENSG00000126561	STAT5A	17:40439564-40463961	OK	6.91518	10.7801	0.640531	1.0461	0.0543	0.9998
ENSG00000152270	ENSG00000152270	PDE3B	11:14665268-14892350	OK	15.2015	10.6697	-0.510692	-1.09128	0.05435	0.9998
ENSG00000179029	ENSG00000179029	TMEM107	17:8076554-8079717	OK	5.3345	2.82631	-0.916433	-1.12728	0.05435	0.9998
ENSG00000136854	ENSG00000136854	STXBP1	9:130374543-130497604	OK	184.178	127.604	-0.52943	-0.905263	0.0544	0.9998
ENSG00000104419	ENSG00000104419	NDRG1	8:134249413-134314265	OK	10.5657	16.5776	0.649852	0.864363	0.0546	0.9998
ENSG00000135097	ENSG00000135097	MSI1	12:120779132-120806983	OK	0.216675	0.710528	1.71336	0.768556	0.05475	0.9998
ENSG00000102575	ENSG00000102575	ACP5	19:11670188-11729950	OK	42.7449	61.1434	0.516442	1.13547	0.0548	0.9998
ENSG00000143476	ENSG00000143476	DTL	1:212208918-212280742	OK	19.9038	13.4377	-0.566757	-1.02207	0.05495	0.9998
ENSG00000123358	ENSG00000123358	NR4A1	12:52416615-52453291	OK	42.5883	59.6062	0.485006	0.989203	0.05505	0.9998
ENSG00000124532	ENSG00000124532	MRS2	6:24403152-24537435	OK	32.1934	48.3162	0.585742	1.18291	0.05505	0.9998
ENSG00000165886	ENSG00000165886	UBTD1	10:99258624-99330966	OK	16.533	23.7589	0.523117	1.15548	0.0551	0.9998
ENSG00000135052	ENSG00000135052	GOLM1	9:88641060-88715088	OK	68.0523	49.7143	-0.452983	-1.06202	0.05515	0.9998
ENSG00000153574	ENSG00000153574	RPIA	2:88991161-89050452	OK	18.0585	12.4004	-0.542298	-1.15114	0.0554	0.9998
ENSG00000259316	ENSG00000259316	CTD-2116N17.1	15:64457715-64679886	OK	0.868248	0.122274	-2.82799	-0.417941	0.0555	0.9998
ENSG00000134802	ENSG00000134802	SLC43A3	11:57154266-57195053	OK	76.0634	104.402	0.45687	0.949603	0.05565	0.9998
ENSG00000137310	ENSG00000137310	TCF19	6:31126318-31148508	OK	33.1827	23.5886	-0.492339	-1.1279	0.05565	0.9998
ENSG00000165091	ENSG00000165091	TMC1	9:75136716-75451267	OK	0.315709	0.65154	1.04526	0.799369	0.05565	0.9998
ENSG00000160469	ENSG00000160469	BRSK1	19:55793439-55823901	OK	3.74689	6.43164	0.779495	1.02695	0.056	0.9998
ENSG00000104998	ENSG00000104998	IL27RA	19:14142559-14163743	OK	0.351759	0.697299	0.987188	1.18113	0.05605	0.9998
ENSG00000205246	ENSG00000205246	RPSAP58	19:23945745-24057503	OK	518.804	741.344	0.514953	1.16448	0.0564	0.9998
ENSG00000273142	ENSG00000273142	RP11-458F8.4	7:66367843-66371284	OK	1.12114	0.647191	-0.792699	-1.15669	0.0566	0.9998
ENSG00000138180	ENSG00000138180	CEP55	10:95256388-95288849	OK	42.0007	30.1669	-0.477445	-1.10714	0.0569	0.9998
ENSG00000196436	ENSG00000196436	NPIPB15	16:74411775-74425978	OK	1.56402	0.791297	-0.982965	-1.20205	0.05705	0.9998
ENSG00000151882	ENSG00000151882	CCL28	5:43376746-43412493	OK	26.8093	18.2421	-0.555462	-1.08117	0.0571	0.9998
ENSG00000139835	ENSG00000139835	GRTP1	13:113978504-114018446	OK	1.25059	2.33044	0.897997	1.17384	0.05745	0.9998
ENSG00000177363	ENSG00000177363	LRRN4CL	11:62453873-62457371	OK	11.8514	17.2412	0.540802	1.17237	0.05745	0.9998
ENSG00000171681	ENSG00000171681	ATF7IP	12:14518609-14651697	OK	6.66431	9.58073	0.52368	0.817885	0.0576	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000102554	ENSG00000102554	KLF5	13:73629113-73651676	OK	1.7343	3.26893	0.914463	0.98723	0.05765	0.9998
ENSG00000143367	ENSG00000143367	TUFT1	1:151512780-151556059	OK	2.22426	3.53828	0.669719	1.04442	0.05815	0.9998
ENSG00000170677	ENSG00000170677	SOCS6	18:67956136-67997436	OK	11.5788	17.0888	0.561563	1.15417	0.0582	0.9998
ENSG00000140379	ENSG00000140379	BCL2A1	15:80253230-80263788	OK	114.514	80.9007	-0.501301	-1.14888	0.05825	0.9998
ENSG00000129667	ENSG00000129667	RHBDF2	17:74466972-74497872	OK	13.4928	8.86239	-0.606425	-0.84667	0.05835	0.9998
ENSG00000163584	ENSG00000163584	RPL22L1	3:170582663-170588272	OK	170.351	117.48	-0.536089	-1.14078	0.0584	0.9998
ENSG00000072182	ENSG00000072182	ASIC4	2:220299567-220403494	OK	0.0973593	0.725472	2.89753	0.647686	0.0587	0.9998
ENSG00000210082	ENSG00000210082	MT-RNR2	MT:1670-3229	OK	1078.47	1648.57	0.612228	1.18385	0.05895	0.9998
ENSG00000111424	ENSG00000111424	VDR	12:48235319-48336831	OK	1.04508	1.91951	0.877128	1.00308	0.059	0.9998
ENSG00000188566	ENSG00000188566	NDOR1	9:140100146-140111461	OK	5.01836	3.19943	-0.649402	-1.18428	0.05915	0.9998
ENSG00000140451	ENSG00000140451	PIF1	15:65107830-65117867	OK	7.9336	4.48188	-0.823872	-1.13518	0.0592	0.9998
ENSG00000165105	ENSG00000165105	RASEF	9:85594499-85678092	OK	4.72365	6.86207	0.538741	1.11914	0.05925	0.9998
ENSG00000136193	ENSG00000136193	SCRN1	7:29959718-30066300	OK	42.0501	59.8293	0.508743	1.08402	0.05935	0.9998
ENSG00000132031	ENSG00000132031	MATN3	2:20189977-20212455	OK	1.25537	0.683789	-0.876486	-1.06186	0.0594	0.9998
ENSG00000134531	ENSG00000134531	EMP1	12:13349649-13369708	OK	44.9271	31.9628	-0.491192	-1.02321	0.05955	0.9998
ENSG00000167105	ENSG00000167105	TMEM92	17:48348766-48358844	OK	0.317842	1.11128	1.80584	0.992656	0.05975	0.9998
ENSG00000172667	ENSG00000172667	ZMAT3	3:178735010-178790067	OK	33.3398	47.6067	0.51392	0.878892	0.05985	0.9998
ENSG00000254332	ENSG00000254332	GS1-44D20.1	8:70041832-70042580	OK	1.28419	0.466598	-1.46061	-1.25467	0.0601	0.9998
ENSG00000259886	ENSG00000259886	U82695.10	X:152689209-152691934	OK	1.61487	2.61573	0.695793	1.13094	0.06035	0.9998
ENSG00000073350	ENSG00000073350	LLGL2	17:73521160-73571289	OK	1.57229	2.59178	0.721074	0.710631	0.0604	0.9998
ENSG00000178096	ENSG00000178096	BOLA1	1:149859018-149872351	OK	27.353	17.8659	-0.614493	-1.17256	0.0604	0.9998
ENSG00000164181	ENSG00000164181	ELOVL7	5:60047617-60140216	OK	2.08148	3.49642	0.74827	1.036	0.06045	0.9998
ENSG00000127528	ENSG00000127528	KLF2	19:16435627-16438685	OK	0.717023	1.4038	0.969248	1.06585	0.06055	0.9998
ENSG00000172058	ENSG00000172058	SERF1A	5:70196491-70214357	OK	9.8227	5.93528	-0.726802	-1.09756	0.0606	0.9998
ENSG00000155640	ENSG00000155640	C10orf12	10:98741040-98745582	OK	1.66208	1.03243	-0.68695	-1.14219	0.06065	0.9998
ENSG00000162576	ENSG00000162576	MXRA8	1:1288068-1297157	OK	0.557092	1.19029	1.09532	0.844369	0.06065	0.9998
ENSG00000168481	ENSG00000168481	LGI3	8:22004337-22021992	OK	89.9828	64.3972	-0.482651	-1.1078	0.06065	0.9998
ENSG00000122223	ENSG00000122223	CD244	1:160799949-160832692	OK	1.05089	2.00161	0.929547	1.02309	0.06075	0.9998
ENSG00000231767	ENSG00000231767	MIR4426	1:192685312-192685783	OK	2.73464	5.45629	0.99657	1.18045	0.06085	0.9998
ENSG00000179862	ENSG00000179862	CITED4	1:41326728-41328018	OK	0.27754	0.686267	1.30607	1.18264	0.0612	0.9998
ENSG00000163531	ENSG00000163531	NFASC	1:204797778-204991950	OK	1.11441	1.84705	0.728933	0.838124	0.06145	0.9998
ENSG00000172292	ENSG00000172292	CERS6	2:169312371-169769881	OK	7.46405	10.9629	0.554603	1.14157	0.06155	0.9998
ENSG00000151491	ENSG00000151491	EPS8	12:15773091-16035263	OK	29.0558	41.1396	0.501698	0.932201	0.06175	0.9998
ENSG00000114251	ENSG00000114251	WNT5A	3:55499742-55523973	OK	2.80498	1.3032	-1.10592	-1.04331	0.06185	0.9998
ENSG00000134690	ENSG00000134690	CDCA8	1:38158089-38175391	OK	21.2932	15.0895	-0.49685	-1.14085	0.06195	0.9998
ENSG00000140859	ENSG00000140859	KIFC3	16:57792128-57896957	OK	16.3876	23.5135	0.520883	0.797761	0.062	0.9998
ENSG00000115457	ENSG00000115457	IGFBP2	2:217497550-217529159	OK	4.70351	7.94709	0.756688	1.15502	0.06205	0.9998
ENSG00000186660	ENSG00000186660	ZFP91	11:58346583-58393198	OK	55.8986	40.8367	-0.452947	-1.12259	0.06215	0.9998
ENSG00000159388	ENSG00000159388	BTG2	1:203274618-203278730	OK	11.4718	16.4574	0.520647	1.13211	0.0622	0.9998
ENSG00000129355	ENSG00000129355	CDKN2D	19:10677137-10679735	OK	26.1638	17.9377	-0.544581	-1.12261	0.06225	0.9998
ENSG00000142920	ENSG00000142920	ADC	1:33546704-33586131	OK	7.46109	12.2476	0.715038	0.937933	0.0624	0.9998
ENSG00000230756	ENSG00000230756	RHOQP3	2:130970442-130971063	OK	66.773	94.8368	0.506182	1.14189	0.06255	0.9998
ENSG00000184838	ENSG00000184838	PRR16	5:119799972-120023027	OK	2.9463	1.36622	-1.10871	-1.03513	0.06265	0.9998
ENSG00000160862	ENSG00000160862	AZGP1	7:99564342-99573780	OK	7.18738	11.0892	0.625615	1.10086	0.0627	0.9998
ENSG00000113761	ENSG00000113761	ZNF346	5:176449696-176508190	OK	6.62971	4.15241	-0.674995	-0.876467	0.06275	0.9998
ENSG00000167930	ENSG00000167930	ITFG3	16:284544-333003	OK	34.3355	22.9895	-0.578726	-0.914719	0.0629	0.9998
ENSG00000198910	ENSG00000198910	L1CAM	X:153126968-153200676	OK	24.2971	36.6931	0.594728	0.732275	0.0632	0.9998
ENSG00000237476	ENSG00000237476	XXbac-B135H6.15	22:21311379-21318967	OK	1.11208	0.392502	-1.50249	-1.21862	0.06325	0.9998
ENSG00000164088	ENSG00000164088	PPM1M	3:52279840-52284613	OK	2.86019	4.86389	0.766	1.0374	0.0634	0.9998
ENSG00000218426	ENSG00000218426	RP11-475C16.1	6:153552454-153668623	OK	667.834	910.514	0.447193	1.10902	0.0634	0.9998
ENSG00000150457	ENSG00000150457	LATS2	13:21547170-21635686	OK	9.923	13.7939	0.475182	0.996305	0.0635	0.9998
ENSG00000184867	ENSG00000184867	ARMCX2	X:100910266-100914876	OK	19.7565	29.1233	0.559843	0.746902	0.0636	0.9998
ENSG00000050820	ENSG00000050820	BCAR1	16:75262927-75301951	OK	7.56711	11.007	0.540601	0.934276	0.0638	0.9998
ENSG00000110881	ENSG00000110881	ASIC1	12:50451330-50477394	OK	5.34733	7.79928	0.544524	0.945048	0.06395	0.9998
ENSG00000101290	ENSG00000101290	CDS2	20:5107431-5178533	OK	16.587	28.4915	0.780482	1.1157	0.064	0.9998
ENSG00000089041	ENSG00000089041	P2RX7	12:121570621-121623876	OK	43.9507	61.5409	0.485658	1.05281	0.0641	0.9998
ENSG00000128245	ENSG00000128245	YWHAH	22:32329506-32353590	OK	151.575	106.725	-0.506126	-1.08514	0.06415	0.9998
ENSG00000095397	ENSG00000095397	DFNB31	9:117164359-117267730	OK	14.298	20.636	0.529344	1.02958	0.0642	0.9998
ENSG00000139239	ENSG00000139239	RPL14P1	12:63359094-63359764	OK	199.026	273.72	0.459746	1.13168	0.0642	0.9998
ENSG00000139618	ENSG00000139618	BRCA2	13:32889610-32973805	OK	0.722542	1.60532	1.15171	0.832866	0.0642	0.9998
ENSG00000145331	ENSG00000145331	TRMT10A	4:100467865-100547070	OK	6.04055	3.56609	-0.760338	-1.04756	0.06425	0.9998
ENSG00000177694	ENSG00000177694	NAALADL2	3:174156362-175523428	OK	0.819779	2.4492	1.579	0.827935	0.06435	0.9998
ENSG00000116819	ENSG00000116819	TFAP2E	1:36035413-36060929	OK	0.753934	1.38761	0.880096	1.14817	0.0645	0.9998
ENSG00000154358	ENSG00000154358	OBSCN	1:228391206-228566577	OK	3.23365	6.0822	0.911431	0.834444	0.06455	0.9998
ENSG00000175414	ENSG00000175414	ARL10	5:175792470-175843570	OK	0.938838	2.69826	1.52308	0.519846	0.0646	0.9998
ENSG00000176771	ENSG00000176771	NCKAP5	2:133429373-134326034	OK	1.81304	4.14519	1.19303	0.830242	0.0646	0.9998
ENSG00000117461	ENSG00000117461	PIK3R3	1:46505811-46651630	OK	14.2397	9.75423	-0.545821	-1.07452	0.06485	0.9998
ENSG00000162889	ENSG00000162889	MAPKAPK2	1:206858288-206907628	OK	26.2089	36.0481	0.459865	0.874198	0.0656	0.9998
ENSG00000272521	ENSG00000272521	RP1-63M2.6	20:32244892-32262269	OK	0	1.54541	inf	#NAME?	0.0656	0.9998
ENSG00000167508	ENSG00000167508	MVD	16:88718342-88729569	OK	22.8636	15.9538	-0.519154	-0.938931	0.06575	0.9998
ENSG00000267512	ENSG00000267512	CTC-250I14.3	19:13228916-13251961	OK	1.54639	0	#NAME?	#NAME?	0.06595	0.9998
ENSG00000138175	ENSG00000138175	ARL3	10:104433487-104474164	OK	9.09932	6.36858	-0.514788	-1.11533	0.06605	0.9998
ENSG00000107242	ENSG00000107242	PIP5K1B	9:71320574-71624092	OK	5.43552	2.94055	-0.886329	-1.07557	0.0661	0.9998
ENSG00000106991	ENSG00000106991	ENG	9:130577290-130617035	OK	14.1137	19.8157	0.489543	1.03063	0.0662	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000087301	ENSG00000087301	TXNDC16	14:52897307-53019240	OK	3.22094	1.75313	-0.877549	-0.883973	0.06625	0.9998
ENSG00000083845	ENSG00000083845	RPS5	19:58897766-58906173	OK	1007.16	1387.09	0.461774	1.09164	0.06635	0.9998
ENSG00000181819	ENSG00000181819	KCTD9P2	X:103810995-105011822	OK	1.44585	0.683117	-1.08171	-1.17535	0.0684	0.9998
ENSG00000006062	ENSG00000006062	MAP3K14	17:43268297-43394414	OK	2.75789	4.2092	0.609984	0.983862	0.06645	0.9998
ENSG00000158106	ENSG00000158106	RHPN1	8:144451056-144466390	OK	2.29742	1.30825	-0.812379	-1.15379	0.0669	0.9998
ENSG00000126883	ENSG00000126883	NUP214	9:134000947-134110057	OK	11.561	8.30169	-0.477786	-0.681339	0.06695	0.9998
ENSG00000180370	ENSG00000180370	PAK2	3:196466727-196559518	OK	33.0154	20.7547	-0.669702	-0.964362	0.06715	0.9998
ENSG00000078674	ENSG00000078674	PCM1	8:17780348-17885478	OK	28.6377	20.154	-0.506852	-0.73445	0.06725	0.9998
ENSG00000119979	ENSG00000119979	FAM45A	10:120863597-120897496	OK	39.31	25.8735	-0.603418	-1.13721	0.06725	0.9998
ENSG00000204899	ENSG00000204899	MZT1	13:73282494-73301825	OK	32.7449	23.5459	-0.475796	-1.1054	0.0673	0.9998
ENSG00000172456	ENSG00000172456	FGGY	1:59762309-60254854	OK	3.10086	1.54545	-1.00464	-0.714974	0.0674	0.9998
ENSG00000015568	ENSG00000015568	RGPD5	2:110550334-110615272	OK	1.43671	0.442033	-1.70054	-0.602592	0.06755	0.9998
ENSG00000101057	ENSG00000101057	MYBL2	20:42295753-42345136	OK	42.57	30.9988	-0.457622	-1.1085	0.06755	0.9998
ENSG00000242876	ENSG00000242876	RN7SL812P	22:20778873-20850170	OK	0	1.38326	inf	#NAME?	0.06825	0.9998
ENSG00000127947	ENSG00000127947	PTPN12	7:77166591-77269388	OK	45.3756	33.6458	-0.431491	-0.917838	0.0683	0.9998
ENSG00000116212	ENSG00000116212	LRRC42	1:54411749-54433841	OK	20.8081	14.2392	-0.547278	-1.11942	0.06835	0.9998
ENSG00000135679	ENSG00000135679	MDM2	12:69201955-69365350	OK	45.5973	75.7918	0.733094	0.890241	0.06835	0.9998
ENSG00000189298	ENSG00000189298	ZKSCAN3	6:28292469-28336947	OK	1.74557	0.939278	-0.894078	-1.12174	0.0684	0.9998
ENSG00000223745	ENSG00000223745	RP4-717I23.3	1:93615298-93835055	OK	3.32588	1.5266	-1.12341	-0.275732	0.0684	0.9998
ENSG00000163428	ENSG00000163428	LRRC58	3:120043355-120068186	OK	15.5495	11.1443	-0.480557	-1.12669	0.0686	0.9998
ENSG00000166402	ENSG00000166402	TUB	11:8040790-8190602	OK	6.46313	9.16587	0.504039	1.07349	0.06865	0.9998
ENSG00000169255	ENSG00000169255	B3GALNT1	3:160801670-160971320	OK	5.7821	11.9658	1.04925	0.766323	0.0687	0.9998
ENSG00000133818	ENSG00000133818	RRAS2	11:14299471-14386052	OK	7.40046	11.0325	0.576068	1.06172	0.0688	0.9998
ENSG00000111913	ENSG00000111913	FAM65B	6:24797548-25057301	OK	4.23603	6.92361	0.70881	1.05773	0.0689	0.9998
ENSG00000130748	ENSG00000130748	TMEM160	19:47549164-47551888	OK	24.3617	36.0447	0.565176	1.09484	0.0689	0.9998
ENSG00000055070	ENSG00000055070	SZRD1	1:16679069-16763919	OK	66.1332	91.6529	0.470805	1.00991	0.0691	0.9998
ENSG00000121152	ENSG00000121152	NCAPH	2:97001524-97039583	OK	24.2362	15.9946	-0.599575	-1.10859	0.0693	0.9998
ENSG00000243701	ENSG00000243701	LINC00883	3:106959538-107101007	OK	7.08649	4.76496	-0.572608	-0.980569	0.0695	0.9998
ENSG00000166986	ENSG00000166986	MARS	12:57853917-57914300	OK	87.7833	63.0866	-0.476612	-0.867389	0.06955	0.9998
ENSG00000131747	ENSG00000131747	TOP2A	17:38544767-38574202	OK	56.3746	41.4881	-0.442348	-1.00981	0.06995	0.9998
ENSG00000155666	ENSG00000155666	KDM8	16:27214806-27233089	OK	0.867589	1.62468	0.905071	0.682248	0.07005	0.9998
ENSG00000178966	ENSG00000178966	RMI1	9:86595625-86618985	OK	7.56569	4.86062	-0.638331	-1.11248	0.0701	0.9998
ENSG00000144893	ENSG00000144893	MED12L	3:150803483-151176497	OK	0.576744	1.24879	1.11453	0.644966	0.07035	0.9998
ENSG00000105369	ENSG00000105369	CD79A	19:42381189-42385439	OK	4.08184	7.96091	0.963712	1.14936	0.0704	0.9998
ENSG00000241741	ENSG00000241741	RPL7AP30	4:113709238-113710034	OK	15.0313	22.4729	0.580218	1.10416	0.0706	0.9998
ENSG00000140497	ENSG00000140497	SCAMP2	15:75136070-75165706	OK	22.6112	33.6033	0.571567	1.06815	0.071	0.9998
ENSG00000082497	ENSG00000082497	SERTAD4	1:210404800-210419976	OK	2.318	1.22158	-0.924139	-0.84902	0.07105	0.9998
ENSG00000129534	ENSG00000129534	MIS18BP1	14:45672392-45722743	OK	11.4491	7.64498	-0.582645	-0.796011	0.0712	0.9998
ENSG00000225649	ENSG00000225649	AC064875.2	2:13106909-13147138	OK	13.6428	8.69529	-0.649835	-1.06483	0.07125	0.9998
ENSG00000109685	ENSG00000109685	WHSC1	4:1873150-1983934	OK	27.9163	20.3666	-0.454904	-0.723378	0.0714	0.9998
ENSG00000128604	ENSG00000128604	IRF5	7:128577665-128590089	OK	0.511751	0.920349	0.846739	0.637238	0.0718	0.9998
ENSG00000197586	ENSG00000197586	ENTPD6	20:25176328-25207370	OK	175.955	241.287	0.455545	0.988839	0.07185	0.9998
ENSG00000157107	ENSG00000157107	FCHO2	5:72251807-72386349	OK	4.65571	7.17832	0.624645	0.820614	0.0719	0.9998
ENSG00000181788	ENSG00000181788	SIAH2	3:150458913-150481264	OK	11.7452	8.20147	-0.51812	-0.944457	0.0724	0.9998
ENSG00000076356	ENSG00000076356	PLXNA2	1:208195586-208417665	OK	8.96304	12.9618	0.532203	0.633533	0.07245	0.9998
ENSG00000070731	ENSG00000070731	ST6GALNAC2	17:74553847-74583038	OK	127.531	75.7827	-0.75091	-0.889566	0.0726	0.9998
ENSG00000188985	ENSG00000188985	DHFRP1	18:23713815-23773319	OK	58.5705	39.8995	-0.553806	-1.09164	0.0726	0.9998
ENSG00000086991	ENSG00000086991	NOX4	11:89057523-89322779	OK	0.930152	1.68238	0.854965	0.843406	0.07265	0.9998
ENSG00000176953	ENSG00000176953	NFATC2IP	16:28962127-28978418	OK	21.3363	14.0745	-0.600221	-0.968118	0.07265	0.9998
ENSG00000169991	ENSG00000169991	IFFO2	1:19166092-19283180	OK	4.54021	8.65494	0.930765	1.02122	0.07275	0.9998
ENSG00000204536	ENSG00000204536	CCHCR1	6:31110215-31126015	OK	18.618	13.1696	-0.499484	-0.803031	0.073	0.9998
ENSG00000163466	ENSG00000163466	ARPC2	2:219081816-219119079	OK	176.306	130.032	-0.439215	-1.04412	0.07315	0.9998
ENSG00000188269	ENSG00000188269	OR7A5	19:14903120-14946188	OK	0.143583	0.787586	2.45555	0.704101	0.07315	0.9998
ENSG00000146054	ENSG00000146054	TRIM7	5:180618923-180632293	OK	1.33677	2.96063	1.14715	1.12107	0.0732	0.9998
ENSG00000069956	ENSG00000069956	MAPK6	15:52121824-52392720	OK	10.5453	16.4901	0.644996	0.797573	0.0733	0.9998
ENSG00000138336	ENSG00000138336	TET1	10:70320412-70454239	OK	0.971802	0.521522	-0.897936	-1.17655	0.0733	0.9998
ENSG00000150593	ENSG00000150593	PDCD4	10:112629500-112679032	OK	26.0091	45.871	0.818564	1.18931	0.07335	0.9998
ENSG00000184564	ENSG00000184564	SLITRK6	13:86366924-86373623	OK	0.873642	0.514506	-0.763854	-1.05162	0.07335	0.9998
ENSG00000170425	ENSG00000170425	ADORA2B	17:15848230-15879060	OK	2.03065	3.37495	0.732924	1.09342	0.07345	0.9998
ENSG00000059804	ENSG00000059804	SLC2A3	12:8071825-8088871	OK	40.0323	27.4546	-0.544116	-0.93294	0.0735	0.9998
ENSG00000144485	ENSG00000144485	HES6	2:239140324-239198743	OK	115.64	157.249	0.443408	1.04368	0.07355	0.9998
ENSG00000103047	ENSG00000103047	TANGO6	16:68877506-69119083	OK	7.10587	4.46399	-0.670677	-0.789133	0.07365	0.9998
ENSG00000152332	ENSG00000152332	UHMK1	1:162467040-162499419	OK	49.9707	68.2117	0.448938	1.05083	0.07385	0.9998
ENSG00000235343	ENSG00000235343	AC005301.8	22:17227758-17229535	OK	1.05894	1.97645	0.900296	1.12094	0.07415	0.9998
ENSG00000065559	ENSG00000065559	MAP2K4	17:11901669-12047147	OK	11.4202	15.6895	0.458208	0.890858	0.0742	0.9998
ENSG00000155465	ENSG00000155465	SLC7A7	14:23242430-23299029	OK	0.763099	1.40171	0.877242	0.581181	0.0742	0.9998
ENSG00000001617	ENSG00000001617	SEMA3F	3:49977439-50226508	OK	1.08862	3.78275	1.79693	0.57801	0.0743	0.9998
ENSG00000005882	ENSG00000005882	PDK2	17:48172100-48207246	OK	18.5927	29.3817	0.660184	1.08189	0.07435	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000181982	ENSG00000181982	CCDC149	4:24807738-24981826	OK	1.30362	2.33421	0.840412	0.916615	0.07435	0.9998
ENSG00000173950	ENSG00000173950	XXYLT1	3:194789007-194991896	OK	28.1913	19.8537	-0.505839	-1.01114	0.0746	0.9998
ENSG00000230592	ENSG00000230592	RPSAP8	X:99410882-99411771	OK	0.689189	1.48314	1.10568	1.11831	0.0746	0.9998
ENSG00000163975	ENSG00000163975	MFI2	3:196715491-196756687	OK	142.475	198.91	0.481407	0.801777	0.07465	0.9998
ENSG00000138759	ENSG00000138759	FRAS1	4:78978723-79465423	OK	0.806379	1.57437	0.965247	0.914216	0.0748	0.9998
ENSG00000224861	ENSG00000224861	YBX1P1	14:66479547-66480507	OK	111.046	151.008	0.443466	1.07501	0.0749	0.9998
ENSG00000169621	ENSG00000169621	APLF	2:68694692-68858004	OK	1.76763	1.11647	-0.662874	-1.03483	0.07505	0.9998
ENSG00000157827	ENSG00000157827	FMNL2	2:153191750-153506348	OK	15.8683	11.5982	-0.45225	-1.02042	0.07515	0.9998
ENSG00000151503	ENSG00000151503	NCAPD3	11:133938819-134117686	OK	17.8592	11.7597	-0.602817	-0.582484	0.0753	0.9998
ENSG00000157992	ENSG00000157992	KRTCAP3	2:27665232-27712656	OK	0.19107	0.665866	1.80113	0.316615	0.07535	0.9998
ENSG00000165171	ENSG00000165171	WBSCR27	7:73248919-73256865	OK	2.63692	1.42136	-0.891582	-1.08087	0.0756	0.9998
ENSG00000003137	ENSG00000003137	CYP26B1	2:72356366-72375167	OK	0.291378	1.00452	1.78555	0.881783	0.07565	0.9998
ENSG00000104447	ENSG00000104447	TRPS1	8:116420723-116821899	OK	1.9016	2.8714	0.594542	0.831229	0.07565	0.9998
ENSG00000234745	ENSG00000234745	HLA-B	6:31321648-31325414	OK	12.8404	18.7615	0.54709	1.04324	0.07565	0.9998
ENSG00000160207	ENSG00000160207	HSF2BP	21:44949071-45079374	OK	0.508098	1.00237	0.980236	1.05125	0.0757	0.9998
ENSG00000178752	ENSG00000178752	FAM132B	2:239067622-239077541	OK	2.69214	1.37023	-0.97434	-1.08786	0.07605	0.9998
ENSG00000136231	ENSG00000136231	IGF2BP3	7:23338357-23510086	OK	14.3667	22.0925	0.62083	0.703272	0.0761	0.9998
ENSG00000092201	ENSG00000092201	SUPT16H	14:21819630-21852425	OK	43.2343	30.7211	-0.492946	-0.959754	0.07615	0.9998
ENSG00000121440	ENSG00000121440	PDZRN3	3:73431583-73675149	OK	6.5942	9.58281	0.539251	0.862404	0.07625	0.9998
ENSG00000166289	ENSG00000166289	PLEKHF1	19:30155962-30166364	OK	3.89616	6.08762	0.643826	1.03728	0.07635	0.9998
ENSG00000173281	ENSG00000173281	PPP1R3B	8:8993764-9009084	OK	26.0688	18.5358	-0.49201	-1.06889	0.0764	0.9998
ENSG00000197457	ENSG00000197457	STMN3	20:62271060-62284780	OK	2.4679	3.80118	0.623167	1.06817	0.07645	0.9998
ENSG00000140988	ENSG00000140988	RPS2	16:2012052-2014861	OK	2011.34	2973.47	0.563994	1.07412	0.0765	0.9998
ENSG00000173599	ENSG00000173599	PC	11:66615703-66725847	OK	14.82	9.23499	-0.682367	-0.508025	0.0766	0.9998
ENSG00000260371	ENSG00000260371	RP11-343C2.9	16:69139466-69442474	OK	0	1.15159	inf	#NAME?	0.0766	0.9998
ENSG00000116649	ENSG00000116649	SRM	1:11114640-11120081	OK	56.3058	76.5976	0.444015	1.04432	0.0767	0.9998
ENSG00000128609	ENSG00000128609	NDUFA5	7:123177050-123198309	OK	76.2293	105.536	0.469324	1.08552	0.0768	0.9998
ENSG00000146963	ENSG00000146963	C7orf55-LUC7L2	7:139024202-139108198	OK	46.2463	31.9955	-0.531469	-1.0405	0.0768	0.9998
ENSG00000148655	ENSG00000148655	C10orf11	10:77360997-78320752	OK	20.6756	13.9579	-0.56684	-0.837267	0.07685	0.9998
ENSG00000136848	ENSG00000136848	DAB2IP	9:124329335-124547809	OK	5.18127	7.32509	0.49954	0.788231	0.0769	0.9998
ENSG00000170312	ENSG00000170312	CDK1	10:62538088-62554610	OK	83.1858	61.5806	-0.433861	-1.042	0.07705	0.9998
ENSG00000240497	ENSG00000240497	RP11-185E8.1	3:171185872-171187422	OK	0.692267	0	#NAME?	#NAME?	0.07705	0.9998
ENSG00000172399	ENSG00000172399	MYOZ2	4:120056938-120108944	OK	1.48391	2.35763	0.667936	1.06061	0.0772	0.9998
ENSG00000174276	ENSG00000174276	ZNHIT2	11:64883874-64885170	OK	6.07545	9.12221	0.586393	1.04967	0.07725	0.9998
ENSG00000165997	ENSG00000165997	ARL5B	10:18948333-18970568	OK	1.75651	2.56697	0.547354	1.07501	0.07735	0.9998
ENSG00000240494	ENSG00000240494	RPS12P28	17:26975373-27029697	OK	0.766803	0	#NAME?	#NAME?	0.07745	0.9998
ENSG00000124208	ENSG00000124208	TMEM189-UBE2V1	20:48697660-48770335	OK	0.861155	0	#NAME?	#NAME?	0.0775	0.9998
ENSG00000137824	ENSG00000137824	RMDN3	15:41028081-41048049	OK	15.0901	21.4153	0.505045	1.03241	0.0775	0.9998
ENSG00000170293	ENSG00000170293	CMTM8	3:32280170-32411817	OK	1.57198	2.75548	0.809717	1.06724	0.0775	0.9998
ENSG00000164087	ENSG00000164087	POC1A	3:52109268-52188706	OK	13.1374	9.08131	-0.532707	-1.08788	0.07755	0.9998
ENSG00000143409	ENSG00000143409	FAM63A	1:150969024-150980851	OK	14.144	9.59334	-0.56008	-0.955334	0.0776	0.9998
ENSG00000072274	ENSG00000072274	TFRC	3:195754053-195809060	OK	168.706	123.149	-0.454108	-0.912674	0.07775	0.9998
ENSG00000148090	ENSG00000148090	AUH	9:93976096-94124195	OK	15.7715	10.6257	-0.569768	-1.04774	0.07775	0.9998
ENSG00000141574	ENSG00000141574	SECTM1	17:80278899-80291950	OK	0.428821	0.933211	1.12183	0.692588	0.07785	0.9998
ENSG00000090316	ENSG00000090316	MAEA	4:1283638-1333935	OK	34.5299	24.8325	-0.475614	-1.03179	0.0779	0.9998
ENSG00000143384	ENSG00000143384	MCL1	1:150547031-150552066	OK	45.1653	61.2968	0.440597	1.01728	0.0779	0.9998
ENSG00000254429	ENSG00000254429	CTD-2562J17.7	11:74971170-74972069	OK	1.04587	2.41438	1.20694	1.10593	0.07795	0.9998
ENSG00000146416	ENSG00000146416	AIG1	6:143381632-143661441	OK	8.84903	5.0772	-0.801487	-1.09186	0.07805	0.9998
ENSG00000124523	ENSG00000124523	SIRT5	6:13574815-13615387	OK	11.3038	7.31447	-0.627984	-1.05879	0.0781	0.9998
ENSG00000125089	ENSG00000125089	SH3TC1	4:8183798-8243530	OK	6.49157	9.90517	0.609614	0.768916	0.07835	0.9998
ENSG00000075240	ENSG00000075240	GRAMD4	22:46971908-47075688	OK	30.4366	19.1472	-0.668674	-0.641761	0.07845	0.9998
ENSG00000139998	ENSG00000139998	RAB15	14:65381078-65569413	OK	8.4356	18.4188	1.12662	0.969288	0.07865	0.9998
ENSG00000221955	ENSG00000221955	SLC12A8	3:124801479-125094198	OK	0.635728	1.40029	1.13925	0.365318	0.0788	0.9998
ENSG00000100139	ENSG00000100139	MICALL1	22:38301663-38338829	OK	16.9395	26.5756	0.649707	1.06071	0.07895	0.9998
ENSG00000121211	ENSG00000121211	MND1	4:154265800-154336270	OK	8.46652	5.3564	-0.660504	-1.02721	0.0792	0.9998
ENSG00000240342	ENSG00000240342	RPS2P5	12:118587605-118810750	OK	373.782	534.2	0.515182	1.09324	0.0793	0.9998
ENSG00000125772	ENSG00000125772	GPCPD1	20:5525084-5591672	OK	2.56196	4.0822	0.672099	0.796131	0.0794	0.9998
ENSG00000233639	ENSG00000233639	LINC01158	2:105424029-105469641	OK	5.17749	2.97599	-0.798883	-1.00315	0.07945	0.9998
ENSG00000117016	ENSG00000117016	RIMS3	1:41086350-41131329	OK	0.893767	1.43759	0.68568	1.03547	0.0795	0.9998
ENSG00000269900	ENSG00000269900	RMRP	9:35657747-35658015	OK	1.06884	3.58156	1.74453	0.974461	0.07955	0.9998
ENSG00000163946	ENSG00000163946	FAM208A	3:56591188-56717265	OK	24.1755	15.3494	-0.655363	-1.06175	0.07985	0.9998
ENSG00000143155	ENSG00000143155	TIPRL	1:168148170-168169950	OK	56.9429	40.3548	-0.496776	-1.04724	0.0799	0.9998
ENSG00000177406	ENSG00000177406	RP11-218M22.1	12:673461-772945	OK	0.639057	0.285502	-1.16244	-0.986524	0.07995	0.9998
ENSG00000085832	ENSG00000085832	EPS15	1:51819934-52027301	OK	13.0207	18.1498	0.479143	0.973328	0.08	0.9998
ENSG00000120137	ENSG00000120137	PANK3	5:167975499-168006605	OK	29.9901	22.3306	-0.425465	-0.743295	0.08015	0.9998
ENSG00000199785	ENSG00000199785	SNORA52	11:799178-812880	OK	17.9508	0	#NAME?	#NAME?	0.08015	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000189343	ENSG00000189343	RPS2P46	17:19342455-19364308	OK	278.628	377.802	0.43929	1.06222	0.08025	0.9998
ENSG00000058335	ENSG00000058335	RASGRF1	15:79252288-79383115	OK	0.876478	1.87268	1.09531	0.867487	0.0803	0.9998
ENSG00000196136	ENSG00000196136	SERPINA3	14:95027427-95090983	OK	1.69358	0.356102	-2.24971	-1.44003	0.08055	0.9998
ENSG00000267436	ENSG00000267436	AC005786.7	19:3506270-3579086	OK	0	1.88361	inf	#NAME?	0.08055	0.9998
ENSG00000158710	ENSG00000158710	TAGLN2	1:159887896-159895522	OK	281.722	390.197	0.469929	1.06545	0.08075	0.9998
ENSG00000065526	ENSG00000065526	SPEN	1:16160559-16266955	OK	8.18877	12.7009	0.633213	0.602176	0.08095	0.9998
ENSG00000256422	ENSG00000256422	RP11-886D15.1	11:104316595-104480049	OK	1.52727	0.664049	-1.20159	-0.990777	0.08105	0.9998
ENSG00000105327	ENSG00000105327	BBC3	19:47724080-47736023	OK	33.3998	48.0852	0.525754	1.05325	0.08115	0.9998
ENSG00000133135	ENSG00000133135	RNF128	X:105937023-106040223	OK	0.611986	1.0799	0.81932	1.00114	0.08115	0.9998
ENSG00000185070	ENSG00000185070	FLRT2	14:85996487-86095034	OK	0.501804	1.20643	1.26555	0.732492	0.0813	0.9998
ENSG00000205670	ENSG00000205670	SMIM11	21:35747778-35780164	OK	17.7835	11.9524	-0.573237	-1.05817	0.0814	0.9998
ENSG00000184787	ENSG00000184787	UBE2G2	21:46188954-46221934	OK	21.8962	33.0576	0.594304	1.00374	0.08145	0.9998
ENSG00000225975	ENSG00000225975	AC074138.3	19:37176341-37178351	OK	1.99698	0.871034	-1.19702	-1.08213	0.08145	0.9998
ENSG00000167363	ENSG00000167363	FN3K	17:80693450-80709073	OK	22.6253	32.4265	0.519234	1.03431	0.08155	0.9998
ENSG00000231991	ENSG00000231991	ANXA2P2	9:33624222-33625532	OK	45.2122	62.1752	0.459626	1.06813	0.0816	0.9998
ENSG00000132953	ENSG00000132953	XPO4	13:21351468-21477187	OK	8.44343	11.58	0.455727	0.815395	0.0819	0.9998
ENSG00000054654	ENSG00000054654	SYNE2	14:64319682-64805317	OK	9.43431	6.28312	-0.586437	-0.503422	0.08195	0.9998
ENSG00000182263	ENSG00000182263	FIGN	2:164449905-164592522	OK	1.17217	1.96766	0.747303	0.720975	0.082	0.9998
ENSG00000134121	ENSG00000134121	CHL1	3:237440-451090	OK	36.4652	21.7749	-0.74385	-0.886362	0.08225	0.9998
ENSG00000106665	ENSG00000106665	CLIP2	7:73703804-73820273	OK	8.12432	5.79028	-0.488614	-0.829183	0.08235	0.9998
ENSG00000138036	ENSG00000138036	DYNC2LI1	2:44001177-44037149	OK	14.0628	9.28199	-0.599373	-1.04103	0.08255	0.9998
ENSG00000102003	ENSG00000102003	SYP	X:49044268-49058913	OK	1.46595	0.84482	-0.795116	-0.759495	0.08265	0.9998
ENSG00000162704	ENSG00000162704	ARPC5	1:183592400-183604892	OK	79.944	107.109	0.422018	1.05302	0.08275	0.9998
ENSG00000163508	ENSG00000163508	EOMES	3:27757439-27764206	OK	1.22664	0.694112	-0.82147	-0.991436	0.08275	0.9998
ENSG00000172071	ENSG00000172071	EIF2AK3	2:88838237-88931339	OK	8.3002	13.7926	0.732672	0.901068	0.08285	0.9998
ENSG00000110696	ENSG00000110696	C11orf58	11:15987994-16778428	OK	105.968	148.799	0.489735	0.972745	0.08295	0.9998
ENSG00000059378	ENSG00000059378	PARP12	7:139723543-139763521	OK	1.03445	1.6977	0.714717	0.704832	0.08315	0.9998
ENSG00000143653	ENSG00000143653	SCCPDH	1:246887348-246931439	OK	35.1172	25.9653	-0.435593	-1.05338	0.08355	0.9998
ENSG00000036672	ENSG00000036672	USP2	11:119225924-119252436	OK	0.871865	1.79854	1.04465	0.902821	0.0838	0.9998
ENSG00000091651	ENSG00000091651	ORC6	16:46723554-46732306	OK	14.1281	9.68464	-0.544802	-1.04822	0.08385	0.9998
ENSG00000102543	ENSG00000102543	CDADC1	13:49822046-49867618	OK	6.96945	12.491	0.841772	1.01632	0.08395	0.9998
ENSG00000149636	ENSG00000149636	DSN1	20:35380193-35402221	OK	23.5463	16.8622	-0.481708	-1.04906	0.08395	0.9998
ENSG00000183323	ENSG00000183323	CCDC125	5:68576001-68628636	OK	3.91184	2.41293	-0.697061	-1.02628	0.08395	0.9998
ENSG00000170456	ENSG00000170456	DENND5B	12:31535156-31768600	OK	7.67875	12.1526	0.662324	1.05636	0.084	0.9998
ENSG00000136940	ENSG00000136940	PDCL	9:125560667-125590910	OK	7.33306	10.5732	0.527928	0.911125	0.0843	0.9998
ENSG00000079482	ENSG00000079482	OPHN1	X:67262185-67653755	OK	4.57734	2.42536	-0.91631	-0.822089	0.08435	0.9998
ENSG00000114738	ENSG00000114738	MAPKAPK3	3:50643920-50686720	OK	22.8354	32.2082	0.496158	1.01107	0.0844	0.9998
ENSG00000165698	ENSG00000165698	C9orf9	9:135600964-135765588	OK	1.89224	1.01275	-0.901819	-0.993269	0.08445	0.9998
ENSG00000237649	ENSG00000237649	KIFC1	6:33359312-33377701	OK	55.456	38.0644	-0.542902	-1.00404	0.08485	0.9998
ENSG00000163605	ENSG00000163605	PPP4R2	3:72937223-73118350	OK	35.391	25.2221	-0.488694	-0.810612	0.0849	0.9998
ENSG00000088035	ENSG00000088035	ALG6	1:63833260-63904233	OK	11.8334	8.13188	-0.541197	-1.01714	0.085	0.9998
ENSG00000165092	ENSG00000165092	ALDH1A1	9:75515577-75695358	OK	15.6781	21.5258	0.45732	1.01139	0.08505	0.9998
ENSG00000072401	ENSG00000072401	UBE2D1	10:60094734-60130513	OK	7.01658	4.64066	-0.59644	-1.05974	0.08515	0.9998
ENSG00000122861	ENSG00000122861	PLAU	10:75668934-75682535	OK	1.13859	0.221996	-2.35864	-0.741441	0.0853	0.9998
ENSG00000178075	ENSG00000178075	GRAMD1C	3:113547028-113666417	OK	5.69022	3.14521	-0.855327	-0.864946	0.0853	0.9998
ENSG00000051108	ENSG00000051108	HERPUD1	16:56965959-56977798	OK	16.5171	23.0987	0.483848	0.955315	0.08535	0.9998
ENSG00000173898	ENSG00000173898	SPTBN2	11:66452718-66496697	OK	3.29774	5.07809	0.622809	0.633351	0.08545	0.9998
ENSG00000236385	ENSG00000236385	RP11-114M1.2	3:177159708-177470093	OK	1.9541	0.907579	-1.10641	-1.06902	0.08545	0.9998
ENSG00000184939	ENSG00000184939	ZFP90	16:68563992-68623415	OK	5.29805	3.37307	-0.651399	-0.650415	0.08555	0.9998
ENSG00000205581	ENSG00000205581	HMGN1	21:40714240-40721573	OK	58.3055	83.5756	0.519449	1.0059	0.08565	0.9998
ENSG00000257411	ENSG00000257411	RP11-603J24.9	12:56473640-56507691	OK	0.79294	0	#NAME?	#NAME?	0.0858	0.9998
ENSG00000260914	ENSG00000260914	RP11-343C2.11	16:69139466-69442474	OK	0	1.00456	inf	#NAME?	0.0859	0.9998
ENSG00000119969	ENSG00000119969	HELLS	10:96305546-96373662	OK	20.3362	13.0244	-0.642827	-1.03139	0.08595	0.9998
ENSG00000171827	ENSG00000171827	ZNF570	19:37902056-37976260	OK	2.55167	1.2633	-1.01424	-0.881475	0.08595	0.9998
ENSG00000170899	ENSG00000170899	GSTA4	6:52842750-52860176	OK	19.7182	13.8487	-0.509776	-1.04229	0.086	0.9998
ENSG00000048991	ENSG00000048991	R3HDM1	2:136289024-136482840	OK	7.86219	5.54321	-0.50421	-0.688969	0.08605	0.9998
ENSG00000005238	ENSG00000005238	FAM214B	9:35104108-35116338	OK	32.3033	44.1025	0.449176	0.988316	0.08615	0.9998
ENSG00000260948	ENSG00000260948	RP11-552M11.8	1:111973667-111975690	OK	0.325132	0.646989	0.992713	1.07812	0.0864	0.9998
ENSG00000072364	ENSG00000072364	AFF4	5:132211070-132299326	OK	5.87598	8.26727	0.492581	0.686309	0.0865	0.9998
ENSG00000169908	ENSG00000169908	TM4SF1	3:149086808-149104370	OK	0.993358	1.69218	0.768501	0.959176	0.0865	0.9998
ENSG00000090470	ENSG00000090470	PDCD7	15:65409716-65426174	OK	13.8529	10.011	-0.468599	-0.808502	0.08655	0.9998
ENSG00000136874	ENSG00000136874	STX17	9:102668914-102732618	OK	11.2428	7.70346	-0.545423	-0.789973	0.08665	0.9998
ENSG00000143126	ENSG00000143126	CELSR2	1:109792640-109818372	OK	8.76424	12.2834	0.487006	0.938354	0.0867	0.9998
ENSG00000235204	ENSG00000235204	RP11-121A14.2	9:127019884-127115586	OK	0.838445	0	#NAME?	#NAME?	0.0867	0.9998
ENSG00000187566	ENSG00000187566	NHLRC1	6:18120717-18122851	OK	2.1252	3.37757	0.668386	1.05638	0.08675	0.9998
ENSG00000048052	ENSG00000048052	HDAC9	7:18126571-19042039	OK	7.0458	10.2906	0.546493	0.800866	0.08725	0.9998
ENSG00000170153	ENSG00000170153	RNF150	4:141780960-142134031	OK	3.56888	2.34639	-0.605031	-0.773785	0.0874	0.9998
ENSG00000163624	ENSG00000163624	CDS1	4:85504131-85572491	OK	1.43676	2.20001	0.614692	0.86967	0.08745	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000161912	ENSG00000161912	ADCY10P1	6:41068760-41108571	OK	0.962202	1.82675	0.924865	0.771861	0.0875	0.9998
ENSG00000145734	ENSG00000145734	BDP1	5:70751441-70863649	OK	7.05336	4.99276	-0.498473	-1.06878	0.0876	0.9998
ENSG00000151208	ENSG00000151208	DLG5	10:79542623-79686378	OK	7.64685	10.5547	0.464949	0.972827	0.0877	0.9998
ENSG00000115844	ENSG00000115844	DLX2	2:172964166-172967628	OK	1.78944	1.0898	-0.715438	-1.06678	0.08775	0.9998
ENSG00000180447	ENSG00000180447	GAS1	9:89559278-89562104	OK	16.0349	11.7579	-0.447583	-1.00986	0.08785	0.9998
ENSG00000137441	ENSG00000137441	FGFBP2	4:15961865-16086001	OK	86.2607	61.4614	-0.489021	-1.05562	0.088	0.9998
ENSG00000166682	ENSG00000166682	TMPRSS5	11:113558271-113577095	OK	0.434253	0.891415	1.03756	0.596595	0.08805	0.9998
ENSG00000085465	ENSG00000085465	OVGP1	1:111956935-111970399	OK	0.328248	0.689024	1.06977	0.758709	0.0884	0.9998
ENSG00000129353	ENSG00000129353	SLC44A2	19:10713132-10755235	OK	9.49942	6.73935	-0.49523	-0.833967	0.0884	0.9998
ENSG00000197459	ENSG00000197459	HIST1H2BH	6:26251878-26252303	OK	6.61042	3.40308	-0.957899	-1.08232	0.0884	0.9998
ENSG00000009307	ENSG00000009307	CSDE1	1:115259533-115301297	OK	168.445	238.879	0.503996	0.81647	0.08845	0.9998
ENSG00000229727	ENSG00000229727	AC013460.1	2:7561391-7590385	OK	0.711401	0.285455	-1.3174	-0.738571	0.0885	0.9998
ENSG00000139737	ENSG00000139737	SLAIN1	13:78272022-78338377	OK	6.01055	8.84003	0.556554	0.903688	0.0886	0.9998
ENSG00000152932	ENSG00000152932	RAB3C	5:57878047-58159241	OK	20.0763	9.37375	-1.09879	-1.1014	0.08885	0.9998
ENSG00000101198	ENSG00000101198	NKAIN4	20:61872135-61904046	OK	6.06027	10.6037	0.807114	1.06912	0.08895	0.9998
ENSG00000077585	ENSG00000077585	GPR137B	1:236305831-236445319	OK	143.855	196.761	0.451829	1.03331	0.089	0.9998
ENSG00000086666	ENSG00000086666	ZFAND6	15:80351909-80430735	OK	61.186	83.3165	0.4454	1.00869	0.08905	0.9998
ENSG00000111371	ENSG00000111371	SLC38A1	12:46576845-46663800	OK	7.40586	11.0432	0.576424	0.637573	0.08905	0.9998
ENSG00000127920	ENSG00000127920	GNG11	7:93551010-93557922	OK	21.2228	28.5834	0.429565	1.03669	0.0891	0.9998
ENSG00000132589	ENSG00000132589	FLOT2	17:27206352-27224697	OK	21.1733	28.552	0.431343	0.976069	0.0891	0.9998
ENSG00000189367	ENSG00000189367	KIAA0408	6:127759550-127840500	OK	1.63981	0.816873	-1.00534	-0.936942	0.0891	0.9998
ENSG00000089723	ENSG00000089723	OTUB2	14:94492674-94515276	OK	1.99001	2.94969	0.567788	0.989444	0.08915	0.9998
ENSG00000119729	ENSG00000119729	RHOQ	2:46717888-46852881	OK	165.421	225.661	0.448016	0.818686	0.0893	0.9998
ENSG00000239306	ENSG00000239306	RBM14	11:66384052-66445392	OK	22.3547	34.9945	0.64655	0.838774	0.0893	0.9998
ENSG00000114107	ENSG00000114107	CEP70	3:138213185-138313380	OK	15.3739	10.5712	-0.540346	-0.976493	0.08935	0.9998
ENSG00000185432	ENSG00000185432	METTL7A	12:51317254-51326300	OK	0.340301	0.853356	1.32634	1.00121	0.0895	0.9998
ENSG00000221914	ENSG00000221914	PPP2R2A	8:26149006-26230196	OK	41.0945	56.2492	0.452889	0.903896	0.08955	0.9998
ENSG00000175183	ENSG00000175183	CSRP2	12:77252494-77274132	OK	50.2883	36.0811	-0.478979	-1.0257	0.08965	0.9998
ENSG00000185920	ENSG00000185920	PTCH1	9:98205261-98279339	OK	4.37304	6.71339	0.618404	0.571736	0.09005	0.9998
ENSG00000021574	ENSG00000021574	SPAST	2:32288679-32382706	OK	5.91717	4.23397	-0.482896	-1.03647	0.0901	0.9998
ENSG00000154654	ENSG00000154654	NCAM2	21:22370632-22915650	OK	5.46451	2.88221	-0.922915	-0.95132	0.09015	0.9998
ENSG00000105767	ENSG00000105767	CADM4	19:44126519-44143991	OK	30.4545	40.9516	0.427268	0.964496	0.0903	0.9998
ENSG00000269728	ENSG00000269728	RP11-145M9.4	3:179113876-179116979	OK	15.467	10.1484	-0.607952	-1.05059	0.0903	0.9998
ENSG00000229472	ENSG00000229472	RP1-64K7.4	20:32570857-32700138	OK	0	1.39846	inf	#NAME?	0.0904	0.9998
ENSG00000167900	ENSG00000167900	TK1	17:76170159-76183314	OK	75.5394	53.6787	-0.49288	-1.03465	0.0905	0.9998
ENSG00000169252	ENSG00000169252	ADRB2	5:148206155-148208196	OK	2.24318	3.49227	0.638621	1.04907	0.0907	0.9998
ENSG00000014824	ENSG00000014824	SLC30A9	4:41992488-42092474	OK	20.9309	30.2919	0.533294	1.02867	0.09075	0.9998
ENSG00000121060	ENSG00000121060	TRIM25	17:54965269-54991399	OK	16.257	22.813	0.488801	0.699441	0.09075	0.9998
ENSG00000131373	ENSG00000131373	HACL1	3:15802210-15687329	OK	19.2505	12.4238	-0.631783	-1.02538	0.09075	0.9998
ENSG00000071246	ENSG00000071246	VASH1	14:77228531-77253067	OK	0.42507	1.05386	1.30991	0.775673	0.09085	0.9998
ENSG00000157693	ENSG00000157693	C9orf91	9:117373485-117408702	OK	41.6764	27.0309	-0.624619	-0.999655	0.09095	0.9998
ENSG00000180917	ENSG00000180917	CMTR2	16:71315291-71323618	OK	3.36762	4.90009	0.541076	0.83468	0.09095	0.9998
ENSG00000105519	ENSG00000105519	CAPS	19:5904851-5915888	OK	1.94616	3.66397	0.91278	0.926689	0.091	0.9998
ENSG00000139146	ENSG00000139146	FAM60A	12:31433517-31479992	OK	11.3517	16.8604	0.570727	0.997636	0.0911	0.9998
ENSG00000177888	ENSG00000177888	ZBTB41	1:197122809-197169672	OK	4.3911	3.15269	-0.477998	-1.0212	0.0912	0.9998
ENSG00000124787	ENSG00000124787	RPP40	6:4994965-5004297	OK	10.6861	16.3721	0.615505	1.00819	0.0913	0.9998
ENSG00000166796	ENSG00000166796	LDHC	11:18433853-18473605	OK	1.094	0.581445	-0.911893	-0.741732	0.09135	0.9998
ENSG00000120370	ENSG00000120370	GORAB	1:170429593-170522587	OK	12.44	8.4863	-0.551781	-0.911843	0.0914	0.9998
ENSG00000172031	ENSG00000172031	EPHX4	1:92495538-92529093	OK	1.75777	2.8772	0.710922	1.01301	0.0917	0.9998
ENSG00000228348	ENSG00000228348	EFCAB14P1	1:35587622-35588085	OK	4.74425	2.45544	-0.950198	-1.06701	0.0918	0.9998
ENSG00000128596	ENSG00000128596	CCDC136	7:128430810-128462186	OK	10.7523	17.441	0.697838	0.956781	0.09195	0.9998
ENSG00000186625	ENSG00000186625	KATNA1	6:149916008-149970108	OK	7.12144	4.67621	-0.60683	-0.993076	0.09195	0.9998
ENSG00000101882	ENSG00000101882	NKAP	X:119059013-119077735	OK	16.6689	11.7697	-0.502085	-1.01971	0.0922	0.9998
ENSG00000109339	ENSG00000109339	MAPK10	4:86936275-87515284	OK	2.51023	3.74808	0.578333	0.60985	0.0922	0.9998
ENSG00000006025	ENSG00000006025	OSBPL7	17:45884737-45899200	OK	4.07422	6.85798	0.75126	0.82777	0.09225	0.9998
ENSG00000234814	ENSG00000234814	SVILP1	10:30960494-31006195	OK	0.692656	0.37956	-0.867813	-0.849341	0.09225	0.9998
ENSG00000214837	ENSG00000214837	RP11-261C10.3	1:243242158-243265035	OK	4.41127	2.40641	-0.874309	-0.990858	0.09255	0.9998
ENSG00000144802	ENSG00000144802	NFKBIZ	3:101498045-101579866	OK	69.5743	47.5543	-0.548977	-0.840368	0.0926	0.9998
ENSG00000134864	ENSG00000134864	GGACT	13:101183809-101241782	OK	2.76174	5.89206	1.0932	1.02085	0.0927	0.9998
ENSG00000198108	ENSG00000198108	CHSY3	5:128795251-129522327	OK	1.09767	2.03957	0.893823	0.873978	0.09295	0.9998
ENSG00000198225	ENSG00000198225	FKBP1C	6:63921350-63922929	OK	3.88583	6.87682	0.82352	0.782491	0.093	0.9998
ENSG00000163071	ENSG00000163071	SPATA18	4:52917496-52963458	OK	2.68771	4.0071	0.576179	0.746612	0.09305	0.9998
ENSG00000142910	ENSG00000142910	TINAGL1	1:32042115-32053288	OK	0.366858	0.720172	0.973118	0.611223	0.0931	0.9998
ENSG00000176720	ENSG00000176720	BOK	2:242483817-242513546	OK	0.392944	0.714851	0.863319	1.0363	0.09315	0.9998
ENSG00000196437	ENSG00000196437	ZNF569	19:37902056-37976260	OK	2.54561	1.50344	-0.759743	-0.850441	0.09315	0.9998
ENSG00000216775	ENSG00000216775	RP1-152L7.5	6:52529945-52533953	OK	2.56698	1.68238	-0.609567	-0.94948	0.09315	0.9998
ENSG00000174130	ENSG00000174130	TLR6	4:38792297-38858438	OK	1.23941	0.711643	-0.800433	-0.785609	0.09325	0.9998
ENSG00000151414	ENSG00000151414	NEK7	1:198126092-198291550	OK	16.809	12.3099	-0.449416	-0.866943	0.09335	0.9998
ENSG00000113140	ENSG00000113140	SPARC	5:151040656-151104343	OK	729.837	502.837	-0.537483	-0.959065	0.09345	0.9998
ENSG00000091490	ENSG00000091490	SEL1L3	4:25749054-25931435	OK	2.50237	4.27311	0.77199	0.743365	0.0935	0.9998
ENSG00000177683	ENSG00000177683	THAP5	7:108110865-108215294	OK	12.1609	6.8905	-0.819564	-0.794823	0.09375	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000157483	ENSG00000157483	MYO1E	15:59427112-59815748	OK	7.10129	13.3203	0.907468	0.886636	0.0938	0.9998
ENSG00000226266	ENSG00000226266	AC009961.3	2:160527218-160568946	OK	3.08463	1.22677	-1.33023	-1.07491	0.0938	0.9998
ENSG00000137947	ENSG00000137947	GTF2B	1:89318614-89357627	OK	14.0291	19.4584	0.471972	0.963188	0.0939	0.9998
ENSG00000132881	ENSG00000132881	RSG1	1:16558194-16563657	OK	2.54336	1.19893	-1.08499	-1.00951	0.09395	0.9998
ENSG00000131389	ENSG00000131389	SLC6A6	3:14444075-14583588	OK	7.69826	10.5005	0.447858	0.852907	0.09415	0.9998
ENSG00000223459	ENSG00000223459	FAM115B	7:143295132-143305111	OK	1.94104	1.22286	-0.666573	-0.976528	0.09415	0.9998
ENSG00000140092	ENSG00000140092	FBLN5	14:92335755-92414331	OK	1.89808	2.92752	0.625138	0.870391	0.09445	0.9998
ENSG00000263165	ENSG00000263165	RP11-810M2.2	17:4046461-4167274	OK	0	0.693507	inf	#NAME?	0.09445	0.9998
ENSG00000143862	ENSG00000143862	ARL8A	1:202091985-202113869	OK	21.3247	29.7484	0.480282	0.838658	0.0945	0.9998
ENSG00000169429	ENSG00000169429	IL8	4:74606222-74609433	OK	80.673	59.8284	-0.431254	-0.97699	0.0946	0.9998
ENSG00000004846	ENSG00000004846	ABCB5	7:20654829-20816658	OK	67.0046	48.9703	-0.452355	-0.962234	0.09475	0.9998
ENSG00000175550	ENSG00000175550	DRAP1	11:65686727-65689032	OK	96.6701	130.024	0.42764	1.00091	0.09475	0.9998
ENSG00000119865	ENSG00000119865	CNRIP1	2:68511302-68547183	OK	8.03654	5.45718	-0.558418	-1.00775	0.09485	0.9998
ENSG00000256929	ENSG00000256929	AC067852.1	17:40610861-40674629	OK	0	3.67373	inf	#NAME?	0.09485	0.9998
ENSG00000168811	ENSG00000168811	IL12A	3:159631188-159943086	OK	0.407671	1.46749	1.84787	1.02778	0.09515	0.9998
ENSG00000101255	ENSG00000101255	TRIB3	20:361260-378203	OK	12.5758	17.0988	0.443244	0.985684	0.0954	0.9998
ENSG00000169379	ENSG00000169379	ARL13B	3:93698982-93847389	OK	7.50654	4.31713	-0.798075	-0.822705	0.09555	0.9998
ENSG00000232445	ENSG00000232445	RP11-132A1.4	7:100951626-100954266	OK	0.288069	0.823158	1.51476	1.06166	0.09565	0.9998
ENSG00000166912	ENSG00000166912	MTMR10	15:31196054-31283810	OK	6.33132	3.86079	-0.713612	-0.806097	0.0959	0.9998
ENSG00000169220	ENSG00000169220	RGS14	5:176784837-176799602	OK	14.4232	21.7535	0.592854	0.89066	0.09605	0.9998
ENSG00000132780	ENSG00000132780	NASP	1:46049517-46084566	OK	55.5463	39.8298	-0.479841	-0.977027	0.0962	0.9998
ENSG00000147894	ENSG00000147894	C9orf72	9:27546543-27573864	OK	5.92484	3.96351	-0.579999	-0.984654	0.09625	0.9998
ENSG00000181754	ENSG00000181754	AMIGO1	1:110046796-110052360	OK	0.421015	0.752684	0.838173	0.976614	0.0965	0.9998
ENSG00000133134	ENSG00000133134	BEX2	X:102564273-102565974	OK	3.83179	6.29992	0.717317	1.03502	0.09665	0.9998
ENSG00000272777	ENSG00000272777	RP11-571L19.8	4:99988406-99989276	OK	0.226502	0.633133	1.48298	1.06464	0.09665	0.9998
ENSG00000116586	ENSG00000116586	LAMTOR2	1:156024542-156028301	OK	138.864	103.018	-0.430777	-1.01836	0.09695	0.9998
ENSG00000167617	ENSG00000167617	CDC42EP5	19:54976209-54984411	OK	0.74396	2.31403	1.63711	0.888099	0.09705	0.9998
ENSG00000134222	ENSG00000134222	PSRC1	1:109822177-109825808	OK	28.1602	20.1467	-0.483115	-0.952366	0.09735	0.9998
ENSG00000138449	ENSG00000138449	SLC40A1	2:190425304-190448484	OK	0.887409	1.43779	0.696178	0.659018	0.0974	0.9998
ENSG00000183137	ENSG00000183137	CEP57L1	6:109416312-109485135	OK	8.65203	5.13245	-0.75339	-1.0185	0.0975	0.9998
ENSG00000244567	ENSG00000244567	AC096772.6	2:208686013-208687493	OK	2.9882	1.80153	-0.730059	-1.01886	0.0976	0.9998
ENSG00000156966	ENSG00000156966	B3GNT7	2:232260253-232265875	OK	1.76315	2.64042	0.582612	0.974585	0.09765	0.9998
ENSG00000165617	ENSG00000165617	DACT1	14:59100684-59115039	OK	7.03651	10.429	0.56767	0.97703	0.09775	0.9998
ENSG00000137331	ENSG00000137331	IER3	6:30710705-30712331	OK	187.99	141.649	-0.408335	-1.01395	0.09805	0.9998
ENSG00000184445	ENSG00000184445	KNTC1	12:123011792-123215390	OK	20.8326	13.9711	-0.576396	-0.782949	0.09835	0.9998
ENSG00000235883	ENSG00000235883	AC012379.1	15:49115931-49255641	OK	0	1.54342	inf	#NAME?	0.09835	0.9998
ENSG00000009780	ENSG00000009780	FAM76A	1:28052489-28089633	OK	6.23598	3.77386	-0.724574	-0.912867	0.0984	0.9998
ENSG00000095932	ENSG00000095932	C19orf77	19:3474404-3480540	OK	0.436887	1.06204	1.2815	0.828177	0.0985	0.9998
ENSG00000166979	ENSG00000166979	EVA1C	21:33784313-33887707	OK	3.5813	5.71894	0.675262	0.956904	0.0985	0.9998
ENSG00000177144	ENSG00000177144	NUDT4P1	1:145139024-145139569	OK	76.5586	104.534	0.449338	1.0047	0.09855	0.9998
ENSG00000242759	ENSG00000242759	LINC00882	3:106555657-106959488	OK	3.87274	2.11533	-0.872474	-0.933776	0.09865	0.9998
ENSG00000165983	ENSG00000165983	PTER	10:16478941-16555736	OK	2.75138	1.6343	-0.751484	-0.985978	0.0987	0.9998
ENSG00000060656	ENSG00000060656	PTPRU	1:29563027-29653325	OK	2.72516	4.14453	0.604866	0.674202	0.09875	0.9998
ENSG00000125633	ENSG00000125633	CCDC93	2:118617002-118771709	OK	11.2005	7.97259	-0.490443	-0.571196	0.09875	0.9998
ENSG00000164096	ENSG00000164096	C4orf3	4:120218206-120225600	OK	59.2943	39.7096	-0.578408	-0.998931	0.09875	0.9998
ENSG00000123364	ENSG00000123364	HOXC13	12:54329111-54340328	OK	1.97385	3.03518	0.620765	1.01773	0.09885	0.9998
ENSG00000189079	ENSG00000189079	ARID2	12:46123447-46301823	OK	2.96656	4.59623	0.631662	0.785704	0.09885	0.9998
ENSG00000153132	ENSG00000153132	CLGN	4:141309608-141349122	OK	2.02586	1.30158	-0.638271	-0.969942	0.0989	0.9998
ENSG00000158882	ENSG00000158882	TOMM40L	1:161195792-161208092	OK	23.9929	17.7878	-0.43172	-0.940119	0.099	0.9998
ENSG00000121621	ENSG00000121621	KIF18A	11:28042166-28355054	OK	6.94712	4.24288	-0.711373	-0.974474	0.09905	0.9998
ENSG00000111911	ENSG00000111911	HINT3	6:126277926-126301387	OK	4.77967	6.69686	0.486574	0.994111	0.0991	0.9998
ENSG00000131238	ENSG00000131238	PPT1	1:40538378-40563375	OK	92.3893	69.0326	-0.420447	-0.900673	0.0992	0.9998
ENSG00000162434	ENSG00000162434	JAK1	1:65210777-65432187	OK	26.9124	19.1792	-0.488725	-0.819476	0.0993	0.9998
ENSG00000100796	ENSG00000100796	SMEK1	14:91923954-91976898	OK	23.9469	34.7279	0.536256	0.966867	0.09945	0.9998
ENSG00000091527	ENSG00000091527	CDV3	3:133292573-133309105	OK	64.9498	90.1283	0.472654	0.886351	0.09955	0.9998
ENSG00000136935	ENSG00000136935	GOLGA1	9:127640645-127905785	OK	9.87705	6.77432	-0.544005	-0.808458	0.09955	0.9998
ENSG00000104368	ENSG00000104368	PLAT	8:42032235-42065242	OK	77.8204	103.031	0.404856	0.955853	0.0996	0.9998
ENSG00000114450	ENSG00000114450	GNB4	3:179116989-179169378	OK	22.2021	16.4984	-0.428373	-0.842682	0.0996	0.9998
ENSG00000155760	ENSG00000155760	FZD7	2:202899309-202903160	OK	4.28051	6.16351	0.525969	1.00579	0.0997	0.9998
ENSG00000149548	ENSG00000149548	CCDC15	11:124824016-124911385	OK	1.47538	0.960209	-0.619669	-0.912116	0.0998	0.9998
ENSG00000260482	ENSG00000260482	CTD-2196E14.9	16:23681331-23686820	OK	6.27099	8.88269	0.502303	1.00075	0.09995	0.9998
ENSG00000187123	ENSG00000187123	LYPD6	2:150186498-150330662	OK	3.52566	2.44887	-0.525778	-0.951935	0.10005	0.9998
ENSG00000138495	ENSG00000138495	COX17	3:119355303-119396301	OK	133.97	99.2771	-0.432382	-0.999761	0.1002	0.9998
ENSG00000109819	ENSG00000109819	PPARGC1A	4:23562545-23905712	OK	11.7627	8.3698	-0.490953	-0.662148	0.10035	0.9998
ENSG00000231686	ENSG00000231686	RP1-203P18.1	X:145701114-145702102	OK	1.56083	2.66295	0.770715	0.988778	0.1006	0.9998
ENSG00000213160	ENSG00000213160	KLHL23	2:170550974-170633499	OK	3.23765	5.17264	0.675955	0.816674	0.1008	0.9998
ENSG00000204310	ENSG00000204310	AGPAT1	6:32116135-32145873	OK	114.236	67.5736	-0.757493	-1.03915	0.10085	0.9998
ENSG00000115520	ENSG00000115520	COQ10B	2:198318146-198340032	OK	19.7146	27.1456	0.461451	1.00135	0.10105	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000171634	ENSG00000171634	BPTF	17:65821639-65980494	OK	30.1127	21.008	-0.519432	-0.590104	0.10105	0.9998
ENSG00000173230	ENSG00000173230	GOLGB1	3:121382045-121468602	OK	10.5965	7.70709	-0.459331	-0.491728	0.10105	0.9998
ENSG00000270069	ENSG00000270069	RP6-99M1.2	X:45604638-45629677	OK	3.40025	5.20463	0.614156	1.00315	0.10105	0.9998
ENSG00000138835	ENSG00000138835	RGS3	9:116207010-116360018	OK	11.2735	15.8144	0.488294	0.893808	0.1011	0.9998
ENSG00000155846	ENSG00000155846	PPARGC1B	5:149109860-149234585	OK	2.04609	3.06475	0.582899	0.826407	0.1011	0.9998
ENSG00000213553	ENSG00000213553	RPLP0P6	2:38633860-38742882	OK	426.837	566.944	0.409522	0.99458	0.10115	0.9998
ENSG00000046604	ENSG00000046604	DSG2	18:29078005-29136874	OK	27.0513	35.5897	0.395762	0.974399	0.1012	0.9998
ENSG00000176387	ENSG00000176387	HSD11B2	16:67464554-67471456	OK	0.288638	0.764727	1.40568	0.725002	0.1012	0.9998
ENSG00000142192	ENSG00000142192	APP	21:27252860-27589700	OK	104.969	139.124	0.406415	0.942494	0.1013	0.9998
ENSG00000158747	ENSG00000158747	NBL1	1:19923472-19984945	OK	238.069	154.742	-0.621517	-1.01646	0.10135	0.9998
ENSG00000111880	ENSG00000111880	RNGTT	6:89319984-89673348	OK	7.48326	5.2662	-0.506905	-1.00665	0.1015	0.9998
ENSG00000105640	ENSG00000105640	RPL18A	19:17970684-17974962	OK	405.483	538.19	0.408473	0.999544	0.1016	0.9998
ENSG00000115827	ENSG00000115827	DCAF17	2:172173918-172341562	OK	7.70575	4.89892	-0.653471	-0.648505	0.10165	0.9998
ENSG00000169302	ENSG00000169302	STK32A	5:146614525-146767415	OK	47.3543	31.5579	-0.585495	-0.975401	0.10165	0.9998
ENSG00000149115	ENSG00000149115	TNKS1BP1	11:57067111-57092426	OK	13.9708	19.7108	0.496572	0.849422	0.102	0.9998
ENSG00000187688	ENSG00000187688	TRPV2	17:16317837-16340317	OK	56.4477	74.135	0.39324	0.780992	0.10215	0.9998
ENSG00000185477	ENSG00000185477	GPRIN3	4:90157536-90229161	OK	0.673288	1.00885	0.583412	1.03364	0.1022	0.9998
ENSG00000125257	ENSG00000125257	ABCC4	13:95672082-95953687	OK	5.70987	7.83116	0.455768	0.937641	0.10225	0.9998
ENSG00000078369	ENSG00000078369	GNB1	1:1716728-1822495	OK	124.976	168.59	0.431867	0.855204	0.1023	0.9998
ENSG00000080986	ENSG00000080986	NDC80	18:2571509-2616634	OK	15.1706	11.0016	-0.463565	-0.873759	0.1023	0.9998
ENSG00000168566	ENSG00000168566	SNRNP48	6:7590431-7612200	OK	8.96837	12.2668	0.451847	0.990047	0.1023	0.9998
ENSG00000090339	ENSG00000090339	ICAM1	19:10362576-10399695	OK	70.8476	49.5321	-0.516355	-1.00289	0.10235	0.9998
ENSG00000168904	ENSG00000168904	LRRC28	15:99791566-99930934	OK	25.1945	17.4713	-0.528116	-0.931788	0.10245	0.9998
ENSG00000087074	ENSG00000087074	PPP1R15A	19:49375648-49379314	OK	41.3388	54.6511	0.402753	0.99497	0.1028	0.9998
ENSG00000182013	ENSG00000182013	PNMAL1	19:46969747-46974820	OK	10.2406	13.8636	0.436995	0.999044	0.1029	0.9998
ENSG00000228327	ENSG00000228327	RP11-206L10.2	1:694411-714006	OK	1.1251	0.592181	-0.925946	-1.02909	0.10295	0.9998
ENSG00000132109	ENSG00000132109	TRIM21	11:4406126-4414926	OK	1.29382	2.08939	0.691443	0.960029	0.10315	0.9998
ENSG00000102882	ENSG00000102882	MAPK3	16:30125425-30134827	OK	47.8175	33.5515	-0.511161	-0.972282	0.10325	0.9998
ENSG00000137573	ENSG00000137573	SULF1	8:70378858-70573150	OK	1.05406	1.90231	0.851799	0.603053	0.10385	0.9998
ENSG00000048740	ENSG00000048740	CELF2	10:11047258-11378674	OK	8.76211	12.7956	0.546301	0.974074	0.1039	0.9998
ENSG00000101752	ENSG00000101752	MIB1	18:19284917-19450918	OK	8.49027	11.5611	0.4454	0.941402	0.10395	0.9998
ENSG00000273456	ENSG00000273456	RP11-686O6.2	2:203239654-203240327	OK	0.509181	1.18395	1.21736	1.00453	0.1041	0.9998
ENSG00000008517	ENSG00000008517	IL32	16:3115297-3137101	OK	2.74256	1.7651	-0.635772	-0.606956	0.10415	0.9998
ENSG00000182871	ENSG00000182871	COL18A1	21:46825051-46964325	OK	5.01483	7.24242	0.530273	0.897378	0.10435	0.9998
ENSG00000107890	ENSG00000107890	ANKRD26	10:27280842-27389421	OK	1.57334	1.0125	-0.635917	-0.733656	0.1044	0.9998
ENSG00000255339	ENSG00000255339	NDUFB8	10:102246398-102319755	OK	0.105141	1.00952	3.26328	0.21531	0.10445	0.9998
ENSG00000125246	ENSG00000125246	CLYBL	13:100258918-100549387	OK	5.28891	3.29104	-0.684427	-0.938899	0.1045	0.9998
ENSG00000123136	ENSG00000123136	DDX39A	19:14519630-14530192	OK	64.2245	48.1931	-0.414298	-0.952782	0.10475	0.9998
ENSG00000143799	ENSG00000143799	PARP1	1:226548391-226595780	OK	85.2355	64.967	-0.391748	-0.835915	0.1049	0.9998
ENSG00000166889	ENSG00000166889	PATL1	11:59383901-59436453	OK	33.3449	25.2861	-0.399125	-0.852719	0.10495	0.9998
ENSG00000132749	ENSG00000132749	MTL5	11:68474907-68519032	OK	0.703702	1.52494	1.11572	0.868987	0.105	0.9998
ENSG00000056097	ENSG00000056097	ZFR	5:32354455-32444867	OK	41.5034	59.2323	0.513155	0.941886	0.10545	0.9998
ENSG00000102265	ENSG00000102265	TIMP1	X:47420515-47479252	OK	26.9019	43.4164	0.690529	0.980185	0.10545	0.9998
ENSG00000186908	ENSG00000186908	ZDHHC17	12:77157367-77247476	OK	17.7166	12.5023	-0.50291	-0.659322	0.1058	0.9998
ENSG00000185033	ENSG00000185033	SEMA4B	15:90703835-90772911	OK	8.91118	6.3923	-0.479283	-0.671708	0.10595	0.9998
ENSG00000267248	ENSG00000267248	CTD-2319I12.4	17:58203895-58213005	OK	1.52378	0.823276	-0.888209	-1.01091	0.106	0.9998
ENSG00000156510	ENSG00000156510	HKDC1	10:70975088-71027904	OK	5.67979	2.60993	-1.12183	-1.06776	0.10605	0.9998
ENSG00000171444	ENSG00000171444	MCC	5:112357795-112824527	OK	8.64944	5.7899	-0.579069	-0.803037	0.1061	0.9998
ENSG00000162377	ENSG00000162377	COA7	1:53152507-53164038	OK	12.7663	18.456	0.531741	0.973077	0.10615	0.9998
ENSG00000110880	ENSG00000110880	CORO1C	12:109038884-109125372	OK	107.309	140.864	0.39253	0.794172	0.1062	0.9998
ENSG00000185480	ENSG00000185480	PARPBP	12:102513955-102591623	OK	15.4618	10.9908	-0.492417	-0.942359	0.1062	0.9998
ENSG00000128011	ENSG00000128011	LRFN1	19:39797207-39811498	OK	2.03615	3.04178	0.57907	0.98785	0.10645	0.9998
ENSG00000147804	ENSG00000147804	SLC39A4	8:145634875-145642279	OK	20.7427	30.5995	0.560904	0.98118	0.1065	0.9998
ENSG00000101363	ENSG00000101363	MANBAL	20:35918040-35945663	OK	54.5318	40.5495	-0.427413	-0.996304	0.1066	0.9998
ENSG00000196923	ENSG00000196923	PDLIM7	5:176910394-176938275	OK	13.0483	18.7085	0.519838	0.923738	0.1066	0.9998
ENSG00000187624	ENSG00000187624	C17orf97	17:254325-273510	OK	0.733495	0.371252	-0.982389	-0.720238	0.1067	0.9998
ENSG00000102081	ENSG00000102081	FMR1	X:146993468-147032645	OK	10.7994	15.4447	0.51616	0.760611	0.1068	0.9998
ENSG00000264019	ENSG00000264019	RP11-6N17.6	17:46018871-46073562	OK	0	1.38062	inf	#NAME?	0.107	0.9998
ENSG00000100599	ENSG00000100599	RIN3	14:92980117-93155339	OK	7.16639	9.80002	0.451539	0.823394	0.1071	0.9998
ENSG00000161326	ENSG00000161326	DUSP14	17:35849936-35873603	OK	19.1504	26.1138	0.44744	0.985532	0.1071	0.9998
ENSG00000101439	ENSG00000101439	CST3	20:23608533-23619110	OK	49.7282	66.9853	0.42978	0.985084	0.10735	0.9998
ENSG00000247556	ENSG00000247556	OIP5-AS1	15:41576187-41624819	OK	18.752	11.4526	-0.711373	-0.85382	0.10755	0.9998
ENSG00000138346	ENSG00000138346	DNA2	10:70173820-70231879	OK	5.5064	3.40567	-0.693171	-0.777809	0.1077	0.9998
ENSG00000183092	ENSG00000183092	BEGAIN	14:101003485-101053750	OK	0.599455	1.1738	0.969468	0.681513	0.1077	0.9998
ENSG00000224260	ENSG00000224260	RP1-272L16.1	1:209701799-209741018	OK	0.51846	1.19436	1.20393	1.0338	0.1078	0.9998
ENSG00000135917	ENSG00000135917	SLC19A3	2:228549925-228582728	OK	0.32757	0.684598	1.06345	0.60293	0.1079	0.9998
ENSG00000213621	ENSG00000213621	RPSAP54	13:21535448-21536334	OK	0.687998	1.36199	0.985238	1.02382	0.10795	0.9998
ENSG00000075711	ENSG00000075711	DLG1	3:196769430-197030618	OK	32.3598	44.9249	0.473315	0.718333	0.108	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000156675	ENSG00000156675	RAB11FIP1	8:37716135-37756985	OK	7.15637	10.0992	0.496937	0.973416	0.108	0.9998
ENSG00000082074	ENSG00000082074	FYB	5:39105337-39274630	OK	1.78318	1.08625	-0.715096	-0.707851	0.10805	0.9998
ENSG00000119986	ENSG00000119986	AVPI1	10:99437180-99447080	OK	32.8333	44.2241	0.429674	0.983034	0.10805	0.9998
ENSG00000169245	ENSG00000169245	CXCL10	4:76932336-77033955	OK	0.817171	0.207703	-1.97612	-1.31562	0.10805	0.9998
ENSG00000269490	ENSG00000269490	SBP1	6:33588141-33679504	OK	0	0.803531	inf	#NAME?	0.1081	0.9998
ENSG00000063761	ENSG00000063761	ADCK1	14:78266425-78401355	OK	4.3033	2.85281	-0.59306	-0.917048	0.1082	0.9998
ENSG00000172927	ENSG00000172927	MYEOV	11:69061604-69182494	OK	0.718006	1.53031	1.09176	0.546028	0.1082	0.9998
ENSG00000105717	ENSG00000105717	PBX4	19:19672521-19729725	OK	2.05771	1.09941	-0.904308	-0.976676	0.1083	0.9998
ENSG00000171680	ENSG00000171680	PLEKHG5	1:6484847-6580121	OK	0.698712	1.14487	0.712408	0.90872	0.1084	0.9998
ENSG00000266258	ENSG00000266258	RP11-41O4.1	18:68002674-68019695	OK	0.529792	1.19898	1.17832	1.00508	0.1084	0.9998
ENSG00000005471	ENSG00000005471	ABCB4	7:87031012-87109751	OK	2.31668	3.33287	0.524705	0.814818	0.1085	0.9998
ENSG00000058804	ENSG00000058804	NDC1	1:54231132-54304533	OK	14.6883	10.5521	-0.477145	-0.962372	0.1085	0.9998
ENSG00000065978	ENSG00000065978	YBX1	1:43148097-43168020	OK	549.555	740.306	0.429858	0.965971	0.1087	0.9998
ENSG00000186193	ENSG00000186193	SAPCD2	9:139952114-139965040	OK	7.0088	5.06816	-0.467704	-0.970489	0.1091	0.9998
ENSG00000004864	ENSG00000004864	SLC25A13	7:95749531-95951459	OK	50.5474	38.168	-0.405274	-0.639575	0.10915	0.9998
ENSG00000124772	ENSG00000124772	CPNE5	6:36708551-36807778	OK	0.844977	0.521482	-0.696295	-0.826138	0.10945	0.9998
ENSG00000117519	ENSG00000117519	CNN3	1:95362506-95392834	OK	84.6312	111.244	0.394469	0.957034	0.1095	0.9998
ENSG00000267001	ENSG00000267001	AC006538.4	19:2714564-2740150	OK	1.41855	0	#NAME?	#NAME?	0.1095	0.9998
ENSG00000218336	ENSG00000218336	TENM3	4:182795590-183724177	OK	0.86599	1.69502	0.968885	0.718057	0.10985	0.9998
ENSG00000107959	ENSG00000107959	PITRM1	10:3179919-3215003	OK	32.8995	24.8068	-0.407327	-0.83403	0.1101	0.9998
ENSG00000120696	ENSG00000120696	KBTBD7	13:41763968-41768702	OK	1.41992	2.0547	0.53312	0.948828	0.11015	0.9998
ENSG00000111358	ENSG00000111358	GTF2H3	12:124118374-124147153	OK	11.002	7.46331	-0.559873	-0.80048	0.1103	0.9998
ENSG00000155974	ENSG00000155974	GRIP1	12:66741210-67197966	OK	1.61512	3.07934	0.930978	0.779254	0.1103	0.9998
ENSG00000138468	ENSG00000138468	SENP7	3:101043048-101232085	OK	8.58123	6.12425	-0.486651	-0.892874	0.11065	0.9998
ENSG00000270673	ENSG00000270673	YTHDF3-AS1	8:64080283-64081001	OK	0.716373	0.219821	-1.70438	-1.16812	0.1107	0.9998
ENSG00000134602	ENSG00000134602	MST4	X:131157292-131209971	OK	5.00533	7.22174	0.528881	0.952804	0.1109	0.9998
ENSG00000064205	ENSG00000064205	WISP2	20:43285091-43379675	OK	0.466025	0.941131	1.01399	0.886366	0.11115	0.9998
ENSG00000084636	ENSG00000084636	COL16A1	1:32083286-32169920	OK	8.53719	14.8579	0.799396	0.759867	0.1112	0.9998
ENSG00000004799	ENSG00000004799	PDK4	7:95212810-95225803	OK	39.3423	52.3644	0.412506	0.848915	0.11125	0.9998
ENSG00000198242	ENSG00000198242	RPL23A	17:27046410-27070473	OK	523.283	696.104	0.411711	0.962547	0.11135	0.9998
ENSG00000176182	ENSG00000176182	MYPOP	19:46393277-46405862	OK	5.36831	3.67126	-0.548192	-0.965876	0.1114	0.9998
ENSG00000005700	ENSG00000005700	IBTK	6:82879699-82957471	OK	20.7008	15.6747	-0.401247	-0.876595	0.1115	0.9998
ENSG00000075945	ENSG00000075945	KIFAP3	1:169890466-170054349	OK	30.7957	23.1757	-0.410118	-0.982227	0.1115	0.9998
ENSG00000138593	ENSG00000138593	SECISBP2L	15:49280672-49338760	OK	9.09802	6.80473	-0.419015	-0.566798	0.1115	0.9998
ENSG00000177685	ENSG00000177685	EFCAB4A	11:818901-842545	OK	0.467069	1.26828	1.44116	0.1729	0.11155	0.9998
ENSG00000075702	ENSG00000075702	WDR62	19:36545782-36596008	OK	8.51778	6.26491	-0.443183	-0.915411	0.1116	0.9998
ENSG00000148943	ENSG00000148943	LIN7C	11:27516122-27528320	OK	5.55001	7.60524	0.454503	0.981107	0.1117	0.9998
ENSG00000065613	ENSG00000065613	SLK	10:105726958-105788991	OK	11.109	8.3863	-0.405623	-0.83449	0.11185	0.9998
ENSG00000225880	ENSG00000225880	LINC00115	1:761585-762902	OK	0.455234	0.875359	0.943266	0.973748	0.11215	0.9998
ENSG00000157741	ENSG00000157741	UBN2	7:138915101-138992982	OK	2.95844	2.18068	-0.440059	-0.884573	0.11225	0.9998
ENSG00000171130	ENSG00000171130	ATP6V0E2	7:149564785-149577784	OK	75.1444	56.9236	-0.400638	-0.926883	0.11225	0.9998
ENSG00000241135	ENSG00000241135	LINC00881	3:156799455-156840793	OK	1.05532	0.41076	-1.36131	-0.906111	0.11235	0.9998
ENSG00000159905	ENSG00000159905	ZNF221	19:44455374-44471861	OK	1.166	0.566828	-1.04059	-0.838921	0.11245	0.9998
ENSG00000183386	ENSG00000183386	FHL3	1:38462441-38471278	OK	4.73449	6.92403	0.548402	0.958388	0.11255	0.9998
ENSG00000232859	ENSG00000232859	LYRM9	17:26083791-26221778	OK	3.66451	1.71173	-1.09817	-1.00358	0.11255	0.9998
ENSG00000115306	ENSG00000115306	SPTBN1	2:54683421-54896812	OK	119.27	160.506	0.4284	0.91442	0.1126	0.9998
ENSG00000143845	ENSG00000143845	ETNK2	1:204100189-204121307	OK	16.8525	22.9983	0.448562	0.932185	0.1126	0.9998
ENSG00000066651	ENSG00000066651	TRMT11	6:126307575-126360422	OK	6.43362	10.0786	0.647597	0.836956	0.1127	0.9998
ENSG00000104983	ENSG00000104983	CCDC61	19:46498338-46526323	OK	4.2259	2.69806	-0.647335	-0.829391	0.1127	0.9998
ENSG00000105372	ENSG00000105372	RPS19	19:42363987-42376994	OK	3266.72	4570.8	0.484604	0.972084	0.11295	0.9998
ENSG00000152056	ENSG00000152056	AP1S3	2:224616402-224702744	OK	7.64339	11.976	0.647861	0.941489	0.11295	0.9998
ENSG00000237172	ENSG00000237172	B3GNT9	16:67143860-67185117	OK	0.961482	2.07088	1.10691	0.99193	0.11305	0.9998
ENSG00000155254	ENSG00000155254	MARVELD1	10:99472929-99477907	OK	10.5207	14.5832	0.47107	0.932012	0.1131	0.9998
ENSG00000133874	ENSG00000133874	RNF122	8:33405272-33424643	OK	8.30471	5.76043	-0.527753	-0.969333	0.11315	0.9998
ENSG00000130309	ENSG00000130309	COLGALT1	19:17666402-17693971	OK	81.4942	106.441	0.385287	0.942543	0.1133	0.9998
ENSG00000225190	ENSG00000225190	PLEKHM1	17:43513265-43568115	OK	15.4046	21.8656	0.505304	0.670501	0.11335	0.9998
ENSG00000139921	ENSG00000139921	TMX1	14:51706879-51722759	OK	31.4506	41.3935	0.396316	0.953819	0.11385	0.9998
ENSG00000159733	ENSG00000159733	ZFYVE28	4:2271308-2420390	OK	1.55274	2.76542	0.832677	0.86411	0.11385	0.9998
ENSG00000084207	ENSG00000084207	GSTP1	11:67351065-67354131	OK	104.688	138.976	0.408739	0.975252	0.11395	0.9998
ENSG00000104765	ENSG00000104765	BNIP3L	8:26236774-26371608	OK	122.797	83.5408	-0.555718	-0.922883	0.11395	0.9998
ENSG00000138829	ENSG00000138829	FBN2	5:127593600-128369335	OK	0.526675	0.967949	0.878018	0.892165	0.11395	0.9998
ENSG00000148925	ENSG00000148925	BTBD10	11:13409547-13484844	OK	23.6489	17.6008	-0.426132	-0.880438	0.1141	0.9998
ENSG00000145390	ENSG00000145390	USP53	4:120113927-120216672	OK	29.0235	20.4575	-0.504588	-0.660068	0.11445	0.9998
ENSG00000092470	ENSG00000092470	WDR76	15:44119160-44160617	OK	3.30511	2.02534	-0.706534	-0.891744	0.11465	0.9998
ENSG00000118412	ENSG00000118412	CASP8AP2	6:90539612-90584155	OK	2.62528	1.65198	-0.668276	-0.911896	0.11495	0.9998
ENSG00000250722	ENSG00000250722	SEPP1	5:42756902-42887494	OK	0.520201	0.982552	0.917464	0.503555	0.11515	0.9998
ENSG00000140326	ENSG00000140326	CDAN1	15:43015756-43029324	OK	3.53807	2.3369	-0.598365	-0.674642	0.11535	0.9998
ENSG00000100211	ENSG00000100211	CBY1	22:39052640-39077825	OK	14.7908	10.0167	-0.562288	-0.942887	0.11545	0.9998
ENSG00000174720	ENSG00000174720	LARP7	4:113434671-113578748	OK	22.5504	15.5082	-0.540123	-0.773073	0.11545	0.9998
ENSG00000164237	ENSG00000164237	CMBL	5:10275986-10308138	OK	31.8261	43.7611	0.459436	0.952866	0.11565	0.9998
ENSG00000176022	ENSG00000176022	B3GALT6	1:1167628-1170421	OK	4.11983	2.82448	-0.544597	-0.968149	0.1157	0.9998
ENSG00000151322	ENSG00000151322	NPAS3	14:33404138-34273382	OK	0.896345	0.456469	-0.973537	-0.547354	0.11575	0.9998
ENSG00000102218	ENSG00000102218	RP2	X:46696374-46741793	OK	5.04472	6.9085	0.453599	0.952492	0.11595	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267194	ENSG00000267194	RP1-193H18.2	17:67547498-67550002	OK	0.823426	1.30678	0.666301	0.939913	0.11595	0.9998
ENSG00000135253	ENSG00000135253	KCP	7:128470430-128550773	OK	0.280315	0.845944	1.59351	0.322258	0.116	0.9998
ENSG00000182141	ENSG00000182141	ZNF708	19:21473961-21512227	OK	2.18693	1.38967	-0.654167	-0.789733	0.11615	0.9998
ENSG00000182952	ENSG00000182952	HMGN4	6:26538632-26546482	OK	32.9349	24.3675	-0.434657	-0.953084	0.11625	0.9998
ENSG00000260086	ENSG00000260086	RP11-42I10.1	16:48657346-48778553	OK	3.6377	1.98992	-0.870313	-0.992601	0.11625	0.9998
ENSG00000152484	ENSG00000152484	USP12	13:27640292-27746033	OK	17.4371	13.1664	-0.405291	-0.957332	0.11635	0.9998
ENSG00000003436	ENSG00000003436	TFPI	2:187866602-188430487	OK	4.07424	2.37284	-0.779917	-0.900452	0.1165	0.9998
ENSG00000143742	ENSG00000143742	SRP9	1:225965530-225978168	OK	141.586	108.476	-0.384305	-0.953547	0.1166	0.9998
ENSG00000125398	ENSG00000125398	SOX9	17:70017991-70216859	OK	2.38578	1.61741	-0.560777	-0.96015	0.11665	0.9998
ENSG00000165724	ENSG00000165724	ZMYND19	9:140476530-140484942	OK	12.2293	17.0743	0.481487	0.956827	0.11665	0.9998
ENSG00000138111	ENSG00000138111	TMEM180	10:104221148-104236802	OK	5.7953	3.28662	-0.818277	-0.916905	0.1168	0.9998
ENSG00000107186	ENSG00000107186	MPDZ	9:13105702-13279589	OK	22.7226	16.8149	-0.434387	-0.805918	0.11685	0.9998
ENSG00000174928	ENSG00000174928	C3orf33	3:155480400-155524140	OK	4.35286	2.91457	-0.578684	-0.940076	0.11685	0.9998
ENSG00000204923	ENSG00000204923	FBXO48	2:68686550-68694390	OK	0.944118	0.618076	-0.611183	-0.961815	0.1169	0.9998
ENSG00000138750	ENSG00000138750	NUP54	4:77035811-77069668	OK	15.9328	11.6897	-0.446758	-0.816807	0.1172	0.9998
ENSG00000204219	ENSG00000204219	TCEA3	1:23707553-23751233	OK	1.22252	2.02647	0.729107	0.843747	0.1172	0.9998
ENSG00000154079	ENSG00000154079	C6orf57	6:71276619-71299272	OK	5.70297	3.78358	-0.59196	-0.927596	0.11745	0.9998
ENSG00000179604	ENSG00000179604	CDC42EP4	17:71279762-71308314	OK	11.6989	8.65451	-0.434846	-0.896631	0.1177	0.9998
ENSG00000139178	ENSG00000139178	C1RL	12:7187512-7275097	OK	5.66305	3.15022	-0.846126	-0.590093	0.11785	0.9998
ENSG00000166750	ENSG00000166750	SLFN5	17:33570054-33600674	OK	14.7836	9.71299	-0.606014	-0.93752	0.11795	0.9998
ENSG00000267519	ENSG00000267519	MIR24-2	19:13945329-13947173	OK	8.15517	11.3762	0.48023	0.892908	0.11795	0.9998
ENSG00000121064	ENSG00000121064	SCPEP1	17:55055465-55084129	OK	65.0089	50.0056	-0.378546	-0.888253	0.1181	0.9998
ENSG00000203778	ENSG00000203778	FAM229B	6:112408801-112423993	OK	16.3636	10.617	-0.624117	-0.949945	0.11835	0.9998
ENSG00000234851	ENSG00000234851	RP11-3P17.3	3:161144214-161166030	OK	768.838	1007.34	0.389802	0.950253	0.11865	0.9998
ENSG00000267633	ENSG00000267633	CTB-5E10.3	19:13875345-13889276	OK	0.143895	1.83955	3.67626	0.221978	0.11865	0.9998
ENSG00000174574	ENSG00000174574	AKIRIN1	1:39456894-39471731	OK	28.2454	37.9707	0.426872	0.943251	0.1187	0.9998
ENSG00000147459	ENSG00000147459	DOCK5	8:25042237-25275598	OK	2.12245	3.24902	0.614275	0.574	0.11885	0.9998
ENSG00000163923	ENSG00000163923	RPL39L	3:186838735-186898696	OK	64.1402	47.6737	-0.428036	-0.952008	0.11885	0.9998
ENSG00000168614	ENSG00000168614	NBPF9	1:144811743-144830413	OK	18.5353	13.263	-0.482868	-0.74104	0.1189	0.9998
ENSG00000173681	ENSG00000173681	CXorf23	X:19930977-19988416	OK	2.43907	3.62498	0.57164	0.766696	0.11905	0.9998
ENSG00000111665	ENSG00000111665	CDCA3	12:6949117-6961230	OK	45.4007	31.7878	-0.514244	-0.971315	0.1192	0.9998
ENSG00000186897	ENSG00000186897	C1QL4	12:49726199-49730971	OK	0.652959	1.09743	0.749068	0.951208	0.11925	0.9998
ENSG00000105976	ENSG00000105976	MET	7:116312443-116438440	OK	154.224	115.607	-0.415805	-0.686603	0.1194	0.9998
ENSG00000263618	ENSG00000263618	RP11-527H14.4	18:14903578-14915627	OK	0.431184	1.06522	1.30478	0.7949	0.1194	0.9998
ENSG00000020577	ENSG00000020577	SAMD4A	14:55033814-55260033	OK	16.0479	21.7429	0.438156	0.686009	0.1195	0.9998
ENSG00000177600	ENSG00000177600	RPLP2	11:799178-812880	OK	722.738	1012.74	0.486716	0.940703	0.1196	0.9998
ENSG00000166847	ENSG00000166847	DCTN5	16:23652712-23681195	OK	41.1749	54.0139	0.391565	0.824877	0.11975	0.9998
ENSG00000140522	ENSG00000140522	RLBP1	15:89753099-89764982	OK	2.94563	4.62758	0.651684	0.744421	0.1199	0.9998
ENSG00000188643	ENSG00000188643	S100A16	1:153579361-153585621	OK	7.86602	11.4471	0.541273	0.947822	0.1199	0.9998
ENSG00000270933	ENSG00000270933	CTD-2227E11.1	7:25988276-25989023	OK	0.924567	1.78734	0.950963	0.985727	0.1199	0.9998
ENSG00000112312	ENSG00000112312	GMNN	6:24775158-24786327	OK	41.3808	30.9094	-0.420919	-0.9188	0.11995	0.9998
ENSG00000171649	ENSG00000171649	ZIK1	19:58082933-58105145	OK	0.536459	1.21483	1.17921	0.710618	0.12	0.9998
ENSG00000133424	ENSG00000133424	LARGE	22:33558211-34318829	OK	13.8042	8.82909	-0.644771	-0.795048	0.1202	0.9998
ENSG00000107165	ENSG00000107165	TYRP1	9:12685438-12822130	OK	1136.22	1667.9	0.553789	0.889565	0.12045	0.9998
ENSG00000090263	ENSG00000090263	MRPS33	7:140705853-140715028	OK	140.363	106.089	-0.403883	-0.946337	0.1206	0.9998
ENSG00000146112	ENSG00000146112	PPP1R18	6:30644165-30655672	OK	37.8697	51.9908	0.457214	0.960894	0.12065	0.9998
ENSG00000076641	ENSG00000076641	PAG1	8:81880044-82024303	OK	13.9108	19.0177	0.451145	0.459003	0.1207	0.9998
ENSG00000114446	ENSG00000114446	IFT57	3:107879658-107941417	OK	11.0717	16.697	0.592717	0.908981	0.1207	0.9998
ENSG00000197818	ENSG00000197818	SLC9A8	20:48429249-48508779	OK	5.1729	3.5986	-0.523538	-0.90497	0.12075	0.9998
ENSG00000158417	ENSG00000158417	EIF5B	2:99613723-100106497	OK	32.2273	20.9603	-0.620622	-0.729868	0.121	0.9998
ENSG00000179085	ENSG00000179085	DPM3	1:155112366-155113071	OK	43.0465	29.6574	-0.537504	-0.965596	0.12115	0.9998
ENSG00000166037	ENSG00000166037	CEP57	11:95502105-95565857	OK	15.7939	11.1363	-0.5041	-0.8415	0.1213	0.9998
ENSG00000160818	ENSG00000160818	GPATCH4	1:156564278-156571288	OK	51.2816	67.7823	0.402468	0.829052	0.1215	0.9998
ENSG00000163093	ENSG00000163093	BBS5	2:170335687-170382772	OK	22.9073	31.8811	0.476891	0.783815	0.1215	0.9998
ENSG00000198914	ENSG00000198914	POU3F3	2:105469742-105542510	OK	1.45379	0.982379	-0.565465	-0.936439	0.1219	0.9998
ENSG00000146918	ENSG00000146918	NCAPG2	7:158424002-158497520	OK	39.7804	30.6047	-0.378305	-0.834769	0.12205	0.9998
ENSG00000013573	ENSG00000013573	DDX11	12:31173696-31257725	OK	16.1553	11.0971	-0.541823	-0.759448	0.1221	0.9998
ENSG00000115310	ENSG00000115310	RTN4	2:55199324-55339757	OK	144.842	199.955	0.465196	0.927401	0.1221	0.9998
ENSG00000170369	ENSG00000170369	CST2	20:23804405-23807368	OK	0.240548	0.664127	1.46514	1.01887	0.12235	0.9998
ENSG00000174151	ENSG00000174151	CYB561D1	1:110036673-110045554	OK	4.80758	3.48627	-0.463625	-0.819079	0.12235	0.9998
ENSG00000055163	ENSG00000055163	CYFIP2	5:156687131-157002783	OK	3.55387	5.94607	0.742546	0.694912	0.12245	0.9998
ENSG00000198816	ENSG00000198816	ZNF358	19:7541760-7585912	OK	15.1579	20.5172	0.436765	0.927927	0.1225	0.9998
ENSG00000227329	ENSG00000227329	RP11-258C19.4	X:53122891-53196196	OK	4.42931	0	#NAME?	#NAME?	0.12255	0.9998
ENSG00000241634	ENSG00000241634	RP11-381E24.1	3:108262213-108262722	OK	1.53964	0.647448	-1.24975	-1.01926	0.12275	0.9998
ENSG00000140534	ENSG00000140534	TICRR	15:90048507-90198682	OK	3.93093	2.46394	-0.673904	-0.942833	0.12315	0.9998
ENSG00000182993	ENSG00000182993	C12orf60	12:14956505-15059520	OK	2.01739	1.06826	-0.917219	-0.823184	0.12315	0.9998
ENSG00000057704	ENSG00000057704	TMCC3	12:94960899-95044338	OK	1.89738	1.2537	-0.597813	-0.71324	0.1233	0.9998
ENSG00000105376	ENSG00000105376	ICAM5	19:10400656-10407454	OK	2.31256	3.62287	0.647644	0.82343	0.12345	0.9998
ENSG00000140853	ENSG00000140853	NLRC5	16:57023396-57117443	OK	0.39702	0.675949	0.767704	0.303393	0.12365	0.9998
ENSG00000167325	ENSG00000167325	RRM1	11:4115936-4160106	OK	65.2491	50.769	-0.36201	-0.78802	0.12365	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000185088	ENSG00000185088	RPS27L	15:63413998-63450220	OK	224.562	312.625	0.477319	0.943544	0.1237	0.9998
ENSG00000178053	ENSG00000178053	MLF1	3:158288951-158325041	OK	29.4164	21.0515	-0.482697	-0.898242	0.12375	0.9998
ENSG00000135968	ENSG00000135968	GCC2	2:109065016-109150652	OK	8.61154	5.98908	-0.523938	-0.684336	0.1238	0.9998
ENSG00000130589	ENSG00000130589	HELZ2	20:62189438-62205592	OK	2.08185	3.64432	0.807781	0.663563	0.1239	0.9998
ENSG00000071539	ENSG00000071539	TRIP13	5:710470-919472	OK	37.0149	23.592	-0.649807	-0.735555	0.124	0.9998
ENSG00000206053	ENSG00000206053	HN1L	16:1662325-1752281	OK	42.4241	30.9887	-0.453143	-0.788783	0.124	0.9998
ENSG00000227242	ENSG00000227242	NBPF13P	1:146490894-146596107	OK	0.373527	0.763742	1.03187	0.943328	0.12415	0.9998
ENSG00000072110	ENSG00000072110	ACTN1	14:69340859-69446157	OK	91.2893	122.188	0.420581	0.827146	0.12425	0.9998
ENSG00000221420	ENSG00000221420	SNORA81	3:186499568-186524847	OK	0	0.886271	inf	#NAME?	0.12425	0.9998
ENSG00000212766	ENSG00000212766	LINC00277	15:69365265-69392275	OK	2.03993	1.26962	-0.684128	-0.701869	0.12435	0.9998
ENSG00000096696	ENSG00000096696	DSP	6:7541807-7586950	OK	1.33762	1.91673	0.518983	0.904906	0.1244	0.9998
ENSG00000114948	ENSG00000114948	ADAM23	2:207308262-207485851	OK	16.3755	21.8953	0.419088	0.936322	0.12445	0.9998
ENSG00000104687	ENSG00000104687	GSR	8:30535582-30585443	OK	32.9825	43.6226	0.403374	0.898545	0.12465	0.9998
ENSG00000112144	ENSG00000112144	ICK	6:52866076-52965671	OK	10.4275	6.75889	-0.625534	-0.954111	0.12465	0.9998
ENSG00000115525	ENSG00000115525	ST3GAL5	2:86066266-86116137	OK	90.4644	69.1989	-0.386601	-0.820899	0.12485	0.9998
ENSG00000168994	ENSG00000168994	PXDC1	6:3722847-3754105	OK	23.1299	31.708	0.455086	0.879331	0.1249	0.9998
ENSG00000118242	ENSG00000118242	MREG	2:216809212-216967506	OK	122.452	91.7349	-0.416673	-0.934396	0.125	0.9998
ENSG00000169679	ENSG00000169679	BUB1	2:111395274-111435691	OK	39.7792	30.4681	-0.384716	-0.872517	0.125	0.9998
ENSG00000186591	ENSG00000186591	UBE2H	7:129470571-129592789	OK	69.086	94.7063	0.455068	0.62606	0.1251	0.9998
ENSG00000120159	ENSG00000120159	CAAP1	9:26840682-26892802	OK	13.4085	9.49096	-0.498517	-0.879262	0.12515	0.9998
ENSG00000137474	ENSG00000137474	MYO7A	11:76839309-76926284	OK	0.464389	0.746907	0.685595	0.63778	0.1253	0.9998
ENSG00000110583	ENSG00000110583	NAA40	11:63706430-63724800	OK	17.0258	12.5084	-0.444827	-0.693431	0.12535	0.9998
ENSG00000115507	ENSG00000115507	OTX1	2:63277191-63284971	OK	1.13103	1.81188	0.679856	0.875658	0.12535	0.9998
ENSG00000158164	ENSG00000158164	TMSB15A	X:101768603-101771712	OK	6.8629	4.38137	-0.647436	-0.930139	0.12535	0.9998
ENSG00000197535	ENSG00000197535	MYO5A	15:52599479-52821247	OK	38.384	52.9428	0.463931	0.784242	0.12535	0.9998
ENSG00000116761	ENSG00000116761	CTH	1:70876900-70905534	OK	4.08868	2.76272	-0.565546	-0.883684	0.1254	0.9998
ENSG00000171298	ENSG00000171298	GAA	17:78075354-78093678	OK	11.8447	8.08811	-0.550366	-0.844172	0.12545	0.9998
ENSG00000232022	ENSG00000232022	RP5-1109J22.1	1:46897800-46911193	OK	0.351417	0.722878	1.04057	0.677881	0.12555	0.9998
ENSG00000176170	ENSG00000176170	SPHK1	17:74305566-74383941	OK	10.1479	19.302	0.92757	0.94459	0.1257	0.9998
ENSG00000107863	ENSG00000107863	ARHGAP21	10:24872537-25012597	OK	20.5793	15.354	-0.422581	-0.621988	0.12575	0.9998
ENSG00000181915	ENSG00000181915	ADO	10:64553321-64568238	OK	13.3751	17.4298	0.382008	0.91011	0.1258	0.9998
ENSG00000249863	ENSG00000249863	RP11-177C12.1	4:37869912-37871599	OK	0.28957	0.663596	1.19639	0.945598	0.1258	0.9998
ENSG00000197355	ENSG00000197355	UAP1L1	9:139971952-139978991	OK	20.3601	26.5579	0.383397	0.864781	0.12595	0.9998
ENSG00000248714	ENSG00000248714	RP11-1079K10.3	17:47366567-47447360	OK	0.631155	0.107531	-2.55325	-0.253318	0.1261	0.9998
ENSG00000092964	ENSG00000092964	DPYSL2	8:26371790-26515694	OK	10.9456	8.30416	-0.398445	-0.860252	0.12615	0.9998
ENSG00000108010	ENSG00000108010	GLRX3	10:131934662-131982785	OK	63.6493	83.081	0.384374	0.90353	0.12625	0.9998
ENSG00000172005	ENSG00000172005	MAL	2:95690937-95719737	OK	0.675805	1.21555	0.846931	0.783492	0.12625	0.9998
ENSG00000235499	ENSG00000235499	AC073046.25	2:74212258-74213470	OK	2.37336	1.00642	-1.23769	-0.991211	0.1263	0.9998
ENSG00000152492	ENSG00000152492	CCDC50	3:190984956-191116459	OK	31.7293	43.0262	0.4394	0.777201	0.1264	0.9998
ENSG00000005469	ENSG00000005469	CROT	7:86974996-87029111	OK	7.01545	10.2517	0.547262	0.798476	0.12655	0.9998
ENSG00000106624	ENSG00000106624	AEBP1	7:44143959-44154161	OK	27.0338	35.6376	0.398636	0.739595	0.12655	0.9998
ENSG00000104856	ENSG00000104856	RELB	19:45504687-45541452	OK	11.6284	8.4813	-0.455299	-0.832068	0.1266	0.9998
ENSG00000148572	ENSG00000148572	NRBF2	10:64893049-64914783	OK	26.4299	34.8381	0.398491	0.935527	0.12665	0.9998
ENSG00000111667	ENSG00000111667	USP5	12:6961291-6975796	OK	34.8506	26.7256	-0.38296	-0.860067	0.12675	0.9998
ENSG00000007237	ENSG00000007237	GAS7	17:9813925-10101868	OK	64.4913	44.6135	-0.531623	-0.701265	0.1269	0.9998
ENSG00000102572	ENSG00000102572	STK24	13:99102454-99231084	OK	49.8662	37.955	-0.393773	-0.919325	0.1269	0.9998
ENSG00000026103	ENSG00000026103	FAS	10:90639490-90775542	OK	5.39195	8.94779	0.730723	0.816624	0.12695	0.9998
ENSG00000168754	ENSG00000168754	FAM178B	2:97541619-97684341	OK	20.1224	15.1236	-0.411999	-0.810463	0.12695	0.9998
ENSG00000229645	ENSG00000229645	LINC00341	14:95873605-95876427	OK	1.5405	2.50316	0.700351	0.895033	0.12695	0.9998
ENSG00000093009	ENSG00000093009	CDC45	22:19466981-19508135	OK	22.3753	16.7619	-0.416723	-0.858297	0.127	0.9998
ENSG00000148450	ENSG00000148450	MSRB2	10:23384434-23410942	OK	28.0034	18.8482	-0.571177	-0.909094	0.12715	0.9998
ENSG00000131236	ENSG00000131236	CAP1	1:40505904-40538321	OK	149.301	194.08	0.378424	0.807608	0.1272	0.9998
ENSG00000137098	ENSG00000137098	SPAG8	9:35792150-35812269	OK	0.75072	0.326131	-1.20282	-0.391201	0.12725	0.9998
ENSG00000135622	ENSG00000135622	SEMA4F	2:74881354-74909186	OK	17.1595	12.4624	-0.461431	-0.735095	0.1274	0.9998
ENSG00000160199	ENSG00000160199	PKNOX1	21:44394619-44453691	OK	4.87805	7.71228	0.660854	0.722921	0.1274	0.9998
ENSG00000105204	ENSG00000105204	DYRK1B	19:40315989-40324841	OK	5.2044	7.50757	0.528614	0.830725	0.12755	0.9998
ENSG00000198780	ENSG00000198780	FAM169A	5:74073398-74163679	OK	3.41174	5.16183	0.597374	0.799136	0.12755	0.9998
ENSG00000163874	ENSG00000163874	ZC3H12A	1:37940152-37949980	OK	1.36258	0.83967	-0.69845	-0.764723	0.1276	0.9998
ENSG00000197557	ENSG00000197557	TTC30A	2:178467816-178483694	OK	1.02654	1.47253	0.520504	0.912151	0.1278	0.9998
ENSG00000205649	ENSG00000205649	HTN3	4:70894129-70902255	OK	1.65431	2.90371	0.811665	0.820226	0.1279	0.9998
ENSG00000093000	ENSG00000093000	NUP50	22:45559721-45583896	OK	34.1437	24.7758	-0.462687	-0.665134	0.12795	0.9998
ENSG00000229083	ENSG00000229083	PSMA6P2	X:12843958-12844952	OK	0.254988	0.693671	1.44382	1.00017	0.12795	0.9998
ENSG00000112425	ENSG00000112425	EPM2A	6:145822718-146058354	OK	1.68183	2.43863	0.536035	0.763771	0.12805	0.9998
ENSG00000112280	ENSG00000112280	COL9A1	6:70924763-71012786	OK	3.86027	2.46124	-0.649317	-0.778271	0.1282	0.9998
ENSG00000166803	ENSG00000166803	KIAA0101	15:64457715-64679886	OK	57.9171	35.8228	-0.693108	-0.955751	0.1282	0.9998
ENSG00000205105	ENSG00000205105	COX17P1	13:47064996-47065397	OK	0.759801	1.75349	1.20653	0.804249	0.1282	0.9998
ENSG00000236830	ENSG00000236830	CBR3-AS1	21:37502668-37528615	OK	0.712966	0.258566	-1.4633	-0.355409	0.1284	0.9998
ENSG00000105825	ENSG00000105825	TFPI2	7:93220884-93540577	OK	37.3127	54.3761	0.543307	0.939533	0.12845	0.9998
ENSG00000175061	ENSG00000175061	FAM211A-AS1	17:16342135-16395467	OK	795.479	1048.68	0.39868	0.918536	0.12845	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226539	ENSG00000226539	AC012512.1	2:224569337-224570055	OK	22.8698	16.0724	-0.508859	-0.940461	0.1285	0.9998
ENSG00000110422	ENSG00000110422	HIPK3	11:33278217-33378569	OK	10.021	13.2734	0.405517	0.907099	0.1286	0.9998
ENSG00000225410	ENSG00000225410	AC107016.1	12:53290976-53346686	OK	0	2.29421	inf	#NAME?	0.1286	0.9998
ENSG00000253978	ENSG00000253978	CTB-178M22.2	5:166711803-167691162	OK	5.8356	3.30417	-0.820593	-0.962523	0.1288	0.9998
ENSG00000111711	ENSG00000111711	GOLT1B	12:21654714-21671342	OK	19.608	28.5099	0.54002	0.882652	0.12905	0.9998
ENSG00000130856	ENSG00000130856	ZNF236	18:74534562-74682683	OK	2.64682	3.87043	0.548235	0.523254	0.12935	0.9998
ENSG00000116266	ENSG00000116266	STXBP3	1:109289295-109352148	OK	18.7808	13.8194	-0.442562	-0.67789	0.12945	0.9998
ENSG00000185737	ENSG00000185737	NRG3	10:83635069-84746935	OK	14.1767	10.3561	-0.45304	-0.928706	0.12945	0.9998
ENSG00000138772	ENSG00000138772	ANXA3	4:79472672-79531597	OK	1.4568	2.24528	0.62409	0.725833	0.12955	0.9998
ENSG00000174405	ENSG00000174405	LIG4	13:108859786-108870716	OK	6.53695	4.74418	-0.46246	-0.931477	0.1296	0.9998
ENSG00000109180	ENSG00000109180	OCIAD1	4:48807228-48863834	OK	59.5358	77.7562	0.385201	0.861464	0.12965	0.9998
ENSG00000166562	ENSG00000166562	SEC11C	18:56806708-56826068	OK	194.25	146.711	-0.404934	-0.918204	0.12965	0.9998
ENSG00000149547	ENSG00000149547	EI24	11:125439111-125551018	OK	45.9091	69.8072	0.604596	0.912447	0.1299	0.9998
ENSG00000128294	ENSG00000128294	TPST2	22:26921457-26992681	OK	7.53124	10.2604	0.446134	0.82775	0.13055	0.9998
ENSG00000128641	ENSG00000128641	MYO1B	2:192093890-192290115	OK	26.193	33.6401	0.361001	0.778157	0.13075	0.9998
ENSG00000229932	ENSG00000229932	YWHAZP3	10:23425851-23426590	OK	50.4362	67.0346	0.410446	0.916355	0.1308	0.9998
ENSG00000049541	ENSG00000049541	RFC2	7:73645828-73668774	OK	37.2939	27.9763	-0.414735	-0.865189	0.1309	0.9998
ENSG00000137831	ENSG00000137831	UACA	15:70946892-71055932	OK	24.4093	17.2595	-0.500039	-0.743167	0.1309	0.9998
ENSG00000150627	ENSG00000150627	WDR17	4:176986984-177103978	OK	4.24925	2.97733	-0.51319	-0.695643	0.1309	0.9998
ENSG00000126091	ENSG00000126091	ST3GAL3	1:44115828-44396831	OK	10.3057	5.65948	-0.864698	-0.591246	0.13095	0.9998
ENSG00000164086	ENSG00000164086	DUSP7	3:52082934-52090566	OK	4.57161	6.32671	0.468755	0.939943	0.13105	0.9998
ENSG00000179262	ENSG00000179262	RAD23A	19:13056668-13064456	OK	79.538	61.2123	-0.377823	-0.916405	0.1311	0.9998
ENSG00000135535	ENSG00000135535	CD164	6:109687716-109703762	OK	39.7004	51.1914	0.366747	0.876983	0.13115	0.9998
ENSG00000151849	ENSG00000151849	CENPJ	13:25457170-25497018	OK	8.76347	6.0665	-0.530639	-0.719809	0.13115	0.9998
ENSG00000270011	ENSG00000270011	ZNF559-ZNF177	19:9434447-9493293	OK	0.986865	0.454036	-1.12004	-0.296005	0.13125	0.9998
ENSG00000112964	ENSG00000112964	GHR	5:42423878-42721979	OK	21.6941	16.4331	-0.400697	-0.900938	0.13145	0.9998
ENSG00000132429	ENSG00000132429	POPDC3	6:105544696-105627870	OK	15.8307	24.5177	0.631104	0.91382	0.1316	0.9998
ENSG00000196924	ENSG00000196924	FLNA	X:153576891-153603006	OK	80.0698	105.326	0.395531	0.64999	0.1316	0.9998
ENSG00000243955	ENSG00000243955	GSTA1	6:52656461-52668708	OK	1.60776	0.866405	-0.891936	-0.83843	0.13165	0.9998
ENSG00000219507	ENSG00000219507	FTH1P8	X:147133752-147134266	OK	51.3067	69.3649	0.435059	0.90028	0.1317	0.9998
ENSG00000179403	ENSG00000179403	VWA1	1:1370240-1378262	OK	2.49644	4.15664	0.735545	0.835676	0.13185	0.9998
ENSG00000241288	ENSG00000241288	RP11-379B18.5	3:125546080-125629115	OK	0.616529	1.24727	1.01653	0.650126	0.13225	0.9998
ENSG00000213062	ENSG00000213062	AL021068.1	1:169455379-169456846	OK	0.509075	0.895535	0.814873	0.903239	0.1323	0.9998
ENSG00000203827	ENSG00000203827	NBPF16	1:148739442-148758311	OK	1.89119	1.29736	-0.543719	-0.907256	0.13235	0.9998
ENSG00000138660	ENSG00000138660	AP1AR	4:113152892-113191203	OK	15.1139	19.9236	0.398607	0.811791	0.1324	0.9998
ENSG00000101639	ENSG00000101639	CEP192	18:12991360-13125051	OK	6.08745	4.46153	-0.4483	-0.622384	0.1325	0.9998
ENSG00000185834	ENSG00000185834	RPL12P4	20:53691154-53691685	OK	27.1368	38.0832	0.488903	0.913876	0.1325	0.9998
ENSG00000115129	ENSG00000115129	TP53I3	2:24299395-24424567	OK	13.9344	20.8208	0.579374	0.920034	0.1327	0.9998
ENSG00000100867	ENSG00000100867	DHRS2	14:24099323-24114848	OK	2.7251	4.01146	0.557819	0.886403	0.13275	0.9998
ENSG00000132640	ENSG00000132640	BTBD3	20:11871370-11907257	OK	18.1517	23.4921	0.372076	0.777307	0.13275	0.9998
ENSG00000143947	ENSG00000143947	RPS27A	2:55401926-55462989	OK	1297.8	1717.09	0.403899	0.918386	0.13275	0.9998
ENSG00000268302	ENSG00000268302	AL035252.1	20:25176328-25207370	OK	0	1.48558	inf	#NAME?	0.13295	0.9998
ENSG00000079215	ENSG00000079215	SLC1A3	5:36606456-36725297	OK	3.15795	5.57995	0.821261	0.839621	0.1331	0.9998
ENSG00000157111	ENSG00000157111	TMEM171	5:72416118-72427644	OK	0.382818	0.754855	0.979541	0.917049	0.13315	0.9998
ENSG00000268655	ENSG00000268655	CTB-60B18.10	19:49521503-49522741	OK	0.230635	0.898135	1.96132	1.21081	0.13315	0.9998
ENSG00000164761	ENSG00000164761	TNFRSF11B	8:119935795-119964439	OK	1.7244	0.896722	-0.943359	-0.831351	0.1332	0.9998
ENSG00000075856	ENSG00000075856	SART3	12:108908961-108955176	OK	22.3153	16.5547	-0.430796	-0.739537	0.13325	0.9998
ENSG00000073008	ENSG00000073008	PVR	19:45041044-45222031	OK	15.0453	21.076	0.486289	0.816194	0.1333	0.9998
ENSG00000107551	ENSG00000107551	RASSF4	10:45306471-45491339	OK	3.94353	2.52008	-0.646019	-0.637361	0.1333	0.9998
ENSG00000142534	ENSG00000142534	RPS11	19:49999621-50002946	OK	1871.74	2458.25	0.393251	0.902472	0.1333	0.9998
ENSG00000121057	ENSG00000121057	AKAP1	17:55162452-55198710	OK	16.3842	21.1868	0.370859	0.775497	0.1336	0.9998
ENSG00000119640	ENSG00000119640	ACYP1	14:75519923-75545126	OK	21.2301	13.8321	-0.618093	-0.970534	0.1337	0.9998
ENSG00000134871	ENSG00000134871	COL4A2	13:110801317-111165374	OK	20.7837	27.5912	0.408755	0.750691	0.1339	0.9998
ENSG00000183648	ENSG00000183648	NDUFB1	14:92582465-92588261	OK	410.899	311.51	-0.399507	-0.926559	0.13405	0.9998
ENSG00000234694	ENSG00000234694	RP1-92O14.3	1:43820354-43824329	OK	0.258519	0.69795	1.43285	0.940224	0.1341	0.9998
ENSG00000196391	ENSG00000196391	ZNF774	15:90895476-90909324	OK	0.608244	1.52775	1.32869	0.762837	0.13415	0.9998
ENSG00000005448	ENSG00000005448	WDR54	2:74648804-74652882	OK	9.12386	6.122	-0.575642	-0.872904	0.1343	0.9998
ENSG00000104936	ENSG00000104936	DMPK	19:46268042-46296060	OK	8.42023	12.9727	0.623551	0.656399	0.1343	0.9998
ENSG00000024526	ENSG00000024526	DEPDC1	1:68939834-69004310	OK	13.4975	9.12953	-0.564078	-0.73714	0.1345	0.9998
ENSG00000140463	ENSG00000140463	BBS4	15:72978526-73030817	OK	14.1092	10.5045	-0.425628	-0.718735	0.1345	0.9998
ENSG00000179104	ENSG00000179104	TMTC2	12:83080658-83528649	OK	15.8614	11.8823	-0.4167	-0.897974	0.1346	0.9998
ENSG00000272005	ENSG00000272005	RP11-91J19.4	8:424454-427966	OK	4.1993	2.96818	-0.500569	-0.916214	0.1346	0.9998
ENSG00000129473	ENSG00000129473	BCL2L2	14:23654524-23795394	OK	23.3793	15.2144	-0.619793	-0.631218	0.13465	0.9998
ENSG00000175087	ENSG00000175087	PDIK1L	1:26437663-26452034	OK	2.67139	1.7797	-0.585958	-0.828527	0.13465	0.9998
ENSG00000111186	ENSG00000111186	WNT5B	12:1639056-1756409	OK	0.305966	0.813379	1.41056	0.462505	0.13475	0.9998
ENSG00000132128	ENSG00000132128	LRRC41	1:46713359-46769280	OK	15.875	21.2795	0.422715	0.906554	0.13475	0.9998
ENSG00000079432	ENSG00000079432	CIC	19:42772688-42799949	OK	25.5135	17.9448	-0.507694	-0.708433	0.1348	0.9998
ENSG00000108861	ENSG00000108861	DUSP3	17:41843488-41856356	OK	94.3563	121.809	0.368432	0.884405	0.1348	0.9998
ENSG00000109929	ENSG00000109929	SC5D	11:121163161-121179403	OK	19.8221	26.0636	0.394927	0.877659	0.1348	0.9998
ENSG00000206140	ENSG00000206140	TMEM191C	22:21820711-21825558	OK	0.809644	1.42017	0.810706	0.653698	0.13515	0.9998
ENSG00000135002	ENSG00000135002	RFK	9:79000432-79009433	OK	13.0939	18.0142	0.460235	0.849603	0.1353	0.9998
ENSG00000134709	ENSG00000134709	HOOK1	1:60280457-60342050	OK	2.97123	4.29968	0.533167	0.673916	0.13545	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000082438	ENSG00000082438	COBLL1	2:165510133-165705844	OK	7.49732	10.1643	0.43907	0.573945	0.1355	0.9998
ENSG00000153560	ENSG00000153560	UBP1	3:33318516-33482863	OK	27.1591	36.2345	0.415929	0.789031	0.13555	0.9998
ENSG00000133069	ENSG00000133069	TMCC2	1:205197303-205242471	OK	81.3982	63.0507	-0.368483	-0.904726	0.13565	0.9998
ENSG00000203880	ENSG00000203880	PCMTD2	20:62887093-62944485	OK	35.2913	24.8648	-0.505206	-0.738155	0.1357	0.9998
ENSG00000172296	ENSG00000172296	SPTLC3	20:12989626-13147411	OK	0.66458	1.29002	0.956878	0.654974	0.1359	0.9998
ENSG00000205269	ENSG00000205269	TMEM170B	6:11537937-11583757	OK	8.54602	4.56572	-0.904412	-0.809094	0.1359	0.9998
ENSG00000132846	ENSG00000132846	ZBED3	5:76367896-76462734	OK	1.4047	2.04702	0.543265	0.740888	0.13595	0.9998
ENSG00000178082	ENSG00000178082	TWF1P1	17:27530440-27531492	OK	16.7093	11.8518	-0.495542	-0.912927	0.13595	0.9998
ENSG00000069248	ENSG00000069248	NUP133	1:229577044-229644103	OK	23.5642	17.9931	-0.389151	-0.823563	0.1361	0.9998
ENSG00000227359	ENSG00000227359	AC017074.2	2:114435278-114461655	OK	0.369749	0.927994	1.32757	0.945872	0.13615	0.9998
ENSG00000154265	ENSG00000154265	ABCA5	17:67143354-67323385	OK	22.8085	16.9007	-0.432487	-0.817685	0.1362	0.9998
ENSG00000120860	ENSG00000120860	CCDC53	12:102406704-102455927	OK	31.8502	22.8774	-0.47738	-0.885905	0.13645	0.9998
ENSG00000003096	ENSG00000003096	KLHL13	X:117031775-117251303	OK	2.52708	3.76672	0.575838	0.618836	0.1365	0.9998
ENSG00000249859	ENSG00000249859	PVT1	8:128806778-129113499	OK	33.0796	47.0285	0.507595	0.904897	0.1366	0.9998
ENSG00000184900	ENSG00000184900	SUMO3	21:46225531-46238694	OK	37.9456	48.9077	0.366128	0.880821	0.1367	0.9998
ENSG00000100426	ENSG00000100426	ZBED4	22:50247489-50283726	OK	7.98353	6.06902	-0.395563	-0.910606	0.13685	0.9998
ENSG00000102401	ENSG00000102401	ARMCX3	X:100877786-100882833	OK	41.7675	54.2522	0.377302	0.798673	0.1369	0.9998
ENSG00000233830	ENSG00000233830	EIF4HP1	7:27497781-27498468	OK	115.73	88.8242	-0.381744	-0.892955	0.1371	0.9998
ENSG00000005810	ENSG00000005810	MYCBP2	13:77618791-77901185	OK	8.85338	12.4447	0.491233	0.780822	0.13725	0.9998
ENSG00000249815	ENSG00000249815	RP11-269F21.3	4:112723956-112993854	OK	2.55729	4.56169	0.834955	0.925746	0.1374	0.9998
ENSG00000136160	ENSG00000136160	EDNRB	13:78469615-79233314	OK	164.154	216.422	0.398801	0.888131	0.1376	0.9998
ENSG00000065534	ENSG00000065534	MYLK	3:123304388-123603178	OK	1.07406	1.65443	0.623249	0.505745	0.1377	0.9998
ENSG00000121289	ENSG00000121289	CEP89	19:33369901-33462897	OK	7.26789	5.28337	-0.460079	-0.802933	0.13785	0.9998
ENSG00000054392	ENSG00000054392	HHAT	1:210501595-210849638	OK	9.49212	12.7579	0.426587	0.907735	0.1379	0.9998
ENSG00000116668	ENSG00000116668	SWT1	1:185126211-185260897	OK	4.328	3.06431	-0.498142	-0.846279	0.13795	0.9998
ENSG00000135315	ENSG00000135315	KIAA1009	6:84833959-84937353	OK	3.02432	1.87558	-0.689272	-0.795373	0.138	0.9998
ENSG00000149084	ENSG00000149084	HSD17B12	11:43577985-43902276	OK	73.4502	95.2034	0.374245	0.72875	0.138	0.9998
ENSG00000235823	ENSG00000235823	LINC00263	10:102133371-102143125	OK	4.5221	3.17855	-0.508624	-0.913663	0.1383	0.9998
ENSG00000196549	ENSG00000196549	MME	3:154741912-154901497	OK	83.9839	120.443	0.520161	0.785353	0.13835	0.9998
ENSG00000178038	ENSG00000178038	ALS2CL	3:46710486-46735194	OK	0.525128	0.951067	0.856877	0.768144	0.1384	0.9998
ENSG00000203849	ENSG00000203849	RP11-417J8.6	1:142618768-142729975	OK	0.936818	1.61271	0.783644	0.915241	0.1384	0.9998
ENSG00000183305	ENSG00000183305	MAGEA2B	X:151883081-151887096	OK	10.2912	17.3973	0.757456	0.912968	0.13845	0.9998
ENSG00000106211	ENSG00000106211	HSPB1	7:75931860-75933612	OK	524.597	677.084	0.368124	0.897199	0.13855	0.9998
ENSG00000234420	ENSG00000234420	ZNF37BP	10:43008957-43048270	OK	3.45074	1.9115	-0.852199	-0.971597	0.13875	0.9998
ENSG00000124782	ENSG00000124782	RREB1	6:7107829-7252213	OK	4.83354	7.63181	0.658944	0.481084	0.13885	0.9998
ENSG00000087076	ENSG00000087076	HSD17B14	19:49316273-49339935	OK	27.2161	37.2812	0.45399	0.899235	0.1391	0.9998
ENSG00000166860	ENSG00000166860	ZBTB39	12:57392617-57400230	OK	4.41642	3.28699	-0.426112	-0.904616	0.1392	0.9998
ENSG00000144677	ENSG00000144677	CTDSPL	3:37903450-38025960	OK	13.7891	19.1647	0.474925	0.737295	0.13935	0.9998
ENSG00000110651	ENSG00000110651	CD81	11:2349978-2418649	OK	549.716	723.633	0.396573	0.873904	0.1394	0.9998
ENSG00000128965	ENSG00000128965	CHAC1	15:41245159-41248710	OK	2.75336	4.36793	0.665758	0.917606	0.1395	0.9998
ENSG00000129474	ENSG00000129474	AJUBA	14:23398817-23451851	OK	2.96024	5.24317	0.824726	0.642911	0.1395	0.9998
ENSG00000172123	ENSG00000172123	SLFN12	17:33738078-33760302	OK	1.19987	1.99218	0.731471	0.736154	0.1397	0.9998
ENSG00000052795	ENSG00000052795	FNIP2	4:159690289-159959912	OK	21.9211	16.198	-0.436508	-0.710602	0.13975	0.9998
ENSG00000134686	ENSG00000134686	PHC2	1:33772366-33896653	OK	56.5486	72.6276	0.361025	0.757387	0.13975	0.9998
ENSG00000233337	ENSG00000233337	UBE2FP3	1:111980135-111980659	OK	0.288645	0.840955	1.54273	1.00411	0.1398	0.9998
ENSG00000185379	ENSG00000185379	RAD51D	17:33332106-33448541	OK	9.01483	5.48292	-0.717355	-0.772801	0.1399	0.9998
ENSG00000196670	ENSG00000196670	ZFP62	5:180274610-180288286	OK	8.62128	5.10567	-0.755802	-0.902889	0.1399	0.9998
ENSG00000185112	ENSG00000185112	FAM43A	3:194406621-194409762	OK	4.7468	6.56728	0.46834	0.902488	0.14005	0.9998
ENSG00000143878	ENSG00000143878	RHOB	2:20646834-20649200	OK	54.8756	70.3306	0.357988	0.893945	0.1402	0.9998
ENSG00000131153	ENSG00000131153	GINS2	16:85645014-85723679	OK	8.44735	5.77797	-0.547936	-0.850598	0.1404	0.9998
ENSG00000197275	ENSG00000197275	RAD54B	8:95384187-95487337	OK	8.40455	6.03571	-0.477648	-0.74459	0.1405	0.9998
ENSG00000172469	ENSG00000172469	MANEA	6:96025418-96057333	OK	2.38647	1.5473	-0.625128	-0.691254	0.14055	0.9998
ENSG00000125629	ENSG00000125629	INSIG2	2:118846027-118868573	OK	18.6281	13.2249	-0.494216	-0.771983	0.1406	0.9998
ENSG00000075303	ENSG00000075303	SLC25A40	7:87462882-87538856	OK	23.8605	13.5226	-0.81925	-0.718618	0.14075	0.9998
ENSG00000055211	ENSG00000055211	GINM1	6:149887429-149912884	OK	13.5354	10.0597	-0.428158	-0.884464	0.1408	0.9998
ENSG00000026950	ENSG00000026950	BTN3A1	6:26402464-26415444	OK	8.90025	6.45633	-0.463132	-0.745845	0.14105	0.9998
ENSG00000105193	ENSG00000105193	RPS16	19:39923846-39926588	OK	1663.58	2163.68	0.379199	0.886047	0.14105	0.9998
ENSG00000126016	ENSG00000126016	AMOT	X:112017730-112084043	OK	16.1524	11.3369	-0.510723	-0.616826	0.14105	0.9998
ENSG00000144224	ENSG00000144224	UBXN4	2:136499188-136542625	OK	16.1564	12.4246	-0.378902	-0.76766	0.14135	0.9998
ENSG00000197180	ENSG00000197180	BX936347.1	X:153656536-153656795	OK	3.05314	0.603047	-2.33995	-1.55965	0.1414	0.9998
ENSG00000109805	ENSG00000109805	NCAPG	4:17812524-18023499	OK	21.6046	15.5815	-0.471507	-0.767673	0.14155	0.9998
ENSG00000105173	ENSG00000105173	CCNE1	19:30302804-30315215	OK	9.2136	6.67574	-0.464838	-0.841995	0.14165	0.9998
ENSG00000109861	ENSG00000109861	CTSC	11:88026759-88070955	OK	18.5353	26.4838	0.514833	0.822413	0.14175	0.9998
ENSG00000143641	ENSG00000143641	GALNT2	1:230193535-230417870	OK	80.3015	60.9273	-0.398339	-0.889614	0.14185	0.9998
ENSG00000038219	ENSG00000038219	BOD1L1	4:13570361-13629347	OK	10.3499	7.4434	-0.475581	-0.695981	0.1424	0.9998
ENSG00000158987	ENSG00000158987	RAPGEF6	5:130759613-131132710	OK	2.25373	3.66163	0.700172	0.563298	0.1425	0.9998
ENSG00000169570	ENSG00000169570	DTWD2	5:118173016-118324240	OK	3.84523	2.65682	-0.533369	-0.872718	0.1426	0.9998
ENSG00000104093	ENSG00000104093	DMXL2	15:51706293-51915030	OK	8.12184	5.98862	-0.439582	-0.466936	0.14275	0.9998
ENSG00000011007	ENSG00000011007	TCEB3	1:24069644-24104777	OK	16.5392	22.0642	0.415817	0.851796	0.14285	0.9998
ENSG00000040275	ENSG00000040275	SPDL1	5:169010637-169031782	OK	15.8844	11.7936	-0.42961	-0.654371	0.143	0.9998
ENSG00000198380	ENSG00000198380	GFPT1	2:69546904-69614382	OK	11.826	8.70896	-0.441391	-0.562967	0.1431	0.9998
ENSG00000065833	ENSG00000065833	ME1	6:83920107-84140797	OK	17.4841	12.8423	-0.445139	-0.886751	0.14315	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000132692	ENSG00000132692	BCAN	1:156611181-156631216	OK	27.2029	20.0732	-0.438492	-0.811412	0.1433	0.9998
ENSG00000147408	ENSG00000147408	CSGALNACT1	8:19261671-19615540	OK	7.22604	10.1613	0.491807	0.708874	0.14345	0.9998
ENSG00000112029	ENSG00000112029	FBXO5	6:153291663-153304714	OK	7.97848	5.7253	-0.478763	-0.906491	0.14355	0.9998
ENSG00000149257	ENSG00000149257	SERPINH1	11:75273100-75283828	OK	32.1024	41.2961	0.363322	0.855628	0.14365	0.9998
ENSG00000073605	ENSG00000073605	GSDMB	17:38060847-38076107	OK	1.11768	0.616986	-0.857196	-0.534522	0.1437	0.9998
ENSG00000223959	ENSG00000223959	AFG3L1P	16:90038993-90068569	OK	11.062	7.09372	-0.640992	-0.855418	0.1437	0.9998
ENSG00000236782	ENSG00000236782	RP11-96L14.7	1:26496361-26498551	OK	0.825818	0.218734	-1.91665	-0.290537	0.1437	0.9998
ENSG00000115963	ENSG00000115963	RND3	2:151324708-151395525	OK	9.41421	13.0145	0.467212	0.823698	0.14405	0.9998
ENSG00000184260	ENSG00000184260	HIST2H2AC	1:149858524-149858961	OK	3.54656	1.94315	-0.868025	-0.887744	0.14415	0.9998
ENSG00000143466	ENSG00000143466	IKBKE	1:206643790-206671061	OK	7.32244	11.5344	0.655549	0.846684	0.1442	0.9998
ENSG00000112984	ENSG00000112984	KIF20A	5:137475454-137549032	OK	32.737	21.4498	-0.609954	-0.739716	0.14425	0.9998
ENSG00000109670	ENSG00000109670	FBXW7	4:153242409-153457253	OK	5.06963	7.23746	0.513602	0.757018	0.14435	0.9998
ENSG00000169718	ENSG00000169718	DUS1L	17:80015381-80023763	OK	125.311	168.566	0.427799	0.895315	0.14455	0.9998
ENSG00000272338	ENSG00000272338	RP11-722E23.2	8:33218360-33218933	OK	0.959452	1.85897	0.954224	0.925071	0.14455	0.9998
ENSG00000077092	ENSG00000077092	RARB	3:25215822-25639423	OK	5.74254	8.0157	0.481139	0.856411	0.14465	0.9998
ENSG00000145349	ENSG00000145349	CAMK2D	4:114372187-114683083	OK	9.91067	13.9234	0.490458	0.882162	0.1448	0.9998
ENSG00000172954	ENSG00000172954	LCLAT1	2:30670091-30867091	OK	6.13966	8.40732	0.453488	0.64666	0.1448	0.9998
ENSG00000141540	ENSG00000141540	TTYH2	17:72209652-72258159	OK	62.9137	82.3357	0.388146	0.729205	0.1449	0.9998
ENSG00000253730	ENSG00000253730	RP11-893F2.13	17:48235693-48238637	OK	0.643125	0.151101	-2.08959	-1.01839	0.14505	0.9998
ENSG00000156804	ENSG00000156804	FBXO32	8:124510128-124553446	OK	35.0354	51.004	0.541799	0.912641	0.1452	0.9998
ENSG00000115107	ENSG00000115107	STEAP3	2:119981383-120023228	OK	0.48999	0.821063	0.744742	0.854451	0.1453	0.9998
ENSG00000204525	ENSG00000204525	HLA-C	6:31236525-31239907	OK	26.5284	35.2055	0.408262	0.873238	0.1453	0.9998
ENSG00000231738	ENSG00000231738	TSPAN19	12:85408093-85430055	OK	0.710324	0.350398	-1.01948	-0.546698	0.14535	0.9998
ENSG00000144115	ENSG00000144115	THNSL2	2:88469834-88486146	OK	0.920206	0.535452	-0.7812	-0.532454	0.14575	0.9998
ENSG00000147364	ENSG00000147364	FBXO25	8:356427-421225	OK	41.7957	31.2986	-0.417257	-0.851073	0.14585	0.9998
ENSG00000251164	ENSG00000251164	HULC	6:8652369-8654079	OK	0.220268	0.670923	1.60688	0.883413	0.14595	0.9998
ENSG00000116584	ENSG00000116584	ARHGEF2	1:155916629-155976861	OK	33.0061	45.1714	0.452679	0.777637	0.1461	0.9998
ENSG00000114796	ENSG00000114796	KLHL24	3:183353355-183402265	OK	31.5534	23.1903	-0.444274	-0.54746	0.1463	0.9998
ENSG00000080839	ENSG00000080839	RBL1	20:35624751-35725581	OK	4.64713	3.32369	-0.483554	-0.771361	0.1465	0.9998
ENSG00000197150	ENSG00000197150	ABCB8	7:150725509-150744869	OK	45.9884	35.0174	-0.393197	-0.763494	0.1466	0.9998
ENSG00000063180	ENSG00000063180	CA11	19:49141198-49184461	OK	4.54889	2.9497	-0.624948	-0.6364	0.1467	0.9998
ENSG00000236537	ENSG00000236537	RP11-732M18.3	6:158703294-158733390	OK	1.31492	2.5716	0.967685	0.899477	0.1468	0.9998
ENSG00000108578	ENSG00000108578	BLMH	17:28565758-28619074	OK	26.7246	20.8194	-0.360236	-0.675594	0.1469	0.9998
ENSG00000185818	ENSG00000185818	NAT8L	4:2061238-2070816	OK	5.48952	7.26943	0.405164	0.882859	0.14705	0.9998
ENSG00000113615	ENSG00000113615	SEC24A	5:133936833-134063513	OK	3.13879	5.24728	0.741363	0.843305	0.14715	0.9998
ENSG00000164951	ENSG00000164951	PDP1	8:94870034-94938294	OK	60.4931	46.7831	-0.370783	-0.81255	0.14715	0.9998
ENSG00000055732	ENSG00000055732	MCOLN3	1:85464829-85598821	OK	21.7596	29.3083	0.429657	0.90897	0.1472	0.9998
ENSG00000149582	ENSG00000149582	TMEM25	11:118307204-118473748	OK	0.568663	0.971034	0.771949	0.139009	0.1472	0.9998
ENSG00000187555	ENSG00000187555	USP7	16:8985950-9060847	OK	28.7481	36.7822	0.355541	0.664911	0.1472	0.9998
ENSG00000076864	ENSG00000076864	RAP1GAP	1:21922707-21995801	OK	6.62782	9.36452	0.498671	0.697349	0.14725	0.9998
ENSG00000260912	ENSG00000260912	RP11-363E7.4	9:19453206-19455171	OK	0.887684	1.40239	0.659771	0.882373	0.14725	0.9998
ENSG00000144580	ENSG00000144580	RQCD1	2:219433302-219461803	OK	30.6294	23.1087	-0.406477	-0.751386	0.1473	0.9998
ENSG00000160200	ENSG00000160200	CBS	21:44473300-44497053	OK	4.54785	6.30295	0.470844	0.751375	0.1473	0.9998
ENSG00000122877	ENSG00000122877	EGR2	10:64571755-64679660	OK	0.877373	0.559044	-0.650229	-0.810441	0.14745	0.9998
ENSG00000109667	ENSG00000109667	SLC2A9	4:9772776-10056560	OK	0.70686	1.39807	0.983944	0.648696	0.14755	0.9998
ENSG00000170345	ENSG00000170345	FOS	14:75745476-75748933	OK	6.53036	4.63217	-0.495473	-0.765484	0.14755	0.9998
ENSG00000182108	ENSG00000182108	DEXI	16:10958770-11036878	OK	36.0373	49.2272	0.449965	0.878178	0.14805	0.9998
ENSG00000101199	ENSG00000101199	ARFGAP1	20:61904136-61921142	OK	81.8424	108.534	0.407228	0.797089	0.14825	0.9998
ENSG00000005893	ENSG00000005893	LAMP2	X:119561681-119603220	OK	153.31	199.024	0.376491	0.858449	0.14845	0.9998
ENSG00000090889	ENSG00000090889	KIF4A	X:69506444-69640682	OK	16.9637	11.4401	-0.568345	-0.809951	0.1488	0.9998
ENSG00000158856	ENSG00000158856	DMTN	8:21906505-21940038	OK	1.96082	3.01824	0.622247	0.658308	0.14885	0.9998
ENSG00000117676	ENSG00000117676	RPS6KA1	1:26856251-26901521	OK	5.83991	7.74888	0.408041	0.684644	0.14895	0.9998
ENSG00000010704	ENSG00000010704	HFE	6:26087508-26098571	OK	10.2838	6.99704	-0.555551	-0.867391	0.149	0.9998
ENSG00000157456	ENSG00000157456	CCNB2	15:59397276-59425449	OK	19.9528	15.0441	-0.407394	-0.85069	0.14905	0.9998
ENSG00000141753	ENSG00000141753	IGFBP4	17:38599701-38613983	OK	1.67154	2.49381	0.577175	0.881719	0.14925	0.9998
ENSG00000186310	ENSG00000186310	NAP1L3	X:92925928-92928567	OK	2.23686	1.51258	-0.564468	-0.894489	0.14925	0.9998
ENSG00000166801	ENSG00000166801	FAM111A	11:58897605-58922512	OK	15.5298	11.1511	-0.477854	-0.653309	0.14935	0.9998
ENSG00000137804	ENSG00000137804	NUSAP1	15:41624891-41673248	OK	39.6295	28.4001	-0.48068	-0.824626	0.14965	0.9998
ENSG00000102038	ENSG00000102038	SMARCA1	X:128580479-128657477	OK	24.733	19.2353	-0.362685	-0.87822	0.14995	0.9998
ENSG00000270127	ENSG00000270127	RP11-526I2.5	15:101087971-101090358	OK	0.405284	0.708875	0.806597	0.904656	0.14995	0.9998
ENSG00000100031	ENSG00000100031	GGT1	22:24936405-25024972	OK	0.999283	2.08493	1.06104	0.206851	0.1502	0.9998
ENSG00000225931	ENSG00000225931	RP3-395M20.7	1:2497848-2501327	OK	0.929329	0.518408	-0.842103	-0.899862	0.1502	0.9998
ENSG00000107745	ENSG00000107745	MICU1	10:74127097-74385899	OK	31.8447	24.2949	-0.390399	-0.832051	0.15025	0.9998
ENSG00000027001	ENSG00000027001	MIPEP	13:24304327-24476794	OK	16.3043	12.3472	-0.40107	-0.851205	0.1503	0.9998
ENSG00000079931	ENSG00000079931	MOXD1	6:132617193-132722684	OK	34.4686	44.152	0.357195	0.83339	0.1503	0.9998
ENSG00000196182	ENSG00000196182	STK40	1:36805224-36851497	OK	22.76	17.0026	-0.420751	-0.759909	0.1503	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000100410	ENSG00000100410	PHF5A	22:41855720-41864729	OK	49.3641	37.9248	-0.380319	-0.797766	0.1505	0.9998
ENSG00000070214	ENSG00000070214	SLC44A1	9:108006902-108201452	OK	34.9396	26.1138	-0.420047	-0.743083	0.15065	0.9998
ENSG00000135919	ENSG00000135919	SERPINE2	2:224839828-224904036	OK	313.848	402.809	0.360031	0.83561	0.1507	0.9998
ENSG00000158615	ENSG00000158615	PPP1R15B	1:204346977-204463852	OK	19.7859	14.5334	-0.445103	-0.863108	0.15095	0.9998
ENSG00000100207	ENSG00000100207	TCF20	22:42556018-42739622	OK	11.7692	15.1987	0.368929	0.681184	0.1511	0.9998
ENSG00000127337	ENSG00000127337	YEATS4	12:69753482-69784576	OK	24.1882	18.2058	-0.40991	-0.870418	0.1514	0.9998
ENSG00000168393	ENSG00000168393	DTYMK	2:242615156-242626406	OK	65.9779	50.9931	-0.371681	-0.86977	0.1517	0.9998
ENSG00000116539	ENSG00000116539	ASH1L	1:155305058-155533775	OK	13.68	10.6222	-0.364989	-0.571838	0.15185	0.9998
ENSG00000197070	ENSG00000197070	ARRDC1	9:140500105-140513358	OK	14.1297	20.5023	0.537055	0.779013	0.15195	0.9998
ENSG00000198015	ENSG00000198015	MRPL42	12:93861263-93897545	OK	61.3599	44.3895	-0.467078	-0.873221	0.15205	0.9998
ENSG00000250961	ENSG00000250961	CTD-2023N9.1	5:56690886-56829251	OK	1.19186	0.259642	-2.19862	-1.82421	0.1521	0.9998
ENSG00000079150	ENSG00000079150	FKBP7	2:179328390-179343327	OK	2.32269	1.29083	-0.847502	-0.771541	0.15215	0.9998
ENSG00000130741	ENSG00000130741	EIF2S3	X:24072832-24096088	OK	89.4878	113.417	0.34187	0.718507	0.15215	0.9998
ENSG00000134291	ENSG00000134291	TMEM106C	12:48357351-48362661	OK	271.363	210.535	-0.366166	-0.834507	0.15215	0.9998
ENSG00000227097	ENSG00000227097	RP11-742N3.1	11:81590892-82429124	OK	1087.38	1387.29	0.351408	0.866626	0.1522	0.9998
ENSG00000167196	ENSG00000167196	FBXO22	15:76196199-76227609	OK	61.4832	83.4146	0.440109	0.854823	0.1523	0.9998
ENSG00000168781	ENSG00000168781	PPIP5K1	15:43825659-43882430	OK	2.87875	1.95013	-0.561873	-0.474419	0.15235	0.9998
ENSG00000260808	ENSG00000260808	CTD-2007L18.5	11:68228185-68384179	OK	0.105869	0.694435	2.71356	0.152623	0.15245	0.9998
ENSG00000084073	ENSG00000084073	ZMPSTE24	1:40723778-40759856	OK	26.0419	33.2481	0.352439	0.774358	0.1525	0.9998
ENSG00000111653	ENSG00000111653	ING4	12:6759445-6772314	OK	15.1508	10.4767	-0.532208	-0.867694	0.1525	0.9998
ENSG00000225353	ENSG00000225353	RP11-292F9.1	9:46270840-46274928	OK	18.9301	13.2375	-0.51605	-0.886453	0.1525	0.9998
ENSG00000225485	ENSG00000225485	ARHGAP23	17:36584661-36668628	OK	0.404204	1.09232	1.43424	0.426233	0.15275	0.9998
ENSG00000106799	ENSG00000106799	TGFBR1	9:101866319-101916474	OK	26.3189	36.0822	0.455192	0.680052	0.1528	0.9998
ENSG00000256771	ENSG00000256771	ZNF253	19:19976694-20006656	OK	0.309099	0.723498	1.22692	0.691698	0.15295	0.9998
ENSG00000142684	ENSG00000142684	ZNF593	1:26496361-26498551	OK	14.8318	19.534	0.397294	0.864166	0.153	0.9998
ENSG00000157654	ENSG00000157654	PALM2-AKAP2	9:112403067-112934792	OK	0.353275	1.05913	1.58402	0.706439	0.153	0.9998
ENSG00000100065	ENSG00000100065	CARD10	22:37886399-37915549	OK	0.683613	1.18369	0.792041	0.651842	0.1534	0.9998
ENSG00000181026	ENSG00000181026	AEN	15:89164526-89175513	OK	27.3069	35.0629	0.36068	0.795848	0.15355	0.9998
ENSG00000108264	ENSG00000108264	TADA2A	17:35766964-35839835	OK	6.03483	4.10564	-0.555707	-0.738564	0.1536	0.9998
ENSG00000151729	ENSG00000151729	SLC25A4	4:186064394-186071536	OK	39.2942	51.468	0.389359	0.863401	0.15365	0.9998
ENSG00000152503	ENSG00000152503	TRIM36	5:114460458-114516243	OK	1.08626	0.685303	-0.664555	-0.574708	0.15395	0.9998
ENSG00000177125	ENSG00000177125	ZBTB34	9:129622943-129648157	OK	4.83329	6.322	0.387374	0.856562	0.15415	0.9998
ENSG00000254701	ENSG00000254701	RP11-1415C14.4	5:69435401-69503572	OK	1.0772	0.218305	-2.30288	-1.03213	0.15415	0.9998
ENSG00000273117	ENSG00000273117	AC144652.1	7:155087627-155089251	OK	1.63581	1.04108	-0.651919	-0.858519	0.15415	0.9998
ENSG00000089057	ENSG00000089057	SLC23A2	20:4833001-4990939	OK	14.1761	18.0883	0.351594	0.783988	0.1546	0.9998
ENSG00000196247	ENSG00000196247	ZNF107	7:64126510-64171404	OK	2.86631	1.63705	-0.808093	-0.838421	0.15465	0.9998
ENSG00000202198	ENSG00000202198	RN7SK	6:52860417-52860748	OK	4.64163	8.29457	0.837535	0.893007	0.1547	0.9998
ENSG00000111145	ENSG00000111145	ELK3	12:96588159-96663613	OK	10.6472	14.4985	0.445424	0.736835	0.1548	0.9998
ENSG00000169925	ENSG00000169925	BRD3	9:136890560-136933657	OK	7.8698	5.0105	-0.651371	-0.62854	0.15485	0.9998
ENSG00000139722	ENSG00000139722	VPS37B	12:123349881-123380991	OK	16.7352	21.4888	0.360701	0.827708	0.1549	0.9998
ENSG00000204775	ENSG00000204775	KM-PA-2	8:145317002-145331153	OK	2.15015	3.10876	0.531903	0.858811	0.15495	0.9998
ENSG00000224940	ENSG00000224940	PRRT4	7:127990378-128001739	OK	2.31693	3.36145	0.53687	0.865188	0.15495	0.9998
ENSG00000122203	ENSG00000122203	KIAA1191	5:175773063-175788971	OK	74.6416	58.3431	-0.355417	-0.71637	0.15515	0.9998
ENSG00000158234	ENSG00000158234	FAIM	3:138327447-138352218	OK	4.75672	7.03899	0.565402	0.83855	0.15515	0.9998
ENSG00000051382	ENSG00000051382	PIK3CB	3:138372859-138553780	OK	37.5569	27.6349	-0.442587	-0.731125	0.1552	0.9998
ENSG00000075218	ENSG00000075218	GTSE1	22:46692637-46726707	OK	25.5362	19.6975	-0.37453	-0.780209	0.15545	0.9998
ENSG00000196712	ENSG00000196712	NF1	17:29335514-29709134	OK	13.3808	17.1358	0.356846	0.471384	0.15565	0.9998
ENSG00000219102	ENSG00000219102	HNRNPA3P12	1:54440641-54441704	OK	6.58817	4.50377	-0.548744	-0.878107	0.15585	0.9998
ENSG00000121691	ENSG00000121691	CAT	11:34460471-34493609	OK	48.2528	61.1284	0.341228	0.749417	0.1561	0.9998
ENSG00000113790	ENSG00000113790	EHHADH	3:184880658-184999778	OK	5.27127	3.83067	-0.460555	-0.67921	0.1564	0.9998
ENSG00000184992	ENSG00000184992	BRI3BP	12:125478245-125515777	OK	7.76979	5.97823	-0.378156	-0.861297	0.1564	0.9998
ENSG00000173193	ENSG00000173193	PARP14	3:122399464-122449687	OK	3.99318	5.44944	0.448571	0.67645	0.15645	0.9998
ENSG00000261879	ENSG00000261879	RP11-333E1.1	17:5095378-5151364	OK	0.788888	0.400065	-0.979585	-0.676991	0.1565	0.9998
ENSG00000118257	ENSG00000118257	NRP2	2:206546713-206662857	OK	86.6707	114.666	0.403826	0.606427	0.1566	0.9998
ENSG00000182310	ENSG00000182310	SPACA6P	19:52188615-52215640	OK	1.74772	3.23933	0.890219	0.744249	0.15665	0.9998
ENSG00000188372	ENSG00000188372	ZP3	7:76018650-76071388	OK	12.1012	8.19569	-0.562212	-0.856056	0.15665	0.9998
ENSG00000226432	ENSG00000226432	CTD-2015B23.2	5:23951456-24178372	OK	1.24336	0.685323	-0.859383	-0.873419	0.1567	0.9998
ENSG00000186814	ENSG00000186814	ZSCAN30	18:32820993-32870196	OK	4.13953	2.46265	-0.749256	-0.580357	0.1568	0.9998
ENSG00000088899	ENSG00000088899	LZTS3	20:3143262-3154192	OK	1.4761	2.08081	0.495361	0.863272	0.15685	0.9998
ENSG00000148700	ENSG00000148700	ADD3	10:111756125-111895323	OK	53.3924	40.5298	-0.397653	-0.491562	0.1569	0.9998
ENSG00000066279	ENSG00000066279	ASPM	1:197053257-197115824	OK	9.13069	6.88109	-0.408086	-0.851686	0.15695	0.9998
ENSG00000090487	ENSG00000090487	SPG21	15:65255361-65282648	OK	75.9177	96.1524	0.340887	0.816651	0.15695	0.9998
ENSG00000181192	ENSG00000181192	DHTKD1	10:12110970-12165224	OK	6.56993	4.86804	-0.432536	-0.543914	0.15695	0.9998
ENSG00000068784	ENSG00000068784	SRBD1	2:45615818-45839304	OK	4.98927	3.6477	-0.451843	-0.784214	0.15705	0.9998
ENSG00000106804	ENSG00000106804	C5	9:123714615-123812554	OK	0.669566	0.385504	-0.796481	-0.461558	0.15705	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000174004	ENSG00000174004	NRROS	3:196366556-196462878	OK	8.75862	15.2464	0.800021	0.842647	0.15725	0.9998
ENSG00000269604	ENSG00000269604	AC005523.2	19:4791727-4795571	OK	0.846614	3.27846	1.95324	0.812514	0.15745	0.9998
ENSG00000165821	ENSG00000165821	SALL2	14:21989231-22005350	OK	0.376798	0.723757	0.941715	0.587121	0.1576	0.9998
ENSG00000070770	ENSG00000070770	CSNK2A2	16:58163432-58251709	OK	18.198	24.5256	0.430513	0.850274	0.1577	0.9998
ENSG00000022267	ENSG00000022267	FHL1	X:135229558-135293518	OK	0.628132	0.994599	0.663047	0.47833	0.15785	0.9998
ENSG00000101608	ENSG00000101608	MYL12A	18:3247478-3261848	OK	187.132	146.324	-0.354886	-0.859453	0.15805	0.9998
ENSG00000100324	ENSG00000100324	TAB1	22:39795745-39833065	OK	10.6814	8.03937	-0.409949	-0.572685	0.1581	0.9998
ENSG00000168785	ENSG00000168785	TSPAN5	4:99391517-99579780	OK	1.19285	1.8213	0.610557	0.595354	0.1582	0.9998
ENSG00000211459	ENSG00000211459	MT-RNR1	MT:647-1601	OK	695.137	932.185	0.423318	0.853046	0.1582	0.9998
ENSG00000105497	ENSG00000105497	ZNF175	19:52074550-52092991	OK	1.44318	2.25253	0.642294	0.740292	0.1583	0.9998
ENSG00000123219	ENSG00000123219	CENPK	5:64813592-64858998	OK	18.6793	13.6208	-0.455636	-0.754228	0.1583	0.9998
ENSG00000170759	ENSG00000170759	KIF5B	10:32297937-32345359	OK	34.2523	26.9265	-0.347173	-0.845918	0.1584	0.9998
ENSG00000130312	ENSG00000130312	MRPL34	19:17402939-17445638	OK	71.9388	109.231	0.602537	0.876991	0.15845	0.9998
ENSG00000131015	ENSG00000131015	ULBP2	6:150263135-150270371	OK	2.84182	1.87794	-0.597668	-0.861669	0.1585	0.9998
ENSG00000144674	ENSG00000144674	GOLGA4	3:37283279-37408242	OK	32.1764	24.3665	-0.401103	-0.704071	0.15855	0.9998
ENSG00000099219	ENSG00000099219	ERMP1	9:5629024-5833117	OK	28.7772	38.1263	0.40586	0.847833	0.15865	0.9998
ENSG00000198934	ENSG00000198934	MAGEE1	X:75648045-75651744	OK	0.789337	0.515446	-0.61482	-0.851604	0.1588	0.9998
ENSG00000171848	ENSG00000171848	RRM2	2:10262454-10271545	OK	110.744	74.3708	-0.574416	-0.840936	0.15885	0.9998
ENSG00000104442	ENSG00000104442	ARMC1	8:66514693-66546442	OK	21.2629	27.0686	0.348279	0.790401	0.1589	0.9998
ENSG00000165802	ENSG00000165802	NSMF	9:140342021-140353786	OK	33.1405	43.1876	0.382021	0.854421	0.15895	0.9998
ENSG00000218208	ENSG00000218208	RP11-367G18.2	6:113902702-113903149	OK	1.63433	2.95075	0.852383	0.833467	0.159	0.9998
ENSG00000198517	ENSG00000198517	MAFK	7:1570349-1600457	OK	11.0655	15.0235	0.441153	0.757157	0.1593	0.9998
ENSG00000273344	ENSG00000273344	PAXIP1-AS1	7:154795157-154797413	OK	2.16999	1.47595	-0.55605	-0.85137	0.15945	0.9998
ENSG00000153982	ENSG00000153982	GDPD1	17:57297827-57353328	OK	4.9243	3.25273	-0.598267	-0.836239	0.15955	0.9998
ENSG00000198054	ENSG00000198054	DSCR8	21:39493544-39679279	OK	0.758374	0.360327	-1.0736	-0.533297	0.15955	0.9998
ENSG00000158008	ENSG00000158008	EXTL1	1:26346374-26362955	OK	0.356969	0.645203	0.853956	0.635515	0.1601	0.9998
ENSG00000034053	ENSG00000034053	APBA2	15:29129628-29410518	OK	2.45228	3.41047	0.47585	0.765806	0.1602	0.9998
ENSG00000113391	ENSG00000113391	FAM172A	5:92953774-93447404	OK	29.2735	15.0107	-0.963601	-0.427603	0.16025	0.9998
ENSG00000137818	ENSG00000137818	RPLP1	15:69745122-69748255	OK	2018.4	2692.46	0.415713	0.837873	0.16035	0.9998
ENSG00000138162	ENSG00000138162	TACC2	10:123748688-124014060	OK	0.949886	1.73021	0.865118	0.535561	0.1604	0.9998
ENSG00000129810	ENSG00000129810	SGOL1	3:20202084-20227919	OK	11.5055	8.32777	-0.466321	-0.839928	0.16045	0.9998
ENSG00000125703	ENSG00000125703	ATG4C	1:63249805-63331184	OK	8.38667	5.28406	-0.666453	-0.819638	0.1605	0.9998
ENSG00000147676	ENSG00000147676	MAL2	8:120177272-120259088	OK	0.3619	0.801842	1.14773	0.598823	0.1605	0.9998
ENSG00000167964	ENSG00000167964	RAB26	16:2190803-2204166	OK	6.2346	9.03152	0.534671	0.804869	0.16055	0.9998
ENSG00000103260	ENSG00000103260	METRN	16:765114-769655	OK	61.2184	86.7746	0.503308	0.860191	0.1606	0.9998
ENSG00000149531	ENSG00000149531	FRG1B	20:29611856-29634010	OK	35.6264	25.9221	-0.458765	-0.859014	0.1606	0.9998
ENSG00000108813	ENSG00000108813	DLX4	17:48046333-48052321	OK	0.435033	0.793925	0.867878	0.734503	0.1607	0.9998
ENSG00000204628	ENSG00000204628	GNB2L1	5:180663908-180699308	OK	1712.45	2293.03	0.421192	0.847499	0.16075	0.9998
ENSG00000244733	ENSG00000244733	RP11-506M13.3	10:81420646-81526085	OK	1.18855	2.20757	0.893255	0.864137	0.1608	0.9998
ENSG00000174899	ENSG00000174899	C3orf55	3:157261034-157395538	OK	3.03538	4.60718	0.602006	0.85152	0.1609	0.9998
ENSG00000065000	ENSG00000065000	AP3D1	19:2100987-2248678	OK	81.0224	60.4312	-0.423026	-0.72093	0.16105	0.9998
ENSG00000104331	ENSG00000104331	IMPAD1	8:57870491-57906403	OK	16.3222	22.4787	0.461725	0.61092	0.1612	0.9998
ENSG00000235554	ENSG00000235554	AC005822.1	17:16520161-16521195	OK	1.92673	1.17955	-0.707915	-0.854873	0.16135	0.9998
ENSG00000124900	ENSG00000124900	TRIM51	11:55650772-55659286	OK	8.17534	11.2031	0.45455	0.853357	0.1614	0.9998
ENSG00000221968	ENSG00000221968	FADS3	11:61640990-61659523	OK	20.5246	27.2145	0.407022	0.778396	0.1615	0.9998
ENSG00000071205	ENSG00000071205	ARHGAP10	4:148653213-148993931	OK	1.99327	2.81996	0.500535	0.77751	0.16155	0.9998
ENSG00000204392	ENSG00000204392	LSM2	6:31765172-31774761	OK	71.6889	55.2622	-0.375457	-0.850572	0.1616	0.9998
ENSG00000258818	ENSG00000258818	RNASE4	14:21152258-21175279	OK	2.85076	1.42628	-0.99909	-0.767328	0.1616	0.9998
ENSG00000125733	ENSG00000125733	TRIP10	19:6737935-6751537	OK	9.22278	12.5589	0.445431	0.682476	0.16165	0.9998
ENSG00000169750	ENSG00000169750	RAC3	17:79989499-79992080	OK	18.8795	25.2707	0.420649	0.848995	0.16175	0.9998
ENSG00000164588	ENSG00000164588	HCN1	5:45259348-45696253	OK	1.47239	1.04206	-0.498728	-0.849976	0.1618	0.9998
ENSG00000227615	ENSG00000227615	RP11-864N7.2	11:74456760-74457159	OK	111.4	145.285	0.383144	0.838982	0.16195	0.9998
ENSG00000071242	ENSG00000071242	RPS6KA2	6:166822851-167370679	OK	5.64271	8.18413	0.536439	0.697047	0.16205	0.9998
ENSG00000124466	ENSG00000124466	LYPD3	19:43964938-43969812	OK	1.89602	2.81271	0.568986	0.810285	0.16205	0.9998
ENSG00000162777	ENSG00000162777	DENND2D	1:111729795-111786062	OK	1.35808	2.34379	0.78728	0.820842	0.1621	0.9998
ENSG00000197977	ENSG00000197977	ELOVL2	6:10980991-11078459	OK	5.89112	4.36691	-0.43193	-0.862252	0.1621	0.9998
ENSG00000185551	ENSG00000185551	NR2F2	15:96670597-96683492	OK	2.33036	3.67845	0.658544	0.690139	0.16215	0.9998
ENSG00000169919	ENSG00000169919	GUSB	7:65425670-65447301	OK	40.1913	31.4921	-0.351892	-0.777892	0.1622	0.9998
ENSG00000228649	ENSG00000228649	AC005682.5	7:22893796-22901021	OK	0.362964	0.794675	1.13054	0.897758	0.1623	0.9998
ENSG00000134574	ENSG00000134574	DDB2	11:47236492-47260767	OK	32.4515	41.5609	0.356942	0.854285	0.16235	0.9998
ENSG00000214973	ENSG00000214973	CHCHD3P3	1:27527324-27527964	OK	0.920642	1.72142	0.902886	0.858591	0.1624	0.9998
ENSG00000144228	ENSG00000144228	SPOPL	2:139259370-139332028	OK	2.41436	3.55836	0.559568	0.670809	0.16295	0.9998
ENSG00000213341	ENSG00000213341	CHUK	10:101909850-101989376	OK	17.5039	11.9067	-0.555907	-0.70439	0.16295	0.9998
ENSG00000268750	ENSG00000268750	CTD-2583A14.10	19:58281022-58427978	OK	0.722803	2.07741	1.52311	0.309627	0.16295	0.9998
ENSG00000164332	ENSG00000164332	UBLCP1	5:158690088-158713044	OK	18.6136	14.2664	-0.38373	-0.836861	0.163	0.9998
ENSG00000167524	ENSG00000167524	SGK494	17:26782769-26972472	OK	3.04019	1.45923	-1.05896	-0.100304	0.16305	0.9998
ENSG00000182287	ENSG00000182287	AP1S2	X:15843928-15873054	OK	133.729	177.26	0.406559	0.777597	0.16315	0.9998
ENSG00000167971	ENSG00000167971	CASKIN1	16:2205698-2246526	OK	0.589779	2.12655	1.85027	0.50184	0.16325	0.9998
ENSG00000172831	ENSG00000172831	CES2	16:66968346-67009051	OK	9.77066	7.35485	-0.40976	-0.663713	0.16325	0.9998
ENSG00000163162	ENSG00000163162	RNF149	2:101887680-101925163	OK	12.1981	16.2243	0.411498	0.742543	0.1633	0.9998
ENSG00000168274	ENSG00000168274	HIST1H2AE	6:26217164-26217711	OK	1.18483	0.539443	-1.13513	-0.90029	0.1634	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000138646	ENSG00000138646	HERC5	4:89378267-89427314	OK	3.84603	5.22017	0.440724	0.82459	0.16365	0.9998
ENSG00000171310	ENSG00000171310	CHST11	12:104849072-105155792	OK	4.54122	7.22463	0.669844	0.689392	0.16365	0.9998
ENSG00000020633	ENSG00000020633	RUNX3	1:25226001-25291612	OK	27.1634	35.2259	0.374973	0.731678	0.1637	0.9998
ENSG00000198908	ENSG00000198908	BHLHB9	X:101975615-102008468	OK	0.566722	0.925916	0.708242	0.581871	0.1637	0.9998
ENSG00000174939	ENSG00000174939	ASPHD1	16:29911695-29940254	OK	0.397226	1.37795	1.79449	0.635216	0.1639	0.9998
ENSG00000176222	ENSG00000176222	ZNF404	19:44376514-44405957	OK	0.330077	0.663595	1.0075	0.748932	0.1639	0.9998
ENSG00000112186	ENSG00000112186	CAP2	6:17393446-17558023	OK	53.3074	68.6389	0.364692	0.842884	0.16405	0.9998
ENSG00000166435	ENSG00000166435	XRRA1	11:74459912-74660245	OK	12.9724	8.17562	-0.66605	-0.53762	0.1641	0.9998
ENSG00000187773	ENSG00000187773	FAM69C	18:72102962-72125179	OK	14.6202	10.8093	-0.435686	-0.853842	0.1641	0.9998
ENSG00000162878	ENSG00000162878	PKDCC	2:42275159-42285668	OK	0.918091	1.66129	0.855594	0.813042	0.1644	0.9998
ENSG00000147588	ENSG00000147588	PMP2	8:82351670-82445510	OK	10.9734	7.95625	-0.463856	-0.831166	0.1646	0.9998
ENSG00000205765	ENSG00000205765	C5orf51	5:41904289-41921738	OK	29.445	23.4239	-0.330045	-0.698428	0.16495	0.9998
ENSG00000126458	ENSG00000126458	RRAS	19:50138548-50143458	OK	4.92971	7.12172	0.530725	0.832601	0.165	0.9998
ENSG00000186448	ENSG00000186448	ZNF197	3:44596684-44727145	OK	0.833964	1.32575	0.668749	0.734863	0.165	0.9998
ENSG00000189221	ENSG00000189221	MAOA	X:43515466-43606068	OK	2.86776	3.98426	0.474389	0.800339	0.165	0.9998
ENSG00000173320	ENSG00000173320	STOX2	4:184774583-184944679	OK	0.596368	1.1578	0.957107	0.607148	0.16505	0.9998
ENSG00000197265	ENSG00000197265	GTF2E2	8:30435834-30515768	OK	22.9057	29.5851	0.36916	0.820376	0.1651	0.9998
ENSG00000158555	ENSG00000158555	GDPD5	11:75145684-75236948	OK	30.7432	42.9632	0.482837	0.700642	0.1652	0.9998
ENSG00000164403	ENSG00000164403	SHROOM1	5:132157832-132166590	OK	1.18825	0.657066	-0.85473	-0.540364	0.1652	0.9998
ENSG00000182934	ENSG00000182934	SRPR	11:126071992-126148026	OK	39.308	51.9921	0.403471	0.796523	0.1656	0.9998
ENSG00000108771	ENSG00000108771	DHX58	17:40253421-40264751	OK	2.25696	1.37006	-0.720142	-0.764618	0.16565	0.9998
ENSG00000224155	ENSG00000224155	RP11-700P18.2	7:56372370-56373219	OK	0.40882	0.824793	1.01257	0.857361	0.1657	0.9998
ENSG00000075539	ENSG00000075539	FRYL	4:48499377-48782339	OK	6.91911	4.89098	-0.500463	-0.488361	0.16575	0.9998
ENSG00000166484	ENSG00000166484	MAPK7	17:19240866-19290553	OK	9.49438	6.41896	-0.564734	-0.689261	0.16575	0.9998
ENSG00000115355	ENSG00000115355	CCDC88A	2:55514977-55647057	OK	10.2553	7.76388	-0.401526	-0.699182	0.1658	0.9998
ENSG00000179859	ENSG00000179859	AC025335.1	17:7816641-7819271	OK	1.59933	1.07481	-0.573394	-0.851019	0.16595	0.9998
ENSG00000172869	ENSG00000172869	DMXL1	5:118342041-118584833	OK	7.16142	4.70382	-0.606411	-0.487995	0.1661	0.9998
ENSG00000182253	ENSG00000182253	SYNM	15:99192199-99675798	OK	45.6897	33.7204	-0.438248	-0.857863	0.1661	0.9998
ENSG00000260018	ENSG00000260018	RP11-505K9.1	16:84150655-84151176	OK	1.06184	0.442157	-1.26394	-0.953831	0.1661	0.9998
ENSG00000142733	ENSG00000142733	MAP3K6	1:27681674-27693383	OK	7.57936	5.39102	-0.491516	-0.610321	0.16625	0.9998
ENSG00000118482	ENSG00000118482	PHF3	6:64345724-66417118	OK	13.5939	10.4904	-0.373894	-0.781745	0.16645	0.9998
ENSG00000168453	ENSG00000168453	HR	8:21971927-21990897	OK	0.509225	0.978813	0.942728	0.59196	0.16655	0.9998
ENSG00000116221	ENSG00000116221	MRPL37	1:54598746-54879152	OK	96.249	72.5219	-0.408354	-0.83104	0.1666	0.9998
ENSG00000182504	ENSG00000182504	CEP97	3:101442768-101489406	OK	6.82873	4.9802	-0.455412	-0.726603	0.1666	0.9998
ENSG00000152042	ENSG00000152042	NBPF11	1:146032646-146253110	OK	2.33536	1.58948	-0.555089	-0.783832	0.16675	0.9998
ENSG00000236698	ENSG00000236698	EIF1AXP1	1:17012115-17012550	OK	34.0049	46.3797	0.447753	0.831866	0.16675	0.9998
ENSG00000151117	ENSG00000151117	TMEM86A	11:18714668-18814268	OK	3.02671	4.32454	0.514795	0.593516	0.16685	0.9998
ENSG00000110330	ENSG00000110330	BIRC2	11:102217941-102249401	OK	28.7132	22.2758	-0.366235	-0.750303	0.16695	0.9998
ENSG00000187792	ENSG00000187792	ZNF70	22:24083768-24093279	OK	1.84271	1.30749	-0.495032	-0.840106	0.1671	0.9998
ENSG00000182118	ENSG00000182118	FAM89A	1:231154703-231175992	OK	99.9081	125.971	0.334423	0.832873	0.16725	0.9998
ENSG00000198237	ENSG00000198237	RP11-98J23.2	5:69171097-69274436	OK	1.98851	1.07615	-0.885802	-0.847883	0.16725	0.9998
ENSG00000107669	ENSG00000107669	ATE1	10:123499938-123711480	OK	18.698	14.1674	-0.400309	-0.733023	0.1674	0.9998
ENSG00000127084	ENSG00000127084	FGD3	9:95709732-95798518	OK	0.363062	0.656611	0.854823	0.422964	0.1674	0.9998
ENSG00000135966	ENSG00000135966	TGFBRAP1	2:105880870-105946986	OK	17.8513	23.0483	0.368625	0.83615	0.16745	0.9998
ENSG00000135655	ENSG00000135655	USP15	12:62102039-62811211	OK	21.2212	14.7156	-0.528163	-0.741261	0.16755	0.9998
ENSG00000130005	ENSG00000130005	GAMT	19:1397090-1401569	OK	19.8368	26.2216	0.402578	0.831224	0.16765	0.9998
ENSG00000105429	ENSG00000105429	MEGF8	19:42829760-42882921	OK	10.8913	8.3767	-0.378717	-0.7676	0.16775	0.9998
ENSG00000171446	ENSG00000171446	KRT27	17:38933059-38938786	OK	2.54655	1.55401	-0.712546	-0.845303	0.1678	0.9998
ENSG00000112715	ENSG00000112715	VEGFA	6:43737920-43754224	OK	53.0721	73.8013	0.475691	0.663445	0.16795	0.9998
ENSG00000090905	ENSG00000090905	TNRC6A	16:24741015-24838953	OK	18.1222	23.4836	0.373895	0.369817	0.16805	0.9998
ENSG00000136932	ENSG00000136932	C9orf156	9:100666770-100684852	OK	5.72192	8.23356	0.525016	0.821115	0.1681	0.9998
ENSG00000126464	ENSG00000126464	PRR12	19:50094899-50129696	OK	3.83497	2.89317	-0.406564	-0.799099	0.16815	0.9998
ENSG00000100292	ENSG00000100292	HMOX1	22:35776353-35790207	OK	14.8867	19.325	0.376448	0.799427	0.16835	0.9998
ENSG00000143756	ENSG00000143756	FBXO28	1:224301788-224349749	OK	21.0645	15.5427	-0.438581	-0.769516	0.1684	0.9998
ENSG00000198597	ENSG00000198597	ZNF536	19:30710572-31204445	OK	3.99685	2.92345	-0.451191	-0.716795	0.1684	0.9998
ENSG00000128342	ENSG00000128342	LIF	22:30635182-30642987	OK	17.4209	12.8881	-0.434776	-0.700758	0.1685	0.9998
ENSG00000164687	ENSG00000164687	FABP5	8:82192105-82197012	OK	16.0656	21.9516	0.450354	0.856957	0.1685	0.9998
ENSG00000186298	ENSG00000186298	PPP1CC	12:111157484-111180744	OK	102.843	130.753	0.346411	0.830649	0.16865	0.9998
ENSG00000164176	ENSG00000164176	EDIL3	5:83236372-83786583	OK	0.417791	0.687056	0.717647	0.676784	0.16875	0.9998
ENSG00000141524	ENSG00000141524	TMC6	17:76000248-76139049	OK	79.8793	104.551	0.388308	0.639035	0.16895	0.9998
ENSG00000118507	ENSG00000118507	AKAP7	6:131456805-131604675	OK	3.0447	2.03727	-0.579667	-0.67197	0.16915	0.9998
ENSG00000146147	ENSG00000146147	MLIP	6:53794779-54131078	OK	6.82766	9.89765	0.535694	0.801351	0.16915	0.9998
ENSG00000233913	ENSG00000233913	CTC-575D19.1	5:168043316-168044059	OK	45.2489	59.1844	0.387333	0.843486	0.1692	0.9998
ENSG00000188517	ENSG00000188517	COL25A1	4:109731876-110223813	OK	2.49107	3.55677	0.513799	0.68588	0.1694	0.9998
ENSG00000160803	ENSG00000160803	UBQLN4	1:156005091-156023585	OK	71.7548	57.1489	-0.32835	-0.73723	0.16945	0.9998
ENSG00000106635	ENSG00000106635	BCL7B	7:72950685-72972332	OK	38.6964	29.4626	-0.393316	-0.818389	0.16955	0.9998
ENSG00000133739	ENSG00000133739	LRRCC1	8:86019381-86058311	OK	4.15134	2.92	-0.507607	-0.84113	0.1699	0.9998
ENSG00000234978	ENSG00000234978	RP11-423O2.5	1:142803223-142827235	OK	1.00995	0.584207	-0.789741	-0.846046	0.16995	0.9998
ENSG00000232838	ENSG00000232838	PET117	20:18118516-18169031	OK	12.7033	8.54805	-0.571531	-0.834491	0.17	0.9998
ENSG00000008311	ENSG00000008311	AASS	7:121715700-121784334	OK	9.53002	7.17193	-0.410117	-0.825854	0.1703	0.9998
ENSG00000117228	ENSG00000117228	GBP1	1:89518001-89531043	OK	0.238946	0.787193	1.72003	0.709911	0.1704	0.9998
ENSG00000125898	ENSG00000125898	FAM110A	20:814357-838106	OK	1.45726	0.938256	-0.635207	-0.802201	0.1704	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000137404	ENSG00000137404	NRM	6:30655823-30659197	OK	17.1739	12.7913	-0.425062	-0.845497	0.1704	0.9998
ENSG00000164651	ENSG00000164651	SP8	7:20823905-20826505	OK	0.693803	1.11906	0.689687	0.843319	0.1704	0.9998
ENSG00000230454	ENSG00000230454	U73166.2	3:50297734-50300790	OK	0.710552	0.0997703	-2.83226	-0.74456	0.1704	0.9998
ENSG00000234535	ENSG00000234535	RP11-37L2.1	13:33929342-34250905	OK	5.48953	2.59142	-1.08294	-0.839958	0.17045	0.9998
ENSG00000170776	ENSG00000170776	AKAP13	15:85923801-86293512	OK	6.1464	8.14668	0.406471	0.483178	0.1705	0.9998
ENSG00000090530	ENSG00000090530	LEPREL1	3:189674516-189862635	OK	20.4527	15.0016	-0.447176	-0.682839	0.17055	0.9998
ENSG00000198960	ENSG00000198960	ARMCX6	X:100870109-100872991	OK	27.7161	36.9786	0.41597	0.816973	0.17055	0.9998
ENSG00000105926	ENSG00000105926	MPP6	7:24612886-24733812	OK	5.57374	8.00999	0.523154	0.799441	0.17075	0.9998
ENSG00000116141	ENSG00000116141	MARK1	1:220701567-220837803	OK	6.7812	10.1651	0.584009	0.498181	0.17075	0.9998
ENSG00000157657	ENSG00000157657	ZNF618	9:116638561-116818871	OK	5.42978	7.35513	0.437858	0.703609	0.17085	0.9998
ENSG00000119630	ENSG00000119630	PGF	14:75408536-75422487	OK	4.3499	6.04194	0.474028	0.809867	0.1709	0.9998
ENSG00000254999	ENSG00000254999	BRK1	3:10157275-10168874	OK	167.626	132.102	-0.343596	-0.837202	0.17095	0.9998
ENSG00000148848	ENSG00000148848	ADAM12	10:127700949-128077024	OK	9.98107	14.9787	0.585645	0.735287	0.171	0.9998
ENSG00000171492	ENSG00000171492	LRRC8D	1:89990394-90402170	OK	16.2821	21.947	0.430739	0.697151	0.17105	0.9998
ENSG00000106714	ENSG00000106714	CNTNAP3	9:39072763-39288312	OK	4.60678	3.35512	-0.457396	-0.693804	0.1711	0.9998
ENSG00000161813	ENSG00000161813	LARP4	12:50720012-50873787	OK	28.2498	21.5896	-0.387902	-0.643899	0.1711	0.9998
ENSG00000196878	ENSG00000196878	LAMB3	1:209788214-209825811	OK	4.72463	7.02855	0.573024	0.844572	0.1712	0.9998
ENSG00000149657	ENSG00000149657	LSM14B	20:60697516-60710434	OK	55.1074	42.9254	-0.360415	-0.815948	0.1713	0.9998
ENSG00000106261	ENSG00000106261	ZKSCAN1	7:99613203-99639312	OK	18.4167	13.6952	-0.42735	-0.73118	0.1714	0.9998
ENSG00000164050	ENSG00000164050	PLXNB1	3:48445260-48471594	OK	18.7247	26.2672	0.488319	0.60562	0.1717	0.9998
ENSG00000059915	ENSG00000059915	PSD	10:104162375-104182893	OK	1.13095	2.47191	1.12809	0.700883	0.172	0.9998
ENSG00000164924	ENSG00000164924	YWHAZ	8:101928752-101965616	OK	469.708	606.55	0.368865	0.748531	0.1722	0.9998
ENSG00000087053	ENSG00000087053	MTMR2	11:95566045-95658479	OK	13.1638	16.7882	0.350869	0.702301	0.1723	0.9998
ENSG00000239264	ENSG00000239264	TXNDC5	6:7727029-8102811	OK	128.732	165.624	0.363546	0.822966	0.1723	0.9998
ENSG00000084764	ENSG00000084764	MAPRE3	2:27070614-27250064	OK	13.5127	17.8	0.397554	0.795039	0.17245	0.9998
ENSG00000204807	ENSG00000204807	FAM27E2	9:45733440-45734896	OK	1.38355	0.845879	-0.709851	-0.851834	0.17245	0.9998
ENSG00000213626	ENSG00000213626	LBH	2:30454396-30546596	OK	9.74282	7.28271	-0.419863	-0.658789	0.17245	0.9998
ENSG00000183960	ENSG00000183960	KCNH8	3:19189945-19577138	OK	0.701827	0.464258	-0.59619	-0.668187	0.1725	0.9998
ENSG00000260644	ENSG00000260644	HERC2P5	16:32752634-32787517	OK	1.02533	0.692765	-0.565651	-0.741675	0.1725	0.9998
ENSG00000104529	ENSG00000104529	EEF1D	8:144661805-144682485	OK	409.23	534.678	0.385759	0.835674	0.17285	0.9998
ENSG00000175115	ENSG00000175115	PACS1	11:65837833-66012218	OK	22.267	17.4394	-0.352561	-0.580377	0.17285	0.9998
ENSG00000162522	ENSG00000162522	KIAA1522	1:33207485-33240571	OK	3.63273	5.05858	0.477679	0.706314	0.1729	0.9998
ENSG00000123552	ENSG00000123552	USP45	6:99880189-99979794	OK	3.005	4.75913	0.663335	0.743401	0.17295	0.9998
ENSG00000186470	ENSG00000186470	BTN3A2	6:26365386-26378546	OK	21.3814	16.403	-0.382399	-0.697052	0.17295	0.9998
ENSG00000101109	ENSG00000101109	STK4	20:43595114-43708600	OK	15.6742	12.1938	-0.362245	-0.696495	0.1731	0.9998
ENSG00000204520	ENSG00000204520	MICA	6:31368478-31445283	OK	47.272	36.7618	-0.362779	-0.83696	0.1734	0.9998
ENSG00000163435	ENSG00000163435	ELF3	1:201951499-201986316	OK	1.78276	0.587358	-1.6018	-0.365413	0.17355	0.9998
ENSG00000141582	ENSG00000141582	CBX4	17:77806954-77813228	OK	29.8759	38.668	0.372159	0.69591	0.1736	0.9998
ENSG00000164603	ENSG00000164603	C7orf60	7:112459201-112579971	OK	8.37032	5.93644	-0.495685	-0.704182	0.17365	0.9998
ENSG00000061656	ENSG00000061656	SPAG4	20:34203813-34208971	OK	2.84039	1.65728	-0.777274	-0.746681	0.17375	0.9998
ENSG00000260619	ENSG00000260619	RP11-775C24.3	15:81283144-81285599	OK	0.438363	0.733568	0.742806	0.864108	0.17375	0.9998
ENSG00000183298	ENSG00000183298	RP11-556K13.1	1:102251891-102254059	OK	0.439737	0.85201	0.95423	0.863321	0.1739	0.9998
ENSG00000120729	ENSG00000120729	MYOT	5:137150021-137387650	OK	0.943649	0.374929	-1.33163	-0.26157	0.17405	0.9998
ENSG00000236943	ENSG00000236943	RP11-640M9.1	1:144275917-144521970	OK	1.12207	0.68038	-0.721747	-0.360335	0.17405	0.9998
ENSG00000113456	ENSG00000113456	RAD1	5:34905368-34926101	OK	57.0243	38.6465	-0.561239	-0.724492	0.1741	0.9998
ENSG00000136159	ENSG00000136159	NUDT15	13:48510621-48621358	OK	18.7051	12.2143	-0.614858	-0.822885	0.1742	0.9998
ENSG00000161671	ENSG00000161671	EMC10	19:50970041-50986608	OK	92.8337	117.134	0.335442	0.829711	0.1743	0.9998
ENSG00000130939	ENSG00000130939	UBE4B	1:10092889-10241297	OK	20.0937	15.3155	-0.391753	-0.67602	0.17435	0.9998
ENSG00000129003	ENSG00000129003	VPS13C	15:62144587-62352672	OK	8.05686	5.96743	-0.433108	-0.584862	0.17455	0.9998
ENSG00000105223	ENSG00000105223	PLD3	19:40825442-40896094	OK	65.2168	46.094	-0.500667	-0.799825	0.17475	0.9998
ENSG00000146409	ENSG00000146409	SLC18B1	6:133090508-133119701	OK	36.3021	28.6096	-0.343555	-0.835577	0.17485	0.9998
ENSG00000108960	ENSG00000108960	MMD	17:53469973-53499353	OK	6.70677	5.04013	-0.412159	-0.759516	0.1749	0.9998
ENSG00000179542	ENSG00000179542	SLITRK4	X:142710595-142723596	OK	0.515528	0.818818	0.667493	0.825321	0.17505	0.9998
ENSG00000215835	ENSG00000215835	RP11-9L18.2	1:166244865-166246834	OK	0.365941	0.629042	0.781544	0.859548	0.17515	0.9998
ENSG00000131584	ENSG00000131584	ACAP3	1:1227755-1260071	OK	15.741	23.4341	0.574081	0.518712	0.1753	0.9998
ENSG00000139168	ENSG00000139168	ZCRB1	12:42632248-42984157	OK	43.918	27.9395	-0.652505	-0.788283	0.1753	0.9998
ENSG00000085760	ENSG00000085760	MTIF2	2:55463730-55496483	OK	28.3835	22.3945	-0.34191	-0.723647	0.17535	0.9998
ENSG00000108510	ENSG00000108510	MED13	17:60019965-60142643	OK	9.97209	12.8998	0.371376	0.573761	0.17535	0.9998
ENSG00000212719	ENSG00000212719	C17orf51	17:21428050-21477781	OK	1.77774	2.6582	0.580405	0.642643	0.17545	0.9998
ENSG00000032742	ENSG00000032742	IFT88	13:21140584-21265503	OK	6.37695	4.34562	-0.553305	-0.73946	0.1755	0.9998
ENSG00000130558	ENSG00000130558	OLFM1	9:137967267-138013025	OK	39.1492	29.3514	-0.415555	-0.775486	0.17565	0.9998
ENSG00000176274	ENSG00000176274	SLC25A53	X:103343897-103401708	OK	2.79501	1.68964	-0.726139	-0.831226	0.17565	0.9998
ENSG00000179476	ENSG00000179476	C14orf28	14:45366497-45381066	OK	1.70905	1.02275	-0.740747	-0.732662	0.1757	0.9998
ENSG00000174233	ENSG00000174233	ADCY6	12:49159974-49182820	OK	15.6305	19.9936	0.355175	0.533502	0.17575	0.9998
ENSG00000233901	ENSG00000233901	RP11-65J3.1	9:132094578-132121817	OK	0.687519	1.19278	0.794855	0.709711	0.1758	0.9998
ENSG00000262194	ENSG00000262194	CTD-3195I5.5	17:3705458-3706676	OK	1.07118	0.441643	-1.27824	-0.959276	0.17595	0.9998
ENSG00000174791	ENSG00000174791	RIN1	11:66097712-66112596	OK	4.12963	7.57919	0.876033	0.66701	0.1761	0.9998
ENSG00000172572	ENSG00000172572	PDE3A	12:20514665-20837315	OK	1.30764	0.682158	-0.938791	-0.744814	0.17625	0.9998
ENSG00000140688	ENSG00000140688	C16orf58	16:31494322-31520630	OK	29.0875	22.9927	-0.339221	-0.742213	0.17635	0.9998
ENSG00000100387	ENSG00000100387	RBX1	22:41253080-41369313	OK	29.9472	41.2489	0.461936	0.818331	0.1764	0.9998
ENSG00000166025	ENSG00000166025	AMOTL1	11:94277005-94658686	OK	4.85309	6.26431	0.368251	0.735227	0.17645	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000189337	ENSG00000189337	KAZN	1:14925199-15478960	OK	7.3797	9.73779	0.400033	0.786747	0.17645	0.9998
ENSG00000149503	ENSG00000149503	INCENP	11:61891444-61920635	OK	51.8941	36.0734	-0.524634	-0.793814	0.1765	0.9998
ENSG00000173846	ENSG00000173846	PLK3	1:45265896-45272957	OK	7.83859	10.7241	0.452185	0.76623	0.17665	0.9998
ENSG00000078043	ENSG00000078043	PIAS2	18:44388352-44627658	OK	12.3638	9.10137	-0.441967	-0.784627	0.1768	0.9998
ENSG00000172301	ENSG00000172301	COPRS	17:30178882-30186356	OK	58.0307	45.2467	-0.359003	-0.819941	0.17685	0.9998
ENSG00000161558	ENSG00000161558	TMEM143	19:48835612-48867494	OK	3.7195	2.53112	-0.555333	-0.635849	0.17705	0.9998
ENSG00000213654	ENSG00000213654	GPSM3	6:32158542-32191844	OK	8.44034	11.4421	0.438982	0.824826	0.17705	0.9998
ENSG00000118298	ENSG00000118298	CA14	1:150227488-150237478	OK	58.5761	41.7636	-0.488067	-0.841785	0.1773	0.9998
ENSG00000213244	ENSG00000213244	HIST2H3DP1	1:120876494-120905159	OK	0.121134	0.82717	2.77157	1.12586	0.1774	0.9998
ENSG00000185442	ENSG00000185442	FAM174B	15:93146139-93353114	OK	1.04422	2.0565	0.97777	0.533403	0.17745	0.9998
ENSG00000063660	ENSG00000063660	GPC1	2:241375087-241407493	OK	5.30016	7.35113	0.471928	0.713448	0.17765	0.9998
ENSG00000068489	ENSG00000068489	PRR11	17:57232859-57292608	OK	46.5886	32.6909	-0.511088	-0.605941	0.1777	0.9998
ENSG00000159228	ENSG00000159228	CBR1	21:37402367-37498938	OK	59.8977	76.5728	0.354332	0.813326	0.1777	0.9998
ENSG00000159208	ENSG00000159208	C1orf51	1:150254952-150259505	OK	13.5882	18.4087	0.438036	0.818441	0.1778	0.9998
ENSG00000067606	ENSG00000067606	PRKCZ	1:1981908-2152177	OK	6.34268	10.5005	0.727291	0.619785	0.17785	0.9998
ENSG00000136942	ENSG00000136942	RPL35	9:127615754-127624260	OK	1743.05	2210.97	0.343067	0.813773	0.17785	0.9998
ENSG00000141639	ENSG00000141639	MAPK4	18:48086447-48258194	OK	14.3084	11.2281	-0.349755	-0.803389	0.1779	0.9998
ENSG00000163840	ENSG00000163840	DTX3L	3:122246770-122294050	OK	3.34918	4.6711	0.479955	0.812058	0.1782	0.9998
ENSG00000118200	ENSG00000118200	CAMSAP2	1:200708685-200829832	OK	10.7644	14.0504	0.384346	0.590196	0.17825	0.9998
ENSG00000214575	ENSG00000214575	CPEB1	15:83205503-83378666	OK	20.1339	25.7624	0.355642	0.667257	0.17825	0.9998
ENSG00000111799	ENSG00000111799	COL12A1	6:75794041-75915767	OK	0.53105	0.897299	0.756742	0.563753	0.1783	0.9998
ENSG00000101230	ENSG00000101230	ISM1	20:13202417-13619587	OK	2.47868	1.42131	-0.802356	-0.857715	0.17845	0.9998
ENSG00000226711	ENSG00000226711	FAM66C	12:8276227-8371507	OK	0.674033	0.367785	-0.873957	-0.513156	0.1786	0.9998
ENSG00000181035	ENSG00000181035	SLC25A42	19:19174807-19223697	OK	1.71336	1.16501	-0.556484	-0.569618	0.17865	0.9998
ENSG00000235821	ENSG00000235821	IFITM4P	6:29718505-29718925	OK	0.231504	0.817039	1.81937	0.965925	0.1787	0.9998
ENSG00000173207	ENSG00000173207	CKS1B	1:154947128-154951725	OK	92.9632	73.1967	-0.344882	-0.809831	0.17875	0.9998
ENSG00000240137	ENSG00000240137	RP11-103G8.2	3:150377671-150438623	OK	0.888878	1.72057	0.952827	0.719727	0.17875	0.9998
ENSG00000197077	ENSG00000197077	KIAA1671	22:25348696-25593415	OK	1.16648	1.59776	0.453888	0.773979	0.1788	0.9998
ENSG00000107104	ENSG00000107104	KANK1	9:213107-746105	OK	34.7693	44.0906	0.34266	0.808206	0.17895	0.9998
ENSG00000102974	ENSG00000102974	CTCF	16:67583116-67673086	OK	12.3367	9.63936	-0.355945	-0.808177	0.1798	0.9998
ENSG00000104738	ENSG00000104738	MCM4	8:48872744-48890720	OK	93.1904	64.4775	-0.531385	-0.645417	0.1798	0.9998
ENSG00000118515	ENSG00000118515	SGK1	6:134490383-134639250	OK	183.948	231.848	0.333882	0.722993	0.1798	0.9998
ENSG00000162402	ENSG00000162402	USP24	1:55532031-55680786	OK	8.13176	10.3459	0.347414	0.485792	0.1798	0.9998
ENSG00000188211	ENSG00000188211	NCR3LG1	11:17373272-17398888	OK	1.20246	1.67766	0.480457	0.805317	0.17985	0.9998
ENSG00000140511	ENSG00000140511	HAPLN3	15:89420518-89438857	OK	0.390254	0.747303	0.937281	0.65907	0.1799	0.9998
ENSG00000122008	ENSG00000122008	POLK	5:74664310-74896969	OK	13.2574	7.00266	-0.920819	-0.895012	0.18015	0.9998
ENSG00000170703	ENSG00000170703	TTLL6	17:46839596-46894576	OK	0.799861	1.33661	0.740751	0.596335	0.18025	0.9998
ENSG00000183765	ENSG00000183765	CHEK2	22:29083730-29153503	OK	11.5036	8.32156	-0.467163	-0.704246	0.1804	0.9998
ENSG00000084444	ENSG00000084444	KIAA1467	12:13197217-13295455	OK	9.45506	7.2538	-0.382349	-0.781724	0.1805	0.9998
ENSG00000109079	ENSG00000109079	TNFAIP1	17:26662627-26684545	OK	20.6851	13.4128	-0.624984	-0.662729	0.1805	0.9998
ENSG00000162290	ENSG00000162290	DCP1A	3:53317446-53381654	OK	8.75234	6.73838	-0.377268	-0.693041	0.1806	0.9998
ENSG00000232833	ENSG00000232833	FAM27E3	9:67784943-67786684	OK	1.03309	0.638984	-0.693111	-0.803222	0.1806	0.9998
ENSG00000143416	ENSG00000143416	SELENBP1	1:151336777-151345209	OK	0.855535	1.32092	0.626648	0.440819	0.18075	0.9998
ENSG00000243449	ENSG00000243449	C4orf48	4:2043688-2045697	OK	51.2481	68.7687	0.424255	0.837268	0.18075	0.9998
ENSG00000092068	ENSG00000092068	SLC7A8	14:23594503-23652883	OK	119.498	93.2608	-0.357648	-0.81767	0.1808	0.9998
ENSG00000197019	ENSG00000197019	SERTAD1	19:40927498-40931932	OK	3.47617	4.77278	0.457333	0.816847	0.1808	0.9998
ENSG00000253552	ENSG00000253552	HOXA-AS2	7:27145802-27197555	OK	0.303636	0.676636	1.15604	0.260214	0.1809	0.9998
ENSG00000258734	ENSG00000258734	RP11-112J1.3	14:59294396-59294894	OK	0.481146	1.08263	1.16999	0.811267	0.181	0.9998
ENSG00000078295	ENSG00000078295	ADCY2	5:7396320-7830194	OK	68.9341	42.0754	-0.71224	-0.852524	0.1812	0.9998
ENSG00000164932	ENSG00000164932	CTHRC1	8:104383742-104395225	OK	142.215	113.229	-0.328833	-0.793096	0.1813	0.9998
ENSG00000212864	ENSG00000212864	RNF208	9:140114706-140116033	OK	0.463979	0.824375	0.829241	0.778671	0.1814	0.9998
ENSG00000100221	ENSG00000100221	JOSD1	22:39081547-39097561	OK	15.1828	11.8734	-0.354698	-0.639169	0.18155	0.9998
ENSG00000172059	ENSG00000172059	KLF11	2:10182975-10194993	OK	6.95158	8.97218	0.368117	0.756273	0.1816	0.9998
ENSG00000224897	ENSG00000224897	POT1-AS1	7:124462439-125019375	OK	0.830525	0.26083	-1.67091	-0.288672	0.1816	0.9998
ENSG00000184007	ENSG00000184007	PTP4A2	1:32307619-32410457	OK	175.871	127.731	-0.461408	-0.768294	0.18165	0.9998
ENSG00000162222	ENSG00000162222	TTC9C	11:62495540-62507765	OK	26.1322	19.4401	-0.426796	-0.734868	0.18175	0.9998
ENSG00000170955	ENSG00000170955	PRKCDBP	11:6340175-6341877	OK	17.5324	23.7413	0.437378	0.821494	0.18175	0.9998
ENSG00000235172	ENSG00000235172	CTB-114C7.3	5:169758432-169760883	OK	1.3399	0.781292	-0.77819	-0.783838	0.18175	0.9998
ENSG00000144868	ENSG00000144868	TMEM108	3:132757234-133116636	OK	5.0633	3.3011	-0.617131	-0.729646	0.18195	0.9998
ENSG00000197594	ENSG00000197594	ENPP1	6:132129155-132216295	OK	3.16036	4.25381	0.428665	0.775107	0.182	0.9998
ENSG00000271976	ENSG00000271976	RP11-884K10.7	3:53880606-53899827	OK	0.846024	1.326	0.648313	0.781444	0.182	0.9998
ENSG00000086205	ENSG00000086205	FOLH1	11:49168186-49230222	OK	0.450586	0.785781	0.802326	0.450531	0.1821	0.9998
ENSG00000186635	ENSG00000186635	ARAP1	11:72396113-72504726	OK	20.3116	27.6187	0.443346	0.533082	0.18215	0.9998
ENSG00000198642	ENSG00000198642	KLHL9	9:21329669-21335379	OK	9.6371	7.42824	-0.375578	-0.811871	0.1822	0.9998
ENSG00000198870	ENSG00000198870	C9orf96	9:136243116-136324508	OK	0.805119	1.98145	1.29928	0.400147	0.18225	0.9998
ENSG00000100097	ENSG00000100097	LGALS1	22:38071614-38075813	OK	730.092	917.321	0.329348	0.807649	0.1823	0.9998
ENSG00000245910	ENSG00000245910	SNHG6	8:67782983-67838633	OK	447.921	596.603	0.413528	0.814077	0.1825	0.9998
ENSG00000196659	ENSG00000196659	TTC30B	2:178413725-178417742	OK	1.39839	1.94469	0.475776	0.818063	0.18255	0.9998
ENSG00000080819	ENSG00000080819	CPOX	3:98216447-98312567	OK	58.4594	79.0389	0.435127	0.737621	0.1828	0.9998
ENSG00000167925	ENSG00000167925	GHDC	17:40340816-40346531	OK	6.46873	8.82922	0.448805	0.712198	0.18285	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000130958	ENSG00000130958	SLC35D2	9:99082987-99145992	OK	41.0874	52.3287	0.348907	0.801433	0.1829	0.9998
ENSG00000240674	ENSG00000240674	RP11-366M4.1	4:165933517-165933997	OK	1.20526	2.24627	0.898185	0.814838	0.183	0.9998
ENSG00000184661	ENSG00000184661	CDCA2	8:25316512-25365436	OK	10.2848	7.8774	-0.384724	-0.750928	0.1831	0.9998
ENSG00000236552	ENSG00000236552	RPL13AP5	10:98510044-98510675	OK	691.319	867.79	0.327995	0.806045	0.18365	0.9998
ENSG00000196867	ENSG00000196867	ZFP28	19:57050316-57078780	OK	1.58215	2.42246	0.614582	0.592678	0.18375	0.9998
ENSG00000159200	ENSG00000159200	RCAN1	21:35885439-35987441	OK	20.0357	15.495	-0.370772	-0.785522	0.1839	0.9998
ENSG00000166508	ENSG00000166508	MCM7	7:99690350-99726118	OK	107.497	80.5857	-0.415702	-0.746701	0.1839	0.9998
ENSG00000136026	ENSG00000136026	CKAP4	12:106631654-106740793	OK	33.814	26.7487	-0.338149	-0.804535	0.18395	0.9998
ENSG00000186468	ENSG00000186468	RPS23	5:81267843-81574396	OK	2510.67	3250.59	0.372628	0.811619	0.184	0.9998
ENSG00000115392	ENSG00000115392	FANCL	2:58134785-58468821	OK	28.6571	20.3106	-0.496659	-0.729277	0.18405	0.9998
ENSG00000151445	ENSG00000151445	VIPAS39	14:77893017-77935817	OK	10.9287	5.09259	-1.10165	-0.670857	0.18405	0.9998
ENSG00000162542	ENSG00000162542	TMCO4	1:20008705-20126438	OK	6.37094	9.12498	0.518316	0.756819	0.1841	0.9998
ENSG00000006042	ENSG00000006042	TMEM98	17:31254927-31272124	OK	71.8856	92.8265	0.368835	0.802267	0.1842	0.9998
ENSG00000135723	ENSG00000135723	FHOD1	16:67263289-67306093	OK	7.42421	10.0161	0.432007	0.638616	0.1843	0.9998
ENSG00000090238	ENSG00000090238	YPEL3	16:30103634-30115437	OK	3.33658	4.89755	0.553691	0.699181	0.18445	0.9998
ENSG00000173638	ENSG00000173638	SLC19A1	21:46825051-46964325	OK	2.66938	4.42025	0.727625	0.595249	0.18445	0.9998
ENSG00000158122	ENSG00000158122	AAED1	9:99401858-99417585	OK	6.12993	8.32117	0.440915	0.658834	0.18455	0.9998
ENSG00000204580	ENSG00000204580	DDR1	6:30844197-30867933	OK	45.3129	56.2718	0.31249	0.544406	0.1846	0.9998
ENSG00000167680	ENSG00000167680	SEMA6B	19:4542599-4559820	OK	2.60196	3.6381	0.483584	0.787512	0.18465	0.9998
ENSG00000228701	ENSG00000228701	TNKS2-AS1	10:93542595-93558048	OK	0.417339	1.0468	1.3267	0.864138	0.1847	0.9998
ENSG00000054983	ENSG00000054983	GALC	14:88176762-88460009	OK	8.02813	10.4089	0.374686	0.659581	0.18475	0.9998
ENSG00000169418	ENSG00000169418	NPR1	1:153651112-153666468	OK	0.577966	0.883641	0.612475	0.740098	0.18505	0.9998
ENSG00000012232	ENSG00000012232	EXTL3	8:28457985-28613116	OK	26.7947	21.4128	-0.323474	-0.683181	0.18515	0.9998
ENSG00000161011	ENSG00000161011	SQSTM1	5:179224596-179334859	OK	379.442	525.494	0.469793	0.781034	0.1853	0.9998
ENSG00000002834	ENSG00000002834	LASP1	17:37026111-37078023	OK	27.2121	34.005	0.321498	0.793958	0.18535	0.9998
ENSG00000180304	ENSG00000180304	OAZ2	15:64979771-65011801	OK	89.103	69.9532	-0.349084	-0.769088	0.1855	0.9998
ENSG00000115808	ENSG00000115808	STRN	2:37070782-37193615	OK	9.51265	7.28877	-0.384172	-0.796997	0.1857	0.9998
ENSG00000176406	ENSG00000176406	RIMS2	8:104495625-105268322	OK	0.525511	1.02556	0.964622	0.563825	0.18575	0.9998
ENSG00000197172	ENSG00000197172	MAGEA6	X:151867213-151870825	OK	62.7869	78.2568	0.317753	0.785257	0.1858	0.9998
ENSG00000177359	ENSG00000177359	RP11-551L14.1	12:31264585-31359088	OK	1.27331	1.84087	0.531796	0.714782	0.1859	0.9998
ENSG00000100614	ENSG00000100614	PPM1A	14:60706838-60765805	OK	25.4104	34.7854	0.453065	0.772049	0.186	0.9998
ENSG00000100307	ENSG00000100307	CBX7	22:39516171-39548679	OK	6.91978	5.22937	-0.404088	-0.595122	0.18615	0.9998
ENSG00000137267	ENSG00000137267	TUBB2A	6:3153902-3157760	OK	64.1051	80.1976	0.32312	0.794249	0.1863	0.9998
ENSG00000235231	ENSG00000235231	AP000351.10	22:24373116-24374043	OK	1.66541	0.859328	-0.954593	-0.73139	0.18635	0.9998
ENSG00000184216	ENSG00000184216	IRAK1	X:153275950-153285440	OK	60.4524	76.9299	0.347744	0.639448	0.1864	0.9998
ENSG00000142731	ENSG00000142731	PLK4	4:128802015-128820350	OK	8.27766	5.73586	-0.529215	-0.698022	0.18645	0.9998
ENSG00000198814	ENSG00000198814	GK	X:30671475-30748725	OK	8.01478	5.88408	-0.445846	-0.563588	0.18655	0.9998
ENSG00000140006	ENSG00000140006	WDR89	14:64063756-64108579	OK	5.33638	3.84687	-0.472174	-0.78691	0.1866	0.9998
ENSG00000116171	ENSG00000116171	SCP2	1:53392900-53517375	OK	49.7909	65.5699	0.397152	0.812428	0.1867	0.9998
ENSG00000146414	ENSG00000146414	SHPRH	6:146136047-146285559	OK	1.98746	1.46658	-0.438474	-0.665768	0.1867	0.9998
ENSG00000131876	ENSG00000131876	SNRPA1	15:101821714-101835487	OK	45.5848	35.2331	-0.371625	-0.778027	0.18685	0.9998
ENSG00000108439	ENSG00000108439	PNPO	17:46018871-46073562	OK	11.7072	19.0194	0.700067	0.688573	0.18715	0.9998
ENSG00000138386	ENSG00000138386	NAB1	2:191511471-191573442	OK	19.4364	14.9902	-0.374743	-0.64848	0.18715	0.9998
ENSG00000197958	ENSG00000197958	RPL12	9:130209952-130213684	OK	1640.19	2093.73	0.352211	0.806645	0.18725	0.9998
ENSG00000243964	ENSG00000243964	RP11-16F15.1	11:9627688-9628156	OK	0.237087	0.747604	1.65685	0.775206	0.1873	0.9998
ENSG00000047056	ENSG00000047056	WDR37	10:1095477-1178237	OK	4.28907	5.67817	0.404763	0.723647	0.18735	0.9998
ENSG00000068001	ENSG00000068001	HYAL2	3:50355220-50365682	OK	25.0551	33.7658	0.430458	0.745297	0.18735	0.9998
ENSG00000141665	ENSG00000141665	FBXO15	18:71740587-71815100	OK	0.711262	0.416574	-0.77181	-0.364205	0.18745	0.9998
ENSG00000225648	ENSG00000225648	SBDSP1	7:72300003-72307909	OK	45.3789	32.8521	-0.466035	-0.821669	0.1875	0.9998
ENSG00000083457	ENSG00000083457	ITGAE	17:3617921-3704537	OK	63.0162	46.9733	-0.423883	-0.816686	0.1878	0.9998
ENSG00000006576	ENSG00000006576	PHTF2	7:77428121-77586818	OK	37.9644	28.5753	-0.409878	-0.69292	0.18785	0.9998
ENSG00000206567	ENSG00000206567	AC022007.5	3:10000400-10052893	OK	1.57403	0.646608	-1.2835	-0.325061	0.18785	0.9998
ENSG00000198221	ENSG00000198221	MLLT4-AS1	6:168224555-168227389	OK	0.667493	0.295154	-1.17729	-0.438283	0.18795	0.9998
ENSG00000167522	ENSG00000167522	ANKRD11	16:89334037-89556969	OK	18.5433	25.9721	0.486064	0.558533	0.18815	0.9998
ENSG00000262758	ENSG00000262758	CTD-3195I5.1	17:3710041-3712148	OK	4.59977	3.36552	-0.450732	-0.802291	0.18825	0.9998
ENSG00000140263	ENSG00000140263	SORD	15:45315301-45369383	OK	14.5436	19.5938	0.430009	0.786814	0.1884	0.9998
ENSG00000241170	ENSG00000241170	RP11-147I3.1	11:74459912-74660245	OK	0.349132	1.09451	1.64844	0.224359	0.18855	0.9998
ENSG00000171084	ENSG00000171084	FAM86JP	3:125635462-125655882	OK	1.53507	0.973579	-0.656931	-0.821794	0.1886	0.9998
ENSG00000134463	ENSG00000134463	ECHDC3	10:11784364-11806069	OK	2.66863	4.15604	0.639108	0.784259	0.18865	0.9998
ENSG00000226221	ENSG00000226221	AC022431.1	5:55800461-55800899	OK	208.938	265.979	0.348236	0.810513	0.1888	0.9998
ENSG00000085999	ENSG00000085999	RAD54L	1:46713359-46769280	OK	7.48669	4.5774	-0.709798	-0.603269	0.1889	0.9998
ENSG00000156869	ENSG00000156869	FRRS1	1:100174258-100232187	OK	0.837923	1.28261	0.614191	0.577032	0.189	0.9998
ENSG00000125676	ENSG00000125676	THOC2	X:122734411-122866906	OK	26.9004	20.3969	-0.399275	-0.585103	0.18905	0.9998
ENSG00000124486	ENSG00000124486	USP9X	X:40944887-41095832	OK	21.4988	26.7947	0.317691	0.582851	0.18915	0.9998
ENSG00000091428	ENSG00000091428	RAPGEF4	2:173541868-173917621	OK	3.59102	2.14918	-0.740604	-0.725334	0.18925	0.9998
ENSG00000141446	ENSG00000141446	ESCO1	18:19109241-19180845	OK	25.0366	19.8006	-0.338495	-0.710674	0.18935	0.9998
ENSG00000100949	ENSG00000100949	RABGGTA	14:24734743-24740945	OK	13.8427	18.1012	0.38696	0.726929	0.18955	0.9998
ENSG00000124225	ENSG00000124225	PMEPA1	20:56223447-56286592	OK	0.902764	1.7615	0.964382	0.660488	0.18965	0.9998
ENSG00000104689	ENSG00000104689	TNFRSF10A	8:23046791-23088439	OK	1.42413	2.24723	0.658064	0.574921	0.1898	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000112972	ENSG00000112972	HMGCS1	5:43287702-43313614	OK	105.768	136.261	0.365468	0.683607	0.1899	0.9998
ENSG00000078808	ENSG00000078808	SDF4	1:1152287-1167411	OK	118.817	92.4108	-0.362611	-0.79107	0.1902	0.9998
ENSG00000105968	ENSG00000105968	H2AFV	7:44866389-44887682	OK	208.57	160.057	-0.381945	-0.78573	0.1902	0.9998
ENSG00000153071	ENSG00000153071	DAB2	5:39284363-39462402	OK	110.794	89.7177	-0.304419	-0.466	0.1903	0.9998
ENSG00000238261	ENSG00000238261	RP11-435B5.5	1:143347957-143467632	OK	9.2391	15.3138	0.729011	0.835273	0.19035	0.9998
ENSG00000100151	ENSG00000100151	PICK1	22:38452317-38471708	OK	14.3125	19.2116	0.424697	0.729301	0.1906	0.9998
ENSG00000100033	ENSG00000100033	PRODH	22:18893540-18924066	OK	1.5962	3.10653	0.960662	0.595662	0.19085	0.9998
ENSG00000198354	ENSG00000198354	DCAF12L2	X:125298336-125300080	OK	0.600014	0.971246	0.69484	0.798339	0.191	0.9998
ENSG00000163507	ENSG00000163507	KIAA1524	3:108268715-108308491	OK	14.389	11.1985	-0.361663	-0.770533	0.19105	0.9998
ENSG00000117153	ENSG00000117153	KLHL12	1:202860227-202897764	OK	25.2376	19.891	-0.343459	-0.800295	0.19125	0.9998
ENSG00000138764	ENSG00000138764	CCNG2	4:78078303-78415440	OK	26.561	19.4255	-0.451359	-0.738277	0.19135	0.9998
ENSG00000119707	ENSG00000119707	RBM25	14:73525138-73588122	OK	30.7289	23.8674	-0.364558	-0.717483	0.1915	0.9998
ENSG00000175175	ENSG00000175175	PPM1E	17:56833229-57058983	OK	1.23348	1.7643	0.516359	0.790591	0.1917	0.9998
ENSG00000224631	ENSG00000224631	RP11-51O6.1	16:61089302-61089868	OK	12.9548	17.8496	0.462398	0.781097	0.19185	0.9998
ENSG00000101935	ENSG00000101935	AMMECR1	X:109437413-109699562	OK	1.68461	2.47864	0.55713	0.579044	0.1919	0.9998
ENSG00000233003	ENSG00000233003	CICP26	1:228162979-228165894	OK	1.04986	0.1996	-2.395	-1.4116	0.19205	0.9998
ENSG00000273033	ENSG00000273033	RP11-67L2.2	3:122605787-122611243	OK	1.68186	2.26909	0.432058	0.797766	0.19205	0.9998
ENSG00000046647	ENSG00000046647	GEMIN8	X:14026397-14048012	OK	3.23621	2.10057	-0.623525	-0.777061	0.1921	0.9998
ENSG00000100767	ENSG00000100767	PAPLN	14:73704204-73741348	OK	1.28993	1.93835	0.587543	0.611482	0.19215	0.9998
ENSG00000100234	ENSG00000100234	TIMP3	22:32908538-33454358	OK	117.405	148.746	0.341353	0.799108	0.1922	0.9998
ENSG00000169562	ENSG00000169562	GJB1	X:70435043-70445366	OK	41.3997	32.7204	-0.339428	-0.794632	0.1922	0.9998
ENSG00000065328	ENSG00000065328	MCM10	10:13203553-13253104	OK	3.72984	2.62685	-0.505781	-0.6037	0.19225	0.9998
ENSG00000258704	ENSG00000258704	RP11-85K15.2	14:35390063-35498773	OK	1.69959	0.461005	-1.88233	-0.343116	0.19225	0.9998
ENSG00000188522	ENSG00000188522	FAM83G	17:18853657-18950950	OK	2.23684	3.00339	0.425125	0.694605	0.19245	0.9998
ENSG00000119403	ENSG00000119403	PHF19	9:123617976-123639606	OK	83.0275	108.973	0.392309	0.78386	0.1925	0.9998
ENSG00000260958	ENSG00000260958	RP11-488I20.8	16:34442273-34518517	OK	23.3009	17.1974	-0.438196	-0.792948	0.1925	0.9998
ENSG00000170185	ENSG00000170185	USP38	4:144106069-144144983	OK	5.33312	6.94575	0.381151	0.796289	0.1926	0.9998
ENSG00000213366	ENSG00000213366	GSTM2	1:110210643-110252171	OK	11.9424	16.0631	0.427664	0.773529	0.1926	0.9998
ENSG00000124140	ENSG00000124140	SLC12A5	20:44637546-44688784	OK	0.700119	1.51652	1.11509	0.600093	0.19265	0.9998
ENSG00000001036	ENSG00000001036	FUCA2	6:143771943-143832827	OK	34.5062	25.6304	-0.429001	-0.799534	0.1928	0.9998
ENSG00000186469	ENSG00000186469	GNG2	14:52292912-52446060	OK	13.9516	10.0971	-0.466493	-0.717341	0.19285	0.9998
ENSG00000176393	ENSG00000176393	RNPEP	1:201951499-201986316	OK	63.3971	50.9261	-0.316011	-0.722766	0.1929	0.9998
ENSG00000156453	ENSG00000156453	PCDH1	5:141232937-141258811	OK	3.93555	2.91484	-0.433145	-0.747434	0.193	0.9998
ENSG00000106701	ENSG00000106701	FSD1L	9:108210076-108314714	OK	2.80743	4.80884	0.77644	0.592813	0.19305	0.9998
ENSG00000108518	ENSG00000108518	PFN1	17:4848946-4860426	OK	574.272	743.972	0.373514	0.783569	0.19305	0.9998
ENSG00000187741	ENSG00000187741	FANCA	16:89773541-89883065	OK	9.97937	6.71956	-0.570581	-0.491303	0.1933	0.9998
ENSG00000188559	ENSG00000188559	RALGAPA2	20:20370195-20693131	OK	2.72334	2.00018	-0.445248	-0.652951	0.1933	0.9998
ENSG00000090054	ENSG00000090054	SPTLC1	9:94794280-94877666	OK	30.026	23.1195	-0.377102	-0.761875	0.1935	0.9998
ENSG00000118246	ENSG00000118246	FASTKD2	2:207602486-207657233	OK	22.8201	28.8616	0.338846	0.769279	0.1937	0.9998
ENSG00000143748	ENSG00000143748	NVL	1:224407314-224518089	OK	26.4814	20.3159	-0.382371	-0.614092	0.19385	0.9998
ENSG00000233762	ENSG00000233762	AC007969.5	2:172373748-172374232	OK	85.2385	110.241	0.371085	0.79577	0.19385	0.9998
ENSG00000259758	ENSG00000259758	CASC7	8:141530254-141539600	OK	6.06516	4.79526	-0.338934	-0.793324	0.19385	0.9998
ENSG00000064042	ENSG00000064042	LIMCH1	4:41361623-41702061	OK	4.20943	5.72445	0.443511	0.623147	0.194	0.9998
ENSG00000258441	ENSG00000258441	LINC00641	14:21668237-21675059	OK	3.31172	4.58098	0.468076	0.780252	0.1941	0.9998
ENSG00000219626	ENSG00000219626	FAM228B	2:24299395-24424567	OK	2.72932	1.26694	-1.10719	-0.57372	0.19425	0.9998
ENSG00000196449	ENSG00000196449	YRDC	1:38268615-38275126	OK	17.7457	24.5573	0.468676	0.808594	0.19435	0.9998
ENSG00000090661	ENSG00000090661	CERS4	19:8271619-8327305	OK	4.93735	6.94453	0.49214	0.695962	0.1944	0.9998
ENSG00000104205	ENSG00000104205	SGK3	8:67579830-67774257	OK	4.56426	6.30151	0.465317	0.589366	0.1944	0.9998
ENSG00000149308	ENSG00000149308	NPAT	11:108027941-108338258	OK	8.26959	4.99157	-0.728322	-0.62682	0.1946	0.9998
ENSG00000234231	ENSG00000234231	AC093616.4	2:88000502-88038766	OK	1.45523	2.18958	0.589401	0.797101	0.1947	0.9998
ENSG00000129055	ENSG00000129055	ANAPC13	3:134196547-134293859	OK	25.4786	36.4093	0.515023	0.797735	0.195	0.9998
ENSG00000143971	ENSG00000143971	ETAA1	2:67624450-67637677	OK	4.69793	3.5169	-0.417721	-0.680965	0.1951	0.9998
ENSG00000213080	ENSG00000213080	RP11-312J18.5	1:160864769-160865866	OK	10.8098	14.4398	0.417714	0.796171	0.1952	0.9998
ENSG00000125351	ENSG00000125351	UPF3B	X:118967984-118986961	OK	7.98885	6.03016	-0.405791	-0.780793	0.19535	0.9998
ENSG00000153094	ENSG00000153094	BCL2L11	2:111876954-111926024	OK	2.27742	1.65497	-0.460593	-0.457791	0.19535	0.9998
ENSG00000186577	ENSG00000186577	C6orf1	6:34214156-34217247	OK	39.0925	30.0429	-0.379865	-0.801832	0.19535	0.9998
ENSG00000133398	ENSG00000133398	MED10	5:6371993-6378707	OK	35.0925	44.8989	0.355519	0.794735	0.19565	0.9998
ENSG00000196378	ENSG00000196378	ZNF34	8:145998498-146012730	OK	1.47768	1.00493	-0.556244	-0.705525	0.19565	0.9998
ENSG00000120215	ENSG00000120215	MLANA	9:5881595-6007904	OK	1222.14	926.822	-0.399049	-0.765102	0.19575	0.9998
ENSG00000028839	ENSG00000028839	TBPL1	6:134273307-134373774	OK	9.80343	14.6573	0.580258	0.754208	0.1958	0.9998
ENSG00000154548	ENSG00000154548	SRSF12	6:89805677-89827800	OK	0.55907	0.897029	0.682125	0.61494	0.19585	0.9998
ENSG00000105663	ENSG00000105663	KMT2B	19:36208920-36229779	OK	6.76333	4.36114	-0.633026	-0.591586	0.19615	0.9998
ENSG00000168936	ENSG00000168936	TMEM129	4:1717678-1723085	OK	11.9764	16.0452	0.421948	0.767988	0.1962	0.9998
ENSG00000134153	ENSG00000134153	EMC7	15:34376217-34394149	OK	41.191	32.4623	-0.343563	-0.770973	0.1963	0.9998
ENSG00000124767	ENSG00000124767	GLO1	6:38643700-38670917	OK	136.714	168.983	0.305719	0.771422	0.19655	0.9998
ENSG00000134532	ENSG00000134532	SOX5	12:23682439-24103966	OK	8.28551	5.90147	-0.489516	-0.609081	0.1969	0.9998
ENSG00000116991	ENSG00000116991	SIPA1L2	1:232533710-232697304	OK	7.49006	5.75628	-0.379842	-0.585586	0.19705	0.9998
ENSG00000118600	ENSG00000118600	TMEM5	12:63952692-64217675	OK	41.6412	32.3158	-0.365773	-0.73767	0.1971	0.9998
ENSG00000162624	ENSG00000162624	LHX8	1:75593514-75627218	OK	0.42772	0.86624	1.0181	0.519723	0.1972	0.9998
ENSG00000136636	ENSG00000136636	KCTD3	1:215740734-215795149	OK	17.7903	22.3848	0.33143	0.69879	0.1973	0.9998
ENSG00000204248	ENSG00000204248	COL11A2	6:33130457-33160276	OK	1.18622	1.93131	0.703205	0.760771	0.1973	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000239883	ENSG00000239883	RP11-175I17.2	10:46349540-46411619	OK	0.742536	0.37617	-0.981077	-0.731693	0.1973	0.9998
ENSG00000180884	ENSG00000180884	ZNF792	19:35447257-35454953	OK	0.466039	0.698543	0.583899	0.786836	0.1975	0.9998
ENSG00000154102	ENSG00000154102	C16orf74	16:85723689-85784735	OK	3.63137	5.31349	0.549144	0.771862	0.1976	0.9998
ENSG00000182704	ENSG00000182704	TSKU	11:76493294-76509198	OK	9.91571	12.7474	0.36242	0.753764	0.1977	0.9998
ENSG00000174684	ENSG00000174684	B3GNT1	11:66112842-66115163	OK	25.593	32.1975	0.331203	0.785979	0.19795	0.9998
ENSG00000163683	ENSG00000163683	SMIM14	4:39500374-39640710	OK	8.26093	4.01521	-1.04083	-0.650556	0.19805	0.9998
ENSG00000213199	ENSG00000213199	ASIC3	7:150745378-150749843	OK	0.768474	1.28667	0.743579	0.644765	0.19805	0.9998
ENSG00000108448	ENSG00000108448	TRIM16L	17:18601310-18639431	OK	16.6362	22.4618	0.433147	0.765804	0.19815	0.9998
ENSG00000128394	ENSG00000128394	APOBEC3F	22:39436608-39483748	OK	1.07609	2.14066	0.992261	0.792204	0.19815	0.9998
ENSG00000111652	ENSG00000111652	COPS7A	12:6832906-6841041	OK	59.4438	47.2318	-0.331767	-0.734822	0.1983	0.9998
ENSG00000162733	ENSG00000162733	DDR2	1:162601162-162757190	OK	1.15177	1.89862	0.721096	0.579417	0.1983	0.9998
ENSG00000135905	ENSG00000135905	DOCK10	2:225629806-225907162	OK	10.2299	6.89516	-0.569136	-0.543101	0.1984	0.9998
ENSG00000135913	ENSG00000135913	USP37	2:219283814-219433084	OK	3.8663	2.88581	-0.42198	-0.492343	0.1984	0.9998
ENSG00000136381	ENSG00000136381	IREB2	15:78729772-78793798	OK	11.0279	14.2403	0.368821	0.487857	0.19845	0.9998
ENSG00000117122	ENSG00000117122	MFAP2	1:17300996-17338423	OK	1.41547	3.2803	1.21255	0.358509	0.19855	0.9998
ENSG00000234975	ENSG00000234975	FTH1P2	1:228823161-228823574	OK	680.532	843.26	0.309316	0.767274	0.19855	0.9998
ENSG00000183779	ENSG00000183779	ZNF703	8:37553268-37557537	OK	23.0549	29.1426	0.338059	0.788442	0.1987	0.9998
ENSG00000160014	ENSG00000160014	CALM3	19:46984052-47114050	OK	202.451	159.218	-0.34657	-0.725461	0.1988	0.9998
ENSG00000102024	ENSG00000102024	PLS3	X:114752489-114885181	OK	50.7049	66.0002	0.380343	0.78183	0.19885	0.9998
ENSG00000167106	ENSG00000167106	FAM102A	9:130696781-130742792	OK	26.8983	35.5243	0.401287	0.548954	0.199	0.9998
ENSG00000174238	ENSG00000174238	PITPNA	17:1420224-1466110	OK	21.0027	28.0441	0.417121	0.642211	0.19905	0.9998
ENSG00000164751	ENSG00000164751	PEX2	8:77892493-77913280	OK	37.8354	26.4083	-0.518746	-0.780319	0.1992	0.9998
ENSG00000007038	ENSG00000007038	PRSS21	16:2867163-2876305	OK	0.301032	0.692032	1.20092	0.531023	0.19925	0.9998
ENSG00000166908	ENSG00000166908	PIP4K2C	12:57984956-57997198	OK	44.5691	55.7011	0.321661	0.600554	0.19925	0.9998
ENSG00000242110	ENSG00000242110	AMACR	5:33986282-34124633	OK	68.2184	89.9946	0.399677	0.780654	0.19925	0.9998
ENSG00000204560	ENSG00000204560	DHX16	6:30614815-30640814	OK	35.1271	26.8496	-0.387683	-0.73931	0.1993	0.9998
ENSG00000198467	ENSG00000198467	TPM2	9:35681988-35691017	OK	2.83636	4.11058	0.5353	0.727657	0.19935	0.9998
ENSG00000101412	ENSG00000101412	E2F1	20:32263488-32274210	OK	37.1073	29.7131	-0.320603	-0.777134	0.1994	0.9998
ENSG00000240280	ENSG00000240280	TCAM1P	17:61926651-61941739	OK	0.97608	0.538066	-0.859215	-0.508858	0.19945	0.9998
ENSG00000169884	ENSG00000169884	WNT10B	12:49359122-49365546	OK	0.756143	1.12701	0.575767	0.56878	0.1995	0.9998
ENSG00000185947	ENSG00000185947	ZNF267	16:31885078-31928668	OK	6.59244	5.01659	-0.394107	-0.640925	0.1995	0.9998
ENSG00000137727	ENSG00000137727	ARHGAP20	11:110447765-110583912	OK	0.839295	0.555459	-0.595496	-0.714054	0.1996	0.9998
ENSG00000228022	ENSG00000228022	HCG20	6:30734601-30760027	OK	1.3452	0.836664	-0.685103	-0.788342	0.1996	0.9998
ENSG00000232803	ENSG00000232803	RP11-93B14.5	20:61272070-61317137	OK	6.98888	10.7917	0.626793	0.830063	0.19965	0.9998
ENSG00000197093	ENSG00000197093	GAL3ST4	7:99756866-99766373	OK	1.55948	2.51167	0.68758	0.748192	0.1997	0.9998
ENSG00000107295	ENSG00000107295	SH3GL2	9:17579079-17797127	OK	0.441335	1.03784	1.23364	0.602298	0.20005	0.9998
ENSG00000198324	ENSG00000198324	FAM109A	12:111798454-111806925	OK	3.51402	4.69539	0.418123	0.73127	0.20005	0.9998
ENSG00000172115	ENSG00000172115	CYCS	7:25159709-25164980	OK	266.701	355.065	0.412858	0.782721	0.2001	0.9998
ENSG00000173933	ENSG00000173933	RBM4	11:66384052-66445392	OK	56.2167	78.3106	0.47821	0.770569	0.2002	0.9998
ENSG00000163029	ENSG00000163029	SMC6	2:17845078-17981509	OK	14.0007	10.3181	-0.440324	-0.650915	0.20035	0.9998
ENSG00000204054	ENSG00000204054	LINC00963	9:132245729-132275965	OK	23.6228	17.262	-0.452577	-0.727969	0.20035	0.9998
ENSG00000176244	ENSG00000176244	ACBD7	10:15057070-15130775	OK	0.404674	0.694758	0.779748	0.642465	0.20045	0.9998
ENSG00000081479	ENSG00000081479	LRP2	2:169983618-170219195	OK	2.23981	1.34086	-0.740224	-0.554813	0.20075	0.9998
ENSG00000086300	ENSG00000086300	SNX10	7:26331540-26416321	OK	86.3555	67.9044	-0.346782	-0.724705	0.2009	0.9998
ENSG00000154864	ENSG00000154864	PIEZO2	18:10661929-11148587	OK	18.3131	22.9697	0.32685	0.454511	0.20095	0.9998
ENSG00000188827	ENSG00000188827	SLX4	16:3631181-3661599	OK	3.2201	2.43147	-0.405275	-0.788297	0.20105	0.9998
ENSG00000160685	ENSG00000160685	ZBTB7B	1:154975126-155006257	OK	16.3941	21.7829	0.410022	0.743172	0.2011	0.9998
ENSG00000015153	ENSG00000015153	YAF2	12:42550905-42632151	OK	15.8071	21.4086	0.437614	0.585947	0.2012	0.9998
ENSG00000260290	ENSG00000260290	CTD-2033A16.2	16:69790438-69791840	OK	1.00543	1.56234	0.635895	0.788153	0.2012	0.9998
ENSG00000163710	ENSG00000163710	PCOLCE2	3:142534763-142608045	OK	9.06785	13.1969	0.541373	0.806264	0.20135	0.9998
ENSG00000111490	ENSG00000111490	TBC1D30	12:65174588-65274812	OK	0.629035	1.11545	0.826415	0.612004	0.20145	0.9998
ENSG00000197566	ENSG00000197566	ZNF624	17:16524050-16557170	OK	1.389	0.936297	-0.569007	-0.56227	0.20145	0.9998
ENSG00000204160	ENSG00000204160	ZDHHC18	1:27153200-27184093	OK	10.4137	6.99198	-0.574705	-0.737881	0.2018	0.9998
ENSG00000185215	ENSG00000185215	TNFAIP2	14:103589778-103603776	OK	7.26846	10.489	0.529156	0.666568	0.20185	0.9998
ENSG00000213741	ENSG00000213741	RPS29	14:50043389-50081390	OK	2828.26	3574.32	0.337755	0.782257	0.2019	0.9998
ENSG00000108018	ENSG00000108018	SORCS1	10:108333420-108924292	OK	9.57301	7.26323	-0.398361	-0.656271	0.20195	0.9998
ENSG00000166949	ENSG00000166949	SMAD3	15:67356100-67487533	OK	9.72812	13.232	0.443796	0.674372	0.2022	0.9998
ENSG00000186340	ENSG00000186340	THBS2	6:169613348-169654139	OK	0.882507	1.2721	0.527534	0.548838	0.2023	0.9998
ENSG00000110911	ENSG00000110911	SLC11A2	12:51373183-51422349	OK	91.6507	73.3701	-0.320953	-0.644518	0.2027	0.9998
ENSG00000107833	ENSG00000107833	NPM3	10:103541081-103543170	OK	43.436	57.8009	0.412202	0.770834	0.20285	0.9998
ENSG00000143819	ENSG00000143819	EPHX1	1:225997793-226070069	OK	77.617	105.319	0.440323	0.765804	0.20285	0.9998
ENSG00000167646	ENSG00000167646	DNAAF3	19:55663136-55691809	OK	0.841518	1.36624	0.699142	0.471413	0.20295	0.9998
ENSG00000144591	ENSG00000144591	GMPPA	2:220299567-220403494	OK	25.4238	19.0105	-0.41938	-0.750659	0.2034	0.9998
ENSG00000131351	ENSG00000131351	HAUS8	19:17160538-17186435	OK	12.7081	9.32838	-0.44605	-0.794672	0.2035	0.9998
ENSG00000261786	ENSG00000261786	RP4-555D20.2	3:44158790-44163857	OK	1.81257	2.41707	0.415225	0.771904	0.2035	0.9998
ENSG00000272556	ENSG00000272556	RP11-638I8.1	7:45854200-45854862	OK	0.632217	0.273224	-1.21033	-0.822138	0.2035	0.9998
ENSG00000054690	ENSG00000054690	PLEKHH1	14:67913800-68067004	OK	59.3766	44.6464	-0.41135	-0.459624	0.20375	0.9998
ENSG00000126107	ENSG00000126107	HECTD3	1:45468211-45477001	OK	18.369	23.2563	0.340351	0.690286	0.2038	0.9998
ENSG00000184634	ENSG00000184634	MED12	X:70338405-70362303	OK	12.7829	9.39536	-0.444197	-0.400925	0.20395	0.9998
ENSG00000111341	ENSG00000111341	MGP	12:14956505-15059520	OK	3.31499	1.40563	-1.23779	-0.867892	0.204	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000164175	ENSG00000164175	SLC45A2	5:33944720-33984835	OK	490.376	627.413	0.355526	0.757926	0.20405	0.9998
ENSG00000173218	ENSG00000173218	VANGL1	1:116184573-116240845	OK	11.3049	15.3613	0.442359	0.743179	0.20435	0.9998
ENSG00000134086	ENSG00000134086	VHL	3:10182691-10193904	OK	18.1924	13.4972	-0.430673	-0.751134	0.2044	0.9998
ENSG00000157224	ENSG00000157224	CLDN12	7:89964536-90839905	OK	43.7266	33.4756	-0.385401	-0.522156	0.2044	0.9998
ENSG00000128591	ENSG00000128591	FLNC	7:128470430-128550773	OK	0.502363	1.93706	1.94707	0.851597	0.20445	0.9998
ENSG00000068793	ENSG00000068793	CYFIP1	15:22892004-23034427	OK	16.8279	10.5688	-0.67104	-0.652458	0.2046	0.9998
ENSG00000147224	ENSG00000147224	PRPS1	X:106871736-106894256	OK	22.9241	29.2625	0.35219	0.746123	0.2048	0.9998
ENSG00000156273	ENSG00000156273	BACH1	21:30565800-31312351	OK	3.23814	4.26161	0.396232	0.546681	0.2048	0.9998
ENSG00000113070	ENSG00000113070	HBEGF	5:139712427-139726216	OK	5.0408	3.79477	-0.409642	-0.735956	0.20495	0.9998
ENSG00000153029	ENSG00000153029	MR1	1:181003066-181031074	OK	4.87569	3.22377	-0.596859	-0.793797	0.20495	0.9998
ENSG00000136197	ENSG00000136197	C7orf25	7:42948324-42988557	OK	2.31291	0.963623	-1.26317	-0.299287	0.205	0.9998
ENSG00000174796	ENSG00000174796	THAP6	4:76404246-76475683	OK	5.94409	3.96294	-0.584886	-0.482636	0.20505	0.9998
ENSG00000196205	ENSG00000196205	EEF1A1P5	9:135894815-135896553	OK	1294.65	1676.62	0.373	0.76896	0.2052	0.9998
ENSG00000186806	ENSG00000186806	VSIG10L	19:51834789-51847371	OK	1.40722	0.967977	-0.539807	-0.775162	0.2053	0.9998
ENSG00000260233	ENSG00000260233	SSSCA1-AS1	11:65337130-65337744	OK	0.851343	1.54927	0.863774	0.79774	0.2053	0.9998
ENSG00000175806	ENSG00000175806	MSRA	8:9911777-10286401	OK	13.9555	18.8169	0.431192	0.749277	0.20545	0.9998
ENSG00000069329	ENSG00000069329	VPS35	16:46690053-46723430	OK	40.0462	30.9456	-0.371932	-0.588367	0.2055	0.9998
ENSG00000138311	ENSG00000138311	ZNF365	10:64133950-64431771	OK	2.18944	2.89198	0.401496	0.675118	0.20555	0.9998
ENSG00000211460	ENSG00000211460	TSN	2:122494678-122525429	OK	80.4282	63.0912	-0.350263	-0.737733	0.20555	0.9998
ENSG00000107957	ENSG00000107957	SH3PXD2A	10:105239359-105615301	OK	36.9294	27.4221	-0.429429	-0.772832	0.2056	0.9998
ENSG00000136717	ENSG00000136717	BIN1	2:127805602-127864931	OK	6.13615	8.14622	0.408798	0.764712	0.20575	0.9998
ENSG00000140474	ENSG00000140474	ULK3	15:75128456-75135687	OK	30.0869	24.1116	-0.31941	-0.653712	0.2058	0.9998
ENSG00000171766	ENSG00000171766	GATM	15:45653321-45694525	OK	1.82587	2.67274	0.549737	0.581697	0.2058	0.9998
ENSG00000079616	ENSG00000079616	KIF22	16:29802039-29816706	OK	34.1083	26.3903	-0.370116	-0.745419	0.20595	0.9998
ENSG00000162702	ENSG00000162702	ZNF281	1:200374067-200379184	OK	8.80309	11.2515	0.35404	0.779939	0.2061	0.9998
ENSG00000140403	ENSG00000140403	DNAJA4	15:78542843-78592136	OK	119.256	153.478	0.363973	0.71904	0.2065	0.9998
ENSG00000112852	ENSG00000112852	PCDHB2	5:140474226-140476962	OK	0.96655	0.647883	-0.57711	-0.776893	0.20665	0.9998
ENSG00000123066	ENSG00000123066	MED13L	12:116395710-116715143	OK	11.01	13.7532	0.320959	0.407941	0.20685	0.9998
ENSG00000129103	ENSG00000129103	SUMF2	7:56131694-56148363	OK	166.476	133.515	-0.318319	-0.698664	0.207	0.9998
ENSG00000184575	ENSG00000184575	XPOT	12:64798129-64844907	OK	44.707	59.5045	0.412498	0.64699	0.20715	0.9998
ENSG00000197043	ENSG00000197043	ANXA6	5:150480272-150537443	OK	46.7864	57.7915	0.304769	0.717996	0.20725	0.9998
ENSG00000221867	ENSG00000221867	MAGEA3	X:151934651-151938240	OK	59.0066	73.0631	0.308266	0.767911	0.2073	0.9998
ENSG00000188846	ENSG00000188846	RPL14	3:40498782-40503861	OK	727.543	911.008	0.324432	0.776097	0.20735	0.9998
ENSG00000222041	ENSG00000222041	LINC00152	2:87754886-87906324	OK	78.2257	99.9752	0.353929	0.779824	0.2074	0.9998
ENSG00000172380	ENSG00000172380	GNG12	1:68167148-68698803	OK	50.3994	63.9157	0.342765	0.765492	0.20745	0.9998
ENSG00000196396	ENSG00000196396	PTPN1	20:49126890-49201299	OK	27.7881	34.3853	0.307324	0.75746	0.20745	0.9998
ENSG00000122970	ENSG00000122970	IFT81	12:110562139-110656602	OK	50.4445	35.6473	-0.500905	-0.78683	0.20775	0.9998
ENSG00000149313	ENSG00000149313	AASDHPPT	11:105921824-105972702	OK	13.7602	20.0417	0.542507	0.764878	0.20775	0.9998
ENSG00000089157	ENSG00000089157	RPLP0	12:120634488-120639038	OK	1718	2246.29	0.386816	0.766827	0.2078	0.9998
ENSG00000110693	ENSG00000110693	SOX6	11:15987994-16778428	OK	6.15992	9.28548	0.592065	0.36335	0.2079	0.9998
ENSG00000135338	ENSG00000135338	LCA5	6:80194707-80247175	OK	2.09551	1.55927	-0.426429	-0.753298	0.208	0.9998
ENSG00000148926	ENSG00000148926	ADM	11:10326226-10328944	OK	72.6033	53.9089	-0.429513	-0.800118	0.208	0.9998
ENSG00000007376	ENSG00000007376	RPUSD1	16:834973-850737	OK	13.1396	19.1714	0.545032	0.772905	0.2081	0.9998
ENSG00000198130	ENSG00000198130	HIBCH	2:190744334-191236391	OK	33.0672	22.9173	-0.528966	-0.665539	0.2081	0.9998
ENSG00000113638	ENSG00000113638	TTC33	5:40714576-40756077	OK	13.3159	10.0427	-0.407002	-0.771876	0.2082	0.9998
ENSG00000205853	ENSG00000205853	RFPL3S	22:32750871-32781618	OK	0.322399	0.907402	1.4929	0.587401	0.2083	0.9998
ENSG00000256001	ENSG00000256001	RP11-575F12.2	12:127629616-127631077	OK	1.47402	0.173261	-3.08874	-0.931975	0.2084	0.9998
ENSG00000117266	ENSG00000117266	CDK18	1:205473722-205501921	OK	4.23	5.71417	0.433886	0.600261	0.20845	0.9998
ENSG00000046774	ENSG00000046774	MAGEC2	X:141290130-141293076	OK	0.713168	1.09428	0.617672	0.773212	0.2086	0.9998
ENSG00000164142	ENSG00000164142	FAM160A1	4:152330367-152584784	OK	1.58895	0.895396	-0.827476	-0.534436	0.20865	0.9998
ENSG00000242028	ENSG00000242028	HYPK	15:44019115-44095241	OK	1.72429	0.55767	-1.62851	-0.122625	0.2087	0.9998
ENSG00000125454	ENSG00000125454	SLC25A19	17:73267449-73285591	OK	11.7233	8.89067	-0.399014	-0.668719	0.2088	0.9998
ENSG00000154839	ENSG00000154839	SKA1	18:47901364-47920543	OK	12.2449	8.90137	-0.460077	-0.744186	0.20885	0.9998
ENSG00000006534	ENSG00000006534	ALDH3B1	11:67776047-67797928	OK	2.95949	2.04312	-0.534572	-0.63801	0.2089	0.9998
ENSG00000163820	ENSG00000163820	FYCO1	3:45959395-46037316	OK	17.3929	23.7628	0.450202	0.72164	0.2092	0.9998
ENSG00000177646	ENSG00000177646	ACAD9	3:128598438-128759585	OK	27.3615	21.9047	-0.320909	-0.697343	0.2094	0.9998
ENSG00000106462	ENSG00000106462	EZH2	7:148504474-148581413	OK	24.839	19.6125	-0.340832	-0.750934	0.2095	0.9998
ENSG00000184922	ENSG00000184922	FMNL1	17:43268297-43394414	OK	0.679439	1.26858	0.900793	0.496616	0.2095	0.9998
ENSG00000166033	ENSG00000166033	HTRA1	10:124221040-124274424	OK	20.9768	26.8867	0.358099	0.757489	0.2098	0.9998
ENSG00000251191	ENSG00000251191	LINC00589	8:29531437-29605625	OK	4.62575	3.1794	-0.540932	-0.776118	0.2098	0.9998
ENSG00000119900	ENSG00000119900	OGFRL1	6:71931159-72130472	OK	4.24679	3.28811	-0.369114	-0.61662	0.20995	0.9998
ENSG00000213430	ENSG00000213430	HSPD1P1	5:21616370-22853731	OK	0.667687	1.29181	0.952151	0.755805	0.20995	0.9998
ENSG00000138641	ENSG00000138641	HERC3	4:89442135-89629693	OK	10.9388	7.09943	-0.623685	-0.499294	0.21005	0.9998
ENSG00000088992	ENSG00000088992	TESC	12:117476727-117537284	OK	1.54948	2.34954	0.600592	0.606635	0.2102	0.9998
ENSG00000170727	ENSG00000170727	BOP1	8:145486054-145515082	OK	17.706	23.2022	0.390023	0.752531	0.2103	0.9998
ENSG00000171843	ENSG00000171843	MLLT3	9:20341662-20622542	OK	10.7688	7.38929	-0.543342	-0.727169	0.21035	0.9998
ENSG00000059728	ENSG00000059728	MXD1	2:70120691-70170077	OK	1.82772	3.02819	0.728409	0.620215	0.2104	0.9998
ENSG00000231121	ENSG00000231121	RP1-34H18.1	12:77718420-77966055	OK	9.64532	1.51206	-2.67332	-0.508964	0.2104	0.9998
ENSG00000141569	ENSG00000141569	TRIM65	17:73876415-73893084	OK	12.7977	16.805	0.393001	0.622165	0.21065	0.9998
ENSG00000178537	ENSG00000178537	SLC25A20	3:48894368-48936426	OK	15.6624	11.8479	-0.402668	-0.773443	0.21065	0.9998
ENSG00000104412	ENSG00000104412	EMC2	8:109455829-109499145	OK	38.6357	30.6535	-0.333885	-0.743724	0.21075	0.9998
ENSG00000130822	ENSG00000130822	PNCK	X:152935184-152962048	OK	0.843684	1.46872	0.799784	0.0971674	0.21085	0.9998
ENSG00000234664	ENSG00000234664	HMGN2P5	15:29991570-30261068	OK	193.15	132.936	-0.538991	-0.764993	0.21085	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000247315	ENSG00000247315	AL034548.1	20:277736-280965	OK	5.74842	3.96469	-0.535957	-0.778286	0.21085	0.9998
ENSG00000102967	ENSG00000102967	DHODH	16:72042486-72058954	OK	3.55418	5.01059	0.495465	0.676448	0.2111	0.9998
ENSG00000104953	ENSG00000104953	TLE6	19:2977443-2995177	OK	4.75965	2.79349	-0.768784	-0.699095	0.2111	0.9998
ENSG00000110851	ENSG00000110851	PRDM4	12:108126642-108155049	OK	11.7445	14.7329	0.327058	0.634162	0.2111	0.9998
ENSG00000119280	ENSG00000119280	C1orf198	1:230972864-231005335	OK	16.4698	20.4479	0.312128	0.728072	0.2111	0.9998
ENSG00000164167	ENSG00000164167	LSM6	4:147096836-147121152	OK	20.5733	15.0558	-0.45045	-0.762647	0.2111	0.9998
ENSG00000108094	ENSG00000108094	CUL2	10:35297478-35379570	OK	14.0489	19.1742	0.448709	0.690301	0.21115	0.9998
ENSG00000146733	ENSG00000146733	PSPH	7:56078743-56119297	OK	16.0637	21.8755	0.445512	0.765233	0.21125	0.9998
ENSG00000172315	ENSG00000172315	TP53RK	20:45313003-45318928	OK	20.8812	16.3037	-0.357003	-0.759148	0.21125	0.9998
ENSG00000196152	ENSG00000196152	ZNF79	9:130186660-130207651	OK	5.08367	3.77559	-0.429168	-0.768165	0.21135	0.9998
ENSG00000113448	ENSG00000113448	PDE4D	5:58264864-59843484	OK	5.56236	7.99374	0.523172	0.640295	0.2114	0.9998
ENSG00000197451	ENSG00000197451	HNRNPAB	5:177631507-177659792	OK	103.194	82.3449	-0.325607	-0.757291	0.2114	0.9998
ENSG00000230490	ENSG00000230490	RP11-141M1.3	13:33929342-34250905	OK	2.44851	1.29132	-0.923058	-0.755483	0.2114	0.9998
ENSG00000072840	ENSG00000072840	EVC	4:5712923-5894785	OK	6.46624	8.30604	0.361233	0.601267	0.2115	0.9998
ENSG00000196611	ENSG00000196611	MMP1	11:102617698-102714534	OK	0.496265	0.814281	0.714415	0.76345	0.2115	0.9998
ENSG00000085415	ENSG00000085415	SEH1L	18:12947131-12991172	OK	14.5901	18.8054	0.366154	0.704271	0.2116	0.9998
ENSG00000144655	ENSG00000144655	CSRNP1	3:39183345-39196053	OK	2.27086	3.11146	0.454348	0.769484	0.2116	0.9998
ENSG00000198408	ENSG00000198408	MGEA5	10:103544199-103578696	OK	33.3062	42.0139	0.335076	0.580827	0.2116	0.9998
ENSG00000236773	ENSG00000236773	RP11-365O16.1	1:224363177-224363408	OK	1.11585	0.174249	-2.67893	-0.819989	0.2116	0.9998
ENSG00000124145	ENSG00000124145	SDC4	20:43953927-43977064	OK	35.1086	27.93	-0.330009	-0.754579	0.2117	0.9998
ENSG00000108799	ENSG00000108799	EZH1	17:40852292-40897071	OK	17.7504	12.184	-0.542867	-0.668103	0.2118	0.9998
ENSG00000117151	ENSG00000117151	CTBS	1:84964007-85040163	OK	7.60654	4.33699	-0.810548	-0.785159	0.21205	0.9998
ENSG00000107201	ENSG00000107201	DDX58	9:32455299-32526322	OK	1.88011	1.3256	-0.504173	-0.755851	0.2121	0.9998
ENSG00000229891	ENSG00000229891	Z83851.1	22:42760405-42765242	OK	0.920243	1.51411	0.718379	0.699902	0.21225	0.9998
ENSG00000135063	ENSG00000135063	FAM189A2	9:71939487-72007371	OK	2.78237	3.92034	0.494665	0.779955	0.21235	0.9998
ENSG00000138326	ENSG00000138326	RPS24	10:79793517-79816570	OK	2738.36	3473.66	0.343147	0.759104	0.2125	0.9998
ENSG00000008394	ENSG00000008394	MGST1	12:16500075-16763528	OK	9.91537	13.4699	0.442	0.614626	0.21255	0.9998
ENSG00000179304	ENSG00000179304	FAM156B	X:52920335-52937587	OK	0.836232	0.573007	-0.545349	-0.556438	0.2127	0.9998
ENSG00000171858	ENSG00000171858	RPS21	20:60962171-60963576	OK	2441.51	3057.28	0.324477	0.763253	0.21275	0.9998
ENSG00000155366	ENSG00000155366	RHOC	1:113243727-113258099	OK	171.035	213.696	0.321271	0.746655	0.21285	0.9998
ENSG00000241556	ENSG00000241556	RP11-490G8.1	12:95861172-95861637	OK	2.12513	3.59761	0.759492	0.780327	0.21285	0.9998
ENSG00000188042	ENSG00000188042	ARL4C	2:235401684-235405697	OK	14.9398	18.8249	0.333482	0.768805	0.2129	0.9998
ENSG00000175548	ENSG00000175548	ALG10B	12:38710379-38717784	OK	2.73059	1.52454	-0.840838	-0.75082	0.21305	0.9998
ENSG00000135951	ENSG00000135951	TSGA10	2:99613723-100106497	OK	3.61375	2.035	-0.828467	-0.104242	0.21315	0.9998
ENSG00000175556	ENSG00000175556	LONRF3	X:118108580-118152318	OK	5.04635	6.72675	0.41467	0.77762	0.21315	0.9998
ENSG00000205560	ENSG00000205560	CPT1B	22:51007289-51052409	OK	1.98705	1.01301	-0.971985	-0.335227	0.21315	0.9998
ENSG00000144713	ENSG00000144713	RPL32	3:12837970-12913415	OK	1702.22	2145.04	0.333588	0.752403	0.2135	0.9998
ENSG00000224550	ENSG00000224550	RP11-270C12.3	1:108047824-108048070	OK	2.23026	0.290329	-2.94145	-1.58933	0.2135	0.9998
ENSG00000137094	ENSG00000137094	DNAJB5	9:34989637-34998897	OK	5.83924	7.62607	0.385158	0.704214	0.21355	0.9998
ENSG00000153044	ENSG00000153044	CENPH	5:68485374-68506184	OK	17.2035	13.1604	-0.386498	-0.739486	0.2136	0.9998
ENSG00000267350	ENSG00000267350	RP1-178F10.3	17:18227535-18229211	OK	6.14657	8.13925	0.405114	0.75798	0.2136	0.9998
ENSG00000162368	ENSG00000162368	CMPK1	1:47799468-47844511	OK	45.757	36.3222	-0.333139	-0.749077	0.2137	0.9998
ENSG00000234297	ENSG00000234297	RP11-54D18.4	9:14987299-15146399	OK	4.62067	3.2492	-0.50802	-0.757324	0.2139	0.9998
ENSG00000162976	ENSG00000162976	PQLC3	2:11295323-11319000	OK	9.09618	11.9719	0.396322	0.692129	0.21395	0.9998
ENSG00000075884	ENSG00000075884	ARHGAP15	2:143848930-144533642	OK	0.905197	0.569653	-0.66815	-0.367842	0.21405	0.9998
ENSG00000142676	ENSG00000142676	RPL11	1:24018268-24022915	OK	1346.9	1676.19	0.315544	0.744355	0.21405	0.9998
ENSG00000117481	ENSG00000117481	NSUN4	1:46805848-46830824	OK	11.1943	14.9087	0.413393	0.751894	0.21425	0.9998
ENSG00000153246	ENSG00000153246	PLA2R1	2:160788518-160919121	OK	1.51029	2.03587	0.430818	0.692715	0.2143	0.9998
ENSG00000168615	ENSG00000168615	ADAM9	8:38854387-38962663	OK	47.3171	58.177	0.298087	0.719821	0.2143	0.9998
ENSG00000205084	ENSG00000205084	TMEM231	16:75562429-75657198	OK	4.77598	2.39589	-0.995236	-0.626448	0.21435	0.9998
ENSG00000065154	ENSG00000065154	OAT	10:126085871-126107545	OK	73.722	90.2741	0.292217	0.673086	0.2144	0.9998
ENSG00000172349	ENSG00000172349	IL16	15:81451915-81616524	OK	35.263	27.244	-0.372217	-0.727033	0.21485	0.9998
ENSG00000179277	ENSG00000179277	MEIS3P1	17:15689931-15690889	OK	2.6095	3.76391	0.528458	0.747599	0.21495	0.9998
ENSG00000184281	ENSG00000184281	TSSC4	11:2421717-2425106	OK	18.3309	23.9662	0.386727	0.771665	0.21495	0.9998
ENSG00000236013	ENSG00000236013	RP3-332B22.1	6:140388571-140414858	OK	1.55504	0.978413	-0.668433	-0.728405	0.21495	0.9998
ENSG00000099385	ENSG00000099385	BCL7C	16:30844946-30906541	OK	13.5086	17.3094	0.357674	0.750764	0.215	0.9998
ENSG00000178295	ENSG00000178295	GEN1	2:17845078-17981509	OK	5.90056	3.71038	-0.669283	-0.47223	0.215	0.9998
ENSG00000132434	ENSG00000132434	LANCL2	7:55433140-55501435	OK	7.12963	9.86796	0.468925	0.722426	0.21515	0.9998
ENSG00000011114	ENSG00000011114	BTBD7	14:93703895-93799438	OK	5.28786	7.27589	0.46044	0.626673	0.21535	0.9998
ENSG00000131944	ENSG00000131944	C19orf40	19:33463114-33469128	OK	4.05017	2.70276	-0.583548	-0.75388	0.21535	0.9998
ENSG00000106348	ENSG00000106348	IMPDH1	7:128032330-128050306	OK	73.0485	89.7903	0.297705	0.663143	0.2154	0.9998
ENSG00000120802	ENSG00000120802	TMPO	12:98906750-98944157	OK	56.066	44.4033	-0.33646	-0.641266	0.2155	0.9998
ENSG00000104870	ENSG00000104870	FCGRT	19:50010072-50029590	OK	3.78636	5.38521	0.508193	0.627105	0.2157	0.9998
ENSG00000119673	ENSG00000119673	ACOT2	14:74034323-74042357	OK	11.8687	15.6206	0.396284	0.640413	0.21575	0.9998
ENSG00000051341	ENSG00000051341	POLQ	3:121150277-121264853	OK	4.83091	3.62555	-0.414094	-0.507665	0.21585	0.9998
ENSG00000106852	ENSG00000106852	LHX6	9:124964855-124991905	OK	2.62309	3.78967	0.530803	0.688601	0.21585	0.9998
ENSG00000074657	ENSG00000074657	ZNF532	18:56529831-56653712	OK	6.72868	9.09355	0.434521	0.49239	0.2159	0.9998
ENSG00000257073	ENSG00000257073	AC011933.1	17:73314156-73401790	OK	8.2911	16.5027	0.993067	0.757219	0.2159	0.9998
ENSG00000116350	ENSG00000116350	SRSF4	1:29474254-29508499	OK	27.0161	21.3364	-0.340504	-0.571411	0.21605	0.9998
ENSG00000162572	ENSG00000162572	SCNN1D	1:1215815-1227409	OK	0.492995	0.973667	0.981854	0.677858	0.2163	0.9998
ENSG00000173674	ENSG00000173674	EIF1AX	X:20142635-20159962	OK	20.3423	28.134	0.467831	0.722594	0.2163	0.9998
ENSG00000233280	ENSG00000233280	CRYBG3	3:97540883-97594132	OK	2.72899	2.04755	-0.414471	-0.757366	0.2164	0.9998
ENSG00000085382	ENSG00000085382	HACE1	6:105175967-105307794	OK	3.81732	2.76809	-0.46367	-0.689797	0.2165	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000092096	ENSG00000092096	SLC22A17	14:23815514-23822121	OK	0.900672	1.34893	0.582746	0.634457	0.2165	0.9998
ENSG00000187801	ENSG00000187801	ZFP69B	1:40915773-40929390	OK	0.937335	0.605442	-0.630576	-0.748619	0.21665	0.9998
ENSG00000232150	ENSG00000232150	ST13P4	13:50601268-51423190	OK	2.18736	4.91403	1.16772	0.749723	0.2169	0.9998
ENSG00000163596	ENSG00000163596	ICA1L	2:203640689-203736708	OK	1.7519	1.26225	-0.472926	-0.369389	0.217	0.9998
ENSG00000205730	ENSG00000205730	ITPRIPL2	16:19125253-19279652	OK	3.72824	4.81198	0.368134	0.747476	0.21705	0.9998
ENSG00000182307	ENSG00000182307	C8orf33	8:146277763-146281416	OK	29.7294	36.9023	0.311821	0.750313	0.2171	0.9998
ENSG00000182400	ENSG00000182400	TRAPPC6B	14:39617014-39639736	OK	6.86031	9.35957	0.448169	0.720806	0.21725	0.9998
ENSG00000249936	ENSG00000249936	RAC1P2	4:46725792-46726625	OK	99.0491	78.3325	-0.338533	-0.758272	0.21725	0.9998
ENSG00000168621	ENSG00000168621	GDNF	5:37812778-37839788	OK	18.6128	14.5217	-0.358083	-0.663054	0.21755	0.9998
ENSG00000120708	ENSG00000120708	TGFBI	5:135364583-135399507	OK	3.54986	4.66537	0.394227	0.584821	0.21765	0.9998
ENSG00000109189	ENSG00000109189	USP46	4:53457137-53525502	OK	10.0816	13.3081	0.40058	0.611513	0.2177	0.9998
ENSG00000133706	ENSG00000133706	LARS	5:145463948-145562223	OK	53.4815	43.332	-0.303608	-0.509335	0.2177	0.9998
ENSG00000167470	ENSG00000167470	MIDN	19:1248551-1259142	OK	15.7872	19.9927	0.34072	0.475668	0.2177	0.9998
ENSG00000103510	ENSG00000103510	KAT8	16:31127074-31142714	OK	17.1066	13.0136	-0.394527	-0.750648	0.2178	0.9998
ENSG00000137200	ENSG00000137200	CMTR1	6:37400994-37450603	OK	25.8353	20.8375	-0.310163	-0.64746	0.2178	0.9998
ENSG00000174080	ENSG00000174080	CTSF	11:66330933-66336312	OK	42.4072	52.6323	0.311641	0.695419	0.2178	0.9998
ENSG00000171723	ENSG00000171723	GPHN	14:66679527-67648520	OK	11.2057	15.4876	0.466874	0.590334	0.2182	0.9998
ENSG00000216490	ENSG00000216490	IFI30	19:18263927-18288927	OK	18.6715	37.85	1.01945	0.691175	0.2183	0.9998
ENSG00000204314	ENSG00000204314	PRRT1	6:32116135-32145873	OK	2.7466	1.40516	-0.966918	-0.133767	0.21835	0.9998
ENSG00000106052	ENSG00000106052	TAX1BP1	7:27773013-28283536	OK	182.013	144.281	-0.335158	-0.680266	0.2185	0.9998
ENSG00000105866	ENSG00000105866	SP4	7:21467651-21554440	OK	2.60379	1.90698	-0.449323	-0.406904	0.21855	0.9998
ENSG00000104299	ENSG00000104299	INTS9	8:28625177-28747759	OK	15.6419	11.4915	-0.444841	-0.669295	0.2188	0.9998
ENSG00000223802	ENSG00000223802	CERS1	19:18979360-19007536	OK	8.17919	11.8411	0.533777	0.753132	0.2188	0.9998
ENSG00000245275	ENSG00000245275	SAP30L-AS1	5:153369687-153825410	OK	0.714293	0.25768	-1.47094	-0.180649	0.2188	0.9998
ENSG00000168040	ENSG00000168040	FADD	11:70049268-70053496	OK	12.398	15.9911	0.36716	0.746493	0.21895	0.9998
ENSG00000179912	ENSG00000179912	R3HDM2	12:57637235-57824788	OK	14.1912	10.5083	-0.43347	-0.643584	0.2191	0.9998
ENSG00000106028	ENSG00000106028	SSBP1	7:141404137-141488440	OK	247.407	306.896	0.310864	0.759294	0.21915	0.9998
ENSG00000228998	ENSG00000228998	RP11-697E2.7	15:90818265-90820841	OK	1.30323	1.85397	0.508528	0.676998	0.21915	0.9998
ENSG00000136938	ENSG00000136938	ANP32B	9:100745642-100778225	OK	88.0093	108.253	0.298678	0.730458	0.21925	0.9998
ENSG00000067836	ENSG00000067836	ROGDI	16:4846968-4852951	OK	9.16003	6.82596	-0.424321	-0.680079	0.21935	0.9998
ENSG00000129911	ENSG00000129911	KLF16	19:1852397-1863567	OK	6.8154	9.07656	0.413346	0.645549	0.21945	0.9998
ENSG00000243444	ENSG00000243444	PALM2	9:112403067-112934792	OK	0.256797	0.638847	1.31484	0.391354	0.2195	0.9998
ENSG00000129657	ENSG00000129657	SEC14L1	17:75082797-75213179	OK	30.462	38.3936	0.333854	0.640947	0.2196	0.9998
ENSG00000107874	ENSG00000107874	CUEDC2	10:104183001-104192418	OK	20.3416	15.6944	-0.374184	-0.734677	0.21975	0.9998
ENSG00000121413	ENSG00000121413	ZSCAN18	19:58570606-58629794	OK	0.708228	0.4319	-0.713518	-0.312048	0.2199	0.9998
ENSG00000185483	ENSG00000185483	ROR1	1:64239692-64647181	OK	3.36382	4.75422	0.499109	0.729054	0.22	0.9998
ENSG00000102054	ENSG00000102054	RBBP7	X:16804549-16888537	OK	96.486	77.2904	-0.32003	-0.679373	0.2201	0.9998
ENSG00000090924	ENSG00000090924	PLEKHG2	19:39903224-39919055	OK	3.7789	5.26209	0.477672	0.441375	0.22015	0.9998
ENSG00000196912	ENSG00000196912	ANKRD36B	2:98108977-98206428	OK	2.65587	1.6479	-0.688558	-0.745224	0.22015	0.9998
ENSG00000141429	ENSG00000141429	GALNT1	18:33161080-33291798	OK	39.7094	50.0689	0.334434	0.684267	0.22045	0.9998
ENSG00000169299	ENSG00000169299	PGM2	4:37828254-37864558	OK	14.0881	17.8916	0.344801	0.740965	0.2205	0.9998
ENSG00000115652	ENSG00000115652	UXS1	2:106709758-106810795	OK	34.1677	42.175	0.303754	0.713061	0.22055	0.9998
ENSG00000171155	ENSG00000171155	C1GALT1C1	X:119759647-119764005	OK	9.64298	7.38311	-0.38525	-0.744633	0.22075	0.9998
ENSG00000203739	ENSG00000203739	RP11-296O14.3	1:173386931-173430501	OK	0.82965	0.487538	-0.766989	-0.77157	0.2209	0.9998
ENSG00000136021	ENSG00000136021	SCYL2	12:100660917-100735502	OK	16.8805	21.1936	0.328273	0.586104	0.22095	0.9998
ENSG00000204305	ENSG00000204305	AGER	6:32146130-32152101	OK	1.41507	0.740114	-0.935056	-0.203256	0.221	0.9998
ENSG00000153233	ENSG00000153233	PTPRR	12:71031852-71314623	OK	0.4672	0.695902	0.574844	0.538623	0.22105	0.9998
ENSG00000163754	ENSG00000163754	GYG1	3:148709127-148745419	OK	29.9624	36.9779	0.303511	0.686854	0.22105	0.9998
ENSG00000116990	ENSG00000116990	MYCL	1:40361097-40367928	OK	0.421146	0.682175	0.695821	0.591137	0.2212	0.9998
ENSG00000136643	ENSG00000136643	RPS6KC1	1:213224588-213448116	OK	16.2933	12.8436	-0.343238	-0.709466	0.22135	0.9998
ENSG00000060138	ENSG00000060138	YBX3	12:10851682-10875911	OK	88.9673	115.196	0.372742	0.731733	0.22155	0.9998
ENSG00000186130	ENSG00000186130	ZBTB6	9:125670334-125675609	OK	6.91946	5.43633	-0.348027	-0.742622	0.222	0.9998
ENSG00000029153	ENSG00000029153	ARNTL2	12:27485786-27599558	OK	1.07861	0.695408	-0.63324	-0.600902	0.22205	0.9998
ENSG00000198752	ENSG00000198752	CDC42BPB	14:103388992-103523799	OK	35.6494	28.2205	-0.337133	-0.601376	0.22205	0.9998
ENSG00000175471	ENSG00000175471	MCTP1	5:93488670-94620279	OK	13.7316	20.0009	0.542571	0.646885	0.2221	0.9998
ENSG00000165813	ENSG00000165813	C10orf118	10:115880620-115933979	OK	4.30009	3.01197	-0.513657	-0.54869	0.2222	0.9998
ENSG00000162998	ENSG00000162998	FRZB	2:183698001-183731890	OK	9.70486	12.2224	0.332749	0.739096	0.22225	0.9998
ENSG00000112659	ENSG00000112659	CUL9	6:43149912-43192325	OK	11.9696	9.26088	-0.370149	-0.429229	0.2226	0.9998
ENSG00000138380	ENSG00000138380	CARF	2:203739504-203879521	OK	1.01783	0.63194	-0.687643	-0.219253	0.22275	0.9998
ENSG00000013306	ENSG00000013306	SLC25A39	17:42396992-42402238	OK	139.232	171.16	0.297851	0.724955	0.2228	0.9998
ENSG00000163513	ENSG00000163513	TGFBR2	3:30647993-30735634	OK	14.8706	18.5078	0.31567	0.749811	0.22295	0.9998
ENSG00000162755	ENSG00000162755	KLHDC9	1:161068150-161070136	OK	1.43646	2.19439	0.611302	0.670438	0.22335	0.9998
ENSG00000214954	ENSG00000214954	LRRC69	8:92114059-92410378	OK	0.666908	0.124506	-2.42127	-0.551066	0.22335	0.9998
ENSG00000006047	ENSG00000006047	YBX2	17:7184985-7197934	OK	1.9049	2.98222	0.64667	0.655624	0.22345	0.9998
ENSG00000105993	ENSG00000105993	DNAJB6	7:157128074-157210133	OK	89.0863	114.536	0.362526	0.709942	0.22355	0.9998
ENSG00000179967	ENSG00000179967	PPP1R14BP3	4:139936942-140098372	OK	63.5373	90.3262	0.507541	0.737809	0.2236	0.9998
ENSG00000132570	ENSG00000132570	PCBD2	5:134240595-134347392	OK	1.58996	1.00805	-0.657413	-0.623472	0.2237	0.9998
ENSG00000242071	ENSG00000242071	RPL7AP6	14:70320847-70499083	OK	320.72	397.263	0.308777	0.748877	0.2237	0.9998
ENSG00000091127	ENSG00000091127	PUS7	7:105080107-105162714	OK	8.91783	11.4934	0.36604	0.535388	0.2238	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000142669	ENSG00000142669	SH3BGRL3	1:26605666-26647014	OK	47.1051	61.5102	0.384942	0.731966	0.22385	0.9998
ENSG00000137338	ENSG00000137338	PGBD1	6:28249313-28270326	OK	3.99365	2.99464	-0.415323	-0.751501	0.2239	0.9998
ENSG00000228495	ENSG00000228495	LINC01013	6:132453054-132490514	OK	1.99396	1.26003	-0.662184	-0.666094	0.2239	0.9998
ENSG00000196083	ENSG00000196083	IL1RAP	3:190231839-190375843	OK	60.1922	78.1205	0.376125	0.705247	0.224	0.9998
ENSG00000102580	ENSG00000102580	DNAJC3	13:96329392-96447243	OK	9.86158	12.2252	0.30997	0.727553	0.2241	0.9998
ENSG00000156414	ENSG00000156414	TDRD9	14:104394798-104519004	OK	22.968	18.6691	-0.298973	-0.673325	0.2241	0.9998
ENSG00000170500	ENSG00000170500	LONRF2	2:100889752-100939195	OK	14.7275	11.2873	-0.383811	-0.700113	0.2241	0.9998
ENSG00000113583	ENSG00000113583	C5orf15	5:133291200-133304478	OK	17.1176	22.1034	0.368789	0.686718	0.22415	0.9998
ENSG00000105514	ENSG00000105514	RAB3D	19:11406823-11465620	OK	1.86243	3.36401	0.852992	0.735444	0.2242	0.9998
ENSG00000108107	ENSG00000108107	RPL28	19:55896712-55919145	OK	547.023	738.915	0.433806	0.759825	0.2242	0.9998
ENSG00000198931	ENSG00000198931	APRT	16:88875746-88878352	OK	54.6377	68.7338	0.331123	0.724993	0.2242	0.9998
ENSG00000142632	ENSG00000142632	ARHGEF19	1:16524348-16539104	OK	1.04403	1.80915	0.793147	0.655361	0.22445	0.9998
ENSG00000170315	ENSG00000170315	UBB	17:16284111-16286059	OK	1403.29	1795.69	0.35573	0.737032	0.2246	0.9998
ENSG00000257524	ENSG00000257524	RP11-203J24.9	9:130628758-130667687	OK	1.29272	0.109567	-3.56054	-0.237857	0.2246	0.9998
ENSG00000263766	ENSG00000263766	RP11-580I16.2	17:45600307-45726786	OK	1.36143	0.419435	-1.69861	-0.146957	0.2247	0.9998
ENSG00000163762	ENSG00000163762	TM4SF18	3:148947142-149052201	OK	2.22747	3.51123	0.656567	0.714419	0.22475	0.9998
ENSG00000240405	ENSG00000240405	RP11-460N16.1	3:70048727-70064469	OK	1.20875	0.687481	-0.81412	-0.66385	0.22495	0.9998
ENSG00000256417	ENSG00000256417	RP11-1038A11.3	12:5399645-5492819	OK	1.26459	0.768334	-0.718862	-0.737792	0.225	0.9998
ENSG00000163001	ENSG00000163001	CCDC104	2:55746739-55773015	OK	33.1278	25.8511	-0.357821	-0.749111	0.2251	0.9998
ENSG00000072518	ENSG00000072518	MARK2	11:63606399-63678491	OK	12.1601	9.4973	-0.35656	-0.694989	0.2252	0.9998
ENSG00000104044	ENSG00000104044	OCA2	15:28000020-28344504	OK	26.3137	21.0694	-0.320665	-0.720699	0.2252	0.9998
ENSG00000175573	ENSG00000175573	C11orf68	11:65684278-65686588	OK	22.1691	27.9785	0.335764	0.746079	0.22535	0.9998
ENSG00000255883	ENSG00000255883	AC099522.2	5:72804509-72805079	OK	0.998506	1.72287	0.786974	0.756191	0.2254	0.9998
ENSG00000114554	ENSG00000114554	PLXNA1	3:126707436-126756235	OK	61.6832	49.369	-0.321273	-0.422591	0.2257	0.9998
ENSG00000128602	ENSG00000128602	SMO	7:128828712-128853386	OK	18.543	22.9174	0.305567	0.637069	0.2258	0.9998
ENSG00000136040	ENSG00000136040	PLXNC1	12:94542498-94853764	OK	49.1753	60.4864	0.298676	0.513731	0.2258	0.9998
ENSG00000080166	ENSG00000080166	DCT	13:95089557-95131936	OK	262.132	209.667	-0.322197	-0.691752	0.226	0.9998
ENSG00000121236	ENSG00000121236	TRIM6	11:5274419-5667019	OK	2.26413	3.26981	0.530254	0.644126	0.22615	0.9998
ENSG00000179588	ENSG00000179588	ZFPM1	16:88519724-88603424	OK	0.431138	1.01306	1.2325	0.527374	0.22615	0.9998
ENSG00000271359	ENSG00000271359	RP11-84C13.1	4:90032650-90033519	OK	1.74933	2.71323	0.63321	0.749876	0.2262	0.9998
ENSG00000149289	ENSG00000149289	ZC3H12C	11:109964086-110042566	OK	9.93667	12.7422	0.358779	0.733507	0.22625	0.9998
ENSG00000104691	ENSG00000104691	UBXN8	8:30589763-30624522	OK	8.56622	11.2988	0.399436	0.676701	0.2263	0.9998
ENSG00000063245	ENSG00000063245	EPN1	19:56186591-56249768	OK	54.8057	44.6551	-0.295501	-0.721466	0.22635	0.9998
ENSG00000166927	ENSG00000166927	MS4A7	11:60102303-60185161	OK	0.746376	1.19745	0.681991	0.480651	0.22645	0.9998
ENSG00000100815	ENSG00000100815	TRIP11	14:92432334-92507240	OK	8.01934	5.34358	-0.585678	-0.60336	0.2265	0.9998
ENSG00000109062	ENSG00000109062	SLC9A3R1	17:72666716-72765492	OK	38.903	48.7915	0.326751	0.736338	0.2265	0.9998
ENSG00000197989	ENSG00000197989	SNHG12	1:28879596-28909495	OK	11.7281	17.7703	0.599494	0.718003	0.22655	0.9998
ENSG00000127507	ENSG00000127507	EMR2	19:14729928-14889353	OK	0.448608	0.913925	1.02662	0.318497	0.2267	0.9998
ENSG00000185787	ENSG00000185787	MORF4L1	15:79051544-79190475	OK	171.85	220.044	0.356647	0.706977	0.22675	0.9998
ENSG00000122694	ENSG00000122694	GLIPR2	9:36136731-36163910	OK	0.797766	1.20656	0.596868	0.703526	0.2268	0.9998
ENSG00000233476	ENSG00000233476	EEF1A1P6	7:22459062-22705152	OK	237.446	294.029	0.308358	0.745433	0.22705	0.9998
ENSG00000214595	ENSG00000214595	EML6	2:54950635-55199157	OK	1.23014	0.680816	-0.85349	-0.492599	0.2271	0.9998
ENSG00000125450	ENSG00000125450	NUP85	17:73201753-73231853	OK	31.4971	25.3396	-0.313829	-0.59695	0.2272	0.9998
ENSG00000108669	ENSG00000108669	CYTH1	17:76670129-76778379	OK	13.9962	10.7619	-0.37911	-0.615691	0.2276	0.9998
ENSG00000183696	ENSG00000183696	UPP1	7:48128224-48148330	OK	165.927	132.203	-0.327797	-0.735504	0.2276	0.9998
ENSG00000121851	ENSG00000121851	POLR3GL	1:145456235-145470388	OK	34.9838	27.4381	-0.350507	-0.726598	0.22765	0.9998
ENSG00000133138	ENSG00000133138	TBC1D8B	X:106045909-106243474	OK	3.29635	2.07278	-0.669299	-0.672244	0.22765	0.9998
ENSG00000146574	ENSG00000146574	CCZ1B	7:6793739-6866401	OK	20.5908	16.4464	-0.324223	-0.663456	0.2277	0.9998
ENSG00000142046	ENSG00000142046	TMEM91	19:41768400-41930910	OK	0.938818	2.27353	1.27602	0.169187	0.22795	0.9998
ENSG00000184979	ENSG00000184979	USP18	22:18632665-18660164	OK	1.87062	2.65067	0.502845	0.718618	0.22795	0.9998
ENSG00000179456	ENSG00000179456	ZBTB18	1:244214584-244220778	OK	9.07535	11.4021	0.32928	0.744574	0.228	0.9998
ENSG00000198081	ENSG00000198081	ZBTB14	18:5289017-5297052	OK	7.13883	5.32451	-0.42304	-0.632624	0.22805	0.9998
ENSG00000271975	ENSG00000271975	RP11-383J24.6	8:125318429-125320617	OK	1.28671	1.81295	0.494649	0.730554	0.2283	0.9998
ENSG00000163328	ENSG00000163328	GPR155	2:175296965-175351822	OK	3.18796	2.28297	-0.481722	-0.581231	0.22835	0.9998
ENSG00000146281	ENSG00000146281	PM20D2	6:89855768-89875284	OK	3.11813	4.01053	0.363108	0.719086	0.2285	0.9998
ENSG00000185924	ENSG00000185924	RTN4RL1	17:1837970-1928639	OK	3.14198	2.31371	-0.441468	-0.724195	0.2285	0.9998
ENSG00000186889	ENSG00000186889	TMEM17	2:62727355-62739029	OK	2.45535	1.75211	-0.48684	-0.742688	0.22855	0.9998
ENSG00000228486	ENSG00000228486	LINC01125	2:98280679-98319527	OK	0.787827	1.06757	0.438376	0.228346	0.2287	0.9998
ENSG00000014138	ENSG00000014138	POLA2	11:65029232-65073060	OK	16.6978	12.1269	-0.46145	-0.74113	0.22875	0.9998
ENSG00000203668	ENSG00000203668	CHML	1:241695433-241965435	OK	5.91801	3.88441	-0.607419	-0.76074	0.2288	0.9998
ENSG00000260947	ENSG00000260947	RP11-384P7.7	9:33697456-33700984	OK	0.720599	0.49022	-0.555767	-0.750908	0.2289	0.9998
ENSG00000145592	ENSG00000145592	RPL37	5:40825363-40835437	OK	3526.3	4493.53	0.349692	0.722477	0.229	0.9998
ENSG00000137714	ENSG00000137714	FDX1	11:110300606-110335605	OK	4.276	5.48316	0.358746	0.712015	0.22905	0.9998
ENSG00000169891	ENSG00000169891	REPS2	X:16964813-17171395	OK	3.04197	2.03902	-0.577131	-0.589964	0.22915	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231500	ENSG00000231500	RPS18	6:33217310-33244287	OK	4361.88	5593.09	0.358694	0.724518	0.2292	0.9998
ENSG00000101871	ENSG00000101871	MID1	X:10413349-10851773	OK	20.1914	28.9564	0.520139	0.715908	0.2295	0.9998
ENSG00000197321	ENSG00000197321	SVIL	10:29698330-30025710	OK	14.7667	10.5483	-0.485332	-0.248369	0.2295	0.9998
ENSG00000177889	ENSG00000177889	UBE2N	12:93799448-93836038	OK	116.663	86.6541	-0.429005	-0.729819	0.2296	0.9998
ENSG00000197121	ENSG00000197121	PGAP1	2:197697727-197792520	OK	4.20047	3.28625	-0.35411	-0.491204	0.2296	0.9998
ENSG00000100600	ENSG00000100600	LGMN	14:93170151-93215047	OK	23.2737	28.7973	0.307236	0.614854	0.2298	0.9998
ENSG00000168944	ENSG00000168944	CEP120	5:122680578-122759286	OK	3.38012	2.57238	-0.393969	-0.617055	0.22985	0.9998
ENSG00000189011	ENSG00000189011	AC138783.12	7:74696065-74714647	OK	3.00427	1.9043	-0.657756	-0.724616	0.23	0.9998
ENSG00000114127	ENSG00000114127	XRN1	3:142025448-142166904	OK	4.47694	5.82051	0.378633	0.391425	0.23005	0.9998
ENSG00000116497	ENSG00000116497	S100PBP	1:33240839-33324476	OK	8.88639	14.0932	0.665332	0.524446	0.2301	0.9998
ENSG00000169762	ENSG00000169762	TAPT1	4:16162127-16321763	OK	6.5063	8.92212	0.45555	0.561167	0.23015	0.9998
ENSG00000261730	ENSG00000261730	RP4-668J24.2	6:1384024-1385301	OK	0.568944	0.933403	0.714213	0.755388	0.23015	0.9998
ENSG00000197568	ENSG00000197568	HHLA3	1:70820487-70851022	OK	5.14942	3.52661	-0.54613	-0.727844	0.2302	0.9998
ENSG00000140854	ENSG00000140854	KATNB1	16:57769641-57791162	OK	6.9958	9.12993	0.384114	0.637321	0.23025	0.9998
ENSG00000138834	ENSG00000138834	MAPK8IP3	16:1756183-1821731	OK	21.8366	16.536	-0.401138	-0.419775	0.2303	0.9998
ENSG00000103202	ENSG00000103202	NME4	16:446724-462487	OK	201.287	251.657	0.322209	0.745201	0.23035	0.9998
ENSG00000092621	ENSG00000092621	PHGDH	1:120202420-120286838	OK	8.99763	11.5074	0.354949	0.710238	0.2304	0.9998
ENSG00000130997	ENSG00000130997	POLN	4:2073644-2243891	OK	0.773549	0.405335	-0.932377	-0.27627	0.2304	0.9998
ENSG00000090097	ENSG00000090097	PCBP4	3:51989329-52023213	OK	28.7145	43.5899	0.602218	0.731997	0.2305	0.9998
ENSG00000108298	ENSG00000108298	RPL19	17:37356535-37360980	OK	1833.96	2304.03	0.329197	0.732695	0.2305	0.9998
ENSG00000146433	ENSG00000146433	TMEM181	6:158957467-159056460	OK	8.34126	10.4762	0.328775	0.727744	0.2306	0.9998
ENSG00000221926	ENSG00000221926	TRIM16	17:15468796-15587625	OK	19.2242	24.1615	0.329784	0.59373	0.2306	0.9998
ENSG00000092140	ENSG00000092140	G2E3	14:30907197-31089269	OK	13.4595	10.566	-0.349199	-0.56685	0.23085	0.9998
ENSG00000227540	ENSG00000227540	RP11-152N13.5	10:74870216-75118617	OK	1.79366	0.691312	-1.3755	-0.153673	0.23085	0.9998
ENSG00000105472	ENSG00000105472	CLEC11A	19:51226585-51228974	OK	5.43207	7.20844	0.408184	0.726341	0.2311	0.9998
ENSG00000127564	ENSG00000127564	PKMYT1	16:3013944-3030540	OK	25.9875	18.269	-0.508421	-0.639152	0.2311	0.9998
ENSG00000103966	ENSG00000103966	EHD4	15:42190949-42264776	OK	13.0847	16.2317	0.310938	0.729307	0.2312	0.9998
ENSG00000154310	ENSG00000154310	TNIK	3:170779127-171178197	OK	6.69798	8.75221	0.385921	0.481074	0.2312	0.9998
ENSG00000225200	ENSG00000225200	AB019441.29	14:106444606-106445233	OK	0.413445	0.847904	1.03621	0.761113	0.23135	0.9998
ENSG00000124608	ENSG00000124608	AARS2	6:44238202-44346694	OK	20.2952	25.2576	0.315579	0.71578	0.2315	0.9998
ENSG00000110921	ENSG00000110921	MVK	12:109991541-110035067	OK	19.8664	14.6756	-0.436908	-0.682642	0.23155	0.9998
ENSG00000111052	ENSG00000111052	LIN7A	12:81186298-81650533	OK	0.558807	1.18375	1.08295	0.683416	0.23155	0.9998
ENSG00000232931	ENSG00000232931	LINC00342	2:96472865-96481963	OK	2.34701	1.62315	-0.532026	-0.696331	0.23155	0.9998
ENSG00000235703	ENSG00000235703	LINC00894	X:149097744-149392815	OK	0.443687	0.886943	0.999298	0.313151	0.23165	0.9998
ENSG00000104518	ENSG00000104518	GSDMD	8:144635376-144645232	OK	9.25223	12.1841	0.397125	0.66274	0.2318	0.9998
ENSG00000114541	ENSG00000114541	FRMD4B	3:69219140-69591734	OK	13.7499	18.7191	0.445092	0.66634	0.2318	0.9998
ENSG00000203836	ENSG00000203836	NBPF24	1:147574427-147634886	OK	1.70627	1.02255	-0.73867	-0.636895	0.2318	0.9998
ENSG00000149231	ENSG00000149231	CCDC82	11:96085932-96123087	OK	10.8818	7.81031	-0.478472	-0.659146	0.23185	0.9998
ENSG00000005486	ENSG00000005486	RHBDD2	7:75471919-75518244	OK	34.532	27.7766	-0.314064	-0.706521	0.2321	0.9998
ENSG00000137812	ENSG00000137812	CASC5	15:40886217-40956540	OK	3.50169	2.58866	-0.435845	-0.43408	0.2321	0.9998
ENSG00000144554	ENSG00000144554	FANCD2	3:10068097-10149915	OK	12.7844	8.64852	-0.563854	-0.580128	0.2321	0.9998
ENSG00000261628	ENSG00000261628	RP11-540B6.3	15:31191682-31192530	OK	1.092	0.339067	-1.68733	-0.901517	0.23215	0.9998
ENSG00000134318	ENSG00000134318	ROCK2	2:11319886-11488456	OK	10.2209	12.8716	0.332664	0.60988	0.23235	0.9998
ENSG00000225159	ENSG00000225159	NPM1P39	1:27533420-27534287	OK	13.7412	18.071	0.395164	0.740886	0.23245	0.9998
ENSG00000087338	ENSG00000087338	GMCL1	2:70056773-70108528	OK	7.37041	5.85606	-0.331815	-0.642894	0.23285	0.9998
ENSG00000175348	ENSG00000175348	TMEM9B	11:8968840-8999074	OK	43.4428	34.5122	-0.332012	-0.726207	0.23285	0.9998
ENSG00000173905	ENSG00000173905	GOLIM4	3:167726464-167813763	OK	16.5071	20.8828	0.339231	0.722985	0.2329	0.9998
ENSG00000124171	ENSG00000124171	PARD6B	20:49348080-49373332	OK	0.703692	0.995513	0.500497	0.628239	0.233	0.9998
ENSG00000014216	ENSG00000014216	CAPN1	11:64945076-64979477	OK	47.3165	57.8468	0.289894	0.573767	0.23305	0.9998
ENSG00000213445	ENSG00000213445	SIPA1	11:65405567-65418401	OK	12.627	16.3699	0.374529	0.582767	0.2331	0.9998
ENSG00000100577	ENSG00000100577	GSTZ1	14:77741298-77797940	OK	18.2428	8.87879	-1.03889	-0.753404	0.2332	0.9998
ENSG00000133619	ENSG00000133619	KRBA1	7:149411871-149431664	OK	10.7133	15.9937	0.578105	0.703825	0.2332	0.9998
ENSG00000182405	ENSG00000182405	PGBD4	15:34394273-34396591	OK	0.811304	0.550922	-0.558393	-0.70509	0.23325	0.9998
ENSG00000180881	ENSG00000180881	CAPS2	12:75628519-75784708	OK	1.88768	1.11991	-0.753235	-0.627598	0.2333	0.9998
ENSG00000269636	ENSG00000269636	AC010441.1	5:150157507-150176297	OK	4.52492	3.39598	-0.414064	-0.716315	0.2333	0.9998
ENSG00000113161	ENSG00000113161	HMGCR	5:74615979-74657929	OK	63.3209	51.4799	-0.298672	-0.516952	0.2335	0.9998
ENSG00000128228	ENSG00000128228	SDF2L1	22:21996549-21998587	OK	58.0174	46.4058	-0.322182	-0.715027	0.23355	0.9998
ENSG00000234129	ENSG00000234129	RP11-120D5.1	X:10865995-11129261	OK	0.951369	0.499829	-0.928572	-0.691694	0.23365	0.9998
ENSG00000230715	ENSG00000230715	RP11-274B21.4	7:128292894-128293719	OK	11.7094	8.184	-0.516794	-0.717218	0.2337	0.9998
ENSG00000205362	ENSG00000205362	MT1A	16:56672577-56673999	OK	0.25658	0.694461	1.43649	0.726899	0.23375	0.9998
ENSG00000064313	ENSG00000064313	TAF2	8:120743014-120845103	OK	15.2833	11.9192	-0.35867	-0.619132	0.23385	0.9998
ENSG00000072501	ENSG00000072501	SMC1A	X:53401069-53458059	OK	25.7477	38.5318	0.581605	0.735242	0.2339	0.9998
ENSG00000100027	ENSG00000100027	YPEL1	22:22006558-22090123	OK	0.635795	0.178867	-1.82968	-0.368675	0.23395	0.9998
ENSG00000240618	ENSG00000240618	RP11-206L10.5	1:694411-714006	OK	1.63039	0.184322	-3.14491	-0.995328	0.2341	0.9998
ENSG00000204439	ENSG00000204439	C6orf47	6:31626074-31628549	OK	11.554	9.12371	-0.340693	-0.716232	0.23415	0.9998
ENSG00000217241	ENSG00000217241	CBX3P9	6:116774176-116774728	OK	4.91085	7.05915	0.523522	0.705414	0.23435	0.9998
ENSG00000144736	ENSG00000144736	SHQ1	3:72798427-72911065	OK	9.80827	7.70779	-0.347682	-0.648947	0.23445	0.9998
ENSG00000206190	ENSG00000206190	ATP10A	15:25922419-26110317	OK	0.977299	1.34155	0.457025	0.484528	0.23455	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000115009	ENSG00000115009	CCL20	2:228678557-228682272	OK	2.02572	1.30574	-0.633567	-0.671296	0.2346	0.9998
ENSG00000236565	ENSG00000236565	HNRNPA3P5	13:66362063-66362896	OK	24.3871	14.8322	-0.717388	-0.723289	0.2346	0.9998
ENSG00000100897	ENSG00000100897	DCAF11	14:24549315-24602058	OK	25.9067	20.4525	-0.341051	-0.546983	0.23465	0.9998
ENSG00000135116	ENSG00000135116	HRK	12:117293948-117319246	OK	2.28321	2.96312	0.376054	0.606817	0.23465	0.9998
ENSG00000101224	ENSG00000101224	CDC25B	20:3767577-3786762	OK	25.761	20.7902	-0.309287	-0.664077	0.2347	0.9998
ENSG00000135074	ENSG00000135074	ADAM19	5:156687131-157002783	OK	2.00262	3.01235	0.589003	0.652809	0.23475	0.9998
ENSG00000227081	ENSG00000227081	RP11-543P15.1	12:3186520-3395730	OK	1386.3	1720.35	0.311469	0.723204	0.23475	0.9998
ENSG00000197256	ENSG00000197256	KANK2	19:11274942-11308467	OK	44.3086	31.8989	-0.474081	-0.649964	0.23505	0.9998
ENSG00000225697	ENSG00000225697	SLC26A6	3:48663155-48672926	OK	49.9011	64.5454	0.371242	0.543471	0.2353	0.9998
ENSG00000120875	ENSG00000120875	DUSP4	8:29190580-29208185	OK	129.336	159.051	0.298362	0.710541	0.23545	0.9998
ENSG00000120798	ENSG00000120798	NR2C1	12:95414004-95467479	OK	20.1992	15.118	-0.418039	-0.661658	0.2355	0.9998
ENSG00000186481	ENSG00000186481	ANKRD20A5P	18:14179095-14252139	OK	1.33943	2.01806	0.591354	0.560563	0.2355	0.9998
ENSG00000250571	ENSG00000250571	GLI4	8:144328990-144359101	OK	7.54377	4.81393	-0.64807	-0.627633	0.23555	0.9998
ENSG00000152558	ENSG00000152558	TMEM123	11:102267062-102369532	OK	89.5432	64.7249	-0.468263	-0.699917	0.2356	0.9998
ENSG00000127314	ENSG00000127314	RAP1B	12:69004618-69054372	OK	59.9926	78.3989	0.386049	0.729362	0.2358	0.9998
ENSG00000082805	ENSG00000082805	ERC1	12:1021242-1605099	OK	7.53942	9.71496	0.365754	0.380977	0.23585	0.9998
ENSG00000228300	ENSG00000228300	C19orf24	19:1275025-1279248	OK	50.2564	64.6553	0.363462	0.730292	0.23585	0.9998
ENSG00000143341	ENSG00000143341	HMCN1	1:185703682-186160085	OK	42.5707	30.0494	-0.502527	-0.436678	0.236	0.9998
ENSG00000165732	ENSG00000165732	DDX21	10:70715883-70744829	OK	38.0267	46.1669	0.279848	0.700354	0.23605	0.9998
ENSG00000102181	ENSG00000102181	CD99L2	X:149934809-150067289	OK	19.018	15.2449	-0.319034	-0.66481	0.23625	0.9998
ENSG00000185697	ENSG00000185697	MYBL1	8:67474409-67526482	OK	8.30046	6.41772	-0.371132	-0.682897	0.2363	0.9998
ENSG00000187955	ENSG00000187955	COL14A1	8:121072018-121384275	OK	8.99957	7.29061	-0.303816	-0.674125	0.2363	0.9998
ENSG00000140525	ENSG00000140525	FANCI	15:89787179-89878092	OK	50.8896	38.1932	-0.414054	-0.376505	0.2364	0.9998
ENSG00000169446	ENSG00000169446	MMGT1	X:135044228-135056222	OK	15.1002	18.6332	0.303315	0.725344	0.2364	0.9998
ENSG00000237749	ENSG00000237749	RP3-423B22.5	1:38021842-38022108	OK	3.3041	5.89682	0.835679	0.719442	0.2364	0.9998
ENSG00000113645	ENSG00000113645	WWC1	5:167718655-167899308	OK	8.2412	10.8141	0.391989	0.545742	0.23645	0.9998
ENSG00000156787	ENSG00000156787	TBC1D31	8:124014799-124164393	OK	7.73965	4.69812	-0.720184	-0.626139	0.23655	0.9998
ENSG00000070501	ENSG00000070501	POLB	8:42195971-42229326	OK	56.3719	70.8407	0.329602	0.722816	0.2368	0.9998
ENSG00000088756	ENSG00000088756	ARHGAP28	18:6728819-6915715	OK	2.25094	3.01998	0.42401	0.4947	0.2369	0.9998
ENSG00000213178	ENSG00000213178	RP11-641D5.1	3:168801286-169381406	OK	447.568	549.438	0.29585	0.719241	0.23695	0.9998
ENSG00000125630	ENSG00000125630	POLR1B	2:113299491-113334635	OK	11.0663	14.0017	0.339428	0.52459	0.237	0.9998
ENSG00000167526	ENSG00000167526	RPL13	16:89627064-89630950	OK	1030.79	1273.91	0.305506	0.721083	0.23705	0.9998
ENSG00000105711	ENSG00000105711	SCN1B	19:35521587-35531352	OK	6.57806	9.03375	0.457664	0.726017	0.2371	0.9998
ENSG00000184949	ENSG00000184949	FAM227A	22:38974124-39052634	OK	0.889269	0.5485	-0.697126	-0.409142	0.23735	0.9998
ENSG00000188467	ENSG00000188467	SLC24A5	15:48413168-48470714	OK	111.493	89.3157	-0.319963	-0.715954	0.2376	0.9998
ENSG00000085449	ENSG00000085449	WDFY1	2:224720432-224810104	OK	98.0744	119.26	0.282162	0.489823	0.2377	0.9998
ENSG00000151229	ENSG00000151229	SLC2A13	12:40019968-40499891	OK	4.91755	3.76862	-0.383904	-0.506523	0.2377	0.9998
ENSG00000108774	ENSG00000108774	RAB5C	17:40265125-40307990	OK	122.862	153.549	0.321652	0.706577	0.23785	0.9998
ENSG00000173890	ENSG00000173890	GPR160	3:169755716-169803191	OK	6.00022	4.50437	-0.413691	-0.65199	0.23785	0.9998
ENSG00000180801	ENSG00000180801	ARSJ	4:114821439-114900883	OK	0.6871	1.04902	0.610451	0.70446	0.23785	0.9998
ENSG00000260158	ENSG00000260158	RP11-67H24.2	16:32820876-32835966	OK	1.33795	0.391967	-1.77122	-1.35009	0.238	0.9998
ENSG00000235720	ENSG00000235720	RP11-340I6.6	7:63348577-63361113	OK	1.14828	0.750804	-0.612961	-0.722717	0.23805	0.9998
ENSG00000070778	ENSG00000070778	PTPN21	14:88851267-89021077	OK	3.6975	2.58702	-0.515259	-0.58748	0.23815	0.9998
ENSG00000182352	ENSG00000182352	C17orf77	17:72575503-72590348	OK	1.17202	0.642149	-0.868021	-0.705149	0.23855	0.9998
ENSG00000138134	ENSG00000138134	STAMBPL1	10:90639490-90775542	OK	6.128	8.57771	0.485176	0.715785	0.23865	0.9998
ENSG00000185252	ENSG00000185252	ZNF74	22:20748404-20762745	OK	6.47917	8.24628	0.347935	0.70982	0.2387	0.9998
ENSG00000137309	ENSG00000137309	HMGA1	6:34204649-34214008	OK	77.2891	94.4169	0.288779	0.721495	0.23875	0.9998
ENSG00000142156	ENSG00000142156	COL6A1	21:47401650-47424964	OK	1.16748	1.71372	0.55373	0.602643	0.23875	0.9998
ENSG00000178860	ENSG00000178860	MSC	8:72740401-73030628	OK	3.27903	5.29783	0.692133	0.698654	0.23885	0.9998
ENSG00000196511	ENSG00000196511	TPK1	7:144149033-144533488	OK	2.64699	1.59368	-0.731993	-0.578688	0.23895	0.9998
ENSG00000197372	ENSG00000197372	ZNF675	19:23708432-23870022	OK	2.05288	1.41703	-0.534777	-0.583742	0.23895	0.9998
ENSG00000129691	ENSG00000129691	ASH2L	8:37962759-38070819	OK	31.5568	23.1317	-0.448084	-0.649766	0.23925	0.9998
ENSG00000255320	ENSG00000255320	RP11-755F10.1	11:66012310-66013710	OK	1.00762	0.39187	-1.3625	-0.867113	0.23925	0.9998
ENSG00000115648	ENSG00000115648	MLPH	2:238394070-238463961	OK	293.954	229.573	-0.356639	-0.708097	0.23955	0.9998
ENSG00000188505	ENSG00000188505	NCCRP1	19:39687600-39692524	OK	0.439495	0.706519	0.684884	0.735515	0.23955	0.9998
ENSG00000115268	ENSG00000115268	RPS15	19:1438357-1440583	OK	1006.49	1235.86	0.296192	0.711598	0.23975	0.9998
ENSG00000175198	ENSG00000175198	PCCA	13:100741268-101182686	OK	6.84815	9.19618	0.42532	0.597093	0.23985	0.9998
ENSG00000205464	ENSG00000205464	ATP6AP1L	5:81575280-81682796	OK	1.43701	0.844436	-0.767006	-0.714169	0.2399	0.9998
ENSG00000171448	ENSG00000171448	ZBTB26	9:125677844-125693779	OK	4.14547	3.12823	-0.406191	-0.725321	0.23995	0.9998
ENSG00000099624	ENSG00000099624	ATP5D	19:1241748-1244824	OK	75.5159	94.2995	0.32047	0.726679	0.24005	0.9998
ENSG00000257923	ENSG00000257923	CUX1	7:101458958-101927249	OK	36.5379	26.8193	-0.446121	-0.63482	0.24005	0.9998
ENSG00000184164	ENSG00000184164	CRELD2	22:50293876-50321188	OK	42.8117	32.8975	-0.380025	-0.723346	0.2404	0.9998
ENSG00000187049	ENSG00000187049	TMEM216	11:61159158-61166335	OK	1.99977	2.91661	0.544456	0.635016	0.2406	0.9998
ENSG00000102796	ENSG00000102796	DHRS12	13:52342128-52378293	OK	8.65065	6.23145	-0.473242	-0.66795	0.2407	0.9998
ENSG00000170903	ENSG00000170903	MSANTD4	11:105866349-105893130	OK	8.09929	5.7547	-0.493055	-0.689496	0.24085	0.9998
ENSG00000175595	ENSG00000175595	ERCC4	16:14014013-14046202	OK	3.82475	5.32113	0.476366	0.526298	0.2409	0.9998
ENSG00000012174	ENSG00000012174	MBTPS2	X:21857753-21903542	OK	10.7132	13.309	0.313019	0.715139	0.24115	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000132688	ENSG00000132688	NES	1:156638554-156647189	OK	14.726	18.2194	0.307112	0.704368	0.24115	0.9998
ENSG00000089737	ENSG00000089737	DDX24	14:94517265-94547591	OK	58.9228	71.9449	0.288066	0.70068	0.24125	0.9998
ENSG00000259623	ENSG00000259623	RP11-156E6.1	17:40004769-40007699	OK	3.07191	2.3348	-0.395834	-0.700318	0.2413	0.9998
ENSG00000122735	ENSG00000122735	DNAI1	9:34398181-34520982	OK	1.53675	0.731304	-1.07134	-0.330205	0.2415	0.9998
ENSG00000108932	ENSG00000108932	SLC16A6	17:66255322-66760023	OK	96.5375	144.636	0.58327	0.716798	0.2417	0.9998
ENSG00000227008	ENSG00000227008	RP3-417G15.1	X:132669772-133119922	OK	154.472	197.733	0.356207	0.711085	0.24205	0.9998
ENSG00000180758	ENSG00000180758	GPR157	1:9160363-9189229	OK	4.35606	5.79479	0.411733	0.533287	0.24225	0.9998
ENSG00000119772	ENSG00000119772	DNMT3A	2:25455844-25565459	OK	6.18213	8.01147	0.373961	0.571238	0.24235	0.9998
ENSG00000244509	ENSG00000244509	APOBEC3C	22:39410087-39429281	OK	18.6166	23.2374	0.319861	0.714999	0.24255	0.9998
ENSG00000105655	ENSG00000105655	ISYNA1	19:18529673-18549111	OK	20.9461	29.0835	0.473519	0.641355	0.2427	0.9998
ENSG00000114923	ENSG00000114923	SLC4A3	2:220492048-220506702	OK	2.62766	3.48378	0.406875	0.613964	0.2427	0.9998
ENSG00000128408	ENSG00000128408	RIBC2	22:45809571-45828376	OK	1.19463	0.553667	-1.10948	-0.805143	0.2427	0.9998
ENSG00000104472	ENSG00000104472	CHRAC1	8:141521396-141527236	OK	21.8574	15.8352	-0.464983	-0.710149	0.24305	0.9998
ENSG00000122126	ENSG00000122126	OCRL	X:128673825-128726538	OK	11.0619	13.6565	0.303993	0.687815	0.24305	0.9998
ENSG00000169330	ENSG00000169330	KIAA1024	15:79724857-79764632	OK	0.942775	0.694826	-0.440262	-0.717615	0.24315	0.9998
ENSG00000167658	ENSG00000167658	EEF2	19:3976053-3985467	OK	955.409	1232.16	0.367003	0.573561	0.24325	0.9998
ENSG00000166004	ENSG00000166004	KIAA1731	11:93394804-93547861	OK	3.09398	1.8399	-0.749834	-0.552367	0.2433	0.9998
ENSG00000106682	ENSG00000106682	EIF4H	7:73588574-73611431	OK	183.383	150.875	-0.281508	-0.688939	0.24345	0.9998
ENSG00000100485	ENSG00000100485	SOS2	14:50583846-50698276	OK	8.19065	10.2257	0.320151	0.654387	0.2437	0.9998
ENSG00000111247	ENSG00000111247	RAD51AP1	12:4647949-4669214	OK	21.1393	15.7684	-0.422892	-0.708221	0.2437	0.9998
ENSG00000100092	ENSG00000100092	SH3BP1	22:38030660-38062941	OK	7.93304	11.1403	0.489848	0.609614	0.24375	0.9998
ENSG00000130193	ENSG00000130193	THEM6	8:143808620-143818345	OK	12.7842	10.1611	-0.331307	-0.704774	0.24375	0.9998
ENSG00000130695	ENSG00000130695	CEP85	1:26560690-26605299	OK	9.89616	7.84174	-0.335696	-0.602895	0.24375	0.9998
ENSG00000010292	ENSG00000010292	NCAPD2	12:6601149-6641121	OK	40.9995	31.6195	-0.374794	-0.519601	0.24425	0.9998
ENSG00000125877	ENSG00000125877	ITPA	20:3189513-3204516	OK	22.3636	28.4113	0.345312	0.715792	0.2443	0.9998
ENSG00000141858	ENSG00000141858	SAMD1	19:14198651-14201848	OK	8.26641	11.2244	0.441305	0.685342	0.2444	0.9998
ENSG00000168300	ENSG00000168300	PCMTD1	8:52730139-52811735	OK	15.5521	11.8061	-0.397583	-0.68402	0.2445	0.9998
ENSG00000128829	ENSG00000128829	EIF2AK4	15:40226346-40327797	OK	8.23284	10.1314	0.299378	0.613851	0.2446	0.9998
ENSG00000175137	ENSG00000175137	SH3BP5L	1:249104647-249120832	OK	13.1546	10.1024	-0.380869	-0.65791	0.24465	0.9998
ENSG00000243137	ENSG00000243137	PSG4	19:43696853-43711451	OK	36.4789	46.0574	0.336372	0.681056	0.2449	0.9998
ENSG00000099377	ENSG00000099377	HSD3B7	16:30996518-31000473	OK	6.24738	8.28113	0.406575	0.69874	0.24505	0.9998
ENSG00000172062	ENSG00000172062	SMN1	5:70220767-70249769	OK	11.5351	9.00558	-0.357137	-0.681635	0.2453	0.9998
ENSG00000120063	ENSG00000120063	GNA13	17:63006832-63052957	OK	46.9477	38.5684	-0.283637	-0.690707	0.2454	0.9998
ENSG00000172318	ENSG00000172318	B3GALT1	2:168671283-168797654	OK	0.588342	0.873436	0.570046	0.695877	0.2454	0.9998
ENSG00000228412	ENSG00000228412	RP4-625H18.2	6:19535174-19840915	OK	1.80471	0.620822	-1.53951	-0.302615	0.2455	0.9998
ENSG00000186594	ENSG00000186594	MIR22HG	17:1614804-1641893	OK	5.71239	8.18135	0.518243	0.4704	0.24555	0.9998
ENSG00000135541	ENSG00000135541	AHI1	6:135604669-136037193	OK	5.37693	3.9478	-0.445735	-0.497182	0.24585	0.9998
ENSG00000161179	ENSG00000161179	YDJC	22:21982377-21984353	OK	17.8986	22.7426	0.345549	0.717656	0.24585	0.9998
ENSG00000085644	ENSG00000085644	ZNF213	16:3160460-3192806	OK	3.49775	2.37395	-0.559137	-0.609794	0.246	0.9998
ENSG00000203813	ENSG00000203813	HIST1H3H	6:27777841-27778314	OK	0.42976	0.915362	1.09081	0.709636	0.2461	0.9998
ENSG00000134107	ENSG00000134107	BHLHE40	3:4938492-5027008	OK	51.565	41.813	-0.302442	-0.579404	0.24625	0.9998
ENSG00000086598	ENSG00000086598	TMED2	12:124066766-124083116	OK	99.3196	124.165	0.322107	0.589534	0.2464	0.9998
ENSG00000160789	ENSG00000160789	LMNA	1:156052363-156109880	OK	513.448	634.535	0.30548	0.656985	0.2464	0.9998
ENSG00000196605	ENSG00000196605	ZNF846	19:9862668-9903856	OK	2.83813	1.79168	-0.663628	-0.677791	0.2465	0.9998
ENSG00000181472	ENSG00000181472	ZBTB2	6:151685251-151712683	OK	5.19709	6.57771	0.339882	0.689222	0.24655	0.9998
ENSG00000189362	ENSG00000189362	TMEM194B	2:191273080-191399448	OK	2.9071	1.49437	-0.960038	-0.428281	0.2467	0.9998
ENSG00000166147	ENSG00000166147	FBN1	15:48700502-48938046	OK	0.439309	0.79236	0.850918	0.51773	0.24675	0.9998
ENSG00000239873	ENSG00000239873	GAPDHP27	1:120101377-120102397	OK	0.39315	0.699334	0.830901	0.711941	0.24675	0.9998
ENSG00000101596	ENSG00000101596	SMCHD1	18:2655736-2833063	OK	10.3861	8.30606	-0.322418	-0.50654	0.24695	0.9998
ENSG00000069493	ENSG00000069493	CLEC2D	12:9817564-9848823	OK	4.01908	2.41344	-0.735778	-0.59538	0.24705	0.9998
ENSG00000135414	ENSG00000135414	GDF11	12:56137063-56236750	OK	7.10018	12.1681	0.777176	0.684178	0.24705	0.9998
ENSG00000169895	ENSG00000169895	SYAP1	X:16737754-16783459	OK	18.1147	14.0679	-0.364758	-0.523858	0.24705	0.9998
ENSG00000196954	ENSG00000196954	CASP4	11:104813592-104840163	OK	19.1468	14.8161	-0.369943	-0.704407	0.2472	0.9998
ENSG00000214021	ENSG00000214021	TTLL3	3:9791627-9896822	OK	5.96413	3.75691	-0.666765	-0.185848	0.2472	0.9998
ENSG00000119632	ENSG00000119632	IFI27L2	14:94594115-94596590	OK	80.639	64.0294	-0.332743	-0.704996	0.2473	0.9998
ENSG00000124614	ENSG00000124614	RPS10	6:34247455-34393902	OK	972.339	1238.78	0.349387	0.727412	0.2475	0.9998
ENSG00000158813	ENSG00000158813	EDA	X:68835910-69259319	OK	0.683043	0.993916	0.541147	0.413944	0.2475	0.9998
ENSG00000135362	ENSG00000135362	PRR5L	11:36317837-36486754	OK	3.7997	2.81952	-0.430436	-0.448749	0.2477	0.9998
ENSG00000179271	ENSG00000179271	GADD45GIP1	19:13064971-13068050	OK	106.035	129.934	0.293235	0.703897	0.24775	0.9998
ENSG00000165516	ENSG00000165516	KLHDC2	14:50234325-50249909	OK	21.2883	17.0732	-0.318324	-0.658969	0.24785	0.9998
ENSG00000178404	ENSG00000178404	DDC8	17:76849058-76921469	OK	0.405582	1.05101	1.37371	0.0456272	0.2479	0.9998
ENSG00000099968	ENSG00000099968	BCL2L13	22:18111620-18213388	OK	67.0138	53.667	-0.320424	-0.666435	0.24805	0.9998
ENSG00000164104	ENSG00000164104	HMGB2	4:174252845-174256276	OK	113.015	91.8162	-0.299689	-0.702353	0.24835	0.9998
ENSG00000112118	ENSG00000112118	MCM3	6:52128806-52149679	OK	46.9665	37.5775	-0.32176	-0.689279	0.2485	0.9998
ENSG00000197756	ENSG00000197756	RPL37A	2:217250010-217443903	OK	2874.73	3621.8	0.333282	0.724446	0.2485	0.9998
ENSG00000104325	ENSG00000104325	DECR1	8:90945563-91064320	OK	42.1406	29.9413	-0.493077	-0.670914	0.2486	0.9998
ENSG00000125378	ENSG00000125378	BMP4	14:54416453-54425479	OK	1.62	2.30083	0.50616	0.565172	0.24865	0.9998
ENSG00000115762	ENSG00000115762	PLEKHB2	2:131862419-132111282	OK	37.0231	45.2969	0.290987	0.670894	0.2487	0.9998
ENSG00000130303	ENSG00000130303	BST2	19:17513747-17516457	OK	0.929172	1.46304	0.654951	0.581565	0.2488	0.9998
ENSG00000103187	ENSG00000103187	COTL1	16:84599199-84651683	OK	53.4745	65.09	0.283584	0.669489	0.24885	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000117298	ENSG00000117298	ECE1	1:21543739-21671997	OK	6.16781	7.94093	0.36455	0.557932	0.24885	0.9998
ENSG00000124785	ENSG00000124785	NRN1	6:5998231-6007200	OK	2.44157	1.62817	-0.584557	-0.72331	0.24895	0.9998
ENSG00000155827	ENSG00000155827	RNF20	9:104296132-104325622	OK	21.6138	17.262	-0.324355	-0.596799	0.24905	0.9998
ENSG00000158864	ENSG00000158864	NDUFS2	1:161154097-161184185	OK	120.588	98.1456	-0.29709	-0.669525	0.24935	0.9998
ENSG00000180340	ENSG00000180340	FZD2	17:42634924-42636907	OK	1.76266	2.43116	0.463891	0.718859	0.24935	0.9998
ENSG00000270055	ENSG00000270055	CTD-3092A11.2	15:30762981-30799826	OK	2.07842	1.49515	-0.475195	-0.707322	0.24935	0.9998
ENSG00000176531	ENSG00000176531	PHLDB3	19:43979105-44009087	OK	10.4517	14.3216	0.454462	0.669628	0.24955	0.9998
ENSG00000000003	ENSG00000000003	TSPAN6	X:99883666-99894988	OK	16.1828	20.185	0.318816	0.694268	0.2496	0.9998
ENSG00000173918	ENSG00000173918	C1QTNF1	17:77015290-77045870	OK	23.2611	18.6931	-0.315417	-0.657848	0.2496	0.9998
ENSG00000226124	ENSG00000226124	FTCDNL1	2:200625266-200715896	OK	1.55964	2.34621	0.589121	0.713861	0.2496	0.9998
ENSG00000034152	ENSG00000034152	MAP2K3	17:21187983-21218552	OK	37.1541	45.8025	0.301906	0.641031	0.24965	0.9998
ENSG00000139433	ENSG00000139433	GLTP	12:110288747-110318293	OK	20.9897	16.9413	-0.309139	-0.635937	0.24975	0.9998
ENSG00000068912	ENSG00000068912	ERLEC1	2:53759809-54087297	OK	35.5977	27.5861	-0.36784	-0.604598	0.25	0.9998
ENSG00000167460	ENSG00000167460	TPM4	19:16177830-16213813	OK	80.1667	65.5713	-0.289938	-0.613132	0.25005	0.9998
ENSG00000118985	ENSG00000118985	ELL2	5:95220801-96143803	OK	5.77375	9.97836	0.789295	0.350016	0.2503	0.9998
ENSG00000173726	ENSG00000173726	TOMM20	1:235272650-235292251	OK	113.897	137.966	0.276578	0.604298	0.25035	0.9998
ENSG00000155868	ENSG00000155868	MED7	5:156512842-156682201	OK	10.0057	7.56024	-0.404318	-0.697506	0.2506	0.9998
ENSG00000138138	ENSG00000138138	ATAD1	10:89511268-89605369	OK	53.051	42.1222	-0.332799	-0.70227	0.2507	0.9998
ENSG00000181544	ENSG00000181544	FANCB	X:14861528-14891191	OK	3.28437	2.34162	-0.488106	-0.611508	0.2508	0.9998
ENSG00000186376	ENSG00000186376	ZNF75D	X:134382866-134478012	OK	1.56077	1.15606	-0.43305	-0.669093	0.2508	0.9998
ENSG00000107625	ENSG00000107625	DDX50	10:70661033-70706603	OK	27.938	22.5265	-0.310609	-0.662856	0.25095	0.9998
ENSG00000147889	ENSG00000147889	CDKN2A	9:21802541-22121096	OK	24.0049	40.3077	0.747726	0.652115	0.25105	0.9998
ENSG00000272086	ENSG00000272086	CTD-2186M15.3	5:32174576-32175378	OK	0.651183	1.0865	0.738552	0.697042	0.25105	0.9998
ENSG00000133997	ENSG00000133997	MED6	14:71047973-71108015	OK	19.6532	25.3643	0.368034	0.714511	0.25125	0.9998
ENSG00000183674	ENSG00000183674	LINC00518	6:10429487-10457014	OK	42.884	34.0418	-0.333131	-0.708286	0.2514	0.9998
ENSG00000125968	ENSG00000125968	ID1	20:30193085-30194318	OK	12.41	16.2189	0.386178	0.707415	0.25145	0.9998
ENSG00000094841	ENSG00000094841	UPRT	X:74493919-74524435	OK	4.47835	5.83307	0.381287	0.677907	0.25155	0.9998
ENSG00000181019	ENSG00000181019	NQO1	16:69740898-69760854	OK	772.151	962.312	0.317622	0.698853	0.25155	0.9998
ENSG00000196155	ENSG00000196155	PLEKHG4	16:67311412-67360666	OK	10.0609	12.8657	0.354765	0.514397	0.25155	0.9998
ENSG00000137693	ENSG00000137693	YAP1	11:101981191-102104154	OK	21.7117	16.6148	-0.386005	-0.698202	0.25165	0.9998
ENSG00000231999	ENSG00000231999	RP5-1007M22.2	1:89990394-90402170	OK	0.676269	0.271623	-1.31599	-0.178766	0.2517	0.9998
ENSG00000144857	ENSG00000144857	BOC	3:112929849-113160457	OK	3.91678	6.26508	0.677664	0.60109	0.25195	0.9998
ENSG00000240972	ENSG00000240972	MIF	22:24198613-24241117	OK	954.904	1222.63	0.356561	0.712005	0.252	0.9998
ENSG00000141140	ENSG00000141140	MYO19	17:34842472-34899284	OK	27.6038	21.3228	-0.372472	-0.473318	0.25205	0.9998
ENSG00000113621	ENSG00000113621	TXNDC15	5:134209492-134237215	OK	11.2552	15.2864	0.441653	0.686555	0.2521	0.9998
ENSG00000122674	ENSG00000122674	CCZ1	7:5938355-6010314	OK	23.6203	18.8846	-0.322811	-0.65159	0.25215	0.9998
ENSG00000204335	ENSG00000204335	SP5	2:171571860-171574588	OK	0.532704	0.852301	0.678029	0.496315	0.25215	0.9998
ENSG00000183763	ENSG00000183763	TRAIP	3:49866033-49894007	OK	8.3355	6.18596	-0.43027	-0.614717	0.2523	0.9998
ENSG00000001084	ENSG00000001084	GCLC	6:53362138-53481969	OK	14.5603	19.1915	0.398427	0.56874	0.25235	0.9998
ENSG00000112306	ENSG00000112306	RPS12	6:133135579-133138703	OK	2104.39	2617.61	0.314848	0.703899	0.25235	0.9998
ENSG00000058262	ENSG00000058262	SEC61A1	3:127770483-128127485	OK	128.385	159.231	0.310643	0.579403	0.25245	0.9998
ENSG00000101294	ENSG00000101294	HM13	20:30102230-30161066	OK	121.438	146.686	0.272517	0.630113	0.25245	0.9998
ENSG00000260141	ENSG00000260141	RP11-19N8.4	16:33054929-33140411	OK	2.35278	1.16002	-1.02022	-0.730218	0.25255	0.9998
ENSG00000150510	ENSG00000150510	FAM124A	13:51796502-51858377	OK	4.58876	3.43069	-0.419605	-0.623873	0.25265	0.9998
ENSG00000137575	ENSG00000137575	SDCBP	8:59465482-59495419	OK	636.484	790.195	0.312085	0.681553	0.2527	0.9998
ENSG00000232434	ENSG00000232434	C9orf172	9:139738866-139741797	OK	0.501217	0.723003	0.528566	0.684473	0.25275	0.9998
ENSG00000100372	ENSG00000100372	SLC25A17	22:41165633-41215403	OK	26.8182	21.4473	-0.32242	-0.656929	0.2528	0.9998
ENSG00000272645	ENSG00000272645	RP11-504P24.8	1:224139095-224141141	OK	3.19097	2.35604	-0.437631	-0.704491	0.25285	0.9998
ENSG00000237238	ENSG00000237238	BMS1P10	9:67327774-67334983	OK	1.37462	0.909665	-0.59562	-0.69593	0.25295	0.9998
ENSG00000232742	ENSG00000232742	RHOQP2	2:132218532-132219150	OK	43.9596	55.5591	0.337845	0.694454	0.253	0.9998
ENSG00000189060	ENSG00000189060	H1F0	22:38201113-38203442	OK	70.7335	58.4843	-0.274346	-0.685492	0.25305	0.9998
ENSG00000156970	ENSG00000156970	BUB1B	15:40453223-40569688	OK	16.9072	13.5584	-0.318443	-0.513935	0.25325	0.9998
ENSG00000007944	ENSG00000007944	MYLIP	6:16129355-16148479	OK	45.8634	56.3178	0.296246	0.698166	0.2534	0.9998
ENSG00000246898	ENSG00000246898	LINC00920	16:66442426-66446038	OK	3.67665	2.75192	-0.417953	-0.704615	0.2536	0.9998
ENSG00000101544	ENSG00000101544	ADNP2	18:77866914-77905406	OK	5.93391	7.40313	0.319152	0.567228	0.25365	0.9998
ENSG00000112902	ENSG00000112902	SEMA5A	5:9001885-9546187	OK	75.4205	59.1032	-0.35172	-0.430485	0.25365	0.9998
ENSG00000166441	ENSG00000166441	RPL27A	11:8703957-8932498	OK	1693.73	2160.7	0.351291	0.691828	0.25365	0.9998
ENSG00000144136	ENSG00000144136	SLC20A1	2:113403433-113421404	OK	22.7786	27.6734	0.280822	0.529159	0.25385	0.9998
ENSG00000168288	ENSG00000168288	MMADHC	2:150426147-150715705	OK	39.7618	48.7394	0.293706	0.689956	0.25395	0.9998
ENSG00000188895	ENSG00000188895	MSL1	17:38278550-38293042	OK	32.9165	26.3352	-0.321819	-0.64658	0.2542	0.9998
ENSG00000267102	ENSG00000267102	RP11-686D22.7	17:33733702-33737247	OK	0.451046	1.31218	1.54062	0.960829	0.25425	0.9998
ENSG00000124688	ENSG00000124688	MAD2L1BP	6:43597276-43608689	OK	76.1275	92.5905	0.282447	0.678871	0.2543	0.9998
ENSG00000161551	ENSG00000161551	ZNF577	19:52359054-52408293	OK	4.39203	6.84269	0.639677	0.565312	0.2543	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000166352	ENSG00000166352	C11orf74	11:36532258-36694823	OK	34.1571	26.1895	-0.383194	-0.691884	0.25435	0.9998
ENSG00000170779	ENSG00000170779	CDCA4	14:105452111-105487485	OK	34.4626	27.6818	-0.316095	-0.695823	0.25455	0.9998
ENSG00000065883	ENSG00000065883	CDK13	7:39989635-40136733	OK	7.9713	9.90651	0.313562	0.617822	0.2546	0.9998
ENSG00000131019	ENSG00000131019	ULBP3	6:150384285-150390231	OK	1.18701	1.80937	0.608155	0.666409	0.2548	0.9998
ENSG00000168490	ENSG00000168490	PHYHIP	8:22077221-22089854	OK	0.654702	1.02954	0.653095	0.575393	0.2548	0.9998
ENSG00000239474	ENSG00000239474	KLHL41	2:170335687-170382772	OK	0.774073	2.51028	1.69731	0.707366	0.2548	0.9998
ENSG00000125611	ENSG00000125611	CHCHD5	2:113341816-113372008	OK	30.9039	23.999	-0.364814	-0.695539	0.25485	0.9998
ENSG00000198795	ENSG00000198795	ZNF521	18:22641889-22932154	OK	0.836842	0.539656	-0.632917	-0.303799	0.2549	0.9998
ENSG00000159842	ENSG00000159842	ABR	17:900356-1132315	OK	52.5609	64.3665	0.292322	0.406716	0.25495	0.9998
ENSG00000089597	ENSG00000089597	GANAB	11:62392297-62414104	OK	168.705	139.513	-0.274101	-0.581376	0.2551	0.9998
ENSG00000123146	ENSG00000123146	CD97	19:14491312-14519537	OK	11.7841	15.0134	0.34941	0.567591	0.2554	0.9998
ENSG00000198901	ENSG00000198901	PRC1	15:91509269-91538859	OK	79.2017	64.9887	-0.285343	-0.52173	0.2554	0.9998
ENSG00000100359	ENSG00000100359	SGSM3	22:40742506-41032706	OK	45.5888	32.9022	-0.470496	-0.555455	0.25545	0.9998
ENSG00000226752	ENSG00000226752	PSMD5-AS1	9:123577773-123616651	OK	0.717579	1.37523	0.938461	0.365279	0.2555	0.9998
ENSG00000128016	ENSG00000128016	ZFP36	19:39897452-39900052	OK	4.38851	5.73559	0.386212	0.656884	0.25555	0.9998
ENSG00000137177	ENSG00000137177	KIF13A	6:17759413-17987854	OK	35.1003	28.3616	-0.307542	-0.519136	0.2556	0.9998
ENSG00000187446	ENSG00000187446	CHP1	15:41523036-41574043	OK	27.2171	33.5773	0.30297	0.556788	0.2556	0.9998
ENSG00000107341	ENSG00000107341	UBE2R2	9:33750514-33920402	OK	22.2882	27.119	0.283026	0.694326	0.25565	0.9998
ENSG00000126934	ENSG00000126934	MAP2K2	19:4090318-4124126	OK	130.704	158.066	0.274232	0.67347	0.25565	0.9998
ENSG00000156482	ENSG00000156482	RPL30	8:98881067-99058697	OK	1861.51	2293.73	0.301219	0.691722	0.25565	0.9998
ENSG00000124214	ENSG00000124214	STAU1	20:47729877-47804904	OK	55.7998	46.0368	-0.277473	-0.65767	0.2557	0.9998
ENSG00000271734	ENSG00000271734	RP1-111B22.3	6:108351452-108351922	OK	0.434132	0.924396	1.09038	0.741904	0.25595	0.9998
ENSG00000074356	ENSG00000074356	C17orf85	17:3714459-3749545	OK	15.5109	11.9321	-0.378437	-0.39686	0.25605	0.9998
ENSG00000101773	ENSG00000101773	RBBP8	18:20279443-20606451	OK	13.3306	10.6738	-0.32066	-0.581416	0.2561	0.9998
ENSG00000198315	ENSG00000198315	ZKSCAN8	6:28109687-28127250	OK	7.9893	6.26433	-0.350908	-0.705511	0.2562	0.9998
ENSG00000163512	ENSG00000163512	AZI2	3:28283074-28390618	OK	61.1066	44.2667	-0.465104	-0.63665	0.25625	0.9998
ENSG00000145675	ENSG00000145675	PIK3R1	5:67511547-67597649	OK	6.96672	9.16007	0.394879	0.449302	0.25635	0.9998
ENSG00000136122	ENSG00000136122	BORA	13:73302060-73590591	OK	9.93086	6.08432	-0.706824	-0.604806	0.2564	0.9998
ENSG00000198951	ENSG00000198951	NAGA	22:42394728-42466846	OK	32.0969	25.7866	-0.315809	-0.699423	0.25705	0.9998
ENSG00000156858	ENSG00000156858	PRR14	16:30662037-30667761	OK	11.7588	9.17272	-0.358313	-0.63835	0.2572	0.9998
ENSG00000157212	ENSG00000157212	PAXIP1	7:154720207-154794794	OK	10.053	7.99778	-0.329958	-0.609359	0.2572	0.9998
ENSG00000161800	ENSG00000161800	RACGAP1	12:50360976-50426919	OK	61.6083	51.0567	-0.271024	-0.491892	0.25735	0.9998
ENSG00000101160	ENSG00000101160	CTSZ	20:57570239-57582302	OK	567.551	700.469	0.303572	0.679987	0.2575	0.9998
ENSG00000232472	ENSG00000232472	EEF1B2P3	X:24712035-25015103	OK	86.3914	61.2457	-0.496279	-0.691343	0.25765	0.9998
ENSG00000155265	ENSG00000155265	GOLGA7B	10:99609995-99790585	OK	21.8126	16.3677	-0.414309	-0.652422	0.25775	0.9998
ENSG00000106105	ENSG00000106105	GARS	7:30536236-30673649	OK	91.9568	115.082	0.323627	0.5769	0.2578	0.9998
ENSG00000072062	ENSG00000072062	PRKACA	19:14202499-14228896	OK	42.044	33.6243	-0.322394	-0.677995	0.25785	0.9998
ENSG00000158639	ENSG00000158639	PAGE5	X:55246787-55250541	OK	2.51281	3.80396	0.598198	0.663746	0.25805	0.9998
ENSG00000178401	ENSG00000178401	DNAJC22	12:49740699-49751309	OK	0.770195	1.15584	0.585645	0.521522	0.2581	0.9998
ENSG00000122862	ENSG00000122862	SRGN	10:70847861-70864567	OK	1.9457	2.74899	0.49861	0.678322	0.25815	0.9998
ENSG00000175322	ENSG00000175322	ZNF519	18:14057455-14132489	OK	2.5266	1.69761	-0.573693	-0.588675	0.25825	0.9998
ENSG00000107872	ENSG00000107872	FBXL15	10:104162375-104182893	OK	5.98675	8.33918	0.478133	0.673022	0.2585	0.9998
ENSG00000133422	ENSG00000133422	MORC2	22:31318294-31364284	OK	6.48352	8.49726	0.390219	0.568805	0.2585	0.9998
ENSG00000125945	ENSG00000125945	ZNF436	1:23685940-23698332	OK	2.88878	2.20055	-0.392596	-0.685522	0.2586	0.9998
ENSG00000087245	ENSG00000087245	MMP2	16:55423611-55540603	OK	4.76344	6.53051	0.455191	0.631029	0.25865	0.9998
ENSG00000139263	ENSG00000139263	LRIG3	12:59265930-59314303	OK	2.33689	3.058	0.388001	0.518539	0.2588	0.9998
ENSG00000178761	ENSG00000178761	FAM219B	15:75192327-75199462	OK	29.3018	23.1291	-0.341281	-0.600686	0.2588	0.9998
ENSG00000239407	ENSG00000239407	LL0XNC01-237H1.2	X:102024088-102161086	OK	1.77526	0.926162	-0.938692	-0.624737	0.2588	0.9998
ENSG00000198825	ENSG00000198825	INPP5F	10:121485608-121588652	OK	66.2354	54.633	-0.277828	-0.534401	0.25885	0.9998
ENSG00000126870	ENSG00000126870	WDR60	7:158649268-158749438	OK	7.18275	5.63589	-0.349893	-0.534341	0.25895	0.9998
ENSG00000167874	ENSG00000167874	TMEM88	17:7758382-7759417	OK	0.88646	1.53992	0.796724	0.69556	0.25915	0.9998
ENSG00000159713	ENSG00000159713	TPPP3	16:67423711-67427438	OK	5.75486	7.98546	0.472595	0.666937	0.2595	0.9998
ENSG00000143633	ENSG00000143633	C1orf131	1:231359508-231376933	OK	12.3417	9.36626	-0.398001	-0.677309	0.25975	0.9998
ENSG00000231389	ENSG00000231389	HLA-DPA1	6:33032345-33054978	OK	10.8863	14.3548	0.399015	0.660322	0.2599	0.9998
ENSG00000075073	ENSG00000075073	TACR2	10:71163658-71176623	OK	0.892253	1.28078	0.521492	0.676405	0.25995	0.9998
ENSG00000145781	ENSG00000145781	COMMD10	5:115419503-115748459	OK	16.9281	21.1415	0.320655	0.669523	0.25995	0.9998
ENSG00000186523	ENSG00000186523	FAM86B1	8:12036205-12051642	OK	2.10008	1.44731	-0.537071	-0.504118	0.26	0.9998
ENSG00000214026	ENSG00000214026	MRPL23	11:1968507-2011150	OK	82.5437	66.8076	-0.305145	-0.677623	0.26	0.9998
ENSG00000141580	ENSG00000141580	WDR45B	17:80477588-80606429	OK	64.0108	48.3114	-0.405953	-0.605891	0.2602	0.9998
ENSG00000228463	ENSG00000228463	AP006222.2	1:227614-267253	OK	1.0005	1.4784	0.563313	0.666283	0.26035	0.9998
ENSG00000233922	ENSG00000233922	AL133493.2	21:47013567-47017005	OK	0.740887	1.23488	0.737047	0.707233	0.2604	0.9998
ENSG00000072135	ENSG00000072135	PTPN18	2:131113579-131132982	OK	8.93361	6.65314	-0.425209	-0.54702	0.2605	0.9998
ENSG00000144635	ENSG00000144635	DYNC1LI1	3:32567462-32612366	OK	21.012	26.0786	0.311651	0.621025	0.2605	0.9998
ENSG00000205629	ENSG00000205629	LCMT1	16:25123049-25189552	OK	36.9818	29.9409	-0.304695	-0.621193	0.2605	0.9998
ENSG00000244342	ENSG00000244342	LINC00698	3:62936104-63110738	OK	0.405797	0.649035	0.67754	0.530064	0.2605	0.9998
ENSG00000255521	ENSG00000255521	RP4-607I7.1	11:35154201-35159579	OK	1.03711	0.432828	-1.2607	-0.919875	0.26065	0.9998
ENSG00000163755	ENSG00000163755	HPS3	3:148847370-148939842	OK	34.5412	42.4843	0.298614	0.63313	0.2609	0.9998
ENSG00000145494	ENSG00000145494	NDUFS6	5:1801513-1816719	OK	114.744	141.54	0.302794	0.677884	0.26115	0.9998
ENSG00000140320	ENSG00000140320	BAHD1	15:40731919-40760441	OK	4.03618	5.19704	0.3647	0.543744	0.2614	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000106367	ENSG00000106367	AP1S1	7:100797677-100804877	OK	118.792	145.564	0.293221	0.684548	0.26145	0.9998
ENSG00000154447	ENSG00000154447	SH3RF1	4:170015406-170192256	OK	2.95671	2.25598	-0.390238	-0.624834	0.26145	0.9998
ENSG00000139437	ENSG00000139437	TCHP	12:110338068-110434194	OK	15.2246	11.0036	-0.468429	-0.542375	0.2616	0.9998
ENSG00000145365	ENSG00000145365	TIFA	4:113195697-113363776	OK	10.8543	7.15541	-0.601161	-0.673705	0.2616	0.9998
ENSG00000141576	ENSG00000141576	RNF157	17:74132413-74236454	OK	22.8962	18.868	-0.279169	-0.56866	0.26215	0.9998
ENSG00000164920	ENSG00000164920	OSR2	8:99956630-99964332	OK	0.765968	1.26035	0.718464	0.514203	0.26215	0.9998
ENSG00000186480	ENSG00000186480	INSIG1	7:155089485-155101945	OK	102.481	126.449	0.3032	0.616173	0.26215	0.9998
ENSG00000105355	ENSG00000105355	PLIN3	19:4838343-4867780	OK	31.5402	38.4906	0.287316	0.666801	0.26225	0.9998
ENSG00000241627	ENSG00000241627	UBQLN4P1	3:148703654-148705455	OK	9.01496	7.05157	-0.354377	-0.679812	0.2623	0.9998
ENSG00000267023	ENSG00000267023	LRRC37A16P	17:66121917-66148609	OK	7.44056	5.9253	-0.328522	-0.663519	0.2626	0.9998
ENSG00000163026	ENSG00000163026	C2orf44	2:24232950-24286551	OK	7.183	5.49287	-0.387027	-0.638234	0.2628	0.9998
ENSG00000225768	ENSG00000225768	RP11-127O4.3	10:106234696-106240032	OK	0.945429	0.570494	-0.728758	-0.707728	0.2629	0.9998
ENSG00000090020	ENSG00000090020	SLC9A1	1:27425305-27493472	OK	5.50015	7.01825	0.351638	0.600211	0.26295	0.9998
ENSG00000157593	ENSG00000157593	SLC35B2	6:44221832-44225291	OK	226.696	187.96	-0.270336	-0.683322	0.263	0.9998
ENSG00000104853	ENSG00000104853	CLPTM1	19:45457841-45496599	OK	47.922	57.6578	0.266826	0.617475	0.26315	0.9998
ENSG00000099942	ENSG00000099942	CRKL	22:21271713-21308037	OK	22.4351	18.5648	-0.273187	-0.676994	0.2633	0.9998
ENSG00000214016	ENSG00000214016	RP6-105D16.1	X:44600332-44601210	OK	2.18546	3.12369	0.515317	0.685617	0.26335	0.9998
ENSG00000250303	ENSG00000250303	RP11-356J5.12	11:112141471-112233257	OK	2.41172	1.56876	-0.620444	-0.705893	0.26335	0.9998
ENSG00000143127	ENSG00000143127	ITGA10	1:145524890-145543868	OK	7.17776	5.22271	-0.458734	-0.553941	0.2635	0.9998
ENSG00000011376	ENSG00000011376	LARS2	3:45429997-45590913	OK	13.8912	11.3671	-0.289309	-0.527831	0.26365	0.9998
ENSG00000169752	ENSG00000169752	NRG4	15:76228309-76352136	OK	0.709453	0.466546	-0.604687	-0.230003	0.2637	0.9998
ENSG00000129484	ENSG00000129484	PARP2	14:20811206-20826064	OK	21.1757	16.911	-0.324449	-0.624545	0.26375	0.9998
ENSG00000188976	ENSG00000188976	NOC2L	1:860259-894689	OK	41.3156	50.0397	0.276388	0.6451	0.264	0.9998
ENSG00000273297	ENSG00000273297	RP11-38M8.1	7:134101041-134117205	OK	3.76563	2.57915	-0.545994	-0.687026	0.26405	0.9998
ENSG00000017621	ENSG00000017621	MAGIX	X:49019060-49024822	OK	0.91215	0.558633	-0.70737	-0.52865	0.2641	0.9998
ENSG00000257681	ENSG00000257681	RP11-341G23.4	12:103981050-104162636	OK	11.7348	15.9901	0.446385	0.664293	0.26415	0.9998
ENSG00000101384	ENSG00000101384	JAG1	20:10618331-10975572	OK	1.75905	2.26548	0.365027	0.678123	0.2643	0.9998
ENSG00000149428	ENSG00000149428	HYOU1	11:118914898-118927913	OK	33.2536	27.6207	-0.26776	-0.506269	0.2643	0.9998
ENSG00000197183	ENSG00000197183	C20orf112	20:31030861-31196695	OK	5.90404	8.76163	0.569496	0.615996	0.2644	0.9998
ENSG00000101333	ENSG00000101333	PLCB4	20:9049409-9461889	OK	14.5727	10.8382	-0.427133	-0.508713	0.26445	0.9998
ENSG00000137962	ENSG00000137962	ARHGAP29	1:94614543-94740624	OK	9.71726	7.73444	-0.329253	-0.660119	0.26455	0.9998
ENSG00000180318	ENSG00000180318	ALX1	12:85673884-85695562	OK	4.34601	5.73925	0.401171	0.678911	0.26465	0.9998
ENSG00000214135	ENSG00000214135	AC024560.3	3:197305083-197354777	OK	21.1074	16.5935	-0.347135	-0.667484	0.2647	0.9998
ENSG00000129195	ENSG00000129195	FAM64A	17:6347734-6459814	OK	17.8371	13.9301	-0.356677	-0.677484	0.26485	0.9998
ENSG00000179979	ENSG00000179979	CRIPAK	4:1385339-1389780	OK	0.972878	0.715346	-0.443618	-0.67729	0.26485	0.9998
ENSG00000106477	ENSG00000106477	CEP41	7:130033611-130082274	OK	34.8619	25.9639	-0.425144	-0.660442	0.26495	0.9998
ENSG00000080224	ENSG00000080224	EPHA6	3:96533424-97471304	OK	0.513423	0.780928	0.605043	0.537957	0.265	0.9998
ENSG00000173621	ENSG00000173621	LRFN4	11:66615703-66725847	OK	4.83496	7.21577	0.577647	0.579922	0.2652	0.9998
ENSG00000100726	ENSG00000100726	TELO2	16:1543344-1662111	OK	19.3805	14.7034	-0.398459	-0.576191	0.26565	0.9998
ENSG00000204386	ENSG00000204386	NEU1	6:31825435-31830683	OK	158.06	130.665	-0.274607	-0.679801	0.26565	0.9998
ENSG00000124370	ENSG00000124370	MCEE	2:71336813-71357369	OK	4.57005	3.2835	-0.476978	-0.65532	0.2658	0.9998
ENSG00000188878	ENSG00000188878	FBF1	17:73893140-73937221	OK	4.61163	2.58398	-0.835679	-0.407689	0.2659	0.9998
ENSG00000142694	ENSG00000142694	EVA1B	1:36771987-36794822	OK	21.0711	31.6699	0.587844	0.640726	0.26605	0.9998
ENSG00000048028	ENSG00000048028	USP28	11:113668595-113746292	OK	7.22552	9.69858	0.424674	0.552707	0.2662	0.9998
ENSG00000136783	ENSG00000136783	NIPSNAP3A	9:107509968-107522403	OK	15.0903	18.778	0.315421	0.674479	0.2662	0.9998
ENSG00000122863	ENSG00000122863	CHST3	10:73724122-73773322	OK	6.99389	8.52542	0.285676	0.674024	0.26625	0.9998
ENSG00000241104	ENSG00000241104	CEACAMP10	19:43715942-43773682	OK	2.08162	1.20666	-0.786692	-0.550645	0.26625	0.9998
ENSG00000159259	ENSG00000159259	CHAF1B	21:37692089-37791313	OK	5.54728	3.76878	-0.557681	-0.633533	0.2664	0.9998
ENSG00000154114	ENSG00000154114	TBCEL	11:120894780-120961484	OK	2.14723	2.78833	0.376929	0.475872	0.2665	0.9998
ENSG00000153147	ENSG00000153147	SMARCA5	4:144434615-144478639	OK	17.7861	14.2212	-0.322703	-0.356137	0.26665	0.9998
ENSG00000213261	ENSG00000213261	AC093106.7	7:131346710-131347383	OK	26.389	20.5925	-0.357817	-0.669109	0.2667	0.9998
ENSG00000007384	ENSG00000007384	RHBDF1	16:108057-126354	OK	14.5027	19.4632	0.424427	0.701994	0.2668	0.9998
ENSG00000106683	ENSG00000106683	LIMK1	7:73497262-73536855	OK	21.4058	26.2309	0.293267	0.665936	0.26685	0.9998
ENSG00000073584	ENSG00000073584	SMARCE1	17:38781213-38821433	OK	87.2007	67.6575	-0.366089	-0.70808	0.2669	0.9998
ENSG00000160957	ENSG00000160957	RECQL4	8:145736666-145743229	OK	17.2694	13.7379	-0.330055	-0.497554	0.26705	0.9998
ENSG00000043462	ENSG00000043462	LCP2	5:169659450-169725231	OK	0.883233	0.558234	-0.661925	-0.511184	0.26715	0.9998
ENSG00000136100	ENSG00000136100	VPS36	13:52986736-53024763	OK	14.0526	17.3332	0.302705	0.435308	0.26725	0.9998
ENSG00000164434	ENSG00000164434	FABP7	6:123100619-123105219	OK	33.7286	27.1566	-0.312668	-0.669338	0.2674	0.9998
ENSG00000173327	ENSG00000173327	MAP3K11	11:65365225-65382853	OK	115.405	95.6514	-0.270847	-0.586228	0.2674	0.9998
ENSG00000178585	ENSG00000178585	CTNNBIP1	1:9908333-9970394	OK	26.662	18.3946	-0.535508	-0.681553	0.2674	0.9998
ENSG00000248643	ENSG00000248643	RBM14-RBM4	11:66384052-66445392	OK	2.74168	0.704806	-1.95976	-0.273781	0.2674	0.9998
ENSG00000273230	ENSG00000273230	RP11-1246C19.1	7:1504132-1507158	OK	1.22629	0.874836	-0.487217	-0.677702	0.2674	0.9998
ENSG00000088325	ENSG00000088325	TPX2	20:30327073-30389608	OK	85.2141	70.5907	-0.271614	-0.675721	0.2675	0.9998
ENSG00000159214	ENSG00000159214	CCDC24	1:44457030-44497139	OK	2.46918	1.62935	-0.599737	-0.61751	0.2676	0.9998
ENSG00000162378	ENSG00000162378	ZYG11B	1:53192125-53293014	OK	6.13157	7.73398	0.334955	0.666664	0.26765	0.9998
ENSG00000106066	ENSG00000106066	CPVL	7:29019582-29603286	OK	38.7575	31.4801	-0.300035	-0.635872	0.26775	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000150594	ENSG00000150594	ADRA2A	10:112836789-112840658	OK	1.63147	1.21631	-0.423653	-0.665251	0.26775	0.9998
ENSG00000125691	ENSG00000125691	RPL23	17:37004117-37010096	OK	1408.3	1715.94	0.285041	0.664654	0.2678	0.9998
ENSG00000126890	ENSG00000126890	CTAG2	X:153880245-153881853	OK	1.17319	0.716573	-0.711253	-0.683158	0.2678	0.9998
ENSG00000109046	ENSG00000109046	WSB1	17:25621101-25640657	OK	48.8761	36.8818	-0.40622	-0.643076	0.2679	0.9998
ENSG00000187840	ENSG00000187840	EIF4EBP1	8:37887858-37917883	OK	79.6794	97.7698	0.295181	0.678094	0.26795	0.9998
ENSG00000226259	ENSG00000226259	GTF2H2B	5:69711178-69743885	OK	3.82317	2.82641	-0.4358	-0.681642	0.26795	0.9998
ENSG00000230487	ENSG00000230487	PSMG3-AS1	7:1606965-1629262	OK	1.89817	0.963147	-0.97878	-0.441613	0.2681	0.9998
ENSG00000244313	ENSG00000244313	RP11-425L10.1	11:46417963-46615675	OK	608.452	762.073	0.324785	0.679562	0.26835	0.9998
ENSG00000012983	ENSG00000012983	MAP4K5	14:50885218-51135049	OK	7.57081	10.0874	0.414029	0.419755	0.2684	0.9998
ENSG00000060069	ENSG00000060069	CTDP1	18:77439800-77514510	OK	8.52127	6.84637	-0.315729	-0.634968	0.2685	0.9998
ENSG00000111788	ENSG00000111788	RP11-22B23.1	12:9429830-9466684	OK	3.00161	2.32127	-0.370822	-0.669744	0.26855	0.9998
ENSG00000155957	ENSG00000155957	TMBIM4	12:66516841-66563852	OK	89.5822	67.6844	-0.404387	-0.516407	0.2688	0.9998
ENSG00000186275	ENSG00000186275	NBPF12	1:146373545-146467744	OK	1.78055	1.34157	-0.408404	-0.440095	0.2688	0.9998
ENSG00000135127	ENSG00000135127	CCDC64	12:120427672-120532298	OK	2.15603	2.95726	0.455884	0.52431	0.26885	0.9998
ENSG00000212802	ENSG00000212802	RPL15P3	6:12514341-12515006	OK	379.798	459.424	0.274593	0.675475	0.26885	0.9998
ENSG00000107968	ENSG00000107968	MAP3K8	10:30722865-30750762	OK	0.947289	0.57831	-0.711962	-0.593608	0.2689	0.9998
ENSG00000153234	ENSG00000153234	NR4A2	2:157180943-157198860	OK	2.09246	1.56729	-0.41693	-0.581134	0.26905	0.9998
ENSG00000249115	ENSG00000249115	HAUS5	19:36103645-36116251	OK	13.1149	10.4586	-0.326523	-0.583111	0.2693	0.9998
ENSG00000269979	ENSG00000269979	RP11-498E2.7	9:125086886-125087594	OK	2.44316	1.64289	-0.572513	-0.671433	0.26935	0.9998
ENSG00000115750	ENSG00000115750	TAF1B	2:9983482-10074545	OK	10.2564	8.03877	-0.351481	-0.536246	0.2694	0.9998
ENSG00000256667	ENSG00000256667	KLRAP1	12:10741076-10752434	OK	0.739144	0.454386	-0.701939	-0.606463	0.2694	0.9998
ENSG00000167635	ENSG00000167635	ZNF146	19:36673187-36737159	OK	34.7649	28.3297	-0.295316	-0.565974	0.26965	0.9998
ENSG00000185420	ENSG00000185420	SMYD3	1:245912641-246670614	OK	26.4366	33.3528	0.335269	0.64964	0.26965	0.9998
ENSG00000163681	ENSG00000163681	SLMAP	3:57741176-57914895	OK	17.2386	21.6333	0.327614	0.556299	0.2698	0.9998
ENSG00000184226	ENSG00000184226	PCDH9	13:66876966-67804468	OK	0.804743	0.579015	-0.474929	-0.668169	0.2699	0.9998
ENSG00000143375	ENSG00000143375	CGN	1:151482985-151511168	OK	4.52954	5.91466	0.384931	0.476325	0.27015	0.9998
ENSG00000170260	ENSG00000170260	ZNF212	7:148936741-148952700	OK	9.02395	7.21664	-0.322432	-0.587461	0.27025	0.9998
ENSG00000243302	ENSG00000243302	RP11-274B21.2	7:128291238-128292388	OK	8.08035	6.13855	-0.396518	-0.672239	0.27045	0.9998
ENSG00000254645	ENSG00000254645	RP11-396O20.2	11:15665430-15780444	OK	1.2527	0.815584	-0.619138	-0.672554	0.27045	0.9998
ENSG00000126947	ENSG00000126947	ARMCX1	X:100805513-100809683	OK	2.9837	3.89811	0.38567	0.654596	0.2706	0.9998
ENSG00000247271	ENSG00000247271	ZBED5-AS1	11:10830843-10928349	OK	4.28964	1.71512	-1.32255	-0.685502	0.2707	0.9998
ENSG00000254893	ENSG00000254893	RP11-466P24.2	5:75377770-75649764	OK	35.4799	47.1774	0.411094	0.675592	0.2707	0.9998
ENSG00000178104	ENSG00000178104	PDE4DIP	1:144836156-145076186	OK	52.019	67.5122	0.376108	0.574648	0.2709	0.9998
ENSG00000238098	ENSG00000238098	ABCA17P	16:2325881-2476700	OK	7.95718	13.0236	0.710797	0.650137	0.2709	0.9998
ENSG00000147684	ENSG00000147684	NDUFB9	8:125500725-125740730	OK	343.76	423.676	0.30156	0.672572	0.2711	0.9998
ENSG00000116833	ENSG00000116833	NR5A2	1:199996729-200146552	OK	0.883742	0.609865	-0.535136	-0.479949	0.27115	0.9998
ENSG00000165113	ENSG00000165113	GKAP1	9:86354335-86444431	OK	1.99627	1.41006	-0.501552	-0.528633	0.2713	0.9998
ENSG00000150403	ENSG00000150403	TMCO3	13:114145309-114204542	OK	26.0008	21.367	-0.283172	-0.548982	0.2714	0.9998
ENSG00000260423	ENSG00000260423	RP13-735L24.1	12:9520059-9550213	OK	2.51061	3.18848	0.344833	0.663769	0.2716	0.9998
ENSG00000124067	ENSG00000124067	SLC12A4	16:67973652-68003504	OK	7.93623	10.1341	0.352687	0.452939	0.27165	0.9998
ENSG00000223953	ENSG00000223953	C1QTNF5	11:119209651-119217383	OK	3.94954	5.37033	0.443328	0.680272	0.27175	0.9998
ENSG00000100526	ENSG00000100526	CDKN3	14:54863566-54886936	OK	79.6827	64.3923	-0.307378	-0.676379	0.2718	0.9998
ENSG00000125319	ENSG00000125319	C17orf53	17:42219273-42239844	OK	4.78765	3.58622	-0.416854	-0.669533	0.2718	0.9998
ENSG00000264462	ENSG00000264462	MIR3648	21:9825831-9826011	OK	0.554543	2.65435	2.25898	1.37943	0.27195	0.9998
ENSG00000084093	ENSG00000084093	REST	4:57774074-57802010	OK	3.61956	4.48423	0.309045	0.487682	0.2723	0.9998
ENSG00000186409	ENSG00000186409	CCDC30	1:42895999-43120335	OK	0.672595	1.39799	1.05554	0.251257	0.2723	0.9998
ENSG00000272198	ENSG00000272198	RP11-309G3.3	1:181060244-181062035	OK	1.95911	2.64508	0.433109	0.671015	0.2723	0.9998
ENSG00000161513	ENSG00000161513	FDXR	17:72858618-72869156	OK	18.1633	22.3915	0.30193	0.654753	0.27235	0.9998
ENSG00000080709	ENSG00000080709	KCNN2	5:113696641-114004107	OK	9.19746	11.5189	0.3247	0.62564	0.2724	0.9998
ENSG00000141480	ENSG00000141480	ARRB2	17:4613783-4624794	OK	11.5413	9.0983	-0.34314	-0.599506	0.2725	0.9998
ENSG00000175866	ENSG00000175866	BAIAP2	17:79008947-79156964	OK	16.8567	21.6769	0.362839	0.577671	0.2725	0.9998
ENSG00000177822	ENSG00000177822	AC108142.1	4:182795590-183724177	OK	0.72065	0.355458	-1.01962	-0.399803	0.2726	0.9998
ENSG00000253320	ENSG00000253320	KB-1507C5.2	8:103838584-103990104	OK	2.08956	1.00747	-1.05247	-0.117429	0.2726	0.9998
ENSG00000070614	ENSG00000070614	NDST1	5:149855093-149937773	OK	26.43	32.3887	0.293315	0.410872	0.27265	0.9998
ENSG00000155252	ENSG00000155252	PI4K2A	10:99344079-99436191	OK	12.1876	15.1486	0.313771	0.670255	0.27265	0.9998
ENSG00000113810	ENSG00000113810	SMC4	3:159943422-160203561	OK	55.3586	45.0989	-0.295714	-0.421412	0.2727	0.9998
ENSG00000102870	ENSG00000102870	ZNF629	16:30789769-30798523	OK	1.33595	1.7726	0.408006	0.678138	0.2728	0.9998
ENSG00000226251	ENSG00000226251	RP11-151I1.3	1:212398619-212412319	OK	2.26289	3.67746	0.700544	0.6091	0.2728	0.9998
ENSG00000140367	ENSG00000140367	UBE2Q2	15:76135621-76193419	OK	13.5345	16.5388	0.289215	0.5915	0.27285	0.9998
ENSG00000095209	ENSG00000095209	TMEM38B	9:108456824-108538893	OK	14.2204	18.696	0.394773	0.581965	0.2729	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000176715	ENSG00000176715	ACSF3	16:89154782-89222254	OK	7.97461	5.82094	-0.454163	-0.587478	0.27295	0.9998
ENSG00000267419	ENSG00000267419	CTC-559E9.6	19:19868174-19945736	OK	1.63058	0.549886	-1.56818	-0.784349	0.27305	0.9998
ENSG00000125944	ENSG00000125944	HNRNPR	1:23630263-23670829	OK	55.5562	67.2851	0.276338	0.649908	0.27315	0.9998
ENSG00000227921	ENSG00000227921	AL353791.1	9:40028619-40032417	OK	0.727607	0.526726	-0.466105	-0.652431	0.27325	0.9998
ENSG00000188234	ENSG00000188234	AGAP4	10:46321041-46349323	OK	0.873064	0.558941	-0.643392	-0.479616	0.2733	0.9998
ENSG00000076928	ENSG00000076928	ARHGEF1	19:42387227-42434302	OK	25.7026	21.1902	-0.27852	-0.519221	0.2737	0.9998
ENSG00000135298	ENSG00000135298	BAI3	6:69345258-70099403	OK	0.785244	0.518545	-0.598674	-0.35808	0.2737	0.9998
ENSG00000137802	ENSG00000137802	MAPKBP1	15:42066631-42120134	OK	6.74562	8.66984	0.362054	0.412734	0.2737	0.9998
ENSG00000134030	ENSG00000134030	CTIF	18:46065416-46389588	OK	4.97252	6.22303	0.323641	0.518794	0.2739	0.9998
ENSG00000150995	ENSG00000150995	ITPR1	3:4535031-4928977	OK	3.2176	4.14036	0.363769	0.410601	0.274	0.9998
ENSG00000169856	ENSG00000169856	ONECUT1	15:53049636-53083273	OK	1.35598	0.898593	-0.593597	-0.617788	0.274	0.9998
ENSG00000070061	ENSG00000070061	IKBKAP	9:111629796-111696396	OK	18.5532	22.4381	0.274287	0.640149	0.27405	0.9998
ENSG00000107282	ENSG00000107282	APBA1	9:72042445-72287222	OK	3.88935	2.61741	-0.571387	-0.416134	0.27405	0.9998
ENSG00000188681	ENSG00000188681	TEKT4P2	21:9907189-9968585	OK	4.75324	6.18695	0.380318	0.674217	0.27405	0.9998
ENSG00000179294	ENSG00000179294	C17orf96	17:36827960-36831187	OK	0.458893	0.656801	0.517298	0.664163	0.27415	0.9998
ENSG00000145147	ENSG00000145147	SLIT2	4:20254882-20622184	OK	0.54235	0.802468	0.56522	0.3469	0.27435	0.9998
ENSG00000163666	ENSG00000163666	HESX1	3:57231943-57260549	OK	0.702763	0.138239	-2.34587	-1.20736	0.2744	0.9998
ENSG00000115266	ENSG00000115266	APC2	19:1446299-1479555	OK	0.635291	1.60108	1.33355	0.499159	0.27455	0.9998
ENSG00000174010	ENSG00000174010	KLHL15	X:24001836-24045303	OK	4.86821	3.93852	-0.305739	-0.660733	0.27455	0.9998
ENSG00000235552	ENSG00000235552	RPL6P27	18:6462142-6463014	OK	290.756	349.461	0.265324	0.663329	0.2747	0.9998
ENSG00000091972	ENSG00000091972	CD200	3:112021324-112081659	OK	11.8212	9.23299	-0.356509	-0.650003	0.27485	0.9998
ENSG00000232274	ENSG00000232274	RP11-782C8.2	1:143118703-143240439	OK	8.4671	12.9922	0.617708	0.664524	0.27485	0.9998
ENSG00000100116	ENSG00000100116	GCAT	22:38203911-38213183	OK	27.0561	21.9917	-0.298999	-0.637948	0.27505	0.9998
ENSG00000109854	ENSG00000109854	HTATIP2	11:20385230-20405329	OK	35.7892	44.4499	0.312654	0.664381	0.27535	0.9998
ENSG00000077942	ENSG00000077942	FBLN1	22:45898117-45997015	OK	0.53455	0.794155	0.571095	0.246878	0.2756	0.9998
ENSG00000072786	ENSG00000072786	STK10	5:171469076-171615390	OK	18.0036	21.48	0.254705	0.397118	0.2757	0.9998
ENSG00000162723	ENSG00000162723	SLAMF9	1:159921281-159924044	OK	7.23171	5.1534	-0.488813	-0.663735	0.27575	0.9998
ENSG00000142541	ENSG00000142541	RPL13A	19:49949554-49995565	OK	983.757	1213.85	0.30322	0.657568	0.27585	0.9998
ENSG00000243452	ENSG00000243452	NBPF15	1:148555978-148596267	OK	33.8782	21.7814	-0.637258	-0.679437	0.276	0.9998
ENSG00000162521	ENSG00000162521	RBBP4	1:33116742-33169197	OK	57.0844	45.0368	-0.341995	-0.630557	0.27605	0.9998
ENSG00000018408	ENSG00000018408	WWTR1	3:149235021-149454501	OK	65.2121	52.114	-0.323468	-0.555682	0.27615	0.9998
ENSG00000144031	ENSG00000144031	ANKRD53	2:71163011-71306935	OK	0.258737	0.669424	1.37143	0.117227	0.27615	0.9998
ENSG00000237356	ENSG00000237356	AL163953.3	14:53635771-54153976	OK	0.9131	0.316279	-1.52957	-0.901215	0.27615	0.9998
ENSG00000168477	ENSG00000168477	TNXB	6:32006041-32096030	OK	0.197289	0.671297	1.76664	0.164776	0.2762	0.9998
ENSG00000110321	ENSG00000110321	EIF4G2	11:10804859-10830657	OK	381.048	466.693	0.292503	0.589078	0.2763	0.9998
ENSG00000115756	ENSG00000115756	HPCAL1	2:10443014-10567743	OK	53.0074	64.2949	0.27851	0.632611	0.2763	0.9998
ENSG00000100479	ENSG00000100479	POLE2	14:50110272-50155140	OK	6.35467	4.75175	-0.419359	-0.589458	0.27635	0.9998
ENSG00000035687	ENSG00000035687	ADSS	1:244515936-244615436	OK	31.2275	37.5884	0.267469	0.62462	0.2764	0.9998
ENSG00000105755	ENSG00000105755	ETHE1	19:44010870-44040282	OK	24.6659	31.0601	0.332544	0.668741	0.2765	0.9998
ENSG00000183943	ENSG00000183943	PRKX	X:3522410-3631649	OK	3.43024	5.41823	0.659511	0.560018	0.2766	0.9998
ENSG00000137269	ENSG00000137269	LRRC1	6:53659294-53788919	OK	6.55778	5.1984	-0.33514	-0.560741	0.27665	0.9998
ENSG00000137312	ENSG00000137312	FLOT1	6:30695485-30710510	OK	253.404	208.512	-0.281309	-0.628829	0.2767	0.9998
ENSG00000164398	ENSG00000164398	ACSL6	5:131142682-131348892	OK	0.957901	1.29928	0.439765	0.370176	0.2767	0.9998
ENSG00000117862	ENSG00000117862	TXNDC12	1:52485802-52556388	OK	25.2125	19.4494	-0.374412	-0.639797	0.27685	0.9998
ENSG00000142453	ENSG00000142453	CARM1	19:10982188-11039357	OK	24.7527	30.9407	0.321919	0.623437	0.277	0.9998
ENSG00000131089	ENSG00000131089	ARHGEF9	X:62854846-63005426	OK	3.16794	4.17936	0.399737	0.629997	0.27725	0.9998
ENSG00000168303	ENSG00000168303	MPLKIP	7:40165621-40174258	OK	2.82879	2.26416	-0.321212	-0.656374	0.2773	0.9998
ENSG00000159761	ENSG00000159761	C16orf86	16:67696847-67702661	OK	0.747775	1.51969	1.0231	0.627066	0.27745	0.9998
ENSG00000260837	ENSG00000260837	RP11-434B12.1	2:8861263-8862816	OK	0.733973	1.07592	0.551769	0.664024	0.27745	0.9998
ENSG00000121957	ENSG00000121957	GPSM2	1:109358519-109506111	OK	16.5124	12.2422	-0.431684	-0.579762	0.27755	0.9998
ENSG00000143797	ENSG00000143797	MBOAT2	2:8992819-9143942	OK	18.7886	14.0431	-0.419995	-0.524091	0.27775	0.9998
ENSG00000151532	ENSG00000151532	VTI1A	10:114206755-114578503	OK	16.8357	12.3682	-0.444892	-0.590225	0.27775	0.9998
ENSG00000126262	ENSG00000126262	FFAR2	19:35934808-35942669	OK	1.82043	1.24122	-0.552515	-0.492752	0.2779	0.9998
ENSG00000126970	ENSG00000126970	ZC4H2	X:64136249-64254593	OK	1.69215	2.43438	0.5247	0.587414	0.27795	0.9998
ENSG00000198521	ENSG00000198521	ZNF43	19:21987751-22034927	OK	0.682281	0.448125	-0.606465	-0.363878	0.27795	0.9998
ENSG00000132681	ENSG00000132681	ATP1A4	1:160121359-160156767	OK	0.796326	0.435803	-0.869684	-0.67111	0.2781	0.9998
ENSG00000261556	ENSG00000261556	RP11-296I10.6	16:70253476-70279519	OK	1.63955	2.49651	0.606615	0.644882	0.2781	0.9998
ENSG00000154734	ENSG00000154734	ADAMTS1	21:28208065-28217728	OK	1.87674	2.97569	0.664996	0.520484	0.27815	0.9998
ENSG00000166925	ENSG00000166925	TSC22D4	7:100054237-100076902	OK	38.2336	46.3142	0.276614	0.633995	0.2783	0.9998
ENSG00000230202	ENSG00000230202	RP11-632C17__A.1	6:118228688-118638839	OK	498.3	601	0.270351	0.660005	0.2783	0.9998
ENSG00000135903	ENSG00000135903	PAX3	2:223064606-223169936	OK	11.5733	14.3971	0.314974	0.629737	0.27835	0.9998
ENSG00000130255	ENSG00000130255	RPL36	19:5674957-5720583	OK	740.6	943.623	0.349517	0.652633	0.2785	0.9998
ENSG00000139083	ENSG00000139083	ETV6	12:11802787-12048336	OK	2.36733	3.0471	0.364178	0.512884	0.2785	0.9998
ENSG00000104549	ENSG00000104549	SQLE	8:126010738-126034525	OK	40.9432	49.4139	0.271294	0.623261	0.27855	0.9998
ENSG00000119616	ENSG00000119616	FCF1	14:75179846-75203394	OK	22.2103	28.4101	0.35518	0.632604	0.2786	0.9998
ENSG00000164741	ENSG00000164741	DLC1	8:12940869-13373167	OK	24.4779	30.1627	0.301285	0.487975	0.27865	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229119	ENSG00000229119	CTB-63M22.1	5:165809309-165809604	OK	301.948	369.716	0.292116	0.66125	0.27865	0.9998
ENSG00000062582	ENSG00000062582	MRPS24	7:43906156-43966010	OK	147.915	188.074	0.346534	0.661717	0.27875	0.9998
ENSG00000174243	ENSG00000174243	DDX23	12:49223546-49246625	OK	38.9721	32.4287	-0.265171	-0.526254	0.27875	0.9998
ENSG00000148175	ENSG00000148175	STOM	9:124101354-124132531	OK	146.688	182.285	0.313449	0.62647	0.2788	0.9998
ENSG00000137692	ENSG00000137692	DCUN1D5	11:102932804-102962944	OK	17.6618	22.0798	0.322096	0.648844	0.27885	0.9998
ENSG00000261594	ENSG00000261594	TPBGL	11:74919098-74954742	OK	2.35588	3.05876	0.37668	0.65293	0.27885	0.9998
ENSG00000001630	ENSG00000001630	CYP51A1	7:91741464-91810039	OK	73.6318	60.8399	-0.275312	-0.650368	0.27925	0.9998
ENSG00000084463	ENSG00000084463	WBP11	12:14939409-14956474	OK	51.1387	42.6556	-0.26168	-0.639269	0.27925	0.9998
ENSG00000115234	ENSG00000115234	SNX17	2:27593388-27599995	OK	87.509	72.5087	-0.271276	-0.646784	0.27925	0.9998
ENSG00000258741	ENSG00000258741	RP11-386M24.4	15:93146139-93353114	OK	16.6956	10.825	-0.625103	-0.615085	0.2797	0.9998
ENSG00000254681	ENSG00000254681	PKD1P5	16:18411798-18495797	OK	0.849345	1.35833	0.677408	0.499022	0.27975	0.9998
ENSG00000261405	ENSG00000261405	RP11-23E10.4	16:33365115-33373402	OK	0.738286	0.162914	-2.18007	-1.11961	0.27975	0.9998
ENSG00000130349	ENSG00000130349	C6orf203	6:107349406-107372546	OK	6.63806	4.8869	-0.441841	-0.665907	0.2798	0.9998
ENSG00000182636	ENSG00000182636	NDN	15:23930564-23932450	OK	2.88231	3.81351	0.403895	0.665756	0.2798	0.9998
ENSG00000106692	ENSG00000106692	FKTN	9:108320410-108403399	OK	6.43973	8.58678	0.415117	0.338742	0.27985	0.9998
ENSG00000196865	ENSG00000196865	NHLRC2	10:115614419-115676953	OK	6.23416	5.10596	-0.288011	-0.439742	0.27985	0.9998
ENSG00000233008	ENSG00000233008	RP11-475O6.1	1:84041458-84326706	OK	0.423421	0.837184	0.983452	0.521038	0.28005	0.9998
ENSG00000144824	ENSG00000144824	PHLDB2	3:111393522-111695364	OK	3.21249	2.49329	-0.365641	-0.498402	0.2801	0.9998
ENSG00000165152	ENSG00000165152	TMEM246	9:104230720-104295819	OK	0.565613	0.787266	0.477036	0.555875	0.2801	0.9998
ENSG00000148803	ENSG00000148803	FUOM	10:135168657-135171529	OK	11.3104	15.136	0.420332	0.682059	0.28035	0.9998
ENSG00000105221	ENSG00000105221	AKT2	19:40736223-40791443	OK	75.0185	94.1273	0.327366	0.561523	0.28045	0.9998
ENSG00000114626	ENSG00000114626	ABTB1	3:127391777-127399768	OK	5.60425	4.26693	-0.393323	-0.564956	0.2805	0.9998
ENSG00000134815	ENSG00000134815	DHX34	19:47852537-47885961	OK	7.97075	9.99626	0.326673	0.566765	0.2805	0.9998
ENSG00000101901	ENSG00000101901	ALG13	X:110909042-111003877	OK	19.0952	25.3797	0.41046	0.634174	0.28055	0.9998
ENSG00000204959	ENSG00000204959	ARHGEF34P	7:143883175-144077725	OK	0.820325	1.29171	0.655012	0.679465	0.28055	0.9998
ENSG00000112078	ENSG00000112078	KCTD20	6:36322418-36458920	OK	50.0531	59.6858	0.253928	0.447482	0.2806	0.9998
ENSG00000115085	ENSG00000115085	ZAP70	2:98330022-98356325	OK	0.752692	1.1474	0.608232	0.435263	0.28075	0.9998
ENSG00000173402	ENSG00000173402	DAG1	3:49506145-49573048	OK	52.9356	64.7517	0.29068	0.417812	0.2808	0.9998
ENSG00000160551	ENSG00000160551	TAOK1	17:27679086-27878922	OK	12.2209	9.91643	-0.301461	-0.395556	0.281	0.9998
ENSG00000103043	ENSG00000103043	VAC14	16:70721341-70835064	OK	13.6234	11.1709	-0.28634	-0.598305	0.28105	0.9998
ENSG00000168806	ENSG00000168806	LCMT2	15:43619973-43622803	OK	1.78434	2.3706	0.409858	0.639387	0.2813	0.9998
ENSG00000198826	ENSG00000198826	ARHGAP11A	15:32898618-32932150	OK	13.923	10.8082	-0.36535	-0.560108	0.2814	0.9998
ENSG00000011465	ENSG00000011465	DCN	12:91539024-91576900	OK	4.23149	2.94278	-0.523984	-0.472644	0.2815	0.9998
ENSG00000125686	ENSG00000125686	MED1	17:37415383-37607539	OK	12.7835	15.8608	0.311176	0.631363	0.2815	0.9998
ENSG00000137842	ENSG00000137842	TMEM62	15:43398422-43513481	OK	1.60721	2.37809	0.565244	0.361279	0.2817	0.9998
ENSG00000184916	ENSG00000184916	JAG2	14:105607317-105647660	OK	2.52912	4.95721	0.970893	0.672298	0.28185	0.9998
ENSG00000104892	ENSG00000104892	KLC3	19:45836691-45874176	OK	0.669182	2.14588	1.6811	0.625417	0.2819	0.9998
ENSG00000160813	ENSG00000160813	PPP1R35	7:100032879-100036127	OK	19.6599	24.9559	0.344128	0.655007	0.2819	0.9998
ENSG00000078814	ENSG00000078814	MYH7B	20:33563205-33680674	OK	0.456515	1.04435	1.19387	0.194969	0.282	0.9998
ENSG00000124006	ENSG00000124006	OBSL1	2:220415450-220440435	OK	20.0797	25.7713	0.360025	0.613417	0.282	0.9998
ENSG00000089053	ENSG00000089053	ANAPC5	12:121746047-121837699	OK	68.8092	82.5477	0.262626	0.623612	0.28205	0.9998
ENSG00000106609	ENSG00000106609	TMEM248	7:66386211-66423538	OK	47.4939	37.2128	-0.351942	-0.585012	0.2823	0.9998
ENSG00000271270	ENSG00000271270	TMCC1-AS1	3:129612713-129637418	OK	0.93663	0.514263	-0.864973	-0.548504	0.2824	0.9998
ENSG00000143554	ENSG00000143554	SLC27A3	1:153746829-153752633	OK	60.5777	78.6242	0.376186	0.631922	0.2825	0.9998
ENSG00000088808	ENSG00000088808	PPP1R13B	14:104200088-104313927	OK	3.96068	5.2251	0.39971	0.456973	0.2826	0.9998
ENSG00000161016	ENSG00000161016	RPL8	8:146015149-146017972	OK	1883.93	2390.78	0.343737	0.666962	0.28265	0.9998
ENSG00000170802	ENSG00000170802	FOXN2	2:48541775-48606433	OK	14.599	11.0055	-0.407639	-0.641487	0.2827	0.9998
ENSG00000099917	ENSG00000099917	MED15	22:20850199-20946505	OK	74.7845	90.5287	0.275636	0.515883	0.28285	0.9998
ENSG00000166997	ENSG00000166997	CNPY4	7:99690350-99726118	OK	30.6323	17.2164	-0.831273	-0.531185	0.283	0.9998
ENSG00000106554	ENSG00000106554	CHCHD3	7:132469628-132766848	OK	149.415	181.624	0.281628	0.637712	0.28305	0.9998
ENSG00000110400	ENSG00000110400	PVRL1	11:119479134-119599794	OK	1.64511	2.47319	0.588188	0.57854	0.28305	0.9998
ENSG00000147010	ENSG00000147010	SH3KBP1	X:19552092-19905719	OK	18.1302	22.6654	0.3221	0.615579	0.28305	0.9998
ENSG00000164631	ENSG00000164631	ZNF12	7:6703604-6748532	OK	11.254	8.50893	-0.403392	-0.360063	0.2831	0.9998
ENSG00000100300	ENSG00000100300	TSPO	22:43547519-43559248	OK	194.823	233.145	0.259066	0.646652	0.28315	0.9998
ENSG00000188613	ENSG00000188613	NANOS1	10:120789227-120793854	OK	35.6035	45.1093	0.341406	0.654671	0.2832	0.9998
ENSG00000126777	ENSG00000126777	KTN1	14:55965995-56168244	OK	75.1555	62.8891	-0.25707	-0.519371	0.2834	0.9998
ENSG00000133466	ENSG00000133466	C1QTNF6	22:37521877-37595425	OK	0.565883	0.862749	0.608437	0.452616	0.2834	0.9998
ENSG00000234405	ENSG00000234405	LL0XNC01-250H12.3	X:102752450-102774417	OK	0.760114	0.155493	-2.28937	-0.862719	0.28345	0.9998
ENSG00000067840	ENSG00000067840	PDZD4	X:153067620-153096020	OK	8.47067	10.6811	0.334519	0.518786	0.28385	0.9998
ENSG00000203306	ENSG00000203306	AP001007.1	11:124932962-124960411	OK	2.49596	3.65828	0.551571	0.655155	0.28405	0.9998
ENSG00000089009	ENSG00000089009	RPL6	12:112842993-112947717	OK	647.731	832.081	0.361329	0.652669	0.28415	0.9998
ENSG00000124356	ENSG00000124356	STAMBP	2:74056085-74100786	OK	24.1135	29.4069	0.286312	0.581774	0.28415	0.9998
ENSG00000268129	ENSG00000268129	RP11-91G21.1	3:142668005-142779567	OK	0.937522	0.0920975	-3.34762	-0.20176	0.2842	0.9998
ENSG00000174206	ENSG00000174206	C12orf66	12:64580095-64616076	OK	2.69858	2.03294	-0.40863	-0.599355	0.28435	0.9998
ENSG00000109534	ENSG00000109534	GAR1	4:110736665-110745893	OK	16.8175	13.188	-0.350736	-0.649789	0.28445	0.9998
ENSG00000197013	ENSG00000197013	ZNF429	19:21579920-21752039	OK	2.27253	1.37648	-0.723311	-0.549425	0.285	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000133119	ENSG00000133119	RFC3	13:34392185-34540695	OK	25.2109	20.7306	-0.282283	-0.655849	0.2854	0.9998
ENSG00000157214	ENSG00000157214	STEAP2	7:89511666-89867451	OK	1.06196	1.71659	0.692822	0.508342	0.28545	0.9998
ENSG00000204186	ENSG00000204186	ZDBF2	2:207139386-207179148	OK	3.08439	2.50195	-0.301935	-0.643221	0.28545	0.9998
ENSG00000205786	ENSG00000205786	AC002511.1	19:35890412-35910287	OK	38.3493	28.7982	-0.41322	-0.634305	0.2855	0.9998
ENSG00000054148	ENSG00000054148	PHPT1	9:139743175-139755249	OK	151.444	183.416	0.276326	0.655655	0.28565	0.9998
ENSG00000123106	ENSG00000123106	CCDC91	12:28286181-28732883	OK	29.0178	23.3598	-0.312914	-0.554365	0.28575	0.9998
ENSG00000129422	ENSG00000129422	MTUS1	8:17433941-17658426	OK	21.1967	25.7068	0.278306	0.454308	0.28595	0.9998
ENSG00000022277	ENSG00000022277	RTFDC1	20:55043646-55101198	OK	200.091	239.6	0.259971	0.619391	0.2861	0.9998
ENSG00000204196	ENSG00000204196	AC011737.2	2:203879601-204091101	OK	93.9746	121.592	0.371705	0.663584	0.2861	0.9998
ENSG00000136861	ENSG00000136861	CDK5RAP2	9:123151146-123342448	OK	33.3496	27.2337	-0.292278	-0.487021	0.28625	0.9998
ENSG00000104946	ENSG00000104946	TBC1D17	19:50372294-50392005	OK	16.2142	10.8055	-0.585501	-0.618596	0.28635	0.9998
ENSG00000113916	ENSG00000113916	BCL6	3:187416046-187463515	OK	8.99862	7.19718	-0.322273	-0.554907	0.28645	0.9998
ENSG00000263004	ENSG00000263004	RP11-166P13.3	17:55155658-55162385	OK	0.903267	0.498198	-0.858434	-0.509824	0.2865	0.9998
ENSG00000118322	ENSG00000118322	ATP10B	5:159990126-160279221	OK	0.936387	0.626901	-0.578867	-0.371836	0.2868	0.9998
ENSG00000166478	ENSG00000166478	ZNF143	11:9481746-9550071	OK	12.0711	16.253	0.429149	0.573427	0.2869	0.9998
ENSG00000050165	ENSG00000050165	DKK3	11:11984652-12031316	OK	0.786041	1.22552	0.640712	0.311019	0.28705	0.9998
ENSG00000228716	ENSG00000228716	DHFR	5:79922046-80172279	OK	17.0105	12.0081	-0.502423	-0.62228	0.2871	0.9998
ENSG00000083544	ENSG00000083544	TDRD3	13:60970590-61148012	OK	11.5711	14.4709	0.322624	0.558986	0.28715	0.9998
ENSG00000171105	ENSG00000171105	INSR	19:7112265-7294045	OK	0.757003	1.04622	0.466811	0.430413	0.2873	0.9998
ENSG00000105088	ENSG00000105088	OLFM2	19:9964393-10047228	OK	2.75137	3.77625	0.456805	0.640783	0.2877	0.9998
ENSG00000214274	ENSG00000214274	ANG	14:21152258-21175279	OK	6.10958	3.98501	-0.61649	-0.619938	0.28775	0.9998
ENSG00000107077	ENSG00000107077	KDM4C	9:6716547-7175648	OK	7.38713	5.87856	-0.329551	-0.494094	0.2878	0.9998
ENSG00000272333	ENSG00000272333	KMT2B	19:36208920-36229779	OK	1.53221	2.82394	0.8821	0.555004	0.2879	0.9998
ENSG00000273055	ENSG00000273055	CTB-13F3.1	7:107531414-107643700	OK	0.831778	2.64022	1.66639	0.174048	0.2881	0.9998
ENSG00000106399	ENSG00000106399	RPA3	7:7676148-8133902	OK	49.6101	34.4148	-0.527604	-0.650721	0.2882	0.9998
ENSG00000101868	ENSG00000101868	POLA1	X:24712035-25015103	OK	8.1229	5.97438	-0.443206	-0.604374	0.2885	0.9998
ENSG00000144199	ENSG00000144199	FAHD2B	2:97749319-97760619	OK	42.5103	34.816	-0.288065	-0.632074	0.28855	0.9998
ENSG00000119965	ENSG00000119965	C10orf88	10:124690418-124768333	OK	7.20409	10.177	0.49842	0.583672	0.2886	0.9998
ENSG00000083535	ENSG00000083535	PIBF1	13:73302060-73590591	OK	5.70591	3.42321	-0.737105	-0.371085	0.289	0.9998
ENSG00000259495	ENSG00000259495	RP11-210M15.2	15:80637194-80695917	OK	1.05641	0.37381	-1.49879	-0.901184	0.2891	0.9998
ENSG00000076604	ENSG00000076604	TRAF4	17:27071001-27077974	OK	73.161	89.9462	0.297987	0.538355	0.2895	0.9998
ENSG00000241313	ENSG00000241313	WWTR1-AS1	3:149235021-149454501	OK	0.951649	0.345002	-1.46382	-0.16923	0.2896	0.9998
ENSG00000254615	ENSG00000254615	RP11-395G23.3	8:107282371-107764922	OK	6.9973	11.887	0.764511	0.613032	0.2896	0.9998
ENSG00000164985	ENSG00000164985	PSIP1	9:15422701-15511017	OK	35.1763	26.8123	-0.391706	-0.443317	0.28965	0.9998
ENSG00000137154	ENSG00000137154	RPS6	9:19375448-19380252	OK	1811.35	2247.72	0.311401	0.642442	0.2897	0.9998
ENSG00000171813	ENSG00000171813	PWWP2B	10:134210671-134231367	OK	5.90563	7.39537	0.324532	0.651737	0.28975	0.9998
ENSG00000117419	ENSG00000117419	ERI3	1:44686741-44820932	OK	43.3767	35.3523	-0.295118	-0.593893	0.2899	0.9998
ENSG00000122786	ENSG00000122786	CALD1	7:134429002-134655479	OK	91.1297	75.1719	-0.277727	-0.542368	0.28995	0.9998
ENSG00000125122	ENSG00000125122	LRRC29	16:67241041-67260951	OK	0.748464	0.485207	-0.625331	-0.495575	0.28995	0.9998
ENSG00000197769	ENSG00000197769	MAP1LC3C	1:242158791-242162375	OK	1.2483	1.80955	0.535672	0.649491	0.29	0.9998
ENSG00000106636	ENSG00000106636	YKT6	7:44240566-44253893	OK	98.655	81.1402	-0.281975	-0.573862	0.29005	0.9998
ENSG00000040608	ENSG00000040608	RTN4R	22:20228937-20270769	OK	10.4204	13.0693	0.326764	0.624736	0.29025	0.9998
ENSG00000178974	ENSG00000178974	FBXO34	14:55729484-55828636	OK	11.1737	13.6744	0.291374	0.590877	0.29035	0.9998
ENSG00000163872	ENSG00000163872	YEATS2	3:183415605-183530413	OK	20.1347	16.3866	-0.297168	-0.434472	0.2904	0.9998
ENSG00000122483	ENSG00000122483	CCDC18	1:93615298-93835055	OK	2.83553	1.52907	-0.890959	-0.237486	0.2905	0.9998
ENSG00000224189	ENSG00000224189	HOXD-AS1	2:177037922-177055688	OK	31.7252	24.1756	-0.392078	-0.57792	0.2905	0.9998
ENSG00000215302	ENSG00000215302	CTD-3092A11.1	15:30762981-30799826	OK	0.642017	0.211196	-1.60403	-0.552006	0.2908	0.9998
ENSG00000106460	ENSG00000106460	TMEM106B	7:12250866-12282993	OK	26.5648	21.0889	-0.333038	-0.552345	0.2909	0.9998
ENSG00000105647	ENSG00000105647	PIK3R2	19:18263927-18288927	OK	26.2651	19.4113	-0.436251	-0.569487	0.29105	0.9998
ENSG00000132388	ENSG00000132388	UBE2G1	17:4172553-4269923	OK	19.4285	24.7077	0.346786	0.639876	0.29105	0.9998
ENSG00000146278	ENSG00000146278	PNRC1	6:89790469-89794879	OK	16.0947	12.4646	-0.368755	-0.654083	0.29105	0.9998
ENSG00000115365	ENSG00000115365	LANCL1	2:211189482-211342376	OK	36.7342	30.3653	-0.2747	-0.599753	0.29135	0.9998
ENSG00000158985	ENSG00000158985	CDC42SE2	5:130581185-130734140	OK	2.87089	3.67681	0.356956	0.451335	0.2915	0.9998
ENSG00000164587	ENSG00000164587	RPS14	5:149822752-149829319	OK	1313.25	1622.07	0.30469	0.652034	0.2915	0.9998
ENSG00000227124	ENSG00000227124	ZNF717	3:75758793-75834734	OK	1.35288	1.97289	0.544279	0.590855	0.2915	0.9998
ENSG00000087586	ENSG00000087586	AURKA	20:54944444-54967393	OK	95.7561	78.0213	-0.295497	-0.632037	0.29165	0.9998
ENSG00000117479	ENSG00000117479	SLC19A2	1:169433146-169455241	OK	32.9648	39.6609	0.266788	0.647723	0.29165	0.9998
ENSG00000213799	ENSG00000213799	ZNF845	19:53837001-53858122	OK	2.44614	1.73575	-0.494947	-0.525544	0.29165	0.9998
ENSG00000101680	ENSG00000101680	LAMA1	18:6941742-7117813	OK	41.8084	50.1496	0.262446	0.413327	0.29185	0.9998
ENSG00000107560	ENSG00000107560	RAB11FIP2	10:119764426-119969663	OK	5.03183	6.57141	0.38512	0.602338	0.2919	0.9998
ENSG00000166073	ENSG00000166073	GPR176	15:39892231-40213093	OK	2.04852	2.65852	0.376036	0.606126	0.2919	0.9998
ENSG00000171219	ENSG00000171219	CDC42BPG	11:64590858-64612041	OK	1.62121	2.17423	0.423432	0.395381	0.29195	0.9998
ENSG00000166343	ENSG00000166343	MSS51	10:75183338-75193319	OK	0.695224	0.472058	-0.558514	-0.626731	0.292	0.9998
ENSG00000167720	ENSG00000167720	SRR	17:1963132-2284352	OK	5.61511	2.52035	-1.15569	-0.285092	0.29205	0.9998
ENSG00000105875	ENSG00000105875	WDR91	7:134868589-134896316	OK	75.6665	96.7021	0.353892	0.486442	0.29225	0.9998
ENSG00000113649	ENSG00000113649	TCERG1	5:145826873-145891524	OK	27.7241	22.6369	-0.292467	-0.492978	0.29255	0.9998
ENSG00000143870	ENSG00000143870	PDIA6	2:10861774-10978103	OK	261.299	217.537	-0.264441	-0.648903	0.29255	0.9998
ENSG00000096080	ENSG00000096080	MRPS18A	6:43612782-43655528	OK	74.9388	90.6594	0.274745	0.645964	0.2926	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000163171	ENSG00000163171	CDC42EP3	2:37827278-37965611	OK	31.8922	42.2325	0.405151	0.623255	0.29265	0.9998
ENSG00000113719	ENSG00000113719	ERGIC1	5:172261277-172379688	OK	60.8777	72.5491	0.253044	0.58865	0.2927	0.9998
ENSG00000221983	ENSG00000221983	UBA52	19:18682539-18731849	OK	1274.07	1558.69	0.290886	0.64518	0.293	0.9998
ENSG00000132405	ENSG00000132405	TBC1D14	4:6910968-7059679	OK	75.8126	90.9788	0.263092	0.513399	0.2932	0.9998
ENSG00000116918	ENSG00000116918	TSNAX	1:231664398-232177018	OK	92.8272	73.7718	-0.331478	-0.612278	0.29325	0.9998
ENSG00000166396	ENSG00000166396	SERPINB7	18:61420168-61472604	OK	1.1266	1.6246	0.52811	0.534155	0.2934	0.9998
ENSG00000178922	ENSG00000178922	HYI	1:43855552-43922666	OK	18.2099	26.7904	0.556988	0.672528	0.29365	0.9998
ENSG00000114268	ENSG00000114268	PFKFB4	3:48555116-48601206	OK	55.1172	44.075	-0.322542	-0.468756	0.2937	0.9998
ENSG00000198677	ENSG00000198677	TTC37	5:94799598-94890711	OK	39.7822	33.3795	-0.253162	-0.442553	0.2937	0.9998
ENSG00000123975	ENSG00000123975	CKS2	9:91926112-91931618	OK	265.494	222.502	-0.254858	-0.630064	0.29375	0.9998
ENSG00000123689	ENSG00000123689	G0S2	1:209834708-209908295	OK	0.298753	0.685507	1.19822	0.889022	0.2939	0.9998
ENSG00000123485	ENSG00000123485	HJURP	2:234684369-234763212	OK	42.911	35.633	-0.268133	-0.541331	0.29405	0.9998
ENSG00000136891	ENSG00000136891	TEX10	9:103064358-103115221	OK	15.8872	19.2863	0.279712	0.600536	0.2941	0.9998
ENSG00000169689	ENSG00000169689	STRA13	17:79976577-79989027	OK	81.2351	61.4315	-0.403123	-0.669576	0.29455	0.9998
ENSG00000180357	ENSG00000180357	ZNF609	15:64752940-64978264	OK	10.3977	12.4596	0.260989	0.480857	0.29455	0.9998
ENSG00000133111	ENSG00000133111	RFXAP	13:37393360-37403241	OK	2.17946	1.66422	-0.389124	-0.5915	0.29485	0.9998
ENSG00000044459	ENSG00000044459	CNTLN	9:17134979-17503921	OK	5.49669	4.32901	-0.344528	-0.586602	0.29495	0.9998
ENSG00000111605	ENSG00000111605	CPSF6	12:69633316-69668138	OK	32.5614	26.4763	-0.298458	-0.594326	0.29495	0.9998
ENSG00000232593	ENSG00000232593	LINC01155	X:53122891-53196196	OK	1.51789	0.955845	-0.667216	-0.571919	0.29505	0.9998
ENSG00000235297	ENSG00000235297	FAUP1	18:72057118-72057532	OK	2.0886	3.30342	0.661428	0.66032	0.29515	0.9998
ENSG00000272792	ENSG00000272792	RP11-141C7.4	3:195366860-195367331	OK	0.654451	0.263364	-1.31323	-0.80298	0.2952	0.9998
ENSG00000105426	ENSG00000105426	PTPRS	19:5158505-5340814	OK	17.0823	22.0771	0.370045	0.442154	0.2953	0.9998
ENSG00000135912	ENSG00000135912	TTLL4	2:219575567-219620139	OK	70.2828	51.7705	-0.441043	-0.621966	0.29535	0.9998
ENSG00000121892	ENSG00000121892	PDS5A	4:39824482-39979576	OK	17.6439	14.5688	-0.276289	-0.537638	0.2954	0.9998
ENSG00000177105	ENSG00000177105	RHOG	11:3848207-3862213	OK	23.8867	29.1051	0.285062	0.628368	0.29555	0.9998
ENSG00000135124	ENSG00000135124	P2RX4	12:121647659-121671909	OK	37.9088	30.0012	-0.337513	-0.642669	0.29565	0.9998
ENSG00000264920	ENSG00000264920	RP11-6N17.4	17:45968620-45973178	OK	7.84175	5.62627	-0.478997	-0.63874	0.29565	0.9998
ENSG00000107331	ENSG00000107331	ABCA2	9:139901685-139931234	OK	10.4068	12.5216	0.266899	0.383642	0.2957	0.9998
ENSG00000104413	ENSG00000104413	ESRP1	8:95653301-95719694	OK	4.48731	5.72919	0.35248	0.607043	0.2958	0.9998
ENSG00000187456	ENSG00000187456	RDM1	17:34245069-34257777	OK	4.84516	3.52196	-0.460164	-0.54204	0.296	0.9998
ENSG00000152049	ENSG00000152049	KCNE4	2:223916531-224063117	OK	3.63791	2.85601	-0.34911	-0.631432	0.29605	0.9998
ENSG00000027869	ENSG00000027869	SH2D2A	1:156776034-156851642	OK	2.72378	3.85421	0.500823	0.608877	0.2961	0.9998
ENSG00000160360	ENSG00000160360	GPSM1	9:139221931-139268133	OK	11.6137	14.4644	0.316673	0.63041	0.2961	0.9998
ENSG00000229956	ENSG00000229956	ZRANB2-AS2	1:71547006-72748417	OK	0.805211	1.2862	0.675678	0.368954	0.2961	0.9998
ENSG00000233225	ENSG00000233225	AC004987.9	7:39856147-39907739	OK	0.885426	1.40615	0.667306	0.648415	0.29615	0.9998
ENSG00000136802	ENSG00000136802	LRRC8A	9:131595220-131680318	OK	29.1551	24.2329	-0.266778	-0.62867	0.29635	0.9998
ENSG00000163931	ENSG00000163931	TKT	3:53258722-53290068	OK	583.752	717.641	0.297906	0.594961	0.29635	0.9998
ENSG00000133640	ENSG00000133640	LRRIQ1	12:85430091-85657002	OK	0.830841	0.44805	-0.890914	-0.572859	0.2965	0.9998
ENSG00000096093	ENSG00000096093	EFHC1	6:52285105-52441713	OK	4.90638	2.36639	-1.05197	-0.658529	0.2967	0.9998
ENSG00000130164	ENSG00000130164	LDLR	19:11200037-11266484	OK	38.866	46.9924	0.273919	0.538328	0.29675	0.9998
ENSG00000272288	ENSG00000272288	RP11-140K17.3	6:34555064-34665247	OK	2.32213	0.756975	-1.61713	-0.155798	0.29695	0.9998
ENSG00000102317	ENSG00000102317	RBM3	X:48431481-48437454	OK	200.49	159.439	-0.330525	-0.633977	0.297	0.9998
ENSG00000167549	ENSG00000167549	CORO6	17:27887564-28513493	OK	0.529715	0.91566	0.789594	0.115208	0.297	0.9998
ENSG00000065029	ENSG00000065029	ZNF76	6:35226685-35263762	OK	8.16861	6.22092	-0.392962	-0.60434	0.2972	0.9998
ENSG00000065882	ENSG00000065882	TBC1D1	4:37892707-38140796	OK	31.8146	23.6743	-0.426364	-0.58987	0.29735	0.9998
ENSG00000053254	ENSG00000053254	FOXN3	14:89591214-90421121	OK	10.4681	7.81642	-0.42142	-0.398221	0.29745	0.9998
ENSG00000261599	ENSG00000261599	HERC2P8	16:33054929-33140411	OK	2.91085	1.97714	-0.558026	-0.642561	0.29755	0.9998
ENSG00000049239	ENSG00000049239	H6PD	1:9294833-9331396	OK	6.37111	5.22623	-0.285774	-0.633272	0.2976	0.9998
ENSG00000180574	ENSG00000180574	EIF2S3L	12:10658200-10675734	OK	6.57385	8.29985	0.336346	0.630377	0.2976	0.9998
ENSG00000273061	ENSG00000273061	RP11-6J24.6	9:4676599-4679502	OK	2.04	0.635603	-1.68237	-1.09891	0.2976	0.9998
ENSG00000127511	ENSG00000127511	SIN3B	19:16940210-16991164	OK	17.259	21.1633	0.294215	0.459274	0.29775	0.9998
ENSG00000078081	ENSG00000078081	LAMP3	3:182840000-182881627	OK	1.15613	1.5655	0.437321	0.550914	0.29785	0.9998
ENSG00000102057	ENSG00000102057	KCND1	X:48818638-48827976	OK	0.609439	0.860298	0.497355	0.505547	0.2982	0.9998
ENSG00000171241	ENSG00000171241	SHCBP1	16:46614465-46655538	OK	18.5136	15.3837	-0.267187	-0.491244	0.2983	0.9998
ENSG00000117133	ENSG00000117133	RPF1	1:84944941-84963473	OK	22.3946	27.2013	0.28053	0.619838	0.29845	0.9998
ENSG00000130723	ENSG00000130723	PRRC2B	9:134269479-134375584	OK	51.9957	40.7484	-0.351649	-0.43098	0.29845	0.9998
ENSG00000162817	ENSG00000162817	C1orf115	1:220863186-220872499	OK	14.102	17.0841	0.276751	0.631307	0.29845	0.9998
ENSG00000010810	ENSG00000010810	FYN	6:111981534-112194655	OK	31.0014	40.3237	0.379293	0.648091	0.29855	0.9998
ENSG00000148308	ENSG00000148308	GTF3C5	9:135906075-135933890	OK	33.9078	27.188	-0.318646	-0.618319	0.29855	0.9998
ENSG00000105409	ENSG00000105409	ATP1A3	19:42470733-42501649	OK	1.08082	1.45731	0.431185	0.470817	0.2986	0.9998
ENSG00000262664	ENSG00000262664	OVCA2	17:1933403-1946724	OK	31.5559	41.2821	0.387606	0.643229	0.2986	0.9998
ENSG00000185127	ENSG00000185127	C6orf120	6:170102232-170124151	OK	9.58286	6.53952	-0.551271	-0.624906	0.29875	0.9998
ENSG00000145041	ENSG00000145041	VPRBP	3:51428730-51534010	OK	14.4282	20.648	0.517116	0.618155	0.2988	0.9998
ENSG00000110700	ENSG00000110700	RPS13	11:17095935-17229530	OK	1063.09	1306.58	0.297533	0.627473	0.29885	0.9998
ENSG00000139793	ENSG00000139793	MBNL2	13:97873687-98046374	OK	25.2984	19.6779	-0.36247	-0.539633	0.29925	0.9998
ENSG00000183495	ENSG00000183495	EP400	12:132434507-132565005	OK	6.90958	5.74805	-0.265525	-0.634317	0.29925	0.9998
ENSG00000139173	ENSG00000139173	TMEM117	12:44229769-44783545	OK	10.9386	13.9649	0.352372	0.583899	0.29935	0.9998
ENSG00000159674	ENSG00000159674	SPON2	4:1160719-1202750	OK	149.928	124.543	-0.267631	-0.583734	0.29935	0.9998
ENSG00000116661	ENSG00000116661	FBXO2	1:11708423-11723384	OK	13.6116	19.9581	0.552134	0.659968	0.2994	0.9998
ENSG00000152495	ENSG00000152495	CAMK4	5:110559350-110830584	OK	0.759161	1.13906	0.585371	0.393344	0.2994	0.9998
ENSG00000050344	ENSG00000050344	NFE2L3	7:26191859-26226745	OK	12.5322	10.0214	-0.322566	-0.469452	0.2996	0.9998
ENSG00000049089	ENSG00000049089	COL9A2	1:40766158-40783488	OK	0.872025	0.605079	-0.527246	-0.354466	0.29965	0.9998
ENSG00000198707	ENSG00000198707	CEP290	12:88373815-88535993	OK	3.26943	2.01005	-0.701807	-0.490143	0.29985	0.9998
ENSG00000203875	ENSG00000203875	SNHG5	6:86370709-86388451	OK	1035.51	1243.72	0.264331	0.635653	0.3003	0.9998
ENSG00000126522	ENSG00000126522	ASL	7:65540784-65629998	OK	17.2138	11.7109	-0.555714	-0.584621	0.30035	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000175395	ENSG00000175395	ZNF25	10:38238499-38265561	OK	2.78104	2.18322	-0.349171	-0.616473	0.3004	0.9998
ENSG00000273281	ENSG00000273281	RP11-339B21.14	9:131068268-131068629	OK	1.52927	2.57756	0.753165	0.636546	0.30045	0.9998
ENSG00000130396	ENSG00000130396	MLLT4	6:168227601-168372703	OK	20.8466	16.5026	-0.337123	-0.483105	0.3005	0.9998
ENSG00000130818	ENSG00000130818	ZNF426	19:9638666-9649303	OK	4.59643	3.47106	-0.405136	-0.618251	0.3006	0.9998
ENSG00000154957	ENSG00000154957	ZNF18	17:11501747-11900827	OK	3.61826	2.8195	-0.359858	-0.57634	0.3006	0.9998
ENSG00000205517	ENSG00000205517	RGL3	19:11488235-11530018	OK	3.77683	5.62205	0.57392	0.415921	0.30065	0.9998
ENSG00000159111	ENSG00000159111	MRPL10	17:45900637-45908900	OK	40.6262	33.6948	-0.269887	-0.634152	0.30075	0.9998
ENSG00000164032	ENSG00000164032	H2AFZ	4:100869242-101136662	OK	805.294	672.279	-0.260456	-0.631275	0.30075	0.9998
ENSG00000110315	ENSG00000110315	RNF141	11:10533224-10562777	OK	24.4444	18.2755	-0.419592	-0.614261	0.30085	0.9998
ENSG00000135387	ENSG00000135387	CAPRIN1	11:34073229-34122703	OK	86.4223	103.012	0.253336	0.609221	0.30085	0.9998
ENSG00000137203	ENSG00000137203	TFAP2A	6:10393418-10419892	OK	108.524	134.216	0.306542	0.598788	0.30085	0.9998
ENSG00000054965	ENSG00000054965	FAM168A	11:73111531-73309234	OK	16.7645	13.5869	-0.303194	-0.564456	0.30095	0.9998
ENSG00000131116	ENSG00000131116	ZNF428	19:44100543-44124026	OK	19.5357	25.3483	0.375774	0.632793	0.30125	0.9998
ENSG00000157978	ENSG00000157978	LDLRAP1	1:25870070-25895377	OK	16.9455	14.0205	-0.273365	-0.581363	0.30125	0.9998
ENSG00000123562	ENSG00000123562	MORF4L2	X:102930423-102946700	OK	156.282	194.86	0.318286	0.557811	0.30145	0.9998
ENSG00000176124	ENSG00000176124	DLEU1	13:50601268-51423190	OK	25.2293	19.8701	-0.344499	-0.578014	0.3015	0.9998
ENSG00000112996	ENSG00000112996	MRPS30	5:44809026-44820530	OK	98.0371	119.588	0.286677	0.633183	0.30155	0.9998
ENSG00000139190	ENSG00000139190	VAMP1	12:6548166-6580153	OK	3.61398	4.95338	0.454822	0.552669	0.3016	0.9998
ENSG00000168890	ENSG00000168890	TMEM150A	2:85825670-85876403	OK	14.3026	7.94784	-0.847644	-0.659386	0.3016	0.9998
ENSG00000198727	ENSG00000198727	MT-CYB	MT:14746-15887	OK	1308.02	1588.11	0.279929	0.613564	0.30205	0.9998
ENSG00000169814	ENSG00000169814	BTD	3:15602210-15687329	OK	17.7252	13.6091	-0.381228	-0.509439	0.3022	0.9998
ENSG00000128881	ENSG00000128881	TTBK2	15:43030931-43213007	OK	2.63944	2.00208	-0.398733	-0.404711	0.30225	0.9998
ENSG00000143387	ENSG00000143387	CTSK	1:150768683-150780799	OK	90.9846	76.5833	-0.248592	-0.610735	0.3024	0.9998
ENSG00000119203	ENSG00000119203	CPSF3	2:9563696-9613230	OK	24.4939	20.2981	-0.271074	-0.578651	0.3026	0.9998
ENSG00000138678	ENSG00000138678	AGPAT9	4:84457066-84527028	OK	2.93851	4.15632	0.500221	0.483106	0.30265	0.9998
ENSG00000147394	ENSG00000147394	ZNF185	X:152082985-152142024	OK	0.917466	1.21933	0.410362	0.542954	0.3028	0.9998
ENSG00000110958	ENSG00000110958	PTGES3	12:57057126-57082159	OK	145.871	122.58	-0.250972	-0.617415	0.30325	0.9998
ENSG00000111554	ENSG00000111554	MDM1	12:68666222-68726161	OK	9.55507	7.653	-0.32024	-0.525178	0.30335	0.9998
ENSG00000111271	ENSG00000111271	ACAD10	12:112123856-112247782	OK	10.7215	8.78114	-0.288026	-0.439701	0.3035	0.9998
ENSG00000086232	ENSG00000086232	EIF2AK1	7:6048875-6098861	OK	81.8331	65.215	-0.32748	-0.51104	0.30355	0.9998
ENSG00000147576	ENSG00000147576	ADHFE1	8:67341262-67430759	OK	2.55319	1.42069	-0.845702	-0.302507	0.30355	0.9998
ENSG00000136235	ENSG00000136235	GPNMB	7:23275585-23314727	OK	396.165	478.279	0.271751	0.58908	0.3038	0.9998
ENSG00000166473	ENSG00000166473	PKD1L2	16:81134479-81253975	OK	0.772303	1.11436	0.528975	0.521035	0.3038	0.9998
ENSG00000232187	ENSG00000232187	FTH1P7	13:23270161-23270713	OK	227.163	270.644	0.252665	0.619173	0.3038	0.9998
ENSG00000233154	ENSG00000233154	RP4-655J12.4	1:116966345-117021464	OK	0.911148	0.421993	-1.11047	-0.594761	0.3038	0.9998
ENSG00000159055	ENSG00000159055	MIS18A	21:33640529-33653299	OK	8.19205	10.2582	0.324476	0.604456	0.30445	0.9998
ENSG00000158402	ENSG00000158402	CDC25C	5:137620953-137685416	OK	8.08758	5.06358	-0.675551	-0.6372	0.30455	0.9998
ENSG00000169100	ENSG00000169100	SLC25A6	X:1505044-1511617	OK	258.194	214.798	-0.265476	-0.622477	0.30465	0.9998
ENSG00000123892	ENSG00000123892	RAB38	11:87831758-87908635	OK	127.255	106.921	-0.251167	-0.619364	0.3047	0.9998
ENSG00000068079	ENSG00000068079	IFI35	17:41158741-41166473	OK	21.9197	17.8506	-0.296261	-0.591394	0.30475	0.9998
ENSG00000145332	ENSG00000145332	KLHL8	4:88081254-88161466	OK	3.513	2.78188	-0.336643	-0.557385	0.30475	0.9998
ENSG00000166598	ENSG00000166598	HSP90B1	12:104235228-104359486	OK	365.689	305.876	-0.257671	-0.544053	0.30475	0.9998
ENSG00000119661	ENSG00000119661	DNAL1	14:74111577-74170435	OK	8.31618	5.0778	-0.711716	-0.634017	0.3048	0.9998
ENSG00000138395	ENSG00000138395	CDK15	2:202655183-202760273	OK	1.27785	1.7952	0.490419	0.498965	0.3048	0.9998
ENSG00000120256	ENSG00000120256	LRP11	6:150139933-150244257	OK	7.57757	9.27413	0.291476	0.49789	0.30495	0.9998
ENSG00000231817	ENSG00000231817	RP11-189B4.6	13:47029269-47060641	OK	4.07263	6.31429	0.632658	0.671595	0.30495	0.9998
ENSG00000088038	ENSG00000088038	CNOT3	19:54641443-54663620	OK	15.0716	12.0314	-0.325025	-0.603856	0.3051	0.9998
ENSG00000007080	ENSG00000007080	CCDC124	19:18043824-18054800	OK	83.1135	68.8744	-0.271116	-0.62314	0.30525	0.9998
ENSG00000169155	ENSG00000169155	ZBTB43	9:129567284-129600489	OK	5.87562	7.88366	0.424124	0.242315	0.3056	0.9998
ENSG00000171914	ENSG00000171914	TLN2	15:62682724-63176233	OK	3.1152	2.2519	-0.468182	-0.279261	0.3058	0.9998
ENSG00000155099	ENSG00000155099	TMEM55A	8:92006023-92053292	OK	37.9269	48.3632	0.350688	0.638138	0.30585	0.9998
ENSG00000176485	ENSG00000176485	PLA2G16	11:63340666-63389143	OK	10.7281	13.8963	0.373309	0.61092	0.30605	0.9998
ENSG00000063601	ENSG00000063601	MTMR1	X:149861434-149933576	OK	8.7658	10.7216	0.290568	0.475594	0.30615	0.9998
ENSG00000115020	ENSG00000115020	PIKFYVE	2:209130990-209223475	OK	18.727	15.618	-0.261908	-0.548723	0.30615	0.9998
ENSG00000128973	ENSG00000128973	CLN6	15:68346516-68549549	OK	37.9033	29.875	-0.343386	-0.562924	0.30645	0.9998
ENSG00000135631	ENSG00000135631	RAB11FIP5	2:73169164-73383849	OK	10.5352	13.0613	0.310082	0.5092	0.30655	0.9998
ENSG00000256673	ENSG00000256673	RP11-599J14.2	12:9550950-9567447	OK	60.4183	75.3006	0.317676	0.632306	0.30665	0.9998
ENSG00000258017	ENSG00000258017	RP11-386G11.10	12:49521564-49541652	OK	1.22743	0.224599	-2.45022	-0.0573574	0.3067	0.9998
ENSG00000130414	ENSG00000130414	NDUFA10	2:240831866-240964819	OK	128.167	101.874	-0.331243	-0.625188	0.3069	0.9998
ENSG00000117155	ENSG00000117155	SSX2IP	1:85109389-85156486	OK	10.62	8.49239	-0.32254	-0.602308	0.30725	0.9998
ENSG00000267041	ENSG00000267041	ZNF850	19:37178513-37263727	OK	1.0625	0.64956	-0.709923	-0.462679	0.3073	0.9998
ENSG00000142279	ENSG00000142279	WTIP	19:34971873-34997258	OK	2.03526	3.31643	0.70442	0.676413	0.3075	0.9998
ENSG00000173295	ENSG00000173295	FAM86B3P	8:8086116-8102387	OK	5.31733	3.77071	-0.495864	-0.568913	0.3075	0.9998
ENSG00000173531	ENSG00000173531	MST1	3:49711434-49761384	OK	2.64945	4.18688	0.660186	0.145185	0.3077	0.9998
ENSG00000161243	ENSG00000161243	FBXO27	19:39481353-39523425	OK	1.64477	2.56644	0.641881	0.472111	0.308	0.9998
ENSG00000076554	ENSG00000076554	TPD52	8:80830951-81143467	OK	49.2627	30.9809	-0.669118	-0.590813	0.30815	0.9998
ENSG00000167987	ENSG00000167987	VPS37C	11:60897727-60929089	OK	10.2295	8.25557	-0.30929	-0.553111	0.30815	0.9998
ENSG00000151806	ENSG00000151806	GUF1	4:44624085-44728612	OK	10.849	13.973	0.365078	0.60339	0.3084	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000196704	ENSG00000196704	AMZ2	17:66242769-66253297	OK	121.308	146.443	0.271657	0.621326	0.3084	0.9998
ENSG00000178449	ENSG00000178449	COX14	12:50505761-50561288	OK	68.0518	52.6942	-0.368989	-0.629217	0.30845	0.9998
ENSG00000267201	ENSG00000267201	AC005624.2	19:2458932-2462183	OK	0.652194	0.166247	-1.97197	-0.957665	0.30845	0.9998
ENSG00000173482	ENSG00000173482	PTPRM	18:7566779-8406951	OK	79.6041	66.929	-0.250212	-0.439293	0.3085	0.9998
ENSG00000102241	ENSG00000102241	HTATSF1	X:135579237-135594505	OK	28.3068	23.3694	-0.276524	-0.618369	0.30855	0.9998
ENSG00000114544	ENSG00000114544	SLC41A3	3:125725197-125820404	OK	25.0328	20.801	-0.267162	-0.524419	0.30855	0.9998
ENSG00000161692	ENSG00000161692	DBF4B	17:42785975-42829632	OK	18.6706	15.1457	-0.301858	-0.572912	0.30855	0.9998
ENSG00000242588	ENSG00000242588	RP11-274B21.1	7:128171751-128269512	OK	5.28059	3.93718	-0.423536	-0.620842	0.30855	0.9998
ENSG00000124496	ENSG00000124496	TRERF1	6:42192668-42419789	OK	0.801101	1.06317	0.408322	0.616752	0.30865	0.9998
ENSG00000141698	ENSG00000141698	NT5C3B	17:39981334-40004636	OK	44.0828	53.4486	0.277937	0.60956	0.30885	0.9998
ENSG00000215414	ENSG00000215414	PSMA6P1	Y:15360258-15592553	OK	1.6476	2.36933	0.524113	0.607168	0.3089	0.9998
ENSG00000243678	ENSG00000243678	NME1-NME2	17:49230896-49249108	OK	1487.48	1865.69	0.326838	0.614103	0.30895	0.9998
ENSG00000230606	ENSG00000230606	AC159540.1	2:98081082-98100408	OK	13.6419	10.1104	-0.432203	-0.56922	0.30905	0.9998
ENSG00000100503	ENSG00000100503	NIN	14:51186480-51297839	OK	35.8902	29.3655	-0.289465	-0.463207	0.3091	0.9998
ENSG00000138604	ENSG00000138604	GLCE	15:69452922-69564556	OK	17.4045	22.9288	0.3977	0.615566	0.30925	0.9998
ENSG00000180263	ENSG00000180263	FGD6	12:95470524-95611258	OK	1.69406	1.22723	-0.465076	-0.520814	0.3093	0.9998
ENSG00000235105	ENSG00000235105	RP11-329A14.1	1:48761043-48937845	OK	6.01751	8.69348	0.530766	0.593855	0.30935	0.9998
ENSG00000056050	ENSG00000056050	C4orf27	4:170650615-170679104	OK	16.1875	13.0313	-0.312894	-0.603915	0.30955	0.9998
ENSG00000143630	ENSG00000143630	HCN3	1:155232658-155271225	OK	8.87669	6.13083	-0.533938	-0.556653	0.30955	0.9998
ENSG00000188735	ENSG00000188735	TMEM120B	12:122150657-122241812	OK	5.25027	7.17021	0.449625	0.593549	0.30975	0.9998
ENSG00000049769	ENSG00000049769	PPP1R3F	X:49126305-49157929	OK	5.07519	6.46209	0.348539	0.622093	0.30995	0.9998
ENSG00000152749	ENSG00000152749	GPR180	13:95254156-95286899	OK	8.37773	7.01532	-0.256051	-0.611282	0.30995	0.9998
ENSG00000117411	ENSG00000117411	B4GALT2	1:44444614-44456840	OK	24.9482	30.7288	0.300655	0.614333	0.31	0.9998
ENSG00000240038	ENSG00000240038	AMY2B	1:104068312-104122156	OK	1.61081	0.917207	-0.812472	-0.49494	0.31	0.9998
ENSG00000168404	ENSG00000168404	MLKL	16:74705752-74734858	OK	0.985164	1.37069	0.476467	0.494421	0.31005	0.9998
ENSG00000073792	ENSG00000073792	IGF2BP2	3:185361526-185542844	OK	64.364	53.8683	-0.256818	-0.428787	0.3103	0.9998
ENSG00000141294	ENSG00000141294	LRRC46	17:45908992-45918699	OK	0.840369	0.320761	-1.38953	-0.440354	0.31035	0.9998
ENSG00000176171	ENSG00000176171	BNIP3	10:133781577-133795435	OK	99.9539	81.9352	-0.286779	-0.613177	0.31045	0.9998
ENSG00000159164	ENSG00000159164	SV2A	1:149874869-149889434	OK	22.6681	27.1496	0.260265	0.622113	0.31055	0.9998
ENSG00000213886	ENSG00000213886	UBD	6:29523291-29601753	OK	1.98214	0.395109	-2.32674	-0.779512	0.31055	0.9998
ENSG00000132535	ENSG00000132535	DLG4	17:7093208-7128592	OK	1.5329	2.72519	0.830088	0.280241	0.31075	0.9998
ENSG00000138092	ENSG00000138092	CENPO	2:25012602-25142708	OK	11.6323	8.24731	-0.496138	-0.541343	0.3108	0.9998
ENSG00000143970	ENSG00000143970	ASXL2	2:25956621-26101385	OK	9.144	7.67223	-0.253179	-0.587035	0.31085	0.9998
ENSG00000163781	ENSG00000163781	TOPBP1	3:133317018-133380737	OK	29.2787	23.457	-0.319835	-0.416676	0.311	0.9998
ENSG00000234797	ENSG00000234797	RPS3AP6	15:60060542-60061347	OK	509.883	608.012	0.253934	0.62374	0.311	0.9998
ENSG00000092421	ENSG00000092421	SEMA6A	5:115779311-115927094	OK	32.4854	39.4545	0.2804	0.434989	0.31115	0.9998
ENSG00000159086	ENSG00000159086	PAXBP1	21:34100425-34144169	OK	8.30289	6.60779	-0.329445	-0.59743	0.31115	0.9998
ENSG00000236166	ENSG00000236166	RP3-523C21.2	6:132406223-132420419	OK	0.713732	0.284995	-1.32444	-0.714568	0.3112	0.9998
ENSG00000215817	ENSG00000215817	ZC3H11B	1:219782858-219786462	OK	4.59529	3.65918	-0.328634	-0.611903	0.31125	0.9998
ENSG00000093217	ENSG00000093217	XYLB	3:38388250-38462839	OK	17.525	14.2179	-0.301707	-0.542932	0.3115	0.9998
ENSG00000134324	ENSG00000134324	LPIN1	2:11817720-11967535	OK	41.3021	50.1616	0.280365	0.406305	0.3117	0.9998
ENSG00000116985	ENSG00000116985	BMP8B	1:40157853-40254533	OK	0.24233	0.744549	1.61939	0.685686	0.3118	0.9998
ENSG00000163536	ENSG00000163536	SERPINI1	3:167453030-167543356	OK	37.6194	29.8717	-0.332698	-0.592397	0.3118	0.9998
ENSG00000260261	ENSG00000260261	RP11-480A16.1	3:195676058-195679566	OK	1.18473	1.54939	0.387148	0.617922	0.3118	0.9998
ENSG00000061337	ENSG00000061337	LZTS1	8:20103675-20161474	OK	41.8741	50.2704	0.263653	0.618443	0.31185	0.9998
ENSG00000197841	ENSG00000197841	ZNF181	19:35225059-35233777	OK	4.97227	3.47564	-0.516626	-0.582786	0.31185	0.9998
ENSG00000119771	ENSG00000119771	KLHL29	2:23608087-23931481	OK	2.66574	3.40865	0.354666	0.609066	0.31195	0.9998
ENSG00000162607	ENSG00000162607	USP1	1:62901967-62917475	OK	16.2196	13.4696	-0.26803	-0.607714	0.312	0.9998
ENSG00000165406	ENSG00000165406	8-Mar	10:45950034-46090354	OK	7.96744	5.79311	-0.459779	-0.61923	0.31205	0.9998
ENSG00000183722	ENSG00000183722	LHFP	13:39917028-40177665	OK	13.8187	11.3615	-0.282473	-0.602478	0.31205	0.9998
ENSG00000161048	ENSG00000161048	NAPEPLD	7:102740222-102790007	OK	10.8086	8.75342	-0.304257	-0.511404	0.3122	0.9998
ENSG00000162231	ENSG00000162231	NXF1	11:62559594-62573774	OK	18.1466	14.8541	-0.288832	-0.504904	0.3122	0.9998
ENSG00000043514	ENSG00000043514	TRIT1	1:40306722-40349183	OK	15.0373	18.7176	0.315854	0.5739	0.3124	0.9998
ENSG00000101440	ENSG00000101440	ASIP	20:32782374-32899608	OK	0.245216	0.876807	1.83821	0.0882815	0.3124	0.9998
ENSG00000133612	ENSG00000133612	AGAP3	7:150782917-150841523	OK	111.156	132.668	0.255235	0.435316	0.3124	0.9998
ENSG00000116793	ENSG00000116793	PHTF1	1:114239452-114302111	OK	6.01521	4.50495	-0.417103	-0.623384	0.3125	0.9998
ENSG00000127980	ENSG00000127980	PEX1	7:92076766-92157845	OK	10.7225	8.08581	-0.407171	-0.450809	0.3126	0.9998
ENSG00000081019	ENSG00000081019	RSBN1	1:114304453-114456708	OK	3.71659	2.45698	-0.597095	-0.419873	0.31265	0.9998
ENSG00000133114	ENSG00000133114	GPALPP1	13:45513383-45657260	OK	13.0621	9.7436	-0.422859	-0.596613	0.3129	0.9998
ENSG00000163191	ENSG00000163191	S100A11	1:151967006-152020383	OK	861.589	1017.72	0.240268	0.603784	0.313	0.9998
ENSG00000085733	ENSG00000085733	CTTN	11:70116805-70282690	OK	154.636	187.748	0.279924	0.485079	0.3131	0.9998
ENSG00000132357	ENSG00000132357	CARD6	5:40841285-40860275	OK	1.34757	1.7521	0.378729	0.595949	0.3131	0.9998
ENSG00000144597	ENSG00000144597	EAF1	3:15422781-15563258	OK	12.2063	15.1478	0.311477	0.553808	0.3131	0.9998
ENSG00000160766	ENSG00000160766	GBAP1	1:155183615-155197214	OK	4.49069	3.21286	-0.483078	-0.609192	0.31315	0.9998
ENSG00000251595	ENSG00000251595	ABCA11P	4:419223-492945	OK	1.41405	2.78067	0.975604	0.709509	0.31315	0.9998
ENSG00000100852	ENSG00000100852	ARHGAP5	14:32544624-32628934	OK	35.0563	42.2839	0.270435	0.530941	0.3132	0.9998
ENSG00000106070	ENSG00000106070	GRB10	7:50657759-50861159	OK	43.5786	35.8978	-0.279724	-0.505058	0.3132	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000166788	ENSG00000166788	SAAL1	11:18091481-18127638	OK	25.5435	21.0653	-0.278085	-0.569849	0.3132	0.9998
ENSG00000181467	ENSG00000181467	RAP2B	3:152880028-152886265	OK	45.682	38.5924	-0.24331	-0.609438	0.31335	0.9998
ENSG00000037749	ENSG00000037749	MFAP3	5:153369687-153825410	OK	16.3343	11.907	-0.456098	-0.407307	0.3136	0.9998
ENSG00000109458	ENSG00000109458	GAB1	4:144256417-144395721	OK	5.76726	4.62016	-0.319944	-0.464836	0.31365	0.9998
ENSG00000057019	ENSG00000057019	DCBLD2	3:98433173-98620533	OK	26.9909	36.6299	0.440549	0.429698	0.31385	0.9998
ENSG00000155754	ENSG00000155754	ALS2CR11	2:202352147-202483901	OK	3.2646	4.20312	0.364553	0.593215	0.3139	0.9998
ENSG00000140450	ENSG00000140450	ARRDC4	15:98462783-98517068	OK	2.9955	2.28338	-0.391624	-0.607055	0.314	0.9998
ENSG00000219481	ENSG00000219481	NBPF1	1:16888813-16940057	OK	18.3772	14.003	-0.39218	-0.470178	0.31405	0.9998
ENSG00000103599	ENSG00000103599	IQCH	15:67493370-67819628	OK	1.48927	0.887968	-0.746026	-0.149397	0.31435	0.9998
ENSG00000102230	ENSG00000102230	PCYT1B	X:24576203-24690794	OK	0.486352	0.769619	0.662143	0.552159	0.3144	0.9998
ENSG00000196227	ENSG00000196227	FAM217B	20:58508818-58523735	OK	10.7145	8.10484	-0.402712	-0.496997	0.31445	0.9998
ENSG00000183337	ENSG00000183337	BCOR	X:39909067-40036582	OK	8.15917	5.9	-0.467707	-0.371227	0.31455	0.9998
ENSG00000174428	ENSG00000174428	GTF2IRD2B	7:74508363-74565623	OK	1.69747	1.05181	-0.690515	-0.468475	0.31475	0.9998
ENSG00000132967	ENSG00000132967	HMGB1P5	3:22423309-22424420	OK	39.4795	32.0824	-0.299325	-0.604077	0.3148	0.9998
ENSG00000140995	ENSG00000140995	DEF8	16:90014332-90034468	OK	45.4182	58.0282	0.353484	0.566052	0.3148	0.9998
ENSG00000220848	ENSG00000220848	RPS18P9	6:149915219-149915679	OK	1.4957	0.895307	-0.740372	-0.6148	0.31485	0.9998
ENSG00000113522	ENSG00000113522	RAD50	5:131877135-131999964	OK	6.41448	5.21318	-0.299169	-0.468226	0.315	0.9998
ENSG00000088340	ENSG00000088340	FER1L4	20:34146506-34195484	OK	0.644252	0.384187	-0.745817	-0.353154	0.3151	0.9998
ENSG00000040199	ENSG00000040199	PHLPP2	16:71657610-71758604	OK	1.91661	1.46674	-0.385947	-0.454073	0.31515	0.9998
ENSG00000172809	ENSG00000172809	RPL38	17:72199720-72209481	OK	2040	2452.27	0.265547	0.613713	0.31515	0.9998
ENSG00000168807	ENSG00000168807	SNTB2	16:69139466-69442474	OK	2.71849	4.42805	0.703868	0.229743	0.3154	0.9998
ENSG00000198933	ENSG00000198933	TBKBP1	17:45771446-45789416	OK	6.18939	8.57874	0.470968	0.598194	0.3154	0.9998
ENSG00000134369	ENSG00000134369	NAV1	1:201592012-201853422	OK	19.4722	13.6313	-0.514493	-0.291002	0.3155	0.9998
ENSG00000143545	ENSG00000143545	RAB13	1:153954126-153958834	OK	210.922	178.328	-0.242176	-0.597893	0.3155	0.9998
ENSG00000241472	ENSG00000241472	PTPRG-AS1	3:61547242-62355005	OK	6.12749	3.71016	-0.723814	-0.276241	0.31555	0.9998
ENSG00000196141	ENSG00000196141	SPATS2L	2:201170603-201346986	OK	29.442	35.7352	0.279472	0.548765	0.3157	0.9998
ENSG00000253797	ENSG00000253797	UTP14C	13:52586533-52607736	OK	2.30657	3.15982	0.45409	0.627528	0.31585	0.9998
ENSG00000242125	ENSG00000242125	SNHG3	1:28832454-28865812	OK	14.6429	19.664	0.425355	0.383274	0.31595	0.9998
ENSG00000130768	ENSG00000130768	SMPDL3B	1:28261503-28294607	OK	0.341403	0.745578	1.12688	0.620531	0.31605	0.9998
ENSG00000146085	ENSG00000146085	MUT	6:49398072-49430904	OK	23.4407	19.7006	-0.250775	-0.612302	0.3161	0.9998
ENSG00000058272	ENSG00000058272	PPP1R12A	12:79968758-80334448	OK	18.2713	14.9024	-0.294037	-0.399446	0.3162	0.9998
ENSG00000138031	ENSG00000138031	ADCY3	2:25012602-25142708	OK	26.5685	19.7903	-0.424923	-0.481835	0.3162	0.9998
ENSG00000128708	ENSG00000128708	HAT1	2:172640879-172947158	OK	66.0628	53.9073	-0.293358	-0.606665	0.31625	0.9998
ENSG00000142686	ENSG00000142686	C1orf216	1:36179475-36185073	OK	14.1208	11.7671	-0.263069	-0.529335	0.31625	0.9998
ENSG00000205302	ENSG00000205302	SNX2	5:122110690-122165803	OK	24.3728	29.4144	0.271253	0.567221	0.3163	0.9998
ENSG00000120925	ENSG00000120925	RNF170	8:42704779-42940931	OK	9.48658	6.30827	-0.588643	-0.392702	0.31645	0.9998
ENSG00000074842	ENSG00000074842	C19orf10	19:4639529-4670382	OK	242.777	204.1	-0.25036	-0.608546	0.3165	0.9998
ENSG00000090266	ENSG00000090266	NDUFB2	7:140218219-140624564	OK	312.536	392.565	0.328906	0.600492	0.31665	0.9998
ENSG00000107566	ENSG00000107566	ERLIN1	10:101909850-101989376	OK	25.8551	19.1117	-0.435987	-0.598542	0.31665	0.9998
ENSG00000153208	ENSG00000153208	MERTK	2:112656055-112787138	OK	13.5991	16.7066	0.296911	0.48795	0.3168	0.9998
ENSG00000260422	ENSG00000260422	RP1-155D22.2	6:164505054-164506693	OK	2.96312	2.20727	-0.42485	-0.620954	0.31685	0.9998
ENSG00000141034	ENSG00000141034	GID4	17:17942605-17971718	OK	3.58351	4.59543	0.358826	0.494627	0.31715	0.9998
ENSG00000214784	ENSG00000214784	AC010468.1	5:110527923-110528740	OK	30.2858	36.9199	0.285756	0.602084	0.31715	0.9998
ENSG00000100592	ENSG00000100592	DAAM1	14:59655363-59838123	OK	37.154	28.9832	-0.358299	-0.528819	0.31725	0.9998
ENSG00000123384	ENSG00000123384	LRP1	12:57482676-57607134	OK	11.7702	14.8152	0.331936	0.427301	0.31735	0.9998
ENSG00000206149	ENSG00000206149	HERC2P9	15:28834637-28930410	OK	3.93236	2.79895	-0.490511	-0.560727	0.31745	0.9998
ENSG00000101040	ENSG00000101040	ZMYND8	20:45837858-45985567	OK	13.8597	11.3256	-0.291315	-0.542588	0.3175	0.9998
ENSG00000109323	ENSG00000109323	MANBA	4:103552659-103682151	OK	13.366	10.6736	-0.324513	-0.495592	0.3175	0.9998
ENSG00000158079	ENSG00000158079	PTPDC1	9:96793075-96872138	OK	9.66355	7.9518	-0.281273	-0.593619	0.3175	0.9998
ENSG00000198860	ENSG00000198860	TSEN15	1:184020810-184043346	OK	38.8189	46.6573	0.265344	0.577142	0.3175	0.9998
ENSG00000113716	ENSG00000113716	HMGXB3	5:149340299-149432386	OK	30.358	36.8235	0.27855	0.487681	0.3176	0.9998
ENSG00000148339	ENSG00000148339	SLC25A25	9:130823511-130871604	OK	13.8405	16.8567	0.284422	0.568756	0.31765	0.9998
ENSG00000111716	ENSG00000111716	LDHB	12:21788275-21928515	OK	1079.14	1297.14	0.265457	0.595483	0.3177	0.9998
ENSG00000023516	ENSG00000023516	AKAP11	13:42846288-42897396	OK	9.22814	7.74188	-0.253357	-0.609244	0.31775	0.9998
ENSG00000178209	ENSG00000178209	PLEC	8:144989320-145050902	OK	20.9637	26.7787	0.353194	0.32426	0.31785	0.9998
ENSG00000260404	ENSG00000260404	RP11-384K6.6	4:119512927-119555914	OK	2.59294	1.98427	-0.38598	-0.608199	0.31785	0.9998
ENSG00000133193	ENSG00000133193	FAM104A	17:71161115-71258491	OK	17.0547	23.295	0.449853	0.437276	0.3179	0.9998
ENSG00000198832	ENSG00000198832	SELM	22:31500757-31516055	OK	16.2753	20.4844	0.331843	0.603583	0.3179	0.9998
ENSG00000198668	ENSG00000198668	CALM1	14:90862845-90874605	OK	219.759	274.579	0.321298	0.590525	0.3181	0.9998
ENSG00000176014	ENSG00000176014	TUBB6	18:12307667-12377313	OK	23.9303	33.2146	0.472983	0.505795	0.31815	0.9998
ENSG00000171867	ENSG00000171867	PRNP	20:4666881-4682236	OK	29.9151	35.9808	0.266352	0.606314	0.3182	0.9998
ENSG00000174099	ENSG00000174099	MSRB3	12:65672422-66036152	OK	25.3786	19.6878	-0.366311	-0.486477	0.31835	0.9998
ENSG00000249910	ENSG00000249910	TRIM51CP	11:48967245-48973447	OK	1.33395	0.956307	-0.480155	-0.570057	0.3184	0.9998
ENSG00000156639	ENSG00000156639	ZFAND3	6:37787274-38122400	OK	75.6197	57.8065	-0.387531	-0.59976	0.31865	0.9998
ENSG00000143436	ENSG00000143436	MRPL9	1:151728016-151766878	OK	86.8616	70.3861	-0.303428	-0.550504	0.3187	0.9998
ENSG00000168724	ENSG00000168724	DNAJC21	5:34929697-34959069	OK	60.9065	50.07	-0.282648	-0.580843	0.3187	0.9998
ENSG00000230629	ENSG00000230629	RPS23P8	X:70182813-70183143	OK	117.156	143.126	0.288861	0.599294	0.3187	0.9998
ENSG00000157036	ENSG00000157036	EXOG	3:38537617-38583652	OK	6.27639	4.86762	-0.366721	-0.517174	0.31875	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000097046	ENSG00000097046	CDC7	1:91966407-91991321	OK	6.2147	4.75474	-0.38632	-0.566387	0.3189	0.9998
ENSG00000180182	ENSG00000180182	MED14	X:40507557-40597950	OK	16.2829	12.6645	-0.362566	-0.436132	0.319	0.9998
ENSG00000226049	ENSG00000226049	TLK2P1	17:31340104-32522956	OK	7.1951	5.85676	-0.296911	-0.608674	0.319	0.9998
ENSG00000111728	ENSG00000111728	ST8SIA1	12:22199107-22589975	OK	42.961	31.0452	-0.468661	-0.572922	0.31915	0.9998
ENSG00000100036	ENSG00000100036	SLC35E4	22:31031638-31065003	OK	3.18657	4.36443	0.453789	0.617944	0.3193	0.9998
ENSG00000139725	ENSG00000139725	RHOF	12:122150657-122241812	OK	1.69845	3.70865	1.12668	0.566756	0.31935	0.9998
ENSG00000197128	ENSG00000197128	ZNF772	19:57874844-57988938	OK	0.930644	1.52835	0.715676	0.346878	0.31955	0.9998
ENSG00000198431	ENSG00000198431	TXNRD1	12:104609556-104744061	OK	131.716	182.643	0.471598	0.454496	0.31955	0.9998
ENSG00000113282	ENSG00000113282	CLINT1	5:157212750-157286183	OK	35.4358	42.1532	0.250436	0.547865	0.31965	0.9998
ENSG00000075223	ENSG00000075223	SEMA3C	7:80371853-80551675	OK	22.5628	18.4086	-0.293564	-0.449339	0.31985	0.9998
ENSG00000168824	ENSG00000168824	NSG1	4:4349866-4712665	OK	106.092	133.166	0.327921	0.616552	0.31985	0.9998
ENSG00000269501	ENSG00000269501	RP11-353N4.6	1:149575344-149637707	OK	1.49493	2.58842	0.791994	0.604067	0.31985	0.9998
ENSG00000168078	ENSG00000168078	PBK	8:27590834-27695612	OK	69.5207	54.4956	-0.351302	-0.598815	0.3199	0.9998
ENSG00000084623	ENSG00000084623	EIF3I	1:32674694-32697205	OK	288.848	344.32	0.253438	0.597866	0.31995	0.9998
ENSG00000172936	ENSG00000172936	MYD88	3:38179968-38184513	OK	10.7163	13.0089	0.279687	0.574707	0.3202	0.9998
ENSG00000152242	ENSG00000152242	C18orf25	18:43753518-43846949	OK	15.3721	12.1813	-0.335653	-0.479214	0.3204	0.9998
ENSG00000128311	ENSG00000128311	TST	22:37406899-37425863	OK	1.78159	3.2854	0.882906	0.562076	0.32045	0.9998
ENSG00000213719	ENSG00000213719	CLIC1	6:31694814-31707540	OK	478.831	570.808	0.25349	0.600694	0.3206	0.9998
ENSG00000110799	ENSG00000110799	VWF	12:6058039-6233936	OK	1.18813	0.935235	-0.345293	-0.424931	0.3207	0.9998
ENSG00000121964	ENSG00000121964	GTDC1	2:144694639-145090135	OK	6.70328	4.97735	-0.42949	-0.542811	0.3207	0.9998
ENSG00000169169	ENSG00000169169	CPT1C	19:50194154-50216988	OK	2.41773	3.32379	0.459178	0.443428	0.3207	0.9998
ENSG00000138587	ENSG00000138587	MNS1	15:56536206-56757335	OK	2.39986	1.77834	-0.432416	-0.549432	0.32075	0.9998
ENSG00000146232	ENSG00000146232	NFKBIE	6:44225902-44233500	OK	21.1188	27.3146	0.371146	0.566756	0.32075	0.9998
ENSG00000179958	ENSG00000179958	DCTPP1	16:30418617-30441396	OK	33.954	41.1712	0.278055	0.604156	0.3208	0.9998
ENSG00000138942	ENSG00000138942	RNF185	22:31556167-31603005	OK	22.9521	19.1632	-0.260287	-0.499357	0.32085	0.9998
ENSG00000241316	ENSG00000241316	RP11-81N13.1	3:67705120-67998137	OK	3.84867	2.85187	-0.432452	-0.603278	0.321	0.9998
ENSG00000120709	ENSG00000120709	FAM53C	5:137620953-137685416	OK	9.86718	12.0041	0.282823	0.511426	0.3211	0.9998
ENSG00000162706	ENSG00000162706	CADM3	1:159141398-159177763	OK	6.77499	5.36173	-0.337522	-0.560441	0.3211	0.9998
ENSG00000146410	ENSG00000146410	MTFR2	6:136552161-136571473	OK	3.34807	2.56679	-0.383364	-0.551239	0.3212	0.9998
ENSG00000228315	ENSG00000228315	GUSBP11	22:23950638-24059543	OK	2.28717	1.50951	-0.599486	-0.493837	0.3212	0.9998
ENSG00000145214	ENSG00000145214	DGKQ	4:952674-998316	OK	7.27378	9.2236	0.342625	0.511848	0.32125	0.9998
ENSG00000214293	ENSG00000214293	RSBN1L-AS1	7:77286976-77325582	OK	9.92651	7.48432	-0.407415	-0.601205	0.32125	0.9998
ENSG00000131127	ENSG00000131127	ZNF141	4:331602-378653	OK	2.85596	2.0834	-0.455041	-0.533005	0.3213	0.9998
ENSG00000101782	ENSG00000101782	RIOK3	18:21032786-21066567	OK	27.4146	22.7544	-0.268804	-0.560494	0.32145	0.9998
ENSG00000184232	ENSG00000184232	OAF	11:120081474-120101041	OK	8.78898	11.1706	0.345941	0.581377	0.32145	0.9998
ENSG00000188501	ENSG00000188501	LCTL	15:66790354-66858317	OK	0.967427	2.18079	1.17263	0.0968115	0.32145	0.9998
ENSG00000135241	ENSG00000135241	PNPLA8	7:108110865-108215294	OK	21.0415	16.196	-0.377602	-0.553439	0.3215	0.9998
ENSG00000011260	ENSG00000011260	UTP18	17:49337888-49375297	OK	40.8916	34.4328	-0.248022	-0.574931	0.32175	0.9998
ENSG00000156875	ENSG00000156875	HIAT1	1:100503652-100598511	OK	23.1126	19.0529	-0.278668	-0.608184	0.32185	0.9998
ENSG00000196352	ENSG00000196352	CD55	1:207494852-207534311	OK	26.7685	32.7888	0.292665	0.608676	0.3219	0.9998
ENSG00000154174	ENSG00000154174	TOMM70A	3:100082274-100175163	OK	31.9145	37.6463	0.238298	0.533196	0.32215	0.9998
ENSG00000089685	ENSG00000089685	BIRC5	17:76210266-76221717	OK	54.0518	44.6937	-0.27427	-0.554146	0.3224	0.9998
ENSG00000178719	ENSG00000178719	GRINA	8:145051320-145101933	OK	119.934	148.436	0.307599	0.632343	0.3224	0.9998
ENSG00000063177	ENSG00000063177	RPL18	19:49118584-49140695	OK	1201.01	1449.41	0.271218	0.606815	0.3225	0.9998
ENSG00000168476	ENSG00000168476	REEP4	8:21995532-21999464	OK	24.7769	20.4426	-0.277414	-0.597683	0.3226	0.9998
ENSG00000214826	ENSG00000214826	DDX12P	12:9570308-9600825	OK	5.00952	4.08217	-0.295338	-0.595721	0.3226	0.9998
ENSG00000105722	ENSG00000105722	ERF	19:42734337-42759309	OK	25.252	32.447	0.361687	0.39935	0.32265	0.9998
ENSG00000006747	ENSG00000006747	SCIN	7:12609750-12693228	OK	34.044	40.2186	0.240463	0.521405	0.3227	0.9998
ENSG00000064666	ENSG00000064666	CNN2	19:1026297-1039068	OK	17.1712	21.613	0.331904	0.589518	0.3227	0.9998
ENSG00000130304	ENSG00000130304	SLC27A1	19:17579577-17632097	OK	18.8957	23.8506	0.335967	0.584797	0.3227	0.9998
ENSG00000145241	ENSG00000145241	CENPC	4:68337520-68411324	OK	4.07795	3.24656	-0.328933	-0.53814	0.3229	0.9998
ENSG00000243433	ENSG00000243433	RP11-148K1.10	7:150725509-150744869	OK	0.73376	0.137961	-2.41104	-0.218045	0.323	0.9998
ENSG00000124243	ENSG00000124243	BCAS4	20:49411430-49493714	OK	2.82454	3.72471	0.39911	0.539832	0.3231	0.9998
ENSG00000079691	ENSG00000079691	LRRC16A	6:25279305-25620758	OK	7.08552	5.92215	-0.258752	-0.528186	0.32325	0.9998
ENSG00000065989	ENSG00000065989	PDE4A	19:10501809-10580305	OK	0.543029	1.05321	0.955695	0.248283	0.3235	0.9998
ENSG00000187815	ENSG00000187815	ZFP69	1:40942886-40974333	OK	0.937751	1.27964	0.448461	0.575115	0.3235	0.9998
ENSG00000175606	ENSG00000175606	TMEM70	8:74884671-74895018	OK	19.1166	23.6491	0.306956	0.579862	0.32365	0.9998
ENSG00000135108	ENSG00000135108	FBXO21	12:117581145-117628336	OK	11.4053	9.47234	-0.267907	-0.576844	0.32375	0.9998
ENSG00000100360	ENSG00000100360	IFT27	22:37154245-37172300	OK	4.87706	3.55253	-0.457165	-0.540374	0.32385	0.9998
ENSG00000154217	ENSG00000154217	PITPNC1	17:65373574-65693372	OK	13.6022	10.7774	-0.335832	-0.574403	0.324	0.9998
ENSG00000197555	ENSG00000197555	SIPA1L1	14:71759441-72207946	OK	4.97336	3.74195	-0.410433	-0.348113	0.32405	0.9998
ENSG00000100399	ENSG00000100399	CHADL	22:41601208-41636938	OK	0.278791	0.873524	1.64766	0.52743	0.32425	0.9998
ENSG00000215908	ENSG00000215908	CROCCP2	1:16944750-16971178	OK	10.2313	8.32298	-0.297822	-0.591918	0.32425	0.9998
ENSG00000185130	ENSG00000185130	HIST1H2BL	6:27775256-27775709	OK	0.65808	0.316766	-1.05485	-0.605788	0.32435	0.9998
ENSG00000176209	ENSG00000176209	SMIM19	8:42273992-42409603	OK	24.5351	17.2181	-0.510923	-0.576711	0.32445	0.9998
ENSG00000163877	ENSG00000163877	SNIP1	1:38000049-38019903	OK	3.03143	2.39443	-0.340318	-0.505071	0.3247	0.9998
ENSG00000176422	ENSG00000176422	SPRYD4	12:56843285-56882198	OK	8.47686	6.85818	-0.305704	-0.590435	0.32475	0.9998
ENSG00000122406	ENSG00000122406	RPL5	1:93297581-93307481	OK	797.269	948.356	0.250363	0.590266	0.32485	0.9998
ENSG00000095713	ENSG00000095713	CRTAC1	10:99609995-99790585	OK	11.4107	16.5642	0.53768	0.533938	0.325	0.9998
ENSG00000243927	ENSG00000243927	MRPS6	21:35445523-35732332	OK	38.957	28.9716	-0.427244	-0.577466	0.3251	0.9998
ENSG00000196455	ENSG00000196455	PIK3R4	3:130397778-130465673	OK	12.3171	10.1737	-0.275826	-0.486628	0.3253	0.9998
ENSG00000271147	ENSG00000271147	RP4-769N13.6	X:101854095-101973607	OK	2.70588	4.92614	0.864361	0.527313	0.32555	0.9998
ENSG00000145107	ENSG00000145107	TM4SF19	3:195938357-196065374	OK	1.44331	3.34941	1.21453	0.328657	0.3256	0.9998
ENSG00000069345	ENSG00000069345	DNAJA2	16:46989298-47007699	OK	15.6897	18.9839	0.274962	0.594492	0.32565	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000174353	ENSG00000174353	STAG3L3	7:72440226-72555749	OK	3.63373	2.7319	-0.411549	-0.610231	0.32565	0.9998
ENSG00000171863	ENSG00000171863	RPS7	2:3622794-3628509	OK	957.951	1143.33	0.255214	0.600958	0.326	0.9998
ENSG00000114346	ENSG00000114346	ECT2	3:172468471-172539264	OK	35.9347	30.294	-0.246347	-0.462887	0.32605	0.9998
ENSG00000268205	ENSG00000268205	CTC-444N24.11	19:57815672-57819930	OK	1.52764	1.93486	0.340926	0.595808	0.32615	0.9998
ENSG00000182979	ENSG00000182979	MTA1	14:105864915-105937066	OK	31.6756	26.1964	-0.274002	-0.520438	0.3263	0.9998
ENSG00000101452	ENSG00000101452	DHX35	20:37590941-37668366	OK	11.0234	9.0519	-0.284271	-0.54585	0.32635	0.9998
ENSG00000234906	ENSG00000234906	APOC2	19:45445494-45452822	OK	11.1385	14.0834	0.338435	0.578377	0.32635	0.9998
ENSG00000204619	ENSG00000204619	PPP1R11	6:30034485-30043664	OK	40.6305	34.1221	-0.251855	-0.600622	0.3264	0.9998
ENSG00000144034	ENSG00000144034	TPRKB	2:73956230-73964527	OK	42.2625	51.8717	0.295571	0.608929	0.3265	0.9998
ENSG00000204389	ENSG00000204389	HSPA1A	6:31777395-31785723	OK	25.5305	20.949	-0.285339	-0.602245	0.3265	0.9998
ENSG00000105058	ENSG00000105058	FAM32A	19:16296190-16302857	OK	45.0753	37.7237	-0.256867	-0.587513	0.32655	0.9998
ENSG00000154122	ENSG00000154122	ANKH	5:14704909-14871887	OK	0.676536	0.488569	-0.469602	-0.317327	0.32655	0.9998
ENSG00000138030	ENSG00000138030	KHK	2:27309614-27341995	OK	3.17065	1.83195	-0.791397	-0.594689	0.32665	0.9998
ENSG00000253716	ENSG00000253716	RP13-582O9.5	8:144362330-144363860	OK	5.72522	8.13689	0.507146	0.600621	0.3268	0.9998
ENSG00000087157	ENSG00000087157	PGS1	17:76374720-76573476	OK	24.4318	30.0083	0.296601	0.550555	0.32715	0.9998
ENSG00000165006	ENSG00000165006	UBAP1	9:34179002-34329198	OK	19.2246	15.2527	-0.333886	-0.627093	0.32715	0.9998
ENSG00000179094	ENSG00000179094	PER1	17:8043789-8066864	OK	5.71924	7.61296	0.412634	0.385121	0.3273	0.9998
ENSG00000148516	ENSG00000148516	ZEB1	10:31476811-31818742	OK	2.57372	2.01459	-0.353373	-0.380174	0.32735	0.9998
ENSG00000151240	ENSG00000151240	DIP2C	10:320129-735683	OK	11.5884	9.21473	-0.330671	-0.434293	0.32735	0.9998
ENSG00000154222	ENSG00000154222	CC2D1B	1:52608045-52831865	OK	21.6984	17.2839	-0.328155	-0.468295	0.32735	0.9998
ENSG00000185345	ENSG00000185345	PARK2	6:161768451-163736524	OK	0.66335	0.453418	-0.548928	-0.467888	0.32735	0.9998
ENSG00000068305	ENSG00000068305	MEF2A	15:100017369-100273766	OK	22.2465	17.9111	-0.312727	-0.451126	0.3274	0.9998
ENSG00000156500	ENSG00000156500	FAM122C	X:133903595-133988640	OK	2.02705	1.0609	-0.934089	-0.331857	0.3276	0.9998
ENSG00000255135	ENSG00000255135	RP11-111M22.3	11:76152381-76155700	OK	3.89186	2.79275	-0.478775	-0.595364	0.32765	0.9998
ENSG00000176225	ENSG00000176225	RTTN	18:67671028-67873181	OK	33.7725	28.3018	-0.254957	-0.461155	0.3277	0.9998
ENSG00000153561	ENSG00000153561	RMND5A	2:86730553-87005164	OK	9.964	6.97834	-0.51384	-0.366265	0.32775	0.9998
ENSG00000147403	ENSG00000147403	RPL10	X:153618314-153650065	OK	1639.85	1990.44	0.279524	0.611525	0.3278	0.9998
ENSG00000161970	ENSG00000161970	RPL26	17:8268880-8286531	OK	1897.64	2261.47	0.253054	0.588395	0.3278	0.9998
ENSG00000184988	ENSG00000184988	TMEM106A	17:41363853-41383338	OK	0.550256	0.828233	0.589934	0.412452	0.3278	0.9998
ENSG00000144231	ENSG00000144231	POLR2D	2:128603839-128615731	OK	22.174	18.3254	-0.275021	-0.583336	0.32795	0.9998
ENSG00000136870	ENSG00000136870	ZNF189	9:104161154-104172942	OK	5.51784	4.45577	-0.308428	-0.601685	0.328	0.9998
ENSG00000076944	ENSG00000076944	STXBP2	19:7694622-7712759	OK	8.85639	11.7204	0.404228	0.443204	0.3281	0.9998
ENSG00000105290	ENSG00000105290	APLP1	19:36316865-36370693	OK	19.1913	24.9284	0.377341	0.577207	0.3281	0.9998
ENSG00000163558	ENSG00000163558	PRKCI	3:169940152-170023769	OK	14.5946	11.7715	-0.310133	-0.336471	0.32815	0.9998
ENSG00000123144	ENSG00000123144	C19orf43	19:12841453-12845589	OK	98.6628	116.948	0.245283	0.599902	0.3282	0.9998
ENSG00000067992	ENSG00000067992	PDK3	X:24483337-24557954	OK	12.9035	10.5285	-0.293465	-0.570334	0.3283	0.9998
ENSG00000083817	ENSG00000083817	ZNF416	19:58082933-58105145	OK	1.02478	1.49798	0.547696	0.566696	0.3283	0.9998
ENSG00000125755	ENSG00000125755	SYMPK	19:46318667-46366548	OK	31.3085	25.5566	-0.292855	-0.450596	0.3283	0.9998
ENSG00000024862	ENSG00000024862	CCDC28A	6:139094656-139114456	OK	9.16585	7.35066	-0.318395	-0.595693	0.32875	0.9998
ENSG00000116906	ENSG00000116906	GNPAT	1:231376952-231413719	OK	39.4307	33.3607	-0.241169	-0.556606	0.3288	0.9998
ENSG00000087884	ENSG00000087884	AAMDC	11:77532154-77705724	OK	31.2492	21.8053	-0.519137	-0.586889	0.32885	0.9998
ENSG00000103342	ENSG00000103342	GSPT1	16:11945505-12009939	OK	55.193	66.8371	0.276163	0.582603	0.32885	0.9998
ENSG00000050438	ENSG00000050438	SLC4A8	12:51745030-51902980	OK	0.590292	0.965801	0.710298	0.288088	0.3289	0.9998
ENSG00000137274	ENSG00000137274	BPHL	6:3118607-3153812	OK	22.6647	17.5817	-0.366374	-0.623329	0.32895	0.9998
ENSG00000169813	ENSG00000169813	HNRNPF	10:43881064-43904614	OK	78.0117	94.3618	0.274512	0.583806	0.329	0.9998
ENSG00000115504	ENSG00000115504	EHBP1	2:62900985-63275775	OK	34.2123	28.4293	-0.267135	-0.43825	0.32925	0.9998
ENSG00000213300	ENSG00000213300	HNRNPA3P6	3:75263781-75264787	OK	113.185	95.7647	-0.241121	-0.590329	0.32935	0.9998
ENSG00000259658	ENSG00000259658	RP11-89K11.1	15:102277301-102285913	OK	0.360184	0.643283	0.836719	0.480455	0.32965	0.9998
ENSG00000179833	ENSG00000179833	SERTAD2	2:64858754-64978139	OK	11.1012	9.19847	-0.271251	-0.36866	0.3298	0.9998
ENSG00000100528	ENSG00000100528	CNIH1	14:54893653-54908149	OK	87.0133	103.653	0.25246	0.580368	0.32985	0.9998
ENSG00000159714	ENSG00000159714	ZDHHC1	16:67428321-67450736	OK	5.24782	6.64925	0.341472	0.557847	0.32985	0.9998
ENSG00000198040	ENSG00000198040	ZNF84	12:133613877-133639885	OK	10.0099	7.81448	-0.357212	-0.451428	0.33	0.9998
ENSG00000135931	ENSG00000135931	ARMC9	2:232063259-232239548	OK	70.8943	87.4577	0.302914	0.54201	0.33025	0.9998
ENSG00000198792	ENSG00000198792	TMEM184B	22:38615297-38669040	OK	31.9139	27.0986	-0.23597	-0.494388	0.33035	0.9998
ENSG00000102387	ENSG00000102387	TAF7L	X:100523240-100548059	OK	4.03505	5.16116	0.355109	0.599001	0.33045	0.9998
ENSG00000167785	ENSG00000167785	ZNF558	19:8920379-8943004	OK	5.12367	4.07491	-0.33041	-0.52488	0.33055	0.9998
ENSG00000077549	ENSG00000077549	CAPZB	1:19665266-19812066	OK	131.163	109.956	-0.254437	-0.586235	0.3307	0.9998
ENSG00000117399	ENSG00000117399	CDC20	1:43824625-43828874	OK	43.2585	36.3941	-0.24928	-0.567518	0.3307	0.9998
ENSG00000082068	ENSG00000082068	WDR70	5:37379313-37753537	OK	34.2305	26.517	-0.368368	-0.592545	0.33085	0.9998
ENSG00000109736	ENSG00000109736	MFSD10	4:2932287-2936586	OK	22.7143	27.5859	0.280331	0.590747	0.33085	0.9998
ENSG00000189067	ENSG00000189067	LITAF	16:11641852-11730237	OK	190.155	225.793	0.24782	0.552235	0.33085	0.9998
ENSG00000078098	ENSG00000078098	FAP	2:163016271-163101661	OK	3.04303	3.91865	0.36485	0.467257	0.33115	0.9998
ENSG00000106537	ENSG00000106537	TSPAN13	7:16793159-16824161	OK	9.6742	11.7538	0.280913	0.583117	0.3312	0.9998
ENSG00000147316	ENSG00000147316	MCPH1	8:6261071-6565730	OK	5.80975	7.25233	0.319969	0.547493	0.3314	0.9998
ENSG00000135837	ENSG00000135837	CEP350	1:179923872-180084015	OK	15.5488	12.0417	-0.36876	-0.315097	0.33155	0.9998
ENSG00000156508	ENSG00000156508	EEF1A1	6:74225472-74280319	OK	2811.2	3591.06	0.35322	0.589447	0.3319	0.9998
ENSG00000078804	ENSG00000078804	TP53INP2	20:33284721-33413452	OK	26.5359	21.0512	-0.334041	-0.525401	0.33195	0.9998
ENSG00000134419	ENSG00000134419	RPS15A	16:18792616-18813000	OK	1568.03	1946.99	0.312298	0.588767	0.332	0.9998
ENSG00000230590	ENSG00000230590	FTX	X:73164158-73513409	OK	0.94737	1.71954	0.860025	0.304699	0.33205	0.9998
ENSG00000114767	ENSG00000114767	RRP9	3:51967445-51975957	OK	17.4712	21.1426	0.275174	0.590158	0.33215	0.9998
ENSG00000180817	ENSG00000180817	PPA1	10:71962585-71993667	OK	104.974	123.46	0.234011	0.581698	0.33215	0.9998
ENSG00000160877	ENSG00000160877	NACC1	19:13228916-13251961	OK	28.7367	23.3367	-0.300292	-0.434798	0.3322	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000162585	ENSG00000162585	C1orf86	1:1981908-2152177	OK	36.2053	47.3487	0.387125	0.60424	0.33225	0.9998
ENSG00000119596	ENSG00000119596	YLPM1	14:75230068-75330537	OK	12.0604	9.89487	-0.285529	-0.431921	0.33255	0.9998
ENSG00000119335	ENSG00000119335	SET	9:131445702-131458679	OK	225.639	275.563	0.288362	0.565751	0.3326	0.9998
ENSG00000128944	ENSG00000128944	KNSTRN	15:40674921-40686447	OK	17.8291	14.067	-0.341924	-0.522683	0.3326	0.9998
ENSG00000083093	ENSG00000083093	PALB2	16:23614487-23652631	OK	7.22226	5.94441	-0.280917	-0.46571	0.3327	0.9998
ENSG00000167384	ENSG00000167384	ZNF180	19:44979853-45004576	OK	1.86289	1.45632	-0.355215	-0.418227	0.33275	0.9998
ENSG00000258301	ENSG00000258301	RP11-488C13.5	14:77228531-77253067	OK	2.92866	2.02531	-0.532096	-0.604843	0.3328	0.9998
ENSG00000123983	ENSG00000123983	ACSL3	2:223725651-223809357	OK	278.069	224.243	-0.310379	-0.469476	0.33325	0.9998
ENSG00000113552	ENSG00000113552	GNPDA1	5:141371313-141392606	OK	72.6477	61.6837	-0.236028	-0.517893	0.3333	0.9998
ENSG00000152104	ENSG00000152104	PTPN14	1:214517514-214725792	OK	7.20219	9.35638	0.377515	0.332338	0.3333	0.9998
ENSG00000075413	ENSG00000075413	MARK3	14:103851728-103970168	OK	32.2355	26.9545	-0.258127	-0.483944	0.33335	0.9998
ENSG00000198840	ENSG00000198840	MT-ND3	MT:10058-10404	OK	1435.67	1691.44	0.236524	0.583358	0.33335	0.9998
ENSG00000138286	ENSG00000138286	FAM149B1	10:74870216-75118617	OK	19.5614	11.8375	-0.724649	-0.512164	0.33345	0.9998
ENSG00000268355	ENSG00000268355	AC006129.1	19:42037565-42038534	OK	0.547115	0.916293	0.743964	0.579815	0.3335	0.9998
ENSG00000068885	ENSG00000068885	IFT80	3:159943422-160203561	OK	20.5361	14.7219	-0.480196	-0.324044	0.33365	0.9998
ENSG00000182481	ENSG00000182481	KPNA2	17:66031634-66042958	OK	233.916	198.276	-0.23848	-0.586653	0.3337	0.9998
ENSG00000102547	ENSG00000102547	CAB39L	13:49882785-50069138	OK	6.43461	4.29903	-0.581841	-0.521799	0.33375	0.9998
ENSG00000235944	ENSG00000235944	ZNF815P	7:5862790-5894066	OK	2.26158	1.60305	-0.496514	-0.566155	0.33425	0.9998
ENSG00000272097	ENSG00000272097	RP11-421M1.8	6:10743556-10747896	OK	0.754775	0.461757	-0.708914	-0.563566	0.3343	0.9998
ENSG00000055483	ENSG00000055483	USP36	17:76783462-76837523	OK	19.4099	23.3425	0.266166	0.484491	0.3349	0.9998
ENSG00000110455	ENSG00000110455	ACCS	11:44087474-44105772	OK	9.54331	12.2673	0.362261	0.517067	0.33495	0.9998
ENSG00000196290	ENSG00000196290	NIF3L1	2:201754049-201768655	OK	25.488	20.8869	-0.287221	-0.600069	0.33495	0.9998
ENSG00000169783	ENSG00000169783	LINGO1	15:77905368-78113242	OK	2.43915	3.15798	0.372624	0.439018	0.335	0.9998
ENSG00000187231	ENSG00000187231	SESTD1	2:179966418-180129517	OK	20.6861	14.8129	-0.481809	-0.553584	0.335	0.9998
ENSG00000010671	ENSG00000010671	BTK	X:100604434-100641183	OK	0.767075	1.63085	1.08818	0.439975	0.33505	0.9998
ENSG00000141736	ENSG00000141736	ERBB2	17:37827374-37887040	OK	5.55967	7.35383	0.403497	0.365895	0.33525	0.9998
ENSG00000171222	ENSG00000171222	SCAND1	20:34541538-34547394	OK	28.9904	23.7287	-0.28894	-0.588885	0.33535	0.9998
ENSG00000108406	ENSG00000108406	DHX40	17:57642885-57685706	OK	40.6634	34.5972	-0.233075	-0.543213	0.33545	0.9998
ENSG00000127948	ENSG00000127948	POR	7:75528517-75623977	OK	33.578	41.5628	0.30778	0.4921	0.33545	0.9998
ENSG00000064726	ENSG00000064726	BTBD1	15:83509837-83772195	OK	56.3033	46.8349	-0.265635	-0.533005	0.3355	0.9998
ENSG00000165684	ENSG00000165684	SNAPC4	9:139270028-139293249	OK	3.17125	3.8808	0.2913	0.590166	0.3357	0.9998
ENSG00000107937	ENSG00000107937	GTPBP4	10:1034337-1095110	OK	19.2295	27.2527	0.503081	0.511434	0.3359	0.9998
ENSG00000180767	ENSG00000180767	CHST13	3:126243125-126277808	OK	0.464138	0.678518	0.547833	0.59739	0.33595	0.9998
ENSG00000139160	ENSG00000139160	METTL20	12:31800093-31882108	OK	1.03582	0.523258	-0.985182	-0.471143	0.336	0.9998
ENSG00000134202	ENSG00000134202	GSTM3	1:110254863-110318050	OK	49.5807	60.1812	0.279535	0.591364	0.33605	0.9998
ENSG00000164708	ENSG00000164708	PGAM2	7:44084238-44109055	OK	6.36581	19.5556	1.61916	0.736111	0.3361	0.9998
ENSG00000139211	ENSG00000139211	AMIGO2	12:47469489-47630443	OK	0.964874	1.32434	0.456863	0.586228	0.33625	0.9998
ENSG00000198947	ENSG00000198947	DMD	X:31115793-33357558	OK	3.50256	4.37378	0.32047	0.379696	0.33665	0.9998
ENSG00000266993	ENSG00000266993	RP4-657D16.3	1:52027537-52344477	OK	0.821925	0.346842	-1.24473	-0.130702	0.3367	0.9998
ENSG00000096654	ENSG00000096654	ZNF184	6:27418521-27440897	OK	2.42113	1.90145	-0.348582	-0.590535	0.3368	0.9998
ENSG00000171703	ENSG00000171703	TCEA2	20:62681188-62703700	OK	8.94272	6.73795	-0.408404	-0.551283	0.337	0.9998
ENSG00000232977	ENSG00000232977	LINC00327	13:24040709-24061603	OK	2.67681	2.00745	-0.415155	-0.594386	0.337	0.9998
ENSG00000134982	ENSG00000134982	APC	5:112043194-112258236	OK	3.50212	5.14124	0.553888	0.283194	0.33705	0.9998
ENSG00000198246	ENSG00000198246	SLC29A3	10:73079014-73123142	OK	0.671344	0.925489	0.463163	0.514485	0.3371	0.9998
ENSG00000261711	ENSG00000261711	RP11-80F22.9	16:34711784-34714852	OK	0.810687	0.508753	-0.67218	-0.529358	0.3371	0.9998
ENSG00000102524	ENSG00000102524	TNFSF13B	13:108903587-108960832	OK	0.920558	1.44326	0.648754	0.459859	0.3374	0.9998
ENSG00000228013	ENSG00000228013	RP11-350G8.5	1:154374803-154441926	OK	0.836484	0.249381	-1.74599	-0.183258	0.3374	0.9998
ENSG00000180573	ENSG00000180573	HIST1H2AC	6:26124372-26139344	OK	14.2067	18.2466	0.361058	0.570819	0.3375	0.9998
ENSG00000123737	ENSG00000123737	EXOSC9	4:122722471-122745087	OK	24.9129	18.3336	-0.442402	-0.536751	0.33765	0.9998
ENSG00000099364	ENSG00000099364	FBXL19	16:30930639-30967832	OK	8.06656	10.35	0.359606	0.530575	0.3377	0.9998
ENSG00000132383	ENSG00000132383	RPA1	17:1682778-1803376	OK	61.8082	47.6201	-0.37623	-0.52198	0.3377	0.9998
ENSG00000163006	ENSG00000163006	CCDC138	2:109403212-109501933	OK	2.95052	2.28041	-0.371676	-0.51089	0.3378	0.9998
ENSG00000213442	ENSG00000213442	RPL18AP3	12:104609556-104744061	OK	957.797	1287.99	0.427325	0.586729	0.3378	0.9998
ENSG00000135929	ENSG00000135929	CYP27A1	2:219646471-219680016	OK	120.899	102.547	-0.237521	-0.556295	0.33785	0.9998
ENSG00000179195	ENSG00000179195	ZNF664	12:124247041-124800570	OK	56.8695	48.0445	-0.243284	-0.420528	0.3379	0.9998
ENSG00000169607	ENSG00000169607	CKAP2L	2:113479062-113522254	OK	13.7384	11.0551	-0.31351	-0.483397	0.3383	0.9998
ENSG00000101400	ENSG00000101400	SNTA1	20:31995760-32031698	OK	19.5109	23.2506	0.252985	0.586421	0.33875	0.9998
ENSG00000165916	ENSG00000165916	PSMC3	11:47440319-47447993	OK	112.562	94.2253	-0.256529	-0.567432	0.3388	0.9998
ENSG00000226869	ENSG00000226869	LHFPL3-AS1	7:103969103-104549001	OK	340.136	285.387	-0.253192	-0.581284	0.3388	0.9998
ENSG00000135049	ENSG00000135049	AGTPBP1	9:88161454-88356944	OK	9.13468	7.33642	-0.316279	-0.524133	0.33885	0.9998
ENSG00000152413	ENSG00000152413	HOMER1	5:78668458-78810040	OK	4.13642	5.70233	0.463168	0.497915	0.339	0.9998
ENSG00000171522	ENSG00000171522	PTGER4	5:40679599-40693837	OK	0.607365	0.935795	0.623629	0.39355	0.33915	0.9998
ENSG00000178718	ENSG00000178718	RPP25	15:75246756-75313837	OK	13.5928	17.537	0.367559	0.583379	0.33915	0.9998
ENSG00000103035	ENSG00000103035	PSMD7	16:74330672-74403724	OK	28.6955	35.004	0.286699	0.571892	0.33925	0.9998
ENSG00000139318	ENSG00000139318	DUSP6	12:89741008-89747048	OK	50.5058	61.9924	0.295641	0.566238	0.33935	0.9998
ENSG00000078237	ENSG00000078237	C12orf5	12:4430370-4462338	OK	37.26	44.2936	0.249471	0.576931	0.33945	0.9998
ENSG00000100523	ENSG00000100523	DDHD1	14:53510685-53620000	OK	4.55656	3.7553	-0.279019	-0.449168	0.3395	0.9998
ENSG00000156697	ENSG00000156697	UTP14A	X:129003039-129091504	OK	11.7045	14.0511	0.263625	0.574353	0.33955	0.9998
ENSG00000198168	ENSG00000198168	SVIP	11:22835344-22966939	OK	75.0118	55.7536	-0.428054	-0.573389	0.33955	0.9998
ENSG00000217128	ENSG00000217128	FNIP1	5:130759613-131132710	OK	5.25939	6.65316	0.339144	0.560567	0.3398	0.9998
ENSG00000160310	ENSG00000160310	PRMT2	21:48055078-48085036	OK	61.7967	50.8121	-0.282357	-0.594945	0.33985	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000100578	ENSG00000100578	KIAA0586	14:58862633-59015216	OK	7.88863	5.64052	-0.483945	-0.41694	0.33995	0.9998
ENSG00000166902	ENSG00000166902	MRPL16	11:59573607-59578345	OK	67.3973	56.4712	-0.255176	-0.587055	0.33995	0.9998
ENSG00000168061	ENSG00000168061	SAC3D1	11:64808372-64826021	OK	11.5433	9.23131	-0.322445	-0.592581	0.33995	0.9998
ENSG00000112983	ENSG00000112983	BRD8	5:137475454-137549032	OK	29.3126	22.3951	-0.388336	-0.357989	0.34	0.9998
ENSG00000023318	ENSG00000023318	ERP44	9:102741460-102861322	OK	10.0852	8.48577	-0.249122	-0.572753	0.34005	0.9998
ENSG00000185803	ENSG00000185803	SLC52A2	8:145575877-145584932	OK	28.8146	34.6572	0.266356	0.556782	0.34005	0.9998
ENSG00000131469	ENSG00000131469	RPL27	17:41150289-41154976	OK	1955.5	2318.03	0.24536	0.577005	0.3401	0.9998
ENSG00000089327	ENSG00000089327	FXYD5	19:35645632-35660786	OK	63.0441	74.7535	0.24578	0.573507	0.34015	0.9998
ENSG00000204388	ENSG00000204388	HSPA1B	6:31795511-31798031	OK	11.7462	9.60195	-0.290801	-0.584909	0.3402	0.9998
ENSG00000250988	ENSG00000250988	RP11-752G15.6	15:83419315-83474822	OK	5.14306	3.34082	-0.622423	-0.587988	0.34035	0.9998
ENSG00000134897	ENSG00000134897	BIVM	13:103451398-103528345	OK	10.7854	7.90721	-0.447844	-0.444919	0.34045	0.9998
ENSG00000142227	ENSG00000142227	EMP3	19:48799713-48833810	OK	224.636	277.101	0.302823	0.521856	0.3406	0.9998
ENSG00000175984	ENSG00000175984	DENND2C	1:115125468-115213043	OK	0.902952	0.631883	-0.514991	-0.504959	0.3406	0.9998
ENSG00000103995	ENSG00000103995	CEP152	15:49005124-49103785	OK	3.41259	2.61746	-0.382699	-0.288245	0.34075	0.9998
ENSG00000163517	ENSG00000163517	HDAC11	3:13518481-13547916	OK	11.5169	9.17126	-0.328559	-0.506206	0.3408	0.9998
ENSG00000122515	ENSG00000122515	ZMIZ2	7:44788179-44809477	OK	18.5516	15.3444	-0.273832	-0.453824	0.34095	0.9998
ENSG00000115539	ENSG00000115539	PDCL3	2:101179151-101193197	OK	19.7148	24.0412	0.286233	0.594641	0.341	0.9998
ENSG00000154305	ENSG00000154305	MIA3	1:222791427-222841354	OK	31.1806	37.6804	0.273163	0.414501	0.34105	0.9998
ENSG00000163644	ENSG00000163644	PPM1K	4:89178771-89205921	OK	4.37695	3.24402	-0.432144	-0.538287	0.34115	0.9998
ENSG00000175040	ENSG00000175040	CHST2	3:142838172-142841800	OK	3.58407	4.41179	0.299765	0.570675	0.3412	0.9998
ENSG00000168538	ENSG00000168538	TRAPPC11	4:184580419-184634745	OK	5.67785	4.66687	-0.28289	-0.462939	0.34135	0.9998
ENSG00000204524	ENSG00000204524	ZNF805	19:57751972-57766503	OK	2.37665	1.83412	-0.37384	-0.580696	0.3414	0.9998
ENSG00000196821	ENSG00000196821	C6orf106	6:34555064-34665247	OK	46.1055	53.9644	0.227068	0.572242	0.3416	0.9998
ENSG00000241978	ENSG00000241978	AKAP2	9:112403067-112934792	OK	8.17619	11.398	0.479284	0.56858	0.3416	0.9998
ENSG00000067057	ENSG00000067057	PFKP	10:3108524-3179904	OK	29.3683	24.8306	-0.242142	-0.528573	0.34165	0.9998
ENSG00000092148	ENSG00000092148	HECTD1	14:31569317-31677010	OK	30.9805	37.2338	0.265252	0.3981	0.34165	0.9998
ENSG00000175970	ENSG00000175970	UNC119B	12:121148237-121161443	OK	19.8005	16.738	-0.242411	-0.455055	0.3417	0.9998
ENSG00000196693	ENSG00000196693	ZNF33B	10:43069632-43134016	OK	0.682601	0.51665	-0.401856	-0.571175	0.3417	0.9998
ENSG00000012822	ENSG00000012822	CALCOCO1	12:54104902-54121529	OK	21.875	18.0664	-0.275975	-0.482519	0.3418	0.9998
ENSG00000223768	ENSG00000223768	LINC00205	21:46713199-46717269	OK	1.23589	1.68513	0.447313	0.579147	0.34195	0.9998
ENSG00000062282	ENSG00000062282	DGAT2	11:75469499-75514460	OK	5.46564	7.33226	0.423867	0.55915	0.342	0.9998
ENSG00000172201	ENSG00000172201	ID4	6:19535174-19840915	OK	17.4029	20.6605	0.247551	0.564582	0.3421	0.9998
ENSG00000075651	ENSG00000075651	PLD1	3:171318194-171528740	OK	21.5568	17.88	-0.269797	-0.409669	0.3422	0.9998
ENSG00000109846	ENSG00000109846	CRYAB	11:111779288-111797596	OK	194.068	233.554	0.267198	0.550844	0.34225	0.9998
ENSG00000082014	ENSG00000082014	SMARCD3	7:150929574-150974982	OK	18.1904	25.853	0.507154	0.515207	0.3423	0.9998
ENSG00000143398	ENSG00000143398	PIP5K1A	1:151170424-151222012	OK	50.1057	58.909	0.233513	0.48535	0.3424	0.9998
ENSG00000166881	ENSG00000166881	TMEM194A	12:57449425-57481846	OK	15.0831	12.7947	-0.237386	-0.547901	0.34255	0.9998
ENSG00000099957	ENSG00000099957	P2RX6	22:21353392-21399306	OK	1.21888	0.701098	-0.797864	-0.36197	0.3426	0.9998
ENSG00000147872	ENSG00000147872	PLIN2	9:19108372-19149288	OK	123.882	146.013	0.237124	0.549363	0.3427	0.9998
ENSG00000267769	ENSG00000267769	CTB-50L17.9	19:4402658-4457819	OK	0.708578	0.127476	-2.4747	-0.204115	0.3427	0.9998
ENSG00000057252	ENSG00000057252	SOAT1	1:179262924-179327815	OK	25.6163	32.4234	0.339972	0.568137	0.34275	0.9998
ENSG00000176994	ENSG00000176994	SMCR8	17:18218623-18226517	OK	5.75402	6.95299	0.273064	0.56515	0.3429	0.9998
ENSG00000101745	ENSG00000101745	ANKRD12	18:9102627-9285983	OK	8.4884	6.01775	-0.496269	-0.295741	0.343	0.9998
ENSG00000132361	ENSG00000132361	CLUH	17:2592679-2616127	OK	31.1193	26.2017	-0.248148	-0.367087	0.3431	0.9998
ENSG00000104064	ENSG00000104064	GABPB1	15:50569388-50659636	OK	10.5758	13.1485	0.314135	0.526223	0.34315	0.9998
ENSG00000114790	ENSG00000114790	ARHGEF26	3:153742189-153975616	OK	4.92695	3.94333	-0.321278	-0.58312	0.34325	0.9998
ENSG00000181555	ENSG00000181555	SETD2	3:47057918-47205457	OK	8.9815	7.46785	-0.266264	-0.409776	0.34325	0.9998
ENSG00000249319	ENSG00000249319	AC068533.7	7:65540784-65629998	OK	0.624127	0.0897821	-2.79734	-0.310412	0.34325	0.9998
ENSG00000071575	ENSG00000071575	TRIB2	2:12857014-12882860	OK	193.414	156.127	-0.308977	-0.531176	0.3435	0.9998
ENSG00000229117	ENSG00000229117	RPL41	12:56510369-56511727	OK	938.473	1110.83	0.243254	0.578987	0.3435	0.9998
ENSG00000242498	ENSG00000242498	C15orf38	15:90373830-90456188	OK	5.53836	3.63351	-0.608094	-0.464962	0.34365	0.9998
ENSG00000154027	ENSG00000154027	AK5	1:77747735-78025651	OK	0.878663	1.30492	0.570579	0.360226	0.3437	0.9998
ENSG00000197283	ENSG00000197283	SYNGAP1	6:33387846-33421466	OK	4.89725	6.41915	0.39041	0.339813	0.34375	0.9998
ENSG00000235674	ENSG00000235674	LDHAP2	1:235824340-236046940	OK	0.738331	0.187607	-1.97655	-0.089051	0.3438	0.9998
ENSG00000164300	ENSG00000164300	SERINC5	5:79407049-79551898	OK	41.0681	48.6409	0.244152	0.575558	0.34385	0.9998
ENSG00000168874	ENSG00000168874	ATOH8	2:85978466-86015189	OK	20.5409	16.3566	-0.328626	-0.560345	0.3439	0.9998
ENSG00000159579	ENSG00000159579	RSPRY1	16:57220048-57274387	OK	6.47881	4.87988	-0.408884	-0.436988	0.34405	0.9998
ENSG00000122547	ENSG00000122547	EEPD1	7:36192757-36341152	OK	3.9373	5.9821	0.603445	0.606059	0.3441	0.9998
ENSG00000141349	ENSG00000141349	G6PC3	17:42148102-42153709	OK	63.5936	53.2993	-0.254765	-0.565808	0.3442	0.9998
ENSG00000014641	ENSG00000014641	MDH1	2:63348517-64054977	OK	349.986	295.618	-0.243565	-0.564402	0.34425	0.9998
ENSG00000116704	ENSG00000116704	SLC35D1	1:67465014-67519782	OK	4.34523	5.26205	0.27619	0.567924	0.3444	0.9998
ENSG00000143631	ENSG00000143631	FLG	1:152140600-152339163	OK	3.73073	4.57815	0.295305	0.575489	0.34455	0.9998
ENSG00000260552	ENSG00000260552	RP11-49I11.1	18:33759958-33767411	OK	1.57404	1.04488	-0.591127	-0.573937	0.3446	0.9998
ENSG00000168575	ENSG00000168575	SLC20A2	8:42273992-42409603	OK	12.1428	15.9377	0.392339	0.433953	0.34465	0.9998
ENSG00000109501	ENSG00000109501	WFS1	4:6271575-6304992	OK	5.71407	7.00576	0.294024	0.477825	0.3447	0.9998
ENSG00000099290	ENSG00000099290	FAM21A	10:51827647-51893269	OK	3.50067	4.52526	0.370367	0.489498	0.3448	0.9998
ENSG00000172893	ENSG00000172893	DHCR7	11:71139238-71163914	OK	71.8211	58.8611	-0.287093	-0.544067	0.3448	0.9998
ENSG00000185278	ENSG00000185278	ZBTB37	1:173832385-173872687	OK	2.26012	1.39004	-0.701275	-0.224419	0.34485	0.9998
ENSG00000104728	ENSG00000104728	ARHGEF10	8:1772141-1906807	OK	15.1191	12.4145	-0.284338	-0.486744	0.3449	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000173041	ENSG00000173041	ZNF680	7:63980261-64023484	OK	3.31462	2.41853	-0.454714	-0.531361	0.3449	0.9998
ENSG00000166471	ENSG00000166471	TMEM41B	11:9302200-9336327	OK	13.3119	10.544	-0.336291	-0.552189	0.345	0.9998
ENSG00000214194	ENSG00000214194	LINC00998	7:112740717-112786385	OK	98.3398	83.4356	-0.237112	-0.571436	0.3451	0.9998
ENSG00000052126	ENSG00000052126	PLEKHA5	12:19282647-19529334	OK	24.6826	29.5887	0.261554	0.452313	0.34515	0.9998
ENSG00000100364	ENSG00000100364	KIAA0930	22:45586218-45636650	OK	39.5662	47.9248	0.276506	0.528307	0.34515	0.9998
ENSG00000181852	ENSG00000181852	RNF41	12:56598284-56615717	OK	23.3088	28.4207	0.286064	0.552555	0.34515	0.9998
ENSG00000165392	ENSG00000165392	WRN	8:30891316-31034683	OK	3.96806	3.19503	-0.312604	-0.456195	0.3453	0.9998
ENSG00000156381	ENSG00000156381	ANKRD9	14:102973178-102976136	OK	26.1974	31.3952	0.261121	0.573866	0.34535	0.9998
ENSG00000119471	ENSG00000119471	HSDL2	9:115142216-115431677	OK	22.4189	17.9298	-0.32236	-0.562503	0.34545	0.9998
ENSG00000169122	ENSG00000169122	FAM110B	8:58907067-59116838	OK	1.38602	2.09882	0.598634	0.460129	0.3455	0.9998
ENSG00000253785	ENSG00000253785	CTC-308K20.3	5:172402513-172403377	OK	1.9058	2.61523	0.45654	0.584644	0.34555	0.9998
ENSG00000110046	ENSG00000110046	ATG2A	11:64662006-64684722	OK	7.19466	8.67691	0.270255	0.417437	0.3458	0.9998
ENSG00000256124	ENSG00000256124	LINC01152	17:70017991-70216859	OK	0.903304	0.312802	-1.52996	-0.425075	0.34585	0.9998
ENSG00000186283	ENSG00000186283	TOR3A	1:179050511-179067158	OK	18.6422	22.3725	0.263152	0.504242	0.3461	0.9998
ENSG00000130881	ENSG00000130881	LRP3	19:33668508-33698694	OK	6.69972	8.34008	0.315959	0.587657	0.3462	0.9998
ENSG00000086061	ENSG00000086061	DNAJA1	9:33025208-33039905	OK	143.975	170.422	0.24329	0.561394	0.3463	0.9998
ENSG00000167232	ENSG00000167232	ZNF91	19:23487792-23578362	OK	1.28312	2.0084	0.646389	0.434837	0.34635	0.9998
ENSG00000124207	ENSG00000124207	CSE1L	20:47662848-47713489	OK	74.8031	87.9654	0.233837	0.56479	0.34645	0.9998
ENSG00000101337	ENSG00000101337	TM9SF4	20:30697308-30755061	OK	31.7418	27.1615	-0.224825	-0.506905	0.3465	0.9998
ENSG00000123700	ENSG00000123700	KCNJ2	17:68163101-68176189	OK	3.73356	2.99265	-0.319127	-0.565659	0.34655	0.9998
ENSG00000087095	ENSG00000087095	NLK	17:26368762-26523407	OK	18.8852	15.7825	-0.258924	-0.524385	0.3466	0.9998
ENSG00000131669	ENSG00000131669	NINJ1	9:95883770-95896570	OK	69.8066	82.3456	0.238328	0.574048	0.3469	0.9998
ENSG00000242299	ENSG00000242299	RP11-234A1.1	3:101292938-101313281	OK	175.454	249.947	0.510532	0.571003	0.34695	0.9998
ENSG00000108679	ENSG00000108679	LGALS3BP	17:76967319-76976191	OK	282.321	331.83	0.233107	0.527198	0.347	0.9998
ENSG00000170113	ENSG00000170113	NIPA1	15:23043276-23115256	OK	5.00715	6.00219	0.2615	0.41277	0.3472	0.9998
ENSG00000175893	ENSG00000175893	ZDHHC21	9:14611068-14693469	OK	3.51267	2.71115	-0.373661	-0.326508	0.3474	0.9998
ENSG00000159399	ENSG00000159399	HK2	2:75059781-75120486	OK	39.4046	46.9054	0.251389	0.570948	0.34745	0.9998
ENSG00000140905	ENSG00000140905	GCSH	16:81087101-81130008	OK	11.1463	14.512	0.38068	0.588463	0.3475	0.9998
ENSG00000151914	ENSG00000151914	DST	6:56322784-56819426	OK	18.5237	14.8105	-0.322753	-0.369933	0.3475	0.9998
ENSG00000126216	ENSG00000126216	TUBGCP3	13:113139324-113242481	OK	15.3903	12.8338	-0.262077	-0.53296	0.34755	0.9998
ENSG00000151552	ENSG00000151552	QDPR	4:17461883-17513857	OK	89.1207	75.5902	-0.237563	-0.561637	0.34765	0.9998
ENSG00000065243	ENSG00000065243	PKN2	1:89003195-89301938	OK	16.9506	14.0897	-0.266698	-0.463299	0.3477	0.9998
ENSG00000125753	ENSG00000125753	VASP	19:46009836-46030241	OK	19.2693	22.8959	0.248781	0.454306	0.34775	0.9998
ENSG00000130244	ENSG00000130244	FAM98C	19:38893774-38916945	OK	9.68083	7.66807	-0.336267	-0.540546	0.34775	0.9998
ENSG00000138688	ENSG00000138688	KIAA1109	4:123073487-123283913	OK	12.8183	10.6303	-0.270011	-0.447777	0.34775	0.9998
ENSG00000154080	ENSG00000154080	CHST9	18:24034873-24770662	OK	10.5051	8.13278	-0.36927	-0.580927	0.34775	0.9998
ENSG00000111961	ENSG00000111961	SASH1	6:148558720-148873186	OK	10.8588	9.19595	-0.239799	-0.555	0.34785	0.9998
ENSG00000165233	ENSG00000165233	C9orf89	9:95858499-95875565	OK	26.7281	33.1992	0.312792	0.552498	0.3479	0.9998
ENSG00000149577	ENSG00000149577	SIDT2	11:117049448-117068160	OK	7.11852	9.27517	0.381797	0.475503	0.34795	0.9998
ENSG00000106617	ENSG00000106617	PRKAG2	7:151253196-151576299	OK	11.2613	13.8083	0.294166	0.462508	0.34825	0.9998
ENSG00000064763	ENSG00000064763	FAR2	12:29302035-29534122	OK	16.3753	22.1784	0.437632	0.378391	0.3483	0.9998
ENSG00000139197	ENSG00000139197	PEX5	12:7319269-7371170	OK	15.474	18.2719	0.239779	0.451949	0.3483	0.9998
ENSG00000186918	ENSG00000186918	ZNF395	8:28203101-28347835	OK	15.0673	12.5441	-0.264419	-0.379433	0.34835	0.9998
ENSG00000085224	ENSG00000085224	ATRX	X:76760355-77041702	OK	7.84022	6.11516	-0.358503	-0.253174	0.34845	0.9998
ENSG00000106333	ENSG00000106333	PCOLCE	7:100169854-100205798	OK	8.52121	4.90588	-0.796547	-0.421485	0.34845	0.9998
ENSG00000170854	ENSG00000170854	MINA	3:97595818-97691301	OK	15.0208	18.5743	0.306341	0.489889	0.34845	0.9998
ENSG00000189266	ENSG00000189266	PNRC2	1:24285598-24289952	OK	33.1879	40.3084	0.280423	0.463082	0.34855	0.9998
ENSG00000102316	ENSG00000102316	MAGED2	X:54834031-54842445	OK	123.2	145.433	0.23935	0.513469	0.34875	0.9998
ENSG00000267756	ENSG00000267756	RP11-411B10.4	18:14057455-14132489	OK	0.743296	0.191576	-1.95602	-0.790641	0.34875	0.9998
ENSG00000135900	ENSG00000135900	MRPL44	2:224822120-224832431	OK	42.6026	50.1527	0.235387	0.571252	0.34895	0.9998
ENSG00000067955	ENSG00000067955	CBFB	16:67063018-67134961	OK	21.5906	27.3699	0.342185	0.520795	0.3491	0.9998
ENSG00000110013	ENSG00000110013	SIAE	11:124492731-124567414	OK	5.82056	4.20923	-0.467602	-0.552306	0.3493	0.9998
ENSG00000139428	ENSG00000139428	MMAB	12:109991541-110035067	OK	35.9292	26.5834	-0.434631	-0.580772	0.3493	0.9998
ENSG00000170889	ENSG00000170889	RPS9	19:54704609-54752862	OK	809.627	954.808	0.237953	0.565486	0.3493	0.9998
ENSG00000101986	ENSG00000101986	ABCD1	X:152990322-153051187	OK	24.2606	30.5379	0.331985	0.513586	0.34935	0.9998
ENSG00000043093	ENSG00000043093	DCUN1D1	3:182655861-182703741	OK	18.9944	24.9234	0.391923	0.534232	0.3494	0.9998
ENSG00000146826	ENSG00000146826	C7orf43	7:99746529-99756338	OK	11.2228	16.4892	0.55509	0.457173	0.34945	0.9998
ENSG00000257261	ENSG00000257261	RP11-96H19.1	12:46777461-46850051	OK	2.54845	1.04977	-1.27954	-0.881325	0.3498	0.9998
ENSG00000243679	ENSG00000243679	RP11-274B21.3	7:128294022-128294776	OK	8.38908	6.46772	-0.375255	-0.570285	0.34985	0.9998
ENSG00000143842	ENSG00000143842	SOX13	1:204042242-204096863	OK	37.3492	31.0572	-0.266151	-0.486086	0.34995	0.9998
ENSG00000272335	ENSG00000272335	RP11-53O19.3	5:44826177-44828694	OK	3.18538	3.97358	0.318976	0.574093	0.34995	0.9998
ENSG00000154237	ENSG00000154237	LRRK1	15:101389765-101626271	OK	3.15774	4.64394	0.556458	0.295014	0.35005	0.9998
ENSG00000142494	ENSG00000142494	SLC47A1	17:19398697-19501235	OK	1.4578	1.9378	0.410628	0.411507	0.35035	0.9998
ENSG00000204116	ENSG00000204116	CHIC1	X:72783035-72906937	OK	3.85144	4.7456	0.301192	0.467156	0.35035	0.9998
ENSG00000170638	ENSG00000170638	TRABD	22:50624343-50638976	OK	19.284	23.0282	0.255998	0.574008	0.3504	0.9998
ENSG00000132010	ENSG00000132010	ZNF20	19:12203077-12267546	OK	2.52487	1.44923	-0.800926	-0.510287	0.3506	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000145779	ENSG00000145779	TNFAIP8	5:118604386-118735383	OK	2.14005	1.46012	-0.55156	-0.493432	0.35065	0.9998
ENSG00000112081	ENSG00000112081	SRSF3	6:36562144-36573377	OK	66.9223	53.8857	-0.312585	-0.54053	0.3508	0.9998
ENSG00000113593	ENSG00000113593	PPWD1	5:64859062-64883376	OK	19.4052	15.9127	-0.286268	-0.524151	0.35085	0.9998
ENSG00000082641	ENSG00000082641	NFE2L1	17:46125690-46138849	OK	95.5855	112.946	0.240765	0.453772	0.3509	0.9998
ENSG00000180818	ENSG00000180818	HOXC10	12:54375292-54449814	OK	15.9242	11.7029	-0.444352	-0.525522	0.3509	0.9998
ENSG00000261609	ENSG00000261609	GAN	16:81348556-81424489	OK	0.791633	1.01721	0.361714	0.436932	0.35115	0.9998
ENSG00000137834	ENSG00000137834	SMAD6	15:66994565-67074338	OK	2.95829	2.20196	-0.42598	-0.542601	0.35125	0.9998
ENSG00000176401	ENSG00000176401	EID2B	19:40021629-40025062	OK	1.85624	1.41092	-0.395744	-0.49881	0.35135	0.9998
ENSG00000130669	ENSG00000130669	PAK4	19:39616409-39673456	OK	21.7014	26.8819	0.308846	0.558543	0.35145	0.9998
ENSG00000139746	ENSG00000139746	RBM26	13:79885961-79998463	OK	16.2111	13.7219	-0.240501	-0.552232	0.3515	0.9998
ENSG00000085982	ENSG00000085982	USP40	2:234384165-234475428	OK	5.97555	4.74701	-0.332051	-0.40869	0.35155	0.9998
ENSG00000176749	ENSG00000176749	CDK5R1	17:30813636-30818274	OK	24.6112	28.9097	0.232239	0.464574	0.3516	0.9998
ENSG00000171475	ENSG00000171475	WIPF2	17:38375555-38440388	OK	7.19966	5.82675	-0.305239	-0.476229	0.35165	0.9998
ENSG00000164209	ENSG00000164209	SLC25A46	5:109624933-110100857	OK	14.8686	17.9363	0.270606	0.560774	0.35185	0.9998
ENSG00000072134	ENSG00000072134	EPN2	17:19118927-19240028	OK	10.4736	13.2641	0.34077	0.325848	0.3519	0.9998
ENSG00000120899	ENSG00000120899	PTK2B	8:27168998-27316903	OK	1.38673	1.92961	0.476626	0.328736	0.35195	0.9998
ENSG00000143514	ENSG00000143514	TP53BP2	1:223967600-224033674	OK	14.8505	17.4595	0.233505	0.403	0.35205	0.9998
ENSG00000167112	ENSG00000167112	TRUB2	9:131071381-131096351	OK	34.2983	41.2909	0.267688	0.549791	0.35215	0.9998
ENSG00000230337	ENSG00000230337	RP4-635E18.6	1:11126674-11162157	OK	0.445265	1.30426	1.5505	0.194458	0.3522	0.9998
ENSG00000131797	ENSG00000131797	CLUHP3	16:31711910-31723305	OK	1.58931	2.08355	0.390643	0.522381	0.35235	0.9998
ENSG00000166333	ENSG00000166333	ILK	11:6624871-6633898	OK	102.755	86.2462	-0.252683	-0.52248	0.3525	0.9998
ENSG00000054523	ENSG00000054523	KIF1B	1:10270862-10441661	OK	10.4848	8.89097	-0.23789	-0.497052	0.3526	0.9998
ENSG00000089094	ENSG00000089094	KDM2B	12:121837843-122031409	OK	9.28449	7.3455	-0.337961	-0.447175	0.3526	0.9998
ENSG00000084090	ENSG00000084090	STARD7	2:96850596-96908359	OK	77.339	89.9473	0.217883	0.471679	0.3528	0.9998
ENSG00000213222	ENSG00000213222	AC093724.2	2:132479947-132524973	OK	2.16203	2.90305	0.425183	0.563035	0.3528	0.9998
ENSG00000079385	ENSG00000079385	CEACAM1	19:42901279-43156507	OK	64.5201	79.5135	0.301452	0.415756	0.35305	0.9998
ENSG00000148019	ENSG00000148019	CEP78	9:80850977-80894606	OK	19.5902	15.8357	-0.306946	-0.545653	0.35325	0.9998
ENSG00000106327	ENSG00000106327	TFR2	7:100218038-100240402	OK	1.33988	0.914766	-0.550627	-0.51167	0.35335	0.9998
ENSG00000142197	ENSG00000142197	DOPEY2	21:37529079-37666572	OK	2.07419	1.54536	-0.424604	-0.35288	0.3534	0.9998
ENSG00000232810	ENSG00000232810	TNF	6:31543343-31546113	OK	0.747653	0.522355	-0.51734	-0.553334	0.35365	0.9998
ENSG00000139372	ENSG00000139372	TDG	12:104359581-104382652	OK	12.758	10.6224	-0.264303	-0.516248	0.35385	0.9998
ENSG00000047188	ENSG00000047188	YTHDC2	5:112849379-112930982	OK	6.28187	5.20923	-0.270123	-0.437842	0.35395	0.9998
ENSG00000094916	ENSG00000094916	CBX5	12:54624723-54745633	OK	17.9101	11.6446	-0.62111	-0.441206	0.35395	0.9998
ENSG00000010539	ENSG00000010539	ZNF200	16:3238211-3286221	OK	4.9176	3.83051	-0.360417	-0.550516	0.3541	0.9998
ENSG00000172590	ENSG00000172590	MRPL52	14:23299087-23304246	OK	128.112	155.711	0.281465	0.554163	0.3541	0.9998
ENSG00000174749	ENSG00000174749	C4orf32	4:113066552-113116412	OK	0.539678	0.685869	0.345835	0.563317	0.3542	0.9998
ENSG00000175279	ENSG00000175279	APITD1	1:10489937-10512210	OK	19.2033	15.6091	-0.298964	-0.546122	0.3546	0.9998
ENSG00000189184	ENSG00000189184	PCDH18	4:138440071-138453648	OK	0.780337	1.09609	0.490191	0.525555	0.35465	0.9998
ENSG00000198909	ENSG00000198909	MAP3K3	17:61699774-61778532	OK	44.4768	36.3187	-0.292343	-0.472866	0.35465	0.9998
ENSG00000222009	ENSG00000222009	BTBD19	1:45274153-45281257	OK	2.55023	3.33714	0.387983	0.480868	0.35465	0.9998
ENSG00000066629	ENSG00000066629	EML1	14:100204029-100408397	OK	0.698181	1.03578	0.569044	0.263781	0.3547	0.9998
ENSG00000137076	ENSG00000137076	TLN1	9:35696944-35758572	OK	45.6612	36.501	-0.323033	-0.27325	0.3547	0.9998
ENSG00000137210	ENSG00000137210	TMEM14B	6:10747991-10979553	OK	170.827	146.192	-0.224675	-0.540638	0.35475	0.9998
ENSG00000143891	ENSG00000143891	GALM	2:38893051-38968379	OK	12.91	10.659	-0.276422	-0.53321	0.35475	0.9998
ENSG00000135686	ENSG00000135686	KLHL36	16:84682130-84701292	OK	10.8819	13.2921	0.288637	0.519713	0.355	0.9998
ENSG00000021826	ENSG00000021826	CPS1	2:211342405-211543831	OK	4.64301	3.60528	-0.364951	-0.386349	0.35505	0.9998
ENSG00000123130	ENSG00000123130	ACOT9	X:23720369-23784592	OK	23.2185	27.7088	0.255066	0.531948	0.3551	0.9998
ENSG00000145868	ENSG00000145868	FBXO38	5:147763497-147822399	OK	10.4248	12.4503	0.256157	0.386512	0.3551	0.9998
ENSG00000244716	ENSG00000244716	RP11-20O24.4	1:109512835-109584850	OK	167.537	202.145	0.270915	0.572917	0.35515	0.9998
ENSG00000174485	ENSG00000174485	DENND4A	15:65903703-66184329	OK	4.94491	3.38063	-0.548652	-0.377808	0.3555	0.9998
ENSG00000165806	ENSG00000165806	CASP7	10:115438941-115490662	OK	8.48273	6.8498	-0.308467	-0.544301	0.3556	0.9998
ENSG00000174799	ENSG00000174799	CEP135	4:56815036-56899529	OK	3.60286	2.71974	-0.405675	-0.53906	0.35585	0.9998
ENSG00000158711	ENSG00000158711	ELK4	1:205577070-205601090	OK	9.32932	7.71447	-0.274204	-0.383391	0.3561	0.9998
ENSG00000151012	ENSG00000151012	SLC7A11	4:138948575-139163503	OK	13.1668	15.423	0.228179	0.473262	0.3562	0.9998
ENSG00000251322	ENSG00000251322	SHANK3	22:51112842-51171726	OK	1.63988	1.33266	-0.299278	-0.558149	0.3562	0.9998
ENSG00000156709	ENSG00000156709	AIFM1	X:129263336-129299861	OK	48.0898	56.2042	0.224948	0.55172	0.35625	0.9998
ENSG00000008838	ENSG00000008838	MED24	17:38175349-38256978	OK	25.578	31.4033	0.29601	0.342454	0.3563	0.9998
ENSG00000169604	ENSG00000169604	ANTXR1	2:69240309-69476459	OK	21.9757	17.7236	-0.310238	-0.515009	0.3563	0.9998
ENSG00000128272	ENSG00000128272	ATF4	22:39915699-39918691	OK	309.872	262.994	-0.236646	-0.566629	0.35635	0.9998
ENSG00000212978	ENSG00000212978	AC016747.3	2:61293005-61391964	OK	3.10587	1.99005	-0.642194	-0.43728	0.3566	0.9998
ENSG00000099795	ENSG00000099795	NDUFB7	19:14676889-14682874	OK	263.457	308.048	0.225588	0.555617	0.3567	0.9998
ENSG00000103485	ENSG00000103485	QPRT	16:29674299-29710020	OK	80.952	101.784	0.33037	0.576633	0.3567	0.9998
ENSG00000111731	ENSG00000111731	C2CD5	12:22601516-22697480	OK	16.7146	14.2471	-0.23044	-0.438787	0.3567	0.9998
ENSG00000256514	ENSG00000256514	AP003419.11	11:67118247-67141648	OK	11.5366	5.64165	-1.03202	-0.548238	0.3568	0.9998
ENSG00000198554	ENSG00000198554	WDHD1	14:55405667-55493823	OK	12.4082	10.0825	-0.299451	-0.492499	0.35685	0.9998
ENSG00000103275	ENSG00000103275	UBE2I	16:1355547-1377019	OK	62.4642	52.3965	-0.253559	-0.521789	0.35695	0.9998
ENSG00000109674	ENSG00000109674	NEIL3	4:178230989-178284097	OK	2.31828	1.831	-0.340421	-0.548235	0.35705	0.9998
ENSG00000173213	ENSG00000173213	RP11-683L23.1	18:47224-73545	OK	1.32627	1.97545	0.574804	0.526674	0.35705	0.9998
ENSG00000226210	ENSG00000226210	ABC7-42389800N19.1	12:73724-91218	OK	8.40761	6.894	-0.286354	-0.555496	0.35705	0.9998
ENSG00000130702	ENSG00000130702	LAMA5	20:60877148-60942368	OK	5.50799	8.73745	0.665687	0.302073	0.3572	0.9998
ENSG00000254813	ENSG00000254813	RP11-252C15.1	8:12623357-12675800	OK	3.55744	4.58616	0.36645	0.540336	0.3573	0.9998
ENSG00000122642	ENSG00000122642	FKBP9	7:32535037-33102409	OK	116.538	90.4397	-0.365772	-0.463942	0.35735	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000143643	ENSG00000143643	TTC13	1:231041988-231114621	OK	11.0437	13.3868	0.277588	0.442957	0.35735	0.9998
ENSG00000236296	ENSG00000236296	GUSBP5	4:144480624-144786225	OK	1.39509	2.13148	0.611498	0.551153	0.3576	0.9998
ENSG00000107672	ENSG00000107672	NSMCE4A	10:123716602-123734732	OK	14.5093	11.8157	-0.296269	-0.551339	0.3577	0.9998
ENSG00000109572	ENSG00000109572	CLCN3	4:170533783-170644824	OK	19.9884	23.7029	0.245901	0.491998	0.35775	0.9998
ENSG00000145425	ENSG00000145425	RPS3A	4:152020724-152246784	OK	956.776	1142.44	0.255867	0.567107	0.3579	0.9998
ENSG00000111859	ENSG00000111859	NEDD9	6:11173684-11382581	OK	29.7705	34.7309	0.222336	0.523181	0.35795	0.9998
ENSG00000125844	ENSG00000125844	RRBP1	20:17594322-17662940	OK	24.9078	30.444	0.289558	0.546316	0.35815	0.9998
ENSG00000217555	ENSG00000217555	CKLF	16:66586465-66613040	OK	45.8081	37.5705	-0.286003	-0.561392	0.3584	0.9998
ENSG00000150630	ENSG00000150630	VEGFC	4:177590771-177713881	OK	1.21536	0.90053	-0.432534	-0.519631	0.35855	0.9998
ENSG00000153363	ENSG00000153363	LINC00467	1:211556144-211605878	OK	15.0083	11.5996	-0.371679	-0.554142	0.3586	0.9998
ENSG00000196313	ENSG00000196313	POM121	7:72349935-72425329	OK	18.7899	22.522	0.261379	0.569922	0.3586	0.9998
ENSG00000113272	ENSG00000113272	THG1L	5:157158204-157168456	OK	6.94917	9.18418	0.402311	0.566957	0.35875	0.9998
ENSG00000183853	ENSG00000183853	KIRREL	1:157963062-158070052	OK	164.537	137.695	-0.256939	-0.550588	0.3588	0.9998
ENSG00000101350	ENSG00000101350	KIF3B	20:30865466-30922814	OK	26.7712	22.9523	-0.222044	-0.555688	0.35885	0.9998
ENSG00000108349	ENSG00000108349	CASC3	17:38296570-38328436	OK	20.365	23.9268	0.232538	0.416726	0.35885	0.9998
ENSG00000196730	ENSG00000196730	DAPK1	9:90112142-90323548	OK	13.8281	11.7826	-0.23094	-0.357823	0.35895	0.9998
ENSG00000132694	ENSG00000132694	ARHGEF11	1:156904631-157015162	OK	42.4463	36.1062	-0.233392	-0.411781	0.35915	0.9998
ENSG00000182903	ENSG00000182903	ZNF721	4:419223-492945	OK	17.2547	12.7788	-0.433246	-0.543033	0.3592	0.9998
ENSG00000132470	ENSG00000132470	ITGB4	17:73717407-73761792	OK	0.686672	1.2406	0.853343	0.215878	0.3593	0.9998
ENSG00000133789	ENSG00000133789	SWAP70	11:9685623-9774538	OK	31.3968	36.9174	0.233683	0.529537	0.35935	0.9998
ENSG00000155850	ENSG00000155850	SLC26A2	5:149340299-149432386	OK	5.2844	3.55361	-0.572454	-0.557439	0.3596	0.9998
ENSG00000225733	ENSG00000225733	FGD5-AS1	3:14860468-15106842	OK	41.3947	31.8343	-0.378866	-0.573138	0.3596	0.9998
ENSG00000116396	ENSG00000116396	KCNC4	1:110753964-110825722	OK	2.74782	3.46119	0.332984	0.547812	0.35965	0.9998
ENSG00000144331	ENSG00000144331	ZNF385B	2:180306708-180726232	OK	0.633294	0.913089	0.52788	0.313337	0.35965	0.9998
ENSG00000066136	ENSG00000066136	NFYC	1:41156051-41237275	OK	21.9033	26.2341	0.260297	0.546827	0.35995	0.9998
ENSG00000225264	ENSG00000225264	ZNRF2P2	7:29638410-29782210	OK	2.16463	3.38487	0.644979	0.578176	0.35995	0.9998
ENSG00000067066	ENSG00000067066	SP100	2:231280656-231444721	OK	19.1494	22.9486	0.26111	0.472882	0.36005	0.9998
ENSG00000186106	ENSG00000186106	ANKRD46	8:101521979-101572012	OK	8.15781	10.1669	0.317624	0.492614	0.3601	0.9998
ENSG00000204138	ENSG00000204138	PHACTR4	1:28696113-28826881	OK	6.15422	5.0799	-0.276778	-0.544271	0.36025	0.9998
ENSG00000081913	ENSG00000081913	PHLPP1	18:60382671-60647666	OK	6.51463	5.46868	-0.25249	-0.418519	0.3603	0.9998
ENSG00000261812	ENSG00000261812	TUBB8P7	16:90159561-90162762	OK	0.658321	0.892732	0.439435	0.51374	0.3603	0.9998
ENSG00000107537	ENSG00000107537	PHYH	10:13319795-13344412	OK	1.84104	1.37191	-0.424328	-0.496527	0.36035	0.9998
ENSG00000197182	ENSG00000197182	FLJ27365	22:46445357-46509808	OK	1.66088	3.48098	1.06755	0.681736	0.3604	0.9998
ENSG00000166747	ENSG00000166747	AP1G1	16:71762912-71843104	OK	19.5438	15.9129	-0.296512	-0.414393	0.3605	0.9998
ENSG00000154727	ENSG00000154727	GABPA	21:27011583-27144771	OK	4.43921	3.11699	-0.510151	-0.513054	0.36055	0.9998
ENSG00000138821	ENSG00000138821	SLC39A8	4:103172197-103371167	OK	18.4474	15.677	-0.234769	-0.502421	0.36075	0.9998
ENSG00000136238	ENSG00000136238	RAC1	7:6414153-6443608	OK	133.85	111.626	-0.261951	-0.539683	0.3608	0.9998
ENSG00000257698	ENSG00000257698	RP11-620J15.3	12:58325310-58329958	OK	17.0259	13.4026	-0.345218	-0.562321	0.36095	0.9998
ENSG00000091513	ENSG00000091513	TF	3:133380841-133497850	OK	0.747895	0.502818	-0.5728	-0.244451	0.361	0.9998
ENSG00000165359	ENSG00000165359	DDX26B	X:134654007-134716435	OK	1.12404	0.832132	-0.433814	-0.427727	0.361	0.9998
ENSG00000138780	ENSG00000138780	GSTCD	4:106473776-106943635	OK	5.86748	4.42886	-0.405806	-0.475042	0.36105	0.9998
ENSG00000143079	ENSG00000143079	CTTNBP2NL	1:112938802-113006078	OK	4.79264	3.8477	-0.316824	-0.504155	0.36125	0.9998
ENSG00000102172	ENSG00000102172	SMS	X:21958690-22025798	OK	443.706	524.858	0.242324	0.557273	0.3613	0.9998
ENSG00000258791	ENSG00000258791	LINC00520	14:56247863-56263406	OK	77.1297	96.2571	0.319608	0.551604	0.36135	0.9998
ENSG00000196301	ENSG00000196301	HLA-DRB9	6:32427597-32441277	OK	0.672966	0.195926	-1.78022	-0.787181	0.36145	0.9998
ENSG00000197299	ENSG00000197299	BLM	15:91260557-91358859	OK	4.94232	4.03073	-0.294147	-0.437605	0.36145	0.9998
ENSG00000205572	ENSG00000205572	SERF1B	5:69321073-69338940	OK	2.24915	1.62257	-0.471101	-0.480272	0.36145	0.9998
ENSG00000196683	ENSG00000196683	TOMM7	7:22852250-22862470	OK	503.007	431.263	-0.222009	-0.545967	0.3615	0.9998
ENSG00000268362	ENSG00000268362	CTD-2017D11.1	19:24216246-24312654	OK	1.06568	1.77673	0.737452	0.561765	0.36165	0.9998
ENSG00000239002	ENSG00000239002	SCARNA10	12:6601149-6641121	OK	0.718567	0.159582	-2.17082	-0.0942487	0.36185	0.9998
ENSG00000109618	ENSG00000109618	SEPSECS	4:25121626-25162204	OK	3.3235	2.63071	-0.337253	-0.429512	0.3619	0.9998
ENSG00000166821	ENSG00000166821	PEX11A	15:90207595-90234014	OK	6.25017	4.81465	-0.376463	-0.560831	0.3619	0.9998
ENSG00000267265	ENSG00000267265	CTC-550B14.7	19:55517560-55582659	OK	0.753235	1.84072	1.2891	0.386216	0.362	0.9998
ENSG00000150867	ENSG00000150867	PIP4K2A	10:22823777-23003484	OK	33.7269	41.3704	0.294696	0.41822	0.3621	0.9998
ENSG00000243199	ENSG00000243199	RP11-408P14.1	4:66185280-66563747	OK	24.1278	30.6301	0.344252	0.554655	0.3622	0.9998
ENSG00000163565	ENSG00000163565	IFI16	1:158969757-159024945	OK	192.83	159.512	-0.273668	-0.560868	0.36235	0.9998
ENSG00000116685	ENSG00000116685	KIAA2013	1:11979647-11986485	OK	23.397	19.8548	-0.236836	-0.561539	0.3624	0.9998
ENSG00000099246	ENSG00000099246	RAB18	10:27793196-27831143	OK	29.1724	36.6722	0.330085	0.540807	0.36245	0.9998
ENSG00000227063	ENSG00000227063	RPL41P1	20:21735865-21736171	OK	96.7773	118.177	0.288205	0.548207	0.36265	0.9998
ENSG00000091009	ENSG00000091009	RBM27	5:145583112-145756526	OK	7.46832	8.91702	0.255777	0.549244	0.3627	0.9998
ENSG00000224081	ENSG00000224081	LINC01057	1:95104016-95285837	OK	2.57347	3.51346	0.44918	0.500601	0.3627	0.9998
ENSG00000114054	ENSG00000114054	PCCB	3:135969147-136471220	OK	35.1608	27.3839	-0.36064	-0.556031	0.36295	0.9998
ENSG00000138617	ENSG00000138617	PARP16	15:65526797-65592956	OK	4.97634	3.84914	-0.370547	-0.5293	0.36295	0.9998
ENSG00000242021	ENSG00000242021	RP11-268G12.3	X:27061023-27417114	OK	1.39366	0.788829	-0.821092	-0.511136	0.36295	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000010310	ENSG00000010310	GIPR	19:46171501-46186982	OK	1.07748	0.694484	-0.633649	-0.39709	0.363	0.9998
ENSG00000214944	ENSG00000214944	ARHGEF28	5:72921982-73237818	OK	0.926809	1.22613	0.403765	0.368137	0.36305	0.9998
ENSG00000136240	ENSG00000136240	KDELR2	7:6448756-6524873	OK	60.9763	74.6094	0.291107	0.533438	0.3632	0.9998
ENSG00000057757	ENSG00000057757	PITHD1	1:24104894-24114722	OK	19.7475	23.7194	0.264399	0.554247	0.36335	0.9998
ENSG00000127586	ENSG00000127586	CHTF18	16:834973-850737	OK	12.5788	9.79773	-0.360474	-0.405715	0.3635	0.9998
ENSG00000033011	ENSG00000033011	ALG1	16:4932507-5147809	OK	14.2812	18.3929	0.365034	0.542777	0.36375	0.9998
ENSG00000228594	ENSG00000228594	C1orf233	1:1533391-1535476	OK	3.30837	4.10435	0.311034	0.542162	0.36375	0.9998
ENSG00000114978	ENSG00000114978	MOB1A	2:74379654-74406025	OK	41.0541	33.2095	-0.305929	-0.484103	0.3638	0.9998
ENSG00000172340	ENSG00000172340	SUCLG2	3:67410883-67705038	OK	36.1778	30.857	-0.229506	-0.550405	0.36395	0.9998
ENSG00000006451	ENSG00000006451	RALA	7:39663081-39747723	OK	43.1012	34.452	-0.323138	-0.55034	0.364	0.9998
ENSG00000099958	ENSG00000099958	DERL3	22:24129149-24181315	OK	3.59434	1.97785	-0.861792	-0.351109	0.36405	0.9998
ENSG00000213339	ENSG00000213339	QTRT1	19:10812105-10824113	OK	27.7244	32.7773	0.241538	0.518254	0.3641	0.9998
ENSG00000218283	ENSG00000218283	MORF4L1P1	1:220321634-220445796	OK	48.8441	65.8386	0.430749	0.552092	0.36425	0.9998
ENSG00000164941	ENSG00000164941	INTS8	8:95825538-96128683	OK	27.258	21.293	-0.356304	-0.287344	0.3644	0.9998
ENSG00000144395	ENSG00000144395	CCDC150	2:197504277-197664449	OK	3.40506	2.26345	-0.58916	-0.215821	0.3647	0.9998
ENSG00000143207	ENSG00000143207	RFWD2	1:175913966-176176629	OK	21.3851	25.2594	0.240215	0.531869	0.3648	0.9998
ENSG00000236439	ENSG00000236439	RP11-175B9.3	1:202317826-202679545	OK	3467.84	4115.91	0.247177	0.564575	0.3648	0.9998
ENSG00000237190	ENSG00000237190	CDKN2AIPNL	5:133737777-133747589	OK	9.22055	7.45755	-0.306151	-0.55226	0.3648	0.9998
ENSG00000164983	ENSG00000164983	TMEM65	8:125324230-125384933	OK	6.96527	8.33065	0.25825	0.551498	0.36495	0.9998
ENSG00000186010	ENSG00000186010	NDUFA13	19:19623226-19648390	OK	255.472	297.67	0.220547	0.545294	0.36495	0.9998
ENSG00000126775	ENSG00000126775	ATG14	14:55833109-55878576	OK	7.4717	8.83991	0.242594	0.546999	0.3652	0.9998
ENSG00000096401	ENSG00000096401	CDC5L	6:44355261-44418163	OK	15.0565	12.8641	-0.227033	-0.539901	0.36525	0.9998
ENSG00000076043	ENSG00000076043	REXO2	11:114262164-114321001	OK	23.8451	29.1382	0.289219	0.496874	0.3653	0.9998
ENSG00000137075	ENSG00000137075	RNF38	9:36336392-36487545	OK	8.43422	9.95983	0.239866	0.466454	0.3654	0.9998
ENSG00000163806	ENSG00000163806	SPDYA	2:28974505-29093167	OK	0.637856	1.31406	1.04273	0.123179	0.36555	0.9998
ENSG00000130224	ENSG00000130224	LRCH2	X:114345184-114468635	OK	2.16855	2.65359	0.291217	0.542135	0.36565	0.9998
ENSG00000112339	ENSG00000112339	HBS1L	6:135281515-135424194	OK	74.7708	60.4103	-0.307682	-0.55339	0.3658	0.9998
ENSG00000269772	ENSG00000269772	RP11-178G16.5	10:75880799-75881121	OK	6.09186	8.45589	0.473073	0.545527	0.3658	0.9998
ENSG00000186073	ENSG00000186073	C15orf41	15:36871811-37110660	OK	5.11904	6.61394	0.369637	0.513988	0.36615	0.9998
ENSG00000249242	ENSG00000249242	TMEM150C	4:83404322-83483510	OK	0.69966	0.486173	-0.525185	-0.422605	0.36635	0.9998
ENSG00000110218	ENSG00000110218	PANX1	11:93862093-93915138	OK	9.0731	10.8141	0.25325	0.542387	0.3668	0.9998
ENSG00000135040	ENSG00000135040	NAA35	9:88556060-88637213	OK	12.6644	15.0236	0.246454	0.539917	0.36725	0.9998
ENSG00000151116	ENSG00000151116	UEVLD	11:18551155-18610294	OK	13.9168	16.7156	0.264366	0.469123	0.36725	0.9998
ENSG00000148303	ENSG00000148303	RPL7A	9:136215068-136218281	OK	1100.13	1298.09	0.238721	0.542639	0.3674	0.9998
ENSG00000214870	ENSG00000214870	AC004540.5	7:26438212-26538594	OK	1.63923	1.09893	-0.576915	-0.531363	0.3674	0.9998
ENSG00000119844	ENSG00000119844	AFTPH	2:64751464-64820139	OK	12.7272	15.1614	0.252487	0.541862	0.36745	0.9998
ENSG00000203855	ENSG00000203855	HSD3BP4	1:120106688-120114734	OK	0.560914	0.886466	0.660285	0.568646	0.36745	0.9998
ENSG00000266037	ENSG00000266037	RN7SL3	14:50320335-50320632	OK	0.226258	0.718404	1.66683	0.700479	0.36745	0.9998
ENSG00000144724	ENSG00000144724	PTPRG	3:61547242-62355005	OK	9.60509	11.9161	0.311038	0.497661	0.36765	0.9998
ENSG00000103148	ENSG00000103148	NPRL3	16:127005-188859	OK	13.9941	10.1722	-0.460188	-0.46886	0.3677	0.9998
ENSG00000010322	ENSG00000010322	NISCH	3:52489133-52527087	OK	17.7863	14.8445	-0.26084	-0.401095	0.36775	0.9998
ENSG00000115760	ENSG00000115760	BIRC6	2:32582095-32843966	OK	12.5106	15.2895	0.28939	0.282978	0.3678	0.9998
ENSG00000267080	ENSG00000267080	ASB16-AS1	17:42247814-42264085	OK	3.95237	3.15649	-0.324401	-0.493543	0.3678	0.9998
ENSG00000176444	ENSG00000176444	CLK2	1:155232658-155271225	OK	41.4115	32.5816	-0.345974	-0.552938	0.3679	0.9998
ENSG00000036054	ENSG00000036054	TBC1D23	3:99979843-100044095	OK	10.6427	12.5456	0.237317	0.519064	0.36795	0.9998
ENSG00000107829	ENSG00000107829	FBXW4	10:103370422-103455052	OK	11.0156	14.0731	0.353385	0.522969	0.36795	0.9998
ENSG00000205041	ENSG00000205041	CTC-425O23.2	19:40736223-40791443	OK	0.249776	0.695971	1.47839	0.200571	0.36795	0.9998
ENSG00000125347	ENSG00000125347	IRF1	5:131817300-131826490	OK	1.71942	1.23243	-0.48042	-0.433773	0.368	0.9998
ENSG00000198034	ENSG00000198034	RPS4X	X:71401202-71527037	OK	1144.27	1394.64	0.285466	0.528374	0.368	0.9998
ENSG00000149806	ENSG00000149806	FAU	11:64888099-64902004	OK	525.53	646.394	0.29864	0.550816	0.36845	0.9998
ENSG00000147162	ENSG00000147162	OGT	X:70752932-70795747	OK	21.7347	25.6495	0.238929	0.395787	0.3685	0.9998
ENSG00000215447	ENSG00000215447	BX322557.10	21:46707966-46711653	OK	1.79328	2.3785	0.407447	0.472941	0.36865	0.9998
ENSG00000167397	ENSG00000167397	VKORC1	16:31085742-31107301	OK	169.471	142.215	-0.252963	-0.553513	0.36875	0.9998
ENSG00000261716	ENSG00000261716	RP11-196G18.22	1:149816064-149820591	OK	2.37874	1.91615	-0.311984	-0.542798	0.36875	0.9998
ENSG00000131061	ENSG00000131061	ZNF341	20:32316736-32398903	OK	1.24294	1.58227	0.348246	0.553501	0.3688	0.9998
ENSG00000117748	ENSG00000117748	RPA2	1:28218034-28241257	OK	17.5407	14.5288	-0.271794	-0.542361	0.36885	0.9998
ENSG00000178917	ENSG00000178917	ZNF852	3:44540461-44552128	OK	2.08453	1.55832	-0.419729	-0.558612	0.36895	0.9998
ENSG00000160058	ENSG00000160058	BSDC1	1:32830703-32860332	OK	25.9732	30.4462	0.229238	0.48861	0.36915	0.9998
ENSG00000161249	ENSG00000161249	DMKN	19:35988121-36004560	OK	20.9304	25.8945	0.30704	0.496622	0.36915	0.9998
ENSG00000162913	ENSG00000162913	C1orf145	1:228391206-228566577	OK	0.489175	1.11306	1.18611	0.335868	0.36915	0.9998
ENSG00000146038	ENSG00000146038	DCDC2	6:24171983-24358512	OK	1.83277	2.54386	0.472998	0.323665	0.3693	0.9998
ENSG00000148840	ENSG00000148840	PPRC1	10:103892786-103910082	OK	11.2252	13.4855	0.264666	0.438115	0.36945	0.9998
ENSG00000180190	ENSG00000180190	TDRP	8:439802-495781	OK	3.52062	4.52307	0.361476	0.365508	0.3696	0.9998
ENSG00000167972	ENSG00000167972	ABCA3	16:2325881-2476700	OK	2.19246	3.38004	0.624491	0.54604	0.36975	0.9998
ENSG00000155363	ENSG00000155363	MOV10	1:113215762-113243368	OK	14.0667	18.0376	0.358727	0.416668	0.3698	0.9998
ENSG00000236849	ENSG00000236849	RP11-151D14.1	9:75486643-75489025	OK	7.87823	10.1297	0.362642	0.557053	0.37015	0.9998
ENSG00000149243	ENSG00000149243	KLHL35	11:75133437-75141674	OK	0.655439	0.917859	0.485811	0.467126	0.3702	0.9998
ENSG00000135547	ENSG00000135547	HEY2	6:125899703-126082415	OK	1.00949	0.770523	-0.389722	-0.531753	0.3703	0.9998
ENSG00000144455	ENSG00000144455	SUMF1	3:3742497-4508965	OK	18.0835	14.5199	-0.316648	-0.551531	0.3704	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000230626	ENSG00000230626	RP11-286H14.4	7:128766571-128770847	OK	1.62526	2.12771	0.388631	0.506448	0.3705	0.9998
ENSG00000236901	ENSG00000236901	MIR600HG	9:125871772-126030855	OK	0.856234	1.45722	0.767145	0.385685	0.37055	0.9998
ENSG00000034063	ENSG00000034063	UHRF1	19:4903091-4962165	OK	4.98019	4.01695	-0.310102	-0.547365	0.3706	0.9998
ENSG00000126457	ENSG00000126457	PRMT1	19:50179042-50193832	OK	102.353	118.184	0.20749	0.502142	0.37095	0.9998
ENSG00000144867	ENSG00000144867	SRPRB	3:133502876-133614680	OK	25.584	40.1989	0.651916	0.581915	0.37095	0.9998
ENSG00000136866	ENSG00000136866	ZFP37	9:115800659-115819039	OK	0.864741	0.63564	-0.444058	-0.551069	0.37105	0.9998
ENSG00000176476	ENSG00000176476	CCDC101	16:28565235-28603111	OK	4.50312	5.67477	0.333635	0.51229	0.37105	0.9998
ENSG00000158458	ENSG00000158458	NRG2	5:139226363-139422884	OK	1.62818	2.36476	0.538434	0.536328	0.3711	0.9998
ENSG00000172046	ENSG00000172046	USP19	3:49145478-49158371	OK	33.5365	28.1532	-0.252436	-0.44326	0.3711	0.9998
ENSG00000186063	ENSG00000186063	AIDA	1:222841354-222908538	OK	32.0642	23.0936	-0.47347	-0.5414	0.37115	0.9998
ENSG00000155229	ENSG00000155229	MMS19	10:99218080-99258551	OK	33.6108	28.8227	-0.221723	-0.466477	0.37145	0.9998
ENSG00000050393	ENSG00000050393	MCUR1	6:13786788-13814800	OK	35.1264	26.4484	-0.409378	-0.514691	0.37155	0.9998
ENSG00000197483	ENSG00000197483	ZNF628	19:55987349-55995854	OK	1.4649	2.07884	0.504976	0.43832	0.37155	0.9998
ENSG00000236947	ENSG00000236947	RP11-98G7.1	1:156416203-156426369	OK	0.732124	0.439215	-0.737162	-0.551102	0.3717	0.9998
ENSG00000109066	ENSG00000109066	TMEM104	17:72772621-72835918	OK	11.1272	13.2141	0.247987	0.478979	0.3718	0.9998
ENSG00000073849	ENSG00000073849	ST6GAL1	3:186648273-186796341	OK	52.058	60.2383	0.210562	0.378676	0.37205	0.9998
ENSG00000236753	ENSG00000236753	MKLN1-AS	7:130626518-131182453	OK	12.7767	7.01731	-0.864527	-0.395104	0.3721	0.9998
ENSG00000124422	ENSG00000124422	USP22	17:20717932-20947073	OK	66.8834	57.5853	-0.215949	-0.355355	0.37215	0.9998
ENSG00000189164	ENSG00000189164	ZNF527	19:37861962-37883968	OK	2.21519	1.72309	-0.362434	-0.43447	0.3722	0.9998
ENSG00000061918	ENSG00000061918	GUCY1B3	4:156680143-156728743	OK	1.40009	1.08959	-0.361734	-0.526456	0.3723	0.9998
ENSG00000079335	ENSG00000079335	CDC14A	1:100810032-100985833	OK	2.39633	1.90379	-0.331953	-0.513348	0.37235	0.9998
ENSG00000198857	ENSG00000198857	HSD3BP5	1:120143962-120151873	OK	2.3299	3.06401	0.395155	0.545717	0.3724	0.9998
ENSG00000072422	ENSG00000072422	RHOBTB1	10:62629195-62761198	OK	8.1093	9.98129	0.299649	0.352749	0.3725	0.9998
ENSG00000143977	ENSG00000143977	SNRPG	2:70508493-70520903	OK	124.067	105.75	-0.230457	-0.536298	0.3725	0.9998
ENSG00000100393	ENSG00000100393	EP300	22:41487789-41593460	OK	7.00441	8.2257	0.231876	0.538993	0.37255	0.9998
ENSG00000186866	ENSG00000186866	POFUT2	21:46683842-46707813	OK	8.66182	6.97005	-0.313502	-0.430884	0.3726	0.9998
ENSG00000171109	ENSG00000171109	MFN1	3:179065479-179112719	OK	36.968	31.7115	-0.221272	-0.415891	0.3727	0.9998
ENSG00000106415	ENSG00000106415	GLCCI1	7:7676148-8133902	OK	3.49771	5.06197	0.533288	0.327724	0.37275	0.9998
ENSG00000137273	ENSG00000137273	FOXF2	6:1390068-1395832	OK	6.30418	7.63707	0.27671	0.540586	0.373	0.9998
ENSG00000144747	ENSG00000144747	TMF1	3:69024364-69129559	OK	12.4998	9.47696	-0.399408	-0.392111	0.3732	0.9998
ENSG00000181938	ENSG00000181938	GINS3	16:58328983-58440048	OK	4.47733	3.64178	-0.297992	-0.485512	0.3732	0.9998
ENSG00000139908	ENSG00000139908	TSSK4	14:24641061-24708448	OK	1.43319	0.824972	-0.79681	-0.099746	0.3733	0.9998
ENSG00000235106	ENSG00000235106	LINC00094	9:136890560-136933657	OK	6.63899	8.66478	0.384201	0.526101	0.3733	0.9998
ENSG00000118729	ENSG00000118729	CASQ2	1:116242627-116311402	OK	0.669676	0.915333	0.450833	0.414171	0.37355	0.9998
ENSG00000163131	ENSG00000163131	CTSS	1:150702671-150738433	OK	2.17353	3.03784	0.483009	0.499629	0.3737	0.9998
ENSG00000163703	ENSG00000163703	CRELD1	3:9975505-9987097	OK	16.261	13.621	-0.255581	-0.461327	0.3737	0.9998
ENSG00000114737	ENSG00000114737	CISH	3:50643920-50686720	OK	1.75016	3.34897	0.936231	0.562445	0.3738	0.9998
ENSG00000138185	ENSG00000138185	ENTPD1	10:97471535-97849995	OK	8.21223	11.1326	0.43895	0.515034	0.37385	0.9998
ENSG00000264956	ENSG00000264956	RP11-1109M24.5	17:21793030-21814739	OK	0.756199	1.04211	0.462668	0.535902	0.37385	0.9998
ENSG00000072958	ENSG00000072958	AP1M1	19:16308388-16346160	OK	46.2924	39.5028	-0.22882	-0.484497	0.3739	0.9998
ENSG00000150316	ENSG00000150316	CWC15	11:94695786-94706776	OK	34.4792	29.08	-0.245696	-0.535492	0.37395	0.9998
ENSG00000160113	ENSG00000160113	NR2F6	19:17342691-17398455	OK	15.7235	20.6039	0.389992	0.540774	0.37395	0.9998
ENSG00000127955	ENSG00000127955	GNAI1	7:79763270-79848718	OK	30.3546	36.6311	0.271152	0.493897	0.3741	0.9998
ENSG00000131018	ENSG00000131018	SYNE1	6:151977825-152958936	OK	4.53838	5.82206	0.359351	0.386523	0.3741	0.9998
ENSG00000136098	ENSG00000136098	NEK3	13:52706774-52733996	OK	8.57036	6.70203	-0.354758	-0.526782	0.3741	0.9998
ENSG00000142168	ENSG00000142168	SOD1	21:33031934-33041244	OK	117.784	136.663	0.214478	0.528607	0.37425	0.9998
ENSG00000117036	ENSG00000117036	ETV3	1:157090982-157108266	OK	25.7131	22.1387	-0.215937	-0.511309	0.37435	0.9998
ENSG00000105197	ENSG00000105197	TIMM50	19:39971051-39984422	OK	186.195	215.771	0.21269	0.509215	0.3744	0.9998
ENSG00000242715	ENSG00000242715	CCDC169	13:36742344-36871979	OK	1.6035	2.24437	0.485086	0.43367	0.3744	0.9998
ENSG00000173418	ENSG00000173418	NAA20	20:19997759-20014299	OK	38.3428	32.512	-0.237981	-0.533248	0.37455	0.9998
ENSG00000090971	ENSG00000090971	NAT14	19:55996370-55998935	OK	20.5247	16.6438	-0.302374	-0.535809	0.37475	0.9998
ENSG00000168496	ENSG00000168496	FEN1	11:61447904-61634826	OK	62.5855	47.2768	-0.404696	-0.538149	0.3748	0.9998
ENSG00000240898	ENSG00000240898	RP11-48B14.1	17:3566195-3599698	OK	0.14281	0.758614	2.40927	0.227802	0.3748	0.9998
ENSG00000197930	ENSG00000197930	ERO1L	14:53106633-53162618	OK	43.7486	36.6444	-0.255647	-0.453796	0.37485	0.9998
ENSG00000158769	ENSG00000158769	F11R	1:160965000-161008780	OK	17.1785	22.3277	0.378232	0.48385	0.37505	0.9998
ENSG00000188130	ENSG00000188130	MAPK12	22:50683611-50700254	OK	7.56679	10.0099	0.403675	0.54878	0.37505	0.9998
ENSG00000196557	ENSG00000196557	CACNA1H	16:1203240-1275257	OK	0.770898	1.04559	0.439708	0.475284	0.3752	0.9998
ENSG00000108423	ENSG00000108423	TUBD1	17:57936850-57970304	OK	5.87742	4.51733	-0.379712	-0.473279	0.37525	0.9998
ENSG00000091986	ENSG00000091986	CCDC80	3:112323406-112368377	OK	2.24366	3.08167	0.457855	0.48411	0.37535	0.9998
ENSG00000255455	ENSG00000255455	RP11-890B15.3	11:130736148-130740142	OK	0.537458	0.703258	0.387902	0.539385	0.37535	0.9998
ENSG00000025770	ENSG00000025770	NCAPH2	22:50946644-50961901	OK	32.0625	27.287	-0.232671	-0.508621	0.3754	0.9998
ENSG00000111707	ENSG00000111707	SUDS3	12:118814184-118855840	OK	15.9532	13.647	-0.225264	-0.438511	0.3754	0.9998
ENSG00000140181	ENSG00000140181	HERC2P2	15:23282280-23378228	OK	6.32816	5.23397	-0.27388	-0.379082	0.37555	0.9998
ENSG00000188647	ENSG00000188647	PTAR1	9:72324437-72374875	OK	32.5843	25.3815	-0.360401	-0.444174	0.37565	0.9998
ENSG00000144366	ENSG00000144366	GULP1	2:189156395-189460653	OK	21.959	27.0695	0.301858	0.496816	0.3757	0.9998
ENSG00000112110	ENSG00000112110	MRPL18	6:160210843-160219468	OK	25.0073	30.0369	0.26439	0.538731	0.37575	0.9998
ENSG00000121361	ENSG00000121361	KCNJ8	12:21788275-21928515	OK	0.266628	0.716285	1.42571	0.0578474	0.37575	0.9998
ENSG00000011132	ENSG00000011132	APBA3	19:3750816-3761697	OK	10.2582	7.99537	-0.359536	-0.520071	0.37585	0.9998
ENSG00000140365	ENSG00000140365	COMMD4	15:75628231-75634268	OK	100.693	85.3185	-0.239032	-0.532039	0.37585	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267323	ENSG00000267323	SLC25A1P5	19:28175487-28475892	OK	0.84634	0.0550479	-3.94248	-0.47044	0.37605	0.9998
ENSG00000235636	ENSG00000235636	NUS1P1	X:47372000-47372882	OK	3.35004	4.32812	0.369562	0.533204	0.37645	0.9998
ENSG00000175854	ENSG00000175854	SWI5	9:131018107-131051269	OK	43.0928	30.429	-0.501999	-0.538874	0.37655	0.9998
ENSG00000013374	ENSG00000013374	NUB1	7:151038784-151110440	OK	46.1813	56.0184	0.278591	0.515084	0.3766	0.9998
ENSG00000139508	ENSG00000139508	SLC46A3	13:29274200-29293107	OK	2.66766	3.31712	0.314357	0.551665	0.3766	0.9998
ENSG00000164877	ENSG00000164877	MICALL2	7:1468100-1499138	OK	3.53229	4.41661	0.322337	0.426825	0.3768	0.9998
ENSG00000108091	ENSG00000108091	CCDC6	10:61548520-61666414	OK	3.40828	4.06153	0.25298	0.518415	0.377	0.9998
ENSG00000135597	ENSG00000135597	REPS1	6:139117062-139309398	OK	13.0651	10.7802	-0.277334	-0.418317	0.3771	0.9998
ENSG00000071794	ENSG00000071794	HLTF	3:148747913-148820610	OK	33.3654	38.8535	0.219693	0.383964	0.37715	0.9998
ENSG00000105607	ENSG00000105607	GCDH	19:13001839-13030090	OK	18.6836	22.6156	0.275547	0.472489	0.37715	0.9998
ENSG00000131037	ENSG00000131037	EPS8L1	19:55583387-55599291	OK	4.23989	5.8668	0.468547	0.517641	0.37715	0.9998
ENSG00000162825	ENSG00000162825	NBPF8	1:144146807-144224481	OK	1.90237	1.24586	-0.61065	-0.52729	0.3774	0.9998
ENSG00000213904	ENSG00000213904	LIPE-AS1	19:42901279-43156507	OK	2.67583	1.18127	-1.17965	-0.110513	0.3774	0.9998
ENSG00000108175	ENSG00000108175	ZMIZ1	10:80828791-81076276	OK	19.9223	16.0794	-0.30917	-0.304448	0.3776	0.9998
ENSG00000138078	ENSG00000138078	PREPL	2:44502598-44589001	OK	28.6027	33.3412	0.221154	0.4285	0.3776	0.9998
ENSG00000149927	ENSG00000149927	DOC2A	16:30003644-30034591	OK	0.459285	0.678533	0.563028	0.13035	0.3776	0.9998
ENSG00000089248	ENSG00000089248	ERP29	12:112451119-112461255	OK	189.438	163.449	-0.212885	-0.51508	0.3777	0.9998
ENSG00000196154	ENSG00000196154	S100A4	1:153516088-153522612	OK	4.65594	7.12437	0.61369	0.593974	0.3779	0.9998
ENSG00000102103	ENSG00000102103	PQBP1	X:48750729-48760420	OK	58.4846	72.0537	0.301015	0.540638	0.37795	0.9998
ENSG00000171262	ENSG00000171262	FAM98B	15:38746327-38779911	OK	8.08383	10.7325	0.408874	0.332513	0.37795	0.9998
ENSG00000118454	ENSG00000118454	ANKRD13C	1:70726270-70820417	OK	8.60492	7.23336	-0.250495	-0.45414	0.37805	0.9998
ENSG00000116922	ENSG00000116922	C1orf109	1:38147241-38157914	OK	8.8211	11.393	0.369111	0.542473	0.3781	0.9998
ENSG00000110063	ENSG00000110063	DCPS	11:126152959-126215644	OK	16.6665	13.6235	-0.290848	-0.529013	0.37815	0.9998
ENSG00000237886	ENSG00000237886	RP11-611D20.2	9:139440624-139444345	OK	0.428316	0.725858	0.76101	0.542245	0.37815	0.9998
ENSG00000213963	ENSG00000213963	AC074286.1	2:178092322-178408564	OK	1.62532	0.811252	-1.0025	-0.181639	0.3782	0.9998
ENSG00000090554	ENSG00000090554	FLT3LG	19:49949554-49995565	OK	0.874495	0.405025	-1.11044	-0.0423078	0.37825	0.9998
ENSG00000255674	ENSG00000255674	AC013718.1	2:135213329-135476570	OK	0.16409	1.76278	3.42529	0.455972	0.3784	0.9998
ENSG00000214485	ENSG00000214485	RPL7P1	5:149432853-149492935	OK	293.335	339.818	0.212215	0.528737	0.37855	0.9998
ENSG00000164190	ENSG00000164190	NIPBL	5:36876860-37066515	OK	7.79377	9.28825	0.253085	0.478766	0.37865	0.9998
ENSG00000095787	ENSG00000095787	WAC	10:28811580-28912041	OK	28.8287	33.8794	0.232902	0.477709	0.37885	0.9998
ENSG00000263470	ENSG00000263470	RP11-160O5.1	17:63096929-63107176	OK	10.3006	8.10698	-0.345495	-0.542152	0.37885	0.9998
ENSG00000162643	ENSG00000162643	WDR63	1:85464829-85598821	OK	2.59176	4.17253	0.686992	0.507633	0.37925	0.9998
ENSG00000135916	ENSG00000135916	ITM2C	2:231729353-231743963	OK	147.83	171.402	0.213444	0.511604	0.37935	0.9998
ENSG00000100802	ENSG00000100802	C14orf93	14:23451906-23479375	OK	6.1416	5.04173	-0.284696	-0.399351	0.3794	0.9998
ENSG00000240463	ENSG00000240463	RPS19P3	14:35025979-35099389	OK	0.213249	0.855107	2.00356	0.154806	0.37945	0.9998
ENSG00000160783	ENSG00000160783	PMF1	1:156182772-156213123	OK	87.9431	102.824	0.225536	0.535082	0.3795	0.9998
ENSG00000137970	ENSG00000137970	RPL7P9	1:97144429-97145176	OK	615.24	715.827	0.218464	0.536254	0.37955	0.9998
ENSG00000152669	ENSG00000152669	CCNO	5:54526979-54529508	OK	3.6612	4.57995	0.323013	0.52662	0.37955	0.9998
ENSG00000154814	ENSG00000154814	OXNAD1	3:16306705-16555533	OK	14.9026	12.2801	-0.279243	-0.529452	0.37965	0.9998
ENSG00000184182	ENSG00000184182	UBE2F	2:238875468-239008054	OK	57.2881	46.033	-0.315568	-0.535161	0.37965	0.9998
ENSG00000162194	ENSG00000162194	C11orf48	11:62414319-62441159	OK	62.3153	79.7509	0.355913	0.548328	0.3798	0.9998
ENSG00000130475	ENSG00000130475	FCHO1	19:17858526-17899377	OK	0.96123	1.21461	0.337545	0.215846	0.3802	0.9998
ENSG00000120318	ENSG00000120318	ARAP3	5:141032967-141061788	OK	6.02606	5.0365	-0.258792	-0.522134	0.38025	0.9998
ENSG00000121671	ENSG00000121671	CRY2	11:45868668-45904798	OK	5.09414	4.25297	-0.260368	-0.402351	0.38025	0.9998
ENSG00000224877	ENSG00000224877	C17orf89	17:79213038-79215081	OK	156.4	186.318	0.252528	0.53081	0.38025	0.9998
ENSG00000132613	ENSG00000132613	MTSS1L	16:70695106-70719969	OK	17.6677	24.9764	0.499454	0.50773	0.38045	0.9998
ENSG00000088387	ENSG00000088387	DOCK9	13:99445740-99738879	OK	17.03	21.6424	0.345781	0.350061	0.3805	0.9998
ENSG00000114942	ENSG00000114942	EEF1B2	2:206979540-207027652	OK	470.021	369.727	-0.346266	-0.543731	0.3805	0.9998
ENSG00000230395	ENSG00000230395	AC092651.1	2:87345656-87348103	OK	0.306021	1.10106	1.8472	0.778951	0.3805	0.9998
ENSG00000197816	ENSG00000197816	CCDC180	9:99918851-100140806	OK	1.7145	1.20887	-0.504129	-0.36051	0.3806	0.9998
ENSG00000122779	ENSG00000122779	TRIM24	7:138145078-138274738	OK	12.1827	14.3918	0.240412	0.466699	0.3809	0.9998
ENSG00000125503	ENSG00000125503	PPP1R12C	19:55602280-55628927	OK	30.5776	25.7161	-0.2498	-0.475303	0.381	0.9998
ENSG00000185246	ENSG00000185246	PRPF39	14:45553301-45604522	OK	13.4067	9.39096	-0.513608	-0.411569	0.381	0.9998
ENSG00000070718	ENSG00000070718	AP3M2	8:42010463-42029191	OK	21.563	18.1341	-0.249853	-0.424417	0.38105	0.9998
ENSG00000164494	ENSG00000164494	PDSS2	6:107473760-107780768	OK	8.20262	6.51636	-0.332018	-0.449034	0.38125	0.9998
ENSG00000185668	ENSG00000185668	POU3F1	1:38509522-38512450	OK	2.7731	2.2204	-0.320685	-0.537471	0.38145	0.9998
ENSG00000108654	ENSG00000108654	DDX5	17:62495733-62658186	OK	274.767	323.25	0.234444	0.474133	0.38155	0.9998
ENSG00000134253	ENSG00000134253	TRIM45	1:117653681-117665209	OK	3.31707	2.59814	-0.35243	-0.525257	0.3818	0.9998
ENSG00000229233	ENSG00000229233	AC011891.5	7:12693803-12694610	OK	1.32418	2.02574	0.613346	0.53611	0.3818	0.9998
ENSG00000118113	ENSG00000118113	MMP8	11:102582525-102597781	OK	31.1906	26.1261	-0.255619	-0.478225	0.38185	0.9998
ENSG00000264247	ENSG00000264247	LINC00909	18:72259009-72777627	OK	2.94109	4.68116	0.670516	0.530768	0.38185	0.9998
ENSG00000153767	ENSG00000153767	GTF2E1	3:120405527-120501916	OK	7.32235	5.77876	-0.341547	-0.436419	0.38195	0.9998
ENSG00000117139	ENSG00000117139	KDM5B	1:202696525-202778598	OK	27.7871	23.8228	-0.222072	-0.461478	0.382	0.9998
ENSG00000228502	ENSG00000228502	EEF1A1P11	1:96912485-96913874	OK	0.73472	1.01899	0.471869	0.546798	0.38215	0.9998
ENSG00000158301	ENSG00000158301	GPRASP2	X:101854095-101973607	OK	2.7061	3.83816	0.504201	0.387063	0.3822	0.9998
ENSG00000213846	ENSG00000213846	AC098614.2	3:27674466-27675211	OK	2.26856	1.64369	-0.464842	-0.529823	0.3822	0.9998
ENSG00000090686	ENSG00000090686	USP48	1:22004790-22110099	OK	51.8308	44.7376	-0.212321	-0.461434	0.38225	0.9998
ENSG00000112578	ENSG00000112578	BYSL	6:41888925-41900784	OK	28.4415	33.6168	0.241183	0.524145	0.3823	0.9998
ENSG00000172531	ENSG00000172531	PPP1CA	11:67159175-67193078	OK	118.31	101.517	-0.220858	-0.527761	0.3823	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000105185	ENSG00000105185	PDCD5	19:33071973-33078358	OK	101.841	86.6437	-0.233152	-0.539424	0.38245	0.9998
ENSG00000121879	ENSG00000121879	PIK3CA	3:178865901-178984790	OK	12.4628	8.83211	-0.496798	-0.506156	0.38245	0.9998
ENSG00000106479	ENSG00000106479	ZNF862	7:149535455-149564568	OK	7.82229	5.36297	-0.544561	-0.519511	0.38285	0.9998
ENSG00000132016	ENSG00000132016	C19orf57	19:13993160-14041692	OK	1.3822	0.748403	-0.885077	-0.31511	0.3829	0.9998
ENSG00000175727	ENSG00000175727	MLXIP	12:122516627-122631894	OK	28.9194	24.5832	-0.234363	-0.37725	0.3829	0.9998
ENSG00000146476	ENSG00000146476	C6orf211	6:151773421-151791236	OK	16.2655	19.307	0.247314	0.517463	0.38295	0.9998
ENSG00000235597	ENSG00000235597	LINC01102	2:105049724-105137290	OK	2.18271	1.68468	-0.373641	-0.512848	0.3831	0.9998
ENSG00000082146	ENSG00000082146	STRADB	2:202241929-202345569	OK	25.4215	36.3728	0.516812	0.420805	0.3832	0.9998
ENSG00000143924	ENSG00000143924	EML4	2:42370377-42559688	OK	14.2688	16.6336	0.221238	0.478298	0.38325	0.9998
ENSG00000186638	ENSG00000186638	KIF24	9:34179002-34329198	OK	2.03094	1.22901	-0.72465	-0.432759	0.3833	0.9998
ENSG00000108262	ENSG00000108262	GIT1	17:27887564-28513493	OK	23.8863	30.3179	0.343987	0.434557	0.3834	0.9998
ENSG00000116984	ENSG00000116984	MTR	1:236958609-237067281	OK	12.5918	10.3976	-0.276239	-0.50109	0.38355	0.9998
ENSG00000106524	ENSG00000106524	ANKMY2	7:16639400-16685442	OK	10.4582	8.72618	-0.261212	-0.471787	0.38365	0.9998
ENSG00000152061	ENSG00000152061	RABGAP1L	1:174084437-174964445	OK	17.8111	15.0617	-0.241891	-0.425641	0.38365	0.9998
ENSG00000020181	ENSG00000020181	GPR124	8:37641708-37707422	OK	7.20225	5.93132	-0.280095	-0.516371	0.3837	0.9998
ENSG00000011638	ENSG00000011638	TMEM159	16:20944432-21191937	OK	8.77039	11.0884	0.338336	0.535724	0.3838	0.9998
ENSG00000122884	ENSG00000122884	P4HA1	10:74766974-74856732	OK	27.6352	23.3572	-0.242644	-0.501333	0.3838	0.9998
ENSG00000125648	ENSG00000125648	SLC25A23	19:6436089-6482568	OK	39.245	33.6734	-0.220898	-0.45264	0.3838	0.9998
ENSG00000139117	ENSG00000139117	CPNE8	12:39040623-39303394	OK	8.93089	7.41219	-0.268903	-0.455322	0.3838	0.9998
ENSG00000162688	ENSG00000162688	AGL	1:100315639-100389579	OK	3.37792	2.84243	-0.249009	-0.497663	0.3838	0.9998
ENSG00000103266	ENSG00000103266	STUB1	16:730223-734529	OK	95.3154	114.748	0.267684	0.511925	0.38385	0.9998
ENSG00000116062	ENSG00000116062	MSH6	2:47922668-48134949	OK	36.0263	26.3652	-0.450412	-0.475329	0.3839	0.9998
ENSG00000164163	ENSG00000164163	ABCE1	4:145888263-146101313	OK	30.8652	37.7432	0.290236	0.41915	0.384	0.9998
ENSG00000181817	ENSG00000181817	LSM10	1:36856838-36863493	OK	43.0861	36.5248	-0.238347	-0.519227	0.38405	0.9998
ENSG00000100749	ENSG00000100749	VRK1	14:97263640-97411731	OK	12.4157	10.3913	-0.256791	-0.492937	0.38425	0.9998
ENSG00000151917	ENSG00000151917	BEND6	6:56819772-56892140	OK	0.850643	1.23596	0.539011	0.437554	0.3843	0.9998
ENSG00000135698	ENSG00000135698	MPHOSPH6	16:82181402-82203831	OK	11.5929	14.0356	0.275848	0.486851	0.38435	0.9998
ENSG00000064933	ENSG00000064933	PMS1	2:190649106-190742355	OK	6.65705	5.35667	-0.313547	-0.427659	0.3844	0.9998
ENSG00000204758	ENSG00000204758	CTC-308K20.1	5:172381788-172396774	OK	0.781202	0.3669	-1.09031	-0.275427	0.3844	0.9998
ENSG00000129682	ENSG00000129682	FGF13	X:137713734-138304939	OK	3.37566	4.38128	0.376183	0.490063	0.38445	0.9998
ENSG00000140416	ENSG00000140416	TPM1	15:63334830-63364114	OK	23.5694	27.9157	0.244162	0.476908	0.3845	0.9998
ENSG00000145741	ENSG00000145741	BTF3	5:72794232-72801460	OK	608.238	706.267	0.215578	0.52812	0.38455	0.9998
ENSG00000162851	ENSG00000162851	TFB2M	1:246703861-246729626	OK	16.2083	19.3286	0.254006	0.526251	0.3847	0.9998
ENSG00000244625	ENSG00000244625	CTA-211A9.5	22:27042391-27176170	OK	9.89505	12.6157	0.350443	0.562365	0.3849	0.9998
ENSG00000143418	ENSG00000143418	CERS2	1:150898738-150948010	OK	190.022	225.4	0.246322	0.50861	0.38505	0.9998
ENSG00000132801	ENSG00000132801	ZSWIM3	20:44486255-44507761	OK	2.14206	1.70681	-0.327701	-0.533276	0.3851	0.9998
ENSG00000105642	ENSG00000105642	KCNN1	19:18062101-18110889	OK	1.09972	1.80916	0.718188	0.474816	0.38515	0.9998
ENSG00000130787	ENSG00000130787	HIP1R	12:123318999-123347507	OK	13.1803	16.0072	0.280332	0.455242	0.3853	0.9998
ENSG00000137965	ENSG00000137965	IFI44	1:79115480-79129763	OK	4.6002	3.53687	-0.379225	-0.494949	0.38535	0.9998
ENSG00000073417	ENSG00000073417	PDE8A	15:85523670-85682376	OK	15.5985	18.5911	0.253207	0.438699	0.38545	0.9998
ENSG00000198712	ENSG00000198712	MT-CO2	MT:7585-8269	OK	9045.7	11095.6	0.294689	0.516777	0.38545	0.9998
ENSG00000182319	ENSG00000182319	SGK223	8:8175257-8244008	OK	4.44847	5.31039	0.25551	0.532872	0.3855	0.9998
ENSG00000196263	ENSG00000196263	ZNF471	19:57019211-57041590	OK	1.27971	0.91419	-0.485248	-0.39796	0.3855	0.9998
ENSG00000214253	ENSG00000214253	FIS1	7:100882738-100895597	OK	162.028	139.778	-0.2131	-0.522285	0.38565	0.9998
ENSG00000119689	ENSG00000119689	DLST	14:75348593-75370448	OK	53.8926	46.6458	-0.208341	-0.446182	0.38575	0.9998
ENSG00000156345	ENSG00000156345	CDK20	9:90581355-90589668	OK	4.10294	5.09671	0.312907	0.527874	0.38575	0.9998
ENSG00000131269	ENSG00000131269	ABCB7	X:74273114-74376567	OK	11.1493	13.2029	0.243896	0.483219	0.3858	0.9998
ENSG00000197020	ENSG00000197020	ZNF100	19:21905567-21950430	OK	0.652035	0.406838	-0.680493	-0.414915	0.38585	0.9998
ENSG00000167280	ENSG00000167280	ENGASE	17:77071020-77084681	OK	12.3007	14.9833	0.284619	0.335058	0.38595	0.9998
ENSG00000164930	ENSG00000164930	FZD6	8:104133259-104345094	OK	20.799	17.414	-0.25626	-0.536326	0.386	0.9998
ENSG00000265681	ENSG00000265681	RPL17	18:47008027-47018906	OK	1181.47	1389.59	0.234075	0.530987	0.38615	0.9998
ENSG00000135749	ENSG00000135749	PCNXL2	1:233086350-233431473	OK	2.71337	3.61408	0.413544	0.234293	0.3862	0.9998
ENSG00000136451	ENSG00000136451	VEZF1	17:56048909-56065620	OK	43.2558	50.6067	0.226433	0.508725	0.38635	0.9998
ENSG00000099910	ENSG00000099910	KLHL22	22:20778873-20850170	OK	14.5801	10.563	-0.464975	-0.418282	0.38655	0.9998
ENSG00000226084	ENSG00000226084	RP4-706A16.3	1:77554674-77685115	OK	176.399	218.432	0.308341	0.543277	0.3866	0.9998
ENSG00000020922	ENSG00000020922	MRE11A	11:94152894-94232749	OK	5.77198	4.63162	-0.31755	-0.456877	0.3867	0.9998
ENSG00000181826	ENSG00000181826	RELL1	4:37455562-37687998	OK	9.72441	7.72212	-0.332614	-0.530921	0.38695	0.9998
ENSG00000114779	ENSG00000114779	ABHD14B	3:51989329-52023213	OK	39.3195	29.032	-0.437599	-0.525046	0.387	0.9998
ENSG00000143578	ENSG00000143578	CREB3L4	1:153931574-153950164	OK	6.85073	4.30076	-0.671668	-0.179797	0.387	0.9998
ENSG00000080200	ENSG00000080200	CRYBG3	3:97595818-97691301	OK	4.25698	3.13733	-0.440292	-0.499549	0.38705	0.9998
ENSG00000167705	ENSG00000167705	RILP	17:1549443-1553371	OK	8.10082	10.0131	0.305746	0.528027	0.38705	0.9998
ENSG00000031081	ENSG00000031081	ARHGAP31	3:119013219-119139561	OK	5.52942	7.06878	0.354333	0.419231	0.38715	0.9998
ENSG00000147905	ENSG00000147905	ZCCHC7	9:37120535-37358146	OK	9.91511	8.15342	-0.282222	-0.525738	0.38715	0.9998
ENSG00000235961	ENSG00000235961	PNMA6C	X:152240818-152340864	OK	0.511289	0.699368	0.451914	0.530379	0.38715	0.9998
ENSG00000103274	ENSG00000103274	NUBP1	16:10837642-10912651	OK	12.3025	14.8137	0.267979	0.504625	0.3875	0.9998
ENSG00000119383	ENSG00000119383	PPP2R4	9:131857088-131911225	OK	124.688	102.932	-0.27664	-0.518483	0.3875	0.9998
ENSG00000147604	ENSG00000147604	RPL7	8:74202505-74268696	OK	408.742	489.267	0.259429	0.522475	0.3875	0.9998
ENSG00000272047	ENSG00000272047	GTF2H5	6:158589383-158620376	OK	2.07829	1.71947	-0.273431	-0.522675	0.3875	0.9998
ENSG00000073711	ENSG00000073711	PPP2R3A	3:135684514-135866733	OK	3.34004	4.15359	0.314493	0.481565	0.38805	0.9998
ENSG00000128578	ENSG00000128578	STRIP2	7:129074273-129128240	OK	9.25909	11.1684	0.27048	0.415051	0.3882	0.9998
ENSG00000138069	ENSG00000138069	RAB1A	2:65283499-65357240	OK	141.214	167.044	0.242338	0.531775	0.3886	0.9998
ENSG00000268521	ENSG00000268521	VN1R83P	19:21472355-21472800	OK	1.35539	0.852774	-0.668476	-0.531486	0.3887	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000174579	ENSG00000174579	MSL2	3:135867763-135916083	OK	8.75098	7.17566	-0.286334	-0.412214	0.38895	0.9998
ENSG00000164647	ENSG00000164647	STEAP1	7:89511666-89867451	OK	11.2845	8.8546	-0.349839	-0.532691	0.3891	0.9998
ENSG00000151413	ENSG00000151413	NUBPL	14:31959161-32330430	OK	15.7987	20.0499	0.343791	0.488953	0.38915	0.9998
ENSG00000169180	ENSG00000169180	XPO6	16:28109299-28223241	OK	51.3546	59.2838	0.207146	0.254984	0.38915	0.9998
ENSG00000229212	ENSG00000229212	RP11-561C5.4	15:85734668-85778026	OK	1.97527	1.46103	-0.435065	-0.436571	0.38915	0.9998
ENSG00000259901	ENSG00000259901	RP5-991G20.4	16:72699068-73093597	OK	1.39256	0.707533	-0.976865	-0.50823	0.38925	0.9998
ENSG00000126778	ENSG00000126778	SIX1	14:61110132-61124977	OK	2.10148	2.90031	0.464806	0.41683	0.3895	0.9998
ENSG00000054267	ENSG00000054267	ARID4B	1:235294497-235507847	OK	10.113	7.82325	-0.370365	-0.33315	0.38985	0.9998
ENSG00000155304	ENSG00000155304	HSPA13	21:15743435-15755805	OK	10.5609	8.57535	-0.300472	-0.513827	0.3899	0.9998
ENSG00000104613	ENSG00000104613	INTS10	8:19674650-19709594	OK	24.5885	28.8197	0.22907	0.327634	0.38995	0.9998
ENSG00000124570	ENSG00000124570	SERPINB6	6:2948392-2972090	OK	92.0461	79.1848	-0.217133	-0.525267	0.3901	0.9998
ENSG00000171960	ENSG00000171960	PPIH	1:43124095-43142429	OK	24.1132	28.8671	0.259604	0.518211	0.39015	0.9998
ENSG00000111897	ENSG00000111897	SERINC1	6:122764498-122792967	OK	35.619	41.0851	0.205967	0.514669	0.39025	0.9998
ENSG00000261167	ENSG00000261167	RP11-517B11.7	3:131173969-131177442	OK	0.636009	0.483279	-0.396191	-0.510863	0.3904	0.9998
ENSG00000267546	ENSG00000267546	RP11-666A8.8	17:74523437-74553765	OK	1.05039	0.51719	-1.02216	-0.214425	0.3904	0.9998
ENSG00000100319	ENSG00000100319	ZMAT5	22:30116072-30163000	OK	22.1061	18.3281	-0.270388	-0.523694	0.39045	0.9998
ENSG00000185238	ENSG00000185238	PRMT3	11:20409075-20530840	OK	14.3533	17.063	0.249494	0.475401	0.39065	0.9998
ENSG00000147416	ENSG00000147416	ATP6V1B2	8:20054877-20084330	OK	197.792	228.725	0.209626	0.48726	0.39075	0.9998
ENSG00000171962	ENSG00000171962	LRRC48	17:17876126-17942523	OK	1.44989	0.997976	-0.538864	-0.210994	0.39075	0.9998
ENSG00000138796	ENSG00000138796	HADH	4:108910869-108956331	OK	32.3375	27.806	-0.217811	-0.484825	0.3908	0.9998
ENSG00000188295	ENSG00000188295	ZNF669	1:247263263-247267674	OK	1.91356	2.4423	0.351977	0.470246	0.3908	0.9998
ENSG00000025423	ENSG00000025423	HSD17B6	12:57106211-57181574	OK	0.68006	0.334416	-1.02402	-0.0574846	0.3909	0.9998
ENSG00000076053	ENSG00000076053	RBM7	11:114262164-114321001	OK	5.0567	7.22884	0.51557	0.495472	0.39095	0.9998
ENSG00000165046	ENSG00000165046	LETM2	8:38243724-38267045	OK	0.849529	1.12646	0.407063	0.3352	0.39095	0.9998
ENSG00000198689	ENSG00000198689	SLC9A6	X:135067597-135129423	OK	7.85767	6.66637	-0.2372	-0.523632	0.39095	0.9998
ENSG00000250479	ENSG00000250479	CHCHD10	22:24105207-24126503	OK	196.277	232.311	0.243167	0.526589	0.391	0.9998
ENSG00000256269	ENSG00000256269	HMBS	11:118955575-118964259	OK	17.9407	15.0886	-0.249782	-0.490264	0.39115	0.9998
ENSG00000112893	ENSG00000112893	MAN2A1	5:109025066-109205326	OK	5.0081	5.97644	0.255022	0.411559	0.3913	0.9998
ENSG00000136108	ENSG00000136108	CKAP2	13:53029563-53050763	OK	29.7329	25.4906	-0.222098	-0.490043	0.3913	0.9998
ENSG00000137171	ENSG00000137171	KLC4	6:43005354-43042837	OK	9.22482	6.96928	-0.404512	-0.360534	0.39135	0.9998
ENSG00000100216	ENSG00000100216	TOMM22	22:39077952-39080818	OK	66.7508	56.963	-0.22876	-0.523381	0.3914	0.9998
ENSG00000211584	ENSG00000211584	SLC48A1	12:48099867-48231681	OK	16.5046	20.5721	0.317821	0.408823	0.3914	0.9998
ENSG00000117289	ENSG00000117289	TXNIP	1:145438468-145442635	OK	31.5939	36.5472	0.210117	0.491442	0.3916	0.9998
ENSG00000266680	ENSG00000266680	RP5-1148A21.3	6:64231665-64293492	OK	0.500084	1.36993	1.45386	0.200903	0.39165	0.9998
ENSG00000164111	ENSG00000164111	ANXA5	4:122589109-122618268	OK	876.353	1025.63	0.22693	0.496936	0.3917	0.9998
ENSG00000127399	ENSG00000127399	LRRC61	7:149941004-150035239	OK	0.520003	0.834442	0.682291	0.47757	0.39175	0.9998
ENSG00000033050	ENSG00000033050	ABCF2	7:150904922-150924316	OK	78.4166	90.6132	0.208563	0.378314	0.3923	0.9998
ENSG00000143314	ENSG00000143314	MRPL24	1:156707094-156711382	OK	178.483	154.557	-0.207648	-0.505823	0.3925	0.9998
ENSG00000138430	ENSG00000138430	OLA1	2:174937174-175113426	OK	89.2141	105.397	0.240496	0.520346	0.39255	0.9998
ENSG00000204304	ENSG00000204304	PBX2	6:32152511-32157963	OK	27.9179	22.7473	-0.295496	-0.497141	0.3928	0.9998
ENSG00000143183	ENSG00000143183	TMCO1	1:165696031-165880855	OK	99.8531	122.628	0.296406	0.502635	0.3929	0.9998
ENSG00000152443	ENSG00000152443	ZNF776	19:58193336-58269527	OK	1.91579	2.61682	0.449876	0.374381	0.3929	0.9998
ENSG00000103257	ENSG00000103257	SLC7A5	16:87863628-87903094	OK	224.177	191.221	-0.2294	-0.5177	0.39295	0.9998
ENSG00000131873	ENSG00000131873	CHSY1	15:101715927-101792137	OK	11.514	13.681	0.248782	0.494297	0.393	0.9998
ENSG00000239213	ENSG00000239213	RP11-85F14.5	3:136537488-136580896	OK	5.13117	3.8095	-0.429687	-0.532057	0.393	0.9998
ENSG00000117505	ENSG00000117505	DR1	1:93615298-93835055	OK	24.3086	31.741	0.384883	0.515166	0.3932	0.9998
ENSG00000149089	ENSG00000149089	APIP	11:34874640-35042138	OK	33.4614	25.8994	-0.369577	-0.53471	0.3932	0.9998
ENSG00000182919	ENSG00000182919	C11orf54	11:93394804-93547861	OK	4.51782	2.97509	-0.602693	-0.350121	0.3932	0.9998
ENSG00000140391	ENSG00000140391	TSPAN3	15:77336021-77376326	OK	240.236	280.178	0.221894	0.50244	0.3934	0.9998
ENSG00000151287	ENSG00000151287	TEX30	13:103418339-103426161	OK	44.8625	38.0112	-0.239084	-0.510332	0.3934	0.9998
ENSG00000225345	ENSG00000225345	SNX18P3	9:38540563-38624987	OK	0.623877	0.98401	0.657411	0.526598	0.3934	0.9998
ENSG00000167670	ENSG00000167670	CHAF1A	19:4402658-4457819	OK	13.4682	9.53676	-0.497986	-0.435065	0.3935	0.9998
ENSG00000214367	ENSG00000214367	HAUS3	4:2073644-2243891	OK	9.53319	7.95743	-0.260657	-0.489878	0.3935	0.9998
ENSG00000116874	ENSG00000116874	WARS2	1:119573838-119869926	OK	4.93879	6.22425	0.333743	0.510296	0.39355	0.9998
ENSG00000141696	ENSG00000141696	LEPREL4	17:39958198-39968856	OK	3.2017	4.06102	0.343005	0.462048	0.39355	0.9998
ENSG00000224722	ENSG00000224722	PRNCR1	8:128098507-128099755	OK	0.590639	0.835033	0.499556	0.52951	0.39365	0.9998
ENSG00000035664	ENSG00000035664	DAPK2	15:64199234-64364232	OK	0.587392	0.801141	0.447733	0.287796	0.39375	0.9998
ENSG00000163319	ENSG00000163319	MRPS18C	4:84377084-84444501	OK	22.8156	28.321	0.311853	0.49171	0.3938	0.9998
ENSG00000112531	ENSG00000112531	QKI	6:163835031-163999628	OK	22.1624	28.3914	0.357343	0.477146	0.39385	0.9998
ENSG00000174652	ENSG00000174652	ZNF266	19:9523271-9546254	OK	9.32292	7.4767	-0.318379	-0.497434	0.3939	0.9998
ENSG00000232116	ENSG00000232116	RP11-187C18.2	9:45484571-45488153	OK	2.78525	4.02419	0.530891	0.524254	0.3939	0.9998
ENSG00000109084	ENSG00000109084	TMEM97	17:26646120-26662515	OK	44.8231	36.2485	-0.30632	-0.508548	0.394	0.9998
ENSG00000178146	ENSG00000178146	RP1-232L22__B.1	X:101033941-101035511	OK	6.80036	5.53405	-0.297274	-0.525824	0.394	0.9998
ENSG00000137513	ENSG00000137513	NARS2	11:77926342-78285919	OK	70.6146	55.7653	-0.3406	-0.419687	0.39405	0.9998
ENSG00000181450	ENSG00000181450	ZNF678	1:227751243-227865144	OK	1.92255	1.27576	-0.591661	-0.395936	0.39405	0.9998
ENSG00000197106	ENSG00000197106	SLC6A17	1:110693107-110744824	OK	28.342	33.0302	0.220842	0.456528	0.39405	0.9998
ENSG00000141098	ENSG00000141098	GFOD2	16:67708433-67753324	OK	4.69952	3.85554	-0.28558	-0.489391	0.3943	0.9998
ENSG00000116604	ENSG00000116604	MEF2D	1:156433518-156470620	OK	37.6029	44.1743	0.232364	0.441374	0.3944	0.9998
ENSG00000145908	ENSG00000145908	ZNF300	5:150226084-150284545	OK	1.58111	1.97695	0.322341	0.521174	0.3944	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000144320	ENSG00000144320	KIAA1715	2:176788619-176867567	OK	26.1677	31.3955	0.262772	0.450909	0.39455	0.9998
ENSG00000267475	ENSG00000267475	CTD-2538C1.2	19:33177994-33182656	OK	0.827548	1.25528	0.601095	0.528396	0.3946	0.9998
ENSG00000112406	ENSG00000112406	HECA	6:139456248-139613276	OK	2.32313	1.91082	-0.281881	-0.521771	0.39465	0.9998
ENSG00000166913	ENSG00000166913	YWHAB	20:43514316-43537173	OK	141.044	121.825	-0.211339	-0.482736	0.39465	0.9998
ENSG00000188662	ENSG00000188662	HILS1	17:48240883-48258539	OK	12.5029	16.2096	0.374591	0.482807	0.39475	0.9998
ENSG00000161681	ENSG00000161681	SHANK1	19:51124563-51222707	OK	0.551611	0.913636	0.727967	0.459222	0.39485	0.9998
ENSG00000244159	ENSG00000244159	RP11-1070A24.1	8:54764367-54871863	OK	0.205237	1.74783	3.0902	0.349045	0.3949	0.9998
ENSG00000166813	ENSG00000166813	KIF7	15:90048507-90198682	OK	3.04002	4.02814	0.406032	0.452959	0.395	0.9998
ENSG00000103326	ENSG00000103326	CAPN15	16:577716-604636	OK	10.626	12.6492	0.251455	0.443719	0.39505	0.9998
ENSG00000135720	ENSG00000135720	DYNC1LI2	16:66754795-66788643	OK	59.4001	69.0749	0.217696	0.362652	0.3951	0.9998
ENSG00000167191	ENSG00000167191	GPRC5B	16:19566561-19897489	OK	30.0649	37.5877	0.32218	0.49834	0.39525	0.9998
ENSG00000150893	ENSG00000150893	FREM2	13:39261265-39460074	OK	0.584921	0.782838	0.420473	0.344754	0.3953	0.9998
ENSG00000064999	ENSG00000064999	ANKS1A	6:34857041-35059179	OK	10.5789	12.2534	0.211996	0.479534	0.39535	0.9998
ENSG00000176490	ENSG00000176490	DIRAS1	19:2714564-2740150	OK	12.1888	15.1121	0.310146	0.479725	0.39535	0.9998
ENSG00000066557	ENSG00000066557	LRRC40	1:70034080-70671303	OK	9.60437	8.10085	-0.245618	-0.516708	0.39555	0.9998
ENSG00000176826	ENSG00000176826	FKBP9L	7:55748766-55780945	OK	10.7523	7.94906	-0.435794	-0.467611	0.3956	0.9998
ENSG00000140848	ENSG00000140848	CPNE2	16:57126448-57181878	OK	6.72537	5.59702	-0.264955	-0.486243	0.39575	0.9998
ENSG00000068354	ENSG00000068354	TBC1D25	X:48397844-48420997	OK	9.5697	11.9031	0.314792	0.472869	0.3959	0.9998
ENSG00000232442	ENSG00000232442	CTD-3184A7.4	20:62258579-62260177	OK	1.60489	2.22976	0.474412	0.536616	0.3961	0.9998
ENSG00000253816	ENSG00000253816	RP11-1415C14.3	5:69515744-69580686	OK	1.39137	0.930965	-0.579704	-0.523993	0.3961	0.9998
ENSG00000169683	ENSG00000169683	LRRC45	17:79976577-79989027	OK	16.6227	13.1768	-0.335153	-0.466635	0.3962	0.9998
ENSG00000185495	ENSG00000185495	RP11-504P24.4	1:224183596-224198314	OK	1.81251	1.24748	-0.538972	-0.472656	0.3962	0.9998
ENSG00000135976	ENSG00000135976	ANKRD36	2:97779232-97930258	OK	2.32686	1.77685	-0.389062	-0.450924	0.39625	0.9998
ENSG00000162104	ENSG00000162104	ADCY9	16:4003387-4166186	OK	11.9356	14.3052	0.26127	0.345542	0.3963	0.9998
ENSG00000234869	ENSG00000234869	RP3-439F8.1	22:46937391-46944093	OK	1.20376	0.939623	-0.357394	-0.516632	0.3963	0.9998
ENSG00000159692	ENSG00000159692	CTBP1	4:1205235-1282079	OK	53.6755	65.6085	0.28962	0.5032	0.39665	0.9998
ENSG00000135972	ENSG00000135972	MRPS9	2:105552868-105719402	OK	30.4495	26.0489	-0.225195	-0.511646	0.39675	0.9998
ENSG00000135336	ENSG00000135336	ORC3	6:88299838-88377169	OK	9.44171	7.84996	-0.266364	-0.412555	0.39685	0.9998
ENSG00000135341	ENSG00000135341	MAP3K7	6:91223291-91296764	OK	12.1273	10.3711	-0.225689	-0.524184	0.397	0.9998
ENSG00000161888	ENSG00000161888	SPC24	19:11200037-11266484	OK	25.2569	16.0375	-0.655227	-0.471635	0.397	0.9998
ENSG00000230207	ENSG00000230207	RPL4P5	9:7477044-7478320	OK	2.16191	2.75027	0.347267	0.49774	0.397	0.9998
ENSG00000065357	ENSG00000065357	DGKA	12:56295196-56347811	OK	3.49933	2.75634	-0.344324	-0.225288	0.39705	0.9998
ENSG00000171135	ENSG00000171135	JAGN1	3:9932237-9936033	OK	20.5693	17.4507	-0.237204	-0.497346	0.3972	0.9998
ENSG00000187068	ENSG00000187068	C3orf70	3:184795837-184870802	OK	3.62108	3.05946	-0.243145	-0.502563	0.3972	0.9998
ENSG00000225278	ENSG00000225278	RP11-782C8.5	1:143118703-143240439	OK	0.713967	0.429397	-0.733545	-0.148172	0.3972	0.9998
ENSG00000140382	ENSG00000140382	HMG20A	15:77712753-77777949	OK	23.5341	28.5923	0.280874	0.429318	0.3974	0.9998
ENSG00000130023	ENSG00000130023	ERMARD	6:170151717-170181680	OK	4.92734	3.83793	-0.360481	-0.438783	0.3975	0.9998
ENSG00000170629	ENSG00000170629	DPY19L2P2	7:102815579-102920857	OK	6.62308	5.52807	-0.260726	-0.52365	0.3975	0.9998
ENSG00000145495	ENSG00000145495	6-Mar	5:10353814-10440500	OK	74.3891	60.3968	-0.300621	-0.453292	0.3976	0.9998
ENSG00000187642	ENSG00000187642	C1orf170	1:901876-917497	OK	2.81271	3.62925	0.367707	0.549195	0.3977	0.9998
ENSG00000111696	ENSG00000111696	NT5DC3	12:104164230-104234975	OK	23.8996	28.1521	0.236253	0.307611	0.3978	0.9998
ENSG00000159063	ENSG00000159063	ALG8	11:77811981-77850706	OK	37.7659	43.5965	0.207129	0.458414	0.39805	0.9998
ENSG00000148824	ENSG00000148824	MTG1	10:135192694-135382916	OK	22.4024	18.0424	-0.312257	-0.487304	0.39815	0.9998
ENSG00000266930	ENSG00000266930	CTD-2085J24.4	19:33366830-33369327	OK	0.664895	0.369631	-0.847042	-0.546919	0.39815	0.9998
ENSG00000008988	ENSG00000008988	RPS20	8:56979853-56987069	OK	1525.13	1776.12	0.219796	0.506101	0.3984	0.9998
ENSG00000272656	ENSG00000272656	RP11-219D15.3	3:138722803-139108574	OK	0.827877	0.125184	-2.72537	-0.113052	0.39845	0.9998
ENSG00000011275	ENSG00000011275	RNF216	7:5659677-5821370	OK	15.8765	18.558	0.225151	0.482456	0.3985	0.9998
ENSG00000089159	ENSG00000089159	PXN	12:120639093-120703574	OK	84.616	100.446	0.247424	0.398782	0.3985	0.9998
ENSG00000136824	ENSG00000136824	SMC2	9:106856540-106903698	OK	13.0497	11.2029	-0.220149	-0.506036	0.39895	0.9998
ENSG00000170852	ENSG00000170852	KBTBD2	7:32535037-33102409	OK	32.1406	23.7772	-0.434818	-0.380653	0.399	0.9998
ENSG00000162745	ENSG00000162745	OLFML2B	1:161952981-161993644	OK	2.03885	1.50388	-0.439068	-0.398207	0.39905	0.9998
ENSG00000141510	ENSG00000141510	TP53	17:7565096-7606820	OK	12.7315	10.4224	-0.288712	-0.437154	0.3991	0.9998
ENSG00000148773	ENSG00000148773	MKI67	10:129894922-129924649	OK	26.5137	23.0077	-0.204622	-0.336549	0.3991	0.9998
ENSG00000175352	ENSG00000175352	NRIP3	11:9002122-9025596	OK	21.1752	18.1595	-0.221645	-0.420483	0.3991	0.9998
ENSG00000115339	ENSG00000115339	GALNT3	2:166604100-166651192	OK	38.9334	33.2404	-0.228072	-0.45126	0.39915	0.9998
ENSG00000213432	ENSG00000213432	RP11-624L12.1	10:95043760-95044315	OK	0.408649	0.720653	0.818444	0.514898	0.3992	0.9998
ENSG00000122644	ENSG00000122644	ARL4A	7:12726480-12730559	OK	52.7645	44.5424	-0.244387	-0.509846	0.39925	0.9998
ENSG00000135747	ENSG00000135747	ZNF670	1:247108848-247242113	OK	2.24568	1.74413	-0.364644	-0.510658	0.39925	0.9998
ENSG00000123095	ENSG00000123095	BHLHE41	12:26272958-26986131	OK	32.1634	24.6087	-0.386251	-0.306679	0.3993	0.9998
ENSG00000118689	ENSG00000118689	FOXO3	6:108881037-109005977	OK	4.79351	4.00483	-0.259342	-0.495457	0.39945	0.9998
ENSG00000164904	ENSG00000164904	ALDH7A1	5:125877532-125931110	OK	26.0618	21.6612	-0.266819	-0.489728	0.3997	0.9998
ENSG00000254806	ENSG00000254806	SYS1-DBNDD2	20:43990576-44039250	OK	0.507804	1.26331	1.31487	0.246297	0.3997	0.9998
ENSG00000027697	ENSG00000027697	IFNGR1	6:137518620-137540586	OK	11.0297	13.0762	0.245544	0.496376	0.39975	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000136997	ENSG00000136997	MYC	8:128747679-128753674	OK	63.9778	74.0336	0.210608	0.511147	0.3998	0.9998
ENSG00000132510	ENSG00000132510	KDM6B	17:7743221-7758114	OK	5.39015	6.58742	0.289387	0.262481	0.39995	0.9998
ENSG00000075131	ENSG00000075131	TIPIN	15:66628543-66679084	OK	7.73857	6.23695	-0.311227	-0.500991	0.4	0.9998
ENSG00000215068	ENSG00000215068	AC025171.1	5:43014515-43192123	OK	0.841631	1.54799	0.879139	0.190671	0.4	0.9998
ENSG00000180336	ENSG00000180336	C17orf104	17:42733761-42767676	OK	0.549284	0.960288	0.805915	0.158127	0.40025	0.9998
ENSG00000138642	ENSG00000138642	HERC6	4:89299890-89364263	OK	2.62016	2.07609	-0.335789	-0.383439	0.4003	0.9998
ENSG00000197063	ENSG00000197063	MAFG	17:79869814-79885590	OK	17.5808	14.9068	-0.238027	-0.506462	0.4003	0.9998
ENSG00000235501	ENSG00000235501	RP4-639F20.1	1:95393121-95428826	OK	1.78069	1.29349	-0.461173	-0.464892	0.4003	0.9998
ENSG00000177000	ENSG00000177000	MTHFR	1:11821843-11908402	OK	9.19115	7.3936	-0.31397	-0.314673	0.4004	0.9998
ENSG00000178202	ENSG00000178202	KDELC2	11:108342831-108369159	OK	8.54814	10.0617	0.235197	0.401662	0.4005	0.9998
ENSG00000171720	ENSG00000171720	HDAC3	5:140894582-141016437	OK	46.638	35.348	-0.399878	-0.361545	0.40055	0.9998
ENSG00000181513	ENSG00000181513	ACBD4	17:43100707-43221548	OK	4.77678	3.01694	-0.662952	-0.230249	0.40055	0.9998
ENSG00000217165	ENSG00000217165	ANKRD18EP	6:39071839-39082965	OK	1.85243	1.25159	-0.565658	-0.499732	0.4006	0.9998
ENSG00000160293	ENSG00000160293	VAV2	9:136627015-136857726	OK	1.07536	1.36046	0.33928	0.423673	0.4007	0.9998
ENSG00000008130	ENSG00000008130	NADK	1:1682670-1711896	OK	26.8263	22.7902	-0.235233	-0.343189	0.4008	0.9998
ENSG00000150637	ENSG00000150637	CD226	18:67068290-67629039	OK	1.19564	0.859752	-0.475788	-0.352423	0.4008	0.9998
ENSG00000214941	ENSG00000214941	ZSWIM7	17:15879873-16256970	OK	10.2385	6.73112	-0.605093	-0.280114	0.40085	0.9998
ENSG00000138050	ENSG00000138050	THUMPD2	2:39963199-40006407	OK	7.26363	8.73411	0.26597	0.485412	0.40095	0.9998
ENSG00000146859	ENSG00000146859	TMEM140	7:134671258-134855547	OK	27.5444	34.3374	0.318023	0.507125	0.40105	0.9998
ENSG00000171067	ENSG00000171067	C11orf24	11:68028802-68039469	OK	73.2109	90.0968	0.299417	0.506723	0.40105	0.9998
ENSG00000115758	ENSG00000115758	ODC1	2:10580093-10588630	OK	45.3707	52.4475	0.209115	0.501161	0.4012	0.9998
ENSG00000237950	ENSG00000237950	RP11-7O11.3	1:44410041-44412223	OK	0.91156	0.565396	-0.689077	-0.445379	0.40135	0.9998
ENSG00000197915	ENSG00000197915	HRNR	1:152140600-152339163	OK	1.0269	1.53225	0.577352	0.500656	0.40145	0.9998
ENSG00000166226	ENSG00000166226	CCT2	12:69979113-69995350	OK	166.335	193.709	0.219804	0.498532	0.4016	0.9998
ENSG00000196678	ENSG00000196678	ERI2	16:20621564-20936328	OK	9.05719	6.25199	-0.534749	-0.340768	0.4016	0.9998
ENSG00000267278	ENSG00000267278	MAP3K14-AS1	17:43268297-43394414	OK	0.700678	0.448099	-0.644933	-0.175581	0.4017	0.9998
ENSG00000266554	ENSG00000266554	RP11-527H14.2	18:14946265-14973769	OK	68.1621	78.695	0.207302	0.507429	0.40195	0.9998
ENSG00000115806	ENSG00000115806	GORASP2	2:171784973-171823639	OK	34.9142	40.7305	0.222298	0.475053	0.40205	0.9998
ENSG00000224167	ENSG00000224167	RP3-522D1.1	1:113362791-113420493	OK	1.49647	0.862676	-0.794674	-0.543505	0.4022	0.9998
ENSG00000161896	ENSG00000161896	IP6K3	6:33689443-33714762	OK	5.20549	6.24374	0.262376	0.513062	0.4024	0.9998
ENSG00000228665	ENSG00000228665	RP11-20O24.1	1:109512835-109584850	OK	0.514957	2.5365	2.30031	0.165229	0.4024	0.9998
ENSG00000166224	ENSG00000166224	SGPL1	10:72575716-72640930	OK	19.9594	16.9207	-0.238278	-0.335853	0.4025	0.9998
ENSG00000183741	ENSG00000183741	CBX6	22:39257454-39268319	OK	15.7746	13.5307	-0.221365	-0.507335	0.4026	0.9998
ENSG00000200087	ENSG00000200087	SNORA73B	1:28832454-28865812	OK	0.666893	3.69183	2.46881	0.39334	0.40265	0.9998
ENSG00000104218	ENSG00000104218	CSPP1	8:67876333-68255912	OK	5.13891	3.37798	-0.605304	-0.272184	0.403	0.9998
ENSG00000108511	ENSG00000108511	HOXB6	17:46618255-46683776	OK	0.69026	0.955695	0.46941	0.415436	0.403	0.9998
ENSG00000197429	ENSG00000197429	IPP	1:46092975-46216322	OK	4.32067	2.38035	-0.860079	-0.425606	0.403	0.9998
ENSG00000198888	ENSG00000198888	MT-ND1	MT:3306-4262	OK	433.403	501.517	0.210589	0.50086	0.40305	0.9998
ENSG00000185008	ENSG00000185008	ROBO2	3:75955845-77699115	OK	4.99968	3.84695	-0.378118	-0.379724	0.4031	0.9998
ENSG00000077498	ENSG00000077498	TYR	11:88910619-89028927	OK	224.278	261.145	0.219562	0.501363	0.40315	0.9998
ENSG00000143889	ENSG00000143889	HNRNPLL	2:38789119-38830728	OK	30.4851	35.6397	0.22538	0.482494	0.4032	0.9998
ENSG00000081985	ENSG00000081985	IL12RB2	1:67773046-67862583	OK	11.1112	14.1839	0.352241	0.501553	0.40325	0.9998
ENSG00000147853	ENSG00000147853	AK3	9:4711154-4742043	OK	44.9565	38.8129	-0.211992	-0.489271	0.40325	0.9998
ENSG00000203724	ENSG00000203724	C1orf53	1:197871776-197876497	OK	3.7495	4.87942	0.380012	0.474317	0.40325	0.9998
ENSG00000124613	ENSG00000124613	ZNF391	6:27342393-27371683	OK	1.08692	0.795232	-0.450793	-0.411407	0.40335	0.9998
ENSG00000167641	ENSG00000167641	PPP1R14A	19:38734674-38795649	OK	0.773933	1.12024	0.533526	0.388102	0.40335	0.9998
ENSG00000251562	ENSG00000251562	MALAT1	11:65265232-65273940	OK	33.5752	28.3482	-0.244143	-0.454317	0.4034	0.9998
ENSG00000166340	ENSG00000166340	TPP1	11:6633999-6640995	OK	65.66	57.4754	-0.19207	-0.373497	0.4035	0.9998
ENSG00000081087	ENSG00000081087	OSTM1	6:108362612-108487058	OK	45.9055	57.7785	0.331865	0.503863	0.40375	0.9998
ENSG00000152253	ENSG00000152253	SPC25	2:169312371-169769881	OK	23.4223	16.7517	-0.483575	-0.484104	0.40375	0.9998
ENSG00000204104	ENSG00000204104	TRAF3IP1	2:239229081-239309541	OK	6.73172	9.02735	0.423326	0.492799	0.4038	0.9998
ENSG00000164758	ENSG00000164758	MED30	8:118532951-118552501	OK	9.70182	7.88293	-0.299523	-0.505698	0.40385	0.9998
ENSG00000112276	ENSG00000112276	BVES	6:105544696-105627870	OK	3.32023	4.1495	0.321654	0.494039	0.40405	0.9998
ENSG00000153904	ENSG00000153904	DDAH1	1:85731930-86043933	OK	4.43508	3.55106	-0.320711	-0.453253	0.40415	0.9998
ENSG00000167193	ENSG00000167193	CRK	17:1323982-1366456	OK	21.4638	24.831	0.210233	0.476923	0.40425	0.9998
ENSG00000197548	ENSG00000197548	ATG7	3:11313994-11766453	OK	16.5219	12.012	-0.459899	-0.339625	0.40425	0.9998
ENSG00000214706	ENSG00000214706	IFRD2	3:50316457-50336899	OK	39.6795	47.0223	0.244951	0.48011	0.40425	0.9998
ENSG00000180448	ENSG00000180448	HMHA1	19:1065921-1095598	OK	3.83513	5.90741	0.623249	0.376713	0.40455	0.9998
ENSG00000160991	ENSG00000160991	ORAI2	7:102067264-102105323	OK	15.9773	20.2103	0.339068	0.449145	0.4046	0.9998
ENSG00000188612	ENSG00000188612	SUMO2	17:73131342-73179078	OK	127.655	151.168	0.243903	0.486743	0.4048	0.9998
ENSG00000180834	ENSG00000180834	MAP6D1	3:183533663-183543382	OK	4.40466	3.56637	-0.304573	-0.414454	0.4049	0.9998
ENSG00000102144	ENSG00000102144	PGK1	X:77320684-77384793	OK	1114.36	922.854	-0.272044	-0.48168	0.405	0.9998
ENSG00000176155	ENSG00000176155	CCDC57	17:80059335-80170706	OK	8.90177	11.1958	0.330798	0.42056	0.40515	0.9998
ENSG00000177565	ENSG00000177565	TBL1XR1	3:176737142-176915261	OK	26.3611	22.4268	-0.233187	-0.303869	0.40515	0.9998
ENSG00000160299	ENSG00000160299	PCNT	21:47744035-47865682	OK	3.54957	2.90796	-0.287638	-0.311998	0.4052	0.9998
ENSG00000215030	ENSG00000215030	RPL13P12	17:17286690-17287326	OK	7.05186	8.81482	0.321928	0.488462	0.4052	0.9998
ENSG00000269837	ENSG00000269837	RP11-15H20.5	19:23437854-23457053	OK	0.401887	0.672123	0.741934	0.419363	0.4052	0.9998
ENSG00000025796	ENSG00000025796	SEC63	6:108188959-108281190	OK	20.3195	16.4127	-0.308054	-0.378353	0.4053	0.9998
ENSG00000105971	ENSG00000105971	CAV2	7:116850546-116148595	OK	80.579	62.5725	-0.364875	-0.523257	0.40535	0.9998
ENSG00000035862	ENSG00000035862	TIMP2	17:76849058-76921469	OK	580.94	689.601	0.247373	0.502456	0.4055	0.9998
ENSG00000106003	ENSG00000106003	LFNG	7:2552162-2568811	OK	4.45853	5.50746	0.30482	0.497164	0.4056	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000152076	ENSG00000152076	CCDC74B	2:130887193-130902707	OK	0.911527	0.649358	-0.489271	-0.350058	0.4056	0.9998
ENSG00000110090	ENSG00000110090	CPT1A	11:68522087-68611878	OK	2.3818	3.11001	0.384871	0.367418	0.40565	0.9998
ENSG00000261431	ENSG00000261431	RP4-616B8.4	20:37590567-37590754	OK	1.01569	2.95928	1.54279	0.944047	0.40575	0.9998
ENSG00000063169	ENSG00000063169	GLTSCR1	19:48110780-48246391	OK	5.28593	3.4055	-0.634289	-0.449486	0.4058	0.9998
ENSG00000100968	ENSG00000100968	NFATC4	14:24834878-24848810	OK	3.13367	4.51904	0.52816	0.429879	0.4058	0.9998
ENSG00000254612	ENSG00000254612	RP11-676M6.1	11:127810807-127811549	OK	18.7141	22.3706	0.257475	0.492471	0.4058	0.9998
ENSG00000114120	ENSG00000114120	SLC25A36	3:140660671-140698775	OK	63.3635	52.2498	-0.278226	-0.421085	0.406	0.9998
ENSG00000170502	ENSG00000170502	NUDT9	4:88343733-88380606	OK	18.2155	15.1397	-0.266838	-0.475496	0.40605	0.9998
ENSG00000146267	ENSG00000146267	FAXC	6:99719044-99797938	OK	11.964	15.4852	0.372193	0.49605	0.40615	0.9998
ENSG00000077254	ENSG00000077254	USP33	1:78161671-78225537	OK	18.4266	21.235	0.20466	0.379796	0.40625	0.9998
ENSG00000146282	ENSG00000146282	RARS2	6:88224095-88299721	OK	13.2894	15.6048	0.231713	0.459725	0.4063	0.9998
ENSG00000109586	ENSG00000109586	GALNT7	4:174053078-174250845	OK	16.832	19.9225	0.243193	0.460708	0.40635	0.9998
ENSG00000169519	ENSG00000169519	METTL15	11:28042166-28355054	OK	8.21746	6.49224	-0.339976	-0.330315	0.4064	0.9998
ENSG00000220583	ENSG00000220583	RPL35P2	6:34231087-34231450	OK	6.45881	8.56579	0.407318	0.510811	0.4065	0.9998
ENSG00000135211	ENSG00000135211	TMEM60	7:77423044-77427897	OK	20.024	16.8726	-0.247046	-0.496495	0.40665	0.9998
ENSG00000224040	ENSG00000224040	HMGN1P4	1:182868999-182922660	OK	0.244422	0.862904	1.81983	0.863448	0.40675	0.9998
ENSG00000262223	ENSG00000262223	RP11-1055B8.3	17:79349800-79359160	OK	34.0334	27.894	-0.286999	-0.496497	0.40675	0.9998
ENSG00000259357	ENSG00000259357	RP11-316M1.12	1:150898738-150948010	OK	0.583491	2.60076	2.15615	0.178017	0.4068	0.9998
ENSG00000182326	ENSG00000182326	C1S	12:7072407-7178336	OK	4.48331	2.58846	-0.792469	-0.215099	0.4069	0.9998
ENSG00000165533	ENSG00000165533	TTC8	14:89290496-89344335	OK	13.0484	15.428	0.241678	0.470876	0.40695	0.9998
ENSG00000173559	ENSG00000173559	NABP1	2:192542793-192561385	OK	12.1382	14.9614	0.301694	0.483457	0.407	0.9998
ENSG00000230189	ENSG00000230189	GS1-124K5.2	7:65670185-65955095	OK	0.675719	0.314849	-1.10176	-0.227293	0.407	0.9998
ENSG00000155755	ENSG00000155755	TMEM237	2:202484906-202508293	OK	27.3612	22.7576	-0.265779	-0.494313	0.40715	0.9998
ENSG00000121390	ENSG00000121390	PSPC1	13:20248763-20357142	OK	21.6169	25.2891	0.226355	0.499086	0.4073	0.9998
ENSG00000118162	ENSG00000118162	KPTN	19:47978400-47987525	OK	12.4586	10.1765	-0.291896	-0.469546	0.4074	0.9998
ENSG00000185269	ENSG00000185269	NOTUM	17:79910387-79919716	OK	0.693586	0.507522	-0.450604	-0.412154	0.40745	0.9998
ENSG00000225138	ENSG00000225138	CTD-2228K2.7	5:473350-524447	OK	82.1342	101.441	0.30459	0.49393	0.40745	0.9998
ENSG00000177082	ENSG00000177082	WDR73	15:85185998-85197574	OK	17.6449	21.1514	0.261504	0.481484	0.40755	0.9998
ENSG00000223546	ENSG00000223546	LINC00630	X:102024088-102161086	OK	4.06722	3.03148	-0.424018	-0.501422	0.40755	0.9998
ENSG00000165716	ENSG00000165716	FAM69B	9:139607021-139622636	OK	37.2826	44.3541	0.250565	0.498242	0.4077	0.9998
ENSG00000064419	ENSG00000064419	TNPO3	7:128594947-128695198	OK	55.2323	48.0026	-0.2024	-0.502791	0.40785	0.9998
ENSG00000143847	ENSG00000143847	PPFIA4	1:202995625-203047868	OK	9.29154	7.37729	-0.332825	-0.31429	0.40785	0.9998
ENSG00000100335	ENSG00000100335	MIEF1	22:39895436-39914137	OK	27.928	32.0184	0.197187	0.409845	0.40835	0.9998
ENSG00000117114	ENSG00000117114	LPHN2	1:81771844-82458120	OK	3.5642	4.35523	0.289171	0.365906	0.40835	0.9998
ENSG00000172671	ENSG00000172671	ZFAND4	10:46111042-46168228	OK	2.08798	2.71837	0.380633	0.476938	0.40845	0.9998
ENSG00000185386	ENSG00000185386	MAPK11	22:50702141-50709196	OK	5.48234	6.64822	0.278176	0.486181	0.4086	0.9998
ENSG00000148481	ENSG00000148481	FAM188A	10:15820168-15902519	OK	10.1314	8.55761	-0.243559	-0.466972	0.4087	0.9998
ENSG00000154639	ENSG00000154639	CXADR	21:18884699-18965897	OK	0.683661	0.980714	0.520551	0.3927	0.4087	0.9998
ENSG00000173020	ENSG00000173020	ADRBK1	11:67033880-67054027	OK	31.1674	26.9238	-0.211158	-0.317559	0.4087	0.9998
ENSG00000189058	ENSG00000189058	APOD	3:195295572-195311076	OK	1.71313	2.24278	0.388658	0.489047	0.4087	0.9998
ENSG00000176623	ENSG00000176623	RMDN1	8:87345502-87777251	OK	39.9605	28.5562	-0.484771	-0.364216	0.40875	0.9998
ENSG00000231764	ENSG00000231764	DLX6-AS1	7:96584452-96643377	OK	0.388672	0.684751	0.817026	0.474482	0.40885	0.9998
ENSG00000141499	ENSG00000141499	WRAP53	17:7565096-7606820	OK	8.53681	6.51423	-0.390101	-0.461064	0.4089	0.9998
ENSG00000059145	ENSG00000059145	UNKL	16:1401923-1464752	OK	5.19624	6.82853	0.394108	0.326583	0.40895	0.9998
ENSG00000215784	ENSG00000215784	FAM72D	1:143896451-143913143	OK	1.85284	1.46274	-0.341063	-0.51474	0.4091	0.9998
ENSG00000232499	ENSG00000232499	RP11-512F24.1	1:113933370-114228545	OK	10.0572	7.60429	-0.40334	-0.498134	0.4092	0.9998
ENSG00000065802	ENSG00000065802	ASB1	2:239335382-239360891	OK	13.113	10.4819	-0.3231	-0.431601	0.4095	0.9998
ENSG00000254598	ENSG00000254598	CSNK2A3	11:11292422-11643552	OK	11.2788	14.0372	0.315642	0.494825	0.4095	0.9998
ENSG00000204920	ENSG00000204920	ZNF155	19:44472013-44506988	OK	1.5063	1.94347	0.367621	0.399946	0.4096	0.9998
ENSG00000125817	ENSG00000125817	CENPB	20:3764497-3767337	OK	11.6562	13.6054	0.223084	0.499447	0.40965	0.9998
ENSG00000174173	ENSG00000174173	TRMT10C	3:101280705-101285290	OK	19.8054	16.7603	-0.240845	-0.498898	0.40965	0.9998
ENSG00000135119	ENSG00000135119	RNFT2	12:117176095-117291436	OK	1.01211	0.761518	-0.410417	-0.424451	0.40975	0.9998
ENSG00000153721	ENSG00000153721	CNKSR3	6:154708637-154831793	OK	1.42011	1.81932	0.357397	0.458811	0.40975	0.9998
ENSG00000130529	ENSG00000130529	TRPM4	19:49660997-49715093	OK	6.00136	8.24485	0.458203	0.506017	0.4098	0.9998
ENSG00000139880	ENSG00000139880	CDH24	14:23516270-23526747	OK	1.96926	2.42242	0.298795	0.50432	0.4099	0.9998
ENSG00000134748	ENSG00000134748	PRPF38A	1:52870235-53019159	OK	17.1392	12.3641	-0.47114	-0.51114	0.40995	0.9998
ENSG00000163625	ENSG00000163625	WDFY3	4:85590703-85932430	OK	7.75297	5.81618	-0.414678	-0.284091	0.40995	0.9998
ENSG00000249481	ENSG00000249481	SPATS1	6:44238202-44346694	OK	2.98272	8.21535	1.46169	0.749727	0.41005	0.9998
ENSG00000118058	ENSG00000118058	KMT2A	11:118307204-118473748	OK	4.43019	3.40937	-0.377866	-0.234743	0.41015	0.9998
ENSG00000172932	ENSG00000172932	ANKRD13D	11:67056017-67069956	OK	19.8678	23.299	0.229835	0.447695	0.41025	0.9998
ENSG00000163812	ENSG00000163812	ZDHHC3	3:44956748-45077563	OK	43.918	34.5665	-0.345439	-0.458151	0.4103	0.9998
ENSG00000184517	ENSG00000184517	ZFP1	16:75182389-75206134	OK	5.632	7.37105	0.388224	0.431166	0.4103	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000104979	ENSG00000104979	C19orf53	19:13875345-13889276	OK	139.827	168.066	0.265386	0.517018	0.41035	0.9998
ENSG00000103121	ENSG00000103121	CMC2	16:81009697-81069364	OK	84.7107	66.5556	-0.347983	-0.51013	0.4106	0.9998
ENSG00000112096	ENSG00000112096	SOD2	6:160090088-160210781	OK	74.9865	51.42	-0.544302	-0.486166	0.4106	0.9998
ENSG00000232380	ENSG00000232380	ZDHHC20P4	13:69559189-69560196	OK	1.03705	1.40819	0.441365	0.495376	0.41065	0.9998
ENSG00000241945	ENSG00000241945	PWP2	21:45527170-45551063	OK	7.46616	6.29779	-0.245521	-0.437225	0.4107	0.9998
ENSG00000102384	ENSG00000102384	CENPI	X:100353177-100418670	OK	13.4744	10.5489	-0.353126	-0.482225	0.4108	0.9998
ENSG00000116285	ENSG00000116285	ERRFI1	1:8064463-8086368	OK	3.12257	3.78194	0.276392	0.46474	0.41115	0.9998
ENSG00000205336	ENSG00000205336	GPR56	16:57644563-57698944	OK	197.178	226.401	0.199383	0.359074	0.41115	0.9998
ENSG00000148344	ENSG00000148344	PTGES	9:132500609-132515326	OK	1.76496	2.26269	0.358406	0.518331	0.41125	0.9998
ENSG00000160208	ENSG00000160208	RRP1B	21:45079428-45115958	OK	8.95563	10.4074	0.216738	0.505878	0.4114	0.9998
ENSG00000235034	ENSG00000235034	C19orf81	19:51124563-51222707	OK	0.381904	0.930417	1.28467	0.449145	0.4114	0.9998
ENSG00000226415	ENSG00000226415	TPI1P1	1:77165473-77166223	OK	27.8184	23.5233	-0.24195	-0.480325	0.4116	0.9998
ENSG00000155984	ENSG00000155984	TMEM185A	X:148678215-148713568	OK	6.55745	8.32918	0.345041	0.448603	0.41185	0.9998
ENSG00000198039	ENSG00000198039	ZNF273	7:64330549-64391344	OK	2.46432	1.89141	-0.381726	-0.467682	0.4119	0.9998
ENSG00000154370	ENSG00000154370	TRIM11	1:228581373-228594541	OK	16.5112	19.279	0.223589	0.42987	0.41205	0.9998
ENSG00000233184	ENSG00000233184	RP11-421L21.3	1:101455178-101552821	OK	2.13395	1.08575	-0.974839	-0.426176	0.4121	0.9998
ENSG00000121210	ENSG00000121210	KIAA0922	4:154387497-154557863	OK	3.09766	2.58394	-0.261604	-0.370899	0.41225	0.9998
ENSG00000230979	ENSG00000230979	AC079250.1	2:47917854-47918385	OK	1.02018	1.52901	0.583772	0.521488	0.41235	0.9998
ENSG00000064225	ENSG00000064225	ST3GAL6	3:98433173-98620533	OK	149.018	179.995	0.272467	0.420593	0.4124	0.9998
ENSG00000243406	ENSG00000243406	MRPS31P5	13:52741843-52908412	OK	4.30155	3.41003	-0.335074	-0.382537	0.4126	0.9998
ENSG00000224411	ENSG00000224411	RP11-1033A18.1	11:27910384-27912580	OK	1.90312	2.47176	0.377176	0.498168	0.4127	0.9998
ENSG00000133773	ENSG00000133773	CCDC59	12:82617459-82873015	OK	30.5353	36.8815	0.272418	0.49145	0.41275	0.9998
ENSG00000141012	ENSG00000141012	GALNS	16:88880141-88933068	OK	11.5053	14.1942	0.303003	0.416959	0.413	0.9998
ENSG00000270557	ENSG00000270557	RP11-546J1.1	2:158733213-158992666	OK	0.524565	0.77835	0.569297	0.507164	0.413	0.9998
ENSG00000186432	ENSG00000186432	KPNA4	3:160212782-160287036	OK	21.7502	26.254	0.271512	0.302226	0.41305	0.9998
ENSG00000073111	ENSG00000073111	MCM2	3:127291911-127341276	OK	10.7985	8.89682	-0.279473	-0.465317	0.4132	0.9998
ENSG00000214182	ENSG00000214182	PTMAP5	13:82264045-82265207	OK	1.47454	0.550723	-1.42087	-0.909617	0.41325	0.9998
ENSG00000127663	ENSG00000127663	KDM4B	19:4969124-5153606	OK	8.99818	10.4111	0.210414	0.408612	0.41335	0.9998
ENSG00000001497	ENSG00000001497	LAS1L	X:64732461-64754655	OK	24.9581	21.3684	-0.224027	-0.436001	0.4134	0.9998
ENSG00000213762	ENSG00000213762	ZNF134	19:58125600-58134724	OK	4.15058	5.01921	0.274146	0.376441	0.4134	0.9998
ENSG00000143622	ENSG00000143622	RIT1	1:155867598-155881195	OK	30.7995	25.3016	-0.283678	-0.496999	0.41345	0.9998
ENSG00000033030	ENSG00000033030	ZCCHC8	12:122957416-122985518	OK	14.6426	12.5268	-0.225154	-0.466108	0.41355	0.9998
ENSG00000124134	ENSG00000124134	KCNS1	20:43720950-43729753	OK	2.06305	2.5066	0.280952	0.494132	0.41355	0.9998
ENSG00000138107	ENSG00000138107	ACTR1A	10:104238985-104262482	OK	64.4399	55.9179	-0.204644	-0.457655	0.41355	0.9998
ENSG00000114405	ENSG00000114405	C3orf14	3:61547242-62355005	OK	63.4023	47.9056	-0.404342	-0.496214	0.4136	0.9998
ENSG00000128573	ENSG00000128573	FOXP2	7:113726381-114333827	OK	1.44807	1.03796	-0.480386	-0.299483	0.4136	0.9998
ENSG00000115159	ENSG00000115159	GPD2	2:157291801-157470247	OK	27.5203	23.6518	-0.218545	-0.363614	0.41365	0.9998
ENSG00000118620	ENSG00000118620	ZNF430	19:21203425-21242856	OK	3.33757	2.46262	-0.438603	-0.371283	0.41375	0.9998
ENSG00000242083	ENSG00000242083	RPL7AP31	4:57204455-57253666	OK	7.11839	9.77993	0.458274	0.495532	0.4139	0.9998
ENSG00000006114	ENSG00000006114	SYNRG	17:35874899-35969544	OK	13.6121	11.4017	-0.255641	-0.432728	0.4141	0.9998
ENSG00000102981	ENSG00000102981	PARD6A	16:67694848-67696681	OK	1.52178	1.15724	-0.395076	-0.476495	0.4141	0.9998
ENSG00000119977	ENSG00000119977	TCTN3	10:97423157-97453900	OK	37.9392	32.8981	-0.205687	-0.472118	0.4141	0.9998
ENSG00000224578	ENSG00000224578	HNRNPA1P48	16:51679666-51681043	OK	66.7235	77.3025	0.21232	0.499183	0.41415	0.9998
ENSG00000260630	ENSG00000260630	SNAI3-AS1	16:88729705-88753594	OK	1.77723	1.20043	-0.566084	-0.511323	0.41425	0.9998
ENSG00000141965	ENSG00000141965	FEM1A	19:4791727-4795571	OK	9.9453	8.23902	-0.271542	-0.499998	0.4143	0.9998
ENSG00000154719	ENSG00000154719	MRPL39	21:26957967-26979829	OK	14.8439	17.6271	0.247928	0.49335	0.41435	0.9998
ENSG00000179950	ENSG00000179950	PUF60	8:144898513-144912029	OK	100.959	116.023	0.20064	0.471225	0.4145	0.9998
ENSG00000119686	ENSG00000119686	FLVCR2	14:76041230-76550928	OK	1.4412	2.46911	0.776721	0.258302	0.4146	0.9998
ENSG00000137161	ENSG00000137161	CNPY3	6:42896937-42907025	OK	65.7313	57.1407	-0.202061	-0.500226	0.4146	0.9998
ENSG00000249992	ENSG00000249992	TMEM158	3:45265957-45267770	OK	5.40038	4.4506	-0.279062	-0.498285	0.41475	0.9998
ENSG00000082482	ENSG00000082482	KCNK2	1:215179117-215410436	OK	0.575508	0.841986	0.54896	0.379261	0.41495	0.9998
ENSG00000166704	ENSG00000166704	ZNF606	19:58488420-58522600	OK	1.10544	1.46241	0.403732	0.395159	0.41495	0.9998
ENSG00000104888	ENSG00000104888	SLC17A7	19:49932657-49945617	OK	0.598778	0.775523	0.373149	0.411149	0.415	0.9998
ENSG00000187630	ENSG00000187630	DHRS4L2	14:24407939-24475617	OK	10.8753	7.97251	-0.447954	-0.484305	0.41505	0.9998
ENSG00000168938	ENSG00000168938	PPIC	5:122179133-122390362	OK	8.03425	9.9414	0.307285	0.494884	0.4153	0.9998
ENSG00000273203	ENSG00000273203	AC006946.16	22:17548710-17551565	OK	2.68274	2.19471	-0.289678	-0.497331	0.4153	0.9998
ENSG00000228696	ENSG00000228696	ARL17B	17:44352149-44439130	OK	2.61472	3.78253	0.532697	0.480553	0.41535	0.9998
ENSG00000172943	ENSG00000172943	PHF8	X:53963108-54075391	OK	5.03903	5.88529	0.223968	0.346942	0.41545	0.9998
ENSG00000051825	ENSG00000051825	MPHOSPH9	12:123636866-123756881	OK	19.3074	14.8678	-0.376964	-0.210116	0.4155	0.9998
ENSG00000143157	ENSG00000143157	POGK	1:166808680-166825581	OK	17.4252	20.4904	0.233773	0.458878	0.4155	0.9998
ENSG00000165487	ENSG00000165487	MICU2	13:22066835-22178353	OK	29.1706	33.6958	0.208054	0.472917	0.4155	0.9998
ENSG00000103152	ENSG00000103152	MPG	16:127005-188859	OK	55.4698	66.7363	0.26677	0.509794	0.41555	0.9998
ENSG00000123600	ENSG00000123600	METTL8	2:172173918-172341562	OK	9.31076	6.75377	-0.463207	-0.415579	0.41555	0.9998
ENSG00000272172	ENSG00000272172	RP13-582O9.7	8:144371845-144380231	OK	0.246617	2.28168	3.20975	0.595496	0.41555	0.9998
ENSG00000114841	ENSG00000114841	DNAH1	3:52350334-52434507	OK	0.656643	1.03887	0.661839	0.3621	0.41585	0.9998
ENSG00000164953	ENSG00000164953	TMEM67	8:94767071-94831462	OK	8.04868	9.70621	0.270155	0.359739	0.41595	0.9998
ENSG00000251003	ENSG00000251003	RP11-152P17.2	8:105602960-107072752	OK	20.2849	24.6119	0.278951	0.499303	0.41605	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000102531	ENSG00000102531	FNDC3A	13:49550047-49783915	OK	24.0225	27.5458	0.197443	0.453712	0.41615	0.9998
ENSG00000237686	ENSG00000237686	RP5-1120P11.	6:43963459-44045689	OK	0.713307	0.493171	-0.532435	-0.464336	0.4162	0.9998
ENSG00000135999	ENSG00000135999	EPC2	2:149402008-149545130	OK	3.25836	2.67393	-0.285183	-0.427278	0.4163	0.9998
ENSG00000084676	ENSG00000084676	NCOA1	2:24714782-24993571	OK	6.81961	7.97459	0.22572	0.399906	0.41635	0.9998
ENSG00000214113	ENSG00000214113	LYRM4	6:5102826-5261172	OK	57.0868	67.6487	0.244906	0.489216	0.41635	0.9998
ENSG00000149480	ENSG00000149480	MTA2	11:62360685-62369312	OK	30.6032	35.1811	0.201121	0.411607	0.4164	0.9998
ENSG00000172006	ENSG00000172006	ZNF554	19:2819871-2835771	OK	1.37789	1.09327	-0.333814	-0.482684	0.4165	0.9998
ENSG00000196652	ENSG00000196652	ZKSCAN5	7:99102273-99132323	OK	8.46261	7.16876	-0.239379	-0.504882	0.4165	0.9998
ENSG00000142208	ENSG00000142208	AKT1	14:105235685-105262088	OK	102.775	119.145	0.213228	0.440019	0.41655	0.9998
ENSG00000175691	ENSG00000175691	ZNF77	19:2933215-2944969	OK	2.38431	1.9276	-0.306765	-0.466573	0.4166	0.9998
ENSG00000213214	ENSG00000213214	ARHGEF35	7:143883175-144077725	OK	1.36158	2.1447	0.65549	0.49291	0.41665	0.9998
ENSG00000130813	ENSG00000130813	C19orf66	19:10196797-10213472	OK	24.1685	20.6835	-0.22465	-0.432815	0.4167	0.9998
ENSG00000167258	ENSG00000167258	CDK12	17:37617763-37721160	OK	10.9998	12.7342	0.211228	0.382075	0.4168	0.9998
ENSG00000197775	ENSG00000197775	DHRS4-AS1	14:24407939-24475617	OK	3.89261	1.99574	-0.963817	-0.556227	0.41685	0.9998
ENSG00000136936	ENSG00000136936	XPA	9:100437190-100459639	OK	7.6615	6.27011	-0.289135	-0.443748	0.41695	0.9998
ENSG00000153814	ENSG00000153814	JAZF1	7:27773013-28283536	OK	23.0086	35.4583	0.62395	0.373103	0.41715	0.9998
ENSG00000103994	ENSG00000103994	ZNF106	15:42705020-42783321	OK	43.6876	50.3273	0.204117	0.376825	0.41725	0.9998
ENSG00000145284	ENSG00000145284	SCD5	4:83550691-83720010	OK	5.1367	4.28702	-0.260866	-0.489269	0.41725	0.9998
ENSG00000011304	ENSG00000011304	PTBP1	19:797074-812327	OK	126.41	106.174	-0.251675	-0.43633	0.4174	0.9998
ENSG00000109919	ENSG00000109919	MTCH2	11:47638866-47664175	OK	154.792	129.351	-0.259035	-0.498318	0.4174	0.9998
ENSG00000137815	ENSG00000137815	RTF1	15:41700605-41775761	OK	8.96353	10.7622	0.263833	0.345552	0.4177	0.9998
ENSG00000250896	ENSG00000250896	RNPS1P1	4:11373598-11374516	OK	5.55043	4.45415	-0.31745	-0.488065	0.4177	0.9998
ENSG00000213918	ENSG00000213918	DNASE1	16:3661728-3767598	OK	4.6402	3.16363	-0.552605	-0.19641	0.41775	0.9998
ENSG00000108561	ENSG00000108561	C1QBP	17:5185557-5372380	OK	169.195	218.362	0.368031	0.488222	0.4178	0.9998
ENSG00000188015	ENSG00000188015	S100A3	1:153516088-153522612	OK	5.59592	4.0065	-0.482032	-0.434609	0.4178	0.9998
ENSG00000147874	ENSG00000147874	HAUS6	9:19053140-19103117	OK	18.6245	15.6391	-0.252046	-0.384284	0.41785	0.9998
ENSG00000129493	ENSG00000129493	HEATR5A	14:31717833-31926716	OK	35.8069	52.074	0.540326	0.469045	0.4179	0.9998
ENSG00000031698	ENSG00000031698	SARS	1:109756539-109780791	OK	77.8841	90.053	0.209445	0.49957	0.41795	0.9998
ENSG00000151967	ENSG00000151967	SCHIP1	3:158680023-159615155	OK	0.902924	1.62311	0.846083	0.282505	0.4181	0.9998
ENSG00000185164	ENSG00000185164	NOMO2	16:18511181-18573533	OK	17.2199	14.998	-0.199303	-0.467613	0.41825	0.9998
ENSG00000238151	ENSG00000238151	MLLT10P1	20:29637798-29638060	OK	0.623382	1.06823	0.777036	0.42588	0.4184	0.9998
ENSG00000063978	ENSG00000063978	RNF4	4:2420700-2734292	OK	28.7004	24.6427	-0.219912	-0.36757	0.41845	0.9998
ENSG00000153140	ENSG00000153140	CETN3	5:89688077-89705603	OK	24.0757	19.8804	-0.276231	-0.49058	0.41855	0.9998
ENSG00000043355	ENSG00000043355	ZIC2	13:100634025-100639018	OK	0.717488	1.08793	0.600555	0.315556	0.4186	0.9998
ENSG00000246763	ENSG00000246763	RGMB-AS1	5:98104353-98134347	OK	0.695365	0.33284	-1.06294	-0.184625	0.4188	0.9998
ENSG00000120664	ENSG00000120664	SPG20OS	13:36875774-36944317	OK	0.751863	0.339529	-1.14693	-0.108578	0.41895	0.9998
ENSG00000140259	ENSG00000140259	MFAP1	15:44096689-44117000	OK	10.0548	8.49224	-0.243673	-0.490757	0.41895	0.9998
ENSG00000213658	ENSG00000213658	LAT	16:28985541-29002104	OK	1.26798	0.855364	-0.567925	-0.126444	0.419	0.9998
ENSG00000123104	ENSG00000123104	ITPR2	12:26272958-26986131	OK	7.67939	6.36718	-0.270337	-0.357002	0.41935	0.9998
ENSG00000146707	ENSG00000146707	POMZP3	7:76139744-77045717	OK	15.3035	12.2783	-0.317746	-0.495112	0.41945	0.9998
ENSG00000132612	ENSG00000132612	VPS4A	16:69139466-69442474	OK	41.6551	31.8789	-0.385892	-0.477363	0.4195	0.9998
ENSG00000269955	ENSG00000269955	LUC7L2	7:139024202-139108198	OK	21.5695	15.8246	-0.446827	-0.499909	0.41955	0.9998
ENSG00000181029	ENSG00000181029	TRAPPC5	19:7741513-7747744	OK	55.3906	64.7998	0.226347	0.490914	0.4196	0.9998
ENSG00000070366	ENSG00000070366	SMG6	17:1963132-2284352	OK	7.01817	5.12981	-0.45219	-0.27932	0.41965	0.9998
ENSG00000165714	ENSG00000165714	LOH12CR1	12:12510012-12619840	OK	9.5237	7.12226	-0.419187	-0.501264	0.41975	0.9998
ENSG00000100714	ENSG00000100714	MTHFD1	14:64854748-65009955	OK	59.2416	48.8713	-0.277622	-0.405713	0.4198	0.9998
ENSG00000204713	ENSG00000204713	TRIM27	6:28870778-28891766	OK	20.4978	23.6813	0.208277	0.41815	0.41985	0.9998
ENSG00000125149	ENSG00000125149	C16orf70	16:67143860-67185117	OK	6.92645	5.66103	-0.291051	-0.420547	0.41995	0.9998
ENSG00000104723	ENSG00000104723	TUSC3	8:15274723-15624158	OK	83.2195	71.169	-0.225671	-0.470945	0.42005	0.9998
ENSG00000182957	ENSG00000182957	SPATA13	13:24553838-24896673	OK	7.84697	9.30927	0.246533	0.253725	0.4202	0.9998
ENSG00000130489	ENSG00000130489	SCO2	22:50961996-50971009	OK	22.4609	27.4847	0.291215	0.498739	0.4204	0.9998
ENSG00000107984	ENSG00000107984	DKK1	10:54074055-54077802	OK	0.759218	1.18291	0.639755	0.361181	0.4205	0.9998
ENSG00000189420	ENSG00000189420	ZFP92	X:152683779-152687087	OK	1.16455	1.51894	0.383295	0.481106	0.4205	0.9998
ENSG00000177337	ENSG00000177337	DLGAP1-AS1	18:3496029-4455335	OK	9.19211	5.48771	-0.74419	-0.439838	0.42055	0.9998
ENSG00000140836	ENSG00000140836	ZFHX3	16:72699068-73093597	OK	0.852833	1.06888	0.325767	0.362617	0.4206	0.9998
ENSG00000144120	ENSG00000144120	TMEM177	2:120436742-120444083	OK	13.826	16.514	0.256313	0.500088	0.42065	0.9998
ENSG00000236675	ENSG00000236675	MTX1P1	1:155200765-155204116	OK	4.05055	5.07455	0.325162	0.480862	0.4209	0.9998
ENSG00000161682	ENSG00000161682	FAM171A2	17:42430582-42441243	OK	2.78546	2.11756	-0.395509	-0.479896	0.42105	0.9998
ENSG00000105486	ENSG00000105486	LIG1	19:48618701-48673860	OK	22.876	19.1317	-0.257867	-0.421298	0.4211	0.9998
ENSG00000082397	ENSG00000082397	EPB41L3	18:5392382-5630699	OK	89.6306	106.029	0.24239	0.40767	0.4215	0.9998
ENSG00000197415	ENSG00000197415	VEPH1	3:156893011-157251408	OK	50.5428	38.1213	-0.40691	-0.476372	0.4215	0.9998
ENSG00000177425	ENSG00000177425	PAWR	12:79968758-80334448	OK	5.68372	8.05271	0.502639	0.261864	0.42155	0.9998
ENSG00000270102	ENSG00000270102	RP11-498E2.8	9:125093145-125093622	OK	1.30798	0.85579	-0.612013	-0.50431	0.42175	0.9998
ENSG00000102109	ENSG00000102109	PCSK1N	X:48689503-48694035	OK	7.62358	9.21138	0.272948	0.472518	0.42185	0.9998
ENSG00000164610	ENSG00000164610	RP9	7:33134408-33149013	OK	26.0619	22.2343	-0.229153	-0.47443	0.42185	0.9998
ENSG00000173926	ENSG00000173926	3-Mar	5:126203405-126366500	OK	1.24746	0.836404	-0.57672	-0.43918	0.42185	0.9998
ENSG00000177873	ENSG00000177873	ZNF619	3:40518603-40531727	OK	1.44742	1.81803	0.328898	0.438418	0.42185	0.9998
ENSG00000174891	ENSG00000174891	RSRC1	3:157814947-158288855	OK	55.9545	46.4493	-0.268597	-0.482946	0.4219	0.9998
ENSG00000005302	ENSG00000005302	MSL3	X:11776277-11793870	OK	8.93098	7.32491	-0.286008	-0.392447	0.422	0.9998
ENSG00000082458	ENSG00000082458	DLG3	X:69664710-69725337	OK	1.51095	1.06474	-0.504958	-0.422694	0.42215	0.9998
ENSG00000006530	ENSG00000006530	AGK	7:141229002-141401953	OK	26.9459	22.2375	-0.277072	-0.437175	0.4222	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000188807	ENSG00000188807	TMEM201	1:9648931-9674935	OK	10.5692	12.2818	0.216662	0.448703	0.4222	0.9998
ENSG00000081386	ENSG00000081386	ZNF510	9:99518146-99540411	OK	5.76009	4.04594	-0.509616	-0.4464	0.42235	0.9998
ENSG00000163932	ENSG00000163932	PRKCD	3:53190024-53226733	OK	56.0039	48.9658	-0.193754	-0.475487	0.42235	0.9998
ENSG00000127914	ENSG00000127914	AKAP9	7:91570180-91739987	OK	5.4092	4.38542	-0.302703	-0.325269	0.4225	0.9998
ENSG00000145020	ENSG00000145020	AMT	3:49454210-49460186	OK	3.1693	2.46583	-0.362092	-0.379081	0.4226	0.9998
ENSG00000104408	ENSG00000104408	EIF3E	8:109213444-109447562	OK	271.041	313.108	0.20815	0.464823	0.42275	0.9998
ENSG00000235174	ENSG00000235174	RPL39P3	6:74078277-74161999	OK	1840.74	2238.95	0.282535	0.504281	0.42285	0.9998
ENSG00000184898	ENSG00000184898	RBM43	2:152104453-152118393	OK	1.29504	1.05187	-0.300048	-0.451088	0.423	0.9998
ENSG00000131094	ENSG00000131094	C1QL1	17:43037060-43045439	OK	1.03791	0.774105	-0.423082	-0.491525	0.42305	0.9998
ENSG00000242889	ENSG00000242889	RN7SL449P	17:55333211-55762046	OK	1.55288	4.79832	1.62758	0.112815	0.4233	0.9998
ENSG00000249915	ENSG00000249915	PDCD6	5:271735-438406	OK	181.359	211.635	0.222732	0.490683	0.42335	0.9998
ENSG00000100330	ENSG00000100330	MTMR3	22:30279143-30573064	OK	12.2692	14.5161	0.24262	0.301476	0.42345	0.9998
ENSG00000223979	ENSG00000223979	SMCR2	17:17577339-17581002	OK	0.684899	1.03943	0.601829	0.48408	0.4236	0.9998
ENSG00000250365	ENSG00000250365	CTD-2213F21.2	14:31717833-31926716	OK	0.525769	1.02658	0.96535	0.132148	0.4236	0.9998
ENSG00000250644	ENSG00000250644	RP11-295K3.1	11:1753639-1785255	OK	0.929162	0.340009	-1.45036	-0.0747098	0.42365	0.9998
ENSG00000253366	ENSG00000253366	RP11-589F5.4	5:70046953-70149508	OK	1.58785	1.12773	-0.493647	-0.46451	0.424	0.9998
ENSG00000083937	ENSG00000083937	CHMP2B	3:87276420-87304698	OK	26.4595	22.1066	-0.259305	-0.47919	0.42405	0.9998
ENSG00000092330	ENSG00000092330	TINF2	14:24708848-24711880	OK	16.7556	19.4756	0.217021	0.447354	0.42405	0.9998
ENSG00000214776	ENSG00000214776	RP11-726G1.1	12:9620147-9728864	OK	21.7564	24.9058	0.195042	0.483588	0.42405	0.9998
ENSG00000129480	ENSG00000129480	DTD2	14:31717833-31926716	OK	12.006	7.28785	-0.720189	-0.441009	0.42415	0.9998
ENSG00000077147	ENSG00000077147	TM9SF3	10:98277865-98347209	OK	54.351	67.4966	0.312507	0.422635	0.4242	0.9998
ENSG00000234287	ENSG00000234287	RP11-761N21.2	3:40803035-40803290	OK	1662.01	1900.26	0.193268	0.483234	0.4242	0.9998
ENSG00000254685	ENSG00000254685	FPGT	1:74663895-75010112	OK	9.34579	7.60762	-0.296871	-0.40544	0.42425	0.9998
ENSG00000128617	ENSG00000128617	OPN1SW	7:128412544-128415844	OK	0.784662	1.06906	0.446195	0.483119	0.42435	0.9998
ENSG00000178150	ENSG00000178150	ZNF114	19:48673948-48790865	OK	1.96578	3.13616	0.673898	0.445188	0.42435	0.9998
ENSG00000215158	ENSG00000215158	RP11-1023L17.1	5:34164802-34244901	OK	2.44741	3.86465	0.65908	0.432177	0.4245	0.9998
ENSG00000138398	ENSG00000138398	PPIG	2:170440849-170497916	OK	22.3055	18.9933	-0.231909	-0.428642	0.42455	0.9998
ENSG00000198894	ENSG00000198894	CIPC	14:77564439-77725838	OK	12.7632	11.001	-0.214359	-0.3539	0.42455	0.9998
ENSG00000259627	ENSG00000259627	RP11-244F12.2	15:63334830-63364114	OK	0.91168	0.156902	-2.53867	-0.379904	0.42455	0.9998
ENSG00000111639	ENSG00000111639	MRPL51	12:6601149-6641121	OK	197.401	154.129	-0.356989	-0.48569	0.4246	0.9998
ENSG00000119523	ENSG00000119523	ALG2	9:101978707-101984238	OK	15.8606	18.5942	0.229401	0.484769	0.4247	0.9998
ENSG00000112695	ENSG00000112695	COX7A2	6:75947390-75960039	OK	307.013	264.185	-0.216748	-0.476669	0.42475	0.9998
ENSG00000145029	ENSG00000145029	NICN1	3:49460378-49466759	OK	4.45083	5.48534	0.301507	0.452713	0.42475	0.9998
ENSG00000162894	ENSG00000162894	FAIM3	1:207077730-207096592	OK	22.2826	26.6354	0.257423	0.478106	0.42475	0.9998
ENSG00000172493	ENSG00000172493	AFF1	4:87797357-88062206	OK	4.79208	5.8226	0.281009	0.326319	0.42475	0.9998
ENSG00000226380	ENSG00000226380	MIR29A	7:130538478-130613408	OK	5.92981	8.38275	0.499437	0.464989	0.42475	0.9998
ENSG00000223705	ENSG00000223705	NSUN5P1	7:74988447-75115548	OK	19.4092	26.8207	0.466608	0.426652	0.4248	0.9998
ENSG00000122512	ENSG00000122512	PMS2	7:6012869-6048756	OK	11.3594	9.75174	-0.22016	-0.454871	0.42485	0.9998
ENSG00000139200	ENSG00000139200	PIANP	12:6802957-6809966	OK	1.60666	2.14229	0.415083	0.351905	0.42485	0.9998
ENSG00000111300	ENSG00000111300	NAA25	12:112464499-112546826	OK	10.1721	12.0112	0.239758	0.370251	0.425	0.9998
ENSG00000080618	ENSG00000080618	CPB2	13:46626940-46687467	OK	0.615574	0.92897	0.5937	0.484386	0.4251	0.9998
ENSG00000178252	ENSG00000178252	WDR6	3:48955220-49060928	OK	30.1142	38.9154	0.369894	0.305084	0.42515	0.9998
ENSG00000253379	ENSG00000253379	RP11-1102P16.1	8:72315674-72504260	OK	1.90364	1.26527	-0.589312	-0.531733	0.4255	0.9998
ENSG00000095739	ENSG00000095739	BAMBI	10:28966270-28971868	OK	110.126	96.2991	-0.193565	-0.484326	0.42565	0.9998
ENSG00000101266	ENSG00000101266	CSNK2A1	20:459115-524465	OK	16.0507	18.5343	0.207563	0.450925	0.4257	0.9998
ENSG00000235374	ENSG00000235374	SSR4P1	21:46491647-46646478	OK	0.503666	1.25003	1.31142	0.257446	0.42575	0.9998
ENSG00000100994	ENSG00000100994	PYGB	20:25228704-25371619	OK	236.451	277.977	0.233422	0.427283	0.42585	0.9998
ENSG00000123728	ENSG00000123728	RAP2C	X:131337052-131623996	OK	13.3883	10.8703	-0.30059	-0.303134	0.42595	0.9998
ENSG00000153317	ENSG00000153317	ASAP1	8:131064352-131455906	OK	21.2287	24.899	0.230074	0.390232	0.426	0.9998
ENSG00000111252	ENSG00000111252	SH2B3	12:111843751-111889427	OK	21.1218	24.3037	0.202447	0.46006	0.4261	0.9998
ENSG00000134440	ENSG00000134440	NARS	18:55267887-55289445	OK	163.532	142.076	-0.202907	-0.411185	0.42625	0.9998
ENSG00000197343	ENSG00000197343	ZNF655	7:99143930-99208439	OK	36.8725	30.803	-0.259472	-0.425111	0.42625	0.9998
ENSG00000214900	ENSG00000214900	C14orf182	14:50448429-50559361	OK	6.68444	5.35052	-0.321127	-0.492933	0.42625	0.9998
ENSG00000108039	ENSG00000108039	XPNPEP1	10:111624523-111683311	OK	62.7346	54.5807	-0.20087	-0.376196	0.4263	0.9998
ENSG00000060762	ENSG00000060762	MPC1	6:166778406-166796486	OK	24.3329	20.6498	-0.236783	-0.482401	0.42635	0.9998
ENSG00000137944	ENSG00000137944	CCBL2	1:89401455-89458643	OK	12.3795	9.68558	-0.354042	-0.48976	0.4264	0.9998
ENSG00000170681	ENSG00000170681	MURC	9:103340360-103350188	OK	0.764856	0.977348	0.353685	0.482754	0.42645	0.9998
ENSG00000134215	ENSG00000134215	VAV3	1:108113781-108537229	OK	25.358	30.2205	0.253088	0.439654	0.4265	0.9998
ENSG00000101997	ENSG00000101997	CCDC22	X:49091926-49121288	OK	8.58041	10.029	0.225065	0.463552	0.42655	0.9998
ENSG00000104808	ENSG00000104808	DHDH	19:49436938-49448226	OK	0.586479	0.856048	0.545613	0.462657	0.42655	0.9998
ENSG00000108055	ENSG00000108055	SMC3	10:112327448-112364394	OK	22.8856	19.9126	-0.200756	-0.475467	0.4266	0.9998
ENSG00000089101	ENSG00000089101	C20orf26	20:20015011-20341346	OK	4.34019	3.11231	-0.47977	-0.31545	0.4268	0.9998
ENSG00000197943	ENSG00000197943	PLCG2	16:81771852-81991899	OK	0.984749	1.27036	0.367411	0.248154	0.4268	0.9998
ENSG00000149273	ENSG00000149273	RPS3	11:75110529-75133324	OK	1710.47	2000.62	0.226055	0.477575	0.42695	0.9998
ENSG00000149532	ENSG00000149532	CPSF7	11:61170120-61258403	OK	24.1954	20.4832	-0.240292	-0.32004	0.42695	0.9998
ENSG00000089177	ENSG00000089177	KIF16B	20:16252748-16554078	OK	4.33939	3.59379	-0.271985	-0.412456	0.42725	0.9998
ENSG00000080371	ENSG00000080371	RAB21	12:72148653-72184699	OK	19.6245	25.1318	0.356852	0.478313	0.4273	0.9998
ENSG00000117877	ENSG00000117877	CD3EAP	19:45882891-45982086	OK	3.23878	6.23741	0.945497	0.54653	0.42735	0.9998
ENSG00000124226	ENSG00000124226	RNF114	20:48552947-48570429	OK	46.8627	40.6876	-0.20385	-0.483646	0.42745	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000138074	ENSG00000138074	SLC5A6	2:27422454-27440046	OK	43.3437	34.9753	-0.309487	-0.400784	0.42745	0.9998
ENSG00000120963	ENSG00000120963	ZNF706	8:102190105-102218421	OK	161.442	189.499	0.231173	0.485459	0.4276	0.9998
ENSG00000122557	ENSG00000122557	HERPUD2	7:35672268-35739023	OK	11.6785	13.8213	0.243042	0.434833	0.4276	0.9998
ENSG00000131788	ENSG00000131788	PIAS3	1:145575232-145589439	OK	35.473	29.966	-0.243394	-0.463612	0.42775	0.9998
ENSG00000107854	ENSG00000107854	TNKS2	10:93558068-93625033	OK	15.1875	17.8408	0.232295	0.479552	0.4278	0.9998
ENSG00000198189	ENSG00000198189	HSD17B11	4:88224940-88312538	OK	38.2533	32.5919	-0.231069	-0.462517	0.4279	0.9998
ENSG00000139668	ENSG00000139668	WDFY2	13:52158643-52336171	OK	7.38216	6.04391	-0.28856	-0.322065	0.42795	0.9998
ENSG00000188215	ENSG00000188215	DCUN1D3	16:20621564-20936328	OK	2.66861	4.20755	0.656889	0.505355	0.42805	0.9998
ENSG00000143486	ENSG00000143486	EIF2D	1:206680878-206785904	OK	42.3432	36.8312	-0.201204	-0.416937	0.42815	0.9998
ENSG00000143933	ENSG00000143933	CALM2	2:47126413-47403740	OK	397.541	469.808	0.240969	0.474861	0.42815	0.9998
ENSG00000253873	ENSG00000253873	PCDHGA11	5:140710251-140892546	OK	5.16573	7.44382	0.527071	0.490746	0.42815	0.9998
ENSG00000255725	ENSG00000255725	RP11-443N24.1	12:25935639-25967105	OK	7.98733	6.11539	-0.385269	-0.476147	0.42825	0.9998
ENSG00000104903	ENSG00000104903	LYL1	19:13209846-13213975	OK	1.27362	1.66514	0.386701	0.498778	0.4283	0.9998
ENSG00000179460	ENSG00000179460	EEF1A1P27	7:20621694-20622829	OK	0.665804	0.901042	0.436497	0.463126	0.4283	0.9998
ENSG00000141756	ENSG00000141756	FKBP10	17:39968931-39979465	OK	3.11248	4.01188	0.366213	0.453664	0.42835	0.9998
ENSG00000213866	ENSG00000213866	YBX1P10	9:35971340-35972315	OK	0.706754	0.966743	0.451926	0.465761	0.42835	0.9998
ENSG00000178988	ENSG00000178988	MRFAP1L1	4:6709427-6711607	OK	23.6732	20.29	-0.222482	-0.488073	0.42855	0.9998
ENSG00000102804	ENSG00000102804	TSC22D1	13:45007654-45151283	OK	29.3208	25.2121	-0.217805	-0.464797	0.4286	0.9998
ENSG00000140443	ENSG00000140443	IGF1R	15:99192199-99675798	OK	12.61	16.6334	0.399516	0.193373	0.42865	0.9998
ENSG00000257033	ENSG00000257033	AL391357.1	1:20959947-20988000	OK	1.60377	0.0611813	-4.71223	-0.0975763	0.42905	0.9998
ENSG00000183785	ENSG00000183785	TUBA8	22:18559292-18629321	OK	4.81296	9.72582	1.0149	0.586539	0.4291	0.9998
ENSG00000114021	ENSG00000114021	NIT2	3:100053544-100075710	OK	49.5881	41.745	-0.248392	-0.478704	0.4292	0.9998
ENSG00000185359	ENSG00000185359	HGS	17:79648203-79670330	OK	52.872	60.6039	0.196907	0.331856	0.42935	0.9998
ENSG00000181804	ENSG00000181804	SLC9A9	3:142984063-143567373	OK	1.18861	0.807452	-0.557829	-0.35862	0.4295	0.9998
ENSG00000135956	ENSG00000135956	TMEM127	2:96914253-96931732	OK	28.1325	32.3552	0.201757	0.458236	0.4296	0.9998
ENSG00000128645	ENSG00000128645	HOXD1	2:177037922-177055688	OK	5.07174	7.99564	0.656731	0.52033	0.4297	0.9998
ENSG00000173575	ENSG00000173575	CHD2	15:93425936-93571237	OK	12.9299	14.8841	0.203055	0.226015	0.4297	0.9998
ENSG00000072858	ENSG00000072858	SIDT1	3:113251142-113348425	OK	0.731043	0.516734	-0.500535	-0.260862	0.42975	0.9998
ENSG00000136877	ENSG00000136877	FPGS	9:130556875-130576606	OK	19.0543	22.2601	0.224343	0.394691	0.42975	0.9998
ENSG00000173272	ENSG00000173272	MZT2A	2:132222472-132250316	OK	52.7026	61.8441	0.230764	0.485435	0.42975	0.9998
ENSG00000214765	ENSG00000214765	SEPT7P2	7:45763378-45808617	OK	11.6716	9.579	-0.285058	-0.46645	0.42975	0.9998
ENSG00000089280	ENSG00000089280	FUS	16:31191430-31203127	OK	219.836	185.714	-0.24335	-0.462664	0.4298	0.9998
ENSG00000187244	ENSG00000187244	BCAM	19:45312327-45324673	OK	1.37459	1.74622	0.345233	0.370336	0.4302	0.9998
ENSG00000184307	ENSG00000184307	ZDHHC23	3:113666747-113807269	OK	2.41665	3.63312	0.588199	0.474355	0.43025	0.9998
ENSG00000144152	ENSG00000144152	FBLN7	2:112895961-112945791	OK	6.50263	7.81864	0.265896	0.481006	0.4303	0.9998
ENSG00000144659	ENSG00000144659	SLC25A38	3:39424838-39438842	OK	7.58124	8.93857	0.237611	0.472205	0.4303	0.9998
ENSG00000177954	ENSG00000177954	RPS27	1:153963234-153964626	OK	2642.31	3053.62	0.208723	0.492866	0.43035	0.9998
ENSG00000070081	ENSG00000070081	NUCB2	11:17229699-17371521	OK	42.3033	35.9974	-0.232878	-0.458426	0.4304	0.9998
ENSG00000256223	ENSG00000256223	ZNF10	12:133707160-133783698	OK	3.40037	2.39449	-0.505975	-0.349946	0.4304	0.9998
ENSG00000235903	ENSG00000235903	CPB2-AS1	13:46626940-46687467	OK	2.49503	3.53992	0.50466	0.507712	0.4306	0.9998
ENSG00000164253	ENSG00000164253	WDR41	5:76506273-76916436	OK	36.5374	29.7354	-0.297192	-0.437103	0.43075	0.9998
ENSG00000242687	ENSG00000242687	AC004893.11	7:98475555-98741723	OK	1.05569	0.531907	-0.988936	-0.131922	0.4309	0.9998
ENSG00000196776	ENSG00000196776	CD47	3:107762144-107809872	OK	28.2034	23.5654	-0.259198	-0.451372	0.4312	0.9998
ENSG00000120686	ENSG00000120686	UFM1	13:38923985-38937140	OK	31.0533	35.948	0.211165	0.447978	0.4315	0.9998
ENSG00000136144	ENSG00000136144	RCBTB1	13:50106081-50159719	OK	15.5515	13.4821	-0.206012	-0.412021	0.4315	0.9998
ENSG00000100628	ENSG00000100628	ASB2	14:94400498-94443137	OK	8.92449	10.4023	0.221061	0.413064	0.43155	0.9998
ENSG00000100580	ENSG00000100580	TMED8	14:77801363-77857840	OK	7.8899	9.06361	0.200078	0.477769	0.4316	0.9998
ENSG00000142002	ENSG00000142002	DPP9	19:4675235-4724685	OK	55.4598	63.1231	0.186725	0.359397	0.4316	0.9998
ENSG00000146263	ENSG00000146263	MMS22L	6:97590036-97731093	OK	4.82446	3.39578	-0.506626	-0.456318	0.4316	0.9998
ENSG00000117899	ENSG00000117899	MESDC2	15:81071683-81282219	OK	44.1173	38.1209	-0.210763	-0.453807	0.43165	0.9998
ENSG00000242631	ENSG00000242631	RP11-508N12.4	9:109625377-109865269	OK	0.128493	2.78254	4.43664	0.341162	0.4317	0.9998
ENSG00000128872	ENSG00000128872	TMOD2	15:52015207-52108565	OK	1.16221	1.5303	0.396949	0.32016	0.4319	0.9998
ENSG00000110697	ENSG00000110697	PITPNM1	11:67259238-67273734	OK	8.6771	10.1112	0.220666	0.324368	0.432	0.9998
ENSG00000205189	ENSG00000205189	ZBTB10	8:81396795-81438500	OK	6.69432	8.08604	0.272495	0.47051	0.432	0.9998
ENSG00000272410	ENSG00000272410	RP11-438J1.1	3:10289706-10362862	OK	1.14795	3.17399	1.46723	0.540824	0.4321	0.9998
ENSG00000013588	ENSG00000013588	GPRC5A	12:13043715-13070871	OK	2.42699	1.63793	-0.5673	-0.428645	0.43215	0.9998
ENSG00000116514	ENSG00000116514	RNF19B	1:33402045-33430286	OK	21.2129	24.4873	0.207093	0.471385	0.43225	0.9998
ENSG00000205578	ENSG00000205578	POM121B	7:72707496-72716496	OK	0.859282	1.08399	0.335149	0.4771	0.43225	0.9998
ENSG00000168209	ENSG00000168209	DDIT4	10:74033677-74035794	OK	145.986	169.485	0.215328	0.456976	0.4323	0.9998
ENSG00000196422	ENSG00000196422	PPP1R26	9:138354572-138380739	OK	9.77407	8.40109	-0.218382	-0.466381	0.43235	0.9998
ENSG00000166452	ENSG00000166452	AKIP1	11:8932685-8954553	OK	31.026	25.9325	-0.258716	-0.494901	0.4324	0.9998
ENSG00000171791	ENSG00000171791	BCL2	18:60790578-60987361	OK	8.61735	6.98821	-0.302322	-0.442909	0.4324	0.9998
ENSG00000095015	ENSG00000095015	MAP3K1	5:56111400-56191979	OK	10.9329	12.5667	0.200926	0.483816	0.43245	0.9998
ENSG00000151553	ENSG00000151553	FAM160B1	10:116581502-116659591	OK	11.7713	10.2652	-0.197511	-0.448266	0.4325	0.9998
ENSG00000145687	ENSG00000145687	SSBP2	5:80708839-81047616	OK	5.54986	4.37702	-0.342503	-0.419297	0.43255	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000213064	ENSG00000213064	SFT2D2	1:168195175-168222263	OK	7.97024	9.37092	0.233568	0.254032	0.43255	0.9998
ENSG00000151304	ENSG00000151304	SRFBP1	5:121297655-121413980	OK	3.39897	2.78359	-0.28815	-0.447708	0.4327	0.9998
ENSG00000244005	ENSG00000244005	NFS1	20:34213952-34288906	OK	39.4068	28.4254	-0.471261	-0.377838	0.4327	0.9998
ENSG00000108826	ENSG00000108826	MRPL27	17:48445217-48450575	OK	108.415	124.849	0.20363	0.476884	0.43275	0.9998
ENSG00000089091	ENSG00000089091	DZANK1	20:18364010-18465287	OK	0.381038	0.702537	0.882642	0.353621	0.43285	0.9998
ENSG00000182986	ENSG00000182986	ZNF320	19:53367042-53400946	OK	0.540936	0.712402	0.397233	0.214894	0.43285	0.9998
ENSG00000196968	ENSG00000196968	FUT11	10:75531934-75540009	OK	15.9682	13.5941	-0.232223	-0.48063	0.43285	0.9998
ENSG00000112697	ENSG00000112697	TMEM30A	6:75962639-75994684	OK	43.0458	37.6725	-0.19236	-0.475644	0.43295	0.9998
ENSG00000062038	ENSG00000062038	CDH3	16:68670091-68756519	OK	2.73331	3.34865	0.292932	0.375999	0.43315	0.9998
ENSG00000169727	ENSG00000169727	GPS1	17:80005777-80015346	OK	92.6875	106.985	0.206964	0.433391	0.43325	0.9998
ENSG00000110811	ENSG00000110811	LEPREL2	12:6930710-6949018	OK	6.34576	7.48819	0.238825	0.427078	0.4333	0.9998
ENSG00000245556	ENSG00000245556	CTD-2037K23.2	5:77638188-77656331	OK	1.08436	0.827157	-0.390607	-0.437543	0.43335	0.9998
ENSG00000000460	ENSG00000000460	C1orf112	1:169631244-169863408	OK	10.2391	7.99189	-0.357484	-0.438505	0.4334	0.9998
ENSG00000138293	ENSG00000138293	NCOA4	10:51565107-51590734	OK	37.5229	42.7129	0.186901	0.453668	0.4335	0.9998
ENSG00000179008	ENSG00000179008	C14orf39	14:60863186-61021634	OK	0.336199	0.801448	1.25329	0.481271	0.4338	0.9998
ENSG00000231273	ENSG00000231273	RP11-343D24.2	6:57690894-57691645	OK	0.701312	1.23546	0.816927	0.522713	0.4338	0.9998
ENSG00000100227	ENSG00000100227	POLDIP3	22:42979726-43010968	OK	29.2304	33.4834	0.195978	0.401647	0.4339	0.9998
ENSG00000175764	ENSG00000175764	TTLL11	9:124584206-124855885	OK	2.15724	1.63728	-0.397891	-0.469951	0.4339	0.9998
ENSG00000248641	ENSG00000248641	HMGA1P2	4:73939092-74124515	OK	0.57724	1.75608	1.60512	0.180371	0.43395	0.9998
ENSG00000112667	ENSG00000112667	DNPH1	6:43193366-43197222	OK	51.3182	59.7462	0.219375	0.473107	0.43405	0.9998
ENSG00000163393	ENSG00000163393	SLC22A15	1:116519118-116612675	OK	1.83561	2.32744	0.342484	0.385444	0.43425	0.9998
ENSG00000196646	ENSG00000196646	ZNF136	19:12273878-12300064	OK	2.59852	2.09512	-0.310654	-0.362976	0.43425	0.9998
ENSG00000197724	ENSG00000197724	PHF2	9:96338688-96441869	OK	7.79935	6.77235	-0.203697	-0.464756	0.43425	0.9998
ENSG00000154655	ENSG00000154655	L3MBTL4	18:5954704-6415236	OK	5.67778	6.68484	0.235567	0.442401	0.4344	0.9998
ENSG00000197238	ENSG00000197238	HIST1H4J	6:27791883-27792257	OK	3.70894	5.04248	0.443127	0.477897	0.4344	0.9998
ENSG00000132563	ENSG00000132563	REEP2	5:137774705-137782658	OK	3.39703	4.23967	0.319679	0.408206	0.43455	0.9998
ENSG00000198478	ENSG00000198478	SH3BGRL2	6:80340999-80413372	OK	1.77947	2.1437	0.268656	0.485111	0.43455	0.9998
ENSG00000170745	ENSG00000170745	KCNS3	2:18059113-18542882	OK	7.96894	9.32309	0.22642	0.451554	0.4346	0.9998
ENSG00000006459	ENSG00000006459	KDM7A	7:139784545-139876835	OK	4.21798	3.43488	-0.296291	-0.373646	0.4347	0.9998
ENSG00000131477	ENSG00000131477	RAMP2	17:40905931-40915059	OK	2.8915	3.76978	0.382665	0.423791	0.43475	0.9998
ENSG00000103852	ENSG00000103852	TTC23	15:99676527-99791428	OK	13.4514	10.8632	-0.308309	-0.400324	0.43485	0.9998
ENSG00000144827	ENSG00000144827	ABHD10	3:111697856-111712210	OK	33.0464	28.3202	-0.22266	-0.450238	0.43485	0.9998
ENSG00000212994	ENSG00000212994	RPS26P6	8:101907973-101908387	OK	0.404733	0.820824	1.0201	0.561799	0.4349	0.9998
ENSG00000137801	ENSG00000137801	THBS1	15:39873279-39891667	OK	3.6025	2.99553	-0.266187	-0.282341	0.435	0.9998
ENSG00000175873	ENSG00000175873	AC004840.9	7:2477397-2487485	OK	1.35851	1.70396	0.326866	0.475967	0.435	0.9998
ENSG00000136631	ENSG00000136631	VPS45	1:150039368-150117505	OK	34.5182	29.9826	-0.203231	-0.442581	0.4351	0.9998
ENSG00000137073	ENSG00000137073	UBAP2	9:33921690-34048947	OK	10.6929	9.19996	-0.216952	-0.414875	0.43515	0.9998
ENSG00000169242	ENSG00000169242	EFNA1	1:155099935-155107333	OK	5.89282	4.652	-0.341106	-0.479768	0.43515	0.9998
ENSG00000131408	ENSG00000131408	NR1H2	19:50815193-50886239	OK	40.7036	46.5687	0.194203	0.467304	0.43525	0.9998
ENSG00000171302	ENSG00000171302	CANT1	17:76987798-77005949	OK	45.2344	39.4969	-0.195683	-0.345659	0.4354	0.9998
ENSG00000165609	ENSG00000165609	NUDT5	10:12171635-12292588	OK	25.4267	19.9518	-0.349823	-0.404842	0.4357	0.9998
ENSG00000006715	ENSG00000006715	VPS41	7:38762562-38971994	OK	63.4916	51.8746	-0.291538	-0.422513	0.4358	0.9998
ENSG00000163602	ENSG00000163602	RYBP	3:72420975-72496069	OK	5.8317	6.72687	0.206018	0.47679	0.43585	0.9998
ENSG00000166681	ENSG00000166681	NGFRAP1	X:102631267-102633005	OK	173.755	197.74	0.186552	0.463519	0.43595	0.9998
ENSG00000171988	ENSG00000171988	JMJD1C	10:64926980-65226323	OK	5.25866	4.50338	-0.223688	-0.368385	0.43595	0.9998
ENSG00000131943	ENSG00000131943	C19orf12	19:30191720-30206364	OK	49.3128	58.5666	0.248114	0.454362	0.43605	0.9998
ENSG00000168056	ENSG00000168056	LTBP3	11:65306275-65326401	OK	15.9713	19.6484	0.298926	0.432478	0.43635	0.9998
ENSG00000130511	ENSG00000130511	SSBP4	19:18529673-18549111	OK	35.268	45.2929	0.360924	0.459771	0.4364	0.9998
ENSG00000225760	ENSG00000225760	LINC00431	13:111635653-111642911	OK	1.97279	1.46308	-0.43123	-0.468666	0.4364	0.9998
ENSG00000156973	ENSG00000156973	PDE6D	2:232597134-232673963	OK	58.0796	47.4588	-0.291357	-0.463827	0.4365	0.9998
ENSG00000110108	ENSG00000110108	TMEM109	11:60680637-60720002	OK	58.0653	50.1743	-0.210727	-0.465642	0.43665	0.9998
ENSG00000188706	ENSG00000188706	ZDHHC9	X:128937263-128977885	OK	13.422	15.5601	0.213249	0.441648	0.43665	0.9998
ENSG00000101191	ENSG00000101191	DIDO1	20:61509089-61569304	OK	19.5842	23.8753	0.28583	0.463138	0.4367	0.9998
ENSG00000137486	ENSG00000137486	ARRB1	11:74975225-75062873	OK	12.7124	14.7664	0.21608	0.439347	0.4368	0.9998
ENSG00000114988	ENSG00000114988	LMAN2L	2:97371665-97405801	OK	9.7623	11.3643	0.219222	0.449264	0.4369	0.9998
ENSG00000153898	ENSG00000153898	MCOLN2	1:85391267-85462796	OK	4.67602	6.01222	0.362616	0.404356	0.43715	0.9998
ENSG00000131779	ENSG00000131779	PEX11B	1:145516251-145523730	OK	32.9173	37.7663	0.198256	0.469883	0.4372	0.9998
ENSG00000124920	ENSG00000124920	MYRF	11:61447904-61634826	OK	1.01595	1.741	0.777087	0.17902	0.43725	0.9998
ENSG00000214455	ENSG00000214455	RCN1P2	13:45911007-45965872	OK	12.3886	23.1899	0.904486	0.10089	0.4375	0.9998
ENSG00000179134	ENSG00000179134	SAMD4B	19:39833035-39876350	OK	70.2928	88.5282	0.33276	0.460244	0.43755	0.9998
ENSG00000196666	ENSG00000196666	FAM180B	11:47608197-47610746	OK	2.50284	3.11039	0.31353	0.464517	0.43755	0.9998
ENSG00000156017	ENSG00000156017	C9orf41	9:77567883-77643339	OK	12.0548	14.0991	0.225999	0.405557	0.4377	0.9998
ENSG00000165121	ENSG00000165121	RP11-213G2.3	9:88430880-88464426	OK	0.739136	0.556772	-0.408753	-0.466151	0.43785	0.9998
ENSG00000165410	ENSG00000165410	CFL2	14:35179592-35184029	OK	46.1028	56.3303	0.289059	0.467348	0.43785	0.9998
ENSG00000151689	ENSG00000151689	INPP1	2:190744334-191236391	OK	10.6331	14.0359	0.400553	0.376997	0.43795	0.9998
ENSG00000076248	ENSG00000076248	UNG	12:109535378-109548797	OK	25.6979	22.2279	-0.209278	-0.474708	0.4381	0.9998
ENSG00000166479	ENSG00000166479	TMX3	18:66340924-66722426	OK	18.5053	16.0082	-0.209123	-0.319804	0.4381	0.9998
ENSG00000116678	ENSG00000116678	LEPR	1:65886247-66107242	OK	0.657268	0.349991	-0.909165	-0.345344	0.4383	0.9998
ENSG00000149743	ENSG00000149743	TRPT1	11:63974149-64001824	OK	37.8298	29.3949	-0.363956	-0.454961	0.4383	0.9998
ENSG00000168484	ENSG00000168484	SFTPC	8:22004337-22021992	OK	31.9732	22.6758	-0.495711	-0.253681	0.43835	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000110057	ENSG00000110057	UNC93B1	11:67758574-67772452	OK	4.25291	5.25307	0.30471	0.42933	0.43845	0.9998
ENSG00000170417	ENSG00000170417	TMEM182	2:103353366-103460352	OK	5.77286	4.45427	-0.374099	-0.462362	0.4385	0.9998
ENSG00000080189	ENSG00000080189	SLC35C2	20:44978166-44993043	OK	41.5724	35.5623	-0.225275	-0.465548	0.43855	0.9998
ENSG00000143774	ENSG00000143774	GUK1	1:228327662-228336685	OK	301.487	345.791	0.197803	0.453642	0.43855	0.9998
ENSG00000108819	ENSG00000108819	PPP1R9B	17:48211103-48227991	OK	20.6127	23.7401	0.203793	0.404125	0.43865	0.9998
ENSG00000164808	ENSG00000164808	SPIDR	8:48173166-48648868	OK	30.6935	25.9487	-0.242268	-0.412758	0.43865	0.9998
ENSG00000225556	ENSG00000225556	C2CD4D	1:151810294-151813033	OK	0.519745	0.697175	0.423718	0.466915	0.43875	0.9998
ENSG00000100403	ENSG00000100403	ZC3H7B	22:41697525-41756151	OK	29.5873	25.9837	-0.187371	-0.473407	0.4389	0.9998
ENSG00000223361	ENSG00000223361	FTH1P10	5:17353803-17355008	OK	47.9664	56.3747	0.233022	0.475682	0.43895	0.9998
ENSG00000091129	ENSG00000091129	NRCAM	7:107788067-108097161	OK	3.71577	4.34949	0.227183	0.316088	0.439	0.9998
ENSG00000125170	ENSG00000125170	DOK4	16:57462080-57521239	OK	1.05738	1.63796	0.631411	0.186468	0.43905	0.9998
ENSG00000184481	ENSG00000184481	FOXO4	X:70316046-70323385	OK	5.0211	4.23763	-0.244746	-0.443918	0.4391	0.9998
ENSG00000187051	ENSG00000187051	RPS19BP1	22:39925097-39928860	OK	74.1517	64.3964	-0.203499	-0.475323	0.4391	0.9998
ENSG00000137497	ENSG00000137497	NUMA1	11:71709586-71823826	OK	43.5151	36.895	-0.238093	-0.274566	0.4393	0.9998
ENSG00000148660	ENSG00000148660	CAMK2G	10:75572258-75634343	OK	5.87484	7.00422	0.253677	0.437849	0.4393	0.9998
ENSG00000272977	ENSG00000272977	CTA-390C10.10	22:25844071-25916821	OK	1.34946	0.939738	-0.522048	-0.479423	0.4394	0.9998
ENSG00000169398	ENSG00000169398	PTK2	8:141667998-142012315	OK	49.872	57.1403	0.196278	0.278999	0.4395	0.9998
ENSG00000233822	ENSG00000233822	HIST1H2BN	6:27806322-27823487	OK	0.687515	1.05703	0.62056	0.440319	0.4395	0.9998
ENSG00000104889	ENSG00000104889	RNASEH2A	19:12873816-12985765	OK	45.7452	36.1775	-0.338528	-0.455342	0.43955	0.9998
ENSG00000125775	ENSG00000125775	SDCBP2	20:1290618-1373806	OK	0.771514	1.54137	0.998449	0.17332	0.4396	0.9998
ENSG00000174840	ENSG00000174840	PDE12	3:57542002-57552571	OK	10.5601	12.3971	0.231378	0.476122	0.4397	0.9998
ENSG00000105248	ENSG00000105248	CCDC94	19:4247075-4269087	OK	9.37016	11.1541	0.251429	0.475665	0.43975	0.9998
ENSG00000071967	ENSG00000071967	CYBRD1	2:172378756-172414643	OK	13.7007	11.6377	-0.235445	-0.428556	0.4398	0.9998
ENSG00000227674	ENSG00000227674	LINC00355	13:64560503-64650144	OK	1.89649	2.33537	0.300322	0.46183	0.4398	0.9998
ENSG00000259132	ENSG00000259132	RP11-298I3.5	14:23398817-23451851	OK	4.448	1.62044	-1.45677	-0.654829	0.4398	0.9998
ENSG00000163349	ENSG00000163349	HIPK1	1:114466621-114520426	OK	8.84851	10.2049	0.205758	0.445745	0.4399	0.9998
ENSG00000234684	ENSG00000234684	SDCBP2-AS1	20:1290618-1373806	OK	0.831426	0.510096	-0.704819	-0.0991588	0.43995	0.9998
ENSG00000102178	ENSG00000102178	UBL4A	X:153712055-153715009	OK	30.5485	34.9589	0.194557	0.372886	0.44005	0.9998
ENSG00000186017	ENSG00000186017	ZNF566	19:36936020-36981942	OK	2.94931	2.29953	-0.359036	-0.403173	0.4401	0.9998
ENSG00000135245	ENSG00000135245	HILPDA	7:128095893-128146656	OK	65.6661	41.4469	-0.663885	-0.598013	0.44015	0.9998
ENSG00000185485	ENSG00000185485	SDHAP1	3:195686618-195717189	OK	15.4271	12.403	-0.314773	-0.474798	0.44015	0.9998
ENSG00000185621	ENSG00000185621	LMLN	3:197687070-197770591	OK	9.28201	7.81502	-0.248188	-0.360121	0.4405	0.9998
ENSG00000172889	ENSG00000172889	EGFL7	9:139543061-139567130	OK	22.136	25.816	0.221869	0.465749	0.4406	0.9998
ENSG00000155629	ENSG00000155629	PIK3AP1	10:98353068-98480271	OK	1.23381	1.54567	0.325115	0.396249	0.44075	0.9998
ENSG00000118564	ENSG00000118564	FBXL5	4:15606161-15739936	OK	18.562	22.0438	0.248023	0.379414	0.4408	0.9998
ENSG00000074696	ENSG00000074696	PTPLAD1	15:65822755-65870687	OK	55.0995	63.4033	0.202517	0.436487	0.441	0.9998
ENSG00000129757	ENSG00000129757	CDKN1C	11:2904442-2907111	OK	2.05119	2.59087	0.336973	0.470881	0.441	0.9998
ENSG00000262001	ENSG00000262001	DLGAP1-AS2	18:3496029-4455335	OK	2.08462	1.20495	-0.790814	-0.535576	0.441	0.9998
ENSG00000143363	ENSG00000143363	PRUNE	1:150980895-151008189	OK	20.5273	17.6608	-0.216991	-0.460887	0.44105	0.9998
ENSG00000168282	ENSG00000168282	MGAT2	14:50087488-50090198	OK	14.3239	16.4939	0.203508	0.460145	0.44105	0.9998
ENSG00000181409	ENSG00000181409	AATK	17:79008947-79156964	OK	2.32359	3.34876	0.527272	0.397032	0.44105	0.9998
ENSG00000099860	ENSG00000099860	GADD45B	19:2476119-2478257	OK	10.4472	12.3955	0.246694	0.396045	0.4414	0.9998
ENSG00000242485	ENSG00000242485	MRPL20	1:1334901-1342693	OK	99.6309	115.76	0.216468	0.457572	0.4414	0.9998
ENSG00000163743	ENSG00000163743	RCHY1	4:76404246-76475683	OK	20.7467	26.7387	0.366045	0.475737	0.44165	0.9998
ENSG00000136011	ENSG00000136011	STAB2	12:103981050-104162636	OK	1.82458	3.82598	1.06826	0.52685	0.4418	0.9998
ENSG00000095139	ENSG00000095139	ARCN1	11:118307204-118473748	OK	28.0297	33.3226	0.249546	0.476427	0.44185	0.9998
ENSG00000252690	ENSG00000252690	SCARNA15	15:83419315-83474822	OK	0.453034	0.687033	0.600762	0.286766	0.44185	0.9998
ENSG00000152804	ENSG00000152804	HHEX	10:94447944-94455403	OK	3.38526	4.28375	0.339605	0.471138	0.44195	0.9998
ENSG00000164099	ENSG00000164099	PRSS12	4:119201192-119274158	OK	6.28857	7.58958	0.271288	0.393576	0.44195	0.9998
ENSG00000146386	ENSG00000146386	ABRACL	6:139349818-139364439	OK	31.7358	37.0091	0.221771	0.469042	0.44205	0.9998
ENSG00000266658	ENSG00000266658	RNA28S5	GL000220.1:113347-118417	OK	65.0448	56.9463	-0.191831	-0.455693	0.4422	0.9998
ENSG00000116001	ENSG00000116001	TIA1	2:70377011-70475792	OK	25.0116	19.716	-0.34323	-0.423074	0.44225	0.9998
ENSG00000151726	ENSG00000151726	ACSL1	4:185676748-185747972	OK	33.7188	38.6123	0.195507	0.438216	0.44245	0.9998
ENSG00000169139	ENSG00000169139	UBE2V2	8:48920959-48977268	OK	57.9354	49.0212	-0.24104	-0.467102	0.44245	0.9998
ENSG00000174013	ENSG00000174013	FBXO45	3:196281055-196315930	OK	10.9158	12.8087	0.230703	0.474017	0.4425	0.9998
ENSG00000258967	ENSG00000258967	HMGN1P3	14:69340859-69446157	OK	0.131919	1.13939	3.11054	0.08307	0.44255	0.9998
ENSG00000165389	ENSG00000165389	SPTSSA	14:34393436-34931980	OK	23.0048	19.4261	-0.243938	-0.465527	0.4426	0.9998
ENSG00000062485	ENSG00000062485	CS	12:56665482-56727837	OK	119.873	103.792	-0.207818	-0.385952	0.44285	0.9998
ENSG00000168243	ENSG00000168243	GNG4	1:235710986-235814054	OK	11.8974	9.58934	-0.311142	-0.463295	0.4429	0.9998
ENSG00000078269	ENSG00000078269	SYNJ2	6:158402887-158520208	OK	2.95785	4.07067	0.460719	0.395404	0.44295	0.9998
ENSG00000248508	ENSG00000248508	SRP14-AS1	15:40331511-40359491	OK	0.756272	0.366188	-1.04632	-0.742325	0.443	0.9998
ENSG00000168653	ENSG00000168653	NDUFS5	1:39491989-39500308	OK	313.362	356.943	0.187864	0.470248	0.4431	0.9998
ENSG00000114999	ENSG00000114999	TTL	2:113239730-113299316	OK	24.1332	29.1472	0.272336	0.423442	0.44315	0.9998
ENSG00000143248	ENSG00000143248	RGS5	1:163080910-163325554	OK	2.41871	1.59054	-0.604719	-0.156761	0.4435	0.9998
ENSG00000153714	ENSG00000153714	LURAP1L	9:12685438-12822130	OK	1.93685	3.95817	1.03112	0.0785647	0.4436	0.9998
ENSG00000134285	ENSG00000134285	FKBP11	12:49297200-49351334	OK	35.2805	52.3405	0.569056	0.411015	0.4437	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000184304	ENSG00000184304	PRKD1	14:30045686-30766249	OK	6.02743	5.16276	-0.223402	-0.375691	0.4437	0.9998
ENSG00000111110	ENSG00000111110	PPM1H	12:63037761-63328817	OK	7.4479	6.47273	-0.20246	-0.395961	0.44395	0.9998
ENSG00000175104	ENSG00000175104	TRAF6	11:36508576-36531822	OK	7.63522	9.07149	0.24867	0.400438	0.444	0.9998
ENSG00000177156	ENSG00000177156	TALDO1	11:747328-765024	OK	93.244	106.113	0.186522	0.457052	0.444	0.9998
ENSG00000125734	ENSG00000125734	GPR108	19:6677714-6737614	OK	19.7517	16.8739	-0.22718	-0.393582	0.44405	0.9998
ENSG00000133316	ENSG00000133316	WDR74	11:62599705-62609281	OK	28.1168	32.6033	0.213586	0.451292	0.4441	0.9998
ENSG00000054277	ENSG00000054277	OPN3	1:241695433-241965435	OK	25.5132	19.9959	-0.351542	-0.461858	0.44425	0.9998
ENSG00000196961	ENSG00000196961	AP2A1	19:50270224-50320633	OK	43.3721	37.8284	-0.197295	-0.437872	0.4443	0.9998
ENSG00000131187	ENSG00000131187	F12	5:176829140-176883283	OK	10.2538	16.1488	0.655278	0.550957	0.4444	0.9998
ENSG00000224271	ENSG00000224271	RP11-191L9.4	22:48027422-48251349	OK	0.465418	0.730758	0.650866	0.446954	0.44445	0.9998
ENSG00000128789	ENSG00000128789	PSMG2	18:12438888-12725739	OK	42.1508	30.3003	-0.476229	-0.488679	0.4445	0.9998
ENSG00000037897	ENSG00000037897	METTL1	12:58156116-58212487	OK	17.8346	24.769	0.473856	0.49976	0.4446	0.9998
ENSG00000128590	ENSG00000128590	DNAJB9	7:108110865-108215294	OK	10.8071	8.22715	-0.393514	-0.423686	0.44505	0.9998
ENSG00000017260	ENSG00000017260	ATP2C1	3:130569438-131100319	OK	44.051	50.8115	0.205982	0.434349	0.4452	0.9998
ENSG00000230082	ENSG00000230082	PRRT3-AS1	3:9987225-9996471	OK	1.54878	2.37513	0.616872	0.464893	0.44525	0.9998
ENSG00000181381	ENSG00000181381	DDX60L	4:169277885-169931426	OK	2.98105	4.06404	0.447095	0.17238	0.44535	0.9998
ENSG00000181588	ENSG00000181588	MEX3D	19:1554667-1568057	OK	4.55116	3.81036	-0.256306	-0.468694	0.44535	0.9998
ENSG00000266501	ENSG00000266501	RP11-766H1.1	17:70642087-71088851	OK	0.112774	0.700218	2.63438	0.356441	0.4455	0.9998
ENSG00000125971	ENSG00000125971	DYNLRB1	20:33104213-33128762	OK	225.84	198.172	-0.188543	-0.466607	0.44575	0.9998
ENSG00000187736	ENSG00000187736	NHEJ1	2:219940038-220035549	OK	13.4731	11.2573	-0.259215	-0.451895	0.446	0.9998
ENSG00000272669	ENSG00000272669	RP3-508I15.21	22:39101727-39190203	OK	0.683851	0.20215	-1.75826	-0.131056	0.446	0.9998
ENSG00000177917	ENSG00000177917	ARL6IP6	2:153508106-153617767	OK	7.79575	4.99755	-0.641466	-0.409193	0.44605	0.9998
ENSG00000091073	ENSG00000091073	DTX2	7:76090992-76135312	OK	6.30259	7.5155	0.253923	0.351809	0.4462	0.9998
ENSG00000080815	ENSG00000080815	PSEN1	14:73603125-73690399	OK	20.773	23.8083	0.196757	0.339904	0.4464	0.9998
ENSG00000133275	ENSG00000133275	CSNK1G2	19:1941187-1981337	OK	33.838	39.1293	0.209608	0.376009	0.4464	0.9998
ENSG00000138735	ENSG00000138735	PDE5A	4:120375945-120550146	OK	2.73084	2.10178	-0.37773	-0.268615	0.4464	0.9998
ENSG00000115350	ENSG00000115350	POLE4	2:75185618-75197255	OK	140.071	163.693	0.224833	0.461841	0.44645	0.9998
ENSG00000138621	ENSG00000138621	PPCDC	15:75315895-75409803	OK	9.94212	7.8286	-0.344799	-0.454798	0.4465	0.9998
ENSG00000001629	ENSG00000001629	ANKIB1	7:91875547-92030698	OK	21.9729	25.0514	0.189165	0.35779	0.4466	0.9998
ENSG00000050327	ENSG00000050327	ARHGEF5	7:143883175-144077725	OK	2.62256	4.11468	0.649803	0.506803	0.4466	0.9998
ENSG00000162772	ENSG00000162772	ATF3	1:212738675-212794119	OK	5.72055	7.20439	0.332723	0.426549	0.44665	0.9998
ENSG00000139531	ENSG00000139531	SUOX	12:56390963-56400425	OK	7.33053	8.56702	0.224875	0.361228	0.4468	0.9998
ENSG00000262621	ENSG00000262621	NAA60	16:3415098-3627401	OK	0.218529	0.672773	1.6223	0.272642	0.44685	0.9998
ENSG00000144847	ENSG00000144847	IGSF11	3:118619403-118864915	OK	21.6291	18.4048	-0.232893	-0.417367	0.4469	0.9998
ENSG00000233539	ENSG00000233539	AC011294.3	7:46713382-46799449	OK	1.52721	1.13372	-0.429838	-0.453294	0.4469	0.9998
ENSG00000254772	ENSG00000254772	EEF1G	11:62327072-62359649	OK	853.786	1016.28	0.251355	0.448177	0.44695	0.9998
ENSG00000197358	ENSG00000197358	BNIP3P1	14:28733595-28735180	OK	8.34643	6.93952	-0.266324	-0.466341	0.4471	0.9998
ENSG00000092010	ENSG00000092010	PSME1	14:24605366-24610797	OK	47.3711	40.4526	-0.227774	-0.467849	0.44725	0.9998
ENSG00000060491	ENSG00000060491	OGFR	20:61431978-61445352	OK	20.94	24.1948	0.208439	0.448878	0.44735	0.9998
ENSG00000084733	ENSG00000084733	RAB10	2:26256975-26360323	OK	78.3884	95.8544	0.290204	0.438733	0.44745	0.9998
ENSG00000108651	ENSG00000108651	UTP6	17:30187922-30228784	OK	31.6376	37.2321	0.234909	0.414581	0.44755	0.9998
ENSG00000130811	ENSG00000130811	EIF3G	19:10216898-10230596	OK	146.139	169.149	0.210953	0.449306	0.44755	0.9998
ENSG00000135148	ENSG00000135148	TRAFD1	12:112563304-112591407	OK	10.0994	8.60459	-0.23109	-0.413268	0.44765	0.9998
ENSG00000135045	ENSG00000135045	C9orf40	9:77561496-77567802	OK	5.26303	4.43458	-0.247097	-0.460791	0.44785	0.9998
ENSG00000163898	ENSG00000163898	LIPH	3:185224049-185270401	OK	0.483792	0.677017	0.484804	0.314798	0.4479	0.9998
ENSG00000185272	ENSG00000185272	RBM11	21:15588450-15600693	OK	2.20081	2.9724	0.433593	0.46833	0.4479	0.9998
ENSG00000163539	ENSG00000163539	CLASP2	3:33537736-33759848	OK	21.1504	18.5319	-0.190674	-0.283955	0.44795	0.9998
ENSG00000173801	ENSG00000173801	JUP	17:39775688-39943183	OK	0.87464	1.56661	0.840887	0.149477	0.44805	0.9998
ENSG00000165458	ENSG00000165458	INPPL1	11:71934744-71956708	OK	70.7558	83.833	0.24467	0.26989	0.4481	0.9998
ENSG00000177697	ENSG00000177697	CD151	11:818901-842545	OK	77.2356	96.428	0.320186	0.442797	0.4481	0.9998
ENSG00000181524	ENSG00000181524	RPL24P4	6:42924082-42924503	OK	17.1735	20.9654	0.287824	0.4603	0.4481	0.9998
ENSG00000100220	ENSG00000100220	RTCB	22:32783568-32808242	OK	79.664	90.1192	0.177906	0.430976	0.4482	0.9998
ENSG00000143013	ENSG00000143013	LMO4	1:87794150-87814606	OK	6.32881	7.69248	0.281515	0.455698	0.4482	0.9998
ENSG00000054118	ENSG00000054118	THRAP3	1:36690016-36770958	OK	28.9961	25.1393	-0.205914	-0.364568	0.4484	0.9998
ENSG00000185684	ENSG00000185684	EP400NL	12:132568827-132613029	OK	2.54325	3.30988	0.380107	0.410017	0.44855	0.9998
ENSG00000178093	ENSG00000178093	TSSK6	19:19623226-19648390	OK	1.18533	0.61168	-0.954436	-0.228846	0.4486	0.9998
ENSG00000136758	ENSG00000136758	YME1L1	10:27399382-27475853	OK	34.4404	39.9131	0.212764	0.446312	0.4488	0.9998
ENSG00000268816	ENSG00000268816	CTD-3093M3.1	19:54697730-54698394	OK	0.578857	0.859077	0.56958	0.472209	0.4488	0.9998
ENSG00000178700	ENSG00000178700	DHFRL1	3:93698982-93847389	OK	1.68563	1.16143	-0.537385	-0.370906	0.4489	0.9998
ENSG00000117586	ENSG00000117586	TNFSF4	1:173152872-173176452	OK	0.795282	1.03558	0.380905	0.352099	0.44905	0.9998
ENSG00000142945	ENSG00000142945	KIF2C	1:45205489-45244451	OK	34.2693	22.2305	-0.62438	-0.368624	0.44905	0.9998
ENSG00000255198	ENSG00000255198	SNHG9	16:2014959-2015510	OK	9.70132	12.6989	0.388454	0.450658	0.44905	0.9998
ENSG00000164329	ENSG00000164329	PAPD4	5:78907942-78982471	OK	20.9646	24.0953	0.200795	0.337645	0.4492	0.9998
ENSG00000100591	ENSG00000100591	AHSA1	14:77893017-77935817	OK	98.8493	117.717	0.252022	0.444485	0.44925	0.9998
ENSG00000143257	ENSG00000143257	NR1I3	1:161195792-161208092	OK	1.4891	1.12403	-0.405758	-0.12899	0.4493	0.9998
ENSG00000168297	ENSG00000168297	PXK	3:58318606-58411748	OK	14.2151	12.1869	-0.22209	-0.426305	0.4493	0.9998
ENSG00000128923	ENSG00000128923	FAM63B	15:59063390-59389618	OK	2.96801	2.10817	-0.493506	-0.416625	0.44935	0.9998
ENSG00000214174	ENSG00000214174	AMZ2P1	17:62962667-62971694	OK	11.4232	9.38076	-0.284186	-0.459715	0.44935	0.9998
ENSG00000095261	ENSG00000095261	PSMD5	9:123577773-123616651	OK	5.47435	6.46289	0.239493	0.311848	0.44945	0.9998
ENSG00000182580	ENSG00000182580	EPHB3	3:183851806-184402546	OK	1.02481	1.94423	0.923846	0.0415734	0.4495	0.9998
ENSG00000074755	ENSG00000074755	ZZEF1	17:3907738-4046314	OK	10.8279	9.2287	-0.230557	-0.34613	0.4496	0.9998
ENSG00000120896	ENSG00000120896	SORBS3	8:22298331-22433301	OK	15.2325	19.3145	0.342536	0.395171	0.4496	0.9998
ENSG00000133433	ENSG00000133433	GSTT2B	22:24299600-24303373	OK	4.67364	3.76808	-0.310718	-0.456697	0.4496	0.9998
ENSG00000187678	ENSG00000187678	SPRY4	5:141689991-142077617	OK	19.9242	22.9482	0.203857	0.378732	0.4498	0.9998
ENSG00000173065	ENSG00000173065	FAM222B	17:27082995-27188085	OK	15.1132	12.2261	-0.305845	-0.345089	0.44985	0.9998
ENSG00000095794	ENSG00000095794	CREM	10:35386933-35501886	OK	62.0639	71.3756	0.201679	0.440658	0.44995	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237094	ENSG00000237094	RP4-669L17.10	1:317719-461954	OK	2.4886	1.76952	-0.491972	-0.349988	0.44995	0.9998
ENSG00000204237	ENSG00000204237	OXLD1	17:79632065-79640934	OK	21.7766	30.983	0.508694	0.49535	0.45	0.9998
ENSG00000196497	ENSG00000196497	IPO4	14:24641061-24708448	OK	20.4001	26.9284	0.400553	0.40417	0.45005	0.9998
ENSG00000159445	ENSG00000159445	THEM4	1:151846059-151882284	OK	52.1608	44.1228	-0.241444	-0.451667	0.45015	0.9998
ENSG00000126856	ENSG00000126856	PRDM7	16:90122973-90158480	OK	2.39836	2.98821	0.317234	0.410815	0.4504	0.9998
ENSG00000148459	ENSG00000148459	PDSS1	10:26986587-27150016	OK	5.2965	7.24982	0.452905	0.38867	0.45045	0.9998
ENSG00000127989	ENSG00000127989	MTERF	7:91321322-91510034	OK	11.8829	10.0008	-0.248767	-0.414243	0.4506	0.9998
ENSG00000164506	ENSG00000164506	STXBP5	6:147163036-147706866	OK	5.97311	6.96481	0.2216	0.43445	0.4507	0.9998
ENSG00000267575	ENSG00000267575	CTC-459F4.3	19:28175487-28475892	OK	11.8465	8.7638	-0.434838	-0.465164	0.4507	0.9998
ENSG00000226054	ENSG00000226054	MEMO1P1	21:37502668-37528615	OK	12.9973	15.9087	0.291602	0.457412	0.45075	0.9998
ENSG00000116251	ENSG00000116251	RPL22	1:6241328-6296032	OK	424.798	524.526	0.304236	0.482215	0.45085	0.9998
ENSG00000167863	ENSG00000167863	ATP5H	17:73028669-73061984	OK	409.798	353.12	-0.214755	-0.455422	0.4511	0.9998
ENSG00000165030	ENSG00000165030	NFIL3	9:94171326-94186144	OK	14.3279	16.5793	0.210551	0.450748	0.45125	0.9998
ENSG00000085117	ENSG00000085117	CD82	11:44585976-44641913	OK	15.3855	18.5445	0.269423	0.44894	0.45135	0.9998
ENSG00000100916	ENSG00000100916	BRMS1L	14:36288429-36536396	OK	4.51065	5.40216	0.260201	0.424391	0.45135	0.9998
ENSG00000131143	ENSG00000131143	COX4I1	16:85805363-85840650	OK	350.095	401.13	0.196327	0.460212	0.4514	0.9998
ENSG00000126709	ENSG00000126709	IFI6	1:27992571-27998729	OK	21.5259	18.244	-0.238656	-0.457112	0.45145	0.9998
ENSG00000198301	ENSG00000198301	SDAD1	4:76831808-76928641	OK	14.7439	12.7658	-0.20783	-0.379311	0.45155	0.9998
ENSG00000198887	ENSG00000198887	SMC5	9:72873936-72969804	OK	6.70033	5.62356	-0.252747	-0.361172	0.4516	0.9998
ENSG00000095485	ENSG00000095485	CWF19L1	10:101989423-102027437	OK	17.3315	20.7448	0.259352	0.45148	0.45175	0.9998
ENSG00000135297	ENSG00000135297	MTO1	6:74171300-74218959	OK	14.9211	17.4291	0.22415	0.351266	0.45175	0.9998
ENSG00000140807	ENSG00000140807	NKD1	16:50582240-50670647	OK	1.79644	2.38935	0.411483	0.374757	0.45195	0.9998
ENSG00000272861	ENSG00000272861	RP11-332H14.1	2:105865860-105866251	OK	0.773321	0.403155	-0.939733	-0.626411	0.45195	0.9998
ENSG00000162433	ENSG00000162433	AK4	1:65613231-65697828	OK	8.76234	6.88663	-0.347518	-0.430509	0.4522	0.9998
ENSG00000214029	ENSG00000214029	ZNF891	12:133692277-133707059	OK	1.44226	1.13429	-0.346547	-0.455084	0.4522	0.9998
ENSG00000011143	ENSG00000011143	MKS1	17:56282802-56345879	OK	9.39679	7.81818	-0.265336	-0.430158	0.4523	0.9998
ENSG00000142798	ENSG00000142798	HSPG2	1:22138757-22263790	OK	12.36	10.5899	-0.222997	-0.22215	0.45235	0.9998
ENSG00000166189	ENSG00000166189	HPS6	10:103825146-103827792	OK	8.21327	9.58484	0.222799	0.459857	0.45245	0.9998
ENSG00000239887	ENSG00000239887	C1orf226	1:162039563-162356600	OK	3.98304	5.09588	0.355459	0.440233	0.45245	0.9998
ENSG00000146122	ENSG00000146122	DAAM2	6:39760141-39902290	OK	37.7367	44.0298	0.222512	0.30788	0.45255	0.9998
ENSG00000256742	ENSG00000256742	RP13-941N14.1	12:121837843-122031409	OK	0.92191	0.300148	-1.61895	-0.224497	0.4526	0.9998
ENSG00000140280	ENSG00000140280	LYSMD2	15:52015207-52108565	OK	4.62311	6.28847	0.443846	0.477435	0.45265	0.9998
ENSG00000154511	ENSG00000154511	FAM69A	1:93307723-93427057	OK	11.9288	10.2634	-0.21694	-0.459263	0.45265	0.9998
ENSG00000256683	ENSG00000256683	ZNF350	19:52452386-52490109	OK	4.68648	3.81945	-0.295138	-0.382468	0.45275	0.9998
ENSG00000178896	ENSG00000178896	EXOSC4	8:145132904-145135550	OK	37.7023	43.7229	0.213735	0.454694	0.45285	0.9998
ENSG00000167815	ENSG00000167815	PRDX2	19:12873816-12985765	OK	0.865617	1.72489	0.994708	0.238341	0.45295	0.9998
ENSG00000004487	ENSG00000004487	KDM1A	1:23345940-23504301	OK	28.9927	34.3854	0.246105	0.429034	0.4531	0.9998
ENSG00000119711	ENSG00000119711	ALDH6A1	14:74318546-74551196	OK	4.01033	2.29139	-0.807499	-0.459909	0.4531	0.9998
ENSG00000063244	ENSG00000063244	U2AF2	19:56165511-56186081	OK	121.846	139.971	0.200068	0.420427	0.45315	0.9998
ENSG00000226852	ENSG00000226852	RP1-212P9.2	1:29194086-29203848	OK	0.730927	0.966885	0.403617	0.469553	0.4532	0.9998
ENSG00000138035	ENSG00000138035	PNPT1	2:55861399-55921045	OK	15.4405	17.7208	0.198723	0.396323	0.45325	0.9998
ENSG00000177169	ENSG00000177169	ULK1	12:132379195-132407712	OK	11.2343	9.58128	-0.229619	-0.43384	0.45325	0.9998
ENSG00000095637	ENSG00000095637	SORBS1	10:97071527-97321171	OK	23.201	20.4349	-0.183152	-0.398059	0.45365	0.9998
ENSG00000104812	ENSG00000104812	GYS1	19:49471381-49496567	OK	31.7426	27.4415	-0.210063	-0.329869	0.45375	0.9998
ENSG00000268201	ENSG00000268201	CTD-3138B18.6	19:58739959-58827023	OK	0.223835	0.629466	1.49169	0.152276	0.4539	0.9998
ENSG00000247626	ENSG00000247626	MARS2	2:198557829-198651486	OK	5.53834	4.72212	-0.230017	-0.446199	0.45405	0.9998
ENSG00000204634	ENSG00000204634	TBC1D8	2:101436613-101886778	OK	12.271	7.44199	-0.721497	-0.172649	0.45415	0.9998
ENSG00000133226	ENSG00000133226	SRRM1	1:24958206-24999758	OK	23.8535	27.3759	0.198705	0.318745	0.45425	0.9998
ENSG00000167555	ENSG00000167555	ZNF528	19:52901101-52921665	OK	1.21966	1.7861	0.550338	0.37126	0.45425	0.9998
ENSG00000015479	ENSG00000015479	MATR3	5:138282408-138667360	OK	140.732	160.112	0.186132	0.356416	0.4543	0.9998
ENSG00000182508	ENSG00000182508	LHFPL1	X:111873875-111923375	OK	0.735708	0.557154	-0.401058	-0.406099	0.4543	0.9998
ENSG00000111737	ENSG00000111737	RAB35	12:120532898-120555306	OK	16.1612	18.7689	0.215807	0.40441	0.4544	0.9998
ENSG00000184110	ENSG00000184110	EIF3C	16:28671016-28752102	OK	13.8467	15.8533	0.19524	0.433489	0.45455	0.9998
ENSG00000167595	ENSG00000167595	C19orf55	19:36249043-36261930	OK	6.92682	5.50824	-0.330602	-0.422718	0.4547	0.9998
ENSG00000170145	ENSG00000170145	SIK2	11:111473114-111637151	OK	3.19825	2.59131	-0.303603	-0.341569	0.4547	0.9998
ENSG00000259976	ENSG00000259976	RP11-553L6.5	3:114033347-114035026	OK	0.876218	0.673777	-0.379018	-0.450218	0.45485	0.9998
ENSG00000149782	ENSG00000149782	PLCB3	11:64018994-64036622	OK	13.2137	11.499	-0.200527	-0.38913	0.45505	0.9998
ENSG00000002919	ENSG00000002919	SNX11	17:46180718-46200436	OK	20.7201	17.9663	-0.205739	-0.423311	0.45515	0.9998
ENSG00000153207	ENSG00000153207	AHCTF1	1:247002399-247095280	OK	19.12	15.7548	-0.279294	-0.307256	0.45535	0.9998
ENSG00000164125	ENSG00000164125	FAM198B	4:159045625-159176563	OK	22.9273	27.0245	0.237204	0.325956	0.45535	0.9998
ENSG00000189403	ENSG00000189403	HMGB1	13:31032883-31191734	OK	277.074	238.865	-0.214078	-0.449066	0.45555	0.9998
ENSG00000215256	ENSG00000215256	DHRS4-AS1	14:24407939-24475617	OK	8.58727	6.61136	-0.377253	-0.473069	0.4556	0.9998
ENSG00000135047	ENSG00000135047	CTSL	9:90340433-90346308	OK	209.209	238.432	0.188633	0.448121	0.45565	0.9998
ENSG00000166153	ENSG00000166153	DEPDC4	12:100550134-100660857	OK	2.00739	1.313	-0.612453	-0.248777	0.45565	0.9998
ENSG00000083223	ENSG00000083223	ZCCHC6	9:88902647-88969369	OK	5.18287	6.52294	0.331771	0.374939	0.4557	0.9998
ENSG00000196743	ENSG00000196743	GM2A	5:150560612-150650001	OK	49.927	43.8531	-0.18714	-0.446616	0.4557	0.9998
ENSG00000125931	ENSG00000125931	CITED1	X:71401202-71527037	OK	32.5063	53.7838	0.726452	0.217479	0.45575	0.9998
ENSG00000225484	ENSG00000225484	RP11-773D16.1	10:81563812-81587358	OK	38.4062	50.7135	0.401029	0.454186	0.4563	0.9998
ENSG00000241404	ENSG00000241404	EGFL8	6:32116135-32145873	OK	17.8796	34.1362	0.93299	0.512851	0.45645	0.9998
ENSG00000101104	ENSG00000101104	PABPC1L	20:43538702-43589127	OK	21.6636	17.3296	-0.322037	-0.371041	0.45665	0.9998
ENSG00000138376	ENSG00000138376	BARD1	2:215590369-215674428	OK	3.70132	3.03599	-0.285871	-0.344571	0.45665	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000135205	ENSG00000135205	CCDC146	7:76139744-77045717	OK	1.52385	0.932917	-0.707902	-0.234687	0.4567	0.9998
ENSG00000146833	ENSG00000146833	TRIM4	7:99473609-99517223	OK	23.0393	26.6135	0.208061	0.415178	0.4568	0.9998
ENSG00000160932	ENSG00000160932	LY6E	8:144063154-144105249	OK	261.232	296.134	0.18092	0.445388	0.45695	0.9998
ENSG00000153885	ENSG00000153885	KCTD15	19:34286837-34306668	OK	22.5748	26.0278	0.205341	0.370815	0.457	0.9998
ENSG00000237611	ENSG00000237611	AL353898.3	1:54519259-54578192	OK	2.29726	0.506065	-2.18252	-0.532945	0.4573	0.9998
ENSG00000258580	ENSG00000258580	RP11-320M16.2	14:32798478-33300567	OK	0.293677	0.816582	1.47537	0.233715	0.4573	0.9998
ENSG00000090565	ENSG00000090565	RAB11FIP3	16:475618-573011	OK	11.8018	9.93991	-0.247698	-0.354762	0.45735	0.9998
ENSG00000164976	ENSG00000164976	KIAA1161	9:34366667-34376851	OK	1.15397	0.945729	-0.287108	-0.400957	0.4574	0.9998
ENSG00000232063	ENSG00000232063	RP11-307E17.8	9:97094757-97123230	OK	1.10885	0.873833	-0.343641	-0.458448	0.4574	0.9998
ENSG00000173757	ENSG00000173757	STAT5B	17:40351185-40428725	OK	14.6712	16.8334	0.198338	0.362299	0.45745	0.9998
ENSG00000120688	ENSG00000120688	WBP4	13:41506055-41658137	OK	9.32351	7.03007	-0.407334	-0.462767	0.45775	0.9998
ENSG00000165494	ENSG00000165494	PCF11	11:82868029-83134559	OK	7.37489	5.62863	-0.389839	-0.353255	0.4578	0.9998
ENSG00000220842	ENSG00000220842	RP11-572P18.1	10:122114176-122114718	OK	129.512	148.853	0.200801	0.452353	0.4579	0.9998
ENSG00000234518	ENSG00000234518	PTGES3P1	1:89569967-89570450	OK	0.790448	1.3716	0.795114	0.591713	0.45795	0.9998
ENSG00000089220	ENSG00000089220	PEBP1	12:118501397-118583389	OK	430.65	499.678	0.214484	0.447245	0.45805	0.9998
ENSG00000181523	ENSG00000181523	SGSH	17:78143790-78227299	OK	19.8818	23.8337	0.261556	0.330562	0.45815	0.9998
ENSG00000126456	ENSG00000126456	IRF3	19:50162825-50177173	OK	19.3031	23.1121	0.259819	0.340992	0.4582	0.9998
ENSG00000185883	ENSG00000185883	ATP6V0C	16:2525146-2581423	OK	170.727	196.918	0.20591	0.443763	0.4582	0.9998
ENSG00000198839	ENSG00000198839	ZNF277	7:111846642-112049678	OK	22.4681	26.4081	0.233105	0.437901	0.4582	0.9998
ENSG00000240344	ENSG00000240344	PPIL3	2:201735629-201754026	OK	11.9528	14.7568	0.30403	0.404953	0.4584	0.9998
ENSG00000141376	ENSG00000141376	BCAS3	17:58754813-59488916	OK	96.4351	121.537	0.333765	0.452478	0.4586	0.9998
ENSG00000120278	ENSG00000120278	PLEKHG1	6:150920998-151164799	OK	1.67248	2.05335	0.295987	0.275881	0.45865	0.9998
ENSG00000189339	ENSG00000189339	SLC35E2B	1:1590785-1624167	OK	11.7676	10.09	-0.22189	-0.446718	0.4587	0.9998
ENSG00000157870	ENSG00000157870	FAM213B	1:2517929-2718286	OK	15.1172	17.3769	0.200983	0.405696	0.4589	0.9998
ENSG00000163481	ENSG00000163481	RNF25	2:219528586-219567439	OK	15.0363	19.2109	0.353477	0.448106	0.4589	0.9998
ENSG00000256121	ENSG00000256121	AC010296.1	5:115779311-115927094	OK	0.185938	1.47669	2.98947	0.270305	0.459	0.9998
ENSG00000224287	ENSG00000224287	MSL3P1	2:234774082-234777090	OK	2.74821	2.25246	-0.286993	-0.455038	0.45905	0.9998
ENSG00000105270	ENSG00000105270	CLIP3	19:36505409-36545664	OK	5.03976	6.26956	0.315008	0.34158	0.45915	0.9998
ENSG00000164638	ENSG00000164638	SLC29A4	7:5313999-5465045	OK	1.56171	3.11644	0.996771	0.433099	0.4592	0.9998
ENSG00000232098	ENSG00000232098	CTD-2619J13.14	19:58912870-58929694	OK	2.01931	1.23092	-0.71413	-0.324509	0.45935	0.9998
ENSG00000252419	ENSG00000252419	RMRPP2	6:5030205-5054657	OK	0.783472	0.291736	-1.42522	-0.559626	0.45935	0.9998
ENSG00000246528	ENSG00000246528	RP11-159H10.3	8:70579281-70767206	OK	1.90467	0.978353	-0.961117	-0.251998	0.4594	0.9998
ENSG00000104131	ENSG00000104131	EIF3J	15:44829254-44955876	OK	23.1942	29.1225	0.328368	0.430607	0.4595	0.9998
ENSG00000168487	ENSG00000168487	BMP1	8:22022248-22069839	OK	25.073	21.9521	-0.191774	-0.406474	0.4595	0.9998
ENSG00000140743	ENSG00000140743	CDR2	16:22357256-22547842	OK	7.97412	9.58274	0.265113	0.352606	0.45955	0.9998
ENSG00000159461	ENSG00000159461	AMFR	16:56395363-56459450	OK	17.9221	21.0395	0.231367	0.397082	0.45985	0.9998
ENSG00000143179	ENSG00000143179	UCK2	1:165696031-165880855	OK	43.4496	54.6939	0.332037	0.431784	0.4601	0.9998
ENSG00000171159	ENSG00000171159	C9orf16	9:130922538-130926207	OK	41.566	48.1841	0.213155	0.441943	0.46015	0.9998
ENSG00000185187	ENSG00000185187	SIGIRR	11:405715-417455	OK	19.0853	22.6741	0.248582	0.438691	0.46025	0.9998
ENSG00000085511	ENSG00000085511	MAP3K4	6:161411349-161538417	OK	4.78204	4.01108	-0.253636	-0.269141	0.46035	0.9998
ENSG00000151694	ENSG00000151694	ADAM17	2:9613786-9695921	OK	12.1495	14.6339	0.268422	0.440699	0.46045	0.9998
ENSG00000260367	ENSG00000260367	RP11-264B17.4	16:28985541-29002104	OK	0.296446	0.847319	1.51513	0.16405	0.4607	0.9998
ENSG00000083857	ENSG00000083857	FAT1	4:187508936-187647876	OK	5.55545	6.57302	0.242652	0.253938	0.4608	0.9998
ENSG00000121486	ENSG00000121486	TRMT1L	1:185087219-185126204	OK	13.5913	17.1024	0.331511	0.455169	0.46095	0.9998
ENSG00000176912	ENSG00000176912	C18orf56	18:596987-712676	OK	0.474688	1.00382	1.08046	0.135884	0.4611	0.9998
ENSG00000188786	ENSG00000188786	MTF1	1:38275238-38325292	OK	2.37756	2.87039	0.271764	0.271229	0.4611	0.9998
ENSG00000005175	ENSG00000005175	RPAP3	12:48057069-48099844	OK	19.3938	23.1498	0.255403	0.395556	0.46115	0.9998
ENSG00000239697	ENSG00000239697	TNFSF12	17:7452207-7464925	OK	4.96407	6.53615	0.396917	0.477073	0.46135	0.9998
ENSG00000023697	ENSG00000023697	DERA	12:16064105-16190220	OK	65.7201	56.8685	-0.208705	-0.450871	0.4615	0.9998
ENSG00000073578	ENSG00000073578	SDHA	5:218355-256815	OK	93.1875	82.58	-0.174344	-0.415277	0.4615	0.9998
ENSG00000172661	ENSG00000172661	FAM21C	10:46201878-46288409	OK	3.22777	4.21405	0.384668	0.357195	0.4615	0.9998
ENSG00000137135	ENSG00000137135	ARHGEF39	9:35658300-35681156	OK	9.25613	6.79719	-0.445471	-0.448573	0.4616	0.9998
ENSG00000255284	ENSG00000255284	AP006621.5	11:777577-784297	OK	1.35202	0.895347	-0.594602	-0.442756	0.46175	0.9998
ENSG00000066583	ENSG00000066583	ISOC1	5:128430443-128449721	OK	4.27222	5.04805	0.240741	0.431935	0.4618	0.9998
ENSG00000259171	ENSG00000259171	AL163636.6	14:21152258-21175279	OK	1.79114	0.980684	-0.869018	-0.54174	0.46185	0.9998
ENSG00000125249	ENSG00000125249	RAP2A	13:98086475-98121382	OK	9.68151	11.0953	0.196642	0.405084	0.46205	0.9998
ENSG00000111850	ENSG00000111850	SMIM8	6:87992695-88109467	OK	3.5987	2.74654	-0.389859	-0.436363	0.4621	0.9998
ENSG00000165943	ENSG00000165943	MOAP1	14:93648540-93651273	OK	36.1533	31.8421	-0.183188	-0.444527	0.46215	0.9998
ENSG00000171368	ENSG00000171368	TPPP	5:612386-693510	OK	13.2423	15.4957	0.226713	0.467276	0.46235	0.9998
ENSG00000137817	ENSG00000137817	PARP6	15:72533521-72671129	OK	16.8296	12.6068	-0.416808	-0.239775	0.4624	0.9998
ENSG00000162063	ENSG00000162063	CCNF	16:2479394-2509980	OK	10.9828	9.59167	-0.195398	-0.438453	0.4624	0.9998
ENSG00000168071	ENSG00000168071	CCDC88B	11:64107694-64125006	OK	3.42532	2.67703	-0.355605	-0.443859	0.4624	0.9998
ENSG00000141279	ENSG00000141279	NPEPPS	17:45600307-45726786	OK	48.9741	43.1329	-0.183232	-0.336421	0.46245	0.9998
ENSG00000049618	ENSG00000049618	ARID1B	6:157099062-157531913	OK	5.25653	6.03375	0.198945	0.389873	0.4625	0.9998
ENSG00000241878	ENSG00000241878	PISD	22:31795508-32058418	OK	10.7413	14.323	0.415171	0.371611	0.46255	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000125814	ENSG00000125814	NAPB	20:23355158-23402125	OK	1.88867	1.53025	-0.303601	-0.392991	0.46275	0.9998
ENSG00000197496	ENSG00000197496	SLC2A10	20:45338125-45364965	OK	0.770095	0.596279	-0.369049	-0.325716	0.46285	0.9998
ENSG00000160602	ENSG00000160602	NEK8	17:27046410-27070473	OK	1.03524	0.630384	-0.715663	-0.0942928	0.463	0.9998
ENSG00000183558	ENSG00000183558	HIST2H2AA3	1:149813504-149814478	OK	0.680314	0.487489	-0.48083	-0.445958	0.46305	0.9998
ENSG00000100505	ENSG00000100505	TRIM9	14:51441979-51562779	OK	4.21406	5.0335	0.256351	0.323222	0.4631	0.9998
ENSG00000138758	ENSG00000138758	11-Sep	4:77870855-77961537	OK	46.9981	54.0524	0.201757	0.227693	0.4631	0.9998
ENSG00000103365	ENSG00000103365	GGA2	16:23474862-23533316	OK	50.4826	61.7044	0.289588	0.366979	0.46315	0.9998
ENSG00000114520	ENSG00000114520	SNX4	3:125165494-125239041	OK	23.8596	27.3572	0.19735	0.427281	0.46315	0.9998
ENSG00000162441	ENSG00000162441	LZIC	1:9982172-10045559	OK	20.0537	16.6221	-0.270765	-0.439527	0.46315	0.9998
ENSG00000125967	ENSG00000125967	NECAB3	20:32244892-32262269	OK	30.5088	26.7267	-0.190946	-0.377367	0.4632	0.9998
ENSG00000177034	ENSG00000177034	MTX3	5:79275583-79287082	OK	6.00374	7.14626	0.251328	0.441702	0.4632	0.9998
ENSG00000178074	ENSG00000178074	C2orf69	2:200775978-200873263	OK	8.38237	6.72485	-0.317856	-0.448249	0.4633	0.9998
ENSG00000237765	ENSG00000237765	FAM200B	4:15606161-15739936	OK	21.2097	15.611	-0.442164	-0.410952	0.46335	0.9998
ENSG00000162244	ENSG00000162244	RPL29	3:52027615-52029958	OK	519.879	589.375	0.181011	0.447506	0.4634	0.9998
ENSG00000232573	ENSG00000232573	RPL3P4	14:99439215-99439638	OK	867.679	983.291	0.180457	0.449561	0.46345	0.9998
ENSG00000234373	ENSG00000234373	SNX18P7	9:33576377-33577012	OK	1.29994	0.930951	-0.481673	-0.45272	0.4635	0.9998
ENSG00000165288	ENSG00000165288	BRWD3	X:79926352-80065187	OK	5.16483	4.33829	-0.251593	-0.395003	0.46355	0.9998
ENSG00000162517	ENSG00000162517	PEF1	1:32083286-32169920	OK	20.9624	24.92	0.249495	0.419006	0.46365	0.9998
ENSG00000180581	ENSG00000180581	SRP9P1	10:93558068-93625033	OK	192.139	131.471	-0.547412	-0.427042	0.4637	0.9998
ENSG00000179218	ENSG00000179218	CALR	19:13049391-13055303	OK	510.973	450.153	-0.182832	-0.428296	0.4639	0.9998
ENSG00000248592	ENSG00000248592	TMEM110-MUSTN1	3:52846990-52931612	OK	1.40787	0.708259	-0.991166	-0.395967	0.4639	0.9998
ENSG00000161920	ENSG00000161920	MED11	17:4634722-4643217	OK	16.1823	13.1577	-0.29851	-0.453502	0.46405	0.9998
ENSG00000101189	ENSG00000101189	MRGBP	20:61427804-61431945	OK	41.2069	36.2163	-0.186244	-0.44354	0.46415	0.9998
ENSG00000112146	ENSG00000112146	FBXO9	6:52866076-52965671	OK	50.8311	61.5164	0.275262	0.380855	0.4642	0.9998
ENSG00000170558	ENSG00000170558	CDH2	18:25530929-25757410	OK	3.12158	3.81001	0.287517	0.347647	0.4642	0.9998
ENSG00000108829	ENSG00000108829	LRRC59	17:48450580-48475249	OK	95.4833	108.221	0.180657	0.440965	0.46425	0.9998
ENSG00000165264	ENSG00000165264	NDUFB6	9:32540541-32573160	OK	69.1196	57.2486	-0.271856	-0.442696	0.46425	0.9998
ENSG00000050748	ENSG00000050748	MAPK9	5:179660142-179719099	OK	34.6944	40.5713	0.225757	0.418773	0.4644	0.9998
ENSG00000254004	ENSG00000254004	ZNF260	19:37001596-37119499	OK	6.52235	4.79458	-0.443987	-0.24681	0.4644	0.9998
ENSG00000215067	ENSG00000215067	AC027763.2	17:6757179-6922978	OK	4.65079	2.95534	-0.654152	-0.17918	0.4645	0.9998
ENSG00000167977	ENSG00000167977	KCTD5	16:2732475-2759031	OK	11.8969	10.2851	-0.210023	-0.428679	0.465	0.9998
ENSG00000180329	ENSG00000180329	CCDC43	17:42733761-42767676	OK	33.9324	38.6844	0.189091	0.419504	0.4651	0.9998
ENSG00000170581	ENSG00000170581	STAT2	12:56735380-56753939	OK	34.5549	29.8971	-0.208884	-0.372098	0.46515	0.9998
ENSG00000102048	ENSG00000102048	ASB9	X:15253409-15288589	OK	25.4964	21.611	-0.238523	-0.44353	0.46525	0.9998
ENSG00000167716	ENSG00000167716	WDR81	17:1614804-1641893	OK	6.99589	8.23367	0.235026	0.291681	0.46525	0.9998
ENSG00000196586	ENSG00000196586	MYO6	6:76458908-76629254	OK	6.29409	5.46747	-0.203124	-0.422649	0.46525	0.9998
ENSG00000251669	ENSG00000251669	FAM86EP	4:3916909-3957148	OK	1.05726	0.772148	-0.453377	-0.365161	0.46535	0.9998
ENSG00000077044	ENSG00000077044	DGKD	2:234263152-234380750	OK	6.68003	5.54942	-0.267517	-0.241022	0.46555	0.9998
ENSG00000229186	ENSG00000229186	ADAM1A	12:112337066-112340042	OK	0.715916	0.544257	-0.395501	-0.450345	0.4657	0.9998
ENSG00000114302	ENSG00000114302	PRKAR2A	3:48782029-48889414	OK	17.7628	21.0214	0.242998	0.36693	0.46575	0.9998
ENSG00000148200	ENSG00000148200	NR6A1	9:127279553-127535206	OK	1.20252	1.56429	0.379441	0.346807	0.46575	0.9998
ENSG00000232938	ENSG00000232938	AC139099.3	17:81159764-81188573	OK	2.463	1.6883	-0.544848	-0.417503	0.46575	0.9998
ENSG00000110756	ENSG00000110756	HPS5	11:18300222-18343745	OK	44.9691	39.7355	-0.178505	-0.352906	0.46585	0.9998
ENSG00000124333	ENSG00000124333	VAMP7	X:155110955-155173433	OK	30.4568	26.7245	-0.188598	-0.385801	0.4659	0.9998
ENSG00000166483	ENSG00000166483	WEE1	11:9595227-9615004	OK	18.2208	15.4355	-0.239329	-0.419001	0.4659	0.9998
ENSG00000107372	ENSG00000107372	ZFAND5	9:74966340-74980163	OK	130.481	157.633	0.272732	0.431066	0.46595	0.9998
ENSG00000131378	ENSG00000131378	RFTN1	3:16306705-16555533	OK	1.21919	0.877918	-0.473764	-0.200722	0.466	0.9998
ENSG00000163067	ENSG00000163067	ZNF2	2:95831176-95850065	OK	2.69245	2.19034	-0.297765	-0.447666	0.46605	0.9998
ENSG00000182512	ENSG00000182512	GLRX5	14:95998633-96011061	OK	42.3753	48.7348	0.201727	0.441356	0.46605	0.9998
ENSG00000188549	ENSG00000188549	C15orf52	15:40623652-40633168	OK	13.4973	16.3753	0.278847	0.347117	0.4661	0.9998
ENSG00000197111	ENSG00000197111	PCBP2	12:53835388-53893847	OK	321.995	276.865	-0.217858	-0.432509	0.46615	0.9998
ENSG00000198355	ENSG00000198355	PIM3	22:50354160-50357728	OK	32.7356	37.0208	0.177475	0.421975	0.46615	0.9998
ENSG00000225791	ENSG00000225791	TRAM2-AS1	6:52442104-52448783	OK	1.47622	1.14564	-0.365756	-0.405489	0.46615	0.9998
ENSG00000106025	ENSG00000106025	TSPAN12	7:120427375-120498456	OK	5.45719	6.47993	0.247818	0.424139	0.4662	0.9998
ENSG00000129968	ENSG00000129968	ABHD17A	19:1876808-1885546	OK	24.0015	27.8446	0.214276	0.438485	0.4662	0.9998
ENSG00000166169	ENSG00000166169	POLL	10:103330316-103369425	OK	17.6427	14.5876	-0.274334	-0.452532	0.4662	0.9998
ENSG00000115091	ENSG00000115091	ACTR3	2:114647536-114720173	OK	118.061	140.725	0.253347	0.447218	0.46625	0.9998
ENSG00000185158	ENSG00000185158	LRRC37B	17:30334890-30380523	OK	5.13577	4.12803	-0.315127	-0.393963	0.46645	0.9998
ENSG00000171722	ENSG00000171722	C1orf111	1:162039563-162356600	OK	0.290879	0.668525	1.20056	0.265036	0.46655	0.9998
ENSG00000032444	ENSG00000032444	PNPLA6	19:7587511-7626650	OK	39.525	34.4666	-0.197566	-0.306991	0.46665	0.9998
ENSG00000184840	ENSG00000184840	TMED9	5:177019158-177023125	OK	172.916	196.763	0.186386	0.440687	0.46675	0.9998
ENSG00000244393	ENSG00000244393	RP11-592B15.3	10:51224680-51371338	OK	0.763913	0.446881	-0.773518	-0.474944	0.46685	0.9998
ENSG00000079462	ENSG00000079462	PAFAH1B3	19:42801184-42814973	OK	61.5194	70.9773	0.206316	0.439257	0.467	0.9998
ENSG00000113966	ENSG00000113966	ARL6	3:97483364-97519953	OK	6.10352	4.81469	-0.342199	-0.448211	0.467	0.9998
ENSG00000183250	ENSG00000183250	C21orf67	21:46352728-46359828	OK	0.551485	0.764579	0.471344	0.405953	0.467	0.9998
ENSG00000023287	ENSG00000023287	RB1CC1	8:53535015-53658403	OK	14.2148	12.5005	-0.185403	-0.306612	0.46705	0.9998
ENSG00000042088	ENSG00000042088	TDP1	14:90421282-90511106	OK	11.5485	9.57872	-0.2698	-0.422173	0.46705	0.9998
ENSG00000117385	ENSG00000117385	LEPRE1	1:43212005-43232755	OK	13.6484	11.7575	-0.215151	-0.367924	0.46715	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000198585	ENSG00000198585	NUDT16	3:131100514-131107674	OK	11.2596	13.3808	0.249001	0.435315	0.46725	0.9998
ENSG00000164902	ENSG00000164902	PHAX	5:125935959-125962944	OK	18.6022	15.2035	-0.291063	-0.444225	0.4673	0.9998
ENSG00000120756	ENSG00000120756	PLS1	3:142315228-142432506	OK	4.26594	3.5686	-0.257508	-0.335388	0.46745	0.9998
ENSG00000068745	ENSG00000068745	IP6K2	3:48725435-48777786	OK	32.5556	37.1547	0.19064	0.40799	0.4675	0.9998
ENSG00000119912	ENSG00000119912	IDE	10:94211440-94333833	OK	10.297	12.306	0.257144	0.377331	0.4675	0.9998
ENSG00000213860	ENSG00000213860	RPL21P75	7:19958603-20257027	OK	264.21	300.108	0.183797	0.435816	0.4676	0.9998
ENSG00000232504	ENSG00000232504	AC105053.4	2:86116402-86118103	OK	0.720147	0.998473	0.471432	0.449683	0.46765	0.9998
ENSG00000164284	ENSG00000164284	GRPEL2	5:148724992-148737205	OK	6.80766	7.86878	0.208981	0.401369	0.46775	0.9998
ENSG00000164850	ENSG00000164850	GPER1	7:1036621-1177896	OK	0.350637	0.675167	0.945266	0.247105	0.4678	0.9998
ENSG00000248690	ENSG00000248690	HAS2-AS1	8:122624355-122656933	OK	4.51401	2.59255	-0.800037	-0.303043	0.46795	0.9998
ENSG00000101460	ENSG00000101460	MAP1LC3A	20:33134657-33148149	OK	34.3057	39.7921	0.214032	0.443039	0.46805	0.9998
ENSG00000048649	ENSG00000048649	RSF1	11:77371040-77532063	OK	16.8642	13.8164	-0.287583	-0.311551	0.46815	0.9998
ENSG00000101019	ENSG00000101019	UQCC1	20:33890368-33999944	OK	24.9857	28.8914	0.209535	0.375101	0.46815	0.9998
ENSG00000067082	ENSG00000067082	KLF6	10:3818187-3827473	OK	48.3181	54.9942	0.186717	0.325291	0.46825	0.9998
ENSG00000246582	ENSG00000246582	RP11-1149O23.3	8:23046791-23088439	OK	0.529298	1.26744	1.25976	0.59251	0.46825	0.9998
ENSG00000103024	ENSG00000103024	NME3	16:1756183-1821731	OK	23.9611	31.3952	0.389846	0.446752	0.4684	0.9998
ENSG00000134759	ENSG00000134759	ELP2	18:33709406-33757909	OK	48.6259	41.9337	-0.213615	-0.351002	0.46845	0.9998
ENSG00000106013	ENSG00000106013	ANKRD7	7:117854726-117882785	OK	7.2133	5.91319	-0.286724	-0.432754	0.4685	0.9998
ENSG00000145996	ENSG00000145996	CDKAL1	6:20534687-21232635	OK	10.356	8.8567	-0.225623	-0.424422	0.4685	0.9998
ENSG00000174748	ENSG00000174748	RPL15	3:23933150-24022109	OK	880.55	1053.5	0.258712	0.444503	0.4685	0.9998
ENSG00000231064	ENSG00000231064	RP11-263K19.4	1:155165378-155183615	OK	1.10622	1.80756	0.708403	0.159237	0.4685	0.9998
ENSG00000198890	ENSG00000198890	PRMT6	1:107599266-107601916	OK	5.5075	4.69527	-0.230187	-0.435591	0.4686	0.9998
ENSG00000158526	ENSG00000158526	TSR2	X:54466833-54522599	OK	25.3104	20.8169	-0.281979	-0.442855	0.46875	0.9998
ENSG00000256525	ENSG00000256525	POLG2	17:62473901-62493154	OK	14.1715	16.7435	0.240611	0.375231	0.46875	0.9998
ENSG00000072041	ENSG00000072041	SLC6A15	12:85253491-85307394	OK	25.0777	28.9794	0.208621	0.412789	0.4689	0.9998
ENSG00000159363	ENSG00000159363	ATP13A2	1:17300996-17338423	OK	45.4698	39.8594	-0.189988	-0.350034	0.46915	0.9998
ENSG00000197375	ENSG00000197375	SLC22A5	5:131520568-131731306	OK	1.38643	2.084	0.587983	0.359768	0.4692	0.9998
ENSG00000198373	ENSG00000198373	WWP2	16:69796208-69975644	OK	7.13235	6.08965	-0.228018	-0.332074	0.4692	0.9998
ENSG00000166900	ENSG00000166900	STX3	11:59480295-59573354	OK	96.6701	82.5689	-0.227471	-0.379941	0.46925	0.9998
ENSG00000183496	ENSG00000183496	MEX3B	15:82334118-82338482	OK	1.10937	1.34913	0.282286	0.437574	0.4694	0.9998
ENSG00000101955	ENSG00000101955	SRPX	X:37208527-38548169	OK	84.0029	71.2428	-0.237695	-0.430142	0.46945	0.9998
ENSG00000138640	ENSG00000138640	FAM13A	4:89630939-90032549	OK	12.4207	10.7523	-0.208105	-0.333649	0.4695	0.9998
ENSG00000148057	ENSG00000148057	IDNK	9:86237963-86259045	OK	2.53488	1.94509	-0.382081	-0.448632	0.46955	0.9998
ENSG00000174374	ENSG00000174374	WBSCR16	7:74441225-74490064	OK	22.9353	26.1203	0.187601	0.431839	0.46965	0.9998
ENSG00000136044	ENSG00000136044	APPL2	12:105567073-105789875	OK	19.7953	17.1634	-0.205824	-0.326413	0.4699	0.9998
ENSG00000224616	ENSG00000224616	RP11-305E17.6	1:100729564-100731676	OK	0.855926	0.530826	-0.689246	-0.458926	0.46995	0.9998
ENSG00000104388	ENSG00000104388	RAB2A	8:61429415-61536186	OK	63.3817	76.7332	0.275785	0.43973	0.47005	0.9998
ENSG00000103316	ENSG00000103316	CRYM	16:21244985-21329912	OK	1.10405	1.42978	0.372982	0.323544	0.4702	0.9998
ENSG00000232527	ENSG00000232527	RP11-14N7.2	1:148928321-148951595	OK	18.2262	23.2485	0.351124	0.428083	0.4702	0.9998
ENSG00000182054	ENSG00000182054	IDH2	15:90626276-90645736	OK	22.9009	19.7672	-0.212295	-0.442704	0.47035	0.9998
ENSG00000019485	ENSG00000019485	PRDM11	11:45115563-45256843	OK	1.03958	1.37548	0.403936	0.406825	0.4704	0.9998
ENSG00000061938	ENSG00000061938	TNK2	3:195590234-195638816	OK	25.8214	29.6631	0.200105	0.370677	0.4704	0.9998
ENSG00000105255	ENSG00000105255	FSD1	19:4304596-4323840	OK	4.12674	4.99748	0.276197	0.391407	0.47045	0.9998
ENSG00000246731	ENSG00000246731	CTD-2514K5.2	17:72199720-72209481	OK	1.47681	0.755166	-0.967615	-0.136078	0.47045	0.9998
ENSG00000238164	ENSG00000238164	RP3-395M20.8	1:2481358-2496821	OK	14.7253	9.52859	-0.62796	-0.277683	0.4705	0.9998
ENSG00000111907	ENSG00000111907	TPD52L1	6:125440194-125623282	OK	24.2788	33.8288	0.478557	0.482865	0.4707	0.9998
ENSG00000196636	ENSG00000196636	ACN9	7:96745901-96811075	OK	22.178	17.6781	-0.327171	-0.430067	0.4707	0.9998
ENSG00000132436	ENSG00000132436	FIGNL1	7:50511830-50518088	OK	23.428	20.4434	-0.196599	-0.329689	0.47075	0.9998
ENSG00000116044	ENSG00000116044	NFE2L2	2:178092322-178408564	OK	51.3002	59.8081	0.221377	0.400099	0.4709	0.9998
ENSG00000170365	ENSG00000170365	SMAD1	4:146402345-146479231	OK	4.33472	3.62356	-0.258528	-0.324789	0.4709	0.9998
ENSG00000119559	ENSG00000119559	C19orf25	19:1446299-1479555	OK	20.6469	17.2274	-0.26122	-0.390874	0.471	0.9998
ENSG00000114030	ENSG00000114030	KPNA1	3:122135053-122233792	OK	35.4085	42.3707	0.25897	0.433448	0.47105	0.9998
ENSG00000085433	ENSG00000085433	WDR47	1:109512835-109584850	OK	4.11271	5.484	0.41514	0.412063	0.4711	0.9998
ENSG00000141933	ENSG00000141933	TPGS1	19:489175-519654	OK	7.87676	9.35723	0.248479	0.449415	0.4712	0.9998
ENSG00000144283	ENSG00000144283	PKP4	2:159313475-159610287	OK	25.6608	22.5115	-0.188905	-0.31394	0.4712	0.9998
ENSG00000214696	ENSG00000214696	AC007347.1	16:53737874-54155853	OK	0.89118	2.3219	1.38152	0.649279	0.4712	0.9998
ENSG00000214435	ENSG00000214435	AS3MT	10:104613979-104661656	OK	3.18669	4.23275	0.409537	0.43797	0.47125	0.9998
ENSG00000103111	ENSG00000103111	MON1B	16:77224731-77478233	OK	10.2887	13.0382	0.341675	0.393997	0.4714	0.9998
ENSG00000235092	ENSG00000235092	AC011747.7	2:8806765-8824583	OK	1.11115	0.712593	-0.640908	-0.134934	0.47145	0.9998
ENSG00000111678	ENSG00000111678	C12orf57	12:7052140-7055166	OK	64.0995	55.3203	-0.212503	-0.437685	0.47155	0.9998
ENSG00000160949	ENSG00000160949	TONSL	8:145654164-145669827	OK	7.1951	6.2495	-0.203273	-0.440977	0.4716	0.9998
ENSG00000244357	ENSG00000244357	RN7SL145P	3:45596885-45786916	OK	0.700685	0.185743	-1.91546	-0.0756469	0.4717	0.9998
ENSG00000137221	ENSG00000137221	TJAP1	6:43445260-43474294	OK	14.7847	12.672	-0.222464	-0.366244	0.47175	0.9998
ENSG00000186187	ENSG00000186187	ZNRF1	16:74907467-75144892	OK	3.1966	4.69618	0.554949	0.442609	0.47175	0.9998
ENSG00000184047	ENSG00000184047	DIABLO	12:122688089-122751068	OK	67.1664	53.3607	-0.331962	-0.445015	0.4718	0.9998
ENSG00000102312	ENSG00000102312	PORCN	X:48367349-48379202	OK	8.84714	7.34908	-0.267648	-0.411058	0.47185	0.9998
ENSG00000127526	ENSG00000127526	SLC35E1	19:16589867-16771253	OK	20.9382	16.5924	-0.335614	-0.280295	0.47205	0.9998
ENSG00000136630	ENSG00000136630	HLX	1:221006104-221058401	OK	16.3397	20.0743	0.296961	0.439975	0.47205	0.9998
ENSG00000149761	ENSG00000149761	NUDT22	11:63974149-64001824	OK	29.6436	23.5437	-0.332379	-0.411312	0.47235	0.9998
ENSG00000255529	ENSG00000255529	POLR2M	15:57884105-58074960	OK	14.5471	11.9592	-0.282602	-0.427939	0.4725	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000133104	ENSG00000133104	SPG20	13:36875774-36944317	OK	45.2929	51.8958	0.196331	0.374474	0.4726	0.9998
ENSG00000106993	ENSG00000106993	CDC37L1	9:4679558-4708398	OK	5.00956	6.03954	0.269754	0.437499	0.47265	0.9998
ENSG00000161714	ENSG00000161714	PLCD3	17:43100707-43221548	OK	14.3963	19.8962	0.466795	0.249798	0.47265	0.9998
ENSG00000099203	ENSG00000099203	TMED1	19:10828754-10946994	OK	22.9928	30.314	0.398804	0.419436	0.4728	0.9998
ENSG00000140987	ENSG00000140987	ZSCAN32	16:3415098-3627401	OK	5.59183	3.91476	-0.514396	-0.389754	0.4728	0.9998
ENSG00000220804	ENSG00000220804	AC093642.5	2:243030783-243102304	OK	10.6142	8.34531	-0.34696	-0.474813	0.47285	0.9998
ENSG00000159069	ENSG00000159069	FBXW5	9:139834886-139839148	OK	45.3297	51.4124	0.181659	0.410514	0.4729	0.9998
ENSG00000132680	ENSG00000132680	KIAA0907	1:155882833-155904191	OK	37.1725	43.371	0.222496	0.36222	0.47305	0.9998
ENSG00000213598	ENSG00000213598	RP11-112J1.1	14:59261371-59261747	OK	1.10631	0.661614	-0.741694	-0.374134	0.4733	0.9998
ENSG00000087903	ENSG00000087903	RFX2	19:5978413-6199583	OK	2.26799	2.89099	0.350152	0.271621	0.47335	0.9998
ENSG00000158716	ENSG00000158716	DUSP23	1:159750721-159752333	OK	151.749	133.379	-0.186152	-0.442447	0.47335	0.9998
ENSG00000105929	ENSG00000105929	ATP6V0A4	7:138391039-138666064	OK	10.4907	7.87771	-0.413269	-0.432524	0.4735	0.9998
ENSG00000164615	ENSG00000164615	CAMLG	5:134074190-134087847	OK	9.26669	11.0009	0.247493	0.423598	0.4735	0.9998
ENSG00000140350	ENSG00000140350	ANP32A	15:69070873-69355083	OK	118.03	101.771	-0.213823	-0.434692	0.47365	0.9998
ENSG00000271853	ENSG00000271853	RP1-178F15.5	1:153591262-153618782	OK	0.640272	0.242217	-1.40239	-0.0357203	0.4738	0.9998
ENSG00000175063	ENSG00000175063	UBE2C	20:44441214-44445596	OK	105.085	92.4804	-0.184334	-0.437444	0.4739	0.9998
ENSG00000108599	ENSG00000108599	AKAP10	17:19807614-19881656	OK	12.8535	11.1053	-0.210909	-0.281854	0.474	0.9998
ENSG00000167771	ENSG00000167771	RCOR2	11:63678692-63684316	OK	0.621827	0.812127	0.385193	0.311607	0.47415	0.9998
ENSG00000178026	ENSG00000178026	FAM211B	22:24936405-25024972	OK	2.25572	3.53086	0.646435	0.189331	0.47415	0.9998
ENSG00000176148	ENSG00000176148	TCP11L1	11:33060962-33213144	OK	9.3974	7.38278	-0.348097	-0.42391	0.4742	0.9998
ENSG00000196459	ENSG00000196459	TRAPPC2	X:13730362-13752754	OK	5.46118	6.93418	0.344511	0.424334	0.4742	0.9998
ENSG00000198793	ENSG00000198793	MTOR	1:11166591-11322564	OK	17.913	15.8663	-0.175043	-0.349375	0.4742	0.9998
ENSG00000163155	ENSG00000163155	LYSMD1	1:151129104-151167797	OK	11.2804	8.25612	-0.450281	-0.418707	0.47435	0.9998
ENSG00000116962	ENSG00000116962	NID1	1:236139129-236228462	OK	10.2095	11.6251	0.187326	0.433463	0.4744	0.9998
ENSG00000248333	ENSG00000248333	CDK11B	1:1567473-1590473	OK	16.3908	13.4665	-0.283505	-0.332899	0.4744	0.9998
ENSG00000215252	ENSG00000215252	GOLGA8B	15:34671268-34880704	OK	9.06003	12.5547	0.470637	0.354812	0.47455	0.9998
ENSG00000159921	ENSG00000159921	GNE	9:36190852-36304921	OK	13.8273	9.4658	-0.546724	-0.459343	0.4747	0.9998
ENSG00000136715	ENSG00000136715	SAP130	2:128698790-128785694	OK	8.64236	7.53252	-0.198292	-0.418973	0.47475	0.9998
ENSG00000169682	ENSG00000169682	SPNS1	16:28985541-29002104	OK	31.4206	35.9634	0.194819	0.399099	0.4748	0.9998
ENSG00000152952	ENSG00000152952	PLOD2	3:145781828-145881440	OK	22.9124	26.1232	0.189203	0.356702	0.47485	0.9998
ENSG00000137601	ENSG00000137601	NEK1	4:170314425-170533780	OK	3.47922	2.98139	-0.222776	-0.408377	0.47495	0.9998
ENSG00000254400	ENSG00000254400	RP11-732A19.8	11:6624871-6633898	OK	0.920642	0.257921	-1.83571	-0.108879	0.47495	0.9998
ENSG00000015171	ENSG00000015171	ZMYND11	10:180404-300577	OK	15.3966	13.2811	-0.213244	-0.399668	0.475	0.9998
ENSG00000112763	ENSG00000112763	BTN2A1	6:26458149-26476849	OK	12.2499	14.0899	0.201899	0.37741	0.4753	0.9998
ENSG00000146535	ENSG00000146535	GNA12	7:2719155-2883958	OK	23.7549	20.4906	-0.213261	-0.403112	0.4753	0.9998
ENSG00000178226	ENSG00000178226	PRSS36	16:31150245-31161415	OK	0.822608	1.16883	0.506789	0.386299	0.47535	0.9998
ENSG00000248964	ENSG00000248964	RP11-94H18.1	8:29672519-29712059	OK	1.22937	0.967766	-0.345186	-0.438935	0.4754	0.9998
ENSG00000103707	ENSG00000103707	MTFMT	15:65294844-65321977	OK	7.11179	8.5203	0.26069	0.398664	0.47545	0.9998
ENSG00000245937	ENSG00000245937	CTC-228N24.3	5:127039081-127418864	OK	5.92722	4.69633	-0.335821	-0.439415	0.47585	0.9998
ENSG00000064393	ENSG00000064393	HIPK2	7:139246315-139720125	OK	10.3608	8.98524	-0.205505	-0.409134	0.4759	0.9998
ENSG00000102893	ENSG00000102893	PHKB	16:47178233-47735434	OK	10.9942	9.1859	-0.259247	-0.300048	0.47595	0.9998
ENSG00000145476	ENSG00000145476	CYP4V2	4:187112673-187179625	OK	2.32356	1.89829	-0.291636	-0.432956	0.476	0.9998
ENSG00000203705	ENSG00000203705	TATDN3	1:212965169-212989968	OK	14.6224	11.8011	-0.309261	-0.391978	0.4761	0.9998
ENSG00000196757	ENSG00000196757	ZNF700	19:12035882-12091196	OK	5.26878	4.50518	-0.225885	-0.435007	0.47615	0.9998
ENSG00000156931	ENSG00000156931	VPS8	3:184529930-184770402	OK	18.0896	16.0835	-0.169576	-0.247664	0.4762	0.9998
ENSG00000138744	ENSG00000138744	NAAA	4:76831808-76928641	OK	0.571245	0.873288	0.612349	0.165553	0.47625	0.9998
ENSG00000205534	ENSG00000205534	RP11-345J4.8	16:29538888-29606395	OK	3.6195	2.9065	-0.316505	-0.438458	0.4765	0.9998
ENSG00000249353	ENSG00000249353	NPM1P27	5:92953774-93447404	OK	647.829	737.944	0.187899	0.435978	0.4766	0.9998
ENSG00000109654	ENSG00000109654	TRIM2	4:154073493-154260472	OK	27.0234	23.6138	-0.194579	-0.29668	0.4767	0.9998
ENSG00000136003	ENSG00000136003	ISCU	12:108956357-108963160	OK	68.6998	78.1706	0.18632	0.42608	0.4769	0.9998
ENSG00000117308	ENSG00000117308	GALE	1:24122088-24127271	OK	41.2044	47.487	0.204736	0.427357	0.4771	0.9998
ENSG00000235863	ENSG00000235863	B3GALT4	6:33244916-33267101	OK	1.14936	2.1712	0.917668	0.179671	0.47715	0.9998
ENSG00000071082	ENSG00000071082	RPL31	2:101436613-101886778	OK	2954.45	3493.7	0.241867	0.435075	0.47725	0.9998
ENSG00000157954	ENSG00000157954	WIPI2	7:5229818-5273457	OK	44.7776	50.8068	0.182244	0.41714	0.4774	0.9998
ENSG00000109475	ENSG00000109475	RPL34	4:109541721-109551568	OK	1158.12	1308.55	0.176189	0.434665	0.47745	0.9998
ENSG00000130779	ENSG00000130779	CLIP1	12:122755978-122907179	OK	23.7286	26.6734	0.168778	0.391066	0.47745	0.9998
ENSG00000148396	ENSG00000148396	SEC16A	9:139334548-139372141	OK	13.9815	12.2653	-0.188931	-0.391839	0.47745	0.9998
ENSG00000040531	ENSG00000040531	CTNS	17:3539761-3564836	OK	13.4306	11.6648	-0.203359	-0.35868	0.47755	0.9998
ENSG00000105982	ENSG00000105982	RNF32	7:156264889-156685924	OK	1.26657	1.84049	0.539162	0.133456	0.47755	0.9998
ENSG00000233325	ENSG00000233325	MIPEPP3	13:21872277-21922860	OK	0.467141	0.839103	0.844991	0.417721	0.4776	0.9998
ENSG00000106268	ENSG00000106268	NUDT1	7:2281856-2290781	OK	86.363	75.5599	-0.192793	-0.440077	0.47765	0.9998
ENSG00000157379	ENSG00000157379	DHRS1	14:24759803-24769039	OK	12.4873	14.624	0.227875	0.43089	0.47765	0.9998
ENSG00000171469	ENSG00000171469	ZNF561	19:9715355-9756572	OK	13.6448	11.3758	-0.262386	-0.34699	0.47785	0.9998
ENSG00000124766	ENSG00000124766	SOX4	6:21593971-21598847	OK	28.4956	25.261	-0.173825	-0.433145	0.4779	0.9998
ENSG00000157778	ENSG00000157778	PSMG3	7:1606965-1629262	OK	34.2702	39.9239	0.220297	0.430368	0.4779	0.9998
ENSG00000134508	ENSG00000134508	CABLES1	18:20714527-21017925	OK	65.4553	74.9777	0.19595	0.356321	0.4781	0.9998
ENSG00000174500	ENSG00000174500	GCSAM	3:111805181-111852152	OK	0.547294	0.769516	0.491635	0.252531	0.47815	0.9998
ENSG00000102125	ENSG00000102125	TAZ	X:153618314-153650065	OK	21.3557	16.924	-0.335546	-0.105459	0.47835	0.9998
ENSG00000156384	ENSG00000156384	SFR1	10:105881815-105886143	OK	4.4752	3.72345	-0.265315	-0.423653	0.47845	0.9998
ENSG00000184545	ENSG00000184545	DUSP8	11:1575273-1620414	OK	4.37024	6.28552	0.524319	0.498919	0.47845	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000164418	ENSG00000164418	GRIK2	6:101846663-102517958	OK	1.89889	1.49449	-0.345496	-0.364187	0.47855	0.9998
ENSG00000160767	ENSG00000160767	FAM189B	1:155216995-155225274	OK	35.4469	31.0255	-0.192205	-0.420614	0.4787	0.9998
ENSG00000107897	ENSG00000107897	ACBD5	10:27484145-27531059	OK	13.0479	15.2494	0.224934	0.425003	0.47885	0.9998
ENSG00000206527	ENSG00000206527	PTPLB	3:123209666-123304032	OK	9.89205	11.2448	0.18492	0.370648	0.4789	0.9998
ENSG00000204632	ENSG00000204632	HLA-G	6:29794743-29798902	OK	87.3597	99.0159	0.180691	0.432905	0.47895	0.9998
ENSG00000121988	ENSG00000121988	ZRANB3	2:135809834-136288806	OK	2.6798	1.57867	-0.763417	-0.293473	0.479	0.9998
ENSG00000075826	ENSG00000075826	SEC31B	10:102246398-102319755	OK	0.825106	0.585551	-0.494783	-0.0801539	0.47905	0.9998
ENSG00000114742	ENSG00000114742	WDR48	3:39093488-39180394	OK	15.5691	18.5668	0.254038	0.370084	0.4791	0.9998
ENSG00000135709	ENSG00000135709	KIAA0513	16:85061374-85127836	OK	3.39858	2.68925	-0.337726	-0.360519	0.47915	0.9998
ENSG00000160323	ENSG00000160323	ADAMTS13	9:136243116-136324508	OK	1.22252	0.740527	-0.723233	-0.322116	0.47915	0.9998
ENSG00000114423	ENSG00000114423	CBLB	3:105374304-105588396	OK	29.8994	26.2469	-0.187968	-0.383061	0.47925	0.9998
ENSG00000100345	ENSG00000100345	MYH9	22:36677326-36784063	OK	66.8718	59.497	-0.168581	-0.393931	0.47935	0.9998
ENSG00000103061	ENSG00000103061	SLC7A6OS	16:68298432-68344849	OK	11.0759	9.15647	-0.274566	-0.2927	0.47935	0.9998
ENSG00000101665	ENSG00000101665	SMAD7	18:46446222-46477081	OK	3.62133	4.2717	0.238291	0.365172	0.4796	0.9998
ENSG00000158552	ENSG00000158552	ZFAND2B	2:220059958-220074373	OK	20.5594	24.0917	0.228733	0.418339	0.4796	0.9998
ENSG00000143740	ENSG00000143740	SNAP47	1:227916239-227968927	OK	29.5945	35.0924	0.245833	0.42098	0.47975	0.9998
ENSG00000158669	ENSG00000158669	AGPAT6	8:41386724-41482520	OK	322.952	396.506	0.296022	0.436963	0.47975	0.9998
ENSG00000168394	ENSG00000168394	TAP1	6:32808493-32827362	OK	13.5314	15.7175	0.216063	0.430078	0.4798	0.9998
ENSG00000084754	ENSG00000084754	HADHA	2:26413503-26513336	OK	117.531	99.7303	-0.236938	-0.392054	0.48	0.9998
ENSG00000179454	ENSG00000179454	KLHL28	14:45393521-45543634	OK	3.36007	2.66001	-0.337057	-0.346669	0.48	0.9998
ENSG00000148841	ENSG00000148841	ITPRIP	10:106071893-106098162	OK	2.21184	2.59739	0.231814	0.422739	0.48005	0.9998
ENSG00000099849	ENSG00000099849	RASSF7	11:537526-564021	OK	5.17899	6.22982	0.26652	0.391005	0.4801	0.9998
ENSG00000236603	ENSG00000236603	RANP1	6:30453716-30454367	OK	14.7733	17.4811	0.24281	0.423961	0.4801	0.9998
ENSG00000044446	ENSG00000044446	PHKA2	X:18908413-19002716	OK	7.39499	6.1379	-0.268801	-0.317917	0.4802	0.9998
ENSG00000129173	ENSG00000129173	E2F8	11:19203577-19302973	OK	1.44363	1.10875	-0.380777	-0.312547	0.48035	0.9998
ENSG00000163041	ENSG00000163041	H3F3A	1:226248412-226259702	OK	21.3663	18.4698	-0.210169	-0.427921	0.48035	0.9998
ENSG00000150712	ENSG00000150712	MTMR12	5:32227099-32313115	OK	26.4653	23.4637	-0.173675	-0.286117	0.48045	0.9998
ENSG00000188342	ENSG00000188342	GTF2F2	13:45694649-45858237	OK	38.0371	43.1517	0.182011	0.42966	0.48065	0.9998
ENSG00000115255	ENSG00000115255	REEP6	19:1491164-1497926	OK	5.82264	4.92301	-0.242131	-0.407004	0.4808	0.9998
ENSG00000184983	ENSG00000184983	NDUFA6	22:42481528-42535938	OK	73.741	64.7416	-0.187774	-0.426391	0.4808	0.9998
ENSG00000214338	ENSG00000214338	SOGA3	6:127759550-127840500	OK	0.936055	0.702195	-0.414721	-0.409037	0.48085	0.9998
ENSG00000105612	ENSG00000105612	DNASE2	19:12986024-12994902	OK	47.0994	41.508	-0.182319	-0.425442	0.4809	0.9998
ENSG00000101407	ENSG00000101407	TTI1	20:36611408-36661870	OK	20.1438	17.7858	-0.179612	-0.39042	0.4811	0.9998
ENSG00000136141	ENSG00000136141	LRCH1	13:47127302-47327175	OK	8.75871	10.0027	0.191605	0.362181	0.4811	0.9998
ENSG00000092871	ENSG00000092871	RFFL	17:33332106-33448541	OK	3.09655	2.48058	-0.319985	-0.240641	0.4812	0.9998
ENSG00000146109	ENSG00000146109	ABT1	6:26597179-26600278	OK	15.3357	17.4666	0.18771	0.42281	0.4813	0.9998
ENSG00000251429	ENSG00000251429	RP11-597D13.7	4:159191529-159199828	OK	1.2237	0.924637	-0.404297	-0.421082	0.4813	0.9998
ENSG00000112242	ENSG00000112242	E2F3	6:20402397-20493941	OK	14.1725	16.087	0.182797	0.426772	0.48145	0.9998
ENSG00000196850	ENSG00000196850	PPTC7	12:110928901-111021125	OK	9.29524	11.1461	0.26197	0.418165	0.48175	0.9998
ENSG00000118707	ENSG00000118707	TGIF2	20:34894257-35274619	OK	7.79402	11.6827	0.583939	0.362763	0.4818	0.9998
ENSG00000168286	ENSG00000168286	THAP11	16:67840667-67906470	OK	10.4458	13.4799	0.36788	0.432001	0.4818	0.9998
ENSG00000197323	ENSG00000197323	TRIM33	1:114935398-115053781	OK	11.9733	10.403	-0.20283	-0.340905	0.48185	0.9998
ENSG00000229809	ENSG00000229809	ZNF688	16:30580666-30597092	OK	6.31161	4.67466	-0.433146	-0.372834	0.48185	0.9998
ENSG00000167699	ENSG00000167699	GLOD4	17:660336-695749	OK	46.3694	39.0719	-0.24704	-0.399237	0.48195	0.9998
ENSG00000008277	ENSG00000008277	ADAM22	7:87563457-87832204	OK	2.5445	3.10199	0.285812	0.35316	0.482	0.9998
ENSG00000272593	ENSG00000272593	RP11-339B21.11	9:131153739-131155789	OK	4.91406	3.8955	-0.335107	-0.429747	0.48205	0.9998
ENSG00000262500	ENSG00000262500	RP11-259G18.2	17:44320971-44322410	OK	0.677899	0.879844	0.376178	0.428377	0.48215	0.9998
ENSG00000257384	ENSG00000257384	RP11-644F5.12	12:56126149-56126432	OK	0.642335	0.295932	-1.11806	-0.507275	0.48225	0.9998
ENSG00000141084	ENSG00000141084	RANBP10	16:67757004-67840555	OK	15.5625	17.728	0.18796	0.38678	0.48235	0.9998
ENSG00000259856	ENSG00000259856	RAB43P1	16:46660315-46660904	OK	9.63625	11.6213	0.270227	0.428399	0.48235	0.9998
ENSG00000055147	ENSG00000055147	FAM114A2	5:153369687-153825410	OK	10.951	7.94476	-0.462994	-0.320673	0.48265	0.9998
ENSG00000141401	ENSG00000141401	IMPA2	18:11981023-12030876	OK	13.2091	11.2239	-0.234957	-0.408256	0.48265	0.9998
ENSG00000116095	ENSG00000116095	PLEKHA3	2:179345194-179381189	OK	9.90695	7.03331	-0.494237	-0.440316	0.4828	0.9998
ENSG00000137700	ENSG00000137700	SLC37A4	11:118868851-118901616	OK	21.5889	15.0096	-0.524403	-0.326041	0.483	0.9998
ENSG00000073464	ENSG00000073464	CLCN4	X:10125023-10205700	OK	2.30935	1.8577	-0.313971	-0.356492	0.4831	0.9998
ENSG00000129282	ENSG00000129282	MRM1	17:34958000-34965407	OK	1.84202	1.49065	-0.305345	-0.417648	0.48315	0.9998
ENSG00000136718	ENSG00000136718	IMP4	2:131095813-131105383	OK	36.506	44.6265	0.289765	0.428812	0.48325	0.9998
ENSG00000183260	ENSG00000183260	ABHD16B	20:62492565-62494341	OK	1.31281	1.04929	-0.323255	-0.428756	0.4833	0.9998
ENSG00000228801	ENSG00000228801	RP11-110G21.1	8:52811884-52859733	OK	1.43709	1.01588	-0.500416	-0.454862	0.4833	0.9998
ENSG00000244300	ENSG00000244300	RP11-475N22.4	3:128198269-128221191	OK	0.39752	0.828211	1.05897	0.558378	0.4833	0.9998
ENSG00000158321	ENSG00000158321	AUTS2	7:69063904-70258054	OK	0.742939	0.549657	-0.434713	-0.221533	0.48335	0.9998
ENSG00000126822	ENSG00000126822	PLEKHG3	14:65170819-65346601	OK	15.2186	13.3426	-0.189805	-0.377573	0.48345	0.9998
ENSG00000147274	ENSG00000147274	RBMX	X:135923089-135962923	OK	88.6103	78.2022	-0.180264	-0.425663	0.48355	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000257386	ENSG00000257386	RP11-56G10.2	12:74931550-74935223	OK	0.00239394	0.859167	8.48741	0.0449113	0.4836	0.9998
ENSG00000249042	ENSG00000249042	CTD-2015H6.3	5:79778111-79838382	OK	5.79358	4.58961	-0.336084	-0.429194	0.48365	0.9998
ENSG00000158161	ENSG00000158161	EYA3	1:28296854-28415207	OK	9.71203	11.6639	0.2642	0.40138	0.4837	0.9998
ENSG00000089876	ENSG00000089876	DHX32	10:127512114-127585005	OK	21.0695	17.4396	-0.272795	-0.379632	0.4838	0.9998
ENSG00000180425	ENSG00000180425	C11orf71	11:114262164-114321001	OK	0.941406	0.275536	-1.77258	-0.308592	0.4838	0.9998
ENSG00000169188	ENSG00000169188	APEX2	X:55026789-55057497	OK	10.4803	9.06503	-0.209296	-0.390208	0.48385	0.9998
ENSG00000065427	ENSG00000065427	KARS	16:75661621-75795770	OK	45.1168	52.2292	0.211191	0.405775	0.48415	0.9998
ENSG00000253719	ENSG00000253719	ATXN7L3B	12:74931550-74935223	OK	18.1508	16.0242	-0.179786	-0.426525	0.48425	0.9998
ENSG00000173517	ENSG00000173517	PEAK1	15:77400470-77712486	OK	12.1613	14.445	0.248274	0.224137	0.4844	0.9998
ENSG00000240771	ENSG00000240771	ARHGEF25	12:58003962-58027138	OK	5.3982	6.59404	0.288683	0.361946	0.48445	0.9998
ENSG00000106771	ENSG00000106771	TMEM245	9:111777431-111882225	OK	22.7068	26.5147	0.223672	0.419966	0.4845	0.9998
ENSG00000256646	ENSG00000256646	PSMA2	7:42948324-42988557	OK	12.7237	8.7265	-0.544048	-0.408714	0.4845	0.9998
ENSG00000178951	ENSG00000178951	ZBTB7A	19:4044361-4066943	OK	7.14738	6.0961	-0.229528	-0.418611	0.48465	0.9998
ENSG00000148225	ENSG00000148225	WDR31	9:116075501-116102578	OK	1.60604	1.28163	-0.325535	-0.304459	0.48475	0.9998
ENSG00000176890	ENSG00000176890	TYMS	18:596987-712676	OK	96.826	83.9141	-0.206482	-0.416461	0.48475	0.9998
ENSG00000116786	ENSG00000116786	PLEKHM2	1:16010826-16076391	OK	37.6271	33.2345	-0.17909	-0.399612	0.4848	0.9998
ENSG00000130560	ENSG00000130560	UBAC1	9:138824814-138853226	OK	27.8265	24.578	-0.179088	-0.404128	0.4848	0.9998
ENSG00000139726	ENSG00000139726	DENR	12:123237320-123255611	OK	31.8191	28.1221	-0.178186	-0.394469	0.4848	0.9998
ENSG00000167895	ENSG00000167895	TMC8	17:76000248-76139049	OK	1.15033	1.80411	0.649234	0.0846543	0.4848	0.9998
ENSG00000245958	ENSG00000245958	RP11-33B1.1	4:120375945-120550146	OK	14.7646	11.8734	-0.314406	-0.408828	0.4848	0.9998
ENSG00000143036	ENSG00000143036	SLC44A3	1:95285897-95360802	OK	4.0277	4.78946	0.249907	0.403258	0.485	0.9998
ENSG00000105619	ENSG00000105619	TFPT	19:54606035-54635140	OK	35.7171	46.554	0.38229	0.42968	0.48505	0.9998
ENSG00000267776	ENSG00000267776	AC006116.24	19:56732680-56904914	OK	0.156856	1.04043	2.72966	0.438358	0.48505	0.9998
ENSG00000091039	ENSG00000091039	OSBPL8	12:76745576-76953589	OK	22.8174	20.1463	-0.17962	-0.325589	0.4851	0.9998
ENSG00000164031	ENSG00000164031	DNAJB14	4:100817404-100867883	OK	11.4085	9.72489	-0.230358	-0.338476	0.4851	0.9998
ENSG00000101811	ENSG00000101811	CSTF2	X:100075383-100095921	OK	11.7886	13.5724	0.203284	0.423452	0.4852	0.9998
ENSG00000116133	ENSG00000116133	DHCR24	1:55315305-55354523	OK	46.3332	41.3243	-0.165054	-0.413016	0.4852	0.9998
ENSG00000176946	ENSG00000176946	THAP4	2:242523819-242613272	OK	26.2318	21.0594	-0.316852	-0.415029	0.4852	0.9998
ENSG00000136261	ENSG00000136261	BZW2	7:16685755-16759523	OK	50.9487	57.5056	0.174657	0.414625	0.48525	0.9998
ENSG00000149311	ENSG00000149311	ATM	11:108027941-108338258	OK	22.0972	17.9443	-0.300333	-0.2589	0.48525	0.9998
ENSG00000163617	ENSG00000163617	KIAA1407	3:113666747-113807269	OK	1.33968	0.896464	-0.579571	-0.229877	0.4853	0.9998
ENSG00000107554	ENSG00000107554	DNMBP	10:101635333-101769676	OK	3.45488	2.98377	-0.2115	-0.401713	0.48535	0.9998
ENSG00000141295	ENSG00000141295	SCRN2	17:45908992-45918699	OK	20.6718	23.945	0.21206	0.414068	0.48535	0.9998
ENSG00000154556	ENSG00000154556	SORBS2	4:186506597-186877806	OK	14.9926	12.5075	-0.261465	-0.360601	0.4854	0.9998
ENSG00000136930	ENSG00000136930	PSMB7	9:127115744-127177723	OK	285.946	320.996	0.166812	0.415036	0.48545	0.9998
ENSG00000163346	ENSG00000163346	PBXIP1	1:154916551-154928599	OK	80.4972	70.6885	-0.187463	-0.403267	0.48555	0.9998
ENSG00000174437	ENSG00000174437	ATP2A2	12:110718560-110788898	OK	125	143.622	0.200344	0.413436	0.48585	0.9998
ENSG00000161654	ENSG00000161654	LSM12	17:42112002-42144987	OK	6.19144	7.22416	0.222556	0.41822	0.4859	0.9998
ENSG00000163214	ENSG00000163214	DHX57	2:39024870-39103075	OK	9.39845	8.23342	-0.190932	-0.338958	0.48595	0.9998
ENSG00000184368	ENSG00000184368	MAP7D2	X:20024830-20135035	OK	5.12144	6.03556	0.236938	0.342616	0.48595	0.9998
ENSG00000014914	ENSG00000014914	MTMR11	1:149900542-149908791	OK	5.31476	4.36271	-0.284782	-0.411818	0.486	0.9998
ENSG00000118965	ENSG00000118965	WDR35	2:20110020-20189892	OK	4.16	4.82657	0.214415	0.382428	0.486	0.9998
ENSG00000108961	ENSG00000108961	RANGRF	17:8191080-8198661	OK	22.5897	26.3624	0.222819	0.427013	0.4861	0.9998
ENSG00000156535	ENSG00000156535	CD109	6:74403625-74538040	OK	24.4963	27.505	0.167131	0.418659	0.4862	0.9998
ENSG00000172840	ENSG00000172840	PDP2	16:66912491-66929657	OK	5.54756	6.55745	0.241282	0.273053	0.4862	0.9998
ENSG00000123064	ENSG00000123064	DDX54	12:113587662-113623284	OK	34.1939	41.2439	0.270439	0.416	0.4863	0.9998
ENSG00000259479	ENSG00000259479	CTD-2008A1.2	15:45118568-45176978	OK	4.06799	4.91263	0.272181	0.424975	0.48645	0.9998
ENSG00000158169	ENSG00000158169	FANCC	9:97861335-98079991	OK	4.97388	4.06132	-0.292424	-0.342536	0.4865	0.9998
ENSG00000109133	ENSG00000109133	TMEM33	4:41937136-41962589	OK	38.5205	46.0343	0.257084	0.412965	0.4867	0.9998
ENSG00000160741	ENSG00000160741	CRTC2	1:153920144-153931101	OK	24.0098	21.062	-0.18898	-0.3182	0.4867	0.9998
ENSG00000169241	ENSG00000169241	SLC50A1	1:155107819-155111329	OK	52.31	45.6257	-0.19724	-0.430175	0.48675	0.9998
ENSG00000178531	ENSG00000178531	CTXN1	19:7989371-8008805	OK	1.46321	3.38202	1.20875	0.55836	0.48675	0.9998
ENSG00000145907	ENSG00000145907	G3BP1	5:151121876-151192346	OK	137.035	162.733	0.247957	0.354756	0.4869	0.9998
ENSG00000148634	ENSG00000148634	HERC4	10:69681664-69835105	OK	19.3385	17.0676	-0.180212	-0.309604	0.487	0.9998
ENSG00000257337	ENSG00000257337	RP11-983P16.4	12:53399941-53458156	OK	7.17574	4.52452	-0.665363	-0.13209	0.48705	0.9998
ENSG00000067191	ENSG00000067191	CACNB1	17:37329542-37353956	OK	1.44073	1.94233	0.430989	0.322196	0.4871	0.9998
ENSG00000151572	ENSG00000151572	ANO4	12:101111303-101522419	OK	0.834222	1.0669	0.354919	0.302027	0.48715	0.9998
ENSG00000189144	ENSG00000189144	ZNF573	19:38226733-38307940	OK	1.6038	1.19304	-0.426848	-0.291714	0.48725	0.9998
ENSG00000250198	ENSG00000250198	RP11-143A12.3	5:8839843-8881637	OK	2.96674	2.44562	-0.278676	-0.334916	0.4874	0.9998
ENSG00000107262	ENSG00000107262	BAG1	9:33218362-33264761	OK	34.9685	39.7408	0.184566	0.411748	0.4877	0.9998
ENSG00000130717	ENSG00000130717	UCK1	9:134378288-134406655	OK	28.0567	23.8136	-0.23656	-0.348585	0.4877	0.9998
ENSG00000164754	ENSG00000164754	RAD21	8:117654368-117889107	OK	88.1455	74.196	-0.248546	-0.366283	0.4877	0.9998
ENSG00000079313	ENSG00000079313	REXO1	19:1815247-1848452	OK	10.9725	9.26746	-0.243643	-0.307357	0.48785	0.9998
ENSG00000079805	ENSG00000079805	DNM2	19:10828754-10946994	OK	45.0455	39.2862	-0.19736	-0.300199	0.48785	0.9998
ENSG00000099194	ENSG00000099194	SCD	10:102106880-102124591	OK	700.782	585.07	-0.260357	-0.418894	0.4879	0.9998
ENSG00000147065	ENSG00000147065	MSN	X:64808256-64961791	OK	107.403	121.072	0.172841	0.420364	0.488	0.9998
ENSG00000182621	ENSG00000182621	PLCB1	20:8112823-8949003	OK	1.83772	1.25397	-0.551412	-0.343659	0.48805	0.9998
ENSG00000219201	ENSG00000219201	RP11-181C21.4	1:78245308-78344106	OK	43.8021	36.6564	-0.256936	-0.407919	0.48805	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000243960	ENSG00000243960	RP11-552M11.4	1:111981259-112005395	OK	1.31153	3.43706	1.38992	0.221679	0.48805	0.9998
ENSG00000145242	ENSG00000145242	EPHA5	4:66185280-66563747	OK	1.28657	1.8314	0.509414	0.460824	0.4881	0.9998
ENSG00000057608	ENSG00000057608	GDI2	10:5807185-5884095	OK	53.1971	59.9784	0.173097	0.419398	0.4882	0.9998
ENSG00000110987	ENSG00000110987	BCL7A	12:122445339-122499948	OK	8.58698	7.42237	-0.210271	-0.410976	0.4883	0.9998
ENSG00000246596	ENSG00000246596	RP11-1277A3.2	5:177038253-177099210	OK	1.41431	0.94407	-0.583132	-0.420178	0.4883	0.9998
ENSG00000212747	ENSG00000212747	FAM127C	X:134154542-134156559	OK	3.26879	3.88211	0.248084	0.424434	0.48835	0.9998
ENSG00000241360	ENSG00000241360	PDXP	22:38030660-38062941	OK	27.3499	23.2629	-0.233503	-0.417244	0.4884	0.9998
ENSG00000105229	ENSG00000105229	PIAS4	19:4007643-4039384	OK	11.962	9.72208	-0.299128	-0.378888	0.48845	0.9998
ENSG00000112159	ENSG00000112159	MDN1	6:90352217-90529442	OK	3.01139	3.464	0.202009	0.248037	0.48845	0.9998
ENSG00000102760	ENSG00000102760	RGCC	13:42031694-42045018	OK	11.5797	13.7786	0.250831	0.404639	0.4885	0.9998
ENSG00000123415	ENSG00000123415	SMUG1	12:54555848-54582778	OK	57.8095	50.0084	-0.209136	-0.402931	0.4886	0.9998
ENSG00000143222	ENSG00000143222	UFC1	1:161122565-161129139	OK	142.232	160.331	0.172812	0.416323	0.4886	0.9998
ENSG00000149136	ENSG00000149136	SSRP1	11:57093076-57103351	OK	100.235	89.2739	-0.167069	-0.419612	0.48865	0.9998
ENSG00000144668	ENSG00000144668	ITGA9	3:37493605-37903271	OK	1.19334	1.51938	0.34847	0.375985	0.4887	0.9998
ENSG00000123684	ENSG00000123684	LPGAT1	1:211916798-212027045	OK	33.9235	30.272	-0.164302	-0.276332	0.489	0.9998
ENSG00000186416	ENSG00000186416	NKRF	X:118722299-118739858	OK	6.23825	7.19163	0.205178	0.415242	0.489	0.9998
ENSG00000147601	ENSG00000147601	TERF1	8:73921098-73960357	OK	16.1853	14.0712	-0.201935	-0.406081	0.48905	0.9998
ENSG00000005073	ENSG00000005073	HOXA11	7:27221128-27233067	OK	0.78363	1.02429	0.386381	0.442708	0.4892	0.9998
ENSG00000105700	ENSG00000105700	KXD1	19:18668571-18680197	OK	52.8922	46.6326	-0.181716	-0.395515	0.48925	0.9998
ENSG00000170469	ENSG00000170469	SPATA24	5:138732251-138739777	OK	5.12533	4.18217	-0.293394	-0.394873	0.4893	0.9998
ENSG00000198265	ENSG00000198265	HELZ	17:65066553-65242105	OK	12.6309	14.5077	0.199862	0.213065	0.4893	0.9998
ENSG00000157227	ENSG00000157227	MMP14	14:23305765-23318236	OK	216.634	190.474	-0.185666	-0.378176	0.48935	0.9998
ENSG00000167315	ENSG00000167315	ACAA2	18:47309868-47721463	OK	33.5826	28.8158	-0.220858	-0.399209	0.48935	0.9998
ENSG00000152795	ENSG00000152795	HNRNPDL	4:83343716-83351294	OK	123.667	109.289	-0.178311	-0.420224	0.4894	0.9998
ENSG00000114784	ENSG00000114784	EIF1B	3:40351174-40353915	OK	51.5812	45.4804	-0.1816	-0.411548	0.48955	0.9998
ENSG00000120616	ENSG00000120616	EPC1	10:32555216-32667726	OK	2.38085	2.86004	0.264561	0.312764	0.48955	0.9998
ENSG00000134278	ENSG00000134278	SPIRE1	18:12438888-12725739	OK	23.3757	27.4516	0.231879	0.349253	0.48955	0.9998
ENSG00000188493	ENSG00000188493	C19orf54	19:41197433-41271294	OK	2.03962	1.39649	-0.546496	-0.253177	0.4897	0.9998
ENSG00000164219	ENSG00000164219	PGGT1B	5:114546526-114599145	OK	5.32319	4.43144	-0.264516	-0.380432	0.48975	0.9998
ENSG00000183530	ENSG00000183530	PRR14L	22:32072241-32146126	OK	8.30609	7.30637	-0.185015	-0.287008	0.48985	0.9998
ENSG00000104365	ENSG00000104365	IKBKB	8:42128819-42189973	OK	17.4729	15.095	-0.211048	-0.27118	0.48995	0.9998
ENSG00000079308	ENSG00000079308	TNS1	2:218664511-218867718	OK	2.01238	2.48308	0.303231	0.2969	0.4901	0.9998
ENSG00000105983	ENSG00000105983	LMBR1	7:156264889-156685924	OK	34.0288	29.8874	-0.187222	-0.297719	0.4901	0.9998
ENSG00000260778	ENSG00000260778	MIR940	16:2303116-2323419	OK	0.433599	0.799791	0.883262	0.0928011	0.49015	0.9998
ENSG00000099875	ENSG00000099875	MKNK2	19:2037469-2051243	OK	52.7849	61.7352	0.225968	0.312172	0.49025	0.9998
ENSG00000101751	ENSG00000101751	POLI	18:51795773-51847636	OK	8.9299	7.63324	-0.226349	-0.34934	0.49025	0.9998
ENSG00000126653	ENSG00000126653	NSRP1	17:27887564-28513493	OK	12.7516	8.64657	-0.56048	-0.325872	0.4903	0.9998
ENSG00000244513	ENSG00000244513	CTD-2013N24.2	3:69024364-69129559	OK	1.0051	1.58458	0.656762	0.11167	0.4904	0.9998
ENSG00000129636	ENSG00000129636	ITFG1	16:47178233-47735434	OK	19.673	16.3869	-0.263679	-0.40043	0.49045	0.9998
ENSG00000161860	ENSG00000161860	SYCE2	19:13001839-13030090	OK	1.37022	0.63191	-1.11661	-0.33126	0.4906	0.9998
ENSG00000185049	ENSG00000185049	NELFA	4:1984440-2043630	OK	10.2913	11.8373	0.201912	0.371324	0.4906	0.9998
ENSG00000105939	ENSG00000105939	ZC3HAV1	7:138728265-138794465	OK	6.45469	7.42047	0.201163	0.393795	0.49065	0.9998
ENSG00000259372	ENSG00000259372	CTD-2240J17.1	15:81702857-81711358	OK	0.468857	0.856133	0.868686	0.498474	0.49065	0.9998
ENSG00000272655	ENSG00000272655	POLR2J4	7:43966036-44058774	OK	4.39198	6.20102	0.497635	0.40804	0.49065	0.9998
ENSG00000149179	ENSG00000149179	C11orf49	11:46958239-47198676	OK	21.0063	16.8617	-0.317068	-0.345056	0.49075	0.9998
ENSG00000128607	ENSG00000128607	KLHDC10	7:129710349-129775560	OK	29.1754	33.8653	0.215056	0.267821	0.4908	0.9998
ENSG00000159658	ENSG00000159658	EFCAB14	1:47098408-47184824	OK	37.393	31.8173	-0.232955	-0.334149	0.4908	0.9998
ENSG00000184831	ENSG00000184831	APOO	X:23851469-23957624	OK	32.6756	28.3508	-0.204823	-0.411346	0.4908	0.9998
ENSG00000167840	ENSG00000167840	ZNF232	17:5008835-5078329	OK	1.87886	2.53882	0.434298	0.403616	0.491	0.9998
ENSG00000182472	ENSG00000182472	CAPN12	19:39138288-39260544	OK	0.678211	1.11932	0.72282	0.0711614	0.491	0.9998
ENSG00000152382	ENSG00000152382	TADA1	1:166825746-166845564	OK	7.32377	6.30558	-0.215957	-0.424661	0.49105	0.9998
ENSG00000168116	ENSG00000168116	KIAA1586	6:56911346-56920023	OK	8.06133	10.1408	0.331087	0.432335	0.4913	0.9998
ENSG00000163689	ENSG00000163689	C3orf67	3:58703091-59035810	OK	8.44302	7.0191	-0.266474	-0.410698	0.49135	0.9998
ENSG00000189319	ENSG00000189319	FAM53B	10:126150402-126480439	OK	22.67	25.8201	0.187709	0.398331	0.4914	0.9998
ENSG00000197771	ENSG00000197771	MCMBP	10:121588971-121652068	OK	32.3495	28.6466	-0.17538	-0.413121	0.4914	0.9998
ENSG00000129696	ENSG00000129696	TTI2	8:33228341-33371119	OK	10.4824	8.19484	-0.355176	-0.394843	0.4915	0.9998
ENSG00000107164	ENSG00000107164	FUBP3	9:133454351-133513739	OK	26.2703	29.6623	0.175196	0.297764	0.49155	0.9998
ENSG00000132294	ENSG00000132294	EFR3A	8:132916334-133025889	OK	15.4234	17.4537	0.178413	0.361075	0.4916	0.9998
ENSG00000177301	ENSG00000177301	KCNA2	1:111136201-111174096	OK	0.438471	0.666232	0.603542	0.250314	0.49175	0.9998
ENSG00000152944	ENSG00000152944	MED21	12:27175478-27219276	OK	26.0507	29.5475	0.181712	0.394059	0.49195	0.9998
ENSG00000197530	ENSG00000197530	MIB2	1:1549137-1565990	OK	9.6347	8.20738	-0.231317	-0.33268	0.49195	0.9998
ENSG00000160408	ENSG00000160408	ST6GALNAC6	9:130628758-130667687	OK	14.7679	11.9798	-0.301855	-0.39996	0.492	0.9998
ENSG00000139517	ENSG00000139517	LNX2	13:28120049-28194541	OK	7.86492	8.92963	0.183168	0.410694	0.49205	0.9998
ENSG00000149182	ENSG00000149182	ARFGAP2	11:46958239-47198676	OK	32.4305	28.3274	-0.195153	-0.316365	0.4921	0.9998
ENSG00000196597	ENSG00000196597	ZNF782	9:99578753-99637905	OK	2.04949	1.52872	-0.422942	-0.327105	0.4921	0.9998
ENSG00000222011	ENSG00000222011	FAM185A	7:102389417-102449672	OK	3.82277	4.62978	0.276325	0.40679	0.4921	0.9998
ENSG00000141026	ENSG00000141026	MED9	17:17380299-17396540	OK	18.9677	16.7185	-0.182101	-0.385762	0.49215	0.9998
ENSG00000131188	ENSG00000131188	PRR7	5:176829140-176883283	OK	14.2583	19.0771	0.420043	0.423628	0.4922	0.9998
ENSG00000186104	ENSG00000186104	CYP2R1	11:14899552-14913798	OK	7.53513	9.12507	0.276204	0.387122	0.49225	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000120049	ENSG00000120049	KCNIP2	10:103578834-103603677	OK	3.80385	3.01213	-0.336678	-0.34654	0.49235	0.9998
ENSG00000096060	ENSG00000096060	FKBP5	6:35541361-35696360	OK	4.45034	3.78456	-0.23379	-0.413734	0.4925	0.9998
ENSG00000182368	ENSG00000182368	FAM27A	9:45727106-45728274	OK	2.60173	2.00864	-0.373254	-0.427415	0.49255	0.9998
ENSG00000261771	ENSG00000261771	DYX1C1-CCPG1	15:55495163-55800432	OK	0.671584	0.245003	-1.45477	-0.265622	0.49275	0.9998
ENSG00000116898	ENSG00000116898	MRPS15	1:36921318-36930038	OK	103.819	116.813	0.170128	0.413317	0.4928	0.9998
ENSG00000047365	ENSG00000047365	ARAP2	4:35949842-36275842	OK	1.60357	1.23978	-0.371205	-0.222564	0.4929	0.9998
ENSG00000157020	ENSG00000157020	SEC13	3:10289706-10362862	OK	76.3368	89.8598	0.235297	0.409647	0.49315	0.9998
ENSG00000081870	ENSG00000081870	HSPB11	1:54382246-54411602	OK	27.5098	23.8376	-0.206708	-0.424356	0.4932	0.9998
ENSG00000177150	ENSG00000177150	FAM210A	18:13663345-13764557	OK	44.801	56.6019	0.33732	0.423596	0.4932	0.9998
ENSG00000178971	ENSG00000178971	CTC1	17:8130190-8173809	OK	6.35176	4.72723	-0.426161	-0.262042	0.4932	0.9998
ENSG00000165495	ENSG00000165495	PKNOX2	11:125034582-125303285	OK	4.33144	3.66886	-0.239516	-0.30695	0.4933	0.9998
ENSG00000135870	ENSG00000135870	RC3H1	1:173900351-173991435	OK	3.13508	2.66141	-0.23631	-0.340439	0.49335	0.9998
ENSG00000259030	ENSG00000259030	FPGT-TNNI3K	1:74663895-75010112	OK	0.326987	0.705968	1.11037	0.226467	0.4935	0.9998
ENSG00000162341	ENSG00000162341	TPCN2	11:68816364-68858072	OK	23.3895	26.7134	0.191702	0.3263	0.4936	0.9998
ENSG00000116096	ENSG00000116096	SPR	2:73114488-73119287	OK	45.1925	50.9583	0.173234	0.413733	0.49365	0.9998
ENSG00000159403	ENSG00000159403	C1R	12:7187512-7275097	OK	16.7471	13.5715	-0.303325	-0.415175	0.49365	0.9998
ENSG00000178035	ENSG00000178035	IMPDH2	3:49061757-49067139	OK	172.512	192.902	0.161175	0.386894	0.49365	0.9998
ENSG00000106772	ENSG00000106772	PRUNE2	9:79226291-79521003	OK	5.07908	4.27932	-0.247185	-0.288991	0.49375	0.9998
ENSG00000144645	ENSG00000144645	OSBPL10	3:31699381-32119072	OK	4.96114	6.20784	0.323418	0.343396	0.49375	0.9998
ENSG00000132386	ENSG00000132386	SERPINF1	17:1665252-1680868	OK	23.9539	27.9252	0.221305	0.385727	0.4938	0.9998
ENSG00000185298	ENSG00000185298	CCDC137	17:79632065-79640934	OK	16.1675	19.896	0.299382	0.312399	0.4939	0.9998
ENSG00000213066	ENSG00000213066	FGFR1OP	6:167412669-167553184	OK	8.09447	6.73082	-0.266154	-0.390334	0.49395	0.9998
ENSG00000125505	ENSG00000125505	MBOAT7	19:54677106-54693733	OK	23.9749	28.0235	0.225111	0.390245	0.494	0.9998
ENSG00000180537	ENSG00000180537	RNF182	6:13924676-13980533	OK	9.26166	10.8426	0.22737	0.373078	0.49405	0.9998
ENSG00000167264	ENSG00000167264	DUS2	16:68021296-68272005	OK	3.47417	2.52579	-0.459936	-0.284973	0.49415	0.9998
ENSG00000166167	ENSG00000166167	BTRC	10:103113819-103317078	OK	9.79785	11.9152	0.282269	0.356051	0.4948	0.9998
ENSG00000174137	ENSG00000174137	FAM53A	4:1619641-1686029	OK	1.02568	0.720841	-0.508828	-0.382364	0.4948	0.9998
ENSG00000125388	ENSG00000125388	GRK4	4:2965334-3042474	OK	2.0882	2.5577	0.292586	0.36383	0.4949	0.9998
ENSG00000133059	ENSG00000133059	DSTYK	1:205111631-205180727	OK	41.0417	46.1386	0.168882	0.417524	0.4949	0.9998
ENSG00000119522	ENSG00000119522	DENND1A	9:126118448-126692431	OK	8.9969	10.4615	0.21759	0.357059	0.495	0.9998
ENSG00000111581	ENSG00000111581	NUP107	12:69068150-69136785	OK	31.5144	26.5989	-0.244644	-0.389513	0.4951	0.9998
ENSG00000197296	ENSG00000197296	FITM2	20:42931477-42939809	OK	12.24	10.8051	-0.179895	-0.419703	0.4951	0.9998
ENSG00000226287	ENSG00000226287	TMEM191A	22:21055219-21058894	OK	2.52245	3.21182	0.348562	0.373683	0.49515	0.9998
ENSG00000255458	ENSG00000255458	RP11-539G18.2	4:39654823-39668264	OK	0.655781	0.365705	-0.842532	-0.481324	0.49515	0.9998
ENSG00000135365	ENSG00000135365	PHF21A	11:45950870-46142985	OK	12.1689	10.5975	-0.199466	-0.272671	0.4954	0.9998
ENSG00000122417	ENSG00000122417	ODF2L	1:86814343-86862023	OK	12.5503	10.6694	-0.23424	-0.334833	0.49545	0.9998
ENSG00000252464	ENSG00000252464	RN7SKP70	5:178029664-178057616	OK	0.998935	0.329228	-1.6013	-0.268511	0.49545	0.9998
ENSG00000131941	ENSG00000131941	RHPN2	19:33469498-33555794	OK	7.90501	9.08147	0.200158	0.352788	0.4955	0.9998
ENSG00000153975	ENSG00000153975	ZUFSP	6:116956780-116989957	OK	4.355	3.64683	-0.256028	-0.416319	0.49555	0.9998
ENSG00000169045	ENSG00000169045	HNRNPH1	5:179041178-179061785	OK	249.524	219.126	-0.187415	-0.293606	0.49565	0.9998
ENSG00000196476	ENSG00000196476	C20orf96	20:251503-271390	OK	2.29939	1.86812	-0.299667	-0.418833	0.49565	0.9998
ENSG00000100316	ENSG00000100316	RPL3	22:39708886-39716394	OK	1235.43	1416.73	0.197556	0.411133	0.4957	0.9998
ENSG00000116106	ENSG00000116106	EPHA4	2:222282746-222439174	OK	10.2755	11.8634	0.207313	0.305836	0.4958	0.9998
ENSG00000169857	ENSG00000169857	AVEN	15:34158427-34357291	OK	4.85599	5.70615	0.232751	0.376805	0.49585	0.9998
ENSG00000187266	ENSG00000187266	EPOR	19:11488235-11530018	OK	11.3702	9.43998	-0.268403	-0.411286	0.4961	0.9998
ENSG00000153406	ENSG00000153406	NMRAL1	16:4511680-4560348	OK	30.7046	37.4995	0.288418	0.375276	0.49615	0.9998
ENSG00000156599	ENSG00000156599	ZDHHC5	11:57435218-57468659	OK	32.1704	28.544	-0.172545	-0.34712	0.49615	0.9998
ENSG00000187650	ENSG00000187650	VMAC	19:5904851-5915888	OK	1.40978	1.84373	0.387156	0.399704	0.49615	0.9998
ENSG00000095066	ENSG00000095066	HOOK2	19:12873816-12985765	OK	7.03253	5.38388	-0.3854	-0.20089	0.4963	0.9998
ENSG00000166263	ENSG00000166263	STXBP4	17:52976747-53241646	OK	5.48055	3.77849	-0.536511	-0.256323	0.49635	0.9998
ENSG00000138496	ENSG00000138496	PARP9	3:122246770-122294050	OK	4.10758	5.11072	0.315237	0.412122	0.4964	0.9998
ENSG00000140740	ENSG00000140740	UQCRC2	16:21963980-21994981	OK	160.281	140.985	-0.185059	-0.34045	0.49645	0.9998
ENSG00000164331	ENSG00000164331	ANKRA2	5:72848159-72877794	OK	13.3627	10.6468	-0.327791	-0.336106	0.4966	0.9998
ENSG00000270820	ENSG00000270820	RP11-355B11.2	2:61698322-61765761	OK	1.05267	0.591821	-0.830821	-0.0608168	0.4966	0.9998
ENSG00000154240	ENSG00000154240	CEP112	17:63524680-64188202	OK	6.3973	4.84364	-0.40137	-0.280169	0.49665	0.9998
ENSG00000163611	ENSG00000163611	SPICE1	3:113161564-113234034	OK	10.2626	8.42052	-0.285409	-0.338501	0.49675	0.9998
ENSG00000198756	ENSG00000198756	COLGALT2	1:183898795-184006863	OK	13.5039	11.8037	-0.194141	-0.415081	0.49675	0.9998
ENSG00000158092	ENSG00000158092	NCK1	3:136581049-136729927	OK	16.7132	19.9986	0.25891	0.370188	0.4968	0.9998
ENSG00000143793	ENSG00000143793	C1orf35	1:228288426-228293112	OK	15.6988	13.6163	-0.205322	-0.398026	0.49705	0.9998
ENSG00000187079	ENSG00000187079	TEAD1	11:12695968-12966298	OK	29.7327	34.5988	0.218673	0.25132	0.49705	0.9998
ENSG00000127666	ENSG00000127666	TICAM1	19:4815943-4831716	OK	4.73207	5.48652	0.213421	0.412381	0.4971	0.9998
ENSG00000228285	ENSG00000228285	LYPLA2P1	6:33333324-33334020	OK	1.87515	2.40142	0.35688	0.416157	0.4971	0.9998
ENSG00000180773	ENSG00000180773	SLC36A4	11:92877340-92931130	OK	7.00143	5.56857	-0.330344	-0.399185	0.49715	0.9998
ENSG00000165029	ENSG00000165029	ABCA1	9:107543282-107691173	OK	13.9372	15.6171	0.164187	0.335987	0.4972	0.9998
ENSG00000160714	ENSG00000160714	UBE2Q1	1:154521052-154531504	OK	108.069	125.916	0.220503	0.291379	0.49725	0.9998
ENSG00000259248	ENSG00000259248	USP3-AS1	15:63796792-63894627	OK	0.879606	0.606087	-0.537334	-0.141124	0.49735	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000111328	ENSG00000111328	CDK2AP1	12:123636866-123756881	OK	178.763	205.234	0.199223	0.416935	0.49745	0.9998
ENSG00000142459	ENSG00000142459	EVI5L	19:7895118-7929862	OK	8.1925	7.15218	-0.19592	-0.367373	0.4976	0.9998
ENSG00000169972	ENSG00000169972	PUSL1	1:1227755-1260071	OK	13.6463	18.3185	0.424792	0.369826	0.4976	0.9998
ENSG00000213983	ENSG00000213983	AP1G2	14:23980968-24048009	OK	15.5659	18.5534	0.253292	0.298163	0.49765	0.9998
ENSG00000183597	ENSG00000183597	TANGO2	22:20004536-20058066	OK	110.008	95.9948	-0.196578	-0.374458	0.4978	0.9998
ENSG00000259969	ENSG00000259969	RP11-999E24.3	14:58460262-58461243	OK	0.734957	0.540938	-0.442196	-0.416963	0.4978	0.9998
ENSG00000105048	ENSG00000105048	TNNT1	19:55644161-55660722	OK	17.7575	20.5032	0.207419	0.391212	0.49785	0.9998
ENSG00000104490	ENSG00000104490	NCALD	8:102698770-103137135	OK	15.0869	13.1758	-0.195403	-0.265192	0.4979	0.9998
ENSG00000110717	ENSG00000110717	NDUFS8	11:67798083-67804111	OK	102.574	115.497	0.171197	0.401724	0.498	0.9998
ENSG00000075426	ENSG00000075426	FOSL2	2:28607275-28640179	OK	5.15513	6.70144	0.378464	0.424465	0.49805	0.9998
ENSG00000106004	ENSG00000106004	HOXA5	7:27145802-27197555	OK	1.53769	2.27185	0.563108	0.305021	0.49825	0.9998
ENSG00000183087	ENSG00000183087	GAS6	13:114518602-114567046	OK	3.23916	3.90923	0.271265	0.386247	0.49825	0.9998
ENSG00000225892	ENSG00000225892	RP11-384K6.2	4:119512927-119555914	OK	2.50382	1.94205	-0.366548	-0.407106	0.49835	0.9998
ENSG00000143379	ENSG00000143379	SETDB1	1:150898738-150948010	OK	27.8759	34.9782	0.32744	0.229777	0.4986	0.9998
ENSG00000197442	ENSG00000197442	MAP3K5	6:136878184-137113656	OK	1.2848	1.06308	-0.273295	-0.350844	0.4986	0.9998
ENSG00000110906	ENSG00000110906	KCTD10	12:109785707-109974507	OK	26.2311	31.83	0.279108	0.301415	0.49885	0.9998
ENSG00000166348	ENSG00000166348	USP54	10:75196185-75385711	OK	16.7688	13.7019	-0.291406	-0.270356	0.49885	0.9998
ENSG00000268621	ENSG00000268621	AC006262.5	19:46604379-46706340	OK	0.805095	1.19194	0.566079	0.376602	0.4989	0.9998
ENSG00000168264	ENSG00000168264	IRF2BP2	1:234740014-234745271	OK	46.5462	57.145	0.295964	0.414711	0.49895	0.9998
ENSG00000242539	ENSG00000242539	AC007620.3	3:179113876-179116979	OK	10.7996	8.77043	-0.300253	-0.396035	0.49895	0.9998
ENSG00000103740	ENSG00000103740	ACSBG1	15:78370149-78538030	OK	0.954211	1.31043	0.457663	0.0903955	0.499	0.9998
ENSG00000171608	ENSG00000171608	PIK3CD	1:9711789-9884584	OK	23.1078	18.3616	-0.331688	-0.277779	0.499	0.9998
ENSG00000176834	ENSG00000176834	VSIG10	12:118501397-118583389	OK	5.24823	7.51736	0.518396	0.0843543	0.4991	0.9998
ENSG00000089775	ENSG00000089775	ZBTB25	14:64854748-65009955	OK	8.37895	5.38877	-0.636814	-0.32137	0.4995	0.9998
ENSG00000116679	ENSG00000116679	IVNS1ABP	1:185265519-185286461	OK	317.534	366.635	0.207432	0.356252	0.49975	0.9998
ENSG00000115548	ENSG00000115548	KDM3A	2:86667769-86719839	OK	32.0916	36.2437	0.175537	0.320884	0.49985	0.9998
ENSG00000165895	ENSG00000165895	ARHGAP42	11:100554892-100862668	OK	3.99263	3.36335	-0.247439	-0.28703	0.49985	0.9998
ENSG00000236493	ENSG00000236493	EIF2S2P3	10:94428501-94429500	OK	0.780335	1.01768	0.383115	0.398615	0.4999	0.9998
ENSG00000105559	ENSG00000105559	PLEKHA4	19:49340353-49371889	OK	5.52405	4.68134	-0.238807	-0.342037	0.49995	0.9998
ENSG00000120699	ENSG00000120699	EXOSC8	13:37523911-37633850	OK	27.6083	21.5946	-0.354433	-0.369365	0.49995	0.9998
ENSG00000075975	ENSG00000075975	MKRN2	3:12525930-12705725	OK	16.4907	21.1581	0.359561	0.413693	0.5	0.9998
ENSG00000198952	ENSG00000198952	SMG5	1:156219014-156252620	OK	47.6547	54.3881	0.190674	0.348409	0.5	0.9998
ENSG00000177640	ENSG00000177640	CASC2	10:119764426-119969663	OK	0.416889	0.715028	0.778338	0.223467	0.5001	0.9998
ENSG00000202058	ENSG00000202058	RN7SKP80	22:42949622-42978044	OK	0.896751	0.288511	-1.63608	-0.28371	0.5001	0.9998
ENSG00000186162	ENSG00000186162	CIDECP	3:10055931-10068049	OK	19.0043	16.3929	-0.213248	-0.414455	0.5002	0.9998
ENSG00000267082	ENSG00000267082	CTC-510F12.2	19:11309970-11373157	OK	0.638819	0.201995	-1.66109	-0.290288	0.5004	0.9998
ENSG00000253895	ENSG00000253895	IGHVII-44-2	14:106938444-106977000	OK	0.0641714	1.72338	4.74717	0.265563	0.50045	0.9998
ENSG00000154917	ENSG00000154917	RAB6B	3:133502876-133614680	OK	38.3829	47.8596	0.318344	0.396248	0.5011	0.9998
ENSG00000163867	ENSG00000163867	ZMYM6	1:35439956-35497569	OK	5.43525	6.49556	0.257108	0.374064	0.5011	0.9998
ENSG00000166164	ENSG00000166164	BRD7	16:50280047-50405391	OK	20.0374	17.1812	-0.221866	-0.353813	0.5011	0.9998
ENSG00000100418	ENSG00000100418	DESI1	22:41994031-42017100	OK	18.599	21.7426	0.225304	0.29304	0.50115	0.9998
ENSG00000137807	ENSG00000137807	KIF23	15:69591285-69740764	OK	46.5041	41.3686	-0.168821	-0.357263	0.50135	0.9998
ENSG00000008441	ENSG00000008441	NFIX	19:13106421-13209610	OK	15.7395	13.5964	-0.211167	-0.390524	0.50145	0.9998
ENSG00000147533	ENSG00000147533	GOLGA7	8:41347914-41368499	OK	37.3579	32.6732	-0.193306	-0.396488	0.50145	0.9998
ENSG00000173145	ENSG00000173145	NOC3L	10:95753745-96122716	OK	11.7021	10.1792	-0.201139	-0.360722	0.5015	0.9998
ENSG00000269246	ENSG00000269246	CTC-246B18.10	19:39818992-39833012	OK	4.99126	2.57895	-0.95262	-0.581468	0.5015	0.9998
ENSG00000081014	ENSG00000081014	AP4E1	15:51200868-51298097	OK	2.41397	2.09557	-0.204064	-0.382755	0.5016	0.9998
ENSG00000185761	ENSG00000185761	ADAMTSL5	19:1505016-1513603	OK	1.47706	1.90515	0.367174	0.335306	0.50165	0.9998
ENSG00000141219	ENSG00000141219	C17orf80	17:71161115-71258491	OK	13.6754	10.7244	-0.350686	-0.40997	0.5017	0.9998
ENSG00000166398	ENSG00000166398	KIAA0355	19:34745441-34850317	OK	6.57458	5.79856	-0.181203	-0.338404	0.50175	0.9998
ENSG00000177951	ENSG00000177951	BET1L	11:127114-207428	OK	16.612	14.6562	-0.180717	-0.364474	0.5018	0.9998
ENSG00000185728	ENSG00000185728	YTHDF3	8:64081111-64125346	OK	17.4318	19.8286	0.185858	0.320633	0.5018	0.9998
ENSG00000055208	ENSG00000055208	TAB2	6:149539061-149732749	OK	10.7908	9.49539	-0.184498	-0.390409	0.5019	0.9998
ENSG00000115271	ENSG00000115271	GCA	2:163175349-163695240	OK	7.78569	9.68878	0.31549	0.385792	0.5019	0.9998
ENSG00000134146	ENSG00000134146	DPH6	15:35473999-35838394	OK	10.7361	8.02812	-0.419331	-0.414433	0.5019	0.9998
ENSG00000111087	ENSG00000111087	GLI1	12:57853917-57914300	OK	1.13381	0.618796	-0.873648	-0.0755885	0.50195	0.9998
ENSG00000257921	ENSG00000257921	RP11-571M6.15	12:58156116-58212487	OK	1.23964	0.578206	-1.10027	-0.129178	0.50195	0.9998
ENSG00000128915	ENSG00000128915	NARG2	15:60711807-60771359	OK	16.3687	12.7417	-0.361389	-0.415676	0.502	0.9998
ENSG00000230195	ENSG00000230195	AC118138.2	7:74765875-74789332	OK	1.07864	0.826092	-0.384835	-0.393208	0.502	0.9998
ENSG00000109762	ENSG00000109762	SNX25	4:186080818-186317053	OK	5.18607	6.37193	0.297089	0.37745	0.5021	0.9998
ENSG00000158406	ENSG00000158406	HIST1H4H	6:26281282-26285762	OK	4.36636	3.35542	-0.379936	-0.396968	0.5021	0.9998
ENSG00000170100	ENSG00000170100	ZNF778	16:89284117-89295363	OK	4.00064	4.89165	0.290093	0.272536	0.5021	0.9998
ENSG00000002016	ENSG00000002016	RAD52	12:1021242-1605099	OK	7.40516	5.45656	-0.44054	-0.226411	0.50215	0.9998
ENSG00000228262	ENSG00000228262	AC073218.2	2:34902645-34963298	OK	2.18613	1.72584	-0.341076	-0.40206	0.50215	0.9998
ENSG00000050426	ENSG00000050426	LETMD1	12:51441744-51454207	OK	38.5323	33.7564	-0.19091	-0.369684	0.50225	0.9998
ENSG00000112079	ENSG00000112079	STK38	6:36461668-36515247	OK	9.72922	8.54706	-0.186896	-0.403376	0.5023	0.9998
ENSG00000186716	ENSG00000186716	BCR	22:23521890-23660224	OK	7.0757	8.4237	0.251581	0.28948	0.5024	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000111641	ENSG00000111641	NOP2	12:6666028-6677857	OK	33.6701	38.2385	0.183558	0.348886	0.50245	0.9998
ENSG00000117450	ENSG00000117450	PRDX1	1:45959537-45988719	OK	348.22	310.679	-0.164575	-0.402177	0.5025	0.9998
ENSG00000121774	ENSG00000121774	KHDRBS1	1:32479429-32568467	OK	55.848	49.5771	-0.171833	-0.415196	0.50255	0.9998
ENSG00000213977	ENSG00000213977	TAX1BP3	17:3566195-3599698	OK	36.1386	41.9917	0.216566	0.406751	0.50255	0.9998
ENSG00000149489	ENSG00000149489	ROM1	11:62369689-62382592	OK	0.787523	1.38707	0.816651	0.209512	0.50275	0.9998
ENSG00000078124	ENSG00000078124	ACER3	11:76571910-76737841	OK	11.8389	14.1008	0.252242	0.319786	0.5029	0.9998
ENSG00000227344	ENSG00000227344	HAUS6P1	7:53255080-53256631	OK	1.90218	1.56392	-0.282485	-0.397277	0.5029	0.9998
ENSG00000106144	ENSG00000106144	CASP2	7:142985307-143004789	OK	15.7471	13.7865	-0.191826	-0.392032	0.50295	0.9998
ENSG00000002330	ENSG00000002330	BAD	11:64037301-64056972	OK	55.3819	47.6605	-0.216621	-0.387843	0.50305	0.9998
ENSG00000150967	ENSG00000150967	ABCB9	12:123405497-123467456	OK	5.95228	8.02634	0.431301	0.240938	0.5031	0.9998
ENSG00000173894	ENSG00000173894	CBX2	17:77751930-77761782	OK	6.12818	7.34809	0.26191	0.351553	0.5032	0.9998
ENSG00000144843	ENSG00000144843	ADPRH	3:119298058-119308792	OK	3.76118	4.39459	0.224545	0.380766	0.50325	0.9998
ENSG00000151292	ENSG00000151292	CSNK1G3	5:122847792-122952739	OK	6.47924	7.68776	0.246739	0.3988	0.5033	0.9998
ENSG00000167912	ENSG00000167912	RP11-25K19.1	8:59717976-60033905	OK	1.24912	0.87059	-0.520848	-0.404973	0.50335	0.9998
ENSG00000166272	ENSG00000166272	WBP1L	10:104503726-104576021	OK	14.9582	13.2933	-0.170235	-0.405803	0.5034	0.9998
ENSG00000254827	ENSG00000254827	SLC22A18AS	11:2909009-2946476	OK	1.95895	3.97984	1.02263	0.468718	0.5034	0.9998
ENSG00000123908	ENSG00000123908	AGO2	8:141541263-141645718	OK	9.4522	11.0409	0.224135	0.2622	0.5037	0.9998
ENSG00000273018	ENSG00000273018	CTD-2303H24.2	17:18414534-18528930	OK	4.86208	3.47434	-0.484835	-0.390839	0.5037	0.9998
ENSG00000101353	ENSG00000101353	MROH8	20:35729628-35870022	OK	1.37229	0.869664	-0.65805	-0.0542117	0.50375	0.9998
ENSG00000144711	ENSG00000144711	IQSEC1	3:12938718-13114617	OK	6.60861	7.51669	0.185749	0.402661	0.50375	0.9998
ENSG00000154328	ENSG00000154328	NEIL2	8:11627147-11644855	OK	16.2679	18.5709	0.191016	0.414333	0.50375	0.9998
ENSG00000164916	ENSG00000164916	FOXK1	7:4683387-4811074	OK	7.09131	8.24339	0.217186	0.284662	0.5038	0.9998
ENSG00000114857	ENSG00000114857	NKTR	3:42589460-42709072	OK	16.4963	13.8377	-0.253546	-0.211499	0.50385	0.9998
ENSG00000182890	ENSG00000182890	GLUD2	X:120181461-120183794	OK	6.70435	5.80357	-0.208157	-0.407584	0.50385	0.9998
ENSG00000026508	ENSG00000026508	CD44	11:35160416-35253949	OK	489.463	583.274	0.252974	0.388128	0.5039	0.9998
ENSG00000116525	ENSG00000116525	TRIM62	1:33611002-33647660	OK	3.36244	3.95546	0.234334	0.375612	0.5039	0.9998
ENSG00000160570	ENSG00000160570	DEDD2	19:42702749-42724292	OK	11.6019	13.3566	0.203183	0.383302	0.504	0.9998
ENSG00000229543	ENSG00000229543	RP11-90J7.2	10:80008504-80115857	OK	1.59531	1.04558	-0.609537	-0.47006	0.50405	0.9998
ENSG00000243339	ENSG00000243339	RN7SL738P	3:196074532-196160242	OK	0.816853	2.32376	1.50832	0.217919	0.50415	0.9998
ENSG00000148120	ENSG00000148120	C9orf3	9:97488982-97849441	OK	15.1614	12.6991	-0.255678	-0.388867	0.50435	0.9998
ENSG00000120832	ENSG00000120832	MTERFD3	12:107349496-107380944	OK	9.14447	6.27177	-0.544028	-0.348922	0.50455	0.9998
ENSG00000134262	ENSG00000134262	AP4B1	1:114304453-114456708	OK	4.61727	3.61901	-0.351446	-0.295378	0.50455	0.9998
ENSG00000137871	ENSG00000137871	ZNF280D	15:56922378-57210769	OK	9.32782	11.7417	0.332034	0.384759	0.50455	0.9998
ENSG00000051596	ENSG00000051596	THOC3	5:175333941-175461683	OK	15.8276	18.0994	0.193503	0.383606	0.5046	0.9998
ENSG00000065970	ENSG00000065970	FOXJ2	12:8185298-8208099	OK	4.43807	3.88986	-0.190214	-0.358954	0.5047	0.9998
ENSG00000100239	ENSG00000100239	PPP6R2	22:50781732-50913454	OK	25.9677	19.612	-0.404983	-0.39621	0.50495	0.9998
ENSG00000164002	ENSG00000164002	EXO5	1:40974412-40982846	OK	1.71246	2.13424	0.317647	0.344411	0.50515	0.9998
ENSG00000049656	ENSG00000049656	CLPTM1L	5:1317858-1345214	OK	163.635	141.674	-0.207909	-0.36155	0.50525	0.9998
ENSG00000198513	ENSG00000198513	ATL1	14:50885218-51135049	OK	1.9882	2.67072	0.425769	0.219953	0.50545	0.9998
ENSG00000159110	ENSG00000159110	IFNAR2	21:34602205-34669539	OK	7.05054	5.5417	-0.347404	-0.398058	0.50585	0.9998
ENSG00000244627	ENSG00000244627	RP3-449O17.1	22:38686696-38794934	OK	2.97973	2.14344	-0.475255	-0.124126	0.5059	0.9998
ENSG00000242349	ENSG00000242349	NPPA-AS1	1:11821843-11908402	OK	2.70683	1.33048	-1.02466	-0.359093	0.50595	0.9998
ENSG00000183444	ENSG00000183444	OR7E38P	7:97595401-97596386	OK	8.80595	10.3541	0.233648	0.412152	0.5061	0.9998
ENSG00000104381	ENSG00000104381	GDAP1	8:75146934-75401107	OK	19.552	16.9231	-0.20832	-0.392359	0.50615	0.9998
ENSG00000168795	ENSG00000168795	ZBTB5	9:37438110-37465396	OK	6.97081	6.13165	-0.185049	-0.40226	0.50625	0.9998
ENSG00000173848	ENSG00000173848	NET1	10:5454513-5500426	OK	4.94464	5.66695	0.196705	0.378716	0.5063	0.9998
ENSG00000227372	ENSG00000227372	TP73-AS1	1:3547330-3663900	OK	0.54286	0.875934	0.690243	0.214656	0.5063	0.9998
ENSG00000164117	ENSG00000164117	FBXO8	4:175157808-175254531	OK	11.6237	9.46731	-0.29604	-0.415958	0.5064	0.9998
ENSG00000184675	ENSG00000184675	AMER1	X:63404996-63425624	OK	0.878686	1.02924	0.228156	0.386382	0.5064	0.9998
ENSG00000100473	ENSG00000100473	COCH	14:31343719-31562818	OK	2.73719	3.86336	0.497162	0.355157	0.5066	0.9998
ENSG00000124074	ENSG00000124074	ENKD1	16:67696847-67702661	OK	3.8035	3.08415	-0.302458	-0.35904	0.5066	0.9998
ENSG00000058673	ENSG00000058673	ZC3H11A	1:203764781-203823252	OK	60.6961	52.8201	-0.200518	-0.347217	0.5067	0.9998
ENSG00000127952	ENSG00000127952	STYXL1	7:75625655-75677322	OK	28.6055	24.5942	-0.217972	-0.420389	0.50675	0.9998
ENSG00000019582	ENSG00000019582	CD74	5:149781199-149792492	OK	4.59807	5.43717	0.241826	0.370944	0.5069	0.9998
ENSG00000116151	ENSG00000116151	MORN1	1:2252691-2323146	OK	6.33056	5.04705	-0.326893	-0.396097	0.50695	0.9998
ENSG00000072694	ENSG00000072694	FCGR2B	1:161475219-161648444	OK	0.547062	0.896388	0.71242	0.408174	0.5071	0.9998
ENSG00000258230	ENSG00000258230	RP11-511H9.3	12:102139274-102224716	OK	0.981732	0.406372	-1.27253	-0.060361	0.5071	0.9998
ENSG00000174775	ENSG00000174775	HRAS	11:532241-537287	OK	49.4989	56.3707	0.18755	0.40376	0.50715	0.9998
ENSG00000188820	ENSG00000188820	FAM26F	6:116781901-116784934	OK	2.84313	3.62662	0.351143	0.394137	0.5074	0.9998
ENSG00000163156	ENSG00000163156	SCNM1	1:151129104-151167797	OK	35.8033	45.8479	0.356765	0.393934	0.50755	0.9998
ENSG00000161381	ENSG00000161381	PLXDC1	17:37213271-37310647	OK	0.731562	0.494752	-0.564275	-0.206299	0.50775	0.9998
ENSG00000167978	ENSG00000167978	SRRM2	16:2787076-2827298	OK	79.0185	90.2892	0.192364	0.19482	0.50775	0.9998
ENSG00000238009	ENSG00000238009	RP11-34P13.7	1:89294-134836	OK	0.652647	0.509958	-0.355925	-0.284245	0.508	0.9998
ENSG00000205609	ENSG00000205609	EIF3CL	16:28390899-28415200	OK	3.76956	4.34723	0.205699	0.392064	0.50805	0.9998
ENSG00000143353	ENSG00000143353	LYPLAL1	1:219259943-219386207	OK	21.8832	17.6586	-0.309447	-0.381138	0.50815	0.9998
ENSG00000144306	ENSG00000144306	SCRN3	2:175260457-175294303	OK	15.5715	18.4402	0.243946	0.393505	0.50815	0.9998
ENSG00000196715	ENSG00000196715	VKORC1L1	7:65338253-65424550	OK	14.2055	16.4922	0.215331	0.393585	0.50815	0.9998
ENSG00000123607	ENSG00000123607	TTC21B	2:166713984-166810353	OK	7.28741	6.33563	-0.201918	-0.284142	0.50825	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000224080	ENSG00000224080	UBE2FP1	3:37034822-37225180	OK	0.800314	0.233517	-1.77704	-0.149015	0.5085	0.9998
ENSG00000128309	ENSG00000128309	MPST	22:37406899-37425863	OK	15.0344	17.6288	0.229665	0.411549	0.50885	0.9998
ENSG00000133935	ENSG00000133935	C14orf1	14:76041230-76550928	OK	24.0554	20.5383	-0.228044	-0.401928	0.50885	0.9998
ENSG00000165502	ENSG00000165502	RPL36AL	14:50085236-50087403	OK	198.075	176.903	-0.163091	-0.40466	0.50895	0.9998
ENSG00000114861	ENSG00000114861	FOXP1	3:71003843-71633140	OK	3.4675	4.16731	0.265223	0.329512	0.509	0.9998
ENSG00000197701	ENSG00000197701	ZNF595	4:53178-88099	OK	1.32887	0.906075	-0.552492	-0.378267	0.50915	0.9998
ENSG00000113360	ENSG00000113360	DROSHA	5:31400603-31532303	OK	43.3891	37.9793	-0.19212	-0.263377	0.50925	0.9998
ENSG00000254667	ENSG00000254667	AP000783.1	11:123301057-123306427	OK	1.12543	1.43398	0.349555	0.395174	0.50935	0.9998
ENSG00000155256	ENSG00000155256	ZFYVE27	10:99496877-99520664	OK	20.3365	22.9957	0.17729	0.325968	0.50955	0.9998
ENSG00000136944	ENSG00000136944	LMX1B	9:129376721-129463312	OK	2.8882	3.77633	0.386818	0.423313	0.5096	0.9998
ENSG00000232388	ENSG00000232388	LINC00493	20:18548063-18550207	OK	33.9816	29.2133	-0.218132	-0.405929	0.50965	0.9998
ENSG00000115685	ENSG00000115685	PPP1R7	2:242045513-242123067	OK	56.6923	48.5575	-0.223456	-0.372961	0.5097	0.9998
ENSG00000056972	ENSG00000056972	TRAF3IP2	6:111620233-111927481	OK	20.6558	26.8937	0.380721	0.398039	0.5098	0.9998
ENSG00000077458	ENSG00000077458	FAM76B	11:95502105-95565857	OK	4.71175	3.67267	-0.359433	-0.237187	0.5098	0.9998
ENSG00000177943	ENSG00000177943	MAMDC4	9:139743175-139755249	OK	0.749346	0.494987	-0.598241	-0.119069	0.50985	0.9998
ENSG00000242086	ENSG00000242086	LINC00969	3:195384932-195467994	OK	16.7744	14.4988	-0.210326	-0.334428	0.50985	0.9998
ENSG00000182087	ENSG00000182087	TMEM259	19:999600-1021117	OK	61.6629	69.242	0.167244	0.334405	0.5099	0.9998
ENSG00000092820	ENSG00000092820	EZR	6:159186772-159241625	OK	31.9505	35.9649	0.170752	0.395791	0.51	0.9998
ENSG00000175216	ENSG00000175216	CKAP5	11:46764597-46867847	OK	69.5544	61.1877	-0.1849	-0.30546	0.51	0.9998
ENSG00000177410	ENSG00000177410	ZFAS1	20:47835883-47905797	OK	261.779	322.623	0.301502	0.427947	0.51	0.9998
ENSG00000180346	ENSG00000180346	TIGD2	4:90033967-90036050	OK	2.82061	3.33492	0.241648	0.406016	0.51	0.9998
ENSG00000182378	ENSG00000182378	PLCXD1	X:192988-220023	OK	21.8281	27.1047	0.312353	0.388578	0.5103	0.9998
ENSG00000141655	ENSG00000141655	TNFRSF11A	18:59992519-60058516	OK	1.47574	1.22601	-0.267473	-0.345802	0.51035	0.9998
ENSG00000220205	ENSG00000220205	VAMP2	17:8043789-8066864	OK	13.9451	11.4006	-0.290649	-0.36692	0.51045	0.9998
ENSG00000261752	ENSG00000261752	RP11-244B22.1	16:34442273-34518517	OK	0.742181	0.130171	-2.51136	-0.622739	0.51065	0.9998
ENSG00000205592	ENSG00000205592	MUC19	12:40787196-40964632	OK	2.18123	2.89243	0.407143	0.318818	0.5107	0.9998
ENSG00000127125	ENSG00000127125	PPCS	1:42895999-43120335	OK	40.7344	46.6329	0.1951	0.413301	0.5108	0.9998
ENSG00000128595	ENSG00000128595	CALU	7:128379345-128411861	OK	386.351	437.051	0.177888	0.342147	0.51095	0.9998
ENSG00000125354	ENSG00000125354	6-Sep	X:118749686-118827333	OK	15.7941	13.495	-0.226965	-0.400907	0.51105	0.9998
ENSG00000039560	ENSG00000039560	RAI14	5:34656341-34832732	OK	83.7162	69.1781	-0.275192	-0.187518	0.5112	0.9998
ENSG00000144579	ENSG00000144579	CTDSP1	2:219262978-219270664	OK	16.6506	14.4604	-0.203465	-0.371622	0.51125	0.9998
ENSG00000260565	ENSG00000260565	ERVK13-1	16:2710349-2723445	OK	2.74742	2.16809	-0.341655	-0.296397	0.5113	0.9998
ENSG00000266173	ENSG00000266173	STRADA	17:61780191-61896677	OK	23.7827	18.0355	-0.399067	-0.256386	0.51135	0.9998
ENSG00000183579	ENSG00000183579	ZNRF3	22:29279579-29453475	OK	6.47467	7.74922	0.259246	0.405191	0.51145	0.9998
ENSG00000146540	ENSG00000146540	C7orf50	7:1036621-1177896	OK	89.1882	78.9228	-0.17641	-0.400238	0.5115	0.9998
ENSG00000178429	ENSG00000178429	RPS3AP5	10:86320198-86321019	OK	9.06028	10.6686	0.235741	0.404336	0.5115	0.9998
ENSG00000225573	ENSG00000225573	RPL35P5	7:66071724-66072094	OK	1.33836	1.85546	0.471316	0.356781	0.5116	0.9998
ENSG00000140521	ENSG00000140521	POLG	15:89787179-89878092	OK	27.0553	32.0776	0.245656	0.204495	0.51165	0.9998
ENSG00000136827	ENSG00000136827	TOR1A	9:132575222-132586413	OK	23.9207	27.1271	0.181479	0.402691	0.5119	0.9998
ENSG00000038382	ENSG00000038382	TRIO	5:14143810-14532235	OK	34.6979	38.8732	0.163929	0.19963	0.51195	0.9998
ENSG00000108786	ENSG00000108786	HSD17B1	17:40688189-40718295	OK	0.477434	0.930267	0.962345	0.208578	0.51195	0.9998
ENSG00000132842	ENSG00000132842	AP3B1	5:77296348-77590579	OK	25.0756	22.3933	-0.163218	-0.320866	0.512	0.9998
ENSG00000166451	ENSG00000166451	CENPN	16:81009697-81069364	OK	48.369	37.919	-0.351162	-0.382912	0.5121	0.9998
ENSG00000130559	ENSG00000130559	CAMSAP1	9:138700332-138799074	OK	9.35722	8.34608	-0.164981	-0.305619	0.5122	0.9998
ENSG00000112576	ENSG00000112576	CCND3	6:41902670-42018095	OK	39.5194	35.3377	-0.161354	-0.365107	0.51225	0.9998
ENSG00000068308	ENSG00000068308	OTUD5	X:48779304-48815648	OK	23.4216	26.4153	0.173537	0.373697	0.5124	0.9998
ENSG00000163320	ENSG00000163320	CGGBP1	3:88101093-88217879	OK	65.1352	55.9082	-0.220379	-0.351175	0.5125	0.9998
ENSG00000216285	ENSG00000216285	RP11-490H24.5	12:104382761-104457961	OK	168.085	147.636	-0.187141	-0.395189	0.51255	0.9998
ENSG00000136943	ENSG00000136943	CTSV	9:99794939-99801925	OK	19.0625	16.6524	-0.195002	-0.397606	0.51265	0.9998
ENSG00000196411	ENSG00000196411	EPHB4	7:100400186-100464631	OK	23.3244	27.6741	0.246696	0.382427	0.51275	0.9998
ENSG00000232160	ENSG00000232160	RAP2C-AS1	X:131337052-131623996	OK	1.65995	0.716567	-1.21197	-0.294638	0.5128	0.9998
ENSG00000198730	ENSG00000198730	CTR9	11:10772533-10801290	OK	23.4036	26.2045	0.163079	0.323602	0.51285	0.9998
ENSG00000175416	ENSG00000175416	CLTB	5:175792470-175843570	OK	44.2285	53.6903	0.279685	0.387124	0.5129	0.9998
ENSG00000156127	ENSG00000156127	BATF	14:75988767-76013358	OK	1.0396	1.337	0.362975	0.352941	0.51295	0.9998
ENSG00000214796	ENSG00000214796	RP11-480I12.5	1:202820955-202830748	OK	8.71693	7.13687	-0.288528	-0.414704	0.51295	0.9998
ENSG00000168259	ENSG00000168259	DNAJC7	17:40118758-40217383	OK	45.3552	56.1472	0.307946	0.352448	0.513	0.9998
ENSG00000142856	ENSG00000142856	ITGB3BP	1:63906440-64125916	OK	26.369	18.3971	-0.519366	-0.347178	0.51335	0.9998
ENSG00000168310	ENSG00000168310	IRF2	4:185308866-185395734	OK	5.35758	6.19174	0.208763	0.30763	0.51335	0.9998
ENSG00000181773	ENSG00000181773	GPR3	1:27719147-27722318	OK	1.14587	1.38809	0.276648	0.395634	0.51335	0.9998
ENSG00000119431	ENSG00000119431	HDHD3	9:116135698-116139279	OK	12.6344	14.6126	0.209861	0.397825	0.5134	0.9998
ENSG00000154127	ENSG00000154127	UBASH3B	11:122526382-122685181	OK	6.52107	7.81111	0.260419	0.340292	0.5135	0.9998
ENSG00000072121	ENSG00000072121	ZFYVE26	14:68168602-68283307	OK	11.0616	9.85104	-0.167215	-0.310963	0.5136	0.9998
ENSG00000160746	ENSG00000160746	ANO10	3:43328003-43775863	OK	24.5846	20.0011	-0.297678	-0.354702	0.5136	0.9998
ENSG00000170144	ENSG00000170144	HNRNPA3	2:177855235-178088686	OK	173.259	145.464	-0.252271	-0.375716	0.5136	0.9998
ENSG00000102043	ENSG00000102043	MTMR8	X:63444075-63615333	OK	1.15251	1.73803	0.592675	0.388556	0.51385	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000143751	ENSG00000143751	SDE2	1:226170402-226187032	OK	9.4078	10.6178	0.174559	0.398355	0.51385	0.9998
ENSG00000074621	ENSG00000074621	SLC24A1	15:65903703-66184329	OK	3.56018	2.50327	-0.508136	-0.167574	0.51395	0.9998
ENSG00000134247	ENSG00000134247	PTGFRN	1:117452678-117532980	OK	14.8869	13.3218	-0.160253	-0.341818	0.51395	0.9998
ENSG00000270504	ENSG00000270504	RP11-420L9.5	6:3722847-3754105	OK	0.996167	1.65387	0.731382	0.404478	0.51395	0.9998
ENSG00000151498	ENSG00000151498	ACAD8	11:134123388-134135749	OK	7.53221	6.45955	-0.221641	-0.36828	0.514	0.9998
ENSG00000174547	ENSG00000174547	MRPL11	11:66202545-66234209	OK	65.1787	73.5914	0.175138	0.397565	0.51405	0.9998
ENSG00000106992	ENSG00000106992	AK1	9:130628758-130667687	OK	70.7697	84.3292	0.2529	0.406596	0.5142	0.9998
ENSG00000225793	ENSG00000225793	RP1-234P15.4	6:75994729-76203454	OK	0.750572	0.511244	-0.553979	-0.372611	0.51425	0.9998
ENSG00000124193	ENSG00000124193	SRSF6	20:42086567-42092245	OK	59.6661	52.6506	-0.180463	-0.398661	0.5144	0.9998
ENSG00000174607	ENSG00000174607	UGT8	4:115519610-115599380	OK	2.02361	2.40672	0.250133	0.34912	0.51445	0.9998
ENSG00000166974	ENSG00000166974	MAPRE2	18:32556891-32723434	OK	14.9297	16.8552	0.175002	0.355751	0.5145	0.9998
ENSG00000008382	ENSG00000008382	MPND	19:4343523-4360083	OK	17.8688	20.4489	0.19458	0.335193	0.51465	0.9998
ENSG00000213397	ENSG00000213397	HAUS7	X:152710177-152775012	OK	15.8876	13.5437	-0.230281	-0.385069	0.51465	0.9998
ENSG00000090932	ENSG00000090932	DLL3	19:39989534-39999121	OK	16.6556	19.0288	0.19218	0.398203	0.51475	0.9998
ENSG00000261221	ENSG00000261221	ZNF865	19:56116770-56128635	OK	3.50973	3.04904	-0.203008	-0.392967	0.51475	0.9998
ENSG00000264070	ENSG00000264070	DND1P1	17:43663236-43664295	OK	1.32618	1.05294	-0.332844	-0.387305	0.51475	0.9998
ENSG00000101850	ENSG00000101850	GPR143	X:9693385-9754337	OK	131.828	148.063	0.16756	0.366492	0.51485	0.9998
ENSG00000138760	ENSG00000138760	SCARB2	4:77079889-77135046	OK	94.7787	83.8781	-0.176268	-0.374074	0.51485	0.9998
ENSG00000242013	ENSG00000242013	USP27X	X:49644469-49647166	OK	1.76287	1.47551	-0.256715	-0.399651	0.5149	0.9998
ENSG00000161021	ENSG00000161021	MAML1	5:179159850-179223648	OK	7.83936	8.922	0.186631	0.260439	0.51495	0.9998
ENSG00000263072	ENSG00000263072	RP11-473M20.14	16:3160460-3192806	OK	3.8887	5.39536	0.472434	0.351596	0.5151	0.9998
ENSG00000119048	ENSG00000119048	UBE2B	5:133706869-133727683	OK	34.8071	29.7482	-0.226583	-0.396499	0.5152	0.9998
ENSG00000258064	ENSG00000258064	RP11-293I14.2	12:72003251-72097836	OK	1.72906	0.347164	-2.3163	-0.34406	0.51525	0.9998
ENSG00000259065	ENSG00000259065	RP5-1021I20.1	14:74181824-74269973	OK	0.300703	0.703621	1.22646	0.194535	0.51525	0.9998
ENSG00000128536	ENSG00000128536	CDHR3	7:105517241-105676877	OK	3.16801	3.8627	0.286031	0.329349	0.5154	0.9998
ENSG00000176399	ENSG00000176399	DMRTA1	9:22446839-22455739	OK	0.827538	0.695786	-0.250181	-0.388812	0.5154	0.9998
ENSG00000187109	ENSG00000187109	NAP1L1	12:76438669-76478813	OK	472.657	539.128	0.189834	0.390143	0.5155	0.9998
ENSG00000245849	ENSG00000245849	RAD51-AS1	15:40978921-41024354	OK	1.44464	0.902034	-0.679452	-0.406794	0.51555	0.9998
ENSG00000142207	ENSG00000142207	URB1	21:33664123-33765335	OK	6.55192	7.75329	0.242892	0.23213	0.51575	0.9998
ENSG00000147180	ENSG00000147180	ZNF711	X:84498996-84528368	OK	3.76912	3.23454	-0.220666	-0.40938	0.51575	0.9998
ENSG00000196177	ENSG00000196177	ACADSB	10:124768494-124817827	OK	15.8106	13.0631	-0.275389	-0.357959	0.5159	0.9998
ENSG00000180354	ENSG00000180354	MTURN	7:30174425-30202378	OK	15.6964	12.8999	-0.283073	-0.401703	0.51595	0.9998
ENSG00000273284	ENSG00000273284	RP11-888D10.4	18:9102627-9285983	OK	1.58248	0.575713	-1.45877	-0.274822	0.51595	0.9998
ENSG00000104312	ENSG00000104312	RIPK2	8:90769974-90803291	OK	11.1114	12.709	0.193817	0.384542	0.516	0.9998
ENSG00000258825	ENSG00000258825	AL133168.3	14:97263640-97411731	OK	0.879167	0.166329	-2.40209	-0.329244	0.51605	0.9998
ENSG00000161217	ENSG00000161217	PCYT1A	3:195938357-196065374	OK	39.2346	34.2419	-0.196363	-0.291861	0.5163	0.9998
ENSG00000104164	ENSG00000104164	BLOC1S6	15:45879320-45983492	OK	19.0844	21.556	0.175697	0.281774	0.5164	0.9998
ENSG00000113119	ENSG00000113119	TMCO6	5:140018324-140042064	OK	6.52582	4.46848	-0.546374	-0.209946	0.5164	0.9998
ENSG00000178188	ENSG00000178188	SH2B1	16:28857920-28885526	OK	17.4776	15.1446	-0.206702	-0.312357	0.5165	0.9998
ENSG00000197102	ENSG00000197102	DYNC1H1	14:102430864-102532565	OK	82.6181	92.6094	0.164702	0.195455	0.5165	0.9998
ENSG00000117318	ENSG00000117318	ID3	1:23884408-23886285	OK	46.5701	53.3183	0.195229	0.393785	0.51665	0.9998
ENSG00000168283	ENSG00000168283	BMI1	10:22604902-22620413	OK	17.2868	20.2417	0.227663	0.25183	0.51665	0.9998
ENSG00000267203	ENSG00000267203	SNRPGP4	17:67143354-67323385	OK	0.90848	2.66448	1.55233	0.274171	0.51675	0.9998
ENSG00000136167	ENSG00000136167	LCP1	13:46700054-46786006	OK	6.44683	7.52448	0.223001	0.354927	0.5168	0.9998
ENSG00000113356	ENSG00000113356	POLR3G	5:89754019-89810370	OK	40.7093	49.5943	0.284816	0.400115	0.517	0.9998
ENSG00000180008	ENSG00000180008	SOCS4	14:55493947-55516206	OK	8.24975	7.18255	-0.199855	-0.236881	0.51705	0.9998
ENSG00000104805	ENSG00000104805	NUCB1	19:49403306-49426629	OK	127.737	112.999	-0.176872	-0.381796	0.5171	0.9998
ENSG00000159788	ENSG00000159788	RGS12	4:3294754-3441640	OK	96.9247	112.838	0.219319	0.207051	0.5173	0.9998
ENSG00000237989	ENSG00000237989	AP001046.5	21:44778026-44782229	OK	1.09984	1.336	0.280629	0.405596	0.51745	0.9998
ENSG00000197563	ENSG00000197563	PIGN	18:59710799-59854351	OK	22.0724	18.9333	-0.221311	-0.284568	0.51755	0.9998
ENSG00000228288	ENSG00000228288	PCAT6	1:202780081-202781284	OK	1.3518	1.7691	0.388131	0.348727	0.51755	0.9998
ENSG00000130770	ENSG00000130770	ATPIF1	1:28562619-28573417	OK	94.956	82.9418	-0.195161	-0.395953	0.5176	0.9998
ENSG00000225439	ENSG00000225439	BOLA3-AS1	2:74375135-74377188	OK	2.80033	2.24223	-0.320663	-0.396128	0.5177	0.9998
ENSG00000145022	ENSG00000145022	TCTA	3:49396577-49453908	OK	15.5939	9.42066	-0.727078	-0.393727	0.5179	0.9998
ENSG00000248049	ENSG00000248049	UBA6-AS1	4:68566997-68995598	OK	5.20944	4.43319	-0.232784	-0.373546	0.5179	0.9998
ENSG00000196632	ENSG00000196632	WNK3	X:54219255-54385075	OK	1.17744	1.37713	0.226011	0.374646	0.5181	0.9998
ENSG00000023041	ENSG00000023041	ZDHHC6	10:114190057-114206672	OK	42.3767	37.6634	-0.170109	-0.306806	0.51815	0.9998
ENSG00000151470	ENSG00000151470	C4orf33	4:129730778-130037795	OK	6.93176	5.21969	-0.409259	-0.335001	0.5183	0.9998
ENSG00000242372	ENSG00000242372	EIF6	20:33703166-33872788	OK	115.275	135.688	0.235211	0.394765	0.5183	0.9998
ENSG00000218510	ENSG00000218510	LINC00339	1:22351680-22357716	OK	6.18834	5.20069	-0.25085	-0.379498	0.51835	0.9998
ENSG00000130347	ENSG00000130347	RTN4IP1	6:107018902-107077373	OK	3.91247	3.33345	-0.231064	-0.349662	0.51845	0.9998
ENSG00000143333	ENSG00000143333	RGS16	1:182567757-182573543	OK	1.4293	1.7065	0.255733	0.39097	0.51855	0.9998
ENSG00000101132	ENSG00000101132	PFDN4	20:52824385-52844591	OK	86.9139	98.2762	0.177257	0.390285	0.5187	0.9998
ENSG00000105447	ENSG00000105447	GRWD1	19:48949029-48985571	OK	18.0759	24.2323	0.422864	0.387013	0.51875	0.9998
ENSG00000136051	ENSG00000136051	KIAA1033	12:105501101-105562912	OK	20.9165	18.5218	-0.175421	-0.247438	0.51875	0.9998
ENSG00000169992	ENSG00000169992	NLGN2	17:7308192-7323179	OK	3.88425	4.55404	0.229514	0.2927	0.51875	0.9998
ENSG00000164414	ENSG00000164414	SLC35A1	6:88117700-88222054	OK	6.77414	5.87442	-0.205591	-0.377761	0.51885	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000120705	ENSG00000120705	ETF1	5:137841783-137878989	OK	81.6112	91.5482	0.165765	0.35186	0.5189	0.9998
ENSG00000105618	ENSG00000105618	PRPF31	19:54606035-54635140	OK	43.7966	35.3682	-0.308364	-0.366756	0.519	0.9998
ENSG00000176978	ENSG00000176978	DPP7	9:140004993-140009629	OK	123.793	139.77	0.175127	0.389871	0.519	0.9998
ENSG00000180015	ENSG00000180015	RP11-756P10.3	4:189659505-189660648	OK	1.59419	1.28346	-0.312786	-0.385438	0.5191	0.9998
ENSG00000165102	ENSG00000165102	HGSNAT	8:42955555-43057998	OK	15.2624	17.1512	0.168329	0.303739	0.5192	0.9998
ENSG00000143753	ENSG00000143753	DEGS1	1:224363457-224381143	OK	63.725	71.1259	0.158516	0.32245	0.5195	0.9998
ENSG00000145945	ENSG00000145945	FAM50B	6:3832166-3855971	OK	6.52833	5.61966	-0.216232	-0.392774	0.5195	0.9998
ENSG00000234456	ENSG00000234456	MAGI2-AS3	7:77646392-79100524	OK	33.6259	27.7136	-0.278977	-0.342377	0.5195	0.9998
ENSG00000253174	ENSG00000253174	RP11-360L9.7	8:41386724-41482520	OK	1.77988	0.765991	-1.21638	-0.103111	0.5197	0.9998
ENSG00000260077	ENSG00000260077	RP11-254F7.2	2:10179218-10180790	OK	1.61323	1.96694	0.285997	0.395161	0.51985	0.9998
ENSG00000139977	ENSG00000139977	NAA30	14:57857261-57882635	OK	8.78176	10.1289	0.205896	0.379153	0.52	0.9998
ENSG00000167074	ENSG00000167074	TEF	22:41763336-41795330	OK	5.71675	5.04076	-0.181555	-0.354475	0.52	0.9998
ENSG00000196700	ENSG00000196700	ZNF512B	20:62588054-62680994	OK	11.2162	14.1407	0.334261	0.40249	0.52005	0.9998
ENSG00000237187	ENSG00000237187	NR2F1-AS1	5:92745064-92930321	OK	6.21009	4.61624	-0.427896	-0.383127	0.5201	0.9998
ENSG00000103494	ENSG00000103494	RPGRIP1L	16:53631594-53737850	OK	2.39444	1.90702	-0.328369	-0.363471	0.5203	0.9998
ENSG00000135617	ENSG00000135617	PRADC1	2:73455133-73460366	OK	35.0286	30.9938	-0.176553	-0.382344	0.52035	0.9998
ENSG00000172239	ENSG00000172239	PAIP1	5:43526368-43557860	OK	122.658	107.547	-0.189665	-0.389962	0.52035	0.9998
ENSG00000146376	ENSG00000146376	ARHGAP18	6:129897276-130031370	OK	5.88233	5.1846	-0.182154	-0.329395	0.5204	0.9998
ENSG00000151474	ENSG00000151474	FRMD4A	10:13628926-14504141	OK	61.0483	72.8666	0.255306	0.380894	0.5204	0.9998
ENSG00000118922	ENSG00000118922	KLF12	13:74260225-74708394	OK	3.83594	3.11951	-0.298258	-0.37323	0.52045	0.9998
ENSG00000117020	ENSG00000117020	AKT3	1:243419319-244014381	OK	44.0009	37.8207	-0.218356	-0.304219	0.5205	0.9998
ENSG00000188763	ENSG00000188763	FZD9	7:72848108-72850450	OK	1.19549	0.978025	-0.289655	-0.400336	0.5205	0.9998
ENSG00000135506	ENSG00000135506	OS9	12:58087737-58115340	OK	136.139	122.372	-0.15381	-0.361448	0.52055	0.9998
ENSG00000129250	ENSG00000129250	KIF1C	17:4901242-4931696	OK	47.3558	57.7977	0.287471	0.375987	0.5206	0.9998
ENSG00000127328	ENSG00000127328	RAB3IP	12:70132460-70748773	OK	7.93455	5.95738	-0.413471	-0.308289	0.52065	0.9998
ENSG00000109606	ENSG00000109606	DHX15	4:24519063-24586173	OK	69.8748	77.7585	0.154229	0.347471	0.5208	0.9998
ENSG00000183723	ENSG00000183723	CMTM4	16:66648652-66730610	OK	8.73941	10.2881	0.235369	0.365451	0.52085	0.9998
ENSG00000228794	ENSG00000228794	LINC01128	1:762987-794826	OK	7.22949	5.71127	-0.340082	-0.367314	0.52085	0.9998
ENSG00000176087	ENSG00000176087	SLC35A4	5:139781398-139973337	OK	37.5633	30.268	-0.311532	-0.35572	0.52105	0.9998
ENSG00000116039	ENSG00000116039	ATP6V1B1	2:71163011-71306935	OK	0.813653	0.518864	-0.649056	-0.0699457	0.5211	0.9998
ENSG00000088812	ENSG00000088812	ATRN	20:3451686-3631769	OK	14.5742	16.4536	0.174987	0.395138	0.52125	0.9998
ENSG00000272734	ENSG00000272734	ADIRF-AS1	10:88695296-88784489	OK	0.866719	1.08335	0.321866	0.356425	0.5213	0.9998
ENSG00000145016	ENSG00000145016	KIAA0226	3:197398263-197514467	OK	14.7572	12.266	-0.266755	-0.192597	0.52135	0.9998
ENSG00000172432	ENSG00000172432	GTPBP2	6:43543886-43596899	OK	48.7808	41.4797	-0.233909	-0.369953	0.5214	0.9998
ENSG00000188483	ENSG00000188483	IER5L	9:131937834-131972827	OK	19.7758	22.1844	0.165811	0.382285	0.5214	0.9998
ENSG00000224023	ENSG00000224023	RP11-383C5.4	10:127371797-127452712	OK	2.64207	1.54487	-0.774181	-0.290339	0.52145	0.9998
ENSG00000132254	ENSG00000132254	ARFIP2	11:6496909-6502666	OK	39.0885	43.887	0.167051	0.380467	0.5215	0.9998
ENSG00000165156	ENSG00000165156	ZHX1	8:124232195-124287781	OK	10.4154	8.78084	-0.24629	-0.312289	0.5216	0.9998
ENSG00000182700	ENSG00000182700	IGIP	5:139505520-139508391	OK	1.39771	1.17224	-0.253798	-0.381953	0.5216	0.9998
ENSG00000119041	ENSG00000119041	GTF3C3	2:197504277-197664449	OK	24.5223	27.9347	0.187966	0.29544	0.52165	0.9998
ENSG00000080007	ENSG00000080007	DDX43	6:74078277-74161999	OK	2.26742	3.16495	0.481132	0.332259	0.5217	0.9998
ENSG00000169554	ENSG00000169554	ZEB2	2:145141647-145282147	OK	23.3044	26.878	0.205824	0.259635	0.5217	0.9998
ENSG00000197056	ENSG00000197056	ZMYM1	1:35525386-35581460	OK	5.27484	4.34228	-0.280675	-0.330639	0.52175	0.9998
ENSG00000163636	ENSG00000163636	PSMD6	3:63989697-64009658	OK	63.584	71.1476	0.162151	0.388961	0.5218	0.9998
ENSG00000183508	ENSG00000183508	FAM46C	1:118148555-118170994	OK	0.944899	1.1093	0.231422	0.383935	0.522	0.9998
ENSG00000185753	ENSG00000185753	CXorf38	X:40488284-40506819	OK	6.49474	7.5314	0.213646	0.363957	0.522	0.9998
ENSG00000198331	ENSG00000198331	HYLS1	11:125753508-125773116	OK	4.97137	4.03303	-0.301781	-0.395182	0.5221	0.9998
ENSG00000032219	ENSG00000032219	ARID4A	14:58765102-58862359	OK	6.0985	5.19615	-0.231011	-0.288948	0.5222	0.9998
ENSG00000121864	ENSG00000121864	ZNF639	3:179040778-179053323	OK	18.3146	20.8475	0.186879	0.377157	0.5222	0.9998
ENSG00000269965	ENSG00000269965	RP11-24B19.4	13:51909908-52126500	OK	0.819228	0.326259	-1.32824	-0.245156	0.5223	0.9998
ENSG00000171865	ENSG00000171865	RNASEH1	2:3579402-3609324	OK	23.6467	26.7895	0.18003	0.380355	0.52265	0.9998
ENSG00000075790	ENSG00000075790	BCAP29	7:107220001-107269943	OK	97.9917	84.0931	-0.220672	-0.385208	0.52275	0.9998
ENSG00000167657	ENSG00000167657	DAPK3	19:3958450-3971121	OK	41.1884	47.3665	0.201628	0.37604	0.5229	0.9998
ENSG00000182872	ENSG00000182872	RBM10	X:47001614-47046212	OK	18.0579	15.0358	-0.264224	-0.373217	0.5229	0.9998
ENSG00000145012	ENSG00000145012	LPP	3:187868993-188608460	OK	15.7435	12.787	-0.300082	-0.219393	0.52305	0.9998
ENSG00000206418	ENSG00000206418	RAB12	18:8609442-8639379	OK	22.3316	25.0376	0.165013	0.350083	0.52325	0.9998
ENSG00000158201	ENSG00000158201	ABHD3	18:19230857-19284766	OK	7.51541	8.62128	0.19805	0.351868	0.5233	0.9998
ENSG00000161791	ENSG00000161791	FMNL3	12:49962000-50158717	OK	5.00342	7.66531	0.615431	0.247391	0.52335	0.9998
ENSG00000166938	ENSG00000166938	DIS3L	15:66570835-66626236	OK	12.7155	11.2116	-0.181596	-0.254474	0.52345	0.9998
ENSG00000184903	ENSG00000184903	IMMP2L	7:110303109-111202573	OK	91.7218	80.9453	-0.180317	-0.393411	0.5235	0.9998
ENSG00000137821	ENSG00000137821	LRRC49	15:71123862-71342414	OK	1.47836	1.85823	0.329938	0.174973	0.5237	0.9998
ENSG00000138463	ENSG00000138463	DIRC2	3:122513641-122599986	OK	17.9689	20.3657	0.180643	0.384579	0.5237	0.9998
ENSG00000080823	ENSG00000080823	MOK	14:102547074-102771537	OK	37.5927	46.7445	0.314342	0.0485284	0.52385	0.9998
ENSG00000112149	ENSG00000112149	CD83	6:14117871-14137149	OK	10.4487	9.18293	-0.186294	-0.389945	0.5239	0.9998
ENSG00000088826	ENSG00000088826	SMOX	20:4101626-4168394	OK	1.5217	1.83651	0.271289	0.271861	0.52405	0.9998
ENSG00000158636	ENSG00000158636	C11orf30	11:76155966-76264069	OK	9.12068	7.67123	-0.249683	-0.309163	0.5241	0.9998
ENSG00000185513	ENSG00000185513	L3MBTL1	20:42136319-42179590	OK	2.53875	3.24021	0.35197	0.327829	0.52415	0.9998
ENSG00000234648	ENSG00000234648	AL162151.3	14:99439650-99439808	OK	61.0548	77.8813	0.351173	0.376045	0.52415	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000243926	ENSG00000243926	TIPARP-AS1	3:156389650-156424559	OK	1.36917	0.632412	-1.11437	-0.123178	0.5242	0.9998
ENSG00000133131	ENSG00000133131	MORC4	X:106045909-106243474	OK	9.51732	8.22559	-0.210437	-0.35551	0.5243	0.9998
ENSG00000139218	ENSG00000139218	SCAF11	12:46312913-46385903	OK	22.1001	19.1178	-0.209136	-0.274269	0.52445	0.9998
ENSG00000101115	ENSG00000101115	SALL4	20:50400580-50419059	OK	7.59855	6.05162	-0.328403	-0.382237	0.5247	0.9998
ENSG00000149091	ENSG00000149091	DGKZ	11:46354454-46402104	OK	36.1088	41.8204	0.211855	0.313213	0.5247	0.9998
ENSG00000101391	ENSG00000101391	CDK5RAP1	20:31946644-31989367	OK	34.2636	30.0528	-0.189177	-0.375153	0.52475	0.9998
ENSG00000103021	ENSG00000103021	CCDC113	16:58265060-58328951	OK	1.29461	0.965835	-0.422674	-0.290884	0.52475	0.9998
ENSG00000113504	ENSG00000113504	SLC12A7	5:1050498-1112150	OK	6.5688	7.53233	0.197467	0.248177	0.52505	0.9998
ENSG00000110711	ENSG00000110711	AIP	11:67250511-67258574	OK	49.4431	55.3245	0.162149	0.377622	0.52515	0.9998
ENSG00000157184	ENSG00000157184	CPT2	1:53662100-53686289	OK	5.60283	4.63866	-0.272446	-0.375081	0.52515	0.9998
ENSG00000204564	ENSG00000204564	C6orf136	6:30614815-30640814	OK	19.3112	14.492	-0.414177	-0.349622	0.52525	0.9998
ENSG00000169062	ENSG00000169062	UPF3A	13:115047058-115071283	OK	20.5529	17.7582	-0.210857	-0.353943	0.5253	0.9998
ENSG00000246985	ENSG00000246985	SOCS2-AS1	12:93936238-93977263	OK	2.49182	3.60079	0.531117	0.370937	0.5254	0.9998
ENSG00000258504	ENSG00000258504	RP11-638I2.6	14:100673743-100772884	OK	0.853714	2.90618	1.7673	0.163023	0.52555	0.9998
ENSG00000083642	ENSG00000083642	PDS5B	13:33160563-33352157	OK	11.2703	9.35865	-0.268158	-0.346005	0.5257	0.9998
ENSG00000168495	ENSG00000168495	POLR3D	8:22102616-22132675	OK	21.4446	18.5942	-0.205765	-0.384486	0.52575	0.9998
ENSG00000134548	ENSG00000134548	C12orf39	12:21679240-21757781	OK	1.75762	1.44523	-0.282322	-0.343583	0.5258	0.9998
ENSG00000174111	ENSG00000174111	SOCS7	17:36508110-36556019	OK	9.81548	12.0908	0.300785	0.387086	0.526	0.9998
ENSG00000181039	ENSG00000181039	ANKRD34A	1:145470507-145475646	OK	1.05797	0.890227	-0.249047	-0.378671	0.5261	0.9998
ENSG00000143919	ENSG00000143919	CAMKMT	2:44589088-44999731	OK	4.92146	6.34453	0.366426	0.407482	0.52615	0.9998
ENSG00000231025	ENSG00000231025	RP11-175O19.4	10:98752206-98755716	OK	1.02562	0.857066	-0.259023	-0.386497	0.52615	0.9998
ENSG00000085998	ENSG00000085998	POMGNT1	1:46654353-46686933	OK	60.8162	54.706	-0.152757	-0.319265	0.52635	0.9998
ENSG00000116675	ENSG00000116675	DNAJC6	1:65713901-65881689	OK	1.43964	1.73464	0.268926	0.298114	0.5264	0.9998
ENSG00000269293	ENSG00000269293	ZSCAN16-AS1	6:28089572-28107456	OK	0.775543	0.507961	-0.61049	-0.375725	0.52645	0.9998
ENSG00000125952	ENSG00000125952	MAX	14:65381078-65569413	OK	28.3933	34.7057	0.289619	0.280027	0.52665	0.9998
ENSG00000174444	ENSG00000174444	RPL4	15:66790354-66858317	OK	1996.53	2333.73	0.225146	0.382376	0.5268	0.9998
ENSG00000180957	ENSG00000180957	PITPNB	22:28247656-29075853	OK	27.0253	30.9484	0.195554	0.370775	0.52705	0.9998
ENSG00000149269	ENSG00000149269	PAK1	11:77032751-77188074	OK	20.6767	23.6724	0.195202	0.325433	0.5271	0.9998
ENSG00000174456	ENSG00000174456	C12orf76	12:110436990-110511491	OK	12.4116	9.89971	-0.326233	-0.262167	0.5271	0.9998
ENSG00000228395	ENSG00000228395	RP11-216B9.6	9:131266978-131314689	OK	1.19152	0.67896	-0.811404	-0.154126	0.5271	0.9998
ENSG00000166181	ENSG00000166181	API5	11:43333512-43516483	OK	59.277	67.6204	0.189988	0.321357	0.5272	0.9998
ENSG00000144848	ENSG00000144848	ATG3	3:112251355-112304424	OK	50.5336	57.2673	0.180468	0.368825	0.5273	0.9998
ENSG00000150455	ENSG00000150455	TIRAP	11:126152959-126215644	OK	4.67805	3.51774	-0.411257	-0.354361	0.5275	0.9998
ENSG00000087088	ENSG00000087088	BAX	19:49458071-49465055	OK	171.475	203.195	0.244862	0.400858	0.5276	0.9998
ENSG00000100462	ENSG00000100462	PRMT5	14:23388664-23398794	OK	57.558	64.5821	0.166118	0.272934	0.52765	0.9998
ENSG00000158062	ENSG00000158062	UBXN11	1:26605666-26647014	OK	12.4858	9.85876	-0.340816	-0.352916	0.5277	0.9998
ENSG00000075568	ENSG00000075568	TMEM131	2:98372798-98612388	OK	16.1106	14.2074	-0.181369	-0.237972	0.52775	0.9998
ENSG00000229644	ENSG00000229644	NAMPTL	10:36810648-36813162	OK	60.0321	51.3651	-0.224946	-0.381905	0.5278	0.9998
ENSG00000261101	ENSG00000261101	RP4-545K15.5	X:100882857-100883508	OK	0.759145	1.02358	0.431175	0.374172	0.52785	0.9998
ENSG00000257252	ENSG00000257252	RP11-486A14.2	12:93710910-93771512	OK	1.69447	0.943388	-0.84491	-0.596693	0.5279	0.9998
ENSG00000155096	ENSG00000155096	AZIN1	8:103838584-103990104	OK	90.6303	101.346	0.161221	0.323169	0.52795	0.9998
ENSG00000167323	ENSG00000167323	STIM1	11:3875547-4114439	OK	20.408	24.5777	0.268216	0.353296	0.52795	0.9998
ENSG00000181191	ENSG00000181191	PJA1	X:68380693-68385636	OK	9.76499	8.4291	-0.212239	-0.381909	0.52815	0.9998
ENSG00000271020	ENSG00000271020	RP11-10C24.1	3:33838640-33839173	OK	0.797371	0.538731	-0.565684	-0.417664	0.52825	0.9998
ENSG00000013016	ENSG00000013016	EHD3	2:31456879-31492313	OK	1.8584	2.17179	0.224825	0.391777	0.52845	0.9998
ENSG00000131504	ENSG00000131504	DIAPH1	5:140894582-141016437	OK	46.4289	41.1908	-0.1727	-0.359572	0.5286	0.9998
ENSG00000143376	ENSG00000143376	SNX27	1:151584513-151671567	OK	18.5878	16.4921	-0.172583	-0.324218	0.5286	0.9998
ENSG00000156469	ENSG00000156469	MTERFD1	8:97251625-97273838	OK	13.3973	11.7248	-0.192376	-0.383072	0.52865	0.9998
ENSG00000197081	ENSG00000197081	IGF2R	6:160390130-160534539	OK	49.4243	57.1809	0.21031	0.277005	0.52875	0.9998
ENSG00000166888	ENSG00000166888	STAT6	12:57482676-57607134	OK	37.143	30.616	-0.278805	-0.275235	0.52885	0.9998
ENSG00000181264	ENSG00000181264	TMEM136	11:120195837-120204391	OK	1.86863	1.52651	-0.291741	-0.357344	0.52885	0.9998
ENSG00000163468	ENSG00000163468	CCT3	1:156278758-156337664	OK	391.151	436.293	0.157573	0.371158	0.5289	0.9998
ENSG00000184602	ENSG00000184602	SNN	16:11762269-11838362	OK	12.189	14.1648	0.216736	0.380193	0.52905	0.9998
ENSG00000170276	ENSG00000170276	HSPB2	11:111779288-111797596	OK	12.3159	18.8991	0.617797	0.437214	0.5291	0.9998
ENSG00000149476	ENSG00000149476	DAK	11:61066922-61136981	OK	13.2268	9.92512	-0.414304	-0.123611	0.52915	0.9998
ENSG00000182196	ENSG00000182196	ARL6IP4	12:123405497-123467456	OK	120.588	137.976	0.194334	0.395219	0.52915	0.9998
ENSG00000096092	ENSG00000096092	TMEM14A	6:52535906-52551386	OK	54.4489	48.5855	-0.164376	-0.379893	0.52925	0.9998
ENSG00000140319	ENSG00000140319	SRP14	15:40327939-40331389	OK	192.587	214.626	0.156312	0.376222	0.52925	0.9998
ENSG00000232411	ENSG00000232411	AC009495.3	2:166651360-166702601	OK	8.53292	6.69444	-0.350076	-0.382847	0.5293	0.9998
ENSG00000120306	ENSG00000120306	CYSTM1	5:139554226-139682706	OK	110.822	131.902	0.251225	0.387858	0.5295	0.9998
ENSG00000188419	ENSG00000188419	CHM	X:85116184-85302566	OK	12.9019	11.3539	-0.184404	-0.335912	0.5295	0.9998
ENSG00000212443	ENSG00000212443	SNORA53	12:98987368-98995946	OK	0.896933	0.270582	-1.72893	-0.0452777	0.5295	0.9998
ENSG00000139687	ENSG00000139687	RB1	13:48877886-49056122	OK	14.5489	16.3234	0.166028	0.339937	0.52955	0.9998
ENSG00000232671	ENSG00000232671	RP11-126K1.2	1:151252499-151300191	OK	0.569205	1.13472	0.995317	0.0889963	0.52955	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000080824	ENSG00000080824	HSP90AA1	14:102547074-102771537	OK	1130.5	1299.71	0.201235	0.37234	0.52965	0.9998
ENSG00000119915	ENSG00000119915	ELOVL3	10:103986084-103989346	OK	1.48492	1.80701	0.283218	0.378054	0.5297	0.9998
ENSG00000205133	ENSG00000205133	TRIQK	8:93895211-94029901	OK	10.7935	9.34123	-0.208478	-0.320983	0.5297	0.9998
ENSG00000017797	ENSG00000017797	RALBP1	18:9475006-9538114	OK	22.0461	24.6013	0.158209	0.369686	0.52975	0.9998
ENSG00000156603	ENSG00000156603	MED19	11:57471185-57479693	OK	14.9728	17.1265	0.193891	0.384678	0.52975	0.9998
ENSG00000259392	ENSG00000259392	RP11-758N13.3	15:33057746-33486897	OK	0.833094	1.69785	1.02716	0.0706124	0.52975	0.9998
ENSG00000110721	ENSG00000110721	CHKA	11:67806482-67888911	OK	29.8338	34.3756	0.204438	0.351734	0.5299	0.9998
ENSG00000132478	ENSG00000132478	UNK	17:73772514-73821886	OK	63.4721	49.0112	-0.373011	-0.346926	0.53005	0.9998
ENSG00000178229	ENSG00000178229	ZNF543	19:57831876-57842144	OK	1.1122	0.938908	-0.24436	-0.37449	0.53005	0.9998
ENSG00000182541	ENSG00000182541	LIMK2	22:31608224-31676066	OK	3.54568	3.01553	-0.233652	-0.321866	0.53005	0.9998
ENSG00000093144	ENSG00000093144	ECHDC1	6:127609854-127664754	OK	26.7049	30.3418	0.184203	0.36411	0.5301	0.9998
ENSG00000115946	ENSG00000115946	PNO1	2:68350067-68488362	OK	16.2808	19.8039	0.28261	0.384826	0.53035	0.9998
ENSG00000051009	ENSG00000051009	FAM160A2	11:6232564-6255941	OK	9.52544	8.23778	-0.209529	-0.333319	0.53045	0.9998
ENSG00000091483	ENSG00000091483	FH	1:241660902-241683061	OK	73.2756	66.1084	-0.148498	-0.348539	0.53045	0.9998
ENSG00000167130	ENSG00000167130	DOLPP1	9:131843378-131852717	OK	8.36081	7.32572	-0.190673	-0.374401	0.53045	0.9998
ENSG00000013364	ENSG00000013364	MVP	16:29817426-29859355	OK	26.0149	21.6396	-0.265665	-0.292978	0.5306	0.9998
ENSG00000167562	ENSG00000167562	ZNF701	19:53030904-53090427	OK	0.975755	1.25924	0.367958	0.333718	0.5308	0.9998
ENSG00000240498	ENSG00000240498	CDKN2B-AS1	9:21802541-22121096	OK	1.12931	0.806246	-0.486152	-0.0811882	0.5308	0.9998
ENSG00000161653	ENSG00000161653	NAGS	17:42081913-42086431	OK	1.46056	1.211	-0.270323	-0.383631	0.53095	0.9998
ENSG00000167553	ENSG00000167553	TUBA1C	12:49578578-49667114	OK	244.851	280.302	0.195077	0.365634	0.531	0.9998
ENSG00000197417	ENSG00000197417	SHPK	17:3468737-3539616	OK	6.62519	7.53009	0.184706	0.37609	0.53105	0.9998
ENSG00000205707	ENSG00000205707	LYRM5	12:25348149-25403870	OK	14.2125	10.1265	-0.489021	-0.344401	0.53105	0.9998
ENSG00000181016	ENSG00000181016	LSMEM1	7:112063022-112131117	OK	1.49519	2.63984	0.82012	0.236689	0.5311	0.9998
ENSG00000214063	ENSG00000214063	TSPAN4	11:842807-867116	OK	83.4129	93.718	0.168055	0.373078	0.5311	0.9998
ENSG00000088854	ENSG00000088854	C20orf194	20:3229950-3388272	OK	2.50322	2.18571	-0.19568	-0.372488	0.5312	0.9998
ENSG00000147133	ENSG00000147133	TAF1	X:70586113-70752224	OK	9.14361	8.01674	-0.189748	-0.260452	0.5312	0.9998
ENSG00000185100	ENSG00000185100	ADSSL1	14:105190522-105213662	OK	9.3133	7.94803	-0.228696	-0.358733	0.5312	0.9998
ENSG00000138771	ENSG00000138771	SHROOM3	4:77356252-77723117	OK	1.59004	1.86747	0.232028	0.218144	0.53125	0.9998
ENSG00000143499	ENSG00000143499	SMYD2	1:214454444-214510474	OK	55.0648	61.4153	0.157468	0.365643	0.53155	0.9998
ENSG00000259318	ENSG00000259318	RP11-454L9.2	14:55833109-55878576	OK	0.592395	1.54971	1.38737	0.234008	0.5317	0.9998
ENSG00000158545	ENSG00000158545	ZC3H18	16:88636788-88698374	OK	8.52869	7.4744	-0.190367	-0.286514	0.53175	0.9998
ENSG00000091947	ENSG00000091947	TMEM101	17:42088555-42101314	OK	40.8751	45.639	0.159044	0.373944	0.53185	0.9998
ENSG00000077454	ENSG00000077454	LRCH4	7:100169854-100205798	OK	22.9605	25.9059	0.174126	0.32653	0.5321	0.9998
ENSG00000172458	ENSG00000172458	IL17D	13:21276265-21297237	OK	8.38972	9.66188	0.203682	0.379134	0.5322	0.9998
ENSG00000006607	ENSG00000006607	FARP2	2:242295657-242449145	OK	70.2828	59.1545	-0.248684	-0.270484	0.53235	0.9998
ENSG00000170175	ENSG00000170175	CHRNB1	17:7323421-7361026	OK	5.61964	4.46573	-0.331583	-0.365188	0.53235	0.9998
ENSG00000219642	ENSG00000219642	BMPR1APS1	6:129204341-129837714	OK	0.492592	0.67606	0.456758	0.388791	0.5325	0.9998
ENSG00000243069	ENSG00000243069	ARHGEF26-AS1	3:153742189-153975616	OK	0.665562	0.448917	-0.568125	-0.163088	0.53255	0.9998
ENSG00000102977	ENSG00000102977	ACD	16:67678821-67694713	OK	7.21682	6.11503	-0.239003	-0.358778	0.5327	0.9998
ENSG00000204576	ENSG00000204576	PRR3	6:30509153-30531500	OK	12.4599	8.94274	-0.478501	-0.35329	0.5328	0.9998
ENSG00000143303	ENSG00000143303	RRNAD1	1:156691682-156706752	OK	17.0754	13.1632	-0.375417	-0.297344	0.5331	0.9998
ENSG00000196739	ENSG00000196739	COL27A1	9:116917839-117074791	OK	15.6288	13.6072	-0.199841	-0.250812	0.5331	0.9998
ENSG00000198886	ENSG00000198886	MT-ND4	MT:10469-12137	OK	3939.24	4634.3	0.234433	0.376263	0.5331	0.9998
ENSG00000083444	ENSG00000083444	PLOD1	1:11994261-12035595	OK	83.4967	74.9591	-0.155616	-0.338392	0.5333	0.9998
ENSG00000108506	ENSG00000108506	INTS2	17:59942730-60005377	OK	7.75655	6.92638	-0.163314	-0.326069	0.5333	0.9998
ENSG00000139354	ENSG00000139354	GAS2L3	12:100967460-101022064	OK	33.6748	29.7433	-0.179107	-0.295099	0.5333	0.9998
ENSG00000109911	ENSG00000109911	ELP4	11:31531296-31805546	OK	10.5048	9.16055	-0.197543	-0.383466	0.53345	0.9998
ENSG00000164120	ENSG00000164120	HPGD	4:175411327-175444305	OK	48.9849	43.2121	-0.180902	-0.360346	0.5335	0.9998
ENSG00000164124	ENSG00000164124	TMEM144	4:159045625-159176563	OK	6.21648	4.86238	-0.354436	-0.225625	0.53365	0.9998
ENSG00000186815	ENSG00000186815	TPCN1	12:113633245-113736390	OK	16.0529	14.2992	-0.166903	-0.234028	0.5337	0.9998
ENSG00000197603	ENSG00000197603	C5orf42	5:37106329-37249530	OK	7.30172	6.47694	-0.172923	-0.192521	0.5337	0.9998
ENSG00000176390	ENSG00000176390	CRLF3	17:29036316-29151794	OK	9.18305	7.93049	-0.211563	-0.361965	0.5338	0.9998
ENSG00000229852	ENSG00000229852	RP11-398K22.12	6:73918805-74020088	OK	1.24917	0.892132	-0.485639	-0.382557	0.5339	0.9998
ENSG00000236255	ENSG00000236255	AC009404.2	2:118591512-118599234	OK	0.686776	0.452309	-0.602531	-0.463418	0.53405	0.9998
ENSG00000157306	ENSG00000157306	RP11-66N24.4	14:23980968-24048009	OK	2.65214	1.74602	-0.603085	-0.26568	0.53415	0.9998
ENSG00000178852	ENSG00000178852	EFCAB13	17:45331211-45518678	OK	2.44699	1.81539	-0.430729	-0.135084	0.53415	0.9998
ENSG00000136378	ENSG00000136378	ADAMTS7	15:79051544-79190475	OK	0.929459	1.4678	0.659193	0.182518	0.53445	0.9998
ENSG00000143033	ENSG00000143033	MTF2	1:93544791-93604638	OK	6.98139	8.02972	0.201835	0.34061	0.53445	0.9998
ENSG00000198680	ENSG00000198680	TUSC1	9:25676395-25678856	OK	6.84453	6.01433	-0.186547	-0.367056	0.53445	0.9998
ENSG00000118705	ENSG00000118705	RPN2	20:35729628-35870022	OK	286.572	257.508	-0.154278	-0.336595	0.53455	0.9998
ENSG00000137414	ENSG00000137414	FAM8A1	6:17600585-17611950	OK	14.0329	12.4948	-0.167483	-0.377556	0.53455	0.9998
ENSG00000197345	ENSG00000197345	MRPL21	11:68658743-68671303	OK	66.5715	74.9492	0.171008	0.382304	0.53455	0.9998
ENSG00000197062	ENSG00000197062	RP5-874C20.3	6:28234787-28245974	OK	9.26033	8.04192	-0.203524	-0.370684	0.5346	0.9998
ENSG00000100478	ENSG00000100478	AP4S1	14:31343719-31562818	OK	3.8837	5.56756	0.519611	0.358254	0.53465	0.9998
ENSG00000100934	ENSG00000100934	SEC23A	14:39501122-39578850	OK	47.7971	54.0747	0.178033	0.325497	0.53465	0.9998
ENSG00000119862	ENSG00000119862	LGALSL	2:64681102-64688515	OK	14.9465	18.5658	0.312842	0.401699	0.53485	0.9998
ENSG00000161904	ENSG00000161904	LEMD2	6:33738978-33756913	OK	55.9939	49.3585	-0.181972	-0.351387	0.5349	0.9998
ENSG00000186111	ENSG00000186111	PIP5K1C	19:3630180-3700477	OK	15.0614	16.9129	0.16727	0.37062	0.5349	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000196505	ENSG00000196505	GDAP2	1:118406106-118472253	OK	10.4525	8.70319	-0.264237	-0.384844	0.5349	0.9998
ENSG00000196550	ENSG00000196550	FAM72A	1:206135292-206155151	OK	3.44063	2.617	-0.394759	-0.395445	0.535	0.9998
ENSG00000061936	ENSG00000061936	SFSWAP	12:132195625-132284282	OK	19.0253	16.9193	-0.169251	-0.324004	0.53515	0.9998
ENSG00000165417	ENSG00000165417	GTF2A1	14:81641795-81687721	OK	13.4072	15.4321	0.202931	0.367614	0.53515	0.9998
ENSG00000167904	ENSG00000167904	TMEM68	8:56608982-56738007	OK	15.4314	12.3914	-0.316526	-0.382235	0.53525	0.9998
ENSG00000100711	ENSG00000100711	ZFYVE21	14:104182066-104200005	OK	29.2366	32.7832	0.16518	0.338525	0.5353	0.9998
ENSG00000243749	ENSG00000243749	ZMYM6NB	1:35439956-35497569	OK	6.97573	5.19727	-0.424592	-0.360758	0.5353	0.9998
ENSG00000071054	ENSG00000071054	MAP4K4	2:102313311-102511150	OK	43.2561	48.41	0.162403	0.334428	0.53535	0.9998
ENSG00000182518	ENSG00000182518	FAM104B	X:55169534-55187743	OK	11.2293	9.57061	-0.230592	-0.368214	0.53535	0.9998
ENSG00000120992	ENSG00000120992	LYPLA1	8:54958937-55014577	OK	53.3877	59.0525	0.145493	0.28926	0.5354	0.9998
ENSG00000178764	ENSG00000178764	ZHX2	8:123793632-123986750	OK	0.643622	0.824528	0.357355	0.321922	0.5354	0.9998
ENSG00000148218	ENSG00000148218	ALAD	9:116148596-116163613	OK	23.6709	21.167	-0.161297	-0.321771	0.5356	0.9998
ENSG00000169231	ENSG00000169231	THBS3	1:155165378-155183615	OK	10.7147	8.39225	-0.352462	-0.322136	0.53565	0.9998
ENSG00000069399	ENSG00000069399	BCL3	19:45250961-45263301	OK	5.853	4.96088	-0.238581	-0.306688	0.5358	0.9998
ENSG00000008294	ENSG00000008294	SPAG9	17:49039534-49198226	OK	50.477	44.7691	-0.173121	-0.26359	0.53585	0.9998
ENSG00000099992	ENSG00000099992	TBC1D10A	22:30681105-30723035	OK	21.92	24.7362	0.174379	0.351077	0.53595	0.9998
ENSG00000165209	ENSG00000165209	STRBP	9:125871772-126030855	OK	16.6191	18.6603	0.167136	0.342717	0.5361	0.9998
ENSG00000185532	ENSG00000185532	PRKG1	10:52750944-54073888	OK	0.666813	0.921062	0.466016	0.312744	0.53625	0.9998
ENSG00000232024	ENSG00000232024	LSM12P1	8:35092974-35654068	OK	50.2845	56.8605	0.177313	0.371813	0.53625	0.9998
ENSG00000168067	ENSG00000168067	MAP4K2	11:64556289-64570713	OK	26.4316	23.522	-0.168251	-0.318091	0.5363	0.9998
ENSG00000185338	ENSG00000185338	SOCS1	16:11343475-11445619	OK	0.674057	1.38955	1.04367	0.470297	0.53635	0.9998
ENSG00000115145	ENSG00000115145	STAM2	2:152973314-153032506	OK	5.46188	6.43886	0.237409	0.328079	0.5364	0.9998
ENSG00000006757	ENSG00000006757	PNPLA4	X:7866287-7895780	OK	12.2021	14.6621	0.264962	0.376277	0.5365	0.9998
ENSG00000175899	ENSG00000175899	A2M	12:9217772-9268825	OK	5.99063	7.02143	0.229057	0.243574	0.5365	0.9998
ENSG00000213443	ENSG00000213443	RP11-75L1.2	12:9817564-9848823	OK	9.67448	11.6536	0.268526	0.364034	0.53655	0.9998
ENSG00000177854	ENSG00000177854	TMEM187	X:153237777-153248646	OK	1.3815	1.79072	0.374304	0.327545	0.5366	0.9998
ENSG00000182796	ENSG00000182796	TMEM198B	12:56137063-56236750	OK	1.62548	1.09042	-0.575981	-0.192437	0.5366	0.9998
ENSG00000108468	ENSG00000108468	CBX1	17:46147413-46178883	OK	75.5318	68.0512	-0.150464	-0.354083	0.53665	0.9998
ENSG00000164091	ENSG00000164091	WDR82	3:52288436-52333083	OK	27.1269	30.1328	0.151608	0.342528	0.53675	0.9998
ENSG00000149599	ENSG00000149599	DUSP15	20:30435439-30539895	OK	6.74363	9.19143	0.446763	0.373951	0.5368	0.9998
ENSG00000059769	ENSG00000059769	DNAJC25	9:114393631-114432526	OK	13.3443	16.9247	0.3429	0.382047	0.53695	0.9998
ENSG00000113273	ENSG00000113273	ARSB	5:78073031-78281910	OK	14.4426	16.2295	0.168284	0.331247	0.53695	0.9998
ENSG00000272869	ENSG00000272869	CTC-487M23.8	5:112043194-112258236	OK	0.560134	1.20741	1.10807	0.138043	0.537	0.9998
ENSG00000233327	ENSG00000233327	USP32P2	17:18414534-18528930	OK	3.39378	2.63499	-0.365096	-0.285541	0.53715	0.9998
ENSG00000135540	ENSG00000135540	NHSL1	6:138723721-139018425	OK	13.721	11.6841	-0.231834	-0.225158	0.5372	0.9998
ENSG00000155438	ENSG00000155438	NIFK	2:122407225-122494499	OK	44.8864	52.1878	0.217434	0.365934	0.5373	0.9998
ENSG00000124813	ENSG00000124813	RUNX2	6:44777053-45632086	OK	1.11756	0.874394	-0.353992	-0.209511	0.5374	0.9998
ENSG00000116489	ENSG00000116489	CAPZA1	1:113009162-113214241	OK	69.3391	78.2712	0.174812	0.330113	0.53745	0.9998
ENSG00000100461	ENSG00000100461	RBM23	14:23369853-23388393	OK	21.6906	24.2121	0.158655	0.272886	0.53755	0.9998
ENSG00000173653	ENSG00000173653	RCE1	11:66511921-66614017	OK	12.0446	14.0126	0.218345	0.349652	0.53755	0.9998
ENSG00000229422	ENSG00000229422	RP11-262H14.5	9:66493571-66494196	OK	0.44296	0.636334	0.522608	0.37786	0.5376	0.9998
ENSG00000261824	ENSG00000261824	LINC00662	19:28175487-28475892	OK	15.6317	12.837	-0.284171	-0.367562	0.5376	0.9998
ENSG00000005194	ENSG00000005194	CIAPIN1	16:57462080-57521239	OK	23.1311	19.1367	-0.27349	-0.302961	0.53765	0.9998
ENSG00000175356	ENSG00000175356	SCUBE2	11:9025708-9159661	OK	58.8463	51.7029	-0.186705	-0.278717	0.5377	0.9998
ENSG00000066322	ENSG00000066322	ELOVL1	1:43829067-43833696	OK	52.947	59.1493	0.15981	0.368538	0.5378	0.9998
ENSG00000213144	ENSG00000213144	RP11-64B16.2	12:119616446-119658936	OK	1.54299	2.03038	0.396017	0.386162	0.53805	0.9998
ENSG00000117984	ENSG00000117984	CTSD	11:1753639-1785255	OK	489.85	554.863	0.179792	0.374284	0.5381	0.9998
ENSG00000132205	ENSG00000132205	EMILIN2	18:2847027-2915991	OK	6.77248	8.0103	0.242172	0.38267	0.5382	0.9998
ENSG00000112874	ENSG00000112874	NUDT12	5:102884555-102898494	OK	3.67728	3.13405	-0.230609	-0.351295	0.53825	0.9998
ENSG00000128692	ENSG00000128692	EIF2S2P4	2:171579718-171627276	OK	52.8096	59.1258	0.162987	0.376621	0.5384	0.9998
ENSG00000075643	ENSG00000075643	MOCOS	18:33767481-33852120	OK	3.07421	2.51373	-0.290383	-0.236824	0.5386	0.9998
ENSG00000127946	ENSG00000127946	HIP1	7:75162620-75368280	OK	10.2604	8.95538	-0.196256	-0.243606	0.5387	0.9998
ENSG00000169258	ENSG00000169258	GPRIN1	5:175969511-176037134	OK	4.55954	3.99594	-0.190351	-0.37935	0.53875	0.9998
ENSG00000151224	ENSG00000151224	MAT1A	10:82031575-82049440	OK	0.758114	0.928818	0.29298	0.268344	0.53885	0.9998
ENSG00000187605	ENSG00000187605	TET3	2:74229839-74335303	OK	2.19766	1.94173	-0.178622	-0.345161	0.53885	0.9998
ENSG00000214110	ENSG00000214110	LDHAP4	9:14921334-14922332	OK	22.4099	19.7192	-0.184536	-0.366131	0.53885	0.9998
ENSG00000154188	ENSG00000154188	ANGPT1	8:108261720-108510283	OK	4.59403	5.392	0.231058	0.361392	0.5389	0.9998
ENSG00000143772	ENSG00000143772	ITPKB	1:226819390-226927024	OK	90.9642	101.121	0.152706	0.36725	0.53895	0.9998
ENSG00000253626	ENSG00000253626	EIF5AL1	10:81272356-81276188	OK	7.06659	7.95187	0.170279	0.373571	0.539	0.9998
ENSG00000107223	ENSG00000107223	EDF1	9:139756570-139760738	OK	356.469	396.045	0.151888	0.377848	0.53905	0.9998
ENSG00000178950	ENSG00000178950	GAK	4:843063-926161	OK	23.5688	20.9447	-0.170297	-0.258428	0.53905	0.9998
ENSG00000088179	ENSG00000088179	PTPN4	2:120517206-120741394	OK	4.93332	6.34246	0.362483	0.333235	0.5391	0.9998
ENSG00000112308	ENSG00000112308	C6orf62	6:24667262-24721064	OK	43.556	49.6693	0.189484	0.316795	0.5391	0.9998
ENSG00000151176	ENSG00000151176	PLBD2	12:113736563-113827203	OK	31.978	35.7405	0.160482	0.37352	0.5395	0.9998
ENSG00000182199	ENSG00000182199	SHMT2	12:57623109-57634498	OK	139.773	156.697	0.164889	0.357032	0.5396	0.9998
ENSG00000196363	ENSG00000196363	WDR5	9:136997363-137025093	OK	18.0488	16.1334	-0.161849	-0.360929	0.53975	0.9998
ENSG00000059758	ENSG00000059758	CDK17	12:96672038-96794338	OK	13.3223	15.0061	0.171712	0.304543	0.5398	0.9998
ENSG00000140598	ENSG00000140598	EFTUD1	15:82422570-82555104	OK	10.7809	9.6492	-0.159995	-0.279602	0.53985	0.9998
ENSG00000105419	ENSG00000105419	MEIS3	19:47906380-47922780	OK	1.63502	1.98168	0.277418	0.284234	0.54005	0.9998
ENSG00000187091	ENSG00000187091	PLCD1	3:38048986-38071253	OK	6.44848	5.56002	-0.213869	-0.293838	0.54005	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000111785	ENSG00000111785	RIC8B	12:106751435-107283090	OK	8.36732	6.98144	-0.261242	-0.281864	0.54015	0.9998
ENSG00000261827	ENSG00000261827	RP11-340F14.5	12:121625358-121625835	OK	24.9561	28.877	0.210529	0.375817	0.5402	0.9998
ENSG00000239523	ENSG00000239523	MYLK-AS1	3:123304388-123603178	OK	0.344422	0.671925	0.964125	0.298992	0.5403	0.9998
ENSG00000160172	ENSG00000160172	FAM86C2P	11:67552743-67572807	OK	1.61978	1.29841	-0.319044	-0.317364	0.54045	0.9998
ENSG00000110367	ENSG00000110367	DDX6	11:118575315-118661858	OK	11.1688	12.5544	0.168715	0.347614	0.54055	0.9998
ENSG00000151366	ENSG00000151366	NDUFC2	11:77726760-77791265	OK	375.72	422.636	0.169758	0.375868	0.54055	0.9998
ENSG00000114200	ENSG00000114200	BCHE	3:165490691-165555260	OK	26.6073	29.813	0.16412	0.347663	0.5406	0.9998
ENSG00000197363	ENSG00000197363	ZNF517	8:146024260-146036554	OK	2.72323	2.32089	-0.230641	-0.347631	0.5406	0.9998
ENSG00000169230	ENSG00000169230	PRELID1	5:176728198-176739758	OK	168.374	188.498	0.162886	0.367316	0.5407	0.9998
ENSG00000256586	ENSG00000256586	AC091171.1	8:21946669-21962409	OK	11.3387	9.00908	-0.331809	-0.368404	0.5408	0.9998
ENSG00000223508	ENSG00000223508	RPL23AP53	8:163185-197342	OK	1.66755	0.991947	-0.749396	-0.458116	0.5409	0.9998
ENSG00000155530	ENSG00000155530	LRGUK	7:133812051-133949343	OK	1.77706	1.51781	-0.227507	-0.34994	0.5413	0.9998
ENSG00000272960	ENSG00000272960	RP11-339B21.15	9:131067439-131067794	OK	0.950376	0.598069	-0.668186	-0.46586	0.5413	0.9998
ENSG00000126461	ENSG00000126461	SCAF1	19:50145381-50161899	OK	13.8871	12.1987	-0.187013	-0.301738	0.5414	0.9998
ENSG00000174028	ENSG00000174028	FAM3C2	X:22277913-23311263	OK	86.5526	96.6804	0.159646	0.3695	0.5414	0.9998
ENSG00000167967	ENSG00000167967	E4F1	16:2273566-2288712	OK	8.90309	10.1493	0.188999	0.300425	0.54145	0.9998
ENSG00000120662	ENSG00000120662	MTRF1	13:41790504-41837742	OK	14.1238	12.0964	-0.223547	-0.364448	0.5415	0.9998
ENSG00000171016	ENSG00000171016	PYGO1	15:55831087-55881145	OK	2.49088	2.11598	-0.235328	-0.369047	0.54155	0.9998
ENSG00000264772	ENSG00000264772	SNORA67	17:7465191-7536700	OK	0.856983	1.61113	0.910731	0.0338765	0.54155	0.9998
ENSG00000005206	ENSG00000005206	SPPL2B	19:2321515-2355099	OK	13.1326	10.8139	-0.280265	-0.281453	0.54175	0.9998
ENSG00000101558	ENSG00000101558	VAPA	18:9913998-9960018	OK	124.104	141.405	0.188286	0.37212	0.5422	0.9998
ENSG00000168389	ENSG00000168389	MFSD2A	1:40420801-40435638	OK	5.80844	5.00982	-0.213392	-0.343557	0.5422	0.9998
ENSG00000087502	ENSG00000087502	ERGIC2	12:29302035-29534122	OK	77.2657	92.468	0.259125	0.375292	0.54225	0.9998
ENSG00000113328	ENSG00000113328	CCNG1	5:162864574-162887146	OK	133.444	149.618	0.165057	0.355563	0.5424	0.9998
ENSG00000183576	ENSG00000183576	SETD3	14:99864082-99947216	OK	26.5485	23.8743	-0.153171	-0.35745	0.5424	0.9998
ENSG00000131791	ENSG00000131791	PRKAB2	1:146626684-146644129	OK	11.7183	13.1032	0.161159	0.29888	0.54245	0.9998
ENSG00000131435	ENSG00000131435	PDLIM4	5:131520568-131731306	OK	1.14268	1.81345	0.666315	0.255755	0.5425	0.9998
ENSG00000198468	ENSG00000198468	FLVCR1-AS1	1:213025449-213031430	OK	3.01696	2.46844	-0.289496	-0.37011	0.5425	0.9998
ENSG00000178567	ENSG00000178567	EPM2AIP1	3:37027356-37034795	OK	1.14364	1.31986	0.206748	0.370636	0.5426	0.9998
ENSG00000049130	ENSG00000049130	KITLG	12:88886569-88974628	OK	2.25963	2.68729	0.250068	0.33438	0.5429	0.9998
ENSG00000148719	ENSG00000148719	DNAJB12	10:74092587-74114988	OK	13.5243	15.1844	0.167037	0.367478	0.543	0.9998
ENSG00000115053	ENSG00000115053	NCL	2:232318241-232348352	OK	323.715	380.75	0.234121	0.357801	0.5431	0.9998
ENSG00000117751	ENSG00000117751	PPP1R8	1:28157288-28178187	OK	18.0901	20.6343	0.189841	0.366341	0.5431	0.9998
ENSG00000079277	ENSG00000079277	MKNK1	1:47004367-47082563	OK	16.2425	19.8745	0.29114	0.351946	0.54315	0.9998
ENSG00000157349	ENSG00000157349	DDX19B	16:70323565-70407286	OK	13.8266	10.7964	-0.356894	-0.332287	0.5432	0.9998
ENSG00000259806	ENSG00000259806	CTD-2196E14.4	16:23681331-23686820	OK	2.80251	7.17259	1.35577	0.592689	0.5432	0.9998
ENSG00000141068	ENSG00000141068	KSR1	17:25783669-25976586	OK	4.95438	6.26127	0.337751	0.290887	0.54325	0.9998
ENSG00000167131	ENSG00000167131	CCDC103	17:42923720-42994305	OK	1.85549	1.11291	-0.737464	-0.119601	0.54325	0.9998
ENSG00000069275	ENSG00000069275	NUCKS1	1:205681946-205719404	OK	89.8645	100.386	0.159733	0.169474	0.5434	0.9998
ENSG00000117394	ENSG00000117394	SLC2A1	1:43391051-43424530	OK	25.3887	29.3455	0.208956	0.334857	0.5435	0.9998
ENSG00000204815	ENSG00000204815	TTC25	17:40086887-40117648	OK	0.631079	0.440328	-0.519242	-0.296814	0.5436	0.9998
ENSG00000089902	ENSG00000089902	RCOR1	14:103058997-103196913	OK	6.64267	7.44913	0.165307	0.290973	0.5437	0.9998
ENSG00000166233	ENSG00000166233	ARIH1	15:72690613-72879692	OK	17.1766	19.4854	0.181947	0.256668	0.5438	0.9998
ENSG00000104957	ENSG00000104957	CCDC130	19:13842573-13874110	OK	17.2915	14.8894	-0.215773	-0.373952	0.54395	0.9998
ENSG00000066926	ENSG00000066926	FECH	18:55215514-55254004	OK	12.6676	14.9824	0.242118	0.340026	0.54405	0.9998
ENSG00000102931	ENSG00000102931	ARL2BP	16:57279009-57287516	OK	20.1058	17.9979	-0.159784	-0.35937	0.54405	0.9998
ENSG00000197044	ENSG00000197044	ZNF441	19:11877814-11894893	OK	2.93783	2.48325	-0.24252	-0.279919	0.54405	0.9998
ENSG00000107290	ENSG00000107290	SETX	9:135136742-135230372	OK	10.0132	11.1783	0.158794	0.227719	0.5443	0.9998
ENSG00000153048	ENSG00000153048	CARHSP1	16:8768421-8962866	OK	37.0537	45.0734	0.282659	0.364737	0.5443	0.9998
ENSG00000171824	ENSG00000171824	EXOSC10	1:11126674-11162157	OK	31.8436	28.3958	-0.165327	-0.273934	0.54435	0.9998
ENSG00000164171	ENSG00000164171	ITGA2	5:51971026-52390609	OK	3.19664	2.6204	-0.286771	-0.357207	0.54455	0.9998
ENSG00000131725	ENSG00000131725	WDR44	X:117480035-117583924	OK	4.45224	3.89724	-0.192079	-0.365788	0.5446	0.9998
ENSG00000227671	ENSG00000227671	MIR3916	1:247353152-247405125	OK	17.7632	15.305	-0.214888	-0.362699	0.5446	0.9998
ENSG00000030582	ENSG00000030582	GRN	17:42422613-42430470	OK	211.799	234.457	0.14663	0.318399	0.5447	0.9998
ENSG00000044574	ENSG00000044574	HSPA5	9:127997131-128003609	OK	110.338	122.505	0.150911	0.355444	0.545	0.9998
ENSG00000132182	ENSG00000132182	NUP210	3:13357736-13461809	OK	7.77257	6.95394	-0.160561	-0.355884	0.54505	0.9998
ENSG00000198920	ENSG00000198920	KIAA0753	17:6481467-6554954	OK	4.39221	5.41911	0.303108	0.227924	0.54505	0.9998
ENSG00000204264	ENSG00000204264	PSMB8	6:32808493-32827362	OK	6.11071	8.38453	0.456389	0.385548	0.5451	0.9998
ENSG00000110047	ENSG00000110047	EHD1	11:64619113-64655768	OK	29.4398	34.1657	0.21478	0.377525	0.54525	0.9998
ENSG00000100304	ENSG00000100304	TTLL12	22:43562627-43583139	OK	24.7	27.3637	0.147754	0.342846	0.5453	0.9998
ENSG00000143621	ENSG00000143621	ILF2	1:153634511-153643524	OK	218.389	241.984	0.148015	0.369598	0.5455	0.9998
ENSG00000138399	ENSG00000138399	FASTKD1	2:170386258-170430385	OK	20.4681	18.1074	-0.1768	-0.322557	0.5456	0.9998
ENSG00000136295	ENSG00000136295	TTYH3	7:2671584-2704436	OK	349.993	311.648	-0.167411	-0.259172	0.5457	0.9998
ENSG00000100490	ENSG00000100490	CDKL1	14:50704280-50883179	OK	0.89686	1.26175	0.492467	0.189072	0.5458	0.9998
ENSG00000133460	ENSG00000133460	SLC2A11	22:24198613-24241117	OK	17.821	24.2152	0.442338	0.154474	0.5458	0.9998
ENSG00000137558	ENSG00000137558	PI15	8:75512009-75779174	OK	21.1195	18.8576	-0.163432	-0.347318	0.5459	0.9998
ENSG00000130299	ENSG00000130299	GTPBP3	19:17445728-17453544	OK	12.7639	14.3777	0.17177	0.297467	0.54595	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000151692	ENSG00000151692	RNF144A	2:7052407-7218011	OK	18.3409	20.7354	0.177033	0.249742	0.54595	0.9998
ENSG00000223496	ENSG00000223496	EXOSC6	16:70284133-70285833	OK	2.96068	2.52431	-0.230043	-0.362027	0.54595	0.9998
ENSG00000066777	ENSG00000066777	ARFGEF1	8:67876333-68255912	OK	12.894	14.7994	0.198842	0.239574	0.5462	0.9998
ENSG00000117000	ENSG00000117000	RLF	1:40627044-40706593	OK	4.76194	4.23767	-0.168277	-0.361095	0.5462	0.9998
ENSG00000204271	ENSG00000204271	SPIN3	X:57002802-57021970	OK	1.01264	1.25986	0.315143	0.370209	0.5462	0.9998
ENSG00000169504	ENSG00000169504	CLIC4	1:25071847-25170815	OK	76.7288	69.2223	-0.148531	-0.360321	0.5463	0.9998
ENSG00000131849	ENSG00000131849	ZNF132	19:58944180-58951589	OK	0.652885	0.797333	0.288354	0.376703	0.54635	0.9998
ENSG00000171443	ENSG00000171443	ZNF524	19:56102745-56114504	OK	2.93614	1.97029	-0.575516	-0.351841	0.54635	0.9998
ENSG00000215421	ENSG00000215421	ZNF407	18:72259009-72777627	OK	2.48105	2.13401	-0.217381	-0.255491	0.54665	0.9998
ENSG00000100056	ENSG00000100056	DGCR14	22:19117791-19132197	OK	12.4224	14.0268	0.175239	0.359898	0.54675	0.9998
ENSG00000114473	ENSG00000114473	IQCG	3:197615945-197687013	OK	4.76918	3.4765	-0.456104	-0.0901279	0.5468	0.9998
ENSG00000153993	ENSG00000153993	SEMA3D	7:84624868-84816171	OK	1.10858	0.878888	-0.334962	-0.356414	0.5468	0.9998
ENSG00000007047	ENSG00000007047	MARK4	19:45574757-45808541	OK	10.3351	13.2868	0.362432	0.227682	0.54685	0.9998
ENSG00000173535	ENSG00000173535	TNFRSF10C	8:22941867-22974950	OK	3.28519	3.84152	0.225699	0.342896	0.54685	0.9998
ENSG00000263006	ENSG00000263006	ROCK1P1	18:109064-122219	OK	0.975204	0.595459	-0.7117	-0.519836	0.54685	0.9998
ENSG00000130522	ENSG00000130522	JUND	19:18390562-18392432	OK	36.3264	42.2622	0.218352	0.356126	0.5469	0.9998
ENSG00000002549	ENSG00000002549	LAP3	4:17578814-17616194	OK	39.8928	44.1829	0.147358	0.35009	0.54705	0.9998
ENSG00000198930	ENSG00000198930	CSAG1	X:151903227-151909518	OK	114.247	127.563	0.159055	0.370651	0.54705	0.9998
ENSG00000128191	ENSG00000128191	DGCR8	22:20067754-20114878	OK	10.2725	8.00639	-0.359569	-0.235782	0.54715	0.9998
ENSG00000168092	ENSG00000168092	PAFAH1B2	11:117014982-117047610	OK	14.8016	16.464	0.153559	0.308534	0.54715	0.9998
ENSG00000186318	ENSG00000186318	BACE1	11:117103340-117283984	OK	3.30355	2.66799	-0.308267	-0.230791	0.5472	0.9998
ENSG00000101493	ENSG00000101493	ZNF516	18:74069643-74207146	OK	7.47009	8.61927	0.206439	0.22177	0.5473	0.9998
ENSG00000136143	ENSG00000136143	SUCLA2	13:48510621-48621358	OK	31.3707	35.5609	0.180872	0.34148	0.5473	0.9998
ENSG00000076003	ENSG00000076003	MCM6	2:136597195-136633996	OK	12.1663	10.897	-0.158952	-0.349735	0.54735	0.9998
ENSG00000108384	ENSG00000108384	RAD51C	17:56769933-56811703	OK	32.2481	28.0114	-0.2032	-0.370417	0.54735	0.9998
ENSG00000172270	ENSG00000172270	BSG	19:567211-583493	OK	242.377	268.509	0.147715	0.36175	0.5474	0.9998
ENSG00000123352	ENSG00000123352	SPATS2	12:49760366-49921205	OK	31.3671	28.1371	-0.156778	-0.257369	0.5476	0.9998
ENSG00000132406	ENSG00000132406	TMEM128	4:4237268-4249950	OK	23.3017	20.5963	-0.178049	-0.378953	0.5476	0.9998
ENSG00000105810	ENSG00000105810	CDK6	7:92234234-92546501	OK	9.55159	8.49051	-0.16989	-0.284492	0.54765	0.9998
ENSG00000122870	ENSG00000122870	BICC1	10:60272899-60591195	OK	2.96141	3.35461	0.179858	0.352267	0.5477	0.9998
ENSG00000150433	ENSG00000150433	TMEM218	11:124966397-124981659	OK	13.6708	11.7459	-0.218943	-0.376097	0.5477	0.9998
ENSG00000109686	ENSG00000109686	SH3D19	4:152020724-152246784	OK	5.26169	7.2971	0.471796	0.15522	0.5478	0.9998
ENSG00000160703	ENSG00000160703	NLRX1	11:119037276-119054725	OK	2.30802	1.99617	-0.209424	-0.263869	0.5479	0.9998
ENSG00000223837	ENSG00000223837	BRD2-IT1	6:32902405-32949282	OK	0.788644	0.262932	-1.58469	-0.0829435	0.5479	0.9998
ENSG00000105135	ENSG00000105135	ILVBL	19:15218213-15236985	OK	59.463	69.5782	0.226644	0.363781	0.54795	0.9998
ENSG00000147174	ENSG00000147174	ACRC	X:70798260-70833433	OK	0.765301	0.588237	-0.37963	-0.343291	0.548	0.9998
ENSG00000258964	ENSG00000258964	RP11-618G20.1	14:62147758-62263146	OK	1.91135	0.721458	-1.4056	-0.217727	0.5481	0.9998
ENSG00000178538	ENSG00000178538	CA8	8:61099905-61193971	OK	41.3705	37.0711	-0.158307	-0.333988	0.54815	0.9998
ENSG00000115325	ENSG00000115325	DOK1	2:74753771-74784681	OK	2.8039	4.01788	0.519	0.184395	0.5484	0.9998
ENSG00000162735	ENSG00000162735	PEX19	1:160185504-160256138	OK	97.4061	84.718	-0.201344	-0.302386	0.54845	0.9998
ENSG00000106628	ENSG00000106628	POLD2	7:44154285-44163957	OK	141.123	125.696	-0.167014	-0.336319	0.5486	0.9998
ENSG00000213465	ENSG00000213465	ARL2	11:64781584-64808044	OK	133.111	119.044	-0.161135	-0.375764	0.5486	0.9998
ENSG00000034713	ENSG00000034713	GABARAPL2	16:75562429-75657198	OK	68.0963	59.7696	-0.188165	-0.355592	0.54865	0.9998
ENSG00000184967	ENSG00000184967	NOC4L	12:132628992-132637013	OK	8.89005	10.146	0.19065	0.35933	0.54865	0.9998
ENSG00000164308	ENSG00000164308	ERAP2	5:96149730-96373219	OK	8.93512	10.9967	0.299517	0.32559	0.5487	0.9998
ENSG00000142102	ENSG00000142102	ATHL1	11:289134-296107	OK	1.72388	2.02316	0.230949	0.310833	0.54875	0.9998
ENSG00000167778	ENSG00000167778	SPRYD3	12:53458387-53473204	OK	23.3354	21.0056	-0.151747	-0.352913	0.54875	0.9998
ENSG00000230903	ENSG00000230903	RPL9P8	15:83023846-83125316	OK	3.75411	1.85578	-1.01645	-0.800566	0.54875	0.9998
ENSG00000234741	ENSG00000234741	GAS5	1:173832385-173872687	OK	535.157	598.078	0.16037	0.364322	0.5489	0.9998
ENSG00000132661	ENSG00000132661	NXT1	20:23327577-23335414	OK	9.54362	8.2679	-0.207015	-0.366768	0.5491	0.9998
ENSG00000138658	ENSG00000138658	C4orf21	4:113434671-113578748	OK	3.60961	2.74083	-0.397232	-0.276917	0.5491	0.9998
ENSG00000182841	ENSG00000182841	RRP7B	22:42949622-42978044	OK	6.19136	7.39094	0.255501	0.363785	0.54915	0.9998
ENSG00000119401	ENSG00000119401	TRIM32	9:119187503-120177348	OK	17.0873	15.0073	-0.187262	-0.322257	0.54945	0.9998
ENSG00000203780	ENSG00000203780	FANK1	10:127585107-127698161	OK	1.0953	0.889609	-0.300082	-0.263353	0.54945	0.9998
ENSG00000186812	ENSG00000186812	ZNF397	18:32820993-32870196	OK	5.97262	4.96882	-0.26546	-0.33685	0.5496	0.9998
ENSG00000006282	ENSG00000006282	SPATA20	17:48609903-48633213	OK	27.1023	30.0504	0.148971	0.294535	0.5498	0.9998
ENSG00000127481	ENSG00000127481	UBR4	1:19398603-19536770	OK	29.7423	34.1918	0.201134	0.204548	0.5498	0.9998
ENSG00000106133	ENSG00000106133	NSUN5P2	7:72349935-72425329	OK	9.19589	13.4065	0.543872	0.41876	0.55025	0.9998
ENSG00000092036	ENSG00000092036	HAUS4	14:23398817-23451851	OK	23.096	19.4427	-0.248414	-0.34894	0.55045	0.9998
ENSG00000135334	ENSG00000135334	AKIRIN2	6:88384789-88411927	OK	8.60577	9.7897	0.185961	0.335089	0.5506	0.9998
ENSG00000203879	ENSG00000203879	GDI1	X:153665265-153671814	OK	81.6349	73.4687	-0.152057	-0.347152	0.5509	0.9998
ENSG00000229419	ENSG00000229419	RALGAPA1P	9:108210076-108314714	OK	3.26904	2.78936	-0.228934	-0.359959	0.5509	0.9998
ENSG00000169914	ENSG00000169914	OTUD3	1:20209005-20239438	OK	6.35539	5.64212	-0.171744	-0.203926	0.55095	0.9998
ENSG00000087087	ENSG00000087087	SRRT	7:100472732-100486285	OK	36.6427	32.5728	-0.169859	-0.282638	0.55105	0.9998
ENSG00000171206	ENSG00000171206	TRIM8	10:104404252-104418164	OK	14.7348	17.1883	0.222198	0.346607	0.55115	0.9998
ENSG00000226659	ENSG00000226659	RP11-137H2.4	10:82213921-82295698	OK	1.89416	0.976811	-0.955407	-0.0667454	0.5512	0.9998
ENSG00000135845	ENSG00000135845	PIGC	1:171810620-172437971	OK	22.2944	19.3937	-0.201095	-0.36782	0.5513	0.9998
ENSG00000159352	ENSG00000159352	PSMD4	1:151227178-151239955	OK	176.426	160.106	-0.140037	-0.342181	0.55135	0.9998
ENSG00000198369	ENSG00000198369	SPRED2	2:65537984-65659771	OK	12.8463	14.3941	0.164126	0.263647	0.5514	0.9998
ENSG00000135736	ENSG00000135736	CCDC102A	16:57546089-57570511	OK	1.63406	1.95087	0.255663	0.361969	0.55145	0.9998
ENSG00000102699	ENSG00000102699	PARP4	13:24982294-25171814	OK	17.9267	19.8049	0.143751	0.334862	0.55175	0.9998
ENSG00000213347	ENSG00000213347	MXD3	5:176728198-176739758	OK	16.8597	10.6828	-0.658292	-0.317407	0.5518	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263753	ENSG00000263753	LINC00667	18:5232874-5246507	OK	14.0592	16.4158	0.223567	0.366025	0.5518	0.9998
ENSG00000114646	ENSG00000114646	CSPG5	3:47603728-47622282	OK	0.747499	0.608879	-0.295916	-0.327168	0.5524	0.9998
ENSG00000082898	ENSG00000082898	XPO1	2:61698322-61765761	OK	80.1525	88.3733	0.140862	0.211878	0.55245	0.9998
ENSG00000101343	ENSG00000101343	CRNKL1	20:20015011-20341346	OK	6.65414	7.77715	0.224991	0.32206	0.55245	0.9998
ENSG00000158109	ENSG00000158109	TPRG1L	1:3541565-3546691	OK	24.1406	26.881	0.155123	0.368132	0.55245	0.9998
ENSG00000124357	ENSG00000124357	NAGK	2:71163011-71306935	OK	59.8677	71.5165	0.256498	0.298851	0.55255	0.9998
ENSG00000141564	ENSG00000141564	RPTOR	17:78518618-78945013	OK	12.9159	14.5831	0.175142	0.333224	0.55255	0.9998
ENSG00000158483	ENSG00000158483	FAM86C1	11:71498555-71532594	OK	2.89493	2.44076	-0.246202	-0.356489	0.5526	0.9998
ENSG00000119333	ENSG00000119333	WDR34	9:131314865-131419066	OK	41.2203	30.6883	-0.425666	-0.344887	0.5528	0.9998
ENSG00000249962	ENSG00000249962	RP11-80H5.5	10:91342744-91410579	OK	0.208114	0.836471	2.00694	0.392013	0.5528	0.9998
ENSG00000008853	ENSG00000008853	RHOBTB2	8:22545171-22941132	OK	7.86311	10.2128	0.377202	0.258974	0.553	0.9998
ENSG00000108187	ENSG00000108187	PBLD	10:70042416-70167051	OK	0.788847	0.53223	-0.567697	-0.11458	0.55305	0.9998
ENSG00000269295	ENSG00000269295	AL358113.1	9:71736208-71870124	OK	1.06223	0.283432	-1.90602	-0.193258	0.55305	0.9998
ENSG00000145632	ENSG00000145632	PLK2	5:57749808-57756087	OK	69.4236	77.3413	0.155811	0.25565	0.55315	0.9998
ENSG00000118181	ENSG00000118181	RPS25	11:118868851-118901616	OK	390.427	436.444	0.160745	0.358699	0.55325	0.9998
ENSG00000157540	ENSG00000157540	DYRK1A	21:38737778-38889753	OK	12.9863	14.9716	0.205238	0.304986	0.5533	0.9998
ENSG00000261064	ENSG00000261064	RP11-1000B6.3	15:32812048-32879814	OK	1.50493	0.537824	-1.48449	-0.669947	0.55335	0.9998
ENSG00000070831	ENSG00000070831	CDC42	1:22379119-22419437	OK	78.3804	86.7202	0.145875	0.348462	0.55345	0.9998
ENSG00000247596	ENSG00000247596	TWF2	3:52255095-52275113	OK	30.4278	33.8797	0.15503	0.35381	0.5536	0.9998
ENSG00000267827	ENSG00000267827	CTC-471J1.8	19:52616343-52680255	OK	0.707602	0.230441	-1.61854	-0.278347	0.5537	0.9998
ENSG00000119699	ENSG00000119699	TGFB3	14:76041230-76550928	OK	1.73915	1.11274	-0.644256	-0.194533	0.55385	0.9998
ENSG00000214389	ENSG00000214389	RPS3AP26	7:97881690-98030380	OK	112.177	139.56	0.315115	0.367658	0.55385	0.9998
ENSG00000161203	ENSG00000161203	AP2M1	3:183851806-184402546	OK	237.701	311.31	0.389203	0.354463	0.5539	0.9998
ENSG00000213462	ENSG00000213462	ERV3-1	7:64432153-64467121	OK	0.721253	0.950445	0.398097	0.313579	0.5539	0.9998
ENSG00000183828	ENSG00000183828	NUDT14	14:105607317-105647660	OK	29.902	35.1635	0.233836	0.353935	0.55395	0.9998
ENSG00000137185	ENSG00000137185	ZSCAN9	6:28192663-28201260	OK	8.88832	7.78069	-0.192011	-0.351843	0.554	0.9998
ENSG00000196839	ENSG00000196839	ADA	20:43160425-43280874	OK	15.1158	18.2402	0.27107	0.369024	0.55435	0.9998
ENSG00000101190	ENSG00000101190	TCFL5	20:61447595-61493115	OK	32.2962	39.9225	0.305839	0.338817	0.55445	0.9998
ENSG00000107317	ENSG00000107317	PTGDS	9:139871955-139880862	OK	0.916357	1.19996	0.389002	0.239789	0.55445	0.9998
ENSG00000044090	ENSG00000044090	CUL7	6:43005354-43042837	OK	6.17628	5.20628	-0.246485	-0.309625	0.5545	0.9998
ENSG00000082516	ENSG00000082516	GEMIN5	5:154266975-154317769	OK	10.1569	11.2607	0.14883	0.350489	0.5545	0.9998
ENSG00000143995	ENSG00000143995	MEIS1	2:66653866-66801001	OK	1.52054	1.27254	-0.256868	-0.203745	0.5545	0.9998
ENSG00000169710	ENSG00000169710	FASN	17:80036213-80056208	OK	112.831	128.118	0.18332	0.240537	0.5545	0.9998
ENSG00000102302	ENSG00000102302	FGD1	X:54466833-54522599	OK	8.36914	9.66911	0.208305	0.358771	0.5546	0.9998
ENSG00000198382	ENSG00000198382	UVRAG	11:75514475-75854239	OK	13.7554	15.3909	0.16208	0.342628	0.55465	0.9998
ENSG00000196937	ENSG00000196937	FAM3C	7:120988904-121036418	OK	49.9727	55.1057	0.14106	0.34408	0.55485	0.9998
ENSG00000177302	ENSG00000177302	TOP3A	17:18174741-18218321	OK	12.3871	10.6985	-0.211435	-0.283027	0.5549	0.9998
ENSG00000154473	ENSG00000154473	BUB3	10:124913792-124924886	OK	79.9367	70.9602	-0.171849	-0.357251	0.55495	0.9998
ENSG00000070371	ENSG00000070371	CLTCL1	22:19166985-19279239	OK	2.44205	2.81031	0.202638	0.268642	0.555	0.9998
ENSG00000214654	ENSG00000214654	RP11-27I1.4	9:123555828-123561848	OK	1.51507	1.14956	-0.398305	-0.344566	0.555	0.9998
ENSG00000221817	ENSG00000221817	RP11-137L10.6	10:75196185-75385711	OK	1.25366	0.894162	-0.487539	-0.101698	0.55515	0.9998
ENSG00000125409	ENSG00000125409	TEKT3	17:15207127-15244958	OK	1.09374	0.837575	-0.384973	-0.277548	0.55535	0.9998
ENSG00000196284	ENSG00000196284	SUPT3H	6:44777053-45632086	OK	12.1684	14.1298	0.215603	0.354176	0.55535	0.9998
ENSG00000108021	ENSG00000108021	FAM208B	10:5726800-5805703	OK	13.8289	15.8754	0.199106	0.190137	0.5554	0.9998
ENSG00000213326	ENSG00000213326	RPS7P11	17:44668034-44834830	OK	87.9977	107.33	0.286519	0.360293	0.5554	0.9998
ENSG00000235912	ENSG00000235912	RP1-159A19.3	1:27975929-27976121	OK	10.5252	13.8759	0.398727	0.353414	0.5555	0.9998
ENSG00000075275	ENSG00000075275	CELSR1	22:46756730-46933067	OK	7.05899	8.11439	0.20102	0.300685	0.55555	0.9998
ENSG00000159899	ENSG00000159899	NPR2	9:35792150-35812269	OK	4.51306	5.12361	0.183054	0.310809	0.5557	0.9998
ENSG00000260537	ENSG00000260537	RP11-529K1.3	16:70323565-70407286	OK	0.549553	1.54679	1.49295	0.359771	0.5557	0.9998
ENSG00000183291	ENSG00000183291	15-Sep	1:87328131-87380107	OK	126.215	140.436	0.154027	0.360019	0.55575	0.9998
ENSG00000188811	ENSG00000188811	NHLRC3	13:39612442-39624246	OK	14.4939	17.2079	0.24763	0.348155	0.55575	0.9998
ENSG00000250742	ENSG00000250742	RP11-834C11.4	12:54519881-54526627	OK	17.4246	19.6445	0.173001	0.350512	0.5558	0.9998
ENSG00000096968	ENSG00000096968	JAK2	9:4985032-5128183	OK	3.49487	3.07444	-0.184914	-0.312033	0.55585	0.9998
ENSG00000018189	ENSG00000018189	RUFY3	4:71569463-71673032	OK	14.0608	15.8099	0.169151	0.277428	0.55595	0.9998
ENSG00000046651	ENSG00000046651	OFD1	X:13752831-13787480	OK	9.63429	8.28694	-0.217339	-0.323597	0.55595	0.9998
ENSG00000144040	ENSG00000144040	SFXN5	2:73169164-73383849	OK	4.6511	5.78545	0.314859	0.162199	0.55595	0.9998
ENSG00000186056	ENSG00000186056	MATN1-AS1	1:31184123-31199674	OK	0.533577	0.739925	0.471682	0.303835	0.5561	0.9998
ENSG00000243989	ENSG00000243989	ACY1	3:51989329-52023213	OK	30.3436	22.8651	-0.408243	-0.346123	0.5562	0.9998
ENSG00000170846	ENSG00000170846	AC093323.3	4:6672451-6677774	OK	3.91015	3.39617	-0.203315	-0.356896	0.55625	0.9998
ENSG00000270344	ENSG00000270344	RP11-734K2.4	12:89813494-89934079	OK	0.353503	0.958304	1.43876	0.223952	0.5564	0.9998
ENSG00000174718	ENSG00000174718	KIAA1551	12:32112303-32146039	OK	3.84751	3.18392	-0.273124	-0.236837	0.55645	0.9998
ENSG00000272779	ENSG00000272779	LL22NC03-80A10.6	22:22657588-22677336	OK	12.0956	10.3384	-0.226469	-0.356282	0.55655	0.9998
ENSG00000248835	ENSG00000248835	AL357673.1	1:54598746-54879152	OK	1.53015	0.520556	-1.55555	-0.462854	0.5566	0.9998
ENSG00000107099	ENSG00000107099	DOCK8	9:213107-746105	OK	0.723163	1.05637	0.546727	0.168303	0.55665	0.9998
ENSG00000183580	ENSG00000183580	FBXL7	5:15500304-15939900	OK	15.4888	17.1394	0.146091	0.3502	0.5568	0.9998
ENSG00000011198	ENSG00000011198	ABHD5	3:43328003-43775863	OK	12.6533	15.9838	0.337094	0.331056	0.5569	0.9998
ENSG00000197147	ENSG00000197147	LRRC8B	1:89990394-90402170	OK	1.95907	1.41533	-0.46903	-0.330492	0.5569	0.9998
ENSG00000168872	ENSG00000168872	DDX19A	16:70323565-70407286	OK	11.9183	10.4401	-0.191042	-0.30993	0.55695	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232559	ENSG00000232559	GS1-124K5.12	7:66010633-66057373	OK	5.87667	4.96111	-0.244336	-0.354461	0.55695	0.9998
ENSG00000213928	ENSG00000213928	IRF9	14:24612573-24636611	OK	18.5258	14.4677	-0.356706	-0.274897	0.557	0.9998
ENSG00000127993	ENSG00000127993	RBM48	7:92158086-92167319	OK	8.6487	9.85377	0.188192	0.345082	0.55705	0.9998
ENSG00000129255	ENSG00000129255	MPDU1	17:7465191-7536700	OK	51.1883	66.1311	0.369514	0.162092	0.55705	0.9998
ENSG00000133026	ENSG00000133026	MYH10	17:8316448-8534079	OK	62.0803	69.3128	0.158987	0.242473	0.5575	0.9998
ENSG00000163629	ENSG00000163629	PTPN13	4:87515467-87736324	OK	5.82837	5.19284	-0.166568	-0.228654	0.5575	0.9998
ENSG00000136271	ENSG00000136271	DDX56	7:44605015-44614650	OK	59.4762	66.0223	0.15064	0.31055	0.55755	0.9998
ENSG00000131462	ENSG00000131462	TUBG1	17:40731530-40767252	OK	62.5759	54.4423	-0.200879	-0.353957	0.55775	0.9998
ENSG00000254122	ENSG00000254122	PCDHGB7	5:140710251-140892546	OK	2.50375	3.62613	0.534337	0.353638	0.5578	0.9998
ENSG00000077514	ENSG00000077514	POLD3	11:74202756-74380162	OK	9.28713	8.03489	-0.208956	-0.316678	0.55785	0.9998
ENSG00000100209	ENSG00000100209	HSCB	22:29083730-29153503	OK	15.5467	12.5712	-0.306481	-0.374999	0.55785	0.9998
ENSG00000198755	ENSG00000198755	RPL10A	6:35436184-35438562	OK	904.118	1001.94	0.148208	0.359579	0.55785	0.9998
ENSG00000189091	ENSG00000189091	SF3B3	16:70557690-70608820	OK	39.0682	32.6974	-0.256819	-0.325925	0.55795	0.9998
ENSG00000124788	ENSG00000124788	ATXN1	6:16299342-16762883	OK	13.0061	15.1924	0.224163	0.276544	0.55805	0.9998
ENSG00000213971	ENSG00000213971	RP11-15H20.6	19:23437854-23457053	OK	1.12233	0.814343	-0.462784	-0.253635	0.55815	0.9998
ENSG00000239467	ENSG00000239467	AC007405.6	2:171627622-171634658	OK	1.29413	0.874515	-0.565429	-0.511706	0.5582	0.9998
ENSG00000213901	ENSG00000213901	SLC23A3	2:219940038-220035549	OK	0.632391	0.849163	0.425224	0.180471	0.55825	0.9998
ENSG00000177383	ENSG00000177383	MAGEF1	3:184428155-184429836	OK	9.97774	8.82681	-0.176821	-0.348602	0.5584	0.9998
ENSG00000120217	ENSG00000120217	CD274	9:5450502-5470566	OK	3.68453	2.71207	-0.44209	-0.394374	0.5585	0.9998
ENSG00000123473	ENSG00000123473	STIL	1:47715810-47779819	OK	5.53551	4.92017	-0.170006	-0.324447	0.55855	0.9998
ENSG00000085231	ENSG00000085231	TAF9	5:68646810-68710628	OK	126.649	142.913	0.174302	0.353856	0.55865	0.9998
ENSG00000011405	ENSG00000011405	PIK3C2A	11:17095935-17229530	OK	17.7346	14.0348	-0.337557	-0.173865	0.5587	0.9998
ENSG00000143507	ENSG00000143507	DUSP10	1:221874765-221915518	OK	105.496	118.103	0.162853	0.355314	0.55875	0.9998
ENSG00000239382	ENSG00000239382	ALKBH6	19:36494208-36505141	OK	13.733	11.6902	-0.232347	-0.349601	0.5588	0.9998
ENSG00000148154	ENSG00000148154	UGCG	9:114659045-114697649	OK	88.1477	80.0404	-0.139196	-0.276127	0.55895	0.9998
ENSG00000270149	ENSG00000270149	RP11-544M22.13	1:160965000-161008780	OK	4.32834	5.88712	0.443748	0.364932	0.55895	0.9998
ENSG00000113269	ENSG00000113269	RNF130	5:179338650-179499118	OK	43.6399	39.4212	-0.146677	-0.333986	0.559	0.9998
ENSG00000165527	ENSG00000165527	ARF6	14:50359809-50361490	OK	93.6831	103.204	0.13964	0.348219	0.559	0.9998
ENSG00000266967	ENSG00000266967	AARSD1	17:41102542-41132545	OK	21.6889	24.534	0.177826	0.315583	0.559	0.9998
ENSG00000165115	ENSG00000165115	KIF27	9:86444570-86536342	OK	2.14883	1.72745	-0.314906	-0.359929	0.5591	0.9998
ENSG00000089820	ENSG00000089820	ARHGAP4	X:153126968-153200676	OK	1.20558	0.920594	-0.389093	-0.0653628	0.5592	0.9998
ENSG00000003393	ENSG00000003393	ALS2	2:202565276-202645912	OK	14.7333	16.5071	0.164002	0.273746	0.55925	0.9998
ENSG00000157823	ENSG00000157823	AP3S2	15:90373830-90456188	OK	30.2074	24.3288	-0.312237	-0.360247	0.55925	0.9998
ENSG00000235173	ENSG00000235173	FAM203A	8:145192671-145195746	OK	1.76627	1.47236	-0.262572	-0.295747	0.55925	0.9998
ENSG00000111615	ENSG00000111615	KRR1	12:75874459-75905416	OK	44.238	37.8804	-0.223834	-0.354903	0.5596	0.9998
ENSG00000125457	ENSG00000125457	MIF4GD	17:73232693-73267308	OK	17.4917	12.8665	-0.443053	-0.257685	0.55965	0.9998
ENSG00000184619	ENSG00000184619	KRBA2	17:8268880-8286531	OK	1.02516	0.536967	-0.932947	-0.10725	0.55965	0.9998
ENSG00000128989	ENSG00000128989	ARPP19	15:52839241-52862080	OK	37.864	44.3543	0.228248	0.333166	0.5597	0.9998
ENSG00000257122	ENSG00000257122	RRN3P3	16:22357256-22547842	OK	1.35639	1.88134	0.471984	0.260328	0.5598	0.9998
ENSG00000163348	ENSG00000163348	PYGO2	1:154929501-154946871	OK	19.2046	15.1139	-0.345572	-0.340631	0.55985	0.9998
ENSG00000131732	ENSG00000131732	ZCCHC9	5:80597408-80609116	OK	48.467	43.3889	-0.159676	-0.34617	0.56025	0.9998
ENSG00000164970	ENSG00000164970	FAM219A	9:34398181-34520982	OK	10.6433	11.8758	0.158077	0.348414	0.56025	0.9998
ENSG00000221978	ENSG00000221978	CCNL2	1:1321090-1334708	OK	65.4431	58.7701	-0.15516	-0.313608	0.5603	0.9998
ENSG00000196220	ENSG00000196220	SRGAP3	3:9022274-9520924	OK	1.8235	1.27976	-0.510838	-0.0949447	0.56045	0.9998
ENSG00000235257	ENSG00000235257	AC093415.2	3:37493605-37903271	OK	7.05176	4.69395	-0.587181	-0.353279	0.56055	0.9998
ENSG00000064199	ENSG00000064199	SPA17	11:124492731-124567414	OK	5.29708	3.23661	-0.710714	-0.378236	0.56065	0.9998
ENSG00000188931	ENSG00000188931	C1orf192	1:161334520-161337664	OK	6.96122	5.94323	-0.228092	-0.352939	0.56075	0.9998
ENSG00000215301	ENSG00000215301	DDX3X	X:41192650-41223725	OK	92.3488	102.42	0.149339	0.313926	0.5609	0.9998
ENSG00000135070	ENSG00000135070	ISCA1	9:88879460-88897676	OK	28.458	25.4289	-0.162368	-0.361901	0.56095	0.9998
ENSG00000198646	ENSG00000198646	NCOA6	20:33284721-33413452	OK	13.8187	12.0517	-0.197384	-0.344097	0.56105	0.9998
ENSG00000260425	ENSG00000260425	LA16c-316G12.2	16:1401923-1464752	OK	1.63377	0.707299	-1.20781	-0.200951	0.56105	0.9998
ENSG00000223803	ENSG00000223803	RPS20P14	3:186617986-186618346	OK	0.754503	0.485339	-0.636533	-0.398596	0.5611	0.9998
ENSG00000213965	ENSG00000213965	NUDT19	19:33182866-33204702	OK	7.60331	8.54673	0.168746	0.352652	0.5612	0.9998
ENSG00000180769	ENSG00000180769	WDFY3-AS2	4:85590703-85932430	OK	0.674912	0.374341	-0.850346	-0.305158	0.56125	0.9998
ENSG00000167779	ENSG00000167779	IGFBP6	12:53491219-53496129	OK	5.57148	6.63297	0.251594	0.35163	0.56145	0.9998
ENSG00000168952	ENSG00000168952	STXBP6	14:25278861-25519503	OK	40.3322	47.0317	0.221702	0.352909	0.56145	0.9998
ENSG00000198837	ENSG00000198837	DENND4B	1:153901976-153919172	OK	28.4393	25.4376	-0.160922	-0.216284	0.56145	0.9998
ENSG00000251056	ENSG00000251056	ANKRD20A17P	4:49504161-49508039	OK	0.672112	0.530656	-0.340923	-0.34477	0.56145	0.9998
ENSG00000111674	ENSG00000111674	ENO2	12:6976282-7032861	OK	156.984	122.386	-0.359175	-0.316203	0.56155	0.9998
ENSG00000123178	ENSG00000123178	SPRYD7	13:50486841-50510626	OK	7.347	6.53345	-0.169311	-0.325518	0.56165	0.9998
ENSG00000245146	ENSG00000245146	LINC01024	5:139452441-139496321	OK	0.768549	1.12476	0.54941	0.205739	0.56165	0.9998
ENSG00000120162	ENSG00000120162	MOB3B	9:27325206-27529779	OK	13.5644	12.2817	-0.143317	-0.348836	0.5619	0.9998
ENSG00000136810	ENSG00000136810	TXN	9:113006090-113018920	OK	343.375	377.933	0.138344	0.346962	0.56195	0.9998
ENSG00000165434	ENSG00000165434	PGM2L1	11:74041362-74197096	OK	1.46312	1.66837	0.189394	0.353911	0.56195	0.9998
ENSG00000198625	ENSG00000198625	MDM4	1:204485510-204542871	OK	8.86341	7.43179	-0.254151	-0.279812	0.56195	0.9998
ENSG00000236624	ENSG00000236624	CCDC163P	1:45959537-45988719	OK	1.33124	0.868817	-0.615648	-0.0994635	0.56225	0.9998
ENSG00000257103	ENSG00000257103	LSM14A	19:34663408-34720420	OK	44.83	52.828	0.236836	0.362072	0.56225	0.9998
ENSG00000066827	ENSG00000066827	ZFAT	8:135490030-135725292	OK	2.81699	3.25508	0.208538	0.248351	0.56245	0.9998
ENSG00000111845	ENSG00000111845	PAK1IP1	6:10671650-10710015	OK	26.2298	29.1369	0.15164	0.350367	0.56245	0.9998
ENSG00000075407	ENSG00000075407	ZNF37A	10:38383263-38414472	OK	2.64356	3.1318	0.244511	0.250153	0.5625	0.9998
ENSG00000172273	ENSG00000172273	HINFP	11:118992296-119006752	OK	4.33536	5.17538	0.255514	0.31501	0.5625	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000169714	ENSG00000169714	CNBP	3:128888326-128902765	OK	196.069	215.572	0.136812	0.341072	0.56255	0.9998
ENSG00000230453	ENSG00000230453	ANKRD18B	9:33524391-33573007	OK	2.1448	2.6896	0.326549	0.28357	0.56255	0.9998
ENSG00000160712	ENSG00000160712	IL6R	1:154374803-154441926	OK	78.4191	90.4244	0.205507	0.320728	0.5627	0.9998
ENSG00000235169	ENSG00000235169	SMIM1	1:3689351-3692546	OK	6.24735	7.53987	0.271295	0.373418	0.5627	0.9998
ENSG00000127081	ENSG00000127081	ZNF484	9:95571669-95661890	OK	1.56633	1.3318	-0.234009	-0.354261	0.56275	0.9998
ENSG00000180673	ENSG00000180673	EXOC5P1	4:63682543-63684512	OK	0.669392	0.814693	0.283405	0.351957	0.56275	0.9998
ENSG00000260874	ENSG00000260874	RP11-715J22.4	16:2479394-2509980	OK	0.645413	0.312169	-1.0479	-0.167021	0.5628	0.9998
ENSG00000206560	ENSG00000206560	ANKRD28	3:15708742-15901278	OK	63.8691	72.152	0.175921	0.281618	0.56285	0.9998
ENSG00000178802	ENSG00000178802	MPI	15:75182345-75191798	OK	27.0156	23.7588	-0.185334	-0.347706	0.5629	0.9998
ENSG00000130204	ENSG00000130204	TOMM40	19:45349431-45406946	OK	46.8661	52.977	0.176821	0.354297	0.56305	0.9998
ENSG00000183474	ENSG00000183474	GTF2H2C	5:68773298-69006341	OK	11.817	9.93559	-0.250183	-0.336846	0.56315	0.9998
ENSG00000179119	ENSG00000179119	SPTY2D1	11:18621333-18656338	OK	7.91889	9.0039	0.185251	0.299662	0.5632	0.9998
ENSG00000186868	ENSG00000186868	MAPT	17:43921016-44105700	OK	7.12078	5.90408	-0.270322	-0.329918	0.5632	0.9998
ENSG00000204842	ENSG00000204842	ATXN2	12:111890017-112038060	OK	16.5511	14.7479	-0.166414	-0.260337	0.5632	0.9998
ENSG00000078747	ENSG00000078747	ITCH	20:32951040-33099198	OK	22.1628	24.7738	0.160674	0.294054	0.56325	0.9998
ENSG00000166848	ENSG00000166848	TERF2IP	16:75661621-75795770	OK	25.2744	21.0137	-0.266343	-0.340318	0.5633	0.9998
ENSG00000185236	ENSG00000185236	RAB11B	19:8428172-8469318	OK	26.7214	23.921	-0.159716	-0.341905	0.5633	0.9998
ENSG00000144468	ENSG00000144468	RHBDD1	2:227700296-227863931	OK	11.1271	9.25425	-0.265889	-0.297919	0.56335	0.9998
ENSG00000174132	ENSG00000174132	FAM174A	5:99871008-99922445	OK	16.8865	18.9408	0.165628	0.34341	0.56335	0.9998
ENSG00000196547	ENSG00000196547	MAN2A2	15:91445447-91465814	OK	34.9182	38.2979	0.133285	0.207617	0.56335	0.9998
ENSG00000141551	ENSG00000141551	CSNK1D	17:80186272-80231607	OK	84.8883	94.9689	0.16189	0.298126	0.5634	0.9998
ENSG00000171853	ENSG00000171853	TRAPPC12	2:3383445-3488865	OK	18.2156	20.5803	0.176087	0.275922	0.5638	0.9998
ENSG00000215154	ENSG00000215154	AC141586.5	16:2653350-2693297	OK	2.68723	2.0581	-0.384806	-0.283512	0.5638	0.9998
ENSG00000228818	ENSG00000228818	RP11-567G24.1	1:240177647-240643504	OK	1.61269	1.2065	-0.418642	-0.337554	0.56385	0.9998
ENSG00000242861	ENSG00000242861	RP11-285F7.2	1:225997793-226070069	OK	3.65182	1.74045	-1.06916	-0.128568	0.5639	0.9998
ENSG00000111276	ENSG00000111276	CDKN1B	12:12867991-12875305	OK	29.8118	33.0484	0.148693	0.352757	0.564	0.9998
ENSG00000108515	ENSG00000108515	ENO3	17:4848946-4860426	OK	6.09366	8.74053	0.520413	0.0900217	0.56405	0.9998
ENSG00000186767	ENSG00000186767	SPIN4	X:62563105-62780951	OK	1.81028	1.42355	-0.346724	-0.356519	0.5641	0.9998
ENSG00000258210	ENSG00000258210	RP11-478C19.2	12:110810704-110888227	OK	0.919235	0.425232	-1.11218	-0.106573	0.5642	0.9998
ENSG00000230896	ENSG00000230896	RP11-767N6.7	1:46092975-46216322	OK	0.669507	0.320497	-1.06279	-0.116165	0.56425	0.9998
ENSG00000258824	ENSG00000258824	CTD-2555O16.2	14:64854748-65009955	OK	1.2759	0.614132	-1.05489	-0.103575	0.5643	0.9998
ENSG00000168016	ENSG00000168016	TRANK1	3:36868310-36986548	OK	2.31165	1.69963	-0.4437	-0.275817	0.56435	0.9998
ENSG00000170542	ENSG00000170542	SERPINB9	6:2887499-2903514	OK	1.1421	0.961726	-0.247988	-0.34146	0.5645	0.9998
ENSG00000117650	ENSG00000117650	NEK2	1:211836113-211848960	OK	32.2358	28.8521	-0.159984	-0.352512	0.56455	0.9998
ENSG00000133195	ENSG00000133195	SLC39A11	17:70642087-71088851	OK	13.4159	16.1707	0.269444	0.345595	0.56455	0.9998
ENSG00000150764	ENSG00000150764	DIXDC1	11:111797867-111893308	OK	2.62159	3.2361	0.303817	0.297082	0.56455	0.9998
ENSG00000164609	ENSG00000164609	SLU7	5:159828647-159848718	OK	48.1487	40.2944	-0.256917	-0.361548	0.56465	0.9998
ENSG00000115468	ENSG00000115468	EFHD1	2:233412778-233547491	OK	16.1216	12.4469	-0.373215	-0.3601	0.56475	0.9998
ENSG00000150540	ENSG00000150540	HNMT	2:138721589-138773930	OK	0.692998	0.518633	-0.418138	-0.228073	0.56475	0.9998
ENSG00000115282	ENSG00000115282	TTC31	2:74699084-74722013	OK	18.1366	15.3877	-0.237125	-0.252468	0.5651	0.9998
ENSG00000151065	ENSG00000151065	DCP1B	12:2055219-2802108	OK	7.75508	6.78046	-0.193759	-0.35319	0.5651	0.9998
ENSG00000173588	ENSG00000173588	CCDC41	12:94542498-94853764	OK	6.9053	4.81441	-0.520347	-0.174898	0.56525	0.9998
ENSG00000185760	ENSG00000185760	KCNQ5	6:73331519-73908574	OK	13.8042	12.2407	-0.173426	-0.188861	0.56525	0.9998
ENSG00000130751	ENSG00000130751	NPAS1	19:47523076-47549033	OK	1.01409	1.27426	0.329473	0.29841	0.5654	0.9998
ENSG00000124299	ENSG00000124299	PEPD	19:33877855-34012700	OK	104.241	114.382	0.133941	0.327584	0.56545	0.9998
ENSG00000270143	ENSG00000270143	AC004257.3	19:15346329-15346819	OK	1.92713	2.42057	0.328892	0.33964	0.56555	0.9998
ENSG00000110619	ENSG00000110619	CARS	11:3022151-3078843	OK	36.434	40.6051	0.156376	0.341899	0.56565	0.9998
ENSG00000136205	ENSG00000136205	TNS3	7:47314751-47622156	OK	23.7247	20.6761	-0.19843	-0.247061	0.56575	0.9998
ENSG00000164742	ENSG00000164742	ADCY1	7:45613738-45762715	OK	52.3105	45.4454	-0.202967	-0.334098	0.5658	0.9998
ENSG00000226696	ENSG00000226696	LENG8-AS1	19:54955990-54974894	OK	1.13414	0.735691	-0.624432	-0.0967701	0.56585	0.9998
ENSG00000100083	ENSG00000100083	GGA1	22:38004480-38029571	OK	49.2949	43.8965	-0.167333	-0.305989	0.56595	0.9998
ENSG00000165507	ENSG00000165507	C10orf10	10:45306471-45491339	OK	1.04498	1.43964	0.462232	0.335249	0.566	0.9998
ENSG00000156103	ENSG00000156103	MMP16	8:89044236-89749363	OK	1.54092	2.03376	0.400356	0.292885	0.5661	0.9998
ENSG00000159387	ENSG00000159387	IRX6	16:55293880-55367500	OK	2.16887	1.87773	-0.207953	-0.325794	0.56615	0.9998
ENSG00000197223	ENSG00000197223	C1D	2:68268261-68338080	OK	22.196	19.4679	-0.189199	-0.353409	0.5662	0.9998
ENSG00000227543	ENSG00000227543	SPAG5-AS1	17:26782769-26972472	OK	0.676868	0.444054	-0.608138	-0.0368537	0.5663	0.9998
ENSG00000041982	ENSG00000041982	TNC	9:117782805-117880536	OK	1.95368	2.26933	0.216071	0.209027	0.5664	0.9998
ENSG00000115363	ENSG00000115363	EVA1A	2:75696427-75796848	OK	24.8181	21.3312	-0.218424	-0.339127	0.5666	0.9998
ENSG00000185624	ENSG00000185624	P4HB	17:79801034-79818570	OK	571.873	513.498	-0.155336	-0.251237	0.5666	0.9998
ENSG00000175265	ENSG00000175265	GOLGA8A	15:34671268-34880704	OK	8.72116	10.8546	0.315719	0.295469	0.56665	0.9998
ENSG00000235363	ENSG00000235363	SNRPGP10	1:205305219-205326218	OK	3.63747	2.1705	-0.744907	-0.586776	0.5669	0.9998
ENSG00000171658	ENSG00000171658	RP11-443P15.2	3:185677731-185698658	OK	1.56166	1.29782	-0.266998	-0.286705	0.56715	0.9998
ENSG00000198855	ENSG00000198855	FICD	12:108908961-108955176	OK	2.69976	1.98096	-0.446629	-0.227757	0.5674	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000182362	ENSG00000182362	YBEY	21:47706250-47717665	OK	7.6809	8.90824	0.213865	0.34387	0.5675	0.9998
ENSG00000249565	ENSG00000249565	SERBP1P5	4:78978723-79465423	OK	6.00491	7.22808	0.26747	0.340324	0.5676	0.9998
ENSG00000107771	ENSG00000107771	CCSER2	10:86088341-86278273	OK	19.764	17.1129	-0.207793	-0.304721	0.56765	0.9998
ENSG00000067208	ENSG00000067208	EVI5	1:92974252-93257961	OK	7.38385	8.72801	0.24128	0.292311	0.5677	0.9998
ENSG00000068971	ENSG00000068971	PPP2R5B	11:64685024-64703360	OK	13.4524	11.8627	-0.181436	-0.26042	0.5677	0.9998
ENSG00000135454	ENSG00000135454	B4GALNT1	12:58003962-58027138	OK	2.85647	2.29584	-0.315213	-0.261298	0.5677	0.9998
ENSG00000167747	ENSG00000167747	C19orf48	19:51300960-51308186	OK	43.2475	38.9509	-0.150961	-0.333769	0.5677	0.9998
ENSG00000142528	ENSG00000142528	ZNF473	19:50479723-50570050	OK	6.26626	5.16542	-0.278717	-0.250644	0.56785	0.9998
ENSG00000087191	ENSG00000087191	PSMC5	17:61896792-61909379	OK	122.825	107.726	-0.189235	-0.342957	0.56795	0.9998
ENSG00000147419	ENSG00000147419	CCDC25	8:27590834-27695612	OK	32.4368	25.6797	-0.337006	-0.34044	0.56805	0.9998
ENSG00000157869	ENSG00000157869	RAB28	4:13362977-13485989	OK	12.9611	14.7038	0.182005	0.2717	0.56805	0.9998
ENSG00000165669	ENSG00000165669	FAM204A	10:120065400-120101840	OK	36.9892	42.2479	0.191775	0.358384	0.56815	0.9998
ENSG00000125834	ENSG00000125834	STK35	20:2082256-2157684	OK	3.02936	2.69495	-0.168752	-0.341498	0.56825	0.9998
ENSG00000147548	ENSG00000147548	WHSC1L1	8:38082735-38239790	OK	24.4646	21.0739	-0.215233	-0.278198	0.5683	0.9998
ENSG00000106009	ENSG00000106009	BRAT1	7:2577510-2595361	OK	28.2707	31.468	0.154577	0.323894	0.56835	0.9998
ENSG00000106723	ENSG00000106723	SPIN1	9:91003333-91093609	OK	17.1385	19.0075	0.149324	0.284032	0.56845	0.9998
ENSG00000174100	ENSG00000174100	MRPL45	17:36452988-36479101	OK	35.0257	38.6963	0.143781	0.337049	0.56845	0.9998
ENSG00000236088	ENSG00000236088	COX10-AS1	17:13659794-13972812	OK	1.45687	1.20165	-0.277859	-0.312535	0.5685	0.9998
ENSG00000163516	ENSG00000163516	ANKZF1	2:220094478-220142892	OK	35.2581	28.7869	-0.292543	-0.302219	0.56855	0.9998
ENSG00000132376	ENSG00000132376	INPP5K	17:1397864-1420182	OK	17.4174	15.4684	-0.171206	-0.286919	0.56865	0.9998
ENSG00000130749	ENSG00000130749	ZC3H4	19:47567443-47713886	OK	7.60695	5.35702	-0.505889	-0.243519	0.56875	0.9998
ENSG00000162927	ENSG00000162927	PUS10	2:61167356-61279125	OK	2.3657	1.69507	-0.480926	-0.313237	0.56875	0.9998
ENSG00000179933	ENSG00000179933	C14orf119	14:23527772-23569665	OK	41.797	31.5334	-0.406523	-0.341504	0.5688	0.9998
ENSG00000268947	ENSG00000268947	AD000684.2	19:35739232-35758867	OK	1.66086	1.23905	-0.42269	-0.341368	0.5688	0.9998
ENSG00000090863	ENSG00000090863	GLG1	16:74485855-74641012	OK	13.6612	15.0989	0.14435	0.313749	0.5689	0.9998
ENSG00000181061	ENSG00000181061	HIGD1A	3:42734154-42846023	OK	124.999	113.611	-0.137815	-0.34487	0.5689	0.9998
ENSG00000196305	ENSG00000196305	IARS	9:94972488-95056038	OK	73.576	66.6428	-0.142786	-0.304718	0.56895	0.9998
ENSG00000099804	ENSG00000099804	CDC34	19:531713-542097	OK	36.2361	32.222	-0.169382	-0.321781	0.56905	0.9998
ENSG00000103490	ENSG00000103490	PYCARD	16:31212805-31214773	OK	91.9452	82.8296	-0.150628	-0.347203	0.56905	0.9998
ENSG00000123965	ENSG00000123965	PMS2P5	7:74306893-74366314	OK	4.95079	4.0453	-0.291413	-0.344548	0.56905	0.9998
ENSG00000135316	ENSG00000135316	SYNCRIP	6:86215213-86353510	OK	54.3061	63.9763	0.236425	0.297389	0.5691	0.9998
ENSG00000158427	ENSG00000158427	TMSB15B	X:103172004-103229570	OK	2.23507	1.7759	-0.331772	-0.342763	0.56925	0.9998
ENSG00000242599	ENSG00000242599	CSAG4	X:151895975-151903184	OK	1.2428	2.27855	0.87452	0.214434	0.56925	0.9998
ENSG00000100938	ENSG00000100938	GMPR2	14:24641061-24708448	OK	50.9259	40.3442	-0.336039	-0.269263	0.5693	0.9998
ENSG00000086504	ENSG00000086504	MRPL28	16:417383-420527	OK	74.9476	82.9152	0.145754	0.348908	0.56935	0.9998
ENSG00000100519	ENSG00000100519	PSMC6	14:53173889-53195305	OK	48.7338	44.1049	-0.143982	-0.324954	0.5694	0.9998
ENSG00000157326	ENSG00000157326	DHRS4	14:24407939-24475617	OK	15.654	12.3038	-0.34742	-0.332001	0.56945	0.9998
ENSG00000171604	ENSG00000171604	CXXC5	5:139026883-139063467	OK	5.19573	5.86095	0.173809	0.27522	0.56945	0.9998
ENSG00000198093	ENSG00000198093	ZNF649	19:52359054-52408293	OK	2.65436	3.2449	0.289809	0.270596	0.56945	0.9998
ENSG00000166579	ENSG00000166579	NDEL1	17:8316448-8534079	OK	21.8924	28.7134	0.391296	0.259023	0.5696	0.9998
ENSG00000157404	ENSG00000157404	KIT	4:55524084-55606881	OK	50.9668	56.6594	0.152757	0.334891	0.56975	0.9998
ENSG00000178982	ENSG00000178982	EIF3K	19:39109734-39127595	OK	262.694	289.142	0.138396	0.341856	0.56975	0.9998
ENSG00000240682	ENSG00000240682	ISY1	3:128806411-128880136	OK	22.5799	18.7007	-0.27195	-0.33461	0.56975	0.9998
ENSG00000120539	ENSG00000120539	MASTL	10:27399382-27475853	OK	6.9077	4.86781	-0.504935	-0.408311	0.5698	0.9998
ENSG00000136068	ENSG00000136068	FLNB	3:57994126-58157982	OK	13.2646	11.8897	-0.157862	-0.242367	0.57	0.9998
ENSG00000144895	ENSG00000144895	EIF2A	3:150259780-150348222	OK	83.3093	98.846	0.246704	0.30008	0.57	0.9998
ENSG00000152527	ENSG00000152527	PLEKHH2	2:43864411-43995126	OK	5.30674	4.66379	-0.186322	-0.209791	0.57015	0.9998
ENSG00000260136	ENSG00000260136	CTD-2270L9.4	16:23399813-23468927	OK	2.79429	4.85011	0.795534	0.385379	0.57015	0.9998
ENSG00000068024	ENSG00000068024	HDAC4	2:239969863-240324058	OK	9.28776	11.2622	0.278083	0.221858	0.5702	0.9998
ENSG00000147852	ENSG00000147852	VLDLR	9:2422701-2660053	OK	32.4591	29.2658	-0.149406	-0.313489	0.5703	0.9998
ENSG00000133678	ENSG00000133678	TMEM254	10:81806615-81852313	OK	24.2384	19.2402	-0.333172	-0.340946	0.57035	0.9998
ENSG00000105854	ENSG00000105854	PON2	7:95034174-95064510	OK	134.623	122.894	-0.131511	-0.302102	0.5705	0.9998
ENSG00000115307	ENSG00000115307	AUP1	2:74753771-74784681	OK	84.6969	95.988	0.180545	0.321904	0.5705	0.9998
ENSG00000164989	ENSG00000164989	CCDC171	9:15552894-16061661	OK	13.1503	15.9604	0.279401	0.34927	0.5705	0.9998
ENSG00000175832	ENSG00000175832	ETV4	17:41561232-41687706	OK	71.3029	61.6134	-0.210717	-0.331915	0.5705	0.9998
ENSG00000198053	ENSG00000198053	SIRPA	20:1875153-1920543	OK	36.7635	33.3582	-0.140234	-0.344095	0.5705	0.9998
ENSG00000204084	ENSG00000204084	INPP5B	1:38326368-38412729	OK	5.78038	5.1061	-0.178942	-0.279776	0.5705	0.9998
ENSG00000172037	ENSG00000172037	LAMB2	3:49158546-49170551	OK	65.3987	73.6724	0.171863	0.214061	0.57055	0.9998
ENSG00000174804	ENSG00000174804	FZD4	11:86502100-86666433	OK	0.496701	0.773545	0.639109	0.342238	0.57055	0.9998
ENSG00000204946	ENSG00000204946	ZNF783	7:148959261-148994403	OK	7.38547	8.41413	0.188124	0.299406	0.57065	0.9998
ENSG00000127445	ENSG00000127445	PIN1	19:9945932-9960358	OK	80.7773	72.9999	-0.146056	-0.342178	0.5709	0.9998
ENSG00000173473	ENSG00000173473	SMARCC1	3:47626761-47823596	OK	22.6017	20.4721	-0.142771	-0.291946	0.57095	0.9998
ENSG00000179526	ENSG00000179526	SHARPIN	8:145153535-145173218	OK	32.7949	27.2407	-0.267708	-0.312492	0.57095	0.9998
ENSG00000048471	ENSG00000048471	SNX29	16:12070593-12704901	OK	5.27834	4.47683	-0.237607	-0.270721	0.5711	0.9998
ENSG00000070961	ENSG00000070961	ATP2B1	12:89954905-90106367	OK	10.1954	11.5485	0.179788	0.247853	0.57115	0.9998
ENSG00000215142	ENSG00000215142	RP11-292B8.1	9:40491621-40633282	OK	1.74171	1.46447	-0.250126	-0.341094	0.57115	0.9998
ENSG00000197170	ENSG00000197170	PSMD12	17:65334031-65362743	OK	48.1878	54.0324	0.165156	0.337704	0.57125	0.9998
ENSG00000153339	ENSG00000153339	TRAPPC8	18:29409135-29533099	OK	16.7297	15.1632	-0.141834	-0.29251	0.57135	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000186615	ENSG00000186615	KTN1-AS1	14:55965995-56168244	OK	2.18006	1.41648	-0.622058	-0.125593	0.57135	0.9998
ENSG00000112137	ENSG00000112137	PHACTR1	6:12717892-13328815	OK	143.592	116.018	-0.307626	-0.337929	0.5714	0.9998
ENSG00000273353	ENSG00000273353	CTA-268H5.12	22:45559721-45583896	OK	0.287722	0.85242	1.56689	0.102149	0.5715	0.9998
ENSG00000077063	ENSG00000077063	CTTNBP2	7:117105837-117514193	OK	16.7891	14.3552	-0.225948	-0.255043	0.5716	0.9998
ENSG00000238227	ENSG00000238227	C9orf69	9:139006426-139010731	OK	15.8331	14.2199	-0.155034	-0.329418	0.57165	0.9998
ENSG00000073921	ENSG00000073921	PICALM	11:85668726-85780924	OK	54.2131	60.2236	0.151688	0.290406	0.57175	0.9998
ENSG00000104313	ENSG00000104313	EYA1	8:72067691-72274467	OK	4.36646	3.79243	-0.203342	-0.325645	0.57175	0.9998
ENSG00000197933	ENSG00000197933	ZNF823	19:11832079-11849824	OK	1.77575	2.07585	0.22527	0.2867	0.5718	0.9998
ENSG00000107263	ENSG00000107263	RAPGEF1	9:134452156-134615461	OK	18.4323	16.199	-0.186328	-0.256455	0.5719	0.9998
ENSG00000228532	ENSG00000228532	RP1-241P17.4	X:114952649-114953685	OK	10.2021	11.6275	0.188674	0.345745	0.57195	0.9998
ENSG00000243113	ENSG00000243113	RP11-480I12.9	1:202830881-202844369	OK	0.661796	0.346211	-0.934735	-0.400899	0.57195	0.9998
ENSG00000222112	ENSG00000222112	RN7SKP16	1:33772366-33896653	OK	0.342326	0.88811	1.37537	0.114997	0.57205	0.9998
ENSG00000181135	ENSG00000181135	ZNF707	8:144766621-144796068	OK	3.47379	4.00303	0.20458	0.221639	0.5721	0.9998
ENSG00000267106	ENSG00000267106	C19orf82	19:9715355-9756572	OK	0.892784	0.582424	-0.616241	-0.175886	0.5721	0.9998
ENSG00000136404	ENSG00000136404	TM6SF1	15:83776158-84108197	OK	1.63652	2.33423	0.512323	0.274866	0.57215	0.9998
ENSG00000165959	ENSG00000165959	CLMN	14:95648276-95786243	OK	5.70404	4.70994	-0.276276	-0.309697	0.5722	0.9998
ENSG00000205444	ENSG00000205444	RP4-529N6.1	6:4610889-4611538	OK	3.77452	3.04958	-0.307684	-0.349094	0.5722	0.9998
ENSG00000078618	ENSG00000078618	NRD1	1:52027537-52344477	OK	53.2957	47.4488	-0.167649	-0.29809	0.5723	0.9998
ENSG00000272677	ENSG00000272677	RP11-127B20.3	4:83273650-83305180	OK	0.993528	0.564658	-0.815183	-0.102814	0.5723	0.9998
ENSG00000172728	ENSG00000172728	FUT10	8:33228341-33371119	OK	7.28672	8.91276	0.290602	0.267781	0.57245	0.9998
ENSG00000102595	ENSG00000102595	UGGT2	13:96453833-96705736	OK	9.8294	8.63955	-0.186148	-0.276667	0.5725	0.9998
ENSG00000116117	ENSG00000116117	PARD3B	2:205410515-206484886	OK	1.90635	2.23485	0.229364	0.247938	0.57255	0.9998
ENSG00000092931	ENSG00000092931	MFSD11	17:74722911-74777531	OK	14.9476	10.8875	-0.457234	-0.262465	0.5726	0.9998
ENSG00000150776	ENSG00000150776	C11orf57	11:111895537-112095422	OK	10.0633	12.6238	0.327046	0.233694	0.5726	0.9998
ENSG00000112624	ENSG00000112624	GLTSCR1L	6:42749764-42836298	OK	1.89328	1.67098	-0.180191	-0.341027	0.57265	0.9998
ENSG00000100412	ENSG00000100412	ACO2	22:41865128-41940610	OK	105.557	94.4652	-0.160166	-0.326668	0.5728	0.9998
ENSG00000105402	ENSG00000105402	NAPA	19:47987538-48018497	OK	72.6773	66.2562	-0.133451	-0.315581	0.5728	0.9998
ENSG00000169926	ENSG00000169926	KLF13	15:31619057-31727868	OK	4.33114	4.80903	0.150997	0.300506	0.5729	0.9998
ENSG00000269609	ENSG00000269609	RP11-18I14.10	10:104209573-104220863	OK	2.63195	3.11413	0.242699	0.304507	0.57295	0.9998
ENSG00000273340	ENSG00000273340	MICE	6:29690551-29716826	OK	2.13157	3.21787	0.594188	0.351195	0.57295	0.9998
ENSG00000057663	ENSG00000057663	ATG5	6:106632350-106773666	OK	9.92011	8.88081	-0.159664	-0.327856	0.573	0.9998
ENSG00000135829	ENSG00000135829	DHX9	1:182808503-182856886	OK	78.6788	86.6266	0.138835	0.213437	0.57305	0.9998
ENSG00000160145	ENSG00000160145	KALRN	3:123798869-124445172	OK	1.63479	1.99914	0.290274	0.26308	0.57305	0.9998
ENSG00000230562	ENSG00000230562	FAM133DP	2:158236235-158236926	OK	5.57385	6.5242	0.227127	0.337071	0.57305	0.9998
ENSG00000009413	ENSG00000009413	REV3L	6:111620233-111927481	OK	5.25417	6.09188	0.213425	0.275421	0.57315	0.9998
ENSG00000106785	ENSG00000106785	TRIM14	9:100819020-100881494	OK	4.2608	5.68348	0.415649	0.253518	0.57315	0.9998
ENSG00000166839	ENSG00000166839	ANKDD1A	15:65134081-65251042	OK	0.650531	0.903697	0.474221	0.106118	0.57315	0.9998
ENSG00000168005	ENSG00000168005	C11orf84	11:63580859-63595190	OK	18.5947	20.8935	0.168166	0.321373	0.5732	0.9998
ENSG00000157181	ENSG00000157181	C1orf27	1:186344889-186390510	OK	15.8575	14.0232	-0.177354	-0.273914	0.57325	0.9998
ENSG00000160087	ENSG00000160087	UBE2J2	1:1189288-1209265	OK	31.3469	34.9653	0.157603	0.324091	0.5733	0.9998
ENSG00000226232	ENSG00000226232	RP11-419C5.2	16:70010199-70099851	OK	1.55593	0.886619	-0.811387	-0.415241	0.57335	0.9998
ENSG00000140931	ENSG00000140931	CMTM3	16:66637776-66647795	OK	9.13746	10.4872	0.198767	0.317187	0.5734	0.9998
ENSG00000197037	ENSG00000197037	ZSCAN25	7:99214568-99230030	OK	5.27692	6.00198	0.185743	0.26726	0.5734	0.9998
ENSG00000081307	ENSG00000081307	UBA5	3:132276981-132593067	OK	26.5848	22.5745	-0.235907	-0.308785	0.5735	0.9998
ENSG00000090857	ENSG00000090857	PDPR	16:70147528-70221264	OK	5.30061	4.67851	-0.180109	-0.25412	0.57355	0.9998
ENSG00000120533	ENSG00000120533	ENY2	8:110253147-110358182	OK	106.698	93.3048	-0.193515	-0.341954	0.57375	0.9998
ENSG00000052802	ENSG00000052802	MSMO1	4:166248774-166264312	OK	68.31	75.2345	0.139296	0.33003	0.5738	0.9998
ENSG00000213073	ENSG00000213073	RP11-288H12.3	6:160390130-160534539	OK	0.726014	1.1983	0.722923	0.0837868	0.57395	0.9998
ENSG00000197757	ENSG00000197757	HOXC6	12:54375292-54449814	OK	4.21166	5.67706	0.430753	0.294535	0.574	0.9998
ENSG00000131773	ENSG00000131773	KHDRBS3	8:136469699-136668965	OK	12.1554	14.0879	0.212862	0.308022	0.57405	0.9998
ENSG00000131475	ENSG00000131475	VPS25	17:40925453-40931617	OK	61.6848	55.8009	-0.144626	-0.338633	0.5741	0.9998
ENSG00000183665	ENSG00000183665	TRMT12	8:125463047-125474391	OK	3.67006	4.18444	0.18923	0.329418	0.5742	0.9998
ENSG00000105887	ENSG00000105887	MTPN	7:135611202-135662101	OK	181.871	203.131	0.159497	0.318909	0.57425	0.9998
ENSG00000185347	ENSG00000185347	C14orf80	14:105952653-105965912	OK	13.7117	12.0621	-0.184919	-0.32681	0.57425	0.9998
ENSG00000154920	ENSG00000154920	EME1	17:48450580-48475249	OK	9.99706	6.86083	-0.54312	-0.218522	0.57435	0.9998
ENSG00000198744	ENSG00000198744	RP5-857K21.11	1:536815-660283	OK	1.10581	2.03432	0.879439	0.0698823	0.5744	0.9998
ENSG00000132323	ENSG00000132323	ILKAP	2:239079041-239112370	OK	40.6945	45.8051	0.170676	0.344397	0.57445	0.9998
ENSG00000070010	ENSG00000070010	UFD1L	22:19318220-19466738	OK	90.9814	76.7966	-0.244529	-0.274324	0.57455	0.9998
ENSG00000138439	ENSG00000138439	FAM117B	2:203499900-203634480	OK	1.38523	1.20396	-0.202336	-0.310934	0.5748	0.9998
ENSG00000101442	ENSG00000101442	ACTR5	20:37377084-37400834	OK	6.43397	7.25345	0.172959	0.338392	0.5749	0.9998
ENSG00000253301	ENSG00000253301	RP11-513O17.2	8:58055247-58153100	OK	0.623645	0.849824	0.446438	0.227333	0.5749	0.9998
ENSG00000124383	ENSG00000124383	MPHOSPH10	2:71357443-71377231	OK	13.321	14.843	0.15608	0.30009	0.57505	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000152380	ENSG00000152380	FAM151B	5:79778111-79838382	OK	1.02673	1.46342	0.511276	0.333162	0.57505	0.9998
ENSG00000133740	ENSG00000133740	E2F5	8:86089459-86132650	OK	7.38974	5.7277	-0.367569	-0.337589	0.57515	0.9998
ENSG00000082781	ENSG00000082781	ITGB5	3:124480794-124620265	OK	90.8719	104.808	0.205843	0.337526	0.5752	0.9998
ENSG00000033327	ENSG00000033327	GAB2	11:77926342-78285919	OK	21.8924	18.934	-0.209453	-0.261576	0.57525	0.9998
ENSG00000078487	ENSG00000078487	ZCWPW1	7:99998448-100031741	OK	1.11156	0.765114	-0.538842	-0.238184	0.57525	0.9998
ENSG00000171621	ENSG00000171621	SPSB1	1:9352938-9429591	OK	30.2947	26.619	-0.186608	-0.338119	0.57525	0.9998
ENSG00000222044	ENSG00000222044	RP5-1039K5.16	22:38339527-38437922	OK	1.59916	0.821294	-0.961348	-0.107536	0.57535	0.9998
ENSG00000150753	ENSG00000150753	CCT5	5:10250032-10267258	OK	362.041	410.686	0.18188	0.326034	0.5754	0.9998
ENSG00000213551	ENSG00000213551	DNAJC9	10:74870216-75118617	OK	22.0755	17.7981	-0.310725	-0.316328	0.5754	0.9998
ENSG00000111843	ENSG00000111843	TMEM14C	6:10723147-10731362	OK	126.743	114.905	-0.141463	-0.345648	0.5756	0.9998
ENSG00000168502	ENSG00000168502	SOGA2	18:8695853-8832776	OK	3.29255	3.89624	0.242876	0.244271	0.5756	0.9998
ENSG00000053900	ENSG00000053900	ANAPC4	4:25378834-25420120	OK	9.45615	8.34909	-0.179633	-0.294919	0.57575	0.9998
ENSG00000143252	ENSG00000143252	SDHC	1:161284046-161332984	OK	182.998	164.006	-0.158083	-0.313482	0.57575	0.9998
ENSG00000122912	ENSG00000122912	SLC25A16	10:70237755-70287231	OK	13.4769	15.236	0.176998	0.293178	0.57595	0.9998
ENSG00000198612	ENSG00000198612	COPS8	2:237968076-238009109	OK	98.3196	107.96	0.134946	0.326602	0.57605	0.9998
ENSG00000204574	ENSG00000204574	ABCF1	6:30539152-30564956	OK	69.8101	78.0843	0.161597	0.29676	0.57605	0.9998
ENSG00000227001	ENSG00000227001	NBPF2P	1:21751117-21754460	OK	1.38077	1.08868	-0.342901	-0.34208	0.57605	0.9998
ENSG00000122299	ENSG00000122299	ZC3H7A	16:11844441-11891123	OK	48.9735	43.6249	-0.16685	-0.259937	0.5761	0.9998
ENSG00000108840	ENSG00000108840	HDAC5	17:42154113-42201070	OK	27.5905	31.0559	0.170696	0.300759	0.57615	0.9998
ENSG00000213463	ENSG00000213463	SYNJ2BP	14:70791797-70883778	OK	13.9471	11.2791	-0.306309	-0.32471	0.5763	0.9998
ENSG00000074527	ENSG00000074527	NTN4	12:96043030-96184930	OK	2.51508	2.16167	-0.218455	-0.251019	0.57635	0.9998
ENSG00000143727	ENSG00000143727	ACP1	2:217729-278283	OK	106.364	117.273	0.14085	0.312764	0.57635	0.9998
ENSG00000126804	ENSG00000126804	ZBTB1	14:64854748-65009955	OK	19.6987	15.8391	-0.314608	-0.296819	0.5764	0.9998
ENSG00000245149	ENSG00000245149	RNF139-AS1	8:125474725-125486817	OK	1.12609	1.3424	0.253489	0.315442	0.5764	0.9998
ENSG00000090372	ENSG00000090372	STRN4	19:47222763-47291851	OK	35.1158	29.6015	-0.246448	-0.249982	0.5765	0.9998
ENSG00000136045	ENSG00000136045	PWP1	12:108079508-108106944	OK	55.9246	61.8927	0.146287	0.330898	0.57655	0.9998
ENSG00000168010	ENSG00000168010	ATG16L2	11:72525352-72853306	OK	6.87466	5.52035	-0.316529	-0.246075	0.57675	0.9998
ENSG00000225241	ENSG00000225241	RP11-640M9.2	1:144593362-144621656	OK	26.8311	23.3541	-0.200228	-0.330017	0.5768	0.9998
ENSG00000101220	ENSG00000101220	C20orf27	20:3734154-3749034	OK	25.9409	28.9738	0.159519	0.343282	0.57685	0.9998
ENSG00000237938	ENSG00000237938	RP11-288I21.1	1:16010826-16076391	OK	0.850185	0.372814	-1.18932	-0.121782	0.57695	0.9998
ENSG00000131748	ENSG00000131748	STARD3	17:37793317-37819737	OK	36.3123	41.1749	0.181307	0.326415	0.577	0.9998
ENSG00000144481	ENSG00000144481	TRPM8	2:234826042-234928166	OK	15.2958	12.7931	-0.257765	-0.318138	0.577	0.9998
ENSG00000205413	ENSG00000205413	SAMD9	7:92728828-92747336	OK	1.9295	1.69361	-0.188124	-0.325948	0.577	0.9998
ENSG00000241935	ENSG00000241935	HOGA1	10:99344079-99436191	OK	0.64315	1.0821	0.750611	0.206108	0.5771	0.9998
ENSG00000170242	ENSG00000170242	USP47	11:11862969-11980870	OK	18.8419	16.8322	-0.162725	-0.314148	0.5774	0.9998
ENSG00000149554	ENSG00000149554	CHEK1	11:125439111-125551018	OK	11.0543	8.44946	-0.387683	-0.227326	0.5775	0.9998
ENSG00000129219	ENSG00000129219	PLD2	17:4710390-4726729	OK	8.2728	7.29657	-0.181156	-0.227981	0.5776	0.9998
ENSG00000224660	ENSG00000224660	SH3BP5-AS1	3:15295690-15382875	OK	1.17453	0.826362	-0.507242	-0.180276	0.5776	0.9998
ENSG00000114686	ENSG00000114686	MRPL3	3:131181055-131221827	OK	86.8225	78.9183	-0.13771	-0.333577	0.57765	0.9998
ENSG00000175643	ENSG00000175643	RMI2	16:11343475-11445619	OK	15.5503	13.7715	-0.175255	-0.338557	0.57765	0.9998
ENSG00000112658	ENSG00000112658	SRF	6:43139036-43149243	OK	14.4351	16.4382	0.18747	0.342631	0.5778	0.9998
ENSG00000168887	ENSG00000168887	C2orf68	2:85825670-85876403	OK	17.0814	12.8537	-0.410242	-0.279717	0.5778	0.9998
ENSG00000123143	ENSG00000123143	PKN1	19:14543864-14582679	OK	47.462	43.2299	-0.134744	-0.323895	0.57785	0.9998
ENSG00000101187	ENSG00000101187	SLCO4A1	20:61272070-61317137	OK	1.49497	2.2385	0.582413	0.310287	0.5779	0.9998
ENSG00000117174	ENSG00000117174	ZNHIT6	1:86115105-86174116	OK	8.58194	9.60923	0.163117	0.337924	0.578	0.9998
ENSG00000151092	ENSG00000151092	NGLY1	3:25760434-25836025	OK	22.9761	25.7708	0.165607	0.319703	0.578	0.9998
ENSG00000236349	ENSG00000236349	SUCLG2P2	12:94942016-94943312	OK	0.777746	0.956938	0.299127	0.342884	0.578	0.9998
ENSG00000127884	ENSG00000127884	ECHS1	10:135175983-135187193	OK	99.7053	90.9293	-0.132925	-0.334514	0.57805	0.9998
ENSG00000100908	ENSG00000100908	EMC9	14:24605366-24610797	OK	13.3374	10.2113	-0.385319	-0.335862	0.57815	0.9998
ENSG00000090447	ENSG00000090447	TFAP4	16:4307186-4323076	OK	4.28067	5.20289	0.281477	0.323557	0.57855	0.9998
ENSG00000227345	ENSG00000227345	PARG	10:51026324-51130715	OK	4.69048	4.1412	-0.179688	-0.316004	0.57855	0.9998
ENSG00000142065	ENSG00000142065	ZFP14	19:36827161-36870101	OK	1.77197	2.23336	0.333861	0.294812	0.57865	0.9998
ENSG00000167377	ENSG00000167377	ZNF23	16:71481499-71598992	OK	2.70862	2.30576	-0.232312	-0.276658	0.57885	0.9998
ENSG00000083799	ENSG00000083799	CYLD	16:50774820-50837249	OK	4.74905	5.36906	0.177031	0.258602	0.5789	0.9998
ENSG00000025800	ENSG00000025800	KPNA6	1:32573638-32642169	OK	13.2152	14.5253	0.136373	0.325275	0.57895	0.9998
ENSG00000100605	ENSG00000100605	ITPK1	14:93403258-93582665	OK	60.3813	51.4208	-0.23175	-0.31986	0.579	0.9998
ENSG00000104081	ENSG00000104081	BMF	15:40380090-40401093	OK	5.09774	4.48795	-0.183802	-0.224281	0.579	0.9998
ENSG00000177595	ENSG00000177595	PIDD	11:799178-812880	OK	5.55057	7.28426	0.392146	0.129731	0.579	0.9998
ENSG00000165312	ENSG00000165312	OTUD1	10:23728197-23731308	OK	1.77826	1.54325	-0.204496	-0.329647	0.57905	0.9998
ENSG00000181007	ENSG00000181007	ZFP82	19:36874021-36909558	OK	2.73704	2.35494	-0.216927	-0.341996	0.57905	0.9998
ENSG00000228852	ENSG00000228852	RP11-57H12.5	1:95582893-95729610	OK	0.934166	0.494025	-0.919094	-0.148563	0.5791	0.9998
ENSG00000104885	ENSG00000104885	DOT1L	19:2100987-2248678	OK	14.4402	11.0264	-0.389137	-0.13226	0.57915	0.9998
ENSG00000141384	ENSG00000141384	TAF4B	18:23805899-23971649	OK	2.20726	1.92915	-0.194286	-0.33445	0.57915	0.9998
ENSG00000186350	ENSG00000186350	RXRA	9:137208943-137332431	OK	8.3097	7.15487	-0.215872	-0.338556	0.5792	0.9998
ENSG00000024048	ENSG00000024048	UBR2	6:42531799-42661242	OK	10.9315	12.0628	0.142068	0.338395	0.57925	0.9998
ENSG00000051523	ENSG00000051523	CYBA	16:88709690-88717560	OK	9.80022	11.2378	0.197477	0.295958	0.57925	0.9998
ENSG00000270041	ENSG00000270041	LL22NC03-N27C7.1	22:24080864-24081476	OK	0.969406	0.728519	-0.412134	-0.349739	0.57925	0.9998
ENSG00000100014	ENSG00000100014	SPECC1L	22:24666785-24924358	OK	13.7319	12.4062	-0.146471	-0.265658	0.5795	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000176024	ENSG00000176024	ZNF613	19:52430399-52452012	OK	2.09886	2.47546	0.239461	0.282195	0.57955	0.9998
ENSG00000108465	ENSG00000108465	CDK5RAP3	17:46018871-46073562	OK	62.6927	56.1313	-0.159491	-0.254885	0.5796	0.9998
ENSG00000121897	ENSG00000121897	LIAS	4:39460619-39479273	OK	4.94238	4.18468	-0.240088	-0.333168	0.5797	0.9998
ENSG00000155380	ENSG00000155380	SLC16A1	1:113454468-113542118	OK	17.7198	19.5194	0.139546	0.298252	0.5797	0.9998
ENSG00000175582	ENSG00000175582	RAB6A	11:73386682-73472182	OK	49.7072	44.5368	-0.158456	-0.325976	0.57985	0.9998
ENSG00000241549	ENSG00000241549	GUSBP2	6:26839262-26924333	OK	3.30548	2.63037	-0.329593	-0.392858	0.57985	0.9998
ENSG00000165476	ENSG00000165476	REEP3	10:65281122-65384883	OK	14.0742	12.7679	-0.140526	-0.336549	0.5799	0.9998
ENSG00000184208	ENSG00000184208	C22orf46	22:42069933-42094140	OK	3.27521	2.36019	-0.472688	-0.226618	0.5799	0.9998
ENSG00000158805	ENSG00000158805	ZNF276	16:89773541-89883065	OK	5.75272	7.23243	0.330236	0.296823	0.57995	0.9998
ENSG00000163832	ENSG00000163832	ELP6	3:47537129-47555251	OK	39.3334	44.0316	0.162784	0.32499	0.57995	0.9998
ENSG00000139990	ENSG00000139990	DCAF5	14:69517597-69619867	OK	19.12	17.2998	-0.144326	-0.287205	0.58	0.9998
ENSG00000152147	ENSG00000152147	GEMIN6	2:38978675-39012142	OK	20.4807	23.3611	0.189845	0.339468	0.58	0.9998
ENSG00000162972	ENSG00000162972	C2orf47	2:200775978-200873263	OK	23.6844	27.9082	0.236756	0.259974	0.58	0.9998
ENSG00000173706	ENSG00000173706	HEG1	3:124684553-124774802	OK	5.91664	4.96413	-0.253237	-0.303953	0.58005	0.9998
ENSG00000135924	ENSG00000135924	DNAJB2	2:220143988-220151622	OK	36.673	32.8766	-0.157655	-0.287787	0.5801	0.9998
ENSG00000151465	ENSG00000151465	CDC123	10:12171635-12292588	OK	29.8087	34.3076	0.202797	0.333182	0.58025	0.9998
ENSG00000157800	ENSG00000157800	SLC37A3	7:139993492-140126050	OK	35.8903	32.6088	-0.138336	-0.239929	0.5803	0.9998
ENSG00000116711	ENSG00000116711	PLA2G4A	1:186798084-186958113	OK	6.3715	7.16458	0.169247	0.340711	0.58035	0.9998
ENSG00000198833	ENSG00000198833	UBE2J1	6:90036343-90062567	OK	15.1245	16.6444	0.138144	0.332306	0.58035	0.9998
ENSG00000204410	ENSG00000204410	MSH5	6:31707724-31733365	OK	15.0513	13.0738	-0.203201	-0.310557	0.5804	0.9998
ENSG00000105699	ENSG00000105699	LSR	19:35739232-35758867	OK	2.32328	2.933	0.336214	0.282055	0.58055	0.9998
ENSG00000178607	ENSG00000178607	ERN1	17:62116501-62208179	OK	2.6436	2.28067	-0.213047	-0.222419	0.58055	0.9998
ENSG00000233868	ENSG00000233868	AC009302.2	2:222808941-222809331	OK	13.7158	16.0175	0.223808	0.332999	0.5806	0.9998
ENSG00000183726	ENSG00000183726	TMEM50A	1:25568727-25756683	OK	55.1372	48.2092	-0.193718	-0.32725	0.58065	0.9998
ENSG00000134265	ENSG00000134265	NAPG	18:10525901-10552758	OK	17.741	20.0056	0.173315	0.32077	0.58075	0.9998
ENSG00000175106	ENSG00000175106	TVP23C	17:15339331-15466909	OK	3.55045	4.71528	0.409342	0.336473	0.58075	0.9998
ENSG00000139410	ENSG00000139410	SDSL	12:113830249-113876081	OK	4.65963	3.99924	-0.220489	-0.30185	0.5808	0.9998
ENSG00000240489	ENSG00000240489	SETP14	3:155705092-155705965	OK	1.19785	1.47821	0.30341	0.342761	0.5808	0.9998
ENSG00000171552	ENSG00000171552	BCL2L1	20:30252254-30311792	OK	68.0142	75.0877	0.142741	0.31325	0.58085	0.9998
ENSG00000213903	ENSG00000213903	LTB4R	14:24769067-24787242	OK	2.533	3.34917	0.402956	0.213858	0.58105	0.9998
ENSG00000158411	ENSG00000158411	MITD1	2:99613723-100106497	OK	25.2399	17.8613	-0.49887	-0.258139	0.5811	0.9998
ENSG00000118217	ENSG00000118217	ATF6	1:161736083-161933860	OK	18.5622	20.3437	0.132211	0.330121	0.58115	0.9998
ENSG00000215126	ENSG00000215126	CBWD7	9:42668607-42714962	OK	0.646134	0.531606	-0.281475	-0.181412	0.58115	0.9998
ENSG00000025708	ENSG00000025708	TYMP	22:50961996-50971009	OK	5.28197	6.58019	0.317053	0.359891	0.58125	0.9998
ENSG00000174886	ENSG00000174886	NDUFA11	19:5865836-5904017	OK	263.101	290.339	0.142121	0.336685	0.5813	0.9998
ENSG00000271793	ENSG00000271793	RP11-321N4.5	6:86215213-86353510	OK	1.02117	2.00047	0.97011	0.141468	0.5813	0.9998
ENSG00000147654	ENSG00000147654	EBAG9	8:110551939-110578225	OK	9.8927	11.2231	0.182037	0.326199	0.5816	0.9998
ENSG00000196295	ENSG00000196295	AC005154.6	7:30536236-30673649	OK	13.9128	11.4412	-0.282181	-0.118675	0.58165	0.9998
ENSG00000146909	ENSG00000146909	NOM1	7:156742416-156765876	OK	18.9448	15.9772	-0.245786	-0.298915	0.58175	0.9998
ENSG00000168884	ENSG00000168884	TNIP2	4:2743374-2758103	OK	15.2669	13.5679	-0.170217	-0.325179	0.58175	0.9998
ENSG00000235033	ENSG00000235033	RP11-61I13.3	6:39760141-39902290	OK	0.984336	1.4229	0.531615	0.0917786	0.5818	0.9998
ENSG00000267740	ENSG00000267740	AC024592.12	19:5865836-5904017	OK	1.60927	3.2011	0.992164	0.198083	0.58185	0.9998
ENSG00000143322	ENSG00000143322	ABL2	1:179068461-179198819	OK	31.1125	34.5726	0.152137	0.191105	0.5819	0.9998
ENSG00000103168	ENSG00000103168	TAF1C	16:84178864-84220669	OK	8.9646	10.1805	0.183502	0.237816	0.58195	0.9998
ENSG00000059588	ENSG00000059588	TARBP1	1:234527058-234614849	OK	22.2373	24.7343	0.153532	0.272021	0.58215	0.9998
ENSG00000273300	ENSG00000273300	AC000068.9	22:19318220-19466738	OK	0.404498	1.12609	1.47712	0.103418	0.58215	0.9998
ENSG00000214960	ENSG00000214960	ISPD	7:16130816-16460947	OK	1.07888	1.30025	0.26926	0.330005	0.5822	0.9998
ENSG00000237380	ENSG00000237380	HOXD-AS2	2:176986338-177037830	OK	6.95003	9.09992	0.388835	0.339653	0.5822	0.9998
ENSG00000125124	ENSG00000125124	BBS2	16:56463044-56554195	OK	12.6253	14.9651	0.245288	0.207454	0.5824	0.9998
ENSG00000128524	ENSG00000128524	ATP6V1F	7:128470430-128550773	OK	338.371	372.013	0.136747	0.33225	0.5824	0.9998
ENSG00000267321	ENSG00000267321	RP11-1094M14.11	17:33895138-33901811	OK	1.91092	1.6129	-0.244615	-0.33166	0.5824	0.9998
ENSG00000179532	ENSG00000179532	DNHD1	11:6502676-6614988	OK	2.28252	1.78681	-0.353237	-0.214977	0.5826	0.9998
ENSG00000166548	ENSG00000166548	TK2	16:66461199-66586447	OK	5.85118	5.14449	-0.185699	-0.282472	0.58265	0.9998
ENSG00000132326	ENSG00000132326	PER2	2:239140324-239198743	OK	0.586535	1.0298	0.812078	0.24259	0.5827	0.9998
ENSG00000142552	ENSG00000142552	RCN3	19:50030874-50050219	OK	2.569	3.05795	0.251354	0.294336	0.5827	0.9998
ENSG00000198464	ENSG00000198464	ZNF480	19:52772823-52871031	OK	22.336	18.1947	-0.295856	-0.325247	0.5827	0.9998
ENSG00000108433	ENSG00000108433	GOSR2	17:45000482-45177689	OK	53.717	60.302	0.166828	0.326035	0.58285	0.9998
ENSG00000158792	ENSG00000158792	SPATA2L	16:89747144-89768113	OK	2.28813	2.96002	0.371442	0.30118	0.58285	0.9998
ENSG00000262147	ENSG00000262147	RP13-638C3.3	17:80477588-80606429	OK	1.17695	0.510657	-1.20462	-0.0788988	0.5829	0.9998
ENSG00000125871	ENSG00000125871	MGME1	20:17922240-18039832	OK	11.7741	14.0638	0.256376	0.309946	0.58295	0.9998
ENSG00000169087	ENSG00000169087	HSPBAP1	3:122458845-122512671	OK	5.7656	6.52489	0.178483	0.330857	0.58295	0.9998
ENSG00000112200	ENSG00000112200	ZNF451	6:56951641-57087078	OK	10.2097	11.6385	0.188954	0.176455	0.5831	0.9998
ENSG00000112039	ENSG00000112039	FANCE	6:35420137-35434880	OK	3.22874	2.83187	-0.189213	-0.331447	0.58315	0.9998
ENSG00000119685	ENSG00000119685	TTLL5	14:76041230-76550928	OK	11.7519	10.1038	-0.217996	-0.172625	0.58315	0.9998
ENSG00000272279	ENSG00000272279	RP11-157J24.2	6:1528598-1529146	OK	1.07482	0.808705	-0.410407	-0.339841	0.5832	0.9998
ENSG00000118873	ENSG00000118873	RAB3GAP2	1:220321634-220445796	OK	15.5447	17.3004	0.154386	0.220954	0.58325	0.9998
ENSG00000205220	ENSG00000205220	PSMB10	16:67927174-67970990	OK	44.077	52.9348	0.264189	0.350245	0.58325	0.9998
ENSG00000065268	ENSG00000065268	WDR18	19:983173-994569	OK	18.0337	20.0883	0.155661	0.316981	0.5833	0.9998
ENSG00000130520	ENSG00000130520	LSM4	19:18417039-18434084	OK	113.328	102.929	-0.138846	-0.326995	0.58335	0.9998
ENSG00000075234	ENSG00000075234	TTC38	22:46663857-46689905	OK	13.6137	15.335	0.17176	0.291053	0.5834	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000104321	ENSG00000104321	TRPA1	8:72740401-73030628	OK	1.77488	0.909224	-0.965013	-0.310141	0.5834	0.9998
ENSG00000259781	ENSG00000259781	RP11-673C5.1	15:71389290-72075722	OK	92.1069	82.4206	-0.160304	-0.337252	0.58345	0.9998
ENSG00000133943	ENSG00000133943	C14orf159	14:91336798-91691976	OK	4.16809	3.35875	-0.311462	-0.177664	0.5835	0.9998
ENSG00000197746	ENSG00000197746	PSAP	10:73576054-73611126	OK	1337.26	1504.09	0.169613	0.300227	0.58355	0.9998
ENSG00000135596	ENSG00000135596	MICAL1	6:109765264-109804440	OK	34.3361	30.5361	-0.169207	-0.271133	0.5836	0.9998
ENSG00000172216	ENSG00000172216	CEBPB	20:48807375-48809212	OK	25.7669	28.4134	0.14105	0.327058	0.5836	0.9998
ENSG00000231989	ENSG00000231989	PPP1R2P3	5:156277548-156279539	OK	2.76955	2.25246	-0.298147	-0.338136	0.5836	0.9998
ENSG00000137806	ENSG00000137806	NDUFAF1	15:41679550-41694717	OK	6.27863	5.40729	-0.215543	-0.331088	0.5837	0.9998
ENSG00000161847	ENSG00000161847	RAVER1	19:10415478-10444316	OK	17.0498	15.3107	-0.155209	-0.307735	0.5837	0.9998
ENSG00000101844	ENSG00000101844	ATG4A	X:107334897-107682727	OK	10.9576	12.2135	0.156551	0.306668	0.58385	0.9998
ENSG00000122068	ENSG00000122068	FYTTD1	3:197398263-197514467	OK	37.4112	43.5834	0.220309	0.292807	0.58395	0.9998
ENSG00000053372	ENSG00000053372	MRTO4	1:19536994-19586622	OK	20.6709	25.0293	0.276021	0.308002	0.58405	0.9998
ENSG00000174282	ENSG00000174282	ZBTB4	17:7362684-7387582	OK	10.4296	11.4773	0.138097	0.334295	0.5841	0.9998
ENSG00000132185	ENSG00000132185	FCRLA	1:161676761-161684142	OK	20.0385	22.5293	0.169028	0.331367	0.58435	0.9998
ENSG00000135766	ENSG00000135766	EGLN1	1:231499496-231560790	OK	149.608	179.305	0.261231	0.314642	0.58435	0.9998
ENSG00000021776	ENSG00000021776	AQR	15:35147731-35262040	OK	4.75814	4.27083	-0.155881	-0.281633	0.58445	0.9998
ENSG00000100401	ENSG00000100401	RANGAP1	22:41641614-41682255	OK	52.5074	47.8749	-0.133251	-0.312666	0.58455	0.9998
ENSG00000123685	ENSG00000123685	BATF3	1:212859759-212873327	OK	1.30902	1.6521	0.335812	0.293904	0.5846	0.9998
ENSG00000267340	ENSG00000267340	RP11-242D8.3	17:41316199-41322420	OK	0.372645	1.44386	1.95405	0.759735	0.5846	0.9998
ENSG00000196876	ENSG00000196876	SCN8A	12:51984049-52206648	OK	2.23278	1.84241	-0.277246	-0.202213	0.58475	0.9998
ENSG00000115239	ENSG00000115239	GPR75-ASB3	2:53759809-54087297	OK	10.8209	8.84781	-0.290433	-0.264857	0.5848	0.9998
ENSG00000151576	ENSG00000151576	QTRTD1	3:113666747-113807269	OK	15.3853	13.562	-0.18198	-0.235677	0.58485	0.9998
ENSG00000143570	ENSG00000143570	SLC39A1	1:153931574-153950164	OK	137.869	155.594	0.174481	0.33595	0.5849	0.9998
ENSG00000170325	ENSG00000170325	PRDM10	11:129769600-129872730	OK	2.82345	3.19652	0.17904	0.268348	0.5849	0.9998
ENSG00000160888	ENSG00000160888	IER2	19:13261228-13265722	OK	14.1445	15.7288	0.153172	0.334044	0.58505	0.9998
ENSG00000152117	ENSG00000152117	AC093838.4	2:132250385-132279146	OK	2.42405	2.0469	-0.243978	-0.30793	0.5851	0.9998
ENSG00000001461	ENSG00000001461	NIPAL3	1:24634045-24799466	OK	10.0503	8.71108	-0.206316	-0.311258	0.5853	0.9998
ENSG00000140526	ENSG00000140526	ABHD2	15:89630308-89745591	OK	62.5999	73.5234	0.232045	0.209468	0.5853	0.9998
ENSG00000149499	ENSG00000149499	EML3	11:62369689-62382592	OK	14.187	15.8177	0.156968	0.254627	0.5853	0.9998
ENSG00000156253	ENSG00000156253	RWDD2B	21:30376704-30391699	OK	10.2644	9.10455	-0.172993	-0.318179	0.5853	0.9998
ENSG00000273271	ENSG00000273271	AP000254.8	21:33031934-33041244	OK	0.529498	1.06482	1.00792	0.125051	0.58535	0.9998
ENSG00000187145	ENSG00000187145	MRPS21	1:150266288-150281414	OK	70.1937	63.7571	-0.138755	-0.331329	0.5854	0.9998
ENSG00000181284	ENSG00000181284	TMEM102	17:7323421-7361026	OK	3.1613	3.83745	0.279632	0.346647	0.58545	0.9998
ENSG00000174996	ENSG00000174996	KLC2	11:66024764-66035600	OK	23.3783	21.0756	-0.149598	-0.277332	0.5855	0.9998
ENSG00000223473	ENSG00000223473	GS1-124K5.3	7:65956082-65958553	OK	0.706571	0.53378	-0.404589	-0.337728	0.5855	0.9998
ENSG00000267280	ENSG00000267280	RP11-332H18.4	17:58754813-59488916	OK	5.30879	3.60289	-0.559229	-0.0909382	0.58555	0.9998
ENSG00000179832	ENSG00000179832	MROH1	8:145202918-145316843	OK	5.05277	5.74723	0.18579	0.320749	0.5857	0.9998
ENSG00000107882	ENSG00000107882	SUFU	10:104263743-104393292	OK	4.61211	5.37234	0.220122	0.339112	0.5858	0.9998
ENSG00000196911	ENSG00000196911	KPNA5	6:117002349-117063029	OK	1.53708	1.8026	0.229891	0.301016	0.5858	0.9998
ENSG00000137561	ENSG00000137561	TTPA	8:63961111-63998612	OK	1.17094	1.38159	0.238656	0.278795	0.586	0.9998
ENSG00000130305	ENSG00000130305	NSUN5	7:72716513-72722864	OK	24.7152	27.4184	0.149747	0.322024	0.5861	0.9998
ENSG00000136052	ENSG00000136052	SLC41A2	12:105196330-105352522	OK	2.21856	2.83823	0.35537	0.242443	0.58625	0.9998
ENSG00000173068	ENSG00000173068	BNC2	9:16409500-16870841	OK	8.37279	9.99958	0.25616	0.285785	0.5863	0.9998
ENSG00000111775	ENSG00000111775	COX6A1	12:120875892-120899389	OK	472.382	528.447	0.161805	0.336505	0.58635	0.9998
ENSG00000167965	ENSG00000167965	MLST8	16:2254248-2261951	OK	26.0675	28.9327	0.150447	0.312731	0.58635	0.9998
ENSG00000063046	ENSG00000063046	EIF4B	12:53399941-53458156	OK	216.5	241.34	0.156702	0.308718	0.5864	0.9998
ENSG00000088280	ENSG00000088280	ASAP3	1:23755055-23811061	OK	1.83098	2.11575	0.208552	0.251981	0.58685	0.9998
ENSG00000157110	ENSG00000157110	RBPMS	8:30239634-30429778	OK	33.4805	28.9815	-0.20819	-0.32998	0.58685	0.9998
ENSG00000157350	ENSG00000157350	ST3GAL2	16:70413337-70473140	OK	9.55063	11.2237	0.232884	0.292915	0.58685	0.9998
ENSG00000187498	ENSG00000187498	COL4A1	13:110801317-111165374	OK	4.82522	6.09249	0.336436	0.320557	0.587	0.9998
ENSG00000234742	ENSG00000234742	AC144530.1	3:197518096-197615307	OK	0.303849	0.62475	1.03992	0.119022	0.587	0.9998
ENSG00000173566	ENSG00000173566	NUDT18	8:21964382-21966932	OK	7.20738	6.35453	-0.181689	-0.329313	0.58725	0.9998
ENSG00000186792	ENSG00000186792	HYAL3	3:50316457-50336899	OK	1.23372	1.98422	0.68555	0.254514	0.5873	0.9998
ENSG00000102878	ENSG00000102878	HSF4	16:67188082-67203848	OK	18.1041	21.588	0.253912	0.256515	0.5874	0.9998
ENSG00000258056	ENSG00000258056	RP11-644F5.11	12:56119106-56124467	OK	3.49474	1.9959	-0.80815	-0.0654591	0.58745	0.9998
ENSG00000272142	ENSG00000272142	RP11-428J1.5	6:5030205-5054657	OK	2.04306	1.57443	-0.375905	-0.333023	0.58745	0.9998
ENSG00000124181	ENSG00000124181	PLCG1	20:39657457-39946312	OK	95.8975	83.9853	-0.191357	-0.20765	0.5876	0.9998
ENSG00000260923	ENSG00000260923	AC137934.1	16:90252404-90289086	OK	3.52363	2.79768	-0.33283	-0.312291	0.58765	0.9998
ENSG00000203791	ENSG00000203791	METTL10	10:126150402-126480439	OK	15.4573	10.2239	-0.596342	-0.430251	0.5877	0.9998
ENSG00000047249	ENSG00000047249	ATP6V1H	8:54628116-54756118	OK	53.5349	58.6714	0.132177	0.312563	0.58775	0.9998
ENSG00000134138	ENSG00000134138	MEIS2	15:37181405-37393504	OK	3.72651	4.24291	0.187231	0.231863	0.5878	0.9998
ENSG00000196367	ENSG00000196367	TRRAP	7:98475555-98741723	OK	11.2235	9.9946	-0.167296	-0.306413	0.5878	0.9998
ENSG00000197619	ENSG00000197619	ZNF615	19:52494584-52511483	OK	1.84954	2.21552	0.260477	0.239665	0.5878	0.9998
ENSG00000113407	ENSG00000113407	TARS	5:33440801-33469644	OK	176.376	194.692	0.14254	0.285488	0.58785	0.9998
ENSG00000268896	ENSG00000268896	RP11-256I23.1	2:220403668-220415317	OK	0.630147	0.290239	-1.11845	-0.107817	0.5879	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000117791	ENSG00000117791	2-Mar	1:220921566-220958150	OK	3.21374	2.66543	-0.269889	-0.321731	0.58795	0.9998
ENSG00000197744	ENSG00000197744	PTMAP2	5:118173016-118324240	OK	4.70845	1.87764	-1.32633	-0.494388	0.58795	0.9998
ENSG00000137124	ENSG00000137124	ALDH1B1	9:38392660-38398658	OK	49.0648	44.8472	-0.129672	-0.325962	0.5881	0.9998
ENSG00000151338	ENSG00000151338	MIPOL1	14:37667117-38021566	OK	2.6873	2.26967	-0.243677	-0.264495	0.5881	0.9998
ENSG00000156958	ENSG00000156958	GALK2	15:49398267-49913128	OK	7.97573	6.38751	-0.320361	-0.225323	0.5881	0.9998
ENSG00000066855	ENSG00000066855	MTFR1	8:66556968-66754557	OK	23.6825	21.333	-0.150734	-0.245382	0.58815	0.9998
ENSG00000183426	ENSG00000183426	NPIPA1	16:15005407-15045915	OK	6.06391	5.04235	-0.266151	-0.290662	0.58815	0.9998
ENSG00000185000	ENSG00000185000	DGAT1	8:145539953-145550573	OK	23.9191	26.6665	0.156865	0.313762	0.58815	0.9998
ENSG00000137216	ENSG00000137216	TMEM63B	6:44081193-44123256	OK	27.8623	23.705	-0.233119	-0.308797	0.5883	0.9998
ENSG00000237149	ENSG00000237149	ZNF503-AS2	10:77029576-77171600	OK	2.99623	2.2085	-0.44008	-0.262421	0.5884	0.9998
ENSG00000181904	ENSG00000181904	C5orf24	5:134094468-134195427	OK	8.55556	7.10111	-0.268818	-0.284218	0.5885	0.9998
ENSG00000140749	ENSG00000140749	IGSF6	16:21608538-21668794	OK	1.94978	3.46029	0.827579	0.0993841	0.5886	0.9998
ENSG00000198182	ENSG00000198182	ZNF607	19:37988062-38210691	OK	1.25183	1.56132	0.318727	0.22881	0.5887	0.9998
ENSG00000120656	ENSG00000120656	TAF12	1:28915834-28969597	OK	10.4452	9.20095	-0.18298	-0.330457	0.58875	0.9998
ENSG00000164654	ENSG00000164654	MIOS	7:7592092-7648560	OK	14.9081	16.7095	0.164571	0.272057	0.58875	0.9998
ENSG00000196150	ENSG00000196150	ZNF250	8:146052848-146127553	OK	2.97633	2.22408	-0.420323	-0.212501	0.58885	0.9998
ENSG00000251580	ENSG00000251580	RP11-539L10.3	4:6672451-6677774	OK	0.890632	0.452378	-0.977299	-0.26079	0.5889	0.9998
ENSG00000025293	ENSG00000025293	PHF20	20:34359895-34538303	OK	15.9521	17.6532	0.146186	0.260328	0.58895	0.9998
ENSG00000149294	ENSG00000149294	NCAM1	11:112830001-113149158	OK	8.76012	7.82623	-0.162632	-0.241723	0.5891	0.9998
ENSG00000067167	ENSG00000067167	TRAM1	8:71485676-71520622	OK	63.5353	57.8723	-0.134684	-0.305104	0.58925	0.9998
ENSG00000159079	ENSG00000159079	C21orf59	21:33948861-33985176	OK	15.9722	14.1609	-0.173646	-0.326678	0.58925	0.9998
ENSG00000176046	ENSG00000176046	NUPR1	16:28548605-28550495	OK	5.53119	6.41244	0.213283	0.33075	0.5893	0.9998
ENSG00000156735	ENSG00000156735	BAG4	8:37962759-38070819	OK	7.23463	8.83335	0.288041	0.29827	0.58935	0.9998
ENSG00000203814	ENSG00000203814	HIST2H2BF	1:149754226-149783928	OK	0.677426	0.909007	0.424228	0.279061	0.58945	0.9998
ENSG00000121274	ENSG00000121274	PAPD5	16:50186828-50269221	OK	3.15681	2.79621	-0.174992	-0.321725	0.5895	0.9998
ENSG00000135473	ENSG00000135473	PAN2	12:56665482-56727837	OK	10.335	8.04498	-0.361384	-0.100891	0.58975	0.9998
ENSG00000172354	ENSG00000172354	GNB2	7:100271153-100276797	OK	144.381	158.862	0.137891	0.325971	0.59005	0.9998
ENSG00000180953	ENSG00000180953	ST20	15:80125926-80217194	OK	37.9458	30.8953	-0.296551	-0.327866	0.5901	0.9998
ENSG00000128039	ENSG00000128039	SRD5A3	4:56212275-56262014	OK	26.4918	22.8652	-0.212394	-0.332422	0.59015	0.9998
ENSG00000133703	ENSG00000133703	KRAS	12:25348149-25403870	OK	12.1816	10.8964	-0.160851	-0.296653	0.59045	0.9998
ENSG00000163904	ENSG00000163904	SENP2	3:185300283-185351339	OK	48.7786	44.0382	-0.147492	-0.285702	0.5905	0.9998
ENSG00000128655	ENSG00000128655	PDE11A	2:178457979-178973066	OK	1.18073	0.992607	-0.250387	-0.228798	0.59065	0.9998
ENSG00000175220	ENSG00000175220	ARHGAP1	11:46698629-46722165	OK	18.4648	16.8035	-0.136015	-0.295113	0.59065	0.9998
ENSG00000237350	ENSG00000237350	CDC42P6	4:22694536-22821198	OK	16.0225	18.26	0.188589	0.32813	0.5907	0.9998
ENSG00000004139	ENSG00000004139	SARM1	17:26684603-26734215	OK	7.54991	6.3119	-0.258385	-0.244905	0.5908	0.9998
ENSG00000112378	ENSG00000112378	PERP	6:138409641-138428648	OK	26.9981	24.6325	-0.13229	-0.328079	0.5908	0.9998
ENSG00000177732	ENSG00000177732	SOX12	20:300956-340304	OK	5.30396	4.424	-0.261718	-0.33341	0.5908	0.9998
ENSG00000259511	ENSG00000259511	UBE2Q2L	15:84839929-84850986	OK	1.65307	2.06518	0.321117	0.324197	0.59085	0.9998
ENSG00000225210	ENSG00000225210	AL589743.1	14:19650017-19718563	OK	11.3464	9.50704	-0.255163	-0.304104	0.5909	0.9998
ENSG00000110841	ENSG00000110841	PPFIBP1	12:27676363-27848497	OK	53.4432	59.9727	0.166301	0.264068	0.59105	0.9998
ENSG00000150991	ENSG00000150991	UBC	12:125396149-125401914	OK	683.777	616.088	-0.150389	-0.259055	0.59105	0.9998
ENSG00000157450	ENSG00000157450	RNF111	15:59063390-59389618	OK	6.40598	7.69261	0.264054	0.19147	0.59145	0.9998
ENSG00000214176	ENSG00000214176	PLEKHM1P	17:62745780-62833272	OK	5.33285	6.33349	0.248093	0.330698	0.59145	0.9998
ENSG00000096717	ENSG00000096717	SIRT1	10:69644426-69678147	OK	5.57821	4.98495	-0.162224	-0.283074	0.5915	0.9998
ENSG00000011454	ENSG00000011454	RABGAP1	9:125703111-125867145	OK	13.8692	15.3207	0.143593	0.247928	0.59165	0.9998
ENSG00000105518	ENSG00000105518	TMEM205	19:11406823-11465620	OK	64.4285	72.3887	0.168066	0.335099	0.59165	0.9998
ENSG00000166716	ENSG00000166716	ZNF592	15:85291865-85349659	OK	7.42267	8.24185	0.151031	0.324517	0.59165	0.9998
ENSG00000100883	ENSG00000100883	SRP54	14:35390063-35498773	OK	34.9332	38.2542	0.13102	0.281095	0.5917	0.9998
ENSG00000129472	ENSG00000129472	RAB2B	14:21927178-21979517	OK	14.3839	10.7869	-0.415172	-0.264284	0.59175	0.9998
ENSG00000227232	ENSG00000227232	WASH7P	1:11868-31109	OK	3.60032	3.11934	-0.206883	-0.326418	0.59175	0.9998
ENSG00000169439	ENSG00000169439	SDC2	8:97505578-97624000	OK	19.5844	23.1518	0.241418	0.322033	0.592	0.9998
ENSG00000168000	ENSG00000168000	BSCL2	11:62457746-62494856	OK	40.3439	32.3654	-0.317901	-0.290944	0.59205	0.9998
ENSG00000185825	ENSG00000185825	BCAP31	X:152965946-152990152	OK	162.496	178.297	0.133877	0.324139	0.59205	0.9998
ENSG00000266977	ENSG00000266977	CTC-459F4.5	19:28175487-28475892	OK	1.1893	0.502342	-1.24337	-0.270423	0.59205	0.9998
ENSG00000125843	ENSG00000125843	AP5S1	20:3801177-3805949	OK	6.19734	5.48147	-0.177087	-0.316578	0.59225	0.9998
ENSG00000146556	ENSG00000146556	WASH2P	2:114341663-114359144	OK	3.81333	3.28068	-0.217059	-0.330054	0.59225	0.9998
ENSG00000198742	ENSG00000198742	SMURF1	7:98475555-98741723	OK	14.0443	12.0237	-0.2241	-0.298483	0.59225	0.9998
ENSG00000144712	ENSG00000144712	CAND2	3:12837970-12913415	OK	1.87779	3.48825	0.893469	0.19474	0.5923	0.9998
ENSG00000154845	ENSG00000154845	PPP4R1	18:9546788-9615238	OK	26.78	24.3092	-0.139654	-0.214224	0.5923	0.9998
ENSG00000177602	ENSG00000177602	GSG2	17:3617921-3704537	OK	3.72018	3.01394	-0.303723	-0.326943	0.5923	0.9998
ENSG00000185565	ENSG00000185565	LSAMP	3:115521234-117716439	OK	12.5967	8.94585	-0.493757	-0.348248	0.5923	0.9998
ENSG00000110435	ENSG00000110435	PDHX	11:34874640-35042138	OK	25.7829	22.8563	-0.173823	-0.293358	0.59245	0.9998
ENSG00000153310	ENSG00000153310	FAM49B	8:130844546-131029375	OK	36.7102	40.4619	0.140383	0.272186	0.59245	0.9998
ENSG00000175741	ENSG00000175741	RWDD4P2	7:39856147-39907739	OK	2.09793	1.57179	-0.416559	-0.296498	0.5926	0.9998
ENSG00000132581	ENSG00000132581	SDF2	17:26975373-27029697	OK	31.1162	39.2009	0.333219	0.286311	0.59265	0.9998
ENSG00000140750	ENSG00000140750	ARHGAP17	16:24930705-25026987	OK	12.354	11.0524	-0.160614	-0.262493	0.59265	0.9998
ENSG00000110442	ENSG00000110442	COMMD9	11:36295050-36310999	OK	37.067	41.2302	0.153564	0.312002	0.5927	0.9998
ENSG00000107789	ENSG00000107789	MINPP1	10:89264631-89313217	OK	9.2747	10.3045	0.151897	0.319174	0.59275	0.9998
ENSG00000213047	ENSG00000213047	DENND1B	1:197473877-197744826	OK	4.69138	5.39676	0.202081	0.272592	0.5928	0.9998
ENSG00000130024	ENSG00000130024	PHF10	6:170102232-170124151	OK	16.2542	14.158	-0.199193	-0.304116	0.59285	0.9998
ENSG00000182165	ENSG00000182165	TP53TG1	7:86954540-86974831	OK	28.3412	24.9144	-0.185922	-0.29341	0.59285	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000198176	ENSG00000198176	TFDP1	13:114239012-114295785	OK	77.1361	68.5903	-0.169402	-0.300358	0.59285	0.9998
ENSG00000110660	ENSG00000110660	SLC35F2	11:107661716-107799019	OK	0.691851	0.548731	-0.334363	-0.240273	0.5929	0.9998
ENSG00000130758	ENSG00000130758	MAP3K10	19:40697650-40721482	OK	10.202	11.4664	0.168562	0.269488	0.5929	0.9998
ENSG00000122687	ENSG00000122687	FTSJ2	7:2273865-2281840	OK	35.1905	31.791	-0.146571	-0.318722	0.59295	0.9998
ENSG00000133243	ENSG00000133243	BTBD2	19:1985446-2034880	OK	26.0462	28.5637	0.13311	0.309345	0.59295	0.9998
ENSG00000134899	ENSG00000134899	ERCC5	13:103451398-103528345	OK	12.4228	9.66314	-0.362426	-0.315644	0.5931	0.9998
ENSG00000150722	ENSG00000150722	PPP1R1C	2:182818967-182996125	OK	3.36785	4.07478	0.274895	0.317991	0.5933	0.9998
ENSG00000224113	ENSG00000224113	RP5-837J1.2	17:33332106-33448541	OK	2.72864	2.00062	-0.447736	-0.347498	0.59335	0.9998
ENSG00000083454	ENSG00000083454	P2RX5	17:3566195-3599698	OK	1.09109	1.49917	0.458387	0.139721	0.59345	0.9998
ENSG00000147144	ENSG00000147144	CCDC120	X:48911100-48927509	OK	2.13467	2.43727	0.191255	0.284982	0.59345	0.9998
ENSG00000154144	ENSG00000154144	TBRG1	11:124492731-124567414	OK	12.4888	10.679	-0.225855	-0.319976	0.59355	0.9998
ENSG00000037241	ENSG00000037241	RPL26L1	5:172381788-172396774	OK	72.5676	65.5358	-0.147043	-0.287582	0.5936	0.9998
ENSG00000155189	ENSG00000155189	AGPAT5	8:6565877-6617184	OK	19.9337	18.0431	-0.143763	-0.306835	0.5936	0.9998
ENSG00000035928	ENSG00000035928	RFC1	4:39289075-39367995	OK	23.4501	21.0924	-0.152877	-0.241649	0.59385	0.9998
ENSG00000140464	ENSG00000140464	PML	15:74287013-74340153	OK	13.7232	12.3564	-0.151354	-0.293584	0.5939	0.9998
ENSG00000161647	ENSG00000161647	MPP3	17:41878166-41910538	OK	4.66345	5.51894	0.242993	0.262693	0.5939	0.9998
ENSG00000129562	ENSG00000129562	DAD1	14:23033804-23058175	OK	248.083	271.238	0.128738	0.321123	0.59395	0.9998
ENSG00000196072	ENSG00000196072	BLOC1S2	10:102033712-102046469	OK	42.716	47.1253	0.141723	0.306277	0.594	0.9998
ENSG00000177855	ENSG00000177855	CACYBPP2	2:184472169-184472847	OK	20.5472	18.1972	-0.175225	-0.320436	0.5941	0.9998
ENSG00000234616	ENSG00000234616	JRK	8:143738873-143764142	OK	10.9925	13.6568	0.313104	0.326367	0.5941	0.9998
ENSG00000162924	ENSG00000162924	REL	2:61108655-61158745	OK	1.6307	1.38261	-0.238092	-0.318304	0.59415	0.9998
ENSG00000108219	ENSG00000108219	TSPAN14	10:82213921-82295698	OK	229.864	264.849	0.204389	0.304313	0.5942	0.9998
ENSG00000132330	ENSG00000132330	SCLY	2:238875468-239008054	OK	19.8861	17.1488	-0.213652	-0.233363	0.5942	0.9998
ENSG00000223865	ENSG00000223865	HLA-DPB1	6:33032345-33054978	OK	2.94651	4.40894	0.581422	0.363329	0.5942	0.9998
ENSG00000127527	ENSG00000127527	EPS15L1	19:16466049-16582896	OK	14.3278	15.8311	0.14394	0.286532	0.59425	0.9998
ENSG00000008256	ENSG00000008256	CYTH3	7:6201406-6312275	OK	48.6947	44.5213	-0.129268	-0.253674	0.59445	0.9998
ENSG00000126878	ENSG00000126878	AIF1L	9:133971862-133998539	OK	1.53766	1.7862	0.216157	0.248341	0.59445	0.9998
ENSG00000134874	ENSG00000134874	DZIP1	13:96085857-96296957	OK	16.7907	15.232	-0.140554	-0.278975	0.5945	0.9998
ENSG00000226958	ENSG00000226958	CTD-2328D6.1	X:108297360-108297792	OK	245.882	222.351	-0.145126	-0.327548	0.5945	0.9998
ENSG00000251569	ENSG00000251569	RP11-724O16.1	2:170335687-170382772	OK	1.19711	2.46437	1.04166	0.438976	0.59455	0.9998
ENSG00000163626	ENSG00000163626	COX18	4:73921796-73935472	OK	5.98139	5.1751	-0.208893	-0.318703	0.59475	0.9998
ENSG00000235957	ENSG00000235957	COX7CP1	13:49550047-49783915	OK	2.58489	5.32472	1.0426	0.0763588	0.5948	0.9998
ENSG00000136270	ENSG00000136270	TBRG4	7:45139698-45151646	OK	79.1195	86.677	0.131615	0.287668	0.595	0.9998
ENSG00000175197	ENSG00000175197	DDIT3	12:57853917-57914300	OK	41.0479	53.7568	0.389139	0.350274	0.595	0.9998
ENSG00000177981	ENSG00000177981	ASB8	12:48541570-48574996	OK	14.9002	13.4712	-0.145455	-0.256711	0.595	0.9998
ENSG00000167118	ENSG00000167118	URM1	9:131133597-131153015	OK	65.0832	58.8473	-0.145308	-0.320338	0.59505	0.9998
ENSG00000240685	ENSG00000240685	RP11-286H14.6	7:128784711-128809538	OK	0.798915	0.392615	-1.02493	-0.158859	0.59505	0.9998
ENSG00000167306	ENSG00000167306	MYO5B	18:47309868-47721463	OK	3.15284	3.97991	0.336084	0.310275	0.5951	0.9998
ENSG00000205937	ENSG00000205937	RNPS1	16:2303116-2323419	OK	77.2408	69.1018	-0.160639	-0.330422	0.59515	0.9998
ENSG00000116459	ENSG00000116459	ATP5F1	1:111981259-112005395	OK	263.725	296.965	0.171259	0.326574	0.5952	0.9998
ENSG00000272578	ENSG00000272578	AP000347.2	22:23950638-24059543	OK	1.60738	1.98617	0.305274	0.198135	0.5953	0.9998
ENSG00000185985	ENSG00000185985	SLITRK2	X:144899349-144907360	OK	2.50972	2.19922	-0.190537	-0.324389	0.5954	0.9998
ENSG00000065485	ENSG00000065485	PDIA5	3:122785908-122992977	OK	11.8586	9.94453	-0.253959	-0.297705	0.5955	0.9998
ENSG00000124549	ENSG00000124549	BTN2A3P	6:26421618-26432611	OK	2.89308	2.52074	-0.198755	-0.294205	0.59555	0.9998
ENSG00000147592	ENSG00000147592	LACTB2	8:71520811-71581409	OK	19.0203	16.9887	-0.162964	-0.308587	0.59565	0.9998
ENSG00000067064	ENSG00000067064	IDI1	10:1034337-1095110	OK	81.0391	72.0414	-0.169792	-0.310902	0.5957	0.9998
ENSG00000130227	ENSG00000130227	XPO7	8:21777179-21864096	OK	37.3383	34.1617	-0.128275	-0.274356	0.5958	0.9998
ENSG00000132823	ENSG00000132823	OSER1	20:42825135-42839431	OK	33.4195	36.6985	0.135034	0.314193	0.59585	0.9998
ENSG00000114993	ENSG00000114993	RTKN	2:74652962-74669549	OK	21.2526	19.1507	-0.150244	-0.295217	0.59595	0.9998
ENSG00000177963	ENSG00000177963	RIC8A	11:207510-215113	OK	49.3864	44.9693	-0.135172	-0.230176	0.596	0.9998
ENSG00000198131	ENSG00000198131	ZNF544	19:58739959-58827023	OK	7.15756	8.66069	0.275013	0.188535	0.59605	0.9998
ENSG00000267858	ENSG00000267858	AC016629.8	19:59070495-59111168	OK	0.799678	0.487051	-0.715346	-0.170093	0.59605	0.9998
ENSG00000168066	ENSG00000168066	SF1	11:64532077-64546258	OK	76.9772	66.8796	-0.202866	-0.323208	0.59615	0.9998
ENSG00000171346	ENSG00000171346	KRT15	17:39669994-39678781	OK	1.44489	1.8199	0.332901	0.321702	0.5962	0.9998
ENSG00000102409	ENSG00000102409	BEX4	X:102470019-102472174	OK	6.64406	7.53986	0.182474	0.325189	0.5964	0.9998
ENSG00000179101	ENSG00000179101	RP11-349N19.2	X:122648323-122648723	OK	19.124	16.5321	-0.210112	-0.322685	0.5965	0.9998
ENSG00000224016	ENSG00000224016	RP11-728K20.1	7:149587827-149606793	OK	2.42021	3.20421	0.40484	0.309106	0.5965	0.9998
ENSG00000255242	ENSG00000255242	C14orf169	14:73945188-74025651	OK	2.70036	4.12932	0.612751	0.393012	0.59655	0.9998
ENSG00000006377	ENSG00000006377	DLX6	7:96584452-96643377	OK	1.23104	0.970609	-0.342915	-0.319269	0.5966	0.9998
ENSG00000115295	ENSG00000115295	CLIP4	2:29320570-29412509	OK	24.4424	21.8419	-0.162293	-0.234091	0.59665	0.9998
ENSG00000232956	ENSG00000232956	SNHG15	7:45022621-45026560	OK	32.8998	37.0823	0.172653	0.333591	0.59665	0.9998
ENSG00000021762	ENSG00000021762	OSBPL5	11:3108345-3187969	OK	3.3117	3.78604	0.19312	0.233202	0.5967	0.9998
ENSG00000171885	ENSG00000171885	AQP4	18:24034873-24770662	OK	0.913315	0.631873	-0.531476	-0.159333	0.5968	0.9998
ENSG00000204681	ENSG00000204681	GABBR1	6:29523291-29601753	OK	10.2376	8.98768	-0.187856	-0.250902	0.59685	0.9998
ENSG00000185842	ENSG00000185842	DNAH14	1:225083963-225586996	OK	22.519	25.9495	0.204564	0.328166	0.59695	0.9998
ENSG00000070476	ENSG00000070476	ZXDC	3:126156443-126194762	OK	15.3242	13.8207	-0.148982	-0.323026	0.5971	0.9998
ENSG00000157500	ENSG00000157500	APPL1	3:57261764-57326710	OK	14.7362	16.2689	0.142755	0.26296	0.5971	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258314	ENSG00000258314	CTD-2314B22.1	14:19611767-19643377	OK	0.937411	0.720722	-0.37924	-0.295382	0.59725	0.9998
ENSG00000076067	ENSG00000076067	RBMS2	12:56915712-56984745	OK	2.95839	2.6095	-0.18104	-0.28161	0.5973	0.9998
ENSG00000004534	ENSG00000004534	RBM6	3:49977439-50226508	OK	26.9124	23.412	-0.201024	-0.219499	0.59745	0.9998
ENSG00000169246	ENSG00000169246	NPIPB3	16:21413557-21531765	OK	6.53738	7.87277	0.26816	0.296551	0.59755	0.9998
ENSG00000262372	ENSG00000262372	RP11-669E14.6	17:44107281-44302733	OK	0.434338	0.932229	1.10187	0.0947558	0.59765	0.9998
ENSG00000180776	ENSG00000180776	ZDHHC20	13:21950262-22033509	OK	23.2327	26.6629	0.198676	0.310898	0.59795	0.9998
ENSG00000105953	ENSG00000105953	OGDH	7:44646170-44748665	OK	41.295	37.5151	-0.138494	-0.317935	0.59805	0.9998
ENSG00000081377	ENSG00000081377	CDC14B	9:99212482-99382112	OK	8.91536	7.52219	-0.24514	-0.225574	0.5981	0.9998
ENSG00000115866	ENSG00000115866	DARS	2:136664246-136779888	OK	23.4097	25.749	0.137409	0.302841	0.59815	0.9998
ENSG00000151135	ENSG00000151135	C12orf23	12:107349496-107380944	OK	20.2728	17.9908	-0.172288	-0.287551	0.59825	0.9998
ENSG00000076770	ENSG00000076770	MBNL3	X:131337052-131623996	OK	1.35819	1.03027	-0.398654	-0.171753	0.5983	0.9998
ENSG00000125991	ENSG00000125991	ERGIC3	20:34129769-34145405	OK	285.903	311.69	0.124584	0.296158	0.59845	0.9998
ENSG00000152404	ENSG00000152404	CWF19L2	11:107197070-107328572	OK	2.62692	2.30613	-0.1879	-0.307577	0.59855	0.9998
ENSG00000259802	ENSG00000259802	CTD-2256P15.2	5:10352812-10353713	OK	1.03936	0.844227	-0.299991	-0.315847	0.59855	0.9998
ENSG00000124399	ENSG00000124399	RP11-663P9.2	4:43900473-43901368	OK	0.791119	1.10203	0.478202	0.323918	0.59865	0.9998
ENSG00000169247	ENSG00000169247	SH3TC2	5:148303201-148442726	OK	10.4947	11.8007	0.169205	0.245134	0.59865	0.9998
ENSG00000263917	ENSG00000263917	RP11-53I6.2	18:29598334-30050447	OK	0.408747	1.0966	1.42376	0.123932	0.59865	0.9998
ENSG00000110237	ENSG00000110237	ARHGEF17	11:73018279-73080136	OK	7.56065	8.60063	0.185932	0.200726	0.5987	0.9998
ENSG00000113368	ENSG00000113368	LMNB1	5:126112314-126172712	OK	14.9409	13.2663	-0.171499	-0.294594	0.5987	0.9998
ENSG00000105948	ENSG00000105948	TTC26	7:138818489-138876732	OK	7.68215	6.75446	-0.18567	-0.306508	0.59875	0.9998
ENSG00000160285	ENSG00000160285	LSS	21:47604992-47648738	OK	33.7168	30.6332	-0.138368	-0.233198	0.5988	0.9998
ENSG00000238105	ENSG00000238105	GOLGA2P5	12:100550134-100660857	OK	0.647118	0.445772	-0.537722	-0.188716	0.5988	0.9998
ENSG00000115998	ENSG00000115998	C2orf42	2:70377011-70475792	OK	4.67982	5.71104	0.2873	0.185678	0.59895	0.9998
ENSG00000123159	ENSG00000123159	GIPC1	19:14588571-14606944	OK	113.258	123.906	0.129642	0.308395	0.599	0.9998
ENSG00000214046	ENSG00000214046	SMIM7	19:16589867-16771253	OK	69.464	58.4569	-0.248893	-0.319121	0.599	0.9998
ENSG00000146700	ENSG00000146700	SRCRB4D	7:76018650-76071388	OK	0.496562	0.763488	0.620631	0.320989	0.5991	0.9998
ENSG00000197971	ENSG00000197971	MBP	18:74686645-74845639	OK	288.721	317.286	0.136109	0.266172	0.59915	0.9998
ENSG00000267100	ENSG00000267100	ILF3-AS1	19:10762537-10764520	OK	1.72416	1.47887	-0.221396	-0.322863	0.59915	0.9998
ENSG00000117475	ENSG00000117475	BLZF1	1:169337207-169429907	OK	21.8548	19.1649	-0.189485	-0.320763	0.5992	0.9998
ENSG00000264364	ENSG00000264364	DYNLL2	17:56160775-56172897	OK	24.8794	27.1527	0.126142	0.315821	0.5992	0.9998
ENSG00000131848	ENSG00000131848	ZSCAN5A	19:56732680-56904914	OK	1.63818	2.08227	0.346061	0.195882	0.59925	0.9998
ENSG00000164291	ENSG00000164291	ARSK	5:94890777-94940768	OK	3.32079	3.87666	0.223286	0.310049	0.5993	0.9998
ENSG00000061676	ENSG00000061676	NCKAP1	2:183773842-183903586	OK	59.4337	65.0224	0.129654	0.241464	0.59935	0.9998
ENSG00000104147	ENSG00000104147	OIP5	15:41576187-41624819	OK	4.18918	2.39795	-0.804865	-0.380251	0.59935	0.9998
ENSG00000160445	ENSG00000160445	ZER1	9:131486723-131534693	OK	10.4412	11.714	0.165944	0.261451	0.59935	0.9998
ENSG00000135090	ENSG00000135090	TAOK3	12:118587605-118810750	OK	28.8481	35.1227	0.283927	0.213251	0.5995	0.9998
ENSG00000165733	ENSG00000165733	BMS1	10:43278248-43330385	OK	6.13233	6.73542	0.135334	0.315602	0.59955	0.9998
ENSG00000105371	ENSG00000105371	ICAM4	19:10362576-10399695	OK	0.554753	0.929113	0.74401	0.0986562	0.5996	0.9998
ENSG00000121207	ENSG00000121207	LRAT	4:155548096-155674270	OK	2.20801	1.90535	-0.212689	-0.257973	0.5996	0.9998
ENSG00000129932	ENSG00000129932	DOHH	19:3490818-3500938	OK	9.57404	8.4977	-0.172055	-0.316126	0.5996	0.9998
ENSG00000175449	ENSG00000175449	RFESD	5:94982457-95034415	OK	4.98077	4.04368	-0.3007	-0.32494	0.5997	0.9998
ENSG00000164933	ENSG00000164933	SLC25A32	8:104410862-104455681	OK	22.2698	19.2798	-0.208	-0.321996	0.59975	0.9998
ENSG00000108528	ENSG00000108528	SLC25A11	17:4840424-4848517	OK	61.9619	54.0544	-0.196968	-0.317256	0.5998	0.9998
ENSG00000154553	ENSG00000154553	PDLIM3	4:186422850-186456766	OK	6.51635	5.74981	-0.180549	-0.29358	0.5999	0.9998
ENSG00000186834	ENSG00000186834	HEXIM1	17:43224683-43248951	OK	20.7776	22.8225	0.135432	0.320502	0.5999	0.9998
ENSG00000154277	ENSG00000154277	UCHL1	4:41222090-41270472	OK	2.23693	2.62577	0.231223	0.280895	0.60015	0.9998
ENSG00000177764	ENSG00000177764	ZCCHC3	20:277736-280965	OK	2.29338	1.87263	-0.29241	-0.320623	0.6003	0.9998
ENSG00000197647	ENSG00000197647	ZNF433	19:12098431-12167127	OK	1.62339	2.05436	0.339676	0.255349	0.60035	0.9998
ENSG00000259071	ENSG00000259071	RP11-247L20.4	14:50704280-50883179	OK	0.217996	0.636408	1.54565	0.193663	0.60035	0.9998
ENSG00000267244	ENSG00000267244	CTB-31O20.4	19:1815247-1848452	OK	0.592153	1.01366	0.775531	0.251372	0.60045	0.9998
ENSG00000136152	ENSG00000136152	COG3	13:46039059-46189874	OK	8.48021	9.53041	0.168438	0.151872	0.6006	0.9998
ENSG00000170161	ENSG00000170161	RP11-262H14.4	9:66513031-66555928	OK	0.90873	0.66472	-0.451104	-0.297527	0.6007	0.9998
ENSG00000205356	ENSG00000205356	TECPR1	7:97843935-97881563	OK	18.0365	15.1242	-0.254061	-0.289394	0.60075	0.9998
ENSG00000111331	ENSG00000111331	OAS3	12:113344581-113455556	OK	0.510571	0.658884	0.367912	0.218781	0.6009	0.9998
ENSG00000245614	ENSG00000245614	DDX11-AS1	12:31173696-31257725	OK	1.30721	0.897775	-0.542067	-0.287041	0.6009	0.9998
ENSG00000251022	ENSG00000251022	THAP9-AS1	4:83739813-83934079	OK	14.8655	18.6945	0.330641	0.223123	0.60095	0.9998
ENSG00000272686	ENSG00000272686	RP11-390E23.6	7:123389121-123391220	OK	1.25346	1.06887	-0.229832	-0.319379	0.60105	0.9998
ENSG00000177409	ENSG00000177409	SAMD9L	7:92759367-92777682	OK	1.36227	1.18151	-0.205379	-0.223291	0.60115	0.9998
ENSG00000123213	ENSG00000123213	NLN	5:64885506-65167553	OK	17.6097	14.7211	-0.25849	-0.257749	0.6015	0.9998
ENSG00000145348	ENSG00000145348	TBCK	4:106962755-107270383	OK	5.53989	4.56255	-0.280017	-0.218216	0.6016	0.9998
ENSG00000003249	ENSG00000003249	DBNDD1	16:90071272-90114181	OK	33.0497	29.3931	-0.16916	-0.312326	0.60175	0.9998
ENSG00000177106	ENSG00000177106	EPS8L2	11:644232-727727	OK	0.77815	0.939015	0.271099	0.0834394	0.6018	0.9998
ENSG00000100979	ENSG00000100979	PLTP	20:44517263-44540794	OK	16.4167	25.8576	0.65542	0.356811	0.60185	0.9998
ENSG00000205923	ENSG00000205923	CEMP1	16:2525146-2581423	OK	0.401369	1.01211	1.33437	0.180448	0.602	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000104142	ENSG00000104142	VPS18	15:41186627-41196173	OK	9.76142	8.85878	-0.139982	-0.29972	0.60205	0.9998
ENSG00000090612	ENSG00000090612	ZNF268	12:133707160-133783698	OK	9.28826	7.22391	-0.362627	-0.311192	0.6021	0.9998
ENSG00000133961	ENSG00000133961	NUMB	14:73741814-73943880	OK	21.3339	19.4021	-0.136938	-0.275218	0.6021	0.9998
ENSG00000248334	ENSG00000248334	WHAMMP2	15:28947099-29002537	OK	0.63425	0.789345	0.315603	0.30449	0.6021	0.9998
ENSG00000075336	ENSG00000075336	TIMM21	18:71815745-71826197	OK	25.9363	28.6646	0.144301	0.310509	0.6022	0.9998
ENSG00000095002	ENSG00000095002	MSH2	2:47630107-47798078	OK	18.5518	16.8748	-0.136688	-0.313907	0.60225	0.9998
ENSG00000215105	ENSG00000215105	TTC3P1	X:74960540-74966749	OK	0.692658	0.53169	-0.381558	-0.327662	0.60225	0.9998
ENSG00000124217	ENSG00000124217	MOCS3	20:49575362-49577820	OK	9.10651	10.09	0.147953	0.309443	0.60235	0.9998
ENSG00000222328	ENSG00000222328	RNU2-2P	11:62599705-62609281	OK	0.883317	1.98146	1.16556	0.269723	0.60235	0.9998
ENSG00000244167	ENSG00000244167	RP4-733B9.1	7:7196564-7288282	OK	0.844305	0.392292	-1.10584	-0.109568	0.60235	0.9998
ENSG00000265222	ENSG00000265222	RP11-466A19.8	17:30819539-31205655	OK	0.412375	0.765837	0.893079	0.0685269	0.60235	0.9998
ENSG00000272182	ENSG00000272182	RP11-802O23.3	3:58413356-58419584	OK	0.273697	0.659893	1.26965	0.144878	0.6025	0.9998
ENSG00000008282	ENSG00000008282	SYPL1	7:105730948-105753022	OK	61.5824	67.3503	0.129166	0.311988	0.60255	0.9998
ENSG00000115459	ENSG00000115459	ELMOD3	2:85569210-85618875	OK	10.3954	8.43107	-0.302158	-0.175926	0.60265	0.9998
ENSG00000180257	ENSG00000180257	ZNF816	19:53430387-53541151	OK	0.672874	0.818373	0.282421	0.184283	0.60265	0.9998
ENSG00000140691	ENSG00000140691	ARMC5	16:31468031-31478487	OK	2.02664	1.71168	-0.243674	-0.307416	0.60275	0.9998
ENSG00000186088	ENSG00000186088	GSAP	7:76139744-77045717	OK	3.67458	3.03165	-0.277476	-0.207556	0.603	0.9998
ENSG00000164038	ENSG00000164038	SLC9B2	4:103941024-104021040	OK	5.3411	6.45445	0.273155	0.271138	0.60305	0.9998
ENSG00000134453	ENSG00000134453	RBM17	10:6130949-6159420	OK	30.4917	26.4928	-0.202817	-0.327851	0.6033	0.9998
ENSG00000151500	ENSG00000151500	THYN1	11:134118172-134123264	OK	15.8694	14.0851	-0.17208	-0.318006	0.6034	0.9998
ENSG00000154429	ENSG00000154429	CCSAP	1:229455149-229479041	OK	9.14084	10.0439	0.135916	0.311223	0.6034	0.9998
ENSG00000125970	ENSG00000125970	RALY	20:32570857-32700138	OK	164.516	143.396	-0.198225	-0.306131	0.60345	0.9998
ENSG00000034510	ENSG00000034510	TMSB10	2:85048773-85134132	OK	857.97	940.609	0.132668	0.324037	0.60365	0.9998
ENSG00000144369	ENSG00000144369	FAM171B	2:187454791-187630685	OK	7.67373	9.63616	0.32853	0.321882	0.60365	0.9998
ENSG00000272909	ENSG00000272909	CTD-2555O16.4	14:64854748-65009955	OK	0.884035	0.479053	-0.883917	-0.147488	0.60365	0.9998
ENSG00000106610	ENSG00000106610	STAG3L4	7:66752527-66786513	OK	17.537	15.0913	-0.216688	-0.311786	0.6037	0.9998
ENSG00000132155	ENSG00000132155	RAF1	3:12525930-12705725	OK	51.5258	57.3588	0.15472	0.285814	0.6037	0.9998
ENSG00000152234	ENSG00000152234	ATP5A1	18:43664109-43708299	OK	344.693	377.28	0.130323	0.30754	0.6037	0.9998
ENSG00000139496	ENSG00000139496	NUPL1	13:25875661-25923938	OK	26.0614	28.4779	0.127925	0.265042	0.60395	0.9998
ENSG00000197324	ENSG00000197324	LRP10	14:23340821-23350789	OK	48.5561	54.341	0.16239	0.317414	0.6041	0.9998
ENSG00000110060	ENSG00000110060	PUS3	11:125753508-125773116	OK	3.72132	4.42336	0.249328	0.296366	0.60415	0.9998
ENSG00000205138	ENSG00000205138	SDHAF1	19:36486089-36487220	OK	6.50636	5.72744	-0.183962	-0.310795	0.60435	0.9998
ENSG00000136146	ENSG00000136146	MED4	13:48627458-48669267	OK	37.3368	33.452	-0.158503	-0.307677	0.6044	0.9998
ENSG00000200816	ENSG00000200816	SNORA38	6:31588496-31605548	OK	4.34601	11.466	1.3996	0.477539	0.6044	0.9998
ENSG00000133606	ENSG00000133606	MKRN1	7:140152839-140179369	OK	68.858	76.238	0.146885	0.261745	0.6046	0.9998
ENSG00000134597	ENSG00000134597	RBMX2	X:129535942-129547317	OK	20.4102	18.4241	-0.147698	-0.290077	0.60475	0.9998
ENSG00000162999	ENSG00000162999	DUSP19	2:183943286-183973247	OK	1.19779	0.955544	-0.325984	-0.309708	0.6049	0.9998
ENSG00000103415	ENSG00000103415	HMOX2	16:4511680-4560348	OK	58.5021	66.0411	0.174875	0.321436	0.60495	0.9998
ENSG00000130830	ENSG00000130830	MPP1	X:154006958-154049282	OK	12.4705	13.775	0.143537	0.269803	0.60495	0.9998
ENSG00000165626	ENSG00000165626	BEND7	10:13480483-13572262	OK	1.07268	1.40137	0.385625	0.269031	0.60495	0.9998
ENSG00000123636	ENSG00000123636	BAZ2B	2:160175489-160473593	OK	7.70605	9.34719	0.27854	0.255974	0.605	0.9998
ENSG00000071189	ENSG00000071189	SNX13	7:17830384-17980124	OK	14.5165	12.8389	-0.177164	-0.269567	0.6052	0.9998
ENSG00000182134	ENSG00000182134	TDRKH	1:151728016-151766878	OK	9.7877	7.88919	-0.311093	-0.316774	0.6053	0.9998
ENSG00000204231	ENSG00000204231	RXRB	6:33161364-33172216	OK	28.4956	23.1805	-0.297825	-0.28981	0.6053	0.9998
ENSG00000162437	ENSG00000162437	RAVER2	1:65210777-65432187	OK	5.43904	4.11099	-0.403866	-0.288652	0.60555	0.9998
ENSG00000261690	ENSG00000261690	AC009133.12	16:29817426-29859355	OK	1.29196	0.697069	-0.890192	-0.103102	0.60555	0.9998
ENSG00000114491	ENSG00000114491	UMPS	3:124449212-124464040	OK	27.8318	31.7929	0.191971	0.308277	0.6056	0.9998
ENSG00000271885	ENSG00000271885	SRSF8	11:94800055-94804388	OK	7.34577	8.41248	0.195619	0.310274	0.60565	0.9998
ENSG00000168268	ENSG00000168268	NT5DC2	3:52529353-52742182	OK	69.6487	58.1646	-0.259956	-0.256601	0.60575	0.9998
ENSG00000144048	ENSG00000144048	DUSP11	2:73989310-74007284	OK	13.4183	12.0555	-0.154502	-0.312779	0.6058	0.9998
ENSG00000165948	ENSG00000165948	IFI27L1	14:94547627-94570192	OK	50.987	45.8864	-0.152063	-0.315201	0.6058	0.9998
ENSG00000151881	ENSG00000151881	C5orf28	5:43444353-43483995	OK	19.6141	17.3468	-0.177222	-0.303046	0.60585	0.9998
ENSG00000188167	ENSG00000188167	TMPPE	3:33038099-33138722	OK	0.800764	0.455836	-0.812864	-0.281964	0.6059	0.9998
ENSG00000100664	ENSG00000100664	EIF5	14:103799880-103811362	OK	138.331	157.799	0.189969	0.297063	0.60605	0.9998
ENSG00000132963	ENSG00000132963	POMP	13:29233240-29253062	OK	104.981	114.562	0.125997	0.316026	0.60615	0.9998
ENSG00000091140	ENSG00000091140	DLD	7:107531414-107643700	OK	82.7949	94.9945	0.198301	0.285492	0.6062	0.9998
ENSG00000163795	ENSG00000163795	ZNF513	2:27600097-27603657	OK	8.77277	9.77084	0.155451	0.278777	0.6063	0.9998
ENSG00000103876	ENSG00000103876	FAH	15:80444831-80479288	OK	123.634	137.289	0.151139	0.291093	0.6065	0.9998
ENSG00000123388	ENSG00000123388	HOXC11	12:54356091-54371427	OK	0.582586	0.709024	0.283365	0.313317	0.6065	0.9998
ENSG00000134186	ENSG00000134186	PRPF38B	1:109234944-109244425	OK	16.8441	15.0571	-0.1618	-0.306595	0.6065	0.9998
ENSG00000058091	ENSG00000058091	CDK14	7:89964536-90839905	OK	4.729	6.28672	0.410773	0.141208	0.6066	0.9998
ENSG00000105662	ENSG00000105662	CRTC1	19:18794486-18893004	OK	3.04581	3.48014	0.192323	0.30996	0.6066	0.9998
ENSG00000230042	ENSG00000230042	AK3P3	7:23145352-23240630	OK	0.463134	0.880256	0.926492	0.125525	0.60665	0.9998
ENSG00000119227	ENSG00000119227	PIGZ	3:196673213-196695931	OK	6.00934	5.21023	-0.20586	-0.310015	0.6067	0.9998
ENSG00000122678	ENSG00000122678	POLM	7:44111845-44122139	OK	10.2452	9.16653	-0.160497	-0.272603	0.6067	0.9998
ENSG00000214391	ENSG00000214391	RP11-121L10.3	11:89984399-90648220	OK	0.685051	0.83997	0.294125	0.32391	0.6068	0.9998
ENSG00000108479	ENSG00000108479	GALK1	17:73717407-73761792	OK	19.5488	21.6036	0.144186	0.29519	0.60685	0.9998
ENSG00000123200	ENSG00000123200	ZC3H13	13:46528599-46626894	OK	37.036	40.6053	0.132737	0.205869	0.607	0.9998
ENSG00000103042	ENSG00000103042	SLC38A7	16:58699012-58719008	OK	4.76038	4.23766	-0.167809	-0.211284	0.6071	0.9998
ENSG00000168517	ENSG00000168517	HEXIM2	17:43224683-43248951	OK	7.64795	4.97673	-0.619875	-0.338979	0.6071	0.9998
ENSG00000108312	ENSG00000108312	UBTF	17:42269172-42301078	OK	32.0102	36.1617	0.17593	0.29122	0.60715	0.9998
ENSG00000230280	ENSG00000230280	HNRNPA1P59	1:202860227-202897764	OK	1.19171	0.574391	-1.05292	-0.239469	0.60715	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000148290	ENSG00000148290	SURF1	9:136218609-136228045	OK	45.2327	40.3102	-0.166221	-0.317483	0.6072	0.9998
ENSG00000228158	ENSG00000228158	TLE1P1	X:64627963-64628565	OK	4.02767	3.34911	-0.266169	-0.297998	0.60725	0.9998
ENSG00000205323	ENSG00000205323	SARNP	12:56137063-56236750	OK	34.7467	28.1136	-0.305608	-0.308386	0.60745	0.9998
ENSG00000174977	ENSG00000174977	AC026271.5	17:18538318-18585575	OK	27.0568	23.7519	-0.187943	-0.308571	0.60755	0.9998
ENSG00000023734	ENSG00000023734	STRAP	12:16035324-16056412	OK	111.56	121.861	0.127425	0.319706	0.6076	0.9998
ENSG00000068120	ENSG00000068120	COASY	17:40688189-40718295	OK	36.8488	41.1628	0.159721	0.263477	0.6076	0.9998
ENSG00000112335	ENSG00000112335	SNX3	6:108532425-108582464	OK	72.6848	79.7325	0.133513	0.312472	0.60765	0.9998
ENSG00000124587	ENSG00000124587	PEX6	6:42928495-42946958	OK	6.96746	7.69426	0.143151	0.306748	0.6077	0.9998
ENSG00000260766	ENSG00000260766	RP11-226L15.5	1:159994742-159996584	OK	1.25978	1.47128	0.223895	0.312849	0.6079	0.9998
ENSG00000072310	ENSG00000072310	SREBF1	17:17584786-17740325	OK	65.3488	57.2069	-0.191971	-0.192564	0.60805	0.9998
ENSG00000073060	ENSG00000073060	SCARB1	12:125261401-125367214	OK	215.14	196.246	-0.132612	-0.289431	0.60805	0.9998
ENSG00000133704	ENSG00000133704	IPO8	12:30781921-30848920	OK	15.6748	14.2749	-0.134971	-0.238184	0.6081	0.9998
ENSG00000267169	ENSG00000267169	CTB-55O6.12	19:14247990-14316999	OK	1.09012	0.749323	-0.540824	-0.217062	0.60815	0.9998
ENSG00000251349	ENSG00000251349	MSANTD3-TMEFF1	9:103189437-103339918	OK	1.19926	2.85954	1.25364	0.418435	0.60825	0.9998
ENSG00000197956	ENSG00000197956	S100A6	1:153506078-153508720	OK	894.114	976.623	0.127344	0.316456	0.6083	0.9998
ENSG00000236992	ENSG00000236992	RPL12L3	20:19804086-19804587	OK	1.19538	1.52728	0.353501	0.311733	0.6083	0.9998
ENSG00000079332	ENSG00000079332	SAR1A	10:71907044-71930279	OK	41.3729	37.1696	-0.154565	-0.2921	0.6084	0.9998
ENSG00000144559	ENSG00000144559	TAMM41	3:11831915-11888393	OK	7.03562	7.9694	0.179795	0.307538	0.6084	0.9998
ENSG00000170775	ENSG00000170775	GPR37	7:124386050-124405681	OK	3.68198	3.29115	-0.16189	-0.299671	0.6084	0.9998
ENSG00000227758	ENSG00000227758	HCG9P5	6:29690551-29716826	OK	1.95904	4.10518	1.0673	0.174776	0.60845	0.9998
ENSG00000215462	ENSG00000215462	AL136218.1	13:49882785-50069138	OK	8.88802	3.93982	-1.17373	-0.238828	0.6085	0.9998
ENSG00000167550	ENSG00000167550	RHEBL1	12:49458467-49463808	OK	6.45818	5.6845	-0.184093	-0.303437	0.60885	0.9998
ENSG00000159256	ENSG00000159256	MORC3	21:37692089-37791313	OK	5.14043	5.83442	0.182699	0.240249	0.6089	0.9998
ENSG00000237846	ENSG00000237846	RP11-216M21.1	9:42250839-42251545	OK	1.63998	1.34169	-0.289631	-0.310544	0.609	0.9998
ENSG00000269893	ENSG00000269893	SNHG8	4:119199863-119200978	OK	72.5742	81.2496	0.162904	0.31198	0.60905	0.9998
ENSG00000138600	ENSG00000138600	SPPL2A	15:50999505-51058005	OK	12.14	10.5488	-0.20269	-0.296676	0.60915	0.9998
ENSG00000156959	ENSG00000156959	LHFPL4	3:9543480-9595486	OK	1.76254	2.07527	0.235647	0.28298	0.60925	0.9998
ENSG00000164323	ENSG00000164323	KIAA1430	4:186080818-186317053	OK	7.75401	8.98668	0.212846	0.289171	0.6095	0.9998
ENSG00000100288	ENSG00000100288	CHKB	22:51007289-51052409	OK	13.4491	16.8734	0.327237	0.316045	0.6096	0.9998
ENSG00000112787	ENSG00000112787	FBRSL1	12:133066136-133161774	OK	15.0862	12.9487	-0.220427	-0.160313	0.6096	0.9998
ENSG00000266964	ENSG00000266964	FXYD1	19:35615416-35645204	OK	2.06175	1.45844	-0.499439	-0.204308	0.60965	0.9998
ENSG00000182831	ENSG00000182831	C16orf72	16:9185504-9215497	OK	10.5536	9.39194	-0.168235	-0.3082	0.6097	0.9998
ENSG00000101298	ENSG00000101298	SNPH	20:1206699-1289972	OK	2.44302	2.1709	-0.170374	-0.315267	0.61025	0.9998
ENSG00000177380	ENSG00000177380	PPFIA3	19:49622645-49654283	OK	6.07523	7.13853	0.232687	0.331201	0.6103	0.9998
ENSG00000134900	ENSG00000134900	TPP2	13:103249352-103331521	OK	19.5534	17.8762	-0.129386	-0.237533	0.61035	0.9998
ENSG00000125107	ENSG00000125107	CNOT1	16:58549382-58663790	OK	37.1906	33.2845	-0.160089	-0.167736	0.6104	0.9998
ENSG00000223482	ENSG00000223482	NUTM2A-AS1	10:88963631-89102369	OK	27.2013	31.4111	0.207597	0.325699	0.61055	0.9998
ENSG00000182944	ENSG00000182944	EWSR1	22:29655840-29696515	OK	74.5441	81.9767	0.13712	0.3035	0.61065	0.9998
ENSG00000197562	ENSG00000197562	RAB40C	16:639356-684116	OK	8.10647	7.3068	-0.149834	-0.268044	0.61075	0.9998
ENSG00000100744	ENSG00000100744	GSKIP	14:96747594-96853625	OK	14.2802	12.2506	-0.221157	-0.282466	0.61085	0.9998
ENSG00000132912	ENSG00000132912	DCTN4	5:150088001-150138671	OK	31.0216	33.7776	0.122791	0.263172	0.61085	0.9998
ENSG00000102189	ENSG00000102189	EEA1	12:93115280-93323107	OK	5.64378	6.2764	0.153275	0.211171	0.6109	0.9998
ENSG00000155330	ENSG00000155330	C16orf87	16:46830518-46865323	OK	4.36874	3.81808	-0.194368	-0.304175	0.61095	0.9998
ENSG00000126243	ENSG00000126243	LRFN3	19:36426259-36436669	OK	8.0057	9.62197	0.265303	0.29437	0.61105	0.9998
ENSG00000228393	ENSG00000228393	LINC01004	7:104581509-104653491	OK	0.753586	0.584734	-0.365992	-0.292134	0.6111	0.9998
ENSG00000131370	ENSG00000131370	SH3BP5	3:15295690-15382875	OK	23.9954	26.4522	0.140634	0.285503	0.61115	0.9998
ENSG00000137218	ENSG00000137218	FRS3	6:41737913-41863099	OK	4.27225	2.49236	-0.777484	-0.324344	0.61115	0.9998
ENSG00000196235	ENSG00000196235	SUPT5H	19:39926795-39967310	OK	46.1864	50.4196	0.126516	0.218723	0.61115	0.9998
ENSG00000081059	ENSG00000081059	TCF7	5:133450401-133706738	OK	3.1827	4.22287	0.407973	0.137657	0.61125	0.9998
ENSG00000068137	ENSG00000068137	PLEKHH3	17:40819931-40829048	OK	9.19631	10.5437	0.197258	0.310131	0.6113	0.9998
ENSG00000128683	ENSG00000128683	GAD1	2:171669722-171717661	OK	6.62729	7.55616	0.189234	0.283797	0.6113	0.9998
ENSG00000237868	ENSG00000237868	AC097533.1	4:122998994-122999473	OK	2.20916	2.72163	0.300974	0.316351	0.6116	0.9998
ENSG00000261373	ENSG00000261373	VPS9D1-AS1	16:89773541-89883065	OK	0.562467	1.04237	0.890023	0.308742	0.61165	0.9998
ENSG00000237499	ENSG00000237499	RP11-356I2.4	6:138144809-138204449	OK	1.02141	0.736627	-0.471555	-0.127776	0.61175	0.9998
ENSG00000171951	ENSG00000171951	SCG2	2:224461657-224467221	OK	2.47548	2.18633	-0.179198	-0.279601	0.6118	0.9998
ENSG00000170571	ENSG00000170571	EMB	5:49692025-49739082	OK	4.27925	3.74168	-0.193672	-0.284033	0.61185	0.9998
ENSG00000137955	ENSG00000137955	RABGGTB	1:76190035-76260764	OK	71.4542	80.7144	0.175808	0.303149	0.612	0.9998
ENSG00000230267	ENSG00000230267	HERC2P4	16:32114565-32199434	OK	0.884188	0.695901	-0.345472	-0.2758	0.6121	0.9998
ENSG00000142409	ENSG00000142409	ZNF787	19:56598731-56632649	OK	15.2996	16.8668	0.140693	0.303885	0.6122	0.9998
ENSG00000107949	ENSG00000107949	BCCIP	10:127512114-127585005	OK	57.3919	64.6122	0.17096	0.313698	0.61225	0.9998
ENSG00000123595	ENSG00000123595	RAB9A	X:13707243-13728625	OK	23.8144	26.7574	0.168099	0.305271	0.6124	0.9998
ENSG00000184402	ENSG00000184402	SS18L1	20:60718821-60757540	OK	31.673	35.1134	0.148769	0.230122	0.6124	0.9998
ENSG00000197409	ENSG00000197409	HIST1H3D	6:26197067-26199521	OK	0.864858	1.18832	0.458386	0.283297	0.6125	0.9998
ENSG00000075142	ENSG00000075142	SRI	7:87834432-87936206	OK	106.074	95.451	-0.152245	-0.314016	0.61265	0.9998
ENSG00000238083	ENSG00000238083	LRRC37A2	17:44588876-44657088	OK	2.53692	2.21685	-0.194566	-0.304449	0.61265	0.9998
ENSG00000080608	ENSG00000080608	KIAA0020	9:2717501-2844241	OK	30.2977	27.6195	-0.133523	-0.250053	0.6127	0.9998
ENSG00000105829	ENSG00000105829	BET1	7:93592073-93640425	OK	28.2264	31.0299	0.136613	0.308045	0.61295	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229874	ENSG00000229874	RP11-312O7.2	1:206135292-206155151	OK	2.32928	3.03169	0.380239	0.297511	0.61295	0.9998
ENSG00000115041	ENSG00000115041	KCNIP3	2:95963051-96051825	OK	12.5209	14.2051	0.182076	0.283376	0.613	0.9998
ENSG00000163930	ENSG00000163930	BAP1	3:52435028-52444366	OK	39.0218	42.4852	0.122681	0.268915	0.613	0.9998
ENSG00000244115	ENSG00000244115	DNAJC25-GNG10	9:114393631-114432526	OK	4.13845	1.95223	-1.08397	-0.369412	0.613	0.9998
ENSG00000100629	ENSG00000100629	CEP128	14:80943329-81636758	OK	3.66784	3.18897	-0.201842	-0.17509	0.6131	0.9998
ENSG00000181704	ENSG00000181704	YIPF6	X:67718164-67757127	OK	22.8992	19.6893	-0.217884	-0.296632	0.61315	0.9998
ENSG00000052841	ENSG00000052841	TTC17	11:43333512-43516483	OK	25.7611	30.2147	0.230058	0.20373	0.6133	0.9998
ENSG00000118503	ENSG00000118503	TNFAIP3	6:138144809-138204449	OK	20.0236	17.8997	-0.161769	-0.227551	0.6133	0.9998
ENSG00000154781	ENSG00000154781	CCDC174	3:14693270-14714166	OK	8.90927	10.5246	0.240391	0.321614	0.61335	0.9998
ENSG00000082196	ENSG00000082196	C1QTNF3	5:33986282-34124633	OK	1.43305	0.943959	-0.602298	-0.141102	0.6134	0.9998
ENSG00000204128	ENSG00000204128	C2orf72	2:231902204-231914434	OK	0.767648	0.59404	-0.369885	-0.227882	0.6134	0.9998
ENSG00000143324	ENSG00000143324	XPR1	1:180601139-180859387	OK	17.5836	19.3636	0.139116	0.23174	0.6135	0.9998
ENSG00000180979	ENSG00000180979	LRRC57	15:42783430-42841000	OK	5.74016	4.70326	-0.287431	-0.263519	0.6135	0.9998
ENSG00000163399	ENSG00000163399	ATP1A1	1:116915289-116961244	OK	496.543	548.842	0.144472	0.291429	0.6136	0.9998
ENSG00000246174	ENSG00000246174	KCTD21-AS1	11:77850816-77925757	OK	2.48716	1.76289	-0.496552	-0.208379	0.6136	0.9998
ENSG00000240087	ENSG00000240087	RP11-254B13.1	12:68946774-68947662	OK	6.69543	7.63113	0.188721	0.30112	0.61365	0.9998
ENSG00000122386	ENSG00000122386	ZNF205	16:3160460-3192806	OK	6.56365	7.65471	0.221851	0.29939	0.6137	0.9998
ENSG00000186312	ENSG00000186312	CA5BP1	X:15693054-15805747	OK	14.549	16.8026	0.207764	0.302339	0.6137	0.9998
ENSG00000232650	ENSG00000232650	RP5-834N19.1	1:119870798-119898805	OK	1.15157	0.878478	-0.39053	-0.282624	0.6137	0.9998
ENSG00000167578	ENSG00000167578	RAB4B	19:41277552-41406413	OK	31.8502	25.7549	-0.306457	-0.27304	0.6138	0.9998
ENSG00000170027	ENSG00000170027	YWHAG	7:75956115-75988348	OK	67.64	73.6678	0.123158	0.304692	0.61385	0.9998
ENSG00000035403	ENSG00000035403	VCL	10:75757871-75879918	OK	26.0217	28.291	0.120627	0.276379	0.6141	0.9998
ENSG00000116560	ENSG00000116560	SFPQ	1:35641978-35658749	OK	87.314	97.8806	0.164811	0.291928	0.61425	0.9998
ENSG00000204592	ENSG00000204592	HLA-E	6:30457243-30461982	OK	76.8237	83.539	0.120898	0.289571	0.61435	0.9998
ENSG00000234964	ENSG00000234964	FABP5P7	11:59480295-59573354	OK	98.2911	131.872	0.424008	0.299547	0.6145	0.9998
ENSG00000270062	ENSG00000270062	RP11-248J18.3	14:51186480-51297839	OK	1.19746	0.606433	-0.981561	-0.0891617	0.6145	0.9998
ENSG00000145293	ENSG00000145293	ENOPH1	4:83351714-83382244	OK	46.8746	42.9635	-0.125694	-0.305553	0.6146	0.9998
ENSG00000162695	ENSG00000162695	SLC30A7	1:101361631-101447309	OK	4.08456	4.83082	0.242088	0.305176	0.61465	0.9998
ENSG00000187534	ENSG00000187534	CTC-471F3.4	19:40448562-40449634	OK	6.21519	7.29951	0.232002	0.301937	0.6147	0.9998
ENSG00000132475	ENSG00000132475	H3F3B	17:73772514-73821886	OK	343.373	394.445	0.200045	0.324287	0.6148	0.9998
ENSG00000234353	ENSG00000234353	AP000347.4	22:23950638-24059543	OK	1.85226	1.01654	-0.865618	-0.320724	0.6148	0.9998
ENSG00000137409	ENSG00000137409	MTCH1	6:36935916-36954074	OK	77.3174	71.021	-0.122546	-0.286522	0.61505	0.9998
ENSG00000169105	ENSG00000169105	CHST14	15:40763159-40765353	OK	4.13508	3.64716	-0.181142	-0.301714	0.6152	0.9998
ENSG00000088247	ENSG00000088247	KHSRP	19:6413358-6424805	OK	126.403	140.366	0.151165	0.301959	0.61535	0.9998
ENSG00000128656	ENSG00000128656	CHN1	2:175664090-175870097	OK	5.4852	6.36498	0.214612	0.27157	0.6156	0.9998
ENSG00000169136	ENSG00000169136	ATF5	19:50392910-50464429	OK	7.58003	9.65592	0.34921	0.293791	0.6158	0.9998
ENSG00000101413	ENSG00000101413	RPRD1B	20:36661947-36720768	OK	21.3461	19.5541	-0.126503	-0.249077	0.6159	0.9998
ENSG00000129515	ENSG00000129515	SNX6	14:35025979-35099389	OK	43.7697	47.8551	0.12874	0.279036	0.61595	0.9998
ENSG00000128626	ENSG00000128626	MRPS12	19:39405905-39466550	OK	51.0585	57.4529	0.170229	0.311198	0.616	0.9998
ENSG00000114735	ENSG00000114735	HEMK1	3:50595461-50622366	OK	14.8072	13.0406	-0.183285	-0.296607	0.61625	0.9998
ENSG00000122484	ENSG00000122484	RPAP2	1:92711958-92867613	OK	10.2523	8.42457	-0.283279	-0.308991	0.61625	0.9998
ENSG00000164068	ENSG00000164068	RNF123	3:49711434-49761384	OK	20.1282	17.1455	-0.231389	-0.223548	0.61635	0.9998
ENSG00000179152	ENSG00000179152	TCAIM	3:44379432-44450943	OK	14.8236	16.3494	0.141339	0.275962	0.6164	0.9998
ENSG00000072832	ENSG00000072832	CRMP1	4:5712923-5894785	OK	3.75044	4.63463	0.305392	0.293793	0.61645	0.9998
ENSG00000267283	ENSG00000267283	AC005306.3	19:1985446-2034880	OK	1.1281	0.64616	-0.803934	-0.140336	0.61645	0.9998
ENSG00000064651	ENSG00000064651	SLC12A2	5:127419457-127525380	OK	2.27101	2.54704	0.165484	0.228392	0.6165	0.9998
ENSG00000164048	ENSG00000164048	ZNF589	3:48282589-48343175	OK	5.70787	4.95004	-0.205511	-0.254835	0.61675	0.9998
ENSG00000203993	ENSG00000203993	C9orf37	9:140500105-140513358	OK	6.8395	8.21716	0.264749	0.310763	0.6168	0.9998
ENSG00000228474	ENSG00000228474	OST4	2:27265231-27294641	OK	392.872	435.658	0.149135	0.302836	0.61685	0.9998
ENSG00000244879	ENSG00000244879	GABPB1-AS1	15:50569388-50659636	OK	1.86471	1.28217	-0.540359	-0.245203	0.61685	0.9998
ENSG00000197714	ENSG00000197714	ZNF460	19:57778587-57804937	OK	1.13593	1.36725	0.267394	0.238379	0.61695	0.9998
ENSG00000101464	ENSG00000101464	PIGU	20:33148345-33264910	OK	27.4179	25.0064	-0.132823	-0.296164	0.617	0.9998
ENSG00000140374	ENSG00000140374	ETFA	15:76352177-76603813	OK	122.529	133.789	0.126832	0.299959	0.61705	0.9998
ENSG00000023572	ENSG00000023572	GLRX2	1:193065597-193075244	OK	20.3499	22.6587	0.155042	0.290718	0.61715	0.9998
ENSG00000110514	ENSG00000110514	MADD	11:47290711-47351582	OK	15.3928	13.9871	-0.138164	-0.191294	0.61725	0.9998
ENSG00000128534	ENSG00000128534	NAA38	7:117824085-117832878	OK	69.923	63.7096	-0.134256	-0.2403	0.6173	0.9998
ENSG00000270346	ENSG00000270346	RP1-90J20.12	6:3020387-3022984	OK	1.88702	2.14741	0.186486	0.297707	0.61735	0.9998
ENSG00000243716	ENSG00000243716	NPIPB5	16:22357256-22547842	OK	5.59796	7.05452	0.333646	0.24159	0.6174	0.9998
ENSG00000105708	ENSG00000105708	ZNF14	19:19821279-19843906	OK	1.42809	1.24717	-0.195422	-0.300679	0.61745	0.9998
ENSG00000198105	ENSG00000198105	ZNF248	10:38091750-38148038	OK	2.42104	2.07086	-0.225398	-0.255848	0.61745	0.9998
ENSG00000112701	ENSG00000112701	SENP6	6:76311224-76427997	OK	30.0576	26.925	-0.158786	-0.278349	0.61755	0.9998
ENSG00000185721	ENSG00000185721	DRG1	22:31795508-32058418	OK	47.9819	54.5843	0.185996	0.293299	0.61755	0.9998
ENSG00000130684	ENSG00000130684	ZNF337	20:25593570-25677477	OK	15.0306	16.8992	0.169055	0.299876	0.6176	0.9998
ENSG00000119899	ENSG00000119899	SLC17A5	6:74303101-74363878	OK	10.6096	9.42357	-0.171027	-0.290426	0.61765	0.9998
ENSG00000134955	ENSG00000134955	SLC37A2	11:124932962-124960411	OK	4.1069	4.93489	0.264968	0.294982	0.61765	0.9998
ENSG00000149929	ENSG00000149929	HIRIP3	16:30003644-30034591	OK	8.70397	7.01983	-0.310239	-0.299203	0.6177	0.9998
ENSG00000144233	ENSG00000144233	AMMECR1L	2:128619203-128643496	OK	16.9565	15.4985	-0.129708	-0.301059	0.61775	0.9998
ENSG00000198556	ENSG00000198556	ZNF789	7:99070463-99101273	OK	11.9015	10.2336	-0.217827	-0.245012	0.61785	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000006118	ENSG00000006118	TMEM132A	11:60680637-60720002	OK	6.30488	4.89734	-0.36447	-0.214374	0.6179	0.9998
ENSG00000167566	ENSG00000167566	NCKAP5L	12:50184928-50236912	OK	13.7316	15.0973	0.13679	0.295544	0.61795	0.9998
ENSG00000177200	ENSG00000177200	CHD9	16:53088944-53363062	OK	5.77895	5.04093	-0.197118	-0.187851	0.618	0.9998
ENSG00000234764	ENSG00000234764	AC008132.12	22:18761177-18830912	OK	4.1041	4.76679	0.215952	0.30343	0.6181	0.9998
ENSG00000122477	ENSG00000122477	LRRC39	1:100598705-100643771	OK	6.84095	8.05402	0.235512	0.308454	0.61815	0.9998
ENSG00000198818	ENSG00000198818	SFT2D1	6:166733215-166756079	OK	28.9816	31.9088	0.138819	0.297389	0.61815	0.9998
ENSG00000235526	ENSG00000235526	RP5-1028L10.2	1:110693107-110744824	OK	0.756954	1.35429	0.839256	0.0827914	0.61825	0.9998
ENSG00000136243	ENSG00000136243	NUPL2	7:23145352-23240630	OK	34.5692	28.575	-0.274732	-0.32959	0.61835	0.9998
ENSG00000137656	ENSG00000137656	BUD13	11:116618885-116643704	OK	5.43233	4.87137	-0.157243	-0.294963	0.61835	0.9998
ENSG00000172164	ENSG00000172164	SNTB1	8:121392999-121825599	OK	6.94071	8.35881	0.268215	0.307259	0.61845	0.9998
ENSG00000174989	ENSG00000174989	FBXW8	12:117348760-117468953	OK	6.49543	5.83703	-0.154191	-0.291858	0.6186	0.9998
ENSG00000159423	ENSG00000159423	ALDH4A1	1:19166092-19283180	OK	6.55751	5.58001	-0.232881	-0.224185	0.61865	0.9998
ENSG00000161960	ENSG00000161960	EIF4A1	17:7465191-7536700	OK	749.707	673.574	-0.154491	-0.270316	0.61865	0.9998
ENSG00000124574	ENSG00000124574	ABCC10	6:43395103-43424370	OK	11.6451	13.072	0.166761	0.225603	0.6187	0.9998
ENSG00000153113	ENSG00000153113	CAST	5:95220801-96143803	OK	92.7061	83.6411	-0.148453	-0.245582	0.61885	0.9998
ENSG00000100442	ENSG00000100442	FKBP3	14:45553301-45604522	OK	82.5373	74.8322	-0.141387	-0.303402	0.6189	0.9998
ENSG00000146872	ENSG00000146872	TLK2	17:60536018-60692842	OK	26.29	23.5224	-0.160478	-0.243618	0.6189	0.9998
ENSG00000113595	ENSG00000113595	TRIM23	5:64885506-65167553	OK	11.3759	8.65575	-0.394248	-0.299955	0.619	0.9998
ENSG00000125962	ENSG00000125962	ARMCX5	X:101854095-101973607	OK	6.79751	7.95496	0.226848	0.299846	0.619	0.9998
ENSG00000064012	ENSG00000064012	CASP8	2:202098165-202152434	OK	11.0354	12.2603	0.151851	0.255256	0.6191	0.9998
ENSG00000121068	ENSG00000121068	TBX2	17:58754813-59488916	OK	43.8843	37.1573	-0.240059	-0.250945	0.6194	0.9998
ENSG00000173275	ENSG00000173275	ZNF449	X:134478720-134497077	OK	5.23859	4.67377	-0.164593	-0.290844	0.6194	0.9998
ENSG00000140332	ENSG00000140332	TLE3	15:70340128-70390515	OK	16.0082	14.0739	-0.185791	-0.228507	0.6195	0.9998
ENSG00000178307	ENSG00000178307	TMEM11	17:21100592-21133348	OK	20.1051	22.2562	0.146646	0.30244	0.6196	0.9998
ENSG00000121690	ENSG00000121690	DEPDC7	11:33037409-33055128	OK	1.92487	2.21956	0.205508	0.301812	0.61965	0.9998
ENSG00000168374	ENSG00000168374	ARF4	3:57557089-57586654	OK	154.145	167.461	0.119532	0.297918	0.6197	0.9998
ENSG00000258890	ENSG00000258890	CEP95	17:62495733-62658186	OK	17.0885	13.4967	-0.340424	-0.0954989	0.6197	0.9998
ENSG00000267058	ENSG00000267058	RP11-15A1.3	19:44376514-44405957	OK	0.929662	0.609837	-0.608283	-0.329548	0.6197	0.9998
ENSG00000143344	ENSG00000143344	RGL1	1:183605219-183897665	OK	3.76454	4.19345	0.155663	0.303374	0.61975	0.9998
ENSG00000145833	ENSG00000145833	DDX46	5:134094468-134195427	OK	22.8794	25.353	0.148105	0.234358	0.61975	0.9998
ENSG00000197380	ENSG00000197380	DACT3	19:47150868-47220384	OK	10.7797	12.7816	0.245756	0.339975	0.61975	0.9998
ENSG00000260895	ENSG00000260895	RP11-554A11.7	11:68870960-68876562	OK	0.638501	0.829082	0.376827	0.314561	0.61975	0.9998
ENSG00000103064	ENSG00000103064	SLC7A6	16:68298432-68344849	OK	17.1189	19.6247	0.197082	0.188794	0.6198	0.9998
ENSG00000256061	ENSG00000256061	DYX1C1	15:55495163-55800432	OK	1.09226	1.52128	0.477976	0.0956463	0.6198	0.9998
ENSG00000135763	ENSG00000135763	URB2	1:229761980-229795946	OK	6.23857	5.65838	-0.140824	-0.268193	0.61985	0.9998
ENSG00000233927	ENSG00000233927	RPS28	19:8367010-8408146	OK	363.325	429.581	0.241668	0.305274	0.61985	0.9998
ENSG00000173821	ENSG00000173821	RNF213	17:78234664-78411886	OK	19.9252	17.8397	-0.159509	-0.156138	0.6199	0.9998
ENSG00000175567	ENSG00000175567	UCP2	11:73685711-73694352	OK	6.57993	5.71432	-0.203489	-0.273304	0.6199	0.9998
ENSG00000232941	ENSG00000232941	AC090186.1	8:52730139-52811735	OK	0.682992	2.07705	1.60459	0.532335	0.61995	0.9998
ENSG00000100888	ENSG00000100888	CHD8	14:21853352-21924285	OK	18.1579	16.6496	-0.125111	-0.144716	0.62005	0.9998
ENSG00000196724	ENSG00000196724	ZNF418	19:58433251-58446761	OK	0.74529	0.927855	0.316098	0.192514	0.62005	0.9998
ENSG00000231023	ENSG00000231023	LINC00326	6:133409218-133427717	OK	1.0413	1.22102	0.229698	0.289488	0.62005	0.9998
ENSG00000153551	ENSG00000153551	CMTM7	3:32433162-32544900	OK	20.9866	26.0556	0.312125	0.315185	0.6201	0.9998
ENSG00000166532	ENSG00000166532	RIMKLB	12:8834195-9039597	OK	15.5109	17.3295	0.159949	0.25039	0.6201	0.9998
ENSG00000037042	ENSG00000037042	TUBG2	17:40811322-40819024	OK	14.0563	12.5195	-0.167035	-0.300995	0.62015	0.9998
ENSG00000135525	ENSG00000135525	MAP7	6:136663874-136873692	OK	2.68275	2.37632	-0.174982	-0.301744	0.6202	0.9998
ENSG00000143469	ENSG00000143469	SYT14	1:210111537-210337636	OK	3.43947	3.84999	0.162665	0.303034	0.62035	0.9998
ENSG00000198042	ENSG00000198042	MAK16	8:33228341-33371119	OK	8.07196	6.61071	-0.288114	-0.277316	0.62035	0.9998
ENSG00000103932	ENSG00000103932	RPAP1	15:41809373-41836467	OK	6.65749	5.99267	-0.151781	-0.194458	0.6204	0.9998
ENSG00000267470	ENSG00000267470	ZNF571-AS1	19:37988062-38210691	OK	0.638014	0.810564	0.345338	0.128927	0.6206	0.9998
ENSG00000156136	ENSG00000156136	DCK	4:71768042-71896631	OK	14.0796	12.1573	-0.211784	-0.27492	0.62065	0.9998
ENSG00000138041	ENSG00000138041	SMEK2	2:55774427-55846015	OK	22.3612	20.5384	-0.122674	-0.271672	0.6207	0.9998
ENSG00000105401	ENSG00000105401	CDC37	19:10501809-10580305	OK	146.131	134.05	-0.124492	-0.295124	0.62075	0.9998
ENSG00000070882	ENSG00000070882	OSBPL3	7:24836157-25021253	OK	8.78887	7.77574	-0.176697	-0.182207	0.6208	0.9998
ENSG00000223960	ENSG00000223960	AC009948.5	2:179278665-179326117	OK	7.76168	5.86941	-0.403153	-0.279899	0.6208	0.9998
ENSG00000004142	ENSG00000004142	POLDIP2	17:26662627-26684545	OK	65.7856	72.8223	0.146608	0.307344	0.62095	0.9998
ENSG00000124593	ENSG00000124593	PRICKLE4	6:41737913-41863099	OK	2.85146	2.10531	-0.437669	-0.115612	0.62095	0.9998
ENSG00000131503	ENSG00000131503	ANKHD1	5:139781398-139973337	OK	49.0571	43.2751	-0.180924	-0.233677	0.62095	0.9998
ENSG00000163132	ENSG00000163132	MSX1	4:4861392-4865663	OK	0.957388	1.11754	0.223154	0.269827	0.62095	0.9998
ENSG00000169738	ENSG00000169738	DCXR	17:79993011-79995608	OK	69.224	76.7133	0.148204	0.311734	0.62105	0.9998
ENSG00000117222	ENSG00000117222	RBBP5	1:205055269-205091143	OK	13.2199	14.4411	0.127471	0.248701	0.6212	0.9998
ENSG00000065150	ENSG00000065150	IPO5	13:98605911-98676551	OK	57.9752	62.9952	0.119806	0.230726	0.6213	0.9998
ENSG00000136111	ENSG00000136111	TBC1D4	13:75858807-76056250	OK	9.7351	10.6222	0.125819	0.284341	0.6214	0.9998
ENSG00000100596	ENSG00000100596	SPTLC2	14:77972339-78083116	OK	6.76261	6.04233	-0.162474	-0.2574	0.62145	0.9998
ENSG00000130706	ENSG00000130706	ADRM1	20:60877148-60942368	OK	102.794	91.652	-0.165522	-0.285174	0.62145	0.9998
ENSG00000173334	ENSG00000173334	TRIB1	8:126442562-126450647	OK	37.9005	34.4027	-0.139697	-0.294831	0.62165	0.9998
ENSG00000134910	ENSG00000134910	STT3A	11:125439111-125551018	OK	41.9834	47.9625	0.192088	0.26168	0.62175	0.9998
ENSG00000162819	ENSG00000162819	BROX	1:222841354-222908538	OK	23.0731	20.0613	-0.201798	-0.256803	0.6218	0.9998
ENSG00000249471	ENSG00000249471	ZNF324B	19:58962970-58969200	OK	1.98248	1.71455	-0.209478	-0.267962	0.62185	0.9998
ENSG00000114391	ENSG00000114391	RPL24	3:101399934-101405626	OK	991.369	908.033	-0.126678	-0.30454	0.62195	0.9998
ENSG00000088930	ENSG00000088930	XRN2	20:21283941-21370463	OK	20.837	19.075	-0.127462	-0.304382	0.62205	0.9998
ENSG00000035681	ENSG00000035681	NSMAF	8:59496062-59572403	OK	24.3685	26.6308	0.128078	0.211616	0.6222	0.9998
ENSG00000037757	ENSG00000037757	MRI1	19:13875345-13889276	OK	13.9868	17.0851	0.288668	0.266489	0.6222	0.9998
ENSG00000137462	ENSG00000137462	TLR2	4:154622651-154626851	OK	1.33703	1.17324	-0.188531	-0.300145	0.6222	0.9998
ENSG00000180596	ENSG00000180596	HIST1H2BC	6:26115100-26124154	OK	4.90629	5.68945	0.213656	0.298798	0.6222	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000196531	ENSG00000196531	NACA	12:57106211-57181574	OK	845.335	930.558	0.138572	0.300609	0.6222	0.9998
ENSG00000257453	ENSG00000257453	RP11-290L1.3	12:76419226-76427712	OK	13.9494	4.79977	-1.53916	-0.278702	0.6222	0.9998
ENSG00000123191	ENSG00000123191	ATP7B	13:52506808-52585630	OK	4.41742	3.9697	-0.154176	-0.254525	0.6223	0.9998
ENSG00000152078	ENSG00000152078	TMEM56	1:95582893-95729610	OK	3.22294	2.78165	-0.212432	-0.186845	0.6223	0.9998
ENSG00000006075	ENSG00000006075	CCL3	17:34400225-34417515	OK	0.762907	1.02686	0.428656	0.379215	0.62245	0.9998
ENSG00000078668	ENSG00000078668	VDAC3	8:42249141-42263415	OK	116.837	107.642	-0.118262	-0.28744	0.6227	0.9998
ENSG00000033800	ENSG00000033800	PIAS1	15:68346516-68549549	OK	10.7138	12.7154	0.247111	0.276965	0.6231	0.9998
ENSG00000151490	ENSG00000151490	PTPRO	12:15260716-15750333	OK	0.807309	0.674239	-0.259861	-0.198333	0.62315	0.9998
ENSG00000070495	ENSG00000070495	JMJD6	17:74708918-74722866	OK	43.1326	47.1519	0.128536	0.280642	0.62325	0.9998
ENSG00000120885	ENSG00000120885	CLU	8:27454433-27472548	OK	11.7087	13.9777	0.255549	0.292414	0.62345	0.9998
ENSG00000261052	ENSG00000261052	SULT1A3	16:30204254-30215631	OK	1.89986	1.379	-0.462275	-0.232042	0.62365	0.9998
ENSG00000134294	ENSG00000134294	SLC38A2	12:46751971-46767561	OK	47.8784	43.7324	-0.130671	-0.212869	0.6238	0.9998
ENSG00000177989	ENSG00000177989	ODF3B	22:50961996-50971009	OK	0.736845	0.990685	0.427066	0.123532	0.62385	0.9998
ENSG00000172725	ENSG00000172725	CORO1B	11:67202980-67211292	OK	73.9932	81.2429	0.13485	0.253901	0.6239	0.9998
ENSG00000180891	ENSG00000180891	CUEDC1	17:55938603-56032684	OK	28.6275	25.1701	-0.185689	-0.300139	0.6239	0.9998
ENSG00000101152	ENSG00000101152	DNAJC5	20:62526517-62567384	OK	41.8967	45.7181	0.125927	0.243638	0.62395	0.9998
ENSG00000066084	ENSG00000066084	DIP2B	12:50898767-51142450	OK	26.6404	24.3517	-0.129592	-0.288204	0.624	0.9998
ENSG00000196405	ENSG00000196405	EVL	14:100437785-100610573	OK	9.97534	11.1622	0.162188	0.231123	0.6241	0.9998
ENSG00000262222	ENSG00000262222	RP11-876N24.4	16:10958770-11036878	OK	1.72291	2.49372	0.533449	0.297843	0.62415	0.9998
ENSG00000143061	ENSG00000143061	IGSF3	1:117117030-117210375	OK	23.1792	25.2453	0.123184	0.292468	0.6242	0.9998
ENSG00000167173	ENSG00000167173	C15orf39	15:75487983-75504510	OK	4.63932	5.15347	0.151632	0.22183	0.62435	0.9998
ENSG00000167378	ENSG00000167378	IRGQ	19:44047191-44100287	OK	6.4474	7.41539	0.201805	0.272776	0.62435	0.9998
ENSG00000138095	ENSG00000138095	LRPPRC	2:44113646-44223144	OK	41.5782	45.7463	0.13783	0.237071	0.6244	0.9998
ENSG00000062194	ENSG00000062194	GPBP1	5:56469774-56560506	OK	42.4727	38.8551	-0.128431	-0.272269	0.6245	0.9998
ENSG00000154059	ENSG00000154059	IMPACT	18:22006579-22033499	OK	16.7893	14.3417	-0.22733	-0.285254	0.6245	0.9998
ENSG00000171714	ENSG00000171714	ANO5	11:22214721-22304903	OK	2.72174	3.02593	0.152849	0.263514	0.62455	0.9998
ENSG00000143156	ENSG00000143156	NME7	1:169074934-169337205	OK	11.1958	9.69257	-0.208005	-0.256736	0.62465	0.9998
ENSG00000160785	ENSG00000160785	SLC25A44	1:156163879-156182587	OK	40.4677	36.7773	-0.137956	-0.202294	0.6248	0.9998
ENSG00000213639	ENSG00000213639	PPP1CB	2:28974505-29093167	OK	86.0467	94.5197	0.135495	0.219376	0.6248	0.9998
ENSG00000175213	ENSG00000175213	ZNF408	11:46722367-46727462	OK	5.67723	6.27905	0.145359	0.269446	0.6249	0.9998
ENSG00000196267	ENSG00000196267	ZNF836	19:52616343-52680255	OK	1.37815	2.1047	0.610884	0.303565	0.62495	0.9998
ENSG00000167393	ENSG00000167393	PPP2R3B	X:294697-347690	OK	3.92237	3.34016	-0.231808	-0.253545	0.6251	0.9998
ENSG00000226137	ENSG00000226137	BAIAP2-AS1	17:79002932-79008501	OK	5.80102	5.24674	-0.144884	-0.302894	0.6251	0.9998
ENSG00000028116	ENSG00000028116	VRK2	2:58134785-58468821	OK	14.6561	16.727	0.190677	0.29092	0.62515	0.9998
ENSG00000061794	ENSG00000061794	MRPS35	12:27863705-27909228	OK	35.0571	32.1206	-0.126209	-0.290724	0.62515	0.9998
ENSG00000158286	ENSG00000158286	RNF207	1:6241328-6296032	OK	2.67778	3.46646	0.372427	0.0678104	0.6252	0.9998
ENSG00000125445	ENSG00000125445	MRPS7	17:73232693-73267308	OK	119.653	133.333	0.156179	0.295244	0.62525	0.9998
ENSG00000046653	ENSG00000046653	GPM6B	X:13789149-13956757	OK	67.697	61.0878	-0.148209	-0.285106	0.6253	0.9998
ENSG00000165804	ENSG00000165804	ZNF219	14:21484921-21572881	OK	10.0695	8.34651	-0.27075	-0.204013	0.6253	0.9998
ENSG00000172594	ENSG00000172594	SMPDL3A	6:123110314-123130865	OK	8.508	7.65161	-0.153056	-0.290653	0.6253	0.9998
ENSG00000106615	ENSG00000106615	RHEB	7:151163097-151217206	OK	208.028	227.571	0.129539	0.292612	0.62535	0.9998
ENSG00000149357	ENSG00000149357	LAMTOR1	11:71709586-71823826	OK	78.2268	65.6721	-0.252381	-0.285454	0.62535	0.9998
ENSG00000145819	ENSG00000145819	ARHGAP26	5:142149948-142608576	OK	7.55233	8.80911	0.222075	0.219237	0.6254	0.9998
ENSG00000164306	ENSG00000164306	PRIMPOL	4:185570766-185655287	OK	2.32862	1.70154	-0.452634	-0.230102	0.6254	0.9998
ENSG00000179837	ENSG00000179837	RBM15B	3:51428730-51534010	OK	9.9109	8.84316	-0.164454	-0.29646	0.6254	0.9998
ENSG00000131495	ENSG00000131495	NDUFA2	5:140018324-140042064	OK	114.185	99.5679	-0.19762	-0.300578	0.62555	0.9998
ENSG00000169609	ENSG00000169609	C15orf40	15:83509837-83772195	OK	18.8734	14.9416	-0.33702	-0.183991	0.62585	0.9998
ENSG00000255494	ENSG00000255494	LINC00681	8:12623357-12675800	OK	2.63114	1.83608	-0.519057	-0.275373	0.62585	0.9998
ENSG00000205571	ENSG00000205571	SMN2	5:69345349-69374349	OK	8.7234	7.69549	-0.180877	-0.276736	0.6259	0.9998
ENSG00000104497	ENSG00000104497	SNX16	8:82704057-82755101	OK	8.08105	7.17326	-0.171914	-0.272655	0.62595	0.9998
ENSG00000144134	ENSG00000144134	RABL2A	2:114384805-114400973	OK	3.32687	2.81357	-0.241767	-0.2788	0.62595	0.9998
ENSG00000170606	ENSG00000170606	HSPA4	5:132387653-132442141	OK	49.097	54.2143	0.143038	0.248071	0.62605	0.9998
ENSG00000213906	ENSG00000213906	LTB4R2	14:24769067-24787242	OK	0.92987	1.51491	0.704134	0.198129	0.62605	0.9998
ENSG00000255098	ENSG00000255098	RP11-481A20.11	8:11870544-11873043	OK	8.82044	7.55812	-0.222822	-0.296185	0.6261	0.9998
ENSG00000234284	ENSG00000234284	ZNF879	5:178450752-178462065	OK	0.627461	0.481155	-0.383022	-0.239837	0.62615	0.9998
ENSG00000233137	ENSG00000233137	RP11-220I1.1	9:37079892-37090398	OK	14.5596	13.1986	-0.141581	-0.208772	0.6263	0.9998
ENSG00000273049	ENSG00000273049	RP11-834C11.12	12:54375292-54449814	OK	0.295143	0.798513	1.4359	0.228204	0.62635	0.9998
ENSG00000020129	ENSG00000020129	NCDN	1:35899090-36032875	OK	9.57376	11.8928	0.312927	0.270013	0.6264	0.9998
ENSG00000152464	ENSG00000152464	RPP38	10:15137383-15210692	OK	8.0323	9.33759	0.217238	0.299189	0.62685	0.9998
ENSG00000163939	ENSG00000163939	PBRM1	3:52529353-52742182	OK	18.3661	21.569	0.231916	0.175755	0.6269	0.9998
ENSG00000166833	ENSG00000166833	NAV2	11:19372270-20143144	OK	38.1743	41.5637	0.12272	0.219882	0.62695	0.9998
ENSG00000123349	ENSG00000123349	PFDN5	12:53689074-53700961	OK	480.892	529.367	0.138556	0.307597	0.627	0.9998
ENSG00000185044	ENSG00000185044	RP11-435B5.4	1:143347957-143467632	OK	1.81496	1.37271	-0.402913	-0.28807	0.627	0.9998
ENSG00000134490	ENSG00000134490	TMEM241	18:20714527-21017925	OK	4.41437	5.87755	0.413008	0.150711	0.6271	0.9998
ENSG00000253200	ENSG00000253200	RP11-582J16.5	8:22462144-22526661	OK	5.71743	3.8463	-0.571894	-0.313469	0.6271	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235261	ENSG00000235261	NICN1-AS1	3:49460378-49466759	OK	1.30232	2.29346	0.816442	0.381023	0.62715	0.9998
ENSG00000089486	ENSG00000089486	CDIP1	16:4560675-4588829	OK	18.4669	20.2416	0.132378	0.282057	0.6272	0.9998
ENSG00000163541	ENSG00000163541	SUCLG1	2:84650646-84687169	OK	104.204	112.941	0.116154	0.278848	0.62725	0.9998
ENSG00000219665	ENSG00000219665	CTD-2006C1.2	19:12098431-12167127	OK	6.32119	7.40961	0.229202	0.282439	0.62725	0.9998
ENSG00000164574	ENSG00000164574	GALNT10	5:153369687-153825410	OK	13.4935	15.806	0.228208	0.197423	0.6273	0.9998
ENSG00000154710	ENSG00000154710	RABGEF1	7:66093867-66309813	OK	7.34623	9.1746	0.320641	0.243828	0.62735	0.9998
ENSG00000119906	ENSG00000119906	FAM178A	10:102670859-102724893	OK	11.7636	12.8831	0.131158	0.213092	0.6274	0.9998
ENSG00000145912	ENSG00000145912	NHP2	5:177557996-177580968	OK	165.73	182.666	0.140374	0.295794	0.6274	0.9998
ENSG00000105220	ENSG00000105220	GPI	19:34850384-34919178	OK	263.755	241.721	-0.125856	-0.290261	0.6275	0.9998
ENSG00000159128	ENSG00000159128	IFNGR2	21:34775201-34852318	OK	35.5351	32.0088	-0.150777	-0.29072	0.62755	0.9998
ENSG00000115649	ENSG00000115649	CNPPD1	2:220036618-220050201	OK	39.5263	33.0336	-0.25888	-0.277187	0.6276	0.9998
ENSG00000128487	ENSG00000128487	SPECC1	17:19912656-20306870	OK	7.25279	8.14057	0.166594	0.252442	0.62765	0.9998
ENSG00000239672	ENSG00000239672	NME1	17:49230896-49249108	OK	382.252	463.888	0.279253	0.286938	0.62765	0.9998
ENSG00000087258	ENSG00000087258	GNAO1	16:56225301-56391356	OK	9.61707	8.24794	-0.221563	-0.229147	0.62775	0.9998
ENSG00000158352	ENSG00000158352	SHROOM4	X:50334646-50557302	OK	1.39714	1.23835	-0.174067	-0.253121	0.62775	0.9998
ENSG00000075391	ENSG00000075391	RASAL2	1:178060642-178448644	OK	8.60218	7.83026	-0.135643	-0.208935	0.6278	0.9998
ENSG00000122741	ENSG00000122741	DCAF10	9:37510888-38069210	OK	15.0171	12.5504	-0.258872	-0.162078	0.6278	0.9998
ENSG00000181929	ENSG00000181929	PRKAG1	12:49388931-49453557	OK	68.3353	56.8546	-0.265353	-0.275095	0.62805	0.9998
ENSG00000258465	ENSG00000258465	DCAF8	1:160185504-160256138	OK	0.464708	0.790445	0.766341	0.103473	0.62815	0.9998
ENSG00000269032	ENSG00000269032	AC016629.7	19:59070495-59111168	OK	0.952446	1.94111	1.02717	0.0893633	0.62825	0.9998
ENSG00000186566	ENSG00000186566	GPATCH8	17:42472651-42580798	OK	15.849	14.5346	-0.124901	-0.204781	0.62835	0.9998
ENSG00000079134	ENSG00000079134	THOC1	18:158382-268050	OK	17.6963	15.0078	-0.237736	-0.194352	0.6285	0.9998
ENSG00000133103	ENSG00000133103	COG6	13:40229763-40365802	OK	13.6262	12.4501	-0.130228	-0.23529	0.6285	0.9998
ENSG00000143811	ENSG00000143811	PYCR2	1:226073981-226111978	OK	44.4694	48.5981	0.128086	0.26346	0.6285	0.9998
ENSG00000114383	ENSG00000114383	TUSC2	3:50355220-50365682	OK	34.1706	39.474	0.208147	0.279825	0.62875	0.9998
ENSG00000115687	ENSG00000115687	PASK	2:242045513-242123067	OK	9.12984	7.77294	-0.232128	-0.214233	0.62875	0.9998
ENSG00000247240	ENSG00000247240	UBL7-AS1	15:74753605-74809300	OK	2.57879	2.144	-0.266392	-0.237241	0.62875	0.9998
ENSG00000058600	ENSG00000058600	POLR3E	16:22308729-22346424	OK	15.384	17.0383	0.14735	0.235295	0.62885	0.9998
ENSG00000067141	ENSG00000067141	NEO1	15:73344050-73597547	OK	19.9648	18.0545	-0.145098	-0.212889	0.62885	0.9998
ENSG00000119392	ENSG00000119392	GLE1	9:131266978-131314689	OK	27.8427	25.5981	-0.121262	-0.292341	0.6289	0.9998
ENSG00000136463	ENSG00000136463	TACO1	17:61678230-61685725	OK	36.6077	39.9602	0.126416	0.296504	0.629	0.9998
ENSG00000170471	ENSG00000170471	RALGAPB	20:37101458-37207504	OK	30.8485	33.7115	0.12804	0.262016	0.629	0.9998
ENSG00000183628	ENSG00000183628	DGCR6	22:18893540-18924066	OK	15.1152	16.9711	0.167082	0.295687	0.629	0.9998
ENSG00000112167	ENSG00000112167	SAYSD1	6:39071839-39082965	OK	8.34589	7.391	-0.175296	-0.291729	0.62905	0.9998
ENSG00000255864	ENSG00000255864	RP11-444D3.1	12:24366189-24715524	OK	2.54401	3.08653	0.278883	0.259736	0.62905	0.9998
ENSG00000187189	ENSG00000187189	TSPYL4	6:116571150-116575261	OK	1.18963	1.04729	-0.183841	-0.29163	0.6292	0.9998
ENSG00000101000	ENSG00000101000	PROCR	20:33703166-33872788	OK	4.08537	9.10972	1.15694	0.46213	0.62925	0.9998
ENSG00000131781	ENSG00000131781	FMO5	1:146644349-146767443	OK	0.543263	0.764202	0.492305	0.0857445	0.6293	0.9998
ENSG00000213853	ENSG00000213853	EMP2	16:10622278-10674555	OK	7.86946	6.6459	-0.243799	-0.284815	0.6293	0.9998
ENSG00000038210	ENSG00000038210	PI4K2B	4:25162262-25280714	OK	11.481	10.0714	-0.188978	-0.217118	0.62935	0.9998
ENSG00000001460	ENSG00000001460	STPG1	1:24634045-24799466	OK	4.18568	4.98397	0.251833	0.201142	0.62945	0.9998
ENSG00000177239	ENSG00000177239	MAN1B1	9:139981378-140003635	OK	38.881	42.3026	0.121683	0.278002	0.6296	0.9998
ENSG00000179818	ENSG00000179818	PCBP1-AS1	2:70187225-70316332	OK	10.3529	11.9501	0.206986	0.090376	0.62975	0.9998
ENSG00000243279	ENSG00000243279	PRAF2	X:48928812-48958108	OK	13.653	15.8658	0.216698	0.28508	0.62975	0.9998
ENSG00000126217	ENSG00000126217	MCF2L	13:113548691-113754053	OK	11.3197	13.0716	0.207605	0.266584	0.6298	0.9998
ENSG00000166546	ENSG00000166546	BEAN1	16:66461199-66586447	OK	0.865496	1.149	0.408776	0.26497	0.6298	0.9998
ENSG00000171223	ENSG00000171223	JUNB	19:12873816-12985765	OK	25.6207	22.1675	-0.208867	-0.298837	0.63	0.9998
ENSG00000170734	ENSG00000170734	POLH	6:43543886-43596899	OK	14.5854	17.1344	0.232366	0.208555	0.63015	0.9998
ENSG00000176973	ENSG00000176973	FAM89B	11:65337900-65341669	OK	25.0231	28.5367	0.18956	0.294253	0.6303	0.9998
ENSG00000059691	ENSG00000059691	PET112	4:152591655-152682175	OK	14.3557	15.8788	0.145482	0.276758	0.6304	0.9998
ENSG00000149196	ENSG00000149196	C11orf73	11:86013252-86056969	OK	18.6537	16.7761	-0.153057	-0.305099	0.63045	0.9998
ENSG00000166347	ENSG00000166347	CYB5A	18:71920529-71959251	OK	71.4415	65.4755	-0.125807	-0.278524	0.63045	0.9998
ENSG00000176986	ENSG00000176986	SEC24C	10:75504119-75531919	OK	40.1036	36.7684	-0.125265	-0.27925	0.63055	0.9998
ENSG00000145730	ENSG00000145730	PAM	5:102089684-102366809	OK	24.1587	21.9499	-0.138324	-0.232161	0.63065	0.9998
ENSG00000270172	ENSG00000270172	RP5-1024G6.8	1:53692563-53710212	OK	3.26708	4.04768	0.309094	0.307293	0.63065	0.9998
ENSG00000130703	ENSG00000130703	OSBPL2	20:60813579-60871268	OK	12.99	14.2058	0.129079	0.282853	0.63095	0.9998
ENSG00000241839	ENSG00000241839	PLEKHO2	15:65134081-65251042	OK	30.2163	27.7526	-0.122708	-0.296357	0.631	0.9998
ENSG00000260727	ENSG00000260727	SLC7A5P1	16:29624424-29624961	OK	5.09082	4.33585	-0.231584	-0.291222	0.631	0.9998
ENSG00000138279	ENSG00000138279	ANXA7	10:75134858-75173834	OK	63.3244	57.6673	-0.135009	-0.283499	0.6312	0.9998
ENSG00000136213	ENSG00000136213	CHST12	7:2443222-2474242	OK	7.70082	8.61723	0.162212	0.28397	0.63125	0.9998
ENSG00000189136	ENSG00000189136	UBE2Q2P1	15:85051115-85123406	OK	3.54294	2.5743	-0.460771	-0.331704	0.63125	0.9998
ENSG00000116030	ENSG00000116030	SUMO1	2:203070902-203103331	OK	90.3808	98.742	0.127647	0.289959	0.63135	0.9998
ENSG00000118816	ENSG00000118816	CCNI	4:77968310-77997158	OK	102.67	113.007	0.138394	0.278607	0.6316	0.9998
ENSG00000185869	ENSG00000185869	ZNF829	19:37288419-37407193	OK	1.17494	0.962392	-0.287888	-0.29516	0.6316	0.9998
ENSG00000104067	ENSG00000104067	TJP1	15:29991570-30261068	OK	4.19754	3.69899	-0.182412	-0.209459	0.6317	0.9998
ENSG00000224975	ENSG00000224975	INE1	X:47050259-47074527	OK	1.12071	0.670122	-0.741916	-0.0899817	0.6317	0.9998
ENSG00000040633	ENSG00000040633	PHF23	17:7138346-7143041	OK	33.8655	37.0834	0.130958	0.266684	0.63175	0.9998
ENSG00000150977	ENSG00000150977	RILPL2	12:123899935-123921264	OK	3.47724	3.93902	0.179892	0.288008	0.6319	0.9998
ENSG00000117569	ENSG00000117569	PTBP2	1:97187220-97289294	OK	3.26353	3.72688	0.191535	0.242898	0.63205	0.9998
ENSG00000221946	ENSG00000221946	FXYD7	19:35615416-35645204	OK	0.488516	0.804364	0.719444	0.28206	0.6321	0.9998
ENSG00000164946	ENSG00000164946	FREM1	9:14734663-14910993	OK	0.817539	0.952787	0.220866	0.180251	0.6322	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000070018	ENSG00000070018	LRP6	12:12202777-12419946	OK	9.55432	10.7854	0.174851	0.174029	0.6323	0.9998
ENSG00000092199	ENSG00000092199	HNRNPC	14:21677294-21737653	OK	287.534	312.886	0.121904	0.286618	0.6323	0.9998
ENSG00000131981	ENSG00000131981	LGALS3	14:55590827-55612126	OK	2096.93	2322.53	0.147422	0.28487	0.6323	0.9998
ENSG00000174165	ENSG00000174165	ZDHHC24	11:66234215-66313709	OK	12.7241	15.4242	0.277633	0.286322	0.6323	0.9998
ENSG00000159335	ENSG00000159335	PTMS	12:6857169-6880116	OK	100.022	116.868	0.224566	0.292152	0.63245	0.9998
ENSG00000204165	ENSG00000204165	CXorf65	X:70323738-70326638	OK	0.694701	0.96277	0.470798	0.285786	0.63245	0.9998
ENSG00000182247	ENSG00000182247	UBE2E2	3:23244510-23633284	OK	19.571	21.5403	0.138321	0.283748	0.6325	0.9998
ENSG00000114315	ENSG00000114315	HES1	3:193853933-193856521	OK	13.7323	12.4494	-0.141499	-0.289276	0.63265	0.9998
ENSG00000122873	ENSG00000122873	CISD1	10:60028817-60049346	OK	33.3233	29.4673	-0.177415	-0.300098	0.6327	0.9998
ENSG00000186235	ENSG00000186235	AC016757.3	2:239133192-239140318	OK	2.19802	2.64783	0.268608	0.305058	0.6329	0.9998
ENSG00000088356	ENSG00000088356	PDRG1	20:30435439-30539895	OK	23.3866	20.7861	-0.170065	-0.299738	0.63295	0.9998
ENSG00000269974	ENSG00000269974	RP11-932O9.10	15:30909160-31065196	OK	0.648422	0.257158	-1.33428	-0.371434	0.633	0.9998
ENSG00000152977	ENSG00000152977	ZIC1	3:147103832-147228080	OK	4.86431	6.09347	0.32503	0.296559	0.63305	0.9998
ENSG00000124120	ENSG00000124120	TTPAL	20:43104525-43123244	OK	10.9702	9.88334	-0.150519	-0.264215	0.63315	0.9998
ENSG00000100105	ENSG00000100105	PATZ1	22:31677578-31742218	OK	14.4161	15.884	0.139889	0.280485	0.63325	0.9998
ENSG00000269929	ENSG00000269929	RP11-2B6.2	9:96928570-96966850	OK	1.71624	1.45842	-0.234851	-0.291313	0.63335	0.9998
ENSG00000261759	ENSG00000261759	RP11-626G11.3	16:19125253-19279652	OK	0.341499	0.891105	1.38371	0.391478	0.6334	0.9998
ENSG00000233588	ENSG00000233588	CYP51A1P2	13:29296522-29298158	OK	1.53823	1.78671	0.216039	0.295233	0.63345	0.9998
ENSG00000029639	ENSG00000029639	TFB1M	6:155054458-155635627	OK	11.0165	9.34038	-0.238115	-0.244531	0.6335	0.9998
ENSG00000166295	ENSG00000166295	ANAPC16	10:73856277-73995618	OK	39.5227	34.972	-0.17648	-0.289607	0.6335	0.9998
ENSG00000171208	ENSG00000171208	NETO2	16:47111613-47177908	OK	8.43632	9.7434	0.207812	0.271027	0.63355	0.9998
ENSG00000116132	ENSG00000116132	PRRX1	1:170631868-170708560	OK	4.65463	4.0217	-0.210861	-0.2141	0.63365	0.9998
ENSG00000089050	ENSG00000089050	RBBP9	20:18467183-18477887	OK	5.11621	5.71204	0.158932	0.270102	0.6338	0.9998
ENSG00000244038	ENSG00000244038	DDOST	1:20959947-20988000	OK	175.887	191.39	0.121864	0.276658	0.6338	0.9998
ENSG00000106263	ENSG00000106263	EIF3B	7:2291404-2420380	OK	118.779	130.532	0.136132	0.226696	0.63385	0.9998
ENSG00000229018	ENSG00000229018	RP11-313P13.3	7:72440226-72555749	OK	1.85945	1.22093	-0.606895	-0.388965	0.63385	0.9998
ENSG00000089916	ENSG00000089916	GPATCH2L	14:76618258-76729817	OK	10.2454	11.4657	0.16234	0.172241	0.6339	0.9998
ENSG00000143369	ENSG00000143369	ECM1	1:150480537-150486265	OK	107.797	116.895	0.116893	0.296133	0.63395	0.9998
ENSG00000172638	ENSG00000172638	EFEMP2	11:65590492-65641063	OK	0.948701	1.30465	0.459635	0.0305188	0.63395	0.9998
ENSG00000108773	ENSG00000108773	KAT2A	17:40265125-40307990	OK	18.3392	21.9278	0.257828	0.24456	0.63405	0.9998
ENSG00000165282	ENSG00000165282	PIGO	9:35088684-35098138	OK	11.2666	12.3839	0.136417	0.269345	0.63405	0.9998
ENSG00000132466	ENSG00000132466	ANKRD17	4:73939092-74124515	OK	14.58	15.848	0.120308	0.225214	0.6342	0.9998
ENSG00000042493	ENSG00000042493	CAPG	2:85621870-85645555	OK	345.134	314.447	-0.134339	-0.292955	0.63425	0.9998
ENSG00000273253	ENSG00000273253	RP3-402G11.26	22:50624343-50638976	OK	0.351779	0.673487	0.936979	0.166954	0.6343	0.9998
ENSG00000107816	ENSG00000107816	LZTS2	10:102756374-102790890	OK	60.3794	66.5878	0.141201	0.269291	0.63435	0.9998
ENSG00000143337	ENSG00000143337	TOR1AIP1	1:179850741-179894135	OK	24.0717	26.4247	0.13455	0.266935	0.63435	0.9998
ENSG00000197329	ENSG00000197329	PELI1	2:64319785-64479993	OK	2.89604	3.24186	0.162742	0.224387	0.63445	0.9998
ENSG00000229043	ENSG00000229043	AC091729.9	7:1191706-1204903	OK	2.35296	1.74562	-0.430736	-0.283763	0.6345	0.9998
ENSG00000206341	ENSG00000206341	HLA-H	6:29855070-29858259	OK	0.532348	0.654115	0.297175	0.295337	0.63455	0.9998
ENSG00000163013	ENSG00000163013	FBXO41	2:73481809-73511559	OK	3.51624	3.10561	-0.179157	-0.219728	0.6346	0.9998
ENSG00000168395	ENSG00000168395	ING5	2:242641449-242668893	OK	6.92913	8.11496	0.22791	0.248639	0.63465	0.9998
ENSG00000183048	ENSG00000183048	SLC25A10	17:79670386-79688042	OK	19.4523	23.3179	0.261499	0.272073	0.6347	0.9998
ENSG00000108592	ENSG00000108592	FTSJ3	17:61896792-61909379	OK	27.497	24.2938	-0.178683	-0.203534	0.63475	0.9998
ENSG00000204977	ENSG00000204977	TRIM13	13:50570023-50595058	OK	14.0066	15.56	0.151739	0.265384	0.6348	0.9998
ENSG00000171953	ENSG00000171953	ATPAF2	17:17876126-17942523	OK	23.2829	20.5581	-0.179567	-0.289025	0.6349	0.9998
ENSG00000196126	ENSG00000196126	HLA-DRB1	6:32546545-32557625	OK	0.790236	0.943588	0.255873	0.289229	0.63495	0.9998
ENSG00000066422	ENSG00000066422	ZBTB11	3:101367732-101398061	OK	9.66112	10.5247	0.123523	0.266316	0.635	0.9998
ENSG00000116752	ENSG00000116752	BCAS2	1:115110177-115124260	OK	33.8843	30.9339	-0.131427	-0.291592	0.6351	0.9998
ENSG00000090674	ENSG00000090674	MCOLN1	19:7587511-7626650	OK	17.9613	21.4796	0.258075	0.249186	0.63515	0.9998
ENSG00000115561	ENSG00000115561	CHMP3	2:86730553-87005164	OK	66.3471	75.5246	0.186913	0.2662	0.6352	0.9998
ENSG00000158467	ENSG00000158467	AHCYL2	7:128864863-129070052	OK	24.5895	26.9586	0.132703	0.251363	0.63525	0.9998
ENSG00000100320	ENSG00000100320	RBFOX2	22:36134782-36424473	OK	30.8855	34.9378	0.177858	0.276736	0.6353	0.9998
ENSG00000262879	ENSG00000262879	RP11-156P1.3	17:45000482-45177689	OK	9.51267	7.09259	-0.423538	-0.224121	0.6353	0.9998
ENSG00000198938	ENSG00000198938	MT-CO3	MT:8365-9990	OK	5818.26	6825.48	0.230342	0.290741	0.63535	0.9998
ENSG00000009830	ENSG00000009830	POMT2	14:77741298-77797940	OK	27.8465	30.8861	0.149466	0.189392	0.6355	0.9998
ENSG00000104133	ENSG00000104133	SPG11	15:44829254-44955876	OK	5.05472	5.73694	0.182651	0.129654	0.6355	0.9998
ENSG00000148296	ENSG00000148296	SURF6	9:136197551-136203235	OK	10.9635	12.0247	0.133291	0.277891	0.63555	0.9998
ENSG00000071127	ENSG00000071127	WDR1	4:10075962-10118573	OK	126.036	138.735	0.138488	0.280681	0.6356	0.9998
ENSG00000116005	ENSG00000116005	PCYOX1	2:70484517-70508323	OK	25.2888	27.7969	0.136426	0.261163	0.63565	0.9998
ENSG00000198171	ENSG00000198171	DDRGK1	20:3170995-3185331	OK	10.933	12.1312	0.150027	0.286422	0.63565	0.9998
ENSG00000125458	ENSG00000125458	NT5C	17:73106046-73127890	OK	26.4699	30.0322	0.182158	0.289187	0.6357	0.9998
ENSG00000157191	ENSG00000157191	NECAP2	1:16767166-16786573	OK	21.7205	19.853	-0.129702	-0.25747	0.6357	0.9998
ENSG00000115163	ENSG00000115163	CENPA	2:26987151-27023935	OK	31.1743	25.6948	-0.278881	-0.28374	0.63575	0.9998
ENSG00000162144	ENSG00000162144	CYB561A3	11:61066922-61136981	OK	55.9314	46.1667	-0.276804	-0.216499	0.63585	0.9998
ENSG00000139343	ENSG00000139343	SNRPF	12:96252705-96336752	OK	41.8335	45.7358	0.128666	0.281546	0.6359	0.9998
ENSG00000198683	ENSG00000198683	AC012615.1	19:1905212-1926016	OK	3.14503	4.59498	0.546983	0.307654	0.6359	0.9998
ENSG00000099977	ENSG00000099977	DDT	22:24309088-24326106	OK	176.017	192.424	0.128569	0.28386	0.636	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000269190	ENSG00000269190	FBXO17	19:39405905-39466550	OK	4.36143	5.53906	0.344841	0.190156	0.6361	0.9998
ENSG00000154153	ENSG00000154153	FAM134B	5:16473146-16630078	OK	13.5964	15.1575	0.156813	0.274276	0.63615	0.9998
ENSG00000137133	ENSG00000137133	HINT2	9:35812956-35854844	OK	33.3403	28.5675	-0.222893	-0.279612	0.6362	0.9998
ENSG00000144785	ENSG00000144785	RP11-977G19.10	12:56665482-56727837	OK	1.64229	0.825533	-0.992311	-0.104158	0.6362	0.9998
ENSG00000153201	ENSG00000153201	RANBP2	2:109335936-109402267	OK	11.7387	12.7323	0.117227	0.23307	0.63625	0.9998
ENSG00000245248	ENSG00000245248	USP2-AS1	11:119252487-119397374	OK	0.637243	0.474052	-0.4268	-0.257775	0.63625	0.9998
ENSG00000167244	ENSG00000167244	IGF2	11:2150341-2182571	OK	1.61328	1.29125	-0.321228	-0.245254	0.63635	0.9998
ENSG00000168924	ENSG00000168924	LETM1	4:1813205-1857974	OK	12.9536	14.2306	0.135636	0.211306	0.63635	0.9998
ENSG00000248919	ENSG00000248919	ATP5J2-PTCD1	7:98923520-99063954	OK	0.497479	0.918645	0.884872	0.0167991	0.63635	0.9998
ENSG00000165138	ENSG00000165138	ANKS6	9:101493610-101559247	OK	8.30864	10.2248	0.299382	0.288284	0.6364	0.9998
ENSG00000259250	ENSG00000259250	RP11-50C13.1	15:58879705-58883875	OK	1.08089	0.849188	-0.348058	-0.29734	0.6365	0.9998
ENSG00000137876	ENSG00000137876	RSL24D1	15:55473003-55489265	OK	23.772	25.8839	0.122792	0.278267	0.63655	0.9998
ENSG00000092841	ENSG00000092841	MYL6	12:56544579-56584068	OK	606.681	669.172	0.141441	0.285983	0.6366	0.9998
ENSG00000134077	ENSG00000134077	THUMPD3	3:9022274-9520924	OK	34.9168	29.2663	-0.254684	-0.242407	0.63675	0.9998
ENSG00000261036	ENSG00000261036	RP11-574H6.1	5:119681601-119740532	OK	2.80069	3.35648	0.261166	0.2869	0.63675	0.9998
ENSG00000259642	ENSG00000259642	C15orf37	15:80125926-80217194	OK	1.76409	1.10253	-0.678111	-0.340309	0.63695	0.9998
ENSG00000151353	ENSG00000151353	TMEM18	2:667334-697371	OK	22.4469	25.0739	0.15967	0.291233	0.6371	0.9998
ENSG00000248098	ENSG00000248098	BCKDHA	19:41768400-41930910	OK	10.4677	7.47117	-0.486538	-0.211099	0.6371	0.9998
ENSG00000103005	ENSG00000103005	USB1	16:58028571-58055522	OK	12.5636	11.3712	-0.143862	-0.257893	0.63715	0.9998
ENSG00000125386	ENSG00000125386	FAM193A	4:2420700-2734292	OK	9.21321	7.47611	-0.301415	-0.199274	0.63715	0.9998
ENSG00000163016	ENSG00000163016	ALMS1P	2:73872045-73912703	OK	0.951637	1.12876	0.246254	0.277103	0.63715	0.9998
ENSG00000167085	ENSG00000167085	PHB	17:47448101-47554350	OK	472.402	519.591	0.137363	0.275413	0.63715	0.9998
ENSG00000168014	ENSG00000168014	C2CD3	11:73723762-74035750	OK	9.86218	8.56471	-0.203503	-0.176701	0.63715	0.9998
ENSG00000068903	ENSG00000068903	SIRT2	19:39369196-39399533	OK	35.2043	38.7263	0.137562	0.250945	0.6372	0.9998
ENSG00000164241	ENSG00000164241	C5orf63	5:126378249-126409184	OK	0.908632	1.12735	0.311167	0.235539	0.63735	0.9998
ENSG00000104884	ENSG00000104884	ERCC2	19:45836691-45874176	OK	20.3933	22.7031	0.154791	0.275197	0.6375	0.9998
ENSG00000179406	ENSG00000179406	LINC00174	7:65670185-65955095	OK	0.751674	0.543619	-0.46751	-0.173297	0.6375	0.9998
ENSG00000102007	ENSG00000102007	PLP2	X:49028272-49042845	OK	60.5257	66.5245	0.136336	0.284607	0.63755	0.9998
ENSG00000104894	ENSG00000104894	CD37	19:49834873-49891338	OK	0.746572	0.589725	-0.340239	-0.10716	0.63755	0.9998
ENSG00000006453	ENSG00000006453	BAIAP2L1	7:97881690-98030380	OK	32.2675	37.9481	0.233946	0.271761	0.6376	0.9998
ENSG00000170604	ENSG00000170604	IRF2BP1	19:46386865-46389376	OK	7.50719	6.80559	-0.141553	-0.284052	0.63765	0.9998
ENSG00000118680	ENSG00000118680	MYL12B	18:3261906-3278282	OK	223.227	241.644	0.114373	0.287995	0.6377	0.9998
ENSG00000259024	ENSG00000259024	TVP23C-CDRT4	17:15339331-15466909	OK	1.65776	1.91112	0.205181	0.258462	0.6377	0.9998
ENSG00000160439	ENSG00000160439	RDH13	19:55517560-55582659	OK	7.75479	7.01851	-0.143923	-0.234968	0.6378	0.9998
ENSG00000164669	ENSG00000164669	INTS4L1	7:64601602-64694600	OK	1.34899	1.15643	-0.22221	-0.274398	0.6378	0.9998
ENSG00000136878	ENSG00000136878	USP20	9:132589568-132644107	OK	10.6544	9.23408	-0.206415	-0.205344	0.63785	0.9998
ENSG00000167182	ENSG00000167182	SP2	17:45973515-46018776	OK	6.79183	7.50301	0.14367	0.290739	0.63795	0.9998
ENSG00000076716	ENSG00000076716	GPC4	X:132434130-132549518	OK	6.975	7.77483	0.156618	0.285888	0.638	0.9998
ENSG00000120158	ENSG00000120158	RCL1	9:4792868-4885917	OK	7.43226	8.35178	0.168282	0.274504	0.638	0.9998
ENSG00000156313	ENSG00000156313	RPGR	X:37208527-38548169	OK	4.1181	3.09076	-0.414019	-0.105333	0.638	0.9998
ENSG00000261010	ENSG00000261010	RARRES2P6	16:34442273-34518517	OK	7.18896	4.69208	-0.615555	-0.333058	0.638	0.9998
ENSG00000120129	ENSG00000120129	DUSP1	5:172185228-172204777	OK	3.79604	4.25584	0.164948	0.288038	0.63805	0.9998
ENSG00000134371	ENSG00000134371	CDC73	1:193091146-193223031	OK	15.3074	16.6373	0.120194	0.285445	0.63815	0.9998
ENSG00000204869	ENSG00000204869	IGFL4	19:46543005-46580376	OK	0.918066	0.782483	-0.230538	-0.219162	0.63815	0.9998
ENSG00000144029	ENSG00000144029	MRPS5	2:95752951-95831158	OK	67.6964	73.9837	0.128128	0.289471	0.6382	0.9998
ENSG00000117620	ENSG00000117620	SLC35A3	1:100433938-100492535	OK	7.63271	8.58179	0.169082	0.283635	0.63835	0.9998
ENSG00000007062	ENSG00000007062	PROM1	4:15961865-16086001	OK	2.4963	3.20222	0.359283	0.146484	0.6384	0.9998
ENSG00000113845	ENSG00000113845	TIMMDC1	3:119217378-119278449	OK	95.2267	104.041	0.127711	0.278972	0.6384	0.9998
ENSG00000160606	ENSG00000160606	TLCD1	17:27046410-27070473	OK	10.3595	16.3109	0.654886	0.28761	0.6385	0.9998
ENSG00000226637	ENSG00000226637	RP6-206I17.3	1:143647637-143745417	OK	0.582207	0.907595	0.640516	0.293522	0.6385	0.9998
ENSG00000144644	ENSG00000144644	GADL1	3:30767691-30936257	OK	1.87503	1.6637	-0.172519	-0.285813	0.63865	0.9998
ENSG00000167548	ENSG00000167548	KMT2D	12:49388931-49453557	OK	11.6712	13.6925	0.230431	0.148203	0.63865	0.9998
ENSG00000177453	ENSG00000177453	NIM1K	5:43192172-43280952	OK	4.527	3.92848	-0.204583	-0.266792	0.63865	0.9998
ENSG00000137764	ENSG00000137764	MAP2K5	15:67835046-68099461	OK	10.0591	11.1165	0.144195	0.223296	0.63885	0.9998
ENSG00000080503	ENSG00000080503	SMARCA2	9:2015341-2193624	OK	13.878	12.4047	-0.161914	-0.213824	0.6389	0.9998
ENSG00000010270	ENSG00000010270	STARD3NL	7:38217823-38270272	OK	40.4022	43.9497	0.121418	0.283029	0.639	0.9998
ENSG00000100297	ENSG00000100297	MCM5	22:35796055-35821423	OK	52.1978	46.2188	-0.175509	-0.288374	0.639	0.9998
ENSG00000257740	ENSG00000257740	RP11-977G19.12	12:56665482-56727837	OK	0.656213	0.321928	-1.02743	-0.0537652	0.639	0.9998
ENSG00000142507	ENSG00000142507	PSMB6	17:4699438-4701790	OK	139.926	129.098	-0.116196	-0.282447	0.63915	0.9998
ENSG00000168234	ENSG00000168234	TTC39C	18:21572736-21715574	OK	18.1811	21.0603	0.212084	0.283186	0.6395	0.9998
ENSG00000128159	ENSG00000128159	TUBGCP6	22:50656117-50683421	OK	9.89205	8.9636	-0.142192	-0.271244	0.6397	0.9998
ENSG00000240857	ENSG00000240857	RDH14	2:18735988-18770838	OK	18.5035	20.5735	0.152989	0.279855	0.6397	0.9998
ENSG00000150990	ENSG00000150990	DHX37	12:125431370-125473668	OK	10.2069	11.2054	0.134652	0.255341	0.63975	0.9998
ENSG00000236528	ENSG00000236528	RP1-125I3.2	1:26186103-26197744	OK	0.642391	0.216469	-1.56929	-0.345777	0.6398	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000130640	ENSG00000130640	TUBGCP2	10:135093134-135166187	OK	30.3833	27.7813	-0.129164	-0.252238	0.63985	0.9998
ENSG00000141971	ENSG00000141971	MVB12A	19:17516502-17544533	OK	42.0846	38.372	-0.133238	-0.286468	0.64	0.9998
ENSG00000131043	ENSG00000131043	AAR2	20:34824380-34858840	OK	24.5207	22.5152	-0.123103	-0.287492	0.6401	0.9998
ENSG00000183405	ENSG00000183405	RPS7P1	17:26782769-26972472	OK	270.828	343.657	0.343592	0.287032	0.6401	0.9998
ENSG00000084652	ENSG00000084652	TXLNA	1:32645286-32663886	OK	25.1105	27.2234	0.116556	0.285784	0.6402	0.9998
ENSG00000076513	ENSG00000076513	ANKRD13A	12:110436990-110511491	OK	18.53	20.5451	0.148934	0.247246	0.64025	0.9998
ENSG00000257949	ENSG00000257949	TEN1	17:73937587-74023533	OK	28.5262	33.3288	0.224484	0.274447	0.64035	0.9998
ENSG00000108557	ENSG00000108557	RAI1	17:17584786-17740325	OK	36.4342	32.168	-0.179669	-0.159991	0.6404	0.9998
ENSG00000232385	ENSG00000232385	RPS3AP25	7:94324338-94325131	OK	11.2598	12.6522	0.168202	0.288466	0.6404	0.9998
ENSG00000047230	ENSG00000047230	CTPS2	X:16606125-16731059	OK	5.79605	6.38217	0.138978	0.245323	0.64045	0.9998
ENSG00000145246	ENSG00000145246	ATP10D	4:47487304-47595503	OK	4.96689	4.3452	-0.192921	-0.21065	0.64045	0.9998
ENSG00000153815	ENSG00000153815	CMIP	16:81478774-81745367	OK	3.23075	2.7979	-0.207525	-0.161744	0.6407	0.9998
ENSG00000125520	ENSG00000125520	SLC2A4RG	20:62289162-62374858	OK	38.6807	45.2705	0.226957	0.238368	0.64095	0.9998
ENSG00000132507	ENSG00000132507	EIF5A	17:7210317-7232712	OK	325.84	356.224	0.12862	0.277609	0.64095	0.9998
ENSG00000188026	ENSG00000188026	RILPL1	12:123942187-124018265	OK	7.31318	6.33659	-0.206793	-0.267476	0.64105	0.9998
ENSG00000104915	ENSG00000104915	STX10	19:13254871-13261197	OK	39.8545	43.5326	0.127355	0.278965	0.6411	0.9998
ENSG00000165271	ENSG00000165271	NOL6	9:33461438-33473928	OK	14.7404	16.0275	0.120781	0.274632	0.64115	0.9998
ENSG00000162994	ENSG00000162994	CLHC1	2:55401926-55462989	OK	2.66156	2.10597	-0.337787	-0.0328894	0.6412	0.9998
ENSG00000100813	ENSG00000100813	ACIN1	14:23527772-23569665	OK	66.9835	59.6494	-0.167298	-0.247763	0.64125	0.9998
ENSG00000166228	ENSG00000166228	PCBD1	10:72642036-72648541	OK	54.3759	49.9872	-0.121409	-0.270998	0.6413	0.9998
ENSG00000227694	ENSG00000227694	AC005884.1	17:58754813-59488916	OK	3.62075	6.09265	0.750782	0.120935	0.6413	0.9998
ENSG00000148356	ENSG00000148356	LRSAM1	9:130213764-130265780	OK	8.80081	7.98444	-0.140446	-0.25202	0.64135	0.9998
ENSG00000187239	ENSG00000187239	FNBP1	9:132649465-132805473	OK	14.8689	16.3558	0.137507	0.244268	0.6414	0.9998
ENSG00000167552	ENSG00000167552	TUBA1A	12:49578578-49667114	OK	104.702	85.9811	-0.284197	-0.278052	0.6415	0.9998
ENSG00000262905	ENSG00000262905	RP5-1029F21.2	17:406410-624957	OK	0.758508	0.302203	-1.32765	-0.183226	0.6416	0.9998
ENSG00000169020	ENSG00000169020	ATP5I	4:666224-683230	OK	402.338	437.843	0.122006	0.287584	0.64175	0.9998
ENSG00000179918	ENSG00000179918	SEPHS2	16:30454951-30457502	OK	21.5618	23.5925	0.129852	0.281203	0.64175	0.9998
ENSG00000174482	ENSG00000174482	LINGO2	9:27948075-28670283	OK	2.19164	1.94059	-0.175516	-0.253267	0.6419	0.9998
ENSG00000236200	ENSG00000236200	KDM4A-AS1	1:44115828-44396831	OK	1.90635	1.36062	-0.486546	-0.124032	0.6419	0.9998
ENSG00000136560	ENSG00000136560	TANK	2:161952741-162111179	OK	28.1998	25.3362	-0.154485	-0.242212	0.64205	0.9998
ENSG00000243335	ENSG00000243335	KCTD7	7:66093867-66309813	OK	24.0461	21.8018	-0.141354	-0.274458	0.64205	0.9998
ENSG00000129991	ENSG00000129991	TNNI3	19:55663136-55691809	OK	1.13939	1.41845	0.316053	0.205987	0.64225	0.9998
ENSG00000213923	ENSG00000213923	CSNK1E	22:38686696-38794934	OK	76.8058	84.7054	0.141239	0.279398	0.64235	0.9998
ENSG00000137145	ENSG00000137145	DENND4C	9:19230432-19374139	OK	10.9772	12.0007	0.128609	0.224115	0.6424	0.9998
ENSG00000171603	ENSG00000171603	CLSTN1	1:9711789-9884584	OK	36.7426	41.2944	0.168492	0.285328	0.6424	0.9998
ENSG00000006695	ENSG00000006695	COX10	17:13972812-14111994	OK	9.47793	10.6041	0.161974	0.273766	0.64245	0.9998
ENSG00000141543	ENSG00000141543	EIF4A3	17:78109012-78120982	OK	77.2563	83.5728	0.113381	0.278338	0.6425	0.9998
ENSG00000172663	ENSG00000172663	TMEM134	11:67231823-67236743	OK	22.6315	20.2857	-0.15787	-0.278783	0.6426	0.9998
ENSG00000173875	ENSG00000173875	ZNF791	19:12490002-12750912	OK	5.18737	4.4855	-0.209735	-0.188873	0.6426	0.9998
ENSG00000226520	ENSG00000226520	KIRREL-IT1	1:157963062-158070052	OK	0.748172	0.405265	-0.884503	-0.0376035	0.6429	0.9998
ENSG00000069849	ENSG00000069849	ATP1B3	3:141594965-141645356	OK	112.994	122.741	0.119376	0.261215	0.643	0.9998
ENSG00000169375	ENSG00000169375	SIN3A	15:75648132-75748183	OK	13.9515	12.4633	-0.162733	-0.17274	0.6431	0.9998
ENSG00000129521	ENSG00000129521	EGLN3	14:34393436-34931980	OK	49.093	34.9307	-0.491024	-0.371513	0.64325	0.9998
ENSG00000093010	ENSG00000093010	COMT	22:19863039-20004331	OK	28.1278	24.239	-0.214668	-0.27407	0.6435	0.9998
ENSG00000203832	ENSG00000203832	NBPF20	1:148250248-148347506	OK	1.7343	1.38952	-0.319766	-0.276009	0.6435	0.9998
ENSG00000266469	ENSG00000266469	CTB-131K11.1	17:37415383-37607539	OK	7.4352	10.3531	0.47762	0.275675	0.6435	0.9998
ENSG00000100814	ENSG00000100814	CCNB1IP1	14:20779526-20801471	OK	56.4012	61.0899	0.115208	0.265401	0.6436	0.9998
ENSG00000198691	ENSG00000198691	ABCA4	1:94458392-94586688	OK	0.489047	0.639517	0.38701	0.18824	0.64365	0.9998
ENSG00000235513	ENSG00000235513	RP4-756G23.5	22:41601208-41636938	OK	0.541527	0.9746	0.847776	0.373642	0.64365	0.9998
ENSG00000074201	ENSG00000074201	CLNS1A	11:77225980-77348850	OK	97.7629	106.765	0.127082	0.282939	0.6437	0.9998
ENSG00000120438	ENSG00000120438	TCP1	6:160090088-160210781	OK	89.2933	78.9392	-0.17781	-0.235511	0.64375	0.9998
ENSG00000181004	ENSG00000181004	BBS12	4:123653856-123666098	OK	1.92	1.71872	-0.159771	-0.259454	0.64375	0.9998
ENSG00000234171	ENSG00000234171	RNASEH1-AS1	2:3579402-3609324	OK	7.72065	5.98009	-0.368554	-0.276281	0.64375	0.9998
ENSG00000168899	ENSG00000168899	VAMP5	2:85811530-85820535	OK	19.7055	17.7105	-0.153993	-0.283993	0.6438	0.9998
ENSG00000234961	ENSG00000234961	RP11-124N14.3	10:17256237-17279592	OK	0.638896	1.07036	0.744435	0.0158068	0.6438	0.9998
ENSG00000130517	ENSG00000130517	PGPEP1	19:18451396-18480760	OK	11.813	10.6279	-0.152518	-0.184822	0.64385	0.9998
ENSG00000109775	ENSG00000109775	UFSP2	4:186317174-186347139	OK	7.94729	9.56181	0.266821	0.245489	0.64395	0.9998
ENSG00000124588	ENSG00000124588	NQO2	6:2988200-3019996	OK	30.2031	27.2764	-0.14704	-0.274986	0.64395	0.9998
ENSG00000136709	ENSG00000136709	WDR33	2:128458595-128568761	OK	15.4924	18.6263	0.265781	0.300492	0.64395	0.9998
ENSG00000026025	ENSG00000026025	VIM	10:17256237-17279592	OK	1858.82	2056.64	0.145902	0.272854	0.64405	0.9998
ENSG00000227077	ENSG00000227077	AC107983.4	17:18414534-18528930	OK	10.1276	13.9103	0.457867	0.283757	0.64405	0.9998
ENSG00000176396	ENSG00000176396	EID2	19:40028889-40030870	OK	4.07263	4.53742	0.155908	0.277719	0.6441	0.9998
ENSG00000118960	ENSG00000118960	HS1BP3	2:20760207-20850849	OK	30.6164	28.1646	-0.120423	-0.283979	0.6442	0.9998
ENSG00000144791	ENSG00000144791	LIMD1	3:45596885-45786916	OK	33.1947	38.1148	0.199399	0.184088	0.6442	0.9998
ENSG00000151657	ENSG00000151657	KIN	10:7792924-7829990	OK	10.4435	9.20057	-0.182816	-0.287097	0.64425	0.9998
ENSG00000164008	ENSG00000164008	C1orf50	1:43232939-43263968	OK	7.14266	6.36274	-0.166813	-0.262433	0.64425	0.9998
ENSG00000039123	ENSG00000039123	SKIV2L2	5:54603587-54830878	OK	35.1665	39.7824	0.177926	0.250713	0.6443	0.9998
ENSG00000147130	ENSG00000147130	ZMYM3	X:70459473-70474996	OK	15.5342	17.1366	0.141626	0.272518	0.64435	0.9998
ENSG00000175906	ENSG00000175906	ARL4D	17:41476326-41478505	OK	11.0566	12.188	0.140553	0.273792	0.64435	0.9998
ENSG00000076382	ENSG00000076382	SPAG5	17:26782769-26972472	OK	35.7655	29.3301	-0.286186	-0.17538	0.6444	0.9998
ENSG00000134308	ENSG00000134308	YWHAQ	2:9724100-9771143	OK	186.972	206.133	0.140753	0.270261	0.6444	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000147862	ENSG00000147862	NFIB	9:14081841-14398982	OK	1.72741	2.00653	0.216089	0.238346	0.6444	0.9998
ENSG00000175931	ENSG00000175931	UBE2O	17:74385531-74449288	OK	19.4174	21.2791	0.132094	0.206539	0.6444	0.9998
ENSG00000238795	ENSG00000238795	SCARNA12	12:7072407-7178336	OK	2.00497	0.983627	-1.0274	-0.0469869	0.6444	0.9998
ENSG00000065600	ENSG00000065600	TMEM206	1:212537272-212588243	OK	15.4555	17.4303	0.173471	0.275492	0.64455	0.9998
ENSG00000119421	ENSG00000119421	NDUFA8	9:124894744-124922098	OK	130.824	141.255	0.110673	0.273667	0.6446	0.9998
ENSG00000111669	ENSG00000111669	TPI1	12:6976282-7032861	OK	798.818	718.155	-0.153571	-0.258072	0.64465	0.9998
ENSG00000234476	ENSG00000234476	RP11-496N12.6	1:225634944-225653045	OK	4.30326	3.71773	-0.211008	-0.276122	0.6447	0.9998
ENSG00000256390	ENSG00000256390	AC092143.1	16:89939999-90005169	OK	30.8293	37.946	0.299647	0.275617	0.6447	0.9998
ENSG00000139132	ENSG00000139132	FGD4	12:32552462-32798984	OK	7.51299	6.66844	-0.172038	-0.203689	0.6448	0.9998
ENSG00000115641	ENSG00000115641	FHL2	2:105974168-106054970	OK	47.2987	51.4962	0.122665	0.281065	0.64485	0.9998
ENSG00000165801	ENSG00000165801	ARHGEF40	14:21484921-21572881	OK	14.0556	15.6023	0.150616	0.247364	0.64485	0.9998
ENSG00000268471	ENSG00000268471	MIR4453	4:153457415-153460415	OK	0.762998	0.588317	-0.375087	-0.162851	0.64485	0.9998
ENSG00000029725	ENSG00000029725	RABEP1	17:5185557-5372380	OK	26.019	31.0998	0.257337	0.173571	0.6451	0.9998
ENSG00000135424	ENSG00000135424	ITGA7	12:56075329-56118489	OK	14.9478	17.1246	0.196141	0.216793	0.64525	0.9998
ENSG00000151693	ENSG00000151693	ASAP2	2:9346893-9563676	OK	11.088	9.56626	-0.212977	-0.221075	0.6455	0.9998
ENSG00000160062	ENSG00000160062	ZBTB8A	1:32930657-33116504	OK	1.17419	0.798229	-0.556796	-0.335466	0.64555	0.9998
ENSG00000227113	ENSG00000227113	RP11-460N20.4	7:64535400-64539158	OK	1.11025	0.675312	-0.717259	-0.358136	0.64585	0.9998
ENSG00000120254	ENSG00000120254	MTHFD1L	6:151186684-151549582	OK	20.6679	24.8955	0.268491	0.304367	0.646	0.9998
ENSG00000065060	ENSG00000065060	UHRF1BP1	6:34759856-34855866	OK	6.33586	6.96767	0.137135	0.276149	0.64605	0.9998
ENSG00000144218	ENSG00000144218	AFF3	2:100162322-100759201	OK	8.44148	9.85649	0.223578	0.215452	0.6461	0.9998
ENSG00000271361	ENSG00000271361	HTATSF1P2	6:3023375-3024006	OK	4.62191	3.99824	-0.209124	-0.280801	0.6461	0.9998
ENSG00000167136	ENSG00000167136	ENDOG	9:131580752-131592100	OK	11.819	14.0624	0.250741	0.276416	0.64625	0.9998
ENSG00000166770	ENSG00000166770	ZNF667-AS1	19:56950693-57012035	OK	16.0037	18.2518	0.189634	0.27173	0.64635	0.9998
ENSG00000169967	ENSG00000169967	MAP3K2	2:128056305-128146041	OK	11.1597	9.85949	-0.178715	-0.223767	0.64635	0.9998
ENSG00000183684	ENSG00000183684	ALYREF	17:79845712-79869340	OK	50.5378	40.9026	-0.305169	-0.244891	0.6465	0.9998
ENSG00000255414	ENSG00000255414	LINC01059	11:123325105-123331118	OK	0.943517	1.08685	0.204031	0.287268	0.64655	0.9998
ENSG00000187866	ENSG00000187866	FAM122A	9:71320574-71624092	OK	4.76073	4.24098	-0.166785	-0.278859	0.6466	0.9998
ENSG00000130544	ENSG00000130544	ZNF557	19:7069454-7087979	OK	2.24231	1.97772	-0.181147	-0.271172	0.64675	0.9998
ENSG00000147251	ENSG00000147251	DOCK11	X:117629860-117820126	OK	0.970929	1.08345	0.158194	0.274143	0.64675	0.9998
ENSG00000197021	ENSG00000197021	CXorf40B	X:149097744-149392815	OK	24.5219	26.9155	0.134368	0.276354	0.6469	0.9998
ENSG00000238045	ENSG00000238045	AC009133.14	16:29817426-29859355	OK	1.07136	0.671557	-0.67386	-0.110694	0.6469	0.9998
ENSG00000104714	ENSG00000104714	ERICH1	8:564745-1212580	OK	14.346	15.8464	0.143509	0.233484	0.64705	0.9998
ENSG00000187164	ENSG00000187164	KIAA1598	10:118592511-118886097	OK	14.9971	16.3378	0.123536	0.282553	0.64705	0.9998
ENSG00000225855	ENSG00000225855	RUSC1-AS1	1:155278538-155300905	OK	12.1881	7.54576	-0.691733	-0.308089	0.64705	0.9998
ENSG00000081791	ENSG00000081791	KIAA0141	5:141303372-141321612	OK	42.9045	38.5979	-0.152607	-0.283428	0.64715	0.9998
ENSG00000268854	ENSG00000268854	CTD-2545M3.2	19:50970041-50986608	OK	4.97487	9.05972	0.864808	0.187791	0.64715	0.9998
ENSG00000126767	ENSG00000126767	ELK1	X:47494919-47510003	OK	18.9286	21.365	0.174679	0.268114	0.64725	0.9998
ENSG00000177628	ENSG00000177628	GBA	1:155204242-155214490	OK	103.718	111.789	0.108117	0.262005	0.6473	0.9998
ENSG00000166012	ENSG00000166012	TAF1D	11:93394804-93547861	OK	35.1914	30.9627	-0.184692	-0.262552	0.64745	0.9998
ENSG00000198586	ENSG00000198586	TLK1	2:171847332-172087824	OK	13.7344	12.4316	-0.143789	-0.231499	0.64745	0.9998
ENSG00000174744	ENSG00000174744	BRMS1	11:66097712-66112596	OK	47.9525	52.4194	0.128496	0.277212	0.64755	0.9998
ENSG00000125651	ENSG00000125651	GTF2F1	19:6379579-6412415	OK	50.1375	55.7702	0.153603	0.265441	0.6477	0.9998
ENSG00000109519	ENSG00000109519	GRPEL1	4:7060632-7069924	OK	27.4758	30.4636	0.148924	0.27579	0.64785	0.9998
ENSG00000135677	ENSG00000135677	GNS	12:65107224-65153227	OK	88.0101	95.0355	0.110798	0.246798	0.64785	0.9998
ENSG00000269449	ENSG00000269449	AC002451.1	7:95171456-95173854	OK	1.63341	1.43767	-0.184155	-0.275061	0.64795	0.9998
ENSG00000197226	ENSG00000197226	TBC1D9B	5:179224596-179334859	OK	52.1244	43.038	-0.276348	-0.162389	0.64805	0.9998
ENSG00000221821	ENSG00000221821	C6orf226	6:42858004-42858554	OK	2.84833	2.40246	-0.245602	-0.278911	0.6482	0.9998
ENSG00000227019	ENSG00000227019	OR7E101P	13:47029269-47060641	OK	0.745076	1.31055	0.814708	0.365842	0.64825	0.9998
ENSG00000132718	ENSG00000132718	SYT11	1:155829299-155854990	OK	2.96322	3.27142	0.142751	0.2691	0.6483	0.9998
ENSG00000110871	ENSG00000110871	COQ5	12:120941076-121015397	OK	23.129	19.6386	-0.236013	-0.251666	0.64835	0.9998
ENSG00000182973	ENSG00000182973	CNOT10	3:32726636-32815367	OK	12.7678	11.7172	-0.123871	-0.205498	0.6484	0.9998
ENSG00000112320	ENSG00000112320	SOBP	6:107811161-107981357	OK	1.53384	1.72256	0.167401	0.226141	0.6485	0.9998
ENSG00000102710	ENSG00000102710	SUPT20H	13:37523911-37633850	OK	22.1318	24.7958	0.163974	0.22637	0.64865	0.9998
ENSG00000248593	ENSG00000248593	DSTNP2	12:6976282-7032861	OK	2.57867	3.80883	0.56272	0.0487523	0.64865	0.9998
ENSG00000105835	ENSG00000105835	NAMPT	7:105888730-105926772	OK	199.662	175.407	-0.18685	-0.249689	0.6487	0.9998
ENSG00000108344	ENSG00000108344	PSMD3	17:38137049-38154213	OK	57.6524	53.4843	-0.108265	-0.264077	0.6487	0.9998
ENSG00000121900	ENSG00000121900	TMEM54	1:33351594-33367039	OK	30.7171	33.6751	0.132639	0.283717	0.6488	0.9998
ENSG00000161040	ENSG00000161040	FBXL13	7:102453307-102715286	OK	1.08159	0.885983	-0.287802	-0.223546	0.6488	0.9998
ENSG00000273226	ENSG00000273226	RP11-513M16.8	9:19375448-19380252	OK	0.679091	1.10448	0.701691	0.0211414	0.64885	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000078177	ENSG00000078177	N4BP2	4:40044536-40159872	OK	0.919155	0.811382	-0.179926	-0.229637	0.64895	0.9998
ENSG00000183172	ENSG00000183172	SMDT1	22:42475694-42480288	OK	57.7016	52.4811	-0.136814	-0.276208	0.6491	0.9998
ENSG00000267254	ENSG00000267254	CTD-2162K18.5	19:37288419-37407193	OK	0.957084	1.48226	0.631082	0.283081	0.6491	0.9998
ENSG00000160710	ENSG00000160710	ADAR	1:154554537-154600475	OK	107.853	99.926	-0.110139	-0.163173	0.64915	0.9998
ENSG00000139289	ENSG00000139289	PHLDA1	12:76419226-76427712	OK	116.847	126.868	0.118704	0.276694	0.6492	0.9998
ENSG00000168913	ENSG00000168913	ENHO	9:34521037-34524239	OK	4.87729	5.50308	0.174159	0.27616	0.64925	0.9998
ENSG00000131165	ENSG00000131165	CHMP1A	16:89710838-89737680	OK	17.9308	16.3845	-0.130107	-0.241688	0.64935	0.9998
ENSG00000153989	ENSG00000153989	NUS1	6:117996664-118031803	OK	8.84925	9.61233	0.119332	0.274699	0.6495	0.9998
ENSG00000101654	ENSG00000101654	RNMT	18:13663345-13764557	OK	29.7213	26.7215	-0.153493	-0.241766	0.64965	0.9998
ENSG00000109320	ENSG00000109320	NFKB1	4:103422485-103538459	OK	12.6951	11.6869	-0.119375	-0.250483	0.6497	0.9998
ENSG00000154582	ENSG00000154582	TCEB1	8:74851403-74884522	OK	118.587	108.413	-0.129404	-0.279431	0.6497	0.9998
ENSG00000183914	ENSG00000183914	DNAH2	17:7620671-7737062	OK	0.72343	1.01084	0.482635	0.288888	0.6497	0.9998
ENSG00000235655	ENSG00000235655	H3F3AP4	2:175411868-175639555	OK	269.753	243.004	-0.150662	-0.274052	0.6499	0.9998
ENSG00000105679	ENSG00000105679	GAPDHS	19:36024313-36038428	OK	11.15	15.2584	0.452558	0.245651	0.65005	0.9998
ENSG00000100644	ENSG00000100644	HIF1A	14:62147758-62263146	OK	44.0938	40.6109	-0.118706	-0.218851	0.6501	0.9998
ENSG00000260924	ENSG00000260924	AC004463.6	22:19158907-19160352	OK	0.563596	0.678785	0.268293	0.281919	0.65015	0.9998
ENSG00000159885	ENSG00000159885	ZNF222	19:44529493-44593766	OK	1.87961	2.33305	0.311786	0.253397	0.6502	0.9998
ENSG00000233937	ENSG00000233937	CTC-338M12.4	5:180663908-180699308	OK	2.20625	3.00408	0.445329	0.0328957	0.65025	0.9998
ENSG00000074317	ENSG00000074317	SNCB	5:176047084-176057530	OK	0.722744	0.596523	-0.276907	-0.201464	0.6503	0.9998
ENSG00000151131	ENSG00000151131	C12orf45	12:105380087-105478355	OK	13.3883	14.8904	0.153409	0.267015	0.6503	0.9998
ENSG00000113231	ENSG00000113231	PDE8B	5:76506273-76916436	OK	0.633744	0.844953	0.414971	0.20559	0.65045	0.9998
ENSG00000101546	ENSG00000101546	RBFA	18:77794345-77854968	OK	17.3626	15.7954	-0.136484	-0.273573	0.6505	0.9998
ENSG00000215527	ENSG00000215527	AP005482.1	18:12438888-12725739	OK	2.2233	1.50002	-0.56772	-0.0773434	0.6506	0.9998
ENSG00000221990	ENSG00000221990	C5orf55	5:441644-443258	OK	2.00213	1.7523	-0.192285	-0.278302	0.65065	0.9998
ENSG00000112294	ENSG00000112294	ALDH5A1	6:24403152-24537435	OK	5.93859	7.01568	0.240461	0.237342	0.6507	0.9998
ENSG00000179899	ENSG00000179899	PHC1P1	12:55804262-55808633	OK	13.4743	12.1027	-0.154887	-0.280078	0.6507	0.9998
ENSG00000216895	ENSG00000216895	AC009403.2	7:155403924-155574179	OK	7.69959	5.23202	-0.557413	-0.206588	0.6507	0.9998
ENSG00000264469	ENSG00000264469	RP11-173M1.8	17:25641668-25642952	OK	2.93362	2.57221	-0.189675	-0.279318	0.6507	0.9998
ENSG00000155508	ENSG00000155508	CNOT8	5:154198050-154256353	OK	22.5531	20.4598	-0.140535	-0.238155	0.65085	0.9998
ENSG00000106049	ENSG00000106049	HIBADH	7:27565060-27702614	OK	56.3689	51.8849	-0.119584	-0.258556	0.6509	0.9998
ENSG00000130812	ENSG00000130812	ANGPTL6	19:10196797-10213472	OK	1.01217	0.641668	-0.657557	-0.215187	0.651	0.9998
ENSG00000165775	ENSG00000165775	FUNDC2	X:154064062-154288578	OK	57.456	63.6485	0.14767	0.270249	0.651	0.9998
ENSG00000007866	ENSG00000007866	TEAD3	6:35441373-35464853	OK	4.83286	4.36671	-0.14633	-0.254649	0.65115	0.9998
ENSG00000186184	ENSG00000186184	POLR1D	13:28194902-28241548	OK	144.654	157.807	0.125557	0.276685	0.6512	0.9998
ENSG00000169019	ENSG00000169019	COMMD8	4:47452684-47465736	OK	25.5524	23.4198	-0.125727	-0.275784	0.65125	0.9998
ENSG00000166896	ENSG00000166896	XRCC6BP1	12:58335323-58351052	OK	8.50064	7.4679	-0.186869	-0.281794	0.6513	0.9998
ENSG00000254477	ENSG00000254477	AP000640.10	11:59480295-59573354	OK	1.47692	0.841661	-0.811278	-0.117556	0.6514	0.9998
ENSG00000092020	ENSG00000092020	PPP2R3C	14:35514112-35786699	OK	24.6325	18.7011	-0.397438	-0.272997	0.6515	0.9998
ENSG00000146834	ENSG00000146834	MEPCE	7:99998448-100031741	OK	11.8127	12.9606	0.133793	0.271866	0.6515	0.9998
ENSG00000100129	ENSG00000100129	EIF3L	22:38226861-38285414	OK	342.72	374.213	0.126829	0.239142	0.65155	0.9998
ENSG00000115128	ENSG00000115128	SF3B14	2:24290453-24299313	OK	119.629	129.177	0.110782	0.269968	0.6516	0.9998
ENSG00000198218	ENSG00000198218	QRICH1	3:49067139-49131796	OK	25.6193	23.5032	-0.12437	-0.208616	0.65165	0.9998
ENSG00000048707	ENSG00000048707	VPS13D	1:12290123-12572099	OK	4.41557	3.98817	-0.146872	-0.147304	0.6517	0.9998
ENSG00000003989	ENSG00000003989	SLC7A2	8:17354596-17428082	OK	4.28553	4.72358	0.140409	0.260744	0.65175	0.9998
ENSG00000135932	ENSG00000135932	CAB39	2:231577559-231685790	OK	25.985	28.0082	0.108172	0.246306	0.65185	0.9998
ENSG00000151090	ENSG00000151090	THRB	3:24158650-24541833	OK	2.07218	2.40483	0.214789	0.188406	0.65185	0.9998
ENSG00000158470	ENSG00000158470	B4GALT5	20:48249481-48330415	OK	34.3259	31.8471	-0.108136	-0.268182	0.6519	0.9998
ENSG00000184486	ENSG00000184486	POU3F2	6:99282579-99286660	OK	4.27312	3.8586	-0.147212	-0.274765	0.6519	0.9998
ENSG00000166823	ENSG00000166823	MESP1	15:90291891-90294541	OK	4.25631	5.2041	0.290045	0.274099	0.65195	0.9998
ENSG00000168101	ENSG00000168101	NUDT16L1	16:4743694-4745860	OK	24.5256	22.4763	-0.125883	-0.275832	0.65195	0.9998
ENSG00000157077	ENSG00000157077	ZFYVE9	1:52608045-52831865	OK	8.48869	9.65369	0.185539	0.274416	0.65205	0.9998
ENSG00000163938	ENSG00000163938	GNL3	3:52529353-52742182	OK	43.6305	51.8643	0.249406	0.214211	0.6521	0.9998
ENSG00000184178	ENSG00000184178	SCFD2	4:53739148-54232242	OK	23.7689	25.7811	0.117237	0.273499	0.65215	0.9998
ENSG00000149292	ENSG00000149292	TTC12	11:113185250-113254266	OK	2.73417	3.24913	0.248948	0.204311	0.6522	0.9998
ENSG00000138768	ENSG00000138768	USO1	4:76649776-76735382	OK	44.6406	38.6994	-0.206044	-0.18744	0.65225	0.9998
ENSG00000161149	ENSG00000161149	TUBA3FP	22:21353392-21399306	OK	1.56559	0.971653	-0.688189	-0.34545	0.65225	0.9998
ENSG00000154274	ENSG00000154274	C4orf19	4:37455562-37687998	OK	2.16145	1.7302	-0.32106	-0.269926	0.6524	0.9998
ENSG00000168827	ENSG00000168827	GFM1	3:158362066-158410364	OK	48.2934	52.2415	0.11337	0.267681	0.6524	0.9998
ENSG00000106290	ENSG00000106290	TAF6	7:99690350-99726118	OK	42.0065	35.2348	-0.253611	-0.198924	0.65245	0.9998
ENSG00000141380	ENSG00000141380	SS18	18:23596577-23671181	OK	39.5106	36.532	-0.113078	-0.229613	0.65255	0.9998
ENSG00000185986	ENSG00000185986	SDHAP3	5:1568636-1594735	OK	0.834209	0.679904	-0.295079	-0.264294	0.6526	0.9998
ENSG00000205726	ENSG00000205726	ITSN1	21:34876237-35349992	OK	4.99497	6.2302	0.318804	0.120483	0.6526	0.9998
ENSG00000112877	ENSG00000112877	CEP72	5:612386-693510	OK	7.14545	5.52126	-0.372028	-0.20775	0.65275	0.9998
ENSG00000136628	ENSG00000136628	EPRS	1:220141942-220220000	OK	50.3382	54.3323	0.110156	0.224241	0.6528	0.9998
ENSG00000075089	ENSG00000075089	ACTR6	12:100550134-100660857	OK	21.8761	19.7899	-0.144591	-0.219585	0.653	0.9998
ENSG00000267459	ENSG00000267459	AC006116.27	19:56732680-56904914	OK	2.00753	0.924995	-1.11791	-0.432287	0.6531	0.9998
ENSG00000079950	ENSG00000079950	STX7	6:132767005-132834337	OK	93.4443	79.5699	-0.231883	-0.265139	0.65315	0.9998
ENSG00000141720	ENSG00000141720	PIP4K2B	17:36921941-36956379	OK	24.6185	22.0661	-0.15791	-0.204366	0.65315	0.9998
ENSG00000068366	ENSG00000068366	ACSL4	X:108866928-108976632	OK	17.7115	16.4032	-0.110712	-0.204822	0.65325	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000144840	ENSG00000144840	RABL3	3:120405527-120501916	OK	7.70378	6.55554	-0.232851	-0.269201	0.6533	0.9998
ENSG00000170166	ENSG00000170166	HOXD4	2:176986338-177037830	OK	8.23025	9.54921	0.214445	0.277201	0.65335	0.9998
ENSG00000272606	ENSG00000272606	RP11-554J4.1	2:55774427-55846015	OK	1.45556	0.8042	-0.855946	-0.122056	0.65335	0.9998
ENSG00000142655	ENSG00000142655	PEX14	1:10516578-10690815	OK	11.4456	9.6842	-0.24109	-0.240167	0.6535	0.9998
ENSG00000178605	ENSG00000178605	GTPBP6	X:220024-230886	OK	15.4886	16.9937	0.133786	0.268869	0.6535	0.9998
ENSG00000168255	ENSG00000168255	POLR2J3	7:102122891-102312088	OK	31.2266	35.2767	0.17594	0.278668	0.65355	0.9998
ENSG00000168291	ENSG00000168291	PDHB	3:58413356-58419584	OK	51.4328	47.5375	-0.113623	-0.272094	0.65355	0.9998
ENSG00000169871	ENSG00000169871	TRIM56	7:100728719-100735017	OK	3.84567	3.43909	-0.161206	-0.236301	0.65365	0.9998
ENSG00000188459	ENSG00000188459	WASF4P	X:47657324-47664188	OK	0.737321	0.861979	0.225361	0.267159	0.65365	0.9998
ENSG00000188603	ENSG00000188603	CLN3	16:28467692-28510291	OK	20.9451	22.6957	0.11581	0.24672	0.65365	0.9998
ENSG00000123091	ENSG00000123091	RNF11	1:51701942-51739127	OK	56.8517	63.7887	0.166097	0.268887	0.6537	0.9998
ENSG00000236739	ENSG00000236739	RP11-370B11.1	9:22646198-22824212	OK	8.67609	7.61456	-0.188284	-0.274227	0.65375	0.9998
ENSG00000141002	ENSG00000141002	TCF25	16:89939999-90005169	OK	42.4264	49.7269	0.229065	0.116816	0.6538	0.9998
ENSG00000123268	ENSG00000123268	ATF1	12:51157492-51214905	OK	15.6763	13.6292	-0.201879	-0.281588	0.65385	0.9998
ENSG00000214087	ENSG00000214087	ARL16	17:79648203-79670330	OK	30.573	25.1019	-0.284459	-0.24913	0.6539	0.9998
ENSG00000198417	ENSG00000198417	MT1F	16:56691605-56694610	OK	2.07357	1.75355	-0.241838	-0.236975	0.65395	0.9998
ENSG00000143393	ENSG00000143393	PI4KB	1:151252499-151300191	OK	68.9465	74.9872	0.121168	0.226978	0.654	0.9998
ENSG00000104361	ENSG00000104361	NIPAL2	8:99202060-99306621	OK	3.29558	3.71584	0.173157	0.167149	0.65405	0.9998
ENSG00000163479	ENSG00000163479	SSR2	1:155978838-155990750	OK	433.355	402.173	-0.107732	-0.267896	0.6541	0.9998
ENSG00000117280	ENSG00000117280	RAB7L1	1:205737113-205744588	OK	28.7697	31.4615	0.129035	0.269323	0.65415	0.9998
ENSG00000172795	ENSG00000172795	DCP2	5:112312398-112356667	OK	5.11658	4.25984	-0.264381	-0.204317	0.65415	0.9998
ENSG00000105186	ENSG00000105186	ANKRD27	19:33087912-33169206	OK	22.9858	24.8831	0.114424	0.211062	0.6542	0.9998
ENSG00000157837	ENSG00000157837	SPPL3	12:121200312-121342174	OK	26.8384	30.7482	0.1962	0.264736	0.6542	0.9998
ENSG00000095321	ENSG00000095321	CRAT	9:131857088-131911225	OK	18.16	14.7142	-0.303561	-0.259111	0.65425	0.9998
ENSG00000134905	ENSG00000134905	CARS2	13:111293758-111373421	OK	18.5546	20.3513	0.133339	0.219152	0.6543	0.9998
ENSG00000139405	ENSG00000139405	RITA1	12:113623330-113630173	OK	22.3382	24.2806	0.120294	0.278305	0.6543	0.9998
ENSG00000270081	ENSG00000270081	RP5-935K16.1	2:128601126-128603261	OK	2.16805	2.4523	0.177737	0.27253	0.6545	0.9998
ENSG00000146143	ENSG00000146143	PRIM2	6:57179602-57513375	OK	10.1939	9.27393	-0.136449	-0.219196	0.65455	0.9998
ENSG00000162065	ENSG00000162065	TBC1D24	16:2525146-2581423	OK	4.21377	3.30185	-0.351836	-0.108272	0.65455	0.9998
ENSG00000162599	ENSG00000162599	NFIA	1:61330930-61928465	OK	2.34564	2.05625	-0.189967	-0.207382	0.6546	0.9998
ENSG00000165699	ENSG00000165699	TSC1	9:135766734-135820020	OK	13.8692	12.3825	-0.163585	-0.240427	0.6546	0.9998
ENSG00000179348	ENSG00000179348	GATA2	3:128198269-128221191	OK	2.17806	2.47476	0.184242	0.254874	0.6547	0.9998
ENSG00000148908	ENSG00000148908	RGS10	10:121259339-121302220	OK	51.449	56.0172	0.122727	0.264178	0.65475	0.9998
ENSG00000236081	ENSG00000236081	AC074389.9	7:1727754-1787590	OK	0.607994	0.815754	0.424077	0.291136	0.65475	0.9998
ENSG00000136514	ENSG00000136514	RTP4	3:187086119-187089864	OK	3.42334	3.03525	-0.173591	-0.271585	0.65485	0.9998
ENSG00000121104	ENSG00000121104	FAM117A	17:47778304-47906458	OK	8.84858	11.3036	0.353265	0.265276	0.6549	0.9998
ENSG00000215424	ENSG00000215424	MCM3AP-AS1	21:47649130-47706211	OK	3.4832	2.63424	-0.403025	-0.189406	0.6551	0.9998
ENSG00000183527	ENSG00000183527	PSMG1	21:40546694-40555777	OK	31.129	28.359	-0.134454	-0.269772	0.6552	0.9998
ENSG00000156239	ENSG00000156239	N6AMT1	21:30244512-30257693	OK	3.05051	2.64497	-0.205797	-0.268202	0.65525	0.9998
ENSG00000175470	ENSG00000175470	PPP2R2D	10:133747954-133773331	OK	19.8991	21.9159	0.139273	0.260943	0.65525	0.9998
ENSG00000131473	ENSG00000131473	ACLY	17:40023160-40086795	OK	88.5787	82.1883	-0.108027	-0.258013	0.6553	0.9998
ENSG00000171094	ENSG00000171094	ALK	2:29415639-30144432	OK	1.53142	1.7023	0.152615	0.215971	0.6553	0.9998
ENSG00000198203	ENSG00000198203	SULT1C2	2:108905094-108926371	OK	2.04589	2.48544	0.280771	0.245701	0.65535	0.9998
ENSG00000197045	ENSG00000197045	GMFB	14:54941201-54955914	OK	34.0848	36.7463	0.108471	0.170127	0.65545	0.9998
ENSG00000111879	ENSG00000111879	FAM184A	6:119134604-119470552	OK	1.13551	0.932889	-0.283567	-0.149727	0.6555	0.9998
ENSG00000151502	ENSG00000151502	VPS26B	11:133938819-134117686	OK	16.3107	14.4807	-0.171686	-0.22056	0.6555	0.9998
ENSG00000163104	ENSG00000163104	SMARCAD1	4:95128761-95212443	OK	7.65562	6.96363	-0.13668	-0.226126	0.65565	0.9998
ENSG00000136875	ENSG00000136875	PRPF4	9:115983807-116055185	OK	17.105	14.1256	-0.276097	-0.2654	0.6557	0.9998
ENSG00000189376	ENSG00000189376	C8orf76	8:124232195-124287781	OK	17.3843	20.0357	0.204789	0.250744	0.65575	0.9998
ENSG00000226976	ENSG00000226976	COX6A1P2	6:37012606-37013177	OK	181.295	196.064	0.112989	0.271559	0.65575	0.9998
ENSG00000173120	ENSG00000173120	KDM2A	11:66886739-67025558	OK	16.9555	15.6457	-0.115994	-0.225486	0.65595	0.9998
ENSG00000145354	ENSG00000145354	CISD2	4:103790134-103940896	OK	24.8157	27.4254	0.144263	0.251585	0.656	0.9998
ENSG00000129187	ENSG00000129187	DCTD	4:183811212-183839089	OK	19.0587	17.2182	-0.146512	-0.256771	0.65615	0.9998
ENSG00000253203	ENSG00000253203	GUSBP3	5:68773298-69006341	OK	1.34423	0.939203	-0.517275	-0.27036	0.6563	0.9998
ENSG00000198863	ENSG00000198863	RUNDC1	17:41132581-41145707	OK	8.97803	8.25282	-0.121511	-0.262877	0.65635	0.9998
ENSG00000164070	ENSG00000164070	HSPA4L	4:128702975-128765195	OK	9.84645	10.8847	0.144628	0.261064	0.65645	0.9998
ENSG00000174106	ENSG00000174106	LEMD3	12:65563350-65642107	OK	5.0321	5.48287	0.12377	0.221026	0.65645	0.9998
ENSG00000166337	ENSG00000166337	TAF10	11:6624871-6633898	OK	105.433	126.866	0.266981	0.267424	0.65655	0.9998
ENSG00000263821	ENSG00000263821	RP11-527H14.1	18:14978737-14979838	OK	0.659048	0.527977	-0.319908	-0.281576	0.6567	0.9998
ENSG00000272240	ENSG00000272240	RP5-855D21.1	8:163185-197342	OK	1.19854	0.84088	-0.511302	-0.272871	0.65675	0.9998
ENSG00000133863	ENSG00000133863	TEX15	8:30689059-30748122	OK	0.889329	1.07912	0.279072	0.240092	0.6569	0.9998
ENSG00000204463	ENSG00000204463	BAG6	6:31606804-31625987	OK	123.016	135.878	0.143464	0.246693	0.65705	0.9998
ENSG00000047634	ENSG00000047634	SCML1	X:17755587-17773105	OK	11.6599	12.7195	0.12549	0.267502	0.65725	0.9998
ENSG00000120725	ENSG00000120725	SIL1	5:138282408-138667360	OK	25.5556	20.7254	-0.302238	-0.138024	0.65725	0.9998
ENSG00000217416	ENSG00000217416	ISCA1P1	5:62072703-62073090	OK	32.6867	29.4341	-0.151214	-0.260963	0.65725	0.9998
ENSG00000148843	ENSG00000148843	PDCD11	10:105156404-105206049	OK	17.6875	16.3381	-0.114489	-0.182182	0.6573	0.9998
ENSG00000029993	ENSG00000029993	HMGB3	X:150148981-150159248	OK	36.3782	32.2765	-0.172589	-0.276924	0.65735	0.9998
ENSG00000141527	ENSG00000141527	CARD14	17:78143790-78227299	OK	2.64351	3.43008	0.375785	0.156847	0.6574	0.9998
ENSG00000143951	ENSG00000143951	WDPCP	2:63348517-64054977	OK	4.82029	5.84985	0.27928	0.090075	0.65745	0.9998
ENSG00000130921	ENSG00000130921	C12orf65	12:123636866-123756881	OK	10.8792	8.38837	-0.375114	-0.20292	0.6575	0.9998
ENSG00000170035	ENSG00000170035	UBE2E3	2:181831974-182264286	OK	77.2304	70.2307	-0.137067	-0.264645	0.65755	0.9998
ENSG00000114503	ENSG00000114503	NCBP2	3:196662272-196669468	OK	91.3506	98.6529	0.110947	0.263079	0.6577	0.9998
ENSG00000120526	ENSG00000120526	NUDCD1	8:110253147-110358182	OK	13.1789	11.5037	-0.196131	-0.269736	0.6577	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000151461	ENSG00000151461	UPF2	10:11962020-12085169	OK	5.34721	4.90294	-0.12514	-0.237068	0.6577	0.9998
ENSG00000233330	ENSG00000233330	RP1-12G14.7	6:149912890-149913799	OK	0.772286	0.534004	-0.532285	-0.318628	0.65795	0.9998
ENSG00000264578	ENSG00000264578	RP11-360L9.8	8:41386724-41482520	OK	5.78227	3.15058	-0.876019	-0.1324	0.65815	0.9998
ENSG00000137563	ENSG00000137563	GGH	8:63927637-63951730	OK	79.4197	73.4269	-0.113189	-0.26382	0.6582	0.9998
ENSG00000176108	ENSG00000176108	CHMP6	17:78965397-78983317	OK	23.2147	21.2979	-0.124327	-0.259293	0.6582	0.9998
ENSG00000147400	ENSG00000147400	CETN2	X:151995516-151999321	OK	27.4372	25.2239	-0.121347	-0.270886	0.65835	0.9998
ENSG00000164118	ENSG00000164118	CEP44	4:175157808-175254531	OK	6.00352	5.18377	-0.211807	-0.211165	0.65845	0.9998
ENSG00000104219	ENSG00000104219	ZDHHC2	8:17013537-17082308	OK	6.67845	8.45279	0.339914	0.256739	0.6585	0.9998
ENSG00000244274	ENSG00000244274	DBNDD2	20:43990576-44039250	OK	3.4995	2.49589	-0.487593	-0.256453	0.65855	0.9998
ENSG00000235314	ENSG00000235314	LINC00957	7:44066549-44081905	OK	1.44863	1.25342	-0.208823	-0.27343	0.65865	0.9998
ENSG00000066135	ENSG00000066135	KDM4A	1:44115828-44396831	OK	13.3698	14.557	0.12273	0.221189	0.65885	0.9998
ENSG00000171055	ENSG00000171055	FEZ2	2:36583068-36873230	OK	28.9931	32.6247	0.170255	0.271492	0.6589	0.9998
ENSG00000187954	ENSG00000187954	CYHR1	8:145674964-145691060	OK	22.3606	24.908	0.15565	0.269245	0.65895	0.9998
ENSG00000147383	ENSG00000147383	NSDHL	X:151999510-152038273	OK	28.4447	26.1863	-0.119348	-0.271155	0.659	0.9998
ENSG00000101447	ENSG00000101447	FAM83D	20:37554954-37581703	OK	22.3125	24.196	0.116917	0.274587	0.65905	0.9998
ENSG00000261596	ENSG00000261596	CTB-31N19.3	16:21608538-21668794	OK	3.93054	6.48992	0.723472	0.0833949	0.6591	0.9998
ENSG00000004777	ENSG00000004777	ARHGAP33	19:36265433-36279724	OK	3.72742	3.07739	-0.276472	-0.146172	0.65915	0.9998
ENSG00000138674	ENSG00000138674	SEC31A	4:83739813-83934079	OK	37.822	41.2729	0.125971	0.199343	0.65915	0.9998
ENSG00000155016	ENSG00000155016	CYP2U1	4:108745718-108899955	OK	7.2536	6.6082	-0.134439	-0.266832	0.65915	0.9998
ENSG00000173258	ENSG00000173258	ZNF483	9:114287438-114393569	OK	0.847873	0.565356	-0.58469	-0.202609	0.65915	0.9998
ENSG00000087266	ENSG00000087266	SH3BP2	4:2794749-2842825	OK	8.51631	9.4812	0.154842	0.198757	0.6592	0.9998
ENSG00000127922	ENSG00000127922	SHFM1	7:96110937-96339203	OK	335.77	305.585	-0.1359	-0.274715	0.6593	0.9998
ENSG00000159873	ENSG00000159873	CCDC117	22:29168661-29185283	OK	10.4032	11.5202	0.147139	0.256027	0.6593	0.9998
ENSG00000131470	ENSG00000131470	PSMC3IP	17:40719085-40729849	OK	11.484	8.50333	-0.433523	-0.281975	0.65935	0.9998
ENSG00000156162	ENSG00000156162	DPY19L4	8:95731930-95806064	OK	17.3949	15.0661	-0.20735	-0.238387	0.6594	0.9998
ENSG00000170619	ENSG00000170619	COMMD5	8:146052848-146127553	OK	17.7092	19.983	0.174277	0.270921	0.65945	0.9998
ENSG00000267680	ENSG00000267680	ZNF224	19:44598491-44637027	OK	9.38045	8.32145	-0.172822	-0.228255	0.65955	0.9998
ENSG00000166133	ENSG00000166133	RPUSD2	15:40861498-40866659	OK	2.64548	2.96011	0.162125	0.262252	0.6596	0.9998
ENSG00000204103	ENSG00000204103	MAFB	20:39314487-39317880	OK	3.67975	4.04785	0.137547	0.261021	0.6596	0.9998
ENSG00000153879	ENSG00000153879	CEBPG	19:33864235-33873592	OK	8.02718	8.73852	0.122495	0.270206	0.6597	0.9998
ENSG00000123297	ENSG00000123297	TSFM	12:58156116-58212487	OK	32.0478	28.108	-0.189242	-0.259332	0.6598	0.9998
ENSG00000185219	ENSG00000185219	ZNF445	3:44481261-44519162	OK	3.12042	2.85806	-0.126708	-0.230344	0.65995	0.9998
ENSG00000254416	ENSG00000254416	RP11-347E10.1	11:110225854-110277124	OK	10.2681	9.09093	-0.175674	-0.269959	0.65995	0.9998
ENSG00000179151	ENSG00000179151	EDC3	15:74890840-74988633	OK	28.3741	31.9152	0.169668	0.227587	0.66	0.9998
ENSG00000083097	ENSG00000083097	DOPEY1	6:83777384-83908651	OK	3.09006	2.55208	-0.275962	-0.145031	0.66005	0.9998
ENSG00000204228	ENSG00000204228	HSD17B8	6:33172418-33174608	OK	10.3603	9.29938	-0.155853	-0.269083	0.66005	0.9998
ENSG00000125912	ENSG00000125912	NCLN	19:3185560-3209573	OK	31.2557	34.1095	0.126057	0.259641	0.6601	0.9998
ENSG00000133983	ENSG00000133983	COX16	14:70791797-70883778	OK	44.2555	39.567	-0.161561	-0.261338	0.66015	0.9998
ENSG00000270728	ENSG00000270728	RP4-657E11.10	1:19623573-19624397	OK	0.737586	0.9279	0.331158	0.266282	0.6602	0.9998
ENSG00000235587	ENSG00000235587	GAPDHP65	X:46299143-46300149	OK	0.679427	0.554201	-0.293908	-0.271577	0.6603	0.9998
ENSG00000133027	ENSG00000133027	PEMT	17:17408876-17513799	OK	45.5517	41.9176	-0.11995	-0.259142	0.66035	0.9998
ENSG00000250471	ENSG00000250471	GMPSP1	4:8176147-8176726	OK	5.25561	6.00457	0.192202	0.269765	0.66045	0.9998
ENSG00000113971	ENSG00000113971	NPHP3	3:132276981-132593067	OK	8.17195	6.98943	-0.225505	-0.151543	0.6605	0.9998
ENSG00000123154	ENSG00000123154	WDR83	19:12754088-12792716	OK	11.8277	8.8136	-0.424366	-0.194483	0.66075	0.9998
ENSG00000168439	ENSG00000168439	STIP1	11:63952743-63972015	OK	132.084	141.992	0.104361	0.235548	0.6609	0.9998
ENSG00000169203	ENSG00000169203	RP11-231C14.4	16:29262828-29519817	OK	3.09069	4.14573	0.423698	0.290824	0.6609	0.9998
ENSG00000068697	ENSG00000068697	LAPTM4A	2:20232410-20251789	OK	89.7332	83.4298	-0.105078	-0.263261	0.66095	0.9998
ENSG00000071889	ENSG00000071889	FAM3A	X:153733349-153744566	OK	21.3362	19.6455	-0.119109	-0.248835	0.6611	0.9998
ENSG00000204469	ENSG00000204469	PRRC2A	6:31588496-31605548	OK	67.5674	63.0149	-0.100634	-0.180603	0.66115	0.9998
ENSG00000143147	ENSG00000143147	GPR161	1:168053996-168106821	OK	36.3945	33.6298	-0.113982	-0.275453	0.6613	0.9998
ENSG00000197498	ENSG00000197498	RPF2	6:111303217-111349466	OK	15.2822	13.6555	-0.162363	-0.26575	0.66145	0.9998
ENSG00000103254	ENSG00000103254	FAM173A	16:770580-791329	OK	19.2917	23.4388	0.280918	0.255793	0.6615	0.9998
ENSG00000049759	ENSG00000049759	NEDD4L	18:55711598-56068772	OK	104.887	96.253	-0.123932	-0.177223	0.6616	0.9998
ENSG00000103507	ENSG00000103507	BCKDK	16:31117427-31124110	OK	30.1187	27.8554	-0.112703	-0.262944	0.6616	0.9998
ENSG00000152556	ENSG00000152556	PFKM	12:48436680-48540187	OK	80.0348	74.1727	-0.10974	-0.216322	0.6617	0.9998
ENSG00000169131	ENSG00000169131	ZNF354A	5:178138592-178157703	OK	7.52818	6.85089	-0.13601	-0.224061	0.6617	0.9998
ENSG00000176681	ENSG00000176681	LRRC37A	17:44352149-44439130	OK	0.711915	0.600052	-0.246618	-0.264314	0.6617	0.9998
ENSG00000088543	ENSG00000088543	C3orf18	3:50595461-50622366	OK	4.33103	3.66959	-0.239092	-0.205063	0.6618	0.9998
ENSG00000213830	ENSG00000213830	CFL1P5	5:68576001-68628636	OK	0.427267	0.857642	1.00524	0.257738	0.66185	0.9998
ENSG00000183520	ENSG00000183520	UTP11L	1:38474929-38490496	OK	22.3918	25.1476	0.16745	0.268471	0.66195	0.9998
ENSG00000107140	ENSG00000107140	TESK1	9:35605366-35647096	OK	12.3565	13.5639	0.134504	0.226398	0.662	0.9998
ENSG00000153575	ENSG00000153575	TUBGCP5	15:22833394-22873892	OK	3.88676	3.53697	-0.136055	-0.204458	0.66205	0.9998
ENSG00000171045	ENSG00000171045	TSNARE1	8:143293440-143484601	OK	6.26649	5.50569	-0.186733	-0.265554	0.6621	0.9998
ENSG00000146830	ENSG00000146830	GIGYF1	7:100277129-100287071	OK	10.9286	11.7602	0.105809	0.198104	0.66215	0.9998
ENSG00000171700	ENSG00000171700	RGS19	20:62704533-62711323	OK	11.0925	12.2425	0.142303	0.235345	0.6622	0.9998
ENSG00000164611	ENSG00000164611	PTTG1	5:159848828-159855748	OK	214.998	231.585	0.107218	0.263929	0.66225	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000076351	ENSG00000076351	SLC46A1	17:26684603-26734215	OK	4.3728	5.18484	0.245744	0.170177	0.66235	0.9998
ENSG00000256616	ENSG00000256616	RP11-815J4.6	18:12073230-12076653	OK	2.14893	2.47494	0.203775	0.265013	0.6624	0.9998
ENSG00000100325	ENSG00000100325	ASCC2	22:30184596-30234271	OK	27.6539	29.845	0.110008	0.191817	0.6625	0.9998
ENSG00000197705	ENSG00000197705	KLHL14	18:30252633-30354376	OK	0.861152	0.971914	0.17456	0.246021	0.6625	0.9998
ENSG00000138413	ENSG00000138413	IDH1	2:209100950-209130798	OK	345.841	319.249	-0.115426	-0.259352	0.66255	0.9998
ENSG00000163040	ENSG00000163040	CCDC74A	2:132285247-132291239	OK	0.890903	1.04767	0.233837	0.228875	0.66255	0.9998
ENSG00000168159	ENSG00000168159	RNF187	1:228674761-228683467	OK	152.655	169.692	0.152644	0.269904	0.66255	0.9998
ENSG00000271781	ENSG00000271781	CTD-2589H19.6	5:612386-693510	OK	1.02223	0.514827	-0.989563	-0.17821	0.66255	0.9998
ENSG00000115289	ENSG00000115289	PCGF1	2:74732169-74735707	OK	28.3585	31.0971	0.132997	0.212192	0.6626	0.9998
ENSG00000138685	ENSG00000138685	FGF2	4:123747862-123844123	OK	1.40225	1.20685	-0.216501	-0.270461	0.6626	0.9998
ENSG00000158966	ENSG00000158966	CACHD1	1:64936427-65158741	OK	1.73343	1.92168	0.148744	0.257338	0.66265	0.9998
ENSG00000088448	ENSG00000088448	ANKRD10	13:111530886-111567416	OK	30.3361	34.6446	0.191593	0.275098	0.6631	0.9998
ENSG00000213780	ENSG00000213780	GTF2H4	6:30875960-30894236	OK	26.9284	23.581	-0.191504	-0.266101	0.6631	0.9998
ENSG00000136153	ENSG00000136153	LMO7	13:76123618-76434004	OK	11.6875	13.0464	0.158682	0.19746	0.66325	0.9998
ENSG00000167491	ENSG00000167491	GATAD2A	19:19496634-19619740	OK	40.8899	46.1205	0.173663	0.249711	0.66345	0.9998
ENSG00000182628	ENSG00000182628	SKA2	17:57059998-57232630	OK	78.4771	66.6902	-0.234797	-0.280075	0.6635	0.9998
ENSG00000158163	ENSG00000158163	DZIP1L	3:137780831-137834660	OK	4.43966	5.08842	0.196768	0.223549	0.66355	0.9998
ENSG00000189241	ENSG00000189241	TSPYL1	6:116575335-116762424	OK	8.12109	8.84629	0.123398	0.26177	0.66355	0.9998
ENSG00000081177	ENSG00000081177	EXD2	14:69649736-69821183	OK	11.0857	10.2045	-0.119486	-0.249808	0.66365	0.9998
ENSG00000151612	ENSG00000151612	ZNF827	4:146601355-146859787	OK	6.9161	6.13456	-0.172998	-0.180576	0.6638	0.9998
ENSG00000188185	ENSG00000188185	LINC00265	7:39773230-39832691	OK	2.60356	2.30372	-0.176519	-0.201944	0.66385	0.9998
ENSG00000074695	ENSG00000074695	LMAN1	18:56995054-57027194	OK	36.6046	34.1067	-0.101969	-0.237798	0.664	0.9998
ENSG00000065371	ENSG00000065371	ROPN1	3:123687367-123711025	OK	15.0245	16.5197	0.13687	0.26462	0.66405	0.9998
ENSG00000116455	ENSG00000116455	WDR77	1:111981259-112005395	OK	34.2574	39.3487	0.199897	0.21446	0.66405	0.9998
ENSG00000105438	ENSG00000105438	KDELR1	19:48885826-48894810	OK	81.9874	76.0139	-0.10914	-0.263688	0.6641	0.9998
ENSG00000127483	ENSG00000127483	HP1BP3	1:21069153-21113816	OK	96.8116	107.522	0.151377	0.240594	0.6641	0.9998
ENSG00000232060	ENSG00000232060	RP11-255N24.4	9:30558877-30559479	OK	0.76139	0.606733	-0.327574	-0.264264	0.66415	0.9998
ENSG00000134333	ENSG00000134333	LDHA	11:18415934-18429972	OK	1227.21	1110.72	-0.14389	-0.260841	0.6642	0.9998
ENSG00000066933	ENSG00000066933	MYO9A	15:72110736-72447800	OK	5.9899	6.57326	0.134079	0.137969	0.66425	0.9998
ENSG00000175697	ENSG00000175697	GPR156	3:119883491-120003941	OK	0.728231	0.883835	0.279381	0.265217	0.66425	0.9998
ENSG00000109265	ENSG00000109265	KIAA1211	4:57036360-57194791	OK	8.51927	7.84699	-0.118591	-0.236227	0.66445	0.9998
ENSG00000110080	ENSG00000110080	ST3GAL4	11:126225534-126875953	OK	128.889	139.335	0.112429	0.259392	0.66455	0.9998
ENSG00000022840	ENSG00000022840	RNF10	12:120941076-121015397	OK	47.7256	52.142	0.127683	0.184451	0.6646	0.9998
ENSG00000159147	ENSG00000159147	DONSON	21:34876237-35349992	OK	14.3119	11.2488	-0.347448	-0.178779	0.66465	0.9998
ENSG00000168778	ENSG00000168778	TCTN2	12:124155659-124192948	OK	10.9198	11.8562	0.118691	0.249335	0.6647	0.9998
ENSG00000258186	ENSG00000258186	SLC7A5P2	16:21413557-21531765	OK	0.425245	1.08704	1.35404	0.341971	0.6649	0.9998
ENSG00000135801	ENSG00000135801	TAF5L	1:229728857-229761794	OK	17.8165	16.4456	-0.115513	-0.220609	0.66495	0.9998
ENSG00000100084	ENSG00000100084	HIRA	22:19318220-19466738	OK	14.658	12.2916	-0.254021	-0.256409	0.665	0.9998
ENSG00000152518	ENSG00000152518	ZFP36L2	2:43393799-43823185	OK	17.6933	19.4814	0.138898	0.262431	0.665	0.9998
ENSG00000158715	ENSG00000158715	SLC45A3	1:205626978-205649587	OK	3.51001	3.87367	0.142226	0.266167	0.665	0.9998
ENSG00000141642	ENSG00000141642	ELAC1	18:48494360-48611415	OK	5.41768	4.14688	-0.385651	-0.22363	0.66505	0.9998
ENSG00000167565	ENSG00000167565	SERTAD3	19:40946750-40950612	OK	8.69651	9.58457	0.140276	0.252631	0.66505	0.9998
ENSG00000132300	ENSG00000132300	PTCD3	2:86333304-86369280	OK	53.6906	60.4013	0.169909	0.255602	0.6651	0.9998
ENSG00000156261	ENSG00000156261	CCT8	21:30428125-30446118	OK	90.3326	97.0027	0.102778	0.258281	0.6651	0.9998
ENSG00000174177	ENSG00000174177	CTU2	16:88772870-88851619	OK	7.74452	9.2221	0.25192	0.241263	0.66515	0.9998
ENSG00000086102	ENSG00000086102	NFX1	9:33290508-33371155	OK	14.5791	15.7877	0.114901	0.246837	0.6652	0.9998
ENSG00000163633	ENSG00000163633	C4orf36	4:87797357-88062206	OK	1.60074	1.27431	-0.329031	-0.104264	0.66535	0.9998
ENSG00000239789	ENSG00000239789	MRPS17	7:55954969-56067874	OK	18.3923	14.4855	-0.344499	-0.259539	0.6654	0.9998
ENSG00000040933	ENSG00000040933	INPP4A	2:99061316-99210853	OK	9.57034	8.80244	-0.120666	-0.216659	0.66545	0.9998
ENSG00000166326	ENSG00000166326	TRIM44	11:35684352-35829775	OK	33.9625	36.8327	0.117044	0.247229	0.66545	0.9998
ENSG00000196535	ENSG00000196535	MYO18A	17:27400527-27507430	OK	19.4532	17.9196	-0.118469	-0.164838	0.6656	0.9998
ENSG00000159792	ENSG00000159792	PSKH1	16:67927174-67970990	OK	6.10457	5.28006	-0.209336	-0.236146	0.66565	0.9998
ENSG00000011009	ENSG00000011009	LYPLA2	1:24117459-24122029	OK	37.0794	40.1464	0.114655	0.246475	0.6657	0.9998
ENSG00000246560	ENSG00000246560	RP11-10L12.4	4:103715539-103790053	OK	2.7154	1.60122	-0.761989	-0.148022	0.6657	0.9998
ENSG00000132356	ENSG00000132356	PRKAA1	5:40759480-40798476	OK	49.1152	54.263	0.143799	0.228911	0.6658	0.9998
ENSG00000183258	ENSG00000183258	DDX41	5:176938577-176944470	OK	66.1584	60.0644	-0.139413	-0.254286	0.66585	0.9998
ENSG00000145736	ENSG00000145736	GTF2H2	5:70330783-70363516	OK	4.88691	4.34283	-0.170287	-0.245933	0.6659	0.9998
ENSG00000196781	ENSG00000196781	TLE1	9:84198597-84304220	OK	34.1657	37.6786	0.141196	0.254243	0.66605	0.9998
ENSG00000205531	ENSG00000205531	NAP1L4	11:2965666-3013607	OK	154.161	167.402	0.11888	0.222648	0.66605	0.9998
ENSG00000084070	ENSG00000084070	SMAP2	1:40810521-40888998	OK	13.4158	14.5962	0.121665	0.233557	0.6662	0.9998
ENSG00000177508	ENSG00000177508	IRX3	16:54317215-54320675	OK	0.686678	0.848319	0.304973	0.188302	0.6662	0.9998
ENSG00000093183	ENSG00000093183	SEC22C	3:42589460-42709072	OK	40.2592	35.0558	-0.199665	-0.234381	0.66635	0.9998
ENSG00000163382	ENSG00000163382	APOA1BP	1:156561553-156564091	OK	289.613	311.618	0.105656	0.260389	0.66635	0.9998
ENSG00000113240	ENSG00000113240	CLK4	5:178029664-178057616	OK	6.08574	6.766	0.152871	0.246286	0.66645	0.9998
ENSG00000196591	ENSG00000196591	HDAC2	6:114254191-114792869	OK	42.4793	46.2219	0.121817	0.238324	0.6665	0.9998
ENSG00000232093	ENSG00000232093	RP11-307C12.11	1:155006299-155035252	OK	1.31893	0.779829	-0.75814	-0.126428	0.6665	0.9998
ENSG00000162885	ENSG00000162885	B3GALNT2	1:235613237-235667781	OK	10.8335	11.8503	0.12943	0.239451	0.6666	0.9998
ENSG00000214300	ENSG00000214300	SPDYE3	7:99905324-99997719	OK	2.85278	2.07462	-0.459525	-0.255601	0.66665	0.9998
ENSG00000160999	ENSG00000160999	SH2B2	7:101928404-101962178	OK	3.76483	4.28621	0.18712	0.260321	0.6669	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000178921	ENSG00000178921	PFAS	17:8130190-8173809	OK	15.0626	13.6853	-0.138345	-0.173436	0.6669	0.9998
ENSG00000267213	ENSG00000267213	AC007773.2	19:32880955-32976801	OK	0.549963	0.932919	0.762416	0.174133	0.6669	0.9998
ENSG00000100439	ENSG00000100439	ABHD4	14:23064714-23081265	OK	9.14267	9.95688	0.123078	0.241159	0.66705	0.9998
ENSG00000142330	ENSG00000142330	CAPN10	2:241526132-241570676	OK	12.6981	13.8872	0.129147	0.214639	0.66705	0.9998
ENSG00000106330	ENSG00000106330	MOSPD3	7:100209724-100213007	OK	18.5508	20.3799	0.135661	0.268927	0.6671	0.9998
ENSG00000219200	ENSG00000219200	RNASEK	17:6757179-6922978	OK	262.814	242.133	-0.118244	-0.260875	0.6672	0.9998
ENSG00000072778	ENSG00000072778	ACADVL	17:7093208-7128592	OK	79.5713	73.4971	-0.114561	-0.225068	0.66725	0.9998
ENSG00000134058	ENSG00000134058	CDK7	5:68530667-68573250	OK	22.7521	20.9017	-0.12238	-0.240913	0.66725	0.9998
ENSG00000167645	ENSG00000167645	YIF1B	19:38795752-38807913	OK	71.3097	77.1723	0.113984	0.261512	0.6673	0.9998
ENSG00000135083	ENSG00000135083	CCNJL	5:159678658-159772403	OK	4.04462	4.59715	0.184736	0.246325	0.66745	0.9998
ENSG00000007392	ENSG00000007392	LUC7L	16:238967-279462	OK	18.7771	20.6858	0.139664	0.271911	0.66765	0.9998
ENSG00000127334	ENSG00000127334	DYRK2	12:68042117-68064699	OK	14.5596	16.039	0.139615	0.238123	0.66765	0.9998
ENSG00000240230	ENSG00000240230	COX19	7:937539-1015235	OK	5.42277	6.08723	0.166756	0.235485	0.66765	0.9998
ENSG00000110917	ENSG00000110917	MLEC	12:121124671-121139667	OK	80.926	86.8793	0.102411	0.157934	0.6677	0.9998
ENSG00000162496	ENSG00000162496	DHRS3	1:12627938-12677737	OK	5.85069	6.4467	0.139955	0.250389	0.6678	0.9998
ENSG00000123131	ENSG00000123131	PRDX4	X:23682378-23704516	OK	115.79	107.586	-0.106016	-0.260383	0.66785	0.9998
ENSG00000265188	ENSG00000265188	RP11-835E18.4	18:5232874-5246507	OK	0.885062	1.89833	1.10088	0.416061	0.66785	0.9998
ENSG00000186364	ENSG00000186364	NUDT17	1:145575232-145589439	OK	7.86793	10.4921	0.415253	0.258406	0.6679	0.9998
ENSG00000130731	ENSG00000130731	C16orf13	16:684428-686358	OK	58.4887	64.091	0.131962	0.265748	0.66795	0.9998
ENSG00000112992	ENSG00000112992	NNT	5:43571695-43707507	OK	111.81	103.598	-0.110058	-0.190119	0.668	0.9998
ENSG00000130158	ENSG00000130158	DOCK6	19:11309970-11373157	OK	5.63751	5.0042	-0.171919	-0.192782	0.6681	0.9998
ENSG00000215271	ENSG00000215271	HOMEZ	14:23654524-23795394	OK	6.53303	4.58159	-0.511905	-0.24533	0.66815	0.9998
ENSG00000075399	ENSG00000075399	VPS9D1	16:89773541-89883065	OK	5.35389	4.5802	-0.225177	-0.206862	0.6682	0.9998
ENSG00000089351	ENSG00000089351	GRAMD1A	19:35485687-35517375	OK	40.937	45.2404	0.144207	0.252277	0.6682	0.9998
ENSG00000141385	ENSG00000141385	AFG3L2	18:12307667-12377313	OK	53.0342	58.16	0.133103	0.227835	0.6682	0.9998
ENSG00000109743	ENSG00000109743	BST1	4:15606161-15739936	OK	0.770074	0.544324	-0.500533	-0.120987	0.6683	0.9998
ENSG00000176101	ENSG00000176101	SSNA1	9:140083098-140084822	OK	66.3468	61.3456	-0.113068	-0.262748	0.6683	0.9998
ENSG00000126012	ENSG00000126012	KDM5C	X:53220502-53254604	OK	24.8339	22.9332	-0.114876	-0.158665	0.66835	0.9998
ENSG00000167380	ENSG00000167380	ZNF226	19:44669225-44682534	OK	13.4711	11.8362	-0.186663	-0.253242	0.66845	0.9998
ENSG00000010803	ENSG00000010803	SCMH1	1:41492871-41707826	OK	11.8072	12.8859	0.126118	0.193653	0.6685	0.9998
ENSG00000159231	ENSG00000159231	CBR3	21:37502668-37528615	OK	7.24183	8.37645	0.209984	0.259995	0.66855	0.9998
ENSG00000198763	ENSG00000198763	MT-ND2	MT:4469-5511	OK	1118.48	1212.63	0.116597	0.262925	0.66855	0.9998
ENSG00000131652	ENSG00000131652	THOC6	16:3072620-3089134	OK	12.7697	15.008	0.233008	0.251972	0.6686	0.9998
ENSG00000103502	ENSG00000103502	CDIPT	16:29869677-29879371	OK	40.1892	43.4849	0.113708	0.262846	0.66865	0.9998
ENSG00000147044	ENSG00000147044	CASK	X:41374186-41782716	OK	11.5711	9.95431	-0.217129	-0.253189	0.66875	0.9998
ENSG00000164258	ENSG00000164258	NDUFS4	5:52856462-52979168	OK	95.1798	102.748	0.110382	0.256439	0.66885	0.9998
ENSG00000138777	ENSG00000138777	PPA2	4:106290233-106395238	OK	81.0479	74.9722	-0.112418	-0.256479	0.66895	0.9998
ENSG00000178425	ENSG00000178425	NT5DC1	6:116422011-116570660	OK	17.691	15.3473	-0.205028	-0.259678	0.66895	0.9998
ENSG00000272341	ENSG00000272341	RP1-151F17.2	6:16764576-16767114	OK	1.60541	1.42705	-0.169903	-0.254955	0.66895	0.9998
ENSG00000242477	ENSG00000242477	CTD-2161E19.1	5:86180047-86180698	OK	2.19804	2.54598	0.212005	0.249769	0.6691	0.9998
ENSG00000123545	ENSG00000123545	NDUFAF4	6:97337188-97345757	OK	27.8443	24.9525	-0.158199	-0.2626	0.66915	0.9998
ENSG00000260075	ENSG00000260075	NSFP1	17:44450220-44564507	OK	10.5742	9.63323	-0.134455	-0.261982	0.66915	0.9998
ENSG00000066185	ENSG00000066185	ZMYND12	1:42895999-43120335	OK	1.33645	0.884146	-0.596054	-0.144197	0.66925	0.9998
ENSG00000173614	ENSG00000173614	NMNAT1	1:9982172-10045559	OK	2.06082	1.61797	-0.349034	-0.231911	0.66925	0.9998
ENSG00000006625	ENSG00000006625	GGCT	7:30536236-30673649	OK	91.1133	78.6316	-0.212552	-0.246336	0.6693	0.9998
ENSG00000100612	ENSG00000100612	DHRS7	14:60558628-60636574	OK	50.5219	56.7017	0.166482	0.255317	0.6693	0.9998
ENSG00000258472	ENSG00000258472	RP11-192H23.4	17:26782769-26972472	OK	0.809039	0.567009	-0.512838	-0.0474717	0.66935	0.9998
ENSG00000108370	ENSG00000108370	RGS9	17:63133548-63223821	OK	1.20744	1.01295	-0.253388	-0.261226	0.6694	0.9998
ENSG00000133030	ENSG00000133030	MPRIP	17:16945858-17140502	OK	58.2682	53.2675	-0.129454	-0.134515	0.6694	0.9998
ENSG00000231074	ENSG00000231074	HCG18	6:30201815-30314661	OK	19.9187	17.3686	-0.197644	-0.2526	0.66945	0.9998
ENSG00000171735	ENSG00000171735	CAMTA1	1:6845383-7829766	OK	58.1333	52.7428	-0.140391	-0.25841	0.66955	0.9998
ENSG00000185585	ENSG00000185585	OLFML2A	9:127539436-127577164	OK	4.06255	3.61727	-0.167485	-0.227193	0.66955	0.9998
ENSG00000111832	ENSG00000111832	RWDD1	6:116892529-116918838	OK	42.3227	45.9225	0.117768	0.242909	0.6697	0.9998
ENSG00000204991	ENSG00000204991	SPIRE2	16:89884586-89937727	OK	4.14301	4.59978	0.150885	0.235125	0.6697	0.9998
ENSG00000120071	ENSG00000120071	KANSL1	17:44107281-44302733	OK	35.4613	31.0874	-0.189916	-0.213094	0.6698	0.9998
ENSG00000255302	ENSG00000255302	EID1	15:49115931-49255641	OK	33.5918	29.2209	-0.201107	-0.256253	0.67015	0.9998
ENSG00000110713	ENSG00000110713	NUP98	11:3686816-3847601	OK	25.4122	27.4993	0.113869	0.164142	0.67025	0.9998
ENSG00000231365	ENSG00000231365	RP11-418J17.1	1:119573838-119869926	OK	1.68708	1.28107	-0.397178	-0.202061	0.67025	0.9998
ENSG00000167394	ENSG00000167394	ZNF668	16:31072163-31085641	OK	3.66065	4.03075	0.138948	0.22178	0.67035	0.9998
ENSG00000139154	ENSG00000139154	AEBP2	12:19556978-19873735	OK	13.5969	15.0389	0.145422	0.246737	0.6706	0.9998
ENSG00000162869	ENSG00000162869	PPP1R21	2:48667736-48742525	OK	9.12717	8.20797	-0.153142	-0.195886	0.6706	0.9998
ENSG00000103199	ENSG00000103199	ZNF500	16:4746512-4817625	OK	4.17085	4.76703	0.192748	0.223025	0.67075	0.9998
ENSG00000053438	ENSG00000053438	NNAT	20:36120873-36156333	OK	0.466452	0.771935	0.726752	0.184913	0.6708	0.9998
ENSG00000230055	ENSG00000230055	CISD3	17:36886487-36906969	OK	24.4236	27.7517	0.184302	0.255748	0.6709	0.9998
ENSG00000092978	ENSG00000092978	GPATCH2	1:217600333-217804424	OK	5.73083	6.24284	0.123457	0.223302	0.671	0.9998
ENSG00000172409	ENSG00000172409	CLP1	11:57405496-57429340	OK	12.3356	14.0257	0.185241	0.263398	0.67105	0.9998
ENSG00000100280	ENSG00000100280	AP1B1	22:29723668-29819182	OK	43.4286	40.3721	-0.105289	-0.240736	0.6711	0.9998
ENSG00000250565	ENSG00000250565	ATP6V1E2	2:46717888-46852881	OK	4.80494	5.9612	0.311086	0.0637508	0.6712	0.9998
ENSG00000265778	ENSG00000265778	RP11-17M16.2	18:74069643-74207146	OK	0.354663	0.683743	0.947006	0.177835	0.6712	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000183401	ENSG00000183401	CCDC159	19:11406823-11465620	OK	10.1317	8.37262	-0.275123	-0.172513	0.6713	0.9998
ENSG00000261971	ENSG00000261971	RP11-473M20.7	16:3096681-3110727	OK	1.12787	0.953044	-0.242989	-0.186174	0.6713	0.9998
ENSG00000116138	ENSG00000116138	DNAJC16	1:15853307-15930121	OK	5.40481	4.84866	-0.156659	-0.173955	0.67135	0.9998
ENSG00000197692	ENSG00000197692	CBX3P7	11:88910619-89028927	OK	2.84527	1.82062	-0.644133	-0.057234	0.67135	0.9998
ENSG00000167637	ENSG00000167637	ZNF283	19:44331443-44353307	OK	3.62482	4.18381	0.206908	0.228826	0.6714	0.9998
ENSG00000111962	ENSG00000111962	UST	6:149068463-149398126	OK	4.44116	3.96456	-0.163773	-0.192884	0.6715	0.9998
ENSG00000198346	ENSG00000198346	ZNF813	19:53970988-54015941	OK	0.674582	0.964305	0.515495	0.163292	0.67155	0.9998
ENSG00000204315	ENSG00000204315	FKBPL	6:32096483-32098068	OK	9.79948	8.90312	-0.138394	-0.259853	0.67155	0.9998
ENSG00000132275	ENSG00000132275	RRP8	11:6616304-6624850	OK	16.3927	18.3875	0.16567	0.258817	0.6716	0.9998
ENSG00000267078	ENSG00000267078	RP11-666A8.9	17:74553847-74583038	OK	4.48889	2.45669	-0.869641	-0.211288	0.6716	0.9998
ENSG00000253352	ENSG00000253352	TUG1	22:31366662-31375381	OK	16.2496	17.6357	0.118096	0.215154	0.67165	0.9998
ENSG00000101574	ENSG00000101574	METTL4	18:2537523-2571508	OK	9.58875	8.59829	-0.157294	-0.218545	0.6717	0.9998
ENSG00000267020	ENSG00000267020	AC011558.5	19:1026297-1039068	OK	2.47235	1.06168	-1.21953	-0.24521	0.67175	0.9998
ENSG00000095564	ENSG00000095564	BTAF1	10:93683525-93790082	OK	17.2924	15.7448	-0.135261	-0.251199	0.67205	0.9998
ENSG00000226445	ENSG00000226445	XXyac-YX65C7_A.2	6:169613348-169654139	OK	0.989717	0.68017	-0.541121	-0.229893	0.6723	0.9998
ENSG00000130764	ENSG00000130764	LRRC47	1:3696783-3713068	OK	24.4827	27.2715	0.155633	0.244379	0.6724	0.9998
ENSG00000100784	ENSG00000100784	RPS6KA5	14:91336798-91691976	OK	14.5601	13.4151	-0.118165	-0.202442	0.67245	0.9998
ENSG00000130816	ENSG00000130816	DNMT1	19:10244020-10341962	OK	40.3055	37.4651	-0.105432	-0.155656	0.67245	0.9998
ENSG00000155744	ENSG00000155744	FAM126B	2:201773695-201950473	OK	5.74695	6.69109	0.219447	0.14175	0.6725	0.9998
ENSG00000184203	ENSG00000184203	PPP1R2	3:195241220-195270209	OK	33.1284	36.4757	0.138869	0.250561	0.6725	0.9998
ENSG00000173992	ENSG00000173992	CCS	11:66357639-66373490	OK	19.6522	21.5122	0.130459	0.260937	0.67265	0.9998
ENSG00000242288	ENSG00000242288	RP11-464F9.1	10:75404638-75490272	OK	0.433911	0.666561	0.61934	0.294344	0.67265	0.9998
ENSG00000158717	ENSG00000158717	RNF166	16:88762902-88772829	OK	5.53554	6.09254	0.138321	0.219531	0.67275	0.9998
ENSG00000228612	ENSG00000228612	HK2P1	X:79827369-79830106	OK	0.883394	0.773236	-0.192149	-0.254341	0.67275	0.9998
ENSG00000131558	ENSG00000131558	EXOC4	7:132937828-133751342	OK	58.8264	54.4535	-0.111439	-0.193841	0.6729	0.9998
ENSG00000139579	ENSG00000139579	NABP2	12:56615798-56623638	OK	33.0561	35.6947	0.110795	0.250675	0.6729	0.9998
ENSG00000214223	ENSG00000214223	HNRNPA1P10	19:11750590-11797382	OK	2.39458	2.03442	-0.23516	-0.262863	0.673	0.9998
ENSG00000129028	ENSG00000129028	THAP10	15:71123862-71342414	OK	1.43682	1.09528	-0.391577	-0.203246	0.67305	0.9998
ENSG00000230074	ENSG00000230074	RP11-195F19.9	9:34638129-34681295	OK	1.9467	0.928425	-1.06817	-0.283428	0.67305	0.9998
ENSG00000171295	ENSG00000171295	ZNF440	19:11925098-11946016	OK	4.57614	4.15529	-0.139182	-0.207531	0.6731	0.9998
ENSG00000157106	ENSG00000157106	SMG1	16:18814404-18937776	OK	11.4763	12.3055	0.100644	0.143719	0.67325	0.9998
ENSG00000163900	ENSG00000163900	TMEM41A	3:185000728-185216845	OK	13.4662	11.7827	-0.192672	-0.226745	0.6733	0.9998
ENSG00000119953	ENSG00000119953	SMNDC1	10:112050487-112064709	OK	19.6648	17.7646	-0.146614	-0.248808	0.67345	0.9998
ENSG00000010404	ENSG00000010404	IDS	X:148558520-148632055	OK	25.2873	22.3367	-0.178997	-0.262137	0.6735	0.9998
ENSG00000169118	ENSG00000169118	CSNK1G1	15:64457715-64679886	OK	6.43764	7.39062	0.199164	0.225898	0.6735	0.9998
ENSG00000185168	ENSG00000185168	LINC00482	17:79277570-79283048	OK	1.34105	1.58969	0.245378	0.216615	0.67355	0.9998
ENSG00000154743	ENSG00000154743	TSEN2	3:12525930-12705725	OK	7.24402	9.06742	0.323903	0.158025	0.67365	0.9998
ENSG00000272564	ENSG00000272564	RP11-548P2.2	2:86131401-86131850	OK	0.727799	0.934264	0.360291	0.262191	0.6737	0.9998
ENSG00000159479	ENSG00000159479	MED8	1:43849587-43855479	OK	26.9234	29.1772	0.115983	0.25373	0.67375	0.9998
ENSG00000162980	ENSG00000162980	ARL5A	2:152645497-152685006	OK	13.6967	15.5638	0.184357	0.240131	0.67375	0.9998
ENSG00000122965	ENSG00000122965	RBM19	12:114254542-114404176	OK	11.4292	12.3288	0.109304	0.247957	0.67385	0.9998
ENSG00000196792	ENSG00000196792	STRN3	14:31343719-31562818	OK	9.74523	10.8418	0.153832	0.178466	0.67385	0.9998
ENSG00000007541	ENSG00000007541	PIGQ	16:616994-634136	OK	13.9558	15.1246	0.116029	0.228786	0.6739	0.9998
ENSG00000108389	ENSG00000108389	MTMR4	17:56566897-56595266	OK	22.1922	23.8807	0.105788	0.176489	0.6739	0.9998
ENSG00000166454	ENSG00000166454	ATMIN	16:81069451-81080963	OK	9.86906	9.0418	-0.126302	-0.2383	0.674	0.9998
ENSG00000227297	ENSG00000227297	RP4-718J7.4	20:56174750-56176256	OK	1.05499	0.880603	-0.260658	-0.258749	0.67405	0.9998
ENSG00000105176	ENSG00000105176	URI1	19:30414550-30506611	OK	56.4574	52.3624	-0.10863	-0.250634	0.67415	0.9998
ENSG00000204623	ENSG00000204623	ZNRD1-AS1	6:29968787-30032686	OK	2.5594	2.17111	-0.237375	-0.249148	0.67415	0.9998
ENSG00000082212	ENSG00000082212	ME2	18:48405418-48474691	OK	20.8322	19.1953	-0.118063	-0.241694	0.6742	0.9998
ENSG00000244198	ENSG00000244198	RP4-545C24.1	7:143883175-144077725	OK	3.33431	2.35277	-0.503024	-0.241704	0.6742	0.9998
ENSG00000088766	ENSG00000088766	CRLS1	20:5986735-6020699	OK	16.6778	15.0832	-0.144991	-0.255561	0.6743	0.9998
ENSG00000182379	ENSG00000182379	NXPH4	12:57610577-57620232	OK	0.887627	1.01799	0.197694	0.234384	0.6744	0.9998
ENSG00000196151	ENSG00000196151	WDSUB1	2:160092303-160143310	OK	13.7742	12.6478	-0.123082	-0.258518	0.6744	0.9998
ENSG00000072954	ENSG00000072954	TMEM38A	19:16771937-16800840	OK	3.78078	3.27002	-0.209383	-0.248302	0.67445	0.9998
ENSG00000139323	ENSG00000139323	POC1B	12:89813494-89934079	OK	12.6507	13.8777	0.133557	0.209311	0.6745	0.9998
ENSG00000017427	ENSG00000017427	IGF1	12:102789644-102874423	OK	1.20766	1.46461	0.278302	0.224782	0.67455	0.9998
ENSG00000225969	ENSG00000225969	LINC00035	7:73149367-73150384	OK	0.920418	1.12964	0.295501	0.258803	0.6746	0.9998
ENSG00000113811	ENSG00000113811	SELK	3:53918436-53926015	OK	68.985	63.8575	-0.111426	-0.254315	0.67465	0.9998
ENSG00000135213	ENSG00000135213	POM121C	7:74988447-75115548	OK	29.0261	33.4095	0.202909	0.222397	0.6747	0.9998
ENSG00000111802	ENSG00000111802	TDP2	6:24650204-24667261	OK	22.5619	20.9149	-0.109359	-0.241175	0.6748	0.9998
ENSG00000152193	ENSG00000152193	RNF219	13:78469615-79233314	OK	7.33177	7.06568	-0.0533339	-0.0223495	0.6748	0.9998
ENSG00000130119	ENSG00000130119	GNL3L	X:54556643-54587504	OK	9.88182	10.7791	0.12539	0.255606	0.675	0.9998
ENSG00000134575	ENSG00000134575	ACP2	11:47260852-47290396	OK	10.8288	9.92963	-0.125064	-0.223518	0.675	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000228451	ENSG00000228451	SDAD1P1	8:26236774-26371608	OK	0.865996	0.563847	-0.619058	-0.134681	0.67515	0.9998
ENSG00000213699	ENSG00000213699	SLC35F6	2:26987151-27023935	OK	14.6879	16.4154	0.160423	0.245528	0.6752	0.9998
ENSG00000239779	ENSG00000239779	WBP1	2:74682149-74688018	OK	39.7059	35.5009	-0.161498	-0.264999	0.6753	0.9998
ENSG00000144935	ENSG00000144935	TRPC1	3:142442915-142526730	OK	4.80519	5.66294	0.236959	0.214183	0.6755	0.9998
ENSG00000242616	ENSG00000242616	GNG10	9:114393631-114432526	OK	43.9063	47.9028	0.125681	0.250482	0.6755	0.9998
ENSG00000170624	ENSG00000170624	SGCD	5:155297353-156194799	OK	17.6868	15.7711	-0.165384	-0.249333	0.67555	0.9998
ENSG00000105928	ENSG00000105928	DFNA5	7:24737971-24809244	OK	56.53	52.5306	-0.105858	-0.235244	0.6756	0.9998
ENSG00000161996	ENSG00000161996	WDR90	16:699310-717833	OK	10.1875	11.2203	0.139299	0.199219	0.6756	0.9998
ENSG00000217325	ENSG00000217325	PRELID1P1	6:126964633-126965536	OK	0.740313	0.892251	0.269313	0.232173	0.6756	0.9998
ENSG00000103018	ENSG00000103018	CYB5B	16:69458427-69500169	OK	67.2994	74.1863	0.14056	0.256343	0.67595	0.9998
ENSG00000165259	ENSG00000165259	HDX	X:83572881-83757487	OK	1.25882	1.46704	0.220831	0.245585	0.67595	0.9998
ENSG00000169564	ENSG00000169564	PCBP1	2:70187225-70316332	OK	150.299	140.015	-0.102257	-0.252107	0.676	0.9998
ENSG00000241547	ENSG00000241547	RP11-4K3__A.5	1:27648650-27662891	OK	0.480669	0.918634	0.934447	0.184725	0.67605	0.9998
ENSG00000270136	ENSG00000270136	MINOS1-NBL1	1:19923472-19984945	OK	9.54697	5.25584	-0.861122	-0.279164	0.67605	0.9998
ENSG00000269176	ENSG00000269176	RP11-727F15.12	11:62538591-62559493	OK	0.948299	0.555197	-0.772342	-0.154755	0.6761	0.9998
ENSG00000126261	ENSG00000126261	UBA2	19:34919256-34960853	OK	93.3622	86.6588	-0.107492	-0.234187	0.67625	0.9998
ENSG00000203485	ENSG00000203485	INF2	14:105155942-105185942	OK	20.2848	22.1576	0.127397	0.24765	0.67645	0.9998
ENSG00000171119	ENSG00000171119	NRTN	19:5823812-5828335	OK	1.9566	2.24549	0.198687	0.255803	0.6765	0.9998
ENSG00000101004	ENSG00000101004	NINL	20:25433340-25566153	OK	5.76451	6.36507	0.142977	0.18957	0.67655	0.9998
ENSG00000172817	ENSG00000172817	CYP7B1	8:65500319-65711318	OK	3.44546	2.94772	-0.225095	-0.254698	0.67655	0.9998
ENSG00000013523	ENSG00000013523	ANGEL1	14:77253587-77292589	OK	13.8162	12.7818	-0.11227	-0.220378	0.67675	0.9998
ENSG00000250067	ENSG00000250067	YJEFN3	19:19623226-19648390	OK	0.716879	0.47005	-0.608917	-0.116436	0.6768	0.9998
ENSG00000223414	ENSG00000223414	LINC00473	6:165740775-166401536	OK	16.9394	15.1323	-0.162747	-0.262692	0.67685	0.9998
ENSG00000225580	ENSG00000225580	RP1-159M24.1	6:112937904-112939082	OK	1.55054	1.77691	0.196605	0.252539	0.677	0.9998
ENSG00000185634	ENSG00000185634	SHC4	15:49115931-49255641	OK	6.53673	7.6164	0.220539	0.226355	0.67705	0.9998
ENSG00000148488	ENSG00000148488	ST8SIA6	10:17360381-17496329	OK	0.805531	0.69412	-0.214754	-0.232017	0.6771	0.9998
ENSG00000231312	ENSG00000231312	AC007246.3	2:39476406-39945103	OK	11.2763	8.39903	-0.425002	-0.235685	0.6771	0.9998
ENSG00000231043	ENSG00000231043	AC007238.1	2:58654933-59290901	OK	10.7396	12.0216	0.162687	0.252288	0.6773	0.9998
ENSG00000166578	ENSG00000166578	IQCD	12:113633245-113736390	OK	1.42079	0.910474	-0.642008	-0.259049	0.67735	0.9998
ENSG00000213401	ENSG00000213401	MAGEA12	X:151895975-151903184	OK	46.4714	49.9924	0.105366	0.252679	0.6774	0.9998
ENSG00000268061	ENSG00000268061	NAPA-AS1	19:47987538-48018497	OK	0.83965	0.535708	-0.64834	-0.128242	0.6774	0.9998
ENSG00000197982	ENSG00000197982	C1orf122	1:38268615-38275126	OK	34.1368	29.9454	-0.188992	-0.233907	0.67745	0.9998
ENSG00000213516	ENSG00000213516	RBMXL1	1:89401455-89458643	OK	3.22375	3.75744	0.221008	0.231734	0.6775	0.9998
ENSG00000268175	ENSG00000268175	AC117395.1	3:149478891-149942977	OK	1.24115	1.97472	0.669973	0.120755	0.6775	0.9998
ENSG00000100603	ENSG00000100603	SNW1	14:78174413-78236085	OK	50.4124	45.7682	-0.139431	-0.240943	0.67765	0.9998
ENSG00000115267	ENSG00000115267	IFIH1	2:163123588-163175213	OK	2.88311	2.60028	-0.148961	-0.243807	0.67775	0.9998
ENSG00000086189	ENSG00000086189	DIMT1	5:61601988-61924409	OK	19.3448	22.7149	0.231695	0.237033	0.6778	0.9998
ENSG00000159023	ENSG00000159023	EPB41	1:29213602-29450447	OK	19.8402	22.6798	0.192986	0.18654	0.6778	0.9998
ENSG00000182552	ENSG00000182552	RWDD4	4:184560787-184580378	OK	5.74313	6.45499	0.168579	0.228464	0.6778	0.9998
ENSG00000100350	ENSG00000100350	FOXRED2	22:36883236-36903148	OK	13.8748	15.2652	0.137781	0.206173	0.67785	0.9998
ENSG00000107779	ENSG00000107779	BMPR1A	10:88516406-88692595	OK	8.42449	7.03796	-0.259432	-0.173303	0.67795	0.9998
ENSG00000236618	ENSG00000236618	PITPNA-AS1	17:1420224-1466110	OK	12.0228	8.23132	-0.546582	-0.261505	0.6781	0.9998
ENSG00000183562	ENSG00000183562	AC131971.1	11:2965666-3013607	OK	0.548992	0.884423	0.687952	0.0989606	0.67815	0.9998
ENSG00000103051	ENSG00000103051	COG4	16:70514470-70557468	OK	12.7021	11.7644	-0.110644	-0.237942	0.6782	0.9998
ENSG00000117691	ENSG00000117691	NENF	1:212606228-212619714	OK	96.681	89.9253	-0.104505	-0.248699	0.67825	0.9998
ENSG00000118900	ENSG00000118900	UBN1	16:4853203-4932361	OK	13.8314	15.5381	0.16786	0.192211	0.67825	0.9998
ENSG00000115825	ENSG00000115825	PRKD3	2:37394962-37551951	OK	128.591	143.212	0.155361	0.163844	0.6783	0.9998
ENSG00000229638	ENSG00000229638	RPL4P4	3:185000728-185216845	OK	33.2197	37.6904	0.182158	0.25199	0.6783	0.9998
ENSG00000184719	ENSG00000184719	RNLS	10:90033620-90344287	OK	24.9741	27.1051	0.118133	0.250594	0.67835	0.9998
ENSG00000198925	ENSG00000198925	ATG9A	2:220074489-220094439	OK	26.9655	29.5488	0.131989	0.187022	0.67835	0.9998
ENSG00000134352	ENSG00000134352	IL6ST	5:55230922-55290821	OK	24.2075	26.3406	0.12183	0.180927	0.6784	0.9998
ENSG00000101474	ENSG00000101474	APMAP	20:24943560-24973615	OK	101.398	108.84	0.102188	0.255015	0.67845	0.9998
ENSG00000230397	ENSG00000230397	SPTLC1P1	10:31476811-31818742	OK	10.8675	6.5944	-0.72071	-0.286519	0.67845	0.9998
ENSG00000142444	ENSG00000142444	C19orf52	19:11039408-11044211	OK	12.8563	11.7792	-0.126233	-0.251725	0.6785	0.9998
ENSG00000233695	ENSG00000233695	GAS6-AS1	13:114518602-114567046	OK	2.77459	3.49773	0.334141	0.250427	0.6785	0.9998
ENSG00000105643	ENSG00000105643	ARRDC2	19:18111940-18124911	OK	6.8215	7.49839	0.136491	0.202248	0.67855	0.9998
ENSG00000147955	ENSG00000147955	SIGMAR1	9:34634718-34637806	OK	107.481	115.251	0.100691	0.242133	0.67855	0.9998
ENSG00000249087	ENSG00000249087	C1orf213	1:23685940-23698332	OK	0.670697	0.843082	0.33001	0.149408	0.67855	0.9998
ENSG00000125885	ENSG00000125885	MCM8	20:5931297-5975852	OK	9.7616	9.0141	-0.114934	-0.250994	0.6787	0.9998
ENSG00000087470	ENSG00000087470	DNM1L	12:32832133-32908836	OK	41.3901	38.4255	-0.107221	-0.171323	0.6789	0.9998
ENSG00000124786	ENSG00000124786	SLC35B3	6:8413300-8435794	OK	15.389	14.0664	-0.129642	-0.247653	0.67895	0.9998
ENSG00000196782	ENSG00000196782	MAML3	4:140586921-141075338	OK	0.65284	0.535417	-0.286065	-0.182669	0.67895	0.9998
ENSG00000172057	ENSG00000172057	ORMDL3	17:38077293-38083854	OK	22.462	20.8513	-0.107348	-0.23337	0.679	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000203546	ENSG00000203546	RP11-176H8.1	14:31717833-31926716	OK	0.929547	1.41012	0.601218	0.105856	0.679	0.9998
ENSG00000140465	ENSG00000140465	CYP1A1	15:75011882-75017951	OK	1.47663	1.6853	0.190692	0.226332	0.67905	0.9998
ENSG00000164961	ENSG00000164961	KIAA0196	8:126036501-126379362	OK	24.5763	22.4189	-0.132551	-0.191852	0.67905	0.9998
ENSG00000166619	ENSG00000166619	BLCAP	20:36120873-36156333	OK	28.9472	31.0698	0.10209	0.233879	0.67905	0.9998
ENSG00000178685	ENSG00000178685	PARP10	8:145051320-145101933	OK	5.26316	6.29783	0.258924	0.125857	0.6793	0.9998
ENSG00000198815	ENSG00000198815	FOXJ3	1:42642209-42804047	OK	11.4651	12.4503	0.118927	0.239607	0.6793	0.9998
ENSG00000232677	ENSG00000232677	LINC00665	19:36803968-36822620	OK	3.23861	3.60905	0.156246	0.229003	0.6793	0.9998
ENSG00000099625	ENSG00000099625	C19orf26	19:1189405-1238026	OK	3.33733	4.12467	0.305586	0.211648	0.67935	0.9998
ENSG00000126746	ENSG00000126746	ZNF384	12:6772425-6798738	OK	23.7369	21.671	-0.131366	-0.235393	0.6794	0.9998
ENSG00000140543	ENSG00000140543	DET1	15:89002706-89089906	OK	4.31267	3.31576	-0.379241	-0.275286	0.6794	0.9998
ENSG00000273058	ENSG00000273058	RP11-385F5.5	1:236681299-236767804	OK	0.47635	0.821026	0.785405	0.0799823	0.6794	0.9998
ENSG00000116213	ENSG00000116213	WRAP73	1:3547330-3663900	OK	14.6898	13.3779	-0.134959	-0.225174	0.67945	0.9998
ENSG00000127863	ENSG00000127863	TNFRSF19	13:24144508-24250232	OK	34.5355	32.1545	-0.103062	-0.237008	0.6795	0.9998
ENSG00000258427	ENSG00000258427	RBM8B	14:60863186-61021634	OK	1.58924	1.24652	-0.350439	-0.251474	0.67955	0.9998
ENSG00000152601	ENSG00000152601	MBNL1	3:151961616-152214602	OK	37.9598	41.6704	0.134551	0.218343	0.6797	0.9998
ENSG00000266820	ENSG00000266820	RP13-104F24.1	17:62745780-62833272	OK	1.54912	0.945956	-0.711604	-0.307707	0.6797	0.9998
ENSG00000153179	ENSG00000153179	RASSF3	12:65004292-65091347	OK	82.7703	90.016	0.121069	0.241821	0.67995	0.9998
ENSG00000196998	ENSG00000196998	WDR45	X:48928812-48958108	OK	26.8373	29.4685	0.134933	0.229351	0.67995	0.9998
ENSG00000272638	ENSG00000272638	GS1-114I9.1	7:30464142-30518400	OK	0.412748	1.00547	1.28454	0.405955	0.67995	0.9998
ENSG00000116698	ENSG00000116698	SMG7	1:183441350-183567381	OK	36.4596	33.7867	-0.109843	-0.172049	0.68	0.9998
ENSG00000138629	ENSG00000138629	UBL7	15:74738317-74753523	OK	36.745	34.0639	-0.109305	-0.241123	0.68005	0.9998
ENSG00000171160	ENSG00000171160	MORN4	10:99344079-99436191	OK	11.7132	8.84184	-0.405713	-0.233202	0.6801	0.9998
ENSG00000169756	ENSG00000169756	LIMS1	2:109150856-109303702	OK	20.0101	18.1282	-0.142487	-0.200236	0.6802	0.9998
ENSG00000204514	ENSG00000204514	ZNF814	19:58281022-58427978	OK	1.31834	1.57429	0.255975	0.106284	0.6804	0.9998
ENSG00000147457	ENSG00000147457	CHMP7	8:23101149-23119512	OK	26.3287	28.2467	0.101447	0.223819	0.6805	0.9998
ENSG00000162552	ENSG00000162552	WNT4	1:22443797-22470462	OK	0.636073	0.779756	0.293831	0.227073	0.6805	0.9998
ENSG00000164975	ENSG00000164975	SNAPC3	9:15422701-15511017	OK	23.0934	20.5908	-0.165478	-0.245828	0.6806	0.9998
ENSG00000272065	ENSG00000272065	U91328.20	6:25963029-26002003	OK	0.389761	0.765102	0.973062	0.141843	0.6806	0.9998
ENSG00000134769	ENSG00000134769	DTNA	18:32073253-32471808	OK	5.59922	5.12373	-0.128033	-0.18812	0.68065	0.9998
ENSG00000152778	ENSG00000152778	IFIT5	10:91174342-91180758	OK	5.72818	6.34807	0.148242	0.249455	0.6807	0.9998
ENSG00000155008	ENSG00000155008	APOOL	X:84258831-84343069	OK	8.09615	7.35416	-0.138675	-0.252238	0.6807	0.9998
ENSG00000236432	ENSG00000236432	AC097662.2	2:228029280-228222550	OK	1.14311	1.56916	0.457034	0.0728799	0.68075	0.9998
ENSG00000096433	ENSG00000096433	ITPR3	6:33588141-33679504	OK	21.7498	19.9243	-0.126473	-0.254886	0.6809	0.9998
ENSG00000183506	ENSG00000183506	PI4KAP2	22:21827288-21871822	OK	5.82018	5.27457	-0.142008	-0.237151	0.68095	0.9998
ENSG00000232310	ENSG00000232310	RP11-557H15.4	6:134846451-134980974	OK	1.80568	2.15804	0.257186	0.234662	0.681	0.9998
ENSG00000270189	ENSG00000270189	RP11-258C19.7	X:53198278-53200096	OK	1.60565	1.4232	-0.174019	-0.249378	0.681	0.9998
ENSG00000112640	ENSG00000112640	PPP2R5D	6:42952236-42981706	OK	33.9166	30.7118	-0.143199	-0.238659	0.68105	0.9998
ENSG00000175730	ENSG00000175730	BAK1P1	20:31276722-31278816	OK	1.36777	1.21329	-0.172908	-0.236278	0.6811	0.9998
ENSG00000259399	ENSG00000259399	TGIF2-C20orf24	20:34894257-35274619	OK	5.92403	2.68076	-1.14394	-0.295405	0.6812	0.9998
ENSG00000101146	ENSG00000101146	RAE1	20:55926065-55954267	OK	41.6468	38.4316	-0.115911	-0.244424	0.6813	0.9998
ENSG00000259426	ENSG00000259426	RP11-253M7.1	15:69591285-69740764	OK	0.488387	0.726994	0.573919	0.0818483	0.6813	0.9998
ENSG00000205838	ENSG00000205838	TTC23L	5:34837653-34899561	OK	1.67258	1.26155	-0.406874	-0.237989	0.6816	0.9998
ENSG00000164466	ENSG00000164466	SFXN1	5:174904064-174956745	OK	64.6637	72.7161	0.169317	0.235128	0.6817	0.9998
ENSG00000273186	ENSG00000273186	RP11-339B21.10	9:131174029-131199626	OK	1.64826	3.111	0.916432	0.208062	0.6818	0.9998
ENSG00000184428	ENSG00000184428	TOP1MT	8:144386553-144442149	OK	19.0515	20.5513	0.109329	0.226891	0.6819	0.9998
ENSG00000243147	ENSG00000243147	MRPL33	2:27994583-28561768	OK	183.202	167.303	-0.130972	-0.250112	0.6819	0.9998
ENSG00000125746	ENSG00000125746	EML2	19:46110251-46148887	OK	25.2342	27.2939	0.1132	0.186612	0.682	0.9998
ENSG00000165675	ENSG00000165675	ENOX2	X:129757349-130037208	OK	8.30453	7.56274	-0.134991	-0.232656	0.682	0.9998
ENSG00000177236	ENSG00000177236	AP006621.1	11:777577-784297	OK	1.23017	0.98062	-0.327092	-0.259557	0.68205	0.9998
ENSG00000128714	ENSG00000128714	HOXD13	2:176957618-176960666	OK	8.2144	7.5352	-0.124508	-0.24823	0.6821	0.9998
ENSG00000175215	ENSG00000175215	CTDSP2	12:58213709-58240522	OK	25.457	27.8944	0.131914	0.206689	0.68225	0.9998
ENSG00000187735	ENSG00000187735	TCEA1	8:54879111-54935089	OK	33.89	31.5905	-0.101368	-0.238061	0.6823	0.9998
ENSG00000229097	ENSG00000229097	CALM2P2	10:71907044-71930279	OK	16.7698	22.8484	0.446224	0.229354	0.6823	0.9998
ENSG00000268262	ENSG00000268262	CTC-246B18.8	19:39797207-39811498	OK	1.16995	1.74858	0.579733	0.290419	0.6823	0.9998
ENSG00000131828	ENSG00000131828	PDHA1	X:19362010-19533379	OK	179.496	163.282	-0.136588	-0.255149	0.68235	0.9998
ENSG00000174365	ENSG00000174365	SNHG11	20:37075220-37079564	OK	7.77884	8.67016	0.156503	0.252868	0.68245	0.9998
ENSG00000179240	ENSG00000179240	RP11-111M22.2	11:76092356-76125663	OK	1.55932	1.30672	-0.254971	-0.228465	0.6825	0.9998
ENSG00000100294	ENSG00000100294	MCAT	22:43528211-43539400	OK	12.1577	11.0953	-0.131932	-0.238389	0.68255	0.9998
ENSG00000183889	ENSG00000183889	NPIPA7	16:16404197-16444447	OK	2.52874	2.22446	-0.184968	-0.175009	0.6826	0.9998
ENSG00000136279	ENSG00000136279	DBNL	7:44084238-44109055	OK	82.8449	89.0056	0.103484	0.237995	0.68265	0.9998
ENSG00000188004	ENSG00000188004	C1orf204	1:159796539-159869953	OK	0.744648	0.914495	0.296416	0.239204	0.68275	0.9998
ENSG00000151014	ENSG00000151014	CCRN4L	4:139936942-140098372	OK	9.03114	7.13155	-0.340692	-0.277163	0.6828	0.9998
ENSG00000266086	ENSG00000266086	RP11-159D12.5	17:56066398-56084707	OK	2.32347	1.32009	-0.815645	-0.137059	0.68295	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000136059	ENSG00000136059	VILL	3:38029549-38048679	OK	2.5975	2.91031	0.164047	0.22217	0.6831	0.9998
ENSG00000196814	ENSG00000196814	MVB12B	9:129089127-129269320	OK	9.76383	8.9928	-0.118676	-0.208865	0.68315	0.9998
ENSG00000225663	ENSG00000225663	FAM195B	17:79780286-79791178	OK	85.9152	79.9101	-0.104536	-0.247429	0.6832	0.9998
ENSG00000182670	ENSG00000182670	TTC3	21:38445525-38575413	OK	41.4536	46.4355	0.16373	0.225617	0.68325	0.9998
ENSG00000169084	ENSG00000169084	DHRSX	X:2137556-2420846	OK	14.5069	17.3822	0.260875	0.258375	0.68345	0.9998
ENSG00000089063	ENSG00000089063	TMEM230	20:5080485-5093749	OK	64.9118	60.4687	-0.102293	-0.231617	0.6835	0.9998
ENSG00000104883	ENSG00000104883	PEX11G	19:7541760-7585912	OK	1.0331	0.59792	-0.788954	-0.264284	0.6835	0.9998
ENSG00000162946	ENSG00000162946	DISC1	1:231664398-232177018	OK	1.51083	2.02737	0.424266	0.146436	0.6835	0.9998
ENSG00000159261	ENSG00000159261	CLDN14	21:37802657-37948867	OK	0.80947	0.669995	-0.272828	-0.224373	0.68365	0.9998
ENSG00000088298	ENSG00000088298	EDEM2	20:33703166-33872788	OK	40.359	35.0658	-0.202823	-0.244789	0.6837	0.9998
ENSG00000226332	ENSG00000226332	RP11-157P1.4	20:60877148-60942368	OK	0.531462	0.846269	0.671152	0.0820491	0.6837	0.9998
ENSG00000172262	ENSG00000172262	ZNF131	5:43014515-43192123	OK	29.7202	27.341	-0.120376	-0.199418	0.68375	0.9998
ENSG00000101444	ENSG00000101444	AHCY	20:32782374-32899608	OK	225.936	242.55	0.102368	0.241622	0.6838	0.9998
ENSG00000137266	ENSG00000137266	SLC22A23	6:3224494-3457256	OK	2.47404	2.98334	0.270057	0.147099	0.68385	0.9998
ENSG00000116161	ENSG00000116161	CACYBP	1:174968299-174992561	OK	118.149	107.441	-0.137055	-0.22956	0.6839	0.9998
ENSG00000106546	ENSG00000106546	AHR	7:17319457-17385776	OK	16.6182	14.7261	-0.174394	-0.217849	0.68395	0.9998
ENSG00000135974	ENSG00000135974	C2orf49	2:105950483-105965668	OK	13.7179	15.494	0.175648	0.248985	0.68395	0.9998
ENSG00000143776	ENSG00000143776	CDC42BPA	1:227177565-227506175	OK	9.1595	9.87572	0.108617	0.217191	0.68395	0.9998
ENSG00000180901	ENSG00000180901	KCTD2	17:73028669-73061984	OK	18.0402	15.6734	-0.202893	-0.219081	0.684	0.9998
ENSG00000118655	ENSG00000118655	DCLRE1B	1:114304453-114456708	OK	3.13468	2.67618	-0.228145	-0.26044	0.68405	0.9998
ENSG00000135940	ENSG00000135940	COX5B	2:98262502-98264846	OK	314.552	336.942	0.0992018	0.246946	0.6842	0.9998
ENSG00000163635	ENSG00000163635	ATXN7	3:63850232-63989138	OK	6.94324	6.38988	-0.119821	-0.196188	0.6842	0.9998
ENSG00000168036	ENSG00000168036	CTNNB1	3:41236327-42003922	OK	513.274	555.645	0.114435	0.212855	0.6842	0.9998
ENSG00000006744	ENSG00000006744	ELAC2	17:12895707-12921504	OK	25.3089	27.1975	0.103827	0.21385	0.68435	0.9998
ENSG00000010626	ENSG00000010626	LRRC23	12:6976282-7032861	OK	8.18676	6.67251	-0.295063	-0.0533531	0.68435	0.9998
ENSG00000183826	ENSG00000183826	BTBD9	6:38136226-38607924	OK	6.28255	7.02348	0.160835	0.212172	0.68435	0.9998
ENSG00000031823	ENSG00000031823	RANBP3	19:5916149-5978153	OK	25.6906	27.8008	0.113885	0.188191	0.6846	0.9998
ENSG00000105393	ENSG00000105393	BABAM1	19:17342691-17398455	OK	61.863	67.5207	0.126252	0.219375	0.68465	0.9998
ENSG00000172197	ENSG00000172197	MBOAT1	6:20100934-20317970	OK	9.92021	9.091	-0.125932	-0.24443	0.6847	0.9998
ENSG00000169902	ENSG00000169902	TPST1	7:65670185-65955095	OK	18.0066	19.654	0.126297	0.239348	0.68475	0.9998
ENSG00000077684	ENSG00000077684	JADE1	4:129730778-130037795	OK	5.48061	4.8424	-0.178616	-0.169479	0.68485	0.9998
ENSG00000166140	ENSG00000166140	ZFYVE19	15:41060066-41106767	OK	9.99126	9.03795	-0.144671	-0.218613	0.68485	0.9998
ENSG00000227855	ENSG00000227855	DPY19L2P3	7:29638410-29782210	OK	0.67328	0.808399	0.263861	0.228173	0.68485	0.9998
ENSG00000100625	ENSG00000100625	SIX4	14:61176245-61191066	OK	2.92881	2.59118	-0.176707	-0.248404	0.6849	0.9998
ENSG00000113384	ENSG00000113384	GOLPH3	5:32124809-32174456	OK	52.0357	55.6294	0.0963472	0.238286	0.6849	0.9998
ENSG00000136527	ENSG00000136527	TRA2B	3:185633693-185655924	OK	108.025	116.652	0.110847	0.230497	0.6849	0.9998
ENSG00000185800	ENSG00000185800	DMWD	19:46268042-46296060	OK	13.5362	15.7348	0.217137	0.238142	0.6849	0.9998
ENSG00000158623	ENSG00000158623	COPG2	7:130125882-130148500	OK	36.8114	33.9745	-0.115699	-0.243583	0.68495	0.9998
ENSG00000110395	ENSG00000110395	CBL	11:119076751-119178859	OK	4.37114	4.69964	0.104541	0.242075	0.6851	0.9998
ENSG00000198563	ENSG00000198563	DDX39B	6:31496493-31526606	OK	180.879	160.396	-0.173381	-0.273961	0.6851	0.9998
ENSG00000120685	ENSG00000120685	PROSER1	13:39584002-39612252	OK	8.77856	9.47025	0.109418	0.172954	0.68515	0.9998
ENSG00000146242	ENSG00000146242	TPBG	6:83072922-83080545	OK	1.06422	1.19758	0.170328	0.252532	0.68515	0.9998
ENSG00000224687	ENSG00000224687	RASAL2-AS1	1:178060642-178448644	OK	0.411373	0.647693	0.654862	0.109094	0.6852	0.9998
ENSG00000198026	ENSG00000198026	ZNF335	20:44577291-44600833	OK	8.69563	9.35262	0.105081	0.230512	0.6853	0.9998
ENSG00000006756	ENSG00000006756	ARSD	X:2822010-2847392	OK	6.77993	5.79426	-0.226647	-0.217188	0.68535	0.9998
ENSG00000117226	ENSG00000117226	GBP3	1:89472348-89488577	OK	1.33709	1.5248	0.189529	0.170032	0.6854	0.9998
ENSG00000232387	ENSG00000232387	SKA2P1	9:125524122-125524512	OK	2.98971	3.52742	0.23861	0.244314	0.6856	0.9998
ENSG00000065457	ENSG00000065457	ADAT1	16:75562429-75657198	OK	22.1903	26.0597	0.231892	0.207919	0.6857	0.9998
ENSG00000235194	ENSG00000235194	PPP1R3E	14:23654524-23795394	OK	3.19311	2.51991	-0.34159	-0.11954	0.68575	0.9998
ENSG00000111364	ENSG00000111364	DDX55	12:124086623-124118313	OK	25.6917	23.0747	-0.154992	-0.194061	0.6858	0.9998
ENSG00000160961	ENSG00000160961	ZNF333	19:14729928-14889353	OK	6.83236	5.75244	-0.24821	-0.213391	0.68595	0.9998
ENSG00000116903	ENSG00000116903	EXOC8	1:231468479-231490769	OK	9.87161	9.01782	-0.130507	-0.247257	0.686	0.9998
ENSG00000155090	ENSG00000155090	KLF10	8:103661006-103668130	OK	7.82283	8.4668	0.114127	0.245818	0.686	0.9998
ENSG00000168661	ENSG00000168661	ZNF30	19:35417806-35436074	OK	3.40914	3.07334	-0.149599	-0.217299	0.686	0.9998
ENSG00000173436	ENSG00000173436	MINOS1	1:19923472-19984945	OK	187.469	147.504	-0.345901	-0.257029	0.68605	0.9998
ENSG00000225163	ENSG00000225163	LINC00618	14:97263640-97411731	OK	0.746815	0.46948	-0.669686	-0.129052	0.68605	0.9998
ENSG00000196922	ENSG00000196922	ZNF252P	8:146198974-146231432	OK	9.55392	8.4544	-0.176391	-0.229213	0.6862	0.9998
ENSG00000225135	ENSG00000225135	RP11-361F15.2	6:147708799-147711601	OK	1.35118	1.54711	0.195363	0.251811	0.6862	0.9998
ENSG00000224138	ENSG00000224138	AC000123.4	7:126986843-127071978	OK	0.713961	0.383103	-0.898113	-0.16612	0.68625	0.9998
ENSG00000162910	ENSG00000162910	MRPL55	1:228294379-228297013	OK	63.8741	69.4296	0.120318	0.228544	0.6863	0.9998
ENSG00000229637	ENSG00000229637	PRAC2	17:46800529-46806540	OK	0.91437	1.91745	1.06834	0.437688	0.68635	0.9998
ENSG00000256268	ENSG00000256268	RP11-221N13.3	12:65672422-66036152	OK	1.39351	0.869465	-0.680525	-0.142106	0.68635	0.9998
ENSG00000183666	ENSG00000183666	GUSBP1	5:21341941-21589481	OK	13.1237	11.7039	-0.165178	-0.229947	0.6864	0.9998
ENSG00000168813	ENSG00000168813	ZNF507	19:32836499-32878573	OK	7.48378	6.89603	-0.118	-0.237944	0.68645	0.9998
ENSG00000138756	ENSG00000138756	BMP2K	4:79697495-79860592	OK	10.5091	11.6725	0.151476	0.17465	0.6866	0.9998
ENSG00000170089	ENSG00000170089	RP11-423H2.1	5:177236407-177410055	OK	7.73035	8.41688	0.122752	0.217679	0.68665	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000224886	ENSG00000224886	BEND3P3	10:81420646-81526085	OK	0.679666	1.20708	0.828626	0.32983	0.6867	0.9998
ENSG00000123094	ENSG00000123094	RASSF8	12:26092261-26232825	OK	17.5702	16.0948	-0.126532	-0.167129	0.68675	0.9998
ENSG00000138614	ENSG00000138614	VWA9	15:65871090-65903627	OK	17.997	19.4126	0.109232	0.225509	0.6868	0.9998
ENSG00000144043	ENSG00000144043	TEX261	2:71163011-71306935	OK	55.0784	50.1173	-0.136177	-0.217447	0.68685	0.9998
ENSG00000095059	ENSG00000095059	DHPS	19:12754088-12792716	OK	67.5354	58.9619	-0.19586	-0.216933	0.6869	0.9998
ENSG00000015676	ENSG00000015676	NUDCD3	7:44418719-44530479	OK	46.3488	41.8392	-0.147676	-0.234288	0.687	0.9998
ENSG00000251192	ENSG00000251192	ZNF674	X:46357161-46404892	OK	1.72429	2.10979	0.291096	0.221134	0.68705	0.9998
ENSG00000101577	ENSG00000101577	LPIN2	18:2916991-3013313	OK	8.65206	9.48816	0.133085	0.218124	0.6871	0.9998
ENSG00000013297	ENSG00000013297	CLDN11	3:170136652-170578169	OK	0.634971	0.556029	-0.191529	-0.139305	0.68715	0.9998
ENSG00000182154	ENSG00000182154	MRPL41	9:140445650-140447007	OK	68.2944	73.2239	0.100549	0.243394	0.6872	0.9998
ENSG00000198258	ENSG00000198258	UBL5	19:9938567-9940791	OK	516.623	482.666	-0.0980841	-0.241099	0.6872	0.9998
ENSG00000205746	ENSG00000205746	RP11-1212A22.1	16:18411798-18495797	OK	1.12857	1.41069	0.3219	0.199562	0.6872	0.9998
ENSG00000136828	ENSG00000136828	RALGPS1	9:129677052-129985445	OK	2.97404	2.58967	-0.199659	-0.180342	0.6873	0.9998
ENSG00000184887	ENSG00000184887	BTBD6	14:105675622-105864484	OK	47.6887	53.1049	0.155198	0.252308	0.6874	0.9998
ENSG00000249509	ENSG00000249509	RP11-402J6.1	4:113434671-113578748	OK	0.711919	1.05999	0.574263	0.113197	0.6874	0.9998
ENSG00000101084	ENSG00000101084	C20orf24	20:34894257-35274619	OK	141.644	155.97	0.138993	0.240968	0.68745	0.9998
ENSG00000215883	ENSG00000215883	CYB5RL	1:54598746-54879152	OK	6.55201	5.09439	-0.363028	-0.154836	0.68745	0.9998
ENSG00000162407	ENSG00000162407	PPAP2B	1:56960418-57110974	OK	0.636141	0.560454	-0.182751	-0.174174	0.6875	0.9998
ENSG00000121310	ENSG00000121310	ECHDC2	1:53361655-53392884	OK	8.79396	10.0964	0.19925	0.27628	0.68755	0.9998
ENSG00000268006	ENSG00000268006	PTOV1-AS1	19:50321538-50364001	OK	4.23257	2.71356	-0.641348	-0.296725	0.68755	0.9998
ENSG00000213015	ENSG00000213015	ZNF580	19:56146381-56164527	OK	6.60251	8.04041	0.284254	0.246642	0.68765	0.9998
ENSG00000090776	ENSG00000090776	EFNB1	X:68048839-68061990	OK	1.52456	1.69483	0.152754	0.245232	0.6877	0.9998
ENSG00000147677	ENSG00000147677	EIF3H	8:117654368-117889107	OK	194.435	221.487	0.187933	0.222941	0.6877	0.9998
ENSG00000121578	ENSG00000121578	B4GALT4	3:118930578-119009513	OK	21.4956	23.0816	0.102706	0.211027	0.68775	0.9998
ENSG00000173465	ENSG00000173465	SSSCA1	11:65337900-65341669	OK	59.2261	65.4733	0.144674	0.245676	0.6878	0.9998
ENSG00000107643	ENSG00000107643	MAPK8	10:49514697-49647403	OK	7.6537	8.87135	0.212997	0.257317	0.6879	0.9998
ENSG00000085662	ENSG00000085662	AKR1B1	7:134127101-134144036	OK	176.602	165.19	-0.096373	-0.23822	0.688	0.9998
ENSG00000058453	ENSG00000058453	CROCC	1:17066767-17299474	OK	2.87449	3.26616	0.184292	0.169051	0.68805	0.9998
ENSG00000153827	ENSG00000153827	TRIP12	2:230628553-230877825	OK	60.6769	65.7164	0.115106	0.152	0.68805	0.9998
ENSG00000146083	ENSG00000146083	RNF44	5:175953697-175965026	OK	12.245	11.2044	-0.128134	-0.198636	0.6881	0.9998
ENSG00000083168	ENSG00000083168	KAT6A	8:41786996-41909508	OK	9.1623	8.51846	-0.105117	-0.177994	0.68815	0.9998
ENSG00000237641	ENSG00000237641	RP11-690I21.1	2:232597134-232673963	OK	0.802924	1.30173	0.697096	0.0792003	0.68815	0.9998
ENSG00000163125	ENSG00000163125	RPRD2	1:150335566-150449042	OK	12.4416	11.5199	-0.111043	-0.238278	0.68825	0.9998
ENSG00000128928	ENSG00000128928	IVD	15:40697685-40728146	OK	9.71121	10.6136	0.128196	0.200266	0.68845	0.9998
ENSG00000183617	ENSG00000183617	MRPL54	19:3762661-3768573	OK	25.8552	28.224	0.126472	0.242822	0.68845	0.9998
ENSG00000109016	ENSG00000109016	DHRS7B	17:21026676-21096578	OK	13.0414	14.2681	0.12969	0.231402	0.68855	0.9998
ENSG00000143624	ENSG00000143624	INTS3	1:153700542-153746555	OK	31.8556	29.7098	-0.100606	-0.241189	0.68855	0.9998
ENSG00000111011	ENSG00000111011	RSRC2	12:122989189-123011547	OK	40.1249	43.494	0.116321	0.217342	0.6888	0.9998
ENSG00000112208	ENSG00000112208	BAG2	6:56951641-57087078	OK	5.36735	6.69924	0.319788	0.238379	0.6888	0.9998
ENSG00000015532	ENSG00000015532	XYLT2	17:48423452-48440499	OK	19.1056	20.4951	0.101285	0.228311	0.68895	0.9998
ENSG00000179091	ENSG00000179091	CYC1	8:145149929-145152428	OK	176.53	188.69	0.0961069	0.241831	0.68905	0.9998
ENSG00000155542	ENSG00000155542	SETD9	5:56195867-56267502	OK	21.1092	17.8403	-0.242733	-0.259681	0.68915	0.9998
ENSG00000157927	ENSG00000157927	RADIL	7:4836685-4923350	OK	1.62887	1.42418	-0.19374	-0.218864	0.68915	0.9998
ENSG00000143224	ENSG00000143224	PPOX	1:161136199-161147803	OK	17.9798	15.2331	-0.239164	-0.177068	0.6892	0.9998
ENSG00000156411	ENSG00000156411	C14orf2	14:104378624-104394606	OK	241.211	224.933	-0.100801	-0.242289	0.6892	0.9998
ENSG00000184014	ENSG00000184014	DENND5A	11:9160371-9286937	OK	33.4117	30.8485	-0.11515	-0.188728	0.6892	0.9998
ENSG00000177879	ENSG00000177879	AP3S1	5:115163892-115249778	OK	35.6091	31.7112	-0.167255	-0.250773	0.68925	0.9998
ENSG00000176894	ENSG00000176894	PXMP2	12:133264191-133299228	OK	12.6898	10.5417	-0.267554	-0.232947	0.68935	0.9998
ENSG00000154124	ENSG00000154124	FAM105B	5:14664772-14699820	OK	21.7767	18.4542	-0.238839	-0.244353	0.6894	0.9998
ENSG00000165525	ENSG00000165525	NEMF	14:50249996-50319921	OK	19.5184	18.1418	-0.105519	-0.176552	0.68945	0.9998
ENSG00000129226	ENSG00000129226	CD68	17:7465191-7536700	OK	51.8348	68.3025	0.398018	0.178998	0.6895	0.9998
ENSG00000135776	ENSG00000135776	ABCB10	1:229652328-229694442	OK	10.596	11.4099	0.10676	0.236594	0.68955	0.9998
ENSG00000134758	ENSG00000134758	RNF138	18:29598334-30050447	OK	12.5967	9.99826	-0.333301	-0.178964	0.6896	0.9998
ENSG00000198836	ENSG00000198836	OPA1	3:193310932-193415612	OK	91.3085	80.3692	-0.184107	-0.232948	0.68965	0.9998
ENSG00000132549	ENSG00000132549	VPS13B	8:100025493-100906290	OK	4.35232	3.7563	-0.212471	-0.159261	0.6897	0.9998
ENSG00000174599	ENSG00000174599	TRAM1L1	4:118004717-118006736	OK	1.24272	1.10057	-0.175247	-0.242585	0.6897	0.9998
ENSG00000020426	ENSG00000020426	MNAT1	14:61201459-61550451	OK	44.2827	38.9608	-0.184723	-0.233825	0.68975	0.9998
ENSG00000100243	ENSG00000100243	CYB5R3	22:43013845-43045574	OK	133.068	142.442	0.0982054	0.241318	0.68975	0.9998
ENSG00000013563	ENSG00000013563	DNASE1L1	X:153618314-153650065	OK	22.6508	16.9438	-0.418802	-0.163404	0.6898	0.9998
ENSG00000170949	ENSG00000170949	ZNF160	19:53569858-53606689	OK	4.827	5.27129	0.12703	0.172867	0.6899	0.9998
ENSG00000169641	ENSG00000169641	LUZP1	1:23345940-23504301	OK	8.56601	9.61876	0.167227	0.198527	0.68995	0.9998
ENSG00000231245	ENSG00000231245	C1DP1	10:32735067-33171802	OK	24.7831	22.244	-0.155943	-0.244647	0.68995	0.9998
ENSG00000158186	ENSG00000158186	MRAS	3:138066538-138124375	OK	6.02242	6.83604	0.182818	0.179199	0.69005	0.9998
ENSG00000188312	ENSG00000188312	CENPP	9:95059639-95432547	OK	2.18912	1.82508	-0.262396	-0.221287	0.69005	0.9998
ENSG00000099994	ENSG00000099994	SUSD2	22:24577226-24585078	OK	0.69815	0.788274	0.175161	0.24066	0.6901	0.9998
ENSG00000130402	ENSG00000130402	ACTN4	19:39138288-39260544	OK	275.809	305.012	0.145194	0.234947	0.6902	0.9998
ENSG00000170340	ENSG00000170340	B3GNT2	2:62423247-62451866	OK	19.2007	17.8422	-0.105864	-0.240299	0.69025	0.9998
ENSG00000225032	ENSG00000225032	RP11-228B15.4	9:130577290-130617035	OK	0.687287	0.397994	-0.788165	-0.224379	0.69025	0.9998
ENSG00000180998	ENSG00000180998	GPR137C	14:53019865-53104431	OK	1.16553	1.03735	-0.168087	-0.215046	0.69035	0.9998
ENSG00000133028	ENSG00000133028	SCO1	17:10583653-10718481	OK	17.781	19.3814	0.124335	0.222262	0.6904	0.9998
ENSG00000239508	ENSG00000239508	PLCH1-AS1	3:155093368-155462856	OK	8.76011	7.94824	-0.140313	-0.246972	0.6904	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000070759	ENSG00000070759	TESK2	1:45794834-45956872	OK	16.9769	15.1118	-0.167892	-0.201342	0.69055	0.9998
ENSG00000214982	ENSG00000214982	PARGP1	10:51623416-51741813	OK	0.662624	0.762802	0.203118	0.237291	0.69055	0.9998
ENSG00000173744	ENSG00000173744	AGFG1	2:228336847-228425930	OK	52.9323	57.9904	0.131666	0.234466	0.6906	0.9998
ENSG00000168883	ENSG00000168883	USP39	2:85825670-85876403	OK	42.947	46.4471	0.113031	0.215748	0.69065	0.9998
ENSG00000170632	ENSG00000170632	ARMC10	7:102715327-102740205	OK	36.389	33.3049	-0.127769	-0.237968	0.69065	0.9998
ENSG00000176105	ENSG00000176105	YES1	18:721587-812547	OK	27.8155	25.3983	-0.131154	-0.177483	0.69065	0.9998
ENSG00000272414	ENSG00000272414	FAM47E-STBD1	4:77135192-77232752	OK	1.56124	1.32439	-0.237365	-0.238506	0.69065	0.9998
ENSG00000095574	ENSG00000095574	IKZF5	10:124690418-124768333	OK	5.66973	6.34505	0.162353	0.155309	0.6907	0.9998
ENSG00000186314	ENSG00000186314	PRELID2	5:144851361-145214932	OK	19.7348	17.8202	-0.147228	-0.242785	0.69075	0.9998
ENSG00000121417	ENSG00000121417	ZNF211	19:58141760-58154147	OK	4.00895	3.61452	-0.14942	-0.203806	0.6908	0.9998
ENSG00000198440	ENSG00000198440	ZNF583	19:56905024-56947404	OK	1.99759	1.62515	-0.297688	-0.201122	0.69095	0.9998
ENSG00000103653	ENSG00000103653	CSK	15:75074397-75095539	OK	28.376	30.4959	0.103947	0.223114	0.6911	0.9998
ENSG00000155621	ENSG00000155621	C9orf85	9:74526425-74600970	OK	17.929	19.5845	0.127413	0.244496	0.69125	0.9998
ENSG00000234009	ENSG00000234009	RPL5P34	22:43172411-43173302	OK	3.69464	4.15	0.167676	0.241101	0.69125	0.9998
ENSG00000155097	ENSG00000155097	ATP6V1C1	8:104032414-104085279	OK	84.7678	92.2225	0.121602	0.208065	0.69135	0.9998
ENSG00000254721	ENSG00000254721	RP11-805J14.5	11:70049268-70053496	OK	1.91725	0.988644	-0.955518	-0.307946	0.6914	0.9998
ENSG00000118369	ENSG00000118369	USP35	11:77850816-77925757	OK	8.74982	9.75956	0.157563	0.233029	0.69145	0.9998
ENSG00000175309	ENSG00000175309	PHYKPL	5:177631507-177659792	OK	10.7199	8.85558	-0.275633	-0.154436	0.6915	0.9998
ENSG00000170439	ENSG00000170439	METTL7B	12:56075329-56118489	OK	1.04217	2.18698	1.06936	0.381115	0.69155	0.9998
ENSG00000257663	ENSG00000257663	RP11-1100L3.7	12:52463029-52502045	OK	1.06746	3.61358	1.75925	0.433838	0.69155	0.9998
ENSG00000188266	ENSG00000188266	HYKK	15:78799905-78829714	OK	3.94884	3.41968	-0.20757	-0.245516	0.69165	0.9998
ENSG00000102225	ENSG00000102225	CDK16	X:47077258-47089396	OK	68.4142	73.4785	0.103026	0.211113	0.6917	0.9998
ENSG00000126602	ENSG00000126602	TRAP1	16:3661728-3767598	OK	85.5355	78.7264	-0.119676	-0.219029	0.6917	0.9998
ENSG00000151687	ENSG00000151687	ANKAR	2:190539015-190630282	OK	1.07626	0.801591	-0.425084	-0.144936	0.69175	0.9998
ENSG00000263142	ENSG00000263142	LRRC37A17P	17:45000482-45177689	OK	1.11231	0.803517	-0.469154	-0.246291	0.6918	0.9998
ENSG00000182551	ENSG00000182551	ADI1	2:3500726-3526968	OK	28.2637	26.3064	-0.103538	-0.241587	0.69195	0.9998
ENSG00000047579	ENSG00000047579	DTNBP1	6:15523031-15663289	OK	34.898	37.9068	0.119311	0.249983	0.6921	0.9998
ENSG00000138381	ENSG00000138381	ASNSD1	2:190526110-190535557	OK	28.2076	25.9693	-0.11928	-0.213986	0.6921	0.9998
ENSG00000140694	ENSG00000140694	PARN	16:14529557-14726585	OK	26.6015	28.8327	0.116195	0.192669	0.69215	0.9998
ENSG00000244291	ENSG00000244291	C7orf13	7:156264889-156685924	OK	2.34223	3.13067	0.418588	0.231648	0.69215	0.9998
ENSG00000132286	ENSG00000132286	TIMM10B	11:6502676-6614988	OK	27.3192	24.3301	-0.167173	-0.24314	0.6922	0.9998
ENSG00000167272	ENSG00000167272	POP5	12:121016566-121019201	OK	44.5547	48.3131	0.116835	0.25666	0.6922	0.9998
ENSG00000180628	ENSG00000180628	PCGF5	10:92979907-93044088	OK	25.383	22.5325	-0.171851	-0.237631	0.69225	0.9998
ENSG00000176058	ENSG00000176058	TPRN	9:140086068-140100090	OK	12.0227	13.4166	0.158252	0.236465	0.6923	0.9998
ENSG00000027847	ENSG00000027847	B4GALT7	5:177027100-177037348	OK	19.0824	17.6213	-0.114917	-0.214228	0.69235	0.9998
ENSG00000160584	ENSG00000160584	SIK3	11:116706466-116969153	OK	3.13965	3.45728	0.139034	0.190232	0.69235	0.9998
ENSG00000018699	ENSG00000018699	TTC27	2:32853098-33046118	OK	6.75287	7.30903	0.11418	0.218679	0.6924	0.9998
ENSG00000258388	ENSG00000258388	PPT2-EGFL8	6:32116135-32145873	OK	3.00562	2.36289	-0.347111	-0.0852436	0.6924	0.9998
ENSG00000048405	ENSG00000048405	ZNF800	7:126986843-127071978	OK	10.1833	9.28136	-0.133796	-0.228604	0.69245	0.9998
ENSG00000250037	ENSG00000250037	RP11-480D4.4	5:8333595-8463208	OK	1.21552	0.579041	-1.06983	-0.428382	0.6925	0.9998
ENSG00000150961	ENSG00000150961	SEC24D	4:119643977-119759838	OK	6.67327	6.17001	-0.113119	-0.193622	0.69255	0.9998
ENSG00000233426	ENSG00000233426	EIF3FP3	2:58478574-58479703	OK	47.4211	50.878	0.101514	0.234997	0.69255	0.9998
ENSG00000108100	ENSG00000108100	CCNY	10:35535952-35860852	OK	13.6153	12.4266	-0.1318	-0.192951	0.69265	0.9998
ENSG00000134287	ENSG00000134287	ARF3	12:49297200-49351334	OK	123.715	136.275	0.139499	0.218708	0.69265	0.9998
ENSG00000105676	ENSG00000105676	ARMC6	19:19101696-19170563	OK	18.8997	21.9682	0.217057	0.222789	0.6927	0.9998
ENSG00000185651	ENSG00000185651	UBE2L3	22:21899632-21978323	OK	75.7303	81.6467	0.108522	0.239153	0.6928	0.9998
ENSG00000167996	ENSG00000167996	FTH1	11:61717292-61735132	OK	8842.5	9956.29	0.171154	0.245949	0.6929	0.9998
ENSG00000138131	ENSG00000138131	LOXL4	10:100007446-100028007	OK	4.27617	3.92638	-0.123118	-0.236304	0.69295	0.9998
ENSG00000125841	ENSG00000125841	NRSN2	20:300956-340304	OK	14.3804	13.1745	-0.126347	-0.218708	0.69305	0.9998
ENSG00000006432	ENSG00000006432	MAP3K9	14:71189242-71276251	OK	4.551	4.99223	0.1335	0.242366	0.6931	0.9998
ENSG00000184209	ENSG00000184209	SNRNP35	12:123942187-124018265	OK	21.9847	19.678	-0.159919	-0.227933	0.69325	0.9998
ENSG00000215417	ENSG00000215417	MIR17HG	13:92000073-92006833	OK	1.92097	1.6316	-0.235543	-0.0978152	0.6933	0.9998
ENSG00000189042	ENSG00000189042	ZNF567	19:37178513-37263727	OK	3.01825	2.65619	-0.184355	-0.18743	0.6934	0.9998
ENSG00000099282	ENSG00000099282	TSPAN15	10:71211228-71267425	OK	2.61905	2.98499	0.188684	0.229458	0.6936	0.9998
ENSG00000221823	ENSG00000221823	PPP3R1	2:68350067-68488362	OK	21.4904	23.7566	0.14464	0.211363	0.6936	0.9998
ENSG00000168172	ENSG00000168172	HOOK3	8:42704779-42940931	OK	6.84494	5.76577	-0.247525	-0.119124	0.6937	0.9998
ENSG00000115364	ENSG00000115364	MRPL19	2:75873908-75938115	OK	40.3851	44.4401	0.138042	0.230899	0.6939	0.9998
ENSG00000138785	ENSG00000138785	INTS12	4:106473776-106943635	OK	15.3994	13.9724	-0.140294	-0.222692	0.6939	0.9998
ENSG00000169627	ENSG00000169627	BOLA2B	16:30204254-30215631	OK	3.97204	4.9552	0.319062	0.237862	0.6939	0.9998
ENSG00000228439	ENSG00000228439	TSTD3	6:99880189-99979794	OK	1.09891	0.773746	-0.506144	-0.192839	0.6939	0.9998
ENSG00000132664	ENSG00000132664	POLR3F	20:18364010-18465287	OK	4.29563	4.72526	0.137526	0.194956	0.69395	0.9998
ENSG00000170579	ENSG00000170579	DLGAP1	18:3496029-4455335	OK	6.21328	7.0288	0.177924	0.135124	0.694	0.9998
ENSG00000103769	ENSG00000103769	RAB11A	15:65903703-66184329	OK	136.674	123.76	-0.143184	-0.241844	0.69405	0.9998
ENSG00000255351	ENSG00000255351	RP11-567I13.1	11:11292422-11643552	OK	4.89984	6.65383	0.441451	0.255075	0.69405	0.9998
ENSG00000088256	ENSG00000088256	GNA11	19:3094407-3124002	OK	27.9084	30.1833	0.113051	0.197346	0.6941	0.9998
ENSG00000106571	ENSG00000106571	GLI3	7:42000547-42277469	OK	7.54118	6.71533	-0.167331	-0.170057	0.69415	0.9998
ENSG00000159202	ENSG00000159202	UBE2Z	17:46952221-47006418	OK	75.8126	82.0039	0.113255	0.198689	0.69415	0.9998
ENSG00000122482	ENSG00000122482	ZNF644	1:91380858-91487829	OK	11.5182	10.3487	-0.154472	-0.222321	0.6942	0.9998
ENSG00000188610	ENSG00000188610	FAM72B	1:120835809-120855681	OK	2.32349	2.68586	0.209091	0.218336	0.6943	0.9998
ENSG00000232940	ENSG00000232940	HCG25	6:33217310-33244287	OK	4.14044	2.72271	-0.604743	-0.0273388	0.69445	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000164053	ENSG00000164053	ATRIP	3:48488113-48509044	OK	4.82836	4.36463	-0.145674	-0.216338	0.6945	0.9998
ENSG00000164305	ENSG00000164305	CASP3	4:185548849-185570663	OK	5.54378	5.08568	-0.124428	-0.211779	0.6946	0.9998
ENSG00000032389	ENSG00000032389	TSSC1	2:3192695-3381653	OK	27.6862	29.6991	0.101252	0.226609	0.6947	0.9998
ENSG00000138613	ENSG00000138613	APH1B	15:63568216-63601325	OK	5.0854	4.4834	-0.181768	-0.209371	0.6947	0.9998
ENSG00000004399	ENSG00000004399	PLXND1	3:129274017-129325661	OK	24.5511	27.6272	0.170302	0.216507	0.69475	0.9998
ENSG00000074964	ENSG00000074964	ARHGEF10L	1:17866329-18024369	OK	6.21117	5.70337	-0.123051	-0.181473	0.69475	0.9998
ENSG00000234719	ENSG00000234719	RP11-166B2.1	16:12021229-12070500	OK	2.87808	2.44965	-0.232532	-0.225698	0.69475	0.9998
ENSG00000010072	ENSG00000010072	SPRTN	1:231468479-231490769	OK	10.5378	9.2514	-0.187826	-0.201678	0.69495	0.9998
ENSG00000047346	ENSG00000047346	FAM214A	15:52870038-53002014	OK	3.37837	3.03907	-0.152701	-0.187465	0.69495	0.9998
ENSG00000266714	ENSG00000266714	MYO15B	17:73584138-73704142	OK	0.838682	0.955208	0.187691	0.0360823	0.69495	0.9998
ENSG00000064652	ENSG00000064652	SNX24	5:122179133-122390362	OK	4.2246	3.44653	-0.293674	-0.205841	0.695	0.9998
ENSG00000138696	ENSG00000138696	BMPR1B	4:95679118-96079599	OK	1.03738	1.20128	0.211629	0.20914	0.69505	0.9998
ENSG00000163577	ENSG00000163577	EIF5A2	3:170606203-170626482	OK	18.5196	15.5311	-0.253893	-0.244631	0.69505	0.9998
ENSG00000164292	ENSG00000164292	RHOBTB3	5:95036952-95160087	OK	27.1098	29.0579	0.100115	0.157858	0.6951	0.9998
ENSG00000273466	ENSG00000273466	RP11-548H3.1	2:219472487-219501907	OK	0.700194	1.15149	0.71767	0.298077	0.6952	0.9998
ENSG00000008513	ENSG00000008513	ST3GAL1	8:134467090-134584183	OK	7.83562	7.1152	-0.139144	-0.164981	0.6953	0.9998
ENSG00000026297	ENSG00000026297	RNASET2	6:166822851-167370679	OK	10.2338	12.0153	0.231536	0.236548	0.69535	0.9998
ENSG00000198492	ENSG00000198492	YTHDF2	1:29063132-29096287	OK	37.2186	34.7413	-0.0993707	-0.237337	0.6954	0.9998
ENSG00000265150	ENSG00000265150	RN7SL2	14:50329270-50329567	OK	2.8632	3.45697	0.271877	0.242916	0.6954	0.9998
ENSG00000161277	ENSG00000161277	THAP8	19:36505409-36545664	OK	6.51462	5.54957	-0.231304	-0.248092	0.69545	0.9998
ENSG00000164663	ENSG00000164663	USP49	6:41737913-41863099	OK	2.51235	3.19498	0.346769	0.122178	0.6955	0.9998
ENSG00000154493	ENSG00000154493	C10orf90	10:128113565-128359079	OK	59.4441	55.1874	-0.107195	-0.231657	0.69555	0.9998
ENSG00000114956	ENSG00000114956	DGUOK	2:74153952-74208568	OK	65.3963	60.6505	-0.10869	-0.238689	0.69565	0.9998
ENSG00000176018	ENSG00000176018	LYSMD3	5:89811427-90460038	OK	9.0381	8.37544	-0.109855	-0.209028	0.69575	0.9998
ENSG00000105556	ENSG00000105556	MIER2	19:305572-344798	OK	7.60622	8.21234	0.110613	0.21907	0.6958	0.9998
ENSG00000242085	ENSG00000242085	RPS20P33	14:105675622-105864484	OK	1.33841	0.861987	-0.634779	-0.0519394	0.69585	0.9998
ENSG00000148187	ENSG00000148187	MRRF	9:124999902-125085743	OK	27.3286	23.6395	-0.209212	-0.25769	0.6959	0.9998
ENSG00000165060	ENSG00000165060	FXN	9:71650174-71715094	OK	21.3425	23.7634	0.155008	0.242027	0.69595	0.9998
ENSG00000140983	ENSG00000140983	RHOT2	16:718085-724174	OK	43.1037	39.9054	-0.11123	-0.210245	0.6961	0.9998
ENSG00000158683	ENSG00000158683	PKD1L1	7:47735327-48019178	OK	2.02962	1.72279	-0.236465	-0.114221	0.69615	0.9998
ENSG00000125848	ENSG00000125848	FLRT3	20:13829892-16033842	OK	1.32087	1.51833	0.200992	0.194296	0.69625	0.9998
ENSG00000035141	ENSG00000035141	FAM136A	2:70523106-70529222	OK	31.8673	34.1274	0.0988567	0.226486	0.69635	0.9998
ENSG00000198804	ENSG00000198804	MT-CO1	MT:5903-7445	OK	6038.13	6732.44	0.157027	0.227748	0.6964	0.9998
ENSG00000157510	ENSG00000157510	AFAP1L1	5:148521045-148721365	OK	19.7039	21.8811	0.151201	0.187074	0.69645	0.9998
ENSG00000116016	ENSG00000116016	EPAS1	2:46520805-46613836	OK	20.4323	21.8555	0.0971431	0.173161	0.6966	0.9998
ENSG00000087269	ENSG00000087269	NOP14	4:2936625-2965112	OK	13.9865	12.9198	-0.11445	-0.237937	0.69675	0.9998
ENSG00000176463	ENSG00000176463	SLCO3A1	15:92396924-92874267	OK	2.14411	2.41042	0.168901	0.170935	0.69675	0.9998
ENSG00000258232	ENSG00000258232	RP11-161H23.5	12:49578578-49667114	OK	70.5517	94.5594	0.422541	0.242461	0.69675	0.9998
ENSG00000001631	ENSG00000001631	KRIT1	7:91828282-91875480	OK	19.8452	18.3319	-0.114437	-0.180629	0.69685	0.9998
ENSG00000183421	ENSG00000183421	RIPK4	21:43159528-43187266	OK	24.4341	22.8073	-0.0994048	-0.237782	0.69685	0.9998
ENSG00000138767	ENSG00000138767	CNOT6L	4:78634540-78740769	OK	4.00734	4.45905	0.154091	0.212429	0.6969	0.9998
ENSG00000198406	ENSG00000198406	BZW1P2	3:115521234-117716439	OK	136.566	125.4	-0.123052	-0.233564	0.6969	0.9998
ENSG00000203950	ENSG00000203950	FAM127B	X:134184961-134186226	OK	24.2486	22.0369	-0.137977	-0.236857	0.69695	0.9998
ENSG00000090432	ENSG00000090432	MUL1	1:20825942-20834654	OK	14.0983	15.1658	0.105308	0.233125	0.697	0.9998
ENSG00000131115	ENSG00000131115	ZNF227	19:44711699-44809199	OK	5.51336	4.90522	-0.168614	-0.195027	0.697	0.9998
ENSG00000255927	ENSG00000255927	AC005000.1	X:114952649-114953685	OK	0.294407	0.743739	1.33698	0.301949	0.697	0.9998
ENSG00000263345	ENSG00000263345	RP1-59D14.5	17:1963132-2284352	OK	0.89616	1.29996	0.536638	0.0703543	0.697	0.9998
ENSG00000115317	ENSG00000115317	HTRA2	2:74753771-74784681	OK	47.2366	40.9776	-0.20507	-0.225282	0.6971	0.9998
ENSG00000187790	ENSG00000187790	FANCM	14:45605142-45670093	OK	3.35682	3.02099	-0.152076	-0.164229	0.6971	0.9998
ENSG00000117523	ENSG00000117523	PRRC2C	1:171454650-171562650	OK	41.9189	38.4881	-0.12319	-0.119518	0.69715	0.9998
ENSG00000204147	ENSG00000204147	ASAH2B	10:52499077-52645435	OK	0.654137	0.767714	0.230976	0.219303	0.69715	0.9998
ENSG00000258515	ENSG00000258515	RP11-203M5.7	14:20914569-20923264	OK	1.48414	0.674951	-1.13677	-0.303277	0.69715	0.9998
ENSG00000087494	ENSG00000087494	PTHLH	12:28111016-28125638	OK	4.00782	3.56372	-0.169437	-0.228851	0.69725	0.9998
ENSG00000160392	ENSG00000160392	C19orf47	19:40825442-40896094	OK	6.14433	7.38509	0.265359	0.181233	0.69725	0.9998
ENSG00000175283	ENSG00000175283	DOLK	9:131683173-131790582	OK	8.25329	10.3084	0.320782	0.238313	0.69725	0.9998
ENSG00000112541	ENSG00000112541	PDE10A	6:165740775-166401536	OK	1.74226	1.44966	-0.265248	-0.200773	0.6973	0.9998
ENSG00000247809	ENSG00000247809	NR2F2-AS1	15:96670597-96883492	OK	1.06526	0.855481	-0.316396	-0.118119	0.6973	0.9998
ENSG00000256005	ENSG00000256005	AC093734.1	7:1570349-1600457	OK	2.48924	3.26768	0.392563	0.252749	0.6973	0.9998
ENSG00000016082	ENSG00000016082	ISL1	5:50668569-50690564	OK	1.0301	1.1576	0.168348	0.223475	0.69735	0.9998
ENSG00000203815	ENSG00000203815	FAM231D	1:149646784-149719362	OK	0.817854	0.61492	-0.411444	-0.252016	0.6975	0.9998
ENSG00000215039	ENSG00000215039	CD27-AS1	12:6548166-6580153	OK	11.5338	9.07921	-0.345232	-0.271931	0.6975	0.9998
ENSG00000173546	ENSG00000173546	CSPG4	15:75966662-76005189	OK	25.2057	26.9449	0.0962624	0.240245	0.69755	0.9998
ENSG00000139537	ENSG00000139537	CCDC65	12:49297200-49351334	OK	0.465398	0.638188	0.455517	0.0375515	0.6976	0.9998
ENSG00000229953	ENSG00000229953	RP11-284F21.7	1:156611181-156631216	OK	0.704116	0.379422	-0.892009	-0.139555	0.6977	0.9998
ENSG00000119537	ENSG00000119537	KDSR	18:60994958-61048862	OK	32.559	36.1782	0.152062	0.225066	0.69775	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000241764	ENSG00000241764	AC002467.7	7:107383261-107402112	OK	4.1333	2.88546	-0.518492	-0.207501	0.69775	0.9998
ENSG00000104881	ENSG00000104881	PPP1R13L	19:45882891-45982086	OK	1.25876	1.56861	0.31748	0.0855469	0.6978	0.9998
ENSG00000106608	ENSG00000106608	URGCP	7:43906156-43966010	OK	12.2741	14.2003	0.210298	0.189582	0.69785	0.9998
ENSG00000197782	ENSG00000197782	ZNF780A	19:40534166-40600313	OK	13.6477	11.0504	-0.304554	-0.256067	0.6979	0.9998
ENSG00000215305	ENSG00000215305	VPS16	20:2815959-3019722	OK	13.0516	11.5891	-0.171454	-0.217699	0.6979	0.9998
ENSG00000090061	ENSG00000090061	CCNK	14:99947505-100070363	OK	17.5151	19.6948	0.169211	0.214132	0.69805	0.9998
ENSG00000122707	ENSG00000122707	RECK	9:36036429-36124448	OK	8.08288	7.3068	-0.14563	-0.24096	0.6981	0.9998
ENSG00000135392	ENSG00000135392	DNAJC14	12:56137063-56236750	OK	18.9321	20.998	0.149416	0.197355	0.6982	0.9998
ENSG00000151923	ENSG00000151923	TIAL1	10:121334198-121356541	OK	61.4834	65.9572	0.101333	0.2042	0.6982	0.9998
ENSG00000204934	ENSG00000204934	ATP6V0E2-AS1	7:149564785-149577784	OK	1.20489	0.754825	-0.674688	-0.264478	0.6982	0.9998
ENSG00000163728	ENSG00000163728	TTC14	3:180319917-180700541	OK	16.1733	13.4215	-0.26907	-0.169238	0.69825	0.9998
ENSG00000111875	ENSG00000111875	ASF1A	6:119134604-119470552	OK	4.5894	5.1207	0.158037	0.217571	0.6983	0.9998
ENSG00000115275	ENSG00000115275	MOGS	2:74688183-74692537	OK	23.5004	25.1718	0.0991224	0.230751	0.6983	0.9998
ENSG00000119688	ENSG00000119688	ABCD4	14:74752125-74769759	OK	19.0456	17.5196	-0.120487	-0.209026	0.69845	0.9998
ENSG00000254614	ENSG00000254614	AP003068.23	11:64945076-64979477	OK	1.04328	1.56121	0.581542	0.103284	0.6985	0.9998
ENSG00000162613	ENSG00000162613	FUBP1	1:78409739-78444794	OK	37.556	35.0128	-0.101162	-0.196579	0.69865	0.9998
ENSG00000240875	ENSG00000240875	LINC00886	3:156465134-156534851	OK	0.718827	0.59276	-0.278196	-0.182865	0.69865	0.9998
ENSG00000106605	ENSG00000106605	BLVRA	7:43798278-43846939	OK	61.6203	66.0983	0.101207	0.236258	0.6987	0.9998
ENSG00000124541	ENSG00000124541	RRP36	6:42989382-43002143	OK	50.3628	54.0251	0.101271	0.234335	0.6987	0.9998
ENSG00000234338	ENSG00000234338	RP11-797H7.1	7:64295657-64297260	OK	0.734751	0.847205	0.205456	0.240831	0.6987	0.9998
ENSG00000171466	ENSG00000171466	ZNF562	19:9759329-9785776	OK	5.78098	5.26697	-0.134343	-0.193497	0.6988	0.9998
ENSG00000040487	ENSG00000040487	PQLC2	1:19638819-19655794	OK	10.7446	11.7571	0.129925	0.23946	0.69885	0.9998
ENSG00000204070	ENSG00000204070	SYS1	20:43990576-44039250	OK	25.4261	27.7435	0.125838	0.224615	0.69885	0.9998
ENSG00000198700	ENSG00000198700	IPO9	1:201592012-201853422	OK	47.4428	40.8154	-0.217076	-0.19255	0.69905	0.9998
ENSG00000204745	ENSG00000204745	AC083899.3	2:87352512-87423770	OK	1.10812	1.22854	0.148824	0.235206	0.69905	0.9998
ENSG00000179041	ENSG00000179041	RRS1	8:67341262-67430759	OK	14.9281	13.2197	-0.175342	-0.249454	0.6992	0.9998
ENSG00000113209	ENSG00000113209	PCDHB5	5:140514799-140517703	OK	1.02405	0.912412	-0.166528	-0.234476	0.69925	0.9998
ENSG00000135740	ENSG00000135740	SLC9A5	16:67263289-67306093	OK	0.578038	0.724481	0.325782	0.134767	0.69925	0.9998
ENSG00000117335	ENSG00000117335	CD46	1:207925401-207968858	OK	72.8318	68.2158	-0.0944629	-0.20988	0.6993	0.9998
ENSG00000114353	ENSG00000114353	GNAI2	3:50263723-50296787	OK	134.853	144.939	0.104058	0.232583	0.6994	0.9998
ENSG00000140961	ENSG00000140961	OSGIN1	16:83932730-83999937	OK	9.14802	10.0784	0.139732	0.229506	0.69945	0.9998
ENSG00000141425	ENSG00000141425	RPRD1A	18:33564349-33647539	OK	41.6014	45.1387	0.117732	0.229352	0.69945	0.9998
ENSG00000137103	ENSG00000137103	TMEM8B	9:35812956-35854844	OK	14.3657	12.7253	-0.174927	-0.232739	0.69955	0.9998
ENSG00000251432	ENSG00000251432	RP11-420A23.1	4:129213905-129440549	OK	0.552432	0.659629	0.255858	0.172851	0.69955	0.9998
ENSG00000025039	ENSG00000025039	RRAGD	6:90074354-90121989	OK	32.564	29.4284	-0.14607	-0.233218	0.69975	0.9998
ENSG00000071243	ENSG00000071243	ING3	7:120590802-120617270	OK	10.384	9.48265	-0.131001	-0.237463	0.69975	0.9998
ENSG00000104643	ENSG00000104643	MTMR9	8:11141924-11185646	OK	4.07498	4.45391	0.12828	0.230455	0.69975	0.9998
ENSG00000116288	ENSG00000116288	PARK7	1:8014350-8045565	OK	266.198	284.626	0.0965686	0.233129	0.69975	0.9998
ENSG00000249908	ENSG00000249908	CTD-2589H19.4	5:710470-919472	OK	4.1441	6.58729	0.668627	0.0724427	0.69975	0.9998
ENSG00000267010	ENSG00000267010	RP11-108P20.1	18:56337711-56421709	OK	0.280263	0.649385	1.21229	0.438459	0.69975	0.9998
ENSG00000126254	ENSG00000126254	RBM42	19:36119931-36128588	OK	48.181	51.5975	0.0988355	0.23905	0.69985	0.9998
ENSG00000229994	ENSG00000229994	RPL5P4	1:35734567-35887659	OK	104.091	115.116	0.145243	0.23984	0.69985	0.9998
ENSG00000268942	ENSG00000268942	CKS1B	5:61601988-61924409	OK	13.9645	8.86202	-0.656054	-0.124765	0.69985	0.9998
ENSG00000153786	ENSG00000153786	ZDHHC7	16:85007786-85045141	OK	18.5407	20.2614	0.128038	0.209747	0.6999	0.9998
ENSG00000070540	ENSG00000070540	WIPI1	17:66255322-66760023	OK	138.359	115.589	-0.259409	-0.190742	0.69995	0.9998
ENSG00000250159	ENSG00000250159	RP11-381K20.2	5:137150021-137387650	OK	3.43967	2.23492	-0.622047	-0.276381	0.69995	0.9998
ENSG00000115694	ENSG00000115694	STK25	2:242295657-242449145	OK	87.6754	98.1119	0.162256	0.188643	0.70005	0.9998
ENSG00000155876	ENSG00000155876	RRAGA	9:19049371-19051019	OK	49.0535	52.3789	0.0946279	0.230102	0.70005	0.9998
ENSG00000272072	ENSG00000272072	CTA-363E19.2	7:106809405-107218906	OK	0.538396	0.832784	0.629276	0.0634491	0.70015	0.9998
ENSG00000236449	ENSG00000236449	AC018890.6	2:175411868-175639555	OK	1.59227	1.15351	-0.465056	-0.135612	0.70025	0.9998
ENSG00000224051	ENSG00000224051	GLTPD1	1:1260135-1264277	OK	9.2994	10.0665	0.114353	0.231462	0.7003	0.9998
ENSG00000197779	ENSG00000197779	ZNF81	X:47696300-47931025	OK	3.5596	4.52649	0.346677	0.227297	0.7004	0.9998
ENSG00000101182	ENSG00000101182	PSMA7	20:60711790-60718496	OK	412.591	440.458	0.0942949	0.233697	0.7005	0.9998
ENSG00000114209	ENSG00000114209	PDCD10	3:167401085-167452727	OK	77.783	72.6029	-0.099429	-0.229573	0.7005	0.9998
ENSG00000166667	ENSG00000166667	SPDYE6	7:101986191-101996889	OK	1.2248	1.04678	-0.226585	-0.239379	0.7005	0.9998
ENSG00000124198	ENSG00000124198	ARFGEF2	20:47538426-47653230	OK	23.5414	25.0822	0.0914639	0.227898	0.7006	0.9998
ENSG00000244218	ENSG00000244218	RN7SL81P	7:128379345-128411861	OK	3.19441	1.90951	-0.742348	-0.0262572	0.70065	0.9998
ENSG00000130985	ENSG00000130985	UBA1	X:47050259-47074527	OK	89.2211	83.7144	-0.0919097	-0.224422	0.7007	0.9998
ENSG00000073905	ENSG00000073905	VDAC1P1	X:80184998-80185846	OK	2.88615	2.54293	-0.182655	-0.239454	0.70075	0.9998
ENSG00000261959	ENSG00000261959	RP11-893F2.14	17:48240883-48258539	OK	3.42369	2.88187	-0.248548	-0.229468	0.7008	0.9998
ENSG00000264112	ENSG00000264112	RP11-159D12.2	17:56066398-56084707	OK	2.8148	1.95814	-0.523547	-0.264258	0.701	0.9998
ENSG00000011243	ENSG00000011243	AKAP8L	19:15464195-15529952	OK	26.158	28.6808	0.132832	0.215742	0.7011	0.9998
ENSG00000179295	ENSG00000179295	PTPN11	12:112842993-112947717	OK	50.8804	57.5034	0.176536	0.200868	0.7012	0.9998
ENSG00000214279	ENSG00000214279	RP11-108K14.4	10:135192694-135382916	OK	0.643937	0.85364	0.406708	0.180765	0.70125	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000162959	ENSG00000162959	MEMO1	2:32090128-32264881	OK	29.3185	32.576	0.151997	0.193754	0.70135	0.9998
ENSG00000160191	ENSG00000160191	PDE9A	21:44073745-44195619	OK	2.35401	2.12396	-0.148366	-0.15165	0.7014	0.9998
ENSG00000196705	ENSG00000196705	ZNF431	19:21324826-21373034	OK	7.3295	6.1635	-0.249965	-0.253592	0.7014	0.9998
ENSG00000272565	ENSG00000272565	RP11-485G4.2	3:141876368-141880820	OK	1.22953	1.11446	-0.14176	-0.230699	0.7014	0.9998
ENSG00000162642	ENSG00000162642	C1orf52	1:85715638-85725355	OK	18.0863	16.433	-0.1383	-0.228414	0.70155	0.9998
ENSG00000105568	ENSG00000105568	PPP2R1A	19:52693291-52734547	OK	107.274	115.97	0.112462	0.228887	0.70165	0.9998
ENSG00000110074	ENSG00000110074	FOXRED1	11:126071992-126148026	OK	12.4287	10.5512	-0.236258	-0.151415	0.7017	0.9998
ENSG00000152256	ENSG00000152256	PDK1	2:173292081-173489823	OK	12.3648	8.96663	-0.463601	-0.219612	0.7017	0.9998
ENSG00000007520	ENSG00000007520	TSR3	16:1383601-1401912	OK	50.5305	46.859	-0.108828	-0.233407	0.70175	0.9998
ENSG00000235398	ENSG00000235398	LINC00623	1:144275917-144521970	OK	6.38159	5.32217	-0.261901	-0.213936	0.70175	0.9998
ENSG00000100395	ENSG00000100395	L3MBTL2	22:41601208-41636938	OK	12.0438	11.151	-0.111119	-0.220468	0.7018	0.9998
ENSG00000142166	ENSG00000142166	IFNAR1	21:34696733-34732168	OK	11.6145	10.644	-0.12588	-0.220239	0.70185	0.9998
ENSG00000260804	ENSG00000260804	RP11-566E18.3	2:217081767-217084915	OK	0.828131	0.93024	0.167745	0.229395	0.7019	0.9998
ENSG00000134825	ENSG00000134825	TMEM258	11:61447904-61634826	OK	93.7797	76.97	-0.28498	-0.235477	0.70195	0.9998
ENSG00000164081	ENSG00000164081	TEX264	3:51575159-51738339	OK	34.2492	38.0928	0.153447	0.226191	0.702	0.9998
ENSG00000170962	ENSG00000170962	PDGFD	11:103777913-104035107	OK	3.98733	3.6676	-0.120586	-0.230009	0.702	0.9998
ENSG00000148399	ENSG00000148399	DPH7	9:140449355-140473387	OK	16.4932	15.1434	-0.123185	-0.235486	0.7022	0.9998
ENSG00000162241	ENSG00000162241	SLC25A45	11:65134908-65151172	OK	2.26512	1.96771	-0.203068	-0.198054	0.7022	0.9998
ENSG00000163521	ENSG00000163521	GLB1L	2:220094478-220142892	OK	15.3217	18.6692	0.285089	0.213552	0.7022	0.9998
ENSG00000087302	ENSG00000087302	C14orf166	14:52456192-52471420	OK	134.679	143.612	0.0926546	0.232218	0.70225	0.9998
ENSG00000152348	ENSG00000152348	ATG10	5:81267843-81574396	OK	8.86899	7.23011	-0.294751	-0.0546783	0.7024	0.9998
ENSG00000182109	ENSG00000182109	RP11-69E11.4	1:39957317-40024379	OK	1.68899	1.36768	-0.304428	-0.248358	0.70245	0.9998
ENSG00000082213	ENSG00000082213	C5orf22	5:31532372-31555165	OK	62.896	68.159	0.115936	0.201958	0.7025	0.9998
ENSG00000102226	ENSG00000102226	USP11	X:47092088-47107727	OK	27.7108	25.9589	-0.0942194	-0.185361	0.7025	0.9998
ENSG00000139624	ENSG00000139624	CERS5	12:50505761-50561288	OK	15.9435	17.5068	0.134942	0.183664	0.7026	0.9998
ENSG00000169085	ENSG00000169085	C8orf46	8:67341262-67430759	OK	7.75946	6.96442	-0.155951	-0.18374	0.70265	0.9998
ENSG00000075239	ENSG00000075239	ACAT1	11:107879458-108018503	OK	32.4596	35.4659	0.127789	0.205108	0.7027	0.9998
ENSG00000260267	ENSG00000260267	RP11-452L6.5	16:31468031-31478487	OK	0.738486	0.60022	-0.29908	-0.219525	0.70285	0.9998
ENSG00000143614	ENSG00000143614	GATAD2B	1:153777200-153895451	OK	12.6457	11.8413	-0.0948273	-0.22977	0.7029	0.9998
ENSG00000170085	ENSG00000170085	SIMC1	5:175665364-175772994	OK	7.25671	6.67791	-0.119919	-0.203869	0.7029	0.9998
ENSG00000135945	ENSG00000135945	REV1	2:99613723-100106497	OK	13.099	11.1386	-0.233878	-0.112539	0.703	0.9998
ENSG00000212998	ENSG00000212998	RBM12B-AS1	8:94225530-94753245	OK	1.54946	0.895245	-0.791411	-0.185153	0.703	0.9998
ENSG00000149485	ENSG00000149485	FADS1	11:61447904-61634826	OK	24.8153	22.1733	-0.162411	-0.142958	0.70305	0.9998
ENSG00000213025	ENSG00000213025	COX20P1	10:70320412-70454239	OK	23.9952	20.3657	-0.236609	-0.212479	0.7031	0.9998
ENSG00000138623	ENSG00000138623	SEMA7A	15:74701629-74726808	OK	7.14706	7.81149	0.128247	0.195888	0.70315	0.9998
ENSG00000171174	ENSG00000171174	RBKS	2:27994583-28561768	OK	1.71043	1.2244	-0.482284	-0.191475	0.7033	0.9998
ENSG00000111642	ENSG00000111642	CHD4	12:6679248-6716642	OK	120.53	110.384	-0.126859	-0.0946819	0.70345	0.9998
ENSG00000109689	ENSG00000109689	STIM2	4:26859299-27027003	OK	7.85704	8.92039	0.18312	0.207629	0.7036	0.9998
ENSG00000204130	ENSG00000204130	RUFY2	10:70042416-70167051	OK	5.06202	6.04324	0.255607	0.145127	0.7036	0.9998
ENSG00000116237	ENSG00000116237	ICMT	1:6241328-6296032	OK	40.7343	35.5753	-0.195366	-0.210398	0.70365	0.9998
ENSG00000213614	ENSG00000213614	HEXA	15:72533521-72671129	OK	174.368	186.261	0.0951868	0.213208	0.70375	0.9998
ENSG00000137522	ENSG00000137522	RNF121	11:71639746-71708643	OK	18.8226	17.1482	-0.134414	-0.22963	0.70385	0.9998
ENSG00000168672	ENSG00000168672	FAM84B	8:127564686-127725660	OK	14.0243	12.6615	-0.147481	-0.208673	0.70385	0.9998
ENSG00000198146	ENSG00000198146	ZNF770	15:35270541-35280488	OK	5.05656	5.44552	0.106915	0.225295	0.70385	0.9998
ENSG00000047849	ENSG00000047849	MAP4	3:47892181-48130769	OK	65.8582	61.7011	-0.0940669	-0.139878	0.7039	0.9998
ENSG00000076555	ENSG00000076555	ACACB	12:109549022-109706031	OK	5.57466	6.42493	0.204798	0.172427	0.70395	0.9998
ENSG00000245281	ENSG00000245281	CTD-2547L16.1	8:17913933-17953903	OK	1.19632	0.884908	-0.435009	-0.0224804	0.704	0.9998
ENSG00000105325	ENSG00000105325	FZR1	19:3506270-3579086	OK	29.653	24.5271	-0.273802	-0.0478394	0.70405	0.9998
ENSG00000164197	ENSG00000164197	RNF180	5:63461670-63668696	OK	2.01896	1.81289	-0.155319	-0.201931	0.7042	0.9998
ENSG00000206503	ENSG00000206503	HLA-A	6:29909036-29913661	OK	165.832	177.255	0.0961086	0.231974	0.7042	0.9998
ENSG00000272323	ENSG00000272323	CTD-2517O10.6	5:34837653-34899561	OK	1.84196	1.60902	-0.19506	-0.232689	0.7042	0.9998
ENSG00000114331	ENSG00000114331	ACAP2	3:194995464-195163807	OK	20.9008	19.5332	-0.097627	-0.0978294	0.70425	0.9998
ENSG00000005243	ENSG00000005243	COPZ2	17:46103532-46115392	OK	5.65002	5.01739	-0.171318	-0.198942	0.7044	0.9998
ENSG00000151893	ENSG00000151893	CACUL1	10:120433678-120514761	OK	17.1274	18.3285	0.0977778	0.137042	0.7044	0.9998
ENSG00000232112	ENSG00000232112	TMA7	3:48473573-48488060	OK	288.752	310.804	0.106178	0.235867	0.7044	0.9998
ENSG00000109118	ENSG00000109118	PHF12	17:27232267-27384234	OK	10.9708	9.96895	-0.138151	-0.201213	0.70445	0.9998
ENSG00000162729	ENSG00000162729	IGSF8	1:160061129-160068733	OK	148.692	159.841	0.104306	0.226445	0.7045	0.9998
ENSG00000089154	ENSG00000089154	GCN1L1	12:120565006-120632513	OK	28.1029	29.8954	0.0892078	0.0971666	0.7047	0.9998
ENSG00000167653	ENSG00000167653	PSCA	8:143738873-143764142	OK	3.99786	5.2438	0.391384	0.244962	0.7047	0.9998
ENSG00000232149	ENSG00000232149	FERP1	X:122734411-122866906	OK	0.678486	0.356179	-0.929716	-0.141221	0.7047	0.9998
ENSG00000214832	ENSG00000214832	UPF3AP2	17:19912656-20306870	OK	3.17659	2.19083	-0.536001	-0.256201	0.70495	0.9998
ENSG00000113643	ENSG00000113643	RARS	5:167913449-167946304	OK	43.7218	46.6221	0.092662	0.221769	0.70505	0.9998
ENSG00000167515	ENSG00000167515	TRAPPC2L	16:88880141-88933068	OK	38.1535	43.2207	0.179906	0.239414	0.70505	0.9998
ENSG00000223509	ENSG00000223509	RP11-632K20.7	15:32812048-32879814	OK	2.03525	1.50836	-0.432217	-0.188602	0.7051	0.9998
ENSG00000072042	ENSG00000072042	RDH11	14:68086514-68162531	OK	65.6601	72.0675	0.134332	0.214912	0.70515	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000104129	ENSG00000104129	DNAJC17	15:41060066-41106767	OK	4.35349	3.59994	-0.274201	-0.215794	0.7052	0.9998
ENSG00000115841	ENSG00000115841	RMDN2	2:38150329-38408997	OK	2.35099	2.63001	0.161802	0.201964	0.70525	0.9998
ENSG00000170871	ENSG00000170871	KIAA0232	4:6783101-6885897	OK	6.66279	6.19555	-0.104893	-0.143263	0.7053	0.9998
ENSG00000224615	ENSG00000224615	RP11-34H11.1	9:46389109-46391556	OK	3.66098	2.11577	-0.791044	-0.422145	0.7053	0.9998
ENSG00000253293	ENSG00000253293	HOXA10	7:27202053-27219880	OK	4.71969	5.27269	0.159847	0.221723	0.70535	0.9998
ENSG00000176998	ENSG00000176998	HCG4	6:29758730-29765588	OK	2.23928	2.60354	0.217438	0.228637	0.70545	0.9998
ENSG00000170348	ENSG00000170348	TMED10	14:75548821-75643334	OK	278.176	249.454	-0.157221	-0.220279	0.7055	0.9998
ENSG00000145014	ENSG00000145014	TMEM44	3:194304739-194393206	OK	10.4884	8.47696	-0.307174	-0.247426	0.70565	0.9998
ENSG00000183773	ENSG00000183773	AIFM3	22:21319395-21353327	OK	0.698029	0.815506	0.224408	0.0548527	0.70565	0.9998
ENSG00000100281	ENSG00000100281	HMGXB4	22:35653444-35691800	OK	17.0699	15.7947	-0.112016	-0.210358	0.7057	0.9998
ENSG00000174912	ENSG00000174912	METTL15P1	3:156431672-156432717	OK	3.35263	2.95618	-0.18156	-0.229517	0.7057	0.9998
ENSG00000159267	ENSG00000159267	HLCS	21:38123188-38362536	OK	4.28265	3.82449	-0.163238	-0.187091	0.7058	0.9998
ENSG00000230269	ENSG00000230269	RP1-40E16.9	6:3182977-3195990	OK	0.792874	0.906744	0.193603	0.228362	0.70595	0.9998
ENSG00000107362	ENSG00000107362	ABHD17B	9:74477367-74525847	OK	10.1848	9.36644	-0.120842	-0.22989	0.70605	0.9998
ENSG00000150687	ENSG00000150687	PRSS23	11:86502100-86666433	OK	50.5679	55.5382	0.135256	0.229005	0.70605	0.9998
ENSG00000114670	ENSG00000114670	NEK11	3:130569438-131100319	OK	2.11452	2.50917	0.246884	0.0777267	0.70615	0.9998
ENSG00000142892	ENSG00000142892	PIGK	1:77554674-77685115	OK	26.4057	22.9852	-0.200143	-0.240008	0.70615	0.9998
ENSG00000176563	ENSG00000176563	CNTD1	17:40950809-40995774	OK	0.677894	0.493774	-0.457209	-0.0770012	0.70615	0.9998
ENSG00000116885	ENSG00000116885	OSCP1	1:36881427-36916086	OK	4.48392	4.97414	0.149687	0.192908	0.7062	0.9998
ENSG00000165490	ENSG00000165490	C11orf82	11:82534543-82782965	OK	4.40217	3.67303	-0.261246	-0.168529	0.7062	0.9998
ENSG00000172009	ENSG00000172009	THOP1	19:2785457-2813599	OK	33.5012	36.1112	0.108234	0.209959	0.7062	0.9998
ENSG00000112282	ENSG00000112282	MED23	6:131894283-131949369	OK	5.3939	5.82521	0.110983	0.198272	0.7063	0.9998
ENSG00000161526	ENSG00000161526	SAP30BP	17:73584138-73704142	OK	45.6244	41.2218	-0.146399	-0.232081	0.70635	0.9998
ENSG00000174136	ENSG00000174136	RGMB	5:98104353-98134347	OK	6.14078	5.63902	-0.122978	-0.208644	0.7064	0.9998
ENSG00000156650	ENSG00000156650	KAT6B	10:76585339-76792380	OK	2.48057	2.68786	0.115787	0.222898	0.70645	0.9998
ENSG00000186871	ENSG00000186871	ERCC6L	X:71401202-71527037	OK	5.65735	3.48181	-0.700291	-0.174889	0.70645	0.9998
ENSG00000141519	ENSG00000141519	CCDC40	17:78010434-78074412	OK	4.08702	3.60147	-0.182463	-0.203906	0.7066	0.9998
ENSG00000146094	ENSG00000146094	DOK3	5:176910394-176938275	OK	0.743356	0.894091	0.26637	0.0867345	0.7066	0.9998
ENSG00000156172	ENSG00000156172	C8orf37	8:96216683-96822364	OK	1.05932	0.953206	-0.152281	-0.22898	0.7067	0.9998
ENSG00000166200	ENSG00000166200	COPS2	15:49398267-49913128	OK	27.9068	30.3599	0.121549	0.222759	0.7067	0.9998
ENSG00000196418	ENSG00000196418	ZNF124	1:247285276-247335318	OK	1.5179	1.31986	-0.201691	-0.212439	0.70675	0.9998
ENSG00000107185	ENSG00000107185	RGP1	9:35696944-35758572	OK	16.2318	13.689	-0.245809	-0.155183	0.7068	0.9998
ENSG00000213123	ENSG00000213123	TCTEX1D2	3:195938357-196065374	OK	5.08746	3.04419	-0.740888	-0.236557	0.7068	0.9998
ENSG00000182810	ENSG00000182810	DDX28	16:68021296-68272005	OK	3.17855	3.70315	0.220383	0.231697	0.70685	0.9998
ENSG00000156219	ENSG00000156219	ART3	4:76932336-77033955	OK	0.687612	0.574768	-0.258614	-0.101629	0.7069	0.9998
ENSG00000054116	ENSG00000054116	TRAPPC3	1:36602172-36615098	OK	56.1461	59.985	0.0954153	0.218165	0.70695	0.9998
ENSG00000131381	ENSG00000131381	ZFYVE20	3:15111579-15140670	OK	13.5371	12.2704	-0.141743	-0.208581	0.70695	0.9998
ENSG00000135828	ENSG00000135828	RNASEL	1:182542768-182558391	OK	2.2802	2.48504	0.124105	0.229503	0.707	0.9998
ENSG00000144730	ENSG00000144730	IL17RD	3:57124009-57204334	OK	3.34371	3.62297	0.115723	0.151892	0.70705	0.9998
ENSG00000186141	ENSG00000186141	POLR3C	1:145592604-145611025	OK	34.1166	31.866	-0.098457	-0.222274	0.70705	0.9998
ENSG00000132256	ENSG00000132256	TRIM5	11:5684424-5959849	OK	6.06058	6.59122	0.12109	0.19889	0.70715	0.9998
ENSG00000177352	ENSG00000177352	CCDC71	3:49199967-49203754	OK	5.98663	5.49075	-0.124741	-0.227367	0.70715	0.9998
ENSG00000160613	ENSG00000160613	PCSK7	11:117070036-117103241	OK	10.7591	12.1023	0.169731	0.200743	0.7072	0.9998
ENSG00000177542	ENSG00000177542	SLC25A22	11:790474-798316	OK	13.4227	14.3746	0.0988513	0.163206	0.7072	0.9998
ENSG00000109536	ENSG00000109536	FRG1	4:190861942-190884359	OK	15.4184	16.7382	0.118495	0.216682	0.70745	0.9998
ENSG00000133265	ENSG00000133265	HSPBP1	19:55773598-55791749	OK	31.2237	33.4725	0.100334	0.215335	0.70745	0.9998
ENSG00000173611	ENSG00000173611	SCAI	9:127640645-127905785	OK	3.13124	2.56332	-0.288722	-0.157028	0.7076	0.9998
ENSG00000120054	ENSG00000120054	CPN1	10:101801949-101841634	OK	55.6921	51.4096	-0.115435	-0.228476	0.70765	0.9998
ENSG00000075213	ENSG00000075213	SEMA3A	7:83585092-84122040	OK	1.29655	1.51813	0.227613	0.159063	0.7077	0.9998
ENSG00000133393	ENSG00000133393	FOPNL	16:15959576-15982482	OK	23.087	21.2846	-0.117269	-0.206878	0.7077	0.9998
ENSG00000101367	ENSG00000101367	MAPRE1	20:31407698-31442063	OK	106.597	113.446	0.0898315	0.226773	0.70775	0.9998
ENSG00000135775	ENSG00000135775	COG2	1:230778234-230829728	OK	18.2854	17.0703	-0.0992084	-0.208783	0.70775	0.9998
ENSG00000162129	ENSG00000162129	CLPB	11:72003468-72145692	OK	17.1597	18.8836	0.138104	0.201784	0.7078	0.9998
ENSG00000133624	ENSG00000133624	ZNF767	7:149244244-149321843	OK	10.8318	9.65834	-0.165424	-0.201185	0.70785	0.9998
ENSG00000134824	ENSG00000134824	FADS2	11:61447904-61634826	OK	9.85416	8.17172	-0.270094	-0.130933	0.70785	0.9998
ENSG00000162849	ENSG00000162849	KIF26B	1:245318286-245872733	OK	0.891677	0.982615	0.140104	0.206902	0.70785	0.9998
ENSG00000160051	ENSG00000160051	IQCC	1:32665986-32674288	OK	3.4537	2.85982	-0.272216	-0.220009	0.7079	0.9998
ENSG00000169410	ENSG00000169410	PTPN9	15:75759461-75918810	OK	16.5813	15.3767	-0.108809	-0.163999	0.7079	0.9998
ENSG00000232637	ENSG00000232637	WI2-3658N16.1	1:146032646-146253110	OK	0.916042	1.14578	0.322844	0.201801	0.7079	0.9998
ENSG00000141013	ENSG00000141013	GAS8	16:90071272-90114181	OK	21.4525	23.9693	0.160042	0.160896	0.70795	0.9998
ENSG00000162929	ENSG00000162929	KIAA1841	2:61293005-61391964	OK	11.733	9.8721	-0.249147	-0.208797	0.70795	0.9998
ENSG00000224864	ENSG00000224864	CTC-260E6.2	19:20188802-20432114	OK	92.5145	99.7456	0.108573	0.230839	0.70795	0.9998
ENSG00000132305	ENSG00000132305	IMMT	2:86371054-86423172	OK	69.8157	65.5302	-0.0913923	-0.218949	0.7081	0.9998
ENSG00000119705	ENSG00000119705	SLIRP	14:78174413-78236085	OK	220.789	244.102	0.144812	0.22423	0.7082	0.9998
ENSG00000075151	ENSG00000075151	EIF4G3	1:21132962-21503377	OK	24.4765	22.9341	-0.0938991	-0.179486	0.70825	0.9998
ENSG00000258634	ENSG00000258634	RP4-773N10.4	1:110574198-110617263	OK	2.60315	2.24433	-0.213973	-0.166494	0.70825	0.9998
ENSG00000149823	ENSG00000149823	VPS51	11:64851694-64883856	OK	57.6569	63.4371	0.137834	0.201324	0.7083	0.9998
ENSG00000261094	ENSG00000261094	RP11-355O1.11	9:125699901-125702612	OK	1.35432	1.17449	-0.205538	-0.230106	0.70835	0.9998
ENSG00000074582	ENSG00000074582	BCS1L	2:219502638-219528166	OK	24.9874	27.5673	0.14176	0.21225	0.70845	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000138193	ENSG00000138193	PLCE1	10:95753745-96122716	OK	0.79127	0.930968	0.234563	0.171984	0.70845	0.9998
ENSG00000142599	ENSG00000142599	RERE	1:8412456-8877702	OK	14.1506	15.3821	0.120388	0.0949535	0.70845	0.9998
ENSG00000066923	ENSG00000066923	STAG3	7:99775185-99869855	OK	3.5596	3.96905	0.157081	0.159241	0.7085	0.9998
ENSG00000166920	ENSG00000166920	C15orf48	15:45722726-45878488	OK	0.735768	0.502289	-0.550733	-0.200582	0.7085	0.9998
ENSG00000178913	ENSG00000178913	TAF7	5:140698056-140700339	OK	20.5151	21.9824	0.0996619	0.228878	0.7086	0.9998
ENSG00000259985	ENSG00000259985	RP11-549B18.1	18:29202209-29266786	OK	1.28448	1.90657	0.569802	0.252452	0.70865	0.9998
ENSG00000175110	ENSG00000175110	MRPS22	3:138722803-139108574	OK	37.0168	43.8231	0.243508	0.218838	0.7087	0.9998
ENSG00000083290	ENSG00000083290	ULK2	17:19674141-19771249	OK	9.46352	10.2295	0.112286	0.156298	0.70895	0.9998
ENSG00000140939	ENSG00000140939	NOL3	16:67204056-67217943	OK	15.1163	13.5834	-0.154262	-0.208361	0.70895	0.9998
ENSG00000198056	ENSG00000198056	PRIM1	12:57106211-57181574	OK	26.3505	19.8083	-0.41172	-0.227475	0.709	0.9998
ENSG00000141141	ENSG00000141141	DDX52	17:35969786-36044255	OK	9.80867	9.04303	-0.117251	-0.209971	0.70905	0.9998
ENSG00000122335	ENSG00000122335	SERAC1	6:158530535-158589312	OK	2.13008	1.93412	-0.139231	-0.189171	0.7091	0.9998
ENSG00000124839	ENSG00000124839	RAB17	2:238482964-238510257	OK	61.2698	66.112	0.109736	0.22132	0.7091	0.9998
ENSG00000131931	ENSG00000131931	THAP1	8:42691816-42698468	OK	5.91031	6.41504	0.118225	0.210215	0.70915	0.9998
ENSG00000182004	ENSG00000182004	SNRPE	1:203830730-203839678	OK	145.123	157.813	0.120934	0.219762	0.7092	0.9998
ENSG00000111666	ENSG00000111666	CHPT1	12:102090724-102137918	OK	73.8332	69.1191	-0.0951839	-0.232165	0.70925	0.9998
ENSG00000116337	ENSG00000116337	AMPD2	1:110158725-110174673	OK	19.9291	21.3178	0.0971817	0.156513	0.70925	0.9998
ENSG00000269897	ENSG00000269897	COMMD3-BMI1	10:22604902-22620413	OK	24.0242	19.6377	-0.290864	-0.226719	0.70925	0.9998
ENSG00000013392	ENSG00000013392	RWDD2A	6:83777384-83908651	OK	2.29606	1.75783	-0.385366	-0.268421	0.7093	0.9998
ENSG00000066427	ENSG00000066427	ATXN3	14:92524895-92572965	OK	15.9937	14.2533	-0.166209	-0.206252	0.7093	0.9998
ENSG00000160298	ENSG00000160298	C21orf58	21:47720094-47743789	OK	1.91077	1.69654	-0.171564	-0.226238	0.7093	0.9998
ENSG00000114631	ENSG00000114631	PODXL2	3:127348023-127391652	OK	50.0207	53.338	0.0926388	0.229151	0.70935	0.9998
ENSG00000136478	ENSG00000136478	TEX2	17:62224586-62340661	OK	27.6314	25.9669	-0.089638	-0.217955	0.7095	0.9998
ENSG00000103222	ENSG00000103222	ABCC1	16:16043433-16236931	OK	12.5315	13.4782	0.105076	0.19279	0.70955	0.9998
ENSG00000253982	ENSG00000253982	CTD-2336O2.1	8:1703943-1734738	OK	24.8211	20.558	-0.27187	-0.240398	0.70985	0.9998
ENSG00000110888	ENSG00000110888	CAPRIN2	12:30862485-30907885	OK	12.737	11.8165	-0.108221	-0.169725	0.70995	0.9998
ENSG00000162526	ENSG00000162526	TSSK3	1:32817121-32829913	OK	0.81392	1.06425	0.386883	0.171641	0.70995	0.9998
ENSG00000105321	ENSG00000105321	CCDC9	19:47759236-47775210	OK	10.9386	9.74792	-0.166261	-0.202982	0.71015	0.9998
ENSG00000229156	ENSG00000229156	RP11-250H24.2	9:69475236-69475614	OK	1.03096	0.78068	-0.401183	-0.270638	0.7102	0.9998
ENSG00000158156	ENSG00000158156	XKR8	1:28261503-28294607	OK	0.780841	0.63948	-0.288129	-0.153542	0.71025	0.9998
ENSG00000129925	ENSG00000129925	TMEM8A	16:420772-442960	OK	116.688	106.315	-0.134309	-0.223058	0.7103	0.9998
ENSG00000126391	ENSG00000126391	FRMD8	11:65154069-65180996	OK	12.4211	13.3717	0.106397	0.174745	0.71035	0.9998
ENSG00000173039	ENSG00000173039	RELA	11:65421066-65430565	OK	36.5474	38.8863	0.0894933	0.168638	0.71035	0.9998
ENSG00000231684	ENSG00000231684	RP11-416K24.2	1:182305135-182305475	OK	1.60102	1.93038	0.269896	0.200146	0.71035	0.9998
ENSG00000113387	ENSG00000113387	SUB1	5:32531738-32604185	OK	279.309	305.003	0.126962	0.229145	0.7105	0.9998
ENSG00000139697	ENSG00000139697	SBNO1	12:123773655-123850660	OK	10.9136	11.6918	0.0993663	0.225098	0.71055	0.9998
ENSG00000167770	ENSG00000167770	OTUB1	11:63742078-63933578	OK	61.1427	69.1248	0.177023	0.218437	0.7106	0.9998
ENSG00000235954	ENSG00000235954	TTC28-AS1	22:28247656-29075853	OK	7.97637	6.4188	-0.313428	-0.15526	0.71065	0.9998
ENSG00000248445	ENSG00000248445	CTB-118N6.3	5:115779311-115927094	OK	4.39232	5.87875	0.420527	0.109995	0.7107	0.9998
ENSG00000271643	ENSG00000271643	RP11-10C24.3	3:33837179-33838442	OK	0.654235	0.561998	-0.219244	-0.225336	0.7107	0.9998
ENSG00000105778	ENSG00000105778	AVL9	7:32535037-33102409	OK	29.2468	25.211	-0.214224	-0.117058	0.7108	0.9998
ENSG00000144959	ENSG00000144959	NCEH1	3:172348038-172429008	OK	13.9485	13.0151	-0.0999212	-0.191636	0.7108	0.9998
ENSG00000144589	ENSG00000144589	STK11IP	2:220462581-220481173	OK	15.0395	13.8743	-0.116342	-0.165056	0.7109	0.9998
ENSG00000109113	ENSG00000109113	RAB34	17:27041298-27045447	OK	50.7475	47.329	-0.100612	-0.221439	0.71095	0.9998
ENSG00000215769	ENSG00000215769	hsa-mir-6080	17:62745780-62833272	OK	1.13967	0.91376	-0.318724	-0.216678	0.711	0.9998
ENSG00000106100	ENSG00000106100	NOD1	7:30464142-30518400	OK	4.18229	4.67923	0.161976	0.215567	0.71105	0.9998
ENSG00000272442	ENSG00000272442	RP11-444E17.6	6:44238202-44346694	OK	0.378199	0.780395	1.04506	0.345013	0.71105	0.9998
ENSG00000204650	ENSG00000204650	CRHR1-IT1	17:43697693-43913194	OK	26.9256	24.4878	-0.136913	-0.222188	0.7111	0.9998
ENSG00000152782	ENSG00000152782	PANK1	10:91342744-91410579	OK	5.18286	4.53717	-0.191956	-0.213058	0.71115	0.9998
ENSG00000235919	ENSG00000235919	ASH1L-AS1	1:155305058-155533775	OK	1.403	1.95404	0.477942	0.120707	0.71115	0.9998
ENSG00000246922	ENSG00000246922	UBAP1L	15:65385337-65407535	OK	4.42449	4.93089	0.156339	0.211213	0.71115	0.9998
ENSG00000108587	ENSG00000108587	GOSR1	17:28804379-28854610	OK	12.1614	10.944	-0.152175	-0.21383	0.7112	0.9998
ENSG00000144566	ENSG00000144566	RAB5A	3:19988570-20053822	OK	31.5168	33.9829	0.108691	0.221382	0.71135	0.9998
ENSG00000052749	ENSG00000052749	RRP12	10:99116114-99185831	OK	9.43459	10.0902	0.096926	0.19739	0.71145	0.9998
ENSG00000204178	ENSG00000204178	TMEM57	1:25757387-25826700	OK	4.71203	4.35783	-0.112736	-0.197045	0.71155	0.9998
ENSG00000196199	ENSG00000196199	MPHOSPH8	13:20207787-20247599	OK	15.5338	14.2995	-0.119444	-0.190631	0.7116	0.9998
ENSG00000138032	ENSG00000138032	PPM1B	2:44394763-44471523	OK	22.1536	20.5283	-0.10993	-0.208792	0.71165	0.9998
ENSG00000169047	ENSG00000169047	IRS1	2:227596032-227664475	OK	4.2564	3.90226	-0.125322	-0.13621	0.7117	0.9998
ENSG00000178694	ENSG00000178694	NSUN3	3:93698982-93847389	OK	5.47335	4.77411	-0.197191	-0.136297	0.7117	0.9998
ENSG00000185437	ENSG00000185437	SH3BGR	21:40817780-40887433	OK	0.99149	0.84967	-0.222695	-0.15732	0.7117	0.9998
ENSG00000142082	ENSG00000142082	SIRT3	11:215457-252983	OK	14.3789	12.3354	-0.221146	-0.157056	0.71175	0.9998
ENSG00000182372	ENSG00000182372	CLN8	8:1703943-1734738	OK	13.2917	15.3656	0.209181	0.236177	0.71175	0.9998
ENSG00000225912	ENSG00000225912	RP13-258O15.1	X:91931517-91931953	OK	1.74527	1.47023	-0.247406	-0.216905	0.71175	0.9998
ENSG00000130713	ENSG00000130713	EXOSC2	9:133569107-133580248	OK	25.7551	23.7359	-0.117784	-0.220842	0.7118	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000253676	ENSG00000253676	TAGLN2P1	8:107282371-107764922	OK	1.45701	2.70518	0.892711	0.240629	0.7118	0.9998
ENSG00000198453	ENSG00000198453	ZNF568	19:37407230-37489602	OK	2.46327	2.24021	-0.136941	-0.196927	0.7119	0.9998
ENSG00000174473	ENSG00000174473	GALNTL6	4:172733404-173962710	OK	1.09985	0.953774	-0.205593	-0.230296	0.71195	0.9998
ENSG00000123575	ENSG00000123575	FAM199X	X:103411300-103440583	OK	12.0971	13.1138	0.116419	0.226205	0.712	0.9998
ENSG00000198162	ENSG00000198162	MAN1A2	1:117910070-118071494	OK	7.80419	8.45217	0.115073	0.151159	0.71205	0.9998
ENSG00000166575	ENSG00000166575	TMEM135	11:86748885-87035401	OK	15.5577	17.0564	0.132691	0.108434	0.71215	0.9998
ENSG00000160326	ENSG00000160326	SLC2A6	9:136336216-136344259	OK	9.48535	8.78911	-0.109984	-0.215329	0.7122	0.9998
ENSG00000172922	ENSG00000172922	RNASEH2C	11:65479466-65488418	OK	40.802	45.8746	0.169057	0.235658	0.7122	0.9998
ENSG00000172159	ENSG00000172159	FRMD3	9:85857904-86153461	OK	11.8892	13.3207	0.164013	0.223892	0.71235	0.9998
ENSG00000150347	ENSG00000150347	ARID5B	10:63661058-63856703	OK	8.49146	9.11339	0.101976	0.215501	0.7124	0.9998
ENSG00000183655	ENSG00000183655	KLHL25	15:86302553-86338261	OK	1.5276	1.68896	0.144867	0.193592	0.7125	0.9998
ENSG00000108958	ENSG00000108958	AC016292.3	17:1682778-1803376	OK	1.71085	1.13767	-0.588634	-0.0675557	0.71255	0.9998
ENSG00000257718	ENSG00000257718	RP11-396F22.1	12:39040623-39303394	OK	0.681881	1.26696	0.893782	0.218049	0.7126	0.9998
ENSG00000106603	ENSG00000106603	COA1	7:43622356-43769316	OK	66.0227	72.5547	0.136107	0.230513	0.71265	0.9998
ENSG00000119801	ENSG00000119801	YPEL5	2:30369806-30383399	OK	42.8179	39.7744	-0.106375	-0.220581	0.71265	0.9998
ENSG00000137710	ENSG00000137710	RDX	11:110045604-110167447	OK	52.4048	48.26	-0.118872	-0.217716	0.7127	0.9998
ENSG00000141905	ENSG00000141905	NFIC	19:3359560-3469215	OK	14.7507	13.3216	-0.147008	-0.210596	0.71285	0.9998
ENSG00000103942	ENSG00000103942	HOMER2	15:83509837-83772195	OK	3.80772	5.10932	0.424204	0.166477	0.7129	0.9998
ENSG00000185950	ENSG00000185950	IRS2	13:110406183-110438915	OK	15.5547	16.5822	0.0922853	0.223458	0.7129	0.9998
ENSG00000165934	ENSG00000165934	CPSF2	14:92588280-92630755	OK	28.1045	30.9035	0.136965	0.207954	0.713	0.9998
ENSG00000142149	ENSG00000142149	HUNK	21:33245627-33416946	OK	0.614824	0.711147	0.209974	0.126116	0.71305	0.9998
ENSG00000184117	ENSG00000184117	NIPSNAP1	22:29901867-29977326	OK	26.4342	29.0834	0.137788	0.2061	0.71315	0.9998
ENSG00000111725	ENSG00000111725	PRKAB1	12:119772516-120119435	OK	8.56746	7.86698	-0.123058	-0.188866	0.71325	0.9998
ENSG00000039068	ENSG00000039068	CDH1	16:68771127-68869451	OK	2.10205	1.88262	-0.159058	-0.143433	0.7134	0.9998
ENSG00000088888	ENSG00000088888	MAVS	20:3827486-3849280	OK	6.66718	6.18211	-0.108977	-0.217829	0.7134	0.9998
ENSG00000177990	ENSG00000177990	DPY19L2	12:63952692-64217675	OK	4.50676	5.36518	0.251537	0.169187	0.7135	0.9998
ENSG00000154518	ENSG00000154518	ATP5G3	2:176040985-176049335	OK	452.816	483.483	0.0945426	0.228585	0.71355	0.9998
ENSG00000224043	ENSG00000224043	CCNT2-AS1	2:135493033-135716912	OK	1.68495	1.16192	-0.536186	-0.19375	0.7137	0.9998
ENSG00000146067	ENSG00000146067	FAM193B	5:176946788-176981542	OK	23.6649	26.2218	0.14802	0.192643	0.7138	0.9998
ENSG00000183196	ENSG00000183196	CHST6	16:75509793-75529305	OK	2.68916	2.44665	-0.136347	-0.224348	0.714	0.9998
ENSG00000104695	ENSG00000104695	PPP2CB	8:30631972-30671830	OK	32.015	34.1876	0.0947257	0.203679	0.71415	0.9998
ENSG00000221819	ENSG00000221819	C16orf3	16:90071272-90114181	OK	0.761629	0.451621	-0.753976	-0.13652	0.7143	0.9998
ENSG00000103363	ENSG00000103363	TCEB2	16:2787076-2827298	OK	297.893	346.832	0.219441	0.210464	0.71435	0.9998
ENSG00000125835	ENSG00000125835	SNRPB	20:2442279-2505348	OK	93.5035	87.4412	-0.0967081	-0.226791	0.71445	0.9998
ENSG00000163389	ENSG00000163389	POGLUT1	3:119187784-119213555	OK	7.60789	6.90795	-0.139237	-0.194784	0.71445	0.9998
ENSG00000271738	ENSG00000271738	RP11-137H2.6	10:82194764-82196869	OK	2.10439	1.90591	-0.142922	-0.220917	0.71455	0.9998
ENSG00000062822	ENSG00000062822	POLD1	19:50887460-50934570	OK	19.6363	17.968	-0.128096	-0.201279	0.71465	0.9998
ENSG00000213024	ENSG00000213024	NUP62	19:50392910-50464429	OK	31.8407	29.7049	-0.100173	-0.189031	0.7147	0.9998
ENSG00000268403	ENSG00000268403	AC132192.1	11:9481746-9550071	OK	2.59436	1.51851	-0.772716	-0.149098	0.71475	0.9998
ENSG00000112473	ENSG00000112473	SLC39A7	6:33161364-33172216	OK	96.1602	103.046	0.0997696	0.219959	0.7148	0.9998
ENSG00000142186	ENSG00000142186	SCYL1	11:65292547-65306175	OK	33.0937	35.2377	0.0905635	0.201757	0.7148	0.9998
ENSG00000166192	ENSG00000166192	SENP8	15:72110736-72447800	OK	1.1306	0.780232	-0.535108	-0.199615	0.7149	0.9998
ENSG00000166173	ENSG00000166173	LARP6	15:71123862-71342414	OK	13.9849	12.3315	-0.181527	-0.215559	0.71505	0.9998
ENSG00000223804	ENSG00000223804	RP6-206I17.1	1:143647637-143745417	OK	2.56185	3.18285	0.313135	0.227065	0.71505	0.9998
ENSG00000070047	ENSG00000070047	PHRF1	11:576485-612222	OK	8.22326	7.67007	-0.100472	-0.229496	0.71515	0.9998
ENSG00000111596	ENSG00000111596	CNOT2	12:70132460-70748773	OK	29.961	32.2063	0.104256	0.152832	0.7153	0.9998
ENSG00000267165	ENSG00000267165	RP11-78A19.3	18:11688954-11909222	OK	15.6555	11.4426	-0.452256	-0.236156	0.71535	0.9998
ENSG00000102871	ENSG00000102871	TRADD	16:67188082-67203848	OK	8.21683	7.32971	-0.164825	-0.201894	0.7154	0.9998
ENSG00000249572	ENSG00000249572	CTD-2203K17.1	5:33424130-33440725	OK	0.736384	0.593504	-0.311199	-0.243089	0.7154	0.9998
ENSG00000185222	ENSG00000185222	WBP5	X:102611372-102613397	OK	57.4886	53.8427	-0.0945264	-0.22069	0.7156	0.9998
ENSG00000004779	ENSG00000004779	NDUFAB1	16:23592322-23607677	OK	152.863	162.854	0.0913469	0.223126	0.7157	0.9998
ENSG00000029364	ENSG00000029364	SLC39A9	14:69846847-69929105	OK	29.9024	27.3533	-0.128546	-0.18828	0.71585	0.9998
ENSG00000161395	ENSG00000161395	PGAP3	17:37827374-37887040	OK	2.69793	2.15134	-0.326617	-0.187942	0.716	0.9998
ENSG00000063176	ENSG00000063176	SPHK2	19:49118584-49140695	OK	9.20381	7.53367	-0.288878	-0.0923509	0.71605	0.9998
ENSG00000166046	ENSG00000166046	TCP11L2	12:106631654-106740793	OK	4.3384	3.33101	-0.381203	-0.167605	0.71615	0.9998
ENSG00000116273	ENSG00000116273	PHF13	1:6650783-6684093	OK	7.94656	6.94705	-0.19393	-0.200752	0.7162	0.9998
ENSG00000154359	ENSG00000154359	LONRF1	8:12579402-12613582	OK	103.931	111.245	0.0981087	0.201031	0.7162	0.9998
ENSG00000223797	ENSG00000223797	ENTPD3-AS1	3:40355292-40494820	OK	5.65112	5.11083	-0.144979	-0.214961	0.71625	0.9998
ENSG00000241458	ENSG00000241458	RPL7P19	5:137809432-137810050	OK	4.18049	3.70204	-0.175352	-0.228528	0.7163	0.9998
ENSG00000167447	ENSG00000167447	SMG8	17:57232859-57292608	OK	16.1256	17.995	0.158246	0.212195	0.71635	0.9998
ENSG00000165169	ENSG00000165169	DYNLT3	X:37208527-38548169	OK	29.9864	26.2934	-0.189607	-0.225136	0.7164	0.9998
ENSG00000184254	ENSG00000184254	ALDH1A3	15:101389765-101626271	OK	34.8143	37.393	0.103088	0.180214	0.7164	0.9998
ENSG00000272688	ENSG00000272688	RP13-270P17.3	18:3066804-3247275	OK	0.972926	0.718651	-0.43704	-0.219021	0.7164	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000242445	ENSG00000242445	RPL7AP11	3:121150277-121264853	OK	7.36309	9.06544	0.300065	0.226303	0.71645	0.9998
ENSG00000049246	ENSG00000049246	PER3	1:7844379-7913572	OK	6.4639	7.09516	0.13443	0.165053	0.7165	0.9998
ENSG00000138085	ENSG00000138085	ATRAID	2:27422454-27440046	OK	101.168	91.6574	-0.142428	-0.221394	0.71655	0.9998
ENSG00000140470	ENSG00000140470	ADAMTS17	15:100510419-100882210	OK	6.99634	5.96994	-0.228886	-0.21729	0.71655	0.9998
ENSG00000273420	ENSG00000273420	CTD-2540B15.13	19:33668508-33698694	OK	2.46017	1.23681	-0.992133	-0.335783	0.71655	0.9998
ENSG00000086065	ENSG00000086065	CHMP5	9:33264939-33281977	OK	73.3309	77.8887	0.0869928	0.215512	0.7166	0.9998
ENSG00000111445	ENSG00000111445	RFC5	12:118451392-118500235	OK	22.539	17.9344	-0.329693	-0.24971	0.7166	0.9998
ENSG00000109332	ENSG00000109332	UBE2D3	4:103715539-103790053	OK	149.325	160.369	0.102945	0.200521	0.7167	0.9998
ENSG00000170037	ENSG00000170037	CNTROB	17:7825176-7853236	OK	18.4775	16.4059	-0.171553	-0.182236	0.7167	0.9998
ENSG00000104964	ENSG00000104964	AES	19:3052907-3063105	OK	167.627	181.031	0.11099	0.175812	0.71675	0.9998
ENSG00000132002	ENSG00000132002	DNAJB1	19:14625581-14676792	OK	79.8499	86.0437	0.107778	0.213472	0.7168	0.9998
ENSG00000101846	ENSG00000101846	STS	X:7137496-7272851	OK	4.68036	5.01159	0.0986512	0.219668	0.71685	0.9998
ENSG00000259897	ENSG00000259897	RP11-244B22.3	16:34442273-34518517	OK	1.0031	0.457412	-1.13289	-0.372298	0.7169	0.9998
ENSG00000074935	ENSG00000074935	TUBE1	6:112375274-112408732	OK	4.69271	4.18856	-0.163965	-0.215474	0.717	0.9998
ENSG00000164182	ENSG00000164182	NDUFAF2	5:60240955-60448853	OK	78.4643	84.0132	0.0985797	0.219508	0.71705	0.9998
ENSG00000172167	ENSG00000172167	MTBP	8:121392999-121825599	OK	5.1002	4.37123	-0.222515	-0.152302	0.71705	0.9998
ENSG00000211451	ENSG00000211451	GNRHR2	1:145475981-145516076	OK	1.21497	0.919879	-0.401403	-0.069174	0.71705	0.9998
ENSG00000176842	ENSG00000176842	IRX5	16:54964773-54968397	OK	0.630731	0.715099	0.181118	0.207024	0.7171	0.9998
ENSG00000234327	ENSG00000234327	AC012146.7	17:5008835-5078329	OK	2.2887	3.0993	0.437416	0.222595	0.7172	0.9998
ENSG00000127419	ENSG00000127419	TMEM175	4:926174-952444	OK	12.6008	11.4844	-0.133833	-0.166233	0.7173	0.9998
ENSG00000176386	ENSG00000176386	CDC26	9:115983807-116055185	OK	12.6368	9.7246	-0.377926	-0.207781	0.7173	0.9998
ENSG00000115677	ENSG00000115677	HDLBP	2:242166678-242293442	OK	199.816	184.978	-0.111324	-0.134472	0.71735	0.9998
ENSG00000125037	ENSG00000125037	EMC3	3:10000400-10052893	OK	99.3732	91.0394	-0.126366	-0.225688	0.71735	0.9998
ENSG00000145901	ENSG00000145901	TNIP1	5:150409505-150473138	OK	34.5314	32.4227	-0.0909055	-0.208906	0.71735	0.9998
ENSG00000049167	ENSG00000049167	ERCC8	5:60169657-60240900	OK	9.00187	8.24469	-0.126761	-0.216373	0.71745	0.9998
ENSG00000162664	ENSG00000162664	ZNF326	1:90460670-90501090	OK	19.1422	17.7297	-0.110592	-0.218235	0.7175	0.9998
ENSG00000160190	ENSG00000160190	SLC37A1	21:43892595-44001550	OK	1.82407	2.01584	0.144214	0.154828	0.71755	0.9998
ENSG00000255769	ENSG00000255769	RP11-152F13.3	15:82751613-82798350	OK	1.13359	0.980771	-0.208914	-0.188905	0.71755	0.9998
ENSG00000166762	ENSG00000166762	CATSPER2	15:43885251-44010458	OK	1.01444	0.832114	-0.285837	-0.135016	0.7176	0.9998
ENSG00000198561	ENSG00000198561	CTNND1	11:57480071-57587018	OK	55.535	50.7944	-0.128728	-0.200559	0.71765	0.9998
ENSG00000269975	ENSG00000269975	RP11-58B17.2	3:9540044-9541253	OK	2.35798	2.62325	0.153805	0.221393	0.71775	0.9998
ENSG00000272087	ENSG00000272087	RP11-379F4.7	3:158410908-158411557	OK	1.33528	1.14525	-0.221481	-0.222654	0.71775	0.9998
ENSG00000272993	ENSG00000272993	RP11-196G18.24	1:149816064-149820591	OK	2.37799	1.70825	-0.477219	-0.249493	0.7178	0.9998
ENSG00000254690	ENSG00000254690	GS1-393G12.12	8:145515279-145538801	OK	0.43045	0.763407	0.826607	0.102013	0.7179	0.9998
ENSG00000268087	ENSG00000268087	CTC-429P9.2	19:16589867-16771253	OK	0.84589	0.493837	-0.776434	-0.0605769	0.718	0.9998
ENSG00000005801	ENSG00000005801	ZNF195	11:3357950-3400448	OK	11.6066	10.5409	-0.138949	-0.188141	0.71805	0.9998
ENSG00000135862	ENSG00000135862	LAMC1	1:182992594-183114727	OK	124.889	113.012	-0.144167	-0.173602	0.71805	0.9998
ENSG00000183718	ENSG00000183718	TRIM52	5:180663908-180699308	OK	5.69246	4.49464	-0.340847	-0.0561987	0.71805	0.9998
ENSG00000166595	ENSG00000166595	FAM96B	16:66965958-66968326	OK	63.7014	59.5075	-0.098254	-0.219065	0.71815	0.9998
ENSG00000086589	ENSG00000086589	RBM22	5:150070355-150080669	OK	17.7165	16.5382	-0.0992949	-0.210756	0.7182	0.9998
ENSG00000204519	ENSG00000204519	ZNF551	19:58193336-58269527	OK	1.67896	1.97426	0.233746	0.152992	0.7182	0.9998
ENSG00000160993	ENSG00000160993	ALKBH4	7:102067264-102105323	OK	7.89784	9.18291	0.217492	0.205946	0.71825	0.9998
ENSG00000182646	ENSG00000182646	FAM156A	X:52976461-53024651	OK	0.891245	0.785235	-0.182698	-0.131921	0.71825	0.9998
ENSG00000198496	ENSG00000198496	NBR2	17:41277626-41305688	OK	1.53554	1.28931	-0.252148	-0.149762	0.71825	0.9998
ENSG00000268565	ENSG00000268565	AC005339.2	19:4639529-4670382	OK	0.834428	0.4561	-0.871438	-0.0560037	0.71825	0.9998
ENSG00000160294	ENSG00000160294	MCM3AP	21:47649130-47706211	OK	18.5202	16.6491	-0.153655	-0.104485	0.71835	0.9998
ENSG00000231181	ENSG00000231181	RP13-15M17.1	1:9599540-9645237	OK	0.486534	0.911843	0.906245	0.217941	0.71835	0.9998
ENSG00000198856	ENSG00000198856	OSTC	4:109571739-109588976	OK	111.022	104.436	-0.0882309	-0.217057	0.71875	0.9998
ENSG00000156171	ENSG00000156171	DRAM2	1:111659954-111727724	OK	46.1615	41.3506	-0.158784	-0.211801	0.7188	0.9998
ENSG00000140400	ENSG00000140400	MAN2C1	15:75648132-75748183	OK	35.206	39.148	0.153117	0.175	0.71895	0.9998
ENSG00000104228	ENSG00000104228	TRIM35	8:27142403-27168836	OK	6.71897	7.43481	0.146054	0.166531	0.719	0.9998
ENSG00000161618	ENSG00000161618	ALDH16A1	19:49949554-49995565	OK	5.2956	6.63165	0.324574	0.0742541	0.719	0.9998
ENSG00000251201	ENSG00000251201	TMED7-TICAM2	5:114914338-114968689	OK	2.54514	2.12877	-0.257724	-0.19469	0.719	0.9998
ENSG00000167799	ENSG00000167799	NUDT8	11:67395408-67397401	OK	7.82534	7.0608	-0.148322	-0.230423	0.7191	0.9998
ENSG00000115216	ENSG00000115216	NRBP1	2:27650656-27665126	OK	46.2784	49.1763	0.0876241	0.20732	0.7192	0.9998
ENSG00000162627	ENSG00000162627	SNX7	1:99127235-99226056	OK	15.6696	16.8358	0.103563	0.2209	0.71925	0.9998
ENSG00000236015	ENSG00000236015	AC011290.5	7:39605974-39649919	OK	1.28664	1.86358	0.534472	0.256964	0.71925	0.9998
ENSG00000077157	ENSG00000077157	PPP1R12B	1:202317826-202679545	OK	5.4407	6.43585	0.242337	0.0661483	0.71935	0.9998
ENSG00000166450	ENSG00000166450	PRTG	15:55903743-56035288	OK	3.26435	3.97082	0.282641	0.224747	0.71935	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000186166	ENSG00000186166	CCDC84	11:118868851-118901616	OK	4.97208	4.13235	-0.266887	-0.0719303	0.71945	0.9998
ENSG00000205981	ENSG00000205981	DNAJC19	3:180701496-181554668	OK	48.2686	52.1055	0.110351	0.221849	0.71955	0.9998
ENSG00000172757	ENSG00000172757	CFL1	11:65590492-65641063	OK	974.403	1048.47	0.105691	0.219593	0.71965	0.9998
ENSG00000140043	ENSG00000140043	PTGR2	14:74318546-74551196	OK	4.72109	3.68563	-0.357208	-0.183091	0.71975	0.9998
ENSG00000271741	ENSG00000271741	RP11-244H3.4	1:35439956-35497569	OK	0.690325	0.914189	0.405215	0.227533	0.71975	0.9998
ENSG00000167625	ENSG00000167625	ZNF526	19:42724422-42732353	OK	3.99758	4.31188	0.109188	0.210285	0.7198	0.9998
ENSG00000082512	ENSG00000082512	TRAF5	1:211499956-211548288	OK	11.8238	12.7146	0.1048	0.205777	0.71995	0.9998
ENSG00000173692	ENSG00000173692	PSMD1	2:231921577-232037541	OK	47.0202	44.3528	-0.0842547	-0.197483	0.72	0.9998
ENSG00000130935	ENSG00000130935	NOL11	17:65713948-65740647	OK	31.0115	33.0296	0.0909534	0.198558	0.72005	0.9998
ENSG00000161267	ENSG00000161267	BDH1	3:197236653-197300194	OK	25.3036	23.0959	-0.13171	-0.225552	0.7201	0.9998
ENSG00000184674	ENSG00000184674	GSTT1	22:24375561-24384680	OK	20.6243	22.238	0.10868	0.176317	0.7202	0.9998
ENSG00000100354	ENSG00000100354	TNRC6B	22:40440820-40731812	OK	4.73852	5.22578	0.14121	0.152911	0.72025	0.9998
ENSG00000147687	ENSG00000147687	TATDN1	8:125500725-125740730	OK	21.5595	17.6409	-0.289396	-0.165788	0.7203	0.9998
ENSG00000131591	ENSG00000131591	C1orf159	1:1017197-1051741	OK	5.23543	4.82961	-0.116399	-0.17411	0.72035	0.9998
ENSG00000204217	ENSG00000204217	BMPR2	2:203241658-203432474	OK	17.0143	18.0849	0.0880387	0.148495	0.72035	0.9998
ENSG00000224790	ENSG00000224790	AP000704.5	21:38123188-38362536	OK	0.375719	0.692937	0.883072	0.155311	0.72035	0.9998
ENSG00000255624	ENSG00000255624	RP11-564D11.3	10:124639245-124658230	OK	0.784613	0.89599	0.1915	0.190723	0.72045	0.9998
ENSG00000112234	ENSG00000112234	FBXL4	6:99316419-99395849	OK	7.11006	7.68946	0.113021	0.218595	0.7205	0.9998
ENSG00000163344	ENSG00000163344	PMVK	1:154897209-154909467	OK	43.4726	40.7815	-0.0921897	-0.21493	0.72055	0.9998
ENSG00000204444	ENSG00000204444	APOM	6:31606804-31625987	OK	1.0191	0.750904	-0.44059	-0.0462265	0.72055	0.9998
ENSG00000140396	ENSG00000140396	NCOA2	8:71021996-71316040	OK	10.0409	10.8399	0.110464	0.14868	0.72065	0.9998
ENSG00000198546	ENSG00000198546	ZNF511	10:135093134-135166187	OK	23.7052	27.8951	0.234805	0.220607	0.72065	0.9998
ENSG00000131778	ENSG00000131778	CHD1L	1:146644349-146767443	OK	57.5587	53.9182	-0.094262	-0.202738	0.7207	0.9998
ENSG00000174780	ENSG00000174780	SRP72	4:57333080-57369839	OK	55.1484	59.3569	0.106096	0.2119	0.72075	0.9998
ENSG00000225830	ENSG00000225830	ERCC6	10:50627322-50747584	OK	3.49313	3.88073	0.151807	0.125941	0.7208	0.9998
ENSG00000137767	ENSG00000137767	SQRDL	15:45879320-45983492	OK	2.80846	2.15279	-0.383571	-0.183843	0.72085	0.9998
ENSG00000152700	ENSG00000152700	SAR1B	5:133936833-134063513	OK	27.3082	30.4847	0.158751	0.206838	0.72085	0.9998
ENSG00000153214	ENSG00000153214	TMEM87B	2:112812799-112876895	OK	8.0098	7.40761	-0.112758	-0.15267	0.72085	0.9998
ENSG00000197774	ENSG00000197774	EME2	16:1823207-1844972	OK	3.77305	4.35441	0.206744	0.122709	0.7209	0.9998
ENSG00000164830	ENSG00000164830	OXR1	8:107282371-107764922	OK	16.6306	15.4106	-0.10992	-0.201242	0.721	0.9998
ENSG00000092203	ENSG00000092203	TOX4	14:21927178-21979517	OK	33.6424	36.8481	0.131309	0.202023	0.72105	0.9998
ENSG00000166987	ENSG00000166987	MBD6	12:57914492-57941114	OK	8.61818	9.93384	0.204968	0.129522	0.72115	0.9998
ENSG00000083099	ENSG00000083099	LYRM2	6:90142888-90348472	OK	18.6245	16.0984	-0.210283	-0.231643	0.7212	0.9998
ENSG00000188243	ENSG00000188243	COMMD6	13:76099349-76123575	OK	148.091	137.828	-0.103614	-0.22513	0.7212	0.9998
ENSG00000155906	ENSG00000155906	RMND1	6:151725988-151773259	OK	10.9823	10.1034	-0.12034	-0.21657	0.7213	0.9998
ENSG00000125534	ENSG00000125534	PPDPF	20:62152076-62153559	OK	148.163	138.47	-0.0976081	-0.214039	0.72135	0.9998
ENSG00000125779	ENSG00000125779	PANK2	20:3868885-3907605	OK	9.95062	9.10796	-0.127658	-0.21199	0.72135	0.9998
ENSG00000163655	ENSG00000163655	GMPS	3:155588324-155661815	OK	64.3705	58.8894	-0.128392	-0.215	0.72135	0.9998
ENSG00000152990	ENSG00000152990	GPR125	4:22346693-22517677	OK	23.5069	24.9773	0.0875327	0.167062	0.7214	0.9998
ENSG00000165280	ENSG00000165280	VCP	9:35056060-35073246	OK	99.1498	105.705	0.0923579	0.17397	0.7214	0.9998
ENSG00000137166	ENSG00000137166	FOXP4	6:41462590-41570122	OK	9.9868	10.6863	0.0976729	0.213492	0.72155	0.9998
ENSG00000182712	ENSG00000182712	CMC4	X:154289896-154384778	OK	10.7571	9.19071	-0.227039	-0.21667	0.72155	0.9998
ENSG00000091640	ENSG00000091640	SPAG7	17:4862520-4871167	OK	28.5861	26.6853	-0.0992691	-0.208211	0.72165	0.9998
ENSG00000248131	ENSG00000248131	CT49	5:12574968-12804475	OK	2.06394	1.78609	-0.2086	-0.221483	0.7217	0.9998
ENSG00000258376	ENSG00000258376	RP4-647C14.2	14:73704204-73741348	OK	1.23366	1.00432	-0.296717	-0.212575	0.722	0.9998
ENSG00000166439	ENSG00000166439	RNF169	11:74459912-74660245	OK	4.80305	5.1998	0.114503	0.194816	0.72205	0.9998
ENSG00000138802	ENSG00000138802	SEC24B	4:110268630-110462052	OK	10.1417	10.8697	0.100012	0.223972	0.7221	0.9998
ENSG00000185880	ENSG00000185880	TRIM69	15:45021185-45060027	OK	1.09693	1.27872	0.221234	0.159336	0.7221	0.9998
ENSG00000226479	ENSG00000226479	TMEM185B	2:120978853-120980984	OK	8.2422	8.90771	0.112025	0.224061	0.7221	0.9998
ENSG00000166971	ENSG00000166971	AKTIP	16:53467888-53538323	OK	7.40706	6.48596	-0.191581	-0.173138	0.7222	0.9998
ENSG00000053524	ENSG00000053524	MCF2L2	3:182895830-183146566	OK	2.03064	2.35607	0.214449	0.163836	0.7223	0.9998
ENSG00000198618	ENSG00000198618	PPIAP22	21:20230096-20230594	OK	807.608	856.142	0.0841942	0.211611	0.72235	0.9998
ENSG00000163161	ENSG00000163161	ERCC3	2:128014865-128051752	OK	30.4719	28.5825	-0.0923487	-0.193005	0.7224	0.9998
ENSG00000243477	ENSG00000243477	NAT6	3:50316457-50336899	OK	4.79988	6.29702	0.39167	0.239598	0.7225	0.9998
ENSG00000137819	ENSG00000137819	PAQR5	15:69591285-69740764	OK	1.30172	1.70206	0.386864	0.12916	0.72255	0.9998
ENSG00000231742	ENSG00000231742	RP11-112L6.4	20:48789086-48793096	OK	0.847995	0.695754	-0.285479	-0.223058	0.7227	0.9998
ENSG00000164169	ENSG00000164169	PRMT10	4:148538533-148605381	OK	4.5018	5.0876	0.176484	0.20955	0.72275	0.9998
ENSG00000176428	ENSG00000176428	VPS37D	7:73082154-73086442	OK	2.18353	2.41169	0.143382	0.212294	0.7228	0.9998
ENSG00000113742	ENSG00000113742	CPEB4	5:173315282-173388979	OK	27.5785	29.9878	0.120835	0.154942	0.72285	0.9998
ENSG00000104231	ENSG00000104231	ZFAND1	8:82613568-82671750	OK	45.2682	48.5923	0.10223	0.209952	0.72295	0.9998
ENSG00000228797	ENSG00000228797	FAM207BP	13:19271142-19271647	OK	1.76235	2.04562	0.215038	0.215437	0.72295	0.9998
ENSG00000237438	ENSG00000237438	CECR7	22:17517459-17541715	OK	29.0244	26.324	-0.140886	-0.211311	0.72295	0.9998
ENSG00000100567	ENSG00000100567	PSMA3	14:58466452-58764857	OK	100.574	90.6726	-0.149519	-0.216874	0.7231	0.9998
ENSG00000115896	ENSG00000115896	PLCL1	2:199164086-199637080	OK	1.30852	1.1876	-0.13988	-0.218	0.7231	0.9998
ENSG00000156928	ENSG00000156928	MALSU1	7:23338357-23510086	OK	84.369	74.9922	-0.169973	-0.206359	0.72315	0.9998
ENSG00000132122	ENSG00000132122	SPATA6	1:48761043-48937845	OK	7.53176	8.27076	0.135032	0.171815	0.7233	0.9998
ENSG00000117625	ENSG00000117625	RCOR3	1:211431718-211489727	OK	19.2237	17.5547	-0.131027	-0.185083	0.72335	0.9998
ENSG00000134987	ENSG00000134987	WDR36	5:110405759-110466200	OK	5.7675	6.24441	0.11462	0.172756	0.72345	0.9998
ENSG00000059122	ENSG00000059122	FLYWCH1	16:2961937-3004277	OK	23.3807	21.7201	-0.106286	-0.177508	0.7235	0.9998
ENSG00000172530	ENSG00000172530	BANP	16:87982849-88110924	OK	4.69805	4.3438	-0.113107	-0.162198	0.7235	0.9998
ENSG00000230733	ENSG00000230733	AC092171.4	7:5470965-5553429	OK	3.97705	3.5582	-0.160553	-0.214278	0.7235	0.9998
ENSG00000112514	ENSG00000112514	CUTA	6:33378175-33386094	OK	306.934	329.74	0.103401	0.212517	0.72355	0.9998
ENSG00000173273	ENSG00000173273	TNKS	8:9412655-9639856	OK	9.80157	10.4765	0.096075	0.144129	0.7237	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000247317	ENSG00000247317	RP11-273G15.2	8:144063154-144105249	OK	3.21531	2.51691	-0.353301	-0.0744366	0.7237	0.9998
ENSG00000245534	ENSG00000245534	RP11-219B17.1	15:60771376-61521518	OK	0.771254	0.581487	-0.407459	-0.179043	0.72385	0.9998
ENSG00000007545	ENSG00000007545	CRAMP1L	16:1662325-1752281	OK	7.86548	6.94786	-0.178965	-0.112721	0.7239	0.9998
ENSG00000071991	ENSG00000071991	CDH19	18:64168319-64271375	OK	1.08211	1.22276	0.176297	0.185497	0.72405	0.9998
ENSG00000176402	ENSG00000176402	GJC3	7:99520891-99546243	OK	0.645028	0.743661	0.205284	0.212712	0.7241	0.9998
ENSG00000123096	ENSG00000123096	SSPN	12:26272958-26986131	OK	2.76044	2.11386	-0.385019	-0.121722	0.7242	0.9998
ENSG00000100109	ENSG00000100109	TFIP11	22:26879842-26908471	OK	19.2401	20.8825	0.11818	0.16336	0.72425	0.9998
ENSG00000112941	ENSG00000112941	PAPD7	5:6714717-6757161	OK	20.49	19.246	-0.0903648	-0.166967	0.72425	0.9998
ENSG00000256923	ENSG00000256923	RP11-449P1.1	12:22852792-23404433	OK	0.969812	1.23024	0.343164	0.22142	0.72425	0.9998
ENSG00000180822	ENSG00000180822	PSMG4	6:3224494-3457256	OK	19.787	16.591	-0.254158	-0.184346	0.7243	0.9998
ENSG00000158604	ENSG00000158604	TMED4	7:44617492-44621886	OK	66.0833	62.1866	-0.0876811	-0.216111	0.72465	0.9998
ENSG00000170322	ENSG00000170322	NFRKB	11:129733530-129765485	OK	4.77891	5.19137	0.119435	0.160954	0.72465	0.9998
ENSG00000149150	ENSG00000149150	SLC43A1	11:57252006-57283259	OK	4.20321	4.6032	0.131146	0.175558	0.7247	0.9998
ENSG00000162139	ENSG00000162139	NEU3	11:74699178-74729938	OK	20.9688	19.5475	-0.101257	-0.173438	0.72475	0.9998
ENSG00000198805	ENSG00000198805	PNP	14:20937112-20945253	OK	17.4696	18.7116	0.0990907	0.203207	0.7248	0.9998
ENSG00000064995	ENSG00000064995	TAF11	6:34759856-34855866	OK	23.8368	21.3522	-0.158807	-0.216525	0.72485	0.9998
ENSG00000141503	ENSG00000141503	MINK1	17:4736682-4806369	OK	31.1248	33.3284	0.0986891	0.161906	0.72485	0.9998
ENSG00000182473	ENSG00000182473	EXOC7	17:74035183-74117657	OK	60.1207	65.2615	0.118371	0.183101	0.72485	0.9998
ENSG00000109111	ENSG00000109111	SUPT6H	17:26975373-27029697	OK	27.0577	28.7919	0.0896249	0.147409	0.7249	0.9998
ENSG00000196302	ENSG00000196302	RP11-497H16.5	5:69812213-69851093	OK	1.75401	2.06678	0.23673	0.221076	0.7249	0.9998
ENSG00000198791	ENSG00000198791	CNOT7	8:17086736-17271037	OK	51.1677	54.9341	0.102468	0.185909	0.72495	0.9998
ENSG00000248527	ENSG00000248527	MTATP6P1	1:536815-660283	OK	514.836	559.898	0.121052	0.212432	0.72495	0.9998
ENSG00000213995	ENSG00000213995	CARKD	13:111267880-111292340	OK	22.6835	21.019	-0.109946	-0.218396	0.725	0.9998
ENSG00000139163	ENSG00000139163	ETNK1	12:22778008-22843599	OK	11.841	13.0053	0.135315	0.140891	0.72515	0.9998
ENSG00000157895	ENSG00000157895	C12orf43	12:121406415-121454305	OK	11.0496	12.0198	0.12141	0.209982	0.72515	0.9998
ENSG00000135093	ENSG00000135093	USP30	12:109460893-109525831	OK	8.74161	8.14359	-0.102235	-0.173094	0.7252	0.9998
ENSG00000140455	ENSG00000140455	USP3	15:63796792-63894627	OK	11.3119	12.1355	0.101393	0.18186	0.72525	0.9998
ENSG00000055332	ENSG00000055332	EIF2AK2	2:37311593-37384208	OK	11.7257	10.4036	-0.172595	-0.172348	0.72535	0.9998
ENSG00000135299	ENSG00000135299	ANKRD6	6:90142888-90348472	OK	6.46486	7.37901	0.190807	0.159925	0.7254	0.9998
ENSG00000116731	ENSG00000116731	PRDM2	1:14026692-14151574	OK	9.45335	8.73425	-0.114143	-0.155391	0.72545	0.9998
ENSG00000257594	ENSG00000257594	GALNT4	12:89813494-89934079	OK	0.675798	0.968283	0.518838	0.244572	0.72545	0.9998
ENSG00000134152	ENSG00000134152	KATNBL1	15:34432874-34502297	OK	12.3851	11.2741	-0.135589	-0.207472	0.7255	0.9998
ENSG00000109794	ENSG00000109794	FAM149A	4:187025572-187093821	OK	2.90896	2.61419	-0.154137	-0.172511	0.7256	0.9998
ENSG00000267757	ENSG00000267757	C19orf83	19:46110251-46148887	OK	1.8547	2.62968	0.503701	0.202387	0.7256	0.9998
ENSG00000104177	ENSG00000104177	MYEF2	15:48413168-48470714	OK	34.0457	28.2021	-0.271668	-0.238847	0.7257	0.9998
ENSG00000011332	ENSG00000011332	DPF1	19:38701645-38720354	OK	3.19034	3.49386	0.131111	0.179948	0.7258	0.9998
ENSG00000125851	ENSG00000125851	PCSK2	20:17206751-17465223	OK	13.7543	15.1908	0.143321	0.205311	0.7258	0.9998
ENSG00000100150	ENSG00000100150	DEPDC5	22:32149943-32303012	OK	7.79516	6.89493	-0.177042	-0.118324	0.72585	0.9998
ENSG00000262410	ENSG00000262410	RP11-388C12.8	17:80693450-80709073	OK	0.92859	1.66063	0.83862	0.245408	0.72585	0.9998
ENSG00000065413	ENSG00000065413	ANKRD44	2:197831740-198175897	OK	19.2733	17.5956	-0.131388	-0.157992	0.7259	0.9998
ENSG00000115425	ENSG00000115425	PECR	2:216809212-216967506	OK	21.2197	17.4312	-0.283737	-0.235359	0.7259	0.9998
ENSG00000120314	ENSG00000120314	WDR55	5:140044260-140086248	OK	13.5379	15.9262	0.234402	0.230965	0.7259	0.9998
ENSG00000157796	ENSG00000157796	WDR19	4:39184023-39287430	OK	6.84098	7.44752	0.122557	0.15795	0.7259	0.9998
ENSG00000090581	ENSG00000090581	GNPTG	16:1401923-1464752	OK	37.3597	34.583	-0.111421	-0.201806	0.72595	0.9998
ENSG00000250021	ENSG00000250021	C15orf38-AP3S2	15:90373830-90456188	OK	8.57807	7.5536	-0.18349	-0.212564	0.72595	0.9998
ENSG00000230658	ENSG00000230658	KLHL7-AS1	7:23140846-23145322	OK	1.97359	1.80231	-0.130981	-0.211186	0.726	0.9998
ENSG00000147536	ENSG00000147536	GINS4	8:41386724-41482520	OK	10.6139	8.24202	-0.364881	-0.0762096	0.7261	0.9998
ENSG00000148343	ENSG00000148343	FAM73B	9:131798899-131834361	OK	9.53	8.72725	-0.12695	-0.169248	0.7261	0.9998
ENSG00000118804	ENSG00000118804	FAM47E-STBD1	4:77135192-77232752	OK	0.7776	0.915604	0.235696	0.227207	0.72615	0.9998
ENSG00000154040	ENSG00000154040	CABYR	18:21718941-21977844	OK	5.26762	6.93427	0.396592	0.240883	0.7262	0.9998
ENSG00000172007	ENSG00000172007	RAB33B	4:140187316-140397763	OK	1.50681	1.12068	-0.427123	-0.156754	0.72625	0.9998
ENSG00000103126	ENSG00000103126	AXIN1	16:337439-402673	OK	10.8784	11.6241	0.0956517	0.201107	0.7263	0.9998
ENSG00000269657	ENSG00000269657	AC079210.1	17:66255322-66760023	OK	0.516261	0.732608	0.50494	0.0495461	0.7264	0.9998
ENSG00000122435	ENSG00000122435	TRMT13	1:100598705-100643771	OK	4.52235	3.87134	-0.224238	-0.185106	0.7265	0.9998
ENSG00000137100	ENSG00000137100	DCTN3	9:34613547-34620515	OK	86.342	92.0095	0.0917201	0.211858	0.7265	0.9998
ENSG00000140386	ENSG00000140386	SCAPER	15:76640525-77197785	OK	10.5679	11.4946	0.12126	0.160243	0.72665	0.9998
ENSG00000135637	ENSG00000135637	CCDC142	2:74699084-74722013	OK	5.55505	4.46218	-0.31605	-0.161209	0.7267	0.9998
ENSG00000148429	ENSG00000148429	USP6NL	10:11495944-11654226	OK	3.97584	4.32288	0.120731	0.210054	0.7268	0.9998
ENSG00000141030	ENSG00000141030	COPS3	17:17150140-17184607	OK	51.7804	55.1279	0.0903763	0.196899	0.72685	0.9998
ENSG00000171148	ENSG00000171148	TADA3	3:9791627-9896822	OK	23.2081	19.7793	-0.230634	-0.208837	0.72685	0.9998
ENSG00000225335	ENSG00000225335	XXbac-B476C20.9	22:18559292-18629321	OK	1.24346	0.837022	-0.571017	-0.138205	0.72685	0.9998
ENSG00000125657	ENSG00000125657	TNFSF9	19:6531009-6535931	OK	1.41034	1.26224	-0.160055	-0.215965	0.72695	0.9998
ENSG00000175946	ENSG00000175946	KLHL38	8:124626464-124670810	OK	1.33472	1.48584	0.154742	0.214683	0.727	0.9998
ENSG00000114270	ENSG00000114270	COL7A1	3:48601505-48632700	OK	0.918655	1.10447	0.265756	0.160254	0.7271	0.9998
ENSG00000205352	ENSG00000205352	PRR13	12:53835388-53893847	OK	133.13	155.514	0.224209	0.215365	0.7271	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000076242	ENSG00000076242	MLH1	3:37034822-37225180	OK	19.0482	17.1587	-0.150712	-0.169581	0.72715	0.9998
ENSG00000228033	ENSG00000228033	AC010967.2	2:52949814-53137158	OK	0.557075	0.690319	0.309392	0.198793	0.72715	0.9998
ENSG00000254473	ENSG00000254473	RP11-522I20.3	9:86274877-86328293	OK	1.36043	0.932776	-0.544456	-0.0857952	0.7272	0.9998
ENSG00000105576	ENSG00000105576	TNPO2	19:12810007-12834825	OK	35.0801	32.9675	-0.0896075	-0.135346	0.7273	0.9998
ENSG00000139174	ENSG00000139174	PRICKLE1	12:42632248-42984157	OK	1.22805	1.55111	0.336927	0.104353	0.7274	0.9998
ENSG00000172264	ENSG00000172264	MACROD2	20:13829892-16033842	OK	0.86901	1.02601	0.239598	0.130118	0.72745	0.9998
ENSG00000160972	ENSG00000160972	PPP1R16A	8:145703351-145732557	OK	13.4117	12.4359	-0.108985	-0.17612	0.7275	0.9998
ENSG00000070950	ENSG00000070950	RAD18	3:8661085-9005457	OK	9.70851	10.5232	0.116258	0.181695	0.72755	0.9998
ENSG00000119943	ENSG00000119943	PYROXD2	10:100143321-100174941	OK	6.99659	6.35674	-0.138366	-0.139982	0.72755	0.9998
ENSG00000063438	ENSG00000063438	AHRR	5:271735-438406	OK	11.3602	10.0085	-0.182771	-0.11343	0.7277	0.9998
ENSG00000115233	ENSG00000115233	PSMD14	2:162164548-162268228	OK	62.3211	66.1221	0.0854111	0.202983	0.7277	0.9998
ENSG00000164221	ENSG00000164221	CCDC112	5:114602884-114632528	OK	3.06662	3.34328	0.124613	0.195183	0.72775	0.9998
ENSG00000273290	ENSG00000273290	CTC-297N7.8	17:10575790-10579323	OK	1.60649	1.75443	0.127087	0.209244	0.7279	0.9998
ENSG00000111450	ENSG00000111450	STX2	12:131274144-131323811	OK	14.4091	13.4763	-0.0965535	-0.186855	0.72795	0.9998
ENSG00000246334	ENSG00000246334	PRR7-AS1	5:176829140-176883283	OK	4.55077	6.00888	0.400983	0.153584	0.728	0.9998
ENSG00000269968	ENSG00000269968	RP5-940J5.9	12:6643092-6647537	OK	163.275	230.623	0.498233	0.0607076	0.728	0.9998
ENSG00000158195	ENSG00000158195	WASF2	1:27730729-27816669	OK	20.1463	21.3818	0.085871	0.200269	0.72805	0.9998
ENSG00000185798	ENSG00000185798	WDR53	3:196281055-196315930	OK	9.77599	11.3975	0.221406	0.205505	0.72825	0.9998
ENSG00000017373	ENSG00000017373	SRCIN1	17:36686250-36762183	OK	0.994836	1.18692	0.254698	0.193413	0.7283	0.9998
ENSG00000132646	ENSG00000132646	PCNA	20:5095598-5107272	OK	66.198	62.0859	-0.0925205	-0.215045	0.7283	0.9998
ENSG00000197858	ENSG00000197858	GPAA1	8:145137492-145141119	OK	79.8688	84.6844	0.0844644	0.189754	0.7283	0.9998
ENSG00000257596	ENSG00000257596	RP11-968A15.2	12:54624723-54745633	OK	1.04117	0.704977	-0.562556	-0.046378	0.7283	0.9998
ENSG00000105698	ENSG00000105698	USF2	19:35759880-35770724	OK	156.069	146.162	-0.094612	-0.207227	0.7284	0.9998
ENSG00000183207	ENSG00000183207	RUVBL2	19:49496704-49520338	OK	74.7177	79.5089	0.0896657	0.209547	0.72845	0.9998
ENSG00000115839	ENSG00000115839	RAB3GAP1	2:135809834-136288806	OK	10.1628	10.8472	0.0940311	0.169553	0.72855	0.9998
ENSG00000143429	ENSG00000143429	AC027612.6	2:91777535-91847998	OK	29.1673	31.8298	0.126027	0.213047	0.7286	0.9998
ENSG00000184702	ENSG00000184702	5-Sep	22:19701986-19712295	OK	19.7336	21.2362	0.105875	0.197214	0.7286	0.9998
ENSG00000198740	ENSG00000198740	ZNF652	17:47366567-47447360	OK	7.24335	6.7863	-0.0940316	-0.206224	0.72865	0.9998
ENSG00000177820	ENSG00000177820	AC004917.1	7:106012696-106410653	OK	0.850008	0.401295	-1.08281	-0.252427	0.7287	0.9998
ENSG00000172650	ENSG00000172650	AGAP5	10:75404638-75490272	OK	0.762193	0.636337	-0.260365	-0.178162	0.7288	0.9998
ENSG00000176533	ENSG00000176533	GNG7	19:2511216-2702707	OK	7.67881	8.2026	0.0951978	0.196499	0.72885	0.9998
ENSG00000072506	ENSG00000072506	HSD17B10	X:53458205-53461320	OK	84.2471	79.3141	-0.0870486	-0.208981	0.72905	0.9998
ENSG00000064703	ENSG00000064703	DDX20	1:112025969-112310638	OK	7.23838	8.14332	0.16995	0.174234	0.7291	0.9998
ENSG00000113312	ENSG00000113312	TTC1	5:159436119-159546430	OK	38.7005	41.556	0.102707	0.214539	0.7291	0.9998
ENSG00000143815	ENSG00000143815	LBR	1:225589203-225616627	OK	24.8288	23.3164	-0.0906705	-0.174558	0.7291	0.9998
ENSG00000254852	ENSG00000254852	NPIPA2	16:14841922-14859270	OK	0.78648	0.898908	0.192763	0.196283	0.7291	0.9998
ENSG00000162302	ENSG00000162302	RPS6KA4	11:64126619-64139687	OK	29.3603	31.2679	0.0908182	0.188159	0.72915	0.9998
ENSG00000139926	ENSG00000139926	FRMD6	14:51921229-52197445	OK	35.6759	37.9578	0.0894486	0.168924	0.7292	0.9998
ENSG00000176340	ENSG00000176340	COX8A	11:63742078-63933578	OK	658.077	611.784	-0.105234	-0.210803	0.7292	0.9998
ENSG00000126001	ENSG00000126001	CEP250	20:34042984-34099804	OK	26.712	24.751	-0.110001	-0.107311	0.72925	0.9998
ENSG00000254673	ENSG00000254673	RP11-598P20.5	8:42704779-42940931	OK	2.38555	6.20182	1.37837	0.362965	0.7293	0.9998
ENSG00000134313	ENSG00000134313	KIDINS220	2:8865407-8977760	OK	16.4042	15.4287	-0.0884463	-0.129205	0.72935	0.9998
ENSG00000171497	ENSG00000171497	PPID	4:159587830-159644548	OK	24.3591	26.7703	0.136168	0.200227	0.72935	0.9998
ENSG00000175130	ENSG00000175130	MARCKSL1	1:32799432-32801980	OK	74.4692	70.1581	-0.086034	-0.211594	0.72935	0.9998
ENSG00000164056	ENSG00000164056	SPRY1	4:124317949-124324910	OK	17.2319	15.8798	-0.117897	-0.198804	0.7294	0.9998
ENSG00000093167	ENSG00000093167	LRRFIP2	3:37034822-37225180	OK	41.2303	45.4493	0.140554	0.174818	0.72945	0.9998
ENSG00000270696	ENSG00000270696	RP11-342K6.1	2:75873908-75938115	OK	5.55559	6.74045	0.278903	0.210674	0.72955	0.9998
ENSG00000166016	ENSG00000166016	ABTB2	11:34172534-34379555	OK	5.50961	5.14879	-0.097717	-0.204555	0.7297	0.9998
ENSG00000149474	ENSG00000149474	CSRP2BP	20:18118516-18169031	OK	3.1043	2.73227	-0.184166	-0.160032	0.72975	0.9998
ENSG00000182010	ENSG00000182010	RTKN2	10:63942793-64028466	OK	4.0208	3.60317	-0.158217	-0.199358	0.7299	0.9998
ENSG00000255498	ENSG00000255498	RP11-618K13.2	11:45907201-45928016	OK	1.78935	0.840632	-1.08989	-0.316697	0.73	0.9998
ENSG00000111229	ENSG00000111229	ARPC3	12:110810704-110888227	OK	243.693	225.993	-0.108787	-0.201573	0.7302	0.9998
ENSG00000119321	ENSG00000119321	FKBP15	9:115913221-115983641	OK	18.0206	16.8852	-0.0938879	-0.193346	0.7302	0.9998
ENSG00000164405	ENSG00000164405	UQCRQ	5:132196872-132203723	OK	236.074	252.194	0.0952948	0.208793	0.7302	0.9998
ENSG00000234268	ENSG00000234268	AP000936.1	11:116706466-116969153	OK	0.670469	1.25984	0.909997	0.137149	0.73025	0.9998
ENSG00000250462	ENSG00000250462	LRRC37BP1	17:28900488-28999807	OK	6.20022	5.47382	-0.17977	-0.198849	0.73025	0.9998
ENSG00000147155	ENSG00000147155	EBP	X:48379545-48387104	OK	73.5318	78.3826	0.092165	0.207829	0.7305	0.9998
ENSG00000151835	ENSG00000151835	SACS	13:23902964-24007841	OK	6.09035	5.60117	-0.120797	-0.155003	0.7305	0.9998
ENSG00000250222	ENSG00000250222	CTC-338M12.5	5:180618923-180632293	OK	2.72308	2.09169	-0.380569	-0.194203	0.7305	0.9998
ENSG00000109971	ENSG00000109971	HSPA8	11:122928196-122933938	OK	1452.08	1589.23	0.130201	0.189936	0.73065	0.9998
ENSG00000170917	ENSG00000170917	NUDT6	4:123747862-123844123	OK	7.25329	6.25114	-0.214517	-0.216385	0.73065	0.9998
ENSG00000213753	ENSG00000213753	CENPBD1P1	19:59070495-59111168	OK	10.8942	10.0652	-0.114183	-0.188123	0.7307	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000124571	ENSG00000124571	XPO5	6:43474706-43543812	OK	22.0124	20.3938	-0.110182	-0.148152	0.73075	0.9998
ENSG00000106688	ENSG00000106688	SLC1A1	9:4490443-4666674	OK	3.43703	3.7387	0.121376	0.190978	0.7308	0.9998
ENSG00000111196	ENSG00000111196	MAGOHB	12:10758611-10766222	OK	19.2949	20.8518	0.111951	0.21319	0.7308	0.9998
ENSG00000113838	ENSG00000113838	TBCCD1	3:186256229-186315061	OK	8.47635	6.92873	-0.290851	-0.189352	0.73085	0.9998
ENSG00000119638	ENSG00000119638	NEK9	14:75548821-75643334	OK	14.5905	17.0798	0.227267	0.126313	0.73085	0.9998
ENSG00000224543	ENSG00000224543	SNRPGP15	19:14588571-14606944	OK	10.0422	15.7648	0.650628	0.144925	0.73085	0.9998
ENSG00000136379	ENSG00000136379	ABHD17C	15:80972024-81047962	OK	6.22013	5.70503	-0.12471	-0.197648	0.7309	0.9998
ENSG00000168758	ENSG00000168758	SEMA4C	2:97525452-97536494	OK	27.5892	29.3643	0.0899614	0.193336	0.7309	0.9998
ENSG00000091157	ENSG00000091157	WDR7	18:54264438-54706076	OK	5.48434	5.9982	0.12921	0.121262	0.731	0.9998
ENSG00000173064	ENSG00000173064	HECTD4	12:112597991-112819896	OK	6.4831	6.99285	0.109196	0.114063	0.731	0.9998
ENSG00000012048	ENSG00000012048	BRCA1	17:41196311-41277500	OK	13.9093	12.8264	-0.116935	-0.163529	0.7311	0.9998
ENSG00000255517	ENSG00000255517	CTD-3074O7.5	11:66234215-66313709	OK	1.54756	1.99544	0.366713	0.0840508	0.7311	0.9998
ENSG00000115904	ENSG00000115904	SOS1	2:39208536-39351486	OK	6.84399	7.37363	0.107538	0.137274	0.73115	0.9998
ENSG00000103591	ENSG00000103591	AAGAB	15:67493370-67819628	OK	43.2045	46.2371	0.0978722	0.20203	0.7312	0.9998
ENSG00000197696	ENSG00000197696	NMB	15:85198359-85201794	OK	14.2388	15.3778	0.11102	0.212321	0.7312	0.9998
ENSG00000202415	ENSG00000202415	RN7SKP269	1:9982172-10045559	OK	0.496683	0.925885	0.898508	0.155415	0.73125	0.9998
ENSG00000132819	ENSG00000132819	RBM38	20:55959215-55984389	OK	8.92675	9.55401	0.0979716	0.197267	0.7313	0.9998
ENSG00000176095	ENSG00000176095	IP6K1	3:49761726-49823975	OK	17.6944	19.3475	0.128856	0.187279	0.7313	0.9998
ENSG00000248235	ENSG00000248235	AC037459.4	8:22435791-22461663	OK	14.8542	18.3688	0.306392	0.201456	0.7313	0.9998
ENSG00000070785	ENSG00000070785	EIF2B3	1:45316449-45452282	OK	21.7896	20.4414	-0.0921507	-0.183313	0.7314	0.9998
ENSG00000152726	ENSG00000152726	FAM21B	10:47894022-47949412	OK	0.647947	0.575069	-0.172141	-0.162865	0.7315	0.9998
ENSG00000087299	ENSG00000087299	L2HGDH	14:50704280-50883179	OK	5.34372	5.93392	0.151139	0.189826	0.73165	0.9998
ENSG00000259006	ENSG00000259006	RP11-566K11.4	16:89939999-90005169	OK	5.30516	9.2748	0.805921	0.227755	0.7317	0.9998
ENSG00000124935	ENSG00000124935	SCGB1D2	11:61976139-62028021	OK	3.79901	3.34963	-0.181622	-0.211486	0.73185	0.9998
ENSG00000269858	ENSG00000269858	EGLN2	19:41277552-41406413	OK	40.2936	44.0391	0.128233	0.196855	0.7319	0.9998
ENSG00000183060	ENSG00000183060	LYSMD4	15:100017369-100273766	OK	4.74795	3.89966	-0.283956	-0.17022	0.73205	0.9998
ENSG00000258608	ENSG00000258608	DNAJC19P9	14:45759238-45759589	OK	14.7476	13.296	-0.149488	-0.21094	0.73205	0.9998
ENSG00000272758	ENSG00000272758	RP11-299J3.8	3:122135053-122233792	OK	15.962	13.3975	-0.252674	-0.186878	0.73205	0.9998
ENSG00000067798	ENSG00000067798	NAV3	12:78224684-78606790	OK	4.27294	3.92555	-0.122335	-0.127306	0.7321	0.9998
ENSG00000102743	ENSG00000102743	SLC25A15	13:41363547-41384247	OK	12.8205	13.7462	0.100579	0.202547	0.7321	0.9998
ENSG00000173511	ENSG00000173511	VEGFB	11:64002009-64006259	OK	124.766	116.92	-0.0936979	-0.207123	0.7321	0.9998
ENSG00000089818	ENSG00000089818	NECAP1	12:8234806-8250367	OK	14.3291	15.2936	0.0939799	0.181688	0.73225	0.9998
ENSG00000122971	ENSG00000122971	ACADS	12:121163537-121177811	OK	6.2471	5.77099	-0.114368	-0.212004	0.73225	0.9998
ENSG00000136603	ENSG00000136603	SKIL	3:170075465-170114623	OK	4.43465	4.88401	0.139247	0.157877	0.73225	0.9998
ENSG00000142937	ENSG00000142937	RPS8	1:45205489-45244451	OK	936.017	877.423	-0.0932619	-0.206334	0.73225	0.9998
ENSG00000185686	ENSG00000185686	PRAME	22:22890122-22909007	OK	395.355	371.834	-0.0884929	-0.199028	0.73225	0.9998
ENSG00000126773	ENSG00000126773	PCNXL4	14:60558628-60636574	OK	20.3541	22.1475	0.121825	0.156563	0.7324	0.9998
ENSG00000171530	ENSG00000171530	TBCA	5:76986990-77164604	OK	312.997	295.487	-0.0830535	-0.205888	0.7324	0.9998
ENSG00000127995	ENSG00000127995	CASD1	7:94138530-94186331	OK	7.29441	7.78823	0.0945045	0.183765	0.7325	0.9998
ENSG00000131171	ENSG00000131171	SH3BGRL	X:80457441-80554046	OK	52.4302	49.3687	-0.086801	-0.201715	0.73255	0.9998
ENSG00000233025	ENSG00000233025	CRYZP1	7:102715327-102740205	OK	0.407818	0.634267	0.637167	0.116589	0.73255	0.9998
ENSG00000104886	ENSG00000104886	PLEKHJ1	19:2100987-2248678	OK	42.0199	33.2386	-0.338214	-0.198348	0.7326	0.9998
ENSG00000115137	ENSG00000115137	DNAJC27	2:25166504-25262563	OK	2.37839	2.18016	-0.125551	-0.145567	0.7327	0.9998
ENSG00000152128	ENSG00000152128	TMEM163	2:135213329-135476570	OK	6.0298	5.54861	-0.119983	-0.205475	0.7327	0.9998
ENSG00000251400	ENSG00000251400	ALDH7A1P1	5:76506273-76916436	OK	1.02191	0.539711	-0.921003	-0.286649	0.7327	0.9998
ENSG00000132768	ENSG00000132768	DPH2	1:44435671-44439041	OK	13.437	14.4157	0.10143	0.180814	0.7328	0.9998
ENSG00000177119	ENSG00000177119	ANO6	12:45566846-45834187	OK	18.8262	19.9649	0.0847257	0.190087	0.7328	0.9998
ENSG00000243251	ENSG00000243251	PGBD3	10:50627322-50747584	OK	1.7689	2.05581	0.216853	0.21232	0.7329	0.9998
ENSG00000132604	ENSG00000132604	TERF2	16:69139466-69442474	OK	8.85664	7.45169	-0.249191	-0.0789628	0.73295	0.9998
ENSG00000185046	ENSG00000185046	ANKS1B	12:99038918-100378432	OK	6.89982	8.05352	0.223061	0.165761	0.73295	0.9998
ENSG00000136273	ENSG00000136273	HUS1	7:47735327-48019178	OK	31.6523	28.9361	-0.129441	-0.207169	0.73305	0.9998
ENSG00000135953	ENSG00000135953	MFSD9	2:103332298-103353347	OK	6.87437	7.61948	0.148465	0.178746	0.73315	0.9998
ENSG00000183020	ENSG00000183020	AP2A2	11:924893-1012239	OK	20.8518	22.1179	0.0850412	0.156444	0.7332	0.9998
ENSG00000071553	ENSG00000071553	ATP6AP1	X:153656977-153664862	OK	134.145	142.454	0.0866955	0.203695	0.7333	0.9998
ENSG00000107960	ENSG00000107960	OBFC1	10:105642299-105677963	OK	12.3372	11.4585	-0.106606	-0.209529	0.73335	0.9998
ENSG00000169851	ENSG00000169851	PCDH7	4:30722036-31148422	OK	14.1443	13.286	-0.0903104	-0.144779	0.73335	0.9998
ENSG00000132424	ENSG00000132424	PNISR	6:99845926-99879249	OK	26.3611	24.5615	-0.102011	-0.18173	0.7334	0.9998
ENSG00000204256	ENSG00000204256	BRD2	6:32902405-32949282	OK	111.408	120.487	0.113032	0.200042	0.7334	0.9998
ENSG00000247572	ENSG00000247572	CKMT2-AS1	5:80243515-80597379	OK	11.2512	10.1254	-0.152096	-0.203598	0.7336	0.9998
ENSG00000136504	ENSG00000136504	KAT7	17:47778304-47906458	OK	17.3285	19.1076	0.140998	0.173059	0.73365	0.9998
ENSG00000130775	ENSG00000130775	THEMIS2	1:28199054-28213196	OK	2.41341	2.6377	0.128206	0.172675	0.7337	0.9998
ENSG00000162385	ENSG00000162385	MAGOH	1:53692563-53710212	OK	35.4011	32.4526	-0.125459	-0.201744	0.7337	0.9998
ENSG00000070269	ENSG00000070269	TMEM260	14:56955071-57197253	OK	8.04539	8.61712	0.0990449	0.149896	0.73375	0.9998
ENSG00000137713	ENSG00000137713	PPP2R1B	11:111473114-111637151	OK	7.81301	8.67405	0.150826	0.190511	0.73375	0.9998
ENSG00000256664	ENSG00000256664	RP11-611O2.3	12:69201955-69365350	OK	19.8879	30.7667	0.629479	0.271733	0.73375	0.9998
ENSG00000257727	ENSG00000257727	CNPY2	12:56665482-56727837	OK	142.831	121.53	-0.232989	-0.245177	0.7338	0.9998
ENSG00000096063	ENSG00000096063	SRPK1	6:35773069-35889119	OK	25.6356	23.8125	-0.106426	-0.163743	0.7339	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000096384	ENSG00000096384	HSP90AB1	6:44214823-44221620	OK	916.618	983.199	0.101163	0.210299	0.7339	0.9998
ENSG00000140941	ENSG00000140941	MAP1LC3B	16:87117167-87438385	OK	29.8083	27.7178	-0.104898	-0.200902	0.7339	0.9998
ENSG00000198799	ENSG00000198799	LRIG2	1:113615830-113674882	OK	2.83801	3.14265	0.147103	0.132344	0.7339	0.9998
ENSG00000152082	ENSG00000152082	MZT2B	2:130908980-130948302	OK	72.6035	81.5815	0.168202	0.217503	0.73395	0.9998
ENSG00000106077	ENSG00000106077	ABHD11	7:73150423-73153197	OK	17.4334	18.7419	0.104418	0.192983	0.734	0.9998
ENSG00000181274	ENSG00000181274	FRAT2	10:99092254-99102770	OK	4.56232	4.21701	-0.113545	-0.205736	0.73405	0.9998
ENSG00000142867	ENSG00000142867	BCL10	1:85731930-86043933	OK	4.00621	4.46675	0.156987	0.20731	0.7341	0.9998
ENSG00000064102	ENSG00000064102	ASUN	12:27058113-27091259	OK	21.0714	22.6265	0.102727	0.189496	0.73435	0.9998
ENSG00000137040	ENSG00000137040	RANBP6	9:6011042-6015618	OK	7.57108	8.07246	0.0925092	0.187672	0.73435	0.9998
ENSG00000073050	ENSG00000073050	XRCC1	19:44047191-44100287	OK	25.5244	23.275	-0.133098	-0.184854	0.7344	0.9998
ENSG00000161091	ENSG00000161091	MFSD12	19:3506270-3579086	OK	1298.56	1424.35	0.133386	0.195396	0.7344	0.9998
ENSG00000171606	ENSG00000171606	ZNF274	19:58694395-58724928	OK	9.46294	10.1775	0.10503	0.182158	0.73445	0.9998
ENSG00000184863	ENSG00000184863	RBM33	7:155403924-155574179	OK	18.7493	20.7343	0.145184	0.197149	0.7345	0.9998
ENSG00000038532	ENSG00000038532	CLEC16A	16:11038344-11276046	OK	10.517	9.83363	-0.0969298	-0.179645	0.73455	0.9998
ENSG00000196975	ENSG00000196975	ANXA4	2:69685128-70053596	OK	49.9536	45.0202	-0.150017	-0.203084	0.73455	0.9998
ENSG00000134698	ENSG00000134698	AGO4	1:36273772-36323491	OK	5.33771	4.86111	-0.134935	-0.106163	0.7347	0.9998
ENSG00000144741	ENSG00000144741	SLC25A26	3:66119284-66551687	OK	20.5855	18.9724	-0.117725	-0.201171	0.7347	0.9998
ENSG00000134852	ENSG00000134852	CLOCK	4:56262123-56414056	OK	9.05578	8.31881	-0.122463	-0.101388	0.73475	0.9998
ENSG00000145723	ENSG00000145723	GIN1	5:102421703-102548500	OK	2.55606	2.03107	-0.331687	-0.130401	0.7348	0.9998
ENSG00000163463	ENSG00000163463	KRTCAP2	1:155141883-155162707	OK	203.704	191.162	-0.0916766	-0.207802	0.7348	0.9998
ENSG00000118579	ENSG00000118579	MED28	4:17616253-17783135	OK	16.8639	19.3096	0.195383	0.180435	0.73485	0.9998
ENSG00000164944	ENSG00000164944	KIAA1429	8:95499920-95565757	OK	17.5939	18.6873	0.0869821	0.149454	0.73485	0.9998
ENSG00000198060	ENSG00000198060	5-Mar	10:94050919-94113721	OK	22.732	24.955	0.134605	0.186653	0.73485	0.9998
ENSG00000256060	ENSG00000256060	TRAPPC2P1	19:57874844-57988938	OK	10.6154	12.2931	0.211679	0.205037	0.7349	0.9998
ENSG00000204387	ENSG00000204387	C6orf48	6:31802384-31807541	OK	248.728	264.403	0.0881662	0.211334	0.73495	0.9998
ENSG00000144401	ENSG00000144401	METTL21A	2:208104373-208490652	OK	11.6438	9.87649	-0.237487	-0.215371	0.73505	0.9998
ENSG00000165678	ENSG00000165678	GHITM	10:85898175-85913001	OK	144.374	153.032	0.0840217	0.208204	0.7351	0.9998
ENSG00000273243	ENSG00000273243	CTA-217C2.2	22:45528900-45559662	OK	0.780406	0.40997	-0.928707	-0.268904	0.7351	0.9998
ENSG00000095951	ENSG00000095951	HIVEP1	6:12007902-12165232	OK	2.253	2.05192	-0.134873	-0.124141	0.73515	0.9998
ENSG00000175581	ENSG00000175581	MRPL48	11:73498360-73576178	OK	41.2772	44.3668	0.104137	0.197684	0.7353	0.9998
ENSG00000173085	ENSG00000173085	COQ2	4:84182688-84206067	OK	8.97802	9.65511	0.104895	0.202547	0.73535	0.9998
ENSG00000105137	ENSG00000105137	SYDE1	19:15218213-15236985	OK	21.9359	24.0479	0.132618	0.173457	0.73555	0.9998
ENSG00000113068	ENSG00000113068	PFDN1	5:139554226-139682706	OK	79.8429	88.2488	0.144412	0.187243	0.73565	0.9998
ENSG00000247903	ENSG00000247903	RP11-421F16.3	12:27124518-27167367	OK	9.06952	11.0734	0.287994	0.202273	0.73565	0.9998
ENSG00000119820	ENSG00000119820	YIPF4	2:32502978-32541663	OK	28.6888	32.0015	0.157652	0.202492	0.73575	0.9998
ENSG00000260032	ENSG00000260032	LINC00657	20:34633543-34638882	OK	38.6099	40.8197	0.0802944	0.20267	0.73585	0.9998
ENSG00000269891	ENSG00000269891	ARHGAP19-SLIT1	10:98757794-99052413	OK	0.938396	0.644834	-0.541269	-0.229828	0.73585	0.9998
ENSG00000143158	ENSG00000143158	MPC2	1:167885966-168045081	OK	54.8741	48.5857	-0.175595	-0.200975	0.73595	0.9998
ENSG00000187240	ENSG00000187240	DYNC2H1	11:102980159-103350591	OK	2.18733	1.95044	-0.165373	-0.134858	0.73595	0.9998
ENSG00000104969	ENSG00000104969	SGTA	19:2754711-2783369	OK	34.1414	32.1981	-0.084547	-0.194046	0.736	0.9998
ENSG00000129292	ENSG00000129292	PHF20L1	8:133787617-133861052	OK	19.1953	18.0048	-0.0923675	-0.179699	0.73605	0.9998
ENSG00000169733	ENSG00000169733	RFNG	17:80005777-80015346	OK	22.7073	25.8627	0.187716	0.146876	0.73605	0.9998
ENSG00000148219	ENSG00000148219	ASTN2	9:119187503-120177348	OK	7.80079	6.72918	-0.213189	-0.196989	0.7361	0.9998
ENSG00000122035	ENSG00000122035	RASL11A	13:27844463-27847827	OK	0.928077	1.15163	0.311363	0.18406	0.73615	0.9998
ENSG00000247400	ENSG00000247400	DNAJC3-AS1	13:96300986-96329179	OK	0.766844	0.646783	-0.245652	-0.159063	0.7362	0.9998
ENSG00000273275	ENSG00000273275	RP11-474G23.2	2:68350067-68488362	OK	2.55094	4.61467	0.855197	0.261393	0.7362	0.9998
ENSG00000168675	ENSG00000168675	LDLRAD4	18:13217496-13652754	OK	3.18916	2.80663	-0.184336	-0.160766	0.7363	0.9998
ENSG00000267216	ENSG00000267216	AC010642.1	19:58739959-58827023	OK	0.449715	0.753526	0.744646	0.316682	0.7365	0.9998
ENSG00000140948	ENSG00000140948	ZCCHC14	16:87439851-87525651	OK	5.81672	6.21575	0.0957216	0.178237	0.7366	0.9998
ENSG00000116957	ENSG00000116957	TBCE	1:235530674-235612283	OK	19.2026	17.8921	-0.101972	-0.181601	0.73665	0.9998
ENSG00000123810	ENSG00000123810	B9D2	19:41768400-41930910	OK	1.22336	1.73727	0.505976	0.0724086	0.73665	0.9998
ENSG00000135521	ENSG00000135521	LTV1	6:143857981-144184949	OK	11.9123	12.8301	0.10708	0.207034	0.7367	0.9998
ENSG00000198945	ENSG00000198945	L3MBTL3	6:130334843-130686570	OK	2.51483	2.77286	0.140913	0.172882	0.7367	0.9998
ENSG00000204371	ENSG00000204371	EHMT2	6:31847535-31865464	OK	28.4301	30.3105	0.0924002	0.190648	0.73675	0.9998
ENSG00000126945	ENSG00000126945	HNRNPH2	X:100645811-100669121	OK	41.5777	38.5621	-0.108626	-0.207408	0.7368	0.9998
ENSG00000261762	ENSG00000261762	RP11-650L12.2	15:78857861-78913637	OK	0.585311	0.760847	0.378402	0.227262	0.7368	0.9998
ENSG00000021355	ENSG00000021355	SERPINB1	6:2832565-2842240	OK	36.2244	38.8512	0.100997	0.200983	0.73685	0.9998
ENSG00000174915	ENSG00000174915	PTDSS2	11:448267-491393	OK	21.2978	22.6938	0.0915973	0.162561	0.7369	0.9998
ENSG00000178952	ENSG00000178952	TUFM	16:28853731-28857729	OK	182.583	194.454	0.0908753	0.190809	0.7369	0.9998
ENSG00000223773	ENSG00000223773	CD99P1	X:2527388-2575270	OK	2.06772	1.81291	-0.189733	-0.19464	0.7369	0.9998
ENSG00000137055	ENSG00000137055	PLAA	9:26904080-27062928	OK	13.4423	14.4364	0.102931	0.186404	0.73695	0.9998
ENSG00000101161	ENSG00000101161	PRPF6	20:62588054-62680994	OK	60.6105	56.3576	-0.104958	-0.204696	0.73705	0.9998
ENSG00000138801	ENSG00000138801	PAPSS1	4:108511432-108641608	OK	27.2304	25.6266	-0.0875763	-0.179694	0.73705	0.9998
ENSG00000198157	ENSG00000198157	HMGN5	X:80369199-80457441	OK	16.3488	14.8165	-0.141979	-0.210802	0.73705	0.9998
ENSG00000170921	ENSG00000170921	TANC2	17:61086916-61509572	OK	10.9076	13.1611	0.270945	0.15664	0.7371	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000213079	ENSG00000213079	SCAF8	6:155054458-155635627	OK	5.85386	5.39956	-0.116546	-0.192587	0.73715	0.9998
ENSG00000258643	ENSG00000258643	BCL2L2-PABPN1	14:23654524-23795394	OK	10.605	8.10699	-0.387508	-0.207926	0.73725	0.9998
ENSG00000259480	ENSG00000259480	RP11-26F2.1	15:23128187-23145997	OK	1.50652	1.68216	0.159094	0.195558	0.73725	0.9998
ENSG00000100146	ENSG00000100146	SOX10	22:38339527-38437922	OK	140.777	150.385	0.0952476	0.199265	0.7373	0.9998
ENSG00000255168	ENSG00000255168	RP11-458D21.5	1:145209118-145370303	OK	2.34693	1.91676	-0.292102	-0.200839	0.7373	0.9998
ENSG00000218422	ENSG00000218422	AC016773.1	4:1723226-1746898	OK	0.79995	0.510482	-0.648049	-0.270615	0.7374	0.9998
ENSG00000130772	ENSG00000130772	MED18	1:28655512-28662476	OK	6.64124	6.0871	-0.125697	-0.190749	0.7375	0.9998
ENSG00000105254	ENSG00000105254	TBCB	19:36602103-36616849	OK	95.9333	102.85	0.100431	0.203136	0.7376	0.9998
ENSG00000196372	ENSG00000196372	ASB13	10:5680829-5708558	OK	5.1617	5.54748	0.103986	0.197915	0.7377	0.9998
ENSG00000156011	ENSG00000156011	PSD3	8:18384810-18942240	OK	7.39238	6.80185	-0.120113	-0.124007	0.73775	0.9998
ENSG00000141985	ENSG00000141985	SH3GL1	19:4360366-4400544	OK	24.777	23.3599	-0.0849673	-0.199187	0.7378	0.9998
ENSG00000090376	ENSG00000090376	IRAK3	12:66582658-66651214	OK	1.46365	1.58524	0.115129	0.175544	0.7379	0.9998
ENSG00000139505	ENSG00000139505	MTMR6	13:25802306-25862147	OK	13.5016	12.6621	-0.092619	-0.177044	0.7379	0.9998
ENSG00000228782	ENSG00000228782	MRPL45P2	17:45527933-45569858	OK	12.6214	13.8427	0.133261	0.202499	0.73795	0.9998
ENSG00000132423	ENSG00000132423	COQ3	6:99817275-99842080	OK	13.3711	12.2846	-0.122259	-0.209434	0.738	0.9998
ENSG00000149177	ENSG00000149177	PTPRJ	11:48002112-48189670	OK	28.1273	29.7195	0.0794427	0.179509	0.738	0.9998
ENSG00000140105	ENSG00000140105	WARS	14:100800124-100996640	OK	151.757	140.147	-0.114822	-0.188082	0.73805	0.9998
ENSG00000148110	ENSG00000148110	HIATL1	9:97136832-97223324	OK	51.0636	48.0131	-0.0888665	-0.199616	0.73815	0.9998
ENSG00000229692	ENSG00000229692	SOS1-IT1	2:39208536-39351486	OK	0.910323	0.647442	-0.491627	-0.133167	0.73815	0.9998
ENSG00000130962	ENSG00000130962	PRRG1	X:37208527-38548169	OK	6.30846	7.32103	0.214758	0.1167	0.7382	0.9998
ENSG00000117713	ENSG00000117713	ARID1A	1:27022523-27108595	OK	11.2776	12.0452	0.0949873	0.185939	0.73825	0.9998
ENSG00000140612	ENSG00000140612	SEC11A	15:85212774-85259947	OK	177.829	167.703	-0.0845793	-0.197282	0.73825	0.9998
ENSG00000141956	ENSG00000141956	PRDM15	21:43218384-43299591	OK	2.08726	1.9205	-0.12013	-0.122423	0.73825	0.9998
ENSG00000215012	ENSG00000215012	C22orf29	22:19744225-19842462	OK	4.55292	4.97825	0.128847	0.152301	0.73825	0.9998
ENSG00000080345	ENSG00000080345	RIF1	2:152266396-152591001	OK	3.23612	3.02113	-0.0991747	-0.127973	0.73845	0.9998
ENSG00000262180	ENSG00000262180	OCLM	1:186344889-186390510	OK	0.471479	0.820902	0.800016	0.1953	0.73855	0.9998
ENSG00000120008	ENSG00000120008	WDR11	10:122521323-122669036	OK	29.9322	28.1519	-0.0884635	-0.148195	0.7386	0.9998
ENSG00000164818	ENSG00000164818	HEATR2	7:588833-829190	OK	23.8733	22.4122	-0.0911145	-0.179589	0.7387	0.9998
ENSG00000230989	ENSG00000230989	HSBP1	16:83841447-83853342	OK	48.3326	45.3252	-0.092685	-0.19257	0.7387	0.9998
ENSG00000233621	ENSG00000233621	LINC01137	1:37920479-37940012	OK	1.1281	1.00612	-0.16509	-0.199836	0.73875	0.9998
ENSG00000271303	ENSG00000271303	SRXN1	20:627258-656823	OK	12.5164	13.3413	0.0920815	0.200386	0.73885	0.9998
ENSG00000160213	ENSG00000160213	CSTB	21:45192392-45196326	OK	188.471	177.288	-0.088244	-0.191085	0.73915	0.9998
ENSG00000060749	ENSG00000060749	QSER1	11:32914723-33014862	OK	6.403	5.99675	-0.094569	-0.155025	0.7393	0.9998
ENSG00000263272	ENSG00000263272	CTC-524C5.2	17:5185557-5372380	OK	1.08754	1.57871	0.537687	0.0910789	0.73945	0.9998
ENSG00000185928	ENSG00000185928	PAGR1	16:29817426-29859355	OK	6.10312	4.57883	-0.41457	-0.223009	0.73955	0.9998
ENSG00000160201	ENSG00000160201	U2AF1	21:44513065-44527697	OK	40.3262	37.6713	-0.0982496	-0.200722	0.73965	0.9998
ENSG00000165912	ENSG00000165912	PACSIN3	11:47199075-47207994	OK	22.1766	23.5942	0.0893945	0.187957	0.73965	0.9998
ENSG00000177225	ENSG00000177225	PDDC1	11:767219-777488	OK	24.2691	22.2289	-0.126684	-0.163811	0.7397	0.9998
ENSG00000147883	ENSG00000147883	CDKN2B	9:21802541-22121096	OK	11.4705	13.7337	0.259799	0.197943	0.73975	0.9998
ENSG00000184009	ENSG00000184009	ACTG1	17:79476996-79494802	OK	3279.94	3631.99	0.147088	0.180135	0.73975	0.9998
ENSG00000224318	ENSG00000224318	CHL1-AS2	3:237440-451090	OK	0.960381	0.699718	-0.456833	-0.0811994	0.73975	0.9998
ENSG00000080947	ENSG00000080947	CROCCP3	1:16787442-16825752	OK	2.48385	2.05661	-0.272308	-0.147332	0.7398	0.9998
ENSG00000114354	ENSG00000114354	TFG	3:100428204-100467810	OK	62.0847	65.7791	0.0833906	0.201973	0.7398	0.9998
ENSG00000258359	ENSG00000258359	PCNPP1	12:112079949-112123790	OK	0.762268	0.50349	-0.598335	-0.105494	0.7398	0.9998
ENSG00000148690	ENSG00000148690	FRA10AC1	10:95427639-95462329	OK	18.7302	17.3506	-0.110384	-0.192596	0.74	0.9998
ENSG00000181856	ENSG00000181856	SLC2A4	17:7184985-7197934	OK	0.681461	0.831243	0.28664	0.228018	0.74	0.9998
ENSG00000270108	ENSG00000270108	RP11-73M18.6	14:104019757-104181841	OK	1.53074	2.24993	0.555652	0.0719435	0.74005	0.9998
ENSG00000134697	ENSG00000134697	GNL2	1:38022519-38061536	OK	27.1029	25.6212	-0.0811089	-0.172451	0.7401	0.9998
ENSG00000110931	ENSG00000110931	CAMKK2	12:121675496-121736111	OK	12.4775	11.7118	-0.0913768	-0.1883	0.7402	0.9998
ENSG00000115966	ENSG00000115966	ATF2	2:175936977-176033250	OK	20.6906	19.4342	-0.0903771	-0.1708	0.74035	0.9998
ENSG00000185418	ENSG00000185418	TARSL2	15:102193800-102264807	OK	3.30797	3.59317	0.119308	0.172154	0.74035	0.9998
ENSG00000244045	ENSG00000244045	TMEM199	17:26684603-26734215	OK	24.2472	20.6571	-0.23118	-0.212027	0.74035	0.9998
ENSG00000064490	ENSG00000064490	RFXANK	19:19256375-19314233	OK	61.2985	55.1645	-0.152112	-0.199563	0.74045	0.9998
ENSG00000013583	ENSG00000013583	HEBP1	12:13080659-13193613	OK	53.3261	50.1854	-0.0875745	-0.202002	0.74055	0.9998
ENSG00000198954	ENSG00000198954	KIAA1279	10:70748486-70776738	OK	21.1272	22.4218	0.0858006	0.191692	0.74055	0.9998
ENSG00000133313	ENSG00000133313	CNDP2	18:72163050-72188366	OK	68.6777	72.8326	0.0847415	0.158527	0.74065	0.9998
ENSG00000175445	ENSG00000175445	LPL	8:19759227-19824769	OK	0.853397	0.738036	-0.209527	-0.0803952	0.74065	0.9998
ENSG00000047621	ENSG00000047621	C12orf4	12:4596893-4647674	OK	8.45017	7.86861	-0.102871	-0.157596	0.74075	0.9998
ENSG00000198964	ENSG00000198964	SGMS1	10:52065359-52401211	OK	2.70232	2.45762	-0.136939	-0.142984	0.74075	0.9998
ENSG00000068394	ENSG00000068394	GPKOW	X:48970333-48980151	OK	15.052	14.1066	-0.0935886	-0.198286	0.7408	0.9998
ENSG00000161955	ENSG00000161955	TNFSF13	17:7452207-7464925	OK	0.795491	0.957943	0.268094	0.155937	0.7408	0.9998
ENSG00000239900	ENSG00000239900	ADSL	22:40742506-41032706	OK	63.3943	58.5147	-0.115552	-0.191439	0.74085	0.9998
ENSG00000151748	ENSG00000151748	SAV1	14:50885218-51135049	OK	18.3919	16.207	-0.182453	-0.198249	0.741	0.9998
ENSG00000165929	ENSG00000165929	TC2N	14:92047039-92333880	OK	0.68866	0.774757	0.169953	0.168757	0.7411	0.9998
ENSG00000181873	ENSG00000181873	IBA57	1:228353515-228369958	OK	3.04766	2.60857	-0.224443	-0.199808	0.7412	0.9998
ENSG00000103512	ENSG00000103512	NOMO1	16:14927537-14990017	OK	48.5825	51.3824	0.0808386	0.184218	0.74125	0.9998
ENSG00000121743	ENSG00000121743	GJA3	13:20712393-20735188	OK	2.40546	2.583	0.102738	0.198277	0.74125	0.9998
ENSG00000160691	ENSG00000160691	SHC1	1:154929501-154946871	OK	100.252	108.306	0.111486	0.169847	0.74125	0.9998
ENSG00000080845	ENSG00000080845	DLGAP4	20:34894257-35274619	OK	44.2505	40.1912	-0.138814	-0.177499	0.7413	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000204356	ENSG00000204356	NELFE	6:31919863-31937532	OK	116.903	108.065	-0.113417	-0.196614	0.74135	0.9998
ENSG00000214753	ENSG00000214753	HNRNPUL2	11:62457746-62494856	OK	24.6611	26.7869	0.119291	0.158807	0.74135	0.9998
ENSG00000198948	ENSG00000198948	MFAP3L	4:170902897-170954182	OK	9.552	8.751	-0.126355	-0.152108	0.7414	0.9998
ENSG00000067900	ENSG00000067900	ROCK1	18:18526866-18691812	OK	8.87045	9.3814	0.0807962	0.121034	0.74145	0.9998
ENSG00000139842	ENSG00000139842	CUL4A	13:113831890-113919399	OK	47.3816	50.9357	0.104351	0.186918	0.7415	0.9998
ENSG00000170364	ENSG00000170364	SETMAR	3:3742497-4508965	OK	5.63602	4.77194	-0.240102	-0.202806	0.74155	0.9998
ENSG00000263563	ENSG00000263563	UBBP4	17:21729600-21731762	OK	1.0498	1.18918	0.179853	0.155343	0.74155	0.9998
ENSG00000014123	ENSG00000014123	UFL1	6:96806249-97003152	OK	5.18213	4.83444	-0.100196	-0.180006	0.7416	0.9998
ENSG00000006125	ENSG00000006125	AP2B1	17:33901813-34053436	OK	66.9481	70.8875	0.0824885	0.168983	0.7417	0.9998
ENSG00000225544	ENSG00000225544	KB-1027C11.4	22:22239620-22240012	OK	0.985135	0.797734	-0.304413	-0.214897	0.7417	0.9998
ENSG00000272752	ENSG00000272752	STAG3L5P-PVRIG2P-PILRB	7:99905324-99997719	OK	4.97119	4.32612	-0.200518	-0.181227	0.74175	0.9998
ENSG00000206120	ENSG00000206120	EGFEM1P	3:167967309-168548387	OK	1.20434	1.35978	0.175138	0.146807	0.7418	0.9998
ENSG00000139910	ENSG00000139910	NOVA1	14:26912298-27066960	OK	2.01276	1.7597	-0.193847	-0.16909	0.74185	0.9998
ENSG00000164362	ENSG00000164362	TERT	5:1253261-1295184	OK	1.46176	1.23783	-0.239885	-0.158394	0.7422	0.9998
ENSG00000204590	ENSG00000204590	GNL1	6:30509153-30531500	OK	53.2904	58.3941	0.131948	0.192638	0.7422	0.9998
ENSG00000120451	ENSG00000120451	SNX19	11:130745330-130786404	OK	12.8581	11.9482	-0.10589	-0.16028	0.74225	0.9998
ENSG00000137193	ENSG00000137193	PIM1	6:37137978-37143202	OK	1.89805	1.70581	-0.154056	-0.191516	0.7423	0.9998
ENSG00000109917	ENSG00000109917	ZNF259	11:116648435-116658766	OK	16.1603	15.1097	-0.0969788	-0.176018	0.7424	0.9998
ENSG00000006007	ENSG00000006007	GDE1	16:19513010-19533467	OK	42.5481	39.5971	-0.1037	-0.200981	0.74245	0.9998
ENSG00000067248	ENSG00000067248	DHX29	5:54529761-54603550	OK	13.0795	12.2952	-0.0892137	-0.173266	0.7425	0.9998
ENSG00000178078	ENSG00000178078	STAP2	19:4324039-4343488	OK	6.3732	6.89708	0.113968	0.180975	0.74255	0.9998
ENSG00000205559	ENSG00000205559	CHKB-AS1	22:51007289-51052409	OK	1.91127	1.18265	-0.692507	-0.170241	0.7426	0.9998
ENSG00000185829	ENSG00000185829	ARL17A	17:44588876-44657088	OK	0.778254	0.879896	0.177092	0.128237	0.74265	0.9998
ENSG00000108591	ENSG00000108591	DRG2	17:17991199-18011285	OK	17.3418	16.3106	-0.088443	-0.176816	0.7428	0.9998
ENSG00000259040	ENSG00000259040	BLOC1S5-TXNDC5	6:7727029-8102811	OK	3.81059	1.94815	-0.967905	-0.291361	0.7428	0.9998
ENSG00000157045	ENSG00000157045	NTAN1	16:15068447-15248421	OK	62.2636	70.4496	0.178203	0.184859	0.74285	0.9998
ENSG00000178660	ENSG00000178660	ARMC10P1	3:94225609-94226464	OK	1.90585	2.13749	0.165484	0.202812	0.74285	0.9998
ENSG00000111348	ENSG00000111348	ARHGDIB	12:15094950-15114662	OK	1.28214	1.13657	-0.173866	-0.15225	0.74295	0.9998
ENSG00000111481	ENSG00000111481	COPZ1	12:54624723-54745633	OK	83.8394	75.1979	-0.156936	-0.165892	0.74295	0.9998
ENSG00000180902	ENSG00000180902	D2HGDH	2:242673993-242708231	OK	5.63422	6.13401	0.122614	0.177626	0.7431	0.9998
ENSG00000138459	ENSG00000138459	SLC35A5	3:112251355-112304424	OK	17.928	16.0689	-0.157946	-0.164996	0.7432	0.9998
ENSG00000169951	ENSG00000169951	ZNF764	16:30535324-30569819	OK	3.29388	2.7063	-0.283465	-0.186381	0.7432	0.9998
ENSG00000005020	ENSG00000005020	SKAP2	7:26706680-27034858	OK	16.183	14.9839	-0.111063	-0.164407	0.74325	0.9998
ENSG00000169758	ENSG00000169758	C15orf27	15:76352177-76603813	OK	0.673198	0.822088	0.288264	0.0799252	0.74325	0.9998
ENSG00000269952	ENSG00000269952	RP11-324I22.3	10:35386933-35501886	OK	1.57114	0.949567	-0.726468	-0.107721	0.7433	0.9998
ENSG00000266783	ENSG00000266783	RP11-715F3.2	18:2537523-2571508	OK	0.405	0.745234	0.879771	0.282244	0.74335	0.9998
ENSG00000141759	ENSG00000141759	TXNL4A	18:77732866-77793949	OK	128.214	119.967	-0.095916	-0.201565	0.7435	0.9998
ENSG00000267348	ENSG00000267348	CTB-179K24.3	19:45574757-45808541	OK	0.947251	0.680218	-0.477749	-0.0529827	0.7435	0.9998
ENSG00000174197	ENSG00000174197	MGA	15:41913421-42062141	OK	2.82673	3.04793	0.108696	0.154615	0.74355	0.9998
ENSG00000198715	ENSG00000198715	C1orf85	1:156252725-156265463	OK	287.349	305.544	0.0885781	0.196553	0.7436	0.9998
ENSG00000144036	ENSG00000144036	EXOC6B	2:72403112-73053170	OK	12.6012	13.3791	0.086422	0.156742	0.74365	0.9998
ENSG00000110427	ENSG00000110427	KIAA1549L	11:33563617-33718247	OK	8.33857	9.01626	0.11273	0.188598	0.7437	0.9998
ENSG00000158480	ENSG00000158480	SPATA2	20:48519927-48532080	OK	14.7374	15.7853	0.0990934	0.205492	0.74375	0.9998
ENSG00000126524	ENSG00000126524	SBDS	7:66452663-66704501	OK	56.7859	53.1333	-0.0959179	-0.200736	0.7438	0.9998
ENSG00000171224	ENSG00000171224	C10orf35	10:71390006-71393352	OK	4.48494	4.09592	-0.1309	-0.193623	0.7438	0.9998
ENSG00000143258	ENSG00000143258	USP21	1:161129239-161135513	OK	24.6339	22.9646	-0.101231	-0.192189	0.74385	0.9998
ENSG00000141570	ENSG00000141570	CBX8	17:77765930-77776326	OK	14.0312	12.7721	-0.135646	-0.192721	0.7439	0.9998
ENSG00000108375	ENSG00000108375	RNF43	17:56378591-56494956	OK	3.14176	2.62495	-0.259287	-0.125145	0.74395	0.9998
ENSG00000145604	ENSG00000145604	SKP2	5:36152090-36184421	OK	31.3643	29.3522	-0.0956522	-0.194629	0.7441	0.9998
ENSG00000166261	ENSG00000166261	ZNF202	11:123594884-123612383	OK	2.44437	2.23874	-0.126776	-0.146391	0.74415	0.9998
ENSG00000254109	ENSG00000254109	RBPMS-AS1	8:30239634-30429778	OK	5.41147	4.09424	-0.402425	-0.219978	0.74415	0.9998
ENSG00000188486	ENSG00000188486	H2AFX	11:118964563-118966177	OK	14.1687	13.2258	-0.0993522	-0.199384	0.7443	0.9998
ENSG00000174839	ENSG00000174839	DENND6A	3:57611183-57678816	OK	7.11422	7.6317	0.101299	0.135787	0.7444	0.9998
ENSG00000068438	ENSG00000068438	FTSJ1	X:48334540-48344752	OK	30.7527	32.9718	0.100518	0.19665	0.74445	0.9998
ENSG00000213689	ENSG00000213689	TREX1	3:48488113-48509044	OK	6.62315	7.85457	0.246015	0.228925	0.74445	0.9998
ENSG00000185989	ENSG00000185989	RASA3	13:114747193-114898086	OK	11.0883	10.4492	-0.085643	-0.189684	0.7445	0.9998
ENSG00000170291	ENSG00000170291	ELP5	17:7143332-7167302	OK	47.7764	56.3577	0.238313	0.20357	0.74455	0.9998
ENSG00000197576	ENSG00000197576	HOXA4	7:27145802-27197555	OK	2.87857	3.30987	0.201419	0.197577	0.7446	0.9998
ENSG00000261188	ENSG00000261188	CTA-445C9.14	22:26908502-26910534	OK	0.6126	0.694343	0.180703	0.198734	0.7446	0.9998
ENSG00000140406	ENSG00000140406	MESDC1	15:81293294-81296342	OK	37.8746	35.8008	-0.081239	-0.201004	0.74465	0.9998
ENSG00000065135	ENSG00000065135	GNAI3	1:110091232-110136975	OK	32.989	31.1907	-0.0808679	-0.198537	0.7447	0.9998
ENSG00000074071	ENSG00000074071	MRPS34	16:1821890-1823156	OK	99.0932	105.057	0.0843133	0.197117	0.74475	0.9998
ENSG00000105053	ENSG00000105053	VRK3	19:50479723-50570050	OK	26.9702	25.0478	-0.106685	-0.176666	0.74475	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000272644	ENSG00000272644	RP11-33O4.1	2:219934075-219934531	OK	0.91152	0.758961	-0.264247	-0.204616	0.7448	0.9998
ENSG00000132635	ENSG00000132635	PCED1A	20:2815959-3019722	OK	7.76755	8.90831	0.197692	0.183858	0.7449	0.9998
ENSG00000171970	ENSG00000171970	ZNF57	19:2900895-2926805	OK	2.3741	2.58258	0.121434	0.184707	0.7449	0.9998
ENSG00000003756	ENSG00000003756	RBM5	3:49977439-50226508	OK	52.8488	49.3065	-0.100093	-0.137091	0.745	0.9998
ENSG00000114650	ENSG00000114650	SCAP	3:47455202-47518616	OK	23.9008	22.6293	-0.0788667	-0.140176	0.745	0.9998
ENSG00000167291	ENSG00000167291	TBC1D16	17:77906141-78009647	OK	285.659	261.143	-0.129452	-0.185606	0.745	0.9998
ENSG00000261526	ENSG00000261526	CTB-31O20.2	19:1874880-1876168	OK	1.85926	1.6818	-0.14472	-0.19645	0.74505	0.9998
ENSG00000260917	ENSG00000260917	RP11-57H14.4	10:114583248-114587485	OK	3.29497	3.06954	-0.102239	-0.198008	0.7451	0.9998
ENSG00000181666	ENSG00000181666	HKR1	19:37803738-37860267	OK	12.2117	11.4447	-0.0935812	-0.141553	0.74525	0.9998
ENSG00000090861	ENSG00000090861	AARS	16:70286197-70323446	OK	54.8073	51.9509	-0.0772191	-0.18096	0.7454	0.9998
ENSG00000227500	ENSG00000227500	SCAMP4	19:1905212-1926016	OK	14.8986	16.3534	0.134407	0.17983	0.7454	0.9998
ENSG00000214783	ENSG00000214783	POLR2J4	7:43966036-44058774	OK	1.28625	0.698418	-0.881006	-0.328116	0.74545	0.9998
ENSG00000267040	ENSG00000267040	RP11-35G9.3	18:55297533-55470333	OK	1.27706	1.11885	-0.190809	-0.193592	0.74545	0.9998
ENSG00000224699	ENSG00000224699	LAMTOR5-AS1	1:110905469-110974982	OK	1.51808	1.34282	-0.176985	-0.0324668	0.74555	0.9998
ENSG00000156876	ENSG00000156876	SASS6	1:100503652-100598511	OK	3.10431	2.61368	-0.248186	-0.203368	0.74565	0.9998
ENSG00000235453	ENSG00000235453	TOPORS-AS1	9:32540541-32573160	OK	5.2763	3.63522	-0.537485	-0.167217	0.7457	0.9998
ENSG00000243725	ENSG00000243725	TTC4	1:55107458-55208330	OK	10.6828	11.5327	0.110443	0.194872	0.7457	0.9998
ENSG00000111321	ENSG00000111321	LTBR	12:6456008-6500733	OK	79.0491	83.4412	0.0780097	0.16006	0.74575	0.9998
ENSG00000137207	ENSG00000137207	YIPF3	6:43474706-43543812	OK	59.6053	54.539	-0.128153	-0.183066	0.74575	0.9998
ENSG00000167986	ENSG00000167986	DDB1	11:61066922-61136981	OK	98.5231	104.865	0.0899946	0.173647	0.7459	0.9998
ENSG00000018610	ENSG00000018610	CXorf56	X:118672111-118699397	OK	10.6146	11.5642	0.123614	0.189058	0.746	0.9998
ENSG00000246877	ENSG00000246877	DNM1P35	15:76016317-76055662	OK	0.872169	0.772916	-0.174296	-0.201472	0.746	0.9998
ENSG00000247828	ENSG00000247828	TMEM161B-AS1	5:87485449-87794514	OK	24.425	20.8238	-0.230126	-0.200297	0.74635	0.9998
ENSG00000272947	ENSG00000272947	RP11-71H17.9	3:124467421-124468120	OK	0.84502	0.721318	-0.22835	-0.19899	0.74645	0.9998
ENSG00000141198	ENSG00000141198	TOM1L1	17:52976747-53241646	OK	21.2025	23.7302	0.162494	0.185203	0.74655	0.9998
ENSG00000114904	ENSG00000114904	NEK4	3:52744799-52804965	OK	13.4495	14.4308	0.101603	0.137545	0.7466	0.9998
ENSG00000123395	ENSG00000123395	C12orf44	12:52463029-52502045	OK	51.2137	54.3279	0.0851635	0.194303	0.7466	0.9998
ENSG00000137478	ENSG00000137478	FCHSD2	11:72525352-72853306	OK	7.93392	7.33895	-0.112461	-0.134438	0.7466	0.9998
ENSG00000121741	ENSG00000121741	ZMYM2	13:20532809-20665968	OK	20.683	19.3945	-0.0927992	-0.144282	0.74665	0.9998
ENSG00000139370	ENSG00000139370	SLC15A4	12:129277738-129308528	OK	23.7774	25.3037	0.0897576	0.172851	0.7467	0.9998
ENSG00000157833	ENSG00000157833	GAREML	2:26395959-26412532	OK	7.27395	6.82406	-0.0921072	-0.143615	0.7467	0.9998
ENSG00000169228	ENSG00000169228	RAB24	5:176728198-176739758	OK	23.8261	19.6478	-0.278177	-0.203407	0.74675	0.9998
ENSG00000079156	ENSG00000079156	OSBPL6	2:179059207-179264160	OK	3.43955	3.18136	-0.112577	-0.156461	0.7469	0.9998
ENSG00000117614	ENSG00000117614	SYF2	1:25549169-25558993	OK	26.1543	24.6102	-0.0877895	-0.19173	0.74695	0.9998
ENSG00000164045	ENSG00000164045	CDC25A	3:48198635-48229892	OK	10.1617	9.40369	-0.111837	-0.175265	0.74695	0.9998
ENSG00000182612	ENSG00000182612	TSPAN10	17:79523912-79615779	OK	82.1339	91.6538	0.158216	0.202289	0.74695	0.9998
ENSG00000174007	ENSG00000174007	CEP19	3:196366556-196462878	OK	2.17141	2.72167	0.325855	0.176571	0.747	0.9998
ENSG00000256663	ENSG00000256663	RP11-424C20.2	12:20514665-20837315	OK	4.34948	3.67489	-0.243141	-0.221804	0.747	0.9998
ENSG00000205659	ENSG00000205659	LIN52	14:74551498-74667936	OK	7.05868	6.50388	-0.118098	-0.167958	0.74705	0.9998
ENSG00000270101	ENSG00000270101	RP11-24B19.3	13:51909908-52126500	OK	3.57676	2.65907	-0.427732	-0.211924	0.74705	0.9998
ENSG00000230880	ENSG00000230880	RP11-417J8.3	1:142618768-142729975	OK	2.40773	3.11811	0.373003	0.234144	0.7471	0.9998
ENSG00000100353	ENSG00000100353	EIF3D	22:36906896-36925483	OK	157.061	166.106	0.08078	0.189962	0.74715	0.9998
ENSG00000160271	ENSG00000160271	RALGDS	9:135973106-136039332	OK	23.0408	24.545	0.0912364	0.118258	0.7472	0.9998
ENSG00000153046	ENSG00000153046	CDYL	6:4706392-4955785	OK	51.4274	54.4491	0.0823727	0.189781	0.74725	0.9998
ENSG00000106948	ENSG00000106948	AKNA	9:117096435-117156685	OK	0.566374	0.634457	0.163766	0.130464	0.7473	0.9998
ENSG00000171425	ENSG00000171425	ZNF581	19:56146381-56164527	OK	20.0337	21.882	0.127313	0.200948	0.7473	0.9998
ENSG00000119812	ENSG00000119812	FAM98A	2:33808724-33824449	OK	59.3591	64.8942	0.12862	0.122958	0.74735	0.9998
ENSG00000154589	ENSG00000154589	LY96	8:74903586-74941322	OK	7.16388	6.48211	-0.144278	-0.193866	0.74735	0.9998
ENSG00000081692	ENSG00000081692	JMJD4	1:227916239-227968927	OK	21.3779	23.7772	0.153454	0.186353	0.7474	0.9998
ENSG00000119231	ENSG00000119231	SENP5	3:196594726-196661585	OK	15.8145	16.8406	0.0906984	0.130291	0.7474	0.9998
ENSG00000180479	ENSG00000180479	ZNF571	19:37988062-38210691	OK	1.11731	0.91101	-0.294491	-0.171066	0.7475	0.9998
ENSG00000204348	ENSG00000204348	DXO	6:31937586-31971298	OK	18.9518	17.5204	-0.113293	-0.201286	0.74755	0.9998
ENSG00000248092	ENSG00000248092	NNT-AS1	5:43571695-43707507	OK	18.6294	16.2725	-0.195145	-0.0928648	0.74755	0.9998
ENSG00000014164	ENSG00000014164	ZC3H3	8:144519824-144623623	OK	4.86531	5.20494	0.0973515	0.187501	0.7476	0.9998
ENSG00000134013	ENSG00000134013	LOXL2	8:23154701-23315208	OK	1.57284	1.90778	0.278528	0.090374	0.7476	0.9998
ENSG00000104356	ENSG00000104356	POP1	8:99129524-99172062	OK	8.85453	8.27214	-0.0981551	-0.176006	0.74775	0.9998
ENSG00000128266	ENSG00000128266	GNAZ	22:23401592-23487208	OK	1.54794	1.41955	-0.124924	-0.163645	0.7478	0.9998
ENSG00000267352	ENSG00000267352	SH3GL1P3	17:66121917-66148609	OK	1.89945	2.70428	0.509662	0.219779	0.7478	0.9998
ENSG00000155970	ENSG00000155970	MICU3	8:16884746-16980153	OK	2.47787	2.76684	0.15914	0.114159	0.74785	0.9998
ENSG00000175324	ENSG00000175324	LSM1	8:37962759-38070819	OK	44.9235	49.9304	0.152447	0.19553	0.74785	0.9998
ENSG00000099991	ENSG00000099991	CABIN1	22:24407641-24574596	OK	22.6339	24.1963	0.0962997	0.123279	0.7479	0.9998
ENSG00000141867	ENSG00000141867	BRD4	19:15347646-15443356	OK	15.5537	14.6518	-0.0861855	-0.140586	0.74795	0.9998
ENSG00000169032	ENSG00000169032	MAP2K1	15:66679154-66790151	OK	26.6278	28.9967	0.122955	0.199894	0.74795	0.9998
ENSG00000229413	ENSG00000229413	AC018638.1	7:128293739-128293989	OK	4.07093	4.75098	0.222866	0.192895	0.74795	0.9998
ENSG00000185641	ENSG00000185641	CTD-2287O16.1	5:115298150-115395815	OK	153.463	162.938	0.0864318	0.191043	0.748	0.9998
ENSG00000113580	ENSG00000113580	NR3C1	5:142657495-142815077	OK	7.20277	7.6825	0.0930228	0.182693	0.74805	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000259583	ENSG00000259583	RP11-66B24.4	15:101389765-101626271	OK	1.41591	1.94345	0.456892	0.149969	0.7481	0.9998
ENSG00000132740	ENSG00000132740	IGHMBP2	11:68671309-68708070	OK	11.48	10.4573	-0.134617	-0.151218	0.74815	0.9998
ENSG00000099797	ENSG00000099797	TECR	19:14625581-14676792	OK	95.5782	84.9548	-0.169987	-0.192374	0.74835	0.9998
ENSG00000101911	ENSG00000101911	PRPS2	X:12809473-12842341	OK	22.6664	24.2246	0.0959155	0.177869	0.74835	0.9998
ENSG00000108474	ENSG00000108474	PIGL	17:15879873-16256970	OK	5.99884	5.19349	-0.207981	-0.0805566	0.74835	0.9998
ENSG00000236859	ENSG00000236859	NIFK-AS1	2:122407225-122494499	OK	2.61427	1.98494	-0.397317	-0.207073	0.7485	0.9998
ENSG00000033178	ENSG00000033178	UBA6	4:68478369-68566897	OK	15.6998	13.727	-0.193728	-0.17663	0.74865	0.9998
ENSG00000162738	ENSG00000162738	VANGL2	1:160370375-160398468	OK	14.7794	15.6764	0.0849993	0.190611	0.74865	0.9998
ENSG00000084112	ENSG00000084112	SSH1	12:109176465-109251366	OK	73.009	78.0119	0.0956208	0.121546	0.7487	0.9998
ENSG00000099308	ENSG00000099308	MAST3	19:18169804-18262502	OK	2.57004	2.75434	0.0999196	0.147932	0.74895	0.9998
ENSG00000113569	ENSG00000113569	NUP155	5:37288238-37371283	OK	30.8681	29.0822	-0.0859788	-0.170707	0.749	0.9998
ENSG00000122033	ENSG00000122033	MTIF3	13:27998680-28024739	OK	48.7869	43.1908	-0.175771	-0.154106	0.749	0.9998
ENSG00000130208	ENSG00000130208	APOC1	19:45417503-45422606	OK	8.92108	8.09592	-0.140023	-0.166034	0.7491	0.9998
ENSG00000233554	ENSG00000233554	RP11-326F20.5	9:33104079-33179981	OK	0.521898	0.743046	0.509683	0.0995948	0.7491	0.9998
ENSG00000153944	ENSG00000153944	MSI2	17:55333211-55762046	OK	128.456	140.559	0.129905	0.166666	0.7492	0.9998
ENSG00000179387	ENSG00000179387	ELMOD2	4:141445311-141474924	OK	12.114	13.2989	0.13463	0.176449	0.74925	0.9998
ENSG00000104611	ENSG00000104611	SH2D4A	8:19171127-19253729	OK	4.33066	4.77834	0.141925	0.169385	0.74935	0.9998
ENSG00000240225	ENSG00000240225	ZNF542	19:56732680-56904914	OK	3.73391	4.14191	0.149609	0.167365	0.74945	0.9998
ENSG00000099341	ENSG00000099341	PSMD8	19:38865175-38874464	OK	162.449	171.766	0.0804528	0.190762	0.7495	0.9998
ENSG00000213096	ENSG00000213096	ZNF254	19:24216246-24312654	OK	2.50866	2.26976	-0.144376	-0.146351	0.74965	0.9998
ENSG00000179010	ENSG00000179010	MRFAP1	4:6641817-6644472	OK	128.287	121.813	-0.0747115	-0.189119	0.7497	0.9998
ENSG00000215548	ENSG00000215548	RP11-764K9.4	9:68427860-68455375	OK	2.02219	1.81235	-0.158056	-0.200485	0.7497	0.9998
ENSG00000240731	ENSG00000240731	RP5-890O3.9	1:1227755-1260071	OK	2.37045	3.51044	0.566493	0.100344	0.7497	0.9998
ENSG00000147140	ENSG00000147140	NONO	X:70503041-70521018	OK	214.769	228.826	0.0914668	0.176399	0.74975	0.9998
ENSG00000165175	ENSG00000165175	MID1IP1	X:38660684-38665790	OK	10.6727	11.375	0.091936	0.192183	0.74975	0.9998
ENSG00000134744	ENSG00000134744	ZCCHC11	1:52870235-53019159	OK	15.0731	13.8044	-0.126854	-0.144554	0.7498	0.9998
ENSG00000119669	ENSG00000119669	IRF2BPL	14:77490887-77495034	OK	15.7832	14.9086	-0.0822468	-0.195034	0.74985	0.9998
ENSG00000174093	ENSG00000174093	RP11-1407O15.2	17:36337710-36421858	OK	15.5817	14.5432	-0.0994989	-0.197278	0.74985	0.9998
ENSG00000204642	ENSG00000204642	HLA-F	6:29690551-29716826	OK	9.91848	10.9886	0.147817	0.182304	0.74985	0.9998
ENSG00000205476	ENSG00000205476	CCDC85C	14:99947505-100070363	OK	14.9946	16.2282	0.114059	0.154041	0.7499	0.9998
ENSG00000197006	ENSG00000197006	METTL9	16:21608538-21668794	OK	551.838	513.905	-0.102744	-0.181283	0.74995	0.9998
ENSG00000181126	ENSG00000181126	HLA-V	6:29758730-29765588	OK	1.48865	1.26086	-0.23959	-0.177557	0.75	0.9998
ENSG00000102901	ENSG00000102901	CENPT	16:67840667-67906470	OK	9.63925	8.53852	-0.174936	-0.150409	0.7501	0.9998
ENSG00000163918	ENSG00000163918	RFC4	3:186499568-186524847	OK	49.7052	39.0841	-0.346814	-0.167599	0.7501	0.9998
ENSG00000119328	ENSG00000119328	FAM206A	9:111696460-111775809	OK	11.0491	12.2911	0.153678	0.147259	0.75015	0.9998
ENSG00000229142	ENSG00000229142	HCG4P8	6:29794743-29798902	OK	1.27886	1.99396	0.640777	0.162255	0.75015	0.9998
ENSG00000266402	ENSG00000266402	SNORA76	17:62223329-62223836	OK	11.4297	8.73049	-0.388657	-0.154402	0.75015	0.9998
ENSG00000126432	ENSG00000126432	PRDX5	11:64085559-64089283	OK	258.727	273.45	0.0798439	0.193789	0.7502	0.9998
ENSG00000134444	ENSG00000134444	KIAA1468	18:59854490-59974355	OK	7.65657	8.27801	0.112586	0.150298	0.7502	0.9998
ENSG00000175826	ENSG00000175826	CTDNEP1	17:7143332-7167302	OK	52.7309	46.5013	-0.181377	-0.193585	0.75025	0.9998
ENSG00000052723	ENSG00000052723	SIKE1	1:115312099-115323306	OK	24.5395	21.5794	-0.18545	-0.176587	0.75035	0.9998
ENSG00000063854	ENSG00000063854	HAGH	16:1845620-1934295	OK	81.0142	74.2286	-0.126199	-0.204652	0.75035	0.9998
ENSG00000100422	ENSG00000100422	CERK	22:47080307-47134158	OK	113.358	107.134	-0.0814714	-0.137666	0.75035	0.9998
ENSG00000132964	ENSG00000132964	CDK8	13:26828275-26979375	OK	20.9059	19.5371	-0.0976917	-0.191912	0.75035	0.9998
ENSG00000164164	ENSG00000164164	OTUD4	4:145888263-146101313	OK	7.91237	8.71819	0.139919	0.132611	0.75045	0.9998
ENSG00000130338	ENSG00000130338	TULP4	6:158733691-158932860	OK	2.9933	3.20841	0.10012	0.196858	0.7505	0.9998
ENSG00000244270	ENSG00000244270	RPL32P29	14:50043389-50081390	OK	2.35867	3.43656	0.542993	0.0509412	0.7505	0.9998
ENSG00000260772	ENSG00000260772	RP11-311C24.1	16:69598996-69738569	OK	1.57452	2.20974	0.488967	0.248841	0.7505	0.9998
ENSG00000078687	ENSG00000078687	TNRC6C	17:76000248-76139049	OK	3.03458	3.65044	0.266574	0.0910116	0.75055	0.9998
ENSG00000131437	ENSG00000131437	KIF3A	5:132024372-132073330	OK	6.50328	7.09577	0.125792	0.157851	0.75055	0.9998
ENSG00000271769	ENSG00000271769	RP11-216P16.2	12:121406415-121454305	OK	0.445021	0.7326	0.719154	0.186892	0.75055	0.9998
ENSG00000158042	ENSG00000158042	MRPL17	11:6702012-6704632	OK	99.6046	92.446	-0.107601	-0.191289	0.7506	0.9998
ENSG00000109390	ENSG00000109390	NDUFC1	4:140187316-140397763	OK	103.704	91.3102	-0.183621	-0.1953	0.75065	0.9998
ENSG00000139116	ENSG00000139116	KIF21A	12:39687029-39837192	OK	13.1922	12.3312	-0.0973758	-0.163737	0.75065	0.9998
ENSG00000197463	ENSG00000197463	CSAG3	X:151876742-151883038	OK	1.83081	2.05554	0.167035	0.19212	0.75065	0.9998
ENSG00000223839	ENSG00000223839	FAM95B1	9:42368302-42474239	OK	2.30732	2.0876	-0.144371	-0.148928	0.7507	0.9998
ENSG00000133315	ENSG00000133315	MACROD1	11:63742078-63933578	OK	20.2328	24.2057	0.25865	0.104912	0.7508	0.9998
ENSG00000213859	ENSG00000213859	KCTD11	17:7255207-7258263	OK	1.12331	1.02535	-0.131644	-0.181094	0.75085	0.9998
ENSG00000240373	ENSG00000240373	SEC62-AS1	3:169657140-169716161	OK	0.893681	0.507091	-0.817517	-0.0626566	0.75085	0.9998
ENSG00000259207	ENSG00000259207	ITGB3	17:45331211-45518678	OK	16.2732	17.2547	0.0844945	0.19319	0.75085	0.9998
ENSG00000231789	ENSG00000231789	RP11-558F24.4	1:9711789-9884584	OK	10.0149	6.29887	-0.668982	-0.257051	0.7509	0.9998
ENSG00000226853	ENSG00000226853	AC010894.3	2:175352116-175353114	OK	1.65961	1.93434	0.220992	0.18855	0.75095	0.9998
ENSG00000258947	ENSG00000258947	TUBB3	16:89939999-90005169	OK	154.72	143.753	-0.106071	-0.1851	0.75095	0.9998
ENSG00000163002	ENSG00000163002	NUP35	2:183982240-184026408	OK	10.8608	10.1724	-0.0944654	-0.182919	0.75105	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000168710	ENSG00000168710	AHCYL1	1:110527307-110566357	OK	42.1228	39.7147	-0.0849293	-0.179012	0.75105	0.9998
ENSG00000122376	ENSG00000122376	FAM35A	10:88810242-88951225	OK	10.824	12.1793	0.170203	0.19317	0.75135	0.9998
ENSG00000254093	ENSG00000254093	PINX1	8:10581277-10697394	OK	22.5781	20.9121	-0.110588	-0.192622	0.75145	0.9998
ENSG00000230798	ENSG00000230798	RP4-792G4.2	1:63786554-63790797	OK	8.1881	7.07832	-0.210122	-0.195187	0.7515	0.9998
ENSG00000236287	ENSG00000236287	ZBED5	11:10830843-10928349	OK	17.6806	16.5745	-0.0932019	-0.168286	0.7515	0.9998
ENSG00000104725	ENSG00000104725	NEFL	8:24808467-24814624	OK	15.4332	14.5428	-0.0857321	-0.188337	0.75155	0.9998
ENSG00000197302	ENSG00000197302	ZNF720	16:31724549-31806190	OK	10.7621	9.59661	-0.165364	-0.19778	0.75155	0.9998
ENSG00000246067	ENSG00000246067	RAB30-AS1	11:82783107-82818003	OK	4.33133	4.84263	0.160982	0.196123	0.75155	0.9998
ENSG00000148341	ENSG00000148341	SH3GLB2	9:131683173-131790582	OK	39.3164	43.8625	0.157857	0.185902	0.75175	0.9998
ENSG00000198393	ENSG00000198393	ZNF26	12:133562950-133589154	OK	4.78024	4.31728	-0.14696	-0.180713	0.75175	0.9998
ENSG00000182359	ENSG00000182359	KBTBD3	11:105921824-105972702	OK	3.25392	2.56406	-0.343748	-0.13447	0.7519	0.9998
ENSG00000184381	ENSG00000184381	PLA2G6	22:38507501-38612518	OK	5.27175	4.68944	-0.168865	-0.103691	0.7519	0.9998
ENSG00000182117	ENSG00000182117	NOP10	15:34633916-34635378	OK	91.3655	96.8628	0.084292	0.19093	0.752	0.9998
ENSG00000234233	ENSG00000234233	KCNH1-IT1	1:210856554-211307457	OK	1.97374	3.07877	0.641423	0.299619	0.752	0.9998
ENSG00000118197	ENSG00000118197	DDX59	1:200593023-200663378	OK	14.3932	13.4557	-0.0971688	-0.180233	0.75215	0.9998
ENSG00000162636	ENSG00000162636	FAM102B	1:109102710-109187522	OK	3.17403	3.39033	0.0951101	0.192155	0.75215	0.9998
ENSG00000215712	ENSG00000215712	TMEM242	6:157710417-157744633	OK	3.07779	3.32181	0.110073	0.183483	0.75215	0.9998
ENSG00000154930	ENSG00000154930	ACSS1	20:24986867-25039616	OK	24.7523	26.1184	0.0775031	0.191867	0.7522	0.9998
ENSG00000262227	ENSG00000262227	RP5-1050D4.5	17:4891000-4900905	OK	0.636243	0.792607	0.317029	0.197695	0.7522	0.9998
ENSG00000241528	ENSG00000241528	RP1-130H16.16	22:30727976-30825045	OK	0.629513	0.421324	-0.579305	-0.0963176	0.75225	0.9998
ENSG00000101624	ENSG00000101624	CEP76	18:12438888-12725739	OK	5.45242	4.55688	-0.258851	-0.122336	0.7523	0.9998
ENSG00000143882	ENSG00000143882	ATP6V1C2	2:10861774-10978103	OK	0.644753	0.477628	-0.432859	-0.0397843	0.7523	0.9998
ENSG00000117500	ENSG00000117500	TMED5	1:93615298-93835055	OK	30.0716	27.2664	-0.141275	-0.176754	0.7525	0.9998
ENSG00000118894	ENSG00000118894	FAM86A	16:4932507-5147809	OK	8.03183	9.16232	0.189983	0.184166	0.7525	0.9998
ENSG00000173852	ENSG00000173852	DPY19L1	7:34968487-35077883	OK	20.5747	19.5336	-0.0749093	-0.165744	0.7525	0.9998
ENSG00000177700	ENSG00000177700	POLR2L	11:818901-842545	OK	308.071	333.955	0.116392	0.188592	0.7525	0.9998
ENSG00000186665	ENSG00000186665	C17orf58	17:65987216-65989765	OK	13.2937	12.4282	-0.0971326	-0.189592	0.75255	0.9998
ENSG00000185904	ENSG00000185904	LINC00839	10:42970990-42990784	OK	1.04907	1.15736	0.141728	0.190909	0.75265	0.9998
ENSG00000168140	ENSG00000168140	VASN	16:4364761-4475706	OK	4.17963	3.42862	-0.285747	-0.213103	0.75285	0.9998
ENSG00000126226	ENSG00000126226	PCID2	13:113831890-113919399	OK	30.7123	27.5088	-0.158922	-0.166149	0.75295	0.9998
ENSG00000146802	ENSG00000146802	TMEM168	7:112402436-112430647	OK	14.9748	16.0567	0.100639	0.163539	0.75295	0.9998
ENSG00000162616	ENSG00000162616	DNAJB4	1:78444858-78604133	OK	8.43499	9.18031	0.122155	0.182716	0.7531	0.9998
ENSG00000176619	ENSG00000176619	LMNB2	19:2389768-2456994	OK	38.0969	35.6679	-0.0950485	-0.156321	0.75315	0.9998
ENSG00000260054	ENSG00000260054	RP11-611L7.1	7:6694494-6696063	OK	11.7077	12.4867	0.0929304	0.186926	0.75315	0.9998
ENSG00000167513	ENSG00000167513	CDT1	16:88869620-88875666	OK	8.45931	7.6395	-0.147063	-0.178531	0.7532	0.9998
ENSG00000196470	ENSG00000196470	SIAH1	16:48198862-48482313	OK	7.90386	6.58816	-0.262681	-0.188413	0.7532	0.9998
ENSG00000047578	ENSG00000047578	KIAA0556	16:27561453-27791690	OK	10.9598	9.98551	-0.134307	-0.149932	0.75325	0.9998
ENSG00000226478	ENSG00000226478	UPF3AP1	17:16592850-16719854	OK	2.20187	1.97312	-0.158249	-0.189164	0.75325	0.9998
ENSG00000241362	ENSG00000241362	RPL36AP43	15:90207595-90234014	OK	0.945668	0.51381	-0.880097	-0.203051	0.75325	0.9998
ENSG00000070756	ENSG00000070756	PABPC1	8:101698043-101735037	OK	341.366	362.966	0.0885137	0.162385	0.7534	0.9998
ENSG00000168096	ENSG00000168096	ANKS3	16:4746512-4817625	OK	5.75488	5.27558	-0.125456	-0.140985	0.75345	0.9998
ENSG00000162813	ENSG00000162813	BPNT1	1:220230823-220263804	OK	28.2622	26.1287	-0.113235	-0.1813	0.7535	0.9998
ENSG00000188917	ENSG00000188917	TRMT2B	X:100264334-100351353	OK	8.60345	8.02305	-0.100765	-0.186043	0.7535	0.9998
ENSG00000127616	ENSG00000127616	SMARCA4	19:11071597-11176071	OK	47.9776	45.4206	-0.0790148	-0.150144	0.75355	0.9998
ENSG00000103174	ENSG00000103174	NAGPA	16:4932507-5147809	OK	10.8192	11.9543	0.143934	0.146639	0.7536	0.9998
ENSG00000131148	ENSG00000131148	EMC8	16:85805363-85840650	OK	16.6712	14.1527	-0.236277	-0.137536	0.7536	0.9998
ENSG00000059377	ENSG00000059377	TBXAS1	7:139246315-139720125	OK	1.40818	1.6761	0.25127	0.0517115	0.75365	0.9998
ENSG00000114982	ENSG00000114982	KANSL3	2:97258906-97370624	OK	15.9886	16.906	0.0804886	0.147915	0.7537	0.9998
ENSG00000110171	ENSG00000110171	TRIM3	11:6469842-6495689	OK	18.4776	20.0436	0.117363	0.171633	0.75375	0.9998
ENSG00000054611	ENSG00000054611	TBC1D22A	22:47158517-47571336	OK	14.7278	13.7487	-0.0992526	-0.189105	0.7538	0.9998
ENSG00000157881	ENSG00000157881	PANK4	1:2439971-2458039	OK	12.0392	12.8277	0.0915191	0.154892	0.75405	0.9998
ENSG00000099399	ENSG00000099399	MAGEB2	X:30233676-30238206	OK	95.5421	90.6646	-0.0755965	-0.187563	0.7541	0.9998
ENSG00000173660	ENSG00000173660	UQCRH	1:46769302-46782448	OK	531.117	503.221	-0.0778384	-0.193573	0.7541	0.9998
ENSG00000170836	ENSG00000170836	PPM1D	17:58677543-58741849	OK	7.09971	7.55689	0.0900334	0.186803	0.75415	0.9998
ENSG00000269888	ENSG00000269888	RP11-3P17.5	3:161144214-161166030	OK	7.42647	10.5844	0.511194	0.0668303	0.7542	0.9998
ENSG00000105855	ENSG00000105855	ITGB8	7:20367921-20455377	OK	19.6377	20.8641	0.0873956	0.184375	0.75445	0.9998
ENSG00000241081	ENSG00000241081	RP11-488C13.1	14:77352719-77353093	OK	2.06626	2.40842	0.221066	0.200262	0.75445	0.9998
ENSG00000139546	ENSG00000139546	TARBP2	12:53893945-53900215	OK	37.3448	35.1117	-0.088957	-0.185709	0.7545	0.9998
ENSG00000144445	ENSG00000144445	KANSL1L	2:210867288-211036115	OK	6.12075	5.37579	-0.187232	-0.145761	0.7545	0.9998
ENSG00000169239	ENSG00000169239	CA5B	X:15693054-15805747	OK	2.4498	2.7728	0.178675	0.127281	0.75455	0.9998
ENSG00000196951	ENSG00000196951	RP11-425I13.3	4:141178439-141306880	OK	2.5469	1.73724	-0.551947	-0.103847	0.75455	0.9998
ENSG00000198862	ENSG00000198862	LTN1	21:30300465-30365270	OK	4.14481	4.40557	0.0880222	0.145381	0.7546	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000008083	ENSG00000008083	JARID2	6:15246526-15522252	OK	38.7651	40.8872	0.0768909	0.181262	0.75475	0.9998
ENSG00000177728	ENSG00000177728	KIAA0195	17:73437239-73496171	OK	39.2311	36.2713	-0.113171	-0.149632	0.75485	0.9998
ENSG00000132952	ENSG00000132952	USPL1	13:31191829-31233686	OK	7.74082	7.22291	-0.0999056	-0.193275	0.75495	0.9998
ENSG00000247993	ENSG00000247993	RP11-79P5.2	5:72740653-72744352	OK	3.55931	2.83926	-0.326083	-0.200958	0.755	0.9998
ENSG00000198498	ENSG00000198498	TMA16	4:164415593-164441691	OK	16.5961	15.2726	-0.119901	-0.187063	0.7552	0.9998
ENSG00000259343	ENSG00000259343	RP11-761I4.3	15:81616717-81666554	OK	17.3801	18.8255	0.115251	0.187491	0.7552	0.9998
ENSG00000183814	ENSG00000183814	LIN9	1:226418849-226497570	OK	5.30523	4.95329	-0.0990267	-0.18807	0.75525	0.9998
ENSG00000121716	ENSG00000121716	PILRB	7:99905324-99997719	OK	14.4694	13.0561	-0.148282	-0.189017	0.75535	0.9998
ENSG00000182606	ENSG00000182606	TRAK1	3:42055293-42267381	OK	17.1396	18.1692	0.0841585	0.185416	0.75535	0.9998
ENSG00000120805	ENSG00000120805	ARL1	12:101786897-101801598	OK	51.2235	47.9989	-0.0938059	-0.183086	0.75545	0.9998
ENSG00000244754	ENSG00000244754	N4BP2L2	13:32974860-33112970	OK	30.74	28.6346	-0.102353	-0.162946	0.75545	0.9998
ENSG00000257379	ENSG00000257379	RP11-793H13.8	12:53835388-53893847	OK	1.76961	1.20425	-0.5553	-0.0893027	0.75545	0.9998
ENSG00000272851	ENSG00000272851	RP11-801F7.1	2:208576263-208626563	OK	0.60303	1.14617	0.926523	0.231793	0.75545	0.9998
ENSG00000123353	ENSG00000123353	ORMDL2	12:56137063-56236750	OK	57.1542	50.8822	-0.167696	-0.182193	0.7555	0.9998
ENSG00000012171	ENSG00000012171	SEMA3B	3:50304989-50314977	OK	7.51838	6.93664	-0.116186	-0.182661	0.75575	0.9998
ENSG00000163138	ENSG00000163138	PACRGL	4:20697904-21950422	OK	10.644	9.87671	-0.107944	-0.166579	0.75575	0.9998
ENSG00000215022	ENSG00000215022	RP1-257A7.4	6:12717892-13328815	OK	1.32928	1.77695	0.418754	0.0519862	0.75575	0.9998
ENSG00000132142	ENSG00000132142	ACACA	17:35441922-35766909	OK	18.6138	20.2818	0.123814	0.131867	0.75585	0.9998
ENSG00000138668	ENSG00000138668	HNRNPD	4:83273650-83305180	OK	107.234	101.305	-0.082067	-0.18543	0.75585	0.9998
ENSG00000226363	ENSG00000226363	AC009336.24	2:177037922-177055688	OK	1.77927	2.9961	0.751797	0.304071	0.75585	0.9998
ENSG00000105397	ENSG00000105397	TYK2	19:10461208-10491352	OK	41.0957	38.1743	-0.106383	-0.14927	0.7559	0.9998
ENSG00000205423	ENSG00000205423	CNEP1R1	16:50058320-50070999	OK	6.53495	6.05799	-0.109337	-0.166628	0.7559	0.9998
ENSG00000265415	ENSG00000265415	CTD-2510F5.4	17:57232859-57292608	OK	16.1358	9.61027	-0.747618	-0.220204	0.75595	0.9998
ENSG00000185710	ENSG00000185710	RP11-645C24.2	16:21845889-21930477	OK	2.88038	2.51958	-0.193078	-0.186939	0.756	0.9998
ENSG00000185043	ENSG00000185043	CIB1	15:90773206-90785315	OK	38.6415	36.4786	-0.0831006	-0.188343	0.75605	0.9998
ENSG00000198898	ENSG00000198898	CAPZA2	7:116451123-116562103	OK	143.526	152.618	0.0886069	0.18512	0.75605	0.9998
ENSG00000133812	ENSG00000133812	SBF2	11:9776316-10315754	OK	15.4711	14.5139	-0.092146	-0.121512	0.7562	0.9998
ENSG00000232460	ENSG00000232460	BMPR1APS2	11:121232558-121233574	OK	1.60944	1.78659	0.150649	0.191819	0.7564	0.9998
ENSG00000164465	ENSG00000164465	DCBLD1	6:117609462-117923691	OK	2.83429	3.1461	0.150578	0.1161	0.75645	0.9998
ENSG00000182318	ENSG00000182318	ZSCAN22	19:58838384-58853698	OK	2.02853	1.8854	-0.105565	-0.19026	0.75645	0.9998
ENSG00000239257	ENSG00000239257	RPL23AP1	6:29690551-29716826	OK	1.75448	3.2257	0.878569	0.301206	0.7565	0.9998
ENSG00000234197	ENSG00000234197	ETV5-AS1	3:185764096-186080026	OK	0.501288	0.74282	0.567373	0.0264295	0.75655	0.9998
ENSG00000039650	ENSG00000039650	PNKP	19:50364460-50371166	OK	18.6011	17.4832	-0.0894248	-0.162065	0.7569	0.9998
ENSG00000254198	ENSG00000254198	RP11-598P20.3	8:42981137-42981540	OK	2.96372	2.60084	-0.188428	-0.188746	0.7569	0.9998
ENSG00000107819	ENSG00000107819	SFXN3	10:102790990-102800998	OK	69.382	65.2733	-0.0880692	-0.152693	0.75695	0.9998
ENSG00000269194	ENSG00000269194	AC006942.4	19:50270224-50320633	OK	1.79588	1.23431	-0.540985	-0.081308	0.75695	0.9998
ENSG00000089693	ENSG00000089693	MLF2	12:6857169-6880116	OK	114.752	122.791	0.0976826	0.185466	0.757	0.9998
ENSG00000091436	ENSG00000091436	MLTK	2:173940162-174146764	OK	11.0209	10.2938	-0.0984656	-0.182814	0.757	0.9998
ENSG00000160007	ENSG00000160007	ARHGAP35	19:47421932-47508334	OK	16.9589	17.8589	0.0745986	0.161939	0.757	0.9998
ENSG00000079819	ENSG00000079819	EPB41L2	6:131160486-131384462	OK	13.3837	14.1988	0.0852945	0.1319	0.7571	0.9998
ENSG00000107862	ENSG00000107862	GBF1	10:104005288-104142656	OK	20.5016	19.4291	-0.0775205	-0.169527	0.7571	0.9998
ENSG00000114062	ENSG00000114062	UBE3A	15:25497371-25684128	OK	35.1467	37.1658	0.0805845	0.188884	0.7572	0.9998
ENSG00000242156	ENSG00000242156	AC000041.8	22:29723668-29819182	OK	12.2236	8.30517	-0.557587	-0.054217	0.7572	0.9998
ENSG00000235454	ENSG00000235454	RP11-678B3.2	7:53929925-53931032	OK	0.58215	0.661898	0.185217	0.18208	0.75735	0.9998
ENSG00000100348	ENSG00000100348	TXN2	22:36863082-36878077	OK	91.388	96.9597	0.0853806	0.189844	0.75755	0.9998
ENSG00000104626	ENSG00000104626	ERI1	8:8859656-8974256	OK	8.98577	9.56128	0.0895624	0.162235	0.75755	0.9998
ENSG00000171161	ENSG00000171161	ZNF672	1:249132408-249143716	OK	14.8029	15.6218	0.077681	0.172414	0.7576	0.9998
ENSG00000188997	ENSG00000188997	KCTD21	11:77850816-77925757	OK	5.7179	6.34967	0.151197	0.135078	0.7576	0.9998
ENSG00000104154	ENSG00000104154	SLC30A4	15:45722726-45878488	OK	1.59726	1.34521	-0.247774	-0.178201	0.75765	0.9998
ENSG00000213920	ENSG00000213920	MDP1	14:24641061-24708448	OK	21.4247	17.6114	-0.282769	-0.111445	0.75765	0.9998
ENSG00000184465	ENSG00000184465	WDR27	6:169857306-170102159	OK	13.6561	12.4722	-0.130831	-0.175909	0.75775	0.9998
ENSG00000163482	ENSG00000163482	STK36	2:219528586-219567439	OK	9.46359	10.6214	0.166513	0.153853	0.7578	0.9998
ENSG00000004838	ENSG00000004838	ZMYND10	3:50378536-50384283	OK	0.807627	0.705788	-0.194453	-0.135674	0.75785	0.9998
ENSG00000149600	ENSG00000149600	COMMD7	20:31290492-31331803	OK	40.4259	42.7312	0.0800103	0.18509	0.75785	0.9998
ENSG00000136732	ENSG00000136732	GYPC	2:127413508-127454246	OK	409.245	431.742	0.077203	0.186392	0.7579	0.9998
ENSG00000239335	ENSG00000239335	RP11-745O10.2	12:66516841-66563852	OK	1.03399	0.707265	-0.547895	-0.0838858	0.7579	0.9998
ENSG00000140718	ENSG00000140718	FTO	16:53737874-54155853	OK	14.6264	13.4763	-0.118143	-0.184936	0.75795	0.9998
ENSG00000248583	ENSG00000248583	RP11-241F15.1	4:49488942-49491571	OK	2.26221	2.52558	0.158881	0.187659	0.75795	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000066697	ENSG00000066697	MSANTD3	9:103189437-103339918	OK	75.1139	79.8779	0.0887176	0.187285	0.758	0.9998
ENSG00000226396	ENSG00000226396	RPS14P3	1:19923472-19984945	OK	1.3722	1.90019	0.46965	0.0395546	0.75805	0.9998
ENSG00000256745	ENSG00000256745	RP11-680H20.1	11:93921614-93922163	OK	12.5135	11.5584	-0.114537	-0.18503	0.7581	0.9998
ENSG00000137494	ENSG00000137494	ANKRD42	11:82868029-83134559	OK	2.00921	2.35692	0.230275	0.147382	0.75815	0.9998
ENSG00000185104	ENSG00000185104	FAF1	1:50905149-51425935	OK	31.8015	29.8716	-0.0903217	-0.183504	0.7582	0.9998
ENSG00000229833	ENSG00000229833	PET100	19:7694622-7712759	OK	49.0089	45.4407	-0.109058	-0.174127	0.7584	0.9998
ENSG00000089123	ENSG00000089123	TASP1	20:13202417-13619587	OK	2.2934	2.55262	0.154487	0.159564	0.75845	0.9998
ENSG00000113734	ENSG00000113734	BNIP1	5:172571164-172591390	OK	12.193	13.0673	0.0999112	0.192821	0.75845	0.9998
ENSG00000111860	ENSG00000111860	CEP85L	6:118781934-119031238	OK	2.37738	2.13876	-0.152597	-0.140581	0.7586	0.9998
ENSG00000124257	ENSG00000124257	NEURL2	20:44517263-44540794	OK	1.54386	2.13594	0.468332	0.0648393	0.7587	0.9998
ENSG00000172732	ENSG00000172732	MUS81	11:65590492-65641063	OK	23.8336	19.8568	-0.263364	-0.0987607	0.7587	0.9998
ENSG00000234996	ENSG00000234996	RP11-480I12.7	1:202830881-202844369	OK	0.69839	0.615932	-0.181263	-0.187026	0.7587	0.9998
ENSG00000138709	ENSG00000138709	LARP1B	4:128982422-129144086	OK	3.9913	3.70015	-0.109273	-0.185661	0.75875	0.9998
ENSG00000169592	ENSG00000169592	INO80E	16:30003644-30034591	OK	37.8238	34.6244	-0.127503	-0.185908	0.75875	0.9998
ENSG00000062650	ENSG00000062650	WAPAL	10:88195012-88281572	OK	14.391	15.3985	0.0976231	0.145812	0.7588	0.9998
ENSG00000173221	ENSG00000173221	GLRX	5:95036952-95160087	OK	18.61	23.3387	0.326641	0.203642	0.7588	0.9998
ENSG00000272579	ENSG00000272579	RP11-101E13.5	1:192981379-193060907	OK	8.8448	10.8075	0.289124	0.129044	0.7588	0.9998
ENSG00000114745	ENSG00000114745	GORASP1	3:39093488-39180394	OK	29.5207	31.6438	0.100195	0.126564	0.75895	0.9998
ENSG00000164022	ENSG00000164022	AIMP1	4:106962755-107270383	OK	29.5194	26.7724	-0.140917	-0.182009	0.75895	0.9998
ENSG00000168038	ENSG00000168038	ULK4	3:41236327-42003922	OK	3.28061	2.77835	-0.239737	-0.0177543	0.759	0.9998
ENSG00000080802	ENSG00000080802	CNOT4	7:135046546-135194875	OK	10.607	11.2819	0.0889877	0.184368	0.75915	0.9998
ENSG00000130311	ENSG00000130311	DDA1	19:17402939-17445638	OK	49.7531	56.4463	0.182091	0.187164	0.75915	0.9998
ENSG00000171984	ENSG00000171984	C20orf196	20:5731038-5844558	OK	2.37332	2.66005	0.164545	0.174837	0.7592	0.9998
ENSG00000184436	ENSG00000184436	THAP7	22:21353392-21399306	OK	18.5946	20.4266	0.135566	0.196153	0.7592	0.9998
ENSG00000185019	ENSG00000185019	UBOX5	20:3087558-3140842	OK	1.48817	1.27828	-0.219332	-0.17119	0.7593	0.9998
ENSG00000272447	ENSG00000272447	RP11-182L21.6	10:81563812-81587358	OK	0.673327	0.500877	-0.426849	-0.213993	0.7594	0.9998
ENSG00000111142	ENSG00000111142	METAP2	12:95867295-95909615	OK	70.2972	74.03	0.0746442	0.155696	0.75955	0.9998
ENSG00000114698	ENSG00000114698	PLSCR4	3:145910125-145968966	OK	3.29947	3.5749	0.115666	0.165429	0.75955	0.9998
ENSG00000132005	ENSG00000132005	RFX1	19:14072349-14117851	OK	2.38646	2.58955	0.11783	0.127697	0.75955	0.9998
ENSG00000167671	ENSG00000167671	UBXN6	19:4402658-4457819	OK	42.0032	45.3621	0.110988	0.171749	0.7596	0.9998
ENSG00000197157	ENSG00000197157	SND1	7:127292233-127732661	OK	155.303	163.314	0.0725595	0.154255	0.7596	0.9998
ENSG00000224046	ENSG00000224046	AC005076.5	7:86780738-86849903	OK	0.706611	0.979417	0.471007	0.0809326	0.7596	0.9998
ENSG00000266835	ENSG00000266835	RP11-838N2.4	18:3466247-3478976	OK	9.05572	8.21066	-0.141331	-0.194632	0.7596	0.9998
ENSG00000103145	ENSG00000103145	HCFC1R1	16:3072620-3089134	OK	89.3036	82.9138	-0.107107	-0.196793	0.75975	0.9998
ENSG00000077809	ENSG00000077809	GTF2I	7:74071993-74306731	OK	112.032	121.676	0.11914	0.17679	0.7598	0.9998
ENSG00000175898	ENSG00000175898	CTD-2369P2.2	19:10244020-10341962	OK	3.55216	4.64483	0.386929	0.188437	0.75985	0.9998
ENSG00000143149	ENSG00000143149	ALDH9A1	1:165631452-165679205	OK	57.3125	54.3211	-0.0773368	-0.18107	0.7599	0.9998
ENSG00000268549	ENSG00000268549	RP11-295P9.8	10:13628926-14504141	OK	0.879738	1.49394	0.76398	0.23021	0.7599	0.9998
ENSG00000116863	ENSG00000116863	ADPRHL2	1:36554475-36559533	OK	12.0185	11.2959	-0.0894508	-0.182839	0.76005	0.9998
ENSG00000177663	ENSG00000177663	IL17RA	22:17565843-17596583	OK	4.00393	4.5588	0.187238	0.165993	0.76005	0.9998
ENSG00000100416	ENSG00000100416	TRMU	22:46726771-46753237	OK	31.8954	33.8487	0.0857522	0.182271	0.76045	0.9998
ENSG00000233994	ENSG00000233994	GDI2P2	1:71547006-72748417	OK	1.44395	1.20675	-0.258894	-0.189724	0.76045	0.9998
ENSG00000225302	ENSG00000225302	RP11-539I5.1	10:118592511-118886097	OK	1.85052	1.26011	-0.554378	-0.148331	0.76055	0.9998
ENSG00000090060	ENSG00000090060	PAPOLA	14:96967146-97033448	OK	104.34	97.5516	-0.0970602	-0.175263	0.76065	0.9998
ENSG00000185339	ENSG00000185339	TCN2	22:30972611-31023265	OK	6.92989	8.6402	0.318232	0.225871	0.76065	0.9998
ENSG00000142556	ENSG00000142556	ZNF614	19:52516017-52533493	OK	2.07714	1.93415	-0.102902	-0.16318	0.7608	0.9998
ENSG00000101335	ENSG00000101335	MYL9	20:34894257-35274619	OK	1.52831	2.15471	0.495553	0.103462	0.76095	0.9998
ENSG00000196812	ENSG00000196812	ZSCAN16	6:28089572-28107456	OK	1.94623	2.16733	0.15524	0.191121	0.76095	0.9998
ENSG00000177788	ENSG00000177788	RP5-1061H20.4	1:229394027-229441641	OK	1.94629	1.26966	-0.616281	-0.121847	0.761	0.9998
ENSG00000141646	ENSG00000141646	SMAD4	18:48494360-48611415	OK	38.2992	34.7273	-0.141241	-0.18619	0.7611	0.9998
ENSG00000162086	ENSG00000162086	ZNF75A	16:3313742-3368852	OK	6.87518	7.77287	0.17705	0.144253	0.7611	0.9998
ENSG00000151151	ENSG00000151151	IPMK	10:59951277-60027694	OK	1.85491	1.73017	-0.100432	-0.182925	0.76115	0.9998
ENSG00000273149	ENSG00000273149	RP11-290D2.6	13:45911007-45965872	OK	0.676752	1.15174	0.767122	0.0232245	0.7613	0.9998
ENSG00000065615	ENSG00000065615	CYB5R4	6:84569361-84677143	OK	12.3527	11.1365	-0.14953	-0.179522	0.7615	0.9998
ENSG00000101052	ENSG00000101052	IFT52	20:42219570-42275936	OK	25.8424	24.4672	-0.0788867	-0.14476	0.76155	0.9998
ENSG00000237732	ENSG00000237732	AC010980.2	2:223181960-223217708	OK	0.751535	0.872019	0.214519	0.127553	0.76155	0.9998
ENSG00000107443	ENSG00000107443	CCNJ	10:97471535-97849995	OK	4.26666	4.90349	0.2007	0.186066	0.7616	0.9998
ENSG00000161013	ENSG00000161013	MGAT4B	5:179224596-179334859	OK	165.045	147.106	-0.166012	-0.123418	0.76165	0.9998
ENSG00000100003	ENSG00000100003	SEC14L2	22:30727976-30825045	OK	8.18018	10.0405	0.295621	0.143258	0.76185	0.9998
ENSG00000105613	ENSG00000105613	MAST1	19:12873816-12985765	OK	8.39635	6.39937	-0.391833	-0.166587	0.76195	0.9998
ENSG00000141252	ENSG00000141252	VPS53	17:406410-624957	OK	27.5751	24.89	-0.147796	-0.161529	0.76195	0.9998
ENSG00000232995	ENSG00000232995	RP11-267N12.3	1:163080910-163325554	OK	2.16563	1.79665	-0.269479	-0.0707358	0.76195	0.9998
ENSG00000105997	ENSG00000105997	HOXA3	7:27145802-27197555	OK	1.64955	1.41361	-0.222689	-0.127278	0.762	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000196123	ENSG00000196123	KIAA0895L	16:67204056-67217943	OK	4.18653	4.61851	0.141674	0.152839	0.7621	0.9998
ENSG00000273261	ENSG00000273261	RP11-531F16.4	3:182511287-182639726	OK	0.645415	0.418009	-0.626693	-0.0764643	0.7622	0.9998
ENSG00000121848	ENSG00000121848	RNF115	1:145611035-145715614	OK	32.4795	29.8258	-0.122967	-0.169069	0.76225	0.9998
ENSG00000198648	ENSG00000198648	STK39	2:168810529-169104651	OK	16.147	17.0632	0.0796176	0.181698	0.76225	0.9998
ENSG00000141741	ENSG00000141741	MIEN1	17:37827374-37887040	OK	61.718	66.0919	0.0987809	0.184065	0.76235	0.9998
ENSG00000239884	ENSG00000239884	RN7SL608P	17:2496503-2588909	OK	1.64771	1.07773	-0.612471	-0.0609141	0.76235	0.9998
ENSG00000166887	ENSG00000166887	VPS39	15:42450898-42500514	OK	11.5721	10.9846	-0.0751661	-0.134139	0.76245	0.9998
ENSG00000213420	ENSG00000213420	GPC2	7:99767228-99774995	OK	3.8692	4.31345	0.156809	0.194294	0.76245	0.9998
ENSG00000125247	ENSG00000125247	TMTC4	13:101256180-101327347	OK	11.3973	12.2708	0.10654	0.163286	0.76255	0.9998
ENSG00000155858	ENSG00000155858	LSM11	5:157170702-157187717	OK	3.24151	3.04303	-0.0911585	-0.18529	0.76255	0.9998
ENSG00000159210	ENSG00000159210	SNF8	17:47006677-47022479	OK	178.139	189.448	0.0888003	0.185459	0.76255	0.9998
ENSG00000213625	ENSG00000213625	LEPROT	1:65886247-66107242	OK	17.7118	19.0614	0.105939	0.115957	0.76255	0.9998
ENSG00000162746	ENSG00000162746	FCRLB	1:161691352-161697933	OK	0.959931	0.874977	-0.133686	-0.158038	0.7626	0.9998
ENSG00000269690	ENSG00000269690	AC096677.1	1:201592012-201853422	OK	6.41546	4.37341	-0.552794	-0.133164	0.7626	0.9998
ENSG00000228175	ENSG00000228175	GEMIN8P4	1:90459151-90459880	OK	1.31061	1.16043	-0.175577	-0.177801	0.76275	0.9998
ENSG00000224424	ENSG00000224424	PRKAR2A-AS1	3:48782029-48889414	OK	0.600003	0.79046	0.397723	0.0687258	0.7628	0.9998
ENSG00000101181	ENSG00000101181	MTG2	20:60758084-60778624	OK	27.4502	25.3121	-0.116989	-0.184879	0.76285	0.9998
ENSG00000145782	ENSG00000145782	ATG12	5:115163892-115249778	OK	22.0463	19.38	-0.185971	-0.177238	0.76285	0.9998
ENSG00000152642	ENSG00000152642	GPD1L	3:32147180-32210205	OK	13.8217	14.5849	0.077537	0.155698	0.7629	0.9998
ENSG00000183513	ENSG00000183513	COA5	2:99215772-99224978	OK	25.132	23.0967	-0.121838	-0.188378	0.76305	0.9998
ENSG00000083896	ENSG00000083896	YTHDC1	4:69176104-69215807	OK	21.1045	19.9156	-0.0836563	-0.147432	0.76315	0.9998
ENSG00000105723	ENSG00000105723	GSK3A	19:42734337-42759309	OK	38.0393	35.1723	-0.113054	-0.18492	0.76335	0.9998
ENSG00000156170	ENSG00000156170	NDUFAF6	8:95825538-96128683	OK	19.5536	16.577	-0.238251	-0.189911	0.7634	0.9998
ENSG00000273154	ENSG00000273154	RP4-583P15.15	20:62289162-62374858	OK	1.07929	0.644755	-0.743255	-0.211452	0.7635	0.9998
ENSG00000188690	ENSG00000188690	UROS	10:127477145-127511817	OK	73.0075	77.0595	0.0779278	0.180711	0.76355	0.9998
ENSG00000260809	ENSG00000260809	CTD-2144E22.10	16:34324871-34339205	OK	1.24979	1.13407	-0.140183	-0.180582	0.76355	0.9998
ENSG00000095906	ENSG00000095906	NUBP2	16:1823207-1844972	OK	44.8976	41.8559	-0.10121	-0.177808	0.7636	0.9998
ENSG00000231663	ENSG00000231663	RP5-827C21.4	1:234507931-234519795	OK	0.498427	0.731504	0.553482	0.0793072	0.7636	0.9998
ENSG00000148335	ENSG00000148335	NTMT1	9:132371162-132398209	OK	45.264	48.1894	0.0903528	0.191157	0.7637	0.9998
ENSG00000157514	ENSG00000157514	TSC22D3	X:106956450-107020572	OK	22.0407	20.8442	-0.0805256	-0.164137	0.7638	0.9998
ENSG00000170271	ENSG00000170271	FAXDC2	5:154198050-154256353	OK	4.44989	3.97896	-0.16138	-0.127707	0.76385	0.9998
ENSG00000213881	ENSG00000213881	NPM1P6	8:61969716-62627155	OK	1.1345	1.6484	0.539013	0.100605	0.76385	0.9998
ENSG00000241127	ENSG00000241127	YAE1D1	7:39605974-39649919	OK	22.4545	20.9952	-0.0969481	-0.1787	0.76385	0.9998
ENSG00000112367	ENSG00000112367	FIG4	6:110012498-110146631	OK	10.3954	9.79966	-0.0851392	-0.166028	0.7639	0.9998
ENSG00000231185	ENSG00000231185	AC005592.2	5:141689991-142077617	OK	3.88739	3.06166	-0.344486	-0.10386	0.7639	0.9998
ENSG00000176371	ENSG00000176371	ZSCAN2	15:85144216-85171027	OK	7.09634	6.4477	-0.138292	-0.176003	0.76395	0.9998
ENSG00000125821	ENSG00000125821	DTD1	20:18568536-18744561	OK	26.4598	27.9742	0.0802951	0.178898	0.764	0.9998
ENSG00000235437	ENSG00000235437	RP11-357C3.3	X:62563105-62780951	OK	12.0418	13.3356	0.147233	0.167833	0.7642	0.9998
ENSG00000131795	ENSG00000131795	RBM8A	1:145475981-145516076	OK	122.707	133.066	0.116927	0.181952	0.76435	0.9998
ENSG00000250474	ENSG00000250474	WBP1LP2	7:107220001-107269943	OK	1.21553	0.801588	-0.600656	-0.114921	0.76435	0.9998
ENSG00000249709	ENSG00000249709	ZNF564	19:12490002-12750912	OK	2.41192	2.70885	0.167495	0.158215	0.7644	0.9998
ENSG00000125652	ENSG00000125652	ALKBH7	19:6372443-6375042	OK	41.3594	44.0067	0.0895055	0.179861	0.7645	0.9998
ENSG00000177463	ENSG00000177463	NR2C2	3:14860468-15106842	OK	12.4994	10.7888	-0.212317	-0.141484	0.7646	0.9998
ENSG00000197608	ENSG00000197608	ZNF841	19:52534631-52599018	OK	3.15421	2.91184	-0.115348	-0.152391	0.7646	0.9998
ENSG00000145088	ENSG00000145088	EAF2	3:121554029-121605373	OK	1.54087	1.38778	-0.150971	-0.16054	0.76465	0.9998
ENSG00000156256	ENSG00000156256	USP16	21:30396575-30426809	OK	10.6355	10.0363	-0.0836545	-0.17058	0.7647	0.9998
ENSG00000138081	ENSG00000138081	FBXO11	2:47922668-48134949	OK	17.9835	16.5848	-0.116808	-0.158442	0.76475	0.9998
ENSG00000215861	ENSG00000215861	WI2-1896O14.1	1:144676873-144679969	OK	1.26609	1.49588	0.240622	0.198681	0.76475	0.9998
ENSG00000257551	ENSG00000257551	HLA-AS1	1:221006104-221058401	OK	0.474642	0.751533	0.662997	0.133563	0.76475	0.9998
ENSG00000178149	ENSG00000178149	DALRD3	3:48955220-49060928	OK	28.7225	33.1331	0.206089	0.155171	0.76485	0.9998
ENSG00000225630	ENSG00000225630	MTND2P28	1:536815-660283	OK	201.996	222.835	0.141647	0.187106	0.7649	0.9998
ENSG00000163866	ENSG00000163866	SMIM12	1:35178337-35325417	OK	26.3117	28.1353	0.0966767	0.180243	0.76495	0.9998
ENSG00000182899	ENSG00000182899	RPL35A	3:197615945-197687013	OK	1587.02	1673.8	0.0767997	0.179904	0.76495	0.9998
ENSG00000269399	ENSG00000269399	CTD-3222D19.7	19:16589867-16771253	OK	0.674272	0.520274	-0.374059	-0.0633732	0.76495	0.9998
ENSG00000126882	ENSG00000126882	FAM78A	9:134133462-134151934	OK	4.45334	4.76062	0.0962617	0.172607	0.765	0.9998
ENSG00000263136	ENSG00000263136	PAGR1	16:29817426-29859355	OK	12.8531	9.75122	-0.398457	-0.199562	0.7651	0.9998
ENSG00000120727	ENSG00000120727	PAIP2	5:138677275-138720242	OK	105.89	100.467	-0.0758449	-0.180428	0.76515	0.9998
ENSG00000136156	ENSG00000136156	ITM2B	13:48807293-48837063	OK	75.9498	70.9373	-0.0985023	-0.181573	0.7652	0.9998
ENSG00000137996	ENSG00000137996	RTCA	1:100731762-100758325	OK	31.5682	29.7741	-0.0844122	-0.182829	0.76525	0.9998
ENSG00000164934	ENSG00000164934	DCAF13	8:104410862-104455681	OK	45.3267	41.5464	-0.125639	-0.176811	0.76525	0.9998
ENSG00000196387	ENSG00000196387	ZNF140	12:133656423-133684130	OK	6.43599	6.95645	0.112189	0.164277	0.76525	0.9998
ENSG00000044115	ENSG00000044115	CTNNA1	5:137946655-138270723	OK	123.121	129.453	0.0723523	0.158644	0.76545	0.9998
ENSG00000136448	ENSG00000136448	NMT1	17:43100707-43221548	OK	95.6811	106.228	0.150851	0.129849	0.76545	0.9998
ENSG00000160404	ENSG00000160404	TOR2A	9:130374543-130497604	OK	13.839	11.0786	-0.320966	-0.11532	0.76545	0.9998
ENSG00000091732	ENSG00000091732	ZC3HC1	7:129593073-129691291	OK	32.412	34.2359	0.0789839	0.176559	0.76565	0.9998
ENSG00000100413	ENSG00000100413	POLR3H	22:41865128-41940610	OK	22.6269	28.1161	0.313359	0.205092	0.76565	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000156374	ENSG00000156374	PCGF6	10:105062552-105110891	OK	6.243	5.84758	-0.0944014	-0.178606	0.76565	0.9998
ENSG00000263934	ENSG00000263934	SNORD3A	17:19091328-19092027	OK	3.11285	3.81849	0.294766	0.186012	0.76565	0.9998
ENSG00000175387	ENSG00000175387	SMAD2	18:45357921-45457515	OK	73.0566	78.0094	0.0946346	0.178312	0.76575	0.9998
ENSG00000100379	ENSG00000100379	KCTD17	22:37447778-37459430	OK	7.62568	8.3106	0.124087	0.179102	0.7658	0.9998
ENSG00000259244	ENSG00000259244	RP11-182J1.12	15:85051115-85123406	OK	1.49848	1.14118	-0.392969	-0.19953	0.7658	0.9998
ENSG00000145685	ENSG00000145685	LHFPL2	5:77781037-78065844	OK	28.0257	29.6689	0.0821998	0.144976	0.7659	0.9998
ENSG00000167766	ENSG00000167766	ZNF83	19:53091757-53193749	OK	5.50056	5.09933	-0.10927	-0.137089	0.76595	0.9998
ENSG00000240184	ENSG00000240184	PCDHGC3	5:140710251-140892546	OK	15.6039	16.8205	0.108309	0.176624	0.76605	0.9998
ENSG00000205758	ENSG00000205758	CRYZL1	21:34876237-35349992	OK	11.2837	9.76516	-0.208531	-0.0688427	0.7661	0.9998
ENSG00000099904	ENSG00000099904	ZDHHC8	22:20116978-20135530	OK	22.4807	20.3973	-0.140314	-0.185046	0.76615	0.9998
ENSG00000263740	ENSG00000263740	RN7SL4P	3:15708742-15901278	OK	32.6064	56.0053	0.780411	0.281094	0.76615	0.9998
ENSG00000090520	ENSG00000090520	DNAJB11	3:186256229-186315061	OK	101.357	107.784	0.0886988	0.17479	0.7662	0.9998
ENSG00000100038	ENSG00000100038	TOP3B	22:22311396-22337213	OK	15.0645	16.144	0.0998457	0.14814	0.7662	0.9998
ENSG00000188739	ENSG00000188739	RBM34	1:235294497-235507847	OK	64.0271	58.4475	-0.131543	-0.167482	0.7662	0.9998
ENSG00000087152	ENSG00000087152	ATXN7L3	17:42269172-42301078	OK	22.4596	24.2799	0.112433	0.126387	0.7663	0.9998
ENSG00000147124	ENSG00000147124	ZNF41	X:47305277-47342345	OK	1.66546	1.51528	-0.136345	-0.150351	0.76635	0.9998
ENSG00000167543	ENSG00000167543	TP53I13	17:27887564-28513493	OK	15.1795	17.6764	0.2197	0.149	0.76635	0.9998
ENSG00000126215	ENSG00000126215	XRCC3	14:104019757-104181841	OK	13.2215	10.8779	-0.281492	-0.147127	0.76645	0.9998
ENSG00000182985	ENSG00000182985	CADM1	11:115039937-115375675	OK	34.7151	32.065	-0.114563	-0.164153	0.7666	0.9998
ENSG00000185808	ENSG00000185808	PIGP	21:38431469-38445470	OK	19.1445	17.8124	-0.104053	-0.181467	0.7666	0.9998
ENSG00000094914	ENSG00000094914	AAAS	12:53701239-53718648	OK	23.7296	22.3114	-0.0889092	-0.179482	0.76665	0.9998
ENSG00000139112	ENSG00000139112	GABARAPL1	12:10365056-10375727	OK	30.657	29.0719	-0.0765928	-0.171433	0.76665	0.9998
ENSG00000162337	ENSG00000162337	LRP5	11:68080076-68216743	OK	9.21607	9.72679	0.0778115	0.134228	0.76665	0.9998
ENSG00000264515	ENSG00000264515	CTC-525D6.1	19:29777917-30055386	OK	0.869795	1.4537	0.740987	0.283235	0.7667	0.9998
ENSG00000114480	ENSG00000114480	GBE1	3:81538849-81811312	OK	34.939	33.1312	-0.07665	-0.164439	0.7668	0.9998
ENSG00000265474	ENSG00000265474	AC010761.9	17:27071001-27077974	OK	1.65102	2.4472	0.567773	0.104152	0.7668	0.9998
ENSG00000142751	ENSG00000142751	GPN2	1:27202623-27216788	OK	17.5605	16.1044	-0.124876	-0.174337	0.76685	0.9998
ENSG00000176871	ENSG00000176871	WSB2	12:118451392-118500235	OK	110.667	104.682	-0.0802012	-0.172396	0.76685	0.9998
ENSG00000164659	ENSG00000164659	KIAA1324L	7:86506221-86689015	OK	4.61967	4.25726	-0.117864	-0.138507	0.76695	0.9998
ENSG00000188177	ENSG00000188177	ZC3H6	2:113033170-113097640	OK	1.60177	1.429	-0.164661	-0.155862	0.767	0.9998
ENSG00000085872	ENSG00000085872	CHERP	19:16589867-16771253	OK	16.0287	14.5167	-0.142943	-0.124552	0.76705	0.9998
ENSG00000119787	ENSG00000119787	ATL2	2:38522021-38604427	OK	32.7055	30.9499	-0.079601	-0.155058	0.7671	0.9998
ENSG00000108306	ENSG00000108306	FBXL20	17:37415383-37607539	OK	2.4695	3.03737	0.298601	0.168841	0.7672	0.9998
ENSG00000120837	ENSG00000120837	NFYB	12:104510854-104532067	OK	9.4142	10.1935	0.114745	0.173211	0.7672	0.9998
ENSG00000213185	ENSG00000213185	FAM24B	10:124591664-124639157	OK	4.71643	4.23123	-0.156618	-0.186616	0.7672	0.9998
ENSG00000250116	ENSG00000250116	RP11-417F21.1	2:46717888-46852881	OK	0.45222	0.640245	0.5016	0.0457436	0.7672	0.9998
ENSG00000100299	ENSG00000100299	ARSA	22:51061181-51066607	OK	17.0228	18.0314	0.08304	0.17303	0.76725	0.9998
ENSG00000115947	ENSG00000115947	ORC4	2:148602085-149275805	OK	16.8658	18.4289	0.127875	0.178949	0.76725	0.9998
ENSG00000189050	ENSG00000189050	RNFT1	17:57970446-58096413	OK	15.8605	14.3694	-0.142444	-0.164151	0.76725	0.9998
ENSG00000230224	ENSG00000230224	PHBP9	10:101989423-102027437	OK	1.16888	0.648237	-0.85054	-0.240007	0.7673	0.9998
ENSG00000112592	ENSG00000112592	TBP	6:170863389-170881958	OK	5.39492	5.03154	-0.100603	-0.174645	0.76735	0.9998
ENSG00000163110	ENSG00000163110	PDLIM5	4:95373036-95589377	OK	12.3906	13.537	0.127669	0.152476	0.76735	0.9998
ENSG00000106868	ENSG00000106868	SUSD1	9:114803064-114937688	OK	1.56561	1.43631	-0.124356	-0.130894	0.76745	0.9998
ENSG00000143390	ENSG00000143390	RFX5	1:151313115-151320503	OK	44.8841	42.6427	-0.0739083	-0.12788	0.76745	0.9998
ENSG00000166822	ENSG00000166822	TMEM170A	16:75327595-75499395	OK	6.38196	5.65263	-0.175078	-0.172193	0.76745	0.9998
ENSG00000043143	ENSG00000043143	JADE2	5:133860002-133918918	OK	19.2929	18.0843	-0.0933329	-0.175742	0.76755	0.9998
ENSG00000254870	ENSG00000254870	ATP6V1G2-DDX39B	6:31496493-31526606	OK	2.66332	1.49293	-0.835078	-0.233897	0.76755	0.9998
ENSG00000204257	ENSG00000204257	HLA-DMA	6:32902405-32949282	OK	18.0196	22.2893	0.306778	0.170904	0.76765	0.9998
ENSG00000215493	ENSG00000215493	XXbac-B562F10.11	22:20778873-20850170	OK	1.20912	0.767297	-0.656095	-0.227117	0.76765	0.9998
ENSG00000002822	ENSG00000002822	MAD1L1	7:1855428-2272878	OK	60.4744	65.0436	0.105084	0.174629	0.7677	0.9998
ENSG00000093100	ENSG00000093100	XXbac-B461K10.4	22:18270414-18507325	OK	4.782	5.72154	0.258788	0.179777	0.7677	0.9998
ENSG00000214192	ENSG00000214192	UBE2V1P2	3:174156362-175523428	OK	4.19043	5.0004	0.254945	0.157783	0.7677	0.9998
ENSG00000180879	ENSG00000180879	SSR4	X:153051220-153063960	OK	248.61	263.923	0.0862336	0.178676	0.76775	0.9998
ENSG00000137393	ENSG00000137393	RNF144B	6:18366966-18469105	OK	4.30106	4.044	-0.0889073	-0.163152	0.7678	0.9998
ENSG00000254837	ENSG00000254837	AP001372.2	11:74202756-74380162	OK	1.4547	1.17911	-0.303017	-0.180695	0.76785	0.9998
ENSG00000228343	ENSG00000228343	RP11-1148L6.5	X:48438161-48439545	OK	1.42363	1.21402	-0.229788	-0.185095	0.76795	0.9998
ENSG00000105373	ENSG00000105373	GLTSCR2	19:48248778-48272097	OK	109.646	115.604	0.0763305	0.170969	0.76805	0.9998
ENSG00000247708	ENSG00000247708	STX18-AS1	4:4349866-4712665	OK	1.61604	1.92671	0.253677	0.0423428	0.76805	0.9998
ENSG00000171421	ENSG00000171421	MRPL36	5:1798499-1801480	OK	48.5282	51.4207	0.0835263	0.176165	0.7681	0.9998
ENSG00000167114	ENSG00000167114	SLC27A4	9:131102924-131123749	OK	19.8926	21.0723	0.0831174	0.183249	0.7682	0.9998
ENSG00000165996	ENSG00000165996	PTPLA	10:17631957-17659376	OK	15.3093	16.4402	0.102815	0.177319	0.76825	0.9998
ENSG00000170832	ENSG00000170832	USP32	17:58256454-58508782	OK	30.0772	31.6296	0.0726049	0.144033	0.76825	0.9998
ENSG00000241837	ENSG00000241837	ATP5O	21:34876237-35349992	OK	131.858	117.957	-0.160729	-0.17296	0.7683	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000099251	ENSG00000099251	HSD17B7P2	10:38645304-38667433	OK	2.72129	2.4836	-0.131857	-0.179894	0.76845	0.9998
ENSG00000147789	ENSG00000147789	ZNF7	8:146052848-146127553	OK	9.37203	10.2633	0.131063	0.150893	0.76845	0.9998
ENSG00000160209	ENSG00000160209	PDXK	21:45138974-45182188	OK	52.766	48.3321	-0.126627	-0.191119	0.76845	0.9998
ENSG00000213398	ENSG00000213398	LCAT	16:67973652-68003504	OK	1.10133	1.32196	0.263441	0.0948426	0.76845	0.9998
ENSG00000010295	ENSG00000010295	IFFO1	12:6647540-6665239	OK	18.113	17.1024	-0.0828246	-0.182796	0.7685	0.9998
ENSG00000182544	ENSG00000182544	MFSD5	12:53645034-53648189	OK	40.3901	43.0651	0.0925181	0.172605	0.7685	0.9998
ENSG00000135914	ENSG00000135914	HTR2B	2:231921577-232037541	OK	1.59336	2.56984	0.689604	0.269863	0.76855	0.9998
ENSG00000214517	ENSG00000214517	PPME1	11:73723762-74035750	OK	24.2997	22.771	-0.0937378	-0.174487	0.76855	0.9998
ENSG00000151006	ENSG00000151006	PRSS53	16:31085742-31107301	OK	0.843315	0.605386	-0.478217	-0.133511	0.7686	0.9998
ENSG00000166924	ENSG00000166924	NYAP1	7:100081549-100092422	OK	0.822096	0.898581	0.128343	0.154176	0.7686	0.9998
ENSG00000198721	ENSG00000198721	ECI2	6:4021500-4157619	OK	88.6055	95.5734	0.109214	0.175475	0.7686	0.9998
ENSG00000226944	ENSG00000226944	RP1-120G22.11	1:6241328-6296032	OK	0.701534	1.01387	0.53129	0.0256138	0.7686	0.9998
ENSG00000005059	ENSG00000005059	CCDC109B	4:110481360-110624739	OK	2.79442	3.15654	0.175795	0.137208	0.76865	0.9998
ENSG00000114126	ENSG00000114126	TFDP2	3:141663269-141868386	OK	23.2243	21.0687	-0.140534	-0.161575	0.7687	0.9998
ENSG00000124562	ENSG00000124562	SNRPC	6:34725182-34741571	OK	149.613	157.277	0.072073	0.179188	0.76875	0.9998
ENSG00000255145	ENSG00000255145	RP11-60I3.5	9:102648607-102668883	OK	0.676756	0.56416	-0.262532	-0.194979	0.76875	0.9998
ENSG00000145545	ENSG00000145545	SRD5A1	5:6633455-6669675	OK	18.6596	17.6398	-0.08109	-0.168045	0.7689	0.9998
ENSG00000177853	ENSG00000177853	ZNF518A	10:97889471-98031344	OK	2.68767	2.48923	-0.110656	-0.133173	0.76895	0.9998
ENSG00000188242	ENSG00000188242	CTD-2228K2.5	5:443272-473213	OK	13.5692	11.4497	-0.24502	-0.15802	0.76895	0.9998
ENSG00000104671	ENSG00000104671	DCTN6	8:29952913-30041156	OK	35.3765	38.6551	0.127866	0.170971	0.76915	0.9998
ENSG00000174032	ENSG00000174032	SLC25A30	13:45967450-45994506	OK	14.3305	13.5029	-0.0858201	-0.132448	0.76915	0.9998
ENSG00000109738	ENSG00000109738	GLRB	4:157997208-158093242	OK	3.09197	2.85895	-0.113042	-0.163232	0.7692	0.9998
ENSG00000079739	ENSG00000079739	PGM1	1:63906440-64125916	OK	57.8509	61.0782	0.0783197	0.17532	0.7693	0.9998
ENSG00000267957	ENSG00000267957	RP11-178G16.4	10:75880012-75880621	OK	5.03993	4.60447	-0.130368	-0.175965	0.76935	0.9998
ENSG00000128791	ENSG00000128791	TWSG1	18:9334764-9402418	OK	11.115	10.4779	-0.0851626	-0.178786	0.7695	0.9998
ENSG00000133597	ENSG00000133597	ADCK2	7:140218219-140624564	OK	12.8473	14.666	0.191015	0.168899	0.7695	0.9998
ENSG00000164548	ENSG00000164548	TRA2A	7:23544398-23571660	OK	26.9698	25.4564	-0.0833205	-0.169631	0.76955	0.9998
ENSG00000106080	ENSG00000106080	FKBP14	7:29959718-30066300	OK	15.4561	17.3751	0.168844	0.113588	0.7696	0.9998
ENSG00000116747	ENSG00000116747	TROVE2	1:192981379-193060907	OK	18.1398	19.8955	0.133281	0.11081	0.7697	0.9998
ENSG00000181163	ENSG00000181163	NPM1	5:170814119-170838141	OK	1671.62	1823.51	0.125476	0.153927	0.7697	0.9998
ENSG00000133519	ENSG00000133519	ZDHHC8P1	22:23732792-23744913	OK	1.22436	1.35911	0.150643	0.162683	0.7698	0.9998
ENSG00000158850	ENSG00000158850	B4GALT3	1:161136199-161147803	OK	91.8742	97.1719	0.0808803	0.157592	0.76985	0.9998
ENSG00000116954	ENSG00000116954	RRAGC	1:39303869-39325495	OK	25.0623	26.3519	0.072388	0.172809	0.7699	0.9998
ENSG00000101417	ENSG00000101417	PXMP4	20:32294511-32308125	OK	9.52947	8.88962	-0.100275	-0.181454	0.77	0.9998
ENSG00000103249	ENSG00000103249	CLCN7	16:1494934-1525581	OK	180.113	167.21	-0.107239	-0.175512	0.77	0.9998
ENSG00000236360	ENSG00000236360	RP11-334A14.2	1:53392900-53517375	OK	2.54476	3.5987	0.499943	0.109089	0.77005	0.9998
ENSG00000124702	ENSG00000124702	KLHDC3	6:42981950-42989036	OK	43.2289	41.0928	-0.0731117	-0.177606	0.7701	0.9998
ENSG00000183354	ENSG00000183354	KIAA2026	9:5881595-6007904	OK	15.5136	12.8393	-0.272965	-0.0495011	0.77015	0.9998
ENSG00000125482	ENSG00000125482	TTF1	9:135251007-135282209	OK	6.142	5.72296	-0.101948	-0.158328	0.7702	0.9998
ENSG00000172789	ENSG00000172789	HOXC5	12:54375292-54449814	OK	1.99448	1.29435	-0.623788	-0.296036	0.7702	0.9998
ENSG00000181481	ENSG00000181481	RNF135	17:29295802-29326929	OK	4.03795	3.77289	-0.0979511	-0.160973	0.7703	0.9998
ENSG00000184708	ENSG00000184708	EIF4ENIF1	22:31795508-32058418	OK	9.77029	10.8219	0.147477	0.0885282	0.7705	0.9998
ENSG00000146757	ENSG00000146757	ZNF92	7:64838711-64866038	OK	3.69324	3.44994	-0.0983164	-0.164067	0.77055	0.9998
ENSG00000100138	ENSG00000100138	NHP2L1	22:42069933-42094140	OK	108.047	115.953	0.101883	0.178205	0.7706	0.9998
ENSG00000234585	ENSG00000234585	CCT6P3	7:64498731-64535091	OK	2.66173	2.46879	-0.108559	-0.176032	0.7706	0.9998
ENSG00000106031	ENSG00000106031	HOXA13	7:27233121-27246878	OK	0.910192	0.837687	-0.119759	-0.164318	0.77065	0.9998
ENSG00000213722	ENSG00000213722	DDAH2	6:31694814-31707540	OK	31.565	39.3248	0.317111	0.205217	0.77065	0.9998
ENSG00000244306	ENSG00000244306	CTD-2314B22.3	14:19812175-19925348	OK	6.97571	6.23412	-0.162154	-0.179245	0.77075	0.9998
ENSG00000272668	ENSG00000272668	RP11-190A12.8	1:159796539-159869953	OK	0.716086	0.436179	-0.71521	-0.311474	0.77075	0.9998
ENSG00000188529	ENSG00000188529	SRSF10	1:24291293-24307417	OK	55.5926	52.4019	-0.0852749	-0.168863	0.7709	0.9998
ENSG00000109680	ENSG00000109680	TBC1D19	4:26578058-26756973	OK	4.01799	3.7117	-0.114395	-0.166617	0.77115	0.9998
ENSG00000112210	ENSG00000112210	RAB23	6:56951641-57087078	OK	7.43846	6.53216	-0.187442	-0.191185	0.77125	0.9998
ENSG00000156504	ENSG00000156504	FAM122B	X:133903595-133988640	OK	17.2356	16.0981	-0.0984994	-0.173024	0.77125	0.9998
ENSG00000163257	ENSG00000163257	DCAF16	4:17802277-17812381	OK	8.55631	8.02785	-0.0919754	-0.142763	0.77125	0.9998
ENSG00000228830	ENSG00000228830	RP4-781K5.2	1:234740014-234745271	OK	22.5535	26.6449	0.240508	0.176908	0.77125	0.9998
ENSG00000257815	ENSG00000257815	RP11-611E13.2	12:70132460-70748773	OK	1.86696	2.45224	0.39341	0.112772	0.77125	0.9998
ENSG00000226508	ENSG00000226508	AC104655.3	2:105760570-105761882	OK	51.2133	47.8752	-0.0972397	-0.181986	0.7713	0.9998
ENSG00000248008	ENSG00000248008	DYNLL1-AS1	12:120907652-120936296	OK	4.60021	3.48451	-0.400743	-0.192637	0.7713	0.9998
ENSG00000214078	ENSG00000214078	CPNE1	20:34213952-34288906	OK	124.987	134.507	0.105905	0.14292	0.77135	0.9998
ENSG00000233276	ENSG00000233276	GPX1	3:49394608-49396033	OK	176.76	185.712	0.071276	0.17679	0.77135	0.9998
ENSG00000164929	ENSG00000164929	BAALC	8:104133259-104345094	OK	5.42016	4.56102	-0.248978	-0.112713	0.7715	0.9998
ENSG00000113369	ENSG00000113369	ARRDC3	5:90664540-90679176	OK	18.4181	17.3904	-0.082835	-0.133911	0.7716	0.9998
ENSG00000146425	ENSG00000146425	DYNLT1	6:159057505-159065771	OK	34.5476	32.5094	-0.0877259	-0.180127	0.77175	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000136699	ENSG00000136699	SMPD4	2:130908980-130948302	OK	13.3244	12.3466	-0.109954	-0.138215	0.7719	0.9998
ENSG00000165650	ENSG00000165650	PDZD8	10:119039999-119134978	OK	7.99296	8.59697	0.105098	0.155238	0.77195	0.9998
ENSG00000102780	ENSG00000102780	DGKH	13:42614175-42830714	OK	1.23551	1.14026	-0.115747	-0.144266	0.772	0.9998
ENSG00000262814	ENSG00000262814	MRPL12	17:79670386-79688042	OK	175.959	166.727	-0.0777529	-0.175185	0.772	0.9998
ENSG00000115415	ENSG00000115415	STAT1	2:191745522-191885686	OK	37.8145	41.1325	0.121336	0.155963	0.7721	0.9998
ENSG00000137822	ENSG00000137822	TUBGCP4	15:43650369-43699293	OK	8.04143	8.73222	0.118895	0.143553	0.7721	0.9998
ENSG00000141959	ENSG00000141959	PFKL	21:45719933-45747259	OK	23.1429	21.9183	-0.0784356	-0.163979	0.7721	0.9998
ENSG00000231527	ENSG00000231527	RP11-374M1.2	9:45108391-45112532	OK	10.3038	9.51289	-0.115215	-0.181213	0.7721	0.9998
ENSG00000273320	ENSG00000273320	RP11-22N19.2	7:105888730-105926772	OK	0.64121	0.440453	-0.541809	-0.0358816	0.7721	0.9998
ENSG00000139637	ENSG00000139637	C12orf10	12:53689074-53700961	OK	33.6805	37.7775	0.165613	0.151632	0.7722	0.9998
ENSG00000087274	ENSG00000087274	ADD1	4:2845583-2931803	OK	47.2278	49.6453	0.0720201	0.138632	0.7723	0.9998
ENSG00000111215	ENSG00000111215	PRR4	12:10977558-11324212	OK	9.19638	9.96706	0.116103	0.152543	0.7723	0.9998
ENSG00000169548	ENSG00000169548	ZNF280A	22:22868059-22874613	OK	1.92675	2.0781	0.109099	0.1708	0.77235	0.9998
ENSG00000126062	ENSG00000126062	TMEM115	3:50384760-50541675	OK	21.8684	23.4587	0.101279	0.175426	0.77245	0.9998
ENSG00000136147	ENSG00000136147	PHF11	13:50069745-50103123	OK	4.2405	4.5711	0.108306	0.152511	0.77265	0.9998
ENSG00000100258	ENSG00000100258	LMF2	22:50941375-50946135	OK	30.4875	32.0787	0.073401	0.160013	0.7728	0.9998
ENSG00000146858	ENSG00000146858	ZC3HAV1L	7:138710451-138720775	OK	8.21142	7.70948	-0.0909987	-0.17638	0.7728	0.9998
ENSG00000179889	ENSG00000179889	PDXDC1	16:15068447-15248421	OK	58.9934	55.3458	-0.09208	-0.120627	0.7728	0.9998
ENSG00000268525	ENSG00000268525	CTB-59C6.3	19:42502472-42585701	OK	0.801447	1.35932	0.762207	0.224546	0.7728	0.9998
ENSG00000266490	ENSG00000266490	CTD-2349P21.9	17:29036316-29151794	OK	1.33218	2.18427	0.713358	0.206205	0.77285	0.9998
ENSG00000116729	ENSG00000116729	WLS	1:68167148-68698803	OK	22.0616	25.1371	0.188283	0.130497	0.7729	0.9998
ENSG00000148143	ENSG00000148143	ZNF462	9:109625377-109865269	OK	3.04613	3.25436	0.0953979	0.10423	0.7729	0.9998
ENSG00000183010	ENSG00000183010	PYCR1	17:79890259-79905477	OK	39.5293	41.7365	0.0783854	0.17555	0.7729	0.9998
ENSG00000225177	ENSG00000225177	RP11-390P2.4	6:138723721-139018425	OK	17.9371	14.8603	-0.271477	-0.19445	0.7729	0.9998
ENSG00000148180	ENSG00000148180	GSN	9:123940414-124095121	OK	178.354	188.787	0.0820143	0.157663	0.77295	0.9998
ENSG00000140829	ENSG00000140829	DHX38	16:72078187-72210777	OK	11.5596	10.9028	-0.0843926	-0.120109	0.773	0.9998
ENSG00000146426	ENSG00000146426	TIAM2	6:155054458-155635627	OK	2.66941	2.30348	-0.212704	-0.117661	0.773	0.9998
ENSG00000149639	ENSG00000149639	SOGA1	20:35405844-35492089	OK	10.6142	11.2989	0.0901834	0.150964	0.773	0.9998
ENSG00000100154	ENSG00000100154	TTC28	22:28247656-29075853	OK	3.94718	4.39161	0.153929	0.0743001	0.7731	0.9998
ENSG00000185163	ENSG00000185163	DDX51	12:132621138-132628880	OK	7.79777	8.48805	0.12237	0.170276	0.77315	0.9998
ENSG00000115368	ENSG00000115368	WDR75	2:190306158-190340291	OK	21.3187	20.2734	-0.0725289	-0.163852	0.7732	0.9998
ENSG00000135604	ENSG00000135604	STX11	6:144471662-144509507	OK	0.64881	0.584889	-0.149634	-0.176294	0.7732	0.9998
ENSG00000247728	ENSG00000247728	RP11-932O9.7	15:30909160-31065196	OK	0.428357	0.649166	0.599773	0.224185	0.7733	0.9998
ENSG00000071282	ENSG00000071282	LMCD1	3:7994491-8653610	OK	14.1771	15.1389	0.0947043	0.17252	0.77335	0.9998
ENSG00000102978	ENSG00000102978	POLR2C	16:57462080-57521239	OK	28.1408	25.7661	-0.127188	-0.173523	0.7735	0.9998
ENSG00000164236	ENSG00000164236	ANKRD33B	5:10564441-10650308	OK	1.29147	1.42002	0.136904	0.173605	0.7735	0.9998
ENSG00000232284	ENSG00000232284	GNG12-AS1	1:68167148-68698803	OK	1.20127	0.932875	-0.364801	-0.0321826	0.7736	0.9998
ENSG00000104375	ENSG00000104375	STK3	8:99413630-99955055	OK	13.5484	14.2996	0.0778569	0.142579	0.7737	0.9998
ENSG00000147526	ENSG00000147526	TACC1	8:38585703-38710546	OK	29.3592	27.7379	-0.081955	-0.118818	0.77375	0.9998
ENSG00000175182	ENSG00000175182	FAM131A	3:183851806-184402546	OK	22.4855	25.8078	0.198812	0.0540962	0.77375	0.9998
ENSG00000198736	ENSG00000198736	MSRB1	16:1988210-1993327	OK	16.2145	17.1546	0.0813072	0.16826	0.77385	0.9998
ENSG00000105136	ENSG00000105136	ZNF419	19:57999078-58029772	OK	3.79196	4.1356	0.125153	0.146817	0.77395	0.9998
ENSG00000168569	ENSG00000168569	TMEM223	11:62538591-62559493	OK	16.6536	18.2183	0.129558	0.167296	0.774	0.9998
ENSG00000082153	ENSG00000082153	BZW1	2:201542955-201688569	OK	113.996	106.139	-0.103031	-0.173121	0.77405	0.9998
ENSG00000108671	ENSG00000108671	PSMD11	17:30771278-30810336	OK	60.4285	65.1145	0.10775	0.164205	0.77405	0.9998
ENSG00000138029	ENSG00000138029	HADHB	2:26413503-26513336	OK	116.83	107.117	-0.125221	-0.176288	0.77405	0.9998
ENSG00000157193	ENSG00000157193	LRP8	1:53711216-53793742	OK	26.4434	28.4974	0.107924	0.162807	0.77405	0.9998
ENSG00000162004	ENSG00000162004	CCDC78	16:770580-791329	OK	5.81583	6.58786	0.179825	0.102733	0.77405	0.9998
ENSG00000178105	ENSG00000178105	DDX10	11:108535751-108811657	OK	8.38778	7.8707	-0.0917983	-0.151428	0.7741	0.9998
ENSG00000134046	ENSG00000134046	MBD2	18:51679078-51751158	OK	30.9638	28.1427	-0.137819	-0.123662	0.7743	0.9998
ENSG00000157933	ENSG00000157933	SKI	1:2160133-2241558	OK	10.6192	11.2225	0.0797238	0.110258	0.7743	0.9998
ENSG00000128585	ENSG00000128585	MKLN1	7:130626518-131182453	OK	28.6806	26.8097	-0.0973186	-0.146711	0.77445	0.9998
ENSG00000224470	ENSG00000224470	ATXN1L	16:71879893-71962913	OK	5.09334	4.69196	-0.11842	-0.132282	0.77445	0.9998
ENSG00000137776	ENSG00000137776	SLTM	15:59063390-59389618	OK	24.1309	22.4346	-0.105158	-0.130747	0.7745	0.9998
ENSG00000125977	ENSG00000125977	EIF2S2	20:32570857-32700138	OK	81.7209	87.5329	0.0991193	0.17413	0.77455	0.9998
ENSG00000105750	ENSG00000105750	ZNF85	19:21106027-21133503	OK	1.17109	1.30173	0.152586	0.123725	0.77475	0.9998
ENSG00000137142	ENSG00000137142	IGFBPL1	9:38408990-38424444	OK	4.10943	3.7939	-0.115257	-0.177278	0.77475	0.9998
ENSG00000155313	ENSG00000155313	USP25	21:17102343-17252377	OK	5.40983	5.0875	-0.0886264	-0.134687	0.77485	0.9998
ENSG00000134375	ENSG00000134375	TIMM17A	1:201924618-201939789	OK	98.7278	103.52	0.0683788	0.170852	0.77495	0.9998
ENSG00000179943	ENSG00000179943	FIZ1	19:56102745-56114504	OK	4.8237	4.40935	-0.129573	-0.141537	0.77495	0.9998
ENSG00000226674	ENSG00000226674	TEX41	2:145425533-145940216	OK	26.7707	24.7391	-0.113861	-0.168155	0.77495	0.9998
ENSG00000254860	ENSG00000254860	TMEM9B-AS1	11:8968840-8999074	OK	1.95275	1.37731	-0.50365	-0.13399	0.775	0.9998
ENSG00000005249	ENSG00000005249	PRKAR2B	7:106685093-106802256	OK	6.78028	7.17077	0.0807845	0.170581	0.77505	0.9998
ENSG00000150477	ENSG00000150477	KIAA1328	18:33877676-34812135	OK	3.32828	3.78963	0.187281	0.105471	0.77505	0.9998
ENSG00000269554	ENSG00000269554	AL590822.2	1:1981908-2152177	OK	0.489139	0.868437	0.828176	0.308783	0.77505	0.9998
ENSG00000156990	ENSG00000156990	RPUSD3	3:9791627-9896822	OK	67.2548	73.7922	0.133831	0.162148	0.7751	0.9998
ENSG00000007923	ENSG00000007923	DNAJC11	1:6684925-6761984	OK	28.3393	30.1335	0.088564	0.156531	0.77525	0.9998
ENSG00000121680	ENSG00000121680	PEX16	11:45931219-45940363	OK	20.9498	22.3323	0.0921895	0.157861	0.77525	0.9998
ENSG00000151320	ENSG00000151320	AKAP6	14:32798478-33300567	OK	5.66792	5.30788	-0.0946839	-0.103807	0.7753	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000187325	ENSG00000187325	TAF9B	X:77385244-77395203	OK	13.4837	12.7875	-0.076488	-0.165386	0.7753	0.9998
ENSG00000136830	ENSG00000136830	FAM129B	9:130267617-130341268	OK	66.3564	63.3114	-0.0677718	-0.143219	0.7754	0.9998
ENSG00000147439	ENSG00000147439	BIN3	8:22462144-22526661	OK	80.4025	73.9523	-0.120645	-0.159851	0.77545	0.9998
ENSG00000243646	ENSG00000243646	IL10RB	21:34602205-34669539	OK	7.46987	6.8942	-0.115699	-0.169592	0.7755	0.9998
ENSG00000163312	ENSG00000163312	HELQ	4:84328495-84377009	OK	4.82263	5.43959	0.17368	0.172984	0.77555	0.9998
ENSG00000107796	ENSG00000107796	ACTA2	10:90639490-90775542	OK	4.7875	5.57237	0.219017	0.169655	0.7757	0.9998
ENSG00000117448	ENSG00000117448	AKR1A1	1:46016214-46035721	OK	42.816	40.3139	-0.0868733	-0.174143	0.7757	0.9998
ENSG00000151093	ENSG00000151093	OXSM	3:25760434-25836025	OK	11.1563	12.4086	0.15348	0.153547	0.7757	0.9998
ENSG00000268516	ENSG00000268516	CTD-3138B18.5	19:58739959-58827023	OK	1.49761	1.17417	-0.351015	-0.167715	0.7758	0.9998
ENSG00000156467	ENSG00000156467	UQCRB	8:97238147-97250262	OK	391.018	413.024	0.0789891	0.178419	0.77585	0.9998
ENSG00000170545	ENSG00000170545	SMAGP	12:51632075-51665146	OK	2.09258	2.55143	0.28602	0.0523295	0.77585	0.9998
ENSG00000163607	ENSG00000163607	GTPBP8	3:112709293-112902148	OK	10.8014	9.52864	-0.180871	-0.154576	0.77595	0.9998
ENSG00000182484	ENSG00000182484	WASH6P	X:155227245-155257848	OK	5.58478	5.1054	-0.129478	-0.170087	0.776	0.9998
ENSG00000183808	ENSG00000183808	RBM12B	8:94225530-94753245	OK	7.67907	8.44286	0.1368	0.108916	0.7761	0.9998
ENSG00000204604	ENSG00000204604	ZNF468	19:53300661-53360902	OK	1.6916	1.53679	-0.138472	-0.115717	0.7761	0.9998
ENSG00000241506	ENSG00000241506	PSMC1P1	3:68684855-68686175	OK	65.9155	62.7315	-0.0714284	-0.174011	0.77625	0.9998
ENSG00000149658	ENSG00000149658	YTHDF1	20:61826780-61847586	OK	31.7336	33.411	0.0743136	0.16251	0.7763	0.9998
ENSG00000099331	ENSG00000099331	MYO9B	19:17186590-17325346	OK	58.0156	61.2976	0.0793893	0.109351	0.77635	0.9998
ENSG00000140104	ENSG00000140104	C14orf79	14:105452111-105487485	OK	3.15606	3.74119	0.245376	0.16468	0.77635	0.9998
ENSG00000137942	ENSG00000137942	FNBP1L	1:93913687-94020218	OK	14.458	13.7349	-0.0740195	-0.16177	0.7765	0.9998
ENSG00000182923	ENSG00000182923	CEP63	3:134196547-134293859	OK	19.5362	18.1256	-0.108123	-0.143793	0.7765	0.9998
ENSG00000152684	ENSG00000152684	PELO	5:51971026-52390609	OK	9.60503	10.4288	0.118709	0.156816	0.7766	0.9998
ENSG00000102393	ENSG00000102393	GLA	X:100645811-100669121	OK	43.5112	39.6727	-0.133238	-0.159834	0.77665	0.9998
ENSG00000234882	ENSG00000234882	EIF3EP1	6:73918805-74020088	OK	0.784139	0.655521	-0.258468	-0.1717	0.77665	0.9998
ENSG00000005100	ENSG00000005100	DHX33	17:5185557-5372380	OK	38.6442	35.1966	-0.134817	-0.168882	0.7767	0.9998
ENSG00000118496	ENSG00000118496	FBXO30	6:146114637-146135889	OK	2.16075	2.04272	-0.0810462	-0.165899	0.77675	0.9998
ENSG00000155393	ENSG00000155393	HEATR3	16:50080339-50155854	OK	6.01643	6.40612	0.0905445	0.136396	0.7768	0.9998
ENSG00000196507	ENSG00000196507	TCEAL3	X:102862378-102885881	OK	20.3384	21.8503	0.103445	0.17518	0.7769	0.9998
ENSG00000143401	ENSG00000143401	ANP32E	1:150190716-150208504	OK	42.5187	44.804	0.0755304	0.147733	0.77695	0.9998
ENSG00000146576	ENSG00000146576	C7orf26	7:6629647-6648357	OK	18.3632	17.104	-0.102485	-0.167352	0.77695	0.9998
ENSG00000233593	ENSG00000233593	RP4-665J23.1	1:91248542-91317207	OK	8.26909	7.61269	-0.119321	-0.175344	0.77695	0.9998
ENSG00000108395	ENSG00000108395	TRIM37	17:57059998-57232630	OK	19.7605	18.3057	-0.11033	-0.147516	0.777	0.9998
ENSG00000163618	ENSG00000163618	CADPS	3:62384021-62861054	OK	18.2165	16.9271	-0.105914	-0.132747	0.77705	0.9998
ENSG00000125827	ENSG00000125827	TMX4	20:7957994-8024159	OK	6.14624	6.57992	0.0983644	0.135924	0.7771	0.9998
ENSG00000243637	ENSG00000243637	AC019221.4	2:234263152-234380750	OK	0.547442	0.823272	0.588663	0.133818	0.7771	0.9998
ENSG00000120509	ENSG00000120509	PDZD11	X:69506444-69640682	OK	91.4465	85.4531	-0.0977943	-0.174611	0.77715	0.9998
ENSG00000204366	ENSG00000204366	ZBTB12	6:31865561-31919861	OK	3.87099	4.15311	0.101492	0.168908	0.77725	0.9998
ENSG00000119004	ENSG00000119004	CYP20A1	2:204103662-204163009	OK	5.01582	5.4049	0.107783	0.1657	0.7774	0.9998
ENSG00000138757	ENSG00000138757	G3BP2	4:76567965-76649709	OK	127.585	121.679	-0.0683809	-0.147169	0.7774	0.9998
ENSG00000185129	ENSG00000185129	PURA	5:139452441-139496321	OK	6.2812	5.89994	-0.090341	-0.148527	0.77745	0.9998
ENSG00000175745	ENSG00000175745	NR2F1	5:92745064-92930321	OK	1.80424	1.55488	-0.214587	-0.163597	0.7775	0.9998
ENSG00000105821	ENSG00000105821	DNAJC2	7:102937868-103629963	OK	22.1712	24.9016	0.167548	0.157081	0.77755	0.9998
ENSG00000084072	ENSG00000084072	PPIE	1:40157853-40254533	OK	44.401	42.1187	-0.0761309	-0.172458	0.7776	0.9998
ENSG00000001167	ENSG00000001167	NFYA	6:40994771-41067715	OK	21.2307	22.6819	0.0953896	0.174437	0.77775	0.9998
ENSG00000138639	ENSG00000138639	ARHGAP24	4:86396266-86923823	OK	13.9695	14.8822	0.091303	0.156223	0.77775	0.9998
ENSG00000253953	ENSG00000253953	PCDHGB4	5:140710251-140892546	OK	0.748783	1.1559	0.626391	0.251628	0.77775	0.9998
ENSG00000197050	ENSG00000197050	ZNF420	19:37498758-37734828	OK	2.52583	2.24868	-0.167683	-0.110715	0.77795	0.9998
ENSG00000249485	ENSG00000249485	RBBP4P1	5:14704909-14871887	OK	0.801648	0.650196	-0.302094	-0.173049	0.778	0.9998
ENSG00000127838	ENSG00000127838	PNKD	2:219135114-219232822	OK	78.8891	72.0496	-0.130835	-0.167468	0.7781	0.9998
ENSG00000137504	ENSG00000137504	CREBZF	11:85370751-85393951	OK	8.06034	8.57695	0.0896228	0.159976	0.7781	0.9998
ENSG00000112304	ENSG00000112304	ACOT13	6:24667262-24721064	OK	23.8393	19.9254	-0.25873	-0.178465	0.77815	0.9998
ENSG00000119242	ENSG00000119242	CCDC92	12:124247041-124800570	OK	12.714	10.7662	-0.239899	-0.156477	0.77815	0.9998
ENSG00000162836	ENSG00000162836	ACP6	1:147101452-147142618	OK	26.2217	24.5329	-0.0960427	-0.169086	0.77815	0.9998
ENSG00000172915	ENSG00000172915	NBEA	13:35516423-36247159	OK	5.97661	5.68252	-0.0727981	-0.150528	0.77815	0.9998
ENSG00000240005	ENSG00000240005	RP11-293A21.1	4:26859299-27027003	OK	1.80414	1.22294	-0.560954	-0.125186	0.77815	0.9998
ENSG00000266441	ENSG00000266441	RP11-91I8.3	18:6728819-6915715	OK	0.711457	0.437222	-0.702409	-0.185776	0.77815	0.9998
ENSG00000105583	ENSG00000105583	WDR83OS	19:12754088-12792716	OK	134.144	148.001	0.141827	0.16501	0.7782	0.9998
ENSG00000122026	ENSG00000122026	RPL21	13:27825445-27830828	OK	18.6416	20.1034	0.108914	0.187969	0.77825	0.9998
ENSG00000260336	ENSG00000260336	RP11-395B7.7	7:100737327-100741248	OK	1.85182	1.98075	0.0971031	0.169434	0.77825	0.9998
ENSG00000231864	ENSG00000231864	RP11-229P13.23	9:139952114-139965040	OK	2.16506	1.34862	-0.682923	-0.282906	0.77835	0.9998
ENSG00000152022	ENSG00000152022	LIX1L	1:145475981-145516076	OK	20.7655	22.5512	0.119019	0.175613	0.77855	0.9998
ENSG00000242193	ENSG00000242193	RP11-568K15.1	1:177893090-178007142	OK	10.7369	10.0877	-0.0899736	-0.150011	0.77855	0.9998
ENSG00000183150	ENSG00000183150	GPR19	12:12813824-12849141	OK	5.87944	6.28932	0.0972239	0.167758	0.77865	0.9998
ENSG00000141127	ENSG00000141127	PRPSAP2	17:18739019-18834581	OK	16.2673	17.1882	0.0794417	0.153795	0.7787	0.9998
ENSG00000189283	ENSG00000189283	FHIT	3:59735035-61237133	OK	10.1993	9.52477	-0.0987147	-0.164724	0.7787	0.9998
ENSG00000124783	ENSG00000124783	SSR1	6:7268538-7418270	OK	125.554	133.424	0.0877109	0.165056	0.77885	0.9998
ENSG00000103319	ENSG00000103319	EEF2K	16:22217602-22300059	OK	8.54778	7.96095	-0.102609	-0.124249	0.7789	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000271971	ENSG00000271971	CTD-2006H14.2	8:94225530-94753245	OK	1.2373	0.817652	-0.597634	-0.140779	0.7789	0.9998
ENSG00000100632	ENSG00000100632	ERH	14:69846847-69929105	OK	91.028	84.2966	-0.110836	-0.167117	0.779	0.9998
ENSG00000260081	ENSG00000260081	RP11-66N11.8	X:152853376-152869808	OK	0.669958	0.471823	-0.505827	-0.109083	0.779	0.9998
ENSG00000179335	ENSG00000179335	CLK3	15:74890840-74988633	OK	41.1095	45.5643	0.148433	0.164043	0.77905	0.9998
ENSG00000154001	ENSG00000154001	PPP2R5E	14:63838074-64010092	OK	13.745	14.7239	0.0992496	0.169363	0.7792	0.9998
ENSG00000265817	ENSG00000265817	FSBP	8:95384187-95487337	OK	1.34547	1.76557	0.39202	0.202659	0.7793	0.9998
ENSG00000204611	ENSG00000204611	ZNF616	19:52616343-52680255	OK	1.94385	2.14763	0.14383	0.134993	0.77935	0.9998
ENSG00000196810	ENSG00000196810	CTBP1-AS2	4:1205235-1282079	OK	2.41494	2.97012	0.29853	0.121069	0.7794	0.9998
ENSG00000270018	ENSG00000270018	RP3-462E2.5	12:112335139-112335710	OK	0.901012	0.781189	-0.205875	-0.170132	0.7794	0.9998
ENSG00000096872	ENSG00000096872	IFT74	9:26904080-27062928	OK	3.76841	3.26546	-0.206668	-0.138778	0.7795	0.9998
ENSG00000227212	ENSG00000227212	PFN1P7	1:148555978-148596267	OK	1.82317	1.24891	-0.545772	-0.117138	0.7795	0.9998
ENSG00000260880	ENSG00000260880	HCCAT5	16:73126247-73127673	OK	1.09573	0.984873	-0.153887	-0.174381	0.7795	0.9998
ENSG00000112679	ENSG00000112679	DUSP22	6:291629-351355	OK	29.6711	27.9946	-0.0839105	-0.151251	0.7797	0.9998
ENSG00000257093	ENSG00000257093	KIAA1147	7:141229002-141401953	OK	3.17663	2.87121	-0.145842	-0.161059	0.7797	0.9998
ENSG00000064932	ENSG00000064932	SBNO2	19:1107635-1174282	OK	27.906	26.4059	-0.0797147	-0.129173	0.77975	0.9998
ENSG00000069966	ENSG00000069966	GNB5	15:52408770-52587995	OK	9.20864	8.59608	-0.099309	-0.163263	0.77975	0.9998
ENSG00000272277	ENSG00000272277	RP1-40E16.12	6:3064224-3115421	OK	1.09586	0.738027	-0.570316	-0.131471	0.7798	0.9998
ENSG00000139641	ENSG00000139641	ESYT1	12:56511942-56538455	OK	31.1653	32.6771	0.0683422	0.135106	0.77985	0.9998
ENSG00000155636	ENSG00000155636	RBM45	2:178977150-179003738	OK	7.30078	6.85235	-0.0914516	-0.165215	0.77985	0.9998
ENSG00000129535	ENSG00000129535	NRL	14:24549315-24602058	OK	0.836436	0.681162	-0.296258	-0.089028	0.77995	0.9998
ENSG00000141627	ENSG00000141627	DYM	18:46550072-46987717	OK	21.1136	22.1761	0.0708302	0.143964	0.78	0.9998
ENSG00000255561	ENSG00000255561	FDXACB1	11:111652918-111756699	OK	0.841606	0.600063	-0.48803	-0.236278	0.78	0.9998
ENSG00000100077	ENSG00000100077	ADRBK2	22:25960815-26125261	OK	10.3132	9.46611	-0.123642	-0.132346	0.78015	0.9998
ENSG00000161981	ENSG00000161981	SNRNP25	16:96406-107669	OK	51.7223	48.5522	-0.091248	-0.168775	0.78025	0.9998
ENSG00000166135	ENSG00000166135	HIF1AN	10:102246398-102319755	OK	28.4892	32.3431	0.183042	0.133262	0.78025	0.9998
ENSG00000168137	ENSG00000168137	SETD5	3:9022274-9520924	OK	33.8807	31.6131	-0.0999379	-0.113798	0.78035	0.9998
ENSG00000004961	ENSG00000004961	HCCS	X:11129420-11683821	OK	34.2405	36.2136	0.0808258	0.167254	0.7804	0.9998
ENSG00000074319	ENSG00000074319	TSG101	11:18477370-18548779	OK	78.5786	74.1103	-0.084462	-0.167496	0.7805	0.9998
ENSG00000061273	ENSG00000061273	HDAC7	12:48099867-48231681	OK	7.49921	8.14935	0.119945	0.109449	0.78055	0.9998
ENSG00000175305	ENSG00000175305	CCNE2	8:95825538-96128683	OK	5.27385	4.03762	-0.385352	-0.174035	0.78055	0.9998
ENSG00000177045	ENSG00000177045	SIX5	19:46268042-46296060	OK	3.3911	2.86758	-0.241922	-0.187573	0.7806	0.9998
ENSG00000269987	ENSG00000269987	RP3-430N8.11	22:31366662-31375381	OK	1.04905	0.63735	-0.718929	-0.1143	0.7806	0.9998
ENSG00000198912	ENSG00000198912	C1orf174	1:3805688-3816857	OK	12.4678	13.2175	0.0842472	0.171774	0.78065	0.9998
ENSG00000162520	ENSG00000162520	SYNC	1:33116742-33169197	OK	3.74412	4.23605	0.178095	0.157583	0.7807	0.9998
ENSG00000144619	ENSG00000144619	CNTN4	3:2140496-3102829	OK	1.385	1.53325	0.146715	0.119951	0.7808	0.9998
ENSG00000168003	ENSG00000168003	SLC3A2	11:62623517-62656352	OK	237.672	226.623	-0.0686734	-0.13577	0.7808	0.9998
ENSG00000261408	ENSG00000261408	TEN1-CDK3	17:73937587-74023533	OK	0.972381	0.691445	-0.491907	-0.211749	0.7808	0.9998
ENSG00000010165	ENSG00000010165	METTL13	1:171750787-171783163	OK	32.279	33.994	0.0746822	0.155714	0.78085	0.9998
ENSG00000172748	ENSG00000172748	ZNF596	8:163185-197342	OK	1.01692	0.877451	-0.212823	-0.126181	0.78085	0.9998
ENSG00000133112	ENSG00000133112	TPT1	13:45911007-45965872	OK	2306	2437.26	0.0798648	0.163969	0.781	0.9998
ENSG00000196204	ENSG00000196204	RNF216P1	7:5013618-5112854	OK	16.2199	14.9926	-0.113513	-0.134143	0.781	0.9998
ENSG00000169629	ENSG00000169629	RGPD8	2:113127668-113192065	OK	0.683917	0.738701	0.11117	0.1188	0.7811	0.9998
ENSG00000105732	ENSG00000105732	ZNF574	19:42502472-42585701	OK	5.84426	6.20056	0.0853779	0.16929	0.7812	0.9998
ENSG00000179115	ENSG00000179115	FARSA	19:13033292-13044851	OK	47.4377	49.7412	0.0684099	0.166508	0.7812	0.9998
ENSG00000198231	ENSG00000198231	DDX42	17:61780191-61896677	OK	59.6878	55.722	-0.0991869	-0.102733	0.7812	0.9998
ENSG00000264538	ENSG00000264538	SUZ12P	17:29036316-29151794	OK	5.64204	6.50288	0.204861	0.173913	0.7812	0.9998
ENSG00000134057	ENSG00000134057	CCNB1	5:68462836-68474072	OK	104.246	98.9646	-0.0750031	-0.16049	0.78155	0.9998
ENSG00000176714	ENSG00000176714	CCDC121	2:27805896-27917840	OK	3.3207	2.40151	-0.467542	-0.165473	0.7816	0.9998
ENSG00000170473	ENSG00000170473	WIBG	12:56295196-56347811	OK	10.4581	11.2991	0.111587	0.174982	0.78165	0.9998
ENSG00000100219	ENSG00000100219	XBP1	22:29190542-29196585	OK	24.8276	26.2036	0.0778221	0.175892	0.78175	0.9998
ENSG00000187676	ENSG00000187676	B3GALTL	13:31774072-31906413	OK	9.74382	9.25638	-0.0740398	-0.166186	0.7819	0.9998
ENSG00000112033	ENSG00000112033	PPARD	6:35310334-35395968	OK	8.5711	9.04824	0.0781574	0.170378	0.782	0.9998
ENSG00000119139	ENSG00000119139	TJP2	9:71736208-71870124	OK	7.43876	7.0547	-0.076477	-0.133584	0.78205	0.9998
ENSG00000178397	ENSG00000178397	FAM220A	7:6369039-6388612	OK	15.2657	14.482	-0.0760266	-0.152768	0.78205	0.9998
ENSG00000107815	ENSG00000107815	C10orf2	10:102729214-102754158	OK	10.8424	9.43817	-0.200108	-0.164831	0.7821	0.9998
ENSG00000141258	ENSG00000141258	SGSM2	17:1963132-2284352	OK	20.614	22.3567	0.117082	0.104316	0.7821	0.9998
ENSG00000137364	ENSG00000137364	TPMT	6:18128541-18155305	OK	34.2094	35.8318	0.0668454	0.166737	0.78215	0.9998
ENSG00000164307	ENSG00000164307	ERAP1	5:95220801-96143803	OK	5.18802	6.0517	0.222157	0.0871559	0.78235	0.9998
ENSG00000134014	ENSG00000134014	ELP3	8:27947189-28048673	OK	18.7119	19.8765	0.087109	0.156549	0.78245	0.9998
ENSG00000163374	ENSG00000163374	YY1AP1	1:155579566-155829191	OK	52.4763	47.4763	-0.144456	-0.153764	0.7825	0.9998
ENSG00000169193	ENSG00000169193	CCDC126	7:23636997-23684327	OK	7.49234	6.88515	-0.121929	-0.180632	0.7825	0.9998
ENSG00000163935	ENSG00000163935	SFMBT1	3:52937587-53164478	OK	10.6179	11.2632	0.0851125	0.119265	0.78255	0.9998
ENSG00000108256	ENSG00000108256	NUFIP2	17:27582853-27621136	OK	21.9517	23.3834	0.0911549	0.104871	0.7826	0.9998
ENSG00000184432	ENSG00000184432	COPB2	3:138722803-139108574	OK	101.789	107.436	0.077905	0.128303	0.78265	0.9998
ENSG00000239569	ENSG00000239569	KMT2E-AS1	7:104653871-105039755	OK	0.97362	1.28936	0.405225	0.0546339	0.78265	0.9998
ENSG00000170043	ENSG00000170043	TRAPPC1	17:7825176-7853236	OK	174.865	163.823	-0.094102	-0.161357	0.7827	0.9998
ENSG00000198169	ENSG00000198169	ZNF251	8:145946297-145981802	OK	4.336	3.9929	-0.118929	-0.161062	0.7827	0.9998
ENSG00000256043	ENSG00000256043	CTSO	4:156845269-156875069	OK	1.01999	0.942286	-0.114318	-0.16556	0.7828	0.9998
ENSG00000113812	ENSG00000113812	ACTR8	3:53901092-53916296	OK	12.6668	13.6424	0.10704	0.155081	0.78285	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000109787	ENSG00000109787	KLF3	4:38614321-38702663	OK	6.20056	6.58897	0.0876532	0.164539	0.78295	0.9998
ENSG00000151458	ENSG00000151458	ANKRD50	4:125585206-125633887	OK	10.704	11.2503	0.0718067	0.16275	0.78295	0.9998
ENSG00000177042	ENSG00000177042	TMEM80	11:644232-727727	OK	5.98113	5.17633	-0.208487	-0.165675	0.78295	0.9998
ENSG00000127191	ENSG00000127191	TRAF2	9:139776363-139821059	OK	14.545	15.3178	0.0746845	0.1471	0.783	0.9998
ENSG00000162430	ENSG00000162430	SEPN1	1:26126666-26185903	OK	36.2545	34.2396	-0.0824952	-0.170825	0.783	0.9998
ENSG00000233006	ENSG00000233006	AC034220.3	5:131520568-131731306	OK	1.47676	1.02296	-0.529687	-0.179195	0.783	0.9998
ENSG00000258315	ENSG00000258315	C17orf49	17:6757179-6922978	OK	43.5603	37.4555	-0.217838	-0.193026	0.7831	0.9998
ENSG00000074219	ENSG00000074219	TEAD2	19:49834873-49891338	OK	7.70744	7.2486	-0.0885499	-0.160611	0.78315	0.9998
ENSG00000122034	ENSG00000122034	GTF3A	13:27998680-28024739	OK	130.532	137.485	0.0748721	0.166168	0.78315	0.9998
ENSG00000259494	ENSG00000259494	MRPL46	15:89002706-89089906	OK	32.2007	29.5725	-0.122837	-0.171484	0.78315	0.9998
ENSG00000196365	ENSG00000196365	LONP1	19:5674957-5720583	OK	43.0098	38.3143	-0.166782	-0.144162	0.7832	0.9998
ENSG00000249459	ENSG00000249459	ZNF286B	17:18538318-18585575	OK	1.2591	1.51321	0.265213	0.0650775	0.7832	0.9998
ENSG00000270607	ENSG00000270607	RP11-359E10.1	11:19372270-20143144	OK	1.35268	1.88293	0.477163	0.0958565	0.7832	0.9998
ENSG00000271430	ENSG00000271430	RP3-368A4.5	X:73164158-73513409	OK	0.663108	0.820329	0.306959	0.185894	0.7832	0.9998
ENSG00000164597	ENSG00000164597	COG5	7:106809405-107218906	OK	39.6749	43.5502	0.134452	0.141043	0.78325	0.9998
ENSG00000265519	ENSG00000265519	CTD-3157E16.1	17:15691100-15691519	OK	1.56709	1.8179	0.214179	0.169651	0.78325	0.9998
ENSG00000227775	ENSG00000227775	RP1-283E3.4	1:1634168-1677431	OK	1.09596	0.868203	-0.33609	-0.106173	0.7833	0.9998
ENSG00000162300	ENSG00000162300	ZFPL1	11:64851694-64883856	OK	25.8981	23.4333	-0.144287	-0.137031	0.78335	0.9998
ENSG00000184779	ENSG00000184779	RPS17	15:82821157-82824972	OK	2.13138	2.32823	0.127443	0.136082	0.78335	0.9998
ENSG00000185305	ENSG00000185305	ARL15	5:53179774-53606412	OK	10.4987	11.4727	0.128001	0.162929	0.7834	0.9998
ENSG00000182568	ENSG00000182568	SATB1	3:17198653-18959184	OK	4.23399	4.67704	0.143581	0.0900187	0.78345	0.9998
ENSG00000065518	ENSG00000065518	NDUFB4	3:120315155-120321347	OK	182.76	174.052	-0.0704317	-0.171307	0.7835	0.9998
ENSG00000105323	ENSG00000105323	HNRNPUL1	19:41768400-41930910	OK	90.8603	86.4604	-0.07161	-0.13684	0.7835	0.9998
ENSG00000166123	ENSG00000166123	GPT2	16:46918289-46965209	OK	3.99577	4.28963	0.10238	0.149372	0.7835	0.9998
ENSG00000166321	ENSG00000166321	NUDT13	10:74870216-75118617	OK	1.03157	0.874354	-0.238558	-0.0313532	0.78355	0.9998
ENSG00000057935	ENSG00000057935	MTA3	2:42721708-42984087	OK	18.2308	19.2598	0.0792148	0.144073	0.7836	0.9998
ENSG00000125744	ENSG00000125744	RTN2	19:45988546-46005768	OK	5.43792	5.91383	0.121039	0.138456	0.7836	0.9998
ENSG00000196466	ENSG00000196466	ZNF799	19:12490002-12750912	OK	0.828652	0.67059	-0.305336	-0.160724	0.78365	0.9998
ENSG00000198522	ENSG00000198522	GPN1	2:27805896-27917840	OK	35.021	31.774	-0.140375	-0.158998	0.7837	0.9998
ENSG00000267034	ENSG00000267034	RP11-384O8.1	2:223181960-223217708	OK	1.0364	1.15929	0.161669	0.171739	0.7837	0.9998
ENSG00000164151	ENSG00000164151	KIAA0947	5:5420776-5490347	OK	15.8917	16.6544	0.0676228	0.145874	0.78375	0.9998
ENSG00000269815	ENSG00000269815	CTD-2278I10.4	19:17402939-17445638	OK	0.439175	0.623917	0.506559	0.0489758	0.7838	0.9998
ENSG00000051620	ENSG00000051620	HEBP2	6:138723721-139018425	OK	11.3433	9.11522	-0.315491	-0.175859	0.78385	0.9998
ENSG00000136521	ENSG00000136521	NDUFB5	3:179322477-179345435	OK	153.211	145.043	-0.0790365	-0.0924746	0.78385	0.9998
ENSG00000185722	ENSG00000185722	ANKFY1	17:4046461-4167274	OK	21.155	22.1924	0.0690635	0.105173	0.78385	0.9998
ENSG00000110768	ENSG00000110768	GTF2H1	11:18343841-18388591	OK	44.5326	46.6774	0.0678642	0.139532	0.7839	0.9998
ENSG00000169957	ENSG00000169957	ZNF768	16:30535324-30569819	OK	24.0988	25.5141	0.0823358	0.169409	0.7839	0.9998
ENSG00000163545	ENSG00000163545	NUAK2	1:205271186-205290883	OK	1.62054	1.73773	0.100726	0.163083	0.78395	0.9998
ENSG00000100225	ENSG00000100225	FBXO7	22:32870662-32894818	OK	165.974	158.225	-0.06898	-0.165239	0.784	0.9998
ENSG00000185453	ENSG00000185453	C19orf68	19:48673948-48790865	OK	1.57381	1.30025	-0.275471	-0.153296	0.78405	0.9998
ENSG00000165629	ENSG00000165629	ATP5C1	10:7830091-7849778	OK	127.514	133.535	0.066568	0.165717	0.7841	0.9998
ENSG00000250264	ENSG00000250264	TAP2	6:32780539-32806599	OK	2.01078	1.45385	-0.467879	-0.202261	0.7841	0.9998
ENSG00000103264	ENSG00000103264	FBXO31	16:87117167-87438385	OK	8.50106	7.6322	-0.155544	-0.0985721	0.78415	0.9998
ENSG00000272003	ENSG00000272003	RP11-23P13.7	15:42120282-42190773	OK	1.41088	1.96799	0.480124	0.228631	0.7842	0.9998
ENSG00000013561	ENSG00000013561	RNF14	5:141323149-141369856	OK	74.867	70.4612	-0.0875011	-0.157491	0.78435	0.9998
ENSG00000089163	ENSG00000089163	SIRT4	12:120740118-120751144	OK	1.94172	1.77003	-0.133558	-0.157106	0.78435	0.9998
ENSG00000172939	ENSG00000172939	OXSR1	3:38206579-38296979	OK	25.4693	24.3324	-0.0658822	-0.143286	0.78435	0.9998
ENSG00000181744	ENSG00000181744	C3orf58	3:143690639-143767561	OK	3.52997	3.2906	-0.101307	-0.131347	0.78435	0.9998
ENSG00000198298	ENSG00000198298	ZNF485	10:44101854-44113351	OK	0.85604	0.754191	-0.182747	-0.139002	0.7844	0.9998
ENSG00000101843	ENSG00000101843	PSMD10	X:107327436-107334848	OK	43.7049	45.9407	0.071976	0.163786	0.78445	0.9998
ENSG00000188785	ENSG00000188785	ZNF548	19:57874844-57988938	OK	5.29851	5.78096	0.125721	0.116459	0.78445	0.9998
ENSG00000070159	ENSG00000070159	PTPN3	9:112137745-112260590	OK	6.88686	7.41095	0.105812	0.138098	0.7845	0.9998
ENSG00000169955	ENSG00000169955	ZNF747	16:30535324-30569819	OK	2.07928	2.49136	0.26085	0.172347	0.7845	0.9998
ENSG00000183793	ENSG00000183793	NPIPA5	16:15457515-15474904	OK	4.48994	4.16529	-0.108279	-0.164882	0.78455	0.9998
ENSG00000178386	ENSG00000178386	ZNF223	19:44529493-44593766	OK	1.53538	1.76846	0.203895	0.139204	0.7846	0.9998
ENSG00000167123	ENSG00000167123	CERCAM	9:131174029-131199626	OK	22.2477	23.3536	0.0699888	0.149183	0.78465	0.9998
ENSG00000112651	ENSG00000112651	MRPL2	6:43005354-43042837	OK	35.4109	32.2909	-0.133066	-0.161008	0.78495	0.9998
ENSG00000174373	ENSG00000174373	RALGAPA1	14:36007557-36278510	OK	9.74351	9.11053	-0.0969055	-0.118223	0.785	0.9998
ENSG00000106344	ENSG00000106344	RBM28	7:127937737-127983962	OK	36.0646	33.4547	-0.108373	-0.153717	0.78505	0.9998
ENSG00000112365	ENSG00000112365	ZBTB24	6:109765264-109804440	OK	3.19437	3.64613	0.190837	0.164054	0.78505	0.9998
ENSG00000082293	ENSG00000082293	COL19A1	6:70576462-70919679	OK	1.99826	2.16992	0.118902	0.098937	0.78515	0.9998
ENSG00000163964	ENSG00000163964	PIGX	3:196366556-196462878	OK	33.7956	31.3177	-0.109859	-0.157698	0.78515	0.9998
ENSG00000254719	ENSG00000254719	RP11-351I24.3	11:9776316-10315754	OK	19.1181	29.2076	0.611405	0.166782	0.78515	0.9998
ENSG00000025434	ENSG00000025434	NR1H3	11:47260852-47290396	OK	2.68545	2.95641	0.13868	0.081011	0.7852	0.9998
ENSG00000259332	ENSG00000259332	ST20-MTHFS	15:80125926-80217194	OK	4.93289	6.41294	0.378553	0.209274	0.7852	0.9998
ENSG00000269990	ENSG00000269990	CTD-3074O7.12	11:66234215-66313709	OK	1.91036	2.40612	0.332859	0.151992	0.78525	0.9998
ENSG00000184886	ENSG00000184886	PIGW	17:34842472-34899284	OK	5.98965	7.10316	0.245988	0.168619	0.7854	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267059	ENSG00000267059	UQCR11	19:1576638-1605480	OK	18.4444	21.6855	0.233547	0.168886	0.7854	0.9998
ENSG00000134780	ENSG00000134780	DAGLA	11:61447904-61634826	OK	1.64981	2.21187	0.422966	0.190643	0.7855	0.9998
ENSG00000126581	ENSG00000126581	BECN1	17:40950809-40995774	OK	50.3593	46.8683	-0.103646	-0.126494	0.78555	0.9998
ENSG00000170791	ENSG00000170791	CHCHD7	8:57124244-57131357	OK	19.5745	20.9421	0.0974267	0.160951	0.78555	0.9998
ENSG00000182240	ENSG00000182240	BACE2	21:42539727-42654445	OK	168.271	158.492	-0.0863787	-0.14929	0.78575	0.9998
ENSG00000136319	ENSG00000136319	TTC5	14:20724716-20774970	OK	9.51424	8.85761	-0.103171	-0.157711	0.78595	0.9998
ENSG00000137106	ENSG00000137106	GRHPR	9:37422662-37436987	OK	106.082	101.19	-0.0681221	-0.163999	0.78595	0.9998
ENSG00000185475	ENSG00000185475	TMEM179B	11:62538591-62559493	OK	35.1129	32.5698	-0.108467	-0.15967	0.7861	0.9998
ENSG00000163848	ENSG00000163848	ZNF148	3:124801479-125094198	OK	8.77597	9.3263	0.0877456	0.131291	0.7862	0.9998
ENSG00000084234	ENSG00000084234	APLP2	11:129936835-130014699	OK	86.4636	90.4914	0.0656874	0.155958	0.7865	0.9998
ENSG00000104524	ENSG00000104524	PYCRL	8:144686082-144691943	OK	3.63141	3.88432	0.0971299	0.156284	0.78665	0.9998
ENSG00000156983	ENSG00000156983	BRPF1	3:9773412-9789702	OK	8.01996	7.57059	-0.0831894	-0.124583	0.7867	0.9998
ENSG00000138363	ENSG00000138363	ATIC	2:216176539-216214487	OK	84.9448	89.6003	0.0769776	0.14676	0.78675	0.9998
ENSG00000104047	ENSG00000104047	DTWD1	15:49913176-49937333	OK	6.24613	5.72103	-0.126688	-0.162515	0.78685	0.9998
ENSG00000145335	ENSG00000145335	SNCA	4:90472506-90763129	OK	292.184	278.02	-0.0716842	-0.155685	0.78685	0.9998
ENSG00000213949	ENSG00000213949	ITGA1	5:51971026-52390609	OK	2.92681	3.40607	0.218779	0.088186	0.78685	0.9998
ENSG00000174109	ENSG00000174109	C16orf91	16:1469744-1479345	OK	9.89661	9.28881	-0.0914408	-0.163056	0.7869	0.9998
ENSG00000165526	ENSG00000165526	RPUSD4	11:126071992-126148026	OK	13.4763	15.1772	0.171484	0.143203	0.78705	0.9998
ENSG00000233218	ENSG00000233218	SNX18P16	1:142618768-142729975	OK	0.727843	0.46372	-0.650375	-0.168927	0.78705	0.9998
ENSG00000119326	ENSG00000119326	CTNNAL1	9:111696460-111775809	OK	22.1139	23.3862	0.0807027	0.164898	0.7871	0.9998
ENSG00000234558	ENSG00000234558	API5P1	X:115238173-115239683	OK	1.84396	1.99435	0.113114	0.161881	0.7871	0.9998
ENSG00000197785	ENSG00000197785	ATAD3A	1:1447530-1470067	OK	22.5314	21.4692	-0.069668	-0.147045	0.78715	0.9998
ENSG00000138101	ENSG00000138101	DTNB	2:25600066-25896503	OK	10.9609	10.3886	-0.0773599	-0.134106	0.78725	0.9998
ENSG00000166401	ENSG00000166401	SERPINB8	18:61616534-61672278	OK	2.41066	2.68958	0.157953	0.147777	0.7873	0.9998
ENSG00000173011	ENSG00000173011	TADA2B	4:6910968-7059679	OK	6.9838	8.24996	0.240376	0.117092	0.7873	0.9998
ENSG00000135624	ENSG00000135624	CCT7	2:73460547-73480149	OK	214.955	225.149	0.066847	0.160012	0.78735	0.9998
ENSG00000143319	ENSG00000143319	ISG20L2	1:156691682-156706752	OK	29.9989	32.3338	0.108133	0.167288	0.78735	0.9998
ENSG00000273047	ENSG00000273047	RP4-583P15.14	20:62289162-62374858	OK	0.819459	1.3041	0.670313	0.0429414	0.78745	0.9998
ENSG00000053501	ENSG00000053501	USE1	19:17326154-17330638	OK	30.3526	28.6193	-0.0848351	-0.163744	0.78755	0.9998
ENSG00000173928	ENSG00000173928	SWSAP1	19:11478798-11487627	OK	1.60067	1.73747	0.118312	0.164749	0.78755	0.9998
ENSG00000196208	ENSG00000196208	GREB1	2:11674241-11782914	OK	51.3154	54.1693	0.0780849	0.123632	0.78755	0.9998
ENSG00000171490	ENSG00000171490	RSL1D1	16:11929055-11945442	OK	114.853	120.806	0.0729085	0.150016	0.78765	0.9998
ENSG00000250251	ENSG00000250251	PKD1P6	16:15068447-15248421	OK	4.89619	4.19759	-0.222098	-0.0656627	0.78765	0.9998
ENSG00000268670	ENSG00000268670	CTD-2622I13.3	19:4044361-4066943	OK	0.627798	0.952726	0.601761	0.143216	0.7877	0.9998
ENSG00000185839	ENSG00000185839	RP4-592A1.2	1:59096512-59097202	OK	168.764	160.024	-0.0767123	-0.163293	0.78775	0.9998
ENSG00000109270	ENSG00000109270	LAMTOR3	4:100799492-100815647	OK	25.2775	26.8126	0.0850569	0.165513	0.78785	0.9998
ENSG00000148842	ENSG00000148842	CNNM2	10:104678049-104953056	OK	4.90312	4.35816	-0.16998	-0.149215	0.78785	0.9998
ENSG00000181045	ENSG00000181045	SLC26A11	17:78143790-78227299	OK	10.4293	11.3043	0.116224	0.107668	0.7879	0.9998
ENSG00000009790	ENSG00000009790	TRAF3IP3	1:209929376-209957904	OK	4.13561	4.60716	0.155777	0.140641	0.78805	0.9998
ENSG00000086827	ENSG00000086827	ZW10	11:113603908-113644533	OK	5.88706	5.56247	-0.081822	-0.165166	0.78805	0.9998
ENSG00000103544	ENSG00000103544	C16orf62	16:19566561-19897489	OK	12.2431	13.5424	0.145515	0.104026	0.78805	0.9998
ENSG00000256294	ENSG00000256294	ZNF225	19:44598491-44637027	OK	1.93782	1.69687	-0.191561	-0.147317	0.78805	0.9998
ENSG00000115816	ENSG00000115816	CEBPZ	2:37394962-37551951	OK	24.4174	28.4618	0.221118	0.135669	0.7881	0.9998
ENSG00000085871	ENSG00000085871	MGST2	4:140586921-141075338	OK	25.5997	23.9401	-0.0967006	-0.164256	0.78815	0.9998
ENSG00000269227	ENSG00000269227	RP11-345P4.6	1:1590785-1624167	OK	0.738351	0.510048	-0.533674	-0.0814078	0.78825	0.9998
ENSG00000225265	ENSG00000225265	RP11-378J18.3	1:222731243-222766374	OK	0.922735	0.674379	-0.452356	-0.188407	0.7884	0.9998
ENSG00000100241	ENSG00000100241	SBF1	22:50781732-50913454	OK	28.7876	30.3421	0.0758743	0.1234	0.78845	0.9998
ENSG00000164889	ENSG00000164889	SLC4A2	7:150750898-150773617	OK	128.151	135.828	0.0839375	0.108822	0.78845	0.9998
ENSG00000083807	ENSG00000083807	SLC27A5	19:58985383-59023780	OK	1.09911	0.882153	-0.317238	-0.128567	0.7885	0.9998
ENSG00000198753	ENSG00000198753	PLXNB3	X:152990322-153051187	OK	15.3206	14.1373	-0.115971	-0.0956594	0.78865	0.9998
ENSG00000100023	ENSG00000100023	PPIL2	22:22006558-22090123	OK	20.4631	21.5399	0.0739837	0.152094	0.78875	0.9998
ENSG00000114395	ENSG00000114395	CYB561D2	3:50384760-50541675	OK	19.5267	21.5822	0.144391	0.159506	0.78885	0.9998
ENSG00000010244	ENSG00000010244	ZNF207	17:30593194-30708905	OK	58.3857	55.2373	-0.0799722	-0.148926	0.7889	0.9998
ENSG00000111237	ENSG00000111237	VPS29	12:110928901-111021125	OK	115.951	108.048	-0.101851	-0.163647	0.78895	0.9998
ENSG00000157014	ENSG00000157014	TATDN2	3:10289706-10362862	OK	17.5096	18.958	0.114664	0.146879	0.78895	0.9998
ENSG00000205903	ENSG00000205903	ZNF316	7:6676952-6694242	OK	10.6563	11.2646	0.0800941	0.164203	0.78895	0.9998
ENSG00000114023	ENSG00000114023	FAM162A	3:122103022-122134882	OK	108.436	102.585	-0.0800228	-0.166997	0.789	0.9998
ENSG00000162909	ENSG00000162909	CAPN2	1:223889294-223963720	OK	85.4497	89.3489	0.0643735	0.132943	0.789	0.9998
ENSG00000181751	ENSG00000181751	C5orf30	5:102594402-102614361	OK	48.011	45.625	-0.0735413	-0.163766	0.78905	0.9998
ENSG00000236829	ENSG00000236829	Z97634.3	16:420772-442960	OK	1.86488	1.45781	-0.35528	-0.0801078	0.7891	0.9998
ENSG00000107651	ENSG00000107651	SEC23IP	10:121652222-121702014	OK	20.0027	19.0187	-0.072776	-0.106473	0.78915	0.9998
ENSG00000119318	ENSG00000119318	RAD23B	9:110045417-110094475	OK	120.576	126.866	0.0733693	0.160529	0.7892	0.9998
ENSG00000127957	ENSG00000127957	PMS2P3	7:75123400-75157478	OK	8.79586	9.4607	0.105123	0.156175	0.78925	0.9998
ENSG00000137872	ENSG00000137872	SEMA6D	15:47476297-48066420	OK	15.5473	16.3742	0.074761	0.115096	0.7893	0.9998
ENSG00000205339	ENSG00000205339	IPO7	11:9406168-9469673	OK	64.611	67.5149	0.0634266	0.124146	0.7893	0.9998
ENSG00000105427	ENSG00000105427	CNFN	19:42891170-42894439	OK	1.91893	1.71983	-0.158035	-0.152104	0.78935	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000144021	ENSG00000144021	CIAO1	2:96931869-96939087	OK	61.9472	59.0251	-0.0697112	-0.156965	0.7894	0.9998
ENSG00000162736	ENSG00000162736	NCSTN	1:160259062-160328742	OK	64.8263	58.3976	-0.150671	-0.123778	0.78945	0.9998
ENSG00000113575	ENSG00000113575	PPP2CA	5:133450401-133706738	OK	52.4135	59.7187	0.188244	0.173175	0.7895	0.9998
ENSG00000215440	ENSG00000215440	NPEPL1	20:57226327-57294294	OK	7.55848	9.24165	0.290055	0.171915	0.7895	0.9998
ENSG00000235477	ENSG00000235477	RP11-122G18.5	1:161337811-161341754	OK	6.2044	5.82462	-0.0911295	-0.167193	0.78955	0.9998
ENSG00000126749	ENSG00000126749	EMG1	12:7072407-7178336	OK	42.9644	48.8849	0.186247	0.153446	0.7896	0.9998
ENSG00000230939	ENSG00000230939	RP11-314C16.1	6:8784410-8785678	OK	3.22231	2.9021	-0.150999	-0.168359	0.78965	0.9998
ENSG00000138382	ENSG00000138382	METTL5	2:170648442-170681441	OK	51.9043	57.7632	0.154296	0.165434	0.7897	0.9998
ENSG00000104973	ENSG00000104973	MED25	19:50321538-50364001	OK	28.4548	26.1014	-0.124543	-0.150676	0.78975	0.9998
ENSG00000157985	ENSG00000157985	AGAP1	2:236402732-237040444	OK	13.6177	12.7798	-0.091618	-0.116767	0.78985	0.9998
ENSG00000225518	ENSG00000225518	RP11-396C23.2	1:226271339-226277993	OK	0.639185	0.742341	0.215848	0.147317	0.78985	0.9998
ENSG00000113108	ENSG00000113108	APBB3	5:139781398-139973337	OK	11.0126	9.9132	-0.151731	-0.0636843	0.78995	0.9998
ENSG00000260114	ENSG00000260114	CTD-2574D22.4	16:29911695-29940254	OK	2.00491	2.30741	0.202741	0.16434	0.79	0.9998
ENSG00000144381	ENSG00000144381	HSPD1	2:198351304-198418423	OK	294.153	311.061	0.0806311	0.150908	0.79005	0.9998
ENSG00000157601	ENSG00000157601	MX1	21:42792230-42831141	OK	0.628435	0.690644	0.136177	0.0725692	0.79005	0.9998
ENSG00000072849	ENSG00000072849	DERL2	17:5374570-5394134	OK	39.3178	42.3783	0.108143	0.157595	0.79015	0.9998
ENSG00000125356	ENSG00000125356	NDUFA1	X:119004496-119010625	OK	170.055	161.912	-0.0707916	-0.163631	0.79015	0.9998
ENSG00000173480	ENSG00000173480	ZNF417	19:58281022-58427978	OK	2.41004	2.74383	0.187136	0.117673	0.79015	0.9998
ENSG00000159593	ENSG00000159593	NAE1	16:66836777-66907159	OK	33.1537	31.6378	-0.06752	-0.140177	0.7903	0.9998
ENSG00000234608	ENSG00000234608	MAPKAPK5-AS1	12:112277570-112334343	OK	12.7823	14.993	0.230142	0.187391	0.7903	0.9998
ENSG00000100068	ENSG00000100068	LRP5L	22:25747384-25801344	OK	2.6312	2.44321	-0.106942	-0.147962	0.79035	0.9998
ENSG00000138867	ENSG00000138867	GUCD1	22:24936405-25024972	OK	45.7324	48.888	0.0962624	0.118473	0.79035	0.9998
ENSG00000123815	ENSG00000123815	ADCK4	19:41197433-41271294	OK	10.3138	9.34556	-0.142229	-0.127788	0.79045	0.9998
ENSG00000267125	ENSG00000267125	CTB-31O20.6	19:1852397-1863567	OK	3.74983	2.58678	-0.535668	-0.208606	0.79045	0.9998
ENSG00000103194	ENSG00000103194	USP10	16:84733583-84813528	OK	14.0645	14.7969	0.0732444	0.127834	0.7905	0.9998
ENSG00000012061	ENSG00000012061	ERCC1	19:45882891-45982086	OK	54.367	57.7793	0.0878224	0.150497	0.79065	0.9998
ENSG00000104880	ENSG00000104880	ARHGEF18	19:7413847-7537363	OK	9.05434	9.58439	0.0820779	0.121429	0.79065	0.9998
ENSG00000134970	ENSG00000134970	TMED7	5:114914338-114968689	OK	15.2338	14.4228	-0.0789239	-0.143412	0.79065	0.9998
ENSG00000174851	ENSG00000174851	YIF1A	11:66036003-66056641	OK	46.3171	51.1435	0.143004	0.152512	0.79065	0.9998
ENSG00000145703	ENSG00000145703	IQGAP2	5:75699073-76031606	OK	2.28342	2.65163	0.215683	0.0903166	0.7907	0.9998
ENSG00000154832	ENSG00000154832	CXXC1	18:47808712-47814674	OK	19.4548	20.7039	0.0897756	0.141989	0.7907	0.9998
ENSG00000213297	ENSG00000213297	ZNF625-ZNF20	19:12203077-12267546	OK	0.770399	0.867847	0.171835	0.155936	0.79075	0.9998
ENSG00000067445	ENSG00000067445	TRO	X:54946894-54957864	OK	8.57113	9.0761	0.0825873	0.121372	0.79095	0.9998
ENSG00000152422	ENSG00000152422	XRCC4	5:82348664-82649606	OK	11.1507	8.93276	-0.319954	-0.236432	0.79095	0.9998
ENSG00000167333	ENSG00000167333	TRIM68	11:4619901-4629489	OK	4.60291	4.89936	0.0900476	0.129263	0.791	0.9998
ENSG00000196950	ENSG00000196950	SLC39A10	2:196440700-196602426	OK	9.05738	8.61414	-0.0723867	-0.122312	0.791	0.9998
ENSG00000100941	ENSG00000100941	PNN	14:39644088-39652422	OK	36.9252	38.5181	0.0609301	0.144362	0.79115	0.9998
ENSG00000120690	ENSG00000120690	ELF1	13:41506055-41658137	OK	17.1182	18.4248	0.106118	0.15572	0.79115	0.9998
ENSG00000154978	ENSG00000154978	VOPP1	7:55503748-55640681	OK	15.5828	16.3149	0.066236	0.147094	0.79115	0.9998
ENSG00000197932	ENSG00000197932	F8A1	X:154064062-154288578	OK	3.23447	2.68549	-0.268345	-0.158463	0.79115	0.9998
ENSG00000198929	ENSG00000198929	NOS1AP	1:162039563-162356600	OK	3.12491	3.49572	0.161773	0.145964	0.79115	0.9998
ENSG00000058063	ENSG00000058063	ATP11B	3:182511287-182639726	OK	27.8104	26.0518	-0.0942402	-0.149538	0.7912	0.9998
ENSG00000081803	ENSG00000081803	CADPS2	7:121958480-122526813	OK	4.6328	4.37463	-0.0827216	-0.158451	0.79125	0.9998
ENSG00000070413	ENSG00000070413	DGCR2	22:19023794-19115962	OK	18.0074	17.0337	-0.0801993	-0.126378	0.7913	0.9998
ENSG00000111203	ENSG00000111203	ITFG2	12:2904118-3050306	OK	11.5173	13.5025	0.229419	0.0720968	0.7913	0.9998
ENSG00000148672	ENSG00000148672	GLUD1	10:88810242-88951225	OK	49.2957	46.7187	-0.0774619	-0.155326	0.7913	0.9998
ENSG00000232656	ENSG00000232656	IDI2-AS1	10:1034337-1095110	OK	1.879	1.42785	-0.396126	-0.0828611	0.7913	0.9998
ENSG00000105516	ENSG00000105516	DBP	19:49118584-49140695	OK	17.2886	20.9188	0.274984	0.101221	0.79135	0.9998
ENSG00000181220	ENSG00000181220	ZNF746	7:149169884-149194908	OK	8.25133	7.83737	-0.0742571	-0.156495	0.79145	0.9998
ENSG00000089639	ENSG00000089639	GMIP	19:19740284-19754476	OK	6.97469	6.55146	-0.0903138	-0.147915	0.7915	0.9998
ENSG00000163322	ENSG00000163322	FAM175A	4:84377084-84444501	OK	3.52552	3.10087	-0.185166	-0.137738	0.7915	0.9998
ENSG00000131979	ENSG00000131979	GCH1	14:55308725-55369570	OK	2.83286	3.03014	0.0971242	0.146468	0.79155	0.9998
ENSG00000168894	ENSG00000168894	RNF181	2:85822847-85824736	OK	152.392	159.652	0.0671447	0.159186	0.7917	0.9998
ENSG00000244405	ENSG00000244405	ETV5	3:185764096-186080026	OK	198.453	184.02	-0.108935	-0.142137	0.7917	0.9998
ENSG00000117054	ENSG00000117054	ACADM	1:76190035-76260764	OK	35.4098	32.6651	-0.116399	-0.157747	0.79175	0.9998
ENSG00000126821	ENSG00000126821	SGPP1	14:64150931-64194757	OK	8.88073	8.44477	-0.0726211	-0.158687	0.79185	0.9998
ENSG00000240204	ENSG00000240204	SMKR1	7:129142319-129152773	OK	0.67566	0.805418	0.253441	0.140874	0.79185	0.9998
ENSG00000126003	ENSG00000126003	PLAGL2	20:30780305-30795594	OK	6.61381	6.28967	-0.0724962	-0.155465	0.7919	0.9998
ENSG00000166188	ENSG00000166188	ZNF319	16:58028571-58055522	OK	1.14096	1.00764	-0.179266	-0.118063	0.792	0.9998
ENSG00000163913	ENSG00000163913	IFT122	3:129158967-129239198	OK	7.15286	6.74751	-0.0841655	-0.0996467	0.79205	0.9998
ENSG00000007202	ENSG00000007202	KIAA0100	17:26782769-26972472	OK	73.9103	69.5354	-0.0880263	-0.108661	0.7921	0.9998
ENSG00000159556	ENSG00000159556	ISL2	15:76629064-76634817	OK	0.748324	0.824154	0.139251	0.153543	0.7921	0.9998
ENSG00000172375	ENSG00000172375	C2CD2L	11:118967212-118989252	OK	5.03824	5.54354	0.137889	0.140803	0.7921	0.9998
ENSG00000203896	ENSG00000203896	LIME1	20:62289162-62374858	OK	1.59798	1.92014	0.264966	0.0592698	0.7921	0.9998
ENSG00000240399	ENSG00000240399	RP1-228P16.1	12:48436680-48540187	OK	0.601862	0.862791	0.519578	0.0358681	0.7923	0.9998
ENSG00000257553	ENSG00000257553	RP11-603J24.17	12:56473640-56507691	OK	3.99113	5.19641	0.380718	0.0438021	0.7923	0.9998
ENSG00000156502	ENSG00000156502	SUPV3L1	10:70939987-70968855	OK	24.0075	25.6341	0.0945808	0.1619	0.7924	0.9998
ENSG00000108883	ENSG00000108883	EFTUD2	17:42923720-42994305	OK	94.6518	100.247	0.0828537	0.126005	0.79245	0.9998
ENSG00000170881	ENSG00000170881	RNF139	8:125486978-125500155	OK	15.9463	16.7441	0.0704359	0.158219	0.79245	0.9998
ENSG00000204839	ENSG00000204839	MROH6	8:144648356-144655141	OK	1.78166	1.98989	0.159466	0.143603	0.79245	0.9998
ENSG00000273237	ENSG00000273237	CTB-119C2.1	7:26191859-26226745	OK	0.444434	0.707947	0.671671	0.193054	0.7926	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000007255	ENSG00000007255	TRAPPC6A	19:45574757-45808541	OK	17.5982	13.5444	-0.377729	-0.209372	0.7927	0.9998
ENSG00000088970	ENSG00000088970	PLK1S1	20:21106623-21227260	OK	3.484	3.73171	0.0990919	0.133413	0.7927	0.9998
ENSG00000114529	ENSG00000114529	C3orf52	3:111805181-111852152	OK	4.59445	4.29513	-0.0971909	-0.144019	0.7927	0.9998
ENSG00000163113	ENSG00000163113	OTUD7B	1:149909704-149982625	OK	21.5676	23.0876	0.0982514	0.157481	0.7927	0.9998
ENSG00000204406	ENSG00000204406	MBD5	2:148602085-149275805	OK	8.23595	6.82307	-0.271513	-0.159962	0.7928	0.9998
ENSG00000213089	ENSG00000213089	PDCL3P5	6:150920998-151164799	OK	1.00255	1.40948	0.491486	0.219661	0.79285	0.9998
ENSG00000187667	ENSG00000187667	WHAMMP3	15:23187727-23208737	OK	1.43937	1.28199	-0.167047	-0.143359	0.7929	0.9998
ENSG00000085185	ENSG00000085185	BCORL1	X:129115082-129192058	OK	4.22311	3.94976	-0.0965393	-0.127754	0.79295	0.9998
ENSG00000230266	ENSG00000230266	XXYLT1-AS2	3:194789007-194991896	OK	1.78947	1.15956	-0.625952	-0.209682	0.79295	0.9998
ENSG00000163453	ENSG00000163453	IGFBP7	4:57829535-58071676	OK	278.172	263.317	-0.0791755	-0.161542	0.793	0.9998
ENSG00000133142	ENSG00000133142	TCEAL4	X:102831158-102842657	OK	100.32	104.892	0.0642963	0.153327	0.79305	0.9998
ENSG00000160193	ENSG00000160193	WDR4	21:44263203-44299678	OK	6.18583	5.80476	-0.091731	-0.148233	0.79305	0.9998
ENSG00000197162	ENSG00000197162	ZNF785	16:30580666-30597092	OK	3.13462	3.38326	0.110126	0.151347	0.79305	0.9998
ENSG00000076662	ENSG00000076662	ICAM3	19:10444451-10450499	OK	14.7138	13.7609	-0.0965922	-0.155685	0.7931	0.9998
ENSG00000145743	ENSG00000145743	FBXL17	5:107194735-107717799	OK	4.38668	4.93057	0.168626	0.158914	0.79315	0.9998
ENSG00000011021	ENSG00000011021	CLCN6	1:11821843-11908402	OK	8.03391	7.48247	-0.102588	-0.110242	0.7932	0.9998
ENSG00000111726	ENSG00000111726	CMAS	12:22199107-22589975	OK	37.6035	40.0799	0.0920104	0.152487	0.79325	0.9998
ENSG00000074855	ENSG00000074855	ANO8	19:17402939-17445638	OK	2.71588	3.1382	0.208514	0.144979	0.7933	0.9998
ENSG00000154529	ENSG00000154529	CNTNAP3B	9:43684901-43924049	OK	0.941821	0.872087	-0.11098	-0.109154	0.79335	0.9998
ENSG00000162694	ENSG00000162694	EXTL2	1:101337942-101361554	OK	11.8204	11.1994	-0.0778581	-0.140833	0.79335	0.9998
ENSG00000250983	ENSG00000250983	RP11-91K8.2	3:133264914-133265116	OK	1.07664	1.08787	0.0149732	0.00677282	0.79335	0.9998
ENSG00000135838	ENSG00000135838	NPL	1:182758427-182799519	OK	12.6244	11.9058	-0.0845486	-0.145573	0.79345	0.9998
ENSG00000171488	ENSG00000171488	LRRC8C	1:89990394-90402170	OK	1.8703	1.6626	-0.169825	-0.125401	0.79345	0.9998
ENSG00000143442	ENSG00000143442	POGZ	1:151375199-151431941	OK	29.4428	27.9957	-0.0727074	-0.0745396	0.7935	0.9998
ENSG00000145040	ENSG00000145040	UCN2	3:48555116-48601206	OK	23.7533	26.5064	0.158213	0.164472	0.79365	0.9998
ENSG00000156232	ENSG00000156232	WHAMM	15:83478379-83503611	OK	2.95317	3.13919	0.08813	0.137361	0.7937	0.9998
ENSG00000240356	ENSG00000240356	RPL23AP7	2:114368078-114384667	OK	7.33546	6.8245	-0.104163	-0.151484	0.7937	0.9998
ENSG00000165861	ENSG00000165861	ZFYVE1	14:73436158-73493920	OK	12.4857	11.8566	-0.0745764	-0.131671	0.79385	0.9998
ENSG00000171150	ENSG00000171150	SOCS5	2:46926090-46990268	OK	7.10635	6.75873	-0.0723566	-0.157632	0.79385	0.9998
ENSG00000157873	ENSG00000157873	TNFRSF14	1:2481358-2496821	OK	246.164	259.428	0.0757165	0.147429	0.794	0.9998
ENSG00000183979	ENSG00000183979	NPB	17:79845712-79869340	OK	0.459737	0.658683	0.518777	0.0459974	0.79405	0.9998
ENSG00000100902	ENSG00000100902	PSMA6	14:35514112-35786699	OK	186.006	197.318	0.0851788	0.155029	0.7941	0.9998
ENSG00000253159	ENSG00000253159	PCDHGA12	5:140710251-140892546	OK	4.24902	4.82468	0.183303	0.161355	0.7941	0.9998
ENSG00000177666	ENSG00000177666	PNPLA2	11:818901-842545	OK	20.8279	23.833	0.194441	0.0991831	0.79415	0.9998
ENSG00000105281	ENSG00000105281	SLC1A5	19:47222763-47291851	OK	55.4444	59.2643	0.0961194	0.158685	0.7942	0.9998
ENSG00000135678	ENSG00000135678	CPM	12:69201955-69365350	OK	13.7927	15.6851	0.185494	0.0661101	0.7942	0.9998
ENSG00000173209	ENSG00000173209	AHSA2	2:61404552-61697904	OK	14.8445	13.3031	-0.158172	-0.0986469	0.7942	0.9998
ENSG00000130844	ENSG00000130844	ZNF331	19:54024234-54083523	OK	4.12835	3.8849	-0.087689	-0.117452	0.79425	0.9998
ENSG00000271843	ENSG00000271843	RP11-245J9.5	3:63989697-64009658	OK	0.740521	0.50276	-0.55867	-0.0787063	0.79425	0.9998
ENSG00000171793	ENSG00000171793	CTPS1	1:41445006-41478235	OK	31.0484	32.6788	0.0738329	0.135546	0.7943	0.9998
ENSG00000233170	ENSG00000233170	RP11-863K10.4	8:37592278-37616619	OK	0.604983	0.820485	0.439582	0.0728982	0.7943	0.9998
ENSG00000122705	ENSG00000122705	CLTA	9:36190852-36304921	OK	184.109	193.681	0.0731252	0.157948	0.79435	0.9998
ENSG00000134461	ENSG00000134461	ANKRD16	10:5903579-5987863	OK	3.24549	2.73383	-0.247512	-0.151528	0.79435	0.9998
ENSG00000105499	ENSG00000105499	PLA2G4C	19:48551099-48614074	OK	6.23688	6.68053	0.0991369	0.127342	0.79455	0.9998
ENSG00000141447	ENSG00000141447	OSBPL1A	18:21718941-21977844	OK	34.8878	36.6076	0.0694193	0.129504	0.79455	0.9998
ENSG00000229400	ENSG00000229400	RP11-3L21.2	1:224572844-224928251	OK	0.68384	0.96613	0.498557	0.0485537	0.7946	0.9998
ENSG00000173226	ENSG00000173226	IQCB1	3:121488609-121553926	OK	12.5876	11.924	-0.0781407	-0.133953	0.79465	0.9998
ENSG00000010361	ENSG00000010361	FUZ	19:50270224-50320633	OK	14.8975	13.2278	-0.171494	-0.116265	0.7947	0.9998
ENSG00000166444	ENSG00000166444	ST5	11:8703957-8932498	OK	36.8516	33.1939	-0.150808	-0.0590875	0.7947	0.9998
ENSG00000055609	ENSG00000055609	KMT2C	7:151832009-152133090	OK	12.115	12.858	0.0858715	0.0819207	0.7948	0.9998
ENSG00000196873	ENSG00000196873	CBWD3	9:70856396-70914929	OK	2.71652	2.51544	-0.110951	-0.157639	0.7949	0.9998
ENSG00000083720	ENSG00000083720	OXCT1	5:41730166-41871059	OK	46.7888	49.0509	0.0681151	0.134039	0.79505	0.9998
ENSG00000118096	ENSG00000118096	IFT46	11:118307204-118473748	OK	5.77625	4.57319	-0.336931	-0.176648	0.79505	0.9998
ENSG00000163251	ENSG00000163251	FZD5	2:208627309-208634287	OK	0.884407	0.944103	0.094234	0.159598	0.79505	0.9998
ENSG00000249286	ENSG00000249286	CTD-2210P15.2	5:43571695-43707507	OK	0.876225	1.14253	0.382854	0.0392596	0.79505	0.9998
ENSG00000132199	ENSG00000132199	ENOSF1	18:596987-712676	OK	17.7102	19.4077	0.132046	0.105201	0.7951	0.9998
ENSG00000153707	ENSG00000153707	PTPRD	9:8314245-10612723	OK	2.74003	2.4368	-0.169203	-0.103327	0.7953	0.9998
ENSG00000125875	ENSG00000125875	TBC1D20	20:416123-443197	OK	10.3926	10.9417	0.0742705	0.161548	0.79535	0.9998
ENSG00000159346	ENSG00000159346	ADIPOR1	1:202909950-202927700	OK	205.977	196.9	-0.0650172	-0.156024	0.79535	0.9998
ENSG00000107036	ENSG00000107036	KIAA1432	9:5629024-5833117	OK	8.8053	9.84662	0.161256	0.117485	0.79545	0.9998
ENSG00000164366	ENSG00000164366	CCDC127	5:196985-218330	OK	5.68811	5.23883	-0.118704	-0.10724	0.79545	0.9998
ENSG00000166068	ENSG00000166068	SPRED1	15:38544526-38649450	OK	7.01508	7.41048	0.079108	0.118036	0.79545	0.9998
ENSG00000261088	ENSG00000261088	RP11-61A14.3	16:66912491-66929657	OK	3.09533	3.49352	0.174589	0.149773	0.79545	0.9998
ENSG00000146729	ENSG00000146729	GBAS	7:55954969-56067874	OK	67.7002	64.3003	-0.0743341	-0.14336	0.7955	0.9998
ENSG00000100124	ENSG00000100124	ANKRD54	22:38226861-38285414	OK	22.4088	19.1807	-0.224417	-0.1173	0.79565	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000169764	ENSG00000169764	UGP2	2:64068073-64118696	OK	57.5863	60.1221	0.0621698	0.142058	0.79565	0.9998
ENSG00000134884	ENSG00000134884	ARGLU1	13:107194020-107220512	OK	36.998	33.6421	-0.13718	-0.162788	0.7957	0.9998
ENSG00000109107	ENSG00000109107	ALDOC	17:26782769-26972472	OK	27.67	21.0948	-0.391432	-0.182354	0.79575	0.9998
ENSG00000175827	ENSG00000175827	AP001266.1	11:65543363-65548273	OK	10.5007	11.3116	0.107313	0.159039	0.7958	0.9998
ENSG00000228933	ENSG00000228933	RP11-268G12.1	X:27061023-27417114	OK	0.782135	0.876459	0.164269	0.155995	0.7958	0.9998
ENSG00000081665	ENSG00000081665	ZNF506	19:19868174-19945736	OK	0.982518	1.09924	0.161946	0.114491	0.79585	0.9998
ENSG00000262877	ENSG00000262877	RP11-1055B8.4	17:79361929-79364056	OK	1.98855	2.14525	0.109429	0.147189	0.79585	0.9998
ENSG00000179523	ENSG00000179523	EIF3J-AS1	15:44719431-44829121	OK	2.36804	1.87133	-0.339632	-0.166275	0.7959	0.9998
ENSG00000224114	ENSG00000224114	RP11-343H5.4	1:206858288-206907628	OK	6.73127	10.71	0.670006	0.265889	0.7959	0.9998
ENSG00000087008	ENSG00000087008	ACOX3	4:8368008-8514337	OK	10.8246	10.0714	-0.104046	-0.14698	0.79595	0.9998
ENSG00000178177	ENSG00000178177	LCORL	4:17812524-18023499	OK	9.71805	8.07571	-0.267079	-0.162871	0.79595	0.9998
ENSG00000143190	ENSG00000143190	POU2F1	1:167190065-167396582	OK	2.49896	2.37287	-0.0746899	-0.0901129	0.79605	0.9998
ENSG00000152454	ENSG00000152454	ZNF256	19:58452200-58459043	OK	1.66281	1.79004	0.106369	0.159027	0.79605	0.9998
ENSG00000118855	ENSG00000118855	MFSD1	3:158414680-158547508	OK	67.2679	70.3432	0.0644931	0.151669	0.79615	0.9998
ENSG00000187186	ENSG00000187186	RP11-195F19.5	9:34638129-34681295	OK	6.88682	5.50185	-0.323922	-0.127437	0.79625	0.9998
ENSG00000116667	ENSG00000116667	C1orf21	1:184356191-184598154	OK	84.1499	91.6846	0.123718	0.151816	0.7963	0.9998
ENSG00000160948	ENSG00000160948	VPS28	8:145648999-145653931	OK	81.05	76.9583	-0.074734	-0.160118	0.7963	0.9998
ENSG00000196214	ENSG00000196214	ZNF766	19:52772823-52871031	OK	3.82457	4.14623	0.116504	0.125944	0.7963	0.9998
ENSG00000171806	ENSG00000171806	METTL18	1:169631244-169863408	OK	7.11265	6.29742	-0.175627	-0.157637	0.79635	0.9998
ENSG00000170445	ENSG00000170445	HARS	5:140044260-140086248	OK	50.9075	55.3295	0.120172	0.157518	0.7964	0.9998
ENSG00000008018	ENSG00000008018	PSMB1	6:170844204-170862429	OK	89.6898	93.8934	0.0660798	0.159101	0.7965	0.9998
ENSG00000110104	ENSG00000110104	CCDC86	11:60603468-60623444	OK	27.3808	28.641	0.0649202	0.148974	0.7965	0.9998
ENSG00000135722	ENSG00000135722	FBXL8	16:67188082-67203848	OK	2.14446	1.79338	-0.257937	-0.12757	0.7965	0.9998
ENSG00000109381	ENSG00000109381	ELF2	4:139936942-140098372	OK	8.48338	7.80683	-0.119903	-0.14204	0.7966	0.9998
ENSG00000214756	ENSG00000214756	METTL12	11:62414319-62441159	OK	4.66888	5.98284	0.357754	0.114992	0.7966	0.9998
ENSG00000129317	ENSG00000129317	PUS7L	12:44122409-44152620	OK	5.72995	5.37341	-0.0926842	-0.131895	0.7967	0.9998
ENSG00000182158	ENSG00000182158	CREB3L2	7:137559724-137686813	OK	13.6636	14.4776	0.0834929	0.132997	0.7967	0.9998
ENSG00000117616	ENSG00000117616	C1orf63	1:25568727-25756683	OK	15.1035	16.4099	0.119683	0.112317	0.79675	0.9998
ENSG00000012211	ENSG00000012211	PRICKLE3	X:49028272-49042845	OK	10.516	9.29062	-0.178736	-0.146625	0.79685	0.9998
ENSG00000018869	ENSG00000018869	ZNF582	19:56732680-56904914	OK	1.12537	1.42203	0.337549	0.162592	0.79685	0.9998
ENSG00000183978	ENSG00000183978	COA3	17:40932695-40950722	OK	62.4059	65.5174	0.0701954	0.155384	0.7969	0.9998
ENSG00000244171	ENSG00000244171	PBX2P1	3:142895126-142897307	OK	0.706055	0.642937	-0.135103	-0.151658	0.7969	0.9998
ENSG00000143473	ENSG00000143473	KCNH1	1:210856554-211307457	OK	5.06682	5.35956	0.081033	0.155525	0.79695	0.9998
ENSG00000161547	ENSG00000161547	SRSF2	17:74722911-74777531	OK	120.813	114.293	-0.0800346	-0.152698	0.79705	0.9998
ENSG00000129680	ENSG00000129680	MAP7D3	X:135295380-135338641	OK	6.71541	6.35595	-0.0793676	-0.133928	0.79715	0.9998
ENSG00000173818	ENSG00000173818	ENDOV	17:78234664-78411886	OK	8.68712	9.62476	0.147873	0.0642012	0.79725	0.9998
ENSG00000099622	ENSG00000099622	CIRBP	19:1259383-1274879	OK	87.125	82.8981	-0.0717465	-0.149241	0.7973	0.9998
ENSG00000135821	ENSG00000135821	GLUL	1:182350838-182361341	OK	411.466	380.52	-0.1128	-0.154976	0.7973	0.9998
ENSG00000126067	ENSG00000126067	PSMB2	1:36067184-36107445	OK	40.6425	42.4565	0.0629951	0.155903	0.7974	0.9998
ENSG00000138303	ENSG00000138303	ASCC1	10:73856277-73995618	OK	12.2704	11.3459	-0.113018	-0.123886	0.7974	0.9998
ENSG00000234636	ENSG00000234636	MED14-AS1	X:40507557-40597950	OK	1.26267	0.880499	-0.52008	-0.129062	0.79745	0.9998
ENSG00000127184	ENSG00000127184	COX7C	5:85913720-85916779	OK	1130.15	1074.89	-0.0723247	-0.15362	0.7975	0.9998
ENSG00000152683	ENSG00000152683	SLC30A6	2:32390932-32449448	OK	7.49344	7.101	-0.0776063	-0.145459	0.7975	0.9998
ENSG00000197713	ENSG00000197713	RPE	2:210867288-211036115	OK	37.3114	39.438	0.0799699	0.134235	0.7975	0.9998
ENSG00000081760	ENSG00000081760	AACS	12:125549924-125627873	OK	11.9731	12.5694	0.0701103	0.131207	0.7976	0.9998
ENSG00000159082	ENSG00000159082	SYNJ1	21:34001068-34100359	OK	3.51158	3.3189	-0.0814168	-0.0936973	0.7976	0.9998
ENSG00000154813	ENSG00000154813	DPH3	3:16299484-16306479	OK	43.4744	40.7951	-0.0917709	-0.155235	0.79765	0.9998
ENSG00000182584	ENSG00000182584	ACTL10	20:32244892-32262269	OK	0.394274	0.629987	0.676122	0.223752	0.79775	0.9998
ENSG00000074266	ENSG00000074266	EED	11:85955585-85989855	OK	8.6382	8.16828	-0.0806984	-0.147189	0.7978	0.9998
ENSG00000164880	ENSG00000164880	INTS1	7:1509912-1545489	OK	29.8894	31.2269	0.0631559	0.114283	0.7978	0.9998
ENSG00000268357	ENSG00000268357	VN1R81P	19:21264964-21308073	OK	2.0728	1.37017	-0.597224	-0.167098	0.7978	0.9998
ENSG00000167702	ENSG00000167702	KIFC2	8:145691425-145701718	OK	11.8	12.6116	0.0959624	0.149766	0.79785	0.9998
ENSG00000106125	ENSG00000106125	FAM188B	7:30692199-30965131	OK	2.40217	2.56591	0.0951352	0.156232	0.7979	0.9998
ENSG00000135486	ENSG00000135486	HNRNPA1	12:54624723-54745633	OK	175.765	189.139	0.105796	0.145719	0.7979	0.9998
ENSG00000234949	ENSG00000234949	AC104667.3	2:238482964-238510257	OK	0.480878	0.654701	0.445166	0.0564084	0.7979	0.9998
ENSG00000151422	ENSG00000151422	FER	5:108083522-108532542	OK	3.64485	3.36295	-0.116132	-0.110688	0.79805	0.9998
ENSG00000213588	ENSG00000213588	ZBTB9	6:33422355-33425325	OK	7.87253	8.29429	0.0752909	0.153415	0.79805	0.9998
ENSG00000134283	ENSG00000134283	PPHLN1	12:42632248-42984157	OK	34.7707	32.4936	-0.0977167	-0.147855	0.79815	0.9998
ENSG00000170222	ENSG00000170222	ADPRM	17:10583653-10718481	OK	7.60334	8.61466	0.180161	0.166356	0.79815	0.9998
ENSG00000130175	ENSG00000130175	PRKCSH	19:11531271-11561783	OK	125.714	120.263	-0.0639434	-0.135525	0.7982	0.9998
ENSG00000229195	ENSG00000229195	AC009495.4	2:166651360-166702601	OK	11.4519	10.3511	-0.145804	-0.15231	0.79825	0.9998
ENSG00000197712	ENSG00000197712	FAM114A1	4:38869297-38947360	OK	17.3177	18.752	0.114794	0.15586	0.79835	0.9998
ENSG00000142657	ENSG00000142657	PGD	1:10458648-10480201	OK	47.7099	45.6771	-0.0628172	-0.146953	0.7984	0.9998
ENSG00000187837	ENSG00000187837	HIST1H1C	6:26055967-26056699	OK	23.6966	25.0463	0.0799206	0.155274	0.7984	0.9998
ENSG00000111790	ENSG00000111790	FGFR1OP2	12:27091315-27119583	OK	24.9382	23.5013	-0.0856167	-0.156896	0.79845	0.9998
ENSG00000256028	ENSG00000256028	RP11-197N18.2	12:123405497-123467456	OK	0.784941	0.804466	0.0354477	0.0158318	0.7985	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000008405	ENSG00000008405	CRY1	12:107385141-107517092	OK	10.2171	9.64467	-0.0831823	-0.130763	0.79855	0.9998
ENSG00000064309	ENSG00000064309	CDON	11:125820010-125933230	OK	3.57253	3.89925	0.126252	0.134967	0.7986	0.9998
ENSG00000111206	ENSG00000111206	FOXM1	12:2904118-3050306	OK	53.7639	49.5964	-0.116402	-0.128437	0.7986	0.9998
ENSG00000235027	ENSG00000235027	AC068580.6	11:1753639-1785255	OK	2.25356	2.97335	0.399887	0.0648564	0.7986	0.9998
ENSG00000123505	ENSG00000123505	AMD1	6:111195972-111216916	OK	17.4417	16.566	-0.0743163	-0.146118	0.79865	0.9998
ENSG00000146828	ENSG00000146828	SLC12A9	7:100400186-100464631	OK	15.2047	16.3813	0.107532	0.125867	0.79865	0.9998
ENSG00000226419	ENSG00000226419	SLC16A1-AS1	1:113454468-113542118	OK	2.03736	2.56377	0.331562	0.12749	0.79865	0.9998
ENSG00000124209	ENSG00000124209	RAB22A	20:56884751-56942563	OK	11.5571	12.0557	0.060937	0.139195	0.7987	0.9998
ENSG00000136770	ENSG00000136770	DNAJC1	10:22045465-22292698	OK	11.9182	12.5418	0.0735768	0.143598	0.7987	0.9998
ENSG00000160959	ENSG00000160959	LRRC14	8:145743375-145754516	OK	14.6547	15.7024	0.0996213	0.143136	0.7987	0.9998
ENSG00000084774	ENSG00000084774	CAD	2:27440257-27466811	OK	14.6068	13.9714	-0.0641695	-0.0947175	0.79875	0.9998
ENSG00000170390	ENSG00000170390	DCLK2	4:150999425-151178609	OK	1.11843	1.20992	0.113438	0.140675	0.7989	0.9998
ENSG00000228638	ENSG00000228638	FCF1P2	3:48282589-48343175	OK	1.3739	2.21539	0.689288	0.211573	0.7989	0.9998
ENSG00000270170	ENSG00000270170	NCBP2-AS2	3:196669493-196670411	OK	15.0777	15.9448	0.0806678	0.153918	0.79895	0.9998
ENSG00000134056	ENSG00000134056	MRPS36	5:68513586-68525956	OK	35.0933	37.713	0.103866	0.141125	0.799	0.9998
ENSG00000166311	ENSG00000166311	SMPD1	11:6411654-6416228	OK	52.8292	55.4571	0.0700353	0.148497	0.799	0.9998
ENSG00000182256	ENSG00000182256	GABRG3	15:27216428-27787137	OK	2.15456	2.34141	0.119979	0.128991	0.79915	0.9998
ENSG00000198722	ENSG00000198722	UNC13B	9:35161998-35405335	OK	14.6951	15.3554	0.0634154	0.139621	0.79915	0.9998
ENSG00000073910	ENSG00000073910	FRY	13:32599450-32870794	OK	1.03153	1.10786	0.102985	0.111476	0.7993	0.9998
ENSG00000100889	ENSG00000100889	PCK2	14:24549315-24602058	OK	4.97061	4.33802	-0.196387	-0.142787	0.7993	0.9998
ENSG00000226091	ENSG00000226091	LINC00937	12:8407122-8549399	OK	0.659355	0.568718	-0.213341	-0.110027	0.7993	0.9998
ENSG00000023330	ENSG00000023330	ALAS1	3:52232101-52248343	OK	39.7718	38.0736	-0.0629519	-0.149598	0.79935	0.9998
ENSG00000164346	ENSG00000164346	NSA2	5:73923233-74072737	OK	59.8395	66.727	0.157172	0.14761	0.7994	0.9998
ENSG00000215021	ENSG00000215021	PHB2	12:7072407-7178336	OK	211.724	222.337	0.0705641	0.149046	0.79945	0.9998
ENSG00000160072	ENSG00000160072	ATAD3B	1:1407142-1433228	OK	15.619	16.9608	0.118896	0.153239	0.79955	0.9998
ENSG00000148158	ENSG00000148158	SNX30	9:115513117-115653193	OK	17.9491	18.7277	0.0612627	0.151389	0.7996	0.9998
ENSG00000162174	ENSG00000162174	ASRGL1	11:62104382-62160882	OK	43.0876	40.4558	-0.0909268	-0.16055	0.7997	0.9998
ENSG00000177030	ENSG00000177030	DEAF1	11:644232-727727	OK	12.0313	12.9182	0.102612	0.132554	0.7997	0.9998
ENSG00000178464	ENSG00000178464	CTD-2192J16.15	19:12754088-12792716	OK	76.7796	86.6585	0.174618	0.158326	0.7998	0.9998
ENSG00000197951	ENSG00000197951	ZNF71	19:57106631-57137849	OK	3.0781	2.85715	-0.107463	-0.129366	0.7998	0.9998
ENSG00000130382	ENSG00000130382	MLLT1	19:6212965-6279959	OK	20.645	21.6266	0.067019	0.150111	0.79995	0.9998
ENSG00000019144	ENSG00000019144	PHLDB1	11:118477154-118550399	OK	16.972	16.0333	-0.0820866	-0.122043	0.80005	0.9998
ENSG00000100106	ENSG00000100106	TRIOBP	22:38077679-38172563	OK	30.4749	32.0376	0.0721448	0.139426	0.80005	0.9998
ENSG00000166166	ENSG00000166166	TRMT61A	14:103995520-104003410	OK	6.03968	6.35999	0.0745523	0.150336	0.80005	0.9998
ENSG00000175879	ENSG00000175879	HOXD8	2:176986338-177037830	OK	5.15009	5.79331	0.169791	0.150523	0.80005	0.9998
ENSG00000129315	ENSG00000129315	CCNT1	12:49082246-49110681	OK	9.33792	8.9222	-0.0657021	-0.132039	0.80015	0.9998
ENSG00000155085	ENSG00000155085	AK9	6:109809108-110012420	OK	0.976022	1.0784	0.14391	0.122009	0.80015	0.9998
ENSG00000237976	ENSG00000237976	RP11-126K1.6	1:151313115-151320503	OK	1.14544	0.849592	-0.431066	-0.0676068	0.80015	0.9998
ENSG00000138698	ENSG00000138698	RAP1GDS1	4:99172838-99365012	OK	26.031	27.3184	0.0696434	0.121701	0.80025	0.9998
ENSG00000101365	ENSG00000101365	IDH3B	20:2639040-2644865	OK	39.4871	41.2713	0.0637564	0.140646	0.8003	0.9998
ENSG00000176903	ENSG00000176903	PNMA1	14:74178493-74181128	OK	13.6141	14.2632	0.0671944	0.150923	0.8003	0.9998
ENSG00000215863	ENSG00000215863	LINC01138	1:147835126-147931933	OK	2.03006	1.60573	-0.33829	-0.168377	0.8003	0.9998
ENSG00000183751	ENSG00000183751	TBL3	16:2022037-2034193	OK	17.7484	18.7564	0.0796923	0.141093	0.80035	0.9998
ENSG00000228409	ENSG00000228409	CCT6P1	7:65216128-65228341	OK	2.30619	2.13434	-0.111719	-0.152123	0.8004	0.9998
ENSG00000268895	ENSG00000268895	A1BG-AS1	19:58856543-58877958	OK	7.07548	6.49312	-0.123915	-0.150693	0.8004	0.9998
ENSG00000211450	ENSG00000211450	C11orf31	11:57480071-57587018	OK	157.546	142.591	-0.14389	-0.143432	0.80045	0.9998
ENSG00000169490	ENSG00000169490	TM2D2	8:38846326-38854343	OK	30.8069	28.78	-0.0981866	-0.148282	0.8005	0.9998
ENSG00000160633	ENSG00000160633	SAFB	19:5587009-5668489	OK	36.5721	38.619	0.0785657	0.110819	0.8007	0.9998
ENSG00000070761	ENSG00000070761	C16orf80	16:58147495-58163354	OK	15.8682	14.9831	-0.0828049	-0.115714	0.80085	0.9998
ENSG00000159199	ENSG00000159199	ATP5G1	17:46952221-47006418	OK	296.825	325.954	0.135059	0.152593	0.80085	0.9998
ENSG00000170464	ENSG00000170464	DNAJC18	5:138744278-138780180	OK	11.9631	10.796	-0.148101	-0.154013	0.8011	0.9998
ENSG00000081026	ENSG00000081026	MAGI3	1:113933370-114228545	OK	2.05435	1.91289	-0.102931	-0.119419	0.80115	0.9998
ENSG00000119650	ENSG00000119650	IFT43	14:76041230-76550928	OK	22.6844	20.1243	-0.172763	-0.143114	0.80115	0.9998
ENSG00000164620	ENSG00000164620	RELL2	5:141016516-141030986	OK	4.93471	5.70042	0.208104	0.180799	0.80115	0.9998
ENSG00000255990	ENSG00000255990	AC034102.1	12:56367696-56388490	OK	16.3649	13.4999	-0.27766	-0.150898	0.8012	0.9998
ENSG00000130733	ENSG00000130733	YIPF2	19:10982188-11039357	OK	26.2934	28.4598	0.114229	0.13902	0.80125	0.9998
ENSG00000256073	ENSG00000256073	C21orf119	21:33765438-33766254	OK	1.45016	1.60157	0.143271	0.157146	0.80125	0.9998
ENSG00000176542	ENSG00000176542	KIAA2018	3:113367231-113415493	OK	2.34411	2.47082	0.0759488	0.14495	0.8013	0.9998
ENSG00000261505	ENSG00000261505	LA16c-358B7.3	16:1355547-1377019	OK	1.31975	1.73446	0.394227	0.199196	0.8013	0.9998
ENSG00000036257	ENSG00000036257	CUL3	2:225334866-225450110	OK	35.9695	34.3969	-0.0644932	-0.152208	0.80135	0.9998
ENSG00000131759	ENSG00000131759	RARA	17:38465443-38513094	OK	22.8948	24.1105	0.0746467	0.152107	0.80135	0.9998
ENSG00000100347	ENSG00000100347	SAMM50	22:44319618-44568829	OK	88.5389	93.6589	0.0811042	0.148848	0.80145	0.9998
ENSG00000100075	ENSG00000100075	SLC25A1	22:19163094-19166343	OK	55.1492	57.5626	0.0617927	0.148228	0.80155	0.9998
ENSG00000236778	ENSG00000236778	INTS6-AS1	13:51909908-52126500	OK	0.807044	0.738594	-0.127865	-0.0303873	0.80155	0.9998
ENSG00000100246	ENSG00000100246	DNAL4	22:39101727-39190203	OK	9.90415	8.32117	-0.251248	-0.149294	0.8016	0.9998
ENSG00000070444	ENSG00000070444	MNT	17:2287353-2304412	OK	9.67341	9.17388	-0.0764933	-0.10277	0.8017	0.9998
ENSG00000120800	ENSG00000120800	UTP20	12:101673886-101780394	OK	10.2365	10.6965	0.0634248	0.143685	0.80175	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000069509	ENSG00000069509	FUNDC1	X:44382884-44402247	OK	13.589	12.864	-0.0790942	-0.154419	0.8018	0.9998
ENSG00000139679	ENSG00000139679	LPAR6	13:48877886-49056122	OK	3.44259	2.94604	-0.22472	-0.112609	0.8018	0.9998
ENSG00000271133	ENSG00000271133	CTA-293F17.1	7:20367921-20455377	OK	1.51939	1.15689	-0.393237	-0.058859	0.8018	0.9998
ENSG00000105341	ENSG00000105341	ATP5SL	19:41937222-41946622	OK	44.9124	42.8905	-0.066456	-0.145087	0.80185	0.9998
ENSG00000149541	ENSG00000149541	B3GAT3	11:62382767-62389647	OK	68.0433	71.0725	0.0628387	0.149325	0.80185	0.9998
ENSG00000107821	ENSG00000107821	KAZALD1	10:102821597-102827888	OK	1.10958	1.23002	0.148673	0.140585	0.8019	0.9998
ENSG00000163170	ENSG00000163170	BOLA3	2:74362524-74375121	OK	108.822	114.148	0.0689361	0.152211	0.8019	0.9998
ENSG00000203446	ENSG00000203446	AC004988.1	7:40174574-40900362	OK	1.30717	1.50775	0.205956	0.148679	0.8019	0.9998
ENSG00000136856	ENSG00000136856	SLC2A8	9:130159420-130170703	OK	15.4245	16.3318	0.0824572	0.13136	0.80195	0.9998
ENSG00000180694	ENSG00000180694	TMEM64	8:91634222-91997485	OK	38.0895	35.9257	-0.0843758	-0.148541	0.80195	0.9998
ENSG00000214407	ENSG00000214407	RP11-221J22.1	3:101659702-101716770	OK	1.78735	1.59615	-0.163225	-0.13947	0.80195	0.9998
ENSG00000139946	ENSG00000139946	PELI2	14:56584531-56768244	OK	7.54529	6.95233	-0.118078	-0.116677	0.80205	0.9998
ENSG00000163738	ENSG00000163738	MTHFD2L	4:74979890-75168816	OK	3.74263	4.04338	0.111511	0.143695	0.8021	0.9998
ENSG00000183891	ENSG00000183891	TTC32	2:20096403-20101747	OK	2.98801	2.75127	-0.119085	-0.154881	0.8021	0.9998
ENSG00000106397	ENSG00000106397	PLOD3	7:100849257-100867471	OK	150.567	157.173	0.0619465	0.119248	0.80215	0.9998
ENSG00000272455	ENSG00000272455	RP4-758J18.13	1:1344475-1345998	OK	1.07379	1.16938	0.12303	0.154161	0.8023	0.9998
ENSG00000254353	ENSG00000254353	RP11-195E2.4	5:70328994-70330227	OK	2.20192	2.01308	-0.129358	-0.153585	0.80235	0.9998
ENSG00000225828	ENSG00000225828	FAM229A	1:32817121-32829913	OK	2.07473	2.24269	0.112307	0.118735	0.8024	0.9998
ENSG00000249592	ENSG00000249592	RP11-440L14.1	4:699536-775637	OK	1.15887	0.937843	-0.305305	-0.0597623	0.8024	0.9998
ENSG00000166794	ENSG00000166794	PPIB	15:64443913-64455404	OK	348.578	363.63	0.0609925	0.152268	0.80245	0.9998
ENSG00000164841	ENSG00000164841	TMEM74	8:109593290-109799844	OK	1.29439	1.20026	-0.108917	-0.146617	0.8025	0.9998
ENSG00000167113	ENSG00000167113	COQ4	9:131071381-131096351	OK	17.9508	16.11	-0.156095	-0.165093	0.8025	0.9998
ENSG00000240759	ENSG00000240759	RP11-25I15.1	12:43040384-43080503	OK	1.38661	1.76155	0.345284	0.213785	0.8025	0.9998
ENSG00000148229	ENSG00000148229	POLE3	9:116169514-116191964	OK	38.9206	37.2645	-0.062731	-0.136042	0.80255	0.9998
ENSG00000136897	ENSG00000136897	MRPL50	9:104149914-104160896	OK	6.7549	7.22099	0.0962617	0.151247	0.80265	0.9998
ENSG00000100532	ENSG00000100532	CGRRF1	14:54976529-55005567	OK	8.00613	7.56881	-0.0810391	-0.139089	0.80275	0.9998
ENSG00000148334	ENSG00000148334	PTGES2	9:130882971-130891481	OK	79.4722	75.482	-0.0743167	-0.149872	0.80275	0.9998
ENSG00000157617	ENSG00000157617	C2CD2	21:43305220-43373999	OK	1.16141	1.05455	-0.139248	-0.0944852	0.80275	0.9998
ENSG00000256546	ENSG00000256546	AC156455.1	12:122501211-122506522	OK	1.01683	0.884936	-0.200431	-0.146617	0.8028	0.9998
ENSG00000154803	ENSG00000154803	FLCN	17:16945858-17140502	OK	15.8484	17.2366	0.121137	0.08878	0.8029	0.9998
ENSG00000198841	ENSG00000198841	KTI12	1:52485802-52556388	OK	6.78909	7.69789	0.181247	0.149844	0.8029	0.9998
ENSG00000236540	ENSG00000236540	AC006547.13	22:20004536-20058066	OK	5.95548	4.81551	-0.306528	-0.10529	0.8029	0.9998
ENSG00000148835	ENSG00000148835	TAF5	10:105127723-105156223	OK	3.20553	2.74313	-0.22474	-0.149271	0.80295	0.9998
ENSG00000158423	ENSG00000158423	RIBC1	X:53401069-53458059	OK	0.885406	0.726347	-0.285679	-0.0561475	0.80295	0.9998
ENSG00000005156	ENSG00000005156	LIG3	17:33254877-33332083	OK	18.3364	19.2856	0.0728145	0.105998	0.803	0.9998
ENSG00000111231	ENSG00000111231	GPN3	12:110890288-110928190	OK	34.39	32.6476	-0.0750149	-0.14354	0.80305	0.9998
ENSG00000170004	ENSG00000170004	CHD3	17:7760002-7816078	OK	34.3331	36.2822	0.0796641	0.123563	0.80305	0.9998
ENSG00000164162	ENSG00000164162	ANAPC10	4:145888263-146101313	OK	14.0115	12.0543	-0.217062	-0.126557	0.8031	0.9998
ENSG00000075420	ENSG00000075420	FNDC3B	3:171757417-172119455	OK	24.8892	23.3986	-0.0890963	-0.0992445	0.8032	0.9998
ENSG00000104343	ENSG00000104343	UBE2W	8:74332238-74791145	OK	12.2162	13.0067	0.0904652	0.130499	0.8033	0.9998
ENSG00000117592	ENSG00000117592	PRDX6	1:173446404-173457946	OK	174.571	166.8	-0.0656987	-0.150888	0.80335	0.9998
ENSG00000128050	ENSG00000128050	PAICS	4:57301906-57327534	OK	111.969	106.981	-0.0657374	-0.14926	0.80335	0.9998
ENSG00000159720	ENSG00000159720	ATP6V0D1	16:67471916-67515140	OK	32.9451	31.5203	-0.0637809	-0.141539	0.80335	0.9998
ENSG00000258900	ENSG00000258900	HNRNPCP1	14:58862633-59015216	OK	0.728338	0.527369	-0.465797	-0.091243	0.80335	0.9998
ENSG00000272812	ENSG00000272812	RP5-855D21.3	8:163185-197342	OK	1.4772	1.25227	-0.238322	-0.153172	0.80335	0.9998
ENSG00000100429	ENSG00000100429	HDAC10	22:50683611-50700254	OK	11.0693	11.8914	0.103351	0.135157	0.8034	0.9998
ENSG00000164039	ENSG00000164039	BDH2	4:103941024-104021040	OK	23.2809	21.918	-0.0870285	-0.150858	0.8035	0.9998
ENSG00000064547	ENSG00000064547	LPAR2	19:19734476-19739739	OK	2.49445	2.2416	-0.154189	-0.140603	0.80365	0.9998
ENSG00000270300	ENSG00000270300	PHACTR2P1	10:121485608-121588652	OK	0.769661	1.04408	0.439932	0.0698363	0.80375	0.9998
ENSG00000223799	ENSG00000223799	IL10RB-AS1	21:34602205-34669539	OK	0.446124	0.651311	0.545902	0.225029	0.80385	0.9998
ENSG00000126562	ENSG00000126562	WNK4	17:40932695-40950722	OK	0.92962	1.1022	0.245673	0.0922297	0.8039	0.9998
ENSG00000204344	ENSG00000204344	STK19	6:31937586-31971298	OK	13.4106	12.2923	-0.125629	-0.151718	0.8039	0.9998
ENSG00000102898	ENSG00000102898	NUTF2	16:67840667-67906470	OK	57.424	61.2847	0.093874	0.148153	0.80405	0.9998
ENSG00000241343	ENSG00000241343	RPL36A	X:100645811-100669121	OK	15.0418	18.1583	0.271653	0.140944	0.80425	0.9998
ENSG00000116035	ENSG00000116035	VAX2	2:71127719-71160576	OK	2.58576	2.39445	-0.110893	-0.151125	0.8043	0.9998
ENSG00000118418	ENSG00000118418	HMGN3	6:79910961-79946514	OK	99.0398	94.8205	-0.062809	-0.150863	0.8043	0.9998
ENSG00000241852	ENSG00000241852	C8orf58	8:22435791-22461663	OK	22.6062	21.1895	-0.0933682	-0.133461	0.80445	0.9998
ENSG00000147535	ENSG00000147535	PPAPDC1B	8:38082735-38239790	OK	9.79655	11.1467	0.186266	0.101232	0.8045	0.9998
ENSG00000177971	ENSG00000177971	IMP3	15:75928479-75954642	OK	33.5341	35.8567	0.0966157	0.153964	0.8045	0.9998
ENSG00000128652	ENSG00000128652	HOXD3	2:176986338-177037830	OK	2.38553	2.64793	0.150556	0.110367	0.80455	0.9998
ENSG00000273306	ENSG00000273306	RP11-527J8.1	2:99613723-100106497	OK	0.746009	1.02475	0.458005	0.0391811	0.80455	0.9998
ENSG00000104907	ENSG00000104907	TRMT1	19:13215715-13228381	OK	23.2487	24.4424	0.0722407	0.138926	0.8046	0.9998
ENSG00000138443	ENSG00000138443	ABI2	2:204192941-204400133	OK	34.7729	32.1809	-0.111758	-0.133627	0.8046	0.9998
ENSG00000250151	ENSG00000250151	ARPC4-TTLL3	3:9791627-9896822	OK	7.54992	5.69992	-0.40552	-0.120865	0.8046	0.9998
ENSG00000111676	ENSG00000111676	ATN1	12:7033625-7051484	OK	21.0445	21.9678	0.0619468	0.145169	0.80465	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000130159	ENSG00000130159	ECSIT	19:11562140-11639989	OK	25.2835	24.0698	-0.0709708	-0.145855	0.80465	0.9998
ENSG00000120053	ENSG00000120053	GOT1	10:101156626-101190381	OK	66.5886	63.746	-0.0629414	-0.142871	0.8047	0.9998
ENSG00000204397	ENSG00000204397	CARD16	11:104896169-104972158	OK	0.716919	0.896607	0.322666	0.151956	0.80475	0.9998
ENSG00000131100	ENSG00000131100	ATP6V1E1	22:18074901-18111584	OK	215.954	225.071	0.0596603	0.149651	0.80485	0.9998
ENSG00000159882	ENSG00000159882	ZNF230	19:44507099-44518078	OK	1.8272	2.00754	0.135799	0.124256	0.80505	0.9998
ENSG00000197892	ENSG00000197892	KIF13B	8:28924795-29120641	OK	7.22898	6.8726	-0.0729349	-0.122902	0.8051	0.9998
ENSG00000187742	ENSG00000187742	SECISBP2	9:91933420-91974557	OK	23.1245	22.0716	-0.0672276	-0.131474	0.80515	0.9998
ENSG00000146676	ENSG00000146676	PURB	7:44915895-44925992	OK	6.67542	6.37878	-0.0655771	-0.149936	0.8052	0.9998
ENSG00000125484	ENSG00000125484	GTF3C4	9:135468383-135570342	OK	5.9715	5.64882	-0.0801446	-0.153045	0.80525	0.9998
ENSG00000054282	ENSG00000054282	SDCCAG8	1:243419319-244014381	OK	15.4359	13.6487	-0.177526	-0.113692	0.8053	0.9998
ENSG00000264608	ENSG00000264608	RP11-192H23.8	17:26782769-26972472	OK	0.749949	0.526458	-0.510475	-0.0194273	0.8053	0.9998
ENSG00000100983	ENSG00000100983	GSS	20:33516235-33543620	OK	75.5829	72.3899	-0.0622717	-0.152818	0.80535	0.9998
ENSG00000158560	ENSG00000158560	DYNC1I1	7:95401865-95739634	OK	6.87098	6.50416	-0.0791539	-0.140974	0.80535	0.9998
ENSG00000000457	ENSG00000000457	SCYL3	1:169631244-169863408	OK	4.42883	3.97234	-0.156936	-0.1705	0.80545	0.9998
ENSG00000105329	ENSG00000105329	TGFB1	19:41768400-41930910	OK	0.565188	0.70196	0.312658	0.0333707	0.80545	0.9998
ENSG00000124104	ENSG00000124104	SNX21	20:44462448-44486045	OK	12.387	13.3688	0.110043	0.139794	0.80545	0.9998
ENSG00000129347	ENSG00000129347	KRI1	19:10654570-10676713	OK	16.8309	15.5565	-0.113594	-0.13221	0.80545	0.9998
ENSG00000137343	ENSG00000137343	ATAT1	6:30594618-30614600	OK	9.59285	9.06907	-0.0810052	-0.145776	0.80545	0.9998
ENSG00000186222	ENSG00000186222	BLOC1S4	4:6717841-6719387	OK	3.44938	3.67474	0.0913052	0.147311	0.80545	0.9998
ENSG00000232372	ENSG00000232372	RP11-504P24.2	1:224170455-224175856	OK	0.690403	0.552547	-0.321343	-0.185592	0.80545	0.9998
ENSG00000068028	ENSG00000068028	RASSF1	3:50367218-50378411	OK	10.2346	9.70527	-0.0766172	-0.152949	0.8055	0.9998
ENSG00000243156	ENSG00000243156	MICAL3	22:18270414-18507325	OK	47.1054	44.3393	-0.087304	-0.0932148	0.8056	0.9998
ENSG00000258311	ENSG00000258311	RP11-644F5.10	12:56075329-56118489	OK	0.786837	0.596996	-0.398345	-0.0649309	0.80575	0.9998
ENSG00000137411	ENSG00000137411	VARS2	6:30875960-30894236	OK	14.4183	13.4383	-0.101545	-0.148631	0.80585	0.9998
ENSG00000101310	ENSG00000101310	SEC23B	20:18488136-18542059	OK	13.1279	13.7758	0.0694964	0.136968	0.8061	0.9998
ENSG00000251666	ENSG00000251666	ZNF346-IT1	5:176449696-176508190	OK	0.6648	0.43829	-0.601035	-0.198271	0.80615	0.9998
ENSG00000175536	ENSG00000175536	LIPT2	11:74202756-74380162	OK	3.64909	2.80633	-0.378855	-0.19201	0.8062	0.9998
ENSG00000147996	ENSG00000147996	CBWD5	9:70432003-70497240	OK	20.3576	21.6081	0.0860028	0.14232	0.80625	0.9998
ENSG00000177426	ENSG00000177426	TGIF1	18:3411605-3458409	OK	42.9313	40.7727	-0.074425	-0.14647	0.80625	0.9998
ENSG00000097021	ENSG00000097021	ACOT7	1:6324328-6454451	OK	126.984	132.319	0.0593709	0.146885	0.8063	0.9998
ENSG00000105202	ENSG00000105202	FBL	19:40325097-40337054	OK	158.012	164.998	0.0624163	0.148885	0.8063	0.9998
ENSG00000146063	ENSG00000146063	TRIM41	5:180649498-180662809	OK	7.79937	8.22905	0.0773678	0.136571	0.8063	0.9998
ENSG00000167461	ENSG00000167461	RAB8A	19:16222438-16269386	OK	28.6868	26.7978	-0.0982704	-0.136767	0.8063	0.9998
ENSG00000164347	ENSG00000164347	GFM2	5:73923233-74072737	OK	30.9382	27.8303	-0.152737	-0.135626	0.80635	0.9998
ENSG00000152439	ENSG00000152439	ZNF773	19:57999078-58029772	OK	2.16214	2.40975	0.15642	0.130879	0.8064	0.9998
ENSG00000170522	ENSG00000170522	ELOVL6	4:110967001-111120355	OK	2.57015	2.77762	0.111997	0.0937905	0.80645	0.9998
ENSG00000139636	ENSG00000139636	LMBR1L	12:49490918-49504683	OK	39.4919	37.7416	-0.0654005	-0.114216	0.8065	0.9998
ENSG00000171574	ENSG00000171574	ZNF584	19:58912870-58929694	OK	6.62312	7.02267	0.0845085	0.127865	0.8065	0.9998
ENSG00000145780	ENSG00000145780	FEM1C	5:114856607-114880591	OK	5.3856	5.13392	-0.0690462	-0.148097	0.80655	0.9998
ENSG00000236397	ENSG00000236397	DDX11L2	2:114341663-114359144	OK	1.1217	0.96042	-0.22395	-0.153182	0.80655	0.9998
ENSG00000126368	ENSG00000126368	NR1D1	17:38175349-38256978	OK	5.87442	6.79579	0.210196	0.160093	0.8066	0.9998
ENSG00000135605	ENSG00000135605	TEC	4:48137799-48271881	OK	0.868639	0.947454	0.125299	0.119147	0.8066	0.9998
ENSG00000145362	ENSG00000145362	ANK2	4:113739264-114304896	OK	13.5046	12.4898	-0.112704	-0.0993695	0.8066	0.9998
ENSG00000197879	ENSG00000197879	MYO1C	17:1367391-1396106	OK	46.1649	48.0372	0.0573552	0.116679	0.8066	0.9998
ENSG00000232561	ENSG00000232561	GTF2IP1	7:74602782-74653438	OK	3.44515	3.25285	-0.0828611	-0.148243	0.8066	0.9998
ENSG00000213593	ENSG00000213593	TMX2	11:57480071-57587018	OK	112.818	103.18	-0.12883	-0.144973	0.80665	0.9998
ENSG00000140990	ENSG00000140990	NDUFB10	16:2009508-2011976	OK	141.817	148.354	0.0650162	0.150391	0.8067	0.9998
ENSG00000162714	ENSG00000162714	ZNF496	1:247460713-247495148	OK	11.9146	11.2224	-0.0863474	-0.146611	0.80675	0.9998
ENSG00000247134	ENSG00000247134	RP11-11N9.4	8:32853695-32902373	OK	7.89263	8.43237	0.0954321	0.151698	0.80675	0.9998
ENSG00000187775	ENSG00000187775	DNAH17	17:76374720-76573476	OK	0.894772	0.768402	-0.219659	-0.0849106	0.8068	0.9998
ENSG00000174306	ENSG00000174306	ZHX3	20:39657457-39946312	OK	9.39382	8.24026	-0.189022	-0.0879252	0.80685	0.9998
ENSG00000196544	ENSG00000196544	C17orf59	17:8091651-8093564	OK	5.72366	6.04582	0.079	0.146154	0.8069	0.9998
ENSG00000185507	ENSG00000185507	IRF7	11:612552-615999	OK	1.85056	2.00411	0.115	0.134234	0.80695	0.9998
ENSG00000132341	ENSG00000132341	RAN	12:131356423-131362223	OK	577.995	604.489	0.0646592	0.148551	0.8071	0.9998
ENSG00000030110	ENSG00000030110	BAK1	6:33540328-33548019	OK	22.2619	21.2809	-0.0650167	-0.149042	0.80725	0.9998
ENSG00000175895	ENSG00000175895	PLEKHF2	8:96146031-96168912	OK	16.3275	15.6051	-0.0652918	-0.141208	0.8073	0.9998
ENSG00000100650	ENSG00000100650	SRSF5	14:70193616-70238722	OK	99.9875	105.756	0.0809205	0.139896	0.80745	0.9998
ENSG00000078403	ENSG00000078403	MLLT10	10:21823093-22032559	OK	9.66054	8.99835	-0.102443	-0.0961643	0.8075	0.9998
ENSG00000204316	ENSG00000204316	MRPL38	17:73893140-73937221	OK	51.2788	53.8567	0.070764	0.130083	0.8076	0.9998
ENSG00000106400	ENSG00000106400	ZNHIT1	7:100849257-100867471	OK	61.0709	68.5235	0.166113	0.137201	0.80765	0.9998
ENSG00000169372	ENSG00000169372	CRADD	12:94071150-94288616	OK	8.3537	8.86024	0.0849293	0.140161	0.8078	0.9998
ENSG00000203667	ENSG00000203667	COX20	1:244998623-245027844	OK	117.511	97.0579	-0.275872	-0.190821	0.8078	0.9998
ENSG00000144504	ENSG00000144504	ANKMY1	2:241418838-241520789	OK	7.0603	6.3883	-0.144298	-0.0814875	0.80795	0.9998
ENSG00000165671	ENSG00000165671	NSD1	5:176560025-176727216	OK	12.8418	13.4883	0.0708663	0.0835899	0.80795	0.9998
ENSG00000170540	ENSG00000170540	ARL6IP1	16:18792616-18813000	OK	116.819	106.801	-0.129359	-0.143266	0.80795	0.9998
ENSG00000184470	ENSG00000184470	TXNRD2	22:19863039-20004331	OK	17.3938	16.3285	-0.0911786	-0.127012	0.80795	0.9998
ENSG00000255154	ENSG00000255154	RPP14	3:58291973-58310422	OK	5.69948	4.25775	-0.42074	-0.201487	0.80795	0.9998
ENSG00000074800	ENSG00000074800	ENO1	1:8921060-8939953	OK	1108.53	1163.32	0.0696044	0.142162	0.808	0.9998
ENSG00000117758	ENSG00000117758	STX12	1:28099693-28150963	OK	18.0397	17.2252	-0.066655	-0.115652	0.808	0.9998
ENSG00000127540	ENSG00000127540	UQCR11	19:1576638-1605480	OK	173.158	186.263	0.105245	0.145688	0.80805	0.9998
ENSG00000186153	ENSG00000186153	WWOX	16:78133309-79246564	OK	2.03033	1.85662	-0.129031	-0.126912	0.80805	0.9998
ENSG00000054967	ENSG00000054967	RELT	11:73087308-73108519	OK	5.46052	5.75141	0.0748774	0.141628	0.8081	0.9998
ENSG00000122958	ENSG00000122958	VPS26A	10:70883267-70932617	OK	38.7598	40.4908	0.0630329	0.135624	0.80815	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229512	ENSG00000229512	AC068580.5	11:1753639-1785255	OK	2.77258	3.62408	0.386385	0.0146253	0.8082	0.9998
ENSG00000132792	ENSG00000132792	CTNNBL1	20:36322407-36500531	OK	36.5484	38.0988	0.0599373	0.136728	0.80825	0.9998
ENSG00000258645	ENSG00000258645	HSPE1P2	14:64063756-64108579	OK	5.9017	7.80105	0.402539	0.19575	0.80825	0.9998
ENSG00000094880	ENSG00000094880	CDC23	5:137475454-137549032	OK	26.0518	24.1422	-0.109823	-0.131022	0.8083	0.9998
ENSG00000163682	ENSG00000163682	RPL9	4:39455743-39460568	OK	236.883	247.405	0.062698	0.148481	0.8083	0.9998
ENSG00000178301	ENSG00000178301	AQP11	11:77225980-77348850	OK	2.02203	2.3783	0.234122	0.123063	0.8083	0.9998
ENSG00000110172	ENSG00000110172	CHORDC1	11:89934327-89956532	OK	19.8866	21.1814	0.0909985	0.14408	0.80835	0.9998
ENSG00000006194	ENSG00000006194	ZNF263	16:3313742-3368852	OK	12.5396	11.6817	-0.102241	-0.141921	0.8085	0.9998
ENSG00000165661	ENSG00000165661	QSOX2	9:139098178-139137687	OK	11.9569	12.4926	0.0632368	0.131782	0.8085	0.9998
ENSG00000256500	ENSG00000256500	RP11-73M18.2	14:104019757-104181841	OK	10.7991	9.38451	-0.202563	-0.148362	0.8085	0.9998
ENSG00000172974	ENSG00000172974	AC007318.5	2:65432136-65433396	OK	104.871	109.392	0.0608961	0.146429	0.80855	0.9998
ENSG00000131650	ENSG00000131650	KREMEN2	16:3013944-3030540	OK	6.05832	7.15822	0.240682	0.166437	0.80865	0.9998
ENSG00000235859	ENSG00000235859	AC006978.6	7:30323922-30452118	OK	1.69894	2.02605	0.254039	0.157755	0.80865	0.9998
ENSG00000269996	ENSG00000269996	RP11-343N15.5	1:121102016-121204983	OK	7.24358	7.85514	0.116935	0.149811	0.80865	0.9998
ENSG00000035115	ENSG00000035115	SH3YL1	2:217729-278283	OK	6.46885	7.02695	0.11939	0.0584951	0.8087	0.9998
ENSG00000148384	ENSG00000148384	INPP5E	9:139323070-139334274	OK	5.43802	5.17986	-0.0701662	-0.142113	0.8087	0.9998
ENSG00000236801	ENSG00000236801	RPL24P8	9:72658496-72873782	OK	0.673393	0.528314	-0.350054	-0.171882	0.8087	0.9998
ENSG00000273192	ENSG00000273192	CITF22-1A6.3	22:50293876-50321188	OK	0.63471	0.977029	0.622305	0.232504	0.8087	0.9998
ENSG00000168612	ENSG00000168612	ZSWIM1	20:44509865-44513905	OK	5.23832	4.9564	-0.0798119	-0.147397	0.80875	0.9998
ENSG00000171817	ENSG00000171817	ZNF540	19:37988062-38210691	OK	0.762656	0.912235	0.258374	0.0879054	0.80875	0.9998
ENSG00000110719	ENSG00000110719	TCIRG1	11:67806482-67888911	OK	12.6943	13.9538	0.136477	0.124871	0.80885	0.9998
ENSG00000178385	ENSG00000178385	PLEKHM3	2:208693026-208890284	OK	3.09111	2.9191	-0.0826048	-0.146516	0.80895	0.9998
ENSG00000255185	ENSG00000255185	PDXDC2P	16:70010199-70099851	OK	2.391	2.01654	-0.245735	-0.12182	0.809	0.9998
ENSG00000213683	ENSG00000213683	AC002056.3	22:51193095-51193862	OK	1.05106	1.16037	0.14275	0.143626	0.80905	0.9998
ENSG00000086758	ENSG00000086758	HUWE1	X:53559056-53713673	OK	39.1865	37.0516	-0.080822	-0.0840489	0.8091	0.9998
ENSG00000124160	ENSG00000124160	NCOA5	20:44689623-44718591	OK	11.4847	12.0841	0.0733937	0.14154	0.8091	0.9998
ENSG00000073169	ENSG00000073169	SELO	22:50639407-50656045	OK	20.1895	21.1706	0.0684576	0.149147	0.80915	0.9998
ENSG00000091656	ENSG00000091656	ZFHX4	8:77316232-77779521	OK	1.46572	1.3805	-0.0864164	-0.0720974	0.80915	0.9998
ENSG00000101974	ENSG00000101974	ATP11C	X:138808504-139027435	OK	4.27828	3.99013	-0.100597	-0.121962	0.80915	0.9998
ENSG00000173456	ENSG00000173456	RNF26	11:119205236-119208023	OK	9.56958	10.0315	0.0680144	0.14523	0.80915	0.9998
ENSG00000266248	ENSG00000266248	CTC-525D6.2	19:29777917-30055386	OK	2.17309	3.5431	0.705268	0.260152	0.8092	0.9998
ENSG00000042317	ENSG00000042317	SPATA7	14:88851267-89021077	OK	5.67163	5.196	-0.126364	-0.117078	0.80925	0.9998
ENSG00000124172	ENSG00000124172	ATP5E	20:57594308-57607437	OK	233.866	250.12	0.0969428	0.142351	0.80925	0.9998
ENSG00000104976	ENSG00000104976	SNAPC2	19:7985200-7988135	OK	13.6865	14.4058	0.073895	0.128938	0.80935	0.9998
ENSG00000109466	ENSG00000109466	KLHL2	4:165995573-166244308	OK	8.55402	7.91806	-0.111454	-0.138622	0.80935	0.9998
ENSG00000145375	ENSG00000145375	SPATA5	4:123844228-124240605	OK	2.11814	1.97554	-0.100549	-0.138915	0.80935	0.9998
ENSG00000023608	ENSG00000023608	SNAPC1	14:62147758-62263146	OK	6.7623	5.88292	-0.200981	-0.144234	0.8094	0.9998
ENSG00000116521	ENSG00000116521	SCAMP3	1:155225769-155232221	OK	183.423	190.671	0.0559167	0.138852	0.8094	0.9998
ENSG00000272711	ENSG00000272711	RP11-259N19.1	2:75059781-75120486	OK	0.809826	1.26268	0.640804	0.122371	0.8095	0.9998
ENSG00000168765	ENSG00000168765	GSTM4	1:110198702-110208118	OK	32.5396	34.0185	0.0641245	0.143919	0.8096	0.9998
ENSG00000259032	ENSG00000259032	ENSAP2	14:83108963-83173169	OK	64.7811	68.2859	0.0760141	0.144804	0.8096	0.9998
ENSG00000099949	ENSG00000099949	LZTR1	22:21319395-21353327	OK	25.1243	23.7728	-0.0797714	-0.114398	0.80965	0.9998
ENSG00000177613	ENSG00000177613	CSTF2T	10:52750944-54073888	OK	5.58709	5.30444	-0.0748976	-0.145555	0.80965	0.9998
ENSG00000258839	ENSG00000258839	MC1R	16:89939999-90005169	OK	16.0613	18.1923	0.179744	0.146449	0.8097	0.9998
ENSG00000058056	ENSG00000058056	USP13	3:179370542-179507189	OK	11.7005	11.1123	-0.0744198	-0.131521	0.80975	0.9998
ENSG00000254986	ENSG00000254986	DPP3	11:66234215-66313709	OK	30.9283	29.2128	-0.0823302	-0.10653	0.80985	0.9998
ENSG00000204308	ENSG00000204308	RNF5	6:32146130-32152101	OK	70.1202	73.1567	0.061161	0.146479	0.81	0.9998
ENSG00000123560	ENSG00000123560	PLP1	X:103028646-103047548	OK	212.944	204.607	-0.0576143	-0.117802	0.81005	0.9998
ENSG00000160688	ENSG00000160688	FLAD1	1:154955813-154965587	OK	30.4331	29.1481	-0.0622393	-0.133082	0.81005	0.9998
ENSG00000182685	ENSG00000182685	BRICD5	16:2254248-2261951	OK	1.94669	1.5968	-0.285847	-0.0727108	0.81005	0.9998
ENSG00000110048	ENSG00000110048	OSBP	11:59341870-59383617	OK	22.0423	21.142	-0.0601611	-0.129562	0.8102	0.9998
ENSG00000134049	ENSG00000134049	IER3IP1	18:44632316-44702745	OK	57.7331	61.1	0.0817744	0.146228	0.8102	0.9998
ENSG00000147437	ENSG00000147437	GNRH1	8:25276775-25282170	OK	0.921359	0.829974	-0.150697	-0.128883	0.8102	0.9998
ENSG00000101247	ENSG00000101247	NDUFAF5	20:13765595-13799067	OK	13.9862	13.0707	-0.0976595	-0.148706	0.81025	0.9998
ENSG00000030066	ENSG00000030066	NUP160	11:47799638-47870107	OK	18.3391	19.1428	0.0618754	0.119407	0.81035	0.9998
ENSG00000120519	ENSG00000120519	SLC10A7	4:147175126-147443123	OK	1.8373	1.98244	0.109689	0.114361	0.81035	0.9998
ENSG00000134452	ENSG00000134452	FBXO18	10:5903579-5987863	OK	13.7142	14.3266	0.0630266	0.100003	0.8104	0.9998
ENSG00000108641	ENSG00000108641	B9D1	17:19240866-19290553	OK	11.3269	10.3169	-0.134739	-0.138772	0.81055	0.9998
ENSG00000078018	ENSG00000078018	MAP2	2:210288781-210598842	OK	5.42608	5.73392	0.0796125	0.111344	0.8106	0.9998
ENSG00000188153	ENSG00000188153	COL4A5	X:107683073-107940775	OK	4.76966	5.01044	0.0710535	0.0923662	0.81065	0.9998
ENSG00000258486	ENSG00000258486	RN7SL1	14:50043389-50081390	OK	91.4237	123.837	0.437804	0.193636	0.8107	0.9998
ENSG00000178502	ENSG00000178502	KLHL11	17:40009796-40021684	OK	2.5083	2.35598	-0.090382	-0.148794	0.81075	0.9998
ENSG00000174943	ENSG00000174943	KCTD13	16:29911695-29940254	OK	16.6901	15.8347	-0.0758999	-0.135385	0.8108	0.9998
ENSG00000197312	ENSG00000197312	DDI2	1:15943994-15995539	OK	7.48959	7.18014	-0.0608747	-0.0967029	0.81095	0.9998
ENSG00000206530	ENSG00000206530	WDR52	3:112929849-113160457	OK	3.44468	3.16428	-0.122491	-0.102904	0.81095	0.9998
ENSG00000256210	ENSG00000256210	AC005255.3	19:14903120-14946188	OK	20.8229	23.0005	0.143492	0.146186	0.81105	0.9998
ENSG00000269973	ENSG00000269973	RP11-95D17.1	2:10076488-10079719	OK	0.805845	0.749916	-0.103772	-0.144957	0.8111	0.9998
ENSG00000140090	ENSG00000140090	SLC24A4	14:92788924-92962596	OK	13.4498	12.4368	-0.112964	-0.0998444	0.81115	0.9998
ENSG00000180098	ENSG00000180098	TRNAU1AP	1:28879596-28909495	OK	17.9048	16.4835	-0.119328	-0.142321	0.81115	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000213380	ENSG00000213380	COG8	16:69139466-69442474	OK	5.54633	7.39338	0.414702	0.224778	0.8112	0.9998
ENSG00000179361	ENSG00000179361	ARID3B	15:74833517-74890472	OK	2.93373	2.77175	-0.0819377	-0.114532	0.81125	0.9998
ENSG00000132467	ENSG00000132467	UTP3	4:71554195-71556267	OK	16.0024	16.7331	0.0644182	0.142359	0.8114	0.9998
ENSG00000182150	ENSG00000182150	ERCC6L2	9:98521512-98776842	OK	10.1917	9.43148	-0.111836	-0.141504	0.8114	0.9998
ENSG00000166411	ENSG00000166411	IDH3A	15:78370149-78538030	OK	56.9753	59.8967	0.0721383	0.132832	0.8115	0.9998
ENSG00000198276	ENSG00000198276	UCKL1	20:62571185-62587769	OK	31.0185	32.4468	0.0649512	0.135237	0.8115	0.9998
ENSG00000104517	ENSG00000104517	UBR5	8:103251621-103425069	OK	29.6391	28.2469	-0.0694121	-0.0821021	0.8116	0.9998
ENSG00000148606	ENSG00000148606	POLR3A	10:79734906-79789303	OK	8.38994	8.75243	0.0610225	0.13257	0.8116	0.9998
ENSG00000173786	ENSG00000173786	CNP	17:40118758-40217383	OK	73.7923	70.1705	-0.0726053	-0.132751	0.8116	0.9998
ENSG00000253683	ENSG00000253683	CTB-79E8.3	5:172068268-172124723	OK	2.58492	3.78878	0.551616	0.193406	0.8116	0.9998
ENSG00000141522	ENSG00000141522	ARHGDIA	17:79825596-79829282	OK	272.676	283.99	0.0586534	0.126443	0.81165	0.9998
ENSG00000169696	ENSG00000169696	ASPSCR1	17:79934682-79975282	OK	23.8118	25.0667	0.0740983	0.135869	0.81165	0.9998
ENSG00000163818	ENSG00000163818	LZTFL1	3:45864807-45957534	OK	8.95226	8.38893	-0.0937663	-0.13587	0.81175	0.9998
ENSG00000163281	ENSG00000163281	GNPDA2	4:44624085-44728612	OK	14.2668	15.3922	0.109543	0.134544	0.81195	0.9998
ENSG00000197472	ENSG00000197472	ZNF695	1:247108848-247242113	OK	0.738086	0.894411	0.277149	0.134116	0.81195	0.9998
ENSG00000082269	ENSG00000082269	FAM135A	6:71122530-71270877	OK	3.88225	4.10151	0.0792595	0.102557	0.812	0.9998
ENSG00000055044	ENSG00000055044	NOP58	2:203130438-203168389	OK	36.0033	37.6089	0.0629437	0.128942	0.8121	0.9998
ENSG00000048828	ENSG00000048828	FAM120A	9:96208775-96328397	OK	55.292	52.9778	-0.0616836	-0.139342	0.8122	0.9998
ENSG00000160908	ENSG00000160908	ZNF394	7:99070463-99101273	OK	13.0238	12.0266	-0.114916	-0.129229	0.8122	0.9998
ENSG00000243667	ENSG00000243667	WDR92	2:68350067-68488362	OK	6.28764	5.56086	-0.177209	-0.117358	0.8122	0.9998
ENSG00000108784	ENSG00000108784	NAGLU	17:40688189-40718295	OK	18.9509	20.5184	0.114651	0.127338	0.81225	0.9998
ENSG00000115935	ENSG00000115935	WIPF1	2:175411868-175639555	OK	10.9037	9.64458	-0.177033	-0.0962911	0.81225	0.9998
ENSG00000160211	ENSG00000160211	G6PD	X:153759605-153796782	OK	60.9872	63.7767	0.0645229	0.134729	0.81225	0.9998
ENSG00000164168	ENSG00000164168	TMEM184C	4:148538533-148605381	OK	13.9722	14.9319	0.0958416	0.143509	0.81225	0.9998
ENSG00000270049	ENSG00000270049	RP11-297D21.4	16:67515216-67521153	OK	0.647295	0.723653	0.160874	0.126044	0.8123	0.9998
ENSG00000107938	ENSG00000107938	EDRF1	10:127371797-127452712	OK	10.2388	9.69881	-0.0781714	-0.13039	0.81235	0.9998
ENSG00000167004	ENSG00000167004	PDIA3	15:44019115-44095241	OK	110.72	118.316	0.0957307	0.12192	0.81235	0.9998
ENSG00000108352	ENSG00000108352	RAPGEFL1	17:38333262-38351908	OK	1.22114	1.33997	0.133976	0.10812	0.8124	0.9998
ENSG00000122783	ENSG00000122783	C7orf49	7:134671258-134855547	OK	52.224	55.6702	0.0921925	0.145346	0.8124	0.9998
ENSG00000225131	ENSG00000225131	PSME2P2	13:49345263-49345965	OK	1.25612	1.23055	-0.0296667	-0.0202375	0.81255	0.9998
ENSG00000146007	ENSG00000146007	ZMAT2	5:140044260-140086248	OK	68.0812	62.6343	-0.120302	-0.147478	0.81265	0.9998
ENSG00000150787	ENSG00000150787	PTS	11:112097087-112140678	OK	24.2722	25.5452	0.0737427	0.144595	0.8127	0.9998
ENSG00000229132	ENSG00000229132	EIF4A1P10	X:91034259-91878229	OK	5.01763	5.33312	0.087975	0.145373	0.8127	0.9998
ENSG00000000419	ENSG00000000419	DPM1	20:49505584-49575092	OK	53.0318	58.1292	0.132405	0.156004	0.81285	0.9998
ENSG00000158158	ENSG00000158158	CNNM4	2:97426638-97477628	OK	4.4402	4.65055	0.0667788	0.134019	0.81295	0.9998
ENSG00000145794	ENSG00000145794	MEGF10	5:126626522-126801429	OK	3.80075	3.56266	-0.0933308	-0.100841	0.81305	0.9998
ENSG00000156398	ENSG00000156398	SFXN2	10:104474294-104503249	OK	6.07808	5.60177	-0.117733	-0.135391	0.81305	0.9998
ENSG00000103226	ENSG00000103226	NOMO3	16:16326351-16388668	OK	34.1611	31.8825	-0.0995895	-0.13284	0.8131	0.9998
ENSG00000261061	ENSG00000261061	RP11-303E16.2	16:81009697-81069364	OK	2.71908	1.77733	-0.613406	-0.195253	0.8131	0.9998
ENSG00000261884	ENSG00000261884	CTC-479C5.12	16:67927174-67970990	OK	3.57907	4.78581	0.419176	0.197124	0.8131	0.9998
ENSG00000119777	ENSG00000119777	TMEM214	2:27255777-27264563	OK	26.2721	25.1829	-0.0610886	-0.118101	0.81315	0.9998
ENSG00000012963	ENSG00000012963	UBR7	14:93651295-93695561	OK	23.0552	21.7564	-0.0836538	-0.119657	0.8132	0.9998
ENSG00000157259	ENSG00000157259	GATAD1	7:92076766-92157845	OK	14.7862	13.9049	-0.0886613	-0.138697	0.8132	0.9998
ENSG00000071994	ENSG00000071994	PDCD2	6:170884382-170893780	OK	31.9129	33.5466	0.0720298	0.142814	0.81325	0.9998
ENSG00000119509	ENSG00000119509	INVS	9:102861537-103063282	OK	12.4953	11.9118	-0.0689922	-0.124897	0.81325	0.9998
ENSG00000172175	ENSG00000172175	MALT1	18:56337711-56421709	OK	8.18537	8.61283	0.0734407	0.137378	0.8133	0.9998
ENSG00000259516	ENSG00000259516	ANP32AP1	15:35473999-35838394	OK	7.4183	6.77622	-0.130608	-0.145789	0.81335	0.9998
ENSG00000066382	ENSG00000066382	MPPED2	11:30406039-30652055	OK	8.37731	7.93459	-0.0783316	-0.13218	0.8134	0.9998
ENSG00000172765	ENSG00000172765	TMCC1	3:129366634-129612419	OK	10.1602	10.9015	0.101594	0.115589	0.8134	0.9998
ENSG00000109790	ENSG00000109790	KLHL5	4:39046658-39128477	OK	13.0935	12.4164	-0.0766099	-0.142228	0.81345	0.9998
ENSG00000164828	ENSG00000164828	SUN1	7:855527-936073	OK	42.6611	40.3241	-0.0812785	-0.101796	0.81345	0.9998
ENSG00000154767	ENSG00000154767	XPC	3:14166439-14242619	OK	11.2092	10.3786	-0.111066	-0.0985845	0.8135	0.9998
ENSG00000213337	ENSG00000213337	ANKRD39	2:97481981-97523832	OK	53.8656	50.7865	-0.0849182	-0.144614	0.8136	0.9998
ENSG00000069974	ENSG00000069974	RAB27A	15:55495163-55800432	OK	68.5582	64.7688	-0.0820306	-0.13554	0.81365	0.9998
ENSG00000155463	ENSG00000155463	OXA1L	14:23171351-23241007	OK	105.286	109.475	0.0562957	0.139254	0.81375	0.9998
ENSG00000166734	ENSG00000166734	CASC4	15:44580926-44719342	OK	9.31587	8.8964	-0.0664695	-0.109816	0.81375	0.9998
ENSG00000107130	ENSG00000107130	NCS1	9:132934856-132999583	OK	41.8308	40.2075	-0.0570998	-0.144895	0.8138	0.9998
ENSG00000156885	ENSG00000156885	COX6A2	16:31439051-31439967	OK	4.30018	4.74259	0.141277	0.155662	0.8138	0.9998
ENSG00000124635	ENSG00000124635	HIST1H2BJ	6:27093675-27100541	OK	5.08376	4.65224	-0.12797	-0.141207	0.81385	0.9998
ENSG00000145050	ENSG00000145050	MANF	3:51422477-51426828	OK	104.104	98.6354	-0.0778478	-0.146654	0.8139	0.9998
ENSG00000107758	ENSG00000107758	PPP3CB	10:75196185-75385711	OK	23.2268	21.6978	-0.0982376	-0.148687	0.814	0.9998
ENSG00000147231	ENSG00000147231	CXorf57	X:105855159-105922672	OK	3.90979	3.65942	-0.0954765	-0.115981	0.814	0.9998
ENSG00000244041	ENSG00000244041	LINC01011	6:2988200-3019996	OK	1.4971	1.22485	-0.28956	-0.165224	0.814	0.9998
ENSG00000064545	ENSG00000064545	TMEM161A	19:19229977-19249322	OK	15.6923	16.4953	0.0719998	0.127364	0.81415	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000144567	ENSG00000144567	FAM134A	2:220036618-220050201	OK	130.537	137.608	0.0761036	0.135802	0.81415	0.9998
ENSG00000160256	ENSG00000160256	FAM207A	21:46359924-46396904	OK	90.7228	86.4977	-0.068802	-0.144576	0.8143	0.9998
ENSG00000075785	ENSG00000075785	RAB7A	3:128444964-128533639	OK	326.067	340.285	0.0615781	0.122228	0.8144	0.9998
ENSG00000047932	ENSG00000047932	GOPC	6:117609462-117923691	OK	5.13989	5.42027	0.0766255	0.140506	0.81445	0.9998
ENSG00000053770	ENSG00000053770	AP5M1	14:57670517-57756797	OK	12.7152	13.8959	0.128113	0.12096	0.81455	0.9998
ENSG00000197114	ENSG00000197114	ZGPAT	20:62289162-62374858	OK	20.2547	22.2774	0.137325	0.130513	0.81455	0.9998
ENSG00000271550	ENSG00000271550	RP11-561N12.7	7:64126510-64171404	OK	0.487083	0.773446	0.667133	0.151886	0.81455	0.9998
ENSG00000180626	ENSG00000180626	ZNF594	17:5082830-5095178	OK	1.49945	1.66589	0.151858	0.144654	0.81465	0.9998
ENSG00000174171	ENSG00000174171	RP11-23P13.6	15:42120282-42190773	OK	0.741003	1.04459	0.49539	0.148601	0.8147	0.9998
ENSG00000153187	ENSG00000153187	HNRNPU	1:244998623-245027844	OK	127.397	121.276	-0.0710347	-0.137656	0.8151	0.9998
ENSG00000176597	ENSG00000176597	B3GNT5	3:182895830-183146566	OK	1.54733	1.67029	0.11032	0.10252	0.8151	0.9998
ENSG00000267528	ENSG00000267528	AC011524.1	19:29374336-29444152	OK	0.742177	0.857625	0.208583	0.14404	0.8151	0.9998
ENSG00000143162	ENSG00000143162	CREG1	1:167498913-167523004	OK	61.1648	63.6305	0.057016	0.141766	0.81515	0.9998
ENSG00000196419	ENSG00000196419	XRCC6	22:42017122-42060044	OK	196.699	204.886	0.0588309	0.14147	0.81515	0.9998
ENSG00000111727	ENSG00000111727	HCFC2	12:104458234-104498639	OK	6.28734	6.60813	0.0717927	0.132322	0.8152	0.9998
ENSG00000175482	ENSG00000175482	POLD4	11:67118247-67141648	OK	38.4765	40.6372	0.0788218	0.148706	0.8152	0.9998
ENSG00000148814	ENSG00000148814	LRRC27	10:134145613-134195010	OK	4.32034	4.01362	-0.106238	-0.129915	0.81525	0.9998
ENSG00000155729	ENSG00000155729	KCTD18	2:201353674-201448505	OK	6.42925	5.84033	-0.138601	-0.128972	0.81525	0.9998
ENSG00000197582	ENSG00000197582	GPX1P1	X:13395306-13421138	OK	44.8842	47.1018	0.0695738	0.143333	0.81525	0.9998
ENSG00000206077	ENSG00000206077	ZDHHC11B	5:710470-919472	OK	7.0683	8.23989	0.221261	0.14739	0.81525	0.9998
ENSG00000113163	ENSG00000113163	COL4A3BP	5:74664310-74896969	OK	25.5544	24.2585	-0.0750827	-0.123125	0.8153	0.9998
ENSG00000198783	ENSG00000198783	ZNF830	17:33254877-33332083	OK	6.17337	5.50613	-0.165018	-0.141516	0.8153	0.9998
ENSG00000132313	ENSG00000132313	MRPL35	2:86426477-86440917	OK	77.8794	73.5368	-0.0827765	-0.146056	0.8154	0.9998
ENSG00000111640	ENSG00000111640	GAPDH	12:6643092-6647537	OK	6299.39	6767.76	0.103466	0.149612	0.81545	0.9998
ENSG00000162408	ENSG00000162408	NOL9	1:6581406-6614595	OK	3.73769	4.0416	0.112778	0.119736	0.81545	0.9998
ENSG00000088833	ENSG00000088833	NSFL1C	20:1422806-1472233	OK	26.4444	27.784	0.071294	0.139956	0.8155	0.9998
ENSG00000111786	ENSG00000111786	SRSF9	12:120899470-120907596	OK	133.33	128.164	-0.0570056	-0.141018	0.81555	0.9998
ENSG00000109099	ENSG00000109099	PMP22	17:15133094-15169024	OK	152.706	146.845	-0.0564655	-0.139951	0.8156	0.9998
ENSG00000184678	ENSG00000184678	HIST2H2BE	1:149856009-149858232	OK	4.03878	3.82118	-0.0798994	-0.140858	0.8156	0.9998
ENSG00000218537	ENSG00000218537	AP000350.4	22:24198613-24241117	OK	0.659943	0.523012	-0.335496	-0.0240668	0.8156	0.9998
ENSG00000235333	ENSG00000235333	PVRIG2P	7:99905324-99997719	OK	1.07686	1.7265	0.681017	0.211173	0.8156	0.9998
ENSG00000157916	ENSG00000157916	RER1	1:2323266-2345236	OK	115.822	122.557	0.0815435	0.133872	0.81565	0.9998
ENSG00000112245	ENSG00000112245	PTP4A1	6:64231665-64293492	OK	78.4465	81.8937	0.0620445	0.104323	0.8157	0.9998
ENSG00000164898	ENSG00000164898	C7orf55	7:139024202-139108198	OK	18.0671	14.3221	-0.335125	-0.140233	0.81575	0.9998
ENSG00000197798	ENSG00000197798	FAM118B	11:126071992-126148026	OK	8.35708	6.89534	-0.277378	-0.170292	0.8158	0.9998
ENSG00000178467	ENSG00000178467	P4HTM	3:48955220-49060928	OK	1.04611	0.901769	-0.214204	-0.0348789	0.8159	0.9998
ENSG00000184162	ENSG00000184162	NR2C2AP	19:19256375-19314233	OK	18.7242	17.0754	-0.132989	-0.135838	0.8159	0.9998
ENSG00000165521	ENSG00000165521	EML5	14:89029252-89259096	OK	0.687471	0.841327	0.291369	0.117364	0.816	0.9998
ENSG00000163875	ENSG00000163875	MEAF6	1:37958175-37980375	OK	33.9068	32.2343	-0.0729809	-0.138824	0.81605	0.9998
ENSG00000188994	ENSG00000188994	ZNF292	6:87860876-87973914	OK	3.00849	2.83356	-0.0864278	-0.0776062	0.81605	0.9998
ENSG00000231889	ENSG00000231889	TRAF3IP2-AS1	6:111620233-111927481	OK	3.54042	4.03116	0.187277	0.0686936	0.81605	0.9998
ENSG00000170468	ENSG00000170468	AC005280.1	14:73945188-74025651	OK	3.98256	3.53612	-0.171526	-0.128717	0.8161	0.9998
ENSG00000185973	ENSG00000185973	TMLHE	X:154695630-154899605	OK	12.5212	11.7315	-0.093983	-0.138885	0.8161	0.9998
ENSG00000006210	ENSG00000006210	CX3CL1	16:57406369-57418960	OK	4.14674	4.36438	0.0737983	0.133403	0.81615	0.9998
ENSG00000066117	ENSG00000066117	SMARCD1	12:50478754-50494495	OK	49.3226	51.6272	0.0658807	0.112026	0.81625	0.9998
ENSG00000131653	ENSG00000131653	TRAF7	16:2205698-2246526	OK	34.5418	36.1195	0.0644339	0.118193	0.81645	0.9998
ENSG00000188313	ENSG00000188313	PLSCR1	3:146232966-146262651	OK	45.6446	43.6573	-0.0642231	-0.133581	0.81645	0.9998
ENSG00000173727	ENSG00000173727	AP000769.1	11:65222727-65234028	OK	4.57566	4.90821	0.101217	0.142209	0.8165	0.9998
ENSG00000174842	ENSG00000174842	GLMN	1:92711958-92867613	OK	4.78585	5.17864	0.113797	0.126946	0.8165	0.9998
ENSG00000179922	ENSG00000179922	ZNF784	19:56132107-56135967	OK	1.22058	1.30704	0.0987449	0.138516	0.81655	0.9998
ENSG00000112584	ENSG00000112584	FAM120B	6:170599790-170716153	OK	7.13584	6.8022	-0.0690818	-0.137789	0.8166	0.9998
ENSG00000132382	ENSG00000132382	MYBBP1A	17:4400688-4458926	OK	17.8047	18.5944	0.0626121	0.120614	0.8166	0.9998
ENSG00000235272	ENSG00000235272	FAM103A2P	6:166822851-167370679	OK	29.3579	33.609	0.195097	0.138661	0.8166	0.9998
ENSG00000166685	ENSG00000166685	COG1	17:71161115-71258491	OK	18.8887	17.6564	-0.0973279	-0.102424	0.81665	0.9998
ENSG00000240990	ENSG00000240990	HOXA11-AS	7:27221128-27233067	OK	0.592405	0.685459	0.210488	0.132506	0.81665	0.9998
ENSG00000270181	ENSG00000270181	BIVM-ERCC5	13:103451398-103528345	OK	4.24021	3.9085	-0.117522	-0.141935	0.81665	0.9998
ENSG00000121903	ENSG00000121903	ZSCAN20	1:33938245-33962107	OK	1.39167	1.48695	0.0955322	0.12595	0.8167	0.9998
ENSG00000227666	ENSG00000227666	CYCSP24	9:96793075-96872138	OK	1.6976	2.27488	0.422293	0.0840645	0.81675	0.9998
ENSG00000273071	ENSG00000273071	RP11-337C18.10	1:146644349-146767443	OK	0.942676	0.651454	-0.533098	-0.0558286	0.8168	0.9998
ENSG00000121753	ENSG00000121753	BAI2	1:32192717-32230494	OK	3.29407	3.52025	0.0958058	0.120236	0.81685	0.9998
ENSG00000172500	ENSG00000172500	FIBP	11:65647279-65656010	OK	58.6942	56.3174	-0.0596366	-0.137369	0.8169	0.9998
ENSG00000106012	ENSG00000106012	IQCE	7:2598631-2654368	OK	13.3934	12.7651	-0.0693095	-0.105061	0.817	0.9998
ENSG00000141179	ENSG00000141179	PCTP	17:53828339-53950300	OK	21.2222	22.133	0.0606232	0.134595	0.817	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000253729	ENSG00000253729	PRKDC	8:48685668-48872743	OK	31.3388	33.0213	0.0754482	0.0837762	0.817	0.9998
ENSG00000106355	ENSG00000106355	LSM5	7:32524950-32534895	OK	80.4712	76.3462	-0.0759174	-0.147914	0.81705	0.9998
ENSG00000110955	ENSG00000110955	ATP5B	12:57031958-57039798	OK	779.591	813.159	0.0608186	0.13343	0.8171	0.9998
ENSG00000163637	ENSG00000163637	PRICKLE2	3:64053639-64440508	OK	1.60978	1.70017	0.0788165	0.0907094	0.8171	0.9998
ENSG00000105227	ENSG00000105227	PRX	19:40899674-40919273	OK	0.897386	0.95616	0.0915245	0.129373	0.81715	0.9998
ENSG00000102786	ENSG00000102786	INTS6	13:51909908-52126500	OK	15.4176	16.1657	0.0683595	0.105165	0.8172	0.9998
ENSG00000139613	ENSG00000139613	SMARCC2	12:56544579-56584068	OK	26.9283	24.5652	-0.13251	-0.103912	0.81725	0.9998
ENSG00000103404	ENSG00000103404	USP31	16:23072726-23160591	OK	4.51626	4.06918	-0.150393	-0.142605	0.8173	0.9998
ENSG00000130479	ENSG00000130479	MAP1S	19:17830050-17845325	OK	8.70186	9.06615	0.0591658	0.10174	0.81735	0.9998
ENSG00000213585	ENSG00000213585	VDAC1	5:133307605-133340824	OK	135.549	130.382	-0.0560701	-0.13605	0.81735	0.9998
ENSG00000102119	ENSG00000102119	EMD	X:153607556-153609883	OK	43.74	45.7416	0.064553	0.14048	0.8174	0.9998
ENSG00000249336	ENSG00000249336	RP11-133G22.1	9:39722429-39817308	OK	0.676037	0.767371	0.182822	0.138986	0.8174	0.9998
ENSG00000169251	ENSG00000169251	NMD3	3:160801670-160971320	OK	40.9844	39.1656	-0.0654861	-0.124357	0.81745	0.9998
ENSG00000215837	ENSG00000215837	SDHAP2	3:195384932-195467994	OK	0.81152	0.595452	-0.446641	-0.177179	0.81755	0.9998
ENSG00000243753	ENSG00000243753	HLA-L	6:30201815-30314661	OK	1.64404	2.03282	0.306239	0.15319	0.81755	0.9998
ENSG00000134882	ENSG00000134882	UBAC2	13:99853027-100038688	OK	49.7624	51.9841	0.0630154	0.140603	0.8176	0.9998
ENSG00000167395	ENSG00000167395	ZNF646	16:31085742-31107301	OK	4.84292	4.34237	-0.157393	-0.0862031	0.81765	0.9998
ENSG00000064115	ENSG00000064115	TM7SF3	12:27124518-27167367	OK	123.535	118.093	-0.0649855	-0.103599	0.8177	0.9998
ENSG00000102897	ENSG00000102897	LYRM1	16:20621564-20936328	OK	17.6321	15.8439	-0.15427	-0.128646	0.8178	0.9998
ENSG00000177192	ENSG00000177192	PUS1	12:132409280-132428406	OK	14.4408	15.2157	0.0754111	0.137654	0.81805	0.9998
ENSG00000244187	ENSG00000244187	TMEM141	9:139685806-139735639	OK	55.7057	49.7517	-0.16308	-0.151131	0.81805	0.9998
ENSG00000099901	ENSG00000099901	RANBP1	22:20067754-20114878	OK	153.636	145.852	-0.0750097	-0.13618	0.81815	0.9998
ENSG00000248275	ENSG00000248275	TRIM52-AS1	5:180663908-180699308	OK	13.1907	11.5166	-0.195805	-0.0234742	0.81815	0.9998
ENSG00000236814	ENSG00000236814	RP11-446E9.1	8:56962596-56963766	OK	2.49245	2.32568	-0.0999123	-0.139999	0.8182	0.9998
ENSG00000147050	ENSG00000147050	KDM6A	X:44732756-44971847	OK	5.93149	5.6239	-0.0768238	-0.10548	0.81825	0.9998
ENSG00000169855	ENSG00000169855	ROBO1	3:78646389-79816965	OK	6.07952	6.43469	0.081914	0.0950585	0.8183	0.9998
ENSG00000100804	ENSG00000100804	PSMB5	14:23485751-23504439	OK	140.708	146.397	0.0571761	0.14172	0.8184	0.9998
ENSG00000108523	ENSG00000108523	RNF167	17:4840424-4848517	OK	56.8394	60.0894	0.0802186	0.119353	0.8184	0.9998
ENSG00000138385	ENSG00000138385	SSB	2:170648442-170681441	OK	69.0948	72.248	0.0643787	0.124299	0.8184	0.9998
ENSG00000231351	ENSG00000231351	AC111200.7	2:87098423-87248975	OK	4.48047	4.087	-0.13261	-0.141642	0.8184	0.9998
ENSG00000152455	ENSG00000152455	SUV39H2	10:14920818-14996431	OK	7.19223	6.64046	-0.115155	-0.135512	0.8185	0.9998
ENSG00000114744	ENSG00000114744	COMMD2	3:149456256-149470286	OK	26.5816	25.0611	-0.0849792	-0.132316	0.8186	0.9998
ENSG00000101898	ENSG00000101898	RP3-324O17.4	20:30102230-30161066	OK	3.53453	4.74791	0.425773	0.100962	0.81865	0.9998
ENSG00000106069	ENSG00000106069	CHN2	7:29019582-29603286	OK	3.01749	3.27998	0.120338	0.0661909	0.8187	0.9998
ENSG00000028310	ENSG00000028310	BRD9	5:710470-919472	OK	36.554	34.2899	-0.0922443	-0.131561	0.81875	0.9998
ENSG00000215630	ENSG00000215630	GUSBP9	5:70435715-70585611	OK	2.45158	2.69055	0.13419	0.125234	0.81875	0.9998
ENSG00000167536	ENSG00000167536	DHRS13	17:27224755-27230089	OK	10.6112	10.0514	-0.0781845	-0.128179	0.8188	0.9998
ENSG00000197863	ENSG00000197863	ZNF790	19:37288419-37407193	OK	1.81004	1.58472	-0.191797	-0.122315	0.81885	0.9998
ENSG00000257851	ENSG00000257851	HNRNPA3P10	12:51984049-52206648	OK	0.635753	0.575979	-0.14245	-0.0564745	0.8189	0.9998
ENSG00000185963	ENSG00000185963	BICD2	9:95473644-95527094	OK	22.3488	23.2523	0.0571719	0.141557	0.81895	0.9998
ENSG00000143702	ENSG00000143702	CEP170	1:243287729-243418650	OK	28.519	29.9677	0.0714847	0.090979	0.819	0.9998
ENSG00000163597	ENSG00000163597	SNHG16	17:74553847-74583038	OK	150.73	160.339	0.0891613	0.126737	0.81905	0.9998
ENSG00000013275	ENSG00000013275	PSMC4	19:40476911-40487348	OK	62.6043	60.1662	-0.0573089	-0.138829	0.81915	0.9998
ENSG00000171132	ENSG00000171132	PRKCE	2:45878483-46415129	OK	11.5532	11.0436	-0.0650784	-0.0939612	0.81915	0.9998
ENSG00000134901	ENSG00000134901	KDELC1	13:103436630-103451357	OK	5.98544	5.69896	-0.0707584	-0.12924	0.8192	0.9998
ENSG00000180089	ENSG00000180089	TMEM86B	19:55738006-55770363	OK	2.63448	2.20844	-0.254494	-0.100954	0.81925	0.9998
ENSG00000141644	ENSG00000141644	MBD1	18:47793251-47808144	OK	24.7736	26.0489	0.0724147	0.113786	0.81935	0.9998
ENSG00000109756	ENSG00000109756	RAPGEF2	4:160025329-160281321	OK	13.773	14.8472	0.108348	0.133452	0.8194	0.9998
ENSG00000165300	ENSG00000165300	SLITRK5	13:88324869-88331871	OK	1.23854	1.31479	0.086183	0.138567	0.8194	0.9998
ENSG00000147118	ENSG00000147118	ZNF182	X:47696300-47931025	OK	2.08724	1.92752	-0.114846	-0.142406	0.8195	0.9998
ENSG00000180228	ENSG00000180228	PRKRA	2:179278665-179326117	OK	23.1062	22.0094	-0.0701614	-0.130115	0.8196	0.9998
ENSG00000198198	ENSG00000198198	SZT2	1:43855552-43922666	OK	3.93457	4.16911	0.0835321	0.0956127	0.81975	0.9998
ENSG00000203760	ENSG00000203760	CENPW	6:126661319-126670021	OK	21.7863	20.6504	-0.0772577	-0.13833	0.81975	0.9998
ENSG00000272186	ENSG00000272186	RP11-110I1.13	11:118938084-118952688	OK	0.655947	0.462925	-0.502801	-0.073284	0.8198	0.9998
ENSG00000134809	ENSG00000134809	TIMM10	11:57295935-57298276	OK	64.733	61.9244	-0.0639921	-0.138588	0.8199	0.9998
ENSG00000136371	ENSG00000136371	MTHFS	15:80125926-80217194	OK	44.5236	47.4417	0.0915848	0.14594	0.8199	0.9998
ENSG00000105171	ENSG00000105171	POP4	19:30094923-30108144	OK	76.5357	80.098	0.0656334	0.141477	0.81995	0.9998
ENSG00000005075	ENSG00000005075	POLR2J	7:102105375-102119354	OK	81.2587	85.5238	0.0738051	0.13663	0.8201	0.9998
ENSG00000138018	ENSG00000138018	EPT1	2:26531040-26618759	OK	9.00182	9.36494	0.0570535	0.113483	0.8202	0.9998
ENSG00000062598	ENSG00000062598	ELMO2	20:44994687-45087915	OK	39.4031	37.8898	-0.0564993	-0.112752	0.82035	0.9998
ENSG00000187601	ENSG00000187601	MAGEH1	X:55478537-55479998	OK	2.37454	2.22993	-0.0906449	-0.134501	0.82035	0.9998
ENSG00000204227	ENSG00000204227	RING1	6:33176271-33180499	OK	38.8837	37.3243	-0.0590501	-0.140589	0.82045	0.9998
ENSG00000077380	ENSG00000077380	DYNC1I2	2:172543918-172604930	OK	52.8738	55.0516	0.0582318	0.128767	0.8205	0.9998
ENSG00000131626	ENSG00000131626	PPFIA1	11:70116805-70282690	OK	27.0413	29.4367	0.122449	0.0903771	0.8206	0.9998
ENSG00000137547	ENSG00000137547	MRPL15	8:55047769-55060461	OK	59.6845	57.2652	-0.0596966	-0.140949	0.8207	0.9998
ENSG00000065665	ENSG00000065665	SEC61A2	10:12171635-12292588	OK	3.4588	3.89413	0.171029	0.0919665	0.82075	0.9998
ENSG00000149716	ENSG00000149716	ORAOV1	11:69455854-69490184	OK	9.07321	10.1087	0.155907	0.0334715	0.8208	0.9998
ENSG00000115084	ENSG00000115084	SLC35F5	2:114462587-114514400	OK	29.2799	30.8404	0.0749084	0.128756	0.82095	0.9998
ENSG00000108984	ENSG00000108984	MAP2K6	17:67410838-67539472	OK	11.4195	10.8868	-0.0689143	-0.134272	0.8211	0.9998
ENSG00000103160	ENSG00000103160	HSDL1	16:84155885-84178797	OK	22.4681	21.5817	-0.0580686	-0.0985195	0.82125	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000176700	ENSG00000176700	SCAND2P	15:85174681-85185695	OK	4.12431	3.87939	-0.0883233	-0.0911309	0.82125	0.9998
ENSG00000170265	ENSG00000170265	ZNF282	7:148892576-148923339	OK	12.7278	13.2813	0.0614118	0.105379	0.82135	0.9998
ENSG00000112812	ENSG00000112812	PRSS16	6:27215479-27224403	OK	0.884472	0.947767	0.0997162	0.0704452	0.8215	0.9998
ENSG00000238121	ENSG00000238121	LINC00426	13:30914406-30951282	OK	1.12957	1.26537	0.163785	0.104822	0.8215	0.9998
ENSG00000123080	ENSG00000123080	CDKN2C	1:51426416-51440305	OK	5.32059	5.03801	-0.0787329	-0.135883	0.82155	0.9998
ENSG00000121749	ENSG00000121749	TBC1D15	12:72233486-72320629	OK	21.3951	20.5009	-0.0615922	-0.123728	0.8217	0.9998
ENSG00000226525	ENSG00000226525	RPS7P10	13:22202551-22203154	OK	8.2664	7.76708	-0.0898863	-0.135219	0.8218	0.9998
ENSG00000251141	ENSG00000251141	RP11-53O19.1	5:44745001-44808879	OK	5.04948	5.43897	0.107198	0.138798	0.8218	0.9998
ENSG00000167842	ENSG00000167842	MIS12	17:5374570-5394134	OK	8.07738	8.66905	0.101987	0.120236	0.82185	0.9998
ENSG00000095380	ENSG00000095380	NANS	9:100819020-100881494	OK	139.066	144.867	0.0589608	0.135027	0.8219	0.9998
ENSG00000115109	ENSG00000115109	EPB41L5	2:120770580-120974855	OK	4.00608	3.767	-0.0887756	-0.0956847	0.8219	0.9998
ENSG00000119402	ENSG00000119402	FBXW2	9:123514255-123555690	OK	35.8105	33.5085	-0.0958555	-0.136193	0.82195	0.9998
ENSG00000226688	ENSG00000226688	ENTPD1-AS1	10:97471535-97849995	OK	7.96202	6.75293	-0.237619	-0.125056	0.822	0.9998
ENSG00000140548	ENSG00000140548	ZNF710	15:90544623-90625439	OK	3.00026	3.21026	0.0976052	0.0948019	0.82205	0.9998
ENSG00000184083	ENSG00000184083	FAM120C	X:54094756-54209714	OK	1.20294	1.35081	0.167257	0.140082	0.82205	0.9998
ENSG00000189190	ENSG00000189190	ZNF600	19:53267447-53290044	OK	3.72697	3.33891	-0.158629	-0.137059	0.82205	0.9998
ENSG00000250802	ENSG00000250802	ZBED3-AS1	5:76367896-76462734	OK	0.903416	0.818227	-0.142889	-0.0621303	0.8221	0.9998
ENSG00000106638	ENSG00000106638	TBL2	7:72983261-72993121	OK	19.114	19.9939	0.0649263	0.119936	0.82225	0.9998
ENSG00000172269	ENSG00000172269	DPAGT1	11:118967212-118989252	OK	10.7053	10.0188	-0.0956151	-0.131335	0.82225	0.9998
ENSG00000141682	ENSG00000141682	PMAIP1	18:57567179-57571538	OK	1.76099	1.64843	-0.0952983	-0.135159	0.8224	0.9998
ENSG00000263620	ENSG00000263620	RP11-599B13.6	17:8043789-8066864	OK	0.659837	1.06785	0.694525	0.123532	0.82245	0.9998
ENSG00000272658	ENSG00000272658	LTB4R2	14:24769067-24787242	OK	1.53693	1.22833	-0.323349	-0.154126	0.82245	0.9998
ENSG00000127720	ENSG00000127720	METTL25	12:82617459-82873015	OK	2.21522	2.49842	0.173567	0.0927144	0.82255	0.9998
ENSG00000070526	ENSG00000070526	ST6GALNAC1	17:74620842-74639920	OK	1.87228	2.00878	0.101525	0.097579	0.8226	0.9998
ENSG00000066379	ENSG00000066379	ZNRD1	6:29968787-30032686	OK	20.4318	19.2122	-0.0887941	-0.135838	0.82265	0.9998
ENSG00000104320	ENSG00000104320	NBN	8:90945563-91064320	OK	12.9345	12.2684	-0.0762842	-0.0931879	0.82265	0.9998
ENSG00000253771	ENSG00000253771	TPTE2P1	13:25498814-25542625	OK	0.764026	0.682257	-0.163305	-0.126073	0.82265	0.9998
ENSG00000172081	ENSG00000172081	MOB3A	19:2071036-2099592	OK	5.3885	5.64666	0.0675142	0.110257	0.8229	0.9998
ENSG00000166262	ENSG00000166262	FAM227B	15:49398267-49913128	OK	1.58247	1.41812	-0.158206	-0.0434404	0.823	0.9998
ENSG00000041880	ENSG00000041880	PARP3	3:51976360-51982883	OK	6.09708	5.73524	-0.088265	-0.131257	0.8232	0.9998
ENSG00000167962	ENSG00000167962	ZNF598	16:2047654-2059824	OK	17.193	16.0883	-0.0958084	-0.141018	0.8232	0.9998
ENSG00000223478	ENSG00000223478	RP11-545E17.3	9:131486723-131534693	OK	4.31125	3.02811	-0.50969	-0.21682	0.82325	0.9998
ENSG00000105552	ENSG00000105552	BCAT2	19:49298318-49314286	OK	19.7529	18.8865	-0.064706	-0.132462	0.82335	0.9998
ENSG00000100836	ENSG00000100836	PABPN1	14:23654524-23795394	OK	57.565	54.2663	-0.0851376	-0.134664	0.8234	0.9998
ENSG00000076258	ENSG00000076258	FMO4	1:171283346-171311223	OK	4.573	4.2102	-0.119254	-0.130336	0.82345	0.9998
ENSG00000155893	ENSG00000155893	ACPL2	3:140947567-141168634	OK	3.52127	4.00519	0.185774	0.0818496	0.82345	0.9998
ENSG00000162512	ENSG00000162512	SDC3	1:31342313-31381608	OK	147.558	156.396	0.0839238	0.111006	0.8235	0.9998
ENSG00000186020	ENSG00000186020	ZNF529	19:37001596-37119499	OK	3.87588	4.155	0.100323	0.0896913	0.82355	0.9998
ENSG00000214975	ENSG00000214975	PPIAP29	6:24797548-25057301	OK	2.12658	1.47366	-0.52913	-0.19696	0.82355	0.9998
ENSG00000273485	ENSG00000273485	RP11-225H22.7	10:105206542-105222452	OK	0.694318	0.451131	-0.622048	-0.131886	0.82365	0.9998
ENSG00000171612	ENSG00000171612	SLC25A33	1:9599540-9645237	OK	4.50254	4.71415	0.0662596	0.13353	0.8237	0.9998
ENSG00000183624	ENSG00000183624	HMCES	3:128997670-129025029	OK	32.5116	31.1561	-0.0614411	-0.130684	0.8237	0.9998
ENSG00000091844	ENSG00000091844	RGS17	6:153325593-153452384	OK	0.607547	0.675942	0.153903	0.124784	0.82375	0.9998
ENSG00000117262	ENSG00000117262	GPR89A	1:145764410-145827103	OK	15.7697	15.0188	-0.0703827	-0.122652	0.82375	0.9998
ENSG00000121350	ENSG00000121350	PYROXD1	12:21590548-21654603	OK	8.08111	8.86866	0.134163	0.113447	0.82375	0.9998
ENSG00000185085	ENSG00000185085	INTS5	11:62414319-62441159	OK	5.43603	4.96779	-0.12995	-0.135048	0.8239	0.9998
ENSG00000227992	ENSG00000227992	AC108463.2	2:111953539-112268567	OK	1.14733	1.53321	0.418272	0.066092	0.8239	0.9998
ENSG00000132600	ENSG00000132600	PRMT7	16:68344876-68482591	OK	30.8201	28.9911	-0.0882626	-0.133085	0.82405	0.9998
ENSG00000160953	ENSG00000160953	MUM1	19:1285889-1378430	OK	17.1929	16.3724	-0.0705442	-0.121199	0.82405	0.9998
ENSG00000132950	ENSG00000132950	ZMYM5	13:20397621-20437776	OK	9.55894	10.0656	0.0745082	0.135919	0.82415	0.9998
ENSG00000227376	ENSG00000227376	FTH1P16	11:77371040-77532063	OK	9.2842	11.2259	0.273986	0.137809	0.8243	0.9998
ENSG00000235082	ENSG00000235082	SUMO1P3	1:160259062-160328742	OK	8.26983	10.3879	0.328971	0.0334922	0.8243	0.9998
ENSG00000162734	ENSG00000162734	PEA15	1:160171988-160185166	OK	254.129	266.489	0.0685154	0.130861	0.82435	0.9998
ENSG00000255112	ENSG00000255112	CHMP1B	18:11688954-11909222	OK	22.1558	21.0234	-0.0756828	-0.139534	0.82435	0.9998
ENSG00000099817	ENSG00000099817	POLR2E	19:1065921-1095598	OK	137.623	131.913	-0.0611272	-0.128221	0.8244	0.9998
ENSG00000120437	ENSG00000120437	ACAT2	6:160090088-160210781	OK	40.1179	36.3483	-0.142356	-0.13897	0.8245	0.9998
ENSG00000135549	ENSG00000135549	PKIB	6:122793075-123047518	OK	1.37403	1.47609	0.103369	0.115725	0.8245	0.9998
ENSG00000136888	ENSG00000136888	ATP6V1G1	9:117350025-117360653	OK	257.957	248.669	-0.0528996	-0.133182	0.8245	0.9998
ENSG00000206573	ENSG00000206573	SETD5-AS1	3:9022274-9520924	OK	23.2949	25.5874	0.13542	0.0680713	0.82455	0.9998
ENSG00000239626	ENSG00000239626	RPSAP41	6:73918805-74020088	OK	0.691997	0.547892	-0.336874	-0.13151	0.82455	0.9998
ENSG00000265678	ENSG00000265678	RP11-1376P16.2	17:80059335-80170706	OK	0.770885	1.14744	0.573828	0.157118	0.8246	0.9998
ENSG00000099785	ENSG00000099785	2-Mar	19:8478153-8503901	OK	13.5235	14.2557	0.0760701	0.131746	0.8247	0.9998
ENSG00000136807	ENSG00000136807	CDK9	9:130547957-130553066	OK	18.7345	19.8057	0.0802215	0.125701	0.82475	0.9998
ENSG00000260442	ENSG00000260442	RP11-22P6.3	16:28889725-28950667	OK	1.58238	1.1524	-0.457447	-0.164273	0.82475	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000269906	ENSG00000269906	RP11-248J18.2	14:50885218-51135049	OK	3.48731	2.35795	-0.56458	-0.191866	0.8248	0.9998
ENSG00000170088	ENSG00000170088	TMEM192	4:165995573-166244308	OK	11.2264	12.0811	0.105857	0.138237	0.82495	0.9998
ENSG00000176783	ENSG00000176783	RUFY1	5:178977558-179037027	OK	13.8574	13.2538	-0.0642568	-0.116718	0.82495	0.9998
ENSG00000180530	ENSG00000180530	NRIP1	21:16333555-16437321	OK	1.25576	1.19263	-0.074419	-0.127648	0.82495	0.9998
ENSG00000258171	ENSG00000258171	RP11-511B23.3	12:93392993-93609455	OK	1.12289	1.21214	0.11035	0.128816	0.825	0.9998
ENSG00000131467	ENSG00000131467	PSME3	17:40950809-40995774	OK	77.4957	73.27	-0.0808924	-0.12968	0.8251	0.9998
ENSG00000142875	ENSG00000142875	PRKACB	1:84543744-84704181	OK	9.36899	8.89079	-0.0755816	-0.115803	0.82515	0.9998
ENSG00000181218	ENSG00000181218	HIST3H2A	1:228645064-228645560	OK	6.47926	6.94102	0.0993202	0.130656	0.8253	0.9998
ENSG00000177173	ENSG00000177173	NAP1L4P1	1:117057156-117113661	OK	0.535763	0.684576	0.353614	0.130837	0.8254	0.9998
ENSG00000188732	ENSG00000188732	FAM221A	7:23719748-23742868	OK	3.4001	3.14733	-0.111448	-0.133599	0.8254	0.9998
ENSG00000116191	ENSG00000116191	RALGPS2	1:178693440-178889238	OK	13.8971	14.6916	0.0802139	0.092708	0.8255	0.9998
ENSG00000105819	ENSG00000105819	PMPCB	7:102937868-103629963	OK	62.988	58.3619	-0.11005	-0.135396	0.82555	0.9998
ENSG00000177479	ENSG00000177479	ARIH2	3:48955220-49060928	OK	63.7907	67.6795	0.0853735	0.0887177	0.8256	0.9998
ENSG00000230373	ENSG00000230373	GOLGA6L5P	15:85051115-85123406	OK	1.24186	1.1412	-0.121954	-0.126593	0.8256	0.9998
ENSG00000173812	ENSG00000173812	EIF1	17:39775688-39943183	OK	726.531	756.513	0.0583413	0.132651	0.82565	0.9998
ENSG00000141101	ENSG00000141101	NOB1	16:69760915-69788843	OK	25.5211	24.4811	-0.0600217	-0.127422	0.8258	0.9998
ENSG00000234494	ENSG00000234494	AC003665.1	17:45973515-46018776	OK	0.857807	0.70267	-0.287807	-0.0986594	0.8258	0.9998
ENSG00000067182	ENSG00000067182	TNFRSF1A	12:6437922-6451280	OK	32.1227	33.6557	0.0672558	0.115988	0.82585	0.9998
ENSG00000125818	ENSG00000125818	PSMF1	20:1093905-1160596	OK	45.9243	48.5946	0.0815381	0.133268	0.82585	0.9998
ENSG00000113300	ENSG00000113300	CNOT6	5:179921411-180005405	OK	15.1108	15.8043	0.0647346	0.0924522	0.8259	0.9998
ENSG00000272518	ENSG00000272518	RP11-26J3.3	8:80830951-81143467	OK	1.77556	2.52314	0.506947	0.15061	0.8259	0.9998
ENSG00000042429	ENSG00000042429	MED17	11:93394804-93547861	OK	8.78964	9.91728	0.174141	0.112661	0.82595	0.9998
ENSG00000233328	ENSG00000233328	PFN1P1	1:171639656-171640079	OK	20.7464	21.9166	0.0791665	0.13178	0.82595	0.9998
ENSG00000167186	ENSG00000167186	COQ7	16:18995255-19091417	OK	11.0085	10.2872	-0.0977634	-0.136464	0.826	0.9998
ENSG00000116691	ENSG00000116691	MIIP	1:12079522-12092102	OK	13.3921	14.0226	0.0663663	0.134048	0.8262	0.9998
ENSG00000117360	ENSG00000117360	PRPF3	1:150293924-150325671	OK	35.3032	36.9092	0.0641814	0.137892	0.82625	0.9998
ENSG00000185090	ENSG00000185090	MANEAL	1:38259473-38266809	OK	14.0525	14.6758	0.0626129	0.135504	0.82625	0.9998
ENSG00000235241	ENSG00000235241	RP11-108M9.5	1:17066767-17299474	OK	3.71485	3.04302	-0.287799	-0.143409	0.82645	0.9998
ENSG00000133302	ENSG00000133302	ANKRD32	5:93488670-94620279	OK	6.26558	5.72712	-0.12964	-0.107242	0.8265	0.9998
ENSG00000179598	ENSG00000179598	PLD6	17:16945858-17140502	OK	2.67187	3.58213	0.422966	0.182378	0.8265	0.9998
ENSG00000270949	ENSG00000270949	RP11-288H12.4	6:160390130-160534539	OK	1.0073	1.34485	0.41695	0.101274	0.82655	0.9998
ENSG00000164683	ENSG00000164683	HEY1	8:80676244-80680098	OK	57.0585	54.8612	-0.0566557	-0.120246	0.8267	0.9998
ENSG00000164543	ENSG00000164543	STK17A	7:43622356-43769316	OK	8.02212	8.83234	0.138812	0.118089	0.8268	0.9998
ENSG00000187118	ENSG00000187118	CMC1	3:28283074-28390618	OK	60.3019	55.3812	-0.122808	-0.134791	0.8268	0.9998
ENSG00000165219	ENSG00000165219	GAPVD1	9:128024072-128129486	OK	17.1424	16.4646	-0.0582028	-0.0814635	0.82705	0.9998
ENSG00000256861	ENSG00000256861	RP11-512M8.5	12:122688089-122751068	OK	1.21312	0.873382	-0.474043	-0.130901	0.82705	0.9998
ENSG00000075914	ENSG00000075914	EXOSC7	3:44956748-45077563	OK	28.7529	30.7989	0.0991704	0.12831	0.82715	0.9998
ENSG00000074054	ENSG00000074054	CLASP1	2:122095351-122407163	OK	13.5265	14.297	0.0799211	0.0885378	0.8272	0.9998
ENSG00000131845	ENSG00000131845	ZNF304	19:57862215-57871266	OK	2.20619	2.32154	0.0735259	0.132623	0.8272	0.9998
ENSG00000137038	ENSG00000137038	TMEM261	9:7796489-7888380	OK	30.0073	27.9913	-0.100336	-0.128021	0.8272	0.9998
ENSG00000160284	ENSG00000160284	SPATC1L	21:47581061-47604390	OK	6.41739	6.77527	0.0782937	0.135471	0.82725	0.9998
ENSG00000241015	ENSG00000241015	TPM3P9	19:53935226-53961515	OK	5.07793	5.55463	0.129452	0.129973	0.82725	0.9998
ENSG00000186026	ENSG00000186026	ZNF284	19:44529493-44593766	OK	0.709534	0.642119	-0.144032	-0.135358	0.8275	0.9998
ENSG00000236058	ENSG00000236058	RP11-215A21.2	10:120631560-120632114	OK	2.11797	2.3217	0.132498	0.127871	0.8275	0.9998
ENSG00000260539	ENSG00000260539	RP11-252A24.7	16:74481324-74483790	OK	2.2824	2.16098	-0.078871	-0.130641	0.8276	0.9998
ENSG00000241975	ENSG00000241975	TCEB1P19	1:89003195-89301938	OK	1.47421	1.09672	-0.426751	-0.0581975	0.82775	0.9998
ENSG00000197763	ENSG00000197763	TXNRD3	3:126290621-126373998	OK	5.45521	5.74118	0.0737135	0.133374	0.8278	0.9998
ENSG00000126790	ENSG00000126790	L3HYPDH	14:59895739-60043549	OK	8.51405	9.81462	0.205086	0.138828	0.8279	0.9998
ENSG00000133639	ENSG00000133639	BTG1	12:92378755-92583436	OK	40.5638	39.0185	-0.0560346	-0.130513	0.8279	0.9998
ENSG00000226510	ENSG00000226510	UPK1A-AS1	19:36157714-36169367	OK	4.76801	4.42386	-0.108083	-0.13159	0.82795	0.9998
ENSG00000267681	ENSG00000267681	CTD-3199J23.6	17:41277626-41305688	OK	1.79004	1.41102	-0.34326	-0.162749	0.82805	0.9998
ENSG00000263013	ENSG00000263013	RP11-876N24.5	16:10958770-11036878	OK	1.54546	1.80424	0.223358	0.0922525	0.8281	0.9998
ENSG00000131149	ENSG00000131149	GSE1	16:85645014-85723679	OK	2.30697	2.13305	-0.113076	-0.0814924	0.82815	0.9998
ENSG00000170215	ENSG00000170215	FAM27B	9:67792166-67794649	OK	0.870107	0.646978	-0.427476	-0.17974	0.8282	0.9998
ENSG00000254835	ENSG00000254835	RNF185-AS1	22:31556167-31603005	OK	9.83861	6.54864	-0.587258	-0.214753	0.8282	0.9998
ENSG00000240522	ENSG00000240522	RPL7AP10	19:21324826-21373034	OK	1.76893	1.47646	-0.260739	-0.136399	0.82825	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000103642	ENSG00000103642	LACTB	15:63413998-63450220	OK	20.868	19.0057	-0.13486	-0.114878	0.8283	0.9998
ENSG00000110536	ENSG00000110536	PTPMT1	11:47487495-47606114	OK	65.5822	74.1998	0.178111	0.136429	0.82835	0.9998
ENSG00000172992	ENSG00000172992	DCAKD	17:43100707-43221548	OK	9.13437	7.90469	-0.208597	-0.0993075	0.82835	0.9998
ENSG00000248905	ENSG00000248905	FMN1	15:33057746-33486897	OK	41.3268	43.7078	0.0808128	0.0849614	0.82835	0.9998
ENSG00000254706	ENSG00000254706	RP11-565P22.6	1:162039563-162356600	OK	1.34414	2.06866	0.622016	0.198475	0.82835	0.9998
ENSG00000227725	ENSG00000227725	GCOM2	4:68566997-68995598	OK	0.650285	0.45146	-0.526473	-0.222212	0.8284	0.9998
ENSG00000116809	ENSG00000116809	ZBTB17	1:16268363-16302627	OK	10.1013	9.65929	-0.0645548	-0.101541	0.82855	0.9998
ENSG00000122778	ENSG00000122778	KIAA1549	7:138391039-138666064	OK	3.06762	3.24927	0.0829935	0.134314	0.82855	0.9998
ENSG00000126247	ENSG00000126247	CAPNS1	19:36630476-36641255	OK	151.948	158.583	0.061659	0.130076	0.82855	0.9998
ENSG00000232545	ENSG00000232545	KB-318B8.7	22:24407641-24574596	OK	0.591755	0.772408	0.384361	0.0471613	0.8286	0.9998
ENSG00000119950	ENSG00000119950	MXI1	10:111967362-112047123	OK	106.258	101.611	-0.0645252	-0.124502	0.82865	0.9998
ENSG00000231908	ENSG00000231908	IDH1-AS1	2:209100950-209130798	OK	2.49606	2.02321	-0.303005	-0.0208741	0.82865	0.9998
ENSG00000156531	ENSG00000156531	PHF6	X:133507282-133562820	OK	11.1498	11.6768	0.0666267	0.130044	0.8287	0.9998
ENSG00000185591	ENSG00000185591	SP1	12:53773959-53810230	OK	15.1214	15.7615	0.0598118	0.10782	0.8287	0.9998
ENSG00000203386	ENSG00000203386	AC009499.1	2:33931952-34522820	OK	8.08841	8.59311	0.0873232	0.135462	0.8287	0.9998
ENSG00000173171	ENSG00000173171	MTX1	1:155165378-155183615	OK	48.3573	50.6464	0.0667259	0.131336	0.8288	0.9998
ENSG00000143627	ENSG00000143627	PKLR	1:155232658-155271225	OK	1.50737	1.1699	-0.365657	-0.16107	0.8289	0.9998
ENSG00000144362	ENSG00000144362	PHOSPHO2	2:170550974-170633499	OK	3.12592	2.79355	-0.162181	-0.124774	0.82905	0.9998
ENSG00000155816	ENSG00000155816	FMN2	1:240177647-240643504	OK	12.8856	11.9895	-0.103996	-0.132404	0.82925	0.9998
ENSG00000196914	ENSG00000196914	ARHGEF12	11:120207786-120360645	OK	9.21796	8.88509	-0.0530612	-0.1167	0.82925	0.9998
ENSG00000131697	ENSG00000131697	NPHP4	1:5922870-6161253	OK	4.27317	4.61495	0.11101	0.0914496	0.82935	0.9998
ENSG00000147121	ENSG00000147121	KRBOX4	X:46306291-46356857	OK	7.78712	8.28516	0.0894396	0.135732	0.82935	0.9998
ENSG00000141526	ENSG00000141526	SLC16A3	17:80186272-80231607	OK	6.26093	5.32094	-0.234698	-0.0901979	0.82945	0.9998
ENSG00000254221	ENSG00000254221	PCDHGB1	5:140710251-140892546	OK	1.44802	1.83053	0.338179	0.166108	0.8295	0.9998
ENSG00000132825	ENSG00000132825	PPP1R3D	20:58508818-58523735	OK	7.53628	7.04437	-0.0973827	-0.126641	0.82955	0.9998
ENSG00000184613	ENSG00000184613	NELL2	12:44902057-45315631	OK	1.38653	1.2932	-0.100536	-0.0806379	0.8296	0.9998
ENSG00000261113	ENSG00000261113	RP11-141O15.1	16:22217602-22300059	OK	1.14491	0.913435	-0.325866	-0.0747486	0.82965	0.9998
ENSG00000088682	ENSG00000088682	COQ9	16:57462080-57521239	OK	19.4036	18.0259	-0.106255	-0.121226	0.82985	0.9998
ENSG00000151834	ENSG00000151834	GABRA2	4:46250443-46477247	OK	1.31573	1.24011	-0.0853927	-0.0892788	0.82985	0.9998
ENSG00000164134	ENSG00000164134	NAA15	4:140187316-140397763	OK	16.2157	17.1214	0.0784107	0.104785	0.82985	0.9998
ENSG00000168769	ENSG00000168769	TET2	4:106067031-106200973	OK	2.48845	2.3832	-0.0623502	-0.111161	0.82985	0.9998
ENSG00000092098	ENSG00000092098	RNF31	14:24612573-24636611	OK	23.5263	25.037	0.0897834	0.0884141	0.82995	0.9998
ENSG00000141424	ENSG00000141424	SLC39A6	18:33688494-33709348	OK	142.769	148.048	0.0523894	0.116781	0.83	0.9998
ENSG00000169282	ENSG00000169282	KCNAB1	3:155755489-156256545	OK	1.68139	1.57149	-0.097526	-0.0903587	0.83	0.9998
ENSG00000156860	ENSG00000156860	FBRS	16:30669751-30682135	OK	11.7643	11.2405	-0.0657086	-0.0990444	0.8301	0.9998
ENSG00000172113	ENSG00000172113	NME6	3:48282589-48343175	OK	26.1177	24.4968	-0.0924339	-0.133018	0.8302	0.9998
ENSG00000183011	ENSG00000183011	LSMD1	17:7760002-7816078	OK	105.296	91.7358	-0.198896	-0.160832	0.83025	0.9998
ENSG00000124459	ENSG00000124459	ZNF45	19:44406152-44439430	OK	4.6299	4.40978	-0.0702728	-0.104715	0.8303	0.9998
ENSG00000181027	ENSG00000181027	FKRP	19:47222763-47291851	OK	6.83227	6.00762	-0.185571	-0.0675954	0.8303	0.9998
ENSG00000137198	ENSG00000137198	GMPR	6:16238810-16295780	OK	66.6795	64.2413	-0.0537414	-0.126815	0.83035	0.9998
ENSG00000065308	ENSG00000065308	TRAM2	6:52285105-52441713	OK	9.12779	9.51775	0.0603556	0.129493	0.8305	0.9998
ENSG00000181830	ENSG00000181830	SLC35C1	11:45825622-45834566	OK	4.47075	4.7181	0.077689	0.125327	0.8305	0.9998
ENSG00000262766	ENSG00000262766	RP11-196G11.4	16:31127074-31142714	OK	0.66737	0.956968	0.519983	0.135399	0.8305	0.9998
ENSG00000272782	ENSG00000272782	RP4-607J23.2	7:97881690-98030380	OK	2.09277	2.58882	0.306878	0.0468433	0.83055	0.9998
ENSG00000086062	ENSG00000086062	B4GALT1	9:33104079-33179981	OK	13.1007	13.6221	0.0562963	0.131621	0.8306	0.9998
ENSG00000122691	ENSG00000122691	TWIST1	7:19060613-19157295	OK	27.4451	29.0391	0.0814457	0.132276	0.8306	0.9998
ENSG00000273388	ENSG00000273388	RP11-401O9.4	17:10195136-10276447	OK	0.814366	0.710474	-0.196895	-0.120952	0.8306	0.9998
ENSG00000136840	ENSG00000136840	ST6GALNAC4	9:130670164-130679317	OK	3.61626	3.86394	0.095575	0.113358	0.83065	0.9998
ENSG00000163050	ENSG00000163050	ADCK3	1:227085236-227175246	OK	8.49563	8.07988	-0.0723877	-0.0980349	0.83065	0.9998
ENSG00000197808	ENSG00000197808	ZNF461	19:37128093-37157755	OK	2.75525	3.02642	0.135425	0.111498	0.8307	0.9998
ENSG00000213676	ENSG00000213676	ATF6B	6:32006041-32096030	OK	51.3955	53.3917	0.0549736	0.108069	0.8307	0.9998
ENSG00000198937	ENSG00000198937	CCDC167	6:37450695-37467698	OK	59.9755	57.4878	-0.0611175	-0.131545	0.83075	0.9998
ENSG00000124224	ENSG00000124224	PPP4R1L	20:56806187-56884495	OK	7.23286	6.81579	-0.0856842	-0.123698	0.83105	0.9998
ENSG00000125901	ENSG00000125901	MRPS26	20:3026590-3028900	OK	18.4098	19.2107	0.0614353	0.125858	0.8311	0.9998
ENSG00000130202	ENSG00000130202	PVRL2	19:45349431-45406946	OK	14.8284	16.0461	0.113859	0.114994	0.8311	0.9998
ENSG00000162396	ENSG00000162396	PARS2	1:55222570-55230187	OK	2.40464	2.27184	-0.0819625	-0.132934	0.8311	0.9998
ENSG00000257303	ENSG00000257303	RP11-977G19.11	12:56665482-56727837	OK	4.70988	6.02339	0.354887	0.0482315	0.83115	0.9998
ENSG00000140025	ENSG00000140025	EFCAB11	14:89591214-90421121	OK	14.2618	12.6105	-0.17753	-0.137309	0.8312	0.9998
ENSG00000179611	ENSG00000179611	DGKZP1	13:44482849-44604597	OK	8.68491	9.05555	0.0602912	0.12808	0.83125	0.9998
ENSG00000103066	ENSG00000103066	PLA2G15	16:68279206-68294961	OK	10.8511	11.3293	0.0622087	0.108828	0.83135	0.9998
ENSG00000169288	ENSG00000169288	MRPL1	4:78783673-78873944	OK	10.2252	9.70118	-0.0758969	-0.124898	0.83135	0.9998
ENSG00000076201	ENSG00000076201	PTPN23	3:47422500-47454931	OK	17.6613	17.037	-0.0519148	-0.10531	0.8314	0.9998
ENSG00000139644	ENSG00000139644	TMBIM6	12:49962000-50158717	OK	339.882	354.275	0.0598344	0.0973665	0.8314	0.9998
ENSG00000182173	ENSG00000182173	TSEN54	17:73512140-73520820	OK	19.1638	18.3065	-0.0660261	-0.110023	0.83155	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000072210	ENSG00000072210	ALDH3A2	17:19551448-19580911	OK	17.6738	18.4683	0.0634364	0.108936	0.8316	0.9998
ENSG00000088986	ENSG00000088986	DYNLL1	12:120907652-120936296	OK	320.403	332.102	0.0517398	0.126276	0.83165	0.9998
ENSG00000224950	ENSG00000224950	RP5-1086K13.1	1:117035644-117041834	OK	1.78907	1.68924	-0.082837	-0.127186	0.83185	0.9998
ENSG00000233237	ENSG00000233237	LINC00472	6:71931159-72130472	OK	0.594846	0.696886	0.228407	0.077915	0.83185	0.9998
ENSG00000010818	ENSG00000010818	HIVEP2	6:143069579-143266338	OK	2.55107	2.40534	-0.0848636	-0.0581671	0.8319	0.9998
ENSG00000153395	ENSG00000153395	LPCAT1	5:1456594-1524092	OK	18.1031	17.3938	-0.0576578	-0.101468	0.8319	0.9998
ENSG00000167528	ENSG00000167528	ZNF641	12:48733790-48836730	OK	3.41391	3.22026	-0.0842472	-0.0929882	0.83195	0.9998
ENSG00000168522	ENSG00000168522	FNTA	8:42704779-42940931	OK	47.2994	49.8446	0.0756153	0.127418	0.83195	0.9998
ENSG00000233984	ENSG00000233984	RPSAP14	X:73164158-73513409	OK	9.76851	11.9045	0.285298	0.156391	0.83195	0.9998
ENSG00000101347	ENSG00000101347	SAMHD1	20:35504523-35580246	OK	4.50615	4.7085	0.0633709	0.116027	0.832	0.9998
ENSG00000233559	ENSG00000233559	AC016831.7	7:130538478-130613408	OK	0.718574	0.873563	0.281774	0.106417	0.832	0.9998
ENSG00000050405	ENSG00000050405	LIMA1	12:50569570-50677329	OK	43.4584	44.9951	0.0501318	0.108501	0.83205	0.9998
ENSG00000163486	ENSG00000163486	SRGAP2	1:206516199-206637783	OK	31.8601	33.6591	0.0792452	0.101033	0.8321	0.9998
ENSG00000133627	ENSG00000133627	ACTR3B	7:152456833-152552463	OK	8.78323	9.37043	0.0933626	0.098663	0.8322	0.9998
ENSG00000164244	ENSG00000164244	PRRC1	5:126853300-126890781	OK	10.7641	10.2206	-0.0747505	-0.127943	0.8322	0.9998
ENSG00000119929	ENSG00000119929	CUTC	10:101419262-101515891	OK	15.331	16.7221	0.125308	0.13546	0.83225	0.9998
ENSG00000068796	ENSG00000068796	KIF2A	5:61601988-61924409	OK	20.225	18.8709	-0.0999779	-0.106448	0.8323	0.9998
ENSG00000182500	ENSG00000182500	ORAI1	12:122064454-122080583	OK	11.2272	11.7322	0.0634776	0.130369	0.8323	0.9998
ENSG00000011052	ENSG00000011052	NME2	17:49230896-49249108	OK	27.0972	34.0957	0.331446	0.095412	0.8325	0.9998
ENSG00000111412	ENSG00000111412	C12orf49	12:117153592-117175875	OK	40.7253	38.6877	-0.074049	-0.124357	0.8325	0.9998
ENSG00000085377	ENSG00000085377	PREP	6:105725439-105850959	OK	15.1386	15.775	0.0594105	0.125782	0.83255	0.9998
ENSG00000162650	ENSG00000162650	ATXN7L2	1:110026100-110035426	OK	1.09958	1.02032	-0.107932	-0.118735	0.83255	0.9998
ENSG00000186787	ENSG00000186787	SPIN2B	X:57144983-57147980	OK	2.09033	2.26103	0.11325	0.128213	0.83255	0.9998
ENSG00000170448	ENSG00000170448	NFXL1	4:47849256-48042188	OK	3.55717	3.38454	-0.0717713	-0.119369	0.8326	0.9998
ENSG00000198824	ENSG00000198824	CHAMP1	13:115079987-115092796	OK	17.614	19.1974	0.124189	0.117911	0.8326	0.9998
ENSG00000269867	ENSG00000269867	CTD-2583A14.8	19:58281022-58427978	OK	1.53749	2.16074	0.490948	0.142499	0.8326	0.9998
ENSG00000171570	ENSG00000171570	RAB4B-EGLN2	19:41277552-41406413	OK	0.929129	0.710228	-0.387597	-0.0401808	0.83265	0.9998
ENSG00000100344	ENSG00000100344	PNPLA3	22:44319618-44568829	OK	5.68803	6.78593	0.254619	0.105733	0.8327	0.9998
ENSG00000003400	ENSG00000003400	CASP10	2:202047603-202094129	OK	1.65891	1.77366	0.0964967	0.103027	0.83275	0.9998
ENSG00000136868	ENSG00000136868	SLC31A1	9:115983807-116055185	OK	30.3017	28.359	-0.0955926	-0.120914	0.83275	0.9998
ENSG00000182809	ENSG00000182809	CRIP2	14:105939298-105946499	OK	20.5807	21.5414	0.0658168	0.12802	0.8328	0.9998
ENSG00000124802	ENSG00000124802	EEF1E1	6:7727029-8102811	OK	46.0027	51.6992	0.168424	0.102215	0.8329	0.9998
ENSG00000182909	ENSG00000182909	LENG9	19:54955990-54974894	OK	1.15965	1.64769	0.506757	0.186082	0.833	0.9998
ENSG00000189306	ENSG00000189306	RRP7A	22:42896584-42915808	OK	37.4822	35.4444	-0.080646	-0.123357	0.83305	0.9998
ENSG00000214413	ENSG00000214413	BBIP1	10:112629500-112679032	OK	20.5253	18.4771	-0.151663	-0.137998	0.8331	0.9998
ENSG00000031003	ENSG00000031003	FAM13B	5:137150021-137387650	OK	9.05428	8.67264	-0.0621287	-0.0891511	0.83315	0.9998
ENSG00000260751	ENSG00000260751	CTD-2196E14.6	16:23533334-23585710	OK	0.799091	0.618615	-0.369316	-0.0591943	0.83315	0.9998
ENSG00000177946	ENSG00000177946	CENPBD1	16:90036198-90038952	OK	2.21998	2.10606	-0.0759982	-0.11864	0.83335	0.9998
ENSG00000237441	ENSG00000237441	RGL2	6:33244916-33267101	OK	39.9274	37.1632	-0.103503	-0.113702	0.83335	0.9998
ENSG00000122497	ENSG00000122497	NBPF14	1:148003641-148025863	OK	5.316	5.09361	-0.0616532	-0.123528	0.8334	0.9998
ENSG00000146457	ENSG00000146457	WTAP	6:160090088-160210781	OK	16.0001	13.8392	-0.209321	-0.127606	0.8334	0.9998
ENSG00000169016	ENSG00000169016	E2F6	2:11584500-11606297	OK	16.0995	16.9677	0.075781	0.125591	0.83345	0.9998
ENSG00000165097	ENSG00000165097	KDM1B	6:18155559-18224084	OK	25.1715	26.1781	0.0565735	0.121403	0.8336	0.9998
ENSG00000112343	ENSG00000112343	TRIM38	6:25963029-26002003	OK	9.3936	9.00595	-0.0607995	-0.126853	0.83365	0.9998
ENSG00000163684	ENSG00000163684	RPP14	3:58291973-58310422	OK	17.9378	17.0577	-0.0725794	-0.113214	0.8337	0.9998
ENSG00000140993	ENSG00000140993	TIGD7	16:3313742-3368852	OK	0.879301	0.987822	0.167895	0.0614874	0.8338	0.9998
ENSG00000180992	ENSG00000180992	MRPL14	6:44081193-44123256	OK	78.2236	73.4976	-0.0899071	-0.123785	0.83385	0.9998
ENSG00000187608	ENSG00000187608	ISG15	1:948802-949920	OK	2.5989	2.40889	-0.10953	-0.130687	0.83385	0.9998
ENSG00000204569	ENSG00000204569	PPP1R10	6:30568176-30594172	OK	8.66096	7.88988	-0.134524	-0.0999742	0.83385	0.9998
ENSG00000087111	ENSG00000087111	PIGS	17:26782769-26972472	OK	35.5614	41.0177	0.205933	0.100911	0.83395	0.9998
ENSG00000105771	ENSG00000105771	SMG9	19:44235300-44259142	OK	13.3986	14.3474	0.0987086	0.128388	0.834	0.9998
ENSG00000132879	ENSG00000132879	FBXO44	1:11708423-11723384	OK	23.659	25.1337	0.0872334	0.124645	0.8341	0.9998
ENSG00000124151	ENSG00000124151	NCOA3	20:46130600-46415360	OK	8.16779	8.51889	0.0607186	0.108807	0.83415	0.9998
ENSG00000037637	ENSG00000037637	FBXO42	1:16573333-16678949	OK	8.00386	8.55064	0.0953369	0.122643	0.83425	0.9998
ENSG00000103888	ENSG00000103888	KIAA1199	15:81071683-81282219	OK	3.79543	4.19475	0.14432	0.0712514	0.8343	0.9998
ENSG00000134590	ENSG00000134590	FAM127A	X:134166332-134167576	OK	34.2978	32.9964	-0.0558099	-0.125551	0.83435	0.9998
ENSG00000160753	ENSG00000160753	RUSC1	1:155278538-155300905	OK	36.0769	39.8044	0.141852	0.118697	0.83435	0.9998
ENSG00000090273	ENSG00000090273	NUDC	1:27216978-27273353	OK	45.7819	47.5688	0.0552397	0.124462	0.83445	0.9998
ENSG00000100764	ENSG00000100764	PSMC1	14:90722838-90738968	OK	23.3315	24.2315	0.0546048	0.121399	0.83445	0.9998
ENSG00000272298	ENSG00000272298	RP11-386M24.8	15:93146139-93353114	OK	1.58777	1.18961	-0.416511	-0.11005	0.83445	0.9998
ENSG00000149634	ENSG00000149634	SPATA25	20:44515127-44516274	OK	0.786106	0.865065	0.138085	0.126779	0.83455	0.9998
ENSG00000248873	ENSG00000248873	SERBP1P6	5:42423878-42721979	OK	2.26793	3.27585	0.530494	0.210965	0.83465	0.9998
ENSG00000058668	ENSG00000058668	ATP2B4	1:203595688-203713209	OK	20.4279	19.755	-0.0483209	-0.0918984	0.83475	0.9998
ENSG00000085365	ENSG00000085365	SCAMP1	5:77656338-77776562	OK	18.3701	19.2484	0.0673747	0.118355	0.83485	0.9998
ENSG00000117143	ENSG00000117143	UAP1	1:162531322-162569627	OK	32.2176	33.4119	0.0525121	0.122567	0.83485	0.9998
ENSG00000143368	ENSG00000143368	SF3B4	1:149895208-149900236	OK	65.8166	63.233	-0.0577719	-0.123479	0.83485	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000130699	ENSG00000130699	TAF4	20:60528524-60640866	OK	7.52652	7.10705	-0.0827319	-0.0727093	0.8349	0.9998
ENSG00000111906	ENSG00000111906	HDDC2	6:125440194-125623282	OK	101.989	97.104	-0.0708179	-0.123724	0.835	0.9998
ENSG00000137628	ENSG00000137628	DDX60	4:169137443-169239958	OK	0.911941	0.858153	-0.0877052	-0.0796287	0.8351	0.9998
ENSG00000185608	ENSG00000185608	MRPL40	22:19318220-19466738	OK	41.811	45.473	0.12113	0.124904	0.8351	0.9998
ENSG00000059573	ENSG00000059573	ALDH18A1	10:97365695-97416463	OK	34.261	33.0481	-0.0520019	-0.116577	0.8352	0.9998
ENSG00000105879	ENSG00000105879	CBLL1	7:107383261-107402112	OK	21.4981	20.526	-0.0667604	-0.110063	0.8353	0.9998
ENSG00000083520	ENSG00000083520	DIS3	13:73302060-73590591	OK	15.0473	14.3246	-0.0710073	-0.114613	0.83535	0.9998
ENSG00000130348	ENSG00000130348	QRSL1	6:107077452-107116292	OK	5.35854	5.59988	0.0635566	0.115353	0.8354	0.9998
ENSG00000146842	ENSG00000146842	TMEM209	7:129804554-129847610	OK	13.351	13.8976	0.0578977	0.119244	0.8354	0.9998
ENSG00000119487	ENSG00000119487	MAPKAP1	9:128199671-128469513	OK	84.182	87.489	0.05559	0.118094	0.83545	0.9998
ENSG00000135164	ENSG00000135164	DMTF1	7:86780738-86849903	OK	28.6506	27.4347	-0.062565	-0.0942122	0.83565	0.9998
ENSG00000260238	ENSG00000260238	PMF1-BGLAP	1:156182772-156213123	OK	6.13625	7.22207	0.235054	0.126017	0.83565	0.9998
ENSG00000272016	ENSG00000272016	RP11-215G15.5	5:10652322-10657928	OK	2.05272	1.94371	-0.0787191	-0.124105	0.83565	0.9998
ENSG00000114026	ENSG00000114026	OGG1	3:9791627-9896822	OK	14.7236	13.0642	-0.172512	-0.116031	0.8357	0.9998
ENSG00000269427	ENSG00000269427	CTC-429P9.1	19:16589867-16771253	OK	3.06637	3.83626	0.32317	0.0558075	0.83575	0.9998
ENSG00000102100	ENSG00000102100	SLC35A2	X:48760458-48769235	OK	11.8828	12.4514	0.0674339	0.119103	0.8358	0.9998
ENSG00000171503	ENSG00000171503	ETFDH	4:159587830-159644548	OK	13.3322	12.522	-0.0904589	-0.108336	0.8358	0.9998
ENSG00000214922	ENSG00000214922	HLA-F-AS1	6:29690551-29716826	OK	12.8962	13.8913	0.107235	0.118019	0.8358	0.9998
ENSG00000134569	ENSG00000134569	LRP4	11:46867962-46940193	OK	7.20148	7.53264	0.0648605	0.0913517	0.8359	0.9998
ENSG00000102221	ENSG00000102221	JADE3	X:46771710-46920641	OK	5.02934	5.25124	0.0622866	0.103727	0.83595	0.9998
ENSG00000104731	ENSG00000104731	KLHDC4	16:87634131-87799598	OK	5.86349	5.49695	-0.0931279	-0.0931448	0.83595	0.9998
ENSG00000140471	ENSG00000140471	LINS	15:101093733-101191910	OK	13.8201	14.6007	0.0792664	0.105133	0.83595	0.9998
ENSG00000145216	ENSG00000145216	FIP1L1	4:54243809-55164414	OK	43.7554	45.5039	0.0565309	0.123281	0.836	0.9998
ENSG00000150456	ENSG00000150456	N6AMT2	13:21302869-21348097	OK	4.34994	4.10231	-0.0845592	-0.122093	0.8361	0.9998
ENSG00000105649	ENSG00000105649	RAB3A	19:18303991-18314884	OK	17.7662	19.4148	0.128021	0.138322	0.83615	0.9998
ENSG00000146701	ENSG00000146701	MDH2	7:75677368-75696826	OK	178.221	186.424	0.064922	0.120424	0.83615	0.9998
ENSG00000163697	ENSG00000163697	APBB2	4:40812043-41218731	OK	7.84735	7.49736	-0.065824	-0.0807397	0.83615	0.9998
ENSG00000162384	ENSG00000162384	C1orf123	1:53662100-53686289	OK	22.8188	21.5959	-0.0794648	-0.125935	0.8363	0.9998
ENSG00000182272	ENSG00000182272	B4GALNT4	11:369795-382116	OK	0.624921	0.704791	0.173522	0.114606	0.8363	0.9998
ENSG00000185340	ENSG00000185340	GAS2L1	22:29702571-29708774	OK	12.706	13.215	0.0566688	0.115576	0.8363	0.9998
ENSG00000256338	ENSG00000256338	RPL41P2	15:28356185-28567298	OK	2.25919	1.71936	-0.393935	-0.0701847	0.83635	0.9998
ENSG00000103351	ENSG00000103351	CLUAP1	16:3415098-3627401	OK	7.61946	8.33532	0.12955	0.107746	0.8364	0.9998
ENSG00000115419	ENSG00000115419	GLS	2:191745522-191885686	OK	60.8585	57.6119	-0.079092	-0.0806062	0.83645	0.9998
ENSG00000169660	ENSG00000169660	HEXDC	17:80347098-80408705	OK	5.45293	4.84929	-0.169258	-0.0779047	0.83645	0.9998
ENSG00000173141	ENSG00000173141	MRP63	13:21750783-21753223	OK	16.3268	15.7012	-0.056361	-0.126338	0.83645	0.9998
ENSG00000254901	ENSG00000254901	MEF2BNB	19:19256375-19314233	OK	30.3012	27.9246	-0.117837	-0.133105	0.83645	0.9998
ENSG00000178234	ENSG00000178234	GALNT11	7:151722758-151819425	OK	58.7252	56.5531	-0.0543749	-0.111112	0.8365	0.9998
ENSG00000104980	ENSG00000104980	TIMM44	19:7989371-8008805	OK	41.4545	39.6575	-0.0639336	-0.124603	0.8367	0.9998
ENSG00000136518	ENSG00000136518	ACTL6A	3:179280667-179322442	OK	51.5618	54.0956	0.0692079	0.112549	0.8368	0.9998
ENSG00000204282	ENSG00000204282	TNRC6C-AS1	17:76000248-76139049	OK	5.07394	6.00346	0.242688	0.136551	0.8368	0.9998
ENSG00000107521	ENSG00000107521	HPS1	10:100175954-100206684	OK	40.3102	42.2242	0.0669266	0.127462	0.837	0.9998
ENSG00000242622	ENSG00000242622	RP11-18H7.1	3:119813741-119855630	OK	1.22159	1.11651	-0.129771	-0.123619	0.837	0.9998
ENSG00000072609	ENSG00000072609	CHFR	12:133345494-133532892	OK	15.6912	16.832	0.101259	0.0948411	0.8373	0.9998
ENSG00000040341	ENSG00000040341	STAU2	8:74332238-74791145	OK	19.4171	18.2742	-0.0875207	-0.101208	0.8375	0.9998
ENSG00000125485	ENSG00000125485	DDX31	9:135468383-135570342	OK	10.3037	11.0698	0.10346	0.127684	0.8375	0.9998
ENSG00000112511	ENSG00000112511	PHF1	6:33378175-33386094	OK	45.5965	42.5923	-0.0983274	-0.110763	0.8376	0.9998
ENSG00000128891	ENSG00000128891	C15orf57	15:40780239-40857256	OK	8.58918	7.90381	-0.119972	-0.120764	0.8376	0.9998
ENSG00000162032	ENSG00000162032	SPSB3	16:1823207-1844972	OK	13.5006	14.6694	0.119794	0.133746	0.83765	0.9998
ENSG00000198720	ENSG00000198720	ANKRD13B	17:27887564-28513493	OK	3.21236	3.7231	0.212872	0.0597044	0.83765	0.9998
ENSG00000065057	ENSG00000065057	NTHL1	16:2089815-2185899	OK	18.7316	20.7768	0.149495	0.114159	0.8377	0.9998
ENSG00000128059	ENSG00000128059	PPAT	4:57259527-57301781	OK	11.3523	10.9081	-0.0575933	-0.104978	0.8377	0.9998
ENSG00000224437	ENSG00000224437	PIGUP1	9:73143978-74061820	OK	1.24699	1.40665	0.173811	0.119293	0.8377	0.9998
ENSG00000019995	ENSG00000019995	ZRANB1	10:126605711-126849739	OK	8.67327	8.20079	-0.0808131	-0.120963	0.83775	0.9998
ENSG00000126603	ENSG00000126603	GLIS2	16:4364761-4475706	OK	1.48339	1.27911	-0.21376	-0.129571	0.83775	0.9998
ENSG00000267855	ENSG00000267855	NDUFA7	19:8367010-8408146	OK	89.7726	81.5453	-0.138674	-0.124928	0.8378	0.9998
ENSG00000117010	ENSG00000117010	ZNF684	1:40997232-41013841	OK	2.91736	2.72212	-0.0999325	-0.123658	0.83785	0.9998
ENSG00000092758	ENSG00000092758	COL9A3	20:61447595-61493115	OK	79.9274	84.0659	0.0728304	0.112937	0.838	0.9998
ENSG00000146856	ENSG00000146856	AGBL3	7:134671258-134855547	OK	3.69265	3.27444	-0.173407	-0.0522627	0.83805	0.9998
ENSG00000242689	ENSG00000242689	CNTF	11:58346583-58393198	OK	0.835416	1.09109	0.385199	0.076454	0.83815	0.9998
ENSG00000267531	ENSG00000267531	AC020922.1	19:55851220-55859488	OK	0.840228	0.646388	-0.378381	-0.18596	0.83815	0.9998
ENSG00000120913	ENSG00000120913	PDLIM2	8:22435791-22461663	OK	22.7393	24.6487	0.116319	0.118541	0.83825	0.9998
ENSG00000187156	ENSG00000187156	LINC00221	14:106938444-106977000	OK	5.94478	5.66845	-0.0686678	-0.123408	0.83825	0.9998
ENSG00000087460	ENSG00000087460	GNAS	20:57393973-57486247	OK	1085.78	1042.05	-0.0593046	-0.121868	0.83835	0.9998
ENSG00000215190	ENSG00000215190	LINC00680	6:58272351-58287779	OK	4.89448	4.63906	-0.0773229	-0.130214	0.83835	0.9998
ENSG00000117395	ENSG00000117395	EBNA1BP2	1:43629845-43739673	OK	56.4563	58.5687	0.0529955	0.125043	0.83845	0.9998
ENSG00000241889	ENSG00000241889	RP11-435F17.3	3:113547028-113666417	OK	0.99455	0.778377	-0.353575	-0.140885	0.83855	0.9998
ENSG00000135930	ENSG00000135930	EIF4E2	2:233412778-233547491	OK	47.0983	44.7604	-0.0734523	-0.102656	0.8386	0.9998
ENSG00000155792	ENSG00000155792	DEPTOR	8:120879658-121063152	OK	2.98316	3.15035	0.0786695	0.112507	0.8386	0.9998
ENSG00000186395	ENSG00000186395	KRT10	17:38974368-38992522	OK	10.826	10.2805	-0.0745872	-0.124962	0.8386	0.9998
ENSG00000168852	ENSG00000168852	TPTE2P5	13:41396431-41495910	OK	0.954828	0.696575	-0.454963	-0.146696	0.8387	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000055130	ENSG00000055130	CUL1	7:148393558-148498128	OK	36.0881	37.3885	0.0510697	0.126081	0.8388	0.9998
ENSG00000171471	ENSG00000171471	MAP1LC3B2	12:116997185-117014425	OK	15.7358	16.4746	0.06619	0.121185	0.8388	0.9998
ENSG00000254531	ENSG00000254531	AP001816.1	4:101944565-102270040	OK	3.82847	3.04576	-0.329965	-0.148631	0.8388	0.9998
ENSG00000267809	ENSG00000267809	NDUFV2P1	19:53727225-53728132	OK	18.5816	19.3915	0.061553	0.121601	0.8388	0.9998
ENSG00000170653	ENSG00000170653	ATF7	12:53900471-54020199	OK	14.9931	16.0099	0.0946698	0.11558	0.83895	0.9998
ENSG00000125743	ENSG00000125743	SNRPD2	19:46190711-46207247	OK	375.033	359.855	-0.0595995	-0.121945	0.839	0.9998
ENSG00000134072	ENSG00000134072	CAMK1	3:9791627-9896822	OK	5.6301	6.96209	0.306359	0.115	0.83905	0.9998
ENSG00000197860	ENSG00000197860	SGTB	5:64885506-65167553	OK	9.80148	8.99945	-0.123162	-0.115565	0.83905	0.9998
ENSG00000148291	ENSG00000148291	SURF2	9:136218609-136228045	OK	32.1709	34.4425	0.098432	0.118923	0.8391	0.9998
ENSG00000213533	ENSG00000213533	TMEM110	3:52846990-52931612	OK	10.2556	10.7604	0.069311	0.0827444	0.8391	0.9998
ENSG00000005955	ENSG00000005955	GGNBP2	17:34900736-34946278	OK	26.4701	27.433	0.0515487	0.108441	0.8393	0.9998
ENSG00000092847	ENSG00000092847	AGO1	1:36335408-36395211	OK	7.36258	7.68834	0.0624624	0.124502	0.8394	0.9998
ENSG00000109445	ENSG00000109445	ZNF330	4:142142040-142155851	OK	43.8082	45.452	0.053142	0.11415	0.83945	0.9998
ENSG00000136720	ENSG00000136720	HS6ST1	2:128994289-129076151	OK	3.51609	3.37182	-0.0604461	-0.11095	0.83945	0.9998
ENSG00000139631	ENSG00000139631	CSAD	12:53551446-53584596	OK	5.3248	5.7829	0.119065	0.078755	0.83945	0.9998
ENSG00000163933	ENSG00000163933	RFT1	3:52937587-53164478	OK	14.0534	12.9363	-0.119498	-0.126001	0.83945	0.9998
ENSG00000111530	ENSG00000111530	CAND1	12:67663060-67713731	OK	59.1922	62.6391	0.0816562	0.108549	0.8395	0.9998
ENSG00000100101	ENSG00000100101	NOL12	22:38077679-38172563	OK	15.2296	13.6667	-0.156215	-0.12429	0.83955	0.9998
ENSG00000139514	ENSG00000139514	SLC7A1	13:30083546-30169825	OK	31.5128	30.4443	-0.049764	-0.118482	0.8396	0.9998
ENSG00000147454	ENSG00000147454	SLC25A37	8:23386317-23432976	OK	18.6187	17.8783	-0.0585399	-0.100819	0.83975	0.9998
ENSG00000240065	ENSG00000240065	PSMB9	6:32808493-32827362	OK	3.38117	2.64816	-0.352534	-0.141934	0.8398	0.9998
ENSG00000261857	ENSG00000261857	MIA	19:41277552-41406413	OK	151.461	162.928	0.10529	0.129423	0.8398	0.9998
ENSG00000085721	ENSG00000085721	RRN3	16:15068447-15248421	OK	13.827	12.6223	-0.131512	-0.114351	0.83985	0.9998
ENSG00000264707	ENSG00000264707	RP11-760N9.1	18:5954704-6415236	OK	1.33709	1.12358	-0.250993	-0.132129	0.8399	0.9998
ENSG00000272913	ENSG00000272913	RP11-440D17.3	2:96190856-96198153	OK	0.770496	0.695328	-0.148093	-0.119548	0.8399	0.9998
ENSG00000119703	ENSG00000119703	ZC2HC1C	14:75519923-75545126	OK	2.34728	2.11769	-0.1485	-0.111071	0.83995	0.9998
ENSG00000107611	ENSG00000107611	CUBN	10:16865962-17171830	OK	2.37671	2.28746	-0.0552167	-0.10831	0.84005	0.9998
ENSG00000166266	ENSG00000166266	CUL5	11:107879458-108018503	OK	5.68893	5.271	-0.110081	-0.110465	0.84015	0.9998
ENSG00000198477	ENSG00000198477	ZNF280B	22:22838766-22863505	OK	3.07631	2.94826	-0.0613356	-0.123322	0.84015	0.9998
ENSG00000141699	ENSG00000141699	FAM134C	17:40731530-40767252	OK	21.0156	19.9002	-0.0786802	-0.0989462	0.8402	0.9998
ENSG00000143543	ENSG00000143543	JTB	1:153931574-153950164	OK	150.968	142.068	-0.0876691	-0.111074	0.84035	0.9998
ENSG00000226562	ENSG00000226562	CYP4F26P	9:33580692-33605289	OK	0.775384	0.858086	0.14621	0.119475	0.84035	0.9998
ENSG00000011258	ENSG00000011258	MBTD1	17:49254785-49337524	OK	4.80171	4.60391	-0.0606863	-0.114452	0.84055	0.9998
ENSG00000197008	ENSG00000197008	ZNF138	7:64254765-64294054	OK	4.92574	5.25402	0.093081	0.125365	0.8406	0.9998
ENSG00000117597	ENSG00000117597	DIEXF	1:210001351-210030910	OK	4.78245	4.61088	-0.0527088	-0.116467	0.84065	0.9998
ENSG00000106305	ENSG00000106305	AIMP2	7:6048875-6098861	OK	27.9461	30.9866	0.148996	0.121732	0.8407	0.9998
ENSG00000056277	ENSG00000056277	ZNF280C	X:129336684-129402873	OK	2.07871	2.17945	0.0682764	0.118465	0.8408	0.9998
ENSG00000103037	ENSG00000103037	SETD6	16:58549382-58663790	OK	8.16717	8.95921	0.133534	0.0784513	0.8408	0.9998
ENSG00000247095	ENSG00000247095	MIR210HG	11:565659-568457	OK	9.26756	8.64488	-0.100343	-0.122096	0.84085	0.9998
ENSG00000119725	ENSG00000119725	ZNF410	14:74318546-74551196	OK	28.1537	26.7372	-0.0744798	-0.108393	0.841	0.9998
ENSG00000245571	ENSG00000245571	AP001258.4	11:58897605-58922512	OK	1.4755	1.19595	-0.303049	-0.102554	0.84105	0.9998
ENSG00000179163	ENSG00000179163	FUCA1	1:24171566-24194784	OK	21.7058	22.5312	0.0538468	0.121062	0.8411	0.9998
ENSG00000197217	ENSG00000197217	ENTPD4	8:23154701-23315208	OK	38.828	40.7036	0.0680588	0.0897591	0.8412	0.9998
ENSG00000230850	ENSG00000230850	RP11-782C8.1	1:143118703-143240439	OK	2.98905	3.48137	0.219971	0.145242	0.8412	0.9998
ENSG00000172845	ENSG00000172845	SP3	2:174771186-174830430	OK	18.4934	19.1674	0.0516425	0.106525	0.8413	0.9998
ENSG00000009844	ENSG00000009844	VTA1	6:142468366-142545826	OK	24.8741	25.9729	0.0623656	0.116481	0.8415	0.9998
ENSG00000146205	ENSG00000146205	ANO7	2:242127923-242164792	OK	1.09106	1.1576	0.0854043	0.0927453	0.84155	0.9998
ENSG00000223749	ENSG00000223749	MIR503HG	X:133677366-133680741	OK	1.03037	1.13923	0.1449	0.0835917	0.8416	0.9998
ENSG00000133250	ENSG00000133250	ZNF414	19:8575461-8579048	OK	4.73416	5.07579	0.100523	0.110291	0.84165	0.9998
ENSG00000188010	ENSG00000188010	MORN2	2:39103102-39202590	OK	52.1984	54.1996	0.0542777	0.119752	0.8417	0.9998
ENSG00000272742	ENSG00000272742	CTB-43P18.1	5:138677275-138720242	OK	1.51994	1.17488	-0.37149	-0.0684199	0.8417	0.9998
ENSG00000262712	ENSG00000262712	RP11-295D4.1	16:4364761-4475706	OK	0.556343	0.812729	0.5468	0.17441	0.84175	0.9998
ENSG00000119599	ENSG00000119599	DCAF4	14:73393039-73426411	OK	6.59759	6.95428	0.0759619	0.105446	0.8418	0.9998
ENSG00000129116	ENSG00000129116	PALLD	4:169277885-169931426	OK	20.2419	19.3775	-0.0629675	-0.101465	0.84195	0.9998
ENSG00000151883	ENSG00000151883	PARP8	5:49961732-50142356	OK	13.9452	13.3588	-0.0619813	-0.0868209	0.84195	0.9998
ENSG00000175600	ENSG00000175600	SUGCT	7:40174574-40900362	OK	10.3342	9.61085	-0.104688	-0.125695	0.842	0.9998
ENSG00000198551	ENSG00000198551	ZNF627	19:11670188-11729950	OK	3.84065	3.47353	-0.144949	-0.0974535	0.84205	0.9998
ENSG00000249590	ENSG00000249590	RP4-539M6.19	22:30727976-30825045	OK	5.42514	4.18359	-0.374919	-0.153037	0.84205	0.9998
ENSG00000254501	ENSG00000254501	AP003068.9	11:64851694-64883856	OK	0.83138	1.12626	0.437961	0.0553966	0.84205	0.9998
ENSG00000121022	ENSG00000121022	COPS5	8:67876333-68255912	OK	45.2887	42.7467	-0.0833352	-0.118373	0.8421	0.9998
ENSG00000225393	ENSG00000225393	RP11-218L14.4	X:154695630-154899605	OK	0.632853	0.468439	-0.43401	-0.107557	0.8421	0.9998
ENSG00000149100	ENSG00000149100	EIF3M	11:32605343-32816204	OK	262.053	272.205	0.0548375	0.122892	0.84215	0.9998
ENSG00000254184	ENSG00000254184	TYW1B	7:72023728-72298777	OK	0.622059	0.676986	0.122075	0.105595	0.8422	0.9998
ENSG00000127837	ENSG00000127837	AAMP	2:219128849-219134980	OK	74.1478	71.3274	-0.0559481	-0.118199	0.84225	0.9998
ENSG00000172785	ENSG00000172785	CBWD1	9:121040-188979	OK	18.2937	19.1126	0.063178	0.117055	0.8423	0.9998
ENSG00000260563	ENSG00000260563	RP13-516M14.1	17:80251591-80252786	OK	1.58467	1.48531	-0.0934148	-0.12125	0.84235	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000113648	ENSG00000113648	H2AFY	5:134363424-134736986	OK	61.1075	58.8444	-0.0544439	-0.116767	0.84245	0.9998
ENSG00000164054	ENSG00000164054	SHISA5	3:48509196-48542259	OK	35.5331	34.3505	-0.0488327	-0.113885	0.8425	0.9998
ENSG00000187626	ENSG00000187626	ZKSCAN4	6:28212400-28227011	OK	2.70876	2.85391	0.0753025	0.119405	0.8425	0.9998
ENSG00000151773	ENSG00000151773	CCDC122	13:44398044-44468068	OK	1.87234	2.18159	0.22054	0.143497	0.84255	0.9998
ENSG00000151876	ENSG00000151876	FBXO4	5:41925355-41941845	OK	6.04597	6.39443	0.0808403	0.12125	0.84255	0.9998
ENSG00000119927	ENSG00000119927	GPAM	10:113909623-113975135	OK	11.6413	11.2383	-0.0508298	-0.090578	0.84265	0.9998
ENSG00000187479	ENSG00000187479	C11orf96	11:43942608-44022707	OK	23.2945	22.4254	-0.0548603	-0.120009	0.84265	0.9998
ENSG00000113318	ENSG00000113318	MSH3	5:79922046-80172279	OK	8.80157	8.33781	-0.0780932	-0.111462	0.8427	0.9998
ENSG00000198399	ENSG00000198399	ITSN2	2:24425732-24583583	OK	16.4035	15.7871	-0.055259	-0.0984011	0.8427	0.9998
ENSG00000196187	ENSG00000196187	TMEM63A	1:225997793-226070069	OK	23.4051	25.0602	0.0985748	0.081537	0.84275	0.9998
ENSG00000273314	ENSG00000273314	RP5-1136G13.2	7:148393558-148498128	OK	0.491633	0.660211	0.425344	0.110265	0.84275	0.9998
ENSG00000187024	ENSG00000187024	PTRH1	9:130374543-130497604	OK	17.0559	21.139	0.309634	0.105408	0.84295	0.9998
ENSG00000113532	ENSG00000113532	ST8SIA4	5:100142638-100238970	OK	0.786817	0.719688	-0.128656	-0.103644	0.84305	0.9998
ENSG00000189180	ENSG00000189180	ZNF33A	10:38299577-38354016	OK	3.0957	3.28919	0.0874666	0.0963582	0.84305	0.9998
ENSG00000180233	ENSG00000180233	ZNRF2	7:30323922-30452118	OK	4.35632	4.54971	0.0626647	0.109442	0.84315	0.9998
ENSG00000188677	ENSG00000188677	PARVB	22:44319618-44568829	OK	89.7345	84.2677	-0.0906837	-0.112328	0.8432	0.9998
ENSG00000215375	ENSG00000215375	MYL5	4:666224-683230	OK	1.64033	1.45556	-0.17242	-0.0446952	0.84325	0.9998
ENSG00000124155	ENSG00000124155	PIGT	20:44044716-44054884	OK	119.212	123.286	0.0484838	0.121342	0.8433	0.9998
ENSG00000141552	ENSG00000141552	ANAPC11	17:79845712-79869340	OK	228.78	215.597	-0.0856292	-0.126436	0.8434	0.9998
ENSG00000204856	ENSG00000204856	FAM216A	12:110890288-110928190	OK	3.953	4.43494	0.165968	0.11798	0.8434	0.9998
ENSG00000134297	ENSG00000134297	PLEKHA8P1	12:45566846-45834187	OK	10.1866	8.70553	-0.226672	-0.0686373	0.84345	0.9998
ENSG00000174669	ENSG00000174669	SLC29A2	11:66115420-66139685	OK	2.0367	1.92567	-0.0808745	-0.119046	0.8435	0.9998
ENSG00000223501	ENSG00000223501	VPS52	6:33217310-33244287	OK	37.2568	31.743	-0.231065	-0.0711884	0.8435	0.9998
ENSG00000260941	ENSG00000260941	LINC00622	1:120140324-120141894	OK	6.09187	6.39552	0.070177	0.12248	0.84355	0.9998
ENSG00000072071	ENSG00000072071	LPHN1	19:14247990-14316999	OK	5.43943	5.73149	0.0754546	0.0836348	0.8436	0.9998
ENSG00000172466	ENSG00000172466	ZNF24	18:32912175-32925446	OK	33.1919	34.2615	0.0457562	0.111859	0.84385	0.9998
ENSG00000100911	ENSG00000100911	PSME2	14:24612573-24636611	OK	100.216	94.8726	-0.0790481	-0.124127	0.84395	0.9998
ENSG00000143321	ENSG00000143321	HDGF	1:156711898-156770607	OK	299.186	286.64	-0.0618042	-0.113679	0.84395	0.9998
ENSG00000160117	ENSG00000160117	ANKLE1	19:17342691-17398455	OK	0.669902	0.760741	0.183455	0.054085	0.8442	0.9998
ENSG00000163788	ENSG00000163788	SNRK	3:43328003-43775863	OK	7.80036	7.38468	-0.0790052	-0.101155	0.84425	0.9998
ENSG00000251474	ENSG00000251474	RPL32P3	3:129100140-129118498	OK	7.47331	7.17087	-0.0595989	-0.0891525	0.84425	0.9998
ENSG00000222019	ENSG00000222019	URAHP	16:90071272-90114181	OK	1.51833	1.28761	-0.237786	-0.0748386	0.84435	0.9998
ENSG00000171757	ENSG00000171757	LRRC34	3:169511215-169530774	OK	2.34625	2.48355	0.0820461	0.0972467	0.8445	0.9998
ENSG00000198858	ENSG00000198858	R3HDM4	19:896502-913240	OK	21.7456	22.5738	0.0539283	0.11507	0.8445	0.9998
ENSG00000183955	ENSG00000183955	SETD8	12:123868319-123893905	OK	21.1324	20.1546	-0.0683466	-0.0986319	0.84455	0.9998
ENSG00000131508	ENSG00000131508	UBE2D2	5:138906015-139008018	OK	58.5681	60.9886	0.0584225	0.117106	0.84465	0.9998
ENSG00000167985	ENSG00000167985	SDHAF2	11:61170120-61258403	OK	38.0322	40.726	0.0987288	0.116056	0.84465	0.9998
ENSG00000272153	ENSG00000272153	RP1-286D6.5	1:3696783-3713068	OK	2.16968	1.59771	-0.441478	-0.114218	0.8447	0.9998
ENSG00000119446	ENSG00000119446	RBM18	9:124999902-125085743	OK	20.1631	18.8904	-0.0940669	-0.108448	0.84475	0.9998
ENSG00000101945	ENSG00000101945	SUV39H1	X:48553944-48595570	OK	6.06906	6.31742	0.0578617	0.112025	0.8448	0.9998
ENSG00000158773	ENSG00000158773	USF1	1:161009040-161015767	OK	42.2534	40.7356	-0.0527757	-0.116281	0.84485	0.9998
ENSG00000171357	ENSG00000171357	LURAP1	1:46654353-46686933	OK	3.1521	2.29488	-0.457895	-0.204805	0.8449	0.9998
ENSG00000272821	ENSG00000272821	CTA-384D8.36	22:50961996-50971009	OK	1.90381	1.4125	-0.430642	-0.176178	0.8449	0.9998
ENSG00000237975	ENSG00000237975	FLG-AS1	1:152140600-152339163	OK	6.49629	7.04846	0.117692	0.104424	0.84495	0.9998
ENSG00000151746	ENSG00000151746	BICD1	12:32257050-32536567	OK	5.54937	5.87495	0.082253	0.10467	0.845	0.9998
ENSG00000109436	ENSG00000109436	TBC1D9	4:141541918-141677274	OK	5.94947	5.74012	-0.0516807	-0.109814	0.84505	0.9998
ENSG00000025772	ENSG00000025772	TOMM34	20:43538702-43589127	OK	30.9975	32.2946	0.0591416	0.119786	0.8451	0.9998
ENSG00000099940	ENSG00000099940	SNAP29	22:21061978-21245506	OK	31.452	28.6197	-0.136145	-0.119461	0.8451	0.9998
ENSG00000157426	ENSG00000157426	AASDH	4:57204455-57253666	OK	4.07537	3.87644	-0.0722004	-0.0933246	0.8451	0.9998
ENSG00000181038	ENSG00000181038	METTL23	17:74722911-74777531	OK	66.1996	72.0068	0.12131	0.116519	0.84515	0.9998
ENSG00000132153	ENSG00000132153	DHX30	3:47844398-47891685	OK	32.1894	31.1398	-0.0478252	-0.100036	0.8452	0.9998
ENSG00000269737	ENSG00000269737	RP11-345P4.7	1:1590785-1624167	OK	0.774616	1.06634	0.461116	0.157338	0.8453	0.9998
ENSG00000162923	ENSG00000162923	WDR26	1:224572844-224928251	OK	81.0013	84.5875	0.0624991	0.110419	0.84535	0.9998
ENSG00000176896	ENSG00000176896	TCEANC	X:13671224-13700083	OK	0.918895	0.986239	0.102037	0.114687	0.84535	0.9998
ENSG00000260342	ENSG00000260342	RP11-1035H13.3	16:18792616-18813000	OK	1.67871	1.3126	-0.354929	-0.0265999	0.84535	0.9998
ENSG00000161958	ENSG00000161958	FGF11	17:7323421-7361026	OK	0.63082	0.731097	0.212835	0.109749	0.8454	0.9998
ENSG00000264501	ENSG00000264501	RN7SL731P	1:10270862-10441661	OK	1.16664	1.56986	0.428282	0.045671	0.8454	0.9998
ENSG00000018236	ENSG00000018236	CNTN1	12:41086243-41466220	OK	7.91541	8.23742	0.057528	0.10041	0.8455	0.9998
ENSG00000137275	ENSG00000137275	RIPK1	6:3064224-3115421	OK	14.1496	14.696	0.05466	0.120601	0.8455	0.9998
ENSG00000224577	ENSG00000224577	LINC01117	2:177494316-177520686	OK	0.835248	0.711336	-0.231674	-0.0886972	0.8455	0.9998
ENSG00000141027	ENSG00000141027	NCOR1	17:15879873-16256970	OK	23.8448	24.9292	0.0641631	0.0607845	0.8457	0.9998
ENSG00000185670	ENSG00000185670	ZBTB3	11:62515790-62521660	OK	2.07747	2.24067	0.109101	0.101234	0.8457	0.9998
ENSG00000237037	ENSG00000237037	NDUFA6-AS1	22:42481528-42535938	OK	2.73284	2.44308	-0.161697	-0.0588244	0.8457	0.9998
ENSG00000136436	ENSG00000136436	CALCOCO2	17:46908349-46943884	OK	61.0029	63.5784	0.0596579	0.109643	0.8458	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000129295	ENSG00000129295	LRRC6	8:133584319-133687838	OK	2.17966	2.03693	-0.0977066	-0.100107	0.84595	0.9998
ENSG00000272273	ENSG00000272273	XXbac-BPG252P9.10	6:30710705-30712331	OK	2.41365	1.91946	-0.330516	-0.0544466	0.84595	0.9998
ENSG00000154380	ENSG00000154380	ENAH	1:225674536-225840844	OK	76.1332	78.9982	0.0532943	0.10475	0.846	0.9998
ENSG00000126768	ENSG00000126768	TIMM17B	X:48750729-48760420	OK	30.9318	32.8466	0.0866561	0.117749	0.8461	0.9998
ENSG00000142327	ENSG00000142327	RNPEPL1	2:241418838-241520789	OK	30.5006	29.225	-0.061632	-0.100072	0.8461	0.9998
ENSG00000259328	ENSG00000259328	RP11-152F13.7	15:82944772-82988374	OK	0.627813	0.687006	0.129987	0.1022	0.8461	0.9998
ENSG00000108272	ENSG00000108272	DHRS11	17:34948227-34957235	OK	11.641	12.2166	0.0696347	0.121414	0.84615	0.9998
ENSG00000132196	ENSG00000132196	HSD17B7	1:162760491-162782607	OK	30.3139	29.2111	-0.0534646	-0.108663	0.84625	0.9998
ENSG00000183077	ENSG00000183077	AFMID	17:76183397-76203782	OK	21.3402	22.4777	0.0749202	0.120651	0.84625	0.9998
ENSG00000064489	ENSG00000064489	MEF2BNB-MEF2B	19:19256375-19314233	OK	12.8523	10.3825	-0.307874	-0.170355	0.8463	0.9998
ENSG00000163166	ENSG00000163166	IWS1	2:128193782-128284462	OK	29.1457	28.1958	-0.0478024	-0.103486	0.8463	0.9998
ENSG00000115942	ENSG00000115942	ORC2	2:201773695-201950473	OK	14.4429	13.3206	-0.116697	-0.0873861	0.8465	0.9998
ENSG00000196458	ENSG00000196458	ZNF605	12:133345494-133532892	OK	2.7134	3.02767	0.158109	0.0737129	0.8465	0.9998
ENSG00000165915	ENSG00000165915	SLC39A13	11:47404698-47438047	OK	27.0203	26.0242	-0.0541858	-0.100754	0.8466	0.9998
ENSG00000272888	ENSG00000272888	AC013394.2	15:93425936-93571237	OK	25.0043	27.5878	0.141853	0.116479	0.8466	0.9998
ENSG00000105677	ENSG00000105677	TMEM147	19:36024313-36038428	OK	303.577	293.095	-0.0506953	-0.117969	0.84665	0.9998
ENSG00000117477	ENSG00000117477	CCDC181	1:169337207-169429907	OK	4.26522	3.81575	-0.160654	-0.127378	0.84665	0.9998
ENSG00000173156	ENSG00000173156	RHOD	11:66824288-66839484	OK	1.17499	1.25468	0.0946683	0.101764	0.84665	0.9998
ENSG00000232119	ENSG00000232119	MCTS1	X:119727864-119754929	OK	36.7265	35.4147	-0.0524721	-0.114668	0.84665	0.9998
ENSG00000069998	ENSG00000069998	CECR5	22:17618400-17646335	OK	30.7967	31.9033	0.050929	0.117394	0.8467	0.9998
ENSG00000167740	ENSG00000167740	CYB5D2	17:4046461-4167274	OK	6.91646	6.03981	-0.19553	-0.101627	0.8467	0.9998
ENSG00000234072	ENSG00000234072	AC074117.10	2:27548715-27593353	OK	1.58477	1.33664	-0.245665	-0.0463935	0.8467	0.9998
ENSG00000142544	ENSG00000142544	CTU1	19:51600862-51611627	OK	3.41237	3.25005	-0.0703108	-0.118159	0.84675	0.9998
ENSG00000147123	ENSG00000147123	NDUFB11	X:47001614-47046212	OK	68.6463	72.024	0.0692943	0.119734	0.84675	0.9998
ENSG00000144524	ENSG00000144524	COPS7B	2:232597134-232673963	OK	34.339	32.6436	-0.0730467	-0.108871	0.8468	0.9998
ENSG00000171823	ENSG00000171823	FBXL14	12:1639056-1756409	OK	4.28387	4.08895	-0.0671822	-0.112123	0.8468	0.9998
ENSG00000147324	ENSG00000147324	MFHAS1	8:8640863-8751155	OK	13.889	14.6101	0.0730228	0.0757878	0.84695	0.9998
ENSG00000158457	ENSG00000158457	TSPAN33	7:128784711-128809538	OK	18.2269	17.5564	-0.0540654	-0.117165	0.847	0.9998
ENSG00000262246	ENSG00000262246	CORO7	16:4364761-4475706	OK	10.7284	11.2217	0.0648568	0.0773403	0.847	0.9998
ENSG00000100104	ENSG00000100104	SRRD	22:26879842-26908471	OK	42.0067	38.9676	-0.108343	-0.114786	0.84705	0.9998
ENSG00000137760	ENSG00000137760	ALKBH8	11:107373451-107436472	OK	2.37748	2.50787	0.0770293	0.102807	0.8471	0.9998
ENSG00000214013	ENSG00000214013	GANC	15:42500610-42704516	OK	7.80122	7.02392	-0.151424	-0.0735618	0.8471	0.9998
ENSG00000127554	ENSG00000127554	GFER	16:2034207-2044276	OK	27.9367	29.6332	0.085053	0.117053	0.84725	0.9998
ENSG00000155561	ENSG00000155561	NUP205	7:135242666-135333505	OK	45.0042	46.3804	0.0434562	0.0900811	0.84725	0.9998
ENSG00000178028	ENSG00000178028	DMAP1	1:44679126-44686353	OK	19.1268	18.3456	-0.0601654	-0.108692	0.84735	0.9998
ENSG00000142230	ENSG00000142230	SAE1	19:47567443-47713886	OK	151.513	146.3	-0.0505054	-0.110996	0.84745	0.9998
ENSG00000100926	ENSG00000100926	TM9SF1	14:24641061-24708448	OK	35.5677	38.9287	0.130266	0.112137	0.8475	0.9998
ENSG00000184785	ENSG00000184785	SMIM10	X:134124967-134126501	OK	0.594905	0.639381	0.104016	0.11582	0.84755	0.9998
ENSG00000125352	ENSG00000125352	RNF113A	X:119004496-119010625	OK	11.0164	12.1952	0.146666	0.116692	0.84765	0.9998
ENSG00000242247	ENSG00000242247	ARFGAP3	22:43192507-43411151	OK	28.0589	30.3068	0.111182	0.0967434	0.84765	0.9998
ENSG00000215041	ENSG00000215041	NEURL4	17:7210317-7232712	OK	13.6859	12.4939	-0.131466	-0.0609111	0.8477	0.9998
ENSG00000255072	ENSG00000255072	PIGY	4:89442135-89629693	OK	7.50013	10.9163	0.5415	0.0755282	0.8477	0.9998
ENSG00000255813	ENSG00000255813	AL162497.1	13:110406183-110438915	OK	10.4743	11.8391	0.176717	0.070993	0.84785	0.9998
ENSG00000128346	ENSG00000128346	C22orf23	22:38339527-38437922	OK	2.58756	3.238	0.323515	0.0734214	0.848	0.9998
ENSG00000149809	ENSG00000149809	TM7SF2	11:64851694-64883856	OK	10.4355	9.47516	-0.139275	-0.0828363	0.848	0.9998
ENSG00000113194	ENSG00000113194	FAF2	5:175874628-175937075	OK	19.1846	18.562	-0.0476006	-0.0882683	0.84805	0.9998
ENSG00000176125	ENSG00000176125	UFSP1	7:100486345-100487339	OK	1.07789	0.99869	-0.110106	-0.120737	0.84805	0.9998
ENSG00000238018	ENSG00000238018	AC093110.3	2:54683421-54896812	OK	1.88256	1.55264	-0.277972	-0.0156411	0.8481	0.9998
ENSG00000114853	ENSG00000114853	ZBTB47	3:42589460-42709072	OK	8.41768	9.17163	0.123756	0.12295	0.8482	0.9998
ENSG00000121542	ENSG00000121542	SEC22A	3:122785908-122992977	OK	18.8197	19.92	0.0819679	0.109658	0.8482	0.9998
ENSG00000203817	ENSG00000203817	FAM72C	1:149438749-149459549	OK	0.632469	0.682392	0.109606	0.0962743	0.8482	0.9998
ENSG00000224858	ENSG00000224858	RPL29P11	3:37034822-37225180	OK	42.5201	37.3107	-0.188556	-0.121264	0.8482	0.9998
ENSG00000252531	ENSG00000252531	SNORA73	2:3622794-3628509	OK	10.9883	8.35091	-0.395961	-0.0143124	0.8482	0.9998
ENSG00000265298	ENSG00000265298	RP13-104F24.3	17:62745780-62833272	OK	1.01183	0.838443	-0.271178	-0.111185	0.8482	0.9998
ENSG00000198899	ENSG00000198899	MT-ATP6	MT:8365-9990	OK	4013.18	4359.73	0.119494	0.114078	0.84825	0.9998
ENSG00000263002	ENSG00000263002	ZNF234	19:44645709-44663156	OK	2.97993	2.84054	-0.0691124	-0.103615	0.84825	0.9998
ENSG00000269982	ENSG00000269982	RP11-1020A11.2	3:10000400-10052893	OK	0.630437	0.547117	-0.204502	-0.0817568	0.8483	0.9998
ENSG00000215790	ENSG00000215790	SLC35E2	1:1634168-1677431	OK	2.77923	2.40919	-0.206139	-0.11638	0.8484	0.9998
ENSG00000005436	ENSG00000005436	GCFC2	2:75873908-75938115	OK	12.4839	13.5389	0.117044	0.107543	0.8485	0.9998
ENSG00000113712	ENSG00000113712	CSNK1A1	5:148871759-148931007	OK	110.801	116.274	0.0695539	0.113057	0.8485	0.9998
ENSG00000230797	ENSG00000230797	YY2	X:21857753-21903542	OK	0.847535	0.683455	-0.310425	-0.142643	0.8486	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226690	ENSG00000226690	AC005281.1	7:12536054-12581536	OK	3.00509	2.8061	-0.0988378	-0.110528	0.84885	0.9998
ENSG00000169612	ENSG00000169612	FAM103A1	15:83509837-83772195	OK	10.4172	11.7994	0.179745	0.114352	0.8489	0.9998
ENSG00000072756	ENSG00000072756	TRNT1	3:3168599-3221394	OK	12.6146	13.3221	0.0787255	0.0974342	0.849	0.9998
ENSG00000132716	ENSG00000132716	DCAF8	1:160185504-160256138	OK	89.0699	84.9652	-0.0680653	-0.0731667	0.849	0.9998
ENSG00000224032	ENSG00000224032	EPB41L4A-AS1	5:111478137-111755013	OK	17.5884	16.2811	-0.111427	-0.113436	0.849	0.9998
ENSG00000125434	ENSG00000125434	SLC25A35	17:8191080-8198661	OK	2.3344	2.12102	-0.138292	-0.109979	0.84905	0.9998
ENSG00000260916	ENSG00000260916	CCPG1	15:55495163-55800432	OK	8.46519	9.33978	0.141847	0.105953	0.84905	0.9998
ENSG00000103091	ENSG00000103091	WDR59	16:74907467-75144892	OK	7.46561	7.12556	-0.067257	-0.0740513	0.84915	0.9998
ENSG00000048342	ENSG00000048342	CC2D2A	4:15471488-15603180	OK	10.8381	10.2437	-0.0813731	-0.0991006	0.8492	0.9998
ENSG00000240891	ENSG00000240891	PLCXD2	3:111393522-111695364	OK	0.67257	0.79565	0.24245	0.0684688	0.8492	0.9998
ENSG00000257621	ENSG00000257621	RP11-349A22.5	14:58466452-58764857	OK	17.476	18.8117	0.106252	0.0784008	0.8494	0.9998
ENSG00000248461	ENSG00000248461	CTD-2207A17.1	5:38025798-38184034	OK	1.68807	1.60259	-0.0749739	-0.112807	0.84945	0.9998
ENSG00000241468	ENSG00000241468	ATP5J2	7:98923520-99063954	OK	863.81	1021.6	0.242045	0.162939	0.8495	0.9998
ENSG00000170860	ENSG00000170860	LSM3	3:14166439-14242619	OK	13.3905	12.575	-0.0906485	-0.107616	0.8496	0.9998
ENSG00000257028	ENSG00000257028	C15ORF37	15:80125926-80217194	OK	2.81186	2.43564	-0.207227	-0.116477	0.84965	0.9998
ENSG00000167674	ENSG00000167674	HDGFRP2	19:4472283-4517716	OK	21.6913	22.475	0.0512079	0.110432	0.8498	0.9998
ENSG00000079246	ENSG00000079246	XRCC5	2:216972186-217071026	OK	163.191	169.477	0.0545304	0.0883939	0.84985	0.9998
ENSG00000101966	ENSG00000101966	XIAP	X:122993573-123047829	OK	7.33445	6.96915	-0.0737069	-0.0722676	0.8499	0.9998
ENSG00000173889	ENSG00000173889	PHC3	3:169804519-169899537	OK	14.2682	15.0214	0.0742234	0.0691729	0.8499	0.9998
ENSG00000255831	ENSG00000255831	AL139385.1	13:111267880-111292340	OK	7.61755	6.72881	-0.178976	-0.115461	0.84995	0.9998
ENSG00000273373	ENSG00000273373	RP5-1074L1.4	1:110905469-110974982	OK	1.08909	0.78909	-0.46486	-0.160567	0.84995	0.9998
ENSG00000108852	ENSG00000108852	MPP2	17:41952724-41987068	OK	8.00373	8.3054	0.0533786	0.105051	0.85005	0.9998
ENSG00000244563	ENSG00000244563	AC006011.4	2:128603839-128615731	OK	3.04872	2.16804	-0.49181	-0.117346	0.85005	0.9998
ENSG00000130283	ENSG00000130283	GDF1	19:18979360-19007536	OK	1.74158	1.91727	0.138651	0.113113	0.8501	0.9998
ENSG00000139826	ENSG00000139826	ABHD13	13:108870726-108886603	OK	3.65284	3.79745	0.0560149	0.115319	0.8501	0.9998
ENSG00000155959	ENSG00000155959	VBP1	X:154425283-154468098	OK	54.5103	56.8596	0.0608739	0.11454	0.8502	0.9998
ENSG00000166529	ENSG00000166529	ZSCAN21	7:99647389-99680171	OK	12.0175	12.7807	0.0888333	0.118063	0.8503	0.9998
ENSG00000168385	ENSG00000168385	2-Sep	2:242166678-242293442	OK	153.78	146.25	-0.0724367	-0.0657757	0.85035	0.9998
ENSG00000198746	ENSG00000198746	GPATCH3	1:27216978-27273353	OK	5.59689	6.11544	0.127831	0.104475	0.85035	0.9998
ENSG00000266753	ENSG00000266753	RP11-690G19.3	17:37408896-37410550	OK	1.49099	1.40702	-0.0836245	-0.1135	0.8504	0.9998
ENSG00000086475	ENSG00000086475	SEPHS1	10:13359423-13390297	OK	27.8044	29.1121	0.0663049	0.112958	0.8505	0.9998
ENSG00000106351	ENSG00000106351	AGFG2	7:100136833-100165842	OK	11.6701	11.1255	-0.068951	-0.111951	0.85055	0.9998
ENSG00000213782	ENSG00000213782	DDX47	12:12878850-12982915	OK	38.3024	41.1748	0.104327	0.109252	0.85055	0.9998
ENSG00000138002	ENSG00000138002	IFT172	2:27665232-27712656	OK	8.03894	7.70256	-0.0616671	-0.069941	0.8506	0.9998
ENSG00000152818	ENSG00000152818	UTRN	6:144606836-145174170	OK	10.1766	9.52364	-0.0956712	-0.0653277	0.85085	0.9998
ENSG00000272962	ENSG00000272962	SLC5A3	21:35445523-35732332	OK	1.76636	1.88024	0.0901383	0.115738	0.85085	0.9998
ENSG00000068654	ENSG00000068654	POLR1A	2:86247338-86333278	OK	12.908	12.4708	-0.0497095	-0.0712919	0.8509	0.9998
ENSG00000242282	ENSG00000242282	AC108488.4	2:3579402-3609324	OK	2.1084	1.80205	-0.226505	-0.0697364	0.85105	0.9998
ENSG00000259845	ENSG00000259845	HERC2P10	15:31107473-31136356	OK	0.63013	0.670572	0.0897432	0.11303	0.8511	0.9998
ENSG00000271936	ENSG00000271936	RP11-443B20.1	2:25012602-25142708	OK	1.46811	1.11175	-0.401129	-0.106066	0.8511	0.9998
ENSG00000172172	ENSG00000172172	MRPL13	8:121392999-121825599	OK	52.715	50.3864	-0.0651784	-0.110227	0.8512	0.9998
ENSG00000198874	ENSG00000198874	TYW1	7:66452663-66704501	OK	7.98525	7.45701	-0.0987405	-0.100907	0.8512	0.9998
ENSG00000203772	ENSG00000203772	SPRN	10:135192694-135382916	OK	1.16875	1.32268	0.178495	0.117711	0.8512	0.9998
ENSG00000100575	ENSG00000100575	TIMM9	14:58862633-59015216	OK	60.5729	64.0177	0.0797995	0.116349	0.85135	0.9998
ENSG00000101193	ENSG00000101193	GID8	20:61569470-61576996	OK	38.9042	37.6793	-0.0461564	-0.103966	0.85135	0.9998
ENSG00000147099	ENSG00000147099	HDAC8	X:71549365-71792953	OK	17.6283	18.4826	0.0682704	0.108838	0.85135	0.9998
ENSG00000238072	ENSG00000238072	RP11-305M3.2	7:128864863-129070052	OK	30.6893	25.0037	-0.295595	-0.114408	0.85145	0.9998
ENSG00000101457	ENSG00000101457	DNTTIP1	20:44420575-44440066	OK	30.862	29.8187	-0.0496119	-0.110053	0.8515	0.9998
ENSG00000130826	ENSG00000130826	DKC1	X:153991030-154005964	OK	34.2425	35.3852	0.0473583	0.0976779	0.8515	0.9998
ENSG00000174738	ENSG00000174738	NR1D2	3:23933150-24022109	OK	12.2376	13.8632	0.179937	0.085933	0.8515	0.9998
ENSG00000020256	ENSG00000020256	ZFP64	20:50668201-50820847	OK	7.73661	7.37144	-0.0697555	-0.106264	0.85155	0.9998
ENSG00000006704	ENSG00000006704	GTF2IRD1	7:73868119-74016931	OK	8.4419	8.82183	0.0635104	0.0952244	0.85165	0.9998
ENSG00000161544	ENSG00000161544	CYGB	17:74523437-74553765	OK	20.833	21.698	0.05869	0.115433	0.85165	0.9998
ENSG00000171428	ENSG00000171428	NAT1	8:18027985-18081198	OK	7.11061	7.44241	0.065797	0.109465	0.8517	0.9998
ENSG00000125656	ENSG00000125656	CLPP	19:6343771-6368919	OK	79.521	82.2812	0.0492258	0.112768	0.85185	0.9998
ENSG00000198466	ENSG00000198466	ZNF587	19:58281022-58427978	OK	5.56578	5.86597	0.0757849	0.0843866	0.85195	0.9998
ENSG00000272498	ENSG00000272498	RP11-415F23.3	3:16306705-16555533	OK	0.949491	0.700095	-0.439605	-0.108752	0.85195	0.9998
ENSG00000261195	ENSG00000261195	CTD-2380F24.1	16:19566561-19897489	OK	0.737379	0.884884	0.263082	0.0288586	0.852	0.9998
ENSG00000083844	ENSG00000083844	ZNF264	19:57702867-57724724	OK	2.60258	2.75737	0.0833491	0.0962788	0.85205	0.9998
ENSG00000198743	ENSG00000198743	SLC5A3	21:35445523-35732332	OK	1.79748	1.91038	0.0878809	0.113238	0.8521	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000164967	ENSG00000164967	RPP25L	9:34610482-34612101	OK	7.10932	7.47008	0.0714132	0.116153	0.85225	0.9998
ENSG00000237004	ENSG00000237004	ZNRF2P1	7:32535037-33102409	OK	0.914514	0.691904	-0.402433	-0.0225105	0.85225	0.9998
ENSG00000139266	ENSG00000139266	9-Mar	12:58117543-58154190	OK	10.3351	12.4525	0.268892	0.147439	0.8523	0.9998
ENSG00000153291	ENSG00000153291	SLC25A27	6:46620677-46703430	OK	3.9257	3.64037	-0.108864	-0.112879	0.85235	0.9998
ENSG00000235298	ENSG00000235298	RP11-575L7.8	9:86582997-86595569	OK	1.28906	1.71231	0.409631	0.0217157	0.85235	0.9998
ENSG00000139719	ENSG00000139719	VPS33A	12:122688089-122751068	OK	16.3862	17.245	0.0736934	0.100019	0.8524	0.9998
ENSG00000171033	ENSG00000171033	PKIA	8:79338337-79517502	OK	6.25556	6.55562	0.0675923	0.10713	0.85245	0.9998
ENSG00000143374	ENSG00000143374	TARS2	1:150459886-150480078	OK	36.3271	35.0884	-0.0500487	-0.0806099	0.85265	0.9998
ENSG00000143498	ENSG00000143498	TAF1A	1:222731243-222766374	OK	7.94405	7.57379	-0.0688594	-0.115362	0.8527	0.9998
ENSG00000257704	ENSG00000257704	PRR24	19:47778141-47778979	OK	2.21441	2.3495	0.0854289	0.108167	0.85275	0.9998
ENSG00000135899	ENSG00000135899	SP110	2:230990025-231268447	OK	7.88216	8.23182	0.0626212	0.0959866	0.8528	0.9998
ENSG00000214655	ENSG00000214655	ZSWIM8	10:75545339-75571589	OK	41.1273	43.0051	0.0644119	0.0666733	0.8529	0.9998
ENSG00000273151	ENSG00000273151	RP11-449P15.2	7:855527-936073	OK	0.534351	0.700108	0.389788	0.155771	0.8529	0.9998
ENSG00000125826	ENSG00000125826	RBCK1	20:388141-411610	OK	25.7652	24.7618	-0.0573041	-0.111797	0.85295	0.9998
ENSG00000168411	ENSG00000168411	RFWD3	16:74655291-74700779	OK	11.2299	11.6183	0.0490516	0.0864759	0.853	0.9998
ENSG00000234127	ENSG00000234127	TRIM26	6:30152231-30181204	OK	20.5797	21.4061	0.056799	0.103872	0.85305	0.9998
ENSG00000242114	ENSG00000242114	MTFP1	22:30727976-30825045	OK	22.2001	19.7906	-0.165754	-0.132444	0.85305	0.9998
ENSG00000258790	ENSG00000258790	KIAA0391	14:35514112-35786699	OK	1.28603	0.967319	-0.410857	-0.121241	0.85305	0.9998
ENSG00000244479	ENSG00000244479	OR2A1-AS1	7:143883175-144077725	OK	4.33285	3.91238	-0.147269	-0.0925049	0.8531	0.9998
ENSG00000104866	ENSG00000104866	PPP1R37	19:45574757-45808541	OK	41.2192	39.6817	-0.0548415	-0.0963871	0.85325	0.9998
ENSG00000181418	ENSG00000181418	DDN	12:49388931-49453557	OK	0.546456	0.742487	0.44226	0.115072	0.85325	0.9998
ENSG00000196967	ENSG00000196967	ZNF585A	19:37498758-37734828	OK	12.188	11.2512	-0.115387	-0.110382	0.85325	0.9998
ENSG00000198924	ENSG00000198924	DCLRE1A	10:115594487-115614142	OK	4.52046	4.69552	0.0548138	0.106689	0.85325	0.9998
ENSG00000226754	ENSG00000226754	RP5-1024G6.5	1:53692563-53710212	OK	0.83442	0.624169	-0.418838	-0.150386	0.8533	0.9998
ENSG00000187187	ENSG00000187187	ZNF546	19:40490040-40523514	OK	0.636695	0.692379	0.120959	0.0673828	0.8534	0.9998
ENSG00000205060	ENSG00000205060	SLC35B4	7:133974083-134001803	OK	38.0869	36.7055	-0.0533016	-0.0695975	0.85345	0.9998
ENSG00000054598	ENSG00000054598	FOXC1	6:1610680-1614127	OK	1.43113	1.50381	0.0714625	0.114086	0.8535	0.9998
ENSG00000170430	ENSG00000170430	MGMT	10:131265447-131566271	OK	15.3451	15.9103	0.0521814	0.111518	0.8535	0.9998
ENSG00000099810	ENSG00000099810	MTAP	9:21802541-22121096	OK	37.8547	35.9074	-0.0761912	-0.103462	0.8537	0.9998
ENSG00000170485	ENSG00000170485	NPAS2	2:101436613-101886778	OK	40.7349	44.5263	0.128394	0.052906	0.8537	0.9998
ENSG00000271742	ENSG00000271742	RP4-680D5.9	1:16009367-16009623	OK	1.32619	1.53527	0.211209	0.156357	0.8537	0.9998
ENSG00000176454	ENSG00000176454	LPCAT4	15:34651105-34659479	OK	8.93076	8.55692	-0.0616923	-0.105521	0.85375	0.9998
ENSG00000259330	ENSG00000259330	LINC00984	15:40617416-40618916	OK	3.77459	3.54561	-0.0902836	-0.11256	0.85375	0.9998
ENSG00000119396	ENSG00000119396	RAB14	9:123940414-124095121	OK	24.2698	26.1957	0.110171	0.112067	0.8538	0.9998
ENSG00000130270	ENSG00000130270	ATP8B3	19:1782073-1812275	OK	1.12244	1.05702	-0.0866364	-0.100415	0.8538	0.9998
ENSG00000248161	ENSG00000248161	RP11-499E18.1	4:103172197-103371167	OK	1.39862	1.19901	-0.222151	-0.055607	0.8538	0.9998
ENSG00000145817	ENSG00000145817	YIPF5	5:143537722-143550278	OK	28.9307	30.1418	0.0591638	0.106772	0.85385	0.9998
ENSG00000185024	ENSG00000185024	BRF1	14:105675622-105864484	OK	12.4039	13.4488	0.116677	0.105484	0.85395	0.9998
ENSG00000263320	ENSG00000263320	RP11-498D10.6	16:71963440-72033877	OK	1.05375	0.985213	-0.0970296	-0.111746	0.85395	0.9998
ENSG00000167302	ENSG00000167302	ENTHD2	17:79202076-79212891	OK	10.9784	10.4885	-0.0658638	-0.0938374	0.85405	0.9998
ENSG00000175054	ENSG00000175054	ATR	3:142168076-142297668	OK	7.13674	6.84767	-0.0596521	-0.0675194	0.8541	0.9998
ENSG00000205542	ENSG00000205542	TMSB4X	X:12993226-12995346	OK	2.84694	2.63619	-0.110956	-0.107766	0.85415	0.9998
ENSG00000246705	ENSG00000246705	H2AFJ	12:14927269-14930936	OK	24.6962	23.6398	-0.0630703	-0.109982	0.85415	0.9998
ENSG00000070182	ENSG00000070182	SPTB	14:65170819-65346601	OK	1.03504	0.931872	-0.151479	-0.0737321	0.8543	0.9998
ENSG00000106689	ENSG00000106689	LHX2	9:126763948-126795580	OK	0.649619	0.597553	-0.120529	-0.0968976	0.85435	0.9998
ENSG00000167110	ENSG00000167110	GOLGA2	9:131018107-131051269	OK	41.1729	39.2912	-0.067489	-0.0948617	0.85435	0.9998
ENSG00000237669	ENSG00000237669	HCG4P3	6:29968787-30032686	OK	0.708896	0.513302	-0.465766	-0.145805	0.8544	0.9998
ENSG00000141428	ENSG00000141428	C18orf21	18:33552045-33559241	OK	27.7402	26.6685	-0.056844	-0.110052	0.85445	0.9998
ENSG00000246089	ENSG00000246089	RP11-115C21.2	8:6261071-6565730	OK	0.757721	0.594626	-0.349686	-0.1371	0.85445	0.9998
ENSG00000119013	ENSG00000119013	NDUFB3	2:201773695-201950473	OK	146.267	139.281	-0.0706078	-0.112409	0.8545	0.9998
ENSG00000143952	ENSG00000143952	VPS54	2:64119279-64246206	OK	17.9931	18.5869	0.0468369	0.108936	0.8545	0.9998
ENSG00000272921	ENSG00000272921	RP11-500M8.7	12:4671369-4960277	OK	1.83757	2.70429	0.557448	0.125895	0.8545	0.9998
ENSG00000103197	ENSG00000103197	TSC2	16:2089815-2185899	OK	18.318	19.1849	0.0667114	0.0647302	0.85455	0.9998
ENSG00000185122	ENSG00000185122	HSF1	8:145515279-145538801	OK	35.7749	34.5943	-0.0484138	-0.0929616	0.85455	0.9998
ENSG00000145882	ENSG00000145882	PCYOX1L	5:148737569-148749216	OK	2.32992	2.22077	-0.0692243	-0.107716	0.8546	0.9998
ENSG00000162413	ENSG00000162413	KLHL21	1:6650783-6684093	OK	12.3384	12.8902	0.0631187	0.108091	0.85465	0.9998
ENSG00000196417	ENSG00000196417	ZNF765	19:53868945-53930574	OK	1.72842	1.62787	-0.0864678	-0.0773808	0.85465	0.9998
ENSG00000146463	ENSG00000146463	ZMYM4	1:35734567-35887659	OK	13.2013	12.3708	-0.0937391	-0.0640613	0.8548	0.9998
ENSG00000229387	ENSG00000229387	AC103801.2	11:22644078-22834601	OK	3.56094	4.66096	0.388369	0.160593	0.8548	0.9998
ENSG00000117593	ENSG00000117593	DARS2	1:173768687-173827684	OK	23.8397	22.9881	-0.0524752	-0.106668	0.8549	0.9998
ENSG00000272842	ENSG00000272842	RP11-513M16.7	9:19230432-19374139	OK	0.653925	0.520923	-0.328054	-0.0455306	0.8549	0.9998
ENSG00000144035	ENSG00000144035	NAT8	2:73867958-73869520	OK	0.665067	0.612442	-0.118927	-0.109935	0.85505	0.9998
ENSG00000048544	ENSG00000048544	MRPS10	6:42174538-42185603	OK	54.5674	56.2292	0.0432792	0.107899	0.8551	0.9998
ENSG00000224837	ENSG00000224837	GCSHP5	1:167885966-168045081	OK	36.5313	40.5562	0.150788	0.113947	0.85515	0.9998
ENSG00000067225	ENSG00000067225	PKM	15:72491369-72524164	OK	1036.13	1074.64	0.0526517	0.103304	0.8552	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000196428	ENSG00000196428	TSC22D2	3:150126121-150184218	OK	18.758	19.5388	0.0588331	0.0978823	0.8553	0.9998
ENSG00000128512	ENSG00000128512	DOCK4	7:111366165-111846466	OK	5.33394	5.05189	-0.0783763	-0.0731328	0.85535	0.9998
ENSG00000235423	ENSG00000235423	RP11-282O18.3	12:123636866-123756881	OK	7.0519	6.14656	-0.198232	-0.0681151	0.8554	0.9998
ENSG00000053371	ENSG00000053371	AKR7A2	1:19630458-19638640	OK	34.0668	32.9518	-0.0480099	-0.106518	0.85545	0.9998
ENSG00000119718	ENSG00000119718	EIF2B2	14:75469613-75476292	OK	42.9225	44.315	0.0460597	0.109378	0.85545	0.9998
ENSG00000135250	ENSG00000135250	SRPK2	7:104653871-105039755	OK	39.454	41.1617	0.061133	0.0882041	0.8556	0.9998
ENSG00000235065	ENSG00000235065	RPL24P2	20:21095363-21095838	OK	4.24336	3.98397	-0.0910008	-0.110136	0.8556	0.9998
ENSG00000156587	ENSG00000156587	UBE2L6	11:57319128-57335757	OK	18.2933	17.5377	-0.0608526	-0.109725	0.8557	0.9998
ENSG00000241973	ENSG00000241973	PI4KA	22:21061978-21245506	OK	23.9969	23.1533	-0.0516296	-0.0764186	0.85575	0.9998
ENSG00000109184	ENSG00000109184	DCUN1D4	4:52709165-52783003	OK	16.7354	17.4252	0.0582775	0.0843864	0.8558	0.9998
ENSG00000107614	ENSG00000107614	TRDMT1	10:17184252-17244053	OK	2.94434	3.12001	0.0836058	0.0846292	0.85585	0.9998
ENSG00000232702	ENSG00000232702	RP3-437C15.1	6:51274878-51275335	OK	21.2834	19.6891	-0.112331	-0.114577	0.85585	0.9998
ENSG00000146373	ENSG00000146373	RNF217	6:125230238-125413779	OK	1.60095	1.69916	0.0858949	0.0699591	0.856	0.9998
ENSG00000171320	ENSG00000171320	ESCO2	8:27590834-27695612	OK	10.5766	11.7231	0.148471	0.0810957	0.856	0.9998
ENSG00000134954	ENSG00000134954	ETS1	11:128328655-128457453	OK	74.4139	71.9439	-0.0487012	-0.107099	0.8561	0.9998
ENSG00000182873	ENSG00000182873	RP11-181G12.2	1:1981908-2152177	OK	0.759495	0.636529	-0.254813	-0.0688625	0.85615	0.9998
ENSG00000254996	ENSG00000254996	ANKHD1-EIF4EBP3	5:139781398-139973337	OK	1.161	1.42021	0.290742	0.0783027	0.85615	0.9998
ENSG00000102921	ENSG00000102921	N4BP1	16:48572636-48654059	OK	9.5573	9.07692	-0.0744003	-0.082615	0.8562	0.9998
ENSG00000112130	ENSG00000112130	RNF8	6:37321747-37362514	OK	24.5211	25.4446	0.0533358	0.111071	0.8562	0.9998
ENSG00000160050	ENSG00000160050	CCDC28B	1:32665986-32674288	OK	19.5452	20.4957	0.0685089	0.109303	0.8562	0.9998
ENSG00000235489	ENSG00000235489	DBF4P1	10:65928714-65930611	OK	1.68527	1.77184	0.0722667	0.103599	0.8563	0.9998
ENSG00000197780	ENSG00000197780	TAF13	1:109605107-109618624	OK	22.6189	21.758	-0.0559855	-0.108559	0.85635	0.9998
ENSG00000119408	ENSG00000119408	NEK6	9:127019884-127115586	OK	53.3168	51.2323	-0.0575372	-0.101163	0.8564	0.9998
ENSG00000259943	ENSG00000259943	RP1-39G22.7	1:40722098-40723639	OK	1.58207	1.49674	-0.0799913	-0.109908	0.8564	0.9998
ENSG00000136161	ENSG00000136161	RCBTB2	13:49063094-49107369	OK	2.80544	2.93161	0.0634651	0.0913765	0.85645	0.9998
ENSG00000138231	ENSG00000138231	DBR1	3:137879853-137893791	OK	8.03455	8.35504	0.0564302	0.0981453	0.85645	0.9998
ENSG00000130638	ENSG00000130638	ATXN10	22:46067677-46241187	OK	98.1951	102.975	0.0685706	0.114123	0.8565	0.9998
ENSG00000111877	ENSG00000111877	MCM9	6:119134604-119470552	OK	2.48575	2.30335	-0.109948	-0.0713407	0.85655	0.9998
ENSG00000196453	ENSG00000196453	ZNF777	7:149128453-149158214	OK	3.75207	3.9064	0.0581536	0.111213	0.85655	0.9998
ENSG00000105656	ENSG00000105656	ELL	19:18552228-18632937	OK	3.26404	3.12784	-0.0614909	-0.0918959	0.8566	0.9998
ENSG00000038002	ENSG00000038002	AGA	4:178351923-178363657	OK	5.8708	5.55366	-0.0801199	-0.100847	0.85665	0.9998
ENSG00000089335	ENSG00000089335	ZNF302	19:35168543-35177302	OK	1.10749	1.17362	0.0836701	0.0712229	0.85665	0.9998
ENSG00000189007	ENSG00000189007	ADAT2	6:143743968-143771810	OK	2.86404	3.03329	0.0828317	0.0927279	0.85665	0.9998
ENSG00000136933	ENSG00000136933	RABEPK	9:127962820-127996437	OK	13.3893	13.913	0.0553554	0.109635	0.8567	0.9998
ENSG00000247679	ENSG00000247679	RP11-1277A3.1	5:177038253-177099210	OK	0.718928	0.662349	-0.118255	-0.118396	0.8567	0.9998
ENSG00000166946	ENSG00000166946	CCNDBP1	15:43398422-43513481	OK	12.5602	13.1146	0.0623229	0.108798	0.8568	0.9998
ENSG00000107021	ENSG00000107021	TBC1D13	9:131549482-131572711	OK	17.9203	17.2997	-0.0508419	-0.0897774	0.85685	0.9998
ENSG00000036549	ENSG00000036549	ZZZ3	1:78028100-78149104	OK	12.9572	13.5097	0.0602492	0.0859838	0.85695	0.9998
ENSG00000181396	ENSG00000181396	OGFOD3	17:80347098-80408705	OK	28.7491	27.3943	-0.069642	-0.0956528	0.85695	0.9998
ENSG00000137074	ENSG00000137074	APTX	9:32972603-33025166	OK	31.0289	32.271	0.0566272	0.107986	0.8571	0.9998
ENSG00000167535	ENSG00000167535	CACNB3	12:49207576-49222724	OK	7.9587	8.29395	0.0595256	0.0892024	0.8571	0.9998
ENSG00000259172	ENSG00000259172	RP11-299G20.2	15:101835623-102065405	OK	0.736293	0.583882	-0.334603	-0.125542	0.8571	0.9998
ENSG00000233404	ENSG00000233404	FLJ20373	2:102313311-102511150	OK	2.08739	2.88665	0.467699	0.181535	0.8572	0.9998
ENSG00000188070	ENSG00000188070	C11orf95	11:63527363-63536113	OK	3.28163	3.153	-0.0576912	-0.101236	0.85725	0.9998
ENSG00000180747	ENSG00000180747	CTD-2547E10.2	16:21413557-21531765	OK	4.54418	4.8941	0.107023	0.105334	0.8573	0.9998
ENSG00000225470	ENSG00000225470	JPX	X:73164158-73513409	OK	15.7335	14.7729	-0.0908852	-0.100678	0.8574	0.9998
ENSG00000204390	ENSG00000204390	HSPA1L	6:31777395-31785723	OK	0.957001	0.79354	-0.270218	-0.117346	0.85745	0.9998
ENSG00000117643	ENSG00000117643	MAN1C1	1:25943958-26112698	OK	2.06927	1.95348	-0.0830805	-0.103888	0.85755	0.9998
ENSG00000258430	ENSG00000258430	RP11-982M15.2	14:105235685-105262088	OK	19.256	22.6702	0.235491	0.11824	0.85755	0.9998
ENSG00000078319	ENSG00000078319	PMS2P1	7:99905324-99997719	OK	15.2929	13.8265	-0.145433	-0.0929299	0.85765	0.9998
ENSG00000126070	ENSG00000126070	AGO3	1:36396318-36538101	OK	4.5503	4.15487	-0.131157	-0.109493	0.8578	0.9998
ENSG00000083842	ENSG00000083842	ZNF8	19:58739959-58827023	OK	1.22234	0.929077	-0.39577	-0.168516	0.85785	0.9998
ENSG00000123427	ENSG00000123427	METTL21B	12:58156116-58212487	OK	3.76531	4.11694	0.128801	0.0921945	0.8579	0.9998
ENSG00000269094	ENSG00000269094	AC006449.1	17:36858704-36886056	OK	5.96942	4.28248	-0.479144	-0.132556	0.8579	0.9998
ENSG00000163902	ENSG00000163902	RPN1	3:128338816-128399918	OK	102.885	99.9236	-0.0421418	-0.104326	0.85795	0.9998
ENSG00000180398	ENSG00000180398	MCFD2	2:47126413-47403740	OK	55.9951	51.3237	-0.125674	-0.0877816	0.85795	0.9998
ENSG00000239521	ENSG00000239521	GATS	7:99775185-99869855	OK	6.23822	6.71258	0.105734	0.105811	0.85795	0.9998
ENSG00000130429	ENSG00000130429	ARPC1B	7:98923520-99063954	OK	813.798	768.822	-0.0820199	-0.103143	0.85815	0.9998
ENSG00000214736	ENSG00000214736	TOMM6	6:41737913-41863099	OK	449.54	463.757	0.0449177	0.105078	0.85815	0.9998
ENSG00000267523	ENSG00000267523	CTD-2537I9.12	19:56165511-56186081	OK	2.02116	1.71727	-0.23506	-0.033201	0.8582	0.9998
ENSG00000132763	ENSG00000132763	MMACHC	1:45959537-45988719	OK	1.68118	2.35392	0.485591	0.170314	0.85825	0.9998
ENSG00000162944	ENSG00000162944	RFTN2	2:198432947-198540769	OK	0.916339	1.00641	0.135264	0.099419	0.85825	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000165819	ENSG00000165819	METTL3	14:21927178-21979517	OK	30.3516	31.8798	0.070874	0.0918944	0.85835	0.9998
ENSG00000120915	ENSG00000120915	EPHX2	8:27348295-27403081	OK	6.6036	6.26161	-0.0767182	-0.0964627	0.8584	0.9998
ENSG00000015475	ENSG00000015475	BID	22:18216905-18257536	OK	21.2652	22.2272	0.063831	0.108278	0.85845	0.9998
ENSG00000162769	ENSG00000162769	FLVCR1	1:213031596-213072705	OK	8.8921	8.38323	-0.0850178	-0.095764	0.85845	0.9998
ENSG00000173548	ENSG00000173548	SNX33	15:75928479-75954642	OK	8.88316	9.40888	0.0829502	0.108674	0.85845	0.9998
ENSG00000184551	ENSG00000184551	AC132872.1	17:80186272-80231607	OK	0.702701	0.900732	0.358188	0.0901654	0.85845	0.9998
ENSG00000123124	ENSG00000123124	WWP1	8:87345502-87777251	OK	21.1913	22.4714	0.0846217	0.0809639	0.8585	0.9998
ENSG00000133083	ENSG00000133083	DCLK1	13:36345477-36705443	OK	17.3996	16.798	-0.0507613	-0.105552	0.8585	0.9998
ENSG00000133641	ENSG00000133641	C12orf29	12:88373815-88535993	OK	18.6554	17.6415	-0.0806216	-0.1032	0.8585	0.9998
ENSG00000034693	ENSG00000034693	PEX3	6:143771943-143832827	OK	8.71376	9.70965	0.156125	0.0833293	0.85855	0.9998
ENSG00000011485	ENSG00000011485	PPP5C	19:46850250-46896238	OK	42.8105	41.3962	-0.0484658	-0.100137	0.8586	0.9998
ENSG00000130956	ENSG00000130956	HABP4	9:99212482-99382112	OK	33.9987	35.2713	0.0530138	0.111244	0.85865	0.9998
ENSG00000145555	ENSG00000145555	MYO10	5:16665394-16936372	OK	207.873	200.823	-0.0497791	-0.0984228	0.85865	0.9998
ENSG00000163291	ENSG00000163291	PAQR3	4:79697495-79860592	OK	15.1178	16.0367	0.0851271	0.0980838	0.8588	0.9998
ENSG00000235238	ENSG00000235238	SUMO2P1	6:29603836-29604120	OK	20.4669	21.5899	0.0770612	0.108866	0.8588	0.9998
ENSG00000267534	ENSG00000267534	S1PR2	19:10244020-10341962	OK	3.09879	4.12	0.410939	0.148489	0.85885	0.9998
ENSG00000114648	ENSG00000114648	KLHL18	3:47205986-47388306	OK	16.5516	18.0183	0.122497	0.110278	0.8589	0.9998
ENSG00000141873	ENSG00000141873	SLC39A3	19:2714564-2740150	OK	39.1123	41.2983	0.0784598	0.11124	0.8589	0.9998
ENSG00000164463	ENSG00000164463	CREBRF	5:172483354-172566291	OK	5.68452	5.40712	-0.0721776	-0.0849634	0.859	0.9998
ENSG00000196189	ENSG00000196189	SEMA4A	1:156117156-156147543	OK	1.02195	0.964895	-0.0828837	-0.0721931	0.85905	0.9998
ENSG00000235043	ENSG00000235043	TECRP1	4:87797357-88062206	OK	96.6046	91.3926	-0.0800146	-0.110429	0.85905	0.9998
ENSG00000143434	ENSG00000143434	SEMA6C	1:151104160-151119104	OK	1.89597	1.77666	-0.0937652	-0.0717839	0.85915	0.9998
ENSG00000198911	ENSG00000198911	SREBF2	22:42227218-42303312	OK	80.7203	83.1503	0.0427901	0.0839942	0.85915	0.9998
ENSG00000023909	ENSG00000023909	GCLM	1:94350760-94374966	OK	8.58531	9.18414	0.0972754	0.102785	0.8592	0.9998
ENSG00000129566	ENSG00000129566	TEP1	14:20833825-20881588	OK	3.63778	3.44925	-0.076774	-0.078998	0.8592	0.9998
ENSG00000137054	ENSG00000137054	POLR1E	9:37485931-37503694	OK	19.1656	19.8193	0.0483853	0.108728	0.8592	0.9998
ENSG00000029363	ENSG00000029363	BCLAF1	6:136578000-136610989	OK	20.4985	21.4447	0.0651004	0.085968	0.85925	0.9998
ENSG00000161298	ENSG00000161298	ZNF382	19:37001596-37119499	OK	2.89564	3.17008	0.130637	0.0745263	0.8593	0.9998
ENSG00000226784	ENSG00000226784	PGAM4	X:77166193-77305892	OK	5.88506	5.43006	-0.116089	-0.110274	0.85945	0.9998
ENSG00000184557	ENSG00000184557	SOCS3	17:76352863-76356158	OK	9.66538	9.31914	-0.0526296	-0.105805	0.8595	0.9998
ENSG00000247796	ENSG00000247796	CTD-2366F13.1	5:52391508-52410956	OK	1.59854	1.31615	-0.280431	-0.14155	0.8595	0.9998
ENSG00000117115	ENSG00000117115	PADI2	1:17393255-17445948	OK	0.660091	0.711938	0.109086	0.0970847	0.85955	0.9998
ENSG00000183340	ENSG00000183340	JRKL	11:96123152-96240738	OK	2.57501	2.46868	-0.0608405	-0.104909	0.85955	0.9998
ENSG00000100029	ENSG00000100029	PES1	22:30972611-31023265	OK	46.9919	48.5872	0.0481664	0.100204	0.85965	0.9998
ENSG00000136104	ENSG00000136104	RNASEH2B	13:51450821-51544592	OK	28.1098	27.159	-0.0496432	-0.100819	0.85965	0.9998
ENSG00000147421	ENSG00000147421	HMBOX1	8:28747910-28922281	OK	10.0339	9.52999	-0.0743299	-0.100825	0.8597	0.9998
ENSG00000188191	ENSG00000188191	PRKAR1B	7:588833-829190	OK	5.94275	6.59148	0.149472	0.106418	0.85975	0.9998
ENSG00000105880	ENSG00000105880	DLX5	7:96649703-96654409	OK	1.42489	1.34384	-0.0844898	-0.0988096	0.8598	0.9998
ENSG00000156298	ENSG00000156298	TSPAN7	X:37208527-38548169	OK	1.58883	1.33393	-0.252282	-0.0678076	0.8598	0.9998
ENSG00000081721	ENSG00000081721	DUSP12	1:161719547-161727028	OK	48.2403	46.6091	-0.0496263	-0.102987	0.8599	0.9998
ENSG00000179222	ENSG00000179222	MAGED1	X:51546102-51645453	OK	37.495	36.3351	-0.0453349	-0.0953426	0.8599	0.9998
ENSG00000110429	ENSG00000110429	FBXO3	11:33762484-33796089	OK	20.1148	19.3962	-0.0524898	-0.090491	0.85995	0.9998
ENSG00000236104	ENSG00000236104	ZBTB22	6:33282182-33285719	OK	5.97348	6.20204	0.0541698	0.104775	0.86005	0.9998
ENSG00000182197	ENSG00000182197	EXT1	8:118806728-119124092	OK	17.9705	17.0695	-0.0742025	-0.10675	0.86015	0.9998
ENSG00000041802	ENSG00000041802	LSG1	3:194304739-194393206	OK	31.3938	30.2765	-0.0522776	-0.0782798	0.8602	0.9998
ENSG00000257026	ENSG00000257026	AC040173.1	16:14165177-14360630	OK	0.809943	0.587765	-0.462581	-0.153137	0.8602	0.9998
ENSG00000125166	ENSG00000125166	GOT2	16:58741034-59142878	OK	34.5254	35.5524	0.0422891	0.102024	0.86025	0.9998
ENSG00000168564	ENSG00000168564	CDKN2AIP	4:184365743-184369351	OK	2.98406	3.12044	0.0644736	0.0978463	0.86025	0.9998
ENSG00000139971	ENSG00000139971	C14orf37	14:58466452-58764857	OK	10.3311	11.212	0.118048	0.0850919	0.8603	0.9998
ENSG00000186951	ENSG00000186951	PPARA	22:46546423-46639653	OK	10.5346	10.061	-0.0663609	-0.0625017	0.8604	0.9998
ENSG00000165898	ENSG00000165898	ISCA2	14:74942894-74963809	OK	27.2293	24.4431	-0.155729	-0.0985997	0.8606	0.9998
ENSG00000248594	ENSG00000248594	AC003029.1	12:112277570-112334343	OK	4.33351	3.51543	-0.301834	-0.135082	0.8607	0.9998
ENSG00000110328	ENSG00000110328	GALNT18	11:11292422-11643552	OK	3.42656	3.18317	-0.106296	-0.109527	0.86075	0.9998
ENSG00000144647	ENSG00000144647	POMGNT2	3:43120723-43147568	OK	18.0713	17.5017	-0.0462102	-0.10579	0.86075	0.9998
ENSG00000145337	ENSG00000145337	PYURF	4:89442135-89629693	OK	85.8636	82.9633	-0.0495733	-0.103177	0.8608	0.9998
ENSG00000108106	ENSG00000108106	UBE2S	19:55896712-55919145	OK	232.393	244.71	0.074509	0.10033	0.86085	0.9998
ENSG00000139133	ENSG00000139133	ALG10	12:34175215-34209675	OK	2.76854	2.58699	-0.0978522	-0.110714	0.86085	0.9998
ENSG00000242802	ENSG00000242802	AP5Z1	7:4815252-4833943	OK	15.8783	15.3348	-0.0502439	-0.0927097	0.86085	0.9998
ENSG00000213058	ENSG00000213058	RP4-765C7.2	1:178060642-178448644	OK	2.71269	2.16915	-0.322594	-0.0688243	0.86095	0.9998
ENSG00000254858	ENSG00000254858	MPV17L2	19:18303991-18314884	OK	17.6005	18.8136	0.0961585	0.0985189	0.86095	0.9998
ENSG00000132024	ENSG00000132024	CC2D1A	19:13993160-14041692	OK	15.1347	15.716	0.054376	0.0900609	0.86105	0.9998
ENSG00000196655	ENSG00000196655	TRAPPC4	11:118868851-118901616	OK	24.4556	22.3234	-0.131607	-0.0737488	0.8611	0.9998
ENSG00000228589	ENSG00000228589	SPCS2P4	1:28421581-28422933	OK	48.8671	47.1945	-0.0502439	-0.107813	0.8611	0.9998
ENSG00000160194	ENSG00000160194	NDUFV3	21:44299753-44333414	OK	10.2935	10.7087	0.0570565	0.104671	0.8612	0.9998
ENSG00000213672	ENSG00000213672	NCKIPSD	3:48701208-48723797	OK	20.9379	20.2538	-0.0479261	-0.0932706	0.8612	0.9998
ENSG00000182963	ENSG00000182963	GJC1	17:42875815-42908184	OK	17.2753	17.9751	0.0572862	0.0917265	0.8613	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000115484	ENSG00000115484	CCT4	2:62095223-62374382	OK	201.608	207.858	0.0440474	0.0964667	0.8614	0.9998
ENSG00000185658	ENSG00000185658	BRWD1	21:40556101-40695144	OK	3.70998	3.55307	-0.0623456	-0.0805725	0.8615	0.9998
ENSG00000164535	ENSG00000164535	DAGLB	7:6448756-6524873	OK	4.5596	5.06181	0.150746	0.0832604	0.8616	0.9998
ENSG00000257218	ENSG00000257218	GATC	12:120875892-120899389	OK	13.6836	15.1303	0.144987	0.0990934	0.8616	0.9998
ENSG00000165355	ENSG00000165355	FBXO33	14:39866872-39901704	OK	7.84117	8.12357	0.0510443	0.0891463	0.86165	0.9998
ENSG00000166507	ENSG00000166507	NDST2	10:75545339-75571589	OK	8.30257	8.91087	0.102008	0.0568177	0.8617	0.9998
ENSG00000186496	ENSG00000186496	ZNF396	18:32946660-32957301	OK	1.34706	1.27677	-0.0773209	-0.0988838	0.8617	0.9998
ENSG00000132670	ENSG00000132670	PTPRA	20:2815959-3019722	OK	19.1271	18.2282	-0.0694464	-0.0968575	0.86175	0.9998
ENSG00000213020	ENSG00000213020	ZNF611	19:53206065-53238326	OK	2.94536	2.7775	-0.0846546	-0.075167	0.86175	0.9998
ENSG00000273179	ENSG00000273179	RP11-20I20.4	4:1160719-1202750	OK	15.9933	11.7171	-0.448859	-0.139725	0.86175	0.9998
ENSG00000079459	ENSG00000079459	FDFT1	8:11653081-11696818	OK	268.713	276.947	0.0435468	0.100253	0.86185	0.9998
ENSG00000165704	ENSG00000165704	HPRT1	X:133594182-133654543	OK	27.2427	28.1539	0.0474649	0.102636	0.86185	0.9998
ENSG00000259086	ENSG00000259086	RP11-134E15.2	14:32741060-32741510	OK	2.92734	2.73292	-0.0991471	-0.107169	0.862	0.9998
ENSG00000163467	ENSG00000163467	TSACC	1:156278758-156337664	OK	1.26814	1.12436	-0.173605	-0.0102715	0.8621	0.9998
ENSG00000220023	ENSG00000220023	AL592183.1	GL000219.1:53830-99642	OK	4.44608	4.66103	0.068114	0.106802	0.8621	0.9998
ENSG00000264281	ENSG00000264281	CTD-2031P19.4	5:55230922-55290821	OK	1.13574	1.39395	0.295547	0.0307773	0.8623	0.9998
ENSG00000271833	ENSG00000271833	RP11-356B19.11	9:129986543-130155939	OK	0.957498	1.17064	0.289957	0.133196	0.8623	0.9998
ENSG00000177548	ENSG00000177548	RABEP2	16:28889725-28950667	OK	7.8284	8.23189	0.0725066	0.0925687	0.86245	0.9998
ENSG00000230154	ENSG00000230154	AC018463.4	2:11319886-11488456	OK	5.23874	4.35714	-0.265839	-0.109307	0.86245	0.9998
ENSG00000198598	ENSG00000198598	MMP17	12:132312937-132336328	OK	104.912	109.377	0.0601273	0.106331	0.8625	0.9998
ENSG00000067596	ENSG00000067596	DHX8	17:41561232-41687706	OK	31.3551	29.8864	-0.0692104	-0.0660781	0.8626	0.9998
ENSG00000160679	ENSG00000160679	CHTOP	1:153591262-153618782	OK	56.9191	62.7752	0.141283	0.0970636	0.86265	0.9998
ENSG00000088305	ENSG00000088305	DNMT3B	20:31350190-31397162	OK	1.82428	1.90245	0.0605292	0.101155	0.86275	0.9998
ENSG00000233384	ENSG00000233384	RP11-100E13.1	1:224572844-224928251	OK	0.867049	1.0992	0.342272	0.0224276	0.86275	0.9998
ENSG00000269131	ENSG00000269131	AC004447.2	19:19101696-19170563	OK	10.4029	9.60401	-0.115276	-0.105999	0.86275	0.9998
ENSG00000272994	ENSG00000272994	RP11-332H14.2	2:105950483-105965668	OK	0.729671	0.613342	-0.250554	-0.126338	0.8628	0.9998
ENSG00000099814	ENSG00000099814	CEP170B	14:105331616-105363107	OK	12.8604	12.4678	-0.0447251	-0.0864233	0.8629	0.9998
ENSG00000101150	ENSG00000101150	TPD52L2	20:62496595-62522898	OK	68.7414	70.7656	0.04187	0.102447	0.8629	0.9998
ENSG00000203288	ENSG00000203288	RP11-98D18.9	1:151728016-151766878	OK	1.21183	1.44095	0.249839	0.0532077	0.86295	0.9998
ENSG00000158887	ENSG00000158887	MPZ	1:161274524-161279762	OK	1.07637	1.14996	0.0954106	0.0877329	0.86325	0.9998
ENSG00000172428	ENSG00000172428	MYEOV2	2:241065979-241076224	OK	206.548	200.324	-0.044142	-0.103803	0.86325	0.9998
ENSG00000230499	ENSG00000230499	AC108463.1	2:111953539-112268567	OK	2.24907	2.81213	0.322332	0.0748935	0.86325	0.9998
ENSG00000089289	ENSG00000089289	IGBP1	X:69353298-69386174	OK	58.3461	56.5856	-0.0442004	-0.107208	0.86335	0.9998
ENSG00000112855	ENSG00000112855	HARS2	5:140044260-140086248	OK	27.8701	26.3042	-0.0834281	-0.0896776	0.8634	0.9998
ENSG00000121406	ENSG00000121406	ZNF549	19:58038692-58071231	OK	2.64107	2.51258	-0.0719513	-0.0881225	0.86345	0.9998
ENSG00000124222	ENSG00000124222	STX16	20:57226327-57294294	OK	60.4508	62.3139	0.0437928	0.0719821	0.86345	0.9998
ENSG00000128563	ENSG00000128563	PRKRIP1	7:102004318-102067123	OK	15.8925	15.3209	-0.0528505	-0.102433	0.8635	0.9998
ENSG00000150459	ENSG00000150459	SAP18	13:21714652-21723221	OK	111.836	116.778	0.0623902	0.106952	0.8635	0.9998
ENSG00000083814	ENSG00000083814	ZNF671	19:58193336-58269527	OK	1.34812	1.46417	0.119125	0.0868165	0.86355	0.9998
ENSG00000180198	ENSG00000180198	RCC1	1:28832454-28865812	OK	18.8674	18.0596	-0.0631269	-0.103697	0.86355	0.9998
ENSG00000099381	ENSG00000099381	SETD1A	16:30968614-30996437	OK	4.2552	4.42565	0.0566618	0.0888119	0.8636	0.9998
ENSG00000105705	ENSG00000105705	SUGP1	19:19386826-19469563	OK	17.7378	16.6752	-0.0891208	-0.0959823	0.8636	0.9998
ENSG00000185745	ENSG00000185745	IFIT1	10:90973325-91174314	OK	2.7098	2.22674	-0.283255	-0.12379	0.8636	0.9998
ENSG00000250397	ENSG00000250397	RP11-1391J7.1	11:842807-867116	OK	1.07909	1.32627	0.297557	0.11586	0.8636	0.9998
ENSG00000181350	ENSG00000181350	FAM211A	17:16342135-16395467	OK	2.41678	2.73151	0.176611	0.0358282	0.86365	0.9998
ENSG00000141441	ENSG00000141441	GAREM	18:29598334-30050447	OK	2.19682	1.88075	-0.224113	-0.0845558	0.8637	0.9998
ENSG00000241990	ENSG00000241990	RP6-109B7.3	22:46445357-46509808	OK	23.4036	24.5643	0.0698364	0.104127	0.86375	0.9998
ENSG00000167721	ENSG00000167721	TSR1	17:1963132-2284352	OK	21.5613	22.5127	0.0622958	0.075393	0.8638	0.9998
ENSG00000114770	ENSG00000114770	ABCC5	3:183637721-183735803	OK	21.0594	20.3492	-0.0494958	-0.0826345	0.86385	0.9998
ENSG00000215193	ENSG00000215193	PEX26	22:18559292-18629321	OK	28.4083	27.063	-0.0699924	-0.101335	0.864	0.9998
ENSG00000254064	ENSG00000254064	CTD-2530N21.4	8:22102616-22132675	OK	1.37694	1.75406	0.349239	0.0863509	0.86405	0.9998
ENSG00000102900	ENSG00000102900	NUP93	16:56764016-56878797	OK	20.8177	21.467	0.0443139	0.0770599	0.8641	0.9998
ENSG00000127080	ENSG00000127080	IPPK	9:95059639-95432547	OK	8.45155	9.16227	0.116489	0.107648	0.8641	0.9998
ENSG00000273439	ENSG00000273439	ZNF8	19:58739959-58827023	OK	1.65671	1.33825	-0.307976	-0.149373	0.86415	0.9998
ENSG00000099960	ENSG00000099960	SLC7A4	22:21353392-21399306	OK	3.81016	4.1172	0.111812	0.101453	0.86425	0.9998
ENSG00000102078	ENSG00000102078	SLC25A14	X:129473873-129507335	OK	15.1958	14.504	-0.0672248	-0.1083	0.8643	0.9998
ENSG00000250786	ENSG00000250786	SNHG18	5:9546311-9550721	OK	15.593	16.1931	0.0544806	0.101756	0.8643	0.9998
ENSG00000170421	ENSG00000170421	KRT8	12:53290976-53346686	OK	1.65582	1.49646	-0.145991	-0.0556861	0.86445	0.9998
ENSG00000198876	ENSG00000198876	DCAF12	9:34084329-34127397	OK	20.429	21.0483	0.0430869	0.0948993	0.86445	0.9998
ENSG00000143294	ENSG00000143294	PRCC	1:156711898-156770607	OK	53.5413	58.3793	0.124804	0.0723237	0.8645	0.9998
ENSG00000152520	ENSG00000152520	PAN3	13:28712642-28869475	OK	8.36202	8.09484	-0.0468485	-0.0998831	0.8645	0.9998
ENSG00000073331	ENSG00000073331	ALPK1	4:113195697-113363776	OK	2.19182	2.34172	0.0954352	0.0619262	0.86455	0.9998
ENSG00000123374	ENSG00000123374	CDK2	12:56347888-56367101	OK	1035.65	1147.04	0.147369	0.0252047	0.86455	0.9998
ENSG00000101888	ENSG00000101888	NXT2	X:108779009-108787919	OK	9.00624	8.67917	-0.0533673	-0.105123	0.8646	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000243811	ENSG00000243811	APOBEC3D	22:39410087-39429281	OK	1.34491	1.09225	-0.300207	-0.0817492	0.8646	0.9998
ENSG00000082701	ENSG00000082701	GSK3B	3:119540169-119813264	OK	28.5485	27.3374	-0.0625409	-0.0862248	0.86465	0.9998
ENSG00000213139	ENSG00000213139	CRYGS	3:186256229-186315061	OK	1.84167	1.589	-0.212897	-0.0499114	0.8647	0.9998
ENSG00000228989	ENSG00000228989	AC133528.2	2:242629828-242633704	OK	2.78197	2.98771	0.102934	0.106755	0.86475	0.9998
ENSG00000163882	ENSG00000163882	POLR2H	3:183851806-184402546	OK	130.134	115.61	-0.170729	-0.0716657	0.8648	0.9998
ENSG00000148935	ENSG00000148935	GAS2	11:22644078-22834601	OK	6.19444	5.62768	-0.138432	-0.0602931	0.86485	0.9998
ENSG00000187713	ENSG00000187713	TMEM203	9:140086068-140100090	OK	20.2489	21.2643	0.0705912	0.0999659	0.86495	0.9998
ENSG00000228519	ENSG00000228519	RP11-298C3.2	X:25663838-25664444	OK	21.3093	22.1615	0.0565768	0.102016	0.86495	0.9998
ENSG00000239415	ENSG00000239415	AP001469.9	21:47649130-47706211	OK	1.01141	0.820965	-0.300971	-0.0865285	0.86495	0.9998
ENSG00000171456	ENSG00000171456	ASXL1	20:30946154-31027122	OK	63.0122	59.0991	-0.0924962	-0.0717761	0.865	0.9998
ENSG00000148300	ENSG00000148300	REXO4	9:136243116-136324508	OK	17.7585	17.1929	-0.0466911	-0.0988427	0.86525	0.9998
ENSG00000175938	ENSG00000175938	ORAI3	16:30930639-30967832	OK	9.81459	9.29894	-0.0778615	-0.100362	0.86525	0.9998
ENSG00000168175	ENSG00000168175	MAPK1IP1L	14:55518348-55536910	OK	57.922	61.9402	0.0967643	0.10885	0.8653	0.9998
ENSG00000226360	ENSG00000226360	RPL10AP6	3:61547242-62355005	OK	2.26348	3.05967	0.434831	0.118848	0.86535	0.9998
ENSG00000170270	ENSG00000170270	C14orf142	14:93651295-93695561	OK	7.58532	6.43747	-0.236717	-0.110185	0.86545	0.9998
ENSG00000198270	ENSG00000198270	TMEM116	12:112369085-112450970	OK	2.24765	2.13006	-0.077519	-0.0721258	0.86545	0.9998
ENSG00000232336	ENSG00000232336	RP11-782C8.3	1:143118703-143240439	OK	1.59693	1.24447	-0.359762	-0.113732	0.86545	0.9998
ENSG00000249341	ENSG00000249341	RP11-317M11.1	4:54243809-55164414	OK	3.55185	2.94332	-0.271124	-0.14757	0.86555	0.9998
ENSG00000175611	ENSG00000175611	LINC00476	9:98521512-98776842	OK	0.842805	0.741093	-0.185544	-0.0729326	0.8656	0.9998
ENSG00000271895	ENSG00000271895	RP4-635E18.8	1:11086579-11107290	OK	0.796142	0.726609	-0.131847	-0.101351	0.8656	0.9998
ENSG00000042753	ENSG00000042753	AP2S1	19:47341392-47354249	OK	125.039	128.952	0.044456	0.101598	0.86565	0.9998
ENSG00000105793	ENSG00000105793	GTPBP10	7:89964536-90839905	OK	17.8544	19.4912	0.126545	0.100067	0.8657	0.9998
ENSG00000169507	ENSG00000169507	SLC38A11	2:165752695-165812035	OK	1.38463	1.30238	-0.0883594	-0.0813288	0.8657	0.9998
ENSG00000256053	ENSG00000256053	APOPT1	14:104019757-104181841	OK	41.7821	37.6531	-0.150117	-0.0977244	0.8658	0.9998
ENSG00000100196	ENSG00000100196	KDELR3	22:38864066-38903665	OK	17.7837	19.7722	0.152919	0.0848562	0.86605	0.9998
ENSG00000152904	ENSG00000152904	GGPS1	1:235294497-235507847	OK	19.7886	21.1552	0.0963405	0.101131	0.86605	0.9998
ENSG00000163364	ENSG00000163364	LINC01116	2:177494316-177520686	OK	7.86852	7.56089	-0.0575373	-0.103601	0.8661	0.9998
ENSG00000167216	ENSG00000167216	KATNAL2	18:44388352-44627658	OK	3.65053	4.07124	0.157361	0.0799813	0.8661	0.9998
ENSG00000078140	ENSG00000078140	UBE2K	4:39699663-39784412	OK	39.6355	37.6354	-0.0747037	-0.101913	0.86615	0.9998
ENSG00000168118	ENSG00000168118	RAB4A	1:229394027-229441641	OK	40.6715	38.9081	-0.0639504	-0.105394	0.86615	0.9998
ENSG00000242294	ENSG00000242294	STAG3L5P	7:99905324-99997719	OK	14.2294	13.0307	-0.126956	-0.107697	0.86615	0.9998
ENSG00000260276	ENSG00000260276	RP11-77H9.2	16:8768421-8962866	OK	0.85303	0.619534	-0.461413	-0.157755	0.86615	0.9998
ENSG00000117410	ENSG00000117410	ATP6V0B	1:44440158-44443967	OK	131.243	135.11	0.0418954	0.100349	0.8662	0.9998
ENSG00000175575	ENSG00000175575	PAAF1	11:73583711-73638790	OK	17.6637	16.7857	-0.0735506	-0.097323	0.8662	0.9998
ENSG00000136908	ENSG00000136908	DPM2	9:130696781-130742792	OK	35.0391	32.7907	-0.095679	-0.102521	0.86625	0.9998
ENSG00000241769	ENSG00000241769	LINC00893	X:148558520-148632055	OK	0.882579	0.949583	0.10557	0.0195524	0.86625	0.9998
ENSG00000184076	ENSG00000184076	UQCR10	22:30163357-30166402	OK	108.176	111.61	0.0450838	0.10276	0.8663	0.9998
ENSG00000132329	ENSG00000132329	RAMP1	2:238767535-238820756	OK	2.99466	2.83768	-0.0776774	-0.103201	0.86645	0.9998
ENSG00000132781	ENSG00000132781	MUTYH	1:45794834-45956872	OK	5.42217	5.72684	0.0788703	0.0473418	0.86645	0.9998
ENSG00000092445	ENSG00000092445	TYRO3	15:41849872-41871536	OK	25.8359	26.6103	0.0426096	0.0954891	0.8665	0.9998
ENSG00000116871	ENSG00000116871	MAP7D1	1:36621179-36646450	OK	30.2509	31.2563	0.0471698	0.0912682	0.8665	0.9998
ENSG00000145414	ENSG00000145414	NAF1	4:164029936-164088073	OK	4.65521	4.4642	-0.0604434	-0.0974049	0.8665	0.9998
ENSG00000228106	ENSG00000228106	RP11-452F19.3	1:222988363-223179337	OK	25.2057	23.9859	-0.0715634	-0.106108	0.8665	0.9998
ENSG00000169905	ENSG00000169905	TOR1AIP2	1:179809101-179846938	OK	21.1112	22.2707	0.0771363	0.100148	0.86665	0.9998
ENSG00000175221	ENSG00000175221	MED16	19:867961-893218	OK	13.9959	13.5478	-0.0469414	-0.089872	0.86675	0.9998
ENSG00000198001	ENSG00000198001	IRAK4	12:44152746-44183346	OK	8.57657	8.8853	0.0510196	0.0833679	0.86675	0.9998
ENSG00000152192	ENSG00000152192	POU4F1	13:78469615-79233314	OK	0.548188	0.663429	0.27527	0.0387843	0.86685	0.9998
ENSG00000013503	ENSG00000013503	POLR3B	12:106751435-107283090	OK	5.15816	5.41706	0.0706517	0.0973084	0.867	0.9998
ENSG00000163807	ENSG00000163807	KIAA1143	3:44779152-44803154	OK	13.2795	12.3312	-0.106894	-0.101387	0.867	0.9998
ENSG00000164815	ENSG00000164815	ORC5	7:103766787-103848495	OK	16.101	16.6341	0.0469949	0.0997438	0.867	0.9998
ENSG00000073614	ENSG00000073614	KDM5A	12:389294-551811	OK	12.1629	12.6641	0.0582478	0.0558411	0.86715	0.9998
ENSG00000150760	ENSG00000150760	DOCK1	10:128593977-129250781	OK	16.2862	16.7655	0.0418402	0.0619706	0.8672	0.9998
ENSG00000164442	ENSG00000164442	CITED2	6:139693392-139695757	OK	8.9103	8.59542	-0.0519055	-0.0999989	0.8673	0.9998
ENSG00000099783	ENSG00000099783	HNRNPM	19:8509650-8553998	OK	108.304	104.987	-0.0448777	-0.099358	0.86735	0.9998
ENSG00000163704	ENSG00000163704	PRRT3	3:9987225-9996471	OK	0.66482	0.70574	0.0861733	0.100267	0.86735	0.9998
ENSG00000260853	ENSG00000260853	RP11-264B17.2	16:28962127-28978418	OK	1.44399	1.15394	-0.32349	-0.0787856	0.86735	0.9998
ENSG00000163462	ENSG00000163462	TRIM46	1:155141883-155162707	OK	2.61091	2.95174	0.177012	0.117315	0.8675	0.9998
ENSG00000108588	ENSG00000108588	CCDC47	17:61780191-61896677	OK	61.17	58.4451	-0.0657427	-0.100354	0.86765	0.9998
ENSG00000135185	ENSG00000135185	TMEM243	7:86780738-86849903	OK	10.7281	11.6196	0.115172	0.0959722	0.86775	0.9998
ENSG00000089234	ENSG00000089234	BRAP	12:112079949-112123790	OK	10.737	11.1167	0.050147	0.0992913	0.8678	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000255857	ENSG00000255857	PXN-AS1	12:120639093-120703574	OK	8.97147	7.90132	-0.183251	-0.0663339	0.8678	0.9998
ENSG00000250318	ENSG00000250318	CTA-963H5.5	22:31031638-31065003	OK	1.17874	0.886977	-0.410273	-0.129796	0.8679	0.9998
ENSG00000196268	ENSG00000196268	ZNF493	19:21579920-21752039	OK	1.34886	1.44921	0.103523	0.0817903	0.86795	0.9998
ENSG00000272520	ENSG00000272520	CTD-2044J15.2	5:6671218-6674499	OK	3.48423	3.35803	-0.0532254	-0.100234	0.86795	0.9998
ENSG00000165672	ENSG00000165672	PRDX3	10:120927214-120938345	OK	132.416	128.647	-0.0416562	-0.104079	0.868	0.9998
ENSG00000180900	ENSG00000180900	SCRIB	8:144873089-144897549	OK	25.1436	24.4296	-0.041558	-0.0639977	0.868	0.9998
ENSG00000224126	ENSG00000224126	UBE2SP2	17:18538318-18585575	OK	87.275	83.3263	-0.0667971	-0.104315	0.868	0.9998
ENSG00000137496	ENSG00000137496	IL18BP	11:71709586-71823826	OK	1.75074	1.95302	0.157744	0.0411009	0.86805	0.9998
ENSG00000254682	ENSG00000254682	RP11-660L16.2	11:71139238-71163914	OK	1.88249	1.53517	-0.29424	-0.0599926	0.86805	0.9998
ENSG00000148337	ENSG00000148337	CIZ1	9:130928342-131017527	OK	47.8202	49.1538	0.039683	0.0762265	0.8681	0.9998
ENSG00000071894	ENSG00000071894	CPSF1	8:145596789-145634753	OK	29.6959	30.8827	0.0565361	0.078733	0.8682	0.9998
ENSG00000231607	ENSG00000231607	DLEU2	13:50601268-51423190	OK	7.91672	8.48079	0.0992961	0.100217	0.8682	0.9998
ENSG00000241697	ENSG00000241697	TMEFF1	9:103189437-103339918	OK	3.43012	4.01688	0.227818	0.115876	0.8682	0.9998
ENSG00000147912	ENSG00000147912	FBXO10	9:37510888-38069210	OK	6.42849	5.90605	-0.122286	-0.0589345	0.8684	0.9998
ENSG00000214717	ENSG00000214717	ZBED1	X:2137556-2420846	OK	3.91447	3.69132	-0.0846792	-0.100063	0.86855	0.9998
ENSG00000197119	ENSG00000197119	SLC25A29	14:100673743-100772884	OK	31.7263	30.2611	-0.0682115	-0.0553571	0.8686	0.9998
ENSG00000177733	ENSG00000177733	HNRNPA0	5:137087074-137090039	OK	34.5878	35.5934	0.0413446	0.102125	0.86865	0.9998
ENSG00000183458	ENSG00000183458	RP11-958N24.1	16:15005407-15045915	OK	1.88564	1.76839	-0.0926218	-0.0931321	0.86865	0.9998
ENSG00000250846	ENSG00000250846	RP11-807H7.1	4:66185280-66563747	OK	2.61373	2.23186	-0.227867	-0.0846187	0.86865	0.9998
ENSG00000132017	ENSG00000132017	DCAF15	19:14041999-14072254	OK	15.1373	14.5357	-0.0585065	-0.0926913	0.8687	0.9998
ENSG00000173442	ENSG00000173442	EHBP1L1	11:65343508-65360121	OK	17.2309	17.7452	0.0424252	0.0876077	0.8687	0.9998
ENSG00000132485	ENSG00000132485	ZRANB2	1:71514537-71546980	OK	28.0405	27.2208	-0.0428019	-0.0846687	0.86875	0.9998
ENSG00000261351	ENSG00000261351	CTD-3185P2.1	15:66679154-66790151	OK	1.31216	1.75084	0.4161	0.12797	0.86875	0.9998
ENSG00000171861	ENSG00000171861	RNMTL1	17:660336-695749	OK	13.3224	14.0532	0.0770408	0.0937752	0.8688	0.9998
ENSG00000230982	ENSG00000230982	DSTNP1	21:48055078-48085036	OK	1.37537	1.70429	0.309351	0.0583301	0.8688	0.9998
ENSG00000100147	ENSG00000100147	CCDC134	22:42196682-42222303	OK	3.96391	3.79486	-0.0628799	-0.0978051	0.8689	0.9998
ENSG00000226268	ENSG00000226268	RP11-61N20.3	11:49455024-49455990	OK	6.66288	6.94169	0.0591405	0.0982855	0.86895	0.9998
ENSG00000005007	ENSG00000005007	UPF1	19:18942746-18979045	OK	18.0484	17.537	-0.0414719	-0.0783989	0.869	0.9998
ENSG00000089022	ENSG00000089022	MAPKAPK5	12:112277570-112334343	OK	27.645	26.646	-0.0530989	-0.0953415	0.869	0.9998
ENSG00000254469	ENSG00000254469	RP11-849H4.2	11:71576554-71639700	OK	1.15138	1.06628	-0.110773	-0.0910639	0.869	0.9998
ENSG00000106089	ENSG00000106089	STX1A	7:73095298-73134002	OK	4.44258	4.86693	0.131613	0.051601	0.86905	0.9998
ENSG00000112031	ENSG00000112031	MTRF1L	6:153304884-153323820	OK	10.0099	9.67224	-0.0495048	-0.0886215	0.86905	0.9998
ENSG00000167981	ENSG00000167981	ZNF597	16:3415098-3627401	OK	1.31682	1.52851	0.215062	0.0912073	0.8691	0.9998
ENSG00000169189	ENSG00000169189	NSMCE1	16:27236311-27301813	OK	31.7137	30.6695	-0.0483027	-0.0980969	0.8691	0.9998
ENSG00000157353	ENSG00000157353	FUK	16:70488323-70514177	OK	3.03507	2.89081	-0.0702522	-0.0764821	0.86915	0.9998
ENSG00000174442	ENSG00000174442	ZWILCH	15:66790354-66858317	OK	15.4387	13.5176	-0.191705	-0.0497065	0.8692	0.9998
ENSG00000233796	ENSG00000233796	AC089999.1	12:113587662-113623284	OK	2.0094	2.55846	0.348513	0.0608941	0.86935	0.9998
ENSG00000129518	ENSG00000129518	EAPP	14:34985134-35008916	OK	17.5593	18.1457	0.0473905	0.098862	0.8694	0.9998
ENSG00000139915	ENSG00000139915	MDGA2	14:47308825-48144157	OK	2.43608	2.55266	0.0674401	0.0734013	0.8694	0.9998
ENSG00000129351	ENSG00000129351	ILF3	19:10764936-10803093	OK	84.657	87.3248	0.0447616	0.0856883	0.86945	0.9998
ENSG00000137492	ENSG00000137492	PRKRIR	11:76060999-76092015	OK	19.3506	18.7344	-0.0466928	-0.082807	0.86945	0.9998
ENSG00000186326	ENSG00000186326	RGS9BP	19:33087912-33169206	OK	0.840822	0.641876	-0.389506	-0.137404	0.86945	0.9998
ENSG00000244560	ENSG00000244560	RP4-800G7.2	7:148959261-148994403	OK	3.54212	3.09223	-0.195968	-0.0803662	0.86945	0.9998
ENSG00000181722	ENSG00000181722	ZBTB20	3:114056940-114866118	OK	0.696495	0.736534	0.080639	0.0472171	0.8695	0.9998
ENSG00000196796	ENSG00000196796	CTB-134H23.2	16:29049922-29064047	OK	0.870207	0.820294	-0.0852184	-0.0968567	0.8695	0.9998
ENSG00000178163	ENSG00000178163	ZNF518B	4:10441497-10459034	OK	3.0351	3.15776	0.0571601	0.0719169	0.86965	0.9998
ENSG00000104635	ENSG00000104635	SLC39A14	8:22224761-22291642	OK	38	39.0224	0.0383032	0.0801716	0.86985	0.9998
ENSG00000138433	ENSG00000138433	CIR1	2:175212749-175260443	OK	14.765	14.2083	-0.0554486	-0.089395	0.8699	0.9998
ENSG00000175203	ENSG00000175203	DCTN2	12:57914492-57941114	OK	129.98	125.331	-0.0525456	-0.0921853	0.8699	0.9998
ENSG00000169223	ENSG00000169223	LMAN2	5:176758562-176778853	OK	147.881	143.113	-0.0472838	-0.0959612	0.86995	0.9998
ENSG00000170310	ENSG00000170310	STX8	17:9153787-9479908	OK	83.2426	80.5842	-0.0468254	-0.0998902	0.86995	0.9998
ENSG00000143549	ENSG00000143549	TPM3	1:154127783-154167124	OK	465.796	482.303	0.0502413	0.100278	0.87005	0.9998
ENSG00000104213	ENSG00000104213	PDGFRL	8:17433941-17658426	OK	1.13281	0.912241	-0.312415	-0.0959697	0.87015	0.9998
ENSG00000221947	ENSG00000221947	XKR9	8:71581599-71702606	OK	1.16783	1.10334	-0.0819479	-0.086893	0.87025	0.9998
ENSG00000006712	ENSG00000006712	PAF1	19:39876491-39881835	OK	30.4831	31.3637	0.0410855	0.093064	0.8703	0.9998
ENSG00000153391	ENSG00000153391	INO80C	18:33023832-33077955	OK	9.61563	9.21143	-0.0619554	-0.0882484	0.8703	0.9998
ENSG00000171163	ENSG00000171163	ZNF692	1:249144204-249153343	OK	28.5904	27.5997	-0.0508786	-0.0994843	0.87035	0.9998
ENSG00000103353	ENSG00000103353	UBFD1	16:23533334-23585710	OK	30.1664	29.116	-0.0511305	-0.0699331	0.8704	0.9998
ENSG00000112769	ENSG00000112769	LAMA4	6:112429962-112672498	OK	9.6051	10.0353	0.0632075	0.0626351	0.8704	0.9998
ENSG00000259605	ENSG00000259605	AC074212.5	19:46268042-46296060	OK	0.924626	1.11228	0.266583	0.0950998	0.8705	0.9998
ENSG00000083635	ENSG00000083635	NUFIP1	13:45513383-45657260	OK	3.72437	3.92874	0.0770706	0.0995881	0.87065	0.9998
ENSG00000065320	ENSG00000065320	NTN1	17:8924858-9147317	OK	0.808487	0.772616	-0.0654725	-0.0927649	0.87075	0.9998
ENSG00000146223	ENSG00000146223	RPL7L1	6:42847355-42857663	OK	35.0937	36.3195	0.0495314	0.0915086	0.87085	0.9998
ENSG00000087995	ENSG00000087995	METTL2A	17:60501227-60527454	OK	17.7159	18.2733	0.0446954	0.0937791	0.87105	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000167797	ENSG00000167797	CDK2AP2	11:67273967-67276120	OK	14.37	14.885	0.0507925	0.0968353	0.87115	0.9998
ENSG00000211456	ENSG00000211456	SACM1L	3:45596885-45786916	OK	39.3097	41.2118	0.0681722	0.078363	0.87115	0.9998
ENSG00000139832	ENSG00000139832	RAB20	13:111175416-111214080	OK	15.0509	15.5844	0.0502521	0.0992787	0.8713	0.9998
ENSG00000173486	ENSG00000173486	FKBP2	11:64008474-64011604	OK	80.5788	83.1644	0.0455658	0.101784	0.8713	0.9998
ENSG00000249456	ENSG00000249456	RP11-298J20.4	10:126605711-126849739	OK	2.31427	2.91812	0.334481	0.0788953	0.8713	0.9998
ENSG00000175782	ENSG00000175782	SLC35E3	12:69139885-69187743	OK	7.70307	7.19448	-0.0985426	-0.0942523	0.87145	0.9998
ENSG00000118263	ENSG00000118263	KLF7	2:207938860-208031991	OK	3.14746	3.30254	0.0693851	0.0763952	0.87155	0.9998
ENSG00000120694	ENSG00000120694	HSPH1	13:31710761-31736525	OK	124.013	120.435	-0.0422358	-0.0928453	0.87155	0.9998
ENSG00000184100	ENSG00000184100	BRD7P2	3:159631188-159943086	OK	2.33437	2.44706	0.0680123	0.0961444	0.8716	0.9998
ENSG00000102908	ENSG00000102908	NFAT5	16:69598996-69738569	OK	4.5427	4.69062	0.0462293	0.0776259	0.87165	0.9998
ENSG00000224831	ENSG00000224831	RP11-651P23.4	3:149478891-149942977	OK	26.8173	29.8136	0.152807	0.0999096	0.8717	0.9998
ENSG00000239482	ENSG00000239482	RP11-90K6.1	3:112021324-112081659	OK	1.21653	1.46309	0.266248	0.0995265	0.87175	0.9998
ENSG00000165644	ENSG00000165644	COMTD1	10:76993726-76995788	OK	14.6126	14.0518	-0.0564508	-0.0966969	0.8718	0.9998
ENSG00000103248	ENSG00000103248	MTHFSD	16:86563781-86588841	OK	4.26637	4.0815	-0.0639121	-0.0787627	0.87185	0.9998
ENSG00000166387	ENSG00000166387	PPFIBP2	11:7534528-7678358	OK	19.7149	20.3825	0.0480415	0.0732198	0.87185	0.9998
ENSG00000263244	ENSG00000263244	RP11-473I1.10	16:9185504-9215497	OK	3.19949	3.42472	0.0981444	0.0986555	0.87185	0.9998
ENSG00000160446	ENSG00000160446	ZDHHC12	9:131464801-131486406	OK	23.2171	24.1399	0.056227	0.0979593	0.8719	0.9998
ENSG00000267317	ENSG00000267317	CTB-25B13.12	19:1446299-1479555	OK	4.258	3.73645	-0.188505	-0.109502	0.87195	0.9998
ENSG00000148985	ENSG00000148985	PGAP2	11:3686816-3847601	OK	16.4066	15.3503	-0.0960108	-0.0722989	0.8721	0.9998
ENSG00000014919	ENSG00000014919	COX15	10:101419262-101515891	OK	20.9951	20.2412	-0.0527592	-0.0829473	0.87215	0.9998
ENSG00000270113	ENSG00000270113	RP11-282O18.6	12:123773655-123850660	OK	1.2439	1.60395	0.366754	0.0781885	0.87215	0.9998
ENSG00000133687	ENSG00000133687	TMTC1	12:29653772-29937692	OK	11.7589	12.1879	0.0517021	0.0957089	0.87225	0.9998
ENSG00000139626	ENSG00000139626	ITGB7	12:53585101-53601091	OK	2.80752	2.95517	0.0739432	0.0736998	0.87225	0.9998
ENSG00000145990	ENSG00000145990	GFOD1	6:13358061-13487894	OK	2.37842	2.46689	0.0526846	0.0875806	0.87225	0.9998
ENSG00000130021	ENSG00000130021	HDHD1	X:6966960-7066231	OK	17.8613	17.3359	-0.043074	-0.0958546	0.8723	0.9998
ENSG00000138594	ENSG00000138594	TMOD3	15:52121824-52392720	OK	9.68561	9.25272	-0.0659658	-0.0833455	0.8724	0.9998
ENSG00000104823	ENSG00000104823	ECH1	19:39306061-39342987	OK	97.6439	104.241	0.0943199	0.095764	0.87245	0.9998
ENSG00000215492	ENSG00000215492	HNRNPA1P7	18:29598334-30050447	OK	136.824	142.365	0.057277	0.102151	0.87245	0.9998
ENSG00000076984	ENSG00000076984	MAP2K7	19:7968727-7979363	OK	12.7563	13.1724	0.0463066	0.0888068	0.8726	0.9998
ENSG00000139180	ENSG00000139180	NDUFA9	12:4671369-4960277	OK	68.9741	72.2065	0.0660748	0.0960855	0.8726	0.9998
ENSG00000124784	ENSG00000124784	RIOK1	6:7268538-7418270	OK	20.0163	18.6857	-0.0992455	-0.0771022	0.87275	0.9998
ENSG00000273046	ENSG00000273046	RP11-834C11.14	12:54375292-54449814	OK	1.7441	1.33451	-0.386177	-0.16413	0.8728	0.9998
ENSG00000104427	ENSG00000104427	ZC2HC1A	8:79578281-79717758	OK	6.51567	6.20125	-0.0713544	-0.0853558	0.87285	0.9998
ENSG00000136169	ENSG00000136169	SETDB2	13:49882785-50069138	OK	8.80394	9.16937	0.0586729	0.0971017	0.87285	0.9998
ENSG00000273311	ENSG00000273311	DGCR11	22:19023794-19115962	OK	0.686535	0.843756	0.297492	0.109543	0.8729	0.9998
ENSG00000184384	ENSG00000184384	MAML2	11:95709761-96076344	OK	1.21601	1.26117	0.0525983	0.095876	0.87295	0.9998
ENSG00000244687	ENSG00000244687	UBE2V1	20:48697660-48770335	OK	101.359	98.4297	-0.0423034	-0.0804793	0.87295	0.9998
ENSG00000267796	ENSG00000267796	LIN37	19:36230057-36245420	OK	6.76148	6.23336	-0.117329	-0.0925085	0.87295	0.9998
ENSG00000097007	ENSG00000097007	ABL1	9:133589332-133763062	OK	20.7608	21.4131	0.0446372	0.0756757	0.873	0.9998
ENSG00000065548	ENSG00000065548	ZC3H15	2:187350882-187374090	OK	58.2457	59.8382	0.0389166	0.093545	0.87305	0.9998
ENSG00000141367	ENSG00000141367	CLTC	17:57697218-57919616	OK	177.622	183.847	0.0496955	0.07197	0.87305	0.9998
ENSG00000097033	ENSG00000097033	SH3GLB1	1:87170258-87213867	OK	29.6206	28.5197	-0.0546407	-0.0949067	0.87325	0.9998
ENSG00000124789	ENSG00000124789	NUP153	6:17615268-17707575	OK	29.0058	28.1812	-0.0416059	-0.100449	0.87325	0.9998
ENSG00000171943	ENSG00000171943	SRGAP2C	1:121102016-121204983	OK	18.1755	17.4469	-0.0590267	-0.0973137	0.87325	0.9998
ENSG00000153896	ENSG00000153896	ZNF599	19:35248980-35264134	OK	3.13601	3.30108	0.0740094	0.0997001	0.8733	0.9998
ENSG00000164073	ENSG00000164073	MFSD8	4:128838959-128960866	OK	3.22517	3.39109	0.0723759	0.0748369	0.87335	0.9998
ENSG00000212907	ENSG00000212907	MT-ND4L	MT:10469-12137	OK	4159.08	4622.91	0.152538	0.0808219	0.87345	0.9998
ENSG00000268573	ENSG00000268573	RP11-158H5.7	18:32820993-32870196	OK	0.872475	0.956074	0.132008	0.103549	0.8735	0.9998
ENSG00000227258	ENSG00000227258	SMIM2-AS1	13:44716681-44817328	OK	0.868803	0.966436	0.153644	0.0894001	0.8736	0.9998
ENSG00000244026	ENSG00000244026	FAM86DP	3:75464220-75484261	OK	14.2742	13.7454	-0.0544691	-0.096002	0.8737	0.9998
ENSG00000104825	ENSG00000104825	NFKBIB	19:39369196-39399533	OK	11.9449	11.1019	-0.105583	-0.10105	0.87375	0.9998
ENSG00000126246	ENSG00000126246	IGFLR1	19:36230057-36245420	OK	5.35362	4.88145	-0.133203	-0.0710437	0.8738	0.9998
ENSG00000149483	ENSG00000149483	TMEM138	11:61066922-61136981	OK	66.2423	61.214	-0.113891	-0.064866	0.87385	0.9998
ENSG00000169598	ENSG00000169598	DFFB	1:3773844-3801993	OK	3.27078	3.43142	0.0691723	0.0860762	0.8739	0.9998
ENSG00000107175	ENSG00000107175	CREB3	9:35696944-35758572	OK	27.8817	24.5159	-0.185603	-0.0959936	0.87395	0.9998
ENSG00000270083	ENSG00000270083	RP1-257I20.14	22:42481528-42535938	OK	0.947582	0.759006	-0.320138	-0.047068	0.87395	0.9998
ENSG00000107404	ENSG00000107404	DVL1	1:1266693-1284730	OK	16.3663	15.8982	-0.0418669	-0.0893395	0.874	0.9998
ENSG00000225096	ENSG00000225096	XXbac-BPG55C20.7	6:58291907-58298496	OK	0.663404	0.786735	0.24599	0.122856	0.874	0.9998
ENSG00000186174	ENSG00000186174	BCL9L	11:118754474-118829269	OK	7.59344	7.99354	0.0740815	0.064716	0.87415	0.9998
ENSG00000247746	ENSG00000247746	USP51	X:55511048-55515635	OK	1.69869	1.6141	-0.0736947	-0.096286	0.87415	0.9998
ENSG00000172345	ENSG00000172345	STARD5	15:81451915-81616524	OK	11.1246	10.1536	-0.131769	-0.088579	0.8742	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000119574	ENSG00000119574	ZBTB45	19:59024896-59050278	OK	3.72453	3.5844	-0.0553248	-0.0899581	0.8743	0.9998
ENSG00000257181	ENSG00000257181	RP11-611O2.5	12:69201955-69365350	OK	5.74993	7.6966	0.420676	0.14312	0.8743	0.9998
ENSG00000139233	ENSG00000139233	LLPH	12:66516841-66563852	OK	41.8763	43.6984	0.0614452	0.0938832	0.87435	0.9998
ENSG00000153443	ENSG00000153443	UBALD1	16:4658883-4665028	OK	8.03693	8.36814	0.0582638	0.092025	0.87435	0.9998
ENSG00000232439	ENSG00000232439	RPL18AP7	3:38537617-38583652	OK	0.691715	0.550381	-0.329747	-0.0873878	0.87435	0.9998
ENSG00000089060	ENSG00000089060	SLC8B1	12:113736563-113827203	OK	3.11328	3.34823	0.104965	0.0686322	0.87445	0.9998
ENSG00000136754	ENSG00000136754	ABI1	10:26986587-27150016	OK	17.0925	17.7275	0.0526292	0.0980367	0.87445	0.9998
ENSG00000185596	ENSG00000185596	WASH3P	15:102500050-102519298	OK	12.3666	11.9031	-0.0551051	-0.0859385	0.87445	0.9998
ENSG00000258655	ENSG00000258655	ARHGAP5-AS1	14:32544624-32628934	OK	7.12371	8.20132	0.203228	0.104606	0.87445	0.9998
ENSG00000080031	ENSG00000080031	PTPRH	19:55692615-55720874	OK	1.55219	1.47405	-0.0745184	-0.072448	0.87455	0.9998
ENSG00000272941	ENSG00000272941	RP11-134L10.1	7:134671258-134855547	OK	2.47724	3.2803	0.405096	0.147898	0.87455	0.9998
ENSG00000165832	ENSG00000165832	TRUB1	10:116697951-116737430	OK	17.1105	17.6804	0.047272	0.0842009	0.8746	0.9998
ENSG00000180964	ENSG00000180964	TCEAL8	X:102507922-102510131	OK	63.9826	65.836	0.041197	0.0989429	0.8746	0.9998
ENSG00000163412	ENSG00000163412	EIF4E3	3:71724566-71805647	OK	2.72758	2.83173	0.0540654	0.0782343	0.87465	0.9998
ENSG00000179988	ENSG00000179988	PSTK	10:124690418-124768333	OK	3.78545	4.2237	0.15804	0.0938631	0.8747	0.9998
ENSG00000163702	ENSG00000163702	IL17RC	3:9958757-9975314	OK	21.8813	21.1168	-0.0513042	-0.0921707	0.87485	0.9998
ENSG00000131459	ENSG00000131459	GFPT2	5:179727689-179780387	OK	4.31708	4.46777	0.0494986	0.08095	0.8749	0.9998
ENSG00000196323	ENSG00000196323	ZBTB44	11:130096571-130184581	OK	4.10854	3.93254	-0.0631624	-0.0791392	0.87495	0.9998
ENSG00000167065	ENSG00000167065	DUSP18	22:31031638-31065003	OK	4.94652	4.67897	-0.0802238	-0.0941053	0.875	0.9998
ENSG00000091317	ENSG00000091317	CMTM6	3:32433162-32544900	OK	22.235	21.553	-0.0449483	-0.0956457	0.8751	0.9998
ENSG00000168906	ENSG00000168906	MAT2A	2:85766287-85788670	OK	116.457	119.899	0.0420174	0.0866821	0.8751	0.9998
ENSG00000215032	ENSG00000215032	GNL3LP1	5:60169657-60240900	OK	0.592206	0.704319	0.25013	0.11309	0.8751	0.9998
ENSG00000218175	ENSG00000218175	AC016739.2	2:177065635-177065980	OK	8.35808	8.8062	0.0753495	0.0956268	0.8751	0.9998
ENSG00000253919	ENSG00000253919	PRKRIRP7	8:79578281-79717758	OK	0.652172	0.572631	-0.187647	-0.0972149	0.8752	0.9998
ENSG00000155115	ENSG00000155115	GTF3C6	6:111279762-111289093	OK	44.8981	46.2296	0.0421626	0.0932871	0.8753	0.9998
ENSG00000169976	ENSG00000169976	SF3B5	6:144416017-144416754	OK	45.9624	44.5952	-0.0435667	-0.0943199	0.8753	0.9998
ENSG00000221988	ENSG00000221988	PPT2	6:32116135-32145873	OK	60.5738	63.6038	0.0704203	0.0840322	0.8753	0.9998
ENSG00000272325	ENSG00000272325	NUDT3	6:34247455-34393902	OK	13.3138	12.4491	-0.0968819	-0.089187	0.8753	0.9998
ENSG00000184305	ENSG00000184305	CCSER1	4:91048685-92523064	OK	1.3982	1.32626	-0.0762097	-0.0637248	0.87535	0.9998
ENSG00000263203	ENSG00000263203	CHTF8	16:69139466-69442474	OK	0.916332	1.25952	0.458935	0.083514	0.87535	0.9998
ENSG00000105404	ENSG00000105404	RABAC1	19:42460832-42463542	OK	78.4008	76.1259	-0.0424795	-0.0984501	0.8754	0.9998
ENSG00000167775	ENSG00000167775	CD320	19:8367010-8408146	OK	102.049	106.124	0.0564848	0.0930569	0.8754	0.9998
ENSG00000113658	ENSG00000113658	SMAD5	5:135465195-135524435	OK	20.2139	19.5098	-0.0511524	-0.0663476	0.87545	0.9998
ENSG00000127603	ENSG00000127603	MACF1	1:39546987-39952849	OK	34.106	35.8424	0.0716394	0.0732407	0.87545	0.9998
ENSG00000182648	ENSG00000182648	LINC01006	7:156264889-156685924	OK	3.49124	2.93894	-0.248443	-0.0694395	0.87545	0.9998
ENSG00000164897	ENSG00000164897	TMUB1	7:150778166-150780633	OK	61.8231	64.0425	0.0508821	0.0995164	0.87555	0.9998
ENSG00000269910	ENSG00000269910	RP11-73M18.10	14:104019757-104181841	OK	6.60316	5.4226	-0.284171	-0.0655312	0.8756	0.9998
ENSG00000174483	ENSG00000174483	BBS1	11:66234215-66313709	OK	9.06322	9.61568	0.0853651	0.0544069	0.87585	0.9998
ENSG00000005981	ENSG00000005981	ASB4	7:95107755-95169544	OK	50.7573	49.3442	-0.040736	-0.0961574	0.8759	0.9998
ENSG00000185361	ENSG00000185361	TNFAIP8L1	19:4639529-4670382	OK	4.0249	3.58062	-0.168743	-0.0939105	0.8759	0.9998
ENSG00000078902	ENSG00000078902	TOLLIP	11:1295600-1330884	OK	38.528	37.1045	-0.054314	-0.0884	0.87595	0.9998
ENSG00000172586	ENSG00000172586	CHCHD1	10:75541804-75543410	OK	64.8639	62.9773	-0.0425838	-0.0979627	0.87595	0.9998
ENSG00000174672	ENSG00000174672	BRSK2	11:1411128-1483919	OK	4.42235	4.24378	-0.0594636	-0.0828671	0.87595	0.9998
ENSG00000269093	ENSG00000269093	AC007773.3	19:32880955-32976801	OK	0.517968	0.68057	0.393881	0.0725738	0.87595	0.9998
ENSG00000108590	ENSG00000108590	MED31	17:6481467-6554954	OK	12.2047	13.8723	0.184767	0.137765	0.876	0.9998
ENSG00000196510	ENSG00000196510	ANAPC7	12:110810704-110888227	OK	61.4383	64.3738	0.0673355	0.0781099	0.876	0.9998
ENSG00000187522	ENSG00000187522	HSPA14	10:14861248-14913740	OK	13.0888	13.5269	0.047497	0.0900608	0.87605	0.9998
ENSG00000130165	ENSG00000130165	ELOF1	19:11661961-11670051	OK	38.5327	37.3961	-0.0431959	-0.0954357	0.8761	0.9998
ENSG00000180667	ENSG00000180667	YOD1	1:207217193-207254369	OK	22.6963	23.8152	0.0694222	0.101323	0.8762	0.9998
ENSG00000263535	ENSG00000263535	AK4P1	17:29335514-29709134	OK	3.82854	2.84119	-0.430301	-0.111577	0.8762	0.9998
ENSG00000121931	ENSG00000121931	LRIF1	1:111486088-111507271	OK	6.91502	7.18182	0.0546169	0.0974344	0.87635	0.9998
ENSG00000227879	ENSG00000227879	PSPC1P1	13:19775776-19801572	OK	2.11918	2.24437	0.0828068	0.0943015	0.8764	0.9998
ENSG00000123992	ENSG00000123992	DNPEP	2:220238267-220268355	OK	29.2448	28.3287	-0.0459161	-0.0764472	0.87645	0.9998
ENSG00000025156	ENSG00000025156	HSF2	6:122720690-122754264	OK	7.42603	7.11594	-0.0615378	-0.094909	0.87655	0.9998
ENSG00000148737	ENSG00000148737	TCF7L2	10:114710008-114927437	OK	5.53409	5.31495	-0.0582906	-0.0802108	0.87655	0.9998
ENSG00000178403	ENSG00000178403	NEUROG2	4:113434671-113578748	OK	0.835235	0.70184	-0.251041	-0.112102	0.87655	0.9998
ENSG00000173542	ENSG00000173542	MOB1B	4:71768042-71896631	OK	9.43957	9.78886	0.0524199	0.0770966	0.87665	0.9998
ENSG00000205664	ENSG00000205664	RP11-706O15.1	X:3735568-3761898	OK	7.28718	7.62786	0.0659179	0.0947304	0.87665	0.9998
ENSG00000178665	ENSG00000178665	ZNF713	7:55954969-56067874	OK	2.07091	1.85633	-0.157816	-0.0456074	0.8767	0.9998
ENSG00000136490	ENSG00000136490	LIMD2	17:61699774-61778532	OK	55.4409	58.5488	0.0786891	0.0977322	0.87675	0.9998
ENSG00000128335	ENSG00000128335	APOL2	22:36622255-36636000	OK	20.1325	20.7855	0.0460563	0.0834372	0.8769	0.9998
ENSG00000145740	ENSG00000145740	SLC30A5	5:68389472-68432221	OK	22.4946	23.3012	0.0508276	0.083362	0.87695	0.9998
ENSG00000081853	ENSG00000081853	PCDHGA2	5:140710251-140892546	OK	0.546938	0.717537	0.391675	0.128355	0.8771	0.9998
ENSG00000185864	ENSG00000185864	NPIPB4	16:21845889-21930477	OK	7.40409	7.06736	-0.0671515	-0.0821493	0.87715	0.9998
ENSG00000119514	ENSG00000119514	GALNT12	9:101569980-101634697	OK	4.02327	3.86248	-0.0588395	-0.0908481	0.8772	0.9998
ENSG00000131242	ENSG00000131242	RAB11FIP4	17:29718641-29865236	OK	22.4294	23.402	0.061239	0.0743079	0.87725	0.9998
ENSG00000069020	ENSG00000069020	MAST4	5:65892175-66465423	OK	1.07218	1.01911	-0.0732422	-0.0432178	0.8773	0.9998
ENSG00000157538	ENSG00000157538	DSCR3	21:38580803-38640785	OK	30.3212	29.3874	-0.0451259	-0.0829878	0.8774	0.9998
ENSG00000164885	ENSG00000164885	CDK5	7:150750898-150773617	OK	58.7362	53.3577	-0.138553	-0.106889	0.8774	0.9998
ENSG00000244676	ENSG00000244676	AL109761.5	21:19135631-19191703	OK	0.803404	1.01148	0.332271	0.0518192	0.8774	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000056586	ENSG00000056586	RC3H2	9:125606834-125667620	OK	11.9127	12.2986	0.0459951	0.0705007	0.87745	0.9998
ENSG00000181924	ENSG00000181924	COA4	11:73583711-73638790	OK	58.1828	56.1855	-0.0503938	-0.0920759	0.87745	0.9998
ENSG00000072415	ENSG00000072415	MPP5	14:67707825-67853233	OK	8.15167	7.54671	-0.111248	-0.0953403	0.87755	0.9998
ENSG00000100722	ENSG00000100722	ZC3H14	14:89029252-89259096	OK	25.401	26.1325	0.0409592	0.0806046	0.8776	0.9998
ENSG00000137720	ENSG00000137720	C11orf1	11:111652918-111756699	OK	7.10493	8.00848	0.172707	0.112893	0.8776	0.9998
ENSG00000140199	ENSG00000140199	SLC12A6	15:34525459-34630261	OK	1.82254	1.89385	0.0553704	0.0618415	0.87765	0.9998
ENSG00000163159	ENSG00000163159	VPS72	1:151129104-151167797	OK	54.4339	52.4581	-0.053339	-0.0940549	0.8777	0.9998
ENSG00000267427	ENSG00000267427	CTC-503J8.6	19:6210389-6212492	OK	20.2022	20.7892	0.0413222	0.091816	0.8777	0.9998
ENSG00000157625	ENSG00000157625	TAB3	X:30845558-30993201	OK	21.0276	20.457	-0.0396877	-0.0882046	0.87775	0.9998
ENSG00000258727	ENSG00000258727	RP11-66N24.3	14:23980968-24048009	OK	1.84121	1.68367	-0.129048	-0.0965554	0.87775	0.9998
ENSG00000244151	ENSG00000244151	RP11-148K1.12	7:150750898-150773617	OK	1.29011	1.5286	0.244716	0.0358106	0.8778	0.9998
ENSG00000228232	ENSG00000228232	GAPDHP1	X:39646385-39647390	OK	0.759936	0.712347	-0.0932966	-0.0895008	0.87785	0.9998
ENSG00000111144	ENSG00000111144	LTA4H	12:96390298-96437298	OK	35.4747	34.5044	-0.040011	-0.0928306	0.87795	0.9998
ENSG00000122565	ENSG00000122565	CBX3	7:26229546-26252976	OK	201.997	213.672	0.0810597	0.0838047	0.87795	0.9998
ENSG00000171792	ENSG00000171792	RHNO1	12:2904118-3050306	OK	28.2638	25.9798	-0.121563	-0.0749952	0.87795	0.9998
ENSG00000128654	ENSG00000128654	MTX2	2:177134122-177202753	OK	86.0539	83.8083	-0.0381479	-0.0908055	0.878	0.9998
ENSG00000172366	ENSG00000172366	FAM195A	16:691812-699200	OK	28.1296	29.0025	0.0440917	0.0919881	0.878	0.9998
ENSG00000109065	ENSG00000109065	NAT9	17:72766685-72772506	OK	30.5427	31.4301	0.0413162	0.0780459	0.87805	0.9998
ENSG00000115524	ENSG00000115524	SF3B1	2:198254507-198299815	OK	101.724	97.6128	-0.059516	-0.0812812	0.8781	0.9998
ENSG00000042286	ENSG00000042286	AIFM2	10:71812551-71892690	OK	6.13114	5.93251	-0.0475111	-0.0909762	0.87815	0.9998
ENSG00000049883	ENSG00000049883	PTCD2	5:71515235-71656052	OK	6.70778	6.22965	-0.106683	-0.0827092	0.87815	0.9998
ENSG00000154229	ENSG00000154229	PRKCA	17:64298753-64806861	OK	3.24026	3.34819	0.047272	0.0794968	0.87815	0.9998
ENSG00000108946	ENSG00000108946	PRKAR1A	17:66255322-66760023	OK	220.941	211.382	-0.0638107	-0.0716594	0.87825	0.9998
ENSG00000204843	ENSG00000204843	DCTN1	2:74425688-74621009	OK	62.3806	64.1309	0.0399216	0.0746274	0.8783	0.9998
ENSG00000218227	ENSG00000218227	RP11-889L3.1	5:177482604-177483195	OK	1.89565	1.78732	-0.0848962	-0.0908849	0.8783	0.9998
ENSG00000205544	ENSG00000205544	TMEM256	17:7283852-7307456	OK	103.889	99.9805	-0.055319	-0.0969088	0.8784	0.9998
ENSG00000262251	ENSG00000262251	RP11-199F11.2	17:7565096-7606820	OK	1.19258	0.928659	-0.360871	-0.129972	0.87845	0.9998
ENSG00000159596	ENSG00000159596	TMEM69	1:46092975-46216322	OK	25.0848	26.7477	0.0926019	0.0892731	0.8785	0.9998
ENSG00000109083	ENSG00000109083	IFT20	17:26646120-26662515	OK	19.3587	17.9682	-0.107539	-0.093597	0.87855	0.9998
ENSG00000167695	ENSG00000167695	FAM57A	17:635651-646206	OK	13.4541	13.9403	0.0512124	0.0926732	0.87855	0.9998
ENSG00000266962	ENSG00000266962	RP11-400F19.6	17:40688189-40718295	OK	2.73433	3.06009	0.162387	0.0910284	0.87865	0.9998
ENSG00000267698	ENSG00000267698	AC002116.7	19:36505409-36545664	OK	0.609823	0.773228	0.342504	0.0860499	0.87865	0.9998
ENSG00000167920	ENSG00000167920	TMEM99	17:38974368-38992522	OK	17.6333	18.497	0.0689872	0.0899637	0.8787	0.9998
ENSG00000197386	ENSG00000197386	HTT	4:3076407-3245676	OK	16.1031	16.6652	0.049501	0.0293833	0.8787	0.9998
ENSG00000089682	ENSG00000089682	RBM41	X:106307649-106362057	OK	6.92059	6.6649	-0.0543127	-0.0839059	0.87875	0.9998
ENSG00000126903	ENSG00000126903	SLC10A3	X:153715644-153719016	OK	7.748	7.4918	-0.048512	-0.0904894	0.87885	0.9998
ENSG00000170906	ENSG00000170906	NDUFA3	19:54606035-54635140	OK	161.932	170.65	0.0756535	0.0891303	0.8789	0.9998
ENSG00000181652	ENSG00000181652	ATG9B	7:150688082-150721586	OK	3.66339	3.99657	0.125582	0.100856	0.8789	0.9998
ENSG00000187140	ENSG00000187140	FOXD3	1:63786554-63790797	OK	1.77463	1.88459	0.0867369	0.0951283	0.8789	0.9998
ENSG00000248278	ENSG00000248278	SUMO2P17	17:46952221-47006418	OK	8.06385	10.1868	0.337168	0.105176	0.8789	0.9998
ENSG00000111269	ENSG00000111269	CREBL2	12:12764760-12798042	OK	29.7314	28.9594	-0.037956	-0.0834609	0.87895	0.9998
ENSG00000131844	ENSG00000131844	MCCC2	5:70883114-70954531	OK	30.7267	29.8954	-0.0395684	-0.0872336	0.87895	0.9998
ENSG00000135457	ENSG00000135457	TFCP2	12:51487445-51566926	OK	15.8215	15.3051	-0.047872	-0.0912766	0.87895	0.9998
ENSG00000196110	ENSG00000196110	ZNF699	19:9402190-9420514	OK	1.25478	1.17437	-0.0955497	-0.0774828	0.87895	0.9998
ENSG00000213757	ENSG00000213757	CTC-451P13.1	5:78532011-78623038	OK	1.44294	1.72267	0.255635	0.124506	0.879	0.9998
ENSG00000120647	ENSG00000120647	CCDC77	12:389294-551811	OK	8.55303	8.058	-0.0860137	-0.0622134	0.87915	0.9998
ENSG00000175066	ENSG00000175066	GK5	3:141882413-141944449	OK	7.10313	6.87502	-0.0470914	-0.0649786	0.87915	0.9998
ENSG00000164430	ENSG00000164430	MB21D1	6:74078277-74161999	OK	2.0481	1.87585	-0.12674	-0.0862394	0.8793	0.9998
ENSG00000226276	ENSG00000226276	AC093382.1	2:216804030-216806442	OK	1.0401	0.952046	-0.127612	-0.095724	0.8793	0.9998
ENSG00000123119	ENSG00000123119	NECAB1	8:91634222-91997485	OK	0.782663	0.649792	-0.268413	-0.104774	0.8794	0.9998
ENSG00000229401	ENSG00000229401	RP1-290I10.7	6:10429487-10457014	OK	0.58522	0.715123	0.289212	0.0551677	0.8794	0.9998
ENSG00000135372	ENSG00000135372	NAT10	11:34127148-34169217	OK	23.7205	23.1313	-0.0362847	-0.0725734	0.87945	0.9998
ENSG00000272030	ENSG00000272030	RP1-178F15.4	1:153591262-153618782	OK	4.77526	5.57793	0.224152	0.0221795	0.87945	0.9998
ENSG00000104290	ENSG00000104290	FZD3	8:28351728-28431775	OK	5.99449	6.24411	0.0588576	0.0781406	0.8795	0.9998
ENSG00000187699	ENSG00000187699	C2orf88	2:190744334-191236391	OK	9.52515	10.2981	0.11257	0.0893567	0.87955	0.9998
ENSG00000218980	ENSG00000218980	FTH1P15	6:56819772-56892140	OK	9.86312	8.96653	-0.137495	-0.0918203	0.87955	0.9998
ENSG00000263020	ENSG00000263020	CSNK2B-LY6G5B-1181	6:31629005-31641553	OK	1.13597	1.39986	0.301358	0.0863427	0.87955	0.9998
ENSG00000129083	ENSG00000129083	COPB1	11:14464985-14665181	OK	61.7109	63.7868	0.0477338	0.0786576	0.8796	0.9998
ENSG00000233270	ENSG00000233270	SNRPEP4	19:5576670-5576949	OK	69.2262	71.8646	0.0539645	0.0951218	0.8797	0.9998
ENSG00000229344	ENSG00000229344	RP5-857K21.7	1:536815-660283	OK	1.50031	1.75218	0.223891	0.022079	0.87975	0.9998
ENSG00000065361	ENSG00000065361	ERBB3	12:56473640-56507691	OK	68.0463	65.594	-0.0529539	-0.0575716	0.87985	0.9998
ENSG00000250914	ENSG00000250914	RP11-1084J3.1	5:33944720-33984835	OK	1.15998	1.35152	0.220492	0.0178371	0.87985	0.9998
ENSG00000145916	ENSG00000145916	RMND5B	5:177557996-177580968	OK	16.5106	15.6348	-0.0786314	-0.074858	0.8799	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258289	ENSG00000258289	CHURC1	14:65381078-65569413	OK	40.6301	43.8427	0.109787	0.0878423	0.87995	0.9998
ENSG00000142864	ENSG00000142864	SERBP1	1:67873492-67896098	OK	107.222	110.273	0.0404725	0.0861169	0.88	0.9998
ENSG00000136819	ENSG00000136819	C9orf78	9:132589568-132644107	OK	34.6841	35.8177	0.0463972	0.0853736	0.88005	0.9998
ENSG00000143458	ENSG00000143458	GABPB2	1:151043053-151098018	OK	3.1718	3.35439	0.080749	0.0889274	0.88005	0.9998
ENSG00000236144	ENSG00000236144	AD000090.2	19:36024313-36038428	OK	3.47988	3.09426	-0.169446	-0.0590715	0.88005	0.9998
ENSG00000143575	ENSG00000143575	HAX1	1:154244986-154248351	OK	184.423	189.306	0.0377025	0.0921302	0.8803	0.9998
ENSG00000073803	ENSG00000073803	MAP3K13	3:185000728-185216845	OK	34.4926	33.0502	-0.0616296	-0.0817966	0.88035	0.9998
ENSG00000236810	ENSG00000236810	RP5-886K2.3	1:24069644-24104777	OK	5.80543	6.42098	0.14539	0.083291	0.88035	0.9998
ENSG00000115421	ENSG00000115421	PAPOLG	2:60983364-61029220	OK	3.60535	3.73378	0.0504957	0.0748388	0.8804	0.9998
ENSG00000203808	ENSG00000203808	BVES-AS1	6:105544696-105627870	OK	1.61259	1.4054	-0.198398	-0.048471	0.88055	0.9998
ENSG00000218226	ENSG00000218226	TATDN2P2	6:158957467-159056460	OK	2.10947	2.30727	0.129308	0.0853349	0.88055	0.9998
ENSG00000228452	ENSG00000228452	RP5-994D16.9	1:43232939-43263968	OK	0.645405	0.550446	-0.229604	-0.0701624	0.8806	0.9998
ENSG00000102996	ENSG00000102996	MMP15	16:58059469-58080805	OK	7.49788	7.28732	-0.0410945	-0.0795308	0.88065	0.9998
ENSG00000185917	ENSG00000185917	SETD4	21:37402367-37498938	OK	5.71841	6.11154	0.0959226	0.062953	0.88065	0.9998
ENSG00000144560	ENSG00000144560	VGLL4	3:11313994-11766453	OK	27.9681	26.9341	-0.0543527	-0.0752131	0.8807	0.9998
ENSG00000186704	ENSG00000186704	DTX2P1	7:76139744-77045717	OK	1.85612	1.57181	-0.239861	-0.135375	0.8808	0.9998
ENSG00000111540	ENSG00000111540	RAB5B	12:56367696-56388490	OK	132.222	135.825	0.0387795	0.0794948	0.88085	0.9998
ENSG00000103550	ENSG00000103550	KNOP1	16:19566561-19897489	OK	30.5925	32.3151	0.0790288	0.07885	0.8809	0.9998
ENSG00000269352	ENSG00000269352	AC018766.5	19:50321538-50364001	OK	3.0516	3.44278	0.174008	0.0422014	0.8809	0.9998
ENSG00000240849	ENSG00000240849	TMEM189	20:48697660-48770335	OK	27.0515	28.5647	0.0785219	0.0925592	0.8812	0.9998
ENSG00000115944	ENSG00000115944	COX7A2L	2:42560685-42652228	OK	164.559	168.564	0.034694	0.0858378	0.8813	0.9998
ENSG00000164105	ENSG00000164105	SAP30	4:174284930-174298683	OK	9.44919	9.78063	0.0497376	0.0882325	0.8814	0.9998
ENSG00000102309	ENSG00000102309	PIN4	X:71401202-71527037	OK	13.1079	14.8165	0.176766	0.0339541	0.8815	0.9998
ENSG00000173153	ENSG00000173153	ESRRA	11:64073043-64085556	OK	42.8895	41.0513	-0.0631975	-0.0858463	0.8815	0.9998
ENSG00000152620	ENSG00000152620	NADK2	5:36192693-36242381	OK	15.8607	15.3815	-0.0442527	-0.0866033	0.88155	0.9998
ENSG00000173451	ENSG00000173451	THAP2	12:72003251-72097836	OK	5.01902	4.52781	-0.148593	-0.0604239	0.8817	0.9998
ENSG00000120458	ENSG00000120458	MSANTD2	11:124636393-124704383	OK	2.21471	2.12742	-0.0580089	-0.0882108	0.88175	0.9998
ENSG00000144028	ENSG00000144028	SNRNP200	2:96940073-96971297	OK	76.775	74.7412	-0.0387318	-0.0810078	0.88175	0.9998
ENSG00000151247	ENSG00000151247	EIF4E	4:99792834-99916145	OK	22.0054	22.8738	0.0558378	0.0899833	0.88175	0.9998
ENSG00000183475	ENSG00000183475	ASB7	15:101093733-101191910	OK	5.03818	5.23904	0.0563988	0.082032	0.88175	0.9998
ENSG00000236364	ENSG00000236364	RP11-525G13.2	1:165696031-165880855	OK	0.826663	0.974271	0.237025	0.0269661	0.8818	0.9998
ENSG00000053702	ENSG00000053702	NRIP2	12:2904118-3050306	OK	0.719044	0.620094	-0.213592	-0.0331888	0.8819	0.9998
ENSG00000184205	ENSG00000184205	TSPYL2	X:53111548-53117722	OK	8.44173	8.10689	-0.0583899	-0.0914899	0.8819	0.9998
ENSG00000168679	ENSG00000168679	SLC16A4	1:110905469-110974982	OK	12.9192	12.0992	-0.0946043	-0.0891365	0.88195	0.9998
ENSG00000205702	ENSG00000205702	CYP2D7P	22:42536213-42540576	OK	0.710502	0.765404	0.107384	0.0728812	0.882	0.9998
ENSG00000233223	ENSG00000233223	AC113189.5	17:7465191-7536700	OK	4.94806	4.49569	-0.138321	-0.00902017	0.882	0.9998
ENSG00000072736	ENSG00000072736	NFATC3	16:68021296-68272005	OK	4.74076	4.55421	-0.0579171	-0.0647869	0.88205	0.9998
ENSG00000181894	ENSG00000181894	ZNF329	19:58637618-58666477	OK	2.61733	2.52621	-0.0511224	-0.0873778	0.88205	0.9998
ENSG00000126785	ENSG00000126785	RHOJ	14:63670831-63759937	OK	5.9735	6.35428	0.0891532	0.0939613	0.88215	0.9998
ENSG00000172426	ENSG00000172426	RSPH9	6:43612782-43655528	OK	1.77665	1.47026	-0.273086	-0.143526	0.88215	0.9998
ENSG00000110497	ENSG00000110497	AMBRA1	11:46417963-46615675	OK	13.6791	14.4706	0.0811492	0.0688614	0.8822	0.9998
ENSG00000115211	ENSG00000115211	EIF2B4	2:27548715-27593353	OK	25.2537	23.9425	-0.0769196	-0.0894645	0.8823	0.9998
ENSG00000261796	ENSG00000261796	ISY1-RAB43	3:128806411-128880136	OK	4.60987	4.84298	0.0711678	0.0885426	0.88235	0.9998
ENSG00000101166	ENSG00000101166	SLMO2	20:57608199-57617964	OK	74.583	77.0155	0.0463016	0.0865658	0.8825	0.9998
ENSG00000167969	ENSG00000167969	ECI1	16:2289395-2302301	OK	35.6826	34.6489	-0.0424109	-0.0909882	0.8826	0.9998
ENSG00000171467	ENSG00000171467	ZNF318	6:43263431-43337216	OK	6.59507	6.42342	-0.0380458	-0.0880748	0.8826	0.9998
ENSG00000143612	ENSG00000143612	C1orf43	1:154179181-154243986	OK	400.198	385.13	-0.0553669	-0.0953046	0.88265	0.9998
ENSG00000116473	ENSG00000116473	RAP1A	1:112025969-112310638	OK	33.1216	34.5518	0.0609908	0.0908807	0.8827	0.9998
ENSG00000235180	ENSG00000235180	LINC00601	10:128102437-128110448	OK	0.759036	0.802244	0.0798729	0.0866443	0.8827	0.9998
ENSG00000258644	ENSG00000258644	SYNJ2BP-COX16	14:70791797-70883778	OK	10.4645	12.9147	0.303511	0.120197	0.8827	0.9998
ENSG00000259366	ENSG00000259366	CTD-2647L4.4	8:28747910-28922281	OK	3.18968	2.76592	-0.205652	-0.0989261	0.8827	0.9998
ENSG00000135437	ENSG00000135437	RDH5	12:56075329-56118489	OK	0.708196	0.772459	0.125311	0.0236522	0.88275	0.9998
ENSG00000137574	ENSG00000137574	TGS1	8:56608982-56738007	OK	6.6458	6.95108	0.0647944	0.0886904	0.88275	0.9998
ENSG00000133895	ENSG00000133895	MEN1	11:64570981-64578766	OK	15.2867	14.8291	-0.0438473	-0.0793286	0.8828	0.9998
ENSG00000233205	ENSG00000233205	AC108479.2	2:88047605-88285309	OK	4.01033	3.70273	-0.115132	-0.0939506	0.88285	0.9998
ENSG00000179981	ENSG00000179981	TSHZ1	18:72922709-73001905	OK	6.89584	6.69681	-0.0422526	-0.0912279	0.8829	0.9998
ENSG00000058729	ENSG00000058729	RIOK2	5:96424778-96772921	OK	14.3232	13.6517	-0.069276	-0.0859609	0.88305	0.9998
ENSG00000132591	ENSG00000132591	ERAL1	17:27082995-27188085	OK	35.5167	34.3352	-0.0488105	-0.0849586	0.88305	0.9998
ENSG00000176809	ENSG00000176809	LRRC37A3	17:62850429-62915598	OK	0.65206	0.611711	-0.0921548	-0.049807	0.88315	0.9998
ENSG00000188002	ENSG00000188002	RP11-43F13.1	5:1594740-1634120	OK	9.19172	8.7659	-0.0684325	-0.0490972	0.88325	0.9998
ENSG00000237188	ENSG00000237188	RP11-337C18.8	1:146644349-146767443	OK	1.48283	1.22469	-0.275935	-0.0717694	0.88335	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000272540	ENSG00000272540	XXbac-BPG252P9.9	6:30687977-30693203	OK	1.89383	1.56916	-0.271319	-0.0123658	0.88335	0.9998
ENSG00000140577	ENSG00000140577	CRTC3	15:91073156-91260372	OK	13.6581	14.0411	0.0398953	0.061717	0.8834	0.9998
ENSG00000104679	ENSG00000104679	R3HCC1	8:23127632-23153792	OK	22.8728	22.2686	-0.0386224	-0.0838221	0.88355	0.9998
ENSG00000129128	ENSG00000129128	SPCS3	4:177229418-177253396	OK	32.7867	31.3791	-0.063308	-0.085622	0.8836	0.9998
ENSG00000160345	ENSG00000160345	C9orf116	9:138387026-138398293	OK	1.68234	1.46743	-0.197183	-0.066894	0.8836	0.9998
ENSG00000197959	ENSG00000197959	DNM3	1:171810620-172437971	OK	2.10902	1.88876	-0.159129	-0.0996772	0.8836	0.9998
ENSG00000175073	ENSG00000175073	VCPIP1	8:67540721-67579452	OK	3.931	4.03743	0.0385405	0.0878437	0.8837	0.9998
ENSG00000163472	ENSG00000163472	TMEM79	1:156252725-156265463	OK	3.13496	2.77204	-0.177497	-0.0542237	0.8838	0.9998
ENSG00000229152	ENSG00000229152	ANKRD10-IT1	13:111530886-111567416	OK	2.141	2.64989	0.307649	0.0826496	0.8838	0.9998
ENSG00000168301	ENSG00000168301	KCTD6	3:58477840-58488087	OK	5.19812	5.0194	-0.0504768	-0.0815564	0.88385	0.9998
ENSG00000187416	ENSG00000187416	LHFPL3	7:103969103-104549001	OK	1.04566	0.887178	-0.237115	-0.0394151	0.88385	0.9998
ENSG00000178980	ENSG00000178980	SEPW1	19:48281828-48287943	OK	80.5126	82.7051	0.0387621	0.0870987	0.8839	0.9998
ENSG00000233016	ENSG00000233016	SNHG7	9:139607021-139622636	OK	26.4299	24.9413	-0.0836334	-0.0833566	0.8839	0.9998
ENSG00000213453	ENSG00000213453	FTH1P3	2:27604060-27632554	OK	1.48218	1.75157	0.240932	0.0415034	0.88395	0.9998
ENSG00000145491	ENSG00000145491	ROPN1L	5:10441401-10472141	OK	0.718643	0.678496	-0.0829353	-0.075619	0.88405	0.9998
ENSG00000128731	ENSG00000128731	HERC2	15:28356185-28567298	OK	7.63246	7.29374	-0.0654906	-0.0497832	0.8841	0.9998
ENSG00000137936	ENSG00000137936	BCAR3	1:94027346-94312706	OK	6.35969	6.5485	0.042207	0.0775091	0.8841	0.9998
ENSG00000110075	ENSG00000110075	PPP6R3	11:68228185-68384179	OK	30.8721	30.0465	-0.039107	-0.0623879	0.8843	0.9998
ENSG00000128203	ENSG00000128203	ASPHD2	22:26825238-26879803	OK	0.937744	1.19804	0.353409	0.1146	0.8843	0.9998
ENSG00000163961	ENSG00000163961	RNF168	3:196195653-196230639	OK	4.89891	4.74814	-0.0450986	-0.0866797	0.8843	0.9998
ENSG00000104872	ENSG00000104872	PIH1D1	19:49949554-49995565	OK	35.3386	31.5764	-0.1624	-0.055112	0.88435	0.9998
ENSG00000205861	ENSG00000205861	C1QTNF9B-AS1	13:24304327-24476794	OK	2.8324	2.47999	-0.191694	-0.0952354	0.88435	0.9998
ENSG00000066739	ENSG00000066739	ATG2B	14:96747594-96853625	OK	6.12842	6.37388	0.0566575	0.0514095	0.8844	0.9998
ENSG00000183605	ENSG00000183605	SFXN4	10:120900278-120925179	OK	21.1929	20.5662	-0.0433055	-0.0854482	0.8844	0.9998
ENSG00000174327	ENSG00000174327	SLC16A13	17:6939393-6943440	OK	1.17986	1.12624	-0.0670971	-0.0874683	0.88445	0.9998
ENSG00000178127	ENSG00000178127	NDUFV2	18:9102627-9285983	OK	112.784	109.087	-0.0480869	-0.0852948	0.88445	0.9998
ENSG00000184056	ENSG00000184056	VPS33B	15:91541645-91565833	OK	14.7591	14.2162	-0.0540742	-0.0733146	0.8845	0.9998
ENSG00000182149	ENSG00000182149	IST1	16:71879893-71962913	OK	55.9685	53.7489	-0.0583794	-0.0873023	0.88455	0.9998
ENSG00000205047	ENSG00000205047	FLJ00104	16:87634131-87799598	OK	0.868771	0.82568	-0.0733943	-0.0895382	0.88455	0.9998
ENSG00000011523	ENSG00000011523	CEP68	2:65283499-65357240	OK	10.6096	11.4275	0.107141	0.0843988	0.8847	0.9998
ENSG00000125375	ENSG00000125375	ATP5S	14:50704280-50883179	OK	9.9414	10.424	0.0683847	0.0814592	0.8847	0.9998
ENSG00000162073	ENSG00000162073	PAQR4	16:3013944-3030540	OK	20.5006	21.2937	0.0547595	0.0842055	0.8848	0.9998
ENSG00000221838	ENSG00000221838	AP4M1	7:99690350-99726118	OK	8.09263	7.33064	-0.142669	-0.0496114	0.8848	0.9998
ENSG00000147164	ENSG00000147164	SNX12	X:70279093-70288273	OK	36.043	36.9537	0.0360016	0.0846151	0.88485	0.9998
ENSG00000106299	ENSG00000106299	WASL	7:123321988-123389121	OK	40.7481	39.7902	-0.0343197	-0.0853746	0.88495	0.9998
ENSG00000118046	ENSG00000118046	STK11	19:1189405-1238026	OK	20.6824	19.9228	-0.0539806	-0.0876075	0.88495	0.9998
ENSG00000155329	ENSG00000155329	ZCCHC10	5:132332676-132362296	OK	13.5834	12.904	-0.0740234	-0.0802554	0.88505	0.9998
ENSG00000181827	ENSG00000181827	RFX7	15:56379477-56535483	OK	2.55249	2.47185	-0.046316	-0.0880453	0.88505	0.9998
ENSG00000127870	ENSG00000127870	RNF6	13:26688546-26796791	OK	29.1084	28.2786	-0.0417228	-0.0581253	0.8851	0.9998
ENSG00000138738	ENSG00000138738	PRDM5	4:121606073-121844025	OK	4.42422	4.59461	0.0545182	0.0788316	0.8851	0.9998
ENSG00000187097	ENSG00000187097	ENTPD5	14:74318546-74551196	OK	4.92434	4.67064	-0.0763102	-0.047667	0.88515	0.9998
ENSG00000023228	ENSG00000023228	NDUFS1	2:206979540-207027652	OK	80.8364	77.1145	-0.0680019	-0.0722344	0.88525	0.9998
ENSG00000159176	ENSG00000159176	CSRP1	1:201452657-201502736	OK	61.7715	60.2417	-0.0361781	-0.086189	0.88525	0.9998
ENSG00000166526	ENSG00000166526	ZNF3	7:99647389-99680171	OK	13.3112	12.8437	-0.0515736	-0.0653871	0.88525	0.9998
ENSG00000083828	ENSG00000083828	ZNF586	19:58281022-58427978	OK	3.7297	3.42482	-0.123031	-0.0635431	0.8853	0.9998
ENSG00000250072	ENSG00000250072	CTC-529P8.1	5:148442879-148489350	OK	2.9	3.06502	0.0798459	0.0696825	0.88535	0.9998
ENSG00000254027	ENSG00000254027	RP11-363E6.3	8:82192105-82197012	OK	0.890913	0.702385	-0.343021	-0.106552	0.88535	0.9998
ENSG00000100647	ENSG00000100647	KIAA0247	14:70078312-70181859	OK	5.31845	5.47019	0.0405842	0.0635328	0.88545	0.9998
ENSG00000138190	ENSG00000138190	EXOC6	10:94590934-94819250	OK	9.68154	10.331	0.0936686	0.0485397	0.88545	0.9998
ENSG00000153037	ENSG00000153037	SRP19	5:112043194-112258236	OK	41.9821	45.0742	0.102529	0.0889577	0.8855	0.9998
ENSG00000232888	ENSG00000232888	RPS11P5	12:133345494-133532892	OK	3.57148	4.31412	0.272547	0.0629584	0.88565	0.9998
ENSG00000152284	ENSG00000152284	TCF7L1	2:85360532-85537511	OK	1.12406	1.1694	0.0570495	0.0701734	0.88575	0.9998
ENSG00000164743	ENSG00000164743	C8orf48	8:134151651-134621191	OK	2.32528	2.42399	0.0599819	0.0878676	0.88575	0.9998
ENSG00000154889	ENSG00000154889	MPPE1	18:11688954-11909222	OK	25.7998	28.0178	0.118983	0.0856125	0.8858	0.9998
ENSG00000176658	ENSG00000176658	MYO1D	17:30819539-31205655	OK	96.249	99.091	0.0419828	0.071682	0.88585	0.9998
ENSG00000127824	ENSG00000127824	TUBA4A	2:220094478-220142892	OK	0.918578	1.00135	0.124474	0.0226679	0.88595	0.9998
ENSG00000173545	ENSG00000173545	ZNF622	5:16451627-16465901	OK	42.1385	41.0939	-0.036213	-0.0869449	0.88595	0.9998
ENSG00000055917	ENSG00000055917	PUM2	2:20448451-20551995	OK	30.3174	29.5758	-0.035732	-0.0592019	0.886	0.9998
ENSG00000173163	ENSG00000173163	COMMD1	2:62095223-62374382	OK	67.1278	60.8638	-0.141326	-0.0988512	0.88615	0.9998
ENSG00000119938	ENSG00000119938	PPP1R3C	10:93388198-93392811	OK	87.1906	84.9234	-0.038011	-0.0905189	0.8863	0.9998
ENSG00000214140	ENSG00000214140	PRCD	17:74523437-74553765	OK	1.81117	1.65115	-0.133447	-0.040583	0.8863	0.9998
ENSG00000186862	ENSG00000186862	PDZD7	10:102756374-102790890	OK	3.48623	3.91985	0.169128	0.075644	0.8864	0.9998
ENSG00000198728	ENSG00000198728	LDB1	10:103867316-103880210	OK	41.6979	42.757	0.0361853	0.0847148	0.8864	0.9998
ENSG00000255103	ENSG00000255103	KIAA0754	1:39546987-39952849	OK	3.85472	4.1531	0.107566	0.0827153	0.8864	0.9998
ENSG00000174953	ENSG00000174953	DHX36	3:153990334-154042286	OK	43.2596	44.6322	0.0450657	0.076047	0.88645	0.9998
ENSG00000198604	ENSG00000198604	BAZ1A	14:35221936-35345665	OK	8.98878	8.66655	-0.0526672	-0.0583949	0.88645	0.9998
ENSG00000004897	ENSG00000004897	CDC27	17:45195068-45266788	OK	39.7894	41.3125	0.0541915	0.0782356	0.88655	0.9998
ENSG00000204152	ENSG00000204152	TIMM23B	10:51371389-51387768	OK	6.71247	6.44627	-0.0583794	-0.0857808	0.8866	0.9998
ENSG00000041357	ENSG00000041357	PSMA4	15:78832746-78841604	OK	121.599	124.683	0.036129	0.0865328	0.88665	0.9998
ENSG00000173581	ENSG00000173581	CCDC106	19:56146381-56164527	OK	8.27915	7.72512	-0.0999264	-0.0866325	0.88665	0.9998
ENSG00000197815	ENSG00000197815	AC122129.1	17:17746827-17875736	OK	0.786767	0.97813	0.314089	0.076107	0.88665	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000077463	ENSG00000077463	SIRT6	19:4174105-4182601	OK	15.1149	15.6171	0.0471551	0.0803238	0.88675	0.9998
ENSG00000058866	ENSG00000058866	DGKG	3:185764096-186080026	OK	9.19205	7.92841	-0.213355	-0.0503755	0.8868	0.9998
ENSG00000181991	ENSG00000181991	MRPS11	15:89002706-89089906	OK	64.2417	62.0271	-0.0506108	-0.0824236	0.88685	0.9998
ENSG00000100601	ENSG00000100601	ALKBH1	14:78138746-78174363	OK	8.84349	8.56175	-0.0467113	-0.0741264	0.8869	0.9998
ENSG00000170873	ENSG00000170873	MTSS1	8:125500725-125740730	OK	7.33258	7.95604	0.117731	0.0471154	0.88695	0.9998
ENSG00000153774	ENSG00000153774	CFDP1	16:75327595-75499395	OK	16.8818	17.5058	0.0523582	0.0764557	0.88705	0.9998
ENSG00000138071	ENSG00000138071	ACTR2	2:65454886-65498387	OK	102.46	104.988	0.0351651	0.0868766	0.8871	0.9998
ENSG00000170919	ENSG00000170919	TPT1-AS1	13:45911007-45965872	OK	7.37023	7.88358	0.0971409	0.0119115	0.8871	0.9998
ENSG00000260456	ENSG00000260456	C16orf95	16:87117167-87438385	OK	3.22168	3.72642	0.209977	0.0644717	0.8871	0.9998
ENSG00000136937	ENSG00000136937	NCBP1	9:100263461-100436030	OK	16.9885	16.5221	-0.0401584	-0.0706169	0.88715	0.9998
ENSG00000073009	ENSG00000073009	IKBKG	X:153759605-153796782	OK	7.79826	8.4501	0.115815	0.0838862	0.88725	0.9998
ENSG00000128581	ENSG00000128581	RABL5	7:100956974-100965104	OK	31.9606	31.0073	-0.0436872	-0.0899742	0.88725	0.9998
ENSG00000183431	ENSG00000183431	SF3A3	1:38422646-38456593	OK	60.4783	58.4615	-0.0489311	-0.0830506	0.8873	0.9998
ENSG00000233838	ENSG00000233838	DPH3P1	20:61447595-61493115	OK	2.55504	3.04137	0.251374	0.0400467	0.8873	0.9998
ENSG00000048392	ENSG00000048392	RRM2B	8:103216729-103251346	OK	17.0729	17.5707	0.0414592	0.0658698	0.88735	0.9998
ENSG00000143178	ENSG00000143178	TBX19	1:168250277-168283664	OK	1.00095	1.04986	0.0688206	0.0895412	0.88735	0.9998
ENSG00000214827	ENSG00000214827	MTCP1	X:154289896-154384778	OK	14.6342	13.2856	-0.139478	-0.0933408	0.8874	0.9998
ENSG00000100997	ENSG00000100997	ABHD12	20:25228704-25371619	OK	92.7374	99.9248	0.107693	0.0735559	0.88745	0.9998
ENSG00000198918	ENSG00000198918	RPL39	X:118920466-118925606	OK	59.3073	61.1948	0.0451973	0.0881252	0.88745	0.9998
ENSG00000167107	ENSG00000167107	ACSF2	17:48503518-48552206	OK	9.93277	9.60569	-0.0483072	-0.0652809	0.8875	0.9998
ENSG00000173110	ENSG00000173110	HSPA6	1:161475219-161648444	OK	0.830457	0.761031	-0.125951	-0.0856675	0.88755	0.9998
ENSG00000237973	ENSG00000237973	hsa-mir-6723	1:536815-660283	OK	43.3482	47.0125	0.117071	0.091668	0.88755	0.9998
ENSG00000088876	ENSG00000088876	ZNF343	20:2442279-2505348	OK	2.49481	2.71738	0.123287	0.0565624	0.88765	0.9998
ENSG00000224629	ENSG00000224629	RP5-1142J19.2	7:156931606-157062066	OK	1.2444	1.21033	-0.0400502	-0.00313754	0.88765	0.9998
ENSG00000250305	ENSG00000250305	KIAA1456	8:12803150-12889012	OK	3.3056	3.44605	0.0600286	0.0707569	0.88765	0.9998
ENSG00000145860	ENSG00000145860	RNF145	5:158584416-158675804	OK	55.8746	54.4863	-0.0363009	-0.0812567	0.8877	0.9998
ENSG00000229931	ENSG00000229931	RP1-151F17.1	6:16299342-16762883	OK	1.70073	1.99882	0.232994	0.059968	0.88775	0.9998
ENSG00000142188	ENSG00000142188	TMEM50B	21:34775201-34852318	OK	8.63519	8.21484	-0.0719957	-0.0607811	0.88785	0.9998
ENSG00000003147	ENSG00000003147	ICA1	7:8152813-8384146	OK	3.9144	4.12441	0.075396	0.0744546	0.8879	0.9998
ENSG00000118690	ENSG00000118690	ARMC2	6:109169618-109295186	OK	1.43622	1.35206	-0.0871197	-0.0858363	0.88795	0.9998
ENSG00000180011	ENSG00000180011	ZADH2	18:72907062-72921303	OK	20.1527	19.3371	-0.0595993	-0.082587	0.888	0.9998
ENSG00000258929	ENSG00000258929	RP11-58E21.3	14:50448429-50559361	OK	2.75038	3.0933	0.169519	0.0689869	0.88805	0.9998
ENSG00000260747	ENSG00000260747	RP11-421N8.1	18:65945038-65945480	OK	13.4377	12.9444	-0.0539553	-0.0822661	0.8881	0.9998
ENSG00000141404	ENSG00000141404	GNAL	18:11688954-11909222	OK	5.65189	5.99851	0.0858694	0.0484769	0.88815	0.9998
ENSG00000184924	ENSG00000184924	PTRHD1	2:25012602-25142708	OK	25.7505	27.7921	0.110078	0.0861852	0.88815	0.9998
ENSG00000168275	ENSG00000168275	COA6	1:234507931-234519795	OK	127.76	124.594	-0.0362013	-0.0874054	0.8882	0.9998
ENSG00000272831	ENSG00000272831	RP11-792A8.4	7:66093867-66309813	OK	3.78726	3.08786	-0.294546	-0.0782452	0.8882	0.9998
ENSG00000136425	ENSG00000136425	CIB2	15:78370149-78538030	OK	28.3444	26.906	-0.0751333	-0.0683896	0.88835	0.9998
ENSG00000184005	ENSG00000184005	ST6GALNAC3	1:76540403-77100286	OK	11.0105	10.4701	-0.0726113	-0.0858846	0.88835	0.9998
ENSG00000096746	ENSG00000096746	HNRNPH3	10:70042416-70167051	OK	105.692	102.182	-0.0487213	-0.083175	0.88845	0.9998
ENSG00000103978	ENSG00000103978	TMEM87A	15:42500610-42704516	OK	25.2347	23.8548	-0.0811297	-0.0682126	0.88845	0.9998
ENSG00000128463	ENSG00000128463	EMC4	15:34517199-34522357	OK	63.3231	64.8661	0.0347326	0.0811445	0.8885	0.9998
ENSG00000170515	ENSG00000170515	PA2G4	12:56473640-56507691	OK	151.896	158.448	0.060921	0.0830853	0.8885	0.9998
ENSG00000155158	ENSG00000155158	TTC39B	9:15163619-15307358	OK	2.08772	1.99904	-0.0626166	-0.0734535	0.88855	0.9998
ENSG00000106246	ENSG00000106246	PTCD1	7:98923520-99063954	OK	10.1201	11.5121	0.185936	0.0519587	0.88895	0.9998
ENSG00000261799	ENSG00000261799	RP11-283I3.6	12:383119-386289	OK	1.18765	1.14257	-0.0558257	-0.0851486	0.889	0.9998
ENSG00000034677	ENSG00000034677	RNF19A	8:101170133-101348446	OK	32.8579	33.6913	0.0361359	0.0529343	0.88905	0.9998
ENSG00000068650	ENSG00000068650	ATP11A	13:113344642-113541482	OK	36.4464	35.474	-0.0390119	-0.053474	0.88905	0.9998
ENSG00000121073	ENSG00000121073	SLC35B1	17:47778304-47906458	OK	103.563	100.139	-0.0485085	-0.0783667	0.8893	0.9998
ENSG00000169221	ENSG00000169221	TBC1D10B	16:30368422-30381585	OK	15.5748	15.9705	0.0362006	0.0718189	0.8893	0.9998
ENSG00000232346	ENSG00000232346	SC22CB-1E7.1	22:32435476-32435883	OK	1.341	1.43441	0.0971434	0.0797214	0.88935	0.9998
ENSG00000060339	ENSG00000060339	CCAR1	10:70480768-70552134	OK	21.6209	21.0162	-0.0409209	-0.0668337	0.88945	0.9998
ENSG00000263826	ENSG00000263826	RP11-573D15.9	3:186499568-186524847	OK	0.803032	0.690289	-0.218258	-0.0235802	0.88945	0.9998
ENSG00000273442	ENSG00000273442	AC006946.17	22:17561590-17562346	OK	0.961355	1.02117	0.0870755	0.0859157	0.88945	0.9998
ENSG00000203472	ENSG00000203472	RP11-77K12.4	16:75509793-75529305	OK	0.779858	0.805859	0.0473166	0.0178532	0.8895	0.9998
ENSG00000164011	ENSG00000164011	ZNF691	1:43312279-43318148	OK	2.64078	2.75054	0.0587502	0.0811305	0.88955	0.9998
ENSG00000120697	ENSG00000120697	ALG5	13:37523911-37633850	OK	21.9386	20.8461	-0.073694	-0.0822798	0.8896	0.9998
ENSG00000148484	ENSG00000148484	RSU1	10:16632609-16859527	OK	27.196	28.0889	0.0466057	0.0849892	0.88965	0.9998
ENSG00000186532	ENSG00000186532	SMYD4	17:1682778-1803376	OK	7.21755	6.78354	-0.0894711	-0.0629089	0.88965	0.9998
ENSG00000146243	ENSG00000146243	IRAK1BP1	6:79577188-79787953	OK	1.5524	1.45197	-0.0964964	-0.0599855	0.8897	0.9998
ENSG00000260051	ENSG00000260051	LA16c-390E6.4	16:1494934-1525581	OK	7.7285	9.4891	0.296083	0.0700209	0.88975	0.9998
ENSG00000129071	ENSG00000129071	MBD4	3:129149786-129158878	OK	15.2168	14.8225	-0.0378792	-0.071187	0.8898	0.9998
ENSG00000253710	ENSG00000253710	ALG11	13:52586533-52607736	OK	8.88091	8.58347	-0.0491457	-0.0809415	0.8899	0.9998
ENSG00000099974	ENSG00000099974	DDTL	22:24309088-24326106	OK	2.93424	3.43747	0.228357	0.11486	0.89	0.9998
ENSG00000147202	ENSG00000147202	DIAPH2	X:95939661-96897588	OK	2.89793	2.802	-0.0485655	-0.0865929	0.89	0.9998
ENSG00000112305	ENSG00000112305	SMAP1	6:71377478-71666741	OK	16.8565	17.2957	0.0371142	0.0786861	0.89005	0.9998
ENSG00000078304	ENSG00000078304	PPP2R5C	14:102228134-102394326	OK	61.9115	60.371	-0.0363505	-0.066748	0.89015	0.9998
ENSG00000243943	ENSG00000243943	ZNF512	2:27805896-27917840	OK	11.6527	10.9233	-0.0932515	-0.0492328	0.89015	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000242574	ENSG00000242574	HLA-DMB	6:32902405-32949282	OK	4.53233	5.181	0.192979	0.0669942	0.8902	0.9998
ENSG00000204778	ENSG00000204778	RP11-15J10.1	9:70181519-70216621	OK	3.82433	3.99712	0.0637518	0.0837658	0.89035	0.9998
ENSG00000106591	ENSG00000106591	MRPL32	7:42948324-42988557	OK	56.2998	53.4883	-0.0739066	-0.0837613	0.8904	0.9998
ENSG00000247516	ENSG00000247516	MIR4458HG	5:8333595-8463208	OK	4.71922	4.51633	-0.0633993	-0.0751342	0.8905	0.9998
ENSG00000161956	ENSG00000161956	SENP3	17:7465191-7536700	OK	37.7075	42.7198	0.180053	0.0812325	0.89055	0.9998
ENSG00000152359	ENSG00000152359	POC5	5:74969948-75013313	OK	9.31864	9.65731	0.0515017	0.0694882	0.8906	0.9998
ENSG00000272599	ENSG00000272599	RP11-152N13.16	10:74870216-75118617	OK	2.13601	1.81865	-0.232055	-0.0394901	0.8906	0.9998
ENSG00000113597	ENSG00000113597	TRAPPC13	5:64885506-65167553	OK	13.3924	12.4589	-0.104228	-0.0784893	0.89065	0.9998
ENSG00000145358	ENSG00000145358	DDIT4L	4:100869242-101136662	OK	1.59043	1.91973	0.271489	0.0562538	0.89065	0.9998
ENSG00000160563	ENSG00000160563	MED27	9:134735493-134955295	OK	18.5965	19.1292	0.0407468	0.0856267	0.8908	0.9998
ENSG00000133835	ENSG00000133835	HSD17B4	5:118788137-118972894	OK	40.6981	39.2897	-0.0508122	-0.064646	0.8909	0.9998
ENSG00000164938	ENSG00000164938	TP53INP1	8:95825538-96128683	OK	10.3598	10.756	0.0541498	0.0761799	0.89095	0.9998
ENSG00000116641	ENSG00000116641	DOCK7	1:62920398-63153969	OK	19.331	19.7885	0.0337472	0.0700672	0.89105	0.9998
ENSG00000118260	ENSG00000118260	CREB1	2:208104373-208490652	OK	21.6448	20.6569	-0.0673947	-0.0810835	0.8911	0.9998
ENSG00000133056	ENSG00000133056	PIK3C2B	1:204346977-204463852	OK	9.82195	10.3079	0.0696674	0.0530431	0.8911	0.9998
ENSG00000179632	ENSG00000179632	MAF1	8:145153535-145173218	OK	56.0553	54.3601	-0.0443029	-0.0821349	0.89115	0.9998
ENSG00000205643	ENSG00000205643	CDPF1	22:46639907-46646576	OK	6.77176	7.07144	0.0624735	0.084614	0.89115	0.9998
ENSG00000242261	ENSG00000242261	RP11-62J1.3	7:127937737-127983962	OK	3.91835	4.47065	0.190237	0.0927995	0.89115	0.9998
ENSG00000115464	ENSG00000115464	USP34	2:61404552-61697904	OK	14.5277	14.1447	-0.0385394	-0.0500288	0.89125	0.9998
ENSG00000179630	ENSG00000179630	LACC1	13:44398044-44468068	OK	2.79044	2.68851	-0.0536833	-0.0662277	0.8913	0.9998
ENSG00000122545	ENSG00000122545	7-Sep	7:35840541-35944917	OK	101.368	103.832	0.0346529	0.0791173	0.89135	0.9998
ENSG00000138400	ENSG00000138400	MDH1B	2:207602486-207657233	OK	1.30836	1.1835	-0.144702	-0.0475352	0.89135	0.9998
ENSG00000213889	ENSG00000213889	PPM1N	19:45988546-46005768	OK	1.32234	1.44914	0.132102	0.0788756	0.89145	0.9998
ENSG00000226085	ENSG00000226085	UQCRFS1P1	22:40139048-40289868	OK	12.229	12.6519	0.0490513	0.0819684	0.8915	0.9998
ENSG00000273000	ENSG00000273000	KB-1572G7.2	22:23950638-24059543	OK	1.57391	1.46111	-0.107285	-0.0598407	0.89155	0.9998
ENSG00000112685	ENSG00000112685	EXOC2	6:485132-693117	OK	29.6214	28.8767	-0.0367368	-0.0712995	0.8916	0.9998
ENSG00000171282	ENSG00000171282	RP11-1055B8.7	17:79369274-79433357	OK	16.9504	17.4964	0.0457355	0.0501099	0.89165	0.9998
ENSG00000108604	ENSG00000108604	SMARCD2	17:61909443-61920425	OK	69.2842	70.9104	0.0334692	0.0746772	0.8917	0.9998
ENSG00000121067	ENSG00000121067	SPOP	17:47676245-47755596	OK	16.4338	16.0334	-0.0355817	-0.060575	0.8918	0.9998
ENSG00000167088	ENSG00000167088	SNRPD1	18:19192227-19213485	OK	54.1423	52.4273	-0.0464367	-0.0705127	0.8918	0.9998
ENSG00000151466	ENSG00000151466	SCLT1	4:129730778-130037795	OK	7.38299	7.08049	-0.060355	-0.0793111	0.89185	0.9998
ENSG00000228540	ENSG00000228540	AC073326.3	7:110303109-111202573	OK	0.664715	0.780219	0.231142	0.0395722	0.89185	0.9998
ENSG00000233966	ENSG00000233966	UBE2SP1	17:15602890-15652629	OK	33.5795	34.845	0.0533734	0.0838881	0.8919	0.9998
ENSG00000099956	ENSG00000099956	SMARCB1	22:24129149-24181315	OK	44.5656	45.6546	0.0348307	0.0809455	0.89195	0.9998
ENSG00000272114	ENSG00000272114	RP1-261G23.7	6:43737920-43754224	OK	45.3699	54.3116	0.259526	0.0579677	0.89195	0.9998
ENSG00000078142	ENSG00000078142	PIK3C3	18:39535170-39667794	OK	31.054	32.4507	0.0634699	0.0892398	0.89205	0.9998
ENSG00000174903	ENSG00000174903	RAB1B	11:66036003-66056641	OK	87.3591	89.6238	0.0369241	0.0821945	0.89205	0.9998
ENSG00000181610	ENSG00000181610	MRPS23	17:55916841-55927417	OK	112.86	115.517	0.0335696	0.0821432	0.89205	0.9998
ENSG00000250615	ENSG00000250615	CTC-564N23.2	5:76367896-76462734	OK	1.49119	1.22602	-0.282486	-0.0882683	0.8921	0.9998
ENSG00000161642	ENSG00000161642	ZNF385A	12:54747444-54891472	OK	5.32543	5.55709	0.0614312	0.0731914	0.89215	0.9998
ENSG00000134108	ENSG00000134108	ARL8B	3:5163904-5229014	OK	59.9875	61.4444	0.0346205	0.0777261	0.8922	0.9998
ENSG00000159131	ENSG00000159131	GART	21:34876237-35349992	OK	32.3044	30.6718	-0.0748159	-0.0503921	0.8922	0.9998
ENSG00000273266	ENSG00000273266	HOXC4	12:54375292-54449814	OK	1.09762	1.12584	0.036625	0.0149697	0.89225	0.9998
ENSG00000141560	ENSG00000141560	FN3KRP	17:80674558-80692019	OK	35.4994	34.6629	-0.0344034	-0.0779884	0.8923	0.9998
ENSG00000168228	ENSG00000168228	ZCCHC4	4:25314406-25372005	OK	6.34208	6.53505	0.0432434	0.0804289	0.8924	0.9998
ENSG00000162852	ENSG00000162852	CNST	1:246729745-246831886	OK	13.4927	13.8359	0.0362369	0.0696455	0.89245	0.9998
ENSG00000174368	ENSG00000174368	PMS2P2	7:74880904-74988262	OK	1.3932	1.31271	-0.0858445	-0.078859	0.89255	0.9998
ENSG00000146677	ENSG00000146677	AC004453.8	7:44418719-44530479	OK	2.52864	2.18231	-0.21251	-0.0444979	0.89265	0.9998
ENSG00000156671	ENSG00000156671	SAMD8	10:76854191-76941881	OK	7.92761	7.70626	-0.0408567	-0.0768732	0.89265	0.9998
ENSG00000170191	ENSG00000170191	NANP	20:25593570-25677477	OK	8.65425	8.30703	-0.059077	-0.0854889	0.89265	0.9998
ENSG00000238142	ENSG00000238142	RP11-108M9.4	1:17066767-17299474	OK	7.94509	7.03068	-0.176399	-0.102688	0.89275	0.9998
ENSG00000240303	ENSG00000240303	ACAD11	3:132276981-132593067	OK	7.99401	8.45951	0.081655	0.0659124	0.8928	0.9998
ENSG00000140943	ENSG00000140943	MBTPS1	16:84087367-84150511	OK	31.5432	30.8585	-0.031659	-0.0655797	0.89285	0.9998
ENSG00000212664	ENSG00000212664	RP11-592N21.1	15:71389290-72075722	OK	2.90361	3.43246	0.241396	0.0905577	0.89285	0.9998
ENSG00000235436	ENSG00000235436	DPY19L2P4	7:89511666-89867451	OK	0.587988	0.675268	0.199673	0.100998	0.89285	0.9998
ENSG00000221944	ENSG00000221944	TIGD1	2:233412778-233547491	OK	0.92977	0.817301	-0.186007	-0.0709208	0.8929	0.9998
ENSG00000236233	ENSG00000236233	RP11-12A20.7	9:67792166-67794649	OK	1.34322	1.29157	-0.0565761	-0.0774879	0.893	0.9998
ENSG00000143537	ENSG00000143537	ADAM15	1:155006299-155035252	OK	57.8703	56.643	-0.0309247	-0.0643859	0.89305	0.9998
ENSG00000161835	ENSG00000161835	GRASP	12:52400723-52409673	OK	6.17697	5.94524	-0.0551629	-0.0689806	0.89315	0.9998
ENSG00000130254	ENSG00000130254	SAFB2	19:5587009-5668489	OK	22.2238	23.0871	0.0549813	0.0537614	0.8932	0.9998
ENSG00000137509	ENSG00000137509	PRCP	11:82534543-82782965	OK	20.7021	20.0865	-0.0435542	-0.0749265	0.8933	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000162419	ENSG00000162419	GMEB1	1:28995243-29045865	OK	2.97925	2.86345	-0.0571947	-0.0796627	0.8934	0.9998
ENSG00000124164	ENSG00000124164	VAPB	20:56964177-57026157	OK	36.9479	38.0823	0.0436275	0.0788894	0.8935	0.9998
ENSG00000122359	ENSG00000122359	ANXA11	10:81910644-81965328	OK	57.9798	59.3427	0.0335208	0.0683847	0.89355	0.9998
ENSG00000224934	ENSG00000224934	RP11-441O15.3	10:101190947-101197874	OK	0.681811	0.710816	0.0601034	0.079663	0.8938	0.9998
ENSG00000135632	ENSG00000135632	SMYD5	2:73441349-73454365	OK	23.3468	22.7498	-0.0373696	-0.0616436	0.89385	0.9998
ENSG00000116857	ENSG00000116857	TMEM9	1:201103899-201140702	OK	61.5648	63.1042	0.0356315	0.0782986	0.8939	0.9998
ENSG00000182858	ENSG00000182858	ALG12	22:50293876-50321188	OK	10.193	9.49377	-0.102525	-0.0840836	0.8939	0.9998
ENSG00000269958	ENSG00000269958	RP11-73M18.8	14:104019757-104181841	OK	10.302	10.0454	-0.036389	-0.0145713	0.8939	0.9998
ENSG00000168818	ENSG00000168818	STX18	4:4349866-4712665	OK	19.0439	17.7925	-0.0980609	-0.0640117	0.89405	0.9998
ENSG00000131446	ENSG00000131446	MGAT1	5:180217540-180242652	OK	45.655	46.8009	0.0357646	0.0644947	0.8941	0.9998
ENSG00000197747	ENSG00000197747	S100A10	1:151955390-151966866	OK	209.996	204.529	-0.0380545	-0.0842151	0.8941	0.9998
ENSG00000139436	ENSG00000139436	GIT2	12:110338068-110434194	OK	19.9618	19.2673	-0.0510863	-0.0685201	0.89415	0.9998
ENSG00000257167	ENSG00000257167	TMPO-AS1	12:98906750-98944157	OK	1.09787	1.3783	0.328186	0.101217	0.89415	0.9998
ENSG00000102984	ENSG00000102984	ZNF821	16:71879893-71962913	OK	3.18327	3.44285	0.113094	0.0550427	0.8943	0.9998
ENSG00000166793	ENSG00000166793	YPEL4	11:57405496-57429340	OK	3.33873	2.96219	-0.172633	-0.0856169	0.89435	0.9998
ENSG00000167604	ENSG00000167604	NFKBID	19:36378554-36393205	OK	1.89162	1.80795	-0.0652705	-0.0674319	0.89435	0.9998
ENSG00000251136	ENSG00000251136	RP11-37B2.1	8:90621637-90769955	OK	2.2654	2.36375	0.0613102	0.0703693	0.8944	0.9998
ENSG00000168434	ENSG00000168434	COG7	16:23399813-23468927	OK	10.1422	10.4964	0.0495137	0.0775579	0.89445	0.9998
ENSG00000083838	ENSG00000083838	ZNF446	19:58985383-59023780	OK	5.22267	5.40536	0.0496027	0.0743213	0.89455	0.9998
ENSG00000119760	ENSG00000119760	SUPT7L	2:27805896-27917840	OK	31.991	33.2588	0.0560706	0.0819678	0.89455	0.9998
ENSG00000068878	ENSG00000068878	PSME4	2:54091203-54532437	OK	14.8046	15.2205	0.0399684	0.0727795	0.8946	0.9998
ENSG00000136682	ENSG00000136682	CBWD2	2:114195267-114253766	OK	8.62979	8.36652	-0.0446965	-0.0810488	0.8946	0.9998
ENSG00000205763	ENSG00000205763	RP9P	7:32535037-33102409	OK	17.037	14.874	-0.195879	-0.0867388	0.89475	0.9998
ENSG00000067369	ENSG00000067369	TP53BP1	15:43699406-43802926	OK	11.7238	12.0048	0.0341678	0.0480467	0.8948	0.9998
ENSG00000100030	ENSG00000100030	MAPK1	22:22108788-22221970	OK	65.6636	68.9099	0.0696188	0.0812986	0.89485	0.9998
ENSG00000146066	ENSG00000146066	HIGD2A	5:175792470-175843570	OK	127.368	122.447	-0.0568461	-0.0828868	0.89485	0.9998
ENSG00000124733	ENSG00000124733	MEA1	6:42952236-42981706	OK	80.439	77.7844	-0.048415	-0.0823643	0.895	0.9998
ENSG00000172336	ENSG00000172336	POP7	7:100303675-100305118	OK	44.1437	45.2537	0.0358296	0.0795362	0.895	0.9998
ENSG00000196357	ENSG00000196357	ZNF565	19:36673187-36737159	OK	1.71289	1.4885	-0.202573	-0.0694166	0.895	0.9998
ENSG00000104835	ENSG00000104835	SARS2	19:39405905-39466550	OK	15.6485	14.9824	-0.0627479	-0.063223	0.8951	0.9998
ENSG00000112293	ENSG00000112293	GPLD1	6:24403152-24537435	OK	0.693587	0.767819	0.146691	0.0349254	0.89525	0.9998
ENSG00000171453	ENSG00000171453	POLR1C	6:43474706-43543812	OK	21.5808	20.1645	-0.097932	-0.0655957	0.8953	0.9998
ENSG00000256591	ENSG00000256591	RP11-286N22.8	11:61170120-61258403	OK	55.5741	58.7428	0.0799983	0.0763104	0.89535	0.9998
ENSG00000070814	ENSG00000070814	TCOF1	5:149737201-149779871	OK	28.0653	28.6923	0.0318805	0.0681844	0.89545	0.9998
ENSG00000266642	ENSG00000266642	RP11-20B24.4	17:27224755-27230089	OK	4.17484	3.86251	-0.112183	-0.0840817	0.8955	0.9998
ENSG00000149923	ENSG00000149923	PPP4C	16:30087298-30096698	OK	76.325	78.1107	0.033364	0.0787872	0.8956	0.9998
ENSG00000016864	ENSG00000016864	GLT8D1	3:52529353-52742182	OK	38.8368	36.7291	-0.0805036	-0.0583322	0.8957	0.9998
ENSG00000185189	ENSG00000185189	NRBP2	8:144915439-144924200	OK	21.245	21.7543	0.0341767	0.0765619	0.8957	0.9998
ENSG00000251675	ENSG00000251675	CTC-458I2.2	5:79407049-79551898	OK	3.72172	4.572	0.296856	0.125944	0.8957	0.9998
ENSG00000141568	ENSG00000141568	FOXK2	17:80477588-80606429	OK	45.4758	47.2809	0.056159	0.0611728	0.89575	0.9998
ENSG00000105617	ENSG00000105617	LENG1	19:54641443-54663620	OK	4.63177	4.92856	0.0896019	0.080597	0.89585	0.9998
ENSG00000242259	ENSG00000242259	C22orf39	22:19318220-19466738	OK	20.1649	18.4022	-0.13197	-0.106649	0.89585	0.9998
ENSG00000129235	ENSG00000129235	TXNDC17	17:6481467-6554954	OK	155.066	150.175	-0.0462387	-0.0780816	0.8959	0.9998
ENSG00000262026	ENSG00000262026	RP11-2C24.6	16:30789769-30798523	OK	1.03889	0.944429	-0.13753	-0.0728412	0.8959	0.9998
ENSG00000120733	ENSG00000120733	KDM3B	5:137688284-137772717	OK	21.4292	20.9536	-0.03238	-0.0576425	0.89595	0.9998
ENSG00000125812	ENSG00000125812	GZF1	20:23342786-23353700	OK	5.16339	4.97736	-0.0529377	-0.0666097	0.89595	0.9998
ENSG00000105738	ENSG00000105738	SIPA1L3	19:38397867-38699012	OK	3.8216	3.96264	0.0522843	0.0435399	0.896	0.9998
ENSG00000145439	ENSG00000145439	CBR4	4:169277885-169931426	OK	4.97938	4.70872	-0.0806293	-0.0574673	0.896	0.9998
ENSG00000120784	ENSG00000120784	ZFP30	19:37988062-38210691	OK	2.81103	2.93461	0.0620738	0.0486422	0.8961	0.9998
ENSG00000189046	ENSG00000189046	ALKBH2	12:109525995-109531436	OK	21.3034	20.6775	-0.04302	-0.0818817	0.8961	0.9998
ENSG00000197258	ENSG00000197258	EIF4BP6	7:103969103-104549001	OK	10.7105	11.7058	0.128202	0.0810842	0.8961	0.9998
ENSG00000172687	ENSG00000172687	ZNF738	19:21541731-21562104	OK	1.53468	1.61582	0.0743295	0.0824093	0.89615	0.9998
ENSG00000262477	ENSG00000262477	AC021224.1	18:29598334-30050447	OK	48.8366	51.5424	0.0777958	0.0793819	0.89615	0.9998
ENSG00000263053	ENSG00000263053	RP11-1055B8.6	17:79369274-79433357	OK	1.52565	1.35351	-0.172723	-0.0305258	0.89615	0.9998
ENSG00000125870	ENSG00000125870	SNRPB2	20:16695488-16722421	OK	28.2552	28.9548	0.0352828	0.0754117	0.8963	0.9998
ENSG00000128699	ENSG00000128699	ORMDL1	2:190635048-190649097	OK	39.5586	38.5805	-0.0361195	-0.0799068	0.8964	0.9998
ENSG00000134243	ENSG00000134243	SORT1	1:109852191-109940573	OK	68.5781	66.9335	-0.0350192	-0.0714376	0.8964	0.9998
ENSG00000108270	ENSG00000108270	AATF	17:35306174-35414171	OK	26.6577	27.265	0.0324953	0.0747205	0.89645	0.9998
ENSG00000182534	ENSG00000182534	MXRA7	17:74668023-74707098	OK	154.771	149.872	-0.0464039	-0.0799135	0.8965	0.9998
ENSG00000204533	ENSG00000204533	AC024580.1	19:56643967-56672262	OK	1.11062	0.97081	-0.19411	-0.0669031	0.8965	0.9998
ENSG00000106853	ENSG00000106853	PTGR1	9:114287438-114393569	OK	38.8758	39.8931	0.0372663	0.079783	0.89655	0.9998
ENSG00000186132	ENSG00000186132	C2orf76	2:120059800-120124404	OK	14.58	15.0444	0.0452371	0.0791483	0.89655	0.9998
ENSG00000177738	ENSG00000177738	CTD-2201E18.3	5:43014515-43192123	OK	3.16454	3.45648	0.12731	0.0766033	0.89665	0.9998
ENSG00000104859	ENSG00000104859	CLASRP	19:45542297-45574214	OK	22.0343	22.7357	0.0452072	0.0640832	0.8968	0.9998
ENSG00000129007	ENSG00000129007	CALML4	15:68346516-68549549	OK	7.39599	6.81627	-0.117761	-0.0671453	0.8968	0.9998
ENSG00000255423	ENSG00000255423	EBLN2	3:72937223-73118350	OK	0.765376	0.639628	-0.258934	-0.0661194	0.89685	0.9998
ENSG00000198000	ENSG00000198000	NOL8	9:95059639-95432547	OK	14.0687	14.5387	0.0474125	0.060786	0.89695	0.9998
ENSG00000118508	ENSG00000118508	RAB32	6:146864828-146876101	OK	157.949	154.505	-0.0318067	-0.0800657	0.897	0.9998
ENSG00000127452	ENSG00000127452	FBXL12	19:9920942-9938492	OK	15.3581	15.8389	0.0444658	0.0762633	0.897	0.9998
ENSG00000164040	ENSG00000164040	PGRMC2	4:129190396-129209984	OK	42.1139	40.9088	-0.0418855	-0.0799016	0.897	0.9998
ENSG00000104904	ENSG00000104904	OAZ1	19:2252250-2273487	OK	583.626	570.505	-0.0328054	-0.0768787	0.89705	0.9998
ENSG00000070423	ENSG00000070423	RNF126	19:647525-663277	OK	28.4069	29.2634	0.0428578	0.0761098	0.8971	0.9998
ENSG00000100823	ENSG00000100823	APEX1	14:20923349-20929771	OK	157.761	161.479	0.0336012	0.0745677	0.8971	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000161980	ENSG00000161980	POLR3K	16:96406-107669	OK	22.2312	23.1342	0.0574386	0.0800822	0.89715	0.9998
ENSG00000004478	ENSG00000004478	FKBP4	12:2904118-3050306	OK	77.3381	80.2993	0.054209	0.0703973	0.8972	0.9998
ENSG00000164093	ENSG00000164093	PITX2	4:111538578-111563279	OK	3.92503	4.07859	0.055366	0.0678323	0.8972	0.9998
ENSG00000174740	ENSG00000174740	PABPC5	X:90669876-90693583	OK	0.696268	0.663796	-0.0689029	-0.0723318	0.89725	0.9998
ENSG00000165688	ENSG00000165688	PMPCA	9:139305109-139318213	OK	41.7498	42.7258	0.0333367	0.0782143	0.8973	0.9998
ENSG00000166199	ENSG00000166199	ALKBH3	11:43902360-43942494	OK	30.5827	29.6722	-0.0436019	-0.0797532	0.8973	0.9998
ENSG00000250461	ENSG00000250461	RP11-631M6.2	5:60628099-60841997	OK	1.33148	1.136	-0.229065	-0.0767841	0.8973	0.9998
ENSG00000108179	ENSG00000108179	PPIF	10:81107224-81115093	OK	48.6434	47.4922	-0.0345548	-0.0772291	0.89735	0.9998
ENSG00000109576	ENSG00000109576	AADAT	4:170981372-171012850	OK	2.97958	3.09425	0.0544807	0.0699539	0.89735	0.9998
ENSG00000112414	ENSG00000112414	GPR126	6:142622990-142767403	OK	5.93739	6.08722	0.0359538	0.0461456	0.89735	0.9998
ENSG00000139291	ENSG00000139291	TMEM19	12:72003251-72097836	OK	25.7618	24.2336	-0.0882254	-0.083357	0.89735	0.9998
ENSG00000163590	ENSG00000163590	PPM1L	3:160473389-160796695	OK	1.48938	1.42837	-0.0603413	-0.0769046	0.89735	0.9998
ENSG00000120742	ENSG00000120742	SERP1	3:150259780-150348222	OK	56.0839	53.8232	-0.05936	-0.0612706	0.8974	0.9998
ENSG00000153790	ENSG00000153790	C7orf31	7:25174315-25219975	OK	5.75629	5.97391	0.0535348	0.0766864	0.89745	0.9998
ENSG00000006016	ENSG00000006016	CRLF1	19:18682539-18731849	OK	3.7072	4.21368	0.184752	0.0311288	0.8976	0.9998
ENSG00000168958	ENSG00000168958	MFF	2:228029280-228222550	OK	61.2412	59.6298	-0.0384688	-0.079049	0.8976	0.9998
ENSG00000128908	ENSG00000128908	INO80	15:41271077-41408552	OK	5.04125	5.23501	0.0544126	0.0580376	0.89765	0.9998
ENSG00000126756	ENSG00000126756	UXT	X:47511196-47519776	OK	100.043	97.7728	-0.0331197	-0.0751182	0.8977	0.9998
ENSG00000165637	ENSG00000165637	VDAC2	10:76969911-76991206	OK	136.034	139.434	0.0356081	0.0794499	0.8977	0.9998
ENSG00000198673	ENSG00000198673	FAM19A2	12:62102039-62811211	OK	0.992972	1.05735	0.0906278	0.0204326	0.8977	0.9998
ENSG00000135446	ENSG00000135446	CDK4	12:58117543-58154190	OK	244.499	251.26	0.0393542	0.0816605	0.8978	0.9998
ENSG00000196376	ENSG00000196376	SLC35F1	6:118228688-118638839	OK	0.782387	0.886153	0.179673	0.0707813	0.8978	0.9998
ENSG00000099822	ENSG00000099822	HCN2	19:589892-617159	OK	3.56751	3.67352	0.0422464	0.0745054	0.89785	0.9998
ENSG00000159917	ENSG00000159917	ZNF235	19:44711699-44809199	OK	2.00353	1.86186	-0.1058	-0.0724526	0.89785	0.9998
ENSG00000185515	ENSG00000185515	BRCC3	X:154289896-154384778	OK	8.84334	9.17251	0.0527246	0.0736201	0.89785	0.9998
ENSG00000106392	ENSG00000106392	C1GALT1	7:7196564-7288282	OK	42.3133	40.8283	-0.0515391	-0.0792332	0.8979	0.9998
ENSG00000006015	ENSG00000006015	C19orf60	19:18682539-18731849	OK	29.8363	32.2751	0.113357	0.0468469	0.898	0.9998
ENSG00000108823	ENSG00000108823	SGCA	17:48240883-48258539	OK	1.70899	1.60772	-0.088133	-0.0415907	0.898	0.9998
ENSG00000139344	ENSG00000139344	AMDHD1	12:96337070-96362370	OK	1.06868	1.02337	-0.0624914	-0.0681016	0.898	0.9998
ENSG00000108061	ENSG00000108061	SHOC2	10:112679300-112773425	OK	14.2885	14.6469	0.0357387	0.0667432	0.89805	0.9998
ENSG00000131375	ENSG00000131375	CAPN7	3:15247658-15294425	OK	18.8745	19.3429	0.0353658	0.0613187	0.8981	0.9998
ENSG00000087448	ENSG00000087448	KLHL42	12:27932753-27955973	OK	11.9319	12.4331	0.0593651	0.0752536	0.89825	0.9998
ENSG00000130340	ENSG00000130340	SNX9	6:158244295-158366109	OK	19.2325	18.8274	-0.0307166	-0.0749126	0.89825	0.9998
ENSG00000184752	ENSG00000184752	NDUFA12	12:95290830-95397546	OK	123.278	126.106	0.0327283	0.0770824	0.89825	0.9998
ENSG00000120334	ENSG00000120334	CENPL	1:173768687-173827684	OK	13.9169	13.2104	-0.0751614	-0.0725779	0.8983	0.9998
ENSG00000242960	ENSG00000242960	FTH1P23	3:72937223-73118350	OK	2.68072	3.18476	0.248561	0.0636753	0.89835	0.9998
ENSG00000122643	ENSG00000122643	NT5C3A	7:32535037-33102409	OK	32.3347	35.7021	0.142923	0.0850293	0.8984	0.9998
ENSG00000124444	ENSG00000124444	ZNF576	19:44100543-44124026	OK	12.8404	12.2116	-0.0724424	-0.0816464	0.89845	0.9998
ENSG00000125995	ENSG00000125995	ROMO1	20:34213952-34288906	OK	254.596	270.294	0.0863213	0.0829058	0.89845	0.9998
ENSG00000141994	ENSG00000141994	DUS3L	19:5782970-5791249	OK	17.8856	18.3948	0.0405061	0.05859	0.89845	0.9998
ENSG00000229273	ENSG00000229273	RP11-104G3.2	9:41954579-41955037	OK	0.840224	0.778309	-0.110431	-0.0809003	0.89845	0.9998
ENSG00000224186	ENSG00000224186	C5orf66	5:134363424-134736986	OK	0.871896	0.786872	-0.148028	-0.0345897	0.8985	0.9998
ENSG00000175390	ENSG00000175390	EIF3F	11:7991797-8023409	OK	163.106	166.689	0.0313449	0.0761719	0.89855	0.9998
ENSG00000261487	ENSG00000261487	AC135048.13	16:30930639-30967832	OK	1.26927	1.47031	0.212124	0.063786	0.89855	0.9998
ENSG00000261790	ENSG00000261790	AC005606.14	16:2034207-2044276	OK	1.14617	1.42418	0.313301	0.100606	0.8986	0.9998
ENSG00000122085	ENSG00000122085	MTERFD2	2:241938254-242041747	OK	21.518	20.8875	-0.0429069	-0.0705975	0.89865	0.9998
ENSG00000164649	ENSG00000164649	CDCA7L	7:21582832-21985702	OK	11.7553	11.4265	-0.0409293	-0.0656987	0.8987	0.9998
ENSG00000166260	ENSG00000166260	COX11	17:52976747-53241646	OK	40.2775	41.5426	0.0446175	0.0596989	0.8987	0.9998
ENSG00000214719	ENSG00000214719	AC005562.1	17:28900488-28999807	OK	7.48057	7.85034	0.0696082	0.0813272	0.8987	0.9998
ENSG00000166275	ENSG00000166275	C10orf32	10:104613979-104661656	OK	12.0041	12.4738	0.055371	0.0766114	0.8988	0.9998
ENSG00000013619	ENSG00000013619	MAMLD1	X:149529688-149682448	OK	0.661525	0.692755	0.0665479	0.0666878	0.89885	0.9998
ENSG00000163249	ENSG00000163249	CCNYL1	2:208576263-208626563	OK	6.80455	7.00775	0.0424521	0.0701911	0.89885	0.9998
ENSG00000259305	ENSG00000259305	ZHX1-C8ORF76	8:124232195-124287781	OK	1.3538	1.27378	-0.0878964	-0.0354674	0.8989	0.9998
ENSG00000078061	ENSG00000078061	ARAF	X:47420515-47479252	OK	19.0831	18.5189	-0.0432957	-0.0654408	0.89925	0.9998
ENSG00000204764	ENSG00000204764	RANBP17	5:170288873-170727019	OK	3.6307	3.74031	0.0429098	0.0518729	0.89925	0.9998
ENSG00000166503	ENSG00000166503	HDGFRP3	15:83776158-84108197	OK	22.3563	23.0302	0.0428468	0.0691547	0.89935	0.9998
ENSG00000175166	ENSG00000175166	PSMD2	3:183851806-184402546	OK	244.533	232.281	-0.0741562	-0.055425	0.8994	0.9998
ENSG00000244480	ENSG00000244480	AC005154.7	7:30536236-30673649	OK	0.969242	0.848503	-0.191937	-0.0277072	0.8994	0.9998
ENSG00000167995	ENSG00000167995	BEST1	11:61717292-61735132	OK	53.0053	49.968	-0.0851323	-0.0142977	0.89945	0.9998
ENSG00000173276	ENSG00000173276	ZBTB21	21:43406939-43445060	OK	4.01073	4.14215	0.0465151	0.0521316	0.89945	0.9998
ENSG00000244398	ENSG00000244398	RP11-466H18.1	11:16799841-17074583	OK	1390.7	1361.42	-0.0306961	-0.0763085	0.89945	0.9998
ENSG00000114416	ENSG00000114416	FXR1	3:180319917-180700541	OK	158.433	154.535	-0.0359394	-0.0737987	0.89955	0.9998
ENSG00000188206	ENSG00000188206	HNRNPU-AS1	1:244998623-245027844	OK	6.30935	5.59638	-0.172998	-0.0392688	0.89965	0.9998
ENSG00000080822	ENSG00000080822	CLDND1	3:98216447-98312567	OK	72.6451	70.3509	-0.0462976	-0.0576075	0.89975	0.9998
ENSG00000254909	ENSG00000254909	RP11-110I1.5	11:118868851-118901616	OK	1.24421	1.21102	-0.0390133	-0.00298922	0.89975	0.9998
ENSG00000102390	ENSG00000102390	PBDC1	X:75392770-75398039	OK	18.055	17.5709	-0.0392078	-0.0793757	0.8998	0.9998
ENSG00000123933	ENSG00000123933	MXD4	4:2249158-2264021	OK	10.242	10.5245	0.0392451	0.0541114	0.8998	0.9998
ENSG00000075624	ENSG00000075624	ACTB	7:5566781-5603415	OK	1061.12	1087.13	0.0349472	0.0723143	0.9	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000079999	ENSG00000079999	KEAP1	19:10596795-10614417	OK	17.7903	17.3607	-0.0352647	-0.0633323	0.9	0.9998
ENSG00000167468	ENSG00000167468	GPX4	19:1103935-1106787	OK	396.279	405.181	0.0320519	0.0768533	0.90005	0.9998
ENSG00000109920	ENSG00000109920	FNBP4	11:47738071-47788995	OK	32.5591	31.7872	-0.034615	-0.0472238	0.9001	0.9998
ENSG00000114547	ENSG00000114547	ROPN1B	3:125687986-125702297	OK	22.1024	21.5095	-0.0392281	-0.0748418	0.9004	0.9998
ENSG00000152240	ENSG00000152240	HAUS1	18:43664109-43708299	OK	22.465	19.1022	-0.233943	-0.0958969	0.9004	0.9998
ENSG00000179886	ENSG00000179886	TIGD5	8:144661805-144682485	OK	3.24326	3.8921	0.263104	0.0998176	0.9004	0.9998
ENSG00000116353	ENSG00000116353	MECR	1:29519384-29557454	OK	19.8034	19.2445	-0.0413004	-0.0683303	0.90045	0.9998
ENSG00000152219	ENSG00000152219	ARL14EP	11:30344597-30359774	OK	17.967	18.5821	0.0485667	0.0733558	0.90055	0.9998
ENSG00000168734	ENSG00000168734	PKIG	20:43160425-43280874	OK	40.0293	41.1918	0.0413032	0.0698291	0.90055	0.9998
ENSG00000255152	ENSG00000255152	MSH5-SAPCD1	6:31707724-31733365	OK	0.737228	0.835672	0.180827	0.0628099	0.90055	0.9998
ENSG00000164684	ENSG00000164684	ZNF704	8:81540685-81787016	OK	27.097	25.4919	-0.0880941	-0.0719399	0.9006	0.9998
ENSG00000100142	ENSG00000100142	POLR2F	22:38339527-38437922	OK	147.473	158.653	0.105419	0.082252	0.90065	0.9998
ENSG00000184068	ENSG00000184068	RP5-821D11.7	22:42227218-42303312	OK	0.725851	0.622541	-0.221505	-0.0391301	0.90065	0.9998
ENSG00000158019	ENSG00000158019	BRE	2:27994583-28561768	OK	17.0453	17.7548	0.0588291	0.0753667	0.90075	0.9998
ENSG00000114388	ENSG00000114388	NPRL2	3:50384760-50541675	OK	15.925	16.6999	0.0685427	0.0747934	0.90085	0.9998
ENSG00000136867	ENSG00000136867	SLC31A2	9:115913221-115983641	OK	8.63151	8.14856	-0.0830677	-0.0769815	0.90085	0.9998
ENSG00000185262	ENSG00000185262	UBALD2	17:74261282-74267375	OK	48.1204	50.4453	0.0680717	0.0769034	0.90085	0.9998
ENSG00000134330	ENSG00000134330	IAH1	2:9613786-9695921	OK	62.6543	60.6535	-0.0468228	-0.0735072	0.90095	0.9998
ENSG00000164338	ENSG00000164338	UTP15	5:72848159-72877794	OK	12.3463	12.7463	0.0460003	0.0662764	0.90095	0.9998
ENSG00000125447	ENSG00000125447	GGA3	17:73232693-73267308	OK	26.9372	25.9667	-0.0529378	-0.044071	0.90105	0.9998
ENSG00000126698	ENSG00000126698	DNAJC8	1:28525966-28559536	OK	71.7331	70.2391	-0.0303658	-0.0736861	0.9011	0.9998
ENSG00000224376	ENSG00000224376	AC017104.6	2:232253686-232259702	OK	1.72268	1.64584	-0.0658261	-0.0737497	0.90125	0.9998
ENSG00000272601	ENSG00000272601	RP11-155G14.5	7:128095893-128146656	OK	0.754571	0.632222	-0.255227	-0.0254233	0.90135	0.9998
ENSG00000166855	ENSG00000166855	CLPX	15:65440556-65477680	OK	26.6578	27.4545	0.0424827	0.0731289	0.9014	0.9998
ENSG00000076685	ENSG00000076685	NT5C2	10:104678049-104953056	OK	32.3336	33.3832	0.046087	0.0483101	0.9015	0.9998
ENSG00000140564	ENSG00000140564	FURIN	15:91411821-91426688	OK	14.9557	15.2812	0.0310634	0.0647135	0.90155	0.9998
ENSG00000110107	ENSG00000110107	PRPF19	11:60658201-60674060	OK	60.6627	61.9591	0.0305077	0.072748	0.9016	0.9998
ENSG00000139718	ENSG00000139718	SETD1B	12:122242085-122270562	OK	3.12429	3.04411	-0.0375046	-0.0740435	0.9016	0.9998
ENSG00000144026	ENSG00000144026	ZNF514	2:95752951-95831158	OK	4.31213	4.67344	0.116085	0.0709039	0.9016	0.9998
ENSG00000105668	ENSG00000105668	UPK1A	19:36157714-36169367	OK	0.762548	0.691525	-0.141048	-0.085884	0.9017	0.9998
ENSG00000104763	ENSG00000104763	ASAH1	8:17913933-17953903	OK	548.711	534.737	-0.0372184	-0.0696116	0.90175	0.9998
ENSG00000099889	ENSG00000099889	ARVCF	22:19863039-20004331	OK	4.7969	5.0829	0.0835514	0.0632739	0.90185	0.9998
ENSG00000267896	ENSG00000267896	AC018766.4	19:50321538-50364001	OK	1.66219	1.3999	-0.247769	-0.0388137	0.90185	0.9998
ENSG00000140545	ENSG00000140545	MFGE8	15:89441915-89456642	OK	82.2741	80.6292	-0.0291366	-0.0645999	0.9019	0.9998
ENSG00000213190	ENSG00000213190	MLLT11	1:151020215-151042801	OK	1.57364	1.48102	-0.087515	-0.0374084	0.9019	0.9998
ENSG00000215695	ENSG00000215695	RSC1A1	1:15943994-15995539	OK	3.18554	2.87804	-0.146448	-0.0793406	0.9019	0.9998
ENSG00000197024	ENSG00000197024	ZNF398	7:148823507-148880116	OK	5.60192	5.75914	0.0399333	0.074369	0.90195	0.9998
ENSG00000154330	ENSG00000154330	PGM5	9:70921443-71145977	OK	9.66733	9.32671	-0.0517481	-0.0696507	0.902	0.9998
ENSG00000234545	ENSG00000234545	FAM133B	7:92190106-92219708	OK	10.2904	10.574	0.0392219	0.0635276	0.9022	0.9998
ENSG00000072803	ENSG00000072803	FBXW11	5:171288552-171433877	OK	34.2409	34.9984	0.0315672	0.0625345	0.90225	0.9998
ENSG00000143590	ENSG00000143590	EFNA3	1:155036206-155060014	OK	4.15794	3.90085	-0.0920798	-0.0829895	0.90225	0.9998
ENSG00000241020	ENSG00000241020	RP11-727A23.1	11:82868029-83134559	OK	1.09783	0.932296	-0.235793	-0.0367048	0.9023	0.9998
ENSG00000116120	ENSG00000116120	FARSB	2:223435254-223521056	OK	36.6922	37.4928	0.0311405	0.0737612	0.90235	0.9998
ENSG00000248932	ENSG00000248932	RP11-319G6.1	3:139108656-139396859	OK	0.945252	0.997789	0.0780361	0.055978	0.90235	0.9998
ENSG00000177576	ENSG00000177576	C18orf32	18:47008027-47018906	OK	60.7553	67.3446	0.148553	0.0987504	0.9025	0.9998
ENSG00000005189	ENSG00000005189	AC004381.6	16:20621564-20936328	OK	4.38422	4.15595	-0.0771422	-0.0459536	0.9026	0.9998
ENSG00000066654	ENSG00000066654	THUMPD1	16:20621564-20936328	OK	8.40351	8.09938	-0.0531808	-0.0616993	0.9026	0.9998
ENSG00000105364	ENSG00000105364	MRPL4	19:10362576-10399695	OK	57.6986	60.6119	0.0710645	0.0777146	0.9026	0.9998
ENSG00000218891	ENSG00000218891	ZNF579	19:56088898-56092211	OK	5.23162	5.39677	0.0448378	0.0634222	0.90275	0.9998
ENSG00000115514	ENSG00000115514	TXNDC9	2:99613723-100106497	OK	35.0706	33.2005	-0.079059	-0.0665988	0.9028	0.9998
ENSG00000162591	ENSG00000162591	MEGF6	1:3406483-3528059	OK	1.93285	1.8548	-0.0594675	-0.0519452	0.90295	0.9998
ENSG00000187147	ENSG00000187147	RNF220	1:44870865-45140227	OK	36.3198	35.2841	-0.041738	-0.0755937	0.903	0.9998
ENSG00000074603	ENSG00000074603	DPP8	15:65734800-65810042	OK	15.2568	15.6686	0.0384241	0.0503593	0.90305	0.9998
ENSG00000103245	ENSG00000103245	NARFL	16:770580-791329	OK	14.037	13.5096	-0.0552548	-0.0591669	0.90305	0.9998
ENSG00000127589	ENSG00000127589	TUBBP1	8:30209388-30211034	OK	48.9095	47.8199	-0.0325061	-0.0763503	0.90305	0.9998
ENSG00000170584	ENSG00000170584	NUDCD2	5:162864574-162887146	OK	14.8662	13.5934	-0.129138	-0.0405366	0.90305	0.9998
ENSG00000188223	ENSG00000188223	AC002398.9	19:36230057-36245420	OK	1.99888	1.62108	-0.30224	-0.109594	0.9031	0.9998
ENSG00000168026	ENSG00000168026	TTC21A	3:39093488-39180394	OK	2.40305	2.2583	-0.0896285	-0.0246632	0.90315	0.9998
ENSG00000178184	ENSG00000178184	PARD6G	18:77905806-78005429	OK	12.1286	11.7718	-0.0430784	-0.0626084	0.90315	0.9998
ENSG00000178691	ENSG00000178691	SUZ12	17:30264036-30328064	OK	17.0719	16.7094	-0.030963	-0.0740802	0.90315	0.9998
ENSG00000236670	ENSG00000236670	KRT18P5	22:20778873-20850170	OK	0.939908	1.13664	0.274183	0.0847254	0.90315	0.9998
ENSG00000164180	ENSG00000164180	TMEM161B	5:87485449-87794514	OK	21.8939	21.3172	-0.0385106	-0.0612643	0.9032	0.9998
ENSG00000231259	ENSG00000231259	AC125232.1	2:87257799-87303536	OK	3.0032	2.90411	-0.0484069	-0.0765203	0.9032	0.9998
ENSG00000153902	ENSG00000153902	LGI4	19:35615416-35645204	OK	1.67178	1.76098	0.0749901	0.0688805	0.9033	0.9998
ENSG00000117859	ENSG00000117859	OSBPL9	1:52027537-52344477	OK	36.7821	35.4029	-0.0551362	-0.0655132	0.90335	0.9998
ENSG00000135482	ENSG00000135482	ZC3H10	12:56511942-56538455	OK	3.94963	3.61801	-0.126521	-0.0669	0.9034	0.9998
ENSG00000181789	ENSG00000181789	COPG1	3:128968448-128996614	OK	99.2865	96.64	-0.0389773	-0.069073	0.9035	0.9998
ENSG00000143450	ENSG00000143450	OAZ3	1:151728016-151766878	OK	1.25417	1.37294	0.130541	0.0294704	0.90365	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000255737	ENSG00000255737	AGAP2-AS1	12:58117543-58154190	OK	11.4283	10.3806	-0.138715	-0.0738505	0.90365	0.9998
ENSG00000175029	ENSG00000175029	CTBP2	10:126605711-126849739	OK	29.4124	30.2254	0.0393352	0.0558612	0.9037	0.9998
ENSG00000138814	ENSG00000138814	PPP3CA	4:101944565-102270040	OK	14.1157	13.7355	-0.0393962	-0.0603336	0.90375	0.9998
ENSG00000139675	ENSG00000139675	HNRNPA1L2	13:53191604-53217919	OK	3.78827	3.67909	-0.0421865	-0.0715129	0.90375	0.9998
ENSG00000124313	ENSG00000124313	IQSEC2	X:53262057-53350522	OK	2.97636	2.84361	-0.0658214	-0.073304	0.9039	0.9998
ENSG00000127774	ENSG00000127774	EMC6	17:3566195-3599698	OK	51.8196	49.9631	-0.0526342	-0.0706696	0.90395	0.9998
ENSG00000171566	ENSG00000171566	PLRG1	4:155456157-155471587	OK	33.7681	33.0196	-0.0323366	-0.0635305	0.90395	0.9998
ENSG00000152223	ENSG00000152223	EPG5	18:43427573-43547240	OK	21.0939	21.6353	0.036559	0.0478175	0.904	0.9998
ENSG00000165752	ENSG00000165752	STK32C	10:134020995-134145351	OK	5.98652	5.80803	-0.0436709	-0.0684698	0.904	0.9998
ENSG00000228109	ENSG00000228109	MFI2-AS1	3:196715491-196756687	OK	8.55507	7.60425	-0.169974	-0.041245	0.904	0.9998
ENSG00000256628	ENSG00000256628	ZBTB11-AS1	3:101367732-101398061	OK	1.06871	0.922269	-0.21261	-0.084178	0.904	0.9998
ENSG00000116977	ENSG00000116977	LGALS8	1:236681299-236767804	OK	21.8226	21.0492	-0.0520588	-0.0497802	0.90405	0.9998
ENSG00000135441	ENSG00000135441	BLOC1S1	12:56075329-56118489	OK	107.361	103.456	-0.0534512	-0.0738271	0.90405	0.9998
ENSG00000231084	ENSG00000231084	CTA-253N17.1	1:185126211-185260897	OK	1.20005	1.43365	0.2566	0.0717887	0.9041	0.9998
ENSG00000152942	ENSG00000152942	RAD17	5:68646810-68710628	OK	17.9778	18.7115	0.0577074	0.0595946	0.90415	0.9998
ENSG00000171204	ENSG00000171204	TMEM126B	11:85339628-85347580	OK	34.2604	35.1522	0.0370718	0.077769	0.90415	0.9998
ENSG00000121989	ENSG00000121989	ACVR2A	2:148602085-149275805	OK	0.981034	1.04479	0.0908434	0.0545881	0.9043	0.9998
ENSG00000204149	ENSG00000204149	AGAP6	10:51748077-51770259	OK	2.78453	2.70089	-0.0439973	-0.075079	0.9043	0.9998
ENSG00000214022	ENSG00000214022	REPIN1	7:150060865-150109558	OK	80.4814	82.3245	0.0326656	0.0621992	0.9043	0.9998
ENSG00000067113	ENSG00000067113	PPAP2A	5:54603587-54830878	OK	11.4912	12.1513	0.0805809	0.0676594	0.90445	0.9998
ENSG00000156515	ENSG00000156515	HK1	10:71029739-71161638	OK	94.3553	96.4382	0.0315002	0.0658984	0.90445	0.9998
ENSG00000258559	ENSG00000258559	AC005519.4	14:74752125-74769759	OK	1.2744	1.52428	0.258302	0.121325	0.90445	0.9998
ENSG00000155975	ENSG00000155975	VPS37A	8:17086736-17271037	OK	23.9084	22.8818	-0.0633205	-0.0631399	0.9045	0.9998
ENSG00000188315	ENSG00000188315	C3orf62	3:49306034-49378145	OK	2.39622	2.58547	0.109671	0.0450492	0.9045	0.9998
ENSG00000204685	ENSG00000204685	STARD7-AS1	2:96850596-96908359	OK	2.27581	2.04729	-0.152669	-0.0424962	0.90455	0.9998
ENSG00000063241	ENSG00000063241	ISOC2	19:55964351-55973710	OK	39.623	40.5198	0.0322912	0.0714621	0.9047	0.9998
ENSG00000160305	ENSG00000160305	DIP2A	21:47878811-47989926	OK	6.84471	6.63951	-0.0439122	-0.0785294	0.9048	0.9998
ENSG00000229944	ENSG00000229944	AC004797.1	17:47448101-47554350	OK	29.4022	35.5227	0.272819	0.12396	0.9049	0.9998
ENSG00000081138	ENSG00000081138	CDH7	18:63417487-63548638	OK	3.65378	3.48479	-0.0683144	-0.0740919	0.905	0.9998
ENSG00000230551	ENSG00000230551	CTB-89H12.4	5:148871759-148931007	OK	12.4519	11.8177	-0.0754198	-0.0724169	0.905	0.9998
ENSG00000272379	ENSG00000272379	RP1-257A7.5	6:12717892-13328815	OK	16.3673	13.9744	-0.228028	-0.0548199	0.90505	0.9998
ENSG00000154642	ENSG00000154642	C21orf91	21:19135631-19191703	OK	17.3489	16.8035	-0.0460835	-0.0683212	0.9051	0.9998
ENSG00000076108	ENSG00000076108	BAZ2A	12:56989379-57030600	OK	31.4664	30.8426	-0.0288869	-0.0372286	0.90515	0.9998
ENSG00000172888	ENSG00000172888	ZNF621	3:40566368-40616176	OK	8.45784	8.67781	0.0370412	0.0588113	0.90515	0.9998
ENSG00000189227	ENSG00000189227	C15orf61	15:67493370-67819628	OK	6.72429	6.28423	-0.097647	-0.0623062	0.90515	0.9998
ENSG00000078699	ENSG00000078699	CBFA2T2	20:32077880-32237842	OK	9.72617	9.99787	0.0397499	0.0659148	0.9052	0.9998
ENSG00000108556	ENSG00000108556	CHRNE	17:4736682-4806369	OK	0.933607	1.05348	0.174272	0.0527199	0.9052	0.9998
ENSG00000156030	ENSG00000156030	ELMSAN1	14:74181824-74269973	OK	7.11492	7.29024	0.0351186	0.0511452	0.9052	0.9998
ENSG00000116198	ENSG00000116198	CEP104	1:3728644-3773778	OK	22.679	21.8386	-0.0544729	-0.0674454	0.9053	0.9998
ENSG00000117682	ENSG00000117682	DHDDS	1:26758772-26797785	OK	20.7792	21.3434	0.0386465	0.0627399	0.9053	0.9998
ENSG00000119782	ENSG00000119782	FKBP1B	2:24232950-24286551	OK	3.01566	3.36936	0.160003	0.091426	0.9053	0.9998
ENSG00000163959	ENSG00000163959	SLC51A	3:195938357-196065374	OK	1.14046	1.20611	0.0807369	0.0150724	0.90535	0.9998
ENSG00000269963	ENSG00000269963	RP11-73M18.9	14:104019757-104181841	OK	3.95674	3.38533	-0.225016	-0.0487974	0.90535	0.9998
ENSG00000186300	ENSG00000186300	ZNF555	19:2841432-2860482	OK	2.29324	2.38887	0.0589416	0.0643166	0.90545	0.9998
ENSG00000242676	ENSG00000242676	ANKRD20A12P	1:142618768-142729975	OK	1.36414	1.46697	0.104848	0.0667135	0.9055	0.9998
ENSG00000157999	ENSG00000157999	ANKRD61	7:6048875-6098861	OK	0.583243	0.66393	0.186935	0.0258481	0.9056	0.9998
ENSG00000197448	ENSG00000197448	GSTK1	7:142941185-142985141	OK	157.203	153.92	-0.0304511	-0.0747362	0.9057	0.9998
ENSG00000102738	ENSG00000102738	MRPS31	13:41303431-41345309	OK	12.0535	12.377	0.0382091	0.071205	0.9058	0.9998
ENSG00000109171	ENSG00000109171	SLAIN2	4:48343338-48428229	OK	17.4999	16.8183	-0.0573126	-0.0505425	0.9058	0.9998
ENSG00000165572	ENSG00000165572	KBTBD6	13:41701704-41706882	OK	3.85146	3.75685	-0.0358817	-0.0698051	0.906	0.9998
ENSG00000092531	ENSG00000092531	SNAP23	15:42783430-42841000	OK	26.2581	25.3721	-0.0495175	-0.0667949	0.9061	0.9998
ENSG00000100918	ENSG00000100918	REC8	14:24641061-24708448	OK	1.17471	1.26337	0.10497	0.01099	0.9061	0.9998
ENSG00000064607	ENSG00000064607	SUGP2	19:19101696-19170563	OK	26.9344	26.2532	-0.0369563	-0.0479888	0.9062	0.9998
ENSG00000225361	ENSG00000225361	PPP1R26-AS1	9:138354572-138380739	OK	0.640601	0.579356	-0.144975	-0.0319862	0.9062	0.9998
ENSG00000071564	ENSG00000071564	TCF3	19:1609290-1652604	OK	31.1472	30.3028	-0.0396475	-0.0669067	0.90625	0.9998
ENSG00000168237	ENSG00000168237	GLYCTK	3:52288436-52333083	OK	4.53513	4.89025	0.108762	0.0579517	0.9063	0.9998
ENSG00000130590	ENSG00000130590	SAMD10	20:62588054-62680994	OK	4.37831	3.92002	-0.159513	-0.0511641	0.90635	0.9998
ENSG00000126249	ENSG00000126249	PDCD2L	19:34850384-34919178	OK	12.9812	14.9929	0.207856	0.0745388	0.90645	0.9998
ENSG00000233844	ENSG00000233844	KCNQ5-IT1	6:73331519-73908574	OK	1.43347	1.70034	0.246312	0.0605259	0.90645	0.9998
ENSG00000153250	ENSG00000153250	RBMS1	2:161128661-161350305	OK	28.1286	27.4921	-0.0330182	-0.0688288	0.9065	0.9998
ENSG00000174628	ENSG00000174628	IQCK	16:19566561-19897489	OK	8.66194	8.07422	-0.101367	-0.0537566	0.9066	0.9998
ENSG00000186687	ENSG00000186687	LYRM7	5:130494719-130541119	OK	4.21024	4.48703	0.0918574	0.0296985	0.9066	0.9998
ENSG00000204568	ENSG00000204568	MRPS18B	6:30568176-30594172	OK	51.7796	50.3336	-0.0408613	-0.0681966	0.9066	0.9998
ENSG00000099899	ENSG00000099899	TRMT2A	22:20067754-20114878	OK	30.6036	31.8585	0.0579773	0.0557864	0.90665	0.9998
ENSG00000115840	ENSG00000115840	SLC25A12	2:172640879-172947158	OK	12.2337	11.7545	-0.0576529	-0.0615718	0.90675	0.9998
ENSG00000116128	ENSG00000116128	BCL9	1:147013181-147098017	OK	13.6704	13.1475	-0.0562602	-0.0573328	0.9068	0.9998
ENSG00000141664	ENSG00000141664	ZCCHC2	18:60190239-60254942	OK	5.12735	5.27071	0.0397839	0.0601216	0.9068	0.9998
ENSG00000115446	ENSG00000115446	UNC50	2:99225041-99234978	OK	23.4261	22.8913	-0.0333183	-0.069092	0.90685	0.9998
ENSG00000141391	ENSG00000141391	SLMO1	18:12407894-12432237	OK	1.82351	1.9069	0.0645158	0.0654452	0.9069	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000233429	ENSG00000233429	HOTAIRM1	7:27132611-27142430	OK	6.21739	5.85108	-0.087606	-0.0817772	0.9069	0.9998
ENSG00000272872	ENSG00000272872	LL22NC03-N14H11.1	22:16147978-16193004	OK	2.06756	2.41212	0.222369	0.100852	0.90695	0.9998
ENSG00000115875	ENSG00000115875	SRSF7	2:38970740-38978636	OK	92.8847	90.8756	-0.0315481	-0.0693562	0.907	0.9998
ENSG00000167523	ENSG00000167523	SPATA33	16:89710838-89737680	OK	2.63138	2.42443	-0.118171	-0.0606512	0.9071	0.9998
ENSG00000004766	ENSG00000004766	CCDC132	7:92861652-92988338	OK	11.9855	12.2338	0.0295794	0.0530966	0.90715	0.9998
ENSG00000119185	ENSG00000119185	ITGB1BP1	2:9346893-9563676	OK	176.008	171.323	-0.0389199	-0.0688165	0.9072	0.9998
ENSG00000163444	ENSG00000163444	TMEM183A	1:202976513-202993976	OK	38.9513	39.9985	0.0382739	0.06972	0.90725	0.9998
ENSG00000100100	ENSG00000100100	PIK3IP1	22:31677578-31742218	OK	1.91956	2.11136	0.137396	0.0740364	0.9073	0.9998
ENSG00000066230	ENSG00000066230	SLC9A3	5:473350-524447	OK	1.11547	1.32967	0.253412	0.103525	0.90735	0.9998
ENSG00000185619	ENSG00000185619	PCGF3	4:699536-775637	OK	21.1273	20.5793	-0.0379142	-0.0610567	0.90735	0.9998
ENSG00000171877	ENSG00000171877	FRMD5	15:44162961-44487450	OK	14.0622	13.7315	-0.0343346	-0.0708936	0.90745	0.9998
ENSG00000114125	ENSG00000114125	RNF7	3:141457045-141466402	OK	71.3091	69.6136	-0.0347179	-0.074559	0.90755	0.9998
ENSG00000189171	ENSG00000189171	S100A13	1:153591262-153618782	OK	365.36	395.674	0.114994	0.0943137	0.9076	0.9998
ENSG00000121039	ENSG00000121039	RDH10	8:74202505-74268696	OK	5.23788	4.73245	-0.146397	-0.0411307	0.9077	0.9998
ENSG00000144158	ENSG00000144158	RP11-395L14.17	2:114415484-114416252	OK	3.03653	2.92957	-0.0517375	-0.0684991	0.90775	0.9998
ENSG00000196981	ENSG00000196981	WDR5B	3:122103022-122134882	OK	1.39736	1.20813	-0.209929	-0.0762023	0.90775	0.9998
ENSG00000258920	ENSG00000258920	FOXN3-AS1	14:89591214-90421121	OK	0.661352	0.788214	0.25317	0.0684677	0.9078	0.9998
ENSG00000114859	ENSG00000114859	CLCN2	3:183851806-184402546	OK	7.32837	6.69594	-0.130206	-0.0181769	0.90785	0.9998
ENSG00000197912	ENSG00000197912	SPG7	16:89557324-89624176	OK	15.9187	15.5755	-0.0314408	-0.0486513	0.90785	0.9998
ENSG00000257270	ENSG00000257270	RP11-521B24.5	14:105864915-105937066	OK	0.767448	0.630271	-0.284097	-0.0419397	0.90785	0.9998
ENSG00000132004	ENSG00000132004	FBXW9	19:12798866-12807457	OK	6.80021	6.61919	-0.038925	-0.0722586	0.9079	0.9998
ENSG00000158863	ENSG00000158863	FAM160B2	8:21946669-21962409	OK	23.3407	24.0949	0.0458764	0.0670989	0.9079	0.9998
ENSG00000099999	ENSG00000099999	RNF215	22:30727976-30825045	OK	6.05399	5.46536	-0.147571	-0.0802737	0.90795	0.9998
ENSG00000187778	ENSG00000187778	MCRS1	12:49932939-49961936	OK	33.7471	33.0184	-0.0314952	-0.0695881	0.908	0.9998
ENSG00000197136	ENSG00000197136	PCNXL3	11:65383243-65404910	OK	17.8302	18.2122	0.0305841	0.0562456	0.908	0.9998
ENSG00000234740	ENSG00000234740	RP11-272P10.2	9:13105702-13279589	OK	0.759125	0.883187	0.218381	0.0259427	0.908	0.9998
ENSG00000101940	ENSG00000101940	WDR13	X:48448429-48463581	OK	31.5215	32.2126	0.0312884	0.063341	0.90805	0.9998
ENSG00000165283	ENSG00000165283	STOML2	9:35099887-35103154	OK	120.381	122.719	0.027747	0.0673786	0.90805	0.9998
ENSG00000143315	ENSG00000143315	PIGM	1:159997461-160001783	OK	3.52937	3.44594	-0.0345136	-0.0683019	0.9082	0.9998
ENSG00000174917	ENSG00000174917	C19orf70	19:5674957-5720583	OK	91.0439	97.2709	0.095445	0.0743421	0.9082	0.9998
ENSG00000175170	ENSG00000175170	FAM182B	20:25744101-25848861	OK	1.02531	1.06739	0.0580253	0.0470728	0.9082	0.9998
ENSG00000233885	ENSG00000233885	YEATS2-AS1	3:183415605-183530413	OK	0.673895	0.749977	0.154322	0.0363436	0.9082	0.9998
ENSG00000129675	ENSG00000129675	ARHGEF6	X:135747705-135864247	OK	1.84395	1.89772	0.0414676	0.072879	0.90825	0.9998
ENSG00000253144	ENSG00000253144	RP11-281O15.7	5:178487415-178510538	OK	0.757488	0.636126	-0.251911	-0.0825255	0.90825	0.9998
ENSG00000176055	ENSG00000176055	MBLAC2	5:89754019-89810370	OK	2.94418	3.12385	0.0854592	0.064124	0.90835	0.9998
ENSG00000133794	ENSG00000133794	ARNTL	11:13298198-13408813	OK	8.28162	8.50271	0.03801	0.0558768	0.9084	0.9998
ENSG00000149557	ENSG00000149557	FEZ1	11:125315645-125369424	OK	2.48737	2.59714	0.0622993	0.0610739	0.9084	0.9998
ENSG00000153107	ENSG00000153107	ANAPC1	2:112523847-112642267	OK	13.9806	14.3928	0.0419267	0.0491779	0.9084	0.9998
ENSG00000067533	ENSG00000067533	RRP15	1:218458628-218511325	OK	14.8935	14.0389	-0.085245	-0.0702107	0.90845	0.9998
ENSG00000142396	ENSG00000142396	ERVK3-1	19:58739959-58827023	OK	39.6716	38.5059	-0.0430274	-0.0690347	0.90845	0.9998
ENSG00000243854	ENSG00000243854	RN7SL67P	12:19282647-19529334	OK	1.03701	0.869589	-0.25403	-0.0267086	0.90845	0.9998
ENSG00000170892	ENSG00000170892	TSEN34	19:54693788-54697585	OK	47.8542	46.8964	-0.0291695	-0.0695713	0.90855	0.9998
ENSG00000174516	ENSG00000174516	PELI3	11:66234215-66313709	OK	5.60661	5.27467	-0.0880476	-0.0689156	0.9086	0.9998
ENSG00000205808	ENSG00000205808	PPAPDC2	9:4490443-4666674	OK	1.18431	1.11223	-0.0905878	-0.0706292	0.90865	0.9998
ENSG00000172828	ENSG00000172828	CES3	16:66968346-67009051	OK	0.640626	0.596073	-0.103994	-0.034622	0.9087	0.9998
ENSG00000103657	ENSG00000103657	HERC1	15:63900816-64126141	OK	19.9959	20.6851	0.0488882	0.0371005	0.90875	0.9998
ENSG00000176248	ENSG00000176248	ANAPC2	9:140069235-140082989	OK	16.5236	16.8979	0.0323145	0.0608283	0.9088	0.9998
ENSG00000127804	ENSG00000127804	METTL16	17:2308855-2415185	OK	7.33367	7.15422	-0.0357412	-0.0474723	0.90885	0.9998
ENSG00000198353	ENSG00000198353	HOXC4	12:54375292-54449814	OK	6.78092	6.44392	-0.0735428	-0.0672089	0.90885	0.9998
ENSG00000104221	ENSG00000104221	BRF2	8:37641708-37707422	OK	7.62864	7.92922	0.0557526	0.0675894	0.9089	0.9998
ENSG00000011422	ENSG00000011422	PLAUR	19:44150246-44174699	OK	1.57589	1.53141	-0.0413091	-0.0453255	0.909	0.9998
ENSG00000161921	ENSG00000161921	CXCL16	17:4634722-4643217	OK	2.5757	2.72643	0.0820519	0.0688325	0.909	0.9998
ENSG00000196642	ENSG00000196642	RABL6	9:139685806-139735639	OK	59.8998	61.4193	0.0361406	0.0693917	0.909	0.9998
ENSG00000179364	ENSG00000179364	PACS2	14:105675622-105864484	OK	22.0109	22.8305	0.0527464	0.0571976	0.90905	0.9998
ENSG00000232320	ENSG00000232320	AC009299.5	2:162164548-162268228	OK	16.0225	17.6017	0.135619	0.067364	0.90905	0.9998
ENSG00000143669	ENSG00000143669	LYST	1:235824340-236046940	OK	150.968	144.933	-0.0588523	-0.0624952	0.90925	0.9998
ENSG00000272661	ENSG00000272661	RP4-548D19.3	7:150929574-150974982	OK	0.915783	1.10984	0.277276	0.0420624	0.90925	0.9998
ENSG00000100028	ENSG00000100028	SNRPD3	22:24936405-25024972	OK	128.891	124.742	-0.0472083	-0.0668186	0.9093	0.9998
ENSG00000224165	ENSG00000224165	DNAJC27-AS1	2:25166504-25262563	OK	1.08332	0.979959	-0.144672	-0.0382906	0.9093	0.9998
ENSG00000165338	ENSG00000165338	HECTD2	10:93170095-93274586	OK	3.19217	3.29263	0.0447029	0.0696766	0.90935	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000204954	ENSG00000204954	C12orf73	12:104235228-104359486	OK	13.8726	13.1653	-0.0754956	-0.0178242	0.90935	0.9998
ENSG00000136811	ENSG00000136811	ODF2	9:131217464-131263571	OK	17.3983	16.9931	-0.0340016	-0.066736	0.90945	0.9998
ENSG00000225422	ENSG00000225422	RBMS1P1	12:66582658-66651214	OK	1.4829	1.36205	-0.122644	-0.0625839	0.9095	0.9998
ENSG00000081181	ENSG00000081181	ARG2	14:68086514-68162531	OK	7.64435	8.51349	0.155357	0.0771303	0.90955	0.9998
ENSG00000161202	ENSG00000161202	DVL3	3:183851806-184402546	OK	44.8827	48.1417	0.101129	0.0526108	0.9096	0.9998
ENSG00000175787	ENSG00000175787	ZNF169	9:97021592-97063736	OK	1.4557	1.51288	0.0555859	0.0625845	0.9096	0.9998
ENSG00000185730	ENSG00000185730	ZNF696	8:144371845-144380231	OK	3.98205	4.12326	0.0502744	0.0653495	0.9096	0.9998
ENSG00000116688	ENSG00000116688	MFN2	1:12040237-12073571	OK	35.5075	34.8491	-0.0270014	-0.0561015	0.9098	0.9998
ENSG00000108296	ENSG00000108296	CWC25	17:36956686-36981734	OK	8.28813	8.5241	0.0405009	0.0611311	0.9099	0.9998
ENSG00000124596	ENSG00000124596	OARD1	6:40994771-41067715	OK	19.5997	18.7142	-0.0667027	-0.0688242	0.90995	0.9998
ENSG00000166582	ENSG00000166582	CENPV	17:15879873-16256970	OK	1.14195	1.06136	-0.105587	-0.019684	0.90995	0.9998
ENSG00000244119	ENSG00000244119	PDCL3P4	3:101431315-101432035	OK	1.25047	1.31081	0.0679899	0.0706619	0.91	0.9998
ENSG00000100321	ENSG00000100321	SYNGR1	22:39745929-39781593	OK	68.7947	70.6885	0.0391786	0.066715	0.91005	0.9998
ENSG00000118762	ENSG00000118762	PKD2	4:88928819-88998929	OK	19.2931	19.8079	0.0379917	0.0630797	0.91005	0.9998
ENSG00000162604	ENSG00000162604	TM2D1	1:62146717-62191095	OK	27.1449	27.8779	0.0384375	0.071819	0.9101	0.9998
ENSG00000204220	ENSG00000204220	PFDN6	6:33244916-33267101	OK	119.948	126.099	0.0721523	0.0709402	0.9101	0.9998
ENSG00000118007	ENSG00000118007	STAG1	3:135969147-136471220	OK	7.64934	7.36037	-0.0555568	-0.0675871	0.91025	0.9998
ENSG00000122507	ENSG00000122507	BBS9	7:33168855-33645680	OK	10.5358	10.2719	-0.0366083	-0.0568148	0.91025	0.9998
ENSG00000256087	ENSG00000256087	ZNF432	19:52534631-52599018	OK	2.44773	2.5499	0.0589962	0.0501113	0.91025	0.9998
ENSG00000148362	ENSG00000148362	C9orf142	9:139886869-139888436	OK	42.1792	41.2164	-0.0333115	-0.0689019	0.9103	0.9998
ENSG00000151779	ENSG00000151779	NBAS	2:15307031-15701454	OK	10.2633	10.4775	0.0297959	0.0546126	0.9103	0.9998
ENSG00000176974	ENSG00000176974	SHMT1	17:18231186-18266856	OK	15.6341	16.0188	0.0350689	0.0608036	0.9103	0.9998
ENSG00000114439	ENSG00000114439	BBX	3:107241782-107530171	OK	20.1704	20.6215	0.0319091	0.0362532	0.91035	0.9998
ENSG00000197948	ENSG00000197948	FCHSD1	5:141016516-141030986	OK	16.0848	16.5896	0.0445888	0.0608455	0.91035	0.9998
ENSG00000211643	ENSG00000211643	IGLV5-52	22:22657588-22677336	OK	0.976399	0.860155	-0.182874	-0.0387019	0.9104	0.9998
ENSG00000204272	ENSG00000204272	RP11-622K12.1	X:56755691-56844813	OK	16.1627	15.7158	-0.0404564	-0.0633556	0.9106	0.9998
ENSG00000169760	ENSG00000169760	NLGN1	3:173114073-174004434	OK	4.23891	4.09323	-0.0504518	-0.0510444	0.91065	0.9998
ENSG00000158435	ENSG00000158435	CNOT11	2:101436613-101886778	OK	40.2279	37.5424	-0.0996759	-0.0501525	0.9107	0.9998
ENSG00000008086	ENSG00000008086	CDKL5	X:18443702-18690229	OK	1.13836	1.17712	0.0482959	0.0649481	0.91075	0.9998
ENSG00000178996	ENSG00000178996	SNX18	5:53813588-53842415	OK	18.1065	17.7637	-0.0275795	-0.0677862	0.91075	0.9998
ENSG00000164713	ENSG00000164713	BRI3	7:97881690-98030380	OK	259.889	267.897	0.0437844	0.0677731	0.9108	0.9998
ENSG00000198690	ENSG00000198690	FAN1	15:31196054-31283810	OK	5.86356	5.6747	-0.0472332	-0.043909	0.9108	0.9998
ENSG00000140265	ENSG00000140265	ZSCAN29	15:43650369-43699293	OK	6.82915	7.08717	0.0535028	0.0505982	0.91085	0.9998
ENSG00000171928	ENSG00000171928	TVP23B	17:18684307-18710027	OK	33.3358	34.0422	0.0302498	0.0668654	0.9109	0.9998
ENSG00000158290	ENSG00000158290	CUL4B	X:119658463-119709649	OK	16.6878	16.3583	-0.0287696	-0.0592661	0.91095	0.9998
ENSG00000159322	ENSG00000159322	ADPGK	15:73043709-73090540	OK	32.8626	33.5173	0.0284575	0.0581631	0.91125	0.9998
ENSG00000011478	ENSG00000011478	QPCTL	19:46190711-46207247	OK	17.025	16.3143	-0.0615127	-0.0512799	0.9113	0.9998
ENSG00000168763	ENSG00000168763	CNNM3	2:97481981-97523832	OK	7.31861	7.01526	-0.0610726	-0.0528449	0.91135	0.9998
ENSG00000148498	ENSG00000148498	PARD3	10:34398487-35104253	OK	9.44306	9.21459	-0.0353333	-0.0575843	0.9114	0.9998
ENSG00000267904	ENSG00000267904	CTC-429P9.5	19:16589867-16771253	OK	0.724122	0.82734	0.192247	0.0185507	0.91145	0.9998
ENSG00000092439	ENSG00000092439	TRPM7	15:50844669-50979012	OK	9.23595	9.05275	-0.0289041	-0.0533358	0.9115	0.9998
ENSG00000175048	ENSG00000175048	ZDHHC14	6:157802164-158099178	OK	2.5899	2.68163	0.0502096	0.0509169	0.91155	0.9998
ENSG00000187098	ENSG00000187098	MITF	3:69788585-70017488	OK	190.912	195.108	0.0313614	0.0671211	0.9116	0.9998
ENSG00000213250	ENSG00000213250	RBMS2P1	12:94542498-94853764	OK	1.86567	1.64435	-0.182173	-0.0318816	0.9117	0.9998
ENSG00000168090	ENSG00000168090	COPS6	7:99686576-99689823	OK	159.932	163.012	0.0275167	0.0672759	0.91195	0.9998
ENSG00000259746	ENSG00000259746	HSPE1P3	15:91073156-91260372	OK	17.2404	19.6939	0.19195	0.0887252	0.91215	0.9998
ENSG00000213638	ENSG00000213638	ADAT3	19:1905212-1926016	OK	3.17338	3.36893	0.0862702	0.0659878	0.91235	0.9998
ENSG00000240086	ENSG00000240086	RP11-657O9.1	3:135074908-135158730	OK	3.42177	3.29589	-0.0540749	-0.0666191	0.91245	0.9998
ENSG00000028203	ENSG00000028203	VEZT	12:95611521-95696566	OK	20.623	20.2254	-0.0280835	-0.0472381	0.9125	0.9998
ENSG00000101361	ENSG00000101361	NOP56	20:2632790-2639039	OK	64.0443	62.5406	-0.0342778	-0.0674358	0.9126	0.9998
ENSG00000086506	ENSG00000086506	HBQ1	16:230451-231180	OK	0.767533	0.820677	0.0965869	0.07575	0.91265	0.9998
ENSG00000171126	ENSG00000171126	KCNG3	2:42669156-42721237	OK	0.762736	0.737639	-0.0482678	-0.068369	0.91275	0.9998
ENSG00000137500	ENSG00000137500	CCDC90B	11:82868029-83134559	OK	18.6027	17.8442	-0.0600553	-0.0703317	0.9128	0.9998
ENSG00000139684	ENSG00000139684	ESD	13:47345390-47371367	OK	104.089	102.123	-0.0275075	-0.0677932	0.9128	0.9998
ENSG00000116754	ENSG00000116754	SRSF11	1:70671364-70718735	OK	61.2013	62.4949	0.0301756	0.0567119	0.9129	0.9998
ENSG00000127463	ENSG00000127463	EMC1	1:19536994-19586622	OK	24.0137	23.4399	-0.0348929	-0.0510411	0.913	0.9998
ENSG00000132676	ENSG00000132676	DAP3	1:155579566-155829191	OK	159.089	154.209	-0.0449453	-0.0620387	0.913	0.9998
ENSG00000234602	ENSG00000234602	MCIDAS	5:54515441-54523143	OK	1.20831	1.24945	0.0483023	0.0617907	0.913	0.9998
ENSG00000260269	ENSG00000260269	CTD-2323K18.1	15:75759461-75918810	OK	1.11766	1.25282	0.164701	0.0393559	0.91305	0.9998
ENSG00000132432	ENSG00000132432	SEC61G	7:54819942-54872621	OK	188.973	185.315	-0.0282013	-0.066946	0.9131	0.9998
ENSG00000129158	ENSG00000129158	SERGEF	11:17809594-18063973	OK	28.5882	27.8205	-0.0392726	-0.0619763	0.91325	0.9998
ENSG00000116580	ENSG00000116580	GON4L	1:155579566-155829191	OK	18.551	17.9193	-0.0499898	-0.0321426	0.91335	0.9998
ENSG00000132824	ENSG00000132824	SERINC3	20:43124861-43150750	OK	94.5217	92.6024	-0.0295952	-0.0634177	0.91335	0.9998
ENSG00000102096	ENSG00000102096	PIM2	X:48770458-48776301	OK	5.59343	5.45436	-0.0363232	-0.0658425	0.9134	0.9998
ENSG00000154608	ENSG00000154608	CEP170P1	4:119388744-119476483	OK	2.41339	2.32322	-0.0549365	-0.0661925	0.91375	0.9998
ENSG00000165118	ENSG00000165118	C9orf64	9:86553225-86571901	OK	4.79959	4.67796	-0.0370316	-0.0611388	0.91375	0.9998
ENSG00000033170	ENSG00000033170	FUT8	14:65877309-66210839	OK	5.94439	5.80297	-0.0347376	-0.0555208	0.9138	0.9998
ENSG00000183208	ENSG00000183208	GDPGP1	15:90773206-90785315	OK	1.31177	1.42706	0.121529	0.0431186	0.9138	0.9998
ENSG00000180423	ENSG00000180423	HARBI1	11:46624410-46696368	OK	3.51979	3.2677	-0.107217	-0.0562693	0.91385	0.9998
ENSG00000111671	ENSG00000111671	SPSB2	12:6976282-7032861	OK	5.56323	5.03155	-0.14492	-0.024104	0.9139	0.9998
ENSG00000115073	ENSG00000115073	ACTR1B	2:98272430-98280570	OK	14.0975	14.4193	0.0325631	0.0644823	0.91395	0.9998
ENSG00000105889	ENSG00000105889	STEAP1B	7:22459062-22705152	OK	14.2468	15.6906	0.139263	0.0732199	0.914	0.9998
ENSG00000136813	ENSG00000136813	KIAA0368	9:114122971-114247025	OK	28.6697	28.0697	-0.0305131	-0.0574574	0.91405	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000161010	ENSG00000161010	C5orf45	5:179224596-179334859	OK	10.8498	11.4269	0.0747635	0.0168965	0.91405	0.9998
ENSG00000239969	ENSG00000239969	RP11-163E9.2	7:102004318-102067123	OK	5.80936	5.26934	-0.140758	-0.081524	0.9142	0.9998
ENSG00000137941	ENSG00000137941	TTLL7	1:84330710-84464833	OK	1.75648	1.82053	0.051672	0.0458453	0.91445	0.9998
ENSG00000244165	ENSG00000244165	P2RY11	19:10216898-10230596	OK	1.32144	1.1904	-0.150664	-0.0247424	0.91445	0.9998
ENSG00000255495	ENSG00000255495	FAM85A	8:12051975-12053789	OK	1.05943	1.02203	-0.0518504	-0.0625624	0.91455	0.9998
ENSG00000261093	ENSG00000261093	CTD-3126B10.1	16:2587964-2653189	OK	1.24661	1.0443	-0.255484	-0.0952838	0.91455	0.9998
ENSG00000134909	ENSG00000134909	ARHGAP32	11:128834954-129149219	OK	6.78579	6.62682	-0.0341999	-0.0446762	0.91465	0.9998
ENSG00000103811	ENSG00000103811	CTSH	15:79213399-79241916	OK	114.474	112.062	-0.0307257	-0.0644979	0.9147	0.9998
ENSG00000197362	ENSG00000197362	ZNF786	7:148766734-148787874	OK	2.53628	2.47105	-0.0375931	-0.0642048	0.9147	0.9998
ENSG00000102098	ENSG00000102098	SCML2	X:18257433-18372847	OK	3.31357	3.40337	0.0385789	0.0665921	0.91475	0.9998
ENSG00000139625	ENSG00000139625	MAP3K12	12:53835388-53893847	OK	10.6774	9.99526	-0.0952414	-0.0383998	0.91475	0.9998
ENSG00000184349	ENSG00000184349	EFNA5	5:106712589-107006596	OK	0.840763	0.788316	-0.0929258	-0.0541137	0.9149	0.9998
ENSG00000272760	ENSG00000272760	RP11-5C23.1	7:154720207-154794794	OK	0.755045	0.630486	-0.260099	-0.0722809	0.9149	0.9998
ENSG00000135778	ENSG00000135778	NTPCR	1:233086350-233431473	OK	55.3599	53.9663	-0.0367821	-0.0649153	0.91495	0.9998
ENSG00000005339	ENSG00000005339	CREBBP	16:3775054-3930727	OK	10.1591	9.94792	-0.030312	-0.0387243	0.91515	0.9998
ENSG00000269343	ENSG00000269343	ZNF587B	19:58281022-58427978	OK	4.57152	4.32735	-0.0791895	-0.0620248	0.91515	0.9998
ENSG00000174227	ENSG00000174227	PIGG	4:492988-533985	OK	22.6399	23.0592	0.0264775	0.0502232	0.9152	0.9998
ENSG00000166130	ENSG00000166130	IKBIP	12:99007182-99038891	OK	17.4681	17.8912	0.0345203	0.0645933	0.91525	0.9998
ENSG00000185627	ENSG00000185627	PSMD13	11:215457-252983	OK	89.6666	91.7127	0.0325513	0.0648663	0.91525	0.9998
ENSG00000259001	ENSG00000259001	RPPH1	14:20811206-20826064	OK	1.50652	1.75673	0.221668	0.0462839	0.91525	0.9998
ENSG00000268543	ENSG00000268543	CTD-2619J13.16	19:58929926-58930677	OK	0.846223	0.896753	0.0836732	0.0668635	0.9153	0.9998
ENSG00000237168	ENSG00000237168	RP11-353N4.3	1:149646784-149719362	OK	0.717339	0.633616	-0.179046	-0.0674526	0.91535	0.9998
ENSG00000150401	ENSG00000150401	DCUN1D2	13:114110133-114145267	OK	10.15	9.83243	-0.0458673	-0.0609009	0.9154	0.9998
ENSG00000152457	ENSG00000152457	DCLRE1C	10:14920818-14996431	OK	3.51514	3.6363	0.0488917	0.0553563	0.91545	0.9998
ENSG00000152465	ENSG00000152465	NMT2	10:15137383-15210692	OK	2.74985	2.64412	-0.0565639	-0.0552972	0.9156	0.9998
ENSG00000125449	ENSG00000125449	ARMC7	17:73106046-73127890	OK	6.98902	6.6942	-0.0621779	-0.0639215	0.91575	0.9998
ENSG00000155368	ENSG00000155368	DBI	2:120124496-120130126	OK	602.122	613.548	0.0271218	0.0675661	0.9159	0.9998
ENSG00000114098	ENSG00000114098	ARMC8	3:137906108-138048728	OK	19.4095	19.8488	0.032287	0.0524828	0.91595	0.9998
ENSG00000189077	ENSG00000189077	TMEM120A	7:75528517-75623977	OK	70.4426	67.9699	-0.0515525	-0.0633979	0.91595	0.9998
ENSG00000186272	ENSG00000186272	ZNF17	19:57874844-57988938	OK	1.81275	1.90377	0.070677	0.0359797	0.916	0.9998
ENSG00000226067	ENSG00000226067	LINC00869	1:149284644-149286975	OK	2.81612	2.92808	0.0562444	0.0628577	0.9161	0.9998
ENSG00000103549	ENSG00000103549	RNF40	16:30709029-30787628	OK	52.648	54.5108	0.0501643	0.0569305	0.9164	0.9998
ENSG00000067221	ENSG00000067221	STOML1	15:74275546-74286963	OK	4.85002	4.97469	0.0366183	0.0599532	0.9165	0.9998
ENSG00000119922	ENSG00000119922	IFIT2	10:90973325-91174314	OK	0.772109	0.909704	0.236593	0.0844407	0.9166	0.9998
ENSG00000175376	ENSG00000175376	EIF1AD	11:65764015-65771620	OK	25.0536	23.9859	-0.0628315	-0.0629795	0.9166	0.9998
ENSG00000183900	ENSG00000183900	AC099522.1	5:72740653-72744352	OK	1.67906	1.62594	-0.0463793	-0.0646549	0.9166	0.9998
ENSG00000144744	ENSG00000144744	UBA3	3:69024364-69129559	OK	36.2948	35.4391	-0.0344204	-0.0574446	0.9167	0.9998
ENSG00000120265	ENSG00000120265	PCMT1	6:150045450-150132556	OK	64.7981	66.1824	0.0304957	0.0617754	0.91675	0.9998
ENSG00000143373	ENSG00000143373	ZNF687	1:151252499-151300191	OK	13.3567	13.8522	0.052555	0.0531012	0.91675	0.9998
ENSG00000146950	ENSG00000146950	SHROOM2	X:9754495-9917483	OK	3.32448	3.24015	-0.0370686	-0.0525619	0.91675	0.9998
ENSG00000108443	ENSG00000108443	RPS6KB1	17:57970446-58096413	OK	15.7242	16.1178	0.0356699	0.057797	0.9168	0.9998
ENSG00000147649	ENSG00000147649	MTDH	8:98656406-98740998	OK	65.9783	67.4853	0.0325812	0.0532858	0.9168	0.9998
ENSG00000164919	ENSG00000164919	COX6C	8:100025493-100906290	OK	529.28	518.553	-0.0295385	-0.0630326	0.9168	0.9998
ENSG00000086712	ENSG00000086712	TXLNG	X:16804549-16888537	OK	5.4144	5.70055	0.0742991	0.0622569	0.91685	0.9998
ENSG00000162062	ENSG00000162062	C16orf59	16:2510080-2518214	OK	13.5206	13.1975	-0.0348975	-0.060633	0.91685	0.9998
ENSG00000167862	ENSG00000167862	ICT1	17:73008764-73017356	OK	30.9761	31.6439	0.0307739	0.0643539	0.91685	0.9998
ENSG00000167081	ENSG00000167081	PBX3	9:128509623-128729656	OK	4.83279	4.69157	-0.0427863	-0.058723	0.917	0.9998
ENSG00000125868	ENSG00000125868	DSTN	20:17550507-17590564	OK	98.606	100.704	0.0303739	0.0669001	0.91705	0.9998
ENSG00000172171	ENSG00000172171	TEFM	17:29224353-29286340	OK	12.909	13.2977	0.042799	0.0608437	0.91705	0.9998
ENSG00000103150	ENSG00000103150	MLYCD	16:83932730-83999937	OK	3.39277	3.52914	0.0568528	0.0604989	0.9172	0.9998
ENSG00000124508	ENSG00000124508	BTN2A2	6:26383323-26395102	OK	27.6254	27.0709	-0.0292552	-0.0555106	0.9172	0.9998
ENSG00000172986	ENSG00000172986	GXYLT2	3:72937223-73118350	OK	3.11175	2.82608	-0.138925	-0.0440896	0.9172	0.9998
ENSG00000100991	ENSG00000100991	TRPC4AP	20:33563205-33680674	OK	59.0399	57.9653	-0.0264986	-0.0641221	0.9173	0.9998
ENSG00000235001	ENSG00000235001	EIF4A1P2	Y:4868266-5610265	OK	0.928322	0.893445	-0.0552453	-0.0623632	0.9173	0.9998
ENSG00000173210	ENSG00000173210	ABLIM3	5:148521045-148721365	OK	15.2333	15.7064	0.0441307	0.060312	0.91745	0.9998
ENSG00000239557	ENSG00000239557	RP11-168J18.6	3:52350334-52434507	OK	1.54945	1.63456	0.0771473	0.0644674	0.91755	0.9998
ENSG00000198961	ENSG00000198961	PJA2	5:108670409-108745695	OK	17.2413	17.5588	0.0263305	0.059395	0.91765	0.9998
ENSG00000235706	ENSG00000235706	DICER1-AS1	14:95552564-95646263	OK	1.1791	1.07426	-0.134343	-0.0289428	0.9177	0.9998
ENSG00000068097	ENSG00000068097	HEATR6	17:58120554-58156292	OK	12.2967	12.5292	0.0270228	0.0461725	0.91785	0.9998
ENSG00000173915	ENSG00000173915	USMG5	10:105127723-105156223	OK	369.128	376.324	0.0278543	0.0611094	0.9179	0.9998
ENSG00000153558	ENSG00000153558	FBXL2	3:33318516-33482863	OK	11.4987	12.0726	0.0702716	0.0620817	0.91795	0.9998
ENSG00000149925	ENSG00000149925	ALDOA	16:30064410-30081778	OK	1955.18	1904.91	-0.0375783	-0.0599126	0.918	0.9998
ENSG00000243056	ENSG00000243056	EIF4EBP3	5:139781398-139973337	OK	4.5094	5.11904	0.182938	0.0419661	0.9181	0.9998
ENSG00000205268	ENSG00000205268	PDE7A	8:66556968-66754557	OK	5.54661	5.34114	-0.0544607	-0.0524008	0.9182	0.9998
ENSG00000105063	ENSG00000105063	PPP6R1	19:55738006-55770363	OK	49.5614	48.7377	-0.0241792	-0.0516933	0.91825	0.9998
ENSG00000141452	ENSG00000141452	C18orf8	18:21083472-21166862	OK	17.2346	17.9955	0.0623295	0.0460971	0.91825	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248866	ENSG00000248866	USP46-AS1	4:53525572-53527835	OK	1.13769	1.09371	-0.0568778	-0.0638262	0.91825	0.9998
ENSG00000253204	ENSG00000253204	RP5-1009N12.1	8:30778575-30778851	OK	1.09103	1.0604	-0.0410789	-0.02096	0.9183	0.9998
ENSG00000189308	ENSG00000189308	LIN54	4:83739813-83934079	OK	6.04341	5.72673	-0.0776527	-0.0672515	0.91855	0.9998
ENSG00000130821	ENSG00000130821	SLC6A8	X:152935184-152962048	OK	85.401	83.83	-0.0267859	-0.0452535	0.9186	0.9998
ENSG00000156052	ENSG00000156052	GNAQ	9:80331002-80646374	OK	17.7746	18.276	0.0401339	0.0492765	0.9186	0.9998
ENSG00000176731	ENSG00000176731	C8orf59	8:86089459-86132650	OK	100.593	96.8452	-0.0547757	-0.0646733	0.9187	0.9998
ENSG00000182774	ENSG00000182774	RPS17L	15:83205503-83378666	OK	0.651186	0.702946	0.110343	0.0196657	0.9187	0.9998
ENSG00000240370	ENSG00000240370	RPL13P5	12:6976282-7032861	OK	2.93922	3.13724	0.0940612	0.00818615	0.9188	0.9998
ENSG00000123570	ENSG00000123570	RAB9B	X:103077251-103087158	OK	1.63565	1.59455	-0.0367203	-0.0619902	0.91885	0.9998
ENSG00000159247	ENSG00000159247	TUBBP5	9:141044564-141071821	OK	6.96978	7.13459	0.0337172	0.0605308	0.9189	0.9998
ENSG00000122490	ENSG00000122490	PQLC1	18:77662419-77711664	OK	16.1488	16.4831	0.0295612	0.0588063	0.91895	0.9998
ENSG00000184897	ENSG00000184897	H1FX	3:129033614-129045068	OK	10.9452	10.7058	-0.0319003	-0.0617802	0.91895	0.9998
ENSG00000237819	ENSG00000237819	AC002454.1	7:92234234-92546501	OK	0.754013	0.815013	0.112234	0.0128952	0.9191	0.9998
ENSG00000105671	ENSG00000105671	DDX49	19:19010322-19057640	OK	24.2258	25.1369	0.0532634	0.0524446	0.9192	0.9998
ENSG00000142961	ENSG00000142961	MOB3C	1:47004367-47082563	OK	1.89065	1.97439	0.0625276	0.053415	0.9192	0.9998
ENSG00000203666	ENSG00000203666	EFCAB2	1:245132651-245290466	OK	14.2543	14.6459	0.0390954	0.0605296	0.9192	0.9998
ENSG00000127580	ENSG00000127580	WDR24	16:734621-755829	OK	4.17455	4.28191	0.0366352	0.0609449	0.91925	0.9998
ENSG00000144642	ENSG00000144642	RBMS3	3:29305684-30051886	OK	0.852075	0.810034	-0.0729979	-0.0400746	0.91925	0.9998
ENSG00000244256	ENSG00000244256	RN7SL130P	1:63906440-64125916	OK	0.764295	0.686224	-0.15545	-0.0114584	0.91925	0.9998
ENSG00000178927	ENSG00000178927	C17orf62	17:80347098-80408705	OK	42.9854	44.1299	0.0379102	0.0503635	0.9193	0.9998
ENSG00000267787	ENSG00000267787	RP11-35G9.5	18:55297533-55470333	OK	0.668054	0.629674	-0.0853598	-0.0567151	0.9193	0.9998
ENSG00000153485	ENSG00000153485	TMEM251	14:93651295-93695561	OK	57.4608	55.8257	-0.0416494	-0.0623192	0.9194	0.9998
ENSG00000268397	ENSG00000268397	AC008443.1	5:180663908-180699308	OK	1.4125	1.57172	0.154099	0.0153625	0.9194	0.9998
ENSG00000267701	ENSG00000267701	RP11-28F1.2	18:60790578-60987361	OK	0.653457	0.618809	-0.0785999	-0.00927815	0.91945	0.9998
ENSG00000231770	ENSG00000231770	TMEM44-AS1	3:194304739-194393206	OK	2.50265	2.7991	0.161507	0.0618482	0.91955	0.9998
ENSG00000129559	ENSG00000129559	NEDD8	14:24641061-24708448	OK	234.603	241.666	0.0427931	0.0607063	0.91965	0.9998
ENSG00000224597	ENSG00000224597	PTCHD3P1	10:29698330-30025710	OK	9.66752	9.26517	-0.0613278	-0.043463	0.91965	0.9998
ENSG00000122378	ENSG00000122378	FAM213A	10:82167584-82192753	OK	78.0357	76.5815	-0.0271378	-0.0630137	0.91975	0.9998
ENSG00000168152	ENSG00000168152	THAP9	4:83739813-83934079	OK	1.42238	1.29138	-0.139395	-0.039078	0.91975	0.9998
ENSG00000234769	ENSG00000234769	WASH4P	16:61552-88321	OK	0.941435	0.970631	0.0440618	0.0479228	0.91985	0.9998
ENSG00000148834	ENSG00000148834	GSTO1	10:105995113-106027217	OK	481.829	473.617	-0.0248003	-0.0611772	0.9199	0.9998
ENSG00000151327	ENSG00000151327	FAM177A1	14:35514112-35786699	OK	50.2176	47.4452	-0.0819313	-0.0609253	0.9199	0.9998
ENSG00000127311	ENSG00000127311	HELB	12:66696324-66737423	OK	0.924961	0.954364	0.0451468	0.0510247	0.91995	0.9998
ENSG00000163608	ENSG00000163608	C3orf17	3:112709293-112902148	OK	33.8676	33.1324	-0.0316612	-0.053099	0.91995	0.9998
ENSG00000169359	ENSG00000169359	SLC33A1	3:155538812-155572218	OK	25.2498	24.703	-0.0315877	-0.0558369	0.92	0.9998
ENSG00000176354	ENSG00000176354	AC097359.1	3:37283279-37408242	OK	1.42818	1.64903	0.207441	0.0652694	0.92	0.9998
ENSG00000160401	ENSG00000160401	C9orf117	9:130374543-130497604	OK	0.633452	0.696225	0.136318	0.0115417	0.92005	0.9998
ENSG00000239305	ENSG00000239305	RNF103	2:86730553-87005164	OK	7.39024	7.78641	0.0753388	0.0499819	0.9201	0.9998
ENSG00000113441	ENSG00000113441	LNPEP	5:96149730-96373219	OK	7.85889	7.65855	-0.0372552	-0.0600893	0.92015	0.9998
ENSG00000138448	ENSG00000138448	ITGAV	2:187454791-187630685	OK	37.6609	38.3862	0.0275205	0.0489234	0.9203	0.9998
ENSG00000153446	ENSG00000153446	C16orf89	16:4932507-5147809	OK	0.979879	1.04473	0.0924511	0.0202018	0.9204	0.9998
ENSG00000197694	ENSG00000197694	SPTAN1	9:131314865-131419066	OK	48.7385	49.5873	0.0249092	0.0406247	0.92055	0.9998
ENSG00000113732	ENSG00000113732	ATP6V0E1	5:172410759-172462448	OK	281.032	286.21	0.0263416	0.0590537	0.9206	0.9998
ENSG00000143553	ENSG00000143553	SNAPIN	1:153631129-153634306	OK	76.451	75.0986	-0.0257489	-0.061715	0.9207	0.9998
ENSG00000119917	ENSG00000119917	IFIT3	10:90973325-91174314	OK	5.68759	6.03301	0.085062	0.0643637	0.92075	0.9998
ENSG00000172830	ENSG00000172830	SSH3	11:67070918-67080078	OK	8.42923	8.61108	0.0307931	0.0478162	0.92075	0.9998
ENSG00000128694	ENSG00000128694	OSGEPL1	2:190539015-190630282	OK	11.9564	11.6987	-0.0314309	-0.0596543	0.9208	0.9998
ENSG00000111361	ENSG00000111361	EIF2B1	12:124086623-124118313	OK	33.878	34.7257	0.0356559	0.057475	0.92085	0.9998
ENSG00000166225	ENSG00000166225	FRS2	12:69864128-69973562	OK	8.40855	8.20147	-0.035974	-0.0459246	0.9209	0.9998
ENSG00000250451	ENSG00000250451	HOXC-AS1	12:54375292-54449814	OK	0.748236	0.831989	0.153071	0.0257235	0.921	0.9998
ENSG00000140632	ENSG00000140632	GLYR1	16:4853203-4932361	OK	33.3073	32.5569	-0.0328714	-0.0420019	0.9211	0.9998
ENSG00000101138	ENSG00000101138	CSTF1	20:54967426-54979518	OK	30.5884	31.1616	0.0267847	0.0569465	0.9212	0.9998
ENSG00000155545	ENSG00000155545	MIER3	5:56195867-56267502	OK	9.09822	8.91038	-0.0300966	-0.0433644	0.9214	0.9998
ENSG00000100568	ENSG00000100568	VTI1B	14:68086514-68162531	OK	92.9974	96.1257	0.0477315	0.0585203	0.92145	0.9998
ENSG00000155275	ENSG00000155275	TRMT44	4:8368008-8514337	OK	3.88271	3.7403	-0.0539118	-0.0498784	0.9215	0.9998
ENSG00000247228	ENSG00000247228	RP11-296I10.3	16:70147528-70221264	OK	1.32924	1.24186	-0.0980919	-0.0568471	0.9216	0.9998
ENSG00000134255	ENSG00000134255	CEPT1	1:111659954-111727724	OK	13.7912	13.2705	-0.0555237	-0.0586007	0.92165	0.9998
ENSG00000180385	ENSG00000180385	EMC3-AS1	3:10000400-10052893	OK	1.28104	1.17885	-0.119934	-0.0315077	0.9217	0.9998
ENSG00000086544	ENSG00000086544	ITPKC	19:41197433-41271294	OK	5.23804	5.04788	-0.0533518	-0.0566144	0.92175	0.9998
ENSG00000136485	ENSG00000136485	DCAF7	17:61627821-61671639	OK	59.0153	57.7088	-0.0322988	-0.0562258	0.9218	0.9998
ENSG00000272870	ENSG00000272870	RP11-798M19.6	4:174284930-174298683	OK	1.07343	1.19395	0.153521	0.0478854	0.9219	0.9998
ENSG00000204351	ENSG00000204351	SKIV2L	6:31919863-31937532	OK	35.4213	36.3577	0.037644	0.042412	0.92195	0.9998
ENSG00000069943	ENSG00000069943	PIGB	15:55495163-55800432	OK	7.03301	7.42832	0.078894	0.0399919	0.92205	0.9998
ENSG00000105258	ENSG00000105258	POLR2I	19:36602103-36616849	OK	54.9016	52.6516	-0.0603725	-0.0648534	0.9221	0.9998
ENSG00000135847	ENSG00000135847	ACBD6	1:180199420-180472089	OK	48.5966	49.6136	0.0298814	0.0577979	0.92215	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000170633	ENSG00000170633	RNF34	12:121837843-122031409	OK	15.6352	15.2245	-0.0384	-0.0572217	0.92235	0.9998
ENSG00000113851	ENSG00000113851	CRBN	3:3168599-3221394	OK	20.7733	20.1829	-0.0415986	-0.0539771	0.9224	0.9998
ENSG00000187607	ENSG00000187607	ZNF286A	17:15602890-15652629	OK	8.24954	8.63124	0.0652543	0.0519705	0.9224	0.9998
ENSG00000113141	ENSG00000113141	IK	5:140018324-140042064	OK	48.2216	49.282	0.0313827	0.0552659	0.9225	0.9998
ENSG00000225137	ENSG00000225137	DYNC1I2P1	10:52024737-52026575	OK	6.16877	6.0388	-0.030721	-0.0575303	0.9225	0.9998
ENSG00000236850	ENSG00000236850	BMS1P20	22:22657588-22677336	OK	4.10381	4.24472	0.0487063	0.058948	0.9225	0.9998
ENSG00000257511	ENSG00000257511	RP11-278C7.1	12:32832133-32908836	OK	0.666548	0.596242	-0.160809	-0.025283	0.92255	0.9998
ENSG00000196656	ENSG00000196656	AC004057.1	4:113739264-114304896	OK	342.483	350.083	0.0316662	0.0572872	0.92265	0.9998
ENSG00000266934	ENSG00000266934	RP11-332H18.3	17:58754813-59488916	OK	1.33889	1.47415	0.138846	0.0172814	0.92265	0.9998
ENSG00000267368	ENSG00000267368	UPK3BL	7:102122891-102312088	OK	2.7421	2.89867	0.0801078	0.0582044	0.92265	0.9998
ENSG00000038358	ENSG00000038358	EDC4	16:67906925-67922758	OK	13.8877	14.2057	0.0326699	0.0469916	0.9227	0.9998
ENSG00000188092	ENSG00000188092	GPR89B	1:147400505-147465753	OK	3.29574	3.40668	0.0477671	0.0585788	0.92275	0.9998
ENSG00000102606	ENSG00000102606	ARHGEF7	13:111766158-111958084	OK	19.5464	19.1395	-0.0303459	-0.0461614	0.9228	0.9998
ENSG00000267493	ENSG00000267493	CIRBP-AS1	19:1259383-1274879	OK	1.76675	1.59028	-0.151816	-0.021376	0.9228	0.9998
ENSG00000118292	ENSG00000118292	C1orf54	1:150237803-150253327	OK	4.62399	5.12982	0.14977	0.036922	0.92285	0.9998
ENSG00000179021	ENSG00000179021	C3orf38	3:88101093-88217879	OK	11.2015	10.4535	-0.0997092	-0.0597028	0.92285	0.9998
ENSG00000250327	ENSG00000250327	RP11-173M11.2	4:187025572-187093821	OK	0.636451	0.697926	0.133025	0.0619156	0.92285	0.9998
ENSG00000156471	ENSG00000156471	PTDSS1	8:97273942-97349223	OK	67.9046	66.4315	-0.0316427	-0.0597325	0.92295	0.9998
ENSG00000234912	ENSG00000234912	LINC00338	17:75082797-75213179	OK	4.84566	5.37909	0.150671	0.0633013	0.92295	0.9998
ENSG00000149932	ENSG00000149932	TMEM219	16:29952205-29984373	OK	70.9737	72.2468	0.0256496	0.0580443	0.9231	0.9998
ENSG00000256545	ENSG00000256545	AL139819.1	10:102106880-102124591	OK	166.166	152.742	-0.121527	-0.0557723	0.92315	0.9998
ENSG00000008300	ENSG00000008300	CELSR3	3:48673901-48700348	OK	2.51907	2.45256	-0.0386032	-0.0383066	0.9232	0.9998
ENSG00000085274	ENSG00000085274	MYNN	3:169490618-169507504	OK	11.5225	11.7534	0.0286223	0.058352	0.9232	0.9998
ENSG00000164576	ENSG00000164576	SAP30L	5:153825516-153840614	OK	21.4129	20.5	-0.062856	-0.0593275	0.9232	0.9998
ENSG00000188825	ENSG00000188825	LINC00910	17:41447212-41466567	OK	0.786352	0.754152	-0.0603205	-0.0392406	0.9232	0.9998
ENSG00000106244	ENSG00000106244	PDAP1	7:98923520-99063954	OK	139.542	127.804	-0.126774	-0.0696364	0.92325	0.9998
ENSG00000106266	ENSG00000106266	SNX8	7:2291404-2420380	OK	72.1753	69.2554	-0.059579	-0.0463187	0.92325	0.9998
ENSG00000180672	ENSG00000180672	AC007362.1	2:206546713-206662857	OK	11.5049	12.6373	0.135439	0.0682487	0.92325	0.9998
ENSG00000111912	ENSG00000111912	NCOA7	6:126102306-126252266	OK	7.48883	7.31996	-0.0329053	-0.0450414	0.9233	0.9998
ENSG00000162775	ENSG00000162775	RBM15	1:110828996-110889299	OK	6.51859	6.65246	0.0293284	0.0608969	0.9233	0.9998
ENSG00000186666	ENSG00000186666	BCDIN3D	12:50184928-50236912	OK	2.74399	2.50192	-0.133242	-0.0582115	0.9233	0.9998
ENSG00000253861	ENSG00000253861	SLC2A3P1	5:167975499-168006605	OK	1.59213	1.85299	0.218896	0.0507849	0.9233	0.9998
ENSG00000257086	ENSG00000257086	RP11-783K16.13	11:64011955-64016966	OK	1.00632	1.12734	0.163835	0.0314885	0.9234	0.9998
ENSG00000108509	ENSG00000108509	CAMTA2	17:4871286-4890972	OK	10.7021	10.9396	0.0316643	0.036731	0.92345	0.9998
ENSG00000259431	ENSG00000259431	THTPA	14:23980968-24048009	OK	6.12194	5.88833	-0.05613	-0.0515233	0.92345	0.9998
ENSG00000081154	ENSG00000081154	PCNP	3:101292938-101313281	OK	134.219	131.264	-0.0321181	-0.0566154	0.92355	0.9998
ENSG00000136574	ENSG00000136574	GATA4	8:11534467-11617511	OK	6.5651	6.72014	0.0336745	0.0545545	0.92355	0.9998
ENSG00000109089	ENSG00000109089	CDR2L	17:72983726-73001895	OK	1.76934	1.81042	0.0331127	0.0556924	0.9236	0.9998
ENSG00000178409	ENSG00000178409	BEND3	6:107386385-107436473	OK	0.949534	0.972747	0.0348452	0.0582615	0.9236	0.9998
ENSG00000184319	ENSG00000184319	RPL23AP82	22:51195375-51239737	OK	19.8353	19.2922	-0.0400554	-0.0576367	0.92365	0.9998
ENSG00000138028	ENSG00000138028	CGREF1	2:27309614-27341995	OK	11.4212	11.6879	0.0332965	0.0593549	0.9237	0.9998
ENSG00000261461	ENSG00000261461	UBE2MP1	16:34404062-34404612	OK	2.0371	1.95993	-0.0557151	-0.0573906	0.9237	0.9998
ENSG00000165275	ENSG00000165275	TRMT10B	9:37510888-38069210	OK	3.158	3.37474	0.0957671	0.0289601	0.92375	0.9998
ENSG00000083812	ENSG00000083812	ZNF324	19:58978422-58984945	OK	2.88222	2.81405	-0.0345313	-0.061081	0.92385	0.9998
ENSG00000066455	ENSG00000066455	GOLGA5	14:93260575-93306308	OK	17.852	17.541	-0.0253508	-0.0584709	0.9239	0.9998
ENSG00000143569	ENSG00000143569	UBAP2L	1:154179181-154243986	OK	117.652	120.811	0.0382283	0.0403314	0.92395	0.9998
ENSG00000184271	ENSG00000184271	POU6F1	12:51580718-51611477	OK	1.36861	1.29748	-0.0769958	-0.0482275	0.92395	0.9998
ENSG00000231811	ENSG00000231811	RP3-527G5.1	6:4345976-4347271	OK	10.3093	10.6322	0.044493	0.0572039	0.92395	0.9998
ENSG00000215717	ENSG00000215717	TMEM167B	1:109630592-109639556	OK	13.9199	14.2649	0.0353244	0.056449	0.924	0.9998
ENSG00000262539	ENSG00000262539	RP11-259G18.3	17:44336916-44337972	OK	2.75124	2.67062	-0.0429069	-0.0607045	0.924	0.9998
ENSG00000162757	ENSG00000162757	C1orf74	1:209929376-209957904	OK	7.01314	6.84015	-0.0360316	-0.0583341	0.92405	0.9998
ENSG00000169093	ENSG00000169093	ASMTL	X:1520661-1572655	OK	4.99025	4.88049	-0.0320882	-0.052727	0.9241	0.9998
ENSG00000270757	ENSG00000270757	HSPE1-MOB4	2:198351304-198418423	OK	10.5657	11.9233	0.174403	0.0393074	0.9241	0.9998
ENSG00000101079	ENSG00000101079	NDRG3	20:35280168-35374533	OK	30.1765	29.6709	-0.024376	-0.058391	0.92425	0.9998
ENSG00000253251	ENSG00000253251	CTC-534A2.2	5:64885506-65167553	OK	2.34629	2.73581	0.221586	0.0831435	0.92435	0.9998
ENSG00000160917	ENSG00000160917	CPSF4	7:98923520-99063954	OK	28.1111	29.624	0.0756287	0.0234741	0.9244	0.9998
ENSG00000165055	ENSG00000165055	METTL2B	7:128095893-128146656	OK	24.9337	26.1033	0.0661347	0.048435	0.92445	0.9998
ENSG00000206417	ENSG00000206417	H1FX-AS1	3:129033614-129045068	OK	1.30702	1.19316	-0.13149	-0.0487993	0.92445	0.9998
ENSG00000114166	ENSG00000114166	KAT2B	3:20081514-20195896	OK	37.6475	37.0153	-0.0244314	-0.0371615	0.9245	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000242198	ENSG00000242198	CTD-2235C13.1	5:74664310-74896969	OK	1.07039	1.19191	0.155148	0.0155987	0.9245	0.9998
ENSG00000188818	ENSG00000188818	ZDHHC11	5:710470-919472	OK	5.83844	5.49364	-0.0878192	-0.0221273	0.9246	0.9998
ENSG00000104897	ENSG00000104897	SF3A2	19:2100987-2248678	OK	18.0784	19.3388	0.0972333	0.0402976	0.92475	0.9998
ENSG00000256786	ENSG00000256786	AP001029.1	18:12407894-12432237	OK	0.702267	0.633735	-0.148141	-0.0556216	0.9249	0.9998
ENSG00000141456	ENSG00000141456	PELP1	17:4574678-4608824	OK	19.8857	20.238	0.0253346	0.0454318	0.92495	0.9998
ENSG00000160336	ENSG00000160336	ZNF761	19:53935226-53961515	OK	2.6238	2.73219	0.058402	0.0530653	0.92495	0.9998
ENSG00000244462	ENSG00000244462	RBM12	20:34213952-34288906	OK	21.2632	22.1688	0.0601723	0.0493711	0.92495	0.9998
ENSG00000116883	ENSG00000116883	RP11-268J15.5	1:36771987-36794822	OK	3.12584	2.94044	-0.0882146	-0.0569735	0.925	0.9998
ENSG00000163945	ENSG00000163945	UVSSA	4:1341053-1381837	OK	3.02406	3.10509	0.0381475	0.0454935	0.925	0.9998
ENSG00000261512	ENSG00000261512	RP11-46D6.1	16:46656772-46658363	OK	0.94898	0.979429	0.045562	0.0558605	0.925	0.9998
ENSG00000119684	ENSG00000119684	MLH3	14:75480466-75518235	OK	6.34474	6.19761	-0.0338494	-0.044653	0.92505	0.9998
ENSG00000181222	ENSG00000181222	POLR2A	17:7387684-7417933	OK	18.4993	18.2209	-0.0218743	-0.0370102	0.92505	0.9998
ENSG00000236338	ENSG00000236338	AC015987.2	7:135611202-135662101	OK	16.6913	14.6596	-0.187253	-0.087233	0.92505	0.9998
ENSG00000177731	ENSG00000177731	FLII	17:18128900-18162230	OK	55.5698	56.614	0.0268559	0.0388318	0.9251	0.9998
ENSG00000085788	ENSG00000085788	DDHD2	8:38082735-38239790	OK	29.0376	29.8611	0.0403447	0.0355709	0.92515	0.9998
ENSG00000119414	ENSG00000119414	PPP6C	9:127908851-127952218	OK	41.994	41.0311	-0.0334648	-0.0568712	0.9252	0.9998
ENSG00000246451	ENSG00000246451	RP11-894P9.1	14:104019757-104181841	OK	5.15136	5.70498	0.147268	0.0587524	0.92525	0.9998
ENSG00000260774	ENSG00000260774	CTD-2083E4.4	5:196985-218330	OK	0.876583	0.81365	-0.107483	-0.0578491	0.92525	0.9998
ENSG00000245970	ENSG00000245970	KB-1208A12.3	8:98881067-99058697	OK	1.00593	0.912751	-0.140237	-0.0156147	0.92535	0.9998
ENSG00000131263	ENSG00000131263	RLIM	X:73805051-73834452	OK	11.5692	11.3747	-0.0244614	-0.0547785	0.92545	0.9998
ENSG00000184588	ENSG00000184588	PDE4B	1:66258196-66840259	OK	8.35138	8.51368	0.0277678	0.0419461	0.92545	0.9998
ENSG00000132793	ENSG00000132793	LPIN3	20:39969559-39995467	OK	12.258	11.9654	-0.0348617	-0.0515163	0.9255	0.9998
ENSG00000147586	ENSG00000147586	MRPS28	8:80830951-81143467	OK	94.8875	91.5663	-0.0514012	-0.0535839	0.92555	0.9998
ENSG00000214193	ENSG00000214193	SH3D21	1:36771987-36794822	OK	10.0578	9.73169	-0.0475497	-0.0574622	0.9256	0.9998
ENSG00000118939	ENSG00000118939	UCHL3	13:76123618-76434004	OK	37.0584	38.0437	0.0378566	0.0548007	0.92565	0.9998
ENSG00000048140	ENSG00000048140	TSPAN17	5:176074387-176086058	OK	31.8352	31.1493	-0.031423	-0.058693	0.9257	0.9998
ENSG00000244425	ENSG00000244425	RN7SL268P	22:24198613-24241117	OK	1.15682	1.02246	-0.178112	-0.00682036	0.9257	0.9998
ENSG00000085719	ENSG00000085719	CPNE3	8:87345502-87777251	OK	31.3226	30.695	-0.029199	-0.0396811	0.92575	0.9998
ENSG00000213240	ENSG00000213240	NOTCH2NL	1:145209118-145370303	OK	19.9305	20.4543	0.0374278	0.0512944	0.92575	0.9998
ENSG00000173137	ENSG00000173137	ADCK5	8:145596789-145634753	OK	4.12771	3.89502	-0.083711	-0.0484176	0.92585	0.9998
ENSG00000186231	ENSG00000186231	KLHL32	6:97372604-97588630	OK	0.668811	0.633824	-0.0775176	-0.0572765	0.92585	0.9998
ENSG00000259918	ENSG00000259918	NDUFA5P11	16:47178233-47735434	OK	0.851672	0.735027	-0.2125	-0.0259147	0.92595	0.9998
ENSG00000103429	ENSG00000103429	BFAR	16:14726671-14763093	OK	110.131	108.113	-0.0266812	-0.0563197	0.926	0.9998
ENSG00000108828	ENSG00000108828	VAT1	17:41166621-41177140	OK	248.515	244.601	-0.0229019	-0.0537213	0.926	0.9998
ENSG00000135537	ENSG00000135537	LACE1	6:108616097-108847999	OK	2.97083	2.84932	-0.0602456	-0.0603377	0.926	0.9998
ENSG00000259820	ENSG00000259820	AC083843.1	8:135804262-135810515	OK	3.45463	3.52087	0.0274013	0.0561152	0.926	0.9998
ENSG00000107518	ENSG00000107518	ATRNL1	10:116853123-117708503	OK	5.59081	5.44807	-0.0373118	-0.0511709	0.92605	0.9998
ENSG00000260708	ENSG00000260708	CTA-29F11.1	22:47157790-47158460	OK	3.4716	3.57407	0.0419673	0.0553	0.92625	0.9998
ENSG00000100564	ENSG00000100564	PIGH	14:67913800-68067004	OK	39.3316	37.6555	-0.0628276	-0.0453152	0.9263	0.9998
ENSG00000133858	ENSG00000133858	ZFC3H1	12:72003251-72097836	OK	9.3926	9.15261	-0.0373405	-0.0305902	0.92635	0.9998
ENSG00000136950	ENSG00000136950	ARPC5L	9:127624408-127640003	OK	33.4475	32.8728	-0.0250019	-0.0558963	0.92635	0.9998
ENSG00000167257	ENSG00000167257	RNF214	11:117103340-117283984	OK	5.84024	6.06235	0.0538502	0.044735	0.9264	0.9998
ENSG00000163510	ENSG00000163510	CWC22	2:180809602-180871840	OK	10.4218	10.6114	0.0260174	0.0563189	0.92645	0.9998
ENSG00000171611	ENSG00000171611	PTCRA	6:42883726-42893573	OK	3.18478	3.09627	-0.0406641	-0.0536868	0.92645	0.9998
ENSG00000182208	ENSG00000182208	MOB2	11:1490686-1522477	OK	19.2004	19.6314	0.0320222	0.0532079	0.92645	0.9998
ENSG00000068323	ENSG00000068323	TFE3	X:48886241-48901012	OK	12.4693	12.2465	-0.0260132	-0.0493263	0.9265	0.9998
ENSG00000229124	ENSG00000229124	VIM-AS1	10:17256237-17279592	OK	0.639514	0.707627	0.146015	0.00444992	0.9265	0.9998
ENSG00000142039	ENSG00000142039	CCDC97	19:41768400-41930910	OK	8.83453	8.31198	-0.0879604	-0.0436396	0.92655	0.9998
ENSG00000164823	ENSG00000164823	OSGIN2	8:90914086-90940116	OK	15.4348	15.8012	0.0338468	0.0541133	0.92655	0.9998
ENSG00000188971	ENSG00000188971	RP11-427H3.3	2:69685128-70053596	OK	4.82886	4.99422	0.0485754	0.0566982	0.92655	0.9998
ENSG00000269940	ENSG00000269940	RP11-73M18.7	14:104019757-104181841	OK	7.37098	8.47434	0.201246	0.0588153	0.92655	0.9998
ENSG00000105672	ENSG00000105672	ETV2	19:36132646-36135773	OK	1.963	1.89222	-0.0529763	-0.0538929	0.9266	0.9998
ENSG00000170248	ENSG00000170248	PDCD6IP	3:33839843-33911194	OK	79.3098	81.2268	0.0344552	0.048504	0.9266	0.9998
ENSG00000235245	ENSG00000235245	RP11-122K13.12	10:135093134-135166187	OK	1.3937	1.57854	0.179668	0.0362493	0.92665	0.9998
ENSG00000096070	ENSG00000096070	BRPF3	6:36114474-36200567	OK	8.16109	8.31275	0.0265645	0.0439932	0.9267	0.9998
ENSG00000204852	ENSG00000204852	TCTN1	12:111051831-111142755	OK	15.2861	14.9829	-0.0289076	-0.0462716	0.9267	0.9998
ENSG00000237984	ENSG00000237984	PTENP1	9:33673501-33677497	OK	1.79143	1.85044	0.0467624	0.0572362	0.9267	0.9998
ENSG00000253706	ENSG00000253706	RP11-758M4.4	8:75512009-75779174	OK	1.18309	1.28142	0.115178	0.0248042	0.9267	0.9998
ENSG00000252481	ENSG00000252481	SCARNA13	14:95998633-96011061	OK	0.827327	0.76887	-0.105718	-0.012133	0.92675	0.9998
ENSG00000198018	ENSG00000198018	ENTPD7	10:101419262-101515891	OK	3.76821	3.95538	0.0699385	0.0559547	0.92685	0.9998
ENSG00000106153	ENSG00000106153	CHCHD2	7:56169261-56174269	OK	520.142	528.127	0.0219798	0.0546851	0.9269	0.9998
ENSG00000137770	ENSG00000137770	CTDSPL2	15:44719431-44829121	OK	5.97501	5.83098	-0.0352025	-0.0441419	0.9269	0.9998
ENSG00000168916	ENSG00000168916	ZNF608	5:123972607-124084500	OK	3.88441	3.97478	0.0331799	0.0452673	0.92695	0.9998
ENSG00000204427	ENSG00000204427	ABHD16A	6:31654725-31685695	OK	17.3485	17.0391	-0.0259595	-0.0510924	0.92695	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000247137	ENSG00000247137	RP11-727A23.5	11:82868029-83134559	OK	2.61084	2.48288	-0.0725028	-0.0222575	0.92695	0.9998
ENSG00000160131	ENSG00000160131	VMA21	X:150564986-150577836	OK	14.0224	13.6288	-0.0410765	-0.0363171	0.927	0.9998
ENSG00000205583	ENSG00000205583	STAG3L1	7:74988447-75115548	OK	1.91144	1.77918	-0.10345	-0.0300948	0.927	0.9998
ENSG00000188428	ENSG00000188428	BLOC1S5	6:7727029-8102811	OK	12.8533	11.9834	-0.1011	-0.0566151	0.92705	0.9998
ENSG00000071051	ENSG00000071051	NCK2	2:106361353-106510730	OK	95.2093	93.4817	-0.0264179	-0.0493737	0.9271	0.9998
ENSG00000140950	ENSG00000140950	TLDC1	16:84511680-84587639	OK	6.04829	5.89932	-0.0359792	-0.0503668	0.9271	0.9998
ENSG00000257365	ENSG00000257365	FNTB	14:65381078-65569413	OK	15.0068	15.6047	0.056363	0.0441264	0.9271	0.9998
ENSG00000214050	ENSG00000214050	FBXO16	8:28203101-28347835	OK	9.98204	10.5512	0.0800032	0.0490875	0.9272	0.9998
ENSG00000196230	ENSG00000196230	TUBB	6:30687977-30693203	OK	1055.74	1034.69	-0.0290606	-0.0532984	0.9274	0.9998
ENSG00000153936	ENSG00000153936	HS2ST1	1:87380330-87634884	OK	14.0782	14.464	0.0389988	0.0476863	0.92755	0.9998
ENSG00000228727	ENSG00000228727	SAPCD1	6:31707724-31733365	OK	1.17955	1.28442	0.122884	0.0456266	0.92755	0.9998
ENSG00000135249	ENSG00000135249	RINT1	7:105172531-105241322	OK	19.2439	19.5929	0.0259267	0.0435474	0.9276	0.9998
ENSG00000206562	ENSG00000206562	METTL6	3:15422781-15563258	OK	15.3764	15.9191	0.0500398	0.0517557	0.92765	0.9998
ENSG00000022976	ENSG00000022976	ZNF839	14:102783713-102829253	OK	4.55971	4.73844	0.0554695	0.0495262	0.9277	0.9998
ENSG00000092108	ENSG00000092108	SCFD1	14:31091317-31291908	OK	29.7976	30.3247	0.0252946	0.0503745	0.9279	0.9998
ENSG00000105991	ENSG00000105991	HOXA1	7:27132611-27142430	OK	3.4597	3.5525	0.0381901	0.054708	0.92795	0.9998
ENSG00000122390	ENSG00000122390	NAA60	16:3415098-3627401	OK	22.1042	21.6313	-0.0312025	-0.0375575	0.928	0.9998
ENSG00000144815	ENSG00000144815	NXPE3	3:101498045-101579866	OK	6.48197	6.94267	0.0990594	0.0540607	0.92805	0.9998
ENSG00000273014	ENSG00000273014	RP11-225B17.2	7:32535037-33102409	OK	1.87927	2.06828	0.138258	0.011902	0.92805	0.9998
ENSG00000145217	ENSG00000145217	SLC26A1	4:952674-998316	OK	0.897456	0.828226	-0.115818	-0.0422024	0.9281	0.9998
ENSG00000182093	ENSG00000182093	WRB	21:40752169-40817731	OK	22.7351	22.3528	-0.0244688	-0.0518474	0.9281	0.9998
ENSG00000167487	ENSG00000167487	KLHL26	19:18747774-18781309	OK	2.50442	2.57496	0.0400751	0.04404	0.92835	0.9998
ENSG00000258664	ENSG00000258664	IFRG15	1:179809101-179846938	OK	9.94537	9.67226	-0.0401722	-0.0149957	0.92835	0.9998
ENSG00000070367	ENSG00000070367	EXOC5	14:57670517-57756797	OK	45.0513	44.1298	-0.0298155	-0.0463664	0.92845	0.9998
ENSG00000246273	ENSG00000246273	SBF2-AS1	11:9776316-10315754	OK	5.20879	4.91873	-0.082663	-0.0433551	0.92845	0.9998
ENSG00000259604	ENSG00000259604	RP11-66B24.1	15:101389765-101626271	OK	1.33225	1.44097	0.11317	0.0186918	0.92845	0.9998
ENSG00000171862	ENSG00000171862	PTEN	10:89618917-89731687	OK	15.7485	16.3606	0.055004	0.0581475	0.9285	0.9998
ENSG00000182185	ENSG00000182185	RAD51B	14:68286495-69196935	OK	8.10039	7.89961	-0.0362115	-0.0394583	0.9286	0.9998
ENSG00000105669	ENSG00000105669	COPE	19:19010322-19057640	OK	115.629	113.5	-0.0268062	-0.0467292	0.92865	0.9998
ENSG00000184277	ENSG00000184277	TM2D3	15:102161846-102192594	OK	22.0856	21.708	-0.0248801	-0.0514488	0.92865	0.9998
ENSG00000205250	ENSG00000205250	E2F4	16:67226071-67232821	OK	19.9808	19.6475	-0.0242692	-0.0483755	0.92865	0.9998
ENSG00000103335	ENSG00000103335	PIEZO1	16:88772870-88851619	OK	10.5365	10.7487	0.0287659	0.0328688	0.9287	0.9998
ENSG00000108582	ENSG00000108582	CPD	17:28705922-28797007	OK	20.4578	20.7973	0.0237418	0.0460718	0.92875	0.9998
ENSG00000058799	ENSG00000058799	YIPF1	1:54317391-54356407	OK	20.3008	19.9154	-0.0276558	-0.0548252	0.9288	0.9998
ENSG00000138686	ENSG00000138686	BBS7	4:122745594-122791652	OK	14.0204	13.6898	-0.0344288	-0.0511613	0.9288	0.9998
ENSG00000135503	ENSG00000135503	ACVR1B	12:52345450-52390862	OK	6.04719	6.15265	0.0249432	0.0458999	0.92885	0.9998
ENSG00000146587	ENSG00000146587	RBAK	7:5013618-5112854	OK	5.4185	5.5349	0.0306656	0.0529743	0.92885	0.9998
ENSG00000113460	ENSG00000113460	BRIX1	5:34905368-34926101	OK	48.1728	49.5113	0.0395383	0.0518959	0.9289	0.9998
ENSG00000156795	ENSG00000156795	WDYHV1	8:124428964-124479470	OK	22.6446	22.1953	-0.0289128	-0.0530151	0.9289	0.9998
ENSG00000241553	ENSG00000241553	ARPC4	3:9791627-9896822	OK	128.043	124.776	-0.0372853	-0.0544902	0.92895	0.9998
ENSG00000247092	ENSG00000247092	SNHG10	14:95998633-96011061	OK	1.66767	1.79746	0.108122	0.0373919	0.929	0.9998
ENSG00000103472	ENSG00000103472	RRN3P2	16:29065052-29231352	OK	0.856667	0.886491	0.0493724	0.0518785	0.9291	0.9998
ENSG00000238103	ENSG00000238103	RPL9P7	X:23851469-23957624	OK	0.889873	0.796585	-0.159771	-0.0442525	0.9291	0.9998
ENSG00000143226	ENSG00000143226	FCGR2A	1:161475219-161648444	OK	6.3505	6.16403	-0.0429953	-0.0480911	0.92915	0.9998
ENSG00000115657	ENSG00000115657	ABCB6	2:220074489-220094439	OK	29.9968	30.6658	0.0318223	0.0422433	0.9292	0.9998
ENSG00000258657	ENSG00000258657	RP11-104E19.1	14:25064928-25126980	OK	12.5854	12.8806	0.0334425	0.0550979	0.9292	0.9998
ENSG00000207110	ENSG00000207110	RNU1-106P	8:128806778-129113499	OK	6.93728	7.2154	0.0567084	0.012195	0.92925	0.9998
ENSG00000099326	ENSG00000099326	MZF1	19:59070495-59111168	OK	4.43926	4.59141	0.048618	0.0502604	0.9293	0.9998
ENSG00000142178	ENSG00000142178	SIK1	21:44834394-44847008	OK	4.16871	4.08451	-0.0294393	-0.046934	0.9293	0.9998
ENSG00000271869	ENSG00000271869	RP11-51J9.5	8:29952913-30041156	OK	0.739192	0.824922	0.158308	0.0167527	0.9293	0.9998
ENSG00000237493	ENSG00000237493	RP11-603J24.7	12:56367696-56388490	OK	42.4091	38.367	-0.144508	-0.0702442	0.9294	0.9998
ENSG00000146776	ENSG00000146776	ATXN7L1	7:105245513-105517050	OK	8.3934	8.0778	-0.0552934	-0.0540582	0.9295	0.9998
ENSG00000256894	ENSG00000256894	RP11-283G6.3	12:26272958-26986131	OK	1.33998	1.23354	-0.119405	-0.0183997	0.9295	0.9998
ENSG00000141562	ENSG00000141562	NARF	17:80412148-80448413	OK	88.9948	90.4945	0.0241094	0.0499665	0.92955	0.9998
ENSG00000119655	ENSG00000119655	NPC2	14:74942894-74963809	OK	338.528	332.244	-0.0270301	-0.0546201	0.9296	0.9998
ENSG00000203326	ENSG00000203326	ZNF525	19:53868945-53930574	OK	1.13373	1.08731	-0.0603115	-0.0335361	0.92965	0.9998
ENSG00000265393	ENSG00000265393	CTD-2517M22.17	8:145736666-145743229	OK	0.92125	1.04897	0.187312	0.0362532	0.92965	0.9998
ENSG00000071537	ENSG00000071537	SEL1L	14:81937892-82000205	OK	30.155	30.7237	0.0269549	0.034782	0.9298	0.9998
ENSG00000115042	ENSG00000115042	FAHD2A	2:96068468-96082364	OK	58.5094	57.3961	-0.027715	-0.0570639	0.9298	0.9998
ENSG00000203727	ENSG00000203727	SAMD5	6:147830062-148275073	OK	0.909823	0.885576	-0.038971	-0.039457	0.9298	0.9998
ENSG00000004059	ENSG00000004059	ARF5	7:127220671-127242198	OK	195.121	199.021	0.0285525	0.0516262	0.92985	0.9998
ENSG00000107902	ENSG00000107902	LHPP	10:126150402-126480439	OK	10.7085	10.165	-0.0751454	-0.0439542	0.92985	0.9998
ENSG00000110274	ENSG00000110274	CEP164	11:117103340-117283984	OK	6.25541	6.0899	-0.038688	-0.0346725	0.92995	0.9998
ENSG00000121005	ENSG00000121005	CRISPLD1	8:75896749-75946793	OK	12.3151	12.652	0.038936	0.0509547	0.92995	0.9998
ENSG00000109452	ENSG00000109452	INPP4B	4:142944312-143768585	OK	62.0892	60.9733	-0.0261651	-0.051053	0.93	0.9998
ENSG00000105856	ENSG00000105856	HBP1	7:106809405-107218906	OK	38.0314	37.1295	-0.0346234	-0.0426944	0.93005	0.9998
ENSG00000162191	ENSG00000162191	UBXN1	11:62443969-62446567	OK	74.8771	76.0766	0.0229273	0.0535793	0.93005	0.9998
ENSG00000108788	ENSG00000108788	MLX	17:40719085-40729849	OK	48.358	49.1573	0.0236507	0.0489863	0.9301	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000163634	ENSG00000163634	THOC7	3:63727968-63849579	OK	90.0019	88.685	-0.0212656	-0.0508787	0.93015	0.9998
ENSG00000164896	ENSG00000164896	FASTK	7:150773710-150777953	OK	76.6339	75.4207	-0.0230233	-0.0502998	0.93015	0.9998
ENSG00000115761	ENSG00000115761	NOL10	2:10710891-10830101	OK	17.102	17.382	0.0234339	0.0500886	0.9302	0.9998
ENSG00000124831	ENSG00000124831	LRRFIP1	2:238536218-238751451	OK	43.2005	43.8334	0.0209819	0.0430797	0.9302	0.9998
ENSG00000132463	ENSG00000132463	GRSF1	4:71681498-71705662	OK	94.5262	96.2043	0.0253872	0.0553665	0.9302	0.9998
ENSG00000172465	ENSG00000172465	TCEAL1	X:102862378-102885881	OK	14.3069	13.9285	-0.0386663	-0.0525018	0.9302	0.9998
ENSG00000115661	ENSG00000115661	STK16	2:220094478-220142892	OK	28.6342	27.6415	-0.0509	-0.0515921	0.9303	0.9998
ENSG00000154035	ENSG00000154035	C17orf103	17:21142182-21156722	OK	4.69727	4.6178	-0.0246184	-0.0511325	0.9303	0.9998
ENSG00000183397	ENSG00000183397	C19orf71	19:3506270-3579086	OK	40.6397	36.8041	-0.143021	-0.0241461	0.9305	0.9998
ENSG00000101557	ENSG00000101557	USP14	18:158382-268050	OK	44.7601	45.633	0.0278621	0.0537977	0.93055	0.9998
ENSG00000173540	ENSG00000173540	GMPPB	3:49711434-49761384	OK	16.3208	15.4732	-0.076942	-0.0530657	0.93055	0.9998
ENSG00000166780	ENSG00000166780	C16orf45	16:15489610-15737023	OK	4.83269	5.14551	0.0904901	0.0414016	0.9306	0.9998
ENSG00000176473	ENSG00000176473	WDR25	14:100800124-100996640	OK	4.69187	4.37282	-0.101598	-0.0399242	0.93065	0.9998
ENSG00000019549	ENSG00000019549	SNAI2	8:49830248-49834299	OK	80.0233	81.2361	0.0216999	0.0545683	0.93085	0.9998
ENSG00000256537	ENSG00000256537	RP11-785H5.1	12:10977558-11324212	OK	12.3262	11.0098	-0.162946	-0.0716746	0.93085	0.9998
ENSG00000173264	ENSG00000173264	GPR137	11:64037301-64056972	OK	18.4906	18.002	-0.0386382	-0.0425118	0.9309	0.9998
ENSG00000265690	ENSG00000265690	RP11-5A19.5	16:67188082-67203848	OK	1.03168	0.943445	-0.12899	-0.0566072	0.9309	0.9998
ENSG00000152689	ENSG00000152689	RASGRP3	2:33661390-33789817	OK	16.486	16.9809	0.0426646	0.0537166	0.931	0.9998
ENSG00000250645	ENSG00000250645	CTD-2228K2.1	5:271735-438406	OK	0.810246	0.913684	0.173334	0.013166	0.931	0.9998
ENSG00000138375	ENSG00000138375	SMARCAL1	2:217250010-217443903	OK	13.849	14.9041	0.105919	0.0458905	0.93105	0.9998
ENSG00000254505	ENSG00000254505	CHMP4A	14:24641061-24708448	OK	49.7864	47.0127	-0.0827017	-0.0581058	0.9313	0.9998
ENSG00000232775	ENSG00000232775	AP000525.10	22:16147978-16193004	OK	0.730925	0.652015	-0.164819	-0.0593515	0.93135	0.9998
ENSG00000243364	ENSG00000243364	EFNA4	1:155036206-155060014	OK	6.35882	6.54539	0.04172	0.0535495	0.93135	0.9998
ENSG00000137502	ENSG00000137502	RAB30	11:82534543-82782965	OK	3.64769	3.52339	-0.0500203	-0.0300131	0.9314	0.9998
ENSG00000205456	ENSG00000205456	TP53TG3D	16:32261940-32267240	OK	0.75434	0.726045	-0.0551561	-0.0369046	0.93145	0.9998
ENSG00000130066	ENSG00000130066	SAT1	X:23801289-23804343	OK	177.129	180.223	0.0249846	0.0551715	0.9315	0.9998
ENSG00000226121	ENSG00000226121	AHCTF1P1	2:162272604-162841792	OK	2.58599	2.53838	-0.0268081	-0.0508543	0.93155	0.9998
ENSG00000110025	ENSG00000110025	SNX15	11:64781584-64808044	OK	6.92062	6.63111	-0.0616506	-0.0392571	0.9316	0.9998
ENSG00000185650	ENSG00000185650	ZFP36L1	14:69254376-69263190	OK	13.5551	13.2906	-0.0284285	-0.0470354	0.9316	0.9998
ENSG00000131724	ENSG00000131724	IL13RA1	X:117861534-117928502	OK	18.2346	18.5219	0.022548	0.0496858	0.9317	0.9998
ENSG00000198900	ENSG00000198900	TOP1	20:39657457-39946312	OK	37.5462	38.6178	0.0405996	0.0515913	0.9317	0.9998
ENSG00000235313	ENSG00000235313	HM13-IT1	20:30102230-30161066	OK	0.931204	1.04362	0.164434	0.0147281	0.9318	0.9998
ENSG00000269439	ENSG00000269439	CTD-3131K8.2	19:17579577-17632097	OK	1.30702	1.39855	0.0976546	0.0152884	0.9318	0.9998
ENSG00000163803	ENSG00000163803	PLB1	2:28680011-28887406	OK	3.79925	3.69298	-0.0409295	-0.0494932	0.93185	0.9998
ENSG00000241685	ENSG00000241685	ARPC1A	7:98923520-99063954	OK	231.35	239.687	0.0510755	0.0475676	0.93185	0.9998
ENSG00000197579	ENSG00000197579	TOPORS	9:32540541-32573160	OK	8.19309	7.9542	-0.0426901	-0.0525665	0.9319	0.9998
ENSG00000160410	ENSG00000160410	SHKBP1	19:41082756-41097305	OK	32.55	33.0155	0.0204887	0.0350831	0.93195	0.9998
ENSG00000197016	ENSG00000197016	ZNF470	19:57078879-57100279	OK	0.892482	0.871942	-0.0335921	-0.0396723	0.93205	0.9998
ENSG00000140553	ENSG00000140553	UNC45A	15:91473409-91506349	OK	42.1085	41.3994	-0.0245015	-0.0443795	0.93215	0.9998
ENSG00000229358	ENSG00000229358	DPY19L1P1	7:32535037-33102409	OK	0.674913	0.739524	0.131897	0.0192972	0.93215	0.9998
ENSG00000134775	ENSG00000134775	FHOD3	18:33877676-34812135	OK	9.16178	8.70866	-0.0731775	-0.0555289	0.9322	0.9998
ENSG00000128951	ENSG00000128951	DUT	15:48604549-48635570	OK	38.3339	37.6091	-0.0275401	-0.0511352	0.93225	0.9998
ENSG00000168002	ENSG00000168002	POLR2G	11:62529015-62534182	OK	111.169	109.536	-0.0213595	-0.0517369	0.93235	0.9998
ENSG00000214401	ENSG00000214401	KANSL1-AS1	17:44107281-44302733	OK	6.85286	6.0834	-0.171829	-0.0741444	0.93235	0.9998
ENSG00000117118	ENSG00000117118	SDHB	1:17345216-17380665	OK	134.224	136.257	0.0216864	0.0513532	0.9324	0.9998
ENSG00000125954	ENSG00000125954	CHURC1-FNTB	14:65381078-65569413	OK	2.23577	2.54398	0.186315	0.0594888	0.93245	0.9998
ENSG00000259363	ENSG00000259363	CTD-2054N24.2	15:100347227-100417353	OK	2.07385	2.14249	0.0469774	0.0507268	0.93255	0.9998
ENSG00000105726	ENSG00000105726	ATP13A1	19:19756006-19774502	OK	22.5276	22.1693	-0.0231299	-0.0445559	0.9326	0.9998
ENSG00000115318	ENSG00000115318	LOXL3	2:74753771-74784681	OK	12.3152	12.9539	0.0729451	0.048941	0.9326	0.9998
ENSG00000179562	ENSG00000179562	GCC1	7:127220671-127242198	OK	15.9641	16.4574	0.0439072	0.0498715	0.9326	0.9998
ENSG00000115241	ENSG00000115241	PPM1G	2:27604060-27632554	OK	69.2126	68.2525	-0.0201537	-0.0508432	0.93265	0.9998
ENSG00000126106	ENSG00000126106	TMEM53	1:44870865-45140227	OK	7.62004	7.27334	-0.0671808	-0.0467218	0.93265	0.9998
ENSG00000198917	ENSG00000198917	C9orf114	9:131580752-131592100	OK	29.3311	30.1391	0.0392093	0.0518352	0.93265	0.9998
ENSG00000228265	ENSG00000228265	RP5-1125A11.1	20:32570857-32700138	OK	1.85929	1.71752	-0.114424	-0.0128522	0.93265	0.9998
ENSG00000152767	ENSG00000152767	FARP1	13:98794815-99102027	OK	42.3701	43.4753	0.0371484	0.0475725	0.9328	0.9998
ENSG00000161204	ENSG00000161204	ABCF3	3:183851806-184402546	OK	39.0467	41.6881	0.0944364	0.0332132	0.9328	0.9998
ENSG00000245680	ENSG00000245680	ZNF585B	19:37498758-37734828	OK	0.883883	0.927123	0.0689056	0.0243609	0.9328	0.9998
ENSG00000172780	ENSG00000172780	RAB43	3:128806411-128880136	OK	5.11291	5.28199	0.0469356	0.0485028	0.9329	0.9998
ENSG00000178498	ENSG00000178498	DTX3	12:57998404-58003587	OK	19.0432	18.6983	-0.0263675	-0.0501339	0.9329	0.9998
ENSG00000214331	ENSG00000214331	RP11-252A24.2	16:74330672-74403724	OK	1.16352	1.24637	0.0992322	0.0477487	0.9329	0.9998
ENSG00000273015	ENSG00000273015	LINC00938	12:46119509-46121558	OK	1.32605	1.29241	-0.0370717	-0.05242	0.93305	0.9998
ENSG00000122218	ENSG00000122218	COPA	1:160259062-160328742	OK	133.9	136.324	0.0258904	0.0427295	0.9333	0.9998
ENSG00000108231	ENSG00000108231	LGI1	10:95517565-95557916	OK	1.57524	1.53655	-0.0358789	-0.0397486	0.93335	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000273338	ENSG00000273338	RP11-386I14.4	1:78444858-78604133	OK	2.7528	2.7675	0.00768523	0.00287227	0.93335	0.9998
ENSG00000142252	ENSG00000142252	GEMIN7	19:45574757-45808541	OK	20.8575	19.6097	-0.0889981	-0.0545568	0.9334	0.9998
ENSG00000179051	ENSG00000179051	RCC2	1:17733255-17766220	OK	34.3514	33.8589	-0.0208342	-0.0503634	0.9334	0.9998
ENSG00000185504	ENSG00000185504	C17orf70	17:79506910-79520987	OK	18.6412	18.3442	-0.0231714	-0.0494178	0.9334	0.9998
ENSG00000186230	ENSG00000186230	ZNF749	19:57874844-57988938	OK	1.64366	1.7327	0.0761049	0.0381114	0.9334	0.9998
ENSG00000250506	ENSG00000250506	CDK3	17:73937587-74023533	OK	2.34261	2.12822	-0.138473	-0.0546613	0.93345	0.9998
ENSG00000160307	ENSG00000160307	S100B	21:48018874-48025121	OK	277.772	273.637	-0.021639	-0.0519509	0.9335	0.9998
ENSG00000115738	ENSG00000115738	ID2	2:8806765-8824583	OK	61.524	60.4175	-0.0261828	-0.050444	0.9336	0.9998
ENSG00000117408	ENSG00000117408	IPO13	1:44412610-44433694	OK	12.6376	12.828	0.0215837	0.033695	0.9336	0.9998
ENSG00000231579	ENSG00000231579	RPL7P21	5:142657495-142815077	OK	0.711521	0.794735	0.159567	0.0343352	0.9336	0.9998
ENSG00000159433	ENSG00000159433	STARD9	15:42867856-43013179	OK	0.794439	0.813796	0.0347301	0.0348809	0.9337	0.9998
ENSG00000132522	ENSG00000132522	GPS2	17:7210317-7232712	OK	50.3574	48.0984	-0.0662146	-0.0484451	0.93385	0.9998
ENSG00000079785	ENSG00000079785	DDX1	2:15731301-15771235	OK	67.4907	68.4335	0.0200149	0.0483558	0.93395	0.9998
ENSG00000105988	ENSG00000105988	NHP2P1	10:93806448-94050844	OK	2.09764	1.98244	-0.0814935	-0.050124	0.93395	0.9998
ENSG00000157216	ENSG00000157216	SSBP3	1:54598746-54879152	OK	19.1111	18.2894	-0.0634057	-0.0435936	0.93395	0.9998
ENSG00000176853	ENSG00000176853	FAM91A1	8:124780695-124827692	OK	33.9246	34.4381	0.0216728	0.0441518	0.93395	0.9998
ENSG00000269374	ENSG00000269374	CTB-50E14.5	19:42901279-43156507	OK	20.4215	22.0348	0.109696	0.0444977	0.93395	0.9998
ENSG00000186352	ENSG00000186352	ANKRD37	4:186317174-186347139	OK	11.0234	11.5534	0.0677502	0.0657721	0.93405	0.9998
ENSG00000108848	ENSG00000108848	LUC7L3	17:48796904-48833574	OK	83.0414	81.7845	-0.0220031	-0.039336	0.9341	0.9998
ENSG00000233527	ENSG00000233527	AC092295.7	19:37001596-37119499	OK	1.6474	1.52101	-0.115156	-0.0406681	0.9341	0.9998
ENSG00000175768	ENSG00000175768	TOMM5	9:37510888-38069210	OK	143.752	147.132	0.0335269	0.0499212	0.93415	0.9998
ENSG00000186575	ENSG00000186575	NF2	22:29999544-30094587	OK	14.2147	14.5007	0.0287338	0.0512779	0.93415	0.9998
ENSG00000261329	ENSG00000261329	CTD-2049O4.1	16:27561453-27791690	OK	1.42285	1.55092	0.124341	0.0364811	0.93415	0.9998
ENSG00000171763	ENSG00000171763	SPATA5L1	15:45694528-45713617	OK	2.43475	2.48817	0.0313118	0.041042	0.93425	0.9998
ENSG00000223374	ENSG00000223374	AC005104.3	2:242166678-242293442	OK	0.740201	0.805842	0.122581	0.00425527	0.93425	0.9998
ENSG00000088727	ENSG00000088727	KIF9	3:47205986-47388306	OK	10.5908	10.1468	-0.0617828	-0.0476462	0.93435	0.9998
ENSG00000172878	ENSG00000172878	METAP1D	2:172640879-172947158	OK	3.36837	3.20568	-0.0714229	-0.0317931	0.93435	0.9998
ENSG00000170275	ENSG00000170275	CRTAP	3:33155470-33189265	OK	353.331	344.967	-0.0345611	-0.0499045	0.9344	0.9998
ENSG00000155903	ENSG00000155903	RASA2	3:141205888-141334184	OK	3.30235	3.23679	-0.0289286	-0.041327	0.93465	0.9998
ENSG00000197728	ENSG00000197728	RPS26	12:56435636-56438116	OK	6.39743	6.26143	-0.0310003	-0.048785	0.93465	0.9998
ENSG00000259917	ENSG00000259917	HNRNPLP2	15:34671268-34880704	OK	2.53677	2.68948	0.0843384	0.0478647	0.9347	0.9998
ENSG00000258985	ENSG00000258985	RP11-368P15.3	14:53503472-53504969	OK	0.737844	0.739055	0.00236641	0.00155928	0.9348	0.9998
ENSG00000134644	ENSG00000134644	PUM1	1:31404352-31538838	OK	19.0886	18.7975	-0.0221706	-0.0358657	0.9349	0.9998
ENSG00000180777	ENSG00000180777	ANKRD30B	18:14728270-14852737	OK	10.1139	10.2946	0.0255457	0.0510852	0.93495	0.9998
ENSG00000100284	ENSG00000100284	TOM1	22:35694830-35743985	OK	24.508	24.1674	-0.0201948	-0.0433433	0.93505	0.9998
ENSG00000101473	ENSG00000101473	ACOT8	20:44462448-44486045	OK	33.8947	34.6082	0.0300577	0.0503921	0.93505	0.9998
ENSG00000155506	ENSG00000155506	LARP1	5:154092461-154197167	OK	66.4818	67.4842	0.0215907	0.0374108	0.93505	0.9998
ENSG00000250899	ENSG00000250899	RP11-253E3.3	12:3150602-3154116	OK	1.23849	1.26694	0.0327684	0.0505556	0.93505	0.9998
ENSG00000105865	ENSG00000105865	DUS4L	7:106809405-107218906	OK	11.5929	12.0787	0.0592236	0.0394669	0.9351	0.9998
ENSG00000115486	ENSG00000115486	GGCX	2:85766287-85788670	OK	32.6115	34.4631	0.0796721	0.0534608	0.93515	0.9998
ENSG00000131051	ENSG00000131051	RBM39	20:34291530-34330234	OK	159.916	157.307	-0.0237254	-0.0450628	0.93515	0.9998
ENSG00000240694	ENSG00000240694	PNMA2	8:26236774-26371608	OK	1.49243	1.65884	0.152508	0.0489213	0.93515	0.9998
ENSG00000133065	ENSG00000133065	SLC41A1	1:205758220-205782876	OK	16.4403	16.6887	0.0216399	0.0443556	0.93525	0.9998
ENSG00000167889	ENSG00000167889	MGAT5B	17:74864537-74965238	OK	18.1292	18.3984	0.021264	0.0421016	0.9353	0.9998
ENSG00000267279	ENSG00000267279	RP11-879F14.2	18:59252978-59421928	OK	0.850269	0.818622	-0.0547225	-0.0463903	0.9353	0.9998
ENSG00000265511	ENSG00000265511	RP11-524F11.1	17:17408876-17513799	OK	0.868818	0.768923	-0.176215	-0.0474074	0.93535	0.9998
ENSG00000116830	ENSG00000116830	TTF2	1:117602924-117650075	OK	19.9026	19.3624	-0.0396977	-0.0499912	0.93545	0.9998
ENSG00000153130	ENSG00000153130	SCOC	4:141178439-141306880	OK	63.5418	62.6851	-0.0195842	-0.047787	0.9355	0.9998
ENSG00000168970	ENSG00000168970	JMJD7-PLA2G4B	15:42120282-42190773	OK	0.937729	0.908135	-0.0462654	-0.0451653	0.9355	0.9998
ENSG00000100226	ENSG00000100226	GTPBP1	22:39101727-39190203	OK	12.613	12.9198	0.0346794	0.0301012	0.93565	0.9998
ENSG00000225031	ENSG00000225031	EIF4BP7	X:110862904-110864717	OK	10.5871	10.7625	0.023703	0.0477063	0.9357	0.9998
ENSG00000123444	ENSG00000123444	KBTBD4	11:47487495-47606114	OK	16.053	15.2636	-0.0727522	-0.0453422	0.93575	0.9998
ENSG00000168646	ENSG00000168646	AXIN2	17:63524680-64188202	OK	9.74936	9.96747	0.0319204	0.0480794	0.9358	0.9998
ENSG00000187609	ENSG00000187609	EXD3	9:140201347-140317714	OK	2.58429	2.52392	-0.0341051	-0.0466904	0.93595	0.9998
ENSG00000125459	ENSG00000125459	MSTO1	1:155579566-155829191	OK	25.9103	25.1265	-0.0443146	-0.0252409	0.936	0.9998
ENSG00000163386	ENSG00000163386	NBPF10	1:145209118-145370303	OK	8.55367	8.77954	0.0376023	0.0516554	0.936	0.9998
ENSG00000232495	ENSG00000232495	AC069287.1	11:127114-207428	OK	3.26379	3.01077	-0.116413	-0.0598402	0.93605	0.9998
ENSG00000067334	ENSG00000067334	DNTTIP2	1:94333372-94345474	OK	19.4274	19.1436	-0.0212259	-0.0443864	0.93615	0.9998
ENSG00000103489	ENSG00000103489	XYLT1	16:17195625-17564738	OK	6.11879	6.22982	0.0259431	0.0312397	0.9362	0.9998
ENSG00000087365	ENSG00000087365	SF3B2	11:65818199-65837090	OK	97.9864	96.7651	-0.0180952	-0.0408273	0.93625	0.9998
ENSG00000115183	ENSG00000115183	TANC1	2:159825145-160089170	OK	20.1963	20.4879	0.0206824	0.0480571	0.9363	0.9998
ENSG00000180867	ENSG00000180867	PDIA3P1	1:146644349-146767443	OK	22.3131	21.2161	-0.0727321	-0.0486557	0.9363	0.9998
ENSG00000213713	ENSG00000213713	PIGCP1	11:33060962-33213144	OK	3.69515	3.33911	-0.146169	-0.0694507	0.9364	0.9998
ENSG00000136444	ENSG00000136444	RSAD1	17:48556160-48563336	OK	29.9686	29.5331	-0.0211218	-0.0425845	0.93655	0.9998
ENSG00000267022	ENSG00000267022	ZNF223	19:44529493-44593766	OK	0.642523	0.668703	0.0576195	0.0447566	0.93665	0.9998
ENSG00000060688	ENSG00000060688	SNRNP40	1:31732416-31769662	OK	21.0802	21.4083	0.0222812	0.0462523	0.9367	0.9998
ENSG00000101346	ENSG00000101346	POFUT1	20:30795682-30826470	OK	35.1438	34.4704	-0.0279127	-0.0456116	0.9367	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000152409	ENSG00000152409	JMY	5:78532011-78623038	OK	1.85708	1.822	-0.0275125	-0.0336558	0.93675	0.9998
ENSG00000241370	ENSG00000241370	RPP21	6:30201815-30314661	OK	68.6563	70.7194	0.0427134	0.0498949	0.9368	0.9998
ENSG00000268995	ENSG00000268995	VN1R82P	19:21324826-21373034	OK	0.931118	0.847569	-0.135633	-0.031423	0.93685	0.9998
ENSG00000150768	ENSG00000150768	DLAT	11:111895537-112095422	OK	13.3232	13.7238	0.042736	0.0490998	0.9369	0.9998
ENSG00000264575	ENSG00000264575	LINC00526	18:5232874-5246507	OK	1.0144	0.90384	-0.16649	-0.070973	0.9369	0.9998
ENSG00000176732	ENSG00000176732	PFN4	2:24299395-24424567	OK	0.636156	0.587399	-0.11504	-0.0303315	0.937	0.9998
ENSG00000108559	ENSG00000108559	NUP88	17:5185557-5372380	OK	24.4835	23.5483	-0.0561855	-0.0266401	0.93705	0.9998
ENSG00000132906	ENSG00000132906	CASP9	1:15783222-15853029	OK	3.57185	3.5028	-0.0281605	-0.0451483	0.93705	0.9998
ENSG00000120948	ENSG00000120948	TARDBP	1:11072413-11085796	OK	70.464	69.4958	-0.0199605	-0.0402261	0.9371	0.9998
ENSG00000143256	ENSG00000143256	PFDN2	1:161070345-161102478	OK	171.214	174.954	0.0311802	0.0471451	0.9371	0.9998
ENSG00000165632	ENSG00000165632	TAF3	10:7860466-8058590	OK	1.58112	1.55122	-0.0275513	-0.0479958	0.93715	0.9998
ENSG00000268812	ENSG00000268812	RP1-102K2.8	22:30635182-30642987	OK	0.776063	0.706755	-0.134964	-0.0292909	0.93715	0.9998
ENSG00000009335	ENSG00000009335	UBE3C	7:156931606-157062066	OK	59.3028	58.5314	-0.0188902	-0.0326983	0.9373	0.9998
ENSG00000141298	ENSG00000141298	SSH2	17:27887564-28513493	OK	18.8359	19.3379	0.0379465	0.0251488	0.9373	0.9998
ENSG00000177311	ENSG00000177311	ZBTB38	3:140947567-141168634	OK	27.2544	26.7636	-0.0262209	-0.0348998	0.93735	0.9998
ENSG00000148832	ENSG00000148832	PAOX	10:135192694-135382916	OK	1.67585	1.75762	0.0687336	0.0440193	0.93745	0.9998
ENSG00000151611	ENSG00000151611	MMAA	4:146539414-146581187	OK	2.45721	2.53396	0.0443707	0.0471357	0.93745	0.9998
ENSG00000230409	ENSG00000230409	TCEA1P2	3:37283279-37408242	OK	22.3238	20.9453	-0.0919523	-0.0426511	0.93745	0.9998
ENSG00000228192	ENSG00000228192	RP11-342M1.3	1:43272722-43312093	OK	1.49163	1.65278	0.148	0.0753519	0.9375	0.9998
ENSG00000134248	ENSG00000134248	LAMTOR5	1:110905469-110974982	OK	219.419	216.142	-0.021711	-0.0478317	0.93755	0.9998
ENSG00000228203	ENSG00000228203	RNF144A-AS1	2:7052407-7218011	OK	0.820799	0.868426	0.081374	0.0209461	0.93755	0.9998
ENSG00000104522	ENSG00000104522	TSTA3	8:144694787-144700218	OK	34.9451	34.4489	-0.0206317	-0.0453385	0.9376	0.9998
ENSG00000272849	ENSG00000272849	RP11-347I19.8	12:122150657-122241812	OK	0.632999	0.57305	-0.143541	-0.0261185	0.93765	0.9998
ENSG00000269899	ENSG00000269899	RP11-589N15.2	8:11700032-11726957	OK	11.8319	12.8332	0.117193	0.00330891	0.9377	0.9998
ENSG00000121481	ENSG00000121481	RNF2	1:185014495-185071740	OK	35.2106	34.6155	-0.0245935	-0.0481981	0.93775	0.9998
ENSG00000197894	ENSG00000197894	ADH5	4:99992131-100009952	OK	67.9636	69.0534	0.0229514	0.0471374	0.93775	0.9998
ENSG00000143198	ENSG00000143198	MGST3	1:165600097-165631033	OK	286.641	282.641	-0.0202757	-0.0476524	0.9378	0.9998
ENSG00000140650	ENSG00000140650	PMM2	16:8768421-8962866	OK	17.1595	16.8067	-0.0299647	-0.0387094	0.93785	0.9998
ENSG00000225507	ENSG00000225507	AC069282.6	7:47735327-48019178	OK	2.87652	2.54872	-0.174552	-0.05559	0.9379	0.9998
ENSG00000123836	ENSG00000123836	PFKFB2	1:207217193-207254369	OK	38.7768	38.0703	-0.0265262	-0.032781	0.93795	0.9998
ENSG00000165689	ENSG00000165689	SDCCAG3	9:139296376-139305061	OK	36.3545	37.0231	0.0262931	0.0451543	0.93795	0.9998
ENSG00000110844	ENSG00000110844	PRPF40B	12:49962000-50158717	OK	8.89455	8.55811	-0.0556304	-0.0129018	0.938	0.9998
ENSG00000178440	ENSG00000178440	LINC00843	10:51623416-51741813	OK	0.822539	0.77425	-0.0872853	-0.042555	0.938	0.9998
ENSG00000273131	ENSG00000273131	RP6-42F4.1	1:120693319-120697146	OK	0.650172	0.635073	-0.0338996	-0.0465389	0.938	0.9998
ENSG00000122140	ENSG00000122140	MRPS2	9:138387026-138398293	OK	30.3141	30.7598	0.0210587	0.0468302	0.9381	0.9998
ENSG00000105443	ENSG00000105443	CYTH2	19:48949029-48985571	OK	41.8358	42.7812	0.0322387	0.0451969	0.9382	0.9998
ENSG00000135926	ENSG00000135926	TMBIM1	2:219135114-219232822	OK	60.8246	61.8745	0.0246902	0.0414753	0.9382	0.9998
ENSG00000188352	ENSG00000188352	FOCAD	9:20658307-21031635	OK	12.186	11.9928	-0.0230589	-0.0302761	0.93825	0.9998
ENSG00000149016	ENSG00000149016	TUT1	11:62327072-62359649	OK	7.44557	6.79724	-0.131433	-0.035362	0.9384	0.9998
ENSG00000157637	ENSG00000157637	SLC38A10	17:79218799-79269347	OK	39.6208	39.0581	-0.0206377	-0.0410552	0.93855	0.9998
ENSG00000129933	ENSG00000129933	MAU2	19:19386826-19469563	OK	14.0825	13.8415	-0.0249087	-0.036029	0.9386	0.9998
ENSG00000171307	ENSG00000171307	ZDHHC16	10:99205926-99217127	OK	34.8957	35.4278	0.0218348	0.0478471	0.9386	0.9998
ENSG00000101216	ENSG00000101216	GMEB2	20:62218954-62258394	OK	6.14749	6.24263	0.0221576	0.0477984	0.93865	0.9998
ENSG00000122591	ENSG00000122591	FAM126A	7:22980877-23053749	OK	22.7887	23.0904	0.018975	0.0348075	0.9387	0.9998
ENSG00000235865	ENSG00000235865	GSN-AS1	9:123940414-124095121	OK	0.827686	0.906199	0.130745	0.0287999	0.93875	0.9998
ENSG00000129625	ENSG00000129625	REEP5	5:112043194-112258236	OK	24.764	25.2925	0.030467	0.0383424	0.9388	0.9998
ENSG00000268030	ENSG00000268030	AC005253.2	19:18668571-18680197	OK	2.14635	2.01614	-0.0902883	-0.0464367	0.9388	0.9998
ENSG00000048162	ENSG00000048162	NOP16	5:175792470-175843570	OK	30.3567	31.5874	0.057336	0.0475388	0.939	0.9998
ENSG00000168701	ENSG00000168701	TMEM208	16:67261005-67263181	OK	32.7641	33.2894	0.0229487	0.0476555	0.939	0.9998
ENSG00000089195	ENSG00000089195	TRMT6	20:5917880-5931182	OK	8.38537	8.2558	-0.0224656	-0.0435095	0.93905	0.9998
ENSG00000101158	ENSG00000101158	NELFCD	20:57556262-57570188	OK	107.067	105.323	-0.0236949	-0.0467495	0.93905	0.9998
ENSG00000128513	ENSG00000128513	POT1	7:124462439-125019375	OK	23.507	23.0862	-0.0260593	-0.0409526	0.93905	0.9998
ENSG00000089006	ENSG00000089006	SNX5	20:17922240-18039832	OK	36.517	35.751	-0.0305845	-0.0458368	0.9391	0.9998
ENSG00000135018	ENSG00000135018	UBQLN1	9:86274877-86328293	OK	60.2413	61.0807	0.0199623	0.0446325	0.9391	0.9998
ENSG00000151575	ENSG00000151575	TEX9	15:56536206-56757335	OK	2.01817	1.94478	-0.0534429	-0.0431877	0.9391	0.9998
ENSG00000213839	ENSG00000213839	RP11-3J10.4	9:37510888-38069210	OK	5.60464	5.03667	-0.154152	-0.044612	0.9391	0.9998
ENSG00000272168	ENSG00000272168	CASC15	6:21665002-22214734	OK	2.83971	2.79093	-0.0249961	-0.0448218	0.9391	0.9998
ENSG00000108294	ENSG00000108294	PSMB3	17:36908988-36920484	OK	140.043	138.267	-0.0184152	-0.0450928	0.9393	0.9998
ENSG00000178741	ENSG00000178741	COX5A	15:75212131-75230509	OK	295.846	300.065	0.0204289	0.0490243	0.93945	0.9998
ENSG00000213742	ENSG00000213742	ZNF337-AS1	20:25593570-25677477	OK	4.64789	4.91494	0.0805984	0.0369154	0.93945	0.9998
ENSG00000124201	ENSG00000124201	ZNFX1	20:47835883-47905797	OK	12.8294	13.2002	0.0411119	0.0417036	0.9395	0.9998
ENSG00000231721	ENSG00000231721	LINC-PINT	7:130626518-131182453	OK	8.65227	8.9963	0.0562518	0.0261939	0.9395	0.9998
ENSG00000130449	ENSG00000130449	ZSWIM6	5:60628099-60841997	OK	5.51292	5.43197	-0.0213406	-0.0454002	0.93955	0.9998
ENSG00000134001	ENSG00000134001	EIF2S1	14:67707825-67853233	OK	148.707	153.766	0.0482639	0.048128	0.93955	0.9998
ENSG00000177303	ENSG00000177303	CASKIN2	17:73496341-73511664	OK	3.56526	3.63145	0.0265385	0.0313804	0.93955	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000111846	ENSG00000111846	GCNT2	6:10492455-10629601	OK	4.83983	4.96561	0.0370142	0.0375321	0.9396	0.9998
ENSG00000103496	ENSG00000103496	STX4	16:31044209-31054296	OK	20.3665	20.6996	0.0234099	0.0462665	0.9397	0.9998
ENSG00000168876	ENSG00000168876	ANKRD49	11:94152894-94232749	OK	4.23885	4.12295	-0.0399966	-0.0389849	0.9397	0.9998
ENSG00000224870	ENSG00000224870	RP4-758J18.2	1:1334901-1342693	OK	7.65198	7.91884	0.0494553	0.0431025	0.9397	0.9998
ENSG00000126814	ENSG00000126814	TRMT5	14:61201459-61550451	OK	10.7408	11.218	0.0627132	0.0407583	0.9398	0.9998
ENSG00000175354	ENSG00000175354	PTPN2	18:12785476-12929642	OK	12.4098	12.6038	0.0223895	0.041637	0.9398	0.9998
ENSG00000008869	ENSG00000008869	HEATR5B	2:37195525-37311485	OK	10.9782	10.8406	-0.0182051	-0.0349094	0.93995	0.9998
ENSG00000103495	ENSG00000103495	MAZ	16:29817426-29859355	OK	94.7514	92.8588	-0.0291072	-0.0425901	0.93995	0.9998
ENSG00000108666	ENSG00000108666	C17orf75	17:30593194-30708905	OK	19.7899	19.2027	-0.0434549	-0.0359389	0.94	0.9998
ENSG00000221886	ENSG00000221886	C5orf54	5:159820154-159827104	OK	1.87002	1.90747	0.0286058	0.0445902	0.94	0.9998
ENSG00000145919	ENSG00000145919	BOD1	5:173034516-173043663	OK	37.3758	36.8596	-0.0200642	-0.0438073	0.94005	0.9998
ENSG00000171729	ENSG00000171729	TMEM51	1:15479027-15546976	OK	18.0289	17.7639	-0.0213594	-0.0460223	0.9401	0.9998
ENSG00000261705	ENSG00000261705	RP11-61A14.2	16:66912491-66929657	OK	3.92328	3.68607	-0.0899762	-0.0467098	0.9401	0.9998
ENSG00000264293	ENSG00000264293	RN7SL657P	1:1334901-1342693	OK	0.784627	0.737763	-0.088849	-0.00947371	0.9401	0.9998
ENSG00000134851	ENSG00000134851	TMEM165	4:56262123-56414056	OK	25.5943	26.1114	0.0288595	0.0432161	0.94015	0.9998
ENSG00000184508	ENSG00000184508	HDDC3	15:91473409-91506349	OK	20.1801	20.979	0.0560108	0.0424058	0.94015	0.9998
ENSG00000231822	ENSG00000231822	AC019097.7	2:99613723-100106497	OK	1.49813	1.37497	-0.123765	-0.0158667	0.9402	0.9998
ENSG00000107338	ENSG00000107338	SHB	9:37510888-38069210	OK	0.580654	0.640497	0.141514	0.0304594	0.9403	0.9998
ENSG00000226564	ENSG00000226564	FTH1P20	2:181737593-181738141	OK	3.28006	3.3643	0.0365847	0.0440268	0.9403	0.9998
ENSG00000108953	ENSG00000108953	YWHAE	17:1247565-1303672	OK	457.356	465.422	0.0252196	0.0451449	0.9404	0.9998
ENSG00000132471	ENSG00000132471	WBP2	17:73841779-73852588	OK	115.08	113.688	-0.0175515	-0.0417731	0.94045	0.9998
ENSG00000170525	ENSG00000170525	PFKFB3	10:6186880-6277495	OK	18.6842	18.9254	0.0185006	0.0339225	0.94045	0.9998
ENSG00000132130	ENSG00000132130	LHX1	17:35294083-35301917	OK	0.933605	0.980611	0.0708686	0.0467385	0.94055	0.9998
ENSG00000155034	ENSG00000155034	FBXL18	7:5470965-5553429	OK	4.64849	4.74436	0.0294518	0.0459061	0.94055	0.9998
ENSG00000258884	ENSG00000258884	CTD-3035D6.2	14:91288708-91294472	OK	0.737011	0.732577	-0.00870619	-0.00578339	0.94055	0.9998
ENSG00000162971	ENSG00000162971	TYW5	2:200775978-200873263	OK	7.33495	7.55871	0.0433523	0.0480755	0.9406	0.9998
ENSG00000165792	ENSG00000165792	METTL17	14:21457928-21467322	OK	29.8741	29.4497	-0.0206437	-0.0410444	0.9406	0.9998
ENSG00000234603	ENSG00000234603	AL356740.1	13:113344642-113541482	OK	19.887	20.4462	0.0400097	0.0149341	0.9406	0.9998
ENSG00000108424	ENSG00000108424	KPNB1	17:45726841-45762871	OK	218.476	214.635	-0.0255945	-0.0394691	0.94065	0.9998
ENSG00000121775	ENSG00000121775	TMEM39B	1:32479429-32568467	OK	5.17361	4.8735	-0.0862138	-0.0501247	0.9407	0.9998
ENSG00000130725	ENSG00000130725	UBE2M	19:59067078-59070327	OK	90.4189	89.192	-0.0197098	-0.0421807	0.9407	0.9998
ENSG00000185344	ENSG00000185344	ATP6V0A2	12:124196864-124246302	OK	9.784	10.0551	0.0394361	0.0452814	0.9407	0.9998
ENSG00000104824	ENSG00000104824	HNRNPL	19:39306061-39342987	OK	152.264	149.821	-0.0233353	-0.047089	0.9408	0.9998
ENSG00000160218	ENSG00000160218	TRAPPC10	21:45432199-45526433	OK	9.98494	10.1514	0.0238478	0.032494	0.94085	0.9998
ENSG00000186472	ENSG00000186472	PCLO	7:82383328-82792246	OK	2.37149	2.4337	0.0373585	0.0288978	0.94085	0.9998
ENSG00000205871	ENSG00000205871	RPS3AP47	15:43398422-43513481	OK	1.10822	0.982115	-0.174278	-0.0592293	0.94095	0.9998
ENSG00000139651	ENSG00000139651	ZNF740	12:53551446-53584596	OK	9.63226	9.47854	-0.0232096	-0.0343873	0.941	0.9998
ENSG00000251396	ENSG00000251396	RP11-163N6.2	8:61297146-61429354	OK	0.967494	0.935348	-0.0487497	-0.0383562	0.941	0.9998
ENSG00000168246	ENSG00000168246	UBTD2	5:171636643-171711075	OK	5.96522	5.87623	-0.0216832	-0.0444537	0.94105	0.9998
ENSG00000267060	ENSG00000267060	PTGES3L	17:41102542-41132545	OK	2.0091	1.88207	-0.0942275	-0.0526267	0.94105	0.9998
ENSG00000160695	ENSG00000160695	VPS11	11:118938084-118952688	OK	11.4485	11.2823	-0.0211035	-0.0433641	0.9411	0.9998
ENSG00000260822	ENSG00000260822	GS1-358P8.4	X:24563632-24568583	OK	5.04762	5.12321	0.0214448	0.0452908	0.94115	0.9998
ENSG00000168488	ENSG00000168488	ATXN2L	16:28834355-28848558	OK	38.9536	38.4371	-0.0192566	-0.0356733	0.9412	0.9998
ENSG00000181404	ENSG00000181404	XXyac-YRM2039.2	9:11986-30891	OK	3.63032	3.56165	-0.027553	-0.0442064	0.9414	0.9998
ENSG00000240616	ENSG00000240616	AD000092.3	19:13001839-13030090	OK	0.854586	0.766077	-0.157736	-0.0434837	0.9414	0.9998
ENSG00000090989	ENSG00000090989	EXOC1	4:56719781-56771200	OK	12.2277	12.0627	-0.0196024	-0.041327	0.94145	0.9998
ENSG00000100982	ENSG00000100982	PCIF1	20:44563266-44576662	OK	19.0025	18.7362	-0.0203605	-0.04733	0.9415	0.9998
ENSG00000165868	ENSG00000165868	HSPA12A	10:118423206-118502085	OK	7.91923	7.80422	-0.021105	-0.0328216	0.9415	0.9998
ENSG00000166136	ENSG00000166136	NDUFB8	10:102246398-102319755	OK	311.134	317.208	0.0278925	0.0467866	0.9415	0.9998
ENSG00000204209	ENSG00000204209	DAXX	6:33286334-33297046	OK	38.1426	37.6037	-0.0205286	-0.0413837	0.94155	0.9998
ENSG00000115274	ENSG00000115274	INO80B	2:74682149-74688018	OK	22.8259	23.3253	0.0312242	0.0422454	0.9416	0.9998
ENSG00000267002	ENSG00000267002	RP11-242D8.1	17:41316199-41322420	OK	1.01061	1.04033	0.0418168	0.0481554	0.94165	0.9998
ENSG00000134716	ENSG00000134716	CYP2J2	1:60358979-60392462	OK	2.05327	2.01367	-0.0280971	-0.0423044	0.9417	0.9998
ENSG00000163719	ENSG00000163719	MTMR14	3:9691116-9744077	OK	19.8679	19.5922	-0.020162	-0.04471	0.9417	0.9998
ENSG00000130714	ENSG00000130714	POMT1	9:134378288-134406655	OK	13.1476	13.5134	0.0395833	0.0382562	0.94175	0.9998
ENSG00000145220	ENSG00000145220	LYAR	4:4269427-4291896	OK	18.253	18.513	0.0204029	0.0431327	0.94175	0.9998
ENSG00000165795	ENSG00000165795	NDRG2	14:21484921-21572881	OK	14.1068	14.4089	0.0305674	0.0284085	0.9419	0.9998
ENSG00000179344	ENSG00000179344	HLA-DQB1	6:32627243-32636160	OK	2.2723	2.37675	0.0648382	0.0629833	0.9419	0.9998
ENSG00000169740	ENSG00000169740	ZNF32	10:44124264-44170151	OK	6.59348	6.70988	0.0252473	0.0414459	0.942	0.9998
ENSG00000102030	ENSG00000102030	NAA10	X:153126968-153200676	OK	114.893	112.035	-0.0363412	-0.043878	0.94205	0.9998
ENSG00000142546	ENSG00000142546	NOSIP	19:50058967-50094272	OK	40.7222	41.2919	0.0200421	0.0451992	0.9421	0.9998
ENSG00000130803	ENSG00000130803	ZNF317	19:9251055-9274100	OK	12.6843	12.4771	-0.0237565	-0.0328955	0.94215	0.9998
ENSG00000183531	ENSG00000183531	Z98256.1	22:32908538-33454358	OK	114.733	124.795	0.121276	0.0604785	0.94215	0.9998
ENSG00000213865	ENSG00000213865	C8orf44	8:67579830-67774257	OK	1.82269	1.7089	-0.0930038	-0.0456766	0.94215	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000061987	ENSG00000061987	MON2	12:62860596-62991363	OK	12.5627	12.7584	0.0223043	0.0330381	0.9422	0.9998
ENSG00000151332	ENSG00000151332	MBIP	14:36767769-36789882	OK	13.9834	14.2041	0.0225966	0.0423081	0.94225	0.9998
ENSG00000162639	ENSG00000162639	HENMT1	1:109190911-109204148	OK	3.47365	3.40779	-0.0276173	-0.0426304	0.94225	0.9998
ENSG00000166024	ENSG00000166024	R3HCC1L	10:99894386-100004654	OK	14.0314	14.2241	0.0196776	0.0452573	0.94225	0.9998
ENSG00000171097	ENSG00000171097	CCBL1	9:131595220-131680318	OK	4.72632	4.4722	-0.0797341	-0.0473871	0.94225	0.9998
ENSG00000087263	ENSG00000087263	OGFOD1	16:56463044-56554195	OK	18.7996	19.3206	0.0394337	0.0352591	0.9423	0.9998
ENSG00000175756	ENSG00000175756	AURKAIP1	1:1309109-1310875	OK	96.1544	97.3358	0.0176184	0.041628	0.9423	0.9998
ENSG00000110066	ENSG00000110066	SUV420H1	11:67922329-67981295	OK	20.8083	20.4989	-0.0216133	-0.0393222	0.9424	0.9998
ENSG00000155130	ENSG00000155130	MARCKS	6:114178540-114184648	OK	24.8049	25.1059	0.0174005	0.0426222	0.9424	0.9998
ENSG00000175467	ENSG00000175467	SART1	11:65729159-65747299	OK	27.4391	27.8928	0.0236576	0.0313162	0.9424	0.9998
ENSG00000257605	ENSG00000257605	RP11-680A11.5	12:53689074-53700961	OK	0.87496	0.949617	0.118129	0.012577	0.9424	0.9998
ENSG00000180806	ENSG00000180806	HOXC9	12:54375292-54449814	OK	7.9082	7.54448	-0.0679276	-0.0482561	0.94245	0.9998
ENSG00000205710	ENSG00000205710	C17orf107	17:4736682-4806369	OK	1.00827	1.08979	0.112177	0.0363741	0.94255	0.9998
ENSG00000106459	ENSG00000106459	NRF1	7:129251554-129396922	OK	6.59852	6.46616	-0.0292341	-0.0411776	0.9426	0.9998
ENSG00000108733	ENSG00000108733	PEX12	17:33901813-34053436	OK	2.8855	2.70439	-0.0935151	-0.0285395	0.9426	0.9998
ENSG00000118523	ENSG00000118523	CTGF	6:132269315-132398533	OK	1.83118	1.8655	0.0267871	0.0412737	0.9427	0.9998
ENSG00000149262	ENSG00000149262	INTS4	11:77532154-77705724	OK	16.2868	16.6257	0.0297075	0.0404464	0.9427	0.9998
ENSG00000172244	ENSG00000172244	C5orf34	5:43484060-43525412	OK	7.57706	7.30218	-0.0533112	-0.036428	0.94275	0.9998
ENSG00000186076	ENSG00000186076	RP11-887P2.3	12:94034597-94035362	OK	90.6259	89.1791	-0.0232183	-0.0457069	0.9428	0.9998
ENSG00000127054	ENSG00000127054	CPSF3L	1:1227755-1260071	OK	37.593	36.8967	-0.0269725	-0.0354576	0.94285	0.9998
ENSG00000168273	ENSG00000168273	SMIM4	3:52529353-52742182	OK	30.8018	29.1858	-0.0777448	-0.0220869	0.94285	0.9998
ENSG00000039319	ENSG00000039319	ZFYVE16	5:79703831-79775169	OK	92.992	94.1592	0.0179951	0.0234808	0.9429	0.9998
ENSG00000188033	ENSG00000188033	ZNF490	19:12490002-12750912	OK	1.38836	1.31372	-0.0797192	-0.038791	0.94305	0.9998
ENSG00000086848	ENSG00000086848	ALG9	11:111652918-111756699	OK	11.298	11.1223	-0.0226139	-0.0380073	0.9431	0.9998
ENSG00000131174	ENSG00000131174	COX7B	X:77154934-77162870	OK	168.282	165.403	-0.024893	-0.0439921	0.9432	0.9998
ENSG00000109220	ENSG00000109220	CHIC2	4:54243809-55164414	OK	4.39822	4.1777	-0.0742129	-0.0369898	0.9433	0.9998
ENSG00000237264	ENSG00000237264	FTH1P11	8:82351670-82445510	OK	6.959	7.5085	0.109645	0.046197	0.9434	0.9998
ENSG00000259456	ENSG00000259456	RP5-914P20.5	20:49505584-49575092	OK	0.784472	0.724409	-0.114917	-0.0157204	0.9434	0.9998
ENSG00000241489	ENSG00000241489	IDS	X:148558520-148632055	OK	2.74432	2.5309	-0.116799	-0.0272744	0.94345	0.9998
ENSG00000197885	ENSG00000197885	NKIRAS1	3:23933150-24022109	OK	15.4469	14.4993	-0.091333	-0.0313089	0.94355	0.9998
ENSG00000134717	ENSG00000134717	BTF3L4	1:52485802-52556388	OK	21.1701	21.7852	0.0413195	0.0419219	0.9437	0.9998
ENSG00000165630	ENSG00000165630	PRPF18	10:13628926-14504141	OK	9.86812	9.41495	-0.0678221	-0.0411182	0.9437	0.9998
ENSG00000170965	ENSG00000170965	PLAC1	X:133699867-133898352	OK	0.76246	0.787042	0.0457795	0.0346853	0.9437	0.9998
ENSG00000259865	ENSG00000259865	RP11-488L18.10	1:247350582-247351828	OK	2.50131	2.55179	0.0288272	0.0414544	0.94375	0.9998
ENSG00000242073	ENSG00000242073	AC006014.7	7:74988447-75115548	OK	1.4829	1.35932	-0.125541	-0.0191623	0.9438	0.9998
ENSG00000137070	ENSG00000137070	IL11RA	9:34638129-34681295	OK	16.5294	16.8669	0.0291539	0.0359142	0.94385	0.9998
ENSG00000241058	ENSG00000241058	NSUN6	10:18429605-18948214	OK	1.84704	1.80744	-0.0312687	-0.0372613	0.94385	0.9998
ENSG00000119778	ENSG00000119778	ATAD2B	2:23971533-24149984	OK	2.37959	2.42143	0.0251449	0.0253621	0.9439	0.9998
ENSG00000148444	ENSG00000148444	COMMD3	10:22604902-22620413	OK	26.5316	27.2468	0.0383727	0.0409185	0.944	0.9998
ENSG00000179965	ENSG00000179965	ZNF771	16:30418617-30441396	OK	2.39285	2.5779	0.107464	0.0678531	0.944	0.9998
ENSG00000198160	ENSG00000198160	MIER1	1:67390577-67454302	OK	7.77004	7.6494	-0.0225739	-0.042581	0.9441	0.9998
ENSG00000068724	ENSG00000068724	TTC7A	2:47126413-47403740	OK	3.8209	3.6897	-0.0504093	-0.0149183	0.9442	0.9998
ENSG00000161533	ENSG00000161533	ACOX1	17:73937587-74023533	OK	17.3446	17.0306	-0.0263626	-0.0378109	0.94425	0.9998
ENSG00000213252	ENSG00000213252	RP11-819M15.1	11:106544737-106889250	OK	1.35755	1.31117	-0.050155	-0.0418094	0.9443	0.9998
ENSG00000114933	ENSG00000114933	INO80D	2:206854308-206951288	OK	1.28011	1.30129	0.0236729	0.0256086	0.9444	0.9998
ENSG00000198538	ENSG00000198538	ZNF28	19:53300661-53360902	OK	4.55287	4.33745	-0.0699297	-0.0325454	0.9444	0.9998
ENSG00000224680	ENSG00000224680	PLA2G12AP1	1:52834348-52834916	OK	0.966198	0.927659	-0.0587257	-0.0505179	0.9444	0.9998
ENSG00000137288	ENSG00000137288	UQCC2	6:33588141-33679504	OK	196.101	200.971	0.0353884	0.0430524	0.94445	0.9998
ENSG00000184986	ENSG00000184986	TMEM121	14:105992939-105996539	OK	4.71258	4.79492	0.0249888	0.0411876	0.94445	0.9998
ENSG00000136710	ENSG00000136710	CCDC115	2:131095813-131105383	OK	10.4631	10.2101	-0.0353076	-0.0427249	0.94455	0.9998
ENSG00000176273	ENSG00000176273	SLC35G1	10:95653729-95715819	OK	17.0854	16.8732	-0.0180283	-0.0391944	0.9447	0.9998
ENSG00000196498	ENSG00000196498	NCOR2	12:124808960-125052135	OK	27.1443	27.6203	0.025077	0.0280575	0.9447	0.9998
ENSG00000023171	ENSG00000023171	GRAMD1B	11:123396343-123498482	OK	31.4978	31.9406	0.0201394	0.0366481	0.94475	0.9998
ENSG00000164978	ENSG00000164978	NUDT2	9:34329503-34343709	OK	15.9991	15.7576	-0.0219482	-0.0425913	0.94475	0.9998
ENSG00000169018	ENSG00000169018	FEM1B	15:68560129-68588203	OK	23.1227	23.5013	0.0234354	0.0363626	0.9448	0.9998
ENSG00000171169	ENSG00000171169	NAIF1	9:130823511-130871604	OK	6.45932	6.69497	0.0516964	0.0369818	0.9448	0.9998
ENSG00000150527	ENSG00000150527	CTAGE5	14:39699434-39856306	OK	5.97105	5.88087	-0.0219571	-0.0391548	0.94485	0.9998
ENSG00000153015	ENSG00000153015	CWC27	5:64064756-64314590	OK	15.8721	15.6583	-0.0195691	-0.0426392	0.94495	0.9998
ENSG00000039523	ENSG00000039523	FAM65A	16:67552320-67580691	OK	10.8035	10.6621	-0.0190075	-0.0287715	0.9451	0.9998
ENSG00000137992	ENSG00000137992	DBT	1:100652474-100715390	OK	2.43116	2.37229	-0.0353623	-0.038861	0.94515	0.9998
ENSG00000147257	ENSG00000147257	GPC3	X:132669772-133119922	OK	8.44436	8.77469	0.0553601	0.0465208	0.94515	0.9998
ENSG00000164024	ENSG00000164024	METAP1	4:99916770-99983964	OK	22.837	22.5699	-0.0169744	-0.0350254	0.9452	0.9998
ENSG00000157240	ENSG00000157240	FZD1	7:90893782-90898123	OK	3.36325	3.41246	0.0209571	0.0407836	0.94525	0.9998
ENSG00000010256	ENSG00000010256	UQCRC1	3:48636434-48648409	OK	281.372	285.375	0.0203783	0.0380772	0.9453	0.9998
ENSG00000091164	ENSG00000091164	TXNL1	18:54264438-54706076	OK	42.2728	42.9535	0.023047	0.0427459	0.94535	0.9998
ENSG00000041988	ENSG00000041988	THAP3	1:6684925-6761984	OK	14.1399	13.6777	-0.0479447	-0.0396107	0.9454	0.9998
ENSG00000071626	ENSG00000071626	DAZAP1	19:1407567-1435719	OK	55.4116	56.2512	0.0216958	0.0388196	0.9455	0.9998
ENSG00000111801	ENSG00000111801	BTN3A3	6:26440699-26453643	OK	2.27347	2.32383	0.0316097	0.0299678	0.94555	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000260955	ENSG00000260955	RP11-30L15.6	8:54955548-54958189	OK	0.752472	0.730557	-0.0426413	-0.0302815	0.94555	0.9998
ENSG00000257913	ENSG00000257913	RP11-386G11.5	12:49388931-49453557	OK	1.42695	1.50263	0.0745521	0.0144262	0.9456	0.9998
ENSG00000213281	ENSG00000213281	NRAS	1:115247089-115259515	OK	19.933	19.6913	-0.0175983	-0.0405736	0.94565	0.9998
ENSG00000170876	ENSG00000170876	TMEM43	3:14166439-14242619	OK	15.9822	16.3206	0.0302252	0.0405891	0.94575	0.9998
ENSG00000187535	ENSG00000187535	IFT140	16:1543344-1662111	OK	5.29969	5.16822	-0.0362401	-0.0331136	0.94575	0.9998
ENSG00000130313	ENSG00000130313	PGLS	19:17579577-17632097	OK	42.1381	43.012	0.0296157	0.0405941	0.9458	0.9998
ENSG00000179241	ENSG00000179241	LDLRAD3	11:35965530-36253686	OK	22.0449	22.3048	0.0169143	0.0381527	0.9459	0.9998
ENSG00000162066	ENSG00000162066	AMDHD2	16:2525146-2581423	OK	25.6451	26.3534	0.0393057	0.0311631	0.946	0.9998
ENSG00000262050	ENSG00000262050	RP11-74E22.3	17:2592679-2616127	OK	0.734096	0.672127	-0.127233	-0.0140151	0.94605	0.9998
ENSG00000008710	ENSG00000008710	PKD1	16:2089815-2185899	OK	14.9031	15.1923	0.0277265	0.0191918	0.94625	0.9998
ENSG00000116791	ENSG00000116791	CRYZ	1:75171169-75232362	OK	34.9612	35.5828	0.0254247	0.0413487	0.9463	0.9998
ENSG00000165782	ENSG00000165782	TMEM55B	14:20923349-20929771	OK	26.2901	25.5309	-0.0422714	-0.0323625	0.94635	0.9998
ENSG00000175334	ENSG00000175334	BANF1	11:65764015-65771620	OK	104.509	105.952	0.0197896	0.0405458	0.94635	0.9998
ENSG00000152433	ENSG00000152433	ZNF547	19:57874844-57988938	OK	0.8149	0.868386	0.0917122	0.0299786	0.94645	0.9998
ENSG00000197620	ENSG00000197620	CXorf40A	X:148558520-148632055	OK	11.0685	11.436	0.0471227	0.0421721	0.94645	0.9998
ENSG00000086015	ENSG00000086015	MAST2	1:46252658-46501796	OK	17.7636	17.5219	-0.0197615	-0.0254885	0.9465	0.9998
ENSG00000104450	ENSG00000104450	SPAG1	8:101170133-101348446	OK	3.79809	3.66289	-0.0522894	-0.0271427	0.9465	0.9998
ENSG00000187961	ENSG00000187961	KLHL17	1:895966-901095	OK	8.78322	8.97992	0.0319517	0.0426899	0.9465	0.9998
ENSG00000134827	ENSG00000134827	TCN1	11:59620272-59634048	OK	0.842042	0.817627	-0.0424494	-0.0316848	0.94655	0.9998
ENSG00000248569	ENSG00000248569	CTC-512J14.5	5:79646839-79647775	OK	2.01893	2.06289	0.0310746	0.0397629	0.94655	0.9998
ENSG00000130177	ENSG00000130177	CDC16	13:115000361-115038198	OK	122.021	123.648	0.0191081	0.0419025	0.9466	0.9998
ENSG00000123411	ENSG00000123411	IKZF4	12:56401442-56435590	OK	1.49221	1.5181	0.0248183	0.0242812	0.94675	0.9998
ENSG00000177427	ENSG00000177427	MIEF2	17:18163847-18169866	OK	5.9393	5.83827	-0.0247526	-0.0342026	0.94675	0.9998
ENSG00000250317	ENSG00000250317	SMIM20	4:25749054-25931435	OK	10.9746	10.7281	-0.0327786	-0.0385584	0.9468	0.9998
ENSG00000153006	ENSG00000153006	SREK1IP1	5:64013970-64064512	OK	8.73228	8.50552	-0.0379583	-0.0332812	0.94685	0.9998
ENSG00000239665	ENSG00000239665	RP11-295P9.3	10:13628926-14504141	OK	8.27106	7.96928	-0.053622	-0.0305955	0.94695	0.9998
ENSG00000267802	ENSG00000267802	AL358333.1	14:52292912-52446060	OK	2.94056	3.06922	0.0617808	0.0112546	0.94695	0.9998
ENSG00000117697	ENSG00000117697	NSL1	1:212899494-212965124	OK	26.9381	27.3296	0.0208186	0.040846	0.947	0.9998
ENSG00000166557	ENSG00000166557	TMED3	15:79603403-79704334	OK	183.478	181.569	-0.0150896	-0.0370773	0.947	0.9998
ENSG00000083750	ENSG00000083750	RRAGB	X:55744171-55785207	OK	3.62467	3.69436	0.0274734	0.0359621	0.94705	0.9998
ENSG00000121058	ENSG00000121058	COIL	17:55015547-55038415	OK	12.4687	12.3184	-0.0174874	-0.0385459	0.94705	0.9998
ENSG00000140830	ENSG00000140830	TXNL4B	16:72078187-72210777	OK	4.03241	4.17019	0.0484682	0.0319221	0.94705	0.9998
ENSG00000180764	ENSG00000180764	PIPSL	10:95717947-95721297	OK	0.871333	0.855241	-0.0268932	-0.0384782	0.94705	0.9998
ENSG00000259952	ENSG00000259952	AC009133.15	16:29817426-29859355	OK	4.40552	5.0232	0.189296	0.045395	0.9471	0.9998
ENSG00000272807	ENSG00000272807	RP11-260M2.1	2:210867288-211036115	OK	0.766616	0.710569	-0.10953	-0.0194696	0.9472	0.9998
ENSG00000099821	ENSG00000099821	POLRMT	19:617222-633597	OK	19.5974	19.8813	0.0207507	0.0281171	0.94725	0.9998
ENSG00000111752	ENSG00000111752	PHC1	12:9066491-9102551	OK	17.2084	16.5748	-0.0541251	-0.0214475	0.94725	0.9998
ENSG00000155287	ENSG00000155287	SLC25A28	10:101370281-101380366	OK	15.6134	15.8611	0.0227016	0.0410078	0.9473	0.9998
ENSG00000177469	ENSG00000177469	PTRF	17:40554469-40575535	OK	10.486	10.36	-0.0174375	-0.0396389	0.9473	0.9998
ENSG00000028528	ENSG00000028528	SNX1	15:64386321-64438289	OK	48.3701	48.947	0.0171053	0.0355929	0.94745	0.9998
ENSG00000115977	ENSG00000115977	AAK1	2:69685128-70053596	OK	5.446	5.27651	-0.0456141	-0.0275971	0.94745	0.9998
ENSG00000251485	ENSG00000251485	AC068134.10	2:232825954-233209060	OK	1.09438	1.1197	0.0329931	0.0113113	0.94745	0.9998
ENSG00000198482	ENSG00000198482	ZNF808	19:53030904-53090427	OK	1.38332	1.41782	0.0355351	0.029982	0.9475	0.9998
ENSG00000235162	ENSG00000235162	C12orf75	12:105567073-105789875	OK	11.1792	11.5173	0.0429828	0.0375819	0.9475	0.9998
ENSG00000149187	ENSG00000149187	CELF1	11:47487495-47606114	OK	40.3814	39.544	-0.0302318	-0.0267709	0.94755	0.9998
ENSG00000051128	ENSG00000051128	HOMER3	19:19010322-19057640	OK	27.7185	26.8511	-0.0458731	-0.0404692	0.94765	0.9998
ENSG00000130810	ENSG00000130810	PPAN	19:10216898-10230596	OK	30.7989	30.0443	-0.035787	-0.0359736	0.94765	0.9998
ENSG00000185220	ENSG00000185220	PGBD2	1:249200394-249214145	OK	2.59513	2.55339	-0.0233923	-0.0367783	0.94765	0.9998
ENSG00000271576	ENSG00000271576	RP11-486G15.2	1:84542013-84543614	OK	0.717688	0.734863	0.0341175	0.0395154	0.9477	0.9998
ENSG00000168256	ENSG00000168256	NKIRAS2	17:40118758-40217383	OK	21.1068	20.4796	-0.0435162	-0.0350431	0.94775	0.9998
ENSG00000196262	ENSG00000196262	PPIA	7:44836278-44864163	OK	1939.09	1965.1	0.0192252	0.0408171	0.94775	0.9998
ENSG00000140575	ENSG00000140575	IQGAP1	15:90931449-91045475	OK	78.8765	80.0176	0.0207221	0.0252763	0.94785	0.9998
ENSG00000152894	ENSG00000152894	PTPRK	6:128289923-128841870	OK	7.04111	7.13775	0.0196673	0.0301296	0.9479	0.9998
ENSG00000203999	ENSG00000203999	RP11-290F20.1	20:48909256-48937879	OK	2.34473	2.39564	0.0309875	0.0385695	0.9479	0.9998
ENSG00000114316	ENSG00000114316	USP4	3:49306034-49378145	OK	24.2005	24.4998	0.017733	0.0361579	0.94795	0.9998
ENSG00000273343	ENSG00000273343	XXbac-B444P24.13	22:20301798-20307603	OK	1.50748	1.65162	0.131741	0.0393266	0.94805	0.9998
ENSG00000166171	ENSG00000166171	DPCD	10:103330316-103369425	OK	22.3094	21.8508	-0.0299639	-0.0376454	0.9481	0.9998
ENSG00000260942	ENSG00000260942	CAPN10-AS1	2:241522116-241526116	OK	0.736349	0.74987	0.0262514	0.0384854	0.9481	0.9998
ENSG00000205208	ENSG00000205208	C4orf46	4:159587830-159644548	OK	6.06853	5.8887	-0.0433981	-0.0390207	0.94815	0.9998
ENSG00000138246	ENSG00000138246	DNAJC13	3:132136369-132257876	OK	21.5105	21.7387	0.0152241	0.0284032	0.9482	0.9998
ENSG00000167615	ENSG00000167615	LENG8	19:54955990-54974894	OK	31.7405	32.2933	0.0249111	0.0227296	0.94825	0.9998
ENSG00000037474	ENSG00000037474	NSUN2	5:6599351-6633404	OK	69.9813	70.7873	0.0165225	0.0367998	0.9483	0.9998
ENSG00000198873	ENSG00000198873	GRK5	10:120967100-121215131	OK	11.4136	11.5634	0.0188092	0.0353779	0.9483	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000112062	ENSG00000112062	MAPK14	6:35995487-36079013	OK	20.548	20.2804	-0.0189147	-0.036328	0.94835	0.9998
ENSG00000183309	ENSG00000183309	ZNF623	8:144718182-144735900	OK	9.2251	9.11187	-0.0178175	-0.0376043	0.94835	0.9998
ENSG00000271452	ENSG00000271452	RP11-342K6.2	2:75873908-75938115	OK	0.741267	0.687661	-0.108297	-0.0122464	0.94835	0.9998
ENSG00000011295	ENSG00000011295	TTC19	17:15879873-16256970	OK	16.0373	15.6991	-0.0307482	-0.034618	0.9484	0.9998
ENSG00000163527	ENSG00000163527	STT3B	3:31574129-31679112	OK	95.1913	94.1705	-0.0155546	-0.0294286	0.9484	0.9998
ENSG00000056661	ENSG00000056661	PCGF2	17:36886487-36906969	OK	14.2804	13.9919	-0.0294451	-0.0386318	0.94845	0.9998
ENSG00000197976	ENSG00000197976	AKAP17A	X:1710485-1721407	OK	7.81992	7.71677	-0.019158	-0.0392152	0.94845	0.9998
ENSG00000264301	ENSG00000264301	RP11-527H14.3	18:14946265-14973769	OK	8.63996	9.35488	0.114694	0.0554362	0.94845	0.9998
ENSG00000101849	ENSG00000101849	TBL1X	X:9431334-9687780	OK	6.49546	6.40779	-0.0196037	-0.028858	0.9485	0.9998
ENSG00000112739	ENSG00000112739	PRPF4B	6:4021500-4157619	OK	38.1548	37.4628	-0.0264056	-0.0315622	0.9485	0.9998
ENSG00000198589	ENSG00000198589	LRBA	4:151185593-151936879	OK	7.48109	7.59835	0.0224363	0.0279899	0.9485	0.9998
ENSG00000144451	ENSG00000144451	SPAG16	2:214149112-215548970	OK	12.6924	12.5144	-0.0203683	-0.0381097	0.9488	0.9998
ENSG00000196504	ENSG00000196504	PRPF40A	2:153508106-153617767	OK	23.7698	23.2433	-0.0323169	-0.0282293	0.94885	0.9998
ENSG00000198786	ENSG00000198786	MT-ND5	MT:12336-14148	OK	923.415	912.432	-0.0172623	-0.0382097	0.94885	0.9998
ENSG00000183283	ENSG00000183283	DAZAP2	12:51632075-51665146	OK	172.855	170.56	-0.0192821	-0.0392808	0.9489	0.9998
ENSG00000034533	ENSG00000034533	ASTE1	3:130569438-131100319	OK	4.00609	3.81904	-0.0689859	-0.0339209	0.94895	0.9998
ENSG00000165028	ENSG00000165028	NIPSNAP3B	9:107526437-107539738	OK	0.843883	0.867777	0.0402809	0.0388258	0.949	0.9998
ENSG00000177932	ENSG00000177932	ZNF354C	5:178487415-178510538	OK	1.01113	0.994145	-0.0244403	-0.0392191	0.949	0.9998
ENSG00000223380	ENSG00000223380	SEC22B	1:145096219-145116922	OK	34.5644	34.1805	-0.0161148	-0.0364014	0.949	0.9998
ENSG00000248587	ENSG00000248587	GDNF-AS1	5:37840539-37875901	OK	9.18947	9.36288	0.0269717	0.0383622	0.949	0.9998
ENSG00000212694	ENSG00000212694	AC084018.1	12:122150657-122241812	OK	4.21477	4.07509	-0.0486216	-0.0334314	0.9491	0.9998
ENSG00000103671	ENSG00000103671	TRIP4	15:64679946-64747502	OK	19.3429	19.5795	0.0175376	0.0347637	0.94915	0.9998
ENSG00000130147	ENSG00000130147	SH3BP4	2:235860616-235964358	OK	76.951	77.8263	0.0163175	0.0318056	0.9492	0.9998
ENSG00000266036	ENSG00000266036	MIR3615	17:72666716-72765492	OK	3.12144	3.3897	0.118947	0.0382428	0.9493	0.9998
ENSG00000169249	ENSG00000169249	ZRSR2	X:15808594-15841383	OK	6.06407	5.97161	-0.0221663	-0.0366447	0.94935	0.9998
ENSG00000100263	ENSG00000100263	RHBDD3	22:29655840-29696515	OK	15.1877	14.5885	-0.0580672	-0.0403246	0.94945	0.9998
ENSG00000116670	ENSG00000116670	MAD2L2	1:11734536-11751707	OK	62.0765	62.8054	0.0168403	0.0392662	0.94945	0.9998
ENSG00000171311	ENSG00000171311	EXOSC1	10:99195898-99205774	OK	42.4703	42.9861	0.0174162	0.0378584	0.9495	0.9998
ENSG00000164849	ENSG00000164849	GPR146	7:1036621-1177896	OK	6.06415	5.73714	-0.0799731	-0.0381975	0.94955	0.9998
ENSG00000236933	ENSG00000236933	RP11-439A17.7	1:120835809-120855681	OK	0.858242	0.910729	0.0856389	0.0382118	0.94955	0.9998
ENSG00000101126	ENSG00000101126	ADNP	20:49505584-49575092	OK	29.9656	30.3906	0.0203191	0.0324269	0.94965	0.9998
ENSG00000154874	ENSG00000154874	CCDC144B	17:18414534-18528930	OK	2.23255	2.16972	-0.0411874	-0.0255072	0.94965	0.9998
ENSG00000177181	ENSG00000177181	RIMKLA	1:42846465-42888249	OK	1.09613	1.14081	0.0576469	0.0430823	0.9497	0.9998
ENSG00000007341	ENSG00000007341	ST7L	1:113009162-113214241	OK	8.61341	8.39819	-0.0365064	-0.0166132	0.94975	0.9998
ENSG00000161914	ENSG00000161914	ZNF653	19:11562140-11639989	OK	2.26156	2.17565	-0.0558707	-0.0266569	0.9498	0.9998
ENSG00000122367	ENSG00000122367	LDB3	10:88428205-88495825	OK	2.09756	2.13485	0.0254231	0.0350347	0.94985	0.9998
ENSG00000148331	ENSG00000148331	ASB6	9:132399170-132404444	OK	18.6777	18.9001	0.0170728	0.037883	0.95	0.9998
ENSG00000162236	ENSG00000162236	STX5	11:62574368-62599560	OK	15.4424	15.6659	0.0207295	0.0402797	0.9502	0.9998
ENSG00000106086	ENSG00000106086	PLEKHA8	7:30067019-30170096	OK	11.8634	12.005	0.0171269	0.0315945	0.9503	0.9998
ENSG00000156873	ENSG00000156873	PHKG2	16:30709029-30787628	OK	16.7649	16.1877	-0.050554	-0.0356149	0.9503	0.9998
ENSG00000165506	ENSG00000165506	DNAAF2	14:50091891-50101948	OK	3.99305	3.93852	-0.0198391	-0.0370553	0.9503	0.9998
ENSG00000180185	ENSG00000180185	FAHD1	16:1845620-1934295	OK	19.3111	18.9021	-0.0308857	-0.0384869	0.9503	0.9998
ENSG00000245060	ENSG00000245060	LINC00847	5:180257956-180262726	OK	5.22978	5.31036	0.0220607	0.0358777	0.9503	0.9998
ENSG00000111077	ENSG00000111077	TENC1	12:53399941-53458156	OK	16.3522	15.9039	-0.0401089	-0.0158626	0.95035	0.9998
ENSG00000185010	ENSG00000185010	F8	X:154064062-154288578	OK	1.94269	1.84736	-0.0725897	-0.0381764	0.9504	0.9998
ENSG00000256594	ENSG00000256594	RP11-705C15.2	12:9787187-9811008	OK	6.17628	6.30973	0.0308412	0.0400432	0.9504	0.9998
ENSG00000071655	ENSG00000071655	MBD3	19:1576638-1605480	OK	27.4186	28.0048	0.0305233	0.0348701	0.9505	0.9998
ENSG00000092208	ENSG00000092208	GEMIN2	14:39583426-39606177	OK	8.88393	8.74821	-0.0222105	-0.0353511	0.9505	0.9998
ENSG00000106245	ENSG00000106245	BUD31	7:98923520-99063954	OK	106.304	110.968	0.0619476	0.0285202	0.9505	0.9998
ENSG00000269951	ENSG00000269951	RP11-797A18.6	15:77336021-77376326	OK	0.901887	0.965515	0.0983512	0.00886433	0.9505	0.9998
ENSG00000128709	ENSG00000128709	HOXD9	2:176986338-177037830	OK	0.784552	0.742962	-0.07858	-0.0396798	0.95055	0.9998
ENSG00000158296	ENSG00000158296	SLC13A3	20:45186462-45304714	OK	4.53448	4.45023	-0.0270591	-0.0325409	0.95055	0.9998
ENSG00000177674	ENSG00000177674	AGTRAP	1:11796140-11814859	OK	38.1714	37.7194	-0.0171834	-0.0370061	0.95055	0.9998
ENSG00000168591	ENSG00000168591	TMUB2	17:42264337-42269099	OK	26.7674	27.1167	0.0187034	0.0404039	0.95075	0.9998
ENSG00000197702	ENSG00000197702	PARVA	11:12398731-12552348	OK	31.5109	31.8748	0.0165668	0.0367887	0.95075	0.9998
ENSG00000116815	ENSG00000116815	CD58	1:117057156-117113661	OK	13.4398	13.6313	0.0204083	0.0376518	0.9508	0.9998
ENSG00000170631	ENSG00000170631	ZNF16	8:146155743-146176274	OK	3.45975	3.40641	-0.0224178	-0.0316197	0.95085	0.9998
ENSG00000168216	ENSG00000168216	LMBRD1	6:70385693-70507003	OK	14.7054	14.5409	-0.0162295	-0.035586	0.9509	0.9998
ENSG00000256569	ENSG00000256569	RP11-173P15.5	12:121148237-121161443	OK	4.50783	4.79534	0.0891989	0.0326721	0.95105	0.9998
ENSG00000272449	ENSG00000272449	RP3-395M20.12	1:2477903-2478899	OK	3.83031	3.90116	0.0264421	0.0394557	0.95105	0.9998
ENSG00000114902	ENSG00000114902	SPCS1	3:52529353-52742182	OK	158.543	154.884	-0.0336814	-0.0393418	0.9511	0.9998
ENSG00000177058	ENSG00000177058	SLC38A9	5:54921672-55112985	OK	9.40588	9.23882	-0.0258553	-0.032062	0.95125	0.9998
ENSG00000272269	ENSG00000272269	RP11-500C11.3	6:17615268-17707575	OK	6.13078	5.88402	-0.0592679	-0.0274138	0.95125	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000272617	ENSG00000272617	RP11-343C2.12	16:69139466-69442474	OK	3.50907	3.25778	-0.107197	-0.0261025	0.9513	0.9998
ENSG00000166377	ENSG00000166377	ATP9B	18:76829284-77138283	OK	4.89584	4.82768	-0.0202277	-0.020291	0.95135	0.9998
ENSG00000239445	ENSG00000239445	ST3GAL6-AS1	3:98433173-98620533	OK	9.56223	9.17673	-0.0593666	-0.0146517	0.9516	0.9998
ENSG00000152133	ENSG00000152133	GPATCH11	2:37311593-37384208	OK	13.1142	13.4127	0.032474	0.0364749	0.95165	0.9998
ENSG00000168556	ENSG00000168556	ING2	4:184426146-184432249	OK	4.51205	4.42746	-0.0273043	-0.0394908	0.95175	0.9998
ENSG00000168802	ENSG00000168802	CHTF8	16:69139466-69442474	OK	26.3063	25.8022	-0.0279126	-0.024928	0.95175	0.9998
ENSG00000100058	ENSG00000100058	CRYBB2P1	22:25844071-25916821	OK	13.1207	13.3642	0.0265308	0.0372008	0.95185	0.9998
ENSG00000102763	ENSG00000102763	VWA8	13:42140972-42535256	OK	8.13798	8.03919	-0.0176203	-0.0259155	0.95185	0.9998
ENSG00000099800	ENSG00000099800	TIMM13	19:2389768-2456994	OK	31.5273	30.6369	-0.0413287	-0.0335655	0.9519	0.9998
ENSG00000067601	ENSG00000067601	PMS2P4	7:66752527-66786513	OK	6.78876	7.16652	0.0781257	0.0410848	0.95195	0.9998
ENSG00000125846	ENSG00000125846	ZNF133	20:18269120-18297640	OK	2.78418	2.83065	0.0238807	0.0320863	0.952	0.9998
ENSG00000163126	ENSG00000163126	ANKRD23	2:97481981-97523832	OK	3.35619	3.5173	0.067647	0.0370716	0.95205	0.9998
ENSG00000182325	ENSG00000182325	FBXL6	8:145575877-145584932	OK	6.41871	6.63346	0.0474774	0.032963	0.95205	0.9998
ENSG00000164077	ENSG00000164077	MON1A	3:49924434-49967606	OK	6.47185	6.56012	0.0195432	0.0358623	0.9522	0.9998
ENSG00000177432	ENSG00000177432	NAP1L5	4:89442135-89629693	OK	3.95218	4.15597	0.0725363	0.0408923	0.9522	0.9998
ENSG00000100811	ENSG00000100811	YY1	14:100673743-100772884	OK	41.831	41.0004	-0.0289369	-0.0343457	0.9523	0.9998
ENSG00000168438	ENSG00000168438	CDC40	6:110501343-110679475	OK	5.26742	5.33698	0.0189291	0.0319541	0.9523	0.9998
ENSG00000177556	ENSG00000177556	ATOX1	5:151121876-151192346	OK	634.296	647.9	0.0306165	0.0363187	0.95235	0.9998
ENSG00000223117	ENSG00000223117	RN7SKP296	3:190231839-190375843	OK	1.5355	1.64662	0.100799	0.00922526	0.9524	0.9998
ENSG00000087253	ENSG00000087253	LPCAT2	16:55542909-55620582	OK	6.57271	6.72633	0.0333294	0.0334814	0.9525	0.9998
ENSG00000257315	ENSG00000257315	ZBED6	1:203764781-203823252	OK	6.19991	5.99806	-0.0477511	-0.0377231	0.9525	0.9998
ENSG00000203843	ENSG00000203843	PFN1P2	1:144593362-144621656	OK	0.648	0.678288	0.065904	0.0118145	0.95255	0.9998
ENSG00000228506	ENSG00000228506	RP11-98I9.4	6:99845926-99879249	OK	0.638052	0.694942	0.123218	0.037	0.95255	0.9998
ENSG00000022567	ENSG00000022567	SLC45A4	8:142217264-142318404	OK	5.94917	5.8324	-0.0285989	-0.0334299	0.9526	0.9998
ENSG00000101246	ENSG00000101246	ARFRP1	20:62289162-62374858	OK	21.0167	20.4709	-0.0379654	-0.0324409	0.9526	0.9998
ENSG00000161036	ENSG00000161036	LRWD1	7:102105375-102119354	OK	18.5285	18.8679	0.0261859	0.0336658	0.9526	0.9998
ENSG00000166886	ENSG00000166886	NAB2	12:57482676-57607134	OK	31.0226	30.3259	-0.0327694	-0.0317418	0.9527	0.9998
ENSG00000177485	ENSG00000177485	ZBTB33	X:119384606-119392253	OK	10.481	10.5883	0.0146916	0.034447	0.9527	0.9998
ENSG00000183155	ENSG00000183155	RABIF	1:202848084-202858263	OK	12.4704	12.6067	0.0156805	0.0342347	0.9527	0.9998
ENSG00000188229	ENSG00000188229	TUBB4B	9:140135664-140142222	OK	265.769	268.452	0.0144895	0.0361378	0.95275	0.9998
ENSG00000188021	ENSG00000188021	UBQLN2	X:56590025-56593443	OK	6.83239	6.91229	0.0167726	0.0355	0.95285	0.9998
ENSG00000203965	ENSG00000203965	EFCAB7	1:63906440-64125916	OK	3.42242	3.59994	0.0729565	0.0228943	0.9529	0.9998
ENSG00000131323	ENSG00000131323	TRAF3	14:103243812-103377837	OK	16.2987	16.5091	0.0185023	0.0337728	0.953	0.9998
ENSG00000138442	ENSG00000138442	WDR12	2:203739504-203879521	OK	57.9062	56.643	-0.0318193	-0.0411288	0.95305	0.9998
ENSG00000172534	ENSG00000172534	HCFC1	X:153213003-153237258	OK	10.3301	10.228	-0.0143369	-0.0330682	0.9531	0.9998
ENSG00000003509	ENSG00000003509	NDUFAF7	2:37394962-37551951	OK	15.2416	14.6567	-0.0564546	-0.0211343	0.9532	0.9998
ENSG00000109881	ENSG00000109881	CCDC34	11:27352373-27385415	OK	12.773	12.6029	-0.0193516	-0.0344485	0.9532	0.9998
ENSG00000123472	ENSG00000123472	ATPAF1	1:47098408-47184824	OK	51.1504	50.1307	-0.0290508	-0.0321844	0.9532	0.9998
ENSG00000169599	ENSG00000169599	NFU1	2:69622881-69664760	OK	37.4301	37.9325	0.0192393	0.0363312	0.9532	0.9998
ENSG00000158828	ENSG00000158828	PINK1	1:20959947-20988000	OK	17.2817	16.6911	-0.0501695	-0.0378139	0.95325	0.9998
ENSG00000163378	ENSG00000163378	EOGT	3:69024364-69129559	OK	4.28334	4.14834	-0.0462034	-0.0247681	0.95325	0.9998
ENSG00000229320	ENSG00000229320	KRT8P12	3:160212782-160287036	OK	2.20107	2.0669	-0.0907357	-0.0266451	0.95325	0.9998
ENSG00000010017	ENSG00000010017	RANBP9	6:13615558-13711796	OK	33.9844	34.483	0.0210126	0.033609	0.9533	0.9998
ENSG00000132603	ENSG00000132603	NIP7	16:69139466-69442474	OK	13.9648	14.3677	0.0410355	0.0202049	0.9535	0.9998
ENSG00000082996	ENSG00000082996	RNF13	3:149478891-149942977	OK	47.673	46.4737	-0.0367568	-0.0301238	0.9536	0.9998
ENSG00000081320	ENSG00000081320	STK17B	2:196998289-197041227	OK	5.87914	5.9642	0.0207229	0.0318425	0.95365	0.9998
ENSG00000253341	ENSG00000253341	RP11-730G20.2	8:75512009-75779174	OK	3.40756	3.55703	0.0619322	0.0237531	0.95365	0.9998
ENSG00000076650	ENSG00000076650	GPATCH1	19:33571785-33621448	OK	4.49679	4.55835	0.0196173	0.0322866	0.9537	0.9998
ENSG00000160124	ENSG00000160124	CCDC58	3:122078437-122102078	OK	45.7174	46.3805	0.0207733	0.0385153	0.95375	0.9998
ENSG00000237854	ENSG00000237854	LINC00674	17:66098048-66111659	OK	3.57796	3.51076	-0.0273529	-0.034507	0.95375	0.9998
ENSG00000084092	ENSG00000084092	NOA1	4:57829535-58071676	OK	9.79911	10.2788	0.0689424	0.0369701	0.9538	0.9998
ENSG00000090013	ENSG00000090013	BLVRB	19:40953695-40971747	OK	52.5662	52.0241	-0.0149561	-0.0334302	0.9539	0.9998
ENSG00000023839	ENSG00000023839	ABCC2	10:101542488-101611949	OK	54.4099	54.9513	0.0142845	0.0283721	0.954	0.9998
ENSG00000115286	ENSG00000115286	NDUFS7	19:1383525-1396466	OK	79.2337	78.3838	-0.0155577	-0.0330833	0.954	0.9998
ENSG00000270015	ENSG00000270015	RP11-540B6.6	15:31196054-31283810	OK	4.02467	4.14885	0.0438429	0.0352006	0.954	0.9998
ENSG00000120868	ENSG00000120868	APAF1	12:99038918-100378432	OK	4.58211	4.51408	-0.0215796	-0.0290218	0.95405	0.9998
ENSG00000140299	ENSG00000140299	BNIP2	15:59887073-59981733	OK	29.6651	30.1537	0.0235672	0.035502	0.9541	0.9998
ENSG00000254470	ENSG00000254470	AP5B1	11:65543363-65548273	OK	6.00074	5.91425	-0.0209446	-0.0348299	0.9541	0.9998
ENSG00000188186	ENSG00000188186	LAMTOR4	7:99746529-99756338	OK	221.098	223.534	0.0158071	0.0336327	0.9542	0.9998
ENSG00000143106	ENSG00000143106	PSMA5	1:109941652-109969062	OK	79.5316	80.3701	0.0151303	0.0351947	0.9543	0.9998
ENSG00000186603	ENSG00000186603	HPDL	1:45792544-45794347	OK	7.11101	7.20994	0.0199328	0.0360077	0.9543	0.9998
ENSG00000173715	ENSG00000173715	C11orf80	11:66511921-66614017	OK	5.34954	5.23504	-0.0312121	-0.0263622	0.9544	0.9998
ENSG00000177051	ENSG00000177051	FBXO46	19:46213886-46234162	OK	4.51757	4.44917	-0.0220109	-0.0315236	0.9544	0.9998
ENSG00000245213	ENSG00000245213	RP11-10K16.1	4:174053078-174250845	OK	1.60709	1.5092	-0.0906655	-0.0248775	0.9544	0.9998
ENSG00000117362	ENSG00000117362	APH1A	1:150237803-150253327	OK	199.023	197.057	-0.0143247	-0.0314098	0.95455	0.9998
ENSG00000187953	ENSG00000187953	PMS2CL	7:6749758-6793493	OK	8.73869	8.91758	0.0292339	0.0341137	0.9546	0.9998
ENSG00000166965	ENSG00000166965	RCCD1	15:91473409-91506349	OK	11.9302	11.633	-0.0364031	-0.0327858	0.95465	0.9998
ENSG00000185115	ENSG00000185115	NDNL2	15:29412456-29862927	OK	6.98336	6.89822	-0.0176976	-0.0332844	0.9547	0.9998
ENSG00000008324	ENSG00000008324	SS18L2	3:42589460-42709072	OK	21.4856	20.6157	-0.0596281	-0.0331636	0.9548	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000117640	ENSG00000117640	MTFR1L	1:26126666-26185903	OK	39.0828	39.8045	0.0271364	0.0330503	0.9548	0.9998
ENSG00000110200	ENSG00000110200	ANAPC15	11:71709586-71823826	OK	36.3902	37.5092	0.0436962	0.0303587	0.95485	0.9998
ENSG00000196159	ENSG00000196159	FAT4	4:126237553-126414087	OK	1.02666	1.04185	0.0211799	0.0203048	0.95485	0.9998
ENSG00000204790	ENSG00000204790	CBWD6	9:69204537-69269662	OK	9.09486	9.24383	0.0234398	0.0369291	0.95485	0.9998
ENSG00000235872	ENSG00000235872	RP11-335O4.3	12:68042117-68064699	OK	0.859022	0.789107	-0.122473	-0.0233736	0.9549	0.9998
ENSG00000092094	ENSG00000092094	OSGEP	14:20914569-20923264	OK	11.7427	11.5387	-0.0252881	-0.0371411	0.95495	0.9998
ENSG00000236264	ENSG00000236264	RPL26P30	11:2349978-2418649	OK	3.26899	3.08936	-0.0815373	-0.00751895	0.95495	0.9998
ENSG00000050130	ENSG00000050130	JKAMP	14:59895739-60043549	OK	47.5253	46.9668	-0.0170554	-0.0335613	0.955	0.9998
ENSG00000196312	ENSG00000196312	HIATL2	9:99660347-99775862	OK	14.4913	14.2916	-0.0200175	-0.0326671	0.955	0.9998
ENSG00000124535	ENSG00000124535	WRNIP1	6:2765647-2787186	OK	67.0351	66.3427	-0.0149782	-0.035462	0.95505	0.9998
ENSG00000082258	ENSG00000082258	CCNT2	2:135493033-135716912	OK	5.18924	5.25188	0.0173111	0.0267388	0.95515	0.9998
ENSG00000243230	ENSG00000243230	RP11-286H14.8	7:128828712-128853386	OK	0.935709	0.866818	-0.11033	-0.0181369	0.95515	0.9998
ENSG00000152953	ENSG00000152953	STK32B	4:5053168-5502725	OK	1.54391	1.52152	-0.0210816	-0.0284722	0.9552	0.9998
ENSG00000178935	ENSG00000178935	ZNF552	19:58281022-58427978	OK	2.96192	2.86627	-0.0473552	-0.023192	0.9552	0.9998
ENSG00000163950	ENSG00000163950	SLBP	4:1694526-1714282	OK	25.3832	25.6858	0.017098	0.0335565	0.95525	0.9998
ENSG00000250568	ENSG00000250568	RP11-333E13.2	4:39824482-39979576	OK	2.8368	3.04827	0.103728	0.0164419	0.95525	0.9998
ENSG00000158941	ENSG00000158941	CCAR2	8:22462144-22526661	OK	72.8113	71.3447	-0.0293559	-0.0250512	0.95535	0.9998
ENSG00000143786	ENSG00000143786	CNIH3	1:224572844-224928251	OK	10.5289	10.8227	0.0397012	0.0136025	0.9554	0.9998
ENSG00000102910	ENSG00000102910	LONP2	16:48198862-48482313	OK	30.5956	30.2593	-0.0159468	-0.0299584	0.95545	0.9998
ENSG00000161265	ENSG00000161265	U2AF1L4	19:36230057-36245420	OK	6.59819	6.79666	0.0427557	0.0285803	0.95545	0.9998
ENSG00000265688	ENSG00000265688	MAFG-AS1	17:79885704-79888629	OK	1.72744	1.69196	-0.0299371	-0.033424	0.95545	0.9998
ENSG00000259948	ENSG00000259948	RP11-326A19.5	15:89630308-89745591	OK	4.24572	4.53468	0.0949914	0.0189628	0.9555	0.9998
ENSG00000269044	ENSG00000269044	CTC-429P9.3	19:16589867-16771253	OK	1.64816	1.77642	0.108121	0.0289432	0.95555	0.9998
ENSG00000116406	ENSG00000116406	EDEM3	1:184659364-184724047	OK	11.1364	11.2625	0.0162435	0.0244908	0.9556	0.9998
ENSG00000119723	ENSG00000119723	COQ6	14:74318546-74551196	OK	20.9407	20.4567	-0.0337375	-0.0291003	0.95565	0.9998
ENSG00000170855	ENSG00000170855	TRIAP1	12:120875892-120899389	OK	34.3286	35.3326	0.041588	0.0331193	0.95565	0.9998
ENSG00000189159	ENSG00000189159	HN1	17:73131342-73179078	OK	123.838	121.34	-0.029403	-0.0321347	0.95565	0.9998
ENSG00000166797	ENSG00000166797	FAM96A	15:64364757-64386217	OK	91.5429	90.6349	-0.0143828	-0.0335734	0.9557	0.9998
ENSG00000159884	ENSG00000159884	CCDC107	9:35658300-35681156	OK	25.7613	26.2094	0.0248759	0.0342459	0.9558	0.9998
ENSG00000164062	ENSG00000164062	APEH	3:49711434-49761384	OK	120.288	122.087	0.0214191	0.0339341	0.9558	0.9998
ENSG00000102753	ENSG00000102753	KPNA3	13:50273446-50367057	OK	12.2802	12.394	0.0133123	0.0303023	0.9559	0.9998
ENSG00000151665	ENSG00000151665	PIGF	2:46717888-46852881	OK	20.1198	19.2282	-0.06539	-0.028894	0.9559	0.9998
ENSG00000156853	ENSG00000156853	ZNF689	16:30597227-30635333	OK	4.08126	4.13093	0.0174522	0.0314953	0.95595	0.9998
ENSG00000132003	ENSG00000132003	ZSWIM4	19:13906273-13943044	OK	2.80249	2.76829	-0.0177117	-0.031572	0.956	0.9998
ENSG00000136536	ENSG00000136536	7-Mar	2:160568999-160761260	OK	41.2668	41.8648	0.0207568	0.0310554	0.956	0.9998
ENSG00000119720	ENSG00000119720	NRDE2	14:90742579-90798481	OK	6.99904	6.8969	-0.0212091	-0.0281941	0.95605	0.9998
ENSG00000160796	ENSG00000160796	NBEAL2	3:46963215-47051193	OK	4.78922	4.86762	0.0234241	0.0215576	0.95605	0.9998
ENSG00000262663	ENSG00000262663	RP11-497H17.1	17:80709939-81009686	OK	0.810907	0.757985	-0.0973657	-0.0108612	0.95605	0.9998
ENSG00000109103	ENSG00000109103	UNC119	17:26782769-26972472	OK	20.2862	21.1786	0.0621103	0.0227641	0.9561	0.9998
ENSG00000010278	ENSG00000010278	CD9	12:6308880-6347425	OK	75.1873	74.4485	-0.0142466	-0.0330551	0.95615	0.9998
ENSG00000227533	ENSG00000227533	SLC2A1-AS1	1:43424719-43449029	OK	0.626525	0.642179	0.0356034	0.0316631	0.95615	0.9998
ENSG00000085978	ENSG00000085978	ATG16L1	2:234118696-234204320	OK	14.5264	14.3587	-0.0167503	-0.0283865	0.9562	0.9998
ENSG00000144535	ENSG00000144535	DIS3L2	2:232825954-233209060	OK	12.2577	12.4378	0.0210509	0.0327166	0.9562	0.9998
ENSG00000249274	ENSG00000249274	PDLIM1P4	3:98433173-98620533	OK	1.77957	1.67764	-0.0850943	-0.012195	0.95625	0.9998
ENSG00000184227	ENSG00000184227	ACOT1	14:73945188-74025651	OK	1.66188	1.72236	0.0515635	0.031817	0.9564	0.9998
ENSG00000134363	ENSG00000134363	FST	5:52776238-52782964	OK	3.50059	3.43751	-0.0262352	-0.0331199	0.95645	0.9998
ENSG00000148358	ENSG00000148358	GPR107	9:132815704-132902448	OK	25.1236	24.8859	-0.0137179	-0.0282683	0.9565	0.9998
ENSG00000175193	ENSG00000175193	PARL	3:183547172-183606237	OK	88.6	87.7211	-0.0143823	-0.0318	0.9565	0.9998
ENSG00000230124	ENSG00000230124	RP5-1180C10.2	1:180199420-180472089	OK	1.72207	1.6138	-0.0936898	-0.0511367	0.95655	0.9998
ENSG00000198695	ENSG00000198695	MT-ND6	MT:14148-14673	OK	1029.42	1019.94	-0.0133536	-0.0329891	0.9566	0.9998
ENSG00000167005	ENSG00000167005	NUDT21	16:56463044-56554195	OK	30.1251	30.9302	0.0380512	0.0376246	0.95665	0.9998
ENSG00000196935	ENSG00000196935	SRGAP1	12:64238072-64541637	OK	8.36712	8.26898	-0.0170231	-0.015997	0.95665	0.9998
ENSG00000113048	ENSG00000113048	MRPS27	5:71515235-71656052	OK	36.1345	36.4656	0.0131572	0.0274557	0.95675	0.9998
ENSG00000150773	ENSG00000150773	PIH1D2	11:111895537-112095422	OK	0.842103	0.816083	-0.0452802	-0.00732011	0.95675	0.9998
ENSG00000268790	ENSG00000268790	CTC-429P9.4	19:16589867-16771253	OK	15.3314	14.1286	-0.117875	-0.0444235	0.95675	0.9998
ENSG00000172965	ENSG00000172965	MIR4435-1HG	2:111953539-112268567	OK	135.53	134.058	-0.015756	-0.0332906	0.9568	0.9998
ENSG00000177868	ENSG00000177868	CCDC23	1:43272722-43312093	OK	15.8358	15.6091	-0.0207987	-0.0319789	0.9568	0.9998
ENSG00000100865	ENSG00000100865	CINP	14:102783713-102829253	OK	48.2971	48.8552	0.016576	0.0315201	0.9569	0.9998
ENSG00000134480	ENSG00000134480	CCNH	5:86563704-86708836	OK	42.6044	43.296	0.0232321	0.032641	0.95695	0.9998
ENSG00000004866	ENSG00000004866	ST7	7:116592499-116870157	OK	48.8169	48.3019	-0.0152983	-0.027953	0.957	0.9998
ENSG00000090615	ENSG00000090615	GOLGA3	12:133345494-133532892	OK	19.0528	18.7472	-0.0233314	-0.0145822	0.957	0.9998
ENSG00000136450	ENSG00000136450	SRSF1	17:56066398-56084707	OK	103.206	102.155	-0.0147776	-0.0312241	0.957	0.9998
ENSG00000164402	ENSG00000164402	8-Sep	5:132083136-132142933	OK	13.3956	13.2549	-0.0152323	-0.0278522	0.95715	0.9998
ENSG00000182446	ENSG00000182446	NPLOC4	17:79523912-79615779	OK	67.1902	66.5105	-0.0146695	-0.0220165	0.95715	0.9998
ENSG00000116750	ENSG00000116750	UCHL5	1:192981379-193060907	OK	49.7651	50.4874	0.0207909	0.0316643	0.9572	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000079974	ENSG00000079974	RABL2B	22:51195375-51239737	OK	8.13826	8.0045	-0.0239103	-0.0288516	0.9573	0.9998
ENSG00000132849	ENSG00000132849	INADL	1:62208148-62629592	OK	3.79951	3.85459	0.0207636	0.0194209	0.9573	0.9998
ENSG00000196696	ENSG00000196696	PDXDC2P	16:70010199-70099851	OK	2.70296	2.63222	-0.0382618	-0.0336272	0.9573	0.9998
ENSG00000167733	ENSG00000167733	HSD11B1L	19:5674957-5720583	OK	6.72299	6.58928	-0.0289808	-0.00659891	0.9574	0.9998
ENSG00000086200	ENSG00000086200	IPO11	5:61601988-61924409	OK	13.1113	12.9133	-0.0219462	-0.0279884	0.9575	0.9998
ENSG00000100441	ENSG00000100441	KHNYN	14:24895737-24912111	OK	22.2344	21.9583	-0.0180328	-0.0305989	0.9575	0.9998
ENSG00000164542	ENSG00000164542	KIAA0895	7:36363829-36493400	OK	4.5309	4.38951	-0.0457358	-0.0208876	0.95755	0.9998
ENSG00000213221	ENSG00000213221	DNLZ	9:139221931-139268133	OK	9.98428	10.2777	0.0417863	0.0315125	0.95755	0.9998
ENSG00000164294	ENSG00000164294	GPX8	5:54408798-54469005	OK	18.2949	18.4999	0.0160732	0.0303404	0.95765	0.9998
ENSG00000262049	ENSG00000262049	RP13-1032I1.7	17:79648203-79670330	OK	1.46136	1.34883	-0.115609	-0.0361019	0.95765	0.9998
ENSG00000262580	ENSG00000262580	RP11-334C17.5	17:78143790-78227299	OK	4.79251	4.63291	-0.048864	-0.0244202	0.9578	0.9998
ENSG00000005812	ENSG00000005812	FBXL3	13:77564794-77601330	OK	13.2858	13.1046	-0.0198136	-0.0266302	0.95795	0.9998
ENSG00000245532	ENSG00000245532	NEAT1	11:65190244-65213011	OK	149.689	147.631	-0.0199725	-0.0343783	0.95795	0.9998
ENSG00000171202	ENSG00000171202	TMEM126A	11:85359010-85367591	OK	30.7846	30.4515	-0.0156984	-0.0318018	0.9583	0.9998
ENSG00000244363	ENSG00000244363	RPL7P23	5:76506273-76916436	OK	1.35491	1.46421	0.11192	0.0327217	0.9583	0.9998
ENSG00000160094	ENSG00000160094	ZNF362	1:33722145-33766320	OK	8.35597	8.25874	-0.0168866	-0.0261775	0.95845	0.9998
ENSG00000164296	ENSG00000164296	TIGD6	5:149340299-149432386	OK	3.44446	3.66399	0.0891398	0.0431906	0.95845	0.9998
ENSG00000205155	ENSG00000205155	PSENEN	19:36230057-36245420	OK	53.0649	52.3746	-0.0188903	-0.0328544	0.9585	0.9998
ENSG00000196118	ENSG00000196118	C16orf93	16:30709029-30787628	OK	3.33035	3.41737	0.0372157	0.00808923	0.95855	0.9998
ENSG00000172613	ENSG00000172613	RAD9A	11:67159175-67193078	OK	8.01661	7.77621	-0.0439245	-0.0256406	0.9586	0.9998
ENSG00000173113	ENSG00000173113	TRMT112	11:64073043-64085556	OK	238.027	240.926	0.0174626	0.0317807	0.9586	0.9998
ENSG00000117533	ENSG00000117533	VAMP4	1:171669299-171711387	OK	11.1783	11.0118	-0.0216492	-0.033331	0.95865	0.9998
ENSG00000123416	ENSG00000123416	TUBA1B	12:49521564-49541652	OK	1153.91	1165.26	0.0141205	0.0306433	0.95865	0.9998
ENSG00000120675	ENSG00000120675	DNAJC15	13:43597338-43683045	OK	31.6644	31.3318	-0.0152298	-0.0311586	0.9587	0.9998
ENSG00000261377	ENSG00000261377	RP11-578F21.12	15:29033388-29101361	OK	10.8268	10.9721	0.0192412	0.0292699	0.9587	0.9998
ENSG00000100242	ENSG00000100242	SUN2	22:39101727-39190203	OK	32.4524	32.0902	-0.0161939	-0.0277753	0.95875	0.9998
ENSG00000068400	ENSG00000068400	GRIPAP1	X:48830133-48858675	OK	12.9327	13.0696	0.0151914	0.0296097	0.9589	0.9998
ENSG00000070610	ENSG00000070610	GBA2	9:35696944-35758572	OK	54.7099	55.6636	0.0249301	0.0255938	0.9589	0.9998
ENSG00000099995	ENSG00000099995	SF3A1	22:30727976-30825045	OK	36.509	37.1734	0.0260164	0.0261499	0.9589	0.9998
ENSG00000163947	ENSG00000163947	ARHGEF3	3:56761445-57114129	OK	15.3853	15.5387	0.0143114	0.0255231	0.9589	0.9998
ENSG00000177707	ENSG00000177707	PVRL3	3:110612554-110994410	OK	7.63763	7.71914	0.0153159	0.0248108	0.9589	0.9998
ENSG00000104774	ENSG00000104774	MAN2B1	19:12754088-12792716	OK	32.2165	32.6955	0.0212902	0.0232671	0.95895	0.9998
ENSG00000170647	ENSG00000170647	TMEM133	11:100862810-100864663	OK	1.47445	1.49722	0.0221079	0.031338	0.95895	0.9998
ENSG00000181090	ENSG00000181090	EHMT1	9:140513443-141019076	OK	15.8109	15.5686	-0.0222855	-0.0272731	0.959	0.9998
ENSG00000145194	ENSG00000145194	ECE2	3:183851806-184402546	OK	5.47736	5.21372	-0.071169	-0.0100431	0.95905	0.9998
ENSG00000162961	ENSG00000162961	DPY30	2:32090128-32264881	OK	76.5017	75.5111	-0.0188045	-0.0314924	0.95905	0.9998
ENSG00000105085	ENSG00000105085	MED26	19:16589867-16771253	OK	3.53117	3.68027	0.0596648	0.0313086	0.9593	0.9998
ENSG00000130724	ENSG00000130724	CHMP2A	19:59062932-59066491	OK	119.135	120.171	0.0124854	0.0304033	0.95945	0.9998
ENSG00000182768	ENSG00000182768	NGRN	15:90792761-90816463	OK	112.698	111.684	-0.0130295	-0.0301431	0.95945	0.9998
ENSG00000262944	ENSG00000262944	RP11-473I1.9	16:9185504-9215497	OK	3.98802	3.83852	-0.0551229	-0.0314498	0.95945	0.9998
ENSG00000116017	ENSG00000116017	ARID3A	19:925780-975939	OK	12.9265	12.7011	-0.0253792	-0.0275065	0.9595	0.9998
ENSG00000127423	ENSG00000127423	AUNIP	1:26126666-26185903	OK	2.84818	3.01065	0.080036	0.0291466	0.9595	0.9998
ENSG00000153487	ENSG00000153487	ING1	13:111293758-111373421	OK	7.71829	7.56815	-0.0283389	-0.0285299	0.9595	0.9998
ENSG00000178233	ENSG00000178233	TMEM151B	6:44238202-44346694	OK	0.616277	0.646277	0.0685744	0.017367	0.9595	0.9998
ENSG00000225151	ENSG00000225151	GOLGA2P7	15:84867599-84898888	OK	3.97954	4.04441	0.0233293	0.0306335	0.9595	0.9998
ENSG00000272048	ENSG00000272048	RP11-458N5.1	2:25450723-25451090	OK	1.60489	1.64457	0.0352357	0.0287278	0.95955	0.9998
ENSG00000002586	ENSG00000002586	CD99	X:2609219-2659350	OK	177.756	179.151	0.0112706	0.0276919	0.9597	0.9998
ENSG00000104324	ENSG00000104324	CPQ	8:97657454-98161882	OK	21.9518	21.7358	-0.0142715	-0.0315323	0.95975	0.9998
ENSG00000006634	ENSG00000006634	DBF4	7:87462882-87538856	OK	24.0219	23.7217	-0.018143	-0.0251861	0.9598	0.9998
ENSG00000235448	ENSG00000235448	RP11-3L8.3	9:12685438-12822130	OK	0.776534	0.826918	0.0906956	0.00241802	0.9598	0.9998
ENSG00000255224	ENSG00000255224	CTD-3065J16.9	8:145132904-145135550	OK	1.51868	1.45218	-0.0645995	-0.0323082	0.96	0.9998
ENSG00000133731	ENSG00000133731	IMPA1	8:82570195-82598928	OK	27.0885	27.3374	0.0131905	0.0256996	0.96005	0.9998
ENSG00000186501	ENSG00000186501	TMEM222	1:27648650-27662891	OK	15.2657	15.1101	-0.01478	-0.0280182	0.96005	0.9998
ENSG00000272140	ENSG00000272140	RP11-574K11.29	10:75404638-75490272	OK	1.19441	1.15147	-0.0528161	-0.0316197	0.96005	0.9998
ENSG00000261616	ENSG00000261616	RP11-6O2.3	15:99676527-99791428	OK	0.791405	0.750097	-0.0773381	-0.040101	0.9601	0.9998
ENSG00000105287	ENSG00000105287	PRKD2	19:47150868-47220384	OK	8.00243	8.16915	0.0297487	0.0286628	0.96025	0.9998
ENSG00000203706	ENSG00000203706	SERTAD4-AS1	1:210404800-210419976	OK	0.892857	0.83657	-0.0939425	-0.0361216	0.9603	0.9998
ENSG00000126453	ENSG00000126453	BCL2L12	19:50162825-50177173	OK	28.3473	27.944	-0.0206725	-0.0294001	0.9604	0.9998
ENSG00000149930	ENSG00000149930	TAOK2	16:29984961-30003582	OK	15.1864	15.0552	-0.012513	-0.0286253	0.96045	0.9998
ENSG00000226328	ENSG00000226328	CTA-217C2.1	22:45528900-45559662	OK	2.60285	2.65342	0.0277604	0.0304139	0.9605	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000133872	ENSG00000133872	TMEM66	8:29920527-29940983	OK	134.438	133.253	-0.01278	-0.0284292	0.96055	0.9998
ENSG00000156304	ENSG00000156304	SCAF4	21:33043345-33104388	OK	5.27994	5.22441	-0.0152523	-0.0293216	0.96055	0.9998
ENSG00000157764	ENSG00000157764	BRAF	7:140218219-140624564	OK	14.8144	15.1029	0.0278238	0.0271214	0.96055	0.9998
ENSG00000217930	ENSG00000217930	PAM16	16:4364761-4475706	OK	54.0016	53.1125	-0.02395	-0.0288511	0.96055	0.9998
ENSG00000145428	ENSG00000145428	RNF175	4:154631276-154681387	OK	3.16069	3.11169	-0.0225404	-0.0257707	0.9606	0.9998
ENSG00000115526	ENSG00000115526	CHST10	2:101008326-101034118	OK	17.6374	17.4555	-0.0149544	-0.026077	0.96065	0.9998
ENSG00000137814	ENSG00000137814	HAUS2	15:42841007-42862192	OK	14.7713	15.0151	0.0236116	0.0296797	0.96065	0.9998
ENSG00000233024	ENSG00000233024	NPIPA7	16:18411798-18495797	OK	0.899236	0.867681	-0.0515348	-0.0272759	0.9607	0.9998
ENSG00000137571	ENSG00000137571	SLCO5A1	8:70579281-70767206	OK	11.6328	11.5135	-0.01487	-0.0273639	0.96075	0.9998
ENSG00000100099	ENSG00000100099	HPS4	22:26825238-26879803	OK	59.8101	59.3088	-0.0121434	-0.0243414	0.96085	0.9998
ENSG00000170296	ENSG00000170296	GABARAP	17:7143332-7167302	OK	321.737	325.609	0.0172583	0.0310586	0.96085	0.9998
ENSG00000130363	ENSG00000130363	RSPH3	6:159393902-159486305	OK	1.08496	1.06465	-0.0272633	-0.0285664	0.9609	0.9998
ENSG00000188599	ENSG00000188599	NPIPP1	16:15068447-15248421	OK	4.92083	4.75266	-0.0501679	-0.0166111	0.9609	0.9998
ENSG00000144909	ENSG00000144909	OSBPL11	3:125247701-125313934	OK	6.24134	6.29952	0.0133861	0.0288965	0.961	0.9998
ENSG00000164327	ENSG00000164327	RICTOR	5:38845959-39074510	OK	7.97183	7.9032	-0.0124738	-0.0215882	0.961	0.9998
ENSG00000204599	ENSG00000204599	TRIM39	6:30201815-30314661	OK	7.64804	7.51125	-0.0260369	-0.023015	0.961	0.9998
ENSG00000258677	ENSG00000258677	RP11-463D19.2	8:74332238-74791145	OK	2.09681	1.98941	-0.0758544	-0.0229119	0.961	0.9998
ENSG00000264577	ENSG00000264577	AC010761.8	17:27046410-27070473	OK	2.64815	2.81477	0.088033	0.0189183	0.961	0.9998
ENSG00000228253	ENSG00000228253	MT-ATP8	MT:8365-9990	OK	6069.16	6286.01	0.0506478	0.0180484	0.96105	0.9998
ENSG00000261253	ENSG00000261253	AC137932.6	16:89334037-89556969	OK	0.649927	0.687849	0.0818144	0.0144926	0.96105	0.9998
ENSG00000005483	ENSG00000005483	KMT2E	7:104653871-105039755	OK	22.6729	23.0019	0.0207825	0.0234225	0.9611	0.9998
ENSG00000183735	ENSG00000183735	TBK1	12:64845659-64895888	OK	16.3864	16.2387	-0.0130654	-0.024213	0.9611	0.9998
ENSG00000124228	ENSG00000124228	DDX27	20:47835883-47905797	OK	38.5022	37.8406	-0.0250043	-0.0287192	0.96115	0.9998
ENSG00000128000	ENSG00000128000	ZNF780B	19:40534166-40600313	OK	2.33643	2.27691	-0.0372299	-0.016242	0.96115	0.9998
ENSG00000106443	ENSG00000106443	PHF14	7:11013498-11209250	OK	14.2333	14.3699	0.0137829	0.0244312	0.9613	0.9998
ENSG00000148297	ENSG00000148297	MED22	9:136205159-136214986	OK	13.7838	13.6615	-0.0128518	-0.0229594	0.9614	0.9998
ENSG00000204673	ENSG00000204673	AKT1S1	19:50372294-50392005	OK	21.637	21.8967	0.0172113	0.0299606	0.9614	0.9998
ENSG00000113558	ENSG00000113558	SKP1	5:133450401-133706738	OK	218.816	215.99	-0.0187588	-0.0307377	0.96145	0.9998
ENSG00000108239	ENSG00000108239	TBC1D12	10:96162260-96295687	OK	2.81626	2.78578	-0.015695	-0.0237706	0.96155	0.9998
ENSG00000159348	ENSG00000159348	CYB5R1	1:202930996-202936408	OK	48.97	48.569	-0.0118608	-0.0273951	0.96155	0.9998
ENSG00000247081	ENSG00000247081	RP11-318M2.2	8:104133259-104345094	OK	3.41886	3.52954	0.0459641	0.0166355	0.96155	0.9998
ENSG00000154783	ENSG00000154783	FGD5	3:14860468-15106842	OK	0.93464	0.881722	-0.0840875	-0.017716	0.9617	0.9998
ENSG00000188641	ENSG00000188641	DPYD	1:97543298-98386605	OK	1.42411	1.44428	0.0202946	0.0244739	0.9617	0.9998
ENSG00000196465	ENSG00000196465	MYL6B	12:56544579-56584068	OK	65.4962	67.2905	0.0389923	0.0297589	0.9619	0.9998
ENSG00000178904	ENSG00000178904	DPY19L3	19:32880955-32976801	OK	7.77057	7.68803	-0.0154076	-0.0202373	0.962	0.9998
ENSG00000100554	ENSG00000100554	ATP6V1D	14:67707825-67853233	OK	135.779	137.706	0.0203401	0.0291732	0.96205	0.9998
ENSG00000273478	ENSG00000273478	RP11-465N4.5	1:201951499-201986316	OK	1.87583	1.99488	0.0887741	0.0190108	0.96205	0.9998
ENSG00000109944	ENSG00000109944	C11orf63	11:122753390-122830506	OK	1.80612	1.78361	-0.0180935	-0.0275477	0.9621	0.9998
ENSG00000145191	ENSG00000145191	EIF2B5	3:183851806-184402546	OK	40.9683	42.5063	0.0531697	0.0187498	0.9621	0.9998
ENSG00000261740	ENSG00000261740	RP11-345J4.5	16:29262828-29519817	OK	9.87301	9.73715	-0.0199898	-0.0298224	0.9621	0.9998
ENSG00000078246	ENSG00000078246	TULP3	12:2904118-3050306	OK	28.8527	29.5837	0.0360991	0.0276573	0.96215	0.9998
ENSG00000060642	ENSG00000060642	PIGV	1:27113962-27124889	OK	6.13588	6.06156	-0.01758	-0.02899	0.9622	0.9998
ENSG00000143093	ENSG00000143093	STRIP1	1:110574198-110617263	OK	12.6146	12.7489	0.0152774	0.024167	0.9622	0.9998
ENSG00000120029	ENSG00000120029	C10orf76	10:103605355-103815950	OK	11.2214	11.0683	-0.0198208	-0.0258023	0.9623	0.9998
ENSG00000134779	ENSG00000134779	TPGS2	18:33877676-34812135	OK	72.0537	71.2752	-0.0156718	-0.0281681	0.9623	0.9998
ENSG00000172339	ENSG00000172339	ALG14	1:95439962-95538501	OK	10.8254	10.5721	-0.0341612	-0.0156164	0.9623	0.9998
ENSG00000145982	ENSG00000145982	FARS2	6:5261276-5771813	OK	22.1369	21.9358	-0.0131673	-0.0285523	0.96235	0.9998
ENSG00000147669	ENSG00000147669	POLR2K	8:101162811-101166230	OK	81.757	81.1194	-0.0112942	-0.0272096	0.9624	0.9998
ENSG00000206432	ENSG00000206432	TMEM200C	18:5882070-5909121	OK	0.828185	0.812948	-0.026789	-0.0286523	0.9624	0.9998
ENSG00000259212	ENSG00000259212	CTD-3065B20.2	15:91073156-91260372	OK	0.673394	0.647652	-0.0562325	-0.00896898	0.96245	0.9998
ENSG00000132561	ENSG00000132561	MATN2	8:98881067-99058697	OK	3.26344	3.36052	0.0422897	0.00876576	0.9625	0.9998
ENSG00000206535	ENSG00000206535	LNP1	3:100082274-100175163	OK	0.867557	0.817412	-0.0858946	-0.0232178	0.9625	0.9998
ENSG00000180229	ENSG00000180229	HERC2P3	15:20587868-20711433	OK	1.27695	1.24791	-0.0331951	-0.0261656	0.96255	0.9998
ENSG00000065183	ENSG00000065183	WDR3	1:118472342-118727846	OK	20.0635	20.4026	0.0241754	0.0268197	0.96265	0.9998
ENSG00000100483	ENSG00000100483	VCPKMT	14:50575349-50583318	OK	5.1245	5.06091	-0.0180146	-0.0305833	0.96265	0.9998
ENSG00000185716	ENSG00000185716	C16orf52	16:22018958-22103552	OK	12.0564	12.2321	0.0208734	0.0275133	0.96265	0.9998
ENSG00000198142	ENSG00000198142	SOWAHC	2:110371910-110376563	OK	3.10985	3.14159	0.0146514	0.028479	0.96265	0.9998
ENSG00000169635	ENSG00000169635	HIC2	22:21771692-21805752	OK	1.61767	1.60104	-0.0149075	-0.0281055	0.9627	0.9998
ENSG00000270804	ENSG00000270804	CTD-2583A14.11	19:58281022-58427978	OK	2.14855	2.03803	-0.076185	-0.0232973	0.9627	0.9998
ENSG00000130734	ENSG00000130734	ATG4D	19:10654570-10676713	OK	32.4952	32.9481	0.0199675	0.0288869	0.96275	0.9998
ENSG00000225377	ENSG00000225377	RP5-1103G7.4	20:300956-340304	OK	1.14493	1.07595	-0.089641	-0.0259038	0.96285	0.9998
ENSG00000108469	ENSG00000108469	RECQL5	17:73584138-73704142	OK	9.23655	9.38284	0.0226703	0.0191396	0.9629	0.9998
ENSG00000136522	ENSG00000136522	MRPL47	3:179280667-179322442	OK	73.1755	72.1884	-0.0195927	-0.0284962	0.9629	0.9998
ENSG00000004975	ENSG00000004975	DVL2	17:7128659-7137864	OK	41.1425	40.7845	-0.0126114	-0.0249683	0.96295	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000136986	ENSG00000136986	DERL1	8:124014799-124164393	OK	39.8355	39.2461	-0.0215062	-0.0275837	0.96295	0.9998
ENSG00000136842	ENSG00000136842	TMOD1	9:100263461-100436030	OK	0.671296	0.726669	0.11435	0.0408567	0.963	0.9998
ENSG00000143420	ENSG00000143420	ENSA	1:150573326-150602088	OK	198.073	196.411	-0.0121607	-0.0267118	0.963	0.9998
ENSG00000163714	ENSG00000163714	U2SURP	3:142668005-142779567	OK	53.3756	52.7923	-0.0158531	-0.0262326	0.96305	0.9998
ENSG00000099204	ENSG00000099204	ABLIM1	10:116190871-116444762	OK	27.8623	27.5758	-0.0149131	-0.0223482	0.96325	0.9998
ENSG00000138434	ENSG00000138434	SSFA2	2:182756559-182795465	OK	41.5305	41.8892	0.0124049	0.0242615	0.96325	0.9998
ENSG00000066044	ENSG00000066044	ELAVL1	19:8023462-8070543	OK	37.5818	37.2322	-0.0134838	-0.0270278	0.9633	0.9998
ENSG00000090006	ENSG00000090006	LTBP4	19:41098788-41135725	OK	10.8156	10.652	-0.021999	-0.0200892	0.9633	0.9998
ENSG00000159140	ENSG00000159140	SON	21:34876237-35349992	OK	31.825	32.1733	0.0157063	0.012427	0.96335	0.9998
ENSG00000223658	ENSG00000223658	AC011242.6	2:43864411-43995126	OK	0.796901	0.751088	-0.0854184	-0.0295356	0.9634	0.9998
ENSG00000163960	ENSG00000163960	UBXN7	3:196074532-196160242	OK	12.139	12.2597	0.0142802	0.0193555	0.96345	0.9998
ENSG00000174446	ENSG00000174446	SNAPC5	15:66679154-66790151	OK	33.5984	34.1576	0.0238129	0.0286093	0.9635	0.9998
ENSG00000160226	ENSG00000160226	C21orf2	21:45748826-45760353	OK	4.32016	4.38298	0.020826	0.0270504	0.96355	0.9998
ENSG00000149212	ENSG00000149212	SESN3	11:94883702-94967268	OK	8.71492	8.78263	0.0111653	0.0227579	0.96365	0.9998
ENSG00000198663	ENSG00000198663	C6orf89	6:36822602-36896740	OK	28.7311	28.2765	-0.0230079	-0.0284811	0.96365	0.9998
ENSG00000149970	ENSG00000149970	CNKSR2	X:21392535-21672813	OK	1.1107	1.13252	0.0280643	0.01811	0.9637	0.9998
ENSG00000268220	ENSG00000268220	RP11-379K17.12	3:169804519-169899537	OK	1.05501	1.09232	0.050138	0.0178998	0.96375	0.9998
ENSG00000140307	ENSG00000140307	GTF2A2	15:59887073-59981733	OK	51.1524	50.3551	-0.0226637	-0.0249652	0.9638	0.9998
ENSG00000205485	ENSG00000205485	AC004980.7	7:76139744-77045717	OK	2.64493	2.55462	-0.0501199	-0.0280692	0.9638	0.9998
ENSG00000255139	ENSG00000255139	AP000442.1	11:59383901-59436453	OK	1.43112	1.50499	0.0726049	0.0133321	0.96385	0.9998
ENSG00000234160	ENSG00000234160	RP11-613M10.6	9:37509146-37510296	OK	3.17404	3.25491	0.036299	0.0303486	0.9639	0.9998
ENSG00000108963	ENSG00000108963	DPH1	17:1933403-1946724	OK	16.2396	16.0696	-0.0151811	-0.0214897	0.96395	0.9998
ENSG00000159685	ENSG00000159685	CHCHD6	3:126423062-126679249	OK	426.297	422.996	-0.0112151	-0.0278609	0.964	0.9998
ENSG00000260257	ENSG00000260257	RP5-1085F17.3	20:31444847-31446557	OK	1.04674	1.03169	-0.020894	-0.0268537	0.964	0.9998
ENSG00000130726	ENSG00000130726	TRIM28	19:59055457-59062089	OK	186.534	188.479	0.0149648	0.0256883	0.96405	0.9998
ENSG00000173409	ENSG00000173409	ARV1	1:231114726-231136341	OK	35.3476	35.0612	-0.0117368	-0.0267595	0.96405	0.9998
ENSG00000174231	ENSG00000174231	PRPF8	17:1553922-1588176	OK	56.7996	57.2272	0.0108202	0.0197741	0.96405	0.9998
ENSG00000172890	ENSG00000172890	NADSYN1	11:71164154-71235153	OK	22.0795	21.8514	-0.0149815	-0.0251243	0.9641	0.9998
ENSG00000256139	ENSG00000256139	RP11-968O1.5	12:109549022-109706031	OK	1.0065	1.0439	0.0526339	0.0188681	0.96415	0.9998
ENSG00000062370	ENSG00000062370	ZNF112	19:44830707-44952766	OK	2.18907	2.2163	0.0178357	0.0210637	0.9643	0.9998
ENSG00000107929	ENSG00000107929	LARP4B	10:855483-977564	OK	10.4146	10.314	-0.0140157	-0.0189673	0.9643	0.9998
ENSG00000258429	ENSG00000258429	PDF	16:69139466-69442474	OK	4.22023	3.95009	-0.0954353	-0.0294178	0.9643	0.9998
ENSG00000249773	ENSG00000249773	MRPS17	7:55954969-56067874	OK	1.31668	1.40232	0.0909159	0.0275102	0.96435	0.9998
ENSG00000225973	ENSG00000225973	RP11-139H15.1	15:55495163-55800432	OK	5.41057	5.67242	0.0681846	0.0246219	0.9644	0.9998
ENSG00000162623	ENSG00000162623	TYW3	1:75171169-75232362	OK	22.172	22.4667	0.0190476	0.0254119	0.96455	0.9998
ENSG00000256940	ENSG00000256940	RP11-783K16.5	11:64011955-64016966	OK	2.90568	3.03237	0.06157	0.0110956	0.96455	0.9998
ENSG00000122550	ENSG00000122550	KLHL7	7:23145352-23240630	OK	44.4328	44.9257	0.0159156	0.0229584	0.9646	0.9998
ENSG00000185900	ENSG00000185900	POMK	8:42948657-42978577	OK	2.71699	2.68366	-0.0178089	-0.024268	0.9646	0.9998
ENSG00000232586	ENSG00000232586	RP11-46A10.4	1:180882289-180992047	OK	0.802726	0.852999	0.0876366	0.0235221	0.9646	0.9998
ENSG00000163686	ENSG00000163686	ABHD6	3:58223232-58281420	OK	10.9384	11.0308	0.0121369	0.0230763	0.96465	0.9998
ENSG00000099330	ENSG00000099330	OCEL1	19:17337012-17340028	OK	10.2184	10.3366	0.0165919	0.025221	0.9647	0.9998
ENSG00000063322	ENSG00000063322	MED29	19:39881942-39891277	OK	13.6831	13.5345	-0.0157537	-0.0232285	0.96475	0.9998
ENSG00000237651	ENSG00000237651	C2orf74	2:61293005-61391964	OK	16.2408	15.9694	-0.0243107	-0.0280749	0.96475	0.9998
ENSG00000140157	ENSG00000140157	NIPA2	15:22892004-23034427	OK	31.4164	31.8324	0.0189783	0.0230105	0.9648	0.9998
ENSG00000141556	ENSG00000141556	TBCD	17:80709939-81009686	OK	41.8907	42.1964	0.0104926	0.0203642	0.9648	0.9998
ENSG00000160049	ENSG00000160049	DFFA	1:10516578-10690815	OK	23.0259	23.2885	0.0163582	0.025863	0.9648	0.9998
ENSG00000100376	ENSG00000100376	FAM118A	22:45704848-45737836	OK	16.672	16.4785	-0.0168384	-0.0258024	0.96485	0.9998
ENSG00000123739	ENSG00000123739	PLA2G12A	4:110631144-110651233	OK	24.1601	23.629	-0.0320626	-0.0219059	0.96485	0.9998
ENSG00000160447	ENSG00000160447	PKN3	9:131464801-131486406	OK	3.833	3.77178	-0.0232277	-0.0235562	0.96485	0.9998
ENSG00000182180	ENSG00000182180	MRPS16	10:74870216-75118617	OK	135.238	132.859	-0.0256086	-0.029063	0.9649	0.9998
ENSG00000133884	ENSG00000133884	DPF2	11:65101224-65120720	OK	24.7726	25.0331	0.0150917	0.0260872	0.96495	0.9998
ENSG00000239322	ENSG00000239322	AC007040.7	2:71163011-71306935	OK	3.88707	3.63678	-0.0960235	-0.0306855	0.96495	0.9998
ENSG00000121766	ENSG00000121766	ZCCHC17	1:31769841-31837783	OK	46.064	45.7022	-0.0113762	-0.0262975	0.9651	0.9998
ENSG00000173960	ENSG00000173960	UBXN2A	2:24150154-24227779	OK	16.1592	15.99	-0.0151903	-0.0244879	0.9651	0.9998
ENSG00000213189	ENSG00000213189	BTF3L4P2	2:159825145-160089170	OK	32.618	34.019	0.0606744	0.0314549	0.9651	0.9998
ENSG00000185946	ENSG00000185946	RNPC3	1:104068312-104122156	OK	8.72578	8.82789	0.0167847	0.0237999	0.96515	0.9998
ENSG00000239857	ENSG00000239857	GET4	7:855527-936073	OK	24.336	24.708	0.0218837	0.0239571	0.9652	0.9998
ENSG00000248503	ENSG00000248503	RP5-1000K24.2	X:77166193-77305892	OK	1.3128	1.38467	0.0768966	0.0150994	0.9652	0.9998
ENSG00000213619	ENSG00000213619	NDUFS3	11:47487495-47606114	OK	186.876	184.667	-0.0171594	-0.0236462	0.96525	0.9998
ENSG00000257742	ENSG00000257742	RP11-350F4.2	12:44112795-44117803	OK	0.912244	0.900991	-0.0179072	-0.0280139	0.96525	0.9998
ENSG00000165185	ENSG00000165185	KIAA1958	9:115142216-115431677	OK	1.78899	1.74484	-0.0360478	-0.0267104	0.9654	0.9998
ENSG00000174606	ENSG00000174606	ANGEL2	1:213165523-213189168	OK	14.2217	14.0476	-0.0177677	-0.0258506	0.96545	0.9998
ENSG00000137168	ENSG00000137168	PPIL1	6:36822602-36896740	OK	36.6155	36.0991	-0.020493	-0.0285045	0.9655	0.9998
ENSG00000204120	ENSG00000204120	GIGYF2	2:233562008-233880595	OK	23.0278	23.1916	0.0102231	0.0140871	0.9655	0.9998
ENSG00000196369	ENSG00000196369	SRGAP2B	1:143913614-144094424	OK	52.2931	51.8036	-0.0135693	-0.0259576	0.96555	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000198892	ENSG00000198892	SHISA4	1:201857807-201861434	OK	39.5958	39.2634	-0.0121629	-0.0262226	0.96555	0.9998
ENSG00000139192	ENSG00000139192	TAPBPL	12:6548166-6580153	OK	4.03513	3.95959	-0.0272632	-0.0231393	0.9656	0.9998
ENSG00000172053	ENSG00000172053	QARS	3:49133364-49142553	OK	163.356	165.066	0.0150215	0.0246985	0.9657	0.9998
ENSG00000177830	ENSG00000177830	CHID1	11:867356-915058	OK	85.1934	84.5339	-0.0112115	-0.0245437	0.9657	0.9998
ENSG00000243789	ENSG00000243789	JMJD7	15:42120282-42190773	OK	2.89863	2.8399	-0.0295313	-0.0252573	0.9657	0.9998
ENSG00000128185	ENSG00000128185	DGCR6L	22:20301798-20307603	OK	44.5867	44.2316	-0.0115376	-0.0261395	0.96575	0.9998
ENSG00000265590	ENSG00000265590	AP000275.65	21:33948861-33985176	OK	2.27301	2.37785	0.0650565	0.0320351	0.96575	0.9998
ENSG00000268713	ENSG00000268713	CTC-444N24.8	19:57772721-57774106	OK	0.787128	0.774125	-0.0240317	-0.0273402	0.96575	0.9998
ENSG00000267683	ENSG00000267683	AC008991.1	19:29374336-29444152	OK	0.943103	0.947676	0.00697906	0.00492211	0.96585	0.9998
ENSG00000071859	ENSG00000071859	FAM50A	X:153672472-153679002	OK	93.8617	93.1886	-0.0103836	-0.0243347	0.966	0.9998
ENSG00000086619	ENSG00000086619	ERO1LB	1:236305831-236445319	OK	2.74496	2.6485	-0.0516096	-0.0211606	0.966	0.9998
ENSG00000168803	ENSG00000168803	ADAL	15:43622871-43646096	OK	5.12493	5.18495	0.0167993	0.0260561	0.966	0.9998
ENSG00000169371	ENSG00000169371	SNUPN	15:75759461-75918810	OK	12.4387	12.2398	-0.023252	-0.023534	0.966	0.9998
ENSG00000115970	ENSG00000115970	THADA	2:43393799-43823185	OK	10.0638	9.94311	-0.0174108	-0.0187106	0.96605	0.9998
ENSG00000067829	ENSG00000067829	IDH3G	X:153051220-153063960	OK	42.2175	41.6169	-0.0206713	-0.0260348	0.96615	0.9998
ENSG00000196756	ENSG00000196756	SNHG17	20:37049234-37063996	OK	55.3353	55.8589	0.013589	0.025797	0.9663	0.9998
ENSG00000254876	ENSG00000254876	RP11-23J9.5	9:99918851-100140806	OK	0.68065	0.658496	-0.0477381	-0.0305777	0.9663	0.9998
ENSG00000198853	ENSG00000198853	RUSC2	9:35490123-35563896	OK	4.37727	4.34122	-0.0119324	-0.0250051	0.9664	0.9998
ENSG00000240024	ENSG00000240024	LINC00888	3:183165395-183173801	OK	19.3075	19.4803	0.0128577	0.0264809	0.96645	0.9998
ENSG00000182095	ENSG00000182095	TNRC18	7:5313999-5465045	OK	13.9584	14.1662	0.02132	0.0224374	0.9665	0.9998
ENSG00000227057	ENSG00000227057	WDR46	6:33244916-33267101	OK	76.1728	75.3993	-0.0147244	-0.0221909	0.9665	0.9998
ENSG00000084731	ENSG00000084731	KIF3C	2:26149470-26205618	OK	28.303	28.0356	-0.0136928	-0.0154656	0.96655	0.9998
ENSG00000221923	ENSG00000221923	ZNF880	19:52873169-52889048	OK	6.73955	6.84708	0.0228362	0.0260163	0.9666	0.9998
ENSG00000106346	ENSG00000106346	USP42	7:6144514-6201195	OK	3.86872	3.83646	-0.0120817	-0.0224475	0.96665	0.9998
ENSG00000119698	ENSG00000119698	PPP4R4	14:94612464-94746072	OK	0.923988	0.90626	-0.0279497	-0.0206917	0.9667	0.9998
ENSG00000166436	ENSG00000166436	TRIM66	11:8633583-8693413	OK	0.885889	0.871487	-0.0236467	-0.0162941	0.9667	0.9998
ENSG00000149792	ENSG00000149792	MRPL49	11:64888099-64902004	OK	29.8805	30.4101	0.0253432	0.022422	0.96675	0.9998
ENSG00000165655	ENSG00000165655	ZNF503	10:77029576-77171600	OK	7.84849	7.91926	0.0129504	0.0246711	0.96675	0.9998
ENSG00000105701	ENSG00000105701	FKBP8	19:18642422-18654887	OK	112.829	113.642	0.0103543	0.0246176	0.9668	0.9998
ENSG00000183255	ENSG00000183255	PTTG1IP	21:46269499-46293752	OK	222.905	221.322	-0.0102833	-0.0229139	0.9668	0.9998
ENSG00000147679	ENSG00000147679	UTP23	8:117654368-117889107	OK	10.7369	10.3826	-0.0484049	-0.0140466	0.96685	0.9998
ENSG00000160828	ENSG00000160828	STAG3L2	7:74071993-74306731	OK	9.78377	9.52498	-0.0386752	-0.0219073	0.96695	0.9998
ENSG00000198843	ENSG00000198843	SELT	3:150259780-150348222	OK	93.7628	95.4418	0.025606	0.0256925	0.96695	0.9998
ENSG00000060971	ENSG00000060971	ACAA1	3:38080695-38178733	OK	54.4625	54.8745	0.0108733	0.0244127	0.96705	0.9998
ENSG00000235531	ENSG00000235531	RP11-383H13.1	8:72740401-73030628	OK	11.9363	12.1758	0.0286667	0.0275487	0.9671	0.9998
ENSG00000135404	ENSG00000135404	CD63	12:56119106-56124467	OK	2912.2	2936.93	0.0121978	0.0243478	0.96715	0.9998
ENSG00000169964	ENSG00000169964	TMEM42	3:44803208-44914868	OK	4.46469	4.59	0.0399323	0.0275671	0.9672	0.9998
ENSG00000080603	ENSG00000080603	SRCAP	16:30709029-30787628	OK	9.63617	9.50696	-0.0194766	-0.0186042	0.96725	0.9998
ENSG00000169217	ENSG00000169217	CD2BP2	16:30362086-30366682	OK	39.0342	38.6894	-0.0127989	-0.0231552	0.96725	0.9998
ENSG00000224546	ENSG00000224546	EIF4BP3	9:98908288-98910138	OK	1.86183	1.84034	-0.0167495	-0.0244107	0.96725	0.9998
ENSG00000139324	ENSG00000139324	TMTC3	12:88536072-88593664	OK	2.82184	2.79616	-0.0131912	-0.0218686	0.9673	0.9998
ENSG00000142089	ENSG00000142089	IFITM3	11:318639-330122	OK	30.6527	30.9028	0.011722	0.0240405	0.9673	0.9998
ENSG00000260260	ENSG00000260260	RP11-304L19.5	16:2204797-2205359	OK	22.3758	22.1204	-0.0165633	-0.0257988	0.9673	0.9998
ENSG00000169567	ENSG00000169567	HINT1	5:130494719-130541119	OK	137.841	138.811	0.0101222	0.0235978	0.9674	0.9998
ENSG00000103356	ENSG00000103356	EARS2	16:23533334-23585710	OK	17.257	17.4829	0.0187605	0.01607	0.96745	0.9998
ENSG00000055950	ENSG00000055950	MRPL43	10:102729214-102754158	OK	87.3147	88.0458	0.0120293	0.0222244	0.9675	0.9998
ENSG00000186001	ENSG00000186001	LRCH3	3:197518096-197615307	OK	19.5782	19.7592	0.0132792	0.0157731	0.96765	0.9998
ENSG00000273138	ENSG00000273138	GS1-293C5.1	7:95034174-95064510	OK	1.56009	1.63162	0.0646736	0.00641381	0.96765	0.9998
ENSG00000110925	ENSG00000110925	CSRNP2	12:51454989-51477447	OK	9.77551	9.69714	-0.0116125	-0.0192095	0.96785	0.9998
ENSG00000137880	ENSG00000137880	GCHFR	15:41056217-41059906	OK	8.24817	8.32925	0.0141121	0.0227143	0.968	0.9998
ENSG00000175105	ENSG00000175105	ZNF654	3:88101093-88217879	OK	7.42579	7.57339	0.0283959	0.0247842	0.96805	0.9998
ENSG00000180104	ENSG00000180104	EXOC3	5:443272-473213	OK	47.8269	48.1925	0.0109862	0.0203451	0.96805	0.9998
ENSG00000171940	ENSG00000171940	ZNF217	20:52169308-52251129	OK	13.1165	13.2116	0.0104204	0.0211324	0.9681	0.9998
ENSG00000117543	ENSG00000117543	DPH5	1:101455178-101552821	OK	28.1897	28.4316	0.0123228	0.0249958	0.96815	0.9998
ENSG00000184207	ENSG00000184207	PGP	16:2261997-2264808	OK	19.4919	19.6298	0.0101714	0.0235769	0.96815	0.9998
ENSG00000272990	ENSG00000272990	RP11-305K5.1	3:155755489-156256545	OK	0.883113	0.839328	-0.0733632	-0.0261667	0.9682	0.9998
ENSG00000171103	ENSG00000171103	TRMT61B	2:28974505-29093167	OK	13.3233	13.6374	0.0336179	0.0159638	0.96825	0.9998
ENSG00000197381	ENSG00000197381	ADARB1	21:46491647-46646478	OK	13.3585	13.2468	-0.0121075	-0.0169266	0.96825	0.9998
ENSG00000117906	ENSG00000117906	RCN2	15:77223959-77242601	OK	151.457	150.452	-0.00960434	-0.0236265	0.9683	0.9998
ENSG00000137449	ENSG00000137449	CPEB2	4:15004297-15447790	OK	5.53172	5.47813	-0.0140459	-0.0251086	0.9683	0.9998
ENSG00000237517	ENSG00000237517	DGCR5	22:18958026-19018755	OK	0.771818	0.756014	-0.0298479	-0.0204833	0.9683	0.9998
ENSG00000180855	ENSG00000180855	ZNF443	19:12490002-12750912	OK	0.686822	0.710723	0.0493507	0.0246646	0.96835	0.9998
ENSG00000121410	ENSG00000121410	A1BG	19:58856543-58877958	OK	36.056	36.5527	0.0197397	0.0236433	0.9684	0.9998
ENSG00000148153	ENSG00000148153	INIP	9:115446205-115480516	OK	13.3807	13.5319	0.0162121	0.0237051	0.9684	0.9998
ENSG00000161542	ENSG00000161542	PRPSAP1	17:74305566-74383941	OK	60.6958	61.3419	0.0152776	0.0224114	0.96845	0.9998
ENSG00000206176	ENSG00000206176	AC023490.1	22:20378813-20380440	OK	3.06188	3.11866	0.0265109	0.0246308	0.96845	0.9998
ENSG00000232630	ENSG00000232630	PRPS1P2	9:127908851-127952218	OK	1.05902	1.12451	0.0865641	0.0213516	0.9685	0.9998
ENSG00000198055	ENSG00000198055	GRK6	5:176829140-176883283	OK	29.3149	29.0389	-0.0136434	-0.0227521	0.96865	0.9998
ENSG00000158793	ENSG00000158793	NIT1	1:161070345-161102478	OK	41.6991	42.2727	0.0197102	0.0205006	0.9687	0.9998
ENSG00000073536	ENSG00000073536	NLE1	17:33448597-33469334	OK	13.0999	12.9898	-0.0121726	-0.0223139	0.96875	0.9998
ENSG00000224531	ENSG00000224531	SMIM13	6:11094265-11138964	OK	15.5937	15.7081	0.0105467	0.0217669	0.9688	0.9998
ENSG00000221909	ENSG00000221909	FAM200A	7:99143930-99208439	OK	4.93535	4.83572	-0.0294221	-0.0255449	0.96885	0.9998
ENSG00000122882	ENSG00000122882	ECD	10:74870216-75118617	OK	23.5761	23.9896	0.0250852	0.0239179	0.9689	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000196526	ENSG00000196526	AFAP1	4:7755816-7942022	OK	1.71905	1.70377	-0.012883	-0.0216323	0.9689	0.9998
ENSG00000269928	ENSG00000269928	RP11-849F2.8	17:8128138-8128798	OK	0.868299	0.886585	0.0300674	0.0275651	0.96895	0.9998
ENSG00000124659	ENSG00000124659	TBCC	6:42712218-42714558	OK	20.3947	20.2434	-0.0107425	-0.0234135	0.969	0.9998
ENSG00000162076	ENSG00000162076	FLYWCH2	16:2933186-2949383	OK	20.4368	20.2694	-0.0118669	-0.0234337	0.96905	0.9998
ENSG00000250999	ENSG00000250999	RP11-1379J22.5	5:179084762-179091433	OK	0.637024	0.624054	-0.0296788	-0.0173683	0.96905	0.9998
ENSG00000173214	ENSG00000173214	KIAA1919	6:111580550-111592370	OK	0.693568	0.686595	-0.0145771	-0.0230071	0.9691	0.9998
ENSG00000178338	ENSG00000178338	ZNF354B	5:178286953-178315123	OK	2.72863	2.76303	0.0180795	0.0232678	0.96915	0.9998
ENSG00000137413	ENSG00000137413	TAF8	6:42018250-42055199	OK	18.6577	18.8899	0.0178453	0.0227303	0.9693	0.9998
ENSG00000198046	ENSG00000198046	ZNF667	19:56950693-57012035	OK	1.21704	1.23667	0.0230898	0.0211014	0.9693	0.9998
ENSG00000103227	ENSG00000103227	LMF1	16:903633-1031663	OK	6.62963	6.7031	0.0159001	0.020413	0.9694	0.9998
ENSG00000173166	ENSG00000173166	RAPH1	2:204192941-204400133	OK	4.16143	4.21122	0.0171561	0.0114493	0.9694	0.9998
ENSG00000176909	ENSG00000176909	MAMSTR	19:49215998-49222978	OK	1.27706	1.26142	-0.0177744	-0.0208379	0.9694	0.9998
ENSG00000260669	ENSG00000260669	AL136419.6	14:24641061-24708448	OK	0.63209	0.607112	-0.0581678	-0.00819214	0.96945	0.9998
ENSG00000204435	ENSG00000204435	CSNK2B	6:31629005-31641553	OK	228.614	227.043	-0.00994598	-0.0231381	0.96955	0.9998
ENSG00000233382	ENSG00000233382	NKAPP1	X:119170200-119379122	OK	1.69164	1.65796	-0.0290112	-0.0216643	0.96955	0.9998
ENSG00000110011	ENSG00000110011	DNAJC4	11:63974149-64001824	OK	21.0459	20.7827	-0.0181556	-0.0198954	0.96985	0.9998
ENSG00000203644	ENSG00000203644	AC083799.1	3:129366634-129612419	OK	4.50867	4.62926	0.0380803	0.0245	0.96985	0.9998
ENSG00000104826	ENSG00000104826	LHB	19:49496704-49520338	OK	0.737426	0.747396	0.0193732	0.0022634	0.9699	0.9998
ENSG00000125304	ENSG00000125304	TM9SF2	13:100153670-100216260	OK	56.886	56.518	-0.00936163	-0.0232693	0.9699	0.9998
ENSG00000103253	ENSG00000103253	HAGHL	16:770580-791329	OK	39.6699	40.1356	0.0168351	0.0210117	0.97	0.9998
ENSG00000166197	ENSG00000166197	NOLC1	10:103911932-103923627	OK	57.1272	56.7699	-0.00905013	-0.0207939	0.97	0.9998
ENSG00000212232	ENSG00000212232	SNORD17	20:17922240-18039832	OK	3.71846	3.81723	0.0378219	0.00545364	0.97005	0.9998
ENSG00000122566	ENSG00000122566	HNRNPA2B1	7:26229546-26252976	OK	580.43	585.187	0.0117752	0.0215966	0.97015	0.9998
ENSG00000272201	ENSG00000272201	U47924.30	12:7072407-7178336	OK	3.10459	2.94758	-0.0748717	-0.0192707	0.97015	0.9998
ENSG00000272836	ENSG00000272836	RP3-402G11.27	22:50639407-50656045	OK	1.01338	1.05202	0.053993	0.010993	0.97015	0.9998
ENSG00000131899	ENSG00000131899	LLGL1	17:18128900-18162230	OK	10.4667	10.6261	0.0217982	0.0232223	0.97025	0.9998
ENSG00000117525	ENSG00000117525	F3	1:94994780-95007356	OK	1.20929	1.22584	0.0196076	0.0195271	0.9703	0.9998
ENSG00000183963	ENSG00000183963	SMTN	22:31460090-31500743	OK	9.81946	9.74599	-0.0108349	-0.0164766	0.9703	0.9998
ENSG00000197903	ENSG00000197903	HIST1H2BK	6:27106072-27114619	OK	58.326	58.7692	0.0109211	0.0222248	0.9703	0.9998
ENSG00000132773	ENSG00000132773	TOE1	1:45794834-45956872	OK	7.0396	7.20112	0.0327288	0.0244262	0.97035	0.9998
ENSG00000235999	ENSG00000235999	RP11-403I13.8	1:149287450-149291743	OK	1.91922	1.90036	-0.0142454	-0.0213277	0.9704	0.9998
ENSG00000257027	ENSG00000257027	RP11-705C15.3	12:9811162-9814681	OK	0.981162	0.992958	0.0172414	0.0242285	0.9704	0.9998
ENSG00000143771	ENSG00000143771	CNIH4	1:224544551-224567161	OK	81.6719	81.0776	-0.0105372	-0.022625	0.97045	0.9998
ENSG00000167202	ENSG00000167202	TBC1D2B	15:78268383-78370066	OK	13.8195	13.7288	-0.00950047	-0.0172072	0.97045	0.9998
ENSG00000214114	ENSG00000214114	MYCBP	1:39325671-39407471	OK	21.4485	21.193	-0.0172879	-0.0217847	0.97045	0.9998
ENSG00000146731	ENSG00000146731	CCT6A	7:56119322-56131682	OK	216.608	215.301	-0.00873565	-0.020348	0.9705	0.9998
ENSG00000218739	ENSG00000218739	CEBPZ-AS1	2:37394962-37551951	OK	27.6442	28.2133	0.0294036	0.0127339	0.97065	0.9998
ENSG00000241280	ENSG00000241280	RP11-221J22.2	3:101659702-101716770	OK	3.0649	3.13608	0.0331266	0.0225866	0.97065	0.9998
ENSG00000125741	ENSG00000125741	OPA3	19:46030684-46105470	OK	5.43959	5.38294	-0.015105	-0.0207099	0.9708	0.9998
ENSG00000138073	ENSG00000138073	PREB	2:27346681-27357543	OK	46.6499	46.9662	0.00975049	0.0223537	0.9708	0.9998
ENSG00000188343	ENSG00000188343	FAM92A1	8:94225530-94753245	OK	24.3239	24.7161	0.0230812	0.024426	0.9708	0.9998
ENSG00000187994	ENSG00000187994	RINL	19:39358469-39368919	OK	6.11314	6.20044	0.0204558	0.0208176	0.97085	0.9998
ENSG00000267270	ENSG00000267270	AC139100.2	18:77905806-78005429	OK	1.41117	1.46105	0.050107	0.0201904	0.9709	0.9998
ENSG00000204438	ENSG00000204438	GPANK1	6:31629005-31641553	OK	13.4407	13.7749	0.0354268	0.022145	0.971	0.9998
ENSG00000067365	ENSG00000067365	METTL22	16:8715539-8740081	OK	13.4334	13.5527	0.0127478	0.0187461	0.97105	0.9998
ENSG00000164252	ENSG00000164252	AGGF1	5:76325075-76361059	OK	15.089	14.9959	-0.00893457	-0.0213799	0.97105	0.9998
ENSG00000172331	ENSG00000172331	BPGM	7:134331559-134364565	OK	31.9648	31.7563	-0.00944346	-0.0221992	0.9712	0.9998
ENSG00000078070	ENSG00000078070	MCCC1	3:182733005-182833863	OK	21.9472	21.7994	-0.00974726	-0.0215813	0.97125	0.9998
ENSG00000124275	ENSG00000124275	MTRR	5:7830490-7906138	OK	41.1468	40.8073	-0.0119496	-0.016474	0.9713	0.9998
ENSG00000106034	ENSG00000106034	CPED1	7:120628730-120937498	OK	1.38584	1.36948	-0.0171245	-0.0159353	0.9714	0.9998
ENSG00000270580	ENSG00000270580	RP11-1186N24.5	16:15068447-15248421	OK	1.52003	1.4613	-0.0568488	-0.00621897	0.97145	0.9998
ENSG00000115541	ENSG00000115541	HSPE1	2:198351304-198418423	OK	269.82	265.587	-0.0228148	-0.0199195	0.9715	0.9998
ENSG00000142687	ENSG00000142687	KIAA0319L	1:35899090-36032875	OK	34.2121	33.955	-0.01088	-0.0154906	0.9716	0.9998
ENSG00000168826	ENSG00000168826	ZBTB49	4:4291923-4323513	OK	1.98987	2.01068	0.0150105	0.016748	0.9717	0.9998
ENSG00000169021	ENSG00000169021	UQCRFS1	19:29698172-29706722	OK	111.459	110.858	-0.00780541	-0.0196062	0.9718	0.9998
ENSG00000236152	ENSG00000236152	MRPS36P1	3:6532165-7783215	OK	3.52506	3.60189	0.0311062	0.0273016	0.97185	0.9998
ENSG00000196236	ENSG00000196236	XPNPEP3	22:41253080-41369313	OK	13.8246	13.9986	0.0180473	0.02299	0.97195	0.9998
ENSG00000140992	ENSG00000140992	PDPK1	16:2587964-2653189	OK	15.6513	15.3143	-0.0314107	-0.0109618	0.972	0.9998
ENSG00000154309	ENSG00000154309	DISP1	1:222988363-223179337	OK	0.909274	0.89631	-0.0207175	-0.0141028	0.972	0.9998
ENSG00000214106	ENSG00000214106	PAXIP1-AS2	7:154720207-154794794	OK	1.8896	1.82492	-0.0502463	-0.0316093	0.97205	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000130332	ENSG00000130332	LSM7	19:2321515-2355099	OK	115.613	116.539	0.0115158	0.0222968	0.9721	0.9998
ENSG00000171316	ENSG00000171316	CHD7	8:61591336-61779465	OK	7.94132	8.0019	0.0109654	0.0113657	0.9721	0.9998
ENSG00000196976	ENSG00000196976	LAGE3	X:153706027-153707596	OK	49.3974	49.6964	0.00870624	0.0197546	0.97225	0.9998
ENSG00000106588	ENSG00000106588	PSMA2	7:42948324-42988557	OK	158.288	157.057	-0.0112666	-0.020243	0.9724	0.9998
ENSG00000033627	ENSG00000033627	ATP6V0A1	17:40610861-40674629	OK	39.6568	39.8942	0.00861155	0.0161961	0.97245	0.9998
ENSG00000112249	ENSG00000112249	ASCC3	6:100956069-101329248	OK	6.86495	6.91201	0.00985681	0.0174481	0.97245	0.9998
ENSG00000234546	ENSG00000234546	RP3-510D11.2	1:9242065-9262678	OK	1.95211	1.9728	0.0152115	0.0191314	0.97245	0.9998
ENSG00000102858	ENSG00000102858	MGRN1	16:4666493-4740975	OK	16.4704	16.3507	-0.0105287	-0.0196112	0.97255	0.9998
ENSG00000065621	ENSG00000065621	GSTO2	10:106028630-106064703	OK	0.817046	0.8295	0.0218232	0.0165781	0.9726	0.9998
ENSG00000185414	ENSG00000185414	MRPL30	2:99613723-100106497	OK	12.5264	12.1408	-0.045116	-0.020095	0.97265	0.9998
ENSG00000166816	ENSG00000166816	LDHD	16:75145757-75150669	OK	1.09665	1.08433	-0.0163107	-0.0192644	0.9727	0.9998
ENSG00000176261	ENSG00000176261	ZBTB8OS	1:32930657-33116504	OK	34.5308	34.2262	-0.0127806	-0.0198537	0.9727	0.9998
ENSG00000162601	ENSG00000162601	MYSM1	1:59120410-59165764	OK	9.01115	8.93887	-0.0116182	-0.0123744	0.97275	0.9998
ENSG00000161057	ENSG00000161057	PSMC2	7:102937868-103629963	OK	89.9473	90.7771	0.0132484	0.0216407	0.9728	0.9998
ENSG00000167619	ENSG00000167619	TMEM145	19:42817476-42829214	OK	1.12732	1.14729	0.0253324	0.0162928	0.9728	0.9998
ENSG00000126858	ENSG00000126858	RHOT1	17:30468244-30580393	OK	16.6558	16.7664	0.00954748	0.0203392	0.973	0.9998
ENSG00000185813	ENSG00000185813	PCYT2	17:79845712-79869340	OK	59.6644	60.2282	0.0135706	0.0181767	0.9731	0.9998
ENSG00000064687	ENSG00000064687	ABCA7	19:1040101-1065571	OK	3.57479	3.5364	-0.0155768	-0.0152686	0.97315	0.9998
ENSG00000134684	ENSG00000134684	YARS	1:33240839-33324476	OK	39.4856	39.1703	-0.0115652	-0.0221671	0.97315	0.9998
ENSG00000005889	ENSG00000005889	ZFX	X:24164341-24234372	OK	6.20801	6.16239	-0.0106402	-0.0148105	0.97325	0.9998
ENSG00000151640	ENSG00000151640	DPYSL4	10:134000403-134019280	OK	6.24287	6.29005	0.0108615	0.0164715	0.97325	0.9998
ENSG00000049860	ENSG00000049860	HEXB	5:73923233-74072737	OK	128.219	129.261	0.0116741	0.0189949	0.9733	0.9998
ENSG00000128918	ENSG00000128918	ALDH1A2	15:58245621-58861151	OK	3.04045	3.07573	0.0166427	0.0133997	0.9733	0.9998
ENSG00000178381	ENSG00000178381	ZFAND2A	7:1191706-1204903	OK	17.084	17.2102	0.0106161	0.0182991	0.9733	0.9998
ENSG00000129197	ENSG00000129197	RPAIN	17:5185557-5372380	OK	24.6295	24.976	0.0201555	0.0108967	0.97345	0.9998
ENSG00000100034	ENSG00000100034	PPM1F	22:22273792-22307209	OK	24.5727	24.7063	0.00782784	0.0169214	0.9735	0.9998
ENSG00000143443	ENSG00000143443	C1orf56	1:151020215-151042801	OK	3.51697	3.53374	0.00686142	0.00271994	0.9735	0.9998
ENSG00000188986	ENSG00000188986	NELFB	9:140149624-140167998	OK	29.9009	29.7306	-0.00824251	-0.0201193	0.97355	0.9998
ENSG00000117868	ENSG00000117868	ESYT2	7:158523685-158622944	OK	37.0317	36.8071	-0.00877457	-0.0206823	0.9736	0.9998
ENSG00000213523	ENSG00000213523	SRA1	5:139781398-139973337	OK	22.826	22.1727	-0.0418896	-0.0276097	0.9736	0.9998
ENSG00000253210	ENSG00000253210	RP11-809O17.1	8:142127376-142205907	OK	0.968091	0.976259	0.0121208	0.00436766	0.9736	0.9998
ENSG00000140153	ENSG00000140153	WDR20	14:102547074-102771537	OK	10.1284	10.2872	0.0224406	0.00267578	0.97365	0.9998
ENSG00000131013	ENSG00000131013	PPIL4	6:149825868-149867174	OK	6.22004	6.17652	-0.0101296	-0.0193915	0.9737	0.9998
ENSG00000126351	ENSG00000126351	THRA	17:38175349-38256978	OK	15.6144	15.4605	-0.0142875	-0.0189867	0.97375	0.9998
ENSG00000162267	ENSG00000162267	ITIH3	3:52828783-52843025	OK	6.66292	6.57553	-0.0190464	-0.0196213	0.97375	0.9998
ENSG00000204922	ENSG00000204922	C11orf83	11:62414319-62441159	OK	14.3272	14.4758	0.0148914	0.0201338	0.9738	0.9998
ENSG00000184857	ENSG00000184857	TMEM186	16:8768421-8962866	OK	4.20168	4.10135	-0.0348645	-0.0195434	0.97395	0.9998
ENSG00000167792	ENSG00000167792	NDUFV1	11:67374322-67380006	OK	129.784	129.053	-0.00814093	-0.0179688	0.9741	0.9998
ENSG00000160055	ENSG00000160055	TMEM234	1:32674694-32697205	OK	11.0034	11.1949	0.0248969	0.0102697	0.97415	0.9998
ENSG00000064601	ENSG00000064601	CTSA	20:44517263-44540794	OK	329.879	331.726	0.00805229	0.018055	0.9742	0.9998
ENSG00000165119	ENSG00000165119	HNRNPK	9:86582997-86595569	OK	326.438	328.284	0.00813629	0.0180133	0.97425	0.9998
ENSG00000140264	ENSG00000140264	SERF2	15:44019115-44095241	OK	280.553	276.899	-0.0189123	-0.0238056	0.97435	0.9998
ENSG00000145979	ENSG00000145979	TBC1D7	6:12717892-13328815	OK	420.792	417.812	-0.0102525	-0.020001	0.97435	0.9998
ENSG00000122481	ENSG00000122481	RWDD3	1:95582893-95729610	OK	11.5377	11.4113	-0.0158917	-0.0198662	0.9744	0.9998
ENSG00000101421	ENSG00000101421	CHMP4B	20:32399109-32442172	OK	86.8817	87.3313	0.00744658	0.0187163	0.97445	0.9998
ENSG00000076321	ENSG00000076321	KLHL20	1:173684079-173755840	OK	16.1243	15.9855	-0.012472	-0.0184957	0.97455	0.9998
ENSG00000082515	ENSG00000082515	MRPL22	5:154320629-154348971	OK	40.2919	40.0082	-0.0101941	-0.0187966	0.97455	0.9998
ENSG00000272654	ENSG00000272654	RP11-422P24.11	1:153950218-153951636	OK	0.959919	0.972448	0.0187084	0.0225436	0.97455	0.9998
ENSG00000078967	ENSG00000078967	UBE2D4	7:43966036-44058774	OK	18.6176	18.7991	0.0139957	0.0205011	0.9746	0.9998
ENSG00000171314	ENSG00000171314	PGAM1	10:99185916-99193198	OK	105.17	104.58	-0.008117	-0.0196881	0.9746	0.9998
ENSG00000197635	ENSG00000197635	DPP4	2:162848750-162931679	OK	0.970189	0.959713	-0.0156628	-0.0127474	0.9746	0.9998
ENSG00000103381	ENSG00000103381	CPPED1	16:12756918-12897874	OK	7.38265	7.43492	0.0101779	0.0196274	0.9747	0.9998
ENSG00000181638	ENSG00000181638	ZFP41	8:144328990-144359101	OK	2.54161	2.50412	-0.0214362	-0.0142485	0.9747	0.9998
ENSG00000255468	ENSG00000255468	RP11-867G23.8	11:66115420-66139685	OK	1.05727	1.09426	0.0496125	0.0240809	0.9747	0.9998
ENSG00000104369	ENSG00000104369	JPH1	8:75146934-75401107	OK	3.42848	3.48926	0.0253498	0.0203791	0.97485	0.9998
ENSG00000142784	ENSG00000142784	WDTC1	1:27561006-27635110	OK	11.97	11.8931	-0.00929132	-0.0206522	0.97495	0.9998
ENSG00000168792	ENSG00000168792	ABHD15	17:27887564-28513493	OK	2.32589	2.24981	-0.04798	-0.0225515	0.97495	0.9998
ENSG00000145715	ENSG00000145715	RASA1	5:86563704-86708836	OK	18.9692	18.8438	-0.00957062	-0.0182741	0.975	0.9998
ENSG00000100266	ENSG00000100266	PACSIN2	22:43192507-43411151	OK	122.255	122.999	0.00875349	0.0165824	0.97505	0.9998
ENSG00000215845	ENSG00000215845	TSTD1	1:160965000-161008780	OK	10.1335	9.84722	-0.0413502	-0.0215256	0.97505	0.9998
ENSG00000250132	ENSG00000250132	RP11-359B12.2	12:1021242-1605099	OK	0.850995	0.870573	0.0328152	0.0062032	0.9752	0.9998
ENSG00000168214	ENSG00000168214	RBPJ	4:26165076-26436541	OK	15.7651	15.6682	-0.00889241	-0.0127391	0.97525	0.9998
ENSG00000187531	ENSG00000187531	SIRT7	17:79869814-79885590	OK	13.7349	13.9004	0.0172786	0.0156563	0.9753	0.9998
ENSG00000197905	ENSG00000197905	TEAD4	12:3068495-3149839	OK	13.3701	13.4494	0.00853189	0.0164351	0.97535	0.9998
ENSG00000185664	ENSG00000185664	PMEL	12:56347888-56367101	OK	8258.75	8140.67	-0.0207756	-0.0125911	0.9754	0.9998
ENSG00000203497	ENSG00000203497	PDCD4-AS1	10:112629500-112679032	OK	0.681251	0.657012	-0.0522683	-0.00992619	0.9754	0.9998
ENSG00000108292	ENSG00000108292	MLLT6	17:36858704-36886056	OK	13.9662	14.0555	0.00919083	0.0132514	0.9755	0.9998
ENSG00000205918	ENSG00000205918	PDPK2	16:2653350-2693297	OK	1.07785	1.10723	0.0387962	0.0255792	0.9755	0.9998
ENSG00000102805	ENSG00000102805	CLN5	13:77564794-77601330	OK	15.994	15.8085	-0.0168284	-0.0176193	0.97555	0.9998
ENSG00000104660	ENSG00000104660	LEPROTL1	8:29952913-30041156	OK	35.9729	35.6215	-0.0141649	-0.0174098	0.9756	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000157470	ENSG00000157470	FAM81A	15:59427112-59815748	OK	5.57898	5.51138	-0.0175894	-0.0130868	0.9756	0.9998
ENSG00000215394	ENSG00000215394	BMS1P18	14:19812175-19925348	OK	0.867053	0.834691	-0.0548789	-0.0182957	0.9757	0.9998
ENSG00000183864	ENSG00000183864	TOB2	22:41829495-41843027	OK	9.74792	9.69307	-0.0081415	-0.0169204	0.97575	0.9998
ENSG00000133247	ENSG00000133247	SUV420H2	19:55851220-55859488	OK	3.48496	3.45669	-0.0117509	-0.0158124	0.9758	0.9998
ENSG00000165416	ENSG00000165416	SUGT1	13:53226843-53275044	OK	34.9837	35.2028	0.00900412	0.0176261	0.9758	0.9998
ENSG00000176102	ENSG00000176102	CSTF3	11:33060962-33213144	OK	21.0153	21.1941	0.0122245	0.0173755	0.9758	0.9998
ENSG00000010219	ENSG00000010219	DYRK4	12:4671369-4960277	OK	29.7956	30.1778	0.0183861	0.0159785	0.97585	0.9998
ENSG00000065491	ENSG00000065491	TBC1D22B	6:37179955-37300746	OK	4.65443	4.68546	0.00958787	0.0189326	0.9759	0.9998
ENSG00000077097	ENSG00000077097	TOP2B	3:25639474-25706430	OK	26.1504	26.3147	0.0090342	0.0196188	0.9759	0.9998
ENSG00000105127	ENSG00000105127	AKAP8	19:15464195-15529952	OK	8.42684	8.50996	0.0141607	0.0172429	0.97595	0.9998
ENSG00000271529	ENSG00000271529	CICP14	7:128296015-128298845	OK	0.823499	0.816158	-0.0129175	-0.0172362	0.976	0.9998
ENSG00000143412	ENSG00000143412	ANXA9	1:150954492-150968110	OK	2.86123	2.84079	-0.0103401	-0.0153977	0.9761	0.9998
ENSG00000266053	ENSG00000266053	RP11-143J12.2	18:9102627-9285983	OK	0.662132	0.677607	0.0333299	0.00404326	0.97615	0.9998
ENSG00000144426	ENSG00000144426	NBEAL1	2:203879601-204091101	OK	3.74108	3.77989	0.0148888	0.0109184	0.9763	0.9998
ENSG00000100425	ENSG00000100425	BRD1	22:50166930-50221160	OK	7.8264	7.86899	0.00782894	0.0131263	0.97635	0.9998
ENSG00000196456	ENSG00000196456	ZNF775	7:150060865-150109558	OK	12.4533	12.2583	-0.0227693	-0.0136519	0.9764	0.9998
ENSG00000124279	ENSG00000124279	FASTKD3	5:7830490-7906138	OK	16.2358	16.034	-0.0180421	-0.01555	0.97645	0.9998
ENSG00000179750	ENSG00000179750	APOBEC3B	22:39378351-39394214	OK	13.4386	13.3584	-0.0086371	-0.0173572	0.9765	0.9998
ENSG00000100731	ENSG00000100731	PCNX	14:71374121-71582099	OK	9.45749	9.5107	0.00809354	0.0102403	0.9766	0.9998
ENSG00000229950	ENSG00000229950	TFAP2A-AS1	6:10393418-10419892	OK	4.57792	4.45598	-0.038948	-0.0115654	0.9766	0.9998
ENSG00000270800	ENSG00000270800	RPS10-NUDT3	6:34247455-34393902	OK	19.1669	19.1906	0.00178233	0.000609115	0.9766	0.9998
ENSG00000120658	ENSG00000120658	ENOX1	13:43787653-44361044	OK	2.70032	2.67686	-0.0125868	-0.0140714	0.97685	0.9998
ENSG00000151690	ENSG00000151690	MFSD6	2:191273080-191399448	OK	9.25819	9.19328	-0.0101508	-0.0133653	0.97685	0.9998
ENSG00000164867	ENSG00000164867	NOS3	7:150688082-150721586	OK	2.25009	2.2908	0.0258648	0.0140914	0.97685	0.9998
ENSG00000166128	ENSG00000166128	RAB8B	15:63481667-63559981	OK	17.9565	17.8109	-0.0117424	-0.0158723	0.9769	0.9998
ENSG00000272093	ENSG00000272093	CTC-365E16.1	5:71656516-71658805	OK	1.95645	1.94135	-0.0111779	-0.0177239	0.9769	0.9998
ENSG00000095319	ENSG00000095319	NUP188	9:131683173-131790582	OK	18.9048	19.0362	0.00999072	0.012075	0.97695	0.9998
ENSG00000220749	ENSG00000220749	RPL21P28	1:212208918-212280742	OK	2.60647	2.70233	0.0521092	0.0162531	0.97695	0.9998
ENSG00000272787	ENSG00000272787	KB-226F1.2	22:24309088-24326106	OK	0.974181	0.944779	-0.0442134	-0.00722924	0.97695	0.9998
ENSG00000164074	ENSG00000164074	C4orf29	4:128838959-128960866	OK	3.08388	3.04869	-0.0165568	-0.0154819	0.977	0.9998
ENSG00000037965	ENSG00000037965	HOXC8	12:54375292-54449814	OK	1.36383	1.33856	-0.0269795	-0.0172923	0.9771	0.9998
ENSG00000079257	ENSG00000079257	LXN	3:158362066-158410364	OK	3.62915	3.77075	0.0552196	0.0201479	0.9771	0.9998
ENSG00000177370	ENSG00000177370	TIMM22	17:900356-1132315	OK	7.95853	8.09213	0.0240179	0.018653	0.97715	0.9998
ENSG00000071462	ENSG00000071462	WBSCR22	7:73095298-73134002	OK	131.8	131.052	-0.00821018	-0.0171908	0.9773	0.9998
ENSG00000175792	ENSG00000175792	RUVBL1	3:127770483-128127485	OK	41.8172	41.2365	-0.0201757	-0.0145781	0.97735	0.9998
ENSG00000135269	ENSG00000135269	TES	7:115850546-116148595	OK	24.6364	24.8509	0.0125062	0.0126465	0.9774	0.9998
ENSG00000269243	ENSG00000269243	CTD-2231E14.8	19:16222438-16269386	OK	15.2636	15.4193	0.0146407	0.0166957	0.97745	0.9998
ENSG00000042445	ENSG00000042445	RETSAT	2:85569210-85618875	OK	56.3804	56.0797	-0.0077132	-0.0150896	0.9776	0.9998
ENSG00000142634	ENSG00000142634	EFHD2	1:15736390-15756839	OK	15.8129	15.73	-0.00758095	-0.0166828	0.97765	0.9998
ENSG00000271870	ENSG00000271870	RP11-97C16.1	3:3168599-3221394	OK	2.66598	2.7609	0.0504754	0.0149248	0.97775	0.9998
ENSG00000075188	ENSG00000075188	NUP37	12:102457132-102513902	OK	22.7076	22.83	0.00775518	0.016103	0.97785	0.9998
ENSG00000197837	ENSG00000197837	HIST4H4	12:14920932-14924065	OK	1.20976	1.22737	0.0208522	0.0169436	0.9779	0.9998
ENSG00000262089	ENSG00000262089	RP11-589P10.5	17:6757179-6922978	OK	1.99807	1.98639	-0.008464	-0.000955957	0.9779	0.9998
ENSG00000112851	ENSG00000112851	ERBB2IP	5:65222302-65378377	OK	30.8052	30.9548	0.0069906	0.0119083	0.97795	0.9998
ENSG00000228274	ENSG00000228274	RP3-508I15.9	22:39052640-39077825	OK	2.1659	2.10027	-0.0443914	-0.0275695	0.97805	0.9998
ENSG00000143761	ENSG00000143761	ARF1	1:228270360-228286912	OK	233.13	234.361	0.00759825	0.0168721	0.9781	0.9998
ENSG00000198455	ENSG00000198455	ZXDB	X:57618268-57623906	OK	1.63811	1.64833	0.00897799	0.0164678	0.97815	0.9998
ENSG00000248487	ENSG00000248487	ABHD14A	3:51989329-52023213	OK	24.3075	24.617	0.0182558	0.0150437	0.97815	0.9998
ENSG00000013288	ENSG00000013288	MAN2B2	4:6576901-6625089	OK	13.7902	13.8562	0.00688476	0.0149518	0.97835	0.9998
ENSG00000104863	ENSG00000104863	LIN7B	19:49617580-49622397	OK	12.0387	12.1377	0.0118187	0.0180164	0.97835	0.9998
ENSG00000176020	ENSG00000176020	AMIGO3	3:49711434-49761384	OK	0.684933	0.719336	0.0707039	0.0208196	0.9785	0.9998
ENSG00000011677	ENSG00000011677	GABRA3	X:151307354-151619830	OK	4.7272	4.69956	-0.00846024	-0.0140795	0.97855	0.9998
ENSG00000013441	ENSG00000013441	CLK1	2:201717731-201729422	OK	30.8438	30.6908	-0.00717398	-0.0133212	0.97855	0.9998
ENSG00000131368	ENSG00000131368	MRPS25	3:14860468-15106842	OK	75.2358	74.4359	-0.0154213	-0.0174874	0.97855	0.9998
ENSG00000114850	ENSG00000114850	SSR3	3:156257928-156272973	OK	208.105	209.516	0.00974941	0.0166668	0.9786	0.9998
ENSG00000143515	ENSG00000143515	ATP8B2	1:154298028-154323783	OK	33.8678	33.6873	-0.00771035	-0.0125603	0.9786	0.9998
ENSG00000149218	ENSG00000149218	ENDOD1	11:94822973-94865809	OK	20.9172	21.0062	0.00612478	0.0148991	0.9786	0.9998
ENSG00000013375	ENSG00000013375	PGM3	6:83777384-83908651	OK	15.5158	15.633	0.01086	0.011724	0.97865	0.9998
ENSG00000075292	ENSG00000075292	ZNF638	2:71503690-71662199	OK	26.4261	26.2458	-0.00987818	-0.0130004	0.97865	0.9998
ENSG00000172775	ENSG00000172775	FAM192A	16:57186377-57220028	OK	30.2272	30.0536	-0.00830933	-0.0147882	0.9787	0.9998
ENSG00000255650	ENSG00000255650	FAM222A-AS1	12:110152032-110211313	OK	1.38975	1.34564	-0.0465308	-0.0174635	0.9788	0.9998
ENSG00000112699	ENSG00000112699	GMDS	6:1624040-2245926	OK	45.3308	45.6153	0.0090277	0.0163305	0.97895	0.9998
ENSG00000141378	ENSG00000141378	PTRH2	17:57697218-57919616	OK	39.1715	41.0242	0.0666722	0.0258704	0.979	0.9998
ENSG00000187720	ENSG00000187720	THSD4	15:71389290-72075722	OK	0.680468	0.669612	-0.0232019	-0.0137082	0.979	0.9998
ENSG00000189114	ENSG00000189114	BLOC1S3	19:45574757-45808541	OK	5.63747	5.73056	0.0236273	0.0131114	0.979	0.9998
ENSG00000188321	ENSG00000188321	ZNF559	19:9434447-9493293	OK	7.89256	7.83721	-0.0101531	-0.0149053	0.9791	0.9998
ENSG00000239282	ENSG00000239282	GATSL3	22:30681105-30723035	OK	3.0416	2.99153	-0.0239467	-0.0138019	0.9791	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000077721	ENSG00000077721	UBE2A	X:118708500-118718381	OK	31.7432	31.8889	0.00660639	0.0148062	0.97915	0.9998
ENSG00000139131	ENSG00000139131	YARS2	12:32832133-32908836	OK	16.3493	16.175	-0.015464	-0.0127251	0.9792	0.9998
ENSG00000176410	ENSG00000176410	DNAJC30	7:73095298-73134002	OK	4.14941	4.22264	0.0252392	0.0161037	0.9792	0.9998
ENSG00000178695	ENSG00000178695	KCTD12	13:77454311-77460540	OK	4.09679	4.11905	0.00782013	0.0163788	0.9792	0.9998
ENSG00000204822	ENSG00000204822	MRPL53	2:74699084-74722013	OK	91.3729	90.7079	-0.0105372	-0.0151694	0.9793	0.9998
ENSG00000126803	ENSG00000126803	HSPA2	14:64854748-65009955	OK	10.9667	10.7695	-0.0261858	-0.0181388	0.97935	0.9998
ENSG00000151148	ENSG00000151148	UBE3B	12:109785707-109974507	OK	25.649	25.3808	-0.0151667	-0.0159445	0.9794	0.9998
ENSG00000170946	ENSG00000170946	DNAJC24	11:31391386-31453396	OK	10.0426	9.96906	-0.0106055	-0.0147539	0.97945	0.9998
ENSG00000180376	ENSG00000180376	CCDC66	3:56591188-56717265	OK	5.37277	5.42678	0.0144294	0.00906285	0.97945	0.9998
ENSG00000139620	ENSG00000139620	KANSL2	12:49047183-49076021	OK	17.3972	17.4999	0.00849344	0.0146229	0.9795	0.9998
ENSG00000180771	ENSG00000180771	SRSF8	11:94800055-94804388	OK	2.37355	2.3526	-0.0127925	-0.016268	0.9795	0.9998
ENSG00000219545	ENSG00000219545	RPA3-AS1	7:7676148-8133902	OK	23.8213	23.9898	0.0101687	0.0120897	0.97955	0.9998
ENSG00000184743	ENSG00000184743	ATL3	11:63391558-63439393	OK	15.8274	15.734	-0.00853803	-0.0155046	0.9796	0.9998
ENSG00000259699	ENSG00000259699	HMGB1P8	15:89630308-89745591	OK	1.49342	1.54129	0.0455212	0.00700932	0.9796	0.9998
ENSG00000105245	ENSG00000105245	NUMBL	19:41172595-41196877	OK	5.36126	5.32753	-0.00910442	-0.013671	0.97965	0.9998
ENSG00000143801	ENSG00000143801	PSEN2	1:227057884-227083806	OK	45.7341	45.5194	-0.00679169	-0.0147292	0.9798	0.9998
ENSG00000230530	ENSG00000230530	LIMD1-AS1	3:45596885-45786916	OK	23.5193	23.0909	-0.0265216	-0.0148364	0.9798	0.9998
ENSG00000188859	ENSG00000188859	FAM78B	1:166026673-166136206	OK	1.94567	1.92868	-0.0126545	-0.0159303	0.97985	0.9998
ENSG00000242798	ENSG00000242798	RP11-506M12.1	7:99690350-99726118	OK	1.26925	1.23013	-0.0451702	-0.00438906	0.97985	0.9998
ENSG00000185009	ENSG00000185009	AP3M1	10:75881523-75910821	OK	43.0955	43.2747	0.00598872	0.0139776	0.9799	0.9998
ENSG00000106976	ENSG00000106976	DNM1	9:130928342-131017527	OK	1.6564	1.69032	0.0292479	0.00990995	0.97995	0.9998
ENSG00000159314	ENSG00000159314	ARHGAP27	17:43471274-43511787	OK	2.23995	2.25728	0.0111147	0.00910223	0.97995	0.9998
ENSG00000160221	ENSG00000160221	C21orf33	21:45553486-45565605	OK	28.7712	28.6317	-0.00700919	-0.0150822	0.97995	0.9998
ENSG00000229729	ENSG00000229729	RP11-159G9.5	3:88101093-88217879	OK	12.4246	12.8017	0.0431309	0.0192711	0.97995	0.9998
ENSG00000154134	ENSG00000154134	ROBO3	11:124735281-124751366	OK	1.4071	1.39633	-0.0110846	-0.010136	0.98	0.9998
ENSG00000073969	ENSG00000073969	NSF	17:44668034-44834830	OK	30.2769	30.1098	-0.00798392	-0.0112178	0.98025	0.9998
ENSG00000182749	ENSG00000182749	PAQR7	1:26186103-26197744	OK	5.72231	5.69381	-0.00720474	-0.01459	0.98025	0.9998
ENSG00000203761	ENSG00000203761	MSTO2P	1:155579566-155829191	OK	3.00827	2.94745	-0.0294666	-0.00812186	0.98025	0.9998
ENSG00000135587	ENSG00000135587	SMPD2	6:109711417-109765122	OK	10.5065	10.5719	0.00894274	0.0150953	0.9803	0.9998
ENSG00000211455	ENSG00000211455	STK38L	12:27396900-27478892	OK	16.2024	16.3187	0.0103169	0.0133457	0.98035	0.9998
ENSG00000105792	ENSG00000105792	C7orf63	7:89874487-89940377	OK	1.01728	1.00628	-0.0156841	-0.0109638	0.9804	0.9998
ENSG00000125510	ENSG00000125510	OPRL1	20:62711525-62731996	OK	1.56807	1.57881	0.00985035	0.0156973	0.9804	0.9998
ENSG00000131023	ENSG00000131023	LATS1	6:149979288-150039392	OK	2.87246	2.85749	-0.00753586	-0.0138697	0.98045	0.9998
ENSG00000153066	ENSG00000153066	TXNDC11	16:11762269-11838362	OK	14.2205	14.1348	-0.00872307	-0.0127271	0.9806	0.9998
ENSG00000187257	ENSG00000187257	RSBN1L	7:77325759-77412339	OK	8.75513	8.80695	0.00851513	0.0132449	0.9807	0.9998
ENSG00000126953	ENSG00000126953	TIMM8A	X:100600648-100604184	OK	9.88521	9.94004	0.00798028	0.0151765	0.9808	0.9998
ENSG00000105483	ENSG00000105483	CARD8	19:48673948-48790865	OK	16.5501	16.4172	-0.0116355	-0.0130846	0.98085	0.9998
ENSG00000165501	ENSG00000165501	LRR1	14:50043389-50081390	OK	22.9294	23.3863	0.0284688	0.0136054	0.98085	0.9998
ENSG00000196588	ENSG00000196588	MKL1	22:40742506-41032706	OK	9.3112	9.41926	0.0166473	0.0086133	0.98085	0.9998
ENSG00000126088	ENSG00000126088	UROD	1:45477818-45481247	OK	73.716	74.0048	0.0056421	0.0132297	0.9809	0.9998
ENSG00000108854	ENSG00000108854	SMURF2	17:62495733-62658186	OK	11.5972	11.811	0.0263551	0.0121889	0.98095	0.9998
ENSG00000109063	ENSG00000109063	MYH3	17:10531842-10560626	OK	0.644321	0.637315	-0.0157714	-0.00997685	0.98095	0.9998
ENSG00000127990	ENSG00000127990	SGCE	7:94214541-94285521	OK	15.2421	15.3117	0.00657259	0.0133995	0.98105	0.9998
ENSG00000160678	ENSG00000160678	S100A1	1:153591262-153618782	OK	1886.61	1877.48	-0.00699874	-0.0134918	0.9812	0.9998
ENSG00000143942	ENSG00000143942	CHAC2	2:53759809-54087297	OK	4.44367	4.34226	-0.0333055	-0.0148707	0.98125	0.9998
ENSG00000176142	ENSG00000176142	TMEM39A	3:119148346-119187677	OK	18.1897	18.3214	0.01041	0.0150819	0.98125	0.9998
ENSG00000060237	ENSG00000060237	WNK1	12:861758-1020618	OK	34.7386	34.9136	0.00725056	0.00796498	0.98135	0.9998
ENSG00000215114	ENSG00000215114	UBXN2B	8:59323822-59364060	OK	14.4169	14.5198	0.0102591	0.0136724	0.98135	0.9998
ENSG00000230724	ENSG00000230724	LINC01001	11:127114-207428	OK	1.43772	1.47216	0.034152	0.0112254	0.98145	0.9998
ENSG00000163884	ENSG00000163884	KLF15	3:126061477-126076285	OK	5.65533	5.62643	-0.00739212	-0.0126285	0.9816	0.9998
ENSG00000248429	ENSG00000248429	RP11-597D13.9	4:159045625-159176563	OK	1.93532	1.90301	-0.024283	-0.0081425	0.9816	0.9998
ENSG00000248668	ENSG00000248668	OXCT1-AS1	5:41730166-41871059	OK	2.18218	2.13084	-0.0343437	-0.00612081	0.9816	0.9998
ENSG00000234857	ENSG00000234857	HNRNPUL2-BSCL2	11:62457746-62494856	OK	27.1812	27.0157	-0.00881291	-0.0137001	0.98165	0.9998
ENSG00000136895	ENSG00000136895	GARNL3	9:129986543-130155939	OK	3.9292	3.89734	-0.0117473	-0.0116471	0.9817	0.9998
ENSG00000177189	ENSG00000177189	RPS6KA3	X:20168028-20285523	OK	28.9359	28.7861	-0.00748956	-0.0121608	0.9818	0.9998
ENSG00000127220	ENSG00000127220	ABHD8	19:17402939-17445638	OK	5.07261	4.9964	-0.0218403	-0.0141751	0.98185	0.9998
ENSG00000133318	ENSG00000133318	RTN3	11:63448917-63527363	OK	56.1757	56.4006	0.00576324	0.0136413	0.98185	0.9998
ENSG00000185324	ENSG00000185324	CDK10	16:89747144-89768113	OK	10.8998	10.8295	-0.0093257	-0.0130315	0.98185	0.9998
ENSG00000258057	ENSG00000258057	BCDIN3D-AS1	12:50184928-50236912	OK	1.23704	1.21235	-0.0290905	-0.00758084	0.98185	0.9998
ENSG00000132394	ENSG00000132394	EEFSEC	3:127770483-128127485	OK	8.67418	9.03459	0.0587313	0.0246999	0.9819	0.9998
ENSG00000100201	ENSG00000100201	DDX17	22:38864066-38903665	OK	105.608	105.197	-0.00562585	-0.0103689	0.98195	0.9998
ENSG00000172766	ENSG00000172766	NAA16	13:41885340-41951166	OK	5.54906	5.58433	0.00914252	0.0119812	0.98205	0.9998
ENSG00000120910	ENSG00000120910	PPP3CC	8:22298331-22433301	OK	10.5263	10.4451	-0.0111806	-0.0128456	0.9821	0.9998
ENSG00000179409	ENSG00000179409	GEMIN4	17:647653-658576	OK	8.78729	8.82577	0.00630362	0.0124226	0.9821	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000112419	ENSG00000112419	PHACTR2	6:143857981-144184949	OK	1.11702	1.10556	-0.0148764	-0.00708638	0.98215	0.9998
ENSG00000131507	ENSG00000131507	NDFIP1	5:141488069-141534005	OK	37.1414	37.0039	-0.0053486	-0.0131225	0.98215	0.9998
ENSG00000152102	ENSG00000152102	FAM168B	2:131805448-131851033	OK	23.4095	23.513	0.00636701	0.0119439	0.98215	0.9998
ENSG00000131067	ENSG00000131067	GGT7	20:33432522-33515769	OK	18.4437	18.6007	0.0122266	0.0101457	0.9822	0.9998
ENSG00000158869	ENSG00000158869	FCER1G	1:161185023-161193421	OK	3.76474	3.73742	-0.0105052	-0.0130389	0.9822	0.9998
ENSG00000188760	ENSG00000188760	TMEM198	2:220403668-220415317	OK	2.29484	2.34002	0.0281274	0.015045	0.9822	0.9998
ENSG00000085063	ENSG00000085063	CD59	11:33719806-33757991	OK	661.974	665.109	0.00681565	0.0137985	0.98225	0.9998
ENSG00000138663	ENSG00000138663	COPS4	4:83955599-83996971	OK	28.6919	28.5816	-0.00555319	-0.0126405	0.98225	0.9998
ENSG00000148730	ENSG00000148730	EIF4EBP2	10:72164134-72188374	OK	28.9739	28.8718	-0.00509113	-0.012815	0.98225	0.9998
ENSG00000119682	ENSG00000119682	AREL1	14:75120139-75179818	OK	21.1398	21.2179	0.00532193	0.00871551	0.9823	0.9998
ENSG00000138297	ENSG00000138297	TIMM23	10:51592079-51623365	OK	30.6218	30.7652	0.00673821	0.0137339	0.9823	0.9998
ENSG00000080298	ENSG00000080298	RFX3	9:3218296-3526004	OK	1.74373	1.73144	-0.010209	-0.00925927	0.98235	0.9998
ENSG00000158796	ENSG00000158796	DEDD	1:161070345-161102478	OK	46.0531	45.7271	-0.0102495	-0.0125693	0.9824	0.9998
ENSG00000120253	ENSG00000120253	NUP43	6:150045450-150132556	OK	11.4447	11.3571	-0.0110768	-0.0116239	0.98265	0.9998
ENSG00000246263	ENSG00000246263	KB-431C1.4	8:103251621-103425069	OK	2.34854	2.26213	-0.0540799	-0.0187478	0.98275	0.9998
ENSG00000169057	ENSG00000169057	MECP2	X:153287023-153363212	OK	20.5798	20.7118	0.00922479	0.0115213	0.98285	0.9998
ENSG00000011451	ENSG00000011451	WIZ	19:15532318-15560762	OK	17.8749	17.9417	0.00538559	0.0122912	0.9829	0.9998
ENSG00000118518	ENSG00000118518	RNF146	6:127587754-127609712	OK	8.57734	8.53711	-0.00678308	-0.0116201	0.98295	0.9998
ENSG00000214309	ENSG00000214309	MBLAC1	7:99690350-99726118	OK	4.07457	3.97238	-0.0366435	-0.0110616	0.98295	0.9998
ENSG00000009954	ENSG00000009954	BAZ1B	7:72854727-72936608	OK	27.9945	28.1007	0.0054611	0.012583	0.98305	0.9998
ENSG00000062716	ENSG00000062716	VMP1	17:57697218-57919616	OK	97.655	96.7985	-0.0127098	-0.00871898	0.98305	0.9998
ENSG00000204859	ENSG00000204859	ZBTB48	1:6640060-6649340	OK	7.50396	7.55826	0.0104011	0.0125387	0.9831	0.9998
ENSG00000249129	ENSG00000249129	SUDS3P1	5:177236407-177410055	OK	1.29559	1.274	-0.02425	-0.0129841	0.9831	0.9998
ENSG00000167220	ENSG00000167220	HDHD2	18:44632316-44702745	OK	41.7569	42.0045	0.00852826	0.0122944	0.98315	0.9998
ENSG00000111325	ENSG00000111325	OGFOD2	12:123405497-123467456	OK	11.3907	11.2943	-0.0122699	-0.00807639	0.98325	0.9998
ENSG00000101236	ENSG00000101236	RNF24	20:3907955-3996229	OK	3.9331	3.90924	-0.00877681	-0.0115868	0.9833	0.9998
ENSG00000154723	ENSG00000154723	ATP5J	21:27011583-27144771	OK	123.347	122.711	-0.00745791	-0.0153358	0.9833	0.9998
ENSG00000108064	ENSG00000108064	TFAM	10:60144781-60158981	OK	13.4223	13.494	0.00768849	0.0115909	0.98335	0.9998
ENSG00000121940	ENSG00000121940	CLCC1	1:109358519-109506111	OK	11.76	11.8292	0.00847286	0.0114219	0.98345	0.9998
ENSG00000116260	ENSG00000116260	QSOX1	1:180123968-180173165	OK	86.7716	87.1078	0.00557853	0.0122284	0.98365	0.9998
ENSG00000213930	ENSG00000213930	GALT	9:34638129-34681295	OK	23.3607	23.2265	-0.00831508	-0.0122332	0.98365	0.9998
ENSG00000115993	ENSG00000115993	TRAK2	2:202241929-202345569	OK	32.4353	32.5575	0.00542555	0.0114009	0.9837	0.9998
ENSG00000166313	ENSG00000166313	APBB1	11:6416354-6440644	OK	17.0634	17.1263	0.00530838	0.0106597	0.9839	0.9998
ENSG00000198121	ENSG00000198121	LPAR1	9:113635542-113800981	OK	1.60409	1.61359	0.00851441	0.0111092	0.98395	0.9998
ENSG00000077235	ENSG00000077235	GTF3C1	16:27470875-27561234	OK	23.9535	24.0322	0.00473017	0.00660659	0.98415	0.9998
ENSG00000156110	ENSG00000156110	ADK	10:75910959-76469061	OK	37.8833	37.7407	-0.00544229	-0.0115982	0.98415	0.9998
ENSG00000131871	ENSG00000131871	VIMP	15:101811021-101817705	OK	35.39	35.5263	0.00554887	0.0118908	0.98425	0.9998
ENSG00000198211	ENSG00000198211	TUBB3	16:89939999-90005169	OK	6.43444	6.47883	0.00991886	0.00482286	0.9843	0.9998
ENSG00000254595	ENSG00000254595	CTD-2010I16.1	11:6502676-6614988	OK	1.19548	1.20331	0.00942272	0.00247584	0.9843	0.9998
ENSG00000141076	ENSG00000141076	CIRH1A	16:69139466-69442474	OK	23.0513	22.8828	-0.0105864	-0.00942692	0.98435	0.9998
ENSG00000230204	ENSG00000230204	FTH1P5	6:50880424-50880969	OK	3.35799	3.34179	-0.00697553	-0.00841692	0.98435	0.9998
ENSG00000165660	ENSG00000165660	FAM175B	10:126490353-126525239	OK	10.4393	10.4816	0.00583555	0.0128739	0.9844	0.9998
ENSG00000219529	ENSG00000219529	AP000580.1	11:77371040-77532063	OK	2.98538	3.01254	0.0130639	0.00280295	0.98445	0.9998
ENSG00000076924	ENSG00000076924	XAB2	19:7684410-7694451	OK	31.1297	31.2237	0.00435046	0.0102676	0.9845	0.9998
ENSG00000254692	ENSG00000254692	TM9SF1	14:24641061-24708448	OK	3.26152	3.36721	0.046007	0.0159506	0.98455	0.9998
ENSG00000161999	ENSG00000161999	JMJD8	16:730223-734529	OK	36.7944	37.044	0.00975363	0.0118144	0.9846	0.9998
ENSG00000215251	ENSG00000215251	FASTKD5	20:3087558-3140842	OK	5.89294	5.92267	0.00726016	0.0114375	0.98465	0.9998
ENSG00000163870	ENSG00000163870	TPRA1	3:127291911-127341276	OK	17.7386	17.6461	-0.00753958	-0.0105393	0.9847	0.9998
ENSG00000116478	ENSG00000116478	HDAC1	1:32757686-32799236	OK	57.904	57.7095	-0.00485552	-0.0104964	0.98475	0.9998
ENSG00000183569	ENSG00000183569	SERHL2	22:42949622-42978044	OK	0.781579	0.772184	-0.0174468	-0.00778174	0.98475	0.9998
ENSG00000007168	ENSG00000007168	PAFAH1B1	17:2496503-2588909	OK	88.5828	89.0955	0.00832629	0.0112993	0.9848	0.9998
ENSG00000115207	ENSG00000115207	GTF3C2	2:27548715-27593353	OK	31.7459	31.8577	0.00506927	0.00792722	0.9848	0.9998
ENSG00000163659	ENSG00000163659	TIPARP	3:156389650-156424559	OK	46.9299	46.7465	-0.00564777	-0.0125367	0.9848	0.9998
ENSG00000175634	ENSG00000175634	RPS6KB2	11:67195930-67202872	OK	33.571	33.4484	-0.00528191	-0.0109623	0.98485	0.9998
ENSG00000127124	ENSG00000127124	HIVEP3	1:41972035-42501596	OK	4.01267	4.03884	0.00938144	0.0112199	0.9849	0.9998
ENSG00000187838	ENSG00000187838	TMEM256-PLSCR3	17:7283852-7307456	OK	14.3774	14.4847	0.0107308	0.0120777	0.98495	0.9998
ENSG00000261054	ENSG00000261054	RP11-6O2.4	15:99192199-99675798	OK	2.49687	2.44457	-0.0305371	-0.00943429	0.98495	0.9998
ENSG00000173914	ENSG00000173914	RBM4B	11:66384052-66445392	OK	9.94652	9.82396	-0.0178878	-0.0093894	0.985	0.9998
ENSG00000181896	ENSG00000181896	ZNF101	19:19779604-19794318	OK	3.49348	3.51575	0.00917158	0.011277	0.98505	0.9998
ENSG00000253426	ENSG00000253426	RP11-10A14.4	8:9009251-9025646	OK	2.58244	2.60466	0.0123559	0.0111994	0.98505	0.9998
ENSG00000090975	ENSG00000090975	PITPNM2	12:123468026-123634562	OK	1.74088	1.72854	-0.0102636	-0.0109968	0.9851	0.9998
ENSG00000186907	ENSG00000186907	RTN4RL2	11:57228021-57245007	OK	2.90296	2.88144	-0.0107309	-0.0104042	0.98525	0.9998
ENSG00000112561	ENSG00000112561	TFEB	6:41651715-41703997	OK	9.40825	9.36649	-0.00641808	-0.00941205	0.9853	0.9998
ENSG00000136925	ENSG00000136925	TSTD2	9:100263461-100436030	OK	8.26831	8.2186	-0.0087004	-0.00858145	0.9853	0.9998
ENSG00000146350	ENSG00000146350	TBC1D32	6:121400639-121655891	OK	0.714353	0.720379	0.0121186	0.00759455	0.98535	0.9998
ENSG00000254635	ENSG00000254635	WAC-AS1	10:28811580-28912041	OK	3.06166	3.09606	0.0161176	0.0102568	0.9854	0.9998
ENSG00000134504	ENSG00000134504	KCTD1	18:24034873-24770662	OK	6.31555	6.37071	0.0125472	0.0113915	0.98545	0.9998
ENSG00000246695	ENSG00000246695	RASSF8-AS1	12:26092261-26232825	OK	5.81773	5.74861	-0.0172423	-0.00966093	0.98545	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000139974	ENSG00000139974	SLC38A6	14:61201459-61550451	OK	26.9411	26.79	-0.00811542	-0.0103087	0.9855	0.9998
ENSG00000239246	ENSG00000239246	RP11-464D20.2	17:60536018-60692842	OK	0.894503	0.877634	-0.0274669	-0.00423901	0.9856	0.9998
ENSG00000197813	ENSG00000197813	CTC-301O7.4	19:49834873-49891338	OK	1.28581	1.3129	0.030073	0.0100192	0.98565	0.9998
ENSG00000127415	ENSG00000127415	IDUA	4:952674-998316	OK	4.22738	4.18395	-0.0148985	-0.00949322	0.9858	0.9998
ENSG00000147471	ENSG00000147471	PROSC	8:37620110-37637283	OK	17.8225	17.914	0.00738277	0.00852296	0.9858	0.9998
ENSG00000253490	ENSG00000253490	AC145110.1	8:29605824-29656008	OK	2.55841	2.57145	0.00733547	0.0120711	0.98585	0.9998
ENSG00000111224	ENSG00000111224	PARP11	12:3900212-4019504	OK	1.6373	1.62896	-0.00736871	-0.00791071	0.9859	0.9998
ENSG00000258297	ENSG00000258297	RP11-658F2.8	11:66384052-66445392	OK	2.40287	2.44773	0.0266917	0.00729896	0.9859	0.9998
ENSG00000176407	ENSG00000176407	KCMF1	2:85198215-85286595	OK	47.5178	47.7747	0.00777986	0.0111878	0.98595	0.9998
ENSG00000169692	ENSG00000169692	AGPAT2	9:139567594-139581875	OK	51.884	51.7226	-0.00449436	-0.0107918	0.98605	0.9998
ENSG00000215513	ENSG00000215513	PI4KAP1	22:20383523-20427835	OK	3.75093	3.76827	0.00665594	0.0107412	0.98625	0.9998
ENSG00000189043	ENSG00000189043	NDUFA4	7:10971577-10979883	OK	187.254	186.515	-0.0057002	-0.00972176	0.9863	0.9998
ENSG00000187391	ENSG00000187391	MAGI2	7:77646392-79100524	OK	1.3169	1.30665	-0.0112749	-0.0078187	0.9864	0.9998
ENSG00000213563	ENSG00000213563	C8orf82	8:145743375-145754516	OK	7.85853	7.91319	0.00999927	0.0107426	0.98645	0.9998
ENSG00000237296	ENSG00000237296	SMG1P1	16:22357256-22547842	OK	2.91771	2.87903	-0.0192524	-0.0114315	0.98645	0.9998
ENSG00000111647	ENSG00000111647	UHRF1BP1L	12:100422232-100536626	OK	6.44013	6.46541	0.00565057	0.00799411	0.9865	0.9998
ENSG00000187860	ENSG00000187860	CCDC157	22:30727976-30825045	OK	1.2252	1.21051	-0.0174022	-0.00474124	0.9865	0.9998
ENSG00000196371	ENSG00000196371	FUT4	11:94277005-94658686	OK	1.04265	1.03211	-0.0146568	-0.0104598	0.9865	0.9998
ENSG00000079387	ENSG00000079387	SENP1	12:48436680-48540187	OK	8.43806	8.35848	-0.01367	-0.00988558	0.9866	0.9998
ENSG00000079435	ENSG00000079435	LIPE	19:42901279-43156507	OK	5.41309	5.35764	-0.0148553	-0.00548136	0.9866	0.9998
ENSG00000159377	ENSG00000159377	PSMB4	1:151372009-151374420	OK	770.996	768.753	-0.00420419	-0.0102255	0.9866	0.9998
ENSG00000138794	ENSG00000138794	CASP6	4:110481360-110624739	OK	8.99947	8.94043	-0.00949675	-0.0107568	0.9867	0.9998
ENSG00000204267	ENSG00000204267	TAP2	6:32780539-32806599	OK	23.3867	23.4863	0.00613117	0.00601956	0.9867	0.9998
ENSG00000110628	ENSG00000110628	SLC22A18	11:2909009-2946476	OK	26.5162	26.6128	0.00524672	0.00951036	0.98675	0.9998
ENSG00000245694	ENSG00000245694	CRNDE	16:54952774-54963101	OK	18.022	17.9536	-0.00548395	-0.0098731	0.98675	0.9998
ENSG00000124380	ENSG00000124380	SNRNP27	2:70120691-70170077	OK	41.2716	41.4367	0.00576028	0.00997289	0.98685	0.9998
ENSG00000175701	ENSG00000175701	LINC00116	2:110969105-111043433	OK	71.2711	71.0261	-0.0049687	-0.0101823	0.9869	0.9998
ENSG00000183647	ENSG00000183647	ZNF530	19:58111252-58124090	OK	1.68599	1.69813	0.0103495	0.00940549	0.9869	0.9998
ENSG00000116127	ENSG00000116127	ALMS1	2:73612885-73837920	OK	3.36697	3.38153	0.00622891	0.00639078	0.987	0.9998
ENSG00000129460	ENSG00000129460	NGDN	14:23938896-23979071	OK	23.0818	23.0105	-0.0044641	-0.00924476	0.98705	0.9998
ENSG00000197965	ENSG00000197965	MPZL1	1:167690428-167761156	OK	61.0566	60.8444	-0.0050242	-0.00892423	0.9871	0.9998
ENSG00000165424	ENSG00000165424	ZCCHC24	10:81142080-81205383	OK	8.43059	8.40498	-0.00438956	-0.00977274	0.98725	0.9998
ENSG00000267009	ENSG00000267009	RP11-120M18.2	17:66255322-66760023	OK	1.2731	1.28885	0.0177356	0.00091194	0.9874	0.9998
ENSG00000129084	ENSG00000129084	PSMA1	11:14464985-14665181	OK	164.337	163.689	-0.00569707	-0.00870442	0.98745	0.9998
ENSG00000135390	ENSG00000135390	ATP5G2	12:54026509-54071192	OK	428.377	429.493	0.00375297	0.00924994	0.98745	0.9998
ENSG00000156050	ENSG00000156050	FAM161B	14:74318546-74551196	OK	1.66458	1.63509	-0.0257893	-0.0126292	0.98745	0.9998
ENSG00000240053	ENSG00000240053	LY6G5B	6:31629005-31641553	OK	4.31162	4.40785	0.0318454	0.0148264	0.9875	0.9998
ENSG00000087206	ENSG00000087206	UIMC1	5:176332005-176449634	OK	13.2688	13.3071	0.00414951	0.0076399	0.98755	0.9998
ENSG00000115540	ENSG00000115540	MOB4	2:198351304-198418423	OK	20.7499	21.0555	0.0210938	0.00880528	0.98765	0.9998
ENSG00000204394	ENSG00000204394	VARS	6:31745294-31763730	OK	55.6813	55.4972	-0.00477778	-0.00857253	0.98765	0.9998
ENSG00000164051	ENSG00000164051	CCDC51	3:48473573-48488060	OK	21.9423	22.097	0.0101327	0.0106301	0.98775	0.9998
ENSG00000213702	ENSG00000213702	AC008865.1	5:96149730-96373219	OK	3.66608	3.62349	-0.0168573	-0.00880834	0.98775	0.9998
ENSG00000107371	ENSG00000107371	EXOSC3	9:37510888-38069210	OK	40.7276	41.2127	0.0170837	0.0128106	0.98785	0.9998
ENSG00000095539	ENSG00000095539	SEMA4G	10:102729214-102754158	OK	5.5289	5.49263	-0.00949441	-0.00655762	0.98795	0.9998
ENSG00000270157	ENSG00000270157	RP5-894A10.6	7:141229002-141401953	OK	1.10719	1.11803	0.0140583	0.00354806	0.988	0.9998
ENSG00000183688	ENSG00000183688	FAM101B	17:289768-295730	OK	13.5746	13.5418	-0.00349112	-0.00813599	0.9881	0.9998
ENSG00000108278	ENSG00000108278	ZNHIT3	17:34842472-34899284	OK	39.3568	39.1373	-0.00807117	-0.00965457	0.98815	0.9998
ENSG00000170234	ENSG00000170234	PWWP2A	5:159436119-159546430	OK	5.0091	5.03903	0.00859557	0.0066349	0.98815	0.9998
ENSG00000133657	ENSG00000133657	ATP13A3	3:194123400-194239008	OK	43.6856	43.5129	-0.00571448	-0.00655495	0.9882	0.9998
ENSG00000188636	ENSG00000188636	LDOC1L	22:44888451-44894178	OK	5.91032	5.8936	-0.00408773	-0.00896727	0.9882	0.9998
ENSG00000003402	ENSG00000003402	CFLAR	2:201980826-202041410	OK	13.7293	13.6762	-0.00559515	-0.00762324	0.98825	0.9998
ENSG00000135272	ENSG00000135272	MDFIC	7:114562208-114659256	OK	30.1731	30.2821	0.00520403	0.00757078	0.98825	0.9998
ENSG00000122692	ENSG00000122692	SMU1	9:33041761-33076665	OK	39.6049	39.4969	-0.00394088	-0.00777625	0.98835	0.9998
ENSG00000151348	ENSG00000151348	EXT2	11:44117098-44266979	OK	49.4457	49.3229	-0.00358901	-0.00869302	0.9884	0.9998
ENSG00000260349	ENSG00000260349	RP11-473I1.5	16:9185504-9215497	OK	2.32405	2.30601	-0.0112422	-0.00339217	0.98855	0.9998
ENSG00000112357	ENSG00000112357	PEX7	6:137143716-137235075	OK	4.58428	4.56579	-0.00582978	-0.00942096	0.9887	0.9998
ENSG00000137265	ENSG00000137265	IRF4	6:391738-411447	OK	23.5181	23.5873	0.0042394	0.00715666	0.9887	0.9998
ENSG00000047315	ENSG00000047315	POLR2B	4:57829535-58071676	OK	34.3866	34.2183	-0.00707849	-0.00574203	0.98875	0.9998
ENSG00000072682	ENSG00000072682	P4HA2	5:131520568-131731306	OK	10.9431	10.9037	-0.00519883	-0.00724104	0.98875	0.9998
ENSG00000164080	ENSG00000164080	RAD54L2	3:51575159-51738339	OK	4.85002	4.86999	0.00592909	0.00705521	0.98875	0.9998
ENSG00000198133	ENSG00000198133	TMEM229B	14:67913800-68067004	OK	31.4987	31.3663	-0.00607673	-0.00568863	0.9888	0.9998
ENSG00000122729	ENSG00000122729	ACO1	9:32384617-32454767	OK	17.3935	17.3507	-0.00356077	-0.00836601	0.98885	0.9998
ENSG00000251369	ENSG00000251369	ZNF550	19:58038692-58071231	OK	2.20327	2.19353	-0.00639559	-0.00733527	0.98885	0.9998
ENSG00000144118	ENSG00000144118	RALB	2:120997639-121052289	OK	42.059	41.9562	-0.00353353	-0.00819292	0.9889	0.9998
ENSG00000154856	ENSG00000154856	APCDD1	18:10454624-10489945	OK	20.9347	21.0462	0.00765833	0.00986458	0.9889	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000228305	ENSG00000228305	AC016734.2	2:63348517-64054977	OK	15.384	15.6584	0.0255003	0.00880336	0.989	0.9998
ENSG00000008128	ENSG00000008128	CDK11A	1:1634168-1677431	OK	16.0172	16.0744	0.00514365	0.00676543	0.98905	0.9998
ENSG00000065911	ENSG00000065911	MTHFD2	2:74425688-74621009	OK	37.5878	37.3282	-0.00999832	-0.008494	0.9891	0.9998
ENSG00000212123	ENSG00000212123	PRR22	19:5782970-5791249	OK	0.634575	0.626296	-0.0189452	-0.00685396	0.9891	0.9998
ENSG00000157911	ENSG00000157911	PEX10	1:2323266-2345236	OK	18.2079	18.2957	0.0069458	0.00641786	0.98915	0.9998
ENSG00000104852	ENSG00000104852	SNRNP70	19:49588675-49611862	OK	96.3195	96.5518	0.00347413	0.0073534	0.98925	0.9998
ENSG00000198363	ENSG00000198363	ASPH	8:61969716-62627155	OK	65.3895	65.2114	-0.00393627	-0.00749923	0.98945	0.9998
ENSG00000106803	ENSG00000106803	SEC61B	9:101984345-101992897	OK	169.538	169.157	-0.00325049	-0.0078154	0.98965	0.9998
ENSG00000140479	ENSG00000140479	PCSK6	15:101835623-102065405	OK	19.1388	19.1894	0.00380198	0.00539604	0.9897	0.9998
ENSG00000120333	ENSG00000120333	MRPS14	1:174968299-174992561	OK	33.1483	32.9913	-0.00684876	-0.00651892	0.98975	0.9998
ENSG00000220785	ENSG00000220785	MTMR9LP	1:32697258-32707221	OK	0.823014	0.827184	0.00729149	0.00803689	0.98985	0.9998
ENSG00000033867	ENSG00000033867	SLC4A7	3:27414213-27525911	OK	6.60049	6.58502	-0.00338638	-0.0052934	0.98995	0.9998
ENSG00000188542	ENSG00000188542	DUSP28	2:241418838-241520789	OK	2.88807	2.86211	-0.0130253	-0.00558424	0.99005	0.9998
ENSG00000122257	ENSG00000122257	RBBP6	16:24549013-24584184	OK	19.197	19.2815	0.00633651	0.00727305	0.99015	0.9998
ENSG00000163798	ENSG00000163798	SLC4A1AP	2:27805896-27917840	OK	16.4341	16.3544	-0.00701232	-0.00800064	0.9902	0.9998
ENSG00000228436	ENSG00000228436	RP5-864K19.4	1:39325671-39407471	OK	1.08139	1.06735	-0.0188478	-0.00446162	0.9902	0.9998
ENSG00000174871	ENSG00000174871	CNIH2	11:66036003-66056641	OK	2.65107	2.67091	0.0107559	0.00264627	0.99025	0.9998
ENSG00000261455	ENSG00000261455	LINC01003	7:152160870-152162634	OK	1.39918	1.39769	-0.00154377	-0.0021606	0.99025	0.9998
ENSG00000133710	ENSG00000133710	SPINK5	5:147405245-147516852	OK	1.05171	1.05775	0.00826584	0.00694559	0.99045	0.9998
ENSG00000110344	ENSG00000110344	UBE4A	11:118230299-118302211	OK	7.98942	8.02235	0.005934	0.0073369	0.9905	0.9998
ENSG00000240036	ENSG00000240036	RP11-587D21.1	11:27528384-27899195	OK	72.3914	72.2091	-0.00363601	-0.00662944	0.9905	0.9998
ENSG00000067704	ENSG00000067704	IARS2	1:220267443-220321380	OK	94.7076	94.9064	0.00302614	0.00761865	0.9906	0.9998
ENSG00000135452	ENSG00000135452	TSPAN31	12:58117543-58154190	OK	24.295	24.4468	0.00898634	0.00579911	0.9906	0.9998
ENSG00000170634	ENSG00000170634	ACYP2	2:54091203-54532437	OK	3.01089	2.98591	-0.0120197	-0.00457789	0.9906	0.9998
ENSG00000267673	ENSG00000267673	FDX1L	19:10415478-10444316	OK	30.5092	30.6582	0.00702765	0.00713863	0.99065	0.9998
ENSG00000125863	ENSG00000125863	MKKS	20:10381656-10414870	OK	29.7605	29.6729	-0.00425497	-0.00760335	0.9907	0.9998
ENSG00000251196	ENSG00000251196	RP11-54F2.1	5:10652322-10657928	OK	1.68828	1.70361	0.0130438	0.00783892	0.9907	0.9998
ENSG00000077312	ENSG00000077312	SNRPA	19:41197433-41271294	OK	45.2181	45.0851	-0.00425228	-0.00602554	0.99075	0.9998
ENSG00000141337	ENSG00000141337	ARSG	17:66255322-66760023	OK	11.1328	11.211	0.0100956	0.00242093	0.99075	0.9998
ENSG00000162783	ENSG00000162783	IER5	1:181057637-181059977	OK	42.495	42.5837	0.00300657	0.00740587	0.9908	0.9998
ENSG00000204370	ENSG00000204370	SDHD	11:111895537-112095422	OK	47.4137	47.2846	-0.00393153	-0.00600825	0.9908	0.9998
ENSG00000008952	ENSG00000008952	SEC62	3:169657140-169716161	OK	55.175	55.0317	-0.00375188	-0.00657413	0.9909	0.9998
ENSG00000167685	ENSG00000167685	ZNF444	19:56643967-56672262	OK	10.4272	10.405	-0.00306473	-0.00535929	0.99095	0.9998
ENSG00000100445	ENSG00000100445	SDR39U1	14:24895737-24912111	OK	22.9557	23.067	0.00697918	0.00684485	0.991	0.9998
ENSG00000110801	ENSG00000110801	PSMD9	12:122326636-122441833	OK	45.7461	45.6359	-0.00347844	-0.00667918	0.99105	0.9998
ENSG00000204253	ENSG00000204253	HNRNPCP2	2:190744334-191236391	OK	12.1757	12.2506	0.00885517	0.00630775	0.99105	0.9998
ENSG00000141668	ENSG00000141668	CBLN2	18:70203914-70305756	OK	0.96486	0.970927	0.00904293	0.00441149	0.9911	0.9998
ENSG00000083123	ENSG00000083123	BCKDHB	6:80816363-81055987	OK	8.72161	8.69946	-0.00366838	-0.00632687	0.9912	0.9998
ENSG00000144161	ENSG00000144161	ZC3H8	2:112969101-113012713	OK	11.3599	11.3895	0.00374738	0.00543455	0.99125	0.9998
ENSG00000160216	ENSG00000160216	AGPAT3	21:45285066-45406417	OK	19.1065	19.0713	-0.00266368	-0.00415019	0.99125	0.9998
ENSG00000241962	ENSG00000241962	C2orf15	2:99613723-100106497	OK	25.1349	25.2571	0.00700107	0.00727594	0.99125	0.9998
ENSG00000091542	ENSG00000091542	ALKBH5	17:18012019-18113268	OK	37.4533	37.3848	-0.00264254	-0.00652437	0.9915	0.9998
ENSG00000214940	ENSG00000214940	NPIPA8	16:18411798-18495797	OK	0.660497	0.671643	0.0241427	0.00679788	0.9915	0.9998
ENSG00000102471	ENSG00000102471	NDFIP2	13:80051498-80130210	OK	22.8352	22.7856	-0.00313614	-0.00596615	0.99155	0.9998
ENSG00000188368	ENSG00000188368	PRR19	19:42801184-42814973	OK	1.05225	1.03556	-0.0230547	-0.00902891	0.9916	0.9998
ENSG00000088367	ENSG00000088367	EPB41L1	20:34679425-34820721	OK	9.48225	9.45406	-0.00429527	-0.00605298	0.9917	0.9998
ENSG00000100296	ENSG00000100296	THOC5	22:29901867-29977326	OK	36.8445	36.7464	-0.00384751	-0.00549415	0.9917	0.9998
ENSG00000185022	ENSG00000185022	MAFF	22:38507501-38612518	OK	14.4518	14.4172	-0.0034528	-0.00676756	0.99175	0.9998
ENSG00000178057	ENSG00000178057	NDUFAF3	3:48955220-49060928	OK	87.7063	88.1406	0.00712657	0.00605765	0.99185	0.9998
ENSG00000233369	ENSG00000233369	RP11-396K3.1	7:72569032-72619657	OK	8.61806	8.6344	0.00273338	0.00551133	0.99185	0.9998
ENSG00000147382	ENSG00000147382	FAM58A	X:152853376-152869808	OK	18.7291	18.6943	-0.00268023	-0.00542353	0.9919	0.9998
ENSG00000166477	ENSG00000166477	LEO1	15:52121824-52392720	OK	7.37806	7.34328	-0.00681712	-0.00623668	0.9919	0.9998
ENSG00000156642	ENSG00000156642	NPTN	15:73735498-73926475	OK	57.8939	58.0112	0.00291951	0.0062518	0.992	0.9998
ENSG00000099984	ENSG00000099984	GSTT2	22:24309088-24326106	OK	13.6119	13.7142	0.0108019	0.00691522	0.9921	0.9998
ENSG00000197961	ENSG00000197961	ZNF121	19:9676403-9695209	OK	3.98796	3.97978	-0.00296142	-0.00541306	0.9921	0.9998
ENSG00000196233	ENSG00000196233	LCOR	10:98592016-98740800	OK	4.9546	4.9686	0.00407072	0.00309143	0.9923	0.9998
ENSG00000259153	ENSG00000259153	RP6-65G23.3	14:71276921-71282120	OK	1.17125	1.16367	-0.0093557	-0.00706823	0.9923	0.9998
ENSG00000227946	ENSG00000227946	AC007383.3	2:206854308-206951288	OK	1.90274	1.91609	0.010091	0.00447054	0.99235	0.9998
ENSG00000236404	ENSG00000236404	RP11-125B21.2	9:2422701-2660053	OK	1.2058	1.19526	-0.0126659	-0.00265321	0.9924	0.9998
ENSG00000253250	ENSG00000253250	C8orf88	8:91634222-91997485	OK	10.6503	10.5731	-0.0104978	-0.00544966	0.99255	0.9998
ENSG00000100890	ENSG00000100890	KIAA0391	14:35514112-35786699	OK	34.0328	33.9158	-0.00497058	-0.00429604	0.9926	0.9998
ENSG00000225921	ENSG00000225921	NOL7	6:13615558-13711796	OK	75.6191	75.7811	0.00308864	0.00515124	0.99265	0.9998
ENSG00000204498	ENSG00000204498	NFKBIL1	6:31496493-31526606	OK	18.4954	18.5937	0.00765253	0.00537488	0.9927	0.9998
ENSG00000230844	ENSG00000230844	ZNF674-AS1	X:46404927-46407843	OK	0.854341	0.851775	-0.00434051	-0.00525412	0.9927	0.9998
ENSG00000114867	ENSG00000114867	EIF4G1	3:183851806-184402546	OK	124.401	124.841	0.00509644	0.00465495	0.9928	0.9998
ENSG00000197852	ENSG00000197852	FAM212B	1:112025969-112310638	OK	1.7916	1.77987	-0.00947688	-0.00408721	0.99285	0.9998
ENSG00000131966	ENSG00000131966	ACTR10	14:58466452-58764857	OK	60.0034	59.8224	-0.00435889	-0.00511588	0.9929	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000108797	ENSG00000108797	CNTNAP1	17:40830906-40851832	OK	9.79793	9.78138	-0.0024391	-0.00409459	0.99295	0.9998
ENSG00000113013	ENSG00000113013	HSPA9	5:137890570-137911133	OK	168.638	168.866	0.0019474	0.00434567	0.99295	0.9998
ENSG00000160352	ENSG00000160352	ZNF714	19:21264964-21308073	OK	6.77096	6.75357	-0.0037115	-0.00461488	0.99295	0.9998
ENSG00000177076	ENSG00000177076	ACER2	9:19408924-19452018	OK	1.63254	1.6388	0.00551627	0.00632671	0.99295	0.9998
ENSG00000145388	ENSG00000145388	METTL14	4:119606522-119636588	OK	7.54402	7.52794	-0.00307871	-0.00446885	0.99305	0.9998
ENSG00000160799	ENSG00000160799	CCDC12	3:46963215-47051193	OK	22.4868	22.5485	0.00395587	0.00525709	0.99305	0.9998
ENSG00000170266	ENSG00000170266	GLB1	3:33038099-33138722	OK	50.3616	50.2932	-0.00196069	-0.0036287	0.9932	0.9998
ENSG00000171617	ENSG00000171617	ENC1	5:73923233-74072737	OK	12.662	12.5978	-0.00733199	-0.00494137	0.99325	0.9998
ENSG00000223820	ENSG00000223820	CFL1P1	10:89511268-89605369	OK	2.35334	2.33713	-0.00996904	-0.00190208	0.99325	0.9998
ENSG00000131069	ENSG00000131069	ACSS2	20:33432522-33515769	OK	57.3827	57.2656	-0.00294651	-0.00364688	0.9934	0.9998
ENSG00000175711	ENSG00000175711	B3GNTL1	17:80709939-81009686	OK	2.64831	2.66784	0.0106009	0.00328863	0.9934	0.9998
ENSG00000147509	ENSG00000147509	RGS20	8:54764367-54871863	OK	42.0408	41.9687	-0.00247574	-0.00476712	0.9935	0.9998
ENSG00000241399	ENSG00000241399	CD302	2:160568999-160761260	OK	15.6875	15.6464	-0.00378205	-0.00379955	0.9935	0.9998
ENSG00000148688	ENSG00000148688	RPP30	10:92631472-92668312	OK	35.3554	35.4176	0.00253608	0.00477892	0.9936	0.9998
ENSG00000122696	ENSG00000122696	SLC25A51	9:37510888-38069210	OK	13.7074	13.7705	0.00662444	0.00478815	0.99365	0.9998
ENSG00000026036	ENSG00000026036	RTEL1-TNFRSF6B	20:62289162-62374858	OK	2.42388	2.43569	0.00701172	0.00424872	0.9937	0.9998
ENSG00000160214	ENSG00000160214	RRP1	21:45209393-45225174	OK	15.9945	16.0294	0.00314597	0.00510616	0.99375	0.9998
ENSG00000198794	ENSG00000198794	SCAMP5	15:75246756-75313837	OK	4.34266	4.33224	-0.0034686	-0.00271547	0.9938	0.9998
ENSG00000111684	ENSG00000111684	LPCAT3	12:7072407-7178336	OK	18.8062	18.8685	0.00477239	0.00320786	0.994	0.9998
ENSG00000134250	ENSG00000134250	NOTCH2	1:120454175-120612240	OK	16.5453	16.5663	0.00183011	0.00360681	0.994	0.9998
ENSG00000163528	ENSG00000163528	CHCHD4	3:14153579-14166370	OK	15.0866	15.0624	-0.00231544	-0.0047767	0.994	0.9998
ENSG00000168397	ENSG00000168397	ATG4B	2:242523819-242613272	OK	47.9083	48.0084	0.00301153	0.00422988	0.994	0.9998
ENSG00000174529	ENSG00000174529	TMEM81	1:205052257-205053645	OK	2.81137	2.80084	-0.00541508	-0.00815104	0.994	0.9998
ENSG00000175662	ENSG00000175662	TOM1L2	17:17746827-17875736	OK	12.5994	12.6202	0.00238146	0.0040043	0.9941	0.9998
ENSG00000156831	ENSG00000156831	NSMCE2	8:126036501-126379362	OK	33.4593	33.3558	-0.00447322	-0.00456839	0.99415	0.9998
ENSG00000164733	ENSG00000164733	CTSB	8:11700032-11726957	OK	2173.68	2177.59	0.00258972	0.00359317	0.99415	0.9998
ENSG00000188554	ENSG00000188554	NBR1	17:41322497-41363708	OK	37.5273	37.4677	-0.00229055	-0.00563641	0.9943	0.9998
ENSG00000123179	ENSG00000123179	EBPL	13:50234858-50265611	OK	33.8129	33.77	-0.001831	-0.00386594	0.99435	0.9998
ENSG00000184154	ENSG00000184154	LRTOMT	11:71709586-71823826	OK	4.19672	4.21288	0.00554407	0.00124937	0.99435	0.9998
ENSG00000233954	ENSG00000233954	RP11-169K16.7	1:16133678-16134194	OK	669.8	668.862	-0.00202132	-0.00432365	0.99435	0.9998
ENSG00000004455	ENSG00000004455	AK2	1:33452552-33546597	OK	153.839	154.099	0.00243482	0.00480932	0.99445	0.9998
ENSG00000124177	ENSG00000124177	CHD6	20:40030740-40247133	OK	26.9384	26.8893	-0.0026304	-0.00275371	0.99455	0.9998
ENSG00000141577	ENSG00000141577	AZI1	17:79163392-79196799	OK	9.99509	10.0073	0.0017635	0.00323874	0.99455	0.9998
ENSG00000185838	ENSG00000185838	GNB1L	22:19744225-19842462	OK	3.28283	3.2709	-0.00525322	-0.00411883	0.99455	0.9998
ENSG00000198718	ENSG00000198718	FAM179B	14:45393521-45543634	OK	5.02098	5.01179	-0.00264346	-0.00274678	0.99455	0.9998
ENSG00000165322	ENSG00000165322	ARHGAP12	10:32094364-32217742	OK	8.03871	8.05061	0.00213531	0.00405907	0.9946	0.9998
ENSG00000155592	ENSG00000155592	ZKSCAN2	16:25247321-25269252	OK	1.52568	1.52292	-0.00261099	-0.00420158	0.99465	0.9998
ENSG00000163660	ENSG00000163660	CCNL1	3:156864296-156878549	OK	67.0625	66.9905	-0.00154918	-0.00268284	0.99485	0.9998
ENSG00000165646	ENSG00000165646	SLC18A2	10:118999110-119038941	OK	1.09526	1.09711	0.00242845	0.00374384	0.99485	0.9998
ENSG00000135317	ENSG00000135317	SNX14	6:86215213-86353510	OK	42.2855	42.1815	-0.00355015	-0.00302693	0.9949	0.9998
ENSG00000112394	ENSG00000112394	SLC16A10	6:111408780-111580237	OK	3.26146	3.25381	-0.00338838	-0.00328495	0.99495	0.9998
ENSG00000188938	ENSG00000188938	FAM120AOS	9:96208775-96328397	OK	24.5025	24.4044	-0.00579186	-0.0044763	0.9951	0.9998
ENSG00000250959	ENSG00000250959	GLUD1P3	10:75490319-75497069	OK	0.644465	0.643816	-0.00145387	-0.00082504	0.9952	0.9998
ENSG00000064961	ENSG00000064961	HMG20B	19:3506270-3579086	OK	419.856	418.738	-0.00384598	-0.00321013	0.99525	0.9998
ENSG00000272780	ENSG00000272780	RP11-822E23.8	17:21428050-21477781	OK	0.728916	0.732139	0.00636361	0.00376091	0.99525	0.9998
ENSG00000119878	ENSG00000119878	CRIPT	2:46717888-46852881	OK	9.51192	9.44419	-0.0103098	-0.00464351	0.9953	0.9998
ENSG00000162928	ENSG00000162928	PEX13	2:61167356-61279125	OK	7.95747	7.94515	-0.00223604	-0.00326498	0.9953	0.9998
ENSG00000164144	ENSG00000164144	ARFIP1	4:153701088-153839615	OK	15.7094	15.7301	0.00189712	0.00362563	0.9953	0.9998
ENSG00000049245	ENSG00000049245	VAMP3	1:7831328-7841492	OK	79.6796	79.7583	0.00142346	0.00330476	0.9954	0.9998
ENSG00000126005	ENSG00000126005	MMP24-AS1	20:33703166-33872788	OK	54.4973	54.3414	-0.004133	-0.00382963	0.9955	0.9998
ENSG00000117602	ENSG00000117602	RCAN3	1:24829386-24882515	OK	6.86971	6.87825	0.00179247	0.00274144	0.9956	0.9998
ENSG00000213246	ENSG00000213246	SUPT4H1	17:56378591-56494956	OK	136.926	137.057	0.00138334	0.00273972	0.9956	0.9998
ENSG00000104960	ENSG00000104960	PTOV1	19:50321538-50364001	OK	73.9701	73.8899	-0.00156568	-0.00263851	0.99565	0.9998
ENSG00000184220	ENSG00000184220	CMSS1	3:99536677-99897447	OK	49.2846	49.338	0.00156272	0.00357496	0.99565	0.9998
ENSG00000115568	ENSG00000115568	ZNF142	2:219502638-219528166	OK	7.25708	7.27324	0.00320924	0.0029073	0.9957	0.9998
ENSG00000206195	ENSG00000206195	AP000525.9	22:16147978-16193004	OK	9.89852	9.88736	-0.00162779	-0.00267769	0.9957	0.9998
ENSG00000167881	ENSG00000167881	SRP68	17:74035183-74117657	OK	56.7991	56.8885	0.00226747	0.00324999	0.99575	0.9998
ENSG00000258366	ENSG00000258366	RTEL1	20:62289162-62374858	OK	13.641	13.6198	-0.00224387	-0.00225366	0.9958	0.9998
ENSG00000135451	ENSG00000135451	TROAP	12:49686413-49725514	OK	67.047	66.9547	-0.00198629	-0.00370184	0.99585	0.9998
ENSG00000241258	ENSG00000241258	CRCP	7:65540784-65629998	OK	12.6959	12.676	-0.00225784	-0.0024839	0.99585	0.9998
ENSG00000118961	ENSG00000118961	C2orf43	2:20883787-21022882	OK	5.77216	5.78028	0.0020274	0.00303262	0.9959	0.9998
ENSG00000224842	ENSG00000224842	RP11-123K19.1	9:129351872-129375979	OK	0.711793	0.712162	0.000748404	0.000492595	0.9959	0.9998
ENSG00000148248	ENSG00000148248	SURF4	9:136228324-136242970	OK	81.1944	81.2798	0.00151681	0.00288102	0.996	0.9998
ENSG00000101695	ENSG00000101695	RNF125	18:29598334-30050447	OK	5.35869	5.37451	0.00425244	0.00163832	0.99605	0.9998
ENSG00000167283	ENSG00000167283	ATP5L	11:118230299-118302211	OK	172.127	171.872	-0.00213653	-0.00340811	0.99605	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000155100	ENSG00000155100	OTUD6B	8:92082423-92099323	OK	7.67581	7.6673	-0.00160013	-0.00308916	0.99615	0.9998
ENSG00000153922	ENSG00000153922	CHD1	5:98190907-98262240	OK	14.0897	14.1012	0.00117807	0.0021271	0.99625	0.9998
ENSG00000182224	ENSG00000182224	CYB5D1	17:7760002-7816078	OK	7.32357	7.34018	0.00326798	0.00198512	0.99625	0.9998
ENSG00000150779	ENSG00000150779	TIMM8B	11:111895537-112095422	OK	25.5882	25.6735	0.00480421	0.00392701	0.9963	0.9998
ENSG00000158806	ENSG00000158806	NPM2	8:21881635-21894408	OK	0.988666	0.986797	-0.00272883	-0.00166654	0.9964	0.9998
ENSG00000170142	ENSG00000170142	UBE2E1	3:23845514-23932807	OK	98.5871	98.6688	0.00119503	0.00284137	0.9964	0.9998
ENSG00000006831	ENSG00000006831	ADIPOR2	12:1797739-1897844	OK	57.7168	57.6832	-0.000840346	-0.00202132	0.99645	0.9998
ENSG00000126214	ENSG00000126214	KLC1	14:104019757-104181841	OK	72.8005	72.7136	-0.00172245	-0.00222008	0.99645	0.9998
ENSG00000120942	ENSG00000120942	UBIAD1	1:11333262-11356106	OK	4.53288	4.53778	0.00156086	0.00287691	0.9965	0.9998
ENSG00000203865	ENSG00000203865	ATP1A1OS	1:116915289-116961244	OK	1.55796	1.5539	-0.00377	-0.000197287	0.9965	0.9998
ENSG00000144182	ENSG00000144182	LIPT1	2:99613723-100106497	OK	4.73557	4.7495	0.00423808	0.00130918	0.99655	0.9998
ENSG00000213186	ENSG00000213186	TRIM59	3:159943422-160203561	OK	2.19588	2.20425	0.00548869	0.00176049	0.9966	0.9998
ENSG00000226381	ENSG00000226381	RP11-119F19.2	10:81420646-81526085	OK	5.04331	5.03465	-0.00248067	-0.00269237	0.9966	0.9998
ENSG00000259417	ENSG00000259417	RP11-2E17.1	15:80487825-80544555	OK	1.63905	1.63805	-0.00087859	-0.00161933	0.99665	0.9998
ENSG00000162298	ENSG00000162298	SYVN1	11:64888099-64902004	OK	12.9846	12.9514	-0.00369267	-0.00210127	0.99675	0.9998
ENSG00000169684	ENSG00000169684	CHRNA5	15:78857861-78913637	OK	9.5425	9.55792	0.00233005	0.0028842	0.9968	0.9998
ENSG00000165512	ENSG00000165512	ZNF22	10:45493145-45676875	OK	4.0325	4.03472	0.000792526	0.00145555	0.9969	0.9998
ENSG00000111885	ENSG00000111885	MAN1A1	6:119498373-119670926	OK	2.29765	2.29986	0.00138557	0.00257135	0.99695	0.9998
ENSG00000225313	ENSG00000225313	RP11-415J8.3	1:33772366-33896653	OK	1.15067	1.15609	0.00677989	0.00118595	0.99695	0.9998
ENSG00000198089	ENSG00000198089	SFI1	22:31795508-32058418	OK	12.6452	12.6287	-0.00188766	-0.00126611	0.997	0.9998
ENSG00000144061	ENSG00000144061	NPHP1	2:110879887-110962643	OK	8.00249	7.99178	-0.00193315	-0.00231386	0.9971	0.9998
ENSG00000088205	ENSG00000088205	DDX18	2:118572225-118589955	OK	42.4694	42.4429	-0.000902069	-0.00168929	0.99715	0.9998
ENSG00000129245	ENSG00000129245	FXR2	17:7465191-7536700	OK	17.0568	17.1801	0.0103926	0.00406996	0.99715	0.9998
ENSG00000141040	ENSG00000141040	ZNF287	17:16454700-16472520	OK	6.35266	6.36526	0.0028588	0.0027277	0.99715	0.9998
ENSG00000164066	ENSG00000164066	INTU	4:128544425-128647892	OK	1.4933	1.49171	-0.00153866	-0.00137472	0.9972	0.9998
ENSG00000117528	ENSG00000117528	ABCD3	1:94883932-94984222	OK	21.5602	21.5749	0.000987801	0.0018887	0.99735	0.9998
ENSG00000247077	ENSG00000247077	PGAM5	12:133264191-133299228	OK	25.5551	25.5285	-0.00150237	-0.00199612	0.99735	0.9998
ENSG00000251247	ENSG00000251247	ZNF345	19:37288419-37407193	OK	1.17075	1.17199	0.00153059	0.000774731	0.99745	0.9998
ENSG00000115828	ENSG00000115828	QPCT	2:37571716-37600465	OK	571.164	570.82	-0.000868225	-0.00197321	0.9975	0.9998
ENSG00000171100	ENSG00000171100	MTM1	X:149737068-149841795	OK	5.38344	5.38745	0.00107471	0.00182953	0.9975	0.9998
ENSG00000168779	ENSG00000168779	SHOX2	3:157814947-158288855	OK	6.07086	6.06208	-0.00208688	-0.00193035	0.99755	0.9998
ENSG00000103423	ENSG00000103423	DNAJA3	16:4475805-4506776	OK	38.9617	38.9837	0.000812231	0.00174197	0.99765	0.9998
ENSG00000084693	ENSG00000084693	AGBL5	2:27265231-27294641	OK	34.3463	34.3802	0.00141998	0.00173635	0.9977	0.9998
ENSG00000089048	ENSG00000089048	ESF1	20:13694968-13765532	OK	5.39219	5.39357	0.000369127	0.000730441	0.99775	0.9998
ENSG00000175224	ENSG00000175224	ATG13	11:46624410-46696368	OK	32.1042	32.0857	-0.000830789	-0.00142612	0.99775	0.9998
ENSG00000236017	ENSG00000236017	ASMTL-AS1	X:1520661-1572655	OK	1.04436	1.04677	0.00332239	0.00142991	0.99775	0.9998
ENSG00000188283	ENSG00000188283	ZNF383	19:37498758-37734828	OK	2.25643	2.25956	0.0020025	0.00163557	0.9978	0.9998
ENSG00000124615	ENSG00000124615	MOCS1	6:39760141-39902290	OK	7.44936	7.43404	-0.00296956	-0.0022064	0.99785	0.9998
ENSG00000184677	ENSG00000184677	ZBTB40	1:22778343-22857650	OK	4.5861	4.58856	0.000773935	0.00169494	0.9979	0.9998
ENSG00000253540	ENSG00000253540	FAM86HP	3:129800673-129839422	OK	0.891821	0.893497	0.00270963	0.00191048	0.998	0.9998
ENSG00000094631	ENSG00000094631	HDAC6	X:48659783-48683392	OK	14.5731	14.5642	-0.000880482	-0.00102322	0.99805	0.9998
ENSG00000214530	ENSG00000214530	STARD10	11:72396113-72504726	OK	26.6591	26.6407	-0.000995131	-0.00115555	0.99805	0.9998
ENSG00000105072	ENSG00000105072	C19orf44	19:16589867-16771253	OK	3.02597	3.03177	0.00276281	0.00133437	0.9981	0.9998
ENSG00000091137	ENSG00000091137	SLC26A4	7:107294420-107358254	OK	6.14863	6.14375	-0.0011449	-0.00168218	0.99815	0.9998
ENSG00000105298	ENSG00000105298	CACTIN	19:3607244-3626813	OK	8.97232	8.97604	0.000598215	0.00117111	0.99815	0.9998
ENSG00000095383	ENSG00000095383	TBC1D2	9:100961310-101017915	OK	1.80752	1.80842	0.000723633	0.00108326	0.9982	0.9998
ENSG00000011105	ENSG00000011105	TSPAN9	12:3186520-3395730	OK	9.56026	9.55007	-0.00153836	-0.00081143	0.99825	0.9998
ENSG00000107951	ENSG00000107951	MTPAP	10:30598729-30663377	OK	6.65953	6.65423	-0.00115056	-0.00133645	0.9983	0.9998
ENSG00000142871	ENSG00000142871	CYR61	1:86046443-86049645	OK	7.39516	7.39202	-0.000613505	-0.00113806	0.9983	0.9998
ENSG00000174695	ENSG00000174695	TMEM167A	5:82348664-82649606	OK	82.8805	82.818	-0.00108947	-0.00147395	0.99835	0.9998
ENSG00000176915	ENSG00000176915	ANKLE2	12:133302253-133338474	OK	31.6236	31.6118	-0.000537933	-0.000931616	0.99835	0.9998
ENSG00000154263	ENSG00000154263	ABCA10	17:67143354-67323385	OK	0.711945	0.711168	-0.00157503	-0.000398536	0.9984	0.9998
ENSG00000156026	ENSG00000156026	MCU	10:74451888-74647452	OK	8.27537	8.27906	0.000643214	0.00125418	0.9984	0.9998
ENSG00000168528	ENSG00000168528	SERINC2	1:31882411-31907525	OK	6.84279	6.8463	0.000739675	0.00141148	0.9984	0.9998
ENSG00000141504	ENSG00000141504	SAT2	17:7465191-7536700	OK	71.6775	71.6148	-0.00126171	-0.000528391	0.99845	0.9998
ENSG00000126267	ENSG00000126267	COX6B1	19:36139124-36149763	OK	351.792	351.908	0.000478205	0.00117738	0.9985	0.9998
ENSG00000172977	ENSG00000172977	KAT5	11:65479466-65488418	OK	27.5632	27.5494	-0.000722229	-0.00106104	0.99865	0.9998
ENSG00000077348	ENSG00000077348	EXOSC5	19:41768400-41930910	OK	17.4171	17.398	-0.00158493	-0.000887359	0.9987	0.9998
ENSG00000183604	ENSG00000183604	RP11-347C12.2	16:30234229-30346695	OK	2.03935	2.03859	-0.000537438	-0.00081988	0.99875	0.9998
ENSG00000163661	ENSG00000163661	PTX3	3:156893011-157251408	OK	9.02399	9.02333	-0.00010502	-0.000101069	0.9988	0.9998
ENSG00000162227	ENSG00000162227	TAF6L	11:62538591-62559493	OK	11.1012	11.1061	0.000645249	0.000501863	0.99905	0.9998
ENSG00000242612	ENSG00000242612	DECR2	16:446724-462487	OK	17.0139	16.9994	-0.00122698	-0.000897811	0.99905	0.9998
ENSG00000006468	ENSG00000006468	ETV1	7:13930852-14031050	OK	10.0081	10.0108	0.000391576	0.000510815	0.9991	0.9998
ENSG00000023191	ENSG00000023191	RNH1	11:494511-507300	OK	82.3748	82.3599	-0.000262146	-0.000622094	0.9991	0.9998
ENSG00000166783	ENSG00000166783	KIAA0430	16:15489610-15737023	OK	13.4208	13.4241	0.000359246	0.000570341	0.9991	0.9998
ENSG00000005022	ENSG00000005022	SLC25A5	X:118599996-118605282	OK	580.921	580.801	-0.000297679	-0.000702938	0.99915	0.9998
ENSG00000140395	ENSG00000140395	WDR61	15:78542843-78592136	OK	107.048	107.005	-0.000587378	-0.000632144	0.99935	0.9998
ENSG00000186260	ENSG00000186260	MKL2	16:14165177-14360630	OK	7.94295	7.94044	-0.000455307	-0.000422498	0.9994	0.9998
ENSG00000198356	ENSG00000198356	ASNA1	19:12847952-12859137	OK	102.968	102.982	0.00019046	0.000473532	0.9994	0.9998
ENSG00000143164	ENSG00000143164	DCAF6	1:167885966-168045081	OK	33.2535	33.2469	-0.000286469	-0.0004377	0.99945	0.9998
ENSG00000166170	ENSG00000166170	BAG5	14:104019757-104181841	OK	11.1321	11.1274	-0.000609023	-0.000569157	0.99945	0.9998

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000249673	ENSG00000249673	NOP14-AS1	4:2936625-2965112	OK	4.30573	4.30466	-0.000357648	-0.000284119	0.99945	0.9998
ENSG00000143493	ENSG00000143493	INTS7	1:212113740-212208884	OK	16.2987	16.2955	-0.000282603	-0.000561683	0.9995	0.9998
ENSG00000159592	ENSG00000159592	GPBP1L1	1:46092975-46216322	OK	31.8509	31.8443	-0.000298194	-0.000394483	0.9995	0.9998
ENSG00000254726	ENSG00000254726	MEX3A	1:156041803-156051789	OK	4.80204	4.80114	-0.000271304	-0.000232086	0.9995	0.9998
ENSG00000118363	ENSG00000118363	SPCS2	11:74660291-74690076	OK	68.4211	68.4337	0.000265202	0.000341938	0.99955	0.9998
ENSG00000075415	ENSG00000075415	SLC25A3	12:98987368-98995946	OK	569.978	569.924	-0.000135839	-0.000320594	0.9996	0.9998
ENSG00000147799	ENSG00000147799	ARHGAP39	8:145754562-145911194	OK	2.23499	2.23534	0.000224464	0.000390192	0.9997	0.9998
ENSG00000103343	ENSG00000103343	ZNF174	16:3415098-3627401	OK	5.8523	5.85127	-0.000254235	-0.000201882	0.99975	0.9998
ENSG00000214160	ENSG00000214160	ALG3	3:183851806-184402546	OK	40.6139	40.6301	0.000575223	0.000178758	0.99975	0.9998
ENSG00000155660	ENSG00000155660	PDIA4	7:148700153-148725733	OK	97.4531	97.4507	-3.53E-05	-8.33E-05	0.9998	0.9998
ENSG00000000005	ENSG00000000005	TNMD	X:99839798-99854882	NOTEST	0	0	0	0	1	1
ENSG00000000938	ENSG00000000938	FGR	1:27938574-27961788	NOTEST	0.0129769	0.011877	-0.12777	0	1	1
ENSG00000000971	ENSG00000000971	CFH	1:196621007-196716634	NOTEST	0.332644	0.224573	-0.566795	0	1	1
ENSG00000001561	ENSG00000001561	ENPP4	6:46097729-46114436	NOTEST	0.0192416	0.0376559	0.968649	0	1	1
ENSG00000001626	ENSG00000001626	CFTR	7:117105837-117514193	NOTEST	0.226979	0.554028	1.2874	0	1	1
ENSG00000002079	ENSG00000002079	MYH16	7:98836416-98908753	NOTEST	0.00679936	0.00547121	-0.31354	0	1	1
ENSG00000002587	ENSG00000002587	HS3ST1	4:11394773-11431389	NOTEST	0.20237	0.595499	1.5571	0	1	1
ENSG00000002726	ENSG00000002726	AOC1	7:150521714-150558592	NOTEST	0.00650634	0.0142835	1.13443	0	1	1
ENSG00000002745	ENSG00000002745	WNT16	7:120965420-120981158	NOTEST	0	0	0	0	1	1
ENSG00000002746	ENSG00000002746	HECW1	7:43152197-43605600	NOTEST	0	0.00579598	inf	0	1	1
ENSG00000002933	ENSG00000002933	TMEM176A	7:150488372-150502208	NOTEST	0	0	0	0	1	1
ENSG00000003987	ENSG00000003987	MTMR7	8:17086736-17271037	NOTEST	0.233866	0.434348	0.893166	0	1	1
ENSG00000004468	ENSG00000004468	CD38	4:15779897-15854853	NOTEST	0.00757472	0.00749941	-0.0144152	0	1	1
ENSG00000004776	ENSG00000004776	HSPB6	19:36245466-36248980	NOTEST	0.0193545	0.102712	2.40786	0	1	1
ENSG00000004809	ENSG00000004809	SLC22A16	6:110745889-110797844	NOTEST	0	0	0	0	1	1
ENSG00000004848	ENSG00000004848	ARX	X:25021810-25034065	NOTEST	0.0616582	0.0672074	0.124326	0	1	1
ENSG00000004939	ENSG00000004939	SLC4A1	17:42325752-42355825	NOTEST	0	0	0	0	1	1
ENSG00000004948	ENSG00000004948	CALCR	7:93053798-93204042	NOTEST	0.107106	0.109534	0.0323437	0	1	1
ENSG00000005001	ENSG00000005001	PRSS22	16:2902727-2909727	NOTEST	0.164458	0.0494722	-1.73303	0	1	1
ENSG00000005102	ENSG00000005102	MEOX1	17:41717755-41739322	NOTEST	0	0	0	0	1	1
ENSG00000005108	ENSG00000005108	THSD7A	7:11221358-11871824	NOTEST	0.037411	0.0732441	0.969251	0	1	1
ENSG00000005187	ENSG00000005187	ACSM3	16:20621564-20936328	NOTEST	0.478489	0.118876	-2.00902	0	1	1
ENSG00000005379	ENSG00000005379	BZRAP1	17:56378591-56494956	NOTEST	0.00463733	0.0321027	2.79133	0	1	1
ENSG00000005381	ENSG00000005381	MPO	17:56347216-56358296	NOTEST	0	0	0	0	1	1
ENSG00000005421	ENSG00000005421	PON1	7:94926987-95025680	NOTEST	0	0	0	0	1	1
ENSG00000005513	ENSG00000005513	SOX8	16:1031807-1036979	NOTEST	0.0691894	0.101034	0.546223	0	1	1
ENSG00000005844	ENSG00000005844	ITGAL	16:30483978-30534506	NOTEST	0	0.0023143	inf	0	1	1
ENSG00000005961	ENSG00000005961	ITGA2B	17:42449547-42466873	NOTEST	0.407737	0.217549	-0.906302	0	1	1
ENSG00000006059	ENSG00000006059	KRT33A	17:39502343-39507064	NOTEST	0	0	0	0	1	1
ENSG00000006071	ENSG00000006071	ABCC8	11:17414431-17498449	NOTEST	0	0	0	0	1	1
ENSG00000006074	ENSG00000006074	CCL18	17:34391639-34399392	NOTEST	0.495519	0.145228	-1.77062	0	1	1
ENSG00000006116	ENSG00000006116	CACNG3	16:24266873-24374122	NOTEST	0	0	0	0	1	1
ENSG00000006128	ENSG00000006128	TAC1	7:97361219-97369784	NOTEST	0.110232	0	#NAME?	0	1	1
ENSG00000006283	ENSG00000006283	CACNA1G	17:48633567-48709301	NOTEST	0.0287297	0.0119547	-1.26497	0	1	1
ENSG00000006555	ENSG00000006555	TTC22	1:55245384-55266940	NOTEST	0	0	0	0	1	1
ENSG00000006606	ENSG00000006606	CCL26	7:75398850-75419214	NOTEST	0	0	0	0	1	1
ENSG00000006611	ENSG00000006611	USH1C	11:17515441-17565963	NOTEST	0	0	0	0	1	1
ENSG00000006659	ENSG00000006659	LGALS14	19:40194945-40200084	NOTEST	0	0	0	0	1	1
ENSG00000006740	ENSG00000006740	ARHGAP44	17:12569206-12894960	NOTEST	0.0868308	0.247886	1.5134	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000006788	ENSG00000006788	MYH13	17:10195136-10276447	NOTEST	0.00255017	0	#NAME?	0	1	1
ENSG00000006837	ENSG00000006837	CDKL3	5:133450401-133706738	NOTEST	0.236311	0.18363	-0.363886	0	1	1
ENSG00000007001	ENSG00000007001	UPP2	2:158733213-158992666	NOTEST	0	0.00508077	inf	0	1	1
ENSG00000007129	ENSG00000007129	CEACAM21	19:42051553-42093197	NOTEST	0.0177441	0.0649325	1.8716	0	1	1
ENSG00000007171	ENSG00000007171	NOS2	17:26083791-26221778	NOTEST	0.154388	0.258532	0.743776	0	1	1
ENSG00000007174	ENSG00000007174	DNAH9	17:11501747-11900827	NOTEST	0.113016	0.0676548	-0.740261	0	1	1
ENSG00000007216	ENSG00000007216	SLC13A2	17:26782769-26972472	NOTEST	0	0	0	0	1	1
ENSG00000007264	ENSG00000007264	MATK	19:3777970-3802127	NOTEST	0.00855357	0.0202733	1.24498	0	1	1
ENSG00000007306	ENSG00000007306	CEACAM7	19:42177234-42210895	NOTEST	0	0	0	0	1	1
ENSG00000007314	ENSG00000007314	SCN4A	17:62015913-62050278	NOTEST	0	0	0	0	1	1
ENSG00000007350	ENSG00000007350	TKTL1	X:153524023-153558700	NOTEST	0.449845	0.517317	0.201621	0	1	1
ENSG00000007372	ENSG00000007372	PAX6	11:31806339-32127301	NOTEST	0.205745	0.514258	1.32163	0	1	1
ENSG00000007402	ENSG00000007402	CACNA2D2	3:50384760-50541675	NOTEST	0.175422	0.206378	0.234457	0	1	1
ENSG00000007516	ENSG00000007516	BAIAP3	16:1383601-1401912	NOTEST	0.329841	0.20405	-0.69285	0	1	1
ENSG00000007908	ENSG00000007908	SELE	1:169631244-169863408	NOTEST	0.0384749	0.0334101	-0.203636	0	1	1
ENSG00000007933	ENSG00000007933	FMO3	1:171060017-171086959	NOTEST	0	0	0	0	1	1
ENSG00000007952	ENSG00000007952	NOX1	X:100098312-100129334	NOTEST	0.011392	0.08206	2.84866	0	1	1
ENSG00000008056	ENSG00000008056	SYN1	X:47420515-47479252	NOTEST	0.00495109	0.0119506	1.27126	0	1	1
ENSG00000008118	ENSG00000008118	CAMK1G	1:209757061-209787283	NOTEST	0.0380185	0.0681456	0.841921	0	1	1
ENSG00000008196	ENSG00000008196	TFAP2B	6:50786435-50815326	NOTEST	0.013234	0.00410927	-1.68729	0	1	1
ENSG00000008197	ENSG00000008197	TFAP2D	6:50681540-50740701	NOTEST	0	0	0	0	1	1
ENSG00000008226	ENSG00000008226	DLEC1	3:38080695-38178733	NOTEST	0.0429533	0.0124482	-1.78684	0	1	1
ENSG00000008323	ENSG00000008323	PLEKHG6	12:6419601-6437672	NOTEST	0.111918	0.00833764	-3.74665	0	1	1
ENSG00000008438	ENSG00000008438	PGLYRP1	19:46498338-46526323	NOTEST	0	0.019117	inf	0	1	1
ENSG00000008516	ENSG00000008516	MMP25	16:3096681-3110727	NOTEST	0.0718335	0.119473	0.733956	0	1	1
ENSG00000009694	ENSG00000009694	TENM1	X:123093082-124097666	NOTEST	0.0222124	0.0183123	-0.278549	0	1	1
ENSG00000009709	ENSG00000009709	PAX7	1:18957499-19075360	NOTEST	0	0	0	0	1	1
ENSG00000009724	ENSG00000009724	MASP2	1:11086579-11107290	NOTEST	0.254643	0.2322	-0.133105	0	1	1
ENSG00000009765	ENSG00000009765	IYD	6:150690027-150727105	NOTEST	0.0020224	0	#NAME?	0	1	1
ENSG00000009950	ENSG00000009950	MLXIPL	7:73007523-73038873	NOTEST	0.00948759	0	#NAME?	0	1	1
ENSG00000010030	ENSG00000010030	ETV7	6:36322418-36458920	NOTEST	0.119442	0.0497046	-1.26486	0	1	1
ENSG00000010282	ENSG00000010282	HHATL	3:42734154-42846023	NOTEST	0	0.0278042	inf	0	1	1
ENSG00000010319	ENSG00000010319	SEMA3G	3:52467068-52479101	NOTEST	0.183136	0.153686	-0.252931	0	1	1
ENSG00000010327	ENSG00000010327	STAB1	3:52529353-52742182	NOTEST	0	0.015737	inf	0	1	1
ENSG00000010379	ENSG00000010379	SLC6A13	12:329788-372039	NOTEST	0.109957	0.0436931	-1.33147	0	1	1
ENSG00000010438	ENSG00000010438	PRSS3	9:33750514-33920402	NOTEST	0	0	0	0	1	1
ENSG00000010610	ENSG00000010610	CD4	12:6896023-6929974	NOTEST	0	0.00354257	inf	0	1	1
ENSG00000010932	ENSG00000010932	FMO1	1:171216718-171255117	NOTEST	0	0.00823829	inf	0	1	1
ENSG00000011028	ENSG00000011028	MRC2	17:60704761-60770958	NOTEST	0.077973	0.0422712	-0.8833	0	1	1
ENSG00000011083	ENSG00000011083	SLC6A7	5:149569519-149669854	NOTEST	0	0.00292124	inf	0	1	1
ENSG00000011201	ENSG00000011201	KAL1	X:8496914-8700227	NOTEST	0.122251	0.139663	0.19211	0	1	1
ENSG00000011347	ENSG00000011347	SYT7	11:61282784-61348620	NOTEST	0.428742	0.617306	0.525875	0	1	1
ENSG00000011590	ENSG00000011590	ZBTB32	19:36195428-36207940	NOTEST	0.135646	0.0801089	-0.759814	0	1	1
ENSG00000011600	ENSG00000011600	TYROBP	19:36395302-36399197	NOTEST	0	0	0	0	1	1
ENSG00000012223	ENSG00000012223	LTF	3:46477135-46526724	NOTEST	0.0137251	0	#NAME?	0	1	1

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ENSG00000012504	ENSG00000012504	NR1H4	12:100867485-100958191	NOTEST	0.0259315	0.00791007	-1.71294	0	1	1
ENSG00000012779	ENSG00000012779	ALOX5	10:45869660-45948569	NOTEST	0	0	0	0	1	1
ENSG00000012817	ENSG00000012817	KDM5D	Y:21865750-21906825	NOTEST	0	0	0	0	1	1
ENSG00000013293	ENSG00000013293	SLC7A14	3:170136652-170578169	NOTEST	0.00299041	0	#NAME?	0	1	1
ENSG00000013725	ENSG00000013725	CD6	11:60739114-60787849	NOTEST	0.0361638	0.13755	1.92734	0	1	1
ENSG00000014257	ENSG00000014257	ACPP	3:132036210-132087142	NOTEST	0.0386846	0.0256686	-0.591753	0	1	1
ENSG00000015285	ENSG00000015285	WAS	X:48534984-48549818	NOTEST	0.469919	0.0882884	-2.41212	0	1	1
ENSG00000015413	ENSG00000015413	DPEP1	16:89679715-89704839	NOTEST	0.0106351	0	#NAME?	0	1	1
ENSG00000015520	ENSG00000015520	NPC1L1	7:44552133-44580914	NOTEST	0.00304499	0.00674171	1.14668	0	1	1
ENSG00000015592	ENSG00000015592	STMN4	8:27092839-27115937	NOTEST	0	0	0	0	1	1
ENSG00000016391	ENSG00000016391	CHDH	3:53528682-53880417	NOTEST	0.00198162	0.0175314	3.14519	0	1	1
ENSG00000016402	ENSG00000016402	IL20RA	6:137321107-137366298	NOTEST	0.129554	0.0163941	-2.98231	0	1	1
ENSG00000016490	ENSG00000016490	CLCA1	1:86934050-86965972	NOTEST	0	0	0	0	1	1
ENSG00000016602	ENSG00000016602	CLCA4	1:87012760-87158886	NOTEST	0	0	0	0	1	1
ENSG00000017483	ENSG00000017483	SLC38A5	X:48316919-48328644	NOTEST	0.0732889	0.094576	0.367879	0	1	1
ENSG00000018280	ENSG00000018280	SLC11A1	2:219246751-219261617	NOTEST	0.00403438	0.0176453	2.12886	0	1	1
ENSG00000018607	ENSG00000018607	ZNF806	2:133066881-133076309	NOTEST	0	0	0	0	1	1
ENSG00000018625	ENSG00000018625	ATP1A2	1:160085548-160113381	NOTEST	0	0.0349446	inf	0	1	1
ENSG00000019102	ENSG00000019102	VSIG2	11:124617367-124635832	NOTEST	0	0	0	0	1	1
ENSG00000019169	ENSG00000019169	MARCO	2:119699741-119752236	NOTEST	0	0	0	0	1	1
ENSG00000019186	ENSG00000019186	CYP24A1	20:52769987-52790512	NOTEST	0.00722303	0.104641	3.8567	0	1	1
ENSG00000019505	ENSG00000019505	SYT13	11:45261851-45307870	NOTEST	0	0.236545	inf	0	1	1
ENSG00000019991	ENSG00000019991	HGF	7:81328321-81399754	NOTEST	0.00460378	0.00179064	-1.36234	0	1	1
ENSG00000020219	ENSG00000020219	CCT8L1P	7:152142561-152144235	NOTEST	0	0	0	0	1	1
ENSG00000021461	ENSG00000021461	CYP3A43	7:99425635-99463718	NOTEST	0	0	0	0	1	1
ENSG00000021488	ENSG00000021488	SLC7A9	19:33321414-33360672	NOTEST	0.0488292	0.0655912	0.425759	0	1	1
ENSG00000021645	ENSG00000021645	NRXN3	14:78708733-80330762	NOTEST	0.00662175	0.0116384	0.813613	0	1	1
ENSG00000021852	ENSG00000021852	C8B	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000022355	ENSG00000022355	GABRA1	5:161274196-161326975	NOTEST	0	0	0	0	1	1
ENSG00000022556	ENSG00000022556	NLRP2	19:55434876-55512510	NOTEST	0	0	0	0	1	1
ENSG00000023892	ENSG00000023892	DEF6	6:35265594-35289548	NOTEST	0.129662	0.235965	0.863824	0	1	1
ENSG00000026559	ENSG00000026559	KCNG1	20:49615906-49639666	NOTEST	0	0.0800938	inf	0	1	1
ENSG00000026652	ENSG00000026652	AGPAT4	6:161551010-161695093	NOTEST	0.426435	0.378786	-0.170944	0	1	1
ENSG00000027644	ENSG00000027644	INSRR	1:156776034-156851642	NOTEST	0	0	0	0	1	1
ENSG00000028137	ENSG00000028137	TNFRSF1B	1:12227059-12269285	NOTEST	0.0244209	0.205821	3.0752	0	1	1
ENSG00000028277	ENSG00000028277	POU2F2	19:42590262-42700737	NOTEST	0.148565	0.372054	1.32442	0	1	1
ENSG00000029534	ENSG00000029534	ANK1	8:41510738-41754280	NOTEST	0.0165837	0.0136135	-0.284722	0	1	1
ENSG00000029559	ENSG00000029559	IBSP	4:88720732-88733074	NOTEST	0	0	0	0	1	1
ENSG00000030304	ENSG00000030304	MUSK	9:113431050-113563859	NOTEST	0	0	0	0	1	1
ENSG00000031544	ENSG00000031544	NR2E3	15:72084976-72110600	NOTEST	0.0223278	0	#NAME?	0	1	1
ENSG00000033122	ENSG00000033122	LRRC7	1:70034080-70671303	NOTEST	0.10669	0.128078	0.263598	0	1	1
ENSG00000034239	ENSG00000034239	EFCAB1	8:49623347-49647870	NOTEST	0	0	0	0	1	1
ENSG00000034971	ENSG00000034971	MYOC	1:171604556-171621823	NOTEST	0	0.0179929	inf	0	1	1
ENSG00000035720	ENSG00000035720	STAP1	4:68424445-68473055	NOTEST	0	0	0	0	1	1
ENSG00000036448	ENSG00000036448	MYOM2	8:1993154-2113475	NOTEST	0.0968394	0.0130199	-2.89487	0	1	1

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ENSG00000036473	ENSG00000036473	OTC	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000036530	ENSG00000036530	CYP46A1	14:100150640-100193638	NOTEST	0	0.00735344	inf	0	1	1
ENSG00000036565	ENSG00000036565	SLC18A1	8:20002365-20040717	NOTEST	0.16394	0.119311	-0.458449	0	1	1
ENSG00000036828	ENSG00000036828	CASR	3:121902529-122005342	NOTEST	0	0	0	0	1	1
ENSG00000037280	ENSG00000037280	FLT4	5:180028505-180076624	NOTEST	0.00510978	0	#NAME?	0	1	1
ENSG00000038295	ENSG00000038295	TLL1	4:166794409-167025047	NOTEST	0	0	0	0	1	1
ENSG00000038427	ENSG00000038427	VCAN	5:82767283-82878122	NOTEST	0.0265239	0.037678	0.50643	0	1	1
ENSG00000038945	ENSG00000038945	MSR1	8:15965386-16424999	NOTEST	0	0	0	0	1	1
ENSG00000039139	ENSG00000039139	DNAH5	5:13690439-13944652	NOTEST	0.0872805	0.126145	0.531352	0	1	1
ENSG00000039537	ENSG00000039537	C6	5:41142335-41261540	NOTEST	0	0	0	0	1	1
ENSG00000039600	ENSG00000039600	SOX30	5:157052686-157098488	NOTEST	0	0.00409727	inf	0	1	1
ENSG00000039987	ENSG00000039987	BEST2	19:12862515-12869272	NOTEST	0	0	0	0	1	1
ENSG00000040731	ENSG00000040731	CDH10	5:24487208-24645087	NOTEST	0.0986362	0.144671	0.55259	0	1	1
ENSG00000041353	ENSG00000041353	RAB27B	18:52385090-52565314	NOTEST	0.00208864	0.00146505	-0.511616	0	1	1
ENSG00000041515	ENSG00000041515	MYO16	13:109248499-109860355	NOTEST	0.271245	0.521887	0.944144	0	1	1
ENSG00000042062	ENSG00000042062	FAM65C	20:49202644-49308065	NOTEST	0.023459	0.0650266	1.47089	0	1	1
ENSG00000042304	ENSG00000042304	C2orf83	2:228474805-228513322	NOTEST	0	0	0	0	1	1
ENSG00000042781	ENSG00000042781	USH2A	1:215796235-216596738	NOTEST	0.0295315	0.0592999	1.00577	0	1	1
ENSG00000042813	ENSG00000042813	ZPBP	7:49813256-50199426	NOTEST	0	0	0	0	1	1
ENSG00000042832	ENSG00000042832	TG	8:133879202-134147147	NOTEST	0.00182892	0	#NAME?	0	1	1
ENSG00000042980	ENSG00000042980	ADAM28	8:24151552-24769586	NOTEST	0.0925727	0.0703891	-0.395235	0	1	1
ENSG00000043039	ENSG00000043039	BARX2	11:129245834-129322171	NOTEST	0	0.00972488	inf	0	1	1
ENSG00000043591	ENSG00000043591	ADRB1	10:115803805-115806667	NOTEST	0.0375697	0.0907343	1.27208	0	1	1
ENSG00000044012	ENSG00000044012	GUCA2B	1:42619091-42621495	NOTEST	0	0	0	0	1	1
ENSG00000046889	ENSG00000046889	PREX2	8:68864352-69149265	NOTEST	0	0	0	0	1	1
ENSG00000047457	ENSG00000047457	CP	3:148847370-148939842	NOTEST	0.160295	0.139401	-0.201489	0	1	1
ENSG00000047597	ENSG00000047597	XK	X:37208527-38548169	NOTEST	0.0992019	0.145382	0.551411	0	1	1
ENSG00000047617	ENSG00000047617	ANO2	12:5641034-6055398	NOTEST	0.179322	0.221407	0.304154	0	1	1
ENSG00000047648	ENSG00000047648	ARHGAP6	X:11129420-11683821	NOTEST	0.0841425	0.233701	1.47376	0	1	1
ENSG00000047662	ENSG00000047662	FAM184B	4:17616253-17783135	NOTEST	0.0296403	0.109734	1.88838	0	1	1
ENSG00000047936	ENSG00000047936	ROS1	6:117609462-117923691	NOTEST	0	0	0	0	1	1
ENSG00000048462	ENSG00000048462	TNFRSF17	16:12021229-12070500	NOTEST	0	0.0721803	inf	0	1	1
ENSG00000048540	ENSG00000048540	LMO3	12:16500075-16763528	NOTEST	0.24887	0.255401	0.0373719	0	1	1
ENSG00000048545	ENSG00000048545	GUCA1A	6:42123143-42147794	NOTEST	0	0	0	0	1	1
ENSG00000049192	ENSG00000049192	ADAMTS6	5:64444562-64777747	NOTEST	0.156229	0.164286	0.0725476	0	1	1
ENSG00000049247	ENSG00000049247	UTS2	1:7844379-7913572	NOTEST	0	0.0304463	inf	0	1	1
ENSG00000049249	ENSG00000049249	TNFRSF9	1:7979906-8000926	NOTEST	0.0524918	0.148758	1.50281	0	1	1
ENSG00000049283	ENSG00000049283	EPN3	17:48609903-48633213	NOTEST	0.0737721	0.187974	1.34938	0	1	1
ENSG00000049319	ENSG00000049319	SRD5A2	2:31747549-31806136	NOTEST	0.00674115	0.00997246	0.564956	0	1	1
ENSG00000049540	ENSG00000049540	ELN	7:73442118-73484237	NOTEST	0.00586434	0.0797433	3.76532	0	1	1
ENSG00000049768	ENSG00000049768	FOXP3	X:49091926-49121288	NOTEST	0.0635541	0.119616	0.912355	0	1	1
ENSG00000050030	ENSG00000050030	KIAA2022	X:73952683-74145282	NOTEST	0	0	0	0	1	1
ENSG00000050555	ENSG00000050555	LAMC3	9:133884468-133969860	NOTEST	0.333179	0.403097	0.27483	0	1	1
ENSG00000050628	ENSG00000050628	PTGER3	1:71318035-71513491	NOTEST	0.153868	0.171465	0.156215	0	1	1
ENSG00000050730	ENSG00000050730	TNIP3	4:122052562-122148621	NOTEST	0	0.0209754	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000050767	ENSG00000050767	COL23A1	5:177664618-178017556	NOTEST	0	0	0	0	1	1
ENSG00000052344	ENSG00000052344	PRSS8	16:31142753-31147083	NOTEST	0	0.0416439	inf	0	1	1
ENSG00000052850	ENSG00000052850	ALX4	11:44281993-44331716	NOTEST	0.0170661	0.0220082	0.36691	0	1	1
ENSG00000053108	ENSG00000053108	FSTL4	5:132496129-132948255	NOTEST	0.478876	0.473156	-0.0173385	0	1	1
ENSG00000053328	ENSG00000053328	METTL24	6:110501343-110679475	NOTEST	0	0	0	0	1	1
ENSG00000053747	ENSG00000053747	LAMA3	18:21269406-21535030	NOTEST	0.308444	0.189699	-0.701293	0	1	1
ENSG00000053918	ENSG00000053918	KCNQ1	11:2465913-2882798	NOTEST	0	0.011643	inf	0	1	1
ENSG00000054179	ENSG00000054179	ENTPD2	9:139942549-139948497	NOTEST	0.0202885	0.0608033	1.58349	0	1	1
ENSG00000054219	ENSG00000054219	LY75	2:160568999-160761260	NOTEST	0.126458	0.085177	-0.570126	0	1	1
ENSG00000054356	ENSG00000054356	PTPRN	2:220154344-220174370	NOTEST	0.0712344	0.0140392	-2.34311	0	1	1
ENSG00000054796	ENSG00000054796	SPO11	20:55904814-55919050	NOTEST	0	0	0	0	1	1
ENSG00000054803	ENSG00000054803	CBLN4	20:54572495-54580528	NOTEST	0	0	0	0	1	1
ENSG00000054938	ENSG00000054938	CHRDL2	11:74407473-74442430	NOTEST	0	0	0	0	1	1
ENSG00000055118	ENSG00000055118	KCNH2	7:150642048-150675403	NOTEST	0.0136584	0.0644709	2.23886	0	1	1
ENSG00000055813	ENSG00000055813	CCDC85A	2:56179292-56613308	NOTEST	0.0608748	0.221263	1.86184	0	1	1
ENSG00000055955	ENSG00000055955	ITIH4	3:52846990-52931612	NOTEST	0.0897862	0.134547	0.583549	0	1	1
ENSG00000055957	ENSG00000055957	ITIH1	3:52811602-52826078	NOTEST	0.0284507	0.0510079	0.842257	0	1	1
ENSG00000056291	ENSG00000056291	NPFFR2	4:72897520-73013784	NOTEST	0.0270362	0.0967656	1.8396	0	1	1
ENSG00000056487	ENSG00000056487	PHF21B	22:45277041-45405880	NOTEST	0.137209	0.186494	0.442754	0	1	1
ENSG00000056678	ENSG00000056678	KIFC1	HSCHR6_MHC_MCF:33529671-33530001	NOTEST	0	0	0	0	1	1
ENSG00000056736	ENSG00000056736	IL17RB	3:53880606-53899827	NOTEST	0.368393	0.346637	-0.0878185	0	1	1
ENSG00000057149	ENSG00000057149	SERPINB3	18:61314812-61391127	NOTEST	0	0	0	0	1	1
ENSG00000057294	ENSG00000057294	PKP2	12:32943678-33049774	NOTEST	0	0.00850029	inf	0	1	1
ENSG00000057468	ENSG00000057468	MSH4	1:76262566-76378923	NOTEST	0.0317333	0.0441182	0.475377	0	1	1
ENSG00000057593	ENSG00000057593	F7	13:113760104-113774995	NOTEST	0	0	0	0	1	1
ENSG00000057657	ENSG00000057657	PRDM1	6:106534194-106557814	NOTEST	0.0813231	0.0482009	-0.754604	0	1	1
ENSG00000058085	ENSG00000058085	LAMC2	1:183155372-183214035	NOTEST	0.0304951	0.102966	1.75551	0	1	1
ENSG00000058404	ENSG00000058404	CAMK2B	7:44256748-44374176	NOTEST	0.00716057	0.177044	4.62789	0	1	1
ENSG00000060303	ENSG00000060303	RPS17P5	6:50824967-50825375	NOTEST	0	0	0	0	1	1
ENSG00000060558	ENSG00000060558	GNA15	19:3136190-3163767	NOTEST	0.0674033	0.0347636	-0.955242	0	1	1
ENSG00000060566	ENSG00000060566	CREB3L3	19:4153597-4173051	NOTEST	0	0	0	0	1	1
ENSG00000060709	ENSG00000060709	RIMBP2	12:130880681-131200826	NOTEST	0	0	0	0	1	1
ENSG00000060718	ENSG00000060718	COL11A1	1:103342022-103574052	NOTEST	0.0169377	0.0368442	1.1212	0	1	1
ENSG00000060982	ENSG00000060982	BCAT1	12:24964294-25113092	NOTEST	0.112858	0.233493	1.04887	0	1	1
ENSG00000061455	ENSG00000061455	PRDM6	5:122422942-122529960	NOTEST	0.0851474	0	#NAME?	0	1	1
ENSG00000061492	ENSG00000061492	WNT8A	5:137419580-137428054	NOTEST	0	0	0	0	1	1
ENSG00000062096	ENSG00000062096	ARSF	X:2959511-3030767	NOTEST	0	0	0	0	1	1
ENSG00000062524	ENSG00000062524	LTK	15:41795835-41806085	NOTEST	0	0	0	0	1	1
ENSG00000063015	ENSG00000063015	SEZ6	17:27232267-27384234	NOTEST	0.1234	0.0789928	-0.643553	0	1	1
ENSG00000063127	ENSG00000063127	SLC6A16	19:49792894-49828482	NOTEST	0.373271	0.26464	-0.496192	0	1	1
ENSG00000063515	ENSG00000063515	GSC2	22:19136088-19137796	NOTEST	0	0	0	0	1	1
ENSG00000064195	ENSG00000064195	DLX3	17:48067368-48072588	NOTEST	0	0.0405156	inf	0	1	1
ENSG00000064201	ENSG00000064201	TSPAN32	11:2316874-2339430	NOTEST	0.0510834	0.0456129	-0.163413	0	1	1
ENSG00000064218	ENSG00000064218	DMRT3	9:976963-991731	NOTEST	0	0	0	0	1	1
ENSG00000064270	ENSG00000064270	ATP2C2	16:84402132-84500967	NOTEST	0.00463022	0.174029	5.2321	0	1	1

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ENSG00000064655	ENSG00000064655	EYA2	20:45523262-45817492	NOTEST	0	0	0	0	1	1
ENSG00000064692	ENSG00000064692	SNCAIP	5:121646991-121814782	NOTEST	0.140165	0.102902	-0.44585	0	1	1
ENSG00000064787	ENSG00000064787	BCAS1	20:52553315-52687304	NOTEST	0.0495651	0.0805059	0.699769	0	1	1
ENSG00000064835	ENSG00000064835	POU1F1	3:87308553-87325737	NOTEST	0	0	0	0	1	1
ENSG00000064886	ENSG00000064886	CHI3L2	1:111729795-111786062	NOTEST	0.276094	0.536938	0.959597	0	1	1
ENSG00000064989	ENSG00000064989	CALCRL	2:187866602-188430487	NOTEST	0.16534	0.27289	0.72288	0	1	1
ENSG00000065325	ENSG00000065325	GLP2R	17:9725522-9795419	NOTEST	0	0	0	0	1	1
ENSG00000065609	ENSG00000065609	SNAP91	6:84262598-84419410	NOTEST	0	0	0	0	1	1
ENSG00000065618	ENSG00000065618	COL17A1	10:105791043-105845760	NOTEST	0.00279187	0	#NAME?	0	1	1
ENSG00000065675	ENSG00000065675	PRKCQ	10:6469104-6622263	NOTEST	0	0	0	0	1	1
ENSG00000065717	ENSG00000065717	TLE2	19:2997635-3047633	NOTEST	0.0871564	0.0512436	-0.766233	0	1	1
ENSG00000066056	ENSG00000066056	TIE1	1:43766663-43788779	NOTEST	0.150719	0.173382	0.202092	0	1	1
ENSG00000066248	ENSG00000066248	NGEF	2:233562008-233880595	NOTEST	0.0742143	0	#NAME?	0	1	1
ENSG00000066294	ENSG00000066294	CD84	1:160506862-160549306	NOTEST	0	0.00463792	inf	0	1	1
ENSG00000066336	ENSG00000066336	SPI1	11:47376410-47400127	NOTEST	0.0506808	0.0464503	-0.125752	0	1	1
ENSG00000066405	ENSG00000066405	CLDN18	3:137717576-137752494	NOTEST	0.0832425	0.0630615	-0.400561	0	1	1
ENSG00000066468	ENSG00000066468	FGFR2	10:123237847-123357972	NOTEST	0	0.0119409	inf	0	1	1
ENSG00000066735	ENSG00000066735	KIF26A	14:104605059-104647231	NOTEST	0.0494184	0.0306826	-0.687629	0	1	1
ENSG00000066813	ENSG00000066813	ACSM2B	16:20547547-20587749	NOTEST	0	0	0	0	1	1
ENSG00000067048	ENSG00000067048	DDX3Y	Y:15016018-15032390	NOTEST	0	0	0	0	1	1
ENSG00000067177	ENSG00000067177	PHKA1	X:71798663-71934167	NOTEST	0.31436	0.483989	0.622554	0	1	1
ENSG00000067646	ENSG00000067646	ZFY	Y:2803111-2870667	NOTEST	0	0	0	0	1	1
ENSG00000067715	ENSG00000067715	SYT1	12:79257772-79897176	NOTEST	0.100902	0.187061	0.890552	0	1	1
ENSG00000067842	ENSG00000067842	ATP2B3	X:152783133-152848397	NOTEST	0	0	0	0	1	1
ENSG00000068078	ENSG00000068078	FGFR3	4:1795033-1810599	NOTEST	0.0150566	0.146897	3.28633	0	1	1
ENSG00000068615	ENSG00000068615	REEP1	2:86441115-86565206	NOTEST	0.0685349	0.152978	1.15841	0	1	1
ENSG00000068781	ENSG00000068781	STON1-GTF2A1L	2:48756521-49003654	NOTEST	0.0454921	0.0236181	-0.945725	0	1	1
ENSG00000068831	ENSG00000068831	RASGRP2	11:64494382-64512928	NOTEST	0	0.088874	inf	0	1	1
ENSG00000068976	ENSG00000068976	PYGM	11:64513860-64527769	NOTEST	0.0135726	0	#NAME?	0	1	1
ENSG00000068985	ENSG00000068985	PAGE1	X:49452052-49460596	NOTEST	0.0553945	0	#NAME?	0	1	1
ENSG00000069011	ENSG00000069011	PITX1	5:134363424-134736986	NOTEST	0	0	0	0	1	1
ENSG00000069018	ENSG00000069018	TRPC7	5:135712035-135732730	NOTEST	0	0	0	0	1	1
ENSG00000069122	ENSG00000069122	GPR116	6:46820248-46922680	NOTEST	0	0.00976527	inf	0	1	1
ENSG00000069188	ENSG00000069188	SDK2	17:71330522-71640228	NOTEST	0.0186182	0.0375431	1.01183	0	1	1
ENSG00000069206	ENSG00000069206	ADAM7	8:24151552-24769586	NOTEST	0	0	0	0	1	1
ENSG00000069431	ENSG00000069431	ABCC9	12:21950334-22094336	NOTEST	0.00329597	0	#NAME?	0	1	1
ENSG00000069482	ENSG00000069482	GAL	11:68451246-68458643	NOTEST	0.0229574	0.358553	3.96515	0	1	1
ENSG00000069535	ENSG00000069535	MAOB	X:43625857-43741693	NOTEST	0.141701	0.154985	0.129276	0	1	1
ENSG00000069667	ENSG00000069667	RORA	15:60771376-61521518	NOTEST	0.275095	0.268661	-0.0341433	0	1	1
ENSG00000069696	ENSG00000069696	DRD4	11:637292-640706	NOTEST	0.114333	0.215574	0.914944	0	1	1
ENSG00000069712	ENSG00000069712	KIAA1107	1:92632541-92650280	NOTEST	0.570423	0.321842	-0.82568	0	1	1
ENSG00000069764	ENSG00000069764	PLA2G10	16:14766404-14788526	NOTEST	0	0.0862779	inf	0	1	1
ENSG00000069812	ENSG00000069812	HES2	1:6472477-6484730	NOTEST	0.252464	0.374368	0.56838	0	1	1
ENSG00000070019	ENSG00000070019	GUCY2C	12:14656594-14910897	NOTEST	0	0	0	0	1	1
ENSG00000070031	ENSG00000070031	SCT	11:626430-627143	NOTEST	0	0.0593188	inf	0	1	1

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ENSG00000070190	ENSG00000070190	DAPP1	4:100737989-100791311	NOTEST	0.0104181	0.0282216	1.43771	0	1	1
ENSG00000070193	ENSG00000070193	FGF10	5:44303645-44414091	NOTEST	0.0146895	0.0332457	1.17839	0	1	1
ENSG00000070388	ENSG00000070388	FGF22	19:639878-643703	NOTEST	0.184391	0.221591	0.265129	0	1	1
ENSG00000070601	ENSG00000070601	FRMPD1	9:37510888-38069210	NOTEST	0.0252678	0.0586097	1.21384	0	1	1
ENSG00000070729	ENSG00000070729	CNGB1	16:57917502-58005020	NOTEST	0	0	0	0	1	1
ENSG00000070748	ENSG00000070748	CHAT	10:50817140-50918307	NOTEST	0	0	0	0	1	1
ENSG00000070886	ENSG00000070886	EPHA8	1:22890056-22930087	NOTEST	0.0521323	0.253599	2.2823	0	1	1
ENSG00000070915	ENSG00000070915	SLC12A3	16:56899118-56949762	NOTEST	0	0	0	0	1	1
ENSG00000070985	ENSG00000070985	TRPM5	11:2425744-2444275	NOTEST	0	0	0	0	1	1
ENSG00000071203	ENSG00000071203	MS4A12	11:60260250-60274903	NOTEST	0	0	0	0	1	1
ENSG00000071677	ENSG00000071677	PRLH	2:238475216-238475818	NOTEST	0	0	0	0	1	1
ENSG00000071909	ENSG00000071909	MYO3B	2:171034654-171551884	NOTEST	0.101729	0.0722306	-0.494043	0	1	1
ENSG00000072080	ENSG00000072080	SPP2	2:234959322-234985778	NOTEST	0.070566	0.0504801	-0.483259	0	1	1
ENSG00000072133	ENSG00000072133	RPS6KA6	X:83318983-83442933	NOTEST	0.00632385	0	#NAME?	0	1	1
ENSG00000072201	ENSG00000072201	LNX1	4:54243809-55164414	NOTEST	0.326004	0.327994	0.00877861	0	1	1
ENSG00000072315	ENSG00000072315	TRPC5	X:111017542-111326004	NOTEST	0.00262003	0	#NAME?	0	1	1
ENSG00000072444	ENSG00000072444	ASAH2C	10:48001602-48055018	NOTEST	0	0	0	0	1	1
ENSG00000072657	ENSG00000072657	TRHDE	12:72332625-73059422	NOTEST	0.066966	0.0236349	-1.50251	0	1	1
ENSG00000072818	ENSG00000072818	ACAP1	17:7239847-7254797	NOTEST	0.442798	0.434589	-0.0269971	0	1	1
ENSG00000072952	ENSG00000072952	MRVI1	11:10562818-10715535	NOTEST	0	0.0143142	inf	0	1	1
ENSG00000073067	ENSG00000073067	CYP2W1	7:1022834-1029276	NOTEST	0.0195513	0.0348364	0.833329	0	1	1
ENSG00000073146	ENSG00000073146	MOV10L1	22:50528307-50600119	NOTEST	0	0	0	0	1	1
ENSG00000073150	ENSG00000073150	PANX2	22:50609159-50618723	NOTEST	0.129099	0.105235	-0.294869	0	1	1
ENSG00000073282	ENSG00000073282	TP63	3:189349204-189615068	NOTEST	0.0179938	0.00232076	-2.95483	0	1	1
ENSG00000073598	ENSG00000073598	FNDC8	17:33448597-33469334	NOTEST	0	0	0	0	1	1
ENSG00000073734	ENSG00000073734	ABCB11	2:169779447-169887832	NOTEST	0	0	0	0	1	1
ENSG00000073737	ENSG00000073737	DHRS9	2:169921298-169952677	NOTEST	0.0120595	0	#NAME?	0	1	1
ENSG00000073754	ENSG00000073754	CD5L	1:157800703-157868046	NOTEST	0.0413221	0.0384436	-0.104171	0	1	1
ENSG00000073756	ENSG00000073756	PTGS2	1:186640922-186649559	NOTEST	0.518478	0.219951	-1.2371	0	1	1
ENSG00000073861	ENSG00000073861	TBX21	17:45810609-45823485	NOTEST	0	0	0	0	1	1
ENSG00000074047	ENSG00000074047	GLI2	2:121493198-121750229	NOTEST	0.0650794	0.143557	1.14135	0	1	1
ENSG00000074181	ENSG00000074181	NOTCH3	19:15270443-15311792	NOTEST	0.146167	0.561882	1.94265	0	1	1
ENSG00000074211	ENSG00000074211	PPP2R2C	4:6322304-6565327	NOTEST	0	0	0	0	1	1
ENSG00000074276	ENSG00000074276	CDHR2	5:175969511-176037134	NOTEST	0.372105	0.251186	-0.566957	0	1	1
ENSG00000074370	ENSG00000074370	ATP2A3	17:3827168-3867736	NOTEST	0.23075	0.212616	-0.118082	0	1	1
ENSG00000074410	ENSG00000074410	CA12	15:63613576-63674360	NOTEST	0.0229419	0.0171821	-0.417083	0	1	1
ENSG00000074416	ENSG00000074416	MGLL	3:127407908-127542051	NOTEST	0.267368	0.368812	0.464057	0	1	1
ENSG00000074590	ENSG00000074590	NUAK1	12:106457117-106533811	NOTEST	0.107887	0.183036	0.762604	0	1	1
ENSG00000074660	ENSG00000074660	SCARF1	17:1537151-1549041	NOTEST	0.0363407	0.0281157	-0.370211	0	1	1
ENSG00000074706	ENSG00000074706	IPCEF1	6:154331630-154677926	NOTEST	0	0	0	0	1	1
ENSG00000074771	ENSG00000074771	NOX3	6:155716503-155777037	NOTEST	0.0143754	0.0684756	2.25199	0	1	1
ENSG00000074803	ENSG00000074803	SLC12A1	15:48481233-48596275	NOTEST	0.210717	0.0651743	-1.69293	0	1	1
ENSG00000074966	ENSG00000074966	TXK	4:48068409-48136273	NOTEST	0.0398942	0.0862085	1.11165	0	1	1
ENSG00000075035	ENSG00000075035	WSCD2	12:108523247-108644314	NOTEST	0	0	0	0	1	1
ENSG00000075043	ENSG00000075043	KCNQ2	20:62037541-62103993	NOTEST	0	0	0	0	1	1

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ENSG00000075290	ENSG00000075290	WNT8B	10:102222797-102243501	NOTEST	0.0277079	0.0168001	-0.721827	0	1	1
ENSG00000075340	ENSG00000075340	ADD2	2:70834749-70995357	NOTEST	0.12489	0.155633	0.317489	0	1	1
ENSG00000075388	ENSG00000075388	FGF4	11:69587796-69590171	NOTEST	0	0	0	0	1	1
ENSG00000075429	ENSG00000075429	CACNG5	17:64831234-64881603	NOTEST	0	0	0	0	1	1
ENSG00000075461	ENSG00000075461	CACNG4	17:64961025-65029514	NOTEST	0	0.00324851	inf	0	1	1
ENSG00000075673	ENSG00000075673	ATP12A	13:25254548-25285921	NOTEST	0.0556271	0.032004	-0.797534	0	1	1
ENSG00000075886	ENSG00000075886	TUBA3D	2:132222472-132250316	NOTEST	0.0432137	0	#NAME?	0	1	1
ENSG00000075891	ENSG00000075891	PAX2	10:102495359-102589698	NOTEST	0	0	0	0	1	1
ENSG00000076344	ENSG00000076344	RGS11	16:284544-333003	NOTEST	0.341052	0.347962	0.0289345	0	1	1
ENSG00000076826	ENSG00000076826	CAMSAP3	19:7660787-7683190	NOTEST	0	0.0245484	inf	0	1	1
ENSG00000077080	ENSG00000077080	ACTL6B	7:100240719-100254084	NOTEST	0	0	0	0	1	1
ENSG00000077238	ENSG00000077238	IL4R	16:27324988-27376099	NOTEST	0.126743	0.358934	1.50182	0	1	1
ENSG00000077264	ENSG00000077264	PAK3	X:110187512-110470589	NOTEST	0.195232	0.354982	0.862553	0	1	1
ENSG00000077274	ENSG00000077274	CAPN6	X:110488330-110513751	NOTEST	0	0	0	0	1	1
ENSG00000077279	ENSG00000077279	DCX	X:110537006-110655603	NOTEST	0	0.00512561	inf	0	1	1
ENSG00000077327	ENSG00000077327	SPAG6	10:22634398-22743153	NOTEST	0.0493662	0	#NAME?	0	1	1
ENSG00000077420	ENSG00000077420	APBB1IP	10:26727131-26856732	NOTEST	0	0	0	0	1	1
ENSG00000077522	ENSG00000077522	ACTN2	1:236849753-236927931	NOTEST	0.00814626	0	#NAME?	0	1	1
ENSG00000077616	ENSG00000077616	NAALAD2	11:89864682-89926062	NOTEST	0.0402741	0.100109	1.31365	0	1	1
ENSG00000077782	ENSG00000077782	FGFR1	8:38268655-38326352	NOTEST	0.190201	0.680545	1.83916	0	1	1
ENSG00000077800	ENSG00000077800	FKBP6	7:72742166-72772634	NOTEST	0.0116424	0.00905039	-0.363333	0	1	1
ENSG00000077935	ENSG00000077935	SMC1B	22:45739943-45809500	NOTEST	0.106444	0.0374019	-1.50891	0	1	1
ENSG00000077943	ENSG00000077943	ITGA8	10:15555947-15762124	NOTEST	0	0.00543469	inf	0	1	1
ENSG00000077984	ENSG00000077984	CST7	20:24929865-24940564	NOTEST	0.133782	0.318165	1.24989	0	1	1
ENSG00000078053	ENSG00000078053	AMPH	7:38423304-38671167	NOTEST	0	0.00350558	inf	0	1	1
ENSG00000078114	ENSG00000078114	NEBL	10:21068901-21463977	NOTEST	0.0634887	0.182854	1.52612	0	1	1
ENSG00000078328	ENSG00000078328	RBFOX1	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000078399	ENSG00000078399	HOXA9	7:27202053-27219880	NOTEST	0.111972	0.425617	1.92641	0	1	1
ENSG00000078401	ENSG00000078401	EDN1	6:12290595-12297427	NOTEST	0.0144453	0	#NAME?	0	1	1
ENSG00000078549	ENSG00000078549	ADCYAP1R1	7:31092075-31151089	NOTEST	0.0086445	0.0230496	1.41488	0	1	1
ENSG00000078579	ENSG00000078579	FGF20	8:16849677-16859690	NOTEST	0.0177555	0.0440265	1.31011	0	1	1
ENSG00000078589	ENSG00000078589	P2RY10	X:78200828-78217451	NOTEST	0	0	0	0	1	1
ENSG00000078596	ENSG00000078596	ITM2A	X:78615880-78623164	NOTEST	0.0383762	0.0369946	-0.052897	0	1	1
ENSG00000078725	ENSG00000078725	BRINP1	9:121915735-122131745	NOTEST	0.0101029	0	#NAME?	0	1	1
ENSG00000078795	ENSG00000078795	PKD2L2	5:137150021-137387650	NOTEST	0.107082	0.149849	0.484791	0	1	1
ENSG00000078898	ENSG00000078898	BPIFB2	20:31595405-31611515	NOTEST	0	0	0	0	1	1
ENSG00000078900	ENSG00000078900	TP73	1:3547330-3663900	NOTEST	0.0351973	0.163524	2.21597	0	1	1
ENSG00000079101	ENSG00000079101	CLUL1	18:596987-712676	NOTEST	0.175959	0.485994	1.4657	0	1	1
ENSG00000079102	ENSG00000079102	RUNX1T1	8:92967202-93115514	NOTEST	0.0543461	0.0130033	-2.0633	0	1	1
ENSG00000079112	ENSG00000079112	CDH17	8:95139398-95229531	NOTEST	0	0	0	0	1	1
ENSG00000079263	ENSG00000079263	SP140	2:230990025-231268447	NOTEST	0.0285441	0.157406	2.46323	0	1	1
ENSG00000079393	ENSG00000079393	DUSP13	10:76854191-76941881	NOTEST	0	0.152148	inf	0	1	1
ENSG00000079557	ENSG00000079557	AFM	4:74347399-74369691	NOTEST	0	0	0	0	1	1
ENSG00000079689	ENSG00000079689	SCGN	6:25652463-25702011	NOTEST	0	0.00904642	inf	0	1	1
ENSG00000079841	ENSG00000079841	RIMS1	6:72596405-73112845	NOTEST	0	0.00153891	inf	0	1	1

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ENSG00000080293	ENSG00000080293	SCTR	2:120197418-120282070	NOTEST	0.0158869	0	#NAME?	0	1	1
ENSG00000080493	ENSG00000080493	SLC4A4	4:72053002-72437804	NOTEST	0.545465	0.554034	0.0224881	0	1	1
ENSG00000080511	ENSG00000080511	RDH8	19:10123924-10132955	NOTEST	0.299181	0.638335	1.0933	0	1	1
ENSG00000080561	ENSG00000080561	MID2	X:107068984-107179210	NOTEST	0	0.0228853	inf	0	1	1
ENSG00000080572	ENSG00000080572	PIH1D3	X:106449861-106487473	NOTEST	0	0	0	0	1	1
ENSG00000080573	ENSG00000080573	COL5A3	19:10070236-10121147	NOTEST	0.220875	0.376446	0.769215	0	1	1
ENSG00000080644	ENSG00000080644	CHRNA3	15:78857861-78913637	NOTEST	0.0539368	0.264629	2.29463	0	1	1
ENSG00000080854	ENSG00000080854	IGSF9B	11:133778458-133826880	NOTEST	0.0283653	0	#NAME?	0	1	1
ENSG00000080910	ENSG00000080910	CFHR2	1:196788886-196928356	NOTEST	0	0	0	0	1	1
ENSG00000081051	ENSG00000081051	AFP	4:74296854-74321891	NOTEST	0	0	0	0	1	1
ENSG00000081052	ENSG00000081052	COL4A4	2:227867426-228028829	NOTEST	0.116874	0.150161	0.361557	0	1	1
ENSG00000081148	ENSG00000081148	IMPG2	3:100941389-101039404	NOTEST	0.129548	0.175367	0.436899	0	1	1
ENSG00000081237	ENSG00000081237	PTPRC	1:198607800-198726545	NOTEST	0.245763	0.199676	-0.299609	0	1	1
ENSG00000081248	ENSG00000081248	CACNA1S	1:201004223-201081694	NOTEST	0.00254862	0.0017882	-0.511206	0	1	1
ENSG00000081277	ENSG00000081277	PKP1	1:201252579-201302121	NOTEST	0	0.0199482	inf	0	1	1
ENSG00000081800	ENSG00000081800	SLC13A1	7:122753584-122840040	NOTEST	0	0	0	0	1	1
ENSG00000081818	ENSG00000081818	PCDHB4	5:140501580-140505201	NOTEST	0.161198	0.21317	0.403175	0	1	1
ENSG00000081842	ENSG00000081842	PCDHA6	5:140165875-140391936	NOTEST	0.0807986	0.0597456	-0.435498	0	1	1
ENSG00000081923	ENSG00000081923	ATP8B1	18:55297533-55470333	NOTEST	0.0273536	0.0620402	1.18147	0	1	1
ENSG00000082126	ENSG00000082126	MPP4	2:202509592-202563417	NOTEST	0.0509331	0.0512805	0.00980527	0	1	1
ENSG00000082175	ENSG00000082175	PGR	11:100900354-101001255	NOTEST	0	0.00263521	inf	0	1	1
ENSG00000082556	ENSG00000082556	OPRK1	8:54090130-54164257	NOTEST	0	0	0	0	1	1
ENSG00000082684	ENSG00000082684	SEMA5B	3:122628040-122747452	NOTEST	0.014815	0	#NAME?	0	1	1
ENSG00000082929	ENSG00000082929	C4orf6	4:5526295-5529528	NOTEST	0	0	0	0	1	1
ENSG00000083067	ENSG00000083067	TRPM3	9:73143978-74061820	NOTEST	0.330331	0.625922	0.922069	0	1	1
ENSG00000083307	ENSG00000083307	GRHL2	8:102473404-102681954	NOTEST	0	0	0	0	1	1
ENSG00000083622	ENSG00000083622	AC000111.6	7:117105837-117514193	NOTEST	0	0	0	0	1	1
ENSG00000083782	ENSG00000083782	EPYC	12:91357455-91398803	NOTEST	0.0657932	0.024583	-1.42028	0	1	1
ENSG00000084110	ENSG00000084110	HAL	12:96366439-96390143	NOTEST	0.0771812	0	#NAME?	0	1	1
ENSG00000084453	ENSG00000084453	SLCO1A2	12:21417533-21572528	NOTEST	0.0417949	0.0295872	-0.498352	0	1	1
ENSG00000084628	ENSG00000084628	NKAIN1	1:31652591-31712401	NOTEST	0.139377	0.164111	0.235674	0	1	1
ENSG00000084674	ENSG00000084674	APOB	2:21224300-21266945	NOTEST	0.00106452	0.0074273	2.80263	0	1	1
ENSG00000084734	ENSG00000084734	GCKR	2:27719708-27746554	NOTEST	0	0	0	0	1	1
ENSG00000085265	ENSG00000085265	FCN1	9:137801430-137809809	NOTEST	0	0	0	0	1	1
ENSG00000085276	ENSG00000085276	MECOM	3:168801286-169381406	NOTEST	0.396831	0.439438	0.147133	0	1	1
ENSG00000085514	ENSG00000085514	PILRA	7:99905324-99997719	NOTEST	0.0496131	0.0962179	0.955584	0	1	1
ENSG00000085552	ENSG00000085552	IGSF9	1:159896828-159915386	NOTEST	0.131561	0.0732739	-0.844357	0	1	1
ENSG00000085741	ENSG00000085741	WNT11	11:75897368-75921780	NOTEST	0.152989	0.103252	-0.567261	0	1	1
ENSG00000086159	ENSG00000086159	AQP6	12:50360976-50426919	NOTEST	0.0545646	0.117037	1.10093	0	1	1
ENSG00000086288	ENSG00000086288	NME8	7:37723398-38065297	NOTEST	0	0	0	0	1	1
ENSG00000086289	ENSG00000086289	EPDR1	7:37723398-38065297	NOTEST	0.500611	0.419276	-0.25579	0	1	1
ENSG00000086548	ENSG00000086548	CEACAM6	19:42212503-42290801	NOTEST	0.0164904	0.0128865	-0.355774	0	1	1
ENSG00000086570	ENSG00000086570	FAT2	5:150883653-150948505	NOTEST	0.301939	0.370047	0.293451	0	1	1
ENSG00000086696	ENSG00000086696	HSD17B2	16:82068608-82173236	NOTEST	0	0	0	0	1	1
ENSG00000086717	ENSG00000086717	PPEF1	X:18694028-18846039	NOTEST	0.300602	0.374324	0.316432	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000086730	ENSG00000086730	LAT2	7:73613981-73644161	NOTEST	0.271115	0.309553	0.191281	0	1	1
ENSG00000086967	ENSG00000086967	MYBPC2	19:50936159-50969578	NOTEST	0.0811744	0.00337117	-4.5897	0	1	1
ENSG00000087085	ENSG00000087085	ACHE	7:100487614-100494594	NOTEST	0.399615	0.570309	0.513135	0	1	1
ENSG00000087116	ENSG00000087116	ADAMTS2	5:178537851-178772431	NOTEST	0	0.00158241	inf	0	1	1
ENSG00000087128	ENSG00000087128	TMPRSS11E	4:69313166-69363322	NOTEST	0.00755781	0	#NAME?	0	1	1
ENSG00000087237	ENSG00000087237	CETP	16:56995761-57017757	NOTEST	0	0	0	0	1	1
ENSG00000087250	ENSG00000087250	MT3	16:56622985-56625000	NOTEST	0.322396	0.10285	-1.6483	0	1	1
ENSG00000087303	ENSG00000087303	NID2	14:52471520-52535712	NOTEST	0.371318	0.47775	0.363598	0	1	1
ENSG00000087495	ENSG00000087495	PHACTR3	20:58152563-58422766	NOTEST	0.110247	0.13325	0.273398	0	1	1
ENSG00000087589	ENSG00000087589	CASS4	20:54987167-55034396	NOTEST	0	0.00942572	inf	0	1	1
ENSG00000087916	ENSG00000087916	SLC6A14	X:115567789-115592625	NOTEST	0	0	0	0	1	1
ENSG00000088002	ENSG00000088002	SULT2B1	19:49055331-49102682	NOTEST	0.341438	0.421151	0.302713	0	1	1
ENSG00000088053	ENSG00000088053	GP6	19:55517560-55582659	NOTEST	0	0	0	0	1	1
ENSG00000088320	ENSG00000088320	REM1	20:30053308-30072708	NOTEST	0	0.00772529	inf	0	1	1
ENSG00000088386	ENSG00000088386	SLC15A1	13:99336054-99404908	NOTEST	0	0	0	0	1	1
ENSG00000088538	ENSG00000088538	DOCK3	3:50712671-51421629	NOTEST	0.0169582	0.0425315	1.32654	0	1	1
ENSG00000088726	ENSG00000088726	TMEM40	3:12775023-12810956	NOTEST	0.0570856	0.321561	2.49389	0	1	1
ENSG00000088782	ENSG00000088782	DEFB127	20:138110-139804	NOTEST	0	0	0	0	1	1
ENSG00000088827	ENSG00000088827	SIGLEC1	20:3667616-3687775	NOTEST	0	0	0	0	1	1
ENSG00000088836	ENSG00000088836	SLC4A11	20:3208062-3219836	NOTEST	0.21963	0.369646	0.75107	0	1	1
ENSG00000088881	ENSG00000088881	EBF4	20:2673523-2740753	NOTEST	0.011718	0.0342846	1.54884	0	1	1
ENSG00000088882	ENSG00000088882	CPXM1	20:2774714-2781283	NOTEST	0.0872776	0.0723886	-0.269848	0	1	1
ENSG00000088926	ENSG00000088926	F11	4:187187098-187476721	NOTEST	0	0	0	0	1	1
ENSG00000089012	ENSG00000089012	SIRPG	20:1609797-1638425	NOTEST	0	0	0	0	1	1
ENSG00000089116	ENSG00000089116	LHX5	12:113899838-113918429	NOTEST	0.00536516	0	#NAME?	0	1	1
ENSG00000089127	ENSG00000089127	OAS1	12:113344581-113455556	NOTEST	0.313868	0.355772	0.180794	0	1	1
ENSG00000089169	ENSG00000089169	RPH3A	12:113008183-113336686	NOTEST	0	0	0	0	1	1
ENSG00000089199	ENSG00000089199	CHGB	20:5892075-5906007	NOTEST	0.0878195	0.0593319	-0.565733	0	1	1
ENSG00000089225	ENSG00000089225	TBX5	12:114791735-114850636	NOTEST	0.00434869	0	#NAME?	0	1	1
ENSG00000089250	ENSG00000089250	NOS1	12:117645946-117889975	NOTEST	0	0	0	0	1	1
ENSG00000089472	ENSG00000089472	HEPH	X:65382390-65488709	NOTEST	0.0698322	0.072911	0.0622432	0	1	1
ENSG00000089558	ENSG00000089558	KCNH4	17:40308908-40333296	NOTEST	0.232865	0.285633	0.294668	0	1	1
ENSG00000089692	ENSG00000089692	LAG3	12:6881677-6887621	NOTEST	0.00823645	0	#NAME?	0	1	1
ENSG00000089847	ENSG00000089847	ANKRD24	19:4183350-4224811	NOTEST	0.0185495	0.0392801	1.08242	0	1	1
ENSG00000090382	ENSG00000090382	LYZ	12:69742120-69748014	NOTEST	0.0198372	0.116625	2.5556	0	1	1
ENSG00000090402	ENSG00000090402	SI	3:164696685-164796283	NOTEST	0	0	0	0	1	1
ENSG00000090512	ENSG00000090512	FETUB	3:186353757-186396029	NOTEST	0	0	0	0	1	1
ENSG00000090534	ENSG00000090534	THPO	3:183851806-184402546	NOTEST	0	0.029091	inf	0	1	1
ENSG00000090539	ENSG00000090539	CHRD	3:183851806-184402546	NOTEST	0.0708702	0.112611	0.668099	0	1	1
ENSG00000090659	ENSG00000090659	CD209	19:7804878-7812464	NOTEST	0	0	0	0	1	1
ENSG00000090920	ENSG00000090920	FCGBP	19:40353962-40440533	NOTEST	0.00348056	0	#NAME?	0	1	1
ENSG00000091010	ENSG00000091010	POU4F3	5:145583112-145756526	NOTEST	0.0293824	0.0540972	0.880605	0	1	1
ENSG00000091106	ENSG00000091106	NLRC4	2:32449521-32490923	NOTEST	0.0689233	0.0720702	0.0644098	0	1	1
ENSG00000091128	ENSG00000091128	LAMB4	7:107663992-107770801	NOTEST	0.0204589	0.0933955	2.19062	0	1	1
ENSG00000091138	ENSG00000091138	SLC26A3	7:107405911-107443670	NOTEST	0	0.00903699	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000091181	ENSG00000091181	IL5RA	3:3111232-3168297	NOTEST	0	0	0	0	1	1
ENSG00000091262	ENSG00000091262	ABCC6	16:16242784-16318118	NOTEST	0.099947	0.191785	0.940253	0	1	1
ENSG00000091482	ENSG00000091482	SMPX	X:21724089-21776281	NOTEST	0.463269	0.507439	0.131383	0	1	1
ENSG00000091536	ENSG00000091536	MYO15A	17:18012019-18113268	NOTEST	0.133705	0.196016	0.551913	0	1	1
ENSG00000091583	ENSG00000091583	APOH	17:64208150-64252643	NOTEST	0	0	0	0	1	1
ENSG00000091592	ENSG00000091592	NLRP1	17:5402746-5522744	NOTEST	0.0185052	0.158111	3.09494	0	1	1
ENSG00000091622	ENSG00000091622	PITPNM3	17:6347734-6459814	NOTEST	0.106544	0.118178	0.149516	0	1	1
ENSG00000091664	ENSG00000091664	SLC17A6	11:22305275-22401049	NOTEST	0.23836	0.295895	0.31194	0	1	1
ENSG00000091704	ENSG00000091704	CPA1	7:130020179-130027955	NOTEST	0	0	0	0	1	1
ENSG00000091831	ENSG00000091831	ESR1	6:151977825-152958936	NOTEST	0.516183	0.524386	0.0227485	0	1	1
ENSG00000091879	ENSG00000091879	ANGPT2	8:6261071-6565730	NOTEST	0.0486756	0.0584904	0.265	0	1	1
ENSG00000092009	ENSG00000092009	CMA1	14:24970799-24977894	NOTEST	0	0	0	0	1	1
ENSG00000092051	ENSG00000092051	JPH4	14:23980968-24048009	NOTEST	0.0536197	0.18437	1.78177	0	1	1
ENSG00000092054	ENSG00000092054	MYH7	14:23881946-23904927	NOTEST	0.0211127	0.0611018	1.5331	0	1	1
ENSG00000092067	ENSG00000092067	CEBPE	14:23586512-23588825	NOTEST	0	0	0	0	1	1
ENSG00000092200	ENSG00000092200	RPGRIP1	14:21756097-21819460	NOTEST	0.00807989	0.017069	1.07897	0	1	1
ENSG00000092295	ENSG00000092295	TGM1	14:24718319-24733638	NOTEST	0.208687	0.615725	1.56094	0	1	1
ENSG00000092345	ENSG00000092345	DAZL	3:16628298-16711813	NOTEST	0	0.0164334	inf	0	1	1
ENSG00000092377	ENSG00000092377	TBL1Y	Y:6778726-6959724	NOTEST	0	0	0	0	1	1
ENSG00000092607	ENSG00000092607	TBX15	1:119425668-119532179	NOTEST	0.00892809	0.0100687	0.173456	0	1	1
ENSG00000092850	ENSG00000092850	TEKT2	1:36549675-36553876	NOTEST	0	0.0691872	inf	0	1	1
ENSG00000092969	ENSG00000092969	TGFB2	1:218519576-218617961	NOTEST	0.270554	0.518498	0.938423	0	1	1
ENSG00000093072	ENSG00000093072	CECR1	22:17660193-17702879	NOTEST	0.0186948	0.0138406	-0.433731	0	1	1
ENSG00000093134	ENSG00000093134	VNN3	6:133043925-133055904	NOTEST	0.0236651	0	#NAME?	0	1	1
ENSG00000094661	ENSG00000094661	OR1I1	19:15197790-15199032	NOTEST	0	0	0	0	1	1
ENSG00000094755	ENSG00000094755	GABRP	5:170174050-170241051	NOTEST	0	0	0	0	1	1
ENSG00000094796	ENSG00000094796	KRT31	17:39549975-39553844	NOTEST	0.018911	0.0391037	1.04808	0	1	1
ENSG00000094963	ENSG00000094963	FMO2	1:171154346-171196927	NOTEST	0	0.0213959	inf	0	1	1
ENSG00000095110	ENSG00000095110	NXPE1	11:114392436-114430617	NOTEST	0	0	0	0	1	1
ENSG00000095203	ENSG00000095203	EPB41L4B	9:111934254-112083244	NOTEST	0.155106	0.269519	0.797132	0	1	1
ENSG00000095303	ENSG00000095303	PTGS1	9:125132823-125157982	NOTEST	0.00701332	0.0120812	0.784598	0	1	1
ENSG00000095370	ENSG00000095370	SH2D3C	9:130500595-130541020	NOTEST	0.126243	0.0985097	-0.357867	0	1	1
ENSG00000095464	ENSG00000095464	PDE6C	10:95372344-95425767	NOTEST	0.00473554	0.216706	5.51607	0	1	1
ENSG00000095585	ENSG00000095585	BLNK	10:97889471-98031344	NOTEST	0	0	0	0	1	1
ENSG00000095587	ENSG00000095587	TLL2	10:98124362-98273675	NOTEST	0.0368059	0.0594187	0.69098	0	1	1
ENSG00000095596	ENSG00000095596	CYP26A1	10:94833231-94837647	NOTEST	0.103521	0.139288	0.428146	0	1	1
ENSG00000095627	ENSG00000095627	TDRD1	10:115939028-115992063	NOTEST	0	0	0	0	1	1
ENSG00000095752	ENSG00000095752	IL11	19:55875756-55881831	NOTEST	0.057171	0.113087	0.984085	0	1	1
ENSG00000095777	ENSG00000095777	MYO3A	10:26223195-26501456	NOTEST	0	0	0	0	1	1
ENSG00000095917	ENSG00000095917	TPSD1	16:1306059-1308532	NOTEST	0.0374577	0	#NAME?	0	1	1
ENSG00000095970	ENSG00000095970	TREM2	6:41126243-41130924	NOTEST	0.0322138	0.0132285	-1.28403	0	1	1
ENSG00000095981	ENSG00000095981	KCNK16	6:39282473-39290744	NOTEST	0.0440678	0	#NAME?	0	1	1
ENSG00000096006	ENSG00000096006	CRISP3	6:49695096-49712150	NOTEST	0	0	0	0	1	1
ENSG00000096088	ENSG00000096088	PGC	6:41704448-41721847	NOTEST	0	0.00961995	inf	0	1	1
ENSG00000096150	ENSG00000096150	RPS18	HSCHR6_MHC_QBL:33146132-33173129	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000096155	ENSG00000096155	BAG6	HSCHR6_MHC_QBL:31597039-31616227	NOTEST	0	0	0	0	1	1
ENSG00000096171	ENSG00000096171	VARS	HSCHR6_MHC_DBB:31727479-31745915	NOTEST	0	0	0	0	1	1
ENSG00000096264	ENSG00000096264	NCR2	6:41303392-41318625	NOTEST	0	0	0	0	1	1
ENSG00000096395	ENSG00000096395	MLN	6:33762449-33771788	NOTEST	0	0	0	0	1	1
ENSG00000096996	ENSG00000096996	IL12RB1	19:18169804-18262502	NOTEST	0.0159545	0.0137077	-0.218984	0	1	1
ENSG00000097096	ENSG00000097096	SYDE2	1:85622555-85666729	NOTEST	0.617884	0.606686	-0.0263842	0	1	1
ENSG00000099139	ENSG00000099139	PCSK5	9:78505559-78977255	NOTEST	0.0100399	0.00123129	-3.0275	0	1	1
ENSG00000099250	ENSG00000099250	NRP1	10:33466419-33625190	NOTEST	0.128023	0.425503	1.73277	0	1	1
ENSG00000099256	ENSG00000099256	PRTFDC1	10:25137535-25241533	NOTEST	0	0	0	0	1	1
ENSG00000099260	ENSG00000099260	PALMD	1:100111498-100160097	NOTEST	0	0	0	0	1	1
ENSG00000099284	ENSG00000099284	H2AFY2	10:71812551-71892690	NOTEST	0.0164192	0.00576877	-1.50905	0	1	1
ENSG00000099337	ENSG00000099337	KCNK6	19:38810483-38819660	NOTEST	0.0167158	0.135909	3.02335	0	1	1
ENSG00000099338	ENSG00000099338	CATSPERG	19:38826414-38861589	NOTEST	0.13971	0.213494	0.61176	0	1	1
ENSG00000099365	ENSG00000099365	STX1B	16:31000576-31021949	NOTEST	0.284443	0.252978	-0.169129	0	1	1
ENSG00000099617	ENSG00000099617	EFNA2	19:1285889-1378430	NOTEST	0.00753098	0.0181539	1.26937	0	1	1
ENSG00000099715	ENSG00000099715	PCDH11Y	Y:4868266-5610265	NOTEST	0	0	0	0	1	1
ENSG00000099721	ENSG00000099721	AMELY	Y:6733958-6742068	NOTEST	0	0	0	0	1	1
ENSG00000099725	ENSG00000099725	PRKY	Y:7142012-7249589	NOTEST	0	0	0	0	1	1
ENSG00000099769	ENSG00000099769	IGFALS	16:1823207-1844972	NOTEST	0.0152672	0.0761973	2.31931	0	1	1
ENSG00000099812	ENSG00000099812	MISP	19:751125-764319	NOTEST	0	0	0	0	1	1
ENSG00000099834	ENSG00000099834	CDHR5	11:616564-626078	NOTEST	0.230048	0.0583951	-1.97802	0	1	1
ENSG00000099864	ENSG00000099864	PALM	19:708952-748329	NOTEST	0.0687143	0.0713012	0.0533158	0	1	1
ENSG00000099866	ENSG00000099866	MADCAM1	19:489175-519654	NOTEST	0.151959	0.118647	-0.357006	0	1	1
ENSG00000099869	ENSG00000099869	IGF2-AS	11:2150341-2182571	NOTEST	0	0	0	0	1	1
ENSG00000099937	ENSG00000099937	SERPIND1	22:21061978-21245506	NOTEST	0.0196614	0.0335143	0.76941	0	1	1
ENSG00000099953	ENSG00000099953	MMP11	22:24105207-24126503	NOTEST	0.637271	0.496414	-0.360362	0	1	1
ENSG00000099954	ENSG00000099954	CECR2	22:17840836-18037850	NOTEST	0.354441	0.200608	-0.821166	0	1	1
ENSG00000099985	ENSG00000099985	OSM	22:30658817-30662829	NOTEST	0.050683	0	#NAME?	0	1	1
ENSG00000099998	ENSG00000099998	GGT5	22:24615621-24641110	NOTEST	0	0	0	0	1	1
ENSG00000100012	ENSG00000100012	SEC14L3	22:30843945-30868036	NOTEST	0	0	0	0	1	1
ENSG00000100024	ENSG00000100024	UPB1	22:24666785-24924358	NOTEST	0	0.0168937	inf	0	1	1
ENSG00000100053	ENSG00000100053	CRYBB3	22:25595816-25603330	NOTEST	0	0.0165986	inf	0	1	1
ENSG00000100055	ENSG00000100055	CYTH4	22:37678067-37711382	NOTEST	0	0	0	0	1	1
ENSG00000100060	ENSG00000100060	MFNG	22:37865100-37882439	NOTEST	0.0341156	0	#NAME?	0	1	1
ENSG00000100078	ENSG00000100078	PLA2G3	22:31530794-31536593	NOTEST	0	0	0	0	1	1
ENSG00000100079	ENSG00000100079	LGALS2	22:37966254-37978623	NOTEST	0.0355383	0	#NAME?	0	1	1
ENSG00000100095	ENSG00000100095	SEZ6L	22:26565439-26779562	NOTEST	0	0	0	0	1	1
ENSG00000100121	ENSG00000100121	GGTLC2	22:22988779-22990368	NOTEST	0	0	0	0	1	1
ENSG00000100122	ENSG00000100122	CRYBB1	22:26995241-27014052	NOTEST	0	0	0	0	1	1
ENSG00000100156	ENSG00000100156	SLC16A8	22:38474140-38480100	NOTEST	0.120132	0.085586	-0.489169	0	1	1
ENSG00000100170	ENSG00000100170	SLC5A1	22:32439018-32509016	NOTEST	0.010959	0.0427513	1.96385	0	1	1
ENSG00000100181	ENSG00000100181	TPTEP1	22:17082776-17185367	NOTEST	0.127067	0.0636405	-0.997575	0	1	1
ENSG00000100191	ENSG00000100191	SLC5A4	22:32601101-32669097	NOTEST	0.222863	0.275002	0.303285	0	1	1
ENSG00000100197	ENSG00000100197	CYP2D6	22:42481528-42535938	NOTEST	0.151405	0.348053	1.20089	0	1	1
ENSG00000100206	ENSG00000100206	DMC1	22:38914953-38966291	NOTEST	0.0800318	0	#NAME?	0	1	1

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ENSG00000100218	ENSG00000100218	RTDR1	22:23401592-23487208	NOTEST	0.0475869	0.0341785	-0.477476	0	1	1
ENSG00000100228	ENSG00000100228	RAB36	22:23487512-23506537	NOTEST	0.315285	0.426979	0.437508	0	1	1
ENSG00000100249	ENSG00000100249	C22orf31	22:29454659-29457832	NOTEST	0	0	0	0	1	1
ENSG00000100253	ENSG00000100253	MIOX	22:50925212-50929077	NOTEST	0	0	0	0	1	1
ENSG00000100276	ENSG00000100276	RASL10A	22:29708921-29715668	NOTEST	0	0	0	0	1	1
ENSG00000100285	ENSG00000100285	NEFH	22:29876218-29887379	NOTEST	0.00411145	0.0060794	0.56428	0	1	1
ENSG00000100298	ENSG00000100298	APOBEC3H	22:39493228-39500072	NOTEST	0.06266	0.141545	1.17565	0	1	1
ENSG00000100302	ENSG00000100302	RASD2	22:35936914-35950048	NOTEST	0.0790779	0.133079	0.750934	0	1	1
ENSG00000100312	ENSG00000100312	ACR	22:51176623-51183762	NOTEST	0.0353052	0.0258742	-0.44837	0	1	1
ENSG00000100314	ENSG00000100314	CABP7	22:30116072-30163000	NOTEST	0.0427864	0.0297237	-0.525538	0	1	1
ENSG00000100336	ENSG00000100336	APOL4	22:36585171-36600886	NOTEST	0	0	0	0	1	1
ENSG00000100341	ENSG00000100341	PNPLA5	22:44275557-44287893	NOTEST	0	0	0	0	1	1
ENSG00000100342	ENSG00000100342	APOL1	22:36649055-36663576	NOTEST	0.0483187	0.25233	2.38465	0	1	1
ENSG00000100346	ENSG00000100346	CACNA1I	22:39966757-40085742	NOTEST	0	0.00856108	inf	0	1	1
ENSG00000100351	ENSG00000100351	GRAP2	22:40297085-40369725	NOTEST	0.348957	0.271009	-0.364708	0	1	1
ENSG00000100362	ENSG00000100362	PVALB	22:37196727-37215780	NOTEST	0	0.0387159	inf	0	1	1
ENSG00000100365	ENSG00000100365	NCF4	22:37243414-37274057	NOTEST	0	0	0	0	1	1
ENSG00000100368	ENSG00000100368	CSF2RB	22:37309669-37336491	NOTEST	0	0.00444196	inf	0	1	1
ENSG00000100373	ENSG00000100373	UPK3A	22:45680862-45691755	NOTEST	0	0	0	0	1	1
ENSG00000100385	ENSG00000100385	IL2RB	22:37521877-37595425	NOTEST	0.0749441	0.271108	1.85498	0	1	1
ENSG00000100427	ENSG00000100427	MLC1	22:50497819-50524331	NOTEST	0	0	0	0	1	1
ENSG00000100433	ENSG00000100433	KCNK10	14:88649112-88793251	NOTEST	0	0	0	0	1	1
ENSG00000100448	ENSG00000100448	CTSG	14:25042727-25045466	NOTEST	0	0	0	0	1	1
ENSG00000100450	ENSG00000100450	GZMH	14:25064928-25126980	NOTEST	0	0.0485651	inf	0	1	1
ENSG00000100453	ENSG00000100453	GZMB	14:25064928-25126980	NOTEST	0.336474	0.282052	-0.254537	0	1	1
ENSG00000100557	ENSG00000100557	C14orf105	14:57936018-57960585	NOTEST	0	0	0	0	1	1
ENSG00000100565	ENSG00000100565	C14orf166B	14:77292714-77336645	NOTEST	0.0505077	0	#NAME?	0	1	1
ENSG00000100583	ENSG00000100583	SAMD15	14:77801363-77857840	NOTEST	0.210354	0.220008	0.0647338	0	1	1
ENSG00000100593	ENSG00000100593	ISM2	14:77940739-77965210	NOTEST	0.0732987	0.0625394	-0.229022	0	1	1
ENSG00000100604	ENSG00000100604	CHGA	14:93389424-93401638	NOTEST	0.140391	0.0805217	-0.802004	0	1	1
ENSG00000100626	ENSG00000100626	GALNT16	14:69649736-69821183	NOTEST	0.095173	0.0148239	-2.68263	0	1	1
ENSG00000100652	ENSG00000100652	SLC10A1	14:70242133-70264006	NOTEST	0.00790796	0.0111126	0.490822	0	1	1
ENSG00000100665	ENSG00000100665	SERPINA4	14:95027427-95090983	NOTEST	0	0	0	0	1	1
ENSG00000100678	ENSG00000100678	SLC8A3	14:70510933-70696904	NOTEST	0	0	0	0	1	1
ENSG00000100721	ENSG00000100721	TCL1A	14:96176303-96223993	NOTEST	0	0	0	0	1	1
ENSG00000100739	ENSG00000100739	BDKRB1	14:96671015-96735304	NOTEST	0.0198945	0.028412	0.514136	0	1	1
ENSG00000100842	ENSG00000100842	EFS	14:23825610-23834961	NOTEST	0.00503926	0.00680135	0.432608	0	1	1
ENSG00000100884	ENSG00000100884	CPNE6	14:24540045-24547309	NOTEST	0.231582	0.290722	0.328113	0	1	1
ENSG00000100985	ENSG00000100985	MMP9	20:44637546-44688784	NOTEST	0.0124129	0.0801389	2.69066	0	1	1
ENSG00000100987	ENSG00000100987	VSX1	20:25051520-25062996	NOTEST	0.0647825	0.100587	0.634771	0	1	1
ENSG00000101017	ENSG00000101017	CD40	20:44746910-44758502	NOTEST	0.150728	0.155666	0.0465055	0	1	1
ENSG00000101049	ENSG00000101049	SGK2	20:42187607-42216877	NOTEST	0.0544961	0.00656949	-3.0523	0	1	1
ENSG00000101074	ENSG00000101074	R3HDML	20:42965625-42983825	NOTEST	0	0	0	0	1	1
ENSG00000101076	ENSG00000101076	HNF4A	20:42984339-43061485	NOTEST	0	0.00328948	inf	0	1	1
ENSG00000101082	ENSG00000101082	SLA2	20:34894257-35274619	NOTEST	0.0074256	0.0320881	2.11146	0	1	1

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ENSG00000101098	ENSG00000101098	RIMS4	20:43380448-43438979	NOTEST	0.135744	0.257822	0.925482	0	1	1
ENSG00000101134	ENSG00000101134	DOK5	20:53092135-53267710	NOTEST	0.038314	0.150132	1.97029	0	1	1
ENSG00000101144	ENSG00000101144	BMP7	20:55743803-55841685	NOTEST	0	0.0288886	inf	0	1	1
ENSG00000101162	ENSG00000101162	TUBB1	20:57594308-57607437	NOTEST	0.175769	0.0868253	-1.0175	0	1	1
ENSG00000101180	ENSG00000101180	HRH3	20:60790025-60795323	NOTEST	0	0	0	0	1	1
ENSG00000101188	ENSG00000101188	NTSR1	20:61340188-61394123	NOTEST	0.0246558	0.0415525	0.753007	0	1	1
ENSG00000101194	ENSG00000101194	SLC17A9	20:61584051-61599949	NOTEST	0.0156464	0.0120363	-0.378442	0	1	1
ENSG00000101200	ENSG00000101200	AVP	20:3063201-3065370	NOTEST	0	0	0	0	1	1
ENSG00000101203	ENSG00000101203	COL20A1	20:61924537-61966203	NOTEST	0.0359395	0.0823475	1.19616	0	1	1
ENSG00000101204	ENSG00000101204	CHRNA4	20:61975419-62009753	NOTEST	0	0	0	0	1	1
ENSG00000101213	ENSG00000101213	PTK6	20:62159777-62168723	NOTEST	0.137654	0.211301	0.618261	0	1	1
ENSG00000101222	ENSG00000101222	SPEF1	20:3758150-3762095	NOTEST	0.164224	0.242479	0.562195	0	1	1
ENSG00000101251	ENSG00000101251	SEL1L2	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000101265	ENSG00000101265	RASSF2	20:4760668-4804291	NOTEST	0.172459	0.351205	1.02606	0	1	1
ENSG00000101276	ENSG00000101276	SLC52A3	20:740723-749131	NOTEST	0.00611848	0.0133476	1.12534	0	1	1
ENSG00000101278	ENSG00000101278	RPS10L	20:814357-838106	NOTEST	0.153351	0.182288	0.249377	0	1	1
ENSG00000101280	ENSG00000101280	ANGPT4	20:853295-896977	NOTEST	0	0.0233871	inf	0	1	1
ENSG00000101282	ENSG00000101282	RSPO4	20:939094-982907	NOTEST	0.0899977	0.204919	1.1871	0	1	1
ENSG00000101292	ENSG00000101292	PROKR2	20:5282316-5297378	NOTEST	0	0	0	0	1	1
ENSG00000101306	ENSG00000101306	MYLK2	20:30407110-30422492	NOTEST	0.0102422	0.0390359	1.93027	0	1	1
ENSG00000101307	ENSG00000101307	SIRPB1	20:1497404-1600707	NOTEST	0.393022	0.487973	0.312194	0	1	1
ENSG00000101311	ENSG00000101311	FERMT1	20:6055491-6104191	NOTEST	0	0.0113583	inf	0	1	1
ENSG00000101323	ENSG00000101323	HAO1	20:7863627-7921121	NOTEST	0	0	0	0	1	1
ENSG00000101327	ENSG00000101327	PDYN	20:1927891-1988163	NOTEST	0	0	0	0	1	1
ENSG00000101331	ENSG00000101331	CCM2L	20:30598244-30619984	NOTEST	0.00631416	0	#NAME?	0	1	1
ENSG00000101336	ENSG00000101336	HCK	20:30639990-30689659	NOTEST	0	0	0	0	1	1
ENSG00000101342	ENSG00000101342	TLDC2	20:35504523-35580246	NOTEST	0.226597	0.117317	-0.949712	0	1	1
ENSG00000101349	ENSG00000101349	PAK7	20:9518035-9819689	NOTEST	0	0	0	0	1	1
ENSG00000101405	ENSG00000101405	OXT	20:3052265-3053163	NOTEST	0	0	0	0	1	1
ENSG00000101425	ENSG00000101425	BPI	20:36838889-36965907	NOTEST	0	0	0	0	1	1
ENSG00000101435	ENSG00000101435	CST9L	20:23545368-23549386	NOTEST	0	0	0	0	1	1
ENSG00000101438	ENSG00000101438	SLC32A1	20:37353104-37358015	NOTEST	0	0	0	0	1	1
ENSG00000101441	ENSG00000101441	CST4	20:23666276-23669677	NOTEST	0	0	0	0	1	1
ENSG00000101443	ENSG00000101443	WFDC2	20:44095909-44110172	NOTEST	0.233393	0.259938	0.155408	0	1	1
ENSG00000101445	ENSG00000101445	PPP1R16B	20:37434347-37551667	NOTEST	0.0045107	0.0239156	2.40653	0	1	1
ENSG00000101446	ENSG00000101446	SPINT3	20:44141100-44144264	NOTEST	0	0	0	0	1	1
ENSG00000101448	ENSG00000101448	EPPIN	20:44162834-44176391	NOTEST	0.032776	0.0139654	-1.23079	0	1	1
ENSG00000101463	ENSG00000101463	SYNDIG1	20:24449834-24647252	NOTEST	0	0	0	0	1	1
ENSG00000101470	ENSG00000101470	TNNC2	20:44451852-44462384	NOTEST	0.148226	0	#NAME?	0	1	1
ENSG00000101489	ENSG00000101489	CELF4	18:34823009-35146000	NOTEST	0.351805	0.470159	0.418376	0	1	1
ENSG00000101542	ENSG00000101542	CDH20	18:59000814-59223006	NOTEST	0	0	0	0	1	1
ENSG00000101605	ENSG00000101605	MYOM1	18:3066804-3247275	NOTEST	0.128337	0.326685	1.34796	0	1	1
ENSG00000101638	ENSG00000101638	ST8SIA5	18:44259080-44340307	NOTEST	0.0309679	0.0248225	-0.319123	0	1	1
ENSG00000101670	ENSG00000101670	LIPG	18:47087068-47119272	NOTEST	0.412215	0.324512	-0.345122	0	1	1
ENSG00000101746	ENSG00000101746	NOL4	18:31431063-31804916	NOTEST	0	0	0	0	1	1

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ENSG00000101812	ENSG00000101812	H2BFM	X:103268268-103297021	NOTEST	0	0.0121996	inf	0	1	1
ENSG00000101825	ENSG00000101825	MXRA5	X:3226605-3264682	NOTEST	0	0	0	0	1	1
ENSG00000101842	ENSG00000101842	VSIG1	X:107288199-107322414	NOTEST	0.0598389	0.0208289	-1.5225	0	1	1
ENSG00000101883	ENSG00000101883	RHOXF1	X:119170200-119379122	NOTEST	0.0455733	0.0175388	-1.37764	0	1	1
ENSG00000101890	ENSG00000101890	GUCY2F	X:108616134-108725301	NOTEST	0.00838305	0	#NAME?	0	1	1
ENSG00000101892	ENSG00000101892	ATP1B4	X:119495966-119516226	NOTEST	0	0	0	0	1	1
ENSG00000101916	ENSG00000101916	TLR8	X:12920935-12941288	NOTEST	0	0	0	0	1	1
ENSG00000101938	ENSG00000101938	CHRDL1	X:109917083-110039286	NOTEST	0.18542	0.366737	0.983947	0	1	1
ENSG00000101951	ENSG00000101951	PAGE4	X:49593862-49598576	NOTEST	0	0.237932	inf	0	1	1
ENSG00000101958	ENSG00000101958	GLRA2	X:14547419-14749934	NOTEST	0	0	0	0	1	1
ENSG00000101977	ENSG00000101977	MCF2	X:138663928-138790386	NOTEST	0.0623495	0.0194909	-1.67758	0	1	1
ENSG00000101981	ENSG00000101981	F9	X:138612916-138645617	NOTEST	0	0	0	0	1	1
ENSG00000102001	ENSG00000102001	CACNA1F	X:49061522-49089833	NOTEST	0	0	0	0	1	1
ENSG00000102010	ENSG00000102010	BMX	X:15402920-15574652	NOTEST	0.0716546	0.0910157	0.345058	0	1	1
ENSG00000102021	ENSG00000102021	LUZP4	X:114524292-114542121	NOTEST	0	0	0	0	1	1
ENSG00000102053	ENSG00000102053	ZC3H12B	X:64708614-64727767	NOTEST	0.0205487	0.0259507	0.336725	0	1	1
ENSG00000102055	ENSG00000102055	PPP1R2P9	X:42636721-42637330	NOTEST	0	0	0	0	1	1
ENSG00000102069	ENSG00000102069	UBE2NL	X:142967172-142968355	NOTEST	0	0	0	0	1	1
ENSG00000102076	ENSG00000102076	OPN1LW	X:153409697-153424507	NOTEST	0	0	0	0	1	1
ENSG00000102080	ENSG00000102080	TEX28P2	X:153424681-153445634	NOTEST	0	0	0	0	1	1
ENSG00000102104	ENSG00000102104	RS1	X:18443702-18690229	NOTEST	0.00562743	0	#NAME?	0	1	1
ENSG00000102128	ENSG00000102128	RAB40AL	X:102192199-102195489	NOTEST	0	0.0835029	inf	0	1	1
ENSG00000102145	ENSG00000102145	GATA1	X:48644961-48652716	NOTEST	0	0	0	0	1	1
ENSG00000102174	ENSG00000102174	PHEX	X:22050558-22269427	NOTEST	0.115227	0.151155	0.391543	0	1	1
ENSG00000102195	ENSG00000102195	GPR50	X:150343663-150349937	NOTEST	0	0	0	0	1	1
ENSG00000102239	ENSG00000102239	BRS3	X:135570045-135575939	NOTEST	0	0	0	0	1	1
ENSG00000102243	ENSG00000102243	VGLL1	X:135614310-135638966	NOTEST	0	0	0	0	1	1
ENSG00000102245	ENSG00000102245	CD40LG	X:135730351-135742549	NOTEST	0	0	0	0	1	1
ENSG00000102271	ENSG00000102271	KLHL4	X:86772751-86925050	NOTEST	0.0487462	0.189612	1.95969	0	1	1
ENSG00000102287	ENSG00000102287	GABRE	X:151121595-151143152	NOTEST	0	0	0	0	1	1
ENSG00000102290	ENSG00000102290	PCDH11X	X:91034259-91878229	NOTEST	0.0157901	0.00470144	-1.74785	0	1	1
ENSG00000102313	ENSG00000102313	ITIH6	X:54775331-54824673	NOTEST	0.0594932	0.103421	0.797728	0	1	1
ENSG00000102349	ENSG00000102349	KLF8	X:56258853-56314322	NOTEST	0	0	0	0	1	1
ENSG00000102359	ENSG00000102359	SRPX2	X:99899214-99926296	NOTEST	0.0151002	0.16219	3.42504	0	1	1
ENSG00000102362	ENSG00000102362	SYTL4	X:99929487-99987110	NOTEST	0.104481	0.131278	0.329388	0	1	1
ENSG00000102383	ENSG00000102383	ZDHHC15	X:74588261-74743337	NOTEST	0	0	0	0	1	1
ENSG00000102385	ENSG00000102385	DRP2	X:100474757-100519486	NOTEST	0.1204	0.0787466	-0.612545	0	1	1
ENSG00000102445	ENSG00000102445	KIAA0226L	13:46916138-47012325	NOTEST	0.0671052	0.146094	1.1224	0	1	1
ENSG00000102452	ENSG00000102452	NALCN	13:101360578-102068843	NOTEST	0.175585	0.197982	0.173196	0	1	1
ENSG00000102466	ENSG00000102466	FGF14	13:102104965-103054807	NOTEST	0.145355	0.101071	-0.524205	0	1	1
ENSG00000102468	ENSG00000102468	HTR2A	13:47405684-47471169	NOTEST	0	0	0	0	1	1
ENSG00000102539	ENSG00000102539	MLNR	13:49794473-49796513	NOTEST	0.0139046	0.0293631	1.07844	0	1	1
ENSG00000102678	ENSG00000102678	FGF9	13:22245521-22278637	NOTEST	0	0	0	0	1	1
ENSG00000102683	ENSG00000102683	SGCG	13:23755090-23899304	NOTEST	0.0238759	0.0424985	0.831857	0	1	1
ENSG00000102755	ENSG00000102755	FLT1	13:28874488-29069265	NOTEST	0.342345	0.513479	0.584855	0	1	1

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ENSG00000102794	ENSG00000102794	IRG1	13:77522631-77532777	NOTEST	0	0	0	0	1	1
ENSG00000102802	ENSG00000102802	MEDAG	13:31456069-31551760	NOTEST	0	0.0162491	inf	0	1	1
ENSG00000102837	ENSG00000102837	OLFM4	13:53602893-53626192	NOTEST	0	0.00382503	inf	0	1	1
ENSG00000102854	ENSG00000102854	MSLN	16:810761-818865	NOTEST	0	0.0182468	inf	0	1	1
ENSG00000102886	ENSG00000102886	GDPD3	16:30116130-30125177	NOTEST	0.478773	0.327808	-0.546493	0	1	1
ENSG00000102890	ENSG00000102890	ELMO3	16:67233013-67237932	NOTEST	0.194741	0.183019	-0.0895589	0	1	1
ENSG00000102891	ENSG00000102891	MT4	16:56598960-56602869	NOTEST	0	0	0	0	1	1
ENSG00000102904	ENSG00000102904	TSNAXIP1	16:67840667-67906470	NOTEST	0.226868	0.0772791	-1.5537	0	1	1
ENSG00000102924	ENSG00000102924	CBLN1	16:49311827-49315742	NOTEST	0	0	0	0	1	1
ENSG00000102934	ENSG00000102934	PLLP	16:57290003-57318599	NOTEST	0.2436	0.298474	0.293093	0	1	1
ENSG00000102935	ENSG00000102935	ZNF423	16:49521434-49891830	NOTEST	0	0	0	0	1	1
ENSG00000102962	ENSG00000102962	CCL22	16:57392683-57400102	NOTEST	0	0.00418317	inf	0	1	1
ENSG00000102970	ENSG00000102970	CCL17	16:57438678-57449974	NOTEST	0.12871	0.470113	1.86888	0	1	1
ENSG00000103023	ENSG00000103023	PRSS54	16:58265060-58328951	NOTEST	0	0	0	0	1	1
ENSG00000103034	ENSG00000103034	NDRG4	16:58496749-58547532	NOTEST	0.249483	0.626374	1.32808	0	1	1
ENSG00000103044	ENSG00000103044	HAS3	16:69139466-69442474	NOTEST	0.128347	0.108133	-0.247233	0	1	1
ENSG00000103056	ENSG00000103056	SMPD3	16:68344876-68482591	NOTEST	0.329059	0.278576	-0.240276	0	1	1
ENSG00000103067	ENSG00000103067	ESRP2	16:68021296-68272005	NOTEST	0.0610303	0.0605151	-0.0122316	0	1	1
ENSG00000103089	ENSG00000103089	FA2H	16:74746852-74808729	NOTEST	0	0	0	0	1	1
ENSG00000103154	ENSG00000103154	NECAB2	16:84002236-84036381	NOTEST	0.0457458	0.120979	1.40304	0	1	1
ENSG00000103175	ENSG00000103175	WFDC1	16:84328251-84363450	NOTEST	0.307453	0.220702	-0.478268	0	1	1
ENSG00000103184	ENSG00000103184	SEC14L5	16:4932507-5147809	NOTEST	0.256646	0.455995	0.82924	0	1	1
ENSG00000103196	ENSG00000103196	CRISPLD2	16:84853589-84954374	NOTEST	0.0457486	0.0562465	0.298035	0	1	1
ENSG00000103200	ENSG00000103200	RP11-723C11.2	7:140135115-140135587	NOTEST	0	0	0	0	1	1
ENSG00000103241	ENSG00000103241	FOXF1	16:86544132-86548076	NOTEST	0	0.0135976	inf	0	1	1
ENSG00000103310	ENSG00000103310	ZP2	16:21206167-21225831	NOTEST	0	0	0	0	1	1
ENSG00000103313	ENSG00000103313	MEFV	16:3292027-3306627	NOTEST	0	0	0	0	1	1
ENSG00000103355	ENSG00000103355	PRSS33	16:2833953-2837949	NOTEST	0.136958	0.584538	2.09356	0	1	1
ENSG00000103375	ENSG00000103375	AQP8	16:25227051-25240261	NOTEST	0.0244407	0	#NAME?	0	1	1
ENSG00000103426	ENSG00000103426	CORO7-PAM16	16:4364761-4475706	NOTEST	0.163033	0.000278261	-9.19451	0	1	1
ENSG00000103449	ENSG00000103449	SALL1	16:51169885-51185278	NOTEST	0	0	0	0	1	1
ENSG00000103460	ENSG00000103460	TOX3	16:52471916-52581714	NOTEST	0.00908484	0.00390533	-1.21802	0	1	1
ENSG00000103522	ENSG00000103522	IL21R	16:27413482-27464714	NOTEST	0	0	0	0	1	1
ENSG00000103528	ENSG00000103528	SYT17	16:19125253-19279652	NOTEST	0.0212796	0.0592771	1.478	0	1	1
ENSG00000103534	ENSG00000103534	TMC5	16:19421817-19510435	NOTEST	0.00762753	0	#NAME?	0	1	1
ENSG00000103546	ENSG00000103546	SLC6A2	16:55689515-55740104	NOTEST	0	0	0	0	1	1
ENSG00000103569	ENSG00000103569	AQP9	15:58245621-58861151	NOTEST	0.0127709	0	#NAME?	0	1	1
ENSG00000103647	ENSG00000103647	CORO2B	15:68871307-69020145	NOTEST	0.215806	0.12927	-0.73934	0	1	1
ENSG00000103710	ENSG00000103710	RASL12	15:65337707-65369028	NOTEST	0.0605015	0.0952477	0.654713	0	1	1
ENSG00000103723	ENSG00000103723	AP3B2	15:83205503-83378666	NOTEST	0.225616	0.129919	-0.79626	0	1	1
ENSG00000103742	ENSG00000103742	IGDCC4	15:65673801-65715410	NOTEST	0.494666	0.445843	-0.149919	0	1	1
ENSG00000103832	ENSG00000103832	GOLGA8UP	15:31083775-31094062	NOTEST	0.0263748	0.0722665	1.45416	0	1	1
ENSG00000104043	ENSG00000104043	ATP8B4	15:50150434-50528592	NOTEST	0	0	0	0	1	1
ENSG00000104055	ENSG00000104055	TGM5	15:43524792-43559055	NOTEST	0.0544504	0.117635	1.1113	0	1	1
ENSG00000104059	ENSG00000104059	FAM189A1	15:29412456-29862927	NOTEST	0	0	0	0	1	1

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ENSG00000104112	ENSG00000104112	SCG3	15:51973549-52013223	NOTEST	0.198238	0.298076	0.588442	0	1	1
ENSG00000104140	ENSG00000104140	RHOV	15:41164411-41166487	NOTEST	0.0623531	0.137344	1.13926	0	1	1
ENSG00000104237	ENSG00000104237	RP1	8:55528626-55543394	NOTEST	0	0.00150335	inf	0	1	1
ENSG00000104267	ENSG00000104267	CA2	8:86239836-86393722	NOTEST	0.0584369	0.00746524	-2.96862	0	1	1
ENSG00000104327	ENSG00000104327	CALB1	8:91070835-91107703	NOTEST	0	0.0917329	inf	0	1	1
ENSG00000104371	ENSG00000104371	DKK4	8:42231585-42234750	NOTEST	0	0.0159777	inf	0	1	1
ENSG00000104415	ENSG00000104415	WISP1	8:134203281-134242587	NOTEST	0.00404317	0	#NAME?	0	1	1
ENSG00000104432	ENSG00000104432	IL7	8:79578281-79717758	NOTEST	0.56536	0.295979	-0.933678	0	1	1
ENSG00000104435	ENSG00000104435	STMN2	8:80523048-80578410	NOTEST	0	0	0	0	1	1
ENSG00000104499	ENSG00000104499	GML	8:143915553-143999259	NOTEST	0	0	0	0	1	1
ENSG00000104537	ENSG00000104537	ANXA13	8:124693033-124749647	NOTEST	0.183978	0.194619	0.0811263	0	1	1
ENSG00000104722	ENSG00000104722	NEFM	8:24769677-24776607	NOTEST	0.426749	0.426846	0.000327265	0	1	1
ENSG00000104755	ENSG00000104755	ADAM2	8:39601253-39695808	NOTEST	0	0	0	0	1	1
ENSG00000104760	ENSG00000104760	FGL1	8:17721888-17767874	NOTEST	0	0	0	0	1	1
ENSG00000104804	ENSG00000104804	TULP2	19:49384221-49401990	NOTEST	0.00938179	0	#NAME?	0	1	1
ENSG00000104814	ENSG00000104814	MAP4K1	19:39078280-39109522	NOTEST	0.184509	0.0908456	-1.0222	0	1	1
ENSG00000104818	ENSG00000104818	CGB2	19:49526125-49552400	NOTEST	0.0245922	0.0347265	0.497834	0	1	1
ENSG00000104827	ENSG00000104827	CGB	19:49526125-49552400	NOTEST	0	0	0	0	1	1
ENSG00000104848	ENSG00000104848	KCNA7	19:49570674-49576198	NOTEST	0.0240556	0.0616144	1.3569	0	1	1
ENSG00000104879	ENSG00000104879	CKM	19:45809671-45826235	NOTEST	0	0.0240966	inf	0	1	1
ENSG00000104899	ENSG00000104899	AMH	19:2249307-2252072	NOTEST	0.0952504	0.0859286	-0.148588	0	1	1
ENSG00000104901	ENSG00000104901	DKKL1	19:49834873-49891338	NOTEST	0.383536	0.341543	-0.167296	0	1	1
ENSG00000104918	ENSG00000104918	RETN	19:7733929-7735334	NOTEST	0	0	0	0	1	1
ENSG00000104921	ENSG00000104921	FCER2	19:7753643-7767032	NOTEST	0	0	0	0	1	1
ENSG00000104938	ENSG00000104938	CLEC4M	19:7828034-7834491	NOTEST	0	0	0	0	1	1
ENSG00000104941	ENSG00000104941	RSPH6A	19:46298967-46318577	NOTEST	0	0	0	0	1	1
ENSG00000104951	ENSG00000104951	IL4I1	19:50392910-50464429	NOTEST	0.418739	0.325711	-0.362461	0	1	1
ENSG00000104967	ENSG00000104967	NOVA2	19:46436991-46476804	NOTEST	0.0447461	0.217181	2.27906	0	1	1
ENSG00000104970	ENSG00000104970	KIR3DX1	19:55043908-55057053	NOTEST	0	0	0	0	1	1
ENSG00000104972	ENSG00000104972	LILRB1	19:55084386-55150343	NOTEST	0	0	0	0	1	1
ENSG00000104974	ENSG00000104974	LILRA1	19:55084386-55150343	NOTEST	0	0	0	0	1	1
ENSG00000105122	ENSG00000105122	RASAL3	19:15562434-15575382	NOTEST	0	0	0	0	1	1
ENSG00000105131	ENSG00000105131	EPHX3	19:15337729-15344246	NOTEST	0.0391948	0.00652029	-2.58765	0	1	1
ENSG00000105141	ENSG00000105141	CASP14	19:15160194-15169104	NOTEST	0	0	0	0	1	1
ENSG00000105143	ENSG00000105143	SLC1A6	19:15060845-15134081	NOTEST	0	0	0	0	1	1
ENSG00000105146	ENSG00000105146	AURKC	19:57742376-57746916	NOTEST	0.390337	0.576246	0.561966	0	1	1
ENSG00000105198	ENSG00000105198	LGALS13	19:40093163-40098116	NOTEST	0	0	0	0	1	1
ENSG00000105205	ENSG00000105205	CLC	19:40221889-40228668	NOTEST	0	0	0	0	1	1
ENSG00000105219	ENSG00000105219	CNTD2	19:40728114-40732597	NOTEST	0.135758	0.427119	1.65361	0	1	1
ENSG00000105246	ENSG00000105246	EBI3	19:4229494-4237528	NOTEST	0	0	0	0	1	1
ENSG00000105251	ENSG00000105251	SHD	19:4278597-4290721	NOTEST	0	0	0	0	1	1
ENSG00000105261	ENSG00000105261	OVOL3	19:36602103-36616849	NOTEST	0	0	0	0	1	1
ENSG00000105278	ENSG00000105278	ZFR2	19:3804021-3869030	NOTEST	0.240508	0.459189	0.933001	0	1	1
ENSG00000105289	ENSG00000105289	TJP3	19:3708106-3750811	NOTEST	0.0294601	0.0694951	1.23815	0	1	1
ENSG00000105352	ENSG00000105352	CEACAM4	19:42125343-42133442	NOTEST	0	0	0	0	1	1

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ENSG00000105357	ENSG00000105357	MYH14	19:50691442-50813802	NOTEST	0.00693149	0.00757717	0.128494	0	1	1
ENSG00000105366	ENSG00000105366	SIGLEC8	19:51954100-51961710	NOTEST	0	0	0	0	1	1
ENSG00000105370	ENSG00000105370	LIM2	19:51883162-51891214	NOTEST	0	0	0	0	1	1
ENSG00000105374	ENSG00000105374	NKG7	19:51874859-51875969	NOTEST	0.0839356	0	#NAME?	0	1	1
ENSG00000105383	ENSG00000105383	CD33	19:51728319-51747115	NOTEST	0	0.031701	inf	0	1	1
ENSG00000105388	ENSG00000105388	CEACAM5	19:42212503-42290801	NOTEST	0	0	0	0	1	1
ENSG00000105392	ENSG00000105392	CRX	19:48322702-48364769	NOTEST	0	0	0	0	1	1
ENSG00000105398	ENSG00000105398	SULT2A1	19:48373722-48389654	NOTEST	0.10678	0.0675799	-0.659971	0	1	1
ENSG00000105428	ENSG00000105428	ZNRF4	19:5455425-5456867	NOTEST	0	0	0	0	1	1
ENSG00000105464	ENSG00000105464	GRIN2D	19:48898131-48948188	NOTEST	0.0966781	0.19573	1.0176	0	1	1
ENSG00000105467	ENSG00000105467	SYNGR4	19:48867651-48879633	NOTEST	0.0395096	0.0139316	-1.50384	0	1	1
ENSG00000105479	ENSG00000105479	CCDC114	19:48799713-48833810	NOTEST	0.447082	0.307579	-0.539582	0	1	1
ENSG00000105492	ENSG00000105492	SIGLEC6	19:52022778-52035110	NOTEST	0	0	0	0	1	1
ENSG00000105501	ENSG00000105501	SIGLEC5	19:52114780-52150151	NOTEST	0	0	0	0	1	1
ENSG00000105507	ENSG00000105507	CABP5	19:48533209-48547310	NOTEST	0	0	0	0	1	1
ENSG00000105509	ENSG00000105509	HAS1	19:52216364-52227247	NOTEST	0.0140272	0	#NAME?	0	1	1
ENSG00000105523	ENSG00000105523	FAM83E	19:49104066-49118111	NOTEST	0.0523779	0.00594672	-3.13879	0	1	1
ENSG00000105538	ENSG00000105538	RASIP1	19:49223843-49243978	NOTEST	0.115794	0.086369	-0.42297	0	1	1
ENSG00000105549	ENSG00000105549	THEG	19:361749-376013	NOTEST	0	0.0116628	inf	0	1	1
ENSG00000105550	ENSG00000105550	FGF21	19:49258815-49261587	NOTEST	0	0	0	0	1	1
ENSG00000105605	ENSG00000105605	CACNG7	19:54412588-54447195	NOTEST	0	0	0	0	1	1
ENSG00000105609	ENSG00000105609	LILRB5	19:54754262-54761164	NOTEST	0	0	0	0	1	1
ENSG00000105610	ENSG00000105610	KLF1	19:12995236-12997995	NOTEST	0.0189647	0.0751848	1.98712	0	1	1
ENSG00000105639	ENSG00000105639	JAK3	19:17935588-17958880	NOTEST	0.0624099	0.173383	1.47412	0	1	1
ENSG00000105641	ENSG00000105641	SLC5A5	19:17982781-18005983	NOTEST	0.00872282	0	#NAME?	0	1	1
ENSG00000105650	ENSG00000105650	PDE4C	19:18315539-18366229	NOTEST	0.262779	0.175575	-0.581765	0	1	1
ENSG00000105664	ENSG00000105664	COMP	19:18893582-18902123	NOTEST	0	0	0	0	1	1
ENSG00000105675	ENSG00000105675	ATP4A	19:36040944-36054560	NOTEST	0.0154558	0.197144	3.67303	0	1	1
ENSG00000105694	ENSG00000105694	TCEB1P28	19:2511216-2702707	NOTEST	0	0	0	0	1	1
ENSG00000105695	ENSG00000105695	MAG	19:35783027-35804707	NOTEST	0.0680897	0.0280717	-1.27832	0	1	1
ENSG00000105696	ENSG00000105696	TMEM59L	19:18682539-18731849	NOTEST	0.0994637	0.216842	1.12441	0	1	1
ENSG00000105697	ENSG00000105697	HAMP	19:35771618-35776046	NOTEST	0	0	0	0	1	1
ENSG00000105707	ENSG00000105707	HPN	19:35531409-35598141	NOTEST	0.162075	0.302937	0.902356	0	1	1
ENSG00000105737	ENSG00000105737	GRIK5	19:42502472-42585701	NOTEST	0.109323	0.220106	1.0096	0	1	1
ENSG00000105784	ENSG00000105784	RUNDC3B	7:87133174-87461611	NOTEST	0.328398	0.338904	0.0454323	0	1	1
ENSG00000105808	ENSG00000105808	RASA4	7:102122891-102312088	NOTEST	0.366762	0.502324	0.453773	0	1	1
ENSG00000105851	ENSG00000105851	PIK3CG	7:106505722-106547590	NOTEST	0	0	0	0	1	1
ENSG00000105852	ENSG00000105852	PON3	7:94926987-95025680	NOTEST	0.180362	0.134443	-0.423904	0	1	1
ENSG00000105877	ENSG00000105877	DNAH11	7:21582832-21985702	NOTEST	0.0489203	0.0194354	-1.33174	0	1	1
ENSG00000105894	ENSG00000105894	PTN	7:136912087-137028611	NOTEST	0.0943351	0.12274	0.37974	0	1	1
ENSG00000105954	ENSG00000105954	NPVF	7:25264188-25268105	NOTEST	0	0	0	0	1	1
ENSG00000105963	ENSG00000105963	ADAP1	7:937539-1015235	NOTEST	0.157949	0.205267	0.378039	0	1	1
ENSG00000105967	ENSG00000105967	TFEC	7:115575201-115799950	NOTEST	0.0138286	0.0922595	2.73804	0	1	1
ENSG00000105989	ENSG00000105989	WNT2	7:116916684-116963343	NOTEST	0	0	0	0	1	1
ENSG00000105996	ENSG00000105996	HOXA2	7:27132611-27142430	NOTEST	0.114761	0.0808012	-0.506186	0	1	1

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ENSG00000106006	ENSG00000106006	HOXA6	7:27145802-27197555	NOTEST	0.458428	0.610871	0.414172	0	1	1
ENSG00000106018	ENSG00000106018	VIPR2	7:158799212-158937649	NOTEST	0.0110404	0	#NAME?	0	1	1
ENSG00000106038	ENSG00000106038	EVX1	7:27281047-27290112	NOTEST	0.0111728	0	#NAME?	0	1	1
ENSG00000106078	ENSG00000106078	COBL	7:50934443-51384515	NOTEST	0.078241	0.161574	1.0462	0	1	1
ENSG00000106113	ENSG00000106113	CRHR2	7:30692199-30965131	NOTEST	0	0.0286764	inf	0	1	1
ENSG00000106123	ENSG00000106123	EPHB6	7:142552791-142568847	NOTEST	0.0126216	0.148522	3.5567	0	1	1
ENSG00000106128	ENSG00000106128	GHRHR	7:30978283-31032869	NOTEST	0	0	0	0	1	1
ENSG00000106178	ENSG00000106178	CCL24	7:75440982-75452674	NOTEST	0	0	0	0	1	1
ENSG00000106236	ENSG00000106236	NPTX2	7:98246608-98259180	NOTEST	0	0	0	0	1	1
ENSG00000106258	ENSG00000106258	CYP3A5	7:99245816-99277621	NOTEST	0.168323	0.230504	0.45356	0	1	1
ENSG00000106302	ENSG00000106302	HYAL4	7:123454192-123517532	NOTEST	0.0186954	0.00516028	-1.85716	0	1	1
ENSG00000106304	ENSG00000106304	SPAM1	7:123565285-123611468	NOTEST	0	0	0	0	1	1
ENSG00000106328	ENSG00000106328	FSCN3	7:127220671-127242198	NOTEST	0.101045	0.169133	0.743155	0	1	1
ENSG00000106331	ENSG00000106331	PAX4	7:127250345-127255982	NOTEST	0	0	0	0	1	1
ENSG00000106336	ENSG00000106336	FBXO24	7:100169854-100205798	NOTEST	0.363931	0.383037	0.0738175	0	1	1
ENSG00000106341	ENSG00000106341	PPP1R17	7:31726328-31748069	NOTEST	0	0	0	0	1	1
ENSG00000106366	ENSG00000106366	SERPINE1	7:100770369-100782547	NOTEST	0.0525357	0.0836119	0.670412	0	1	1
ENSG00000106384	ENSG00000106384	MOGAT3	7:100838287-100844302	NOTEST	0	0.0053206	inf	0	1	1
ENSG00000106410	ENSG00000106410	NOBOX	7:144094332-144107320	NOTEST	0	0	0	0	1	1
ENSG00000106436	ENSG00000106436	MYL10	7:101256604-101272576	NOTEST	0.497541	0.284772	-0.805005	0	1	1
ENSG00000106483	ENSG00000106483	SFRP4	7:37723398-38065297	NOTEST	0	0	0	0	1	1
ENSG00000106484	ENSG00000106484	MEST	7:130125882-130148500	NOTEST	0.223304	0.186767	-0.257767	0	1	1
ENSG00000106511	ENSG00000106511	MEOX2	7:15650836-15726437	NOTEST	0	0.0153695	inf	0	1	1
ENSG00000106526	ENSG00000106526	ACTR3C	7:149941004-150035239	NOTEST	0.256681	0.521277	1.02207	0	1	1
ENSG00000106536	ENSG00000106536	POU6F2	7:39017597-39532694	NOTEST	0.0171705	0.0082034	-1.06563	0	1	1
ENSG00000106538	ENSG00000106538	RARRES2	7:150035407-150038763	NOTEST	0.0378783	0.110837	1.549	0	1	1
ENSG00000106540	ENSG00000106540	AC004837.3	7:39605974-39649919	NOTEST	0	0	0	0	1	1
ENSG00000106541	ENSG00000106541	AGR2	7:16831434-16873057	NOTEST	0	0	0	0	1	1
ENSG00000106560	ENSG00000106560	GIMAP2	7:150382784-150390729	NOTEST	0.0232421	0.0798101	1.77983	0	1	1
ENSG00000106565	ENSG00000106565	TMEM176B	7:150488372-150502208	NOTEST	0.0649149	0.0647456	-0.00376687	0	1	1
ENSG00000106631	ENSG00000106631	MYL7	7:44178462-44180931	NOTEST	0	0	0	0	1	1
ENSG00000106633	ENSG00000106633	GCK	7:44183871-44237769	NOTEST	0.0625729	0.0183343	-1.77099	0	1	1
ENSG00000106648	ENSG00000106648	GALNTL5	7:151653463-151717019	NOTEST	0	0	0	0	1	1
ENSG00000106686	ENSG00000106686	SPATA6L	9:4490443-4666674	NOTEST	0.565164	0.396096	-0.512817	0	1	1
ENSG00000106809	ENSG00000106809	OGN	9:95059639-95432547	NOTEST	0	0	0	0	1	1
ENSG00000106819	ENSG00000106819	ASPN	9:95059639-95432547	NOTEST	0.037324	0	#NAME?	0	1	1
ENSG00000106823	ENSG00000106823	ECM2	9:95059639-95432547	NOTEST	0	0	0	0	1	1
ENSG00000106829	ENSG00000106829	TLE4	9:82186687-82341658	NOTEST	0.162663	0.259299	0.672728	0	1	1
ENSG00000106927	ENSG00000106927	AMBP	9:116822406-116840752	NOTEST	0	0.0554748	inf	0	1	1
ENSG00000106952	ENSG00000106952	TNFSF8	9:117656002-117692697	NOTEST	0	0.00665144	inf	0	1	1
ENSG00000107014	ENSG00000107014	RLN2	9:5299867-5304969	NOTEST	0	0	0	0	1	1
ENSG00000107018	ENSG00000107018	RLN1	9:5334968-5339873	NOTEST	0	0.0553056	inf	0	1	1
ENSG00000107105	ENSG00000107105	ELAVL2	9:23690101-23826335	NOTEST	0	0	0	0	1	1
ENSG00000107147	ENSG00000107147	KCNT1	9:138594030-138684992	NOTEST	0	0.0117631	inf	0	1	1
ENSG00000107159	ENSG00000107159	CA9	9:35658300-35681156	NOTEST	0.310939	0.106267	-1.54894	0	1	1

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ENSG00000107187	ENSG00000107187	LHX3	9:139088095-139096955	NOTEST	0	0.00525487	inf	0	1	1
ENSG00000107249	ENSG00000107249	GLIS3	9:3824126-4348392	NOTEST	0.0985532	0.181164	0.87832	0	1	1
ENSG00000107447	ENSG00000107447	DNTT	10:98052441-98098321	NOTEST	0	0.0121945	inf	0	1	1
ENSG00000107485	ENSG00000107485	GATA3	10:8095566-8117161	NOTEST	0	0	0	0	1	1
ENSG00000107562	ENSG00000107562	CXCL12	10:44793037-44881941	NOTEST	0	0	0	0	1	1
ENSG00000107593	ENSG00000107593	PKD2L1	10:102047902-102090243	NOTEST	0.0070512	0	#NAME?	0	1	1
ENSG00000107618	ENSG00000107618	RBP3	10:48381486-48390991	NOTEST	0	0	0	0	1	1
ENSG00000107623	ENSG00000107623	GDF10	10:48425814-48438976	NOTEST	0	0.0045607	inf	0	1	1
ENSG00000107719	ENSG00000107719	PALD1	10:72238576-72328205	NOTEST	0.0156146	0.0284924	0.867676	0	1	1
ENSG00000107731	ENSG00000107731	UNC5B	10:72972326-73062621	NOTEST	0.027445	0.0380032	0.469576	0	1	1
ENSG00000107736	ENSG00000107736	CDH23	10:73156690-73575702	NOTEST	0.0166585	0.0111837	-0.574859	0	1	1
ENSG00000107738	ENSG00000107738	C10orf54	10:73156690-73575702	NOTEST	0.131559	0.490065	1.89727	0	1	1
ENSG00000107742	ENSG00000107742	SPOCK2	10:73818792-73848790	NOTEST	0.0859932	0.121505	0.498716	0	1	1
ENSG00000107807	ENSG00000107807	TLX1	10:102849077-102899468	NOTEST	0	0	0	0	1	1
ENSG00000107831	ENSG00000107831	FGF8	10:103529898-103535854	NOTEST	0	0.0236289	inf	0	1	1
ENSG00000107859	ENSG00000107859	PITX3	10:103989942-104001231	NOTEST	0	0.00946209	inf	0	1	1
ENSG00000107864	ENSG00000107864	CPEB3	10:93806448-94050844	NOTEST	0.270864	0.327644	0.274562	0	1	1
ENSG00000107954	ENSG00000107954	NEURL1	10:105239359-105615301	NOTEST	0.0857651	0.145586	0.76341	0	1	1
ENSG00000108001	ENSG00000108001	EBF3	10:131633546-131762105	NOTEST	0.352698	0.134699	-1.3887	0	1	1
ENSG00000108176	ENSG00000108176	DNAJC12	10:69556426-69597924	NOTEST	0.301033	0.493595	0.713408	0	1	1
ENSG00000108242	ENSG00000108242	CYP2C18	10:96443250-96613017	NOTEST	0.00614679	0.0523883	3.09134	0	1	1
ENSG00000108244	ENSG00000108244	KRT23	17:39077681-39132178	NOTEST	0.108784	0.234003	1.10505	0	1	1
ENSG00000108255	ENSG00000108255	CRYBA1	17:27573880-27581512	NOTEST	0	0.0246003	inf	0	1	1
ENSG00000108309	ENSG00000108309	RUNDC3A	17:42376941-42396039	NOTEST	0.268935	0.487063	0.85685	0	1	1
ENSG00000108342	ENSG00000108342	CSF3	17:38171613-38174066	NOTEST	0	0	0	0	1	1
ENSG00000108381	ENSG00000108381	ASPA	17:3343312-3461289	NOTEST	0.290668	0.451956	0.636808	0	1	1
ENSG00000108405	ENSG00000108405	P2RX1	17:3799885-3819794	NOTEST	0	0	0	0	1	1
ENSG00000108417	ENSG00000108417	KRT37	17:39558667-39581301	NOTEST	0	0	0	0	1	1
ENSG00000108442	ENSG00000108442	TVP23BP2	2:74785009-74875465	NOTEST	0	0	0	0	1	1
ENSG00000108452	ENSG00000108452	ZNF29P	17:15468796-15587625	NOTEST	0	0	0	0	1	1
ENSG00000108516	ENSG00000108516	AC003958.6	17:39490883-39491985	NOTEST	0	0	0	0	1	1
ENSG00000108576	ENSG00000108576	SLC6A4	17:28521336-28563020	NOTEST	0.0857642	0.0248058	-1.7897	0	1	1
ENSG00000108602	ENSG00000108602	ALDH3A1	17:19640994-19652256	NOTEST	0.117836	0.0478518	-1.30013	0	1	1
ENSG00000108622	ENSG00000108622	ICAM2	17:62073430-62097994	NOTEST	0.0548119	0.0573999	0.0665592	0	1	1
ENSG00000108684	ENSG00000108684	ASIC2	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000108688	ENSG00000108688	CCL7	17:32597239-32599261	NOTEST	0	0	0	0	1	1
ENSG00000108700	ENSG00000108700	CCL8	17:32646054-32648421	NOTEST	0	0	0	0	1	1
ENSG00000108702	ENSG00000108702	CCL1	17:32687346-32690250	NOTEST	0	0	0	0	1	1
ENSG00000108753	ENSG00000108753	HNF1B	17:36046434-36108563	NOTEST	0	0	0	0	1	1
ENSG00000108759	ENSG00000108759	KRT32	17:39616062-39623681	NOTEST	0	0	0	0	1	1
ENSG00000108785	ENSG00000108785	HSD17B1P1	17:40688189-40718295	NOTEST	0.16064	0.0695483	-1.20774	0	1	1
ENSG00000108798	ENSG00000108798	ABI3	17:47280152-47300587	NOTEST	0	0	0	0	1	1
ENSG00000108821	ENSG00000108821	COL1A1	17:48260649-48278993	NOTEST	0.34525	0.463804	0.425873	0	1	1
ENSG00000108825	ENSG00000108825	PTGES3L-AARSD1	17:41102542-41132545	NOTEST	0.369001	0.459792	0.317355	0	1	1
ENSG00000108839	ENSG00000108839	ALOX12	17:6757179-6922978	NOTEST	0.304422	0.129273	-1.23565	0	1	1

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ENSG00000108846	ENSG00000108846	ABCC3	17:48712137-48769613	NOTEST	0.0400396	0.093313	1.22065	0	1	1
ENSG00000108849	ENSG00000108849	PPY	17:42018171-42019836	NOTEST	0.145198	0.425624	1.55155	0	1	1
ENSG00000108878	ENSG00000108878	CACNG1	17:65040705-65052909	NOTEST	0	0	0	0	1	1
ENSG00000108947	ENSG00000108947	EFNB3	17:7608519-7614696	NOTEST	0.193151	0.219245	0.182811	0	1	1
ENSG00000108950	ENSG00000108950	FAM20A	17:66255322-66760023	NOTEST	0.460532	0.520721	0.17721	0	1	1
ENSG00000109047	ENSG00000109047	RCVRN	17:9799636-9808938	NOTEST	0	0.0189028	inf	0	1	1
ENSG00000109061	ENSG00000109061	MYH1	17:10286448-10527203	NOTEST	0.0045762	0	#NAME?	0	1	1
ENSG00000109072	ENSG00000109072	VTN	17:26684603-26734215	NOTEST	0.270388	0.427203	0.659892	0	1	1
ENSG00000109101	ENSG00000109101	FOXN1	17:26782769-26972472	NOTEST	0	0	0	0	1	1
ENSG00000109132	ENSG00000109132	PHOX2B	4:41746098-41826136	NOTEST	0	0	0	0	1	1
ENSG00000109158	ENSG00000109158	GABRA4	4:46920916-47428461	NOTEST	0	0	0	0	1	1
ENSG00000109163	ENSG00000109163	GNRHR	4:68566997-68995598	NOTEST	0.00745162	0	#NAME?	0	1	1
ENSG00000109181	ENSG00000109181	UGT2B10	4:69681710-69696914	NOTEST	0	0	0	0	1	1
ENSG00000109182	ENSG00000109182	CWH43	4:48988263-49064098	NOTEST	0	0	0	0	1	1
ENSG00000109193	ENSG00000109193	SULT1E1	4:70657589-70725870	NOTEST	0	0	0	0	1	1
ENSG00000109205	ENSG00000109205	ODAM	4:71062212-71070293	NOTEST	0	0	0	0	1	1
ENSG00000109208	ENSG00000109208	SMR3A	4:71226477-71232875	NOTEST	0	0	0	0	1	1
ENSG00000109255	ENSG00000109255	NMU	4:56461395-56502865	NOTEST	0.310365	0.476453	0.618365	0	1	1
ENSG00000109272	ENSG00000109272	PF4V1	4:74718905-74719872	NOTEST	0.163344	0.262211	0.68281	0	1	1
ENSG00000109321	ENSG00000109321	AREG	4:75310850-75320726	NOTEST	0	0	0	0	1	1
ENSG00000109424	ENSG00000109424	UCP1	4:141480587-141489959	NOTEST	0	0	0	0	1	1
ENSG00000109471	ENSG00000109471	IL2	4:123372624-123377880	NOTEST	0	0	0	0	1	1
ENSG00000109472	ENSG00000109472	CPE	4:166282345-166419472	NOTEST	0.448467	0.358353	-0.323622	0	1	1
ENSG00000109511	ENSG00000109511	ANXA10	4:168867824-169108841	NOTEST	0	0	0	0	1	1
ENSG00000109610	ENSG00000109610	SOD3	4:24791533-24802464	NOTEST	0	0.131636	inf	0	1	1
ENSG00000109625	ENSG00000109625	CPZ	4:8560451-8621488	NOTEST	0	0.0229336	inf	0	1	1
ENSG00000109684	ENSG00000109684	CLNK	4:10488018-10686489	NOTEST	0.0452639	0	#NAME?	0	1	1
ENSG00000109705	ENSG00000109705	NKX3-2	4:13542453-13546674	NOTEST	0.36445	0.496081	0.444854	0	1	1
ENSG00000109758	ENSG00000109758	HGFAC	4:3443613-3451211	NOTEST	0.109706	0.184884	0.752974	0	1	1
ENSG00000109771	ENSG00000109771	LRP2BP	4:186080818-186317053	NOTEST	0.189416	0.197119	0.0575129	0	1	1
ENSG00000109851	ENSG00000109851	DBX1	11:20177700-20182159	NOTEST	0	0	0	0	1	1
ENSG00000109906	ENSG00000109906	ZBTB16	11:113930314-114227293	NOTEST	0	0	0	0	1	1
ENSG00000109927	ENSG00000109927	TECTA	11:120971881-121062202	NOTEST	0.0531687	0.0687431	0.370638	0	1	1
ENSG00000109943	ENSG00000109943	CRTAM	11:122709207-122743347	NOTEST	0.0129253	0	#NAME?	0	1	1
ENSG00000109956	ENSG00000109956	B3GAT1	11:134248397-134281812	NOTEST	0	0.00310951	inf	0	1	1
ENSG00000109991	ENSG00000109991	P2RX3	11:57105847-57138073	NOTEST	0	0	0	0	1	1
ENSG00000110002	ENSG00000110002	VWA5A	11:123986068-124018428	NOTEST	0	0.00681945	inf	0	1	1
ENSG00000110076	ENSG00000110076	NRXN2	11:64373645-64490660	NOTEST	0.160658	0.103838	-0.629659	0	1	1
ENSG00000110077	ENSG00000110077	MS4A6A	11:59939080-59952139	NOTEST	0.130079	0.154078	0.244267	0	1	1
ENSG00000110079	ENSG00000110079	MS4A4A	11:60048013-60076445	NOTEST	0.0809251	0.0674617	-0.262517	0	1	1
ENSG00000110148	ENSG00000110148	CCKBR	11:6280965-6293357	NOTEST	0	0	0	0	1	1
ENSG00000110169	ENSG00000110169	HPX	11:6452278-6463847	NOTEST	0.0471497	0.129062	1.45275	0	1	1
ENSG00000110195	ENSG00000110195	FOLR1	11:71874365-71920285	NOTEST	0	0.0759496	inf	0	1	1
ENSG00000110203	ENSG00000110203	FOLR3	11:71825914-71850936	NOTEST	0	0	0	0	1	1
ENSG00000110243	ENSG00000110243	APOA5	11:116660082-116663136	NOTEST	0	0	0	0	1	1

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ENSG00000110245	ENSG00000110245	APOC3	11:116700421-116703788	NOTEST	0	0	0	0	1	1
ENSG00000110318	ENSG00000110318	KIAA1377	11:101761404-101871789	NOTEST	0.3061	0.281416	-0.121298	0	1	1
ENSG00000110324	ENSG00000110324	IL10RA	11:117857062-117872196	NOTEST	0	0	0	0	1	1
ENSG00000110347	ENSG00000110347	MMP12	11:102733466-102745764	NOTEST	0	0.0129282	inf	0	1	1
ENSG00000110375	ENSG00000110375	UPK2	11:118754474-118829269	NOTEST	0.0364409	0	#NAME?	0	1	1
ENSG00000110436	ENSG00000110436	SLC1A2	11:35272752-35442549	NOTEST	0.00992973	0.0783999	2.98102	0	1	1
ENSG00000110446	ENSG00000110446	SLC15A3	11:60680637-60720002	NOTEST	0.0611845	0.0427357	-0.517725	0	1	1
ENSG00000110448	ENSG00000110448	CD5	11:60869866-60895324	NOTEST	0	0	0	0	1	1
ENSG00000110484	ENSG00000110484	SCGB2A2	11:62037626-62040628	NOTEST	0	0	0	0	1	1
ENSG00000110665	ENSG00000110665	C11orf21	11:2316874-2339430	NOTEST	0	0	0	0	1	1
ENSG00000110675	ENSG00000110675	ELMOD1	11:107461816-107537505	NOTEST	0	0	0	0	1	1
ENSG00000110680	ENSG00000110680	CALCA	11:14926542-15103888	NOTEST	0	0	0	0	1	1
ENSG00000110723	ENSG00000110723	EXPH5	11:108376157-108464465	NOTEST	0.0834011	0.0725052	-0.201981	0	1	1
ENSG00000110777	ENSG00000110777	POU2AF1	11:111222976-111328876	NOTEST	0.115958	0.0452304	-1.35824	0	1	1
ENSG00000110786	ENSG00000110786	PTPN5	11:18714668-18814268	NOTEST	0	0	0	0	1	1
ENSG00000110848	ENSG00000110848	CD69	12:9905081-9913497	NOTEST	0.0456643	0.0286204	-0.674024	0	1	1
ENSG00000110876	ENSG00000110876	SELPLG	12:109015685-109035094	NOTEST	0.129917	0.0738687	-0.814552	0	1	1
ENSG00000110887	ENSG00000110887	DAO	12:109252707-109294819	NOTEST	0	0	0	0	1	1
ENSG00000110900	ENSG00000110900	TSPAN11	12:31079361-31149534	NOTEST	0.200337	0.345601	0.786678	0	1	1
ENSG00000110934	ENSG00000110934	BIN2	12:51674821-51718452	NOTEST	0.0147585	0	#NAME?	0	1	1
ENSG00000110944	ENSG00000110944	IL23A	12:56732662-56734193	NOTEST	0.357532	0.151923	-1.23473	0	1	1
ENSG00000110975	ENSG00000110975	SYT10	12:33527172-33592754	NOTEST	0	0	0	0	1	1
ENSG00000111012	ENSG00000111012	CYP27B1	12:58156116-58212487	NOTEST	0.112898	0.277753	1.29878	0	1	1
ENSG00000111046	ENSG00000111046	MYF6	12:81101276-81103253	NOTEST	0	0	0	0	1	1
ENSG00000111049	ENSG00000111049	MYF5	12:81110690-81113452	NOTEST	0	0	0	0	1	1
ENSG00000111058	ENSG00000111058	ACSS3	12:81186298-81650533	NOTEST	0.0630623	0.0143551	-2.13521	0	1	1
ENSG00000111181	ENSG00000111181	SLC6A12	12:299242-323736	NOTEST	0.142517	0.371003	1.3803	0	1	1
ENSG00000111199	ENSG00000111199	TRPV4	12:110220889-110271241	NOTEST	0.0237201	0.0354735	0.580633	0	1	1
ENSG00000111218	ENSG00000111218	PRMT8	12:3490514-3703139	NOTEST	0	0	0	0	1	1
ENSG00000111241	ENSG00000111241	FGF6	12:4537320-4554780	NOTEST	0	0	0	0	1	1
ENSG00000111245	ENSG00000111245	MYL2	12:111348622-111358526	NOTEST	0.0233546	0	#NAME?	0	1	1
ENSG00000111249	ENSG00000111249	CUX2	12:111471827-111788358	NOTEST	0	0.0156024	inf	0	1	1
ENSG00000111254	ENSG00000111254	AKAP3	12:4671369-4960277	NOTEST	0.425382	0.249177	-0.771587	0	1	1
ENSG00000111262	ENSG00000111262	KCNA1	12:5019070-5040527	NOTEST	0	0	0	0	1	1
ENSG00000111275	ENSG00000111275	ALDH2	12:112123856-112247782	NOTEST	0.134365	0.183771	0.451747	0	1	1
ENSG00000111291	ENSG00000111291	GPRC5D	12:13080659-13193613	NOTEST	0.0312447	0	#NAME?	0	1	1
ENSG00000111305	ENSG00000111305	GSG1	12:13197217-13295455	NOTEST	0.0461407	0.0198913	-1.2139	0	1	1
ENSG00000111319	ENSG00000111319	SCNN1A	12:6456008-6500733	NOTEST	0.0460707	0.0837065	0.861491	0	1	1
ENSG00000111335	ENSG00000111335	OAS2	12:113344581-113455556	NOTEST	0.291683	0.45476	0.640705	0	1	1
ENSG00000111339	ENSG00000111339	ART4	12:14956505-15059520	NOTEST	0.00540419	0	#NAME?	0	1	1
ENSG00000111344	ENSG00000111344	RASAL1	12:113536623-113574044	NOTEST	0.217238	0.201814	-0.106253	0	1	1
ENSG00000111404	ENSG00000111404	RERGL	12:18233802-18801348	NOTEST	0.0644763	0	#NAME?	0	1	1
ENSG00000111405	ENSG00000111405	ENDOU	12:48099867-48231681	NOTEST	0.112585	0.223392	0.988556	0	1	1
ENSG00000111432	ENSG00000111432	FZD10	12:130647003-130650285	NOTEST	0	0	0	0	1	1

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ENSG00000111452	ENSG00000111452	GPR133	12:131438451-131626014	NOTEST	0.103364	0.363397	1.81381	0	1	1
ENSG00000111536	ENSG00000111536	IL26	12:68383224-68628466	NOTEST	0	0	0	0	1	1
ENSG00000111537	ENSG00000111537	IFNG	12:68383224-68628466	NOTEST	0	0	0	0	1	1
ENSG00000111644	ENSG00000111644	ACRBP	12:6747240-6756626	NOTEST	0.0520695	0.0697896	0.422573	0	1	1
ENSG00000111664	ENSG00000111664	GNB3	12:6949117-6961230	NOTEST	0.589441	0.440738	-0.419425	0	1	1
ENSG00000111679	ENSG00000111679	PTPN6	12:7055630-7070479	NOTEST	0.0546412	0.0725828	0.409639	0	1	1
ENSG00000111700	ENSG00000111700	SLCO1B3	12:20963635-21392180	NOTEST	0	0	0	0	1	1
ENSG00000111701	ENSG00000111701	APOBEC1	12:7801995-7818499	NOTEST	0	0	0	0	1	1
ENSG00000111704	ENSG00000111704	NANOG	12:7940389-7948655	NOTEST	0	0	0	0	1	1
ENSG00000111713	ENSG00000111713	GYS2	12:21679240-21757781	NOTEST	0.0050176	0.0156085	1.63726	0	1	1
ENSG00000111729	ENSG00000111729	CLEC4A	12:8276227-8371507	NOTEST	0.151108	0.167829	0.151415	0	1	1
ENSG00000111732	ENSG00000111732	AICDA	12:8754761-8765467	NOTEST	0.0951795	0.0269611	-1.81977	0	1	1
ENSG00000111780	ENSG00000111780	AL021546.6	12:120875892-120899389	NOTEST	0.133371	0.0602406	-1.14664	0	1	1
ENSG00000111783	ENSG00000111783	RFX4	12:106751435-107283090	NOTEST	0	0.243143	inf	0	1	1
ENSG00000111796	ENSG00000111796	KLRB1	12:9747146-9760482	NOTEST	0.0422451	0	#NAME?	0	1	1
ENSG00000111816	ENSG00000111816	FRK	6:116252311-116381921	NOTEST	0.14462	0.0551569	-1.39065	0	1	1
ENSG00000111817	ENSG00000111817	DSE	6:116575335-116762424	NOTEST	0.348713	0.203932	-0.773947	0	1	1
ENSG00000111834	ENSG00000111834	RSPH4A	6:116937641-116954148	NOTEST	0.0674176	0.00843226	-2.99913	0	1	1
ENSG00000111837	ENSG00000111837	MAK	6:10747991-10979553	NOTEST	0.261027	0.14735	-0.824948	0	1	1
ENSG00000111863	ENSG00000111863	ADTRP	6:11712286-11807279	NOTEST	0.532858	0.104096	-2.35584	0	1	1
ENSG00000111886	ENSG00000111886	GABRR2	6:89966926-90025018	NOTEST	0.0756952	0.0617842	-0.292962	0	1	1
ENSG00000111971	ENSG00000111971	LY6G5C	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000111981	ENSG00000111981	ULBP1	6:150285142-150294846	NOTEST	0.00999711	0.0404938	2.01812	0	1	1
ENSG00000112038	ENSG00000112038	OPRM1	6:154331630-154677926	NOTEST	0	0	0	0	1	1
ENSG00000112041	ENSG00000112041	TULP1	6:35465650-35480715	NOTEST	0	0	0	0	1	1
ENSG00000112053	ENSG00000112053	SLC26A8	6:35911290-35992645	NOTEST	0	0	0	0	1	1
ENSG00000112077	ENSG00000112077	RHAG	6:49572870-49604552	NOTEST	0	0	0	0	1	1
ENSG00000112115	ENSG00000112115	IL17A	6:52051184-52055436	NOTEST	0	0	0	0	1	1
ENSG00000112116	ENSG00000112116	IL17F	6:52101478-52109335	NOTEST	0	0	0	0	1	1
ENSG00000112139	ENSG00000112139	MDGA1	6:37600283-37667082	NOTEST	0.261269	0.540099	1.04768	0	1	1
ENSG00000112164	ENSG00000112164	GLP1R	6:39016573-39055519	NOTEST	0	0	0	0	1	1
ENSG00000112175	ENSG00000112175	BMP5	6:55618442-55740362	NOTEST	0	0	0	0	1	1
ENSG00000112182	ENSG00000112182	BACH2	6:90636247-91006627	NOTEST	0.595992	0.592347	-0.00884977	0	1	1
ENSG00000112195	ENSG00000112195	TREML2	6:41158014-41168932	NOTEST	0	0	0	0	1	1
ENSG00000112212	ENSG00000112212	TSPO2	6:40994771-41067715	NOTEST	0.0517107	0	#NAME?	0	1	1
ENSG00000112214	ENSG00000112214	FHL5	6:97010423-97064512	NOTEST	0	0	0	0	1	1
ENSG00000112218	ENSG00000112218	GPR63	6:97233012-97285353	NOTEST	0.23827	0.465902	0.967428	0	1	1
ENSG00000112232	ENSG00000112232	KHDRBS2	6:62340137-62996132	NOTEST	0.546846	0.450296	-0.280261	0	1	1
ENSG00000112238	ENSG00000112238	PRDM13	6:100054605-100063454	NOTEST	0.388787	0.310618	-0.32384	0	1	1
ENSG00000112246	ENSG00000112246	SIM1	6:100832890-100912805	NOTEST	0.00391272	0.00559343	0.51556	0	1	1
ENSG00000112273	ENSG00000112273	HDGFL1	6:22569677-22571892	NOTEST	0	0	0	0	1	1
ENSG00000112297	ENSG00000112297	AIM1	6:106959729-107018326	NOTEST	0.487303	0.590271	0.276556	0	1	1
ENSG00000112299	ENSG00000112299	VNN1	6:133002728-133035188	NOTEST	0.0151796	0.0225147	0.568735	0	1	1
ENSG00000112303	ENSG00000112303	VNN2	6:133065008-133084598	NOTEST	0.0493017	0.049552	0.00730563	0	1	1
ENSG00000112309	ENSG00000112309	B3GAT2	6:71377478-71666741	NOTEST	0.149264	0.0585838	-1.34929	0	1	1

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ENSG00000112333	ENSG00000112333	NR2E1	6:108487261-108510013	NOTEST	0.0907965	0.025377	-1.83911	0	1	1
ENSG00000112337	ENSG00000112337	SLC17A2	6:25912981-25930946	NOTEST	0	0	0	0	1	1
ENSG00000112379	ENSG00000112379	KIAA1244	6:138483057-138665800	NOTEST	0.376302	0.334583	-0.169529	0	1	1
ENSG00000112459	ENSG00000112459	OR14J1	HSCHR6_MHC_MCF:29274636-29275753	NOTEST	0	0	0	0	1	1
ENSG00000112461	ENSG00000112461	OR5V1	HSCHR6_MHC_MCF:29323243-29424633	NOTEST	0	0	0	0	1	1
ENSG00000112462	ENSG00000112462	OR12D3	6:29323006-29424848	NOTEST	0	0	0	0	1	1
ENSG00000112474	ENSG00000112474	HSD17B8	HSCHR6_MHC_QBL:33101244-33103438	NOTEST	0	0	0	0	1	1
ENSG00000112486	ENSG00000112486	CCR6	6:167412669-167553184	NOTEST	0	0	0	0	1	1
ENSG00000112493	ENSG00000112493	TAPBP	HSCHR6_MHC_COX:33189080-33203772	NOTEST	0	0	0	0	1	1
ENSG00000112494	ENSG00000112494	UNC93A	6:167684656-167729507	NOTEST	0	0	0	0	1	1
ENSG00000112499	ENSG00000112499	SLC22A2	6:160592092-160698670	NOTEST	0	0	0	0	1	1
ENSG00000112530	ENSG00000112530	PACRG	6:161768451-163736524	NOTEST	0.204116	0.074558	-1.45296	0	1	1
ENSG00000112539	ENSG00000112539	C6orf118	6:165693152-165723096	NOTEST	0.00905016	0.00702626	-0.365187	0	1	1
ENSG00000112559	ENSG00000112559	MDFI	6:41604619-41621984	NOTEST	0.102703	0.117719	0.19686	0	1	1
ENSG00000112562	ENSG00000112562	SMOC2	6:168841830-169073984	NOTEST	0	0	0	0	1	1
ENSG00000112599	ENSG00000112599	GUCA1B	6:42152138-42162654	NOTEST	0.0889866	0.0691746	-0.363346	0	1	1
ENSG00000112619	ENSG00000112619	PRPH2	6:42664339-42690312	NOTEST	0.00529816	0	#NAME?	0	1	1
ENSG00000112706	ENSG00000112706	IMPG1	6:76630831-76782395	NOTEST	0.0526582	0.0375998	-0.485933	0	1	1
ENSG00000112761	ENSG00000112761	WISP3	6:112375274-112408732	NOTEST	0.019699	0.0143896	-0.453099	0	1	1
ENSG00000112782	ENSG00000112782	CLIC5	6:45868044-46048132	NOTEST	0	0	0	0	1	1
ENSG00000112796	ENSG00000112796	ENPP5	6:46126923-46138708	NOTEST	0.0226393	0	#NAME?	0	1	1
ENSG00000112799	ENSG00000112799	LY86	6:6346697-6655216	NOTEST	0	0	0	0	1	1
ENSG00000112818	ENSG00000112818	MEP1A	6:46761126-46807515	NOTEST	0	0	0	0	1	1
ENSG00000112837	ENSG00000112837	TBX18	6:85397068-85474237	NOTEST	0.100672	0.03561	-1.49931	0	1	1
ENSG00000112936	ENSG00000112936	C7	5:40909353-40983041	NOTEST	0.196977	0.195436	-0.0113319	0	1	1
ENSG00000113073	ENSG00000113073	SLC4A9	5:139739786-139780952	NOTEST	0.0699632	0.0747988	0.0964181	0	1	1
ENSG00000113083	ENSG00000113083	LOX	5:121297655-121413980	NOTEST	0.350183	0.613033	0.807855	0	1	1
ENSG00000113088	ENSG00000113088	GZMK	5:54273691-54338672	NOTEST	0	0	0	0	1	1
ENSG00000113100	ENSG00000113100	CDH9	5:26880708-27121257	NOTEST	0	0	0	0	1	1
ENSG00000113196	ENSG00000113196	HAND1	5:153854531-153857824	NOTEST	0	0.00666221	inf	0	1	1
ENSG00000113205	ENSG00000113205	PCDHB3	5:140479828-140483406	NOTEST	0.489038	0.335697	-0.542788	0	1	1
ENSG00000113211	ENSG00000113211	PCDHB6	5:140529682-140532868	NOTEST	0.432773	0.399423	-0.115695	0	1	1
ENSG00000113212	ENSG00000113212	PCDHB7	5:140552242-140555957	NOTEST	0.137715	0.19052	0.468254	0	1	1
ENSG00000113248	ENSG00000113248	PCDHB15	5:140625146-140627799	NOTEST	0.491392	0.460648	-0.0932079	0	1	1
ENSG00000113249	ENSG00000113249	HAVCR1	5:156456423-156486130	NOTEST	0	0	0	0	1	1
ENSG00000113262	ENSG00000113262	GRM6	5:178396390-178423207	NOTEST	0	0	0	0	1	1
ENSG00000113263	ENSG00000113263	ITK	5:156512842-156682201	NOTEST	0.0918033	0.29262	1.67241	0	1	1
ENSG00000113296	ENSG00000113296	THBS4	5:79287133-79379477	NOTEST	0.308934	0.258285	-0.258336	0	1	1
ENSG00000113302	ENSG00000113302	IL12B	5:158737940-158789842	NOTEST	0	0	0	0	1	1
ENSG00000113303	ENSG00000113303	BTNL8	5:180326076-180377906	NOTEST	0	0	0	0	1	1
ENSG00000113319	ENSG00000113319	RASGRF2	5:80243515-80597379	NOTEST	0.173553	0.203602	0.230372	0	1	1
ENSG00000113327	ENSG00000113327	GABRG2	5:161494545-161582542	NOTEST	0.0442063	0	#NAME?	0	1	1
ENSG00000113361	ENSG00000113361	CDH6	5:31094083-31329253	NOTEST	0	0.0026429	inf	0	1	1
ENSG00000113389	ENSG00000113389	NPR3	5:32689175-32791819	NOTEST	0.0206964	0.00729523	-1.50435	0	1	1
ENSG00000113396	ENSG00000113396	SLC27A6	5:127593600-128369335	NOTEST	0.0379795	0.0152626	-1.31522	0	1	1

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ENSG00000113430	ENSG00000113430	IRX4	5:1877540-1887350	NOTEST	0	0	0	0	1	1
ENSG00000113492	ENSG00000113492	AGXT2	5:34998205-35048198	NOTEST	0	0	0	0	1	1
ENSG00000113494	ENSG00000113494	PRLR	5:35048860-35230794	NOTEST	0	0	0	0	1	1
ENSG00000113520	ENSG00000113520	IL4	5:132009677-132018368	NOTEST	0	0	0	0	1	1
ENSG00000113525	ENSG00000113525	IL5	5:131877135-131999964	NOTEST	0	0.0994469	inf	0	1	1
ENSG00000113555	ENSG00000113555	PCDH12	5:141323149-141369856	NOTEST	0.0711605	0.0500481	-0.507762	0	1	1
ENSG00000113578	ENSG00000113578	FGF1	5:141689991-142077617	NOTEST	0.228609	0.621077	1.44189	0	1	1
ENSG00000113594	ENSG00000113594	LIFR	5:38475064-38671318	NOTEST	0.220136	0.193928	-0.182878	0	1	1
ENSG00000113600	ENSG00000113600	C9	5:39284363-39462402	NOTEST	0.0219795	0	#NAME?	0	1	1
ENSG00000113721	ENSG00000113721	PDGFRB	5:149493399-149535435	NOTEST	0.062769	0.118248	0.913687	0	1	1
ENSG00000113722	ENSG00000113722	CDX1	5:149546357-149564120	NOTEST	0	0	0	0	1	1
ENSG00000113749	ENSG00000113749	HRH2	5:175085032-175113245	NOTEST	0.428296	0.573058	0.420075	0	1	1
ENSG00000113763	ENSG00000113763	UNC5A	5:176237477-176326333	NOTEST	0.00457143	0	#NAME?	0	1	1
ENSG00000113805	ENSG00000113805	CNTN3	3:74311718-74570291	NOTEST	0.00871817	0	#NAME?	0	1	1
ENSG00000113889	ENSG00000113889	KNG1	3:186435037-186478330	NOTEST	0	0	0	0	1	1
ENSG00000113905	ENSG00000113905	HRG	3:186353757-186396029	NOTEST	0	0	0	0	1	1
ENSG00000113924	ENSG00000113924	HGD	3:120347019-120401418	NOTEST	0	0	0	0	1	1
ENSG00000113946	ENSG00000113946	CLDN16	3:190040329-190129932	NOTEST	0.090204	0.247829	1.45808	0	1	1
ENSG00000114013	ENSG00000114013	CD86	3:121774212-121839983	NOTEST	0	0	0	0	1	1
ENSG00000114113	ENSG00000114113	RBP2	3:139108656-139396859	NOTEST	0	0	0	0	1	1
ENSG00000114115	ENSG00000114115	RBP1	3:139108656-139396859	NOTEST	0.0883881	0.0144074	-2.61704	0	1	1
ENSG00000114124	ENSG00000114124	GRK7	3:141496989-141537332	NOTEST	0	0	0	0	1	1
ENSG00000114204	ENSG00000114204	SERPINI2	3:167159576-167371771	NOTEST	0	0.0717003	inf	0	1	1
ENSG00000114248	ENSG00000114248	LRRC31	3:169556966-169587718	NOTEST	0	0	0	0	1	1
ENSG00000114279	ENSG00000114279	FGF12	3:191857183-192485553	NOTEST	0.0734483	0.132072	0.846527	0	1	1
ENSG00000114349	ENSG00000114349	GNAT1	3:50229044-50233949	NOTEST	0.104342	0.0218879	-2.25311	0	1	1
ENSG00000114374	ENSG00000114374	USP9Y	Y:14813159-14972764	NOTEST	0	0	0	0	1	1
ENSG00000114378	ENSG00000114378	HYAL1	3:50337319-50349812	NOTEST	0.241409	0.328194	0.443069	0	1	1
ENSG00000114455	ENSG00000114455	HHLA2	3:108015375-108097132	NOTEST	0	0	0	0	1	1
ENSG00000114487	ENSG00000114487	MORC1	3:108677085-108836989	NOTEST	0.0794586	0.192145	1.27392	0	1	1
ENSG00000114638	ENSG00000114638	UPK1B	3:118864996-118924000	NOTEST	0	0	0	0	1	1
ENSG00000114654	ENSG00000114654	EFCC1	3:128598438-128759585	NOTEST	0	0.0151585	inf	0	1	1
ENSG00000114656	ENSG00000114656	KIAA1257	3:128598438-128759585	NOTEST	0	0.06011	inf	0	1	1
ENSG00000114757	ENSG00000114757	PEX5L	3:179512745-179754841	NOTEST	0.109551	0.0803062	-0.448021	0	1	1
ENSG00000114771	ENSG00000114771	AADAC	3:151451703-151645963	NOTEST	0	0	0	0	1	1
ENSG00000114786	ENSG00000114786	ABHD14A-ACY1	3:51989329-52023213	NOTEST	0.553461	0.430081	-0.363871	0	1	1
ENSG00000114805	ENSG00000114805	PLCH1	3:155093368-155462856	NOTEST	0.0964715	0.0764716	-0.335179	0	1	1
ENSG00000114812	ENSG00000114812	VIPR1	3:42530790-42579059	NOTEST	0.0620061	0.106449	0.779686	0	1	1
ENSG00000114854	ENSG00000114854	TNNC1	3:52485117-52488086	NOTEST	0.225586	0.0212863	-3.40567	0	1	1
ENSG00000115008	ENSG00000115008	IL1A	2:113531491-113542167	NOTEST	0.0152085	0.0106849	-0.509306	0	1	1
ENSG00000115112	ENSG00000115112	TFCP2L1	2:121974162-122042783	NOTEST	0.0211851	0.0305882	0.529926	0	1	1
ENSG00000115138	ENSG00000115138	POMC	2:25383721-25391772	NOTEST	0	0	0	0	1	1
ENSG00000115155	ENSG00000115155	OTOF	2:26680070-26781566	NOTEST	0.0149258	0.00503091	-1.56891	0	1	1
ENSG00000115165	ENSG00000115165	CYTIP	2:158271130-158345473	NOTEST	0.0607433	0.00552362	-3.45904	0	1	1
ENSG00000115194	ENSG00000115194	SLC30A3	2:27476551-27504367	NOTEST	0.0943571	0.14279	0.597689	0	1	1

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ENSG00000115221	ENSG00000115221	ITGB6	2:160956176-161128399	NOTEST	0.0921212	0.0715662	-0.364256	0	1	1
ENSG00000115252	ENSG00000115252	PDE1A	2:183004762-183387919	NOTEST	0.0920093	0.0123877	-2.89288	0	1	1
ENSG00000115257	ENSG00000115257	PCSK4	19:1481426-1490751	NOTEST	0.431492	0.511273	0.24476	0	1	1
ENSG00000115263	ENSG00000115263	GCG	2:162999391-163008914	NOTEST	0	0	0	0	1	1
ENSG00000115297	ENSG00000115297	TLX2	2:74740589-74744274	NOTEST	0	0.0106195	inf	0	1	1
ENSG00000115353	ENSG00000115353	TACR1	2:75273589-75426826	NOTEST	0.00559652	0.0125804	1.16857	0	1	1
ENSG00000115361	ENSG00000115361	ACADL	2:211036241-211095107	NOTEST	0.373503	0.528637	0.501157	0	1	1
ENSG00000115380	ENSG00000115380	EFEMP1	2:56093101-56151274	NOTEST	0.0931481	0.207941	1.15857	0	1	1
ENSG00000115386	ENSG00000115386	REG1A	2:79347487-79350545	NOTEST	0	0	0	0	1	1
ENSG00000115423	ENSG00000115423	DNAH6	2:84743578-85046713	NOTEST	0.143968	0.00890656	-4.01474	0	1	1
ENSG00000115474	ENSG00000115474	KCNJ13	2:233562008-233880595	NOTEST	0.60567	0.386518	-0.647995	0	1	1
ENSG00000115488	ENSG00000115488	NEU2	2:233897381-233899767	NOTEST	0	0	0	0	1	1
ENSG00000115523	ENSG00000115523	GNLY	2:85912297-85925977	NOTEST	0	0	0	0	1	1
ENSG00000115590	ENSG00000115590	IL1R2	2:102608305-102645006	NOTEST	0	0.0111865	inf	0	1	1
ENSG00000115592	ENSG00000115592	PRKAG3	2:219687105-219696809	NOTEST	0.0357523	0.111293	1.63826	0	1	1
ENSG00000115593	ENSG00000115593	SMYD1	2:88367298-88412906	NOTEST	0.027076	0.129191	2.25442	0	1	1
ENSG00000115594	ENSG00000115594	IL1R1	2:102681003-102798568	NOTEST	0.0195236	0.00618062	-1.6594	0	1	1
ENSG00000115596	ENSG00000115596	WNT6	2:219724543-219738955	NOTEST	0	0.0454115	inf	0	1	1
ENSG00000115598	ENSG00000115598	IL1RL2	2:102803432-102856462	NOTEST	0	0	0	0	1	1
ENSG00000115602	ENSG00000115602	IL1RL1	2:102927961-103015218	NOTEST	0	0	0	0	1	1
ENSG00000115604	ENSG00000115604	IL18R1	2:102927961-103015218	NOTEST	0	0.12731	inf	0	1	1
ENSG00000115607	ENSG00000115607	IL18RAP	2:103035148-103069025	NOTEST	0	0	0	0	1	1
ENSG00000115616	ENSG00000115616	SLC9A2	2:103236165-103327777	NOTEST	0.0102274	0	#NAME?	0	1	1
ENSG00000115665	ENSG00000115665	SLC5A7	2:108602978-108630450	NOTEST	0	0	0	0	1	1
ENSG00000115705	ENSG00000115705	TPO	2:1377994-1547483	NOTEST	0	0.00828255	inf	0	1	1
ENSG00000115718	ENSG00000115718	PROC	2:128176002-128186822	NOTEST	0.0540763	0.036254	-0.576858	0	1	1
ENSG00000115850	ENSG00000115850	LCT	2:136545409-136594750	NOTEST	0.00243129	0	#NAME?	0	1	1
ENSG00000115919	ENSG00000115919	KYNU	2:143635066-143799890	NOTEST	0.132571	0.247124	0.898468	0	1	1
ENSG00000115934	ENSG00000115934	RP11-153K16.2	12:22852792-23404433	NOTEST	0	0	0	0	1	1
ENSG00000116014	ENSG00000116014	KISS1R	19:917286-921015	NOTEST	0.0359505	0.0159639	-1.1712	0	1	1
ENSG00000116031	ENSG00000116031	CD207	2:71057346-71062952	NOTEST	0.0667642	0.0123083	-2.43945	0	1	1
ENSG00000116032	ENSG00000116032	GRIN3B	19:999600-1021117	NOTEST	0.0181775	0.0256391	0.496191	0	1	1
ENSG00000116147	ENSG00000116147	TNR	1:175276353-175712906	NOTEST	0	0	0	0	1	1
ENSG00000116157	ENSG00000116157	GPX7	1:53068043-53074723	NOTEST	0	0.010923	inf	0	1	1
ENSG00000116176	ENSG00000116176	TPSG1	16:1203240-1275257	NOTEST	0.0288817	0.0458128	0.665597	0	1	1
ENSG00000116183	ENSG00000116183	PAPPA2	1:176432306-176814735	NOTEST	0.0143313	0.0138406	-0.0502623	0	1	1
ENSG00000116194	ENSG00000116194	ANGPTL1	1:178693440-178889238	NOTEST	0.0845646	0.0370315	-1.1913	0	1	1
ENSG00000116218	ENSG00000116218	NPHS2	1:179334854-179545087	NOTEST	0	0	0	0	1	1
ENSG00000116254	ENSG00000116254	CHD5	1:6161852-6240183	NOTEST	0.012689	0.0356718	1.4912	0	1	1
ENSG00000116299	ENSG00000116299	KIAA1324	1:109648572-109749401	NOTEST	0.0777913	0.14148	0.862913	0	1	1
ENSG00000116329	ENSG00000116329	OPRD1	1:29138653-29190208	NOTEST	0.524085	0.548172	0.06483	0	1	1
ENSG00000116544	ENSG00000116544	DLGAP3	1:35331036-35395186	NOTEST	0.00869366	0.00642736	-0.435737	0	1	1
ENSG00000116574	ENSG00000116574	RHOU	1:228870823-228882416	NOTEST	0.108405	0.104778	-0.0490907	0	1	1
ENSG00000116652	ENSG00000116652	DLEU2L	1:63906440-64125916	NOTEST	0.0558429	0.161272	1.53005	0	1	1
ENSG00000116690	ENSG00000116690	PRG4	1:186265404-186344825	NOTEST	0	0.00306694	inf	0	1	1

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ENSG00000116701	ENSG00000116701	NCF2	1:183441350-183567381	NOTEST	0.0134607	0.132038	3.29413	0	1	1
ENSG00000116703	ENSG00000116703	PDC	1:186412697-186430254	NOTEST	0	0	0	0	1	1
ENSG00000116721	ENSG00000116721	PRAMEF1	1:12851545-12856777	NOTEST	0	0	0	0	1	1
ENSG00000116726	ENSG00000116726	PRAMEF12	1:12834983-12838049	NOTEST	0	0	0	0	1	1
ENSG00000116745	ENSG00000116745	RPE65	1:68894504-68915642	NOTEST	0.00608892	0.00900652	0.564784	0	1	1
ENSG00000116748	ENSG00000116748	AMPD1	1:115215718-115238239	NOTEST	0.0121641	0.00520949	-1.22341	0	1	1
ENSG00000116771	ENSG00000116771	AGMAT	1:15853307-15930121	NOTEST	0.105964	0.256659	1.27628	0	1	1
ENSG00000116774	ENSG00000116774	OLFML3	1:114522062-114524876	NOTEST	0.093512	0.113478	0.279184	0	1	1
ENSG00000116783	ENSG00000116783	TNNI3K	1:74663895-75010112	NOTEST	0.0886916	0.0205511	-2.10958	0	1	1
ENSG00000116785	ENSG00000116785	CFHR3	1:196743924-196763203	NOTEST	0	0	0	0	1	1
ENSG00000116824	ENSG00000116824	CD2	1:117297006-117311850	NOTEST	0	0	0	0	1	1
ENSG00000116852	ENSG00000116852	KIF21B	1:200938519-200992828	NOTEST	0.206067	0.477826	1.21337	0	1	1
ENSG00000116882	ENSG00000116882	HAO2	1:119911401-119936753	NOTEST	0.0811283	0.0176481	-2.20069	0	1	1
ENSG00000116981	ENSG00000116981	NT5C1A	1:40124792-40137710	NOTEST	0.0447808	0.0819568	0.871984	0	1	1
ENSG00000116983	ENSG00000116983	HPCAL4	1:40144319-40157361	NOTEST	0.156153	0.244596	0.64744	0	1	1
ENSG00000116996	ENSG00000116996	ZP4	1:238025474-238091621	NOTEST	0.0347812	0.114375	1.71739	0	1	1
ENSG00000117009	ENSG00000117009	KMO	1:241695433-241965435	NOTEST	0.071178	0.406401	2.5134	0	1	1
ENSG00000117013	ENSG00000117013	KCNQ4	1:41249683-41306124	NOTEST	0.104727	0.23983	1.19538	0	1	1
ENSG00000117069	ENSG00000117069	ST6GALNAC5	1:77333125-77531396	NOTEST	0.583874	0.585669	0.00442836	0	1	1
ENSG00000117090	ENSG00000117090	SLAMF1	1:160577889-160617085	NOTEST	0.162341	0.195326	0.266856	0	1	1
ENSG00000117091	ENSG00000117091	CD48	1:160639937-160681641	NOTEST	0.301894	0.0792828	-1.92896	0	1	1
ENSG00000117148	ENSG00000117148	ACTL8	1:18081807-18153558	NOTEST	0	0.044781	inf	0	1	1
ENSG00000117152	ENSG00000117152	RGS4	1:163038564-163046592	NOTEST	0.148967	0.168362	0.176576	0	1	1
ENSG00000117154	ENSG00000117154	IGSF21	1:18434239-18704977	NOTEST	0	0	0	0	1	1
ENSG00000117215	ENSG00000117215	PLA2G2D	1:20438431-20446050	NOTEST	0	0.00416976	inf	0	1	1
ENSG00000117242	ENSG00000117242	PINK1-AS	1:20959947-20988000	NOTEST	0.559633	0.510565	-0.132387	0	1	1
ENSG00000117245	ENSG00000117245	KIF17	1:20990506-21044510	NOTEST	0.319151	0.252476	-0.338096	0	1	1
ENSG00000117281	ENSG00000117281	CD160	1:145611035-145715614	NOTEST	0.111075	0.28521	1.36049	0	1	1
ENSG00000117322	ENSG00000117322	CR2	1:207627574-207663240	NOTEST	0	0.0271351	inf	0	1	1
ENSG00000117400	ENSG00000117400	MPL	1:43803477-43818443	NOTEST	0	0.0117326	inf	0	1	1
ENSG00000117407	ENSG00000117407	ARTN	1:44398991-44402913	NOTEST	0.0714007	0.0888375	0.31523	0	1	1
ENSG00000117425	ENSG00000117425	PTCH2	1:45285515-45308735	NOTEST	0.0708762	0.0838528	0.242556	0	1	1
ENSG00000117472	ENSG00000117472	TSPAN1	1:46505811-46651630	NOTEST	0.402742	0.50716	0.332584	0	1	1
ENSG00000117480	ENSG00000117480	FAAH	1:46859936-46879520	NOTEST	0.47715	0.446383	-0.0961598	0	1	1
ENSG00000117501	ENSG00000117501	MROH9	1:170904611-171033906	NOTEST	0.0835763	0.125333	0.584603	0	1	1
ENSG00000117507	ENSG00000117507	FMO6P	1:171106878-171130707	NOTEST	0	0	0	0	1	1
ENSG00000117560	ENSG00000117560	FASLG	1:172628153-172636014	NOTEST	0	0	0	0	1	1
ENSG00000117594	ENSG00000117594	HSD11B1	1:209834708-209908295	NOTEST	0	0	0	0	1	1
ENSG00000117595	ENSG00000117595	IRF6	1:209959035-209979465	NOTEST	0	0.0136791	inf	0	1	1
ENSG00000117598	ENSG00000117598	LPPR5	1:99355805-99614408	NOTEST	0.0267438	0.035351	0.402547	0	1	1
ENSG00000117600	ENSG00000117600	LPPR4	1:99729508-99775146	NOTEST	0.481838	0.448491	-0.103469	0	1	1
ENSG00000117601	ENSG00000117601	SERPINC1	1:173872946-173886516	NOTEST	0.0535934	0.0229367	-1.2244	0	1	1
ENSG00000117707	ENSG00000117707	PROX1	1:213991093-214214595	NOTEST	0.111559	0.117476	0.0745665	0	1	1
ENSG00000117834	ENSG00000117834	SLC5A9	1:48688356-48714316	NOTEST	0.319144	0.17945	-0.830629	0	1	1
ENSG00000117971	ENSG00000117971	CHRNB4	15:78916460-79027837	NOTEST	0.0591375	0.112053	0.922041	0	1	1

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ENSG00000117983	ENSG00000117983	MUC5B	11:1244295-1283406	NOTEST	0.0130787	0.0390191	1.57696	0	1	1
ENSG00000118004	ENSG00000118004	COLEC11	2:3642425-3692048	NOTEST	0.0881778	0.0822299	-0.100751	0	1	1
ENSG00000118017	ENSG00000118017	A4GNT	3:137842559-137851229	NOTEST	0.0168278	0.026916	0.677617	0	1	1
ENSG00000118094	ENSG00000118094	TREH	11:118477154-118550399	NOTEST	0	0.0441685	inf	0	1	1
ENSG00000118137	ENSG00000118137	APOA1	11:116706466-116969153	NOTEST	0	0.0276511	inf	0	1	1
ENSG00000118156	ENSG00000118156	ZNF541	19:48023941-48059113	NOTEST	0.121433	0.0776659	-0.644813	0	1	1
ENSG00000118160	ENSG00000118160	SLC8A2	19:47931273-47975425	NOTEST	0.122619	0.347698	1.50365	0	1	1
ENSG00000118194	ENSG00000118194	TNNT2	1:201328135-201368736	NOTEST	0	0	0	0	1	1
ENSG00000118231	ENSG00000118231	CRYGD	2:208986330-208989225	NOTEST	0	0	0	0	1	1
ENSG00000118245	ENSG00000118245	TNP1	2:217536827-217858802	NOTEST	0	0	0	0	1	1
ENSG00000118271	ENSG00000118271	TTR	18:29171688-29178974	NOTEST	0	0.0280233	inf	0	1	1
ENSG00000118307	ENSG00000118307	CASC1	12:25261353-25348096	NOTEST	0.397166	0.168266	-1.239	0	1	1
ENSG00000118308	ENSG00000118308	LRMP	12:25173935-25261268	NOTEST	0	0.0107048	inf	0	1	1
ENSG00000118407	ENSG00000118407	FILIP1	6:75994729-76203454	NOTEST	0.0220648	0.00272815	-3.01576	0	1	1
ENSG00000118432	ENSG00000118432	CNR1	6:88849582-88876078	NOTEST	0.00666682	0.00214409	-1.63663	0	1	1
ENSG00000118434	ENSG00000118434	SPACA1	6:88757506-88776550	NOTEST	0	0	0	0	1	1
ENSG00000118473	ENSG00000118473	SGIP1	1:66999065-67213982	NOTEST	0.0042729	0.00519312	0.281386	0	1	1
ENSG00000118491	ENSG00000118491	ZC2HC1B	6:144185572-144259483	NOTEST	0	0	0	0	1	1
ENSG00000118492	ENSG00000118492	ADGB	6:146920100-147136598	NOTEST	0.0629602	0	#NAME?	0	1	1
ENSG00000118495	ENSG00000118495	PLAGL1	6:144261436-144385735	NOTEST	0.0100754	0	#NAME?	0	1	1
ENSG00000118514	ENSG00000118514	ALDH8A1	6:135238527-135271260	NOTEST	0.0485412	0.00737479	-2.71853	0	1	1
ENSG00000118520	ENSG00000118520	ARG1	6:131894283-131949369	NOTEST	0	0	0	0	1	1
ENSG00000118526	ENSG00000118526	TCF21	6:133561735-134216691	NOTEST	0.00677194	0.0122691	0.857383	0	1	1
ENSG00000118557	ENSG00000118557	PMFBP1	16:72078187-72210777	NOTEST	0.463092	0.18782	-1.30195	0	1	1
ENSG00000118702	ENSG00000118702	GHRH	20:35879488-35890238	NOTEST	0.0958785	0.0561721	-0.771354	0	1	1
ENSG00000118733	ENSG00000118733	OLFM3	1:102268129-102462586	NOTEST	0	0.0510004	inf	0	1	1
ENSG00000118777	ENSG00000118777	ABCG2	4:89011415-89152474	NOTEST	0.350633	0.584768	0.737902	0	1	1
ENSG00000118849	ENSG00000118849	RARRES1	3:158414680-158547508	NOTEST	0.13015	0.0800519	-0.701164	0	1	1
ENSG00000118898	ENSG00000118898	PPL	16:4932507-5147809	NOTEST	0.0411687	0.142393	1.79025	0	1	1
ENSG00000118903	ENSG00000118903	BTF3P11	13:77502199-77502970	NOTEST	0	0	0	0	1	1
ENSG00000118946	ENSG00000118946	PCDH17	13:58205943-58303445	NOTEST	0.132059	0.059169	-1.15827	0	1	1
ENSG00000118971	ENSG00000118971	CCND2	12:4357930-4414516	NOTEST	0	0.00165119	inf	0	1	1
ENSG00000118972	ENSG00000118972	FGF23	12:4477392-4488894	NOTEST	0	0	0	0	1	1
ENSG00000118976	ENSG00000118976	HIN1L	12:3900212-4019504	NOTEST	0.010256	0.00360015	-1.51034	0	1	1
ENSG00000118990	ENSG00000118990	GLRXP3	5:161178453-161178774	NOTEST	0	0	0	0	1	1
ENSG00000118997	ENSG00000118997	DNAH7	2:196602426-196933536	NOTEST	0.191348	0.399124	1.06064	0	1	1
ENSG00000119121	ENSG00000119121	TRPM6	9:77337410-77503010	NOTEST	0.173544	0.224816	0.373443	0	1	1
ENSG00000119125	ENSG00000119125	GDA	9:74729510-74872109	NOTEST	0.00287297	0.0157663	2.45623	0	1	1
ENSG00000119147	ENSG00000119147	C2orf40	2:106679701-106694615	NOTEST	0	0.0259283	inf	0	1	1
ENSG00000119283	ENSG00000119283	TRIM67	1:231297857-231357302	NOTEST	0.370302	0.505336	0.44854	0	1	1
ENSG00000119411	ENSG00000119411	BSPRY	9:116111820-116133513	NOTEST	0.0145432	0.037876	1.38094	0	1	1
ENSG00000119440	ENSG00000119440	LCN1P1	9:136100291-136103993	NOTEST	0	0	0	0	1	1
ENSG00000119457	ENSG00000119457	SLC46A2	9:115513117-115653193	NOTEST	0.110968	0.102479	-0.114805	0	1	1
ENSG00000119535	ENSG00000119535	CSF3R	1:36931643-36948879	NOTEST	0.018103	0.0384685	1.08745	0	1	1
ENSG00000119547	ENSG00000119547	ONECUT2	18:55102916-55158529	NOTEST	0.170064	0.213075	0.325285	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000119608	ENSG00000119608	PROX2	14:75230068-75330537	NOTEST	0.0707761	0.132435	0.903948	0	1	1
ENSG00000119614	ENSG00000119614	VSX2	14:74706174-74729441	NOTEST	0	0	0	0	1	1
ENSG00000119636	ENSG00000119636	CCDC176	14:74318546-74551196	NOTEST	0.562585	0.424151	-0.407491	0	1	1
ENSG00000119660	ENSG00000119660	RP11-293M10.4	14:75758808-75761016	NOTEST	0	0.171446	inf	0	1	1
ENSG00000119714	ENSG00000119714	GPR68	14:91698875-91720269	NOTEST	0.0624518	0.0339179	-0.880695	0	1	1
ENSG00000119715	ENSG00000119715	ESRRB	14:76776956-77227731	NOTEST	0.0236486	0.0218146	-0.116462	0	1	1
ENSG00000119737	ENSG00000119737	GPR75	2:53759809-54087297	NOTEST	0.408598	0.487433	0.254522	0	1	1
ENSG00000119866	ENSG00000119866	BCL11A	2:60678301-60780702	NOTEST	0	0.0918109	inf	0	1	1
ENSG00000119888	ENSG00000119888	EPCAM	2:47572296-47614740	NOTEST	0.248205	0.457822	0.883256	0	1	1
ENSG00000119913	ENSG00000119913	TECTB	10:114043492-114064793	NOTEST	0.0222481	0.0172824	-0.364379	0	1	1
ENSG00000119919	ENSG00000119919	NKX2-3	10:101292689-101296278	NOTEST	0	0	0	0	1	1
ENSG00000119973	ENSG00000119973	PRLHR	10:120352915-120355160	NOTEST	0	0	0	0	1	1
ENSG00000120051	ENSG00000120051	CCDC147	10:106113521-106214848	NOTEST	0.0522283	0.179154	1.7783	0	1	1
ENSG00000120055	ENSG00000120055	C10orf95	10:104209573-104220863	NOTEST	0.0733628	0.223212	1.60529	0	1	1
ENSG00000120057	ENSG00000120057	SFRP5	10:99526507-99531709	NOTEST	0.0858508	0.0201316	-2.09237	0	1	1
ENSG00000120068	ENSG00000120068	HOXB8	17:46684593-46712294	NOTEST	0	0	0	0	1	1
ENSG00000120075	ENSG00000120075	HOXB5	17:46618255-46683776	NOTEST	0.0798576	0.0370675	-1.10728	0	1	1
ENSG00000120088	ENSG00000120088	CRHR1	17:43697693-43913194	NOTEST	0	0	0	0	1	1
ENSG00000120093	ENSG00000120093	HOXB3	17:46618255-46683776	NOTEST	0.112513	0.111434	-0.0139027	0	1	1
ENSG00000120094	ENSG00000120094	HOXB1	17:46605887-46608359	NOTEST	0	0	0	0	1	1
ENSG00000120149	ENSG00000120149	MSX2	5:174151535-174157896	NOTEST	0.0332324	0	#NAME?	0	1	1
ENSG00000120156	ENSG00000120156	TEK	9:27109138-27230173	NOTEST	0	0.00888528	inf	0	1	1
ENSG00000120160	ENSG00000120160	EQTN	9:27284655-27297137	NOTEST	0.317179	0.357002	0.170639	0	1	1
ENSG00000120210	ENSG00000120210	INSL6	9:5131978-5185668	NOTEST	0	0	0	0	1	1
ENSG00000120211	ENSG00000120211	INSL4	9:5231418-5235304	NOTEST	0	0	0	0	1	1
ENSG00000120235	ENSG00000120235	IFNA6	9:21349833-21351377	NOTEST	0	0	0	0	1	1
ENSG00000120242	ENSG00000120242	IFNA8	9:21409145-21410184	NOTEST	0	0	0	0	1	1
ENSG00000120251	ENSG00000120251	GRIA2	4:158125333-158287227	NOTEST	0.0102192	0.00401	-1.34962	0	1	1
ENSG00000120262	ENSG00000120262	CCDC170	6:151815164-151942328	NOTEST	0.421477	0.237821	-0.825582	0	1	1
ENSG00000120279	ENSG00000120279	MYCT1	6:153019029-153045702	NOTEST	0.122154	0.180228	0.561124	0	1	1
ENSG00000120280	ENSG00000120280	CXorf21	X:30576940-30595961	NOTEST	0	0	0	0	1	1
ENSG00000120289	ENSG00000120289	MAGEB4	X:30260056-30270155	NOTEST	0	0	0	0	1	1
ENSG00000120322	ENSG00000120322	PCDHB8	5:140557370-140560081	NOTEST	0.241557	0.218259	-0.146324	0	1	1
ENSG00000120324	ENSG00000120324	PCDHB10	5:140571941-140575215	NOTEST	0.319288	0.320453	0.00525496	0	1	1
ENSG00000120327	ENSG00000120327	PCDHB14	5:140602930-140605858	NOTEST	0.232065	0.253463	0.127244	0	1	1
ENSG00000120328	ENSG00000120328	PCDHB12	5:140588268-140591696	NOTEST	0.207615	0.217029	0.0639796	0	1	1
ENSG00000120329	ENSG00000120329	SLC25A2	5:140682195-140683612	NOTEST	0	0.00838472	inf	0	1	1
ENSG00000120332	ENSG00000120332	TNN	1:175036993-175117202	NOTEST	0	0.0117064	inf	0	1	1
ENSG00000120337	ENSG00000120337	TNFSF18	1:172745044-173033155	NOTEST	0.00828998	0	#NAME?	0	1	1
ENSG00000120341	ENSG00000120341	SEC16B	1:177893090-178007142	NOTEST	0.359235	0.245876	-0.546998	0	1	1
ENSG00000120436	ENSG00000120436	GPR31	6:167559901-167610401	NOTEST	0	0	0	0	1	1
ENSG00000120440	ENSG00000120440	TTLL2	6:167738573-167797998	NOTEST	0	0	0	0	1	1
ENSG00000120457	ENSG00000120457	KCNJ5	11:128761250-128790930	NOTEST	0	0.00564302	inf	0	1	1
ENSG00000120471	ENSG00000120471	TP53AIP1	11:128804625-128813040	NOTEST	0.0467827	0.0448217	-0.061779	0	1	1
ENSG00000120498	ENSG00000120498	TEX11	X:69748789-70128581	NOTEST	0	0	0	0	1	1

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ENSG00000120500	ENSG00000120500	ARR3	X:69488154-69501690	NOTEST	0.071647	0.0637339	-0.168845	0	1	1
ENSG00000120549	ENSG00000120549	KIAA1217	10:23983674-24836772	NOTEST	0.0859219	0.0665004	-0.369663	0	1	1
ENSG00000120555	ENSG00000120555	SEPT7P9	10:38671996-38691844	NOTEST	0.0519367	0.0854832	0.718886	0	1	1
ENSG00000120563	ENSG00000120563	LYZL1	10:29577989-29607257	NOTEST	0	0	0	0	1	1
ENSG00000120586	ENSG00000120586	MRC1	10:18098351-18200091	NOTEST	0.00535869	0.00439082	-0.287389	0	1	1
ENSG00000120594	ENSG00000120594	PLXDC2	10:20105167-20578785	NOTEST	0	0	0	0	1	1
ENSG00000120645	ENSG00000120645	IQSEC3	12:175930-291565	NOTEST	0.00221774	0	#NAME?	0	1	1
ENSG00000120659	ENSG00000120659	TNFSF11	13:43136871-43182149	NOTEST	0	0.00587316	inf	0	1	1
ENSG00000120669	ENSG00000120669	SOHLH2	13:36742344-36871979	NOTEST	0.286327	0.25883	-0.145657	0	1	1
ENSG00000120738	ENSG00000120738	EGR1	5:137801178-137805004	NOTEST	0.368811	0.18981	-0.958326	0	1	1
ENSG00000120820	ENSG00000120820	GLT8D2	12:104382761-104457961	NOTEST	0.0818009	0.0222649	-1.87735	0	1	1
ENSG00000120903	ENSG00000120903	CHRNA2	8:27317278-27337400	NOTEST	0	0	0	0	1	1
ENSG00000120907	ENSG00000120907	ADRA1A	8:26605666-26724790	NOTEST	0	0	0	0	1	1
ENSG00000120937	ENSG00000120937	NPPB	1:11917520-11918988	NOTEST	0	0	0	0	1	1
ENSG00000120949	ENSG00000120949	TNFRSF8	1:12123433-12204264	NOTEST	0	0	0	0	1	1
ENSG00000120952	ENSG00000120952	PRAMEF2	1:12916940-12921764	NOTEST	0	0	0	0	1	1
ENSG00000121053	ENSG00000121053	EPX	17:56270097-56282535	NOTEST	0.0434612	0.0268775	-0.693331	0	1	1
ENSG00000121075	ENSG00000121075	TBX4	17:59529764-59562471	NOTEST	0.0746492	0.0902156	0.273249	0	1	1
ENSG00000121089	ENSG00000121089	NACA3P	4:165864441-165865089	NOTEST	0.0311419	0	#NAME?	0	1	1
ENSG00000121101	ENSG00000121101	TEX14	17:56597197-56769416	NOTEST	0.162808	0.201367	0.306659	0	1	1
ENSG00000121270	ENSG00000121270	ABCC11	16:48198862-48482313	NOTEST	0.165912	0.182442	0.137016	0	1	1
ENSG00000121281	ENSG00000121281	ADCY7	16:50280047-50405391	NOTEST	0.218642	0.218348	-0.00194149	0	1	1
ENSG00000121297	ENSG00000121297	TSHZ3	19:31765850-31908700	NOTEST	0	0.00416354	inf	0	1	1
ENSG00000121314	ENSG00000121314	TAS2R8	12:10958649-10959892	NOTEST	0	0	0	0	1	1
ENSG00000121316	ENSG00000121316	PLBD1	12:14656594-14910897	NOTEST	0.0682135	0.0164282	-2.05388	0	1	1
ENSG00000121318	ENSG00000121318	TAS2R10	12:10977558-11324212	NOTEST	0.0511569	0.0120141	-2.0902	0	1	1
ENSG00000121335	ENSG00000121335	PRB2	12:11504756-11653975	NOTEST	0	0	0	0	1	1
ENSG00000121351	ENSG00000121351	IAPP	12:21417533-21572528	NOTEST	0	0	0	0	1	1
ENSG00000121377	ENSG00000121377	TAS2R7	12:10954130-10955226	NOTEST	0	0	0	0	1	1
ENSG00000121380	ENSG00000121380	BCL2L14	12:12202777-12419946	NOTEST	0	0.0338403	inf	0	1	1
ENSG00000121381	ENSG00000121381	TAS2R9	12:10961692-10962767	NOTEST	0	0	0	0	1	1
ENSG00000121388	ENSG00000121388	RP11-408E5.4	13:19756172-19761496	NOTEST	0	0	0	0	1	1
ENSG00000121446	ENSG00000121446	RGSL1	1:182419255-182529734	NOTEST	0	0	0	0	1	1
ENSG00000121454	ENSG00000121454	LHX4	1:180199420-180472089	NOTEST	0.395663	0.360823	-0.132977	0	1	1
ENSG00000121552	ENSG00000121552	CSTA	3:122044090-122060819	NOTEST	0	0.0380128	inf	0	1	1
ENSG00000121570	ENSG00000121570	DPPA4	3:109044987-109056419	NOTEST	0	0	0	0	1	1
ENSG00000121577	ENSG00000121577	POPDC2	3:119355303-119396301	NOTEST	0.22296	0.113871	-0.969377	0	1	1
ENSG00000121594	ENSG00000121594	CD80	3:119217378-119278449	NOTEST	0.279488	0.209031	-0.419073	0	1	1
ENSG00000121634	ENSG00000121634	GJA8	1:147374945-147381393	NOTEST	0	0	0	0	1	1
ENSG00000121742	ENSG00000121742	GJB6	13:20796109-20806534	NOTEST	0	0	0	0	1	1
ENSG00000121764	ENSG00000121764	HCRTR1	1:32083286-32169920	NOTEST	0	0.0378531	inf	0	1	1
ENSG00000121797	ENSG00000121797	CCRL2	3:46448653-46454488	NOTEST	0	0	0	0	1	1
ENSG00000121807	ENSG00000121807	CCR2	3:46395224-46402419	NOTEST	0	0	0	0	1	1
ENSG00000121853	ENSG00000121853	GHSR	3:172162922-172166246	NOTEST	0	0	0	0	1	1
ENSG00000121858	ENSG00000121858	TNFSF10	3:172223297-172241297	NOTEST	0	0.0225389	inf	0	1	1

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ENSG00000121871	ENSG00000121871	SLITRK3	3:164904507-164914897	NOTEST	0.0761823	0.133669	0.811143	0	1	1
ENSG00000121895	ENSG00000121895	TMEM156	4:38968364-39034542	NOTEST	0	0.0302102	inf	0	1	1
ENSG00000121898	ENSG00000121898	CPXM2	10:125465722-125699783	NOTEST	0.389086	0.188624	-1.04458	0	1	1
ENSG00000121904	ENSG00000121904	CSMD2	1:33979608-34631443	NOTEST	0.00206763	0	#NAME?	0	1	1
ENSG00000121905	ENSG00000121905	HPCA	1:33351594-33367039	NOTEST	0.162401	0.459502	1.50051	0	1	1
ENSG00000121933	ENSG00000121933	ADORA3	1:112025969-112310638	NOTEST	0.212815	0.24775	0.219286	0	1	1
ENSG00000121966	ENSG00000121966	CXCR4	2:136871918-136875735	NOTEST	0.102611	0.0152766	-2.74779	0	1	1
ENSG00000122012	ENSG00000122012	SV2C	5:75377770-75649764	NOTEST	0.0195178	0.0228178	0.225367	0	1	1
ENSG00000122025	ENSG00000122025	FLT3	13:28577410-28674729	NOTEST	0	0	0	0	1	1
ENSG00000122043	ENSG00000122043	LINC00544	13:30510041-30524625	NOTEST	0	0	0	0	1	1
ENSG00000122121	ENSG00000122121	XPNPEP2	X:128872949-128903514	NOTEST	0	0	0	0	1	1
ENSG00000122122	ENSG00000122122	SASH3	X:128913954-128930939	NOTEST	0	0	0	0	1	1
ENSG00000122133	ENSG00000122133	PAEP	9:138453601-138458801	NOTEST	0.281206	0.336408	0.258584	0	1	1
ENSG00000122136	ENSG00000122136	OBP2A	9:138437984-138441815	NOTEST	0	0	0	0	1	1
ENSG00000122145	ENSG00000122145	TBX22	X:79270254-79287268	NOTEST	0.377682	0.358878	-0.0736764	0	1	1
ENSG00000122176	ENSG00000122176	FMOD	1:203309755-203320617	NOTEST	0.469195	0.623268	0.409664	0	1	1
ENSG00000122180	ENSG00000122180	MYOG	1:203052259-203055164	NOTEST	0	0	0	0	1	1
ENSG00000122188	ENSG00000122188	LAX1	1:203734303-203745361	NOTEST	0	0	0	0	1	1
ENSG00000122194	ENSG00000122194	PLG	6:161123269-161174347	NOTEST	0	0	0	0	1	1
ENSG00000122224	ENSG00000122224	LY9	1:160765863-160798051	NOTEST	0	0.00212122	inf	0	1	1
ENSG00000122254	ENSG00000122254	HS3ST2	16:22825497-22927659	NOTEST	0.00708206	0	#NAME?	0	1	1
ENSG00000122304	ENSG00000122304	PRM2	16:11343475-11445619	NOTEST	0	0	0	0	1	1
ENSG00000122375	ENSG00000122375	OPN4	10:88414313-88426605	NOTEST	0	0	0	0	1	1
ENSG00000122420	ENSG00000122420	PTGFR	1:78695282-79005434	NOTEST	0	0.00499914	inf	0	1	1
ENSG00000122432	ENSG00000122432	SPATA1	1:84964007-85040163	NOTEST	0.0804599	0.140725	0.806534	0	1	1
ENSG00000122543	ENSG00000122543	OCM	7:5919457-5925993	NOTEST	0	0	0	0	1	1
ENSG00000122548	ENSG00000122548	KIAA0087	7:26572739-26578407	NOTEST	0	0.00870294	inf	0	1	1
ENSG00000122584	ENSG00000122584	NXPH1	7:8473584-8792593	NOTEST	0	0	0	0	1	1
ENSG00000122585	ENSG00000122585	NPY	7:24323781-24331484	NOTEST	0	0	0	0	1	1
ENSG00000122592	ENSG00000122592	HOXA7	7:27145802-27197555	NOTEST	0.196694	0.256539	0.383223	0	1	1
ENSG00000122641	ENSG00000122641	INHBA	7:41706765-41818986	NOTEST	0	0.0310431	inf	0	1	1
ENSG00000122679	ENSG00000122679	RAMP3	7:45197389-45225901	NOTEST	0.0128923	0	#NAME?	0	1	1
ENSG00000122711	ENSG00000122711	SPINK4	9:33218362-33264761	NOTEST	0	0	0	0	1	1
ENSG00000122718	ENSG00000122718	OR2S2	9:35957104-35958151	NOTEST	0	0	0	0	1	1
ENSG00000122728	ENSG00000122728	TAF1L	9:32629451-32648683	NOTEST	0.0167137	0.00898621	-0.895247	0	1	1
ENSG00000122733	ENSG00000122733	KIAA1045	9:34957483-34982541	NOTEST	0.127959	0.200449	0.647559	0	1	1
ENSG00000122756	ENSG00000122756	CNTFR	9:34551429-34590121	NOTEST	0.2219	0.474943	1.09784	0	1	1
ENSG00000122787	ENSG00000122787	AKR1D1	7:137687069-137802732	NOTEST	0	0	0	0	1	1
ENSG00000122824	ENSG00000122824	NUDT10	X:51075082-51080377	NOTEST	0.0239097	0.136471	2.51292	0	1	1
ENSG00000122852	ENSG00000122852	SFTPA1	10:81370694-81375196	NOTEST	0	0	0	0	1	1
ENSG00000122859	ENSG00000122859	NEUROG3	10:71331453-71332994	NOTEST	0	0	0	0	1	1
ENSG00000122872	ENSG00000122872	ARL4P	10:61786055-62493248	NOTEST	0	0	0	0	1	1
ENSG00000122986	ENSG00000122986	HVCN1	12:111051831-111142755	NOTEST	0.0634533	0.112758	0.829464	0	1	1
ENSG00000123009	ENSG00000123009	NME2P1	12:120719939-120720632	NOTEST	0.174481	0.632267	1.85746	0	1	1
ENSG00000123165	ENSG00000123165	ACTRT1	X:127184942-127186382	NOTEST	0	0	0	0	1	1

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ENSG00000123171	ENSG00000123171	CCDC70	13:52436116-52440366	NOTEST	0	0.0225224	inf	0	1	1
ENSG00000123201	ENSG00000123201	GUCY1B2	13:51568646-51654998	NOTEST	0.0101253	0.00662626	-0.611699	0	1	1
ENSG00000123243	ENSG00000123243	ITIH5	10:7601231-7708961	NOTEST	0.207973	0.425077	1.03133	0	1	1
ENSG00000123307	ENSG00000123307	NEUROD4	12:55413728-55423798	NOTEST	0	0	0	0	1	1
ENSG00000123329	ENSG00000123329	ARHGAP9	12:57853917-57914300	NOTEST	0.037418	0	#NAME?	0	1	1
ENSG00000123338	ENSG00000123338	NCKAP1L	12:54891494-54937889	NOTEST	0	0	0	0	1	1
ENSG00000123342	ENSG00000123342	MMP19	12:56137063-56236750	NOTEST	0.0196487	0.00744239	-1.40059	0	1	1
ENSG00000123360	ENSG00000123360	PDE1B	12:54943133-54982443	NOTEST	0.00750434	0.0342691	2.19111	0	1	1
ENSG00000123405	ENSG00000123405	NFE2	12:54624723-54745633	NOTEST	0.162548	0.206159	0.342893	0	1	1
ENSG00000123407	ENSG00000123407	HOXC12	12:54348617-54352745	NOTEST	7.11E-07	0.00364649	12.3238	0	1	1
ENSG00000123447	ENSG00000123447	TYRL	11:49426526-49437299	NOTEST	0.284256	0.131581	-1.11124	0	1	1
ENSG00000123453	ENSG00000123453	SARDH	9:136528681-136605077	NOTEST	0.0655717	0.209067	1.67282	0	1	1
ENSG00000123454	ENSG00000123454	DBH	9:136501481-136524466	NOTEST	0.0160885	0	#NAME?	0	1	1
ENSG00000123500	ENSG00000123500	COL10A1	6:116422011-116570660	NOTEST	0.00858619	0.00333509	-1.36429	0	1	1
ENSG00000123561	ENSG00000123561	SERPINA7	X:105277196-105282729	NOTEST	0	0	0	0	1	1
ENSG00000123569	ENSG00000123569	H2BFWT	X:103265718-103268259	NOTEST	0	0	0	0	1	1
ENSG00000123572	ENSG00000123572	NRK	X:105066535-105202602	NOTEST	0.0446376	0.0505398	0.17916	0	1	1
ENSG00000123576	ENSG00000123576	ESX1	X:103494718-103499614	NOTEST	0	0	0	0	1	1
ENSG00000123584	ENSG00000123584	MAGEA9B	X:148663308-148669116	NOTEST	0	0	0	0	1	1
ENSG00000123594	ENSG00000123594	ATXN3L	X:13328770-13338518	NOTEST	0	0	0	0	1	1
ENSG00000123609	ENSG00000123609	NMI	2:152126978-152146571	NOTEST	0.496943	0.233831	-1.08761	0	1	1
ENSG00000123610	ENSG00000123610	TNFAIP6	2:152214105-152236560	NOTEST	0.0550031	0.00835109	-2.71948	0	1	1
ENSG00000123838	ENSG00000123838	C4BPA	1:207277606-207318317	NOTEST	0	0	0	0	1	1
ENSG00000123843	ENSG00000123843	C4BPB	1:207262186-207273338	NOTEST	0	0	0	0	1	1
ENSG00000123870	ENSG00000123870	ZNF137P	19:53091757-53193749	NOTEST	0.368455	0.498761	0.436861	0	1	1
ENSG00000123901	ENSG00000123901	GPR83	11:94110476-94134585	NOTEST	0	0.00870506	inf	0	1	1
ENSG00000123977	ENSG00000123977	DAW1	2:228735769-228789060	NOTEST	0.0295274	0.191089	2.69412	0	1	1
ENSG00000123999	ENSG00000123999	INHA	2:220415450-220440435	NOTEST	0.11452	0.0436537	-1.39143	0	1	1
ENSG00000124003	ENSG00000124003	MOGAT1	2:223536504-223574649	NOTEST	0	0	0	0	1	1
ENSG00000124019	ENSG00000124019	FAM124B	2:225243414-225266802	NOTEST	0	0	0	0	1	1
ENSG00000124089	ENSG00000124089	MC3R	20:54823787-54824871	NOTEST	0.151137	0.0392424	-1.94538	0	1	1
ENSG00000124091	ENSG00000124091	GCNT7	20:55043646-55101198	NOTEST	0.0676411	0.102459	0.599068	0	1	1
ENSG00000124092	ENSG00000124092	CTCFL	20:56071034-56100708	NOTEST	0.246746	0.472596	0.937581	0	1	1
ENSG00000124097	ENSG00000124097	HMGB1P1	20:56063447-56064083	NOTEST	0.0589358	0.124632	1.08046	0	1	1
ENSG00000124102	ENSG00000124102	PI3	20:43803516-43805185	NOTEST	0	0	0	0	1	1
ENSG00000124103	ENSG00000124103	FAM209A	20:55043646-55101198	NOTEST	0.110073	0.0624401	-0.817916	0	1	1
ENSG00000124107	ENSG00000124107	SLPI	20:43880879-43883205	NOTEST	0	0	0	0	1	1
ENSG00000124116	ENSG00000124116	WFDC3	20:44376582-44420571	NOTEST	0.193891	0.0845069	-1.1981	0	1	1
ENSG00000124143	ENSG00000124143	ARHGAP40	20:37230576-37279678	NOTEST	0	0	0	0	1	1
ENSG00000124157	ENSG00000124157	SEMG2	20:43849940-43853099	NOTEST	0	0.00613809	inf	0	1	1
ENSG00000124159	ENSG00000124159	MATN4	20:43922084-43945803	NOTEST	0.0829019	0.0843157	0.0243948	0	1	1
ENSG00000124191	ENSG00000124191	TOX2	20:42543503-42698256	NOTEST	0.100958	0.572132	2.5026	0	1	1
ENSG00000124194	ENSG00000124194	GDAP1L1	20:42875886-42909013	NOTEST	0.0951699	0.227434	1.25687	0	1	1
ENSG00000124196	ENSG00000124196	GTSF1L	20:42354803-42355638	NOTEST	0	0	0	0	1	1
ENSG00000124203	ENSG00000124203	ZNF831	20:57766074-57834168	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000124205	ENSG00000124205	EDN3	20:57875481-57901047	NOTEST	0	0	0	0	1	1
ENSG00000124212	ENSG00000124212	PTGIS	20:48120410-48184683	NOTEST	0.0640242	0.213434	1.7371	0	1	1
ENSG00000124215	ENSG00000124215	CDH26	20:58533470-58609066	NOTEST	0.337266	0.202101	-0.738813	0	1	1
ENSG00000124216	ENSG00000124216	SNAI1	20:48599535-48605423	NOTEST	0.177122	0.516119	1.54296	0	1	1
ENSG00000124227	ENSG00000124227	ANKRD60	20:56793550-56803709	NOTEST	0	0	0	0	1	1
ENSG00000124232	ENSG00000124232	RBPJL	20:43922084-43945803	NOTEST	0	0.00717652	inf	0	1	1
ENSG00000124233	ENSG00000124233	SEMG1	20:43835637-43838413	NOTEST	0	0	0	0	1	1
ENSG00000124237	ENSG00000124237	C20orf85	20:56725959-56736206	NOTEST	0	0	0	0	1	1
ENSG00000124249	ENSG00000124249	KCNK15	20:43285091-43379675	NOTEST	0.343105	0.402544	0.230495	0	1	1
ENSG00000124251	ENSG00000124251	TP53TG5	20:43990576-44039250	NOTEST	0	0.0927628	inf	0	1	1
ENSG00000124253	ENSG00000124253	PCK1	20:56136135-56141513	NOTEST	0	0	0	0	1	1
ENSG00000124256	ENSG00000124256	ZBP1	20:56178901-56195632	NOTEST	0	0.0224923	inf	0	1	1
ENSG00000124260	ENSG00000124260	MAGEA10	X:151282525-151307033	NOTEST	0.0294364	0.0290632	-0.0184075	0	1	1
ENSG00000124302	ENSG00000124302	CHST8	19:34112860-34264414	NOTEST	0	0	0	0	1	1
ENSG00000124334	ENSG00000124334	IL9R	X:155227245-155257848	NOTEST	0.00836646	0.0062008	-0.432163	0	1	1
ENSG00000124343	ENSG00000124343	XG	X:2670090-2734539	NOTEST	0.253004	0.22406	-0.17528	0	1	1
ENSG00000124374	ENSG00000124374	PAIP2B	2:71409868-71454213	NOTEST	0.41817	0.274312	-0.608272	0	1	1
ENSG00000124391	ENSG00000124391	IL17C	16:88704998-88706881	NOTEST	0	0	0	0	1	1
ENSG00000124406	ENSG00000124406	ATP8A1	4:42410389-42659122	NOTEST	0.357389	0.561558	0.65194	0	1	1
ENSG00000124429	ENSG00000124429	POF1B	X:84532401-84634748	NOTEST	0.00711233	0	#NAME?	0	1	1
ENSG00000124440	ENSG00000124440	HIF3A	19:46800302-46846690	NOTEST	0	0	0	0	1	1
ENSG00000124449	ENSG00000124449	IRGC	19:44220161-44224173	NOTEST	0	0	0	0	1	1
ENSG00000124467	ENSG00000124467	PSG8	19:43256837-43359870	NOTEST	0.100158	0.232676	1.21604	0	1	1
ENSG00000124469	ENSG00000124469	CEACAM8	19:42901279-43156507	NOTEST	0	0.0310193	inf	0	1	1
ENSG00000124479	ENSG00000124479	NDP	X:43808021-43832750	NOTEST	0.0709051	0.00628037	-3.49697	0	1	1
ENSG00000124490	ENSG00000124490	CRISP2	6:49660072-49681274	NOTEST	0	0	0	0	1	1
ENSG00000124491	ENSG00000124491	F13A1	6:6144317-6321246	NOTEST	0	0.0027226	inf	0	1	1
ENSG00000124493	ENSG00000124493	GRM4	6:33989627-34123399	NOTEST	0	0.0233666	inf	0	1	1
ENSG00000124507	ENSG00000124507	PACSIN1	6:34433915-34503006	NOTEST	0.0432789	0.0279238	-0.63217	0	1	1
ENSG00000124529	ENSG00000124529	HIST1H4B	6:26027123-26027480	NOTEST	0	0.062158	inf	0	1	1
ENSG00000124557	ENSG00000124557	BTN1A1	6:26501448-26510650	NOTEST	0	0	0	0	1	1
ENSG00000124564	ENSG00000124564	SLC17A3	6:25833293-25882623	NOTEST	0	0	0	0	1	1
ENSG00000124568	ENSG00000124568	SLC17A1	6:25783124-25832287	NOTEST	0	0	0	0	1	1
ENSG00000124575	ENSG00000124575	HIST1H1D	6:26234439-26235216	NOTEST	0.253373	0.147458	-0.780955	0	1	1
ENSG00000124578	ENSG00000124578	HIST1H4G	6:26246885-26247259	NOTEST	0	0	0	0	1	1
ENSG00000124602	ENSG00000124602	UNC5CL	6:40994771-41067715	NOTEST	0.0735719	0.0889992	0.274638	0	1	1
ENSG00000124610	ENSG00000124610	HIST1H1A	6:26017259-26018040	NOTEST	0	0	0	0	1	1
ENSG00000124657	ENSG00000124657	OR2B6	6:27925018-27925960	NOTEST	0.0385289	0.0600632	0.640541	0	1	1
ENSG00000124664	ENSG00000124664	SPDEF	6:34505578-34524110	NOTEST	0.0178848	0.00766298	-1.22275	0	1	1
ENSG00000124678	ENSG00000124678	TCP11	6:35085847-35116387	NOTEST	0.0673645	0.0247835	-1.44261	0	1	1
ENSG00000124693	ENSG00000124693	HIST1H3B	6:26031816-26032288	NOTEST	0.148018	0.288636	0.963483	0	1	1
ENSG00000124701	ENSG00000124701	APOBEC2	6:40994771-41067715	NOTEST	0.0151745	0.067596	2.15529	0	1	1
ENSG00000124713	ENSG00000124713	GNMT	6:42928495-42946958	NOTEST	0.0300637	0	#NAME?	0	1	1
ENSG00000124721	ENSG00000124721	DNAH8	6:38683116-38998301	NOTEST	0.00415431	0.052883	3.67012	0	1	1
ENSG00000124731	ENSG00000124731	TREM1	6:41235663-41254457	NOTEST	0	0.103188	inf	0	1	1

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ENSG00000124743	ENSG00000124743	KLHL31	6:53512698-53530506	NOTEST	0.0509824	0.067323	0.4011	0	1	1
ENSG00000124749	ENSG00000124749	COL21A1	6:55921387-56258892	NOTEST	0	0.00841161	inf	0	1	1
ENSG00000124780	ENSG00000124780	KCNK17	6:39266776-39282329	NOTEST	0	0	0	0	1	1
ENSG00000124812	ENSG00000124812	CRISP1	6:49801969-49844809	NOTEST	0	0	0	0	1	1
ENSG00000124818	ENSG00000124818	OPN5	6:47749717-47800516	NOTEST	0	0.0129608	inf	0	1	1
ENSG00000124827	ENSG00000124827	GCM2	6:10747991-10979553	NOTEST	0	0	0	0	1	1
ENSG00000124835	ENSG00000124835	AC105760.3	2:237957241-237964810	NOTEST	0.0130492	0	#NAME?	0	1	1
ENSG00000124875	ENSG00000124875	CXCL6	4:74702213-74714781	NOTEST	0	0	0	0	1	1
ENSG00000124882	ENSG00000124882	EREG	4:75230859-75254468	NOTEST	0.00333868	0	#NAME?	0	1	1
ENSG00000124915	ENSG00000124915	RP11-467L20.10	11:61447904-61634826	NOTEST	0.00745772	0	#NAME?	0	1	1
ENSG00000124939	ENSG00000124939	SCGB2A1	11:61976139-62028021	NOTEST	0	0	0	0	1	1
ENSG00000125046	ENSG00000125046	SSUH2	3:8661085-9005457	NOTEST	0.107881	0.35121	1.70289	0	1	1
ENSG00000125084	ENSG00000125084	WNT1	12:49372397-49375459	NOTEST	0	0	0	0	1	1
ENSG00000125144	ENSG00000125144	MT1G	16:56700642-56701977	NOTEST	0	0.0855848	inf	0	1	1
ENSG00000125207	ENSG00000125207	PIWIL1	12:130822431-130857182	NOTEST	0	0	0	0	1	1
ENSG00000125245	ENSG00000125245	GPR18	13:99853027-100038688	NOTEST	0.0998356	0.214468	1.10313	0	1	1
ENSG00000125255	ENSG00000125255	SLC10A2	13:103696349-103719196	NOTEST	0	0	0	0	1	1
ENSG00000125266	ENSG00000125266	EFNB2	13:107142078-107187462	NOTEST	0.376308	0.353991	-0.0881996	0	1	1
ENSG00000125285	ENSG00000125285	SOX21	13:95361885-95364389	NOTEST	0	0.0044706	inf	0	1	1
ENSG00000125337	ENSG00000125337	KIF25	6:168393501-168445769	NOTEST	0	0	0	0	1	1
ENSG00000125363	ENSG00000125363	AMELX	X:11129420-11683821	NOTEST	0	0	0	0	1	1
ENSG00000125384	ENSG00000125384	PTGER2	14:52781022-52795324	NOTEST	0.00671382	0	#NAME?	0	1	1
ENSG00000125385	ENSG00000125385	RP11-297B17.2	9:37046831-37047234	NOTEST	0	0	0	0	1	1
ENSG00000125414	ENSG00000125414	MYH2	17:10286448-10527203	NOTEST	0	0	0	0	1	1
ENSG00000125430	ENSG00000125430	HS3ST3B1	17:14204399-14252721	NOTEST	0	0.00437515	inf	0	1	1
ENSG00000125462	ENSG00000125462	C1orf61	1:156374041-156400493	NOTEST	0.379943	0.404922	0.0918623	0	1	1
ENSG00000125492	ENSG00000125492	BARHL1	9:135457571-135465653	NOTEST	0	0.0600367	inf	0	1	1
ENSG00000125498	ENSG00000125498	KIR2DL1	19:55235968-55378662	NOTEST	0	0	0	0	1	1
ENSG00000125508	ENSG00000125508	SRMS	20:62172162-62178857	NOTEST	0	0	0	0	1	1
ENSG00000125514	ENSG00000125514	LINC00029	20:61640734-61716423	NOTEST	0	0	0	0	1	1
ENSG00000125522	ENSG00000125522	NPBWR2	20:62737172-62738524	NOTEST	0	0	0	0	1	1
ENSG00000125531	ENSG00000125531	C20orf195	20:62184372-62188061	NOTEST	0	0	0	0	1	1
ENSG00000125533	ENSG00000125533	BHLHE23	20:61637330-61638387	NOTEST	0	0	0	0	1	1
ENSG00000125538	ENSG00000125538	IL1B	2:113587327-113594480	NOTEST	0.104912	0.103298	-0.022368	0	1	1
ENSG00000125551	ENSG00000125551	PLGLB2	2:88047605-88285309	NOTEST	0.0095795	5.06E-06	-10.8878	0	1	1
ENSG00000125571	ENSG00000125571	IL37	2:113670547-113676459	NOTEST	0	0	0	0	1	1
ENSG00000125618	ENSG00000125618	PAX8	2:113969098-114036527	NOTEST	0.0103832	0.00666292	-0.640025	0	1	1
ENSG00000125631	ENSG00000125631	HTR5BP	2:118617002-118771709	NOTEST	0.0529048	0.0537155	0.0219394	0	1	1
ENSG00000125637	ENSG00000125637	PSD4	2:113914901-113966973	NOTEST	0.0267716	0.0445103	0.733434	0	1	1
ENSG00000125650	ENSG00000125650	PSPN	19:6375158-6379069	NOTEST	0.287109	0.238934	-0.264987	0	1	1
ENSG00000125675	ENSG00000125675	GRIA3	X:122318005-122624766	NOTEST	0.00743256	0.0946699	3.67098	0	1	1
ENSG00000125695	ENSG00000125695	RP11-51F16.8	17:61780191-61896677	NOTEST	0	0	0	0	1	1
ENSG00000125726	ENSG00000125726	CD70	19:6583193-6604114	NOTEST	0.0940932	0.205162	1.1246	0	1	1
ENSG00000125730	ENSG00000125730	C3	19:6677714-6737614	NOTEST	0.426858	0.139285	-1.61571	0	1	1

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ENSG00000125731	ENSG00000125731	SH2D3A	19:6752170-6767599	NOTEST	0.181608	0.164703	-0.140957	0	1	1
ENSG00000125735	ENSG00000125735	TNFSF14	19:6663147-6670599	NOTEST	0	0	0	0	1	1
ENSG00000125740	ENSG00000125740	FOSB	19:45882891-45982086	NOTEST	0.129625	0.282937	1.12613	0	1	1
ENSG00000125780	ENSG00000125780	TGM3	20:2276646-2321724	NOTEST	0	0	0	0	1	1
ENSG00000125787	ENSG00000125787	GNRH2	20:3024267-3026393	NOTEST	0	0.0178699	inf	0	1	1
ENSG00000125788	ENSG00000125788	DEFB126	20:123009-126392	NOTEST	0.0613827	0.377851	2.62191	0	1	1
ENSG00000125798	ENSG00000125798	FOXA2	20:22561642-22566093	NOTEST	0	0	0	0	1	1
ENSG00000125804	ENSG00000125804	FAM182A	20:26035290-26073683	NOTEST	0.143198	0.00212685	-6.07315	0	1	1
ENSG00000125810	ENSG00000125810	CD93	20:23059985-23066977	NOTEST	0	0.0138113	inf	0	1	1
ENSG00000125813	ENSG00000125813	PAX1	20:21686296-21696620	NOTEST	0	0	0	0	1	1
ENSG00000125815	ENSG00000125815	CST8	20:23471737-23476655	NOTEST	0	0	0	0	1	1
ENSG00000125816	ENSG00000125816	NKX2-4	20:21376004-21381029	NOTEST	0.0287393	0.0201886	-0.509481	0	1	1
ENSG00000125820	ENSG00000125820	NKX2-2	20:21491647-21494664	NOTEST	0.0294609	0.0363817	0.304412	0	1	1
ENSG00000125823	ENSG00000125823	CSTL1	20:23420321-23425567	NOTEST	0	0	0	0	1	1
ENSG00000125831	ENSG00000125831	CST11	20:23431039-23433494	NOTEST	0	0	0	0	1	1
ENSG00000125845	ENSG00000125845	BMP2	20:6748310-6760927	NOTEST	0	0	0	0	1	1
ENSG00000125850	ENSG00000125850	OVOL2	20:17922240-18039832	NOTEST	0.0181387	0.0754741	2.05691	0	1	1
ENSG00000125861	ENSG00000125861	GFRA4	20:3639938-3644046	NOTEST	0	0	0	0	1	1
ENSG00000125864	ENSG00000125864	BFSP1	20:17474549-17549865	NOTEST	0.349243	0.503293	0.527167	0	1	1
ENSG00000125869	ENSG00000125869	LAMP5	20:9485826-9511171	NOTEST	0	0	0	0	1	1
ENSG00000125872	ENSG00000125872	LRRN4	20:6021423-6034695	NOTEST	0	0	0	0	1	1
ENSG00000125878	ENSG00000125878	TCF15	20:584440-591042	NOTEST	0	0.00833985	inf	0	1	1
ENSG00000125879	ENSG00000125879	OTOR	20:16729002-16750707	NOTEST	0	0	0	0	1	1
ENSG00000125888	ENSG00000125888	BANF2	20:17674316-17716516	NOTEST	0	0	0	0	1	1
ENSG00000125895	ENSG00000125895	TMEM74B	20:1161204-1166059	NOTEST	0.151097	0.292025	0.950615	0	1	1
ENSG00000125899	ENSG00000125899	C20orf187	20:11008407-11010014	NOTEST	0	0	0	0	1	1
ENSG00000125900	ENSG00000125900	SIRPD	20:1497404-1600707	NOTEST	0	0	0	0	1	1
ENSG00000125903	ENSG00000125903	DEFB129	20:207898-210527	NOTEST	0	0	0	0	1	1
ENSG00000125910	ENSG00000125910	S1PR4	19:3172343-3180329	NOTEST	0.0398114	0.0162222	-1.29522	0	1	1
ENSG00000125965	ENSG00000125965	GDF5	20:34020826-34042568	NOTEST	0.0121462	0	#NAME?	0	1	1
ENSG00000125966	ENSG00000125966	MMP24	20:33703166-33872788	NOTEST	0.274445	0.320426	0.223476	0	1	1
ENSG00000125975	ENSG00000125975	C20orf173	20:34108568-34117481	NOTEST	0	0	0	0	1	1
ENSG00000125997	ENSG00000125997	BPIFB9P	20:31935525-31942250	NOTEST	0	0.0959963	inf	0	1	1
ENSG00000125998	ENSG00000125998	FAM83C	20:33873053-33880204	NOTEST	0	0	0	0	1	1
ENSG00000125999	ENSG00000125999	BPIFB1	20:31861285-31897684	NOTEST	0	0	0	0	1	1
ENSG00000126010	ENSG00000126010	GRPR	X:16141678-16189587	NOTEST	0.200064	0.309624	0.630054	0	1	1
ENSG00000126218	ENSG00000126218	F10	13:113777127-113803843	NOTEST	0.096019	0.0504605	-0.928167	0	1	1
ENSG00000126231	ENSG00000126231	PROZ	13:113812967-113826694	NOTEST	0.0318157	0.0255135	-0.31848	0	1	1
ENSG00000126233	ENSG00000126233	SLURP1	8:143822361-143823829	NOTEST	0	0	0	0	1	1
ENSG00000126251	ENSG00000126251	GPR42	19:35861830-35863855	NOTEST	0	0	0	0	1	1
ENSG00000126259	ENSG00000126259	KIRREL2	19:36316865-36370693	NOTEST	0.175262	0.266211	0.603056	0	1	1
ENSG00000126264	ENSG00000126264	HCST	19:36393381-36395279	NOTEST	0.270605	0.24451	-0.146299	0	1	1
ENSG00000126266	ENSG00000126266	FFAR1	19:35842444-35843367	NOTEST	0	0	0	0	1	1
ENSG00000126337	ENSG00000126337	KRT36	17:39642387-39648798	NOTEST	0.0182853	0.0156687	-0.222799	0	1	1
ENSG00000126353	ENSG00000126353	CCR7	17:38710020-38721724	NOTEST	0.1246	0.0687048	-0.858823	0	1	1

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ENSG00000126460	ENSG00000126460	PRRG2	19:50058967-50094272	NOTEST	0.476322	0.13606	-1.80769	0	1	1
ENSG00000126467	ENSG00000126467	TSKS	19:50243009-50266587	NOTEST	0	0	0	0	1	1
ENSG00000126500	ENSG00000126500	FLRT1	11:63742078-63933578	NOTEST	0.211061	0.287312	0.444957	0	1	1
ENSG00000126542	ENSG00000126542	PTPN20CP	10:49272333-49327498	NOTEST	0	0	0	0	1	1
ENSG00000126545	ENSG00000126545	CSN1S1	4:70796798-70812289	NOTEST	0	0	0	0	1	1
ENSG00000126549	ENSG00000126549	STATH	4:70861646-70868287	NOTEST	0	0.0318729	inf	0	1	1
ENSG00000126583	ENSG00000126583	PRKCG	19:54382443-54410906	NOTEST	0	0	0	0	1	1
ENSG00000126733	ENSG00000126733	DACH2	X:85403461-86087607	NOTEST	0.274004	0.306491	0.161646	0	1	1
ENSG00000126759	ENSG00000126759	CFP	X:47483611-47489704	NOTEST	0.0847264	0.0318215	-1.41281	0	1	1
ENSG00000126838	ENSG00000126838	PZP	12:9301435-9360966	NOTEST	0	0	0	0	1	1
ENSG00000126860	ENSG00000126860	EVI2A	17:29335514-29709134	NOTEST	0.126706	0.274228	1.11389	0	1	1
ENSG00000126861	ENSG00000126861	OMG	17:29335514-29709134	NOTEST	0.0442737	0.0319113	-0.472382	0	1	1
ENSG00000126895	ENSG00000126895	AVPR2	X:153126968-153200676	NOTEST	0	0.0434628	inf	0	1	1
ENSG00000126950	ENSG00000126950	TMEM35	X:100264334-100351353	NOTEST	0	0	0	0	1	1
ENSG00000126952	ENSG00000126952	NXF5	X:101087084-101112549	NOTEST	0	0	0	0	1	1
ENSG00000127074	ENSG00000127074	RGS13	1:192605274-192629390	NOTEST	0.0115124	0.00895122	-0.363026	0	1	1
ENSG00000127083	ENSG00000127083	OMD	9:95059639-95432547	NOTEST	0	0	0	0	1	1
ENSG00000127129	ENSG00000127129	EDN2	1:41944445-41950344	NOTEST	0	0.0305382	inf	0	1	1
ENSG00000127152	ENSG00000127152	BCL11B	14:99635623-99737861	NOTEST	0	0	0	0	1	1
ENSG00000127241	ENSG00000127241	MASP1	3:186935941-187009810	NOTEST	0	0	0	0	1	1
ENSG00000127249	ENSG00000127249	ATP13A4	3:193119865-193310900	NOTEST	0.0698682	7.37E-06	-13.2112	0	1	1
ENSG00000127252	ENSG00000127252	HRASLS	3:192958913-193096632	NOTEST	0.0166042	0	#NAME?	0	1	1
ENSG00000127318	ENSG00000127318	IL22	12:68642021-68647387	NOTEST	0	0	0	0	1	1
ENSG00000127324	ENSG00000127324	TSPAN8	12:71518864-71980090	NOTEST	0.071624	0	#NAME?	0	1	1
ENSG00000127325	ENSG00000127325	BEST3	12:70037139-70093256	NOTEST	0	0	0	0	1	1
ENSG00000127362	ENSG00000127362	TAS2R3	7:141404137-141488440	NOTEST	0.0610531	0.119843	0.973013	0	1	1
ENSG00000127364	ENSG00000127364	TAS2R4	7:141404137-141488440	NOTEST	0.287879	0.295491	0.0376545	0	1	1
ENSG00000127366	ENSG00000127366	TAS2R5	7:141490016-141491166	NOTEST	0.382476	0.182501	-1.06747	0	1	1
ENSG00000127377	ENSG00000127377	CRYGN	7:151124768-151137899	NOTEST	0.0669735	0.283475	2.08156	0	1	1
ENSG00000127412	ENSG00000127412	TRPV5	7:142605266-142630905	NOTEST	0	0.0053533	inf	0	1	1
ENSG00000127472	ENSG00000127472	PLA2G5	1:20354671-20417683	NOTEST	0	0	0	0	1	1
ENSG00000127515	ENSG00000127515	OR7A10	19:14951759-14952689	NOTEST	0	0	0	0	1	1
ENSG00000127529	ENSG00000127529	OR7C2	19:15052300-15053260	NOTEST	0	0	0	0	1	1
ENSG00000127530	ENSG00000127530	OR7C1	19:14903120-14946188	NOTEST	0	0.0129028	inf	0	1	1
ENSG00000127533	ENSG00000127533	F2RL3	19:16999670-17003417	NOTEST	0	0	0	0	1	1
ENSG00000127561	ENSG00000127561	SYNGR3	16:2034207-2044276	NOTEST	0.385488	0.513339	0.413226	0	1	1
ENSG00000127578	ENSG00000127578	WFIKKN1	16:639356-684116	NOTEST	0.0669418	0.164229	1.29473	0	1	1
ENSG00000127585	ENSG00000127585	FBXL16	16:734621-755829	NOTEST	0.347434	0.540324	0.637086	0	1	1
ENSG00000127588	ENSG00000127588	GNG13	16:834973-850737	NOTEST	0	0.0440774	inf	0	1	1
ENSG00000127743	ENSG00000127743	IL17B	5:148750886-148783765	NOTEST	0	0.147092	inf	0	1	1
ENSG00000127780	ENSG00000127780	OR1E2	17:3336163-3337135	NOTEST	0	0	0	0	1	1
ENSG00000127831	ENSG00000127831	VIL1	2:219283814-219433084	NOTEST	0	0.00384313	inf	0	1	1
ENSG00000127903	ENSG00000127903	ZNF835	19:57174019-57183151	NOTEST	0	0.106883	inf	0	1	1
ENSG00000127928	ENSG00000127928	GNGT1	7:93220884-93540577	NOTEST	0.0404823	0	#NAME?	0	1	1
ENSG00000127951	ENSG00000127951	FGL2	7:76139744-77045717	NOTEST	0	0	0	0	1	1

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ENSG00000128040	ENSG00000128040	SPINK2	4:57676025-57687908	NOTEST	0	0.20267	inf	0	1	1
ENSG00000128045	ENSG00000128045	RASL11B	4:53728456-53733000	NOTEST	0.108766	0.131957	0.278838	0	1	1
ENSG00000128052	ENSG00000128052	KDR	4:55919226-55991756	NOTEST	0.406532	0.410469	0.0139019	0	1	1
ENSG00000128165	ENSG00000128165	ADM2	22:50919984-50924869	NOTEST	0.119964	0.269215	1.16615	0	1	1
ENSG00000128218	ENSG00000128218	VPREB3	22:24094929-24096655	NOTEST	0	0	0	0	1	1
ENSG00000128242	ENSG00000128242	GAL3ST1	22:30950621-30970574	NOTEST	0	0.085421	inf	0	1	1
ENSG00000128250	ENSG00000128250	RFPL1	22:29832817-29874164	NOTEST	0.0777572	0.0435578	-0.836046	0	1	1
ENSG00000128253	ENSG00000128253	RFPL2	22:32586421-32600718	NOTEST	0.302366	0.252857	-0.257975	0	1	1
ENSG00000128254	ENSG00000128254	C22orf24	22:32329506-32353590	NOTEST	0.151807	0.0337971	-2.16727	0	1	1
ENSG00000128262	ENSG00000128262	POM121L9P	22:24647795-24661493	NOTEST	0	0.0125131	inf	0	1	1
ENSG00000128268	ENSG00000128268	MGAT3	22:39853348-39888199	NOTEST	0.00851466	0.0360996	2.08396	0	1	1
ENSG00000128271	ENSG00000128271	ADORA2A	22:24666785-24924358	NOTEST	0.216783	0.454569	1.06824	0	1	1
ENSG00000128274	ENSG00000128274	A4GALT	22:43088126-43117304	NOTEST	0.00841515	0.0436878	2.37617	0	1	1
ENSG00000128276	ENSG00000128276	RFPL3	22:32750871-32781618	NOTEST	3.46E-05	2.86E-05	-0.273638	0	1	1
ENSG00000128284	ENSG00000128284	APOL3	22:36536371-36562225	NOTEST	0.0138151	0.0285613	1.04781	0	1	1
ENSG00000128285	ENSG00000128285	MCHR1	22:41074753-41078818	NOTEST	0.0738048	0.0110137	-2.74442	0	1	1
ENSG00000128310	ENSG00000128310	GALR3	22:38219388-38221502	NOTEST	0	0.0117105	inf	0	1	1
ENSG00000128313	ENSG00000128313	APOL5	22:36113918-36125530	NOTEST	0	0	0	0	1	1
ENSG00000128322	ENSG00000128322	IGLL1	22:23909250-23922495	NOTEST	0	0	0	0	1	1
ENSG00000128340	ENSG00000128340	RAC2	22:37621300-37640488	NOTEST	0.0902669	0.582935	2.69107	0	1	1
ENSG00000128383	ENSG00000128383	APOBEC3A	22:39348745-39359188	NOTEST	0	0	0	0	1	1
ENSG00000128422	ENSG00000128422	KRT17	17:39775688-39943183	NOTEST	0	0.00827946	inf	0	1	1
ENSG00000128438	ENSG00000128438	TBC1D27	17:16826228-16875432	NOTEST	0	0	0	0	1	1
ENSG00000128482	ENSG00000128482	RNF112	17:19314437-19320589	NOTEST	0.284715	0.0278545	-3.35353	0	1	1
ENSG00000128510	ENSG00000128510	CPA4	7:129932973-129964020	NOTEST	0.0579733	0.424548	2.87247	0	1	1
ENSG00000128519	ENSG00000128519	TAS2R16	7:122634758-122635754	NOTEST	0	0	0	0	1	1
ENSG00000128567	ENSG00000128567	PODXL	7:131185020-131242976	NOTEST	0.0218501	0.0548013	1.32657	0	1	1
ENSG00000128594	ENSG00000128594	LRRC4	7:127292233-127732661	NOTEST	0.00812172	0.0273041	1.74926	0	1	1
ENSG00000128606	ENSG00000128606	LRRC17	7:102453307-102715286	NOTEST	0.05095	0.0390688	-0.383065	0	1	1
ENSG00000128610	ENSG00000128610	FEZF1	7:121941447-121950745	NOTEST	0.0760939	0.0749035	-0.0227476	0	1	1
ENSG00000128710	ENSG00000128710	HOXD10	2:176968943-176984670	NOTEST	0.222123	0.0636907	-1.80221	0	1	1
ENSG00000128713	ENSG00000128713	HOXD11	2:176968943-176984670	NOTEST	0.34533	0.34133	-0.0168113	0	1	1
ENSG00000128739	ENSG00000128739	SNRPN	15:25068793-25492435	NOTEST	0.0349996	0.15507	2.14751	0	1	1
ENSG00000128802	ENSG00000128802	GDF2	10:48413091-48416853	NOTEST	0	0	0	0	1	1
ENSG00000128805	ENSG00000128805	ARHGAP22	10:49654076-49864310	NOTEST	0.0136059	0.132207	3.28049	0	1	1
ENSG00000128815	ENSG00000128815	WDFY4	10:49892920-50323554	NOTEST	0.00609141	0	#NAME?	0	1	1
ENSG00000128833	ENSG00000128833	MYO5C	15:52408770-52587995	NOTEST	0.154302	0.324447	1.07222	0	1	1
ENSG00000128849	ENSG00000128849	CGNL1	15:57668164-57842925	NOTEST	0.00800739	0.0126332	0.657819	0	1	1
ENSG00000128886	ENSG00000128886	ELL3	15:44019115-44095241	NOTEST	0.633914	0.632038	-0.00427762	0	1	1
ENSG00000128917	ENSG00000128917	DLL4	15:41221537-41231237	NOTEST	0	0.00329061	inf	0	1	1
ENSG00000129009	ENSG00000129009	ISLR	15:74445140-74471567	NOTEST	0	0	0	0	1	1
ENSG00000129038	ENSG00000129038	LOXL1	15:74200423-74244478	NOTEST	0.257902	0.38133	0.564216	0	1	1
ENSG00000129048	ENSG00000129048	ACKR4	3:132276981-132593067	NOTEST	0.0633635	0.045879	-0.465817	0	1	1
ENSG00000129151	ENSG00000129151	BBOX1	11:27062271-27241660	NOTEST	0	0	0	0	1	1

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ENSG00000129159	ENSG00000129159	KCNC1	11:17756358-17804602	NOTEST	0.0184747	0.0212916	0.204728	0	1	1
ENSG00000129167	ENSG00000129167	TPH1	11:17809594-18063973	NOTEST	0.211776	0.149363	-0.50371	0	1	1
ENSG00000129170	ENSG00000129170	CSRP3	11:19203577-19302973	NOTEST	0	0	0	0	1	1
ENSG00000129194	ENSG00000129194	SOX15	17:7465191-7536700	NOTEST	0.259494	0.226457	-0.19646	0	1	1
ENSG00000129204	ENSG00000129204	USP6	17:5008835-5078329	NOTEST	0.310725	0.320671	0.0454539	0	1	1
ENSG00000129214	ENSG00000129214	SHBG	17:7465191-7536700	NOTEST	0.20529	0.145411	-0.497525	0	1	1
ENSG00000129221	ENSG00000129221	AIPL1	17:6297012-6338519	NOTEST	0	0	0	0	1	1
ENSG00000129244	ENSG00000129244	ATP1B2	17:7549944-7561086	NOTEST	0.0379185	0.11482	1.5984	0	1	1
ENSG00000129270	ENSG00000129270	MMP28	17:34083267-34122711	NOTEST	0	0	0	0	1	1
ENSG00000129277	ENSG00000129277	CCL4	17:34430982-34433014	NOTEST	0	0	0	0	1	1
ENSG00000129354	ENSG00000129354	AP1M2	19:10683346-10697991	NOTEST	0.0438165	0.334983	2.93454	0	1	1
ENSG00000129437	ENSG00000129437	KLK14	19:51580751-51587502	NOTEST	0.107653	0.0108716	-3.30776	0	1	1
ENSG00000129450	ENSG00000129450	SIGLEC9	19:51628164-51639908	NOTEST	0.0335325	0	#NAME?	0	1	1
ENSG00000129451	ENSG00000129451	KLK10	19:51515994-51523431	NOTEST	0	0.00918165	inf	0	1	1
ENSG00000129455	ENSG00000129455	KLK8	19:51446558-51515385	NOTEST	0.0894847	0	#NAME?	0	1	1
ENSG00000129465	ENSG00000129465	RIPK3	14:24787554-24809251	NOTEST	0	0	0	0	1	1
ENSG00000129467	ENSG00000129467	ADCY4	14:24787554-24809251	NOTEST	0	0.0482442	inf	0	1	1
ENSG00000129514	ENSG00000129514	FOXA1	14:38059188-38672128	NOTEST	0.103044	0.0907568	-0.18318	0	1	1
ENSG00000129538	ENSG00000129538	RNASE1	14:21269386-21271437	NOTEST	0.440786	0.579715	0.395267	0	1	1
ENSG00000129595	ENSG00000129595	EPB41L4A	5:111478137-111755013	NOTEST	0.130887	0.299172	1.19265	0	1	1
ENSG00000129596	ENSG00000129596	CDO1	5:115140429-115152651	NOTEST	0.263148	0.356011	0.436044	0	1	1
ENSG00000129646	ENSG00000129646	QRICH2	17:74270129-74303761	NOTEST	0.147762	0.325259	1.13831	0	1	1
ENSG00000129654	ENSG00000129654	FOXJ1	17:74132413-74236454	NOTEST	0.00601249	0.00467117	-0.364181	0	1	1
ENSG00000129673	ENSG00000129673	AANAT	17:74449432-74466199	NOTEST	0.134352	0.0523828	-1.35885	0	1	1
ENSG00000129744	ENSG00000129744	ART1	11:3666357-3685646	NOTEST	0	0	0	0	1	1
ENSG00000129749	ENSG00000129749	CHRNA10	11:3686816-3847601	NOTEST	0.230856	0.134017	-0.784576	0	1	1
ENSG00000129816	ENSG00000129816	TTTY1B	Y:6258471-6292186	NOTEST	0	0	0	0	1	1
ENSG00000129824	ENSG00000129824	RPS4Y1	Y:2709526-2800041	NOTEST	0	0	0	0	1	1
ENSG00000129845	ENSG00000129845	TTTY1	Y:9578192-9611898	NOTEST	0	0	0	0	1	1
ENSG00000129862	ENSG00000129862	VCY1B	Y:16168096-16168838	NOTEST	0	0	0	0	1	1
ENSG00000129864	ENSG00000129864	VCY	Y:16097651-16098393	NOTEST	0	0	0	0	1	1
ENSG00000129873	ENSG00000129873	CDY2B	Y:19989289-19992100	NOTEST	0	0	0	0	1	1
ENSG00000129910	ENSG00000129910	CDH15	16:89238174-89261900	NOTEST	0.00554962	0.0172456	1.63577	0	1	1
ENSG00000129951	ENSG00000129951	LPPR3	19:812517-821967	NOTEST	0.0210408	0.0720775	1.77636	0	1	1
ENSG00000129965	ENSG00000129965	INS-IGF2	11:2150341-2182571	NOTEST	0	0	0	0	1	1
ENSG00000129988	ENSG00000129988	LBP	20:36974758-37005665	NOTEST	0.0150301	0.026448	0.815303	0	1	1
ENSG00000129990	ENSG00000129990	SYT5	19:55663136-55691809	NOTEST	0.155484	0.163819	0.0753395	0	1	1
ENSG00000129993	ENSG00000129993	CBFA2T3	16:88941265-89043612	NOTEST	0.0452361	0	#NAME?	0	1	1
ENSG00000130032	ENSG00000130032	PRRG3	X:150863595-150874396	NOTEST	0	0	0	0	1	1
ENSG00000130035	ENSG00000130035	GALNT8	12:4671369-4960277	NOTEST	0.129311	0.0508365	-1.34691	0	1	1
ENSG00000130037	ENSG00000130037	KCNA5	12:5153084-5155949	NOTEST	0	0.00387054	inf	0	1	1
ENSG00000130038	ENSG00000130038	EFCAB4B	12:3715798-3873985	NOTEST	0.0151849	0.0659932	2.11968	0	1	1
ENSG00000130045	ENSG00000130045	NXNL2	9:91150015-91199189	NOTEST	0	0.00897601	inf	0	1	1
ENSG00000130052	ENSG00000130052	STARD8	X:67867507-67945684	NOTEST	0.342837	0.603007	0.814653	0	1	1

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ENSG00000130054	ENSG00000130054	FAM155B	X:68725083-68752351	NOTEST	0.293328	0.306207	0.061992	0	1	1
ENSG00000130055	ENSG00000130055	GDPD2	X:69642880-69653240	NOTEST	0.0187746	0	#NAME?	0	1	1
ENSG00000130167	ENSG00000130167	TSPAN16	19:11406823-11465620	NOTEST	0	0	0	0	1	1
ENSG00000130173	ENSG00000130173	C19orf80	19:11309970-11373157	NOTEST	0.127707	0.044364	-1.52537	0	1	1
ENSG00000130176	ENSG00000130176	CNN1	19:11649531-11661138	NOTEST	0.0816133	0.133982	0.715167	0	1	1
ENSG00000130182	ENSG00000130182	ZSCAN10	16:3138890-3149318	NOTEST	0	0.0260541	inf	0	1	1
ENSG00000130201	ENSG00000130201	EXOC3L2	19:45574757-45808541	NOTEST	0	0.0308521	inf	0	1	1
ENSG00000130222	ENSG00000130222	GADD45G	9:92219927-92221470	NOTEST	0.0184243	0.0117026	-0.654773	0	1	1
ENSG00000130226	ENSG00000130226	DPP6	7:153584181-154685995	NOTEST	0	0	0	0	1	1
ENSG00000130234	ENSG00000130234	ACE2	X:15579155-15620271	NOTEST	0.0347079	0.0187885	-0.885411	0	1	1
ENSG00000130287	ENSG00000130287	NCAN	19:19322781-19363042	NOTEST	0	0.0105368	inf	0	1	1
ENSG00000130294	ENSG00000130294	KIF1A	2:241653180-241759725	NOTEST	0.0382072	0.322892	3.07914	0	1	1
ENSG00000130300	ENSG00000130300	PLVAP	19:17462256-17488159	NOTEST	0	0	0	0	1	1
ENSG00000130307	ENSG00000130307	USHBP1	19:17342691-17398455	NOTEST	0.0393016	0.030613	-0.360441	0	1	1
ENSG00000130368	ENSG00000130368	MAS1	6:160327973-160329108	NOTEST	0	0	0	0	1	1
ENSG00000130377	ENSG00000130377	ACSBG2	19:5978413-6199583	NOTEST	0.0870397	0.0203371	-2.09756	0	1	1
ENSG00000130383	ENSG00000130383	FUT5	19:5865836-5904017	NOTEST	0.171065	0.49194	1.52393	0	1	1
ENSG00000130385	ENSG00000130385	BMP15	X:50653783-50659607	NOTEST	0	0	0	0	1	1
ENSG00000130413	ENSG00000130413	STK33	11:8413417-8615836	NOTEST	0.401358	0.602775	0.58673	0	1	1
ENSG00000130427	ENSG00000130427	EPO	7:100318422-100321323	NOTEST	0	0.00996063	inf	0	1	1
ENSG00000130433	ENSG00000130433	CACNG6	19:54495541-54515923	NOTEST	0	0	0	0	1	1
ENSG00000130477	ENSG00000130477	UNC13A	19:17712136-17799401	NOTEST	0.0713178	0.0188523	-1.91952	0	1	1
ENSG00000130487	ENSG00000130487	KLHDC7B	22:50986461-50989451	NOTEST	0.0105362	0.00369864	-1.51028	0	1	1
ENSG00000130508	ENSG00000130508	PXDN	2:1635658-1748624	NOTEST	0	0	0	0	1	1
ENSG00000130518	ENSG00000130518	KIAA1683	19:18367907-18385319	NOTEST	0.0362508	0.0268093	-0.435282	0	1	1
ENSG00000130528	ENSG00000130528	HRC	19:49654454-49658681	NOTEST	0.00670775	0.124859	4.21833	0	1	1
ENSG00000130538	ENSG00000130538	OR11H1	22:16448823-16449805	NOTEST	0	0	0	0	1	1
ENSG00000130540	ENSG00000130540	SULT4A1	22:44220388-44258398	NOTEST	0.16114	0.458443	1.50843	0	1	1
ENSG00000130545	ENSG00000130545	CRB3	19:6436089-6482568	NOTEST	0.0563112	0.12593	1.16113	0	1	1
ENSG00000130561	ENSG00000130561	SAG	2:234216461-234255701	NOTEST	0	0	0	0	1	1
ENSG00000130584	ENSG00000130584	ZBTB46	20:62375018-62462597	NOTEST	0.257345	0.3885	0.59421	0	1	1
ENSG00000130592	ENSG00000130592	LSP1	11:1874199-1913497	NOTEST	0	0.115946	inf	0	1	1
ENSG00000130595	ENSG00000130595	TNNT3	11:1940791-1959936	NOTEST	0	0.0122582	inf	0	1	1
ENSG00000130598	ENSG00000130598	TNNI2	11:1860218-1862910	NOTEST	0	0	0	0	1	1
ENSG00000130612	ENSG00000130612	CYP2G1P	19:41277552-41406413	NOTEST	0	0	0	0	1	1
ENSG00000130635	ENSG00000130635	COL5A1	9:137533619-137736686	NOTEST	0.00178983	0.0230033	3.68395	0	1	1
ENSG00000130643	ENSG00000130643	CALY	10:135093134-135166187	NOTEST	0	0	0	0	1	1
ENSG00000130649	ENSG00000130649	CYP2E1	10:135192694-135382916	NOTEST	0.529472	0.39105	-0.437199	0	1	1
ENSG00000130653	ENSG00000130653	PNPLA7	9:140354403-140444986	NOTEST	0.341239	0.36088	0.080738	0	1	1
ENSG00000130656	ENSG00000130656	HBZ	16:202685-216767	NOTEST	0.0721221	0	#NAME?	0	1	1
ENSG00000130675	ENSG00000130675	MNX1	7:156786744-156803345	NOTEST	0.03071	0	#NAME?	0	1	1
ENSG00000130700	ENSG00000130700	GATA5	20:61038552-61051026	NOTEST	0	0	0	0	1	1
ENSG00000130701	ENSG00000130701	RBBP8NL	20:60985292-61002589	NOTEST	0.01024	0	#NAME?	0	1	1
ENSG00000130711	ENSG00000130711	PRDM12	9:133539980-133558368	NOTEST	0.0116553	0.0145365	0.318696	0	1	1
ENSG00000130720	ENSG00000130720	FIBCD1	9:133777824-133820907	NOTEST	0.0158592	0.0326642	1.04239	0	1	1

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ENSG00000130755	ENSG00000130755	GMFG	19:39818992-39833012	NOTEST	0.250936	0.138386	-0.858617	0	1	1
ENSG00000130762	ENSG00000130762	ARHGEF16	1:3370989-3397677	NOTEST	0.316116	0.474588	0.586222	0	1	1
ENSG00000130783	ENSG00000130783	CCDC62	12:123258873-123312075	NOTEST	0.0344641	0.0187154	-0.88087	0	1	1
ENSG00000130827	ENSG00000130827	PLXNA3	X:153686620-153701989	NOTEST	0.26641	0.567958	1.09213	0	1	1
ENSG00000130876	ENSG00000130876	SLC7A10	19:33699569-33716756	NOTEST	0	0	0	0	1	1
ENSG00000130940	ENSG00000130940	CASZ1	1:10696660-10856707	NOTEST	0.227825	0.383136	0.749933	0	1	1
ENSG00000130943	ENSG00000130943	PKDREJ	22:46651559-46659219	NOTEST	0.0535679	0.0550929	0.040499	0	1	1
ENSG00000130948	ENSG00000130948	HSD17B3	9:98997587-99064434	NOTEST	0	0.0188812	inf	0	1	1
ENSG00000130950	ENSG00000130950	NUTM2F	9:97077604-97090926	NOTEST	0	0	0	0	1	1
ENSG00000130957	ENSG00000130957	FBP2	9:97317350-97356075	NOTEST	0	0.00921611	inf	0	1	1
ENSG00000130988	ENSG00000130988	RGN	X:46937774-46952712	NOTEST	0.0323634	0.0750292	1.21309	0	1	1
ENSG00000131002	ENSG00000131002	TXLNG2P	Y:21729198-21768160	NOTEST	0	0	0	0	1	1
ENSG00000131007	ENSG00000131007	TTTY9B	Y:20652800-20790963	NOTEST	0	0	0	0	1	1
ENSG00000131042	ENSG00000131042	LILRB2	19:54777674-54785039	NOTEST	0	0	0	0	1	1
ENSG00000131044	ENSG00000131044	TTLL9	20:30435439-30539895	NOTEST	0.0640254	0.0902558	0.495375	0	1	1
ENSG00000131050	ENSG00000131050	BPIFA2	20:31749573-31769218	NOTEST	0	0	0	0	1	1
ENSG00000131055	ENSG00000131055	COX4I2	20:30225690-30232809	NOTEST	0	0	0	0	1	1
ENSG00000131059	ENSG00000131059	BPIFA3	20:31805115-31815564	NOTEST	0	0	0	0	1	1
ENSG00000131068	ENSG00000131068	DEFB118	20:29956420-29961726	NOTEST	0	0	0	0	1	1
ENSG00000131095	ENSG00000131095	GFAP	17:42923720-42994305	NOTEST	0	0.0706757	inf	0	1	1
ENSG00000131096	ENSG00000131096	PYY	17:42030105-42081837	NOTEST	0.0168396	0.0401441	1.25333	0	1	1
ENSG00000131097	ENSG00000131097	HIGD1B	17:42923720-42994305	NOTEST	0	0.040498	inf	0	1	1
ENSG00000131126	ENSG00000131126	TEX101	19:43905647-43922763	NOTEST	0	0	0	0	1	1
ENSG00000131142	ENSG00000131142	CCL25	19:8117650-8127534	NOTEST	0	0	0	0	1	1
ENSG00000131152	ENSG00000131152	RP11-178L8.4	16:87117167-87438385	NOTEST	0.494431	0.495297	0.00252451	0	1	1
ENSG00000131183	ENSG00000131183	SLC34A1	5:176806235-176825849	NOTEST	0.0538234	0.0682633	0.342877	0	1	1
ENSG00000131203	ENSG00000131203	IDO1	8:39759793-39873910	NOTEST	0	0	0	0	1	1
ENSG00000131233	ENSG00000131233	GJA9	1:39325671-39407471	NOTEST	0.00913751	0.0742797	3.02309	0	1	1
ENSG00000131264	ENSG00000131264	CDX4	X:72667089-72675081	NOTEST	0	0	0	0	1	1
ENSG00000131355	ENSG00000131355	EMR3	19:14729928-14889353	NOTEST	0	0	0	0	1	1
ENSG00000131379	ENSG00000131379	C3orf20	3:14716605-14814541	NOTEST	0	0	0	0	1	1
ENSG00000131386	ENSG00000131386	GALNT15	3:16216155-16273499	NOTEST	0.0288875	0.0450108	0.639827	0	1	1
ENSG00000131398	ENSG00000131398	KCNC3	19:50815193-50886239	NOTEST	0.0168767	0.0138897	-0.281021	0	1	1
ENSG00000131400	ENSG00000131400	NAPSA	19:50815193-50886239	NOTEST	0.0718148	0.230969	1.68534	0	1	1
ENSG00000131401	ENSG00000131401	NAPSB	19:50815193-50886239	NOTEST	0	0	0	0	1	1
ENSG00000131471	ENSG00000131471	AOC3	17:41003200-41010147	NOTEST	0.108049	0.09236	-0.22634	0	1	1
ENSG00000131480	ENSG00000131480	AOC2	17:40996616-41002724	NOTEST	0.164082	0.295465	0.848572	0	1	1
ENSG00000131482	ENSG00000131482	G6PC	17:41052813-41065386	NOTEST	0	0	0	0	1	1
ENSG00000131484	ENSG00000131484	RP11-798G7.5	17:43578684-43640596	NOTEST	0	0.20559	inf	0	1	1
ENSG00000131538	ENSG00000131538	TTTY6	Y:24585086-24631739	NOTEST	0	0	0	0	1	1
ENSG00000131548	ENSG00000131548	TTTY6B	Y:24246960-24293631	NOTEST	0	0	0	0	1	1
ENSG00000131620	ENSG00000131620	ANO1	11:69924407-70035634	NOTEST	0.00780796	0.0439869	2.49406	0	1	1
ENSG00000131634	ENSG00000131634	TMEM204	16:1543344-1662111	NOTEST	0.171653	0.231567	0.431941	0	1	1
ENSG00000131668	ENSG00000131668	BARX1	9:96713904-96717654	NOTEST	0	0.00907079	inf	0	1	1
ENSG00000131686	ENSG00000131686	CA6	1:9005925-9035151	NOTEST	0.0235199	0	#NAME?	0	1	1

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ENSG00000131730	ENSG00000131730	CKMT2	5:80243515-80597379	NOTEST	0.132823	0.287837	1.11575	0	1	1
ENSG00000131737	ENSG00000131737	KRT34	17:39533901-39538655	NOTEST	0	0.0278234	inf	0	1	1
ENSG00000131738	ENSG00000131738	KRT33B	17:39519745-39526052	NOTEST	0	0	0	0	1	1
ENSG00000131746	ENSG00000131746	TNS4	17:38632079-38657849	NOTEST	0	0	0	0	1	1
ENSG00000131771	ENSG00000131771	PPP1R1B	17:37782992-37792879	NOTEST	0.0431219	0.301451	2.80543	0	1	1
ENSG00000131808	ENSG00000131808	FSHB	11:30252562-30256808	NOTEST	0	0	0	0	1	1
ENSG00000131831	ENSG00000131831	RAI2	X:17818168-17879457	NOTEST	0	0	0	0	1	1
ENSG00000131864	ENSG00000131864	USP29	19:57630505-57643294	NOTEST	0	0	0	0	1	1
ENSG00000131885	ENSG00000131885	KRT17P1	17:16744056-16749197	NOTEST	0	0	0	0	1	1
ENSG00000131910	ENSG00000131910	NR0B2	1:27216978-27273353	NOTEST	0	0	0	0	1	1
ENSG00000131914	ENSG00000131914	LIN28A	1:26737268-26756213	NOTEST	0	0	0	0	1	1
ENSG00000131951	ENSG00000131951	LRRC9	14:60386140-60558501	NOTEST	0	0	0	0	1	1
ENSG00000131969	ENSG00000131969	ABHD12B	14:51314839-51411454	NOTEST	0.312968	0.194578	-0.685666	0	1	1
ENSG00000131982	ENSG00000131982	UBE2L2	12:20514665-20837315	NOTEST	0	0	0	0	1	1
ENSG00000132000	ENSG00000132000	PODNL1	19:14041999-14072254	NOTEST	0.0448744	0.0235533	-0.929962	0	1	1
ENSG00000132026	ENSG00000132026	RTBDN	19:12873816-12985765	NOTEST	0.287201	0.342775	0.2552	0	1	1
ENSG00000132139	ENSG00000132139	GAS2L2	17:34071529-34079897	NOTEST	0.0107844	0.0172761	0.679828	0	1	1
ENSG00000132141	ENSG00000132141	CCT6B	17:33254877-33332083	NOTEST	0.207555	0.349575	0.75211	0	1	1
ENSG00000132164	ENSG00000132164	SLC6A11	3:10857884-10982419	NOTEST	0	0	0	0	1	1
ENSG00000132204	ENSG00000132204	LINC00470	18:1254383-1408345	NOTEST	0.0858604	0.169183	0.978522	0	1	1
ENSG00000132207	ENSG00000132207	SLX1A	16:30204254-30215631	NOTEST	0.353773	0.554555	0.648506	0	1	1
ENSG00000132259	ENSG00000132259	CNGA4	11:6255994-6265659	NOTEST	0	0.0136876	inf	0	1	1
ENSG00000132274	ENSG00000132274	TRIM22	11:5684424-5959849	NOTEST	0.195639	0.514296	1.3944	0	1	1
ENSG00000132297	ENSG00000132297	HHLA1	8:133036466-133123406	NOTEST	0.00377491	0	#NAME?	0	1	1
ENSG00000132321	ENSG00000132321	IQCA1	2:237232793-237416185	NOTEST	0	0	0	0	1	1
ENSG00000132334	ENSG00000132334	PTPRE	10:129705324-129884119	NOTEST	0.0195747	0	#NAME?	0	1	1
ENSG00000132359	ENSG00000132359	RAP1GAP2	17:2680349-2941033	NOTEST	0.00330951	0.0473689	3.83925	0	1	1
ENSG00000132437	ENSG00000132437	DDC	7:50526133-50633154	NOTEST	0.0206289	0.243816	3.56305	0	1	1
ENSG00000132446	ENSG00000132446	FTHL17	X:31089359-31090170	NOTEST	0	0	0	0	1	1
ENSG00000132464	ENSG00000132464	ENAM	4:71494460-71552533	NOTEST	0	0	0	0	1	1
ENSG00000132465	ENSG00000132465	IGJ	4:71494460-71552533	NOTEST	0.0992162	0.226366	1.19001	0	1	1
ENSG00000132498	ENSG00000132498	ANKRD20A3	9:43064965-43133544	NOTEST	0.327989	0.207228	-0.662428	0	1	1
ENSG00000132514	ENSG00000132514	CLEC10A	17:6977855-6983626	NOTEST	0	0	0	0	1	1
ENSG00000132517	ENSG00000132517	SLC52A1	17:4935894-4955304	NOTEST	0.0435434	0.0246999	-0.817947	0	1	1
ENSG00000132518	ENSG00000132518	GUCY2D	17:7905911-7923657	NOTEST	0.304758	0.319446	0.0679085	0	1	1
ENSG00000132530	ENSG00000132530	XAF1	17:6658765-6678966	NOTEST	0	0.00301997	inf	0	1	1
ENSG00000132554	ENSG00000132554	RGS22	8:100973163-101143496	NOTEST	0.00729423	0	#NAME?	0	1	1
ENSG00000132622	ENSG00000132622	HSPA12B	20:3713313-3733758	NOTEST	0.188695	0.228178	0.274105	0	1	1
ENSG00000132623	ENSG00000132623	ANKEF1	20:9966735-10349424	NOTEST	0	0.0299323	inf	0	1	1
ENSG00000132631	ENSG00000132631	SCP2D1	20:18790371-18810797	NOTEST	0	0	0	0	1	1
ENSG00000132639	ENSG00000132639	SNAP25	20:9966735-10349424	NOTEST	0	0	0	0	1	1
ENSG00000132671	ENSG00000132671	SSTR4	20:23012178-23019873	NOTEST	0	0	0	0	1	1
ENSG00000132677	ENSG00000132677	RHBG	1:156339002-156355011	NOTEST	0.0387513	0.0357362	-0.116859	0	1	1
ENSG00000132693	ENSG00000132693	CRP	1:159682078-159684379	NOTEST	0	0	0	0	1	1

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ENSG00000132698	ENSG00000132698	RAB25	1:156030950-156040295	NOTEST	0	0.0286319	inf	0	1	1
ENSG00000132702	ENSG00000132702	HAPLN2	1:156589085-156595517	NOTEST	0.0615065	0.0531206	-0.211467	0	1	1
ENSG00000132703	ENSG00000132703	APCS	1:159557614-159558655	NOTEST	0	0	0	0	1	1
ENSG00000132704	ENSG00000132704	FCRL2	1:157715522-157746922	NOTEST	0	0	0	0	1	1
ENSG00000132744	ENSG00000132744	ACY3	11:67410025-67418130	NOTEST	0	0.0389664	inf	0	1	1
ENSG00000132746	ENSG00000132746	ALDH3B2	11:67429632-67448671	NOTEST	0.144886	0.29054	1.00382	0	1	1
ENSG00000132821	ENSG00000132821	VSTM2L	20:36531498-36573752	NOTEST	0.0487112	0.0982688	1.01248	0	1	1
ENSG00000132832	ENSG00000132832	RP11-445H22.3	20:43285091-43379675	NOTEST	0.0552701	0.0785115	0.506405	0	1	1
ENSG00000132837	ENSG00000132837	DMGDH	5:78293437-78531861	NOTEST	0	0	0	0	1	1
ENSG00000132840	ENSG00000132840	BHMT2	5:78293437-78531861	NOTEST	0	0.00844962	inf	0	1	1
ENSG00000132854	ENSG00000132854	KANK4	1:62702650-62785085	NOTEST	0	0	0	0	1	1
ENSG00000132855	ENSG00000132855	ANGPTL3	1:62920398-63153969	NOTEST	0	0.0122979	inf	0	1	1
ENSG00000132872	ENSG00000132872	SYT4	18:40847842-40857615	NOTEST	0	0	0	0	1	1
ENSG00000132874	ENSG00000132874	SLC14A2	18:42792959-43332485	NOTEST	0.00953227	0	#NAME?	0	1	1
ENSG00000132911	ENSG00000132911	NMUR2	5:151771092-151812929	NOTEST	0	0.0171454	inf	0	1	1
ENSG00000132915	ENSG00000132915	PDE6A	5:149237518-149324356	NOTEST	0	0.0040072	inf	0	1	1
ENSG00000132932	ENSG00000132932	ATP8A2	13:25946208-26599989	NOTEST	0.376968	0.0695342	-2.43865	0	1	1
ENSG00000132938	ENSG00000132938	MTUS2	13:29598747-30077892	NOTEST	0.0298832	0.0193072	-0.630195	0	1	1
ENSG00000132958	ENSG00000132958	TPTE2	13:19997016-20110903	NOTEST	0	0	0	0	1	1
ENSG00000132965	ENSG00000132965	ALOX5AP	13:31309644-31338556	NOTEST	0	0	0	0	1	1
ENSG00000132972	ENSG00000132972	RNF17	13:25338289-25454059	NOTEST	0	0	0	0	1	1
ENSG00000132975	ENSG00000132975	GPR12	13:27329340-27334922	NOTEST	0	0	0	0	1	1
ENSG00000133019	ENSG00000133019	CHRM3	1:239549864-240080255	NOTEST	0.0474838	0.0850976	0.841683	0	1	1
ENSG00000133020	ENSG00000133020	MYH8	17:10286448-10527203	NOTEST	0	0	0	0	1	1
ENSG00000133048	ENSG00000133048	CHI3L1	1:203148058-203155877	NOTEST	0.039314	0.0655882	0.738394	0	1	1
ENSG00000133055	ENSG00000133055	MYBPH	1:203136938-203144941	NOTEST	0	0	0	0	1	1
ENSG00000133063	ENSG00000133063	CHIT1	1:203181954-203242769	NOTEST	0	0	0	0	1	1
ENSG00000133067	ENSG00000133067	LGR6	1:202163028-202288909	NOTEST	0	0	0	0	1	1
ENSG00000133101	ENSG00000133101	CCNA1	13:37005966-37017019	NOTEST	0.00829213	0	#NAME?	0	1	1
ENSG00000133105	ENSG00000133105	RXFP2	13:32313673-32377009	NOTEST	0	0	0	0	1	1
ENSG00000133106	ENSG00000133106	EPSTI1	13:43460523-43566407	NOTEST	0.243758	0.194196	-0.327933	0	1	1
ENSG00000133107	ENSG00000133107	TRPC4	13:38210772-38444562	NOTEST	0.00644418	0.0368827	2.51688	0	1	1
ENSG00000133110	ENSG00000133110	POSTN	13:38136719-38172981	NOTEST	0.0337306	0.0165727	-1.02524	0	1	1
ENSG00000133115	ENSG00000133115	STOML3	13:39540061-39565203	NOTEST	0.0147293	0.00631864	-1.221	0	1	1
ENSG00000133116	ENSG00000133116	KL	13:33590206-33640282	NOTEST	0	0.00740118	inf	0	1	1
ENSG00000133124	ENSG00000133124	IRS4	X:107963178-107982133	NOTEST	0.0668481	0.120261	0.847213	0	1	1
ENSG00000133136	ENSG00000133136	GNG5P2	X:109437413-109699562	NOTEST	0	0.0318733	inf	0	1	1
ENSG00000133149	ENSG00000133149	TEX13A	X:103810995-105011822	NOTEST	0	0	0	0	1	1
ENSG00000133216	ENSG00000133216	EPHB2	1:23037331-23241818	NOTEST	0.0671886	0.184948	1.46083	0	1	1
ENSG00000133246	ENSG00000133246	PRAM1	19:8554939-8567996	NOTEST	0.0135035	0	#NAME?	0	1	1
ENSG00000133256	ENSG00000133256	PDE6B	4:619372-664571	NOTEST	0	0	0	0	1	1
ENSG00000133317	ENSG00000133317	LGALS12	11:63273555-63284246	NOTEST	0.0118421	0	#NAME?	0	1	1
ENSG00000133321	ENSG00000133321	RARRES3	11:63304280-63313934	NOTEST	0	0.0199938	inf	0	1	1
ENSG00000133328	ENSG00000133328	HRASLS2	11:63320241-63330855	NOTEST	0	0.062803	inf	0	1	1
ENSG00000133392	ENSG00000133392	MYH11	16:15737123-15950890	NOTEST	0.180338	0.187165	0.0536104	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000133401	ENSG00000133401	PDZD2	5:31639516-32122047	NOTEST	0.264973	0.409825	0.629161	0	1	1
ENSG00000133454	ENSG00000133454	MYO18B	22:26138110-26427007	NOTEST	0	0.00186268	inf	0	1	1
ENSG00000133475	ENSG00000133475	GGT2	22:21562261-21581926	NOTEST	0	0.00689315	inf	0	1	1
ENSG00000133477	ENSG00000133477	FAM83F	22:40390952-40440534	NOTEST	0	0	0	0	1	1
ENSG00000133488	ENSG00000133488	SEC14L4	22:30879340-30901698	NOTEST	0	0	0	0	1	1
ENSG00000133561	ENSG00000133561	GIMAP6	7:150322462-150329473	NOTEST	0	0.0464589	inf	0	1	1
ENSG00000133574	ENSG00000133574	GIMAP4	7:150264364-150271041	NOTEST	0	0	0	0	1	1
ENSG00000133661	ENSG00000133661	SFTPD	10:81664653-81742370	NOTEST	0.0377138	0.0386494	0.0353516	0	1	1
ENSG00000133665	ENSG00000133665	DYDC2	10:82095860-82127829	NOTEST	0.0441765	0.233094	2.39956	0	1	1
ENSG00000133742	ENSG00000133742	CA1	8:86239836-86393722	NOTEST	0	0	0	0	1	1
ENSG00000133800	ENSG00000133800	LYVE1	11:10562818-10715535	NOTEST	0	0.0105024	inf	0	1	1
ENSG00000133808	ENSG00000133808	MICALCL	11:12297626-12380691	NOTEST	0.0351871	0.010887	-1.69244	0	1	1
ENSG00000133878	ENSG00000133878	DUSP26	8:33448855-33457624	NOTEST	0.00895736	0	#NAME?	0	1	1
ENSG00000133937	ENSG00000133937	GSC	14:95234552-95236562	NOTEST	0	0	0	0	1	1
ENSG00000133958	ENSG00000133958	UNC79	14:93799564-94174222	NOTEST	0	0	0	0	1	1
ENSG00000133962	ENSG00000133962	CATSPERB	14:92047039-92333880	NOTEST	0	0.0101357	inf	0	1	1
ENSG00000133980	ENSG00000133980	VRTN	14:74769771-74826711	NOTEST	0	0	0	0	1	1
ENSG00000133985	ENSG00000133985	TTC9	14:71108503-71142077	NOTEST	0.0188722	0.022872	0.277324	0	1	1
ENSG00000134007	ENSG00000134007	ADAM20	14:70892528-71014181	NOTEST	0.0056596	0	#NAME?	0	1	1
ENSG00000134020	ENSG00000134020	PEBP4	8:22545171-22941132	NOTEST	0	0	0	0	1	1
ENSG00000134028	ENSG00000134028	ADAMDEC1	8:24151552-24769586	NOTEST	0	0	0	0	1	1
ENSG00000134042	ENSG00000134042	MRO	18:48324573-48351772	NOTEST	0.57458	0.403903	-0.508501	0	1	1
ENSG00000134061	ENSG00000134061	CD180	5:66478102-66492627	NOTEST	0	0	0	0	1	1
ENSG00000134070	ENSG00000134070	IRAK2	3:10206548-10285427	NOTEST	0.408599	0.387044	-0.0781886	0	1	1
ENSG00000134115	ENSG00000134115	CNTN6	3:1134259-1445901	NOTEST	0.538553	0.476734	-0.175904	0	1	1
ENSG00000134183	ENSG00000134183	GNAT2	1:110145888-110155679	NOTEST	0.135236	0.0989909	-0.450111	0	1	1
ENSG00000134184	ENSG00000134184	GSTM1	1:110210643-110252171	NOTEST	0	0.0818829	inf	0	1	1
ENSG00000134193	ENSG00000134193	REG4	1:120336640-120354283	NOTEST	0	0	0	0	1	1
ENSG00000134198	ENSG00000134198	TSPAN2	1:115590631-115632121	NOTEST	0	0	0	0	1	1
ENSG00000134200	ENSG00000134200	TSHB	1:115572414-115576941	NOTEST	0	0	0	0	1	1
ENSG00000134201	ENSG00000134201	GSTM5	1:110254863-110318050	NOTEST	0	0	0	0	1	1
ENSG00000134207	ENSG00000134207	SYT6	1:114631912-114696541	NOTEST	0	0	0	0	1	1
ENSG00000134216	ENSG00000134216	CHIA	1:111833483-111866697	NOTEST	0	0	0	0	1	1
ENSG00000134240	ENSG00000134240	HMGCS2	1:120290618-120311528	NOTEST	0	0	0	0	1	1
ENSG00000134242	ENSG00000134242	PTPN22	1:114304453-114456708	NOTEST	0	0.0201017	inf	0	1	1
ENSG00000134245	ENSG00000134245	WNT2B	1:113009162-113214241	NOTEST	0.218782	0.294445	0.428502	0	1	1
ENSG00000134249	ENSG00000134249	ADAM30	1:120436155-120439118	NOTEST	0	0	0	0	1	1
ENSG00000134256	ENSG00000134256	CD101	1:117544381-117602112	NOTEST	0.0625175	0.211718	1.75981	0	1	1
ENSG00000134258	ENSG00000134258	VTCN1	1:117686208-117753556	NOTEST	0.0328888	0.00553117	-2.57194	0	1	1
ENSG00000134259	ENSG00000134259	NGF	1:115825654-115910693	NOTEST	0	0	0	0	1	1
ENSG00000134317	ENSG00000134317	GRHL1	2:10085340-10142411	NOTEST	0.611265	0.521225	-0.229891	0	1	1
ENSG00000134321	ENSG00000134321	RSAD2	2:6980700-7038370	NOTEST	0	0.0272114	inf	0	1	1
ENSG00000134323	ENSG00000134323	MYCN	2:16060520-16087129	NOTEST	0	0.00429005	inf	0	1	1
ENSG00000134326	ENSG00000134326	CMPK2	2:6980700-7038370	NOTEST	0.30419	0.323069	0.0868723	0	1	1
ENSG00000134339	ENSG00000134339	SAA2	11:18252895-18270190	NOTEST	0.160966	0.235562	0.549353	0	1	1

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ENSG00000134343	ENSG00000134343	ANO3	11:26210669-26684835	NOTEST	0	0.0191088	inf	0	1	1
ENSG00000134365	ENSG00000134365	CFHR4	1:196788886-196928356	NOTEST	0	0	0	0	1	1
ENSG00000134376	ENSG00000134376	CRB1	1:197170591-197447585	NOTEST	0.173172	0.182406	0.074952	0	1	1
ENSG00000134389	ENSG00000134389	CFHR5	1:196946666-196978804	NOTEST	0	0	0	0	1	1
ENSG00000134398	ENSG00000134398	ERN2	16:23688976-23724821	NOTEST	0	0	0	0	1	1
ENSG00000134438	ENSG00000134438	RAX	18:56934266-56941318	NOTEST	0	0	0	0	1	1
ENSG00000134443	ENSG00000134443	GRP	18:56887399-56898006	NOTEST	0	0	0	0	1	1
ENSG00000134460	ENSG00000134460	IL2RA	10:6052651-6104288	NOTEST	0	0	0	0	1	1
ENSG00000134470	ENSG00000134470	IL15RA	10:5990854-6020150	NOTEST	0	0	0	0	1	1
ENSG00000134489	ENSG00000134489	HRH4	18:22040592-22059921	NOTEST	0.0192156	0.0359904	0.905334	0	1	1
ENSG00000134516	ENSG00000134516	DOCK2	5:169064250-169510386	NOTEST	0.279089	0.290634	0.0584784	0	1	1
ENSG00000134533	ENSG00000134533	RERG	12:15260716-15750333	NOTEST	0.240588	0.1316	-0.870408	0	1	1
ENSG00000134538	ENSG00000134538	SLCO1B1	12:20963635-21392180	NOTEST	0	0	0	0	1	1
ENSG00000134539	ENSG00000134539	KLRD1	12:10378656-10469850	NOTEST	0	0	0	0	1	1
ENSG00000134545	ENSG00000134545	KLRC1	12:10564910-10607284	NOTEST	0	0	0	0	1	1
ENSG00000134551	ENSG00000134551	PRH2	12:10977558-11324212	NOTEST	0.121485	0	#NAME?	0	1	1
ENSG00000134571	ENSG00000134571	MYBPC3	11:47352956-47374253	NOTEST	0.0102988	0	#NAME?	0	1	1
ENSG00000134588	ENSG00000134588	USP26	X:132158658-132231137	NOTEST	0	0	0	0	1	1
ENSG00000134595	ENSG00000134595	SOX3	X:139585151-139587225	NOTEST	0	0	0	0	1	1
ENSG00000134612	ENSG00000134612	FOLH1B	11:89371682-89431886	NOTEST	0.072563	0.172424	1.24865	0	1	1
ENSG00000134627	ENSG00000134627	PIWIL4	11:94277005-94658686	NOTEST	0.265289	0.30536	0.202948	0	1	1
ENSG00000134640	ENSG00000134640	MTNR1B	11:92702885-92718232	NOTEST	0	0	0	0	1	1
ENSG00000134668	ENSG00000134668	SPOCD1	1:32254730-32281652	NOTEST	0.398724	0.479375	0.265764	0	1	1
ENSG00000134755	ENSG00000134755	DSC2	18:28645939-28742819	NOTEST	0.0172694	0.0467383	1.43638	0	1	1
ENSG00000134757	ENSG00000134757	DSG3	18:29027757-29058665	NOTEST	0	0	0	0	1	1
ENSG00000134760	ENSG00000134760	DSG1	18:28898051-29006951	NOTEST	0.00880878	0.0193484	1.1352	0	1	1
ENSG00000134762	ENSG00000134762	DSC3	18:28569973-28622781	NOTEST	0.00790246	0.0114473	0.534629	0	1	1
ENSG00000134765	ENSG00000134765	DSC1	18:28645939-28742819	NOTEST	0	0	0	0	1	1
ENSG00000134812	ENSG00000134812	GIF	11:59596740-59612974	NOTEST	0	0	0	0	1	1
ENSG00000134817	ENSG00000134817	APLNR	11:57001050-57004709	NOTEST	0	0.00947448	inf	0	1	1
ENSG00000134830	ENSG00000134830	C5AR2	19:47835403-47846606	NOTEST	0	0	0	0	1	1
ENSG00000134873	ENSG00000134873	CLDN10	13:96085857-96296957	NOTEST	0.0183758	0.0840348	2.19318	0	1	1
ENSG00000134917	ENSG00000134917	ADAMTS8	11:130274819-130298888	NOTEST	0	0	0	0	1	1
ENSG00000134940	ENSG00000134940	ACRV1	11:125439111-125551018	NOTEST	0.283208	0.0454693	-2.6389	0	1	1
ENSG00000134962	ENSG00000134962	KLB	4:39408472-39453156	NOTEST	0.00502464	0.00176245	-1.51144	0	1	1
ENSG00000134986	ENSG00000134986	NREP	5:110831730-111353006	NOTEST	0.560466	0.307232	-0.867297	0	1	1
ENSG00000135077	ENSG00000135077	HAVCR2	5:156512842-156682201	NOTEST	0	0.0707077	inf	0	1	1
ENSG00000135094	ENSG00000135094	SDS	12:113830249-113876081	NOTEST	0.0770381	0.355482	2.20613	0	1	1
ENSG00000135100	ENSG00000135100	HNF1A	12:121406415-121454305	NOTEST	0.303769	0.362493	0.254981	0	1	1
ENSG00000135111	ENSG00000135111	TBX3	12:115108058-115121969	NOTEST	0.0163843	0.0163375	-0.00412648	0	1	1
ENSG00000135114	ENSG00000135114	OASL	12:121458094-121477045	NOTEST	0.0337287	0.0109034	-1.6292	0	1	1
ENSG00000135144	ENSG00000135144	DTX1	12:113494513-113535833	NOTEST	0.0148756	0.0677344	2.18694	0	1	1
ENSG00000135175	ENSG00000135175	OCM2	7:97613995-97620481	NOTEST	0	0	0	0	1	1
ENSG00000135220	ENSG00000135220	UGT2A3	4:69794180-69817509	NOTEST	0	0	0	0	1	1
ENSG00000135222	ENSG00000135222	CSN2	4:70820973-70826725	NOTEST	0	0	0	0	1	1

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ENSG00000135226	ENSG00000135226	UGT2B28	4:70146216-70160768	NOTEST	0	0	0	0	1	1
ENSG00000135248	ENSG00000135248	FAM71F1	7:128349114-128371797	NOTEST	0	0.0255235	inf	0	1	1
ENSG00000135312	ENSG00000135312	HTR1B	6:78171947-78173490	NOTEST	0	0	0	0	1	1
ENSG00000135314	ENSG00000135314	KHDC1	6:73918805-74020088	NOTEST	0.409516	0.394772	-0.0528991	0	1	1
ENSG00000135324	ENSG00000135324	MRAP2	6:84743474-84800600	NOTEST	0.0435376	0.197596	2.18222	0	1	1
ENSG00000135333	ENSG00000135333	EPHA7	6:93949737-94129265	NOTEST	0.28852	0.129914	-1.15111	0	1	1
ENSG00000135346	ENSG00000135346	CGA	6:87795215-87804824	NOTEST	0.0506697	0	#NAME?	0	1	1
ENSG00000135355	ENSG00000135355	GJA10	6:90604187-90605839	NOTEST	0	0	0	0	1	1
ENSG00000135363	ENSG00000135363	LMO2	11:33880121-33913836	NOTEST	0.241286	0.421343	0.804248	0	1	1
ENSG00000135373	ENSG00000135373	EHF	11:34642639-34682604	NOTEST	0.0133911	0.0734449	2.45538	0	1	1
ENSG00000135374	ENSG00000135374	ELF5	11:34500339-34535352	NOTEST	0	0	0	0	1	1
ENSG00000135378	ENSG00000135378	PRRG4	11:32851488-32879669	NOTEST	0.495325	0.622269	0.329164	0	1	1
ENSG00000135406	ENSG00000135406	PRPH	12:49686413-49725514	NOTEST	0.104173	0.176556	0.761149	0	1	1
ENSG00000135407	ENSG00000135407	AVIL	12:58156116-58212487	NOTEST	0.171462	0.0912956	-0.909273	0	1	1
ENSG00000135409	ENSG00000135409	AMHR2	12:53817638-53825318	NOTEST	0.106147	0.0770626	-0.461958	0	1	1
ENSG00000135413	ENSG00000135413	LACRT	12:55024594-55028679	NOTEST	0	0	0	0	1	1
ENSG00000135423	ENSG00000135423	GLS2	12:56843285-56882198	NOTEST	0.425812	0.258453	-0.720317	0	1	1
ENSG00000135426	ENSG00000135426	TESPA1	12:55341801-55378530	NOTEST	0	0	0	0	1	1
ENSG00000135436	ENSG00000135436	FAM186B	12:49962000-50158717	NOTEST	0.280565	0.395764	0.496306	0	1	1
ENSG00000135439	ENSG00000135439	AGAP2	12:58117543-58154190	NOTEST	0.012485	0.0152765	0.291113	0	1	1
ENSG00000135443	ENSG00000135443	KRT85	12:52753789-52761265	NOTEST	0	0	0	0	1	1
ENSG00000135447	ENSG00000135447	PPP1R1A	12:54943133-54982443	NOTEST	0	0	0	0	1	1
ENSG00000135472	ENSG00000135472	FAIM2	12:50260678-50298000	NOTEST	0	0.0145173	inf	0	1	1
ENSG00000135477	ENSG00000135477	KRT121P	12:52626303-52702947	NOTEST	0	0	0	0	1	1
ENSG00000135480	ENSG00000135480	KRT7	12:52626303-52702947	NOTEST	0.0585486	0.139817	1.25583	0	1	1
ENSG00000135502	ENSG00000135502	SLC26A10	12:58003962-58027138	NOTEST	0.33725	0.293388	-0.201006	0	1	1
ENSG00000135517	ENSG00000135517	MIP	12:56843285-56882198	NOTEST	0.0180937	0.00859143	-1.07452	0	1	1
ENSG00000135519	ENSG00000135519	KCNH3	12:49932939-49961936	NOTEST	0.0838494	0.100833	0.266097	0	1	1
ENSG00000135569	ENSG00000135569	TAAR5	6:132909730-132910877	NOTEST	0	0	0	0	1	1
ENSG00000135577	ENSG00000135577	NMBR	6:142379466-142410356	NOTEST	0	0	0	0	1	1
ENSG00000135625	ENSG00000135625	EGR4	2:73518057-73520833	NOTEST	0.00674737	0	#NAME?	0	1	1
ENSG00000135638	ENSG00000135638	EMX1	2:73143388-73162020	NOTEST	0.0188461	0	#NAME?	0	1	1
ENSG00000135643	ENSG00000135643	KCNMB4	12:70760055-70828072	NOTEST	0.184029	0.193694	0.0738447	0	1	1
ENSG00000135697	ENSG00000135697	BCMO1	16:81272052-81324747	NOTEST	0.0159636	0	#NAME?	0	1	1
ENSG00000135702	ENSG00000135702	CHST5	16:75562429-75657198	NOTEST	0.0346212	0.104702	1.59656	0	1	1
ENSG00000135744	ENSG00000135744	AGT	1:230838268-230937749	NOTEST	0.0520439	0.358058	2.78239	0	1	1
ENSG00000135750	ENSG00000135750	KCNK1	1:233749749-233808258	NOTEST	0	0	0	0	1	1
ENSG00000135773	ENSG00000135773	CAPN9	1:230838268-230937749	NOTEST	0	0	0	0	1	1
ENSG00000135824	ENSG00000135824	RGS8	1:182615238-182653711	NOTEST	0	0	0	0	1	1
ENSG00000135835	ENSG00000135835	KIAA1614	1:180882289-180992047	NOTEST	0.244693	0.350078	0.516703	0	1	1
ENSG00000135898	ENSG00000135898	GPR55	2:231772032-231825781	NOTEST	0.235933	0.413152	0.808297	0	1	1
ENSG00000135902	ENSG00000135902	CHRND	2:233390702-233401377	NOTEST	0.00941416	0	#NAME?	0	1	1
ENSG00000135925	ENSG00000135925	WNT10A	2:219745084-219764303	NOTEST	0.023806	0.0238138	0.000470275	0	1	1
ENSG00000135960	ENSG00000135960	EDAR	2:109510926-109605828	NOTEST	0.00662727	0	#NAME?	0	1	1
ENSG00000135973	ENSG00000135973	GPR45	2:105858199-105859924	NOTEST	0.12666	0.170059	0.425078	0	1	1

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ENSG00000136002	ENSG00000136002	ARHGEF4	2:131588550-131804836	NOTEST	0.471503	0.493454	0.0656475	0	1	1
ENSG00000136010	ENSG00000136010	ALDH1L2	12:105380087-105478355	NOTEST	0.454949	0.383084	-0.248043	0	1	1
ENSG00000136014	ENSG00000136014	USP44	12:95910335-95945266	NOTEST	0.305426	0.582594	0.93167	0	1	1
ENSG00000136099	ENSG00000136099	PCDH8	13:53418108-53422775	NOTEST	0	0	0	0	1	1
ENSG00000136110	ENSG00000136110	LECT1	13:53277398-53313947	NOTEST	0	0	0	0	1	1
ENSG00000136114	ENSG00000136114	THSD1	13:52951304-52980629	NOTEST	0.287577	0.317201	0.141452	0	1	1
ENSG00000136149	ENSG00000136149	RPL13AP25	13:55014838-55015450	NOTEST	0.412192	0.402556	-0.0341255	0	1	1
ENSG00000136155	ENSG00000136155	SCEL	13:78109808-78219398	NOTEST	0.00670436	0.00395448	-0.761613	0	1	1
ENSG00000136206	ENSG00000136206	SPDYE1	7:43966036-44058774	NOTEST	0.251063	0.203792	-0.300958	0	1	1
ENSG00000136237	ENSG00000136237	RAPGEF5	7:22157855-22396763	NOTEST	0.468736	0.580321	0.308076	0	1	1
ENSG00000136250	ENSG00000136250	AOAH	7:36552455-36764154	NOTEST	0	0	0	0	1	1
ENSG00000136267	ENSG00000136267	DGKB	7:14184673-15014402	NOTEST	0	0	0	0	1	1
ENSG00000136275	ENSG00000136275	C7orf69	7:47735327-48019178	NOTEST	0.144554	0.141808	-0.02767	0	1	1
ENSG00000136286	ENSG00000136286	MYO1G	7:45002260-45018697	NOTEST	0.0197531	0.033533	0.763506	0	1	1
ENSG00000136297	ENSG00000136297	MMD2	7:4945619-4998844	NOTEST	0	0	0	0	1	1
ENSG00000136305	ENSG00000136305	CIDEB	14:24769067-24787242	NOTEST	0.231683	0.473436	1.03102	0	1	1
ENSG00000136315	ENSG00000136315	RP11-84C10.2	14:21366143-21404414	NOTEST	0	0	0	0	1	1
ENSG00000136327	ENSG00000136327	NKX2-8	14:37049783-37051812	NOTEST	0.142483	0.299844	1.07342	0	1	1
ENSG00000136352	ENSG00000136352	NKX2-1	14:36942411-36992221	NOTEST	0	7.63E-07	inf	0	1	1
ENSG00000136367	ENSG00000136367	ZFHX2	14:23980968-24048009	NOTEST	0.206458	0.386318	0.903938	0	1	1
ENSG00000136383	ENSG00000136383	ALPK3	15:85359910-85416713	NOTEST	0.0273791	0.0583672	1.09209	0	1	1
ENSG00000136449	ENSG00000136449	MYCBPAP	17:48585744-48608862	NOTEST	0.495146	0.570096	0.203351	0	1	1
ENSG00000136457	ENSG00000136457	CHAD	17:48503518-48552206	NOTEST	0.341378	0.423536	0.311113	0	1	1
ENSG00000136487	ENSG00000136487	GH2	17:61957577-61959295	NOTEST	0	0	0	0	1	1
ENSG00000136488	ENSG00000136488	CSH1	17:61972274-61974021	NOTEST	0	0	0	0	1	1
ENSG00000136531	ENSG00000136531	SCN2A	2:166095911-166248818	NOTEST	0.0316776	0.0517024	0.706765	0	1	1
ENSG00000136535	ENSG00000136535	TBR1	2:162272604-162841792	NOTEST	0	0.00572116	inf	0	1	1
ENSG00000136541	ENSG00000136541	ERMN	2:158175136-158184225	NOTEST	0.0180022	0.129198	2.84334	0	1	1
ENSG00000136542	ENSG00000136542	GALNT5	2:158114109-158170723	NOTEST	0.0327058	0.0541068	0.726262	0	1	1
ENSG00000136546	ENSG00000136546	SCN7A	2:167260082-167350757	NOTEST	0	0	0	0	1	1
ENSG00000136573	ENSG00000136573	BLK	8:11351509-11422113	NOTEST	0.0553227	0.0484282	-0.192026	0	1	1
ENSG00000136634	ENSG00000136634	IL10	1:206940946-206945839	NOTEST	0.108188	0.169306	0.646089	0	1	1
ENSG00000136653	ENSG00000136653	RASSF5	1:206680878-206785904	NOTEST	0.234622	0.528685	1.17207	0	1	1
ENSG00000136688	ENSG00000136688	IL36G	2:113730779-113743242	NOTEST	0.0145041	0	#NAME?	0	1	1
ENSG00000136689	ENSG00000136689	IL1RN	2:113864790-113891593	NOTEST	0	0	0	0	1	1
ENSG00000136694	ENSG00000136694	IL36A	2:113763037-113765621	NOTEST	0	0	0	0	1	1
ENSG00000136695	ENSG00000136695	IL36RN	2:113816214-113822959	NOTEST	0	0	0	0	1	1
ENSG00000136696	ENSG00000136696	IL36B	2:113779667-113810444	NOTEST	0	0	0	0	1	1
ENSG00000136697	ENSG00000136697	IL1F10	2:113825546-113833427	NOTEST	0	0	0	0	1	1
ENSG00000136698	ENSG00000136698	CFC1	2:131350338-131357123	NOTEST	0	0	0	0	1	1
ENSG00000136750	ENSG00000136750	GAD2	10:26505235-26593487	NOTEST	0	0	0	0	1	1
ENSG00000136826	ENSG00000136826	KLF4	9:110247132-110252763	NOTEST	0.238199	0.603818	1.34195	0	1	1
ENSG00000136834	ENSG00000136834	OR1J1	9:125239219-125240235	NOTEST	0	0	0	0	1	1
ENSG00000136839	ENSG00000136839	OR13C9	9:107379528-107380485	NOTEST	0	0	0	0	1	1
ENSG00000136859	ENSG00000136859	ANGPTL2	9:129677052-129985445	NOTEST	0	0.00589543	inf	0	1	1

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ENSG00000136869	ENSG00000136869	TLR4	9:120466609-120479149	NOTEST	0.00577832	0.00727802	0.332896	0	1	1
ENSG00000136872	ENSG00000136872	ALDOB	9:104182859-104198105	NOTEST	0	0.00963537	inf	0	1	1
ENSG00000136881	ENSG00000136881	BAAT	9:104121213-104145801	NOTEST	0.152269	0.527489	1.79252	0	1	1
ENSG00000136883	ENSG00000136883	KIF12	9:116848405-116861507	NOTEST	0.138179	0.418596	1.59902	0	1	1
ENSG00000136918	ENSG00000136918	WDR38	9:127615754-127624260	NOTEST	0.0137392	0	#NAME?	0	1	1
ENSG00000136928	ENSG00000136928	GABBR2	9:101050390-101471479	NOTEST	0.00265659	0.0196488	2.88679	0	1	1
ENSG00000136929	ENSG00000136929	HEMGN	9:100689072-100707138	NOTEST	0	0	0	0	1	1
ENSG00000136931	ENSG00000136931	NR5A1	9:127243515-127269709	NOTEST	0	0	0	0	1	1
ENSG00000136939	ENSG00000136939	OR1L4	9:125486268-125487204	NOTEST	0	0	0	0	1	1
ENSG00000136960	ENSG00000136960	ENPP2	8:120569325-120685693	NOTEST	0.35136	0.333529	-0.0751386	0	1	1
ENSG00000137033	ENSG00000137033	IL33	9:6215804-6257983	NOTEST	0.0552511	0.124633	1.17361	0	1	1
ENSG00000137077	ENSG00000137077	CCL21	9:34709001-34710121	NOTEST	0	0	0	0	1	1
ENSG00000137078	ENSG00000137078	SIT1	9:35649291-35650937	NOTEST	0	0	0	0	1	1
ENSG00000137080	ENSG00000137080	IFNA21	9:21165635-21166659	NOTEST	0	0	0	0	1	1
ENSG00000137090	ENSG00000137090	DMRT1	9:841689-969090	NOTEST	0.00933996	0	#NAME?	0	1	1
ENSG00000137101	ENSG00000137101	CD72	9:35605366-35647096	NOTEST	0.114098	0.0392979	-1.53775	0	1	1
ENSG00000137197	ENSG00000137197	CDSN	HSCHR6_MHC_COX:31075026-31100333	NOTEST	0	0	0	0	1	1
ENSG00000137204	ENSG00000137204	SLC22A7	6:43263431-43337216	NOTEST	0	0	0	0	1	1
ENSG00000137225	ENSG00000137225	CAPN11	6:44126547-44152139	NOTEST	0.0232349	0.0250966	0.111198	0	1	1
ENSG00000137251	ENSG00000137251	TINAG	6:54172656-54254950	NOTEST	0	0	0	0	1	1
ENSG00000137252	ENSG00000137252	HCRTR2	6:55039049-55147418	NOTEST	0	0	0	0	1	1
ENSG00000137259	ENSG00000137259	HIST1H2AB	6:26033319-26033796	NOTEST	0.13923	0.180335	0.373206	0	1	1
ENSG00000137261	ENSG00000137261	KIAA0319	6:24544331-24646383	NOTEST	0.0799032	0.0221469	-1.85115	0	1	1
ENSG00000137270	ENSG00000137270	GCM1	6:52991761-53013627	NOTEST	0.0229002	0.00402001	-2.51009	0	1	1
ENSG00000137313	ENSG00000137313	TRIM26	HSCHR6_MHC_QBL:30141749-30170728	NOTEST	0	0	0	0	1	1
ENSG00000137321	ENSG00000137321	RANP1	HSCHR6_MHC_SSTO:30445151-30445802	NOTEST	0	0	0	0	1	1
ENSG00000137332	ENSG00000137332	DDR1	HSCHR6_MHC_COX:30838645-30857829	NOTEST	0	0	0	0	1	1
ENSG00000137345	ENSG00000137345	MOG	HSCHR6_MHC_QBL:29624679-29640072	NOTEST	0	0	0	0	1	1
ENSG00000137384	ENSG00000137384	TRIM15	HSCHR6_MHC_QBL:30120532-30130023	NOTEST	0	0	0	0	1	1
ENSG00000137392	ENSG00000137392	CLPS	6:35762758-35765088	NOTEST	0	0	0	0	1	1
ENSG00000137394	ENSG00000137394	TRIM10	HSCHR6_MHC_QBL:30109272-30118261	NOTEST	0	0	0	0	1	1
ENSG00000137397	ENSG00000137397	TRIM31	HSCHR6_MHC_QBL:30060242-30072064	NOTEST	0	0	0	0	1	1
ENSG00000137403	ENSG00000137403	HLA-F	HSCHR6_MHC_COX:29684536-29710797	NOTEST	0	0	0	0	1	1
ENSG00000137434	ENSG00000137434	C6orf52	6:10671650-10710015	NOTEST	0.554335	0.273053	-1.02158	0	1	1
ENSG00000137440	ENSG00000137440	FGFBP1	4:15937191-15940363	NOTEST	0	0.0355382	inf	0	1	1
ENSG00000137463	ENSG00000137463	MGARP	4:140187316-140397763	NOTEST	0.0231148	0.0396273	0.777674	0	1	1
ENSG00000137473	ENSG00000137473	TTC29	4:147627789-147867034	NOTEST	0	0	0	0	1	1
ENSG00000137491	ENSG00000137491	SLCO2B1	11:74810216-74917594	NOTEST	0.580121	0.581698	0.00391554	0	1	1
ENSG00000137507	ENSG00000137507	LRRC32	11:76368099-76381791	NOTEST	0.0702146	0.0835382	0.250664	0	1	1
ENSG00000137634	ENSG00000137634	NXPE4	11:114441312-114466484	NOTEST	0	0	0	0	1	1
ENSG00000137642	ENSG00000137642	SORL1	11:121318039-121504402	NOTEST	0.567015	0.563369	-0.00930764	0	1	1
ENSG00000137648	ENSG00000137648	TMPRSS4	11:117886486-117992605	NOTEST	0	0	0	0	1	1
ENSG00000137672	ENSG00000137672	TRPC6	11:101322294-101743293	NOTEST	0	0	0	0	1	1
ENSG00000137673	ENSG00000137673	MMP7	11:102391238-102401484	NOTEST	0.0155685	0	#NAME?	0	1	1
ENSG00000137674	ENSG00000137674	MMP20	11:102447565-102498801	NOTEST	0.00832	0	#NAME?	0	1	1

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ENSG00000137675	ENSG00000137675	MMP27	11:102562217-102576537	NOTEST	0	0	0	0	1	1
ENSG00000137691	ENSG00000137691	C11orf70	11:101918173-101955291	NOTEST	0.0829072	0.0294845	-1.49154	0	1	1
ENSG00000137699	ENSG00000137699	TRIM29	11:119981982-120056237	NOTEST	0.0184412	0.0245093	0.410395	0	1	1
ENSG00000137707	ENSG00000137707	BTG4	11:111338250-111383079	NOTEST	0	0.0406731	inf	0	1	1
ENSG00000137709	ENSG00000137709	POU2F3	11:120107348-120190653	NOTEST	0.0477558	0	#NAME?	0	1	1
ENSG00000137726	ENSG00000137726	FXYD6	11:117298488-117748201	NOTEST	0.127891	0.298539	1.223	0	1	1
ENSG00000137731	ENSG00000137731	FXYD2	11:117298488-117748201	NOTEST	0	0	0	0	1	1
ENSG00000137745	ENSG00000137745	MMP13	11:102813723-102826463	NOTEST	0	0	0	0	1	1
ENSG00000137747	ENSG00000137747	TMPRSS13	11:117771357-117800174	NOTEST	0	0	0	0	1	1
ENSG00000137757	ENSG00000137757	CASP5	11:104864961-104893895	NOTEST	0	0	0	0	1	1
ENSG00000137766	ENSG00000137766	UNC13C	15:54305100-54920806	NOTEST	0.154339	0.288977	0.904848	0	1	1
ENSG00000137808	ENSG00000137808	RP11-809H16.2	15:69070873-69355083	NOTEST	0	0.018784	inf	0	1	1
ENSG00000137809	ENSG00000137809	ITGA11	15:68594049-68724501	NOTEST	0.0479332	0.122185	1.34997	0	1	1
ENSG00000137825	ENSG00000137825	ITPKA	15:41785590-41795747	NOTEST	0.263294	0.318567	0.274925	0	1	1
ENSG00000137841	ENSG00000137841	PLCB2	15:40570376-40600136	NOTEST	0.248929	0.592045	1.24997	0	1	1
ENSG00000137843	ENSG00000137843	PAK6	15:40453223-40569688	NOTEST	0.0108326	0.0618472	2.51333	0	1	1
ENSG00000137857	ENSG00000137857	DUOX1	15:45384847-45493373	NOTEST	0.0742206	0.0452079	-0.715245	0	1	1
ENSG00000137860	ENSG00000137860	SLC28A2	15:45543883-45571449	NOTEST	0.0106387	0	#NAME?	0	1	1
ENSG00000137868	ENSG00000137868	STRA6	15:74471806-74628813	NOTEST	0.0324633	0	#NAME?	0	1	1
ENSG00000137869	ENSG00000137869	CYP19A1	15:51329684-51630807	NOTEST	0.0829087	0.206327	1.31534	0	1	1
ENSG00000137875	ENSG00000137875	BCL2L10	15:52401459-52404972	NOTEST	0	0	0	0	1	1
ENSG00000137877	ENSG00000137877	SPTBN5	15:42120282-42190773	NOTEST	0.0558914	0.0955902	0.774235	0	1	1
ENSG00000137878	ENSG00000137878	GCOM1	15:57884105-58074960	NOTEST	0.0267683	0.0270067	0.0127913	0	1	1
ENSG00000137948	ENSG00000137948	BRDT	1:92414927-92479983	NOTEST	0	0	0	0	1	1
ENSG00000137959	ENSG00000137959	IFI44L	1:79085606-79111830	NOTEST	0.135103	0.0883956	-0.612009	0	1	1
ENSG00000137960	ENSG00000137960	GIPC2	1:78444858-78604133	NOTEST	0	0	0	0	1	1
ENSG00000137968	ENSG00000137968	SLC44A5	1:75667815-76076801	NOTEST	0.0858981	0.243793	1.50496	0	1	1
ENSG00000137975	ENSG00000137975	CLCA2	1:86889768-86922241	NOTEST	0.0293268	0.0561242	0.936404	0	1	1
ENSG00000137976	ENSG00000137976	DNASE2B	1:84864214-84880701	NOTEST	0.0746704	0.0714462	-0.0636782	0	1	1
ENSG00000138039	ENSG00000138039	LHCGR	2:48756521-49003654	NOTEST	0	0	0	0	1	1
ENSG00000138061	ENSG00000138061	CYP1B1	2:38150329-38408997	NOTEST	0.201465	0.130779	-0.623395	0	1	1
ENSG00000138068	ENSG00000138068	SULT6B1	2:37394962-37551951	NOTEST	0	0.0192971	inf	0	1	1
ENSG00000138075	ENSG00000138075	ABCG5	2:44039610-44066004	NOTEST	0.0103779	0.00445459	-1.22015	0	1	1
ENSG00000138079	ENSG00000138079	SLC3A1	2:44502598-44589001	NOTEST	0.043951	0.0836857	0.929087	0	1	1
ENSG00000138080	ENSG00000138080	EMILIN1	2:27301434-27309271	NOTEST	0.110656	0.29037	1.39181	0	1	1
ENSG00000138083	ENSG00000138083	SIX3	2:45167292-45173216	NOTEST	0.0287126	0.0681418	1.24686	0	1	1
ENSG00000138100	ENSG00000138100	TRIM54	2:27505259-27531313	NOTEST	0.0278168	0.078456	1.49593	0	1	1
ENSG00000138109	ENSG00000138109	CYP2C9	10:96698414-96749147	NOTEST	0	0	0	0	1	1
ENSG00000138115	ENSG00000138115	CYP2C8	10:96796529-96829254	NOTEST	0	0	0	0	1	1
ENSG00000138135	ENSG00000138135	CH25H	10:90965693-90967071	NOTEST	0.155461	0.27941	0.845828	0	1	1
ENSG00000138136	ENSG00000138136	LBX1	10:102986732-103029905	NOTEST	0	0.0237339	inf	0	1	1
ENSG00000138152	ENSG00000138152	BTBD16	10:124030820-124097677	NOTEST	0.423421	0.174904	-1.27553	0	1	1
ENSG00000138161	ENSG00000138161	CUZD1	10:124591664-124639157	NOTEST	0.334461	0.375188	0.165774	0	1	1
ENSG00000138207	ENSG00000138207	RBP4	10:95326421-95364237	NOTEST	0	0	0	0	1	1
ENSG00000138271	ENSG00000138271	GPR87	3:150803483-151176497	NOTEST	0.0187519	0.0072668	-1.36764	0	1	1

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ENSG00000138294	ENSG00000138294	MSMB	10:51549497-51562517	NOTEST	0	0	0	0	1	1
ENSG00000138308	ENSG00000138308	PLA2G12B	10:74694927-74714536	NOTEST	0	0	0	0	1	1
ENSG00000138315	ENSG00000138315	OIT3	10:74653338-74692791	NOTEST	0	0.00475441	inf	0	1	1
ENSG00000138316	ENSG00000138316	ADAMTS14	10:72432558-72522197	NOTEST	0.134933	0.136572	0.0174108	0	1	1
ENSG00000138347	ENSG00000138347	MYPN	10:69865911-69971774	NOTEST	0.00335577	0.0249702	2.89549	0	1	1
ENSG00000138356	ENSG00000138356	AOX1	2:201450590-201541787	NOTEST	0.0189732	0.0371769	0.970442	0	1	1
ENSG00000138378	ENSG00000138378	STAT4	2:191886251-192016322	NOTEST	0.21798	0.122086	-0.836302	0	1	1
ENSG00000138379	ENSG00000138379	MSTN	2:190744334-191236391	NOTEST	0.00560262	0	#NAME?	0	1	1
ENSG00000138411	ENSG00000138411	HECW2	2:197059093-197458416	NOTEST	0.157913	0.082071	-0.94419	0	1	1
ENSG00000138435	ENSG00000138435	CHRNA1	2:175411868-175639555	NOTEST	0.0907377	0.274325	1.59611	0	1	1
ENSG00000138472	ENSG00000138472	GUCA1C	3:108626638-108672742	NOTEST	0.0372493	0	#NAME?	0	1	1
ENSG00000138483	ENSG00000138483	CCDC54	3:106959538-107101007	NOTEST	0.0504995	0.0412041	-0.29348	0	1	1
ENSG00000138615	ENSG00000138615	CILP	15:65488336-65503826	NOTEST	0.0166601	0	#NAME?	0	1	1
ENSG00000138622	ENSG00000138622	HCN4	15:73612199-73661605	NOTEST	0.00210433	0	#NAME?	0	1	1
ENSG00000138650	ENSG00000138650	PCDH10	4:134070469-134129356	NOTEST	0.11808	0.0908156	-0.378753	0	1	1
ENSG00000138653	ENSG00000138653	NDST4	4:115748918-116035032	NOTEST	0.285541	0.283052	-0.0126297	0	1	1
ENSG00000138669	ENSG00000138669	PRKG2	4:82009836-82136218	NOTEST	0.0475694	0	#NAME?	0	1	1
ENSG00000138670	ENSG00000138670	RASGEF1B	4:82347546-82965397	NOTEST	0.0169877	0.0764845	2.17068	0	1	1
ENSG00000138675	ENSG00000138675	FGF5	4:81187752-81884910	NOTEST	0.247706	0.186797	-0.407154	0	1	1
ENSG00000138684	ENSG00000138684	IL21	4:123533782-123610311	NOTEST	0	0	0	0	1	1
ENSG00000138722	ENSG00000138722	MMRN1	4:90800682-90875780	NOTEST	0.010193	0	#NAME?	0	1	1
ENSG00000138741	ENSG00000138741	TRPC3	4:122800181-122872909	NOTEST	0.123215	0.0734134	-0.747059	0	1	1
ENSG00000138755	ENSG00000138755	CXCL9	4:76831808-76928641	NOTEST	0.0231253	0.00855112	-1.43529	0	1	1
ENSG00000138769	ENSG00000138769	CDKL2	4:76503214-76555900	NOTEST	0.218747	0.173693	-0.33272	0	1	1
ENSG00000138792	ENSG00000138792	ENPEP	4:111286888-111486441	NOTEST	0.00395413	0.0299716	2.92216	0	1	1
ENSG00000138813	ENSG00000138813	C4orf17	4:100432160-100463460	NOTEST	0	0	0	0	1	1
ENSG00000138823	ENSG00000138823	MTTP	4:100467865-100547070	NOTEST	0.113775	0.127247	0.161452	0	1	1
ENSG00000138892	ENSG00000138892	TTLL8	22:50453551-50495364	NOTEST	0	0	0	0	1	1
ENSG00000138944	ENSG00000138944	KIAA1644	22:44639546-44708731	NOTEST	0.0302642	0.0508679	0.749143	0	1	1
ENSG00000138964	ENSG00000138964	PARVG	22:44568835-44615413	NOTEST	0	0.0753986	inf	0	1	1
ENSG00000139044	ENSG00000139044	B4GALNT3	12:569529-672675	NOTEST	0.0641242	0.395807	2.62585	0	1	1
ENSG00000139053	ENSG00000139053	PDE6H	12:15125955-15134799	NOTEST	0	0	0	0	1	1
ENSG00000139055	ENSG00000139055	ERP27	12:15066968-15092016	NOTEST	0.0501075	0.0703777	0.490092	0	1	1
ENSG00000139144	ENSG00000139144	PIK3C2G	12:18233802-18801348	NOTEST	0	0.0126682	inf	0	1	1
ENSG00000139151	ENSG00000139151	PLCZ1	12:18836102-18890991	NOTEST	0	0	0	0	1	1
ENSG00000139155	ENSG00000139155	SLCO1C1	12:20848288-20906320	NOTEST	0	0	0	0	1	1
ENSG00000139193	ENSG00000139193	CD27	12:6548166-6580153	NOTEST	0.113587	0.0743616	-0.611173	0	1	1
ENSG00000139194	ENSG00000139194	RBP5	12:7276279-7281538	NOTEST	0.0941168	0.032568	-1.531	0	1	1
ENSG00000139209	ENSG00000139209	SLC38A4	12:47158545-47226191	NOTEST	0.00580767	0	#NAME?	0	1	1
ENSG00000139219	ENSG00000139219	COL2A1	12:48366747-48398269	NOTEST	0.138315	0.166492	0.267491	0	1	1
ENSG00000139220	ENSG00000139220	PPFIA2	12:81652044-82153332	NOTEST	0.139328	0	#NAME?	0	1	1
ENSG00000139223	ENSG00000139223	ANP32D	12:48866447-48866843	NOTEST	0	0	0	0	1	1
ENSG00000139269	ENSG00000139269	INHBE	12:57846105-57853063	NOTEST	0.0382078	0.201147	2.39631	0	1	1
ENSG00000139278	ENSG00000139278	GLIPR1	12:75874459-75905416	NOTEST	0.314565	0.427083	0.441158	0	1	1
ENSG00000139287	ENSG00000139287	TPH2	12:72332625-73059422	NOTEST	0	0.0153076	inf	0	1	1

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ENSG00000139292	ENSG00000139292	LGR5	12:71518864-71980090	NOTEST	0	0.00265564	inf	0	1	1
ENSG00000139304	ENSG00000139304	PTPRQ	12:80799773-81072802	NOTEST	0	0	0	0	1	1
ENSG00000139330	ENSG00000139330	KERA	12:91444267-91451760	NOTEST	0	0	0	0	1	1
ENSG00000139351	ENSG00000139351	SYCP3	12:102090724-102137918	NOTEST	0.153635	0.316317	1.04186	0	1	1
ENSG00000139352	ENSG00000139352	ASCL1	12:103230662-103354294	NOTEST	0.00645412	0.0135987	1.07517	0	1	1
ENSG00000139364	ENSG00000139364	TMEM132B	12:125671381-126146917	NOTEST	0	0.00553857	inf	0	1	1
ENSG00000139445	ENSG00000139445	FOXN4	12:109715783-109747025	NOTEST	0.0592332	0.0295257	-1.00443	0	1	1
ENSG00000139515	ENSG00000139515	PDX1	13:28407580-28500368	NOTEST	0	0.0139894	inf	0	1	1
ENSG00000139540	ENSG00000139540	SLC39A5	12:56623832-56652175	NOTEST	0.0196731	0	#NAME?	0	1	1
ENSG00000139547	ENSG00000139547	RDH16	12:57345218-57353158	NOTEST	0.0186749	0.0295903	0.664025	0	1	1
ENSG00000139549	ENSG00000139549	DHH	12:49483203-49488602	NOTEST	0.0389031	0.0898203	1.20716	0	1	1
ENSG00000139567	ENSG00000139567	ACVRL1	12:52300691-52317145	NOTEST	0.00375962	0.202719	5.75275	0	1	1
ENSG00000139572	ENSG00000139572	GPR84	12:54747444-54891472	NOTEST	0	0.00870562	inf	0	1	1
ENSG00000139574	ENSG00000139574	NPFF	12:53900471-54020199	NOTEST	0.122094	0.342995	1.4902	0	1	1
ENSG00000139597	ENSG00000139597	N4BP2L1	13:32974860-33112970	NOTEST	0.118743	0.177723	0.581795	0	1	1
ENSG00000139610	ENSG00000139610	CELA1	12:51722226-51740463	NOTEST	0	0	0	0	1	1
ENSG00000139648	ENSG00000139648	KRT71	12:52937692-52946931	NOTEST	0	0	0	0	1	1
ENSG00000139656	ENSG00000139656	SMIM2	13:44716681-44817328	NOTEST	0.0228164	0	#NAME?	0	1	1
ENSG00000139714	ENSG00000139714	MORN3	12:122089023-122110537	NOTEST	0.0767493	0.0625744	-0.29458	0	1	1
ENSG00000139767	ENSG00000139767	SRRM4	12:119419299-119600856	NOTEST	0	0	0	0	1	1
ENSG00000139780	ENSG00000139780	METTL21C	13:103338093-103346854	NOTEST	0	0.0251857	inf	0	1	1
ENSG00000139797	ENSG00000139797	RNF113B	13:98794815-99102027	NOTEST	0	0.00867891	inf	0	1	1
ENSG00000139800	ENSG00000139800	ZIC5	13:100615217-100624163	NOTEST	0.066553	0.145963	1.13303	0	1	1
ENSG00000139865	ENSG00000139865	TTC6	14:38059188-38672128	NOTEST	0.00437297	0	#NAME?	0	1	1
ENSG00000139874	ENSG00000139874	SSTR1	14:38677203-38682272	NOTEST	0	0	0	0	1	1
ENSG00000139890	ENSG00000139890	REM2	14:23352373-23356895	NOTEST	0.133573	0.146901	0.137213	0	1	1
ENSG00000139899	ENSG00000139899	CBLN3	14:24895737-24912111	NOTEST	0.193878	0.139535	-0.474523	0	1	1
ENSG00000139914	ENSG00000139914	FITM1	14:24549315-24602058	NOTEST	0.047826	0.0333364	-0.520695	0	1	1
ENSG00000139970	ENSG00000139970	RTN1	14:60062693-60337684	NOTEST	0.171457	0.109993	-0.640425	0	1	1
ENSG00000139973	ENSG00000139973	SYT16	14:62453802-62568431	NOTEST	0	0	0	0	1	1
ENSG00000139985	ENSG00000139985	ADAM21	14:70892528-71014181	NOTEST	0.0265776	0.0332527	0.323258	0	1	1
ENSG00000139988	ENSG00000139988	RDH12	14:68168602-68283307	NOTEST	0.163169	0.200145	0.294675	0	1	1
ENSG00000140009	ENSG00000140009	ESR2	14:64319682-64805317	NOTEST	0.407126	0.363333	-0.164181	0	1	1
ENSG00000140015	ENSG00000140015	KCNH5	14:63173286-63568755	NOTEST	0	0	0	0	1	1
ENSG00000140022	ENSG00000140022	STON2	14:81726999-81902809	NOTEST	0.47512	0.466956	-0.0250043	0	1	1
ENSG00000140030	ENSG00000140030	GPR65	14:88471467-88481955	NOTEST	0	0	0	0	1	1
ENSG00000140057	ENSG00000140057	AK7	14:96858447-96955764	NOTEST	0.363221	0.15971	-1.18539	0	1	1
ENSG00000140067	ENSG00000140067	FAM181A	14:94371075-94395954	NOTEST	0	0	0	0	1	1
ENSG00000140093	ENSG00000140093	SERPINA10	14:94749649-94759608	NOTEST	0	0	0	0	1	1
ENSG00000140107	ENSG00000140107	SLC25A47	14:100789673-100796715	NOTEST	0.0107525	0	#NAME?	0	1	1
ENSG00000140254	ENSG00000140254	DUOXA1	15:45384847-45493373	NOTEST	0	0	0	0	1	1
ENSG00000140274	ENSG00000140274	DUOXA2	15:45384847-45493373	NOTEST	0.0213766	0	#NAME?	0	1	1
ENSG00000140279	ENSG00000140279	DUOX2	15:45384847-45493373	NOTEST	0	0	0	0	1	1
ENSG00000140284	ENSG00000140284	SLC27A2	15:50150434-50528592	NOTEST	0.0211869	0.0227794	0.104557	0	1	1
ENSG00000140285	ENSG00000140285	FGF7	15:49398267-49913128	NOTEST	0.128515	0.0662955	-0.954959	0	1	1

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ENSG00000140287	ENSG00000140287	HDC	15:50534143-50558223	NOTEST	0	0.0190925	inf	0	1	1
ENSG00000140297	ENSG00000140297	GCNT3	15:59887073-59981733	NOTEST	0.0135736	0.154686	3.51046	0	1	1
ENSG00000140323	ENSG00000140323	DISP2	15:40650435-40663257	NOTEST	0.343438	0.461953	0.427697	0	1	1
ENSG00000140368	ENSG00000140368	PSTPIP1	15:77285699-77329673	NOTEST	0.23247	0.390065	0.746668	0	1	1
ENSG00000140398	ENSG00000140398	NEIL1	15:75639295-75648087	NOTEST	0.209866	0.402647	0.940045	0	1	1
ENSG00000140459	ENSG00000140459	CYP11A1	15:74630099-74660081	NOTEST	0	0	0	0	1	1
ENSG00000140478	ENSG00000140478	GOLGA6D	15:75575175-75586816	NOTEST	0.0137754	0	#NAME?	0	1	1
ENSG00000140481	ENSG00000140481	CCDC33	15:74471806-74628813	NOTEST	0	0	0	0	1	1
ENSG00000140488	ENSG00000140488	CELF6	15:72533521-72671129	NOTEST	0.156563	0.0466526	-1.74672	0	1	1
ENSG00000140505	ENSG00000140505	CYP1A2	15:75041184-75048543	NOTEST	0	0.0180766	inf	0	1	1
ENSG00000140506	ENSG00000140506	LMAN1L	15:75105056-75124141	NOTEST	0	0.0210361	inf	0	1	1
ENSG00000140519	ENSG00000140519	RHCG	15:89998679-90039844	NOTEST	0.348045	0.573451	0.720398	0	1	1
ENSG00000140527	ENSG00000140527	WDR93	15:90234027-90286869	NOTEST	0.0610363	0.0546696	-0.158929	0	1	1
ENSG00000140538	ENSG00000140538	NTRK3	15:88418229-88814297	NOTEST	0	0	0	0	1	1
ENSG00000140557	ENSG00000140557	ST8SIA2	15:92937057-93011958	NOTEST	0.300309	0.211966	-0.502617	0	1	1
ENSG00000140563	ENSG00000140563	MCTP2	15:94774766-95023632	NOTEST	0.250935	0.318603	0.344448	0	1	1
ENSG00000140600	ENSG00000140600	SH3GL3	15:84115979-84287495	NOTEST	0.011007	0.0171116	0.636553	0	1	1
ENSG00000140623	ENSG00000140623	12-Sep	16:4827669-4846533	NOTEST	0	0	0	0	1	1
ENSG00000140675	ENSG00000140675	SLC5A2	16:31494322-31520630	NOTEST	0.0586125	0.109874	0.956656	0	1	1
ENSG00000140678	ENSG00000140678	ITGAX	16:31366454-31394318	NOTEST	0.112651	0.373674	1.72992	0	1	1
ENSG00000140795	ENSG00000140795	MYLK3	16:46740890-46825952	NOTEST	0.103542	0.161312	0.639637	0	1	1
ENSG00000140798	ENSG00000140798	ABCC12	16:48116883-48189929	NOTEST	0	0	0	0	1	1
ENSG00000140832	ENSG00000140832	MARVELD3	16:71657610-71758604	NOTEST	0	0.00420912	inf	0	1	1
ENSG00000140835	ENSG00000140835	CHST4	16:71481499-71598992	NOTEST	0	0	0	0	1	1
ENSG00000140839	ENSG00000140839	CLEC18B	16:74442528-74455368	NOTEST	0	0	0	0	1	1
ENSG00000140873	ENSG00000140873	ADAMTS18	16:77224731-77478233	NOTEST	0	0	0	0	1	1
ENSG00000140876	ENSG00000140876	NUDT7	16:77756410-77776897	NOTEST	0.266908	0.237944	-0.165723	0	1	1
ENSG00000140932	ENSG00000140932	CMTM2	16:66613350-66622178	NOTEST	0	0	0	0	1	1
ENSG00000140937	ENSG00000140937	CDH11	16:64977655-65160015	NOTEST	0.0120819	0.0634902	2.39368	0	1	1
ENSG00000140945	ENSG00000140945	CDH13	16:82660407-83841439	NOTEST	0	0.0147863	inf	0	1	1
ENSG00000140955	ENSG00000140955	ADAD2	16:84224743-84230774	NOTEST	0	0	0	0	1	1
ENSG00000140968	ENSG00000140968	IRF8	16:85932408-85956215	NOTEST	0	0	0	0	1	1
ENSG00000140986	ENSG00000140986	RPL3L	16:1993974-2007607	NOTEST	0.0355237	0.010926	-1.70101	0	1	1
ENSG00000141028	ENSG00000141028	CDRT15P1	17:13659794-13972812	NOTEST	0.0377989	0.0294362	-0.360751	0	1	1
ENSG00000141052	ENSG00000141052	MYOCD	17:12569206-12894960	NOTEST	0	0	0	0	1	1
ENSG00000141086	ENSG00000141086	CTRL	16:67927174-67970990	NOTEST	0.294178	0.414063	0.49316	0	1	1
ENSG00000141096	ENSG00000141096	DPEP3	16:68009565-68014732	NOTEST	0	0	0	0	1	1
ENSG00000141150	ENSG00000141150	RASL10B	17:34058667-34070540	NOTEST	0.0833789	0.10438	0.324094	0	1	1
ENSG00000141161	ENSG00000141161	UNC45B	17:33474835-33518721	NOTEST	0	0	0	0	1	1
ENSG00000141194	ENSG00000141194	OR4D1	17:56232493-56233517	NOTEST	0	0	0	0	1	1
ENSG00000141200	ENSG00000141200	KIF2B	17:51900238-51902573	NOTEST	0	0	0	0	1	1
ENSG00000141255	ENSG00000141255	SPATA22	17:3343312-3461289	NOTEST	0.0142073	0.0787084	2.46989	0	1	1
ENSG00000141293	ENSG00000141293	SKAP1	17:46210801-46507637	NOTEST	0	0	0	0	1	1
ENSG00000141314	ENSG00000141314	RHBDL3	17:30593194-30708905	NOTEST	0.0385064	0	#NAME?	0	1	1
ENSG00000141316	ENSG00000141316	SPACA3	17:31297393-31324895	NOTEST	0	0.25597	inf	0	1	1

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ENSG00000141338	ENSG00000141338	ABCA8	17:66863432-66951533	NOTEST	0.199438	0.216452	0.118105	0	1	1
ENSG00000141371	ENSG00000141371	C17orf64	17:58256454-58508782	NOTEST	0.0191077	0.0134948	-0.501744	0	1	1
ENSG00000141431	ENSG00000141431	ASXL3	18:31158578-31331156	NOTEST	0	0	0	0	1	1
ENSG00000141433	ENSG00000141433	ADCYAP1	18:894435-912173	NOTEST	0	0	0	0	1	1
ENSG00000141434	ENSG00000141434	MEP1B	18:29598334-30050447	NOTEST	0.0346826	0.00539497	-2.68452	0	1	1
ENSG00000141437	ENSG00000141437	SLC25A52	18:29339524-29340843	NOTEST	0.0129372	0.0144874	0.163269	0	1	1
ENSG00000141448	ENSG00000141448	GATA6	18:19749403-19785192	NOTEST	0.0619056	0.100717	0.702164	0	1	1
ENSG00000141449	ENSG00000141449	GREB1L	18:18822202-19105378	NOTEST	0.104974	0.174154	0.730333	0	1	1
ENSG00000141469	ENSG00000141469	SLC14A1	18:42792959-43332485	NOTEST	0	0.0264449	inf	0	1	1
ENSG00000141485	ENSG00000141485	SLC13A5	17:6588031-6616886	NOTEST	0	0	0	0	1	1
ENSG00000141497	ENSG00000141497	ZMYND15	17:4643318-4649411	NOTEST	0	0.0337334	inf	0	1	1
ENSG00000141505	ENSG00000141505	ASGR1	17:7076749-7082883	NOTEST	0.168934	0.594922	1.81624	0	1	1
ENSG00000141506	ENSG00000141506	PIK3R5	17:8782232-8869029	NOTEST	0.098965	0.222106	1.16626	0	1	1
ENSG00000141579	ENSG00000141579	ZNF750	17:80709939-81009686	NOTEST	0.01177	0.0202487	0.782708	0	1	1
ENSG00000141622	ENSG00000141622	RNF165	18:43906771-44043103	NOTEST	0.15787	0.0828344	-0.930435	0	1	1
ENSG00000141738	ENSG00000141738	GRB7	17:37894179-37903544	NOTEST	0.163016	0.391667	1.26462	0	1	1
ENSG00000141744	ENSG00000141744	PNMT	17:37824233-37826728	NOTEST	0.0249699	0	#NAME?	0	1	1
ENSG00000141748	ENSG00000141748	ARL5C	17:37313146-37323737	NOTEST	0	0	0	0	1	1
ENSG00000141750	ENSG00000141750	STAC2	17:37366788-37382125	NOTEST	0.0288845	0.0605835	1.17215	0	1	1
ENSG00000141837	ENSG00000141837	CACNA1A	19:13317255-13734804	NOTEST	0.0831913	0.179788	1.11179	0	1	1
ENSG00000141854	ENSG00000141854	hsa-mir-1199	19:14183347-14185874	NOTEST	0.440856	0.542652	0.29972	0	1	1
ENSG00000141946	ENSG00000141946	ZIM3	19:57645417-57656570	NOTEST	0	0	0	0	1	1
ENSG00000141968	ENSG00000141968	VAV1	19:6772724-6857377	NOTEST	0	0.00439114	inf	0	1	1
ENSG00000141977	ENSG00000141977	CIB3	19:16272178-16284336	NOTEST	0	0	0	0	1	1
ENSG00000141979	ENSG00000141979	CTD-3222D19.2	19:16589867-16771253	NOTEST	0	0	0	0	1	1
ENSG00000142025	ENSG00000142025	DMRTC2	19:42348805-42356401	NOTEST	0	0	0	0	1	1
ENSG00000142163	ENSG00000142163	OR1E3	17:3019716-3020660	NOTEST	0	0	0	0	1	1
ENSG00000142173	ENSG00000142173	COL6A2	21:47518010-47552763	NOTEST	0.0525192	0.0819202	0.641374	0	1	1
ENSG00000142182	ENSG00000142182	DNMT3L	21:45666221-45682099	NOTEST	0	0	0	0	1	1
ENSG00000142185	ENSG00000142185	TRPM2	21:45770045-45862964	NOTEST	0.230666	0.207899	-0.149924	0	1	1
ENSG00000142224	ENSG00000142224	IL19	1:206972214-207016324	NOTEST	0	0.0534372	inf	0	1	1
ENSG00000142233	ENSG00000142233	NTN5	19:49141198-49184461	NOTEST	0.00658637	0	#NAME?	0	1	1
ENSG00000142235	ENSG00000142235	LMTK3	19:48988527-49016446	NOTEST	0.0389969	0.101675	1.38253	0	1	1
ENSG00000142273	ENSG00000142273	CBLC	19:45281125-45303891	NOTEST	0.021238	0	#NAME?	0	1	1
ENSG00000142303	ENSG00000142303	ADAMTS10	19:8645125-8675620	NOTEST	0	0.087276	inf	0	1	1
ENSG00000142319	ENSG00000142319	SLC6A3	5:1392908-1445545	NOTEST	0	0	0	0	1	1
ENSG00000142347	ENSG00000142347	MYO1F	19:8585673-8642461	NOTEST	0.0998416	0.0344209	-1.53636	0	1	1
ENSG00000142405	ENSG00000142405	NLRP12	19:54296856-54327648	NOTEST	0.00643426	0	#NAME?	0	1	1
ENSG00000142408	ENSG00000142408	CACNG8	19:54466293-54493469	NOTEST	0.00312125	0.00255935	-0.286346	0	1	1
ENSG00000142449	ENSG00000142449	FBN3	19:8130285-8214730	NOTEST	0	0	0	0	1	1
ENSG00000142484	ENSG00000142484	TM4SF5	17:4675178-4686506	NOTEST	0	0	0	0	1	1
ENSG00000142511	ENSG00000142511	GPR32	19:51273720-51274989	NOTEST	0	0	0	0	1	1
ENSG00000142512	ENSG00000142512	SIGLEC10	19:51913274-51921057	NOTEST	0	0	0	0	1	1
ENSG00000142513	ENSG00000142513	ACPT	19:51293671-51298481	NOTEST	0	0	0	0	1	1
ENSG00000142515	ENSG00000142515	KLK3	19:51358170-51364020	NOTEST	0	0	0	0	1	1

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ENSG00000142530	ENSG00000142530	FAM71E1	19:50970041-50986608	NOTEST	0.316467	0.32056	0.0185376	0	1	1
ENSG00000142538	ENSG00000142538	PTH2	19:49925670-49926698	NOTEST	0	0	0	0	1	1
ENSG00000142539	ENSG00000142539	CTD-2545M3.6	19:50887460-50934570	NOTEST	0.0109935	0.0234807	1.09483	0	1	1
ENSG00000142549	ENSG00000142549	IGLON5	19:51815101-51833608	NOTEST	0.0943395	0.032713	-1.528	0	1	1
ENSG00000142583	ENSG00000142583	SLC2A5	1:9095165-9148537	NOTEST	0.0707559	0.148564	1.07016	0	1	1
ENSG00000142606	ENSG00000142606	MMEL1	1:2517929-2718286	NOTEST	0.0709805	0.269058	1.92242	0	1	1
ENSG00000142609	ENSG00000142609	C1orf222	1:1853395-1935276	NOTEST	0.0430552	0	#NAME?	0	1	1
ENSG00000142611	ENSG00000142611	PRDM16	1:2985731-3355185	NOTEST	0.366851	0.364774	-0.00819077	0	1	1
ENSG00000142615	ENSG00000142615	CELA2A	1:15783222-15853029	NOTEST	0	0	0	0	1	1
ENSG00000142619	ENSG00000142619	PADI3	1:17575592-17610728	NOTEST	0.00889125	0.00727704	-0.289035	0	1	1
ENSG00000142621	ENSG00000142621	FHAD1	1:15573767-15726779	NOTEST	0.128075	0.206151	0.686712	0	1	1
ENSG00000142623	ENSG00000142623	PADI1	1:17531620-17572500	NOTEST	0.127925	0.196659	0.620397	0	1	1
ENSG00000142661	ENSG00000142661	MYOM3	1:24367324-24438665	NOTEST	0	0	0	0	1	1
ENSG00000142675	ENSG00000142675	CNKSR1	1:26503893-26516377	NOTEST	0.173998	0.0494206	-1.81589	0	1	1
ENSG00000142677	ENSG00000142677	IL22RA1	1:24446260-24469611	NOTEST	0.0532737	0.113151	1.08675	0	1	1
ENSG00000142698	ENSG00000142698	C1orf94	1:34632483-34684732	NOTEST	0	0	0	0	1	1
ENSG00000142700	ENSG00000142700	DMRTA2	1:50883221-50889172	NOTEST	0.0055631	0	#NAME?	0	1	1
ENSG00000142748	ENSG00000142748	FCN3	1:27695602-27701315	NOTEST	0	0	0	0	1	1
ENSG00000142765	ENSG00000142765	SYTL1	1:27668512-27680421	NOTEST	0.103309	0.0776567	-0.41178	0	1	1
ENSG00000142789	ENSG00000142789	CELA3A	1:22328148-22339032	NOTEST	0	0	0	0	1	1
ENSG00000142959	ENSG00000142959	BEST4	1:45249256-45253377	NOTEST	0.0158328	0.0178646	0.174191	0	1	1
ENSG00000142973	ENSG00000142973	CYP4B1	1:47223509-47285085	NOTEST	0	0	0	0	1	1
ENSG00000143001	ENSG00000143001	TMEM61	1:55446464-55457966	NOTEST	0	0	0	0	1	1
ENSG00000143006	ENSG00000143006	DMRTB1	1:53925071-53933161	NOTEST	0	0	0	0	1	1
ENSG00000143028	ENSG00000143028	SYPL2	1:110009179-110024759	NOTEST	0.106247	0.189522	0.834943	0	1	1
ENSG00000143032	ENSG00000143032	BARHL2	1:91177095-91182794	NOTEST	0.0888069	0.0812985	-0.127444	0	1	1
ENSG00000143105	ENSG00000143105	KCNA10	1:111059838-111061797	NOTEST	0	0	0	0	1	1
ENSG00000143107	ENSG00000143107	FNDC7	1:109255278-109285365	NOTEST	0	0.00697925	inf	0	1	1
ENSG00000143110	ENSG00000143110	C1orf162	1:112016413-112021134	NOTEST	0.189405	0.353533	0.900372	0	1	1
ENSG00000143119	ENSG00000143119	CD53	1:111415774-111442550	NOTEST	0.0398156	0.0653526	0.71491	0	1	1
ENSG00000143125	ENSG00000143125	PROK1	1:110993821-110999976	NOTEST	0.0358598	0.0188468	-0.928048	0	1	1
ENSG00000143140	ENSG00000143140	GJA5	1:147228331-147245484	NOTEST	0.0577572	0.0305573	-0.918486	0	1	1
ENSG00000143167	ENSG00000143167	GPA33	1:167021787-167059868	NOTEST	0	0	0	0	1	1
ENSG00000143184	ENSG00000143184	XCL1	1:168545710-168551315	NOTEST	0.0124179	0.078281	2.65624	0	1	1
ENSG00000143185	ENSG00000143185	XCL2	1:168510002-168513235	NOTEST	0	0	0	0	1	1
ENSG00000143194	ENSG00000143194	MAEL	1:166958345-166991451	NOTEST	0.0892409	0.173784	0.961518	0	1	1
ENSG00000143195	ENSG00000143195	ILDR2	1:166882442-166944719	NOTEST	0.00673137	0.00435018	-0.629827	0	1	1
ENSG00000143196	ENSG00000143196	DPT	1:168664696-168698502	NOTEST	0	0	0	0	1	1
ENSG00000143199	ENSG00000143199	ADCY10	1:167778624-167883453	NOTEST	0.00623451	0.0217275	1.80117	0	1	1
ENSG00000143217	ENSG00000143217	PVRL4	1:161040784-161059389	NOTEST	0.0570309	0.295426	2.37298	0	1	1
ENSG00000143278	ENSG00000143278	F13B	1:197008320-197036397	NOTEST	0	0.0159358	inf	0	1	1
ENSG00000143297	ENSG00000143297	FCRL5	1:157483166-157522310	NOTEST	0	0	0	0	1	1
ENSG00000143318	ENSG00000143318	CASQ1	1:160160284-160171676	NOTEST	0.484289	0.17252	-1.48911	0	1	1
ENSG00000143340	ENSG00000143340	FAM163A	1:179712297-179787326	NOTEST	0.0673806	0.142403	1.07957	0	1	1
ENSG00000143355	ENSG00000143355	LHX9	1:197881036-197904608	NOTEST	0.0463449	0.0710625	0.616678	0	1	1

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ENSG00000143365	ENSG00000143365	RORC	1:151772739-151804348	NOTEST	0.0241047	0.0889956	1.88442	0	1	1
ENSG00000143382	ENSG00000143382	ADAMTSL4	1:150521039-150533413	NOTEST	0.205181	0.215927	0.0736483	0	1	1
ENSG00000143452	ENSG00000143452	HORMAD1	1:150670535-150693364	NOTEST	0.0537159	0.0639884	0.252461	0	1	1
ENSG00000143494	ENSG00000143494	VASH2	1:213123861-213165379	NOTEST	0.247966	0.127347	-0.961379	0	1	1
ENSG00000143502	ENSG00000143502	SUSD4	1:223394160-223537544	NOTEST	0	0	0	0	1	1
ENSG00000143512	ENSG00000143512	HHIPL2	1:222695601-222721445	NOTEST	0.0247103	0.0555568	1.16885	0	1	1
ENSG00000143520	ENSG00000143520	FLG2	1:152140600-152339163	NOTEST	0.0431459	0.0751606	0.800754	0	1	1
ENSG00000143536	ENSG00000143536	CRNN	1:152346429-152417932	NOTEST	0.0155458	0	#NAME?	0	1	1
ENSG00000143546	ENSG00000143546	S100A8	1:153362507-153363664	NOTEST	0	0	0	0	1	1
ENSG00000143552	ENSG00000143552	NUP210L	1:153965160-154127592	NOTEST	0.0176377	0.0101288	-0.800197	0	1	1
ENSG00000143556	ENSG00000143556	S100A7	1:153430219-153433177	NOTEST	0	0	0	0	1	1
ENSG00000143595	ENSG00000143595	AQP10	1:154293565-154297801	NOTEST	0	0	0	0	1	1
ENSG00000143603	ENSG00000143603	KCNN3	1:154669930-154842756	NOTEST	0.0219475	0.132597	2.59493	0	1	1
ENSG00000143632	ENSG00000143632	ACTA1	1:229566991-229569845	NOTEST	0.0337555	0.0426655	0.337946	0	1	1
ENSG00000143674	ENSG00000143674	MLK4	1:233463513-233520894	NOTEST	0.0144297	0.0620172	2.10363	0	1	1
ENSG00000143768	ENSG00000143768	LEFTY2	1:226124110-226129189	NOTEST	0	0	0	0	1	1
ENSG00000143816	ENSG00000143816	WNT9A	1:228106356-228135599	NOTEST	0.0297442	0.032842	0.142935	0	1	1
ENSG00000143839	ENSG00000143839	REN	1:204123943-204135465	NOTEST	0	0	0	0	1	1
ENSG00000143850	ENSG00000143850	PLEKHA6	1:204187978-204346793	NOTEST	0.0423459	0.0125815	-1.75092	0	1	1
ENSG00000143851	ENSG00000143851	PTPN7	1:202116140-202130716	NOTEST	0.00746173	0.0220211	1.56131	0	1	1
ENSG00000143858	ENSG00000143858	SYT2	1:202317826-202679545	NOTEST	0.0102478	0.00166953	-2.61781	0	1	1
ENSG00000143867	ENSG00000143867	OSR1	2:19551245-19558414	NOTEST	0	0	0	0	1	1
ENSG00000143869	ENSG00000143869	GDF7	2:20866423-20873418	NOTEST	0	0.00816007	inf	0	1	1
ENSG00000143921	ENSG00000143921	ABCG8	2:44066102-44105605	NOTEST	0	0.0176939	inf	0	1	1
ENSG00000143954	ENSG00000143954	REG3G	2:79252811-79255631	NOTEST	0.0216797	0	#NAME?	0	1	1
ENSG00000143994	ENSG00000143994	ABHD1	2:27346681-27357543	NOTEST	0.220421	0.154239	-0.515098	0	1	1
ENSG00000144010	ENSG00000144010	TRIM43B	2:96142714-96150479	NOTEST	0	0	0	0	1	1
ENSG00000144015	ENSG00000144015	TRIM43	2:96257765-96265526	NOTEST	0	0.0076383	inf	0	1	1
ENSG00000144045	ENSG00000144045	DQX1	2:74745257-74753463	NOTEST	0.0136837	0.124075	3.18068	0	1	1
ENSG00000144057	ENSG00000144057	ST6GAL2	2:107418055-107503564	NOTEST	0	0	0	0	1	1
ENSG00000144063	ENSG00000144063	MALL	2:110841446-110874143	NOTEST	0.0672339	0.0116372	-2.53044	0	1	1
ENSG00000144119	ENSG00000144119	C1QL2	2:119913818-119916465	NOTEST	0	0	0	0	1	1
ENSG00000144130	ENSG00000144130	NT5DC4	2:113479062-113522254	NOTEST	0.0402696	0.00506731	-2.9904	0	1	1
ENSG00000144140	ENSG00000144140	RP11-143M1.7	9:52451-88826	NOTEST	0	0	0	0	1	1
ENSG00000144188	ENSG00000144188	TRIM43CP	2:97691717-97697373	NOTEST	0	0	0	0	1	1
ENSG00000144191	ENSG00000144191	CNGA3	2:98947851-99015064	NOTEST	0	0	0	0	1	1
ENSG00000144214	ENSG00000144214	LYG1	2:99613723-100106497	NOTEST	0.120685	0.110632	-0.125478	0	1	1
ENSG00000144227	ENSG00000144227	NXPH2	2:139428341-139537918	NOTEST	0	0	0	0	1	1
ENSG00000144229	ENSG00000144229	THSD7B	2:137523114-138435287	NOTEST	0	0.0292764	inf	0	1	1
ENSG00000144230	ENSG00000144230	GPR17	2:128395955-128439360	NOTEST	0.0157055	0.0513597	1.70936	0	1	1
ENSG00000144278	ENSG00000144278	GALNT13	2:154728425-155313950	NOTEST	0.0238508	0.0200018	-0.25391	0	1	1
ENSG00000144285	ENSG00000144285	SCN1A	2:166813908-167232503	NOTEST	0.00374203	0.0151226	2.01481	0	1	1
ENSG00000144290	ENSG00000144290	SLC4A10	2:162272604-162841792	NOTEST	0.107584	0.129244	0.264633	0	1	1
ENSG00000144339	ENSG00000144339	TMEFF2	2:192699027-193060435	NOTEST	0.0403888	0.119971	1.57065	0	1	1
ENSG00000144406	ENSG00000144406	UNC80	2:210636716-210864024	NOTEST	0.25837	0.436693	0.757183	0	1	1

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ENSG00000144407	ENSG00000144407	PTH2R	2:209224437-209719227	NOTEST	0.0116844	0.0333308	1.51228	0	1	1
ENSG00000144410	ENSG00000144410	CPO	2:207804277-207834198	NOTEST	0.0143084	0	#NAME?	0	1	1
ENSG00000144452	ENSG00000144452	ABCA12	2:215674952-216003151	NOTEST	0.0161004	0.146914	3.18981	0	1	1
ENSG00000144460	ENSG00000144460	NYAP2	2:226265363-226518734	NOTEST	0	0	0	0	1	1
ENSG00000144476	ENSG00000144476	ACKR3	2:237476429-237491001	NOTEST	0	0	0	0	1	1
ENSG00000144488	ENSG00000144488	ESPNL	2:239008797-239041928	NOTEST	0.0263094	0.00669954	-1.97344	0	1	1
ENSG00000144550	ENSG00000144550	CPNE9	3:9745490-9771592	NOTEST	0.100849	0.111304	0.142308	0	1	1
ENSG00000144583	ENSG00000144583	4-Mar	2:217122587-217236750	NOTEST	0	0	0	0	1	1
ENSG00000144596	ENSG00000144596	GRIP2	3:14444075-14583588	NOTEST	0.00600035	0.0102888	0.777955	0	1	1
ENSG00000144648	ENSG00000144648	ACKR2	3:42846243-43101703	NOTEST	0.135202	0.236044	0.803942	0	1	1
ENSG00000144649	ENSG00000144649	FAM198A	3:42846243-43101703	NOTEST	0	0.0798947	inf	0	1	1
ENSG00000144671	ENSG00000144671	SLC22A14	3:38323784-38360066	NOTEST	0.0255253	0.094788	1.89278	0	1	1
ENSG00000144681	ENSG00000144681	STAC	3:36421835-36589499	NOTEST	0.0457929	0.0408571	-0.164538	0	1	1
ENSG00000144771	ENSG00000144771	LRTM1	3:54156573-55108584	NOTEST	0	0	0	0	1	1
ENSG00000144792	ENSG00000144792	ZNF660	3:44596684-44727145	NOTEST	0	0	0	0	1	1
ENSG00000144810	ENSG00000144810	COL8A1	3:99357318-99518070	NOTEST	0.0460143	0.112446	1.28908	0	1	1
ENSG00000144820	ENSG00000144820	GPR128	3:100328432-100414323	NOTEST	0	0	0	0	1	1
ENSG00000144821	ENSG00000144821	MYH15	3:108099215-108248169	NOTEST	0.159046	0.0886206	-0.843733	0	1	1
ENSG00000144834	ENSG00000144834	TAGLN3	3:111717510-111732734	NOTEST	0	0.0220292	inf	0	1	1
ENSG00000144852	ENSG00000144852	NR1I2	3:119499330-119537332	NOTEST	0	0	0	0	1	1
ENSG00000144891	ENSG00000144891	AGTR1	3:148415570-148460795	NOTEST	0	0	0	0	1	1
ENSG00000144908	ENSG00000144908	ALDH1L1	3:125822411-125929012	NOTEST	0.130854	0.144758	0.145678	0	1	1
ENSG00000144962	ENSG00000144962	SPATA16	3:172607147-172859058	NOTEST	0.01535	0.00539226	-1.50928	0	1	1
ENSG00000145002	ENSG00000145002	FAM86B2	8:12282912-12293915	NOTEST	0.179997	0.205145	0.18867	0	1	1
ENSG00000145063	ENSG00000145063	AC062028.1	2:11239976-11272947	NOTEST	0.0519309	0.0287037	-0.855357	0	1	1
ENSG00000145075	ENSG00000145075	CCDC39	3:180319917-180700541	NOTEST	0.258403	0.176732	-0.54806	0	1	1
ENSG00000145087	ENSG00000145087	STXBP5L	3:120626918-121143608	NOTEST	0.238226	0.186193	-0.355538	0	1	1
ENSG00000145103	ENSG00000145103	ILDR1	3:121706169-121741051	NOTEST	0.00722607	0.0056147	-0.364002	0	1	1
ENSG00000145113	ENSG00000145113	MUC4	3:195473635-195539148	NOTEST	0.00418475	0.0230163	2.45945	0	1	1
ENSG00000145192	ENSG00000145192	AHSG	3:186330711-186339107	NOTEST	0.0537302	0.0461347	-0.219881	0	1	1
ENSG00000145198	ENSG00000145198	VWA5B2	3:183851806-184402546	NOTEST	0.0235028	0.00681863	-1.78528	0	1	1
ENSG00000145244	ENSG00000145244	CORIN	4:47596014-47840123	NOTEST	0.0778353	0.0165283	-2.23548	0	1	1
ENSG00000145248	ENSG00000145248	SLC10A4	4:48485359-48491213	NOTEST	0.0607772	0.177524	1.54641	0	1	1
ENSG00000145283	ENSG00000145283	SLC10A6	4:87744620-87770416	NOTEST	0	0	0	0	1	1
ENSG00000145287	ENSG00000145287	PLAC8	4:84011200-84058228	NOTEST	0.0871564	0.0770878	-0.177105	0	1	1
ENSG00000145309	ENSG00000145309	CABS1	4:71200682-71202833	NOTEST	0	0	0	0	1	1
ENSG00000145321	ENSG00000145321	GC	4:72607409-72669758	NOTEST	0	0	0	0	1	1
ENSG00000145384	ENSG00000145384	FABP2	4:120238404-120243545	NOTEST	0	0.0155162	inf	0	1	1
ENSG00000145416	ENSG00000145416	1-Mar	4:164445449-165305202	NOTEST	0.395803	0.377858	-0.0669373	0	1	1
ENSG00000145423	ENSG00000145423	SFRP2	4:154701743-154710272	NOTEST	0	0.0248446	inf	0	1	1
ENSG00000145451	ENSG00000145451	GLRA3	4:175558064-175750465	NOTEST	0.00824445	0	#NAME?	0	1	1
ENSG00000145526	ENSG00000145526	CDH18	5:19473059-20575982	NOTEST	0.291375	0.277413	-0.0708437	0	1	1
ENSG00000145536	ENSG00000145536	ADAMTS16	5:5140442-5320417	NOTEST	0.0488148	0.12013	1.2992	0	1	1
ENSG00000145569	ENSG00000145569	FAM105A	5:14581883-14615116	NOTEST	0.0164982	0.00912744	-0.854026	0	1	1
ENSG00000145623	ENSG00000145623	OSMR	5:38845959-39074510	NOTEST	0.126362	0.083058	-0.605376	0	1	1

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ENSG00000145626	ENSG00000145626	UGT3A1	5:35951111-36001130	NOTEST	0	0	0	0	1	1
ENSG00000145642	ENSG00000145642	FAM159B	5:63986134-64013917	NOTEST	0	0	0	0	1	1
ENSG00000145649	ENSG00000145649	GZMA	5:54398475-54406080	NOTEST	0.0375675	0.0289753	-0.374663	0	1	1
ENSG00000145681	ENSG00000145681	HAPLN1	5:82933623-83017432	NOTEST	0.0331428	0.0935975	1.49778	0	1	1
ENSG00000145692	ENSG00000145692	BHMT	5:78293437-78531861	NOTEST	0	0.00448408	inf	0	1	1
ENSG00000145700	ENSG00000145700	ANKRD31	5:74364099-74532703	NOTEST	0.0968499	0.0765909	-0.338577	0	1	1
ENSG00000145708	ENSG00000145708	CRHBP	5:76248537-76276983	NOTEST	0	0.0485301	inf	0	1	1
ENSG00000145721	ENSG00000145721	LIX1	5:96424778-96772921	NOTEST	0.0614241	0.0119789	-2.35831	0	1	1
ENSG00000145757	ENSG00000145757	SPATA9	5:94982457-95034415	NOTEST	0.11284	0.0807072	-0.483508	0	1	1
ENSG00000145777	ENSG00000145777	TSLP	5:110405759-110466200	NOTEST	0.111752	0.124119	0.151433	0	1	1
ENSG00000145808	ENSG00000145808	ADAMTS19	5:128795251-129522327	NOTEST	0	0	0	0	1	1
ENSG00000145824	ENSG00000145824	CXCL14	5:134895266-134970564	NOTEST	0.00938628	0.0131971	0.491596	0	1	1
ENSG00000145826	ENSG00000145826	LECT2	5:135257967-135290723	NOTEST	0	0	0	0	1	1
ENSG00000145832	ENSG00000145832	SLC25A48	5:135170337-135224326	NOTEST	0	0	0	0	1	1
ENSG00000145835	ENSG00000145835	CDKN2AIPNLP2	2:27050036-27050388	NOTEST	0	0	0	0	1	1
ENSG00000145839	ENSG00000145839	IL9	5:135227934-135231516	NOTEST	0	0	0	0	1	1
ENSG00000145850	ENSG00000145850	TIMD4	5:156346292-156390266	NOTEST	0	0.0298961	inf	0	1	1
ENSG00000145861	ENSG00000145861	C1QTNF2	5:159774757-159797648	NOTEST	0.0517052	0.151143	1.54754	0	1	1
ENSG00000145863	ENSG00000145863	GABRA6	5:160715435-161129599	NOTEST	0	0	0	0	1	1
ENSG00000145864	ENSG00000145864	GABRB2	5:160715435-161129599	NOTEST	0.0518153	0.0659434	0.347849	0	1	1
ENSG00000145879	ENSG00000145879	SPINK7	5:147647742-147763346	NOTEST	0	0	0	0	1	1
ENSG00000145888	ENSG00000145888	GLRA1	5:151202073-151304403	NOTEST	0	0.00639614	inf	0	1	1
ENSG00000145911	ENSG00000145911	N4BP3	5:177540443-177553088	NOTEST	0.151555	0.17525	0.209569	0	1	1
ENSG00000145920	ENSG00000145920	CPLX2	5:175223312-175311023	NOTEST	0	0	0	0	1	1
ENSG00000145934	ENSG00000145934	TENM2	5:166711803-167691162	NOTEST	0.0440521	0.0118957	-1.88877	0	1	1
ENSG00000145936	ENSG00000145936	KCNMB1	5:169780490-170163636	NOTEST	0	0	0	0	1	1
ENSG00000145949	ENSG00000145949	MYLK4	6:2663862-2751200	NOTEST	0.0755487	0.0616246	-0.293901	0	1	1
ENSG00000145965	ENSG00000145965	C6ORF50	6:3982908-3984372	NOTEST	0.196184	0.0915795	-1.09911	0	1	1
ENSG00000145975	ENSG00000145975	FAM217A	6:4021500-4157619	NOTEST	0.142168	0	#NAME?	0	1	1
ENSG00000146001	ENSG00000146001	PCDHB18	5:140613937-140617101	NOTEST	0.0283008	0.0526027	0.894296	0	1	1
ENSG00000146005	ENSG00000146005	PSD2	5:139175405-139224051	NOTEST	0.16033	0.193505	0.271328	0	1	1
ENSG00000146006	ENSG00000146006	LRRTM2	5:137946655-138270723	NOTEST	0.0580979	0.013868	-2.06673	0	1	1
ENSG00000146013	ENSG00000146013	GFRA3	5:137588067-137610360	NOTEST	0	0	0	0	1	1
ENSG00000146039	ENSG00000146039	SLC17A4	6:25754926-25781419	NOTEST	0.00687546	0.00701002	0.0279624	0	1	1
ENSG00000146047	ENSG00000146047	HIST1H2BA	6:25727136-25727573	NOTEST	0	0	0	0	1	1
ENSG00000146049	ENSG00000146049	KAAG1	6:24171983-24358512	NOTEST	0.352549	0.355898	0.0136393	0	1	1
ENSG00000146070	ENSG00000146070	PLA2G7	6:46620677-46703430	NOTEST	0.0260148	0	#NAME?	0	1	1
ENSG00000146090	ENSG00000146090	RASGEF1C	5:179527794-179636153	NOTEST	0.0824467	0.0892023	0.11362	0	1	1
ENSG00000146151	ENSG00000146151	HMGCLL1	6:55299166-55444012	NOTEST	0	0.0290647	inf	0	1	1
ENSG00000146166	ENSG00000146166	LGSN	6:63985855-64029882	NOTEST	0	0	0	0	1	1
ENSG00000146192	ENSG00000146192	FGD2	6:36973421-36996846	NOTEST	0.0213064	0	#NAME?	0	1	1
ENSG00000146197	ENSG00000146197	SCUBE3	6:35182189-35220856	NOTEST	0.19895	0.367127	0.883874	0	1	1
ENSG00000146215	ENSG00000146215	CRIP3	6:43263431-43337216	NOTEST	0	0	0	0	1	1
ENSG00000146216	ENSG00000146216	TTBK1	6:43211417-43255997	NOTEST	0	0.0188881	inf	0	1	1
ENSG00000146221	ENSG00000146221	TCTE1	6:44238202-44346694	NOTEST	0.0589841	0.228067	1.95106	0	1	1

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ENSG00000146233	ENSG00000146233	CYP39A1	6:46517540-46620523	NOTEST	0.161932	0.122798	-0.399106	0	1	1
ENSG00000146250	ENSG00000146250	PRSS35	6:84222193-84235423	NOTEST	0.346992	0.266852	-0.378862	0	1	1
ENSG00000146276	ENSG00000146276	GABRR1	6:89887219-89940997	NOTEST	0	0	0	0	1	1
ENSG00000146352	ENSG00000146352	CLVS2	6:123317115-123394072	NOTEST	0	0.00092046	inf	0	1	1
ENSG00000146360	ENSG00000146360	GPR6	6:110299513-110301921	NOTEST	0	0	0	0	1	1
ENSG00000146374	ENSG00000146374	RSPO3	6:127439748-127518910	NOTEST	0	0	0	0	1	1
ENSG00000146378	ENSG00000146378	TAAR2	6:132938160-132945414	NOTEST	0	0	0	0	1	1
ENSG00000146383	ENSG00000146383	TAAR6	6:132891460-132892498	NOTEST	0.213651	0.189083	-0.176234	0	1	1
ENSG00000146385	ENSG00000146385	TAAR8	6:132873831-132874860	NOTEST	0.0315768	0.0539581	0.772975	0	1	1
ENSG00000146399	ENSG00000146399	TAAR1	6:132966122-132967142	NOTEST	0	0	0	0	1	1
ENSG00000146411	ENSG00000146411	SLC2A12	6:134273307-134373774	NOTEST	0.423822	0.448518	0.0817081	0	1	1
ENSG00000146453	ENSG00000146453	PNLDC1	6:160221297-160241736	NOTEST	0	0	0	0	1	1
ENSG00000146469	ENSG00000146469	VIP	6:153071932-153080900	NOTEST	0.0248761	0.0630685	1.34216	0	1	1
ENSG00000146477	ENSG00000146477	SLC22A3	6:160769299-160932156	NOTEST	0	0	0	0	1	1
ENSG00000146521	ENSG00000146521	C6orf123	6:168185216-168198927	NOTEST	0	0	0	0	1	1
ENSG00000146530	ENSG00000146530	VWDE	7:12370510-12443567	NOTEST	0.507085	0.439051	-0.207839	0	1	1
ENSG00000146555	ENSG00000146555	SDK1	7:3303663-4308632	NOTEST	0	0	0	0	1	1
ENSG00000146618	ENSG00000146618	FERD3L	7:19183915-19185876	NOTEST	0	0	0	0	1	1
ENSG00000146648	ENSG00000146648	EGFR	7:55086713-55324313	NOTEST	0.00884655	0.0088658	0.00313576	0	1	1
ENSG00000146666	ENSG00000146666	LINC00525	7:47735327-48019178	NOTEST	0.0148097	0.0115182	-0.362626	0	1	1
ENSG00000146678	ENSG00000146678	IGFBP1	7:45927955-45933267	NOTEST	0	0.00872124	inf	0	1	1
ENSG00000146722	ENSG00000146722	AC006014.8	7:74988447-75115548	NOTEST	0	0	0	0	1	1
ENSG00000146755	ENSG00000146755	TRIM50	7:72726534-72742085	NOTEST	0	0	0	0	1	1
ENSG00000146809	ENSG00000146809	ASB15	7:123207063-123277951	NOTEST	0.0105771	0.00410619	-1.36507	0	1	1
ENSG00000146839	ENSG00000146839	ZAN	7:100331248-100395419	NOTEST	0	0	0	0	1	1
ENSG00000146857	ENSG00000146857	STRA8	7:134916730-134943244	NOTEST	0.018069	0.0127333	-0.504912	0	1	1
ENSG00000146904	ENSG00000146904	EPHA1	7:143078172-143220542	NOTEST	0.118944	0.483511	2.02327	0	1	1
ENSG00000146910	ENSG00000146910	CNPY1	7:155266900-155326557	NOTEST	0.0503629	0.0970107	0.945781	0	1	1
ENSG00000146926	ENSG00000146926	ASB10	7:150872784-150884919	NOTEST	0.0692394	0.169045	1.28774	0	1	1
ENSG00000146938	ENSG00000146938	NLGN4X	X:5758677-6146904	NOTEST	0.0427613	0.0505262	0.240725	0	1	1
ENSG00000146955	ENSG00000146955	RAB19	7:139993492-140126050	NOTEST	0	0	0	0	1	1
ENSG00000146966	ENSG00000146966	DENND2A	7:140218219-140624564	NOTEST	0.269799	0.398383	0.562269	0	1	1
ENSG00000147003	ENSG00000147003	TMEM27	X:15645440-15683154	NOTEST	0.0508214	0.023829	-1.09272	0	1	1
ENSG00000147027	ENSG00000147027	TMEM47	X:34645180-34675405	NOTEST	0.0505659	0.025894	-0.96555	0	1	1
ENSG00000147036	ENSG00000147036	LANCL3	X:37208527-38548169	NOTEST	0	0.0435677	inf	0	1	1
ENSG00000147041	ENSG00000147041	SYTL5	X:37208527-38548169	NOTEST	0.185028	0.224367	0.278116	0	1	1
ENSG00000147059	ENSG00000147059	SPIN2A	X:57160962-57164058	NOTEST	0	0.0136224	inf	0	1	1
ENSG00000147081	ENSG00000147081	AKAP4	X:49955405-49965664	NOTEST	0	0	0	0	1	1
ENSG00000147082	ENSG00000147082	CCNB3	X:49967363-50094909	NOTEST	0.280493	0.219165	-0.355946	0	1	1
ENSG00000147100	ENSG00000147100	SLC16A2	X:73641084-73753752	NOTEST	0.533071	0.565757	0.0858544	0	1	1
ENSG00000147113	ENSG00000147113	CXorf36	X:45007618-45193162	NOTEST	0.00634102	0	#NAME?	0	1	1
ENSG00000147117	ENSG00000147117	ZNF157	X:47229981-47273704	NOTEST	0.065221	0.0209817	-1.63621	0	1	1
ENSG00000147119	ENSG00000147119	CHST7	X:46433218-46457843	NOTEST	0.0520933	0.103957	0.996815	0	1	1
ENSG00000147127	ENSG00000147127	RAB41	X:69501942-69504852	NOTEST	0.186037	0.298993	0.68452	0	1	1
ENSG00000147138	ENSG00000147138	GPR174	X:78426468-78427726	NOTEST	0	0	0	0	1	1

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ENSG00000147145	ENSG00000147145	LPAR4	X:78003205-78012591	NOTEST	0	0	0	0	1	1
ENSG00000147160	ENSG00000147160	AWAT2	X:69260391-69269788	NOTEST	0	0	0	0	1	1
ENSG00000147166	ENSG00000147166	ITGB1BP2	X:70521583-70525221	NOTEST	0.111366	0.0602734	-0.885713	0	1	1
ENSG00000147168	ENSG00000147168	IL2RG	X:70327253-70331958	NOTEST	0.106196	0.0355453	-1.579	0	1	1
ENSG00000147183	ENSG00000147183	CPXCR1	X:88002225-88009786	NOTEST	0	0	0	0	1	1
ENSG00000147206	ENSG00000147206	NXF3	X:102330737-102348157	NOTEST	0	0	0	0	1	1
ENSG00000147223	ENSG00000147223	RIPPLY1	X:106045909-106243474	NOTEST	0	0	0	0	1	1
ENSG00000147234	ENSG00000147234	FRMPD3	X:106756212-106848481	NOTEST	0.134856	0.114273	-0.23894	0	1	1
ENSG00000147246	ENSG00000147246	HTR2C	X:113818550-114144624	NOTEST	0.00331101	0	#NAME?	0	1	1
ENSG00000147255	ENSG00000147255	IGSF1	X:130407479-130533677	NOTEST	0.02201	0	#NAME?	0	1	1
ENSG00000147256	ENSG00000147256	ARHGAP36	X:130192215-130223857	NOTEST	0	0	0	0	1	1
ENSG00000147262	ENSG00000147262	GPR119	X:129518318-129519511	NOTEST	0	0	0	0	1	1
ENSG00000147378	ENSG00000147378	FATE1	X:150884506-150891666	NOTEST	0	0	0	0	1	1
ENSG00000147380	ENSG00000147380	OPN1MW	X:153448106-153461633	NOTEST	0	0	0	0	1	1
ENSG00000147381	ENSG00000147381	MAGEA4	X:151072902-151093642	NOTEST	0	0.259399	inf	0	1	1
ENSG00000147402	ENSG00000147402	GABRQ	X:151806636-151825999	NOTEST	0.00989526	0.0174999	0.822537	0	1	1
ENSG00000147432	ENSG00000147432	CHRNB3	8:42552518-42592550	NOTEST	0	0	0	0	1	1
ENSG00000147443	ENSG00000147443	DOK2	8:21766383-21771371	NOTEST	0.00841429	0.0439163	2.38384	0	1	1
ENSG00000147465	ENSG00000147465	STAR	8:37962759-38070819	NOTEST	0	0.0407309	inf	0	1	1
ENSG00000147481	ENSG00000147481	SNTG1	8:50822348-51706678	NOTEST	0	0	0	0	1	1
ENSG00000147485	ENSG00000147485	PXDNL	8:52170247-52722005	NOTEST	0.00677515	0	#NAME?	0	1	1
ENSG00000147488	ENSG00000147488	ST18	8:53023398-53373519	NOTEST	0	0	0	0	1	1
ENSG00000147570	ENSG00000147570	DNAJC5B	8:66933794-67012751	NOTEST	0	0	0	0	1	1
ENSG00000147571	ENSG00000147571	CRH	8:67088619-67090960	NOTEST	0	0	0	0	1	1
ENSG00000147573	ENSG00000147573	TRIM55	8:67039130-67087720	NOTEST	0	0	0	0	1	1
ENSG00000147596	ENSG00000147596	PRDM14	8:70963885-70983928	NOTEST	0	0	0	0	1	1
ENSG00000147606	ENSG00000147606	SLC26A7	8:92114059-92410378	NOTEST	0.048371	0.00845412	-2.51642	0	1	1
ENSG00000147613	ENSG00000147613	PSKH2	8:86999551-87166457	NOTEST	0	0	0	0	1	1
ENSG00000147614	ENSG00000147614	ATP6V0D2	8:86999551-87166457	NOTEST	0.0850804	0.210972	1.31015	0	1	1
ENSG00000147642	ENSG00000147642	SYBU	8:110586206-110704020	NOTEST	0.308652	0.32295	0.0653256	0	1	1
ENSG00000147647	ENSG00000147647	DPYS	8:105342551-105479281	NOTEST	0.0441186	0.115624	1.38998	0	1	1
ENSG00000147655	ENSG00000147655	RSPO2	8:108911543-109095913	NOTEST	0	0	0	0	1	1
ENSG00000147689	ENSG00000147689	FAM83A	8:124191199-124222314	NOTEST	0	0	0	0	1	1
ENSG00000147697	ENSG00000147697	GSDMC	8:130760441-130799134	NOTEST	0	0.0218713	inf	0	1	1
ENSG00000147724	ENSG00000147724	FAM135B	8:139142265-139509065	NOTEST	0	0	0	0	1	1
ENSG00000147753	ENSG00000147753	TTTY7	Y:6317508-6325947	NOTEST	0	0	0	0	1	1
ENSG00000147761	ENSG00000147761	TTTY7B	Y:9544432-9552871	NOTEST	0	0	0	0	1	1
ENSG00000147869	ENSG00000147869	CER1	9:14719721-14722715	NOTEST	0	0	0	0	1	1
ENSG00000147873	ENSG00000147873	IFNA5	9:21304612-21305312	NOTEST	0	0	0	0	1	1
ENSG00000147885	ENSG00000147885	IFNA16	9:21216371-21217310	NOTEST	0.128685	0	#NAME?	0	1	1
ENSG00000147896	ENSG00000147896	IFNK	9:27325206-27529779	NOTEST	0	0	0	0	1	1
ENSG00000147926	ENSG00000147926	SPATA31A3	9:40700290-40713709	NOTEST	0	0	0	0	1	1
ENSG00000148053	ENSG00000148053	NTRK2	9:87283465-87638505	NOTEST	0.182113	0.173951	-0.0661486	0	1	1
ENSG00000148082	ENSG00000148082	SHC3	9:91628059-91793682	NOTEST	0	0	0	0	1	1
ENSG00000148123	ENSG00000148123	LPPR1	9:103790990-104087417	NOTEST	0	0	0	0	1	1

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ENSG00000148136	ENSG00000148136	OR13C4	9:107288533-107289490	NOTEST	0	0	0	0	1	1
ENSG00000148156	ENSG00000148156	ACTL7B	9:111616870-111619239	NOTEST	0	0	0	0	1	1
ENSG00000148204	ENSG00000148204	CRB2	9:126118448-126692431	NOTEST	0.0081474	0.00933861	0.196868	0	1	1
ENSG00000148215	ENSG00000148215	OR5C1	9:125551149-125552237	NOTEST	0	0	0	0	1	1
ENSG00000148288	ENSG00000148288	GBGT1	9:135973106-136039332	NOTEST	0.307618	0.419035	0.445929	0	1	1
ENSG00000148346	ENSG00000148346	LCN2	9:130911349-130915734	NOTEST	0	0	0	0	1	1
ENSG00000148357	ENSG00000148357	HMCN2	9:133259835-133309510	NOTEST	0	0	0	0	1	1
ENSG00000148377	ENSG00000148377	IDI2	10:1034337-1095110	NOTEST	0	0	0	0	1	1
ENSG00000148386	ENSG00000148386	LCN9	9:138555167-138558268	NOTEST	0	0	0	0	1	1
ENSG00000148408	ENSG00000148408	CACNA1B	9:140513443-141019076	NOTEST	0.0561575	0.00298189	-4.23518	0	1	1
ENSG00000148426	ENSG00000148426	PROSER2	10:11865337-11936699	NOTEST	0.392762	0.411909	0.0686701	0	1	1
ENSG00000148468	ENSG00000148468	FAM171A1	10:15253641-15413061	NOTEST	0	0	0	0	1	1
ENSG00000148482	ENSG00000148482	SLC39A12	10:18240767-18332221	NOTEST	0.101279	0.201192	0.990234	0	1	1
ENSG00000148483	ENSG00000148483	TMEM236	10:17794250-17842867	NOTEST	0.00609885	0	#NAME?	0	1	1
ENSG00000148513	ENSG00000148513	ANKRD30A	10:37414784-37673039	NOTEST	0	0	0	0	1	1
ENSG00000148541	ENSG00000148541	FAM13C	10:60936349-61122939	NOTEST	0.12504	0.0326806	-1.93588	0	1	1
ENSG00000148584	ENSG00000148584	A1CF	10:52499077-52645435	NOTEST	0	0	0	0	1	1
ENSG00000148600	ENSG00000148600	CDHR1	10:85954409-85979377	NOTEST	0.0396432	0.0336109	-0.238146	0	1	1
ENSG00000148602	ENSG00000148602	LRIT1	10:85991348-86001217	NOTEST	0	0	0	0	1	1
ENSG00000148604	ENSG00000148604	RGR	10:86004808-86019716	NOTEST	0.597309	0.335566	-0.831881	0	1	1
ENSG00000148671	ENSG00000148671	ADIRF	10:88695296-88784489	NOTEST	0.165159	0.565255	1.77505	0	1	1
ENSG00000148677	ENSG00000148677	ANKRD1	10:92671852-92681033	NOTEST	0.0461874	0.260644	2.49651	0	1	1
ENSG00000148680	ENSG00000148680	HTR7	10:92500577-92617671	NOTEST	0.0405175	0.0655358	0.693739	0	1	1
ENSG00000148702	ENSG00000148702	HABP2	10:115310595-115423886	NOTEST	0.0443687	0.131129	1.56338	0	1	1
ENSG00000148704	ENSG00000148704	VAX1	10:118888031-118897812	NOTEST	0.439512	0.445894	0.0207955	0	1	1
ENSG00000148734	ENSG00000148734	NPFFR1	10:72007084-72043432	NOTEST	0.00305911	0.00119032	-1.36176	0	1	1
ENSG00000148735	ENSG00000148735	PLEKHS1	10:115511212-115543188	NOTEST	0.0384309	0.080696	1.07023	0	1	1
ENSG00000148795	ENSG00000148795	CYP17A1	10:104590287-104597290	NOTEST	0.00874119	0.00679206	-0.36398	0	1	1
ENSG00000148798	ENSG00000148798	INA	10:105036919-105050108	NOTEST	0.0281814	0.307423	3.44741	0	1	1
ENSG00000148826	ENSG00000148826	NKX6-2	10:134598296-134599556	NOTEST	0	0	0	0	1	1
ENSG00000148828	ENSG00000148828	CT476828.1	GL000228.1:30529-32226	NOTEST	0	0	0	0	1	1
ENSG00000148942	ENSG00000148942	SLC5A12	11:26688565-26744974	NOTEST	0	0	0	0	1	1
ENSG00000148948	ENSG00000148948	LRRC4C	11:40135752-41481323	NOTEST	0	0	0	0	1	1
ENSG00000148965	ENSG00000148965	SAA4	11:18252895-18270190	NOTEST	0.049088	0	#NAME?	0	1	1
ENSG00000149021	ENSG00000149021	SCGB1A1	11:62172574-62194196	NOTEST	0	0	0	0	1	1
ENSG00000149043	ENSG00000149043	SYT8	11:1848708-1858751	NOTEST	0	0	0	0	1	1
ENSG00000149050	ENSG00000149050	ZNF214	11:7020548-7041599	NOTEST	0.039148	0.0454161	0.214264	0	1	1
ENSG00000149054	ENSG00000149054	ZNF215	11:6947634-7005863	NOTEST	0.431266	0.481312	0.158395	0	1	1
ENSG00000149090	ENSG00000149090	PAMR1	11:35453369-35551848	NOTEST	0	0	0	0	1	1
ENSG00000149124	ENSG00000149124	GLYAT	11:58407898-58499447	NOTEST	0	0.0398544	inf	0	1	1
ENSG00000149131	ENSG00000149131	SERPING1	11:57364859-57382326	NOTEST	0.148303	0.170579	0.201899	0	1	1
ENSG00000149133	ENSG00000149133	OR5F1	11:55761156-55762101	NOTEST	0	0	0	0	1	1
ENSG00000149201	ENSG00000149201	CCDC81	11:86085777-86134151	NOTEST	0.0610535	0.0494667	-0.303617	0	1	1
ENSG00000149256	ENSG00000149256	TENM4	11:78363875-79151992	NOTEST	0.0534795	0.108342	1.01853	0	1	1
ENSG00000149295	ENSG00000149295	DRD2	11:113276042-113346413	NOTEST	0	0.0282621	inf	0	1	1

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ENSG00000149300	ENSG00000149300	C11orf52	11:111779288-111797596	NOTEST	0.043199	0.124747	1.52994	0	1	1
ENSG00000149305	ENSG00000149305	HTR3B	11:113775398-113817287	NOTEST	0	0.0235412	inf	0	1	1
ENSG00000149328	ENSG00000149328	GLB1L2	11:134201767-134248235	NOTEST	0.0295542	0.129011	2.12606	0	1	1
ENSG00000149346	ENSG00000149346	SLX4IP	20:10415950-10617477	NOTEST	0.615831	0.546649	-0.171919	0	1	1
ENSG00000149380	ENSG00000149380	P4HA3	11:73723762-74035750	NOTEST	0.144856	0.0823478	-0.814821	0	1	1
ENSG00000149403	ENSG00000149403	GRIK4	11:120382467-120859613	NOTEST	0	0.105196	inf	0	1	1
ENSG00000149418	ENSG00000149418	ST14	11:130029456-130080271	NOTEST	0.00440933	0	#NAME?	0	1	1
ENSG00000149435	ENSG00000149435	GGTLC1	20:23965689-23969416	NOTEST	0	0	0	0	1	1
ENSG00000149443	ENSG00000149443	C20orf78	20:18790371-18810797	NOTEST	0	0	0	0	1	1
ENSG00000149451	ENSG00000149451	ADAM33	20:3648611-3662893	NOTEST	0.00524761	0.0583195	3.47425	0	1	1
ENSG00000149452	ENSG00000149452	SLC22A8	11:62756625-62783311	NOTEST	0	0	0	0	1	1
ENSG00000149488	ENSG00000149488	TMC2	20:2517252-2622430	NOTEST	0.0139043	0	#NAME?	0	1	1
ENSG00000149506	ENSG00000149506	ZP1	11:60635034-60643166	NOTEST	0.0545946	0.0537571	-0.0223029	0	1	1
ENSG00000149507	ENSG00000149507	OOSP2	11:59807747-59815517	NOTEST	0	0	0	0	1	1
ENSG00000149516	ENSG00000149516	MS4A3	11:59824059-59838601	NOTEST	0	0	0	0	1	1
ENSG00000149527	ENSG00000149527	PLCH2	1:2357418-2436969	NOTEST	0.0222317	0.0148442	-0.582713	0	1	1
ENSG00000149534	ENSG00000149534	MS4A2	11:59855733-59863444	NOTEST	0.0157769	0	#NAME?	0	1	1
ENSG00000149564	ENSG00000149564	ESAM	11:124617367-124635832	NOTEST	0.0364656	0.0278943	-0.386566	0	1	1
ENSG00000149571	ENSG00000149571	KIRREL3	11:126225534-126875953	NOTEST	0.323106	0.477067	0.562185	0	1	1
ENSG00000149573	ENSG00000149573	MPZL2	11:118124117-118135251	NOTEST	0.0550358	0.0312891	-0.81471	0	1	1
ENSG00000149575	ENSG00000149575	SCN2B	11:118032665-118047388	NOTEST	0.0094735	0	#NAME?	0	1	1
ENSG00000149591	ENSG00000149591	TAGLN	11:117070036-117103241	NOTEST	0.586881	0.517936	-0.180294	0	1	1
ENSG00000149596	ENSG00000149596	JPH2	20:42740334-42816218	NOTEST	0.0934679	0.17575	0.910984	0	1	1
ENSG00000149609	ENSG00000149609	C20orf144	20:32244892-32262269	NOTEST	0.0501672	0.138653	1.46666	0	1	1
ENSG00000149633	ENSG00000149633	KIAA1755	20:36838889-36965907	NOTEST	0.155478	0.137838	-0.173732	0	1	1
ENSG00000149635	ENSG00000149635	OCSTAMP	20:45169584-45179213	NOTEST	0	0.00616434	inf	0	1	1
ENSG00000149646	ENSG00000149646	CNBD2	20:34556511-34618622	NOTEST	0.0420936	0.0387618	-0.118965	0	1	1
ENSG00000149651	ENSG00000149651	SPINT4	20:44350989-44354469	NOTEST	0	0	0	0	1	1
ENSG00000149654	ENSG00000149654	CDH22	20:44802371-44937137	NOTEST	0	0	0	0	1	1
ENSG00000149656	ENSG00000149656	LINC00266-1	20:62887093-62944485	NOTEST	0.127184	0.216581	0.767993	0	1	1
ENSG00000149735	ENSG00000149735	GPHA2	11:64685024-64703360	NOTEST	0	0	0	0	1	1
ENSG00000149742	ENSG00000149742	SLC22A9	11:63137260-63177766	NOTEST	0	0	0	0	1	1
ENSG00000149781	ENSG00000149781	FERMT3	11:63974149-64001824	NOTEST	0.144568	0.201771	0.480969	0	1	1
ENSG00000149922	ENSG00000149922	TBX6	16:30097113-30103208	NOTEST	0.587404	0.359783	-0.707225	0	1	1
ENSG00000149926	ENSG00000149926	FAM57B	16:30034654-30064299	NOTEST	0.205655	0.0796319	-1.36881	0	1	1
ENSG00000149968	ENSG00000149968	MMP3	11:102617698-102714534	NOTEST	0.0733454	0.0557766	-0.395046	0	1	1
ENSG00000149972	ENSG00000149972	CNTN5	11:98891682-100229616	NOTEST	0.0190924	0.0356533	0.901041	0	1	1
ENSG00000150045	ENSG00000150045	KLRF1	12:9980076-9997606	NOTEST	0.588581	0.586794	-0.00438518	0	1	1
ENSG00000150048	ENSG00000150048	CLEC1A	12:10222152-10264226	NOTEST	0	0	0	0	1	1
ENSG00000150051	ENSG00000150051	MKX	10:27961803-28056723	NOTEST	0	0	0	0	1	1
ENSG00000150054	ENSG00000150054	MPP7	10:28339921-28623415	NOTEST	0	0.0515776	inf	0	1	1
ENSG00000150076	ENSG00000150076	C10ORF68	10:32735067-33171802	NOTEST	0.0565926	0.00973156	-2.53987	0	1	1
ENSG00000150165	ENSG00000150165	ANXA8L1	10:47011752-47174093	NOTEST	0	0	0	0	1	1
ENSG00000150175	ENSG00000150175	FRMPD2P2	10:46657134-46681603	NOTEST	0	0.00981623	inf	0	1	1
ENSG00000150201	ENSG00000150201	FXYD4	10:43867089-43871783	NOTEST	0	0	0	0	1	1

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ENSG00000150244	ENSG00000150244	TRIM48	11:55029657-55038595	NOTEST	0.231954	0.469902	1.01852	0	1	1
ENSG00000150261	ENSG00000150261	OR8K1	11:56113420-56114507	NOTEST	0	0	0	0	1	1
ENSG00000150269	ENSG00000150269	OR5M9	11:56229944-56230877	NOTEST	0	0	0	0	1	1
ENSG00000150275	ENSG00000150275	PCDH15	10:55562530-57387702	NOTEST	0.00221696	0	#NAME?	0	1	1
ENSG00000150276	ENSG00000150276	PPIAP26	13:53394631-53395153	NOTEST	0	0	0	0	1	1
ENSG00000150281	ENSG00000150281	CTF1	16:30907927-30914881	NOTEST	0.0867012	0.0471787	-0.877915	0	1	1
ENSG00000150337	ENSG00000150337	FCGR1A	1:149754226-149783928	NOTEST	0.0237484	0.0868392	1.87052	0	1	1
ENSG00000150361	ENSG00000150361	KLHL1	13:70274725-70713561	NOTEST	0	0.00530699	inf	0	1	1
ENSG00000150394	ENSG00000150394	CDH8	16:61681145-62070939	NOTEST	0.0370448	0.0262512	-0.49689	0	1	1
ENSG00000150471	ENSG00000150471	LPHN3	4:62066975-63031272	NOTEST	0.129476	0.197134	0.606487	0	1	1
ENSG00000150526	ENSG00000150526	MIA2	14:39699434-39856306	NOTEST	0	0	0	0	1	1
ENSG00000150556	ENSG00000150556	LYPD6B	2:149894620-150071776	NOTEST	0.041844	0.0357857	-0.22564	0	1	1
ENSG00000150625	ENSG00000150625	GPM6A	4:176554084-176923815	NOTEST	0.341672	0.494787	0.534195	0	1	1
ENSG00000150628	ENSG00000150628	SPATA4	4:177105788-177116822	NOTEST	0.165244	0.203411	0.299802	0	1	1
ENSG00000150636	ENSG00000150636	CCDC102B	18:66340924-66722426	NOTEST	0.268079	0.173108	-0.630982	0	1	1
ENSG00000150656	ENSG00000150656	CNDP1	18:72201674-72254448	NOTEST	0.0966997	0.131892	0.447775	0	1	1
ENSG00000150667	ENSG00000150667	FSIP1	15:39892231-40213093	NOTEST	0.158314	0.055743	-1.50593	0	1	1
ENSG00000150672	ENSG00000150672	DLG2	11:83166054-85338966	NOTEST	0.516162	0.182343	-1.50116	0	1	1
ENSG00000150676	ENSG00000150676	CCDC83	11:85566143-85634725	NOTEST	0	0	0	0	1	1
ENSG00000150681	ENSG00000150681	RGS18	1:192127586-192154945	NOTEST	0	0	0	0	1	1
ENSG00000150732	ENSG00000150732	RP11-134C1.1	1:188036428-188036656	NOTEST	0	0	0	0	1	1
ENSG00000150750	ENSG00000150750	C11orf53	11:111126706-111157126	NOTEST	0	0	0	0	1	1
ENSG00000150782	ENSG00000150782	IL18	11:111895537-112095422	NOTEST	0	0.037828	inf	0	1	1
ENSG00000150783	ENSG00000150783	TEX12	11:111895537-112095422	NOTEST	0.0241246	0.0187843	-0.360974	0	1	1
ENSG00000150873	ENSG00000150873	C2orf50	2:11273178-11286916	NOTEST	0.0236415	0.0442957	0.905841	0	1	1
ENSG00000150907	ENSG00000150907	FOXO1	13:41129803-41240734	NOTEST	0.546236	0.609827	0.158874	0	1	1
ENSG00000151005	ENSG00000151005	TKTL2	4:164392256-164395047	NOTEST	0	0	0	0	1	1
ENSG00000151023	ENSG00000151023	ENKUR	10:25270907-25305089	NOTEST	0.0326559	0.039433	0.272062	0	1	1
ENSG00000151033	ENSG00000151033	LYZL2	10:30900717-30918691	NOTEST	0	0	0	0	1	1
ENSG00000151062	ENSG00000151062	CACNA2D4	12:1901122-2032033	NOTEST	0.152961	0.0326299	-2.2289	0	1	1
ENSG00000151067	ENSG00000151067	CACNA1C	12:2055219-2802108	NOTEST	0	0.00164262	inf	0	1	1
ENSG00000151079	ENSG00000151079	KCNA6	12:4671369-4960277	NOTEST	0	0	0	0	1	1
ENSG00000151136	ENSG00000151136	BTBD11	12:107712189-108053419	NOTEST	0	0	0	0	1	1
ENSG00000151150	ENSG00000151150	ANK3	10:61786055-62493248	NOTEST	0.386294	0.358411	-0.108085	0	1	1
ENSG00000151164	ENSG00000151164	RAD9B	12:110928901-111021125	NOTEST	0.20278	0.125627	-0.690773	0	1	1
ENSG00000151276	ENSG00000151276	MAGI1	3:65339199-66024509	NOTEST	0.0498045	0.00920835	-2.43526	0	1	1
ENSG00000151303	ENSG00000151303	AGAP11	10:88695296-88784489	NOTEST	0.00606783	0	#NAME?	0	1	1
ENSG00000151360	ENSG00000151360	ALLC	2:3705784-3836122	NOTEST	0	0	0	0	1	1
ENSG00000151364	ENSG00000151364	KCTD14	11:77726760-77791265	NOTEST	0.0448778	0.0075937	-2.56313	0	1	1
ENSG00000151365	ENSG00000151365	THRSP	11:77726760-77791265	NOTEST	0.0148086	0.0230245	0.636735	0	1	1
ENSG00000151376	ENSG00000151376	ME3	11:86142631-86383678	NOTEST	0.63765	0.491647	-0.375142	0	1	1
ENSG00000151379	ENSG00000151379	MSGN1	2:17997762-17998368	NOTEST	0	0	0	0	1	1
ENSG00000151388	ENSG00000151388	ADAMTS12	5:33523639-33892297	NOTEST	0.229999	0.22922	-0.00489674	0	1	1
ENSG00000151418	ENSG00000151418	ATP6V1G3	1:198492351-198510075	NOTEST	0	0	0	0	1	1
ENSG00000151468	ENSG00000151468	CCDC3	10:12938626-13180291	NOTEST	0	0.00902078	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000151475	ENSG00000151475	SLC25A31	4:128651532-128695448	NOTEST	0	0	0	0	1	1
ENSG00000151577	ENSG00000151577	DRD3	3:113847498-113918254	NOTEST	0	0	0	0	1	1
ENSG00000151615	ENSG00000151615	POU4F2	4:147560044-147563626	NOTEST	0	0	0	0	1	1
ENSG00000151617	ENSG00000151617	EDNRA	4:148402068-148466106	NOTEST	0.0233438	0.116763	2.32247	0	1	1
ENSG00000151623	ENSG00000151623	NR3C2	4:148999912-149365850	NOTEST	0.560735	0.608151	0.117112	0	1	1
ENSG00000151631	ENSG00000151631	AKR1C6P	10:4914092-4934167	NOTEST	0	0	0	0	1	1
ENSG00000151632	ENSG00000151632	AKR1C2	10:5029966-5060223	NOTEST	0	0	0	0	1	1
ENSG00000151650	ENSG00000151650	VENTX	10:135050907-135055433	NOTEST	0	0	0	0	1	1
ENSG00000151651	ENSG00000151651	ADAM8	10:135075906-135090372	NOTEST	0.0472481	0.0649022	0.458012	0	1	1
ENSG00000151655	ENSG00000151655	ITIH2	10:7745231-7791483	NOTEST	0	0.024345	inf	0	1	1
ENSG00000151702	ENSG00000151702	FLI1	11:128499547-128683162	NOTEST	0.0706009	0.0372915	-0.920841	0	1	1
ENSG00000151704	ENSG00000151704	KCNJ1	11:128706209-128737268	NOTEST	0	0	0	0	1	1
ENSG00000151715	ENSG00000151715	TMEM45B	11:129685713-129729898	NOTEST	0	0.00505697	inf	0	1	1
ENSG00000151778	ENSG00000151778	SERP2	13:44947800-44971850	NOTEST	0.0187773	0.0599074	1.67375	0	1	1
ENSG00000151789	ENSG00000151789	ZNF385D	3:21459914-22414812	NOTEST	0	0	0	0	1	1
ENSG00000151790	ENSG00000151790	TDO2	4:156750880-156841558	NOTEST	0.0888396	0.0486226	-0.869576	0	1	1
ENSG00000151812	ENSG00000151812	SLC35F4	14:58030639-58448912	NOTEST	0	0	0	0	1	1
ENSG00000151838	ENSG00000151838	CCDC175	14:59895739-60043549	NOTEST	0	0	0	0	1	1
ENSG00000151846	ENSG00000151846	PABPC3	13:25670299-25673389	NOTEST	0.0285632	0.0158333	-0.851199	0	1	1
ENSG00000151892	ENSG00000151892	GFRA1	10:117816443-118032979	NOTEST	0.0425203	0.0684888	0.687717	0	1	1
ENSG00000151948	ENSG00000151948	GLT1D1	12:129337971-129469509	NOTEST	0	0.00747949	inf	0	1	1
ENSG00000151952	ENSG00000151952	TMEM132D	12:129556269-130388211	NOTEST	0	0	0	0	1	1
ENSG00000151962	ENSG00000151962	RBM46	4:155675907-155749965	NOTEST	0.0125342	0.0202215	0.690012	0	1	1
ENSG00000151963	ENSG00000151963	RP11-775A3.1	10:38172521-38173037	NOTEST	0	0	0	0	1	1
ENSG00000152034	ENSG00000152034	MCHR2	6:100367785-100524289	NOTEST	0	0	0	0	1	1
ENSG00000152086	ENSG00000152086	TUBA3E	2:130949317-130956034	NOTEST	0	0.00843131	inf	0	1	1
ENSG00000152092	ENSG00000152092	ASTN1	1:176826437-177134109	NOTEST	0.00870508	0	#NAME?	0	1	1
ENSG00000152093	ENSG00000152093	CFC1B	2:131273569-131285579	NOTEST	0	0	0	0	1	1
ENSG00000152137	ENSG00000152137	HSPB8	12:119616446-119658936	NOTEST	0.12373	0.0689926	-0.84268	0	1	1
ENSG00000152154	ENSG00000152154	TMEM178A	2:39476406-39945103	NOTEST	0.246692	0.0822319	-1.58494	0	1	1
ENSG00000152207	ENSG00000152207	CYSLTR2	13:49280950-49283498	NOTEST	0.0113005	0	#NAME?	0	1	1
ENSG00000152208	ENSG00000152208	GRID2	4:93225549-94695707	NOTEST	0.00861925	0	#NAME?	0	1	1
ENSG00000152213	ENSG00000152213	ARL11	13:50202434-50208008	NOTEST	0	0	0	0	1	1
ENSG00000152214	ENSG00000152214	RIT2	18:40323191-40695657	NOTEST	0	0	0	0	1	1
ENSG00000152217	ENSG00000152217	SETBP1	18:42260137-42648475	NOTEST	0.381368	0.359949	-0.0833922	0	1	1
ENSG00000152254	ENSG00000152254	G6PC2	2:169312371-169769881	NOTEST	0	0	0	0	1	1
ENSG00000152266	ENSG00000152266	PTH	11:13513601-13517728	NOTEST	0	0	0	0	1	1
ENSG00000152268	ENSG00000152268	SPON1	11:13983913-14295237	NOTEST	0.0245694	0.149349	2.60376	0	1	1
ENSG00000152292	ENSG00000152292	SH2D6	2:85645843-85664152	NOTEST	0.354135	0.193165	-0.874467	0	1	1
ENSG00000152315	ENSG00000152315	KCNK13	14:90528108-90652201	NOTEST	0.0366935	0.00934404	-1.97341	0	1	1
ENSG00000152377	ENSG00000152377	SPOCK1	5:136310986-136934068	NOTEST	0.330604	0.194451	-0.765701	0	1	1
ENSG00000152402	ENSG00000152402	GUCY1A2	11:106544737-106889250	NOTEST	0.380614	0.50491	0.407696	0	1	1
ENSG00000152430	ENSG00000152430	BOLL	2:198557829-198651486	NOTEST	0	0	0	0	1	1
ENSG00000152463	ENSG00000152463	OLAH	10:15057070-15130775	NOTEST	0	0	0	0	1	1
ENSG00000152467	ENSG00000152467	ZSCAN1	19:58545399-58565999	NOTEST	0	0	0	0	1	1

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ENSG00000152475	ENSG00000152475	ZNF837	19:58878984-58892427	NOTEST	0.315399	0.111777	-1.49655	0	1	1
ENSG00000152487	ENSG00000152487	ARL5B-AS1	10:18429605-18948214	NOTEST	0.217792	0.176323	-0.304731	0	1	1
ENSG00000152578	ENSG00000152578	GRIA4	11:105480720-105852819	NOTEST	0.0304889	0.0638678	1.06681	0	1	1
ENSG00000152580	ENSG00000152580	IGSF10	3:150803483-151176497	NOTEST	0.131166	0.23064	0.814253	0	1	1
ENSG00000152582	ENSG00000152582	SPEF2	5:35617945-35827120	NOTEST	0.168809	0.288708	0.774217	0	1	1
ENSG00000152583	ENSG00000152583	SPARCL1	4:88394486-88452213	NOTEST	0.024079	0.0182314	-0.401349	0	1	1
ENSG00000152591	ENSG00000152591	DSPP	4:88489186-88655108	NOTEST	0	0	0	0	1	1
ENSG00000152592	ENSG00000152592	DMP1	4:88489186-88655108	NOTEST	0	0	0	0	1	1
ENSG00000152595	ENSG00000152595	MEPE	4:88742562-88767969	NOTEST	0	0	0	0	1	1
ENSG00000152611	ENSG00000152611	CAPSL	5:35904396-35938881	NOTEST	0	0	0	0	1	1
ENSG00000152661	ENSG00000152661	GJA1	6:121756837-121770873	NOTEST	0	0	0	0	1	1
ENSG00000152670	ENSG00000152670	DDX4	5:54921672-55112985	NOTEST	0.0376075	0	#NAME?	0	1	1
ENSG00000152672	ENSG00000152672	CLEC4F	2:71035774-71047732	NOTEST	0.0146106	0	#NAME?	0	1	1
ENSG00000152705	ENSG00000152705	CATSPER3	5:134240595-134347392	NOTEST	0.0395884	0.0708863	0.840431	0	1	1
ENSG00000152760	ENSG00000152760	TCTEX1D1	1:67218141-67244470	NOTEST	0	0	0	0	1	1
ENSG00000152763	ENSG00000152763	WDR78	1:67278567-67390570	NOTEST	0.474479	0.375746	-0.336587	0	1	1
ENSG00000152766	ENSG00000152766	ANKRD22	10:90581888-90611575	NOTEST	0	0	0	0	1	1
ENSG00000152779	ENSG00000152779	SLC16A12	10:91190050-91316398	NOTEST	0	0	0	0	1	1
ENSG00000152784	ENSG00000152784	PRDM8	4:81104433-81125483	NOTEST	0.0701559	0.0547665	-0.357271	0	1	1
ENSG00000152785	ENSG00000152785	BMP3	4:81952118-81978685	NOTEST	0	0	0	0	1	1
ENSG00000152822	ENSG00000152822	GRM1	6:146348781-146758734	NOTEST	0.0195612	0.014496	-0.43234	0	1	1
ENSG00000152910	ENSG00000152910	CNTNAP4	16:76311175-76692375	NOTEST	0.0922223	0.119611	0.375159	0	1	1
ENSG00000152926	ENSG00000152926	ZNF117	7:64432153-64467121	NOTEST	0.0627339	0.0672342	0.099949	0	1	1
ENSG00000152931	ENSG00000152931	PART1	5:58264864-59843484	NOTEST	0.0209342	0.0288953	0.464975	0	1	1
ENSG00000152936	ENSG00000152936	IFLTD1	12:25562226-25801513	NOTEST	0	0.0771615	inf	0	1	1
ENSG00000152939	ENSG00000152939	MARVELD2	5:68710938-68740157	NOTEST	0.0276725	0.0290626	0.0707144	0	1	1
ENSG00000152954	ENSG00000152954	NRSN1	6:24126349-24155128	NOTEST	0.0477663	0	#NAME?	0	1	1
ENSG00000152969	ENSG00000152969	JAKMIP1	4:6027925-6202318	NOTEST	0	0	0	0	1	1
ENSG00000153002	ENSG00000153002	CPB1	3:148508888-148677899	NOTEST	0.0593889	0.0810047	0.447813	0	1	1
ENSG00000153012	ENSG00000153012	LGI2	4:25000468-25032501	NOTEST	0.00428019	0.0286607	2.74333	0	1	1
ENSG00000153060	ENSG00000153060	TEKT5	16:10721357-10788802	NOTEST	0.167254	0.24314	0.539741	0	1	1
ENSG00000153064	ENSG00000153064	BANK1	4:102332442-102995969	NOTEST	0.0215711	0.027511	0.350908	0	1	1
ENSG00000153086	ENSG00000153086	ACMSD	2:135493033-135716912	NOTEST	0.0389097	0	#NAME?	0	1	1
ENSG00000153093	ENSG00000153093	ACOXL	2:111490149-111875799	NOTEST	0	0	0	0	1	1
ENSG00000153157	ENSG00000153157	SYCP2L	6:10747991-10979553	NOTEST	0.0111166	0.0244449	1.13682	0	1	1
ENSG00000153162	ENSG00000153162	BMP6	6:7727029-8102811	NOTEST	0.0262872	0.039827	0.599382	0	1	1
ENSG00000153165	ENSG00000153165	RGPD3	2:107021445-107084832	NOTEST	0.0797984	0.0906052	0.183233	0	1	1
ENSG00000153230	ENSG00000153230	OR14K1	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000153237	ENSG00000153237	CCDC148	2:159023161-159313265	NOTEST	0.538241	0.557474	0.0506536	0	1	1
ENSG00000153253	ENSG00000153253	SCN3A	2:165848493-166060577	NOTEST	0.0391602	0.133035	1.76434	0	1	1
ENSG00000153266	ENSG00000153266	FEZF2	3:62355355-62359999	NOTEST	0	0	0	0	1	1
ENSG00000153283	ENSG00000153283	CD96	3:111011565-111384597	NOTEST	0.0866334	0.263599	1.60535	0	1	1
ENSG00000153292	ENSG00000153292	GPR110	6:46965439-47010099	NOTEST	0	0.0298711	inf	0	1	1
ENSG00000153294	ENSG00000153294	GPR115	6:47624171-47689757	NOTEST	0	0	0	0	1	1
ENSG00000153303	ENSG00000153303	FRMD1	6:168456424-168482237	NOTEST	0	0	0	0	1	1

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ENSG00000153347	ENSG00000153347	FAM81B	5:94727047-94786158	NOTEST	0	0	0	0	1	1
ENSG00000153404	ENSG00000153404	PLEKHG4B	5:140372-190085	NOTEST	0.0224167	0.0330773	0.561272	0	1	1
ENSG00000153495	ENSG00000153495	TEX29	13:111968530-111996596	NOTEST	0.0783733	0	#NAME?	0	1	1
ENSG00000153498	ENSG00000153498	SPACA7	13:113030632-113089003	NOTEST	0	0	0	0	1	1
ENSG00000153531	ENSG00000153531	ADPRHL1	13:114076259-114107839	NOTEST	0.204131	0.0525664	-1.95728	0	1	1
ENSG00000153563	ENSG00000153563	CD8A	2:87011728-87035519	NOTEST	0.0278427	0.0667506	1.26148	0	1	1
ENSG00000153666	ENSG00000153666	GOLGA8I	15:23255241-23268823	NOTEST	0.508654	0.324134	-0.650091	0	1	1
ENSG00000153684	ENSG00000153684	GOLGA8F	15:28623766-28637170	NOTEST	0	0	0	0	1	1
ENSG00000153779	ENSG00000153779	TGIF2LX	X:89176880-89177882	NOTEST	0	0	0	0	1	1
ENSG00000153789	ENSG00000153789	FAM92B	16:85131964-85146114	NOTEST	0	0	0	0	1	1
ENSG00000153802	ENSG00000153802	TMPRSS11D	4:68566997-68995598	NOTEST	0	0	0	0	1	1
ENSG00000153820	ENSG00000153820	SPHKAP	2:228844665-229046361	NOTEST	0	0	0	0	1	1
ENSG00000153822	ENSG00000153822	KCNJ16	17:68013464-68131749	NOTEST	0.0172089	0.0440503	1.356	0	1	1
ENSG00000153823	ENSG00000153823	PID1	2:229715241-230136001	NOTEST	0.0887277	0.0465322	-0.931154	0	1	1
ENSG00000153832	ENSG00000153832	FBXO36	2:230628553-230877825	NOTEST	0.192974	0.150883	-0.354971	0	1	1
ENSG00000153923	ENSG00000153923	CLCA3P	1:87012760-87158886	NOTEST	0	0	0	0	1	1
ENSG00000153930	ENSG00000153930	ANKFN1	17:54188318-54589020	NOTEST	0	0	0	0	1	1
ENSG00000153933	ENSG00000153933	DGKE	17:54869273-54946036	NOTEST	0.437987	0.478557	0.1278	0	1	1
ENSG00000153956	ENSG00000153956	CACNA2D1	7:81575759-82073114	NOTEST	0.0661249	0.0482831	-0.453675	0	1	1
ENSG00000153976	ENSG00000153976	HS3ST3A1	17:13399005-13505244	NOTEST	0	0	0	0	1	1
ENSG00000154007	ENSG00000154007	ASB17	1:76384557-76398116	NOTEST	0	0	0	0	1	1
ENSG00000154016	ENSG00000154016	GRAP	17:18853657-18950950	NOTEST	0.104603	0.13539	0.3722	0	1	1
ENSG00000154025	ENSG00000154025	SLC5A10	17:18853657-18950950	NOTEST	0.0401306	0.119088	1.56925	0	1	1
ENSG00000154096	ENSG00000154096	THY1	11:119252487-119397374	NOTEST	0.251367	0.56347	1.16454	0	1	1
ENSG00000154099	ENSG00000154099	DNAAF1	16:84178864-84220669	NOTEST	0.0301741	0.0569545	0.916497	0	1	1
ENSG00000154118	ENSG00000154118	JPH3	16:87634131-87799598	NOTEST	0.0217522	0.0204668	-0.0878707	0	1	1
ENSG00000154133	ENSG00000154133	ROBO4	11:124753586-124768396	NOTEST	0	0.027633	inf	0	1	1
ENSG00000154143	ENSG00000154143	PANX3	11:124481385-124490252	NOTEST	0	0.00697934	inf	0	1	1
ENSG00000154162	ENSG00000154162	CDH12	5:21616370-22853731	NOTEST	0.170853	0.259228	0.601463	0	1	1
ENSG00000154165	ENSG00000154165	GPR15	3:98216447-98312567	NOTEST	0	0	0	0	1	1
ENSG00000154175	ENSG00000154175	ABI3BP	3:100467999-100712359	NOTEST	0.068914	0.113953	0.725576	0	1	1
ENSG00000154198	ENSG00000154198	CYP4Z2P	1:47308766-47366109	NOTEST	0	0	0	0	1	1
ENSG00000154227	ENSG00000154227	CERS3	15:100913143-101085200	NOTEST	0.0514457	0.039109	-0.395549	0	1	1
ENSG00000154252	ENSG00000154252	GAL3ST2	2:242716239-242743623	NOTEST	0.0247737	0.0174292	-0.507299	0	1	1
ENSG00000154258	ENSG00000154258	ABCA9	17:66970628-67057205	NOTEST	0.0274767	0.0735315	1.42015	0	1	1
ENSG00000154262	ENSG00000154262	ABCA6	17:67074842-67138029	NOTEST	0.0762911	0.148932	0.965067	0	1	1
ENSG00000154269	ENSG00000154269	ENPP3	6:131949581-132068553	NOTEST	0.0707855	0.191663	1.43705	0	1	1
ENSG00000154316	ENSG00000154316	TDH	8:11197145-11332224	NOTEST	0	0	0	0	1	1
ENSG00000154319	ENSG00000154319	FAM167A	8:11197145-11332224	NOTEST	0.0941038	0.124929	0.408784	0	1	1
ENSG00000154342	ENSG00000154342	WNT3A	1:228194751-228248961	NOTEST	0	0	0	0	1	1
ENSG00000154415	ENSG00000154415	PPP1R3A	7:113516831-113715975	NOTEST	0	0	0	0	1	1
ENSG00000154438	ENSG00000154438	ASZ1	7:117003275-117068177	NOTEST	0	0	0	0	1	1
ENSG00000154451	ENSG00000154451	GBP5	1:89724632-89738544	NOTEST	0	0	0	0	1	1
ENSG00000154478	ENSG00000154478	GPR26	10:125425870-125454123	NOTEST	0	0	0	0	1	1
ENSG00000154479	ENSG00000154479	CCDC173	2:170501934-170550943	NOTEST	0.0341398	0.0219628	-0.636394	0	1	1

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ENSG00000154537	ENSG00000154537	FAM27C	9:44990313-44991483	NOTEST	0	0	0	0	1	1
ENSG00000154545	ENSG00000154545	MAGED4	X:51927918-51935364	NOTEST	0	0	0	0	1	1
ENSG00000154611	ENSG00000154611	PSMA8	18:23713815-23773319	NOTEST	0.104149	0.10024	-0.0551805	0	1	1
ENSG00000154620	ENSG00000154620	TMSB4Y	Y:15815446-15817904	NOTEST	0	0	0	0	1	1
ENSG00000154645	ENSG00000154645	CHODL	21:19273579-19639690	NOTEST	0.302672	0.218114	-0.472673	0	1	1
ENSG00000154646	ENSG00000154646	TMPRSS15	21:19641432-19858917	NOTEST	0.00393288	0.00887018	1.17338	0	1	1
ENSG00000154678	ENSG00000154678	PDE1C	7:31790792-32338941	NOTEST	0.11844	0.137321	0.213404	0	1	1
ENSG00000154721	ENSG00000154721	JAM2	21:27011583-27144771	NOTEST	0.0597568	0.0425694	-0.489286	0	1	1
ENSG00000154736	ENSG00000154736	ADAMTS5	21:28261694-28338832	NOTEST	0.00334276	0	#NAME?	0	1	1
ENSG00000154760	ENSG00000154760	SLFN13	17:33762114-33775856	NOTEST	0.00514369	0	#NAME?	0	1	1
ENSG00000154764	ENSG00000154764	WNT7A	3:13857754-13921618	NOTEST	0	0	0	0	1	1
ENSG00000154768	ENSG00000154768	C17orf50	17:34083267-34122711	NOTEST	0.0175356	0	#NAME?	0	1	1
ENSG00000154898	ENSG00000154898	CCDC144CP	17:19912656-20306870	NOTEST	0.0405153	0.0203543	-0.993135	0	1	1
ENSG00000154914	ENSG00000154914	USP43	17:9479943-9633008	NOTEST	0	0	0	0	1	1
ENSG00000154928	ENSG00000154928	EPHB1	3:134316642-134979309	NOTEST	0.105217	0.21239	1.01335	0	1	1
ENSG00000154975	ENSG00000154975	CA10	17:49707673-50237377	NOTEST	0.0411279	0.0538101	0.387761	0	1	1
ENSG00000154997	ENSG00000154997	14-Sep	7:55861236-55930482	NOTEST	0	0	0	0	1	1
ENSG00000155011	ENSG00000155011	DKK2	4:107842958-108223027	NOTEST	0.109551	0.206652	0.915601	0	1	1
ENSG00000155026	ENSG00000155026	RSPH10B	7:5938355-6010314	NOTEST	0.0161401	0.0040355	-1.99983	0	1	1
ENSG00000155052	ENSG00000155052	CNTNAP5	2:124782863-125672864	NOTEST	0	0.0602477	inf	0	1	1
ENSG00000155066	ENSG00000155066	PROM2	2:95940200-95957056	NOTEST	0.0409847	0.118567	1.53254	0	1	1
ENSG00000155070	ENSG00000155070	UNC93B2	7:6895115-6899461	NOTEST	0	0.0218908	inf	0	1	1
ENSG00000155087	ENSG00000155087	ODF1	8:103563799-103573245	NOTEST	0	0	0	0	1	1
ENSG00000155093	ENSG00000155093	PTPRN2	7:157331749-158380480	NOTEST	0	0.00229678	inf	0	1	1
ENSG00000155249	ENSG00000155249	OR4K1	14:20403766-20404842	NOTEST	0	0	0	0	1	1
ENSG00000155269	ENSG00000155269	GPR78	4:8560451-8621488	NOTEST	0	0	0	0	1	1
ENSG00000155282	ENSG00000155282	RP11-195B21.3	9:67926760-67987998	NOTEST	0.288034	0.18383	-0.647867	0	1	1
ENSG00000155307	ENSG00000155307	SAMSN1	21:15857548-16031142	NOTEST	0	0	0	0	1	1
ENSG00000155367	ENSG00000155367	PPM1J	1:113243727-113258099	NOTEST	0.305195	0.565213	0.889063	0	1	1
ENSG00000155428	ENSG00000155428	TRIM74	7:72430015-72439997	NOTEST	0.012597	0.019583	0.636519	0	1	1
ENSG00000155495	ENSG00000155495	MAGEC1	X:140991679-140997174	NOTEST	0.167445	0.297179	0.827645	0	1	1
ENSG00000155511	ENSG00000155511	GRIA1	5:152869174-153193429	NOTEST	0	0	0	0	1	1
ENSG00000155622	ENSG00000155622	XAGE2B	X:52112172-52118823	NOTEST	0	0	0	0	1	1
ENSG00000155657	ENSG00000155657	TTN	2:179385909-179914813	NOTEST	0.0503819	0.00896757	-2.49011	0	1	1
ENSG00000155659	ENSG00000155659	VSIG4	X:65241579-65259967	NOTEST	0	0	0	0	1	1
ENSG00000155714	ENSG00000155714	PDZD9	16:21995185-22012433	NOTEST	0.1373	0.0349891	-1.97236	0	1	1
ENSG00000155719	ENSG00000155719	OTOA	16:21689834-21772050	NOTEST	0.0346213	0.0562452	0.700069	0	1	1
ENSG00000155749	ENSG00000155749	ALS2CR12	2:202152993-202222121	NOTEST	0.272413	0.48327	0.827032	0	1	1
ENSG00000155761	ENSG00000155761	SPAG17	1:118472342-118727846	NOTEST	0.00455247	0.0100101	1.13673	0	1	1
ENSG00000155833	ENSG00000155833	CYLC2	9:105757592-105780770	NOTEST	0	0	0	0	1	1
ENSG00000155849	ENSG00000155849	ELMO1	7:36893960-37488852	NOTEST	0	0.0395378	inf	0	1	1
ENSG00000155875	ENSG00000155875	FAM154A	9:18927655-19033251	NOTEST	0.0173064	0	#NAME?	0	1	1
ENSG00000155886	ENSG00000155886	SLC24A2	9:19507449-19786926	NOTEST	0.00140387	0.00675699	2.26697	0	1	1
ENSG00000155890	ENSG00000155890	TRIM42	3:140396880-140419992	NOTEST	0	0	0	0	1	1

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ENSG00000155897	ENSG00000155897	ADCY8	8:131792546-132054672	NOTEST	0	0	0	0	1	1
ENSG00000155918	ENSG00000155918	RAET1L	6:150339469-150346668	NOTEST	0	0	0	0	1	1
ENSG00000155926	ENSG00000155926	SLA	8:133879202-134147147	NOTEST	0	0	0	0	1	1
ENSG00000155961	ENSG00000155961	RAB39B	X:154487525-154493874	NOTEST	0.0589083	0.0872112	0.566044	0	1	1
ENSG00000155962	ENSG00000155962	CLIC2	X:154505499-154563966	NOTEST	0.0599968	0.126918	1.08094	0	1	1
ENSG00000155966	ENSG00000155966	AFF2	X:147582138-148082193	NOTEST	0.310669	0.397733	0.35642	0	1	1
ENSG00000155980	ENSG00000155980	KIF5A	12:57943780-57980415	NOTEST	0.0783457	0.116461	0.571917	0	1	1
ENSG00000156006	ENSG00000156006	NAT2	8:18248754-18258728	NOTEST	0.023458	0	#NAME?	0	1	1
ENSG00000156009	ENSG00000156009	MAGEA8	X:149009940-149014609	NOTEST	0.0270524	0.0129914	-1.0582	0	1	1
ENSG00000156042	ENSG00000156042	TTC18	10:74870216-75118617	NOTEST	0.0418117	0.0459744	0.136926	0	1	1
ENSG00000156049	ENSG00000156049	GNA14	9:80037994-80263223	NOTEST	0.0116248	0	#NAME?	0	1	1
ENSG00000156076	ENSG00000156076	WIF1	12:65444405-65515346	NOTEST	0.145526	0.149554	0.0393874	0	1	1
ENSG00000156096	ENSG00000156096	UGT2B4	4:70345882-70391732	NOTEST	0	0	0	0	1	1
ENSG00000156097	ENSG00000156097	GPR61	1:110082493-110091028	NOTEST	0.16163	0.120763	-0.420515	0	1	1
ENSG00000156113	ENSG00000156113	KCNMA1	10:78629358-79398353	NOTEST	0	0.0071432	inf	0	1	1
ENSG00000156140	ENSG00000156140	ADAMTS3	4:73146685-73434516	NOTEST	0.138347	0.426211	1.62328	0	1	1
ENSG00000156150	ENSG00000156150	ALX3	1:110574198-110617263	NOTEST	0	0	0	0	1	1
ENSG00000156194	ENSG00000156194	PPEF2	4:76781019-76823724	NOTEST	0	0.00355712	inf	0	1	1
ENSG00000156206	ENSG00000156206	C15orf26	15:81299373-81441516	NOTEST	0.213195	0.547681	1.36116	0	1	1
ENSG00000156218	ENSG00000156218	ADAMTSL3	15:84322837-84708594	NOTEST	0.140075	0.496819	1.82652	0	1	1
ENSG00000156222	ENSG00000156222	SLC28A1	15:85427884-85518876	NOTEST	0.0496002	0.0757355	0.610626	0	1	1
ENSG00000156234	ENSG00000156234	CXCL13	4:78432906-78532988	NOTEST	0.0261932	0.0111879	-1.22726	0	1	1
ENSG00000156265	ENSG00000156265	MAP3K7CL	21:30449791-30548210	NOTEST	0.238584	0.303683	0.348067	0	1	1
ENSG00000156269	ENSG00000156269	NAA11	4:79892901-80247204	NOTEST	0.0662577	0.15689	1.24359	0	1	1
ENSG00000156282	ENSG00000156282	CLDN17	21:31538240-31538971	NOTEST	0	0	0	0	1	1
ENSG00000156284	ENSG00000156284	CLDN8	21:31586323-31588391	NOTEST	0	0.00706671	inf	0	1	1
ENSG00000156299	ENSG00000156299	TIAM1	21:32490733-32932800	NOTEST	0.410437	0.407631	-0.00989731	0	1	1
ENSG00000156395	ENSG00000156395	SORCS3	10:106400858-107024993	NOTEST	0	0.00995785	inf	0	1	1
ENSG00000156413	ENSG00000156413	FUT6	19:5830620-5839742	NOTEST	0	0	0	0	1	1
ENSG00000156427	ENSG00000156427	FGF18	5:170846659-170884627	NOTEST	0.0311867	0.0549438	0.817026	0	1	1
ENSG00000156463	ENSG00000156463	SH3RF2	5:145316141-145461354	NOTEST	0	0.0695831	inf	0	1	1
ENSG00000156466	ENSG00000156466	GDF6	8:97154561-97173020	NOTEST	0	0	0	0	1	1
ENSG00000156486	ENSG00000156486	KCNS2	8:99413630-99955055	NOTEST	0.00999401	0.00641379	-0.639886	0	1	1
ENSG00000156564	ENSG00000156564	LRFN2	6:40359324-40555204	NOTEST	0	0	0	0	1	1
ENSG00000156574	ENSG00000156574	NODAL	10:72192070-72207707	NOTEST	0.0346254	0.00698871	-2.30873	0	1	1
ENSG00000156575	ENSG00000156575	PRG3	11:57144241-57148623	NOTEST	0	0	0	0	1	1
ENSG00000156687	ENSG00000156687	UNC5D	8:35092974-35654068	NOTEST	0	0.00412775	inf	0	1	1
ENSG00000156689	ENSG00000156689	GLYATL2	11:58601541-58671688	NOTEST	0.0112748	0.0354178	1.65138	0	1	1
ENSG00000156711	ENSG00000156711	MAPK13	6:36095585-36107842	NOTEST	0.262822	0.113828	-1.20723	0	1	1
ENSG00000156738	ENSG00000156738	MS4A1	11:60223224-60238233	NOTEST	0.0420704	0.0870823	1.04957	0	1	1
ENSG00000156750	ENSG00000156750	AQP7P3	9:42845767-42876505	NOTEST	0.0327642	0.014355	-1.19057	0	1	1
ENSG00000156755	ENSG00000156755	IGKV1OR-2	9:69777098-69777953	NOTEST	0	0	0	0	1	1
ENSG00000156886	ENSG00000156886	ITGAD	16:31404632-31437826	NOTEST	0	0.0145757	inf	0	1	1
ENSG00000156920	ENSG00000156920	GPR112	X:135383121-135519215	NOTEST	0	0	0	0	1	1
ENSG00000156925	ENSG00000156925	ZIC3	X:136648300-136659850	NOTEST	0	0	0	0	1	1

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ENSG00000156968	ENSG00000156968	MPV17L	16:15489610-15737023	NOTEST	0	0.0163575	inf	0	1	1
ENSG00000157005	ENSG00000157005	SST	3:187386693-187388187	NOTEST	0	0	0	0	1	1
ENSG00000157017	ENSG00000157017	GHRL	3:10289706-10362862	NOTEST	0.0366841	0.0166643	-1.13839	0	1	1
ENSG00000157021	ENSG00000157021	FAM92A1P1	15:41455359-41456572	NOTEST	0.412601	0.322108	-0.357205	0	1	1
ENSG00000157060	ENSG00000157060	SHCBP1L	1:182868999-182922660	NOTEST	0	0	0	0	1	1
ENSG00000157064	ENSG00000157064	NMNAT2	1:183217371-183387737	NOTEST	0.200106	0.12481	-0.681029	0	1	1
ENSG00000157087	ENSG00000157087	ATP2B2	3:10365706-10749716	NOTEST	0.00493983	0	#NAME?	0	1	1
ENSG00000157093	ENSG00000157093	LYZL4	3:42438569-42452092	NOTEST	0	0	0	0	1	1
ENSG00000157103	ENSG00000157103	SLC6A1	3:11034409-11080933	NOTEST	0	0.00266342	inf	0	1	1
ENSG00000157119	ENSG00000157119	KLHL40	3:42727010-42734036	NOTEST	0	0.0152581	inf	0	1	1
ENSG00000157131	ENSG00000157131	C8A	1:57320478-57383894	NOTEST	0	0	0	0	1	1
ENSG00000157150	ENSG00000157150	TIMP4	3:12045875-12232900	NOTEST	0	0	0	0	1	1
ENSG00000157152	ENSG00000157152	SYN2	3:12045875-12232900	NOTEST	0	0	0	0	1	1
ENSG00000157168	ENSG00000157168	NRG1	8:31496901-32622548	NOTEST	0	0	0	0	1	1
ENSG00000157211	ENSG00000157211	CDCP2	1:54598746-54879152	NOTEST	0	0	0	0	1	1
ENSG00000157219	ENSG00000157219	HTR5A	7:154858776-154877459	NOTEST	0	0.00420912	inf	0	1	1
ENSG00000157303	ENSG00000157303	SUSD3	9:95820988-95847420	NOTEST	0.221788	0.294327	0.40824	0	1	1
ENSG00000157315	ENSG00000157315	TMED6	16:69139466-69442474	NOTEST	0.114781	0.0423682	-1.43783	0	1	1
ENSG00000157322	ENSG00000157322	CLEC18A	16:69984809-69998141	NOTEST	0.0157885	0	#NAME?	0	1	1
ENSG00000157330	ENSG00000157330	C1orf158	1:12806162-12823847	NOTEST	0	0	0	0	1	1
ENSG00000157335	ENSG00000157335	CLEC18C	16:70147528-70221264	NOTEST	0	0	0	0	1	1
ENSG00000157343	ENSG00000157343	ARMC12	6:35704808-35716856	NOTEST	0.0970786	0.126674	0.383894	0	1	1
ENSG00000157358	ENSG00000157358	PRAMEF15	1:13641972-13648988	NOTEST	0	0	0	0	1	1
ENSG00000157368	ENSG00000157368	IL34	16:70613797-70694585	NOTEST	0.0712576	0.0956954	0.425406	0	1	1
ENSG00000157388	ENSG00000157388	CACNA1D	3:53528682-53880417	NOTEST	0.41535	0.445858	0.102257	0	1	1
ENSG00000157399	ENSG00000157399	ARSE	X:2852698-2886286	NOTEST	0.533178	0.517828	-0.0421448	0	1	1
ENSG00000157423	ENSG00000157423	HYDIN	16:70841280-71264625	NOTEST	0.100765	0.0651671	-0.628785	0	1	1
ENSG00000157429	ENSG00000157429	ZNF19	16:71481499-71598992	NOTEST	0.498933	0.492903	-0.0175407	0	1	1
ENSG00000157445	ENSG00000157445	CACNA2D3	3:54156573-55108584	NOTEST	0	0	0	0	1	1
ENSG00000157502	ENSG00000157502	MUM1L1	X:105412297-105452949	NOTEST	0.447951	0.425925	-0.0727442	0	1	1
ENSG00000157542	ENSG00000157542	KCNJ6	21:38979677-39288749	NOTEST	0	0	0	0	1	1
ENSG00000157551	ENSG00000157551	KCNJ15	21:39493544-39679279	NOTEST	0	0.013512	inf	0	1	1
ENSG00000157554	ENSG00000157554	ERG	21:39751948-40033704	NOTEST	0	0	0	0	1	1
ENSG00000157557	ENSG00000157557	ETS2	21:40177230-40196879	NOTEST	0.0447561	0.00931523	-2.26442	0	1	1
ENSG00000157570	ENSG00000157570	TSPAN18	11:44740941-44972840	NOTEST	0	0	0	0	1	1
ENSG00000157578	ENSG00000157578	LCA5L	21:40752169-40817731	NOTEST	0.116617	0.0860727	-0.438145	0	1	1
ENSG00000157613	ENSG00000157613	CREB3L1	11:46299211-46342972	NOTEST	0.0180451	0.106553	2.56189	0	1	1
ENSG00000157653	ENSG00000157653	C9orf43	9:116169514-116191964	NOTEST	0.331512	0.455423	0.458147	0	1	1
ENSG00000157703	ENSG00000157703	SVOPL	7:138279029-138386097	NOTEST	0	0	0	0	1	1
ENSG00000157734	ENSG00000157734	SNX22	15:64443913-64455404	NOTEST	0.338465	0.458074	0.436576	0	1	1
ENSG00000157765	ENSG00000157765	SLC34A2	4:25656922-25680370	NOTEST	0.00375867	0	#NAME?	0	1	1
ENSG00000157766	ENSG00000157766	ACAN	15:89346673-89418585	NOTEST	0.0153481	0.0772281	2.33107	0	1	1
ENSG00000157782	ENSG00000157782	CABP1	12:121067907-121105127	NOTEST	0.15531	0.148759	-0.0621742	0	1	1
ENSG00000157828	ENSG00000157828	RPS4Y2	Y:22918049-22942918	NOTEST	0	0	0	0	1	1
ENSG00000157851	ENSG00000157851	DPYSL5	2:27070614-27250064	NOTEST	0.0547136	0.100831	0.88197	0	1	1

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ENSG00000157856	ENSG00000157856	DRC1	2:26624783-26679579	NOTEST	0.0179907	0.0154292	-0.221591	0	1	1
ENSG00000157884	ENSG00000157884	CIB4	2:26804069-26864236	NOTEST	0	0	0	0	1	1
ENSG00000157890	ENSG00000157890	MEGF11	15:66187416-66546085	NOTEST	0.00533123	0.0123071	1.20695	0	1	1
ENSG00000157950	ENSG00000157950	SSX2B	X:52780317-52790617	NOTEST	0	0	0	0	1	1
ENSG00000157965	ENSG00000157965	SSX8	X:52651984-52662998	NOTEST	0.0189449	0	#NAME?	0	1	1
ENSG00000158014	ENSG00000158014	SLC30A2	1:26363742-26372624	NOTEST	0.223839	0.219979	-0.0250959	0	1	1
ENSG00000158023	ENSG00000158023	WDR66	12:122326636-122441833	NOTEST	0.119289	0.158591	0.410857	0	1	1
ENSG00000158055	ENSG00000158055	GRHL3	1:24634045-24799466	NOTEST	0	0.00437537	inf	0	1	1
ENSG00000158077	ENSG00000158077	NLRP14	11:7041676-7092539	NOTEST	0	0	0	0	1	1
ENSG00000158089	ENSG00000158089	GALNT14	2:31133332-31378068	NOTEST	0	0	0	0	1	1
ENSG00000158104	ENSG00000158104	HPD	12:122277432-122301502	NOTEST	0.0312733	0.016742	-0.901458	0	1	1
ENSG00000158113	ENSG00000158113	LRRC43	12:122652284-122688018	NOTEST	0.421669	0.568699	0.431553	0	1	1
ENSG00000158125	ENSG00000158125	XDH	2:31557186-31637581	NOTEST	0.00754722	0.00397915	-0.923487	0	1	1
ENSG00000158220	ENSG00000158220	ESYT3	3:138153427-138200528	NOTEST	0.130489	0.407721	1.64366	0	1	1
ENSG00000158258	ENSG00000158258	CLSTN2	3:139654026-140296239	NOTEST	0.00105838	0.00469154	2.14821	0	1	1
ENSG00000158270	ENSG00000158270	COLEC12	18:319360-500722	NOTEST	0.0141308	0.0376011	1.41193	0	1	1
ENSG00000158315	ENSG00000158315	RHBDL2	1:39325671-39407471	NOTEST	0.0165222	0.0648411	1.9725	0	1	1
ENSG00000158428	ENSG00000158428	C2orf62	2:219135114-219232822	NOTEST	0.0157308	0	#NAME?	0	1	1
ENSG00000158445	ENSG00000158445	KCNB1	20:47980413-48099184	NOTEST	0.00356268	0.00267505	-0.413399	0	1	1
ENSG00000158473	ENSG00000158473	CD1D	1:158149736-158154686	NOTEST	0.0930848	0.119475	0.360092	0	1	1
ENSG00000158477	ENSG00000158477	CD1A	1:158223926-158228059	NOTEST	0	0	0	0	1	1
ENSG00000158481	ENSG00000158481	CD1C	1:158259575-158263420	NOTEST	0	0	0	0	1	1
ENSG00000158482	ENSG00000158482	SNX29P1	16:21391312-21403412	NOTEST	0.0909514	0.13953	0.617408	0	1	1
ENSG00000158485	ENSG00000158485	CD1B	1:158297740-158301321	NOTEST	0	0	0	0	1	1
ENSG00000158486	ENSG00000158486	DNAH3	16:20944432-21191937	NOTEST	0.00739314	0.00565191	-0.38745	0	1	1
ENSG00000158488	ENSG00000158488	CD1E	1:158323253-158327343	NOTEST	0	0	0	0	1	1
ENSG00000158497	ENSG00000158497	HMHB1	5:142985192-143208337	NOTEST	0	0	0	0	1	1
ENSG00000158517	ENSG00000158517	NCF1	7:74071993-74306731	NOTEST	0	0.0260148	inf	0	1	1
ENSG00000158525	ENSG00000158525	CPA5	7:129984629-130008571	NOTEST	0	0	0	0	1	1
ENSG00000158528	ENSG00000158528	PPP1R9A	7:94536513-94925727	NOTEST	0.318068	0.436259	0.45585	0	1	1
ENSG00000158553	ENSG00000158553	POM121L2	6:27253681-27279949	NOTEST	0.00977758	0	#NAME?	0	1	1
ENSG00000158571	ENSG00000158571	PFKFB1	X:54959393-55024967	NOTEST	0.0398947	0.085713	1.10332	0	1	1
ENSG00000158578	ENSG00000158578	ALAS2	X:55026789-55057497	NOTEST	0.0166039	0.0146576	-0.179868	0	1	1
ENSG00000158691	ENSG00000158691	ZSCAN12	6:28346731-28367511	NOTEST	0.085365	0.0684403	-0.3188	0	1	1
ENSG00000158714	ENSG00000158714	SLAMF8	1:159796539-159869953	NOTEST	0.146837	0.169779	0.209447	0	1	1
ENSG00000158731	ENSG00000158731	OR10J6P	1:159568087-159569017	NOTEST	0	0	0	0	1	1
ENSG00000158748	ENSG00000158748	HTR6	1:19991779-20006055	NOTEST	0	0	0	0	1	1
ENSG00000158786	ENSG00000158786	PLA2G2F	1:20465818-20476879	NOTEST	0	0	0	0	1	1
ENSG00000158815	ENSG00000158815	FGF17	8:21899908-21906320	NOTEST	0.0175024	0.0194074	0.149055	0	1	1
ENSG00000158816	ENSG00000158816	VWA5B1	1:20617411-20681387	NOTEST	0	0	0	0	1	1
ENSG00000158825	ENSG00000158825	CDA	1:20915440-20945401	NOTEST	0.0922456	0.0354954	-1.37785	0	1	1
ENSG00000158859	ENSG00000158859	ADAMTS4	1:161154097-161184185	NOTEST	0.0973832	0.0591816	-0.718525	0	1	1
ENSG00000158865	ENSG00000158865	SLC5A11	16:24857161-24922949	NOTEST	0.0153647	0	#NAME?	0	1	1
ENSG00000158874	ENSG00000158874	APOA2	1:161185023-161193421	NOTEST	0	0	0	0	1	1
ENSG00000158901	ENSG00000158901	WFDC8	20:44179791-44207965	NOTEST	0	0	0	0	1	1

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ENSG00000158955	ENSG00000158955	WNT9B	17:44910566-44964096	NOTEST	0	0	0	0	1	1
ENSG00000159123	ENSG00000159123	DMRTC1	X:72091858-72163653	NOTEST	0	0	0	0	1	1
ENSG00000159166	ENSG00000159166	LAD1	1:201328135-201368736	NOTEST	0.0261311	0.0237458	-0.138093	0	1	1
ENSG00000159173	ENSG00000159173	TNNI1	1:201373624-201398994	NOTEST	0	0	0	0	1	1
ENSG00000159182	ENSG00000159182	PRAC1	17:46799083-46799884	NOTEST	0	0	0	0	1	1
ENSG00000159186	ENSG00000159186	AC007383.6	2:207100959-207101595	NOTEST	0	0	0	0	1	1
ENSG00000159189	ENSG00000159189	C1QC	1:22970122-22974603	NOTEST	0	0	0	0	1	1
ENSG00000159197	ENSG00000159197	KCNE2	21:35736322-35747647	NOTEST	0.0878347	0.120122	0.451635	0	1	1
ENSG00000159212	ENSG00000159212	CLIC6	21:36041687-36090525	NOTEST	0.023707	0.140543	2.56763	0	1	1
ENSG00000159217	ENSG00000159217	IGF2BP1	17:47072627-47133012	NOTEST	0.111407	0.131631	0.24066	0	1	1
ENSG00000159224	ENSG00000159224	GIP	17:47035915-47045958	NOTEST	0	0	0	0	1	1
ENSG00000159239	ENSG00000159239	C2orf81	2:74641303-74648718	NOTEST	0.496492	0.331067	-0.584647	0	1	1
ENSG00000159248	ENSG00000159248	GJD2	15:35043232-35047166	NOTEST	0	0	0	0	1	1
ENSG00000159251	ENSG00000159251	ACTC1	15:35047284-35105124	NOTEST	0	0	0	0	1	1
ENSG00000159263	ENSG00000159263	SIM2	21:38071072-38122218	NOTEST	0.101191	0.20731	1.0347	0	1	1
ENSG00000159289	ENSG00000159289	GOLGA6A	15:74362197-74374891	NOTEST	0.00494199	0	#NAME?	0	1	1
ENSG00000159307	ENSG00000159307	SCUBE1	22:43593288-43739394	NOTEST	0.0304457	0.0329661	0.114746	0	1	1
ENSG00000159337	ENSG00000159337	PLA2G4D	15:42359206-42386752	NOTEST	0	0	0	0	1	1
ENSG00000159339	ENSG00000159339	PADI4	1:17634689-17690499	NOTEST	0	0	0	0	1	1
ENSG00000159374	ENSG00000159374	M1AP	2:74785009-74875465	NOTEST	0.233339	0.248243	0.0893233	0	1	1
ENSG00000159398	ENSG00000159398	CES5A	16:55880065-55989943	NOTEST	0.0682635	0.00587083	-3.53948	0	1	1
ENSG00000159409	ENSG00000159409	CELF3	1:151673501-151702281	NOTEST	0.0287693	0.0810707	1.49465	0	1	1
ENSG00000159450	ENSG00000159450	TCHH	1:152078792-152086556	NOTEST	0.00220691	0.00309611	0.488433	0	1	1
ENSG00000159455	ENSG00000159455	LCE2B	1:152647770-152659877	NOTEST	0	0	0	0	1	1
ENSG00000159495	ENSG00000159495	TGM7	15:43568477-43594970	NOTEST	0	0	0	0	1	1
ENSG00000159496	ENSG00000159496	RGL4	22:23950638-24059543	NOTEST	0.0770741	0.13006	0.754863	0	1	1
ENSG00000159516	ENSG00000159516	SPRR2G	1:153122057-153123345	NOTEST	0	0	0	0	1	1
ENSG00000159527	ENSG00000159527	PGLYRP3	1:153270337-153283194	NOTEST	0	0	0	0	1	1
ENSG00000159588	ENSG00000159588	CCDC17	1:46085715-46089729	NOTEST	0.214476	0.0444349	-2.27105	0	1	1
ENSG00000159618	ENSG00000159618	GPR114	16:57576332-57625593	NOTEST	0.00792018	0	#NAME?	0	1	1
ENSG00000159625	ENSG00000159625	CCDC135	16:57702098-57765717	NOTEST	0	0	0	0	1	1
ENSG00000159640	ENSG00000159640	ACE	17:61554421-61599209	NOTEST	0	0.00468382	inf	0	1	1
ENSG00000159648	ENSG00000159648	TEPP	16:58010338-58022020	NOTEST	0	0.00527114	inf	0	1	1
ENSG00000159650	ENSG00000159650	UROC1	3:126200123-126236616	NOTEST	0.277458	0.254376	-0.12531	0	1	1
ENSG00000159708	ENSG00000159708	LRRC36	16:67360700-67419106	NOTEST	0.47026	0.567631	0.271494	0	1	1
ENSG00000159712	ENSG00000159712	ANKRD18CP	9:99918851-100140806	NOTEST	0.0148423	0	#NAME?	0	1	1
ENSG00000159723	ENSG00000159723	AGRP	16:67515216-67521153	NOTEST	0	0.0604677	inf	0	1	1
ENSG00000159753	ENSG00000159753	RLTPR	16:67678821-67694713	NOTEST	0.172804	0.168876	-0.0331725	0	1	1
ENSG00000159763	ENSG00000159763	PIP	7:142829169-142836839	NOTEST	0	0	0	0	1	1
ENSG00000159784	ENSG00000159784	FAM131B	7:143050492-143059863	NOTEST	0.0134255	0	#NAME?	0	1	1
ENSG00000159860	ENSG00000159860	FAM115D	7:143318042-143534026	NOTEST	0.0238833	0.00976316	-1.29058	0	1	1
ENSG00000159871	ENSG00000159871	LYPD5	19:44300080-44331358	NOTEST	0	0.0670184	inf	0	1	1
ENSG00000159904	ENSG00000159904	ZNF890P	7:5160869-5184177	NOTEST	0.425923	0.227181	-0.906751	0	1	1
ENSG00000159915	ENSG00000159915	ZNF233	19:44711699-44809199	NOTEST	0.132927	0.0919814	-0.531224	0	1	1
ENSG00000159958	ENSG00000159958	TNFRSF13C	22:42321044-42322822	NOTEST	0.0556236	0.0277399	-1.00373	0	1	1

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ENSG00000160013	ENSG00000160013	PTGIR	19:47123724-47128375	NOTEST	0.00800602	0	#NAME?	0	1	1
ENSG00000160097	ENSG00000160097	FNDC5	1:33327868-33338083	NOTEST	0.0989214	0.0633298	-0.643398	0	1	1
ENSG00000160111	ENSG00000160111	CPAMD8	19:17003757-17137625	NOTEST	0.265652	0.181491	-0.549643	0	1	1
ENSG00000160161	ENSG00000160161	CILP2	19:19649056-19657468	NOTEST	0.111204	0.0598232	-0.894437	0	1	1
ENSG00000160179	ENSG00000160179	ABCG1	21:43619798-43717354	NOTEST	0.370376	0.617946	0.738492	0	1	1
ENSG00000160180	ENSG00000160180	TFF3	21:43731776-43735761	NOTEST	0.281282	0.407841	0.535991	0	1	1
ENSG00000160181	ENSG00000160181	TFF2	21:43766465-43771237	NOTEST	0	0	0	0	1	1
ENSG00000160182	ENSG00000160182	TFF1	21:43782390-43786703	NOTEST	0	0	0	0	1	1
ENSG00000160183	ENSG00000160183	TMPRSS3	21:43791998-43816955	NOTEST	0.114207	0	#NAME?	0	1	1
ENSG00000160185	ENSG00000160185	UBASH3A	21:43824007-43867791	NOTEST	0	0	0	0	1	1
ENSG00000160188	ENSG00000160188	RSPH1	21:43892595-44001550	NOTEST	0.124321	0.0136696	-3.18502	0	1	1
ENSG00000160202	ENSG00000160202	CRYAA	21:44589117-44592915	NOTEST	0	0	0	0	1	1
ENSG00000160219	ENSG00000160219	GAB3	X:153903528-153979858	NOTEST	0.0415786	0.060674	0.545237	0	1	1
ENSG00000160223	ENSG00000160223	ICOSLG	21:45642873-45660849	NOTEST	0.0938032	0.152551	0.701578	0	1	1
ENSG00000160224	ENSG00000160224	AIRE	21:45705720-45718531	NOTEST	0	0	0	0	1	1
ENSG00000160229	ENSG00000160229	ZNF66	19:20959109-20991922	NOTEST	0.043962	0.0833981	0.923756	0	1	1
ENSG00000160233	ENSG00000160233	LRRC3	21:45875368-45878739	NOTEST	0.262943	0.397469	0.596093	0	1	1
ENSG00000160255	ENSG00000160255	ITGB2	21:46305867-46351904	NOTEST	0.19719	0.165905	-0.249235	0	1	1
ENSG00000160282	ENSG00000160282	FTCD	21:47556175-47575481	NOTEST	0.0395915	0.0734968	0.89249	0	1	1
ENSG00000160318	ENSG00000160318	CLDND2	19:51848422-51872257	NOTEST	0.37795	0.228983	-0.722951	0	1	1
ENSG00000160321	ENSG00000160321	ZNF208	19:22115759-22193751	NOTEST	0.00777311	0.00272759	-1.51086	0	1	1
ENSG00000160339	ENSG00000160339	FCN2	9:137772653-137779924	NOTEST	0	0	0	0	1	1
ENSG00000160349	ENSG00000160349	LCN1	9:138413283-138418378	NOTEST	0	0	0	0	1	1
ENSG00000160396	ENSG00000160396	HIPK4	19:40825442-40896094	NOTEST	0.013024	0	#NAME?	0	1	1
ENSG00000160460	ENSG00000160460	SPTBN4	19:40972147-41082370	NOTEST	0.576419	0.626574	0.120367	0	1	1
ENSG00000160471	ENSG00000160471	COX6B2	19:55860673-55874628	NOTEST	0.0220276	0.00699753	-1.6544	0	1	1
ENSG00000160472	ENSG00000160472	TMEM190	19:55888203-55889612	NOTEST	0	0	0	0	1	1
ENSG00000160505	ENSG00000160505	NLRP4	19:56296769-56393220	NOTEST	0	0	0	0	1	1
ENSG00000160539	ENSG00000160539	PPAPDC3	9:134165080-134184649	NOTEST	0.130569	0.184476	0.498616	0	1	1
ENSG00000160593	ENSG00000160593	AMICA1	11:118064454-118095809	NOTEST	0.0467687	0.00863298	-2.43761	0	1	1
ENSG00000160654	ENSG00000160654	CD3G	11:118215058-118225876	NOTEST	0	0	0	0	1	1
ENSG00000160683	ENSG00000160683	CXCR5	11:118754474-118829269	NOTEST	0.169736	0.00750051	-4.50016	0	1	1
ENSG00000160716	ENSG00000160716	CHRNB2	1:154540256-154552502	NOTEST	0.190084	0.191529	0.0109238	0	1	1
ENSG00000160781	ENSG00000160781	PAQR6	1:156213205-156217881	NOTEST	0.351843	0.22409	-0.650857	0	1	1
ENSG00000160791	ENSG00000160791	CCR5	3:46406445-46448550	NOTEST	0	0	0	0	1	1
ENSG00000160801	ENSG00000160801	PTH1R	3:46899361-46945287	NOTEST	0	0.0187384	inf	0	1	1
ENSG00000160808	ENSG00000160808	MYL3	3:46899361-46945287	NOTEST	0	0.0153381	inf	0	1	1
ENSG00000160838	ENSG00000160838	LRRC71	1:156890441-156902886	NOTEST	0.015047	0	#NAME?	0	1	1
ENSG00000160844	ENSG00000160844	GATS	7:99775185-99869855	NOTEST	0	0	0	0	1	1
ENSG00000160856	ENSG00000160856	FCRL3	1:157644110-157670647	NOTEST	0	0.0182539	inf	0	1	1
ENSG00000160868	ENSG00000160868	CYP3A4	7:99354603-99381888	NOTEST	0	0.00582108	inf	0	1	1
ENSG00000160870	ENSG00000160870	CYP3A7	7:99302659-99332819	NOTEST	0.104262	0.0470598	-1.14765	0	1	1
ENSG00000160882	ENSG00000160882	CYP11B1	8:143915553-143999259	NOTEST	0	0	0	0	1	1
ENSG00000160883	ENSG00000160883	HK3	5:176237477-176326333	NOTEST	0	0.00635095	inf	0	1	1

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ENSG00000160886	ENSG00000160886	LY6K	8:143781528-143808391	NOTEST	0.0466359	0.103829	1.1547	0	1	1
ENSG00000160951	ENSG00000160951	PTGER1	19:14583277-14586174	NOTEST	0.0356442	0.0990213	1.47407	0	1	1
ENSG00000160963	ENSG00000160963	COL26A1	7:101006100-101202304	NOTEST	0.417008	0.332513	-0.326662	0	1	1
ENSG00000160973	ENSG00000160973	FOXH1	8:145691425-145701718	NOTEST	0.0457938	0.0144813	-1.66096	0	1	1
ENSG00000160994	ENSG00000160994	CCDC105	19:15060845-15134081	NOTEST	0	0	0	0	1	1
ENSG00000161031	ENSG00000161031	PGLYRP2	19:15579455-15609767	NOTEST	0	0	0	0	1	1
ENSG00000161055	ENSG00000161055	SCGB3A1	5:180017102-180018540	NOTEST	0	0.0942392	inf	0	1	1
ENSG00000161082	ENSG00000161082	CELF5	19:3224700-3303001	NOTEST	0.0969838	0.0079487	-3.60895	0	1	1
ENSG00000161103	ENSG00000161103	AC008132.13	22:18834323-18848562	NOTEST	0	0.00200634	inf	0	1	1
ENSG00000161132	ENSG00000161132	XXbac-B444P24.10	22:20287282-20300739	NOTEST	0	0.0305669	inf	0	1	1
ENSG00000161133	ENSG00000161133	USP41	22:20692437-20745048	NOTEST	0.0362421	0.194648	2.42513	0	1	1
ENSG00000161180	ENSG00000161180	CCDC116	22:21987004-21991616	NOTEST	0.0299171	0.0575097	0.942835	0	1	1
ENSG00000161270	ENSG00000161270	NPHS1	19:36316865-36370693	NOTEST	0.017938	0.0370206	1.04531	0	1	1
ENSG00000161281	ENSG00000161281	COX7A1	19:36641823-36643771	NOTEST	0	0.0177481	inf	0	1	1
ENSG00000161328	ENSG00000161328	LRRC56	11:537526-564021	NOTEST	0.50614	0.531625	0.0708726	0	1	1
ENSG00000161405	ENSG00000161405	IKZF3	17:37921197-38020441	NOTEST	0.164088	0.094691	-0.793175	0	1	1
ENSG00000161509	ENSG00000161509	GRIN2C	17:72838161-72857627	NOTEST	0.22258	0.298984	0.425746	0	1	1
ENSG00000161570	ENSG00000161570	CCL5	17:34195970-34212867	NOTEST	0.324032	0.324116	0.00037559	0	1	1
ENSG00000161572	ENSG00000161572	LYZL6	17:34261521-34270703	NOTEST	0	0	0	0	1	1
ENSG00000161573	ENSG00000161573	CCL16	17:34303528-34308532	NOTEST	0	0	0	0	1	1
ENSG00000161574	ENSG00000161574	CCL15-CCL14	17:34310326-34338658	NOTEST	0	1.05E-06	inf	0	1	1
ENSG00000161583	ENSG00000161583	TBC1D3G	17:34580901-34808104	NOTEST	0.20744	0.049096	-2.07902	0	1	1
ENSG00000161594	ENSG00000161594	KLHL10	17:39981334-40004636	NOTEST	0.0740502	0.0228259	-1.69783	0	1	1
ENSG00000161609	ENSG00000161609	CCDC155	19:49891474-49921251	NOTEST	0.212132	0.135233	-0.64952	0	1	1
ENSG00000161610	ENSG00000161610	HCRT	17:40336077-40337470	NOTEST	0	0	0	0	1	1
ENSG00000161634	ENSG00000161634	DCD	12:55038374-55042277	NOTEST	0	0	0	0	1	1
ENSG00000161640	ENSG00000161640	SIGLEC11	19:50392910-50464429	NOTEST	0	0	0	0	1	1
ENSG00000161643	ENSG00000161643	SIGLEC16	19:50472856-50479071	NOTEST	0	0.00939203	inf	0	1	1
ENSG00000161649	ENSG00000161649	CD300LG	17:41924515-41940997	NOTEST	0.0192615	0.0599008	1.63686	0	1	1
ENSG00000161652	ENSG00000161652	IZUMO2	19:50655804-50666452	NOTEST	0	0	0	0	1	1
ENSG00000161664	ENSG00000161664	ASB16	17:42247814-42264085	NOTEST	0.388138	0.357878	-0.117103	0	1	1
ENSG00000161798	ENSG00000161798	AQP5	12:50344523-50359464	NOTEST	0.158173	0.220619	0.480054	0	1	1
ENSG00000161807	ENSG00000161807	OR7G1	19:9225273-9226439	NOTEST	0	0	0	0	1	1
ENSG00000161849	ENSG00000161849	KRT84	12:52771595-52800139	NOTEST	0	0	0	0	1	1
ENSG00000161850	ENSG00000161850	KRT82	12:52771595-52800139	NOTEST	0	0	0	0	1	1
ENSG00000161905	ENSG00000161905	ALOX15	17:4534196-4545589	NOTEST	0	0.0409727	inf	0	1	1
ENSG00000161911	ENSG00000161911	TREML1	6:41117079-41122075	NOTEST	0	0	0	0	1	1
ENSG00000161929	ENSG00000161929	SCIMP	17:5095378-5151364	NOTEST	0.0211767	0.0741889	1.80872	0	1	1
ENSG00000161939	ENSG00000161939	RNASEK-C17orf49	17:6757179-6922978	NOTEST	0.104937	0.199808	0.929086	0	1	1
ENSG00000161940	ENSG00000161940	BCL6B	17:6926338-6933609	NOTEST	0.100955	0.0163877	-2.62303	0	1	1
ENSG00000161944	ENSG00000161944	ASGR2	17:7004640-7019019	NOTEST	0	0.0462607	inf	0	1	1
ENSG00000161973	ENSG00000161973	CCDC42	17:8633251-8648537	NOTEST	0	0	0	0	1	1
ENSG00000161992	ENSG00000161992	C16orf11	16:610421-615528	NOTEST	0.00726213	0.0175054	1.26934	0	1	1
ENSG00000162006	ENSG00000162006	MSLNL	16:819427-833370	NOTEST	0	0	0	0	1	1

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ENSG00000162009	ENSG00000162009	SSTR5	16:1114092-1131454	NOTEST	0	0	0	0	1	1
ENSG00000162039	ENSG00000162039	MEIOB	16:1845620-1934295	NOTEST	0.0100859	0.00757826	-0.412394	0	1	1
ENSG00000162040	ENSG00000162040	HS3ST6	16:1961463-1968441	NOTEST	0	0	0	0	1	1
ENSG00000162068	ENSG00000162068	NTN3	16:2521499-2524146	NOTEST	0.0572773	0.0772912	0.432341	0	1	1
ENSG00000162069	ENSG00000162069	CCDC64B	16:3072620-3089134	NOTEST	0.313573	0.126814	-1.30609	0	1	1
ENSG00000162078	ENSG00000162078	ZG16B	16:2880169-2888967	NOTEST	0	0.0721287	inf	0	1	1
ENSG00000162105	ENSG00000162105	SHANK2	11:70313960-70963623	NOTEST	0.0143369	0.00538035	-1.41396	0	1	1
ENSG00000162148	ENSG00000162148	PPP1R32	11:61170120-61258403	NOTEST	0	0.0395168	inf	0	1	1
ENSG00000162188	ENSG00000162188	GNG3	11:62457746-62494856	NOTEST	0.0628172	0.0457153	-0.458483	0	1	1
ENSG00000162344	ENSG00000162344	FGF19	11:69512999-69519410	NOTEST	0	0.00458278	inf	0	1	1
ENSG00000162365	ENSG00000162365	CYP4A22	1:47533159-47646011	NOTEST	0	0	0	0	1	1
ENSG00000162366	ENSG00000162366	PDZK1IP1	1:47649264-47656716	NOTEST	0	0	0	0	1	1
ENSG00000162367	ENSG00000162367	TAL1	1:47681961-47697892	NOTEST	0	0.00642376	inf	0	1	1
ENSG00000162373	ENSG00000162373	BEND5	1:48998526-50489585	NOTEST	0.0965012	0.234571	1.2814	0	1	1
ENSG00000162374	ENSG00000162374	ELAVL4	1:50513685-50669458	NOTEST	0.150923	0.084283	-0.840501	0	1	1
ENSG00000162383	ENSG00000162383	SLC1A7	1:53552854-53608289	NOTEST	0	0.00534395	inf	0	1	1
ENSG00000162390	ENSG00000162390	ACOT11	1:55007929-55104865	NOTEST	0.241931	0.376983	0.639903	0	1	1
ENSG00000162391	ENSG00000162391	FAM151A	1:55007929-55104865	NOTEST	0	0	0	0	1	1
ENSG00000162398	ENSG00000162398	C1orf177	1:55271735-55307925	NOTEST	0	0	0	0	1	1
ENSG00000162399	ENSG00000162399	BSND	1:55464605-55476556	NOTEST	0	0.00349479	inf	0	1	1
ENSG00000162409	ENSG00000162409	PRKAA2	1:57110994-57181008	NOTEST	0.0618756	0.0572829	-0.111265	0	1	1
ENSG00000162415	ENSG00000162415	ZSWIM5	1:45482070-45771881	NOTEST	0.549833	0.311789	-0.818421	0	1	1
ENSG00000162426	ENSG00000162426	SLC45A1	1:8377885-8404227	NOTEST	0.0265087	0.0146165	-0.858865	0	1	1
ENSG00000162438	ENSG00000162438	CTRC	1:15764934-15775737	NOTEST	0	0	0	0	1	1
ENSG00000162456	ENSG00000162456	KNCN	1:47004367-47082563	NOTEST	0	0	0	0	1	1
ENSG00000162458	ENSG00000162458	FBLIM1	1:16083101-16113089	NOTEST	0.0453889	0.141478	1.64016	0	1	1
ENSG00000162460	ENSG00000162460	TMEM82	1:16010826-16076391	NOTEST	0	0	0	0	1	1
ENSG00000162461	ENSG00000162461	SLC25A34	1:16010826-16076391	NOTEST	0.324404	0.384244	0.24423	0	1	1
ENSG00000162482	ENSG00000162482	AKR7A3	1:19609051-19615744	NOTEST	0.191849	0.18955	-0.0173881	0	1	1
ENSG00000162490	ENSG00000162490	DRAXIN	1:11751785-11785914	NOTEST	0.0194739	0.0173712	-0.164846	0	1	1
ENSG00000162493	ENSG00000162493	PDPN	1:13909959-13944452	NOTEST	0	0	0	0	1	1
ENSG00000162494	ENSG00000162494	LRRC38	1:13801444-13842765	NOTEST	0	0.0159986	inf	0	1	1
ENSG00000162510	ENSG00000162510	MATN1	1:31184123-31199674	NOTEST	0.0529365	0.109821	1.05282	0	1	1
ENSG00000162511	ENSG00000162511	LAPTM5	1:31205315-31230667	NOTEST	0	0.0300227	inf	0	1	1
ENSG00000162543	ENSG00000162543	UBXN10	1:20510734-20522541	NOTEST	0	0.00876264	inf	0	1	1
ENSG00000162545	ENSG00000162545	CAMK2N1	1:20808883-20812713	NOTEST	0.266907	0.341403	0.355141	0	1	1
ENSG00000162551	ENSG00000162551	ALPL	1:21835857-21904905	NOTEST	0.0552042	0.0578024	0.0663495	0	1	1
ENSG00000162571	ENSG00000162571	TTLL10	1:1108435-1133315	NOTEST	0	0	0	0	1	1
ENSG00000162592	ENSG00000162592	CCDC27	1:3668961-3688209	NOTEST	0	0	0	0	1	1
ENSG00000162594	ENSG00000162594	IL23R	1:67557847-67725662	NOTEST	0	0.013843	inf	0	1	1
ENSG00000162595	ENSG00000162595	DIRAS3	1:68167148-68698803	NOTEST	0	0.035816	inf	0	1	1
ENSG00000162598	ENSG00000162598	C1orf87	1:60452940-60539442	NOTEST	0	0	0	0	1	1
ENSG00000162614	ENSG00000162614	NEXN	1:78347032-78409580	NOTEST	0.196773	0.36342	0.885108	0	1	1
ENSG00000162618	ENSG00000162618	ELTD1	1:79355448-79472403	NOTEST	0	0	0	0	1	1
ENSG00000162620	ENSG00000162620	LRRIQ3	1:74491698-74663871	NOTEST	0.569143	0.429724	-0.405378	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000162621	ENSG00000162621	LRRC53	1:74663895-75010112	NOTEST	0	0	0	0	1	1
ENSG00000162630	ENSG00000162630	B3GALT2	1:193091146-193223031	NOTEST	0.0364383	0.0216135	-0.753521	0	1	1
ENSG00000162631	ENSG00000162631	NTNG1	1:107682628-108026080	NOTEST	0.368618	0.521878	0.501586	0	1	1
ENSG00000162641	ENSG00000162641	AKNAD1	1:109358519-109506111	NOTEST	0.0616671	0.132023	1.09822	0	1	1
ENSG00000162654	ENSG00000162654	GBP4	1:89646830-89664615	NOTEST	0.0248806	0	#NAME?	0	1	1
ENSG00000162669	ENSG00000162669	HFM1	1:91726322-91870426	NOTEST	0.387672	0.319433	-0.279323	0	1	1
ENSG00000162670	ENSG00000162670	BRINP3	1:190066791-190446759	NOTEST	0.186951	0.201473	0.107932	0	1	1
ENSG00000162676	ENSG00000162676	GFI1	1:92940318-92952433	NOTEST	0.0554911	0.044452	-0.320006	0	1	1
ENSG00000162685	ENSG00000162685	LSP1P3	5:28925706-28927696	NOTEST	0	0	0	0	1	1
ENSG00000162687	ENSG00000162687	KCNT2	1:196194908-196578355	NOTEST	0.0814572	0.0747691	-0.123601	0	1	1
ENSG00000162692	ENSG00000162692	VCAM1	1:101185297-101204601	NOTEST	0	0	0	0	1	1
ENSG00000162699	ENSG00000162699	DNAJA1P5	1:102268129-102462586	NOTEST	0	0	0	0	1	1
ENSG00000162711	ENSG00000162711	NLRP3	1:247579457-247612410	NOTEST	0	0.00443219	inf	0	1	1
ENSG00000162722	ENSG00000162722	TRIM58	1:248020500-248060449	NOTEST	0.147152	0.270451	0.878058	0	1	1
ENSG00000162727	ENSG00000162727	OR2M5	1:248308449-248309388	NOTEST	0	0	0	0	1	1
ENSG00000162728	ENSG00000162728	KCNJ9	1:160051359-160060353	NOTEST	0.0111407	0	#NAME?	0	1	1
ENSG00000162739	ENSG00000162739	SLAMF6	1:160454819-160493052	NOTEST	0	0	0	0	1	1
ENSG00000162747	ENSG00000162747	FCGR3B	1:161475219-161648444	NOTEST	0	0	0	0	1	1
ENSG00000162753	ENSG00000162753	SLC9C2	1:173469602-173639001	NOTEST	2.46E-05	1.21E-05	-1.01838	0	1	1
ENSG00000162761	ENSG00000162761	LMX1A	1:165171103-165325952	NOTEST	0	0	0	0	1	1
ENSG00000162763	ENSG00000162763	LRRC52	1:165446077-165551713	NOTEST	0	0.0298961	inf	0	1	1
ENSG00000162771	ENSG00000162771	FAM71A	1:212797625-212800120	NOTEST	0	0	0	0	1	1
ENSG00000162779	ENSG00000162779	AXDND1	1:179334854-179545087	NOTEST	0.207615	0.0239917	-3.1133	0	1	1
ENSG00000162782	ENSG00000162782	TDRD5	1:179560747-179660407	NOTEST	0.00442494	0.00654469	0.564668	0	1	1
ENSG00000162804	ENSG00000162804	SNED1	2:241938254-242041747	NOTEST	0.17699	0.452511	1.35429	0	1	1
ENSG00000162814	ENSG00000162814	SPATA17	1:217804665-218045038	NOTEST	0.397983	0.191278	-1.05703	0	1	1
ENSG00000162840	ENSG00000162840	MT2P1	4:69242040-69242226	NOTEST	0	0	0	0	1	1
ENSG00000162843	ENSG00000162843	WDR64	1:241695433-241965435	NOTEST	0.0175869	0	#NAME?	0	1	1
ENSG00000162873	ENSG00000162873	KLHDC8A	1:205305219-205326218	NOTEST	0.0268453	0	#NAME?	0	1	1
ENSG00000162877	ENSG00000162877	PM20D1	1:205797149-205819260	NOTEST	0	0	0	0	1	1
ENSG00000162881	ENSG00000162881	OXER1	2:42989641-42991401	NOTEST	0	0	0	0	1	1
ENSG00000162882	ENSG00000162882	HAAO	2:42994228-43019733	NOTEST	0	0	0	0	1	1
ENSG00000162888	ENSG00000162888	C1orf147	1:206643790-206671061	NOTEST	0.126776	0.129664	0.0325045	0	1	1
ENSG00000162891	ENSG00000162891	IL20	1:207038698-207042568	NOTEST	0.384741	0.611521	0.668515	0	1	1
ENSG00000162896	ENSG00000162896	PIGR	1:207101862-207119811	NOTEST	0.00361502	0.00871142	1.2689	0	1	1
ENSG00000162897	ENSG00000162897	FCAMR	1:207131309-207143970	NOTEST	0	0.00999516	inf	0	1	1
ENSG00000162931	ENSG00000162931	TRIM17	1:228595081-228604562	NOTEST	0.305315	0.489233	0.680223	0	1	1
ENSG00000162947	ENSG00000162947	AC007364.1	2:150426147-150715705	NOTEST	0	0	0	0	1	1
ENSG00000162949	ENSG00000162949	CAPN13	2:30945636-31043408	NOTEST	0	0	0	0	1	1
ENSG00000162951	ENSG00000162951	LRRTM1	2:79384131-80875905	NOTEST	0	0	0	0	1	1
ENSG00000162975	ENSG00000162975	KCNF1	2:11052062-11054350	NOTEST	0	0	0	0	1	1
ENSG00000162981	ENSG00000162981	FAM84A	2:14772809-14790933	NOTEST	0	0.00290004	inf	0	1	1
ENSG00000162989	ENSG00000162989	KCNJ3	2:155554810-155714863	NOTEST	0.0477213	0.118968	1.31786	0	1	1
ENSG00000162992	ENSG00000162992	NEUROD1	2:182401402-182545603	NOTEST	0	0	0	0	1	1
ENSG00000162997	ENSG00000162997	PRORSD1P	2:55509454-55511658	NOTEST	0.252735	0.362171	0.519046	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000163009	ENSG00000163009	C2orf48	2:10281508-10351851	NOTEST	0.158631	0.139068	-0.189884	0	1	1
ENSG00000163012	ENSG00000163012	ZSWIM2	2:187692561-187713935	NOTEST	0	0	0	0	1	1
ENSG00000163017	ENSG00000163017	ACTG2	2:74119440-74146992	NOTEST	0.0374119	0	#NAME?	0	1	1
ENSG00000163032	ENSG00000163032	VSNL1	2:17720392-17838285	NOTEST	0	0	0	0	1	1
ENSG00000163046	ENSG00000163046	ANKRD30BL	2:132905163-133015542	NOTEST	0	0	0	0	1	1
ENSG00000163053	ENSG00000163053	SLC16A14	2:230899697-230933715	NOTEST	0	0	0	0	1	1
ENSG00000163060	ENSG00000163060	TEKT4	2:95533230-95613086	NOTEST	0.011133	0	#NAME?	0	1	1
ENSG00000163064	ENSG00000163064	EN1	2:119599746-119605254	NOTEST	0.0429946	0.00456269	-3.2362	0	1	1
ENSG00000163072	ENSG00000163072	NOSTRIN	2:169312371-169769881	NOTEST	0.374308	0.269824	-0.472208	0	1	1
ENSG00000163075	ENSG00000163075	PCDP1	2:120302007-120419827	NOTEST	0	0	0	0	1	1
ENSG00000163081	ENSG00000163081	CCDC140	2:223064606-223169936	NOTEST	0.120919	0.100892	-0.261229	0	1	1
ENSG00000163082	ENSG00000163082	SGPP2	2:223289235-223425667	NOTEST	0.0366297	0.0574203	0.648548	0	1	1
ENSG00000163083	ENSG00000163083	INHBB	2:121103718-121109384	NOTEST	0.0137435	0	#NAME?	0	1	1
ENSG00000163092	ENSG00000163092	XIRP2	2:167744996-168116263	NOTEST	0	0.000952844	inf	0	1	1
ENSG00000163098	ENSG00000163098	BIRC8	19:53792855-53794875	NOTEST	0	0	0	0	1	1
ENSG00000163106	ENSG00000163106	HPGDS	4:95219685-95264027	NOTEST	0	0	0	0	1	1
ENSG00000163114	ENSG00000163114	PDHA2	4:96761238-96762625	NOTEST	0	0	0	0	1	1
ENSG00000163116	ENSG00000163116	STPG2	4:98105243-99064391	NOTEST	0.010028	0	#NAME?	0	1	1
ENSG00000163121	ENSG00000163121	NEURL3	2:97163382-97173846	NOTEST	0.287297	0.261945	-0.133279	0	1	1
ENSG00000163141	ENSG00000163141	BNIPL	1:151009045-151020076	NOTEST	0.181767	0.186508	0.0371436	0	1	1
ENSG00000163145	ENSG00000163145	C1QTNF7	4:15004297-15447790	NOTEST	0	0	0	0	1	1
ENSG00000163154	ENSG00000163154	TNFAIP8L2	1:151129104-151167797	NOTEST	0.100596	0.0218625	-2.20204	0	1	1
ENSG00000163157	ENSG00000163157	TMOD4	1:151129104-151167797	NOTEST	0.104078	0.0111596	-3.22131	0	1	1
ENSG00000163202	ENSG00000163202	LCE3D	1:152551856-152552980	NOTEST	0	0	0	0	1	1
ENSG00000163206	ENSG00000163206	SMCP	1:152850792-152857523	NOTEST	0	0	0	0	1	1
ENSG00000163207	ENSG00000163207	IVL	1:152881020-152884362	NOTEST	0	0	0	0	1	1
ENSG00000163209	ENSG00000163209	SPRR3	1:152974222-152976332	NOTEST	0	0	0	0	1	1
ENSG00000163216	ENSG00000163216	SPRR2D	1:153012200-153014407	NOTEST	0.0290663	0	#NAME?	0	1	1
ENSG00000163217	ENSG00000163217	BMP10	2:69092612-69098649	NOTEST	0.019073	0	#NAME?	0	1	1
ENSG00000163218	ENSG00000163218	PGLYRP4	1:153302595-153321316	NOTEST	0	0	0	0	1	1
ENSG00000163219	ENSG00000163219	ARHGAP25	2:68906732-69053965	NOTEST	0.0766961	0.162642	1.08448	0	1	1
ENSG00000163220	ENSG00000163220	S100A9	1:153330329-153333503	NOTEST	0	0	0	0	1	1
ENSG00000163221	ENSG00000163221	S100A12	1:153346183-153348125	NOTEST	0	0	0	0	1	1
ENSG00000163235	ENSG00000163235	TGFA	2:70674411-70781325	NOTEST	0.0548024	0.0696077	0.345006	0	1	1
ENSG00000163239	ENSG00000163239	TDRD10	1:154474694-154520623	NOTEST	0.105663	0.0148156	-2.83428	0	1	1
ENSG00000163254	ENSG00000163254	CRYGC	2:208992860-208994554	NOTEST	0.0324341	0.218679	2.75324	0	1	1
ENSG00000163263	ENSG00000163263	C1orf189	1:154171847-154178809	NOTEST	0	0	0	0	1	1
ENSG00000163273	ENSG00000163273	NPPC	2:232786529-232791113	NOTEST	0.312907	0.57213	0.870611	0	1	1
ENSG00000163283	ENSG00000163283	ALPP	2:233243243-233247599	NOTEST	0	0	0	0	1	1
ENSG00000163285	ENSG00000163285	GABRG1	4:46037785-46126098	NOTEST	0.00404876	0.00157499	-1.36213	0	1	1
ENSG00000163286	ENSG00000163286	ALPPL2	2:233271552-233275424	NOTEST	0	0	0	0	1	1
ENSG00000163288	ENSG00000163288	GABRB1	4:46920916-47428461	NOTEST	0.107585	0.262593	1.28735	0	1	1
ENSG00000163293	ENSG00000163293	NIPAL1	4:47849256-48042188	NOTEST	0.108979	0.360911	1.72759	0	1	1
ENSG00000163295	ENSG00000163295	ALPI	2:233320832-233324742	NOTEST	0	0	0	0	1	1
ENSG00000163331	ENSG00000163331	DAPL1	2:159651828-159719797	NOTEST	0.073876	0.0592213	-0.318989	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000163352	ENSG00000163352	LENEP	1:154966061-154966791	NOTEST	0	0.0301282	inf	0	1	1
ENSG00000163354	ENSG00000163354	DCST2	1:154975126-155006257	NOTEST	0.157548	0.281702	0.83838	0	1	1
ENSG00000163357	ENSG00000163357	DCST1	1:155006299-155035252	NOTEST	0.0998573	0.0307487	-1.69934	0	1	1
ENSG00000163359	ENSG00000163359	COL6A3	2:238232645-238323018	NOTEST	0.0544686	0.0521531	-0.0626728	0	1	1
ENSG00000163362	ENSG00000163362	C1orf106	1:200860175-200884863	NOTEST	0.102558	0.0354138	-1.53406	0	1	1
ENSG00000163376	ENSG00000163376	KBTBD8	3:67048726-67061634	NOTEST	0.517328	0.540722	0.0638083	0	1	1
ENSG00000163377	ENSG00000163377	FAM19A4	3:68780916-68981761	NOTEST	0	0.00491839	inf	0	1	1
ENSG00000163380	ENSG00000163380	LMOD3	3:69156022-69172183	NOTEST	0.0207086	0.0372071	0.845348	0	1	1
ENSG00000163394	ENSG00000163394	CCKAR	4:26483021-26492084	NOTEST	0	0	0	0	1	1
ENSG00000163395	ENSG00000163395	IGFN1	1:201159952-201198080	NOTEST	0.0348763	0.141144	2.01685	0	1	1
ENSG00000163406	ENSG00000163406	SLC15A2	3:121612935-121662949	NOTEST	0.0653196	0.134005	1.0367	0	1	1
ENSG00000163421	ENSG00000163421	PROK2	3:71820806-71834357	NOTEST	0	0	0	0	1	1
ENSG00000163424	ENSG00000163424	C3orf30	3:118864996-118924000	NOTEST	0	0.048576	inf	0	1	1
ENSG00000163431	ENSG00000163431	LMOD1	1:201862969-201915715	NOTEST	0.0658807	0.0445116	-0.565674	0	1	1
ENSG00000163440	ENSG00000163440	PDCL2	4:56422691-56458379	NOTEST	0	0	0	0	1	1
ENSG00000163449	ENSG00000163449	TMEM169	2:216809212-216967506	NOTEST	0.530908	0.354807	-0.581428	0	1	1
ENSG00000163464	ENSG00000163464	CXCR1	2:219027567-219031718	NOTEST	0	0	0	0	1	1
ENSG00000163485	ENSG00000163485	ADORA1	1:203059781-203136533	NOTEST	0.140884	0.209123	0.569839	0	1	1
ENSG00000163491	ENSG00000163491	NEK10	3:27151575-27410951	NOTEST	0.226688	0.540466	1.2535	0	1	1
ENSG00000163492	ENSG00000163492	CCDC141	2:179385909-179914813	NOTEST	0.145791	0.0634012	-1.20132	0	1	1
ENSG00000163497	ENSG00000163497	FEV	2:219845808-219850379	NOTEST	0	0	0	0	1	1
ENSG00000163499	ENSG00000163499	CRYBA2	2:219854910-219858143	NOTEST	0.104863	0.065549	-0.677861	0	1	1
ENSG00000163501	ENSG00000163501	IHH	2:219919141-219925189	NOTEST	0.00801899	0.0118655	0.565276	0	1	1
ENSG00000163515	ENSG00000163515	RETNLB	3:108462270-108476231	NOTEST	0	0	0	0	1	1
ENSG00000163518	ENSG00000163518	FCRL4	1:157543538-157567870	NOTEST	0	0	0	0	1	1
ENSG00000163519	ENSG00000163519	TRAT1	3:108541544-108573852	NOTEST	0	0	0	0	1	1
ENSG00000163520	ENSG00000163520	FBLN2	3:13573823-13679922	NOTEST	0.0363155	0.0466338	0.360788	0	1	1
ENSG00000163530	ENSG00000163530	DPPA2	3:109012634-109035364	NOTEST	0	0.0295503	inf	0	1	1
ENSG00000163534	ENSG00000163534	FCRL1	1:157764192-157789895	NOTEST	0	0	0	0	1	1
ENSG00000163554	ENSG00000163554	SPTA1	1:158580495-158656488	NOTEST	0.333708	0.292882	-0.188266	0	1	1
ENSG00000163563	ENSG00000163563	MNDA	1:158801106-158819296	NOTEST	0	0	0	0	1	1
ENSG00000163564	ENSG00000163564	PYHIN1	1:158900585-158946844	NOTEST	0.0479497	0.208666	2.1216	0	1	1
ENSG00000163568	ENSG00000163568	AIM2	1:159032273-159116886	NOTEST	0.100066	0.0933457	-0.100297	0	1	1
ENSG00000163576	ENSG00000163576	EFHB	3:19920963-19988517	NOTEST	0.196467	0.00990448	-4.31006	0	1	1
ENSG00000163581	ENSG00000163581	SLC2A2	3:170714136-170744539	NOTEST	0	0	0	0	1	1
ENSG00000163586	ENSG00000163586	FABP1	2:88422509-88427635	NOTEST	0	0	0	0	1	1
ENSG00000163599	ENSG00000163599	CTLA4	2:204732508-204738683	NOTEST	0.121815	0.428183	1.81354	0	1	1
ENSG00000163600	ENSG00000163600	ICOS	2:204801470-204826300	NOTEST	0	0	0	0	1	1
ENSG00000163606	ENSG00000163606	CD200R1	3:112640055-112693969	NOTEST	0.044879	0.0151419	-1.56749	0	1	1
ENSG00000163612	ENSG00000163612	FAM86KP	4:9155021-9167177	NOTEST	0	0	0	0	1	1
ENSG00000163623	ENSG00000163623	NKX6-1	4:85413139-85419603	NOTEST	0.44574	0.458643	0.0411697	0	1	1
ENSG00000163630	ENSG00000163630	SYNPR	3:63213990-63602597	NOTEST	0.0427731	0.0995391	1.21856	0	1	1
ENSG00000163631	ENSG00000163631	ALB	4:74262830-74287129	NOTEST	0.137774	0.0879484	-0.647572	0	1	1
ENSG00000163632	ENSG00000163632	C3orf49	3:63727968-63849579	NOTEST	0	0.0634716	inf	0	1	1
ENSG00000163638	ENSG00000163638	ADAMTS9	3:64501332-64997143	NOTEST	0.00495504	0.0236364	2.25404	0	1	1

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ENSG00000163645	ENSG00000163645	FAM194A	3:150377671-150438623	NOTEST	0.0236744	0.0364163	0.621256	0	1	1
ENSG00000163646	ENSG00000163646	CLRN1	3:150570270-150798513	NOTEST	0	0	0	0	1	1
ENSG00000163673	ENSG00000163673	DCLK3	3:36753912-36781352	NOTEST	0	0	0	0	1	1
ENSG00000163687	ENSG00000163687	DNASE1L3	3:58177983-58200424	NOTEST	0	0.034967	inf	0	1	1
ENSG00000163694	ENSG00000163694	RBM47	4:40425271-40632892	NOTEST	0.187894	0.0938675	-1.00122	0	1	1
ENSG00000163701	ENSG00000163701	IL17RE	3:9944295-9958086	NOTEST	0.172129	0.269719	0.647964	0	1	1
ENSG00000163705	ENSG00000163705	FANCD2OS	3:10068097-10149915	NOTEST	0	0	0	0	1	1
ENSG00000163736	ENSG00000163736	PPBP	4:74852754-74853914	NOTEST	0	0	0	0	1	1
ENSG00000163737	ENSG00000163737	PF4	4:74846793-74847841	NOTEST	0.0343071	0.0242914	-0.498057	0	1	1
ENSG00000163746	ENSG00000163746	PLSCR2	3:146109149-146213778	NOTEST	0.0452843	0	#NAME?	0	1	1
ENSG00000163749	ENSG00000163749	CCDC158	4:77234153-77343021	NOTEST	0.0178741	0.0321814	0.848352	0	1	1
ENSG00000163751	ENSG00000163751	CPA3	3:148508888-148677899	NOTEST	0	0	0	0	1	1
ENSG00000163792	ENSG00000163792	TCF23	2:27371871-27376378	NOTEST	0	0	0	0	1	1
ENSG00000163793	ENSG00000163793	DNAJC5G	2:27476551-27504367	NOTEST	0	0	0	0	1	1
ENSG00000163794	ENSG00000163794	UCN	2:27505259-27531313	NOTEST	0.253904	0.197438	-0.362889	0	1	1
ENSG00000163810	ENSG00000163810	TGM4	3:44916099-44956482	NOTEST	0	0	0	0	1	1
ENSG00000163814	ENSG00000163814	CDCP1	3:45123769-45187914	NOTEST	0.0563999	0.0946082	0.746271	0	1	1
ENSG00000163815	ENSG00000163815	CLEC3B	3:44956748-45077563	NOTEST	0.0276862	0	#NAME?	0	1	1
ENSG00000163817	ENSG00000163817	SLC6A20	3:45796941-45838027	NOTEST	0.00596175	0.00205176	-1.53887	0	1	1
ENSG00000163823	ENSG00000163823	CCR1	3:46205095-46308197	NOTEST	0.0174033	0.0651349	1.90407	0	1	1
ENSG00000163825	ENSG00000163825	RTP3	3:46538980-46542439	NOTEST	0	0	0	0	1	1
ENSG00000163827	ENSG00000163827	LRRC2	3:46556912-46668033	NOTEST	0.0165468	0.0523181	1.66076	0	1	1
ENSG00000163833	ENSG00000163833	FBXO40	3:121311965-121349139	NOTEST	0.00774127	0.00601275	-0.364545	0	1	1
ENSG00000163864	ENSG00000163864	NMNAT3	3:139108656-139396859	NOTEST	0.0694493	0.0978904	0.495207	0	1	1
ENSG00000163873	ENSG00000163873	GRIK3	1:37261127-37499730	NOTEST	0.00332591	0.00374521	0.171299	0	1	1
ENSG00000163879	ENSG00000163879	DNALI1	1:38022519-38061536	NOTEST	0.0044095	0.0301707	2.77446	0	1	1
ENSG00000163885	ENSG00000163885	CCDC37	3:126113781-126155399	NOTEST	0.111715	0	#NAME?	0	1	1
ENSG00000163888	ENSG00000163888	CAMK2N2	3:183851806-184402546	NOTEST	0.256459	0.369469	0.526726	0	1	1
ENSG00000163909	ENSG00000163909	HEYL	1:40089824-40105617	NOTEST	0	0	0	0	1	1
ENSG00000163914	ENSG00000163914	RHO	3:129247482-129254012	NOTEST	0	0	0	0	1	1
ENSG00000163915	ENSG00000163915	C3orf65	3:185361526-185542844	NOTEST	0.00847189	0.00595352	-0.508942	0	1	1
ENSG00000163958	ENSG00000163958	ZDHHC19	3:195924319-195938308	NOTEST	0.105659	0.12592	0.253094	0	1	1
ENSG00000163982	ENSG00000163982	OTOP1	4:4190529-4228616	NOTEST	0	0	0	0	1	1
ENSG00000163993	ENSG00000163993	S100P	4:6694795-6698897	NOTEST	0	0	0	0	1	1
ENSG00000163995	ENSG00000163995	ABLIM2	4:7967038-8160559	NOTEST	0.477299	0.199523	-1.25834	0	1	1
ENSG00000164007	ENSG00000164007	CLDN19	1:43198763-43205925	NOTEST	0	0	0	0	1	1
ENSG00000164010	ENSG00000164010	ERMAP	1:43272722-43312093	NOTEST	0.619765	0.347177	-0.836051	0	1	1
ENSG00000164035	ENSG00000164035	EMCN	4:101316497-101801283	NOTEST	0.0614634	0.0531563	-0.209485	0	1	1
ENSG00000164037	ENSG00000164037	SLC9B1	4:103790134-103940896	NOTEST	0.447145	0.22949	-0.962311	0	1	1
ENSG00000164047	ENSG00000164047	CAMP	3:48264836-48266981	NOTEST	0	0	0	0	1	1
ENSG00000164049	ENSG00000164049	FBXW12	3:48413708-48442666	NOTEST	0	0	0	0	1	1
ENSG00000164061	ENSG00000164061	BSN	3:49591921-49708978	NOTEST	0.112393	0.0778656	-0.529488	0	1	1
ENSG00000164076	ENSG00000164076	CAMKV	3:49895420-49907655	NOTEST	0	0.0914604	inf	0	1	1
ENSG00000164078	ENSG00000164078	MST1R	3:49924434-49967606	NOTEST	0.0656553	0.166364	1.34136	0	1	1
ENSG00000164082	ENSG00000164082	GRM2	3:51741085-51752629	NOTEST	0.0757332	0.0111449	-2.76455	0	1	1

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ENSG00000164106	ENSG00000164106	SCRG1	4:174305851-174327531	NOTEST	0.0429053	0.0128314	-1.74148	0	1	1
ENSG00000164107	ENSG00000164107	HAND2	4:174446119-174512475	NOTEST	0	0	0	0	1	1
ENSG00000164112	ENSG00000164112	TMEM155	4:122680087-122687962	NOTEST	0	0	0	0	1	1
ENSG00000164113	ENSG00000164113	ADAD1	4:123300120-123350957	NOTEST	0	0	0	0	1	1
ENSG00000164116	ENSG00000164116	GUCY1A3	4:156587862-156653501	NOTEST	0.233479	0.187024	-0.320074	0	1	1
ENSG00000164122	ENSG00000164122	ASB5	4:177134823-177198722	NOTEST	0	0.0378166	inf	0	1	1
ENSG00000164123	ENSG00000164123	C4orf45	4:159690289-159959912	NOTEST	0	0.0423615	inf	0	1	1
ENSG00000164128	ENSG00000164128	NPY1R	4:164245112-164273086	NOTEST	0	0	0	0	1	1
ENSG00000164129	ENSG00000164129	NPY5R	4:164245112-164273086	NOTEST	0	0	0	0	1	1
ENSG00000164136	ENSG00000164136	IL15	4:142557751-142655140	NOTEST	0.266493	0.174294	-0.612576	0	1	1
ENSG00000164161	ENSG00000164161	HHIP	4:145564073-145666423	NOTEST	0	0.0912748	inf	0	1	1
ENSG00000164185	ENSG00000164185	ZNF474	5:121464456-121518353	NOTEST	0.0543499	0.00582037	-3.22309	0	1	1
ENSG00000164188	ENSG00000164188	RANBP3L	5:36248535-36302216	NOTEST	0.0101266	0.0378864	1.90352	0	1	1
ENSG00000164199	ENSG00000164199	GPR98	5:89811427-90460038	NOTEST	0.0823264	0.0447254	-0.880261	0	1	1
ENSG00000164220	ENSG00000164220	F2RL2	5:75699073-76031606	NOTEST	0	0.00675731	inf	0	1	1
ENSG00000164251	ENSG00000164251	F2RL1	5:76114757-76131140	NOTEST	0.0340076	0.150774	2.14846	0	1	1
ENSG00000164256	ENSG00000164256	PRDM9	5:23507263-23528706	NOTEST	0.00421892	0	#NAME?	0	1	1
ENSG00000164265	ENSG00000164265	SCGB3A2	5:147250244-147286101	NOTEST	0	0	0	0	1	1
ENSG00000164270	ENSG00000164270	HTR4	5:147830594-148056798	NOTEST	0	0	0	0	1	1
ENSG00000164283	ENSG00000164283	ESM1	5:54273691-54338672	NOTEST	0	0	0	0	1	1
ENSG00000164287	ENSG00000164287	CDC20B	5:54408798-54469005	NOTEST	0.0219635	0.0234587	0.0950136	0	1	1
ENSG00000164299	ENSG00000164299	SPZ1	5:79615443-79617661	NOTEST	0	0.0210484	inf	0	1	1
ENSG00000164303	ENSG00000164303	ENPP6	4:185009858-185142383	NOTEST	0	0	0	0	1	1
ENSG00000164304	ENSG00000164304	CAGE1	6:7268538-7418270	NOTEST	0.0799171	0.0761341	-0.069963	0	1	1
ENSG00000164309	ENSG00000164309	CMYA5	5:78985699-79112013	NOTEST	0.129737	0.0741607	-0.806862	0	1	1
ENSG00000164318	ENSG00000164318	EGFLAM	5:38258510-38468441	NOTEST	0	0	0	0	1	1
ENSG00000164325	ENSG00000164325	TMEM174	5:72469021-72470970	NOTEST	0	0	0	0	1	1
ENSG00000164326	ENSG00000164326	CARTPT	5:71014989-71016875	NOTEST	0	0	0	0	1	1
ENSG00000164330	ENSG00000164330	EBF1	5:158122927-158526769	NOTEST	0.107847	0.182818	0.761425	0	1	1
ENSG00000164334	ENSG00000164334	FAM170A	5:118788137-118972894	NOTEST	0.0315413	0	#NAME?	0	1	1
ENSG00000164342	ENSG00000164342	TLR3	4:186990305-187009223	NOTEST	0.158756	0.204592	0.365935	0	1	1
ENSG00000164344	ENSG00000164344	KLKB1	4:187112673-187179625	NOTEST	0	0	0	0	1	1
ENSG00000164363	ENSG00000164363	SLC6A18	5:1225469-1246304	NOTEST	0	0	0	0	1	1
ENSG00000164379	ENSG00000164379	FOXQ1	6:1312674-1314992	NOTEST	0.00691709	0.0194348	1.49041	0	1	1
ENSG00000164385	ENSG00000164385	C6orf195	6:2622146-2634837	NOTEST	0.0999907	0.0712704	-0.488491	0	1	1
ENSG00000164393	ENSG00000164393	GPR111	6:47624171-47689757	NOTEST	0.00759232	0.0183023	1.26941	0	1	1
ENSG00000164399	ENSG00000164399	IL3	5:131396221-131398897	NOTEST	0	0	0	0	1	1
ENSG00000164400	ENSG00000164400	CSF2	5:131409482-131411859	NOTEST	0	0.0188815	inf	0	1	1
ENSG00000164404	ENSG00000164404	GDF9	5:132196872-132203723	NOTEST	0.0695358	0.0124815	-2.47797	0	1	1
ENSG00000164406	ENSG00000164406	LEAP2	5:132208013-132210738	NOTEST	0.272842	0.22029	-0.308661	0	1	1
ENSG00000164411	ENSG00000164411	GJB7	6:87992695-88109467	NOTEST	0	0	0	0	1	1
ENSG00000164438	ENSG00000164438	TLX3	5:170736287-170739138	NOTEST	0	0.00790106	inf	0	1	1
ENSG00000164440	ENSG00000164440	TXLNB	6:139456248-139613276	NOTEST	0.0149386	0.0103274	-0.532558	0	1	1
ENSG00000164451	ENSG00000164451	FAM26D	6:116813459-116880031	NOTEST	0.069325	0	#NAME?	0	1	1

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ENSG00000164483	ENSG00000164483	SAMD3	6:130334843-130686570	NOTEST	0.0157752	0	#NAME?	0	1	1
ENSG00000164484	ENSG00000164484	TMEM200A	6:130686878-130764208	NOTEST	0	0	0	0	1	1
ENSG00000164485	ENSG00000164485	IL22RA2	6:137464967-137494785	NOTEST	0	0	0	0	1	1
ENSG00000164488	ENSG00000164488	DACT2	6:168693509-168720434	NOTEST	0	0	0	0	1	1
ENSG00000164500	ENSG00000164500	C7orf72	7:49813256-50199426	NOTEST	0	0	0	0	1	1
ENSG00000164508	ENSG00000164508	HIST1H2AA	6:25726290-25726790	NOTEST	0	0	0	0	1	1
ENSG00000164509	ENSG00000164509	IL31RA	5:55147206-55218678	NOTEST	0	0.0193511	inf	0	1	1
ENSG00000164512	ENSG00000164512	ANKRD55	5:55395506-55529186	NOTEST	0.0110252	0.0318869	1.53215	0	1	1
ENSG00000164520	ENSG00000164520	RAET1E	6:150139933-150244257	NOTEST	0.0657431	0.00541559	-3.60165	0	1	1
ENSG00000164530	ENSG00000164530	PI16	6:36922208-36932613	NOTEST	0	0	0	0	1	1
ENSG00000164532	ENSG00000164532	TBX20	7:35242041-35293758	NOTEST	0	0	0	0	1	1
ENSG00000164556	ENSG00000164556	FAM183B	7:38724945-38726637	NOTEST	0	0	0	0	1	1
ENSG00000164591	ENSG00000164591	MYOZ3	5:150040435-150058927	NOTEST	0.00952075	0.0362767	1.9299	0	1	1
ENSG00000164600	ENSG00000164600	NEUROD6	7:31377074-31380508	NOTEST	0	0	0	0	1	1
ENSG00000164604	ENSG00000164604	GPR85	7:112718385-112727833	NOTEST	0.317073	0.313793	-0.0150008	0	1	1
ENSG00000164616	ENSG00000164616	FBXL21	5:135257967-135290723	NOTEST	0	0	0	0	1	1
ENSG00000164619	ENSG00000164619	BMPER	7:33944522-34195484	NOTEST	0.0478116	0.0498224	0.0594318	0	1	1
ENSG00000164621	ENSG00000164621	SMAD5-AS1	5:135465195-135524435	NOTEST	0.0102109	0.0103339	0.0172714	0	1	1
ENSG00000164626	ENSG00000164626	KCNK5	6:39156748-39197226	NOTEST	0.0199078	0.0396775	0.994987	0	1	1
ENSG00000164645	ENSG00000164645	C7orf62	7:88388681-88966346	NOTEST	0	0	0	0	1	1
ENSG00000164674	ENSG00000164674	SYTL3	6:159071045-159185908	NOTEST	0.280324	0.358445	0.354655	0	1	1
ENSG00000164675	ENSG00000164675	IQUB	7:123092453-123175131	NOTEST	0.446811	0.225733	-0.985051	0	1	1
ENSG00000164690	ENSG00000164690	SHH	7:155592679-155604967	NOTEST	0	0	0	0	1	1
ENSG00000164691	ENSG00000164691	TAGAP	6:159393902-159486305	NOTEST	0.0743376	0.113199	0.606694	0	1	1
ENSG00000164692	ENSG00000164692	COL1A2	7:94023872-94060544	NOTEST	0.082573	0.150202	0.863159	0	1	1
ENSG00000164694	ENSG00000164694	FNDC1	6:159586940-159693141	NOTEST	0.0395755	0.00929531	-2.09003	0	1	1
ENSG00000164695	ENSG00000164695	CHMP4C	8:82613568-82671750	NOTEST	0	0	0	0	1	1
ENSG00000164707	ENSG00000164707	SLC13A4	7:135347243-135433594	NOTEST	0.0787047	0.0146416	-2.42638	0	1	1
ENSG00000164729	ENSG00000164729	SLC35G3	17:33519538-33521412	NOTEST	0	0	0	0	1	1
ENSG00000164736	ENSG00000164736	SOX17	8:55370494-55373448	NOTEST	0	0	0	0	1	1
ENSG00000164740	ENSG00000164740	SEPT7P5	7:62956176-62962914	NOTEST	0	0	0	0	1	1
ENSG00000164744	ENSG00000164744	SUN3	7:48026744-48068716	NOTEST	0.229157	0.271707	0.245719	0	1	1
ENSG00000164749	ENSG00000164749	HNF4G	8:76320148-76479078	NOTEST	0.373336	0.48049	0.364034	0	1	1
ENSG00000164756	ENSG00000164756	SLC30A8	8:117962511-118188953	NOTEST	0	0	0	0	1	1
ENSG00000164764	ENSG00000164764	SBSPON	8:73976774-74036323	NOTEST	0.195136	0.168791	-0.209237	0	1	1
ENSG00000164776	ENSG00000164776	PHKG1	7:56148439-56160689	NOTEST	0.33161	0.416039	0.327231	0	1	1
ENSG00000164794	ENSG00000164794	KCNV1	8:110975873-110988076	NOTEST	0.380486	0.283011	-0.426982	0	1	1
ENSG00000164796	ENSG00000164796	CSMD3	8:113235156-114449328	NOTEST	0.0575532	0.0315078	-0.869187	0	1	1
ENSG00000164816	ENSG00000164816	DEFA5	8:6912830-6914256	NOTEST	0	0	0	0	1	1
ENSG00000164821	ENSG00000164821	DEFA4	8:6793343-6795860	NOTEST	0	0	0	0	1	1
ENSG00000164822	ENSG00000164822	DEFA6	8:6782214-6783598	NOTEST	0	0	0	0	1	1
ENSG00000164825	ENSG00000164825	DEFB1	8:6666037-6742798	NOTEST	0	0	0	0	1	1
ENSG00000164845	ENSG00000164845	FAM86FP	12:8385107-8395544	NOTEST	0.405201	0.127956	-1.66299	0	1	1
ENSG00000164853	ENSG00000164853	UNCX	7:1272542-1276954	NOTEST	0.00791217	0	#NAME?	0	1	1

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ENSG00000164855	ENSG00000164855	TMEM184A	7:1570349-1600457	NOTEST	0.150403	0.436199	1.53615	0	1	1
ENSG00000164871	ENSG00000164871	SPAG11B	8:7300205-7321196	NOTEST	0	0	0	0	1	1
ENSG00000164879	ENSG00000164879	CA3	8:86239836-86393722	NOTEST	0	0	0	0	1	1
ENSG00000164893	ENSG00000164893	SLC7A13	8:87226280-87333375	NOTEST	0	0	0	0	1	1
ENSG00000164900	ENSG00000164900	GBX1	7:150845675-150871832	NOTEST	0	0.0273544	inf	0	1	1
ENSG00000164935	ENSG00000164935	DCSTAMP	8:105342551-105479281	NOTEST	0	0.0282803	inf	0	1	1
ENSG00000164949	ENSG00000164949	GEM	8:95261480-95274578	NOTEST	0.282243	0.559877	0.988171	0	1	1
ENSG00000164972	ENSG00000164972	C9orf24	9:34379016-34397830	NOTEST	0	0.0935925	inf	0	1	1
ENSG00000165023	ENSG00000165023	DIRAS2	9:93372113-93405386	NOTEST	0.00704816	0	#NAME?	0	1	1
ENSG00000165025	ENSG00000165025	SYK	9:93564068-93660831	NOTEST	0.0206376	0.0212425	0.0416758	0	1	1
ENSG00000165059	ENSG00000165059	PRKACG	9:71627468-71629039	NOTEST	0	0	0	0	1	1
ENSG00000165061	ENSG00000165061	ZMAT4	8:40388108-40755352	NOTEST	0	0	0	0	1	1
ENSG00000165066	ENSG00000165066	NKX6-3	8:41502696-41508855	NOTEST	0	0	0	0	1	1
ENSG00000165071	ENSG00000165071	TMEM71	8:133697252-133772958	NOTEST	0.0456968	0	#NAME?	0	1	1
ENSG00000165072	ENSG00000165072	MAMDC2	9:72658496-72873782	NOTEST	0.0793966	0.0867221	0.127323	0	1	1
ENSG00000165076	ENSG00000165076	PRSS37	7:141536085-141541287	NOTEST	0.02352	0	#NAME?	0	1	1
ENSG00000165078	ENSG00000165078	CPA6	8:68334359-68658620	NOTEST	0	0	0	0	1	1
ENSG00000165084	ENSG00000165084	C8orf34	8:69215702-69731257	NOTEST	0.0203681	0	#NAME?	0	1	1
ENSG00000165120	ENSG00000165120	SSMEM1	7:129847699-129856683	NOTEST	0	0	0	0	1	1
ENSG00000165124	ENSG00000165124	SVEP1	9:113127530-113342160	NOTEST	0.0212818	0.046627	1.13155	0	1	1
ENSG00000165125	ENSG00000165125	TRPV6	7:142568955-142590199	NOTEST	0.00144823	0	#NAME?	0	1	1
ENSG00000165131	ENSG00000165131	C7orf34	7:142636439-142637955	NOTEST	0	0	0	0	1	1
ENSG00000165140	ENSG00000165140	FBP1	9:97365414-97402531	NOTEST	0	0	0	0	1	1
ENSG00000165164	ENSG00000165164	CXorf22	X:35937850-36008269	NOTEST	0	0	0	0	1	1
ENSG00000165168	ENSG00000165168	CYBB	X:37208527-38548169	NOTEST	0	0.00528788	inf	0	1	1
ENSG00000165178	ENSG00000165178	NCF1C	7:74572444-74587848	NOTEST	0	0	0	0	1	1
ENSG00000165181	ENSG00000165181	C9orf84	9:114448452-114557288	NOTEST	0.0229977	0.0244525	0.0884892	0	1	1
ENSG00000165182	ENSG00000165182	CXorf58	X:23851469-23957624	NOTEST	0	0.0279402	inf	0	1	1
ENSG00000165186	ENSG00000165186	PTCHD1	X:23352132-23422489	NOTEST	0.00197554	0	#NAME?	0	1	1
ENSG00000165188	ENSG00000165188	RNF183	9:116059372-116065656	NOTEST	0.00895196	0	#NAME?	0	1	1
ENSG00000165192	ENSG00000165192	ASB11	X:15298052-15333778	NOTEST	0.163802	0.174106	0.0880155	0	1	1
ENSG00000165194	ENSG00000165194	PCDH19	X:99546641-99665271	NOTEST	0.00872784	0.0094849	0.120008	0	1	1
ENSG00000165197	ENSG00000165197	FIGF	X:15363712-15402498	NOTEST	0.357526	0.300485	-0.250757	0	1	1
ENSG00000165202	ENSG00000165202	OR1Q1	9:125372193-125401964	NOTEST	0	0	0	0	1	1
ENSG00000165204	ENSG00000165204	OR1K1	9:125560667-125590910	NOTEST	0	0	0	0	1	1
ENSG00000165215	ENSG00000165215	CLDN3	7:73183327-73184600	NOTEST	0	0	0	0	1	1
ENSG00000165246	ENSG00000165246	NLGN4Y	Y:16634517-16957530	NOTEST	0	0	0	0	1	1
ENSG00000165269	ENSG00000165269	AQP7	9:33384764-33402643	NOTEST	0	0.0228462	inf	0	1	1
ENSG00000165272	ENSG00000165272	AQP3	9:33441151-33447609	NOTEST	0.035405	0.159729	2.1736	0	1	1
ENSG00000165309	ENSG00000165309	ARMC3	10:23216952-23326518	NOTEST	0.442971	0.529105	0.256344	0	1	1
ENSG00000165323	ENSG00000165323	FAT3	11:92085261-92629618	NOTEST	0.000810821	0	#NAME?	0	1	1
ENSG00000165325	ENSG00000165325	CCDC67	11:93063136-93171653	NOTEST	0	0	0	0	1	1
ENSG00000165349	ENSG00000165349	SLC7A3	X:70145431-70150975	NOTEST	0	0	0	0	1	1
ENSG00000165370	ENSG00000165370	GPR101	X:136112306-136113833	NOTEST	0	0	0	0	1	1
ENSG00000165376	ENSG00000165376	CLDN2	X:106045909-106243474	NOTEST	0.0195349	0.0118538	-0.720705	0	1	1

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ENSG00000165379	ENSG00000165379	LRFN5	14:42076772-42373752	NOTEST	0.0668975	0.0212932	-1.65156	0	1	1
ENSG00000165383	ENSG00000165383	LRRC18	10:49892920-50323554	NOTEST	0	0	0	0	1	1
ENSG00000165388	ENSG00000165388	ZNF488	10:48355023-48373866	NOTEST	0	0	0	0	1	1
ENSG00000165390	ENSG00000165390	ANXA8	10:48247668-48279200	NOTEST	0	0	0	0	1	1
ENSG00000165409	ENSG00000165409	TSHR	14:80943329-81636758	NOTEST	0.0750265	0.11666	0.636831	0	1	1
ENSG00000165443	ENSG00000165443	PHYHIPL	10:60936349-61122939	NOTEST	0.00825074	0	#NAME?	0	1	1
ENSG00000165449	ENSG00000165449	SLC16A9	10:61410522-61495760	NOTEST	0	0.00937317	inf	0	1	1
ENSG00000165457	ENSG00000165457	FOLR2	11:71927644-71932994	NOTEST	0	0.0901467	inf	0	1	1
ENSG00000165462	ENSG00000165462	PHOX2A	11:71934744-71956708	NOTEST	0	0	0	0	1	1
ENSG00000165471	ENSG00000165471	MBL2	10:54525139-54531460	NOTEST	0	0.00613517	inf	0	1	1
ENSG00000165474	ENSG00000165474	GJB2	13:20761608-20767037	NOTEST	0.438525	0.182676	-1.26337	0	1	1
ENSG00000165478	ENSG00000165478	HEPACAM	11:124789088-124806308	NOTEST	0.0350093	0.00303804	-3.52652	0	1	1
ENSG00000165496	ENSG00000165496	RPL10L	14:47120221-47121028	NOTEST	0	0	0	0	1	1
ENSG00000165509	ENSG00000165509	MAGEC3	X:140926101-140985618	NOTEST	0.0320656	0	#NAME?	0	1	1
ENSG00000165511	ENSG00000165511	C10orf25	10:45493145-45676875	NOTEST	0.0357603	0.0276862	-0.369192	0	1	1
ENSG00000165548	ENSG00000165548	TMEM63C	14:77564439-77725838	NOTEST	0.0161356	0.00685444	-1.23513	0	1	1
ENSG00000165553	ENSG00000165553	NGB	14:77731825-77737655	NOTEST	0	0.0485387	inf	0	1	1
ENSG00000165555	ENSG00000165555	NOXRED1	14:77860363-77889860	NOTEST	0.141585	0.141496	-0.000908854	0	1	1
ENSG00000165556	ENSG00000165556	CDX2	13:28536273-28545276	NOTEST	0.00690652	0.00268468	-1.36321	0	1	1
ENSG00000165566	ENSG00000165566	AMER2	13:25735821-25746426	NOTEST	0	0	0	0	1	1
ENSG00000165568	ENSG00000165568	AKR1E2	10:4828820-4890254	NOTEST	0.0401436	0.115841	1.52891	0	1	1
ENSG00000165583	ENSG00000165583	SSX5	X:48045655-48056199	NOTEST	0.610302	0.281652	-1.11561	0	1	1
ENSG00000165584	ENSG00000165584	SSX3	X:48205862-48216142	NOTEST	0.0433204	0	#NAME?	0	1	1
ENSG00000165588	ENSG00000165588	OTX2	14:57267424-57277197	NOTEST	0	0	0	0	1	1
ENSG00000165591	ENSG00000165591	FAAH2	X:57313138-57515629	NOTEST	0.0704446	0.00636859	-3.46744	0	1	1
ENSG00000165606	ENSG00000165606	DRGX	10:50572236-50603497	NOTEST	0	0	0	0	1	1
ENSG00000165621	ENSG00000165621	OXGR1	13:97637972-97646984	NOTEST	0.0130966	0.00545826	-1.26268	0	1	1
ENSG00000165623	ENSG00000165623	UCMA	10:13263766-13276334	NOTEST	0	0	0	0	1	1
ENSG00000165633	ENSG00000165633	VSTM4	10:49892920-50323554	NOTEST	0	0	0	0	1	1
ENSG00000165643	ENSG00000165643	SOHLH1	9:138585252-138591374	NOTEST	0	0.0381912	inf	0	1	1
ENSG00000165659	ENSG00000165659	DACH1	13:72012097-72441330	NOTEST	0.184659	0.182302	-0.018528	0	1	1
ENSG00000165682	ENSG00000165682	CLEC1B	12:10100735-10183205	NOTEST	0	0	0	0	1	1
ENSG00000165685	ENSG00000165685	TMEM52B	12:10310901-10344400	NOTEST	0	0	0	0	1	1
ENSG00000165694	ENSG00000165694	FRMD7	X:131211020-131262048	NOTEST	0.0249686	0.050031	1.00271	0	1	1
ENSG00000165695	ENSG00000165695	AK8	9:135600964-135765588	NOTEST	0.0749916	0.047793	-0.649931	0	1	1
ENSG00000165702	ENSG00000165702	GFI1B	9:135820931-135867083	NOTEST	0.050162	0.0438195	-0.195022	0	1	1
ENSG00000165730	ENSG00000165730	STOX1	10:70587297-70655188	NOTEST	0.181422	0.223102	0.298353	0	1	1
ENSG00000165731	ENSG00000165731	RET	10:43572474-43625799	NOTEST	0.0142053	0.00593221	-1.25979	0	1	1
ENSG00000165757	ENSG00000165757	KIAA1462	10:30301728-30404423	NOTEST	0.00457621	0.00726047	0.665909	0	1	1
ENSG00000165762	ENSG00000165762	OR4K2	14:20344390-20345468	NOTEST	0	0	0	0	1	1
ENSG00000165794	ENSG00000165794	SLC39A2	14:21467413-21470030	NOTEST	0	0	0	0	1	1
ENSG00000165799	ENSG00000165799	RNASE7	14:21484921-21572881	NOTEST	0.0197776	0.0260952	0.399921	0	1	1
ENSG00000165805	ENSG00000165805	C12orf50	12:88373815-88535993	NOTEST	0.0199111	0	#NAME?	0	1	1
ENSG00000165807	ENSG00000165807	PPP1R36	14:65016619-65063254	NOTEST	0.115298	0.186705	0.695394	0	1	1
ENSG00000165810	ENSG00000165810	BTNL9	5:180467224-180488523	NOTEST	0	0.0031322	inf	0	1	1

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ENSG00000165816	ENSG00000165816	VWA2	10:115999017-116051272	NOTEST	0.00566176	0	#NAME?	0	1	1
ENSG00000165828	ENSG00000165828	PRAP1	10:135093134-135166187	NOTEST	0	0.0227355	inf	0	1	1
ENSG00000165837	ENSG00000165837	FAM194B	13:46039059-46189874	NOTEST	0.26921	0.243232	-0.1464	0	1	1
ENSG00000165841	ENSG00000165841	CYP2C19	10:96443250-96613017	NOTEST	0.000608607	0	#NAME?	0	1	1
ENSG00000165862	ENSG00000165862	PNLIPRP2	10:118380464-118404654	NOTEST	0.0675727	0	#NAME?	0	1	1
ENSG00000165863	ENSG00000165863	C10orf82	10:118423206-118502085	NOTEST	0.0257863	0.00768878	-1.74578	0	1	1
ENSG00000165874	ENSG00000165874	FAM35BP	10:46897591-46971400	NOTEST	0.0432809	0.148347	1.77717	0	1	1
ENSG00000165879	ENSG00000165879	FRAT1	10:99079021-99081672	NOTEST	0.217477	0.221747	0.0280528	0	1	1
ENSG00000165887	ENSG00000165887	ANKRD2	10:99332197-99343641	NOTEST	0.405182	0.397444	-0.027817	0	1	1
ENSG00000165899	ENSG00000165899	OTOGL	12:80603232-80772870	NOTEST	0.0511454	0.052135	0.0276465	0	1	1
ENSG00000165905	ENSG00000165905	GYLTL1B	11:45943171-45950647	NOTEST	0.097213	0.0815306	-0.253807	0	1	1
ENSG00000165917	ENSG00000165917	RAPSN	11:47459307-47470730	NOTEST	0.0633943	0.00696067	-3.18705	0	1	1
ENSG00000165935	ENSG00000165935	SMCO2	12:27619742-27655118	NOTEST	0.0395535	0.110393	1.48078	0	1	1
ENSG00000165949	ENSG00000165949	IFI27	14:94571181-94583033	NOTEST	0.431041	0.251438	-0.777623	0	1	1
ENSG00000165953	ENSG00000165953	SERPINA12	14:94953610-94984181	NOTEST	0.126156	0.034944	-1.85209	0	1	1
ENSG00000165966	ENSG00000165966	PDZRN4	12:41582249-41968392	NOTEST	0.00529946	0.0360525	2.76618	0	1	1
ENSG00000165970	ENSG00000165970	SLC6A5	11:20620945-20680831	NOTEST	0	0	0	0	1	1
ENSG00000165972	ENSG00000165972	CCDC38	12:96252705-96336752	NOTEST	0	0.0280858	inf	0	1	1
ENSG00000165973	ENSG00000165973	NELL1	11:20691116-21597227	NOTEST	0	0	0	0	1	1
ENSG00000165985	ENSG00000165985	C1QL3	10:16555741-16564004	NOTEST	0.0475	0.0528357	0.153585	0	1	1
ENSG00000165995	ENSG00000165995	CACNB2	10:18429605-18948214	NOTEST	0.0670112	0.0998104	0.574788	0	1	1
ENSG00000166002	ENSG00000166002	SMCO4	11:93211637-93276674	NOTEST	0.0951263	0.0530492	-0.842514	0	1	1
ENSG00000166006	ENSG00000166006	KCNC2	12:75414748-75603648	NOTEST	0	0	0	0	1	1
ENSG00000166007	ENSG00000166007	TRIM51HP	11:55059358-55065746	NOTEST	0.375443	0.385792	0.0392315	0	1	1
ENSG00000166008	ENSG00000166008	MAGEA9	X:148863583-148869397	NOTEST	0	0	0	0	1	1
ENSG00000166013	ENSG00000166013	TRIM53BP	11:89575164-89584138	NOTEST	0	0	0	0	1	1
ENSG00000166035	ENSG00000166035	LIPC	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000166049	ENSG00000166049	PASD1	X:150732093-150845211	NOTEST	0.0467602	0.0655521	0.487361	0	1	1
ENSG00000166069	ENSG00000166069	TMCO5A	15:38214139-38259925	NOTEST	0	0	0	0	1	1
ENSG00000166086	ENSG00000166086	JAM3	11:133938819-134117686	NOTEST	0.464085	0.484574	0.0623294	0	1	1
ENSG00000166090	ENSG00000166090	IL25	14:23842017-23845612	NOTEST	0	0	0	0	1	1
ENSG00000166091	ENSG00000166091	CMTM5	14:23846016-23848981	NOTEST	0.180193	0	#NAME?	0	1	1
ENSG00000166104	ENSG00000166104	hsa-mir-7162	15:62520094-62545434	NOTEST	0.178831	0.318992	0.834921	0	1	1
ENSG00000166105	ENSG00000166105	GLB1L3	11:134144138-134189458	NOTEST	0.00827792	0	#NAME?	0	1	1
ENSG00000166106	ENSG00000166106	ADAMTS15	11:130318868-130346532	NOTEST	0	0.00189495	inf	0	1	1
ENSG00000166111	ENSG00000166111	SVOP	12:109458638-109459045	NOTEST	0	0	0	0	1	1
ENSG00000166118	ENSG00000166118	SPATA19	11:133710525-133715433	NOTEST	0	0	0	0	1	1
ENSG00000166126	ENSG00000166126	AMN	14:103388992-103523799	NOTEST	0.00855395	0.0269701	1.6567	0	1	1
ENSG00000166143	ENSG00000166143	PPP1R14D	15:41107649-41120907	NOTEST	0	0	0	0	1	1
ENSG00000166145	ENSG00000166145	SPINT1	15:41128005-41150405	NOTEST	0.248701	0.519237	1.06198	0	1	1
ENSG00000166148	ENSG00000166148	AVPR1A	12:63539013-63544722	NOTEST	0.0109687	0	#NAME?	0	1	1
ENSG00000166152	ENSG00000166152	C16orf78	16:49407733-49433342	NOTEST	0	0	0	0	1	1
ENSG00000166157	ENSG00000166157	TPTE	21:10906200-11098980	NOTEST	0.0664851	0.0540808	-0.297915	0	1	1
ENSG00000166159	ENSG00000166159	LRTM2	12:1901122-2032033	NOTEST	0.00875439	0	#NAME?	0	1	1
ENSG00000166160	ENSG00000166160	OPN1MW2	X:153485224-153498755	NOTEST	0	0	0	0	1	1

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ENSG00000166183	ENSG00000166183	ASPG	14:104552015-104579098	NOTEST	0.0299115	0.0485482	0.698716	0	1	1
ENSG00000166206	ENSG00000166206	GABRB3	15:26788692-27194354	NOTEST	0	0.0199828	inf	0	1	1
ENSG00000166211	ENSG00000166211	SPIC	12:101869198-101880775	NOTEST	0	0	0	0	1	1
ENSG00000166220	ENSG00000166220	TBATA	10:72530994-72545157	NOTEST	0	0	0	0	1	1
ENSG00000166246	ENSG00000166246	C16orf71	16:4746512-4817625	NOTEST	0.0504494	0.0933843	0.888344	0	1	1
ENSG00000166250	ENSG00000166250	CLMP	11:122943034-123098985	NOTEST	0.0935835	0.205069	1.13178	0	1	1
ENSG00000166257	ENSG00000166257	SCN3B	11:123499894-123525952	NOTEST	0.0189203	0.0257061	0.442174	0	1	1
ENSG00000166265	ENSG00000166265	CYYR1	21:27750870-27945603	NOTEST	0	0	0	0	1	1
ENSG00000166268	ENSG00000166268	MYRFL	12:70132460-70748773	NOTEST	0.0129372	0	#NAME?	0	1	1
ENSG00000166278	ENSG00000166278	C2	6:31865561-31919861	NOTEST	0.253461	0.239332	-0.0827456	0	1	1
ENSG00000166292	ENSG00000166292	TMEM100	17:53796987-53809482	NOTEST	0	0	0	0	1	1
ENSG00000166317	ENSG00000166317	SYNPO2L	10:75404638-75490272	NOTEST	0.0686047	0.281548	2.037	0	1	1
ENSG00000166323	ENSG00000166323	C11orf65	11:108027941-108338258	NOTEST	0.0973007	0.0695331	-0.484751	0	1	1
ENSG00000166329	ENSG00000166329	CCDC182	17:55821841-55822673	NOTEST	0	0	0	0	1	1
ENSG00000166342	ENSG00000166342	NETO1	18:70409548-70535381	NOTEST	0	0	0	0	1	1
ENSG00000166349	ENSG00000166349	RAG1	11:36532258-36694823	NOTEST	0.32855	0.129411	-1.34415	0	1	1
ENSG00000166351	ENSG00000166351	POTED	21:14982497-15013906	NOTEST	0	0	0	0	1	1
ENSG00000166359	ENSG00000166359	WDR88	19:33622995-33666701	NOTEST	0.0618205	0.0287335	-1.10535	0	1	1
ENSG00000166363	ENSG00000166363	OR10A5	11:6866882-6867936	NOTEST	0	0	0	0	1	1
ENSG00000166368	ENSG00000166368	OR2D2	11:6912720-6913830	NOTEST	0	0	0	0	1	1
ENSG00000166391	ENSG00000166391	MOGAT2	11:75428863-75444003	NOTEST	0	0	0	0	1	1
ENSG00000166394	ENSG00000166394	CYB5R2	11:7686330-7698453	NOTEST	0.187061	0.453373	1.27719	0	1	1
ENSG00000166405	ENSG00000166405	RIC3	11:8040790-8190602	NOTEST	0.013236	0.0383029	1.53298	0	1	1
ENSG00000166407	ENSG00000166407	LMO1	11:8245850-8290263	NOTEST	0.527403	0.38642	-0.448738	0	1	1
ENSG00000166408	ENSG00000166408	OR5P1P	11:7710668-7927502	NOTEST	0	0	0	0	1	1
ENSG00000166415	ENSG00000166415	WDR72	15:53805937-54055075	NOTEST	0.349533	0.254704	-0.456611	0	1	1
ENSG00000166426	ENSG00000166426	CRABP1	15:78632665-78640572	NOTEST	0	0	0	0	1	1
ENSG00000166428	ENSG00000166428	PLD4	14:105391152-105399574	NOTEST	0	0	0	0	1	1
ENSG00000166432	ENSG00000166432	ZMAT1	X:101137261-101187004	NOTEST	0.0182163	0.0158653	-0.199357	0	1	1
ENSG00000166446	ENSG00000166446	CDYL2	16:80631802-80838226	NOTEST	0	0	0	0	1	1
ENSG00000166448	ENSG00000166448	TMEM130	7:98444110-98468394	NOTEST	0	0	0	0	1	1
ENSG00000166455	ENSG00000166455	C16orf46	16:81087101-81130008	NOTEST	0.447622	0.270642	-0.725898	0	1	1
ENSG00000166482	ENSG00000166482	MFAP4	17:19240866-19290553	NOTEST	0.0948817	0.0533955	-0.829412	0	1	1
ENSG00000166492	ENSG00000166492	FAM86GP	11:3431581-3443726	NOTEST	0	0	0	0	1	1
ENSG00000166501	ENSG00000166501	PRKCB	16:23847321-24231932	NOTEST	0.322799	0.264482	-0.287466	0	1	1
ENSG00000166509	ENSG00000166509	CLEC3A	16:78048579-78100658	NOTEST	0	0	0	0	1	1
ENSG00000166510	ENSG00000166510	CCDC68	18:52568739-52626739	NOTEST	0	0	0	0	1	1
ENSG00000166523	ENSG00000166523	CLEC4E	12:8685900-8693559	NOTEST	0	0	0	0	1	1
ENSG00000166527	ENSG00000166527	CLEC4D	12:8662070-8674962	NOTEST	0	0	0	0	1	1
ENSG00000166530	ENSG00000166530	HSBP1P2	4:111173026-111173255	NOTEST	0	0	0	0	1	1
ENSG00000166535	ENSG00000166535	A2ML1	12:8834195-9039597	NOTEST	0	0.00325093	inf	0	1	1
ENSG00000166558	ENSG00000166558	SLC38A8	16:84043271-84076241	NOTEST	0.100314	0.163516	0.704903	0	1	1
ENSG00000166569	ENSG00000166569	CPLX4	18:56942387-56985881	NOTEST	0	0.0117948	inf	0	1	1
ENSG00000166573	ENSG00000166573	GALR1	18:74962504-74980858	NOTEST	0	0	0	0	1	1
ENSG00000166589	ENSG00000166589	CDH16	16:66942024-66952887	NOTEST	0	0.0056251	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000166592	ENSG00000166592	RRAD	16:66955581-66959547	NOTEST	0	0.0265339	inf	0	1	1
ENSG00000166596	ENSG00000166596	WDR16	17:9479943-9633008	NOTEST	0	0	0	0	1	1
ENSG00000166603	ENSG00000166603	MC4R	18:58038563-58040001	NOTEST	0	0	0	0	1	1
ENSG00000166634	ENSG00000166634	SERPINB12	18:61223392-61234244	NOTEST	0.0141804	0.00998267	-0.506399	0	1	1
ENSG00000166664	ENSG00000166664	CHRFAM7A	15:30653442-30686052	NOTEST	0.0463404	0	#NAME?	0	1	1
ENSG00000166669	ENSG00000166669	ATF7IP2	16:10420290-10577495	NOTEST	0.070958	0.037458	-0.921693	0	1	1
ENSG00000166670	ENSG00000166670	MMP10	11:102617698-102714534	NOTEST	0	0	0	0	1	1
ENSG00000166676	ENSG00000166676	TVP23A	16:10837642-10912651	NOTEST	0.0528975	0.0212222	-1.31762	0	1	1
ENSG00000166689	ENSG00000166689	PLEKHA7	11:16799841-17074583	NOTEST	0.242307	0.347859	0.521665	0	1	1
ENSG00000166693	ENSG00000166693	OR5M13P	11:56364901-56365838	NOTEST	0	0	0	0	1	1
ENSG00000166707	ENSG00000166707	ZCCHC18	X:103343897-103401708	NOTEST	0.157852	0.157137	-0.00655265	0	1	1
ENSG00000166736	ENSG00000166736	HTR3A	11:113845602-113861035	NOTEST	0	0	0	0	1	1
ENSG00000166741	ENSG00000166741	NNMT	11:113930314-114227293	NOTEST	0.124924	0.228497	0.87113	0	1	1
ENSG00000166743	ENSG00000166743	ACSM1	16:20621564-20936328	NOTEST	0	0	0	0	1	1
ENSG00000166748	ENSG00000166748	AGBL1	15:86685226-87572283	NOTEST	0	0	0	0	1	1
ENSG00000166763	ENSG00000166763	STRCP1	15:43885251-44010458	NOTEST	0	0	0	0	1	1
ENSG00000166787	ENSG00000166787	SAA3P	11:18134018-18137679	NOTEST	0	0	0	0	1	1
ENSG00000166800	ENSG00000166800	LDHAL6A	11:18477370-18548779	NOTEST	0.0409227	0.0219623	-0.897873	0	1	1
ENSG00000166819	ENSG00000166819	PLIN1	15:90207595-90234014	NOTEST	0.0207085	0.0549268	1.40729	0	1	1
ENSG00000166825	ENSG00000166825	ANPEP	15:90328119-90358633	NOTEST	0.011882	0.0227821	0.939125	0	1	1
ENSG00000166828	ENSG00000166828	SCNN1G	16:23194035-23228204	NOTEST	0	0	0	0	1	1
ENSG00000166840	ENSG00000166840	GLYATL1	11:58672870-58826132	NOTEST	0	0	0	0	1	1
ENSG00000166856	ENSG00000166856	GPR182	12:57388229-57392225	NOTEST	0.017685	0.0290039	0.713721	0	1	1
ENSG00000166862	ENSG00000166862	CACNG2	22:36959967-37099603	NOTEST	0	0	0	0	1	1
ENSG00000166863	ENSG00000166863	TAC3	12:57403783-57444982	NOTEST	0	0	0	0	1	1
ENSG00000166866	ENSG00000166866	MYO1A	12:57403783-57444982	NOTEST	0	0	0	0	1	1
ENSG00000166869	ENSG00000166869	CHP2	16:23765947-23770272	NOTEST	0	0	0	0	1	1
ENSG00000166884	ENSG00000166884	OR4D6	11:59224410-59225464	NOTEST	0	0	0	0	1	1
ENSG00000166897	ENSG00000166897	ELFN2	22:37735623-37823505	NOTEST	0.0631133	0.194323	1.62244	0	1	1
ENSG00000166917	ENSG00000166917	MIR202HG	10:135059981-135061395	NOTEST	0	0	0	0	1	1
ENSG00000166922	ENSG00000166922	SCG5	15:32933876-32989299	NOTEST	0.149828	0.235292	0.651146	0	1	1
ENSG00000166923	ENSG00000166923	GREM1	15:33009470-33026870	NOTEST	0.0692392	0.00465759	-3.89393	0	1	1
ENSG00000166926	ENSG00000166926	MS4A6E	11:60102303-60185161	NOTEST	0.0376075	0	#NAME?	0	1	1
ENSG00000166928	ENSG00000166928	MS4A14	11:60102303-60185161	NOTEST	0.0711885	0.0693743	-0.0372422	0	1	1
ENSG00000166930	ENSG00000166930	MS4A5	11:60197061-60222687	NOTEST	0	0	0	0	1	1
ENSG00000166947	ENSG00000166947	EPB42	15:43398422-43513481	NOTEST	0.0380215	0.049071	0.368054	0	1	1
ENSG00000166948	ENSG00000166948	TGM6	20:2361553-2413399	NOTEST	0	0	0	0	1	1
ENSG00000166959	ENSG00000166959	MS4A8	11:60467046-60483284	NOTEST	0	0.0368621	inf	0	1	1
ENSG00000166960	ENSG00000166960	CCDC178	18:30413416-31021065	NOTEST	0	0	0	0	1	1
ENSG00000166961	ENSG00000166961	MS4A15	11:60524425-60544205	NOTEST	0	0	0	0	1	1
ENSG00000166963	ENSG00000166963	MAP1A	15:43803155-43823818	NOTEST	0.493485	0.312186	-0.660603	0	1	1
ENSG00000166984	ENSG00000166984	TCP10L2	6:167559901-167610401	NOTEST	0	0	0	0	1	1
ENSG00000167011	ENSG00000167011	NAT16	7:100813773-100823557	NOTEST	0.153758	0.578931	1.91273	0	1	1
ENSG00000167014	ENSG00000167014	C15orf43	15:45248899-45271427	NOTEST	0	0	0	0	1	1
ENSG00000167034	ENSG00000167034	NKX3-1	8:23536205-23540440	NOTEST	0.103016	0.118028	0.19627	0	1	1

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ENSG00000167046	ENSG00000167046	RP11-93B14.6	20:61272070-61317137	NOTEST	0	0.00654944	inf	0	1	1
ENSG00000167077	ENSG00000167077	MEI1	22:42095502-42195460	NOTEST	0.0705576	0.129798	0.87939	0	1	1
ENSG00000167080	ENSG00000167080	B4GALNT2	17:47209821-47247351	NOTEST	0	0	0	0	1	1
ENSG00000167083	ENSG00000167083	GNGT2	17:47280152-47300587	NOTEST	0	0	0	0	1	1
ENSG00000167094	ENSG00000167094	TTC16	9:130374543-130497604	NOTEST	0.00547052	0.0505905	3.20912	0	1	1
ENSG00000167098	ENSG00000167098	SUN5	20:31571578-31592239	NOTEST	0	0	0	0	1	1
ENSG00000167100	ENSG00000167100	SAMD14	17:48172100-48207246	NOTEST	0.334393	0.463071	0.469689	0	1	1
ENSG00000167103	ENSG00000167103	PIP5KL1	9:130683157-130693076	NOTEST	0.189192	0.409028	1.11235	0	1	1
ENSG00000167104	ENSG00000167104	BPIFB6	20:31619453-31631853	NOTEST	0	0	0	0	1	1
ENSG00000167117	ENSG00000167117	LINC00483	17:48838389-48844918	NOTEST	0	0	0	0	1	1
ENSG00000167139	ENSG00000167139	TBC1D21	15:74165948-74181555	NOTEST	0	0	0	0	1	1
ENSG00000167157	ENSG00000167157	PRRX2	9:132427919-132484875	NOTEST	0.02797	0.164362	2.55492	0	1	1
ENSG00000167165	ENSG00000167165	UGT1A6	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000167178	ENSG00000167178	ISLR2	15:74392651-74430881	NOTEST	0.0642887	0	#NAME?	0	1	1
ENSG00000167183	ENSG00000167183	PRR15L	17:46018871-46073562	NOTEST	0	0.0498209	inf	0	1	1
ENSG00000167194	ENSG00000167194	C16orf92	16:30034654-30064299	NOTEST	0	0	0	0	1	1
ENSG00000167195	ENSG00000167195	GOLGA6C	15:75550939-75562540	NOTEST	0	0	0	0	1	1
ENSG00000167207	ENSG00000167207	NOD2	16:50727513-50766988	NOTEST	0.00344159	0.0635914	4.20768	0	1	1
ENSG00000167208	ENSG00000167208	SNX20	16:50700121-50715264	NOTEST	0.00810634	0.00525603	-0.625077	0	1	1
ENSG00000167210	ENSG00000167210	LOXHD1	18:44056934-44236996	NOTEST	0	0	0	0	1	1
ENSG00000167230	ENSG00000167230	C17orf78	17:35441922-35766909	NOTEST	0	0	0	0	1	1
ENSG00000167236	ENSG00000167236	CCL23	17:34340095-34345005	NOTEST	0	0	0	0	1	1
ENSG00000167261	ENSG00000167261	DPEP2	16:68021296-68272005	NOTEST	0	0.00684338	inf	0	1	1
ENSG00000167281	ENSG00000167281	RBFOX3	17:77085426-77613550	NOTEST	0	0.0410822	inf	0	1	1
ENSG00000167286	ENSG00000167286	CD3D	11:118209668-118213459	NOTEST	0	0	0	0	1	1
ENSG00000167311	ENSG00000167311	ART5	11:3659732-3663546	NOTEST	0	0.168312	inf	0	1	1
ENSG00000167332	ENSG00000167332	OR51E2	11:4701400-4719084	NOTEST	0	0	0	0	1	1
ENSG00000167346	ENSG00000167346	MMP26	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000167355	ENSG00000167355	AC104389.28	11:5274419-5667019	NOTEST	0.014972	0	#NAME?	0	1	1
ENSG00000167359	ENSG00000167359	OR51I1	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000167360	ENSG00000167360	OR51Q1	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000167371	ENSG00000167371	PRRT2	16:29817426-29859355	NOTEST	0.475272	0.460886	-0.0443435	0	1	1
ENSG00000167383	ENSG00000167383	ZNF229	19:44830707-44952766	NOTEST	0.286797	0.507601	0.823666	0	1	1
ENSG00000167390	ENSG00000167390	POM121L3P	20:23969928-23971091	NOTEST	0	0	0	0	1	1
ENSG00000167414	ENSG00000167414	GNG8	19:47137332-47137942	NOTEST	0	0	0	0	1	1
ENSG00000167419	ENSG00000167419	LPO	17:56282802-56345879	NOTEST	0.00928165	0.0199532	1.10417	0	1	1
ENSG00000167434	ENSG00000167434	CA4	17:58227296-58248260	NOTEST	0	0	0	0	1	1
ENSG00000167459	ENSG00000167459	LINC00905	19:16142116-16152926	NOTEST	0	0	0	0	1	1
ENSG00000167476	ENSG00000167476	JSRP1	19:2252250-2273487	NOTEST	0.157469	0.0452338	-1.79959	0	1	1
ENSG00000167483	ENSG00000167483	FAM129C	19:17634109-17664648	NOTEST	0	0.0391385	inf	0	1	1
ENSG00000167494	ENSG00000167494	NOS2P2	17:18400885-18404348	NOTEST	0	0	0	0	1	1
ENSG00000167525	ENSG00000167525	PROCA1	17:27030214-27038872	NOTEST	0.265462	0.21286	-0.318596	0	1	1
ENSG00000167531	ENSG00000167531	LALBA	12:48961466-48963849	NOTEST	0	0	0	0	1	1
ENSG00000167554	ENSG00000167554	ZNF610	19:52772823-52871031	NOTEST	0.15139	0.0709542	-1.09331	0	1	1

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ENSG00000167588	ENSG00000167588	GPD1	12:50497601-50505102	NOTEST	0.425687	0.391564	-0.120543	0	1	1
ENSG00000167600	ENSG00000167600	CYP2S1	19:41698953-41713444	NOTEST	0.0859732	0.153376	0.835115	0	1	1
ENSG00000167601	ENSG00000167601	AXL	19:41725107-41767671	NOTEST	0.0522303	0.217775	2.05988	0	1	1
ENSG00000167612	ENSG00000167612	ANKRD33	12:52281743-52285448	NOTEST	0	0	0	0	1	1
ENSG00000167613	ENSG00000167613	LAIR1	19:54865361-54882165	NOTEST	0	0	0	0	1	1
ENSG00000167614	ENSG00000167614	TTYH1	19:54926392-54948080	NOTEST	0.0516889	0.022454	-1.20288	0	1	1
ENSG00000167618	ENSG00000167618	LAIR2	19:55009099-55021897	NOTEST	0	0	0	0	1	1
ENSG00000167633	ENSG00000167633	KIR3DL1	19:55235968-55378662	NOTEST	0	0	0	0	1	1
ENSG00000167634	ENSG00000167634	NLRP7	19:55434876-55512510	NOTEST	0	0	0	0	1	1
ENSG00000167642	ENSG00000167642	SPINT2	19:38734674-38795649	NOTEST	0.260215	0.312204	0.262783	0	1	1
ENSG00000167644	ENSG00000167644	C19orf33	19:38734674-38795649	NOTEST	0	0.370288	inf	0	1	1
ENSG00000167654	ENSG00000167654	ATCAY	19:3879861-3928077	NOTEST	0.00543373	0.145357	4.74152	0	1	1
ENSG00000167656	ENSG00000167656	LY6D	8:143866295-143893536	NOTEST	0	0	0	0	1	1
ENSG00000167664	ENSG00000167664	TMIGD2	19:4292228-4302428	NOTEST	0	0	0	0	1	1
ENSG00000167676	ENSG00000167676	PLIN4	19:4472283-4517716	NOTEST	0.0731934	0.0615	-0.251125	0	1	1
ENSG00000167701	ENSG00000167701	GPT	8:145703351-145732557	NOTEST	0.0756103	0.139082	0.879279	0	1	1
ENSG00000167703	ENSG00000167703	SLC43A2	17:1472560-1532180	NOTEST	0.421481	0.561086	0.412754	0	1	1
ENSG00000167711	ENSG00000167711	SERPINF2	17:1646129-1658562	NOTEST	0.21783	0.324752	0.576134	0	1	1
ENSG00000167723	ENSG00000167723	TRPV3	17:3343312-3461289	NOTEST	0.0557163	0.0684395	0.296731	0	1	1
ENSG00000167741	ENSG00000167741	GGT6	17:4460221-4464113	NOTEST	0.0113678	0	#NAME?	0	1	1
ENSG00000167748	ENSG00000167748	KLK1	19:51322403-51327043	NOTEST	0.0213645	0.0441868	1.0484	0	1	1
ENSG00000167749	ENSG00000167749	KLK4	19:51409607-51413994	NOTEST	0.0490136	0.057919	0.240854	0	1	1
ENSG00000167751	ENSG00000167751	KLK2	19:51364823-51383823	NOTEST	0.177577	0.551953	1.6361	0	1	1
ENSG00000167754	ENSG00000167754	KLK5	19:51446558-51515385	NOTEST	0	0	0	0	1	1
ENSG00000167755	ENSG00000167755	KLK6	19:51446558-51515385	NOTEST	0.0125628	0	#NAME?	0	1	1
ENSG00000167757	ENSG00000167757	KLK11	19:51525471-51531295	NOTEST	0	0	0	0	1	1
ENSG00000167759	ENSG00000167759	KLK13	19:51559462-51568371	NOTEST	0.119778	0.167593	0.484601	0	1	1
ENSG00000167765	ENSG00000167765	AC018755.1	19:52095035-52097630	NOTEST	0.228639	0.179272	-0.350924	0	1	1
ENSG00000167767	ENSG00000167767	KRT80	12:52562779-52585784	NOTEST	0.212352	0.573013	1.43211	0	1	1
ENSG00000167768	ENSG00000167768	KRT1	12:53068519-53074191	NOTEST	0	0	0	0	1	1
ENSG00000167769	ENSG00000167769	ACER1	19:6306152-6333640	NOTEST	0	0	0	0	1	1
ENSG00000167772	ENSG00000167772	ANGPTL4	19:8428172-8469318	NOTEST	0.220488	0.16936	-0.38061	0	1	1
ENSG00000167774	ENSG00000167774	NDUFA7	19:8367010-8408146	NOTEST	0.00255124	0.00299956	0.233551	0	1	1
ENSG00000167780	ENSG00000167780	SOAT2	12:53497301-53518322	NOTEST	0	0	0	0	1	1
ENSG00000167791	ENSG00000167791	CABP2	11:67286382-67290899	NOTEST	0	0	0	0	1	1
ENSG00000167798	ENSG00000167798	C3P1	19:10148478-10184811	NOTEST	0.00799482	0	#NAME?	0	1	1
ENSG00000167800	ENSG00000167800	TBX10	11:67398773-67407031	NOTEST	0	0	0	0	1	1
ENSG00000167807	ENSG00000167807	CTD-2369P2.10	19:10415478-10444316	NOTEST	0.176072	0.089555	-0.975322	0	1	1
ENSG00000167822	ENSG00000167822	OR8J3	11:55904246-55905194	NOTEST	0	0	0	0	1	1
ENSG00000167825	ENSG00000167825	OR5I1	11:55702931-55703876	NOTEST	0	0	0	0	1	1
ENSG00000167850	ENSG00000167850	CD300C	17:72537246-72542282	NOTEST	0	0	0	0	1	1
ENSG00000167851	ENSG00000167851	CD300A	17:72462554-72480933	NOTEST	0	0	0	0	1	1
ENSG00000167858	ENSG00000167858	TEKT1	17:6679541-6735080	NOTEST	0	0	0	0	1	1
ENSG00000167861	ENSG00000167861	HID1	17:72946837-72971823	NOTEST	0.0617463	0.200566	1.69965	0	1	1

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ENSG00000167880	ENSG00000167880	EVPL	17:73937587-74023533	NOTEST	0.265808	0.357596	0.427943	0	1	1
ENSG00000167910	ENSG00000167910	CYP7A1	8:59402736-59412795	NOTEST	0.0256908	0.0320833	0.320568	0	1	1
ENSG00000167914	ENSG00000167914	GSDMA	17:38119225-38134019	NOTEST	0	0	0	0	1	1
ENSG00000167916	ENSG00000167916	KRT24	17:38854242-38860002	NOTEST	0	0	0	0	1	1
ENSG00000167941	ENSG00000167941	SOST	17:41831098-41836156	NOTEST	0	0	0	0	1	1
ENSG00000167945	ENSG00000167945	PRR25	16:855442-863861	NOTEST	0	0.0222463	inf	0	1	1
ENSG00000167968	ENSG00000167968	DNASE1L2	16:2273566-2288712	NOTEST	0.0404431	0.0639356	0.660727	0	1	1
ENSG00000167970	ENSG00000167970	AC009065.1	16:2303116-2323419	NOTEST	0.182599	0	#NAME?	0	1	1
ENSG00000167984	ENSG00000167984	NLRC3	16:3415098-3627401	NOTEST	0.0614356	0.130758	1.08975	0	1	1
ENSG00000167992	ENSG00000167992	VWCE	11:61025761-61062896	NOTEST	0.206214	0.34672	0.749632	0	1	1
ENSG00000168004	ENSG00000168004	HRASLS5	11:63228875-63258666	NOTEST	0	0	0	0	1	1
ENSG00000168032	ENSG00000168032	ENTPD3	3:40355292-40494820	NOTEST	0.0202737	0.00393789	-2.36411	0	1	1
ENSG00000168060	ENSG00000168060	NAALADL1	11:64808372-64826021	NOTEST	0.0743926	0	#NAME?	0	1	1
ENSG00000168062	ENSG00000168062	BATF2	11:64755414-64764517	NOTEST	0.557036	0.522219	-0.0931163	0	1	1
ENSG00000168065	ENSG00000168065	SLC22A11	11:64323097-64340347	NOTEST	0	0	0	0	1	1
ENSG00000168070	ENSG00000168070	C11orf85	11:64704988-64739557	NOTEST	0.114175	0.13759	0.269129	0	1	1
ENSG00000168077	ENSG00000168077	SCARA3	8:27491384-27534293	NOTEST	0.00893631	0.0440664	2.30193	0	1	1
ENSG00000168079	ENSG00000168079	SCARA5	8:27727398-27850244	NOTEST	0.272092	0.42569	0.645706	0	1	1
ENSG00000168081	ENSG00000168081	PNOC	8:28107579-28200872	NOTEST	0	0.0302065	inf	0	1	1
ENSG00000168122	ENSG00000168122	ZNF355P	21:14467625-14486111	NOTEST	0	0	0	0	1	1
ENSG00000168124	ENSG00000168124	OR1F1	16:3238211-3286221	NOTEST	0.185974	0.157019	-0.24416	0	1	1
ENSG00000168126	ENSG00000168126	OR2W6P	6:27905242-27906181	NOTEST	0	0	0	0	1	1
ENSG00000168129	ENSG00000168129	AC098817.5	2:83083926-83084885	NOTEST	0	0	0	0	1	1
ENSG00000168131	ENSG00000168131	OR2B2	6:27878962-27880174	NOTEST	0	0	0	0	1	1
ENSG00000168135	ENSG00000168135	KCNJ4	22:38820292-38851205	NOTEST	0.0504405	0.0952561	0.917228	0	1	1
ENSG00000168143	ENSG00000168143	FAM83B	6:54711568-54806820	NOTEST	0.00991368	0.015032	0.600541	0	1	1
ENSG00000168148	ENSG00000168148	HIST3H3	1:228612545-228613026	NOTEST	0	0	0	0	1	1
ENSG00000168158	ENSG00000168158	OR2C1	16:3405888-3406924	NOTEST	0	0.013351	inf	0	1	1
ENSG00000168229	ENSG00000168229	PTGDR	14:52734430-52743442	NOTEST	0	0	0	0	1	1
ENSG00000168242	ENSG00000168242	HIST1H2BI	6:26273143-26273622	NOTEST	0	0	0	0	1	1
ENSG00000168260	ENSG00000168260	C14orf183	14:50448429-50559361	NOTEST	0	0.0143657	inf	0	1	1
ENSG00000168263	ENSG00000168263	KCNV2	9:2717501-2844241	NOTEST	0.0207291	0.0338533	0.707641	0	1	1
ENSG00000168267	ENSG00000168267	PTF1A	10:23481255-23483181	NOTEST	0	0	0	0	1	1
ENSG00000168269	ENSG00000168269	FOXI1	5:169532900-169536727	NOTEST	0	0	0	0	1	1
ENSG00000168280	ENSG00000168280	KIF5C	2:149624038-149883273	NOTEST	0.308945	0.585137	0.921425	0	1	1
ENSG00000168298	ENSG00000168298	HIST1H1E	6:26156558-26157343	NOTEST	0.185493	0.329349	0.828254	0	1	1
ENSG00000168306	ENSG00000168306	ACOX2	3:58490862-58523046	NOTEST	0.091194	0.259306	1.50764	0	1	1
ENSG00000168309	ENSG00000168309	FAM107A	3:58549843-58652575	NOTEST	0	0	0	0	1	1
ENSG00000168314	ENSG00000168314	MOBP	3:39508688-39570970	NOTEST	0	0	0	0	1	1
ENSG00000168329	ENSG00000168329	CX3CR1	3:39304984-39323226	NOTEST	0	0.0271396	inf	0	1	1
ENSG00000168333	ENSG00000168333	C8orf22	8:49966869-49988649	NOTEST	0	0	0	0	1	1
ENSG00000168334	ENSG00000168334	XIRP1	3:39224700-39234087	NOTEST	0.00612402	0	#NAME?	0	1	1
ENSG00000168348	ENSG00000168348	INSM2	14:36003247-36006260	NOTEST	0.00944409	0.00366866	-1.36416	0	1	1
ENSG00000168350	ENSG00000168350	DEGS2	14:100612755-100626500	NOTEST	0	0.0423401	inf	0	1	1
ENSG00000168356	ENSG00000168356	SCN11A	3:38887259-38992052	NOTEST	0.00526204	0.00207513	-1.34242	0	1	1

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ENSG00000168367	ENSG00000168367	LINC00917	16:86365449-86383289	NOTEST	0	0	0	0	1	1
ENSG00000168379	ENSG00000168379	HLA-DPB2	HSCHR6_MHC_SSTO:33219847-33236168	NOTEST	0	0	0	0	1	1
ENSG00000168384	ENSG00000168384	HLA-DPA1	HSCHR6_MHC_MCF:33065821-33088426	NOTEST	0	0	0	0	1	1
ENSG00000168386	ENSG00000168386	FILIP1L	3:99536677-99897447	NOTEST	0	0.00536681	inf	0	1	1
ENSG00000168398	ENSG00000168398	BDKRB2	14:96671015-96735304	NOTEST	0	0	0	0	1	1
ENSG00000168405	ENSG00000168405	CMAHP	6:25081547-25166793	NOTEST	0.017938	0.0683146	1.92917	0	1	1
ENSG00000168412	ENSG00000168412	MTNR1A	4:187187098-187476721	NOTEST	0	0	0	0	1	1
ENSG00000168418	ENSG00000168418	KCNG4	16:84255822-84273356	NOTEST	0.0219795	0.0645865	1.55508	0	1	1
ENSG00000168421	ENSG00000168421	RHOH	4:40192672-40248587	NOTEST	0	0	0	0	1	1
ENSG00000168427	ENSG00000168427	KLHL30	2:239047362-239061588	NOTEST	0.0118402	0.0864788	2.86865	0	1	1
ENSG00000168447	ENSG00000168447	SCNN1B	16:23289551-23392620	NOTEST	0	0	0	0	1	1
ENSG00000168452	ENSG00000168452	PPT2	HSCHR6_MHC_MANN:32155582-32185300	NOTEST	0	0	0	0	1	1
ENSG00000168454	ENSG00000168454	TXNDC2	18:9885762-9889272	NOTEST	0.0100969	0.00753259	-0.422689	0	1	1
ENSG00000168468	ENSG00000168468	ATF6B	HSCHR6_MHC_DBB:31981893-32071805	NOTEST	0	0	0	0	1	1
ENSG00000168491	ENSG00000168491	CCDC110	4:186347393-186393417	NOTEST	0.188602	0.145905	-0.370316	0	1	1
ENSG00000168497	ENSG00000168497	SDPR	2:192699027-193060435	NOTEST	0	0	0	0	1	1
ENSG00000168505	ENSG00000168505	GBX2	2:237073878-237203570	NOTEST	0.0409041	0.0829899	1.02069	0	1	1
ENSG00000168509	ENSG00000168509	HFE2	1:145413094-145417545	NOTEST	0	0	0	0	1	1
ENSG00000168515	ENSG00000168515	SCGB1D1	11:61957687-61961011	NOTEST	0	0	0	0	1	1
ENSG00000168530	ENSG00000168530	MYL1	2:211154873-211179914	NOTEST	0.0287631	0	#NAME?	0	1	1
ENSG00000168539	ENSG00000168539	CHRM1	11:62676150-62689279	NOTEST	0	0.0261319	inf	0	1	1
ENSG00000168542	ENSG00000168542	COL3A1	2:189839045-189877472	NOTEST	0.0027644	0.00387888	0.488673	0	1	1
ENSG00000168546	ENSG00000168546	GFRA2	8:21547914-21669869	NOTEST	0	0.00855572	inf	0	1	1
ENSG00000168582	ENSG00000168582	CRYGA	2:209025463-209028300	NOTEST	0	0	0	0	1	1
ENSG00000168589	ENSG00000168589	DYNLRB2	16:80099732-80597032	NOTEST	0	0	0	0	1	1
ENSG00000168594	ENSG00000168594	ADAM29	4:175750818-175900532	NOTEST	0	0	0	0	1	1
ENSG00000168619	ENSG00000168619	ADAM18	8:39442007-39587583	NOTEST	0	0	0	0	1	1
ENSG00000168630	ENSG00000168630	SPINT5P	20:44376582-44420571	NOTEST	0	0	0	0	1	1
ENSG00000168631	ENSG00000168631	DPCR1	6:30908748-30922639	NOTEST	0.00289546	0	#NAME?	0	1	1
ENSG00000168634	ENSG00000168634	WFDC13	20:44313291-44337456	NOTEST	0	0	0	0	1	1
ENSG00000168658	ENSG00000168658	VWA3B	2:98703578-98929762	NOTEST	0.0111664	0	#NAME?	0	1	1
ENSG00000168671	ENSG00000168671	UGT3A2	5:36035118-36071460	NOTEST	0.0320447	0.0730695	1.18918	0	1	1
ENSG00000168676	ENSG00000168676	KCTD19	16:67311412-67360666	NOTEST	0.27606	0.161291	-0.775315	0	1	1
ENSG00000168685	ENSG00000168685	IL7R	5:35852796-35879705	NOTEST	0.00601592	0.00803268	0.417094	0	1	1
ENSG00000168702	ENSG00000168702	LRP1B	2:140988991-142895399	NOTEST	0.00736917	0	#NAME?	0	1	1
ENSG00000168703	ENSG00000168703	WFDC12	20:43752065-43753106	NOTEST	0	0	0	0	1	1
ENSG00000168743	ENSG00000168743	NPNT	4:106473776-106943635	NOTEST	0	0.0080835	inf	0	1	1
ENSG00000168746	ENSG00000168746	C20orf62	20:43080623-43093984	NOTEST	0	0.021851	inf	0	1	1
ENSG00000168748	ENSG00000168748	CA7	16:66836777-66907159	NOTEST	0	0	0	0	1	1
ENSG00000168757	ENSG00000168757	TSPY2	Y:6114263-6117060	NOTEST	0	0	0	0	1	1
ENSG00000168772	ENSG00000168772	CXXC4	4:105389468-106041157	NOTEST	0.326068	0.131326	-1.31202	0	1	1
ENSG00000168787	ENSG00000168787	OR12D2	6:29323006-29424848	NOTEST	0	0	0	0	1	1
ENSG00000168828	ENSG00000168828	OR13J1	9:35869374-35870461	NOTEST	0	0	0	0	1	1
ENSG00000168830	ENSG00000168830	HTR1E	6:87647023-87726349	NOTEST	0	0	0	0	1	1
ENSG00000168875	ENSG00000168875	SOX14	3:137483578-137484396	NOTEST	0.0420597	0	#NAME?	0	1	1

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ENSG00000168878	ENSG00000168878	SFTPB	2:85884436-85895864	NOTEST	0	0.00340863	inf	0	1	1
ENSG00000168903	ENSG00000168903	BTNL3	5:180415844-180433727	NOTEST	0	0	0	0	1	1
ENSG00000168907	ENSG00000168907	PLA2G4F	15:42433331-42448839	NOTEST	0	0	0	0	1	1
ENSG00000168917	ENSG00000168917	SLC35G2	3:136537488-136580896	NOTEST	0.120866	0.269395	1.15632	0	1	1
ENSG00000168918	ENSG00000168918	INPP5D	2:233924676-234116549	NOTEST	0.0482605	0.0666043	0.464772	0	1	1
ENSG00000168925	ENSG00000168925	CTRB1	16:75252897-75258822	NOTEST	0	0	0	0	1	1
ENSG00000168928	ENSG00000168928	CTRB2	16:75237993-75241083	NOTEST	0	0	0	0	1	1
ENSG00000168930	ENSG00000168930	TRIM49	11:89530822-89541743	NOTEST	0	0	0	0	1	1
ENSG00000168939	ENSG00000168939	SPRY3	X:154997473-155012121	NOTEST	0.222704	0.215362	-0.0483624	0	1	1
ENSG00000168955	ENSG00000168955	TM4SF20	2:228226871-228246711	NOTEST	0	0	0	0	1	1
ENSG00000168959	ENSG00000168959	GRM5	11:88237743-88799113	NOTEST	1.11E-07	0.0240287	17.7222	0	1	1
ENSG00000168961	ENSG00000168961	LGALS9	17:25783669-25976586	NOTEST	0.0455028	0.114155	1.32697	0	1	1
ENSG00000168967	ENSG00000168967	PMCHL1	5:21616370-22853731	NOTEST	0	0	0	0	1	1
ENSG00000168992	ENSG00000168992	OR7E102P	2:96212278-96213315	NOTEST	0.0351719	0.0136707	-1.36334	0	1	1
ENSG00000168993	ENSG00000168993	CPLX1	4:778744-819986	NOTEST	0.32424	0.261484	-0.31034	0	1	1
ENSG00000168995	ENSG00000168995	SIGLEC7	19:51645555-51685222	NOTEST	0	0.00729063	inf	0	1	1
ENSG00000169006	ENSG00000169006	NTSR2	2:11798303-11810290	NOTEST	0	0	0	0	1	1
ENSG00000169026	ENSG00000169026	MFSD7	4:666224-683230	NOTEST	0	0.0701788	inf	0	1	1
ENSG00000169031	ENSG00000169031	COL4A3	2:228029280-228222550	NOTEST	0.00862887	0.00131414	-2.71506	0	1	1
ENSG00000169035	ENSG00000169035	KLK7	19:51446558-51515385	NOTEST	0	0	0	0	1	1
ENSG00000169040	ENSG00000169040	PMCHL2	5:70647681-70742396	NOTEST	0	0	0	0	1	1
ENSG00000169059	ENSG00000169059	VCX3A	X:6451658-6453159	NOTEST	0.0699523	0.386119	2.4646	0	1	1
ENSG00000169064	ENSG00000169064	ZBBX	3:166958074-167099134	NOTEST	0.271334	0.0667171	-2.02394	0	1	1
ENSG00000169067	ENSG00000169067	ACTBL2	5:56690886-56829251	NOTEST	0.0375004	0.00398005	-3.23605	0	1	1
ENSG00000169071	ENSG00000169071	ROR2	9:94325372-94712444	NOTEST	0.00951107	0	#NAME?	0	1	1
ENSG00000169075	ENSG00000169075	BRD7P3	6:118781934-119031238	NOTEST	0.0206495	0	#NAME?	0	1	1
ENSG00000169083	ENSG00000169083	AR	X:66764464-66950461	NOTEST	0.0344985	0.0360479	0.0633804	0	1	1
ENSG00000169116	ENSG00000169116	PARM1	4:75858304-75975325	NOTEST	0	0	0	0	1	1
ENSG00000169126	ENSG00000169126	ARMC4	10:28064114-28287977	NOTEST	0	0	0	0	1	1
ENSG00000169129	ENSG00000169129	AFAP1L2	10:116054582-116164515	NOTEST	0.339851	0.444403	0.386967	0	1	1
ENSG00000169154	ENSG00000169154	GOT1L1	8:37791798-37797647	NOTEST	0	0	0	0	1	1
ENSG00000169164	ENSG00000169164	RP11-167P23.2	X:55681141-55683447	NOTEST	0	0	0	0	1	1
ENSG00000169174	ENSG00000169174	PCSK9	1:55505220-55530525	NOTEST	0.0506471	0.15733	1.63525	0	1	1
ENSG00000169181	ENSG00000169181	GSG1L	16:27798849-28074830	NOTEST	0.0204642	0.0255246	0.318791	0	1	1
ENSG00000169184	ENSG00000169184	MN1	22:28144264-28197486	NOTEST	0.0112725	0.00141046	-2.99857	0	1	1
ENSG00000169194	ENSG00000169194	IL13	5:131877135-131999964	NOTEST	0	0	0	0	1	1
ENSG00000169202	ENSG00000169202	OR10G1P	14:22070048-22070976	NOTEST	0	0	0	0	1	1
ENSG00000169208	ENSG00000169208	OR10G3	14:22037933-22038875	NOTEST	0	0	0	0	1	1
ENSG00000169213	ENSG00000169213	RAB3B	1:52373627-52456436	NOTEST	0.00351538	0.0191441	2.44515	0	1	1
ENSG00000169214	ENSG00000169214	OR6F1	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000169218	ENSG00000169218	RSPO1	1:38076950-38100595	NOTEST	0	0	0	0	1	1
ENSG00000169224	ENSG00000169224	GCSAML	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000169248	ENSG00000169248	CXCL11	4:76932336-77033955	NOTEST	0.0394775	0.187524	2.24798	0	1	1
ENSG00000169253	ENSG00000169253	RP11-220D10.1	9:111389112-111389430	NOTEST	0	0	0	0	1	1

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ENSG00000169260	ENSG00000169260	ZNF311	HSCHR6_MHC_QBL:28962561-28973093	NOTEST	0	0	0	0	1	1
ENSG00000169271	ENSG00000169271	HSPB3	5:53751444-53752207	NOTEST	0	0.0177179	inf	0	1	1
ENSG00000169291	ENSG00000169291	SHE	1:154442247-154474589	NOTEST	0.00269008	0.0391311	3.8626	0	1	1
ENSG00000169313	ENSG00000169313	P2RY12	3:150803483-151176497	NOTEST	0	0.014639	inf	0	1	1
ENSG00000169314	ENSG00000169314	C22orf15	22:24105207-24126503	NOTEST	0.0311738	0.053096	0.768267	0	1	1
ENSG00000169325	ENSG00000169325	GUSBP12	7:57268437-57271304	NOTEST	0	0	0	0	1	1
ENSG00000169327	ENSG00000169327	OR5AU1	14:21623025-21624222	NOTEST	0	0	0	0	1	1
ENSG00000169340	ENSG00000169340	PDILT	16:20370491-20416059	NOTEST	0	0	0	0	1	1
ENSG00000169344	ENSG00000169344	UMOD	16:20344373-20367623	NOTEST	0	0	0	0	1	1
ENSG00000169347	ENSG00000169347	GP2	16:20320893-20339130	NOTEST	0	0	0	0	1	1
ENSG00000169385	ENSG00000169385	RNASE2	14:21423610-21424595	NOTEST	0	0	0	0	1	1
ENSG00000169393	ENSG00000169393	ELSPBP1	19:48497907-48528410	NOTEST	0	0	0	0	1	1
ENSG00000169397	ENSG00000169397	RNASE3	14:21359557-21360507	NOTEST	0	0	0	0	1	1
ENSG00000169402	ENSG00000169402	RSPH10B2	7:6793739-6866401	NOTEST	0.044344	0.0247372	-0.84206	0	1	1
ENSG00000169403	ENSG00000169403	PTAFR	1:28473676-28520447	NOTEST	0.0562659	0.0485114	-0.213937	0	1	1
ENSG00000169413	ENSG00000169413	RNASE6	14:21249209-21250626	NOTEST	0	0.0259508	inf	0	1	1
ENSG00000169427	ENSG00000169427	KCNK9	8:140613080-140715299	NOTEST	0	0.12488	inf	0	1	1
ENSG00000169432	ENSG00000169432	SCN9A	2:166813908-167232503	NOTEST	0.147671	0.190796	0.369643	0	1	1
ENSG00000169435	ENSG00000169435	RASSF6	4:74437266-74486348	NOTEST	0	0.0194181	inf	0	1	1
ENSG00000169436	ENSG00000169436	COL22A1	8:139600477-139926249	NOTEST	0.0181441	0.167278	3.20468	0	1	1
ENSG00000169442	ENSG00000169442	CD52	1:26605666-26647014	NOTEST	0	0	0	0	1	1
ENSG00000169469	ENSG00000169469	SPRR1B	1:153003677-153005376	NOTEST	0	0	0	0	1	1
ENSG00000169474	ENSG00000169474	SPRR1A	1:152956556-152958289	NOTEST	0	0	0	0	1	1
ENSG00000169484	ENSG00000169484	OR4K14	14:20482418-20483352	NOTEST	0	0	0	0	1	1
ENSG00000169488	ENSG00000169488	OR4K15	14:20443602-20444818	NOTEST	0	0	0	0	1	1
ENSG00000169495	ENSG00000169495	HTRA4	8:38831682-38846181	NOTEST	0.00771888	0.00599763	-0.363999	0	1	1
ENSG00000169508	ENSG00000169508	GPR183	13:99853027-100038688	NOTEST	0.0097133	0	#NAME?	0	1	1
ENSG00000169509	ENSG00000169509	CRCT1	1:152486977-152488486	NOTEST	0	0	0	0	1	1
ENSG00000169515	ENSG00000169515	CCDC8	19:46913628-46916841	NOTEST	0	0.00342711	inf	0	1	1
ENSG00000169550	ENSG00000169550	MUC15	11:26210669-26684835	NOTEST	0.0050609	0.00603199	0.253239	0	1	1
ENSG00000169575	ENSG00000169575	VPREB1	22:22599086-22599927	NOTEST	0	0	0	0	1	1
ENSG00000169583	ENSG00000169583	CLIC3	9:139889086-139891255	NOTEST	0.0751176	0.137148	0.868514	0	1	1
ENSG00000169594	ENSG00000169594	BNC1	15:83776158-84108197	NOTEST	0.00895206	0.00347802	-1.36395	0	1	1
ENSG00000169605	ENSG00000169605	GKN1	2:69201704-69208106	NOTEST	0.0231003	0.0509728	1.14182	0	1	1
ENSG00000169618	ENSG00000169618	PROKR1	2:68870720-68882708	NOTEST	0.305793	0.152428	-1.00443	0	1	1
ENSG00000169662	ENSG00000169662	BCRP6	22:21645048-21648875	NOTEST	0	0	0	0	1	1
ENSG00000169668	ENSG00000169668	BCRP2	22:21457304-21482352	NOTEST	0.026663	0.0500502	0.908537	0	1	1
ENSG00000169676	ENSG00000169676	DRD5	4:9772776-10056560	NOTEST	0	0	0	0	1	1
ENSG00000169688	ENSG00000169688	MT1B	16:56682159-56687116	NOTEST	0	0	0	0	1	1
ENSG00000169704	ENSG00000169704	GP9	3:128779609-128781249	NOTEST	0	0	0	0	1	1
ENSG00000169715	ENSG00000169715	MT1E	16:56659386-56661024	NOTEST	0	0	0	0	1	1
ENSG00000169717	ENSG00000169717	ACTRT2	1:2938045-2939465	NOTEST	0	0	0	0	1	1
ENSG00000169744	ENSG00000169744	LDB2	4:16402052-16900432	NOTEST	0	0	0	0	1	1
ENSG00000169763	ENSG00000169763	PRYP3	Y:25827586-25840726	NOTEST	0	0	0	0	1	1
ENSG00000169777	ENSG00000169777	TAS2R1	5:9621488-9903938	NOTEST	0.0227978	0.0275857	0.275027	0	1	1

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ENSG00000169789	ENSG00000169789	PRY	Y:24636543-24660784	NOTEST	0	0	0	0	1	1
ENSG00000169800	ENSG00000169800	RBMY1F	Y:24314688-24329129	NOTEST	0	0	0	0	1	1
ENSG00000169807	ENSG00000169807	PRY2	Y:24217902-24242154	NOTEST	0	0	0	0	1	1
ENSG00000169811	ENSG00000169811	RBMY1HP	Y:23655404-23663854	NOTEST	0	0	0	0	1	1
ENSG00000169836	ENSG00000169836	TACR3	4:104469901-104640973	NOTEST	0.00533836	0	#NAME?	0	1	1
ENSG00000169840	ENSG00000169840	GSX1	13:28366779-28368905	NOTEST	0	0	0	0	1	1
ENSG00000169849	ENSG00000169849	TSPY14P	Y:23630043-23632569	NOTEST	0	0	0	0	1	1
ENSG00000169860	ENSG00000169860	P2RY1	3:152552735-152555841	NOTEST	0.282736	0.322848	0.191403	0	1	1
ENSG00000169861	ENSG00000169861	IGHV1OR21-1	21:10862621-10863067	NOTEST	0	0	0	0	1	1
ENSG00000169862	ENSG00000169862	CTNND2	5:10971951-11904155	NOTEST	0	0	0	0	1	1
ENSG00000169876	ENSG00000169876	MUC17	7:100663352-100702020	NOTEST	0	0	0	0	1	1
ENSG00000169877	ENSG00000169877	AHSP	16:31539184-31540124	NOTEST	0	0	0	0	1	1
ENSG00000169885	ENSG00000169885	CALML6	1:1846265-1848735	NOTEST	0.0403789	0.0122001	-1.72671	0	1	1
ENSG00000169894	ENSG00000169894	MUC3A	7:100547186-100611410	NOTEST	0.0278004	0.0120908	-1.2012	0	1	1
ENSG00000169896	ENSG00000169896	ITGAM	16:31271310-31344213	NOTEST	0.13708	0.210383	0.617999	0	1	1
ENSG00000169900	ENSG00000169900	PYDC1	16:31225341-31236510	NOTEST	0	0	0	0	1	1
ENSG00000169903	ENSG00000169903	TM4SF4	3:149191760-149221068	NOTEST	0	0	0	0	1	1
ENSG00000169906	ENSG00000169906	S100G	X:16606125-16731059	NOTEST	0	0	0	0	1	1
ENSG00000169918	ENSG00000169918	OTUD7A	15:31775328-32162992	NOTEST	0.430642	0.352885	-0.28729	0	1	1
ENSG00000169933	ENSG00000169933	FRMPD4	X:12156584-12742642	NOTEST	0.0189884	0.0650284	1.77595	0	1	1
ENSG00000169946	ENSG00000169946	ZFPM2	8:105602960-107072752	NOTEST	0.261188	0.140253	-0.897058	0	1	1
ENSG00000169953	ENSG00000169953	HSFY2	Y:20835918-20991373	NOTEST	0	0	0	0	1	1
ENSG00000169962	ENSG00000169962	TAS1R3	1:1266693-1284730	NOTEST	0.0218817	0.0205586	-0.0899795	0	1	1
ENSG00000169981	ENSG00000169981	ZNF35	3:44596684-44727145	NOTEST	0.0393156	0.00644772	-2.60824	0	1	1
ENSG00000169989	ENSG00000169989	TIGD4	4:153690505-153700916	NOTEST	0.248304	0.283249	0.189964	0	1	1
ENSG00000169994	ENSG00000169994	MYO7B	2:128293377-128395304	NOTEST	0	0	0	0	1	1
ENSG00000170006	ENSG00000170006	TMEM154	4:153539783-153601317	NOTEST	0.0135483	0.0715842	2.40152	0	1	1
ENSG00000170011	ENSG00000170011	MYRIP	3:39850404-40301812	NOTEST	0.134154	0.329133	1.29478	0	1	1
ENSG00000170044	ENSG00000170044	ZPLD1	3:101818087-102198685	NOTEST	0.0507895	0.0444585	-0.192073	0	1	1
ENSG00000170049	ENSG00000170049	KCNAB3	17:7825176-7853236	NOTEST	0.148068	0.0595552	-1.31397	0	1	1
ENSG00000170054	ENSG00000170054	SERPINA9	14:94896969-94946026	NOTEST	0	0	0	0	1	1
ENSG00000170074	ENSG00000170074	FAM153A	5:177109294-177221397	NOTEST	0	0	0	0	1	1
ENSG00000170075	ENSG00000170075	GPR37L1	1:202091985-202113869	NOTEST	0.0551931	0.0371451	-0.571317	0	1	1
ENSG00000170091	ENSG00000170091	NSG2	5:173472606-173670504	NOTEST	0.00651071	0.0202328	1.63581	0	1	1
ENSG00000170092	ENSG00000170092	AC018720.10	7:75123400-75157478	NOTEST	0.38046	0.374783	-0.0216924	0	1	1
ENSG00000170099	ENSG00000170099	SERPINA6	14:94770584-94789731	NOTEST	0	0.0207171	inf	0	1	1
ENSG00000170122	ENSG00000170122	FOXD4	9:116236-118417	NOTEST	0.0724843	0.0902781	0.316707	0	1	1
ENSG00000170128	ENSG00000170128	GPR25	1:200842082-200843306	NOTEST	0	0	0	0	1	1
ENSG00000170152	ENSG00000170152	RP11-374M1.7	9:44997776-44999352	NOTEST	0	0	0	0	1	1
ENSG00000170160	ENSG00000170160	CCDC144A	17:16592850-16719854	NOTEST	0.474739	0.430035	-0.142679	0	1	1
ENSG00000170162	ENSG00000170162	VGLL2	6:117586720-117594728	NOTEST	0	0.0232809	inf	0	1	1
ENSG00000170165	ENSG00000170165	CR848007.2	9:44051023-44069881	NOTEST	0.120917	0.00755325	-4.00077	0	1	1
ENSG00000170178	ENSG00000170178	HOXD12	2:176964457-176966408	NOTEST	0.140315	0.0724215	-0.954179	0	1	1
ENSG00000170180	ENSG00000170180	GYPA	4:144833483-145061904	NOTEST	0	0	0	0	1	1
ENSG00000170190	ENSG00000170190	SLC16A5	17:73083821-73102257	NOTEST	0.0816823	0.0478807	-0.770581	0	1	1

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ENSG00000170209	ENSG00000170209	ANKK1	11:113258512-113271140	NOTEST	0.0113244	0.00439696	-1.36486	0	1	1
ENSG00000170214	ENSG00000170214	ADRA1B	5:159343789-159399551	NOTEST	0	0	0	0	1	1
ENSG00000170217	ENSG00000170217	RP11-12A20.2	9:67784943-67786684	NOTEST	0	0	0	0	1	1
ENSG00000170231	ENSG00000170231	FABP6	5:159614373-159665742	NOTEST	0	0.155272	inf	0	1	1
ENSG00000170236	ENSG00000170236	USP50	15:50716576-50838905	NOTEST	0	0	0	0	1	1
ENSG00000170255	ENSG00000170255	MRGPRX1	11:18955359-18961268	NOTEST	0	0	0	0	1	1
ENSG00000170262	ENSG00000170262	MRAP	21:33664123-33765335	NOTEST	0	0	0	0	1	1
ENSG00000170279	ENSG00000170279	C7orf33	7:148287656-148312952	NOTEST	0	0	0	0	1	1
ENSG00000170289	ENSG00000170289	CNGB3	8:87345502-87777251	NOTEST	0	0	0	0	1	1
ENSG00000170290	ENSG00000170290	SLN	11:107578103-107595135	NOTEST	0	0	0	0	1	1
ENSG00000170298	ENSG00000170298	LGALS9B	17:20352707-20370852	NOTEST	0	0	0	0	1	1
ENSG00000170323	ENSG00000170323	FABP4	8:82351670-82445510	NOTEST	0	0	0	0	1	1
ENSG00000170324	ENSG00000170324	FRMPD2	10:49364600-49482941	NOTEST	0	0	0	0	1	1
ENSG00000170356	ENSG00000170356	OR2A20P	7:143883175-144077725	NOTEST	0	0	0	0	1	1
ENSG00000170367	ENSG00000170367	CST5	20:23856571-23860387	NOTEST	0	0	0	0	1	1
ENSG00000170370	ENSG00000170370	EMX2	10:119184704-119309056	NOTEST	0	0	0	0	1	1
ENSG00000170373	ENSG00000170373	CST1	20:23728189-23731905	NOTEST	0.0306884	0	#NAME?	0	1	1
ENSG00000170374	ENSG00000170374	SP7	12:53720361-53739099	NOTEST	0	0	0	0	1	1
ENSG00000170379	ENSG00000170379	FAM115C	7:143318042-143534026	NOTEST	0.113728	0.0563286	-1.01364	0	1	1
ENSG00000170381	ENSG00000170381	SEMA3E	7:82993221-83278326	NOTEST	0.106311	0.249747	1.23218	0	1	1
ENSG00000170382	ENSG00000170382	LRRN2	1:204586297-204654861	NOTEST	0.0256888	0.0107163	-1.26134	0	1	1
ENSG00000170396	ENSG00000170396	ZNF804A	2:185463092-185804219	NOTEST	0.0578681	0.0680463	0.233748	0	1	1
ENSG00000170409	ENSG00000170409	CTA-313A17.2	7:101967673-101969945	NOTEST	0	0	0	0	1	1
ENSG00000170412	ENSG00000170412	GPRC5C	17:72420989-72447792	NOTEST	0	0.0158522	inf	0	1	1
ENSG00000170419	ENSG00000170419	VSTM2A	7:54610017-54639419	NOTEST	0	0	0	0	1	1
ENSG00000170423	ENSG00000170423	KRT78	12:53231587-53242876	NOTEST	0	0	0	0	1	1
ENSG00000170426	ENSG00000170426	SDR9C7	12:57316937-57328189	NOTEST	0	0	0	0	1	1
ENSG00000170454	ENSG00000170454	KRT75	12:52801363-52828309	NOTEST	0	0.00535933	inf	0	1	1
ENSG00000170458	ENSG00000170458	CD14	5:140011312-140013286	NOTEST	0.0514929	0.0312597	-0.720071	0	1	1
ENSG00000170465	ENSG00000170465	KRT6C	12:52862299-52867569	NOTEST	0	0	0	0	1	1
ENSG00000170476	ENSG00000170476	MZB1	5:138723168-138725770	NOTEST	0.0222334	0	#NAME?	0	1	1
ENSG00000170477	ENSG00000170477	KRT4	12:53200332-53208335	NOTEST	0	0	0	0	1	1
ENSG00000170482	ENSG00000170482	SLC23A1	5:138677275-138720242	NOTEST	0.0823477	0.113274	0.46002	0	1	1
ENSG00000170484	ENSG00000170484	KRT74	12:52959565-52967609	NOTEST	0	0	0	0	1	1
ENSG00000170486	ENSG00000170486	KRT72	12:52979372-53012343	NOTEST	0	0	0	0	1	1
ENSG00000170498	ENSG00000170498	KISS1	1:204159468-204165614	NOTEST	0.02761	0	#NAME?	0	1	1
ENSG00000170509	ENSG00000170509	HSD17B13	4:88224940-88312538	NOTEST	0.0397541	0.00937741	-2.08384	0	1	1
ENSG00000170516	ENSG00000170516	COX7B2	4:46736843-46911252	NOTEST	0	0	0	0	1	1
ENSG00000170523	ENSG00000170523	KRT83	12:52708084-52715182	NOTEST	0.0157938	0	#NAME?	0	1	1
ENSG00000170537	ENSG00000170537	TMC7	16:18995255-19091417	NOTEST	0.0414622	0.0507334	0.29114	0	1	1
ENSG00000170549	ENSG00000170549	IRX1	5:3596167-3601517	NOTEST	0	0	0	0	1	1
ENSG00000170561	ENSG00000170561	IRX2	5:2745958-2755508	NOTEST	0	0	0	0	1	1
ENSG00000170577	ENSG00000170577	SIX2	2:45232299-45236569	NOTEST	0	0	0	0	1	1
ENSG00000170590	ENSG00000170590	LINC00266-3	6:131909-145083	NOTEST	0.0758038	0.100594	0.408207	0	1	1
ENSG00000170605	ENSG00000170605	OR9K2	12:55523464-55524586	NOTEST	0	0	0	0	1	1

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ENSG00000170608	ENSG00000170608	FOXA3	19:46367246-46377055	NOTEST	0	0.00634756	inf	0	1	1
ENSG00000170613	ENSG00000170613	FAM71B	5:156512842-156682201	NOTEST	0	0	0	0	1	1
ENSG00000170615	ENSG00000170615	SLC26A5	7:102937868-103629963	NOTEST	0.0656582	0	#NAME?	0	1	1
ENSG00000170616	ENSG00000170616	SCRT1	8:145554227-145559943	NOTEST	0.00411715	0.00288962	-0.510767	0	1	1
ENSG00000170627	ENSG00000170627	GTSF1	12:54747444-54891472	NOTEST	0.0234653	0.293117	3.64288	0	1	1
ENSG00000170667	ENSG00000170667	RASA4B	7:102122891-102312088	NOTEST	0.189887	0.299788	0.658802	0	1	1
ENSG00000170683	ENSG00000170683	OR10A3	11:7960080-7961141	NOTEST	0	0	0	0	1	1
ENSG00000170684	ENSG00000170684	ZNF296	19:45574757-45808541	NOTEST	0.00944183	0.0506607	2.42373	0	1	1
ENSG00000170688	ENSG00000170688	OR5E1P	11:7710668-7927502	NOTEST	0	0	0	0	1	1
ENSG00000170689	ENSG00000170689	HOXB9	17:46684593-46712294	NOTEST	0.0811794	0.082801	0.0285341	0	1	1
ENSG00000170743	ENSG00000170743	SYT9	11:7260008-7490273	NOTEST	0	0.0142776	inf	0	1	1
ENSG00000170748	ENSG00000170748	RBMXL2	11:7110164-7112379	NOTEST	0	0	0	0	1	1
ENSG00000170777	ENSG00000170777	TPD52L3	9:6328348-6331900	NOTEST	0	0	0	0	1	1
ENSG00000170782	ENSG00000170782	OR10A4	11:6897855-6898850	NOTEST	0	0	0	0	1	1
ENSG00000170786	ENSG00000170786	SDR16C5	8:57212568-57233335	NOTEST	0	0.00691365	inf	0	1	1
ENSG00000170788	ENSG00000170788	DYDC1	10:82095860-82127829	NOTEST	0	0	0	0	1	1
ENSG00000170790	ENSG00000170790	OR10A2	11:6890923-6891976	NOTEST	0	0	0	0	1	1
ENSG00000170801	ENSG00000170801	HTRA3	4:8271491-8308838	NOTEST	0.0370661	0.0162661	-1.18823	0	1	1
ENSG00000170803	ENSG00000170803	OR2AG1	11:6806247-6807245	NOTEST	0	0	0	0	1	1
ENSG00000170807	ENSG00000170807	LMOD2	7:123295860-123304344	NOTEST	0.0136561	0.0497765	1.86592	0	1	1
ENSG00000170819	ENSG00000170819	BFSP2	3:133118838-133194066	NOTEST	0.384378	0.358655	-0.0999283	0	1	1
ENSG00000170820	ENSG00000170820	FSHR	2:49189295-49381676	NOTEST	0.00875574	0	#NAME?	0	1	1
ENSG00000170827	ENSG00000170827	CELP	9:135957925-135962742	NOTEST	0.0137774	0	#NAME?	0	1	1
ENSG00000170835	ENSG00000170835	CEL	9:135937364-135947248	NOTEST	0.102255	0.154596	0.596328	0	1	1
ENSG00000170837	ENSG00000170837	GPR27	3:71724566-71805647	NOTEST	0.036659	0.186672	2.34827	0	1	1
ENSG00000170848	ENSG00000170848	PSG6	19:43406230-43423715	NOTEST	0.0148969	0	#NAME?	0	1	1
ENSG00000170858	ENSG00000170858	LILRP2	19:55219699-55224955	NOTEST	0	0	0	0	1	1
ENSG00000170866	ENSG00000170866	LILRA3	19:54799853-54809952	NOTEST	0	0	0	0	1	1
ENSG00000170890	ENSG00000170890	PLA2G1B	12:120759913-120765592	NOTEST	0.07042	0	#NAME?	0	1	1
ENSG00000170891	ENSG00000170891	CYTL1	4:5016312-5021199	NOTEST	0.37481	0.224836	-0.737283	0	1	1
ENSG00000170893	ENSG00000170893	TRH	3:129693147-129696781	NOTEST	0	0	0	0	1	1
ENSG00000170909	ENSG00000170909	OSCAR	19:54597932-54606000	NOTEST	0	0	0	0	1	1
ENSG00000170920	ENSG00000170920	OR7G3	19:9236687-9237626	NOTEST	0	0	0	0	1	1
ENSG00000170923	ENSG00000170923	OR7G2	19:9212944-9213982	NOTEST	0	0	0	0	1	1
ENSG00000170925	ENSG00000170925	TEX13B	X:107224093-107225600	NOTEST	0	0.0107199	inf	0	1	1
ENSG00000170927	ENSG00000170927	PKHD1	6:51464520-51952423	NOTEST	0.0160228	0.0220251	0.459027	0	1	1
ENSG00000170929	ENSG00000170929	OR1M1	19:9203854-9204889	NOTEST	0	0	0	0	1	1
ENSG00000170935	ENSG00000170935	NCBP2L	X:107020962-107037912	NOTEST	0	0	0	0	1	1
ENSG00000170948	ENSG00000170948	MBD3L1	19:8943073-8954016	NOTEST	0	0	0	0	1	1
ENSG00000170950	ENSG00000170950	PGK2	6:49753365-49755053	NOTEST	0.0177555	0	#NAME?	0	1	1
ENSG00000170953	ENSG00000170953	OR8B12	11:124412577-124413575	NOTEST	0	0	0	0	1	1
ENSG00000170954	ENSG00000170954	ZNF415	19:53611131-53662328	NOTEST	0.00757226	0.154411	4.3499	0	1	1
ENSG00000170956	ENSG00000170956	CEACAM3	19:42300368-42315591	NOTEST	0	0.0359592	inf	0	1	1
ENSG00000170959	ENSG00000170959	DCDC1	11:30851915-31391357	NOTEST	0.121991	0.0594535	-1.03695	0	1	1
ENSG00000170967	ENSG00000170967	DDI1	11:103777913-104035107	NOTEST	0	0	0	0	1	1

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ENSG00000170983	ENSG00000170983	LINC00208	8:11433821-11438851	NOTEST	0	0	0	0	1	1
ENSG00000170989	ENSG00000170989	S1PR1	1:101702443-101707074	NOTEST	0.0348951	0.0569413	0.706448	0	1	1
ENSG00000171014	ENSG00000171014	OR4D5	11:123810249-123811344	NOTEST	0	0	0	0	1	1
ENSG00000171044	ENSG00000171044	XKR6	8:10753554-11058875	NOTEST	0	0	0	0	1	1
ENSG00000171049	ENSG00000171049	FPR2	19:52248424-52329442	NOTEST	0	0	0	0	1	1
ENSG00000171051	ENSG00000171051	FPR1	19:52248424-52329442	NOTEST	0	0	0	0	1	1
ENSG00000171053	ENSG00000171053	PATE1	11:125616187-125619762	NOTEST	0	0	0	0	1	1
ENSG00000171054	ENSG00000171054	OR13H1	X:130677949-130679030	NOTEST	0	0	0	0	1	1
ENSG00000171056	ENSG00000171056	SOX7	8:10581277-10697394	NOTEST	0.212701	0.213729	0.00695296	0	1	1
ENSG00000171060	ENSG00000171060	C8orf74	8:10463858-10569697	NOTEST	0	0	0	0	1	1
ENSG00000171101	ENSG00000171101	SIGLEC17P	19:51645555-51685222	NOTEST	0.0474512	0.0116048	-2.03173	0	1	1
ENSG00000171102	ENSG00000171102	OBP2B	9:136080663-136084630	NOTEST	0	0	0	0	1	1
ENSG00000171115	ENSG00000171115	GIMAP8	7:150147717-150176480	NOTEST	0	0.00259695	inf	0	1	1
ENSG00000171116	ENSG00000171116	HSFX1	X:148855725-148858525	NOTEST	0	0	0	0	1	1
ENSG00000171121	ENSG00000171121	KCNMB3	3:178865901-178984790	NOTEST	0.272895	0.3307	0.277177	0	1	1
ENSG00000171124	ENSG00000171124	FUT3	19:5842898-5858250	NOTEST	0.0530724	0.0678324	0.354012	0	1	1
ENSG00000171129	ENSG00000171129	HSFX2	X:148674171-148676974	NOTEST	0	0	0	0	1	1
ENSG00000171133	ENSG00000171133	OR2K2	9:114089762-114090800	NOTEST	0	0	0	0	1	1
ENSG00000171136	ENSG00000171136	RLN3	19:14138959-14142369	NOTEST	0	0	0	0	1	1
ENSG00000171180	ENSG00000171180	OR2M4	1:248402230-248403166	NOTEST	0	0	0	0	1	1
ENSG00000171189	ENSG00000171189	GRIK1	21:30565800-31312351	NOTEST	0	0.00862285	inf	0	1	1
ENSG00000171195	ENSG00000171195	MUC7	4:71296208-71348714	NOTEST	0.435805	0.489674	0.168139	0	1	1
ENSG00000171199	ENSG00000171199	PROL1	4:71263598-71275911	NOTEST	0	0	0	0	1	1
ENSG00000171201	ENSG00000171201	SMR3B	4:71235809-71255961	NOTEST	0	0	0	0	1	1
ENSG00000171209	ENSG00000171209	CSN3	4:71108304-71117145	NOTEST	0	0	0	0	1	1
ENSG00000171217	ENSG00000171217	CLDN20	6:155054458-155635627	NOTEST	0.0832741	0.0201443	-2.0475	0	1	1
ENSG00000171227	ENSG00000171227	TMEM37	2:120187476-120196096	NOTEST	0	0.03709	inf	0	1	1
ENSG00000171234	ENSG00000171234	UGT2B7	4:69917080-69978705	NOTEST	0	0	0	0	1	1
ENSG00000171236	ENSG00000171236	LRG1	19:4522542-4540486	NOTEST	0	0.00402688	inf	0	1	1
ENSG00000171243	ENSG00000171243	SOSTDC1	7:16501105-16621193	NOTEST	0.0245963	0.0482713	0.972725	0	1	1
ENSG00000171246	ENSG00000171246	NPTX1	17:78440947-78451643	NOTEST	0.0160813	0.0235592	0.550902	0	1	1
ENSG00000171291	ENSG00000171291	ZNF439	19:11959540-11994565	NOTEST	0.0833446	0.0667145	-0.32109	0	1	1
ENSG00000171303	ENSG00000171303	KCNK3	2:26915618-26956288	NOTEST	0	0	0	0	1	1
ENSG00000171345	ENSG00000171345	KRT19	17:39679868-39684560	NOTEST	0	0.0239352	inf	0	1	1
ENSG00000171360	ENSG00000171360	KRT38	17:39592697-39597173	NOTEST	0	0	0	0	1	1
ENSG00000171385	ENSG00000171385	KCND3	1:112313283-112531777	NOTEST	0.00596333	0.00144172	-2.04833	0	1	1
ENSG00000171388	ENSG00000171388	APLN	X:128779239-128788933	NOTEST	0.115238	0.136951	0.249038	0	1	1
ENSG00000171396	ENSG00000171396	KRTAP4-4	17:39315909-39316983	NOTEST	0	0	0	0	1	1
ENSG00000171401	ENSG00000171401	KRT13	17:39657232-39661957	NOTEST	0	0	0	0	1	1
ENSG00000171402	ENSG00000171402	XAGE3	X:52891556-52897099	NOTEST	0	0	0	0	1	1
ENSG00000171403	ENSG00000171403	KRT9	17:39722095-39728310	NOTEST	0	0.0154075	inf	0	1	1
ENSG00000171405	ENSG00000171405	XAGE5	X:52841227-52847325	NOTEST	0	0	0	0	1	1
ENSG00000171408	ENSG00000171408	PDE7B	6:136172833-136546733	NOTEST	0.310022	0.146928	-1.07726	0	1	1
ENSG00000171431	ENSG00000171431	KRT20	17:39032192-39041479	NOTEST	0	0	0	0	1	1
ENSG00000171433	ENSG00000171433	GLOD5	X:48620153-48632064	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000171435	ENSG00000171435	KSR2	12:117890816-118406788	NOTEST	0	0	0	0	1	1
ENSG00000171450	ENSG00000171450	CDK5R2	2:219809350-219826876	NOTEST	0.256847	0.238707	-0.105672	0	1	1
ENSG00000171451	ENSG00000171451	DSEL	18:65173818-65566856	NOTEST	0.184092	0.116828	-0.656039	0	1	1
ENSG00000171459	ENSG00000171459	OR1L6	9:125512018-125513062	NOTEST	0	0	0	0	1	1
ENSG00000171462	ENSG00000171462	DLK2	6:43395103-43424370	NOTEST	0.420226	0.279279	-0.589458	0	1	1
ENSG00000171476	ENSG00000171476	HOPX	4:57514154-57548065	NOTEST	0	0	0	0	1	1
ENSG00000171478	ENSG00000171478	SPACA5B	X:47990038-47991995	NOTEST	0	0	0	0	1	1
ENSG00000171481	ENSG00000171481	OR1L3	9:125437314-125438432	NOTEST	0	0	0	0	1	1
ENSG00000171483	ENSG00000171483	SSX6	X:47967366-47980068	NOTEST	0	0	0	0	1	1
ENSG00000171484	ENSG00000171484	OR1B1	9:125372193-125401964	NOTEST	0	0	0	0	1	1
ENSG00000171487	ENSG00000171487	NLRP5	19:56511091-56573179	NOTEST	0	0	0	0	1	1
ENSG00000171489	ENSG00000171489	SPACA5	X:47696300-47931025	NOTEST	0	0	0	0	1	1
ENSG00000171495	ENSG00000171495	MROH2B	5:40998118-41071444	NOTEST	0.00750208	0	#NAME?	0	1	1
ENSG00000171496	ENSG00000171496	OR1L8	9:125329777-125330838	NOTEST	0	0	0	0	1	1
ENSG00000171501	ENSG00000171501	OR1N2	9:125315390-125316493	NOTEST	0	0	0	0	1	1
ENSG00000171502	ENSG00000171502	COL24A1	1:86194915-86622626	NOTEST	0.0669478	0.17173	1.35903	0	1	1
ENSG00000171505	ENSG00000171505	OR1N1	9:125288636-125289572	NOTEST	0	0	0	0	1	1
ENSG00000171509	ENSG00000171509	RXFP1	4:159236462-159574524	NOTEST	0	0.00328451	inf	0	1	1
ENSG00000171517	ENSG00000171517	LPAR3	1:85277284-85358896	NOTEST	0.234757	0.566226	1.27021	0	1	1
ENSG00000171532	ENSG00000171532	NEUROD2	17:37759788-37766030	NOTEST	0	0	0	0	1	1
ENSG00000171533	ENSG00000171533	MAP6	11:75294240-75380165	NOTEST	0	0.0138872	inf	0	1	1
ENSG00000171540	ENSG00000171540	OTP	5:76924537-76935513	NOTEST	0	0.00596126	inf	0	1	1
ENSG00000171551	ENSG00000171551	ECEL1	2:233344536-233352538	NOTEST	0	0	0	0	1	1
ENSG00000171557	ENSG00000171557	FGG	4:155525285-155534119	NOTEST	0	0.0579487	inf	0	1	1
ENSG00000171560	ENSG00000171560	FGA	4:155504277-155511918	NOTEST	0	0	0	0	1	1
ENSG00000171561	ENSG00000171561	OR2AT4	11:74799757-74800799	NOTEST	0	0	0	0	1	1
ENSG00000171564	ENSG00000171564	FGB	4:155484107-155492238	NOTEST	0	0	0	0	1	1
ENSG00000171587	ENSG00000171587	DSCAM	21:41382925-42219065	NOTEST	0	0	0	0	1	1
ENSG00000171595	ENSG00000171595	DNAI2	17:72270385-72311023	NOTEST	0.0147674	0.00572848	-1.3662	0	1	1
ENSG00000171596	ENSG00000171596	NMUR1	2:232387870-232395206	NOTEST	0.0903926	0.259	1.51867	0	1	1
ENSG00000171631	ENSG00000171631	P2RY6	11:72975549-73009662	NOTEST	0.027077	0.038678	0.514443	0	1	1
ENSG00000171643	ENSG00000171643	S100Z	5:76145825-76217475	NOTEST	0	0	0	0	1	1
ENSG00000171657	ENSG00000171657	GPR82	X:41374186-41782716	NOTEST	0.0443377	0.0112628	-1.97697	0	1	1
ENSG00000171659	ENSG00000171659	GPR34	X:41374186-41782716	NOTEST	0.00903502	0.0217808	1.26945	0	1	1
ENSG00000171671	ENSG00000171671	SHANK2-AS3	11:70313960-70963623	NOTEST	0	0	0	0	1	1
ENSG00000171695	ENSG00000171695	C20orf201	20:62711525-62731996	NOTEST	0.373326	0.338261	-0.142298	0	1	1
ENSG00000171711	ENSG00000171711	DEFB4A	8:7752150-7754233	NOTEST	0	0	0	0	1	1
ENSG00000171724	ENSG00000171724	VAT1L	16:77822426-78014004	NOTEST	0	0	0	0	1	1
ENSG00000171747	ENSG00000171747	LGALS4	19:39292310-39304004	NOTEST	0	0	0	0	1	1
ENSG00000171759	ENSG00000171759	PAH	12:103230662-103354294	NOTEST	0	0.00291966	inf	0	1	1
ENSG00000171772	ENSG00000171772	SYCE1	10:135192694-135382916	NOTEST	0.0583646	0.012459	-2.22791	0	1	1
ENSG00000171773	ENSG00000171773	NXNL1	19:17546317-17571763	NOTEST	0	0.0135496	inf	0	1	1
ENSG00000171777	ENSG00000171777	RASGRP4	19:38893774-38916945	NOTEST	0	0	0	0	1	1
ENSG00000171786	ENSG00000171786	NHLH1	1:160336856-160342638	NOTEST	0.0747722	0.034881	-1.10006	0	1	1
ENSG00000171790	ENSG00000171790	SLFNL1	1:41481268-41488909	NOTEST	0.161817	0.201648	0.317474	0	1	1

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ENSG00000171794	ENSG00000171794	UTF1	10:135043777-135045062	NOTEST	0	0	0	0	1	1
ENSG00000171798	ENSG00000171798	KNDC1	10:134973950-135039916	NOTEST	0.0691394	0.0561814	-0.299415	0	1	1
ENSG00000171804	ENSG00000171804	WDR87	19:38375462-38397317	NOTEST	0	0	0	0	1	1
ENSG00000171811	ENSG00000171811	TTC40	10:134621895-134756327	NOTEST	0.0150784	0.0939501	2.63941	0	1	1
ENSG00000171812	ENSG00000171812	COL8A2	1:36560836-36590821	NOTEST	0.0778374	0.111114	0.513504	0	1	1
ENSG00000171815	ENSG00000171815	PCDHB1	5:140430978-140433512	NOTEST	0	0	0	0	1	1
ENSG00000171819	ENSG00000171819	ANGPTL7	1:11166591-11322564	NOTEST	0.0684999	0.0422988	-0.695487	0	1	1
ENSG00000171840	ENSG00000171840	NINJ2	12:673461-772945	NOTEST	0.161525	0.133862	-0.271012	0	1	1
ENSG00000171847	ENSG00000171847	FAM90A1	12:8373855-8380214	NOTEST	0.0123768	0.00480397	-1.36534	0	1	1
ENSG00000171855	ENSG00000171855	IFNB1	9:21077103-21077943	NOTEST	0	0	0	0	1	1
ENSG00000171860	ENSG00000171860	C3AR1	12:8210897-8219067	NOTEST	0.0154941	0.0573004	1.88682	0	1	1
ENSG00000171864	ENSG00000171864	PRND	20:4702555-4709106	NOTEST	0	0	0	0	1	1
ENSG00000171872	ENSG00000171872	KLF17	1:44584521-44600812	NOTEST	0.00501713	0	#NAME?	0	1	1
ENSG00000171873	ENSG00000171873	ADRA1D	20:4201328-4229721	NOTEST	0	0	0	0	1	1
ENSG00000171889	ENSG00000171889	MIR31HG	9:21455482-21559668	NOTEST	0.0992731	0.117307	0.240818	0	1	1
ENSG00000171903	ENSG00000171903	CYP4F11	19:16023176-16045677	NOTEST	0	0	0	0	1	1
ENSG00000171916	ENSG00000171916	LGALS9C	17:18380050-18398259	NOTEST	0	0	0	0	1	1
ENSG00000171931	ENSG00000171931	FBXW10	17:18647325-18682662	NOTEST	0.00973681	0.0218972	1.16923	0	1	1
ENSG00000171936	ENSG00000171936	OR10H3	19:15852202-15853153	NOTEST	0	0	0	0	1	1
ENSG00000171942	ENSG00000171942	OR10H2	19:15838833-15839862	NOTEST	0	0	0	0	1	1
ENSG00000171944	ENSG00000171944	OR52A5	11:5152921-5153872	NOTEST	0	0	0	0	1	1
ENSG00000171954	ENSG00000171954	CYP4F22	19:15619303-15663128	NOTEST	0	0	0	0	1	1
ENSG00000171956	ENSG00000171956	FOXB1	15:60296420-60353929	NOTEST	0	0	0	0	1	1
ENSG00000171987	ENSG00000171987	C11orf40	11:4592652-4599050	NOTEST	0	0	0	0	1	1
ENSG00000171989	ENSG00000171989	LDHAL6B	15:59427112-59815748	NOTEST	0	0.00699404	inf	0	1	1
ENSG00000171992	ENSG00000171992	SYNPO	5:149980641-150038782	NOTEST	0.132168	0.228796	0.791692	0	1	1
ENSG00000171999	ENSG00000171999	OR52P2P	11:4452552-4453507	NOTEST	0	0	0	0	1	1
ENSG00000172000	ENSG00000172000	ZNF556	19:2867332-2878515	NOTEST	0	0	0	0	1	1
ENSG00000172014	ENSG00000172014	ANKRD20A4	9:69381811-69425560	NOTEST	0.168068	0.106565	-0.657313	0	1	1
ENSG00000172016	ENSG00000172016	REG3A	2:79384131-80875905	NOTEST	0	0	0	0	1	1
ENSG00000172020	ENSG00000172020	GAP43	3:115342170-115440337	NOTEST	0.017719	0	#NAME?	0	1	1
ENSG00000172023	ENSG00000172023	REG1B	2:79312155-79315145	NOTEST	0	0	0	0	1	1
ENSG00000172061	ENSG00000172061	LRRC15	3:194075975-194090472	NOTEST	0.0424173	0.420783	3.31035	0	1	1
ENSG00000172073	ENSG00000172073	TEX37	2:88824168-88829102	NOTEST	0	0.0168027	inf	0	1	1
ENSG00000172116	ENSG00000172116	CD8B	2:87042461-87092827	NOTEST	0	0	0	0	1	1
ENSG00000172137	ENSG00000172137	CALB2	16:71392615-71424341	NOTEST	0	0.0893878	inf	0	1	1
ENSG00000172139	ENSG00000172139	SLC9C1	3:111859733-112013105	NOTEST	0.0627539	0.025364	-1.30692	0	1	1
ENSG00000172146	ENSG00000172146	OR1A1	17:3118914-3119844	NOTEST	0	0	0	0	1	1
ENSG00000172148	ENSG00000172148	AC005255.6	19:14974597-14975527	NOTEST	0	0	0	0	1	1
ENSG00000172150	ENSG00000172150	OR1A2	17:3100812-3101742	NOTEST	0	0	0	0	1	1
ENSG00000172154	ENSG00000172154	OR8I2	11:55860752-55861762	NOTEST	0	0	0	0	1	1
ENSG00000172155	ENSG00000172155	LCE1D	1:152769226-152770657	NOTEST	0	0	0	0	1	1
ENSG00000172156	ENSG00000172156	CCL11	17:32612686-32615353	NOTEST	0	0	0	0	1	1
ENSG00000172179	ENSG00000172179	PRL	6:22260652-22318027	NOTEST	0	0.0185913	inf	0	1	1
ENSG00000172186	ENSG00000172186	HMGN1P35	X:68393966-68394560	NOTEST	0	0	0	0	1	1

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ENSG00000172199	ENSG00000172199	OR8U1	11:56143099-56144029	NOTEST	0	0	0	0	1	1
ENSG00000172208	ENSG00000172208	OR4X2	11:48266607-48267622	NOTEST	0	0	0	0	1	1
ENSG00000172209	ENSG00000172209	GPR22	7:106809405-107218906	NOTEST	0.0151069	0.00377099	-2.00219	0	1	1
ENSG00000172215	ENSG00000172215	CXCR6	3:45959395-46037316	NOTEST	0.0146616	0.0957236	2.70683	0	1	1
ENSG00000172232	ENSG00000172232	AZU1	19:825096-832017	NOTEST	0	0	0	0	1	1
ENSG00000172236	ENSG00000172236	TPSAB1	16:1290696-1292555	NOTEST	0.0562231	0.0334873	-0.74755	0	1	1
ENSG00000172238	ENSG00000172238	ATOH1	4:94750041-94751221	NOTEST	0	0.0438366	inf	0	1	1
ENSG00000172243	ENSG00000172243	CLEC7A	12:10269375-10282857	NOTEST	0.0694095	0.00458472	-3.92023	0	1	1
ENSG00000172250	ENSG00000172250	SERHL	22:42896584-42915808	NOTEST	0.0212283	0.128912	2.60232	0	1	1
ENSG00000172260	ENSG00000172260	NEGR1	1:71547006-72748417	NOTEST	0.374176	0.283619	-0.399764	0	1	1
ENSG00000172283	ENSG00000172283	PRYP4	Y:28121659-28134216	NOTEST	0	0	0	0	1	1
ENSG00000172288	ENSG00000172288	CDY1	Y:27768263-27771049	NOTEST	0	0	0	0	1	1
ENSG00000172289	ENSG00000172289	OR10V1	11:59480295-59573354	NOTEST	0	0	0	0	1	1
ENSG00000172294	ENSG00000172294	CSPG4P4Y	Y:27624415-27633809	NOTEST	0	0	0	0	1	1
ENSG00000172297	ENSG00000172297	GOLGA2P3Y	Y:27600707-27606719	NOTEST	0	0	0	0	1	1
ENSG00000172320	ENSG00000172320	OR5A1	11:59210616-59211667	NOTEST	0	0	0	0	1	1
ENSG00000172322	ENSG00000172322	CLEC12A	12:10100735-10183205	NOTEST	0	0	0	0	1	1
ENSG00000172324	ENSG00000172324	OR5A2	11:59189415-59190449	NOTEST	0	0	0	0	1	1
ENSG00000172332	ENSG00000172332	AC012005.2	Y:26355713-26361728	NOTEST	0	0	0	0	1	1
ENSG00000172342	ENSG00000172342	CSPG4P3Y	Y:26325462-26338017	NOTEST	0	0	0	0	1	1
ENSG00000172346	ENSG00000172346	CSDC2	22:41956766-41985894	NOTEST	0.0402697	0.0225899	-0.834014	0	1	1
ENSG00000172348	ENSG00000172348	RCAN2	6:46188474-46459709	NOTEST	0.0325655	0.334124	3.35897	0	1	1
ENSG00000172350	ENSG00000172350	ABCG4	11:119019721-119033360	NOTEST	0.423242	0.32371	-0.386779	0	1	1
ENSG00000172352	ENSG00000172352	CDY1B	Y:26191375-26194166	NOTEST	0	0	0	0	1	1
ENSG00000172361	ENSG00000172361	CCDC11	18:47753562-47792892	NOTEST	0.141985	0.105484	-0.428712	0	1	1
ENSG00000172362	ENSG00000172362	OR5B12	11:58206592-58207646	NOTEST	0.0613421	0	#NAME?	0	1	1
ENSG00000172365	ENSG00000172365	OR5B2	11:58189737-58190786	NOTEST	0	0	0	0	1	1
ENSG00000172367	ENSG00000172367	PDZD3	11:119056165-119067479	NOTEST	0	0.00465046	inf	0	1	1
ENSG00000172377	ENSG00000172377	OR9I1	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000172381	ENSG00000172381	OR6Q1	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000172382	ENSG00000172382	PRSS27	16:2762418-2770552	NOTEST	0.280573	0.0482614	-2.53943	0	1	1
ENSG00000172403	ENSG00000172403	SYNPO2	4:119809995-119982402	NOTEST	0.0978569	0.068611	-0.512234	0	1	1
ENSG00000172404	ENSG00000172404	DNAJB7	22:41253080-41369313	NOTEST	0.0146558	0.0101075	-0.536044	0	1	1
ENSG00000172410	ENSG00000172410	INSL5	1:67263423-67266939	NOTEST	0	0	0	0	1	1
ENSG00000172421	ENSG00000172421	EFCAB3	17:60447578-60493837	NOTEST	0.0196602	0	#NAME?	0	1	1
ENSG00000172425	ENSG00000172425	TTC36	11:118307204-118473748	NOTEST	0	0.112506	inf	0	1	1
ENSG00000172457	ENSG00000172457	OR9G4	11:56510302-56511287	NOTEST	0	0	0	0	1	1
ENSG00000172459	ENSG00000172459	OR5AR1	11:56431137-56432163	NOTEST	0	0	0	0	1	1
ENSG00000172460	ENSG00000172460	PRSS30P	16:2889568-2892745	NOTEST	0.109514	0.196031	0.839963	0	1	1
ENSG00000172461	ENSG00000172461	FUT9	6:96463859-96663488	NOTEST	0	0	0	0	1	1
ENSG00000172464	ENSG00000172464	OR5AP2	11:56408941-56409947	NOTEST	0	0	0	0	1	1
ENSG00000172468	ENSG00000172468	HSFY1	Y:20652800-20790963	NOTEST	0	0	0	0	1	1
ENSG00000172476	ENSG00000172476	RAB40A	X:102752450-102774417	NOTEST	0.433917	0.359443	-0.271656	0	1	1
ENSG00000172478	ENSG00000172478	C2orf54	2:241825464-241836306	NOTEST	0	0.00662912	inf	0	1	1

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ENSG00000172487	ENSG00000172487	OR8J1	11:56127690-56128764	NOTEST	0	0	0	0	1	1
ENSG00000172489	ENSG00000172489	OR5T3	11:56019675-56020698	NOTEST	0	0	0	0	1	1
ENSG00000172497	ENSG00000172497	ACOT12	5:80625823-80689998	NOTEST	0.27461	0.222724	-0.302128	0	1	1
ENSG00000172508	ENSG00000172508	CARNS1	11:67159175-67193078	NOTEST	0.0600606	0.0560214	-0.10044	0	1	1
ENSG00000172519	ENSG00000172519	OR10H5	19:15904760-15905892	NOTEST	0	0	0	0	1	1
ENSG00000172524	ENSG00000172524	TRIM40	HSCHR6_MHC_QBL:30093434-30106063	NOTEST	0	0	0	0	1	1
ENSG00000172538	ENSG00000172538	FAM170B	10:50329883-50359592	NOTEST	0	0	0	0	1	1
ENSG00000172543	ENSG00000172543	CTSW	11:65647279-65656010	NOTEST	0	0.0775007	inf	0	1	1
ENSG00000172548	ENSG00000172548	NIPAL4	5:156687131-157002783	NOTEST	0.28329	0.349781	0.304172	0	1	1
ENSG00000172551	ENSG00000172551	MUCL1	12:55224302-55252177	NOTEST	0	0	0	0	1	1
ENSG00000172554	ENSG00000172554	SNTG2	2:946553-1371385	NOTEST	0	0	0	0	1	1
ENSG00000172568	ENSG00000172568	FNDC9	5:156687131-157002783	NOTEST	0	0	0	0	1	1
ENSG00000172575	ENSG00000172575	RASGRP1	15:38780303-38857776	NOTEST	0.150229	0.217721	0.535314	0	1	1
ENSG00000172578	ENSG00000172578	KLHL6	3:183205318-183273477	NOTEST	0.312739	0.168382	-0.89322	0	1	1
ENSG00000172602	ENSG00000172602	RND1	12:49250927-49259681	NOTEST	0.337454	0.274082	-0.300088	0	1	1
ENSG00000172640	ENSG00000172640	OR10AD1	12:48596080-48597170	NOTEST	0.0484845	0.0113827	-2.09068	0	1	1
ENSG00000172653	ENSG00000172653	C17orf66	17:34136458-34195895	NOTEST	0.00823694	0	#NAME?	0	1	1
ENSG00000172673	ENSG00000172673	THEMIS	6:128029216-128239776	NOTEST	0.00404982	0	#NAME?	0	1	1
ENSG00000172680	ENSG00000172680	MOS	8:57025500-57026541	NOTEST	0	0	0	0	1	1
ENSG00000172689	ENSG00000172689	MS4A10	11:60552820-60568778	NOTEST	0	0	0	0	1	1
ENSG00000172716	ENSG00000172716	SLFN11	17:33677323-33700720	NOTEST	0	0.0800538	inf	0	1	1
ENSG00000172717	ENSG00000172717	FAM71D	14:67656109-67695267	NOTEST	0.0582125	0.0675191	0.213968	0	1	1
ENSG00000172724	ENSG00000172724	CCL19	9:34689563-34691274	NOTEST	0	0	0	0	1	1
ENSG00000172733	ENSG00000172733	PURG	8:30853320-30891231	NOTEST	0.0966236	0.123232	0.350925	0	1	1
ENSG00000172738	ENSG00000172738	TMEM217	6:37179955-37300746	NOTEST	0.0240747	0.154634	2.68327	0	1	1
ENSG00000172742	ENSG00000172742	OR4D9	11:59282385-59283330	NOTEST	0	0	0	0	1	1
ENSG00000172746	ENSG00000172746	RP11-344H11.4	1:27306655-27307466	NOTEST	0.0849462	0.0355048	-1.25854	0	1	1
ENSG00000172752	ENSG00000172752	COL6A5	3:130064358-130203688	NOTEST	0.00477797	0.0248347	2.37789	0	1	1
ENSG00000172769	ENSG00000172769	OR5B3	11:58169936-58170882	NOTEST	0	0	0	0	1	1
ENSG00000172771	ENSG00000172771	EFCAB12	3:129120163-129147494	NOTEST	0.0983502	0.0862489	-0.189422	0	1	1
ENSG00000172772	ENSG00000172772	OR10W1	11:58034263-58035732	NOTEST	0	0	0	0	1	1
ENSG00000172774	ENSG00000172774	OR1S1	11:57982216-57983195	NOTEST	0	0	0	0	1	1
ENSG00000172782	ENSG00000172782	FADS6	17:72873427-72889708	NOTEST	0	0	0	0	1	1
ENSG00000172794	ENSG00000172794	RAB37	17:72666716-72765492	NOTEST	0.501369	0.345528	-0.537069	0	1	1
ENSG00000172799	ENSG00000172799	ZBTB8OSP2	2:232298633-232299137	NOTEST	0	0	0	0	1	1
ENSG00000172803	ENSG00000172803	SNX32	11:65590492-65641063	NOTEST	0.286074	0.436809	0.610616	0	1	1
ENSG00000172818	ENSG00000172818	OVOL1	11:65554492-65564690	NOTEST	0.0366765	0.0351311	-0.0621052	0	1	1
ENSG00000172824	ENSG00000172824	CES4A	16:67022491-67043661	NOTEST	0	0	0	0	1	1
ENSG00000172850	ENSG00000172850	LSM2	HSCHR6_MHC_QBL:31755420-31765001	NOTEST	0	0	0	0	1	1
ENSG00000172867	ENSG00000172867	KRT2	12:53038341-53045948	NOTEST	0	0	0	0	1	1
ENSG00000172900	ENSG00000172900	AP002387.1	11:71093646-71134469	NOTEST	0	0	0	0	1	1
ENSG00000172901	ENSG00000172901	AQPEP	5:115298150-115395815	NOTEST	0.0121535	0	#NAME?	0	1	1
ENSG00000172912	ENSG00000172912	COX6B1P3	22:40742506-41032706	NOTEST	0	0	0	0	1	1
ENSG00000172935	ENSG00000172935	MRGPRF	11:68771861-68785915	NOTEST	0.021075	0.0471852	1.1628	0	1	1

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ENSG00000172940	ENSG00000172940	SLC22A13	3:38307302-38319806	NOTEST	0.0186882	0.0655535	1.81055	0	1	1
ENSG00000172955	ENSG00000172955	ADH6	4:100010007-100222513	NOTEST	0	0	0	0	1	1
ENSG00000172967	ENSG00000172967	XKR3	22:17264301-17302589	NOTEST	0.0470632	0.0220694	-1.09255	0	1	1
ENSG00000172969	ENSG00000172969	FRG2C	3:75713480-75716371	NOTEST	0.0311754	0.0790076	1.34158	0	1	1
ENSG00000172971	ENSG00000172971	UNC93B3	3:75668656-75673000	NOTEST	0	0	0	0	1	1
ENSG00000172985	ENSG00000172985	SH3RF3	2:109745803-110262207	NOTEST	0	0.00480658	inf	0	1	1
ENSG00000172987	ENSG00000172987	HPSE2	10:100218874-100995619	NOTEST	0.268787	0.178107	-0.593723	0	1	1
ENSG00000172995	ENSG00000172995	ARPP21	3:35680436-35835988	NOTEST	0	0	0	0	1	1
ENSG00000173013	ENSG00000173013	CCDC96	4:6910968-7059679	NOTEST	0.285577	0.167609	-0.768779	0	1	1
ENSG00000173040	ENSG00000173040	EVC2	4:5544498-5711275	NOTEST	0.225722	0.340003	0.590999	0	1	1
ENSG00000173077	ENSG00000173077	1-Dec	9:117904096-118164923	NOTEST	0	0.0197607	inf	0	1	1
ENSG00000173080	ENSG00000173080	RXFP4	1:155911479-155912625	NOTEST	0	0.0118428	inf	0	1	1
ENSG00000173083	ENSG00000173083	HPSE	4:84213613-84256306	NOTEST	0.273794	0.188829	-0.536015	0	1	1
ENSG00000173088	ENSG00000173088	C10orf131	10:97471535-97849995	NOTEST	0.0694023	0.144818	1.06119	0	1	1
ENSG00000173093	ENSG00000173093	CCDC63	12:111284572-111345339	NOTEST	0	0	0	0	1	1
ENSG00000173114	ENSG00000173114	LRRN3	7:110303109-111202573	NOTEST	0.245934	0.173872	-0.500241	0	1	1
ENSG00000173124	ENSG00000173124	C10orf129	10:96953956-96990901	NOTEST	0	0	0	0	1	1
ENSG00000173157	ENSG00000173157	ADAMTS20	12:43747668-43945724	NOTEST	0	0	0	0	1	1
ENSG00000173175	ENSG00000173175	ADCY5	3:123001142-123168605	NOTEST	0.325104	0.391418	0.267808	0	1	1
ENSG00000173198	ENSG00000173198	CYSLTR1	X:77526960-77583048	NOTEST	0	0	0	0	1	1
ENSG00000173200	ENSG00000173200	PARP15	3:122296448-122357894	NOTEST	0.0473721	0.0145725	-1.70079	0	1	1
ENSG00000173208	ENSG00000173208	ABCD2	12:39943834-40013553	NOTEST	0.0538927	0.103773	0.945272	0	1	1
ENSG00000173212	ENSG00000173212	MAB21L3	1:116654375-116677861	NOTEST	0.00971267	0.034796	1.84098	0	1	1
ENSG00000173227	ENSG00000173227	SYT12	11:66774248-66818334	NOTEST	0	0	0	0	1	1
ENSG00000173231	ENSG00000173231	TERF1P1	21:15148406-15149587	NOTEST	0	0	0	0	1	1
ENSG00000173237	ENSG00000173237	C11orf86	11:66742747-66744475	NOTEST	0	0	0	0	1	1
ENSG00000173239	ENSG00000173239	LIPM	10:90562486-90580303	NOTEST	0	0	0	0	1	1
ENSG00000173250	ENSG00000173250	GPR151	5:145892665-145895753	NOTEST	0	0	0	0	1	1
ENSG00000173253	ENSG00000173253	DMRT2	9:1050353-1057552	NOTEST	0.0896529	0.156679	0.80539	0	1	1
ENSG00000173261	ENSG00000173261	PLAC8L1	5:145463948-145562223	NOTEST	0.0330108	0	#NAME?	0	1	1
ENSG00000173262	ENSG00000173262	SLC2A14	12:7965107-8043744	NOTEST	0.187867	0.135299	-0.473558	0	1	1
ENSG00000173267	ENSG00000173267	SNCG	10:88695296-88784489	NOTEST	0.0948045	0.182652	0.946072	0	1	1
ENSG00000173269	ENSG00000173269	MMRN2	10:88695296-88784489	NOTEST	0.144233	0.122352	-0.237365	0	1	1
ENSG00000173285	ENSG00000173285	OR10K1	1:158435271-158436344	NOTEST	0	0	0	0	1	1
ENSG00000173302	ENSG00000173302	GPR148	2:131486642-131487909	NOTEST	0	0	0	0	1	1
ENSG00000173335	ENSG00000173335	CST9	20:23583046-23586513	NOTEST	0	0	0	0	1	1
ENSG00000173338	ENSG00000173338	KCNK7	11:65360325-65363467	NOTEST	0.0891495	0.0840535	-0.0849179	0	1	1
ENSG00000173349	ENSG00000173349	SFT2D3	2:128458595-128568761	NOTEST	0	0.073966	inf	0	1	1
ENSG00000173357	ENSG00000173357	AC007967.3	Y:8774264-8784114	NOTEST	0	0	0	0	1	1
ENSG00000173366	ENSG00000173366	TLR9	3:52255095-52275113	NOTEST	0	0	0	0	1	1
ENSG00000173369	ENSG00000173369	C1QB	1:22979254-22988031	NOTEST	0	0	0	0	1	1
ENSG00000173372	ENSG00000173372	C1QA	1:22962998-22966101	NOTEST	0	0	0	0	1	1
ENSG00000173376	ENSG00000173376	NDNF	4:121956767-122001631	NOTEST	0.577334	0.257866	-1.16278	0	1	1
ENSG00000173389	ENSG00000173389	IQCF1	3:51928891-51937351	NOTEST	0	0	0	0	1	1

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ENSG00000173401	ENSG00000173401	GLIPR1L1	12:75628519-75784708	NOTEST	0.0636643	0	#NAME?	0	1	1
ENSG00000173404	ENSG00000173404	INSM1	20:20348764-20351590	NOTEST	0.0258178	0.00827302	-1.64188	0	1	1
ENSG00000173406	ENSG00000173406	DAB1	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000173421	ENSG00000173421	CCDC36	3:49235860-49295537	NOTEST	0	0.0279121	inf	0	1	1
ENSG00000173431	ENSG00000173431	RNASE8	14:21484921-21572881	NOTEST	0.0591967	0	#NAME?	0	1	1
ENSG00000173432	ENSG00000173432	SAA1	11:18287720-18291524	NOTEST	0.102765	0.0255373	-2.00867	0	1	1
ENSG00000173452	ENSG00000173452	TMEM196	7:19758932-19813221	NOTEST	0	0	0	0	1	1
ENSG00000173464	ENSG00000173464	RNASE11	14:21051050-21078043	NOTEST	0	0	0	0	1	1
ENSG00000173467	ENSG00000173467	AGR3	7:16899028-16921611	NOTEST	0	0	0	0	1	1
ENSG00000173503	ENSG00000173503	LTA	HSCHR6_MHC_QBL:31530069-31532342	NOTEST	0	0	0	0	1	1
ENSG00000173530	ENSG00000173530	TNFRSF10D	8:22993100-23021543	NOTEST	0	0	0	0	1	1
ENSG00000173557	ENSG00000173557	C2orf70	2:26785449-26802400	NOTEST	0.372557	0.557257	0.580882	0	1	1
ENSG00000173567	ENSG00000173567	GPR113	2:26531040-26618759	NOTEST	0.00776727	0.0289978	1.90046	0	1	1
ENSG00000173572	ENSG00000173572	NLRP13	19:56403064-56443702	NOTEST	0	0	0	0	1	1
ENSG00000173578	ENSG00000173578	XCR1	3:46058515-46069234	NOTEST	0	0.0297965	inf	0	1	1
ENSG00000173585	ENSG00000173585	CCR9	3:45864807-45957534	NOTEST	0.0296133	0.0188469	-0.651913	0	1	1
ENSG00000173597	ENSG00000173597	SULT1B1	4:70586879-70653679	NOTEST	0	0	0	0	1	1
ENSG00000173610	ENSG00000173610	UGT2A1	4:70454134-70518967	NOTEST	0	0	0	0	1	1
ENSG00000173612	ENSG00000173612	GPRC6A	6:117113247-117150200	NOTEST	0	0	0	0	1	1
ENSG00000173626	ENSG00000173626	TRAPPC3L	6:116813459-116880031	NOTEST	0	0	0	0	1	1
ENSG00000173627	ENSG00000173627	APOBEC4	1:183605219-183897665	NOTEST	0	0	0	0	1	1
ENSG00000173641	ENSG00000173641	HSPB7	1:16340522-16360545	NOTEST	0.483653	0.547044	0.177685	0	1	1
ENSG00000173662	ENSG00000173662	TAS1R1	1:6615240-6639817	NOTEST	0.0257666	0	#NAME?	0	1	1
ENSG00000173673	ENSG00000173673	HES3	1:6304251-6305638	NOTEST	0.0519498	0	#NAME?	0	1	1
ENSG00000173678	ENSG00000173678	SPDYE2B	7:102122891-102312088	NOTEST	0	0	0	0	1	1
ENSG00000173679	ENSG00000173679	OR1L1	9:125423844-125424927	NOTEST	0	0	0	0	1	1
ENSG00000173698	ENSG00000173698	GPR64	X:19007426-19140755	NOTEST	0.0163504	0.0176118	0.10722	0	1	1
ENSG00000173699	ENSG00000173699	SPATA3	2:231860835-231889770	NOTEST	0	0	0	0	1	1
ENSG00000173702	ENSG00000173702	MUC13	3:124624288-124672663	NOTEST	0	0.021352	inf	0	1	1
ENSG00000173705	ENSG00000173705	SUSD5	3:33191536-33260707	NOTEST	0.428623	0.441751	0.0435255	0	1	1
ENSG00000173714	ENSG00000173714	WFIKKN2	17:48912010-48919709	NOTEST	0	0	0	0	1	1
ENSG00000173728	ENSG00000173728	C1orf100	1:244515936-244615436	NOTEST	0.0443383	0.0312827	-0.503187	0	1	1
ENSG00000173762	ENSG00000173762	CD7	17:80272743-80275478	NOTEST	0	0.0294096	inf	0	1	1
ENSG00000173769	ENSG00000173769	TOPAZ1	3:44283377-44373590	NOTEST	0	0	0	0	1	1
ENSG00000173805	ENSG00000173805	HAP1	17:39775688-39943183	NOTEST	0.145594	0.324264	1.15522	0	1	1
ENSG00000173809	ENSG00000173809	TDRD12	19:33210658-33320483	NOTEST	0.0308665	0.00653842	-2.23903	0	1	1
ENSG00000173810	ENSG00000173810	PPIAP7	1:101736430-101736919	NOTEST	0	0	0	0	1	1
ENSG00000173811	ENSG00000173811	CCDC13-AS1	3:42734154-42846023	NOTEST	0.0725293	0.00555812	-3.70589	0	1	1
ENSG00000173825	ENSG00000173825	TIGD3	11:65122237-65125084	NOTEST	0.179448	0.19444	0.11576	0	1	1
ENSG00000173826	ENSG00000173826	KCNH6	17:61600694-61626338	NOTEST	0	0.0041141	inf	0	1	1
ENSG00000173838	ENSG00000173838	10-Mar	17:60776604-60885705	NOTEST	0	0.00364272	inf	0	1	1
ENSG00000173862	ENSG00000173862	RP11-89N17.1	7:33765592-33768068	NOTEST	0.0334893	0	#NAME?	0	1	1
ENSG00000173867	ENSG00000173867	RP11-97O12.7	15:89002706-89089906	NOTEST	0.195256	0.0687923	-1.50505	0	1	1
ENSG00000173868	ENSG00000173868	PHOSPHO1	17:47300723-47308128	NOTEST	0.504949	0.608862	0.269977	0	1	1

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ENSG00000173908	ENSG00000173908	KRT28	17:38948454-38956211	NOTEST	0	0	0	0	1	1
ENSG00000173917	ENSG00000173917	HOXB2	17:46618255-46683776	NOTEST	0.0603311	0.080849	0.422328	0	1	1
ENSG00000173930	ENSG00000173930	SLCO4C1	5:101569689-101632253	NOTEST	0	0.00201801	inf	0	1	1
ENSG00000173947	ENSG00000173947	PIFO	1:111888909-111895635	NOTEST	0.370149	0.455214	0.298436	0	1	1
ENSG00000173954	ENSG00000173954	SNURFL	X:138444198-138444541	NOTEST	0	0	0	0	1	1
ENSG00000173966	ENSG00000173966	RP11-18M17.1	4:54243809-55164414	NOTEST	0	0	0	0	1	1
ENSG00000173976	ENSG00000173976	RAX2	19:3769086-3772233	NOTEST	0	0	0	0	1	1
ENSG00000173988	ENSG00000173988	LRRC63	13:46786082-46851501	NOTEST	0.385722	0.308671	-0.321493	0	1	1
ENSG00000173991	ENSG00000173991	TCAP	17:37820439-37822808	NOTEST	0.3113	0.367706	0.240247	0	1	1
ENSG00000174015	ENSG00000174015	SPERT	13:46276445-46288694	NOTEST	0	0	0	0	1	1
ENSG00000174016	ENSG00000174016	FAM46D	X:79591002-79700810	NOTEST	0.107301	0.0888496	-0.272224	0	1	1
ENSG00000174038	ENSG00000174038	C9orf131	9:35041091-35045988	NOTEST	0	0	0	0	1	1
ENSG00000174059	ENSG00000174059	CD34	1:208057593-208084747	NOTEST	0.238378	0.230626	-0.0476992	0	1	1
ENSG00000174083	ENSG00000174083	PIK3R6	17:8706040-8770994	NOTEST	0.00709528	0	#NAME?	0	1	1
ENSG00000174123	ENSG00000174123	TLR10	4:38773859-38784611	NOTEST	0.0170574	0.0146396	-0.220524	0	1	1
ENSG00000174125	ENSG00000174125	TLR1	4:38792297-38858438	NOTEST	0.178063	0.328068	0.881609	0	1	1
ENSG00000174145	ENSG00000174145	KIAA1239	4:37245841-37451087	NOTEST	0	0	0	0	1	1
ENSG00000174156	ENSG00000174156	GSTA3	6:52761436-52774483	NOTEST	0	0	0	0	1	1
ENSG00000174175	ENSG00000174175	SELP	1:169558086-169599431	NOTEST	0	0	0	0	1	1
ENSG00000174194	ENSG00000174194	AGAP8	10:51224680-51371338	NOTEST	0.393991	0.4599	0.223159	0	1	1
ENSG00000174196	ENSG00000174196	FAM21D	10:51187937-51192032	NOTEST	0.145814	0.101644	-0.520597	0	1	1
ENSG00000174225	ENSG00000174225	ARL13A	X:100224696-100245818	NOTEST	0	0.00765698	inf	0	1	1
ENSG00000174226	ENSG00000174226	SNX31	8:101585115-101675643	NOTEST	0.0135757	0	#NAME?	0	1	1
ENSG00000174236	ENSG00000174236	REP15	12:27849320-27863703	NOTEST	0.421118	0.376198	-0.162732	0	1	1
ENSG00000174255	ENSG00000174255	ZNF80	3:113933159-113956425	NOTEST	0	0	0	0	1	1
ENSG00000174279	ENSG00000174279	EVX2	2:176942199-176948641	NOTEST	0.0147326	0.0340884	1.21027	0	1	1
ENSG00000174292	ENSG00000174292	TNK1	17:7283852-7307456	NOTEST	0.0601629	0.22126	1.8788	0	1	1
ENSG00000174325	ENSG00000174325	DIRC1	2:189463517-189704171	NOTEST	0	0	0	0	1	1
ENSG00000174326	ENSG00000174326	SLC16A11	17:6944948-6947242	NOTEST	0.0589402	0.0333205	-0.822845	0	1	1
ENSG00000174332	ENSG00000174332	GLIS1	1:53971909-54199877	NOTEST	0.010166	0.0341818	1.74948	0	1	1
ENSG00000174339	ENSG00000174339	OR2Y1	5:180166041-180167099	NOTEST	0	0	0	0	1	1
ENSG00000174343	ENSG00000174343	CHRNA9	4:40337345-40357234	NOTEST	0	0	0	0	1	1
ENSG00000174348	ENSG00000174348	PODN	1:53527853-53551174	NOTEST	0.0275587	0.0333408	0.274781	0	1	1
ENSG00000174358	ENSG00000174358	SLC6A19	5:1201709-1225232	NOTEST	0	0	0	0	1	1
ENSG00000174370	ENSG00000174370	C11orf45	11:128761250-128790930	NOTEST	0.570886	0.542824	-0.0727179	0	1	1
ENSG00000174384	ENSG00000174384	RP11-313P13.4	7:72440226-72555749	NOTEST	0	0	0	0	1	1
ENSG00000174403	ENSG00000174403	C20orf166-AS1	20:61141549-61167971	NOTEST	0	0	0	0	1	1
ENSG00000174407	ENSG00000174407	C20orf166	20:61141549-61167971	NOTEST	0	0	0	0	1	1
ENSG00000174408	ENSG00000174408	PPIAP24	13:107516163-107516634	NOTEST	0	0	0	0	1	1
ENSG00000174417	ENSG00000174417	TRHR	8:110098849-110131813	NOTEST	0	0	0	0	1	1
ENSG00000174418	ENSG00000174418	RPL35P9	13:107078120-107078470	NOTEST	0	0	0	0	1	1
ENSG00000174429	ENSG00000174429	ABRA	8:107771710-107782473	NOTEST	0	0	0	0	1	1
ENSG00000174448	ENSG00000174448	STARD6	18:51850727-51911588	NOTEST	0	0	0	0	1	1
ENSG00000174450	ENSG00000174450	GOLGA6L2	15:23684644-23692381	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000174453	ENSG00000174453	VWC2L	2:214149112-215548970	NOTEST	0	0	0	0	1	1
ENSG00000174460	ENSG00000174460	ZCCHC12	X:117957752-117960931	NOTEST	0.0274676	0.0728185	1.40657	0	1	1
ENSG00000174469	ENSG00000174469	CNTNAP2	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000174495	ENSG00000174495	AC005017.2	7:28318829-28319319	NOTEST	0	0	0	0	1	1
ENSG00000174498	ENSG00000174498	IGDCC3	15:65619464-65670378	NOTEST	0.00966893	0.085193	3.13931	0	1	1
ENSG00000174502	ENSG00000174502	SLC26A9	1:205882175-205912588	NOTEST	0	0	0	0	1	1
ENSG00000174514	ENSG00000174514	MFSD4	1:205538012-205572046	NOTEST	0.139761	0.247405	0.823916	0	1	1
ENSG00000174521	ENSG00000174521	TTC9B	19:40721964-40724306	NOTEST	0.143872	0.240096	0.738829	0	1	1
ENSG00000174527	ENSG00000174527	MYO1H	12:109785707-109974507	NOTEST	0	0.00533326	inf	0	1	1
ENSG00000174562	ENSG00000174562	KLK15	19:51328544-51354345	NOTEST	0	0	0	0	1	1
ENSG00000174564	ENSG00000174564	IL20RB	3:136581049-136729927	NOTEST	0.171609	0.424386	1.30625	0	1	1
ENSG00000174567	ENSG00000174567	GOLT1A	1:204167287-204183220	NOTEST	0.172513	0.016225	-3.41042	0	1	1
ENSG00000174572	ENSG00000174572	RP11-209A2.1	6:27179022-27179692	NOTEST	0	0	0	0	1	1
ENSG00000174576	ENSG00000174576	NPAS4	11:66188474-66194178	NOTEST	0	0	0	0	1	1
ENSG00000174586	ENSG00000174586	ZNF497	19:58856543-58877958	NOTEST	0.27219	0.400745	0.558072	0	1	1
ENSG00000174595	ENSG00000174595	KLF14	7:130417400-130418888	NOTEST	0.185472	0.25642	0.467305	0	1	1
ENSG00000174600	ENSG00000174600	CMKLR1	12:108681820-108733118	NOTEST	0.00863202	0.00210871	-2.03334	0	1	1
ENSG00000174611	ENSG00000174611	KY	3:134316642-134979309	NOTEST	0.00383536	0	#NAME?	0	1	1
ENSG00000174640	ENSG00000174640	SLCO2A1	3:133651539-133771028	NOTEST	0	0.00803708	inf	0	1	1
ENSG00000174667	ENSG00000174667	OR7D4	19:9324525-9325542	NOTEST	0	0	0	0	1	1
ENSG00000174677	ENSG00000174677	VN1R6P	19:53818389-53819296	NOTEST	0	0	0	0	1	1
ENSG00000174678	ENSG00000174678	FAM47DP	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000174680	ENSG00000174680	GRIK1-AS1	21:30565800-31312351	NOTEST	0	0	0	0	1	1
ENSG00000174697	ENSG00000174697	LEP	7:127881336-127897681	NOTEST	0	0	0	0	1	1
ENSG00000174715	ENSG00000174715	RP11-79L9.2	3:138362715-138363536	NOTEST	0	0.0316794	inf	0	1	1
ENSG00000174721	ENSG00000174721	FGFBP3	10:93666345-93669240	NOTEST	0.346077	0.432137	0.320396	0	1	1
ENSG00000174776	ENSG00000174776	WDR49	3:167159576-167371771	NOTEST	0.0879138	0.106561	0.277512	0	1	1
ENSG00000174788	ENSG00000174788	PCP2	19:7694622-7712759	NOTEST	0.343741	0.407866	0.246771	0	1	1
ENSG00000174792	ENSG00000174792	C4orf26	4:76481257-76491095	NOTEST	0	0	0	0	1	1
ENSG00000174807	ENSG00000174807	CD248	11:66080323-66086708	NOTEST	0	0.00436927	inf	0	1	1
ENSG00000174808	ENSG00000174808	BTC	4:75669968-75719896	NOTEST	0.0661517	0.00436196	-3.92273	0	1	1
ENSG00000174827	ENSG00000174827	PDZK1	1:145726917-145764074	NOTEST	0.218954	0.33616	0.618519	0	1	1
ENSG00000174837	ENSG00000174837	EMR1	19:6887576-6940470	NOTEST	0.0112079	0.0338766	1.59578	0	1	1
ENSG00000174844	ENSG00000174844	DNAH12	3:57327726-57530071	NOTEST	0.00714253	0.0188261	1.39823	0	1	1
ENSG00000174876	ENSG00000174876	AMY1B	1:104230036-104239302	NOTEST	0	0	0	0	1	1
ENSG00000174885	ENSG00000174885	NLRP6	11:278364-285359	NOTEST	0	0.00415752	inf	0	1	1
ENSG00000174898	ENSG00000174898	CATSPERD	19:5720687-5778745	NOTEST	0	0	0	0	1	1
ENSG00000174914	ENSG00000174914	OR9G1	11:56467863-56468781	NOTEST	0.0198835	0.0140194	-0.504148	0	1	1
ENSG00000174930	ENSG00000174930	VN2R1P	3:155737434-155755475	NOTEST	0	0	0	0	1	1
ENSG00000174937	ENSG00000174937	OR5M3	11:56236963-56238014	NOTEST	0	0	0	0	1	1
ENSG00000174938	ENSG00000174938	SEZ6L2	16:29882479-29910868	NOTEST	0.20665	0.301425	0.544609	0	1	1
ENSG00000174942	ENSG00000174942	OR5R1	11:56184733-56185708	NOTEST	0	0	0	0	1	1
ENSG00000174944	ENSG00000174944	P2RY14	3:150803483-151176497	NOTEST	0	0	0	0	1	1
ENSG00000174945	ENSG00000174945	AMZ1	7:2719155-2883958	NOTEST	0.052844	0.0815653	0.626217	0	1	1
ENSG00000174946	ENSG00000174946	GPR171	3:150803483-151176497	NOTEST	0	0	0	0	1	1

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ENSG00000174948	ENSG00000174948	GPR149	3:154055460-154147504	NOTEST	0	0	0	0	1	1
ENSG00000174950	ENSG00000174950	CD164L2	1:27705665-27709870	NOTEST	0	0.0148847	inf	0	1	1
ENSG00000174951	ENSG00000174951	FUT1	19:49251267-49258647	NOTEST	0.013157	0.0184173	0.48523	0	1	1
ENSG00000174957	ENSG00000174957	OR5J2	11:55944093-55945032	NOTEST	0.0740125	0	#NAME?	0	1	1
ENSG00000174963	ENSG00000174963	ZIC4	3:147103832-147228080	NOTEST	0.49673	0.440529	-0.173223	0	1	1
ENSG00000174970	ENSG00000174970	OR10AG1	11:55734974-55735990	NOTEST	0	0	0	0	1	1
ENSG00000174982	ENSG00000174982	OR4S2	11:55418379-55419315	NOTEST	0	0	0	0	1	1
ENSG00000174990	ENSG00000174990	CA5A	16:87921624-87970135	NOTEST	0	0	0	0	1	1
ENSG00000174992	ENSG00000174992	ZG16	16:29789560-29793096	NOTEST	0	0	0	0	1	1
ENSG00000175003	ENSG00000175003	SLC22A1	6:160542820-160579750	NOTEST	0.0347769	0.0498794	0.520312	0	1	1
ENSG00000175018	ENSG00000175018	TEX36	10:127262939-127371713	NOTEST	0	0	0	0	1	1
ENSG00000175065	ENSG00000175065	DSG4	18:28898051-29006951	NOTEST	0	0.00305843	inf	0	1	1
ENSG00000175077	ENSG00000175077	RTP1	3:186914877-186925417	NOTEST	0	0	0	0	1	1
ENSG00000175084	ENSG00000175084	DES	2:220283098-220291461	NOTEST	0	0.0172355	inf	0	1	1
ENSG00000175093	ENSG00000175093	SPSB4	3:140770243-140867453	NOTEST	0	0	0	0	1	1
ENSG00000175097	ENSG00000175097	RAG2	11:36532258-36694823	NOTEST	0.0403932	0.213828	2.40427	0	1	1
ENSG00000175121	ENSG00000175121	WFDC5	20:43738092-43743813	NOTEST	0	0	0	0	1	1
ENSG00000175143	ENSG00000175143	OR2T1	1:248569295-248570405	NOTEST	0	0	0	0	1	1
ENSG00000175147	ENSG00000175147	TMEM51-AS1	1:14925199-15478960	NOTEST	0.208088	0.118313	-0.814577	0	1	1
ENSG00000175161	ENSG00000175161	CADM2	3:85008131-86123579	NOTEST	0	0.0201991	inf	0	1	1
ENSG00000175164	ENSG00000175164	ABO	9:136125787-136150617	NOTEST	0	0	0	0	1	1
ENSG00000175189	ENSG00000175189	INHBC	12:57828542-57844611	NOTEST	0.00815551	0	#NAME?	0	1	1
ENSG00000175202	ENSG00000175202	HIGD2B	15:72968123-72978490	NOTEST	0	0	0	0	1	1
ENSG00000175206	ENSG00000175206	NPPA	1:11821843-11908402	NOTEST	0.129383	0.112287	-0.204455	0	1	1
ENSG00000175229	ENSG00000175229	GAL3ST3	11:65809422-65816651	NOTEST	0	0	0	0	1	1
ENSG00000175262	ENSG00000175262	C1orf127	1:11006527-11042094	NOTEST	0.012181	0	#NAME?	0	1	1
ENSG00000175264	ENSG00000175264	CHST1	11:45670426-45687172	NOTEST	0	0.0131541	inf	0	1	1
ENSG00000175267	ENSG00000175267	VWA3A	16:22103858-22168287	NOTEST	0	0	0	0	1	1
ENSG00000175274	ENSG00000175274	TP53I11	11:44740941-44972840	NOTEST	0.0492531	0.130505	1.40582	0	1	1
ENSG00000175287	ENSG00000175287	PHYHD1	9:131683173-131790582	NOTEST	0.0723851	0	#NAME?	0	1	1
ENSG00000175302	ENSG00000175302	ANKRD30BP1	21:14756569-14800094	NOTEST	0.363101	0.243461	-0.576681	0	1	1
ENSG00000175311	ENSG00000175311	ANKS4B	16:21244985-21329912	NOTEST	0	0	0	0	1	1
ENSG00000175315	ENSG00000175315	CST6	11:65779311-65780976	NOTEST	0	0	0	0	1	1
ENSG00000175318	ENSG00000175318	GRAMD2	15:72452147-72490126	NOTEST	0.0731383	0.202284	1.46768	0	1	1
ENSG00000175319	ENSG00000175319	NF1P5	18:14152997-14157341	NOTEST	0	0	0	0	1	1
ENSG00000175325	ENSG00000175325	PROP1	5:177419235-177423243	NOTEST	0	0.0276972	inf	0	1	1
ENSG00000175329	ENSG00000175329	ISX	22:35318598-35483380	NOTEST	0	0.0122442	inf	0	1	1
ENSG00000175336	ENSG00000175336	APOF	12:56754352-56756607	NOTEST	0.00981898	0	#NAME?	0	1	1
ENSG00000175344	ENSG00000175344	CHRNA7	15:32322690-32464722	NOTEST	0.042739	0.0347289	-0.299416	0	1	1
ENSG00000175393	ENSG00000175393	OR10A6	11:7949179-7950209	NOTEST	0	0	0	0	1	1
ENSG00000175398	ENSG00000175398	OR10P1	12:56030643-56031638	NOTEST	0	0	0	0	1	1
ENSG00000175426	ENSG00000175426	PCSK1	5:95220801-96143803	NOTEST	0.0126557	0	#NAME?	0	1	1
ENSG00000175463	ENSG00000175463	TBC1D10C	11:67159175-67193078	NOTEST	0.136057	0.0425911	-1.67558	0	1	1
ENSG00000175485	ENSG00000175485	OR52W1	11:6220375-6221489	NOTEST	0	0.0110917	inf	0	1	1
ENSG00000175489	ENSG00000175489	LRRC25	19:18501953-18508427	NOTEST	0	0.0159521	inf	0	1	1

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ENSG00000175497	ENSG00000175497	DPP10	2:115199875-116603328	NOTEST	0	0	0	0	1	1
ENSG00000175505	ENSG00000175505	CLCF1	11:67118247-67141648	NOTEST	0.186967	0.305462	0.708208	0	1	1
ENSG00000175509	ENSG00000175509	RP11-395L14.13	2:114425054-114426198	NOTEST	0.0281864	0	#NAME?	0	1	1
ENSG00000175513	ENSG00000175513	TSGA10IP	11:65712915-65727434	NOTEST	0	0	0	0	1	1
ENSG00000175514	ENSG00000175514	GPR152	11:67218771-67226699	NOTEST	0	0	0	0	1	1
ENSG00000175518	ENSG00000175518	UBQLNL	11:5274419-5667019	NOTEST	0.0194802	0.0274861	0.496698	0	1	1
ENSG00000175520	ENSG00000175520	UBQLN3	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000175535	ENSG00000175535	PNLIP	10:118305442-118327367	NOTEST	0	0	0	0	1	1
ENSG00000175538	ENSG00000175538	KCNE3	11:74041362-74197096	NOTEST	0	0	0	0	1	1
ENSG00000175544	ENSG00000175544	CABP4	11:67218771-67226699	NOTEST	0	0.00926419	inf	0	1	1
ENSG00000175564	ENSG00000175564	UCP3	11:73711325-73720480	NOTEST	0.0929391	0.0557286	-0.737869	0	1	1
ENSG00000175591	ENSG00000175591	P2RY2	11:72929342-72947397	NOTEST	0.0637965	0.086584	0.440625	0	1	1
ENSG00000175604	ENSG00000175604	RP11-276H1.3	16:12070593-12704901	NOTEST	0	0.0198607	inf	0	1	1
ENSG00000175619	ENSG00000175619	OR4B1	11:48238343-48239314	NOTEST	0	0	0	0	1	1
ENSG00000175646	ENSG00000175646	PRM1	16:11343475-11445619	NOTEST	0	0	0	0	1	1
ENSG00000175658	ENSG00000175658	DRD5P2	1:148900614-148903715	NOTEST	0	0	0	0	1	1
ENSG00000175664	ENSG00000175664	TEX26	13:31456069-31551760	NOTEST	0	0	0	0	1	1
ENSG00000175676	ENSG00000175676	GOLGA8EP	15:23435095-23448420	NOTEST	0	0	0	0	1	1
ENSG00000175699	ENSG00000175699	LINC00521	14:94463615-94478040	NOTEST	0	0	0	0	1	1
ENSG00000175707	ENSG00000175707	C1orf172	1:27276052-27286897	NOTEST	0.071535	0.108186	0.596786	0	1	1
ENSG00000175718	ENSG00000175718	RBMXL3	X:114345184-114468635	NOTEST	0	0	0	0	1	1
ENSG00000175728	ENSG00000175728	C11orf44	11:130542850-130587247	NOTEST	0	0	0	0	1	1
ENSG00000175746	ENSG00000175746	C15orf54	15:39157522-39719396	NOTEST	0	0	0	0	1	1
ENSG00000175749	ENSG00000175749	EIF3KP1	5:102368079-102368735	NOTEST	0	0.0739707	inf	0	1	1
ENSG00000175766	ENSG00000175766	EIF4E1B	5:176057682-176073642	NOTEST	0	0	0	0	1	1
ENSG00000175772	ENSG00000175772	LINC01106	2:111132714-111142219	NOTEST	0.120757	0.152446	0.336192	0	1	1
ENSG00000175773	ENSG00000175773	RP11-121M22.1	11:130184887-130263688	NOTEST	0	0	0	0	1	1
ENSG00000175779	ENSG00000175779	C15orf53	15:38988798-38992239	NOTEST	0	0	0	0	1	1
ENSG00000175785	ENSG00000175785	PRIMA1	14:94184643-94254827	NOTEST	0.00770684	0	#NAME?	0	1	1
ENSG00000175793	ENSG00000175793	SFN	1:27189632-27190947	NOTEST	0.0259649	0.12049	2.21428	0	1	1
ENSG00000175800	ENSG00000175800	OR52B3P	11:4399511-4400457	NOTEST	0	0	0	0	1	1
ENSG00000175809	ENSG00000175809	ZNF645	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000175820	ENSG00000175820	CCDC168	13:103381800-103389159	NOTEST	0.00785688	0	#NAME?	0	1	1
ENSG00000175841	ENSG00000175841	FAM172BP	3:101237710-101242731	NOTEST	0	0	0	0	1	1
ENSG00000175857	ENSG00000175857	GAPT	5:57787261-57792917	NOTEST	0.0138036	0	#NAME?	0	1	1
ENSG00000175868	ENSG00000175868	CALCB	11:14926542-15103888	NOTEST	0.0165208	0.0833034	2.33409	0	1	1
ENSG00000175874	ENSG00000175874	CREG2	2:101962012-102004057	NOTEST	0.0859306	0.0333751	-1.3644	0	1	1
ENSG00000175877	ENSG00000175877	WBSCR28	7:73275488-73280223	NOTEST	0	0	0	0	1	1
ENSG00000175886	ENSG00000175886	RPL7AP66	18:36786887-37380282	NOTEST	0.129497	0.314189	1.27872	0	1	1
ENSG00000175894	ENSG00000175894	TSPEAR	21:45917774-46131495	NOTEST	0.00391215	0.00303892	-0.364404	0	1	1
ENSG00000175911	ENSG00000175911	AC127496.1	17:78965397-78983317	NOTEST	0.232201	0.281843	0.27952	0	1	1
ENSG00000175920	ENSG00000175920	DOK7	4:3465032-3503200	NOTEST	0.0477889	0.0760046	0.66941	0	1	1
ENSG00000175928	ENSG00000175928	LRRN1	3:3742497-4508965	NOTEST	0.0728649	0.00570991	-3.67369	0	1	1
ENSG00000175967	ENSG00000175967	RP11-544L8__B.4	6:114225301-114242806	NOTEST	0.00712621	0	#NAME?	0	1	1

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ENSG00000175985	ENSG00000175985	PLEKHD1	14:69951408-69995215	NOTEST	0	0.00703274	inf	0	1	1
ENSG00000176007	ENSG00000176007	FAM220BP	9:38527093-38527909	NOTEST	0	0	0	0	1	1
ENSG00000176009	ENSG00000176009	ASCL3	11:8959118-8964580	NOTEST	0	0	0	0	1	1
ENSG00000176029	ENSG00000176029	C11orf16	11:8932685-8954553	NOTEST	0.00854994	0.00689612	-0.31013	0	1	1
ENSG00000176034	ENSG00000176034	CHDC2	X:36053907-36163187	NOTEST	0	0	0	0	1	1
ENSG00000176040	ENSG00000176040	TMPRSS7	3:111753689-111800116	NOTEST	0	0.0205674	inf	0	1	1
ENSG00000176043	ENSG00000176043	RP1-146I3.1	14:73393039-73426411	NOTEST	0	0	0	0	1	1
ENSG00000176049	ENSG00000176049	JAKMIP2	5:146967989-147162338	NOTEST	0.230184	0.293234	0.349259	0	1	1
ENSG00000176054	ENSG00000176054	RPL23P2	21:30369933-30370354	NOTEST	0.1712	0.185264	0.113901	0	1	1
ENSG00000176075	ENSG00000176075	LINC00302	1:152627952-152629280	NOTEST	0	0	0	0	1	1
ENSG00000176076	ENSG00000176076	KCNE1L	X:108866928-108976632	NOTEST	0.0323927	0.181237	2.48414	0	1	1
ENSG00000176082	ENSG00000176082	AL357153.1	14:70892528-71014181	NOTEST	0.0195803	0.0266837	0.446559	0	1	1
ENSG00000176083	ENSG00000176083	ZNF683	1:26688124-26701013	NOTEST	0	0	0	0	1	1
ENSG00000176092	ENSG00000176092	AIM1L	1:26648349-26680621	NOTEST	0	0.420777	inf	0	1	1
ENSG00000176115	ENSG00000176115	AQP7P4	9:67032330-67048373	NOTEST	0	0	0	0	1	1
ENSG00000176134	ENSG00000176134	AL445665.1	9:69650262-69660358	NOTEST	0	0	0	0	1	1
ENSG00000176136	ENSG00000176136	MC5R	18:13824153-13826861	NOTEST	0.0302919	0.09082	1.58408	0	1	1
ENSG00000176153	ENSG00000176153	GPX2	14:65381078-65569413	NOTEST	0.0489577	0.051658	0.0774578	0	1	1
ENSG00000176160	ENSG00000176160	HSF5	17:56497527-56565745	NOTEST	0	0	0	0	1	1
ENSG00000176165	ENSG00000176165	FOXG1	14:29235049-29238870	NOTEST	0	0	0	0	1	1
ENSG00000176177	ENSG00000176177	ENTHD1	22:40139048-40289868	NOTEST	0.308236	0.51699	0.746098	0	1	1
ENSG00000176183	ENSG00000176183	CH17-12M21.1	5:97674447-97675536	NOTEST	0	0	0	0	1	1
ENSG00000176194	ENSG00000176194	CIDEA	18:12254317-12277594	NOTEST	0	0	0	0	1	1
ENSG00000176198	ENSG00000176198	OR11H4	14:20710897-20711979	NOTEST	0	0	0	0	1	1
ENSG00000176200	ENSG00000176200	OR4D11	11:59271048-59271984	NOTEST	0	0	0	0	1	1
ENSG00000176219	ENSG00000176219	OR11H6	14:20691790-20692964	NOTEST	0	0	0	0	1	1
ENSG00000176227	ENSG00000176227	CTAGE15	7:143268818-143271480	NOTEST	0	0	0	0	1	1
ENSG00000176230	ENSG00000176230	OR4K17	14:20585565-20586597	NOTEST	0	0	0	0	1	1
ENSG00000176231	ENSG00000176231	OR10H4	19:16059817-16060768	NOTEST	0	0	0	0	1	1
ENSG00000176232	ENSG00000176232	RP5-1193P9.4	7:63440762-63441855	NOTEST	0	0	0	0	1	1
ENSG00000176236	ENSG00000176236	C10orf111	10:15137383-15210692	NOTEST	0.0655792	0.028627	-1.19586	0	1	1
ENSG00000176239	ENSG00000176239	OR51B6	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000176243	ENSG00000176243	CDV3P1	3:96495788-96496527	NOTEST	0	0	0	0	1	1
ENSG00000176246	ENSG00000176246	OR4L1	14:20528203-20529142	NOTEST	0	0	0	0	1	1
ENSG00000176253	ENSG00000176253	OR4K13	14:20502002-20502919	NOTEST	0	0	0	0	1	1
ENSG00000176256	ENSG00000176256	HMGB4	1:33979608-34631443	NOTEST	0	0	0	0	1	1
ENSG00000176268	ENSG00000176268	CYCSP34	13:41396431-41495910	NOTEST	0.330107	0	#NAME?	0	1	1
ENSG00000176269	ENSG00000176269	OR4F21	8:116048-117043	NOTEST	0	0.043488	inf	0	1	1
ENSG00000176281	ENSG00000176281	OR4K5	14:20388740-20389818	NOTEST	0	0	0	0	1	1
ENSG00000176289	ENSG00000176289	IDSP1	X:148558520-148632055	NOTEST	0.216811	0.205339	-0.0784251	0	1	1
ENSG00000176290	ENSG00000176290	OR4K3	14:20336400-20337302	NOTEST	0	0	0	0	1	1
ENSG00000176293	ENSG00000176293	ZNF135	19:58570606-58629794	NOTEST	0.0813886	0.0441911	-0.881071	0	1	1
ENSG00000176294	ENSG00000176294	OR4N2	14:20187173-20296531	NOTEST	0	0	0	0	1	1
ENSG00000176299	ENSG00000176299	OR4M1	14:20187173-20296531	NOTEST	0	0	0	0	1	1
ENSG00000176302	ENSG00000176302	FOXR1	11:118842416-118852001	NOTEST	0	0	0	0	1	1

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ENSG00000176305	ENSG00000176305	AC087269.1	8:8559447-8561616	NOTEST	0.00234165	0.0668702	4.83576	0	1	1
ENSG00000176312	ENSG00000176312	OR4H12P	14:20187173-20296531	NOTEST	0	0	0	0	1	1
ENSG00000176318	ENSG00000176318	FOXN3P1	X:101801661-101803141	NOTEST	0	0	0	0	1	1
ENSG00000176320	ENSG00000176320	RP11-404O13.5	1:158167711-158173667	NOTEST	0	0	0	0	1	1
ENSG00000176343	ENSG00000176343	RPL37AP8	11:111759922-111760198	NOTEST	0	0.0993726	inf	0	1	1
ENSG00000176349	ENSG00000176349	AC110781.3	7:1855428-2272878	NOTEST	0.010623	0.0205762	0.953792	0	1	1
ENSG00000176358	ENSG00000176358	TAC4	17:47915670-47926199	NOTEST	0.0698152	0.112446	0.687622	0	1	1
ENSG00000176378	ENSG00000176378	PFN1P10	1:21766620-21811498	NOTEST	0.0944504	0	#NAME?	0	1	1
ENSG00000176381	ENSG00000176381	PRR18	6:166719167-166721936	NOTEST	0	0.00455493	inf	0	1	1
ENSG00000176383	ENSG00000176383	B3GNT4	12:122688089-122751068	NOTEST	0.408009	0.313256	-0.381262	0	1	1
ENSG00000176395	ENSG00000176395	CEACAM20	19:45005728-45033811	NOTEST	0	0	0	0	1	1
ENSG00000176435	ENSG00000176435	CLEC14A	14:38723307-38725574	NOTEST	0	0	0	0	1	1
ENSG00000176472	ENSG00000176472	ZNF575	19:44010870-44040282	NOTEST	0.431625	0.318597	-0.438047	0	1	1
ENSG00000176495	ENSG00000176495	OR5AN1	11:59131884-59132921	NOTEST	0	0	0	0	1	1
ENSG00000176510	ENSG00000176510	OR10AC1P	7:143078172-143220542	NOTEST	0	0	0	0	1	1
ENSG00000176515	ENSG00000176515	AL033381.1	6:1080163-1105181	NOTEST	0.0218683	0.00319369	-2.77554	0	1	1
ENSG00000176532	ENSG00000176532	PRR15	7:29603426-29606911	NOTEST	0	0	0	0	1	1
ENSG00000176540	ENSG00000176540	OR4C5	11:48387036-48388017	NOTEST	0	0	0	0	1	1
ENSG00000176547	ENSG00000176547	OR4C3	11:48346471-48347507	NOTEST	0	0	0	0	1	1
ENSG00000176555	ENSG00000176555	OR4S1	11:48327774-48328704	NOTEST	0	0	0	0	1	1
ENSG00000176566	ENSG00000176566	DCAF4L2	8:88882972-88886296	NOTEST	0.00471001	0.0036589	-0.364319	0	1	1
ENSG00000176567	ENSG00000176567	OR4X1	11:48285412-48286330	NOTEST	0	0	0	0	1	1
ENSG00000176571	ENSG00000176571	CNBD1	8:87878669-88767946	NOTEST	0.0568135	0.0827759	0.542976	0	1	1
ENSG00000176584	ENSG00000176584	DMBT1P1	10:124516209-124558696	NOTEST	0	0	0	0	1	1
ENSG00000176593	ENSG00000176593	CTD-2368P22.1	19:58488420-58522600	NOTEST	0.244408	0.302817	0.309153	0	1	1
ENSG00000176595	ENSG00000176595	KBTBD11	8:1919562-1955102	NOTEST	0.132799	0.16528	0.315665	0	1	1
ENSG00000176601	ENSG00000176601	MAP3K19	2:135722060-135805038	NOTEST	0	0	0	0	1	1
ENSG00000176605	ENSG00000176605	C14orf177	14:99177949-99184098	NOTEST	0	0	0	0	1	1
ENSG00000176635	ENSG00000176635	HORMAD2	22:30279143-30573064	NOTEST	0	0.00593499	inf	0	1	1
ENSG00000176641	ENSG00000176641	RNF152	18:59475295-59561480	NOTEST	0.32506	0.498181	0.615964	0	1	1
ENSG00000176654	ENSG00000176654	NANOGP1	12:8045171-8052736	NOTEST	0	0	0	0	1	1
ENSG00000176659	ENSG00000176659	C20orf197	20:58630979-58648008	NOTEST	0	0	0	0	1	1
ENSG00000176678	ENSG00000176678	FOXL1	16:86609973-86615303	NOTEST	0	0	0	0	1	1
ENSG00000176679	ENSG00000176679	TGIF2LY	Y:3447081-3448082	NOTEST	0	0	0	0	1	1
ENSG00000176692	ENSG00000176692	FOXC2	16:86598750-86602539	NOTEST	0	0	0	0	1	1
ENSG00000176695	ENSG00000176695	OR4F17	19:107470-111696	NOTEST	0	0	0	0	1	1
ENSG00000176697	ENSG00000176697	BDNF	11:27528384-27899195	NOTEST	0.258945	0.408077	0.656194	0	1	1
ENSG00000176716	ENSG00000176716	OR10AB1P	11:7710668-7927502	NOTEST	0	0	0	0	1	1
ENSG00000176723	ENSG00000176723	ZNF843	16:31445568-31454346	NOTEST	0.192507	0.194179	0.0124702	0	1	1
ENSG00000176728	ENSG00000176728	TTTY14	Y:21034386-21239302	NOTEST	0	0	0	0	1	1
ENSG00000176734	ENSG00000176734	TRIL	7:28992973-28998961	NOTEST	0.0374997	0.0775662	1.04855	0	1	1
ENSG00000176742	ENSG00000176742	OR51V1	11:5220964-5221930	NOTEST	0	0	0	0	1	1
ENSG00000176746	ENSG00000176746	MAGEB6	X:26210556-26213763	NOTEST	0	0.0242141	inf	0	1	1
ENSG00000176748	ENSG00000176748	OR52Z1	11:5172238-5207612	NOTEST	0	0	0	0	1	1

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ENSG00000176753	ENSG00000176753	C15orf56	15:40453223-40569688	NOTEST	0	0.00589737	inf	0	1	1
ENSG00000176754	ENSG00000176754	LINC00303	1:204001574-204010393	NOTEST	0.0316109	0	#NAME?	0	1	1
ENSG00000176761	ENSG00000176761	ZNF285B	19:44971857-44977444	NOTEST	0.0875418	0.0725588	-0.270821	0	1	1
ENSG00000176769	ENSG00000176769	TCERG1L	10:132890653-133109984	NOTEST	0.00606891	0	#NAME?	0	1	1
ENSG00000176774	ENSG00000176774	MAGEB18	X:26156459-26158852	NOTEST	0	0	0	0	1	1
ENSG00000176782	ENSG00000176782	DEFB104A	8:7693992-7698764	NOTEST	0	0	0	0	1	1
ENSG00000176787	ENSG00000176787	OR52E2	11:5079879-5080857	NOTEST	0	0	0	0	1	1
ENSG00000176788	ENSG00000176788	BASP1	5:17065706-17276943	NOTEST	0.0435011	0.0651692	0.583139	0	1	1
ENSG00000176797	ENSG00000176797	DEFB103A	8:7738725-7740186	NOTEST	0	0	0	0	1	1
ENSG00000176798	ENSG00000176798	OR51L1	11:5020212-5021160	NOTEST	0	0	0	0	1	1
ENSG00000176812	ENSG00000176812	RP11-629O4.1	X:25212497-25213324	NOTEST	0	0	0	0	1	1
ENSG00000176824	ENSG00000176824	AC009951.1	2:145141647-145282147	NOTEST	0.0159347	0	#NAME?	0	1	1
ENSG00000176840	ENSG00000176840	MIR7-3HG	19:4769116-4772545	NOTEST	0	0	0	0	1	1
ENSG00000176855	ENSG00000176855	KRT18P28	1:182928208-182929540	NOTEST	0	0	0	0	1	1
ENSG00000176857	ENSG00000176857	GJA1P1	5:108083522-108532542	NOTEST	0.0152737	0	#NAME?	0	1	1
ENSG00000176868	ENSG00000176868	AL358781.1	9:134269479-134375584	NOTEST	0.0590714	0	#NAME?	0	1	1
ENSG00000176879	ENSG00000176879	OR51G1	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000176882	ENSG00000176882	RP11-432M24.4	13:50194449-50194784	NOTEST	0	0	0	0	1	1
ENSG00000176884	ENSG00000176884	GRIN1	9:140032841-140063207	NOTEST	0.0710158	0.382152	2.42793	0	1	1
ENSG00000176887	ENSG00000176887	SOX11	2:5832798-5848227	NOTEST	0	0	0	0	1	1
ENSG00000176893	ENSG00000176893	OR51G2	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000176895	ENSG00000176895	OR51A7	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000176900	ENSG00000176900	OR51T1	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000176904	ENSG00000176904	OR51H1P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000176907	ENSG00000176907	C8orf4	8:40010988-40012821	NOTEST	0	0	0	0	1	1
ENSG00000176919	ENSG00000176919	C8G	9:139839697-139841426	NOTEST	0.280341	0.427281	0.608003	0	1	1
ENSG00000176920	ENSG00000176920	FUT2	19:49199227-49209207	NOTEST	0.210361	0.141112	-0.576032	0	1	1
ENSG00000176922	ENSG00000176922	OR51S1	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000176923	ENSG00000176923	OR7A15P	19:15037869-15038836	NOTEST	0	0	0	0	1	1
ENSG00000176925	ENSG00000176925	OR51F2	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000176927	ENSG00000176927	EFCAB5	17:27887564-28513493	NOTEST	0.572156	0.250101	-1.1939	0	1	1
ENSG00000176928	ENSG00000176928	GCNT4	5:74323288-74326724	NOTEST	0.121192	0.0807654	-0.585484	0	1	1
ENSG00000176933	ENSG00000176933	TOB2P1	6:28185420-28186655	NOTEST	0.509406	0.461109	-0.143708	0	1	1
ENSG00000176937	ENSG00000176937	OR52R1	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000176945	ENSG00000176945	MUC20	3:195384932-195467994	NOTEST	0.35167	0.243944	-0.527676	0	1	1
ENSG00000176951	ENSG00000176951	OR51N1P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000176956	ENSG00000176956	LY6H	8:144239330-144242128	NOTEST	0	0	0	0	1	1
ENSG00000176970	ENSG00000176970	RPL7L1P11	X:147546227-147546948	NOTEST	0	0	0	0	1	1
ENSG00000176971	ENSG00000176971	FIBIN	11:27015627-27018630	NOTEST	0	0	0	0	1	1
ENSG00000176979	ENSG00000176979	TRIM60	4:165953104-165962896	NOTEST	0	0	0	0	1	1
ENSG00000176984	ENSG00000176984	AP000679.2	11:119981982-120056237	NOTEST	0	0	0	0	1	1
ENSG00000176988	ENSG00000176988	FMR1NB	X:147062848-147108187	NOTEST	0	0	0	0	1	1
ENSG00000177023	ENSG00000177023	DEFB104B	8:7327829-7332604	NOTEST	0	0	0	0	1	1
ENSG00000177025	ENSG00000177025	C19orf18	19:58469804-58485902	NOTEST	0	0.0140763	inf	0	1	1

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ENSG00000177096	ENSG00000177096	FAM109B	22:42470254-42475445	NOTEST	0.0192815	0	#NAME?	0	1	1
ENSG00000177098	ENSG00000177098	SCN4B	11:118004091-118023603	NOTEST	0.160099	0.233289	0.543153	0	1	1
ENSG00000177103	ENSG00000177103	DSCAML1	11:117298488-117748201	NOTEST	0	0	0	0	1	1
ENSG00000177108	ENSG00000177108	ZDHHC22	14:77564439-77725838	NOTEST	0.0128828	0.00712791	-0.853897	0	1	1
ENSG00000177112	ENSG00000177112	MRVI1-AS1	11:10562818-10715535	NOTEST	0.0714183	0.210854	1.56188	0	1	1
ENSG00000177133	ENSG00000177133	LINC00982	1:2976178-2985001	NOTEST	0	0	0	0	1	1
ENSG00000177138	ENSG00000177138	FAM9B	X:8992272-9132680	NOTEST	0	0.106363	inf	0	1	1
ENSG00000177143	ENSG00000177143	CETN1	18:580366-581524	NOTEST	0	0	0	0	1	1
ENSG00000177151	ENSG00000177151	OR2T35	1:248801587-248802559	NOTEST	0	0	0	0	1	1
ENSG00000177174	ENSG00000177174	OR14C36	1:248512076-248513015	NOTEST	0	0	0	0	1	1
ENSG00000177182	ENSG00000177182	CLVS1	8:61969716-62627155	NOTEST	0.0154205	0.00720994	-1.09679	0	1	1
ENSG00000177186	ENSG00000177186	OR2M7	1:248486893-248487899	NOTEST	0	0	0	0	1	1
ENSG00000177191	ENSG00000177191	B3GNT8	19:41931263-41934635	NOTEST	0.0538006	0.0345767	-0.637822	0	1	1
ENSG00000177197	ENSG00000177197	PCNPP5	13:48877886-49056122	NOTEST	0	0.105537	inf	0	1	1
ENSG00000177201	ENSG00000177201	OR2T12	1:248457917-248458880	NOTEST	0	0	0	0	1	1
ENSG00000177202	ENSG00000177202	SPACA4	19:49104066-49118111	NOTEST	0	0	0	0	1	1
ENSG00000177212	ENSG00000177212	OR2T33	1:248436072-248437138	NOTEST	0	0	0	0	1	1
ENSG00000177233	ENSG00000177233	OR2M1P	1:248285233-248286184	NOTEST	0	0	0	0	1	1
ENSG00000177234	ENSG00000177234	C10orf85	10:122357720-122359629	NOTEST	0.01709	0.07381	2.11066	0	1	1
ENSG00000177238	ENSG00000177238	TRIM72	16:31225341-31236510	NOTEST	0.0135726	0.0105335	-0.365705	0	1	1
ENSG00000177243	ENSG00000177243	DEFB103B	8:7286409-7287870	NOTEST	0	0	0	0	1	1
ENSG00000177257	ENSG00000177257	DEFB4B	8:7272381-7274385	NOTEST	0	0	0	0	1	1
ENSG00000177261	ENSG00000177261	ENSAP3	2:215562450-215562788	NOTEST	0	0	0	0	1	1
ENSG00000177272	ENSG00000177272	KCNA3	1:111214309-111217655	NOTEST	0	0	0	0	1	1
ENSG00000177275	ENSG00000177275	OR2AJ1	1:248097070-248098057	NOTEST	0	0	0	0	1	1
ENSG00000177283	ENSG00000177283	FZD8	10:35927176-35930362	NOTEST	0	0.0226768	inf	0	1	1
ENSG00000177291	ENSG00000177291	GJD4	10:35894337-35897863	NOTEST	0	0	0	0	1	1
ENSG00000177294	ENSG00000177294	FBXO39	17:6679541-6735080	NOTEST	0	0	0	0	1	1
ENSG00000177300	ENSG00000177300	CLDN22	4:184020445-184241930	NOTEST	0	0.0267162	inf	0	1	1
ENSG00000177306	ENSG00000177306	OR7E125P	8:7104247-7105874	NOTEST	0	0	0	0	1	1
ENSG00000177324	ENSG00000177324	BEND2	X:18181050-18239024	NOTEST	0	0.00543165	inf	0	1	1
ENSG00000177335	ENSG00000177335	C8orf31	8:144120625-144141359	NOTEST	0	0.0101701	inf	0	1	1
ENSG00000177338	ENSG00000177338	LINC00469	17:71733992-71824659	NOTEST	0	0	0	0	1	1
ENSG00000177340	ENSG00000177340	AC024940.1	12:31433517-31479992	NOTEST	0	0.0223691	inf	0	1	1
ENSG00000177350	ENSG00000177350	RPL13AP3	14:56214925-56239921	NOTEST	0	0	0	0	1	1
ENSG00000177354	ENSG00000177354	C10orf71	10:50507186-50535537	NOTEST	0	0	0	0	1	1
ENSG00000177369	ENSG00000177369	RP1-62O9.3	17:47325600-47336024	NOTEST	0	0	0	0	1	1
ENSG00000177374	ENSG00000177374	HIC1	17:1957447-1962981	NOTEST	0.0878991	0.262981	1.58104	0	1	1
ENSG00000177398	ENSG00000177398	UMODL1	21:43483067-43563563	NOTEST	0	0	0	0	1	1
ENSG00000177400	ENSG00000177400	OR7E8P	8:12541662-12542662	NOTEST	0	0	0	0	1	1
ENSG00000177414	ENSG00000177414	UBE2U	1:64669309-64733051	NOTEST	0	0.0811461	inf	0	1	1
ENSG00000177418	ENSG00000177418	AC006001.1	7:66010633-66057373	NOTEST	0	0	0	0	1	1
ENSG00000177447	ENSG00000177447	CBX3P1	11:27528384-27899195	NOTEST	0	0	0	0	1	1
ENSG00000177452	ENSG00000177452	RP4-597J3.1	1:64239692-64647181	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000177459	ENSG00000177459	C8orf47	8:99076538-99105838	NOTEST	0	0.00725849	inf	0	1	1
ENSG00000177462	ENSG00000177462	OR2T8	1:248084319-248085258	NOTEST	0	0	0	0	1	1
ENSG00000177464	ENSG00000177464	GPR4	19:46030684-46105470	NOTEST	0	0.0284809	inf	0	1	1
ENSG00000177465	ENSG00000177465	ACOT4	14:74058409-74063200	NOTEST	0.369567	0.461802	0.32144	0	1	1
ENSG00000177468	ENSG00000177468	OLIG3	6:137813335-137815531	NOTEST	0.0146677	0.0056983	-1.36404	0	1	1
ENSG00000177476	ENSG00000177476	OR2G3	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000177483	ENSG00000177483	RBM44	2:238536218-238751451	NOTEST	0.052413	0.013738	-1.93175	0	1	1
ENSG00000177489	ENSG00000177489	OR2G2	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000177494	ENSG00000177494	ZBED2	3:111011565-111384597	NOTEST	0	0.0102665	inf	0	1	1
ENSG00000177504	ENSG00000177504	VCX2	X:8137988-8139308	NOTEST	0	0	0	0	1	1
ENSG00000177511	ENSG00000177511	ST8SIA3	18:55018043-55038962	NOTEST	0	0	0	0	1	1
ENSG00000177519	ENSG00000177519	RPRM	2:154277190-154449801	NOTEST	0	0	0	0	1	1
ENSG00000177535	ENSG00000177535	OR2B11	1:247614254-247615308	NOTEST	0	0	0	0	1	1
ENSG00000177551	ENSG00000177551	NHLH2	1:116378997-116386538	NOTEST	0.00634383	0.00163487	-1.95618	0	1	1
ENSG00000177553	ENSG00000177553	RP11-56N19.5	1:11821843-11908402	NOTEST	0	0	0	0	1	1
ENSG00000177558	ENSG00000177558	FAM187B	19:35715702-35719632	NOTEST	0	0	0	0	1	1
ENSG00000177570	ENSG00000177570	SAMD12	8:119201697-119634234	NOTEST	0.193794	0.273524	0.497138	0	1	1
ENSG00000177575	ENSG00000177575	CD163	12:7499280-7656489	NOTEST	0	0	0	0	1	1
ENSG00000177586	ENSG00000177586	OR7E149P	12:8589998-8591021	NOTEST	0	0	0	0	1	1
ENSG00000177590	ENSG00000177590	RP5-1051J4.6	7:150413644-150487837	NOTEST	0	0	0	0	1	1
ENSG00000177596	ENSG00000177596	AL355390.1	13:74987093-74993252	NOTEST	0	0	0	0	1	1
ENSG00000177599	ENSG00000177599	ZNF491	19:11906898-11920437	NOTEST	0.106315	0.110493	0.0556056	0	1	1
ENSG00000177614	ENSG00000177614	PGBD5	1:230457391-230561475	NOTEST	0.0440671	0.0369508	-0.254096	0	1	1
ENSG00000177627	ENSG00000177627	C12orf54	12:48876285-48894744	NOTEST	0	0	0	0	1	1
ENSG00000177669	ENSG00000177669	MBOAT4	8:29952913-30041156	NOTEST	0.0422587	0	#NAME?	0	1	1
ENSG00000177673	ENSG00000177673	C2orf57	2:232457574-232458994	NOTEST	0	0.028674	inf	0	1	1
ENSG00000177675	ENSG00000177675	CD163L1	12:7499280-7656489	NOTEST	0.0922575	0.0779917	-0.242346	0	1	1
ENSG00000177684	ENSG00000177684	DEFB114	6:49927961-49931818	NOTEST	0	0	0	0	1	1
ENSG00000177688	ENSG00000177688	SUMO4	6:149539061-149732749	NOTEST	0	0.0225784	inf	0	1	1
ENSG00000177689	ENSG00000177689	MAGEB10	X:27826106-27841131	NOTEST	0	0	0	0	1	1
ENSG00000177692	ENSG00000177692	DNAJC28	21:34860496-34864027	NOTEST	0.373143	0.335063	-0.155297	0	1	1
ENSG00000177693	ENSG00000177693	OR4F4	15:102462244-102463298	NOTEST	0	0	0	0	1	1
ENSG00000177699	ENSG00000177699	RP11-16K12.1	15:79252288-79383115	NOTEST	0.140978	0.259446	0.879962	0	1	1
ENSG00000177706	ENSG00000177706	FAM20C	7:182934-300711	NOTEST	0.139499	0.329151	1.23849	0	1	1
ENSG00000177710	ENSG00000177710	SLC35G5	8:11188396-11189717	NOTEST	0.0129147	0.0411841	1.67307	0	1	1
ENSG00000177721	ENSG00000177721	ANXA2R	5:43014515-43192123	NOTEST	0.321933	0.331389	0.0417672	0	1	1
ENSG00000177725	ENSG00000177725	AC105206.1	8:22022248-22069839	NOTEST	0.0269775	0.00997794	-1.43494	0	1	1
ENSG00000177736	ENSG00000177736	RP11-474P12.3	9:127640645-127905785	NOTEST	0.0790147	0.0714091	-0.146015	0	1	1
ENSG00000177752	ENSG00000177752	YIPF7	4:44624085-44728612	NOTEST	0.146772	0.0472502	-1.63518	0	1	1
ENSG00000177757	ENSG00000177757	FAM87B	1:714149-755214	NOTEST	0.0167526	0	#NAME?	0	1	1
ENSG00000177770	ENSG00000177770	CDKN2AIPNLP1	1:226680888-226681190	NOTEST	0	0	0	0	1	1
ENSG00000177776	ENSG00000177776	RPS2P2	14:74844520-74845121	NOTEST	0	0	0	0	1	1
ENSG00000177791	ENSG00000177791	MYOZ1	10:75391411-75401515	NOTEST	0.0501938	0.0836667	0.737144	0	1	1
ENSG00000177800	ENSG00000177800	TMEM78	1:229385382-229387557	NOTEST	0	0	0	0	1	1

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ENSG00000177807	ENSG00000177807	KCNJ10	1:160007256-160049611	NOTEST	0.584571	0.41644	-0.489267	0	1	1
ENSG00000177839	ENSG00000177839	PCDHB9	5:140566892-140571111	NOTEST	0.135928	0.12399	-0.132619	0	1	1
ENSG00000177842	ENSG00000177842	ZNF620	3:40547482-40560227	NOTEST	0.542654	0.386594	-0.489215	0	1	1
ENSG00000177875	ENSG00000177875	C12orf68	12:48577365-48579709	NOTEST	0.305919	0.187403	-0.707012	0	1	1
ENSG00000177910	ENSG00000177910	SPATA31C2	9:90744219-90753361	NOTEST	0	0	0	0	1	1
ENSG00000177938	ENSG00000177938	CAPZA3	12:18891044-18892121	NOTEST	0	0	0	0	1	1
ENSG00000177947	ENSG00000177947	ODF3	11:127114-207428	NOTEST	0	0	0	0	1	1
ENSG00000177984	ENSG00000177984	LCN15	9:139654085-139660707	NOTEST	0	0.0826719	inf	0	1	1
ENSG00000177992	ENSG00000177992	SPATA31E1	9:90497740-90503814	NOTEST	0	0	0	0	1	1
ENSG00000177993	ENSG00000177993	ZNRF3-AS1	22:29279579-29453475	NOTEST	0	0.0267538	inf	0	1	1
ENSG00000177994	ENSG00000177994	C2orf73	2:54557170-54610879	NOTEST	0.0763572	0.105204	0.462358	0	1	1
ENSG00000178015	ENSG00000178015	GPR150	5:94955781-94957846	NOTEST	0.073964	0.1441	0.962175	0	1	1
ENSG00000178021	ENSG00000178021	TSPYL6	2:54091203-54532437	NOTEST	0.0050789	0	#NAME?	0	1	1
ENSG00000178031	ENSG00000178031	ADAMTSL1	9:18473891-18910948	NOTEST	0.0407783	0.0384961	-0.083087	0	1	1
ENSG00000178033	ENSG00000178033	FAM26E	6:116813459-116880031	NOTEST	0.0015448	0.00480542	1.63724	0	1	1
ENSG00000178055	ENSG00000178055	PRSS42	3:46871031-46875585	NOTEST	0	0	0	0	1	1
ENSG00000178081	ENSG00000178081	ULK4P3	15:30395922-30423960	NOTEST	0.261248	0.19512	-0.421057	0	1	1
ENSG00000178084	ENSG00000178084	HTR3C	3:183770834-183778459	NOTEST	0	0	0	0	1	1
ENSG00000178107	ENSG00000178107	RP11-998D10.4	14:21576201-21584862	NOTEST	0.0791103	0	#NAME?	0	1	1
ENSG00000178115	ENSG00000178115	GOLGA8Q	15:30844182-30854704	NOTEST	0.129669	0.0309565	-2.06652	0	1	1
ENSG00000178125	ENSG00000178125	PPP1R42	8:67876333-68255912	NOTEST	0.0162913	0	#NAME?	0	1	1
ENSG00000178130	ENSG00000178130	FAM27L	17:21825296-21826499	NOTEST	0	0	0	0	1	1
ENSG00000178162	ENSG00000178162	FAR2P2	2:131174327-131199048	NOTEST	0.00388656	0	#NAME?	0	1	1
ENSG00000178171	ENSG00000178171	AMER3	2:131501110-131525707	NOTEST	0	0	0	0	1	1
ENSG00000178172	ENSG00000178172	SPINK6	5:147582356-147594700	NOTEST	0	0	0	0	1	1
ENSG00000178175	ENSG00000178175	ZNF366	5:71738478-71803554	NOTEST	0.00405864	0	#NAME?	0	1	1
ENSG00000178187	ENSG00000178187	ZNF454	5:178368191-178393434	NOTEST	0	0	0	0	1	1
ENSG00000178193	ENSG00000178193	RP4-682C21.5	1:76175687-76189696	NOTEST	0	0	0	0	1	1
ENSG00000178199	ENSG00000178199	ZC3H12D	6:149768793-149806197	NOTEST	0.0255158	0.0138622	-0.880234	0	1	1
ENSG00000178201	ENSG00000178201	VN1R1	19:57874844-57988938	NOTEST	0.161974	0.144442	-0.165276	0	1	1
ENSG00000178206	ENSG00000178206	CYP4F31P	2:131862419-132111282	NOTEST	0	0.0111088	inf	0	1	1
ENSG00000178217	ENSG00000178217	SH2D4B	10:82297657-82406316	NOTEST	0.0392923	0.0357814	-0.135037	0	1	1
ENSG00000178222	ENSG00000178222	RNF212	4:1050037-1107350	NOTEST	0	0	0	0	1	1
ENSG00000178235	ENSG00000178235	SLITRK1	13:84451343-84456528	NOTEST	0	0.00713689	inf	0	1	1
ENSG00000178243	ENSG00000178243	C9orf62	9:138235094-138238408	NOTEST	0.0153494	0.00658309	-1.22135	0	1	1
ENSG00000178248	ENSG00000178248	AP000345.1	22:23804272-23829167	NOTEST	0	0	0	0	1	1
ENSG00000178257	ENSG00000178257	PRM3	16:11343475-11445619	NOTEST	0	0	0	0	1	1
ENSG00000178279	ENSG00000178279	TNP2	16:11343475-11445619	NOTEST	0	0	0	0	1	1
ENSG00000178287	ENSG00000178287	SPAG11A	8:7705397-7726389	NOTEST	0	0	0	0	1	1
ENSG00000178297	ENSG00000178297	TMPRSS9	19:2389768-2456994	NOTEST	0.4825	0.478625	-0.0116339	0	1	1
ENSG00000178342	ENSG00000178342	KCNG2	18:77623667-77660184	NOTEST	0.167805	0.236023	0.492145	0	1	1
ENSG00000178343	ENSG00000178343	SHISA3	4:42399855-42404504	NOTEST	0	0	0	0	1	1
ENSG00000178358	ENSG00000178358	OR2D3	11:6942204-6943264	NOTEST	0	0	0	0	1	1

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ENSG00000178363	ENSG00000178363	CALML3	10:5556206-5568225	NOTEST	0	0	0	0	1	1
ENSG00000178372	ENSG00000178372	CALML5	10:5540657-5541533	NOTEST	0	0	0	0	1	1
ENSG00000178394	ENSG00000178394	HTR1A	5:63253719-63276870	NOTEST	0	0	0	0	1	1
ENSG00000178395	ENSG00000178395	C1orf65	1:223568714-223568812	NOTEST	0	0	0	0	1	1
ENSG00000178412	ENSG00000178412	RP11-567M16.3	18:77398927-77439745	NOTEST	0.0158004	0	#NAME?	0	1	1
ENSG00000178430	ENSG00000178430	AC006111.1	16:3661728-3767598	NOTEST	0.0901394	0.0500776	-0.847992	0	1	1
ENSG00000178445	ENSG00000178445	GLDC	9:6532463-6645650	NOTEST	0.315014	0.553947	0.814331	0	1	1
ENSG00000178457	ENSG00000178457	LINC00314	21:29385681-29395552	NOTEST	0	0	0	0	1	1
ENSG00000178458	ENSG00000178458	H3F3AP6	4:140586921-141075338	NOTEST	0.123641	0.138192	0.160516	0	1	1
ENSG00000178460	ENSG00000178460	MCMDC2	8:67782983-67838633	NOTEST	0.484797	0.580708	0.260433	0	1	1
ENSG00000178462	ENSG00000178462	TUBAL3	10:5435060-5446793	NOTEST	0	0	0	0	1	1
ENSG00000178473	ENSG00000178473	UCN3	10:5406971-5416169	NOTEST	0	0	0	0	1	1
ENSG00000178503	ENSG00000178503	NECAP1P1	7:37625102-37625932	NOTEST	0	0	0	0	1	1
ENSG00000178522	ENSG00000178522	AMBN	4:71457972-71473005	NOTEST	0	0.0415587	inf	0	1	1
ENSG00000178550	ENSG00000178550	AC010170.1	3:45265957-45267770	NOTEST	0	0	0	0	1	1
ENSG00000178556	ENSG00000178556	CKS1BP6	X:30635570-30635810	NOTEST	0.197797	0.462034	1.22398	0	1	1
ENSG00000178562	ENSG00000178562	CD28	2:204571197-204603635	NOTEST	0.032203	0.0586738	0.865518	0	1	1
ENSG00000178568	ENSG00000178568	ERBB4	2:212240445-213403565	NOTEST	0.177311	0.558199	1.6545	0	1	1
ENSG00000178573	ENSG00000178573	MAF	16:79619739-79634611	NOTEST	0.0281582	0.0344942	0.292798	0	1	1
ENSG00000178586	ENSG00000178586	OR6B3	2:240984493-240985489	NOTEST	0	0	0	0	1	1
ENSG00000178591	ENSG00000178591	DEFB125	20:67890-77735	NOTEST	0	0	0	0	1	1
ENSG00000178596	ENSG00000178596	GAPDHP29	1:94767593-94768578	NOTEST	0.0182466	0	#NAME?	0	1	1
ENSG00000178597	ENSG00000178597	PSAPL1	4:7194264-7744554	NOTEST	0	0	0	0	1	1
ENSG00000178602	ENSG00000178602	OTOS	2:241078445-241083979	NOTEST	0	0	0	0	1	1
ENSG00000178623	ENSG00000178623	GPR35	2:241526132-241570676	NOTEST	0.096222	0.0196766	-2.28988	0	1	1
ENSG00000178631	ENSG00000178631	ACTG1P1	3:139108656-139396859	NOTEST	0.0592479	0.0120532	-2.29734	0	1	1
ENSG00000178636	ENSG00000178636	RP11-455G16.1	4:120113927-120216672	NOTEST	0.0139625	0.0266212	0.931024	0	1	1
ENSG00000178642	ENSG00000178642	AL513477.1	1:2252691-2323146	NOTEST	0.110632	0.0985141	-0.167366	0	1	1
ENSG00000178645	ENSG00000178645	C10orf53	10:50817140-50918307	NOTEST	0	0	0	0	1	1
ENSG00000178654	ENSG00000178654	RP11-366I21.1	9:7597822-7598377	NOTEST	0	0	0	0	1	1
ENSG00000178662	ENSG00000178662	CSRNP3	2:166326156-166545917	NOTEST	0.190373	0.18065	-0.0756301	0	1	1
ENSG00000178690	ENSG00000178690	DYNAP	18:52254987-52266724	NOTEST	0	0	0	0	1	1
ENSG00000178715	ENSG00000178715	RP11-169K16.8	1:16154723-16155167	NOTEST	0	0	0	0	1	1
ENSG00000178722	ENSG00000178722	C5orf64	5:60933534-61047590	NOTEST	0.0446865	0.177149	1.98705	0	1	1
ENSG00000178723	ENSG00000178723	GLULP4	9:34917171-34918293	NOTEST	0.0284513	0	#NAME?	0	1	1
ENSG00000178732	ENSG00000178732	GP5	3:194115549-194119995	NOTEST	0.00446093	0	#NAME?	0	1	1
ENSG00000178734	ENSG00000178734	C13orf45	13:76445186-76457947	NOTEST	0.0151091	0.0117463	-0.363214	0	1	1
ENSG00000178750	ENSG00000178750	STX19	3:93698982-93847389	NOTEST	0	0.0233978	inf	0	1	1
ENSG00000178762	ENSG00000178762	HIST1H2BPS1	6:25732009-25732390	NOTEST	0	0	0	0	1	1
ENSG00000178772	ENSG00000178772	CPN2	3:194060493-194072057	NOTEST	0	0	0	0	1	1
ENSG00000178776	ENSG00000178776	C5orf46	5:147250244-147286101	NOTEST	0	0.0633237	inf	0	1	1
ENSG00000178789	ENSG00000178789	CD300LB	17:72517312-72527613	NOTEST	0	0	0	0	1	1
ENSG00000178795	ENSG00000178795	GDPD4	11:76927602-77012732	NOTEST	0	0.0303864	inf	0	1	1
ENSG00000178796	ENSG00000178796	RIIAD1	1:151673501-151702281	NOTEST	0.00494104	0.0416488	3.07539	0	1	1
ENSG00000178803	ENSG00000178803	ADORA2AAS1	22:24666785-24924358	NOTEST	0.04362	0.0373436	-0.224128	0	1	1

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ENSG00000178809	ENSG00000178809	TRIM73	7:74988447-75115548	NOTEST	0	0.080729	inf	0	1	1
ENSG00000178814	ENSG00000178814	OPLAH	8:145104029-145118735	NOTEST	0.114055	0.23985	1.07241	0	1	1
ENSG00000178821	ENSG00000178821	TMEM52	1:1849028-1850712	NOTEST	0.0553985	0.0882954	0.672492	0	1	1
ENSG00000178826	ENSG00000178826	TMEM139	7:142941185-142985141	NOTEST	0.240375	0.443448	0.883475	0	1	1
ENSG00000178828	ENSG00000178828	RNF186	1:20140522-20145995	NOTEST	0	0	0	0	1	1
ENSG00000178836	ENSG00000178836	AC114812.5	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000178863	ENSG00000178863	CEBPA-AS1	19:33793762-33800293	NOTEST	0.00983339	0.013828	0.491835	0	1	1
ENSG00000178882	ENSG00000178882	FAM101A	12:124247041-124800570	NOTEST	0.0142604	0	#NAME?	0	1	1
ENSG00000178894	ENSG00000178894	AC073416.1	2:90137997-90138233	NOTEST	0	0	0	0	1	1
ENSG00000178919	ENSG00000178919	FOXE1	9:100615535-100618986	NOTEST	0	0	0	0	1	1
ENSG00000178928	ENSG00000178928	TPRX1	19:48304499-48322308	NOTEST	0	0	0	0	1	1
ENSG00000178934	ENSG00000178934	LGALS7B	19:39279850-39282389	NOTEST	0	0	0	0	1	1
ENSG00000178947	ENSG00000178947	LINC00086	X:134555867-134561999	NOTEST	0.069937	0.101454	0.536692	0	1	1
ENSG00000178965	ENSG00000178965	C1orf173	1:75033794-75139422	NOTEST	0.00546259	0.00663793	0.281149	0	1	1
ENSG00000178972	ENSG00000178972	AC097658.1	4:144256417-144395721	NOTEST	0.0754705	0.0589968	-0.355275	0	1	1
ENSG00000178977	ENSG00000178977	LINC00324	17:8123959-8127361	NOTEST	0.0733037	0.0273007	-1.42495	0	1	1
ENSG00000178997	ENSG00000178997	EXD1	15:41474922-41522941	NOTEST	0	0.0631875	inf	0	1	1
ENSG00000179002	ENSG00000179002	TAS1R2	1:19166092-19283180	NOTEST	0	0	0	0	1	1
ENSG00000179023	ENSG00000179023	KLHDC7A	1:18807423-18812478	NOTEST	0	0	0	0	1	1
ENSG00000179028	ENSG00000179028	RP11-363G10.2	X:51942962-51946358	NOTEST	0	0	0	0	1	1
ENSG00000179031	ENSG00000179031	LL0XNC01-131B10.2	X:100165700-100166478	NOTEST	0	0.0190374	inf	0	1	1
ENSG00000179038	ENSG00000179038	AP001885.1	11:66886739-67025558	NOTEST	0	0.0107199	inf	0	1	1
ENSG00000179044	ENSG00000179044	EXOC3L1	16:67218268-67224107	NOTEST	0.0392479	0.0753151	0.940325	0	1	1
ENSG00000179046	ENSG00000179046	TRIML2	4:189012426-189030757	NOTEST	0	0	0	0	1	1
ENSG00000179055	ENSG00000179055	OR13D1	9:107456659-107457766	NOTEST	0	0	0	0	1	1
ENSG00000179057	ENSG00000179057	IGSF22	11:18714668-18814268	NOTEST	0	0.0338411	inf	0	1	1
ENSG00000179058	ENSG00000179058	C9orf50	9:132371162-132398209	NOTEST	0.0390945	0.0216193	-0.854647	0	1	1
ENSG00000179059	ENSG00000179059	ZFP42	4:188916924-188926204	NOTEST	0	0.00420513	inf	0	1	1
ENSG00000179061	ENSG00000179061	AC012074.1	2:25592041-25598714	NOTEST	0.0751589	0.181991	1.27585	0	1	1
ENSG00000179066	ENSG00000179066	AC020907.1	19:35531409-35598141	NOTEST	0.0651815	0.0210293	-1.63206	0	1	1
ENSG00000179071	ENSG00000179071	CCDC89	11:85394892-85397320	NOTEST	0.00657995	0	#NAME?	0	1	1
ENSG00000179073	ENSG00000179073	TAAR3	6:132929363-132930441	NOTEST	0	0	0	0	1	1
ENSG00000179082	ENSG00000179082	C9orf106	9:132083294-132087184	NOTEST	0	0.00350558	inf	0	1	1
ENSG00000179083	ENSG00000179083	FAM133A	X:92929011-92967273	NOTEST	0.104994	0.0519626	-1.01476	0	1	1
ENSG00000179088	ENSG00000179088	C12orf42	12:103631368-103889749	NOTEST	0.0359173	0	#NAME?	0	1	1
ENSG00000179097	ENSG00000179097	HTR1F	3:88039845-88042919	NOTEST	0	0.0115397	inf	0	1	1
ENSG00000179111	ENSG00000179111	HES7	17:8023907-8027410	NOTEST	0.195779	0.163684	-0.258313	0	1	1
ENSG00000179131	ENSG00000179131	RP11-458F8.3	7:66379567-66379930	NOTEST	0.15417	0	#NAME?	0	1	1
ENSG00000179133	ENSG00000179133	C10orf67	10:23556123-23634110	NOTEST	0.0205271	0.11848	2.52904	0	1	1
ENSG00000179136	ENSG00000179136	LINC00670	17:12453098-12546171	NOTEST	0	0	0	0	1	1
ENSG00000179141	ENSG00000179141	MTUS2-AS1	13:29598747-30077892	NOTEST	0.0718615	0.103794	0.530434	0	1	1
ENSG00000179142	ENSG00000179142	CYP11B2	8:143915553-143999259	NOTEST	0	0	0	0	1	1
ENSG00000179144	ENSG00000179144	GIMAP7	7:150211917-150218161	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000179148	ENSG00000179148	ALOXE3	17:7999217-8022365	NOTEST	0	0.012418	inf	0	1	1
ENSG00000179157	ENSG00000179157	RPS2P28	6:43263431-43337216	NOTEST	0	0	0	0	1	1
ENSG00000179165	ENSG00000179165	PXT1	6:36322418-36458920	NOTEST	0.00766707	0.00538678	-0.509253	0	1	1
ENSG00000179168	ENSG00000179168	GGN	19:38874904-38878722	NOTEST	0.113914	0.155245	0.446602	0	1	1
ENSG00000179170	ENSG00000179170	OR7E97P	3:125465926-125466941	NOTEST	0	0	0	0	1	1
ENSG00000179172	ENSG00000179172	HNRNPCL1	1:12907260-12908578	NOTEST	0	0	0	0	1	1
ENSG00000179178	ENSG00000179178	TMEM125	1:43629845-43739673	NOTEST	0	0	0	0	1	1
ENSG00000179213	ENSG00000179213	SIGLECL1	19:51749602-51774433	NOTEST	0	0	0	0	1	1
ENSG00000179219	ENSG00000179219	LINC00311	16:85316563-85319569	NOTEST	0	0.00748628	inf	0	1	1
ENSG00000179242	ENSG00000179242	CDH4	20:59827481-60515673	NOTEST	0.117194	0.112815	-0.0549396	0	1	1
ENSG00000179253	ENSG00000179253	RP11-429E11.3	20:59827481-60515673	NOTEST	0	0	0	0	1	1
ENSG00000179256	ENSG00000179256	SMCO3	12:14956505-15059520	NOTEST	0.192485	0.13143	-0.550449	0	1	1
ENSG00000179270	ENSG00000179270	C2orf71	2:29179476-29297127	NOTEST	0	0	0	0	1	1
ENSG00000179284	ENSG00000179284	DAND5	19:13075972-13085567	NOTEST	0.0522667	0.0209458	-1.31923	0	1	1
ENSG00000179292	ENSG00000179292	TMEM151A	11:66059340-66064135	NOTEST	0.300403	0.402524	0.422176	0	1	1
ENSG00000179296	ENSG00000179296	CTGLF12P	10:49217897-49239729	NOTEST	0.0911239	0.0243327	-1.90493	0	1	1
ENSG00000179299	ENSG00000179299	NSUN7	4:40751913-40812002	NOTEST	0.00931491	0	#NAME?	0	1	1
ENSG00000179300	ENSG00000179300	ZCCHC5	X:77911565-77914825	NOTEST	0	0	0	0	1	1
ENSG00000179314	ENSG00000179314	WSCD1	17:5675553-6027747	NOTEST	0	0.0133205	inf	0	1	1
ENSG00000179331	ENSG00000179331	RAB39A	11:107799228-107834208	NOTEST	0	0	0	0	1	1
ENSG00000179342	ENSG00000179342	GS1-124K5.9	7:65970141-65971210	NOTEST	0	0.0128597	inf	0	1	1
ENSG00000179363	ENSG00000179363	TMEM31	X:102962151-102983583	NOTEST	0.0756659	0.0207501	-1.86652	0	1	1
ENSG00000179381	ENSG00000179381	OR4K11P	21:14916602-14917506	NOTEST	0	0	0	0	1	1
ENSG00000179388	ENSG00000179388	EGR3	8:22545171-22941132	NOTEST	0.352936	0.165725	-1.09061	0	1	1
ENSG00000179397	ENSG00000179397	C1orf101	1:244617678-244804479	NOTEST	0.081654	0.0868311	0.0886883	0	1	1
ENSG00000179399	ENSG00000179399	GPC5	13:92050928-93519490	NOTEST	0.204638	0.220083	0.104973	0	1	1
ENSG00000179407	ENSG00000179407	DNAJB8	3:128181281-128191160	NOTEST	0	0	0	0	1	1
ENSG00000179412	ENSG00000179412	HNRNPCP5	1:13182959-13184326	NOTEST	0	0	0	0	1	1
ENSG00000179420	ENSG00000179420	OR6W1P	7:142759426-142760735	NOTEST	0	0	0	0	1	1
ENSG00000179428	ENSG00000179428	AC073072.5	7:22765013-22771621	NOTEST	0.082192	0.0696499	-0.238878	0	1	1
ENSG00000179443	ENSG00000179443	OR13C6P	9:35991332-35992282	NOTEST	0	0	0	0	1	1
ENSG00000179447	ENSG00000179447	RP5-1027G4.3	20:19193289-19703581	NOTEST	0	0	0	0	1	1
ENSG00000179449	ENSG00000179449	AC124309.1	15:23888690-23891175	NOTEST	0	0.00545115	inf	0	1	1
ENSG00000179452	ENSG00000179452	RP11-380B22.1	1:181205523-181207740	NOTEST	0	0	0	0	1	1
ENSG00000179455	ENSG00000179455	MKRN3	15:23810453-23873064	NOTEST	0.0222656	0.0181977	-0.291061	0	1	1
ENSG00000179467	ENSG00000179467	AL109806.1	20:55043646-55101198	NOTEST	0	0	0	0	1	1
ENSG00000179468	ENSG00000179468	OR9A2	7:142723244-142724282	NOTEST	0	0	0	0	1	1
ENSG00000179477	ENSG00000179477	ALOX12B	17:7975953-7991021	NOTEST	0	0.137392	inf	0	1	1
ENSG00000179520	ENSG00000179520	SLC17A8	12:100750856-100815837	NOTEST	0.037021	0.027492	-0.429332	0	1	1
ENSG00000179528	ENSG00000179528	LBX2	2:74724643-74731805	NOTEST	0.211452	0.0825057	-1.35776	0	1	1
ENSG00000179546	ENSG00000179546	HTR1D	1:23516992-23521222	NOTEST	0.00557462	0.0264316	2.24532	0	1	1
ENSG00000179564	ENSG00000179564	LSMEM2	3:50316457-50336899	NOTEST	0.0535185	0.234245	2.12991	0	1	1
ENSG00000179571	ENSG00000179571	NBPF23	1:149089874-149130302	NOTEST	0	0	0	0	1	1
ENSG00000179577	ENSG00000179577	AP003471.1	8:105342551-105479281	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000179580	ENSG00000179580	RNF151	16:2016823-2018976	NOTEST	0	0	0	0	1	1
ENSG00000179583	ENSG00000179583	CIITA	16:10958770-11036878	NOTEST	0.499302	0.403121	-0.3087	0	1	1
ENSG00000179593	ENSG00000179593	ALOX15B	17:7942334-7952452	NOTEST	0.0133484	0	#NAME?	0	1	1
ENSG00000179600	ENSG00000179600	GPHB5	14:63779548-63785593	NOTEST	0	0	0	0	1	1
ENSG00000179603	ENSG00000179603	GRM8	7:126078651-126893348	NOTEST	0.00437973	0	#NAME?	0	1	1
ENSG00000179615	ENSG00000179615	OR2AP1	12:55828520-55979255	NOTEST	0	0	0	0	1	1
ENSG00000179626	ENSG00000179626	OR6C4	12:55828520-55979255	NOTEST	0	0	0	0	1	1
ENSG00000179636	ENSG00000179636	TPPP2	14:21484921-21572881	NOTEST	0	0	0	0	1	1
ENSG00000179639	ENSG00000179639	FCER1A	1:159259503-159278014	NOTEST	0.0250056	0.0720803	1.52735	0	1	1
ENSG00000179673	ENSG00000179673	RPRML	17:45000482-45177689	NOTEST	0	0	0	0	1	1
ENSG00000179674	ENSG00000179674	ARL14	3:160394947-160396233	NOTEST	0	0	0	0	1	1
ENSG00000179676	ENSG00000179676	LINC00305	18:61747242-62090836	NOTEST	0	0	0	0	1	1
ENSG00000179695	ENSG00000179695	OR6C2	12:55828520-55979255	NOTEST	0	0	0	0	1	1
ENSG00000179698	ENSG00000179698	KIAA1875	8:145153535-145173218	NOTEST	0.0229793	0.0105897	-1.11768	0	1	1
ENSG00000179709	ENSG00000179709	NLRP8	19:56459197-56499995	NOTEST	0	0	0	0	1	1
ENSG00000179715	ENSG00000179715	PCED1B	12:47469489-47630443	NOTEST	0.318617	0.599234	0.911296	0	1	1
ENSG00000179743	ENSG00000179743	RP11-169K16.9	1:16160559-16266955	NOTEST	0.428743	0.507265	0.242626	0	1	1
ENSG00000179751	ENSG00000179751	SYCN	19:39693470-39694906	NOTEST	0	0	0	0	1	1
ENSG00000179755	ENSG00000179755	CTD-2144E22.5	16:34256506-34258621	NOTEST	0.0453413	0	#NAME?	0	1	1
ENSG00000179761	ENSG00000179761	PIPOX	17:27232267-27384234	NOTEST	0.158523	0.187795	0.244472	0	1	1
ENSG00000179766	ENSG00000179766	ATP8B5P	9:35406751-35483026	NOTEST	0.0577767	0.0463318	-0.318487	0	1	1
ENSG00000179772	ENSG00000179772	FOXS1	20:30432102-30433420	NOTEST	0	0	0	0	1	1
ENSG00000179774	ENSG00000179774	ATOH7	10:69990385-69991871	NOTEST	0.106697	0.15836	0.569694	0	1	1
ENSG00000179776	ENSG00000179776	CDH5	16:66400532-66438686	NOTEST	0.0152792	0.0117103	-0.383798	0	1	1
ENSG00000179796	ENSG00000179796	LRRC3B	3:26664296-26752267	NOTEST	0	0	0	0	1	1
ENSG00000179799	ENSG00000179799	OR7E22P	3:75405666-75406654	NOTEST	0	0	0	0	1	1
ENSG00000179813	ENSG00000179813	FAM216B	13:43355685-43365683	NOTEST	0.0135661	0.0071481	-0.924369	0	1	1
ENSG00000179820	ENSG00000179820	MYADM	19:54357834-54379691	NOTEST	0.0279653	0.107949	1.94864	0	1	1
ENSG00000179826	ENSG00000179826	MRGPRX3	11:18142501-18160027	NOTEST	0.152476	0.116471	-0.388605	0	1	1
ENSG00000179840	ENSG00000179840	C1orf200	1:9711789-9884584	NOTEST	0	0	0	0	1	1
ENSG00000179841	ENSG00000179841	AKAP5	14:64854748-65009955	NOTEST	0.360251	0.255607	-0.495076	0	1	1
ENSG00000179846	ENSG00000179846	NKPD1	19:45574757-45808541	NOTEST	0.0353515	0.0273612	-0.369639	0	1	1
ENSG00000179869	ENSG00000179869	ABCA13	7:48211054-48687092	NOTEST	0.00928151	0.0386684	2.05872	0	1	1
ENSG00000179873	ENSG00000179873	NLRP11	19:56296769-56393220	NOTEST	0.00512262	0.00358671	-0.514223	0	1	1
ENSG00000179902	ENSG00000179902	C1orf194	1:109648572-109749401	NOTEST	0.0600798	0	#NAME?	0	1	1
ENSG00000179909	ENSG00000179909	ZNF154	19:58193336-58269527	NOTEST	0.0523734	0.0592936	0.179043	0	1	1
ENSG00000179913	ENSG00000179913	B3GNT3	19:17905636-17923891	NOTEST	0	0	0	0	1	1
ENSG00000179914	ENSG00000179914	ITLN1	1:160846328-160854960	NOTEST	0	0	0	0	1	1
ENSG00000179915	ENSG00000179915	NRXN1	2:50145642-51259674	NOTEST	0	0.00266456	inf	0	1	1
ENSG00000179919	ENSG00000179919	OR10A7	12:55614808-55615759	NOTEST	0	0	0	0	1	1
ENSG00000179921	ENSG00000179921	GPBAR1	2:219124218-219128582	NOTEST	0.00810654	0	#NAME?	0	1	1
ENSG00000179930	ENSG00000179930	ZNF648	1:182023704-182030847	NOTEST	0.0479251	0.0944567	0.978871	0	1	1
ENSG00000179934	ENSG00000179934	CCR8	3:39371196-39375171	NOTEST	0	0	0	0	1	1
ENSG00000179935	ENSG00000179935	LINC00652	20:18768294-18774979	NOTEST	0	0	0	0	1	1
ENSG00000179938	ENSG00000179938	GOLGA8J	15:30375157-30385702	NOTEST	0.0155719	0.00603933	-1.36649	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000179954	ENSG00000179954	SSC5D	19:55999770-56030465	NOTEST	0.0320161	0.0393536	0.297701	0	1	1
ENSG00000179978	ENSG00000179978	RP11-1319K7.1	5:69390201-69424261	NOTEST	0.109353	0.0619448	-0.819935	0	1	1
ENSG00000179994	ENSG00000179994	SPDYE7P	7:72333320-72341076	NOTEST	0	0	0	0	1	1
ENSG00000179997	ENSG00000179997	AC010894.4	2:175366679-175367043	NOTEST	0	0	0	0	1	1
ENSG00000180016	ENSG00000180016	OR1E1	17:3300397-3301704	NOTEST	0	0	0	0	1	1
ENSG00000180019	ENSG00000180019	AC079741.2	7:112063022-112131117	NOTEST	0	0	0	0	1	1
ENSG00000180035	ENSG00000180035	ZNF48	16:30389426-30411429	NOTEST	0.545044	0.60692	0.155134	0	1	1
ENSG00000180042	ENSG00000180042	OR1R1P	17:3181192-3290132	NOTEST	0	0	0	0	1	1
ENSG00000180043	ENSG00000180043	FAM71E2	19:55860673-55874628	NOTEST	0	0	0	0	1	1
ENSG00000180044	ENSG00000180044	C3orf80	3:159943422-160203561	NOTEST	0.094753	0.104883	0.146543	0	1	1
ENSG00000180053	ENSG00000180053	NKX2-6	8:23559963-23564111	NOTEST	0	0	0	0	1	1
ENSG00000180061	ENSG00000180061	TMEM150B	19:55824168-55845416	NOTEST	0	0	0	0	1	1
ENSG00000180066	ENSG00000180066	C10orf91	10:134257830-134262912	NOTEST	0.0136755	0.0491311	1.84505	0	1	1
ENSG00000180068	ENSG00000180068	OR3A4P	17:3181192-3290132	NOTEST	0	0	0	0	1	1
ENSG00000180071	ENSG00000180071	ANKRD18A	9:38540563-38624987	NOTEST	0.255231	0.262536	0.0407152	0	1	1
ENSG00000180081	ENSG00000180081	CTC-451A6.4	19:22934984-22937677	NOTEST	0	0	0	0	1	1
ENSG00000180083	ENSG00000180083	WFDC11	20:44277201-44298909	NOTEST	0	0	0	0	1	1
ENSG00000180090	ENSG00000180090	OR3A1	17:3181192-3290132	NOTEST	0	0	0	0	1	1
ENSG00000180096	ENSG00000180096	1-Sep	16:30389426-30411429	NOTEST	0.0908692	0.0378608	-1.26309	0	1	1
ENSG00000180105	ENSG00000180105	AC017081.2	2:207274810-207275633	NOTEST	0.0455626	0.190173	2.06139	0	1	1
ENSG00000180113	ENSG00000180113	TDRD6	6:46620677-46703430	NOTEST	0.0469687	0.00695101	-2.75641	0	1	1
ENSG00000180116	ENSG00000180116	C12orf40	12:40019968-40499891	NOTEST	0.00928661	0	#NAME?	0	1	1
ENSG00000180138	ENSG00000180138	CSNK1A1L	13:37677397-37679803	NOTEST	0	0	0	0	1	1
ENSG00000180139	ENSG00000180139	ACTA2-AS1	10:90639490-90775542	NOTEST	0.113128	0.0309068	-1.87196	0	1	1
ENSG00000180150	ENSG00000180150	HMGN2P9	22:43911996-44208217	NOTEST	0	0	0	0	1	1
ENSG00000180152	ENSG00000180152	AC079753.4	2:113610904-113611699	NOTEST	0	0	0	0	1	1
ENSG00000180155	ENSG00000180155	LYNX1	8:143844533-143859640	NOTEST	0.138368	0.557935	2.01159	0	1	1
ENSG00000180172	ENSG00000180172	RPS12P23	13:21668456-21668853	NOTEST	0.0657647	0	#NAME?	0	1	1
ENSG00000180176	ENSG00000180176	TH	11:2185158-2193107	NOTEST	0.0217599	0.192324	3.14379	0	1	1
ENSG00000180178	ENSG00000180178	FAR2P1	2:130748028-130808704	NOTEST	0.0839531	0	#NAME?	0	1	1
ENSG00000180189	ENSG00000180189	HMGB1P14	14:58466452-58764857	NOTEST	0.123187	0.237862	0.949276	0	1	1
ENSG00000180205	ENSG00000180205	WFDC9	20:44236577-44259907	NOTEST	0	0	0	0	1	1
ENSG00000180209	ENSG00000180209	MYLPF	16:30382254-30389312	NOTEST	0	0	0	0	1	1
ENSG00000180210	ENSG00000180210	F2	11:46740729-46761056	NOTEST	0.00884868	0.0304314	1.78203	0	1	1
ENSG00000180211	ENSG00000180211	RP1-278E11.3	6:39926152-39926572	NOTEST	0.291104	0.222138	-0.390077	0	1	1
ENSG00000180219	ENSG00000180219	FAM71C	12:99038918-100378432	NOTEST	0	0.0142042	inf	0	1	1
ENSG00000180221	ENSG00000180221	TPT1P10	10:59951277-60027694	NOTEST	0	0	0	0	1	1
ENSG00000180230	ENSG00000180230	NACAP2	10:121756597-121757221	NOTEST	0	0	0	0	1	1
ENSG00000180245	ENSG00000180245	RRH	4:110749149-110765760	NOTEST	0.0115667	0.0162714	0.492357	0	1	1
ENSG00000180251	ENSG00000180251	SLC9A4	2:103089761-103150431	NOTEST	0	0	0	0	1	1
ENSG00000180259	ENSG00000180259	PRNT	20:4711927-4721314	NOTEST	0	0	0	0	1	1
ENSG00000180264	ENSG00000180264	GPR144	9:127213422-127239379	NOTEST	0	0	0	0	1	1
ENSG00000180269	ENSG00000180269	GPR139	16:20042806-20085239	NOTEST	0	0	0	0	1	1
ENSG00000180279	ENSG00000180279	CTD-2568A17.5	19:51320936-51322134	NOTEST	0.0917388	0.188455	1.03862	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000180284	ENSG00000180284	RP5-1055C14.6	X:102906662-102907034	NOTEST	0	0	0	0	1	1
ENSG00000180287	ENSG00000180287	PLD5	1:242246287-242687998	NOTEST	0	0	0	0	1	1
ENSG00000180305	ENSG00000180305	WFDC10A	20:44236577-44259907	NOTEST	0	0	0	0	1	1
ENSG00000180316	ENSG00000180316	PNPLA1	6:36210979-36276372	NOTEST	0	0	0	0	1	1
ENSG00000180332	ENSG00000180332	KCTD4	13:45694649-45858237	NOTEST	0	0	0	0	1	1
ENSG00000180344	ENSG00000180344	AL035460.1	20:2673523-2740753	NOTEST	0	0	0	0	1	1
ENSG00000180347	ENSG00000180347	CCDC129	7:31553703-31698334	NOTEST	0	0	0	0	1	1
ENSG00000180353	ENSG00000180353	HCLS1	3:121350245-121379774	NOTEST	0.0896438	0.0447629	-1.0019	0	1	1
ENSG00000180383	ENSG00000180383	DEFB124	20:30053308-30072708	NOTEST	0	0	0	0	1	1
ENSG00000180386	ENSG00000180386	KRTAP9-7	17:39431910-39432949	NOTEST	0	0	0	0	1	1
ENSG00000180389	ENSG00000180389	ATP5EP2	13:28519342-28519727	NOTEST	0.0692618	0.0495308	-0.483734	0	1	1
ENSG00000180409	ENSG00000180409	OR10AA1P	1:158778188-158779125	NOTEST	0	0	0	0	1	1
ENSG00000180422	ENSG00000180422	LINC00304	16:89225553-89230653	NOTEST	0.0978424	0.0637249	-0.618604	0	1	1
ENSG00000180424	ENSG00000180424	DEFB123	20:30028321-30038060	NOTEST	0	0	0	0	1	1
ENSG00000180432	ENSG00000180432	CYP8B1	3:42846243-43101703	NOTEST	0.00392975	0	#NAME?	0	1	1
ENSG00000180433	ENSG00000180433	OR6K6	1:158724509-158725681	NOTEST	0	0	0	0	1	1
ENSG00000180437	ENSG00000180437	OR6K4P	1:158693902-158694902	NOTEST	0	0	0	0	1	1
ENSG00000180438	ENSG00000180438	TPRXL	3:13974552-14124311	NOTEST	0	0	0	0	1	1
ENSG00000180440	ENSG00000180440	SERTM1	13:37248048-37271976	NOTEST	0.00489153	0	#NAME?	0	1	1
ENSG00000180458	ENSG00000180458	CTD-3064H18.4	19:37988062-38210691	NOTEST	0.00479673	0.0396375	3.04674	0	1	1
ENSG00000180475	ENSG00000180475	OR10Q1	11:57995353-57996390	NOTEST	0	0	0	0	1	1
ENSG00000180481	ENSG00000180481	GLIPR1L2	12:75784849-75826468	NOTEST	0.299492	0.370459	0.306795	0	1	1
ENSG00000180483	ENSG00000180483	DEFB119	20:29964966-29978406	NOTEST	0	0	0	0	1	1
ENSG00000180509	ENSG00000180509	KCNE1	21:35818987-35884573	NOTEST	0.0461503	0.0799277	0.792355	0	1	1
ENSG00000180525	ENSG00000180525	PRR26	10:320129-735683	NOTEST	0.0212031	0.0722764	1.76925	0	1	1
ENSG00000180532	ENSG00000180532	ZSCAN4	19:58180302-58190520	NOTEST	0	0	0	0	1	1
ENSG00000180535	ENSG00000180535	BHLHA15	7:97840738-97842291	NOTEST	0.0475316	0.215054	2.17774	0	1	1
ENSG00000180539	ENSG00000180539	C9orf139	9:139901685-139931234	NOTEST	0	0.00633145	inf	0	1	1
ENSG00000180543	ENSG00000180543	TSPYL5	8:98285716-98290176	NOTEST	0	0	0	0	1	1
ENSG00000180549	ENSG00000180549	FUT7	9:139901685-139931234	NOTEST	0	0	0	0	1	1
ENSG00000180592	ENSG00000180592	SKIDA1	10:21802406-21814611	NOTEST	0.154109	0.0803583	-0.939428	0	1	1
ENSG00000180610	ENSG00000180610	ZBTB12P1	4:39699663-39784412	NOTEST	0.0693759	0.012142	-2.51442	0	1	1
ENSG00000180611	ENSG00000180611	MB21D2	3:192514603-192635950	NOTEST	0.0316176	0.0898274	1.50643	0	1	1
ENSG00000180613	ENSG00000180613	GSX2	4:54243809-55164414	NOTEST	0	0	0	0	1	1
ENSG00000180616	ENSG00000180616	SSTR2	17:71161115-71258491	NOTEST	0	0.0116242	inf	0	1	1
ENSG00000180636	ENSG00000180636	OR4E1	14:22138202-22139150	NOTEST	0	0	0	0	1	1
ENSG00000180638	ENSG00000180638	SLC47A2	17:19581600-19622292	NOTEST	0.0380342	0.0181163	-1.07001	0	1	1
ENSG00000180644	ENSG00000180644	PRF1	10:72357103-72362531	NOTEST	0	0	0	0	1	1
ENSG00000180658	ENSG00000180658	OR2A4	6:131949581-132068553	NOTEST	0	0	0	0	1	1
ENSG00000180660	ENSG00000180660	MAB21L1	13:35516423-36247159	NOTEST	0.096872	0.0887355	-0.126568	0	1	1
ENSG00000180662	ENSG00000180662	RPL21P8	14:65877309-66210839	NOTEST	0	0	0	0	1	1
ENSG00000180663	ENSG00000180663	VN1R3	16:31814267-31820165	NOTEST	0	0	0	0	1	1
ENSG00000180697	ENSG00000180697	C3orf22	3:126243125-126277808	NOTEST	0	0	0	0	1	1
ENSG00000180708	ENSG00000180708	OR10K2	1:158389717-158390656	NOTEST	0	0	0	0	1	1

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ENSG00000180714	ENSG00000180714	OR5AZ1P	11:57684768-57685711	NOTEST	0	0	0	0	1	1
ENSG00000180720	ENSG00000180720	CHRM4	11:46406639-46408107	NOTEST	0.0322447	0.0332272	0.0433	0	1	1
ENSG00000180723	ENSG00000180723	OR51A9P	11:4682082-4682993	NOTEST	0	0	0	0	1	1
ENSG00000180725	ENSG00000180725	AC015871.1	15:80282246-80282948	NOTEST	0	0	0	0	1	1
ENSG00000180745	ENSG00000180745	CLRN3	10:129676104-129691211	NOTEST	0	0	0	0	1	1
ENSG00000180770	ENSG00000180770	OR7E129P	3:129740395-129741363	NOTEST	0	0	0	0	1	1
ENSG00000180772	ENSG00000180772	AGTR2	X:115301974-115306225	NOTEST	0.00547797	0.0208952	1.93146	0	1	1
ENSG00000180785	ENSG00000180785	OR51E1	11:4664649-4676718	NOTEST	0	0	0	0	1	1
ENSG00000180787	ENSG00000180787	ZFP3	17:4981542-4999669	NOTEST	0.100343	0.131365	0.388646	0	1	1
ENSG00000180803	ENSG00000180803	RP11-467D10.2	13:25946208-26599989	NOTEST	0	0	0	0	1	1
ENSG00000180815	ENSG00000180815	MAP3K15	X:19362010-19533379	NOTEST	0.00945974	0.0603161	2.67267	0	1	1
ENSG00000180846	ENSG00000180846	CSNK1G2-AS1	19:1941187-1981337	NOTEST	0	0.060925	inf	0	1	1
ENSG00000180861	ENSG00000180861	C12orf36	12:13524022-13540101	NOTEST	0	0	0	0	1	1
ENSG00000180869	ENSG00000180869	C1orf180	1:85093912-85100703	NOTEST	0	0	0	0	1	1
ENSG00000180871	ENSG00000180871	CXCR2	2:218990011-219001976	NOTEST	0	0	0	0	1	1
ENSG00000180872	ENSG00000180872	DEFB112	6:50011287-50016364	NOTEST	0	0	0	0	1	1
ENSG00000180875	ENSG00000180875	GREM2	1:240652872-240775449	NOTEST	0.28262	0.228036	-0.309601	0	1	1
ENSG00000180878	ENSG00000180878	C11orf42	11:6226795-6232362	NOTEST	0.1169	0.059557	-0.972933	0	1	1
ENSG00000180909	ENSG00000180909	OR52B1P	11:6128913-6206806	NOTEST	0	0	0	0	1	1
ENSG00000180910	ENSG00000180910	TTTY11	Y:8651350-8685423	NOTEST	0	0	0	0	1	1
ENSG00000180913	ENSG00000180913	OR56B3P	11:6128913-6206806	NOTEST	0	0	0	0	1	1
ENSG00000180914	ENSG00000180914	OXTR	3:8661085-9005457	NOTEST	0.307105	0.359989	0.22922	0	1	1
ENSG00000180919	ENSG00000180919	OR56B4	11:6128913-6206806	NOTEST	0	0	0	0	1	1
ENSG00000180926	ENSG00000180926	OR7E18P	19:9371690-9372392	NOTEST	0	0	0	0	1	1
ENSG00000180929	ENSG00000180929	GPR62	3:51989329-52023213	NOTEST	0	0.0109369	inf	0	1	1
ENSG00000180934	ENSG00000180934	OR56A1	11:6047900-6048971	NOTEST	0	0	0	0	1	1
ENSG00000180938	ENSG00000180938	ZNF572	8:125985539-125991631	NOTEST	0.55981	0.458886	-0.286801	0	1	1
ENSG00000180974	ENSG00000180974	OR52E4	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000180987	ENSG00000180987	AC123768.1	15:32885656-32896179	NOTEST	0	0	0	0	1	1
ENSG00000180988	ENSG00000180988	OR52N2	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000180999	ENSG00000180999	C1orf105	1:171810620-172437971	NOTEST	0.0510305	0	#NAME?	0	1	1
ENSG00000181001	ENSG00000181001	OR52N1	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000181009	ENSG00000181009	OR52N5	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000181013	ENSG00000181013	C17orf47	17:56597197-56769416	NOTEST	0	0	0	0	1	1
ENSG00000181017	ENSG00000181017	OR56B2P	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000181023	ENSG00000181023	OR56B1	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000181031	ENSG00000181031	RPH3AL	17:62292-236045	NOTEST	0.113954	0.052258	-1.12472	0	1	1
ENSG00000181036	ENSG00000181036	FCRL6	1:159770300-159786041	NOTEST	0.202339	0.0766996	-1.39949	0	1	1
ENSG00000181072	ENSG00000181072	CHRM2	7:136370305-136866854	NOTEST	0	0	0	0	1	1
ENSG00000181074	ENSG00000181074	OR52N4	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000181085	ENSG00000181085	MAPK15	8:144798428-144804628	NOTEST	0	0.0754014	inf	0	1	1
ENSG00000181092	ENSG00000181092	ADIPOQ	3:186560462-186576252	NOTEST	0.00337454	3.22E-07	-13.3559	0	1	1
ENSG00000181097	ENSG00000181097	RP11-429J17.2	8:144766621-144796068	NOTEST	0.103053	0.147547	0.517784	0	1	1
ENSG00000181101	ENSG00000181101	SDCCAG3P2	1:175013761-175014784	NOTEST	0	0	0	0	1	1

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ENSG00000181123	ENSG00000181123	RP4-539M6.14	22:30879340-30901698	NOTEST	0	0	0	0	1	1
ENSG00000181143	ENSG00000181143	MUC16	19:8959519-9092018	NOTEST	0	0	0	0	1	1
ENSG00000181171	ENSG00000181171	FER1L6-AS1	8:124864226-125183763	NOTEST	0	0	0	0	1	1
ENSG00000181195	ENSG00000181195	PENK	8:57349232-57472382	NOTEST	0.113167	0.0773507	-0.548968	0	1	1
ENSG00000181201	ENSG00000181201	HIST3H2BA	1:228651803-228652327	NOTEST	0	0	0	0	1	1
ENSG00000181211	ENSG00000181211	HECW1-IT1	7:43152197-43605600	NOTEST	0.00890366	0	#NAME?	0	1	1
ENSG00000181214	ENSG00000181214	OR8G2P	11:124095436-124096365	NOTEST	0	0	0	0	1	1
ENSG00000181215	ENSG00000181215	C4orf50	4:5958844-5991545	NOTEST	0	0	0	0	1	1
ENSG00000181227	ENSG00000181227	RP4-682C21.2	1:76190035-76260764	NOTEST	0.216625	0.227211	0.0688353	0	1	1
ENSG00000181234	ENSG00000181234	TMEM132C	12:128751947-129192460	NOTEST	0	0	0	0	1	1
ENSG00000181240	ENSG00000181240	SLC25A41	19:6426047-6433790	NOTEST	0.054571	0.0324633	-0.749327	0	1	1
ENSG00000181260	ENSG00000181260	MTHFD2P7	3:179182133-179183116	NOTEST	0	0	0	0	1	1
ENSG00000181273	ENSG00000181273	OR5AK2	11:56756346-56757342	NOTEST	0	0	0	0	1	1
ENSG00000181282	ENSG00000181282	OR5AK3P	11:56738324-56739621	NOTEST	0	0	0	0	1	1
ENSG00000181291	ENSG00000181291	TMEM132E	17:32907767-32966337	NOTEST	0	0	0	0	1	1
ENSG00000181296	ENSG00000181296	OR5G1P	11:56542736-56543682	NOTEST	0	0	0	0	1	1
ENSG00000181322	ENSG00000181322	NME9	3:137906108-138048728	NOTEST	0.161975	0.191106	0.238601	0	1	1
ENSG00000181323	ENSG00000181323	SPEM1	17:7323421-7361026	NOTEST	0	0	0	0	1	1
ENSG00000181325	ENSG00000181325	OR9G3P	11:56507654-56508572	NOTEST	0	0	0	0	1	1
ENSG00000181333	ENSG00000181333	HEPHL1	11:93754526-93846917	NOTEST	0.00861058	0.0113749	0.401667	0	1	1
ENSG00000181355	ENSG00000181355	OFCC1	6:9596342-10211841	NOTEST	0.52331	0.502359	-0.0589479	0	1	1
ENSG00000181358	ENSG00000181358	CTAGE10P	13:50464726-50467134	NOTEST	0	0	0	0	1	1
ENSG00000181359	ENSG00000181359	HSP90AA6P	4:171502620-171526601	NOTEST	0	0	0	0	1	1
ENSG00000181371	ENSG00000181371	OR5M8	11:56257824-56258871	NOTEST	0	0	0	0	1	1
ENSG00000181374	ENSG00000181374	CCL13	17:32683470-32685629	NOTEST	0	0	0	0	1	1
ENSG00000181378	ENSG00000181378	CCDC108	2:219866936-219906249	NOTEST	0.118031	0.0989161	-0.254884	0	1	1
ENSG00000181392	ENSG00000181392	SYNE4	19:36494208-36505141	NOTEST	0.014724	0.0337161	1.19527	0	1	1
ENSG00000181395	ENSG00000181395	OR5AL1	11:56180171-56181156	NOTEST	0	0	0	0	1	1
ENSG00000181408	ENSG00000181408	UTS2R	17:80332152-80333462	NOTEST	0	0	0	0	1	1
ENSG00000181433	ENSG00000181433	SAGE1	X:134971373-134995220	NOTEST	0.00548126	0.0108533	0.985555	0	1	1
ENSG00000181444	ENSG00000181444	ZNF467	7:149461270-149470568	NOTEST	0.0490598	0.295262	2.58938	0	1	1
ENSG00000181449	ENSG00000181449	SOX2	3:180701496-181554668	NOTEST	0.0936824	0.174508	0.897447	0	1	1
ENSG00000181464	ENSG00000181464	CDRT1	17:15468796-15587625	NOTEST	0	0	0	0	1	1
ENSG00000181495	ENSG00000181495	AC026703.1	5:32689175-32791819	NOTEST	0.00549215	0	#NAME?	0	1	1
ENSG00000181499	ENSG00000181499	OR6T1	11:123813491-123814580	NOTEST	0	0	0	0	1	1
ENSG00000181511	ENSG00000181511	RP4-655L22.4	X:119866947-119867250	NOTEST	0	0	0	0	1	1
ENSG00000181514	ENSG00000181514	RP3-474G15.1	6:73308178-73309362	NOTEST	0	0	0	0	1	1
ENSG00000181518	ENSG00000181518	OR8D4	11:123777108-123778183	NOTEST	0	0	0	0	1	1
ENSG00000181541	ENSG00000181541	MAB21L2	4:151185593-151936879	NOTEST	0	0	0	0	1	1
ENSG00000181552	ENSG00000181552	EDDM3B	14:21236585-21239107	NOTEST	0	0	0	0	1	1
ENSG00000181562	ENSG00000181562	EDDM3A	14:21214050-21216539	NOTEST	0	0	0	0	1	1
ENSG00000181577	ENSG00000181577	C6orf223	6:43963459-44045689	NOTEST	0.191647	0.249753	0.382049	0	1	1
ENSG00000181585	ENSG00000181585	TMIE	3:46742822-46752376	NOTEST	0.0415534	0.037888	-0.133227	0	1	1

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ENSG00000181616	ENSG00000181616	OR52H1	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000181617	ENSG00000181617	FDCSP	4:71091787-71100969	NOTEST	0.0376075	0.0292868	-0.360771	0	1	1
ENSG00000181619	ENSG00000181619	GPR135	14:59895739-60043549	NOTEST	0.460579	0.511003	0.149885	0	1	1
ENSG00000181625	ENSG00000181625	SLX1B	16:29262828-29519817	NOTEST	0.183052	0.302641	0.725352	0	1	1
ENSG00000181626	ENSG00000181626	ANKRD62	18:12093851-12129748	NOTEST	0.00406158	0	#NAME?	0	1	1
ENSG00000181631	ENSG00000181631	P2RY13	3:150803483-151176497	NOTEST	0	0	0	0	1	1
ENSG00000181634	ENSG00000181634	TNFSF15	9:117546914-117568406	NOTEST	0.00410976	0.0326544	2.99015	0	1	1
ENSG00000181656	ENSG00000181656	GPR88	1:101003692-101007574	NOTEST	0	0	0	0	1	1
ENSG00000181689	ENSG00000181689	OR8K3	11:56085782-56086721	NOTEST	0	0	0	0	1	1
ENSG00000181693	ENSG00000181693	OR8H1	11:56057528-56058566	NOTEST	0	0	0	0	1	1
ENSG00000181698	ENSG00000181698	OR5T1	11:56043028-56044146	NOTEST	0	0	0	0	1	1
ENSG00000181705	ENSG00000181705	RP11-11L12.2	6:81208912-81209109	NOTEST	0	0	0	0	1	1
ENSG00000181718	ENSG00000181718	OR5T2	11:55999489-56000737	NOTEST	0	0	0	0	1	1
ENSG00000181733	ENSG00000181733	OR2Z1	19:8841315-8842371	NOTEST	0	0	0	0	1	1
ENSG00000181741	ENSG00000181741	FDX1P1	20:32951040-33099198	NOTEST	0	0.0304463	inf	0	1	1
ENSG00000181752	ENSG00000181752	OR8K5	11:55926869-55927793	NOTEST	0	0	0	0	1	1
ENSG00000181761	ENSG00000181761	OR8H3	11:55889848-55890787	NOTEST	0	0	0	0	1	1
ENSG00000181767	ENSG00000181767	OR8H2	11:55872518-55873457	NOTEST	0	0	0	0	1	1
ENSG00000181778	ENSG00000181778	TMEM252	9:71151495-71155783	NOTEST	0	0.0538351	inf	0	1	1
ENSG00000181780	ENSG00000181780	OR5J1P	11:55838505-55839525	NOTEST	0	0.0733937	inf	0	1	1
ENSG00000181781	ENSG00000181781	ODF3L2	19:463345-474983	NOTEST	0.0245335	0.100215	2.03028	0	1	1
ENSG00000181785	ENSG00000181785	OR5AS1	11:55797894-55798869	NOTEST	0	0	0	0	1	1
ENSG00000181786	ENSG00000181786	ACTL9	19:8807750-8809172	NOTEST	0	0	0	0	1	1
ENSG00000181790	ENSG00000181790	BAI1	8:143530790-143626370	NOTEST	0.181501	0.201574	0.151335	0	1	1
ENSG00000181791	ENSG00000181791	AC009041.1	16:1114092-1131454	NOTEST	0	0	0	0	1	1
ENSG00000181798	ENSG00000181798	LINC00471	2:232373136-232379050	NOTEST	0.0534725	0.0989956	0.888568	0	1	1
ENSG00000181800	ENSG00000181800	CELF2-AS1	10:11047258-11378674	NOTEST	0.198543	0.178074	-0.156971	0	1	1
ENSG00000181803	ENSG00000181803	OR6S1	14:21108854-21109850	NOTEST	0	0	0	0	1	1
ENSG00000181837	ENSG00000181837	OR5D17P	11:55522451-55523433	NOTEST	0	0	0	0	1	1
ENSG00000181847	ENSG00000181847	TIGIT	3:113995759-114029135	NOTEST	0.00530965	0.0247107	2.21845	0	1	1
ENSG00000181867	ENSG00000181867	FTMT	5:121187649-121188519	NOTEST	0	0	0	0	1	1
ENSG00000181885	ENSG00000181885	CLDN7	17:7143332-7167302	NOTEST	0.0140512	0.114397	3.02529	0	1	1
ENSG00000181903	ENSG00000181903	OR4C6	11:55432613-55433671	NOTEST	0	0.0403944	inf	0	1	1
ENSG00000181908	ENSG00000181908	AP003774.4	11:64216545-64219126	NOTEST	0.00685641	0	#NAME?	0	1	1
ENSG00000181927	ENSG00000181927	OR4P4	11:55405833-55406772	NOTEST	0	0	0	0	1	1
ENSG00000181935	ENSG00000181935	OR4C16	11:55339603-55340536	NOTEST	0	0	0	0	1	1
ENSG00000181939	ENSG00000181939	OR4C15	11:55321782-55322895	NOTEST	0	0	0	0	1	1
ENSG00000181943	ENSG00000181943	OR4A21P	11:55258627-55259618	NOTEST	0	0	0	0	1	1
ENSG00000181950	ENSG00000181950	OR4A13P	11:55234246-55235188	NOTEST	0.0192644	0	#NAME?	0	1	1
ENSG00000181958	ENSG00000181958	OR4A15	11:55135359-55136394	NOTEST	0	0	0	0	1	1
ENSG00000181961	ENSG00000181961	OR4A16	11:55110626-55111707	NOTEST	0	0	0	0	1	1
ENSG00000181963	ENSG00000181963	OR52K2	11:4470524-4471591	NOTEST	0	0	0	0	1	1
ENSG00000181965	ENSG00000181965	NEUROG1	5:134869990-134871639	NOTEST	0	0	0	0	1	1
ENSG00000181977	ENSG00000181977	PYY3	X:49920806-49921019	NOTEST	0	0	0	0	1	1

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ENSG00000181995	ENSG00000181995	LINC00301	11:60383208-60454622	NOTEST	0	0	0	0	1	1
ENSG00000181997	ENSG00000181997	AQP7P2	9:69633977-69650004	NOTEST	0	0	0	0	1	1
ENSG00000182000	ENSG00000182000	RP11-651P23.2	3:149478891-149942977	NOTEST	0	0	0	0	1	1
ENSG00000182021	ENSG00000182021	RP11-381O7.3	9:67017399-67032072	NOTEST	0.254848	0.560264	1.13647	0	1	1
ENSG00000182022	ENSG00000182022	CHST15	10:125767183-125853206	NOTEST	0.113056	0.0687854	-0.716867	0	1	1
ENSG00000182035	ENSG00000182035	ADIG	20:37209837-37217106	NOTEST	0	0	0	0	1	1
ENSG00000182040	ENSG00000182040	USH1G	17:72912175-72919351	NOTEST	0	0.00307483	inf	0	1	1
ENSG00000182048	ENSG00000182048	TRPC2	11:3631130-3658789	NOTEST	0	0	0	0	1	1
ENSG00000182050	ENSG00000182050	MGAT4C	12:86372515-87232775	NOTEST	0.0118591	0.00834284	-0.50738	0	1	1
ENSG00000182053	ENSG00000182053	TRIM49B	11:49050503-49059579	NOTEST	0.0117312	0	#NAME?	0	1	1
ENSG00000182057	ENSG00000182057	Z83851.3	22:42556018-42739622	NOTEST	0.307211	0.155626	-0.981144	0	1	1
ENSG00000182070	ENSG00000182070	OR52A1	11:5172238-5207612	NOTEST	0	0	0	0	1	1
ENSG00000182077	ENSG00000182077	PTCHD3	10:27687115-27703297	NOTEST	0	0	0	0	1	1
ENSG00000182083	ENSG00000182083	OR6B2	2:240968840-240969906	NOTEST	0	0	0	0	1	1
ENSG00000182103	ENSG00000182103	FAM181B	11:82443052-82444906	NOTEST	0.0656252	0.0342855	-0.936651	0	1	1
ENSG00000182107	ENSG00000182107	TMEM30B	14:61654276-62125414	NOTEST	0	0	0	0	1	1
ENSG00000182111	ENSG00000182111	ZNF716	7:57509882-57533252	NOTEST	0.0053309	0.0193604	1.86065	0	1	1
ENSG00000182132	ENSG00000182132	KCNIP1	5:169780490-170163636	NOTEST	0	0	0	0	1	1
ENSG00000182156	ENSG00000182156	ENPP7	17:77704680-77716021	NOTEST	0	0	0	0	1	1
ENSG00000182162	ENSG00000182162	P2RY8	X:1581464-1656000	NOTEST	0	0	0	0	1	1
ENSG00000182168	ENSG00000182168	UNC5C	4:96083654-96473608	NOTEST	0.175373	0.236378	0.430667	0	1	1
ENSG00000182170	ENSG00000182170	MRGPRG	11:3239173-3244361	NOTEST	0	0	0	0	1	1
ENSG00000182175	ENSG00000182175	RGMA	15:93586635-93632433	NOTEST	0	0.0241566	inf	0	1	1
ENSG00000182177	ENSG00000182177	ASB18	2:237073878-237203570	NOTEST	0	0	0	0	1	1
ENSG00000182179	ENSG00000182179	UBA7	3:49842639-49851379	NOTEST	0.282507	0.635079	1.16865	0	1	1
ENSG00000182183	ENSG00000182183	FAM159A	1:53099015-53135355	NOTEST	0	0	0	0	1	1
ENSG00000182187	ENSG00000182187	CRYGB	2:209007296-209010892	NOTEST	0.0582933	0	#NAME?	0	1	1
ENSG00000182195	ENSG00000182195	LDOC1	X:140269933-140271310	NOTEST	0.113738	0.257319	1.17784	0	1	1
ENSG00000182217	ENSG00000182217	HIST2H4B	1:149824180-149832714	NOTEST	0	0	0	0	1	1
ENSG00000182218	ENSG00000182218	HHIPL1	14:100111446-100146906	NOTEST	0.178308	0.311997	0.807161	0	1	1
ENSG00000182223	ENSG00000182223	ZAR1	4:48492268-48496406	NOTEST	0	0.0179102	inf	0	1	1
ENSG00000182230	ENSG00000182230	FAM153B	5:175476680-175559261	NOTEST	0	0.00766678	inf	0	1	1
ENSG00000182242	ENSG00000182242	TEX28P1	X:153461811-153482755	NOTEST	0	0	0	0	1	1
ENSG00000182255	ENSG00000182255	KCNA4	11:30031287-30038570	NOTEST	0.256351	0.258638	0.0128117	0	1	1
ENSG00000182257	ENSG00000182257	C22orf26	22:46445357-46509808	NOTEST	0.0978206	0.147437	0.591885	0	1	1
ENSG00000182261	ENSG00000182261	NLRP10	11:7980970-7986973	NOTEST	0	0	0	0	1	1
ENSG00000182264	ENSG00000182264	IZUMO1	19:49244108-49250166	NOTEST	0	0.00509658	inf	0	1	1
ENSG00000182271	ENSG00000182271	TMIGD1	17:28643350-28661077	NOTEST	0	0	0	0	1	1
ENSG00000182308	ENSG00000182308	DCAF4L1	4:41983712-41988476	NOTEST	0.176715	0.10557	-0.743223	0	1	1
ENSG00000182315	ENSG00000182315	MBD3L3	19:7056219-7058651	NOTEST	0	0	0	0	1	1
ENSG00000182324	ENSG00000182324	KCNJ14	19:48949029-48985571	NOTEST	0.189466	0.291527	0.621691	0	1	1
ENSG00000182327	ENSG00000182327	GLTPD2	17:4692253-4693685	NOTEST	0.0522979	0.0393925	-0.408831	0	1	1
ENSG00000182329	ENSG00000182329	AC079354.1	2:202937977-203062585	NOTEST	0	0	0	0	1	1
ENSG00000182330	ENSG00000182330	PRAMEF8	1:13386645-13390765	NOTEST	0	0	0	0	1	1

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ENSG00000182334	ENSG00000182334	OR5P3	11:7710668-7927502	NOTEST	0	0	0	0	1	1
ENSG00000182346	ENSG00000182346	DAOA	13:106111403-106158030	NOTEST	0.0291214	0	#NAME?	0	1	1
ENSG00000182347	ENSG00000182347	RP11-39K24.9	9:4985032-5128183	NOTEST	0.0157501	0	#NAME?	0	1	1
ENSG00000182348	ENSG00000182348	ZNF804B	7:88388681-88966346	NOTEST	0	0	0	0	1	1
ENSG00000182351	ENSG00000182351	CRIP1P4	22:25108258-25108489	NOTEST	0	0	0	0	1	1
ENSG00000182365	ENSG00000182365	OR5F2P	11:55782492-55783433	NOTEST	0	0	0	0	1	1
ENSG00000182366	ENSG00000182366	FAM87A	8:325930-333174	NOTEST	0.0180125	0.00902218	-0.997453	0	1	1
ENSG00000182376	ENSG00000182376	RP5-1142A6.8	16:88772870-88851619	NOTEST	0	0	0	0	1	1
ENSG00000182383	ENSG00000182383	RPL27AP5	5:74213550-74319753	NOTEST	0	0	0	0	1	1
ENSG00000182389	ENSG00000182389	CACNB4	2:152689289-152965716	NOTEST	0.0663398	0.0640122	-0.0515278	0	1	1
ENSG00000182393	ENSG00000182393	IFNL1	19:39786964-39789313	NOTEST	0	0	0	0	1	1
ENSG00000182397	ENSG00000182397	DNM1P46	15:100330360-100347132	NOTEST	0.378668	0.272522	-0.474558	0	1	1
ENSG00000182404	ENSG00000182404	RP1-86D1.3	6:128289923-128841870	NOTEST	0	0	0	0	1	1
ENSG00000182415	ENSG00000182415	CDY2A	Y:20137666-20140477	NOTEST	0	0	0	0	1	1
ENSG00000182447	ENSG00000182447	OTOL1	3:161214595-161221730	NOTEST	0.0875946	0.17403	0.990423	0	1	1
ENSG00000182450	ENSG00000182450	KCNK4	11:64058773-64072242	NOTEST	0	0	0	0	1	1
ENSG00000182459	ENSG00000182459	TEX19	17:80317122-80321652	NOTEST	0.0893888	0.19101	1.09548	0	1	1
ENSG00000182463	ENSG00000182463	TSHZ2	20:51588945-52120853	NOTEST	0	0.000866664	inf	0	1	1
ENSG00000182477	ENSG00000182477	OR2B8P	6:28021005-28021943	NOTEST	0	0	0	0	1	1
ENSG00000182487	ENSG00000182487	NCF1B	7:72634610-72649979	NOTEST	0	0	0	0	1	1
ENSG00000182489	ENSG00000182489	XKRX	X:100168430-100184422	NOTEST	0.0110891	0.0105728	-0.0687826	0	1	1
ENSG00000182492	ENSG00000182492	BGN	X:152710177-152775012	NOTEST	0.0621272	0.111778	0.847339	0	1	1
ENSG00000182502	ENSG00000182502	ABHD17AP5	22:22469235-22472374	NOTEST	0.0203746	0.0733167	1.84737	0	1	1
ENSG00000182511	ENSG00000182511	FES	15:91426924-91439006	NOTEST	0.0969148	0.00544802	-4.15291	0	1	1
ENSG00000182521	ENSG00000182521	TBPL2	14:55880258-55923444	NOTEST	0	0	0	0	1	1
ENSG00000182531	ENSG00000182531	OR7E115P	10:15049859-15050883	NOTEST	0	0	0	0	1	1
ENSG00000182533	ENSG00000182533	CAV3	3:8661085-9005457	NOTEST	0	0	0	0	1	1
ENSG00000182545	ENSG00000182545	RNASE10	14:20973695-20979328	NOTEST	0	0.0326536	inf	0	1	1
ENSG00000182557	ENSG00000182557	SPNS3	17:4336982-4391503	NOTEST	0	0	0	0	1	1
ENSG00000182565	ENSG00000182565	OR4C2P	11:48441761-48442825	NOTEST	0	0	0	0	1	1
ENSG00000182566	ENSG00000182566	CLEC4G	19:7793842-7798792	NOTEST	0	0	0	0	1	1
ENSG00000182572	ENSG00000182572	HIST1H3I	6:27839622-27840099	NOTEST	0.145604	0.0690199	-1.07697	0	1	1
ENSG00000182574	ENSG00000182574	RP3-341D10.1	X:100211581-100212528	NOTEST	0	0	0	0	1	1
ENSG00000182575	ENSG00000182575	NXPH3	17:47572654-47661189	NOTEST	0.120682	0.107805	-0.162786	0	1	1
ENSG00000182578	ENSG00000182578	CSF1R	5:149432853-149492935	NOTEST	0.0195645	0.0196494	0.00624164	0	1	1
ENSG00000182583	ENSG00000182583	VCX	X:7810302-7812184	NOTEST	0.086804	0.212625	1.29248	0	1	1
ENSG00000182585	ENSG00000182585	EPGN	4:75174189-75181024	NOTEST	0	0	0	0	1	1
ENSG00000182586	ENSG00000182586	LINC00334	21:46654254-46678645	NOTEST	0	0.0322326	inf	0	1	1
ENSG00000182591	ENSG00000182591	KRTAP11-1	21:32252965-32253874	NOTEST	0	0	0	0	1	1
ENSG00000182600	ENSG00000182600	C2orf82	2:233562008-233880595	NOTEST	0.361749	0.363159	0.00561488	0	1	1
ENSG00000182601	ENSG00000182601	HS3ST4	16:25703346-26149009	NOTEST	0	0	0	0	1	1
ENSG00000182611	ENSG00000182611	HIST1H2AJ	6:27782111-27782607	NOTEST	0.268024	0.103697	-1.36998	0	1	1
ENSG00000182613	ENSG00000182613	OR2V2	5:180581942-180582890	NOTEST	0	0	0	0	1	1
ENSG00000182625	ENSG00000182625	RP11-123C21.1	15:58887402-59042177	NOTEST	0	0	0	0	1	1

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ENSG00000182632	ENSG00000182632	CCNYL2	10:42903615-42967688	NOTEST	0.0446948	0.0317334	-0.494106	0	1	1
ENSG00000182634	ENSG00000182634	OR10G7	11:123908772-123909717	NOTEST	0	0	0	0	1	1
ENSG00000182645	ENSG00000182645	CCDC172	10:118083939-118139541	NOTEST	0	0	0	0	1	1
ENSG00000182652	ENSG00000182652	OR4Q3	14:20187173-20296531	NOTEST	0	0	0	0	1	1
ENSG00000182667	ENSG00000182667	NTM	11:131240372-132206716	NOTEST	0.0114746	0.122158	3.41223	0	1	1
ENSG00000182674	ENSG00000182674	KCNB2	8:73449625-73850584	NOTEST	0	0	0	0	1	1
ENSG00000182676	ENSG00000182676	PPP1R27	17:79791367-79792926	NOTEST	0.0242583	0.0532382	1.13398	0	1	1
ENSG00000182687	ENSG00000182687	GALR2	17:74035183-74117657	NOTEST	0	0.0272009	inf	0	1	1
ENSG00000182698	ENSG00000182698	RESP18	2:220192130-220197899	NOTEST	0	0	0	0	1	1
ENSG00000182707	ENSG00000182707	FXYD6P3	X:73094902-73095470	NOTEST	0	0	0	0	1	1
ENSG00000182722	ENSG00000182722	SEPHS1P1	7:64312774-64313732	NOTEST	0	0	0	0	1	1
ENSG00000182732	ENSG00000182732	RGS6	14:72399155-73061833	NOTEST	0	0	0	0	1	1
ENSG00000182742	ENSG00000182742	HOXB4	17:46618255-46683776	NOTEST	0	0.0278168	inf	0	1	1
ENSG00000182747	ENSG00000182747	SLC35D3	6:137243401-137246777	NOTEST	0.00678747	0.00953495	0.490352	0	1	1
ENSG00000182752	ENSG00000182752	PAPPA	9:118916082-119164601	NOTEST	0.312193	0.493119	0.659495	0	1	1
ENSG00000182759	ENSG00000182759	MAFA	8:144501351-144512576	NOTEST	0	0	0	0	1	1
ENSG00000182771	ENSG00000182771	GRID1	10:87359311-88126250	NOTEST	0.0250037	0.0101807	-1.2963	0	1	1
ENSG00000182776	ENSG00000182776	RP11-114H20.1	X:51793955-51797351	NOTEST	0	0	0	0	1	1
ENSG00000182782	ENSG00000182782	HCAR2	12:123011792-123215390	NOTEST	0	0.00555039	inf	0	1	1
ENSG00000182783	ENSG00000182783	OR2T29	1:248712056-248727140	NOTEST	0	0	0	0	1	1
ENSG00000182791	ENSG00000182791	CCDC87	11:66357639-66373490	NOTEST	0.0520381	0.097344	0.903524	0	1	1
ENSG00000182793	ENSG00000182793	GSTA5	6:52696452-52710893	NOTEST	0	0	0	0	1	1
ENSG00000182795	ENSG00000182795	C1orf116	1:207191865-207206101	NOTEST	0.133184	0.25198	0.91989	0	1	1
ENSG00000182798	ENSG00000182798	MAGEB17	X:16141678-16189587	NOTEST	0.0361368	0.034604	-0.0625283	0	1	1
ENSG00000182814	ENSG00000182814	FUNDC2P2	2:84517805-84519326	NOTEST	0	0	0	0	1	1
ENSG00000182816	ENSG00000182816	KRTAP13-2	21:31743708-31744557	NOTEST	0	0	0	0	1	1
ENSG00000182824	ENSG00000182824	AC008132.1	22:18721426-18745407	NOTEST	0.00879815	0	#NAME?	0	1	1
ENSG00000182836	ENSG00000182836	PLCXD3	5:41307055-41510730	NOTEST	0.101209	0.0415333	-1.285	0	1	1
ENSG00000182851	ENSG00000182851	GPIHBP1	8:144295067-144299044	NOTEST	0	0	0	0	1	1
ENSG00000182853	ENSG00000182853	VMO1	17:4688579-4689728	NOTEST	0.0549024	0	#NAME?	0	1	1
ENSG00000182854	ENSG00000182854	OR4F15	15:102358365-102359350	NOTEST	0.0182466	0	#NAME?	0	1	1
ENSG00000182866	ENSG00000182866	LCK	1:32716839-32751766	NOTEST	0	0	0	0	1	1
ENSG00000182870	ENSG00000182870	GALNT9	12:132680923-132905935	NOTEST	0.0287027	0.032382	0.174004	0	1	1
ENSG00000182885	ENSG00000182885	GPR97	16:57702098-57765717	NOTEST	0.014226	0.0361628	1.34598	0	1	1
ENSG00000182888	ENSG00000182888	RP11-558O12.1	X:3635189-3635641	NOTEST	0	0	0	0	1	1
ENSG00000182896	ENSG00000182896	TMEM95	17:7258441-7260538	NOTEST	0	0	0	0	1	1
ENSG00000182898	ENSG00000182898	TCHHL1	1:152056619-152061540	NOTEST	0	0	0	0	1	1
ENSG00000182901	ENSG00000182901	RGS7	1:240928856-241520530	NOTEST	0	0	0	0	1	1
ENSG00000182902	ENSG00000182902	SLC25A18	22:18043138-18073760	NOTEST	0.208473	0.185755	-0.166466	0	1	1
ENSG00000182912	ENSG00000182912	C21orf90	21:45917774-46131495	NOTEST	0.0370675	0.109905	1.56803	0	1	1
ENSG00000182916	ENSG00000182916	TCEAL7	X:102585123-102587254	NOTEST	0	0	0	0	1	1
ENSG00000182921	ENSG00000182921	CCDC75P1	3:73231651-73232442	NOTEST	0	0.0169119	inf	0	1	1
ENSG00000182931	ENSG00000182931	WFDC10B	20:44313291-44337456	NOTEST	0	0	0	0	1	1
ENSG00000182938	ENSG00000182938	OTOP3	17:72931813-72946087	NOTEST	0	0	0	0	1	1

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ENSG00000182965	ENSG00000182965	NPM1P14	7:112160542-112161725	NOTEST	0	0	0	0	1	1
ENSG00000182968	ENSG00000182968	SOX1	13:112721912-112726020	NOTEST	0	0	0	0	1	1
ENSG00000182974	ENSG00000182974	OR4M2	15:22278009-22413497	NOTEST	0	0	0	0	1	1
ENSG00000182983	ENSG00000182983	ZNF662	3:42846243-43101703	NOTEST	0	0.00514189	inf	0	1	1
ENSG00000183016	ENSG00000183016	IQCA1P1	7:150888066-150902582	NOTEST	0	0.0583945	inf	0	1	1
ENSG00000183018	ENSG00000183018	SPNS2	17:4400688-4458926	NOTEST	0.222698	0.407892	0.873101	0	1	1
ENSG00000183019	ENSG00000183019	C19orf59	19:7741513-7747744	NOTEST	0	0.00740379	inf	0	1	1
ENSG00000183022	ENSG00000183022	TPM3P8	2:231280656-231444721	NOTEST	0	0	0	0	1	1
ENSG00000183023	ENSG00000183023	SLC8A1	2:40013592-40838193	NOTEST	0.518772	0.448238	-0.210834	0	1	1
ENSG00000183024	ENSG00000183024	OR1G1	17:3029877-3030875	NOTEST	0	0	0	0	1	1
ENSG00000183032	ENSG00000183032	SLC25A21	14:37116287-37643016	NOTEST	0.338063	0.148964	-1.18233	0	1	1
ENSG00000183034	ENSG00000183034	OTOP2	17:72920369-72930007	NOTEST	0	0	0	0	1	1
ENSG00000183035	ENSG00000183035	CYLC1	X:83116153-83141705	NOTEST	0	0	0	0	1	1
ENSG00000183036	ENSG00000183036	PCP4	21:41239242-41301322	NOTEST	0	0	0	0	1	1
ENSG00000183038	ENSG00000183038	GGTLC3	22:20366205-20368028	NOTEST	0.0211549	0	#NAME?	0	1	1
ENSG00000183044	ENSG00000183044	ABAT	16:8768421-8962866	NOTEST	0.163143	0.249164	0.610962	0	1	1
ENSG00000183049	ENSG00000183049	CAMK1D	10:12391480-12877545	NOTEST	0	0	0	0	1	1
ENSG00000183054	ENSG00000183054	RGPD6	2:111271388-111334762	NOTEST	0.102434	0.20719	1.01627	0	1	1
ENSG00000183055	ENSG00000183055	FAM133CP	10:60272899-60591195	NOTEST	0.027869	0.0672933	1.2718	0	1	1
ENSG00000183066	ENSG00000183066	WBP2NL	22:42394728-42466846	NOTEST	0.0605041	0.0519344	-0.220342	0	1	1
ENSG00000183067	ENSG00000183067	IGSF5	21:41117333-41174023	NOTEST	0.00783701	0.0588163	2.90784	0	1	1
ENSG00000183072	ENSG00000183072	NKX2-5	5:172659111-172662360	NOTEST	0	0	0	0	1	1
ENSG00000183086	ENSG00000183086	GATSL1	7:74379082-74438803	NOTEST	0	0.0255603	inf	0	1	1
ENSG00000183090	ENSG00000183090	FREM3	4:144480624-144786225	NOTEST	0.00452891	0.0126713	1.48433	0	1	1
ENSG00000183091	ENSG00000183091	NEB	2:152266396-152591001	NOTEST	0.405379	0.263514	-0.621391	0	1	1
ENSG00000183098	ENSG00000183098	GPC6	13:93879094-95059655	NOTEST	0.0368115	0.147766	2.00508	0	1	1
ENSG00000183103	ENSG00000183103	LYPD4	19:42341147-42348760	NOTEST	0	0	0	0	1	1
ENSG00000183111	ENSG00000183111	ARHGEF37	5:148931509-149014531	NOTEST	0.196585	0.373299	0.925179	0	1	1
ENSG00000183114	ENSG00000183114	FAM43B	1:20878931-20881512	NOTEST	0	0	0	0	1	1
ENSG00000183117	ENSG00000183117	CSMD1	8:2792874-4852494	NOTEST	0.157889	0.28846	0.869462	0	1	1
ENSG00000183122	ENSG00000183122	OR2A3P	7:143854318-143855271	NOTEST	0	0	0	0	1	1
ENSG00000183128	ENSG00000183128	CALHM3	10:105232560-105238997	NOTEST	0	0	0	0	1	1
ENSG00000183130	ENSG00000183130	OR2T11	1:248789419-248790491	NOTEST	0	0	0	0	1	1
ENSG00000183134	ENSG00000183134	PTGDR2	11:60603468-60623444	NOTEST	0.00988447	0.0374478	1.92165	0	1	1
ENSG00000183145	ENSG00000183145	RIPPLY3	21:38378449-38391959	NOTEST	0.0143906	0.0399176	1.47189	0	1	1
ENSG00000183146	ENSG00000183146	CYorf17	Y:23544839-23548246	NOTEST	0	0	0	0	1	1
ENSG00000183148	ENSG00000183148	ANKRD20A2	9:42368302-42474239	NOTEST	0.165529	0.0493152	-1.74698	0	1	1
ENSG00000183153	ENSG00000183153	GJD3	17:38516906-38520945	NOTEST	0.151522	0.0331536	-2.19229	0	1	1
ENSG00000183154	ENSG00000183154	RP11-863K10.7	8:37592278-37616619	NOTEST	0.0455196	0.040304	-0.175564	0	1	1
ENSG00000183160	ENSG00000183160	TMEM119	12:108983621-108992096	NOTEST	0	0.0933978	inf	0	1	1
ENSG00000183166	ENSG00000183166	CALN1	7:71244475-71912136	NOTEST	0.0608117	0.0484336	-0.328341	0	1	1
ENSG00000183169	ENSG00000183169	POM121L1P	22:22981647-22986944	NOTEST	0	0	0	0	1	1
ENSG00000183171	ENSG00000183171	RP11-49C9.2	X:149097744-149392815	NOTEST	0.0362278	0.0669955	0.886967	0	1	1
ENSG00000183185	ENSG00000183185	GABRR3	3:97705516-97754148	NOTEST	0	0	0	0	1	1

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ENSG00000183186	ENSG00000183186	C2CD4C	19:405437-409139	NOTEST	0	0.00788307	inf	0	1	1
ENSG00000183199	ENSG00000183199	HSP90AB3P	4:88812994-88815167	NOTEST	0.195046	0.101263	-0.945708	0	1	1
ENSG00000183206	ENSG00000183206	POTEC	18:14507337-14543584	NOTEST	0	0	0	0	1	1
ENSG00000183214	ENSG00000183214	MICA	HSCHR6_MHC_QBL:31357609-31374165	NOTEST	0	0	0	0	1	1
ENSG00000183230	ENSG00000183230	CTNNA3	10:67672275-69455927	NOTEST	0.00509546	0.00450424	-0.177927	0	1	1
ENSG00000183239	ENSG00000183239	RP5-1120P11.4	6:44056978-44057433	NOTEST	0	0.0779844	inf	0	1	1
ENSG00000183242	ENSG00000183242	WT1-AS	11:32409320-32480315	NOTEST	0	0.0223754	inf	0	1	1
ENSG00000183246	ENSG00000183246	RIMBP3C	22:21899632-21978323	NOTEST	0	0	0	0	1	1
ENSG00000183248	ENSG00000183248	CTD-3193O13.9	19:7933604-7939326	NOTEST	0.0597447	0.183311	1.61741	0	1	1
ENSG00000183249	ENSG00000183249	NF1P3	21:15373247-15377600	NOTEST	0	0	0	0	1	1
ENSG00000183251	ENSG00000183251	OR51B4	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000183269	ENSG00000183269	OR52E8	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000183273	ENSG00000183273	CCDC60	12:119772516-120119435	NOTEST	0	0	0	0	1	1
ENSG00000183281	ENSG00000183281	PLGLB1	2:87098423-87248975	NOTEST	0.0188268	0	#NAME?	0	1	1
ENSG00000183287	ENSG00000183287	CCBE1	18:57098171-57364644	NOTEST	0.0132675	0.0532746	2.00555	0	1	1
ENSG00000183292	ENSG00000183292	AC140481.2	2:131328401-131348036	NOTEST	0	0	0	0	1	1
ENSG00000183303	ENSG00000183303	OR5P2	11:7710668-7927502	NOTEST	0	0	0	0	1	1
ENSG00000183304	ENSG00000183304	FAM9A	X:8758835-8769424	NOTEST	0	0.00855662	inf	0	1	1
ENSG00000183307	ENSG00000183307	CECR6	22:17597188-17602257	NOTEST	0.0190412	0.0351943	0.886214	0	1	1
ENSG00000183308	ENSG00000183308	AC005037.3	2:201773695-201950473	NOTEST	0.132024	0.149748	0.181733	0	1	1
ENSG00000183310	ENSG00000183310	OR2T34	1:248737021-248738080	NOTEST	0	0	0	0	1	1
ENSG00000183311	ENSG00000183311	TUBB	HSCHR6_MHC_QBL:30677511-30682738	NOTEST	0	0	0	0	1	1
ENSG00000183313	ENSG00000183313	OR52L1	11:6007121-6008215	NOTEST	0	0	0	0	1	1
ENSG00000183317	ENSG00000183317	EPHA10	1:38179551-38230805	NOTEST	0.0437892	0.0531513	0.279528	0	1	1
ENSG00000183318	ENSG00000183318	SPDYE4	17:8656423-8661877	NOTEST	0	0	0	0	1	1
ENSG00000183324	ENSG00000183324	C15orf60	15:73735498-73926475	NOTEST	0	0	0	0	1	1
ENSG00000183336	ENSG00000183336	BOLA2	16:29262828-29519817	NOTEST	0	0	0	0	1	1
ENSG00000183346	ENSG00000183346	C10orf107	10:63422718-63526524	NOTEST	0.188817	0.0236506	-2.99704	0	1	1
ENSG00000183347	ENSG00000183347	GBP6	1:89829616-89852020	NOTEST	0.0156407	0	#NAME?	0	1	1
ENSG00000183378	ENSG00000183378	OVCH2	11:7710668-7927502	NOTEST	0.00974087	0	#NAME?	0	1	1
ENSG00000183379	ENSG00000183379	SYNDIG1L	14:74872595-74892805	NOTEST	0	0	0	0	1	1
ENSG00000183385	ENSG00000183385	TTTY8	Y:9528708-9531566	NOTEST	0	0	0	0	1	1
ENSG00000183389	ENSG00000183389	OR56A4	11:6023215-6024424	NOTEST	0	0	0	0	1	1
ENSG00000183395	ENSG00000183395	PMCH	12:102513955-102591623	NOTEST	0.0359571	0.225266	2.64728	0	1	1
ENSG00000183396	ENSG00000183396	TMEM89	3:48658191-48659288	NOTEST	0	0.0235464	inf	0	1	1
ENSG00000183423	ENSG00000183423	LRIT3	4:110769357-110793471	NOTEST	0.00943358	0.0185749	0.977479	0	1	1
ENSG00000183432	ENSG00000183432	ZBTB8OSP1	4:151185593-151936879	NOTEST	0	0	0	0	1	1
ENSG00000183434	ENSG00000183434	TFDP3	X:132350696-132352376	NOTEST	0	0	0	0	1	1
ENSG00000183439	ENSG00000183439	TRIM61	4:165869230-165899980	NOTEST	0	0	0	0	1	1
ENSG00000183454	ENSG00000183454	GRIN2A	16:9852375-10276611	NOTEST	0.412875	0.307369	-0.425734	0	1	1
ENSG00000183461	ENSG00000183461	XAGE1C	X:52511760-52516905	NOTEST	0	0	0	0	1	1
ENSG00000183463	ENSG00000183463	URAD	13:28551850-28562791	NOTEST	0	0	0	0	1	1
ENSG00000183470	ENSG00000183470	AC009365.3	7:132333552-132413528	NOTEST	0	0	0	0	1	1
ENSG00000183473	ENSG00000183473	SSTR3	22:37600277-37608362	NOTEST	0	0	0	0	1	1

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ENSG00000183476	ENSG00000183476	SH2D7	15:78370149-78538030	NOTEST	0.0805721	0.101839	0.33794	0	1	1
ENSG00000183479	ENSG00000183479	TREX2	X:152710177-152775012	NOTEST	0.191816	0.538436	1.48905	0	1	1
ENSG00000183484	ENSG00000183484	GPR132	14:105515727-105531782	NOTEST	0.0710103	0	#NAME?	0	1	1
ENSG00000183486	ENSG00000183486	MX2	21:42733869-42781317	NOTEST	0.0355497	0.0259067	-0.456512	0	1	1
ENSG00000183504	ENSG00000183504	AL132868.1	4:1873150-1983934	NOTEST	0.161918	0	#NAME?	0	1	1
ENSG00000183514	ENSG00000183514	TDGF1P2	2:228734798-228735360	NOTEST	0	0	0	0	1	1
ENSG00000183535	ENSG00000183535	COL18A1-AS1	21:46825051-46964325	NOTEST	0	0.00481228	inf	0	1	1
ENSG00000183542	ENSG00000183542	KLRC4	12:10516367-10562745	NOTEST	0	0.000273781	inf	0	1	1
ENSG00000183549	ENSG00000183549	ACSM5	16:20420855-20458322	NOTEST	0.0216836	0	#NAME?	0	1	1
ENSG00000183559	ENSG00000183559	C10orf120	10:124457224-124459338	NOTEST	0	0	0	0	1	1
ENSG00000183560	ENSG00000183560	FOLR4	11:94038758-94040887	NOTEST	0	0	0	0	1	1
ENSG00000183566	ENSG00000183566	BPIFA4P	20:31781390-31798268	NOTEST	0	0	0	0	1	1
ENSG00000183570	ENSG00000183570	PCBP3	21:47063607-47362368	NOTEST	0.00960496	0.0127784	0.411861	0	1	1
ENSG00000183571	ENSG00000183571	PGPEP1L	15:99192199-99675798	NOTEST	0	0	0	0	1	1
ENSG00000183574	ENSG00000183574	RNF5	HSCHR6_MHC_QBL:32103753-32106193	NOTEST	0	0	0	0	1	1
ENSG00000183578	ENSG00000183578	TNFAIP8L3	15:51329684-51630807	NOTEST	0.0128546	0	#NAME?	0	1	1
ENSG00000183586	ENSG00000183586	HMGN3P1	1:152346429-152417932	NOTEST	0	0	0	0	1	1
ENSG00000183598	ENSG00000183598	HIST2H3D	1:149784825-149785236	NOTEST	0.178499	0.382611	1.09996	0	1	1
ENSG00000183607	ENSG00000183607	GKN2	2:69172363-69180102	NOTEST	0	0	0	0	1	1
ENSG00000183621	ENSG00000183621	ZNF438	10:31109135-31320866	NOTEST	0.285612	0.289274	0.0183759	0	1	1
ENSG00000183625	ENSG00000183625	CCR3	3:46205095-46308197	NOTEST	0	0	0	0	1	1
ENSG00000183629	ENSG00000183629	GOLGA8G	15:28764756-28778160	NOTEST	0	0	0	0	1	1
ENSG00000183631	ENSG00000183631	CXorf64	X:125953746-125955769	NOTEST	0	0	0	0	1	1
ENSG00000183632	ENSG00000183632	TP53TG3	16:32684851-32690152	NOTEST	0.266996	0.144293	-0.887821	0	1	1
ENSG00000183638	ENSG00000183638	RP1L1	8:10463858-10569697	NOTEST	0.0426794	0.0435918	0.030517	0	1	1
ENSG00000183640	ENSG00000183640	KRTAP8-1	21:32185015-32185570	NOTEST	0	0	0	0	1	1
ENSG00000183643	ENSG00000183643	C15orf32	15:93014883-93044347	NOTEST	0	0	0	0	1	1
ENSG00000183644	ENSG00000183644	C11orf88	11:111384767-111407756	NOTEST	0	0	0	0	1	1
ENSG00000183653	ENSG00000183653	GRIK1-AS2	21:30565800-31312351	NOTEST	0	0	0	0	1	1
ENSG00000183654	ENSG00000183654	11-Mar	5:16067247-16185694	NOTEST	0	0	0	0	1	1
ENSG00000183657	ENSG00000183657	PP13439	3:171318194-171528740	NOTEST	0.144724	0.0685642	-1.07778	0	1	1
ENSG00000183662	ENSG00000183662	FAM19A1	3:68053358-68594776	NOTEST	0.0085027	0	#NAME?	0	1	1
ENSG00000183663	ENSG00000183663	RP11-44N17.1	8:97080956-97081909	NOTEST	0.0189934	0	#NAME?	0	1	1
ENSG00000183671	ENSG00000183671	GPR1	2:207040039-207082771	NOTEST	0	0.00491143	inf	0	1	1
ENSG00000183675	ENSG00000183675	PTPN20B	10:48736873-48827966	NOTEST	0.00844331	0	#NAME?	0	1	1
ENSG00000183678	ENSG00000183678	CTAG1A	X:153813406-153815075	NOTEST	0	0	0	0	1	1
ENSG00000183682	ENSG00000183682	BMP8A	1:39957317-40024379	NOTEST	0.0292928	0.090524	1.62776	0	1	1
ENSG00000183690	ENSG00000183690	EFHC2	X:44007127-44202918	NOTEST	0.0129533	0.0287423	1.14986	0	1	1
ENSG00000183691	ENSG00000183691	NOG	17:54671059-54672951	NOTEST	0.0469102	0.0323649	-0.53547	0	1	1
ENSG00000183695	ENSG00000183695	MRGPRX2	11:19076001-19082228	NOTEST	0	0	0	0	1	1
ENSG00000183704	ENSG00000183704	SLC9B1P1	Y:13496240-13524717	NOTEST	0	0	0	0	1	1
ENSG00000183706	ENSG00000183706	OR4N4	15:22278009-22413497	NOTEST	0	0	0	0	1	1
ENSG00000183709	ENSG00000183709	IFNL2	19:39759153-39760732	NOTEST	0	0	0	0	1	1
ENSG00000183715	ENSG00000183715	OPCML	11:132284870-133402414	NOTEST	0	0	0	0	1	1
ENSG00000183729	ENSG00000183729	NPBWR1	8:53850990-53853677	NOTEST	0	0	0	0	1	1

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ENSG00000183733	ENSG00000183733	FIGLA	2:71004441-71017775	NOTEST	0	0	0	0	1	1
ENSG00000183734	ENSG00000183734	ASCL2	11:2289724-2292182	NOTEST	0	0	0	0	1	1
ENSG00000183742	ENSG00000183742	MACC1	7:19958603-20257027	NOTEST	0.0105341	0.0142302	0.433894	0	1	1
ENSG00000183747	ENSG00000183747	ACSM2A	16:20462782-20498991	NOTEST	0	0	0	0	1	1
ENSG00000183748	ENSG00000183748	MRC1L1	10:17851361-17953178	NOTEST	0.00297008	0.00230697	-0.364504	0	1	1
ENSG00000183753	ENSG00000183753	BPY2	Y:25119965-25151612	NOTEST	0	0	0	0	1	1
ENSG00000183760	ENSG00000183760	PAPL	19:39574552-39602133	NOTEST	0	0	0	0	1	1
ENSG00000183770	ENSG00000183770	FOXL2	3:138663065-138665982	NOTEST	0.00540814	0.0237326	2.13367	0	1	1
ENSG00000183775	ENSG00000183775	KCTD16	5:143550395-143865249	NOTEST	0.078555	0.0201387	-1.96373	0	1	1
ENSG00000183778	ENSG00000183778	B3GALT5	21:40928368-41098012	NOTEST	0	0	0	0	1	1
ENSG00000183780	ENSG00000183780	SLC35F3	1:234040678-234460262	NOTEST	0	0	0	0	1	1
ENSG00000183783	ENSG00000183783	KCTD8	4:44175925-44450824	NOTEST	0	0	0	0	1	1
ENSG00000183784	ENSG00000183784	C9orf66	9:213107-746105	NOTEST	0.0389136	0.0419651	0.108915	0	1	1
ENSG00000183791	ENSG00000183791	TCEB3C	18:44388352-44627658	NOTEST	0	0	0	0	1	1
ENSG00000183795	ENSG00000183795	BPY2B	Y:26753706-26785354	NOTEST	0	0	0	0	1	1
ENSG00000183798	ENSG00000183798	EMILIN3	20:39969559-39995467	NOTEST	0.0551827	0.0251237	-1.13517	0	1	1
ENSG00000183801	ENSG00000183801	OLFML1	11:7490917-7533746	NOTEST	0.104088	0.155009	0.574555	0	1	1
ENSG00000183807	ENSG00000183807	FAM162B	6:117073362-117086886	NOTEST	0	0.0513465	inf	0	1	1
ENSG00000183813	ENSG00000183813	CCR4	3:32993065-32997841	NOTEST	0	0.00713124	inf	0	1	1
ENSG00000183822	ENSG00000183822	CTA-833B7.2	22:37243414-37274057	NOTEST	0	0	0	0	1	1
ENSG00000183831	ENSG00000183831	ANKRD45	1:173469602-173639001	NOTEST	0.203249	0.264393	0.37944	0	1	1
ENSG00000183833	ENSG00000183833	MAATS1	3:119421868-119485949	NOTEST	0.070566	0.20231	1.51952	0	1	1
ENSG00000183837	ENSG00000183837	PNMA3	X:152224765-152228827	NOTEST	0.126838	0.431595	1.76669	0	1	1
ENSG00000183840	ENSG00000183840	GPR39	2:133174146-133429152	NOTEST	0.0376491	0	#NAME?	0	1	1
ENSG00000183844	ENSG00000183844	FAM3B	21:42676138-42729358	NOTEST	0.0820839	0.15785	0.943385	0	1	1
ENSG00000183850	ENSG00000183850	ZNF730	19:23258002-23330021	NOTEST	0	0	0	0	1	1
ENSG00000183862	ENSG00000183862	CNGA2	X:150906922-150913776	NOTEST	0	0	0	0	1	1
ENSG00000183873	ENSG00000183873	SCN5A	3:38589547-38691164	NOTEST	0.118132	0.139866	0.24365	0	1	1
ENSG00000183876	ENSG00000183876	ARSI	5:149675905-149718870	NOTEST	0.388167	0.341613	-0.184315	0	1	1
ENSG00000183878	ENSG00000183878	UTY	Y:15360258-15592553	NOTEST	0	0	0	0	1	1
ENSG00000183888	ENSG00000183888	C1orf64	1:16330730-16335302	NOTEST	0	0.0194251	inf	0	1	1
ENSG00000183908	ENSG00000183908	LRRC55	11:56949220-56959191	NOTEST	0.00566916	0.0240654	2.08575	0	1	1
ENSG00000183909	ENSG00000183909	OR4G2P	15:102467007-102467910	NOTEST	0	0	0	0	1	1
ENSG00000183911	ENSG00000183911	RPL21P132	X:100594904-100595922	NOTEST	0	0.036311	inf	0	1	1
ENSG00000183918	ENSG00000183918	SH2D1A	X:123093082-124097666	NOTEST	0	0.0456651	inf	0	1	1
ENSG00000183921	ENSG00000183921	SDR42E2	16:22177617-22203075	NOTEST	0.0113969	0.018724	0.716254	0	1	1
ENSG00000183929	ENSG00000183929	DUSP5P1	1:228744884-228788150	NOTEST	0.128025	0.279322	1.1255	0	1	1
ENSG00000183935	ENSG00000183935	HTR7P1	12:13080659-13193613	NOTEST	0.334062	0.345874	0.0501329	0	1	1
ENSG00000183938	ENSG00000183938	TRBV21OR9-2	9:33629118-33629584	NOTEST	0	0	0	0	1	1
ENSG00000183941	ENSG00000183941	HIST2H4A	1:149804220-149812765	NOTEST	0	0.0451618	inf	0	1	1
ENSG00000183971	ENSG00000183971	NPW	16:2059926-2070756	NOTEST	0.172308	0.111805	-0.624	0	1	1
ENSG00000183977	ENSG00000183977	PP2D1	3:19988570-20053822	NOTEST	0.0474117	0.152679	1.68719	0	1	1
ENSG00000183981	ENSG00000183981	MAGEA13P	X:137564902-137565955	NOTEST	0	0	0	0	1	1
ENSG00000184012	ENSG00000184012	TMPRSS2	21:42836477-42903043	NOTEST	0.0274069	0.0144236	-0.926106	0	1	1
ENSG00000184022	ENSG00000184022	OR2T10	1:248756051-248757100	NOTEST	0	0	0	0	1	1

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ENSG00000184029	ENSG00000184029	DSCR4	21:39323727-39493454	NOTEST	0.0490077	0	#NAME?	0	1	1
ENSG00000184032	ENSG00000184032	KRTAP20-2	21:32007554-32007938	NOTEST	0	0	0	0	1	1
ENSG00000184033	ENSG00000184033	CTAG1B	X:153845864-153847533	NOTEST	0	0	0	0	1	1
ENSG00000184040	ENSG00000184040	TMEM236	10:18041217-18089855	NOTEST	0.0432356	0.0468407	0.115543	0	1	1
ENSG00000184055	ENSG00000184055	OR7E87P	11:71292900-71319086	NOTEST	0	0	0	0	1	1
ENSG00000184058	ENSG00000184058	TBX1	22:19744225-19842462	NOTEST	0	0	0	0	1	1
ENSG00000184060	ENSG00000184060	ADAP2	17:29224353-29286340	NOTEST	0	0.0173216	inf	0	1	1
ENSG00000184084	ENSG00000184084	CTD-2372A4.1	5:72921982-73237818	NOTEST	0	0	0	0	1	1
ENSG00000184106	ENSG00000184106	TREML3P	6:41176291-41190382	NOTEST	0	0	0	0	1	1
ENSG00000184108	ENSG00000184108	TRIML1	4:189060572-189068897	NOTEST	0	0	0	0	1	1
ENSG00000184111	ENSG00000184111	RP11-366I13.3	10:94353042-94415150	NOTEST	0	0	0	0	1	1
ENSG00000184113	ENSG00000184113	CLDN5	22:19510546-19515068	NOTEST	0.0732108	0.0368514	-0.990335	0	1	1
ENSG00000184115	ENSG00000184115	RP13-1039J1.2	2:111143953-111230652	NOTEST	0	0	0	0	1	1
ENSG00000184139	ENSG00000184139	RPL7AP28	4:132778497-132779068	NOTEST	0	0	0	0	1	1
ENSG00000184140	ENSG00000184140	OR4F6	15:102345901-102346876	NOTEST	0	0	0	0	1	1
ENSG00000184144	ENSG00000184144	CNTN2	1:205012324-205047627	NOTEST	0.037447	0.118263	1.65908	0	1	1
ENSG00000184148	ENSG00000184148	SPRR4	1:152943141-152945050	NOTEST	0	0	0	0	1	1
ENSG00000184155	ENSG00000184155	OR10J5	1:159504792-159505842	NOTEST	0	0	0	0	1	1
ENSG00000184156	ENSG00000184156	KCNQ3	8:133133107-133493200	NOTEST	0.00369206	0.00984846	1.41547	0	1	1
ENSG00000184160	ENSG00000184160	ADRA2C	4:3768074-3770251	NOTEST	0	0.00533423	inf	0	1	1
ENSG00000184163	ENSG00000184163	FAM132A	1:1177825-1182102	NOTEST	0.170431	0.659316	1.95178	0	1	1
ENSG00000184166	ENSG00000184166	OR1D2	17:2995351-2996290	NOTEST	0	0	0	0	1	1
ENSG00000184185	ENSG00000184185	KCNJ12	17:21279508-21323179	NOTEST	0.0622276	0.177116	1.50907	0	1	1
ENSG00000184188	ENSG00000184188	CTC-512J14.7	5:79595496-79598666	NOTEST	0	0	0	0	1	1
ENSG00000184194	ENSG00000184194	GPR173	X:53078272-53109797	NOTEST	0	0.00267392	inf	0	1	1
ENSG00000184206	ENSG00000184206	GOLGA6L4	15:84904524-84914120	NOTEST	0.537481	0.445025	-0.272327	0	1	1
ENSG00000184210	ENSG00000184210	DGAT2L6	X:69397332-69425395	NOTEST	0	0	0	0	1	1
ENSG00000184221	ENSG00000184221	OLIG1	21:34285956-34444726	NOTEST	0.159587	0.185438	0.2166	0	1	1
ENSG00000184224	ENSG00000184224	C11orf72	11:67370350-67374177	NOTEST	0.0575371	0.0496051	-0.214005	0	1	1
ENSG00000184247	ENSG00000184247	AC100791.1	17:77906141-78009647	NOTEST	0	0	0	0	1	1
ENSG00000184258	ENSG00000184258	CDR1	X:139865424-139866723	NOTEST	0	0	0	0	1	1
ENSG00000184261	ENSG00000184261	KCNK12	2:47630107-47798078	NOTEST	0.00490433	0.0130045	1.40688	0	1	1
ENSG00000184270	ENSG00000184270	HIST2H2AB	1:149859018-149872351	NOTEST	0.10055	0.0381686	-1.39745	0	1	1
ENSG00000184274	ENSG00000184274	LINC00315	21:46720159-46725172	NOTEST	0	0.0248439	inf	0	1	1
ENSG00000184276	ENSG00000184276	DEFB108B	11:71544245-71548756	NOTEST	0	0	0	0	1	1
ENSG00000184292	ENSG00000184292	TACSTD2	1:59041098-59043166	NOTEST	0	0	0	0	1	1
ENSG00000184293	ENSG00000184293	CLECL1	12:9868455-9885895	NOTEST	0	0	0	0	1	1
ENSG00000184302	ENSG00000184302	SIX6	14:60863186-61021634	NOTEST	0.0159405	0.0408588	1.35795	0	1	1
ENSG00000184303	ENSG00000184303	DRD5P1	2:91872472-91902771	NOTEST	0	0	0	0	1	1
ENSG00000184313	ENSG00000184313	MROH7	1:55107458-55208330	NOTEST	0.0489083	0.00212218	-4.52647	0	1	1
ENSG00000184321	ENSG00000184321	OR51J1	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000184324	ENSG00000184324	CSAG2	X:151922444-151928738	NOTEST	0.024035	0.0170906	-0.491931	0	1	1
ENSG00000184330	ENSG00000184330	S100A7A	1:153388999-153395701	NOTEST	0	0	0	0	1	1
ENSG00000184343	ENSG00000184343	SRPK3	X:152990322-153051187	NOTEST	0.0224109	0.123611	2.46353	0	1	1
ENSG00000184344	ENSG00000184344	GDF3	12:7842377-7848372	NOTEST	0	0	0	0	1	1

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ENSG00000184347	ENSG00000184347	SLIT3	5:168081517-168728133	NOTEST	0.339153	0.333333	-0.0249714	0	1	1
ENSG00000184348	ENSG00000184348	HIST1H2AK	6:27805657-27806117	NOTEST	0.256913	0.378642	0.559553	0	1	1
ENSG00000184350	ENSG00000184350	MRGPRE	11:3247290-3254068	NOTEST	0	0	0	0	1	1
ENSG00000184351	ENSG00000184351	KRTAP19-1	21:31852017-31852663	NOTEST	0.062546	0.273335	2.12768	0	1	1
ENSG00000184357	ENSG00000184357	HIST1H1B	6:27834569-27835359	NOTEST	0.399946	0.124179	-1.68739	0	1	1
ENSG00000184361	ENSG00000184361	SPATA32	17:43268297-43394414	NOTEST	0.0376366	0.0224033	-0.748426	0	1	1
ENSG00000184374	ENSG00000184374	COLEC10	8:120007690-120118821	NOTEST	0	0	0	0	1	1
ENSG00000184378	ENSG00000184378	ACTRT3	3:169484708-169489831	NOTEST	0.244932	0.391277	0.675807	0	1	1
ENSG00000184385	ENSG00000184385	C21orf128	21:43483067-43563563	NOTEST	0	0.00529624	inf	0	1	1
ENSG00000184388	ENSG00000184388	PABPC1L2B	X:72223351-72225551	NOTEST	0	0	0	0	1	1
ENSG00000184389	ENSG00000184389	A3GALT2	1:33772366-33896653	NOTEST	0	0	0	0	1	1
ENSG00000184394	ENSG00000184394	OR4N5	14:20611894-20612821	NOTEST	0	0	0	0	1	1
ENSG00000184408	ENSG00000184408	KCND2	7:119913721-120392568	NOTEST	0.07873	0.0069349	-3.50497	0	1	1
ENSG00000184414	ENSG00000184414	RP11-44M6.3	7:100167753-100168759	NOTEST	0.0177876	0.0903326	2.34437	0	1	1
ENSG00000184423	ENSG00000184423	AC090043.1	3:1637460-1637929	NOTEST	0	0	0	0	1	1
ENSG00000184434	ENSG00000184434	LRRC19	9:26904080-27062928	NOTEST	0.0674477	0.105631	0.647191	0	1	1
ENSG00000184441	ENSG00000184441	AP001062.7	21:45748826-45760353	NOTEST	0.33505	0.405502	0.275334	0	1	1
ENSG00000184451	ENSG00000184451	CCR10	17:40830906-40851832	NOTEST	0.504105	0.421116	-0.259508	0	1	1
ENSG00000184454	ENSG00000184454	NCMAP	1:24882601-24935819	NOTEST	0.00392368	0	#NAME?	0	1	1
ENSG00000184459	ENSG00000184459	BPIFC	22:32809833-32860471	NOTEST	0	0	0	0	1	1
ENSG00000184471	ENSG00000184471	C1QTNF8	16:1140004-1146244	NOTEST	0	0	0	0	1	1
ENSG00000184478	ENSG00000184478	OR56A3	11:5968569-5969591	NOTEST	0	0	0	0	1	1
ENSG00000184490	ENSG00000184490	AP000351.9	22:24366749-24370882	NOTEST	0	0	0	0	1	1
ENSG00000184492	ENSG00000184492	FOXD4L1	2:114256660-114258728	NOTEST	0.0156575	0.0286677	0.872572	0	1	1
ENSG00000184494	ENSG00000184494	NEU1	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000184497	ENSG00000184497	TMEM255B	13:114462215-114514926	NOTEST	0.0332324	0.140862	2.08362	0	1	1
ENSG00000184502	ENSG00000184502	GAST	17:39775688-39943183	NOTEST	0	0	0	0	1	1
ENSG00000184507	ENSG00000184507	NUTM1	15:34635515-34649938	NOTEST	0	0	0	0	1	1
ENSG00000184515	ENSG00000184515	BEX5	X:101408679-101411029	NOTEST	0.0395409	0.168963	2.09529	0	1	1
ENSG00000184523	ENSG00000184523	PTGER4P2	9:66499742-66499994	NOTEST	0	0.13589	inf	0	1	1
ENSG00000184524	ENSG00000184524	CEND1	11:787103-790123	NOTEST	0.383983	0.149216	-1.36364	0	1	1
ENSG00000184530	ENSG00000184530	C6orf58	6:127840599-127912962	NOTEST	0.170606	0.075364	-1.17872	0	1	1
ENSG00000184544	ENSG00000184544	DHRS7C	17:9674750-9725388	NOTEST	0	0	0	0	1	1
ENSG00000184560	ENSG00000184560	C17orf74	17:7323421-7361026	NOTEST	0.0375126	0.00936535	-2.00197	0	1	1
ENSG00000184566	ENSG00000184566	AC132216.1	11:33880121-33913836	NOTEST	0	0	0	0	1	1
ENSG00000184571	ENSG00000184571	PIWIL3	22:25115000-25170687	NOTEST	0.00445563	0	#NAME?	0	1	1
ENSG00000184574	ENSG00000184574	LPAR5	12:6728000-6745613	NOTEST	0.0058833	0.00413138	-0.510001	0	1	1
ENSG00000184586	ENSG00000184586	KRTAP7-1	21:32201356-32202078	NOTEST	0	0.000236461	inf	0	1	1
ENSG00000184596	ENSG00000184596	AF207550.1	X:48779304-48815648	NOTEST	0.497976	0.381226	-0.385427	0	1	1
ENSG00000184599	ENSG00000184599	FAM19A3	1:113263040-113269857	NOTEST	0.125005	0.159123	0.348152	0	1	1
ENSG00000184601	ENSG00000184601	C14orf180	14:104941014-105071984	NOTEST	0	0	0	0	1	1
ENSG00000184608	ENSG00000184608	C8orf12	8:11197145-11332224	NOTEST	0	0	0	0	1	1
ENSG00000184611	ENSG00000184611	KCNH7	2:163175349-163695240	NOTEST	0.00680109	0.00921832	0.438737	0	1	1
ENSG00000184612	ENSG00000184612	RPL7P26	6:17393446-17558023	NOTEST	0.271899	0.168337	-0.691713	0	1	1

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ENSG00000184616	ENSG00000184616	AC004166.6	7:74306893-74366314	NOTEST	0.256839	0.215677	-0.251996	0	1	1
ENSG00000184617	ENSG00000184617	ZNF840	20:45113099-45121279	NOTEST	0	0	0	0	1	1
ENSG00000184624	ENSG00000184624	ZNF72P	22:16634897-16651926	NOTEST	0	0	0	0	1	1
ENSG00000184635	ENSG00000184635	ZNF93	19:20011721-20074273	NOTEST	0.295857	0.409899	0.470369	0	1	1
ENSG00000184647	ENSG00000184647	PRSS55	8:10340387-10411676	NOTEST	0	0.0162123	inf	0	1	1
ENSG00000184650	ENSG00000184650	ODF4	17:8243181-8249364	NOTEST	0	0	0	0	1	1
ENSG00000184659	ENSG00000184659	FOXD4L4	9:70426622-70429731	NOTEST	0	0	0	0	1	1
ENSG00000184669	ENSG00000184669	OR7E14P	11:16799841-17074583	NOTEST	0	0	0	0	1	1
ENSG00000184672	ENSG00000184672	RALYL	8:85095021-85834079	NOTEST	0.356269	0.191947	-0.89226	0	1	1
ENSG00000184682	ENSG00000184682	C11orf89	11:1874199-1913497	NOTEST	0	0	0	0	1	1
ENSG00000184697	ENSG00000184697	CLDN6	16:3064712-3072384	NOTEST	0	0.00872268	inf	0	1	1
ENSG00000184698	ENSG00000184698	OR51M1	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000184709	ENSG00000184709	LRRC26	9:140063209-140066861	NOTEST	0.0286168	0.149017	2.38054	0	1	1
ENSG00000184716	ENSG00000184716	SERINC4	15:44019115-44095241	NOTEST	0.0497042	0.0403787	-0.299773	0	1	1
ENSG00000184724	ENSG00000184724	KRTAP6-1	21:31985749-31986249	NOTEST	0	0	0	0	1	1
ENSG00000184730	ENSG00000184730	APOBR	16:28467692-28510291	NOTEST	0	0	0	0	1	1
ENSG00000184731	ENSG00000184731	FAM110C	2:38813-46870	NOTEST	0.0082756	0	#NAME?	0	1	1
ENSG00000184735	ENSG00000184735	DDX53	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000184741	ENSG00000184741	OR5AQ1P	11:55821839-55822779	NOTEST	0	0	0	0	1	1
ENSG00000184750	ENSG00000184750	MAGEA2	X:151918386-151922364	NOTEST	0.0492849	0.180181	1.87023	0	1	1
ENSG00000184761	ENSG00000184761	AC013269.5	2:131296667-131307456	NOTEST	0	0	0	0	1	1
ENSG00000184774	ENSG00000184774	RP11-480I12.4	1:202789393-202796353	NOTEST	0.0133605	0.00938423	-0.509661	0	1	1
ENSG00000184786	ENSG00000184786	TCTE3	6:170140209-170151655	NOTEST	0.0704122	0.0175388	-2.00528	0	1	1
ENSG00000184788	ENSG00000184788	SATL1	X:84347292-84364054	NOTEST	0.564488	0.426872	-0.403138	0	1	1
ENSG00000184789	ENSG00000184789	OR4C10P	11:48453768-48454699	NOTEST	0	0	0	0	1	1
ENSG00000184792	ENSG00000184792	OSBP2	22:31089768-31303811	NOTEST	0.334889	0.609409	0.863727	0	1	1
ENSG00000184795	ENSG00000184795	UNC93B5	11:67479172-67483476	NOTEST	0.13163	0.151483	0.202668	0	1	1
ENSG00000184809	ENSG00000184809	C21orf88	21:40928368-41098012	NOTEST	0	0	0	0	1	1
ENSG00000184811	ENSG00000184811	TUSC5	17:1182956-1204281	NOTEST	0	0	0	0	1	1
ENSG00000184814	ENSG00000184814	PRR23B	3:138722803-139108574	NOTEST	0	0	0	0	1	1
ENSG00000184825	ENSG00000184825	HIST1H2AH	6:27114860-27115317	NOTEST	0.447576	0.501853	0.165131	0	1	1
ENSG00000184828	ENSG00000184828	ZBTB7C	18:45553043-45937123	NOTEST	0	0.00545564	inf	0	1	1
ENSG00000184844	ENSG00000184844	CYCSP45	X:153106705-153107020	NOTEST	0	0.246863	inf	0	1	1
ENSG00000184845	ENSG00000184845	DRD1	5:174867041-174871211	NOTEST	0	0	0	0	1	1
ENSG00000184856	ENSG00000184856	LINC00308	21:23470935-23488847	NOTEST	0	0	0	0	1	1
ENSG00000184860	ENSG00000184860	SDR42E1	16:82031220-82045093	NOTEST	0.0217381	0.0487556	1.16534	0	1	1
ENSG00000184881	ENSG00000184881	OR51B2	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000184895	ENSG00000184895	SRY	Y:2654895-2655740	NOTEST	0	0	0	0	1	1
ENSG00000184905	ENSG00000184905	TCEAL2	X:101380659-101382683	NOTEST	0	0	0	0	1	1
ENSG00000184906	ENSG00000184906	AC129778.2	9:42845767-42876505	NOTEST	0.372232	0.221893	-0.746334	0	1	1
ENSG00000184908	ENSG00000184908	CLCNKB	1:16370271-16383803	NOTEST	0.0151697	0.0546157	1.84813	0	1	1
ENSG00000184909	ENSG00000184909	C1ORF220	1:178482211-178518024	NOTEST	0	0.0137177	inf	0	1	1
ENSG00000184911	ENSG00000184911	DMRTC1B	X:71996832-72068636	NOTEST	0	0	0	0	1	1
ENSG00000184923	ENSG00000184923	NUTM2A	10:88963631-89102369	NOTEST	0.0293819	0.0747912	1.34794	0	1	1
ENSG00000184925	ENSG00000184925	LCN12	9:139844002-139849949	NOTEST	0.1479	0	#NAME?	0	1	1

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ENSG00000184937	ENSG00000184937	WT1	11:32409320-32480315	NOTEST	0.0229298	0.0205386	-0.158881	0	1	1
ENSG00000184945	ENSG00000184945	AQP12A	2:241631261-241637900	NOTEST	0	0	0	0	1	1
ENSG00000184954	ENSG00000184954	OR6C70	12:55828520-55979255	NOTEST	0	0	0	0	1	1
ENSG00000184956	ENSG00000184956	MUC6	11:1012820-1036706	NOTEST	0.00531225	0.00147209	-1.85146	0	1	1
ENSG00000184961	ENSG00000184961	AL772307.1	9:42128838-42129419	NOTEST	0.0362317	0.0282122	-0.360932	0	1	1
ENSG00000184984	ENSG00000184984	CHRM5	15:34158427-34357291	NOTEST	0	0	0	0	1	1
ENSG00000184985	ENSG00000184985	SORCS2	4:7194264-7744554	NOTEST	0	0	0	0	1	1
ENSG00000184991	ENSG00000184991	TTTY13	Y:23745485-23756552	NOTEST	0	0	0	0	1	1
ENSG00000184995	ENSG00000184995	IFNE	9:21455482-21559668	NOTEST	0.032145	0.00802912	-2.00128	0	1	1
ENSG00000184999	ENSG00000184999	SLC22A10	11:62847411-63137190	NOTEST	0	0	0	0	1	1
ENSG00000185002	ENSG00000185002	RFX6	6:117198374-117253326	NOTEST	0.00847653	0	#NAME?	0	1	1
ENSG00000185013	ENSG00000185013	NT5C1B	2:18735988-18770838	NOTEST	0.0199906	0	#NAME?	0	1	1
ENSG00000185015	ENSG00000185015	CA13	8:86132815-86196302	NOTEST	0.37522	0.460129	0.294304	0	1	1
ENSG00000185020	ENSG00000185020	RP11-111G23.1	9:40293024-40339528	NOTEST	0.462266	0.335755	-0.461314	0	1	1
ENSG00000185028	ENSG00000185028	LRRC14B	5:191625-195468	NOTEST	0	0	0	0	1	1
ENSG00000185031	ENSG00000185031	SLC2A3P2	1:65437907-65468159	NOTEST	0	0	0	0	1	1
ENSG00000185037	ENSG00000185037	ZNF733P	7:62751895-62764434	NOTEST	0	0	0	0	1	1
ENSG00000185038	ENSG00000185038	MROH2A	2:234684369-234763212	NOTEST	0.00286962	0.00850645	1.5677	0	1	1
ENSG00000185040	ENSG00000185040	AC004980.11	7:76139744-77045717	NOTEST	0.0417852	0.0478955	0.196897	0	1	1
ENSG00000185041	ENSG00000185041	RP11-321E2.6	5:17498333-17498936	NOTEST	0	0	0	0	1	1
ENSG00000185052	ENSG00000185052	SLC24A3	20:19193289-19703581	NOTEST	0	0	0	0	1	1
ENSG00000185053	ENSG00000185053	SGCZ	8:13947372-15095848	NOTEST	0	0	0	0	1	1
ENSG00000185055	ENSG00000185055	EFCAB10	7:105172531-105241322	NOTEST	0.103069	0.17956	0.80086	0	1	1
ENSG00000185056	ENSG00000185056	C5orf47	5:173400781-173433143	NOTEST	0.0261072	0.0529969	1.02146	0	1	1
ENSG00000185065	ENSG00000185065	AC000068.5	22:19318220-19466738	NOTEST	0.0946791	0.073588	-0.363576	0	1	1
ENSG00000185069	ENSG00000185069	KRT76	12:53161938-53171129	NOTEST	0	0	0	0	1	1
ENSG00000185074	ENSG00000185074	OR7E31P	9:92978320-92979206	NOTEST	0	0	0	0	1	1
ENSG00000185078	ENSG00000185078	AC093698.1	2:208896106-208896677	NOTEST	0	0	0	0	1	1
ENSG00000185087	ENSG00000185087	FAM169B	15:98980390-99057611	NOTEST	0	0	0	0	1	1
ENSG00000185097	ENSG00000185097	OR4F16	1:536815-660283	NOTEST	0	0	0	0	1	1
ENSG00000185101	ENSG00000185101	ANO9	11:417932-442011	NOTEST	0.0837786	0.307975	1.87816	0	1	1
ENSG00000185105	ENSG00000185105	MYADML2	17:79890259-79905477	NOTEST	0.0127312	0.00494174	-1.36528	0	1	1
ENSG00000185128	ENSG00000185128	TBC1D3F	17:36283970-36294915	NOTEST	0.162926	0.0795956	-1.03346	0	1	1
ENSG00000185133	ENSG00000185133	INPP5J	22:31518716-31530682	NOTEST	0.0992283	0.123606	0.31693	0	1	1
ENSG00000185149	ENSG00000185149	NPY2R	4:156127680-156138230	NOTEST	0	0	0	0	1	1
ENSG00000185155	ENSG00000185155	MIXL1	1:226411318-226414755	NOTEST	0.0146673	0.131365	3.16291	0	1	1
ENSG00000185156	ENSG00000185156	MFSD6L	17:8700435-8702667	NOTEST	0	0	0	0	1	1
ENSG00000185162	ENSG00000185162	AP001324.1	11:74407473-74442430	NOTEST	0	0	0	0	1	1
ENSG00000185176	ENSG00000185176	AQP12B	2:241615834-241622323	NOTEST	0	0	0	0	1	1
ENSG00000185177	ENSG00000185177	ZNF479	7:57187320-57207571	NOTEST	0	0	0	0	1	1
ENSG00000185182	ENSG00000185182	GOLGA8DP	15:22704720-22715604	NOTEST	0	0	0	0	1	1
ENSG00000185186	ENSG00000185186	LINC00313	21:44881973-44899414	NOTEST	0	0	0	0	1	1
ENSG00000185198	ENSG00000185198	PRSS57	19:685520-695460	NOTEST	0	0	0	0	1	1
ENSG00000185201	ENSG00000185201	IFITM2	11:307630-315272	NOTEST	0.23776	0.361442	0.604255	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000185203	ENSG00000185203	WASIR1	X:155227245-155257848	NOTEST	0	0	0	0	1	1
ENSG00000185221	ENSG00000185221	GAPDHP24	1:215044076-215045059	NOTEST	0	0	0	0	1	1
ENSG00000185231	ENSG00000185231	MC2R	18:13882042-13915706	NOTEST	0	0	0	0	1	1
ENSG00000185245	ENSG00000185245	GP1BA	17:4835591-4838325	NOTEST	0.112292	0.0373225	-1.58914	0	1	1
ENSG00000185247	ENSG00000185247	MAGEA11	X:148769893-148798926	NOTEST	0.0571361	0.0453843	-0.33221	0	1	1
ENSG00000185250	ENSG00000185250	PPIL6	6:109711417-109765122	NOTEST	0.285981	0.344824	0.269943	0	1	1
ENSG00000185254	ENSG00000185254	TEX28	X:153498929-153523796	NOTEST	0	0	0	0	1	1
ENSG00000185261	ENSG00000185261	KIAA0825	5:93488670-94620279	NOTEST	0.156225	0.0253419	-2.62403	0	1	1
ENSG00000185264	ENSG00000185264	TEX33	22:37387162-37403882	NOTEST	0	0	0	0	1	1
ENSG00000185267	ENSG00000185267	CDNF	10:14861248-14913740	NOTEST	0.442136	0.250516	-0.819588	0	1	1
ENSG00000185271	ENSG00000185271	KLHL33	14:20896969-20903801	NOTEST	0	0	0	0	1	1
ENSG00000185274	ENSG00000185274	WBSCR17	7:70597154-71178585	NOTEST	0	0	0	0	1	1
ENSG00000185275	ENSG00000185275	CD24P4	Y:21034386-21239302	NOTEST	0	0.445256	inf	0	1	1
ENSG00000185290	ENSG00000185290	NUPR1L	7:56182373-56184093	NOTEST	0	0	0	0	1	1
ENSG00000185291	ENSG00000185291	IL3RA	X:1455508-1501578	NOTEST	0	0.14134	inf	0	1	1
ENSG00000185294	ENSG00000185294	SPPL2C	17:43921016-44105700	NOTEST	0	0	0	0	1	1
ENSG00000185296	ENSG00000185296	CTD-2139B15.1	5:17306489-17307069	NOTEST	0	0	0	0	1	1
ENSG00000185303	ENSG00000185303	SFTPA2	10:81315607-81320153	NOTEST	0	0	0	0	1	1
ENSG00000185304	ENSG00000185304	RGPD2	2:88047605-88285309	NOTEST	0.19935	0.233696	0.229326	0	1	1
ENSG00000185306	ENSG00000185306	C12orf56	12:64616116-64790845	NOTEST	0	0.0331919	inf	0	1	1
ENSG00000185313	ENSG00000185313	SCN10A	3:38738292-38835501	NOTEST	0	0	0	0	1	1
ENSG00000185319	ENSG00000185319	SSXP4	X:52627543-52632339	NOTEST	0	0	0	0	1	1
ENSG00000185332	ENSG00000185332	TMEM105	17:79285073-79304474	NOTEST	0	0.112337	inf	0	1	1
ENSG00000185352	ENSG00000185352	HS6ST3	13:96743092-97485671	NOTEST	0	0	0	0	1	1
ENSG00000185372	ENSG00000185372	OR2V1	5:180551356-180552304	NOTEST	0	0	0	0	1	1
ENSG00000185385	ENSG00000185385	OR7A17	19:14991137-14992264	NOTEST	0	0	0	0	1	1
ENSG00000185390	ENSG00000185390	FGF7P2	21:14721585-14722969	NOTEST	0	0	0	0	1	1
ENSG00000185404	ENSG00000185404	SP140L	2:230990025-231268447	NOTEST	0.0799439	0.185209	1.2121	0	1	1
ENSG00000185433	ENSG00000185433	LINC00158	21:26758132-26804013	NOTEST	0	0	0	0	1	1
ENSG00000185436	ENSG00000185436	IFNLR1	1:24480646-24514449	NOTEST	0.00951407	0.0311573	1.71143	0	1	1
ENSG00000185448	ENSG00000185448	FAM47A	X:34147868-34150447	NOTEST	0	0	0	0	1	1
ENSG00000185467	ENSG00000185467	KPNA7	7:98771196-98805129	NOTEST	0	0	0	0	1	1
ENSG00000185479	ENSG00000185479	KRT6B	12:52840434-52845910	NOTEST	0	0.00546602	inf	0	1	1
ENSG00000185482	ENSG00000185482	STAC3	12:57637235-57824788	NOTEST	0.0753675	0.101148	0.424448	0	1	1
ENSG00000185499	ENSG00000185499	MUC1	1:155141883-155162707	NOTEST	0.30307	0.513012	0.759338	0	1	1
ENSG00000185518	ENSG00000185518	SV2B	15:91643179-91844539	NOTEST	0	0	0	0	1	1
ENSG00000185519	ENSG00000185519	FAM131C	1:16384263-16400127	NOTEST	0.211418	0.347854	0.718382	0	1	1
ENSG00000185522	ENSG00000185522	C11orf35	11:537526-564021	NOTEST	0.302665	0.481471	0.669726	0	1	1
ENSG00000185523	ENSG00000185523	C1orf227	1:213003482-213020991	NOTEST	0	0	0	0	1	1
ENSG00000185527	ENSG00000185527	PDE6G	17:79617488-79630142	NOTEST	0.185201	0.20449	0.142935	0	1	1
ENSG00000185554	ENSG00000185554	NXF2	X:101470279-101581634	NOTEST	0	0	0	0	1	1
ENSG00000185559	ENSG00000185559	DLK1	14:101192041-101201539	NOTEST	0	0	0	0	1	1
ENSG00000185561	ENSG00000185561	TLCD2	17:1611063-1613732	NOTEST	0.496791	0.312193	-0.6702	0	1	1
ENSG00000185594	ENSG00000185594	SPATA8	15:97326618-97328845	NOTEST	0	0	0	0	1	1
ENSG00000185607	ENSG00000185607	ACTBP7	15:44162961-44487450	NOTEST	0.0311696	0.0782159	1.32732	0	1	1

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ENSG00000185610	ENSG00000185610	DBX2	12:45408454-45496890	NOTEST	0	0	0	0	1	1
ENSG00000185615	ENSG00000185615	PDIA2	16:333151-337215	NOTEST	0.141298	0.191872	0.441401	0	1	1
ENSG00000185630	ENSG00000185630	PBX1	1:164524820-164868533	NOTEST	0.00966257	0.0278066	1.52495	0	1	1
ENSG00000185631	ENSG00000185631	AC017079.3	2:128960934-128961349	NOTEST	0	0	0	0	1	1
ENSG00000185633	ENSG00000185633	NDUFA4L2	12:57623109-57634498	NOTEST	0.13923	0.270702	0.959232	0	1	1
ENSG00000185638	ENSG00000185638	FTH1P14	X:34165152-34165703	NOTEST	0	0	0	0	1	1
ENSG00000185640	ENSG00000185640	KRT79	12:53215193-53228079	NOTEST	0.0196616	0.00841869	-1.22371	0	1	1
ENSG00000185652	ENSG00000185652	NTF3	12:5541277-5630702	NOTEST	0.107086	0.174501	0.704459	0	1	1
ENSG00000185662	ENSG00000185662	SMIM23	5:171212875-171221602	NOTEST	0	0	0	0	1	1
ENSG00000185666	ENSG00000185666	SYN3	22:32908538-33454358	NOTEST	0.308057	0.252883	-0.284725	0	1	1
ENSG00000185669	ENSG00000185669	SNAI3	16:88729705-88753594	NOTEST	0.139787	0.243109	0.798372	0	1	1
ENSG00000185674	ENSG00000185674	LYG2	2:99613723-100106497	NOTEST	0.0645188	0.0226226	-1.51196	0	1	1
ENSG00000185681	ENSG00000185681	MORN5	9:124922189-124962367	NOTEST	0.576081	0.328697	-0.809513	0	1	1
ENSG00000185689	ENSG00000185689	C6orf201	6:4021500-4157619	NOTEST	0.360036	0.370755	0.0423262	0	1	1
ENSG00000185700	ENSG00000185700	TTTY8B	Y:6338813-6341671	NOTEST	0	0	0	0	1	1
ENSG00000185701	ENSG00000185701	OR5M5P	11:56294043-56294979	NOTEST	0	0	0	0	1	1
ENSG00000185736	ENSG00000185736	ADARB2	10:1228072-1779670	NOTEST	0.0164244	0	#NAME?	0	1	1
ENSG00000185739	ENSG00000185739	SRL	16:4239374-4292081	NOTEST	0	0	0	0	1	1
ENSG00000185742	ENSG00000185742	C11orf87	11:109225811-109454633	NOTEST	0	0.00182358	inf	0	1	1
ENSG00000185751	ENSG00000185751	XAGE2	X:52380350-52387001	NOTEST	0	0	0	0	1	1
ENSG00000185758	ENSG00000185758	CLDN24	4:184242916-184243579	NOTEST	0	0	0	0	1	1
ENSG00000185774	ENSG00000185774	KCNIP4	4:20697904-21950422	NOTEST	0.334586	0.54572	0.705784	0	1	1
ENSG00000185775	ENSG00000185775	SPATA31A6	9:43624506-43630730	NOTEST	0.00367769	0	#NAME?	0	1	1
ENSG00000185792	ENSG00000185792	NLRP9	19:56186591-56249768	NOTEST	0.0134537	0.00629332	-1.09611	0	1	1
ENSG00000185811	ENSG00000185811	IKZF1	7:50343719-50472799	NOTEST	0	0	0	0	1	1
ENSG00000185821	ENSG00000185821	OR6C76	12:55820037-55820976	NOTEST	0	0	0	0	1	1
ENSG00000185823	ENSG00000185823	NPAP1	15:24920540-24928593	NOTEST	0	0	0	0	1	1
ENSG00000185837	ENSG00000185837	CECR5-AS1	22:17618400-17646335	NOTEST	0.100145	0.289612	1.53203	0	1	1
ENSG00000185847	ENSG00000185847	RP1-46F2.2	12:111374388-111396012	NOTEST	0	0.0599277	inf	0	1	1
ENSG00000185860	ENSG00000185860	C1orf110	1:162794247-162838605	NOTEST	0	0	0	0	1	1
ENSG00000185862	ENSG00000185862	EVI2B	17:29335514-29709134	NOTEST	0.0105705	0.077521	2.87454	0	1	1
ENSG00000185863	ENSG00000185863	TMEM210	9:140063209-140066861	NOTEST	0	0	0	0	1	1
ENSG00000185873	ENSG00000185873	TMPRSS11B	4:69048009-69111438	NOTEST	0	0	0	0	1	1
ENSG00000185885	ENSG00000185885	IFITM1	11:307630-315272	NOTEST	0.0333435	0.0187709	-0.828908	0	1	1
ENSG00000185888	ENSG00000185888	PRSS38	1:228003393-228034171	NOTEST	0	0.0298106	inf	0	1	1
ENSG00000185894	ENSG00000185894	BPY2C	Y:27177047-27208695	NOTEST	0	0	0	0	1	1
ENSG00000185897	ENSG00000185897	FFAR3	19:35849361-35851387	NOTEST	0	0.0354331	inf	0	1	1
ENSG00000185899	ENSG00000185899	TAS2R60	7:143078172-143220542	NOTEST	0	0	0	0	1	1
ENSG00000185903	ENSG00000185903	OR11N1P	X:130407479-130533677	NOTEST	0	0	0	0	1	1
ENSG00000185905	ENSG00000185905	C16orf54	16:29753783-29759620	NOTEST	0	0.0135016	inf	0	1	1
ENSG00000185915	ENSG00000185915	KLHL34	X:21673608-21676448	NOTEST	0.0333851	0.0699158	1.06641	0	1	1
ENSG00000185926	ENSG00000185926	OR4C46	11:51515281-51516211	NOTEST	0	0	0	0	1	1
ENSG00000185933	ENSG00000185933	CALHM1	10:105206542-105222452	NOTEST	0.00515487	0	#NAME?	0	1	1
ENSG00000185940	ENSG00000185940	KRTAP5-5	11:1651032-1652160	NOTEST	0	0	0	0	1	1
ENSG00000185942	ENSG00000185942	NKAIN3	8:63161149-63912211	NOTEST	0.427594	0.132478	-1.69049	0	1	1

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ENSG00000185945	ENSG00000185945	NXF2B	X:101615315-101726732	NOTEST	0	0	0	0	1	1
ENSG00000185955	ENSG00000185955	C7orf61	7:100054237-100076902	NOTEST	0	0.16381	inf	0	1	1
ENSG00000185958	ENSG00000185958	FAM186A	12:50720012-50873787	NOTEST	0	0	0	0	1	1
ENSG00000185960	ENSG00000185960	SHOX	X:585078-620146	NOTEST	0	0	0	0	1	1
ENSG00000185962	ENSG00000185962	LCE3A	1:152595309-152595579	NOTEST	0	0	0	0	1	1
ENSG00000185966	ENSG00000185966	LCE3E	1:152538129-152539248	NOTEST	0	0	0	0	1	1
ENSG00000185972	ENSG00000185972	CCIN	9:36169388-36171329	NOTEST	0	0	0	0	1	1
ENSG00000185974	ENSG00000185974	GRK1	13:114321469-114440708	NOTEST	0.00868309	0	#NAME?	0	1	1
ENSG00000185978	ENSG00000185978	H2AFB3	X:154689079-154689596	NOTEST	0	0	0	0	1	1
ENSG00000185982	ENSG00000185982	DEFB128	20:168493-170322	NOTEST	0	0	0	0	1	1
ENSG00000185988	ENSG00000185988	PLK5	19:1524072-1535455	NOTEST	0	0.0209163	inf	0	1	1
ENSG00000185990	ENSG00000185990	F8A3	X:154686575-154688276	NOTEST	0	0	0	0	1	1
ENSG00000186007	ENSG00000186007	LEMD1	1:205342379-205438152	NOTEST	0.131883	0.0225518	-2.54794	0	1	1
ENSG00000186008	ENSG00000186008	RPS4XP21	19:34583444-34584215	NOTEST	0	0.0181112	inf	0	1	1
ENSG00000186009	ENSG00000186009	ATP4B	13:114303118-114312501	NOTEST	0	0	0	0	1	1
ENSG00000186019	ENSG00000186019	AC084219.4	19:44598491-44637027	NOTEST	0.219849	0.204551	-0.104053	0	1	1
ENSG00000186038	ENSG00000186038	HTR3E	3:183812905-183824783	NOTEST	0	0	0	0	1	1
ENSG00000186047	ENSG00000186047	DLEU7	13:50601268-51423190	NOTEST	0.0729028	0.0632344	-0.205266	0	1	1
ENSG00000186049	ENSG00000186049	KRT73	12:52979372-53012343	NOTEST	0	0	0	0	1	1
ENSG00000186051	ENSG00000186051	TAL2	9:108424737-108425367	NOTEST	0	0.0229021	inf	0	1	1
ENSG00000186074	ENSG00000186074	CD300LF	17:72666716-72765492	NOTEST	0	0	0	0	1	1
ENSG00000186075	ENSG00000186075	ZPBP2	17:38024416-38034149	NOTEST	0	0	0	0	1	1
ENSG00000186081	ENSG00000186081	KRT5	12:52908358-52914471	NOTEST	0	0	0	0	1	1
ENSG00000186082	ENSG00000186082	KRT18P14	11:35881798-35883048	NOTEST	0	0	0	0	1	1
ENSG00000186086	ENSG00000186086	NBPF6	1:108803817-109013624	NOTEST	0	0	0	0	1	1
ENSG00000186090	ENSG00000186090	HTR3D	3:183749331-183757157	NOTEST	0	0	0	0	1	1
ENSG00000186092	ENSG00000186092	OR4F5	1:69090-70008	NOTEST	0	0	0	0	1	1
ENSG00000186094	ENSG00000186094	AGBL4	1:48998526-50489585	NOTEST	0.195139	0.205872	0.0772497	0	1	1
ENSG00000186103	ENSG00000186103	ARGFX	3:121289550-121305481	NOTEST	0	0	0	0	1	1
ENSG00000186105	ENSG00000186105	LRRC70	5:61601988-61924409	NOTEST	0.138691	0.371314	1.42077	0	1	1
ENSG00000186113	ENSG00000186113	OR5D14	11:55563031-55563976	NOTEST	0	0	0	0	1	1
ENSG00000186115	ENSG00000186115	CYP4F2	19:15988832-16008930	NOTEST	0	0	0	0	1	1
ENSG00000186117	ENSG00000186117	OR5L1	11:55578853-55579952	NOTEST	0	0	0	0	1	1
ENSG00000186118	ENSG00000186118	TEX38	1:47098408-47184824	NOTEST	0	0	0	0	1	1
ENSG00000186119	ENSG00000186119	OR5D18	11:55587085-55588073	NOTEST	0	0	0	0	1	1
ENSG00000186124	ENSG00000186124	OR9M1P	11:55623067-55623988	NOTEST	0	0	0	0	1	1
ENSG00000186136	ENSG00000186136	TAS2R42	12:11338598-11339543	NOTEST	0	0	0	0	1	1
ENSG00000186143	ENSG00000186143	C2orf53	2:27359722-27362278	NOTEST	0	0	0	0	1	1
ENSG00000186146	ENSG00000186146	DEFB131	4:9446259-9452240	NOTEST	0	0	0	0	1	1
ENSG00000186148	ENSG00000186148	AC013271.3	2:110690737-110742667	NOTEST	0	0	0	0	1	1
ENSG00000186150	ENSG00000186150	UBL4B	1:110655061-110656569	NOTEST	0.0938239	0.0604968	-0.633098	0	1	1
ENSG00000186152	ENSG00000186152	LILRP1	19:55208382-55212683	NOTEST	0	0	0	0	1	1
ENSG00000186160	ENSG00000186160	CYP4Z1	1:47533159-47646011	NOTEST	0	0	0	0	1	1
ENSG00000186163	ENSG00000186163	U66059.29	7:141965649-141972054	NOTEST	0	0	0	0	1	1
ENSG00000186188	ENSG00000186188	FFAR4	10:95326421-95364237	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000186190	ENSG00000186190	BPIFB3	20:31643229-31661434	NOTEST	0	0	0	0	1	1
ENSG00000186191	ENSG00000186191	BPIFB4	20:31667449-31699557	NOTEST	0	0	0	0	1	1
ENSG00000186197	ENSG00000186197	EDARADD	1:236511561-236648214	NOTEST	0.065461	0.115551	0.819821	0	1	1
ENSG00000186198	ENSG00000186198	SLC51B	15:65337707-65369028	NOTEST	0.0352864	0.0616242	0.804384	0	1	1
ENSG00000186204	ENSG00000186204	CYP4F12	19:15783566-15807984	NOTEST	0	0	0	0	1	1
ENSG00000186207	ENSG00000186207	LCE5A	1:152483319-152484653	NOTEST	0.11076	0.0501827	-1.14217	0	1	1
ENSG00000186212	ENSG00000186212	SOWAHB	4:77816081-77819002	NOTEST	0	0	0	0	1	1
ENSG00000186223	ENSG00000186223	SSU72P4	11:4308731-4309313	NOTEST	0	0	0	0	1	1
ENSG00000186226	ENSG00000186226	LCE1E	1:152758689-152760902	NOTEST	0	0	0	0	1	1
ENSG00000186232	ENSG00000186232	SSU72P3	11:4351094-4351679	NOTEST	0	0	0	0	1	1
ENSG00000186234	ENSG00000186234	FAM86MP	4:9694118-9704578	NOTEST	0	0	0	0	1	1
ENSG00000186244	ENSG00000186244	RP11-1079K10.1	17:47448101-47554350	NOTEST	0	0	0	0	1	1
ENSG00000186265	ENSG00000186265	BTLA	3:112182814-112218408	NOTEST	0	0.0391459	inf	0	1	1
ENSG00000186268	ENSG00000186268	OR10D4P	11:123964288-123965239	NOTEST	0	0	0	0	1	1
ENSG00000186280	ENSG00000186280	KDM4D	11:94706844-94732682	NOTEST	0.558749	0.447776	-0.319424	0	1	1
ENSG00000186281	ENSG00000186281	GPAT2	2:96676298-96705199	NOTEST	0.0193524	0.0265164	0.454372	0	1	1
ENSG00000186288	ENSG00000186288	PABPC1L2A	X:72297114-72299351	NOTEST	0	0	0	0	1	1
ENSG00000186297	ENSG00000186297	GABRA5	15:26788692-27194354	NOTEST	0.0502676	0.550686	3.45353	0	1	1
ENSG00000186301	ENSG00000186301	MST1P2	1:16972068-16976914	NOTEST	0.383158	0.325549	-0.235066	0	1	1
ENSG00000186306	ENSG00000186306	OR10T2	1:158368311-158369256	NOTEST	0	0	0	0	1	1
ENSG00000186322	ENSG00000186322	GOLGA6L17P	15:82804002-82810874	NOTEST	0.204166	0.33702	0.723088	0	1	1
ENSG00000186328	ENSG00000186328	RP11-140K17.2	6:34683389-34683717	NOTEST	0	0	0	0	1	1
ENSG00000186329	ENSG00000186329	TMEM212	3:171561138-171656505	NOTEST	0	0	0	0	1	1
ENSG00000186334	ENSG00000186334	SLC36A3	5:150656322-150683327	NOTEST	0	0	0	0	1	1
ENSG00000186335	ENSG00000186335	SLC36A2	5:150694538-150727151	NOTEST	0	0	0	0	1	1
ENSG00000186354	ENSG00000186354	C9orf47	9:91605777-91619925	NOTEST	0	0	0	0	1	1
ENSG00000186367	ENSG00000186367	KIAA1024L	5:128795251-129522327	NOTEST	0	0	0	0	1	1
ENSG00000186369	ENSG00000186369	LINC00643	14:62570095-62596352	NOTEST	0	0	0	0	1	1
ENSG00000186377	ENSG00000186377	CYP4X1	1:47427035-47516423	NOTEST	0	0	0	0	1	1
ENSG00000186393	ENSG00000186393	KRT26	17:38922489-38928414	NOTEST	0	0	0	0	1	1
ENSG00000186399	ENSG00000186399	GOLGA8R	15:30695942-30706463	NOTEST	0.302311	0.343914	0.186013	0	1	1
ENSG00000186400	ENSG00000186400	OR10X1	1:158548708-158549689	NOTEST	0	0	0	0	1	1
ENSG00000186407	ENSG00000186407	CD300E	17:72606025-72619897	NOTEST	0	0	0	0	1	1
ENSG00000186417	ENSG00000186417	GLDN	15:51633825-51700210	NOTEST	0.00799309	0	#NAME?	0	1	1
ENSG00000186431	ENSG00000186431	FCAR	19:55385703-55401838	NOTEST	0	0	0	0	1	1
ENSG00000186439	ENSG00000186439	TRDN	6:123537482-123958238	NOTEST	0	0	0	0	1	1
ENSG00000186440	ENSG00000186440	OR6P1	1:158532440-158533394	NOTEST	0	0	0	0	1	1
ENSG00000186442	ENSG00000186442	KRT3	12:53183468-53189901	NOTEST	0	0	0	0	1	1
ENSG00000186446	ENSG00000186446	ZNF501	3:44771087-44778575	NOTEST	0.562842	0.42252	-0.413711	0	1	1
ENSG00000186451	ENSG00000186451	SPATA12	3:56761445-57114129	NOTEST	0.0331199	0.07014	1.08254	0	1	1
ENSG00000186452	ENSG00000186452	TMPRSS12	12:51236702-51281667	NOTEST	0	0	0	0	1	1
ENSG00000186453	ENSG00000186453	FAM228A	2:24299395-24424567	NOTEST	0	0	0	0	1	1
ENSG00000186458	ENSG00000186458	DEFB132	20:238376-241737	NOTEST	0	0	0	0	1	1
ENSG00000186462	ENSG00000186462	NAP1L2	X:72432134-72434684	NOTEST	0	0	0	0	1	1
ENSG00000186466	ENSG00000186466	AQP7P1	9:67272037-67298632	NOTEST	0	0	0	0	1	1

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ENSG00000186474	ENSG00000186474	KLK12	19:51532347-51538486	NOTEST	0	0	0	0	1	1
ENSG00000186479	ENSG00000186479	RGS7BP	5:63802083-63908139	NOTEST	0	0	0	0	1	1
ENSG00000186487	ENSG00000186487	MYT1L	2:1792884-2335032	NOTEST	0	0	0	0	1	1
ENSG00000186493	ENSG00000186493	C5orf38	5:2745958-2755508	NOTEST	0	0	0	0	1	1
ENSG00000186508	ENSG00000186508	OR9I2P	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000186509	ENSG00000186509	OR9Q1	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000186510	ENSG00000186510	CLCNKA	1:16340522-16360545	NOTEST	0.0609094	0.242679	1.99431	0	1	1
ENSG00000186513	ENSG00000186513	OR9Q2	11:57957905-57958990	NOTEST	0	0	0	0	1	1
ENSG00000186517	ENSG00000186517	ARHGAP30	1:161016735-161039760	NOTEST	0.0442857	0.0611535	0.465594	0	1	1
ENSG00000186526	ENSG00000186526	CYP4F8	19:15726028-15741448	NOTEST	0	0	0	0	1	1
ENSG00000186529	ENSG00000186529	CYP4F3	19:15751706-15773635	NOTEST	0	0	0	0	1	1
ENSG00000186530	ENSG00000186530	XKR5	8:6666037-6742798	NOTEST	0	0	0	0	1	1
ENSG00000186543	ENSG00000186543	CROCCP5	1:21760810-21764051	NOTEST	0	0	0	0	1	1
ENSG00000186562	ENSG00000186562	DEFB105A	8:7679487-7681411	NOTEST	0	0	0	0	1	1
ENSG00000186564	ENSG00000186564	FOXD2	1:47901688-47906363	NOTEST	0.329381	0.27925	-0.238199	0	1	1
ENSG00000186567	ENSG00000186567	CEACAM19	19:45041044-45222031	NOTEST	0.0714882	0.0850098	0.249923	0	1	1
ENSG00000186572	ENSG00000186572	DEFB107A	8:7669241-7673238	NOTEST	0	0	0	0	1	1
ENSG00000186579	ENSG00000186579	DEFB106A	8:7682693-7686575	NOTEST	0	0	0	0	1	1
ENSG00000186583	ENSG00000186583	SPATC1	8:145051320-145101933	NOTEST	0	0	0	0	1	1
ENSG00000186599	ENSG00000186599	DEFB105B	8:7345190-7347115	NOTEST	0	0	0	0	1	1
ENSG00000186628	ENSG00000186628	FSD2	15:83419315-83474822	NOTEST	0.014531	0.0100548	-0.531245	0	1	1
ENSG00000186642	ENSG00000186642	PDE2A	11:72287184-72385635	NOTEST	0.356551	0.285342	-0.321413	0	1	1
ENSG00000186645	ENSG00000186645	SPDYE9P	7:76139744-77045717	NOTEST	0.0153712	0.0158553	0.0447319	0	1	1
ENSG00000186648	ENSG00000186648	LRRC16B	14:24521205-24538937	NOTEST	0.598153	0.430227	-0.475418	0	1	1
ENSG00000186652	ENSG00000186652	PRG2	11:57154266-57195053	NOTEST	0	0	0	0	1	1
ENSG00000186675	ENSG00000186675	MAGEE2	X:75002822-75005079	NOTEST	0.00711938	0	#NAME?	0	1	1
ENSG00000186676	ENSG00000186676	EEF1GP1	7:124462439-125019375	NOTEST	0	0	0	0	1	1
ENSG00000186678	ENSG00000186678	RP11-266I3.7	X:55199149-55202459	NOTEST	0	0	0	0	1	1
ENSG00000186684	ENSG00000186684	CYP27C1	2:127941695-127977654	NOTEST	0.0154618	0.0430631	1.47775	0	1	1
ENSG00000186710	ENSG00000186710	CCDC42B	12:113587662-113623284	NOTEST	0.0389836	0.00993976	-1.97158	0	1	1
ENSG00000186714	ENSG00000186714	CCDC73	11:32605343-32816204	NOTEST	0.0507452	0.0498753	-0.0249449	0	1	1
ENSG00000186715	ENSG00000186715	MST1L	1:17066767-17299474	NOTEST	0.394942	0.260892	-0.598188	0	1	1
ENSG00000186723	ENSG00000186723	OR10H1	19:15917816-15918936	NOTEST	0	0	0	0	1	1
ENSG00000186732	ENSG00000186732	MPPED1	22:43807201-43903728	NOTEST	0	0	0	0	1	1
ENSG00000186743	ENSG00000186743	TPI1P3	6:116252311-116381921	NOTEST	0	0	0	0	1	1
ENSG00000186765	ENSG00000186765	FSCN2	17:79495421-79504156	NOTEST	0.137182	0.156566	0.190673	0	1	1
ENSG00000186766	ENSG00000186766	FOXI2	10:129535498-129539450	NOTEST	0	0	0	0	1	1
ENSG00000186777	ENSG00000186777	ZNF732	4:264463-299110	NOTEST	0.00734474	0.0103195	0.490586	0	1	1
ENSG00000186788	ENSG00000186788	SPATA31D3	9:84542935-84592004	NOTEST	0	0	0	0	1	1
ENSG00000186790	ENSG00000186790	FOXE3	1:47881743-47883723	NOTEST	0	0	0	0	1	1
ENSG00000186795	ENSG00000186795	KCNK18	10:118956999-118969810	NOTEST	0	0	0	0	1	1
ENSG00000186803	ENSG00000186803	IFNA10	9:21206179-21207142	NOTEST	0	0	0	0	1	1
ENSG00000186807	ENSG00000186807	ANXA8L2	10:47740329-47770871	NOTEST	0	0	0	0	1	1
ENSG00000186810	ENSG00000186810	CXCR3	X:70835765-70838367	NOTEST	0.01022	0	#NAME?	0	1	1

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ENSG00000186825	ENSG00000186825	C2orf27B	2:132552533-132559234	NOTEST	0	0	0	0	1	1
ENSG00000186827	ENSG00000186827	TNFRSF4	1:1146705-1149518	NOTEST	0	0.0493341	inf	0	1	1
ENSG00000186831	ENSG00000186831	KRT17P2	17:18330174-18335162	NOTEST	0	0	0	0	1	1
ENSG00000186832	ENSG00000186832	KRT16	17:39766029-39772151	NOTEST	0	0	0	0	1	1
ENSG00000186838	ENSG00000186838	SELV	19:40005752-40011326	NOTEST	0	0	0	0	1	1
ENSG00000186842	ENSG00000186842	LINC00846	21:33944547-33948191	NOTEST	0.00924166	0.00649592	-0.508619	0	1	1
ENSG00000186844	ENSG00000186844	LCE1A	1:152799948-152800573	NOTEST	0	0.0254707	inf	0	1	1
ENSG00000186847	ENSG00000186847	KRT14	17:39738530-39743173	NOTEST	0.104999	0.138955	0.404245	0	1	1
ENSG00000186854	ENSG00000186854	TRABD2A	2:85048773-85134132	NOTEST	0.0107385	0.0418579	1.96271	0	1	1
ENSG00000186860	ENSG00000186860	KRTAP17-1	17:39471172-39471947	NOTEST	0	0	0	0	1	1
ENSG00000186867	ENSG00000186867	QRFPR	4:122250466-122302214	NOTEST	0.177925	0.319635	0.845156	0	1	1
ENSG00000186881	ENSG00000186881	OR13F1	9:107266454-107267547	NOTEST	0	0	0	0	1	1
ENSG00000186886	ENSG00000186886	OR5D3P	11:55493593-55494634	NOTEST	0	0	0	0	1	1
ENSG00000186891	ENSG00000186891	TNFRSF18	1:1138887-1142071	NOTEST	0	0	0	0	1	1
ENSG00000186895	ENSG00000186895	FGF3	11:69624991-69633792	NOTEST	0	0	0	0	1	1
ENSG00000186910	ENSG00000186910	SERPINA11	14:94896969-94946026	NOTEST	0	0	0	0	1	1
ENSG00000186912	ENSG00000186912	P2RY4	X:69478015-69479654	NOTEST	0.0183528	0.0293441	0.677072	0	1	1
ENSG00000186919	ENSG00000186919	ZACN	17:74035183-74117657	NOTEST	0.10141	0.0292733	-1.79254	0	1	1
ENSG00000186924	ENSG00000186924	KRTAP22-1	21:31973413-31973612	NOTEST	0	0	0	0	1	1
ENSG00000186925	ENSG00000186925	KRTAP19-6	21:31913853-31914183	NOTEST	0	0	0	0	1	1
ENSG00000186930	ENSG00000186930	KRTAP6-2	21:31970908-31971219	NOTEST	0	0	0	0	1	1
ENSG00000186940	ENSG00000186940	CHCHD2P9	9:82006218-82006674	NOTEST	0	0.114794	inf	0	1	1
ENSG00000186943	ENSG00000186943	OR13C8	9:107331448-107332411	NOTEST	0	0	0	0	1	1
ENSG00000186952	ENSG00000186952	TMEM232	5:109624933-110100857	NOTEST	0.62871	0.292184	-1.10552	0	1	1
ENSG00000186960	ENSG00000186960	C14orf23	14:29241909-29299410	NOTEST	0	0	0	0	1	1
ENSG00000186965	ENSG00000186965	KRTAP19-2	21:31859361-31859755	NOTEST	0	0	0	0	1	1
ENSG00000186967	ENSG00000186967	KRTAP19-4	21:31869141-31869451	NOTEST	0	0	0	0	1	1
ENSG00000186970	ENSG00000186970	KRTAP15-1	21:31812596-31813070	NOTEST	0	0	0	0	1	1
ENSG00000186971	ENSG00000186971	KRTAP13-4	21:31802571-31803216	NOTEST	0	0	0	0	1	1
ENSG00000186973	ENSG00000186973	FAM183A	1:43610823-43622067	NOTEST	0.0763009	0.0665915	-0.196363	0	1	1
ENSG00000186976	ENSG00000186976	EFCAB6	22:43911996-44208217	NOTEST	0.114945	0.073453	-0.646052	0	1	1
ENSG00000186977	ENSG00000186977	KRTAP19-5	21:31873974-31874435	NOTEST	0	0	0	0	1	1
ENSG00000186980	ENSG00000186980	KRTAP23-1	21:31720716-31720924	NOTEST	0	0	0	0	1	1
ENSG00000186994	ENSG00000186994	KANK3	19:8367010-8408146	NOTEST	0.0541364	0.203853	1.91286	0	1	1
ENSG00000186998	ENSG00000186998	EMID1	22:29601839-29655586	NOTEST	0.19177	0.185357	-0.0490752	0	1	1
ENSG00000187003	ENSG00000187003	ACTL7A	9:111624602-111626035	NOTEST	0	0	0	0	1	1
ENSG00000187005	ENSG00000187005	KRTAP21-1	21:32127438-32127746	NOTEST	0	0	0	0	1	1
ENSG00000187008	ENSG00000187008	PKD1L3	16:71963440-72033877	NOTEST	0.00295589	0.00666578	1.17318	0	1	1
ENSG00000187010	ENSG00000187010	RHD	1:25568727-25756683	NOTEST	0.0151144	0.04234	1.48609	0	1	1
ENSG00000187012	ENSG00000187012	LINC00207	22:44965218-44968221	NOTEST	0	0	0	0	1	1
ENSG00000187013	ENSG00000187013	C17orf82	17:59489111-59490641	NOTEST	0.414088	0.429684	0.0533369	0	1	1
ENSG00000187017	ENSG00000187017	ESPN	1:6484847-6580121	NOTEST	0.294846	0.458136	0.635814	0	1	1
ENSG00000187021	ENSG00000187021	PNLIPRP1	10:118349896-118368687	NOTEST	0	0	0	0	1	1
ENSG00000187026	ENSG00000187026	KRTAP21-2	21:32119111-32119551	NOTEST	0	0	0	0	1	1

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ENSG00000187033	ENSG00000187033	SAMD7	3:169629359-169656963	NOTEST	0	0	0	0	1	1
ENSG00000187037	ENSG00000187037	GPR141	7:37723398-38065297	NOTEST	0	0.0154635	inf	0	1	1
ENSG00000187045	ENSG00000187045	TMPRSS6	22:37461475-37505603	NOTEST	0	0.00390679	inf	0	1	1
ENSG00000187048	ENSG00000187048	CYP4A11	1:47394848-47407156	NOTEST	0	0	0	0	1	1
ENSG00000187054	ENSG00000187054	TMPRSS11A	4:68566997-68995598	NOTEST	0	0.00375061	inf	0	1	1
ENSG00000187060	ENSG00000187060	RP11-187C18.3	9:45562978-45563576	NOTEST	0.500817	0.46514	-0.106617	0	1	1
ENSG00000187066	ENSG00000187066	TMEM262	11:64851694-64883856	NOTEST	0.550245	0.577608	0.0700162	0	1	1
ENSG00000187080	ENSG00000187080	OR2AK2	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000187082	ENSG00000187082	DEFB106B	8:7340025-7343922	NOTEST	0	0	0	0	1	1
ENSG00000187094	ENSG00000187094	CCK	3:42299316-42307699	NOTEST	0	0	0	0	1	1
ENSG00000187103	ENSG00000187103	FUNDC2P3	6:146348781-146758734	NOTEST	0	0	0	0	1	1
ENSG00000187105	ENSG00000187105	HEATR4	14:73945188-74025651	NOTEST	0.055272	0.128971	1.22243	0	1	1
ENSG00000187116	ENSG00000187116	LILRA5	19:54818352-54850421	NOTEST	0	0	0	0	1	1
ENSG00000187122	ENSG00000187122	SLIT1	10:98757794-99052413	NOTEST	0	0	0	0	1	1
ENSG00000187134	ENSG00000187134	AKR1C1	10:4934795-5025475	NOTEST	0.025923	0.0220945	-0.230551	0	1	1
ENSG00000187144	ENSG00000187144	SPATA21	1:16679069-16763919	NOTEST	0	0	0	0	1	1
ENSG00000187151	ENSG00000187151	ANGPTL5	11:101761404-101871789	NOTEST	0	0	0	0	1	1
ENSG00000187166	ENSG00000187166	H1FNT	12:48722762-48724062	NOTEST	0	0.0102256	inf	0	1	1
ENSG00000187170	ENSG00000187170	LCE4A	1:152680635-152681967	NOTEST	0	0	0	0	1	1
ENSG00000187172	ENSG00000187172	BAGE2	21:10906200-11098980	NOTEST	0.057802	0.085462	0.564164	0	1	1
ENSG00000187173	ENSG00000187173	LCE2A	1:152670839-152671918	NOTEST	0.176425	0.231306	0.390745	0	1	1
ENSG00000187175	ENSG00000187175	KRTAP12-1	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000187180	ENSG00000187180	LCE2C	1:152647770-152659877	NOTEST	0	0	0	0	1	1
ENSG00000187185	ENSG00000187185	CTD-2600O9.1	16:57792128-57896957	NOTEST	0	0	0	0	1	1
ENSG00000187191	ENSG00000187191	DAZ3	Y:26909215-26959626	NOTEST	0	0	0	0	1	1
ENSG00000187210	ENSG00000187210	GCNT1	9:79034751-79122332	NOTEST	0.0101932	0.0386041	1.92115	0	1	1
ENSG00000187223	ENSG00000187223	LCE2D	1:152635871-152637135	NOTEST	0	0	0	0	1	1
ENSG00000187229	ENSG00000187229	RP11-161I2.1	8:18384810-18942240	NOTEST	0	0	0	0	1	1
ENSG00000187238	ENSG00000187238	LCE3B	1:152586286-152586574	NOTEST	0	0	0	0	1	1
ENSG00000187242	ENSG00000187242	KRT12	17:39007051-39023462	NOTEST	0.00875665	0.027915	1.67259	0	1	1
ENSG00000187243	ENSG00000187243	MAGED4B	X:51804922-51812368	NOTEST	0	0	0	0	1	1
ENSG00000187258	ENSG00000187258	NPSR1	7:34386123-34917944	NOTEST	0	0	0	0	1	1
ENSG00000187260	ENSG00000187260	WDR86	7:151038784-151110440	NOTEST	0.219531	0.144247	-0.605882	0	1	1
ENSG00000187268	ENSG00000187268	FAM9C	X:13053736-13062801	NOTEST	0	0	0	0	1	1
ENSG00000187272	ENSG00000187272	KRTAP9-8	17:39394296-39395256	NOTEST	0	0	0	0	1	1
ENSG00000187288	ENSG00000187288	CIDEC	3:9908397-9921938	NOTEST	0	0.0208774	inf	0	1	1
ENSG00000187323	ENSG00000187323	DCC	18:49866541-51094653	NOTEST	0.0100217	0.0106961	0.093944	0	1	1
ENSG00000187372	ENSG00000187372	PCDHB13	5:140593508-140596993	NOTEST	0.390427	0.380959	-0.0354184	0	1	1
ENSG00000187398	ENSG00000187398	LUZP2	11:24518515-25104150	NOTEST	0.0112853	0.0615955	2.44838	0	1	1
ENSG00000187461	ENSG00000187461	AL583828.1	6:13358061-13487894	NOTEST	0	0	0	0	1	1
ENSG00000187472	ENSG00000187472	RP11-67P15.1	6:99228132-99241868	NOTEST	0	0	0	0	1	1
ENSG00000187474	ENSG00000187474	FPR3	19:52248424-52329442	NOTEST	0	0	0	0	1	1
ENSG00000187475	ENSG00000187475	HIST1H1T	6:26107639-26108364	NOTEST	0.0492689	0	#NAME?	0	1	1
ENSG00000187481	ENSG00000187481	HSD3BP1	1:120009843-120016426	NOTEST	0.0158004	0.186993	3.56495	0	1	1
ENSG00000187483	ENSG00000187483	SERPINA13P	14:95107061-95113331	NOTEST	0	0	0	0	1	1

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ENSG00000187486	ENSG00000187486	KCNJ11	11:17407405-17410878	NOTEST	0	0	0	0	1	1
ENSG00000187492	ENSG00000187492	CDHR4	3:49828164-49837268	NOTEST	0	0	0	0	1	1
ENSG00000187504	ENSG00000187504	RPL7P48	17:49579848-49580594	NOTEST	0	0	0	0	1	1
ENSG00000187510	ENSG00000187510	PLEKHG7	12:93115280-93323107	NOTEST	0	0	0	0	1	1
ENSG00000187513	ENSG00000187513	GJA4	1:35178337-35325417	NOTEST	0	0	0	0	1	1
ENSG00000187516	ENSG00000187516	CXorf27	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000187527	ENSG00000187527	ATP13A5	3:192958913-193096632	NOTEST	0	0	0	0	1	1
ENSG00000187533	ENSG00000187533	C4orf40	4:70999332-71042516	NOTEST	0	0.00225884	inf	0	1	1
ENSG00000187536	ENSG00000187536	TPM3P7	2:25956621-26101385	NOTEST	0	0	0	0	1	1
ENSG00000187537	ENSG00000187537	POTEM	14:19983558-20020272	NOTEST	0	0.00167403	inf	0	1	1
ENSG00000187545	ENSG00000187545	PRAMEF10	1:12952726-12958101	NOTEST	0	0	0	0	1	1
ENSG00000187546	ENSG00000187546	AGMO	7:15239942-15601640	NOTEST	0.310514	0.0934074	-1.73305	0	1	1
ENSG00000187550	ENSG00000187550	SBK2	19:56041099-56048456	NOTEST	0	0	0	0	1	1
ENSG00000187553	ENSG00000187553	CYP26C1	10:94821020-94828454	NOTEST	0.0511496	0.0473309	-0.111939	0	1	1
ENSG00000187554	ENSG00000187554	TLR5	1:223282747-223316624	NOTEST	0.185474	0.192786	0.05578	0	1	1
ENSG00000187556	ENSG00000187556	NANOS3	19:13972876-13991571	NOTEST	0.11246	0.136043	0.274643	0	1	1
ENSG00000187559	ENSG00000187559	FOXD4L3	9:70917275-70920000	NOTEST	0	0	0	0	1	1
ENSG00000187569	ENSG00000187569	DPPA3	12:7864049-7870155	NOTEST	0	0	0	0	1	1
ENSG00000187581	ENSG00000187581	COX8C	14:93799564-94174222	NOTEST	0	0	0	0	1	1
ENSG00000187583	ENSG00000187583	PLEKHN1	1:901876-917497	NOTEST	0.390104	0.603346	0.629128	0	1	1
ENSG00000187589	ENSG00000187589	TERF1P2	18:14377544-14378756	NOTEST	0	0.0113564	inf	0	1	1
ENSG00000187595	ENSG00000187595	ZNF385C	17:40118758-40217383	NOTEST	0.276146	0.405599	0.554621	0	1	1
ENSG00000187600	ENSG00000187600	TMEM247	2:46656328-46711564	NOTEST	0	0	0	0	1	1
ENSG00000187612	ENSG00000187612	OR5W2	11:55681125-55682058	NOTEST	0	0	0	0	1	1
ENSG00000187616	ENSG00000187616	TMEM8C	9:136379707-136393734	NOTEST	0	0	0	0	1	1
ENSG00000187621	ENSG00000187621	TCL6	14:96116834-96158980	NOTEST	0.113525	0	#NAME?	0	1	1
ENSG00000187627	ENSG00000187627	RGPD1	2:87098423-87248975	NOTEST	0.0565783	0.100145	0.823772	0	1	1
ENSG00000187634	ENSG00000187634	SAMD11	1:860259-894689	NOTEST	0.0850664	0.269563	1.66396	0	1	1
ENSG00000187653	ENSG00000187653	TMSB4XP8	4:91048685-92523064	NOTEST	0.317179	0.0911103	-1.79961	0	1	1
ENSG00000187657	ENSG00000187657	TSPY13P	Y:9743203-9745748	NOTEST	0	0	0	0	1	1
ENSG00000187658	ENSG00000187658	C5orf52	5:157098560-157107151	NOTEST	0	0	0	0	1	1
ENSG00000187664	ENSG00000187664	HAPLN4	19:19366449-19384200	NOTEST	0	0.00317335	inf	0	1	1
ENSG00000187672	ENSG00000187672	ERC2	3:55542335-56502391	NOTEST	0.104121	0.103268	-0.0118601	0	1	1
ENSG00000187682	ENSG00000187682	ERAS	X:48687282-48688548	NOTEST	0	0	0	0	1	1
ENSG00000187686	ENSG00000187686	KRT18P59	11:124983056-124996677	NOTEST	0.00937837	0.0170937	0.866054	0	1	1
ENSG00000187689	ENSG00000187689	AMTN	4:71384256-71398459	NOTEST	0	0	0	0	1	1
ENSG00000187690	ENSG00000187690	CXorf67	X:51139362-51208513	NOTEST	0.00848642	0.0125581	0.565395	0	1	1
ENSG00000187695	ENSG00000187695	RP11-723O4.6	3:128598438-128759585	NOTEST	0.00711612	0.00590757	-0.268525	0	1	1
ENSG00000187701	ENSG00000187701	OR2T27	1:248813231-248814185	NOTEST	0	0	0	0	1	1
ENSG00000187714	ENSG00000187714	SLC18A3	10:50817140-50918307	NOTEST	0	0	0	0	1	1
ENSG00000187715	ENSG00000187715	KBTBD12	3:127634074-127706514	NOTEST	0	0	0	0	1	1
ENSG00000187721	ENSG00000187721	GTF2IP3	13:19520894-19636858	NOTEST	0	0	0	0	1	1
ENSG00000187726	ENSG00000187726	DNAJB13	11:73661363-73681411	NOTEST	0	0	0	0	1	1
ENSG00000187730	ENSG00000187730	GABRD	1:1950779-1962192	NOTEST	0	0	0	0	1	1
ENSG00000187733	ENSG00000187733	AMY1C	1:104293027-104301312	NOTEST	0	0	0	0	1	1

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ENSG00000187747	ENSG00000187747	OR52B6	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000187753	ENSG00000187753	C9orf153	9:88835179-88874572	NOTEST	0.00887174	0.0919328	3.37329	0	1	1
ENSG00000187754	ENSG00000187754	SSX7	X:52673139-52683950	NOTEST	0	0	0	0	1	1
ENSG00000187758	ENSG00000187758	ADH1A	4:100010007-100222513	NOTEST	0	0	0	0	1	1
ENSG00000187762	ENSG00000187762	HSPE1P11	6:34857041-35059179	NOTEST	0.105504	0.0826268	-0.352612	0	1	1
ENSG00000187763	ENSG00000187763	OR2B7P	6:28014211-28015145	NOTEST	0	0	0	0	1	1
ENSG00000187764	ENSG00000187764	SEMA4D	9:91975701-92113045	NOTEST	0.49351	0.366071	-0.430956	0	1	1
ENSG00000187766	ENSG00000187766	KRTAP10-8	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000187772	ENSG00000187772	LIN28B	6:105404922-105531207	NOTEST	0.0317718	0.0708976	1.15799	0	1	1
ENSG00000187783	ENSG00000187783	TMEM72	10:45306471-45491339	NOTEST	0	0	0	0	1	1
ENSG00000187786	ENSG00000187786	SCXB	8:145317002-145331153	NOTEST	0	0	0	0	1	1
ENSG00000187791	ENSG00000187791	FAM205CP	9:34889060-34895775	NOTEST	0	0	0	0	1	1
ENSG00000187796	ENSG00000187796	CARD9	9:139221931-139268133	NOTEST	0.0543983	0.039587	-0.458534	0	1	1
ENSG00000187800	ENSG00000187800	PEAR1	1:156863489-156886226	NOTEST	0.0685209	0.00484763	-3.82119	0	1	1
ENSG00000187806	ENSG00000187806	TMEM202	15:72690613-72879692	NOTEST	0	0	0	0	1	1
ENSG00000187808	ENSG00000187808	SOWAHD	X:118892575-118894164	NOTEST	0.368866	0.489185	0.407283	0	1	1
ENSG00000187811	ENSG00000187811	AP000867.1	11:71292900-71319086	NOTEST	0	0	0	0	1	1
ENSG00000187812	ENSG00000187812	RP11-24M17.5	15:76067893-76079239	NOTEST	0	0	0	0	1	1
ENSG00000187821	ENSG00000187821	HELT	4:185939994-185941958	NOTEST	0	0	0	0	1	1
ENSG00000187823	ENSG00000187823	ZCCHC16	X:111697726-111700473	NOTEST	0	0	0	0	1	1
ENSG00000187824	ENSG00000187824	TMEM220	17:10583653-10718481	NOTEST	0.496202	0.476508	-0.0584278	0	1	1
ENSG00000187833	ENSG00000187833	C2orf78	2:74011315-74044274	NOTEST	0	0.00362775	inf	0	1	1
ENSG00000187847	ENSG00000187847	OR7E25P	19:9314983-9315893	NOTEST	0	0	0	0	1	1
ENSG00000187848	ENSG00000187848	P2RX2	12:133195365-133198972	NOTEST	0	0.00789507	inf	0	1	1
ENSG00000187855	ENSG00000187855	ASCL4	12:108168161-108170421	NOTEST	0	0	0	0	1	1
ENSG00000187857	ENSG00000187857	OR6C75	12:55758894-55759833	NOTEST	0	0	0	0	1	1
ENSG00000187862	ENSG00000187862	TTC24	1:156549518-156556562	NOTEST	0.00825037	0	#NAME?	0	1	1
ENSG00000187867	ENSG00000187867	PALM3	19:14164176-14169971	NOTEST	0.0734644	0.170918	1.21819	0	1	1
ENSG00000187870	ENSG00000187870	RNFT1P3	17:20646645-20657814	NOTEST	0	0	0	0	1	1
ENSG00000187871	ENSG00000187871	GFRAL	6:55192266-55267291	NOTEST	0	0.00599811	inf	0	1	1
ENSG00000187889	ENSG00000187889	C1orf168	1:57184476-57285369	NOTEST	0.00750026	0	#NAME?	0	1	1
ENSG00000187893	ENSG00000187893	CXXC1P1	X:47566589-47612855	NOTEST	0	0	0	0	1	1
ENSG00000187900	ENSG00000187900	OR5H7P	3:97952494-98176742	NOTEST	0	0	0	0	1	1
ENSG00000187902	ENSG00000187902	SHISA7	19:55940106-55954230	NOTEST	0.0194074	0.0144746	-0.423079	0	1	1
ENSG00000187904	ENSG00000187904	AC097382.5	4:6910968-7059679	NOTEST	0.0654247	0.0250512	-1.38495	0	1	1
ENSG00000187905	ENSG00000187905	AC002472.13	22:21400248-21418457	NOTEST	0	0	0	0	1	1
ENSG00000187908	ENSG00000187908	DMBT1	10:124320180-124403252	NOTEST	0.00763276	0.0104514	0.453416	0	1	1
ENSG00000187912	ENSG00000187912	CLEC17A	19:14693895-14721969	NOTEST	0.03891	0.00971405	-2.002	0	1	1
ENSG00000187918	ENSG00000187918	OR51I2	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000187922	ENSG00000187922	LCN10	9:139632618-139642980	NOTEST	0.10073	0.522583	2.37517	0	1	1
ENSG00000187942	ENSG00000187942	LDLRAD2	1:22138757-22263790	NOTEST	0.128793	0.0810412	-0.668325	0	1	1
ENSG00000187944	ENSG00000187944	C2orf66	2:197669725-197675000	NOTEST	0.136953	0.0944779	-0.535628	0	1	1
ENSG00000187950	ENSG00000187950	OVCH1	12:29542226-29650619	NOTEST	0.0570301	0.0657287	0.2048	0	1	1
ENSG00000187952	ENSG00000187952	HS6ST1P1	1:21754795-21756030	NOTEST	0.336297	0.352822	0.0692041	0	1	1
ENSG00000187957	ENSG00000187957	DNER	2:230222344-230579274	NOTEST	0.251486	0.53444	1.08755	0	1	1

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ENSG00000187959	ENSG00000187959	CPSF4L	17:71161115-71258491	NOTEST	0	0.00946756	inf	0	1	1
ENSG00000187969	ENSG00000187969	ZCCHC13	X:73524024-73524868	NOTEST	0	0	0	0	1	1
ENSG00000187979	ENSG00000187979	AC008079.9	22:18660804-18688682	NOTEST	0	0	0	0	1	1
ENSG00000187980	ENSG00000187980	PLA2G2C	1:20487745-20503917	NOTEST	0	0	0	0	1	1
ENSG00000187984	ENSG00000187984	ANKRD19P	9:95571669-95661890	NOTEST	0.0665324	0.0694097	0.0610793	0	1	1
ENSG00000187987	ENSG00000187987	ZSCAN23	6:28399706-28411279	NOTEST	0.075518	0.0877272	0.216204	0	1	1
ENSG00000187988	ENSG00000187988	RP11-405L18.2	9:37477145-37478314	NOTEST	0.154371	0.0518562	-1.57382	0	1	1
ENSG00000187990	ENSG00000187990	HIST1H2BG	6:26216427-26216872	NOTEST	0.460952	0.207622	-1.15066	0	1	1
ENSG00000187997	ENSG00000187997	C17orf99	17:76142433-76162258	NOTEST	0	0	0	0	1	1
ENSG00000187999	ENSG00000187999	HNRNPA1P61	2:33861568-33862492	NOTEST	0	0	0	0	1	1
ENSG00000188000	ENSG00000188000	OR7D2	19:9296278-9299493	NOTEST	0.00487867	0	#NAME?	0	1	1
ENSG00000188001	ENSG00000188001	TPRG1	3:188659503-189043093	NOTEST	0.130604	0.0568643	-1.1996	0	1	1
ENSG00000188011	ENSG00000188011	CXXC11	2:242811751-242815975	NOTEST	0	0	0	0	1	1
ENSG00000188029	ENSG00000188029	CTSL3P	9:90387367-90401799	NOTEST	0	0	0	0	1	1
ENSG00000188032	ENSG00000188032	C19orf67	19:14192430-14196687	NOTEST	0.0118246	0	#NAME?	0	1	1
ENSG00000188037	ENSG00000188037	CLCN1	7:143013218-143049176	NOTEST	0	0	0	0	1	1
ENSG00000188038	ENSG00000188038	NRN1L	16:67906925-67922758	NOTEST	0.00848386	0	#NAME?	0	1	1
ENSG00000188039	ENSG00000188039	NWD1	19:16830786-16928774	NOTEST	0	0	0	0	1	1
ENSG00000188050	ENSG00000188050	RNF133	7:121958480-122526813	NOTEST	0.0233151	0.0181213	-0.363581	0	1	1
ENSG00000188051	ENSG00000188051	TMEM221	19:17546317-17571763	NOTEST	0.025329	0.00593316	-2.09392	0	1	1
ENSG00000188056	ENSG00000188056	TREML4	6:41196061-41206620	NOTEST	0	0	0	0	1	1
ENSG00000188060	ENSG00000188060	RAB42	1:28915834-28969597	NOTEST	0.00834807	0	#NAME?	0	1	1
ENSG00000188064	ENSG00000188064	WNT7B	22:46316241-46373009	NOTEST	0	0	0	0	1	1
ENSG00000188069	ENSG00000188069	OR51F1	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000188073	ENSG00000188073	PMS2P10	7:74880904-74988262	NOTEST	0.0238804	0.0712853	1.57778	0	1	1
ENSG00000188076	ENSG00000188076	SCGB1C1	11:127114-207428	NOTEST	0	0	0	0	1	1
ENSG00000188078	ENSG00000188078	RP5-1119A7.1	22:36932702-36933651	NOTEST	0	0	0	0	1	1
ENSG00000188086	ENSG00000188086	PRSS45	3:46753604-46854064	NOTEST	0	0	0	0	1	1
ENSG00000188089	ENSG00000188089	PLA2G4E	15:42264960-42343388	NOTEST	0	0	0	0	1	1
ENSG00000188095	ENSG00000188095	MESP2	15:90303821-90321982	NOTEST	0.238026	0.42638	0.841021	0	1	1
ENSG00000188100	ENSG00000188100	FAM25A	10:88695296-88784489	NOTEST	0	0	0	0	1	1
ENSG00000188101	ENSG00000188101	ALOX15P2	9:95675437-95683842	NOTEST	0	0	0	0	1	1
ENSG00000188107	ENSG00000188107	EYS	6:64345724-66417118	NOTEST	0.035763	0.0467943	0.387866	0	1	1
ENSG00000188112	ENSG00000188112	C6orf132	6:42068855-42110357	NOTEST	0	0.00172507	inf	0	1	1
ENSG00000188120	ENSG00000188120	DAZ1	Y:25275501-25345241	NOTEST	0	0	0	0	1	1
ENSG00000188124	ENSG00000188124	OR2AG2	11:6789217-6790286	NOTEST	0	0	0	0	1	1
ENSG00000188133	ENSG00000188133	TMEM215	9:32783496-32787397	NOTEST	0.283476	0.379777	0.421926	0	1	1
ENSG00000188152	ENSG00000188152	NUTM2G	9:99660347-99775862	NOTEST	0.233446	0.208163	-0.165372	0	1	1
ENSG00000188155	ENSG00000188155	KRTAP10-6	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000188158	ENSG00000188158	NHS	X:17393542-17754114	NOTEST	0	0	0	0	1	1
ENSG00000188162	ENSG00000188162	OTOG	11:17568919-17668697	NOTEST	0	0	0	0	1	1
ENSG00000188163	ENSG00000188163	FAM166A	9:140135664-140142222	NOTEST	0.118068	0.0901643	-0.388984	0	1	1
ENSG00000188171	ENSG00000188171	ZNF626	19:20718630-20844402	NOTEST	0.0595442	0.00179869	-5.04894	0	1	1
ENSG00000188175	ENSG00000188175	HEPACAM2	7:92817898-92855837	NOTEST	0.00785715	0	#NAME?	0	1	1
ENSG00000188176	ENSG00000188176	SMTNL2	17:4487293-4511614	NOTEST	0	0.00660156	inf	0	1	1

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ENSG00000188199	ENSG00000188199	NUTM2B	10:81420646-81526085	NOTEST	0.031269	0.0620802	0.989399	0	1	1
ENSG00000188219	ENSG00000188219	POTEE	2:131862419-132111282	NOTEST	0	0	0	0	1	1
ENSG00000188227	ENSG00000188227	ZNF793	19:37988062-38210691	NOTEST	0.0575381	0.0867346	0.592091	0	1	1
ENSG00000188257	ENSG00000188257	PLA2G2A	1:20301924-20306932	NOTEST	0	0	0	0	1	1
ENSG00000188263	ENSG00000188263	IL17REL	22:50432941-50451088	NOTEST	0	0	0	0	1	1
ENSG00000188277	ENSG00000188277	C15orf62	15:41060066-41106767	NOTEST	0.38226	0.329921	-0.212435	0	1	1
ENSG00000188279	ENSG00000188279	FAM25C	10:49199648-49207818	NOTEST	0	0	0	0	1	1
ENSG00000188280	ENSG00000188280	FAM230A	22:20692437-20745048	NOTEST	0.00171026	0.0013283	-0.364638	0	1	1
ENSG00000188282	ENSG00000188282	RUFY4	2:218899682-218955304	NOTEST	0	0.0187587	inf	0	1	1
ENSG00000188293	ENSG00000188293	IGFL1	19:46732220-46734500	NOTEST	0	0	0	0	1	1
ENSG00000188305	ENSG00000188305	C19orf35	19:2274630-2282181	NOTEST	0	0.034738	inf	0	1	1
ENSG00000188306	ENSG00000188306	LRRIQ4	3:169539709-169555563	NOTEST	0.0504459	0.041862	-0.269094	0	1	1
ENSG00000188314	ENSG00000188314	OR7D1P	19:9345819-9346812	NOTEST	0	0	0	0	1	1
ENSG00000188316	ENSG00000188316	ENO4	10:118592511-118886097	NOTEST	0.408217	0.16932	-1.26959	0	1	1
ENSG00000188322	ENSG00000188322	SBK1	16:28303839-28335170	NOTEST	0.120871	0.0662517	-0.867443	0	1	1
ENSG00000188324	ENSG00000188324	OR6C6	12:55677533-55706860	NOTEST	0	0	0	0	1	1
ENSG00000188334	ENSG00000188334	BSPH1	19:48471302-48495427	NOTEST	0	0	0	0	1	1
ENSG00000188338	ENSG00000188338	SLC38A3	3:50242678-50258411	NOTEST	0	0.0396555	inf	0	1	1
ENSG00000188340	ENSG00000188340	OR6N2	1:158746471-158747425	NOTEST	0	0	0	0	1	1
ENSG00000188365	ENSG00000188365	AC092171.2	7:5313999-5465045	NOTEST	0	0	0	0	1	1
ENSG00000188373	ENSG00000188373	C10orf99	10:85933493-85945050	NOTEST	0	0	0	0	1	1
ENSG00000188375	ENSG00000188375	H3F3C	12:31944122-31945175	NOTEST	0.0168396	0	#NAME?	0	1	1
ENSG00000188379	ENSG00000188379	IFNA2	9:21384253-21385396	NOTEST	0	0	0	0	1	1
ENSG00000188383	ENSG00000188383	AC018892.9	2:97746834-97748986	NOTEST	0.438308	0.130293	-1.75018	0	1	1
ENSG00000188384	ENSG00000188384	CSPG4P8	15:82751613-82798350	NOTEST	0	0	0	0	1	1
ENSG00000188385	ENSG00000188385	JAKMIP3	10:133918174-133999466	NOTEST	0.0186239	0.00555098	-1.74634	0	1	1
ENSG00000188386	ENSG00000188386	PPP3R2	9:104331634-104500862	NOTEST	0	0	0	0	1	1
ENSG00000188388	ENSG00000188388	GOLGA6L3	15:85783702-85790410	NOTEST	0.471267	0.270765	-0.799502	0	1	1
ENSG00000188389	ENSG00000188389	PDCD1	2:242792032-242801060	NOTEST	0	0	0	0	1	1
ENSG00000188393	ENSG00000188393	CLEC2A	12:10051271-10084980	NOTEST	0	0	0	0	1	1
ENSG00000188394	ENSG00000188394	GPR21	9:125703111-125867145	NOTEST	0	0	0	0	1	1
ENSG00000188396	ENSG00000188396	TCTEX1D4	1:45265896-45272957	NOTEST	0.0816793	0.0718017	-0.185952	0	1	1
ENSG00000188399	ENSG00000188399	ANKRD36P1	Y:28555961-28566682	NOTEST	0	0	0	0	1	1
ENSG00000188403	ENSG00000188403	IGHV1OR15-9	15:20169918-20170354	NOTEST	0	0	0	0	1	1
ENSG00000188404	ENSG00000188404	SELL	1:169631244-169863408	NOTEST	0.32582	0.458562	0.493043	0	1	1
ENSG00000188408	ENSG00000188408	MAGEB5	X:26234285-26236387	NOTEST	0	0	0	0	1	1
ENSG00000188424	ENSG00000188424	XXbac-B33L19.3	22:20326327-20350457	NOTEST	0	0	0	0	1	1
ENSG00000188425	ENSG00000188425	NANOS2	19:46416474-46418036	NOTEST	0.0581313	0.00750787	-2.95284	0	1	1
ENSG00000188438	ENSG00000188438	RP11-1396O13.14	4:9400929-9405291	NOTEST	0	0	0	0	1	1
ENSG00000188439	ENSG00000188439	OR4P1P	11:55450714-55453636	NOTEST	0	0	0	0	1	1
ENSG00000188451	ENSG00000188451	SRP72P2	6:158658367-158663829	NOTEST	0	0	0	0	1	1
ENSG00000188460	ENSG00000188460	ACTBP11	1:224051427-224052553	NOTEST	0	0	0	0	1	1
ENSG00000188474	ENSG00000188474	ZNF788	19:12203077-12267546	NOTEST	0.284951	0.25148	-0.180269	0	1	1
ENSG00000188477	ENSG00000188477	AC003003.5	16:19297060-19333467	NOTEST	0	0	0	0	1	1

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ENSG00000188487	ENSG00000188487	INSC	11:15133969-15268754	NOTEST	0.0105681	0.025486	1.26999	0	1	1
ENSG00000188488	ENSG00000188488	SERPINA5	14:95027427-95090983	NOTEST	0.0564553	0.0986204	0.804776	0	1	1
ENSG00000188508	ENSG00000188508	KRTDAP	19:35978225-35986460	NOTEST	0.094601	0	#NAME?	0	1	1
ENSG00000188511	ENSG00000188511	C22orf34	22:49808175-50051190	NOTEST	0.0206303	0	#NAME?	0	1	1
ENSG00000188512	ENSG00000188512	RP1-273G13.2	8:33462373-33896526	NOTEST	0	0.155297	inf	0	1	1
ENSG00000188523	ENSG00000188523	C9orf171	9:135285429-135448704	NOTEST	0.126092	0.152352	0.272935	0	1	1
ENSG00000188525	ENSG00000188525	AC010969.1	2:10143285-10146158	NOTEST	0	0	0	0	1	1
ENSG00000188536	ENSG00000188536	HBA2	16:222845-223709	NOTEST	0	0	0	0	1	1
ENSG00000188558	ENSG00000188558	OR2G6	1:248684915-248685964	NOTEST	0	0	0	0	1	1
ENSG00000188573	ENSG00000188573	FBLL1	5:167956120-167957639	NOTEST	0.26611	0.331852	0.318516	0	1	1
ENSG00000188580	ENSG00000188580	NKAIN2	6:124125285-125146803	NOTEST	0.00911561	0	#NAME?	0	1	1
ENSG00000188581	ENSG00000188581	KRTAP1-1	17:39196810-39197713	NOTEST	0	0.0605147	inf	0	1	1
ENSG00000188582	ENSG00000188582	PAQR9	3:142668005-142779567	NOTEST	0.242462	0.50087	1.04667	0	1	1
ENSG00000188585	ENSG00000188585	LINC00083	1:178465030-178468769	NOTEST	0	0	0	0	1	1
ENSG00000188596	ENSG00000188596	C12orf55	12:96883348-97269333	NOTEST	0.101092	0.207837	1.03978	0	1	1
ENSG00000188611	ENSG00000188611	ASAH2	10:51942537-52008370	NOTEST	0.416921	0.206751	-1.01188	0	1	1
ENSG00000188620	ENSG00000188620	HMX3	10:124895477-124897257	NOTEST	0	0	0	0	1	1
ENSG00000188624	ENSG00000188624	IGFL3	19:46604379-46706340	NOTEST	0	0	0	0	1	1
ENSG00000188626	ENSG00000188626	GOLGA8M	15:28947099-29002537	NOTEST	0.10785	0.142677	0.403719	0	1	1
ENSG00000188629	ENSG00000188629	ZNF177	19:9434447-9493293	NOTEST	0.37521	0.435037	0.213439	0	1	1
ENSG00000188646	ENSG00000188646	RP11-361A23.2	12:75057553-75057921	NOTEST	0	0	0	0	1	1
ENSG00000188649	ENSG00000188649	CC2D2B	10:97471535-97849995	NOTEST	0.192242	0.139494	-0.462721	0	1	1
ENSG00000188655	ENSG00000188655	RNASE9	14:21024251-21029090	NOTEST	0	0	0	0	1	1
ENSG00000188656	ENSG00000188656	TSPY7P	Y:9195405-9235047	NOTEST	0	0	0	0	1	1
ENSG00000188659	ENSG00000188659	FAM154B	15:82555150-82577271	NOTEST	0.49431	0.522667	0.0804784	0	1	1
ENSG00000188660	ENSG00000188660	LINC00319	21:44866480-44873773	NOTEST	0.00524146	0.00368033	-0.510132	0	1	1
ENSG00000188668	ENSG00000188668	OR7E90P	2:159731153-159732182	NOTEST	0	0	0	0	1	1
ENSG00000188672	ENSG00000188672	RHCE	1:25568727-25756683	NOTEST	0.106635	0.0432679	-1.30131	0	1	1
ENSG00000188674	ENSG00000188674	C2orf80	2:209030066-209054797	NOTEST	0.143316	0.116807	-0.295073	0	1	1
ENSG00000188676	ENSG00000188676	IDO2	8:39759793-39873910	NOTEST	0	0	0	0	1	1
ENSG00000188686	ENSG00000188686	SCXA	8:145486054-145515082	NOTEST	0.101351	0.123046	0.279828	0	1	1
ENSG00000188687	ENSG00000188687	SLC4A5	2:74425688-74621009	NOTEST	0.316413	0.546112	0.787387	0	1	1
ENSG00000188691	ENSG00000188691	RP11-451K18.7	11:5988406-5989724	NOTEST	0	0	0	0	1	1
ENSG00000188693	ENSG00000188693	CTB-161K23.1	7:91741464-91810039	NOTEST	0.0106667	0	#NAME?	0	1	1
ENSG00000188694	ENSG00000188694	KRTAP24-1	21:31653628-31655276	NOTEST	0	0	0	0	1	1
ENSG00000188707	ENSG00000188707	ZBED6CL	7:149941004-150035239	NOTEST	0.201607	0.246709	0.291266	0	1	1
ENSG00000188710	ENSG00000188710	QRFP	9:133768814-133769225	NOTEST	0.363961	0.0482442	-2.91536	0	1	1
ENSG00000188712	ENSG00000188712	OR13D3P	9:107484615-107485552	NOTEST	0	0	0	0	1	1
ENSG00000188716	ENSG00000188716	DUPD1	10:76797593-76818272	NOTEST	0	0	0	0	1	1
ENSG00000188722	ENSG00000188722	AL391005.1	10:129534322-129534969	NOTEST	0	0	0	0	1	1
ENSG00000188729	ENSG00000188729	OSTN	3:190917029-190983404	NOTEST	0	0	0	0	1	1
ENSG00000188730	ENSG00000188730	VWC2	7:49813256-50199426	NOTEST	0	0	0	0	1	1
ENSG00000188738	ENSG00000188738	FSIP2	2:186584600-186698017	NOTEST	0.0585032	0.0142434	-2.03822	0	1	1
ENSG00000188747	ENSG00000188747	NOXA1	9:140317801-140336268	NOTEST	0.168217	0.304366	0.855478	0	1	1

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ENSG00000188755	ENSG00000188755	TBC1D3P2	17:60342065-60374387	NOTEST	0	0	0	0	1	1
ENSG00000188761	ENSG00000188761	BCL2L15	1:114304453-114456708	NOTEST	0.0270376	0.0397999	0.557795	0	1	1
ENSG00000188765	ENSG00000188765	TMSB4XP2	2:3642425-3692048	NOTEST	0	0	0	0	1	1
ENSG00000188766	ENSG00000188766	SPRED3	19:38879060-38886881	NOTEST	0.368318	0.612691	0.734209	0	1	1
ENSG00000188770	ENSG00000188770	OPTC	1:203463270-203477992	NOTEST	0	0.02707	inf	0	1	1
ENSG00000188771	ENSG00000188771	PLET1	11:112097087-112140678	NOTEST	0	0	0	0	1	1
ENSG00000188778	ENSG00000188778	ADRB3	8:37820515-37824483	NOTEST	0	0	0	0	1	1
ENSG00000188779	ENSG00000188779	SKOR1	15:68112041-68166204	NOTEST	0.0150437	0.0291666	0.955163	0	1	1
ENSG00000188782	ENSG00000188782	CATSPER4	1:26517051-26529459	NOTEST	0	0	0	0	1	1
ENSG00000188784	ENSG00000188784	PLA2G2E	1:20246501-20250110	NOTEST	0	0	0	0	1	1
ENSG00000188800	ENSG00000188800	TMCO2	1:40711618-40717363	NOTEST	0	0	0	0	1	1
ENSG00000188801	ENSG00000188801	ZNF322P1	9:99918851-100140806	NOTEST	0.155366	0.118377	-0.392283	0	1	1
ENSG00000188803	ENSG00000188803	SHISA6	17:11144579-11467380	NOTEST	0	0	0	0	1	1
ENSG00000188816	ENSG00000188816	HMX2	10:124907637-124910188	NOTEST	0.0184924	0	#NAME?	0	1	1
ENSG00000188817	ENSG00000188817	SNTN	3:63638343-63664696	NOTEST	0	0	0	0	1	1
ENSG00000188822	ENSG00000188822	CNR2	1:24197015-24285549	NOTEST	0.00291814	0	#NAME?	0	1	1
ENSG00000188828	ENSG00000188828	GLRA4	X:102962151-102983583	NOTEST	0	0.00710641	inf	0	1	1
ENSG00000188831	ENSG00000188831	DPPA3P2	14:36840369-36841588	NOTEST	0	0	0	0	1	1
ENSG00000188833	ENSG00000188833	ENTPD8	9:140317801-140336268	NOTEST	0.0247193	0.017843	-0.470283	0	1	1
ENSG00000188848	ENSG00000188848	BEND4	4:42112954-42154895	NOTEST	0.00313612	0	#NAME?	0	1	1
ENSG00000188850	ENSG00000188850	RP11-159F24.2	5:43336265-43348818	NOTEST	0	0	0	0	1	1
ENSG00000188856	ENSG00000188856	RPSAP47	8:81471104-81471992	NOTEST	0.0207156	0.0161116	-0.362617	0	1	1
ENSG00000188868	ENSG00000188868	ZNF563	19:12428290-12444534	NOTEST	0.0622784	0.0818857	0.394879	0	1	1
ENSG00000188869	ENSG00000188869	TMC3	15:81616717-81666554	NOTEST	0.256808	0.256527	-0.00158167	0	1	1
ENSG00000188873	ENSG00000188873	RPL10AP2	8:48001194-48110484	NOTEST	0.0615098	0	#NAME?	0	1	1
ENSG00000188877	ENSG00000188877	POTEA	8:43147625-43218661	NOTEST	0	0	0	0	1	1
ENSG00000188883	ENSG00000188883	KLRG2	7:139137435-139168458	NOTEST	0.00733024	0.0396766	2.43636	0	1	1
ENSG00000188886	ENSG00000188886	ASTL	2:96789588-96804175	NOTEST	0	0	0	0	1	1
ENSG00000188888	ENSG00000188888	GPR179	17:36481412-36499730	NOTEST	0.0407678	0.0068356	-2.57629	0	1	1
ENSG00000188897	ENSG00000188897	CTD-3088G3.8	16:11453701-11617444	NOTEST	0.213544	0.289476	0.438908	0	1	1
ENSG00000188909	ENSG00000188909	BSX	11:122848277-122852428	NOTEST	0	0	0	0	1	1
ENSG00000188910	ENSG00000188910	GJB3	1:35178337-35325417	NOTEST	0	0	0	0	1	1
ENSG00000188916	ENSG00000188916	FAM196A	10:128593977-129250781	NOTEST	0.00498622	0.0193963	1.95976	0	1	1
ENSG00000188921	ENSG00000188921	PTPLAD2	9:20658307-21031635	NOTEST	0.414874	0.40977	-0.0178579	0	1	1
ENSG00000188933	ENSG00000188933	USP32P1	17:16592850-16719854	NOTEST	0.157768	0.190452	0.271619	0	1	1
ENSG00000188937	ENSG00000188937	NYX	X:41306686-41334963	NOTEST	0.0139701	0.0688388	2.30088	0	1	1
ENSG00000188958	ENSG00000188958	UTS2B	3:190984956-191116459	NOTEST	0	0.137435	inf	0	1	1
ENSG00000188959	ENSG00000188959	C9orf152	9:112952327-112970469	NOTEST	0.010547	0.00906332	-0.218723	0	1	1
ENSG00000188981	ENSG00000188981	MSANTD1	4:3246095-3273465	NOTEST	0.0464145	0.0244823	-0.922836	0	1	1
ENSG00000188984	ENSG00000188984	AADACL3	1:12776117-12788726	NOTEST	0	0	0	0	1	1
ENSG00000188987	ENSG00000188987	HIST1H4D	6:26188937-26189304	NOTEST	0.151073	0	#NAME?	0	1	1
ENSG00000188991	ENSG00000188991	SLC15A5	12:16341418-16430619	NOTEST	0	0	0	0	1	1
ENSG00000188992	ENSG00000188992	LIPI	21:15399741-15583166	NOTEST	0	0	0	0	1	1
ENSG00000188993	ENSG00000188993	LRRC66	4:52859867-52883786	NOTEST	0.0235277	0.0315721	0.424293	0	1	1

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ENSG00000188996	ENSG00000188996	HUS1B	6:485132-693117	NOTEST	0.0665103	0.238168	1.84033	0	1	1
ENSG00000189001	ENSG00000189001	SBSN	19:36014268-36019253	NOTEST	0.104701	0.07623	-0.457842	0	1	1
ENSG00000189002	ENSG00000189002	PROSP	3:90251465-90306565	NOTEST	0.0151151	0	#NAME?	0	1	1
ENSG00000189013	ENSG00000189013	KIR2DL4	19:55235968-55378662	NOTEST	0	0	0	0	1	1
ENSG00000189014	ENSG00000189014	FAM35DP	10:47379726-47420712	NOTEST	0.0791974	0.208156	1.39414	0	1	1
ENSG00000189023	ENSG00000189023	MAGEB16	X:35816458-35821852	NOTEST	0	0	0	0	1	1
ENSG00000189030	ENSG00000189030	VHLL	1:156268414-156269428	NOTEST	0.0176188	0.0124144	-0.505101	0	1	1
ENSG00000189037	ENSG00000189037	DUSP21	X:44703248-44704130	NOTEST	0	0	0	0	1	1
ENSG00000189045	ENSG00000189045	ANKDD1B	5:74907283-74967671	NOTEST	0.125032	0.0568497	-1.13707	0	1	1
ENSG00000189051	ENSG00000189051	RNF222	17:8294021-8301144	NOTEST	0	0	0	0	1	1
ENSG00000189052	ENSG00000189052	CGB5	19:49526125-49552400	NOTEST	0	0	0	0	1	1
ENSG00000189056	ENSG00000189056	RELN	7:102937868-103629963	NOTEST	0.12164	0.0723995	-0.748567	0	1	1
ENSG00000189064	ENSG00000189064	GAGE2A	X:49354131-49361430	NOTEST	0	0	0	0	1	1
ENSG00000189068	ENSG00000189068	VSTM1	19:54544078-54567207	NOTEST	0	0	0	0	1	1
ENSG00000189089	ENSG00000189089	RIMKLBP1	21:37402367-37498938	NOTEST	0	0.053538	inf	0	1	1
ENSG00000189090	ENSG00000189090	FAM25B	10:47177203-47181681	NOTEST	0	0	0	0	1	1
ENSG00000189099	ENSG00000189099	PRSS48	4:152020724-152246784	NOTEST	0	0	0	0	1	1
ENSG00000189108	ENSG00000189108	IL1RAPL2	X:103810995-105011822	NOTEST	0	0	0	0	1	1
ENSG00000189120	ENSG00000189120	SP6	17:45922278-45933240	NOTEST	0.0122873	0.00318017	-1.95	0	1	1
ENSG00000189127	ENSG00000189127	ANKRD34B	5:79852573-79866307	NOTEST	0.0181783	0.0510534	1.48979	0	1	1
ENSG00000189129	ENSG00000189129	PLAC9	10:81891437-81905115	NOTEST	0.257718	0.422119	0.711859	0	1	1
ENSG00000189132	ENSG00000189132	FAM47B	X:34960912-34963034	NOTEST	0	0	0	0	1	1
ENSG00000189134	ENSG00000189134	NKAPL	6:28227097-28228736	NOTEST	0	0	0	0	1	1
ENSG00000189139	ENSG00000189139	FSCB	14:44973544-44976482	NOTEST	0	0	0	0	1	1
ENSG00000189143	ENSG00000189143	CLDN4	7:73213871-73247014	NOTEST	0.00899534	0.188949	4.39268	0	1	1
ENSG00000189145	ENSG00000189145	RP11-77G22.2	X:40767236-40767644	NOTEST	0	0	0	0	1	1
ENSG00000189149	ENSG00000189149	CRYM-AS1	16:21244985-21329912	NOTEST	0.380816	0.437613	0.200563	0	1	1
ENSG00000189152	ENSG00000189152	GRAPL	17:19030781-19062489	NOTEST	0	0	0	0	1	1
ENSG00000189157	ENSG00000189157	FAM47E	4:77135192-77232752	NOTEST	0.13438	0.236286	0.814218	0	1	1
ENSG00000189166	ENSG00000189166	TNRC18P3	7:57059594-57076856	NOTEST	0	0.014204	inf	0	1	1
ENSG00000189167	ENSG00000189167	ZAR1L	13:32877836-32889481	NOTEST	0	0	0	0	1	1
ENSG00000189169	ENSG00000189169	KRTAP10-12	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000189181	ENSG00000189181	OR14I1	1:248844627-248845629	NOTEST	0	0	0	0	1	1
ENSG00000189182	ENSG00000189182	KRT77	12:53083409-53097247	NOTEST	0	0	0	0	1	1
ENSG00000189186	ENSG00000189186	DCAF8L2	X:27608498-27766908	NOTEST	0.0379921	0	#NAME?	0	1	1
ENSG00000189195	ENSG00000189195	BTBD8	1:92545861-92613393	NOTEST	0.531381	0.318757	-0.737287	0	1	1
ENSG00000189196	ENSG00000189196	LINC00994	3:64053639-64440508	NOTEST	0	0.0053323	inf	0	1	1
ENSG00000189212	ENSG00000189212	DPY19L2P1	7:35119600-35225934	NOTEST	0.134285	0.222215	0.726653	0	1	1
ENSG00000189223	ENSG00000189223	PAX8-AS1	2:113969098-114036527	NOTEST	0.107465	0.111203	0.0493267	0	1	1
ENSG00000189229	ENSG00000189229	AC069277.2	3:6532165-7783215	NOTEST	0	0.012662	inf	0	1	1
ENSG00000189233	ENSG00000189233	NUGGC	8:27879480-27941388	NOTEST	0	0	0	0	1	1
ENSG00000189238	ENSG00000189238	LINC00943	12:127210815-127256957	NOTEST	0	0	0	0	1	1
ENSG00000189252	ENSG00000189252	SPANXN3	X:142372753-142605303	NOTEST	0.0354534	0	#NAME?	0	1	1
ENSG00000189253	ENSG00000189253	TRIM64B	11:89602449-89609185	NOTEST	0	0	0	0	1	1
ENSG00000189269	ENSG00000189269	C22orf43	22:23950638-24059543	NOTEST	0.0239218	0.051209	1.09807	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000189275	ENSG00000189275	AL450307.1	10:133604733-133622535	NOTEST	0	0	0	0	1	1
ENSG00000189280	ENSG00000189280	GJB5	1:35178337-35325417	NOTEST	0	0	0	0	1	1
ENSG00000189292	ENSG00000189292	FAM150B	2:279557-301515	NOTEST	0	0	0	0	1	1
ENSG00000189295	ENSG00000189295	ANKRD62P1-PARP4P3	22:17082776-17185367	NOTEST	0.151141	0.0348327	-2.11738	0	1	1
ENSG00000189299	ENSG00000189299	FOXR2	X:55649832-55652621	NOTEST	0	0.0207632	inf	0	1	1
ENSG00000189316	ENSG00000189316	RP11-797H7.5	7:64330549-64391344	NOTEST	0	0	0	0	1	1
ENSG00000189320	ENSG00000189320	FAM180A	7:135347243-135433594	NOTEST	0.0300158	0.040949	0.448108	0	1	1
ENSG00000189325	ENSG00000189325	C6orf222	6:36283533-36304662	NOTEST	0	0	0	0	1	1
ENSG00000189326	ENSG00000189326	SPANXN4	X:142113703-142122488	NOTEST	0	0	0	0	1	1
ENSG00000189332	ENSG00000189332	RP11-113D6.10	11:18230684-18236109	NOTEST	0	0.0210242	inf	0	1	1
ENSG00000189334	ENSG00000189334	S100A14	1:153586730-153589462	NOTEST	0.017506	0.0259687	0.568928	0	1	1
ENSG00000189348	ENSG00000189348	FAM90A27P	19:53784807-53788200	NOTEST	0	0	0	0	1	1
ENSG00000189350	ENSG00000189350	FAM179A	2:29179476-29297127	NOTEST	0.0389915	0.0118527	-1.71794	0	1	1
ENSG00000189357	ENSG00000189357	SPATA31D4	9:84542935-84592004	NOTEST	0	0	0	0	1	1
ENSG00000189366	ENSG00000189366	ALG1L	3:125635462-125655882	NOTEST	0.042938	0.0237659	-0.853358	0	1	1
ENSG00000189369	ENSG00000189369	GSPT2	X:51486480-51489324	NOTEST	0	0.0479736	inf	0	1	1
ENSG00000189372	ENSG00000189372	RP6-149D17.1	X:107334897-107682727	NOTEST	0	0	0	0	1	1
ENSG00000189375	ENSG00000189375	TBC1D28	17:18538318-18585575	NOTEST	0	0	0	0	1	1
ENSG00000189377	ENSG00000189377	CXCL17	19:42901279-43156507	NOTEST	0	0.0115348	inf	0	1	1
ENSG00000189393	ENSG00000189393	FAM90A14P	8:7572964-7575975	NOTEST	0	0	0	0	1	1
ENSG00000189398	ENSG00000189398	OR7E12P	11:3402190-3430208	NOTEST	0.0338135	0	#NAME?	0	1	1
ENSG00000189401	ENSG00000189401	OTUD6A	X:69282340-69284029	NOTEST	0	0	0	0	1	1
ENSG00000189409	ENSG00000189409	MMP23B	1:1567473-1590473	NOTEST	0	0	0	0	1	1
ENSG00000189419	ENSG00000189419	SPATA41	15:100884661-100890438	NOTEST	0.213044	0.201109	-0.0831736	0	1	1
ENSG00000189423	ENSG00000189423	USP32P3	17:20318859-20334321	NOTEST	0.23069	0.0545252	-2.08096	0	1	1
ENSG00000189430	ENSG00000189430	NCR1	19:55417507-55427508	NOTEST	0	0	0	0	1	1
ENSG00000189431	ENSG00000189431	RASSF10	11:13022636-13032647	NOTEST	0.187046	0.241932	0.371207	0	1	1
ENSG00000189433	ENSG00000189433	GJB4	1:35178337-35325417	NOTEST	0	0	0	0	1	1
ENSG00000194270	ENSG00000194270	Y_RNA	2:42721708-42984087	NOTEST	0	0	0	0	1	1
ENSG00000194297	ENSG00000194297	RNU1-75P	1:119870798-119898805	NOTEST	0	0	0	0	1	1
ENSG00000194717	ENSG00000194717	MIR494	14:101495970-101496051	NOTEST	0	0	0	0	1	1
ENSG00000195024	ENSG00000195024	RNU1-15P	7:21420980-21421124	NOTEST	0	0	0	0	1	1
ENSG00000195401	ENSG00000195401	Y_RNA	10:70480768-70552134	NOTEST	0	0	0	0	1	1
ENSG00000196071	ENSG00000196071	OR2L13	1:248099362-248264224	NOTEST	0.0524066	0.00686348	-2.93274	0	1	1
ENSG00000196081	ENSG00000196081	ZNF724P	19:23404400-23433192	NOTEST	0.533482	0.389529	-0.453706	0	1	1
ENSG00000196082	ENSG00000196082	AC140061.1	12:50706111-50706217	NOTEST	0	0	0	0	1	1
ENSG00000196085	ENSG00000196085	AC013442.1	2:35444442-35444670	NOTEST	0	0	0	0	1	1
ENSG00000196090	ENSG00000196090	PTPRT	20:40701391-41818610	NOTEST	0	0	0	0	1	1
ENSG00000196091	ENSG00000196091	MYBPC1	12:101962130-102079796	NOTEST	0.00857958	0.0685599	2.99839	0	1	1
ENSG00000196092	ENSG00000196092	PAX5	9:36833271-37034103	NOTEST	0	0	0	0	1	1
ENSG00000196095	ENSG00000196095	AC126182.1	3:120262891-120263292	NOTEST	0	0	0	0	1	1
ENSG00000196096	ENSG00000196096	AC079610.2	2:214141275-214148929	NOTEST	0	0	0	0	1	1
ENSG00000196098	ENSG00000196098	OR5K4	3:97952494-98176742	NOTEST	0	0	0	0	1	1
ENSG00000196099	ENSG00000196099	OR6M1	11:123676042-123677095	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000196101	ENSG00000196101	HLA-DRB3	HSCHR6_MHC_QBL:32417556-32430644	NOTEST	0	0	0	0	1	1
ENSG00000196104	ENSG00000196104	SPOCK3	4:167654534-168155947	NOTEST	0.184382	0.31316	0.764199	0	1	1
ENSG00000196109	ENSG00000196109	ZNF676	19:22361892-22379753	NOTEST	0.00968006	0.0117506	0.279644	0	1	1
ENSG00000196114	ENSG00000196114	RP3-391O22.3	6:34544034-34544433	NOTEST	0	0	0	0	1	1
ENSG00000196115	ENSG00000196115	ADAM5	8:39172109-39274897	NOTEST	0	0	0	0	1	1
ENSG00000196119	ENSG00000196119	OR8A1	11:124439892-124441037	NOTEST	0	0	0	0	1	1
ENSG00000196131	ENSG00000196131	VN1R2	19:53761544-53765090	NOTEST	0	0	0	0	1	1
ENSG00000196132	ENSG00000196132	MYT1	20:62783143-62873604	NOTEST	0.217825	0.422991	0.957456	0	1	1
ENSG00000196138	ENSG00000196138	AC005831.1	12:3715798-3873985	NOTEST	0	0	0	0	1	1
ENSG00000196139	ENSG00000196139	AKR1C3	10:5077545-5149878	NOTEST	0	0.0771608	inf	0	1	1
ENSG00000196143	ENSG00000196143	OR11H13P	14:19806436-19807415	NOTEST	0	0	0	0	1	1
ENSG00000196156	ENSG00000196156	KRTAP4-3	17:39323483-39324424	NOTEST	0	0	0	0	1	1
ENSG00000196166	ENSG00000196166	C8orf86	8:38368351-38386180	NOTEST	0	0	0	0	1	1
ENSG00000196167	ENSG00000196167	COLCA1	11:111164113-111179460	NOTEST	0.0107173	0.113389	3.40327	0	1	1
ENSG00000196169	ENSG00000196169	KIF19	17:72322348-72351959	NOTEST	0	0	0	0	1	1
ENSG00000196171	ENSG00000196171	OR6K2	1:158669368-158670486	NOTEST	0	0	0	0	1	1
ENSG00000196172	ENSG00000196172	ZNF681	19:23921996-23941693	NOTEST	0.0552972	0.161734	1.54834	0	1	1
ENSG00000196176	ENSG00000196176	HIST1H4A	6:26021906-26022278	NOTEST	0	0	0	0	1	1
ENSG00000196183	ENSG00000196183	RPS2P4	14:105302330-105303221	NOTEST	0	0.0305884	inf	0	1	1
ENSG00000196184	ENSG00000196184	OR10J1	1:159315955-159453166	NOTEST	0	0	0	0	1	1
ENSG00000196188	ENSG00000196188	CTSE	1:206317458-206332104	NOTEST	0.218063	0.526085	1.27055	0	1	1
ENSG00000196193	ENSG00000196193	AC034229.1	5:10201620-10201960	NOTEST	0	0	0	0	1	1
ENSG00000196196	ENSG00000196196	HRCT1	9:35906188-35907138	NOTEST	0.0190666	0.139183	2.86787	0	1	1
ENSG00000196209	ENSG00000196209	SIRPB2	20:1422806-1472233	NOTEST	0	0	0	0	1	1
ENSG00000196218	ENSG00000196218	RYR1	19:38924338-39078204	NOTEST	0.0225507	0.313633	3.79783	0	1	1
ENSG00000196224	ENSG00000196224	KRTAP5-3	11:1628794-1629693	NOTEST	0	0	0	0	1	1
ENSG00000196226	ENSG00000196226	HIST1H2BB	6:26043454-26043885	NOTEST	0.0570913	0.0445347	-0.35834	0	1	1
ENSG00000196228	ENSG00000196228	SULT1C3	2:108863650-108881807	NOTEST	0	0	0	0	1	1
ENSG00000196231	ENSG00000196231	OR2J2	HSCHR6_MHC_MCF:29141458-29142499	NOTEST	0	0	0	0	1	1
ENSG00000196240	ENSG00000196240	OR2T2	1:248616076-248617130	NOTEST	0	0	0	0	1	1
ENSG00000196242	ENSG00000196242	OR2C3	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000196243	ENSG00000196243	LINC00615	12:91299398-91348953	NOTEST	0	0	0	0	1	1
ENSG00000196248	ENSG00000196248	OR10S1	11:123847367-123848488	NOTEST	0	0	0	0	1	1
ENSG00000196260	ENSG00000196260	SFTA2	6:30899129-30899952	NOTEST	0	0	0	0	1	1
ENSG00000196266	ENSG00000196266	OR10J3	1:159283459-159284449	NOTEST	0	0	0	0	1	1
ENSG00000196273	ENSG00000196273	LINC00523	14:101123586-101146221	NOTEST	0	0	0	0	1	1
ENSG00000196274	ENSG00000196274	AC090519.1	15:44580926-44719342	NOTEST	0	0	0	0	1	1
ENSG00000196275	ENSG00000196275	GTF2IRD2	7:74071993-74306731	NOTEST	0.57563	0.178645	-1.68804	0	1	1
ENSG00000196277	ENSG00000196277	GRM7	3:6532165-7783215	NOTEST	0	0	0	0	1	1
ENSG00000196289	ENSG00000196289	BECN1P1	1:242121038-242122364	NOTEST	0	0	0	0	1	1
ENSG00000196296	ENSG00000196296	ATP2A1	16:28889725-28950667	NOTEST	0.35605	0.542783	0.608293	0	1	1
ENSG00000196299	ENSG00000196299	NCRNA00171	HSCHR6_MHC_SSTO:29957256-30022268	NOTEST	0	0	0	0	1	1
ENSG00000196326	ENSG00000196326	AKR1CL1	10:5202774-5260912	NOTEST	0	0	0	0	1	1
ENSG00000196329	ENSG00000196329	GIMAP5	7:150413644-150487837	NOTEST	0.00700519	0	#NAME?	0	1	1
ENSG00000196331	ENSG00000196331	HIST1H2BO	6:27861202-27861669	NOTEST	0.23791	0.340729	0.518206	0	1	1

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ENSG00000196335	ENSG00000196335	STK31	7:23749785-23872132	NOTEST	0.0175742	0	#NAME?	0	1	1
ENSG00000196337	ENSG00000196337	CGB7	19:49557530-49568333	NOTEST	0.131728	0.0645945	-1.02808	0	1	1
ENSG00000196338	ENSG00000196338	NLGN3	X:70364680-70391051	NOTEST	0.128753	0.180324	0.485979	0	1	1
ENSG00000196341	ENSG00000196341	OR8D1	11:124179707-124180733	NOTEST	0	0	0	0	1	1
ENSG00000196344	ENSG00000196344	ADH7	4:100333417-100356894	NOTEST	0.0128664	0.0100023	-0.363277	0	1	1
ENSG00000196345	ENSG00000196345	ZKSCAN7	3:44596684-44727145	NOTEST	0.0113366	0.0118271	0.061112	0	1	1
ENSG00000196350	ENSG00000196350	ZNF729	19:22469209-22499978	NOTEST	0.00433607	0	#NAME?	0	1	1
ENSG00000196353	ENSG00000196353	CPNE4	3:131252398-132004254	NOTEST	0	0	0	0	1	1
ENSG00000196355	ENSG00000196355	AC021860.1	4:38614321-38702663	NOTEST	0.0117917	0.0322898	1.4533	0	1	1
ENSG00000196358	ENSG00000196358	NTNG2	9:135037333-135119921	NOTEST	0.00925938	0.0226999	1.2937	0	1	1
ENSG00000196361	ENSG00000196361	ELAVL3	19:11562140-11639989	NOTEST	0	0	0	0	1	1
ENSG00000196364	ENSG00000196364	PRSS29P	16:1310952-1313846	NOTEST	0	0	0	0	1	1
ENSG00000196366	ENSG00000196366	C9orf163	9:139377946-139380518	NOTEST	0.0880451	0.162474	0.883893	0	1	1
ENSG00000196374	ENSG00000196374	HIST1H2BM	6:27782821-27783267	NOTEST	0.155298	0.0384495	-2.014	0	1	1
ENSG00000196381	ENSG00000196381	ZNF781	19:37988062-38210691	NOTEST	0.0588473	0.405982	2.78637	0	1	1
ENSG00000196383	ENSG00000196383	OR4Q2	14:20470321-20471265	NOTEST	0	0	0	0	1	1
ENSG00000196388	ENSG00000196388	INCA1	17:4891000-4900905	NOTEST	0.431184	0.311264	-0.470164	0	1	1
ENSG00000196390	ENSG00000196390	CTD-2503O16.3	5:74213550-74319753	NOTEST	0	0	0	0	1	1
ENSG00000196395	ENSG00000196395	RP13-77O11.11	X:52853315-52858317	NOTEST	0	0	0	0	1	1
ENSG00000196400	ENSG00000196400	BX255923.1	9:69204537-69269662	NOTEST	0	0	0	0	1	1
ENSG00000196403	ENSG00000196403	OR10D1P	11:124029127-124030063	NOTEST	0	0	0	0	1	1
ENSG00000196406	ENSG00000196406	SPANXD	X:140785567-140786896	NOTEST	0	0.070197	inf	0	1	1
ENSG00000196407	ENSG00000196407	THEM5	1:151814352-151826173	NOTEST	0.018269	0.0805	2.13959	0	1	1
ENSG00000196408	ENSG00000196408	NOXO1	16:2022037-2034193	NOTEST	0.0668975	0.113185	0.75866	0	1	1
ENSG00000196415	ENSG00000196415	PRTN3	19:840962-848175	NOTEST	0.0635814	0.0135426	-2.2311	0	1	1
ENSG00000196420	ENSG00000196420	S100A5	1:153509622-153514241	NOTEST	0	0.0214447	inf	0	1	1
ENSG00000196421	ENSG00000196421	LINC00176	20:62588054-62680994	NOTEST	0.186213	0.240092	0.366635	0	1	1
ENSG00000196427	ENSG00000196427	NBPF4	1:108765962-108786689	NOTEST	0.00641786	0.0289913	2.17546	0	1	1
ENSG00000196431	ENSG00000196431	CRYBA4	22:27017927-27026636	NOTEST	0	0	0	0	1	1
ENSG00000196433	ENSG00000196433	ASMT	X:1733893-1761974	NOTEST	0.06988	0.0423577	-0.722254	0	1	1
ENSG00000196460	ENSG00000196460	RFX8	2:102013822-102091165	NOTEST	0	0	0	0	1	1
ENSG00000196468	ENSG00000196468	FGF16	X:76709647-76712769	NOTEST	0	0	0	0	1	1
ENSG00000196472	ENSG00000196472	RP13-644M16.4	4:70047377-70082484	NOTEST	0	0	0	0	1	1
ENSG00000196475	ENSG00000196475	GK2	4:80327507-80329372	NOTEST	0	0	0	0	1	1
ENSG00000196482	ENSG00000196482	ESRRG	1:216676587-217311097	NOTEST	0.0861861	0.0926345	0.104095	0	1	1
ENSG00000196502	ENSG00000196502	SULT1A1	16:28616902-28634946	NOTEST	0.0867229	0.139373	0.684466	0	1	1
ENSG00000196503	ENSG00000196503	ARL9	4:57371508-57390614	NOTEST	0.170205	0.191518	0.170212	0	1	1
ENSG00000196517	ENSG00000196517	SLC6A9	1:44457030-44497139	NOTEST	0.246459	0.395029	0.680614	0	1	1
ENSG00000196532	ENSG00000196532	HIST1H3C	6:26045638-26046097	NOTEST	0.450947	0.538526	0.256057	0	1	1
ENSG00000196533	ENSG00000196533	C1orf186	1:206238871-206306131	NOTEST	0	0	0	0	1	1
ENSG00000196534	ENSG00000196534	OR9K1P	12:55509316-55510257	NOTEST	0	0	0	0	1	1
ENSG00000196539	ENSG00000196539	OR2T3	1:248636626-248637634	NOTEST	0	0	0	0	1	1
ENSG00000196542	ENSG00000196542	SPTSSB	3:161062579-161090668	NOTEST	0	0	0	0	1	1
ENSG00000196553	ENSG00000196553	LINC00238	14:66679527-67648520	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000196559	ENSG00000196559	LINC00610	11:36290833-36294909	NOTEST	0.134406	0.0993369	-0.436195	0	1	1
ENSG00000196562	ENSG00000196562	SULF2	20:46130600-46415360	NOTEST	0.0685795	0.252767	1.88196	0	1	1
ENSG00000196564	ENSG00000196564	RP3-499B10.3	X:18856826-18857570	NOTEST	0	0	0	0	1	1
ENSG00000196565	ENSG00000196565	HBG2	11:5274419-5667019	NOTEST	0.209486	0	#NAME?	0	1	1
ENSG00000196566	ENSG00000196566	RP11-57C13.3	10:89367741-89507462	NOTEST	0	0	0	0	1	1
ENSG00000196569	ENSG00000196569	LAMA2	6:129204341-129837714	NOTEST	0.276903	0.369752	0.417174	0	1	1
ENSG00000196570	ENSG00000196570	PFN3	5:176827107-176827637	NOTEST	0	0	0	0	1	1
ENSG00000196578	ENSG00000196578	OR5AC2	3:97806016-97806946	NOTEST	0	0	0	0	1	1
ENSG00000196581	ENSG00000196581	AJAP1	1:4714791-4852594	NOTEST	0.151642	0.14531	-0.0615364	0	1	1
ENSG00000196589	ENSG00000196589	CTB-25J19.1	19:7019310-7021442	NOTEST	0	0	0	0	1	1
ENSG00000196593	ENSG00000196593	ANKRD20A19P	13:24513695-24520921	NOTEST	0.11758	0.0119174	-3.3025	0	1	1
ENSG00000196600	ENSG00000196600	SLC22A25	11:62847411-63137190	NOTEST	0	0	0	0	1	1
ENSG00000196604	ENSG00000196604	POTEF	2:130831107-130886795	NOTEST	0	0.00567757	inf	0	1	1
ENSG00000196610	ENSG00000196610	HLA-DQB2	HSCHR6_MHC_QBL:32652597-32660056	NOTEST	0	0	0	0	1	1
ENSG00000196616	ENSG00000196616	ADH1B	4:100226120-100242558	NOTEST	0	0	0	0	1	1
ENSG00000196620	ENSG00000196620	UGT2B15	4:69512347-69536346	NOTEST	0.00779178	0.0236374	1.60105	0	1	1
ENSG00000196622	ENSG00000196622	RIMBP3	22:20456002-20461786	NOTEST	0	0.00185609	inf	0	1	1
ENSG00000196628	ENSG00000196628	TCF4	18:52889561-53332018	NOTEST	0	0.00826046	inf	0	1	1
ENSG00000196634	ENSG00000196634	RP3-337D23.3	6:147163036-147706866	NOTEST	0.0987165	0	#NAME?	0	1	1
ENSG00000196639	ENSG00000196639	HRH1	3:11178778-11305243	NOTEST	0	0	0	0	1	1
ENSG00000196644	ENSG00000196644	GPR89C	1:145883867-145924373	NOTEST	0.156559	0.236487	0.595059	0	1	1
ENSG00000196648	ENSG00000196648	GOLGA6L20	15:83023846-83125316	NOTEST	0.235004	0.198534	-0.243303	0	1	1
ENSG00000196653	ENSG00000196653	ZNF502	3:44754134-44765323	NOTEST	0.327319	0.450289	0.460154	0	1	1
ENSG00000196660	ENSG00000196660	SLC30A10	1:219858768-220131989	NOTEST	0.495559	0.458368	-0.11255	0	1	1
ENSG00000196661	ENSG00000196661	OR8B3	11:124266277-124267264	NOTEST	0	0	0	0	1	1
ENSG00000196664	ENSG00000196664	TLR7	X:12885201-12908499	NOTEST	0.0116728	0.00672724	-0.795061	0	1	1
ENSG00000196668	ENSG00000196668	LINC00173	12:116971226-116974323	NOTEST	0.646463	0.497578	-0.377644	0	1	1
ENSG00000196674	ENSG00000196674	Z98881.1	16:639356-684116	NOTEST	0.0825759	0	#NAME?	0	1	1
ENSG00000196684	ENSG00000196684	HSH2D	19:16222438-16269386	NOTEST	0	0	0	0	1	1
ENSG00000196689	ENSG00000196689	TRPV1	17:3468737-3539616	NOTEST	0.573884	0.237772	-1.27118	0	1	1
ENSG00000196711	ENSG00000196711	FAM150A	8:53446596-53478067	NOTEST	0	0	0	0	1	1
ENSG00000196734	ENSG00000196734	LCE1B	1:152784446-152785585	NOTEST	0	0	0	0	1	1
ENSG00000196735	ENSG00000196735	HLA-DQA1	6:32595955-32614839	NOTEST	0	0.019998	inf	0	1	1
ENSG00000196741	ENSG00000196741	CXorf24	X:47342969-47344207	NOTEST	0.39747	0.311695	-0.350712	0	1	1
ENSG00000196747	ENSG00000196747	HIST1H2AI	6:27775898-27776429	NOTEST	0.601389	0.368325	-0.707317	0	1	1
ENSG00000196748	ENSG00000196748	CLPSL2	6:35744370-35747329	NOTEST	0	0	0	0	1	1
ENSG00000196758	ENSG00000196758	AC079612.1	2:240499994-240507788	NOTEST	0	0	0	0	1	1
ENSG00000196767	ENSG00000196767	POU3F4	X:82761030-82764775	NOTEST	0	0	0	0	1	1
ENSG00000196772	ENSG00000196772	OR14A16	1:247978101-247979031	NOTEST	0	0	0	0	1	1
ENSG00000196774	ENSG00000196774	ANKRD20A1	9:67926760-67987998	NOTEST	0.145283	0.0734575	-0.983882	0	1	1
ENSG00000196777	ENSG00000196777	AL162574.1	13:107594561-107594907	NOTEST	0	0	0	0	1	1
ENSG00000196778	ENSG00000196778	OR52K1	11:4510108-4511138	NOTEST	0	0	0	0	1	1
ENSG00000196787	ENSG00000196787	HIST1H2AG	6:27100831-27103070	NOTEST	0.581765	0.561703	-0.0506275	0	1	1
ENSG00000196793	ENSG00000196793	ZNF239	10:44051791-44070066	NOTEST	0.180435	0.38005	1.07471	0	1	1

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ENSG00000196800	ENSG00000196800	SPINK14	5:147549295-147554961	NOTEST	0	0	0	0	1	1
ENSG00000196805	ENSG00000196805	SPRR2B	1:153042699-153113927	NOTEST	0	0	0	0	1	1
ENSG00000196811	ENSG00000196811	CHRNG	2:233404436-233411113	NOTEST	0.0142047	0.0211104	0.571586	0	1	1
ENSG00000196826	ENSG00000196826	ZNF709	19:12490002-12750912	NOTEST	0.020584	0.211161	3.35875	0	1	1
ENSG00000196832	ENSG00000196832	OR11G2	14:20665494-20666605	NOTEST	0	0	0	0	1	1
ENSG00000196834	ENSG00000196834	POTEI	2:131217027-131267239	NOTEST	0	0.00152092	inf	0	1	1
ENSG00000196844	ENSG00000196844	PATE2	11:125646007-125648714	NOTEST	0.107016	0.0834209	-0.359343	0	1	1
ENSG00000196859	ENSG00000196859	KRT39	17:39077681-39132178	NOTEST	0	0	0	0	1	1
ENSG00000196860	ENSG00000196860	TOMM20L	14:58862633-59015216	NOTEST	0.131303	0.606501	2.2076	0	1	1
ENSG00000196861	ENSG00000196861	AC002994.1	17:59667793-59668563	NOTEST	0	0.0972303	inf	0	1	1
ENSG00000196862	ENSG00000196862	RGPD4	2:108443387-108507297	NOTEST	0.0273681	0.0434702	0.667531	0	1	1
ENSG00000196866	ENSG00000196866	HIST1H2AD	6:26197067-26199521	NOTEST	0.471727	0.728148	0.626279	0	1	1
ENSG00000196872	ENSG00000196872	KIAA1211L	2:99410308-99552722	NOTEST	0.0520912	0.163411	1.64939	0	1	1
ENSG00000196890	ENSG00000196890	HIST3H2BB	1:228645807-228646259	NOTEST	0.0990664	0.607613	2.61669	0	1	1
ENSG00000196893	ENSG00000196893	AC090286.4	17:18853657-18950950	NOTEST	0	0	0	0	1	1
ENSG00000196900	ENSG00000196900	C5orf48	5:125967413-125971979	NOTEST	0	0	0	0	1	1
ENSG00000196917	ENSG00000196917	HCAR1	12:123011792-123215390	NOTEST	0	0.00422562	inf	0	1	1
ENSG00000196927	ENSG00000196927	AC009093.1	16:29259549-29261449	NOTEST	0	0	0	0	1	1
ENSG00000196932	ENSG00000196932	TMEM26	10:63166400-63241714	NOTEST	0.0855931	0.0289054	-1.56616	0	1	1
ENSG00000196933	ENSG00000196933	RPS26P11	X:71130937-71363424	NOTEST	0	0.190461	inf	0	1	1
ENSG00000196934	ENSG00000196934	RIMBP3B	22:21737662-21743446	NOTEST	0	0	0	0	1	1
ENSG00000196936	ENSG00000196936	OR2L8	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000196944	ENSG00000196944	OR2T4	1:248524882-248525929	NOTEST	0	0	0	0	1	1
ENSG00000196946	ENSG00000196946	ZNF705A	12:8276227-8371507	NOTEST	0	0	0	0	1	1
ENSG00000196960	ENSG00000196960	RP11-192P3.5	10:31476811-31818742	NOTEST	0	0	0	0	1	1
ENSG00000196963	ENSG00000196963	PCDHB16	5:140560979-140565793	NOTEST	0.607254	0.555125	-0.129489	0	1	1
ENSG00000196966	ENSG00000196966	HIST1H3E	6:26225382-26225844	NOTEST	0.548295	0.556324	0.0209732	0	1	1
ENSG00000196970	ENSG00000196970	NXF4	X:101804892-101826623	NOTEST	0	0	0	0	1	1
ENSG00000196972	ENSG00000196972	LINC00087	X:134193714-134257880	NOTEST	0.412511	0.214003	-0.946799	0	1	1
ENSG00000196979	ENSG00000196979	AL360004.1	9:132902888-132906498	NOTEST	0	0	0	0	1	1
ENSG00000196987	ENSG00000196987	LCA10	X:153126968-153200676	NOTEST	0.0797939	0.0214759	-1.89356	0	1	1
ENSG00000196990	ENSG00000196990	FAM163B	9:136444078-136451319	NOTEST	0	0	0	0	1	1
ENSG00000196993	ENSG00000196993	NPIPB9	16:28763107-28784128	NOTEST	0	0	0	0	1	1
ENSG00000197015	ENSG00000197015	AL353898.1	1:54474411-54483856	NOTEST	0	0	0	0	1	1
ENSG00000197023	ENSG00000197023	OR51A8P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000197038	ENSG00000197038	RBMY1A3P	Y:9148738-9160483	NOTEST	0	0	0	0	1	1
ENSG00000197046	ENSG00000197046	SIGLEC15	18:43405476-43424045	NOTEST	0.130302	0.188244	0.530741	0	1	1
ENSG00000197047	ENSG00000197047	Z73979.1	22:32908538-33454358	NOTEST	0	0	0	0	1	1
ENSG00000197054	ENSG00000197054	ZNF763	19:12035882-12091196	NOTEST	0.144117	0.200158	0.473899	0	1	1
ENSG00000197057	ENSG00000197057	DTHD1	4:36283243-36394032	NOTEST	0.00573373	0.018391	1.68146	0	1	1
ENSG00000197061	ENSG00000197061	HIST1H4C	6:26104103-26104518	NOTEST	0.587335	0.666654	0.182754	0	1	1
ENSG00000197067	ENSG00000197067	OR2T32P	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000197071	ENSG00000197071	AC010243.1	5:87485449-87794514	NOTEST	0.139531	0	#NAME?	0	1	1
ENSG00000197079	ENSG00000197079	KRT35	17:39632940-39637392	NOTEST	0	0	0	0	1	1
ENSG00000197083	ENSG00000197083	ZNF300P1	5:150310206-150325851	NOTEST	0.207278	0.259806	0.325868	0	1	1

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ENSG00000197084	ENSG00000197084	LCE1C	1:152777310-152779107	NOTEST	0	0	0	0	1	1
ENSG00000197085	ENSG00000197085	NPSR1-AS1	7:34386123-34917944	NOTEST	0	0	0	0	1	1
ENSG00000197092	ENSG00000197092	GOLGA6L16P	Y:27641797-27648105	NOTEST	0	0	0	0	1	1
ENSG00000197099	ENSG00000197099	RP11-573D15.8	3:186435037-186478330	NOTEST	0	0.0175093	inf	0	1	1
ENSG00000197110	ENSG00000197110	IFNL3	19:39734245-39735646	NOTEST	0	0	0	0	1	1
ENSG00000197123	ENSG00000197123	ZNF679	7:63688851-63727309	NOTEST	0	0	0	0	1	1
ENSG00000197124	ENSG00000197124	ZNF682	19:20107866-20150315	NOTEST	0.170815	0.0473038	-1.8524	0	1	1
ENSG00000197125	ENSG00000197125	OR8B8	11:124310021-124311054	NOTEST	0	0	0	0	1	1
ENSG00000197134	ENSG00000197134	ZNF257	19:22235253-22274282	NOTEST	0.0996777	0.0752433	-0.405707	0	1	1
ENSG00000197140	ENSG00000197140	ADAM32	8:38964508-39142430	NOTEST	0.0434736	0.0435538	0.00265618	0	1	1
ENSG00000197142	ENSG00000197142	ACSL5	10:114133775-114188138	NOTEST	0.0421082	0.198205	2.23482	0	1	1
ENSG00000197146	ENSG00000197146	AL133458.1	6:166822851-167370679	NOTEST	0.193436	0.30586	0.661015	0	1	1
ENSG00000197149	ENSG00000197149	RP11-452G18.2	11:17229699-17371521	NOTEST	0	0	0	0	1	1
ENSG00000197153	ENSG00000197153	HIST1H3J	6:27858092-27860963	NOTEST	0.096828	0.189703	0.970248	0	1	1
ENSG00000197161	ENSG00000197161	OR4C4P	11:48366899-48373999	NOTEST	0	0	0	0	1	1
ENSG00000197165	ENSG00000197165	SULT1A2	16:28603263-28608430	NOTEST	0	0.0125648	inf	0	1	1
ENSG00000197168	ENSG00000197168	NEK5	13:52611092-52703214	NOTEST	0.3426	0.300051	-0.191318	0	1	1
ENSG00000197171	ENSG00000197171	OR2B4P	6:29258487-29259430	NOTEST	0	0	0	0	1	1
ENSG00000197176	ENSG00000197176	RP11-76E12.1	14:98098983-98152995	NOTEST	0	0	0	0	1	1
ENSG00000197177	ENSG00000197177	GPR123	10:134884432-134945179	NOTEST	0	0	0	0	1	1
ENSG00000197181	ENSG00000197181	PIWIL2	8:22132809-22215076	NOTEST	0.244941	0.380623	0.63593	0	1	1
ENSG00000197185	ENSG00000197185	SSXP1	X:52635581-52640808	NOTEST	0	0	0	0	1	1
ENSG00000197191	ENSG00000197191	C9orf169	9:140119086-140120763	NOTEST	0.38259	0.370359	-0.046874	0	1	1
ENSG00000197208	ENSG00000197208	SLC22A4	5:131520568-131731306	NOTEST	0.0895516	0.0636037	-0.49361	0	1	1
ENSG00000197210	ENSG00000197210	KB-1592A4.15	22:21457304-21482352	NOTEST	0	0.00547652	inf	0	1	1
ENSG00000197213	ENSG00000197213	ZSCAN5B	19:56700938-56709289	NOTEST	0	0.0132884	inf	0	1	1
ENSG00000197214	ENSG00000197214	TCEA1P1	9:99830030-99830910	NOTEST	0	0	0	0	1	1
ENSG00000197233	ENSG00000197233	OR1J2	9:125273080-125274022	NOTEST	0	0	0	0	1	1
ENSG00000197241	ENSG00000197241	SLC2A7	1:9063358-9086404	NOTEST	0.0197056	0	#NAME?	0	1	1
ENSG00000197245	ENSG00000197245	FAM110D	1:26485510-26489119	NOTEST	0.0418796	0.0308777	-0.43968	0	1	1
ENSG00000197251	ENSG00000197251	LINC00336	6:33551514-33561115	NOTEST	0	0	0	0	1	1
ENSG00000197253	ENSG00000197253	TPSB2	16:1277271-1280214	NOTEST	0.0738568	0.0683208	-0.112406	0	1	1
ENSG00000197254	ENSG00000197254	AP000445.1	11:58407898-58499447	NOTEST	0	0	0	0	1	1
ENSG00000197261	ENSG00000197261	C6orf141	6:49518112-49529620	NOTEST	0	0	0	0	1	1
ENSG00000197262	ENSG00000197262	CCL4L2	17:34580901-34808104	NOTEST	0	0	0	0	1	1
ENSG00000197263	ENSG00000197263	OR8D2	11:124189133-124190184	NOTEST	0	0	0	0	1	1
ENSG00000197272	ENSG00000197272	IL27	16:28510682-28523372	NOTEST	0	0	0	0	1	1
ENSG00000197273	ENSG00000197273	GUCA2A	1:42628361-42630389	NOTEST	0.143794	0.0264512	-2.4426	0	1	1
ENSG00000197279	ENSG00000197279	ZNF165	6:28046569-28057341	NOTEST	0.253965	0.208155	-0.286971	0	1	1
ENSG00000197284	ENSG00000197284	RP11-589F5.3	5:70046953-70149508	NOTEST	0	0	0	0	1	1
ENSG00000197291	ENSG00000197291	RAMP2-AS1	17:40905931-40915059	NOTEST	0.13142	0.337016	1.35863	0	1	1
ENSG00000197301	ENSG00000197301	RP11-366L20.2	12:66151799-66360075	NOTEST	0.558013	0.469447	-0.249336	0	1	1
ENSG00000197308	ENSG00000197308	GATA3-AS1	10:8092412-8095447	NOTEST	0	0	0	0	1	1
ENSG00000197309	ENSG00000197309	OR10D3	11:124055922-124056952	NOTEST	0	0	0	0	1	1

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ENSG00000197320	ENSG00000197320	AC060834.2	7:9765869-9767915	NOTEST	0	0	0	0	1	1
ENSG00000197322	ENSG00000197322	C17orf102	17:32901141-32906388	NOTEST	0	0	0	0	1	1
ENSG00000197332	ENSG00000197332	ZNF833P	19:11750590-11797382	NOTEST	0.0976569	0.0808678	-0.272156	0	1	1
ENSG00000197334	ENSG00000197334	AC032027.1	8:57868646-57868875	NOTEST	0.22712	0.178929	-0.344064	0	1	1
ENSG00000197353	ENSG00000197353	LYPD2	8:143831567-143833952	NOTEST	0	0	0	0	1	1
ENSG00000197360	ENSG00000197360	ZNF98	19:22573820-22715287	NOTEST	0	0	0	0	1	1
ENSG00000197361	ENSG00000197361	FBXL22	15:63796792-63894627	NOTEST	0.124192	0.0579561	-1.09954	0	1	1
ENSG00000197364	ENSG00000197364	S100A7L2	1:153409533-153412425	NOTEST	0	0	0	0	1	1
ENSG00000197376	ENSG00000197376	OR8S1	12:48901136-48923680	NOTEST	0	0	0	0	1	1
ENSG00000197385	ENSG00000197385	ZNF860	3:31699381-32119072	NOTEST	0.0345392	0.0157923	-1.12901	0	1	1
ENSG00000197403	ENSG00000197403	OR6N1	1:158735465-158736492	NOTEST	0	0	0	0	1	1
ENSG00000197405	ENSG00000197405	C5AR1	19:47793279-47825323	NOTEST	0.0125587	0.00487463	-1.36533	0	1	1
ENSG00000197406	ENSG00000197406	DIO3	14:102027687-102029789	NOTEST	0	0	0	0	1	1
ENSG00000197408	ENSG00000197408	CYP2B6	19:41497203-41524303	NOTEST	0	0	0	0	1	1
ENSG00000197410	ENSG00000197410	DCHS2	4:155153398-155412930	NOTEST	0.0762974	0.0921059	0.271659	0	1	1
ENSG00000197414	ENSG00000197414	GOLGA6L1	15:22736245-22746002	NOTEST	0	0	0	0	1	1
ENSG00000197416	ENSG00000197416	FABP12	8:82351670-82445510	NOTEST	0	0	0	0	1	1
ENSG00000197421	ENSG00000197421	GGT3P	22:18761177-18830912	NOTEST	0	0.00531977	inf	0	1	1
ENSG00000197428	ENSG00000197428	OR51D1	11:4660944-4662068	NOTEST	0	0	0	0	1	1
ENSG00000197430	ENSG00000197430	OPALIN	10:98102972-98119092	NOTEST	0.0169544	0	#NAME?	0	1	1
ENSG00000197437	ENSG00000197437	OR13G1	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000197445	ENSG00000197445	C16orf47	16:73160535-73178346	NOTEST	0	0	0	0	1	1
ENSG00000197446	ENSG00000197446	CYP2F1	19:41620336-41634271	NOTEST	0	0	0	0	1	1
ENSG00000197454	ENSG00000197454	OR2L5	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000197461	ENSG00000197461	PDGFA	7:536894-559933	NOTEST	0.0286763	0.0969251	1.75701	0	1	1
ENSG00000197462	ENSG00000197462	AC005276.1	7:125557924-125573886	NOTEST	0	0	0	0	1	1
ENSG00000197465	ENSG00000197465	GYPE	4:144792019-144826716	NOTEST	0.0185383	0	#NAME?	0	1	1
ENSG00000197467	ENSG00000197467	COL13A1	10:71561643-71724031	NOTEST	0.00538891	0.0788293	3.87067	0	1	1
ENSG00000197468	ENSG00000197468	RP11-747H12.1	4:8951355-8952285	NOTEST	0	0	0	0	1	1
ENSG00000197471	ENSG00000197471	SPN	16:29674299-29710020	NOTEST	0	0	0	0	1	1
ENSG00000197475	ENSG00000197475	ADAM3A	8:39308563-39380371	NOTEST	0	0	0	0	1	1
ENSG00000197476	ENSG00000197476	RP11-170L3.7	16:31973383-31985682	NOTEST	0	0	0	0	1	1
ENSG00000197479	ENSG00000197479	PCDHB11	5:140579182-140582618	NOTEST	0.343114	0.21433	-0.678854	0	1	1
ENSG00000197487	ENSG00000197487	GALP	19:56687388-56697144	NOTEST	0	0	0	0	1	1
ENSG00000197497	ENSG00000197497	ZNF665	19:53667390-53696639	NOTEST	0	0	0	0	1	1
ENSG00000197502	ENSG00000197502	AL627171.1	14:50249996-50319921	NOTEST	0	0	0	0	1	1
ENSG00000197503	ENSG00000197503	LINC00477	12:24719897-24737483	NOTEST	0	0	0	0	1	1
ENSG00000197506	ENSG00000197506	SLC28A3	9:86890371-86955672	NOTEST	0.251594	0.0497396	-2.33863	0	1	1
ENSG00000197520	ENSG00000197520	FAM177B	1:222910548-222924147	NOTEST	0	0	0	0	1	1
ENSG00000197532	ENSG00000197532	OR6Y1	1:158516917-158517895	NOTEST	0	0	0	0	1	1
ENSG00000197536	ENSG00000197536	C5orf56	5:131746327-131811736	NOTEST	0.551333	0.459588	-0.262585	0	1	1
ENSG00000197549	ENSG00000197549	PRAMENP	22:22345495-22398340	NOTEST	0	0	0	0	1	1
ENSG00000197550	ENSG00000197550	RP11-460N11.2	9:69830287-69848759	NOTEST	0.0412098	0.0595336	0.530716	0	1	1
ENSG00000197558	ENSG00000197558	SSPO	7:149473130-149531068	NOTEST	0.00207674	0.0514516	4.63082	0	1	1
ENSG00000197561	ENSG00000197561	ELANE	19:851013-856242	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000197565	ENSG00000197565	COL4A6	X:107334897-107682727	NOTEST	0.0484421	0.108386	1.16184	0	1	1
ENSG00000197575	ENSG00000197575	RPS17P2	5:116051928-116052387	NOTEST	0	0	0	0	1	1
ENSG00000197580	ENSG00000197580	BCO2	11:111895537-112095422	NOTEST	0.491631	0.567445	0.206903	0	1	1
ENSG00000197584	ENSG00000197584	KCNMB2	3:177919837-178578193	NOTEST	0.00696496	0.0303201	2.12209	0	1	1
ENSG00000197585	ENSG00000197585	AC107218.3	2:214149112-215548970	NOTEST	0	0	0	0	1	1
ENSG00000197587	ENSG00000197587	DMBX1	1:46972667-46979898	NOTEST	0.0307721	0.0153906	-0.999572	0	1	1
ENSG00000197588	ENSG00000197588	KLKP1	19:51385351-51399654	NOTEST	0	0	0	0	1	1
ENSG00000197591	ENSG00000197591	OR11L1	1:248004198-248005254	NOTEST	0	0	0	0	1	1
ENSG00000197595	ENSG00000197595	C13orf35	13:113301357-113338811	NOTEST	0.00717441	0.0212284	1.56506	0	1	1
ENSG00000197599	ENSG00000197599	CCDC154	16:1484383-1494557	NOTEST	0.411937	0.0625972	-2.71825	0	1	1
ENSG00000197604	ENSG00000197604	AC022532.1	10:72192070-72207707	NOTEST	1.30E-07	0	#NAME?	0	1	1
ENSG00000197614	ENSG00000197614	MFAP5	12:8786962-8815484	NOTEST	0	0.00389954	inf	0	1	1
ENSG00000197616	ENSG00000197616	MYH6	14:23851198-23877486	NOTEST	0	0	0	0	1	1
ENSG00000197617	ENSG00000197617	VN1R5	1:247419373-247420445	NOTEST	0	0.0397658	inf	0	1	1
ENSG00000197627	ENSG00000197627	UBE2Q2P12	15:85034710-85045612	NOTEST	0	0	0	0	1	1
ENSG00000197629	ENSG00000197629	MPEG1	11:58938902-58980424	NOTEST	0	0.00244051	inf	0	1	1
ENSG00000197632	ENSG00000197632	SERPINB2	18:61538925-61609601	NOTEST	0.0983569	0.076217	-0.367912	0	1	1
ENSG00000197641	ENSG00000197641	SERPINB13	18:61254222-61271873	NOTEST	0	0	0	0	1	1
ENSG00000197644	ENSG00000197644	AC106870.2	2:29415639-30144432	NOTEST	0	0	0	0	1	1
ENSG00000197646	ENSG00000197646	PDCD1LG2	9:5510544-5571282	NOTEST	0	0	0	0	1	1
ENSG00000197651	ENSG00000197651	CCER1	12:91299398-91348953	NOTEST	0	0	0	0	1	1
ENSG00000197653	ENSG00000197653	DNAH10	12:124247041-124800570	NOTEST	0.149466	0.561365	1.90912	0	1	1
ENSG00000197658	ENSG00000197658	SLC22A24	11:62847411-63137190	NOTEST	0	0	0	0	1	1
ENSG00000197665	ENSG00000197665	AC007952.6	17:19030781-19062489	NOTEST	0	0	0	0	1	1
ENSG00000197670	ENSG00000197670	RP4-724E16.2	20:52169308-52251129	NOTEST	0.119133	0.110974	-0.102342	0	1	1
ENSG00000197674	ENSG00000197674	OR51C1P	11:4701400-4719084	NOTEST	0	0	0	0	1	1
ENSG00000197681	ENSG00000197681	TBC1D3	17:36337710-36421858	NOTEST	0.140752	0.116325	-0.274986	0	1	1
ENSG00000197683	ENSG00000197683	KRTAP26-1	21:31691451-31692607	NOTEST	0	0	0	0	1	1
ENSG00000197697	ENSG00000197697	HIST1H2BE	6:26183957-26184454	NOTEST	0.0911236	0.0647358	-0.493261	0	1	1
ENSG00000197704	ENSG00000197704	FRMPD2P1	10:48844035-48868504	NOTEST	0.0355836	0.00888571	-2.00165	0	1	1
ENSG00000197706	ENSG00000197706	OR6C74	12:55640981-55642086	NOTEST	0	0	0	0	1	1
ENSG00000197721	ENSG00000197721	CR1L	1:207818457-207911761	NOTEST	0	0.101371	inf	0	1	1
ENSG00000197723	ENSG00000197723	HSPB9	17:40265125-40307990	NOTEST	0.0950434	0.123593	0.378942	0	1	1
ENSG00000197727	ENSG00000197727	AL022341.1	16:691038-691688	NOTEST	0	0	0	0	1	1
ENSG00000197734	ENSG00000197734	C14orf178	14:78174413-78236085	NOTEST	0.0644454	0	#NAME?	0	1	1
ENSG00000197745	ENSG00000197745	SCGB1D4	11:62063753-62066536	NOTEST	0	0	0	0	1	1
ENSG00000197748	ENSG00000197748	WDR96	10:105889645-105992120	NOTEST	0.461083	0.381032	-0.275115	0	1	1
ENSG00000197753	ENSG00000197753	LHFPL5	6:35773069-35889119	NOTEST	0	0	0	0	1	1
ENSG00000197768	ENSG00000197768	C9orf173	9:140145712-140147934	NOTEST	0.0691662	0.0230415	-1.58583	0	1	1
ENSG00000197776	ENSG00000197776	KLHDC1	14:50159822-50219870	NOTEST	0.459429	0.218694	-1.07093	0	1	1
ENSG00000197786	ENSG00000197786	OR5B17	11:58125596-58126542	NOTEST	0	0	0	0	1	1
ENSG00000197790	ENSG00000197790	OR52M1	11:4566420-4567374	NOTEST	0	0	0	0	1	1
ENSG00000197794	ENSG00000197794	IGKV7-3	2:89214596-89214894	NOTEST	0	0	0	0	1	1
ENSG00000197805	ENSG00000197805	BX649597.1	9:43313698-43314502	NOTEST	0	0	0	0	1	1
ENSG00000197822	ENSG00000197822	OCLN	5:68773298-69006341	NOTEST	0.403548	0.451771	0.16285	0	1	1

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ENSG00000197826	ENSG00000197826	C4orf22	4:81187752-81884910	NOTEST	0	0	0	0	1	1
ENSG00000197830	ENSG00000197830	AC011385.1	5:137881628-137882992	NOTEST	0.10522	0.23872	1.18191	0	1	1
ENSG00000197838	ENSG00000197838	CYP2A13	19:41594376-41602100	NOTEST	0	0	0	0	1	1
ENSG00000197844	ENSG00000197844	AL358813.1	1:149646784-149719362	NOTEST	0	0	0	0	1	1
ENSG00000197846	ENSG00000197846	HIST1H2BF	6:26199747-26200942	NOTEST	0.0673044	0.152843	1.18328	0	1	1
ENSG00000197847	ENSG00000197847	SLC22A20	11:64981310-65010228	NOTEST	0.0118993	0.00924898	-0.363504	0	1	1
ENSG00000197849	ENSG00000197849	OR8G1	11:124120422-124135763	NOTEST	0	0	0	0	1	1
ENSG00000197857	ENSG00000197857	ZNF44	19:12305829-12405702	NOTEST	0.355327	0.452574	0.349005	0	1	1
ENSG00000197859	ENSG00000197859	ADAMTSL2	9:136397285-136440641	NOTEST	0.00754511	0.00586509	-0.363389	0	1	1
ENSG00000197866	ENSG00000197866	OR5M12P	11:56396407-56397345	NOTEST	0	0	0	0	1	1
ENSG00000197870	ENSG00000197870	PRB3	12:11418856-11422739	NOTEST	0	0	0	0	1	1
ENSG00000197872	ENSG00000197872	FAM49A	2:16730726-16847599	NOTEST	0	0	0	0	1	1
ENSG00000197880	ENSG00000197880	MDS2	1:23907984-23967058	NOTEST	0	0	0	0	1	1
ENSG00000197882	ENSG00000197882	OR7E13P	11:86502100-86666433	NOTEST	0	0.0337417	inf	0	1	1
ENSG00000197887	ENSG00000197887	OR1S2	11:57970673-57971653	NOTEST	0	0	0	0	1	1
ENSG00000197888	ENSG00000197888	UGT2B17	4:69402901-69434245	NOTEST	0	0.00547449	inf	0	1	1
ENSG00000197889	ENSG00000197889	MEIG1	10:15001437-15030049	NOTEST	0.0442043	0.0790364	0.838331	0	1	1
ENSG00000197891	ENSG00000197891	SLC22A12	11:64358112-64369820	NOTEST	0	0	0	0	1	1
ENSG00000197893	ENSG00000197893	NRAP	10:115310595-115423886	NOTEST	0.0376648	0.0314391	-0.260656	0	1	1
ENSG00000197901	ENSG00000197901	SLC22A6	11:62703856-62752455	NOTEST	0	0	0	0	1	1
ENSG00000197910	ENSG00000197910	FAM25G	10:48247668-48279200	NOTEST	0	0	0	0	1	1
ENSG00000197914	ENSG00000197914	HIST1H4K	6:27798951-27799305	NOTEST	0	0	0	0	1	1
ENSG00000197919	ENSG00000197919	IFNA1	9:21440439-21441315	NOTEST	0	0	0	0	1	1
ENSG00000197921	ENSG00000197921	HES5	1:2460183-2461684	NOTEST	0	0	0	0	1	1
ENSG00000197927	ENSG00000197927	C2orf27A	2:132479947-132524973	NOTEST	0.061683	0.0855603	0.472069	0	1	1
ENSG00000197928	ENSG00000197928	ZNF677	19:53731576-53758151	NOTEST	0.268344	0.490573	0.870383	0	1	1
ENSG00000197934	ENSG00000197934	AP001597.1	21:27750870-27945603	NOTEST	0.00827731	0.00643278	-0.363721	0	1	1
ENSG00000197935	ENSG00000197935	ZNF311	6:28962561-28973093	NOTEST	0.13125	0.179723	0.453452	0	1	1
ENSG00000197937	ENSG00000197937	ZNF347	19:53611131-53662328	NOTEST	0.359645	0.46754	0.378516	0	1	1
ENSG00000197938	ENSG00000197938	OR5H2	3:97952494-98176742	NOTEST	0	0	0	0	1	1
ENSG00000197953	ENSG00000197953	AADACL2	3:151451703-151645963	NOTEST	0	0	0	0	1	1
ENSG00000197978	ENSG00000197978	GOLGA6L9	15:82647359-82748784	NOTEST	0.0379324	0.0903913	1.25276	0	1	1
ENSG00000197980	ENSG00000197980	LEKR1	3:156543269-156763918	NOTEST	0.580584	0.588157	0.0186966	0	1	1
ENSG00000197984	ENSG00000197984	OR51A8P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000197990	ENSG00000197990	ZNF734P	7:62910196-62917065	NOTEST	0	0	0	0	1	1
ENSG00000197991	ENSG00000197991	PCDH20	13:61983817-62002220	NOTEST	0.016117	0.0744336	2.20737	0	1	1
ENSG00000197992	ENSG00000197992	CLEC9A	12:10183275-10218565	NOTEST	0	0	0	0	1	1
ENSG00000197993	ENSG00000197993	KEL	7:142638200-142659768	NOTEST	0.129488	0.186164	0.523764	0	1	1
ENSG00000198003	ENSG00000198003	CCDC151	19:11531271-11561783	NOTEST	0	0	0	0	1	1
ENSG00000198010	ENSG00000198010	DLGAP2	8:1449531-1656642	NOTEST	0	0	0	0	1	1
ENSG00000198019	ENSG00000198019	FCGR1B	1:120906027-120935937	NOTEST	0	0	0	0	1	1
ENSG00000198021	ENSG00000198021	SPANXA1	X:140590842-140738057	NOTEST	0	0	0	0	1	1
ENSG00000198022	ENSG00000198022	RP11-432N13.4	X:134807305-134819866	NOTEST	0	0	0	0	1	1
ENSG00000198028	ENSG00000198028	ZNF560	19:9577182-9609283	NOTEST	0.011962	0.0401914	1.74843	0	1	1

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ENSG00000198035	ENSG00000198035	AGAP9	10:48187415-48237508	NOTEST	0.292328	0.221285	-0.401686	0	1	1
ENSG00000198049	ENSG00000198049	AVPR1B	1:206223975-206231639	NOTEST	0	0	0	0	1	1
ENSG00000198062	ENSG00000198062	POTEH	22:16255354-16287937	NOTEST	0.00844298	0	#NAME?	0	1	1
ENSG00000198064	ENSG00000198064	RP11-347C12.1	16:30234229-30346695	NOTEST	0.229555	0.137997	-0.734198	0	1	1
ENSG00000198074	ENSG00000198074	AKR1B10	7:134212343-134226160	NOTEST	0.0597101	0.0919429	0.622765	0	1	1
ENSG00000198075	ENSG00000198075	SULT1C4	2:108994366-109004513	NOTEST	0	0	0	0	1	1
ENSG00000198077	ENSG00000198077	CYP2A7	19:41277552-41406413	NOTEST	0	0	0	0	1	1
ENSG00000198082	ENSG00000198082	H2AFB1	X:154064062-154288578	NOTEST	0	0	0	0	1	1
ENSG00000198083	ENSG00000198083	KRTAP9-9	17:39411635-39412616	NOTEST	0	0	0	0	1	1
ENSG00000198088	ENSG00000198088	NUP62CL	X:106366656-106449670	NOTEST	0	0	0	0	1	1
ENSG00000198090	ENSG00000198090	KRTAP4-6	17:39295684-39296739	NOTEST	0	0	0	0	1	1
ENSG00000198092	ENSG00000198092	TMPRSS11F	4:68566997-68995598	NOTEST	0	0	0	0	1	1
ENSG00000198099	ENSG00000198099	ADH4	4:100010007-100222513	NOTEST	0.00750055	0	#NAME?	0	1	1
ENSG00000198100	ENSG00000198100	AL138751.1	9:74526425-74600970	NOTEST	0	0	0	0	1	1
ENSG00000198104	ENSG00000198104	OR2T6	1:248550909-248551836	NOTEST	0	0	0	0	1	1
ENSG00000198106	ENSG00000198106	SNX29P2	16:29262828-29519817	NOTEST	0.138249	0.112522	-0.297055	0	1	1
ENSG00000198113	ENSG00000198113	TOR4A	9:140172200-140177093	NOTEST	0.0284185	0.0458656	0.690582	0	1	1
ENSG00000198125	ENSG00000198125	MB	22:36002810-36033998	NOTEST	0.309248	0.157895	-0.969802	0	1	1
ENSG00000198128	ENSG00000198128	OR2L3	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000198129	ENSG00000198129	DEFB107B	8:7353367-7366833	NOTEST	0	0	0	0	1	1
ENSG00000198134	ENSG00000198134	RP11-267J23.4	12:12202777-12419946	NOTEST	0	0	0	0	1	1
ENSG00000198143	ENSG00000198143	BX247900.1	HSCHR6_MHC_SSTO:31059238-31062047	NOTEST	0	0	0	0	1	1
ENSG00000198150	ENSG00000198150	AC135178.1	17:8261730-8263538	NOTEST	0.174646	0.132328	-0.400323	0	1	1
ENSG00000198153	ENSG00000198153	ZNF849P	19:22817125-22899793	NOTEST	0	0	0	0	1	1
ENSG00000198155	ENSG00000198155	ZNF876P	4:206398-249774	NOTEST	0.17428	0.230823	0.405382	0	1	1
ENSG00000198156	ENSG00000198156	NPIPB6	16:28353875-28374829	NOTEST	0.0241486	0.0169678	-0.509143	0	1	1
ENSG00000198161	ENSG00000198161	PPIAL4C	1:149553002-149553787	NOTEST	0.0241916	0	#NAME?	0	1	1
ENSG00000198173	ENSG00000198173	FAM47C	X:37026431-37029739	NOTEST	0	0	0	0	1	1
ENSG00000198178	ENSG00000198178	CLEC4C	12:7882010-7904201	NOTEST	0	0	0	0	1	1
ENSG00000198183	ENSG00000198183	BPIFA1	20:31823800-31831115	NOTEST	0	0	0	0	1	1
ENSG00000198185	ENSG00000198185	ZNF334	20:45129700-45142198	NOTEST	0	0	0	0	1	1
ENSG00000198205	ENSG00000198205	ZXDA	X:57931863-57937067	NOTEST	0.446614	0.39225	-0.187255	0	1	1
ENSG00000198216	ENSG00000198216	CACNA1E	1:181382237-181777219	NOTEST	0	0	0	0	1	1
ENSG00000198217	ENSG00000198217	OR51H2P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000198223	ENSG00000198223	CSF2RA	X:1387692-1429274	NOTEST	0	0.0941208	inf	0	1	1
ENSG00000198250	ENSG00000198250	ANTXRL	10:47657580-47701443	NOTEST	0.0558236	0.036593	-0.609307	0	1	1
ENSG00000198251	ENSG00000198251	CTC-490E21.13	19:41414376-41416754	NOTEST	0	0	0	0	1	1
ENSG00000198261	ENSG00000198261	OR5BB1P	11:59158826-59159765	NOTEST	0	0	0	0	1	1
ENSG00000198271	ENSG00000198271	KRTAP4-5	17:39305177-39306054	NOTEST	0	0	0	0	1	1
ENSG00000198277	ENSG00000198277	RP11-468N14.09	4:69780639-69790459	NOTEST	0	0	0	0	1	1
ENSG00000198283	ENSG00000198283	OR5B21	11:58274647-58275578	NOTEST	0.0195433	0	#NAME?	0	1	1
ENSG00000198284	ENSG00000198284	NUP210P1	3:126379451-126390782	NOTEST	0	0	0	0	1	1
ENSG00000198286	ENSG00000198286	CARD11	7:2945774-3083579	NOTEST	0	0	0	0	1	1

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ENSG00000198300	ENSG00000198300	PEG3	19:57202053-57352097	NOTEST	0	0	0	0	1	1
ENSG00000198305	ENSG00000198305	SPDYE8P	7:72440226-72555749	NOTEST	0.0127748	0.0104424	-0.29084	0	1	1
ENSG00000198307	ENSG00000198307	H2AFB2	X:154610427-154610944	NOTEST	0	0	0	0	1	1
ENSG00000198312	ENSG00000198312	BMS1P9	9:66960612-66964189	NOTEST	0.335863	0.138769	-1.27519	0	1	1
ENSG00000198326	ENSG00000198326	TMEM239	20:2795613-2800930	NOTEST	0	0	0	0	1	1
ENSG00000198327	ENSG00000198327	HIST1H4F	6:26240560-26240976	NOTEST	0.0605672	0.146591	1.27519	0	1	1
ENSG00000198336	ENSG00000198336	MYL4	17:45277811-45301045	NOTEST	0	0	0	0	1	1
ENSG00000198339	ENSG00000198339	HIST1H4I	6:27106072-27114619	NOTEST	0.160137	0.179946	0.168265	0	1	1
ENSG00000198342	ENSG00000198342	ZNF442	19:12460184-12476719	NOTEST	0.00855944	0.018682	1.12606	0	1	1
ENSG00000198358	ENSG00000198358	RP11-544M22.1	1:160901528-160924589	NOTEST	0.142455	0.260877	0.87286	0	1	1
ENSG00000198366	ENSG00000198366	HIST1H3A	6:26020717-26021186	NOTEST	0.0932176	0	#NAME?	0	1	1
ENSG00000198367	ENSG00000198367	OR7A11P	19:15027227-15028192	NOTEST	0	0	0	0	1	1
ENSG00000198374	ENSG00000198374	HIST1H2AL	6:27833033-27833606	NOTEST	0.258669	0	#NAME?	0	1	1
ENSG00000198384	ENSG00000198384	TPTE2P3	13:53063127-53161222	NOTEST	0.0513024	0	#NAME?	0	1	1
ENSG00000198388	ENSG00000198388	AC092291.1	16:14529557-14726585	NOTEST	0	0	0	0	1	1
ENSG00000198390	ENSG00000198390	KRTAP13-1	21:31768391-31769136	NOTEST	0	0	0	0	1	1
ENSG00000198398	ENSG00000198398	TMEM207	3:190146443-190167665	NOTEST	0.0443829	0	#NAME?	0	1	1
ENSG00000198400	ENSG00000198400	NTRK1	1:156776034-156851642	NOTEST	0.0462972	0.102805	1.15092	0	1	1
ENSG00000198414	ENSG00000198414	TATDN2P1	X:44007127-44202918	NOTEST	0	0	0	0	1	1
ENSG00000198416	ENSG00000198416	CTD-2173L22.4	9:39443803-39464526	NOTEST	0.0345629	0.0469493	0.44188	0	1	1
ENSG00000198429	ENSG00000198429	ZNF69	19:11998598-12025144	NOTEST	0.0146271	0.200874	3.77957	0	1	1
ENSG00000198434	ENSG00000198434	AF241725.1	21:23006772-23007049	NOTEST	0	0	0	0	1	1
ENSG00000198435	ENSG00000198435	NRARP	9:140194082-140196703	NOTEST	0	0.00851343	inf	0	1	1
ENSG00000198443	ENSG00000198443	KRTAP4-1	17:39340353-39341594	NOTEST	0	0	0	0	1	1
ENSG00000198444	ENSG00000198444	F8A2	X:154611748-154613449	NOTEST	0.083741	0.0576052	-0.539736	0	1	1
ENSG00000198445	ENSG00000198445	CCT8L2	22:17071666-17073700	NOTEST	0	0	0	0	1	1
ENSG00000198452	ENSG00000198452	OR14L1P	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000198454	ENSG00000198454	C9orf141	9:139863694-139866442	NOTEST	0	0	0	0	1	1
ENSG00000198457	ENSG00000198457	CYP21A2	HSCHR6_MHC_SSTO:31965199-32027628	NOTEST	0	0	0	0	1	1
ENSG00000198471	ENSG00000198471	RTP2	3:187416046-187463515	NOTEST	0	0	0	0	1	1
ENSG00000198483	ENSG00000198483	ANKRD35	1:145549229-145568526	NOTEST	0	0.0278376	inf	0	1	1
ENSG00000198488	ENSG00000198488	B3GNT6	11:76745384-76753096	NOTEST	0	0.00496152	inf	0	1	1
ENSG00000198491	ENSG00000198491	RP11-208N14.4	3:186914877-186925417	NOTEST	0	0	0	0	1	1
ENSG00000198502	ENSG00000198502	HLA-DRB5	6:32485119-32498064	NOTEST	0.0248077	0	#NAME?	0	1	1
ENSG00000198515	ENSG00000198515	CNGA1	4:47849256-48042188	NOTEST	0	0.00469781	inf	0	1	1
ENSG00000198518	ENSG00000198518	HIST1H4E	6:26204857-26206266	NOTEST	0.231136	0.311156	0.428897	0	1	1
ENSG00000198520	ENSG00000198520	C1orf228	1:45140363-45191263	NOTEST	0.150812	0.119498	-0.335766	0	1	1
ENSG00000198523	ENSG00000198523	PLN	6:118781934-119031238	NOTEST	0.0780915	0.0665697	-0.2303	0	1	1
ENSG00000198526	ENSG00000198526	PABPC1P2	2:147345011-147346878	NOTEST	0	0	0	0	1	1
ENSG00000198535	ENSG00000198535	C2CD4A	15:62359175-62363116	NOTEST	0.00819359	0	#NAME?	0	1	1
ENSG00000198542	ENSG00000198542	ITGBL1	13:102104965-103054807	NOTEST	0.0109844	0.00793718	-0.468755	0	1	1
ENSG00000198547	ENSG00000198547	C20orf203	20:31219427-31261743	NOTEST	0	0.0022544	inf	0	1	1
ENSG00000198553	ENSG00000198553	KCNRG	13:50570023-50595058	NOTEST	0.33285	0.342582	0.0415741	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000198555	ENSG00000198555	RP11-598D12.4	16:33775378-33790097	NOTEST	0	0.00514187	inf	0	1	1
ENSG00000198558	ENSG00000198558	HIST1H4L	6:27840925-27841289	NOTEST	0	0	0	0	1	1
ENSG00000198566	ENSG00000198566	ZNF658B	9:41588822-41609544	NOTEST	0.0338729	0.0214922	-0.656321	0	1	1
ENSG00000198569	ENSG00000198569	SLC34A3	9:140125208-140131006	NOTEST	0.0137595	0.0301395	1.13123	0	1	1
ENSG00000198570	ENSG00000198570	RD3	1:211649863-211666259	NOTEST	0	0.00795258	inf	0	1	1
ENSG00000198573	ENSG00000198573	SPANXC	X:140335595-140336629	NOTEST	0	0	0	0	1	1
ENSG00000198574	ENSG00000198574	SH2D1B	1:162365055-162381928	NOTEST	0	0.0929105	inf	0	1	1
ENSG00000198576	ENSG00000198576	ARC	8:143692404-143696833	NOTEST	0.11064	0.229257	1.05109	0	1	1
ENSG00000198580	ENSG00000198580	AC073343.1	7:6703604-6748532	NOTEST	0.0294731	0.0466212	0.661587	0	1	1
ENSG00000198590	ENSG00000198590	C3orf35	3:37427759-37476988	NOTEST	0.311067	0.191511	-0.699802	0	1	1
ENSG00000198601	ENSG00000198601	OR2M2	1:248343287-248344331	NOTEST	0	0	0	0	1	1
ENSG00000198610	ENSG00000198610	AKR1C4	10:5202774-5260912	NOTEST	0	0	0	0	1	1
ENSG00000198624	ENSG00000198624	CCDC69	5:150560612-150650001	NOTEST	0.353882	0.52566	0.570864	0	1	1
ENSG00000198626	ENSG00000198626	RYR2	1:237205504-237997288	NOTEST	0.0300165	0.0194959	-0.622587	0	1	1
ENSG00000198632	ENSG00000198632	AC004878.3	7:74880904-74988262	NOTEST	0.137105	0.547788	1.99833	0	1	1
ENSG00000198633	ENSG00000198633	ZNF534	19:52932439-52955568	NOTEST	0	0	0	0	1	1
ENSG00000198643	ENSG00000198643	FAM3D	3:58549843-58652575	NOTEST	0.0534093	0	#NAME?	0	1	1
ENSG00000198650	ENSG00000198650	TAT	16:71599562-71612090	NOTEST	0	0	0	0	1	1
ENSG00000198657	ENSG00000198657	OR8B4	11:124293806-124294789	NOTEST	0	0	0	0	1	1
ENSG00000198658	ENSG00000198658	ABHD17AP2	1:146032646-146253110	NOTEST	0	0	0	0	1	1
ENSG00000198670	ENSG00000198670	LPA	6:160952514-161097555	NOTEST	0	0	0	0	1	1
ENSG00000198671	ENSG00000198671	RP11-168J19.2	12:65411247-65413586	NOTEST	0	0	0	0	1	1
ENSG00000198674	ENSG00000198674	OR10G6	11:123864869-123865868	NOTEST	0	0	0	0	1	1
ENSG00000198678	ENSG00000198678	OR5BS1P	12:48953664-48956739	NOTEST	0	0	0	0	1	1
ENSG00000198681	ENSG00000198681	MAGEA1	X:152481521-152486115	NOTEST	0.317713	0.481362	0.599396	0	1	1
ENSG00000198685	ENSG00000198685	C3orf27	3:128290842-128294929	NOTEST	0	0.00456756	inf	0	1	1
ENSG00000198692	ENSG00000198692	EIF1AY	Y:22737610-22755040	NOTEST	0	0	0	0	1	1
ENSG00000198703	ENSG00000198703	OR10R3P	1:158444243-158464676	NOTEST	0	0	0	0	1	1
ENSG00000198704	ENSG00000198704	GPX6	6:28471072-28502729	NOTEST	0	0	0	0	1	1
ENSG00000198711	ENSG00000198711	SSBP3-AS1	1:54598746-54879152	NOTEST	0.0490447	0.16864	1.78178	0	1	1
ENSG00000198719	ENSG00000198719	DLL1	6:170591293-170599561	NOTEST	0.00494529	0	#NAME?	0	1	1
ENSG00000198723	ENSG00000198723	C19orf45	19:7541760-7585912	NOTEST	0	0.14803	inf	0	1	1
ENSG00000198729	ENSG00000198729	PPP1R14C	6:150464211-150571493	NOTEST	0.243522	0.320734	0.397324	0	1	1
ENSG00000198732	ENSG00000198732	SMOC1	14:70320847-70499083	NOTEST	0.027141	0.0173427	-0.646149	0	1	1
ENSG00000198734	ENSG00000198734	F5	1:169483403-169555826	NOTEST	0.00823229	0.00689687	-0.255351	0	1	1
ENSG00000198738	ENSG00000198738	SMIM11P1	6:86445461-86445639	NOTEST	0	0	0	0	1	1
ENSG00000198739	ENSG00000198739	LRRTM3	10:67672275-69455927	NOTEST	0	0	0	0	1	1
ENSG00000198750	ENSG00000198750	GATSL2	7:74807498-74867509	NOTEST	0.509083	0.496288	-0.036724	0	1	1
ENSG00000198754	ENSG00000198754	OXCT2	1:40157853-40254533	NOTEST	0.041504	0.0335349	-0.307584	0	1	1
ENSG00000198758	ENSG00000198758	EPS8L3	1:110254863-110318050	NOTEST	0	0	0	0	1	1
ENSG00000198759	ENSG00000198759	EGFL6	X:13587723-13651694	NOTEST	0.00668834	0.0150904	1.17392	0	1	1
ENSG00000198765	ENSG00000198765	SYCP1	1:115397423-115537991	NOTEST	0	0	0	0	1	1
ENSG00000198768	ENSG00000198768	APCDD1L	20:57034156-57090187	NOTEST	0	0	0	0	1	1
ENSG00000198771	ENSG00000198771	RCSD1	1:167596621-167675486	NOTEST	0.0269115	0.0284844	0.0819478	0	1	1
ENSG00000198774	ENSG00000198774	RASSF9	12:86198330-86230348	NOTEST	0.261356	0.0825188	-1.66322	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000198785	ENSG00000198785	GRIN3A	9:104331634-104500862	NOTEST	0.0265887	0.0466068	0.80973	0	1	1
ENSG00000198787	ENSG00000198787	OR4D12P	4:4128385-4129296	NOTEST	0	0	0	0	1	1
ENSG00000198788	ENSG00000198788	MUC2	11:1074874-1104419	NOTEST	0	0	0	0	1	1
ENSG00000198796	ENSG00000198796	ALPK2	18:56148478-56296189	NOTEST	0	0.0050767	inf	0	1	1
ENSG00000198797	ENSG00000198797	BRINP2	1:177140632-177251558	NOTEST	0	0	0	0	1	1
ENSG00000198798	ENSG00000198798	MAGEB3	X:30248552-30255607	NOTEST	0.00696576	0.00489296	-0.509573	0	1	1
ENSG00000198807	ENSG00000198807	PAX9	14:37116287-37643016	NOTEST	0.19061	0.292834	0.619461	0	1	1
ENSG00000198812	ENSG00000198812	LRRC10	12:70002350-70004942	NOTEST	0	0	0	0	1	1
ENSG00000198821	ENSG00000198821	CD247	1:167399876-167487847	NOTEST	0.0978885	0.0722588	-0.437966	0	1	1
ENSG00000198822	ENSG00000198822	GRM3	7:86273229-86494200	NOTEST	1.45E-05	0.0218318	10.559	0	1	1
ENSG00000198829	ENSG00000198829	SUCNR1	3:151451703-151645963	NOTEST	0.0267551	0.0717083	1.42233	0	1	1
ENSG00000198835	ENSG00000198835	GJC2	1:228337552-228347527	NOTEST	0.0215025	0.0156389	-0.459365	0	1	1
ENSG00000198838	ENSG00000198838	RYR3	15:33603162-34158303	NOTEST	0.083371	0.29779	1.83668	0	1	1
ENSG00000198842	ENSG00000198842	DUSP27	1:167063281-167098402	NOTEST	0	0	0	0	1	1
ENSG00000198844	ENSG00000198844	ARHGEF15	17:8213558-8225829	NOTEST	0.0550523	0.00293769	-4.22805	0	1	1
ENSG00000198846	ENSG00000198846	TOX	8:59717976-60033905	NOTEST	0.41613	0.599502	0.526731	0	1	1
ENSG00000198848	ENSG00000198848	CES1	16:55836762-55867249	NOTEST	0	0	0	0	1	1
ENSG00000198851	ENSG00000198851	CD3E	11:118175259-118186890	NOTEST	0	0	0	0	1	1
ENSG00000198854	ENSG00000198854	C1orf68	1:152691997-152692905	NOTEST	0	0	0	0	1	1
ENSG00000198865	ENSG00000198865	CCDC152	5:42756902-42887494	NOTEST	0.0393851	0.0538485	0.451255	0	1	1
ENSG00000198868	ENSG00000198868	MIR4461	5:134240595-134347392	NOTEST	0	0.090772	inf	0	1	1
ENSG00000198877	ENSG00000198877	OR5D13	11:55540913-55541858	NOTEST	0	0	0	0	1	1
ENSG00000198879	ENSG00000198879	SFMBT2	10:7200585-7453450	NOTEST	0	0	0	0	1	1
ENSG00000198881	ENSG00000198881	ASB12	X:63444075-63615333	NOTEST	0	0	0	0	1	1
ENSG00000198883	ENSG00000198883	PNMA5	X:152157367-152162671	NOTEST	0	0	0	0	1	1
ENSG00000198885	ENSG00000198885	ITPRIPL1	2:96991068-96994091	NOTEST	0	0.00713063	inf	0	1	1
ENSG00000198889	ENSG00000198889	DCAF12L1	X:125683368-125686834	NOTEST	0	0	0	0	1	1
ENSG00000198915	ENSG00000198915	RASGEF1A	10:43689982-43762367	NOTEST	0.0359418	0.214014	2.57397	0	1	1
ENSG00000198923	ENSG00000198923	RP11-290L1.7	12:75956981-76377795	NOTEST	0	0	0	0	1	1
ENSG00000198932	ENSG00000198932	GPRASP1	X:101854095-101973607	NOTEST	0.191761	0.161596	-0.24692	0	1	1
ENSG00000198939	ENSG00000198939	ZFP2	5:178322894-178360213	NOTEST	0.0222954	0.0382472	0.778608	0	1	1
ENSG00000198944	ENSG00000198944	SOWAHA	5:132149032-132152488	NOTEST	0.00816606	0	#NAME?	0	1	1
ENSG00000198946	ENSG00000198946	SSX4B	X:48261523-48271344	NOTEST	0	0	0	0	1	1
ENSG00000198963	ENSG00000198963	RORB	9:77100466-77308093	NOTEST	0.379513	0.344556	-0.139413	0	1	1
ENSG00000198965	ENSG00000198965	OR10R2	1:158444243-158464676	NOTEST	0	0	0	0	1	1
ENSG00000198967	ENSG00000198967	OR10Z1	1:158576228-158577170	NOTEST	0	0	0	0	1	1
ENSG00000198972	ENSG00000198972	MIRLET7E	19:52188615-52215640	NOTEST	0	0	0	0	1	1
ENSG00000198973	ENSG00000198973	MIR375	2:219866361-219866431	NOTEST	0	0	0	0	1	1
ENSG00000198974	ENSG00000198974	MIR30E	1:41156051-41237275	NOTEST	0	0	0	0	1	1
ENSG00000198975	ENSG00000198975	MIRLET7A2	11:122017228-122017301	NOTEST	0	0	0	0	1	1
ENSG00000198976	ENSG00000198976	MIR429	1:1104384-1104467	NOTEST	0	0	0	0	1	1
ENSG00000198982	ENSG00000198982	MIR380	14:101491330-101491441	NOTEST	0	0	0	0	1	1
ENSG00000198983	ENSG00000198983	MIR449A	5:54408798-54469005	NOTEST	0	0	0	0	1	1
ENSG00000198984	ENSG00000198984	MIR345	14:100774195-100774293	NOTEST	0	0	0	0	1	1
ENSG00000198986	ENSG00000198986	MIRLET7A3	22:46445357-46509808	NOTEST	0	0	0	0	1	1

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ENSG00000198987	ENSG00000198987	MIR16-2	3:159943422-160203561	NOTEST	0	0	0	0	1	1
ENSG00000198995	ENSG00000198995	MIR340	5:179338650-179499118	NOTEST	0	0	0	0	1	1
ENSG00000198997	ENSG00000198997	MIR107	10:91342744-91410579	NOTEST	0	0	0	0	1	1
ENSG00000199001	ENSG00000199001	MIR448	X:113818550-114144624	NOTEST	0	0	0	0	1	1
ENSG00000199004	ENSG00000199004	MIR21	17:57697218-57919616	NOTEST	0	0	0	0	1	1
ENSG00000199005	ENSG00000199005	MIR370	14:101361106-101402336	NOTEST	0	0	0	0	1	1
ENSG00000199012	ENSG00000199012	MIR412	14:101531783-101531874	NOTEST	0	0	0	0	1	1
ENSG00000199015	ENSG00000199015	MIR377	14:101528342-101528476	NOTEST	0	0	0	0	1	1
ENSG00000199017	ENSG00000199017	MIR1-1	20:61141549-61167971	NOTEST	0	0	0	0	1	1
ENSG00000199020	ENSG00000199020	MIR381	14:101511493-101518132	NOTEST	0	0	0	0	1	1
ENSG00000199023	ENSG00000199023	MIR339	7:1036621-1177896	NOTEST	0	0	0	0	1	1
ENSG00000199024	ENSG00000199024	MIR103A2	20:3868885-3907605	NOTEST	0	0	0	0	1	1
ENSG00000199025	ENSG00000199025	MIR369	14:101531917-101532024	NOTEST	0	0	0	0	1	1
ENSG00000199030	ENSG00000199030	MIRLET7C	21:17442841-17999716	NOTEST	0	0	0	0	1	1
ENSG00000199031	ENSG00000199031	MIR371A	19:54290850-54291423	NOTEST	0	0	0	0	1	1
ENSG00000199032	ENSG00000199032	MIR425	3:48955220-49060928	NOTEST	0	0	0	0	1	1
ENSG00000199035	ENSG00000199035	MIR103A1	5:167975499-168006605	NOTEST	0	0	0	0	1	1
ENSG00000199036	ENSG00000199036	MIR219-1	6:33175611-33175721	NOTEST	0	0	0	0	1	1
ENSG00000199038	ENSG00000199038	MIR210	11:565659-568457	NOTEST	0	0	0	0	1	1
ENSG00000199043	ENSG00000199043	MIR335	7:130125882-130148500	NOTEST	0	0	0	0	1	1
ENSG00000199047	ENSG00000199047	MIR378A	5:149109860-149234585	NOTEST	0	0	0	0	1	1
ENSG00000199051	ENSG00000199051	MIR361	X:85116184-85302566	NOTEST	0	0	0	0	1	1
ENSG00000199053	ENSG00000199053	MIR324	17:7093208-7128592	NOTEST	0	0	0	0	1	1
ENSG00000199059	ENSG00000199059	MIR135B	1:205342379-205438152	NOTEST	0	0	0	0	1	1
ENSG00000199065	ENSG00000199065	MIR101-2	9:4792868-4885917	NOTEST	0	0	0	0	1	1
ENSG00000199066	ENSG00000199066	MIR330	19:46110251-46148887	NOTEST	0	0	0	0	1	1
ENSG00000199069	ENSG00000199069	MIR323A	14:101492068-101492154	NOTEST	0	0	0	0	1	1
ENSG00000199071	ENSG00000199071	MIR423	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000199072	ENSG00000199072	MIRLET7F1	9:96928570-96966850	NOTEST	0	0	0	0	1	1
ENSG00000199075	ENSG00000199075	MIR26A1	3:37903450-38025960	NOTEST	0	0	0	0	1	1
ENSG00000199077	ENSG00000199077	MIR129-2	11:43577985-43902276	NOTEST	0	0	0	0	1	1
ENSG00000199080	ENSG00000199080	MIR133B	6:52011611-52015917	NOTEST	0	0	0	0	1	1
ENSG00000199082	ENSG00000199082	MIR342	14:100437785-100610573	NOTEST	0	0	0	0	1	1
ENSG00000199085	ENSG00000199085	MIR148A	7:25989538-25989606	NOTEST	0	0	0	0	1	1
ENSG00000199088	ENSG00000199088	MIR379	14:101488365-101488491	NOTEST	0	0	0	0	1	1
ENSG00000199090	ENSG00000199090	MIR326	11:74975225-75062873	NOTEST	0	0	0	0	1	1
ENSG00000199092	ENSG00000199092	MIR410	14:101532248-101532328	NOTEST	0	0	0	0	1	1
ENSG00000199094	ENSG00000199094	MIR30C2	6:71931159-72130472	NOTEST	0	0	0	0	1	1
ENSG00000199095	ENSG00000199095	MIR372	19:54290850-54291423	NOTEST	0	0	0	0	1	1
ENSG00000199102	ENSG00000199102	MIR302C	4:113434671-113578748	NOTEST	0	0	0	0	1	1
ENSG00000199104	ENSG00000199104	MIR346	10:87359311-88126250	NOTEST	0	0	0	0	1	1
ENSG00000199107	ENSG00000199107	MIR409	14:101531636-101531715	NOTEST	0	0	0	0	1	1
ENSG00000199109	ENSG00000199109	MIR411	14:101489661-101489757	NOTEST	0	0	0	0	1	1
ENSG00000199121	ENSG00000199121	MIR26B	2:219262978-219270664	NOTEST	0	0	0	0	1	1
ENSG00000199122	ENSG00000199122	MIR148B	12:54624723-54745633	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000199127	ENSG00000199127	MIR383	8:13947372-15095848	NOTEST	0	0	0	0	1	1
ENSG00000199130	ENSG00000199130	MIR365A	16:14396144-14420210	NOTEST	0	0	0	0	1	1
ENSG00000199132	ENSG00000199132	MIR450A1	X:133674370-133674461	NOTEST	0	0	0	0	1	1
ENSG00000199133	ENSG00000199133	MIRLET7D	9:96928570-96966850	NOTEST	0	0	0	0	1	1
ENSG00000199135	ENSG00000199135	MIR101-1	1:65524116-65524191	NOTEST	0	0	0	0	1	1
ENSG00000199143	ENSG00000199143	MIR373	19:54291958-54292027	NOTEST	0	0	0	0	1	1
ENSG00000199145	ENSG00000199145	MIR302D	4:113434671-113578748	NOTEST	0	0	0	0	1	1
ENSG00000199150	ENSG00000199150	MIRLET7G	3:52288436-52333083	NOTEST	0	0	0	0	1	1
ENSG00000199151	ENSG00000199151	MIR337	14:101340829-101340922	NOTEST	0	0	0	0	1	1
ENSG00000199153	ENSG00000199153	MIR30D	8:135817118-135817188	NOTEST	0	0	0	0	1	1
ENSG00000199156	ENSG00000199156	MIR422A	15:64163128-64163218	NOTEST	0	0	0	0	1	1
ENSG00000199157	ENSG00000199157	MIR208A	14:23851198-23877486	NOTEST	0	0	0	0	1	1
ENSG00000199158	ENSG00000199158	MIR96	7:129414531-129414609	NOTEST	0	0	0	0	1	1
ENSG00000199161	ENSG00000199161	MIR126	9:139543061-139567130	NOTEST	0	0	0	0	1	1
ENSG00000199165	ENSG00000199165	MIRLET7A1	9:96928570-96966850	NOTEST	0	0	0	0	1	1
ENSG00000199168	ENSG00000199168	MIR374A	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000199169	ENSG00000199169	MIR367	4:113434671-113578748	NOTEST	0	0	0	0	1	1
ENSG00000199172	ENSG00000199172	MIR331	12:95702195-95702289	NOTEST	0	0	0	0	1	1
ENSG00000199177	ENSG00000199177	MIR31	9:21455482-21559668	NOTEST	0	0	0	0	1	1
ENSG00000199179	ENSG00000199179	MIRLET7I	12:62995530-63007855	NOTEST	0	0	0	0	1	1
ENSG00000199187	ENSG00000199187	MIR365B	17:29898160-29902678	NOTEST	0	0	0	0	1	1
ENSG00000199196	ENSG00000199196	SNORA25	13:34674847-34674975	NOTEST	0	0	0	0	1	1
ENSG00000199197	ENSG00000199197	RN7SKP72	18:1254383-1408345	NOTEST	0	0	0	0	1	1
ENSG00000199200	ENSG00000199200	Y_RNA	10:34398487-35104253	NOTEST	0	0	0	0	1	1
ENSG00000199201	ENSG00000199201	Y_RNA	10:74870216-75118617	NOTEST	0	0	0	0	1	1
ENSG00000199202	ENSG00000199202	RNA5SP289	9:98521512-98776842	NOTEST	0	0	0	0	1	1
ENSG00000199203	ENSG00000199203	Y_RNA	2:211130686-211130798	NOTEST	0	0	0	0	1	1
ENSG00000199204	ENSG00000199204	Y_RNA	18:31431063-31804916	NOTEST	0	0	0	0	1	1
ENSG00000199212	ENSG00000199212	RNU105C	8:55243246-55243455	NOTEST	0	0	0	0	1	1
ENSG00000199214	ENSG00000199214	Y_RNA	15:25922419-26110317	NOTEST	0	0	0	0	1	1
ENSG00000199217	ENSG00000199217	RNU6-1123P	11:119479134-119599794	NOTEST	0	0	0	0	1	1
ENSG00000199218	ENSG00000199218	RN7SKP184	20:51588945-52120853	NOTEST	0	0	0	0	1	1
ENSG00000199219	ENSG00000199219	RNU6-500P	5:172789136-172789243	NOTEST	0	0	0	0	1	1
ENSG00000199220	ENSG00000199220	Y_RNA	12:115095753-115095867	NOTEST	0	0	0	0	1	1
ENSG00000199222	ENSG00000199222	Y_RNA	10:21770644-21770746	NOTEST	0	0	0	0	1	1
ENSG00000199223	ENSG00000199223	Y_RNA	19:6572966-6573068	NOTEST	0	0	0	0	1	1
ENSG00000199224	ENSG00000199224	Y_RNA	7:115473326-115473427	NOTEST	0	0	0	0	1	1
ENSG00000199226	ENSG00000199226	RNU6-50P	X:46357161-46404892	NOTEST	0	0	0	0	1	1
ENSG00000199231	ENSG00000199231	snoU2_19	7:62636317-62636397	NOTEST	0	0	0	0	1	1
ENSG00000199235	ENSG00000199235	RNU6-1063P	11:87359380-87359441	NOTEST	0	0	0	0	1	1
ENSG00000199237	ENSG00000199237	RNU6-834P	12:49962000-50158717	NOTEST	0	0	0	0	1	1
ENSG00000199240	ENSG00000199240	RNA5SP46	1:43629845-43739673	NOTEST	0	0	0	0	1	1
ENSG00000199241	ENSG00000199241	Y_RNA	1:240861619-240861729	NOTEST	0	0	0	0	1	1
ENSG00000199245	ENSG00000199245	Y_RNA	12:88824218-88824327	NOTEST	0	0	0	0	1	1
ENSG00000199246	ENSG00000199246	RNU6-896P	6:154002581-154002688	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000199248	ENSG00000199248	RNU6-28P	22:31795508-32058418	NOTEST	0	0	0	0	1	1
ENSG00000199251	ENSG00000199251	RNU6-664P	2:208545256-208545363	NOTEST	0	0	0	0	1	1
ENSG00000199260	ENSG00000199260	RNU6-874P	11:128834954-129149219	NOTEST	0	0	0	0	1	1
ENSG00000199262	ENSG00000199262	MIR3607	5:85913720-85916779	NOTEST	0	0	0	0	1	1
ENSG00000199263	ENSG00000199263	Y_RNA	16:68508455-68508567	NOTEST	0	0	0	0	1	1
ENSG00000199266	ENSG00000199266	SNORA60	20:37075220-37079564	NOTEST	0	0	0	0	1	1
ENSG00000199270	ENSG00000199270	RNA5S12	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000199272	ENSG00000199272	RNU6-349P	18:6454960-6455067	NOTEST	0	0	0	0	1	1
ENSG00000199273	ENSG00000199273	Y_RNA	7:40165621-40174258	NOTEST	0	0	0	0	1	1
ENSG00000199276	ENSG00000199276	RNA5SP26	13:38210772-38444562	NOTEST	0	0	0	0	1	1
ENSG00000199279	ENSG00000199279	RNU6-661P	5:61601988-61924409	NOTEST	0	0	0	0	1	1
ENSG00000199282	ENSG00000199282	SNORA9	13:73160817-73160948	NOTEST	0	0	0	0	1	1
ENSG00000199283	ENSG00000199283	RNU1-58P	7:139941669-139941832	NOTEST	0	0	0	0	1	1
ENSG00000199285	ENSG00000199285	Y_RNA	14:39456484-39456587	NOTEST	0	0	0	0	1	1
ENSG00000199286	ENSG00000199286	RNU6-1094P	3:96327657-96327761	NOTEST	0	0	0	0	1	1
ENSG00000199287	ENSG00000199287	Y_RNA	20:40328259-40328355	NOTEST	0	0	0	0	1	1
ENSG00000199289	ENSG00000199289	RNU6-502P	6:26519578-26519686	NOTEST	0	0	0	0	1	1
ENSG00000199290	ENSG00000199290	Y_RNA	6:29718147-29718249	NOTEST	0	0	0	0	1	1
ENSG00000199291	ENSG00000199291	Y_RNA	14:31717833-31926716	NOTEST	0	0	0	0	1	1
ENSG00000199293	ENSG00000199293	SNORA21	17:37004117-37010096	NOTEST	0	0	0	0	1	1
ENSG00000199295	ENSG00000199295	RNU6-1312P	2:83884858-83884966	NOTEST	0	0	0	0	1	1
ENSG00000199299	ENSG00000199299	RNA5SP430	16:75894945-75895055	NOTEST	0	0	0	0	1	1
ENSG00000199301	ENSG00000199301	RNU6-208P	16:71657610-71758604	NOTEST	0	0	0	0	1	1
ENSG00000199303	ENSG00000199303	Y_RNA	6:100090112-100090223	NOTEST	0	0	0	0	1	1
ENSG00000199306	ENSG00000199306	RNU6-858P	3:197615945-197687013	NOTEST	0	0	0	0	1	1
ENSG00000199308	ENSG00000199308	RNU6-222P	19:55380393-55380500	NOTEST	0	0	0	0	1	1
ENSG00000199311	ENSG00000199311	SNORD115-34	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000199313	ENSG00000199313	RNU4-82P	9:127640645-127905785	NOTEST	0	0	0	0	1	1
ENSG00000199315	ENSG00000199315	RNA5SP347	11:97528463-97528582	NOTEST	0	0	0	0	1	1
ENSG00000199318	ENSG00000199318	RNA5SP52	1:87918922-87919056	NOTEST	0	0	0	0	1	1
ENSG00000199319	ENSG00000199319	RN7SKP25	3:142315228-142432506	NOTEST	0	0	0	0	1	1
ENSG00000199321	ENSG00000199321	SNORD60	10:128468270-128468343	NOTEST	0	0	0	0	1	1
ENSG00000199322	ENSG00000199322	RNA5SP183	5:54921672-55112985	NOTEST	0	0	0	0	1	1
ENSG00000199325	ENSG00000199325	RNU4-39P	11:66382434-66382561	NOTEST	0	0	0	0	1	1
ENSG00000199326	ENSG00000199326	RNU6-1298P	4:89011415-89152474	NOTEST	0	0	0	0	1	1
ENSG00000199327	ENSG00000199327	RNU6-230P	3:124801479-125094198	NOTEST	0	0	0	0	1	1
ENSG00000199331	ENSG00000199331	Y_RNA	9:111777431-111882225	NOTEST	0	0	0	0	1	1
ENSG00000199332	ENSG00000199332	Y_RNA	6:31368478-31445283	NOTEST	0	0	0	0	1	1
ENSG00000199334	ENSG00000199334	RNA5S11	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000199335	ENSG00000199335	RNU6-204P	4:3045827-3045934	NOTEST	0	0	0	0	1	1
ENSG00000199337	ENSG00000199337	RNA5S3	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000199347	ENSG00000199347	RNU5E-1	1:11968208-11968328	NOTEST	0	0	0	0	1	1
ENSG00000199348	ENSG00000199348	RNU6-766P	2:169312371-169769881	NOTEST	0	0	0	0	1	1
ENSG00000199349	ENSG00000199349	Y_RNA	1:206921324-206921437	NOTEST	0	0	0	0	1	1
ENSG00000199350	ENSG00000199350	RNA5SP432	16:84043271-84076241	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000199352	ENSG00000199352	RNA5S1	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000199354	ENSG00000199354	RNA5SP273	8:91233715-91632298	NOTEST	0	0	0	0	1	1
ENSG00000199357	ENSG00000199357	Y_RNA	18:21032786-21066567	NOTEST	0	0	0	0	1	1
ENSG00000199360	ENSG00000199360	RNU6-1115P	6:111177619-111177725	NOTEST	0	0	0	0	1	1
ENSG00000199361	ENSG00000199361	RNU1-150P	5:40269659-40269821	NOTEST	0	0	0	0	1	1
ENSG00000199362	ENSG00000199362	Y_RNA	11:75514475-75854239	NOTEST	0	0	0	0	1	1
ENSG00000199363	ENSG00000199363	SNORA63	3:183165395-183173801	NOTEST	0	0	0	0	1	1
ENSG00000199364	ENSG00000199364	RNA5SP327	10:112404154-112599227	NOTEST	0	0	0	0	1	1
ENSG00000199366	ENSG00000199366	Y_RNA	18:21083472-21166862	NOTEST	0	0	0	0	1	1
ENSG00000199368	ENSG00000199368	RNU6-1084P	8:11197145-11332224	NOTEST	0	0	0	0	1	1
ENSG00000199370	ENSG00000199370	U3	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000199373	ENSG00000199373	RNA5SP453	18:29598334-30050447	NOTEST	0	0	0	0	1	1
ENSG00000199377	ENSG00000199377	RNU5F-1	1:45140363-45191263	NOTEST	0	0	0	0	1	1
ENSG00000199378	ENSG00000199378	Y_RNA	5:99357507-99357610	NOTEST	0	0	0	0	1	1
ENSG00000199381	ENSG00000199381	RNU6-79P	13:73302060-73590591	NOTEST	0	0	0	0	1	1
ENSG00000199385	ENSG00000199385	RNU6-369P	1:44856393-44856495	NOTEST	0	0	0	0	1	1
ENSG00000199390	ENSG00000199390	SNORD114-7	14:101426845-101433377	NOTEST	0	0	0	0	1	1
ENSG00000199392	ENSG00000199392	SNORA25	18:75133574-75272719	NOTEST	0	0	0	0	1	1
ENSG00000199394	ENSG00000199394	RNU6-600P	12:49285912-49286011	NOTEST	0	0	0	0	1	1
ENSG00000199395	ENSG00000199395	RNA5SP93	2:56179292-56613308	NOTEST	0	0	0	0	1	1
ENSG00000199396	ENSG00000199396	RNA5S5	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000199398	ENSG00000199398	Y_RNA	5:159435451-159435553	NOTEST	0	0	0	0	1	1
ENSG00000199400	ENSG00000199400	RNY4P19	2:230899697-230933715	NOTEST	0	0	0	0	1	1
ENSG00000199402	ENSG00000199402	RNA5SP308	10:29135336-29170827	NOTEST	0	0	0	0	1	1
ENSG00000199404	ENSG00000199404	RNA5SP250	7:152290057-152290176	NOTEST	0	0	0	0	1	1
ENSG00000199405	ENSG00000199405	SNORA1	8:56792371-56923940	NOTEST	0	0	0	0	1	1
ENSG00000199407	ENSG00000199407	RNA5SP301	10:13628926-14504141	NOTEST	0	0	0	0	1	1
ENSG00000199409	ENSG00000199409	Y_RNA	5:149432853-149492935	NOTEST	0	0	0	0	1	1
ENSG00000199410	ENSG00000199410	Y_RNA	X:16930337-16930440	NOTEST	0	0	0	0	1	1
ENSG00000199411	ENSG00000199411	SNORD62	9:139981378-140003635	NOTEST	0	0	0	0	1	1
ENSG00000199415	ENSG00000199415	RNA5SP370	12:104510854-104532067	NOTEST	0	0	0	0	1	1
ENSG00000199420	ENSG00000199420	RN7SKP170	4:15004297-15447790	NOTEST	0	0	0	0	1	1
ENSG00000199422	ENSG00000199422	VTRNA3-1P	X:53489149-53489251	NOTEST	0	0	0	0	1	1
ENSG00000199424	ENSG00000199424	Y_RNA	X:135653863-135653974	NOTEST	0	0	0	0	1	1
ENSG00000199426	ENSG00000199426	RNU1-108P	17:56597197-56769416	NOTEST	0	0	0	0	1	1
ENSG00000199432	ENSG00000199432	Y_RNA	9:67764521-67764633	NOTEST	0	0	0	0	1	1
ENSG00000199436	ENSG00000199436	SNORD9	14:21853352-21924285	NOTEST	0	0	0	0	1	1
ENSG00000199440	ENSG00000199440	Y_RNA	14:78266425-78401355	NOTEST	0	0	0	0	1	1
ENSG00000199442	ENSG00000199442	Y_RNA	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000199444	ENSG00000199444	Y_RNA	19:12199059-12199161	NOTEST	0	0	0	0	1	1
ENSG00000199446	ENSG00000199446	RNU6-543P	10:64869898-64870006	NOTEST	0	0	0	0	1	1
ENSG00000199448	ENSG00000199448	RNU6-845P	16:46503252-46603009	NOTEST	0	0	0	0	1	1
ENSG00000199450	ENSG00000199450	RNA5SP276	8:116962735-117337297	NOTEST	0	0	0	0	1	1
ENSG00000199453	ENSG00000199453	SNORD115-12	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000199454	ENSG00000199454	RNA5SP388	14:78644145-78644264	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000199455	ENSG00000199455	RNA5SP191	5:128795251-129522327	NOTEST	0	0	0	0	1	1
ENSG00000199458	ENSG00000199458	RNU4-35P	6:121775126-121775267	NOTEST	0	0	0	0	1	1
ENSG00000199459	ENSG00000199459	Y_RNA	1:85731930-86043933	NOTEST	0	0	0	0	1	1
ENSG00000199460	ENSG00000199460	RNU6-1216P	2:69240309-69476459	NOTEST	0	0	0	0	1	1
ENSG00000199461	ENSG00000199461	Y_RNA	14:21147569-21147671	NOTEST	0	0	0	0	1	1
ENSG00000199466	ENSG00000199466	Y_RNA	10:126150402-126480439	NOTEST	0	0	0	0	1	1
ENSG00000199468	ENSG00000199468	RNU6-556P	5:156241140-156241245	NOTEST	0	0	0	0	1	1
ENSG00000199469	ENSG00000199469	RNU1-62P	3:72625841-72626005	NOTEST	0	0	0	0	1	1
ENSG00000199470	ENSG00000199470	SNORA64	7:12740382-12740514	NOTEST	0	0	0	0	1	1
ENSG00000199471	ENSG00000199471	Y_RNA	1:202860227-202897764	NOTEST	0	0	0	0	1	1
ENSG00000199472	ENSG00000199472	Y_RNA	14:74318546-74551196	NOTEST	0	0	0	0	1	1
ENSG00000199473	ENSG00000199473	SNORA63	7:17412824-17412950	NOTEST	0	0	0	0	1	1
ENSG00000199474	ENSG00000199474	SNORA27	16:12936343-12936467	NOTEST	0	0	0	0	1	1
ENSG00000199475	ENSG00000199475	RN7SKP104	7:97228244-97228572	NOTEST	0	0	0	0	1	1
ENSG00000199476	ENSG00000199476	Y_RNA	3:48282589-48343175	NOTEST	0	0	0	0	1	1
ENSG00000199477	ENSG00000199477	SNORA31	13:45911007-45965872	NOTEST	0	3.69922	inf	0	1	1
ENSG00000199480	ENSG00000199480	RNA5SP357	14:107092676-107092791	NOTEST	0	0	0	0	1	1
ENSG00000199482	ENSG00000199482	RNU6-633P	16:10590128-10590231	NOTEST	0	0	0	0	1	1
ENSG00000199483	ENSG00000199483	RNU4-15P	9:86211358-86211499	NOTEST	0	0	0	0	1	1
ENSG00000199487	ENSG00000199487	Y_RNA	5:41963969-41964071	NOTEST	0	0	0	0	1	1
ENSG00000199488	ENSG00000199488	RNU1-70P	3:170712658-170712822	NOTEST	0	0	0	0	1	1
ENSG00000199489	ENSG00000199489	SNORD115-25	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000199490	ENSG00000199490	Y_RNA	20:48537133-48537231	NOTEST	0	0	0	0	1	1
ENSG00000199492	ENSG00000199492	RNU6-1313P	17:48043438-48043540	NOTEST	0	0	0	0	1	1
ENSG00000199497	ENSG00000199497	RNU1-94P	20:30435439-30539895	NOTEST	0	0	0	0	1	1
ENSG00000199506	ENSG00000199506	RNU6-247P	12:96186306-96186413	NOTEST	0	0	0	0	1	1
ENSG00000199508	ENSG00000199508	RNA5SP110	2:165714941-165715056	NOTEST	0	0	0	0	1	1
ENSG00000199509	ENSG00000199509	RNA5SP477	20:21106623-21227260	NOTEST	0	0	0	0	1	1
ENSG00000199512	ENSG00000199512	RNU6-212P	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000199514	ENSG00000199514	RNU6-235P	3:38323784-38360066	NOTEST	0	0	0	0	1	1
ENSG00000199515	ENSG00000199515	Y_RNA	22:41461557-41461650	NOTEST	0	0	0	0	1	1
ENSG00000199516	ENSG00000199516	Y_RNA	7:129593073-129691291	NOTEST	0	0	0	0	1	1
ENSG00000199520	ENSG00000199520	RNU6-386P	3:75955845-77699115	NOTEST	0	0	0	0	1	1
ENSG00000199523	ENSG00000199523	RNA5SP226	6:165740775-166401536	NOTEST	0	0	0	0	1	1
ENSG00000199525	ENSG00000199525	RNA5SP295	9:114980714-115095947	NOTEST	0	0	0	0	1	1
ENSG00000199529	ENSG00000199529	RNU6-462P	4:102332442-102995969	NOTEST	0	0	0	0	1	1
ENSG00000199530	ENSG00000199530	Y_RNA	4:83739813-83934079	NOTEST	0	0	0	0	1	1
ENSG00000199535	ENSG00000199535	RNA5SP305	10:24872537-25012597	NOTEST	0	0	0	0	1	1
ENSG00000199536	ENSG00000199536	RNU6-315P	3:169804519-169899537	NOTEST	0	0	0	0	1	1
ENSG00000199540	ENSG00000199540	Y_RNA	5:140372-190085	NOTEST	0	0	0	0	1	1
ENSG00000199545	ENSG00000199545	RNA5SP195	5:138282408-138667360	NOTEST	0	0	0	0	1	1
ENSG00000199546	ENSG00000199546	Y_RNA	3:49306034-49378145	NOTEST	0	0	0	0	1	1
ENSG00000199550	ENSG00000199550	Y_RNA	11:2349978-2418649	NOTEST	0	0	0	0	1	1
ENSG00000199551	ENSG00000199551	RNU6-545P	12:12202777-12419946	NOTEST	0	0	0	0	1	1
ENSG00000199552	ENSG00000199552	SNORA63	5:40655064-40655196	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000199556	ENSG00000199556	RNA5SP361	12:45511553-45511671	NOTEST	0	0	0	0	1	1
ENSG00000199562	ENSG00000199562	RNU6-37P	1:10270862-10441661	NOTEST	0	0	0	0	1	1
ENSG00000199564	ENSG00000199564	RNA5SP502	X:41152050-41152169	NOTEST	0	0	0	0	1	1
ENSG00000199565	ENSG00000199565	Y_RNA	1:153698727-153698829	NOTEST	0	0	0	0	1	1
ENSG00000199566	ENSG00000199566	SNORA64	12:47739948-47740080	NOTEST	0	0	0	0	1	1
ENSG00000199567	ENSG00000199567	Y_RNA	X:85116184-85302566	NOTEST	0	0	0	0	1	1
ENSG00000199568	ENSG00000199568	RNU5A-1	15:65526797-65592956	NOTEST	0	0	0	0	1	1
ENSG00000199570	ENSG00000199570	RNU6-228P	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000199571	ENSG00000199571	SNORA22	12:40019968-40499891	NOTEST	0	0	0	0	1	1
ENSG00000199572	ENSG00000199572	RNA5SP174	4:190936292-190936410	NOTEST	0	0	0	0	1	1
ENSG00000199574	ENSG00000199574	SNORD18C	15:66790354-66858317	NOTEST	0	0	0	0	1	1
ENSG00000199575	ENSG00000199575	SNORD114-1	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000199577	ENSG00000199577	RNU6-822P	3:20310456-20310562	NOTEST	0	0	0	0	1	1
ENSG00000199580	ENSG00000199580	Y_RNA	15:75246756-75313837	NOTEST	0	0	0	0	1	1
ENSG00000199584	ENSG00000199584	Y_RNA	12:128103880-128103992	NOTEST	0	0	0	0	1	1
ENSG00000199585	ENSG00000199585	RNA5SP119	2:212240445-213403565	NOTEST	0	0	0	0	1	1
ENSG00000199591	ENSG00000199591	Y_RNA	3:47892181-48130769	NOTEST	0	0	0	0	1	1
ENSG00000199592	ENSG00000199592	RNA5SP321	10:78629358-79398353	NOTEST	0	0	0	0	1	1
ENSG00000199593	ENSG00000199593	SNORD114-14	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000199594	ENSG00000199594	RNU6-1301P	3:37034822-37225180	NOTEST	0	0	0	0	1	1
ENSG00000199595	ENSG00000199595	Y_RNA	1:161669295-161669397	NOTEST	0	0	0	0	1	1
ENSG00000199598	ENSG00000199598	RNU6-859P	21:45285066-45406417	NOTEST	0	0	0	0	1	1
ENSG00000199601	ENSG00000199601	RNU6-562P	X:74422537-74422644	NOTEST	0	0	0	0	1	1
ENSG00000199603	ENSG00000199603	RNU6-951P	2:38150329-38408997	NOTEST	0	0	0	0	1	1
ENSG00000199605	ENSG00000199605	RNY4P24	13:52951304-52980629	NOTEST	0	0	0	0	1	1
ENSG00000199609	ENSG00000199609	RNA5SP124	3:14436147-14436257	NOTEST	0	0	0	0	1	1
ENSG00000199620	ENSG00000199620	RNA5SP258	8:25994395-25994514	NOTEST	0	0	0	0	1	1
ENSG00000199622	ENSG00000199622	RN7SKP20	X:13587723-13651694	NOTEST	0	0	0	0	1	1
ENSG00000199626	ENSG00000199626	RNU6-989P	2:187866602-188430487	NOTEST	0	0	0	0	1	1
ENSG00000199627	ENSG00000199627	RNU6-1010P	7:130626518-131182453	NOTEST	0	0	0	0	1	1
ENSG00000199629	ENSG00000199629	RNU1-14P	7:53433750-53433902	NOTEST	0	0	0	0	1	1
ENSG00000199630	ENSG00000199630	Y_RNA	6:90539612-90584155	NOTEST	0	0	0	0	1	1
ENSG00000199631	ENSG00000199631	SNORD33	19:49949554-49995565	NOTEST	0	0	0	0	1	1
ENSG00000199633	ENSG00000199633	SNORA63	15:78370149-78538030	NOTEST	0	0	0	0	1	1
ENSG00000199634	ENSG00000199634	RNU4-79P	4:159236462-159574524	NOTEST	0	0	0	0	1	1
ENSG00000199635	ENSG00000199635	Y_RNA	9:21160233-21160335	NOTEST	0	0	0	0	1	1
ENSG00000199636	ENSG00000199636	Y_RNA	18:22006579-22033499	NOTEST	0	0	0	0	1	1
ENSG00000199638	ENSG00000199638	RNA5SP319	10:70173820-70231879	NOTEST	0	0	0	0	1	1
ENSG00000199640	ENSG00000199640	RN7SKP294	8:50242768-50243106	NOTEST	0	0	0	0	1	1
ENSG00000199641	ENSG00000199641	Y_RNA	7:74880904-74988262	NOTEST	0	0	0	0	1	1
ENSG00000199643	ENSG00000199643	RNU4-90P	5:90566543-90566684	NOTEST	0	0	0	0	1	1
ENSG00000199645	ENSG00000199645	RNU6-1330P	5:74073398-74163679	NOTEST	0	0	0	0	1	1
ENSG00000199646	ENSG00000199646	RNU6-1272P	7:138391039-138666064	NOTEST	0	0	0	0	1	1
ENSG00000199652	ENSG00000199652	RNU1-35P	8:136754585-136754738	NOTEST	0	0	0	0	1	1
ENSG00000199654	ENSG00000199654	RNA5SP389	HG1592_PATCH:10710300-107103123	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000199664	ENSG00000199664	RNU6-1266P	10:79536708-79536813	NOTEST	0	0	0	0	1	1
ENSG00000199666	ENSG00000199666	U3	1:91123306-91123520	NOTEST	0	0	0	0	1	1
ENSG00000199667	ENSG00000199667	Y_RNA	8:101170133-101348446	NOTEST	0	0	0	0	1	1
ENSG00000199668	ENSG00000199668	Y_RNA	16:11343475-11445619	NOTEST	0	0	0	0	1	1
ENSG00000199672	ENSG00000199672	RNU4-21P	1:229652328-229694442	NOTEST	0	0	0	0	1	1
ENSG00000199673	ENSG00000199673	SNORD16	15:66790354-66858317	NOTEST	0	0	0	0	1	1
ENSG00000199674	ENSG00000199674	RNU6-862P	17:15879873-16256970	NOTEST	0	0	0	0	1	1
ENSG00000199676	ENSG00000199676	Y_RNA	20:34359895-34538303	NOTEST	0	0	0	0	1	1
ENSG00000199677	ENSG00000199677	Y_RNA	5:132328790-132328892	NOTEST	0	0	0	0	1	1
ENSG00000199678	ENSG00000199678	RNY4P5	8:124014799-124164393	NOTEST	0	0	0	0	1	1
ENSG00000199683	ENSG00000199683	RN7SKP185	20:36603557-36603883	NOTEST	0	0	0	0	1	1
ENSG00000199687	ENSG00000199687	RNU1-38P	2:85955316-85955460	NOTEST	0	0	0	0	1	1
ENSG00000199691	ENSG00000199691	RN7SKP173	20:37377084-37400834	NOTEST	0	0.159707	inf	0	1	1
ENSG00000199695	ENSG00000199695	RNU6-1128P	22:31608224-31676066	NOTEST	0	0	0	0	1	1
ENSG00000199697	ENSG00000199697	RNU6-446P	17:60704761-60770958	NOTEST	0	0	0	0	1	1
ENSG00000199698	ENSG00000199698	Y_RNA	21:24804500-24804602	NOTEST	0	0	0	0	1	1
ENSG00000199700	ENSG00000199700	RNU6-223P	7:135611202-135662101	NOTEST	0	0	0	0	1	1
ENSG00000199701	ENSG00000199701	Y_RNA	8:95725942-95726040	NOTEST	0	0	0	0	1	1
ENSG00000199702	ENSG00000199702	RNU6-170P	18:12304089-12304193	NOTEST	0	0	0	0	1	1
ENSG00000199704	ENSG00000199704	SNORD115-29	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000199705	ENSG00000199705	Y_RNA	X:122990911-122991013	NOTEST	0	0	0	0	1	1
ENSG00000199709	ENSG00000199709	RNU4-23P	11:122753390-122830506	NOTEST	0	0	0	0	1	1
ENSG00000199710	ENSG00000199710	Y_RNA	1:111307029-111307128	NOTEST	0	0	0	0	1	1
ENSG00000199711	ENSG00000199711	Y_RNA	7:99520891-99546243	NOTEST	0	0	0	0	1	1
ENSG00000199712	ENSG00000199712	SNORD115-2	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000199713	ENSG00000199713	U8	18:56481111-56501596	NOTEST	0	0	0	0	1	1
ENSG00000199715	ENSG00000199715	Y_RNA	6:18273395-18273497	NOTEST	0	0	0	0	1	1
ENSG00000199716	ENSG00000199716	Y_RNA	14:23337026-23337126	NOTEST	0	0	0	0	1	1
ENSG00000199719	ENSG00000199719	RN7SKP74	20:18269120-18297640	NOTEST	0.312642	0	#NAME?	0	1	1
ENSG00000199727	ENSG00000199727	U3	2:105149230-105149442	NOTEST	0	0	0	0	1	1
ENSG00000199728	ENSG00000199728	RNU6-655P	18:75796738-75796845	NOTEST	0	0	0	0	1	1
ENSG00000199730	ENSG00000199730	RN7SKP95	15:58887402-59042177	NOTEST	0	0	0	0	1	1
ENSG00000199731	ENSG00000199731	RNU6-1079P	5:32227099-32313115	NOTEST	0	0	0	0	1	1
ENSG00000199732	ENSG00000199732	Y_RNA	8:97273942-97349223	NOTEST	0	0	0	0	1	1
ENSG00000199733	ENSG00000199733	RNA5SP307	10:26727131-26856732	NOTEST	0	0	0	0	1	1
ENSG00000199735	ENSG00000199735	RNU6-227P	17:74652401-74652504	NOTEST	0	0	0	0	1	1
ENSG00000199739	ENSG00000199739	RNU6-552P	14:45743561-45743680	NOTEST	0	0	0	0	1	1
ENSG00000199740	ENSG00000199740	Y_RNA	12:51333709-51333809	NOTEST	0	0	0	0	1	1
ENSG00000199744	ENSG00000199744	SNORD36A	9:136215068-136218281	NOTEST	0	0	0	0	1	1
ENSG00000199751	ENSG00000199751	Y_RNA	X:70586113-70752224	NOTEST	0	0	0	0	1	1
ENSG00000199753	ENSG00000199753	SNORD104	17:62223329-62223836	NOTEST	0	0	0	0	1	1
ENSG00000199755	ENSG00000199755	Y_RNA	14:67707825-67853233	NOTEST	0	0	0	0	1	1
ENSG00000199756	ENSG00000199756	Y_RNA	1:29208237-29208347	NOTEST	0	0	0	0	1	1
ENSG00000199762	ENSG00000199762	Y_RNA	6:47445524-47594999	NOTEST	0	0	0	0	1	1
ENSG00000199764	ENSG00000199764	Y_RNA	7:114701590-114871409	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000199765	ENSG00000199765	RNU6-363P	5:31595671-31595776	NOTEST	0	0	0	0	1	1
ENSG00000199767	ENSG00000199767	RNU6-78P	13:25946208-26599989	NOTEST	0	0	0	0	1	1
ENSG00000199769	ENSG00000199769	U3	X:69748789-70128581	NOTEST	0	0	0	0	1	1
ENSG00000199771	ENSG00000199771	RNA5SP426	16:50890524-50913189	NOTEST	0	0	0	0	1	1
ENSG00000199773	ENSG00000199773	RNU1-76P	5:7980258-7980417	NOTEST	0	0	0	0	1	1
ENSG00000199780	ENSG00000199780	Y_RNA	4:60399503-60399616	NOTEST	0	0	0	0	1	1
ENSG00000199781	ENSG00000199781	Y_RNA	2:233562008-233880595	NOTEST	0	0	0	0	1	1
ENSG00000199782	ENSG00000199782	SNORD115-9	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000199783	ENSG00000199783	SNORD56	22:25202235-25323545	NOTEST	0	0	0	0	1	1
ENSG00000199784	ENSG00000199784	RNU6-1287P	15:56536206-56757335	NOTEST	0	0	0	0	1	1
ENSG00000199786	ENSG00000199786	RNA5SP188	5:101466710-101466839	NOTEST	0	0	0	0	1	1
ENSG00000199787	ENSG00000199787	SNORA42	16:30418617-30441396	NOTEST	0	0	0	0	1	1
ENSG00000199788	ENSG00000199788	RNY3P2	13:49550047-49783915	NOTEST	0	0	0	0	1	1
ENSG00000199790	ENSG00000199790	RNU6-836P	4:40812043-41218731	NOTEST	0	0	0	0	1	1
ENSG00000199791	ENSG00000199791	RNU6-451P	2:231451835-231451942	NOTEST	0	0	0	0	1	1
ENSG00000199792	ENSG00000199792	RNU6-1233P	3:174156362-175523428	NOTEST	0	0	0	0	1	1
ENSG00000199796	ENSG00000199796	RNU6-924P	19:46800302-46846690	NOTEST	0	0	0	0	1	1
ENSG00000199797	ENSG00000199797	Y_RNA	22:28247656-29075853	NOTEST	0	0	0	0	1	1
ENSG00000199798	ENSG00000199798	SNORD114-5	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000199801	ENSG00000199801	Y_RNA	17:67982126-67982235	NOTEST	0	0	0	0	1	1
ENSG00000199803	ENSG00000199803	RNU6-1159P	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000199804	ENSG00000199804	RNA5SP383	14:24612573-24636611	NOTEST	0	0	0	0	1	1
ENSG00000199805	ENSG00000199805	RNU1-134P	20:62526517-62567384	NOTEST	0	0	0	0	1	1
ENSG00000199806	ENSG00000199806	RNA5SP491	21:38123188-38362536	NOTEST	0	0	0	0	1	1
ENSG00000199809	ENSG00000199809	RNA5SP374	12:119256608-119271341	NOTEST	0	0	0	0	1	1
ENSG00000199812	ENSG00000199812	RNU6-428P	3:146289263-146289370	NOTEST	0	0	0	0	1	1
ENSG00000199814	ENSG00000199814	RNU6-1260P	9:14734663-14910993	NOTEST	0	0	0	0	1	1
ENSG00000199815	ENSG00000199815	SNORA43	3:8661085-9005457	NOTEST	0	0	0	0	1	1
ENSG00000199824	ENSG00000199824	RNU6-199P	12:51487445-51566926	NOTEST	0	0	0	0	1	1
ENSG00000199827	ENSG00000199827	RNU6-1290P	2:175894496-175894605	NOTEST	0	0	0	0	1	1
ENSG00000199831	ENSG00000199831	RN7SKP291	1:55842198-55842525	NOTEST	0	0	0	0	1	1
ENSG00000199832	ENSG00000199832	Y_RNA	X:106366656-106449670	NOTEST	0	0	0	0	1	1
ENSG00000199833	ENSG00000199833	SNORD115-21	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000199836	ENSG00000199836	RNU1-47P	14:100411651-100411814	NOTEST	0	0	0	0	1	1
ENSG00000199837	ENSG00000199837	RNA5SP71	1:182868999-182922660	NOTEST	0	0	0	0	1	1
ENSG00000199839	ENSG00000199839	RNA5SP150	3:180701496-181554668	NOTEST	0	0	0	0	1	1
ENSG00000199840	ENSG00000199840	Y_RNA	1:184140847-184140957	NOTEST	0	0	0	0	1	1
ENSG00000199843	ENSG00000199843	RNA5SP358	12:38555267-38555384	NOTEST	0	0	0	0	1	1
ENSG00000199845	ENSG00000199845	RNA5SP375	12:123767462-123767581	NOTEST	0	0	0	0	1	1
ENSG00000199846	ENSG00000199846	RNU1-72P	7:129074273-129128240	NOTEST	1.34642	0	#NAME?	0	1	1
ENSG00000199849	ENSG00000199849	RNU5F-6P	1:164320509-164320625	NOTEST	0	0	0	0	1	1
ENSG00000199851	ENSG00000199851	U3	6:27983345-27983553	NOTEST	0	0	0	0	1	1
ENSG00000199855	ENSG00000199855	RNU6-490P	10:27280842-27389421	NOTEST	0	0	0	0	1	1
ENSG00000199856	ENSG00000199856	U3	18:7566779-8406951	NOTEST	0	0	0	0	1	1
ENSG00000199857	ENSG00000199857	SNORD50	4:77234153-77343021	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000199858	ENSG00000199858	RNU6-1120P	3:177725459-177725567	NOTEST	0	0	0	0	1	1
ENSG00000199859	ENSG00000199859	RNU6-582P	4:158122713-158122820	NOTEST	0	0	0	0	1	1
ENSG00000199862	ENSG00000199862	Y_RNA	4:127949261-127949374	NOTEST	0	0	0	0	1	1
ENSG00000199865	ENSG00000199865	RNU6-495P	22:41763336-41795330	NOTEST	0	0	0	0	1	1
ENSG00000199866	ENSG00000199866	Y_RNA	2:173292081-173489823	NOTEST	0	0	0	0	1	1
ENSG00000199867	ENSG00000199867	Y_RNA	18:59992519-60058516	NOTEST	0	0	0	0	1	1
ENSG00000199870	ENSG00000199870	Y_RNA	7:74880904-74988262	NOTEST	0	0	0	0	1	1
ENSG00000199872	ENSG00000199872	RNU6-942P	2:26256975-26360323	NOTEST	0	0	0	0	1	1
ENSG00000199874	ENSG00000199874	RNA5SP452	18:21718941-21977844	NOTEST	0	0	0	0	1	1
ENSG00000199875	ENSG00000199875	Y_RNA	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000199876	ENSG00000199876	RN7SKP131	22:20455668-20455969	NOTEST	0	0	0	0	1	1
ENSG00000199878	ENSG00000199878	RN7SKP149	X:142285033-142285377	NOTEST	0	0	0	0	1	1
ENSG00000199879	ENSG00000199879	RNU1-120P	1:147735750-147735907	NOTEST	0	0	0	0	1	1
ENSG00000199880	ENSG00000199880	RNU6-888P	5:137450865-137475132	NOTEST	0	0	0	0	1	1
ENSG00000199881	ENSG00000199881	Y_RNA	10:93806448-94050844	NOTEST	0	0	0	0	1	1
ENSG00000199883	ENSG00000199883	RN7SKP90	11:16799841-17074583	NOTEST	0	0	0	0	1	1
ENSG00000199884	ENSG00000199884	Y_RNA	2:153140863-153140974	NOTEST	0	0	0	0	1	1
ENSG00000199885	ENSG00000199885	RNU6-330P	X:73899887-73899994	NOTEST	0	0	0	0	1	1
ENSG00000199886	ENSG00000199886	RNU6-249P	12:42632248-42984157	NOTEST	0	0	0	0	1	1
ENSG00000199890	ENSG00000199890	Y_RNA	1:111981259-112005395	NOTEST	0	0	0	0	1	1
ENSG00000199892	ENSG00000199892	RNU1-17P	5:180156585-180156737	NOTEST	0	0	0	0	1	1
ENSG00000199894	ENSG00000199894	snoU2_19	4:111286888-111486441	NOTEST	0	0	0	0	1	1
ENSG00000199895	ENSG00000199895	Y_RNA	12:92378755-92583436	NOTEST	0	0	0	0	1	1
ENSG00000199899	ENSG00000199899	Y_RNA	12:113587662-113623284	NOTEST	0	0	0	0	1	1
ENSG00000199900	ENSG00000199900	RNA5SP463	19:7951861-7951981	NOTEST	0	0	0	0	1	1
ENSG00000199901	ENSG00000199901	Y_RNA	4:53652703-53652805	NOTEST	0	0	0	0	1	1
ENSG00000199903	ENSG00000199903	RNU6-1273P	12:51431281-51431385	NOTEST	0	0	0	0	1	1
ENSG00000199905	ENSG00000199905	RNU6-492P	9:110237316-110237420	NOTEST	0	0	0	0	1	1
ENSG00000199906	ENSG00000199906	RNU5B-2P	3:40540381-40540494	NOTEST	0	0	0	0	1	1
ENSG00000199910	ENSG00000199910	RNA5S10	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000199911	ENSG00000199911	Y_RNA	5:24910702-24910804	NOTEST	0	0	0	0	1	1
ENSG00000199912	ENSG00000199912	Y_RNA	12:7952956-7953063	NOTEST	0	0	0	0	1	1
ENSG00000199913	ENSG00000199913	Y_RNA	7:72440226-72555749	NOTEST	0	0	0	0	1	1
ENSG00000199914	ENSG00000199914	SNORD114-16	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000199920	ENSG00000199920	RNU4-44P	X:133699867-133898352	NOTEST	0	0	0	0	1	1
ENSG00000199921	ENSG00000199921	RNU6-161P	1:77218819-77218925	NOTEST	0	0	0	0	1	1
ENSG00000199924	ENSG00000199924	RNU6-1252P	4:53361014-53361118	NOTEST	0	0	0	0	1	1
ENSG00000199927	ENSG00000199927	U3	3:30345812-30346027	NOTEST	0	0	0	0	1	1
ENSG00000199929	ENSG00000199929	RNA5SP405	16:25703346-26149009	NOTEST	0	0	0	0	1	1
ENSG00000199932	ENSG00000199932	RNU1-18P	6:122532793-122532957	NOTEST	0	0	0	0	1	1
ENSG00000199933	ENSG00000199933	Y_RNA	12:102090724-102137918	NOTEST	0	0	0	0	1	1
ENSG00000199934	ENSG00000199934	SNORD81	1:86057962-86058039	NOTEST	0	0	0	0	1	1
ENSG00000199936	ENSG00000199936	Y_RNA	2:85687266-85687375	NOTEST	0	0	0	0	1	1
ENSG00000199938	ENSG00000199938	Y_RNA	6:38136226-38607924	NOTEST	0	0	0	0	1	1
ENSG00000199940	ENSG00000199940	RN7SKP75	7:70597154-71178585	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000199942	ENSG00000199942	SNORD114-19	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000199944	ENSG00000199944	RNU6-653P	6:109307639-109416022	NOTEST	0	0	0	0	1	1
ENSG00000199949	ENSG00000199949	Y_RNA	16:86259185-86309351	NOTEST	0	0	0	0	1	1
ENSG00000199953	ENSG00000199953	RNA5SP443	17:43404731-43404863	NOTEST	0	0	0	0	1	1
ENSG00000199959	ENSG00000199959	SNORA2	1:84743003-84743140	NOTEST	0	0	0	0	1	1
ENSG00000199960	ENSG00000199960	SNORD115-14	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000199961	ENSG00000199961	SNORD1B	17:74553847-74583038	NOTEST	0	0	0	0	1	1
ENSG00000199962	ENSG00000199962	Y_RNA	21:18884699-18965897	NOTEST	0	0	0	0	1	1
ENSG00000199963	ENSG00000199963	RNU6-605P	1:39325671-39407471	NOTEST	0	0	0	0	1	1
ENSG00000199964	ENSG00000199964	Y_RNA	2:65061189-65061291	NOTEST	0	0	0	0	1	1
ENSG00000199968	ENSG00000199968	SNORD115-19	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000199970	ENSG00000199970	SNORD115-3	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000199971	ENSG00000199971	RNU6-797P	7:139909362-139909471	NOTEST	0	0	0	0	1	1
ENSG00000199975	ENSG00000199975	RN7SKP243	11:73498360-73576178	NOTEST	0	0.0832015	inf	0	1	1
ENSG00000199977	ENSG00000199977	SNORA73	18:19284917-19450918	NOTEST	0	0	0	0	1	1
ENSG00000199979	ENSG00000199979	Y_RNA	16:68877506-69119083	NOTEST	0	0	0	0	1	1
ENSG00000199980	ENSG00000199980	Y_RNA	14:35390063-35498773	NOTEST	0	0	0	0	1	1
ENSG00000199985	ENSG00000199985	RNA5SP264	8:36394908-36636682	NOTEST	0	0	0	0	1	1
ENSG00000199986	ENSG00000199986	RNU6-486P	3:180284505-180319723	NOTEST	0	0	0	0	1	1
ENSG00000199990	ENSG00000199990	VTRNA1-1	5:140090859-140090958	NOTEST	0	0	0	0	1	1
ENSG00000199994	ENSG00000199994	RNA5SP145	3:150803483-151176497	NOTEST	0	0	0	0	1	1
ENSG00000200003	ENSG00000200003	RNU6-986P	2:27665232-27712656	NOTEST	0	0	0	0	1	1
ENSG00000200008	ENSG00000200008	Y_RNA	15:33603162-34158303	NOTEST	0	0	0	0	1	1
ENSG00000200011	ENSG00000200011	Y_RNA	12:93854500-93854602	NOTEST	0	0	0	0	1	1
ENSG00000200013	ENSG00000200013	RNU6-623P	17:58677543-58741849	NOTEST	0	0	0	0	1	1
ENSG00000200021	ENSG00000200021	RNA5SP448	17:72413732-72413843	NOTEST	0	0	0	0	1	1
ENSG00000200024	ENSG00000200024	Y_RNA	4:88665103-88665205	NOTEST	0	0	0	0	1	1
ENSG00000200026	ENSG00000200026	U8	9:38147424-38147558	NOTEST	0	0	0	0	1	1
ENSG00000200028	ENSG00000200028	RNA5SP98	2:76974844-77820445	NOTEST	0	0	0	0	1	1
ENSG00000200029	ENSG00000200029	RNU6-642P	2:219765532-219795358	NOTEST	0	0	0	0	1	1
ENSG00000200033	ENSG00000200033	RNU6-403P	1:222001007-222014008	NOTEST	0	0	0	0	1	1
ENSG00000200034	ENSG00000200034	RNU4-73P	2:9880771-9880912	NOTEST	0	0	0	0	1	1
ENSG00000200036	ENSG00000200036	RNA5SP65	1:166958345-166991451	NOTEST	0	0	0	0	1	1
ENSG00000200037	ENSG00000200037	RNA5SP32	13:72552225-72552344	NOTEST	0	0	0	0	1	1
ENSG00000200040	ENSG00000200040	Y_RNA	6:76630831-76782395	NOTEST	0	0	0	0	1	1
ENSG00000200041	ENSG00000200041	Y_RNA	9:77796435-77796537	NOTEST	0	0	0	0	1	1
ENSG00000200042	ENSG00000200042	U3	14:92047039-92333880	NOTEST	0	0	0	0	1	1
ENSG00000200047	ENSG00000200047	RN7SKP115	11:100554892-100862668	NOTEST	0	0	0	0	1	1
ENSG00000200048	ENSG00000200048	RNU6-812P	2:79109753-79109860	NOTEST	0	0	0	0	1	1
ENSG00000200049	ENSG00000200049	Y_RNA	4:144207445-144251011	NOTEST	0	0	0	0	1	1
ENSG00000200051	ENSG00000200051	SNORD45	5:139781398-139973337	NOTEST	0	0	0	0	1	1
ENSG00000200052	ENSG00000200052	Y_RNA	3:164840500-164840611	NOTEST	0	0	0	0	1	1
ENSG00000200057	ENSG00000200057	RN7SKP63	22:21743479-21743780	NOTEST	0	0	0	0	1	1
ENSG00000200058	ENSG00000200058	RNA5SP218	6:134490383-134639250	NOTEST	0	0	0	0	1	1
ENSG00000200059	ENSG00000200059	Y_RNA	16:2089815-2185899	NOTEST	0	0	0	0	1	1

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ENSG00000200060	ENSG00000200060	Y_RNA	12:109132259-109132380	NOTEST	0	0	0	0	1	1
ENSG00000200062	ENSG00000200062	RNU4-58P	16:59574029-59574170	NOTEST	0	0	0	0	1	1
ENSG00000200063	ENSG00000200063	SNORA30	17:76374720-76573476	NOTEST	0	0	0	0	1	1
ENSG00000200064	ENSG00000200064	RNY4P9	13:50482769-50482866	NOTEST	0	0	0	0	1	1
ENSG00000200065	ENSG00000200065	Y_RNA	5:32124809-32174456	NOTEST	0	0	0	0	1	1
ENSG00000200066	ENSG00000200066	Y_RNA	12:133656423-133684130	NOTEST	0	0	0	0	1	1
ENSG00000200070	ENSG00000200070	RNU4-80P	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000200072	ENSG00000200072	SNORD44	13:112706391-112706452	NOTEST	0	0	0	0	1	1
ENSG00000200075	ENSG00000200075	SNORA25	8:130844546-131029375	NOTEST	0	0	0	0	1	1
ENSG00000200079	ENSG00000200079	RNA5SP326	10:109221317-109221427	NOTEST	0	0	0	0	1	1
ENSG00000200084	ENSG00000200084	SNORD68	16:89627064-89630950	NOTEST	0	0	0	0	1	1
ENSG00000200085	ENSG00000200085	Y_RNA	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000200086	ENSG00000200086	RNU6-433P	2:55199324-55339757	NOTEST	0	0	0	0	1	1
ENSG00000200089	ENSG00000200089	SNORD114-31	14:101459572-101459647	NOTEST	0	0	0	0	1	1
ENSG00000200090	ENSG00000200090	Y_RNA	11:47738071-47788995	NOTEST	0	0	0	0	1	1
ENSG00000200091	ENSG00000200091	RN7SKP163	6:76311224-76427997	NOTEST	0	0.0725181	inf	0	1	1
ENSG00000200095	ENSG00000200095	RNU6-181P	15:101093733-101191910	NOTEST	0	0	0	0	1	1
ENSG00000200097	ENSG00000200097	RNU6-1167P	10:35535952-35860852	NOTEST	0	0	0	0	1	1
ENSG00000200101	ENSG00000200101	RNU6-508P	2:59444842-60327335	NOTEST	0	0	0	0	1	1
ENSG00000200102	ENSG00000200102	RNU6-252P	14:21576201-21584862	NOTEST	0	0	0	0	1	1
ENSG00000200105	ENSG00000200105	RNU6-251P	12:15773091-16035263	NOTEST	0	0	0	0	1	1
ENSG00000200106	ENSG00000200106	RNU6-984P	9:111934254-112083244	NOTEST	0	0	0	0	1	1
ENSG00000200107	ENSG00000200107	RNU6-1249P	17:53604324-53638938	NOTEST	0	0	0	0	1	1
ENSG00000200108	ENSG00000200108	RNU6-774P	4:84717588-85214565	NOTEST	0	0	0	0	1	1
ENSG00000200112	ENSG00000200112	SNORD56	12:116248163-116323942	NOTEST	0	0	0	0	1	1
ENSG00000200113	ENSG00000200113	SNORA51	7:36893960-37488852	NOTEST	0	0	0	0	1	1
ENSG00000200114	ENSG00000200114	RNA5SP123	3:12525930-12705725	NOTEST	0	0	0	0	1	1
ENSG00000200115	ENSG00000200115	RNA5SP440	17:36886487-36906969	NOTEST	0	0	0	0	1	1
ENSG00000200118	ENSG00000200118	Y_RNA	3:169940152-170023769	NOTEST	0	0	0	0	1	1
ENSG00000200120	ENSG00000200120	Y_RNA	15:49398267-49913128	NOTEST	0	0	0	0	1	1
ENSG00000200121	ENSG00000200121	Y_RNA	2:176040985-176049335	NOTEST	0	0	0	0	1	1
ENSG00000200127	ENSG00000200127	Y_RNA	17:41149932-41150024	NOTEST	0	0	0	0	1	1
ENSG00000200130	ENSG00000200130	SNORA63	7:64792308-64792386	NOTEST	0	0	0	0	1	1
ENSG00000200131	ENSG00000200131	RN7SKP77	9:109378338-109464943	NOTEST	0	0	0	0	1	1
ENSG00000200132	ENSG00000200132	RNU6-1021P	18:14507337-14543584	NOTEST	0	0	0	0	1	1
ENSG00000200135	ENSG00000200135	Y_RNA	12:112563304-112591407	NOTEST	0	0	0	0	1	1
ENSG00000200138	ENSG00000200138	Y_RNA	16:28109299-28223241	NOTEST	0	0	0	0	1	1
ENSG00000200139	ENSG00000200139	RNU6-778P	1:199857286-199857389	NOTEST	0	0	0	0	1	1
ENSG00000200141	ENSG00000200141	Y_RNA	9:34179002-34329198	NOTEST	0	0	0	0	1	1
ENSG00000200142	ENSG00000200142	Y_RNA	15:91509269-91538859	NOTEST	0	0	0	0	1	1
ENSG00000200146	ENSG00000200146	RNU6-544P	11:80239003-80239110	NOTEST	0	0	0	0	1	1
ENSG00000200150	ENSG00000200150	SNORD113	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000200151	ENSG00000200151	RN7SKP231	8:92555151-92919847	NOTEST	0	0	0	0	1	1
ENSG00000200152	ENSG00000200152	RNU6-216P	11:74660291-74690076	NOTEST	0	126.934	inf	0	1	1
ENSG00000200153	ENSG00000200153	RNU6-23P	16:70479195-70479302	NOTEST	0	0	0	0	1	1

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ENSG00000200154	ENSG00000200154	SNORD103A	1:31404352-31538838	NOTEST	0	0	0	0	1	1
ENSG00000200156	ENSG00000200156	RNU5B-1	15:65597014-65597130	NOTEST	0	0	0	0	1	1
ENSG00000200161	ENSG00000200161	RN7SKP145	5:148495740-148496043	NOTEST	0	0	0	0	1	1
ENSG00000200162	ENSG00000200162	Y_RNA	3:153102722-153697975	NOTEST	0	0	0	0	1	1
ENSG00000200163	ENSG00000200163	SNORD115-18	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200164	ENSG00000200164	Y_RNA	16:69139466-69442474	NOTEST	0	0	0	0	1	1
ENSG00000200168	ENSG00000200168	RNA5SP350	11:110910821-110910932	NOTEST	0	0	0	0	1	1
ENSG00000200169	ENSG00000200169	RNU5D-1	1:45196726-45196842	NOTEST	0	0	0	0	1	1
ENSG00000200170	ENSG00000200170	Y_RNA	10:73856277-73995618	NOTEST	0	0	0	0	1	1
ENSG00000200171	ENSG00000200171	Y_RNA	1:44619056-44619152	NOTEST	0	0	0	0	1	1
ENSG00000200174	ENSG00000200174	Y_RNA	1:62660502-62678000	NOTEST	0	0	0	0	1	1
ENSG00000200175	ENSG00000200175	RNU6-1309P	1:150782180-150849244	NOTEST	0	0	0	0	1	1
ENSG00000200176	ENSG00000200176	RNU1-19P	10:88516406-88692595	NOTEST	0	0	0	0	1	1
ENSG00000200179	ENSG00000200179	Y_RNA	19:36673187-36737159	NOTEST	0	0	0	0	1	1
ENSG00000200181	ENSG00000200181	SNORD85	1:31404352-31538838	NOTEST	0	0	0	0	1	1
ENSG00000200183	ENSG00000200183	RNU6-238P	12:50898767-51142450	NOTEST	0	0	0	0	1	1
ENSG00000200184	ENSG00000200184	RNU1-20P	3:191857183-192485553	NOTEST	0	0	0	0	1	1
ENSG00000200189	ENSG00000200189	RNU6-832P	7:68590256-68590363	NOTEST	0	0	0	0	1	1
ENSG00000200191	ENSG00000200191	U8	8:72727728-72727860	NOTEST	0	0	0	0	1	1
ENSG00000200197	ENSG00000200197	RNU1-21P	11:123634634-123634797	NOTEST	0	0	0	0	1	1
ENSG00000200198	ENSG00000200198	RN7SKP211	6:106352247-106352562	NOTEST	0	0	0	0	1	1
ENSG00000200201	ENSG00000200201	Y_RNA	11:3686393-3686489	NOTEST	0	0	0	0	1	1
ENSG00000200204	ENSG00000200204	RNU1-22P	16:3115297-3137101	NOTEST	0	0	0	0	1	1
ENSG00000200206	ENSG00000200206	SNORD74	15:86685226-87572283	NOTEST	0	0	0	0	1	1
ENSG00000200208	ENSG00000200208	Y_RNA	20:23438220-23438322	NOTEST	0	0	0	0	1	1
ENSG00000200209	ENSG00000200209	Y_RNA	19:38734674-38795649	NOTEST	0	0	0	0	1	1
ENSG00000200211	ENSG00000200211	RNY4P27	13:95988359-95988455	NOTEST	0	0	0	0	1	1
ENSG00000200213	ENSG00000200213	RNU6-992P	21:37402367-37498938	NOTEST	0	0	0	0	1	1
ENSG00000200215	ENSG00000200215	SNORD113-6	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000200216	ENSG00000200216	RNU6-745P	15:70485574-70485683	NOTEST	0	0	0	0	1	1
ENSG00000200217	ENSG00000200217	RNU6-839P	10:110999396-110999504	NOTEST	0	0	0	0	1	1
ENSG00000200218	ENSG00000200218	RNU6-697P	10:70587297-70655188	NOTEST	0	0	0	0	1	1
ENSG00000200220	ENSG00000200220	RNU6-179P	1:153965160-154127592	NOTEST	0	0	0	0	1	1
ENSG00000200222	ENSG00000200222	U3	3:64053639-64440508	NOTEST	0	0	0	0	1	1
ENSG00000200224	ENSG00000200224	RNU6-626P	6:56322784-56819426	NOTEST	0	0	0	0	1	1
ENSG00000200225	ENSG00000200225	RNA5SP382	14:20883145-20883257	NOTEST	0	0	0	0	1	1
ENSG00000200227	ENSG00000200227	RNA5SP197	5:150816606-150871942	NOTEST	0	0	0	0	1	1
ENSG00000200231	ENSG00000200231	RNU1-23P	20:24217890-24218034	NOTEST	0	0	0	0	1	1
ENSG00000200235	ENSG00000200235	SNORA27	5:139781398-139973337	NOTEST	0	0	0	0	1	1
ENSG00000200237	ENSG00000200237	SNORA70	19:9920942-9938492	NOTEST	0	0	0	0	1	1
ENSG00000200238	ENSG00000200238	RNA5SP133	3:55542335-56502391	NOTEST	0	0	0	0	1	1
ENSG00000200241	ENSG00000200241	Y_RNA	2:86371054-86423172	NOTEST	0	0	0	0	1	1
ENSG00000200243	ENSG00000200243	RN7SKP79	5:6848239-6848575	NOTEST	0	0	0	0	1	1
ENSG00000200246	ENSG00000200246	RNA5SP263	8:31496901-32622548	NOTEST	0	0	0	0	1	1
ENSG00000200247	ENSG00000200247	RNU6-254P	12:19556978-19873735	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000200248	ENSG00000200248	RNA5SP214	6:117381844-117381962	NOTEST	0	0	0	0	1	1
ENSG00000200250	ENSG00000200250	RNU6-1147P	2:128056305-128146041	NOTEST	0	0	0	0	1	1
ENSG00000200252	ENSG00000200252	Y_RNA	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000200253	ENSG00000200253	RNU6-529P	10:88800994-88801098	NOTEST	0	0	0	0	1	1
ENSG00000200254	ENSG00000200254	RNU6-536P	1:42895999-43120335	NOTEST	0	0	0	0	1	1
ENSG00000200256	ENSG00000200256	Y_RNA	11:75514475-75854239	NOTEST	0	0	0	0	1	1
ENSG00000200257	ENSG00000200257	RNU6-97P	17:74722911-74777531	NOTEST	0	0	0	0	1	1
ENSG00000200259	ENSG00000200259	SNORD35A	19:49949554-49995565	NOTEST	0	0	0	0	1	1
ENSG00000200261	ENSG00000200261	Y_RNA	9:114803064-114937688	NOTEST	0	0	0	0	1	1
ENSG00000200262	ENSG00000200262	Y_RNA	1:51567905-51613752	NOTEST	0	0	0	0	1	1
ENSG00000200267	ENSG00000200267	RNU6-66P	13:73687051-73687155	NOTEST	0	0	0	0	1	1
ENSG00000200269	ENSG00000200269	RNU6-838P	4:48068409-48136273	NOTEST	0	0	0	0	1	1
ENSG00000200270	ENSG00000200270	Y_RNA	3:191359117-191359213	NOTEST	0	0	0	0	1	1
ENSG00000200274	ENSG00000200274	RNU4-32P	12:109991541-110035067	NOTEST	0	4.87681	inf	0	1	1
ENSG00000200275	ENSG00000200275	RNA5SP199	5:155272446-155272538	NOTEST	0	0	0	0	1	1
ENSG00000200278	ENSG00000200278	RNA5SP352	11:124492731-124567414	NOTEST	0	0	0	0	1	1
ENSG00000200279	ENSG00000200279	SNORD114-10	14:101433388-101433460	NOTEST	0	0	0	0	1	1
ENSG00000200281	ENSG00000200281	RNU6-624P	2:228844665-229046361	NOTEST	0	0	0	0	1	1
ENSG00000200283	ENSG00000200283	Y_RNA	2:29179476-29297127	NOTEST	0	0	0	0	1	1
ENSG00000200287	ENSG00000200287	Y_RNA	2:144654830-144654929	NOTEST	0	0	0	0	1	1
ENSG00000200288	ENSG00000200288	SNORA18	3:177159708-177470093	NOTEST	0	0	0	0	1	1
ENSG00000200291	ENSG00000200291	Y_RNA	X:117031775-117251303	NOTEST	0	0	0	0	1	1
ENSG00000200293	ENSG00000200293	RNA5SP393	15:42120282-42190773	NOTEST	0	0	0	0	1	1
ENSG00000200294	ENSG00000200294	SNORA36	10:73856277-73995618	NOTEST	0	0	0	0	1	1
ENSG00000200295	ENSG00000200295	RNU6-527P	6:107018902-107077373	NOTEST	0	0	0	0	1	1
ENSG00000200296	ENSG00000200296	RNU1-83P	12:63037761-63328817	NOTEST	0	0	0	0	1	1
ENSG00000200298	ENSG00000200298	Y_RNA	14:72399155-73061833	NOTEST	0	0	0	0	1	1
ENSG00000200301	ENSG00000200301	RNA5SP483	20:33703166-33872788	NOTEST	0	0	0	0	1	1
ENSG00000200303	ENSG00000200303	RNU6-940P	12:49369325-49369429	NOTEST	0	0	0	0	1	1
ENSG00000200304	ENSG00000200304	RNU6-1255P	8:131064352-131455906	NOTEST	0	0	0	0	1	1
ENSG00000200305	ENSG00000200305	Y_RNA	15:40213242-40218081	NOTEST	0	0	0	0	1	1
ENSG00000200309	ENSG00000200309	Y_RNA	12:49521564-49541652	NOTEST	0	0	0	0	1	1
ENSG00000200310	ENSG00000200310	RNA5SP215	6:121007766-121007888	NOTEST	0	0	0	0	1	1
ENSG00000200312	ENSG00000200312	RN7SKP255	14:89591214-90421121	NOTEST	0	0.0744683	inf	0	1	1
ENSG00000200313	ENSG00000200313	RNA5-8SP7	20:5326651-5326806	NOTEST	0	0	0	0	1	1
ENSG00000200314	ENSG00000200314	Y_RNA	6:106902702-106902804	NOTEST	0	0	0	0	1	1
ENSG00000200318	ENSG00000200318	U3	15:59052665-59052880	NOTEST	0	0	0	0	1	1
ENSG00000200320	ENSG00000200320	SNORA63	3:186499568-186524847	NOTEST	0	0	0	0	1	1
ENSG00000200325	ENSG00000200325	Y_RNA	20:29543690-29543802	NOTEST	0	0	0	0	1	1
ENSG00000200326	ENSG00000200326	RNA5SP391	15:27216428-27787137	NOTEST	0	0	0	0	1	1
ENSG00000200327	ENSG00000200327	RNA5SP62	1:163438285-163438395	NOTEST	0	0	0	0	1	1
ENSG00000200331	ENSG00000200331	RNU6-183P	5:77610739-77610849	NOTEST	0	0	0	0	1	1
ENSG00000200332	ENSG00000200332	Y_RNA	22:42017122-42060044	NOTEST	0	0	0	0	1	1
ENSG00000200334	ENSG00000200334	Y_RNA	5:149237518-149324356	NOTEST	0	0	0	0	1	1
ENSG00000200336	ENSG00000200336	RNA5SP333	11:18252895-18270190	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000200338	ENSG00000200338	RNU1-49P	4:41746098-41826136	NOTEST	0	0	0	0	1	1
ENSG00000200340	ENSG00000200340	RNU1-105P	6:47749717-47800516	NOTEST	0	0	0	0	1	1
ENSG00000200343	ENSG00000200343	RNA5S8	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000200344	ENSG00000200344	Y_RNA	1:8014350-8045565	NOTEST	0	0	0	0	1	1
ENSG00000200345	ENSG00000200345	RNU6-485P	12:7187512-7275097	NOTEST	0	0	0	0	1	1
ENSG00000200347	ENSG00000200347	RNU6-963P	5:125877532-125931110	NOTEST	0	0	0	0	1	1
ENSG00000200350	ENSG00000200350	RNU6-1285P	4:155456157-155471587	NOTEST	0	0	0	0	1	1
ENSG00000200351	ENSG00000200351	Y_RNA	5:98264874-98330717	NOTEST	0	0	0	0	1	1
ENSG00000200354	ENSG00000200354	SNORA71D	20:37049234-37063996	NOTEST	0	0	0	0	1	1
ENSG00000200355	ENSG00000200355	SNORA72	3:172468471-172539264	NOTEST	0	0	0	0	1	1
ENSG00000200356	ENSG00000200356	RNU6-833P	10:74870216-75118617	NOTEST	0	0	0	0	1	1
ENSG00000200360	ENSG00000200360	RNU6-792P	1:112025969-112310638	NOTEST	0	0	0	0	1	1
ENSG00000200361	ENSG00000200361	Y_RNA	3:106407524-106407626	NOTEST	0	0	0	0	1	1
ENSG00000200366	ENSG00000200366	RNU6-511P	3:93695872-93695979	NOTEST	0	0	0	0	1	1
ENSG00000200367	ENSG00000200367	SNORD113-8	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000200369	ENSG00000200369	RNU6-666P	10:27604048-27604155	NOTEST	0	0	0	0	1	1
ENSG00000200370	ENSG00000200370	RNA5S17	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000200372	ENSG00000200372	RNU5E-8P	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000200376	ENSG00000200376	RNU5E-10P	11:47487495-47606114	NOTEST	0	0	0	0	1	1
ENSG00000200377	ENSG00000200377	SNORD56	2:154277190-154449801	NOTEST	0	0	0	0	1	1
ENSG00000200378	ENSG00000200378	RNU5B-4P	5:138783595-138783706	NOTEST	0	0	0	0	1	1
ENSG00000200379	ENSG00000200379	RN7SKP45	3:55542335-56502391	NOTEST	0	0	0	0	1	1
ENSG00000200381	ENSG00000200381	RNA5S4	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000200385	ENSG00000200385	SNORA42	14:38059188-38672128	NOTEST	0	0	0	0	1	1
ENSG00000200388	ENSG00000200388	RNU6-618P	12:31535156-31768600	NOTEST	0	0	0	0	1	1
ENSG00000200389	ENSG00000200389	RNU6-509P	3:141594965-141645356	NOTEST	0	0	0	0	1	1
ENSG00000200390	ENSG00000200390	Y_RNA	2:128587320-128587426	NOTEST	0	0	0	0	1	1
ENSG00000200391	ENSG00000200391	Y_RNA	15:44119160-44160617	NOTEST	0	0	0	0	1	1
ENSG00000200393	ENSG00000200393	RNU6-698P	19:54156938-54157045	NOTEST	0	0	0	0	1	1
ENSG00000200394	ENSG00000200394	SNORA38B	17:65713948-65740647	NOTEST	0	0	0	0	1	1
ENSG00000200397	ENSG00000200397	Y_RNA	7:86780738-86849903	NOTEST	0	0	0	0	1	1
ENSG00000200398	ENSG00000200398	SNORD115-24	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200403	ENSG00000200403	RNU6-1099P	1:19630458-19638640	NOTEST	0	0	0	0	1	1
ENSG00000200406	ENSG00000200406	SNORD114-23	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000200407	ENSG00000200407	RNU6-1169P	15:41700605-41775761	NOTEST	0	0	0	0	1	1
ENSG00000200408	ENSG00000200408	RNA5SP74	1:204485510-204542871	NOTEST	0	0	0	0	1	1
ENSG00000200411	ENSG00000200411	RNA5SP346	11:96123152-96240738	NOTEST	0	0	0	0	1	1
ENSG00000200413	ENSG00000200413	SNORD114-26	14:101453382-101453454	NOTEST	0	0	0	0	1	1
ENSG00000200418	ENSG00000200418	SNORA63	3:186499568-186524847	NOTEST	0	28.3332	inf	0	1	1
ENSG00000200419	ENSG00000200419	Y_RNA	15:45879320-45983492	NOTEST	0	0	0	0	1	1
ENSG00000200421	ENSG00000200421	Y_RNA	1:38179551-38230805	NOTEST	0	0	0	0	1	1
ENSG00000200422	ENSG00000200422	SNORD45	X:86401735-86401807	NOTEST	0	0	0	0	1	1
ENSG00000200424	ENSG00000200424	RNU6-1155P	16:58741034-59142878	NOTEST	0	0	0	0	1	1
ENSG00000200427	ENSG00000200427	Y_RNA	6:86487356-86487473	NOTEST	0	0	0	0	1	1
ENSG00000200428	ENSG00000200428	Y_RNA	12:50898767-51142450	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000200431	ENSG00000200431	RNU4-81P	X:69664710-69725337	NOTEST	0	0	0	0	1	1
ENSG00000200432	ENSG00000200432	Y_RNA	2:128825373-128825475	NOTEST	0	0	0	0	1	1
ENSG00000200434	ENSG00000200434	RNA5-8SP2	16:33965425-33965577	NOTEST	0	0	0	0	1	1
ENSG00000200436	ENSG00000200436	Y_RNA	X:111873875-111923375	NOTEST	0	0	0	0	1	1
ENSG00000200437	ENSG00000200437	RNU6-799P	17:15207127-15244958	NOTEST	0	0	0	0	1	1
ENSG00000200443	ENSG00000200443	RNU6-1066P	22:27431849-27431954	NOTEST	0	0	0	0	1	1
ENSG00000200444	ENSG00000200444	RNU6-1339P	15:84322837-84708594	NOTEST	0	0	0	0	1	1
ENSG00000200446	ENSG00000200446	RNU6-1085P	7:35969767-35969874	NOTEST	0	0	0	0	1	1
ENSG00000200448	ENSG00000200448	Y_RNA	22:43158865-43158965	NOTEST	0	0	0	0	1	1
ENSG00000200455	ENSG00000200455	RNU6-1112P	4:40044536-40159872	NOTEST	0	0	0	0	1	1
ENSG00000200456	ENSG00000200456	RNU6-1097P	7:44543371-44543478	NOTEST	0	0	0	0	1	1
ENSG00000200462	ENSG00000200462	RNU6-727P	5:86716157-86716264	NOTEST	0	0	0	0	1	1
ENSG00000200463	ENSG00000200463	SNORD118	17:8076554-8079717	NOTEST	0	0	0	0	1	1
ENSG00000200468	ENSG00000200468	RNA5SP403	16:9658246-9658354	NOTEST	0	0	0	0	1	1
ENSG00000200469	ENSG00000200469	RNU6-112P	4:89178771-89205921	NOTEST	0	0	0	0	1	1
ENSG00000200471	ENSG00000200471	RNU6-1125P	7:54688717-54688824	NOTEST	0	0	0	0	1	1
ENSG00000200472	ENSG00000200472	RN7SKP44	18:29298855-29299171	NOTEST	0.101313	0.229672	1.18075	0	1	1
ENSG00000200473	ENSG00000200473	RNA5SP507	X:69472891-69473012	NOTEST	0	0	0	0	1	1
ENSG00000200475	ENSG00000200475	RN7SKP162	12:13679787-14133053	NOTEST	0	0	0	0	1	1
ENSG00000200478	ENSG00000200478	SNORD115-41	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200480	ENSG00000200480	SNORD114-28	14:101455466-101455538	NOTEST	0	0	0	0	1	1
ENSG00000200483	ENSG00000200483	RNU6-1017P	12:132299807-132299913	NOTEST	0	0	0	0	1	1
ENSG00000200484	ENSG00000200484	RNU6-1244P	10:32683485-32683593	NOTEST	0	0	0	0	1	1
ENSG00000200485	ENSG00000200485	Y_RNA	11:33218092-33218183	NOTEST	0	0	0	0	1	1
ENSG00000200486	ENSG00000200486	SNORD115-11	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200487	ENSG00000200487	RNA5SP322	10:87359311-88126250	NOTEST	0	0	0	0	1	1
ENSG00000200488	ENSG00000200488	RN7SKP203	2:76672204-76672536	NOTEST	0	0	0	0	1	1
ENSG00000200492	ENSG00000200492	U3	6:92829239-92829349	NOTEST	0	0	0	0	1	1
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ENSG00000200495	ENSG00000200495	RNU6-1205P	1:249200394-249214145	NOTEST	0	0	0	0	1	1
ENSG00000200496	ENSG00000200496	U8	11:123172097-123172231	NOTEST	0	0	0	0	1	1
ENSG00000200502	ENSG00000200502	Y_RNA	9:37120535-37358146	NOTEST	0	0	0	0	1	1
ENSG00000200503	ENSG00000200503	SNORD115-5	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200506	ENSG00000200506	Y_RNA	14:99947505-100070363	NOTEST	0	0	0	0	1	1
ENSG00000200508	ENSG00000200508	Y_RNA	1:64239692-64647181	NOTEST	0	0	0	0	1	1
ENSG00000200510	ENSG00000200510	RNY4P2	17:41084864-41084959	NOTEST	0	0	0	0	1	1
ENSG00000200516	ENSG00000200516	RNA5SP378	12:132285859-132285979	NOTEST	0	0	0	0	1	1
ENSG00000200520	ENSG00000200520	RNU6-1214P	4:140187316-140397763	NOTEST	0	0	0	0	1	1
ENSG00000200521	ENSG00000200521	Y_RNA	4:158689164-158689265	NOTEST	0	0	0	0	1	1
ENSG00000200522	ENSG00000200522	RNU6-957P	6:110931180-111137161	NOTEST	0	0	0	0	1	1
ENSG00000200525	ENSG00000200525	RNU6-1209P	8:95825538-96128683	NOTEST	0	0	0	0	1	1
ENSG00000200526	ENSG00000200526	RNY4P14	13:40229763-40365802	NOTEST	0	0	0	0	1	1
ENSG00000200527	ENSG00000200527	RNA5SP457	18:47309868-47721463	NOTEST	0	0	0	0	1	1
ENSG00000200528	ENSG00000200528	RNU6-1331P	8:54764367-54871863	NOTEST	0	0	0	0	1	1
ENSG00000200530	ENSG00000200530	SNORD35B	19:49999621-50002946	NOTEST	0	0	0	0	1	1

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ENSG00000200534	ENSG00000200534	SNORA33	6:133135579-133138703	NOTEST	0	0	0	0	1	1
ENSG00000200536	ENSG00000200536	SNORA25	1:110753964-110825722	NOTEST	0	0	0	0	1	1
ENSG00000200537	ENSG00000200537	RNY4P6	11:116706466-116969153	NOTEST	0	0	0	0	1	1
ENSG00000200538	ENSG00000200538	U3	17:46210801-46507637	NOTEST	0	0	0	0	1	1
ENSG00000200544	ENSG00000200544	Y_RNA	9:33290508-33371155	NOTEST	0	0	0	0	1	1
ENSG00000200545	ENSG00000200545	U3	10:19492778-20079330	NOTEST	0	0	0	0	1	1
ENSG00000200547	ENSG00000200547	Y_RNA	1:116966345-117021464	NOTEST	0	0	0	0	1	1
ENSG00000200550	ENSG00000200550	RNU6-137P	2:42721708-42984087	NOTEST	0	0	0	0	1	1
ENSG00000200552	ENSG00000200552	Y_RNA	7:101977280-101977382	NOTEST	0	0	0	0	1	1
ENSG00000200553	ENSG00000200553	Y_RNA	4:120858711-120885448	NOTEST	0	0	0	0	1	1
ENSG00000200554	ENSG00000200554	RNU6-1020P	9:128024072-128129486	NOTEST	0	0	0	0	1	1
ENSG00000200555	ENSG00000200555	RNU6-525P	5:179871508-179871612	NOTEST	0	0	0	0	1	1
ENSG00000200556	ENSG00000200556	RNU6-103P	16:58496749-58547532	NOTEST	0	0	0	0	1	1
ENSG00000200558	ENSG00000200558	RNA5SP429	16:68771127-68869451	NOTEST	0	0	0	0	1	1
ENSG00000200560	ENSG00000200560	RNU6-288P	17:61627821-61671639	NOTEST	0	0	0	0	1	1
ENSG00000200563	ENSG00000200563	RNU6-640P	2:86730553-87005164	NOTEST	0	0	0	0	1	1
ENSG00000200564	ENSG00000200564	SNORD115-39	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200566	ENSG00000200566	RNU5F-7P	X:15934311-15934426	NOTEST	0	0	0	0	1	1
ENSG00000200570	ENSG00000200570	RNU6-829P	9:96137837-96137949	NOTEST	0	0	0	0	1	1
ENSG00000200571	ENSG00000200571	RNU6-1284P	3:135969147-136471220	NOTEST	0	0	0	0	1	1
ENSG00000200572	ENSG00000200572	Y_RNA	X:133276257-133276370	NOTEST	0	0	0	0	1	1
ENSG00000200575	ENSG00000200575	RNU6-414P	1:62208148-62629592	NOTEST	0	0	0	0	1	1
ENSG00000200579	ENSG00000200579	Y_RNA	3:38048986-38071253	NOTEST	0	0	0	0	1	1
ENSG00000200587	ENSG00000200587	RNA5SP514	X:131072873-131072984	NOTEST	0	0	0	0	1	1
ENSG00000200591	ENSG00000200591	Y_RNA	1:32930657-33116504	NOTEST	0	0	0	0	1	1
ENSG00000200593	ENSG00000200593	SNORD115-33	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200594	ENSG00000200594	RNU6-824P	6:155054458-155635627	NOTEST	0	0	0	0	1	1
ENSG00000200597	ENSG00000200597	RNU1-87P	6:37787274-38122400	NOTEST	0	0	0	0	1	1
ENSG00000200600	ENSG00000200600	Y_RNA	5:23951456-24178372	NOTEST	0	0	0	0	1	1
ENSG00000200601	ENSG00000200601	RNA5SP50	1:74215199-74215306	NOTEST	0	0	0	0	1	1
ENSG00000200605	ENSG00000200605	Y_RNA	15:50150434-50528592	NOTEST	0	0	0	0	1	1
ENSG00000200606	ENSG00000200606	Y_RNA	15:59867826-59867922	NOTEST	0	0	0	0	1	1
ENSG00000200608	ENSG00000200608	SNORD114-11	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000200610	ENSG00000200610	Y_RNA	3:106234743-106234845	NOTEST	0	0	0	0	1	1
ENSG00000200612	ENSG00000200612	SNORD114-25	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000200613	ENSG00000200613	RNA5SP349	11:108991604-108991713	NOTEST	0	0	0	0	1	1
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ENSG00000200616	ENSG00000200616	Y_RNA	3:178815518-178815628	NOTEST	0	0	0	0	1	1
ENSG00000200619	ENSG00000200619	RNA5SP447	17:65264225-65264344	NOTEST	0	0	0	0	1	1
ENSG00000200620	ENSG00000200620	SNORA7	X:15693054-15805747	NOTEST	0	0	0	0	1	1
ENSG00000200622	ENSG00000200622	RNU6-1059P	4:96789817-96789915	NOTEST	0	0	0	0	1	1
ENSG00000200623	ENSG00000200623	SNORD18A	15:66790354-66858317	NOTEST	0	0	0	0	1	1
ENSG00000200624	ENSG00000200624	RNA5S6	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000200626	ENSG00000200626	RNA5SP325	10:108333420-108924292	NOTEST	0	0	0	0	1	1
ENSG00000200629	ENSG00000200629	Y_RNA	7:128784711-128809538	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000200630	ENSG00000200630	Y_RNA	8:12940869-13373167	NOTEST	0	0	0	0	1	1
ENSG00000200632	ENSG00000200632	SNORD113-7	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000200635	ENSG00000200635	Y_RNA	X:55609165-55609267	NOTEST	0	0	0	0	1	1
ENSG00000200636	ENSG00000200636	SNORD114-27	14:101454497-101454567	NOTEST	0	0	0	0	1	1
ENSG00000200637	ENSG00000200637	RNU5F-3P	18:5954704-6415236	NOTEST	0	0	0	0	1	1
ENSG00000200638	ENSG00000200638	SNORD115-37	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200645	ENSG00000200645	RNU6-1210P	18:14728270-14852737	NOTEST	0	0	0	0	1	1
ENSG00000200646	ENSG00000200646	Y_RNA	19:56732680-56904914	NOTEST	0	0	0	0	1	1
ENSG00000200648	ENSG00000200648	RNU6-226P	5:175130900-175131007	NOTEST	0	0	0	0	1	1
ENSG00000200649	ENSG00000200649	RNA5SP343	11:73723762-74035750	NOTEST	0	0	0	0	1	1
ENSG00000200650	ENSG00000200650	RNA5SP114	2:188577542-189152418	NOTEST	0	0	0	0	1	1
ENSG00000200651	ENSG00000200651	Y_RNA	17:75253818-75496678	NOTEST	0	0	0	0	1	1
ENSG00000200652	ENSG00000200652	SNORA25	16:28109299-28223241	NOTEST	0	0	0	0	1	1
ENSG00000200653	ENSG00000200653	RNU4-92P	14:89286640-89286776	NOTEST	0	0	0	0	1	1
ENSG00000200656	ENSG00000200656	SNORA5B	7:45139698-45151646	NOTEST	0	1.49607	inf	0	1	1
ENSG00000200658	ENSG00000200658	Y_RNA	4:99094934-99095030	NOTEST	0	0	0	0	1	1
ENSG00000200661	ENSG00000200661	SNORD116-10	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200662	ENSG00000200662	Y_RNA	X:102411047-102411139	NOTEST	0	0	0	0	1	1
ENSG00000200664	ENSG00000200664	Y_RNA	2:136545409-136594750	NOTEST	0	0	0	0	1	1
ENSG00000200665	ENSG00000200665	RNU6-1188P	12:116395710-116715143	NOTEST	0	0	0	0	1	1
ENSG00000200670	ENSG00000200670	RNU6-912P	7:65279658-65279762	NOTEST	0	0	0	0	1	1
ENSG00000200673	ENSG00000200673	RN7SKP174	7:144546847-144547177	NOTEST	0	0	0	0	1	1
ENSG00000200674	ENSG00000200674	RN7SKP160	1:173760685-173761025	NOTEST	0	0	0	0	1	1
ENSG00000200677	ENSG00000200677	SNORD18	15:91260557-91358859	NOTEST	0	0	0	0	1	1
ENSG00000200680	ENSG00000200680	SNORD115-4	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200681	ENSG00000200681	RNU6-263P	6:18307203-18307310	NOTEST	0	0	0	0	1	1
ENSG00000200683	ENSG00000200683	RNU6-379P	22:41253080-41369313	NOTEST	0	0	0	0	1	1
ENSG00000200685	ENSG00000200685	Y_RNA	11:13690216-13753893	NOTEST	0	0	0	0	1	1
ENSG00000200686	ENSG00000200686	RNY3P3	13:78469615-79233314	NOTEST	0	0	0	0	1	1
ENSG00000200687	ENSG00000200687	RNA5SP335	11:19372270-20143144	NOTEST	0	0	0	0	1	1
ENSG00000200688	ENSG00000200688	Y_RNA	12:112464499-112546826	NOTEST	0	0	0	0	1	1
ENSG00000200693	ENSG00000200693	U3	14:64118014-64118217	NOTEST	0.716797	0.249091	-1.52489	0	1	1
ENSG00000200701	ENSG00000200701	RNU6-674P	2:85360532-85537511	NOTEST	0	0	0	0	1	1
ENSG00000200702	ENSG00000200702	Y_RNA	X:44260848-44260950	NOTEST	0	0	0	0	1	1
ENSG00000200703	ENSG00000200703	RNU6-873P	3:87780551-87842779	NOTEST	0	0	0	0	1	1
ENSG00000200706	ENSG00000200706	SNORD45	6:38136226-38607924	NOTEST	0	0	0	0	1	1
ENSG00000200708	ENSG00000200708	RN7SKP93	2:134353661-134353970	NOTEST	0	0	0	0	1	1
ENSG00000200709	ENSG00000200709	RNA5SP27	13:46039059-46189874	NOTEST	0	0	0	0	1	1
ENSG00000200711	ENSG00000200711	RNA5SP28	13:50601268-51423190	NOTEST	0	0	0	0	1	1
ENSG00000200713	ENSG00000200713	RNU6-682P	8:8753322-8753428	NOTEST	0	0	0	0	1	1
ENSG00000200714	ENSG00000200714	Y_RNA	8:66504965-66505055	NOTEST	0	0	0	0	1	1
ENSG00000200718	ENSG00000200718	RN7SKP103	2:133174146-133429152	NOTEST	0	0	0	0	1	1
ENSG00000200719	ENSG00000200719	RNA5SP260	8:28747910-28922281	NOTEST	0	0	0	0	1	1
ENSG00000200720	ENSG00000200720	RNU6-931P	4:45482046-45482153	NOTEST	0	0	0	0	1	1
ENSG00000200726	ENSG00000200726	SNORD115-8	15:25068793-25492435	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000200731	ENSG00000200731	RNU1-124P	8:42704779-42940931	NOTEST	0	0	0	0	1	1
ENSG00000200732	ENSG00000200732	RNU6-194P	6:119498373-119670926	NOTEST	0	0	0	0	1	1
ENSG00000200733	ENSG00000200733	SNORD38	13:90489423-90489491	NOTEST	0	0	0	0	1	1
ENSG00000200735	ENSG00000200735	RNY4P8	17:38375555-38440388	NOTEST	0	0	0	0	1	1
ENSG00000200737	ENSG00000200737	Y_RNA	10:99116114-99185831	NOTEST	0	0	0	0	1	1
ENSG00000200738	ENSG00000200738	RNA5SP472	19:32734870-32734989	NOTEST	0	0	0	0	1	1
ENSG00000200741	ENSG00000200741	RNA5SP161	4:56963555-56963670	NOTEST	0	0	0	0	1	1
ENSG00000200742	ENSG00000200742	Y_RNA	14:55965995-56168244	NOTEST	0	0	0	0	1	1
ENSG00000200745	ENSG00000200745	RNU1-31P	2:237073878-237203570	NOTEST	0	0	0	0	1	1
ENSG00000200750	ENSG00000200750	Y_RNA	18:19284917-19450918	NOTEST	0	0	0	0	1	1
ENSG00000200752	ENSG00000200752	Y_RNA	18:48485636-48485749	NOTEST	0	0	0	0	1	1
ENSG00000200753	ENSG00000200753	SNORD56	7:20367921-20455377	NOTEST	0	0	0	0	1	1
ENSG00000200754	ENSG00000200754	Y_RNA	21:18884699-18965897	NOTEST	0	0	0	0	1	1
ENSG00000200755	ENSG00000200755	RNA5SP68	1:173900351-173991435	NOTEST	0	0	0	0	1	1
ENSG00000200756	ENSG00000200756	RNU6-236P	5:139064229-139125808	NOTEST	0	0	0	0	1	1
ENSG00000200757	ENSG00000200757	SNORD115-16	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200759	ENSG00000200759	RNU6-884P	1:150980895-151008189	NOTEST	0	0	0	0	1	1
ENSG00000200761	ENSG00000200761	RN7SKP113	4:4922496-4922791	NOTEST	0	0	0	0	1	1
ENSG00000200763	ENSG00000200763	RNU6-961P	2:20375565-20375670	NOTEST	0	0	0	0	1	1
ENSG00000200764	ENSG00000200764	Y_RNA	2:208552683-208552783	NOTEST	0	0	0	0	1	1
ENSG00000200769	ENSG00000200769	Y_RNA	7:91828282-91875480	NOTEST	0	0	0	0	1	1
ENSG00000200774	ENSG00000200774	RNU6-478P	10:84827717-84827827	NOTEST	0	0	0	0	1	1
ENSG00000200779	ENSG00000200779	RNU6-105P	2:71503690-71662199	NOTEST	0	0	0	0	1	1
ENSG00000200783	ENSG00000200783	RN7SKP180	17:70642087-71088851	NOTEST	0	0	0	0	1	1
ENSG00000200785	ENSG00000200785	SNORD8	14:21853352-21924285	NOTEST	0	0	0	0	1	1
ENSG00000200786	ENSG00000200786	RNA5SP234	7:79283424-79283543	NOTEST	0	0	0	0	1	1
ENSG00000200788	ENSG00000200788	Y_RNA	9:130213764-130265780	NOTEST	0	0	0	0	1	1
ENSG00000200789	ENSG00000200789	RNU1-65P	10:85763087-85763235	NOTEST	0	0	0	0	1	1
ENSG00000200790	ENSG00000200790	RNU6-631P	15:22051852-22083227	NOTEST	0	0	0	0	1	1
ENSG00000200792	ENSG00000200792	SNORA80	21:33664123-33765335	NOTEST	0	2.57506	inf	0	1	1
ENSG00000200794	ENSG00000200794	RN7SKP250	12:110100667-110100988	NOTEST	0	0	0	0	1	1
ENSG00000200795	ENSG00000200795	RNU4-1	12:120730899-120731040	NOTEST	0	1.91258	inf	0	1	1
ENSG00000200796	ENSG00000200796	RNU6-753P	1:38862330-38862437	NOTEST	0	0	0	0	1	1
ENSG00000200799	ENSG00000200799	RNU6-770P	6:108616097-108847999	NOTEST	0	0	0	0	1	1
ENSG00000200800	ENSG00000200800	RNU1-130P	1:96691456-96691616	NOTEST	0	0	0	0	1	1
ENSG00000200801	ENSG00000200801	SNORD115-28	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200806	ENSG00000200806	RNA5SP275	8:108896721-108896839	NOTEST	0	0	0	0	1	1
ENSG00000200807	ENSG00000200807	RNU1-32P	2:60586350-60618510	NOTEST	0	0	0	0	1	1
ENSG00000200812	ENSG00000200812	SNORD115-6	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200814	ENSG00000200814	RNU6-595P	12:62102039-62811211	NOTEST	0	0	0	0	1	1
ENSG00000200815	ENSG00000200815	RNU6-1091P	7:50503077-50503184	NOTEST	0	0	0	0	1	1
ENSG00000200817	ENSG00000200817	RNU6-899P	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000200818	ENSG00000200818	RNU6-1204P	14:57279900-57618895	NOTEST	0	0	0	0	1	1
ENSG00000200822	ENSG00000200822	Y_RNA	2:223269703-223269814	NOTEST	0	0	0	0	1	1

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ENSG00000200827	ENSG00000200827	RNU6-324P	18:12093851-12129748	NOTEST	0	0	0	0	1	1
ENSG00000200829	ENSG00000200829	Y_RNA	2:20680604-20680716	NOTEST	0	0	0	0	1	1
ENSG00000200830	ENSG00000200830	RN7SKP134	12:14656594-14910897	NOTEST	0	0	0	0	1	1
ENSG00000200831	ENSG00000200831	SNORD36B	9:136215068-136218281	NOTEST	0	0	0	0	1	1
ENSG00000200832	ENSG00000200832	SNORD114-4	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000200833	ENSG00000200833	Y_RNA	5:72395899-72396009	NOTEST	0	0	0	0	1	1
ENSG00000200834	ENSG00000200834	Y_RNA	9:33750514-33920402	NOTEST	0	0	0	0	1	1
ENSG00000200839	ENSG00000200839	RNA5SP48	1:52373627-52456436	NOTEST	0	0	0	0	1	1
ENSG00000200840	ENSG00000200840	RNU6-82P	13:28712642-28869475	NOTEST	0	0	0	0	1	1
ENSG00000200842	ENSG00000200842	Y_RNA	17:60019965-60142643	NOTEST	0	0	0	0	1	1
ENSG00000200843	ENSG00000200843	RNY4P4	3:135969147-136471220	NOTEST	0	0	0	0	1	1
ENSG00000200847	ENSG00000200847	Y_RNA	7:23531410-23531512	NOTEST	0	0	0	0	1	1
ENSG00000200849	ENSG00000200849	Y_RNA	10:10274573-10274675	NOTEST	0	0	0	0	1	1
ENSG00000200852	ENSG00000200852	RNA5SP499	X:8992272-9132680	NOTEST	0	0	0	0	1	1
ENSG00000200855	ENSG00000200855	Y_RNA	11:107879458-108018503	NOTEST	0	0	0	0	1	1
ENSG00000200857	ENSG00000200857	Y_RNA	7:68972495-68972608	NOTEST	0	0	0	0	1	1
ENSG00000200860	ENSG00000200860	Y_RNA	14:66644244-66644353	NOTEST	0	0	0	0	1	1
ENSG00000200867	ENSG00000200867	RN7SKP36	4:7113814-7114126	NOTEST	0	0	0	0	1	1
ENSG00000200869	ENSG00000200869	RNU6-457P	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000200871	ENSG00000200871	RNU6-810P	22:29469065-29564321	NOTEST	0	0	0	0	1	1
ENSG00000200872	ENSG00000200872	RNA5SP456	18:46001857-46001971	NOTEST	0	0	0	0	1	1
ENSG00000200873	ENSG00000200873	RNA5SP399	15:72110736-72447800	NOTEST	0	0	0	0	1	1
ENSG00000200874	ENSG00000200874	Y_RNA	7:75123400-75157478	NOTEST	0	0	0	0	1	1
ENSG00000200875	ENSG00000200875	RNU6-340P	18:2649759-2649866	NOTEST	0	0	0	0	1	1
ENSG00000200877	ENSG00000200877	RNU6-560P	11:85864268-85864376	NOTEST	0	0	0	0	1	1
ENSG00000200879	ENSG00000200879	SNORD14E	11:122928196-122933938	NOTEST	0	0	0	0	1	1
ENSG00000200882	ENSG00000200882	RNU6-681P	3:176737142-176915261	NOTEST	0	0	0	0	1	1
ENSG00000200883	ENSG00000200883	Y_RNA	18:9102627-9285983	NOTEST	0	0	0	0	1	1
ENSG00000200884	ENSG00000200884	Y_RNA	5:96149730-96373219	NOTEST	0	0	0	0	1	1
ENSG00000200885	ENSG00000200885	RNU1-146P	12:19877368-19877533	NOTEST	0	0	0	0	1	1
ENSG00000200887	ENSG00000200887	RNU6-598P	10:30588497-30588602	NOTEST	0	0	0	0	1	1
ENSG00000200888	ENSG00000200888	Y_RNA	17:43100707-43221548	NOTEST	0	0	0	0	1	1
ENSG00000200889	ENSG00000200889	RNU4-13P	17:57614719-57614860	NOTEST	0	0	0	0	1	1
ENSG00000200890	ENSG00000200890	RNA5SP99	2:81723337-81723451	NOTEST	0	0	0	0	1	1
ENSG00000200891	ENSG00000200891	SNORD74	10:89754374-89754452	NOTEST	0	0	0	0	1	1
ENSG00000200893	ENSG00000200893	RNU6-944P	16:20621564-20936328	NOTEST	0	0	0	0	1	1
ENSG00000200895	ENSG00000200895	RN7SKP245	6:132129155-132216295	NOTEST	0	0	0	0	1	1
ENSG00000200897	ENSG00000200897	SNORD74	12:107712189-108053419	NOTEST	0	0	0	0	1	1
ENSG00000200898	ENSG00000200898	RNU6-1243P	11:61705365-61705472	NOTEST	0	0	0	0	1	1
ENSG00000200902	ENSG00000200902	RNU6-627P	2:164145504-164145606	NOTEST	0	0	0	0	1	1
ENSG00000200903	ENSG00000200903	RNU1-42P	17:47026722-47026882	NOTEST	0	0	0	0	1	1
ENSG00000200906	ENSG00000200906	RNU6-854P	X:77081860-77151090	NOTEST	0	0	0	0	1	1
ENSG00000200913	ENSG00000200913	SNORD46	1:45205489-45244451	NOTEST	0	0	0	0	1	1
ENSG00000200914	ENSG00000200914	RNA5SP435	17:6481467-6554954	NOTEST	0	0	0	0	1	1

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ENSG00000200922	ENSG00000200922	Y_RNA	9:74477367-74525847	NOTEST	0	0	0	0	1	1
ENSG00000200924	ENSG00000200924	RNU6-1048P	2:44113646-44223144	NOTEST	0	0	0	0	1	1
ENSG00000200926	ENSG00000200926	RNU6-960P	6:111408780-111580237	NOTEST	0	0	0	0	1	1
ENSG00000200935	ENSG00000200935	RNU6-1090P	10:118297694-118297788	NOTEST	0	0	0	0	1	1
ENSG00000200941	ENSG00000200941	RNU6-694P	9:4386409-4386556	NOTEST	0	0	0	0	1	1
ENSG00000200942	ENSG00000200942	RNU6-501P	1:201592012-201853422	NOTEST	0	0	0	0	1	1
ENSG00000200949	ENSG00000200949	SNORD115-32	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200953	ENSG00000200953	Y_RNA	12:51487445-51566926	NOTEST	0	0	0	0	1	1
ENSG00000200957	ENSG00000200957	RNU6-801P	6:19535174-19840915	NOTEST	0	0	0	0	1	1
ENSG00000200959	ENSG00000200959	SNORA74A	5:138282408-138667360	NOTEST	0.74529	1.42304	0.933097	0	1	1
ENSG00000200963	ENSG00000200963	RNU6-289P	4:112252567-112252674	NOTEST	0	0	0	0	1	1
ENSG00000200966	ENSG00000200966	RN7SKP87	9:103340360-103350188	NOTEST	0.331702	0	#NAME?	0	1	1
ENSG00000200969	ENSG00000200969	SNORD95	9:84503832-84503900	NOTEST	0	0	0	0	1	1
ENSG00000200972	ENSG00000200972	RNU5A-8P	1:210501595-210849638	NOTEST	0	0	0	0	1	1
ENSG00000200974	ENSG00000200974	RNU4-87P	4:165995573-166244308	NOTEST	0	0	0	0	1	1
ENSG00000200975	ENSG00000200975	RNU1-7P	1:8266493-8266657	NOTEST	0	0	0	0	1	1
ENSG00000200976	ENSG00000200976	Y_RNA	22:30116072-30163000	NOTEST	0	0	0	0	1	1
ENSG00000200980	ENSG00000200980	Y_RNA	16:4932507-5147809	NOTEST	0	0	0	0	1	1
ENSG00000200982	ENSG00000200982	Y_RNA	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000200983	ENSG00000200983	SNORA3	11:8703957-8932498	NOTEST	0	0	0	0	1	1
ENSG00000200985	ENSG00000200985	RNA5SP493	22:22108788-22221970	NOTEST	0	0	0	0	1	1
ENSG00000200986	ENSG00000200986	RNU6-819P	8:48001194-48110484	NOTEST	0	0	0	0	1	1
ENSG00000200987	ENSG00000200987	SNORD115-30	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000200991	ENSG00000200991	SNORA25	15:85359910-85416713	NOTEST	0	0	0	0	1	1
ENSG00000200997	ENSG00000200997	RNU1-85P	17:56597197-56769416	NOTEST	0	0	0	0	1	1
ENSG00000200998	ENSG00000200998	Y_RNA	4:79553426-79553539	NOTEST	0	0	0	0	1	1
ENSG00000200999	ENSG00000200999	SNORD74	4:26578058-26756973	NOTEST	0	0	0	0	1	1
ENSG00000201000	ENSG00000201000	RNA5SP516	X:141498838-141498957	NOTEST	0	0	0	0	1	1
ENSG00000201001	ENSG00000201001	RNU6-270P	10:29049627-29049732	NOTEST	0	0	0	0	1	1
ENSG00000201003	ENSG00000201003	SNORA58	1:54231132-54304533	NOTEST	0	0	0	0	1	1
ENSG00000201006	ENSG00000201006	Y_RNA	2:121408848-121408950	NOTEST	0	0	0	0	1	1
ENSG00000201009	ENSG00000201009	SNORD46	7:132437782-132437886	NOTEST	0	0	0	0	1	1
ENSG00000201010	ENSG00000201010	RN7SKP224	2:48168834-48468122	NOTEST	0	0	0	0	1	1
ENSG00000201012	ENSG00000201012	Y_RNA	6:135604669-136037193	NOTEST	0	0	0	0	1	1
ENSG00000201013	ENSG00000201013	Y_RNA	2:234263152-234380750	NOTEST	0	0	0	0	1	1
ENSG00000201014	ENSG00000201014	RNA5SP232	7:71244475-71912136	NOTEST	0	0	0	0	1	1
ENSG00000201015	ENSG00000201015	RNU6-280P	6:68256543-68256647	NOTEST	0	0	0	0	1	1
ENSG00000201016	ENSG00000201016	RNU6-374P	5:25701325-25701433	NOTEST	0	0	0	0	1	1
ENSG00000201021	ENSG00000201021	RNU6-743P	20:42034112-42034218	NOTEST	0	0	0	0	1	1
ENSG00000201023	ENSG00000201023	Y_RNA	6:109612230-109676266	NOTEST	0	0	0	0	1	1
ENSG00000201025	ENSG00000201025	SNORD74	21:17442841-17999716	NOTEST	0	0	0	0	1	1
ENSG00000201026	ENSG00000201026	Y_RNA	5:2184823-2184934	NOTEST	0	0	0	0	1	1
ENSG00000201027	ENSG00000201027	RN7SKP107	14:89591214-90421121	NOTEST	0	0	0	0	1	1
ENSG00000201028	ENSG00000201028	RNU6-151P	1:112025969-112310638	NOTEST	0	0	0	0	1	1

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ENSG00000201032	ENSG00000201032	RNU6-704P	1:200890121-200935658	NOTEST	0	0	0	0	1	1
ENSG00000201033	ENSG00000201033	RNU1-96P	3:27555361-27555523	NOTEST	0	0	0	0	1	1
ENSG00000201034	ENSG00000201034	Y_RNA	16:475618-573011	NOTEST	0	0	0	0	1	1
ENSG00000201035	ENSG00000201035	RNA5SP469	19:21264964-21308073	NOTEST	0	0	0	0	1	1
ENSG00000201036	ENSG00000201036	SNORD113	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000201041	ENSG00000201041	RNA5SP242	7:128337492-128337610	NOTEST	0	0	0	0	1	1
ENSG00000201042	ENSG00000201042	SNORA38	12:119287158-119346735	NOTEST	0	0	0	0	1	1
ENSG00000201044	ENSG00000201044	RNU6-268P	2:231577559-231685790	NOTEST	0	0	0	0	1	1
ENSG00000201047	ENSG00000201047	Y_RNA	10:74766974-74856732	NOTEST	0	0	0	0	1	1
ENSG00000201048	ENSG00000201048	Y_RNA	6:10671650-10710015	NOTEST	0	0	0	0	1	1
ENSG00000201050	ENSG00000201050	RNU6-668P	4:165675215-165724947	NOTEST	0	0	0	0	1	1
ENSG00000201059	ENSG00000201059	RNA5SP336	11:20691116-21597227	NOTEST	0	0	0	0	1	1
ENSG00000201065	ENSG00000201065	RNU6-461P	3:102473907-102474014	NOTEST	0	0	0	0	1	1
ENSG00000201066	ENSG00000201066	RN7SKP280	7:154973590-154973894	NOTEST	0	0	0	0	1	1
ENSG00000201070	ENSG00000201070	RNU4-84P	2:99398872-99399011	NOTEST	0	0	0	0	1	1
ENSG00000201071	ENSG00000201071	Y_RNA	15:64386321-64438289	NOTEST	0	0	0	0	1	1
ENSG00000201074	ENSG00000201074	Y_RNA	9:96180136-96180248	NOTEST	0	0	0	0	1	1
ENSG00000201075	ENSG00000201075	Y_RNA	16:14369361-14369457	NOTEST	0	0	0	0	1	1
ENSG00000201076	ENSG00000201076	RNU4-51P	2:61108655-61158745	NOTEST	0	0	0	0	1	1
ENSG00000201077	ENSG00000201077	RNU6-188P	15:42705020-42783321	NOTEST	0	0	0	0	1	1
ENSG00000201078	ENSG00000201078	RN7SKP214	22:37447778-37459430	NOTEST	0	0	0	0	1	1
ENSG00000201080	ENSG00000201080	RNU6-372P	10:104613979-104661656	NOTEST	0	0	0	0	1	1
ENSG00000201084	ENSG00000201084	Y_RNA	15:32467447-32467552	NOTEST	0	0	0	0	1	1
ENSG00000201085	ENSG00000201085	RNU6-173P	4:189042684-189042788	NOTEST	0	0	0	0	1	1
ENSG00000201086	ENSG00000201086	RNA5SP394	15:50150434-50528592	NOTEST	0	0	0	0	1	1
ENSG00000201088	ENSG00000201088	Y_RNA	2:175129605-175129709	NOTEST	0	0	0	0	1	1
ENSG00000201095	ENSG00000201095	RNU6-266P	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000201096	ENSG00000201096	RNA5SP387	14:76041230-76550928	NOTEST	0	0	0	0	1	1
ENSG00000201097	ENSG00000201097	RNU6-366P	14:92732045-92732151	NOTEST	0	0	0	0	1	1
ENSG00000201098	ENSG00000201098	RNY1	7:148684227-148684340	NOTEST	0	0	0	0	1	1
ENSG00000201102	ENSG00000201102	Y_RNA	2:177855235-178088686	NOTEST	0	0	0	0	1	1
ENSG00000201104	ENSG00000201104	RNU6-11P	7:123430658-123430765	NOTEST	0	0	0	0	1	1
ENSG00000201105	ENSG00000201105	RNU1-137P	1:145944937-145945104	NOTEST	0	0	0	0	1	1
ENSG00000201109	ENSG00000201109	RNA5SP245	7:129593073-129691291	NOTEST	0	0	0	0	1	1
ENSG00000201113	ENSG00000201113	RNU6-647P	2:32390932-32449448	NOTEST	0	0	0	0	1	1
ENSG00000201114	ENSG00000201114	Y_RNA	1:114935398-115053781	NOTEST	0	0	0	0	1	1
ENSG00000201118	ENSG00000201118	Y_RNA	9:19053140-19103117	NOTEST	0	0	0	0	1	1
ENSG00000201119	ENSG00000201119	RNU1-33P	6:145784373-145784535	NOTEST	0	0	0	0	1	1
ENSG00000201121	ENSG00000201121	Y_RNA	3:101367732-101398061	NOTEST	0	0	0	0	1	1
ENSG00000201126	ENSG00000201126	RNU6-773P	1:171454650-171562650	NOTEST	0	0	0	0	1	1
ENSG00000201129	ENSG00000201129	SNORA58	1:154179181-154243986	NOTEST	0	0	0	0	1	1
ENSG00000201133	ENSG00000201133	SNORA4	7:50934443-51384515	NOTEST	0	0	0	0	1	1
ENSG00000201134	ENSG00000201134	Y_RNA	1:151814211-151814313	NOTEST	0	0	0	0	1	1
ENSG00000201135	ENSG00000201135	RNU6-777P	1:12123433-12204264	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000201136	ENSG00000201136	RNU6-353P	15:43885251-44010458	NOTEST	0	0	0	0	1	1
ENSG00000201138	ENSG00000201138	Y_RNA	7:74988447-75115548	NOTEST	0	0	0	0	1	1
ENSG00000201140	ENSG00000201140	RN7SKP128	9:119187503-120177348	NOTEST	0	0	0	0	1	1
ENSG00000201142	ENSG00000201142	RNVU1-8	1:146490894-146596107	NOTEST	0	0	0	0	1	1
ENSG00000201143	ENSG00000201143	SNORD115-42	15:25492491-25492573	NOTEST	0	0	0	0	1	1
ENSG00000201145	ENSG00000201145	RNA5SP175	4:190938850-190938969	NOTEST	0	0	0	0	1	1
ENSG00000201148	ENSG00000201148	RNA5SP42	1:33979608-34631443	NOTEST	0	0	0	0	1	1
ENSG00000201151	ENSG00000201151	SNORD56	20:33703166-33872788	NOTEST	0	0	0	0	1	1
ENSG00000201153	ENSG00000201153	RNU6-371P	1:62702650-62785085	NOTEST	0	0	0	0	1	1
ENSG00000201155	ENSG00000201155	RNU1-24P	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000201157	ENSG00000201157	SNORA62	8:18384810-18942240	NOTEST	0	0	0	0	1	1
ENSG00000201160	ENSG00000201160	Y_RNA	2:25919944-25920057	NOTEST	0	0	0	0	1	1
ENSG00000201161	ENSG00000201161	RN7SKP10	13:110567442-110567767	NOTEST	0	0	0	0	1	1
ENSG00000201162	ENSG00000201162	RNU6-454P	3:15295690-15382875	NOTEST	0	0	0	0	1	1
ENSG00000201164	ENSG00000201164	RNU4-36P	16:68563992-68623415	NOTEST	0	0	0	0	1	1
ENSG00000201165	ENSG00000201165	RNU6-1229P	7:64483581-64483688	NOTEST	0	0	0	0	1	1
ENSG00000201168	ENSG00000201168	RNA5SP368	12:102139274-102224716	NOTEST	0	0	0	0	1	1
ENSG00000201170	ENSG00000201170	RNU1-132P	1:245297228-245297392	NOTEST	0	0	0	0	1	1
ENSG00000201176	ENSG00000201176	RNU6-853P	4:169277885-169931426	NOTEST	0	0	0	0	1	1
ENSG00000201178	ENSG00000201178	Y_RNA	17:30819539-31205655	NOTEST	0	0	0	0	1	1
ENSG00000201179	ENSG00000201179	RNU6-1322P	7:104653871-105039755	NOTEST	0	0	0	0	1	1
ENSG00000201180	ENSG00000201180	RNU6-115P	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000201182	ENSG00000201182	RNU6-670P	3:10068097-10149915	NOTEST	0	0	0	0	1	1
ENSG00000201183	ENSG00000201183	RNVU1-12	1:147835126-147931933	NOTEST	0	0	0	0	1	1
ENSG00000201184	ENSG00000201184	RNU4-68P	14:104019757-104181841	NOTEST	0	0	0	0	1	1
ENSG00000201185	ENSG00000201185	RNA5SP202	6:4428196-4428315	NOTEST	0	0	0	0	1	1
ENSG00000201186	ENSG00000201186	RNU4-33P	4:120255483-120299388	NOTEST	0	0	0	0	1	1
ENSG00000201196	ENSG00000201196	Y_RNA	10:54612366-54612463	NOTEST	0	0	0	0	1	1
ENSG00000201198	ENSG00000201198	RNU6-879P	12:57637235-57824788	NOTEST	0	0	0	0	1	1
ENSG00000201201	ENSG00000201201	RN7SKP118	16:67311412-67360666	NOTEST	0	0	0	0	1	1
ENSG00000201204	ENSG00000201204	Y_RNA	11:95206435-95206538	NOTEST	0	0	0	0	1	1
ENSG00000201207	ENSG00000201207	Y_RNA	6:31629005-31641553	NOTEST	0	0	0	0	1	1
ENSG00000201208	ENSG00000201208	Y_RNA	12:113587662-113623284	NOTEST	0	0	0	0	1	1
ENSG00000201209	ENSG00000201209	SNORD42	22:28247656-29075853	NOTEST	0	0	0	0	1	1
ENSG00000201210	ENSG00000201210	RNA5SP139	3:127634074-127706514	NOTEST	0	0	0	0	1	1
ENSG00000201216	ENSG00000201216	Y_RNA	8:103838584-103990104	NOTEST	0	0	0	0	1	1
ENSG00000201217	ENSG00000201217	Y_RNA	3:151961616-152214602	NOTEST	0	0	0	0	1	1
ENSG00000201218	ENSG00000201218	Y_RNA	7:7142203-7142312	NOTEST	0	0	0	0	1	1
ENSG00000201221	ENSG00000201221	RNU4-40P	20:34359895-34538303	NOTEST	0	0	0	0	1	1
ENSG00000201223	ENSG00000201223	RNU6-1305P	5:36152090-36184421	NOTEST	0	0	0	0	1	1
ENSG00000201227	ENSG00000201227	RNA5-8SP3	9:111696460-111775809	NOTEST	0	0	0	0	1	1
ENSG00000201228	ENSG00000201228	Y_RNA	12:31535156-31768600	NOTEST	0	0	0	0	1	1
ENSG00000201229	ENSG00000201229	SNORA63	3:183165395-183173801	NOTEST	0	0	0	0	1	1
ENSG00000201231	ENSG00000201231	RNU4-50P	8:59717976-60033905	NOTEST	0	0	0	0	1	1
ENSG00000201239	ENSG00000201239	Y_RNA	17:80347098-80408705	NOTEST	0	0	0	0	1	1

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ENSG00000201241	ENSG00000201241	RNU6-978P	15:20083768-20093074	NOTEST	0	0	0	0	1	1
ENSG00000201242	ENSG00000201242	RNY1P1	13:27976612-27976724	NOTEST	0	0	0	0	1	1
ENSG00000201243	ENSG00000201243	RNU6-654P	11:108873191-108908694	NOTEST	0	0	0	0	1	1
ENSG00000201245	ENSG00000201245	SNORA25	13:100258918-100549387	NOTEST	0	0	0	0	1	1
ENSG00000201247	ENSG00000201247	SNORD114-13	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000201253	ENSG00000201253	RNU4-10P	13:73765664-73765804	NOTEST	0	0	0	0	1	1
ENSG00000201255	ENSG00000201255	RNU6-990P	17:28687480-28687584	NOTEST	0	0	0	0	1	1
ENSG00000201260	ENSG00000201260	RNU6-1075P	10:16249819-16249926	NOTEST	0	0	0	0	1	1
ENSG00000201263	ENSG00000201263	SNORD114-6	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000201264	ENSG00000201264	SNORD73	4:152020724-152246784	NOTEST	0	0	0	0	1	1
ENSG00000201270	ENSG00000201270	RNU6-755P	1:164949271-164949374	NOTEST	0	0	0	0	1	1
ENSG00000201271	ENSG00000201271	RNU1-112P	X:71960529-71960693	NOTEST	0	0	0	0	1	1
ENSG00000201273	ENSG00000201273	RNU6-776P	1:22328148-22339032	NOTEST	0	0	0	0	1	1
ENSG00000201274	ENSG00000201274	RNA5SP192	5:132184268-132184388	NOTEST	0	0	0	0	1	1
ENSG00000201277	ENSG00000201277	Y_RNA	5:172681192-172681293	NOTEST	0	0	0	0	1	1
ENSG00000201279	ENSG00000201279	Y_RNA	11:3666357-3685646	NOTEST	0	0	0	0	1	1
ENSG00000201282	ENSG00000201282	Y_RNA	7:72440226-72555749	NOTEST	0	0	0	0	1	1
ENSG00000201283	ENSG00000201283	RNU6-489P	17:36267500-36267607	NOTEST	0	0	0	0	1	1
ENSG00000201285	ENSG00000201285	5S_rRNA	X:147062848-147108187	NOTEST	0	0	0	0	1	1
ENSG00000201287	ENSG00000201287	RN7SKP171	9:37510888-38069210	NOTEST	0	0	0	0	1	1
ENSG00000201288	ENSG00000201288	RNU6-1047P	3:126959810-126959917	NOTEST	0	0	0	0	1	1
ENSG00000201289	ENSG00000201289	RN7SKP76	16:61681145-62070939	NOTEST	0	0	0	0	1	1
ENSG00000201291	ENSG00000201291	RNU1-34P	6:75994729-76203454	NOTEST	0	0	0	0	1	1
ENSG00000201292	ENSG00000201292	RNU6-153P	6:166622890-166622994	NOTEST	0	0	0	0	1	1
ENSG00000201294	ENSG00000201294	RNU6-1019P	20:3229950-3388272	NOTEST	0	0	0	0	1	1
ENSG00000201296	ENSG00000201296	RNU4-41P	12:98811673-98811816	NOTEST	0	0	0	0	1	1
ENSG00000201297	ENSG00000201297	Y_RNA	4:126237553-126414087	NOTEST	0	0	0	0	1	1
ENSG00000201298	ENSG00000201298	RNU6-1164P	5:133936833-134063513	NOTEST	0	0	0	0	1	1
ENSG00000201300	ENSG00000201300	SNORD115-27	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000201301	ENSG00000201301	RNA5SP130	3:49504547-49504661	NOTEST	0	0	0	0	1	1
ENSG00000201302	ENSG00000201302	SNORA65	9:130209952-130213684	NOTEST	0	0	0	0	1	1
ENSG00000201308	ENSG00000201308	RNU6-512P	2:136289024-136482840	NOTEST	0	0	0	0	1	1
ENSG00000201309	ENSG00000201309	Y_RNA	6:134490383-134639250	NOTEST	0	0	0	0	1	1
ENSG00000201311	ENSG00000201311	Y_RNA	2:82534190-82534292	NOTEST	0	0	0	0	1	1
ENSG00000201312	ENSG00000201312	RNA5SP72	1:184984082-184984199	NOTEST	0	0	0	0	1	1
ENSG00000201314	ENSG00000201314	Y_RNA	4:146879279-146879392	NOTEST	0	0	0	0	1	1
ENSG00000201315	ENSG00000201315	RN7SKP227	3:36726530-36726860	NOTEST	0	0	0	0	1	1
ENSG00000201316	ENSG00000201316	SNORA7	8:51927580-51927725	NOTEST	0	0	0	0	1	1
ENSG00000201317	ENSG00000201317	RNU4-59P	1:92974252-93257961	NOTEST	0	0	0	0	1	1
ENSG00000201318	ENSG00000201318	SNORD114-30	14:101458255-101458327	NOTEST	0	0	0	0	1	1
ENSG00000201321	ENSG00000201321	RNA5S9	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000201324	ENSG00000201324	RNU6-361P	12:109304657-109372439	NOTEST	0	0	0	0	1	1
ENSG00000201325	ENSG00000201325	RNA5SP142	3:137236975-137237097	NOTEST	0	0	0	0	1	1
ENSG00000201326	ENSG00000201326	SNORD115-22	15:25068793-25492435	NOTEST	0	0	0	0	1	1

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ENSG00000201329	ENSG00000201329	U3	8:43233440-43233652	NOTEST	0	0	0	0	1	1
ENSG00000201330	ENSG00000201330	SNORD32B	6:29523291-29601753	NOTEST	0	0	0	0	1	1
ENSG00000201331	ENSG00000201331	SNORD115-23	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000201339	ENSG00000201339	Y_RNA	3:93591880-93692910	NOTEST	0	0	0	0	1	1
ENSG00000201340	ENSG00000201340	Y_RNA	17:48770550-48785285	NOTEST	0	0	0	0	1	1
ENSG00000201341	ENSG00000201341	RNU6-421P	X:49687224-49863892	NOTEST	0	0	0	0	1	1
ENSG00000201342	ENSG00000201342	RNU4-38P	3:169755716-169803191	NOTEST	0	0	0	0	1	1
ENSG00000201343	ENSG00000201343	Y_RNA	3:176737142-176915261	NOTEST	0	0	0	0	1	1
ENSG00000201346	ENSG00000201346	U3	20:3229950-3388272	NOTEST	0	0	0	0	1	1
ENSG00000201347	ENSG00000201347	RNA5SP69	1:178530047-178530164	NOTEST	0	0	0	0	1	1
ENSG00000201348	ENSG00000201348	RNU105B	20:8112823-8949003	NOTEST	0.311053	0	#NAME?	0	1	1
ENSG00000201351	ENSG00000201351	Y_RNA	14:90528108-90652201	NOTEST	0	0	0	0	1	1
ENSG00000201354	ENSG00000201354	Y_RNA	7:140218219-140624564	NOTEST	0	0	0	0	1	1
ENSG00000201355	ENSG00000201355	RNA5S14	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000201356	ENSG00000201356	RNA5SP500	X:28605515-29974840	NOTEST	0	0	0	0	1	1
ENSG00000201358	ENSG00000201358	RN7SKP193	14:50448429-50559361	NOTEST	0	0	0	0	1	1
ENSG00000201361	ENSG00000201361	RNA5SP433	16:84296420-84296534	NOTEST	0	0	0	0	1	1
ENSG00000201363	ENSG00000201363	Y_RNA	20:42965625-42983825	NOTEST	0	0	0	0	1	1
ENSG00000201364	ENSG00000201364	RN7SKP37	10:22045465-22292698	NOTEST	0	0	0	0	1	1
ENSG00000201365	ENSG00000201365	Y_RNA	8:67540721-67579452	NOTEST	0	0	0	0	1	1
ENSG00000201367	ENSG00000201367	RNU6-522P	6:15246526-15522252	NOTEST	0	0	0	0	1	1
ENSG00000201368	ENSG00000201368	U3	5:35429165-35429378	NOTEST	0	0	0	0	1	1
ENSG00000201370	ENSG00000201370	Y_RNA	5:16473146-16630078	NOTEST	0	0	0	0	1	1
ENSG00000201371	ENSG00000201371	Y_RNA	16:27561453-27791690	NOTEST	0	0	0	0	1	1
ENSG00000201372	ENSG00000201372	RNU6-1251P	20:42101652-42101759	NOTEST	0	0	0	0	1	1
ENSG00000201376	ENSG00000201376	SNORA70	14:51706879-51722759	NOTEST	0	0	0	0	1	1
ENSG00000201377	ENSG00000201377	RNY4P23	X:69506444-69640682	NOTEST	0	0	0	0	1	1
ENSG00000201378	ENSG00000201378	Y_RNA	17:17876126-17942523	NOTEST	0	0	0	0	1	1
ENSG00000201379	ENSG00000201379	RNU4-76P	6:121863631-121863772	NOTEST	0	0	0	0	1	1
ENSG00000201382	ENSG00000201382	RNU6-558P	12:117176095-117291436	NOTEST	0	0	0	0	1	1
ENSG00000201384	ENSG00000201384	SNORA32	14:77564439-77725838	NOTEST	0	0	0	0	1	1
ENSG00000201386	ENSG00000201386	RNU6-1163P	6:113292694-113292801	NOTEST	0	0	0	0	1	1
ENSG00000201388	ENSG00000201388	SNORA68	19:33087912-33169206	NOTEST	0	0	0	0	1	1
ENSG00000201390	ENSG00000201390	RNU6-1141P	10:21823093-22032559	NOTEST	0	0	0	0	1	1
ENSG00000201392	ENSG00000201392	RNU6-1078P	X:71130937-71363424	NOTEST	0	0	0	0	1	1
ENSG00000201393	ENSG00000201393	SNORA71	10:80127263-80127380	NOTEST	0	0	0	0	1	1
ENSG00000201394	ENSG00000201394	RNA5SP140	3:133380841-133497850	NOTEST	0	0	0	0	1	1
ENSG00000201395	ENSG00000201395	RN7SKP257	14:37063043-37063352	NOTEST	0	0	0	0	1	1
ENSG00000201398	ENSG00000201398	U8	3:153725155-153725291	NOTEST	0	0	0	0	1	1
ENSG00000201403	ENSG00000201403	SNORD14B	11:17095935-17229530	NOTEST	0	0	0	0	1	1
ENSG00000201405	ENSG00000201405	Y_RNA	1:23685940-23698332	NOTEST	0	0	0	0	1	1
ENSG00000201407	ENSG00000201407	SNORA68	X:24151302-24151434	NOTEST	0	0	0	0	1	1
ENSG00000201410	ENSG00000201410	snoZ40	3:86174365-86174437	NOTEST	0	0	0	0	1	1
ENSG00000201412	ENSG00000201412	Y_RNA	10:94470255-94470365	NOTEST	0	0	0	0	1	1
ENSG00000201413	ENSG00000201413	RNA5SP141	3:134316642-134979309	NOTEST	0	0	0	0	1	1

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ENSG00000201415	ENSG00000201415	RNA5SP204	6:17722016-17722134	NOTEST	0	0	0	0	1	1
ENSG00000201420	ENSG00000201420	RNA5SP512	X:110909042-111003877	NOTEST	0	0	0	0	1	1
ENSG00000201421	ENSG00000201421	Y_RNA	1:185126211-185260897	NOTEST	0	0	0	0	1	1
ENSG00000201423	ENSG00000201423	RN7SKP246	5:143914916-143915233	NOTEST	0	0	0	0	1	1
ENSG00000201425	ENSG00000201425	Y_RNA	2:175664090-175870097	NOTEST	0	0	0	0	1	1
ENSG00000201426	ENSG00000201426	Y_RNA	3:110445867-110445968	NOTEST	0	0	0	0	1	1
ENSG00000201428	ENSG00000201428	RN7SKP71	12:112597991-112819896	NOTEST	0	0.226561	inf	0	1	1
ENSG00000201431	ENSG00000201431	RNU6-1277P	14:38059188-38672128	NOTEST	0	0	0	0	1	1
ENSG00000201432	ENSG00000201432	Y_RNA	7:36363829-36493400	NOTEST	0	0	0	0	1	1
ENSG00000201433	ENSG00000201433	RNU6-335P	4:184580419-184634745	NOTEST	0	0	0	0	1	1
ENSG00000201435	ENSG00000201435	RNU4-24P	12:96672038-96794338	NOTEST	0	0	0	0	1	1
ENSG00000201436	ENSG00000201436	RNU6-660P	5:16941951-16942060	NOTEST	0	0	0	0	1	1
ENSG00000201439	ENSG00000201439	RNU4-67P	12:25557221-25557362	NOTEST	0	0	0	0	1	1
ENSG00000201440	ENSG00000201440	RNA5SP515	X:134562092-134562210	NOTEST	0	0	0	0	1	1
ENSG00000201441	ENSG00000201441	RNU6-646P	3:196366556-196462878	NOTEST	0	0	0	0	1	1
ENSG00000201442	ENSG00000201442	Y_RNA	6:17737688-17737790	NOTEST	0	0	0	0	1	1
ENSG00000201443	ENSG00000201443	RNU6-309P	X:108069993-108070099	NOTEST	0	0	0	0	1	1
ENSG00000201444	ENSG00000201444	RNU6-1082P	9:120466609-120479149	NOTEST	0	0	0	0	1	1
ENSG00000201447	ENSG00000201447	RNA5SP509	X:76287129-76287248	NOTEST	0	0	0	0	1	1
ENSG00000201448	ENSG00000201448	SNORA63	1:36881427-36916086	NOTEST	0	0	0	0	1	1
ENSG00000201450	ENSG00000201450	RNU6-149P	X:47211241-47211348	NOTEST	0	0	0	0	1	1
ENSG00000201451	ENSG00000201451	Y_RNA	9:136204564-136204661	NOTEST	0	0	0	0	1	1
ENSG00000201452	ENSG00000201452	RNU6-1317P	3:174156362-175523428	NOTEST	0	0	0	0	1	1
ENSG00000201457	ENSG00000201457	SNORA55	1:40026487-40042462	NOTEST	0	0	0	0	1	1
ENSG00000201458	ENSG00000201458	RNU4-4P	3:172468471-172539264	NOTEST	0	0	0	0	1	1
ENSG00000201464	ENSG00000201464	Y_RNA	6:80011679-80011783	NOTEST	0	0	0	0	1	1
ENSG00000201465	ENSG00000201465	SNORA51	7:137872743-137872875	NOTEST	0	0	0	0	1	1
ENSG00000201466	ENSG00000201466	Y_RNA	18:12760715-12760817	NOTEST	0	0	0	0	1	1
ENSG00000201467	ENSG00000201467	SNORA16	X:16964813-17171395	NOTEST	0	0	0	0	1	1
ENSG00000201469	ENSG00000201469	RNA5SP379	12:133300530-133300643	NOTEST	0	0	0	0	1	1
ENSG00000201470	ENSG00000201470	RNY4P7	2:128458595-128568761	NOTEST	0	0	0	0	1	1
ENSG00000201474	ENSG00000201474	RNU6-164P	5:161904896-161904999	NOTEST	0	0	0	0	1	1
ENSG00000201476	ENSG00000201476	RNA5SP353	12:13593817-13593935	NOTEST	0	0	0	0	1	1
ENSG00000201482	ENSG00000201482	SNORD115-17	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000201483	ENSG00000201483	Y_RNA	6:7107829-7252213	NOTEST	0	0	0	0	1	1
ENSG00000201487	ENSG00000201487	SNORD45B	1:76190035-76260764	NOTEST	0	0	0	0	1	1
ENSG00000201489	ENSG00000201489	Y_RNA	17:7440412-7440513	NOTEST	0	0	0	0	1	1
ENSG00000201491	ENSG00000201491	RNU4-75P	1:100250295-100250441	NOTEST	0	0	0	0	1	1
ENSG00000201492	ENSG00000201492	RNA5SP78	1:229652328-229694442	NOTEST	0	24.9933	inf	0	1	1
ENSG00000201493	ENSG00000201493	RNU1-141P	1:218303136-218303294	NOTEST	0	0	0	0	1	1
ENSG00000201496	ENSG00000201496	RN7SKP275	4:5053168-5502725	NOTEST	0.337336	0	#NAME?	0	1	1
ENSG00000201498	ENSG00000201498	Y_RNA	20:32951040-33099198	NOTEST	0	0	0	0	1	1
ENSG00000201499	ENSG00000201499	RNU6-312P	2:201735629-201754026	NOTEST	0	0	0	0	1	1
ENSG00000201500	ENSG00000201500	SNORD113	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000201501	ENSG00000201501	Y_RNA	20:49126890-49201299	NOTEST	0	0	0	0	1	1

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ENSG00000201502	ENSG00000201502	SNORD74	12:93659792-93659872	NOTEST	0	0	0	0	1	1
ENSG00000201509	ENSG00000201509	Y_RNA	15:38780303-38857776	NOTEST	0	0	0	0	1	1
ENSG00000201510	ENSG00000201510	RN7SKP217	15:76640525-77197785	NOTEST	0	0	0	0	1	1
ENSG00000201511	ENSG00000201511	Y_RNA	3:101366264-101366366	NOTEST	0	0	0	0	1	1
ENSG00000201512	ENSG00000201512	SNORA71C	20:37049234-37063996	NOTEST	0	2.77953	inf	0	1	1
ENSG00000201516	ENSG00000201516	SNORA51	4:176986984-177103978	NOTEST	0	0	0	0	1	1
ENSG00000201517	ENSG00000201517	RNU6-707P	X:48013295-48015369	NOTEST	0	0	0	0	1	1
ENSG00000201518	ENSG00000201518	RNA5SP513	X:128570506-128570624	NOTEST	0	0	0	0	1	1
ENSG00000201519	ENSG00000201519	RNU6-645P	6:15246526-15522252	NOTEST	0	0	0	0	1	1
ENSG00000201523	ENSG00000201523	RNA5SP205	6:19438513-19438649	NOTEST	0	0	0	0	1	1
ENSG00000201524	ENSG00000201524	RNU6-450P	17:57924798-57924905	NOTEST	0	0	0	0	1	1
ENSG00000201527	ENSG00000201527	RNA5SP478	20:23141493-23141608	NOTEST	0	0	0	0	1	1
ENSG00000201529	ENSG00000201529	Y_RNA	14:68084018-68084132	NOTEST	0	0	0	0	1	1
ENSG00000201532	ENSG00000201532	RNA5SP194	5:138282408-138667360	NOTEST	0	0	0	0	1	1
ENSG00000201533	ENSG00000201533	RN7SKP237	4:140586921-141075338	NOTEST	0	0	0	0	1	1
ENSG00000201535	ENSG00000201535	Y_RNA	11:118706718-118706819	NOTEST	0	0	0	0	1	1
ENSG00000201541	ENSG00000201541	SNORA1	16:24266873-24374122	NOTEST	0	0	0	0	1	1
ENSG00000201542	ENSG00000201542	SNORA62	1:35734567-35887659	NOTEST	0	0	0	0	1	1
ENSG00000201544	ENSG00000201544	SNORA16B	1:212458878-212535200	NOTEST	0	0	0	0	1	1
ENSG00000201545	ENSG00000201545	RNU4-85P	3:19988570-20053822	NOTEST	0	0	0	0	1	1
ENSG00000201547	ENSG00000201547	Y_RNA	17:65373574-65693372	NOTEST	0	0	0	0	1	1
ENSG00000201548	ENSG00000201548	Y_RNA	10:90345394-90345490	NOTEST	0	0	0	0	1	1
ENSG00000201549	ENSG00000201549	Y_RNA	12:7936998-7937107	NOTEST	0	0	0	0	1	1
ENSG00000201550	ENSG00000201550	RNU6-726P	3:130569438-131100319	NOTEST	0	0	0	0	1	1
ENSG00000201554	ENSG00000201554	Y_RNA	3:101043048-101232085	NOTEST	0	0	0	0	1	1
ENSG00000201555	ENSG00000201555	Y_RNA	6:31745294-31763730	NOTEST	0	0	0	0	1	1
ENSG00000201557	ENSG00000201557	SNORD114-15	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000201558	ENSG00000201558	RNVU1-6	1:145382756-145382920	NOTEST	0	0	0	0	1	1
ENSG00000201560	ENSG00000201560	RNU6-973P	7:65324646-65324753	NOTEST	0	0	0	0	1	1
ENSG00000201563	ENSG00000201563	Y_RNA	12:32832133-32908836	NOTEST	0	0	0	0	1	1
ENSG00000201564	ENSG00000201564	RN7SKP50	11:9685623-9774538	NOTEST	0	0	0	0	1	1
ENSG00000201565	ENSG00000201565	Y_RNA	7:66752527-66786513	NOTEST	0	0	0	0	1	1
ENSG00000201566	ENSG00000201566	Y_RNA	7:36893960-37488852	NOTEST	0	0	0	0	1	1
ENSG00000201567	ENSG00000201567	RNA5SP510	X:94837062-94837161	NOTEST	0	0	0	0	1	1
ENSG00000201569	ENSG00000201569	SNORD114-17	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000201570	ENSG00000201570	RNU4-56P	3:39850404-40301812	NOTEST	0	0	0	0	1	1
ENSG00000201573	ENSG00000201573	Y_RNA	14:50885218-51135049	NOTEST	0	0	0	0	1	1
ENSG00000201574	ENSG00000201574	RNU1-93P	2:231921577-232037541	NOTEST	0	0	0	0	1	1
ENSG00000201579	ENSG00000201579	RNU6-343P	12:56915712-56984745	NOTEST	0	0	0	0	1	1
ENSG00000201581	ENSG00000201581	RN7SKP78	10:6186880-6277495	NOTEST	0	0	0	0	1	1
ENSG00000201583	ENSG00000201583	RN7SKP191	9:107859036-107859342	NOTEST	0	0	0	0	1	1
ENSG00000201584	ENSG00000201584	Y_RNA	2:121798185-121798286	NOTEST	0	0	0	0	1	1
ENSG00000201586	ENSG00000201586	RNU6-593P	11:17095935-17229530	NOTEST	0	0	0	0	1	1
ENSG00000201588	ENSG00000201588	RNA5S2	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000201591	ENSG00000201591	RNU6-99P	11:39282656-39282763	NOTEST	0	0	0	0	1	1

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ENSG00000201592	ENSG00000201592	snoU2_19	X:20142635-20159962	NOTEST	0	0	0	0	1	1
ENSG00000201594	ENSG00000201594	RNA5SP517	X:145508973-145509090	NOTEST	0	0	0	0	1	1
ENSG00000201595	ENSG00000201595	RNA5SP132	3:51575159-51738339	NOTEST	0	0	0	0	1	1
ENSG00000201596	ENSG00000201596	Y_RNA	1:185603204-185603314	NOTEST	0	0	0	0	1	1
ENSG00000201598	ENSG00000201598	RNU6-219P	18:56472499-56472606	NOTEST	0	0	0	0	1	1
ENSG00000201600	ENSG00000201600	RN7SKP124	3:139108656-139396859	NOTEST	0	0	0	0	1	1
ENSG00000201602	ENSG00000201602	Y_RNA	1:248758225-248758334	NOTEST	0	0	0	0	1	1
ENSG00000201604	ENSG00000201604	RNU6-740P	10:92682487-92682592	NOTEST	0	0	0	0	1	1
ENSG00000201607	ENSG00000201607	RNU4-16P	7:94536513-94925727	NOTEST	0	0	0	0	1	1
ENSG00000201608	ENSG00000201608	RNU4-42P	1:160362557-160362699	NOTEST	0	0	0	0	1	1
ENSG00000201609	ENSG00000201609	RNU4-28P	1:19837086-19837227	NOTEST	0	0	0	0	1	1
ENSG00000201610	ENSG00000201610	RNA5SP84	2:11657522-11657629	NOTEST	0	0	0	0	1	1
ENSG00000201612	ENSG00000201612	RN7SKP15	12:27959014-27959323	NOTEST	0	0	0	0	1	1
ENSG00000201613	ENSG00000201613	RNU6-200P	6:126911432-126911539	NOTEST	0	0	0	0	1	1
ENSG00000201614	ENSG00000201614	RNU4-19P	1:155864071-155864177	NOTEST	0	0	0	0	1	1
ENSG00000201616	ENSG00000201616	RNU1-91P	11:3022151-3078843	NOTEST	0	0	0	0	1	1
ENSG00000201618	ENSG00000201618	RNA5SP505	X:53935487-53935595	NOTEST	0	0	0	0	1	1
ENSG00000201619	ENSG00000201619	SNORA67	1:179068461-179198819	NOTEST	0	0	0	0	1	1
ENSG00000201620	ENSG00000201620	RNA5SP51	1:86194915-86622626	NOTEST	0	0	0	0	1	1
ENSG00000201622	ENSG00000201622	RNU6-621P	3:197687070-197770591	NOTEST	0	0	0	0	1	1
ENSG00000201623	ENSG00000201623	RNU6-923P	5:33523639-33892297	NOTEST	0	0	0	0	1	1
ENSG00000201624	ENSG00000201624	Y_RNA	12:34135399-34135501	NOTEST	0	0	0	0	1	1
ENSG00000201627	ENSG00000201627	Y_RNA	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000201628	ENSG00000201628	RNU4-7P	6:150647758-150647899	NOTEST	0	0	0	0	1	1
ENSG00000201633	ENSG00000201633	Y_RNA	4:84557348-84557443	NOTEST	0	0	0	0	1	1
ENSG00000201634	ENSG00000201634	SNORD115-48	15:25497371-25684128	NOTEST	0	0	0	0	1	1
ENSG00000201635	ENSG00000201635	Y_RNA	3:45864807-45957534	NOTEST	0	0	0	0	1	1
ENSG00000201638	ENSG00000201638	RNY4P16	1:234973719-234973820	NOTEST	0	0	0	0	1	1
ENSG00000201640	ENSG00000201640	RN7SKP28	4:97231851-97740015	NOTEST	0	0	0	0	1	1
ENSG00000201641	ENSG00000201641	RNU6-1187P	4:78071480-78071590	NOTEST	0	0	0	0	1	1
ENSG00000201642	ENSG00000201642	RNU6-865P	3:100467999-100712359	NOTEST	0	0	0	0	1	1
ENSG00000201643	ENSG00000201643	SNORA14A	7:75528517-75623977	NOTEST	3.53478	0	#NAME?	0	1	1
ENSG00000201644	ENSG00000201644	Y_RNA	4:76567965-76649709	NOTEST	0	0	0	0	1	1
ENSG00000201648	ENSG00000201648	RNU4-91P	3:174156362-175523428	NOTEST	0	0	0	0	1	1
ENSG00000201649	ENSG00000201649	Y_RNA	2:201170603-201346986	NOTEST	0	0	0	0	1	1
ENSG00000201654	ENSG00000201654	RNU6-7	14:32671250-32671357	NOTEST	0	0	0	0	1	1
ENSG00000201658	ENSG00000201658	RNU6-283P	6:31337910-31338017	NOTEST	0	0	0	0	1	1
ENSG00000201659	ENSG00000201659	RNU12-2P	X:46992069-46992225	NOTEST	0	0	0	0	1	1
ENSG00000201660	ENSG00000201660	SNORA20	X:5328162-5328292	NOTEST	0	0	0	0	1	1
ENSG00000201662	ENSG00000201662	RNU6-60P	13:49550047-49783915	NOTEST	0	0	0	0	1	1
ENSG00000201663	ENSG00000201663	Y_RNA	12:7965107-8043744	NOTEST	0	0	0	0	1	1
ENSG00000201665	ENSG00000201665	RN7SKP6	13:57459417-57459736	NOTEST	0	0	0	0	1	1
ENSG00000201666	ENSG00000201666	SNORD74	X:28605515-29974840	NOTEST	0	0	0	0	1	1
ENSG00000201668	ENSG00000201668	Y_RNA	18:47309868-47721463	NOTEST	0	0	0	0	1	1
ENSG00000201671	ENSG00000201671	RNA5SP90	2:31395923-31456724	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000201672	ENSG00000201672	SNORD113-4	14:101402827-101402902	NOTEST	0	0	0	0	1	1
ENSG00000201674	ENSG00000201674	U3	X:113187478-113187691	NOTEST	0	0	0	0	1	1
ENSG00000201675	ENSG00000201675	SNORD32A	19:49949554-49995565	NOTEST	0	0	0	0	1	1
ENSG00000201676	ENSG00000201676	Y_RNA	4:60698892-60698994	NOTEST	0	0	0	0	1	1
ENSG00000201678	ENSG00000201678	Y_RNA	12:49297200-49351334	NOTEST	0	0	0	0	1	1
ENSG00000201679	ENSG00000201679	SNORD115-15	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000201680	ENSG00000201680	Y_RNA	6:31462657-31478901	NOTEST	0	0	0	0	1	1
ENSG00000201683	ENSG00000201683	Y_RNA	6:20500405-20500507	NOTEST	0	0	0	0	1	1
ENSG00000201684	ENSG00000201684	RN7SKP239	11:67118247-67141648	NOTEST	0	0	0	0	1	1
ENSG00000201687	ENSG00000201687	RNU6-1107P	11:113668595-113746292	NOTEST	0	0	0	0	1	1
ENSG00000201689	ENSG00000201689	SNORD114-29	14:101456427-101456497	NOTEST	0	0	0	0	1	1
ENSG00000201690	ENSG00000201690	RNY1P2	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000201695	ENSG00000201695	RNA5SP334	11:18287720-18291524	NOTEST	0	0	0	0	1	1
ENSG00000201699	ENSG00000201699	RNU1-59P	1:144534037-144534199	NOTEST	0	0	0	0	1	1
ENSG00000201700	ENSG00000201700	SNORD113-3	14:101361106-101402336	NOTEST	0	0	0	0	1	1
ENSG00000201701	ENSG00000201701	SNORA25	3:31699381-32119072	NOTEST	0	0	0	0	1	1
ENSG00000201704	ENSG00000201704	RNA5SP396	15:59866301-59866421	NOTEST	0	0	0	0	1	1
ENSG00000201707	ENSG00000201707	RNU6-818P	4:89011415-89152474	NOTEST	0	0	0	0	1	1
ENSG00000201708	ENSG00000201708	RNA5SP359	12:38557204-38557317	NOTEST	0	0	0	0	1	1
ENSG00000201709	ENSG00000201709	RNU6-688P	15:65522198-65522305	NOTEST	0	0	0	0	1	1
ENSG00000201710	ENSG00000201710	SNORD113	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000201711	ENSG00000201711	RNU6-1303P	9:80037994-80263223	NOTEST	0	0	0	0	1	1
ENSG00000201713	ENSG00000201713	RNA5SP125	3:24729409-25215796	NOTEST	0	0	0	0	1	1
ENSG00000201715	ENSG00000201715	RN7SKP133	5:17345724-17346064	NOTEST	0	0	0	0	1	1
ENSG00000201723	ENSG00000201723	Y_RNA	18:76304095-76304188	NOTEST	0	0	0	0	1	1
ENSG00000201724	ENSG00000201724	Y_RNA	15:100017369-100273766	NOTEST	0	0	0	0	1	1
ENSG00000201725	ENSG00000201725	RNU6-304P	1:8943485-8943592	NOTEST	0	0	0	0	1	1
ENSG00000201727	ENSG00000201727	RNA5SP173	4:179327848-179327984	NOTEST	0	0	0	0	1	1
ENSG00000201728	ENSG00000201728	RNA5SP479	20:23355158-23402125	NOTEST	0	0	0	0	1	1
ENSG00000201733	ENSG00000201733	SNORA43	11:66200233-66200373	NOTEST	0	0	0	0	1	1
ENSG00000201736	ENSG00000201736	RNA5SP160	4:40812043-41218731	NOTEST	0	0	0	0	1	1
ENSG00000201737	ENSG00000201737	RNU1-133P	2:201542955-201688569	NOTEST	0	0	0	0	1	1
ENSG00000201741	ENSG00000201741	Y_RNA	17:17363757-17363836	NOTEST	0	0	0	0	1	1
ENSG00000201742	ENSG00000201742	RNU6-563P	20:46121721-46121829	NOTEST	0	0	0	0	1	1
ENSG00000201744	ENSG00000201744	RNU6-34P	4:97073447-97073554	NOTEST	0	0	0	0	1	1
ENSG00000201746	ENSG00000201746	RNU6-828P	1:10092889-10241297	NOTEST	0	0	0	0	1	1
ENSG00000201747	ENSG00000201747	RNU6-534P	7:7676148-8133902	NOTEST	0	0	0	0	1	1
ENSG00000201749	ENSG00000201749	Y_RNA	9:117373485-117408702	NOTEST	0	0	0	0	1	1
ENSG00000201752	ENSG00000201752	RNU6-119P	4:117760434-117760541	NOTEST	0	0	0	0	1	1
ENSG00000201754	ENSG00000201754	SNORD52	6:31802384-31807541	NOTEST	0	0	0	0	1	1
ENSG00000201756	ENSG00000201756	Y_RNA	11:76092356-76125663	NOTEST	0	0	0	0	1	1
ENSG00000201758	ENSG00000201758	RN7SKP55	1:245107211-245107518	NOTEST	0	0	0	0	1	1
ENSG00000201761	ENSG00000201761	RNU6-336P	8:22291903-22292010	NOTEST	0	0	0	0	1	1
ENSG00000201763	ENSG00000201763	RNA5SP267	8:60368443-60368569	NOTEST	0	0	0	0	1	1
ENSG00000201766	ENSG00000201766	RNA5SP302	10:14560555-14816896	NOTEST	0	0	0	0	1	1

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ENSG00000201772	ENSG00000201772	SNORA5C	7:45139698-45151646	NOTEST	0	0	0	0	1	1
ENSG00000201774	ENSG00000201774	Y_RNA	7:10941604-10941701	NOTEST	0	0	0	0	1	1
ENSG00000201775	ENSG00000201775	RNU6-1325P	4:60699780-60699885	NOTEST	0	0	0	0	1	1
ENSG00000201778	ENSG00000201778	Y_RNA	3:156864296-156878549	NOTEST	0	0	0	0	1	1
ENSG00000201780	ENSG00000201780	RNU6-275P	12:8637341-8637448	NOTEST	0	0	0	0	1	1
ENSG00000201782	ENSG00000201782	RN7SKP226	8:129232749-129233049	NOTEST	0	0	0	0	1	1
ENSG00000201785	ENSG00000201785	SNORD117	6:31496493-31526606	NOTEST	0	0	0	0	1	1
ENSG00000201786	ENSG00000201786	Y_RNA	4:154073493-154260472	NOTEST	0	0	0	0	1	1
ENSG00000201788	ENSG00000201788	Y_RNA	12:44902057-45315631	NOTEST	0	0	0	0	1	1
ENSG00000201789	ENSG00000201789	RNU6-1071P	1:145149739-145149840	NOTEST	0	0	0	0	1	1
ENSG00000201790	ENSG00000201790	RNA5SP189	5:105258694-105258809	NOTEST	0	0	0	0	1	1
ENSG00000201791	ENSG00000201791	SNORA63	1:178693440-178889238	NOTEST	0	0	0	0	1	1
ENSG00000201792	ENSG00000201792	RNU6-1192P	17:34580901-34808104	NOTEST	0	0	0	0	1	1
ENSG00000201793	ENSG00000201793	RN7SKP9	13:99853027-100038688	NOTEST	0	0	0	0	1	1
ENSG00000201794	ENSG00000201794	RN7SKP130	7:2945774-3083579	NOTEST	0	0	0	0	1	1
ENSG00000201796	ENSG00000201796	RNU6-392P	7:105848612-105848713	NOTEST	0	0	0	0	1	1
ENSG00000201800	ENSG00000201800	Y_RNA	3:125165494-125239041	NOTEST	0	0	0	0	1	1
ENSG00000201801	ENSG00000201801	RNU5E-4P	1:11969864-11969984	NOTEST	0	0	0	0	1	1
ENSG00000201805	ENSG00000201805	RNU6-1180P	2:113844381-113844488	NOTEST	0	0	0	0	1	1
ENSG00000201806	ENSG00000201806	RNU4-8P	2:98280679-98319527	NOTEST	0	0	0	0	1	1
ENSG00000201807	ENSG00000201807	SNORA27	6:137143716-137235075	NOTEST	0	0	0	0	1	1
ENSG00000201809	ENSG00000201809	U8	12:74154468-74192507	NOTEST	0	0	0	0	1	1
ENSG00000201810	ENSG00000201810	U8	3:180260488-180260624	NOTEST	0	0	0	0	1	1
ENSG00000201811	ENSG00000201811	SNORA71	20:37070678-37070812	NOTEST	0	0	0	0	1	1
ENSG00000201812	ENSG00000201812	RNA5SP488	21:15399741-15583166	NOTEST	0	0	0	0	1	1
ENSG00000201813	ENSG00000201813	RNU6-915P	2:196440700-196602426	NOTEST	0	0	0	0	1	1
ENSG00000201815	ENSG00000201815	RNU6-526P	8:9106926-9293715	NOTEST	0	0	0	0	1	1
ENSG00000201816	ENSG00000201816	SNORA73	18:53548918-53858493	NOTEST	0	0	0	0	1	1
ENSG00000201818	ENSG00000201818	RNY4P17	4:169277885-169931426	NOTEST	0	0	0	0	1	1
ENSG00000201820	ENSG00000201820	Y_RNA	14:51706879-51722759	NOTEST	0	0	0	0	1	1
ENSG00000201821	ENSG00000201821	RNU4-9P	13:21547170-21635686	NOTEST	0	0	0	0	1	1
ENSG00000201822	ENSG00000201822	RNA5SP149	3:179879673-179879765	NOTEST	0	0	0	0	1	1
ENSG00000201823	ENSG00000201823	SNORD48	6:31802384-31807541	NOTEST	0	0	0	0	1	1
ENSG00000201825	ENSG00000201825	RNU6-1131P	18:44746292-44775554	NOTEST	0	0	0	0	1	1
ENSG00000201826	ENSG00000201826	RNU6-867P	X:75465366-75465473	NOTEST	0	0	0	0	1	1
ENSG00000201827	ENSG00000201827	SNORA33	3:133270029-133270159	NOTEST	0	0	0	0	1	1
ENSG00000201830	ENSG00000201830	Y_RNA	9:100666770-100684852	NOTEST	0	0	0	0	1	1
ENSG00000201831	ENSG00000201831	SNORD115-1	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000201839	ENSG00000201839	SNORD114-3	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000201843	ENSG00000201843	Y_RNA	9:136177952-136178046	NOTEST	0	0	0	0	1	1
ENSG00000201846	ENSG00000201846	RNA5SP166	4:149479098-149479200	NOTEST	0	0	0	0	1	1
ENSG00000201847	ENSG00000201847	SNORD31	13:107820882-108519083	NOTEST	0	0	0	0	1	1
ENSG00000201850	ENSG00000201850	Y_RNA	16:68021296-68272005	NOTEST	0	0	0	0	1	1
ENSG00000201852	ENSG00000201852	RNU6-702P	18:19749403-19785192	NOTEST	0	0	0	0	1	1

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ENSG00000201853	ENSG00000201853	snosnR60_Z15	2:125886408-125886490	NOTEST	0	0	0	0	1	1
ENSG00000201856	ENSG00000201856	RNA5SP331	11:13929030-13929137	NOTEST	0	0	0	0	1	1
ENSG00000201860	ENSG00000201860	Y_RNA	3:191358923-191359026	NOTEST	0	0	0	0	1	1
ENSG00000201861	ENSG00000201861	RNA5SP298	10:320129-735683	NOTEST	0	0	0	0	1	1
ENSG00000201862	ENSG00000201862	Y_RNA	7:72440226-72555749	NOTEST	0	0	0	0	1	1
ENSG00000201863	ENSG00000201863	SNORA51	4:40044536-40159872	NOTEST	0	0	0	0	1	1
ENSG00000201867	ENSG00000201867	Y_RNA	11:34172534-34379555	NOTEST	0	0	0	0	1	1
ENSG00000201868	ENSG00000201868	Y_RNA	1:35661569-35661663	NOTEST	0	0	0	0	1	1
ENSG00000201869	ENSG00000201869	RNU6-294P	5:63802083-63908139	NOTEST	0	0	0	0	1	1
ENSG00000201875	ENSG00000201875	RN7SKP178	2:206765353-206765682	NOTEST	0	0	0	0	1	1
ENSG00000201876	ENSG00000201876	RNA5SP97	2:74153952-74208568	NOTEST	0	0	0	0	1	1
ENSG00000201881	ENSG00000201881	Y_RNA	10:74413922-74414034	NOTEST	0	0	0	0	1	1
ENSG00000201882	ENSG00000201882	snoU2-30	X:20142635-20159962	NOTEST	0	0	0	0	1	1
ENSG00000201884	ENSG00000201884	Y_RNA	10:123499938-123711480	NOTEST	0	0	0	0	1	1
ENSG00000201885	ENSG00000201885	Y_RNA	7:76139744-77045717	NOTEST	0	0	0	0	1	1
ENSG00000201892	ENSG00000201892	Y_RNA	2:140988991-142895399	NOTEST	0	0	0	0	1	1
ENSG00000201894	ENSG00000201894	RNU6-967P	19:32278053-32278161	NOTEST	0	0	0	0	1	1
ENSG00000201896	ENSG00000201896	RN7SKP153	8:120724069-120724385	NOTEST	0	0	0	0	1	1
ENSG00000201898	ENSG00000201898	SNORA72	1:224363457-224381143	NOTEST	0	0	0	0	1	1
ENSG00000201899	ENSG00000201899	SNORD114-24	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000201900	ENSG00000201900	Y_RNA	1:115259533-115301297	NOTEST	0	0	0	0	1	1
ENSG00000201901	ENSG00000201901	RN7SKP48	4:86021648-86021976	NOTEST	0	0	0	0	1	1
ENSG00000201907	ENSG00000201907	SNORD115-38	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000201909	ENSG00000201909	RNU6-590P	12:13612603-13612710	NOTEST	0	0	0	0	1	1
ENSG00000201910	ENSG00000201910	RNU1-140P	5:103415611-103441104	NOTEST	0	0	0	0	1	1
ENSG00000201912	ENSG00000201912	RN7SKP189	X:144138627-144138957	NOTEST	0	0	0	0	1	1
ENSG00000201913	ENSG00000201913	Y_RNA	7:99905324-99997719	NOTEST	0	0	0	0	1	1
ENSG00000201916	ENSG00000201916	Y_RNA	22:20778873-20850170	NOTEST	0	0	0	0	1	1
ENSG00000201919	ENSG00000201919	RNU6-1022P	1:22303513-22325135	NOTEST	0	0	0	0	1	1
ENSG00000201920	ENSG00000201920	RNA5SP442	17:39775688-39943183	NOTEST	0	0	0	0	1	1
ENSG00000201922	ENSG00000201922	RNU1-43P	3:102878803-102878968	NOTEST	0	0	0	0	1	1
ENSG00000201923	ENSG00000201923	RNA5SP485	20:44179791-44207965	NOTEST	0	0	0	0	1	1
ENSG00000201925	ENSG00000201925	RNA5S15	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000201931	ENSG00000201931	RNA5SP172	4:178366132-178598280	NOTEST	0	0	0	0	1	1
ENSG00000201933	ENSG00000201933	Y_RNA	7:43136330-43136443	NOTEST	0	0	0	0	1	1
ENSG00000201938	ENSG00000201938	Y_RNA	9:98865360-98865456	NOTEST	0	0	0	0	1	1
ENSG00000201939	ENSG00000201939	RNA5SP224	6:153480354-153480480	NOTEST	0	0	0	0	1	1
ENSG00000201942	ENSG00000201942	RNA5SP363	12:79968758-80334448	NOTEST	0	0	0	0	1	1
ENSG00000201943	ENSG00000201943	SNORD115-10	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000201944	ENSG00000201944	SNORA72	1:205681946-205719404	NOTEST	0	0	0	0	1	1
ENSG00000201945	ENSG00000201945	SNORA70	12:121544845-121544977	NOTEST	0	0	0	0	1	1
ENSG00000201950	ENSG00000201950	SNORD113-9	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000201954	ENSG00000201954	RNU6-673P	10:77360997-78320752	NOTEST	0	0	0	0	1	1
ENSG00000201955	ENSG00000201955	RNY3P1	5:78293437-78531861	NOTEST	0	0	0	0	1	1
ENSG00000201957	ENSG00000201957	SNORA25	3:178865901-178984790	NOTEST	0	0	0	0	1	1

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ENSG00000201959	ENSG00000201959	Y_RNA	7:76139744-77045717	NOTEST	0	0	0	0	1	1
ENSG00000201962	ENSG00000201962	RNA5SP126	3:25215822-25639423	NOTEST	0	0	0	0	1	1
ENSG00000201965	ENSG00000201965	Y_RNA	3:38080695-38178733	NOTEST	0	0	0	0	1	1
ENSG00000201966	ENSG00000201966	RNA5-8SP4	19:24187159-24187309	NOTEST	0	0	0	0	1	1
ENSG00000201967	ENSG00000201967	RN7SKP22	19:33321414-33360672	NOTEST	0	0	0	0	1	1
ENSG00000201968	ENSG00000201968	RNA5SP138	3:126283407-126283521	NOTEST	0	0	0	0	1	1
ENSG00000201969	ENSG00000201969	SNORD115-20	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000201980	ENSG00000201980	SNORA62	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000201984	ENSG00000201984	Y_RNA	21:30449791-30548210	NOTEST	0	0	0	0	1	1
ENSG00000201987	ENSG00000201987	Y_RNA	1:164524820-164868533	NOTEST	0	0	0	0	1	1
ENSG00000201988	ENSG00000201988	Y_RNA	6:30695485-30710510	NOTEST	0	0	0	0	1	1
ENSG00000201990	ENSG00000201990	Y_RNA	7:6012869-6048756	NOTEST	0	0	0	0	1	1
ENSG00000201992	ENSG00000201992	SNORD115-35	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000201998	ENSG00000201998	SNORA23	11:9406168-9469673	NOTEST	0.527853	0	#NAME?	0	1	1
ENSG00000201999	ENSG00000201999	RNA5SP428	16:66335711-66335843	NOTEST	0	0	0	0	1	1
ENSG00000202000	ENSG00000202000	RNU1-36P	4:88921388-88921553	NOTEST	0	1.90643	inf	0	1	1
ENSG00000202001	ENSG00000202001	Y_RNA	8:101767328-101767423	NOTEST	0	0	0	0	1	1
ENSG00000202008	ENSG00000202008	Y_RNA	2:202241929-202345569	NOTEST	0	0	0	0	1	1
ENSG00000202012	ENSG00000202012	RNY4P15	2:88529087-88529183	NOTEST	0	0	0	0	1	1
ENSG00000202014	ENSG00000202014	Y_RNA	4:48137799-48271881	NOTEST	0	0	0	0	1	1
ENSG00000202016	ENSG00000202016	RNU6-619P	2:223289235-223425667	NOTEST	0	0	0	0	1	1
ENSG00000202017	ENSG00000202017	RNU6-806P	5:58264864-59843484	NOTEST	0	0	0	0	1	1
ENSG00000202019	ENSG00000202019	Y_RNA	22:31608224-31676066	NOTEST	0	0	0	0	1	1
ENSG00000202021	ENSG00000202021	Y_RNA	7:74696065-74714647	NOTEST	0	0	0	0	1	1
ENSG00000202023	ENSG00000202023	SNORD81	7:136912087-137028611	NOTEST	0	0	0	0	1	1
ENSG00000202024	ENSG00000202024	RNU6-934P	X:100580391-100580498	NOTEST	0	0	0	0	1	1
ENSG00000202025	ENSG00000202025	RNU6-1240P	1:186265404-186344825	NOTEST	0	0	0	0	1	1
ENSG00000202026	ENSG00000202026	RNU6-1134P	17:30040771-30040872	NOTEST	0	0	0	0	1	1
ENSG00000202027	ENSG00000202027	Y_RNA	1:155092965-155093074	NOTEST	0	0	0	0	1	1
ENSG00000202029	ENSG00000202029	RNU6-580P	2:159825145-160089170	NOTEST	0	0	0	0	1	1
ENSG00000202031	ENSG00000202031	SNORD38A	1:45205489-45244451	NOTEST	0	0	0	0	1	1
ENSG00000202034	ENSG00000202034	RNU6-399P	12:62860596-62991363	NOTEST	0	0	0	0	1	1
ENSG00000202035	ENSG00000202035	Y_RNA	7:72818117-72818219	NOTEST	0	0	0	0	1	1
ENSG00000202039	ENSG00000202039	RNU6-215P	7:5219691-5219793	NOTEST	0	0	0	0	1	1
ENSG00000202041	ENSG00000202041	Y_RNA	1:240177647-240643504	NOTEST	0	0	0	0	1	1
ENSG00000202044	ENSG00000202044	RNA5SP223	6:151977825-152958936	NOTEST	0	0	0	0	1	1
ENSG00000202046	ENSG00000202046	Y_RNA	2:120770580-120974855	NOTEST	0	0	0	0	1	1
ENSG00000202047	ENSG00000202047	RNA5SP324	10:98353068-98480271	NOTEST	0	0	0	0	1	1
ENSG00000202048	ENSG00000202048	SNORD114-20	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000202050	ENSG00000202050	RNU6-391P	6:24365878-24365982	NOTEST	0	0	0	0	1	1
ENSG00000202051	ENSG00000202051	RNU6-382P	X:146908796-146908902	NOTEST	0	0	0	0	1	1
ENSG00000202054	ENSG00000202054	RNA5SP152	4:8368008-8514337	NOTEST	0	0	0	0	1	1
ENSG00000202056	ENSG00000202056	RNA5SP19	1:228743493-228743602	NOTEST	0	0	0	0	1	1
ENSG00000202059	ENSG00000202059	SNORA1	2:203879601-204091101	NOTEST	0	0	0	0	1	1
ENSG00000202060	ENSG00000202060	RNA5SP455	18:41651547-41651666	NOTEST	0	0	0	0	1	1

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ENSG00000202064	ENSG00000202064	RNVU1-11	1:147835126-147931933	NOTEST	0	0	0	0	1	1
ENSG00000202067	ENSG00000202067	Y_RNA	12:57621756-57621880	NOTEST	0	0	0	0	1	1
ENSG00000202069	ENSG00000202069	RNU4-66P	6:72362176-72362314	NOTEST	0	0	0	0	1	1
ENSG00000202070	ENSG00000202070	RNU6-1175P	11:69918539-69921575	NOTEST	0	0	0	0	1	1
ENSG00000202071	ENSG00000202071	Y_RNA	3:65339199-66024509	NOTEST	0	0	0	0	1	1
ENSG00000202072	ENSG00000202072	Y_RNA	7:138100224-138100319	NOTEST	0	0	0	0	1	1
ENSG00000202074	ENSG00000202074	RNU6-715P	2:148253005-148253108	NOTEST	0	0	0	0	1	1
ENSG00000202077	ENSG00000202077	RNU1-60P	17:56597197-56769416	NOTEST	0	0	0	0	1	1
ENSG00000202078	ENSG00000202078	Y_RNA	1:160259062-160328742	NOTEST	0	0	0	0	1	1
ENSG00000202079	ENSG00000202079	Y_RNA	1:247458136-247458243	NOTEST	0	0	0	0	1	1
ENSG00000202081	ENSG00000202081	RNU6-1280P	15:85923801-86293512	NOTEST	0	0	0	0	1	1
ENSG00000202082	ENSG00000202082	RNU6-290P	1:171387782-171387889	NOTEST	0	0	0	0	1	1
ENSG00000202089	ENSG00000202089	RNU6-1306P	11:63606399-63678491	NOTEST	0	0	0	0	1	1
ENSG00000202092	ENSG00000202092	RNA5SP190	5:118781410-118781528	NOTEST	0	0	0	0	1	1
ENSG00000202093	ENSG00000202093	SNORD58C	18:47008027-47018906	NOTEST	0	0	0	0	1	1
ENSG00000202095	ENSG00000202095	RNU6-1172P	8:97443281-97443388	NOTEST	0	0	0	0	1	1
ENSG00000202099	ENSG00000202099	RNU6-234P	2:239321282-239321386	NOTEST	0	0	0	0	1	1
ENSG00000202100	ENSG00000202100	Y_RNA	17:30771278-30810336	NOTEST	0	0	0	0	1	1
ENSG00000202103	ENSG00000202103	RNU4-12P	6:86702738-86702877	NOTEST	0	0	0	0	1	1
ENSG00000202105	ENSG00000202105	Y_RNA	5:122846129-122846231	NOTEST	0	0	0	0	1	1
ENSG00000202107	ENSG00000202107	SNORD103B	1:31404352-31538838	NOTEST	0	0	0	0	1	1
ENSG00000202111	ENSG00000202111	VTRNA1-2	5:140098509-140098598	NOTEST	0	0	0	0	1	1
ENSG00000202112	ENSG00000202112	RNU6-690P	8:96216683-96822364	NOTEST	0	0	0	0	1	1
ENSG00000202119	ENSG00000202119	RNU6-302P	6:151186684-151549582	NOTEST	0	0	0	0	1	1
ENSG00000202124	ENSG00000202124	RNY4P3	16:50080339-50155854	NOTEST	0	0	0	0	1	1
ENSG00000202125	ENSG00000202125	RNU1-100P	3:142025448-142166904	NOTEST	0	0	0	0	1	1
ENSG00000202129	ENSG00000202129	RNY5P1	1:35893416-35893494	NOTEST	0	0	0	0	1	1
ENSG00000202137	ENSG00000202137	Y_RNA	2:202655183-202760273	NOTEST	0	0	0	0	1	1
ENSG00000202140	ENSG00000202140	Y_RNA	1:50905149-51425935	NOTEST	0	0	0	0	1	1
ENSG00000202141	ENSG00000202141	Y_RNA	2:183773842-183903586	NOTEST	0	0	0	0	1	1
ENSG00000202142	ENSG00000202142	SNORD114-18	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000202144	ENSG00000202144	Y_RNA	X:19362010-19533379	NOTEST	0	0	0	0	1	1
ENSG00000202146	ENSG00000202146	Y_RNA	12:54452037-54519776	NOTEST	0	0	0	0	1	1
ENSG00000202147	ENSG00000202147	RNA5SP329	11:6038225-6038344	NOTEST	0	0	0	0	1	1
ENSG00000202150	ENSG00000202150	RNU6-407P	20:33563205-33680674	NOTEST	0	0	0	0	1	1
ENSG00000202151	ENSG00000202151	RNY4P28	13:60761871-60761964	NOTEST	0	0	0	0	1	1
ENSG00000202157	ENSG00000202157	RNU4-11P	5:83099372-83099504	NOTEST	0	0	0	0	1	1
ENSG00000202159	ENSG00000202159	RNU6-742P	18:55297533-55470333	NOTEST	0	0	0	0	1	1
ENSG00000202160	ENSG00000202160	RNU5E-7P	2:16005058-16005175	NOTEST	0	0	0	0	1	1
ENSG00000202164	ENSG00000202164	RNA5SP117	2:209785270-209785388	NOTEST	0	0	0	0	1	1
ENSG00000202167	ENSG00000202167	RNU1-114P	1:149146713-149146879	NOTEST	0	0	0	0	1	1
ENSG00000202169	ENSG00000202169	Y_RNA	4:62066975-63031272	NOTEST	0	0	0	0	1	1
ENSG00000202172	ENSG00000202172	RNU6-1327P	9:213107-746105	NOTEST	0	0	0	0	1	1
ENSG00000202174	ENSG00000202174	RNA5-8SP5	2:132905163-133015542	NOTEST	0	0	0	0	1	1

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ENSG00000202175	ENSG00000202175	RNA5SP128	3:33533474-33533590	NOTEST	0	0	0	0	1	1
ENSG00000202177	ENSG00000202177	Y_RNA	3:101659702-101716770	NOTEST	0	0	0	0	1	1
ENSG00000202178	ENSG00000202178	Y_RNA	7:74880904-74988262	NOTEST	0	0	0	0	1	1
ENSG00000202182	ENSG00000202182	Y_RNA	14:64314978-64315080	NOTEST	0	0	0	0	1	1
ENSG00000202183	ENSG00000202183	SNORA4	X:81816649-81816796	NOTEST	0	0	0	0	1	1
ENSG00000202184	ENSG00000202184	RNU6-1283P	1:245912641-246670614	NOTEST	0	0	0	0	1	1
ENSG00000202186	ENSG00000202186	RNU6-497P	20:46113021-46113125	NOTEST	0	0	0	0	1	1
ENSG00000202187	ENSG00000202187	RNA5SP355	12:28286181-28732883	NOTEST	0	0	0	0	1	1
ENSG00000202188	ENSG00000202188	SNORD115-31	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000202189	ENSG00000202189	SNORA30	9:20658307-21031635	NOTEST	0	0	0	0	1	1
ENSG00000202190	ENSG00000202190	Y_RNA	10:61786055-62493248	NOTEST	0	0	0	0	1	1
ENSG00000202191	ENSG00000202191	SNORD113-1	14:101361106-101402336	NOTEST	0	0	0	0	1	1
ENSG00000202193	ENSG00000202193	RNA5SP427	16:53371364-53371483	NOTEST	0	0	0	0	1	1
ENSG00000202195	ENSG00000202195	Y_RNA	2:51259738-52635055	NOTEST	0	0	0	0	1	1
ENSG00000202199	ENSG00000202199	RNU1-115P	X:132372684-132372844	NOTEST	0	0	0	0	1	1
ENSG00000202200	ENSG00000202200	Y_RNA	6:129082861-129082953	NOTEST	0	0	0	0	1	1
ENSG00000202205	ENSG00000202205	RNU6-1034P	17:27679086-27878922	NOTEST	0	0	0	0	1	1
ENSG00000202206	ENSG00000202206	RNU6-169P	2:196313255-196380423	NOTEST	0	0	0	0	1	1
ENSG00000202211	ENSG00000202211	Y_RNA	15:43524792-43559055	NOTEST	0	0	0	0	1	1
ENSG00000202215	ENSG00000202215	RNU1-51P	4:190630692-190630868	NOTEST	0	0	0	0	1	1
ENSG00000202216	ENSG00000202216	SNORA43	2:180799127-180799265	NOTEST	0	0	0	0	1	1
ENSG00000202217	ENSG00000202217	RN7SKP47	9:77337410-77503010	NOTEST	0	0	0	0	1	1
ENSG00000202220	ENSG00000202220	Y_RNA	8:74884671-74895018	NOTEST	0	0	0	0	1	1
ENSG00000202222	ENSG00000202222	Y_RNA	1:40306722-40349183	NOTEST	0	0	0	0	1	1
ENSG00000202224	ENSG00000202224	Y_RNA	18:2621088-2621200	NOTEST	0	0	0	0	1	1
ENSG00000202225	ENSG00000202225	RNA5SP240	7:120621479-120621607	NOTEST	0	0	0	0	1	1
ENSG00000202227	ENSG00000202227	RNU6-282P	2:48667736-48742525	NOTEST	0	0	0	0	1	1
ENSG00000202229	ENSG00000202229	RNU6-1138P	14:23594503-23652883	NOTEST	0	0	0	0	1	1
ENSG00000202231	ENSG00000202231	SNORA9	X:100075383-100095921	NOTEST	0	0	0	0	1	1
ENSG00000202233	ENSG00000202233	U3	7:25304274-25304377	NOTEST	0	0	0	0	1	1
ENSG00000202237	ENSG00000202237	RNU6-53P	13:29274200-29293107	NOTEST	0	0	0	0	1	1
ENSG00000202239	ENSG00000202239	RNU6-396P	21:47878811-47989926	NOTEST	0	0	0	0	1	1
ENSG00000202240	ENSG00000202240	RNU6-737P	18:54951832-54951939	NOTEST	0	0	0	0	1	1
ENSG00000202241	ENSG00000202241	RN7SKP186	6:30832026-30832329	NOTEST	0	0	0	0	1	1
ENSG00000202242	ENSG00000202242	RNU6-1276P	8:27590834-27695612	NOTEST	0	0	0	0	1	1
ENSG00000202245	ENSG00000202245	RNU6-728P	10:124105204-124105308	NOTEST	0	0	0	0	1	1
ENSG00000202248	ENSG00000202248	RNA5SP85	2:11674241-11782914	NOTEST	0	0	0	0	1	1
ENSG00000202249	ENSG00000202249	RNU5E-5P	12:101860482-101860598	NOTEST	0	0	0	0	1	1
ENSG00000202250	ENSG00000202250	RNU6-443P	18:41412123-41412230	NOTEST	0	0	0	0	1	1
ENSG00000202251	ENSG00000202251	Y_RNA	17:7169373-7169485	NOTEST	0	0	0	0	1	1
ENSG00000202252	ENSG00000202252	SNORD14C	11:122928196-122933938	NOTEST	0	0	0	0	1	1
ENSG00000202254	ENSG00000202254	Y_RNA	1:100257217-100257309	NOTEST	0	0	0	0	1	1
ENSG00000202255	ENSG00000202255	Y_RNA	20:35280168-35374533	NOTEST	0	0	0	0	1	1
ENSG00000202257	ENSG00000202257	RNA5S16	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000202259	ENSG00000202259	RNU6-1318P	1:100433938-100492535	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000202260	ENSG00000202260	RN7SKP69	20:17550507-17590564	NOTEST	0	0	0	0	1	1
ENSG00000202261	ENSG00000202261	SNORD115-44	15:25496005-25496087	NOTEST	0	0	0	0	1	1
ENSG00000202263	ENSG00000202263	RNA5SP22	1:78444858-78604133	NOTEST	0	0	0	0	1	1
ENSG00000202264	ENSG00000202264	RNA5SP77	1:227748881-227749001	NOTEST	0	0	0	0	1	1
ENSG00000202265	ENSG00000202265	RNU6-596P	8:58202110-58202208	NOTEST	0	0	0	0	1	1
ENSG00000202268	ENSG00000202268	U3	3:45296901-45297112	NOTEST	0	0	0	0	1	1
ENSG00000202269	ENSG00000202269	U8	5:15110894-15111029	NOTEST	0	0	0	0	1	1
ENSG00000202270	ENSG00000202270	SNORD114-12	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000202272	ENSG00000202272	Y_RNA	X:23791108-23801073	NOTEST	0	0	0	0	1	1
ENSG00000202273	ENSG00000202273	Y_RNA	7:6201406-6312275	NOTEST	0	0	0	0	1	1
ENSG00000202275	ENSG00000202275	SNORD51	14:104200088-104313927	NOTEST	0	0	0	0	1	1
ENSG00000202276	ENSG00000202276	Y_RNA	11:8703957-8932498	NOTEST	0	0	0	0	1	1
ENSG00000202279	ENSG00000202279	Y_RNA	X:135898635-135898733	NOTEST	0	0	0	0	1	1
ENSG00000202281	ENSG00000202281	RNA5SP235	7:82383328-82792246	NOTEST	0	0	0	0	1	1
ENSG00000202283	ENSG00000202283	SNORA33	6:104031009-104031143	NOTEST	0	0	0	0	1	1
ENSG00000202285	ENSG00000202285	RNU6-117P	6:107165326-107235416	NOTEST	0	0	0	0	1	1
ENSG00000202290	ENSG00000202290	RNA5SP37	13:97873687-98046374	NOTEST	0	0	0	0	1	1
ENSG00000202293	ENSG00000202293	SNORD114-22	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000202296	ENSG00000202296	RNU6-1335P	7:56407923-56408030	NOTEST	0	0	0	0	1	1
ENSG00000202297	ENSG00000202297	Y_RNA	10:94050919-94113721	NOTEST	0	0	0	0	1	1
ENSG00000202300	ENSG00000202300	RNU6-487P	1:203288123-203288227	NOTEST	0	0	0	0	1	1
ENSG00000202304	ENSG00000202304	RNU6-1130P	X:129444045-129444152	NOTEST	0	0	0	0	1	1
ENSG00000202306	ENSG00000202306	Y_RNA	14:93799564-94174222	NOTEST	0	0	0	0	1	1
ENSG00000202308	ENSG00000202308	RNU6-996P	9:110425420-110425527	NOTEST	0	0	0	0	1	1
ENSG00000202309	ENSG00000202309	Y_RNA	2:39355966-39356068	NOTEST	0	0	0	0	1	1
ENSG00000202310	ENSG00000202310	Y_RNA	8:101170133-101348446	NOTEST	0	0	0	0	1	1
ENSG00000202313	ENSG00000202313	RNU1-64P	6:11487458-11516699	NOTEST	0	0	0	0	1	1
ENSG00000202314	ENSG00000202314	SNORD6	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000202317	ENSG00000202317	RNU1-84P	11:66160919-66161083	NOTEST	0	0	0	0	1	1
ENSG00000202318	ENSG00000202318	Y_RNA	12:6308880-6347425	NOTEST	0	0	0	0	1	1
ENSG00000202322	ENSG00000202322	RNA5SP131	3:50384760-50541675	NOTEST	0	0	0	0	1	1
ENSG00000202324	ENSG00000202324	RNA5SP366	12:99038918-100378432	NOTEST	0	0	0	0	1	1
ENSG00000202329	ENSG00000202329	RNU6-609P	1:199983816-199983923	NOTEST	0	0	0	0	1	1
ENSG00000202331	ENSG00000202331	RNA5SP167	4:150828711-150828827	NOTEST	0	0	0	0	1	1
ENSG00000202332	ENSG00000202332	Y_RNA	17:73428070-73428168	NOTEST	0	0	0	0	1	1
ENSG00000202334	ENSG00000202334	RNA5SP238	7:113726381-114333827	NOTEST	0	0	0	0	1	1
ENSG00000202335	ENSG00000202335	SNORD50	12:110928901-111021125	NOTEST	0	0	0	0	1	1
ENSG00000202336	ENSG00000202336	RNU6-359P	16:68021296-68272005	NOTEST	0	0	0	0	1	1
ENSG00000202337	ENSG00000202337	RNU6-8	14:32672368-32672475	NOTEST	0	0	0	0	1	1
ENSG00000202339	ENSG00000202339	RNU4-45P	21:23577510-23577651	NOTEST	0	0	0	0	1	1
ENSG00000202341	ENSG00000202341	RNU6-1051P	2:237923846-237923948	NOTEST	0	0	0	0	1	1
ENSG00000202343	ENSG00000202343	SNORA2	6:149915760-149915895	NOTEST	0	0	0	0	1	1
ENSG00000202344	ENSG00000202344	RN7SKP208	2:56178788-56179149	NOTEST	0	0	0	0	1	1
ENSG00000202345	ENSG00000202345	Y_RNA	5:168081517-168728133	NOTEST	0	0	0	0	1	1
ENSG00000202347	ENSG00000202347	RNU1-16P	13:114110133-114145267	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000202350	ENSG00000202350	RNU6-326P	7:45883232-45883339	NOTEST	0	0	0	0	1	1
ENSG00000202351	ENSG00000202351	RN7SKP204	6:13547935-13548245	NOTEST	0	0	0	0	1	1
ENSG00000202354	ENSG00000202354	RNY3	7:148680846-148680948	NOTEST	0	0	0	0	1	1
ENSG00000202356	ENSG00000202356	RNA5SP277	8:120879658-121063152	NOTEST	0	0	0	0	1	1
ENSG00000202357	ENSG00000202357	Y_RNA	19:11488235-11530018	NOTEST	0	0	0	0	1	1
ENSG00000202358	ENSG00000202358	RNU6-652P	4:56719781-56771200	NOTEST	0	0	0	0	1	1
ENSG00000202360	ENSG00000202360	RN7SKP249	8:102150186-102150541	NOTEST	0	0	0	0	1	1
ENSG00000202361	ENSG00000202361	Y_RNA	17:59942730-60005377	NOTEST	0	0	0	0	1	1
ENSG00000202363	ENSG00000202363	SNORA62	3:39448179-39454033	NOTEST	0	0	0	0	1	1
ENSG00000202368	ENSG00000202368	Y_RNA	12:97373305-97373407	NOTEST	0	0	0	0	1	1
ENSG00000202373	ENSG00000202373	SNORD115-43	15:25494344-25494426	NOTEST	0	0	0	0	1	1
ENSG00000202374	ENSG00000202374	SNORA62	4:68566997-68995598	NOTEST	0	0	0	0	1	1
ENSG00000202377	ENSG00000202377	SNORA25	7:115221368-115221496	NOTEST	0	0	0	0	1	1
ENSG00000202379	ENSG00000202379	SNORA70	3:108268715-108308491	NOTEST	0	0	0	0	1	1
ENSG00000202380	ENSG00000202380	RNU1-55P	20:5870700-5870858	NOTEST	0	0	0	0	1	1
ENSG00000202382	ENSG00000202382	Y_RNA	2:85569210-85618875	NOTEST	0	0	0	0	1	1
ENSG00000202383	ENSG00000202383	RNA5SP279	9:1333836-1333953	NOTEST	0	0	0	0	1	1
ENSG00000202385	ENSG00000202385	Y_RNA	1:89472348-89488577	NOTEST	0	0	0	0	1	1
ENSG00000202386	ENSG00000202386	RNA5SP211	6:106897255-106897372	NOTEST	0	0	0	0	1	1
ENSG00000202388	ENSG00000202388	Y_RNA	3:121744041-121744151	NOTEST	0	0	0	0	1	1
ENSG00000202389	ENSG00000202389	SNORA70	17:26349355-26349490	NOTEST	0	0	0	0	1	1
ENSG00000202392	ENSG00000202392	RN7SKP292	4:6910968-7059679	NOTEST	0	0	0	0	1	1
ENSG00000202395	ENSG00000202395	RN7SKP1	13:37740488-37740795	NOTEST	0	0	0	0	1	1
ENSG00000202398	ENSG00000202398	RNU6-61P	13:80943560-80943669	NOTEST	0	0	0	0	1	1
ENSG00000202399	ENSG00000202399	Y_RNA	8:98784540-98784653	NOTEST	0	0	0	0	1	1
ENSG00000202400	ENSG00000202400	SNORD82	2:232318241-232348352	NOTEST	0	0	0	0	1	1
ENSG00000202402	ENSG00000202402	Y_RNA	14:31713966-31714067	NOTEST	0	0	0	0	1	1
ENSG00000202406	ENSG00000202406	RN7SKP187	7:111846642-112049678	NOTEST	0	0	0	0	1	1
ENSG00000202407	ENSG00000202407	Y_RNA	X:105669797-105669899	NOTEST	0	0	0	0	1	1
ENSG00000202408	ENSG00000202408	RNU1-122P	1:147801123-147816764	NOTEST	0	0	0	0	1	1
ENSG00000202410	ENSG00000202410	Y_RNA	X:93433003-93433105	NOTEST	0	0	0	0	1	1
ENSG00000202411	ENSG00000202411	RNA5SP259	8:28351728-28431775	NOTEST	0	0	0	0	1	1
ENSG00000202412	ENSG00000202412	Y_RNA	3:129366634-129612419	NOTEST	0	0	0	0	1	1
ENSG00000202414	ENSG00000202414	Y_RNA	20:25176328-25207370	NOTEST	0	0	0	0	1	1
ENSG00000202417	ENSG00000202417	Y_RNA	5:132211070-132299326	NOTEST	0	0	0	0	1	1
ENSG00000202422	ENSG00000202422	RNA5SP30	13:58565483-58565598	NOTEST	0	0	0	0	1	1
ENSG00000202423	ENSG00000202423	RNU6-827P	2:79109572-79109678	NOTEST	0	0	0	0	1	1
ENSG00000202427	ENSG00000202427	RNU6-744P	2:114435278-114461655	NOTEST	0	0	0	0	1	1
ENSG00000202428	ENSG00000202428	RNU6-108P	3:57327726-57530071	NOTEST	0	0	0	0	1	1
ENSG00000202429	ENSG00000202429	RNU4-48P	2:128193782-128284462	NOTEST	0	0	0	0	1	1
ENSG00000202430	ENSG00000202430	RNA5SP88	2:24714782-24993571	NOTEST	0	0	0	0	1	1
ENSG00000202431	ENSG00000202431	RNU6-438P	7:34337107-34337210	NOTEST	0	0	0	0	1	1
ENSG00000202433	ENSG00000202433	RNU6-54P	13:71033595-71033702	NOTEST	0	0	0	0	1	1
ENSG00000202434	ENSG00000202434	SNORA4	2:198254507-198299815	NOTEST	0	0	0	0	1	1
ENSG00000202438	ENSG00000202438	Y_RNA	6:130895140-130895257	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000202440	ENSG00000202440	SNORD42	4:83323790-83323859	NOTEST	0	0	0	0	1	1
ENSG00000202441	ENSG00000202441	RNY4P10	6:33161364-33172216	NOTEST	0	0	0	0	1	1
ENSG00000202444	ENSG00000202444	RNU5E-6P	1:45285515-45308735	NOTEST	0	0	0	0	1	1
ENSG00000202445	ENSG00000202445	RNU6-669P	9:97258556-97275161	NOTEST	0	0	0	0	1	1
ENSG00000202449	ENSG00000202449	SNORA63	4:14472088-14889793	NOTEST	0	0	0	0	1	1
ENSG00000202459	ENSG00000202459	Y_RNA	14:103058997-103196913	NOTEST	0	0	0	0	1	1
ENSG00000202461	ENSG00000202461	Y_RNA	1:12079522-12092102	NOTEST	0	0	0	0	1	1
ENSG00000202468	ENSG00000202468	RNU4-17P	18:57830799-57830940	NOTEST	0	0	0	0	1	1
ENSG00000202469	ENSG00000202469	Y_RNA	X:9983601-10112518	NOTEST	0	0	0	0	1	1
ENSG00000202470	ENSG00000202470	Y_RNA	12:95611521-95696566	NOTEST	0	0	0	0	1	1
ENSG00000202471	ENSG00000202471	RNU4-20P	12:59980573-59980724	NOTEST	0	0	0	0	1	1
ENSG00000202472	ENSG00000202472	RNA5SP248	7:139993492-140126050	NOTEST	0	0	0	0	1	1
ENSG00000202473	ENSG00000202473	RN7SKP81	X:142178132-142178463	NOTEST	0	0	0	0	1	1
ENSG00000202474	ENSG00000202474	RNA5SP283	9:66457284-66469310	NOTEST	0	0	0	0	1	1
ENSG00000202476	ENSG00000202476	Y_RNA	16:30465317-30465418	NOTEST	0	0	0	0	1	1
ENSG00000202478	ENSG00000202478	RNU6-81P	13:64357933-64358037	NOTEST	0	0	0	0	1	1
ENSG00000202479	ENSG00000202479	SNORD14	2:25166504-25262563	NOTEST	0	0	0	0	1	1
ENSG00000202482	ENSG00000202482	U3	X:71945975-71946190	NOTEST	0	0	0	0	1	1
ENSG00000202485	ENSG00000202485	RNU6-499P	4:83095699-83095806	NOTEST	0	0	0	0	1	1
ENSG00000202487	ENSG00000202487	Y_RNA	10:128593977-129250781	NOTEST	0	0	0	0	1	1
ENSG00000202490	ENSG00000202490	RNU6-597P	14:64063756-64108579	NOTEST	0	0	0	0	1	1
ENSG00000202491	ENSG00000202491	RNU6-716P	1:199977632-199977735	NOTEST	0	0	0	0	1	1
ENSG00000202495	ENSG00000202495	Y_RNA	X:49935840-49935941	NOTEST	0	0	0	0	1	1
ENSG00000202496	ENSG00000202496	RNVU1-20	1:149575344-149637707	NOTEST	0	0	0	0	1	1
ENSG00000202497	ENSG00000202497	RNU6-898P	16:68877506-69119083	NOTEST	0	0	0	0	1	1
ENSG00000202498	ENSG00000202498	SNORD116	1:215796235-216596738	NOTEST	0	0	0	0	1	1
ENSG00000202499	ENSG00000202499	SNORD115-36	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000202502	ENSG00000202502	RNA5SP151	3:182895830-183146566	NOTEST	0	0	0	0	1	1
ENSG00000202503	ENSG00000202503	SNORD34	19:49949554-49995565	NOTEST	0	0	0	0	1	1
ENSG00000202508	ENSG00000202508	Y_RNA	10:13480483-13572262	NOTEST	0	0	0	0	1	1
ENSG00000202512	ENSG00000202512	RN7SKP230	5:109025066-109205326	NOTEST	0	0	0	0	1	1
ENSG00000202513	ENSG00000202513	RNU6-805P	10:74127097-74385899	NOTEST	0	0	0	0	1	1
ENSG00000202514	ENSG00000202514	Y_RNA	8:42704779-42940931	NOTEST	0	0	0	0	1	1
ENSG00000202515	ENSG00000202515	VTRNA1-3	5:140105742-140105831	NOTEST	0	0	0	0	1	1
ENSG00000202517	ENSG00000202517	SNORA64	3:39850404-40301812	NOTEST	0	0	0	0	1	1
ENSG00000202521	ENSG00000202521	RNA5S7	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000202522	ENSG00000202522	Y_RNA	11:72396113-72504726	NOTEST	0	21.29	inf	0	1	1
ENSG00000202523	ENSG00000202523	Y_RNA	9:86595625-86618985	NOTEST	0	0	0	0	1	1
ENSG00000202526	ENSG00000202526	RNA5S13	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000202528	ENSG00000202528	RNU6-650P	7:148730148-148730259	NOTEST	0	0	0	0	1	1
ENSG00000202529	ENSG00000202529	SNORD18B	15:66790354-66858317	NOTEST	0	0	0	0	1	1
ENSG00000202532	ENSG00000202532	RNU6-395P	2:128601126-128603261	NOTEST	0	0	0	0	1	1
ENSG00000202533	ENSG00000202533	Y_RNA	5:131746327-131811736	NOTEST	0	0	0	0	1	1
ENSG00000202534	ENSG00000202534	RNU6-1329P	12:93346414-93346521	NOTEST	0	0	0	0	1	1
ENSG00000202536	ENSG00000202536	Y_RNA	4:113676972-113677073	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000202537	ENSG00000202537	U8	2:86574184-86574318	NOTEST	0	0	0	0	1	1
ENSG00000202542	ENSG00000202542	Y_RNA	15:48604549-48635570	NOTEST	0	0	0	0	1	1
ENSG00000202560	ENSG00000202560	MIR539	14:101511493-101518132	NOTEST	0	0	0	0	1	1
ENSG00000202566	ENSG00000202566	MIR421	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000202569	ENSG00000202569	MIR146B	10:104196268-104196341	NOTEST	0	0	0	0	1	1
ENSG00000202601	ENSG00000202601	MIR582	5:58264864-59843484	NOTEST	0	0	0	0	1	1
ENSG00000202609	ENSG00000202609	MIR488	1:176826437-177134109	NOTEST	0	0	0	0	1	1
ENSG00000203257	ENSG00000203257	AL691479.1	1:230451437-230451976	NOTEST	0	0	0	0	1	1
ENSG00000203258	ENSG00000203258	RP11-47J17.2	11:12695968-12966298	NOTEST	0	0	0	0	1	1
ENSG00000203260	ENSG00000203260	AL356475.1	1:169890466-170054349	NOTEST	0	0	0	0	1	1
ENSG00000203262	ENSG00000203262	RP5-961K14.2	X:95325667-95326777	NOTEST	0	0	0	0	1	1
ENSG00000203266	ENSG00000203266	RP11-560A15.3	20:55689970-55697148	NOTEST	0	0	0	0	1	1
ENSG00000203268	ENSG00000203268	AL445199.1	10:134884432-134945179	NOTEST	0	0	0	0	1	1
ENSG00000203276	ENSG00000203276	AL353898.2	1:54497346-54519177	NOTEST	0.0705395	0.0709808	0.00899675	0	1	1
ENSG00000203279	ENSG00000203279	RP11-498P14.5	9:99918851-100140806	NOTEST	0.432084	0.279146	-0.63029	0	1	1
ENSG00000203280	ENSG00000203280	CTA-221G9.11	22:25348696-25593415	NOTEST	0.0190666	0.0148273	-0.362793	0	1	1
ENSG00000203281	ENSG00000203281	AL590489.1	6:107473760-107780768	NOTEST	0	0	0	0	1	1
ENSG00000203284	ENSG00000203284	AL591516.1	6:107473760-107780768	NOTEST	0	0	0	0	1	1
ENSG00000203285	ENSG00000203285	AL591516.2	6:107473760-107780768	NOTEST	0	0	0	0	1	1
ENSG00000203286	ENSG00000203286	AL365202.1	9:3218296-3526004	NOTEST	0	0	0	0	1	1
ENSG00000203301	ENSG00000203301	AL590822.1	1:1981908-2152177	NOTEST	0.0645413	0.085316	0.402594	0	1	1
ENSG00000203305	ENSG00000203305	AC010525.1	19:56186591-56249768	NOTEST	0.132682	0.0578133	-1.1985	0	1	1
ENSG00000203307	ENSG00000203307	RP11-375H19.2	1:166026673-166136206	NOTEST	0	0.0273427	inf	0	1	1
ENSG00000203314	ENSG00000203314	AC015815.1	17:75082797-75213179	NOTEST	0	0	0	0	1	1
ENSG00000203315	ENSG00000203315	AC015815.2	17:75082797-75213179	NOTEST	0	0	0	0	1	1
ENSG00000203316	ENSG00000203316	AC015815.3	17:75082797-75213179	NOTEST	0	0	0	0	1	1
ENSG00000203317	ENSG00000203317	AC015815.4	17:75077628-75077716	NOTEST	0	0	0	0	1	1
ENSG00000203318	ENSG00000203318	AC015815.5	17:75076717-75076850	NOTEST	0	0	0	0	1	1
ENSG00000203321	ENSG00000203321	RP11-197P3.4	9:77567883-77643339	NOTEST	0	0.126815	inf	0	1	1
ENSG00000203325	ENSG00000203325	RP11-277A4.4	1:32479429-32568467	NOTEST	0	0	0	0	1	1
ENSG00000203327	ENSG00000203327	AC012358.7	2:55401926-55462989	NOTEST	0.0599799	0.137596	1.19788	0	1	1
ENSG00000203334	ENSG00000203334	AP003027.1	11:108828444-108830523	NOTEST	0	0	0	0	1	1
ENSG00000203335	ENSG00000203335	AC006019.3	7:153584181-154685995	NOTEST	0	0	0	0	1	1
ENSG00000203343	ENSG00000203343	AC009107.1	16:58265060-58328951	NOTEST	0	0.0169586	inf	0	1	1
ENSG00000203344	ENSG00000203344	AC018696.2	2:91693218-91693945	NOTEST	0	0	0	0	1	1
ENSG00000203346	ENSG00000203346	AL162458.1	20:44637546-44688784	NOTEST	0	0	0	0	1	1
ENSG00000203356	ENSG00000203356	RP11-296A18.3	1:51660766-51700768	NOTEST	0	0	0	0	1	1
ENSG00000203362	ENSG00000203362	RP3-337H4.8	6:43543886-43596899	NOTEST	0.609382	0.383634	-0.667615	0	1	1
ENSG00000203363	ENSG00000203363	AC012454.4	2:85912297-85925977	NOTEST	0	0	0	0	1	1
ENSG00000203364	ENSG00000203364	RP11-370F5.4	9:95909321-95910838	NOTEST	0	0	0	0	1	1
ENSG00000203372	ENSG00000203372	RP11-101E5.1	9:65467782-65469026	NOTEST	0	0	0	0	1	1
ENSG00000203377	ENSG00000203377	AC131568.1	8:131064352-131455906	NOTEST	0	0	0	0	1	1
ENSG00000203384	ENSG00000203384	AL591516.3	6:107473760-107780768	NOTEST	0	0	0	0	1	1
ENSG00000203387	ENSG00000203387	AC074019.2	2:229216835-229217931	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000203392	ENSG00000203392	AC105020.1	15:75966662-76005189	NOTEST	0.0766567	0.161822	1.07793	0	1	1
ENSG00000203394	ENSG00000203394	RP5-930J4.4	1:21069153-21113816	NOTEST	0	0	0	0	1	1
ENSG00000203395	ENSG00000203395	AC015969.3	2:68588345-68624585	NOTEST	0	0	0	0	1	1
ENSG00000203396	ENSG00000203396	RP11-217O12.1	9:107090600-107091677	NOTEST	0	0	0	0	1	1
ENSG00000203397	ENSG00000203397	RP13-36G14.3	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000203400	ENSG00000203400	AP001187.1	11:64657297-64657758	NOTEST	0	0	0	0	1	1
ENSG00000203401	ENSG00000203401	AC009061.1	16:67464554-67471456	NOTEST	0.100273	0.158176	0.657602	0	1	1
ENSG00000203402	ENSG00000203402	RP11-571E6.3	X:47157250-47158120	NOTEST	0	0	0	0	1	1
ENSG00000203403	ENSG00000203403	AC020907.2	19:35615416-35645204	NOTEST	0.0236587	0.0386045	0.706398	0	1	1
ENSG00000203408	ENSG00000203408	OR6C71P	12:55770581-55771520	NOTEST	0	0	0	0	1	1
ENSG00000203411	ENSG00000203411	AC090519.2	15:44571084-44571275	NOTEST	0	0	0	0	1	1
ENSG00000203413	ENSG00000203413	ACTBP6	8:85860819-85861909	NOTEST	0	0	0	0	1	1
ENSG00000203414	ENSG00000203414	BTBD7P1	10:13198683-13200136	NOTEST	0	0	0	0	1	1
ENSG00000203415	ENSG00000203415	AC016734.1	2:63348517-64054977	NOTEST	0	0	0	0	1	1
ENSG00000203416	ENSG00000203416	FAM32B	22:17660193-17702879	NOTEST	0	0	0	0	1	1
ENSG00000203418	ENSG00000203418	AC131571.1	11:31531296-31805546	NOTEST	0	0	0	0	1	1
ENSG00000203421	ENSG00000203421	AC140061.2	12:50711461-50711558	NOTEST	0	0	0	0	1	1
ENSG00000203422	ENSG00000203422	AC140061.3	12:50710652-50710749	NOTEST	0	0	0	0	1	1
ENSG00000203423	ENSG00000203423	AC140061.4	12:50710005-50710100	NOTEST	0	0	0	0	1	1
ENSG00000203424	ENSG00000203424	AC140061.5	12:50707797-50707894	NOTEST	0	0	0	0	1	1
ENSG00000203425	ENSG00000203425	AC140061.6	12:50706429-50706526	NOTEST	0	0	0	0	1	1
ENSG00000203426	ENSG00000203426	AC140061.7	12:50698424-50698530	NOTEST	0	0	0	0	1	1
ENSG00000203427	ENSG00000203427	AC140061.8	12:50697569-50697669	NOTEST	0	0	0	0	1	1
ENSG00000203428	ENSG00000203428	AC140061.9	12:50695576-50695673	NOTEST	0	0	0	0	1	1
ENSG00000203430	ENSG00000203430	AC140061.10	12:50688916-50689013	NOTEST	0	0	0	0	1	1
ENSG00000203431	ENSG00000203431	AC140061.11	12:50684743-50684840	NOTEST	0	0	0	0	1	1
ENSG00000203432	ENSG00000203432	AC008147.1	12:50683976-50684073	NOTEST	0	0	0	0	1	1
ENSG00000203433	ENSG00000203433	AC008147.2	12:50678448-50678545	NOTEST	0	0	0	0	1	1
ENSG00000203434	ENSG00000203434	RP11-163F15.1	10:110307732-110321573	NOTEST	0	0	0	0	1	1
ENSG00000203435	ENSG00000203435	AC104600.1	2:196602426-196933536	NOTEST	0.0118719	0.0378555	1.67295	0	1	1
ENSG00000203436	ENSG00000203436	AC109925.1	4:95371801-95372043	NOTEST	0	0	0	0	1	1
ENSG00000203437	ENSG00000203437	RP11-820K3.3	12:31535156-31768600	NOTEST	0	0.0189435	inf	0	1	1
ENSG00000203438	ENSG00000203438	AL512625.1	9:66473374-66473673	NOTEST	0	0	0	0	1	1
ENSG00000203441	ENSG00000203441	LINC00449	13:100151980-100153306	NOTEST	0.0211886	0.03296	0.637433	0	1	1
ENSG00000203442	ENSG00000203442	AC008555.1	19:35328792-35351480	NOTEST	0	0	0	0	1	1
ENSG00000203443	ENSG00000203443	AC092964.1	3:171757417-172119455	NOTEST	0	0.273115	inf	0	1	1
ENSG00000203457	ENSG00000203457	AC068896.1	10:126490353-126525239	NOTEST	0	0	0	0	1	1
ENSG00000203462	ENSG00000203462	RP11-814E24.1	7:56390496-56391294	NOTEST	0	0	0	0	1	1
ENSG00000203463	ENSG00000203463	SLC44A4	HSCHR6_MHC_MANN:31870630-31870874	NOTEST	0	0	0	0	1	1
ENSG00000203465	ENSG00000203465	AC061975.2	17:26603011-26644809	NOTEST	0	0	0	0	1	1
ENSG00000203469	ENSG00000203469	RP5-1113E3.3	1:10516578-10690815	NOTEST	0	0	0	0	1	1
ENSG00000203471	ENSG00000203471	AL359697.1	10:22045465-22292698	NOTEST	0	0	0	0	1	1
ENSG00000203473	ENSG00000203473	AC105036.1	15:75759461-75918810	NOTEST	0	0	0	0	1	1
ENSG00000203477	ENSG00000203477	AC061975.3	17:26603011-26644809	NOTEST	0	0	0	0	1	1
ENSG00000203478	ENSG00000203478	AC061975.4	17:26603011-26644809	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000203479	ENSG00000203479	AC061975.5	17:26581510-26581655	NOTEST	0	0	0	0	1	1
ENSG00000203480	ENSG00000203480	AC061975.6	17:26568404-26568558	NOTEST	0	0	0	0	1	1
ENSG00000203482	ENSG00000203482	AC061975.7	17:26547061-26547215	NOTEST	0	0	0	0	1	1
ENSG00000203483	ENSG00000203483	AC100852.1	17:26368762-26523407	NOTEST	0	0	0	0	1	1
ENSG00000203484	ENSG00000203484	AC100852.2	17:26368762-26523407	NOTEST	0	0	0	0	1	1
ENSG00000203489	ENSG00000203489	HMGB1P39	6:75994729-76203454	NOTEST	0	0	0	0	1	1
ENSG00000203492	ENSG00000203492	OR2N1P	6:29105656-29106593	NOTEST	0	0	0	0	1	1
ENSG00000203496	ENSG00000203496	RP11-291L22.4	10:38741914-38755104	NOTEST	0	0.0590193	inf	0	1	1
ENSG00000203498	ENSG00000203498	RP11-556O15.1	6:6993423-6995787	NOTEST	0	0	0	0	1	1
ENSG00000203499	ENSG00000203499	FAM83H-AS1	8:144816309-144828507	NOTEST	0.186028	0.385587	1.05154	0	1	1
ENSG00000203504	ENSG00000203504	AC131571.2	11:31531296-31805546	NOTEST	0	0	0	0	1	1
ENSG00000203505	ENSG00000203505	AC003079.1	7:95107755-95169544	NOTEST	0	0	0	0	1	1
ENSG00000203506	ENSG00000203506	RBMS3-AS2	3:29305684-30051886	NOTEST	0	0	0	0	1	1
ENSG00000203507	ENSG00000203507	AC103801.1	11:22644078-22834601	NOTEST	0	0	0	0	1	1
ENSG00000203511	ENSG00000203511	AL353662.1	9:34179002-34329198	NOTEST	0	0	0	0	1	1
ENSG00000203512	ENSG00000203512	AL353662.2	9:34179002-34329198	NOTEST	0	0	0	0	1	1
ENSG00000203513	ENSG00000203513	AL353662.3	9:34169686-34169934	NOTEST	0	0	0	0	1	1
ENSG00000203518	ENSG00000203518	AL023807.1	6:17759413-17987854	NOTEST	0	0	0	0	1	1
ENSG00000203520	ENSG00000203520	RP11-697H9.3	11:63340666-63389143	NOTEST	0	0	0	0	1	1
ENSG00000203523	ENSG00000203523	TAS2R2P	7:12530720-12531630	NOTEST	0.0803952	0.0425162	-0.919095	0	1	1
ENSG00000203527	ENSG00000203527	Z99756.1	22:43593288-43739394	NOTEST	0	0	0	0	1	1
ENSG00000203531	ENSG00000203531	AC016712.1	2:223536504-223574649	NOTEST	0	0	0	0	1	1
ENSG00000203542	ENSG00000203542	AL353671.1	9:32540541-32573160	NOTEST	0	0	0	0	1	1
ENSG00000203543	ENSG00000203543	AL353671.2	9:32540541-32573160	NOTEST	0	0	0	0	1	1
ENSG00000203544	ENSG00000203544	BX248133.1	HSCHR6_MHC_SSTO:31735248-31822599	NOTEST	0	0	0	0	1	1
ENSG00000203547	ENSG00000203547	AL135901.1	13:50234858-50265611	NOTEST	0	0	0	0	1	1
ENSG00000203560	ENSG00000203560	OR52J1P	11:5125382-5126314	NOTEST	0	0	0	0	1	1
ENSG00000203562	ENSG00000203562	AC004771.1	17:4871286-4890972	NOTEST	0.227257	0.469338	1.0463	0	1	1
ENSG00000203563	ENSG00000203563	AC138951.1	5:21341941-21589481	NOTEST	0.140977	0	#NAME?	0	1	1
ENSG00000203565	ENSG00000203565	RP13-259N13.2	10:33973682-33975992	NOTEST	0	0	0	0	1	1
ENSG00000203572	ENSG00000203572	AC090519.3	15:44580926-44719342	NOTEST	0	0	0	0	1	1
ENSG00000203573	ENSG00000203573	AC090519.4	15:44580926-44719342	NOTEST	0	0	0	0	1	1
ENSG00000203574	ENSG00000203574	AC090519.5	15:44580926-44719342	NOTEST	0	0	0	0	1	1
ENSG00000203575	ENSG00000203575	AC090519.6	15:44580926-44719342	NOTEST	0	0	0	0	1	1
ENSG00000203576	ENSG00000203576	AC090519.7	15:44575956-44576117	NOTEST	0	0	0	0	1	1
ENSG00000203578	ENSG00000203578	AC073940.1	15:44564039-44564218	NOTEST	0	0	0	0	1	1
ENSG00000203581	ENSG00000203581	OR1F2P	16:3238211-3286221	NOTEST	0	0.0732741	inf	0	1	1
ENSG00000203583	ENSG00000203583	AL021707.1	22:39101727-39190203	NOTEST	0.332002	0	#NAME?	0	1	1
ENSG00000203585	ENSG00000203585	RP11-542B15.1	12:67913608-67960906	NOTEST	0	0.00654493	inf	0	1	1
ENSG00000203588	ENSG00000203588	IGBP1-AS1	X:69353298-69386174	NOTEST	0.0800792	0.0623741	-0.360482	0	1	1
ENSG00000203589	ENSG00000203589	RP5-886K2.1	1:24032290-24033424	NOTEST	0	0.0339486	inf	0	1	1
ENSG00000203593	ENSG00000203593	RP5-1096D14.6	12:2055219-2802108	NOTEST	0	0	0	0	1	1
ENSG00000203594	ENSG00000203594	AC116351.1	5:987294-997423	NOTEST	0	0	0	0	1	1
ENSG00000203601	ENSG00000203601	LINC00970	1:168873142-169056243	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000203602	ENSG00000203602	AL137059.1	13:27998680-28024739	NOTEST	0.482437	0.566365	0.23139	0	1	1
ENSG00000203605	ENSG00000203605	RP11-335E6.2	1:63604920-63628824	NOTEST	0	0	0	0	1	1
ENSG00000203606	ENSG00000203606	AC004832.1	22:30831530-30832234	NOTEST	0	0.0109882	inf	0	1	1
ENSG00000203614	ENSG00000203614	AL512652.1	13:21276265-21297237	NOTEST	0.0270439	0.091937	1.76535	0	1	1
ENSG00000203615	ENSG00000203615	AC069200.1	4:56262123-56414056	NOTEST	0	0	0	0	1	1
ENSG00000203616	ENSG00000203616	RHOT1P2	21:15281894-15352758	NOTEST	0	0	0	0	1	1
ENSG00000203618	ENSG00000203618	GP1BB	22:19701986-19712295	NOTEST	0.00401931	0.158114	5.29787	0	1	1
ENSG00000203620	ENSG00000203620	RP11-84A19.2	1:32307619-32410457	NOTEST	0.00713243	0.00553157	-0.366706	0	1	1
ENSG00000203623	ENSG00000203623	C6orf47	HSCHR6_MHC_QBL:31616314-31618789	NOTEST	0	0	0	0	1	1
ENSG00000203624	ENSG00000203624	MRPS18B	HSCHR6_MHC_QBL:30557687-30583682	NOTEST	0	0	0	0	1	1
ENSG00000203630	ENSG00000203630	AL136531.1	20:1290618-1373806	NOTEST	0.0385427	0.009035	-2.09286	0	1	1
ENSG00000203632	ENSG00000203632	AC007690.1	3:186648273-186796341	NOTEST	0.415047	0.280833	-0.563564	0	1	1
ENSG00000203635	ENSG00000203635	AC144450.2	2:1624281-1629191	NOTEST	0	0	0	0	1	1
ENSG00000203643	ENSG00000203643	AC012456.3	2:11817720-11967535	NOTEST	0	0	0	0	1	1
ENSG00000203645	ENSG00000203645	LINC00501	3:177012229-177041206	NOTEST	0	0	0	0	1	1
ENSG00000203647	ENSG00000203647	AC106827.1	3:65339199-66024509	NOTEST	0	0	0	0	1	1
ENSG00000203648	ENSG00000203648	AC007618.3	12:2055219-2802108	NOTEST	0	0	0	0	1	1
ENSG00000203650	ENSG00000203650	RP4-562J12.2	X:117973518-118015978	NOTEST	0.0928304	0.171203	0.883037	0	1	1
ENSG00000203652	ENSG00000203652	AC099048.1	3:29305684-30051886	NOTEST	0	0	0	0	1	1
ENSG00000203659	ENSG00000203659	AL353671.3	9:32540541-32573160	NOTEST	0	0	0	0	1	1
ENSG00000203661	ENSG00000203661	OR2T5	1:248651884-248652898	NOTEST	0	0	0	0	1	1
ENSG00000203663	ENSG00000203663	OR2L2	1:248099362-248264224	NOTEST	0	0.0119905	inf	0	1	1
ENSG00000203664	ENSG00000203664	OR2W5	1:247654369-247655710	NOTEST	0	0	0	0	1	1
ENSG00000203684	ENSG00000203684	IBA57-AS1	1:228351786-228353213	NOTEST	0	0.0384485	inf	0	1	1
ENSG00000203685	ENSG00000203685	C1orf95	1:226736500-226796915	NOTEST	0.00710626	0.113258	3.99438	0	1	1
ENSG00000203688	ENSG00000203688	RP11-351J23.1	6:168080305-168084467	NOTEST	0.0174819	0.0552713	1.66067	0	1	1
ENSG00000203690	ENSG00000203690	TCP10	6:167738573-167797998	NOTEST	0	0	0	0	1	1
ENSG00000203691	ENSG00000203691	AC092811.1	1:225589203-225616627	NOTEST	0.394643	0.176878	-1.1578	0	1	1
ENSG00000203697	ENSG00000203697	CAPN8	1:223711348-223853436	NOTEST	0	0.0844562	inf	0	1	1
ENSG00000203709	ENSG00000203709	C1orf132	1:207974862-208042495	NOTEST	0.0573382	0.0741289	0.370538	0	1	1
ENSG00000203710	ENSG00000203710	CR1	1:207669491-207813992	NOTEST	0.00451524	0.0147775	1.71052	0	1	1
ENSG00000203711	ENSG00000203711	C6orf99	6:159290970-159331385	NOTEST	0.0713038	0.180872	1.34291	0	1	1
ENSG00000203721	ENSG00000203721	LINC00862	1:200311671-200343482	NOTEST	0.135712	0.180394	0.410596	0	1	1
ENSG00000203722	ENSG00000203722	RAET1G	6:150139933-150244257	NOTEST	0.0202633	0.0804157	1.9886	0	1	1
ENSG00000203729	ENSG00000203729	LINC00272	1:182376755-182383950	NOTEST	0	0	0	0	1	1
ENSG00000203730	ENSG00000203730	TEDDM1	1:182367251-182369751	NOTEST	0	0	0	0	1	1
ENSG00000203733	ENSG00000203733	GJE1	6:142454226-142456288	NOTEST	0	0	0	0	1	1
ENSG00000203734	ENSG00000203734	ECT2L	6:139117062-139309398	NOTEST	0.0353106	0.0224751	-0.651776	0	1	1
ENSG00000203737	ENSG00000203737	GPR52	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000203740	ENSG00000203740	METTL11B	1:170115141-170136931	NOTEST	0.138404	0.062905	-1.13764	0	1	1
ENSG00000203747	ENSG00000203747	FCGR3A	1:161475219-161648444	NOTEST	0	0	0	0	1	1
ENSG00000203756	ENSG00000203756	TMEM244	6:130152388-130182692	NOTEST	0	0	0	0	1	1
ENSG00000203757	ENSG00000203757	OR6K3	1:158686957-158687953	NOTEST	0	0	0	0	1	1
ENSG00000203758	ENSG00000203758	OR10T1P	1:158414857-158415804	NOTEST	0	0	0	0	1	1
ENSG00000203781	ENSG00000203781	AL591704.9	1:153399495-153400877	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000203782	ENSG00000203782	LOR	1:153232175-153234598	NOTEST	0	0	0	0	1	1
ENSG00000203783	ENSG00000203783	PRR9	1:153190059-153191793	NOTEST	0	0.00988094	inf	0	1	1
ENSG00000203784	ENSG00000203784	LELP1	1:153175918-153177596	NOTEST	0	0	0	0	1	1
ENSG00000203785	ENSG00000203785	SPRR2E	1:153042699-153113927	NOTEST	0	0	0	0	1	1
ENSG00000203786	ENSG00000203786	KPRP	1:152730505-152734529	NOTEST	0	0	0	0	1	1
ENSG00000203795	ENSG00000203795	FAM24A	10:124670216-124672627	NOTEST	0	0	0	0	1	1
ENSG00000203797	ENSG00000203797	DDO	6:110712973-110736765	NOTEST	0	0.0241566	inf	0	1	1
ENSG00000203799	ENSG00000203799	CCDC162P	6:109612230-109676266	NOTEST	0	0	0	0	1	1
ENSG00000203801	ENSG00000203801	LINC00222	6:109072856-109091145	NOTEST	0	0	0	0	1	1
ENSG00000203804	ENSG00000203804	ADAMTSL4-AS1	1:150533479-150533969	NOTEST	0.179995	0	#NAME?	0	1	1
ENSG00000203809	ENSG00000203809	LINC00577	6:105384168-105388402	NOTEST	0	0	0	0	1	1
ENSG00000203811	ENSG00000203811	HIST2H3C	1:149804220-149812765	NOTEST	0	0	0	0	1	1
ENSG00000203812	ENSG00000203812	HIST2H2AA4	1:149822642-149823191	NOTEST	0	0	0	0	1	1
ENSG00000203818	ENSG00000203818	HIST2H3PS2	1:149369293-149429348	NOTEST	0.0592679	0.197058	1.73329	0	1	1
ENSG00000203819	ENSG00000203819	HIST2H2BC	1:149821759-149822339	NOTEST	0.383303	0.300197	-0.352576	0	1	1
ENSG00000203825	ENSG00000203825	RP11-744H18.1	1:149036434-149067496	NOTEST	0	0	0	0	1	1
ENSG00000203835	ENSG00000203835	ABHD17AP1	1:147574427-147634886	NOTEST	0.110073	0.178197	0.695016	0	1	1
ENSG00000203852	ENSG00000203852	HIST2H3A	1:149824180-149832714	NOTEST	0	0	0	0	1	1
ENSG00000203857	ENSG00000203857	HSD3B1	1:120049820-120057681	NOTEST	0	0	0	0	1	1
ENSG00000203858	ENSG00000203858	HSD3BP2	1:119981623-119988709	NOTEST	0	0.0500248	inf	0	1	1
ENSG00000203859	ENSG00000203859	HSD3B2	1:119957553-119965658	NOTEST	0.026596	0.0816107	1.61755	0	1	1
ENSG00000203863	ENSG00000203863	AL079342.1	6:89674245-89676685	NOTEST	0	0	0	0	1	1
ENSG00000203864	ENSG00000203864	C1orf137	1:117236733-117249225	NOTEST	0	0	0	0	1	1
ENSG00000203867	ENSG00000203867	RBM20	10:112404154-112599227	NOTEST	0.135325	0.314984	1.21884	0	1	1
ENSG00000203870	ENSG00000203870	SMIM9	X:154051622-154062937	NOTEST	0	0	0	0	1	1
ENSG00000203871	ENSG00000203871	C6orf164	6:87992695-88109467	NOTEST	0.160253	0.023365	-2.77793	0	1	1
ENSG00000203872	ENSG00000203872	C6orf163	6:87992695-88109467	NOTEST	0.342083	0.258282	-0.405396	0	1	1
ENSG00000203876	ENSG00000203876	RP11-451M19.3	10:111701028-111713649	NOTEST	0.077366	0.0129463	-2.57916	0	1	1
ENSG00000203877	ENSG00000203877	RIPPLY2	6:84562984-84567234	NOTEST	0	0.033063	inf	0	1	1
ENSG00000203878	ENSG00000203878	CHIAP2	1:111822680-111828738	NOTEST	0	0	0	0	1	1
ENSG00000203883	ENSG00000203883	SOX18	20:62588054-62680994	NOTEST	0.318851	0.575064	0.850843	0	1	1
ENSG00000203886	ENSG00000203886	CYP17A1-AS1	10:104590287-104597290	NOTEST	0.439204	0.0691544	-2.667	0	1	1
ENSG00000203897	ENSG00000203897	SPATA42	1:109358519-109506111	NOTEST	0	0	0	0	1	1
ENSG00000203900	ENSG00000203900	RP11-261N11.8	20:61975419-62009753	NOTEST	0	0	0	0	1	1
ENSG00000203902	ENSG00000203902	PNMA6B	X:152341457-152343394	NOTEST	0	0	0	0	1	1
ENSG00000203907	ENSG00000203907	OOEP	6:74078277-74161999	NOTEST	0	0.0773899	inf	0	1	1
ENSG00000203908	ENSG00000203908	KHDC3L	6:74072399-74073894	NOTEST	0	0	0	0	1	1
ENSG00000203909	ENSG00000203909	DPPA5	6:74062784-74064018	NOTEST	0	0	0	0	1	1
ENSG00000203910	ENSG00000203910	C1orf146	1:92683496-92711370	NOTEST	0	0	0	0	1	1
ENSG00000203914	ENSG00000203914	HSP90B3P	1:92100567-92109639	NOTEST	0	0	0	0	1	1
ENSG00000203923	ENSG00000203923	SPANXN1	X:144328347-144337632	NOTEST	0	0	0	0	1	1
ENSG00000203924	ENSG00000203924	SPANXN2	X:142795054-142804516	NOTEST	0	0.12222	inf	0	1	1
ENSG00000203926	ENSG00000203926	SPANXA2	X:140590842-140738057	NOTEST	0	0	0	0	1	1
ENSG00000203930	ENSG00000203930	LINC00632	X:139791931-139854844	NOTEST	0.0269095	0	#NAME?	0	1	1
ENSG00000203933	ENSG00000203933	CXorf66	X:139037883-139047679	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000203942	ENSG00000203942	C10orf62	10:99344079-99436191	NOTEST	0.027762	0.0648276	1.22349	0	1	1
ENSG00000203943	ENSG00000203943	SAMD13	1:84764048-84863514	NOTEST	0.379875	0.27246	-0.479481	0	1	1
ENSG00000203952	ENSG00000203952	CCDC160	X:133371076-133380237	NOTEST	0.467655	0.48232	0.0445442	0	1	1
ENSG00000203963	ENSG00000203963	C1orf141	1:67557847-67725662	NOTEST	0	0	0	0	1	1
ENSG00000203970	ENSG00000203970	DEFB110	6:49976850-49989694	NOTEST	0	0	0	0	1	1
ENSG00000203971	ENSG00000203971	RP13-379L11.2	20:56532181-56534716	NOTEST	0	0	0	0	1	1
ENSG00000203972	ENSG00000203972	GLYATL3	6:49467670-49494760	NOTEST	0	0	0	0	1	1
ENSG00000203985	ENSG00000203985	LDLRAD1	1:54474411-54483856	NOTEST	0	0	0	0	1	1
ENSG00000203987	ENSG00000203987	RP11-188C12.3	9:140513443-141019076	NOTEST	0	0	0	0	1	1
ENSG00000203989	ENSG00000203989	RHOXF2B	X:119170200-119379122	NOTEST	0	0	0	0	1	1
ENSG00000203995	ENSG00000203995	ZYG11A	1:53308182-53360670	NOTEST	0.00393756	0.00858612	1.12471	0	1	1
ENSG00000204001	ENSG00000204001	LCN8	9:139648837-139652678	NOTEST	0	0	0	0	1	1
ENSG00000204003	ENSG00000204003	LCN6	9:139632618-139642980	NOTEST	0.023351	0.0698682	1.58115	0	1	1
ENSG00000204006	ENSG00000204006	C1orf185	1:51567905-51613752	NOTEST	0	0	0	0	1	1
ENSG00000204007	ENSG00000204007	GLT6D1	9:138515501-138531386	NOTEST	0	0	0	0	1	1
ENSG00000204010	ENSG00000204010	IFIT1B	10:90973325-91174314	NOTEST	0	0	0	0	1	1
ENSG00000204011	ENSG00000204011	COL5A1-AS1	9:137533619-137736686	NOTEST	0	0	0	0	1	1
ENSG00000204019	ENSG00000204019	CT83	X:115592848-115594164	NOTEST	0	0	0	0	1	1
ENSG00000204020	ENSG00000204020	LIPN	10:90521162-90537999	NOTEST	0	0	0	0	1	1
ENSG00000204021	ENSG00000204021	LIPK	10:90484300-90512543	NOTEST	0	0	0	0	1	1
ENSG00000204022	ENSG00000204022	LIPJ	10:90346509-90366733	NOTEST	0	0.0427621	inf	0	1	1
ENSG00000204025	ENSG00000204025	TRPC5OS	X:111017542-111326004	NOTEST	0.00563598	0.00833588	0.564668	0	1	1
ENSG00000204031	ENSG00000204031	LCN1P2	9:136184628-136185304	NOTEST	0	0	0	0	1	1
ENSG00000204033	ENSG00000204033	LRIT2	10:85980253-85985345	NOTEST	0.00510334	0	#NAME?	0	1	1
ENSG00000204038	ENSG00000204038	AL359195.1	10:82009465-82013395	NOTEST	0.00395066	0.00277264	-0.510836	0	1	1
ENSG00000204044	ENSG00000204044	RP11-465L10.10	20:44637546-44688784	NOTEST	0.024974	0.0814963	1.70631	0	1	1
ENSG00000204049	ENSG00000204049	AL391421.1	10:79542623-79686378	NOTEST	0	0	0	0	1	1
ENSG00000204052	ENSG00000204052	LRRC73	6:43474706-43543812	NOTEST	0.167972	0.245926	0.550004	0	1	1
ENSG00000204053	ENSG00000204053	MYCLP1	X:106515811-106516888	NOTEST	0	0	0	0	1	1
ENSG00000204055	ENSG00000204055	RP11-247A12.2	9:131937834-131972827	NOTEST	0.09028	0.00773509	-3.54492	0	1	1
ENSG00000204060	ENSG00000204060	FOXO6	1:41827593-41849262	NOTEST	0.0187342	0.0145488	-0.364774	0	1	1
ENSG00000204065	ENSG00000204065	TCEAL5	X:102528618-102531800	NOTEST	0	0	0	0	1	1
ENSG00000204071	ENSG00000204071	TCEAL6	X:101395447-101397942	NOTEST	0	0.0142223	inf	0	1	1
ENSG00000204072	ENSG00000204072	RP4-545K15.3	X:100852487-100853649	NOTEST	0	0	0	0	1	1
ENSG00000204086	ENSG00000204086	RPA4	X:95939661-96897588	NOTEST	0.0630851	0.0236921	-1.41289	0	1	1
ENSG00000204091	ENSG00000204091	TDRG1	6:40302692-40347624	NOTEST	0	0	0	0	1	1
ENSG00000204092	ENSG00000204092	LINC00951	6:40302692-40347624	NOTEST	0	0	0	0	1	1
ENSG00000204099	ENSG00000204099	NEU4	2:242749406-242758739	NOTEST	0.13318	0.141021	0.0825315	0	1	1
ENSG00000204110	ENSG00000204110	RP1-153P14.8	6:37475123-37503392	NOTEST	0	0	0	0	1	1
ENSG00000204113	ENSG00000204113	BMP2KL	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000204117	ENSG00000204117	RP4-640H8.2	20:36305311-36311636	NOTEST	0	0	0	0	1	1
ENSG00000204118	ENSG00000204118	NAP1L6	X:72345875-72347919	NOTEST	0	0	0	0	1	1
ENSG00000204119	ENSG00000204119	LINC00684	X:72091858-72163653	NOTEST	0	0	0	0	1	1
ENSG00000204121	ENSG00000204121	AC068134.5	2:233280527-233284526	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000204131	ENSG00000204131	NHSL2	X:71130937-71363424	NOTEST	0.00921935	0	#NAME?	0	1	1
ENSG00000204136	ENSG00000204136	GGTA1P	9:124137518-124262306	NOTEST	0	0.0199944	inf	0	1	1
ENSG00000204140	ENSG00000204140	CLPSL1	6:35748793-35761452	NOTEST	0	0	0	0	1	1
ENSG00000204148	ENSG00000204148	LINC00474	9:118650447-118687486	NOTEST	0	0	0	0	1	1
ENSG00000204150	ENSG00000204150	CTGLF11P	10:47708306-47730235	NOTEST	0.166981	0.0859694	-0.95779	0	1	1
ENSG00000204161	ENSG00000204161	C10orf128	10:50362772-50396630	NOTEST	0	0	0	0	1	1
ENSG00000204164	ENSG00000204164	BMS1P5	10:48901101-48950972	NOTEST	0.261462	0.236589	-0.144217	0	1	1
ENSG00000204169	ENSG00000204169	AGAP7	10:51464161-51486327	NOTEST	0.0820643	0.0442919	-0.889713	0	1	1
ENSG00000204172	ENSG00000204172	AGAP10	10:47186202-47243502	NOTEST	0.0851194	0.0397174	-1.09972	0	1	1
ENSG00000204173	ENSG00000204173	LRRC37A5P	9:114287438-114393569	NOTEST	0	0	0	0	1	1
ENSG00000204174	ENSG00000204174	NPY4R	10:47011752-47174093	NOTEST	0	0	0	0	1	1
ENSG00000204175	ENSG00000204175	GPRIN2	10:46994086-47005643	NOTEST	0	0	0	0	1	1
ENSG00000204176	ENSG00000204176	SYT15	10:46897591-46971400	NOTEST	0.0475965	0.0311651	-0.610923	0	1	1
ENSG00000204177	ENSG00000204177	BMS1P1	10:46737611-46761205	NOTEST	0.148398	0.0892344	-0.733801	0	1	1
ENSG00000204179	ENSG00000204179	PTPN20A	10:46549954-46641045	NOTEST	0	0	0	0	1	1
ENSG00000204183	ENSG00000204183	GDF5OS	20:34020826-34042568	NOTEST	0	0	0	0	1	1
ENSG00000204187	ENSG00000204187	LINC00619	10:44340753-44346070	NOTEST	0	0	0	0	1	1
ENSG00000204188	ENSG00000204188	GGNBP1	6:33551514-33561115	NOTEST	0.0188249	0.0454205	1.2707	0	1	1
ENSG00000204193	ENSG00000204193	TXNDC8	9:113065800-113100127	NOTEST	0	0	0	0	1	1
ENSG00000204194	ENSG00000204194	RPL12P1	6:33359312-33377701	NOTEST	0.208544	0.268636	0.365296	0	1	1
ENSG00000204195	ENSG00000204195	AWAT1	X:69454504-69460477	NOTEST	0	0	0	0	1	1
ENSG00000204197	ENSG00000204197	KIFC1	HSCHR6_MHC_QBL:33288142-33306509	NOTEST	0	0	0	0	1	1
ENSG00000204221	ENSG00000204221	WDR46	HSCHR6_MHC_COX:33168490-33188786	NOTEST	0	0	0	0	1	1
ENSG00000204241	ENSG00000204241	RP11-713P17.3	11:133902166-133916744	NOTEST	0	0	0	0	1	1
ENSG00000204246	ENSG00000204246	OR13C3	9:107298029-107299137	NOTEST	0	0	0	0	1	1
ENSG00000204250	ENSG00000204250	LINC00587	9:105281917-105419796	NOTEST	0	0	0	0	1	1
ENSG00000204252	ENSG00000204252	HLA-DOA	6:32971954-32977389	NOTEST	0	0.0385671	inf	0	1	1
ENSG00000204261	ENSG00000204261	TAPSAR1	6:32808493-32827362	NOTEST	0.324897	0.236941	-0.455456	0	1	1
ENSG00000204262	ENSG00000204262	COL5A2	2:189896621-190044605	NOTEST	0.465608	0.502092	0.108835	0	1	1
ENSG00000204276	ENSG00000204276	HLA-DQA2	HSCHR6_MHC_COX:32632815-32638891	NOTEST	0	0	0	0	1	1
ENSG00000204277	ENSG00000204277	RP11-219G17.4	17:76257429-76274573	NOTEST	0	0	0	0	1	1
ENSG00000204278	ENSG00000204278	TMEM235	17:76227390-76237068	NOTEST	0	0	0	0	1	1
ENSG00000204279	ENSG00000204279	PAGE3	X:55284847-55291279	NOTEST	0	0	0	0	1	1
ENSG00000204283	ENSG00000204283	FLJ45079	17:75875108-75878659	NOTEST	0	0	0	0	1	1
ENSG00000204287	ENSG00000204287	HLA-DRA	6:32407618-32412823	NOTEST	0.225239	0.285791	0.343502	0	1	1
ENSG00000204290	ENSG00000204290	BTNL2	6:32361739-32374905	NOTEST	0	0	0	0	1	1
ENSG00000204293	ENSG00000204293	OR8B2	11:124252290-124253258	NOTEST	0	0	0	0	1	1
ENSG00000204296	ENSG00000204296	C6orf10	6:32256302-32339684	NOTEST	0.0358028	0.035811	0.000329827	0	1	1
ENSG00000204300	ENSG00000204300	TMEM225	11:123753632-123756349	NOTEST	0	0	0	0	1	1
ENSG00000204301	ENSG00000204301	NOTCH4	6:32158542-32191844	NOTEST	0.453598	0.203109	-1.15916	0	1	1
ENSG00000204306	ENSG00000204306	AP002348.1	11:120382467-120859613	NOTEST	0	0	0	0	1	1
ENSG00000204311	ENSG00000204311	DFNB59	2:179278665-179326117	NOTEST	0.246983	0.291363	0.238403	0	1	1
ENSG00000204323	ENSG00000204323	SMIM5	17:73584138-73704142	NOTEST	0.140923	0.223315	0.664171	0	1	1
ENSG00000204334	ENSG00000204334	ERICH2	2:171640295-171655481	NOTEST	0.335003	0.0244627	-3.77552	0	1	1
ENSG00000204338	ENSG00000204338	CYP21A1P	6:31973412-31976228	NOTEST	0	0.00641108	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000204345	ENSG00000204345	CD300LD	17:72575503-72590348	NOTEST	0	0	0	0	1	1
ENSG00000204347	ENSG00000204347	BTBD17	17:72352554-72358085	NOTEST	0	0	0	0	1	1
ENSG00000204352	ENSG00000204352	C9orf129	9:95947197-96108696	NOTEST	0.0235949	0.0117463	-1.00627	0	1	1
ENSG00000204359	ENSG00000204359	CFB	HSCHR6_MHC_MANN:31927378-31957964	NOTEST	0	0	0	0	1	1
ENSG00000204361	ENSG00000204361	NXPE2	11:114549107-114579362	NOTEST	0	0	0	0	1	1
ENSG00000204362	ENSG00000204362	RP11-380J14.1	1:17516277-17524112	NOTEST	0	0	0	0	1	1
ENSG00000204363	ENSG00000204363	SPANXN5	X:52825183-52827141	NOTEST	0	0	0	0	1	1
ENSG00000204364	ENSG00000204364	C2	HSCHR6_MHC_MANN:31927378-31957964	NOTEST	0	0	0	0	1	1
ENSG00000204365	ENSG00000204365	C10orf126	10:29135336-29170827	NOTEST	0.303958	0.500116	0.718393	0	1	1
ENSG00000204368	ENSG00000204368	RP11-552E4.3	X:48072225-48077445	NOTEST	0	0	0	0	1	1
ENSG00000204375	ENSG00000204375	XAGE1E	X:52541052-52546197	NOTEST	0	0.0638112	inf	0	1	1
ENSG00000204376	ENSG00000204376	XAGE1D	X:52528158-52533303	NOTEST	0	0	0	0	1	1
ENSG00000204377	ENSG00000204377	C1orf134	1:16555367-16556038	NOTEST	0	0.13589	inf	0	1	1
ENSG00000204379	ENSG00000204379	XAGE1A	X:52255218-52260363	NOTEST	0	0	0	0	1	1
ENSG00000204380	ENSG00000204380	AC005042.4	2:159313475-159610287	NOTEST	0.393268	0.201281	-0.966299	0	1	1
ENSG00000204381	ENSG00000204381	LAYN	11:111411004-111432264	NOTEST	0.00968916	0.0947191	3.28921	0	1	1
ENSG00000204382	ENSG00000204382	XAGE1B	X:52235227-52243954	NOTEST	0	0	0	0	1	1
ENSG00000204385	ENSG00000204385	SLC44A4	6:31830968-31846823	NOTEST	0	0.0203151	inf	0	1	1
ENSG00000204393	ENSG00000204393	RP11-410N8.4	20:31030861-31196695	NOTEST	0	0.0365544	inf	0	1	1
ENSG00000204398	ENSG00000204398	RP11-65D24.2	13:112240547-112324955	NOTEST	0	0	0	0	1	1
ENSG00000204399	ENSG00000204399	AC012306.2	2:128688900-128689014	NOTEST	0	0	0	0	1	1
ENSG00000204403	ENSG00000204403	CASP12	11:104756444-104769397	NOTEST	0	0	0	0	1	1
ENSG00000204414	ENSG00000204414	CSHL1	17:61986956-61996198	NOTEST	0	0	0	0	1	1
ENSG00000204420	ENSG00000204420	C6orf25	6:31686370-31694491	NOTEST	0.00667459	0.00518581	-0.36411	0	1	1
ENSG00000204421	ENSG00000204421	LY6G6C	6:31686370-31694491	NOTEST	0	0	0	0	1	1
ENSG00000204422	ENSG00000204422	XXbac-BPG32J3.20	6:31654725-31685695	NOTEST	0	0	0	0	1	1
ENSG00000204424	ENSG00000204424	LY6G6F	6:31654725-31685695	NOTEST	0	0	0	0	1	1
ENSG00000204428	ENSG00000204428	LY6G5C	6:31644460-31651817	NOTEST	0.356261	0.370099	0.054977	0	1	1
ENSG00000204429	ENSG00000204429	RP11-1E11.1	9:90795587-90796362	NOTEST	0.0245922	0	#NAME?	0	1	1
ENSG00000204434	ENSG00000204434	POTEKP	2:132349324-132384839	NOTEST	0	0.00458349	inf	0	1	1
ENSG00000204437	ENSG00000204437	CTSLP6	10:81630130-81633659	NOTEST	0	0	0	0	1	1
ENSG00000204442	ENSG00000204442	FAM155A	13:107820882-108519083	NOTEST	0	0	0	0	1	1
ENSG00000204446	ENSG00000204446	C9orf170	9:89763558-89774471	NOTEST	0.00484051	0.0150638	1.63785	0	1	1
ENSG00000204449	ENSG00000204449	TRIM49C	11:89764273-89806558	NOTEST	0	0	0	0	1	1
ENSG00000204450	ENSG00000204450	TRIM64	11:89701671-89708396	NOTEST	0	0	0	0	1	1
ENSG00000204455	ENSG00000204455	TRIM51BP	11:89586007-89596061	NOTEST	0.133536	0.0510739	-1.38657	0	1	1
ENSG00000204456	ENSG00000204456	RP11-313I2.10	11:89499607-89502004	NOTEST	0	0	0	0	1	1
ENSG00000204460	ENSG00000204460	AC079586.1	2:129999745-130031421	NOTEST	0	0	0	0	1	1
ENSG00000204464	ENSG00000204464	C1orf195	1:15479027-15546976	NOTEST	0	0	0	0	1	1
ENSG00000204466	ENSG00000204466	DGKK	X:50108407-50213737	NOTEST	0.00370069	0	#NAME?	0	1	1
ENSG00000204471	ENSG00000204471	TBC1D3P4	17:18296793-18304275	NOTEST	0	0	0	0	1	1
ENSG00000204472	ENSG00000204472	AIF1	6:31582960-31584798	NOTEST	0	0	0	0	1	1
ENSG00000204475	ENSG00000204475	NCR3	6:31553900-31560762	NOTEST	0.0663983	0.0558772	-0.248887	0	1	1
ENSG00000204478	ENSG00000204478	PRAMEF20	1:13736906-13747803	NOTEST	0	0	0	0	1	1
ENSG00000204479	ENSG00000204479	PRAMEF17	1:13716091-13719089	NOTEST	0	0	0	0	1	1

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ENSG00000204480	ENSG00000204480	PRAMEF19	1:13694888-13698405	NOTEST	0	0	0	0	1	1
ENSG00000204481	ENSG00000204481	PRAMEF14	1:13668268-13673511	NOTEST	0	0	0	0	1	1
ENSG00000204482	ENSG00000204482	LST1	6:31553900-31560762	NOTEST	0.00894118	0	#NAME?	0	1	1
ENSG00000204485	ENSG00000204485	XX-FW84067D5.1	1:13607430-13611550	NOTEST	0	0	0	0	1	1
ENSG00000204486	ENSG00000204486	PRAMEF21	1:13516065-13526943	NOTEST	0	0	0	0	1	1
ENSG00000204487	ENSG00000204487	LTB	HSCHR6_MHC_COX:31535743-31537711	NOTEST	0	0	0	0	1	1
ENSG00000204488	ENSG00000204488	PRAMEF16	1:13495253-13498260	NOTEST	0	0	0	0	1	1
ENSG00000204490	ENSG00000204490	TNF	HSCHR6_MHC_COX:31530755-31533525	NOTEST	0	0	0	0	1	1
ENSG00000204491	ENSG00000204491	PRAMEF18	1:13474688-13477522	NOTEST	0	0	0	0	1	1
ENSG00000204495	ENSG00000204495	PRAMEF13	1:13447413-13452656	NOTEST	0	0	0	0	1	1
ENSG00000204501	ENSG00000204501	PRAMEF9	1:13421175-13428191	NOTEST	0	0	0	0	1	1
ENSG00000204502	ENSG00000204502	PRAMEF5	1:13359818-13369057	NOTEST	0	0	0	0	1	1
ENSG00000204503	ENSG00000204503	PRAMEF3	1:13328195-13331692	NOTEST	0	0	0	0	1	1
ENSG00000204505	ENSG00000204505	PRAMEF25	1:13140455-13145000	NOTEST	0	0	0	0	1	1
ENSG00000204508	ENSG00000204508	PRAMEF22	1:12998180-13117751	NOTEST	0	0	0	0	1	1
ENSG00000204510	ENSG00000204510	PRAMEF7	1:12976449-12980569	NOTEST	0	0	0	0	1	1
ENSG00000204511	ENSG00000204511	MCCD1	6:31496493-31526606	NOTEST	0	0.0147325	inf	0	1	1
ENSG00000204513	ENSG00000204513	PRAMEF11	1:12884467-12891264	NOTEST	0	0	0	0	1	1
ENSG00000204518	ENSG00000204518	AADACL4	1:12704565-12727097	NOTEST	0	0	0	0	1	1
ENSG00000204528	ENSG00000204528	PSORS1C3	6:31126318-31148508	NOTEST	0	0	0	0	1	1
ENSG00000204529	ENSG00000204529	GUCY2EP	11:76386122-76418685	NOTEST	0	0	0	0	1	1
ENSG00000204531	ENSG00000204531	POU5F1	6:31126318-31148508	NOTEST	0.181043	0.0653551	-1.46996	0	1	1
ENSG00000204532	ENSG00000204532	ZSCAN5C	19:56713669-56720821	NOTEST	0.0376868	0.00791273	-2.25181	0	1	1
ENSG00000204538	ENSG00000204538	PSORS1C2	6:31082526-31107869	NOTEST	0.0303417	0.054755	0.851689	0	1	1
ENSG00000204539	ENSG00000204539	CDSN	6:31082526-31107869	NOTEST	0.00804405	8.99E-07	-13.127	0	1	1
ENSG00000204540	ENSG00000204540	PSORS1C1	6:31082526-31107869	NOTEST	0.0585342	0.146641	1.32494	0	1	1
ENSG00000204542	ENSG00000204542	C6orf15	6:31078999-31080336	NOTEST	0	0	0	0	1	1
ENSG00000204544	ENSG00000204544	MUC21	6:30951494-30957680	NOTEST	0	0	0	0	1	1
ENSG00000204547	ENSG00000204547	DEFB122	20:30009238-30016983	NOTEST	0	0	0	0	1	1
ENSG00000204548	ENSG00000204548	DEFB121	20:29992647-30000641	NOTEST	0	0	0	0	1	1
ENSG00000204555	ENSG00000204555	RP4-610C12.2	20:29449473-29449652	NOTEST	0	0	0	0	1	1
ENSG00000204556	ENSG00000204556	CTD-2514C3.1	20:25999467-26001320	NOTEST	0.324969	0.631763	0.959083	0	1	1
ENSG00000204566	ENSG00000204566	C10orf115	10:23492744-23528745	NOTEST	0	0	0	0	1	1
ENSG00000204571	ENSG00000204571	KRTAP5-11	11:71292900-71319086	NOTEST	0	0	0	0	1	1
ENSG00000204572	ENSG00000204572	KRTAP5-10	11:71276608-71279980	NOTEST	0.030531	0.0130194	-1.22961	0	1	1
ENSG00000204577	ENSG00000204577	LILRB3	19:54704609-54752862	NOTEST	0.00666261	0.0295332	2.14818	0	1	1
ENSG00000204581	ENSG00000204581	AC096670.3	2:111490149-111875799	NOTEST	0	0	0	0	1	1
ENSG00000204583	ENSG00000204583	LRCOL1	12:133179735-133187037	NOTEST	0.0227116	0.0877589	1.95011	0	1	1
ENSG00000204584	ENSG00000204584	RP11-304F15.3	17:47915670-47926199	NOTEST	0.213057	0.0870103	-1.29198	0	1	1
ENSG00000204588	ENSG00000204588	LINC01123	2:110744515-110753717	NOTEST	0.222841	0.293792	0.398776	0	1	1
ENSG00000204595	ENSG00000204595	DPRX	19:54135309-54140263	NOTEST	0	0	0	0	1	1
ENSG00000204603	ENSG00000204603	RP11-638F5.1	12:131649555-131697476	NOTEST	0	0	0	0	1	1
ENSG00000204610	ENSG00000204610	TRIM15	6:30130992-30140473	NOTEST	0	0	0	0	1	1
ENSG00000204612	ENSG00000204612	FOXB2	9:79634570-79635869	NOTEST	0	0	0	0	1	1

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ENSG00000204613	ENSG00000204613	TRIM10	6:30119721-30128711	NOTEST	0	0	0	0	1	1
ENSG00000204614	ENSG00000204614	TRIM40	6:30103884-30116512	NOTEST	0	0	0	0	1	1
ENSG00000204616	ENSG00000204616	TRIM31	6:30070673-30082501	NOTEST	0	0	0	0	1	1
ENSG00000204618	ENSG00000204618	RNF39	6:30034485-30043664	NOTEST	0.0696618	0.046081	-0.596196	0	1	1
ENSG00000204620	ENSG00000204620	AC115618.1	X:48431481-48437454	NOTEST	0.0789299	0.0793475	0.00761225	0	1	1
ENSG00000204622	ENSG00000204622	HLA-J	6:29968787-30032686	NOTEST	0.163249	0.0738224	-1.14494	0	1	1
ENSG00000204624	ENSG00000204624	PTCHD2	1:11539222-11597641	NOTEST	0.00588951	0.00413214	-0.511258	0	1	1
ENSG00000204625	ENSG00000204625	HCG9	6:29942888-29946183	NOTEST	0.0865316	0.0215286	-2.00697	0	1	1
ENSG00000204637	ENSG00000204637	AC068538.2	2:101125738-101126077	NOTEST	0	0	0	0	1	1
ENSG00000204640	ENSG00000204640	NMS	2:101086943-101099742	NOTEST	0	0	0	0	1	1
ENSG00000204644	ENSG00000204644	ZFP57	6:29640168-29648887	NOTEST	0	0	0	0	1	1
ENSG00000204645	ENSG00000204645	SSX4	X:48242862-48252785	NOTEST	0	0	0	0	1	1
ENSG00000204648	ENSG00000204648	SSX9	X:48156250-48165614	NOTEST	0	0	0	0	1	1
ENSG00000204652	ENSG00000204652	RPS26P8	17:43685908-43686349	NOTEST	0.0549858	0.162699	1.56507	0	1	1
ENSG00000204653	ENSG00000204653	ASPDH	19:51014856-51017947	NOTEST	0.241758	0.0548451	-2.14013	0	1	1
ENSG00000204655	ENSG00000204655	MOG	6:29624757-29640149	NOTEST	0	0.0957055	inf	0	1	1
ENSG00000204657	ENSG00000204657	OR2H2	6:29523291-29601753	NOTEST	0.0166556	0.116632	2.80789	0	1	1
ENSG00000204658	ENSG00000204658	RP11-218C14.2	20:23564281-23567147	NOTEST	0	0	0	0	1	1
ENSG00000204659	ENSG00000204659	CBY3	5:179105583-179157926	NOTEST	0.0241916	0.0717965	1.56941	0	1	1
ENSG00000204661	ENSG00000204661	C5orf60	5:179068544-179072047	NOTEST	0	0	0	0	1	1
ENSG00000204662	ENSG00000204662	CST9LP1	20:23528400-23531289	NOTEST	0	0	0	0	1	1
ENSG00000204663	ENSG00000204663	CST13P	20:23499782-23522655	NOTEST	0	0	0	0	1	1
ENSG00000204666	ENSG00000204666	CTD-2126E3.1	19:50479723-50570050	NOTEST	0.0199115	0.0255801	0.361415	0	1	1
ENSG00000204669	ENSG00000204669	C9orf57	9:74666291-74687733	NOTEST	0	0	0	0	1	1
ENSG00000204670	ENSG00000204670	IGKV1OR2-3	2:97725681-97726152	NOTEST	0	0	0	0	1	1
ENSG00000204671	ENSG00000204671	IL31	12:122652284-122688018	NOTEST	0	0	0	0	1	1
ENSG00000204677	ENSG00000204677	FAM153C	5:177433405-177482560	NOTEST	0	0	0	0	1	1
ENSG00000204682	ENSG00000204682	CASC10	10:21781586-21786191	NOTEST	0.129443	0.199484	0.623959	0	1	1
ENSG00000204683	ENSG00000204683	C10orf113	10:21068901-21463977	NOTEST	0	0	0	0	1	1
ENSG00000204684	ENSG00000204684	RP5-1004I9.1	20:22380988-22401281	NOTEST	0	0	0	0	1	1
ENSG00000204687	ENSG00000204687	MAS1L	6:29454473-29455738	NOTEST	0.0246931	0.0298653	0.274361	0	1	1
ENSG00000204688	ENSG00000204688	OR2H1	6:29424957-29432105	NOTEST	0	0	0	0	1	1
ENSG00000204689	ENSG00000204689	OR10C1	HSCHR6_MHC_MCF:29323243-29424633	NOTEST	0	0	0	0	1	1
ENSG00000204690	ENSG00000204690	OR12D2	HSCHR6_MHC_MCF:29323243-29424633	NOTEST	0	0	0	0	1	1
ENSG00000204692	ENSG00000204692	OR12D3	HSCHR6_MHC_MCF:29323243-29424633	NOTEST	0	0	0	0	1	1
ENSG00000204694	ENSG00000204694	OR11A1	6:29323006-29424848	NOTEST	0	0	0	0	1	1
ENSG00000204695	ENSG00000204695	OR14J1	6:29274402-29275519	NOTEST	0	0	0	0	1	1
ENSG00000204697	ENSG00000204697	OR2U1P	6:29191749-29258217	NOTEST	0	0	0	0	1	1
ENSG00000204699	ENSG00000204699	UBTFL3	2:96285391-96296321	NOTEST	0	0	0	0	1	1
ENSG00000204700	ENSG00000204700	OR2J2	6:29141310-29142351	NOTEST	0	0	0	0	1	1
ENSG00000204701	ENSG00000204701	OR2J3	6:29079667-29080603	NOTEST	0	0	0	0	1	1
ENSG00000204702	ENSG00000204702	OR2J1	6:29068385-29069658	NOTEST	0	0	0	0	1	1
ENSG00000204703	ENSG00000204703	OR2B3	6:29053984-29055090	NOTEST	0	0	0	0	1	1
ENSG00000204704	ENSG00000204704	OR2W1	6:29011989-29013017	NOTEST	0	0	0	0	1	1
ENSG00000204705	ENSG00000204705	UBTFL5	2:96111910-96122840	NOTEST	0	0	0	0	1	1

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ENSG00000204706	ENSG00000204706	MAMDC2-AS1	9:72658496-72873782	NOTEST	0.0691909	0.0380296	-0.863458	0	1	1
ENSG00000204709	ENSG00000204709	C6orf100	6:28911653-28912314	NOTEST	0	0	0	0	1	1
ENSG00000204710	ENSG00000204710	SPDYC	11:64937624-64940715	NOTEST	0	0	0	0	1	1
ENSG00000204711	ENSG00000204711	C9orf135	9:72435708-72521148	NOTEST	0.0282346	0.0199567	-0.500593	0	1	1
ENSG00000204717	ENSG00000204717	AC073464.11	2:95461552-95472197	NOTEST	0	0	0	0	1	1
ENSG00000204718	ENSG00000204718	CNN2P12	13:19300845-19301554	NOTEST	0	0	0	0	1	1
ENSG00000204740	ENSG00000204740	MALRD1	10:19492778-20079330	NOTEST	0	0	0	0	1	1
ENSG00000204752	ENSG00000204752	AC025278.1	19:7011513-7013338	NOTEST	0	0	0	0	1	1
ENSG00000204754	ENSG00000204754	CTC-281M20.1	5:174346084-174422516	NOTEST	0	0	0	0	1	1
ENSG00000204767	ENSG00000204767	FAM196B	5:169064250-169510386	NOTEST	0.0908329	0.21805	1.26337	0	1	1
ENSG00000204771	ENSG00000204771	CTD-3232M19.2	8:145462708-145485885	NOTEST	0	0	0	0	1	1
ENSG00000204776	ENSG00000204776	IGKV1OR-3	9:70394237-70395090	NOTEST	0	0	0	0	1	1
ENSG00000204779	ENSG00000204779	FOXD4L5	9:70175706-70178815	NOTEST	0	0	0	0	1	1
ENSG00000204780	ENSG00000204780	IGKV1OR9-1	9:70143768-70144432	NOTEST	0	0	0	0	1	1
ENSG00000204787	ENSG00000204787	REG1P	2:79362628-79365553	NOTEST	0	0	0	0	1	1
ENSG00000204788	ENSG00000204788	CR769776.1	9:69377901-69380597	NOTEST	0.0291268	0.00564979	-2.36608	0	1	1
ENSG00000204789	ENSG00000204789	ZNF204P	6:27325603-27339304	NOTEST	0.366807	0.187966	-0.964551	0	1	1
ENSG00000204791	ENSG00000204791	CTD-3065J16.6	8:145104029-145118735	NOTEST	0	0	0	0	1	1
ENSG00000204793	ENSG00000204793	FOXD4L6	9:69199479-69202204	NOTEST	0	0	0	0	1	1
ENSG00000204794	ENSG00000204794	PGM5P1	9:68726628-68809906	NOTEST	0.483533	0.406468	-0.250473	0	1	1
ENSG00000204801	ENSG00000204801	RP11-96J15.2	9:46786248-46787634	NOTEST	0.233305	0	#NAME?	0	1	1
ENSG00000204802	ENSG00000204802	RP11-111F5.4	9:46685428-46746500	NOTEST	0.443551	0.649332	0.549858	0	1	1
ENSG00000204805	ENSG00000204805	FAM27E4	9:44997776-44999352	NOTEST	0.460865	0.16027	-1.52384	0	1	1
ENSG00000204813	ENSG00000204813	RP11-34H11.3	9:46385690-46387222	NOTEST	0	0	0	0	1	1
ENSG00000204814	ENSG00000204814	RP11-160N1.10	9:44867570-44870528	NOTEST	0.0266662	0	#NAME?	0	1	1
ENSG00000204816	ENSG00000204816	RP11-475I24.1	9:44343365-44345689	NOTEST	0.0696626	0.04025	-0.791394	0	1	1
ENSG00000204818	ENSG00000204818	BX649563.4	9:44170446-44175727	NOTEST	0	0.0112109	inf	0	1	1
ENSG00000204828	ENSG00000204828	FOXD4L2	9:42717233-42720342	NOTEST	0.0101094	0	#NAME?	0	1	1
ENSG00000204832	ENSG00000204832	ST8SIA6-AS1	10:17360381-17496329	NOTEST	0	0	0	0	1	1
ENSG00000204837	ENSG00000204837	RP11-204M4.2	9:41961614-42019580	NOTEST	0.221899	0.236374	0.0911699	0	1	1
ENSG00000204844	ENSG00000204844	FAM74A3	9:40715661-40722679	NOTEST	0	0	0	0	1	1
ENSG00000204848	ENSG00000204848	SPATA31A2	9:39884974-39891210	NOTEST	0	0.00803113	inf	0	1	1
ENSG00000204849	ENSG00000204849	SPATA31A1	9:39355698-39361956	NOTEST	0.00366498	0	#NAME?	0	1	1
ENSG00000204850	ENSG00000204850	AC011484.1	19:46984052-47114050	NOTEST	0.00815999	0.0395101	2.27558	0	1	1
ENSG00000204851	ENSG00000204851	PNMAL2	19:46984052-47114050	NOTEST	0	0.00312841	inf	0	1	1
ENSG00000204860	ENSG00000204860	FAM201A	9:38540563-38624987	NOTEST	0.203534	0.277872	0.449151	0	1	1
ENSG00000204866	ENSG00000204866	IGFL2	19:46604379-46706340	NOTEST	0	0.0754444	inf	0	1	1
ENSG00000204872	ENSG00000204872	AC092653.5	2:73927753-73928432	NOTEST	0.0877229	0.0206735	-2.08517	0	1	1
ENSG00000204873	ENSG00000204873	KRTAP9-3	17:39388714-39389705	NOTEST	0	0	0	0	1	1
ENSG00000204876	ENSG00000204876	AC021218.2	7:155755325-155759037	NOTEST	0	0	0	0	1	1
ENSG00000204880	ENSG00000204880	KRTAP4-8	17:39253232-39254393	NOTEST	0	0	0	0	1	1
ENSG00000204882	ENSG00000204882	GPR20	8:142366599-142377367	NOTEST	0	0	0	0	1	1
ENSG00000204887	ENSG00000204887	KRTAP1-4	17:39185948-39186356	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000204889	ENSG00000204889	KRT40	17:39133967-39143387	NOTEST	0	0	0	0	1	1
ENSG00000204894	ENSG00000204894	RP11-208G20.2	7:151832009-152133090	NOTEST	0	0	0	0	1	1
ENSG00000204897	ENSG00000204897	KRT25	17:38904272-38911584	NOTEST	0	0	0	0	1	1
ENSG00000204904	ENSG00000204904	CXorf31	X:46746851-46759138	NOTEST	0.0848812	0.0661276	-0.360193	0	1	1
ENSG00000204909	ENSG00000204909	SPINK9	5:147647742-147763346	NOTEST	0	0	0	0	1	1
ENSG00000204913	ENSG00000204913	LRRC3C	17:38097726-38101000	NOTEST	0	0	0	0	1	1
ENSG00000204915	ENSG00000204915	RP6-99M1.1	X:45590240-45591177	NOTEST	0	0	0	0	1	1
ENSG00000204918	ENSG00000204918	PRR20B	13:57721621-57724643	NOTEST	0	0	0	0	1	1
ENSG00000204919	ENSG00000204919	PRR20A	13:57715051-57718073	NOTEST	0	0	0	0	1	1
ENSG00000204928	ENSG00000204928	GRXCR2	5:145239295-145252531	NOTEST	0.025788	0.0182139	-0.501662	0	1	1
ENSG00000204929	ENSG00000204929	AC074391.1	2:65663844-66311773	NOTEST	0.0819807	0	#NAME?	0	1	1
ENSG00000204930	ENSG00000204930	FAM221B	9:35812956-35854844	NOTEST	0	0	0	0	1	1
ENSG00000204933	ENSG00000204933	CD177P1	19:43876893-43883276	NOTEST	0	0.0593188	inf	0	1	1
ENSG00000204936	ENSG00000204936	CD177	19:43857810-43873122	NOTEST	0.0696565	0.179868	1.36861	0	1	1
ENSG00000204947	ENSG00000204947	ZNF425	7:148799875-148823438	NOTEST	0.545902	0.572103	0.0676335	0	1	1
ENSG00000204949	ENSG00000204949	FAM83A-AS1	8:124191199-124222314	NOTEST	0	0	0	0	1	1
ENSG00000204950	ENSG00000204950	LRRC10B	11:61276271-61278482	NOTEST	0	0.0159828	inf	0	1	1
ENSG00000204952	ENSG00000204952	FBXO47	17:37092684-37123655	NOTEST	0.00696903	0	#NAME?	0	1	1
ENSG00000204956	ENSG00000204956	PCDHGA1	5:140710251-140892546	NOTEST	0.482624	0.602484	0.320024	0	1	1
ENSG00000204957	ENSG00000204957	AC006486.1	19:42734337-42759309	NOTEST	0.104286	0.0444684	-1.2297	0	1	1
ENSG00000204960	ENSG00000204960	BLACE	7:155149679-155160629	NOTEST	0	0	0	0	1	1
ENSG00000204961	ENSG00000204961	PCDHA9	5:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000204962	ENSG00000204962	PCDHA8	5:140165875-140391936	NOTEST	0	0.0314831	inf	0	1	1
ENSG00000204963	ENSG00000204963	PCDHA7	5:140165875-140391936	NOTEST	0.0122204	0.0199816	0.709382	0	1	1
ENSG00000204965	ENSG00000204965	PCDHA5	5:140165875-140391936	NOTEST	0.0350015	0.0279244	-0.325892	0	1	1
ENSG00000204967	ENSG00000204967	PCDHA4	5:140165875-140391936	NOTEST	0.0803939	0.0957851	0.252716	0	1	1
ENSG00000204969	ENSG00000204969	PCDHA2	5:140165875-140391936	NOTEST	0.0412959	0.0042602	-3.277	0	1	1
ENSG00000204970	ENSG00000204970	PCDHA1	5:140165875-140391936	NOTEST	0.0234542	0.101453	2.11289	0	1	1
ENSG00000204971	ENSG00000204971	RP11-807H22.7	11:71874365-71920285	NOTEST	0	0	0	0	1	1
ENSG00000204978	ENSG00000204978	C19orf69	19:41949062-41950670	NOTEST	0.019165	0.01351	-0.504451	0	1	1
ENSG00000204979	ENSG00000204979	MS4A13	11:60282885-60310194	NOTEST	0	0	0	0	1	1
ENSG00000204982	ENSG00000204982	PRSS3P4	9:33613845-33614007	NOTEST	0	0	0	0	1	1
ENSG00000204983	ENSG00000204983	PRSS1	7:142457318-142460923	NOTEST	0	0	0	0	1	1
ENSG00000204989	ENSG00000204989	OR4D8P	11:59259124-59260054	NOTEST	0	0	0	0	1	1
ENSG00000204990	ENSG00000204990	RP5-842K16.1	7:140774031-141180180	NOTEST	0	0	0	0	1	1
ENSG00000204993	ENSG00000204993	AC139712.2	2:52797785-52799660	NOTEST	0	0	0	0	1	1
ENSG00000205002	ENSG00000205002	AARD	8:117950437-117956726	NOTEST	0.270077	0.317161	0.231844	0	1	1
ENSG00000205015	ENSG00000205015	RP11-46C24.3	16:89232790-89235555	NOTEST	0	0	0	0	1	1
ENSG00000205018	ENSG00000205018	RP11-830F9.6	16:88941265-89043612	NOTEST	0	0	0	0	1	1
ENSG00000205020	ENSG00000205020	CCL4L1	17:34538309-34540280	NOTEST	0	0	0	0	1	1
ENSG00000205021	ENSG00000205021	CCL3L1	17:34580901-34808104	NOTEST	0	0	0	0	1	1
ENSG00000205022	ENSG00000205022	PABPN1L	16:88880141-88933068	NOTEST	0	0	0	0	1	1
ENSG00000205025	ENSG00000205025	OR5G5P	11:56569331-56587980	NOTEST	0	0	0	0	1	1
ENSG00000205029	ENSG00000205029	OR5D16	11:55606227-55607214	NOTEST	0	0	0	0	1	1

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ENSG00000205030	ENSG00000205030	OR5L2	11:55594694-55595630	NOTEST	0	0	0	0	1	1
ENSG00000205035	ENSG00000205035	RP11-707M1.1	11:49580097-49831971	NOTEST	0	0	0	0	1	1
ENSG00000205037	ENSG00000205037	RP11-863P13.4	16:88121646-88134591	NOTEST	0.00900857	0.00316168	-1.5106	0	1	1
ENSG00000205038	ENSG00000205038	PKHD1L1	8:110374705-110542559	NOTEST	0	0.11566	inf	0	1	1
ENSG00000205044	ENSG00000205044	RP11-56P9.11	11:49035494-49037446	NOTEST	0	0	0	0	1	1
ENSG00000205045	ENSG00000205045	SLFN12L	17:33791267-33864880	NOTEST	0	0	0	0	1	1
ENSG00000205054	ENSG00000205054	LINC01121	2:45392008-45550434	NOTEST	0	0	0	0	1	1
ENSG00000205056	ENSG00000205056	RP11-693J15.5	12:92813869-92885867	NOTEST	0	0	0	0	1	1
ENSG00000205057	ENSG00000205057	CLLU1OS	12:92813869-92885867	NOTEST	0	0	0	0	1	1
ENSG00000205076	ENSG00000205076	LGALS7	19:39261610-39264132	NOTEST	0	0	0	0	1	1
ENSG00000205078	ENSG00000205078	SYCE1L	16:77224731-77478233	NOTEST	0.279893	0.110269	-1.34385	0	1	1
ENSG00000205081	ENSG00000205081	CXorf30	X:36246734-36458375	NOTEST	0	0	0	0	1	1
ENSG00000205085	ENSG00000205085	FAM71F2	7:128312341-128326929	NOTEST	0.311956	0.316857	0.0224876	0	1	1
ENSG00000205086	ENSG00000205086	C2orf91	2:42162507-42181406	NOTEST	0	0	0	0	1	1
ENSG00000205089	ENSG00000205089	CCNI2	5:132083136-132142933	NOTEST	0.014377	0.570198	5.30963	0	1	1
ENSG00000205090	ENSG00000205090	TMEM240	1:1470553-1475833	NOTEST	0.15428	0.225101	0.545019	0	1	1
ENSG00000205097	ENSG00000205097	FRG2	4:190945505-190948412	NOTEST	0	0	0	0	1	1
ENSG00000205100	ENSG00000205100	HSP90AA4P	4:190394118-190396346	NOTEST	0	0	0	0	1	1
ENSG00000205106	ENSG00000205106	CTD-2210P24.4	11:45792982-45793909	NOTEST	0	0.0241885	inf	0	1	1
ENSG00000205108	ENSG00000205108	FAM205A	9:34723051-34729464	NOTEST	0	0	0	0	1	1
ENSG00000205111	ENSG00000205111	CDKL4	2:39402786-39456729	NOTEST	0.0585796	0.142258	1.28004	0	1	1
ENSG00000205116	ENSG00000205116	TMEM88B	1:1361507-1363167	NOTEST	0	0	0	0	1	1
ENSG00000205126	ENSG00000205126	ACCSL	11:44069530-44081527	NOTEST	0.25221	0.268663	0.0911695	0	1	1
ENSG00000205129	ENSG00000205129	C4orf47	4:186347393-186393417	NOTEST	0.122872	0.261835	1.0915	0	1	1
ENSG00000205143	ENSG00000205143	ARID3C	9:34621375-34628104	NOTEST	0	0.00930932	inf	0	1	1
ENSG00000205147	ENSG00000205147	AC016586.1	19:4041126-4043154	NOTEST	0.0159948	0.0112386	-0.509141	0	1	1
ENSG00000205148	ENSG00000205148	AC016251.1	15:96670597-96883492	NOTEST	0	0	0	0	1	1
ENSG00000205174	ENSG00000205174	C7orf66	7:108524031-108524644	NOTEST	0	0	0	0	1	1
ENSG00000205176	ENSG00000205176	REXO1L1P	8:86568694-86575726	NOTEST	0.00216445	0	#NAME?	0	1	1
ENSG00000205177	ENSG00000205177	C11orf91	11:33719806-33757991	NOTEST	0.0386922	0.393567	3.34649	0	1	1
ENSG00000205181	ENSG00000205181	LINC00654	20:5476712-5485259	NOTEST	0.00499842	0.00350649	-0.511444	0	1	1
ENSG00000205184	ENSG00000205184	SLC10A5P1	8:82546591-82547897	NOTEST	0	0	0	0	1	1
ENSG00000205186	ENSG00000205186	FABP9	8:82351670-82445510	NOTEST	0	0	0	0	1	1
ENSG00000205209	ENSG00000205209	SCGB2B2	19:35084233-35166604	NOTEST	0	0	0	0	1	1
ENSG00000205212	ENSG00000205212	CCDC144NL	17:20717932-20947073	NOTEST	0	0.00395803	inf	0	1	1
ENSG00000205215	ENSG00000205215	AC015818.3	17:20422624-20432000	NOTEST	0	0	0	0	1	1
ENSG00000205217	ENSG00000205217	FAM106B	17:20318859-20334321	NOTEST	0	0	0	0	1	1
ENSG00000205221	ENSG00000205221	VIT	2:36923832-37041935	NOTEST	0.0126614	0	#NAME?	0	1	1
ENSG00000205231	ENSG00000205231	TTLL10-AS1	1:1108435-1133315	NOTEST	0	0	0	0	1	1
ENSG00000205236	ENSG00000205236	RP11-514P8.6	7:102122891-102312088	NOTEST	0.0663124	0.0278747	-1.25032	0	1	1
ENSG00000205238	ENSG00000205238	SPDYE2	7:102122891-102312088	NOTEST	0.114201	0.193715	0.762357	0	1	1
ENSG00000205240	ENSG00000205240	OR7E36P	13:42005424-42006446	NOTEST	0	0	0	0	1	1
ENSG00000205266	ENSG00000205266	AL353997.3	17:18319041-18328411	NOTEST	0	0	0	0	1	1
ENSG00000205267	ENSG00000205267	DGAT2L7P	7:100845042-100846807	NOTEST	0	0	0	0	1	1

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ENSG00000205271	ENSG00000205271	CSPG4P10	15:83128127-83182928	NOTEST	0.117425	0.120975	0.0429798	0	1	1
ENSG00000205274	ENSG00000205274	TRBV20OR9-2	9:33617759-33618504	NOTEST	0.242269	0.615912	1.34612	0	1	1
ENSG00000205275	ENSG00000205275	CSPG4P9	15:82944772-82988374	NOTEST	0	0.00752574	inf	0	1	1
ENSG00000205277	ENSG00000205277	MUC12	7:100612903-100662230	NOTEST	0.0589462	0.0997234	0.758534	0	1	1
ENSG00000205279	ENSG00000205279	CTXN3	5:126984735-126999721	NOTEST	0	0	0	0	1	1
ENSG00000205281	ENSG00000205281	GOLGA6L10	15:82635129-82641706	NOTEST	0.0739336	0.135619	0.87526	0	1	1
ENSG00000205293	ENSG00000205293	RP11-1112C15.	8:58890916-58896685	NOTEST	0	0	0	0	1	1
ENSG00000205300	ENSG00000205300	RP11-352D3.2	20:4050798-4055812	NOTEST	0	0	0	0	1	1
ENSG00000205301	ENSG00000205301	RP11-542P2.1	4:141363415-141419531	NOTEST	0	0	0	0	1	1
ENSG00000205307	ENSG00000205307	SAP25	7:100169854-100205798	NOTEST	0	0	0	0	1	1
ENSG00000205312	ENSG00000205312	AC022596.2	17:16750948-16756091	NOTEST	0	0	0	0	1	1
ENSG00000205318	ENSG00000205318	GCNT6	6:10633992-10647501	NOTEST	0	0	0	0	1	1
ENSG00000205325	ENSG00000205325	AC005863.1	17:14670899-14683520	NOTEST	0	0	0	0	1	1
ENSG00000205327	ENSG00000205327	OR6C68	12:55828520-55979255	NOTEST	0	0	0	0	1	1
ENSG00000205328	ENSG00000205328	OR6C65	12:55794213-55795289	NOTEST	0	0	0	0	1	1
ENSG00000205329	ENSG00000205329	OR6C3	12:55725484-55726420	NOTEST	0	0	0	0	1	1
ENSG00000205330	ENSG00000205330	OR6C1	12:55714345-55715408	NOTEST	0	0	0	0	1	1
ENSG00000205331	ENSG00000205331	OR6C72P	12:55677533-55706860	NOTEST	0	0	0	0	1	1
ENSG00000205333	ENSG00000205333	GOLGA2P1	8:87345502-87777251	NOTEST	0	0	0	0	1	1
ENSG00000205334	ENSG00000205334	AC074091.13	2:27928652-27938599	NOTEST	0.00998374	0.00429056	-1.21842	0	1	1
ENSG00000205358	ENSG00000205358	MT1H	16:56703725-56705041	NOTEST	0	0	0	0	1	1
ENSG00000205359	ENSG00000205359	SLCO6A1	5:101707485-101834720	NOTEST	0	0	0	0	1	1
ENSG00000205360	ENSG00000205360	MT1CP	16:56682159-56687116	NOTEST	0	0	0	0	1	1
ENSG00000205361	ENSG00000205361	MT1DP	16:56677616-56678698	NOTEST	0	0	0	0	1	1
ENSG00000205363	ENSG00000205363	C15orf59	15:74032140-74045088	NOTEST	0.103632	0.209555	1.01586	0	1	1
ENSG00000205364	ENSG00000205364	MT1M	16:56662970-56667898	NOTEST	0	0	0	0	1	1
ENSG00000205396	ENSG00000205396	LINC00661	19:16126096-16138272	NOTEST	0	0	0	0	1	1
ENSG00000205403	ENSG00000205403	CFI	4:110661851-110723335	NOTEST	0.223703	0.327986	0.552051	0	1	1
ENSG00000205409	ENSG00000205409	OR52E6	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000205412	ENSG00000205412	HNRNPA1P20	3:147878697-147997885	NOTEST	0	0	0	0	1	1
ENSG00000205414	ENSG00000205414	RP11-401P9.6	16:50582240-50670647	NOTEST	0.047998	0.0256189	-0.905763	0	1	1
ENSG00000205420	ENSG00000205420	KRT6A	12:52880957-52887041	NOTEST	0	0	0	0	1	1
ENSG00000205424	ENSG00000205424	AL592528.1	21:47063607-47362368	NOTEST	0	0	0	0	1	1
ENSG00000205426	ENSG00000205426	KRT81	12:52626303-52702947	NOTEST	0.042239	0.359036	3.08748	0	1	1
ENSG00000205433	ENSG00000205433	SNRPGP6	10:118168767-118168987	NOTEST	0	0	0	0	1	1
ENSG00000205436	ENSG00000205436	EXOC3L4	14:103566480-103576896	NOTEST	0.348601	0.318758	-0.129115	0	1	1
ENSG00000205439	ENSG00000205439	KRTAP12-3	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000205441	ENSG00000205441	KRTAP10-7	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000205442	ENSG00000205442	IZUMO3	9:24542949-24545944	NOTEST	0	0	0	0	1	1
ENSG00000205445	ENSG00000205445	KRTAP10-2	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000205449	ENSG00000205449	NBPF22P	5:85578277-85592281	NOTEST	0	0	0	0	1	1
ENSG00000205452	ENSG00000205452	RP11-812E19.3	16:33775378-33790097	NOTEST	0	0	0	0	1	1
ENSG00000205457	ENSG00000205457	TP53TG3C	16:33202881-33264727	NOTEST	0.0994365	0.12208	0.295982	0	1	1
ENSG00000205482	ENSG00000205482	AC007000.12	7:76139744-77045717	NOTEST	0.0353371	0.104328	1.56187	0	1	1
ENSG00000205488	ENSG00000205488	CALML3-AS1	10:5556206-5568225	NOTEST	0	0	0	0	1	1

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ENSG00000205494	ENSG00000205494	OR52A4	11:5141848-5145743	NOTEST	0	0	0	0	1	1
ENSG00000205495	ENSG00000205495	OR52J3	11:5067755-5068691	NOTEST	0	0	0	0	1	1
ENSG00000205496	ENSG00000205496	OR51A2	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000205497	ENSG00000205497	OR51A4	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000205500	ENSG00000205500	AC013472.3	2:27070614-27250064	NOTEST	0.014988	0	#NAME?	0	1	1
ENSG00000205502	ENSG00000205502	C2CD4B	15:62455733-62457482	NOTEST	0	0.0254328	inf	0	1	1
ENSG00000205505	ENSG00000205505	AC006014.10	7:74880904-74988262	NOTEST	0.0433127	0.0175055	-1.30698	0	1	1
ENSG00000205506	ENSG00000205506	AC004878.6	7:74880904-74988262	NOTEST	0	0	0	0	1	1
ENSG00000205508	ENSG00000205508	AC004878.5	7:74880904-74988262	NOTEST	0	0	0	0	1	1
ENSG00000205509	ENSG00000205509	AC138783.11	7:74696065-74714647	NOTEST	0.00884532	0	#NAME?	0	1	1
ENSG00000205537	ENSG00000205537	RP11-89H19.1	12:48235319-48336831	NOTEST	0	0	0	0	1	1
ENSG00000205549	ENSG00000205549	C9orf92	9:16203932-16276311	NOTEST	0	0	0	0	1	1
ENSG00000205562	ENSG00000205562	RP11-497E19.1	14:85991476-85996332	NOTEST	0	0.00732302	inf	0	1	1
ENSG00000205565	ENSG00000205565	RP11-497H16.6	5:69803905-69808422	NOTEST	0.0586553	0.0368325	-0.671281	0	1	1
ENSG00000205579	ENSG00000205579	DYNLL1P1	14:81712637-81712907	NOTEST	0	0	0	0	1	1
ENSG00000205580	ENSG00000205580	AC006995.8	7:72440226-72555749	NOTEST	0	0	0	0	1	1
ENSG00000205584	ENSG00000205584	AC005488.11	7:72440226-72555749	NOTEST	0	0	0	0	1	1
ENSG00000205593	ENSG00000205593	DENND6B	22:50747458-50765489	NOTEST	0.569679	0.221903	-1.36022	0	1	1
ENSG00000205595	ENSG00000205595	AREGB	4:75418300-75514664	NOTEST	0	0	0	0	1	1
ENSG00000205596	ENSG00000205596	RP5-1132H15.2	7:65535890-65536305	NOTEST	0	0	0	0	1	1
ENSG00000205611	ENSG00000205611	RP4-610C12.4	20:29513581-29521213	NOTEST	0.0264048	0.0165105	-0.67742	0	1	1
ENSG00000205622	ENSG00000205622	AF064858.6	21:40249214-40328392	NOTEST	0	0	0	0	1	1
ENSG00000205625	ENSG00000205625	RP11-15G8.1	6:155027776-155028929	NOTEST	0	0	0	0	1	1
ENSG00000205628	ENSG00000205628	GS1-179L18.1	7:53723201-53879624	NOTEST	0.0170619	0.00696426	-1.29273	0	1	1
ENSG00000205632	ENSG00000205632	WI2-81516E3.1	22:49288728-49294198	NOTEST	0	0	0	0	1	1
ENSG00000205634	ENSG00000205634	LINC00898	22:48016791-48027318	NOTEST	0.0103784	0.0273171	1.39621	0	1	1
ENSG00000205636	ENSG00000205636	LINC00583	9:13927969-13945609	NOTEST	0	0	0	0	1	1
ENSG00000205639	ENSG00000205639	MFSD2B	2:24232950-24286551	NOTEST	0	0.0164515	inf	0	1	1
ENSG00000205642	ENSG00000205642	VCX3B	X:8432870-8434550	NOTEST	0.269019	0.207234	-0.376448	0	1	1
ENSG00000205644	ENSG00000205644	CTD-2375G15.1	5:64444562-64777747	NOTEST	0	0	0	0	1	1
ENSG00000205653	ENSG00000205653	RP3-416J7.5	6:181465-206392	NOTEST	0	0	0	0	1	1
ENSG00000205662	ENSG00000205662	RP11-706O15.7	X:3847909-3855896	NOTEST	0	0	0	0	1	1
ENSG00000205663	ENSG00000205663	RP11-706O15.5	X:3809478-3838787	NOTEST	0	0.0112718	inf	0	1	1
ENSG00000205667	ENSG00000205667	ARSH	X:2924653-2951612	NOTEST	0.00871553	0	#NAME?	0	1	1
ENSG00000205669	ENSG00000205669	ACOT6	14:74077648-74100644	NOTEST	7.88E-07	0	#NAME?	0	1	1
ENSG00000205677	ENSG00000205677	LYPLA2P1	HSCHR6_MHC_MCF:33503673-33504369	NOTEST	0	0	0	0	1	1
ENSG00000205678	ENSG00000205678	TECRL	4:65140974-65275186	NOTEST	0	0	0	0	1	1
ENSG00000205682	ENSG00000205682	RP11-798L4.1	4:62066975-63031272	NOTEST	0	0	0	0	1	1
ENSG00000205683	ENSG00000205683	DPF3	14:73086003-73360809	NOTEST	0.129586	0.107661	-0.267411	0	1	1
ENSG00000205695	ENSG00000205695	RP11-15H7.2	6:139981064-139982650	NOTEST	0	0	0	0	1	1
ENSG00000205696	ENSG00000205696	ADARB2-AS1	10:1228072-1779670	NOTEST	0	0	0	0	1	1
ENSG00000205704	ENSG00000205704	LINC00634	22:42348168-42354937	NOTEST	0.108717	0	#NAME?	0	1	1
ENSG00000205716	ENSG00000205716	AC007248.6	2:102866316-102866715	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000205718	ENSG00000205718	MBD3L4	19:7037758-7040190	NOTEST	0	0	0	0	1	1
ENSG00000205740	ENSG00000205740	AL359878.1	10:1017096-1034281	NOTEST	0.00871553	0	#NAME?	0	1	1
ENSG00000205744	ENSG00000205744	DENND1C	19:6436089-6482568	NOTEST	0.0210493	0.123904	2.55738	0	1	1
ENSG00000205745	ENSG00000205745	PP13004	7:36118693-36125346	NOTEST	0	0	0	0	1	1
ENSG00000205754	ENSG00000205754	SLCO1B7	12:20963635-21392180	NOTEST	0	0	0	0	1	1
ENSG00000205755	ENSG00000205755	CRLF2	X:1314889-1331616	NOTEST	0	0	0	0	1	1
ENSG00000205767	ENSG00000205767	CTD-2302E22.1	14:64034670-64035027	NOTEST	0	0	0	0	1	1
ENSG00000205771	ENSG00000205771	CATSPER2P1	15:44019115-44095241	NOTEST	0.0343865	0.0415837	0.274178	0	1	1
ENSG00000205775	ENSG00000205775	GAGE2E	X:49197606-49204923	NOTEST	0	0	0	0	1	1
ENSG00000205777	ENSG00000205777	GAGE1	X:49363627-49373139	NOTEST	0	0.0193569	inf	0	1	1
ENSG00000205784	ENSG00000205784	ARRDC5	19:4890448-4902879	NOTEST	0	0	0	0	1	1
ENSG00000205790	ENSG00000205790	AC005594.3	19:4675235-4724685	NOTEST	0.0934566	0.135358	0.534414	0	1	1
ENSG00000205791	ENSG00000205791	LOH12CR2	12:12508341-12510001	NOTEST	0.286125	0.0975238	-1.55282	0	1	1
ENSG00000205794	ENSG00000205794	RP11-333E13.4	4:40044536-40159872	NOTEST	0.0742071	0.0604563	-0.295665	0	1	1
ENSG00000205795	ENSG00000205795	CYS1	2:10196906-10221071	NOTEST	0.0418414	0.0134837	-1.63371	0	1	1
ENSG00000205809	ENSG00000205809	KLRC2	12:10564910-10607284	NOTEST	0.00552114	0.126642	4.51965	0	1	1
ENSG00000205810	ENSG00000205810	KLRC3	12:10564910-10607284	NOTEST	0.0366429	0.152844	2.06045	0	1	1
ENSG00000205821	ENSG00000205821	AC006435.1	17:2308855-2415185	NOTEST	0	0	0	0	1	1
ENSG00000205822	ENSG00000205822	TPTE2P6	13:24982294-25171814	NOTEST	0.295876	0.22964	-0.365619	0	1	1
ENSG00000205830	ENSG00000205830	AC024132.1	4:27209126-27283847	NOTEST	0	0	0	0	1	1
ENSG00000205832	ENSG00000205832	C16orf96	16:4606490-4650715	NOTEST	0.0228185	0.0278897	0.289523	0	1	1
ENSG00000205835	ENSG00000205835	GMNC	3:190570665-190610218	NOTEST	0	0.00331216	inf	0	1	1
ENSG00000205837	ENSG00000205837	LINC00487	2:6868308-6910442	NOTEST	0	0	0	0	1	1
ENSG00000205846	ENSG00000205846	CLEC6A	12:8608521-8630926	NOTEST	0	0	0	0	1	1
ENSG00000205847	ENSG00000205847	OR7E91P	2:71163011-71306935	NOTEST	0	0	0	0	1	1
ENSG00000205850	ENSG00000205850	AL359736.1	13:24553838-24896673	NOTEST	0	0	0	0	1	1
ENSG00000205856	ENSG00000205856	C22orf42	22:32544992-32555309	NOTEST	0.0668076	0.0436493	-0.614055	0	1	1
ENSG00000205857	ENSG00000205857	NANOGNB	12:7917811-7926717	NOTEST	0	0	0	0	1	1
ENSG00000205858	ENSG00000205858	LRRC72	7:16501105-16621193	NOTEST	0	0	0	0	1	1
ENSG00000205863	ENSG00000205863	C1QTNF9B	13:24304327-24476794	NOTEST	0.0419997	0.0642056	0.612321	0	1	1
ENSG00000205864	ENSG00000205864	KRTAP5-6	11:1718424-1718985	NOTEST	0	0	0	0	1	1
ENSG00000205865	ENSG00000205865	FAM99B	11:1704498-1706859	NOTEST	0	0	0	0	1	1
ENSG00000205866	ENSG00000205866	FAM99A	11:1686826-1689086	NOTEST	0	0	0	0	1	1
ENSG00000205867	ENSG00000205867	KRTAP5-2	11:1575273-1620414	NOTEST	0.023641	0.0366577	0.632829	0	1	1
ENSG00000205869	ENSG00000205869	KRTAP5-1	11:1575273-1620414	NOTEST	0.0192644	0.160907	3.06221	0	1	1
ENSG00000205879	ENSG00000205879	FAM90A2P	8:12029710-12036084	NOTEST	0.0185255	0.0102472	-0.854284	0	1	1
ENSG00000205882	ENSG00000205882	DEFB134	8:11850691-11853821	NOTEST	0.14759	0.152922	0.051196	0	1	1
ENSG00000205883	ENSG00000205883	DEFB135	8:11839829-11842099	NOTEST	0	0.167626	inf	0	1	1
ENSG00000205884	ENSG00000205884	DEFB136	8:11831445-11832108	NOTEST	0	0	0	0	1	1
ENSG00000205885	ENSG00000205885	C1RL-AS1	12:7187512-7275097	NOTEST	0.266508	0.539904	1.01852	0	1	1
ENSG00000205890	ENSG00000205890	RP11-473M20.5	16:3072620-3089134	NOTEST	0	0	0	0	1	1
ENSG00000205897	ENSG00000205897	OR7E136P	7:6906288-6907303	NOTEST	0	0	0	0	1	1
ENSG00000205898	ENSG00000205898	RP11-3B12.4	7:124462439-125019375	NOTEST	0.0737263	0	#NAME?	0	1	1
ENSG00000205899	ENSG00000205899	BHLHA9	17:1173852-1174754	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000205913	ENSG00000205913	SRRM2-AS1	16:2787076-2827298	NOTEST	0.514143	0.465691	-0.142797	0	1	1
ENSG00000205916	ENSG00000205916	DAZ4	Y:26980007-27053183	NOTEST	0	0	0	0	1	1
ENSG00000205922	ENSG00000205922	ONECUT3	19:1752371-1780987	NOTEST	0	0.00439187	inf	0	1	1
ENSG00000205927	ENSG00000205927	OLIG2	21:34285956-34444726	NOTEST	0.0866437	0.126829	0.549722	0	1	1
ENSG00000205929	ENSG00000205929	C21orf62	21:34144410-34266043	NOTEST	0	0	0	0	1	1
ENSG00000205930	ENSG00000205930	C21orf49	21:34144410-34266043	NOTEST	0.430571	0.17717	-1.28111	0	1	1
ENSG00000205936	ENSG00000205936	PPP1R12BP2	Y:25525630-25538844	NOTEST	0	0	0	0	1	1
ENSG00000205940	ENSG00000205940	HSP90AB2P	4:13335037-13340281	NOTEST	0.0454171	0.0449899	-0.0136322	0	1	1
ENSG00000205944	ENSG00000205944	DAZ2	Y:25365593-25437503	NOTEST	0	0	0	0	1	1
ENSG00000205946	ENSG00000205946	USP17L6P	4:9369599-9370796	NOTEST	0	0	0	0	1	1
ENSG00000205955	ENSG00000205955	HSP90AA5P	3:183833139-183835686	NOTEST	0	0	0	0	1	1
ENSG00000205959	ENSG00000205959	RP11-689P11.2	4:8368008-8514337	NOTEST	0.0549739	0.19577	1.83234	0	1	1
ENSG00000205971	ENSG00000205971	AC074389.6	7:1727754-1787590	NOTEST	0	0	0	0	1	1
ENSG00000205976	ENSG00000205976	RP11-404K5.2	5:7299886-7306705	NOTEST	0	0	0	0	1	1
ENSG00000205989	ENSG00000205989	DEFB109	8:7812535-7866277	NOTEST	0	0	0	0	1	1
ENSG00000206013	ENSG00000206013	IFITM5	11:298199-299526	NOTEST	0	0	0	0	1	1
ENSG00000206014	ENSG00000206014	OR7E161P	8:11786100-11787072	NOTEST	0	0	0	0	1	1
ENSG00000206026	ENSG00000206026	SMIM21	18:73118966-73139658	NOTEST	0	0	0	0	1	1
ENSG00000206028	ENSG00000206028	CTA-373H7.7	22:27042391-27176170	NOTEST	0.027314	0.0606244	1.15026	0	1	1
ENSG00000206034	ENSG00000206034	DEFB109P1B	8:7159132-7212876	NOTEST	0	0	0	0	1	1
ENSG00000206042	ENSG00000206042	DEFA7P	8:6896092-6896961	NOTEST	0	0	0	0	1	1
ENSG00000206043	ENSG00000206043	C18orf63	18:71983047-72026422	NOTEST	0	0	0	0	1	1
ENSG00000206044	ENSG00000206044	AC005841.1	12:2904118-3050306	NOTEST	0.218692	0.486501	1.15354	0	1	1
ENSG00000206047	ENSG00000206047	DEFA1	8:6835170-6837602	NOTEST	0	0	0	0	1	1
ENSG00000206052	ENSG00000206052	DOK6	18:67068290-67629039	NOTEST	0.0163594	0.0620618	1.92358	0	1	1
ENSG00000206062	ENSG00000206062	RP13-212L9.1	X:90562779-90563877	NOTEST	0	0	0	0	1	1
ENSG00000206066	ENSG00000206066	IGLL3P	22:25714222-25716047	NOTEST	0	0	0	0	1	1
ENSG00000206069	ENSG00000206069	TMEM211	22:25331076-25342662	NOTEST	0	0	0	0	1	1
ENSG00000206072	ENSG00000206072	SERPINB11	18:61314812-61391127	NOTEST	0	0	0	0	1	1
ENSG00000206073	ENSG00000206073	SERPINB4	18:61304492-61311532	NOTEST	0	0	0	0	1	1
ENSG00000206075	ENSG00000206075	SERPINB5	18:61143993-61172318	NOTEST	0	0	0	0	1	1
ENSG00000206082	ENSG00000206082	LINC01002	19:197074-205074	NOTEST	0	0	0	0	1	1
ENSG00000206090	ENSG00000206090	AP000350.7	22:24282184-24284985	NOTEST	0	0	0	0	1	1
ENSG00000206102	ENSG00000206102	KRTAP19-8	21:32410477-32410795	NOTEST	0	0	0	0	1	1
ENSG00000206104	ENSG00000206104	KRTAP20-3	21:32015182-32015455	NOTEST	0	0	0	0	1	1
ENSG00000206105	ENSG00000206105	KRTAP20-4	21:31992945-31993169	NOTEST	0	0	0	0	1	1
ENSG00000206106	ENSG00000206106	KRTAP22-2	21:31962423-31962716	NOTEST	0	0.272339	inf	0	1	1
ENSG00000206107	ENSG00000206107	KRTAP27-1	21:31709330-31710012	NOTEST	0	0	0	0	1	1
ENSG00000206113	ENSG00000206113	RP11-503N18.1	4:2420700-2734292	NOTEST	0	0.040721	inf	0	1	1
ENSG00000206114	ENSG00000206114	FAM138D	12:147051-149350	NOTEST	0	0	0	0	1	1
ENSG00000206127	ENSG00000206127	GOLGA8O	15:32737306-32747835	NOTEST	0.144074	0.194321	0.431634	0	1	1
ENSG00000206129	ENSG00000206129	CTD-2008L17.2	18:53548918-53858493	NOTEST	0	0	0	0	1	1
ENSG00000206142	ENSG00000206142	FAM230C	22:21655278-21679331	NOTEST	0	0	0	0	1	1
ENSG00000206144	ENSG00000206144	RP11-400K9.2	8:54449619-54452860	NOTEST	0	0	0	0	1	1
ENSG00000206145	ENSG00000206145	P2RX6P	22:21353392-21399306	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206147	ENSG00000206147	RP11-106A1.2	9:6532463-6645650	NOTEST	0	0	0	0	1	1
ENSG00000206150	ENSG00000206150	RNASE13	14:21484921-21572881	NOTEST	0	0	0	0	1	1
ENSG00000206159	ENSG00000206159	GYG2P1	Y:14474826-14532255	NOTEST	0	0	0	0	1	1
ENSG00000206168	ENSG00000206168	Z69890.1	16:281132-281471	NOTEST	0	0.275831	inf	0	1	1
ENSG00000206172	ENSG00000206172	HBA1	16:226678-227521	NOTEST	0	0	0	0	1	1
ENSG00000206177	ENSG00000206177	HBM	16:202685-216767	NOTEST	0.0443351	0.192979	2.12192	0	1	1
ENSG00000206178	ENSG00000206178	HBZP1	16:202685-216767	NOTEST	0	0	0	0	1	1
ENSG00000206181	ENSG00000206181	TCEB3B	18:44388352-44627658	NOTEST	0.00516606	0.0040139	-0.364057	0	1	1
ENSG00000206187	ENSG00000206187	RP11-1084I9.1	15:26147506-26298267	NOTEST	0	0.0303864	inf	0	1	1
ENSG00000206192	ENSG00000206192	ANKRD20A9P	13:19390857-19446107	NOTEST	0	0	0	0	1	1
ENSG00000206199	ENSG00000206199	ANKUB1	3:149478891-149942977	NOTEST	0.0727801	0.128872	0.824327	0	1	1
ENSG00000206203	ENSG00000206203	TSSK2	22:19117791-19132197	NOTEST	0.054941	0	#NAME?	0	1	1
ENSG00000206206	ENSG00000206206	DAXX	HSCHR6_MHC_DBB:33264260-33274971	NOTEST	0	0	0	0	1	1
ENSG00000206208	ENSG00000206208	TAPBP	HSCHR6_MHC_MCF:33437817-33452509	NOTEST	0	0	0	0	1	1
ENSG00000206228	ENSG00000206228	HNRNPA1P4	8:83203858-83204614	NOTEST	0.0466061	0.0753726	0.693523	0	1	1
ENSG00000206232	ENSG00000206232	TAPSAR1	HSCHR6_MHC_DBB:32786474-32825559	NOTEST	0	0	0	0	1	1
ENSG00000206235	ENSG00000206235	TAP2	HSCHR6_MHC_MANN:32943408-32960357	NOTEST	0	0	0	0	1	1
ENSG00000206237	ENSG00000206237	HLA-DQB1	HSCHR6_MHC_COX:32542404-32557884	NOTEST	0	0	0	0	1	1
ENSG00000206240	ENSG00000206240	HLA-DRB1	HSCHR6_MHC_COX:32475946-32506554	NOTEST	0	0	0	0	1	1
ENSG00000206245	ENSG00000206245	C6orf10	HSCHR6_MHC_MANN:32299913-32391764	NOTEST	0	0	0	0	1	1
ENSG00000206249	ENSG00000206249	CTD-2308N23.2	20:36838889-36965907	NOTEST	0	0	0	0	1	1
ENSG00000206256	ENSG00000206256	PPT2	HSCHR6_MHC_COX:32064597-32094350	NOTEST	0	0	0	0	1	1
ENSG00000206258	ENSG00000206258	TNXB	HSCHR6_MHC_MCF:32082522-32172461	NOTEST	0	0	0	0	1	1
ENSG00000206260	ENSG00000206260	PRR23A	3:138722803-139108574	NOTEST	0	0	0	0	1	1
ENSG00000206262	ENSG00000206262	C3orf72	3:138666075-138672293	NOTEST	0.00441064	0.0127704	1.53375	0	1	1
ENSG00000206268	ENSG00000206268	NELFE	HSCHR6_MHC_DBB:31902054-31919714	NOTEST	0	0	0	0	1	1
ENSG00000206279	ENSG00000206279	DAXX	HSCHR6_MHC_QBL:33215185-33225897	NOTEST	0	0	0	0	1	1
ENSG00000206280	ENSG00000206280	ZBTB22	HSCHR6_MHC_QBL:33211031-33214569	NOTEST	0	0	0	0	1	1
ENSG00000206281	ENSG00000206281	TAPBP	HSCHR6_MHC_QBL:33196313-33211013	NOTEST	0	0	0	0	1	1
ENSG00000206282	ENSG00000206282	RGL2	HSCHR6_MHC_QBL:33175726-33196019	NOTEST	0	0	0	0	1	1
ENSG00000206283	ENSG00000206283	PFDN6	HSCHR6_MHC_QBL:33175726-33196019	NOTEST	0	0	0	0	1	1
ENSG00000206284	ENSG00000206284	WDR46	HSCHR6_MHC_QBL:33175726-33196019	NOTEST	0	0	0	0	1	1
ENSG00000206285	ENSG00000206285	B3GALT4	HSCHR6_MHC_QBL:33173758-33175444	NOTEST	0	0	0	0	1	1
ENSG00000206286	ENSG00000206286	VPS52	HSCHR6_MHC_QBL:33146132-33173129	NOTEST	0	0	0	0	1	1
ENSG00000206287	ENSG00000206287	RING1	HSCHR6_MHC_QBL:33105101-33109329	NOTEST	0	0	0	0	1	1
ENSG00000206288	ENSG00000206288	SLC39A7	HSCHR6_MHC_QBL:33090189-33101042	NOTEST	0	0	0	0	1	1
ENSG00000206289	ENSG00000206289	RXRB	HSCHR6_MHC_QBL:33090189-33101042	NOTEST	0	0	0	0	1	1
ENSG00000206290	ENSG00000206290	COL11A2	HSCHR6_MHC_QBL:33059283-33089101	NOTEST	0	0	0	0	1	1
ENSG00000206291	ENSG00000206291	HLA-DPA1	HSCHR6_MHC_QBL:32961399-32984034	NOTEST	0	0	0	0	1	1
ENSG00000206292	ENSG00000206292	HLA-DOA	HSCHR6_MHC_QBL:32900650-32906085	NOTEST	0	0	0	0	1	1
ENSG00000206296	ENSG00000206296	TAPSAR1	HSCHR6_MHC_QBL:32737203-32776334	NOTEST	0	0	0	0	1	1
ENSG00000206297	ENSG00000206297	TAP1	HSCHR6_MHC_QBL:32737203-32776334	NOTEST	0	0	0	0	1	1
ENSG00000206298	ENSG00000206298	PSMB8	HSCHR6_MHC_QBL:32737203-32776334	NOTEST	0	0	0	0	1	1
ENSG00000206299	ENSG00000206299	TAP2	HSCHR6_MHC_QBL:32718319-32735268	NOTEST	0	0	0	0	1	1
ENSG00000206301	ENSG00000206301	HLA-DQA2	HSCHR6_MHC_MCF:32742903-32748772	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206302	ENSG00000206302	HLA-DQB1	HSCHR6_MHC_QBL:32547664-32563145	NOTEST	0	0	0	0	1	1
ENSG00000206305	ENSG00000206305	HLA-DQA1	HSCHR6_MHC_QBL:32538583-32544863	NOTEST	0	0	0	0	1	1
ENSG00000206306	ENSG00000206306	HLA-DRB1	HSCHR6_MHC_QBL:32481202-32511820	NOTEST	0	0	0	0	1	1
ENSG00000206308	ENSG00000206308	HLA-DRA	HSCHR6_MHC_QBL:32365089-32370300	NOTEST	0	0	0	0	1	1
ENSG00000206310	ENSG00000206310	C6orf10	HSCHR6_MHC_QBL:32218296-32297155	NOTEST	0	0	0	0	1	1
ENSG00000206312	ENSG00000206312	NOTCH4	HSCHR6_MHC_QBL:32116163-32149468	NOTEST	0	0	0	0	1	1
ENSG00000206314	ENSG00000206314	GPSM3	HSCHR6_MHC_QBL:32116163-32149468	NOTEST	0	0	0	0	1	1
ENSG00000206315	ENSG00000206315	PBX2	HSCHR6_MHC_QBL:32110132-32115584	NOTEST	0	0	0	0	1	1
ENSG00000206320	ENSG00000206320	AGER	HSCHR6_MHC_QBL:32106367-32109724	NOTEST	0	0	0	0	1	1
ENSG00000206324	ENSG00000206324	AGPAT1	HSCHR6_MHC_QBL:32073754-32103496	NOTEST	0	0	0	0	1	1
ENSG00000206329	ENSG00000206329	PPT2	HSCHR6_MHC_QBL:32073754-32103496	NOTEST	0	0	0	0	1	1
ENSG00000206331	ENSG00000206331	PRRT1	HSCHR6_MHC_QBL:32073754-32103496	NOTEST	0	0	0	0	1	1
ENSG00000206337	ENSG00000206337	HCP5	6:31368478-31445283	NOTEST	0.43575	0.576185	0.403031	0	1	1
ENSG00000206338	ENSG00000206338	CYP21A2	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000206340	ENSG00000206340	C4A	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000206342	ENSG00000206342	STK19	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000206344	ENSG00000206344	HCG27	6:31162976-31171745	NOTEST	0.190876	0.08489	-1.16897	0	1	1
ENSG00000206346	ENSG00000206346	DXO	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000206353	ENSG00000206353	SKIV2L	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000206355	ENSG00000206355	CCHCR1	HSCHR6_MHC_DBB:31103948-31119721	NOTEST	0	0	0	0	1	1
ENSG00000206356	ENSG00000206356	RP11-93O17.2	5:98858014-98861166	NOTEST	0	0	0	0	1	1
ENSG00000206357	ENSG00000206357	NELFE	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000206366	ENSG00000206366	ZBTB12	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000206372	ENSG00000206372	C2	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000206376	ENSG00000206376	EHMT2	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000206378	ENSG00000206378	SLC44A4	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000206379	ENSG00000206379	FLOT1	HSCHR6_MHC_DBB:30685746-30700772	NOTEST	0	0	0	0	1	1
ENSG00000206380	ENSG00000206380	C6orf48	HSCHR6_MHC_QBL:31792646-31797799	NOTEST	0	0	0	0	1	1
ENSG00000206383	ENSG00000206383	HSPA1L	HSCHR6_MHC_QBL:31767646-31773092	NOTEST	0	0	0	0	1	1
ENSG00000206384	ENSG00000206384	COL6A6	3:130279177-130396999	NOTEST	0.0234726	0.0212571	-0.143029	0	1	1
ENSG00000206394	ENSG00000206394	CLIC1	HSCHR6_MHC_QBL:31685047-31697781	NOTEST	0	0	0	0	1	1
ENSG00000206395	ENSG00000206395	DDAH2	HSCHR6_MHC_QBL:31685047-31697781	NOTEST	0	0	0	0	1	1
ENSG00000206396	ENSG00000206396	C6orf25	HSCHR6_MHC_QBL:31676606-31684720	NOTEST	0	0	0	0	1	1
ENSG00000206398	ENSG00000206398	LY6G6C	HSCHR6_MHC_QBL:31676606-31684720	NOTEST	0	0	0	0	1	1
ENSG00000206401	ENSG00000206401	LY6G6E	HSCHR6_MHC_QBL:31664900-31675931	NOTEST	0	0	0	0	1	1
ENSG00000206402	ENSG00000206402	LY6G6D	HSCHR6_MHC_QBL:31664900-31675931	NOTEST	0	0	0	0	1	1
ENSG00000206403	ENSG00000206403	ABHD16A	HSCHR6_MHC_QBL:31644971-31661447	NOTEST	0	0	0	0	1	1
ENSG00000206404	ENSG00000206404	LY6G5C	HSCHR6_MHC_QBL:31634706-31642059	NOTEST	0	0	0	0	1	1
ENSG00000206406	ENSG00000206406	CSNK2B	HSCHR6_MHC_QBL:31619245-31631569	NOTEST	0	0	0	0	1	1
ENSG00000206408	ENSG00000206408	GPANK1	HSCHR6_MHC_QBL:31619245-31631569	NOTEST	0	0	0	0	1	1
ENSG00000206409	ENSG00000206409	APOM	HSCHR6_MHC_QBL:31597039-31616227	NOTEST	0	0	0	0	1	1
ENSG00000206412	ENSG00000206412	GNL1	HSCHR6_MHC_APD:30517399-30529581	NOTEST	0	0	0	0	1	1
ENSG00000206422	ENSG00000206422	LRRC30	18:7231122-7232045	NOTEST	0	0	0	0	1	1
ENSG00000206427	ENSG00000206427	PRRC2A	HSCHR6_MHC_QBL:31578693-31595788	NOTEST	0	0	0	0	1	1
ENSG00000206428	ENSG00000206428	AIF1	HSCHR6_MHC_QBL:31573204-31575042	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206430	ENSG00000206430	NCR3	HSCHR6_MHC_QBL:31544143-31551005	NOTEST	0	0	0	0	1	1
ENSG00000206433	ENSG00000206433	LST1	HSCHR6_MHC_QBL:31544143-31551005	NOTEST	0	0	0	0	1	1
ENSG00000206435	ENSG00000206435	HLA-C	HSCHR6_MHC_SSTO:31229146-31232539	NOTEST	0	0	0	0	1	1
ENSG00000206437	ENSG00000206437	LTB	HSCHR6_MHC_QBL:31538574-31540542	NOTEST	0	0	0	0	1	1
ENSG00000206439	ENSG00000206439	TNF	HSCHR6_MHC_QBL:31533584-31536356	NOTEST	0	0	0	0	1	1
ENSG00000206440	ENSG00000206440	NFKBIL1	HSCHR6_MHC_QBL:31504920-31516872	NOTEST	0	0	0	0	1	1
ENSG00000206444	ENSG00000206444	HLA-V	HSCHR6_MHC_QBL:29756043-29762764	NOTEST	0	0	0	0	1	1
ENSG00000206445	ENSG00000206445	ATP6V1G2	HSCHR6_MHC_QBL:31486777-31504899	NOTEST	0	0	0	0	1	1
ENSG00000206446	ENSG00000206446	DAQB-335A13.8	HSCHR6_MHC_COX:29684536-29710797	NOTEST	0	0	0	0	1	1
ENSG00000206447	ENSG00000206447	MCCD1	HSCHR6_MHC_QBL:31486777-31504899	NOTEST	0	0	0	0	1	1
ENSG00000206448	ENSG00000206448	PPIAP30	10:15137383-15210692	NOTEST	0	0	0	0	1	1
ENSG00000206449	ENSG00000206449	MICB	HSCHR6_MHC_QBL:31456184-31469201	NOTEST	0	0	0	0	1	1
ENSG00000206450	ENSG00000206450	HLA-B	HSCHR6_MHC_QBL:31311767-31315097	NOTEST	0	0	0	0	1	1
ENSG00000206452	ENSG00000206452	HLA-C	HSCHR6_MHC_QBL:31226379-31229751	NOTEST	0	0	0	0	1	1
ENSG00000206454	ENSG00000206454	POU5F1	HSCHR6_MHC_QBL:31118772-31130942	NOTEST	0	0	0	0	1	1
ENSG00000206455	ENSG00000206455	TCF19	HSCHR6_MHC_QBL:31118772-31130942	NOTEST	0	0	0	0	1	1
ENSG00000206457	ENSG00000206457	CCHCR1	HSCHR6_MHC_QBL:31102652-31118444	NOTEST	0	0	0	0	1	1
ENSG00000206458	ENSG00000206458	PSORS1C1	HSCHR6_MHC_QBL:31074947-31100262	NOTEST	0	0	0	0	1	1
ENSG00000206459	ENSG00000206459	PSORS1C2	HSCHR6_MHC_QBL:31074947-31100262	NOTEST	0	0	0	0	1	1
ENSG00000206460	ENSG00000206460	CDSN	HSCHR6_MHC_QBL:31074947-31100262	NOTEST	0	0	0	0	1	1
ENSG00000206461	ENSG00000206461	C6orf15	HSCHR6_MHC_QBL:31071420-31072757	NOTEST	0	0	0	0	1	1
ENSG00000206463	ENSG00000206463	C6orf205	HSCHR6_MHC_QBL:30941072-30947468	NOTEST	0	0	0	0	1	1
ENSG00000206465	ENSG00000206465	SFTA2	HSCHR6_MHC_QBL:30888703-30889526	NOTEST	0	0	0	0	1	1
ENSG00000206466	ENSG00000206466	GABBR1	HSCHR6_MHC_MCF:29523203-29600766	NOTEST	0	0	0	0	1	1
ENSG00000206467	ENSG00000206467	OR2H2	HSCHR6_MHC_MCF:29523203-29600766	NOTEST	0	0	0	0	1	1
ENSG00000206468	ENSG00000206468	UBD	HSCHR6_MHC_MCF:29523203-29600766	NOTEST	0	0	0	0	1	1
ENSG00000206470	ENSG00000206470	MAS1L	HSCHR6_MHC_MCF:29454258-29455523	NOTEST	0	0	0	0	1	1
ENSG00000206471	ENSG00000206471	OR2H1	HSCHR6_MHC_MCF:29424742-29431890	NOTEST	0	0	0	0	1	1
ENSG00000206472	ENSG00000206472	OR11A1	HSCHR6_MHC_MCF:29323243-29424633	NOTEST	0	0	0	0	1	1
ENSG00000206474	ENSG00000206474	OR10C1	6:29323006-29424848	NOTEST	0	0	0	0	1	1
ENSG00000206476	ENSG00000206476	VARS2	HSCHR6_MHC_QBL:30865548-30883835	NOTEST	0	0	0	0	1	1
ENSG00000206478	ENSG00000206478	IER3	HSCHR6_MHC_QBL:30700507-30701863	NOTEST	0	0	0	0	1	1
ENSG00000206480	ENSG00000206480	FLOT1	HSCHR6_MHC_QBL:30685020-30700042	NOTEST	0	0	0	0	1	1
ENSG00000206481	ENSG00000206481	MDC1	HSCHR6_MHC_QBL:30657118-30675200	NOTEST	0	0	0	0	1	1
ENSG00000206483	ENSG00000206483	TXNRD3NB	3:126290621-126373998	NOTEST	0.0102146	0	#NAME?	0	1	1
ENSG00000206484	ENSG00000206484	NRM	HSCHR6_MHC_QBL:30645359-30648733	NOTEST	0	0	0	0	1	1
ENSG00000206485	ENSG00000206485	PPP1R18	HSCHR6_MHC_QBL:30633701-30645208	NOTEST	0	0	0	0	1	1
ENSG00000206486	ENSG00000206486	DHX16	HSCHR6_MHC_QBL:30604325-30630349	NOTEST	0	0	0	0	1	1
ENSG00000206487	ENSG00000206487	C6orf136	HSCHR6_MHC_QBL:30604325-30630349	NOTEST	0	0	0	0	1	1
ENSG00000206488	ENSG00000206488	ATAT1	HSCHR6_MHC_QBL:30584128-30604110	NOTEST	0	0	0	0	1	1
ENSG00000206489	ENSG00000206489	PPP1R10	HSCHR6_MHC_QBL:30557687-30583682	NOTEST	0	0	0	0	1	1
ENSG00000206490	ENSG00000206490	ABCF1	HSCHR6_MHC_QBL:30528661-30554466	NOTEST	0	0	0	0	1	1
ENSG00000206491	ENSG00000206491	PRR3	HSCHR6_MHC_QBL:30498659-30521007	NOTEST	0	0	0	0	1	1
ENSG00000206492	ENSG00000206492	GNL1	HSCHR6_MHC_QBL:30498659-30521007	NOTEST	0	0	0	0	1	1
ENSG00000206493	ENSG00000206493	HLA-E	HSCHR6_MHC_QBL:30446761-30451500	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206495	ENSG00000206495	TRIM39	HSCHR6_MHC_QBL:30191333-30304165	NOTEST	0	0	0	0	1	1
ENSG00000206500	ENSG00000206500	RNF39	HSCHR6_MHC_QBL:30024067-30033205	NOTEST	0	0	0	0	1	1
ENSG00000206501	ENSG00000206501	PPP1R11	HSCHR6_MHC_QBL:30024067-30033205	NOTEST	0	0	0	0	1	1
ENSG00000206502	ENSG00000206502	ZNRD1	HSCHR6_MHC_QBL:29958304-30022269	NOTEST	0	0	0	0	1	1
ENSG00000206504	ENSG00000206504	HCG9	HSCHR6_MHC_QBL:29932283-29935585	NOTEST	0	0	0	0	1	1
ENSG00000206505	ENSG00000206505	HLA-A	HSCHR6_MHC_QBL:29898416-29903057	NOTEST	0	0	0	0	1	1
ENSG00000206506	ENSG00000206506	HLA-G	HSCHR6_MHC_QBL:29791931-29796106	NOTEST	0	0	0	0	1	1
ENSG00000206507	ENSG00000206507	HLA-V	HSCHR6_MHC_APD:29758889-29765609	NOTEST	0	0	0	0	1	1
ENSG00000206508	ENSG00000206508	DAQB-335A13.26	HSCHR6_MHC_QBL:29688013-29714292	NOTEST	0	0	0	0	1	1
ENSG00000206509	ENSG00000206509	HLA-F	HSCHR6_MHC_QBL:29688013-29714292	NOTEST	0	0	0	0	1	1
ENSG00000206510	ENSG00000206510	ZFP57	HSCHR6_MHC_QBL:29640091-29648802	NOTEST	0	0	0	0	1	1
ENSG00000206511	ENSG00000206511	GABBR1	HSCHR6_MHC_QBL:29523309-29600897	NOTEST	0	0	0	0	1	1
ENSG00000206512	ENSG00000206512	OR2H2	HSCHR6_MHC_QBL:29523309-29600897	NOTEST	0	0	0	0	1	1
ENSG00000206513	ENSG00000206513	UBD	HSCHR6_MHC_QBL:29523309-29600897	NOTEST	0	0	0	0	1	1
ENSG00000206515	ENSG00000206515	MAS1L	HSCHR6_MHC_QBL:29454361-29455626	NOTEST	0	0	0	0	1	1
ENSG00000206516	ENSG00000206516	OR2H1	HSCHR6_MHC_QBL:29424844-29431993	NOTEST	0	0	0	0	1	1
ENSG00000206517	ENSG00000206517	OR11A1	HSCHR6_MHC_QBL:29384950-29424735	NOTEST	0	0	0	0	1	1
ENSG00000206519	ENSG00000206519	RPL13AP	HSCHR6_MHC_QBL:29523309-29600897	NOTEST	0	0	0	0	1	1
ENSG00000206522	ENSG00000206522	OR2J3	HSCHR6_MHC_QBL:29079674-29080610	NOTEST	0	0	0	0	1	1
ENSG00000206523	ENSG00000206523	OR2J1	HSCHR6_MHC_QBL:29068728-29069667	NOTEST	0	0	0	0	1	1
ENSG00000206524	ENSG00000206524	OR2B3	HSCHR6_MHC_QBL:29053986-29055092	NOTEST	0	0	0	0	1	1
ENSG00000206525	ENSG00000206525	OR2W1	HSCHR6_MHC_QBL:29011989-29013017	NOTEST	0	0	0	0	1	1
ENSG00000206526	ENSG00000206526	C6orf100	HSCHR6_MHC_QBL:28911656-28912317	NOTEST	0	0	0	0	1	1
ENSG00000206531	ENSG00000206531	CD200R1L	3:112534555-112565703	NOTEST	0	0	0	0	1	1
ENSG00000206532	ENSG00000206532	RP11-553A10.1	3:110607230-110612323	NOTEST	0.188593	0.0854837	-1.14156	0	1	1
ENSG00000206536	ENSG00000206536	OR5K3	3:97952494-98176742	NOTEST	0	0	0	0	1	1
ENSG00000206538	ENSG00000206538	VGLL3	3:86987118-87040269	NOTEST	0.00406807	0.00101814	-1.99841	0	1	1
ENSG00000206549	ENSG00000206549	PRSS50	3:46753604-46854064	NOTEST	0	0.00934847	inf	0	1	1
ENSG00000206552	ENSG00000206552	KRBOX1-AS1	3:42846243-43101703	NOTEST	0	0	0	0	1	1
ENSG00000206557	ENSG00000206557	TRIM71	3:32859509-32939318	NOTEST	0.0520263	0.150851	1.53581	0	1	1
ENSG00000206559	ENSG00000206559	ZCWPW2	3:28390636-28579613	NOTEST	0.612756	0.345341	-0.82729	0	1	1
ENSG00000206561	ENSG00000206561	COLQ	3:15422781-15563258	NOTEST	0.270805	0.0909514	-1.57408	0	1	1
ENSG00000206579	ENSG00000206579	XKR4	8:56014948-56454613	NOTEST	0	0	0	0	1	1
ENSG00000206582	ENSG00000206582	Y_RNA	20:33104213-33128762	NOTEST	0	0	0	0	1	1
ENSG00000206583	ENSG00000206583	RNU6-1292P	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000206585	ENSG00000206585	RNVU1-9	1:147511003-147511167	NOTEST	0	0	0	0	1	1
ENSG00000206587	ENSG00000206587	RNU6-46P	11:67653947-67673821	NOTEST	0	0	0	0	1	1
ENSG00000206588	ENSG00000206588	RNU1-28P	14:35025431-35025595	NOTEST	0	0	0	0	1	1
ENSG00000206589	ENSG00000206589	RNU6-354P	15:44019115-44095241	NOTEST	0	0	0	0	1	1
ENSG00000206590	ENSG00000206590	RNU6-132P	15:90234027-90286869	NOTEST	0	0	0	0	1	1
ENSG00000206592	ENSG00000206592	SNORA18	5:78293437-78531861	NOTEST	0	0	0	0	1	1
ENSG00000206593	ENSG00000206593	RNU6-47P	5:108083522-108532542	NOTEST	0	0	0	0	1	1
ENSG00000206595	ENSG00000206595	RNU6-877P	1:51819934-52027301	NOTEST	0	0	0	0	1	1
ENSG00000206596	ENSG00000206596	RNU1-27P	14:35015919-35016083	NOTEST	0	0	0	0	1	1
ENSG00000206597	ENSG00000206597	SNORA57	11:62414319-62441159	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206598	ENSG00000206598	RNU6-1286P	6:121675499-121675606	NOTEST	0	0	0	0	1	1
ENSG00000206599	ENSG00000206599	RNU6-841P	19:50267780-50267887	NOTEST	0	0	0	0	1	1
ENSG00000206600	ENSG00000206600	RNU6-25P	3:194789007-194991896	NOTEST	0	0	0	0	1	1
ENSG00000206601	ENSG00000206601	RNU6-431P	4:109571739-109588976	NOTEST	0	0	0	0	1	1
ENSG00000206602	ENSG00000206602	SNORD58A	18:47008027-47018906	NOTEST	0	0	0	0	1	1
ENSG00000206603	ENSG00000206603	SNORA22	7:56119322-56131682	NOTEST	0	5.70356	inf	0	1	1
ENSG00000206604	ENSG00000206604	RNU6-425P	3:141663269-141868386	NOTEST	0	0	0	0	1	1
ENSG00000206605	ENSG00000206605	RNU6-946P	10:26986587-27150016	NOTEST	0	0	0	0	1	1
ENSG00000206606	ENSG00000206606	RNU6-1296P	5:50463374-50463481	NOTEST	0	0	0	0	1	1
ENSG00000206609	ENSG00000206609	SNORD116-11	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000206611	ENSG00000206611	SNORD24	9:136215068-136218281	NOTEST	0	0	0	0	1	1
ENSG00000206612	ENSG00000206612	SNORA2A	12:49047183-49076021	NOTEST	0	0	0	0	1	1
ENSG00000206613	ENSG00000206613	RNU6-1336P	4:169277885-169931426	NOTEST	0	0	0	0	1	1
ENSG00000206614	ENSG00000206614	RNU6-477P	5:168979452-168979559	NOTEST	0	0	0	0	1	1
ENSG00000206615	ENSG00000206615	RNU6-338P	22:31784718-31784823	NOTEST	0	0	0	0	1	1
ENSG00000206616	ENSG00000206616	RNU6-741P	15:24022583-24022690	NOTEST	0	0	0	0	1	1
ENSG00000206617	ENSG00000206617	RNY1P5	13:74863236-74863351	NOTEST	0	0	0	0	1	1
ENSG00000206618	ENSG00000206618	RNU6-1264P	17:6110482-6110589	NOTEST	0	0	0	0	1	1
ENSG00000206620	ENSG00000206620	SNORD45C	1:76190035-76260764	NOTEST	0	0	0	0	1	1
ENSG00000206621	ENSG00000206621	SNORD116-14	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000206622	ENSG00000206622	SNORA69	X:118920466-118925606	NOTEST	0	0	0	0	1	1
ENSG00000206623	ENSG00000206623	RNU6-979P	7:27773013-28283536	NOTEST	0	0	0	0	1	1
ENSG00000206624	ENSG00000206624	RNU1-39P	5:178286953-178315123	NOTEST	0.00987517	0	#NAME?	0	1	1
ENSG00000206625	ENSG00000206625	RNU6-1	15:68112041-68166204	NOTEST	0	0	0	0	1	1
ENSG00000206627	ENSG00000206627	RNU6-969P	1:53192125-53293014	NOTEST	0	0	0	0	1	1
ENSG00000206629	ENSG00000206629	RNU1-63P	4:68283022-68333969	NOTEST	0	0	0	0	1	1
ENSG00000206630	ENSG00000206630	SNORD60	16:2204797-2205359	NOTEST	0	0	0	0	1	1
ENSG00000206631	ENSG00000206631	RNU6-657P	10:95753745-96122716	NOTEST	0	0	0	0	1	1
ENSG00000206633	ENSG00000206633	SNORA80B	2:10580093-10588630	NOTEST	0	0	0	0	1	1
ENSG00000206634	ENSG00000206634	SNORA22	7:65216128-65228341	NOTEST	0	10.7086	inf	0	1	1
ENSG00000206635	ENSG00000206635	RNU6-1062P	1:151584513-151671567	NOTEST	0	0	0	0	1	1
ENSG00000206636	ENSG00000206636	Y_RNA	12:8128854-8128956	NOTEST	0	0	0	0	1	1
ENSG00000206637	ENSG00000206637	SNORA70	1:201947588-201947723	NOTEST	0	0	0	0	1	1
ENSG00000206638	ENSG00000206638	RNU6-672P	11:72525352-72853306	NOTEST	0	0	0	0	1	1
ENSG00000206639	ENSG00000206639	Y_RNA	X:21857753-21903542	NOTEST	0	0	0	0	1	1
ENSG00000206640	ENSG00000206640	Y_RNA	1:185126211-185260897	NOTEST	0	0	0	0	1	1
ENSG00000206641	ENSG00000206641	RNU6-449P	15:54056400-54056507	NOTEST	0	0	0	0	1	1
ENSG00000206644	ENSG00000206644	RNU6-1279P	3:196074532-196160242	NOTEST	0	0	0	0	1	1
ENSG00000206645	ENSG00000206645	Y_RNA	3:37034822-37225180	NOTEST	0	0	0	0	1	1
ENSG00000206646	ENSG00000206646	Y_RNA	X:67262185-67653755	NOTEST	0	0	0	0	1	1
ENSG00000206647	ENSG00000206647	SNORA2	2:10281508-10351851	NOTEST	0	0	0	0	1	1
ENSG00000206649	ENSG00000206649	SNORA20	8:81177762-81252075	NOTEST	0	0	0	0	1	1
ENSG00000206650	ENSG00000206650	SNORA70G	12:69004618-69054372	NOTEST	0	0	0	0	1	1
ENSG00000206651	ENSG00000206651	Y_RNA	1:156433518-156470620	NOTEST	0	0	0	0	1	1
ENSG00000206652	ENSG00000206652	RNU1-1	1:16840616-16840780	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206654	ENSG00000206654	RNU6-608P	1:39546987-39952849	NOTEST	0	0	0	0	1	1
ENSG00000206656	ENSG00000206656	SNORD116-17	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000206658	ENSG00000206658	RNU6-1039P	9:113127530-113342160	NOTEST	0	0	0	0	1	1
ENSG00000206659	ENSG00000206659	Y_RNA	1:174968299-174992561	NOTEST	0	0	0	0	1	1
ENSG00000206660	ENSG00000206660	Y_RNA	10:32345673-32345767	NOTEST	0	0	0	0	1	1
ENSG00000206661	ENSG00000206661	SNORA70	8:4985800-4985934	NOTEST	0	0	0	0	1	1
ENSG00000206662	ENSG00000206662	Y_RNA	12:17863867-17863980	NOTEST	0	0	0	0	1	1
ENSG00000206663	ENSG00000206663	Y_RNA	X:20003175-20003277	NOTEST	0	0	0	0	1	1
ENSG00000206665	ENSG00000206665	RNU6-573P	4:35497519-35497625	NOTEST	0	0	0	0	1	1
ENSG00000206668	ENSG00000206668	Y_RNA	GL000195.1:37433-37534	NOTEST	0	0	0	0	1	1
ENSG00000206669	ENSG00000206669	Y_RNA	19:37288419-37407193	NOTEST	0	0	0	0	1	1
ENSG00000206671	ENSG00000206671	RNU6-471P	6:27564190-27564296	NOTEST	0	0	0	0	1	1
ENSG00000206672	ENSG00000206672	Y_RNA	6:68335248-68335357	NOTEST	0	0	0	0	1	1
ENSG00000206674	ENSG00000206674	RNU6-945P	19:40805384-40805491	NOTEST	0	0	0	0	1	1
ENSG00000206675	ENSG00000206675	RNU6-32P	4:39289075-39367995	NOTEST	0	0	0	0	1	1
ENSG00000206676	ENSG00000206676	Y_RNA	15:37181405-37393504	NOTEST	0	0	0	0	1	1
ENSG00000206677	ENSG00000206677	Y_RNA	X:40352091-40352192	NOTEST	0	0	0	0	1	1
ENSG00000206678	ENSG00000206678	RNU6-144P	8:138117594-138117701	NOTEST	0	0	0	0	1	1
ENSG00000206679	ENSG00000206679	Y_RNA	1:95582893-95729610	NOTEST	0	0	0	0	1	1
ENSG00000206680	ENSG00000206680	SNORD21	1:93297581-93307481	NOTEST	0	0	0	0	1	1
ENSG00000206681	ENSG00000206681	RNU6-730P	6:165740775-166401536	NOTEST	0	0	0	0	1	1
ENSG00000206682	ENSG00000206682	Y_RNA	5:31400603-31532303	NOTEST	0	0	0	0	1	1
ENSG00000206684	ENSG00000206684	RNU6-157P	1:171810620-172437971	NOTEST	0	0	0	0	1	1
ENSG00000206685	ENSG00000206685	RNU6-1189P	X:46937774-46952712	NOTEST	0	0	0	0	1	1
ENSG00000206686	ENSG00000206686	RNU6-1036P	5:180434280-180434384	NOTEST	0	0	0	0	1	1
ENSG00000206687	ENSG00000206687	RNU1-109P	18:721587-812547	NOTEST	0	0	0	0	1	1
ENSG00000206688	ENSG00000206688	SNORD116-18	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000206690	ENSG00000206690	Y_RNA	11:87831758-87908635	NOTEST	0	0	0	0	1	1
ENSG00000206692	ENSG00000206692	Y_RNA	1:171216718-171255117	NOTEST	0	0	0	0	1	1
ENSG00000206693	ENSG00000206693	SNORA56	X:153991030-154005964	NOTEST	0	0	0	0	1	1
ENSG00000206694	ENSG00000206694	RNVU1-3	1:143647637-143745417	NOTEST	0	0	0	0	1	1
ENSG00000206695	ENSG00000206695	RNU6-442P	8:126913194-126913298	NOTEST	0	0	0	0	1	1
ENSG00000206697	ENSG00000206697	RNY1P8	13:73801283-73801397	NOTEST	0	0	0	0	1	1
ENSG00000206698	ENSG00000206698	RNU1-73P	5:96424778-96772921	NOTEST	0	0.654506	inf	0	1	1
ENSG00000206699	ENSG00000206699	Y_RNA	8:100025493-100906290	NOTEST	0	0	0	0	1	1
ENSG00000206700	ENSG00000206700	RNU6-723P	1:48761043-48937845	NOTEST	0	0	0	0	1	1
ENSG00000206701	ENSG00000206701	RNU6-1040P	8:85095021-85834079	NOTEST	0	0	0	0	1	1
ENSG00000206702	ENSG00000206702	RNU1-11P	6:12717892-13328815	NOTEST	0	0	0	0	1	1
ENSG00000206703	ENSG00000206703	RNU6-128P	4:159690289-159959912	NOTEST	0	0	0	0	1	1
ENSG00000206704	ENSG00000206704	Y_RNA	1:29213602-29450447	NOTEST	0	0	0	0	1	1
ENSG00000206705	ENSG00000206705	Y_RNA	7:135777672-136122174	NOTEST	0	0	0	0	1	1
ENSG00000206706	ENSG00000206706	Y_RNA	16:16404197-16444447	NOTEST	0	0	0	0	1	1
ENSG00000206708	ENSG00000206708	RNU6-1227P	3:39067477-39067584	NOTEST	0	0	0	0	1	1
ENSG00000206709	ENSG00000206709	RNU6-1080P	7:72742166-72772634	NOTEST	0	0	0	0	1	1
ENSG00000206710	ENSG00000206710	RNU6-147P	20:48588642-48588749	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206711	ENSG00000206711	Y_RNA	4:167234086-167234186	NOTEST	0	0	0	0	1	1
ENSG00000206712	ENSG00000206712	RNU6-26P	3:98433173-98620533	NOTEST	0	0	0	0	1	1
ENSG00000206713	ENSG00000206713	Y_RNA	17:73083821-73102257	NOTEST	0	0	0	0	1	1
ENSG00000206714	ENSG00000206714	Y_RNA	5:77612859-77612961	NOTEST	0	0	0	0	1	1
ENSG00000206715	ENSG00000206715	RNU6-444P	6:88117700-88222054	NOTEST	0	0	0	0	1	1
ENSG00000206716	ENSG00000206716	RNU6-133P	X:21232754-21232861	NOTEST	0	0	0	0	1	1
ENSG00000206717	ENSG00000206717	Y_RNA	6:34759856-34855866	NOTEST	0	0	0	0	1	1
ENSG00000206718	ENSG00000206718	RNU6-546P	2:156186932-156187039	NOTEST	0	0	0	0	1	1
ENSG00000206719	ENSG00000206719	Y_RNA	8:114963114-114963227	NOTEST	0	0	0	0	1	1
ENSG00000206721	ENSG00000206721	Y_RNA	3:119883491-120003941	NOTEST	0	0	0	0	1	1
ENSG00000206722	ENSG00000206722	RNU6-1074P	4:140177810-140177914	NOTEST	0	0	0	0	1	1
ENSG00000206723	ENSG00000206723	RNU6-1056P	X:48553944-48595570	NOTEST	0	0	0	0	1	1
ENSG00000206724	ENSG00000206724	RNU6-756P	8:125272886-125272993	NOTEST	0	0	0	0	1	1
ENSG00000206725	ENSG00000206725	RNU6-1027P	2:230628553-230877825	NOTEST	0	0	0	0	1	1
ENSG00000206726	ENSG00000206726	RNU6-259P	2:125746795-125746902	NOTEST	0	0	0	0	1	1
ENSG00000206727	ENSG00000206727	SNORD116-9	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000206728	ENSG00000206728	Y_RNA	3:23244510-23633284	NOTEST	0	0	0	0	1	1
ENSG00000206729	ENSG00000206729	RNU6-1126P	7:55857060-55857167	NOTEST	0	0	0	0	1	1
ENSG00000206730	ENSG00000206730	RNU6-468P	17:17408876-17513799	NOTEST	0	0	0	0	1	1
ENSG00000206731	ENSG00000206731	SNORA36	2:27805896-27917840	NOTEST	0	0	0	0	1	1
ENSG00000206732	ENSG00000206732	RNU6-936P	2:24714782-24993571	NOTEST	0	0	0	0	1	1
ENSG00000206733	ENSG00000206733	RNU6-641P	X:36040055-36040162	NOTEST	0	0	0	0	1	1
ENSG00000206734	ENSG00000206734	Y_RNA	17:45600307-45726786	NOTEST	0	0	0	0	1	1
ENSG00000206737	ENSG00000206737	RNVU1-18	1:149224057-149224221	NOTEST	0	0.701066	inf	0	1	1
ENSG00000206738	ENSG00000206738	Y_RNA	4:2420700-2734292	NOTEST	0	0	0	0	1	1
ENSG00000206739	ENSG00000206739	Y_RNA	22:19023794-19115962	NOTEST	0	0	0	0	1	1
ENSG00000206741	ENSG00000206741	Y_RNA	5:172206984-172207097	NOTEST	0	0	0	0	1	1
ENSG00000206743	ENSG00000206743	RNU6-484P	5:37379313-37753537	NOTEST	0	0	0	0	1	1
ENSG00000206744	ENSG00000206744	RNU6-620P	5:82933623-83017432	NOTEST	0	0	0	0	1	1
ENSG00000206745	ENSG00000206745	RNU6-643P	6:41270203-41270310	NOTEST	0	0	0	0	1	1
ENSG00000206746	ENSG00000206746	RNU6-142P	18:60382671-60647666	NOTEST	0	0	0	0	1	1
ENSG00000206747	ENSG00000206747	RNU6-245P	X:67759284-67759391	NOTEST	0	0	0	0	1	1
ENSG00000206749	ENSG00000206749	RNU6-1083P	12:58156116-58212487	NOTEST	0	0	0	0	1	1
ENSG00000206750	ENSG00000206750	Y_RNA	GL000205.1:81438-81539	NOTEST	0	0	0	0	1	1
ENSG00000206751	ENSG00000206751	Y_RNA	14:73086003-73360809	NOTEST	0	0	0	0	1	1
ENSG00000206752	ENSG00000206752	RNU6-1323P	X:115984806-115984913	NOTEST	0	0	0	0	1	1
ENSG00000206754	ENSG00000206754	SNORD101	6:133135579-133138703	NOTEST	0	0	0	0	1	1
ENSG00000206755	ENSG00000206755	SNORA30	16:30709029-30787628	NOTEST	0	0	0	0	1	1
ENSG00000206756	ENSG00000206756	Y_RNA	10:75910959-76469061	NOTEST	0	0	0	0	1	1
ENSG00000206758	ENSG00000206758	RNU6-317P	19:49296408-49296515	NOTEST	0	0	0	0	1	1
ENSG00000206759	ENSG00000206759	RNU6-787P	3:66119284-66551687	NOTEST	0	0	0	0	1	1
ENSG00000206760	ENSG00000206760	SNORA6	3:39448179-39454033	NOTEST	0	0	0	0	1	1
ENSG00000206761	ENSG00000206761	U3	14:101611817-101612032	NOTEST	0	0	0	0	1	1
ENSG00000206762	ENSG00000206762	RNU6-418P	1:205538012-205572046	NOTEST	0	0	0	0	1	1
ENSG00000206763	ENSG00000206763	RNU6-10P	7:92234234-92546501	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206764	ENSG00000206764	RNU6-152P	1:182296202-182296309	NOTEST	0	0	0	0	1	1
ENSG00000206765	ENSG00000206765	RNU6-203P	X:132665750-132665854	NOTEST	0	0	0	0	1	1
ENSG00000206766	ENSG00000206766	RNU6-435P	18:21718941-21977844	NOTEST	0	0	0	0	1	1
ENSG00000206767	ENSG00000206767	RNU6-949P	1:28002113-28002220	NOTEST	0	0	0	0	1	1
ENSG00000206768	ENSG00000206768	Y_RNA	14:69517597-69619867	NOTEST	0	0	0	0	1	1
ENSG00000206769	ENSG00000206769	RNU6-116P	18:59000814-59223006	NOTEST	0	0	0	0	1	1
ENSG00000206770	ENSG00000206770	Y_RNA	5:72064528-72064638	NOTEST	0	0	0	0	1	1
ENSG00000206772	ENSG00000206772	RNU6-44P	11:112141471-112233257	NOTEST	0	0	0	0	1	1
ENSG00000206774	ENSG00000206774	RNU6-211P	5:79661544-79661651	NOTEST	0	0	0	0	1	1
ENSG00000206775	ENSG00000206775	SNORD37	19:3976053-3985467	NOTEST	0	0	0	0	1	1
ENSG00000206776	ENSG00000206776	SNORA32	8:120400587-120400709	NOTEST	0	0	0	0	1	1
ENSG00000206777	ENSG00000206777	RNU6-637P	3:169437974-169438081	NOTEST	0	0	0	0	1	1
ENSG00000206778	ENSG00000206778	RNU6-213P	16:15959576-15982482	NOTEST	0	0	0	0	1	1
ENSG00000206779	ENSG00000206779	Y_RNA	1:28696113-28826881	NOTEST	0	0	0	0	1	1
ENSG00000206780	ENSG00000206780	SNORA75	4:17322368-17322505	NOTEST	0	0	0	0	1	1
ENSG00000206781	ENSG00000206781	Y_RNA	15:64679946-64747502	NOTEST	0	0	0	0	1	1
ENSG00000206782	ENSG00000206782	RNU6-224P	4:132194396-132194503	NOTEST	0	0	0	0	1	1
ENSG00000206783	ENSG00000206783	RNU6-292P	11:71709586-71823826	NOTEST	0	0	0	0	1	1
ENSG00000206784	ENSG00000206784	Y_RNA	9:37120535-37358146	NOTEST	0	0	0	0	1	1
ENSG00000206785	ENSG00000206785	SNORA15	7:65216128-65228341	NOTEST	0	0	0	0	1	1
ENSG00000206786	ENSG00000206786	RNU6-701P	5:118342041-118584833	NOTEST	0	0	0	0	1	1
ENSG00000206787	ENSG00000206787	RNU6-76P	13:19454193-19454297	NOTEST	0	0	0	0	1	1
ENSG00000206788	ENSG00000206788	RNU6-629P	2:178487979-178973066	NOTEST	0	0	0	0	1	1
ENSG00000206790	ENSG00000206790	Y_RNA	12:100550134-100660857	NOTEST	0	0	0	0	1	1
ENSG00000206791	ENSG00000206791	RNU1-129P	1:147486648-147486815	NOTEST	0	0	0	0	1	1
ENSG00000206792	ENSG00000206792	Y_RNA	X:12072942-12073045	NOTEST	0	0	0	0	1	1
ENSG00000206795	ENSG00000206795	Y_RNA	X:12156584-12742642	NOTEST	0	0	0	0	1	1
ENSG00000206796	ENSG00000206796	RNU6-811P	10:37414784-37673039	NOTEST	0	0	0	0	1	1
ENSG00000206797	ENSG00000206797	Y_RNA	20:416123-443197	NOTEST	0	0	0	0	1	1
ENSG00000206799	ENSG00000206799	SNORA32	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000206800	ENSG00000206800	RNY3P7	13:78109808-78219398	NOTEST	0	0	0	0	1	1
ENSG00000206801	ENSG00000206801	RNU6-639P	20:42425076-42425183	NOTEST	0	0	0	0	1	1
ENSG00000206802	ENSG00000206802	RNU6-926P	21:27252860-27589700	NOTEST	0	0	0	0	1	1
ENSG00000206803	ENSG00000206803	RNU6-968P	1:236078714-236078821	NOTEST	0	0	0	0	1	1
ENSG00000206804	ENSG00000206804	RNU6-1293P	9:69891207-69901481	NOTEST	0	0	0	0	1	1
ENSG00000206805	ENSG00000206805	Y_RNA	17:46556458-46556560	NOTEST	0	0	0	0	1	1
ENSG00000206806	ENSG00000206806	Y_RNA	11:40135752-41481323	NOTEST	0	0	0	0	1	1
ENSG00000206807	ENSG00000206807	RNU6-815P	3:20549135-20549248	NOTEST	0	0	0	0	1	1
ENSG00000206808	ENSG00000206808	Y_RNA	11:33060962-33213144	NOTEST	0	0	0	0	1	1
ENSG00000206811	ENSG00000206811	SNORA10	16:2012052-2014861	NOTEST	0	0	0	0	1	1
ENSG00000206812	ENSG00000206812	RNU6-38P	13:75683723-75683830	NOTEST	0	0	0	0	1	1
ENSG00000206813	ENSG00000206813	Y_RNA	22:42095502-42195460	NOTEST	0	0	0	0	1	1
ENSG00000206814	ENSG00000206814	Y_RNA	5:17065706-17276943	NOTEST	0	0	0	0	1	1
ENSG00000206815	ENSG00000206815	RNU6-483P	3:57534564-57534672	NOTEST	0	0	0	0	1	1
ENSG00000206816	ENSG00000206816	Y_RNA	11:77371040-77532063	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206817	ENSG00000206817	Y_RNA	1:91726322-91870426	NOTEST	0	0	0	0	1	1
ENSG00000206818	ENSG00000206818	RNU6-849P	7:79541419-79541524	NOTEST	0	0	0	0	1	1
ENSG00000206819	ENSG00000206819	RNU6-260P	5:157212750-157286183	NOTEST	0	0	0	0	1	1
ENSG00000206820	ENSG00000206820	RNU1-138P	4:114341478-114341642	NOTEST	0	0	0	0	1	1
ENSG00000206822	ENSG00000206822	Y_RNA	14:64063756-64108579	NOTEST	0	0	0	0	1	1
ENSG00000206824	ENSG00000206824	Y_RNA	17:48450580-48475249	NOTEST	0	0	0	0	1	1
ENSG00000206826	ENSG00000206826	RNU6-974P	X:81256668-81256776	NOTEST	0	0	0	0	1	1
ENSG00000206827	ENSG00000206827	RNU6-1032P	18:20227544-20227651	NOTEST	0	0	0	0	1	1
ENSG00000206828	ENSG00000206828	RNVU1-5	1:144275917-144521970	NOTEST	0	0	0	0	1	1
ENSG00000206832	ENSG00000206832	RNU6V	1:110091232-110136975	NOTEST	0	0	0	0	1	1
ENSG00000206833	ENSG00000206833	RNU6-20P	16:57792128-57896957	NOTEST	0	0	0	0	1	1
ENSG00000206834	ENSG00000206834	SNORA1	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000206835	ENSG00000206835	RNU1-74P	1:232967762-232967933	NOTEST	0	0	0	0	1	1
ENSG00000206836	ENSG00000206836	RNU6-1029P	2:198312468-198312575	NOTEST	0	0	0	0	1	1
ENSG00000206838	ENSG00000206838	SNORA5A	7:45139698-45151646	NOTEST	3.77699	2.77942	-0.442454	0	1	1
ENSG00000206839	ENSG00000206839	RNU6-746P	4:56160656-56160765	NOTEST	0	0	0	0	1	1
ENSG00000206840	ENSG00000206840	Y_RNA	10:38283790-38283903	NOTEST	0	0	0	0	1	1
ENSG00000206841	ENSG00000206841	RNU6-409P	22:51112842-51171726	NOTEST	0	0	0	0	1	1
ENSG00000206842	ENSG00000206842	RNU6-413P	10:23076321-23076428	NOTEST	0	0	0	0	1	1
ENSG00000206843	ENSG00000206843	RNU6-206P	7:139000036-139000140	NOTEST	0	0	0	0	1	1
ENSG00000206844	ENSG00000206844	Y_RNA	X:9754495-9917483	NOTEST	0	0	0	0	1	1
ENSG00000206845	ENSG00000206845	RNU6-209P	5:163723701-164598649	NOTEST	0	0	0	0	1	1
ENSG00000206846	ENSG00000206846	Y_RNA	15:30909160-31065196	NOTEST	0	0	0	0	1	1
ENSG00000206847	ENSG00000206847	Y_RNA	11:128834954-129149219	NOTEST	0	0	0	0	1	1
ENSG00000206848	ENSG00000206848	RNU6-890P	6:42531799-42661242	NOTEST	0	0	0	0	1	1
ENSG00000206849	ENSG00000206849	SNORA18	15:32220505-32220637	NOTEST	0	0	0	0	1	1
ENSG00000206850	ENSG00000206850	Y_RNA	12:131391382-131391494	NOTEST	0	0	0	0	1	1
ENSG00000206852	ENSG00000206852	RNU6-895P	8:41119480-41167016	NOTEST	0	0	0	0	1	1
ENSG00000206853	ENSG00000206853	SNORA51	8:60049930-60050061	NOTEST	0	0	0	0	1	1
ENSG00000206854	ENSG00000206854	RNY3P5	13:61363693-61363795	NOTEST	0	0	0	0	1	1
ENSG00000206855	ENSG00000206855	RNU6-571P	10:70661033-70706603	NOTEST	0	0	0	0	1	1
ENSG00000206856	ENSG00000206856	RNU6-427P	6:139117062-139309398	NOTEST	0	0	0	0	1	1
ENSG00000206857	ENSG00000206857	RNU6-214P	6:120847439-120847546	NOTEST	0	0	0	0	1	1
ENSG00000206858	ENSG00000206858	Y_RNA	11:10747449-10747551	NOTEST	0	0	0	0	1	1
ENSG00000206859	ENSG00000206859	RNU6-767P	17:16945858-17140502	NOTEST	0	0	0	0	1	1
ENSG00000206862	ENSG00000206862	Y_RNA	X:117629860-117820126	NOTEST	0	0	0	0	1	1
ENSG00000206863	ENSG00000206863	RNU5A-6P	18:21572736-21715574	NOTEST	0	0	0	0	1	1
ENSG00000206864	ENSG00000206864	RNU6-207P	X:103810995-105011822	NOTEST	0	0	0	0	1	1
ENSG00000206865	ENSG00000206865	Y_RNA	18:54264438-54706076	NOTEST	0	0	0	0	1	1
ENSG00000206866	ENSG00000206866	RNU6-187P	2:177794712-177794818	NOTEST	0	0	0	0	1	1
ENSG00000206867	ENSG00000206867	RNU6-356P	8:40890410-40890517	NOTEST	0	0	0	0	1	1
ENSG00000206869	ENSG00000206869	SNORA70F	2:165510133-165705844	NOTEST	0	0	0	0	1	1
ENSG00000206870	ENSG00000206870	RNU6-398P	14:61201459-61550451	NOTEST	0	0	0	0	1	1
ENSG00000206871	ENSG00000206871	RNU6-533P	8:36167101-36167208	NOTEST	0	0	0	0	1	1
ENSG00000206875	ENSG00000206875	RNU6-761P	6:41902670-42018095	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206877	ENSG00000206877	RNU6-1103P	7:24576950-24577057	NOTEST	0	0	0	0	1	1
ENSG00000206878	ENSG00000206878	SNORA51	1:228788182-228788307	NOTEST	0	0	0	0	1	1
ENSG00000206880	ENSG00000206880	RNU6-1310P	1:168232612-168232719	NOTEST	0	0	0	0	1	1
ENSG00000206881	ENSG00000206881	RNU6-190P	6:17615268-17707575	NOTEST	0	0	0	0	1	1
ENSG00000206882	ENSG00000206882	RNA5SP87	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000206885	ENSG00000206885	SNORA75	2:232318241-232348352	NOTEST	0	2.41972	inf	0	1	1
ENSG00000206886	ENSG00000206886	SNORA70	6:82473740-82473873	NOTEST	0	0	0	0	1	1
ENSG00000206887	ENSG00000206887	RNU6-1008P	1:224407314-224518089	NOTEST	0	0	0	0	1	1
ENSG00000206888	ENSG00000206888	RNU6-48P	1:27648650-27662891	NOTEST	0	0	0	0	1	1
ENSG00000206889	ENSG00000206889	RNU6-1200P	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000206891	ENSG00000206891	RNU6-217P	3:77860891-77860995	NOTEST	0	0	0	0	1	1
ENSG00000206892	ENSG00000206892	RNU6-42P	3:196466727-196559518	NOTEST	0	0	0	0	1	1
ENSG00000206895	ENSG00000206895	Y_RNA	7:4836685-4923350	NOTEST	0	0	0	0	1	1
ENSG00000206896	ENSG00000206896	RNU6-1124P	X:42033531-42033638	NOTEST	0	0	0	0	1	1
ENSG00000206897	ENSG00000206897	SNORA9	12:124086623-124118313	NOTEST	0	0	0	0	1	1
ENSG00000206898	ENSG00000206898	SNORA51	2:10436172-10436306	NOTEST	0	0	0	0	1	1
ENSG00000206899	ENSG00000206899	RNU6-36P	12:98107189-98155637	NOTEST	0	0	0	0	1	1
ENSG00000206900	ENSG00000206900	RNU6-98P	X:131714144-131714251	NOTEST	0	0	0	0	1	1
ENSG00000206901	ENSG00000206901	SNORA72	2:140268993-140269125	NOTEST	0	0	0	0	1	1
ENSG00000206902	ENSG00000206902	Y_RNA	3:53317446-53381654	NOTEST	0	0	0	0	1	1
ENSG00000206903	ENSG00000206903	SNORA24	15:65526797-65592956	NOTEST	0	0	0	0	1	1
ENSG00000206905	ENSG00000206905	Y_RNA	1:180488151-180488255	NOTEST	0	0	0	0	1	1
ENSG00000206906	ENSG00000206906	RNU6-458P	14:19119514-19119621	NOTEST	0	0	0	0	1	1
ENSG00000206907	ENSG00000206907	RNU6-1013P	9:114602107-114602214	NOTEST	0	0	0	0	1	1
ENSG00000206908	ENSG00000206908	RNU1-136P	6:53084058-53084222	NOTEST	0	0	0	0	1	1
ENSG00000206909	ENSG00000206909	SNORA70	5:170792598-170794697	NOTEST	0	0	0	0	1	1
ENSG00000206910	ENSG00000206910	SNORA29	6:160090088-160210781	NOTEST	0	0	0	0	1	1
ENSG00000206911	ENSG00000206911	Y_RNA	11:93551397-93583697	NOTEST	0	0	0	0	1	1
ENSG00000206912	ENSG00000206912	Y_RNA	5:23299263-23299371	NOTEST	0	0	0	0	1	1
ENSG00000206913	ENSG00000206913	SNORA7	11:73723762-74035750	NOTEST	0	0	0	0	1	1
ENSG00000206914	ENSG00000206914	Y_RNA	12:123237320-123255611	NOTEST	0	0	0	0	1	1
ENSG00000206915	ENSG00000206915	RNU6-439P	2:49460932-49461038	NOTEST	0	0	0	0	1	1
ENSG00000206917	ENSG00000206917	RNU1-52P	17:56597197-56769416	NOTEST	0	0	0	0	1	1
ENSG00000206918	ENSG00000206918	RNU6-1181P	3:57327726-57530071	NOTEST	0	0	0	0	1	1
ENSG00000206920	ENSG00000206920	RNY1P6	13:52158643-52336171	NOTEST	0	0	0	0	1	1
ENSG00000206921	ENSG00000206921	RNU6-481P	1:161371078-161371185	NOTEST	0	0	0	0	1	1
ENSG00000206922	ENSG00000206922	RNU6-80P	13:73280154-73280261	NOTEST	0	0	0	0	1	1
ENSG00000206923	ENSG00000206923	RNU6-432P	9:113635542-113800981	NOTEST	0	0	0	0	1	1
ENSG00000206924	ENSG00000206924	RNU6-689P	14:75480466-75518235	NOTEST	0	0	0	0	1	1
ENSG00000206925	ENSG00000206925	Y_RNA	19:40825442-40896094	NOTEST	0	0	0	0	1	1
ENSG00000206926	ENSG00000206926	RNU6-1024P	3:15422781-15563258	NOTEST	0	0	0	0	1	1
ENSG00000206927	ENSG00000206927	Y_RNA	16:18411798-18495797	NOTEST	0	0	0	0	1	1
ENSG00000206929	ENSG00000206929	Y_RNA	12:101840602-101840710	NOTEST	0	0	0	0	1	1
ENSG00000206931	ENSG00000206931	RNU6-1042P	1:150670535-150693364	NOTEST	0	0	0	0	1	1
ENSG00000206932	ENSG00000206932	RNU6-4P	3:180701496-181554668	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206935	ENSG00000206935	RNU6-514P	1:23345940-23504301	NOTEST	0	0	0	0	1	1
ENSG00000206936	ENSG00000206936	RNU4-52P	X:48928812-48958108	NOTEST	0	0	0	0	1	1
ENSG00000206937	ENSG00000206937	SNORA70B	2:61404552-61697904	NOTEST	0	0	0	0	1	1
ENSG00000206938	ENSG00000206938	RNU4-31P	7:156264889-156685924	NOTEST	0	0	0	0	1	1
ENSG00000206939	ENSG00000206939	RNU6-281P	3:70857500-70857603	NOTEST	0	0	0	0	1	1
ENSG00000206941	ENSG00000206941	SNORD15A	11:75110529-75133324	NOTEST	0	0	0	0	1	1
ENSG00000206944	ENSG00000206944	RNU6-708P	18:45553043-45937123	NOTEST	0	0	0	0	1	1
ENSG00000206946	ENSG00000206946	RNU6-156P	9:66693276-66759372	NOTEST	0	0	0	0	1	1
ENSG00000206947	ENSG00000206947	SNORA20	7:39017597-39532694	NOTEST	0	0	0	0	1	1
ENSG00000206948	ENSG00000206948	SNORA36A	X:153991030-154005964	NOTEST	0	0	0	0	1	1
ENSG00000206949	ENSG00000206949	RNU6-1324P	8:67341262-67430759	NOTEST	0	0	0	0	1	1
ENSG00000206950	ENSG00000206950	Y_RNA	8:13947372-15095848	NOTEST	0	0	0	0	1	1
ENSG00000206951	ENSG00000206951	Y_RNA	2:33170405-33170518	NOTEST	0	0	0	0	1	1
ENSG00000206952	ENSG00000206952	SNORA50	16:58549382-58663790	NOTEST	0	0	0	0	1	1
ENSG00000206954	ENSG00000206954	RNU6-1201P	17:46147413-46178883	NOTEST	0	0	0	0	1	1
ENSG00000206957	ENSG00000206957	Y_RNA	15:44957929-45003514	NOTEST	0	0	0	0	1	1
ENSG00000206958	ENSG00000206958	SNORA70	5:87485449-87794514	NOTEST	0	0	0	0	1	1
ENSG00000206959	ENSG00000206959	Y_RNA	20:52161153-52161264	NOTEST	0	0	0	0	1	1
ENSG00000206960	ENSG00000206960	RNU6-793P	6:14646765-14646869	NOTEST	0	0	0	0	1	1
ENSG00000206961	ENSG00000206961	SNORA51	2:170550974-170633499	NOTEST	0	0	0	0	1	1
ENSG00000206962	ENSG00000206962	RNU6-74P	13:42140972-42535256	NOTEST	0	0	0	0	1	1
ENSG00000206963	ENSG00000206963	RNU6-675P	2:127460414-127460518	NOTEST	0	0	0	0	1	1
ENSG00000206964	ENSG00000206964	Y_RNA	2:55513153-55513264	NOTEST	0	0	0	0	1	1
ENSG00000206965	ENSG00000206965	RNU6-5P	2:175411868-175639555	NOTEST	0	0	0	0	1	1
ENSG00000206967	ENSG00000206967	Y_RNA	11:108027941-108338258	NOTEST	0	0	0	0	1	1
ENSG00000206968	ENSG00000206968	RNVU1-16	1:148766937-148767102	NOTEST	0	0	0	0	1	1
ENSG00000206969	ENSG00000206969	RNU6-1316P	14:103243812-103377837	NOTEST	0	0	0	0	1	1
ENSG00000206970	ENSG00000206970	RNU6-474P	2:204646759-204646866	NOTEST	0	0	0	0	1	1
ENSG00000206972	ENSG00000206972	RNU6-17P	15:30546604-30546711	NOTEST	0	0	0	0	1	1
ENSG00000206973	ENSG00000206973	RNU6-1145P	2:61832750-61832857	NOTEST	0	0	0	0	1	1
ENSG00000206974	ENSG00000206974	RNU6-1144P	6:108613969-108614073	NOTEST	0	0	0	0	1	1
ENSG00000206975	ENSG00000206975	RNU6-13P	8:57829642-57829749	NOTEST	0	0	0	0	1	1
ENSG00000206976	ENSG00000206976	SNORA7	11:3875547-4114439	NOTEST	0	0	0	0	1	1
ENSG00000206977	ENSG00000206977	SNORA8	6:41737913-41863099	NOTEST	0	0	0	0	1	1
ENSG00000206978	ENSG00000206978	Y_RNA	4:159985448-159985550	NOTEST	0	0	0	0	1	1
ENSG00000206979	ENSG00000206979	SNORD61	X:135923089-135962923	NOTEST	0	0	0	0	1	1
ENSG00000206980	ENSG00000206980	RNU6-662P	1:151720072-151720176	NOTEST	0	0	0	0	1	1
ENSG00000206981	ENSG00000206981	RNU6-40P	1:31970418-31970525	NOTEST	0	0	0	0	1	1
ENSG00000206982	ENSG00000206982	Y_RNA	6:128905534-128905636	NOTEST	0	0	0	0	1	1
ENSG00000206983	ENSG00000206983	RNU6-49P	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000206985	ENSG00000206985	RNU6-198P	2:39208536-39351486	NOTEST	0	0	0	0	1	1
ENSG00000206987	ENSG00000206987	U8	15:32684982-32727434	NOTEST	0	0	0	0	1	1
ENSG00000206989	ENSG00000206989	SNORD63	5:137890570-137911133	NOTEST	0	0	0	0	1	1
ENSG00000206990	ENSG00000206990	Y_RNA	1:165631452-165679205	NOTEST	0	0	0	0	1	1
ENSG00000206991	ENSG00000206991	RNU6-610P	15:43885251-44010458	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000206992	ENSG00000206992	RNU6-574P	12:52345450-52390862	NOTEST	0	0	0	0	1	1
ENSG00000206995	ENSG00000206995	Y_RNA	15:52408770-52587995	NOTEST	0	0	0	0	1	1
ENSG00000206996	ENSG00000206996	RNU6-842P	8:12901858-12901965	NOTEST	0	0	0	0	1	1
ENSG00000206997	ENSG00000206997	RNU6-524P	5:95220801-96143803	NOTEST	0	0	0	0	1	1
ENSG00000206998	ENSG00000206998	Y_RNA	20:42079798-42079900	NOTEST	0	0	0	0	1	1
ENSG00000206999	ENSG00000206999	RNU6-622P	1:75648729-75648832	NOTEST	0	0	0	0	1	1
ENSG00000207000	ENSG00000207000	RNU6-820P	9:71320574-71624092	NOTEST	0	0	0	0	1	1
ENSG00000207001	ENSG00000207001	SNORD116-2	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207002	ENSG00000207002	SNORA5	3:123304388-123603178	NOTEST	0	0	0	0	1	1
ENSG00000207003	ENSG00000207003	RNU6-611P	19:45542297-45574214	NOTEST	0	0	0	0	1	1
ENSG00000207004	ENSG00000207004	RNU6-301P	14:51921229-52197445	NOTEST	0	0	0	0	1	1
ENSG00000207005	ENSG00000207005	RNU1-2	1:17066767-17299474	NOTEST	0	0	0	0	1	1
ENSG00000207007	ENSG00000207007	RNU6-891P	4:71717846-71717957	NOTEST	0	0	0	0	1	1
ENSG00000207008	ENSG00000207008	SNORA54	11:2965666-3013607	NOTEST	0	0	0	0	1	1
ENSG00000207009	ENSG00000207009	Y_RNA	4:1619641-1686029	NOTEST	0	0	0	0	1	1
ENSG00000207010	ENSG00000207010	RNU6-1295P	12:12442160-12442263	NOTEST	0	0	0	0	1	1
ENSG00000207011	ENSG00000207011	RNY4P13	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000207012	ENSG00000207012	RNU6-72P	13:86158882-86158988	NOTEST	0	0	0	0	1	1
ENSG00000207013	ENSG00000207013	RNU6-804P	5:85958960-85959067	NOTEST	0	0	0	0	1	1
ENSG00000207014	ENSG00000207014	SNORD116-3	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207016	ENSG00000207016	SNORA36C	2:69685128-70053596	NOTEST	0	0	0	0	1	1
ENSG00000207019	ENSG00000207019	RNU6-167P	18:28898051-29006951	NOTEST	0	0	0	0	1	1
ENSG00000207020	ENSG00000207020	Y_RNA	5:138906015-139008018	NOTEST	0	0	0	0	1	1
ENSG00000207021	ENSG00000207021	Y_RNA	17:79523912-79615779	NOTEST	0	0	0	0	1	1
ENSG00000207022	ENSG00000207022	SNORA51	1:93307723-93427057	NOTEST	0	0	0	0	1	1
ENSG00000207023	ENSG00000207023	RNU6-975P	6:74171300-74218959	NOTEST	0	0	0	0	1	1
ENSG00000207024	ENSG00000207024	Y_RNA	11:64058773-64072242	NOTEST	0	0	0	0	1	1
ENSG00000207025	ENSG00000207025	Y_RNA	X:18414113-18414215	NOTEST	0	0	0	0	1	1
ENSG00000207026	ENSG00000207026	RNU6-472P	12:34076308-34076415	NOTEST	0	0	0	0	1	1
ENSG00000207027	ENSG00000207027	SNORA67	8:23663741-23663890	NOTEST	0	0	0	0	1	1
ENSG00000207029	ENSG00000207029	RNU6-43P	10:104263743-104393292	NOTEST	0	0	0	0	1	1
ENSG00000207031	ENSG00000207031	SNORD59A	12:57031958-57039798	NOTEST	0	0	0	0	1	1
ENSG00000207032	ENSG00000207032	Y_RNA	9:34379016-34397830	NOTEST	0	0	0	0	1	1
ENSG00000207033	ENSG00000207033	RNU6-154P	X:115532007-115532113	NOTEST	0	0	0	0	1	1
ENSG00000207034	ENSG00000207034	Y_RNA	18:2655736-2833063	NOTEST	0	0	0	0	1	1
ENSG00000207036	ENSG00000207036	Y_RNA	8:71021996-71316040	NOTEST	0	0	0	0	1	1
ENSG00000207037	ENSG00000207037	RNU6-339P	15:85427884-85518876	NOTEST	0	0	0	0	1	1
ENSG00000207039	ENSG00000207039	Y_RNA	1:153758195-153758297	NOTEST	0	0	0	0	1	1
ENSG00000207041	ENSG00000207041	RNU6-3P	X:140212214-140212321	NOTEST	0	0	0	0	1	1
ENSG00000207042	ENSG00000207042	RNU6-196P	16:21608538-21668794	NOTEST	0	0	0	0	1	1
ENSG00000207044	ENSG00000207044	RNU6-1226P	6:112429962-112672498	NOTEST	0	0	0	0	1	1
ENSG00000207045	ENSG00000207045	RNU6-532P	7:95959949-95960056	NOTEST	0	0	0	0	1	1
ENSG00000207046	ENSG00000207046	RNU6-886P	14:37667117-38021566	NOTEST	0	0	0	0	1	1
ENSG00000207047	ENSG00000207047	SNORD51	2:206979540-207027652	NOTEST	0	0	0	0	1	1
ENSG00000207049	ENSG00000207049	Y_RNA	2:237061714-237061816	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207051	ENSG00000207051	SNORA27	13:27825445-27830828	NOTEST	0	0	0	0	1	1
ENSG00000207052	ENSG00000207052	RNU6-378P	5:32227099-32313115	NOTEST	0	0	0	0	1	1
ENSG00000207053	ENSG00000207053	RNU6-937P	20:34359895-34538303	NOTEST	0	0	0	0	1	1
ENSG00000207056	ENSG00000207056	RNU1-8P	1:6845383-7829766	NOTEST	0	0	0	0	1	1
ENSG00000207058	ENSG00000207058	RNU6-784P	4:71568734-71568840	NOTEST	0	0	0	0	1	1
ENSG00000207060	ENSG00000207060	RNU6-480P	5:50351186-50351293	NOTEST	0	0	0	0	1	1
ENSG00000207061	ENSG00000207061	Y_RNA	7:155978815-155978917	NOTEST	0	0	0	0	1	1
ENSG00000207062	ENSG00000207062	SNORA15	7:64498731-64535091	NOTEST	0	0	0	0	1	1
ENSG00000207063	ENSG00000207063	SNORD116-1	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207065	ENSG00000207065	RNU5A-2P	4:82255456-82255572	NOTEST	0	0	0	0	1	1
ENSG00000207067	ENSG00000207067	SNORA72	8:98881067-99058697	NOTEST	0	0	0	0	1	1
ENSG00000207068	ENSG00000207068	RNU6-463P	10:107294416-107294523	NOTEST	0	0	0	0	1	1
ENSG00000207069	ENSG00000207069	Y_RNA	2:25166504-25262563	NOTEST	0	0	0	0	1	1
ENSG00000207071	ENSG00000207071	RNU6-1207P	10:45684237-45684344	NOTEST	0	0	0	0	1	1
ENSG00000207072	ENSG00000207072	RNU6-39P	18:66340924-66722426	NOTEST	0	0	0	0	1	1
ENSG00000207073	ENSG00000207073	Y_RNA	19:50058967-50094272	NOTEST	0	0	0	0	1	1
ENSG00000207075	ENSG00000207075	Y_RNA	4:37701516-37701624	NOTEST	0	0	0	0	1	1
ENSG00000207076	ENSG00000207076	RNU6-1113P	6:43441923-43442030	NOTEST	0	0	0	0	1	1
ENSG00000207077	ENSG00000207077	RNU6-1119P	5:99489375-99489483	NOTEST	0	0	0	0	1	1
ENSG00000207080	ENSG00000207080	Y_RNA	1:184284791-184284899	NOTEST	0	0	0	0	1	1
ENSG00000207081	ENSG00000207081	RNU6-616P	X:134052339-134052446	NOTEST	0	0	0	0	1	1
ENSG00000207082	ENSG00000207082	RNU6-171P	1:164524820-164868533	NOTEST	0	0	0	0	1	1
ENSG00000207083	ENSG00000207083	RNU6-22P	16:69139466-69442474	NOTEST	0	0	0	0	1	1
ENSG00000207084	ENSG00000207084	SNORA72	3:160414716-160414848	NOTEST	0	0	0	0	1	1
ENSG00000207086	ENSG00000207086	Y_RNA	2:9724100-9771143	NOTEST	0	0	0	0	1	1
ENSG00000207087	ENSG00000207087	RNU6-242P	2:43318525-43318632	NOTEST	0	0	0	0	1	1
ENSG00000207088	ENSG00000207088	SNORA7B	3:129100140-129118498	NOTEST	0	0	0	0	1	1
ENSG00000207089	ENSG00000207089	RNU6-921P	14:69202638-69202745	NOTEST	0	0	0	0	1	1
ENSG00000207090	ENSG00000207090	RNU6-517P	7:120628730-120937498	NOTEST	0	0	0	0	1	1
ENSG00000207091	ENSG00000207091	Y_RNA	15:34525459-34630261	NOTEST	0	0	0	0	1	1
ENSG00000207092	ENSG00000207092	Y_RNA	18:9102627-9285983	NOTEST	0	0	0	0	1	1
ENSG00000207093	ENSG00000207093	SNORD116-8	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207094	ENSG00000207094	SNORA67	7:88078406-88078546	NOTEST	0	0	0	0	1	1
ENSG00000207095	ENSG00000207095	RNU6-424P	1:28020241-28020346	NOTEST	0	0	0	0	1	1
ENSG00000207097	ENSG00000207097	RNU6-614P	21:14410480-14439354	NOTEST	0	0	0	0	1	1
ENSG00000207098	ENSG00000207098	SNORA70	21:34144410-34266043	NOTEST	0	0	0	0	1	1
ENSG00000207099	ENSG00000207099	RNU6-166P	12:65444405-65515346	NOTEST	0	0	0	0	1	1
ENSG00000207100	ENSG00000207100	SNORA8	X:132286781-132286920	NOTEST	0	0	0	0	1	1
ENSG00000207101	ENSG00000207101	Y_RNA	8:41510738-41754280	NOTEST	0	0	0	0	1	1
ENSG00000207104	ENSG00000207104	RNU6-434P	X:54219255-54385075	NOTEST	0	0	0	0	1	1
ENSG00000207105	ENSG00000207105	Y_RNA	15:49280672-49338760	NOTEST	0	0	0	0	1	1
ENSG00000207106	ENSG00000207106	RNVU1-4	1:144275917-144521970	NOTEST	0	0	0	0	1	1
ENSG00000207108	ENSG00000207108	Y_RNA	1:185599559-185599660	NOTEST	0	0	0	0	1	1
ENSG00000207109	ENSG00000207109	SNORD38	3:53317446-53381654	NOTEST	0	0	0	0	1	1
ENSG00000207112	ENSG00000207112	SNORA25	11:93394804-93547861	NOTEST	0	0	0	0	1	1

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ENSG00000207113	ENSG00000207113	RNU6-16P	11:88237743-88799113	NOTEST	0	0	0	0	1	1
ENSG00000207114	ENSG00000207114	RNU6-348P	3:171222033-171222140	NOTEST	0	0	0	0	1	1
ENSG00000207115	ENSG00000207115	RNU6-364P	7:95970451-95970558	NOTEST	0	0	0	0	1	1
ENSG00000207116	ENSG00000207116	RNU6-31P	2:201694731-201694839	NOTEST	0	0	0	0	1	1
ENSG00000207117	ENSG00000207117	Y_RNA	2:160175489-160473593	NOTEST	0	0	0	0	1	1
ENSG00000207118	ENSG00000207118	SNORD14D	11:122928196-122933938	NOTEST	0	0	0	0	1	1
ENSG00000207119	ENSG00000207119	U3	15:69750280-69750488	NOTEST	0	0	0	0	1	1
ENSG00000207121	ENSG00000207121	RNU6-1230P	4:150855527-150855635	NOTEST	0	0	0	0	1	1
ENSG00000207122	ENSG00000207122	RNU6-591P	X:38940432-38940538	NOTEST	0	0	0	0	1	1
ENSG00000207123	ENSG00000207123	Y_RNA	17:60199680-60199782	NOTEST	0	0	0	0	1	1
ENSG00000207124	ENSG00000207124	RNU6-163P	10:4557143-4557249	NOTEST	0	0	0	0	1	1
ENSG00000207127	ENSG00000207127	Y_RNA	17:47448101-47554350	NOTEST	0	0	0	0	1	1
ENSG00000207128	ENSG00000207128	RNU6-729P	8:10332074-10339484	NOTEST	0	0	0	0	1	1
ENSG00000207129	ENSG00000207129	RNA5SP187	5:87485449-87794514	NOTEST	0	0	0	0	1	1
ENSG00000207130	ENSG00000207130	SNORA24	3:128433413-128433548	NOTEST	0	0	0	0	1	1
ENSG00000207131	ENSG00000207131	Y_RNA	6:88535890-88536003	NOTEST	0	0	0	0	1	1
ENSG00000207132	ENSG00000207132	Y_RNA	17:28671520-28671622	NOTEST	0	0	0	0	1	1
ENSG00000207133	ENSG00000207133	SNORD116-7	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207134	ENSG00000207134	RNU6-106P	1:155305058-155533775	NOTEST	0	0	0	0	1	1
ENSG00000207135	ENSG00000207135	RNU6-452P	10:27620285-27630181	NOTEST	0	0	0	0	1	1
ENSG00000207136	ENSG00000207136	RNU6-769P	12:50898767-51142450	NOTEST	0	0	0	0	1	1
ENSG00000207137	ENSG00000207137	SNORD116-13	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207138	ENSG00000207138	RNU6-869P	8:127517007-127517114	NOTEST	0	0	0	0	1	1
ENSG00000207139	ENSG00000207139	Y_RNA	1:197473877-197744826	NOTEST	0	0	0	0	1	1
ENSG00000207141	ENSG00000207141	RNU6-802P	14:24821262-24821363	NOTEST	0	0	0	0	1	1
ENSG00000207142	ENSG00000207142	Y_RNA	12:42632248-42984157	NOTEST	0	0	0	0	1	1
ENSG00000207144	ENSG00000207144	RNU6-1297P	1:155305058-155533775	NOTEST	0	0	0	0	1	1
ENSG00000207145	ENSG00000207145	SNORA18	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000207146	ENSG00000207146	Y_RNA	X:107683073-107940775	NOTEST	0	0	0	0	1	1
ENSG00000207147	ENSG00000207147	SNORA51	21:41382925-42219065	NOTEST	0	0	0	0	1	1
ENSG00000207148	ENSG00000207148	Y_RNA	4:122250223-122250325	NOTEST	0	0	0	0	1	1
ENSG00000207149	ENSG00000207149	RNU6-465P	1:120669561-120669662	NOTEST	0	0	0	0	1	1
ENSG00000207150	ENSG00000207150	RNU6-185P	15:87975288-88247083	NOTEST	0	0	0	0	1	1
ENSG00000207151	ENSG00000207151	Y_RNA	X:11129420-11683821	NOTEST	0	0	0	0	1	1
ENSG00000207153	ENSG00000207153	RNU6-933P	11:60739114-60787849	NOTEST	0	0	0	0	1	1
ENSG00000207154	ENSG00000207154	RNU1-46P	18:48810102-48810266	NOTEST	0	0	0	0	1	1
ENSG00000207155	ENSG00000207155	Y_RNA	4:141541918-141677274	NOTEST	0	0	0	0	1	1
ENSG00000207156	ENSG00000207156	RNU6-505P	3:146627471-147088443	NOTEST	0	0	0	0	1	1
ENSG00000207157	ENSG00000207157	RNY3P4	13:23726724-23726825	NOTEST	0	0	0	0	1	1
ENSG00000207158	ENSG00000207158	RNU6-929P	20:55361036-55361143	NOTEST	0	0	0	0	1	1
ENSG00000207160	ENSG00000207160	RNU6-1289P	18:23805899-23971649	NOTEST	0	0	0	0	1	1
ENSG00000207161	ENSG00000207161	Y_RNA	2:148229700-148229811	NOTEST	0	0	0	0	1	1
ENSG00000207162	ENSG00000207162	RNU6-549P	15:64752940-64978264	NOTEST	0	0	0	0	1	1
ENSG00000207163	ENSG00000207163	RNU6-905P	3:14444075-14583588	NOTEST	0	0	0	0	1	1
ENSG00000207164	ENSG00000207164	Y_RNA	14:29299449-29497969	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207165	ENSG00000207165	SNORA70	X:153618314-153650065	NOTEST	0	0	0	0	1	1
ENSG00000207166	ENSG00000207166	SNORA68	19:17970684-17974962	NOTEST	0	1.21431	inf	0	1	1
ENSG00000207167	ENSG00000207167	RNU6-1340P	16:18995255-19091417	NOTEST	0	0	0	0	1	1
ENSG00000207168	ENSG00000207168	SNORA15	7:56119322-56131682	NOTEST	0	0	0	0	1	1
ENSG00000207169	ENSG00000207169	RNU6-24P	17:74305566-74383941	NOTEST	0	0	0	0	1	1
ENSG00000207170	ENSG00000207170	RNU6-1215P	2:18735988-18770838	NOTEST	0	0	0	0	1	1
ENSG00000207171	ENSG00000207171	SNORA51	4:169277885-169931426	NOTEST	0	0	0	0	1	1
ENSG00000207172	ENSG00000207172	RNU6-1162P	14:64063756-64108579	NOTEST	0	0	0	0	1	1
ENSG00000207173	ENSG00000207173	Y_RNA	16:58116971-58117072	NOTEST	0	0	0	0	1	1
ENSG00000207174	ENSG00000207174	SNORD116-15	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207175	ENSG00000207175	RNU1-67P	X:118533022-118588441	NOTEST	0	0	0	0	1	1
ENSG00000207176	ENSG00000207176	Y_RNA	12:32548983-32549081	NOTEST	0	0	0	0	1	1
ENSG00000207177	ENSG00000207177	SNORA51	5:109624933-110100857	NOTEST	0	0	0	0	1	1
ENSG00000207178	ENSG00000207178	RNU6-1122P	2:183738568-183738675	NOTEST	0	0	0	0	1	1
ENSG00000207180	ENSG00000207180	RNU6-411P	6:71892314-71892421	NOTEST	0	0	0	0	1	1
ENSG00000207181	ENSG00000207181	SNORA14B	1:235272650-235292251	NOTEST	0	0	0	0	1	1
ENSG00000207182	ENSG00000207182	RNU1-44P	4:147501199-147501362	NOTEST	0	0	0	0	1	1
ENSG00000207183	ENSG00000207183	RNU6-843P	2:11988747-12718474	NOTEST	0	0	0	0	1	1
ENSG00000207184	ENSG00000207184	Y_RNA	7:129593073-129691291	NOTEST	0	0	0	0	1	1
ENSG00000207185	ENSG00000207185	RNU6-1157P	11:118307204-118473748	NOTEST	0	0	0	0	1	1
ENSG00000207186	ENSG00000207186	RNA5SP122	2:242523819-242613272	NOTEST	0	0	0	0	1	1
ENSG00000207187	ENSG00000207187	SNORA64	2:30410299-30410432	NOTEST	0	0	0	0	1	1
ENSG00000207188	ENSG00000207188	RNU6-569P	4:136236572-136236677	NOTEST	0	0	0	0	1	1
ENSG00000207189	ENSG00000207189	Y_RNA	12:123773655-123850660	NOTEST	0	0	0	0	1	1
ENSG00000207190	ENSG00000207190	RNU6-809P	1:64239692-64647181	NOTEST	0	0	0	0	1	1
ENSG00000207191	ENSG00000207191	SNORD116-5	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207192	ENSG00000207192	RNU6-649P	2:4992866-4992973	NOTEST	0	0	0	0	1	1
ENSG00000207193	ENSG00000207193	Y_RNA	6:16232461-16232561	NOTEST	0	0	0	0	1	1
ENSG00000207194	ENSG00000207194	RNU6-1026P	1:50905149-51425935	NOTEST	0	0	0	0	1	1
ENSG00000207195	ENSG00000207195	Y_RNA	4:40812043-41218731	NOTEST	0	0	0	0	1	1
ENSG00000207196	ENSG00000207196	Y_RNA	11:70313960-70963623	NOTEST	0	0	0	0	1	1
ENSG00000207197	ENSG00000207197	SNORD116-12	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207198	ENSG00000207198	RNU6-1195P	4:40812043-41218731	NOTEST	0	0	0	0	1	1
ENSG00000207199	ENSG00000207199	SNORD38	8:38854387-38962663	NOTEST	0	0	0	0	1	1
ENSG00000207200	ENSG00000207200	RNU6-45P	11:63737941-63738048	NOTEST	0	0	0	0	1	1
ENSG00000207201	ENSG00000207201	RNU1-148P	8:23934509-23934671	NOTEST	0	0	0	0	1	1
ENSG00000207202	ENSG00000207202	RNU6-800P	X:10413349-10851773	NOTEST	0	0	0	0	1	1
ENSG00000207203	ENSG00000207203	RNU6-71P	13:36742344-36871979	NOTEST	0	0	0	0	1	1
ENSG00000207204	ENSG00000207204	RNU6-393P	7:98392340-98392447	NOTEST	0	0	0	0	1	1
ENSG00000207205	ENSG00000207205	RNVU1-15	1:148604907-148605072	NOTEST	0	0	0	0	1	1
ENSG00000207206	ENSG00000207206	RNU6-1035P	9:84304627-84391815	NOTEST	0	0	0	0	1	1
ENSG00000207207	ENSG00000207207	Y_RNA	2:85645843-85664152	NOTEST	0	0	0	0	1	1
ENSG00000207208	ENSG00000207208	RNU6-790P	14:102228134-102394326	NOTEST	0	0	0	0	1	1
ENSG00000207209	ENSG00000207209	Y_RNA	1:146891925-146892027	NOTEST	0	0	0	0	1	1
ENSG00000207210	ENSG00000207210	Y_RNA	5:172479454-172479558	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207212	ENSG00000207212	Y_RNA	17:36337710-36421858	NOTEST	0	0	0	0	1	1
ENSG00000207213	ENSG00000207213	Y_RNA	1:11059918-11060002	NOTEST	0	0	0	0	1	1
ENSG00000207214	ENSG00000207214	RNU6-102P	7:124287772-124287876	NOTEST	0	0	0	0	1	1
ENSG00000207215	ENSG00000207215	U3	8:98370492-98370702	NOTEST	0	0	0	0	1	1
ENSG00000207217	ENSG00000207217	SNORA42	7:6048875-6098861	NOTEST	0	0	0	0	1	1
ENSG00000207218	ENSG00000207218	Y_RNA	2:42084410-42084512	NOTEST	0	0	0	0	1	1
ENSG00000207220	ENSG00000207220	RNU1-57P	X:113193201-113193367	NOTEST	0	0	0	0	1	1
ENSG00000207221	ENSG00000207221	SNORA70E	11:82534543-82782965	NOTEST	0	0	0	0	1	1
ENSG00000207222	ENSG00000207222	RNU6-456P	5:133835868-133835975	NOTEST	0	0	0	0	1	1
ENSG00000207223	ENSG00000207223	Y_RNA	15:64752940-64978264	NOTEST	0	0	0	0	1	1
ENSG00000207225	ENSG00000207225	RNU6-692P	2:148165909-148166016	NOTEST	0	0	0	0	1	1
ENSG00000207227	ENSG00000207227	RNU6-900P	22:38287353-38287455	NOTEST	0	0	0	0	1	1
ENSG00000207229	ENSG00000207229	Y_RNA	5:54273691-54338672	NOTEST	0	0	0	0	1	1
ENSG00000207231	ENSG00000207231	Y_RNA	4:186317174-186347139	NOTEST	0	0	0	0	1	1
ENSG00000207233	ENSG00000207233	SNORA37	18:51679078-51751158	NOTEST	0	0	0	0	1	1
ENSG00000207234	ENSG00000207234	RNU6-125P	1:89003195-89301938	NOTEST	0	0	0	0	1	1
ENSG00000207235	ENSG00000207235	Y_RNA	17:57297827-57353328	NOTEST	0	0	0	0	1	1
ENSG00000207237	ENSG00000207237	RNU6-110P	1:26286257-26324648	NOTEST	0	0	0	0	1	1
ENSG00000207240	ENSG00000207240	Y_RNA	18:28898051-29006951	NOTEST	0	0	0	0	1	1
ENSG00000207241	ENSG00000207241	SNORD45A	1:76190035-76260764	NOTEST	0	0	0	0	1	1
ENSG00000207242	ENSG00000207242	RNU6-1065P	17:10752857-10784212	NOTEST	0	0	0	0	1	1
ENSG00000207243	ENSG00000207243	Y_RNA	16:228552-228655	NOTEST	0	0	0	0	1	1
ENSG00000207244	ENSG00000207244	SNORA70	8:8818709-8836535	NOTEST	0	0	0	0	1	1
ENSG00000207245	ENSG00000207245	SNORD116-29	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207247	ENSG00000207247	Y_RNA	6:137255902-137256004	NOTEST	0	0	0	0	1	1
ENSG00000207248	ENSG00000207248	RNU6-1005P	16:21608538-21668794	NOTEST	0	0	0	0	1	1
ENSG00000207249	ENSG00000207249	SNORA72	2:105349691-105349820	NOTEST	0	0	0	0	1	1
ENSG00000207251	ENSG00000207251	RNU6-342P	3:27151575-27410951	NOTEST	0	0	0	0	1	1
ENSG00000207252	ENSG00000207252	Y_RNA	11:24477456-24477556	NOTEST	0	0	0	0	1	1
ENSG00000207255	ENSG00000207255	RNU6-1117P	2:35696670-35696774	NOTEST	0	0	0	0	1	1
ENSG00000207256	ENSG00000207256	RNU6-880P	1:43457108-43457215	NOTEST	0	0	0	0	1	1
ENSG00000207257	ENSG00000207257	RNU6-18P	15:32576352-32576459	NOTEST	0	0	0	0	1	1
ENSG00000207258	ENSG00000207258	Y_RNA	8:38585703-38710546	NOTEST	0	0	0	0	1	1
ENSG00000207260	ENSG00000207260	RNU6-35P	4:110834039-110933422	NOTEST	0	0	0	0	1	1
ENSG00000207261	ENSG00000207261	RNU6-738P	5:26880708-27121257	NOTEST	0	0	0	0	1	1
ENSG00000207263	ENSG00000207263	SNORD116-16	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207264	ENSG00000207264	RNU6-15P	10:21610889-21610996	NOTEST	0	0	0	0	1	1
ENSG00000207265	ENSG00000207265	Y_RNA	19:52762328-52762440	NOTEST	0	0	0	0	1	1
ENSG00000207266	ENSG00000207266	RNU6-1241P	16:27798849-28074830	NOTEST	0	0	0	0	1	1
ENSG00000207267	ENSG00000207267	RNU6-1081P	2:11319886-11488456	NOTEST	0	0	0	0	1	1
ENSG00000207268	ENSG00000207268	SNORA70C	9:119187503-120177348	NOTEST	0	0	0	0	1	1
ENSG00000207269	ENSG00000207269	RN7SKP62	5:100068761-100069090	NOTEST	0	0	0	0	1	1
ENSG00000207270	ENSG00000207270	RNU6-601P	2:150426147-150715705	NOTEST	0	0	0	0	1	1
ENSG00000207271	ENSG00000207271	Y_RNA	10:36914942-36915066	NOTEST	0	0	0	0	1	1
ENSG00000207274	ENSG00000207274	SNORA70	2:215674952-216003151	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207275	ENSG00000207275	RNU6-441P	10:83635069-84746935	NOTEST	0	0	0	0	1	1
ENSG00000207276	ENSG00000207276	RNU6-1160P	9:98997587-99064434	NOTEST	0	0	0	0	1	1
ENSG00000207277	ENSG00000207277	RNA5SP284	9:68397877-68409893	NOTEST	0	0	0	0	1	1
ENSG00000207278	ENSG00000207278	RNU6-831P	18:3496029-4455335	NOTEST	0	0	0	0	1	1
ENSG00000207279	ENSG00000207279	SNORD116-24	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207280	ENSG00000207280	SNORD20	2:232318241-232348352	NOTEST	0	0	0	0	1	1
ENSG00000207281	ENSG00000207281	Y_RNA	19:40825442-40896094	NOTEST	0	0	0	0	1	1
ENSG00000207282	ENSG00000207282	Y_RNA	20:18094110-18094223	NOTEST	0	0	0	0	1	1
ENSG00000207283	ENSG00000207283	Y_RNA	3:5127862-5127964	NOTEST	0	0	0	0	1	1
ENSG00000207286	ENSG00000207286	Y_RNA	6:25279305-25620758	NOTEST	0	0	0	0	1	1
ENSG00000207287	ENSG00000207287	RNU6-1274P	10:98502923-98503030	NOTEST	0	0	0	0	1	1
ENSG00000207289	ENSG00000207289	RNU6-1235P	15:21941146-21968151	NOTEST	0	0	0	0	1	1
ENSG00000207290	ENSG00000207290	Y_RNA	5:127593600-128369335	NOTEST	0	0	0	0	1	1
ENSG00000207291	ENSG00000207291	RNU6-30P	X:100888993-100889100	NOTEST	0	0	0	0	1	1
ENSG00000207292	ENSG00000207292	Y_RNA	6:149916008-149970108	NOTEST	0	0	0	0	1	1
ENSG00000207293	ENSG00000207293	Y_RNA	5:56464934-56465036	NOTEST	0	0	0	0	1	1
ENSG00000207294	ENSG00000207294	Y_RNA	16:15068447-15248421	NOTEST	0	0	0	0	1	1
ENSG00000207295	ENSG00000207295	RNU6-851P	2:39103102-39202590	NOTEST	0	0	0	0	1	1
ENSG00000207296	ENSG00000207296	RNU6-140P	19:39287641-39287749	NOTEST	0	0	0	0	1	1
ENSG00000207297	ENSG00000207297	SNORD7	17:33895138-33901811	NOTEST	0	0	0	0	1	1
ENSG00000207298	ENSG00000207298	RNU6-83P	13:99445740-99738879	NOTEST	0	0	0	0	1	1
ENSG00000207299	ENSG00000207299	SNORD56	11:89851558-89851629	NOTEST	0	0	0	0	1	1
ENSG00000207300	ENSG00000207300	Y_RNA	6:138105510-138105623	NOTEST	0	0	0	0	1	1
ENSG00000207302	ENSG00000207302	Y_RNA	1:26203986-26204096	NOTEST	0	0	0	0	1	1
ENSG00000207303	ENSG00000207303	Y_RNA	2:217122587-217236750	NOTEST	0	0	0	0	1	1
ENSG00000207304	ENSG00000207304	SNORA8	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000207305	ENSG00000207305	Y_RNA	20:2433655-2433763	NOTEST	0	0	0	0	1	1
ENSG00000207306	ENSG00000207306	RNU6-1152P	17:46210801-46507637	NOTEST	0	0	0	0	1	1
ENSG00000207307	ENSG00000207307	RNU6-145P	4:77356252-77723117	NOTEST	0	0	0	0	1	1
ENSG00000207308	ENSG00000207308	RNU6-878P	11:2342947-2343057	NOTEST	0	0	0	0	1	1
ENSG00000207309	ENSG00000207309	RNU4-70P	6:97097328-97097467	NOTEST	0	0	0	0	1	1
ENSG00000207310	ENSG00000207310	RNU6-1127P	3:119013219-119139561	NOTEST	0	0	0	0	1	1
ENSG00000207312	ENSG00000207312	RNU6-429P	5:10971951-11904155	NOTEST	0	0	0	0	1	1
ENSG00000207313	ENSG00000207313	SNORA2B	12:49047183-49076021	NOTEST	0	0	0	0	1	1
ENSG00000207316	ENSG00000207316	Y_RNA	3:88480340-88480459	NOTEST	0	0	0	0	1	1
ENSG00000207317	ENSG00000207317	Y_RNA	5:139226363-139422884	NOTEST	0	0	0	0	1	1
ENSG00000207318	ENSG00000207318	RNU6-1184P	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000207319	ENSG00000207319	Y_RNA	2:207516344-207583120	NOTEST	0	0	0	0	1	1
ENSG00000207320	ENSG00000207320	Y_RNA	X:3522410-3631649	NOTEST	0	0	0	0	1	1
ENSG00000207321	ENSG00000207321	RNU6-160P	1:153302595-153321316	NOTEST	0	0	0	0	1	1
ENSG00000207322	ENSG00000207322	RNU1-89P	4:136917083-136917247	NOTEST	0	0	0	0	1	1
ENSG00000207323	ENSG00000207323	RNU6-901P	3:153102722-153697975	NOTEST	0	0	0	0	1	1
ENSG00000207325	ENSG00000207325	RNY1P4	13:33160563-33352157	NOTEST	0	0	0	0	1	1
ENSG00000207326	ENSG00000207326	Y_RNA	1:245912641-246670614	NOTEST	0	0	0	0	1	1
ENSG00000207327	ENSG00000207327	RNU6-883P	10:75196185-75385711	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207328	ENSG00000207328	RNU6-636P	1:37669210-37669317	NOTEST	0	0	0	0	1	1
ENSG00000207329	ENSG00000207329	Y_RNA	9:112086964-112087076	NOTEST	0	0	0	0	1	1
ENSG00000207330	ENSG00000207330	RNU6-73P	13:28402899-28403006	NOTEST	0	0	0	0	1	1
ENSG00000207331	ENSG00000207331	RNU6-1263P	3:98621267-98737406	NOTEST	0	0	0	0	1	1
ENSG00000207332	ENSG00000207332	RNU6-146P	X:3522410-3631649	NOTEST	0	0	0	0	1	1
ENSG00000207333	ENSG00000207333	RNU6-680P	5:74969948-75013313	NOTEST	0	0	0	0	1	1
ENSG00000207334	ENSG00000207334	RNU6-12P	8:119988751-119988858	NOTEST	0	0	0	0	1	1
ENSG00000207336	ENSG00000207336	RNU6-658P	5:73923233-74072737	NOTEST	0	0	0	0	1	1
ENSG00000207338	ENSG00000207338	RNU6-296P	7:123092453-123175131	NOTEST	0	0	0	0	1	1
ENSG00000207339	ENSG00000207339	RNU1-69P	12:56268461-56268625	NOTEST	0	0	0	0	1	1
ENSG00000207340	ENSG00000207340	RNVU1-10	1:147834501-147834665	NOTEST	0	0	0	0	1	1
ENSG00000207341	ENSG00000207341	RNA5SP64	1:166011480-166011587	NOTEST	0	0	0	0	1	1
ENSG00000207342	ENSG00000207342	Y_RNA	14:89290496-89344335	NOTEST	0	0	0	0	1	1
ENSG00000207343	ENSG00000207343	RNU6-225P	22:20771086-20771189	NOTEST	0	0	0	0	1	1
ENSG00000207344	ENSG00000207344	SNORA22	7:64498731-64535091	NOTEST	0	0	0	0	1	1
ENSG00000207345	ENSG00000207345	RNU6-1222P	6:148558720-148873186	NOTEST	0	0	0	0	1	1
ENSG00000207347	ENSG00000207347	RNU6-306P	10:21823093-22032559	NOTEST	0	0	0	0	1	1
ENSG00000207349	ENSG00000207349	RNVU1-17	1:149194105-149194269	NOTEST	0	0	0	0	1	1
ENSG00000207351	ENSG00000207351	Y_RNA	3:183804578-183804691	NOTEST	0	0	0	0	1	1
ENSG00000207352	ENSG00000207352	RNU6-540P	5:64885506-65167553	NOTEST	0	0	0	0	1	1
ENSG00000207355	ENSG00000207355	RNU6-1257P	20:24943560-24973615	NOTEST	0	0	0	0	1	1
ENSG00000207356	ENSG00000207356	Y_RNA	1:40410561-40410670	NOTEST	0	0	0	0	1	1
ENSG00000207357	ENSG00000207357	RNU6-2	19:1021520-1021627	NOTEST	0	0	0	0	1	1
ENSG00000207359	ENSG00000207359	RNU6-925P	8:90912948-90913052	NOTEST	0	0	0	0	1	1
ENSG00000207360	ENSG00000207360	RNU6-14P	9:15552894-16061661	NOTEST	0	0	0	0	1	1
ENSG00000207361	ENSG00000207361	RNU6-178P	8:28203101-28347835	NOTEST	0	0	0	0	1	1
ENSG00000207362	ENSG00000207362	RNU6-422P	10:101989423-102027437	NOTEST	0	0	0	0	1	1
ENSG00000207363	ENSG00000207363	Y_RNA	X:107068984-107179210	NOTEST	0	0	0	0	1	1
ENSG00000207364	ENSG00000207364	RNU6-939P	2:37558912-37559019	NOTEST	0	0	0	0	1	1
ENSG00000207365	ENSG00000207365	Y_RNA	12:93392993-93609455	NOTEST	0	0	0	0	1	1
ENSG00000207366	ENSG00000207366	RNU6-297P	14:48810428-48810535	NOTEST	0	0	0	0	1	1
ENSG00000207367	ENSG00000207367	RNU6-29P	X:48634407-48635486	NOTEST	0	0	0	0	1	1
ENSG00000207368	ENSG00000207368	Y_RNA	3:194995464-195163807	NOTEST	0	0	0	0	1	1
ENSG00000207369	ENSG00000207369	RNU6-665P	8:48173166-48648868	NOTEST	0	0	0	0	1	1
ENSG00000207370	ENSG00000207370	Y_RNA	3:193310932-193415612	NOTEST	0	0	0	0	1	1
ENSG00000207371	ENSG00000207371	Y_RNA	6:41873091-41888877	NOTEST	0	0	0	0	1	1
ENSG00000207375	ENSG00000207375	SNORD116-23	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207378	ENSG00000207378	RNU6-748P	8:99413630-99955055	NOTEST	0	0	0	0	1	1
ENSG00000207379	ENSG00000207379	Y_RNA	1:93851267-93851374	NOTEST	0	0	0	0	1	1
ENSG00000207380	ENSG00000207380	Y_RNA	20:5931297-5975852	NOTEST	0	0	0	0	1	1
ENSG00000207381	ENSG00000207381	RNU6-950P	12:54624723-54745633	NOTEST	0	0	0	0	1	1
ENSG00000207382	ENSG00000207382	Y_RNA	17:60704761-60770958	NOTEST	0	0	0	0	1	1
ENSG00000207383	ENSG00000207383	Y_RNA	2:113337060-113337161	NOTEST	0	0	0	0	1	1
ENSG00000207384	ENSG00000207384	Y_RNA	4:140121548-140121667	NOTEST	0	0	0	0	1	1
ENSG00000207385	ENSG00000207385	RNU6-310P	4:53739148-54232242	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207386	ENSG00000207386	Y_RNA	2:206854308-206951288	NOTEST	0	0	0	0	1	1
ENSG00000207387	ENSG00000207387	Y_RNA	12:71031852-71314623	NOTEST	0	0	0	0	1	1
ENSG00000207389	ENSG00000207389	RNU1-4	1:17066767-17299474	NOTEST	0	0	0	0	1	1
ENSG00000207390	ENSG00000207390	Y_RNA	17:4046461-4167274	NOTEST	0	0	0	0	1	1
ENSG00000207391	ENSG00000207391	Y_RNA	5:78830675-78830777	NOTEST	0	0	0	0	1	1
ENSG00000207392	ENSG00000207392	SNORA20	6:160090088-160210781	NOTEST	0	0	0	0	1	1
ENSG00000207393	ENSG00000207393	RNU6-136P	2:219433302-219461803	NOTEST	0	0	0	0	1	1
ENSG00000207394	ENSG00000207394	RNU6-1060P	6:23125208-23125315	NOTEST	0	0	0	0	1	1
ENSG00000207395	ENSG00000207395	Y_RNA	15:69591285-69740764	NOTEST	0	0	0	0	1	1
ENSG00000207397	ENSG00000207397	RNU6-1179P	19:22738062-22738169	NOTEST	0	0	0	0	1	1
ENSG00000207399	ENSG00000207399	RNU6-1011P	8:104397188-104397295	NOTEST	0	0	0	0	1	1
ENSG00000207401	ENSG00000207401	Y_RNA	9:113635542-113800981	NOTEST	0	0	0	0	1	1
ENSG00000207402	ENSG00000207402	RNU6-959P	2:191886251-192016322	NOTEST	0	0	0	0	1	1
ENSG00000207403	ENSG00000207403	Y_RNA	6:121699942-121700044	NOTEST	0	0	0	0	1	1
ENSG00000207404	ENSG00000207404	Y_RNA	5:108083522-108532542	NOTEST	0	0	0	0	1	1
ENSG00000207405	ENSG00000207405	SNORA64	16:2012052-2014861	NOTEST	0	3.11599	inf	0	1	1
ENSG00000207406	ENSG00000207406	SNORA41	2:206979540-207027652	NOTEST	0	0	0	0	1	1
ENSG00000207407	ENSG00000207407	SNORA1	11:19372270-20143144	NOTEST	0	0	0	0	1	1
ENSG00000207408	ENSG00000207408	Y_RNA	X:53353766-53353879	NOTEST	0	0	0	0	1	1
ENSG00000207410	ENSG00000207410	SNORA8	17:65267584-65267723	NOTEST	0	0	0	0	1	1
ENSG00000207411	ENSG00000207411	Y_RNA	2:43848016-43848123	NOTEST	0	0	0	0	1	1
ENSG00000207412	ENSG00000207412	RNU6-455P	14:31959161-32330430	NOTEST	0	0	0	0	1	1
ENSG00000207414	ENSG00000207414	RNU6-768P	12:101549270-101604185	NOTEST	0	0	0	0	1	1
ENSG00000207415	ENSG00000207415	RNU6-1151P	8:9106926-9293715	NOTEST	0	0	0	0	1	1
ENSG00000207416	ENSG00000207416	Y_RNA	21:38123188-38362536	NOTEST	0	0	0	0	1	1
ENSG00000207417	ENSG00000207417	Y_RNA	8:75146934-75401107	NOTEST	0	0	0	0	1	1
ENSG00000207418	ENSG00000207418	RNVU1-7	1:145969269-145969433	NOTEST	0	0	0	0	1	1
ENSG00000207419	ENSG00000207419	SNORA67	6:11710051-11710193	NOTEST	0	0	0	0	1	1
ENSG00000207420	ENSG00000207420	Y_RNA	5:175969511-176037134	NOTEST	0	0	0	0	1	1
ENSG00000207421	ENSG00000207421	SNORD38B	1:45205489-45244451	NOTEST	0	0	0	0	1	1
ENSG00000207422	ENSG00000207422	RNU6-813P	6:151815164-151942328	NOTEST	0	0	0	0	1	1
ENSG00000207425	ENSG00000207425	Y_RNA	16:15005407-15045915	NOTEST	0	0	0	0	1	1
ENSG00000207426	ENSG00000207426	Y_RNA	X:95939661-96897588	NOTEST	0	0	0	0	1	1
ENSG00000207428	ENSG00000207428	RNU6-95P	4:68566997-68995598	NOTEST	0	0	0	0	1	1
ENSG00000207430	ENSG00000207430	U8	15:30864940-30892918	NOTEST	0	0	0	0	1	1
ENSG00000207431	ENSG00000207431	RNU6-906P	6:111303217-111349466	NOTEST	0	0	0	0	1	1
ENSG00000207432	ENSG00000207432	U8	15:30395922-30423960	NOTEST	0	0	0	0	1	1
ENSG00000207433	ENSG00000207433	RNU6-246P	9:15544185-15544292	NOTEST	0	0	0	0	1	1
ENSG00000207434	ENSG00000207434	RNU6-1072P	1:12982373-12982480	NOTEST	0	0	0	0	1	1
ENSG00000207435	ENSG00000207435	RNU6-114P	X:3490897-3491002	NOTEST	0	0	0	0	1	1
ENSG00000207438	ENSG00000207438	Y_RNA	10:70237755-70287231	NOTEST	0	0	0	0	1	1
ENSG00000207439	ENSG00000207439	Y_RNA	5:64419195-64419301	NOTEST	0	0	0	0	1	1
ENSG00000207440	ENSG00000207440	RNU6-541P	14:31569317-31677010	NOTEST	0	0	0	0	1	1
ENSG00000207441	ENSG00000207441	RNU6-21P	16:62221443-62221550	NOTEST	0	0	0	0	1	1
ENSG00000207442	ENSG00000207442	SNORD116-6	15:25068793-25492435	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207443	ENSG00000207443	RNU6-417P	7:62471840-62471947	NOTEST	0	0	0	0	1	1
ENSG00000207444	ENSG00000207444	SNORD56B	14:71759441-72207946	NOTEST	0	0	0	0	1	1
ENSG00000207445	ENSG00000207445	SNORD15B	11:75110529-75133324	NOTEST	0	1.37975	inf	0	1	1
ENSG00000207448	ENSG00000207448	RNU6-520P	4:71567471-71567575	NOTEST	0	0	0	0	1	1
ENSG00000207449	ENSG00000207449	RNU6-19P	15:65822755-65870687	NOTEST	0	0	0	0	1	1
ENSG00000207450	ENSG00000207450	Y_RNA	8:48685668-48872743	NOTEST	0	0	0	0	1	1
ENSG00000207451	ENSG00000207451	RNU6-291P	1:11166591-11322564	NOTEST	0	0	0	0	1	1
ENSG00000207452	ENSG00000207452	RNU6-606P	5:86563704-86708836	NOTEST	0	0	0	0	1	1
ENSG00000207453	ENSG00000207453	RNU6-535P	10:7528664-7528771	NOTEST	0	0	0	0	1	1
ENSG00000207454	ENSG00000207454	RNU6-1104P	7:100913218-100913322	NOTEST	0	0	0	0	1	1
ENSG00000207455	ENSG00000207455	RNU6-331P	22:30279143-30573064	NOTEST	0	0	0	0	1	1
ENSG00000207456	ENSG00000207456	RNU6-997P	2:53759809-54087297	NOTEST	0	0	0	0	1	1
ENSG00000207457	ENSG00000207457	RNU6-476P	22:42069933-42094140	NOTEST	0	0	0	0	1	1
ENSG00000207458	ENSG00000207458	RNY3P9	13:40800963-40801069	NOTEST	0	0	0	0	1	1
ENSG00000207459	ENSG00000207459	RNU6-1311P	5:133936833-134063513	NOTEST	0	0	0	0	1	1
ENSG00000207460	ENSG00000207460	SNORD116-19	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000207461	ENSG00000207461	RNU6-253P	6:117609462-117923691	NOTEST	0	0	0	0	1	1
ENSG00000207462	ENSG00000207462	RNU6-376P	11:118573050-118573156	NOTEST	0	0	0	0	1	1
ENSG00000207465	ENSG00000207465	RNU6-734P	6:146920100-147136598	NOTEST	0	0	0	0	1	1
ENSG00000207466	ENSG00000207466	Y_RNA	1:39416496-39416597	NOTEST	0	0	0	0	1	1
ENSG00000207467	ENSG00000207467	Y_RNA	12:49203693-49203799	NOTEST	0	0	0	0	1	1
ENSG00000207468	ENSG00000207468	SNORA19	10:120794355-120840316	NOTEST	0	0	0	0	1	1
ENSG00000207472	ENSG00000207472	RNU6-41P	1:182951346-182951453	NOTEST	0	0	0	0	1	1
ENSG00000207473	ENSG00000207473	Y_RNA	10:74870216-75118617	NOTEST	0	0	0	0	1	1
ENSG00000207474	ENSG00000207474	RNY1P7	13:25254548-25285921	NOTEST	0	0	0	0	1	1
ENSG00000207475	ENSG00000207475	SNORA42	1:155882833-155904191	NOTEST	0	0	0	0	1	1
ENSG00000207476	ENSG00000207476	RNU6-286P	21:14982497-15013906	NOTEST	0	0	0	0	1	1
ENSG00000207477	ENSG00000207477	RNU6-318P	12:31516414-31522235	NOTEST	0	0	0	0	1	1
ENSG00000207480	ENSG00000207480	Y_RNA	4:89206093-89252573	NOTEST	0	0	0	0	1	1
ENSG00000207481	ENSG00000207481	Y_RNA	4:41305253-41305354	NOTEST	0	0	0	0	1	1
ENSG00000207483	ENSG00000207483	RNU6-1067P	10:28956847-28956954	NOTEST	0	0	0	0	1	1
ENSG00000207484	ENSG00000207484	Y_RNA	15:52121824-52392720	NOTEST	0	0	0	0	1	1
ENSG00000207486	ENSG00000207486	RNU6-1044P	X:72617366-72617473	NOTEST	0	0	0	0	1	1
ENSG00000207488	ENSG00000207488	Y_RNA	7:89874487-89940377	NOTEST	0	0	0	0	1	1
ENSG00000207490	ENSG00000207490	RNU6-987P	6:25279305-25620758	NOTEST	0	0	0	0	1	1
ENSG00000207491	ENSG00000207491	RNU6-423P	1:212859759-212873327	NOTEST	0	0	0	0	1	1
ENSG00000207492	ENSG00000207492	RNU6-713P	12:40787196-40964632	NOTEST	0	0	0	0	1	1
ENSG00000207493	ENSG00000207493	SNORA46	16:58549382-58663790	NOTEST	0	0	0	0	1	1
ENSG00000207494	ENSG00000207494	Y_RNA	10:126490353-126525239	NOTEST	0	0	0	0	1	1
ENSG00000207495	ENSG00000207495	RNY3P10	13:70274725-70713561	NOTEST	0	0	0	0	1	1
ENSG00000207496	ENSG00000207496	SNORA7A	3:12837970-12913415	NOTEST	0	3.61086	inf	0	1	1
ENSG00000207497	ENSG00000207497	Y_RNA	4:186506597-186877806	NOTEST	0	0	0	0	1	1
ENSG00000207499	ENSG00000207499	Y_RNA	6:106868580-106868682	NOTEST	0	0	0	0	1	1
ENSG00000207500	ENSG00000207500	SNORD102	13:27825445-27830828	NOTEST	0	0	0	0	1	1
ENSG00000207502	ENSG00000207502	SNORA42	1:116164492-116164626	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207503	ENSG00000207503	SNORA32	21:42911132-42911253	NOTEST	0	0	0	0	1	1
ENSG00000207504	ENSG00000207504	RNU6-1031P	1:68006809-68006916	NOTEST	0	0	0	0	1	1
ENSG00000207505	ENSG00000207505	RNU6-1105P	3:186489629-186489736	NOTEST	0	0	0	0	1	1
ENSG00000207507	ENSG00000207507	RNU6-9	19:893483-893590	NOTEST	0	0	0	0	1	1
ENSG00000207508	ENSG00000207508	RNU6-1237P	1:40627044-40706593	NOTEST	0	0	0	0	1	1
ENSG00000207511	ENSG00000207511	RNU6-771P	1:13384734-13384841	NOTEST	0	0	0	0	1	1
ENSG00000207512	ENSG00000207512	Y_RNA	3:38537617-38583652	NOTEST	0	0	0	0	1	1
ENSG00000207513	ENSG00000207513	RNU1-3	1:16993279-16993443	NOTEST	0	0	0	0	1	1
ENSG00000207514	ENSG00000207514	RNU6-385P	16:72410602-72410659	NOTEST	0	0	0	0	1	1
ENSG00000207515	ENSG00000207515	RNU6-555P	X:89852233-89852339	NOTEST	0	0	0	0	1	1
ENSG00000207516	ENSG00000207516	SNORA41	15:45722726-45878488	NOTEST	0	0	0	0	1	1
ENSG00000207518	ENSG00000207518	RNU6-59P	13:22066835-22178353	NOTEST	0	0	0	0	1	1
ENSG00000207523	ENSG00000207523	SNORA66	1:93297581-93307481	NOTEST	0	0	0	0	1	1
ENSG00000207524	ENSG00000207524	RNU6-33P	4:89442135-89629693	NOTEST	0	0	0	0	1	1
ENSG00000207525	ENSG00000207525	Y_RNA	16:74485855-74641012	NOTEST	0	0	0	0	1	1
ENSG00000207546	ENSG00000207546	MIR548C	12:65004292-65091347	NOTEST	0	0	0	0	1	1
ENSG00000207547	ENSG00000207547	MIR25	7:99690350-99726118	NOTEST	0	0	0	0	1	1
ENSG00000207548	ENSG00000207548	MIR217	2:56179292-56613308	NOTEST	0	0	0	0	1	1
ENSG00000207549	ENSG00000207549	MIR521-2	19:54219847-54219934	NOTEST	0	0	0	0	1	1
ENSG00000207550	ENSG00000207550	MIR99B	19:52188615-52215640	NOTEST	0	0	0	0	1	1
ENSG00000207551	ENSG00000207551	MIR608	10:102729214-102754158	NOTEST	0	0	0	0	1	1
ENSG00000207552	ENSG00000207552	MIR633	17:61012762-61044171	NOTEST	0	0	0	0	1	1
ENSG00000207553	ENSG00000207553	MIR518C	19:54211988-54212089	NOTEST	0	0	0	0	1	1
ENSG00000207554	ENSG00000207554	MIR647	20:62571185-62587769	NOTEST	0	0	0	0	1	1
ENSG00000207555	ENSG00000207555	MIR520F	19:54185412-54185499	NOTEST	0	0	0	0	1	1
ENSG00000207556	ENSG00000207556	MIR636	17:74722911-74777531	NOTEST	0	0	0	0	1	1
ENSG00000207558	ENSG00000207558	MIR487A	14:101518782-101518862	NOTEST	0	0	0	0	1	1
ENSG00000207559	ENSG00000207559	MIR578	4:166282345-166419472	NOTEST	0	0	0	0	1	1
ENSG00000207561	ENSG00000207561	MIR635	17:66255322-66760023	NOTEST	0	0	0	0	1	1
ENSG00000207562	ENSG00000207562	MIR34C	11:111384163-111384240	NOTEST	0	0	0	0	1	1
ENSG00000207563	ENSG00000207563	MIR23B	9:97488982-97849441	NOTEST	0	0	0	0	1	1
ENSG00000207568	ENSG00000207568	MIR203	14:104583741-104583851	NOTEST	0	0	0	0	1	1
ENSG00000207569	ENSG00000207569	MIR433	14:101346991-101351184	NOTEST	0	0	0	0	1	1
ENSG00000207571	ENSG00000207571	MIR615	12:54375292-54449814	NOTEST	0	0	0	0	1	1
ENSG00000207572	ENSG00000207572	MIR363	X:133303407-133303482	NOTEST	0	0	0	0	1	1
ENSG00000207573	ENSG00000207573	MIR550A2	7:32535037-33102409	NOTEST	0	0	0	0	1	1
ENSG00000207574	ENSG00000207574	MIR661	8:144989320-145050902	NOTEST	0	0	0	0	1	1
ENSG00000207575	ENSG00000207575	MIR649	22:21353392-21399306	NOTEST	0	0	0	0	1	1
ENSG00000207577	ENSG00000207577	MIR587	6:107165326-107235416	NOTEST	0	0	0	0	1	1
ENSG00000207578	ENSG00000207578	MIR583	5:95220801-96143803	NOTEST	0	0	0	0	1	1
ENSG00000207579	ENSG00000207579	MIR662	16:819427-833370	NOTEST	0	0	0	0	1	1
ENSG00000207580	ENSG00000207580	MIR526B	19:54197646-54197729	NOTEST	0	0	0	0	1	1
ENSG00000207581	ENSG00000207581	MIR199B	9:130928342-131017527	NOTEST	0	0	0	0	1	1
ENSG00000207582	ENSG00000207582	MIR30B	8:135812762-135812850	NOTEST	0	0	0	0	1	1
ENSG00000207583	ENSG00000207583	MIR606	10:77312215-77312311	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207584	ENSG00000207584	MIR196B	7:27202053-27219880	NOTEST	0	0	0	0	1	1
ENSG00000207585	ENSG00000207585	MIR181D	19:13972876-13991571	NOTEST	0	0	0	0	1	1
ENSG00000207586	ENSG00000207586	MIR135A2	12:97825430-97958813	NOTEST	0	0	0	0	1	1
ENSG00000207587	ENSG00000207587	MIR544A	14:101511493-101518132	NOTEST	0	0	0	0	1	1
ENSG00000207588	ENSG00000207588	MIR593	7:127292233-127732661	NOTEST	0	0	0	0	1	1
ENSG00000207589	ENSG00000207589	MIR508	X:146318430-146318545	NOTEST	0	0	0	0	1	1
ENSG00000207590	ENSG00000207590	MIR215	1:220267443-220321380	NOTEST	0	0	0	0	1	1
ENSG00000207594	ENSG00000207594	MIR520A	19:54194134-54194219	NOTEST	0	0	0	0	1	1
ENSG00000207595	ENSG00000207595	MIR181A2	9:127279553-127535206	NOTEST	0	0	0	0	1	1
ENSG00000207597	ENSG00000207597	MIR490	7:136370305-136866854	NOTEST	0	0	0	0	1	1
ENSG00000207598	ENSG00000207598	MIR124-3	20:61798148-61812255	NOTEST	0	0	0	0	1	1
ENSG00000207599	ENSG00000207599	MIR520E	19:54178964-54179051	NOTEST	0	0	0	0	1	1
ENSG00000207600	ENSG00000207600	MIR598	8:10753554-11058875	NOTEST	0	0	0	0	1	1
ENSG00000207601	ENSG00000207601	MIR611	11:61447904-61634826	NOTEST	0	0	0	0	1	1
ENSG00000207602	ENSG00000207602	MIR106A	X:133304227-133304308	NOTEST	0	0	0	0	1	1
ENSG00000207603	ENSG00000207603	MIR7-1	9:86582997-86595569	NOTEST	0	0	0	0	1	1
ENSG00000207604	ENSG00000207604	MIR206	6:52009146-52009232	NOTEST	0	0	0	0	1	1
ENSG00000207605	ENSG00000207605	MIR191	3:48955220-49060928	NOTEST	0	0	0	0	1	1
ENSG00000207606	ENSG00000207606	MIR554	1:151512780-151556059	NOTEST	0	0	0	0	1	1
ENSG00000207607	ENSG00000207607	MIR200A	1:1103242-1103332	NOTEST	0	0	0	0	1	1
ENSG00000207608	ENSG00000207608	MIR127	14:101346991-101351184	NOTEST	0	0	0	0	1	1
ENSG00000207609	ENSG00000207609	MIR491	9:20658307-21031635	NOTEST	0	0	0	0	1	1
ENSG00000207611	ENSG00000207611	MIR149	2:241375087-241407493	NOTEST	0	0	0	0	1	1
ENSG00000207612	ENSG00000207612	MIR604	10:29698330-30025710	NOTEST	0	0	0	0	1	1
ENSG00000207613	ENSG00000207613	MIR181C	19:13972876-13991571	NOTEST	0	0	0	0	1	1
ENSG00000207614	ENSG00000207614	MIR193A	17:29887014-29887102	NOTEST	0	0	0	0	1	1
ENSG00000207615	ENSG00000207615	MIR515-2	19:54188262-54188345	NOTEST	0	0	0	0	1	1
ENSG00000207616	ENSG00000207616	MIR515-1	19:54182256-54182339	NOTEST	0	0	0	0	1	1
ENSG00000207617	ENSG00000207617	MIR3074	9:97488982-97849441	NOTEST	0	0	0	0	1	1
ENSG00000207619	ENSG00000207619	MIR585	5:168081517-168728133	NOTEST	0	0	0	0	1	1
ENSG00000207620	ENSG00000207620	MIR516A2	19:54264386-54264476	NOTEST	0	0	0	0	1	1
ENSG00000207621	ENSG00000207621	MIR224	X:151121595-151143152	NOTEST	0	0	0	0	1	1
ENSG00000207622	ENSG00000207622	MIR619	12:109176465-109251366	NOTEST	0	0	0	0	1	1
ENSG00000207624	ENSG00000207624	MIR194-1	1:220267443-220321380	NOTEST	0	0	0	0	1	1
ENSG00000207625	ENSG00000207625	MIR128-2	3:35680436-35835988	NOTEST	0	0	0	0	1	1
ENSG00000207626	ENSG00000207626	MIR562	2:232825954-233209060	NOTEST	0	0	0	0	1	1
ENSG00000207627	ENSG00000207627	MIR581	5:53179774-53606412	NOTEST	0	0	0	0	1	1
ENSG00000207628	ENSG00000207628	MIR651	X:8095005-8095102	NOTEST	0	0	0	0	1	1
ENSG00000207629	ENSG00000207629	MIR526A1	19:54209505-54209590	NOTEST	0	0	0	0	1	1
ENSG00000207630	ENSG00000207630	MIR7-3	19:4769116-4772545	NOTEST	0	0	0	0	1	1
ENSG00000207631	ENSG00000207631	MIR641	19:40736223-40791443	NOTEST	0	0	0	0	1	1
ENSG00000207632	ENSG00000207632	MIR588	6:126805776-126805859	NOTEST	0	0	0	0	1	1
ENSG00000207633	ENSG00000207633	MIR505	X:138808504-139027435	NOTEST	0	0	0	0	1	1
ENSG00000207634	ENSG00000207634	MIR521-1	19:54251889-54251976	NOTEST	0	0	0	0	1	1
ENSG00000207635	ENSG00000207635	MIR499A	20:33563205-33680674	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207636	ENSG00000207636	MIR631	15:75639295-75648087	NOTEST	0	0	0	0	1	1
ENSG00000207637	ENSG00000207637	MIR595	7:157331749-158380480	NOTEST	0	0	0	0	1	1
ENSG00000207638	ENSG00000207638	MIR99A	21:17442841-17999716	NOTEST	0	0	0	0	1	1
ENSG00000207639	ENSG00000207639	MIR193B	16:14396144-14420210	NOTEST	0	0	0	0	1	1
ENSG00000207641	ENSG00000207641	MIR510	X:146353852-146353926	NOTEST	0	0	0	0	1	1
ENSG00000207642	ENSG00000207642	MIR571	4:331602-378653	NOTEST	0	0	0	0	1	1
ENSG00000207643	ENSG00000207643	Z95704.1	4:53178-88099	NOTEST	0	0	0	0	1	1
ENSG00000207644	ENSG00000207644	MIR512-2	19:54172410-54172508	NOTEST	0	0	0	0	1	1
ENSG00000207645	ENSG00000207645	MIR512-1	19:54169926-54170024	NOTEST	0	0	0	0	1	1
ENSG00000207646	ENSG00000207646	MIR655	14:101511493-101518132	NOTEST	0	0	0	0	1	1
ENSG00000207647	ENSG00000207647	MIR153-1	2:220154344-220174370	NOTEST	0	0	0	0	1	1
ENSG00000207648	ENSG00000207648	MIR192	11:64658608-64658718	NOTEST	0	0	0	0	1	1
ENSG00000207649	ENSG00000207649	MIR138-2	16:56892429-56892513	NOTEST	0	0	0	0	1	1
ENSG00000207650	ENSG00000207650	MIR570	3:195384932-195467994	NOTEST	0	0	0	0	1	1
ENSG00000207651	ENSG00000207651	MIR28	3:187868993-188608460	NOTEST	0	0	0	0	1	1
ENSG00000207652	ENSG00000207652	MIR621	13:41384901-41384997	NOTEST	0	0	0	0	1	1
ENSG00000207653	ENSG00000207653	MIR558	2:32582095-32843966	NOTEST	0	0	0	0	1	1
ENSG00000207654	ENSG00000207654	MIR128-1	2:136289024-136482840	NOTEST	0	0	0	0	1	1
ENSG00000207656	ENSG00000207656	MIR489	7:93053798-93204042	NOTEST	0	0	0	0	1	1
ENSG00000207688	ENSG00000207688	MIR548AA2	17:65373574-65693372	NOTEST	0	0	0	0	1	1
ENSG00000207689	ENSG00000207689	MIR548A2	6:135560297-135560394	NOTEST	0	0	0	0	1	1
ENSG00000207690	ENSG00000207690	MIR630	15:72690613-72879692	NOTEST	0	0	0	0	1	1
ENSG00000207691	ENSG00000207691	MIR183	7:129414744-129414854	NOTEST	0	0	0	0	1	1
ENSG00000207692	ENSG00000207692	MIR592	7:126078651-126893348	NOTEST	0	0	0	0	1	1
ENSG00000207693	ENSG00000207693	MIR602	9:140513443-141019076	NOTEST	0	0	0	0	1	1
ENSG00000207695	ENSG00000207695	MIR184	15:79484048-79590580	NOTEST	0	0	0	0	1	1
ENSG00000207696	ENSG00000207696	MIR659	22:38226861-38285414	NOTEST	0	0	0	0	1	1
ENSG00000207697	ENSG00000207697	MIR573	4:24519063-24586173	NOTEST	0	0	0	0	1	1
ENSG00000207698	ENSG00000207698	MIR32	9:111777431-111882225	NOTEST	0	0	0	0	1	1
ENSG00000207699	ENSG00000207699	MIR518A2	19:54242586-54242673	NOTEST	0	0	0	0	1	1
ENSG00000207701	ENSG00000207701	MIR597	8:9412655-9639856	NOTEST	0	0	0	0	1	1
ENSG00000207702	ENSG00000207702	MIR211	15:31293263-31453476	NOTEST	0	0	0	0	1	1
ENSG00000207703	ENSG00000207703	MIR7-2	15:89155055-89155165	NOTEST	0	0	0	0	1	1
ENSG00000207704	ENSG00000207704	MIR548D1	8:124332089-124428590	NOTEST	0	0	0	0	1	1
ENSG00000207705	ENSG00000207705	MIR129-1	7:127847923-127847996	NOTEST	0	0	0	0	1	1
ENSG00000207706	ENSG00000207706	MIR518F	19:54203268-54203355	NOTEST	0	0	0	0	1	1
ENSG00000207707	ENSG00000207707	MIR639	19:14625581-14676792	NOTEST	0	0	0	0	1	1
ENSG00000207708	ENSG00000207708	MIR141	12:7072407-7178336	NOTEST	0	0	0	0	1	1
ENSG00000207709	ENSG00000207709	MIR197	1:110141514-110141589	NOTEST	0	0	0	0	1	1
ENSG00000207710	ENSG00000207710	MIR20B	X:133303838-133303907	NOTEST	0	0	0	0	1	1
ENSG00000207711	ENSG00000207711	MIR525	19:54200786-54200871	NOTEST	0	0	0	0	1	1
ENSG00000207712	ENSG00000207712	MIR627	15:42450898-42500514	NOTEST	0	0	0	0	1	1
ENSG00000207713	ENSG00000207713	MIR200C	12:7072407-7178336	NOTEST	0	0	0	0	1	1
ENSG00000207714	ENSG00000207714	MIR584	5:148303201-148442726	NOTEST	0	0	0	0	1	1
ENSG00000207715	ENSG00000207715	AC009065.2	16:2303116-2323419	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207716	ENSG00000207716	MIR572	4:11370450-11370545	NOTEST	0	0	0	0	1	1
ENSG00000207717	ENSG00000207717	MIR551B	3:167967309-168548387	NOTEST	0	0	0	0	1	1
ENSG00000207719	ENSG00000207719	MIR623	13:99853027-100038688	NOTEST	0	0	0	0	1	1
ENSG00000207720	ENSG00000207720	MIR555	1:155305058-155533775	NOTEST	0	0	0	0	1	1
ENSG00000207721	ENSG00000207721	MIR186	1:71514537-71546980	NOTEST	0	0	0	0	1	1
ENSG00000207722	ENSG00000207722	MIR520B	19:54204480-54204541	NOTEST	0	0	0	0	1	1
ENSG00000207725	ENSG00000207725	MIR222	X:45604638-45629677	NOTEST	0	0	0	0	1	1
ENSG00000207726	ENSG00000207726	MIR455	9:116917839-117074791	NOTEST	0	0	0	0	1	1
ENSG00000207728	ENSG00000207728	MIR449B	5:54408798-54469005	NOTEST	0	0	0	0	1	1
ENSG00000207729	ENSG00000207729	MIR556	1:162039563-162356600	NOTEST	0	0	0	0	1	1
ENSG00000207730	ENSG00000207730	MIR200B	1:1102483-1102578	NOTEST	0	0	0	0	1	1
ENSG00000207731	ENSG00000207731	MIR506	X:146312237-146312361	NOTEST	0	0	0	0	1	1
ENSG00000207732	ENSG00000207732	MIR218-1	4:20254882-20622184	NOTEST	0	0	0	0	1	1
ENSG00000207733	ENSG00000207733	MIR637	19:3958450-3971121	NOTEST	0	0	0	0	1	1
ENSG00000207734	ENSG00000207734	MIR517A	19:54215521-54215608	NOTEST	0	0	0	0	1	1
ENSG00000207735	ENSG00000207735	MIR520D	19:54223349-54223436	NOTEST	0	0	0	0	1	1
ENSG00000207736	ENSG00000207736	MIR657	17:79008947-79156964	NOTEST	0	0	0	0	1	1
ENSG00000207737	ENSG00000207737	MIR181B2	9:127279553-127535206	NOTEST	0	0	0	0	1	1
ENSG00000207738	ENSG00000207738	MIR520C	19:54210706-54210793	NOTEST	0	0	0	0	1	1
ENSG00000207739	ENSG00000207739	MIR218-2	5:168081517-168728133	NOTEST	0	0	0	0	1	1
ENSG00000207741	ENSG00000207741	MIR590	7:73588574-73611431	NOTEST	0	0	0	0	1	1
ENSG00000207742	ENSG00000207742	MIR382	14:101520637-101520723	NOTEST	0	0	0	0	1	1
ENSG00000207743	ENSG00000207743	MIR495	14:101500091-101500173	NOTEST	0	0	0	0	1	1
ENSG00000207744	ENSG00000207744	MIR10B	2:176986338-177037830	NOTEST	0	0	0	0	1	1
ENSG00000207746	ENSG00000207746	MIR575	4:83550691-83720010	NOTEST	0	0	0	0	1	1
ENSG00000207747	ENSG00000207747	MIR518D	19:54238130-54238217	NOTEST	0	0	0	0	1	1
ENSG00000207749	ENSG00000207749	MIR299	14:101490113-101490215	NOTEST	0	0	0	0	1	1
ENSG00000207750	ENSG00000207750	MIR553	1:100731762-100758325	NOTEST	0	0	0	0	1	1
ENSG00000207751	ENSG00000207751	MIR130B	22:22006558-22090123	NOTEST	0	0	0	0	1	1
ENSG00000207752	ENSG00000207752	MIR199A1	19:10828754-10946994	NOTEST	0	0	0	0	1	1
ENSG00000207753	ENSG00000207753	MIR452	X:151121595-151143152	NOTEST	0	0	0	0	1	1
ENSG00000207754	ENSG00000207754	MIR487B	14:101511493-101518132	NOTEST	0	0	0	0	1	1
ENSG00000207755	ENSG00000207755	MIR450A2	X:133674537-133674637	NOTEST	0	0	0	0	1	1
ENSG00000207756	ENSG00000207756	MIR580	5:36098513-36152063	NOTEST	0	0	0	0	1	1
ENSG00000207757	ENSG00000207757	MIR93	7:99690350-99726118	NOTEST	0	0	0	0	1	1
ENSG00000207758	ENSG00000207758	MIR532	X:49687224-49863892	NOTEST	0	0	0	0	1	1
ENSG00000207759	ENSG00000207759	MIR181A1	1:198776621-198906558	NOTEST	0	0	0	0	1	1
ENSG00000207761	ENSG00000207761	MIR329-1	14:101493121-101493201	NOTEST	0	0	0	0	1	1
ENSG00000207762	ENSG00000207762	MIR329-2	14:101493436-101493520	NOTEST	0	0	0	0	1	1
ENSG00000207763	ENSG00000207763	MIR617	12:81186298-81650533	NOTEST	0	0	0	0	1	1
ENSG00000207764	ENSG00000207764	MIR133A2	20:61141549-61167971	NOTEST	0	0	0	0	1	1
ENSG00000207765	ENSG00000207765	AL132780.1	14:23485751-23504439	NOTEST	0	0	0	0	1	1
ENSG00000207766	ENSG00000207766	MIR626	15:41913421-42062141	NOTEST	0	0	0	0	1	1
ENSG00000207767	ENSG00000207767	MIR516A1	19:54259994-54260084	NOTEST	0	0	0	0	1	1
ENSG00000207768	ENSG00000207768	MIR188	X:49687224-49863892	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207769	ENSG00000207769	MIR586	6:44777053-45632086	NOTEST	0	0	0	0	1	1
ENSG00000207770	ENSG00000207770	MIR568	3:114035321-114035416	NOTEST	0	0	0	0	1	1
ENSG00000207771	ENSG00000207771	MIR550A1	7:30323922-30452118	NOTEST	0	0	0	0	1	1
ENSG00000207773	ENSG00000207773	MIR642A	19:46171501-46186982	NOTEST	0	0	0	0	1	1
ENSG00000207775	ENSG00000207775	MIR548A1	6:18572014-18572111	NOTEST	0	0	0	0	1	1
ENSG00000207776	ENSG00000207776	MIR551A	1:3406483-3528059	NOTEST	0	0	0	0	1	1
ENSG00000207778	ENSG00000207778	MIR122	18:56118305-56118390	NOTEST	0	0	0	0	1	1
ENSG00000207779	ENSG00000207779	MIR15B	3:159943422-160203561	NOTEST	0	0	0	0	1	1
ENSG00000207780	ENSG00000207780	MIR648	22:18270414-18507325	NOTEST	0	0	0	0	1	1
ENSG00000207781	ENSG00000207781	MIR625	14:65877309-66210839	NOTEST	0	0	0	0	1	1
ENSG00000207782	ENSG00000207782	MIR150	19:50003780-50004614	NOTEST	0	0	0	0	1	1
ENSG00000207783	ENSG00000207783	MIR564	3:44803208-44914868	NOTEST	0	0	0	0	1	1
ENSG00000207784	ENSG00000207784	MIR542	X:133675370-133675467	NOTEST	0	0	0	0	1	1
ENSG00000207785	ENSG00000207785	MIR500A	X:49687224-49863892	NOTEST	0	0	0	0	1	1
ENSG00000207788	ENSG00000207788	MIR519C	19:54189722-54189809	NOTEST	0	0	0	0	1	1
ENSG00000207789	ENSG00000207789	MIR26A2	12:58213709-58240522	NOTEST	0	0	0	0	1	1
ENSG00000207797	ENSG00000207797	MIR187	18:33484780-33484889	NOTEST	0	0	0	0	1	1
ENSG00000207798	ENSG00000207798	MIR216A	2:56179292-56613308	NOTEST	0	0	0	0	1	1
ENSG00000207799	ENSG00000207799	MIR520G	19:54225419-54225509	NOTEST	0	0	0	0	1	1
ENSG00000207800	ENSG00000207800	MIR504	X:137713734-138304939	NOTEST	0	0	0	0	1	1
ENSG00000207802	ENSG00000207802	MIR646	20:58662894-59102516	NOTEST	0	0	0	0	1	1
ENSG00000207803	ENSG00000207803	MIR518A1	19:54234259-54234344	NOTEST	0	0	0	0	1	1
ENSG00000207804	ENSG00000207804	MIR599	8:100025493-100906290	NOTEST	0	0	0	0	1	1
ENSG00000207805	ENSG00000207805	MIR483	11:2150341-2182571	NOTEST	0	0	0	0	1	1
ENSG00000207806	ENSG00000207806	MIR522	19:54254464-54254551	NOTEST	0	0	0	0	1	1
ENSG00000207807	ENSG00000207807	MIR95	4:7967038-8160559	NOTEST	0	0	0	0	1	1
ENSG00000207808	ENSG00000207808	MIR27A	19:13947253-13947331	NOTEST	0	0	0	0	1	1
ENSG00000207810	ENSG00000207810	MIR519E	19:54183193-54183277	NOTEST	0	0	0	0	1	1
ENSG00000207811	ENSG00000207811	MIR34B	11:111383662-111383746	NOTEST	0	0	0	0	1	1
ENSG00000207812	ENSG00000207812	MIR19B2	X:133303700-133303797	NOTEST	0	0	0	0	1	1
ENSG00000207813	ENSG00000207813	MIR605	10:52750944-54073888	NOTEST	0	0	0	0	1	1
ENSG00000207814	ENSG00000207814	MIR147A	9:123007256-123007328	NOTEST	0	0	0	0	1	1
ENSG00000207815	ENSG00000207815	MIR563	3:15915277-15915356	NOTEST	0	0	0	0	1	1
ENSG00000207816	ENSG00000207816	MIR124-2	8:65285884-65296344	NOTEST	0	0	0	0	1	1
ENSG00000207817	ENSG00000207817	MIR614	12:13043715-13070871	NOTEST	0	0	0	0	1	1
ENSG00000207818	ENSG00000207818	MIR105-2	X:151307354-151619830	NOTEST	0	0	0	0	1	1
ENSG00000207819	ENSG00000207819	MIR9-3	15:89904809-89939471	NOTEST	0	0	0	0	1	1
ENSG00000207820	ENSG00000207820	MIR545	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000207821	ENSG00000207821	MIR640	19:19496634-19619740	NOTEST	0	0	0	0	1	1
ENSG00000207825	ENSG00000207825	MIR519B	19:54198466-54198547	NOTEST	0	0	0	0	1	1
ENSG00000207826	ENSG00000207826	MIR596	8:1765396-1765473	NOTEST	0	0	0	0	1	1
ENSG00000207827	ENSG00000207827	MIR30A	6:71931159-72130472	NOTEST	0	0	0	0	1	1
ENSG00000207830	ENSG00000207830	D86994.1	22:23040273-23040892	NOTEST	0	0	0	0	1	1
ENSG00000207832	ENSG00000207832	D87024.1	22:23198719-23198813	NOTEST	0	0	0	0	1	1
ENSG00000207833	ENSG00000207833	D86998.1	22:23134976-23135496	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207834	ENSG00000207834	D86994.2	22:23006897-23007377	NOTEST	0	0	0	0	1	1
ENSG00000207835	ENSG00000207835	D87015.1	22:23101184-23101707	NOTEST	0	0	0	0	1	1
ENSG00000207836	ENSG00000207836	MIR650	22:23165152-23165787	NOTEST	0	0	0	0	1	1
ENSG00000207837	ENSG00000207837	MIR517B	19:54224329-54224396	NOTEST	0	0	0	0	1	1
ENSG00000207838	ENSG00000207838	MIR517C	19:54244566-54244661	NOTEST	0	0	0	0	1	1
ENSG00000207839	ENSG00000207839	MIR33B	17:17584786-17740325	NOTEST	0	0	0	0	1	1
ENSG00000207844	ENSG00000207844	AC061975.8	17:26603011-26644809	NOTEST	0	0	0	0	1	1
ENSG00000207846	ENSG00000207846	AL035088.1	X:106671859-106672691	NOTEST	0	0	0	0	1	1
ENSG00000207849	ENSG00000207849	AC108867.1	4:136292331-136293079	NOTEST	0	0	0	0	1	1
ENSG00000207857	ENSG00000207857	AC097639.1	3:32280170-32411817	NOTEST	0	0	0	0	1	1
ENSG00000207858	ENSG00000207858	MIR622	13:90882637-90883936	NOTEST	0	0	0	0	1	1
ENSG00000207861	ENSG00000207861	MIR520H	19:54245765-54245853	NOTEST	0	0	0	0	1	1
ENSG00000207862	ENSG00000207862	MIR518B	19:54205990-54206073	NOTEST	0	0	0	0	1	1
ENSG00000207863	ENSG00000207863	MIR125B2	21:17442841-17999716	NOTEST	0	0	0	0	1	1
ENSG00000207864	ENSG00000207864	MIR27B	9:97488982-97849441	NOTEST	0	0	0	0	1	1
ENSG00000207865	ENSG00000207865	MIR34A	1:9211726-9211836	NOTEST	0	0	0	0	1	1
ENSG00000207866	ENSG00000207866	MIR514A2	X:146363460-146363548	NOTEST	0	0	0	0	1	1
ENSG00000207867	ENSG00000207867	MIR514A3	X:146366158-146366246	NOTEST	0	0	0	0	1	1
ENSG00000207868	ENSG00000207868	MIR514A1	X:146360764-146360862	NOTEST	0	0	0	0	1	1
ENSG00000207869	ENSG00000207869	MIR498	19:54177450-54177574	NOTEST	0	0	0	0	1	1
ENSG00000207870	ENSG00000207870	MIR221	X:45604638-45629677	NOTEST	0	0	0	0	1	1
ENSG00000207871	ENSG00000207871	MIR513B	X:146280561-146280645	NOTEST	0	0	0	0	1	1
ENSG00000207873	ENSG00000207873	MIR513A1	X:146294980-146295109	NOTEST	0	0	0	0	1	1
ENSG00000207874	ENSG00000207874	MIR610	11:28042166-28355054	NOTEST	0	0	0	0	1	1
ENSG00000207875	ENSG00000207875	MIRLET7B	22:46445357-46509808	NOTEST	0	0	0	0	1	1
ENSG00000207895	ENSG00000207895	AL161652.1	10:94200967-94201061	NOTEST	0	0	0	0	1	1
ENSG00000207922	ENSG00000207922	MIR566	3:49977439-50226508	NOTEST	0	0	0	0	1	1
ENSG00000207923	ENSG00000207923	MIR559	2:47572296-47614740	NOTEST	0	0	0	0	1	1
ENSG00000207924	ENSG00000207924	MIR196A2	12:54375292-54449814	NOTEST	0	0	0	0	1	1
ENSG00000207925	ENSG00000207925	MIR516B2	19:54228695-54228780	NOTEST	0	0	0	0	1	1
ENSG00000207926	ENSG00000207926	MIR135A1	3:52288436-52333083	NOTEST	0	0	0	0	1	1
ENSG00000207927	ENSG00000207927	MIR302A	4:113434671-113578748	NOTEST	0	0	0	0	1	1
ENSG00000207928	ENSG00000207928	MIR632	17:30593194-30708905	NOTEST	0	0	0	0	1	1
ENSG00000207930	ENSG00000207930	MIR603	10:23983674-24836772	NOTEST	0	0	0	0	1	1
ENSG00000207931	ENSG00000207931	MIR577	4:115519610-115599380	NOTEST	0	0	0	0	1	1
ENSG00000207932	ENSG00000207932	MIR33A	22:42227218-42303312	NOTEST	0	0	0	0	1	1
ENSG00000207933	ENSG00000207933	MIR9-1	1:156374041-156400493	NOTEST	0	0	0	0	1	1
ENSG00000207934	ENSG00000207934	MIR654	14:101506555-101506636	NOTEST	0	0	0	0	1	1
ENSG00000207935	ENSG00000207935	MIR204	9:73143978-74061820	NOTEST	0	0	0	0	1	1
ENSG00000207937	ENSG00000207937	MIR511-1	10:17851361-17953178	NOTEST	0	0	0	0	1	1
ENSG00000207938	ENSG00000207938	MIR511-2	10:18098351-18200091	NOTEST	0	0	0	0	1	1
ENSG00000207939	ENSG00000207939	MIR223	X:65238711-65238821	NOTEST	0	0	0	0	1	1
ENSG00000207940	ENSG00000207940	MIR567	3:111805181-111852152	NOTEST	0	0	0	0	1	1
ENSG00000207941	ENSG00000207941	MIR552	1:35135199-35135295	NOTEST	0	0	0	0	1	1
ENSG00000207942	ENSG00000207942	MIR136	14:101346991-101351184	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207943	ENSG00000207943	MIR634	17:64298753-64806861	NOTEST	0	0	0	0	1	1
ENSG00000207944	ENSG00000207944	MIR574	4:38869297-38947360	NOTEST	0	0	0	0	1	1
ENSG00000207945	ENSG00000207945	MIR658	22:38226861-38285414	NOTEST	0	0	0	0	1	1
ENSG00000207946	ENSG00000207946	MIR516B1	19:54240098-54240188	NOTEST	0	0	0	0	1	1
ENSG00000207947	ENSG00000207947	MIR152	17:46103532-46115392	NOTEST	0	0	0	0	1	1
ENSG00000207948	ENSG00000207948	MIR328	16:67233013-67237932	NOTEST	0	0	0	0	1	1
ENSG00000207949	ENSG00000207949	MIR214	1:171810620-172437971	NOTEST	0	0	0	0	1	1
ENSG00000207951	ENSG00000207951	MIR561	2:189156395-189460653	NOTEST	0	0	0	0	1	1
ENSG00000207952	ENSG00000207952	MIR624	14:31343719-31562818	NOTEST	0	0	0	0	1	1
ENSG00000207954	ENSG00000207954	MIR138-1	3:44155703-44155802	NOTEST	0	0	0	0	1	1
ENSG00000207955	ENSG00000207955	MIR219-2	9:131153739-131155789	NOTEST	0.0111835	0.0356583	1.67287	0	1	1
ENSG00000207956	ENSG00000207956	MIR579	5:32354455-32444867	NOTEST	0	0	0	0	1	1
ENSG00000207957	ENSG00000207957	MIR105-1	X:151307354-151619830	NOTEST	0	0	0	0	1	1
ENSG00000207959	ENSG00000207959	MIR656	14:101533060-101533138	NOTEST	0	0	0	0	1	1
ENSG00000207960	ENSG00000207960	MIR153-2	7:157331749-158380480	NOTEST	0	0	0	0	1	1
ENSG00000207961	ENSG00000207961	MIR496	14:101526909-101527011	NOTEST	0	0	0	0	1	1
ENSG00000207962	ENSG00000207962	MIR30C1	1:41156051-41237275	NOTEST	0	0	0	0	1	1
ENSG00000207963	ENSG00000207963	MIR569	3:170779127-171178197	NOTEST	0	0	0	0	1	1
ENSG00000207964	ENSG00000207964	MIR628	15:55495163-55800432	NOTEST	0	0	0	0	1	1
ENSG00000207965	ENSG00000207965	MIR629	15:70340128-70390515	NOTEST	0	0	0	0	1	1
ENSG00000207967	ENSG00000207967	MIR620	12:116395710-116715143	NOTEST	0	0	0	0	1	1
ENSG00000207969	ENSG00000207969	MIR507	X:146312501-146312595	NOTEST	0	0	0	0	1	1
ENSG00000207970	ENSG00000207970	MIR660	X:49687224-49863892	NOTEST	0	0	0	0	1	1
ENSG00000207971	ENSG00000207971	MIR125B1	11:121899062-121987031	NOTEST	0	0	0	0	1	1
ENSG00000207972	ENSG00000207972	MIR638	19:10828754-10946994	NOTEST	0	0	0	0	1	1
ENSG00000207973	ENSG00000207973	MIR589	7:5470965-5553429	NOTEST	0	0	0	0	1	1
ENSG00000207974	ENSG00000207974	MIR557	1:168344761-168344859	NOTEST	0	0	0	0	1	1
ENSG00000207975	ENSG00000207975	MIR181B1	1:198776621-198906558	NOTEST	0	0	0	0	1	1
ENSG00000207976	ENSG00000207976	MIR607	10:98588425-98588521	NOTEST	0	0	0	0	1	1
ENSG00000207977	ENSG00000207977	MIR524	19:54214255-54214342	NOTEST	0	0	0	0	1	1
ENSG00000207978	ENSG00000207978	MIR154	14:101526091-101526175	NOTEST	0	0	0	0	1	1
ENSG00000207979	ENSG00000207979	MIR527	19:54257271-54257356	NOTEST	0	0	0	0	1	1
ENSG00000207980	ENSG00000207980	MIR23A	19:13947400-13947473	NOTEST	0	0	0	0	1	1
ENSG00000207981	ENSG00000207981	MIR519D	19:54216600-54216688	NOTEST	0	0	0	0	1	1
ENSG00000207982	ENSG00000207982	MIR548B	6:119134604-119470552	NOTEST	0	0	0	0	1	1
ENSG00000207983	ENSG00000207983	MIR613	12:12878850-12982915	NOTEST	0	0	0	0	1	1
ENSG00000207984	ENSG00000207984	MIR513A2	X:146307343-146307470	NOTEST	0	0	0	0	1	1
ENSG00000207986	ENSG00000207986	AC136932.1	16:33961051-33962503	NOTEST	0	0	0	0	1	1
ENSG00000207987	ENSG00000207987	MIR518E	19:54233091-54233179	NOTEST	0	0	0	0	1	1
ENSG00000207988	ENSG00000207988	MIR576	4:110268630-110462052	NOTEST	0	0	0	0	1	1
ENSG00000207989	ENSG00000207989	MIR493	14:101335396-101335485	NOTEST	0	0	0	0	1	1
ENSG00000207990	ENSG00000207990	MIR182	7:129410222-129410332	NOTEST	0	0	0	0	1	1
ENSG00000207991	ENSG00000207991	MIR601	9:126118448-126692431	NOTEST	0	0	0	0	1	1
ENSG00000207992	ENSG00000207992	MIR519A1	19:54255650-54255735	NOTEST	0	0	0	0	1	1
ENSG00000207993	ENSG00000207993	MIR134	14:101521007-101521110	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000207994	ENSG00000207994	MIR100	11:122022936-122023016	NOTEST	0	0	0	0	1	1
ENSG00000207995	ENSG00000207995	MIR325	X:76225828-76225926	NOTEST	0	0	0	0	1	1
ENSG00000207996	ENSG00000207996	MIR301A	17:57059998-57232630	NOTEST	0	0	0	0	1	1
ENSG00000207997	ENSG00000207997	MIR644A	20:32951040-33099198	NOTEST	0	0	0	0	1	1
ENSG00000208000	ENSG00000208000	MIR509-1	X:146342049-146342143	NOTEST	0	0	0	0	1	1
ENSG00000208001	ENSG00000208001	MIR431	14:101346991-101351184	NOTEST	0	0	0	0	1	1
ENSG00000208002	ENSG00000208002	MIR643	19:52772823-52871031	NOTEST	0	0	0	0	1	1
ENSG00000208003	ENSG00000208003	MIR549	15:81071683-81282219	NOTEST	0	0	0	0	1	1
ENSG00000208004	ENSG00000208004	MIR323B	14:101522555-101522637	NOTEST	0	0	0	0	1	1
ENSG00000208005	ENSG00000208005	MIR503	X:133677366-133680741	NOTEST	0	0	0	0	1	1
ENSG00000208006	ENSG00000208006	MIR16-1	13:50601268-51423190	NOTEST	0	0	0	0	1	1
ENSG00000208008	ENSG00000208008	MIR125A	19:52188615-52215640	NOTEST	0	0	0	0	1	1
ENSG00000208009	ENSG00000208009	MIR130A	11:57405496-57429340	NOTEST	0	0	0	0	1	1
ENSG00000208012	ENSG00000208012	MIRLET7F2	X:53559056-53713673	NOTEST	0	0	0	0	1	1
ENSG00000208013	ENSG00000208013	MIR652	X:109245858-109425962	NOTEST	0	0	0	0	1	1
ENSG00000208014	ENSG00000208014	MIR653	7:93053798-93204042	NOTEST	0	0	0	0	1	1
ENSG00000208015	ENSG00000208015	MIR362	X:49687224-49863892	NOTEST	0	0	0	0	1	1
ENSG00000208016	ENSG00000208016	MIR523	19:54201638-54201725	NOTEST	0	0	0	0	1	1
ENSG00000208017	ENSG00000208017	MIR140	16:69796208-69975644	NOTEST	0	0	0	0	1	1
ENSG00000208018	ENSG00000208018	MIR645	20:49202322-49202416	NOTEST	0	0	0	0	1	1
ENSG00000208022	ENSG00000208022	MIR618	12:81186298-81650533	NOTEST	0	0	0	0	1	1
ENSG00000208023	ENSG00000208023	MIR185	22:20004536-20058066	NOTEST	0	0	0	0	1	1
ENSG00000208024	ENSG00000208024	MIR199A2	1:171810620-172437971	NOTEST	0	0	0	0	1	1
ENSG00000208025	ENSG00000208025	MIR591	7:95749531-95951459	NOTEST	0	0	0	0	1	1
ENSG00000208027	ENSG00000208027	MIR485	14:101521737-101521848	NOTEST	0	0	0	0	1	1
ENSG00000208028	ENSG00000208028	MIR616	12:57853917-57914300	NOTEST	0	0	0	0	1	1
ENSG00000208032	ENSG00000208032	MIR548A3	8:105496596-105496693	NOTEST	0	0	0	0	1	1
ENSG00000208033	ENSG00000208033	MIR609	10:105889645-105992120	NOTEST	0	0	0	0	1	1
ENSG00000208034	ENSG00000208034	MIR92A2	X:133303567-133303642	NOTEST	0	0	0	0	1	1
ENSG00000208035	ENSG00000208035	MIR143	5:148808480-148808586	NOTEST	0	0	0	0	1	1
ENSG00000208036	ENSG00000208036	MIR106B	7:99690350-99726118	NOTEST	0	0	0	0	1	1
ENSG00000208037	ENSG00000208037	MIR320A	8:22102474-22102556	NOTEST	0	0	0	0	1	1
ENSG00000208038	ENSG00000208038	MIR492	12:95227922-95228934	NOTEST	0	0	0	0	1	1
ENSG00000208308	ENSG00000208308	SNORA40	2:135809834-136288806	NOTEST	0	0	0	0	1	1
ENSG00000208317	ENSG00000208317	SNORD78	1:173832385-173872687	NOTEST	0	0	0	0	1	1
ENSG00000208772	ENSG00000208772	SNORD94	2:86333304-86369280	NOTEST	7.72853	6.02549	-0.359116	0	1	1
ENSG00000208797	ENSG00000208797	SNORD73A	4:152020724-152246784	NOTEST	0	0	0	0	1	1
ENSG00000208839	ENSG00000208839	SNORA35	X:113818550-114144624	NOTEST	0	0	0	0	1	1
ENSG00000208883	ENSG00000208883	SNORD96B	X:109437413-109699562	NOTEST	0	0	0	0	1	1
ENSG00000208892	ENSG00000208892	SNORA49	12:132434507-132565005	NOTEST	0	0	0	0	1	1
ENSG00000209042	ENSG00000209042	SNORD12C	20:47835883-47905797	NOTEST	0	0	0	0	1	1
ENSG00000209082	ENSG00000209082	MT-TL1	MT:3229-3304	NOTEST	0	0	0	0	1	1
ENSG00000209480	ENSG00000209480	SNORD83B	22:39708886-39716394	NOTEST	0	0	0	0	1	1
ENSG00000209482	ENSG00000209482	SNORD83A	22:39708886-39716394	NOTEST	0	0	0	0	1	1
ENSG00000209582	ENSG00000209582	SNORA48	17:7465191-7536700	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000209645	ENSG00000209645	SNORD105	19:10216898-10230596	NOTEST	0	0	0	0	1	1
ENSG00000209702	ENSG00000209702	SNORD41	19:12810007-12834825	NOTEST	0	0	0	0	1	1
ENSG00000210049	ENSG00000210049	MT-TF	MT:576-647	NOTEST	0	0	0	0	1	1
ENSG00000210077	ENSG00000210077	MT-TV	MT:1601-1670	NOTEST	0	0	0	0	1	1
ENSG00000210100	ENSG00000210100	MT-TI	MT:4262-4400	NOTEST	0	0	0	0	1	1
ENSG00000210107	ENSG00000210107	MT-TQ	MT:4262-4400	NOTEST	0	0	0	0	1	1
ENSG00000210112	ENSG00000210112	MT-TM	MT:4401-4469	NOTEST	0	0	0	0	1	1
ENSG00000210117	ENSG00000210117	MT-TW	MT:5511-5579	NOTEST	0	0	0	0	1	1
ENSG00000210127	ENSG00000210127	MT-TA	MT:5586-5655	NOTEST	0	0	0	0	1	1
ENSG00000210135	ENSG00000210135	MT-TN	MT:5656-5729	NOTEST	0	0	0	0	1	1
ENSG00000210140	ENSG00000210140	MT-TC	MT:5760-5891	NOTEST	0	0	0	0	1	1
ENSG00000210144	ENSG00000210144	MT-TY	MT:5760-5891	NOTEST	0	0	0	0	1	1
ENSG00000210151	ENSG00000210151	MT-TS1	MT:7445-7514	NOTEST	0	0	0	0	1	1
ENSG00000210154	ENSG00000210154	MT-TD	MT:7517-7585	NOTEST	0	0	0	0	1	1
ENSG00000210156	ENSG00000210156	MT-TK	MT:8294-8364	NOTEST	0	0	0	0	1	1
ENSG00000210164	ENSG00000210164	MT-TG	MT:9990-10058	NOTEST	0	0	0	0	1	1
ENSG00000210174	ENSG00000210174	MT-TR	MT:10404-10469	NOTEST	0	0	0	0	1	1
ENSG00000210176	ENSG00000210176	MT-TH	MT:12137-12206	NOTEST	0	0	0	0	1	1
ENSG00000210181	ENSG00000210181	RNU6ATAC4P	3:37009681-37009807	NOTEST	0	0	0	0	1	1
ENSG00000210184	ENSG00000210184	MT-TS2	MT:12206-12265	NOTEST	0	0	0	0	1	1
ENSG00000210191	ENSG00000210191	MT-TL2	MT:12265-12336	NOTEST	0	0	0	0	1	1
ENSG00000210194	ENSG00000210194	MT-TE	MT:14673-14742	NOTEST	0	0	0	0	1	1
ENSG00000210195	ENSG00000210195	MT-TT	MT:15887-15953	NOTEST	0	0	0	0	1	1
ENSG00000210196	ENSG00000210196	MT-TP	MT:15955-16023	NOTEST	0	0	0	0	1	1
ENSG00000210678	ENSG00000210678	RNU6ATAC2P	5:55593390-55593516	NOTEST	0	0	0	0	1	1
ENSG00000210709	ENSG00000210709	RNU6ATAC3P	17:44994135-45000400	NOTEST	0	0	0	0	1	1
ENSG00000210741	ENSG00000210741	MIR196A1	17:46684593-46712294	NOTEST	0	0	0	0	1	1
ENSG00000210825	ENSG00000210825	SNORA40	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000210839	ENSG00000210839	RNU6ATAC5P	4:73892464-73892590	NOTEST	0	0	0	0	1	1
ENSG00000210841	ENSG00000210841	RNU6ATAC26P	3:57605173-57605299	NOTEST	0	0	0	0	1	1
ENSG00000211137	ENSG00000211137	MIR190A	15:62682724-63176233	NOTEST	0	0	0	0	1	1
ENSG00000211445	ENSG00000211445	GPX3	5:150400123-150408554	NOTEST	0.282204	0.389526	0.464983	0	1	1
ENSG00000211448	ENSG00000211448	DIO2	14:80663872-80921812	NOTEST	0.0540599	0.172713	1.67575	0	1	1
ENSG00000211452	ENSG00000211452	DIO1	1:54356911-54376759	NOTEST	0.0631242	0.0140428	-2.16837	0	1	1
ENSG00000211454	ENSG00000211454	AKR7L	1:19592475-19600688	NOTEST	0.0557911	0.0310316	-0.846298	0	1	1
ENSG00000211482	ENSG00000211482	AC092574.1	4:403597-403704	NOTEST	0	0	0	0	1	1
ENSG00000211483	ENSG00000211483	AC018450.1	3:142884489-142884579	NOTEST	0	0	0	0	1	1
ENSG00000211491	ENSG00000211491	MIR320D1	13:41301963-41302011	NOTEST	0	0	0	0	1	1
ENSG00000211495	ENSG00000211495	AL009174.1	X:132669772-133119922	NOTEST	0	0	0	0	1	1
ENSG00000211498	ENSG00000211498	AC093311.1	5:93488670-94620279	NOTEST	0	0	0	0	1	1
ENSG00000211499	ENSG00000211499	AC110056.1	11:29298235-29298352	NOTEST	0	0	0	0	1	1
ENSG00000211508	ENSG00000211508	AL359538.1	13:25183216-25183313	NOTEST	0	0	0	0	1	1
ENSG00000211510	ENSG00000211510	AL590726.1	9:30773461-30774730	NOTEST	0	0	0	0	1	1
ENSG00000211513	ENSG00000211513	MIR320E	19:47150868-47220384	NOTEST	0	0	0	0	1	1
ENSG00000211514	ENSG00000211514	MIR454	17:57059998-57232630	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000211515	ENSG00000211515	AC079005.1	17:58754813-59488916	NOTEST	0	0	0	0	1	1
ENSG00000211517	ENSG00000211517	MIR671	7:150929574-150974982	NOTEST	0	0	0	0	1	1
ENSG00000211518	ENSG00000211518	AC006988.1	7:88269834-88269941	NOTEST	0	0	0	0	1	1
ENSG00000211519	ENSG00000211519	MIR147B	15:45722726-45878488	NOTEST	0	0	0	0	1	1
ENSG00000211520	ENSG00000211520	MIR216B	2:56179292-56613308	NOTEST	0	0	0	0	1	1
ENSG00000211524	ENSG00000211524	MIR718	X:153275950-153285440	NOTEST	0	0	0	0	1	1
ENSG00000211525	ENSG00000211525	BX323860.1	1:230184928-230184997	NOTEST	0	0	0	0	1	1
ENSG00000211526	ENSG00000211526	AL121869.1	X:91034259-91878229	NOTEST	0	0	0	0	1	1
ENSG00000211528	ENSG00000211528	AP001525.1	18:13823913-13823985	NOTEST	0	0	0	0	1	1
ENSG00000211530	ENSG00000211530	AL354933.1	6:72294423-72295609	NOTEST	0	0	0	0	1	1
ENSG00000211532	ENSG00000211532	MIR526A2	19:54230175-54230240	NOTEST	0	0	0	0	1	1
ENSG00000211534	ENSG00000211534	AL121588.1	20:37900182-37900258	NOTEST	0	0	0	0	1	1
ENSG00000211535	ENSG00000211535	MIR711	3:48601505-48632700	NOTEST	0	0	0	0	1	1
ENSG00000211538	ENSG00000211538	MIR501	X:49687224-49863892	NOTEST	0	0	0	0	1	1
ENSG00000211542	ENSG00000211542	AC007436.1	12:9280378-9281241	NOTEST	0	0	0	0	1	1
ENSG00000211543	ENSG00000211543	MIR320B1	1:117214370-117214449	NOTEST	0	0	0	0	1	1
ENSG00000211544	ENSG00000211544	AC069286.1	7:3303663-4308632	NOTEST	0	0	0	0	1	1
ENSG00000211553	ENSG00000211553	AC118278.1	4:123965-157779	NOTEST	0	0	0	0	1	1
ENSG00000211554	ENSG00000211554	AC096645.1	1:203968372-203968471	NOTEST	0	0	0	0	1	1
ENSG00000211556	ENSG00000211556	AL157702.1	9:116554637-116554719	NOTEST	0	0	0	0	1	1
ENSG00000211562	ENSG00000211562	AC103686.1	8:48685668-48872743	NOTEST	0	0	0	0	1	1
ENSG00000211563	ENSG00000211563	MIR338	17:79008947-79156964	NOTEST	0	0	0	0	1	1
ENSG00000211566	ENSG00000211566	AC114788.1	2:239894623-239894706	NOTEST	0	0	0	0	1	1
ENSG00000211568	ENSG00000211568	MIR670	11:43577985-43902276	NOTEST	0	0	0	0	1	1
ENSG00000211571	ENSG00000211571	AC010525.2	19:56186591-56249768	NOTEST	0	0	0	0	1	1
ENSG00000211573	ENSG00000211573	AC125238.1	2:204629017-204630316	NOTEST	0	0	0	0	1	1
ENSG00000211574	ENSG00000211574	MIR770	14:101245746-101327368	NOTEST	0	0	0	0	1	1
ENSG00000211575	ENSG00000211575	MIR760	1:94027346-94312706	NOTEST	0	0	0	0	1	1
ENSG00000211577	ENSG00000211577	AC090673.1	12:66151799-66360075	NOTEST	0	0	0	0	1	1
ENSG00000211578	ENSG00000211578	MIR766	X:118749686-118827333	NOTEST	0	0	0	0	1	1
ENSG00000211579	ENSG00000211579	MIR759	13:53384178-53384274	NOTEST	0	0	0	0	1	1
ENSG00000211580	ENSG00000211580	MIR769	19:46498338-46526323	NOTEST	0	0	0	0	1	1
ENSG00000211581	ENSG00000211581	MIR765	1:156904631-157015162	NOTEST	0	0	0	0	1	1
ENSG00000211582	ENSG00000211582	MIR758	14:101492356-101492444	NOTEST	0	0	0	0	1	1
ENSG00000211583	ENSG00000211583	MIR767	X:151307354-151619830	NOTEST	0	0	0	0	1	1
ENSG00000211588	ENSG00000211588	AL023913.1	20:9966735-10349424	NOTEST	0	0	0	0	1	1
ENSG00000211590	ENSG00000211590	MIR802	21:36160097-37376965	NOTEST	0	0	0	0	1	1
ENSG00000211591	ENSG00000211591	MIR762	16:30844946-30906541	NOTEST	0	0	0	0	1	1
ENSG00000211592	ENSG00000211592	IGKC	2:89109983-89165653	NOTEST	0	0	0	0	1	1
ENSG00000211593	ENSG00000211593	IGKJ5	2:89109983-89165653	NOTEST	0	0	0	0	1	1
ENSG00000211594	ENSG00000211594	IGKJ4	2:89109983-89165653	NOTEST	0	0	0	0	1	1
ENSG00000211595	ENSG00000211595	IGKJ3	2:89109983-89165653	NOTEST	0	0	0	0	1	1
ENSG00000211596	ENSG00000211596	IGKJ2	2:89109983-89165653	NOTEST	0	0	0	0	1	1
ENSG00000211597	ENSG00000211597	IGKJ1	2:89109983-89165653	NOTEST	0	0	0	0	1	1
ENSG00000211598	ENSG00000211598	IGKV4-1	2:89184912-89185669	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000211599	ENSG00000211599	IGKV5-2	2:89196747-89197300	NOTEST	0	0	0	0	1	1
ENSG00000211611	ENSG00000211611	IGKV6-21	2:89459234-89459850	NOTEST	0	0	0	0	1	1
ENSG00000211619	ENSG00000211619	IGKV2-40	2:89629872-89630186	NOTEST	0	0	0	0	1	1
ENSG00000211623	ENSG00000211623	IGKV2D-26	2:90024731-90025512	NOTEST	0	0	0	0	1	1
ENSG00000211625	ENSG00000211625	IGKV3D-20	2:90077679-90078311	NOTEST	0	0	0	0	1	1
ENSG00000211626	ENSG00000211626	IGKV6D-41	2:90108503-90109080	NOTEST	0	0	0	0	1	1
ENSG00000211630	ENSG00000211630	IGKV1D-13	2:90192767-90193424	NOTEST	0	0	0	0	1	1
ENSG00000211632	ENSG00000211632	IGKV3D-11	2:90211642-90212253	NOTEST	0	0	0	0	1	1
ENSG00000211633	ENSG00000211633	IGKV1D-42	2:90229044-90229531	NOTEST	0	0	0	0	1	1
ENSG00000211637	ENSG00000211637	IGLV4-69	22:22345495-22398340	NOTEST	0	0	0	0	1	1
ENSG00000211638	ENSG00000211638	IGLV8-61	22:22453109-22453622	NOTEST	0	0	0	0	1	1
ENSG00000211639	ENSG00000211639	IGLV4-60	22:22516591-22517074	NOTEST	0	0	0	0	1	1
ENSG00000211640	ENSG00000211640	IGLV6-57	22:22550112-22550860	NOTEST	0	0	0	0	1	1
ENSG00000211641	ENSG00000211641	IGLV11-55	22:22556056-22556600	NOTEST	0	0	0	0	1	1
ENSG00000211642	ENSG00000211642	IGLV10-54	22:22569183-22569660	NOTEST	0	0	0	0	1	1
ENSG00000211644	ENSG00000211644	IGLV1-51	22:22657588-22677336	NOTEST	0.194302	0.138787	-0.485423	0	1	1
ENSG00000211645	ENSG00000211645	IGLV1-50	22:22681657-22682172	NOTEST	0	0	0	0	1	1
ENSG00000211647	ENSG00000211647	IGLV5-48	22:22707288-22707781	NOTEST	0	0	0	0	1	1
ENSG00000211648	ENSG00000211648	IGLV1-47	22:22712086-22712608	NOTEST	0	0	0	0	1	1
ENSG00000211649	ENSG00000211649	IGLV7-46	22:22723981-22724454	NOTEST	0	0	0	0	1	1
ENSG00000211650	ENSG00000211650	IGLV5-45	22:22730354-22730874	NOTEST	0	0	0	0	1	1
ENSG00000211651	ENSG00000211651	IGLV1-44	22:22735134-22735715	NOTEST	0	0	0	0	1	1
ENSG00000211652	ENSG00000211652	IGLV7-43	22:22749355-22749827	NOTEST	0	0	0	0	1	1
ENSG00000211653	ENSG00000211653	IGLV1-40	22:22764097-22764614	NOTEST	0	0	0	0	1	1
ENSG00000211654	ENSG00000211654	IGLV5-37	22:22781875-22782371	NOTEST	0	0	0	0	1	1
ENSG00000211655	ENSG00000211655	IGLV1-36	22:22786295-22786802	NOTEST	0	0	0	0	1	1
ENSG00000211656	ENSG00000211656	IGLV2-33	22:22930625-22931145	NOTEST	0	0	0	0	1	1
ENSG00000211657	ENSG00000211657	IGLV3-32	22:22936997-22937501	NOTEST	0	0	0	0	1	1
ENSG00000211658	ENSG00000211658	IGLV3-27	22:23010757-23011276	NOTEST	0	0	0	0	1	1
ENSG00000211659	ENSG00000211659	IGLV3-25	22:23029189-23029735	NOTEST	0	0	0	0	1	1
ENSG00000211660	ENSG00000211660	IGLV2-23	22:23040273-23040892	NOTEST	0	0	0	0	1	1
ENSG00000211661	ENSG00000211661	IGLV3-22	22:23046749-23047307	NOTEST	0	0	0	0	1	1
ENSG00000211662	ENSG00000211662	IGLV3-21	22:23054173-23055688	NOTEST	0	0	0	0	1	1
ENSG00000211663	ENSG00000211663	IGLV3-19	22:23063107-23063630	NOTEST	0	0	0	0	1	1
ENSG00000211664	ENSG00000211664	IGLV2-18	22:23077062-23077584	NOTEST	0	0	0	0	1	1
ENSG00000211665	ENSG00000211665	IGLV3-16	22:23089869-23090398	NOTEST	0	0	0	0	1	1
ENSG00000211666	ENSG00000211666	IGLV2-14	22:23101184-23101707	NOTEST	0	0	0	0	1	1
ENSG00000211667	ENSG00000211667	IGLV3-12	22:23114316-23115079	NOTEST	0	0	0	0	1	1
ENSG00000211668	ENSG00000211668	IGLV2-11	22:23134976-23135496	NOTEST	0	0	0	0	1	1
ENSG00000211669	ENSG00000211669	IGLV3-10	22:23154243-23154782	NOTEST	0	0	0	0	1	1
ENSG00000211670	ENSG00000211670	IGLV3-9	22:23161506-23162253	NOTEST	0	0	0	0	1	1
ENSG00000211671	ENSG00000211671	IGLV2-8	22:23165152-23165787	NOTEST	0	0	0	0	1	1
ENSG00000211672	ENSG00000211672	IGLV4-3	22:23213685-23214214	NOTEST	0	0	0	0	1	1
ENSG00000211673	ENSG00000211673	IGLV3-1	22:23222885-23223576	NOTEST	0	0	0	0	1	1
ENSG00000211674	ENSG00000211674	IGLJ1	22:23229959-23238287	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000211675	ENSG00000211675	IGLC1	22:23229959-23238287	NOTEST	0	0	0	0	1	1
ENSG00000211676	ENSG00000211676	IGLJ2	22:23241660-23241835	NOTEST	0	0	0	0	1	1
ENSG00000211677	ENSG00000211677	IGLC2	22:23243155-23243617	NOTEST	0	0	0	0	1	1
ENSG00000211678	ENSG00000211678	IGLJ3	22:23247029-23247205	NOTEST	0	0	0	0	1	1
ENSG00000211679	ENSG00000211679	IGLC3	22:23248511-23248973	NOTEST	0	0	0	0	1	1
ENSG00000211680	ENSG00000211680	IGLJ4	22:23252743-23252776	NOTEST	0	0	0	0	1	1
ENSG00000211681	ENSG00000211681	IGLJ5	22:23256407-23256479	NOTEST	0	0	0	0	1	1
ENSG00000211682	ENSG00000211682	IGLJ6	22:23260303-23260373	NOTEST	0	0	0	0	1	1
ENSG00000211683	ENSG00000211683	KB-1572G7.3	22:23950638-24059543	NOTEST	0.0493316	0	#NAME?	0	1	1
ENSG00000211684	ENSG00000211684	IGLJ7	22:23263561-23263607	NOTEST	0	0	0	0	1	1
ENSG00000211685	ENSG00000211685	IGLC7	22:23264765-23265203	NOTEST	0	0	0	0	1	1
ENSG00000211687	ENSG00000211687	TRGJ2	7:38292980-38293030	NOTEST	0	0	0	0	1	1
ENSG00000211688	ENSG00000211688	TRGJP2	7:38295937-38295997	NOTEST	0	0	0	0	1	1
ENSG00000211689	ENSG00000211689	TRGC1	7:38297479-38305279	NOTEST	0	0	0	0	1	1
ENSG00000211690	ENSG00000211690	TRGJ1	7:38309091-38309141	NOTEST	0	0	0	0	1	1
ENSG00000211691	ENSG00000211691	TRGJP	7:38313187-38313248	NOTEST	0	0	0	0	1	1
ENSG00000211692	ENSG00000211692	TRGJP1	7:38315859-38315919	NOTEST	0	0	0	0	1	1
ENSG00000211693	ENSG00000211693	TRGV11	7:38331216-38331679	NOTEST	0	0	0	0	1	1
ENSG00000211694	ENSG00000211694	TRGV10	7:38339411-38339923	NOTEST	0	0	0	0	1	1
ENSG00000211695	ENSG00000211695	TRGV9	7:38356617-38358462	NOTEST	0	0	0	0	1	1
ENSG00000211696	ENSG00000211696	TRGV8	7:38369943-38370536	NOTEST	0	0	0	0	1	1
ENSG00000211697	ENSG00000211697	TRGV5	7:38388955-38389623	NOTEST	0.0779781	0.0942276	0.27308	0	1	1
ENSG00000211698	ENSG00000211698	TRGV4	7:38393315-38394118	NOTEST	0	0.0203105	inf	0	1	1
ENSG00000211699	ENSG00000211699	TRGV3	7:38398112-38398763	NOTEST	0.115966	0.0316143	-1.87505	0	1	1
ENSG00000211701	ENSG00000211701	TRGV1	7:38407186-38407770	NOTEST	0	0	0	0	1	1
ENSG00000211706	ENSG00000211706	TRBV6-1	7:142028120-142028610	NOTEST	0	0	0	0	1	1
ENSG00000211707	ENSG00000211707	TRBV7-1	7:142032005-142032527	NOTEST	0	0	0	0	1	1
ENSG00000211710	ENSG00000211710	TRBV4-1	7:142013006-142013489	NOTEST	0	0	0	0	1	1
ENSG00000211713	ENSG00000211713	TRBV6-4	7:142250702-142251158	NOTEST	0	0	0	0	1	1
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ENSG00000211715	ENSG00000211715	TRBV5-3	7:142242280-142242747	NOTEST	0	0	0	0	1	1
ENSG00000211716	ENSG00000211716	TRBV9	7:142239536-142240058	NOTEST	0	0	0	0	1	1
ENSG00000211717	ENSG00000211717	TRBV10-1	7:142231572-142232090	NOTEST	0	0	0	0	1	1
ENSG00000211720	ENSG00000211720	TRBV11-1	7:142223819-142224284	NOTEST	0	0	0	0	1	1
ENSG00000211721	ENSG00000211721	TRBV6-5	7:142180514-142181016	NOTEST	0	0	0	0	1	1
ENSG00000211724	ENSG00000211724	TRBV6-6	7:142161930-142162407	NOTEST	0	0	0	0	1	1
ENSG00000211725	ENSG00000211725	TRBV5-5	7:142148927-142149399	NOTEST	0	0	0	0	1	1
ENSG00000211727	ENSG00000211727	TRBV7-6	7:142139277-142139815	NOTEST	0	0	0	0	1	1
ENSG00000211728	ENSG00000211728	TRBV5-6	7:142131411-142131918	NOTEST	0	0	0	0	1	1
ENSG00000211731	ENSG00000211731	TRBV5-7	7:142111392-142111859	NOTEST	0	0	0	0	1	1
ENSG00000211732	ENSG00000211732	TRBV6-9	7:142104120-142104553	NOTEST	0	0	0	0	1	1
ENSG00000211734	ENSG00000211734	TRBV5-1	7:142020495-142021363	NOTEST	0	0	0	0	1	1
ENSG00000211739	ENSG00000211739	TRBV12-2	7:142190637-142191080	NOTEST	0	0	0	0	1	1
ENSG00000211745	ENSG00000211745	TRBV4-2	7:142045251-142045816	NOTEST	0	0	0	0	1	1
ENSG00000211746	ENSG00000211746	TRBV19	7:142326362-142327046	NOTEST	0	0	0	0	1	1

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ENSG00000211747	ENSG00000211747	TRBV20-1	7:142334162-142334913	NOTEST	0.0613132	0.0437546	-0.486763	0	1	1
ENSG00000211749	ENSG00000211749	TRBV23-1	7:142353467-142353964	NOTEST	0	0	0	0	1	1
ENSG00000211750	ENSG00000211750	TRBV24-1	7:142364197-142364710	NOTEST	0	0.170854	inf	0	1	1
ENSG00000211751	ENSG00000211751	TRBV25-1	7:142378571-142379076	NOTEST	0	0	0	0	1	1
ENSG00000211752	ENSG00000211752	TRBV27	7:142423172-142423688	NOTEST	0	0	0	0	1	1
ENSG00000211753	ENSG00000211753	TRBV28	7:142428483-142428984	NOTEST	0	0	0	0	1	1
ENSG00000211764	ENSG00000211764	TRBJ2-1	7:142494048-142494098	NOTEST	0	0	0	0	1	1
ENSG00000211765	ENSG00000211765	TRBJ2-2	7:142494243-142494294	NOTEST	0	0	0	0	1	1
ENSG00000211766	ENSG00000211766	TRBJ2-2P	7:142494380-142494426	NOTEST	0	0	0	0	1	1
ENSG00000211767	ENSG00000211767	TRBJ2-3	7:142494530-142494579	NOTEST	0	0	0	0	1	1
ENSG00000211768	ENSG00000211768	TRBJ2-4	7:142494681-142494731	NOTEST	0	0	0	0	1	1
ENSG00000211769	ENSG00000211769	TRBJ2-5	7:142494802-142494850	NOTEST	0	0	0	0	1	1
ENSG00000211770	ENSG00000211770	TRBJ2-6	7:142494922-142494975	NOTEST	0	0	0	0	1	1
ENSG00000211771	ENSG00000211771	TRBJ2-7	7:142495139-142495186	NOTEST	0	0	0	0	1	1
ENSG00000211772	ENSG00000211772	TRBC2	7:142498724-142500432	NOTEST	0	0	0	0	1	1
ENSG00000211776	ENSG00000211776	TRAV2	14:22180543-22181066	NOTEST	0	0	0	0	1	1
ENSG00000211777	ENSG00000211777	TRAV3	14:22191959-22192568	NOTEST	0	0	0	0	1	1
ENSG00000211778	ENSG00000211778	TRAV4	14:22204433-22205264	NOTEST	0	0	0	0	1	1
ENSG00000211779	ENSG00000211779	TRAV5	14:22217461-22217989	NOTEST	0	0	0	0	1	1
ENSG00000211780	ENSG00000211780	TRAV6	14:22236728-22237320	NOTEST	0	0	0	0	1	1
ENSG00000211781	ENSG00000211781	TRAV7	14:22251209-22251720	NOTEST	0	0	0	0	1	1
ENSG00000211782	ENSG00000211782	TRAV8-1	14:22265458-22266058	NOTEST	0	0	0	0	1	1
ENSG00000211783	ENSG00000211783	TRAV9-1	14:22279673-22280149	NOTEST	0	0	0	0	1	1
ENSG00000211784	ENSG00000211784	TRAV10	14:22293635-22294239	NOTEST	0	0	0	0	1	1
ENSG00000211785	ENSG00000211785	TRAV12-1	14:22309421-22309956	NOTEST	0	0	0	0	1	1
ENSG00000211786	ENSG00000211786	TRAV8-2	14:22314718-22315403	NOTEST	0	0	0	0	1	1
ENSG00000211787	ENSG00000211787	TRAV8-3	14:22320734-22321183	NOTEST	0	0	0	0	1	1
ENSG00000211788	ENSG00000211788	TRAV13-1	14:22337019-22337546	NOTEST	0	0	0	0	1	1
ENSG00000211789	ENSG00000211789	TRAV12-2	14:22356036-22356682	NOTEST	0	0	0	0	1	1
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ENSG00000211793	ENSG00000211793	TRAV9-2	14:22409312-22409848	NOTEST	0	0	0	0	1	1
ENSG00000211794	ENSG00000211794	TRAV12-3	14:22433679-22434290	NOTEST	0	0	0	0	1	1
ENSG00000211795	ENSG00000211795	TRAV8-6	14:22446698-22447360	NOTEST	0	0	0	0	1	1
ENSG00000211796	ENSG00000211796	TRAV16	14:22458734-22459177	NOTEST	0	0	0	0	1	1
ENSG00000211797	ENSG00000211797	TRAV17	14:22465777-22466407	NOTEST	0	0	0	0	1	1
ENSG00000211798	ENSG00000211798	TRAV18	14:22471344-22471912	NOTEST	0.103652	0.117952	0.186446	0	1	1
ENSG00000211799	ENSG00000211799	TRAV19	14:22475750-22476420	NOTEST	0	0.039112	inf	0	1	1
ENSG00000211800	ENSG00000211800	TRAV20	14:22508839-22509399	NOTEST	0	0	0	0	1	1
ENSG00000211801	ENSG00000211801	TRAV21	14:22520772-22521315	NOTEST	0	0	0	0	1	1
ENSG00000211802	ENSG00000211802	TRAV22	14:22538819-22539471	NOTEST	0	0	0	0	1	1
ENSG00000211803	ENSG00000211803	TRAV23DV6	14:22554683-22555238	NOTEST	0	0	0	0	1	1
ENSG00000211804	ENSG00000211804	TRDV1	14:22564308-22564896	NOTEST	0	0	0	0	1	1
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ENSG00000211807	ENSG00000211807	TRAV26-1	14:22591275-22592243	NOTEST	0	0	0	0	1	1
ENSG00000211808	ENSG00000211808	TRAV8-7	14:22600514-22600996	NOTEST	0	0	0	0	1	1
ENSG00000211809	ENSG00000211809	TRAV27	14:22615948-22616587	NOTEST	0	0	0	0	1	1
ENSG00000211810	ENSG00000211810	TRAV29DV5	14:22631133-22631766	NOTEST	0	0	0	0	1	1
ENSG00000211812	ENSG00000211812	TRAV26-2	14:22670476-22671262	NOTEST	0	0	0	0	1	1
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ENSG00000211814	ENSG00000211814	TRAV35	14:22689791-22690371	NOTEST	0	0	0	0	1	1
ENSG00000211815	ENSG00000211815	TRAV36DV7	14:22694640-22695149	NOTEST	0	0	0	0	1	1
ENSG00000211816	ENSG00000211816	TRAV38-1	14:22739850-22740446	NOTEST	0	0	0	0	1	1
ENSG00000211817	ENSG00000211817	TRAV38-2DV8	14:22748987-22749631	NOTEST	0	0	0	0	1	1
ENSG00000211818	ENSG00000211818	TRAV39	14:22771938-22772438	NOTEST	0	0	0	0	1	1
ENSG00000211819	ENSG00000211819	TRAV40	14:22782921-22783351	NOTEST	0	0	0	0	1	1
ENSG00000211820	ENSG00000211820	TRAV41	14:22788619-22789123	NOTEST	0.0894092	0	#NAME?	0	1	1
ENSG00000211821	ENSG00000211821	TRDV2	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000211825	ENSG00000211825	TRDJ1	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000211826	ENSG00000211826	TRDJ4	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000211827	ENSG00000211827	TRDJ2	14:22849082-22951948	NOTEST	0	0	0	0	1	1
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ENSG00000211831	ENSG00000211831	TRAJ61	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000211832	ENSG00000211832	TRAJ59	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000211833	ENSG00000211833	TRAJ58	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000211834	ENSG00000211834	TRAJ57	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000211835	ENSG00000211835	TRAJ56	14:22849082-22951948	NOTEST	0	0	0	0	1	1
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ENSG00000211837	ENSG00000211837	TRAJ53	14:22951992-22952058	NOTEST	0	0	0	0	1	1
ENSG00000211838	ENSG00000211838	TRAJ52	14:22955215-22955284	NOTEST	0	0	0	0	1	1
ENSG00000211839	ENSG00000211839	TRAJ50	14:22957580-22957640	NOTEST	0	0	0	0	1	1
ENSG00000211840	ENSG00000211840	TRAJ49	14:22958475-22958531	NOTEST	0	0	0	0	1	1
ENSG00000211841	ENSG00000211841	TRAJ48	14:22959478-22959541	NOTEST	0	0	0	0	1	1
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ENSG00000211843	ENSG00000211843	TRAJ46	14:22962388-22962451	NOTEST	0	0	0	0	1	1
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ENSG00000211846	ENSG00000211846	TRAJ43	14:22964895-22964949	NOTEST	0	0	0	0	1	1
ENSG00000211847	ENSG00000211847	TRAJ42	14:22965871-22965937	NOTEST	0	0	0	0	1	1
ENSG00000211848	ENSG00000211848	TRAJ41	14:22966641-22966703	NOTEST	0	0	0	0	1	1
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ENSG00000211851	ENSG00000211851	TRAJ38	14:22971214-22971276	NOTEST	0	0	0	0	1	1
ENSG00000211852	ENSG00000211852	TRAJ37	14:22972734-22972797	NOTEST	0	0	0	0	1	1
ENSG00000211853	ENSG00000211853	TRAJ36	14:22974095-22974155	NOTEST	0	0	0	0	1	1
ENSG00000211854	ENSG00000211854	TRAJ35	14:22975628-22975687	NOTEST	0	0	0	0	1	1
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ENSG00000211858	ENSG00000211858	TRAJ31	14:22979950-22980007	NOTEST	0	0	0	0	1	1
ENSG00000211859	ENSG00000211859	TRAJ30	14:22981833-22981890	NOTEST	0	0	0	0	1	1
ENSG00000211860	ENSG00000211860	TRAJ29	14:22982920-22982980	NOTEST	0	0	0	0	1	1
ENSG00000211861	ENSG00000211861	TRAJ28	14:22984600-22984666	NOTEST	0	0	0	0	1	1
ENSG00000211862	ENSG00000211862	TRAJ27	14:22985250-22985309	NOTEST	0	0	0	0	1	1
ENSG00000211863	ENSG00000211863	TRAJ26	14:22987423-22987483	NOTEST	0	0	0	0	1	1
ENSG00000211864	ENSG00000211864	TRAJ25	14:22987789-22987849	NOTEST	0	0	0	0	1	1
ENSG00000211865	ENSG00000211865	TRAJ24	14:22988946-22989009	NOTEST	0	0	0	0	1	1
ENSG00000211866	ENSG00000211866	TRAJ23	14:22989393-22989456	NOTEST	0	0	0	0	1	1
ENSG00000211867	ENSG00000211867	TRAJ22	14:22991015-22991078	NOTEST	0	0	0	0	1	1
ENSG00000211868	ENSG00000211868	TRAJ21	14:22992572-22992627	NOTEST	0	0	0	0	1	1
ENSG00000211869	ENSG00000211869	TRAJ20	14:22993295-22993352	NOTEST	0	0	0	0	1	1
ENSG00000211870	ENSG00000211870	TRAJ19	14:22994232-22994292	NOTEST	0	0	0	0	1	1
ENSG00000211871	ENSG00000211871	TRAJ18	14:22994619-22994685	NOTEST	0	0	0	0	1	1
ENSG00000211872	ENSG00000211872	TRAJ17	14:22995811-22995874	NOTEST	0	0	0	0	1	1
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ENSG00000211874	ENSG00000211874	TRAJ15	14:22998579-22998641	NOTEST	0	0	0	0	1	1
ENSG00000211875	ENSG00000211875	TRAJ14	14:22999277-22999329	NOTEST	0	0	0	0	1	1
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ENSG00000211877	ENSG00000211877	TRAJ12	14:23000888-23000948	NOTEST	0	0	0	0	1	1
ENSG00000211878	ENSG00000211878	TRAJ11	14:23001451-23001511	NOTEST	0	0	0	0	1	1
ENSG00000211879	ENSG00000211879	TRAJ10	14:23002444-23002508	NOTEST	0	0	0	0	1	1
ENSG00000211880	ENSG00000211880	TRAJ9	14:23004501-23004562	NOTEST	0	0	0	0	1	1
ENSG00000211881	ENSG00000211881	TRAJ8	14:23005091-23005151	NOTEST	0	0	0	0	1	1
ENSG00000211882	ENSG00000211882	TRAJ7	14:23006566-23006625	NOTEST	0	0	0	0	1	1
ENSG00000211883	ENSG00000211883	TRAJ6	14:23008015-23008077	NOTEST	0	0	0	0	1	1
ENSG00000211884	ENSG00000211884	TRAJ5	14:23009189-23009249	NOTEST	0	0	0	0	1	1
ENSG00000211885	ENSG00000211885	TRAJ4	14:23011141-23011204	NOTEST	0	0	0	0	1	1
ENSG00000211886	ENSG00000211886	TRAJ3	14:23012121-23012183	NOTEST	0	0	0	0	1	1
ENSG00000211887	ENSG00000211887	TRAJ2	14:23013014-23013080	NOTEST	0	0	0	0	1	1
ENSG00000211888	ENSG00000211888	TRAJ1	14:23013980-23014042	NOTEST	0	0	0	0	1	1
ENSG00000211890	ENSG00000211890	IGHA2	14:106053225-106054732	NOTEST	0	0.0128311	inf	0	1	1
ENSG00000211891	ENSG00000211891	IGHE	14:106064027-106071694	NOTEST	0	0	0	0	1	1
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ENSG00000211893	ENSG00000211893	IGHG2	14:106109388-106115394	NOTEST	0	0	0	0	1	1
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ENSG00000211898	ENSG00000211898	IGHD	14:106303098-106312010	NOTEST	0	0	0	0	1	1
ENSG00000211899	ENSG00000211899	IGHM	14:106320348-106322323	NOTEST	0	0	0	0	1	1
ENSG00000211900	ENSG00000211900	IGHJ6	14:106329407-106329468	NOTEST	0	0	0	0	1	1
ENSG00000211904	ENSG00000211904	IGHJ2	14:106331408-106331460	NOTEST	0	0	0	0	1	1
ENSG00000211905	ENSG00000211905	IGHJ1	14:106331616-106331668	NOTEST	0	0	0	0	1	1

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ENSG00000211907	ENSG00000211907	IGHD1-26	14:106346891-106346911	NOTEST	0	0	0	0	1	1
ENSG00000211909	ENSG00000211909	IGHD5-24	14:106349760-106349780	NOTEST	0	0	0	0	1	1
ENSG00000211911	ENSG00000211911	IGHD3-22	14:106351888-106351919	NOTEST	0	0	0	0	1	1
ENSG00000211912	ENSG00000211912	IGHD2-21	14:106354408-106354436	NOTEST	0	0	0	0	1	1
ENSG00000211914	ENSG00000211914	IGHD6-19	14:106355941-106362435	NOTEST	0	0	0	0	1	1
ENSG00000211915	ENSG00000211915	IGHD5-18	14:106355941-106362435	NOTEST	0	0	0	0	1	1
ENSG00000211917	ENSG00000211917	IGHD3-16	14:106355941-106362435	NOTEST	0	0	0	0	1	1
ENSG00000211918	ENSG00000211918	IGHD2-15	14:106363814-106363845	NOTEST	0	0	0	0	1	1
ENSG00000211920	ENSG00000211920	IGHD6-13	14:106366999-106367020	NOTEST	0	0	0	0	1	1
ENSG00000211921	ENSG00000211921	IGHD5-12	14:106368506-106368529	NOTEST	0	0	0	0	1	1
ENSG00000211923	ENSG00000211923	IGHD3-10	14:106370354-106370385	NOTEST	0	0	0	0	1	1
ENSG00000211924	ENSG00000211924	IGHD3-9	14:106370538-106370569	NOTEST	0	0	0	0	1	1
ENSG00000211925	ENSG00000211925	IGHD2-8	14:106373068-106373099	NOTEST	0	0	0	0	1	1
ENSG00000211928	ENSG00000211928	IGHD5-5	14:106378115-106378135	NOTEST	0	0	0	0	1	1
ENSG00000211930	ENSG00000211930	IGHD3-3	14:106380217-106380248	NOTEST	0	0	0	0	1	1
ENSG00000211931	ENSG00000211931	IGHD2-2	14:106382684-106382715	NOTEST	0	0	0	0	1	1
ENSG00000211933	ENSG00000211933	IGHV6-1	14:106405610-106406108	NOTEST	0	0	0	0	1	1
ENSG00000211934	ENSG00000211934	IGHV1-2	14:106452670-106453170	NOTEST	0	0	0	0	1	1
ENSG00000211935	ENSG00000211935	IGHV1-3	14:106471245-106471723	NOTEST	0	0	0	0	1	1
ENSG00000211936	ENSG00000211936	IGHV4-4	14:106478109-106478603	NOTEST	0	0	0	0	1	1
ENSG00000211937	ENSG00000211937	IGHV2-5	14:106494134-106494597	NOTEST	0	0	0	0	1	1
ENSG00000211938	ENSG00000211938	IGHV3-7	14:106518399-106518932	NOTEST	0	0	0	0	1	1
ENSG00000211939	ENSG00000211939	IGHV1-8	14:106539078-106539577	NOTEST	0	0	0	0	1	1
ENSG00000211940	ENSG00000211940	IGHV3-9	14:106552284-106552809	NOTEST	0	0	0	0	1	1
ENSG00000211941	ENSG00000211941	IGHV3-11	14:106573232-106573800	NOTEST	0	0	0	0	1	1
ENSG00000211942	ENSG00000211942	IGHV3-13	14:106586136-106586667	NOTEST	0	0	0	0	1	1
ENSG00000211943	ENSG00000211943	IGHV3-15	14:106610312-106610852	NOTEST	0	0	0	0	1	1
ENSG00000211944	ENSG00000211944	IGHV3-16	14:106621893-106622419	NOTEST	0	0	0	0	1	1
ENSG00000211945	ENSG00000211945	IGHV1-18	14:106641562-106642056	NOTEST	0	0	0	0	1	1
ENSG00000211946	ENSG00000211946	IGHV3-20	14:106667580-106668095	NOTEST	0	0	0	0	1	1
ENSG00000211947	ENSG00000211947	IGHV3-21	14:106691672-106692203	NOTEST	0	0	0	0	1	1
ENSG00000211949	ENSG00000211949	IGHV3-23	14:106725200-106725733	NOTEST	0	0	0	0	1	1
ENSG00000211950	ENSG00000211950	IGHV1-24	14:106733143-106733639	NOTEST	0	0	0	0	1	1
ENSG00000211951	ENSG00000211951	IGHV2-26	14:106757649-106758116	NOTEST	0	0	0	0	1	1
ENSG00000211952	ENSG00000211952	IGHV4-28	14:106780512-106781017	NOTEST	0	0	0	0	1	1
ENSG00000211953	ENSG00000211953	IGHV3-30	14:106791004-106791536	NOTEST	0	0	0	0	1	1
ENSG00000211955	ENSG00000211955	IGHV3-33	14:106815721-106816253	NOTEST	0	0	0	0	1	1
ENSG00000211956	ENSG00000211956	IGHV4-34	14:106829593-106830076	NOTEST	0	0.0505568	inf	0	1	1
ENSG00000211957	ENSG00000211957	IGHV3-35	14:106845322-106845789	NOTEST	0	0	0	0	1	1
ENSG00000211958	ENSG00000211958	IGHV3-38	14:106866405-106866934	NOTEST	0	0	0	0	1	1
ENSG00000211959	ENSG00000211959	IGHV4-39	14:106877618-106878126	NOTEST	0.116866	0	#NAME?	0	1	1
ENSG00000211961	ENSG00000211961	IGHV1-45	14:106938444-106977000	NOTEST	0	0	0	0	1	1
ENSG00000211962	ENSG00000211962	IGHV1-46	14:106938444-106977000	NOTEST	0	0	0	0	1	1
ENSG00000211964	ENSG00000211964	IGHV3-48	14:106993813-106994346	NOTEST	0	0	0	0	1	1
ENSG00000211965	ENSG00000211965	IGHV3-49	14:107012937-107013477	NOTEST	0	0	0	0	1	1

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ENSG00000211966	ENSG00000211966	IGHV5-51	14:107034728-107035221	NOTEST	0	0	0	0	1	1
ENSG00000211967	ENSG00000211967	IGHV3-53	14:107048671-107049341	NOTEST	0	0	0	0	1	1
ENSG00000211968	ENSG00000211968	IGHV1-58	14:107078372-107078869	NOTEST	0	0	0	0	1	1
ENSG00000211970	ENSG00000211970	IGHV4-61	14:107095125-107095662	NOTEST	0	0	0	0	1	1
ENSG00000211972	ENSG00000211972	IGHV3-66	14:107131032-107131560	NOTEST	0	0	0	0	1	1
ENSG00000211973	ENSG00000211973	IGHV1-69	14:107169930-107170428	NOTEST	0	0	0	0	1	1
ENSG00000211974	ENSG00000211974	IGHV2-70	14:107178819-107179338	NOTEST	0	0	0	0	1	1
ENSG00000211976	ENSG00000211976	IGHV3-73	14:107210931-107211471	NOTEST	0	0	0	0	1	1
ENSG00000211978	ENSG00000211978	IGHV5-78	14:107259337-107259632	NOTEST	0	0	0	0	1	1
ENSG00000211979	ENSG00000211979	IGHV7-81	14:107282791-107283280	NOTEST	0	0	0	0	1	1
ENSG00000211983	ENSG00000211983	AL138919.1	6:88557262-88557350	NOTEST	0	0	0	0	1	1
ENSG00000211984	ENSG00000211984	AC079117.2	2:76974844-77820445	NOTEST	0	0	0	0	1	1
ENSG00000211987	ENSG00000211987	AC104802.1	2:225104178-225104273	NOTEST	0	0	0	0	1	1
ENSG00000211990	ENSG00000211990	AL117209.1	14:103243812-103377837	NOTEST	0	0	0	0	1	1
ENSG00000211991	ENSG00000211991	MIR676	X:68835910-69259319	NOTEST	0	0	0	0	1	1
ENSG00000211995	ENSG00000211995	AP000428.1	8:108261720-108510283	NOTEST	0	0	0	0	1	1
ENSG00000211996	ENSG00000211996	Z97352.1	6:130068881-130068964	NOTEST	0	0	0	0	1	1
ENSG00000211997	ENSG00000211997	MIR708	11:78363875-79151992	NOTEST	0	0	0	0	1	1
ENSG00000212001	ENSG00000212001	AC009297.1	2:154728425-155313950	NOTEST	0	0	0	0	1	1
ENSG00000212007	ENSG00000212007	AL596329.1	13:62334416-62334509	NOTEST	0	0	0	0	1	1
ENSG00000212013	ENSG00000212013	MIR509-2	X:146340277-146340368	NOTEST	0	0	0	0	1	1
ENSG00000212014	ENSG00000212014	MIR509-3	X:146341169-146341244	NOTEST	0	0	0	0	1	1
ENSG00000212017	ENSG00000212017	MIR548U	6:57179602-57513375	NOTEST	0	0	0	0	1	1
ENSG00000212022	ENSG00000212022	AC080032.1	15:94133095-94651167	NOTEST	0	0	0	0	1	1
ENSG00000212024	ENSG00000212024	MIR550A3	7:29638410-29782210	NOTEST	0	0	0	0	1	1
ENSG00000212025	ENSG00000212025	AC011748.1	2:34608854-34860407	NOTEST	0	0	0	0	1	1
ENSG00000212027	ENSG00000212027	MIR374B	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000212030	ENSG00000212030	AP002498.1	11:76571910-76737841	NOTEST	0	0	0	0	1	1
ENSG00000212031	ENSG00000212031	AC117444.1	3:96385037-96385123	NOTEST	0	0	0	0	1	1
ENSG00000212032	ENSG00000212032	AC007486.1	X:120466407-120466492	NOTEST	0	0	0	0	1	1
ENSG00000212034	ENSG00000212034	AC084262.1	8:29127490-29127578	NOTEST	0	0	0	0	1	1
ENSG00000212036	ENSG00000212036	AC016575.1	5:14910666-14910749	NOTEST	0	0	0	0	1	1
ENSG00000212037	ENSG00000212037	AL049831.1	14:26641371-26641464	NOTEST	0	0	0	0	1	1
ENSG00000212039	ENSG00000212039	AL592205.1	1:97368254-97368348	NOTEST	0	0	0	0	1	1
ENSG00000212040	ENSG00000212040	MIR543	14:101498323-101498401	NOTEST	0	0	0	0	1	1
ENSG00000212044	ENSG00000212044	CR812485.1	1:149323330-149323422	NOTEST	0	0	0	0	1	1
ENSG00000212045	ENSG00000212045	AC109351.1	4:29751817-29751932	NOTEST	0	0	0	0	1	1
ENSG00000212049	ENSG00000212049	AL590007.1	13:39261265-39460074	NOTEST	0	0	0	0	1	1
ENSG00000212051	ENSG00000212051	MIR320C2	18:21718941-21977844	NOTEST	0	0	0	0	1	1
ENSG00000212054	ENSG00000212054	AL354764.1	13:60970590-61148012	NOTEST	0	0	0	0	1	1
ENSG00000212055	ENSG00000212055	AC122136.1	2:216743555-216743642	NOTEST	0	0	0	0	1	1
ENSG00000212057	ENSG00000212057	AL139318.1	13:95089557-95131936	NOTEST	0	0	0	0	1	1
ENSG00000212061	ENSG00000212061	AC016543.1	14:76776956-77227731	NOTEST	0	0	0	0	1	1
ENSG00000212063	ENSG00000212063	AC112693.1	15:93829463-93829552	NOTEST	0	0	0	0	1	1
ENSG00000212065	ENSG00000212065	AL591034.1	6:53321244-53321330	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000212066	ENSG00000212066	AL645941.1	6:32902405-32949282	NOTEST	0	0	0	0	1	1
ENSG00000212067	ENSG00000212067	AP005227.1	18:7566779-8406951	NOTEST	0	0	0	0	1	1
ENSG00000212070	ENSG00000212070	AC112219.1	3:72311472-72311579	NOTEST	0	0	0	0	1	1
ENSG00000212071	ENSG00000212071	AL162511.1	14:36665685-36665774	NOTEST	0	0	0	0	1	1
ENSG00000212072	ENSG00000212072	AL353147.1	10:19492778-20079330	NOTEST	0	0	0	0	1	1
ENSG00000212073	ENSG00000212073	AC121332.1	3:130569438-131100319	NOTEST	0	0	0	0	1	1
ENSG00000212075	ENSG00000212075	AC112778.1	X:25224486-25224577	NOTEST	0	0	0	0	1	1
ENSG00000212076	ENSG00000212076	MIR761	1:52027537-52344477	NOTEST	0	0	0	0	1	1
ENSG00000212082	ENSG00000212082	AC010368.1	5:34998205-35048198	NOTEST	0	0	0	0	1	1
ENSG00000212084	ENSG00000212084	AL121914.1	20:55035321-55035413	NOTEST	0	0	0	0	1	1
ENSG00000212085	ENSG00000212085	AC105245.1	18:26776405-26776492	NOTEST	0	0	0	0	1	1
ENSG00000212086	ENSG00000212086	AL390119.1	1:164953138-164953229	NOTEST	0	0	0	0	1	1
ENSG00000212089	ENSG00000212089	AP002490.1	11:71709586-71823826	NOTEST	0	0	0	0	1	1
ENSG00000212091	ENSG00000212091	AC013268.1	2:110879887-110962643	NOTEST	0	0	0	0	1	1
ENSG00000212093	ENSG00000212093	AP000807.1	11:68228185-68384179	NOTEST	0	0	0	0	1	1
ENSG00000212094	ENSG00000212094	AC092765.1	1:222186348-222186432	NOTEST	0	0	0	0	1	1
ENSG00000212095	ENSG00000212095	AC096922.1	3:68684066-68684160	NOTEST	0	0	0	0	1	1
ENSG00000212098	ENSG00000212098	AL390966.1	X:94389277-94389371	NOTEST	0	0	0	0	1	1
ENSG00000212099	ENSG00000212099	AL035467.1	6:72248586-72248679	NOTEST	0	0	0	0	1	1
ENSG00000212100	ENSG00000212100	MIR764	X:113818550-114144624	NOTEST	0	0	0	0	1	1
ENSG00000212101	ENSG00000212101	AL080276.1	6:153325593-153452384	NOTEST	0	0	0	0	1	1
ENSG00000212102	ENSG00000212102	MIR301B	22:22006558-22090123	NOTEST	0	0	0	0	1	1
ENSG00000212104	ENSG00000212104	AC026877.1	3:75955845-77699115	NOTEST	0	0	0	0	1	1
ENSG00000212111	ENSG00000212111	AL121584.1	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000212114	ENSG00000212114	AC093267.1	5:122110690-122165803	NOTEST	0	0	0	0	1	1
ENSG00000212122	ENSG00000212122	TSSK1B	5:112357795-112824527	NOTEST	0	0	0	0	1	1
ENSG00000212124	ENSG00000212124	TAS2R19	12:10977558-11324212	NOTEST	0.136727	0.145631	0.0910133	0	1	1
ENSG00000212125	ENSG00000212125	TAS2R15	12:10977558-11324212	NOTEST	0.176587	0.10553	-0.742722	0	1	1
ENSG00000212126	ENSG00000212126	TAS2R50	12:10977558-11324212	NOTEST	0	0	0	0	1	1
ENSG00000212127	ENSG00000212127	TAS2R14	12:10977558-11324212	NOTEST	0.61312	0.446045	-0.458981	0	1	1
ENSG00000212128	ENSG00000212128	TAS2R13	12:10977558-11324212	NOTEST	0	0	0	0	1	1
ENSG00000212133	ENSG00000212133	RNU6-1168P	2:88683012-88683116	NOTEST	0	0	0	0	1	1
ENSG00000212134	ENSG00000212134	SNORA40	20:29964121-29964249	NOTEST	0	0	0	0	1	1
ENSG00000212135	ENSG00000212135	SNORD67	11:46764597-46867847	NOTEST	0	0	0	0	1	1
ENSG00000212136	ENSG00000212136	RNU6-696P	21:38417829-38417936	NOTEST	0	0	0	0	1	1
ENSG00000212138	ENSG00000212138	RNA5SP372	12:109460893-109525831	NOTEST	0	0	0	0	1	1
ENSG00000212140	ENSG00000212140	RNU6-1320P	2:95476790-95523027	NOTEST	0	0	0	0	1	1
ENSG00000212144	ENSG00000212144	U8	1:234729020-234729148	NOTEST	0	0	0	0	1	1
ENSG00000212145	ENSG00000212145	U8	3:41236327-42003922	NOTEST	0	0	0	0	1	1
ENSG00000212146	ENSG00000212146	RNU6-910P	3:196068479-196068586	NOTEST	0	0	0	0	1	1
ENSG00000212147	ENSG00000212147	RNU6-1106P	6:105404922-105531207	NOTEST	0	0	0	0	1	1
ENSG00000212149	ENSG00000212149	SNORA40	17:41092591-41092719	NOTEST	0	0	0	0	1	1
ENSG00000212153	ENSG00000212153	RNU1-82P	7:141404137-141488440	NOTEST	0	0	0	0	1	1
ENSG00000212154	ENSG00000212154	RNA5SP377	12:132145607-132145719	NOTEST	0	0	0	0	1	1
ENSG00000212156	ENSG00000212156	RNU6-576P	10:2241580-2241682	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000212157	ENSG00000212157	RNU6-1319P	1:224163847-224163951	NOTEST	0	0	0	0	1	1
ENSG00000212158	ENSG00000212158	SNORD66	3:183851806-184402546	NOTEST	0	0	0	0	1	1
ENSG00000212160	ENSG00000212160	RNU6-205P	4:111199340-111199447	NOTEST	0	0	0	0	1	1
ENSG00000212161	ENSG00000212161	SNORD64	1:159796539-159869953	NOTEST	0	0	0	0	1	1
ENSG00000212163	ENSG00000212163	SNORD91A	17:1963132-2284352	NOTEST	0	0	0	0	1	1
ENSG00000212165	ENSG00000212165	U3	20:16963476-16963678	NOTEST	0	0	0	0	1	1
ENSG00000212167	ENSG00000212167	RNU6-763P	2:175886941-175887047	NOTEST	0	0	0	0	1	1
ENSG00000212168	ENSG00000212168	SNORD78	2:57771669-57771734	NOTEST	0	0	0	0	1	1
ENSG00000212170	ENSG00000212170	RNU1-77P	15:82422570-82555104	NOTEST	0	0	0	0	1	1
ENSG00000212171	ENSG00000212171	RNA5SP86	2:20601387-20601485	NOTEST	0	0	0	0	1	1
ENSG00000212172	ENSG00000212172	RNU1-149P	12:22199107-22589975	NOTEST	0	0	0	0	1	1
ENSG00000212174	ENSG00000212174	Y_RNA	1:52027537-52344477	NOTEST	0	0	0	0	1	1
ENSG00000212175	ENSG00000212175	SNORA12	2:55774427-55846015	NOTEST	0	0	0	0	1	1
ENSG00000212176	ENSG00000212176	RNA5SP207	6:41207257-41207364	NOTEST	0	0	0	0	1	1
ENSG00000212181	ENSG00000212181	SNORA48	2:148602085-149275805	NOTEST	0	0	0	0	1	1
ENSG00000212182	ENSG00000212182	U3	2:114737145-114764879	NOTEST	0	0	0	0	1	1
ENSG00000212184	ENSG00000212184	RNU6-440P	2:202792161-202792266	NOTEST	0	0	0	0	1	1
ENSG00000212186	ENSG00000212186	RNU6-258P	17:19912656-20306870	NOTEST	0	0	0	0	1	1
ENSG00000212187	ENSG00000212187	SNORA26	1:212113740-212208884	NOTEST	0	0	0	0	1	1
ENSG00000212189	ENSG00000212189	RNU6-328P	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000212190	ENSG00000212190	RNU6-298P	17:29158987-29222887	NOTEST	0	0	0	0	1	1
ENSG00000212191	ENSG00000212191	SNORD65	4:179607039-179607110	NOTEST	0	0	0	0	1	1
ENSG00000212195	ENSG00000212195	U3	17:56597197-56769416	NOTEST	0	0	0	0	1	1
ENSG00000212197	ENSG00000212197	RNY3P6	13:100153670-100216260	NOTEST	0	0	0	0	1	1
ENSG00000212199	ENSG00000212199	RNU6-127P	2:131862419-132111282	NOTEST	0	0	0	0	1	1
ENSG00000212204	ENSG00000212204	RNA5SP91	2:33172038-33624576	NOTEST	0	0	0	0	1	1
ENSG00000212205	ENSG00000212205	Y_RNA	1:211916798-212027045	NOTEST	0	0	0	0	1	1
ENSG00000212206	ENSG00000212206	SNORA69	17:8232900-8233037	NOTEST	0	0	0	0	1	1
ENSG00000212207	ENSG00000212207	RNU6-1321P	X:41374186-41782716	NOTEST	0	0	0	0	1	1
ENSG00000212211	ENSG00000212211	U3	3:59735035-61237133	NOTEST	0	0	0	0	1	1
ENSG00000212214	ENSG00000212214	SNORA48	X:3450157-3450292	NOTEST	0	0	0	0	1	1
ENSG00000212215	ENSG00000212215	RNU6-913P	5:60933534-61047590	NOTEST	0	0	0	0	1	1
ENSG00000212216	ENSG00000212216	RNU6-816P	22:16255354-16287937	NOTEST	0	0	0	0	1	1
ENSG00000212219	ENSG00000212219	RNU6-604P	7:151597359-151597459	NOTEST	0	0	0	0	1	1
ENSG00000212221	ENSG00000212221	RNU6-220P	8:144386553-144442149	NOTEST	0	0	0	0	1	1
ENSG00000212224	ENSG00000212224	SNORA26	20:40341117-40341239	NOTEST	0	0	0	0	1	1
ENSG00000212226	ENSG00000212226	RNU6-907P	4:90052002-90052104	NOTEST	0	0	0	0	1	1
ENSG00000212228	ENSG00000212228	SNORA48	16:11343475-11445619	NOTEST	0	0	0	0	1	1
ENSG00000212229	ENSG00000212229	SNORD65	6:67920300-67920373	NOTEST	0	0	0	0	1	1
ENSG00000212230	ENSG00000212230	RNU6-747P	1:243242158-243265035	NOTEST	0	0	0	0	1	1
ENSG00000212237	ENSG00000212237	RNA5SP18	1:228744884-228788150	NOTEST	0	0	0	0	1	1
ENSG00000212238	ENSG00000212238	RNA5SP244	7:129251554-129396922	NOTEST	0	92.6895	inf	0	1	1
ENSG00000212240	ENSG00000212240	RNU6-930P	6:28870778-28891766	NOTEST	0	0	0	0	1	1
ENSG00000212241	ENSG00000212241	Y_RNA	X:114345184-114468635	NOTEST	0	0	0	0	1	1
ENSG00000212242	ENSG00000212242	RNA5SP219	6:136878184-137113656	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000212246	ENSG00000212246	RNU6-360P	2:208693026-208890284	NOTEST	0	0	0	0	1	1
ENSG00000212247	ENSG00000212247	RNU6-278P	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000212248	ENSG00000212248	RNU6-750P	1:100433938-100492535	NOTEST	0	0	0	0	1	1
ENSG00000212249	ENSG00000212249	U8	5:68128411-68257985	NOTEST	0	0	0	0	1	1
ENSG00000212251	ENSG00000212251	RNA5SP376	12:131784184-131784296	NOTEST	0	0	0	0	1	1
ENSG00000212254	ENSG00000212254	RNU6-124P	9:113127530-113342160	NOTEST	0	0	0	0	1	1
ENSG00000212257	ENSG00000212257	RNU6-1176P	1:65488650-65488757	NOTEST	0	0	0	0	1	1
ENSG00000212258	ENSG00000212258	RNA5SP176	5:6933782-7190925	NOTEST	0	0	0	0	1	1
ENSG00000212259	ENSG00000212259	RNU6-308P	5:94799598-94890711	NOTEST	0	0	0	0	1	1
ENSG00000212260	ENSG00000212260	RNU6-724P	5:68773298-69006341	NOTEST	0	0	0	0	1	1
ENSG00000212264	ENSG00000212264	SNORD65	7:23338357-23510086	NOTEST	0	0	0	0	1	1
ENSG00000212265	ENSG00000212265	RNA5SP185	5:55556159-55556273	NOTEST	0	0	0	0	1	1
ENSG00000212266	ENSG00000212266	SNORA40	1:118231242-118231364	NOTEST	0	0	0	0	1	1
ENSG00000212269	ENSG00000212269	RNU6-788P	3:23682979-23683083	NOTEST	0	0	0	0	1	1
ENSG00000212270	ENSG00000212270	SNORD37	14:26275853-26275918	NOTEST	0	0	0	0	1	1
ENSG00000212273	ENSG00000212273	SNORA40	8:134656840-134656968	NOTEST	0	0	0	0	1	1
ENSG00000212276	ENSG00000212276	RNA5SP292	9:109606029-109606147	NOTEST	0	0	0	0	1	1
ENSG00000212277	ENSG00000212277	SNORD43	11:74407473-74442430	NOTEST	0	0	0	0	1	1
ENSG00000212278	ENSG00000212278	SNORD81	5:18236231-18236305	NOTEST	0	0	0	0	1	1
ENSG00000212279	ENSG00000212279	SNORD77	15:74753605-74809300	NOTEST	0	0	0	0	1	1
ENSG00000212280	ENSG00000212280	RNA5SP256	8:17433941-17658426	NOTEST	0	0	0	0	1	1
ENSG00000212282	ENSG00000212282	RNU6-578P	4:12314211-12314314	NOTEST	0	0	0	0	1	1
ENSG00000212283	ENSG00000212283	SNORD89	2:101887680-101925163	NOTEST	0	0	0	0	1	1
ENSG00000212289	ENSG00000212289	RNA5SP339	11:27528384-27899195	NOTEST	0	0	0	0	1	1
ENSG00000212290	ENSG00000212290	RNA5SP424	16:47178233-47735434	NOTEST	0	0	0	0	1	1
ENSG00000212292	ENSG00000212292	RNU6-239P	1:154267978-154268077	NOTEST	0	0	0	0	1	1
ENSG00000212293	ENSG00000212293	SNORA16	13:32974860-33112970	NOTEST	0	0	0	0	1	1
ENSG00000212295	ENSG00000212295	SNORD28	6:156699883-156699958	NOTEST	0	0	0	0	1	1
ENSG00000212296	ENSG00000212296	SNORD72	5:40825363-40835437	NOTEST	0	0	0	0	1	1
ENSG00000212297	ENSG00000212297	RNU6-821P	3:197780392-197807591	NOTEST	0	0	0	0	1	1
ENSG00000212298	ENSG00000212298	RNU6-1009P	12:64580095-64616076	NOTEST	0	0	0	0	1	1
ENSG00000212302	ENSG00000212302	SNORD41	14:23171351-23241007	NOTEST	0	0	0	0	1	1
ENSG00000212303	ENSG00000212303	RNU6-1154P	7:135347243-135433594	NOTEST	0	0	0	0	1	1
ENSG00000212304	ENSG00000212304	SNORD12	20:47835883-47905797	NOTEST	0	0	0	0	1	1
ENSG00000212305	ENSG00000212305	RNU6-679P	5:12297510-12297616	NOTEST	0	0	0	0	1	1
ENSG00000212306	ENSG00000212306	Y_RNA	15:101093733-101191910	NOTEST	0	0	0	0	1	1
ENSG00000212308	ENSG00000212308	RNA5SP23	1:78695282-79005434	NOTEST	0	0	0	0	1	1
ENSG00000212309	ENSG00000212309	SNORD70	2:203130438-203168389	NOTEST	0	0	0	0	1	1
ENSG00000212312	ENSG00000212312	RNA5SP109	2:163175349-163695240	NOTEST	0	0	0	0	1	1
ENSG00000212314	ENSG00000212314	RNU6-1307P	19:54767804-54767913	NOTEST	0	0	0	0	1	1
ENSG00000212316	ENSG00000212316	RNU6-1228P	9:77812986-77813093	NOTEST	0	0	0	0	1	1
ENSG00000212319	ENSG00000212319	Y_RNA	3:101347153-101347250	NOTEST	0	0	0	0	1	1
ENSG00000212321	ENSG00000212321	U3	X:121974278-121974497	NOTEST	0	0	0	0	1	1
ENSG00000212324	ENSG00000212324	RNU6-129P	10:85524113-85524220	NOTEST	0	0	0	0	1	1
ENSG00000212325	ENSG00000212325	Y_RNA	10:102158108-102158203	NOTEST	0	0	0	0	1	1

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ENSG00000212327	ENSG00000212327	RNU6-882P	3:9958757-9975314	NOTEST	0	0	0	0	1	1
ENSG00000212329	ENSG00000212329	RNU6-316P	18:14179095-14252139	NOTEST	0	0	0	0	1	1
ENSG00000212330	ENSG00000212330	RNU6-244P	14:102829299-102968818	NOTEST	0	0	0	0	1	1
ENSG00000212331	ENSG00000212331	RNA5SP297	10:180404-300577	NOTEST	0	0	0	0	1	1
ENSG00000212332	ENSG00000212332	RNU6-780P	10:88195012-88281572	NOTEST	0	0	0	0	1	1
ENSG00000212333	ENSG00000212333	RNA5SP213	6:114254191-114792869	NOTEST	0	0	0	0	1	1
ENSG00000212335	ENSG00000212335	Y_RNA	14:23321824-23321937	NOTEST	0	0	0	0	1	1
ENSG00000212336	ENSG00000212336	RNA5SP210	6:82201155-82462491	NOTEST	0	0	0	0	1	1
ENSG00000212338	ENSG00000212338	SNORA67	1:179068461-179198819	NOTEST	0	0	0	0	1	1
ENSG00000212340	ENSG00000212340	RNU6-739P	3:64497430-64497533	NOTEST	0	0	0	0	1	1
ENSG00000212342	ENSG00000212342	SNORA12	8:131064352-131455906	NOTEST	0	0	0	0	1	1
ENSG00000212344	ENSG00000212344	RNU6-823P	3:127770483-128127485	NOTEST	0	0	0	0	1	1
ENSG00000212345	ENSG00000212345	RNU6-700P	12:9776717-9776824	NOTEST	0	0	0	0	1	1
ENSG00000212347	ENSG00000212347	SNORD77	X:45752346-45752414	NOTEST	0	0	0	0	1	1
ENSG00000212348	ENSG00000212348	RNU6-1300P	8:74960911-74961019	NOTEST	0	0	0	0	1	1
ENSG00000212354	ENSG00000212354	RNU6-1242P	18:36786887-37380282	NOTEST	0	0	0	0	1	1
ENSG00000212358	ENSG00000212358	RNU6-837P	12:17224331-17224439	NOTEST	0	0	0	0	1	1
ENSG00000212359	ENSG00000212359	RNU6-550P	4:121606073-121844025	NOTEST	0	0	0	0	1	1
ENSG00000212360	ENSG00000212360	RNU6-1177P	1:62208148-62629592	NOTEST	0	0	0	0	1	1
ENSG00000212363	ENSG00000212363	SNORA40	5:74178480-74178608	NOTEST	0	0	0	0	1	1
ENSG00000212365	ENSG00000212365	RNA5SP332	11:13983913-14295237	NOTEST	0	0	0	0	1	1
ENSG00000212366	ENSG00000212366	RNU6-1246P	1:73183345-73183452	NOTEST	0	0	0	0	1	1
ENSG00000212368	ENSG00000212368	RNU6-1000P	4:77234153-77343021	NOTEST	0	0	0	0	1	1
ENSG00000212370	ENSG00000212370	RNU6-482P	5:112043194-112258236	NOTEST	0	0	0	0	1	1
ENSG00000212371	ENSG00000212371	SNORA46	14:77893017-77935817	NOTEST	0	0.995482	inf	0	1	1
ENSG00000212373	ENSG00000212373	RNA5SP171	4:167654534-168155947	NOTEST	0	0	0	0	1	1
ENSG00000212374	ENSG00000212374	RNU6-401P	15:84322837-84708594	NOTEST	0	0	0	0	1	1
ENSG00000212377	ENSG00000212377	SNORD37	13:73028039-73028105	NOTEST	0	0	0	0	1	1
ENSG00000212378	ENSG00000212378	SNORD78	2:72403112-73053170	NOTEST	0	0	0	0	1	1
ENSG00000212379	ENSG00000212379	RNU6-269P	16:58328983-58440048	NOTEST	0	0	0	0	1	1
ENSG00000212380	ENSG00000212380	SNORD115-45	15:25497371-25684128	NOTEST	0	0	0	0	1	1
ENSG00000212382	ENSG00000212382	RNU6-159P	16:27798849-28074830	NOTEST	0	0	0	0	1	1
ENSG00000212383	ENSG00000212383	SNORA48	12:57216768-57268052	NOTEST	0	0	0	0	1	1
ENSG00000212384	ENSG00000212384	SNORD113-2	14:101361106-101402336	NOTEST	0	0	0	0	1	1
ENSG00000212385	ENSG00000212385	RNU6-817P	1:116915289-116961244	NOTEST	0	0	0	0	1	1
ENSG00000212387	ENSG00000212387	RNU6-1055P	4:187187098-187476721	NOTEST	0	0	0	0	1	1
ENSG00000212388	ENSG00000212388	RNU6-796P	15:85427884-85518876	NOTEST	0	0	0	0	1	1
ENSG00000212389	ENSG00000212389	RNU6-1275P	2:148602085-149275805	NOTEST	0	0	0	0	1	1
ENSG00000212391	ENSG00000212391	SNORA48	2:227700296-227863931	NOTEST	0	0	0	0	1	1
ENSG00000212392	ENSG00000212392	Y_RNA	3:57327726-57530071	NOTEST	0	0	0	0	1	1
ENSG00000212395	ENSG00000212395	SNORA67	9:134658246-134658345	NOTEST	0	0	0	0	1	1
ENSG00000212396	ENSG00000212396	RNA5SP323	10:95256388-95288849	NOTEST	0	0	0	0	1	1
ENSG00000212397	ENSG00000212397	snosnR66	11:112263840-112492452	NOTEST	0	0	0	0	1	1
ENSG00000212398	ENSG00000212398	RNU6-1248P	1:223877752-223877816	NOTEST	0	0	0	0	1	1
ENSG00000212402	ENSG00000212402	SNORA74B	5:172410759-172462448	NOTEST	0	0	0	0	1	1

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ENSG00000212404	ENSG00000212404	Y_RNA	2:183692850-183692948	NOTEST	0	0	0	0	1	1
ENSG00000212407	ENSG00000212407	RNU6-663P	8:32769010-32769116	NOTEST	0	0	0	0	1	1
ENSG00000212409	ENSG00000212409	RNY4P18	9:113859604-113859693	NOTEST	0	0	0	0	1	1
ENSG00000212410	ENSG00000212410	RNU6-932P	2:158733213-158992666	NOTEST	0	0	0	0	1	1
ENSG00000212411	ENSG00000212411	SNORD115	10:29698330-30025710	NOTEST	0	0	0	0	1	1
ENSG00000212413	ENSG00000212413	RNU11-3P	10:105062552-105110891	NOTEST	0	0	0	0	1	1
ENSG00000212414	ENSG00000212414	SNORD77	8:100973163-101143496	NOTEST	0	0	0	0	1	1
ENSG00000212415	ENSG00000212415	SNORD77	15:33057746-33486897	NOTEST	0	0	0	0	1	1
ENSG00000212418	ENSG00000212418	Y_RNA	17:74668023-74707098	NOTEST	0	0	0	0	1	1
ENSG00000212420	ENSG00000212420	RNU6-1111P	15:90373830-90456188	NOTEST	0	0	0	0	1	1
ENSG00000212421	ENSG00000212421	SNORA26	9:89875364-89875500	NOTEST	0	0	0	0	1	1
ENSG00000212422	ENSG00000212422	U3	7:10262423-10262637	NOTEST	0	0	0	0	1	1
ENSG00000212424	ENSG00000212424	RNU1-119P	15:45118568-45176978	NOTEST	0	0	0	0	1	1
ENSG00000212425	ENSG00000212425	RNA5SP105	2:137523114-138435287	NOTEST	0	0	0	0	1	1
ENSG00000212428	ENSG00000212428	SNORD115	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000212429	ENSG00000212429	RNU11-6P	8:81540685-81787016	NOTEST	0	0	0	0	1	1
ENSG00000212432	ENSG00000212432	SNORA75	12:9570308-9600825	NOTEST	0	4.54088	inf	0	1	1
ENSG00000212433	ENSG00000212433	RNA5SP252	8:10463858-10569697	NOTEST	0	0	0	0	1	1
ENSG00000212434	ENSG00000212434	U3	X:68835910-69259319	NOTEST	0	0	0	0	1	1
ENSG00000212440	ENSG00000212440	SNORA75	12:9429830-9466684	NOTEST	0	0	0	0	1	1
ENSG00000212441	ENSG00000212441	RNU6-1269P	9:42368302-42474239	NOTEST	0	0	0	0	1	1
ENSG00000212442	ENSG00000212442	RNU6-243P	3:35298331-35298438	NOTEST	0	0	0	0	1	1
ENSG00000212445	ENSG00000212445	SNORA48	16:68021296-68272005	NOTEST	0	0	0	0	1	1
ENSG00000212446	ENSG00000212446	RNU6-131P	17:42213250-42213357	NOTEST	0	0	0	0	1	1
ENSG00000212447	ENSG00000212447	SNORD90	9:125606834-125667620	NOTEST	0	0	0	0	1	1
ENSG00000212448	ENSG00000212448	Y_RNA	12:96011464-96011562	NOTEST	0	0	0	0	1	1
ENSG00000212450	ENSG00000212450	RNU6-241P	7:45829183-45829287	NOTEST	0	0	0	0	1	1
ENSG00000212451	ENSG00000212451	RNU11-4P	8:127564686-127725660	NOTEST	0	0	0	0	1	1
ENSG00000212452	ENSG00000212452	SNORD69	3:52529353-52742182	NOTEST	0	0	0	0	1	1
ENSG00000212454	ENSG00000212454	RNA5SP286	9:76365887-76365993	NOTEST	0	0	0	0	1	1
ENSG00000212455	ENSG00000212455	SNORA40	2:18059113-18542882	NOTEST	0	0	0	0	1	1
ENSG00000212456	ENSG00000212456	RNVU1-13	1:147994145-147994313	NOTEST	0	0	0	0	1	1
ENSG00000212457	ENSG00000212457	RNU6-644P	5:115419503-115748459	NOTEST	0	0	0	0	1	1
ENSG00000212458	ENSG00000212458	SNORA48	4:1107426-1147514	NOTEST	0	0	0	0	1	1
ENSG00000212459	ENSG00000212459	RNU6-695P	1:90719013-90719117	NOTEST	0	0	0	0	1	1
ENSG00000212460	ENSG00000212460	RNU6-460P	5:137450865-137475132	NOTEST	0	0	0	0	1	1
ENSG00000212461	ENSG00000212461	SNORA17	12:72003251-72097836	NOTEST	0	0	0	0	1	1
ENSG00000212464	ENSG00000212464	SNORA12	10:101989423-102027437	NOTEST	0	0	0	0	1	1
ENSG00000212466	ENSG00000212466	RNU6-952P	11:102184452-102184560	NOTEST	0	0	0	0	1	1
ENSG00000212468	ENSG00000212468	RNU6-754P	6:45868044-46048132	NOTEST	0	0	0	0	1	1
ENSG00000212469	ENSG00000212469	RNU6-1158P	17:54948530-54948637	NOTEST	0	0	0	0	1	1
ENSG00000212473	ENSG00000212473	RNU1-101P	8:70990140-70990267	NOTEST	0	0	0	0	1	1
ENSG00000212475	ENSG00000212475	RNU6-400P	12:33729029-33729135	NOTEST	0	0	0	0	1	1
ENSG00000212479	ENSG00000212479	U3	21:30552746-30552960	NOTEST	0	0	0	0	1	1
ENSG00000212482	ENSG00000212482	RNU6-530P	7:77646392-79100524	NOTEST	0	0	0	0	1	1

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ENSG00000212485	ENSG00000212485	RNU6-1197P	8:74964574-75012088	NOTEST	0	0	0	0	1	1
ENSG00000212489	ENSG00000212489	RNU6-1109P	3:189883205-189883312	NOTEST	0	0	0	0	1	1
ENSG00000212490	ENSG00000212490	SNORA26	4:53588784-53617807	NOTEST	0	0	0	0	1	1
ENSG00000212493	ENSG00000212493	SNORD19	3:52529353-52742182	NOTEST	0	0	0	0	1	1
ENSG00000212495	ENSG00000212495	RNU6-332P	X:93258813-93258921	NOTEST	0	0	0	0	1	1
ENSG00000212496	ENSG00000212496	RNU6-1093P	12:50569570-50677329	NOTEST	0	0	0	0	1	1
ENSG00000212497	ENSG00000212497	RNA5SP465	19:12098431-12167127	NOTEST	0	0	0	0	1	1
ENSG00000212498	ENSG00000212498	SNORD86	20:2632790-2639039	NOTEST	0	0	0	0	1	1
ENSG00000212499	ENSG00000212499	RNA5SP300	10:12938626-13180291	NOTEST	0	0	0	0	1	1
ENSG00000212505	ENSG00000212505	RNA5SP299	10:8698678-8698794	NOTEST	0	0	0	0	1	1
ENSG00000212510	ENSG00000212510	RNU6-972P	X:135747705-135864247	NOTEST	0	0	0	0	1	1
ENSG00000212511	ENSG00000212511	U3	15:37144840-37145059	NOTEST	0	0	0	0	1	1
ENSG00000212512	ENSG00000212512	Y_RNA	1:150854926-150855011	NOTEST	0	0	0	0	1	1
ENSG00000212516	ENSG00000212516	RNU6-1268P	14:19983558-20020272	NOTEST	0	0	0	0	1	1
ENSG00000212517	ENSG00000212517	SNORA26	20:5095598-5107272	NOTEST	0	0	0	0	1	1
ENSG00000212518	ENSG00000212518	RNU11-5P	14:29945989-29946118	NOTEST	0	0	0	0	1	1
ENSG00000212520	ENSG00000212520	RNU6-1250P	10:69556426-69597924	NOTEST	0	0	0	0	1	1
ENSG00000212521	ENSG00000212521	RNU6-918P	9:100794511-100794617	NOTEST	0	0	0	0	1	1
ENSG00000212522	ENSG00000212522	Y_RNA	14:56535160-56535245	NOTEST	0	0	0	0	1	1
ENSG00000212525	ENSG00000212525	RNA5SP212	6:108532425-108582464	NOTEST	0	0	0	0	1	1
ENSG00000212526	ENSG00000212526	RNU6-466P	15:31196054-31283810	NOTEST	0	0	0	0	1	1
ENSG00000212527	ENSG00000212527	RNA5SP63	1:163479273-163479385	NOTEST	0	0	0	0	1	1
ENSG00000212528	ENSG00000212528	SNORD115-47	15:25497371-25684128	NOTEST	0	0	0	0	1	1
ENSG00000212529	ENSG00000212529	SNORA57	5:171636643-171711075	NOTEST	0	0	0	0	1	1
ENSG00000212532	ENSG00000212532	SNORD66	6:51329487-51329563	NOTEST	0	0	0	0	1	1
ENSG00000212533	ENSG00000212533	SNORA75	12:31173696-31257725	NOTEST	0	0	0	0	1	1
ENSG00000212534	ENSG00000212534	SNORD70	2:203130438-203168389	NOTEST	0	0	0	0	1	1
ENSG00000212535	ENSG00000212535	RNU6-808P	12:95611521-95696566	NOTEST	0	0	0	0	1	1
ENSG00000212536	ENSG00000212536	RNA5SP474	20:5079032-5079122	NOTEST	0	0	0	0	1	1
ENSG00000212538	ENSG00000212538	U3	1:163892906-163893109	NOTEST	0	0	0	0	1	1
ENSG00000212539	ENSG00000212539	U3	18:54264438-54706076	NOTEST	0	0	0	0	1	1
ENSG00000212541	ENSG00000212541	RNU6-510P	1:38457133-38457241	NOTEST	0	0	0	0	1	1
ENSG00000212542	ENSG00000212542	RNA5SP496	22:31677578-31742218	NOTEST	0	0	0	0	1	1
ENSG00000212544	ENSG00000212544	RNVU1-19	1:149514089-149514256	NOTEST	0	0	0	0	1	1
ENSG00000212545	ENSG00000212545	RNU6-337P	7:77646392-79100524	NOTEST	0	0	0	0	1	1
ENSG00000212546	ENSG00000212546	RNU6-995P	X:80191932-80192039	NOTEST	0	0	0	0	1	1
ENSG00000212549	ENSG00000212549	RNA5SP354	12:26272958-26986131	NOTEST	0	0	0	0	1	1
ENSG00000212550	ENSG00000212550	RNU1-78P	15:45295061-45295226	NOTEST	0	0	0	0	1	1
ENSG00000212551	ENSG00000212551	U3	11:31806339-32127301	NOTEST	0	0	0	0	1	1
ENSG00000212552	ENSG00000212552	SNORD91B	17:1963132-2284352	NOTEST	0	0	0	0	1	1
ENSG00000212553	ENSG00000212553	SNORD116	13:40431271-40431364	NOTEST	0	0	0	0	1	1
ENSG00000212555	ENSG00000212555	RNU6-192P	20:17884405-17884505	NOTEST	0	0	0	0	1	1
ENSG00000212556	ENSG00000212556	Y_RNA	3:126921214-126921316	NOTEST	0	0	0	0	1	1
ENSG00000212558	ENSG00000212558	SNORA26	2:10230331-10230446	NOTEST	0	0	0	0	1	1
ENSG00000212559	ENSG00000212559	RNA5SP35	13:93879094-95059655	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000212560	ENSG00000212560	RNU6-630P	X:41998677-41998783	NOTEST	0	0	0	0	1	1
ENSG00000212561	ENSG00000212561	RNU6-381P	5:44066725-44066833	NOTEST	0	0	0	0	1	1
ENSG00000212564	ENSG00000212564	RNU6-1326P	21:16986601-16986708	NOTEST	0	0	0	0	1	1
ENSG00000212565	ENSG00000212565	SNORA68	17:46952221-47006418	NOTEST	0	0	0	0	1	1
ENSG00000212567	ENSG00000212567	SNORA57	5:40759480-40798476	NOTEST	0	0	0	0	1	1
ENSG00000212568	ENSG00000212568	RNU6-1254P	7:66356174-66356278	NOTEST	0	0	0	0	1	1
ENSG00000212569	ENSG00000212569	Y_RNA	22:51108231-51108329	NOTEST	0	0	0	0	1	1
ENSG00000212571	ENSG00000212571	RNA5SP482	20:30638390-30638508	NOTEST	0	0	0	0	1	1
ENSG00000212572	ENSG00000212572	RNU6-903P	18:9615261-9619361	NOTEST	0	0	0	0	1	1
ENSG00000212576	ENSG00000212576	RNA5SP467	19:12203077-12267546	NOTEST	0	0	0	0	1	1
ENSG00000212579	ENSG00000212579	SNORA40	6:35541361-35696360	NOTEST	0	0	0	0	1	1
ENSG00000212580	ENSG00000212580	SNORA75	2:50116005-50116124	NOTEST	0	0	0	0	1	1
ENSG00000212581	ENSG00000212581	U8	2:186526500-186526633	NOTEST	0	0	0	0	1	1
ENSG00000212582	ENSG00000212582	Y_RNA	16:53088944-53363062	NOTEST	0	0	0	0	1	1
ENSG00000212584	ENSG00000212584	RNU6-587P	X:100946552-100946658	NOTEST	0	0	0	0	1	1
ENSG00000212585	ENSG00000212585	Y_RNA	3:74215202-74215290	NOTEST	0	0	0	0	1	1
ENSG00000212586	ENSG00000212586	SNORA8	6:38683116-38998301	NOTEST	0	0	0	0	1	1
ENSG00000212587	ENSG00000212587	SNORA40	6:111169748-111169876	NOTEST	0	0	0	0	1	1
ENSG00000212588	ENSG00000212588	SNORA26	4:53578596-53586998	NOTEST	0	0	0	0	1	1
ENSG00000212589	ENSG00000212589	SNORA17	10:115580217-115580349	NOTEST	0	0	0	0	1	1
ENSG00000212590	ENSG00000212590	SNORA26	7:152306397-152306519	NOTEST	0	0	0	0	1	1
ENSG00000212593	ENSG00000212593	SNORA75	16:23399813-23468927	NOTEST	0	0	0	0	1	1
ENSG00000212594	ENSG00000212594	U8	12:103981050-104162636	NOTEST	0	0	0	0	1	1
ENSG00000212595	ENSG00000212595	5S_rRNA	X:150194766-150194878	NOTEST	0	0	0	0	1	1
ENSG00000212597	ENSG00000212597	RNU6-876P	11:128834954-129149219	NOTEST	0	0	0	0	1	1
ENSG00000212598	ENSG00000212598	U3	3:90079433-90079644	NOTEST	0	0	0	0	1	1
ENSG00000212599	ENSG00000212599	RNU6-279P	12:59759998-59804952	NOTEST	0	0	0	0	1	1
ENSG00000212601	ENSG00000212601	RNA5SP53	1:93913687-94020218	NOTEST	0	0	0	0	1	1
ENSG00000212604	ENSG00000212604	SNORA48	15:26147506-26298267	NOTEST	0	0	0	0	1	1
ENSG00000212605	ENSG00000212605	RNU1-56P	X:70240124-70240288	NOTEST	0	0	0	0	1	1
ENSG00000212607	ENSG00000212607	SNORA45	11:8703957-8932498	NOTEST	4.67982	0	#NAME?	0	1	1
ENSG00000212608	ENSG00000212608	SNORA26	3:53421739-53421863	NOTEST	0	0	0	0	1	1
ENSG00000212609	ENSG00000212609	RNU1-139P	21:20717464-20717629	NOTEST	0	0	0	0	1	1
ENSG00000212610	ENSG00000212610	U3	1:218715032-218715241	NOTEST	0	0	0	0	1	1
ENSG00000212611	ENSG00000212611	SNORD30	X:113260260-113260330	NOTEST	0	0	0	0	1	1
ENSG00000212612	ENSG00000212612	RNU6-1239P	14:19553364-19590078	NOTEST	0	0	0	0	1	1
ENSG00000212615	ENSG00000212615	SNORD58	14:45553301-45604522	NOTEST	0	0	0	0	1	1
ENSG00000212618	ENSG00000212618	snoMBII-202	17:18847311-18847386	NOTEST	0	0	0	0	1	1
ENSG00000212620	ENSG00000212620	SNORA75	4:80748624-80798924	NOTEST	0	0	0	0	1	1
ENSG00000212623	ENSG00000212623	RNU6-493P	X:80156255-80156363	NOTEST	0	0	0	0	1	1
ENSG00000212624	ENSG00000212624	SNORA26	1:52027537-52344477	NOTEST	0	0	0	0	1	1
ENSG00000212625	ENSG00000212625	RNA5SP397	15:60771376-61521518	NOTEST	0	0	0	0	1	1
ENSG00000212626	ENSG00000212626	SNORA48	18:7301017-7301151	NOTEST	0	0	0	0	1	1
ENSG00000212628	ENSG00000212628	RNA5SP241	7:120628730-120937498	NOTEST	0	0	0	0	1	1
ENSG00000212643	ENSG00000212643	ZRSR1	5:112043194-112258236	NOTEST	0.403967	0.0904064	-2.15974	0	1	1

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ENSG00000212657	ENSG00000212657	KRTAP16-1	17:39463951-39465505	NOTEST	0	0	0	0	1	1
ENSG00000212658	ENSG00000212658	KRTAP29-1	17:39458077-39459103	NOTEST	0	0	0	0	1	1
ENSG00000212659	ENSG00000212659	KRTAP9-6	17:39421590-39422893	NOTEST	0	0	0	0	1	1
ENSG00000212663	ENSG00000212663	RP1-122K4.3	X:13998184-14006939	NOTEST	0	0	0	0	1	1
ENSG00000212670	ENSG00000212670	AL161915.1	1:54519259-54578192	NOTEST	0.478535	0.453331	-0.0780603	0	1	1
ENSG00000212673	ENSG00000212673	AL136115.1	1:32307619-32410457	NOTEST	0.157848	0.11163	-0.499807	0	1	1
ENSG00000212695	ENSG00000212695	RP11-134K1.2	9:8314245-10612723	NOTEST	0	0	0	0	1	1
ENSG00000212710	ENSG00000212710	CTAGE1	18:19993563-19997878	NOTEST	0	0	0	0	1	1
ENSG00000212712	ENSG00000212712	AP002414.1	18:12056674-12057821	NOTEST	0	0	0	0	1	1
ENSG00000212717	ENSG00000212717	DEFB117	20:29948577-29948733	NOTEST	0	0	0	0	1	1
ENSG00000212721	ENSG00000212721	KRTAP4-11	17:39273432-39274606	NOTEST	0	0	0	0	1	1
ENSG00000212722	ENSG00000212722	KRTAP4-9	17:39261583-39262740	NOTEST	0	0	0	0	1	1
ENSG00000212724	ENSG00000212724	KRTAP2-3	17:39215494-39216344	NOTEST	0.123838	0.125044	0.0139818	0	1	1
ENSG00000212725	ENSG00000212725	KRTAP2-1	17:39202792-39203568	NOTEST	0	0	0	0	1	1
ENSG00000212734	ENSG00000212734	C17orf100	17:6554970-6558328	NOTEST	0.316068	0.257207	-0.297308	0	1	1
ENSG00000212743	ENSG00000212743	DKFZP667F0711	10:6392277-6394723	NOTEST	0	0.0101435	inf	0	1	1
ENSG00000212768	ENSG00000212768	AC114546.1	15:35270541-35280488	NOTEST	0.000685955	0.00979631	3.83605	0	1	1
ENSG00000212769	ENSG00000212769	HMGN2P8	10:85841184-85841751	NOTEST	0	0	0	0	1	1
ENSG00000212789	ENSG00000212789	ST13P5	11:18283528-18284638	NOTEST	0.225998	0.464779	1.04023	0	1	1
ENSG00000212807	ENSG00000212807	OR2A42	7:143883175-144077725	NOTEST	0	0	0	0	1	1
ENSG00000212829	ENSG00000212829	RPS26P3	9:8314245-10612723	NOTEST	0.112038	0.0873881	-0.358479	0	1	1
ENSG00000212855	ENSG00000212855	TTTY2	Y:9578192-9611898	NOTEST	0	0	0	0	1	1
ENSG00000212856	ENSG00000212856	TTTY2B	Y:6258471-6292186	NOTEST	0	0	0	0	1	1
ENSG00000212857	ENSG00000212857	AL356585.1	GL000212.1:64251-65919	NOTEST	0.209022	0.321219	0.619901	0	1	1
ENSG00000212866	ENSG00000212866	HSPA1B	HSCHR6_MHC_QBL:31785765-31788290	NOTEST	0	0	0	0	1	1
ENSG00000212884	ENSG00000212884	AC011841.1	GL000205.1:117168-119085	NOTEST	0	0.0119549	inf	0	1	1
ENSG00000212899	ENSG00000212899	KRTAP3-3	17:39149685-39150385	NOTEST	0	0	0	0	1	1
ENSG00000212900	ENSG00000212900	KRTAP3-2	17:39155446-39156138	NOTEST	0	0	0	0	1	1
ENSG00000212901	ENSG00000212901	KRTAP3-1	17:39164772-39175576	NOTEST	0.10079	0.0250486	-2.00855	0	1	1
ENSG00000212916	ENSG00000212916	MAP10	1:232940642-232946092	NOTEST	0.0129628	0.0188317	0.538781	0	1	1
ENSG00000212928	ENSG00000212928	AL391152.1	14:57670517-57756797	NOTEST	0	0	0	0	1	1
ENSG00000212930	ENSG00000212930	RP11-414H23.2	5:90519235-90519784	NOTEST	0	0	0	0	1	1
ENSG00000212932	ENSG00000212932	RPL23AP4	21:48110675-48111157	NOTEST	0	0	0	0	1	1
ENSG00000212933	ENSG00000212933	KRTAP12-4	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000212935	ENSG00000212935	KRTAP10-3	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000212938	ENSG00000212938	KRTAP6-3	21:31964758-31965394	NOTEST	0	0	0	0	1	1
ENSG00000212939	ENSG00000212939	RP1-29C18.10	22:49808175-50051190	NOTEST	0	0	0	0	1	1
ENSG00000212951	ENSG00000212951	RP11-211N8.3	9:46842615-46846025	NOTEST	0.0932831	0.114301	0.293145	0	1	1
ENSG00000212952	ENSG00000212952	BX088651.1	9:44400716-44404440	NOTEST	0	0.0648664	inf	0	1	1
ENSG00000212961	ENSG00000212961	HNRNPA1P40	11:74041362-74197096	NOTEST	0	0	0	0	1	1
ENSG00000212989	ENSG00000212989	RP11-351E7.2	8:73341854-73342347	NOTEST	0	0	0	0	1	1
ENSG00000212993	ENSG00000212993	POU5F1B	8:128302061-128494384	NOTEST	0.228546	0.19167	-0.253862	0	1	1
ENSG00000212997	ENSG00000212997	AC023632.1	8:95499920-95565757	NOTEST	0.00882323	0.0211999	1.26468	0	1	1
ENSG00000212999	ENSG00000212999	AC117834.1	8:93895211-94029901	NOTEST	0	6.13E-05	inf	0	1	1

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ENSG00000213003	ENSG00000213003	BTF3P12	8:71021996-71316040	NOTEST	0	0	0	0	1	1
ENSG00000213005	ENSG00000213005	PTTG3P	8:67579830-67774257	NOTEST	0	0	0	0	1	1
ENSG00000213013	ENSG00000213013	RPS15AP36	19:58727545-58727927	NOTEST	0	0.0502394	inf	0	1	1
ENSG00000213014	ENSG00000213014	VN2R17P	19:56732680-56904914	NOTEST	0.0224712	0	#NAME?	0	1	1
ENSG00000213016	ENSG00000213016	AC008746.9	19:55032905-55033214	NOTEST	0	0	0	0	1	1
ENSG00000213018	ENSG00000213018	AL590762.11	X:70586113-70752224	NOTEST	0.113747	0.044364	-1.35837	0	1	1
ENSG00000213022	ENSG00000213022	KLK9	19:51446558-51515385	NOTEST	0	0	0	0	1	1
ENSG00000213023	ENSG00000213023	SYT3	19:51124563-51222707	NOTEST	0.125689	0.207317	0.721985	0	1	1
ENSG00000213026	ENSG00000213026	CFL1P4	1:242156486-242156984	NOTEST	0	0	0	0	1	1
ENSG00000213028	ENSG00000213028	RP11-108F13.2	1:229824745-229825651	NOTEST	0	0	0	0	1	1
ENSG00000213029	ENSG00000213029	SPHAR	1:229394027-229441641	NOTEST	0	0	0	0	1	1
ENSG00000213030	ENSG00000213030	CGB8	19:49526125-49552400	NOTEST	0	0	0	0	1	1
ENSG00000213032	ENSG00000213032	NDUFA3P3	1:226151878-226152128	NOTEST	0	0	0	0	1	1
ENSG00000213033	ENSG00000213033	AURKAPS1	1:220321634-220445796	NOTEST	0.196821	0.158159	-0.315511	0	1	1
ENSG00000213035	ENSG00000213035	RPL23AP80	19:48297723-48298177	NOTEST	0	0.0418327	inf	0	1	1
ENSG00000213036	ENSG00000213036	RP11-365D23.4	1:214517514-214725792	NOTEST	0	0	0	0	1	1
ENSG00000213041	ENSG00000213041	RP11-383G10.3	1:205111631-205180727	NOTEST	0.111313	0.0607322	-0.874085	0	1	1
ENSG00000213045	ENSG00000213045	RP11-532L16.1	1:200298288-200298805	NOTEST	0	0.103786	inf	0	1	1
ENSG00000213046	ENSG00000213046	EEF1A1P32	1:197473877-197744826	NOTEST	0	0	0	0	1	1
ENSG00000213048	ENSG00000213048	OR5S1P	2:241048518-241049469	NOTEST	0	0	0	0	1	1
ENSG00000213049	ENSG00000213049	HNRNPA1P34	12:9180127-9181685	NOTEST	0	0	0	0	1	1
ENSG00000213050	ENSG00000213050	TPM3P1	7:116592499-116870157	NOTEST	0	0	0	0	1	1
ENSG00000213051	ENSG00000213051	RPL5P5	1:185126211-185260897	NOTEST	0.0376204	0.0145078	-1.37468	0	1	1
ENSG00000213055	ENSG00000213055	AC064852.5	2:233562008-233880595	NOTEST	0.0294254	0	#NAME?	0	1	1
ENSG00000213057	ENSG00000213057	C1orf220	1:178482211-178518024	NOTEST	0.515077	0.575444	0.159888	0	1	1
ENSG00000213060	ENSG00000213060	RP4-612B18.3	1:171750787-171783163	NOTEST	0.0588944	0	#NAME?	0	1	1
ENSG00000213061	ENSG00000213061	PFN1P11	10:104597767-104605230	NOTEST	0	0	0	0	1	1
ENSG00000213063	ENSG00000213063	RPL29P7	1:168873142-169056243	NOTEST	0	0	0	0	1	1
ENSG00000213065	ENSG00000213065	RP3-431P23.2	6:168167762-168169248	NOTEST	0	0	0	0	1	1
ENSG00000213067	ENSG00000213067	RP11-760D2.10	7:56665071-56666035	NOTEST	0	0	0	0	1	1
ENSG00000213068	ENSG00000213068	RP11-277B15.1	1:167131659-167132074	NOTEST	0	0	0	0	1	1
ENSG00000213069	ENSG00000213069	KRT8P40	2:177855235-178088686	NOTEST	0	0.091576	inf	0	1	1
ENSG00000213070	ENSG00000213070	HMGB3P6	1:164326003-164326601	NOTEST	0	0	0	0	1	1
ENSG00000213071	ENSG00000213071	LPAL2	6:160769299-160932156	NOTEST	0.0174646	0	#NAME?	0	1	1
ENSG00000213075	ENSG00000213075	RPL31P11	1:161653484-161655042	NOTEST	0.0214154	0.0235341	0.136104	0	1	1
ENSG00000213076	ENSG00000213076	yR211F11.2	6:159342302-159343182	NOTEST	0	0	0	0	1	1
ENSG00000213077	ENSG00000213077	FAM106A	17:18414534-18528930	NOTEST	0.403912	0.253106	-0.674298	0	1	1
ENSG00000213078	ENSG00000213078	RP5-933K21.2	6:157787021-157787955	NOTEST	0	0	0	0	1	1
ENSG00000213081	ENSG00000213081	AC012362.3	2:209224437-209719227	NOTEST	0	0	0	0	1	1
ENSG00000213082	ENSG00000213082	PPP1R14BP2	2:208546313-208546757	NOTEST	0	0	0	0	1	1
ENSG00000213083	ENSG00000213083	AC010731.6	2:207516344-207583120	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000213085	ENSG00000213085	CCDC19	1:159796539-159869953	NOTEST	0.205754	0.228457	0.150996	0	1	1
ENSG00000213087	ENSG00000213087	RP11-613F7.1	6:151186684-151549582	NOTEST	0.123625	0	#NAME?	0	1	1
ENSG00000213088	ENSG00000213088	DARC	1:159141398-159177763	NOTEST	0.111819	0.121275	0.117117	0	1	1
ENSG00000213090	ENSG00000213090	AC007256.5	2:202241929-202345569	NOTEST	0.070058	0.0509125	-0.46053	0	1	1
ENSG00000213091	ENSG00000213091	PHBP1	6:150363681-150364489	NOTEST	0	0	0	0	1	1
ENSG00000213100	ENSG00000213100	KRT18P68	X:45842799-45843799	NOTEST	0	0	0	0	1	1
ENSG00000213104	ENSG00000213104	NPM1P46	2:198244424-198245616	NOTEST	0	0.0301939	inf	0	1	1
ENSG00000213107	ENSG00000213107	AHCYP5	2:196440700-196602426	NOTEST	0	0	0	0	1	1
ENSG00000213108	ENSG00000213108	BTF3L4P3	6:137865033-137865509	NOTEST	0	0	0	0	1	1
ENSG00000213109	ENSG00000213109	RP11-55K22.2	6:137143716-137235075	NOTEST	0.013192	0	#NAME?	0	1	1
ENSG00000213110	ENSG00000213110	AC019178.2	2:190744334-191236391	NOTEST	0	0	0	0	1	1
ENSG00000213111	ENSG00000213111	COX5BP2	6:136172833-136546733	NOTEST	0	0.0707771	inf	0	1	1
ENSG00000213113	ENSG00000213113	TUBB8P8	3:197846591-197847649	NOTEST	0.172358	0.254907	0.564563	0	1	1
ENSG00000213115	ENSG00000213115	AC104131.1	2:188577542-189152418	NOTEST	0.0264263	0	#NAME?	0	1	1
ENSG00000213117	ENSG00000213117	RP3-352A20.1	6:135219011-135219897	NOTEST	0	0	0	0	1	1
ENSG00000213118	ENSG00000213118	CHCHD2P4	6:134714279-134715038	NOTEST	0.106106	0	#NAME?	0	1	1
ENSG00000213120	ENSG00000213120	LIN28AP1	2:184125369-184125774	NOTEST	0	0	0	0	1	1
ENSG00000213121	ENSG00000213121	AL590867.1	6:153552454-153668623	NOTEST	0	0	0	0	1	1
ENSG00000213122	ENSG00000213122	RPL23AP46	6:133318689-133319179	NOTEST	0	0	0	0	1	1
ENSG00000213126	ENSG00000213126	AC092642.1	2:180306708-180726232	NOTEST	0	0	0	0	1	1
ENSG00000213128	ENSG00000213128	RPL32P31	17:78516002-78516405	NOTEST	0	0	0	0	1	1
ENSG00000213130	ENSG00000213130	EEF1DP5	6:128901257-128902029	NOTEST	0	0	0	0	1	1
ENSG00000213131	ENSG00000213131	YWHAZP4	6:127676900-127677934	NOTEST	0.0829842	0	#NAME?	0	1	1
ENSG00000213132	ENSG00000213132	AC022498.1	3:187868993-188608460	NOTEST	0	0	0	0	1	1
ENSG00000213133	ENSG00000213133	PPP1R14BP5	6:126579066-126579501	NOTEST	0	0	0	0	1	1
ENSG00000213135	ENSG00000213135	AC015815.6	17:75082797-75213179	NOTEST	0	0	0	0	1	1
ENSG00000213137	ENSG00000213137	ARF1P2	12:121200312-121342174	NOTEST	0	0	0	0	1	1
ENSG00000213140	ENSG00000213140	ELK2AP	14:106138644-106139651	NOTEST	0	0	0	0	1	1
ENSG00000213145	ENSG00000213145	CRIP1	14:105952653-105965912	NOTEST	0.454129	0.350807	-0.372423	0	1	1
ENSG00000213147	ENSG00000213147	RPL23AP60	10:135515570-135516024	NOTEST	0	0	0	0	1	1
ENSG00000213148	ENSG00000213148	AC073465.1	2:174296076-174296540	NOTEST	0	0	0	0	1	1
ENSG00000213149	ENSG00000213149	CNN2P9	6:111179441-111180350	NOTEST	0	0.0141914	inf	0	1	1
ENSG00000213150	ENSG00000213150	RP11-346C16.2	6:110931180-111137161	NOTEST	0	0	0	0	1	1
ENSG00000213152	ENSG00000213152	RPL7AP60	12:112597991-112819896	NOTEST	0.0913943	0.115099	0.332699	0	1	1
ENSG00000213153	ENSG00000213153	RP11-259P6.3	11:133734771-133735522	NOTEST	0	0	0	0	1	1
ENSG00000213155	ENSG00000213155	RP11-252O18.3	3:181584138-181584942	NOTEST	0	0	0	0	1	1
ENSG00000213157	ENSG00000213157	RP11-259P15.1	3:180319917-180700541	NOTEST	0	0	0	0	1	1
ENSG00000213158	ENSG00000213158	GAPDHP36	3:179918923-179930896	NOTEST	0	0	0	0	1	1
ENSG00000213159	ENSG00000213159	CEND1P1	14:104917315-104917770	NOTEST	0	0	0	0	1	1
ENSG00000213165	ENSG00000213165	AC090425.1	3:179322477-179345435	NOTEST	0	0	0	0	1	1
ENSG00000213167	ENSG00000213167	AL591516.4	6:107473760-107780768	NOTEST	0	0	0	0	1	1
ENSG00000213169	ENSG00000213169	RP11-393N4.2	3:174095033-174095795	NOTEST	0	0	0	0	1	1
ENSG00000213170	ENSG00000213170	RP11-81B10.2	10:127700949-128077024	NOTEST	0	0	0	0	1	1

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ENSG00000213171	ENSG00000213171	LINGO4	1:151772739-151804348	NOTEST	0	0	0	0	1	1
ENSG00000213172	ENSG00000213172	RP1-228H13.2	1:40810521-40888998	NOTEST	0	0	0	0	1	1
ENSG00000213174	ENSG00000213174	RP11-373E16.1	3:170136652-170578169	NOTEST	0	0	0	0	1	1
ENSG00000213176	ENSG00000213176	RPL13P6	14:103388992-103523799	NOTEST	0	0	0	0	1	1
ENSG00000213177	ENSG00000213177	PRDX2P4	6:100583939-100584539	NOTEST	0	0	0	0	1	1
ENSG00000213179	ENSG00000213179	RPL17P41	17:65780868-65781409	NOTEST	0	0	0	0	1	1
ENSG00000213180	ENSG00000213180	RPL36AP48	17:65066553-65242105	NOTEST	0	0	0	0	1	1
ENSG00000213181	ENSG00000213181	OR10N1P	11:123975806-123976675	NOTEST	0	0	0	0	1	1
ENSG00000213182	ENSG00000213182	OR10D5P	11:123925576-123926414	NOTEST	0	0	0	0	1	1
ENSG00000213183	ENSG00000213183	RPS7P8	6:97096364-97096945	NOTEST	0	0	0	0	1	1
ENSG00000213184	ENSG00000213184	RP11-335F8.2	11:122888345-122889369	NOTEST	0	0	0	0	1	1
ENSG00000213187	ENSG00000213187	COPS5P1	6:93780104-93813102	NOTEST	0	0	0	0	1	1
ENSG00000213188	ENSG00000213188	YBX1P4	7:151825963-151826771	NOTEST	0.042732	0.018139	-1.23622	0	1	1
ENSG00000213194	ENSG00000213194	AC016732.2	2:158067358-158068051	NOTEST	0	0	0	0	1	1
ENSG00000213197	ENSG00000213197	AC012066.1	2:153191750-153506348	NOTEST	0.0806565	0.0627783	-0.361525	0	1	1
ENSG00000213201	ENSG00000213201	FABP5P10	2:151974468-152043109	NOTEST	0	0	0	0	1	1
ENSG00000213203	ENSG00000213203	GIMAP1	7:150413644-150487837	NOTEST	0	0	0	0	1	1
ENSG00000213204	ENSG00000213204	C6orf165	6:88117700-88222054	NOTEST	0.044823	0.034085	-0.395103	0	1	1
ENSG00000213205	ENSG00000213205	STRADBP1	7:150209646-150210927	NOTEST	0.0243335	0.0104008	-1.22624	0	1	1
ENSG00000213209	ENSG00000213209	AC005229.7	7:148334270-148334679	NOTEST	0	0	0	0	1	1
ENSG00000213210	ENSG00000213210	AC005229.5	7:148277492-148277891	NOTEST	0	0	0	0	1	1
ENSG00000213211	ENSG00000213211	KRT18P64	6:85995793-86000567	NOTEST	0	0	0	0	1	1
ENSG00000213212	ENSG00000213212	NCLP1	9:139685806-139735639	NOTEST	0.0699061	0.0689925	-0.0189774	0	1	1
ENSG00000213213	ENSG00000213213	CCDC183	9:139685806-139735639	NOTEST	0.57544	0.584918	0.0235674	0	1	1
ENSG00000213215	ENSG00000213215	OR2F1	7:143651936-143694405	NOTEST	0	0	0	0	1	1
ENSG00000213216	ENSG00000213216	RP11-355O1.7	9:125703111-125867145	NOTEST	0	0	0	0	1	1
ENSG00000213218	ENSG00000213218	CSH2	17:61949371-61951126	NOTEST	0	0	0	0	1	1
ENSG00000213225	ENSG00000213225	AC018804.7	2:130986948-130989679	NOTEST	0.0143929	0.0548494	1.93012	0	1	1
ENSG00000213226	ENSG00000213226	RP11-337C18.4	1:146790827-146791942	NOTEST	0	0	0	0	1	1
ENSG00000213228	ENSG00000213228	RPL12P38	17:58511038-58513357	NOTEST	0.179995	0	#NAME?	0	1	1
ENSG00000213231	ENSG00000213231	TCL1B	14:96116834-96158980	NOTEST	0	0	0	0	1	1
ENSG00000213232	ENSG00000213232	PPP1R2P10	13:64385146-64385741	NOTEST	0	0	0	0	1	1
ENSG00000213233	ENSG00000213233	RPL23AP62	11:112263840-112492452	NOTEST	0	0	0	0	1	1
ENSG00000213234	ENSG00000213234	ST13P10	11:112097087-112140678	NOTEST	0	0.0634897	inf	0	1	1
ENSG00000213235	ENSG00000213235	EEF1A1P16	12:17143603-17145017	NOTEST	0.12705	0.164021	0.368488	0	1	1
ENSG00000213236	ENSG00000213236	YWHAZP2	2:127315011-127315739	NOTEST	0.0266679	0.156933	2.55697	0	1	1
ENSG00000213237	ENSG00000213237	AC008155.1	7:138088939-138089268	NOTEST	0	0	0	0	1	1
ENSG00000213238	ENSG00000213238	AC008155.2	7:137982832-137983229	NOTEST	0	0	0	0	1	1
ENSG00000213239	ENSG00000213239	NPM1P32	2:122407225-122494499	NOTEST	0.0343331	0.129394	1.9141	0	1	1
ENSG00000213247	ENSG00000213247	RP11-479A21.1	10:112864713-112865006	NOTEST	0	0	0	0	1	1
ENSG00000213253	ENSG00000213253	CTC-250I14.1	19:13268772-13269602	NOTEST	0.0452843	0.233469	2.36615	0	1	1
ENSG00000213260	ENSG00000213260	YWHAZP5	10:107446079-107446809	NOTEST	0.0531449	0.0375444	-0.501331	0	1	1
ENSG00000213262	ENSG00000213262	AL365331.2	1:118183433-118184261	NOTEST	0	0	0	0	1	1
ENSG00000213264	ENSG00000213264	NIP7P2	3:132120096-132120640	NOTEST	0	0	0	0	1	1

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ENSG00000213265	ENSG00000213265	TSGA13	7:130295819-130372268	NOTEST	0	0.00556522	inf	0	1	1
ENSG00000213269	ENSG00000213269	AC004386.4	X:73595959-73596720	NOTEST	0	0	0	0	1	1
ENSG00000213270	ENSG00000213270	RPL6P25	12:83545109-83545969	NOTEST	0	0	0	0	1	1
ENSG00000213272	ENSG00000213272	RP11-613M5.1	12:76956073-77009211	NOTEST	0.0472291	0	#NAME?	0	1	1
ENSG00000213275	ENSG00000213275	IFITM9P	11:69061604-69182494	NOTEST	0	0	0	0	1	1
ENSG00000213277	ENSG00000213277	MARCKSL1P1	10:104678049-104953056	NOTEST	0.154848	0.150773	-0.0384699	0	1	1
ENSG00000213279	ENSG00000213279	RP1-29C18.9	22:49808175-50051190	NOTEST	0	0.0047242	inf	0	1	1
ENSG00000213280	ENSG00000213280	RP11-212P7.1	7:128171751-128269512	NOTEST	0.107203	0.20965	0.967643	0	1	1
ENSG00000213285	ENSG00000213285	AC138031.1	5:180898963-180899431	NOTEST	0	0	0	0	1	1
ENSG00000213287	ENSG00000213287	RP11-680L20.1	11:86748885-87035401	NOTEST	0	0	0	0	1	1
ENSG00000213290	ENSG00000213290	PGK1P2	19:12490002-12750912	NOTEST	0	0.0454147	inf	0	1	1
ENSG00000213291	ENSG00000213291	RP11-420H19.3	7:124462439-125019375	NOTEST	0	0	0	0	1	1
ENSG00000213293	ENSG00000213293	CTD-2666L21.3	19:12305829-12405702	NOTEST	0	0.0480449	inf	0	1	1
ENSG00000213295	ENSG00000213295	AC092106.2	2:106863824-106864197	NOTEST	0	0	0	0	1	1
ENSG00000213296	ENSG00000213296	RP5-1106E3.1	7:124120577-124121449	NOTEST	0	0	0	0	1	1
ENSG00000213301	ENSG00000213301	HMGB3P11	2:105387739-105388343	NOTEST	0	0	0	0	1	1
ENSG00000213302	ENSG00000213302	RP11-560I19.2	7:121874584-121874957	NOTEST	0	0	0	0	1	1
ENSG00000213303	ENSG00000213303	CTC-398G3.2	19:11562140-11639989	NOTEST	0.56505	0.205844	-1.45682	0	1	1
ENSG00000213304	ENSG00000213304	CTC-398G3.1	19:11562140-11639989	NOTEST	0.436394	0.314197	-0.473961	0	1	1
ENSG00000213305	ENSG00000213305	HNRNPCP6	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000213307	ENSG00000213307	RPL18P11	15:78916460-79027837	NOTEST	0	0	0	0	1	1
ENSG00000213309	ENSG00000213309	RPL9P18	6:64325731-64326266	NOTEST	0	0	0	0	1	1
ENSG00000213310	ENSG00000213310	CYCSP19	7:121038505-121038821	NOTEST	0	0	0	0	1	1
ENSG00000213312	ENSG00000213312	RPL7AP34	6:64231665-64293492	NOTEST	0	0	0	0	1	1
ENSG00000213315	ENSG00000213315	CTD-3035D6.1	14:91006931-91282823	NOTEST	0.113744	0.0470723	-1.27284	0	1	1
ENSG00000213316	ENSG00000213316	LTC4S	5:179159850-179223648	NOTEST	0	0.154223	inf	0	1	1
ENSG00000213318	ENSG00000213318	RP11-331F4.1	16:75226362-75227145	NOTEST	0	0	0	0	1	1
ENSG00000213328	ENSG00000213328	RP11-281O15.2	5:178322894-178360213	NOTEST	0	0	0	0	1	1
ENSG00000213331	ENSG00000213331	RP11-713C19.2	4:188891426-188892438	NOTEST	0	0	0	0	1	1
ENSG00000213332	ENSG00000213332	SLC25A5P6	4:187187098-187476721	NOTEST	0	0	0	0	1	1
ENSG00000213333	ENSG00000213333	NPM1P50	11:74790309-74791176	NOTEST	0.0213408	0.0150533	-0.503535	0	1	1
ENSG00000213335	ENSG00000213335	CLNS1AP1	6:54349966-54350648	NOTEST	0	0	0	0	1	1
ENSG00000213338	ENSG00000213338	ATF4P1	X:153850678-153851751	NOTEST	0	0	0	0	1	1
ENSG00000213343	ENSG00000213343	RP11-118B13.1	12:66431014-66431494	NOTEST	0	0	0	0	1	1
ENSG00000213344	ENSG00000213344	PCNPP3	12:66038113-66057079	NOTEST	0	0.0352086	inf	0	1	1
ENSG00000213352	ENSG00000213352	GAPDHP44	12:63037761-63328817	NOTEST	0	0	0	0	1	1
ENSG00000213355	ENSG00000213355	CNN2P8	2:95403081-95403994	NOTEST	0	0	0	0	1	1
ENSG00000213356	ENSG00000213356	AC018696.6	2:91734173-91734450	NOTEST	0	0	0	0	1	1
ENSG00000213358	ENSG00000213358	AC092933.4	3:196254209-196255662	NOTEST	0	0	0	0	1	1
ENSG00000213361	ENSG00000213361	RP4-778K6.1	7:104653871-105039755	NOTEST	0	0	0	0	1	1
ENSG00000213362	ENSG00000213362	FTH1P12	9:15527130-15527681	NOTEST	0.111611	0.152641	0.451657	0	1	1
ENSG00000213363	ENSG00000213363	RPS3P6	12:62102039-62811211	NOTEST	0	0.0758069	inf	0	1	1
ENSG00000213365	ENSG00000213365	AP000593.6	11:71991194-71992222	NOTEST	0	0	0	0	1	1

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ENSG00000213368	ENSG00000213368	ST13P11	11:94277005-94658686	NOTEST	0	0	0	0	1	1
ENSG00000213370	ENSG00000213370	RANP6	4:174554878-174555522	NOTEST	0	0	0	0	1	1
ENSG00000213371	ENSG00000213371	NAP1L1P3	3:120524712-120525592	NOTEST	0	0	0	0	1	1
ENSG00000213373	ENSG00000213373	LINC00671	17:41026686-41050751	NOTEST	0	0	0	0	1	1
ENSG00000213375	ENSG00000213375	AC068279.1	2:87596355-87596632	NOTEST	0	0	0	0	1	1
ENSG00000213376	ENSG00000213376	GAPDHP71	5:173763297-173959460	NOTEST	0	0	0	0	1	1
ENSG00000213383	ENSG00000213383	AC104297.1	3:17198653-18959184	NOTEST	0	0	0	0	1	1
ENSG00000213384	ENSG00000213384	EIF4E2P1	20:20370195-20693131	NOTEST	0	0	0	0	1	1
ENSG00000213385	ENSG00000213385	RP11-577H5.1	7:102389417-102449672	NOTEST	0.441085	0.179213	-1.29938	0	1	1
ENSG00000213386	ENSG00000213386	RP11-779O18.2	5:172185228-172204777	NOTEST	0	0.0185053	inf	0	1	1
ENSG00000213391	ENSG00000213391	RP11-66N11.6	X:152871971-152872343	NOTEST	0	0	0	0	1	1
ENSG00000213393	ENSG00000213393	RP11-546B8.1	5:170772346-170772634	NOTEST	0	0	0	0	1	1
ENSG00000213394	ENSG00000213394	RP4-747G18.5	7:100846894-100847776	NOTEST	0	0.0147337	inf	0	1	1
ENSG00000213399	ENSG00000213399	AC022210.2	2:85142909-85143789	NOTEST	0.0477568	0.193135	2.01583	0	1	1
ENSG00000213400	ENSG00000213400	RPL12P18	2:85048773-85134132	NOTEST	0	0	0	0	1	1
ENSG00000213402	ENSG00000213402	PTPRCAP	11:67202980-67211292	NOTEST	0.334848	0.322159	-0.0557326	0	1	1
ENSG00000213403	ENSG00000213403	CISD1P1	2:20026009-20026336	NOTEST	0	0	0	0	1	1
ENSG00000213406	ENSG00000213406	ANXA2P1	4:154073493-154260472	NOTEST	0.0556236	0.0905392	0.702845	0	1	1
ENSG00000213409	ENSG00000213409	RP11-658F2.3	11:66511921-66614017	NOTEST	0	0.0763178	inf	0	1	1
ENSG00000213410	ENSG00000213410	AC009951.2	2:145141647-145282147	NOTEST	0	0	0	0	1	1
ENSG00000213411	ENSG00000213411	RBM22P2	13:31032883-31191734	NOTEST	0.0327686	0.0217928	-0.58846	0	1	1
ENSG00000213412	ENSG00000213412	HNRNPA1P33	10:47011752-47174093	NOTEST	0.0706059	0	#NAME?	0	1	1
ENSG00000213413	ENSG00000213413	PVRIG	7:99775185-99869855	NOTEST	0.584049	0.53114	-0.136997	0	1	1
ENSG00000213414	ENSG00000213414	CTB-47B8.5	5:157411665-157416998	NOTEST	0	0	0	0	1	1
ENSG00000213416	ENSG00000213416	KRTAP4-12	17:39279342-39280419	NOTEST	0	0	0	0	1	1
ENSG00000213417	ENSG00000213417	KRTAP2-4	17:39221368-39222131	NOTEST	0	0	0	0	1	1
ENSG00000213421	ENSG00000213421	RP11-84O12.2	1:101052204-101052987	NOTEST	0	0	0	0	1	1
ENSG00000213423	ENSG00000213423	RBMX2P2	X:140355254-140358349	NOTEST	0	0	0	0	1	1
ENSG00000213424	ENSG00000213424	KRT222	17:38781213-38821433	NOTEST	0	0	0	0	1	1
ENSG00000213431	ENSG00000213431	RP11-301G23.1	3:100467999-100712359	NOTEST	0	0	0	0	1	1
ENSG00000213433	ENSG00000213433	RP11-54C4.1	5:151121876-151192346	NOTEST	0.250744	0.354332	0.498885	0	1	1
ENSG00000213434	ENSG00000213434	VTI1BP2	4:184404642-184405338	NOTEST	0.0282938	0.0199984	-0.500606	0	1	1
ENSG00000213435	ENSG00000213435	ATP6V0CP3	6:42694971-42695438	NOTEST	0	0	0	0	1	1
ENSG00000213438	ENSG00000213438	YBX2P1	10:125751425-125752185	NOTEST	0	0	0	0	1	1
ENSG00000213439	ENSG00000213439	OR5AC1	3:97783315-97784240	NOTEST	0	0	0	0	1	1
ENSG00000213440	ENSG00000213440	H2AFZP1	21:45432199-45526433	NOTEST	0	0	0	0	1	1
ENSG00000213448	ENSG00000213448	RPS23P2	4:138369240-138369655	NOTEST	0	0	0	0	1	1
ENSG00000213449	ENSG00000213449	GAPDHP28	10:93426536-93427539	NOTEST	0	0	0	0	1	1
ENSG00000213450	ENSG00000213450	VDAC1P7	3:75955845-77699115	NOTEST	0	0	0	0	1	1
ENSG00000213451	ENSG00000213451	OR6C69P	12:55656322-55657215	NOTEST	0	0	0	0	1	1
ENSG00000213452	ENSG00000213452	AKR1B1P2	3:74185109-74186043	NOTEST	0	0	0	0	1	1
ENSG00000213455	ENSG00000213455	AC091654.7	7:98083430-98083929	NOTEST	0	0	0	0	1	1
ENSG00000213461	ENSG00000213461	RP13-235E23.1	6:41275903-41276303	NOTEST	0	0	0	0	1	1
ENSG00000213467	ENSG00000213467	HMGB1P37	9:124282094-124282703	NOTEST	0	0.0240113	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000213468	ENSG00000213468	RP11-453F18__B.1	X:130836677-130964671	NOTEST	0.326318	0.215476	-0.59875	0	1	1
ENSG00000213470	ENSG00000213470	RP11-972K6.1	12:54026509-54071192	NOTEST	0	0	0	0	1	1
ENSG00000213471	ENSG00000213471	TTLL13	15:90792761-90816463	NOTEST	0	0	0	0	1	1
ENSG00000213478	ENSG00000213478	CFL1P2	1:51623459-51624143	NOTEST	0	0.0699226	inf	0	1	1
ENSG00000213480	ENSG00000213480	RP11-364P2.2	4:122250466-122302214	NOTEST	0.0200175	0	#NAME?	0	1	1
ENSG00000213483	ENSG00000213483	NDUFAF4P2	7:93220884-93540577	NOTEST	0	0	0	0	1	1
ENSG00000213484	ENSG00000213484	EIF4A1P8	10:93806448-94050844	NOTEST	0	0	0	0	1	1
ENSG00000213486	ENSG00000213486	AC108039.1	2:61937210-61938113	NOTEST	0	0	0	0	1	1
ENSG00000213487	ENSG00000213487	ASS1P4	X:3285189-3286423	NOTEST	0	0	0	0	1	1
ENSG00000213488	ENSG00000213488	CTB-85P21.1	5:143901702-143902551	NOTEST	0	0	0	0	1	1
ENSG00000213489	ENSG00000213489	RP13-147D17.1	X:124460745-124461870	NOTEST	0	0	0	0	1	1
ENSG00000213492	ENSG00000213492	NT5C3AP1	4:118349551-118612343	NOTEST	0.065981	0.0563396	-0.227902	0	1	1
ENSG00000213493	ENSG00000213493	ACTN4P1	4:117519316-117520767	NOTEST	0.0116029	0.0649757	2.48542	0	1	1
ENSG00000213494	ENSG00000213494	CCL14	17:34310326-34338658	NOTEST	0	0	0	0	1	1
ENSG00000213495	ENSG00000213495	RP11-416L21.1	2:60938618-60939055	NOTEST	0	0	0	0	1	1
ENSG00000213498	ENSG00000213498	TPT1P13	X:120997550-120998049	NOTEST	0	0	0	0	1	1
ENSG00000213500	ENSG00000213500	LAP3P2	6:36641593-36643047	NOTEST	0	0	0	0	1	1
ENSG00000213509	ENSG00000213509	PPIAP16	3:57927544-57928031	NOTEST	0	0.113662	inf	0	1	1
ENSG00000213512	ENSG00000213512	GBP7	1:89571814-89641723	NOTEST	0	0	0	0	1	1
ENSG00000213513	ENSG00000213513	RP13-39P12.2	10:79540094-79541634	NOTEST	0.0739336	0.0998499	0.43353	0	1	1
ENSG00000213514	ENSG00000213514	RP11-428P16.2	10:79490523-79494527	NOTEST	0.0612977	0.0588989	-0.057593	0	1	1
ENSG00000213519	ENSG00000213519	AC132008.1	3:197305083-197354777	NOTEST	0	0	0	0	1	1
ENSG00000213522	ENSG00000213522	RAC1P5	4:107842958-108223027	NOTEST	0	0	0	0	1	1
ENSG00000213525	ENSG00000213525	RP11-383B24.3	10:76504143-76504465	NOTEST	0	0	0	0	1	1
ENSG00000213526	ENSG00000213526	SETP8	X:116097016-116097644	NOTEST	0	0	0	0	1	1
ENSG00000213527	ENSG00000213527	RP11-591L14.1	15:80044030-80044391	NOTEST	0.0778829	0	#NAME?	0	1	1
ENSG00000213529	ENSG00000213529	RP11-432F4.2	9:115124993-115125396	NOTEST	0	0	0	0	1	1
ENSG00000213530	ENSG00000213530	MTHFD2P5	7:82219163-82220007	NOTEST	0	0	0	0	1	1
ENSG00000213536	ENSG00000213536	GNG5P1	6:166650456-166657197	NOTEST	0	0	0	0	1	1
ENSG00000213538	ENSG00000213538	KRT8P41	11:9025708-9159661	NOTEST	0	0	0	0	1	1
ENSG00000213539	ENSG00000213539	YBX1P6	9:112295109-112296612	NOTEST	0	0	0	0	1	1
ENSG00000213540	ENSG00000213540	RP11-486G15.1	1:84543744-84704181	NOTEST	0.0860374	0	#NAME?	0	1	1
ENSG00000213542	ENSG00000213542	RP11-467H10.1	7:76139744-77045717	NOTEST	0.238425	0.329689	0.467571	0	1	1
ENSG00000213543	ENSG00000213543	RARRES2P2	10:135450911-135451396	NOTEST	0	0	0	0	1	1
ENSG00000213547	ENSG00000213547	VN1R64P	16:31558018-31559058	NOTEST	0	0	0	0	1	1
ENSG00000213548	ENSG00000213548	AC005522.6	7:75991084-75991430	NOTEST	0	0	0	0	1	1
ENSG00000213549	ENSG00000213549	AC005077.8	7:75742343-75742718	NOTEST	0	0.0519726	inf	0	1	1
ENSG00000213556	ENSG00000213556	RP11-3J11.1	9:111598612-111598877	NOTEST	0	0	0	0	1	1
ENSG00000213557	ENSG00000213557	RP11-240E2.2	9:110802493-110802873	NOTEST	0	0	0	0	1	1
ENSG00000213558	ENSG00000213558	HMGN2P32	9:110220318-110220587	NOTEST	0	0	0	0	1	1
ENSG00000213559	ENSG00000213559	HNRNPA1P64	1:80916767-80917689	NOTEST	0	0	0	0	1	1
ENSG00000213560	ENSG00000213560	RP11-386I14.3	1:78444858-78604133	NOTEST	0	0	0	0	1	1
ENSG00000213561	ENSG00000213561	RP11-386I14.2	1:78444858-78604133	NOTEST	0	0	0	0	1	1
ENSG00000213568	ENSG00000213568	HNRNPA1P13	5:135764580-135765543	NOTEST	0	0	0	0	1	1

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ENSG00000213574	ENSG00000213574	LDHAP5	10:120692185-120692807	NOTEST	0	0.0256406	inf	0	1	1
ENSG00000213578	ENSG00000213578	CPLX3	15:75105056-75124141	NOTEST	0	0.00936197	inf	0	1	1
ENSG00000213579	ENSG00000213579	RP4-595K12.1	1:75667815-76076801	NOTEST	0	0	0	0	1	1
ENSG00000213587	ENSG00000213587	RP11-646D13.1	3:50712671-51421629	NOTEST	0	0	0	0	1	1
ENSG00000213590	ENSG00000213590	RP11-229P13.2	9:139830291-139831613	NOTEST	0.049265	0.00907946	-2.43988	0	1	1
ENSG00000213592	ENSG00000213592	AP000662.9	11:57480071-57587018	NOTEST	0.175455	0.0366316	-2.25994	0	1	1
ENSG00000213594	ENSG00000213594	GAPDHP25	2:38512551-38513552	NOTEST	0	0	0	0	1	1
ENSG00000213599	ENSG00000213599	SLX1A-SULT1A3	16:30204254-30215631	NOTEST	0.270555	0.140682	-0.943479	0	1	1
ENSG00000213600	ENSG00000213600	U73169.1	3:50263723-50296787	NOTEST	0.0770851	0.362364	2.23291	0	1	1
ENSG00000213601	ENSG00000213601	KRT18P19	2:190175988-190176693	NOTEST	0	0	0	0	1	1
ENSG00000213604	ENSG00000213604	RP11-444K7.8	11:55972600-55973101	NOTEST	0	0	0	0	1	1
ENSG00000213605	ENSG00000213605	AC111200.2	2:87098423-87248975	NOTEST	0	0	0	0	1	1
ENSG00000213606	ENSG00000213606	AKR1B10P1	10:69510041-69510983	NOTEST	0	0	0	0	1	1
ENSG00000213607	ENSG00000213607	OR4A45P	11:48600987-48601888	NOTEST	0	0	0	0	1	1
ENSG00000213608	ENSG00000213608	SLC25A14P1	4:84377084-84444501	NOTEST	0.0372095	0.0158242	-1.23354	0	1	1
ENSG00000213609	ENSG00000213609	RP11-170M17.2	10:65424423-65750328	NOTEST	0.0912465	0.0168027	-2.44108	0	1	1
ENSG00000213612	ENSG00000213612	FAM220CP	9:99883940-99884771	NOTEST	0	0	0	0	1	1
ENSG00000213613	ENSG00000213613	RP11-380G5.3	10:89618917-89731687	NOTEST	0.0421996	0.200639	2.2493	0	1	1
ENSG00000213620	ENSG00000213620	AL121657.4	2:31513627-31514470	NOTEST	0	0	0	0	1	1
ENSG00000213622	ENSG00000213622	AL163952.1	14:56464931-56465307	NOTEST	0	0	0	0	1	1
ENSG00000213630	ENSG00000213630	RP11-772E11.1	5:125999028-125999260	NOTEST	0	0	0	0	1	1
ENSG00000213640	ENSG00000213640	RP11-797H7.3	7:64323376-64324748	NOTEST	0	0	0	0	1	1
ENSG00000213641	ENSG00000213641	RPL7AP4	14:55965995-56168244	NOTEST	0	0	0	0	1	1
ENSG00000213642	ENSG00000213642	RP11-561N12.5	7:64029805-64030815	NOTEST	0	0	0	0	1	1
ENSG00000213643	ENSG00000213643	VN1R37P	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000213644	ENSG00000213644	RP11-165H4.3	7:63642087-63643271	NOTEST	0	0	0	0	1	1
ENSG00000213645	ENSG00000213645	SLC25A1P3	7:63391518-63392346	NOTEST	0	0	0	0	1	1
ENSG00000213648	ENSG00000213648	SULT1A4	16:29262828-29519817	NOTEST	0.234491	0.304198	0.37548	0	1	1
ENSG00000213650	ENSG00000213650	RP11-760D2.7	7:56635598-56636551	NOTEST	0	0.0210924	inf	0	1	1
ENSG00000213652	ENSG00000213652	HMGB3P30	X:111933142-111933748	NOTEST	0	0	0	0	1	1
ENSG00000213653	ENSG00000213653	RPL22P22	X:81761882-81762261	NOTEST	0	0	0	0	1	1
ENSG00000213655	ENSG00000213655	CTD-2347I17.1	5:122571772-122572064	NOTEST	0	0	0	0	1	1
ENSG00000213657	ENSG00000213657	RP11-346D6.4	10:54148871-54149248	NOTEST	0	0	0	0	1	1
ENSG00000213659	ENSG00000213659	RSU1P3	10:52750944-54073888	NOTEST	0	0	0	0	1	1
ENSG00000213661	ENSG00000213661	RP11-510I6.2	5:120951941-120952502	NOTEST	0	0	0	0	1	1
ENSG00000213663	ENSG00000213663	CTD-2158P22.1	5:118788137-118972894	NOTEST	0	0	0	0	1	1
ENSG00000213664	ENSG00000213664	RPS16P8	17:25607507-25607938	NOTEST	0	0	0	0	1	1
ENSG00000213667	ENSG00000213667	PGGT1BP1	10:52486706-52487729	NOTEST	0	0	0	0	1	1
ENSG00000213669	ENSG00000213669	RP11-476B13.2	9:95439224-95439689	NOTEST	0	0	0	0	1	1
ENSG00000213671	ENSG00000213671	OLA1P2	17:20678954-20680218	NOTEST	0	0	0	0	1	1
ENSG00000213673	ENSG00000213673	SLC25A5P3	7:54487136-54488021	NOTEST	0.0380488	0	#NAME?	0	1	1

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ENSG00000213686	ENSG00000213686	DUSP8P1	10:48952490-48981273	NOTEST	0	0	0	0	1	1
ENSG00000213690	ENSG00000213690	RP11-513D4.1	1:242246287-242687998	NOTEST	0	0	0	0	1	1
ENSG00000213693	ENSG00000213693	SEC14L1P1	11:43902360-43942494	NOTEST	0.598218	0.419273	-0.512781	0	1	1
ENSG00000213694	ENSG00000213694	S1PR3	9:91605777-91619925	NOTEST	0.0132878	0.0163715	0.301082	0	1	1
ENSG00000213695	ENSG00000213695	RPS7P14	X:73629352-73629935	NOTEST	0	0	0	0	1	1
ENSG00000213697	ENSG00000213697	CTBP2P6	11:43543585-43544814	NOTEST	0	0	0	0	1	1
ENSG00000213698	ENSG00000213698	RP1-172N19.4	X:71947801-71948646	NOTEST	0	0	0	0	1	1
ENSG00000213700	ENSG00000213700	RPL17P50	10:74765590-74766353	NOTEST	0.299774	0.437709	0.5461	0	1	1
ENSG00000213701	ENSG00000213701	SETP22	5:96392105-96393062	NOTEST	0.034512	0	#NAME?	0	1	1
ENSG00000213703	ENSG00000213703	RP5-849H19.2	1:62920398-63153969	NOTEST	0	0.0280922	inf	0	1	1
ENSG00000213704	ENSG00000213704	EEF1A1P15	X:97644509-97645917	NOTEST	0	0	0	0	1	1
ENSG00000213706	ENSG00000213706	AL590762.7	X:70572267-70572838	NOTEST	0	0	0	0	1	1
ENSG00000213707	ENSG00000213707	HMGB1P10	22:26921457-26992681	NOTEST	0.0702351	0.118454	0.754061	0	1	1
ENSG00000213708	ENSG00000213708	SLC16A14P1	8:107227990-107229446	NOTEST	0	0	0	0	1	1
ENSG00000213711	ENSG00000213711	PHBP7	9:88513817-88514631	NOTEST	0	0	0	0	1	1
ENSG00000213714	ENSG00000213714	FAM209B	20:55108301-55111576	NOTEST	0.394183	0.575839	0.546799	0	1	1
ENSG00000213716	ENSG00000213716	FABP5P5	5:95220801-96143803	NOTEST	0	0	0	0	1	1
ENSG00000213717	ENSG00000213717	AC004692.5	7:43152197-43605600	NOTEST	0	0	0	0	1	1
ENSG00000213721	ENSG00000213721	HMGN2P30	7:42000547-42277469	NOTEST	0	0	0	0	1	1
ENSG00000213724	ENSG00000213724	PRDX2P2	10:35253996-35255187	NOTEST	0	0	0	0	1	1
ENSG00000213726	ENSG00000213726	RPS2P52	19:685520-695460	NOTEST	0	0	0	0	1	1
ENSG00000213727	ENSG00000213727	LA16c-60G3.7	22:16399956-16436527	NOTEST	0	0	0	0	1	1
ENSG00000213729	ENSG00000213729	AC098828.3	2:20355378-20355818	NOTEST	0	0	0	0	1	1
ENSG00000213730	ENSG00000213730	POLD2P1	5:92603134-92604131	NOTEST	0	0	0	0	1	1
ENSG00000213731	ENSG00000213731	RAB5CP1	10:75910959-76469061	NOTEST	0	0	0	0	1	1
ENSG00000213735	ENSG00000213735	ANAPC10P1	1:52608045-52831865	NOTEST	0.0385894	0.0273546	-0.496421	0	1	1
ENSG00000213736	ENSG00000213736	RP11-662I13.1	12:25120060-25120438	NOTEST	0	0	0	0	1	1
ENSG00000213739	ENSG00000213739	AC007679.1	2:206813814-206814869	NOTEST	0	0	0	0	1	1
ENSG00000213740	ENSG00000213740	SERBP1P1	X:68003314-68004909	NOTEST	0.331953	0.4282	0.367304	0	1	1
ENSG00000213744	ENSG00000213744	RPS10P14	7:36893960-37488852	NOTEST	0	0	0	0	1	1
ENSG00000213747	ENSG00000213747	RP13-278H16.2	X:69748789-70128581	NOTEST	0	0	0	0	1	1
ENSG00000213750	ENSG00000213750	KB-1683C8.1	8:98636430-98637307	NOTEST	0	0	0	0	1	1
ENSG00000213752	ENSG00000213752	CTA-268H5.9	22:45671479-45671966	NOTEST	0	0	0	0	1	1
ENSG00000213754	ENSG00000213754	RP11-284B18.3	X:63444075-63615333	NOTEST	0	0.0421585	inf	0	1	1
ENSG00000213755	ENSG00000213755	RP11-342F17.1	5:78668458-78810040	NOTEST	0	0	0	0	1	1
ENSG00000213759	ENSG00000213759	UGT2B11	4:70047377-70082484	NOTEST	0	0	0	0	1	1
ENSG00000213760	ENSG00000213760	ATP6V1G2	6:31496493-31526606	NOTEST	0.47773	0.568713	0.251505	0	1	1
ENSG00000213761	ENSG00000213761	MT1P1	9:98175548-98175731	NOTEST	0	0	0	0	1	1
ENSG00000213763	ENSG00000213763	ACTBP2	5:76986990-77164604	NOTEST	0	0.0464758	inf	0	1	1
ENSG00000213770	ENSG00000213770	FAM210CP	10:27638645-27639219	NOTEST	0	0	0	0	1	1
ENSG00000213771	ENSG00000213771	KRT8P37	10:8555649-8557069	NOTEST	0	0	0	0	1	1
ENSG00000213772	ENSG00000213772	RP11-385J23.1	2:9346893-9563676	NOTEST	0	0.0638549	inf	0	1	1

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ENSG00000213777	ENSG00000213777	CTD-2224J9.8	19:53970988-54015941	NOTEST	0	0	0	0	1	1
ENSG00000213778	ENSG00000213778	HNRNPA1P32	10:30806544-30807790	NOTEST	0	0	0	0	1	1
ENSG00000213779	ENSG00000213779	RP11-452G18.1	11:17095935-17229530	NOTEST	0	0	0	0	1	1
ENSG00000213781	ENSG00000213781	PSMC1P2	7:27501384-27502588	NOTEST	0	0	0	0	1	1
ENSG00000213783	ENSG00000213783	RPL35P4	7:27308975-27309297	NOTEST	0	0	0	0	1	1
ENSG00000213785	ENSG00000213785	RP11-449L13.2	11:15987994-16778428	NOTEST	0	0.0252948	inf	0	1	1
ENSG00000213786	ENSG00000213786	NHP2P2	7:27087787-27088247	NOTEST	0	0	0	0	1	1
ENSG00000213787	ENSG00000213787	RPL7AP38	7:26706680-27034858	NOTEST	0	0	0	0	1	1
ENSG00000213790	ENSG00000213790	OLA1P1	22:42481528-42535938	NOTEST	0.19639	0.270435	0.461562	0	1	1
ENSG00000213791	ENSG00000213791	RP11-941H19.2	8:81177762-81252075	NOTEST	0	0	0	0	1	1
ENSG00000213793	ENSG00000213793	ZNF888	19:53418448-53427328	NOTEST	0	4.87588	inf	0	1	1
ENSG00000213798	ENSG00000213798	AC004129.9	7:25251788-25252584	NOTEST	0	0	0	0	1	1
ENSG00000213801	ENSG00000213801	ZNF816-ZNF321P	19:53430387-53541151	NOTEST	0.171198	0.0223178	-2.93939	0	1	1
ENSG00000213809	ENSG00000213809	KLRK1	12:10516367-10562745	NOTEST	0.110699	0.0167009	-2.72864	0	1	1
ENSG00000213816	ENSG00000213816	CNN2P4	9:43997829-43998733	NOTEST	0	0	0	0	1	1
ENSG00000213820	ENSG00000213820	RPL13P2	20:44728156-44728815	NOTEST	0	0	0	0	1	1
ENSG00000213822	ENSG00000213822	CEACAM18	19:51979837-51994206	NOTEST	0	0	0	0	1	1
ENSG00000213828	ENSG00000213828	AC017028.1	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000213842	ENSG00000213842	SUGT1P2	3:32726636-32815367	NOTEST	0.0361949	0.159095	2.13603	0	1	1
ENSG00000213849	ENSG00000213849	AC104306.1	3:32549446-32549817	NOTEST	0	0	0	0	1	1
ENSG00000213851	ENSG00000213851	RP11-324J13.1	4:43412057-43412954	NOTEST	0	0	0	0	1	1
ENSG00000213854	ENSG00000213854	CNN2P6	3:31223242-31224142	NOTEST	0.0407491	0.0793794	0.961997	0	1	1
ENSG00000213856	ENSG00000213856	VDAC1P2	X:49397102-49397952	NOTEST	0.105669	0.0478803	-1.14205	0	1	1
ENSG00000213857	ENSG00000213857	RP11-12M9.4	22:41470183-41471243	NOTEST	0	0	0	0	1	1
ENSG00000213862	ENSG00000213862	CTD-2270N23.1	15:47476297-48066420	NOTEST	0.111626	0.0354934	-1.65305	0	1	1
ENSG00000213863	ENSG00000213863	XX-C2158C12.2	6:171034284-171037576	NOTEST	0	0	0	0	1	1
ENSG00000213864	ENSG00000213864	EEF1B2P2	5:67455045-67455721	NOTEST	0.0588294	0	#NAME?	0	1	1
ENSG00000213867	ENSG00000213867	RP11-829H16.2	14:31091317-31291908	NOTEST	0	0	0	0	1	1
ENSG00000213871	ENSG00000213871	TAF9BP1	3:25760434-25836025	NOTEST	0	0.0806156	inf	0	1	1
ENSG00000213872	ENSG00000213872	AC092798.2	3:25760434-25836025	NOTEST	0.180047	0.0931463	-0.950801	0	1	1
ENSG00000213873	ENSG00000213873	RP11-678D18.1	8:66289826-66290346	NOTEST	0	0	0	0	1	1
ENSG00000213875	ENSG00000213875	AC005019.2	7:13911480-13912138	NOTEST	0	0	0	0	1	1
ENSG00000213876	ENSG00000213876	RPL7AP64	17:7044248-7044911	NOTEST	0	0	0	0	1	1
ENSG00000213877	ENSG00000213877	CFL1P7	3:25215822-25639423	NOTEST	0	0.114024	inf	0	1	1
ENSG00000213880	ENSG00000213880	RPL7AP7	6:29770971-29771768	NOTEST	0.158177	0.085453	-0.888337	0	1	1
ENSG00000213882	ENSG00000213882	CYB5P4	20:22866307-22866706	NOTEST	0	0	0	0	1	1
ENSG00000213885	ENSG00000213885	RPL13AP7	21:26734134-26734745	NOTEST	0.350775	0.276159	-0.345046	0	1	1
ENSG00000213888	ENSG00000213888	AC005003.1	22:31742874-31744670	NOTEST	0.480411	0.572181	0.252204	0	1	1
ENSG00000213891	ENSG00000213891	RPL3P6	5:60628099-60841997	NOTEST	0	0	0	0	1	1
ENSG00000213892	ENSG00000213892	CEACAM16	19:45041044-45222031	NOTEST	0	0	0	0	1	1
ENSG00000213896	ENSG00000213896	RP11-546M4.1	5:58264864-59843484	NOTEST	0	0	0	0	1	1

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ENSG00000213908	ENSG00000213908	CYP2A7P1	19:41530171-41533625	NOTEST	0	0	0	0	1	1
ENSG00000213911	ENSG00000213911	OR2G1P	6:29191749-29258217	NOTEST	0	0	0	0	1	1
ENSG00000213916	ENSG00000213916	RPL13P	6:28827401-28832407	NOTEST	0	0	0	0	1	1
ENSG00000213917	ENSG00000213917	RPL5P8	2:214149112-215548970	NOTEST	0	0	0	0	1	1
ENSG00000213921	ENSG00000213921	LEUTX	19:40267234-40276775	NOTEST	0	0	0	0	1	1
ENSG00000213922	ENSG00000213922	AC011500.1	19:39926795-39967310	NOTEST	0.150006	0	#NAME?	0	1	1
ENSG00000213924	ENSG00000213924	HNRNPH1P2	X:142760231-142761441	NOTEST	0	0	0	0	1	1
ENSG00000213925	ENSG00000213925	NPM1P33	2:204637353-204638225	NOTEST	0	0	0	0	1	1
ENSG00000213926	ENSG00000213926	MSRB1P1	19:39745555-39745909	NOTEST	0	0	0	0	1	1
ENSG00000213927	ENSG00000213927	CCL27	9:34638129-34681295	NOTEST	0.0569882	0.00911888	-2.64373	0	1	1
ENSG00000213931	ENSG00000213931	HBE1	11:5274419-5667019	NOTEST	0.0452847	0.202093	2.15792	0	1	1
ENSG00000213934	ENSG00000213934	HBG1	11:5269312-5271122	NOTEST	0	0	0	0	1	1
ENSG00000213935	ENSG00000213935	AC092610.12	7:4836685-4923350	NOTEST	0	0	0	0	1	1
ENSG00000213937	ENSG00000213937	CLDN9	16:3062456-3064506	NOTEST	0	0	0	0	1	1
ENSG00000213938	ENSG00000213938	SEPHS1P6	2:200524273-200525452	NOTEST	0.0147343	0.0542535	1.88054	0	1	1
ENSG00000213939	ENSG00000213939	RP11-314A20.1	17:4574678-4608824	NOTEST	0.442536	0.0917687	-2.26972	0	1	1
ENSG00000213940	ENSG00000213940	RP11-94D20.1	5:52502390-52503006	NOTEST	0	0	0	0	1	1
ENSG00000213942	ENSG00000213942	RP1-102E24.1	12:6518802-6519179	NOTEST	0	0	0	0	1	1
ENSG00000213943	ENSG00000213943	KRT18P17	3:12828891-12830170	NOTEST	0	0.0399059	inf	0	1	1
ENSG00000213946	ENSG00000213946	DNAJB1P1	2:192699027-193060435	NOTEST	0	0	0	0	1	1
ENSG00000213950	ENSG00000213950	RPS10P2	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000213953	ENSG00000213953	AC018867.1	2:187350882-187374090	NOTEST	0	0	0	0	1	1
ENSG00000213954	ENSG00000213954	RP11-280O24.1	9:14068930-14069416	NOTEST	0	0	0	0	1	1
ENSG00000213956	ENSG00000213956	RP11-269M20.1	5:49928957-49929436	NOTEST	0	0	0	0	1	1
ENSG00000213958	ENSG00000213958	KRT18P29	2:182818967-182996125	NOTEST	0	0	0	0	1	1
ENSG00000213959	ENSG00000213959	RP5-1100H13.3	20:37230576-37279678	NOTEST	0	0	0	0	1	1
ENSG00000213962	ENSG00000213962	API5P2	2:178487979-178973066	NOTEST	0.0447676	0	#NAME?	0	1	1
ENSG00000213964	ENSG00000213964	CHCHD4P4	3:11178778-11305243	NOTEST	0	0	0	0	1	1
ENSG00000213967	ENSG00000213967	ZNF726	19:24097677-24140732	NOTEST	0.536273	0.434602	-0.303272	0	1	1
ENSG00000213970	ENSG00000213970	RP11-264F23.1	12:4430370-4462338	NOTEST	0.158864	0.353236	1.15284	0	1	1
ENSG00000213972	ENSG00000213972	RP3-522P13.2	6:25272427-25273979	NOTEST	0	0	0	0	1	1
ENSG00000213973	ENSG00000213973	ZNF99	19:22939006-22966909	NOTEST	0	0	0	0	1	1
ENSG00000213976	ENSG00000213976	CTD-2561J22.2	19:21565666-21569979	NOTEST	0.110131	0.0262127	-2.07089	0	1	1
ENSG00000213979	ENSG00000213979	RPL7AP14	20:36073134-36073936	NOTEST	0	0	0	0	1	1
ENSG00000213981	ENSG00000213981	AC007277.3	2:171034654-171551884	NOTEST	0	0	0	0	1	1
ENSG00000213985	ENSG00000213985	AC078899.1	19:20188802-20432114	NOTEST	0.355668	0.569104	0.678159	0	1	1
ENSG00000213987	ENSG00000213987	RP11-399E6.2	1:41708044-41750533	NOTEST	0	0	0	0	1	1
ENSG00000213988	ENSG00000213988	ZNF90	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000213994	ENSG00000213994	RP11-414H17.5	10:6186880-6277495	NOTEST	0	0	0	0	1	1
ENSG00000213996	ENSG00000213996	TM6SF2	19:19366449-19384200	NOTEST	0.0111332	0.12434	3.48136	0	1	1
ENSG00000213997	ENSG00000213997	PGAM1P7	X:46464752-46618490	NOTEST	0	0.0204194	inf	0	1	1

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ENSG00000214003	ENSG00000214003	ATP5F1P3	7:152446163-152446820	NOTEST	0	0	0	0	1	1
ENSG00000214006	ENSG00000214006	AL353671.4	9:32540541-32573160	NOTEST	0	0	0	0	1	1
ENSG00000214009	ENSG00000214009	PCNAP3	X:45918185-45918963	NOTEST	0	0	0	0	1	1
ENSG00000214012	ENSG00000214012	KRT18P38	6:19535174-19840915	NOTEST	0	0	0	0	1	1
ENSG00000214015	ENSG00000214015	RP11-414H17.2	10:6113476-6113881	NOTEST	0	0	0	0	1	1
ENSG00000214018	ENSG00000214018	RRM2P3	X:44007127-44202918	NOTEST	0	0	0	0	1	1
ENSG00000214019	ENSG00000214019	RP6-218J18.2	X:43888577-43890167	NOTEST	0.191095	0.238088	0.317207	0	1	1
ENSG00000214020	ENSG00000214020	FTLP4	9:30935482-30935975	NOTEST	0	0	0	0	1	1
ENSG00000214024	ENSG00000214024	AC012501.1	2:154227125-154227578	NOTEST	0	0	0	0	1	1
ENSG00000214025	ENSG00000214025	ATP5F1P4	2:154015451-154016197	NOTEST	0	0	0	0	1	1
ENSG00000214027	ENSG00000214027	ARPC3P5	6:15935012-15935546	NOTEST	0	0	0	0	1	1
ENSG00000214031	ENSG00000214031	RP11-169L17.3	X:40619356-40620523	NOTEST	0	0	0	0	1	1
ENSG00000214035	ENSG00000214035	AC073310.4	7:144707053-144708086	NOTEST	0	0	0	0	1	1
ENSG00000214039	ENSG00000214039	RP11-474D1.3	12:130509037-130529602	NOTEST	0	0	0	0	1	1
ENSG00000214041	ENSG00000214041	PGAM1P4	3:9022274-9520924	NOTEST	0.0256543	0	#NAME?	0	1	1
ENSG00000214042	ENSG00000214042	IFNA7	9:21201467-21202204	NOTEST	0.175137	0	#NAME?	0	1	1
ENSG00000214043	ENSG00000214043	RP5-944M2.3	12:126927026-126957336	NOTEST	0	0	0	0	1	1
ENSG00000214045	ENSG00000214045	RP6-186E3.1	X:40218435-40219979	NOTEST	0	0	0	0	1	1
ENSG00000214047	ENSG00000214047	RPS11P7	X:39724677-39725142	NOTEST	0	0	0	0	1	1
ENSG00000214049	ENSG00000214049	UCA1	19:15937854-15947130	NOTEST	0	0.17619	inf	0	1	1
ENSG00000214051	ENSG00000214051	ARF4P3	13:101360578-102068843	NOTEST	0	0	0	0	1	1
ENSG00000214062	ENSG00000214062	RPL7P17	4:78003555-78004279	NOTEST	0	0.0189776	inf	0	1	1
ENSG00000214064	ENSG00000214064	RPL6P5	2:146094797-146095625	NOTEST	0	0	0	0	1	1
ENSG00000214067	ENSG00000214067	RP11-549L6.2	10:111967362-112047123	NOTEST	0	0	0	0	1	1
ENSG00000214070	ENSG00000214070	AC011999.1	2:136655524-136656548	NOTEST	0	0.0420071	inf	0	1	1
ENSG00000214071	ENSG00000214071	RP11-31H15.2	X:37095923-37096474	NOTEST	0	0	0	0	1	1
ENSG00000214073	ENSG00000214073	RPL21P17	3:1947334-1947809	NOTEST	0	0	0	0	1	1
ENSG00000214074	ENSG00000214074	RPL23AP39	3:1771753-1772158	NOTEST	0	0	0	0	1	1
ENSG00000214076	ENSG00000214076	CPSF1P1	22:32601101-32669097	NOTEST	0.0200534	0.0230212	0.199115	0	1	1
ENSG00000214077	ENSG00000214077	GNAQP1	2:132181373-132182440	NOTEST	0.0663057	0.0233528	-1.50554	0	1	1
ENSG00000214081	ENSG00000214081	CYP4F30P	2:131437622-131476404	NOTEST	0	0	0	0	1	1
ENSG00000214089	ENSG00000214089	RP11-256K7.1	10:44910096-44910601	NOTEST	0	0	0	0	1	1
ENSG00000214093	ENSG00000214093	RP11-247I13.3	22:31795508-32058418	NOTEST	0.0519204	0.287529	2.46933	0	1	1
ENSG00000214097	ENSG00000214097	SMCO1	3:196233747-196242237	NOTEST	0	0	0	0	1	1
ENSG00000214100	ENSG00000214100	AC079776.2	2:130680434-130704276	NOTEST	0	0	0	0	1	1
ENSG00000214102	ENSG00000214102	WEE2	7:141404137-141488440	NOTEST	0	0.0263434	inf	0	1	1
ENSG00000214105	ENSG00000214105	CTD-2116F7.1	17:77681074-77686081	NOTEST	0	0.00518355	inf	0	1	1
ENSG00000214107	ENSG00000214107	MAGEB1	X:30260056-30270155	NOTEST	0.0736872	0.165615	1.16835	0	1	1
ENSG00000214108	ENSG00000214108	TPT1P5	5:31639516-32122047	NOTEST	0	0.0301228	inf	0	1	1
ENSG00000214109	ENSG00000214109	AC008686.1	19:13890883-13900972	NOTEST	0	0	0	0	1	1
ENSG00000214111	ENSG00000214111	RP1-258N20.3	X:25047661-25048352	NOTEST	0.0525627	0.0631439	0.264605	0	1	1
ENSG00000214121	ENSG00000214121	TDPX2	9:12972841-12973437	NOTEST	0.099587	0.0544274	-0.871624	0	1	1
ENSG00000214124	ENSG00000214124	SNRPEP9	X:24483337-24557954	NOTEST	0	0	0	0	1	1

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ENSG00000214128	ENSG00000214128	TMEM213	7:138391039-138666064	NOTEST	0	0	0	0	1	1
ENSG00000214132	ENSG00000214132	RP11-420O16.2	5:19473059-20575982	NOTEST	0	0	0	0	1	1
ENSG00000214141	ENSG00000214141	ACTN4P2	1:38242341-38245090	NOTEST	0	0	0	0	1	1
ENSG00000214142	ENSG00000214142	RPL7P60	7:99728586-99738305	NOTEST	0	0	0	0	1	1
ENSG00000214144	ENSG00000214144	RP11-488L18.1	1:247353152-247405125	NOTEST	0	0	0	0	1	1
ENSG00000214145	ENSG00000214145	LINC00887	3:194014253-194030592	NOTEST	0	0.0132125	inf	0	1	1
ENSG00000214146	ENSG00000214146	RP11-699L21.1	3:193675160-193788759	NOTEST	0.22883	0.399558	0.80413	0	1	1
ENSG00000214147	ENSG00000214147	RP11-332P22.2	3:190548753-190549962	NOTEST	0	0	0	0	1	1
ENSG00000214161	ENSG00000214161	SDC4P	22:30877297-30877898	NOTEST	0	0	0	0	1	1
ENSG00000214164	ENSG00000214164	AC018696.5	2:91723048-91723916	NOTEST	0	0	0	0	1	1
ENSG00000214167	ENSG00000214167	AC005544.1	17:64961025-65029514	NOTEST	0	0	0	0	1	1
ENSG00000214178	ENSG00000214178	PPIAP23	13:91924334-91924831	NOTEST	0	0	0	0	1	1
ENSG00000214179	ENSG00000214179	AC112200.1	5:10541567-10541807	NOTEST	0	0	0	0	1	1
ENSG00000214181	ENSG00000214181	DDX6P2	13:86927754-86929524	NOTEST	0	0	0	0	1	1
ENSG00000214184	ENSG00000214184	AC012487.2	2:109065016-109150652	NOTEST	0.287233	0.171325	-0.745483	0	1	1
ENSG00000214185	ENSG00000214185	XPOTP1	20:32782374-32899608	NOTEST	0.0454094	0.0342792	-0.405659	0	1	1
ENSG00000214188	ENSG00000214188	ST7-OT4	7:116592499-116870157	NOTEST	0.354148	0.260111	-0.445225	0	1	1
ENSG00000214189	ENSG00000214189	ZNF788	19:12203077-12267546	NOTEST	5.69E-05	0.130432	11.1628	0	1	1
ENSG00000214190	ENSG00000214190	RP11-12D24.7	9:5357972-5437878	NOTEST	0	0.0242914	inf	0	1	1
ENSG00000214195	ENSG00000214195	HMGN2P31	9:5311443-5311716	NOTEST	0	0	0	0	1	1
ENSG00000214198	ENSG00000214198	RP11-642P15.1	12:104235228-104359486	NOTEST	0.418091	0.232495	-0.846613	0	1	1
ENSG00000214199	ENSG00000214199	EEF1A1P12	2:107313786-107315132	NOTEST	0.386032	0.572297	0.568045	0	1	1
ENSG00000214200	ENSG00000214200	TPM3P2	20:32500128-32501142	NOTEST	0	0	0	0	1	1
ENSG00000214203	ENSG00000214203	RPS4XP1	12:100402829-100403616	NOTEST	0.024113	0.11641	2.27133	0	1	1
ENSG00000214204	ENSG00000214204	HNRNPA1P43	1:116399530-116400440	NOTEST	0	0.0141721	inf	0	1	1
ENSG00000214207	ENSG00000214207	KRT18P10	Y:4868266-5610265	NOTEST	0	0	0	0	1	1
ENSG00000214210	ENSG00000214210	RP11-208P4.1	3:163719393-163720253	NOTEST	0	0	0	0	1	1
ENSG00000214211	ENSG00000214211	CTAGE14P	2:168570172-168572575	NOTEST	0	0	0	0	1	1
ENSG00000214212	ENSG00000214212	C19orf38	19:10947250-10980466	NOTEST	0.0654977	0.0198751	-1.72048	0	1	1
ENSG00000214215	ENSG00000214215	C12orf74	12:93096618-93102325	NOTEST	0	0	0	0	1	1
ENSG00000214216	ENSG00000214216	IQCJ	3:158680023-159615155	NOTEST	0.0380507	0	#NAME?	0	1	1
ENSG00000214222	ENSG00000214222	TUBBP2	13:41958908-41959319	NOTEST	0	0	0	0	1	1
ENSG00000214226	ENSG00000214226	C17orf67	17:54869273-54946036	NOTEST	0.353883	0.372641	0.0745118	0	1	1
ENSG00000214237	ENSG00000214237	FAM188B2	3:150570270-150798513	NOTEST	0	0	0	0	1	1
ENSG00000214239	ENSG00000214239	AL591025.1	6:158957467-159056460	NOTEST	0	0	0	0	1	1
ENSG00000214243	ENSG00000214243	AC004980.10	7:76139744-77045717	NOTEST	0.169902	0.103386	-0.716668	0	1	1
ENSG00000214244	ENSG00000214244	SETP21	5:58264864-59843484	NOTEST	0	0.0454213	inf	0	1	1
ENSG00000214245	ENSG00000214245	HDHD1P3	20:31635322-31635958	NOTEST	0	0	0	0	1	1
ENSG00000214248	ENSG00000214248	AC010336.1	19:7953389-7968427	NOTEST	0.0308083	0.0309861	0.00830114	0	1	1
ENSG00000214249	ENSG00000214249	CTAGE11P	13:75812079-75814432	NOTEST	0	0	0	0	1	1
ENSG00000214252	ENSG00000214252	AZGP1P2	7:100930762-100933052	NOTEST	0	0	0	0	1	1
ENSG00000214254	ENSG00000214254	AC136896.2	15:27216428-27787137	NOTEST	0	0	0	0	1	1
ENSG00000214255	ENSG00000214255	RPS2P6	18:68096395-68098361	NOTEST	0	0	0	0	1	1

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ENSG00000214259	ENSG00000214259	RP11-568J23.1	16:85849478-85850142	NOTEST	0	0	0	0	1	1
ENSG00000214262	ENSG00000214262	ANKRD36BP1	1:168195175-168222263	NOTEST	0	0.0178825	inf	0	1	1
ENSG00000214263	ENSG00000214263	RPSAP53	13:67840976-67841838	NOTEST	0.0214953	0.0518749	1.27102	0	1	1
ENSG00000214264	ENSG00000214264	RP11-356J5.5	11:111895537-112095422	NOTEST	0.0570495	0.0549819	-0.0532573	0	1	1
ENSG00000214265	ENSG00000214265	SNURF	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000214266	ENSG00000214266	STARP1	13:65883986-65885085	NOTEST	0	0	0	0	1	1
ENSG00000214268	ENSG00000214268	RPS3AP33	8:7048422-7049085	NOTEST	0	0	0	0	1	1
ENSG00000214269	ENSG00000214269	LGMNP1	13:65532228-65533528	NOTEST	0.013155	0	#NAME?	0	1	1
ENSG00000214273	ENSG00000214273	AGGF1P1	4:190962496-190964569	NOTEST	0.133164	0.0651411	-1.03156	0	1	1
ENSG00000214278	ENSG00000214278	CTD-2228K2.2	5:271735-438406	NOTEST	0.0230286	0.017921	-0.36178	0	1	1
ENSG00000214280	ENSG00000214280	RP11-553K23.2	3:139108656-139396859	NOTEST	0	0.0233557	inf	0	1	1
ENSG00000214281	ENSG00000214281	HMGN2P39	13:59584465-59584738	NOTEST	0	0	0	0	1	1
ENSG00000214282	ENSG00000214282	KRT8P14	X:45491536-45492978	NOTEST	0	0.00821922	inf	0	1	1
ENSG00000214283	ENSG00000214283	RP11-85F14.1	3:136581049-136729927	NOTEST	0	0	0	0	1	1
ENSG00000214285	ENSG00000214285	NPS	10:129347612-129350935	NOTEST	0	0	0	0	1	1
ENSG00000214286	ENSG00000214286	PDCL3P3	3:17198653-18959184	NOTEST	0	0	0	0	1	1
ENSG00000214288	ENSG00000214288	HMGB3P13	3:134156446-134157053	NOTEST	0	0	0	0	1	1
ENSG00000214289	ENSG00000214289	RPL39P5	3:134070693-134094321	NOTEST	0.0691515	0	#NAME?	0	1	1
ENSG00000214290	ENSG00000214290	COLCA2	11:111164113-111179460	NOTEST	0.0119485	0.037887	1.66487	0	1	1
ENSG00000214295	ENSG00000214295	FOXO1B	5:180526139-180527666	NOTEST	0	0	0	0	1	1
ENSG00000214297	ENSG00000214297	ALDOAP2	10:127262939-127371713	NOTEST	0	0.0127601	inf	0	1	1
ENSG00000214298	ENSG00000214298	MRPS21P6	10:126855245-126855506	NOTEST	0	0	0	0	1	1
ENSG00000214301	ENSG00000214301	RP11-91K8.4	3:133209667-133210349	NOTEST	0	0	0	0	1	1
ENSG00000214305	ENSG00000214305	AP001024.1	11:107650218-107652316	NOTEST	0	0	0	0	1	1
ENSG00000214306	ENSG00000214306	AP001024.2	11:107643128-107647344	NOTEST	0	0	0	0	1	1
ENSG00000214313	ENSG00000214313	AZGP1P1	7:99578384-99585158	NOTEST	0	0	0	0	1	1
ENSG00000214314	ENSG00000214314	AC073063.1	7:98923520-99063954	NOTEST	0	0	0	0	1	1
ENSG00000214318	ENSG00000214318	ATP5G1P6	18:61143993-61172318	NOTEST	0	0	0	0	1	1
ENSG00000214319	ENSG00000214319	CXADRP1	21:15048342-15049437	NOTEST	0.0292931	0.0478865	0.709057	0	1	1
ENSG00000214321	ENSG00000214321	CBX1P4	X:17300759-17301216	NOTEST	0	0	0	0	1	1
ENSG00000214322	ENSG00000214322	CBX1P2	X:16964813-17171395	NOTEST	0	0	0	0	1	1
ENSG00000214324	ENSG00000214324	C3orf56	3:126911973-126917025	NOTEST	0	0	0	0	1	1
ENSG00000214325	ENSG00000214325	AC025287.1	16:75661621-75795770	NOTEST	0	0	0	0	1	1
ENSG00000214326	ENSG00000214326	RPL31P1	21:44949071-45079374	NOTEST	0	0	0	0	1	1
ENSG00000214329	ENSG00000214329	SLC9B1P2	2:92071101-92119740	NOTEST	0	0	0	0	1	1
ENSG00000214330	ENSG00000214330	ABCD1P5	2:92028626-92031828	NOTEST	0	0	0	0	1	1
ENSG00000214335	ENSG00000214335	CTAGE16P	13:59102748-59105160	NOTEST	0.00662693	0	#NAME?	0	1	1
ENSG00000214336	ENSG00000214336	FOXI3	2:88747725-88752131	NOTEST	0	0	0	0	1	1
ENSG00000214342	ENSG00000214342	ATP5F1P2	7:94367963-94368723	NOTEST	0	0	0	0	1	1
ENSG00000214344	ENSG00000214344	OR4F13P	15:102382321-102390527	NOTEST	0.00788696	0	#NAME?	0	1	1
ENSG00000214347	ENSG00000214347	CTB-180A7.8	19:6379579-6412415	NOTEST	0	0	0	0	1	1
ENSG00000214351	ENSG00000214351	OR1X5P	5:177236407-177410055	NOTEST	0	0	0	0	1	1
ENSG00000214353	ENSG00000214353	VAC14-AS1	16:70721341-70835064	NOTEST	0.0996288	0.0878652	-0.18127	0	1	1
ENSG00000214354	ENSG00000214354	AC133644.3	2:87754886-87906324	NOTEST	0	0	0	0	1	1

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ENSG00000214359	ENSG00000214359	RPL18P10	13:50601268-51423190	NOTEST	0	0.118545	inf	0	1	1
ENSG00000214360	ENSG00000214360	EFCAB9	5:171621175-171630456	NOTEST	0	0.0197705	inf	0	1	1
ENSG00000214362	ENSG00000214362	RP11-7D5.2	10:97354354-97355129	NOTEST	0	0.0191321	inf	0	1	1
ENSG00000214366	ENSG00000214366	RP11-138H14.1	8:13947372-15095848	NOTEST	0	0	0	0	1	1
ENSG00000214369	ENSG00000214369	AC009967.3	2:170646602-170647395	NOTEST	0	0	0	0	1	1
ENSG00000214374	ENSG00000214374	RPLP2P1	6:27932952-27933292	NOTEST	0	0	0	0	1	1
ENSG00000214376	ENSG00000214376	VSTM5	11:93551397-93583697	NOTEST	0	0.0486158	inf	0	1	1
ENSG00000214380	ENSG00000214380	RP11-457K10.2	3:109634822-109635787	NOTEST	0	0	0	0	1	1
ENSG00000214381	ENSG00000214381	LINC00488	3:108897011-108904104	NOTEST	0.0595965	0.135179	1.18157	0	1	1
ENSG00000214397	ENSG00000214397	DKFZP779J2370	15:100017369-100273766	NOTEST	0.185616	0.090922	-1.02962	0	1	1
ENSG00000214402	ENSG00000214402	LCNL1	9:139871955-139880862	NOTEST	0.00968799	0.00739719	-0.389219	0	1	1
ENSG00000214405	ENSG00000214405	RP11-40M23.1	3:103781882-103782426	NOTEST	0	0	0	0	1	1
ENSG00000214414	ENSG00000214414	TRIM77	11:89443466-89451040	NOTEST	0	0	0	0	1	1
ENSG00000214415	ENSG00000214415	GNAT3	7:79959507-80308593	NOTEST	0.0150326	0	#NAME?	0	1	1
ENSG00000214417	ENSG00000214417	KRT18P13	9:100461203-100463016	NOTEST	0	0	0	0	1	1
ENSG00000214424	ENSG00000214424	FAM149B1P1	15:97300216-97301826	NOTEST	0.0187256	0.0393977	1.0731	0	1	1
ENSG00000214425	ENSG00000214425	LRRC37A4P	17:43578684-43640596	NOTEST	0	0	0	0	1	1
ENSG00000214428	ENSG00000214428	NPM1P10	6:104473414-104474638	NOTEST	0	0	0	0	1	1
ENSG00000214429	ENSG00000214429	CYCSP6	2:78639918-78640220	NOTEST	0	0	0	0	1	1
ENSG00000214432	ENSG00000214432	AC068831.10	15:91565848-91579841	NOTEST	0.196072	0.197183	0.00815224	0	1	1
ENSG00000214433	ENSG00000214433	AC091167.3	15:90835193-90838915	NOTEST	0	0	0	0	1	1
ENSG00000214434	ENSG00000214434	NIFKP1	10:30669102-30669991	NOTEST	0	0	0	0	1	1
ENSG00000214439	ENSG00000214439	FAM185BP	7:76139744-77045717	NOTEST	0.213643	0.317138	0.569912	0	1	1
ENSG00000214447	ENSG00000214447	FAM187A	17:42923720-42994305	NOTEST	0.423732	0.518579	0.291411	0	1	1
ENSG00000214456	ENSG00000214456	PLIN5	19:4522542-4540486	NOTEST	0.19495	0.270218	0.471023	0	1	1
ENSG00000214457	ENSG00000214457	RPL7P29	6:87647023-87726349	NOTEST	0	0	0	0	1	1
ENSG00000214460	ENSG00000214460	TPT1P6	6:86137170-86137684	NOTEST	0	0	0	0	1	1
ENSG00000214465	ENSG00000214465	SMARCE1P6	2:26372072-26373600	NOTEST	0.0142125	0	#NAME?	0	1	1
ENSG00000214479	ENSG00000214479	AL139333.1	6:83777384-83908651	NOTEST	0	0	0	0	1	1
ENSG00000214484	ENSG00000214484	AC074008.1	2:73597146-73598020	NOTEST	0	0	0	0	1	1
ENSG00000214487	ENSG00000214487	OR7E148P	12:8580235-8581206	NOTEST	0	0	0	0	1	1
ENSG00000214491	ENSG00000214491	SEC14L6	22:30918785-30942669	NOTEST	0	0	0	0	1	1
ENSG00000214510	ENSG00000214510	SPINK13	5:147647742-147763346	NOTEST	0	0.0342403	inf	0	1	1
ENSG00000214511	ENSG00000214511	HIGD1C	12:51347704-51364289	NOTEST	0	0	0	0	1	1
ENSG00000214513	ENSG00000214513	NOTO	2:73429385-73439641	NOTEST	0.0161761	0.00447538	-1.85378	0	1	1
ENSG00000214514	ENSG00000214514	KRT42P	17:39775688-39943183	NOTEST	0	0	0	0	1	1
ENSG00000214518	ENSG00000214518	KRTAP2-2	17:39210749-39211482	NOTEST	0.0264306	0	#NAME?	0	1	1
ENSG00000214525	ENSG00000214525	AC130709.1	2:68694692-68858004	NOTEST	0.0259643	0.020086	-0.370338	0	1	1
ENSG00000214526	ENSG00000214526	AP000343.1	22:23664729-23665114	NOTEST	0	0	0	0	1	1
ENSG00000214533	ENSG00000214533	KRT18P33	2:65663844-66311773	NOTEST	0.0170328	0	#NAME?	0	1	1
ENSG00000214534	ENSG00000214534	ZNF705E	11:71498555-71532594	NOTEST	0.0354417	0.00995891	-1.83139	0	1	1
ENSG00000214535	ENSG00000214535	RPS15AP1	20:21106623-21227260	NOTEST	0.134785	0.144512	0.100533	0	1	1
ENSG00000214541	ENSG00000214541	RPS4XP3	20:55176756-55177169	NOTEST	0	0	0	0	1	1
ENSG00000214544	ENSG00000214544	GTF2IRD2P1	7:72656901-72694143	NOTEST	0.0796642	0.0486617	-0.711146	0	1	1

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ENSG00000214546	ENSG00000214546	AC087491.2	17:37775865-37778766	NOTEST	0	0.0259873	inf	0	1	1
ENSG00000214548	ENSG00000214548	MEG3	14:101245746-101327368	NOTEST	0.0062073	0	#NAME?	0	1	1
ENSG00000214549	ENSG00000214549	SDHCP2	10:93806448-94050844	NOTEST	0	0	0	0	1	1
ENSG00000214552	ENSG00000214552	COPS8P2	3:68053358-68594776	NOTEST	0	0.177819	inf	0	1	1
ENSG00000214553	ENSG00000214553	LRRC37A11P	17:37183529-37209458	NOTEST	0	0.00955519	inf	0	1	1
ENSG00000214556	ENSG00000214556	C17orf98	17:36991340-36997708	NOTEST	0	0	0	0	1	1
ENSG00000214558	ENSG00000214558	RP11-74E24.2	6:64345724-66417118	NOTEST	0.470216	0.603221	0.359364	0	1	1
ENSG00000214559	ENSG00000214559	RP11-323J4.1	4:99172838-99365012	NOTEST	0	0	0	0	1	1
ENSG00000214560	ENSG00000214560	RPL21P41	3:66687572-66687836	NOTEST	0	0	0	0	1	1
ENSG00000214561	ENSG00000214561	RBBP4P4	6:58446018-58447307	NOTEST	0	0	0	0	1	1
ENSG00000214562	ENSG00000214562	NUTM2D	10:89102492-89130452	NOTEST	0.117415	0.216913	0.885504	0	1	1
ENSG00000214563	ENSG00000214563	GAPDHP15	6:58291907-58298496	NOTEST	0.119658	0	#NAME?	0	1	1
ENSG00000214566	ENSG00000214566	GAPDHP41	6:57686968-57687949	NOTEST	0.0669496	0	#NAME?	0	1	1
ENSG00000214578	ENSG00000214578	HMGN2P15	17:40904897-40905817	NOTEST	0.30614	0.338354	0.144341	0	1	1
ENSG00000214581	ENSG00000214581	RP11-80F22.10	16:34681268-34683395	NOTEST	0	0	0	0	1	1
ENSG00000214584	ENSG00000214584	PGGT1BP2	10:81651903-81652931	NOTEST	0	0	0	0	1	1
ENSG00000214593	ENSG00000214593	RP11-65N13.6	9:128024072-128129486	NOTEST	0	0	0	0	1	1
ENSG00000214597	ENSG00000214597	TMEM249	8:145575877-145584932	NOTEST	0.00933811	0.00694125	-0.427935	0	1	1
ENSG00000214602	ENSG00000214602	CTBP2P5	2:49142405-49143669	NOTEST	0	0	0	0	1	1
ENSG00000214604	ENSG00000214604	NPM1P36	6:55804587-55805422	NOTEST	0	0	0	0	1	1
ENSG00000214607	ENSG00000214607	ADAM24P	8:17327026-17329127	NOTEST	0	0	0	0	1	1
ENSG00000214612	ENSG00000214612	RPS19P1	20:18485276-18485710	NOTEST	0	0	0	0	1	1
ENSG00000214614	ENSG00000214614	RP11-989E6.3	16:32888789-32900195	NOTEST	0.0356519	0.00690889	-2.36745	0	1	1
ENSG00000214617	ENSG00000214617	SLC6A10P	16:32888789-32900195	NOTEST	0.0146103	0.0228118	0.6428	0	1	1
ENSG00000214626	ENSG00000214626	POLR3DP1	10:75910959-76469061	NOTEST	0	0.0114888	inf	0	1	1
ENSG00000214628	ENSG00000214628	RP11-392M9.2	X:95939661-96897588	NOTEST	0	0	0	0	1	1
ENSG00000214629	ENSG00000214629	RPSAP6	10:75910959-76469061	NOTEST	0	0	0	0	1	1
ENSG00000214641	ENSG00000214641	RP11-793K1.1	6:51401952-51402341	NOTEST	0	0	0	0	1	1
ENSG00000214642	ENSG00000214642	DEFB113	6:49936389-49937338	NOTEST	0	0	0	0	1	1
ENSG00000214643	ENSG00000214643	DEFB133	6:49913813-49917157	NOTEST	0	0	0	0	1	1
ENSG00000214645	ENSG00000214645	AL162389.1	9:110539470-110540419	NOTEST	0	0	0	0	1	1
ENSG00000214646	ENSG00000214646	RP11-114H24.4	15:78232252-78236924	NOTEST	0.0344663	0	#NAME?	0	1	1
ENSG00000214650	ENSG00000214650	RP11-83B20.1	12:124808960-125052135	NOTEST	0.0644317	0.0520394	-0.308167	0	1	1
ENSG00000214651	ENSG00000214651	RP11-477J21.2	9:123940414-124095121	NOTEST	0	0	0	0	1	1
ENSG00000214652	ENSG00000214652	RP11-3N2.13	7:63505820-63545179	NOTEST	0.0739223	0	#NAME?	0	1	1
ENSG00000214653	ENSG00000214653	HNRNPA3P3	X:139114502-139115665	NOTEST	0	0.0108263	inf	0	1	1
ENSG00000214657	ENSG00000214657	RP11-120J4.1	2:16010062-16010367	NOTEST	0	0	0	0	1	1
ENSG00000214659	ENSG00000214659	KRT8P26	11:65494409-65495685	NOTEST	0.0244447	0	#NAME?	0	1	1
ENSG00000214660	ENSG00000214660	SLC29A4P2	7:63016975-63022966	NOTEST	0	0	0	0	1	1
ENSG00000214668	ENSG00000214668	SLC29A4P1	7:57081991-57087980	NOTEST	0	0	0	0	1	1
ENSG00000214669	ENSG00000214669	RP11-18B16.1	9:116521273-116521699	NOTEST	0	0	0	0	1	1
ENSG00000214670	ENSG00000214670	AC007956.1	14:75120139-75179818	NOTEST	0.353384	0.283005	-0.320408	0	1	1
ENSG00000214671	ENSG00000214671	RPL6P12	4:170015406-170192256	NOTEST	0	0	0	0	1	1
ENSG00000214676	ENSG00000214676	RPL9P16	4:169277885-169931426	NOTEST	0	0	0	0	1	1

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ENSG00000214681	ENSG00000214681	IQCF5	3:51907611-51909783	NOTEST	0	0	0	0	1	1
ENSG00000214684	ENSG00000214684	AC003045.1	7:117080035-117080834	NOTEST	0.0274061	0	#NAME?	0	1	1
ENSG00000214686	ENSG00000214686	IQCF6	3:51812579-51813009	NOTEST	0	0	0	0	1	1
ENSG00000214688	ENSG00000214688	C10orf105	10:73156690-73575702	NOTEST	0	0	0	0	1	1
ENSG00000214691	ENSG00000214691	AC104654.1	2:42104213-42121179	NOTEST	0	0	0	0	1	1
ENSG00000214694	ENSG00000214694	ARHGEF33	2:39103102-39202590	NOTEST	0.222491	0.0555683	-2.00141	0	1	1
ENSG00000214695	ENSG00000214695	NPAP1P2	10:81620328-81621562	NOTEST	0	0	0	0	1	1
ENSG00000214700	ENSG00000214700	C12orf71	12:27233990-27235447	NOTEST	0.034512	0	#NAME?	0	1	1
ENSG00000214702	ENSG00000214702	RP11-247C2.1	15:74387925-74390758	NOTEST	0	0	0	0	1	1
ENSG00000214708	ENSG00000214708	AC090616.2	17:30468244-30580393	NOTEST	0.0684494	0.0245945	-1.4767	0	1	1
ENSG00000214711	ENSG00000214711	CAPN14	2:31395923-31456724	NOTEST	0.111801	0.101675	-0.136965	0	1	1
ENSG00000214720	ENSG00000214720	KRT18P49	X:106671859-106672691	NOTEST	0	0	0	0	1	1
ENSG00000214725	ENSG00000214725	CDIPT-AS1	16:29869677-29879371	NOTEST	0.361675	0.204408	-0.823239	0	1	1
ENSG00000214727	ENSG00000214727	RPL5P35	22:50151274-50152628	NOTEST	0	0	0	0	1	1
ENSG00000214732	ENSG00000214732	RP1-139D8.6	6:42123143-42147794	NOTEST	0	0	0	0	1	1
ENSG00000214733	ENSG00000214733	RP11-429J17.8	8:144871089-144872629	NOTEST	0	0.10864	inf	0	1	1
ENSG00000214743	ENSG00000214743	MRPS5P3	5:126478773-126478939	NOTEST	0	0	0	0	1	1
ENSG00000214745	ENSG00000214745	RP11-541I5.1	X:55934555-56041606	NOTEST	0	0	0	0	1	1
ENSG00000214748	ENSG00000214748	RP11-332E4.1	X:136407130-136407208	NOTEST	0	0	0	0	1	1
ENSG00000214754	ENSG00000214754	AC004870.5	7:46930222-47118726	NOTEST	0	0	0	0	1	1
ENSG00000214759	ENSG00000214759	CTD-2509G16.1	14:65703197-65785508	NOTEST	0	0	0	0	1	1
ENSG00000214760	ENSG00000214760	RPL21P1	12:122755978-122907179	NOTEST	0	0	0	0	1	1
ENSG00000214761	ENSG00000214761	HNRNPA1P15	9:128199671-128469513	NOTEST	0	0	0	0	1	1
ENSG00000214770	ENSG00000214770	RP11-544I20.2	14:64319682-64805317	NOTEST	0.23584	0.152971	-0.624555	0	1	1
ENSG00000214772	ENSG00000214772	RP11-174G6.1	12:14656594-14910897	NOTEST	0	0	0	0	1	1
ENSG00000214773	ENSG00000214773	RP11-717D12.1	3:47626761-47823596	NOTEST	0.0214617	0	#NAME?	0	1	1
ENSG00000214782	ENSG00000214782	MS4A18	11:60496788-60511685	NOTEST	0	0	0	0	1	1
ENSG00000214787	ENSG00000214787	MS4A4E	11:59968725-60010561	NOTEST	0.235384	0.0521629	-2.17392	0	1	1
ENSG00000214788	ENSG00000214788	OOSP1	11:59705927-59712807	NOTEST	0	0	0	0	1	1
ENSG00000214794	ENSG00000214794	KRT18P42	5:108924038-108925293	NOTEST	0	0	0	0	1	1
ENSG00000214797	ENSG00000214797	RP11-1036E20.9	11:59036348-59051506	NOTEST	0	0	0	0	1	1
ENSG00000214803	ENSG00000214803	RP11-37N22.1	8:125204911-125259639	NOTEST	0.0145041	0	#NAME?	0	1	1
ENSG00000214807	ENSG00000214807	NPM1P31	10:126556078-126556895	NOTEST	0	0	0	0	1	1
ENSG00000214810	ENSG00000214810	CYCSP55	6:34187215-34187843	NOTEST	0	0	0	0	1	1
ENSG00000214812	ENSG00000214812	RP5-1053E7.3	1:28446959-28447832	NOTEST	0	0	0	0	1	1
ENSG00000214814	ENSG00000214814	FER1L6	8:124864226-125183763	NOTEST	0.0219569	0.0174957	-0.327678	0	1	1
ENSG00000214815	ENSG00000214815	AC008265.2	7:138125434-138126983	NOTEST	0	0	0	0	1	1
ENSG00000214819	ENSG00000214819	CDRT15L2	17:20483036-20484224	NOTEST	0	0	0	0	1	1
ENSG00000214820	ENSG00000214820	MPRIPP1	3:44596684-44727145	NOTEST	0.13987	0.19097	0.449255	0	1	1
ENSG00000214821	ENSG00000214821	HMGB1P4	2:171034654-171551884	NOTEST	0	0	0	0	1	1
ENSG00000214822	ENSG00000214822	KRT16P3	17:20404825-20415670	NOTEST	0	0	0	0	1	1
ENSG00000214823	ENSG00000214823	NXT1P1	13:39743772-39744088	NOTEST	0.101313	0	#NAME?	0	1	1
ENSG00000214825	ENSG00000214825	EI24P3	3:44566235-44567297	NOTEST	0	0	0	0	1	1
ENSG00000214835	ENSG00000214835	RPL23AP6	20:9966735-10349424	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000214841	ENSG00000214841	AC005493.1	7:34386123-34917944	NOTEST	0	0	0	0	1	1
ENSG00000214842	ENSG00000214842	RAD51AP2	2:17691850-17699706	NOTEST	0	0	0	0	1	1
ENSG00000214843	ENSG00000214843	ZFYVE9P2	2:17465558-17466162	NOTEST	0	0	0	0	1	1
ENSG00000214844	ENSG00000214844	AC007952.1	17:19030781-19062489	NOTEST	0	0	0	0	1	1
ENSG00000214846	ENSG00000214846	RP11-115L11.1	4:15606161-15739936	NOTEST	0	0.0233557	inf	0	1	1
ENSG00000214851	ENSG00000214851	LINC00612	12:9208181-9217666	NOTEST	0.0145456	0.0113017	-0.364047	0	1	1
ENSG00000214853	ENSG00000214853	RP11-509M23.1	5:84295737-84296113	NOTEST	0	0	0	0	1	1
ENSG00000214854	ENSG00000214854	AL031590.1	22:39656864-39657063	NOTEST	0	0	0	0	1	1
ENSG00000214855	ENSG00000214855	APOC1P1	19:45430060-45434643	NOTEST	0	0	0	0	1	1
ENSG00000214856	ENSG00000214856	KRT16P1	17:18335364-18346209	NOTEST	0	0	0	0	1	1
ENSG00000214857	ENSG00000214857	SHFM1P1	5:81188308-81188540	NOTEST	0	0	0	0	1	1
ENSG00000214860	ENSG00000214860	EVPLL	17:18280975-18292961	NOTEST	0	0	0	0	1	1
ENSG00000214866	ENSG00000214866	DCDC2C	2:3705784-3836122	NOTEST	0	0	0	0	1	1
ENSG00000214867	ENSG00000214867	SRSF9P1	21:37667470-37668000	NOTEST	0.0413773	0.0293589	-0.49504	0	1	1
ENSG00000214869	ENSG00000214869	TPM3P4	7:27063355-27064526	NOTEST	0	0	0	0	1	1
ENSG00000214871	ENSG00000214871	AC005082.1	7:23145352-23240630	NOTEST	0	0	0	0	1	1
ENSG00000214872	ENSG00000214872	SMTNL1	11:57308978-57318108	NOTEST	0.0100472	0.00668521	-0.587742	0	1	1
ENSG00000214875	ENSG00000214875	MED28P1	10:70748486-70776738	NOTEST	0	0.0552372	inf	0	1	1
ENSG00000214878	ENSG00000214878	RPL5P31	13:51656983-51746524	NOTEST	0	0	0	0	1	1
ENSG00000214880	ENSG00000214880	OR7E5P	11:55746178-55753881	NOTEST	0	0	0	0	1	1
ENSG00000214881	ENSG00000214881	TMEM14D	10:70304245-70304590	NOTEST	0.247707	0.132766	-0.899746	0	1	1
ENSG00000214883	ENSG00000214883	RP11-574M7.2	11:50368212-50381487	NOTEST	0	0	0	0	1	1
ENSG00000214886	ENSG00000214886	FAM177A1P1	4:99792834-99916145	NOTEST	0	0	0	0	1	1
ENSG00000214888	ENSG00000214888	XXyac-YM21GA2.7	9:90471929-90474314	NOTEST	0	0	0	0	1	1
ENSG00000214889	ENSG00000214889	RPS9P1	21:37502668-37528615	NOTEST	0.394294	0.356956	-0.143528	0	1	1
ENSG00000214890	ENSG00000214890	CTD-2299I21.1	5:78293437-78531861	NOTEST	0	0	0	0	1	1
ENSG00000214891	ENSG00000214891	TRIM64C	11:49075265-49080664	NOTEST	0	0	0	0	1	1
ENSG00000214892	ENSG00000214892	USP8P1	6:31243348-31246531	NOTEST	0	0	0	0	1	1
ENSG00000214894	ENSG00000214894	LINC00243	6:30766430-30798436	NOTEST	0	0.029607	inf	0	1	1
ENSG00000214896	ENSG00000214896	RPSAP55	15:53177791-53178667	NOTEST	0	0	0	0	1	1
ENSG00000214897	ENSG00000214897	U82695.5	X:152662420-152664307	NOTEST	0	0	0	0	1	1
ENSG00000214903	ENSG00000214903	RPS15AP3	14:47308825-48144157	NOTEST	0	0	0	0	1	1
ENSG00000214904	ENSG00000214904	DUTP8	4:98105243-99064391	NOTEST	0	0	0	0	1	1
ENSG00000214908	ENSG00000214908	RP11-229M1.2	9:88989880-88990621	NOTEST	0	0	0	0	1	1
ENSG00000214914	ENSG00000214914	RPL23AP3	21:37388376-37388844	NOTEST	0	0	0	0	1	1
ENSG00000214915	ENSG00000214915	XX-FW80269A6.1	X:150684022-150684717	NOTEST	0	0	0	0	1	1
ENSG00000214917	ENSG00000214917	RP11-53I6.1	18:29598334-30050447	NOTEST	0	0	0	0	1	1
ENSG00000214919	ENSG00000214919	AC104472.1	3:155093368-155462856	NOTEST	0	0.00817432	inf	0	1	1
ENSG00000214921	ENSG00000214921	AC003102.1	17:42325752-42355825	NOTEST	0	0	0	0	1	1
ENSG00000214925	ENSG00000214925	RP3-507I15.1	X:140232662-140233358	NOTEST	0	0	0	0	1	1
ENSG00000214929	ENSG00000214929	SPATA31D1	9:84603686-84610171	NOTEST	0	0	0	0	1	1
ENSG00000214930	ENSG00000214930	KRT8P6	X:137569823-137571030	NOTEST	0	0	0	0	1	1
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ENSG00000214946	ENSG00000214946	TBC1D26	17:15602890-15652629	NOTEST	0	0	0	0	1	1
ENSG00000214955	ENSG00000214955	AP000318.2	21:35445523-35732332	NOTEST	0	0	0	0	1	1
ENSG00000214961	ENSG00000214961	RP11-355K23B.1	X:133406316-133407688	NOTEST	0	0.00961194	inf	0	1	1
ENSG00000214967	ENSG00000214967	NPIPA7	16:16472911-16487811	NOTEST	0	0	0	0	1	1
ENSG00000214970	ENSG00000214970	CTC-297N7.7	17:10286448-10527203	NOTEST	0	0	0	0	1	1
ENSG00000214976	ENSG00000214976	VDAC2P1	21:17442841-17999716	NOTEST	0	0	0	0	1	1
ENSG00000214978	ENSG00000214978	RP11-477N12.3	17:9674750-9725388	NOTEST	0	0	0	0	1	1
ENSG00000214980	ENSG00000214980	RP11-274J2.1	4:84717588-85214565	NOTEST	0	0	0	0	1	1
ENSG00000214985	ENSG00000214985	AL591516.5	6:107473760-107780768	NOTEST	0	0	0	0	1	1
ENSG00000214986	ENSG00000214986	FAM25D	10:51214506-51216406	NOTEST	0	0	0	0	1	1
ENSG00000214988	ENSG00000214988	RPL7AP26	4:83404322-83483510	NOTEST	0	0.0179975	inf	0	1	1
ENSG00000214992	ENSG00000214992	AKAP17BP	X:118383308-118391633	NOTEST	0	0	0	0	1	1
ENSG00000214998	ENSG00000214998	AC006465.4	7:7676148-8133902	NOTEST	0	0	0	0	1	1
ENSG00000214999	ENSG00000214999	AC129492.6	17:7975953-7991021	NOTEST	0	0	0	0	1	1
ENSG00000215000	ENSG00000215000	RP1-31B8.1	X:108585041-108585926	NOTEST	0	0	0	0	1	1
ENSG00000215002	ENSG00000215002	RP11-446H13.2	10:108309863-108310879	NOTEST	0	0	0	0	1	1
ENSG00000215003	ENSG00000215003	RPL15P20	16:16025553-16026151	NOTEST	0	0	0	0	1	1
ENSG00000215004	ENSG00000215004	MESTP4	3:29128886-29130090	NOTEST	0	0	0	0	1	1
ENSG00000215005	ENSG00000215005	HSPD1P7	21:30259601-30261594	NOTEST	0	0	0	0	1	1
ENSG00000215006	ENSG00000215006	CHCHD2P2	5:68629755-68630076	NOTEST	0.196119	0	#NAME?	0	1	1
ENSG00000215007	ENSG00000215007	DNAJA1P3	X:106594879-106596073	NOTEST	0	0	0	0	1	1
ENSG00000215009	ENSG00000215009	ACSM4	12:7456879-7481320	NOTEST	0	0	0	0	1	1
ENSG00000215014	ENSG00000215014	AL645728.1	1:1510354-1511373	NOTEST	0.148407	0.209355	0.49639	0	1	1
ENSG00000215016	ENSG00000215016	RPL24P7	3:23175862-23176315	NOTEST	0.210617	0.0374839	-2.49028	0	1	1
ENSG00000215018	ENSG00000215018	COL28A1	7:7395833-7575484	NOTEST	0.0101455	0.0503818	2.31207	0	1	1
ENSG00000215020	ENSG00000215020	AL591684.1	10:48247668-48279200	NOTEST	0	0	0	0	1	1
ENSG00000215023	ENSG00000215023	AC114730.5	2:242716239-242743623	NOTEST	0	0	0	0	1	1
ENSG00000215024	ENSG00000215024	DUSP8P2	10:48169664-48175810	NOTEST	0	0	0	0	1	1
ENSG00000215029	ENSG00000215029	TCP11X2	X:101615315-101726732	NOTEST	0	0	0	0	1	1
ENSG00000215033	ENSG00000215033	AL603965.1	10:47740329-47770871	NOTEST	0	0	0	0	1	1
ENSG00000215034	ENSG00000215034	DSTNP4	3:39255683-39256163	NOTEST	0	0	0	0	1	1
ENSG00000215035	ENSG00000215035	FDPSP5	X:44335272-44336668	NOTEST	0	0	0	0	1	1
ENSG00000215037	ENSG00000215037	VENTXP2	13:84481435-84481916	NOTEST	0	0	0	0	1	1
ENSG00000215043	ENSG00000215043	GLULP6	2:194994077-194994990	NOTEST	0.0200175	0	#NAME?	0	1	1
ENSG00000215044	ENSG00000215044	AHCYP1	10:47594378-47595651	NOTEST	0	0	0	0	1	1
ENSG00000215045	ENSG00000215045	GRID2IP	7:6537092-6591067	NOTEST	0.00487728	0.00721337	0.564598	0	1	1
ENSG00000215046	ENSG00000215046	TCP11X1	X:101470279-101581634	NOTEST	0	0	0	0	1	1
ENSG00000215048	ENSG00000215048	HLA-DPB1	HSCHR6_MHC_QBL:32961399-32984034	NOTEST	0	0	0	0	1	1
ENSG00000215049	ENSG00000215049	PRDX2P1	13:30776766-30881621	NOTEST	0	0	0	0	1	1
ENSG00000215054	ENSG00000215054	HNRNPCP10	X:143922297-143923181	NOTEST	0	0	0	0	1	1
ENSG00000215057	ENSG00000215057	PKMP5	6:5972644-5974245	NOTEST	0	0	0	0	1	1
ENSG00000215063	ENSG00000215063	RPL21P2	20:4040279-4040760	NOTEST	0.0479096	0	#NAME?	0	1	1
ENSG00000215065	ENSG00000215065	DUSP8P4	10:47253594-47259683	NOTEST	0	0	0	0	1	1

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ENSG00000215070	ENSG00000215070	XRCC6P5	X:98716599-98976156	NOTEST	0	0	0	0	1	1
ENSG00000215077	ENSG00000215077	BRD2	HSCHR6_MHC_QBL:32831135-32878022	NOTEST	0	0	0	0	1	1
ENSG00000215085	ENSG00000215085	RP11-471G13.2	X:94839301-94839941	NOTEST	0	0	0	0	1	1
ENSG00000215086	ENSG00000215086	NPM1P24	10:74653338-74692791	NOTEST	0.0375675	0.0640622	0.769988	0	1	1
ENSG00000215088	ENSG00000215088	RPS5P3	21:34853886-34854502	NOTEST	0	0	0	0	1	1
ENSG00000215089	ENSG00000215089	KRT18P11	X:91034259-91878229	NOTEST	0	0	0	0	1	1
ENSG00000215093	ENSG00000215093	EEF1A1P29	X:85403461-86087607	NOTEST	0	0.0226171	inf	0	1	1
ENSG00000215094	ENSG00000215094	RP11-244K5.7	6:150272968-150273375	NOTEST	0	0	0	0	1	1
ENSG00000215096	ENSG00000215096	IFITM8P	8:64297396-64388040	NOTEST	0	0	0	0	1	1
ENSG00000215097	ENSG00000215097	DUSP8P3	10:46772793-46778894	NOTEST	0	0	0	0	1	1
ENSG00000215102	ENSG00000215102	TERF1P4	X:83003832-83004947	NOTEST	0	0.0122322	inf	0	1	1
ENSG00000215104	ENSG00000215104	CHMP1B2P	X:79528829-79565669	NOTEST	0	0.0703603	inf	0	1	1
ENSG00000215110	ENSG00000215110	RP11-790I12.1	4:70255207-70267799	NOTEST	0	0	0	0	1	1
ENSG00000215112	ENSG00000215112	FAM74A5	9:39371061-39376913	NOTEST	0	0	0	0	1	1
ENSG00000215113	ENSG00000215113	CXorf49B	X:70983139-70987054	NOTEST	0	0	0	0	1	1
ENSG00000215115	ENSG00000215115	CXorf49	X:70934220-70938135	NOTEST	0	0	0	0	1	1
ENSG00000215117	ENSG00000215117	LINC00588	8:58192101-58197290	NOTEST	0	0	0	0	1	1
ENSG00000215120	ENSG00000215120	AL590763.5	X:70586113-70752224	NOTEST	0.010809	0	#NAME?	0	1	1
ENSG00000215124	ENSG00000215124	RP3-420J14.1	6:11861858-11863203	NOTEST	0	0	0	0	1	1
ENSG00000215127	ENSG00000215127	SYT14L	4:68566997-68995598	NOTEST	0.0938746	0.0726122	-0.370522	0	1	1
ENSG00000215131	ENSG00000215131	C16orf90	16:3415098-3627401	NOTEST	0	0.015695	inf	0	1	1
ENSG00000215146	ENSG00000215146	RP11-313J2.1	10:42827313-42863422	NOTEST	0.0763598	0.0578687	-0.40003	0	1	1
ENSG00000215148	ENSG00000215148	PRSS41	16:2848485-2855148	NOTEST	0	0	0	0	1	1
ENSG00000215149	ENSG00000215149	KRT18P32	1:238643683-238701605	NOTEST	0	0	0	0	1	1
ENSG00000215151	ENSG00000215151	ABCD1P2	10:38894548-38898740	NOTEST	0	0	0	0	1	1
ENSG00000215156	ENSG00000215156	RP11-1023L17.2	5:34164802-34244901	NOTEST	0.0408139	0.0729096	0.837049	0	1	1
ENSG00000215159	ENSG00000215159	RP11-629N8.3	12:65153300-65173098	NOTEST	0	0	0	0	1	1
ENSG00000215160	ENSG00000215160	OR7E122P	3:8661085-9005457	NOTEST	0	0	0	0	1	1
ENSG00000215162	ENSG00000215162	LINC00269	X:68399399-68429767	NOTEST	0	0	0	0	1	1
ENSG00000215165	ENSG00000215165	RP11-403F21.3	9:38478467-38479347	NOTEST	0	0	0	0	1	1
ENSG00000215168	ENSG00000215168	RP11-30M20.1	X:65275428-65276429	NOTEST	0	0	0	0	1	1
ENSG00000215174	ENSG00000215174	RP13-487C10.1	X:57703499-57706693	NOTEST	0	0	0	0	1	1
ENSG00000215177	ENSG00000215177	IGLV8OR8-1	8:48114066-48114520	NOTEST	0	0	0	0	1	1
ENSG00000215179	ENSG00000215179	MAPK6PS4	8:47884098-47886240	NOTEST	0	0	0	0	1	1
ENSG00000215182	ENSG00000215182	MUC5AC	11:1212759-1222364	NOTEST	0	0	0	0	1	1
ENSG00000215183	ENSG00000215183	MSMP	9:35696944-35758572	NOTEST	0	0	0	0	1	1
ENSG00000215184	ENSG00000215184	RP11-8L18.2	10:34398487-35104253	NOTEST	0	0	0	0	1	1
ENSG00000215186	ENSG00000215186	GOLGA6B	15:72947078-72958735	NOTEST	0.00756551	0	#NAME?	0	1	1
ENSG00000215187	ENSG00000215187	FAM166B	9:35490123-35563896	NOTEST	0.136364	0.12887	-0.081546	0	1	1
ENSG00000215196	ENSG00000215196	AC091878.1	5:17065706-17276943	NOTEST	0.00536128	0.0275518	2.3615	0	1	1
ENSG00000215197	ENSG00000215197	PGAM4P1	X:54698417-54699071	NOTEST	0	0	0	0	1	1
ENSG00000215198	ENSG00000215198	RP11-182N22.7	9:35147406-35149181	NOTEST	0	0	0	0	1	1
ENSG00000215199	ENSG00000215199	YWHAZP6	9:34922180-34922918	NOTEST	0	0	0	0	1	1

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ENSG00000215206	ENSG00000215206	TRBV24OR9-2	9:33649044-33649612	NOTEST	0	0	0	0	1	1
ENSG00000215208	ENSG00000215208	KRT18P60	12:65672422-66036152	NOTEST	0.0131937	0	#NAME?	0	1	1
ENSG00000215210	ENSG00000215210	RBMXP2	9:30689102-30690270	NOTEST	0	0	0	0	1	1
ENSG00000215217	ENSG00000215217	C5orf49	5:7830490-7906138	NOTEST	0.198965	0.217197	0.126486	0	1	1
ENSG00000215218	ENSG00000215218	UBE2QL1	5:6448735-6495022	NOTEST	0	0	0	0	1	1
ENSG00000215221	ENSG00000215221	UBA52P6	9:21802541-22121096	NOTEST	0.273981	0.270541	-0.0182285	0	1	1
ENSG00000215223	ENSG00000215223	CYP51A1P3	6:148558720-148873186	NOTEST	0	0.00831108	inf	0	1	1
ENSG00000215227	ENSG00000215227	RP11-308K19.2	10:13628926-14504141	NOTEST	0	0	0	0	1	1
ENSG00000215231	ENSG00000215231	LINC01020	5:5034471-5078424	NOTEST	0	0	0	0	1	1
ENSG00000215236	ENSG00000215236	RPL7P33	9:15361390-15362132	NOTEST	0	0	0	0	1	1
ENSG00000215237	ENSG00000215237	RP11-54D18.2	9:14987299-15146399	NOTEST	0.0278216	0.0681394	1.29228	0	1	1
ENSG00000215241	ENSG00000215241	RP11-266K4.9	12:8385107-8395544	NOTEST	0.0530266	0.170551	1.68541	0	1	1
ENSG00000215244	ENSG00000215244	RP11-563J2.2	10:6319649-6377944	NOTEST	0.0511278	0.0417621	-0.291914	0	1	1
ENSG00000215246	ENSG00000215246	RP11-43F13.3	5:987294-997423	NOTEST	0.070824	0.071589	0.0154996	0	1	1
ENSG00000215262	ENSG00000215262	KCNU1	8:36641841-36793646	NOTEST	0.0599281	0.158735	1.40531	0	1	1
ENSG00000215263	ENSG00000215263	AC025750.7	2:42721708-42984087	NOTEST	0	0	0	0	1	1
ENSG00000215264	ENSG00000215264	RP1-84O15.1	8:34085956-34204249	NOTEST	0	0	0	0	1	1
ENSG00000215267	ENSG00000215267	AKR1C7P	10:5317135-5330433	NOTEST	0	0	0	0	1	1
ENSG00000215268	ENSG00000215268	LA16c-60G3.8	22:16399956-16436527	NOTEST	0	0	0	0	1	1
ENSG00000215269	ENSG00000215269	GAGE12G	X:49335036-49342357	NOTEST	0	0	0	0	1	1
ENSG00000215270	ENSG00000215270	LA16c-60H5.7	22:16100516-16124973	NOTEST	0.289571	0.275434	-0.0722113	0	1	1
ENSG00000215274	ENSG00000215274	GAGE10	X:49160147-49176323	NOTEST	0	0	0	0	1	1
ENSG00000215277	ENSG00000215277	C14orf164	14:23654524-23795394	NOTEST	0.0474549	0	#NAME?	0	1	1
ENSG00000215278	ENSG00000215278	RPS7P6	4:17429318-17429897	NOTEST	0	0	0	0	1	1
ENSG00000215283	ENSG00000215283	HMGB3P24	9:36190852-36304921	NOTEST	0	0.0233686	inf	0	1	1
ENSG00000215284	ENSG00000215284	RP11-198M15.1	X:46464752-46618490	NOTEST	0	0.0217082	inf	0	1	1
ENSG00000215286	ENSG00000215286	RP5-1158E12.2	X:45772552-45776475	NOTEST	0	0	0	0	1	1
ENSG00000215288	ENSG00000215288	RP11-613H2.1	8:26868663-26869888	NOTEST	0	0	0	0	1	1
ENSG00000215296	ENSG00000215296	TMCO5B	15:33527752-33539822	NOTEST	0	0	0	0	1	1
ENSG00000215297	ENSG00000215297	RP11-62E14.2	9:3218296-3526004	NOTEST	0	0	0	0	1	1
ENSG00000215298	ENSG00000215298	FP15737	8:23386317-23432976	NOTEST	0.376476	0.312316	-0.269551	0	1	1
ENSG00000215304	ENSG00000215304	RP13-395E19.3	15:32684982-32727434	NOTEST	0.0160403	0	#NAME?	0	1	1
ENSG00000215306	ENSG00000215306	AL135998.1	14:23242430-23299029	NOTEST	0	0	0	0	1	1
ENSG00000215307	ENSG00000215307	RBBP4P3	6:57841106-57842388	NOTEST	0	0	0	0	1	1
ENSG00000215310	ENSG00000215310	RP6-60B16.1	X:33429060-33430290	NOTEST	0	0	0	0	1	1
ENSG00000215311	ENSG00000215311	NPM1P12	7:149031114-149031948	NOTEST	0	0	0	0	1	1
ENSG00000215313	ENSG00000215313	RPL6P30	X:16216550-16217412	NOTEST	0	0	0	0	1	1
ENSG00000215317	ENSG00000215317	THUMPD1P1	21:30274100-30276019	NOTEST	0	0	0	0	1	1
ENSG00000215319	ENSG00000215319	RP11-98L4.1	X:9754495-9917483	NOTEST	0	0.0545518	inf	0	1	1
ENSG00000215323	ENSG00000215323	OR7E84P	4:9470745-9471694	NOTEST	0	0	0	0	1	1
ENSG00000215325	ENSG00000215325	ASS1P10	5:144602172-144609617	NOTEST	0.130911	0.0745956	-0.811426	0	1	1
ENSG00000215326	ENSG00000215326	GPX1P2	21:28515662-28516268	NOTEST	0	0	0	0	1	1
ENSG00000215328	ENSG00000215328	HSPA1A	HSCHR6_MHC_QBL:31773490-31775973	NOTEST	0	0	0	0	1	1

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ENSG00000215339	ENSG00000215339	ZNF705C	8:12213644-12216900	NOTEST	0	0	0	0	1	1
ENSG00000215343	ENSG00000215343	ZNF705D	8:11961897-11973025	NOTEST	0	0	0	0	1	1
ENSG00000215346	ENSG00000215346	AF131215.5	8:10753554-11058875	NOTEST	0	0	0	0	1	1
ENSG00000215347	ENSG00000215347	SLC25A5P1	22:42394728-42466846	NOTEST	0.193795	0.165673	-0.226192	0	1	1
ENSG00000215349	ENSG00000215349	MRPL3P1	13:19864732-19918965	NOTEST	0.0172304	0.0133975	-0.362988	0	1	1
ENSG00000215351	ENSG00000215351	PPIAP1	21:22200444-22200940	NOTEST	0	0	0	0	1	1
ENSG00000215353	ENSG00000215353	C1QBPP	21:21131672-21132442	NOTEST	0	0	0	0	1	1
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ENSG00000215356	ENSG00000215356	ZNF705B	8:7783858-7812271	NOTEST	0	0	0	0	1	1
ENSG00000215357	ENSG00000215357	HSPD1P8	13:79423365-79425343	NOTEST	0	0	0	0	1	1
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ENSG00000215367	ENSG00000215367	TMED11P	4:1107426-1147514	NOTEST	0	0	0	0	1	1
ENSG00000215368	ENSG00000215368	RP11-190I17.4	18:5132747-5133228	NOTEST	0	0	0	0	1	1
ENSG00000215369	ENSG00000215369	RPL37P3	21:19266509-19266802	NOTEST	0	0	0	0	1	1
ENSG00000215371	ENSG00000215371	DEFB108P2	8:7213038-7243080	NOTEST	0	0	0	0	1	1
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ENSG00000215374	ENSG00000215374	FAM66B	8:7159132-7212876	NOTEST	0.0499054	0.0496053	-0.00870243	0	1	1
ENSG00000215378	ENSG00000215378	DEFT1P	8:6844699-6847243	NOTEST	0	0	0	0	1	1
ENSG00000215380	ENSG00000215380	AC090625.1	11:35272752-35442549	NOTEST	0	0	0	0	1	1
ENSG00000215381	ENSG00000215381	RP5-1057J7.1	1:23571257-23571717	NOTEST	0	0	0	0	1	1
ENSG00000215386	ENSG00000215386	LINC00478	21:17442841-17999716	NOTEST	0.231533	0.31408	0.439916	0	1	1
ENSG00000215388	ENSG00000215388	ACTG1P3	20:1093905-1160596	NOTEST	0.146284	0.0870784	-0.748383	0	1	1
ENSG00000215397	ENSG00000215397	SCRT2	20:627258-656823	NOTEST	0	0	0	0	1	1
ENSG00000215398	ENSG00000215398	RP11-754I20.1	14:19110202-19118336	NOTEST	0.358835	0	#NAME?	0	1	1
ENSG00000215399	ENSG00000215399	HMGB3P7	13:102104965-103054807	NOTEST	0	0	0	0	1	1
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ENSG00000215405	ENSG00000215405	GOLGA6L6	15:20737093-20747114	NOTEST	0	0	0	0	1	1
ENSG00000215409	ENSG00000215409	RP11-748L13.2	10:27620285-27630181	NOTEST	0	0	0	0	1	1
ENSG00000215418	ENSG00000215418	PEX12P1	13:90644084-90645132	NOTEST	0	0	0	0	1	1
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ENSG00000215430	ENSG00000215430	OR7E156P	13:64316497-64316945	NOTEST	0	0	0	0	1	1
ENSG00000215431	ENSG00000215431	AC015989.1	18:60382671-60647666	NOTEST	0	0	0	0	1	1
ENSG00000215432	ENSG00000215432	OR7E104P	13:64402972-64418258	NOTEST	0	0	0	0	1	1
ENSG00000215441	ENSG00000215441	CTAGE12P	9:27608379-27610743	NOTEST	0	0	0	0	1	1
ENSG00000215444	ENSG00000215444	RP5-827A12.2	20:50213052-50385173	NOTEST	0	0	0	0	1	1
ENSG00000215448	ENSG00000215448	SRMP1	20:46488531-46489416	NOTEST	0	0	0	0	1	1
ENSG00000215450	ENSG00000215450	RP5-890O15.3	20:45523262-45817492	NOTEST	0	0	0	0	1	1
ENSG00000215452	ENSG00000215452	ZNF663P	20:44994687-45087915	NOTEST	0	0	0	0	1	1
ENSG00000215454	ENSG00000215454	KRTAP10-4	21:45917774-46131495	NOTEST	0	0	0	0	1	1
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ENSG00000215456	ENSG00000215456	BCRP4	22:22972531-22978624	NOTEST	0	0	0	0	1	1
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ENSG00000215464	ENSG00000215464	AP000354.2	22:24665313-24666102	NOTEST	0	0	0	0	1	1
ENSG00000215467	ENSG00000215467	RPL27AP	20:42281162-42281931	NOTEST	0.105689	0	#NAME?	0	1	1
ENSG00000215472	ENSG00000215472	RPL17-C18orf32	18:47008027-47018906	NOTEST	0.578298	0	#NAME?	0	1	1
ENSG00000215474	ENSG00000215474	SKOR2	18:44746292-44775554	NOTEST	0	0	0	0	1	1
ENSG00000215475	ENSG00000215475	SIAH3	13:46354404-46425871	NOTEST	0	0	0	0	1	1
ENSG00000215477	ENSG00000215477	RCN1P1	6:87831410-87832406	NOTEST	0	0	0	0	1	1
ENSG00000215478	ENSG00000215478	CES5AP1	22:23701789-23729918	NOTEST	0	0.0143834	inf	0	1	1
ENSG00000215480	ENSG00000215480	OR7E37P	13:42016905-42017786	NOTEST	0	0	0	0	1	1
ENSG00000215481	ENSG00000215481	BCRP3	22:25028881-25055114	NOTEST	0	0	0	0	1	1
ENSG00000215482	ENSG00000215482	CALM2P3	13:41744835-41745284	NOTEST	0	0	0	0	1	1
ENSG00000215483	ENSG00000215483	LINC00598	13:41025130-41055143	NOTEST	0	0	0	0	1	1
ENSG00000215486	ENSG00000215486	ARL2BPP3	13:37363468-37369187	NOTEST	0	0	0	0	1	1
ENSG00000215498	ENSG00000215498	FAM230B	22:21522046-21546445	NOTEST	0	0	0	0	1	1
ENSG00000215504	ENSG00000215504	AP000974.1	11:85563599-85565986	NOTEST	0.0443567	0.0345386	-0.36094	0	1	1
ENSG00000215506	ENSG00000215506	TPTE2P4	Y:28654359-28725837	NOTEST	0	0	0	0	1	1
ENSG00000215507	ENSG00000215507	RBMY2DP	Y:28269820-28279455	NOTEST	0	0	0	0	1	1
ENSG00000215512	ENSG00000215512	AP005901.1	18:15307661-15330281	NOTEST	0	0	0	0	1	1
ENSG00000215515	ENSG00000215515	IFIT1P1	13:32889610-32973805	NOTEST	0.0116211	0.00817404	-0.507621	0	1	1
ENSG00000215520	ENSG00000215520	RPS4XP4	1:20852481-20853244	NOTEST	0	0	0	0	1	1
ENSG00000215522	ENSG00000215522	DDR1	HSCHR6_MHC_QBL:30838341-30857525	NOTEST	0	0	0	0	1	1
ENSG00000215523	ENSG00000215523	LINC00243	HSCHR6_MHC_QBL:30755938-30787964	NOTEST	0	0	0	0	1	1
ENSG00000215529	ENSG00000215529	EFCAB8	20:31547650-31549006	NOTEST	0	0.00941618	inf	0	1	1
ENSG00000215533	ENSG00000215533	LINC00189	21:30565800-31312351	NOTEST	0	0.0666366	inf	0	1	1
ENSG00000215537	ENSG00000215537	ZNF736P11Y	Y:25012690-25013903	NOTEST	0	0	0	0	1	1
ENSG00000215540	ENSG00000215540	AC009947.3	Y:25683454-25693089	NOTEST	0	0	0	0	1	1
ENSG00000215544	ENSG00000215544	BCRP7	22:18834323-18848562	NOTEST	0	0.0883552	inf	0	1	1
ENSG00000215545	ENSG00000215545	DEFB116	20:29891014-29896388	NOTEST	0	0	0	0	1	1
ENSG00000215546	ENSG00000215546	DKKL1P1	20:29861972-29862670	NOTEST	0	0	0	0	1	1
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ENSG00000215549	ENSG00000215549	AL138815.1	13:25946208-26599989	NOTEST	0	0	0	0	1	1
ENSG00000215553	ENSG00000215553	KRT18P3	20:22713439-22714727	NOTEST	0	0	0	0	1	1
ENSG00000215559	ENSG00000215559	ANKRD20A11P	21:15281894-15352758	NOTEST	0.015939	0.0155322	-0.0372964	0	1	1
ENSG00000215560	ENSG00000215560	TTTY5	Y:24442944-24445023	NOTEST	0	0	0	0	1	1
ENSG00000215562	ENSG00000215562	CNN2P7	21:15199016-15199948	NOTEST	0	0	0	0	1	1
ENSG00000215565	ENSG00000215565	AP003041.1	11:129936835-130014699	NOTEST	0	0	0	0	1	1
ENSG00000215567	ENSG00000215567	RP11-79C23.1	15:20083768-20093074	NOTEST	0	0	0	0	1	1
ENSG00000215568	ENSG00000215568	GAB4	22:17442825-17489112	NOTEST	0	0	0	0	1	1
ENSG00000215571	ENSG00000215571	GRK6P1	13:21872277-21922860	NOTEST	0.011049	0	#NAME?	0	1	1
ENSG00000215572	ENSG00000215572	ESRRAP1	13:20126710-20144428	NOTEST	0	0	0	0	1	1
ENSG00000215580	ENSG00000215580	BCORP1	Y:21617316-21665039	NOTEST	0	0	0	0	1	1
ENSG00000215583	ENSG00000215583	ASS1P6	Y:14043241-14044475	NOTEST	0	0	0	0	1	1
ENSG00000215586	ENSG00000215586	RP5-836E8.1	20:7812444-7812969	NOTEST	0	0	0	0	1	1
ENSG00000215589	ENSG00000215589	RP5-967N21.2	20:5908730-5909964	NOTEST	0	0	0	0	1	1

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ENSG00000215601	ENSG00000215601	TSPY24P	Y:8148238-8150250	NOTEST	0	0	0	0	1	1
ENSG00000215603	ENSG00000215603	ZNF92P1Y	Y:7721726-7722917	NOTEST	0	0	0	0	1	1
ENSG00000215604	ENSG00000215604	ZNF962P	13:19041311-19059588	NOTEST	0	0	0	0	1	1
ENSG00000215606	ENSG00000215606	KRT18P35	3:141189475-141190744	NOTEST	0	0	0	0	1	1
ENSG00000215608	ENSG00000215608	AL356585.2	GL000212.1:126293-128249	NOTEST	0.00832	0	#NAME?	0	1	1
ENSG00000215611	ENSG00000215611	AC002321.1	GL000201.1:26347-27637	NOTEST	0	0	0	0	1	1
ENSG00000215612	ENSG00000215612	HMX1	4:8847801-8873543	NOTEST	0	0	0	0	1	1
ENSG00000215615	ENSG00000215615	AL354822.1	GL000218.1:38791-97421	NOTEST	0.205039	0.056623	-1.85644	0	1	1
ENSG00000215616	ENSG00000215616	AC002321.2	GL000201.1:3904-22432	NOTEST	0	0	0	0	1	1
ENSG00000215621	ENSG00000215621	AC174470.1	17:79780286-79791178	NOTEST	0.300618	0.614616	1.03175	0	1	1
ENSG00000215635	ENSG00000215635	AC145205.1	GL000204.1:44536-47211	NOTEST	0	0	0	0	1	1
ENSG00000215641	ENSG00000215641	TRIM27	HSCHR6_MHC_QBL:28870782-28891770	NOTEST	0	0	0	0	1	1
ENSG00000215642	ENSG00000215642	AL360154.1	GL000192.1:180635-212206	NOTEST	0	0	0	0	1	1
ENSG00000215644	ENSG00000215644	GCGR	17:79762007-79771889	NOTEST	0	0	0	0	1	1
ENSG00000215689	ENSG00000215689	MGC39584	GL000193.1:49251-88375	NOTEST	0.0286035	0.0366189	0.356396	0	1	1
ENSG00000215692	ENSG00000215692	AC114730.8	2:242673993-242708231	NOTEST	0	0.0672666	inf	0	1	1
ENSG00000215699	ENSG00000215699	SRSF10	GL000191.1:36276-50281	NOTEST	0.034001	0.0783573	1.20449	0	1	1
ENSG00000215700	ENSG00000215700	PNRC2	GL000191.1:29662-33264	NOTEST	0.142142	0.224354	0.658444	0	1	1
ENSG00000215704	ENSG00000215704	CELA2B	1:15783222-15853029	NOTEST	0	0	0	0	1	1
ENSG00000215705	ENSG00000215705	AC011841.2	GL000205.1:122919-123169	NOTEST	0	0	0	0	1	1
ENSG00000215713	ENSG00000215713	CU179654.1	GL000236.1:5814-7152	NOTEST	0	0	0	0	1	1
ENSG00000215719	ENSG00000215719	AL356585.3	GL000212.1:35321-36221	NOTEST	0	0	0	0	1	1
ENSG00000215720	ENSG00000215720	RP1-21O18.3	1:15479027-15546976	NOTEST	0	0	0	0	1	1
ENSG00000215734	ENSG00000215734	MRPL20P1	21:38366942-38367375	NOTEST	0	0	0	0	1	1
ENSG00000215749	ENSG00000215749	GOLGA6L18	15:82930437-82939159	NOTEST	0.0470797	0.0130372	-1.85247	0	1	1
ENSG00000215750	ENSG00000215750	AC145212.1	GL000194.1:53589-56132	NOTEST	0.0366331	0.0634998	0.793604	0	1	1
ENSG00000215760	ENSG00000215760	TAF9BP2	10:116569133-116570929	NOTEST	0	0	0	0	1	1
ENSG00000215764	ENSG00000215764	KIR2DL2	GL000209.1:7890-96246	NOTEST	0	0	0	0	1	1
ENSG00000215765	ENSG00000215765	CTB-61M7.1	19:55235968-55378662	NOTEST	0	0	0	0	1	1
ENSG00000215771	ENSG00000215771	LRRC37A14P	22:41487789-41593460	NOTEST	0.0510305	0	#NAME?	0	1	1
ENSG00000215785	ENSG00000215785	CFL1P6	1:11051034-11051854	NOTEST	0	0	0	0	1	1
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ENSG00000215791	ENSG00000215791	AL645728.2	1:1477052-1510249	NOTEST	0.25612	0.0970711	-1.39971	0	1	1
ENSG00000215795	ENSG00000215795	RP11-488L18.3	1:247347114-247348784	NOTEST	0.00990757	0	#NAME?	0	1	1
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ENSG00000215802	ENSG00000215802	RFKP1	1:240928856-241520530	NOTEST	0	0	0	0	1	1
ENSG00000215805	ENSG00000215805	RP11-438O11.1	1:240136086-240137545	NOTEST	0	0	0	0	1	1
ENSG00000215807	ENSG00000215807	KRT18P65	6:112682638-112684039	NOTEST	0	0	0	0	1	1
ENSG00000215808	ENSG00000215808	LINC01139	1:238643683-238701605	NOTEST	0.0197347	0.0160956	-0.294073	0	1	1
ENSG00000215811	ENSG00000215811	BTNL10	1:228696355-228700006	NOTEST	0	0	0	0	1	1
ENSG00000215812	ENSG00000215812	ZNF847P	1:227884592-227894412	NOTEST	0	0	0	0	1	1
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ENSG00000215838	ENSG00000215838	RP11-466F5.6	1:165631452-165679205	NOTEST	0.310286	0.0931604	-1.73581	0	1	1
ENSG00000215840	ENSG00000215840	RP11-122G18.7	1:161375857-161376872	NOTEST	0.0589349	0	#NAME?	0	1	1
ENSG00000215841	ENSG00000215841	RP11-800A3.2	11:72926042-72926958	NOTEST	0	0	0	0	1	1
ENSG00000215846	ENSG00000215846	MPTX1	1:159246292-159247282	NOTEST	0	0	0	0	1	1
ENSG00000215853	ENSG00000215853	RPTN	1:152126070-152131704	NOTEST	0	0	0	0	1	1
ENSG00000215859	ENSG00000215859	RP6-74O6.2	1:147466093-147484460	NOTEST	0	0	0	0	1	1
ENSG00000215860	ENSG00000215860	PDZK1P1	1:145924387-145942619	NOTEST	0	0	0	0	1	1
ENSG00000215864	ENSG00000215864	NBPF7	1:120377387-120387779	NOTEST	0	0	0	0	1	1
ENSG00000215866	ENSG00000215866	RP11-426L16.8	1:113362791-113420493	NOTEST	0.411782	0.28445	-0.533703	0	1	1
ENSG00000215867	ENSG00000215867	KRT18P57	1:112025969-112310638	NOTEST	0	0	0	0	1	1
ENSG00000215869	ENSG00000215869	RP11-364B6.1	1:104615631-104619709	NOTEST	0	0	0	0	1	1
ENSG00000215871	ENSG00000215871	RP5-837M10.1	1:100797359-100798173	NOTEST	0	0	0	0	1	1
ENSG00000215873	ENSG00000215873	FEN1P1	1:91726322-91870426	NOTEST	0	0	0	0	1	1
ENSG00000215874	ENSG00000215874	CAPNS1P1	1:89859591-89860224	NOTEST	0	0	0	0	1	1
ENSG00000215875	ENSG00000215875	ST13P20	1:81771844-82458120	NOTEST	0	0	0	0	1	1
ENSG00000215878	ENSG00000215878	MARCKSL1P2	6:138723721-139018425	NOTEST	0	0	0	0	1	1
ENSG00000215881	ENSG00000215881	RP11-65D24.1	13:112240547-112324955	NOTEST	0	0	0	0	1	1
ENSG00000215887	ENSG00000215887	ZNF859P	1:48998526-50489585	NOTEST	0	0	0	0	1	1
ENSG00000215893	ENSG00000215893	RP4-635E8.1	1:41492871-41707826	NOTEST	0	0	0	0	1	1
ENSG00000215895	ENSG00000215895	RP11-334L9.1	1:39174602-39176562	NOTEST	0.0150386	0.00583342	-1.36625	0	1	1
ENSG00000215899	ENSG00000215899	RP11-439L8.2	1:31960435-31961777	NOTEST	0	0	0	0	1	1
ENSG00000215900	ENSG00000215900	SEPW1P	1:31567833-31568405	NOTEST	0	0	0	0	1	1
ENSG00000215902	ENSG00000215902	AL353354.1	1:28525966-28559536	NOTEST	0	0	0	0	1	1
ENSG00000215905	ENSG00000215905	RP11-4M23.7	1:24334370-24335009	NOTEST	0	0	0	0	1	1
ENSG00000215906	ENSG00000215906	LACTBL1	1:23279535-23291831	NOTEST	0	0	0	0	1	1
ENSG00000215909	ENSG00000215909	RP4-597A16.3	1:13881495-13882189	NOTEST	0	0	0	0	1	1
ENSG00000215910	ENSG00000215910	C1orf167	1:11821843-11908402	NOTEST	0	0	0	0	1	1
ENSG00000215912	ENSG00000215912	TTC34	1:2517929-2718286	NOTEST	0.0158497	0	#NAME?	0	1	1
ENSG00000215914	ENSG00000215914	MMP23A	1:1631368-1633249	NOTEST	0	0	0	0	1	1
ENSG00000215915	ENSG00000215915	ATAD3C	1:1385068-1405538	NOTEST	0.132214	0.174191	0.397797	0	1	1
ENSG00000215921	ENSG00000215921	AL731568.1	10:77360997-78320752	NOTEST	0	0	0	0	1	1
ENSG00000215922	ENSG00000215922	AC092965.1	3:166743200-166743287	NOTEST	0	0	0	0	1	1
ENSG00000215923	ENSG00000215923	AC007528.1	12:16500075-16763528	NOTEST	0	0	0	0	1	1
ENSG00000215924	ENSG00000215924	BX284613.1	1:170904611-171033906	NOTEST	0	0	0	0	1	1
ENSG00000215925	ENSG00000215925	AL157788.1	10:120765301-120765411	NOTEST	0	0	0	0	1	1
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ENSG00000215933	ENSG00000215933	BX119917.1	X:71364033-71381600	NOTEST	0	0	0	0	1	1
ENSG00000215934	ENSG00000215934	AC013731.1	2:158592957-158732374	NOTEST	0	0	0	0	1	1
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ENSG00000215939	ENSG00000215939	MIR873	9:28888876-28888953	NOTEST	0	0	0	0	1	1
ENSG00000215941	ENSG00000215941	AC116038.1	3:38887259-38992052	NOTEST	0	0	0	0	1	1
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ENSG00000215948	ENSG00000215948	AC055873.1	15:97634491-97634582	NOTEST	0	0	0	0	1	1
ENSG00000215952	ENSG00000215952	MIR921	1:166026673-166136206	NOTEST	0	0	0	0	1	1
ENSG00000215953	ENSG00000215953	AC026700.1	5:84823861-84823952	NOTEST	0	0	0	0	1	1
ENSG00000215954	ENSG00000215954	AP002884.1	11:112097087-112140678	NOTEST	0	0	0	0	1	1
ENSG00000215957	ENSG00000215957	MIR300	14:101507699-101507782	NOTEST	0	0	0	0	1	1
ENSG00000215958	ENSG00000215958	AC021818.1	15:70077753-70077843	NOTEST	0	0	0	0	1	1
ENSG00000215960	ENSG00000215960	AC068292.1	2:4276017-4276108	NOTEST	0	0	0	0	1	1
ENSG00000215961	ENSG00000215961	MIR297	4:111781737-111781803	NOTEST	0	0	0	0	1	1
ENSG00000215964	ENSG00000215964	AC055813.1	17:41825567-41825631	NOTEST	0	0	0	0	1	1
ENSG00000215966	ENSG00000215966	MIR876	9:28863623-28863704	NOTEST	0	0	0	0	1	1
ENSG00000215968	ENSG00000215968	AC007560.2	2:50145642-51259674	NOTEST	0	0	0	0	1	1
ENSG00000215972	ENSG00000215972	AL360176.1	10:127512114-127585005	NOTEST	0	0	0	0	1	1
ENSG00000215973	ENSG00000215973	MIR933	2:175936977-176033250	NOTEST	0	0	0	0	1	1
ENSG00000215976	ENSG00000215976	AC078819.1	12:104359581-104382652	NOTEST	0	0	0	0	1	1
ENSG00000215977	ENSG00000215977	AC130365.1	8:7705397-7726389	NOTEST	0	0	0	0	1	1
ENSG00000215979	ENSG00000215979	AL021917.1	6:26365386-26378546	NOTEST	0	0	0	0	1	1
ENSG00000215983	ENSG00000215983	AC092756.1	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000215984	ENSG00000215984	AC110769.1	2:114737145-114764879	NOTEST	0	0	0	0	1	1
ENSG00000215991	ENSG00000215991	MIR208B	14:23881946-23904927	NOTEST	0	0	0	0	1	1
ENSG00000215993	ENSG00000215993	AC079603.1	12:43685297-43685383	NOTEST	0	0	0	0	1	1
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ENSG00000215998	ENSG00000215998	MIR935	19:54466293-54493469	NOTEST	0	0	0	0	1	1
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ENSG00000216014	ENSG00000216014	AL512505.1	13:40226714-40226806	NOTEST	0	0	0	0	1	1
ENSG00000216015	ENSG00000216015	AL354936.1	6:124061578-124061677	NOTEST	0	0	0	0	1	1
ENSG00000216017	ENSG00000216017	AL139429.1	20:19193289-19703581	NOTEST	0	0	0	0	1	1
ENSG00000216020	ENSG00000216020	AC026320.1	3:191693742-191693813	NOTEST	0	0	0	0	1	1
ENSG00000216022	ENSG00000216022	AC068062.1	10:52750944-54073888	NOTEST	0	0	0	0	1	1
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ENSG00000216031	ENSG00000216031	MIR298	20:57393280-57393368	NOTEST	0	0	0	0	1	1
ENSG00000216032	ENSG00000216032	AL445258.1	X:145072384-145072455	NOTEST	0	0	0	0	1	1
ENSG00000216035	ENSG00000216035	MIR938	10:29698330-30025710	NOTEST	0	0	0	0	1	1
ENSG00000216037	ENSG00000216037	AL356479.1	1:95970531-95970619	NOTEST	0	0	0	0	1	1
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ENSG00000216045	ENSG00000216045	AL356693.1	1:5875930-5876019	NOTEST	0	0	0	0	1	1
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ENSG00000216055	ENSG00000216055	AC097372.1	4:147043355-147043436	NOTEST	0	0	0	0	1	1
ENSG00000216056	ENSG00000216056	MIR891A	X:145109311-145109390	NOTEST	0	0	0	0	1	1
ENSG00000216058	ENSG00000216058	MIR944	3:189349204-189615068	NOTEST	0	0	0	0	1	1
ENSG00000216060	ENSG00000216060	MIR934	X:135614310-135638966	NOTEST	0	0	0	0	1	1
ENSG00000216064	ENSG00000216064	MIR891B	X:145082570-145082649	NOTEST	0	0	0	0	1	1
ENSG00000216067	ENSG00000216067	AC104457.1	1:100810032-100985833	NOTEST	0	0	0	0	1	1
ENSG00000216069	ENSG00000216069	MIR875	8:100025493-100906290	NOTEST	0	0	0	0	1	1
ENSG00000216070	ENSG00000216070	AL158155.1	9:37120535-37358146	NOTEST	0	0	0	0	1	1
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ENSG00000216073	ENSG00000216073	AP003730.1	11:97749780-97813762	NOTEST	0	0	0	0	1	1
ENSG00000216075	ENSG00000216075	MIR890	X:145075792-145075869	NOTEST	0	0	0	0	1	1
ENSG00000216076	ENSG00000216076	AC002066.2	7:115850546-116148595	NOTEST	0	0	0	0	1	1
ENSG00000216077	ENSG00000216077	MIR887	5:15500304-15939900	NOTEST	0	0	0	0	1	1
ENSG00000216081	ENSG00000216081	AC010146.2	2:137301940-137302050	NOTEST	0	0	0	0	1	1
ENSG00000216083	ENSG00000216083	MIR936	10:105791043-105845760	NOTEST	0	0	0	0	1	1
ENSG00000216084	ENSG00000216084	AC131213.1	12:73184230-73184425	NOTEST	0	0	0	0	1	1
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ENSG00000216093	ENSG00000216093	AC009305.2	2:31133332-31378068	NOTEST	0	0	0	0	1	1
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ENSG00000216098	ENSG00000216098	MIR892B	X:145078715-145078792	NOTEST	0	0	0	0	1	1
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ENSG00000216100	ENSG00000216100	AC138710.1	17:21481083-21481171	NOTEST	0	0	0	0	1	1
ENSG00000216101	ENSG00000216101	MIR877	6:30539152-30564956	NOTEST	0	0	0	0	1	1
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ENSG00000216105	ENSG00000216105	MIR943	4:1984440-2043630	NOTEST	0	0	0	0	1	1
ENSG00000216109	ENSG00000216109	AL713999.1	1:155204242-155214490	NOTEST	0	0	0	0	1	1
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ENSG00000216123	ENSG00000216123	AC012119.1	8:23564653-23647000	NOTEST	0	0	0	0	1	1
ENSG00000216125	ENSG00000216125	AC109496.1	5:83236372-83786583	NOTEST	0	0	0	0	1	1
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ENSG00000216131	ENSG00000216131	AC025284.1	16:77224731-77478233	NOTEST	0	0	0	0	1	1
ENSG00000216133	ENSG00000216133	MIR939	8:145596789-145634753	NOTEST	0	0	0	0	1	1
ENSG00000216135	ENSG00000216135	MIR885	3:10365706-10749716	NOTEST	0	0	0	0	1	1
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ENSG00000216141	ENSG00000216141	MIR941-2	20:62526517-62567384	NOTEST	0	0	0	0	1	1
ENSG00000216154	ENSG00000216154	AC109357.1	4:123844228-124240605	NOTEST	0	0	0	0	1	1
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ENSG00000216168	ENSG00000216168	AC100832.1	17:57059998-57232630	NOTEST	0	0	0	0	1	1
ENSG00000216169	ENSG00000216169	AC098650.1	3:29305684-30051886	NOTEST	0	0	0	0	1	1
ENSG00000216171	ENSG00000216171	MIR513C	X:146271221-146271305	NOTEST	0	0	0	0	1	1
ENSG00000216173	ENSG00000216173	AL132819.1	14:99828627-99828716	NOTEST	0	0	0	0	1	1
ENSG00000216179	ENSG00000216179	MIR541	14:101530831-101530915	NOTEST	0	0	0	0	1	1
ENSG00000216181	ENSG00000216181	AL391056.1	9:132353754-132353841	NOTEST	0	0	0	0	1	1
ENSG00000216182	ENSG00000216182	AL137024.1	9:118916082-119164601	NOTEST	0	0	0	0	1	1
ENSG00000216184	ENSG00000216184	AC048346.1	3:139654026-140296239	NOTEST	0	0	0	0	1	1
ENSG00000216191	ENSG00000216191	AC009234.2	2:50145642-51259674	NOTEST	0	0	0	0	1	1
ENSG00000216192	ENSG00000216192	MIR920	12:24365354-24365429	NOTEST	0	0	0	0	1	1
ENSG00000216193	ENSG00000216193	AC009336.1	2:176968943-176984670	NOTEST	0	0	0	0	1	1
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ENSG00000216205	ENSG00000216205	AC036178.1	18:18526866-18691812	NOTEST	0	0	0	0	1	1
ENSG00000216206	ENSG00000216206	AF228730.1	8:6973420-6973570	NOTEST	0	0	0	0	1	1
ENSG00000216265	ENSG00000216265	FABP12P1	6:149539061-149732749	NOTEST	0	0	0	0	1	1
ENSG00000216306	ENSG00000216306	KRT19P2	12:95227922-95228934	NOTEST	0	0	0	0	1	1
ENSG00000216307	ENSG00000216307	RP3-400B16.2	6:4189349-4190040	NOTEST	0.028566	0	#NAME?	0	1	1
ENSG00000216316	ENSG00000216316	RP3-354N19.3	6:119498373-119670926	NOTEST	0	0.0281438	inf	0	1	1
ENSG00000216324	ENSG00000216324	RP3-382I10.2	6:88117700-88222054	NOTEST	0	0	0	0	1	1
ENSG00000216331	ENSG00000216331	HIST1H1PS1	6:26195793-26195999	NOTEST	0.321896	0.236071	-0.447378	0	1	1
ENSG00000216347	ENSG00000216347	RP3-334F4.2	6:54467284-54467948	NOTEST	0	0	0	0	1	1
ENSG00000216352	ENSG00000216352	RP11-486E2.1	6:81265557-81266906	NOTEST	0	0	0	0	1	1
ENSG00000216359	ENSG00000216359	RP11-360O19.1	6:10492455-10629601	NOTEST	0.0215064	0	#NAME?	0	1	1
ENSG00000216360	ENSG00000216360	RP1-182O16.2	6:5817653-5818599	NOTEST	0.0891833	0.0270199	-1.72275	0	1	1
ENSG00000216364	ENSG00000216364	MRPL42P2	6:16171836-16172262	NOTEST	0	0	0	0	1	1
ENSG00000216365	ENSG00000216365	RPL37P15	6:70576462-70919679	NOTEST	0	0	0	0	1	1
ENSG00000216368	ENSG00000216368	RP3-486D24.1	6:9596342-10211841	NOTEST	0	0	0	0	1	1
ENSG00000216378	ENSG00000216378	RP3-344J20.1	6:100625084-100626068	NOTEST	0	0	0	0	1	1
ENSG00000216412	ENSG00000216412	RPL12P2	6:37059087-37059582	NOTEST	0	0	0	0	1	1
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ENSG00000216471	ENSG00000216471	RPSAP43	6:114254191-114792869	NOTEST	0	0	0	0	1	1
ENSG00000216475	ENSG00000216475	RP1-91J24.1	6:144578169-144578760	NOTEST	0	0	0	0	1	1
ENSG00000216480	ENSG00000216480	RP3-393E18.1	6:159947093-159947559	NOTEST	0	0	0	0	1	1
ENSG00000216516	ENSG00000216516	RP11-317M22.1	6:160584570-160584787	NOTEST	0	0	0	0	1	1

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ENSG00000216519	ENSG00000216519	RP3-406A7.1	6:136639098-136639374	NOTEST	0	0	0	0	1	1
ENSG00000216522	ENSG00000216522	AC011718.1	22:20610446-20616201	NOTEST	0	0	0	0	1	1
ENSG00000216523	ENSG00000216523	RP3-435K13.1	6:85676114-85676343	NOTEST	0	0	0	0	1	1
ENSG00000216548	ENSG00000216548	RP11-471B18.1	6:141243593-141244047	NOTEST	0	0	0	0	1	1
ENSG00000216560	ENSG00000216560	LINC00955	4:3578595-3592438	NOTEST	0	0	0	0	1	1
ENSG00000216588	ENSG00000216588	IGSF23	19:45041044-45222031	NOTEST	0	0.0269151	inf	0	1	1
ENSG00000216613	ENSG00000216613	RP3-406A7.5	6:136663874-136873692	NOTEST	0.0364114	0	#NAME?	0	1	1
ENSG00000216616	ENSG00000216616	RP11-550C4.4	6:47720563-47720976	NOTEST	0	0	0	0	1	1
ENSG00000216621	ENSG00000216621	RP11-244K5.6	6:150255662-150257918	NOTEST	0	0	0	0	1	1
ENSG00000216624	ENSG00000216624	GAPDHP72	6:166477778-166478788	NOTEST	0	0.0124739	inf	0	1	1
ENSG00000216629	ENSG00000216629	OR2W4P	6:27944927-27945853	NOTEST	0	0	0	0	1	1
ENSG00000216636	ENSG00000216636	RPL7P25	6:34555064-34665247	NOTEST	0	0	0	0	1	1
ENSG00000216639	ENSG00000216639	RP3-355L5.3	6:105725439-105850959	NOTEST	0.025788	0.0622566	1.27153	0	1	1
ENSG00000216642	ENSG00000216642	RP1-95L4.3	6:143381632-143661441	NOTEST	0	0	0	0	1	1
ENSG00000216649	ENSG00000216649	GAGE12E	X:49315935-49323252	NOTEST	0	0	0	0	1	1
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ENSG00000216663	ENSG00000216663	RP11-506B6.5	6:112429962-112672498	NOTEST	0	0	0	0	1	1
ENSG00000216671	ENSG00000216671	CCNYL3	16:34262755-34318684	NOTEST	0	0	0	0	1	1
ENSG00000216676	ENSG00000216676	RP1-15D7.1	6:27620380-27620604	NOTEST	0	0	0	0	1	1
ENSG00000216687	ENSG00000216687	RP11-278J20.2	6:58397997-58399412	NOTEST	0	0	0	0	1	1
ENSG00000216708	ENSG00000216708	CIR1P3	11:34452426-34453196	NOTEST	0	0	0	0	1	1
ENSG00000216710	ENSG00000216710	COX6A1P3	6:121102365-121102658	NOTEST	0	0	0	0	1	1
ENSG00000216713	ENSG00000216713	MTND4P13	6:153990013-153991036	NOTEST	0	0	0	0	1	1
ENSG00000216718	ENSG00000216718	RP3-522P13.1	6:25245583-25261959	NOTEST	0	0	0	0	1	1
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ENSG00000216740	ENSG00000216740	ANXA2P3	10:66585328-66586336	NOTEST	0	0	0	0	1	1
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ENSG00000216762	ENSG00000216762	VN1R13P	6:27028143-27029028	NOTEST	0	0	0	0	1	1
ENSG00000216777	ENSG00000216777	PRRC2CP1	Y:3417692-3417851	NOTEST	0	0	0	0	1	1
ENSG00000216781	ENSG00000216781	RP1-290I10.2	6:10365825-10366815	NOTEST	0	0	0	0	1	1
ENSG00000216802	ENSG00000216802	RP11-390P2.2	6:138723721-139018425	NOTEST	0	0.0768823	inf	0	1	1
ENSG00000216809	ENSG00000216809	RP11-57K17.1	6:118773631-118776155	NOTEST	0.012623	0.0320535	1.34443	0	1	1
ENSG00000216811	ENSG00000216811	RP1-69B13.2	6:146348781-146758734	NOTEST	0	0	0	0	1	1
ENSG00000216813	ENSG00000216813	RP11-812I20.2	6:47445524-47594999	NOTEST	0	0	0	0	1	1
ENSG00000216817	ENSG00000216817	R3HDM2P2	6:104465507-104467623	NOTEST	0	0	0	0	1	1
ENSG00000216819	ENSG00000216819	TUBB2BP1	6:3177277-3179998	NOTEST	0.0600412	0.100717	0.746289	0	1	1
ENSG00000216824	ENSG00000216824	ZNF736P10Y	Y:8286831-8287941	NOTEST	0	0	0	0	1	1
ENSG00000216829	ENSG00000216829	BX005214.1	9:44302231-44303807	NOTEST	0.0874412	0	#NAME?	0	1	1
ENSG00000216835	ENSG00000216835	RBMXP1	6:48181339-48182530	NOTEST	0	0	0	0	1	1
ENSG00000216844	ENSG00000216844	AC009494.3	Y:23005141-23005596	NOTEST	0	0	0	0	1	1
ENSG00000216853	ENSG00000216853	RP3-399J4.1	6:95156457-95156897	NOTEST	0	0	0	0	1	1

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ENSG00000216859	ENSG00000216859	RP11-448N11.1	6:63170844-63171408	NOTEST	0	0	0	0	1	1
ENSG00000216863	ENSG00000216863	LY86-AS1	6:6346697-6655216	NOTEST	0	0	0	0	1	1
ENSG00000216866	ENSG00000216866	RPS2P55	X:40794197-40795117	NOTEST	0.36199	0.29734	-0.283836	0	1	1
ENSG00000216867	ENSG00000216867	AC114776.1	2:111391523-111391910	NOTEST	0.267417	0.322396	0.269743	0	1	1
ENSG00000216901	ENSG00000216901	AL022393.7	6:28143965-28144452	NOTEST	0.0877275	0.0366312	-1.25996	0	1	1
ENSG00000216902	ENSG00000216902	RP1-161C16.1	6:85967045-85967412	NOTEST	0	0	0	0	1	1
ENSG00000216904	ENSG00000216904	SOCS5P5	6:113543367-113545274	NOTEST	0	0	0	0	1	1
ENSG00000216906	ENSG00000216906	RP11-350J20.9	6:150139933-150244257	NOTEST	0	0	0	0	1	1
ENSG00000216913	ENSG00000216913	RP4-753D5.3	6:50865327-50865938	NOTEST	0	0	0	0	1	1
ENSG00000216915	ENSG00000216915	RP1-97D16.1	6:27704778-27706273	NOTEST	0.0968187	0.0333762	-1.53647	0	1	1
ENSG00000216917	ENSG00000216917	RP5-988G15.1	6:132101860-132102452	NOTEST	0	0	0	0	1	1
ENSG00000216921	ENSG00000216921	AC131097.4	2:242823513-243026289	NOTEST	0	0	0	0	1	1
ENSG00000216937	ENSG00000216937	CCDC7	10:32735067-33171802	NOTEST	0.581838	0.515339	-0.175096	0	1	1
ENSG00000216938	ENSG00000216938	RPL7P58	X:26704142-26706072	NOTEST	0	0	0	0	1	1
ENSG00000216966	ENSG00000216966	RP11-568A7.1	6:167622118-167622385	NOTEST	0	0	0	0	1	1
ENSG00000216977	ENSG00000216977	RPL21P65	6:107077452-107116292	NOTEST	0	0.0392448	inf	0	1	1
ENSG00000216990	ENSG00000216990	HSPD1P10	6:87992695-88109467	NOTEST	0	0	0	0	1	1
ENSG00000216998	ENSG00000216998	CYP2AC1P	6:49533636-49547879	NOTEST	0	0	0	0	1	1
ENSG00000217004	ENSG00000217004	RP3-329A5.1	6:35226685-35263762	NOTEST	0	0	0	0	1	1
ENSG00000217026	ENSG00000217026	RPL10P1	21:28731203-28820898	NOTEST	0	0	0	0	1	1
ENSG00000217027	ENSG00000217027	TPT1P4	6:144521583-144522102	NOTEST	0	0	0	0	1	1
ENSG00000217030	ENSG00000217030	RP11-428J1.2	6:4979305-4979728	NOTEST	0	0.0420005	inf	0	1	1
ENSG00000217041	ENSG00000217041	RP11-346C16.1	6:110931180-111137161	NOTEST	0	0	0	0	1	1
ENSG00000217044	ENSG00000217044	RP11-331O9.4	6:153987600-153989241	NOTEST	0	0	0	0	1	1
ENSG00000217060	ENSG00000217060	RP11-30P6.1	6:85995793-86000567	NOTEST	0.0294578	0.0302117	0.0364571	0	1	1
ENSG00000217067	ENSG00000217067	RP11-448N11.2	6:63257331-63258177	NOTEST	0	0	0	0	1	1
ENSG00000217075	ENSG00000217075	AC007401.2	2:36583068-36873230	NOTEST	0	0	0	0	1	1
ENSG00000217078	ENSG00000217078	RP1-13D10.3	6:16163607-16163993	NOTEST	0.130791	0.0492989	-1.40763	0	1	1
ENSG00000217083	ENSG00000217083	RP1-245M18.2	6:24797548-25057301	NOTEST	0	0	0	0	1	1
ENSG00000217085	ENSG00000217085	HMGB3P19	6:154259567-154260127	NOTEST	0	0	0	0	1	1
ENSG00000217089	ENSG00000217089	RPS29P13	6:117369832-117370001	NOTEST	0	0	0	0	1	1
ENSG00000217094	ENSG00000217094	PPIAP31	10:32477250-32477745	NOTEST	0.485678	0.475954	-0.0291794	0	1	1
ENSG00000217120	ENSG00000217120	RP1-76C18.1	6:103450388-103451772	NOTEST	0	0	0	0	1	1
ENSG00000217130	ENSG00000217130	RP3-375P9.2	6:34711952-34712450	NOTEST	0.266368	0.239418	-0.15389	0	1	1
ENSG00000217135	ENSG00000217135	RP1-140K8.3	6:3922080-3922380	NOTEST	0	0	0	0	1	1
ENSG00000217139	ENSG00000217139	RP11-129H15.4	6:122004070-122005418	NOTEST	0	0	0	0	1	1
ENSG00000217159	ENSG00000217159	LARP1P1	6:26158348-26171577	NOTEST	0	0	0	0	1	1
ENSG00000217160	ENSG00000217160	RP11-331O9.1	6:153986841-153987525	NOTEST	0	0	0	0	1	1
ENSG00000217169	ENSG00000217169	MTHFD2P2	6:87647023-87726349	NOTEST	0	0	0	0	1	1
ENSG00000217178	ENSG00000217178	RP11-9G10.1	6:74779166-75443995	NOTEST	0	0	0	0	1	1
ENSG00000217179	ENSG00000217179	MTCYBP2	Y:21033987-21034158	NOTEST	0	0	0	0	1	1
ENSG00000217181	ENSG00000217181	RP11-360O19.5	6:10492455-10629601	NOTEST	0	0	0	0	1	1

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ENSG00000217227	ENSG00000217227	RP1-319M7.2	6:38136226-38607924	NOTEST	0	0	0	0	1	1
ENSG00000217228	ENSG00000217228	RP1-152L7.1	6:52630077-52643145	NOTEST	0	0	0	0	1	1
ENSG00000217231	ENSG00000217231	RP3-340H11.2	6:144261436-144385735	NOTEST	0	0	0	0	1	1
ENSG00000217236	ENSG00000217236	SP9	2:175199673-175203220	NOTEST	0.0112719	0	#NAME?	0	1	1
ENSG00000217239	ENSG00000217239	RP1-182O16.1	6:5788578-5788932	NOTEST	0	0	0	0	1	1
ENSG00000217258	ENSG00000217258	AC007249.3	2:10592444-10595678	NOTEST	0	0	0	0	1	1
ENSG00000217261	ENSG00000217261	POM121L4P	22:21044216-21053226	NOTEST	0	0	0	0	1	1
ENSG00000217268	ENSG00000217268	TXNP7	6:74714235-74714528	NOTEST	0	0	0	0	1	1
ENSG00000217272	ENSG00000217272	RP1-263J7.2	6:86880164-86880736	NOTEST	0	0	0	0	1	1
ENSG00000217275	ENSG00000217275	RP1-34B20.4	6:26202383-26202882	NOTEST	0.168822	0.132819	-0.346043	0	1	1
ENSG00000217281	ENSG00000217281	LYPLA2P1	HSCHR6_MHC_APD:33316720-33317416	NOTEST	0	0	0	0	1	1
ENSG00000217289	ENSG00000217289	AC018865.5	2:130748028-130808704	NOTEST	0	0	0	0	1	1
ENSG00000217314	ENSG00000217314	UQCRFS1P3	6:19535174-19840915	NOTEST	0	0	0	0	1	1
ENSG00000217315	ENSG00000217315	OR2W2P	6:28001724-28002633	NOTEST	0	0	0	0	1	1
ENSG00000217327	ENSG00000217327	RPS7P5	1:240175945-240176526	NOTEST	0	0	0	0	1	1
ENSG00000217330	ENSG00000217330	SSXP10	6:118781934-119031238	NOTEST	0	0	0	0	1	1
ENSG00000217331	ENSG00000217331	RP11-304C16.3	6:97120004-97120845	NOTEST	0	0	0	0	1	1
ENSG00000217334	ENSG00000217334	RP11-33E24.3	6:86441088-86441729	NOTEST	0	0	0	0	1	1
ENSG00000217372	ENSG00000217372	TUBB4BP7	6:153219181-153220415	NOTEST	0.0254211	0.0108612	-1.22684	0	1	1
ENSG00000217377	ENSG00000217377	AK4P5	6:80787445-80788079	NOTEST	0	0	0	0	1	1
ENSG00000217379	ENSG00000217379	RP11-254A17.1	6:19143925-19144391	NOTEST	0	0	0	0	1	1
ENSG00000217385	ENSG00000217385	PSMC1P11	6:4702696-4704013	NOTEST	0	0	0	0	1	1
ENSG00000217404	ENSG00000217404	RPS4XP9	6:127004180-127004992	NOTEST	0	0	0	0	1	1
ENSG00000217408	ENSG00000217408	PRELID1P2	6:25652463-25702011	NOTEST	0	0	0	0	1	1
ENSG00000217414	ENSG00000217414	RP11-528A10.2	6:18363647-18365654	NOTEST	0	0	0	0	1	1
ENSG00000217442	ENSG00000217442	SYCE3	22:50989540-51001334	NOTEST	0.10055	0	#NAME?	0	1	1
ENSG00000217447	ENSG00000217447	RP3-366N23.4	6:167738573-167797998	NOTEST	0	0	0	0	1	1
ENSG00000217455	ENSG00000217455	AC091801.1	7:3179867-3214287	NOTEST	0	0	0	0	1	1
ENSG00000217477	ENSG00000217477	RP11-184C23.1	6:63902976-63903535	NOTEST	0	0	0	0	1	1
ENSG00000217482	ENSG00000217482	HMGB1P17	6:135604669-136037193	NOTEST	0	0	0	0	1	1
ENSG00000217483	ENSG00000217483	RP11-135M8__A.1	6:73232342-73232940	NOTEST	0	0	0	0	1	1
ENSG00000217488	ENSG00000217488	RP11-474L11.5	6:76311224-76427997	NOTEST	0	0.0197548	inf	0	1	1
ENSG00000217495	ENSG00000217495	RP1-95L4.2	6:143381632-143661441	NOTEST	0	0	0	0	1	1
ENSG00000217512	ENSG00000217512	RP11-477E3.2	6:79577188-79787953	NOTEST	0.0537949	0	#NAME?	0	1	1
ENSG00000217514	ENSG00000217514	RP3-495O10.1	6:163784241-163784495	NOTEST	0	0	0	0	1	1
ENSG00000217527	ENSG00000217527	RPS16P5	6:53132195-53213947	NOTEST	0	0	0	0	1	1
ENSG00000217539	ENSG00000217539	IQCB2P	6:27978500-27980133	NOTEST	0	0	0	0	1	1
ENSG00000217557	ENSG00000217557	RP11-157L10.1	6:161768451-163736524	NOTEST	0	0	0	0	1	1
ENSG00000217566	ENSG00000217566	TDGF1P4	6:3941515-3942035	NOTEST	0	0	0	0	1	1
ENSG00000217576	ENSG00000217576	RP11-248G5.8	13:52741843-52908412	NOTEST	0.026597	0.0214766	-0.308498	0	1	1
ENSG00000217585	ENSG00000217585	RP1-13D10.5	6:16107852-16108824	NOTEST	0	0	0	0	1	1
ENSG00000217612	ENSG00000217612	RP1-28C20.1	6:145810765-145813228	NOTEST	0	0	0	0	1	1

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ENSG00000217624	ENSG00000217624	RP11-204C16.4	X:41374186-41782716	NOTEST	0.0526776	0.0186045	-1.50154	0	1	1
ENSG00000217631	ENSG00000217631	RP1-142O9.2	6:49241240-49241435	NOTEST	0	0	0	0	1	1
ENSG00000217643	ENSG00000217643	PTGES3P2	2:25956621-26101385	NOTEST	0	0	0	0	1	1
ENSG00000217644	ENSG00000217644	RP4-803A2.1	1:33445542-33446073	NOTEST	0.0417845	0	#NAME?	0	1	1
ENSG00000217646	ENSG00000217646	HIST1H2BPS2	6:27831839-27832179	NOTEST	0	0	0	0	1	1
ENSG00000217648	ENSG00000217648	RP1-95L4.4	6:143663382-143664520	NOTEST	0.0307183	0.0324453	0.0789117	0	1	1
ENSG00000217653	ENSG00000217653	RP11-63K6.1	6:90352217-90529442	NOTEST	0.0466875	0	#NAME?	0	1	1
ENSG00000217680	ENSG00000217680	RP11-415D17.1	6:75994729-76203454	NOTEST	0	0	0	0	1	1
ENSG00000217684	ENSG00000217684	RPS3AP24	6:141082665-141083399	NOTEST	0	0	0	0	1	1
ENSG00000217686	ENSG00000217686	NUS1P4	13:99262545-99263130	NOTEST	0	0	0	0	1	1
ENSG00000217702	ENSG00000217702	MGC10955	2:74361598-74362521	NOTEST	0	0	0	0	1	1
ENSG00000217707	ENSG00000217707	SERPINB8P1	6:3049068-3049445	NOTEST	0	0	0	0	1	1
ENSG00000217716	ENSG00000217716	RPS10P3	9:90631214-90631708	NOTEST	0.0919688	0	#NAME?	0	1	1
ENSG00000217718	ENSG00000217718	AC064847.4	2:26109832-26110075	NOTEST	0	0	0	0	1	1
ENSG00000217733	ENSG00000217733	CCT7P1	6:150139933-150244257	NOTEST	0	0	0	0	1	1
ENSG00000217746	ENSG00000217746	RP1-303A1.1	6:7727029-8102811	NOTEST	0	0	0	0	1	1
ENSG00000217767	ENSG00000217767	RP11-160A9.2	6:71377478-71666741	NOTEST	0.192452	0.164369	-0.227563	0	1	1
ENSG00000217769	ENSG00000217769	RP11-76H14.2	6:87606835-87607139	NOTEST	0	0.0793655	inf	0	1	1
ENSG00000217770	ENSG00000217770	FEM1AP3	6:112686905-112688646	NOTEST	0	0	0	0	1	1
ENSG00000217776	ENSG00000217776	RP11-156F23.2	6:87779873-87780179	NOTEST	0	0	0	0	1	1
ENSG00000217783	ENSG00000217783	LDHAL6FP	6:157710417-157744633	NOTEST	0	0	0	0	1	1
ENSG00000217786	ENSG00000217786	RP3-508D13.1	6:80036284-80036924	NOTEST	0	0	0	0	1	1
ENSG00000217791	ENSG00000217791	ASS1P9	5:53154995-53156231	NOTEST	0	0	0	0	1	1
ENSG00000217792	ENSG00000217792	KIR3DL2	GL000209.1:147648-156325	NOTEST	0	0	0	0	1	1
ENSG00000217805	ENSG00000217805	RP11-191A15.2	6:25181586-25181973	NOTEST	0	0	0	0	1	1
ENSG00000217809	ENSG00000217809	FAT1P1	20:10618331-10975572	NOTEST	0	0	0	0	1	1
ENSG00000217811	ENSG00000217811	HNRNPDP2	6:64345724-66417118	NOTEST	0	0	0	0	1	1
ENSG00000217824	ENSG00000217824	SNRPEP6	6:148888513-148888790	NOTEST	0	0	0	0	1	1
ENSG00000217825	ENSG00000217825	AC099552.4	7:154988272-154990165	NOTEST	0.025923	0.01831	-0.501605	0	1	1
ENSG00000217835	ENSG00000217835	RP6-159A1.2	X:65176130-65177038	NOTEST	0.0403067	0.0142108	-1.50403	0	1	1
ENSG00000217862	ENSG00000217862	HIST1H4PS1	6:27774852-27775117	NOTEST	0	0	0	0	1	1
ENSG00000217874	ENSG00000217874	OR4F7P	6:170948693-170949624	NOTEST	0	0	0	0	1	1
ENSG00000217878	ENSG00000217878	RP11-534P19.1	6:165530683-165531013	NOTEST	0	0	0	0	1	1
ENSG00000217889	ENSG00000217889	KRT18P48	X:152869951-152870803	NOTEST	0	0	0	0	1	1
ENSG00000217896	ENSG00000217896	ZNF839P1	Y:21034386-21239302	NOTEST	0	0	0	0	1	1
ENSG00000217897	ENSG00000217897	HSPE1P8	1:39546987-39952849	NOTEST	0	0	0	0	1	1
ENSG00000217929	ENSG00000217929	CICP18	6:131909-145083	NOTEST	0.0157891	0	#NAME?	0	1	1
ENSG00000217950	ENSG00000217950	AC073869.20	2:132200166-132202467	NOTEST	0.0167518	0.00588578	-1.50901	0	1	1
ENSG00000218014	ENSG00000218014	KRT19P1	6:72294423-72295609	NOTEST	0	0	0	0	1	1
ENSG00000218016	ENSG00000218016	ZNF192P2	6:28155827-28157210	NOTEST	0	0	0	0	1	1
ENSG00000218018	ENSG00000218018	RP4-800J21.3	20:55959215-55984389	NOTEST	0.12471	0.0367317	-1.76348	0	1	1
ENSG00000218020	ENSG00000218020	PRKRIRP5	6:11487458-11516699	NOTEST	0	0	0	0	1	1
ENSG00000218027	ENSG00000218027	RP11-157J24.1	6:1513932-1515524	NOTEST	0.0673456	0.0679847	0.013627	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000218029	ENSG00000218029	RP1-232L24.2	6:80064159-80064430	NOTEST	0	0	0	0	1	1
ENSG00000218048	ENSG00000218048	RP3-407E4.4	6:64150670-64153485	NOTEST	0	0	0	0	1	1
ENSG00000218049	ENSG00000218049	RPL31P33	6:53233467-53233807	NOTEST	0	0	0	0	1	1
ENSG00000218052	ENSG00000218052	ADAMTS7P4	15:85798599-85873565	NOTEST	0.0527487	0	#NAME?	0	1	1
ENSG00000218069	ENSG00000218069	RSL24D1P1	6:27748397-27748890	NOTEST	0.0860374	0.0327749	-1.39237	0	1	1
ENSG00000218073	ENSG00000218073	RP1-13D10.2	6:16161156-16161642	NOTEST	0.377204	0.137284	-1.45818	0	1	1
ENSG00000218089	ENSG00000218089	DNAJA1P4	6:114254191-114792869	NOTEST	0	0	0	0	1	1
ENSG00000218107	ENSG00000218107	RP1-261G23.4	6:43673685-43674488	NOTEST	0.0235024	0	#NAME?	0	1	1
ENSG00000218109	ENSG00000218109	KIRREL3-AS3	11:126225534-126875953	NOTEST	0	0	0	0	1	1
ENSG00000218125	ENSG00000218125	AP000567.27	21:31898863-31899019	NOTEST	0	0	0	0	1	1
ENSG00000218143	ENSG00000218143	ERHP2	6:53794779-54131078	NOTEST	0	0	0	0	1	1
ENSG00000218153	ENSG00000218153	KRT18P22	6:116778485-116779832	NOTEST	0	0	0	0	1	1
ENSG00000218173	ENSG00000218173	RP11-427E4.1	6:105135115-105135546	NOTEST	0	0	0	0	1	1
ENSG00000218180	ENSG00000218180	SLC25A5P7	6:121974940-121975836	NOTEST	0	0	0	0	1	1
ENSG00000218186	ENSG00000218186	KRT8P43	6:24544331-24646383	NOTEST	0	0	0	0	1	1
ENSG00000218187	ENSG00000218187	RP11-325O24.1	6:127976004-127976423	NOTEST	0	0	0	0	1	1
ENSG00000218189	ENSG00000218189	POM121L14P	6:58263735-58265293	NOTEST	0	0	0	0	1	1
ENSG00000218194	ENSG00000218194	HLFP1	6:132996023-132996522	NOTEST	0	0	0	0	1	1
ENSG00000218198	ENSG00000218198	RPS20P32	13:27591687-27592046	NOTEST	0	0	0	0	1	1
ENSG00000218213	ENSG00000218213	FTH1P26	6:133561735-134216691	NOTEST	0	0	0	0	1	1
ENSG00000218233	ENSG00000218233	NEPNP	6:117954868-117966250	NOTEST	0	0	0	0	1	1
ENSG00000218261	ENSG00000218261	RP11-96J19.1	6:53243300-53243659	NOTEST	0	0	0	0	1	1
ENSG00000218265	ENSG00000218265	RPS4XP7	6:13521497-13522277	NOTEST	0	0	0	0	1	1
ENSG00000218274	ENSG00000218274	RP3-407E4.3	6:64104911-64107011	NOTEST	0	0	0	0	1	1
ENSG00000218281	ENSG00000218281	HIST1H2APS3	6:26233349-26233483	NOTEST	0	0	0	0	1	1
ENSG00000218297	ENSG00000218297	OR2J4P	HSCHR6_MHC_QBL:29143288-29163375	NOTEST	0	0	0	0	1	1
ENSG00000218300	ENSG00000218300	RP11-63K6.4	6:90586262-90586597	NOTEST	0	0	0	0	1	1
ENSG00000218305	ENSG00000218305	AC006024.4	7:48959360-48965612	NOTEST	0	0.020963	inf	0	1	1
ENSG00000218313	ENSG00000218313	RP11-393I2.2	6:87860876-87973914	NOTEST	0	0.0136876	inf	0	1	1
ENSG00000218337	ENSG00000218337	RP4-724P12.1	6:49045348-49045688	NOTEST	0	0	0	0	1	1
ENSG00000218346	ENSG00000218346	VN1R14P	6:26630781-26632007	NOTEST	0	0	0	0	1	1
ENSG00000218347	ENSG00000218347	HNRNPA1P1	6:27490854-27492118	NOTEST	0	0	0	0	1	1
ENSG00000218350	ENSG00000218350	LYPLA1P3	6:71874778-71875473	NOTEST	0.30274	0.278935	-0.118149	0	1	1
ENSG00000218351	ENSG00000218351	RPS3AP23	6:141956786-141957640	NOTEST	0	0	0	0	1	1
ENSG00000218357	ENSG00000218357	LL22NC03-75H12.2	22:47857047-47882860	NOTEST	0	0	0	0	1	1
ENSG00000218358	ENSG00000218358	RAET1K	6:150319154-150326293	NOTEST	0.166976	0.201497	0.271118	0	1	1
ENSG00000218359	ENSG00000218359	SUMO2P13	6:17582264-17582536	NOTEST	0	0	0	0	1	1
ENSG00000218363	ENSG00000218363	SLC25A20P1	6:52111257-52112160	NOTEST	0	0	0	0	1	1
ENSG00000218410	ENSG00000218410	AC012078.2	Y:3719264-3720910	NOTEST	0	0	0	0	1	1
ENSG00000218416	ENSG00000218416	AC110619.2	2:241375087-241407493	NOTEST	0.0194948	0	#NAME?	0	1	1
ENSG00000218418	ENSG00000218418	RP11-296E7.1	6:80774002-80779916	NOTEST	0.241275	0.192568	-0.325308	0	1	1
ENSG00000218424	ENSG00000218424	NDUFS5P1	6:136663874-136873692	NOTEST	0	0	0	0	1	1
ENSG00000218428	ENSG00000218428	NIP7P3	6:116422011-116570660	NOTEST	0	0	0	0	1	1

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ENSG00000218454	ENSG00000218454	HNRNPA1P19	17:20674370-20674740	NOTEST	0	0	0	0	1	1
ENSG00000218459	ENSG00000218459	RPS27P15	6:74303101-74363878	NOTEST	0	0.13589	inf	0	1	1
ENSG00000218472	ENSG00000218472	RP1-140K8.2	6:3914155-3914526	NOTEST	0	0	0	0	1	1
ENSG00000218475	ENSG00000218475	RP11-93K7.1	6:101846663-102517958	NOTEST	0	0	0	0	1	1
ENSG00000218476	ENSG00000218476	RP11-108N13.1	6:23102907-23103774	NOTEST	0	0	0	0	1	1
ENSG00000218483	ENSG00000218483	RP11-554D15.2	6:74779166-75443995	NOTEST	0	0	0	0	1	1
ENSG00000218490	ENSG00000218490	FCF1P10	6:113332138-113332617	NOTEST	0	0	0	0	1	1
ENSG00000218497	ENSG00000218497	ZNF84	GL000223.1:42780-68787	NOTEST	0	0	0	0	1	1
ENSG00000218499	ENSG00000218499	RP3-422G23.3	6:138714509-138714681	NOTEST	0	0	0	0	1	1
ENSG00000218502	ENSG00000218502	H2AFZP3	13:99853027-100038688	NOTEST	0.137256	0.0490693	-1.48397	0	1	1
ENSG00000218512	ENSG00000218512	SPTLC1P2	6:23856925-23857046	NOTEST	0	0	0	0	1	1
ENSG00000218520	ENSG00000218520	RP11-184C23.4	6:63938991-63940015	NOTEST	0	0	0	0	1	1
ENSG00000218521	ENSG00000218521	RP11-420A21.1	6:37787274-38122400	NOTEST	0	0	0	0	1	1
ENSG00000218536	ENSG00000218536	AP002530.2	6:102526746-102527430	NOTEST	0	0	0	0	1	1
ENSG00000218549	ENSG00000218549	OR4K12P	21:14953364-14954325	NOTEST	0	0	0	0	1	1
ENSG00000218561	ENSG00000218561	RP1-253B10.1	6:87439425-87439826	NOTEST	0	0.14429	inf	0	1	1
ENSG00000218565	ENSG00000218565	RP11-12A2.1	6:139659154-139660717	NOTEST	0	0	0	0	1	1
ENSG00000218574	ENSG00000218574	HNRNPA1P37	6:5261276-5771813	NOTEST	0	0	0	0	1	1
ENSG00000218577	ENSG00000218577	RP3-416J7.1	6:167606-170631	NOTEST	0	0	0	0	1	1
ENSG00000218582	ENSG00000218582	GAPDHP63	6:80662721-80663728	NOTEST	0	0	0	0	1	1
ENSG00000218586	ENSG00000218586	RP4-791C19.1	7:55001391-55005877	NOTEST	0.0193064	0.0131234	-0.556942	0	1	1
ENSG00000218596	ENSG00000218596	RP11-2J18.1	6:157099062-157531913	NOTEST	0	0.0559728	inf	0	1	1
ENSG00000218617	ENSG00000218617	RP3-407E4.2	6:64102126-64102511	NOTEST	0	0	0	0	1	1
ENSG00000218631	ENSG00000218631	RP3-395C13.1	6:157793587-157794203	NOTEST	0	0	0	0	1	1
ENSG00000218632	ENSG00000218632	RPL7P28	6:109612230-109676266	NOTEST	0	0	0	0	1	1
ENSG00000218643	ENSG00000218643	RPL5P20	6:19348411-19349307	NOTEST	0	0	0	0	1	1
ENSG00000218672	ENSG00000218672	AC008060.7	7:155174770-155189051	NOTEST	0	0.0236539	inf	0	1	1
ENSG00000218676	ENSG00000218676	BRD7P4	6:111620233-111927481	NOTEST	0	0.0077309	inf	0	1	1
ENSG00000218682	ENSG00000218682	AC010150.1	2:25956621-26101385	NOTEST	0.171271	0.031488	-2.44341	0	1	1
ENSG00000218689	ENSG00000218689	RPL5P21	6:130077442-130078257	NOTEST	0	0	0	0	1	1
ENSG00000218690	ENSG00000218690	HIST1H2APS4	6:26272420-26272768	NOTEST	0	0	0	0	1	1
ENSG00000218698	ENSG00000218698	ST13P16	6:88117700-88222054	NOTEST	0	0	0	0	1	1
ENSG00000218713	ENSG00000218713	RP1-34L19.1	6:53071395-53073495	NOTEST	0	0	0	0	1	1
ENSG00000218716	ENSG00000218716	RPL12P23	6:170514992-170515482	NOTEST	0	0	0	0	1	1
ENSG00000218725	ENSG00000218725	RP11-174C7.2	6:130122052-130123359	NOTEST	0.122536	0.146759	0.260246	0	1	1
ENSG00000218728	ENSG00000218728	KRT18P44	X:127848483-127849768	NOTEST	0	0	0	0	1	1
ENSG00000218730	ENSG00000218730	RP3-453I5.2	6:90636247-91006627	NOTEST	0	0	0	0	1	1
ENSG00000218732	ENSG00000218732	RP5-1046G13.2	6:72596405-73112845	NOTEST	0	0	0	0	1	1
ENSG00000218748	ENSG00000218748	DBIP1	6:80146624-80146884	NOTEST	0	0	0	0	1	1
ENSG00000218749	ENSG00000218749	RP3-340B19.5	6:35541361-35696360	NOTEST	0	0	0	0	1	1
ENSG00000218754	ENSG00000218754	RPL18AP8	3:96338147-96338675	NOTEST	0	0	0	0	1	1
ENSG00000218757	ENSG00000218757	RP3-472M2.2	6:155054458-155635627	NOTEST	0	0	0	0	1	1

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ENSG00000218772	ENSG00000218772	FAM8A6P	6:134846451-134980974	NOTEST	0.158473	0.0838469	-0.918407	0	1	1
ENSG00000218776	ENSG00000218776	RP11-331O9.3	6:153987600-153989241	NOTEST	0	0	0	0	1	1
ENSG00000218792	ENSG00000218792	HSPD1P16	6:153019029-153045702	NOTEST	0	0	0	0	1	1
ENSG00000218793	ENSG00000218793	RP3-382I10.3	6:88117700-88222054	NOTEST	0	0	0	0	1	1
ENSG00000218803	ENSG00000218803	GSTM2P1	6:111368070-111368724	NOTEST	0.12302	0.336555	1.45195	0	1	1
ENSG00000218806	ENSG00000218806	RP3-369A17.2	6:24742529-24752149	NOTEST	0	0	0	0	1	1
ENSG00000218809	ENSG00000218809	RP1-229K20.5	6:41235663-41254457	NOTEST	0	0	0	0	1	1
ENSG00000218813	ENSG00000218813	RP11-59D5__B.3	6:64345724-66417118	NOTEST	0	0	0	0	1	1
ENSG00000218819	ENSG00000218819	TDRD15	2:21346788-21366144	NOTEST	0	0.0114273	inf	0	1	1
ENSG00000218823	ENSG00000218823	PAPOLB	7:4836685-4923350	NOTEST	0	0	0	0	1	1
ENSG00000218834	ENSG00000218834	RP11-361F19.1	6:69308095-69308285	NOTEST	0	0	0	0	1	1
ENSG00000218839	ENSG00000218839	FAM138C	9:34393-35856	NOTEST	0	0	0	0	1	1
ENSG00000218857	ENSG00000218857	RP1-209B5.2	6:131456805-131604675	NOTEST	0.0149874	0	#NAME?	0	1	1
ENSG00000218868	ENSG00000218868	CNN3P1	6:6346697-6655216	NOTEST	0	0	0	0	1	1
ENSG00000218870	ENSG00000218870	SLC25A6P6	6:71373204-71373982	NOTEST	0	0	0	0	1	1
ENSG00000218872	ENSG00000218872	RP11-249L21.2	6:109169618-109295186	NOTEST	0	0	0	0	1	1
ENSG00000218890	ENSG00000218890	NUFIP1P	6:66803323-66804802	NOTEST	0.0752985	0.0689868	-0.126302	0	1	1
ENSG00000218893	ENSG00000218893	SUMO2P12	6:12319684-12319824	NOTEST	0	0	0	0	1	1
ENSG00000218896	ENSG00000218896	TUBB8P2	6:143743968-143771810	NOTEST	0	0	0	0	1	1
ENSG00000218902	ENSG00000218902	PTMAP3	20:17922240-18039832	NOTEST	0	0	0	0	1	1
ENSG00000218965	ENSG00000218965	NACAP7	6:90131817-90132767	NOTEST	0	0	0	0	1	1
ENSG00000218976	ENSG00000218976	RP11-528A10.1	6:18366966-18469105	NOTEST	0.0236253	0	#NAME?	0	1	1
ENSG00000218986	ENSG00000218986	RP1-137F1.3	6:39297765-39693181	NOTEST	0.0582052	0	#NAME?	0	1	1
ENSG00000218991	ENSG00000218991	CCNG1P1	6:133002728-133035188	NOTEST	0	0	0	0	1	1
ENSG00000218996	ENSG00000218996	RP1-99E18.2	6:151186684-151549582	NOTEST	0	0.0245782	inf	0	1	1
ENSG00000219016	ENSG00000219016	CTA-299D3.8	22:48885271-49246724	NOTEST	0	0	0	0	1	1
ENSG00000219023	ENSG00000219023	RP3-340B19.2	6:35523649-35524041	NOTEST	0	0.267183	inf	0	1	1
ENSG00000219027	ENSG00000219027	RPS3AP2	16:1527830-1528584	NOTEST	0	0	0	0	1	1
ENSG00000219039	ENSG00000219039	AC005102.1	7:75464980-75465459	NOTEST	0	0	0	0	1	1
ENSG00000219041	ENSG00000219041	IGKV1OR2-118	2:91679086-91679734	NOTEST	0.125132	0	#NAME?	0	1	1
ENSG00000219061	ENSG00000219061	TRIM51FP	11:49854691-49860872	NOTEST	0	0.00976661	inf	0	1	1
ENSG00000219073	ENSG00000219073	CELA3B	1:22303513-22325135	NOTEST	0	0.0159099	inf	0	1	1
ENSG00000219074	ENSG00000219074	SOD1P1	6:53061517-53061957	NOTEST	0	0	0	0	1	1
ENSG00000219085	ENSG00000219085	NPM1P37	6:70385693-70507003	NOTEST	0.0211283	0.0807947	1.93509	0	1	1
ENSG00000219087	ENSG00000219087	RP3-433F14.2	6:92436876-92437223	NOTEST	0	0	0	0	1	1
ENSG00000219088	ENSG00000219088	RP3-359N14.1	6:106114200-106115873	NOTEST	0	0	0	0	1	1
ENSG00000219095	ENSG00000219095	RP11-323I14__A.1	6:55921387-56258892	NOTEST	0	0	0	0	1	1
ENSG00000219133	ENSG00000219133	RP11-203F10.6	1:204187978-204346793	NOTEST	0.136494	0.287577	1.07511	0	1	1
ENSG00000219135	ENSG00000219135	RP11-129H15.3	6:122001117-122001605	NOTEST	0	0	0	0	1	1
ENSG00000219139	ENSG00000219139	RP11-304C16.2	6:97101149-97102018	NOTEST	0	0	0	0	1	1

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ENSG00000219149	ENSG00000219149	RP11-214N16.2	9:79164197-79164687	NOTEST	0	0	0	0	1	1
ENSG00000219150	ENSG00000219150	RP11-569A2.2	6:110931180-111137161	NOTEST	0	0	0	0	1	1
ENSG00000219159	ENSG00000219159	AC011298.2	2:241625750-241629831	NOTEST	0	0	0	0	1	1
ENSG00000219163	ENSG00000219163	HMGB1P20	6:53100418-53101095	NOTEST	0	0	0	0	1	1
ENSG00000219186	ENSG00000219186	FTH1P19	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000219188	ENSG00000219188	CACYBPP3	6:158936636-158937261	NOTEST	0	0	0	0	1	1
ENSG00000219190	ENSG00000219190	RP1-253B10.2	6:87478239-87478650	NOTEST	0	0	0	0	1	1
ENSG00000219222	ENSG00000219222	RP11-480N24.3	6:43263431-43337216	NOTEST	0	0	0	0	1	1
ENSG00000219240	ENSG00000219240	RP11-63K6.5	6:90595874-90597567	NOTEST	0	0	0	0	1	1
ENSG00000219249	ENSG00000219249	AMZ2P2	6:159071045-159185908	NOTEST	0	0	0	0	1	1
ENSG00000219253	ENSG00000219253	RPS6P7	6:78205835-78206388	NOTEST	0	0	0	0	1	1
ENSG00000219257	ENSG00000219257	NPM1P38	6:100367785-100524289	NOTEST	0	0	0	0	1	1
ENSG00000219262	ENSG00000219262	OR2E1P	6:28423424-28423918	NOTEST	0	0	0	0	1	1
ENSG00000219273	ENSG00000219273	RP1-217P22.2	6:38683116-38998301	NOTEST	0	0	0	0	1	1
ENSG00000219274	ENSG00000219274	RPS20P2	16:1379078-1379778	NOTEST	0	0	0	0	1	1
ENSG00000219280	ENSG00000219280	VN1R8P	21:14815693-14861497	NOTEST	0	0	0	0	1	1
ENSG00000219284	ENSG00000219284	RP11-151M7.1	6:127954102-127956466	NOTEST	0	0	0	0	1	1
ENSG00000219294	ENSG00000219294	PIP5K1P1	6:7727029-8102811	NOTEST	0.0297127	0.00777219	-1.93469	0	1	1
ENSG00000219297	ENSG00000219297	MRPL42P3	6:144457586-144457912	NOTEST	0	0	0	0	1	1
ENSG00000219298	ENSG00000219298	RP11-472G23.3	6:150298606-150300241	NOTEST	0	0	0	0	1	1
ENSG00000219302	ENSG00000219302	RP11-174C7.3	6:130140781-130141315	NOTEST	0	0	0	0	1	1
ENSG00000219314	ENSG00000219314	RP1-273P12.1	6:17381597-17382351	NOTEST	0	0	0	0	1	1
ENSG00000219329	ENSG00000219329	RP11-397G5.2	6:111244768-111245310	NOTEST	0	0	0	0	1	1
ENSG00000219355	ENSG00000219355	RPL31P52	12:120875892-120899389	NOTEST	0.22661	0.0590189	-1.94096	0	1	1
ENSG00000219361	ENSG00000219361	RP11-250B2.2	6:81179787-81180145	NOTEST	0.0791103	0	#NAME?	0	1	1
ENSG00000219368	ENSG00000219368	ZNF299P	21:24437812-24503528	NOTEST	0	0	0	0	1	1
ENSG00000219374	ENSG00000219374	EEF1A1P42	6:49325858-49328093	NOTEST	0	0	0	0	1	1
ENSG00000219375	ENSG00000219375	RP11-69L16.3	6:7268538-7418270	NOTEST	0	0	0	0	1	1
ENSG00000219384	ENSG00000219384	RP11-491H9.3	6:44777053-45632086	NOTEST	0	0	0	0	1	1
ENSG00000219387	ENSG00000219387	ATF1P1	6:93596968-93598299	NOTEST	0	0	0	0	1	1
ENSG00000219391	ENSG00000219391	AC019129.1	2:44293032-44293293	NOTEST	0	0	0	0	1	1
ENSG00000219392	ENSG00000219392	RP1-265C24.5	6:28083405-28084329	NOTEST	0.154398	0.172155	0.157056	0	1	1
ENSG00000219395	ENSG00000219395	HSPA8P15	6:151725988-151773259	NOTEST	0.112731	0.200767	0.832631	0	1	1
ENSG00000219404	ENSG00000219404	RP11-524C21.1	6:21665002-22214734	NOTEST	0	0	0	0	1	1
ENSG00000219409	ENSG00000219409	RP11-106E7.1	6:144606836-145174170	NOTEST	0	0	0	0	1	1
ENSG00000219410	ENSG00000219410	RP4-761J14.8	12:6772425-6798738	NOTEST	0.202173	0.25777	0.350495	0	1	1
ENSG00000219430	ENSG00000219430	MBL3P	10:81342053-81344633	NOTEST	0	0	0	0	1	1
ENSG00000219433	ENSG00000219433	RP11-350J20.4	6:150045450-150132556	NOTEST	0.0541601	0	#NAME?	0	1	1
ENSG00000219435	ENSG00000219435	TEX40	11:64058773-64072242	NOTEST	0.0779035	0.105012	0.430796	0	1	1
ENSG00000219438	ENSG00000219438	FAM19A5	22:48885271-49246724	NOTEST	0	0	0	0	1	1
ENSG00000219445	ENSG00000219445	RP11-3B12.3	7:124462439-125019375	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000219451	ENSG00000219451	RPL23P8	7:20866944-20867372	NOTEST	0	0.172458	inf	0	1	1
ENSG00000219453	ENSG00000219453	RP4-810F7.1	6:23649723-23650002	NOTEST	0	0	0	0	1	1
ENSG00000219463	ENSG00000219463	RPSAP42	6:138316406-138317284	NOTEST	0	0	0	0	1	1
ENSG00000219470	ENSG00000219470	RP3-337H4.6	6:43474706-43543812	NOTEST	0.104495	0.534301	2.35421	0	1	1
ENSG00000219487	ENSG00000219487	RP11-365H23.1	6:149433144-149433808	NOTEST	0	0	0	0	1	1
ENSG00000219491	ENSG00000219491	TPT1P8	8:36641841-36793646	NOTEST	0	0	0	0	1	1
ENSG00000219492	ENSG00000219492	RP11-1396O13.13	4:9385742-9390709	NOTEST	0	0	0	0	1	1
ENSG00000219500	ENSG00000219500	RP11-15J23.1	6:87141961-87142387	NOTEST	0	0	0	0	1	1
ENSG00000219532	ENSG00000219532	RP3-323K23.3	6:132129155-132216295	NOTEST	0	0	0	0	1	1
ENSG00000219547	ENSG00000219547	RPL17P25	6:81083731-81084286	NOTEST	0	0	0	0	1	1
ENSG00000219549	ENSG00000219549	RP11-374I15.1	6:96077990-96080805	NOTEST	0	0	0	0	1	1
ENSG00000219553	ENSG00000219553	RP1-281H8.3	6:149812702-149813425	NOTEST	0	0	0	0	1	1
ENSG00000219559	ENSG00000219559	RP11-346C16.4	6:110883377-110883818	NOTEST	0	0	0	0	1	1
ENSG00000219565	ENSG00000219565	ZNF259P1	6:109103328-109108256	NOTEST	0	0	0	0	1	1
ENSG00000219575	ENSG00000219575	RP1-288M22.1	6:72260660-72261346	NOTEST	0	0	0	0	1	1
ENSG00000219582	ENSG00000219582	HNRNPA1P58	6:24002051-24002658	NOTEST	0	0	0	0	1	1
ENSG00000219592	ENSG00000219592	NCSTNP1	21:28864436-28864580	NOTEST	0	0	0	0	1	1
ENSG00000219604	ENSG00000219604	RP11-132M7.2	6:85397068-85474237	NOTEST	0	0	0	0	1	1
ENSG00000219607	ENSG00000219607	PPP1R3G	6:5085719-5087455	NOTEST	0.173841	0.214915	0.305994	0	1	1
ENSG00000219608	ENSG00000219608	HIGD1AP16	20:34359895-34538303	NOTEST	0	0	0	0	1	1
ENSG00000219619	ENSG00000219619	RP11-126M14.1	6:115679661-115679916	NOTEST	0	0	0	0	1	1
ENSG00000219622	ENSG00000219622	RP11-291C6.1	6:150825946-150831436	NOTEST	0	0	0	0	1	1
ENSG00000219627	ENSG00000219627	CYCSP17	6:95952057-95952372	NOTEST	0	0	0	0	1	1
ENSG00000219653	ENSG00000219653	GCNT1P4	6:64345724-66417118	NOTEST	0	0	0	0	1	1
ENSG00000219666	ENSG00000219666	RP11-174C7.1	6:130104913-130105190	NOTEST	0	0	0	0	1	1
ENSG00000219669	ENSG00000219669	RP1-20N4.1	6:71785266-71786078	NOTEST	0	0	0	0	1	1
ENSG00000219681	ENSG00000219681	RP11-191A15.4	6:25218915-25219297	NOTEST	0	0	0	0	1	1
ENSG00000219682	ENSG00000219682	RP3-425P12.4	6:25081547-25166793	NOTEST	0.516798	0.528871	0.0333156	0	1	1
ENSG00000219693	ENSG00000219693	RP11-262H14.11	9:66513031-66555928	NOTEST	0	0	0	0	1	1
ENSG00000219699	ENSG00000219699	RP11-325O24.2	6:127980568-127981724	NOTEST	0	0	0	0	1	1
ENSG00000219700	ENSG00000219700	PTCHD3P3	6:109609773-109611706	NOTEST	0	0	0	0	1	1
ENSG00000219702	ENSG00000219702	RP5-991C6.2	6:82473927-82474220	NOTEST	0	0	0	0	1	1
ENSG00000219703	ENSG00000219703	RP1-92C8.2	6:117609462-117923691	NOTEST	0	0	0	0	1	1
ENSG00000219712	ENSG00000219712	RP11-532F6.2	6:485132-693117	NOTEST	0.0255914	0	#NAME?	0	1	1
ENSG00000219722	ENSG00000219722	RPL26P20	6:76209420-76209852	NOTEST	0	0	0	0	1	1
ENSG00000219736	ENSG00000219736	RP11-560O20.1	6:75558792-75560200	NOTEST	0	0	0	0	1	1
ENSG00000219738	ENSG00000219738	XXbac-BPG34I8.3	6:27528600-27529523	NOTEST	0	0	0	0	1	1
ENSG00000219747	ENSG00000219747	RP1-292B18.1	6:151186684-151549582	NOTEST	0	0.153458	inf	0	1	1

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ENSG00000219757	ENSG00000219757	RP11-793L10.1	6:102901241-102901667	NOTEST	0	0	0	0	1	1
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ENSG00000219770	ENSG00000219770	VN1R11P	6:27051058-27051926	NOTEST	0	0	0	0	1	1
ENSG00000219773	ENSG00000219773	RP11-506B6.3	6:112677042-112677916	NOTEST	0	0.0775734	inf	0	1	1
ENSG00000219776	ENSG00000219776	RPL21P67	6:131790198-131790676	NOTEST	0	0	0	0	1	1
ENSG00000219784	ENSG00000219784	RP1-172I22.1	6:121799418-121801054	NOTEST	0	0	0	0	1	1
ENSG00000219790	ENSG00000219790	OSTCP6	6:56819772-56892140	NOTEST	0	0	0	0	1	1
ENSG00000219797	ENSG00000219797	PPIAP9	6:31487256-31488068	NOTEST	0	0	0	0	1	1
ENSG00000219806	ENSG00000219806	ATP5F1P6	6:139935574-139936341	NOTEST	0	0	0	0	1	1
ENSG00000219807	ENSG00000219807	ARF1P1	7:94463215-94463759	NOTEST	0	0	0	0	1	1
ENSG00000219814	ENSG00000219814	XX-C2158C6.2	6:171054605-171055065	NOTEST	0	0	0	0	1	1
ENSG00000219863	ENSG00000219863	RPL31P28	6:53219485-53219863	NOTEST	0	0	0	0	1	1
ENSG00000219867	ENSG00000219867	RP11-40G16.1	6:92525560-92526146	NOTEST	0	0	0	0	1	1
ENSG00000219870	ENSG00000219870	RP11-430A19.2	X:9147425-9147647	NOTEST	0	0	0	0	1	1
ENSG00000219881	ENSG00000219881	GAPDHP42	6:70385693-70507003	NOTEST	0.0518115	0.0285178	-0.861408	0	1	1
ENSG00000219891	ENSG00000219891	ZSCAN12P1	6:28058931-28061442	NOTEST	0.0781161	0.0988593	0.339757	0	1	1
ENSG00000219902	ENSG00000219902	RPL35P3	6:105725439-105850959	NOTEST	0	0	0	0	1	1
ENSG00000219926	ENSG00000219926	RP11-394A14.2	13:64402972-64418258	NOTEST	0.012543	0	#NAME?	0	1	1
ENSG00000219928	ENSG00000219928	RP11-40C6.2	9:90112142-90323548	NOTEST	0	0	0	0	1	1
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ENSG00000219932	ENSG00000219932	RPL12P8	10:69634089-69634672	NOTEST	0.222993	0	#NAME?	0	1	1
ENSG00000219940	ENSG00000219940	SPTLC1P3	6:63937389-63937648	NOTEST	0	0	0	0	1	1
ENSG00000219941	ENSG00000219941	KRT18P50	6:96438982-96440225	NOTEST	0	0	0	0	1	1
ENSG00000219951	ENSG00000219951	RP11-378G13.2	6:83920107-84140797	NOTEST	0	0.0435409	inf	0	1	1
ENSG00000219986	ENSG00000219986	BTF3P7	6:6795147-6795635	NOTEST	0	0	0	0	1	1
ENSG00000219992	ENSG00000219992	RP11-420L9.2	6:3754332-3755074	NOTEST	0	0	0	0	1	1
ENSG00000219993	ENSG00000219993	RP11-288G3.3	6:7506435-7506782	NOTEST	0	0	0	0	1	1
ENSG00000220008	ENSG00000220008	LINGO3	19:2289773-2308156	NOTEST	0	0	0	0	1	1
ENSG00000220030	ENSG00000220030	RP1-91N13.1	6:61996402-61996816	NOTEST	0	0	0	0	1	1
ENSG00000220032	ENSG00000220032	RP11-17M16.1	18:74207476-74210045	NOTEST	0.1173	0.200915	0.776385	0	1	1
ENSG00000220069	ENSG00000220069	RPL7P27	6:86796132-86796852	NOTEST	0	0	0	0	1	1
ENSG00000220076	ENSG00000220076	RP1-207H1.2	6:38683116-38998301	NOTEST	0	0	0	0	1	1
ENSG00000220091	ENSG00000220091	LAP3P1	6:83602116-83775560	NOTEST	0	0	0	0	1	1
ENSG00000220105	ENSG00000220105	RP11-307I14.2	9:4781474-4782078	NOTEST	0	0	0	0	1	1
ENSG00000220110	ENSG00000220110	RP1-6P5.2	6:128960332-128960798	NOTEST	0	0	0	0	1	1
ENSG00000220113	ENSG00000220113	MTCYBP4	6:133471706-133471955	NOTEST	0	0	0	0	1	1
ENSG00000220125	ENSG00000220125	MRPL32P1	X:48441480-48441727	NOTEST	0	0	0	0	1	1
ENSG00000220130	ENSG00000220130	RP1-72A23.3	6:89711266-89711533	NOTEST	0	0	0	0	1	1
ENSG00000220131	ENSG00000220131	RP4-570O12.2	6:88974876-88975230	NOTEST	0	0	0	0	1	1
ENSG00000220132	ENSG00000220132	AF238380.8	X:49676226-49676969	NOTEST	0	0	0	0	1	1
ENSG00000220139	ENSG00000220139	RP3-354N19.1	6:119480461-119480641	NOTEST	0	0	0	0	1	1
ENSG00000220154	ENSG00000220154	RP11-46B11.2	6:79987821-79988144	NOTEST	0	0	0	0	1	1

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ENSG00000220161	ENSG00000220161	RP1-37N7.3	17:18314472-18317694	NOTEST	0.0578705	0.0525286	-0.139725	0	1	1
ENSG00000220181	ENSG00000220181	RP11-486M3.2	6:154870650-154871376	NOTEST	0	0	0	0	1	1
ENSG00000220184	ENSG00000220184	HMGB3P18	6:122179324-122179914	NOTEST	0	0	0	0	1	1
ENSG00000220201	ENSG00000220201	ZGLP1	19:10415478-10444316	NOTEST	0.237404	0.100138	-1.24535	0	1	1
ENSG00000220204	ENSG00000220204	RP1-53C18.3	11:34426209-34426496	NOTEST	0	0	0	0	1	1
ENSG00000220212	ENSG00000220212	OR4F1P	6:105918-106856	NOTEST	0	0	0	0	1	1
ENSG00000220237	ENSG00000220237	RPS24P12	6:107473760-107780768	NOTEST	0	0.148886	inf	0	1	1
ENSG00000220240	ENSG00000220240	RP11-76H14.5	6:87607264-87607401	NOTEST	0	0	0	0	1	1
ENSG00000220248	ENSG00000220248	ZNF402P	22:17338508-17341608	NOTEST	0	0	0	0	1	1
ENSG00000220256	ENSG00000220256	AC093802.1	2:240684553-240724577	NOTEST	0	0	0	0	1	1
ENSG00000220267	ENSG00000220267	ACTBP8	6:88985600-88986708	NOTEST	0.0577633	0	#NAME?	0	1	1
ENSG00000220291	ENSG00000220291	RP3-455E7.1	6:85865384-85877467	NOTEST	0	0	0	0	1	1
ENSG00000220305	ENSG00000220305	HNRNPH1P1	6:160090088-160210781	NOTEST	0	0	0	0	1	1
ENSG00000220311	ENSG00000220311	RPL35AP18	6:80673931-80674236	NOTEST	0	0	0	0	1	1
ENSG00000220323	ENSG00000220323	HIST2H2BD	1:149814607-149815100	NOTEST	0.132164	0	#NAME?	0	1	1
ENSG00000220326	ENSG00000220326	RP11-129H15.1	6:121962154-121962367	NOTEST	0	0	0	0	1	1
ENSG00000220340	ENSG00000220340	RP3-433F14.1	6:92436876-92437223	NOTEST	0	0	0	0	1	1
ENSG00000220343	ENSG00000220343	RP11-440K22.1	3:166783552-166784113	NOTEST	0	0	0	0	1	1
ENSG00000220347	ENSG00000220347	RP11-230C9.1	6:156983183-156983571	NOTEST	0	0	0	0	1	1
ENSG00000220349	ENSG00000220349	RP3-431A14.4	6:36704826-36705763	NOTEST	0	0	0	0	1	1
ENSG00000220370	ENSG00000220370	RP3-399J4.2	6:95054454-95054680	NOTEST	0	0	0	0	1	1
ENSG00000220377	ENSG00000220377	RP1-152L7.3	6:52552727-52568623	NOTEST	0	0	0	0	1	1
ENSG00000220378	ENSG00000220378	KRT8P42	6:134490383-134639250	NOTEST	0.0483789	0.226956	2.22996	0	1	1
ENSG00000220379	ENSG00000220379	OR2J4P	HSCHR6_MHC_MCF:29149438-29150374	NOTEST	0	0	0	0	1	1
ENSG00000220391	ENSG00000220391	HCG4B	HSCHR6_MHC_QBL:29883749-29888221	NOTEST	0	0	0	0	1	1
ENSG00000220392	ENSG00000220392	FCF1P5	6:111620233-111927481	NOTEST	0	0	0	0	1	1
ENSG00000220412	ENSG00000220412	RP11-95M15.2	6:138026559-138028338	NOTEST	0.0813948	0.148134	0.863891	0	1	1
ENSG00000220418	ENSG00000220418	TUBB3P1	6:89966926-90025018	NOTEST	0	0	0	0	1	1
ENSG00000220446	ENSG00000220446	RP3-520B18.1	6:5261276-5771813	NOTEST	0	0	0	0	1	1
ENSG00000220447	ENSG00000220447	RP1-276J11.2	6:121702617-121703006	NOTEST	0	0	0	0	1	1
ENSG00000220472	ENSG00000220472	RP11-69L16.5	6:7268538-7418270	NOTEST	0.150783	0.0788959	-0.934452	0	1	1
ENSG00000220483	ENSG00000220483	SLC25A51P1	6:66498309-66499180	NOTEST	0	0	0	0	1	1
ENSG00000220494	ENSG00000220494	YAP1P1	6:147728024-147729417	NOTEST	0.0243074	0.0482014	0.987683	0	1	1
ENSG00000220505	ENSG00000220505	EIF4EBP2P3	6:98264584-98847748	NOTEST	0	0	0	0	1	1
ENSG00000220506	ENSG00000220506	RP3-415N12.1	6:111620233-111927481	NOTEST	0	0.0217536	inf	0	1	1
ENSG00000220514	ENSG00000220514	RP11-331O9.6	6:153989723-153989993	NOTEST	0	0	0	0	1	1
ENSG00000220515	ENSG00000220515	PGAM1P10	6:73331519-73908574	NOTEST	0	0.0177784	inf	0	1	1
ENSG00000220517	ENSG00000220517	ASS1P1	6:24797548-25057301	NOTEST	0	0	0	0	1	1
ENSG00000220522	ENSG00000220522	RP1-177A13.1	6:127737679-127738097	NOTEST	0	0	0	0	1	1
ENSG00000220537	ENSG00000220537	RP3-492P14.2	6:82973712-82974691	NOTEST	0	0	0	0	1	1
ENSG00000220540	ENSG00000220540	RP1-298M8.1	20:17168778-17168989	NOTEST	0	0	0	0	1	1
ENSG00000220541	ENSG00000220541	RP5-1170D6.1	X:112765752-112766265	NOTEST	0	0	0	0	1	1

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ENSG00000220550	ENSG00000220550	OR10C1	HSCHR6_MHC_QBL:29384950-29424735	NOTEST	0	0	0	0	1	1
ENSG00000220553	ENSG00000220553	RPL5P19	6:92723559-92724452	NOTEST	0	0	0	0	1	1
ENSG00000220556	ENSG00000220556	RP1-202I21.3	6:39007378-39007761	NOTEST	0	0	0	0	1	1
ENSG00000220557	ENSG00000220557	HMGB1P13	6:133189356-133189998	NOTEST	0	0	0	0	1	1
ENSG00000220563	ENSG00000220563	PKMP3	6:86369609-86370324	NOTEST	0.0546107	0.0424942	-0.361916	0	1	1
ENSG00000220575	ENSG00000220575	HTR5A-AS1	7:154858776-154877459	NOTEST	0	0	0	0	1	1
ENSG00000220581	ENSG00000220581	VN1R12P	6:27001213-27002089	NOTEST	0	0	0	0	1	1
ENSG00000220585	ENSG00000220585	DDX18P6	10:92806922-92821916	NOTEST	0	0	0	0	1	1
ENSG00000220586	ENSG00000220586	TUBBP9	6:39960553-39967972	NOTEST	0	0	0	0	1	1
ENSG00000220598	ENSG00000220598	SSR1P1	6:150690027-150727105	NOTEST	0	0	0	0	1	1
ENSG00000220600	ENSG00000220600	RP3-509I19.6	6:139117062-139309398	NOTEST	0	0	0	0	1	1
ENSG00000220614	ENSG00000220614	RP11-480N24.4	6:43263431-43337216	NOTEST	0	0	0	0	1	1
ENSG00000220635	ENSG00000220635	KRASP1	6:54635380-54635932	NOTEST	0	0	0	0	1	1
ENSG00000220643	ENSG00000220643	RP3-391O22.1	6:34555064-34665247	NOTEST	0	0	0	0	1	1
ENSG00000220660	ENSG00000220660	RP3-406A7.3	6:136663874-136873692	NOTEST	0	0	0	0	1	1
ENSG00000220666	ENSG00000220666	RCC2P7	6:56296747-56298011	NOTEST	0	0	0	0	1	1
ENSG00000220685	ENSG00000220685	RP11-530A18.1	6:5066028-5067216	NOTEST	0.187233	0.141484	-0.404195	0	1	1
ENSG00000220693	ENSG00000220693	AC011498.1	19:4472283-4517716	NOTEST	0	0.0062315	inf	0	1	1
ENSG00000220694	ENSG00000220694	RP3-403A15.1	6:127756780-127757334	NOTEST	0	0	0	0	1	1
ENSG00000220695	ENSG00000220695	RP1-121G13.3	6:100956069-101329248	NOTEST	0.0449857	0	#NAME?	0	1	1
ENSG00000220702	ENSG00000220702	RP1-32I10.10	22:44761430-44762164	NOTEST	0	0	0	0	1	1
ENSG00000220721	ENSG00000220721	OR1F12	6:28041093-28042011	NOTEST	0	0	0	0	1	1
ENSG00000220725	ENSG00000220725	RP11-228O6.2	6:55545439-55545819	NOTEST	0	0	0	0	1	1
ENSG00000220730	ENSG00000220730	RP11-474L11.3	6:76295837-76296177	NOTEST	0	0	0	0	1	1
ENSG00000220733	ENSG00000220733	RP11-331O9.5	6:153989311-153989497	NOTEST	0	0	0	0	1	1
ENSG00000220734	ENSG00000220734	RP3-510O8.3	6:35733684-35734704	NOTEST	0	0	0	0	1	1
ENSG00000220739	ENSG00000220739	RP11-277I20.3	6:144606836-145174170	NOTEST	0	0	0	0	1	1
ENSG00000220744	ENSG00000220744	RPL5P18	6:127683657-127684548	NOTEST	0	0.0290968	inf	0	1	1
ENSG00000220745	ENSG00000220745	RP1-101K10.4	6:153280493-153280740	NOTEST	0	0	0	0	1	1
ENSG00000220748	ENSG00000220748	RP1-59B16.1	6:23972106-23973169	NOTEST	0	0	0	0	1	1
ENSG00000220758	ENSG00000220758	VN1R10P	6:27292577-27293742	NOTEST	0	0	0	0	1	1
ENSG00000220771	ENSG00000220771	RP3-322L4.2	6:21602358-21602614	NOTEST	0	0	0	0	1	1
ENSG00000220773	ENSG00000220773	RP3-334F4.1	6:54489402-54490286	NOTEST	0	0	0	0	1	1
ENSG00000220793	ENSG00000220793	RPL21P119	16:9250218-9250761	NOTEST	0.0961224	0.187868	0.966777	0	1	1
ENSG00000220823	ENSG00000220823	AC018692.1	GL000193.1:92419-92496	NOTEST	0	0	0	0	1	1
ENSG00000220831	ENSG00000220831	NDUFA5P9	6:86923954-86924297	NOTEST	0	0	0	0	1	1
ENSG00000220867	ENSG00000220867	HSPE1P26	6:158244295-158366109	NOTEST	0.273613	0.317754	0.215774	0	1	1
ENSG00000220868	ENSG00000220868	MRPL35P1	6:13924676-13980533	NOTEST	0	0	0	0	1	1
ENSG00000220871	ENSG00000220871	DNAJC19P6	6:90352217-90529442	NOTEST	0	0	0	0	1	1
ENSG00000220875	ENSG00000220875	HIST1H3PS1	6:26322103-26322520	NOTEST	0.113725	0.134772	0.244963	0	1	1
ENSG00000220884	ENSG00000220884	MESTP1	6:129204341-129837714	NOTEST	0	0	0	0	1	1
ENSG00000220890	ENSG00000220890	HCG27	HSCHR6_MHC_QBL:31157982-31164195	NOTEST	0	0	0	0	1	1
ENSG00000220891	ENSG00000220891	LL22NC03-63E9.3	22:22890122-22909007	NOTEST	0.0344064	0.0263408	-0.385381	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000220903	ENSG00000220903	FRG2C	GL000222.1:86429-89304	NOTEST	0	0	0	0	1	1
ENSG00000220908	ENSG00000220908	RP11-127B16.1	6:93432720-93433547	NOTEST	0	0	0	0	1	1
ENSG00000220913	ENSG00000220913	RP11-235G24.2	6:161293919-161339681	NOTEST	0	0	0	0	1	1
ENSG00000220918	ENSG00000220918	RP1-92C4.1	6:80564400-80565349	NOTEST	0	0	0	0	1	1
ENSG00000220920	ENSG00000220920	RP3-525L6.2	6:17759413-17987854	NOTEST	0.150312	0.123075	-0.288426	0	1	1
ENSG00000220924	ENSG00000220924	OSTCP4	4:113606210-113606659	NOTEST	0	0	0	0	1	1
ENSG00000220925	ENSG00000220925	IGBP1-AS2	X:69353298-69386174	NOTEST	0	0	0	0	1	1
ENSG00000220937	ENSG00000220937	HNRNPA1P41	9:4944669-4945902	NOTEST	0	0	0	0	1	1
ENSG00000220948	ENSG00000220948	TRIM51GP	11:48997052-49003247	NOTEST	0.025194	0.0971374	1.94695	0	1	1
ENSG00000220949	ENSG00000220949	CTC-499B15.1	19:11867347-11870748	NOTEST	0	0	0	0	1	1
ENSG00000220960	ENSG00000220960	RP1-72A23.1	6:89769346-89769828	NOTEST	0	0	0	0	1	1
ENSG00000220981	ENSG00000220981	AL391384.1	13:73302060-73590591	NOTEST	0	0	0	0	1	1
ENSG00000220982	ENSG00000220982	AC009784.1	7:135777672-136122174	NOTEST	0	0	0	0	1	1
ENSG00000220984	ENSG00000220984	AC025674.1	8:58055247-58153100	NOTEST	0	0	0	0	1	1
ENSG00000220986	ENSG00000220986	SNORA50	5:68456632-68456766	NOTEST	0	0	0	0	1	1
ENSG00000220987	ENSG00000220987	AC084368.1	7:95749531-95951459	NOTEST	0	0	0	0	1	1
ENSG00000220988	ENSG00000220988	SNORD88C	19:51300960-51308186	NOTEST	0	0	0	0	1	1
ENSG00000220989	ENSG00000220989	AC063944.1	3:106959538-107101007	NOTEST	0	0	0	0	1	1
ENSG00000220990	ENSG00000220990	AL450423.1	13:53941979-53942091	NOTEST	0	0	0	0	1	1
ENSG00000220992	ENSG00000220992	AL158151.1	9:131992850-131992996	NOTEST	0	0	0	0	1	1
ENSG00000220993	ENSG00000220993	AC007611.1	16:48657346-48778553	NOTEST	0	0	0	0	1	1
ENSG00000220994	ENSG00000220994	AC011841.3	GL000205.1:152039-152122	NOTEST	0	0	0	0	1	1
ENSG00000220996	ENSG00000220996	AC034236.1	5:115298150-115395815	NOTEST	0	0	0	0	1	1
ENSG00000220997	ENSG00000220997	AL161651.1	10:30598729-30663377	NOTEST	0	0	0	0	1	1
ENSG00000220999	ENSG00000220999	AC012671.1	2:88762284-88762370	NOTEST	0	0	0	0	1	1
ENSG00000221000	ENSG00000221000	AC116165.1	15:22704720-22715604	NOTEST	0	0	0	0	1	1
ENSG00000221002	ENSG00000221002	AC022120.1	5:160657056-160657154	NOTEST	0	0	0	0	1	1
ENSG00000221003	ENSG00000221003	AC131254.1	8:29779028-29811240	NOTEST	0	0	0	0	1	1
ENSG00000221005	ENSG00000221005	AL161723.1	X:89045333-89045450	NOTEST	0	0	0	0	1	1
ENSG00000221007	ENSG00000221007	AL354984.1	20:56493939-56494091	NOTEST	0	0	0	0	1	1
ENSG00000221008	ENSG00000221008	AC136698.1	15:84867599-84898888	NOTEST	0	0	0	0	1	1
ENSG00000221010	ENSG00000221010	AL008708.1	X:102323792-102323914	NOTEST	0	0	0	0	1	1
ENSG00000221011	ENSG00000221011	AC079804.1	7:7034845-7034949	NOTEST	0	0	0	0	1	1
ENSG00000221015	ENSG00000221015	RNU6ATAC29P	3:51575159-51738339	NOTEST	0	0	0	0	1	1
ENSG00000221016	ENSG00000221016	AC002558.1	17:45195068-45266788	NOTEST	0	0	0	0	1	1
ENSG00000221017	ENSG00000221017	MIR1323	19:54175221-54175294	NOTEST	0	0	0	0	1	1
ENSG00000221018	ENSG00000221018	AC136365.1	8:39601253-39695808	NOTEST	0	0	0	0	1	1
ENSG00000221019	ENSG00000221019	AC127526.1	11:3490548-3602441	NOTEST	0	0	0	0	1	1
ENSG00000221020	ENSG00000221020	AC107993.1	17:40551026-40551109	NOTEST	0	0	0	0	1	1
ENSG00000221021	ENSG00000221021	AL035697.1	6:161768451-163736524	NOTEST	0	0	0	0	1	1
ENSG00000221023	ENSG00000221023	RNU6ATAC19P	2:182603332-182603442	NOTEST	0	0	0	0	1	1
ENSG00000221025	ENSG00000221025	MIR1250	17:79008947-79156964	NOTEST	0	0	0	0	1	1
ENSG00000221026	ENSG00000221026	AL592063.1	1:213783038-213783183	NOTEST	0	0	0	0	1	1
ENSG00000221027	ENSG00000221027	AC068020.1	8:7996349-7996453	NOTEST	0	0	0	0	1	1
ENSG00000221028	ENSG00000221028	MIR1231	1:201592012-201853422	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000221029	ENSG00000221029	AC016194.1	8:76698599-76698695	NOTEST	0	0	0	0	1	1
ENSG00000221030	ENSG00000221030	AC010930.1	11:4467871-4467957	NOTEST	0	0	0	0	1	1
ENSG00000221031	ENSG00000221031	CoTC_ribozyme	11:5245677-5245869	NOTEST	0	0	0	0	1	1
ENSG00000221032	ENSG00000221032	AL590683.1	1:24554406-24554520	NOTEST	0	0	0	0	1	1
ENSG00000221033	ENSG00000221033	MIR1272	15:65032090-65067786	NOTEST	0	0	0	0	1	1
ENSG00000221035	ENSG00000221035	MIR486	8:41510738-41754280	NOTEST	0	0	0	0	1	1
ENSG00000221036	ENSG00000221036	MIR1193	14:101496388-101496466	NOTEST	0	0	0	0	1	1
ENSG00000221037	ENSG00000221037	AC090099.1	11:18161732-18211168	NOTEST	0	0	0	0	1	1
ENSG00000221038	ENSG00000221038	RNU6ATAC7P	17:29890786-29890913	NOTEST	0	0	0	0	1	1
ENSG00000221039	ENSG00000221039	MIR1286	22:20228937-20270769	NOTEST	0	0	0	0	1	1
ENSG00000221040	ENSG00000221040	U3	1:116821227-116821442	NOTEST	0	0	0	0	1	1
ENSG00000221041	ENSG00000221041	AP001537.1	21:19933582-20132321	NOTEST	0	0	0	0	1	1
ENSG00000221042	ENSG00000221042	CPEB3_ribozyme	10:93806448-94050844	NOTEST	0	0	0	0	1	1
ENSG00000221043	ENSG00000221043	U3	5:149075311-149075522	NOTEST	0	0	0	0	1	1
ENSG00000221044	ENSG00000221044	U3	17:42102388-42102591	NOTEST	0	0	0	0	1	1
ENSG00000221046	ENSG00000221046	RNU6ATAC38P	20:44376582-44420571	NOTEST	0	0	0	0	1	1
ENSG00000221048	ENSG00000221048	AC079781.1	7:97535283-97535431	NOTEST	0	0	0	0	1	1
ENSG00000221050	ENSG00000221050	AC091304.1	15:28623766-28637170	NOTEST	0	0	0	0	1	1
ENSG00000221051	ENSG00000221051	AC118344.1	19:40697650-40721482	NOTEST	0	0	0	0	1	1
ENSG00000221052	ENSG00000221052	MIR1266	15:52408770-52587995	NOTEST	0	0	0	0	1	1
ENSG00000221053	ENSG00000221053	AC115286.1	1:34632483-34684732	NOTEST	0	0	0	0	1	1
ENSG00000221055	ENSG00000221055	MIR1302-3	2:114340535-114340673	NOTEST	0	0	0	0	1	1
ENSG00000221058	ENSG00000221058	AC090666.1	18:51612955-51613026	NOTEST	0	0	0	0	1	1
ENSG00000221059	ENSG00000221059	RNU6ATAC6P	3:87959369-87959495	NOTEST	0	0	0	0	1	1
ENSG00000221060	ENSG00000221060	SNORA11	14:70270919-70271048	NOTEST	0	0	0	0	1	1
ENSG00000221062	ENSG00000221062	MIR1292	20:2632790-2639039	NOTEST	0	0	0	0	1	1
ENSG00000221063	ENSG00000221063	MIR1296	10:64926980-65226323	NOTEST	0	0	0	0	1	1
ENSG00000221065	ENSG00000221065	MIR1233-2	15:34671268-34880704	NOTEST	0	0	0	0	1	1
ENSG00000221066	ENSG00000221066	SNORD111	16:70557690-70608820	NOTEST	0	0	0	0	1	1
ENSG00000221067	ENSG00000221067	MIR1280	3:127770483-128127485	NOTEST	0	0	0	0	1	1
ENSG00000221069	ENSG00000221069	AC000029.1	22:23401592-23487208	NOTEST	0	0	0	0	1	1
ENSG00000221070	ENSG00000221070	AC008625.1	5:153369687-153825410	NOTEST	0	0	0	0	1	1
ENSG00000221072	ENSG00000221072	AC124853.1	19:48401989-48402073	NOTEST	0	0	0	0	1	1
ENSG00000221073	ENSG00000221073	AC112198.2	5:54104037-54168379	NOTEST	0	0	0	0	1	1
ENSG00000221074	ENSG00000221074	AC078851.2	2:140584260-140584350	NOTEST	0	0	0	0	1	1
ENSG00000221075	ENSG00000221075	AC119751.1	4:49597626-49597709	NOTEST	0	0	0	0	1	1
ENSG00000221077	ENSG00000221077	AL117190.1	14:101361106-101402336	NOTEST	0	0	0	0	1	1
ENSG00000221079	ENSG00000221079	AC083829.1	4:89378267-89427314	NOTEST	0	0	0	0	1	1
ENSG00000221081	ENSG00000221081	MIR320D2	X:140008336-140008384	NOTEST	0	0	0	0	1	1
ENSG00000221082	ENSG00000221082	AC119751.2	4:49600631-49600714	NOTEST	0	0	0	0	1	1
ENSG00000221083	ENSG00000221083	SNORA77	1:8412456-8877702	NOTEST	0	0	0	0	1	1
ENSG00000221084	ENSG00000221084	AP000547.1	22:17079606-17079694	NOTEST	0	0	0	0	1	1
ENSG00000221085	ENSG00000221085	AC096664.3	2:63348517-64054977	NOTEST	0	0	0	0	1	1
ENSG00000221087	ENSG00000221087	AC096546.1	2:73612885-73837920	NOTEST	0	0	0	0	1	1
ENSG00000221091	ENSG00000221091	MIR1302-5	20:49202644-49308065	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000221093	ENSG00000221093	SNORA3	8:57033800-57033911	NOTEST	0	0	0	0	1	1
ENSG00000221094	ENSG00000221094	AL671972.1	10:63875973-63876060	NOTEST	0	0	0	0	1	1
ENSG00000221095	ENSG00000221095	AC135995.1	15:82751613-82798350	NOTEST	0	0	0	0	1	1
ENSG00000221096	ENSG00000221096	AC092757.1	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000221100	ENSG00000221100	AL138706.1	13:37523911-37633850	NOTEST	0	0	0	0	1	1
ENSG00000221101	ENSG00000221101	AL391417.1	6:87183204-87183313	NOTEST	0	0	0	0	1	1
ENSG00000221102	ENSG00000221102	SNORA11B	14:91336798-91691976	NOTEST	0	0	0	0	1	1
ENSG00000221104	ENSG00000221104	AC092865.1	12:8407122-8549399	NOTEST	0	0	0	0	1	1
ENSG00000221105	ENSG00000221105	AL159997.1	9:135037333-135119921	NOTEST	0	0	0	0	1	1
ENSG00000221108	ENSG00000221108	AL845259.1	10:135470738-135474139	NOTEST	0	0	0	0	1	1
ENSG00000221110	ENSG00000221110	AL449083.1	9:75906035-75906143	NOTEST	0	0	0	0	1	1
ENSG00000221111	ENSG00000221111	AL590726.2	9:30771094-30771197	NOTEST	0	0	0	0	1	1
ENSG00000221112	ENSG00000221112	AP000908.1	11:113930314-114227293	NOTEST	0	0	0	0	1	1
ENSG00000221113	ENSG00000221113	AC104133.1	7:155664584-155664701	NOTEST	0	0	0	0	1	1
ENSG00000221114	ENSG00000221114	RNU6ATAC30P	14:50110272-50155140	NOTEST	0	0	0	0	1	1
ENSG00000221115	ENSG00000221115	AC020910.1	19:35213328-35213429	NOTEST	0	0	0	0	1	1
ENSG00000221116	ENSG00000221116	SNORD110	20:2632790-2639039	NOTEST	0	0	0	0	1	1
ENSG00000221118	ENSG00000221118	AC112249.1	4:77356252-77723117	NOTEST	0	0	0	0	1	1
ENSG00000221120	ENSG00000221120	MIR1224	3:183851806-184402546	NOTEST	0	0	0	0	1	1
ENSG00000221121	ENSG00000221121	AC083811.1	12:82617459-82873015	NOTEST	0	0	0	0	1	1
ENSG00000221122	ENSG00000221122	AC098869.1	4:40425271-40632892	NOTEST	0	0	0	0	1	1
ENSG00000221123	ENSG00000221123	AC104417.1	8:143026859-143026986	NOTEST	0	0	0	0	1	1
ENSG00000221125	ENSG00000221125	U3	19:50392910-50464429	NOTEST	0	0	0	0	1	1
ENSG00000221126	ENSG00000221126	AC092265.1	1:30117391-30117525	NOTEST	0	0	0	0	1	1
ENSG00000221128	ENSG00000221128	AC007450.1	12:11694328-11743303	NOTEST	0	0	0	0	1	1
ENSG00000221130	ENSG00000221130	AP001482.1	11:88845877-88845992	NOTEST	0	0	0	0	1	1
ENSG00000221131	ENSG00000221131	AC008410.1	5:154404273-154404360	NOTEST	0	0	0	0	1	1
ENSG00000221132	ENSG00000221132	AL035422.1	X:100673274-100788446	NOTEST	0	0	0	0	1	1
ENSG00000221134	ENSG00000221134	AC007339.1	16:49521434-49891830	NOTEST	0	0	0	0	1	1
ENSG00000221135	ENSG00000221135	AC021078.1	5:148931509-149014531	NOTEST	0	0	0	0	1	1
ENSG00000221136	ENSG00000221136	AC131094.1	4:176394152-176394259	NOTEST	0	0	0	0	1	1
ENSG00000221137	ENSG00000221137	AC013751.1	8:87345502-87777251	NOTEST	0	0	0	0	1	1
ENSG00000221139	ENSG00000221139	SNORD23	18:18822202-19105378	NOTEST	0	0	0	0	1	1
ENSG00000221141	ENSG00000221141	AC126323.1	15:62520094-62545434	NOTEST	0	0	0	0	1	1
ENSG00000221142	ENSG00000221142	AC104405.1	2:133174146-133429152	NOTEST	0	0	0	0	1	1
ENSG00000221145	ENSG00000221145	AL136987.1	1:192460257-192460350	NOTEST	0	0	0	0	1	1
ENSG00000221147	ENSG00000221147	MIR1270-2	19:20451077-20607775	NOTEST	0	0	0	0	1	1
ENSG00000221148	ENSG00000221148	SNORA3	12:84577102-84577227	NOTEST	0	0	0	0	1	1
ENSG00000221156	ENSG00000221156	AC007551.1	7:35840541-35944917	NOTEST	0	0	0	0	1	1
ENSG00000221157	ENSG00000221157	AC009196.1	7:36893960-37488852	NOTEST	0	0	0	0	1	1
ENSG00000221159	ENSG00000221159	AL356741.1	10:69681664-69835105	NOTEST	0	0	0	0	1	1
ENSG00000221160	ENSG00000221160	MIR1281	22:41487789-41593460	NOTEST	0	0	0	0	1	1
ENSG00000221163	ENSG00000221163	AL138963.1	13:45874148-45874235	NOTEST	0	0	0	0	1	1
ENSG00000221164	ENSG00000221164	SNORA11	10:74870216-75118617	NOTEST	0	4.52997	inf	0	1	1
ENSG00000221165	ENSG00000221165	AL359983.1	1:245318286-245872733	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000221167	ENSG00000221167	AC008397.1	19:18520503-18520592	NOTEST	0	0	0	0	1	1
ENSG00000221169	ENSG00000221169	AC013444.2	2:143635066-143799890	NOTEST	0	0	0	0	1	1
ENSG00000221170	ENSG00000221170	MIR1304	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000221172	ENSG00000221172	AC091096.1	8:93577670-93667722	NOTEST	0	0	0	0	1	1
ENSG00000221173	ENSG00000221173	AL161908.1	9:129338808-129338909	NOTEST	0	0	0	0	1	1
ENSG00000221174	ENSG00000221174	AL050327.1	20:57090434-57194944	NOTEST	0	0	0	0	1	1
ENSG00000221175	ENSG00000221175	AL391538.1	6:48817559-48817639	NOTEST	0	0	0	0	1	1
ENSG00000221176	ENSG00000221176	MIR1207	8:128806778-129113499	NOTEST	0	0	0	0	1	1
ENSG00000221177	ENSG00000221177	AC126339.1	15:82944772-82988374	NOTEST	0	0	0	0	1	1
ENSG00000221178	ENSG00000221178	AC008045.1	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000221179	ENSG00000221179	AC016670.1	2:79384131-80875905	NOTEST	0	0	0	0	1	1
ENSG00000221180	ENSG00000221180	AB019440.1	14:106663245-106665214	NOTEST	0	0	0	0	1	1
ENSG00000221181	ENSG00000221181	AC078899.5	19:20451077-20607775	NOTEST	0	0	0	0	1	1
ENSG00000221182	ENSG00000221182	SNORD98	10:70480768-70552134	NOTEST	0	0	0	0	1	1
ENSG00000221183	ENSG00000221183	AC093897.1	4:78978723-79465423	NOTEST	0	0	0	0	1	1
ENSG00000221184	ENSG00000221184	MIR1254-1	10:70480768-70552134	NOTEST	0	0	0	0	1	1
ENSG00000221185	ENSG00000221185	AC103816.1	8:85095021-85834079	NOTEST	0	0	0	0	1	1
ENSG00000221186	ENSG00000221186	AC114798.1	4:183747380-183747518	NOTEST	0	0	0	0	1	1
ENSG00000221187	ENSG00000221187	MIR548M	X:94318139-94318225	NOTEST	0	0	0	0	1	1
ENSG00000221189	ENSG00000221189	AC108211.1	4:157217712-157217798	NOTEST	0	0	0	0	1	1
ENSG00000221190	ENSG00000221190	MIR1184-3	X:154611748-154613449	NOTEST	0	0	0	0	1	1
ENSG00000221191	ENSG00000221191	AL662890.1	6:28743692-28743800	NOTEST	0	0	0	0	1	1
ENSG00000221192	ENSG00000221192	AC004745.1	7:96920825-96920908	NOTEST	0	0	0	0	1	1
ENSG00000221195	ENSG00000221195	AC008780.1	5:56938721-56938813	NOTEST	0	0	0	0	1	1
ENSG00000221198	ENSG00000221198	AL138696.1	13:50601268-51423190	NOTEST	0	0	0	0	1	1
ENSG00000221199	ENSG00000221199	AC114765.3	2:220970376-221569286	NOTEST	0	0	0	0	1	1
ENSG00000221200	ENSG00000221200	MIR1253	17:2627713-2652714	NOTEST	0	0	0	0	1	1
ENSG00000221201	ENSG00000221201	AL031655.1	20:8112823-8949003	NOTEST	0	0	0	0	1	1
ENSG00000221202	ENSG00000221202	AC012050.1	15:47476297-48066420	NOTEST	0	0	0	0	1	1
ENSG00000221203	ENSG00000221203	MIR1262	1:68167148-68698803	NOTEST	0	0	0	0	1	1
ENSG00000221204	ENSG00000221204	AC106795.1	5:177236407-177410055	NOTEST	0	0	0	0	1	1
ENSG00000221206	ENSG00000221206	RNU6ATAC15P	3:110270691-110270812	NOTEST	0	0	0	0	1	1
ENSG00000221210	ENSG00000221210	AP001137.1	21:22370632-22915650	NOTEST	0	0	0	0	1	1
ENSG00000221211	ENSG00000221211	AC078794.1	3:122628040-122747452	NOTEST	0	0	0	0	1	1
ENSG00000221214	ENSG00000221214	MIR548E	10:112679300-112773425	NOTEST	0	0	0	0	1	1
ENSG00000221216	ENSG00000221216	RNU6ATAC27P	1:28696113-28826881	NOTEST	0	0	0	0	1	1
ENSG00000221217	ENSG00000221217	AL359851.1	X:121002719-121002809	NOTEST	0	0	0	0	1	1
ENSG00000221218	ENSG00000221218	AC009997.1	15:56053214-56053300	NOTEST	0	0	0	0	1	1
ENSG00000221219	ENSG00000221219	AC110298.1	4:54243809-55164414	NOTEST	0	0	0	0	1	1
ENSG00000221220	ENSG00000221220	AL035045.1	20:17823226-17823372	NOTEST	0	0	0	0	1	1
ENSG00000221221	ENSG00000221221	AL139815.1	10:23363311-23363407	NOTEST	0	0	0	0	1	1
ENSG00000221222	ENSG00000221222	AL139139.1	1:87380330-87634884	NOTEST	0	0	0	0	1	1
ENSG00000221225	ENSG00000221225	AL138837.1	1:33907625-33907712	NOTEST	0	0	0	0	1	1
ENSG00000221226	ENSG00000221226	AC092724.1	16:77744197-77744281	NOTEST	0	0	0	0	1	1
ENSG00000221227	ENSG00000221227	MIR1305	4:182795590-183724177	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000221230	ENSG00000221230	MIR548L	11:94152894-94232749	NOTEST	0	0	0	0	1	1
ENSG00000221232	ENSG00000221232	AC012047.1	10:77360997-78320752	NOTEST	0	0	0	0	1	1
ENSG00000221233	ENSG00000221233	AC007842.1	19:40490040-40523514	NOTEST	0	0	0	0	1	1
ENSG00000221234	ENSG00000221234	AC009495.1	2:166651360-166702601	NOTEST	0	0	0	0	1	1
ENSG00000221235	ENSG00000221235	AC110813.1	4:151185593-151936879	NOTEST	0	0	0	0	1	1
ENSG00000221236	ENSG00000221236	AL137190.1	14:96603187-96603280	NOTEST	0	0	0	0	1	1
ENSG00000221237	ENSG00000221237	AC106736.1	16:71365091-71365202	NOTEST	0	0	0	0	1	1
ENSG00000221238	ENSG00000221238	MIR1285-2	2:70480049-70480137	NOTEST	0	0	0	0	1	1
ENSG00000221240	ENSG00000221240	MIR1258	2:180306708-180726232	NOTEST	0	0	0	0	1	1
ENSG00000221241	ENSG00000221241	SNORD88A	19:51300960-51308186	NOTEST	0	0	0	0	1	1
ENSG00000221244	ENSG00000221244	AC116351.2	5:1004301-1004392	NOTEST	0	0	0	0	1	1
ENSG00000221245	ENSG00000221245	SNORA11	4:120375945-120550146	NOTEST	0	0	0	0	1	1
ENSG00000221246	ENSG00000221246	AC144522.1	12:111051831-111142755	NOTEST	0	0	0	0	1	1
ENSG00000221247	ENSG00000221247	AC136704.1	15:84944426-84950601	NOTEST	0	0	0	0	1	1
ENSG00000221249	ENSG00000221249	AC004980.1	7:76139744-77045717	NOTEST	0	0	0	0	1	1
ENSG00000221250	ENSG00000221250	AC120045.1	15:30375157-30385702	NOTEST	0	0	0	0	1	1
ENSG00000221251	ENSG00000221251	MIR1263	3:163889258-163889344	NOTEST	0	0	0	0	1	1
ENSG00000221252	ENSG00000221252	U3	6:42192668-42419789	NOTEST	0	0	0	0	1	1
ENSG00000221254	ENSG00000221254	AL163952.2	14:56542197-56542284	NOTEST	0	0	0	0	1	1
ENSG00000221255	ENSG00000221255	RNU6ATAC37P	2:7716971-7717102	NOTEST	0	0	0	0	1	1
ENSG00000221257	ENSG00000221257	AC012175.1	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000221258	ENSG00000221258	AC011465.1	19:38397867-38699012	NOTEST	0	0	0	0	1	1
ENSG00000221259	ENSG00000221259	AC002978.1	12:111471827-111788358	NOTEST	0	0	0	0	1	1
ENSG00000221260	ENSG00000221260	AC083810.1	12:82617459-82873015	NOTEST	0	0	0	0	1	1
ENSG00000221261	ENSG00000221261	MIR1208	8:129162361-129162434	NOTEST	0	0	0	0	1	1
ENSG00000221262	ENSG00000221262	AC005159.1	7:81575759-82073114	NOTEST	0	0	0	0	1	1
ENSG00000221263	ENSG00000221263	MIR548P	5:100142638-100238970	NOTEST	0	0	0	0	1	1
ENSG00000221264	ENSG00000221264	MIR1284	3:71003843-71633140	NOTEST	0	0	0	0	1	1
ENSG00000221265	ENSG00000221265	MIR1255A	4:101944565-102270040	NOTEST	0	0	0	0	1	1
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ENSG00000221267	ENSG00000221267	MIR1236	6:31919863-31937532	NOTEST	0	0	0	0	1	1
ENSG00000221269	ENSG00000221269	MIR1302-8	9:99918851-100140806	NOTEST	0	0	0	0	1	1
ENSG00000221270	ENSG00000221270	AC130888.1	3:129902365-129902466	NOTEST	0	0	0	0	1	1
ENSG00000221272	ENSG00000221272	AC067742.1	10:63661058-63856703	NOTEST	0	0	0	0	1	1
ENSG00000221273	ENSG00000221273	MIR1237	11:64126619-64139687	NOTEST	0	0	0	0	1	1
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ENSG00000221278	ENSG00000221278	AC003658.1	X:14783096-14783239	NOTEST	0	0	0	0	1	1
ENSG00000221279	ENSG00000221279	AC005161.1	7:110303109-111202573	NOTEST	0	0	0	0	1	1
ENSG00000221280	ENSG00000221280	AC026366.1	12:118587605-118810750	NOTEST	0	0	0	0	1	1
ENSG00000221281	ENSG00000221281	AC002485.1	6:67069317-67069392	NOTEST	0	0	0	0	1	1
ENSG00000221286	ENSG00000221286	AC092289.1	16:72459383-72698908	NOTEST	0	0	0	0	1	1
ENSG00000221287	ENSG00000221287	MIR1289-2	5:132496129-132948255	NOTEST	0	0	0	0	1	1
ENSG00000221288	ENSG00000221288	MIR663B	2:132905163-133015542	NOTEST	0	0	0	0	1	1
ENSG00000221289	ENSG00000221289	AC013406.1	2:148224197-148224282	NOTEST	0	0	0	0	1	1
ENSG00000221290	ENSG00000221290	MIR1182	1:231154703-231175992	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000221291	ENSG00000221291	AC090660.1	18:49866541-51094653	NOTEST	0	0	0	0	1	1
ENSG00000221293	ENSG00000221293	AC009987.1	10:125465722-125699783	NOTEST	0	0	0	0	1	1
ENSG00000221294	ENSG00000221294	AL021394.1	20:46130600-46415360	NOTEST	0	0	0	0	1	1
ENSG00000221295	ENSG00000221295	AC134698.1	8:43415810-43415916	NOTEST	0	0	0	0	1	1
ENSG00000221296	ENSG00000221296	MIR548T	4:174053078-174250845	NOTEST	0	0	0	0	1	1
ENSG00000221297	ENSG00000221297	AL590708.1	9:131018107-131051269	NOTEST	0	0	0	0	1	1
ENSG00000221299	ENSG00000221299	Z83826.1	X:134021655-134049297	NOTEST	0	0	0	0	1	1
ENSG00000221300	ENSG00000221300	SNORD75	2:42667516-42667576	NOTEST	0	0	0	0	1	1
ENSG00000221301	ENSG00000221301	AC116562.1	4:4086060-4086208	NOTEST	0	0	0	0	1	1
ENSG00000221302	ENSG00000221302	AC018628.1	17:60019965-60142643	NOTEST	0	0	0	0	1	1
ENSG00000221303	ENSG00000221303	SNORA79	14:81641795-81687721	NOTEST	0	0	0	0	1	1
ENSG00000221304	ENSG00000221304	AC068706.1	2:177248154-177248304	NOTEST	0	0	0	0	1	1
ENSG00000221305	ENSG00000221305	MIR548I3	8:7946462-7946611	NOTEST	0	0	0	0	1	1
ENSG00000221307	ENSG00000221307	AC092745.1	12:8407122-8549399	NOTEST	0	0	0	0	1	1
ENSG00000221309	ENSG00000221309	AC091167.1	15:90835193-90838915	NOTEST	0	0	0	0	1	1
ENSG00000221310	ENSG00000221310	AC008967.1	5:110831730-111353006	NOTEST	0	0	0	0	1	1
ENSG00000221312	ENSG00000221312	AL109922.1	6:64345724-66417118	NOTEST	0	0	0	0	1	1
ENSG00000221313	ENSG00000221313	AC010207.1	3:134128885-134128982	NOTEST	0	0	0	0	1	1
ENSG00000221314	ENSG00000221314	AC093700.1	4:159690289-159959912	NOTEST	0	0	0	0	1	1
ENSG00000221316	ENSG00000221316	AL445204.1	13:107773380-107773471	NOTEST	0	0	0	0	1	1
ENSG00000221317	ENSG00000221317	AL513487.1	X:121605577-121605671	NOTEST	0	0	0	0	1	1
ENSG00000221318	ENSG00000221318	AC135983.1	15:32737306-32747835	NOTEST	0	0	0	0	1	1
ENSG00000221319	ENSG00000221319	AL441988.1	20:29637161-29637300	NOTEST	0	0	0	0	1	1
ENSG00000221320	ENSG00000221320	AC023385.1	8:9911777-10286401	NOTEST	0	0	0	0	1	1
ENSG00000221321	ENSG00000221321	AC016764.1	2:121792648-121792794	NOTEST	0	0	0	0	1	1
ENSG00000221322	ENSG00000221322	AC116533.1	11:17095498-17095582	NOTEST	0	0	0	0	1	1
ENSG00000221323	ENSG00000221323	MIR1178	12:120123594-120315095	NOTEST	0	0	0	0	1	1
ENSG00000221324	ENSG00000221324	AL590787.1	13:25802306-25862147	NOTEST	0	0	0	0	1	1
ENSG00000221325	ENSG00000221325	MIR1200	7:36893960-37488852	NOTEST	0	0	0	0	1	1
ENSG00000221326	ENSG00000221326	AL121652.1	2:32090128-32264881	NOTEST	0	0	0	0	1	1
ENSG00000221328	ENSG00000221328	AL117333.1	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000221330	ENSG00000221330	AC009159.1	16:79703551-79703634	NOTEST	0	0	0	0	1	1
ENSG00000221331	ENSG00000221331	MIR548Q	10:12391480-12877545	NOTEST	0	0	0	0	1	1
ENSG00000221332	ENSG00000221332	U3	6:75994729-76203454	NOTEST	0	0	0	0	1	1
ENSG00000221333	ENSG00000221333	MIR548K	11:70116805-70282690	NOTEST	0	0	0	0	1	1
ENSG00000221334	ENSG00000221334	AC119751.3	4:49600439-49600522	NOTEST	0	0	0	0	1	1
ENSG00000221335	ENSG00000221335	AP000745.1	21:19264027-19264116	NOTEST	0	0	0	0	1	1
ENSG00000221336	ENSG00000221336	AL356137.1	6:140981759-140981850	NOTEST	0	0	0	0	1	1
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ENSG00000221340	ENSG00000221340	RNU6ATAC18P	1:12627938-12677737	NOTEST	0	0	0	0	1	1
ENSG00000221343	ENSG00000221343	AC010422.1	19:12490002-12750912	NOTEST	0	0	0	0	1	1
ENSG00000221344	ENSG00000221344	AC068946.1	2:220074489-220094439	NOTEST	0	0	0	0	1	1
ENSG00000221345	ENSG00000221345	U3	6:71836596-71836808	NOTEST	0	0	0	0	1	1
ENSG00000221346	ENSG00000221346	AL356458.1	1:47968175-47968311	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000221347	ENSG00000221347	AC096649.4	2:176121977-176319368	NOTEST	0	0	0	0	1	1
ENSG00000221348	ENSG00000221348	MIR548F5	X:31115793-33357558	NOTEST	0	0	0	0	1	1
ENSG00000221351	ENSG00000221351	AC068570.1	8:129832039-129832124	NOTEST	0	0	0	0	1	1
ENSG00000221352	ENSG00000221352	AL356214.1	10:95368342-95368456	NOTEST	0	0	0	0	1	1
ENSG00000221354	ENSG00000221354	AC131280.1	15:20767699-20781019	NOTEST	0	0	0	0	1	1
ENSG00000221355	ENSG00000221355	MIR1288	17:15879873-16256970	NOTEST	0	0	0	0	1	1
ENSG00000221356	ENSG00000221356	AC004492.1	7:106809405-107218906	NOTEST	0	0	0	0	1	1
ENSG00000221357	ENSG00000221357	AC104387.1	11:40135752-41481323	NOTEST	0	0	0	0	1	1
ENSG00000221358	ENSG00000221358	AC026150.1	15:30896328-30906764	NOTEST	0	0	0	0	1	1
ENSG00000221359	ENSG00000221359	AL355512.1	10:112188597-112255962	NOTEST	0	0	0	0	1	1
ENSG00000221362	ENSG00000221362	AC106860.1	4:161925028-161925110	NOTEST	0	0	0	0	1	1
ENSG00000221363	ENSG00000221363	RNU6ATAC20P	18:19710563-19710690	NOTEST	0	0	0	0	1	1
ENSG00000221365	ENSG00000221365	MIR1228	12:57482676-57607134	NOTEST	0	0	0	0	1	1
ENSG00000221366	ENSG00000221366	MIR1306	22:20067754-20114878	NOTEST	0	0	0	0	1	1
ENSG00000221369	ENSG00000221369	MIR548G	4:148265780-148265869	NOTEST	0	0	0	0	1	1
ENSG00000221371	ENSG00000221371	MIR1265	10:13628926-14504141	NOTEST	0	0	0	0	1	1
ENSG00000221372	ENSG00000221372	AC010739.1	2:41823525-41823632	NOTEST	0	0	0	0	1	1
ENSG00000221373	ENSG00000221373	AC010297.1	5:175874628-175937075	NOTEST	0	0	0	0	1	1
ENSG00000221374	ENSG00000221374	AC007242.1	2:202655183-202760273	NOTEST	0	0	0	0	1	1
ENSG00000221375	ENSG00000221375	RNU6ATAC23P	X:138808504-139027435	NOTEST	0	0	0	0	1	1
ENSG00000221376	ENSG00000221376	SNORA77	15:69591285-69740764	NOTEST	0	0	0	0	1	1
ENSG00000221377	ENSG00000221377	AC073255.1	2:30655218-30655314	NOTEST	0	0	0	0	1	1
ENSG00000221378	ENSG00000221378	AL096864.1	10:83635069-84746935	NOTEST	0	0	0	0	1	1
ENSG00000221379	ENSG00000221379	AC004460.1	15:31083775-31094062	NOTEST	0	0	0	0	1	1
ENSG00000221380	ENSG00000221380	AC108696.1	3:84339262-84339404	NOTEST	0	0	0	0	1	1
ENSG00000221381	ENSG00000221381	SNORD88B	19:51300960-51308186	NOTEST	0	0	0	0	1	1
ENSG00000221382	ENSG00000221382	AC096971.1	3:70927810-70927943	NOTEST	0	0	0	0	1	1
ENSG00000221383	ENSG00000221383	AC016907.1	2:30273931-30366670	NOTEST	0	0	0	0	1	1
ENSG00000221384	ENSG00000221384	AC023798.1	3:21459914-22414812	NOTEST	0	0	0	0	1	1
ENSG00000221385	ENSG00000221385	AL354984.2	20:56642511-56642663	NOTEST	0	0	0	0	1	1
ENSG00000221386	ENSG00000221386	AC002979.1	12:111471827-111788358	NOTEST	0	0	0	0	1	1
ENSG00000221387	ENSG00000221387	RNU6ATAC8P	8:103433424-103433550	NOTEST	0	0	0	0	1	1
ENSG00000221388	ENSG00000221388	AC093865.1	2:213446080-214017151	NOTEST	0	0	0	0	1	1
ENSG00000221389	ENSG00000221389	AC010754.1	18:21269406-21535030	NOTEST	0	0	0	0	1	1
ENSG00000221390	ENSG00000221390	MIR1295A	1:171060017-171086959	NOTEST	0	0	0	0	1	1
ENSG00000221391	ENSG00000221391	AC013489.1	15:89002706-89089906	NOTEST	0	0	0	0	1	1
ENSG00000221392	ENSG00000221392	Z73964.1	X:103065313-103065438	NOTEST	0	0	0	0	1	1
ENSG00000221393	ENSG00000221393	MIR1302-6	7:18126571-19042039	NOTEST	0	0	0	0	1	1
ENSG00000221394	ENSG00000221394	MIR1229	5:179224596-179334859	NOTEST	0	0	0	0	1	1
ENSG00000221395	ENSG00000221395	AC099506.1	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000221396	ENSG00000221396	AF064863.1	21:41382925-42219065	NOTEST	0	0	0	0	1	1
ENSG00000221397	ENSG00000221397	AC011841.4	GL000205.1:138776-138857	NOTEST	0	0	0	0	1	1
ENSG00000221398	ENSG00000221398	SNORA11	21:35818987-35884573	NOTEST	0	0	0	0	1	1
ENSG00000221400	ENSG00000221400	U3	10:43912697-43912888	NOTEST	0	0	0	0	1	1
ENSG00000221401	ENSG00000221401	AC025594.1	7:128470430-128550773	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000221402	ENSG00000221402	AL353664.1	10:121883643-121883738	NOTEST	0	0	0	0	1	1
ENSG00000221403	ENSG00000221403	AC096633.1	1:199996729-200146552	NOTEST	0	0	0	0	1	1
ENSG00000221405	ENSG00000221405	AC123768.2	15:32885656-32896179	NOTEST	0	0	0	0	1	1
ENSG00000221406	ENSG00000221406	MIR320B2	1:224407314-224518089	NOTEST	0	0	0	0	1	1
ENSG00000221407	ENSG00000221407	U85056.4	4:190979056-190984160	NOTEST	0	0	0	0	1	1
ENSG00000221409	ENSG00000221409	AC068506.1	18:32073253-32471808	NOTEST	0	0	0	0	1	1
ENSG00000221410	ENSG00000221410	MIR1238	19:10654570-10676713	NOTEST	0	0	0	0	1	1
ENSG00000221411	ENSG00000221411	MIR1227	19:2100987-2248678	NOTEST	0	0	0	0	1	1
ENSG00000221412	ENSG00000221412	AC124861.2	2:241201131-241201277	NOTEST	0	0	0	0	1	1
ENSG00000221413	ENSG00000221413	AC023593.1	3:127348023-127391652	NOTEST	0	0	0	0	1	1
ENSG00000221415	ENSG00000221415	AC118282.1	4:49200223-49200306	NOTEST	0	0	0	0	1	1
ENSG00000221416	ENSG00000221416	AL133232.1	20:55293941-55294025	NOTEST	0	0	0	0	1	1
ENSG00000221417	ENSG00000221417	MIR1257	20:60528524-60640866	NOTEST	0	0	0	0	1	1
ENSG00000221418	ENSG00000221418	AC003968.1	7:125680282-125680354	NOTEST	0	0	0	0	1	1
ENSG00000221419	ENSG00000221419	MIR1287	10:100143321-100174941	NOTEST	0	0	0	0	1	1
ENSG00000221421	ENSG00000221421	MIR1283-1	19:54191734-54191821	NOTEST	0	0	0	0	1	1
ENSG00000221423	ENSG00000221423	AL031602.1	1:33391894-33392000	NOTEST	0	0	0	0	1	1
ENSG00000221424	ENSG00000221424	AC090954.1	3:15175889-15176037	NOTEST	0	0	0	0	1	1
ENSG00000221425	ENSG00000221425	AL157904.1	1:117447771-117447916	NOTEST	0	0	0	0	1	1
ENSG00000221427	ENSG00000221427	AL121819.1	14:59237869-59237964	NOTEST	0	0	0	0	1	1
ENSG00000221428	ENSG00000221428	AC006150.2	7:14184673-15014402	NOTEST	0	0	0	0	1	1
ENSG00000221429	ENSG00000221429	AC018635.1	7:127930056-127930144	NOTEST	0	0	0	0	1	1
ENSG00000221430	ENSG00000221430	MIR1294	5:153369687-153825410	NOTEST	0	0	0	0	1	1
ENSG00000221431	ENSG00000221431	AC092925.1	3:147629192-147629288	NOTEST	0	0	0	0	1	1
ENSG00000221432	ENSG00000221432	AC079834.2	2:222282746-222439174	NOTEST	0	0	0	0	1	1
ENSG00000221434	ENSG00000221434	AL132671.1	6:117609462-117923691	NOTEST	0	0	0	0	1	1
ENSG00000221436	ENSG00000221436	MIR548F3	5:109624933-110100857	NOTEST	0	0	0	0	1	1
ENSG00000221437	ENSG00000221437	AC068058.1	10:125465722-125699783	NOTEST	0	0	0	0	1	1
ENSG00000221438	ENSG00000221438	AC114877.1	3:26795427-26795567	NOTEST	0	0	0	0	1	1
ENSG00000221439	ENSG00000221439	RNU4ATAC16P	12:861758-1020618	NOTEST	0	0	0	0	1	1
ENSG00000221440	ENSG00000221440	RNU6ATAC31P	4:89011415-89152474	NOTEST	0	0	0	0	1	1
ENSG00000221442	ENSG00000221442	MIR548F4	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000221443	ENSG00000221443	AC017083.3	2:68500235-68500338	NOTEST	0	0	0	0	1	1
ENSG00000221444	ENSG00000221444	AC139426.1	15:32684982-32727434	NOTEST	0	0	0	0	1	1
ENSG00000221445	ENSG00000221445	MIR1301	2:25455844-25565459	NOTEST	0	0	0	0	1	1
ENSG00000221446	ENSG00000221446	AC099805.1	8:72315674-72504260	NOTEST	0	0	0	0	1	1
ENSG00000221447	ENSG00000221447	AL591415.1	1:48086764-48086849	NOTEST	0	0	0	0	1	1
ENSG00000221448	ENSG00000221448	AL118509.1	20:16252748-16554078	NOTEST	0	0	0	0	1	1
ENSG00000221449	ENSG00000221449	AL109618.1	20:6209440-6209595	NOTEST	0	0	0	0	1	1
ENSG00000221450	ENSG00000221450	AL589675.1	9:2907072-3053408	NOTEST	0	0	0	0	1	1
ENSG00000221451	ENSG00000221451	AL354984.3	20:56551073-56551149	NOTEST	0	0	0	0	1	1
ENSG00000221454	ENSG00000221454	AC005631.1	7:152133979-152140272	NOTEST	0	0	0	0	1	1
ENSG00000221455	ENSG00000221455	U3	6:93500170-93500382	NOTEST	0	0	0	0	1	1
ENSG00000221456	ENSG00000221456	MIR1202	6:156267930-156268013	NOTEST	0	0	0	0	1	1
ENSG00000221457	ENSG00000221457	AC092958.1	3:147795945-147805816	NOTEST	0	0	0	0	1	1

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ENSG00000221459	ENSG00000221459	SNORA11C	X:47229981-47273704	NOTEST	0	0	0	0	1	1
ENSG00000221461	ENSG00000221461	U3	8:124191199-124222314	NOTEST	0	0	0	0	1	1
ENSG00000221463	ENSG00000221463	MIR1277	X:117480035-117583924	NOTEST	0	0	0	0	1	1
ENSG00000221464	ENSG00000221464	MIR1271	5:175792470-175843570	NOTEST	0	0	0	0	1	1
ENSG00000221465	ENSG00000221465	AL162502.1	10:98592016-98740800	NOTEST	0	0	0	0	1	1
ENSG00000221466	ENSG00000221466	MIR548AJ2	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000221467	ENSG00000221467	AC132803.1	5:144577337-144577422	NOTEST	0	0	0	0	1	1
ENSG00000221468	ENSG00000221468	RNU6ATAC11P	10:43837233-43837358	NOTEST	0	0	0	0	1	1
ENSG00000221469	ENSG00000221469	AL133260.1	6:151186684-151549582	NOTEST	0	0	0	0	1	1
ENSG00000221470	ENSG00000221470	AL132875.1	6:80536509-80536602	NOTEST	0	0	0	0	1	1
ENSG00000221471	ENSG00000221471	AC098847.1	18:57416908-57416989	NOTEST	0	0	0	0	1	1
ENSG00000221473	ENSG00000221473	AL138710.1	13:107820882-108519083	NOTEST	0	0	0	0	1	1
ENSG00000221474	ENSG00000221474	AC068754.1	3:121902529-122005342	NOTEST	0	0	0	0	1	1
ENSG00000221475	ENSG00000221475	SNORA11D	X:51927918-51935364	NOTEST	0	0	0	0	1	1
ENSG00000221476	ENSG00000221476	MIR1827	15:78268383-78370066	NOTEST	0	0	0	0	1	1
ENSG00000221477	ENSG00000221477	AC108739.1	3:95885660-95885746	NOTEST	0	0	0	0	1	1
ENSG00000221478	ENSG00000221478	AC092329.1	19:23369033-23369139	NOTEST	0	0	0	0	1	1
ENSG00000221479	ENSG00000221479	MIR1251	12:97825430-97958813	NOTEST	0	0	0	0	1	1
ENSG00000221484	ENSG00000221484	AC027807.1	15:84322837-84708594	NOTEST	0	0	0	0	1	1
ENSG00000221485	ENSG00000221485	AC145212.2	GL000194.1:84476-84559	NOTEST	0	0	0	0	1	1
ENSG00000221486	ENSG00000221486	AC000003.1	17:9813925-10101868	NOTEST	0	0	0	0	1	1
ENSG00000221487	ENSG00000221487	AC069294.1	7:99302659-99332819	NOTEST	0	0	0	0	1	1
ENSG00000221488	ENSG00000221488	AC092017.1	1:211384330-211384424	NOTEST	0	0	0	0	1	1
ENSG00000221489	ENSG00000221489	AC007358.1	2:202817979-202818059	NOTEST	0	0	0	0	1	1
ENSG00000221491	ENSG00000221491	SNORA34	12:49047183-49076021	NOTEST	0	2.41885	inf	0	1	1
ENSG00000221492	ENSG00000221492	AL162430.1	1:51656554-51656630	NOTEST	0	0	0	0	1	1
ENSG00000221493	ENSG00000221493	MIR320C1	18:19230857-19284766	NOTEST	0	0	0	0	1	1
ENSG00000221494	ENSG00000221494	MIR548I4	X:83480759-83480836	NOTEST	0	0	0	0	1	1
ENSG00000221495	ENSG00000221495	AC098680.1	4:38240233-38240317	NOTEST	0	0	0	0	1	1
ENSG00000221496	ENSG00000221496	U3	17:42376941-42396039	NOTEST	0	1.00951	inf	0	1	1
ENSG00000221497	ENSG00000221497	AL034449.1	21:17065526-17065622	NOTEST	0	0	0	0	1	1
ENSG00000221498	ENSG00000221498	SNORA77	2:183928962-183929074	NOTEST	0	0	0	0	1	1
ENSG00000221499	ENSG00000221499	AC078881.1	4:178366132-178598280	NOTEST	0	0	0	0	1	1
ENSG00000221500	ENSG00000221500	SNORD100	6:133135579-133138703	NOTEST	0	0	0	0	1	1
ENSG00000221502	ENSG00000221502	MIR1245A	2:189839045-189877472	NOTEST	0	0	0	0	1	1
ENSG00000221504	ENSG00000221504	AC011456.1	19:32413789-32436304	NOTEST	0	0	0	0	1	1
ENSG00000221505	ENSG00000221505	AL030997.1	X:142372753-142605303	NOTEST	0	0	0	0	1	1
ENSG00000221506	ENSG00000221506	AC092038.1	3:23244510-23633284	NOTEST	0	0	0	0	1	1
ENSG00000221507	ENSG00000221507	RNU6ATAC40P	7:144148773-144148910	NOTEST	0	0	0	0	1	1
ENSG00000221510	ENSG00000221510	MIR548O	7:102004318-102067123	NOTEST	0	0	0	0	1	1
ENSG00000221511	ENSG00000221511	AC090825.1	15:100330360-100347132	NOTEST	0	0	0	0	1	1
ENSG00000221514	ENSG00000221514	SNORD111B	16:70557690-70608820	NOTEST	0	0	0	0	1	1
ENSG00000221515	ENSG00000221515	AC007333.1	16:52271993-52314211	NOTEST	0	0	0	0	1	1
ENSG00000221516	ENSG00000221516	AP002806.1	11:130981829-130981910	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000221517	ENSG00000221517	AC010724.1	15:83128127-83182928	NOTEST	0	0	0	0	1	1
ENSG00000221518	ENSG00000221518	RNU6ATAC16P	3:52529353-52742182	NOTEST	0	0	0	0	1	1
ENSG00000221519	ENSG00000221519	AL390071.1	13:35516423-36247159	NOTEST	0	0	0	0	1	1
ENSG00000221520	ENSG00000221520	MIR1285-1	7:91828282-91875480	NOTEST	0	0	0	0	1	1
ENSG00000221521	ENSG00000221521	AL158151.2	9:131857088-131911225	NOTEST	0	0	0	0	1	1
ENSG00000221523	ENSG00000221523	AC079080.1	4:185188509-185188584	NOTEST	0	0	0	0	1	1
ENSG00000221524	ENSG00000221524	AC074391.2	2:65663844-66311773	NOTEST	0	0	0	0	1	1
ENSG00000221525	ENSG00000221525	MIR1185-1	14:101509313-101509399	NOTEST	0	0	0	0	1	1
ENSG00000221526	ENSG00000221526	AC040162.1	16:67906925-67922758	NOTEST	0	0	0	0	1	1
ENSG00000221527	ENSG00000221527	RNU6ATAC41P	8:101752029-101752155	NOTEST	0	0	0	0	1	1
ENSG00000221528	ENSG00000221528	AC016597.1	16:27561453-27791690	NOTEST	0	0	0	0	1	1
ENSG00000221529	ENSG00000221529	AC105227.1	18:47927310-47927418	NOTEST	0	0	0	0	1	1
ENSG00000221530	ENSG00000221530	AC005037.2	2:201707908-201708022	NOTEST	0	0	0	0	1	1
ENSG00000221531	ENSG00000221531	AC074091.1	2:27799388-27805588	NOTEST	0	0	0	0	1	1
ENSG00000221532	ENSG00000221532	AC007353.1	16:34442273-34518517	NOTEST	0	0	0	0	1	1
ENSG00000221533	ENSG00000221533	MIR1184-1	X:154064062-154288578	NOTEST	0	0	0	0	1	1
ENSG00000221534	ENSG00000221534	AC090079.1	17:51614873-51614965	NOTEST	0	0	0	0	1	1
ENSG00000221535	ENSG00000221535	AC027319.1	19:4889214-4889310	NOTEST	0	0	0	0	1	1
ENSG00000221536	ENSG00000221536	AC091643.1	18:64320645-64320738	NOTEST	0	0	0	0	1	1
ENSG00000221537	ENSG00000221537	MIR548H1	14:64319682-64805317	NOTEST	0	0	0	0	1	1
ENSG00000221538	ENSG00000221538	AL365361.1	1:111195563-111195653	NOTEST	0	0	0	0	1	1
ENSG00000221539	ENSG00000221539	SNORD99	1:28879596-28909495	NOTEST	0	0	0	0	1	1
ENSG00000221540	ENSG00000221540	MIR1180	17:19240866-19290553	NOTEST	0	0	0	0	1	1
ENSG00000221541	ENSG00000221541	AC079753.1	2:113601887-113601988	NOTEST	0	0	0	0	1	1
ENSG00000221542	ENSG00000221542	AC016405.2	8:123793632-123986750	NOTEST	0	0	0	0	1	1
ENSG00000221544	ENSG00000221544	AL359709.1	6:105629023-105629107	NOTEST	0	0	0	0	1	1
ENSG00000221545	ENSG00000221545	MIR1255B2	1:167885966-168045081	NOTEST	0	0	0	0	1	1
ENSG00000221547	ENSG00000221547	AL359853.1	1:179679384-179679481	NOTEST	0	0	0	0	1	1
ENSG00000221548	ENSG00000221548	MIR1283-2	19:54261485-54261572	NOTEST	0	0	0	0	1	1
ENSG00000221550	ENSG00000221550	AL645859.1	1:29563027-29653325	NOTEST	0	0	0	0	1	1
ENSG00000221551	ENSG00000221551	AP000478.1	11:79403422-79403573	NOTEST	0	0	0	0	1	1
ENSG00000221552	ENSG00000221552	MIR1303	5:154065335-154065421	NOTEST	0	0	0	0	1	1
ENSG00000221553	ENSG00000221553	AC004924.1	11:67700684-67700833	NOTEST	0	0	0	0	1	1
ENSG00000221555	ENSG00000221555	AC068669.1	17:38296570-38328436	NOTEST	0	0	0	0	1	1
ENSG00000221556	ENSG00000221556	AC103794.1	11:15987994-16778428	NOTEST	0	0	0	0	1	1
ENSG00000221558	ENSG00000221558	AC024082.1	7:137687069-137802732	NOTEST	0	0	0	0	1	1
ENSG00000221559	ENSG00000221559	AL357519.1	6:114026034-114026125	NOTEST	0	0	0	0	1	1
ENSG00000221560	ENSG00000221560	MIR1302-1	12:113008183-113336686	NOTEST	0	0	0	0	1	1
ENSG00000221561	ENSG00000221561	AC087069.1	7:36552455-36764154	NOTEST	0	0	0	0	1	1
ENSG00000221562	ENSG00000221562	RNU6ATAC10P	5:128795251-129522327	NOTEST	0	0	0	0	1	1
ENSG00000221563	ENSG00000221563	MIR1269A	4:67142541-67142646	NOTEST	0	0	0	0	1	1
ENSG00000221564	ENSG00000221564	RNU6ATAC42P	12:65277173-65376304	NOTEST	0	0	0	0	1	1
ENSG00000221565	ENSG00000221565	AP004242.1	11:93063136-93171653	NOTEST	0	0	0	0	1	1
ENSG00000221566	ENSG00000221566	MIR1181	19:10501809-10580305	NOTEST	0	0	0	0	1	1
ENSG00000221567	ENSG00000221567	AF228730.2	8:7055961-7056110	NOTEST	0	0	0	0	1	1

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ENSG00000221570	ENSG00000221570	AC011841.5	GL000205.1:165362-165438	NOTEST	0	0	0	0	1	1
ENSG00000221571	ENSG00000221571	RNU6ATAC35P	1:220998961-220999389	NOTEST	0	0	0	0	1	1
ENSG00000221573	ENSG00000221573	AC099535.1	3:27151575-27410951	NOTEST	0	0	0	0	1	1
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ENSG00000221576	ENSG00000221576	AC004543.1	7:19758932-19813221	NOTEST	0	0	0	0	1	1
ENSG00000221578	ENSG00000221578	AL049798.1	1:168717033-168717120	NOTEST	0	0	0	0	1	1
ENSG00000221579	ENSG00000221579	AC093162.1	2:85360532-85537511	NOTEST	0	0	0	0	1	1
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ENSG00000221581	ENSG00000221581	AL353707.1	9:83349156-83349244	NOTEST	0	0	0	0	1	1
ENSG00000221583	ENSG00000221583	RNU6ATAC21P	6:10222268-10222394	NOTEST	0	0	0	0	1	1
ENSG00000221584	ENSG00000221584	AC008747.1	19:35051690-35051801	NOTEST	0	0	0	0	1	1
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ENSG00000221586	ENSG00000221586	MIR1261	11:89984399-90648220	NOTEST	0	0	0	0	1	1
ENSG00000221589	ENSG00000221589	AC100817.1	8:56589791-56589883	NOTEST	0	0	0	0	1	1
ENSG00000221590	ENSG00000221590	AC009299.1	2:162164548-162268228	NOTEST	0	0	0	0	1	1
ENSG00000221591	ENSG00000221591	AL161740.1	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000221593	ENSG00000221593	AC026150.2	15:30844182-30854704	NOTEST	0	0	0	0	1	1
ENSG00000221594	ENSG00000221594	MIR548F1	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000221595	ENSG00000221595	AC010458.1	19:48551099-48614074	NOTEST	0	0	0	0	1	1
ENSG00000221597	ENSG00000221597	BX088702.1	GL000199.1:1175-1259	NOTEST	0	0	0	0	1	1
ENSG00000221598	ENSG00000221598	MIR1249	22:45586218-45636650	NOTEST	0	0	0	0	1	1
ENSG00000221599	ENSG00000221599	AL136446.1	6:114254191-114792869	NOTEST	0	0	0	0	1	1
ENSG00000221601	ENSG00000221601	RNU4ATAC2P	5:158737940-158789842	NOTEST	0	0	0	0	1	1
ENSG00000221602	ENSG00000221602	AC133041.1	3:75589199-75629150	NOTEST	0	0	0	0	1	1
ENSG00000221603	ENSG00000221603	MIR1184-2	X:154686575-154688276	NOTEST	0	0	0	0	1	1
ENSG00000221604	ENSG00000221604	MIR1293	12:50569570-50677329	NOTEST	0	0	0	0	1	1
ENSG00000221606	ENSG00000221606	AL356131.1	6:62056769-62056882	NOTEST	0	0	0	0	1	1
ENSG00000221607	ENSG00000221607	AP005718.1	11:108340181-108340279	NOTEST	0	0	0	0	1	1
ENSG00000221608	ENSG00000221608	AC079235.1	2:227867426-228028829	NOTEST	0	0	0	0	1	1
ENSG00000221610	ENSG00000221610	AC107890.1	8:113235156-114449328	NOTEST	0	0	0	0	1	1
ENSG00000221611	ENSG00000221611	SNORD88	12:13080659-13193613	NOTEST	0	0	0	0	1	1
ENSG00000221612	ENSG00000221612	AC106775.1	5:136310986-136934068	NOTEST	0	0	0	0	1	1
ENSG00000221613	ENSG00000221613	AL161452.1	9:138420456-138420546	NOTEST	0	0	0	0	1	1
ENSG00000221614	ENSG00000221614	MIR1185-2	14:101510534-101510620	NOTEST	0	0	0	0	1	1
ENSG00000221615	ENSG00000221615	AC140132.1	5:21616370-22853731	NOTEST	0	0	0	0	1	1
ENSG00000221616	ENSG00000221616	MIR548H4	8:26906369-26906480	NOTEST	0	0	0	0	1	1
ENSG00000221617	ENSG00000221617	AC138123.1	12:93392993-93609455	NOTEST	0	0	0	0	1	1
ENSG00000221618	ENSG00000221618	AC093817.1	4:158509299-158509387	NOTEST	0	0	0	0	1	1
ENSG00000221619	ENSG00000221619	AC012671.3	2:88594110-88594198	NOTEST	0	0	0	0	1	1
ENSG00000221621	ENSG00000221621	AC009835.1	18:30106104-30106185	NOTEST	0	0	0	0	1	1
ENSG00000221623	ENSG00000221623	AC090150.1	8:27005220-27005309	NOTEST	0	0	0	0	1	1
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ENSG00000221628	ENSG00000221628	MIR1302-4	2:208104373-208490652	NOTEST	0	0	0	0	1	1
ENSG00000221629	ENSG00000221629	AL162614.1	11:30851915-31391357	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000221631	ENSG00000221631	AP000897.1	18:7566779-8406951	NOTEST	0	0	0	0	1	1
ENSG00000221633	ENSG00000221633	U3	3:108677085-108836989	NOTEST	0	0	0	0	1	1
ENSG00000221634	ENSG00000221634	MIR1276	15:86302553-86338261	NOTEST	0	0	0	0	1	1
ENSG00000221635	ENSG00000221635	BX255972.1	6:34433915-34503006	NOTEST	0	0	0	0	1	1
ENSG00000221637	ENSG00000221637	AC105252.1	4:134482010-134482089	NOTEST	0	0	0	0	1	1
ENSG00000221638	ENSG00000221638	U3	2:75855078-75855293	NOTEST	0	0	0	0	1	1
ENSG00000221639	ENSG00000221639	SNORA3	4:74124925-74183670	NOTEST	0	0	0	0	1	1
ENSG00000221641	ENSG00000221641	MIR1268A	15:22513228-22513280	NOTEST	0	0	0	0	1	1
ENSG00000221643	ENSG00000221643	SNORA77	1:203595688-203713209	NOTEST	0	0	0	0	1	1
ENSG00000221644	ENSG00000221644	AC027238.1	8:122198997-122199132	NOTEST	0	0	0	0	1	1
ENSG00000221645	ENSG00000221645	AL157791.1	14:39699434-39856306	NOTEST	0	0	0	0	1	1
ENSG00000221649	ENSG00000221649	MIR1233-1	15:34671268-34880704	NOTEST	0	0	0	0	1	1
ENSG00000221650	ENSG00000221650	MIR1267	13:107820882-108519083	NOTEST	0	0	0	0	1	1
ENSG00000221653	ENSG00000221653	AC007131.3	2:59444842-60327335	NOTEST	0	0	0	0	1	1
ENSG00000221654	ENSG00000221654	AC013402.1	2:105185274-105185378	NOTEST	0	0	0	0	1	1
ENSG00000221655	ENSG00000221655	AL354978.1	1:66999065-67213982	NOTEST	0	0	0	0	1	1
ENSG00000221656	ENSG00000221656	MIR1225	16:2089815-2185899	NOTEST	0	0	0	0	1	1
ENSG00000221657	ENSG00000221657	AC097455.1	4:152330367-152584784	NOTEST	0	0	0	0	1	1
ENSG00000221659	ENSG00000221659	AC104441.1	3:21179754-21179833	NOTEST	0	0	0	0	1	1
ENSG00000221660	ENSG00000221660	AC022861.1	8:68334359-68658620	NOTEST	0	0	0	0	1	1
ENSG00000221662	ENSG00000221662	MIR1290	1:19166092-19283180	NOTEST	0	0	0	0	1	1
ENSG00000221664	ENSG00000221664	AC095030.1	1:77747735-78025651	NOTEST	0	0	0	0	1	1
ENSG00000221665	ENSG00000221665	AL591708.1	X:94148499-94148592	NOTEST	0	0	0	0	1	1
ENSG00000221666	ENSG00000221666	AC011841.6	GL000205.1:136234-136317	NOTEST	0	0	0	0	1	1
ENSG00000221667	ENSG00000221667	MIR1825	20:30795682-30826470	NOTEST	0	0	0	0	1	1
ENSG00000221669	ENSG00000221669	MIR548N	7:34968487-35077883	NOTEST	0	0	0	0	1	1
ENSG00000221670	ENSG00000221670	AL596092.1	13:29598747-30077892	NOTEST	0	0	0	0	1	1
ENSG00000221672	ENSG00000221672	Z97351.1	22:47158517-47571336	NOTEST	0	0	0	0	1	1
ENSG00000221673	ENSG00000221673	U3	1:220136027-220136206	NOTEST	0	0	0	0	1	1
ENSG00000221676	ENSG00000221676	RNU6ATAC	9:137029560-137029686	NOTEST	6.9915	0	#NAME?	0	1	1
ENSG00000221677	ENSG00000221677	AL161898.1	13:33590206-33640282	NOTEST	0	0	0	0	1	1
ENSG00000221679	ENSG00000221679	AC087237.1	12:19928384-20162871	NOTEST	0	0	0	0	1	1
ENSG00000221680	ENSG00000221680	MIR1278	1:193091146-193223031	NOTEST	0	0	0	0	1	1
ENSG00000221681	ENSG00000221681	AC092902.1	3:125546080-125629115	NOTEST	0	0	0	0	1	1
ENSG00000221683	ENSG00000221683	AC104837.1	1:79152744-79152845	NOTEST	0	0	0	0	1	1
ENSG00000221684	ENSG00000221684	BX276092.1	X:70979234-70979305	NOTEST	0	0	0	0	1	1
ENSG00000221685	ENSG00000221685	AL354775.1	13:66438304-66438398	NOTEST	0	0	0	0	1	1
ENSG00000221686	ENSG00000221686	AC096579.1	2:89065323-89106126	NOTEST	0	0	0	0	1	1
ENSG00000221689	ENSG00000221689	AC092646.3	2:124439682-124439791	NOTEST	0	0	0	0	1	1
ENSG00000221690	ENSG00000221690	AC004875.1	7:121214722-121214808	NOTEST	0	0	0	0	1	1
ENSG00000221691	ENSG00000221691	AC090825.2	15:100291923-100292010	NOTEST	0	0	0	0	1	1
ENSG00000221692	ENSG00000221692	AC011841.7	GL000205.1:164642-164725	NOTEST	0	0	0	0	1	1
ENSG00000221693	ENSG00000221693	AL590226.1	9:139588587-139588714	NOTEST	0	0	0	0	1	1
ENSG00000221695	ENSG00000221695	AL390335.1	14:41818496-41818570	NOTEST	0	0	0	0	1	1

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ENSG00000221697	ENSG00000221697	MIR1275	6:33967748-33967828	NOTEST	0	0	0	0	1	1
ENSG00000221698	ENSG00000221698	MIR548H3	17:13399005-13505244	NOTEST	0	0	0	0	1	1
ENSG00000221699	ENSG00000221699	AC024610.1	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000221701	ENSG00000221701	AC005284.1	17:10957104-10957252	NOTEST	0	0	0	0	1	1
ENSG00000221702	ENSG00000221702	AL356270.1	1:87012760-87158886	NOTEST	0	0	0	0	1	1
ENSG00000221703	ENSG00000221703	MIR302E	11:7255996-7256068	NOTEST	0	0	0	0	1	1
ENSG00000221704	ENSG00000221704	AC012305.1	2:236402732-237040444	NOTEST	0	0	0	0	1	1
ENSG00000221705	ENSG00000221705	SNORA11E	X:51804922-51812368	NOTEST	0	0	0	0	1	1
ENSG00000221706	ENSG00000221706	AC090573.1	8:127153919-127154003	NOTEST	0	0	0	0	1	1
ENSG00000221707	ENSG00000221707	AL592294.1	1:45482070-45771881	NOTEST	0	0	0	0	1	1
ENSG00000221708	ENSG00000221708	AL353733.1	9:8314245-10612723	NOTEST	0	0	0	0	1	1
ENSG00000221710	ENSG00000221710	MIR1298	X:113818550-114144624	NOTEST	0	0	0	0	1	1
ENSG00000221711	ENSG00000221711	SNORD75	4:78623899-78623957	NOTEST	0	0	0	0	1	1
ENSG00000221714	ENSG00000221714	AC130352.1	8:12384246-12384350	NOTEST	0	0	0	0	1	1
ENSG00000221716	ENSG00000221716	SNORA11	X:54834031-54842445	NOTEST	0	0	0	0	1	1
ENSG00000221717	ENSG00000221717	AL583860.1	10:128113565-128359079	NOTEST	0	0	0	0	1	1
ENSG00000221718	ENSG00000221718	AC046143.1	3:194304739-194393206	NOTEST	0	0	0	0	1	1
ENSG00000221719	ENSG00000221719	SNORA3	16:2846408-2846533	NOTEST	0	0	0	0	1	1
ENSG00000221720	ENSG00000221720	AC096951.1	1:77333125-77531396	NOTEST	0	0	0	0	1	1
ENSG00000221721	ENSG00000221721	AC010455.1	5:27986281-27986392	NOTEST	0	0	0	0	1	1
ENSG00000221723	ENSG00000221723	AC019322.1	15:30695942-30706463	NOTEST	0	0	0	0	1	1
ENSG00000221724	ENSG00000221724	AC078855.1	3:108015375-108097132	NOTEST	0	0	0	0	1	1
ENSG00000221725	ENSG00000221725	RNU6ATAC25P	16:70841280-71264625	NOTEST	0	0	0	0	1	1
ENSG00000221726	ENSG00000221726	AL031653.1	20:7677532-7677624	NOTEST	0	0	0	0	1	1
ENSG00000221729	ENSG00000221729	AL590285.1	X:36595469-36595565	NOTEST	0	0	0	0	1	1
ENSG00000221730	ENSG00000221730	AL162419.1	9:4378422-4378494	NOTEST	0	0	0	0	1	1
ENSG00000221731	ENSG00000221731	AC091321.1	18:27063292-27063388	NOTEST	0	0	0	0	1	1
ENSG00000221732	ENSG00000221732	AC006452.1	7:140218219-140624564	NOTEST	0	0	0	0	1	1
ENSG00000221733	ENSG00000221733	AL109843.1	1:67557847-67725662	NOTEST	0	0	0	0	1	1
ENSG00000221734	ENSG00000221734	AL390240.1	9:117546914-117568406	NOTEST	0	0	0	0	1	1
ENSG00000221736	ENSG00000221736	AC003681.1	22:30279143-30573064	NOTEST	0	0	0	0	1	1
ENSG00000221737	ENSG00000221737	MIR548I1	3:125493556-125516796	NOTEST	0	0	0	0	1	1
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ENSG00000221740	ENSG00000221740	SNORD93	7:22893796-22901021	NOTEST	0	0	0	0	1	1
ENSG00000221741	ENSG00000221741	AC093304.1	5:166711803-167691162	NOTEST	0	0	0	0	1	1
ENSG00000221743	ENSG00000221743	Z95152.1	6:36108274-36108365	NOTEST	0	0	0	0	1	1
ENSG00000221744	ENSG00000221744	AL512635.1	9:20295001-20295086	NOTEST	0	0	0	0	1	1
ENSG00000221745	ENSG00000221745	MIR1197	14:101491900-101491988	NOTEST	0	0	0	0	1	1
ENSG00000221746	ENSG00000221746	AL645730.1	1:48998526-50489585	NOTEST	0	0	0	0	1	1
ENSG00000221747	ENSG00000221747	AC118282.2	4:49200031-49200114	NOTEST	0	0	0	0	1	1
ENSG00000221748	ENSG00000221748	AL049647.1	20:19193289-19703581	NOTEST	0	0	0	0	1	1
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ENSG00000221750	ENSG00000221750	SNORA11	X:54946894-54957864	NOTEST	0	0	0	0	1	1
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ENSG00000221754	ENSG00000221754	MIR1260A	14:77731825-77737655	NOTEST	0	0	0	0	1	1
ENSG00000221755	ENSG00000221755	MIR720	3:164059128-164059238	NOTEST	0	0	0	0	1	1
ENSG00000221756	ENSG00000221756	AL159977.1	13:27894149-27894296	NOTEST	0	0	0	0	1	1
ENSG00000221760	ENSG00000221760	MIR548J	22:26921457-26992681	NOTEST	0	0	0	0	1	1
ENSG00000221762	ENSG00000221762	AC092786.1	2:137402677-137402762	NOTEST	0	0	0	0	1	1
ENSG00000221763	ENSG00000221763	MIR1289-1	20:34020826-34042568	NOTEST	0	0	0	0	1	1
ENSG00000221764	ENSG00000221764	AC107068.1	4:47849256-48042188	NOTEST	0	0	0	0	1	1
ENSG00000221766	ENSG00000221766	AC084872.1	7:145813452-148118090	NOTEST	0	0	0	0	1	1
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ENSG00000221770	ENSG00000221770	AC010203.1	12:100550134-100660857	NOTEST	0	0	0	0	1	1
ENSG00000221771	ENSG00000221771	MIR1205	8:128806778-129113499	NOTEST	0	0	0	0	1	1
ENSG00000221772	ENSG00000221772	AL353141.1	9:118916082-119164601	NOTEST	0	0	0	0	1	1
ENSG00000221774	ENSG00000221774	AC016821.1	10:71029739-71161638	NOTEST	0	0	0	0	1	1
ENSG00000221777	ENSG00000221777	AL160056.1	1:98838940-98839055	NOTEST	0	0	0	0	1	1
ENSG00000221778	ENSG00000221778	AC034236.2	5:115298150-115395815	NOTEST	0	0	0	0	1	1
ENSG00000221779	ENSG00000221779	AL590403.1	6:33989627-34123399	NOTEST	0	0	0	0	1	1
ENSG00000221781	ENSG00000221781	AL359815.1	1:21918903-21919041	NOTEST	0	0	0	0	1	1
ENSG00000221782	ENSG00000221782	MIR548F2	2:212240445-213403565	NOTEST	0	0	0	0	1	1
ENSG00000221783	ENSG00000221783	MIR1183	7:21467651-21554440	NOTEST	0	0	0	0	1	1
ENSG00000221785	ENSG00000221785	AC120045.2	15:30427351-30437770	NOTEST	0	0	0	0	1	1
ENSG00000221786	ENSG00000221786	AC004673.1	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000221788	ENSG00000221788	MIR1252	12:79257772-79897176	NOTEST	0	0	0	0	1	1
ENSG00000221789	ENSG00000221789	AC130462.1	16:68021296-68272005	NOTEST	0	0	0	0	1	1
ENSG00000221790	ENSG00000221790	AC011467.1	19:22779058-22791303	NOTEST	0	0	0	0	1	1
ENSG00000221792	ENSG00000221792	MIR1282	15:44019115-44095241	NOTEST	0	0	0	0	1	1
ENSG00000221793	ENSG00000221793	AC103863.1	8:116962735-117337297	NOTEST	0	0	0	0	1	1
ENSG00000221795	ENSG00000221795	MIR1324	3:75679913-75680009	NOTEST	0	0	0	0	1	1
ENSG00000221796	ENSG00000221796	AL356739.1	6:145669893-145669985	NOTEST	0	0	0	0	1	1
ENSG00000221798	ENSG00000221798	AC092812.1	1:96352095-96352182	NOTEST	0	0	0	0	1	1
ENSG00000221799	ENSG00000221799	AC132068.1	16:72699068-73093597	NOTEST	0	0	0	0	1	1
ENSG00000221801	ENSG00000221801	MIR548H2	16:11343475-11445619	NOTEST	0	0	0	0	1	1
ENSG00000221802	ENSG00000221802	MIR1234	8:145596789-145634753	NOTEST	0	0	0	0	1	1
ENSG00000221803	ENSG00000221803	SNORD23	19:48248778-48272097	NOTEST	0	0	0	0	1	1
ENSG00000221804	ENSG00000221804	AC021749.1	11:39883055-39883144	NOTEST	0	0	0	0	1	1
ENSG00000221806	ENSG00000221806	RNU6ATAC34P	20:18568536-18744561	NOTEST	0	0	0	0	1	1
ENSG00000221807	ENSG00000221807	AC069227.1	12:103230662-103354294	NOTEST	0	0	0	0	1	1
ENSG00000221808	ENSG00000221808	MIR1256	1:21132962-21503377	NOTEST	0	0	0	0	1	1
ENSG00000221809	ENSG00000221809	AC074051.1	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000221810	ENSG00000221810	AC026781.1	5:92053138-92053220	NOTEST	0	0	0	0	1	1
ENSG00000221813	ENSG00000221813	OR6B1	7:143701021-143702068	NOTEST	0	0	0	0	1	1
ENSG00000221818	ENSG00000221818	EBF2	8:25699245-25902913	NOTEST	0	0	0	0	1	1
ENSG00000221826	ENSG00000221826	PSG3	19:43225789-43244721	NOTEST	0	0.0181105	inf	0	1	1
ENSG00000221836	ENSG00000221836	OR2A5	7:143747460-143748473	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000221837	ENSG00000221837	KRTAP10-9	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000221840	ENSG00000221840	OR4A5	11:51411377-51412448	NOTEST	0	0	0	0	1	1
ENSG00000221843	ENSG00000221843	C2orf16	2:27799388-27805588	NOTEST	0.0986128	0.153646	0.639764	0	1	1
ENSG00000221844	ENSG00000221844	RP11-404E6.1	9:76089293-76090989	NOTEST	0	0	0	0	1	1
ENSG00000221845	ENSG00000221845	C7orf65	7:47694841-47701246	NOTEST	0	0	0	0	1	1
ENSG00000221849	ENSG00000221849	AC018880.1	2:104144077-104145719	NOTEST	0	0	0	0	1	1
ENSG00000221852	ENSG00000221852	KRTAP1-5	17:39182277-39183454	NOTEST	0	0	0	0	1	1
ENSG00000221855	ENSG00000221855	TAS2R41	7:143078172-143220542	NOTEST	0	0	0	0	1	1
ENSG00000221857	ENSG00000221857	CTD-2527I21.4	19:35615416-35645204	NOTEST	0	0	0	0	1	1
ENSG00000221858	ENSG00000221858	OR2A12	7:143792140-143793186	NOTEST	0	0	0	0	1	1
ENSG00000221859	ENSG00000221859	KRTAP10-10	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000221864	ENSG00000221864	KRTAP12-2	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000221866	ENSG00000221866	PLXNA4	7:131808090-132333447	NOTEST	0.00230372	0.0177925	2.94923	0	1	1
ENSG00000221870	ENSG00000221870	TMEM257	X:144908927-144911368	NOTEST	0.0445472	0.0924776	1.05377	0	1	1
ENSG00000221874	ENSG00000221874	ZNF321P	19:53430387-53541151	NOTEST	0	0.0477866	inf	0	1	1
ENSG00000221878	ENSG00000221878	PSG7	19:43428285-43441330	NOTEST	0.0436014	0.0901664	1.04822	0	1	1
ENSG00000221879	ENSG00000221879	MRPS21P3	1:197170591-197447585	NOTEST	0	0	0	0	1	1
ENSG00000221880	ENSG00000221880	KRTAP1-3	17:39190141-39191107	NOTEST	0	0	0	0	1	1
ENSG00000221882	ENSG00000221882	OR3A2	17:3181192-3290132	NOTEST	0	0	0	0	1	1
ENSG00000221883	ENSG00000221883	ARIH2OS	3:48955220-49060928	NOTEST	0.433093	0.322425	-0.425714	0	1	1
ENSG00000221887	ENSG00000221887	HMSD	18:61616534-61672278	NOTEST	0.0960709	0.0622059	-0.627048	0	1	1
ENSG00000221888	ENSG00000221888	OR1C1	1:247920675-247921982	NOTEST	0	0	0	0	1	1
ENSG00000221891	ENSG00000221891	FAM218BP	4:165850645-165851103	NOTEST	0	0	0	0	1	1
ENSG00000221900	ENSG00000221900	POM121L12	7:53103348-53104617	NOTEST	0	0	0	0	1	1
ENSG00000221910	ENSG00000221910	OR2F2	7:143632258-143633372	NOTEST	0	0	0	0	1	1
ENSG00000221916	ENSG00000221916	C19orf73	19:49617580-49622397	NOTEST	0.515587	0.546393	0.0837228	0	1	1
ENSG00000221931	ENSG00000221931	OR6X1	11:123624195-123625253	NOTEST	0	0	0	0	1	1
ENSG00000221932	ENSG00000221932	HEPN1	11:124789088-124806308	NOTEST	0.078369	0.00918329	-3.0932	0	1	1
ENSG00000221933	ENSG00000221933	OR2A25	7:143771274-143772288	NOTEST	0	0	0	0	1	1
ENSG00000221937	ENSG00000221937	TAS2R40	7:142919129-142920162	NOTEST	0	0	0	0	1	1
ENSG00000221938	ENSG00000221938	OR2A14	7:143826150-143827162	NOTEST	0	0	0	0	1	1
ENSG00000221949	ENSG00000221949	C12orf61	12:62995530-63007855	NOTEST	0.0945008	0.109072	0.20688	0	1	1
ENSG00000221953	ENSG00000221953	C1orf229	1:247273461-247275719	NOTEST	0.0142319	0.00499869	-1.50951	0	1	1
ENSG00000221954	ENSG00000221954	OR4C12	11:50003008-50004071	NOTEST	0	0	0	0	1	1
ENSG00000221957	ENSG00000221957	KIR2DS4	19:55235968-55378662	NOTEST	0	0	0	0	1	1
ENSG00000221961	ENSG00000221961	PRR21	2:240981229-240982399	NOTEST	0	0	0	0	1	1
ENSG00000221962	ENSG00000221962	TMEM14E	3:151961616-152214602	NOTEST	0.0132017	0	#NAME?	0	1	1
ENSG00000221963	ENSG00000221963	APOL6	22:36044441-36064456	NOTEST	0.115593	0.200086	0.79156	0	1	1
ENSG00000221970	ENSG00000221970	OR2A1	7:143883175-144077725	NOTEST	0.0745998	0.115921	0.635892	0	1	1
ENSG00000221971	ENSG00000221971	TTC4P1	7:46030503-46040497	NOTEST	0	0	0	0	1	1
ENSG00000221972	ENSG00000221972	C3orf36	3:133646991-133648656	NOTEST	0	0	0	0	1	1
ENSG00000221974	ENSG00000221974	GTF2H4	HSCHR6_MHC_QBL:30865548-30883835	NOTEST	0	0	0	0	1	1
ENSG00000221977	ENSG00000221977	OR4E2	14:22133296-22134238	NOTEST	0	0	0	0	1	1
ENSG00000221986	ENSG00000221986	MYBPHL	1:109834986-109849663	NOTEST	0.0123662	0.0970191	2.97186	0	1	1
ENSG00000221989	ENSG00000221989	OR2A2	7:143806606-143807657	NOTEST	0	0	0	0	1	1

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ENSG00000221995	ENSG00000221995	TIAF1	17:27400527-27507430	NOTEST	0.322402	0.386232	0.260606	0	1	1
ENSG00000221996	ENSG00000221996	OR52B4	11:4388492-4389616	NOTEST	0	0	0	0	1	1
ENSG00000222000	ENSG00000222000	AC092675.3	2:98947851-99015064	NOTEST	0	0	0	0	1	1
ENSG00000222001	ENSG00000222001	AC106876.2	2:233562008-233880595	NOTEST	0	0	0	0	1	1
ENSG00000222004	ENSG00000222004	C7orf71	7:26677489-26686889	NOTEST	0	0	0	0	1	1
ENSG00000222005	ENSG00000222005	LINC01118	2:47043806-47086146	NOTEST	0.0634286	0	#NAME?	0	1	1
ENSG00000222007	ENSG00000222007	AC064874.1	2:236402732-237040444	NOTEST	0	0	0	0	1	1
ENSG00000222012	ENSG00000222012	AC005481.5	7:157331749-158380480	NOTEST	0	0	0	0	1	1
ENSG00000222014	ENSG00000222014	RAB6C	2:130724164-130740311	NOTEST	0.0143456	0.0194676	0.440464	0	1	1
ENSG00000222017	ENSG00000222017	AC011997.1	2:198557829-198651486	NOTEST	0	0	0	0	1	1
ENSG00000222018	ENSG00000222018	C21orf140	21:35747778-35780164	NOTEST	0.0507832	0.169584	1.73957	0	1	1
ENSG00000222020	ENSG00000222020	AC062017.1	2:239969863-240324058	NOTEST	0.278334	0.232975	-0.256642	0	1	1
ENSG00000222022	ENSG00000222022	AC112721.1	2:238330062-238333919	NOTEST	0	0	0	0	1	1
ENSG00000222024	ENSG00000222024	AC004945.1	7:77646392-79100524	NOTEST	0	0.0142237	inf	0	1	1
ENSG00000222028	ENSG00000222028	PSMB11	14:23511375-23513269	NOTEST	0	0	0	0	1	1
ENSG00000222030	ENSG00000222030	AC007131.1	2:59444842-60327335	NOTEST	0	0	0	0	1	1
ENSG00000222031	ENSG00000222031	AC023469.1	2:151839019-151905288	NOTEST	0	0	0	0	1	1
ENSG00000222032	ENSG00000222032	AC112721.2	2:238337562-238343465	NOTEST	0	0	0	0	1	1
ENSG00000222033	ENSG00000222033	LINC01124	2:171568960-171571077	NOTEST	0.0428994	0.0167568	-1.35621	0	1	1
ENSG00000222035	ENSG00000222035	AC079354.3	2:202937977-203062585	NOTEST	0	0.00356806	inf	0	1	1
ENSG00000222036	ENSG00000222036	POTEG	14:19553364-19590078	NOTEST	0	0	0	0	1	1
ENSG00000222037	ENSG00000222037	IGLC6	22:23261706-23262023	NOTEST	0	0	0	0	1	1
ENSG00000222038	ENSG00000222038	POTEJ	2:131369053-131415664	NOTEST	0	0	0	0	1	1
ENSG00000222040	ENSG00000222040	ADRA2B	2:96778706-96781984	NOTEST	0.0823399	0.154647	0.909316	0	1	1
ENSG00000222042	ENSG00000222042	AP000233.4	21:26541744-26706139	NOTEST	0	0	0	0	1	1
ENSG00000222043	ENSG00000222043	AC079305.10	2:178092322-178408564	NOTEST	0.0481402	0	#NAME?	0	1	1
ENSG00000222046	ENSG00000222046	DCDC2B	1:32674694-32697205	NOTEST	0.0192604	0.0666608	1.7912	0	1	1
ENSG00000222047	ENSG00000222047	C10orf55	10:75668934-75682535	NOTEST	0	0.0196561	inf	0	1	1
ENSG00000222051	ENSG00000222051	RNU6-1165P	10:103370422-103455052	NOTEST	0	0	0	0	1	1
ENSG00000222054	ENSG00000222054	RNA5SP177	5:9621488-9903938	NOTEST	0	0	0	0	1	1
ENSG00000222055	ENSG00000222055	AC092117.1	16:2762418-2770552	NOTEST	0	0	0	0	1	1
ENSG00000222057	ENSG00000222057	RNU4-62P	3:121350245-121379774	NOTEST	0	0	0	0	1	1
ENSG00000222064	ENSG00000222064	AC108137.1	15:74183749-74183828	NOTEST	0	0	0	0	1	1
ENSG00000222066	ENSG00000222066	AL163760.1	14:98797968-98798087	NOTEST	0	0	0	0	1	1
ENSG00000222067	ENSG00000222067	RNU4-86P	11:126071992-126148026	NOTEST	0	0	0	0	1	1
ENSG00000222068	ENSG00000222068	RN7SKP154	2:133429373-134326034	NOTEST	0	0	0	0	1	1
ENSG00000222069	ENSG00000222069	RN7SKP285	1:103957500-104068105	NOTEST	0	0	0	0	1	1
ENSG00000222070	ENSG00000222070	AC010150.2	2:25945060-25945165	NOTEST	0	0	0	0	1	1
ENSG00000222071	ENSG00000222071	MIR1915	10:21781586-21786191	NOTEST	0	0	0	0	1	1
ENSG00000222072	ENSG00000222072	Y_RNA	10:102666930-102667037	NOTEST	0	0	0	0	1	1
ENSG00000222076	ENSG00000222076	RNU2-3P	15:96289032-96289223	NOTEST	0	0	0	0	1	1
ENSG00000222078	ENSG00000222078	RN7SKP110	6:90636247-91006627	NOTEST	0	0	0	0	1	1
ENSG00000222079	ENSG00000222079	AC020636.1	3:150570270-150798513	NOTEST	0	0	0	0	1	1
ENSG00000222080	ENSG00000222080	AL356310.1	1:211809247-211827923	NOTEST	0	0	0	0	1	1

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ENSG00000222086	ENSG00000222086	AC010609.1	5:156512842-156682201	NOTEST	0	0	0	0	1	1
ENSG00000222087	ENSG00000222087	RNU6-721P	18:15307661-15330281	NOTEST	0	0	0	0	1	1
ENSG00000222092	ENSG00000222092	RNU6-908P	10:29698330-30025710	NOTEST	0	0	0	0	1	1
ENSG00000222094	ENSG00000222094	RNU2-65P	15:72110736-72447800	NOTEST	0	0	0	0	1	1
ENSG00000222095	ENSG00000222095	SNORD113	14:101460593-101460667	NOTEST	0	0	0	0	1	1
ENSG00000222096	ENSG00000222096	AC019051.1	2:220970376-221569286	NOTEST	0	0	0	0	1	1
ENSG00000222099	ENSG00000222099	RN7SKP32	8:47979643-47979946	NOTEST	0	0	0	0	1	1
ENSG00000222100	ENSG00000222100	RNA5SP316	10:51224680-51371338	NOTEST	0	0	0	0	1	1
ENSG00000222101	ENSG00000222101	AC091705.2	7:25610287-25610378	NOTEST	0	0	0	0	1	1
ENSG00000222102	ENSG00000222102	RN7SKP232	5:151040656-151104343	NOTEST	0	0	0	0	1	1
ENSG00000222107	ENSG00000222107	RN7SKP117	5:124686560-124686824	NOTEST	0	0	0	0	1	1
ENSG00000222108	ENSG00000222108	RNA5SP317	10:51623416-51741813	NOTEST	0	0	0	0	1	1
ENSG00000222109	ENSG00000222109	AC093515.1	16:7949339-7949433	NOTEST	0	0	0	0	1	1
ENSG00000222111	ENSG00000222111	RN7SKP148	5:175055190-175055465	NOTEST	0	0	0	0	1	1
ENSG00000222114	ENSG00000222114	RNU6-985P	X:136770049-136770153	NOTEST	0	0	0	0	1	1
ENSG00000222117	ENSG00000222117	AL391867.1	9:105057658-105057746	NOTEST	0	0	0	0	1	1
ENSG00000222118	ENSG00000222118	RNA5SP487	20:54780107-54780229	NOTEST	0	0	0	0	1	1
ENSG00000222120	ENSG00000222120	RNA5SP81	1:242246287-242687998	NOTEST	0	0	0	0	1	1
ENSG00000222121	ENSG00000222121	AL512290.1	6:136172833-136546733	NOTEST	0	0	0	0	1	1
ENSG00000222122	ENSG00000222122	RNU6-648P	X:114266989-114267096	NOTEST	0	0	0	0	1	1
ENSG00000222123	ENSG00000222123	RNA5SP390	15:25922419-26110317	NOTEST	0	0	0	0	1	1
ENSG00000222126	ENSG00000222126	RNU2-9P	2:149583259-149583404	NOTEST	0	0	0	0	1	1
ENSG00000222129	ENSG00000222129	RNA5SP36	13:95303650-95303783	NOTEST	0	0	0	0	1	1
ENSG00000222133	ENSG00000222133	AC003666.1	X:10125023-10205700	NOTEST	0	0	0	0	1	1
ENSG00000222139	ENSG00000222139	RNU6-380P	15:80956112-80956219	NOTEST	0	0	0	0	1	1
ENSG00000222145	ENSG00000222145	SNORA73	6:89319984-89673348	NOTEST	0	0	0	0	1	1
ENSG00000222146	ENSG00000222146	RNU4-37P	8:113160970-113161054	NOTEST	0	0	0	0	1	1
ENSG00000222148	ENSG00000222148	RNY4P30	13:50463769-50463864	NOTEST	0	0	0	0	1	1
ENSG00000222150	ENSG00000222150	RNA5SP239	7:116584339-116584468	NOTEST	0	0	0	0	1	1
ENSG00000222152	ENSG00000222152	RNU6-1166P	20:34357706-34357789	NOTEST	0	0	0	0	1	1
ENSG00000222154	ENSG00000222154	RN7SKP218	7:53557840-53558132	NOTEST	0	0	0	0	1	1
ENSG00000222158	ENSG00000222158	AP003471.2	8:105342551-105479281	NOTEST	0	0	0	0	1	1
ENSG00000222160	ENSG00000222160	Y_RNA	12:107712189-108053419	NOTEST	0	0	0	0	1	1
ENSG00000222161	ENSG00000222161	Z97356.1	X:105066535-105202602	NOTEST	0	0	0	0	1	1
ENSG00000222162	ENSG00000222162	RN7SKP151	11:13298198-13408813	NOTEST	0	0	0	0	1	1
ENSG00000222164	ENSG00000222164	RN7SKP266	7:18126571-19042039	NOTEST	0	0	0	0	1	1
ENSG00000222168	ENSG00000222168	Y_RNA	1:59187950-59188044	NOTEST	0	0	0	0	1	1
ENSG00000222169	ENSG00000222169	AL162590.1	9:33041761-33076665	NOTEST	0	0	0	0	1	1
ENSG00000222170	ENSG00000222170	RNU6-257P	16:48657346-48778553	NOTEST	0	0	0	0	1	1
ENSG00000222174	ENSG00000222174	RN7SKP146	18:586516-586850	NOTEST	0	0	0	0	1	1
ENSG00000222177	ENSG00000222177	RNU4-30P	16:68344876-68482591	NOTEST	0	0	0	0	1	1
ENSG00000222178	ENSG00000222178	RNA5SP181	5:36485444-36485542	NOTEST	0	0	0	0	1	1
ENSG00000222179	ENSG00000222179	RN7SKP26	18:43563501-43652238	NOTEST	0	0	0	0	1	1

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ENSG00000222185	ENSG00000222185	SNORD113	14:101464803-101464878	NOTEST	0	0	0	0	1	1
ENSG00000222190	ENSG00000222190	MIR1910	16:85723689-85784735	NOTEST	0	0	0	0	1	1
ENSG00000222192	ENSG00000222192	Y_RNA	10:89322844-89322943	NOTEST	0	0	0	0	1	1
ENSG00000222196	ENSG00000222196	AC121157.1	4:100869242-101136662	NOTEST	0	0	0	0	1	1
ENSG00000222197	ENSG00000222197	AL359836.1	10:119039999-119134978	NOTEST	0	0	0	0	1	1
ENSG00000222202	ENSG00000222202	RNU4-26P	9:20341662-20622542	NOTEST	0	0	0	0	1	1
ENSG00000222203	ENSG00000222203	Y_RNA	X:100523240-100548059	NOTEST	0	0	0	0	1	1
ENSG00000222205	ENSG00000222205	RNA5SP266	8:58039213-58039321	NOTEST	0	0	0	0	1	1
ENSG00000222206	ENSG00000222206	Y_RNA	4:27209126-27283847	NOTEST	0	0	0	0	1	1
ENSG00000222207	ENSG00000222207	RNA5SP407	16:34969009-34969119	NOTEST	0	0	0	0	1	1
ENSG00000222208	ENSG00000222208	RNA5SP129	3:37283279-37408242	NOTEST	0	0	0	0	1	1
ENSG00000222209	ENSG00000222209	RNA5SP56	1:118806994-118807112	NOTEST	0	0	0	0	1	1
ENSG00000222210	ENSG00000222210	RN7SKP65	12:58371747-58372060	NOTEST	0	0	0	0	1	1
ENSG00000222213	ENSG00000222213	RNU6-588P	5:148931509-149014531	NOTEST	0	0	0	0	1	1
ENSG00000222219	ENSG00000222219	AC091736.1	7:135482753-135482857	NOTEST	0	0	0	0	1	1
ENSG00000222220	ENSG00000222220	RN7SKP129	7:94430825-94431124	NOTEST	0	0	0	0	1	1
ENSG00000222222	ENSG00000222222	RNU2-17P	1:150209314-150209504	NOTEST	0.438829	0	#NAME?	0	1	1
ENSG00000222224	ENSG00000222224	Y_RNA	2:29117508-29171088	NOTEST	0	0	0	0	1	1
ENSG00000222225	ENSG00000222225	RNU6-447P	11:127114-207428	NOTEST	0	0	0	0	1	1
ENSG00000222226	ENSG00000222226	AC006926.1	7:118102552-118102648	NOTEST	0	0	0	0	1	1
ENSG00000222230	ENSG00000222230	RNA5SP158	4:38760411-38760513	NOTEST	0	0	0	0	1	1
ENSG00000222231	ENSG00000222231	RNU2-54P	8:77177777-77177967	NOTEST	0	0	0	0	1	1
ENSG00000222232	ENSG00000222232	RNA5SP89	2:28906841-28906949	NOTEST	0	0	0	0	1	1
ENSG00000222235	ENSG00000222235	AL157392.1	10:13628926-14504141	NOTEST	0	0	0	0	1	1
ENSG00000222236	ENSG00000222236	RNA5SP163	4:72607409-72669758	NOTEST	0	0	0	0	1	1
ENSG00000222238	ENSG00000222238	RNU2-43P	10:103067285-103067475	NOTEST	0	0	0	0	1	1
ENSG00000222240	ENSG00000222240	RN7SKP156	1:188124969-188125311	NOTEST	0	0	0	0	1	1
ENSG00000222244	ENSG00000222244	RNA5SP431	16:79298350-79298470	NOTEST	0	0	0	0	1	1
ENSG00000222246	ENSG00000222246	MIR1471	2:232756951-232757008	NOTEST	0	0	0	0	1	1
ENSG00000222248	ENSG00000222248	RNA5SP201	6:3064224-3115421	NOTEST	0	0	0	0	1	1
ENSG00000222249	ENSG00000222249	RNU6-262P	11:119076751-119178859	NOTEST	0	0	0	0	1	1
ENSG00000222251	ENSG00000222251	RNA5SP95	2:61167356-61279125	NOTEST	0	0	0	0	1	1
ENSG00000222255	ENSG00000222255	RNU6-101P	12:102139274-102224716	NOTEST	0	0	0	0	1	1
ENSG00000222257	ENSG00000222257	RN7SKP199	4:45997135-45997440	NOTEST	0	0	0	0	1	1
ENSG00000222259	ENSG00000222259	RN7SKP114	9:34049963-34050242	NOTEST	0	0	0	0	1	1
ENSG00000222262	ENSG00000222262	AC092846.1	4:24422798-24422924	NOTEST	0	0	0	0	1	1
ENSG00000222266	ENSG00000222266	RNU6-757P	5:133936833-134063513	NOTEST	0	0	0	0	1	1
ENSG00000222267	ENSG00000222267	RNU6-892P	8:20087289-20087388	NOTEST	0	0	0	0	1	1
ENSG00000222268	ENSG00000222268	RNA5SP425	16:47178233-47735434	NOTEST	0	0	0	0	1	1
ENSG00000222274	ENSG00000222274	AC018690.1	2:100136564-100136694	NOTEST	0	0	0	0	1	1
ENSG00000222276	ENSG00000222276	RNU2-33P	14:96747594-96853625	NOTEST	0	0	0	0	1	1
ENSG00000222281	ENSG00000222281	RN7SKP111	20:11781110-11851363	NOTEST	0	0	0	0	1	1
ENSG00000222282	ENSG00000222282	RNU6-584P	1:38326368-38412729	NOTEST	0	0	0	0	1	1
ENSG00000222285	ENSG00000222285	RNA5SP193	5:136304888-136304995	NOTEST	0	0	0	0	1	1

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ENSG00000222287	ENSG00000222287	RNU6-1043P	16:30709029-30787628	NOTEST	0	0	0	0	1	1
ENSG00000222293	ENSG00000222293	RNU2-36P	9:89037852-89038043	NOTEST	0	0	0	0	1	1
ENSG00000222296	ENSG00000222296	Y_RNA	9:130577290-130617035	NOTEST	0	0	0	0	1	1
ENSG00000222297	ENSG00000222297	RNU6-1156P	11:125439111-125551018	NOTEST	0	0	0	0	1	1
ENSG00000222298	ENSG00000222298	AL031655.2	20:8112823-8949003	NOTEST	0	0	0	0	1	1
ENSG00000222299	ENSG00000222299	AC009142.1	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000222300	ENSG00000222300	RNU2-21P	2:159792309-159792497	NOTEST	0	0	0	0	1	1
ENSG00000222301	ENSG00000222301	RNY5P8	13:103451398-103528345	NOTEST	0	0	0	0	1	1
ENSG00000222302	ENSG00000222302	RNA5SP371	12:107712189-108053419	NOTEST	0	0	0	0	1	1
ENSG00000222303	ENSG00000222303	RNU6-935P	X:50334646-50557302	NOTEST	0	0	0	0	1	1
ENSG00000222305	ENSG00000222305	Y_RNA	10:92631472-92668312	NOTEST	0	0	0	0	1	1
ENSG00000222306	ENSG00000222306	Y_RNA	4:113195227-113195309	NOTEST	0	0	0	0	1	1
ENSG00000222308	ENSG00000222308	RNA5SP198	5:151202073-151304403	NOTEST	0	0	0	0	1	1
ENSG00000222309	ENSG00000222309	AL391839.1	10:32555216-32667726	NOTEST	0	0	0	0	1	1
ENSG00000222311	ENSG00000222311	AC084882.1	15:47476297-48066420	NOTEST	0	0	0	0	1	1
ENSG00000222312	ENSG00000222312	RNA5SP178	5:16033337-16033465	NOTEST	0	0	0	0	1	1
ENSG00000222313	ENSG00000222313	RN7SKP267	X:147582138-148082193	NOTEST	0	0	0	0	1	1
ENSG00000222314	ENSG00000222314	RNU6-1118P	10:38712552-38712656	NOTEST	0	0	0	0	1	1
ENSG00000222316	ENSG00000222316	AC008581.1	5:76367896-76462734	NOTEST	0	0	0	0	1	1
ENSG00000222317	ENSG00000222317	RNA5SP118	2:210288781-210598842	NOTEST	0	0	0	0	1	1
ENSG00000222320	ENSG00000222320	RNU6-1050P	18:29409135-29533099	NOTEST	0	0	0	0	1	1
ENSG00000222321	ENSG00000222321	MIR1912	X:113818550-114144624	NOTEST	0	0	0	0	1	1
ENSG00000222326	ENSG00000222326	MIR1908	11:61447904-61634826	NOTEST	0	0	0	0	1	1
ENSG00000222327	ENSG00000222327	RNU6-855P	9:114803064-114937688	NOTEST	0	0	0	0	1	1
ENSG00000222329	ENSG00000222329	RNU6-1076P	19:223157-223261	NOTEST	0	0	0	0	1	1
ENSG00000222331	ENSG00000222331	AC104434.1	3:43252232-43252363	NOTEST	0	0	0	0	1	1
ENSG00000222333	ENSG00000222333	AC093680.1	4:107336862-107336942	NOTEST	0	0	0	0	1	1
ENSG00000222334	ENSG00000222334	AC105242.1	8:78199051-78199131	NOTEST	0	0	0	0	1	1
ENSG00000222335	ENSG00000222335	Y_RNA	3:195924319-195938308	NOTEST	0	0	0	0	1	1
ENSG00000222337	ENSG00000222337	RN7SKP225	9:102046303-102046655	NOTEST	0	0	0	0	1	1
ENSG00000222338	ENSG00000222338	RNU6-174P	12:3715798-3873985	NOTEST	0	0	0	0	1	1
ENSG00000222339	ENSG00000222339	AP000807.2	11:68228185-68384179	NOTEST	0	0	0	0	1	1
ENSG00000222343	ENSG00000222343	RN7SKP139	15:47476297-48066420	NOTEST	0	0	0	0	1	1
ENSG00000222344	ENSG00000222344	RNU6-613P	2:230628553-230877825	NOTEST	0	0	0	0	1	1
ENSG00000222345	ENSG00000222345	SNORD19	3:52529353-52742182	NOTEST	0	0	0	0	1	1
ENSG00000222346	ENSG00000222346	RNA5SP237	7:111366165-111846466	NOTEST	0	0	0	0	1	1
ENSG00000222348	ENSG00000222348	RNU6-814P	3:10206548-10285427	NOTEST	0	0	0	0	1	1
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ENSG00000222352	ENSG00000222352	RN7SKP221	22:21899632-21978323	NOTEST	0	0	0	0	1	1
ENSG00000222355	ENSG00000222355	RNU2-29P	7:53723201-53879624	NOTEST	0	0	0	0	1	1
ENSG00000222356	ENSG00000222356	RNU6-710P	9:114758914-114759019	NOTEST	0	0	0	0	1	1
ENSG00000222357	ENSG00000222357	RNU2-20P	3:167967309-168548387	NOTEST	0	0	0	0	1	1
ENSG00000222359	ENSG00000222359	RNU6-355P	16:90168678-90244752	NOTEST	0	0	0	0	1	1
ENSG00000222361	ENSG00000222361	RNU6-1186P	15:98589895-98836406	NOTEST	0	0	0	0	1	1
ENSG00000222363	ENSG00000222363	RNU4-34P	17:27679086-27878922	NOTEST	0	0	0	0	1	1

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ENSG00000222365	ENSG00000222365	SNORD12B	20:47835883-47905797	NOTEST	0	0	0	0	1	1
ENSG00000222370	ENSG00000222370	SNORA36B	1:220321634-220445796	NOTEST	0	0	0	0	1	1
ENSG00000222371	ENSG00000222371	RN7SKP202	10:69865911-69971774	NOTEST	0	0	0	0	1	1
ENSG00000222373	ENSG00000222373	RNY5P5	6:25192640-25192718	NOTEST	0	0	0	0	1	1
ENSG00000222374	ENSG00000222374	AC022021.1	10:28339921-28623415	NOTEST	0	0	0	0	1	1
ENSG00000222375	ENSG00000222375	RN7SKP127	16:29742371-29742725	NOTEST	0	0	0	0	1	1
ENSG00000222376	ENSG00000222376	RN7SKP152	2:166813908-167232503	NOTEST	0	0	0	0	1	1
ENSG00000222378	ENSG00000222378	RNA5SP44	1:39546987-39952849	NOTEST	0	0	0	0	1	1
ENSG00000222383	ENSG00000222383	RNA5SP203	6:10747991-10979553	NOTEST	0	0	0	0	1	1
ENSG00000222385	ENSG00000222385	RN7SKP158	11:28042166-28355054	NOTEST	0	0	0	0	1	1
ENSG00000222386	ENSG00000222386	RN7SKP86	7:102937868-103629963	NOTEST	0	0	0	0	1	1
ENSG00000222389	ENSG00000222389	RNU2-28P	3:81538849-81811312	NOTEST	0	0	0	0	1	1
ENSG00000222391	ENSG00000222391	AL137118.1	13:49326224-49326292	NOTEST	0	0	0	0	1	1
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ENSG00000222395	ENSG00000222395	Y_RNA	18:29598334-30050447	NOTEST	0	0	0	0	1	1
ENSG00000222397	ENSG00000222397	RN7SKP229	1:181808607-181808909	NOTEST	0	0	0	0	1	1
ENSG00000222398	ENSG00000222398	RNU6-554P	15:43885251-44010458	NOTEST	0	0	0	0	1	1
ENSG00000222399	ENSG00000222399	RNU6-791P	1:222676973-222677077	NOTEST	0	0	0	0	1	1
ENSG00000222404	ENSG00000222404	RN7SKP281	2:158114109-158170723	NOTEST	0	0	0	0	1	1
ENSG00000222405	ENSG00000222405	RNU4-65P	12:70837563-70837703	NOTEST	0	0	0	0	1	1
ENSG00000222406	ENSG00000222406	RNA5SP314	10:48901101-48950972	NOTEST	0	0	0	0	1	1
ENSG00000222407	ENSG00000222407	RNA5SP80	1:231417159-231417270	NOTEST	0	0	0	0	1	1
ENSG00000222408	ENSG00000222408	AL160279.1	9:90359815-90359908	NOTEST	0	0	0	0	1	1
ENSG00000222409	ENSG00000222409	AC103996.1	15:94133095-94651167	NOTEST	0	0	0	0	1	1
ENSG00000222411	ENSG00000222411	RNY5P3	3:170136652-170578169	NOTEST	0	0	0	0	1	1
ENSG00000222412	ENSG00000222412	Y_RNA	10:32044969-32045064	NOTEST	0	0	0	0	1	1
ENSG00000222413	ENSG00000222413	RN7SKP125	9:119187503-120177348	NOTEST	0	0	0	0	1	1
ENSG00000222414	ENSG00000222414	RNU2-59P	10:103113819-103317078	NOTEST	0	0	0	0	1	1
ENSG00000222416	ENSG00000222416	RNA5SP274	8:94225530-94753245	NOTEST	0	0	0	0	1	1
ENSG00000222418	ENSG00000222418	RNA5SP113	2:182818967-182996125	NOTEST	0	0	0	0	1	1
ENSG00000222419	ENSG00000222419	RNA5SP511	X:103105725-103105840	NOTEST	0	0	0	0	1	1
ENSG00000222421	ENSG00000222421	Y_RNA	9:130577290-130617035	NOTEST	0	0	0	0	1	1
ENSG00000222426	ENSG00000222426	RNU2-50P	9:34179002-34329198	NOTEST	0	0	0	0	1	1
ENSG00000222427	ENSG00000222427	RNA5SP338	11:22644078-22834601	NOTEST	0	0	0	0	1	1
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ENSG00000222430	ENSG00000222430	Y_RNA	10:103605355-103815950	NOTEST	0	0	0	0	1	1
ENSG00000222431	ENSG00000222431	RNU6-141P	6:20402397-20493941	NOTEST	0	0	0	0	1	1
ENSG00000222432	ENSG00000222432	Y_RNA	7:77428121-77586818	NOTEST	0	0	0	0	1	1
ENSG00000222436	ENSG00000222436	RN7SKP278	10:110700726-110701068	NOTEST	0	0	0	0	1	1
ENSG00000222437	ENSG00000222437	AC118282.3	4:49199219-49199301	NOTEST	0	0	0	0	1	1
ENSG00000222438	ENSG00000222438	RNU6-1077P	12:131354280-131354382	NOTEST	0	0	0	0	1	1
ENSG00000222439	ENSG00000222439	RNU6-994P	20:61968690-61968801	NOTEST	0	0	0	0	1	1
ENSG00000222440	ENSG00000222440	RNU2-26P	X:91034259-91878229	NOTEST	0	0	0	0	1	1

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ENSG00000222449	ENSG00000222449	RNU6-1140P	2:238471807-238471913	NOTEST	0	0	0	0	1	1
ENSG00000222451	ENSG00000222451	RN7SKP143	10:91923407-91923717	NOTEST	0	0	0	0	1	1
ENSG00000222452	ENSG00000222452	RN7SKP59	9:80780380-80780694	NOTEST	0	0	0	0	1	1
ENSG00000222455	ENSG00000222455	RNA5SP296	9:130577290-130617035	NOTEST	0	0	0	0	1	1
ENSG00000222457	ENSG00000222457	RNU6-121P	1:154270125-154270224	NOTEST	0	0	0	0	1	1
ENSG00000222459	ENSG00000222459	RNA5SP293	9:110681146-110681259	NOTEST	0	0	0	0	1	1
ENSG00000222460	ENSG00000222460	RN7SKP271	20:34213952-34288906	NOTEST	0.0987956	0	#NAME?	0	1	1
ENSG00000222463	ENSG00000222463	AP005138.1	18:4775052-5004536	NOTEST	0	0	0	0	1	1
ENSG00000222465	ENSG00000222465	RNU2-5P	9:72658496-72873782	NOTEST	0	0	0	0	1	1
ENSG00000222467	ENSG00000222467	Y_RNA	2:122095351-122407163	NOTEST	0	0	0	0	1	1
ENSG00000222468	ENSG00000222468	RNA5SP261	8:31455614-31455720	NOTEST	0	0	0	0	1	1
ENSG00000222472	ENSG00000222472	RN7SKP7	13:97593534-97636426	NOTEST	0	0	0	0	1	1
ENSG00000222477	ENSG00000222477	RNU2-23P	11:64915054-64915249	NOTEST	0	0	0	0	1	1
ENSG00000222481	ENSG00000222481	AC012150.1	12:29273715-29273815	NOTEST	0	0	0	0	1	1
ENSG00000222482	ENSG00000222482	AC005071.1	7:99775185-99869855	NOTEST	0	0	0	0	1	1
ENSG00000222486	ENSG00000222486	RNU6-77P	13:81824572-81876542	NOTEST	0	0	0	0	1	1
ENSG00000222488	ENSG00000222488	RNU6-285P	8:73921098-73960357	NOTEST	0	0	0	0	1	1
ENSG00000222489	ENSG00000222489	SNORA79	14:20779526-20801471	NOTEST	4.04496	0	#NAME?	0	1	1
ENSG00000222490	ENSG00000222490	RNU6-712P	3:90233783-90233883	NOTEST	0	0	0	0	1	1
ENSG00000222492	ENSG00000222492	AC092069.1	19:13069668-13069761	NOTEST	0	0	0	0	1	1
ENSG00000222493	ENSG00000222493	Y_RNA	12:2904118-3050306	NOTEST	0	0	0	0	1	1
ENSG00000222494	ENSG00000222494	AC091178.1	17:37213271-37310647	NOTEST	0	0	0	0	1	1
ENSG00000222496	ENSG00000222496	RN7SKP200	2:207086038-207086358	NOTEST	0	0	0	0	1	1
ENSG00000222499	ENSG00000222499	RN7SKP177	3:156543269-156763918	NOTEST	0	0	0	0	1	1
ENSG00000222500	ENSG00000222500	RNA5SP475	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000222501	ENSG00000222501	RNU4-25P	8:128806778-129113499	NOTEST	0	0	0	0	1	1
ENSG00000222503	ENSG00000222503	Y_RNA	10:105239359-105615301	NOTEST	0	0	0	0	1	1
ENSG00000222506	ENSG00000222506	Y_RNA	3:170779127-171178197	NOTEST	0	0	0	0	1	1
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ENSG00000222511	ENSG00000222511	Y_RNA	1:8412456-8877702	NOTEST	0	0	0	0	1	1
ENSG00000222512	ENSG00000222512	AL137019.1	9:111121131-111121209	NOTEST	0	0	0	0	1	1
ENSG00000222514	ENSG00000222514	RN7SKP223	7:137687069-137802732	NOTEST	0	0	0	0	1	1
ENSG00000222515	ENSG00000222515	RN7SKP240	6:21665002-22214734	NOTEST	0	0	0	0	1	1
ENSG00000222518	ENSG00000222518	AL645819.1	X:124796898-124796989	NOTEST	0	0	0	0	1	1
ENSG00000222520	ENSG00000222520	RNA5SP451	18:19508945-19509055	NOTEST	0	0	0	0	1	1
ENSG00000222521	ENSG00000222521	AC026956.1	15:82334118-82338482	NOTEST	0	0	0	0	1	1
ENSG00000222522	ENSG00000222522	RNU6-519P	8:48891973-48892081	NOTEST	0	0	0	0	1	1
ENSG00000222524	ENSG00000222524	RN7SKP109	19:56186591-56249768	NOTEST	0	0	0	0	1	1
ENSG00000222526	ENSG00000222526	AC060835.1	4:138149281-138149385	NOTEST	0	0	0	0	1	1
ENSG00000222529	ENSG00000222529	Y_RNA	11:118841207-118841305	NOTEST	0	0	0	0	1	1
ENSG00000222532	ENSG00000222532	MIR1468	X:63005881-63005967	NOTEST	0	0	0	0	1	1
ENSG00000222533	ENSG00000222533	RNU6-705P	5:180728967-180729071	NOTEST	0	0	0	0	1	1
ENSG00000222536	ENSG00000222536	RNU2-39P	2:72403112-73053170	NOTEST	0	0	0	0	1	1

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ENSG00000222544	ENSG00000222544	RNU6-735P	12:95832512-95832619	NOTEST	0	0	0	0	1	1
ENSG00000222545	ENSG00000222545	AC080037.1	17:70642087-71088851	NOTEST	0	0	0	0	1	1
ENSG00000222546	ENSG00000222546	RNA5SP251	8:2792874-4852494	NOTEST	0	0	0	0	1	1
ENSG00000222548	ENSG00000222548	AC006534.1	17:65809697-65809770	NOTEST	0	0	0	0	1	1
ENSG00000222551	ENSG00000222551	AC106732.1	5:73567506-73567590	NOTEST	0	0	0	0	1	1
ENSG00000222552	ENSG00000222552	RNA5SP60	1:159141398-159177763	NOTEST	0	0	0	0	1	1
ENSG00000222558	ENSG00000222558	RNU6-1064P	9:110560024-110560128	NOTEST	0	0	0	0	1	1
ENSG00000222560	ENSG00000222560	RNU4-43P	5:26012997-26013134	NOTEST	0	0	0	0	1	1
ENSG00000222561	ENSG00000222561	RNU6-1025P	11:924893-1012239	NOTEST	0	0	0	0	1	1
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ENSG00000222570	ENSG00000222570	AF216667.1	8:133693145-133693248	NOTEST	0	0	0	0	1	1
ENSG00000222574	ENSG00000222574	RN7SKP61	3:78210848-78211143	NOTEST	0	0	0	0	1	1
ENSG00000222578	ENSG00000222578	RNA5SP345	11:95566045-95658479	NOTEST	0	0	0	0	1	1
ENSG00000222579	ENSG00000222579	Y_RNA	12:105196330-105352522	NOTEST	0	0	0	0	1	1
ENSG00000222581	ENSG00000222581	RNU2-47P	9:12300265-12300451	NOTEST	0	0	0	0	1	1
ENSG00000222582	ENSG00000222582	RNU2-66P	4:155675907-155749965	NOTEST	0	0	0	0	1	1
ENSG00000222583	ENSG00000222583	RN7SKP222	3:191810910-191811225	NOTEST	0	0	0	0	1	1
ENSG00000222585	ENSG00000222585	RNA5SP494	22:25960815-26125261	NOTEST	0	0	0	0	1	1
ENSG00000222586	ENSG00000222586	AC010999.1	15:57210820-57591479	NOTEST	0	0	0	0	1	1
ENSG00000222588	ENSG00000222588	SNORA19	10:120794355-120840316	NOTEST	0	0	0	0	1	1
ENSG00000222589	ENSG00000222589	RN7SKP159	8:5768466-5768758	NOTEST	0	0	0	0	1	1
ENSG00000222591	ENSG00000222591	AC118345.2	2:66466631-66466786	NOTEST	0	0	0	0	1	1
ENSG00000222592	ENSG00000222592	RNU6-887P	4:39400768-39400868	NOTEST	0	0	0	0	1	1
ENSG00000222594	ENSG00000222594	RN7SKP235	4:145888263-146101313	NOTEST	0	0	0	0	1	1
ENSG00000222596	ENSG00000222596	AL445523.1	X:64435116-64435222	NOTEST	0	0	0	0	1	1
ENSG00000222598	ENSG00000222598	RNU2-49P	5:115110015-115110199	NOTEST	0	0	0	0	1	1
ENSG00000222601	ENSG00000222601	Y_RNA	12:120941076-121015397	NOTEST	0	0	0	0	1	1
ENSG00000222602	ENSG00000222602	AL136160.1	13:37302738-37302829	NOTEST	0	0	0	0	1	1
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ENSG00000222609	ENSG00000222609	RNU4-69P	5:120046392-120046535	NOTEST	0	0	0	0	1	1
ENSG00000222610	ENSG00000222610	RNU6-402P	5:98190907-98262240	NOTEST	0	0	0	0	1	1
ENSG00000222611	ENSG00000222611	AL355388.1	1:156041803-156051789	NOTEST	0	0	0	0	1	1
ENSG00000222612	ENSG00000222612	RNU2-52P	20:39652844-39653034	NOTEST	0	0	0	0	1	1
ENSG00000222613	ENSG00000222613	Y_RNA	4:141700192-141700295	NOTEST	0	0	0	0	1	1
ENSG00000222614	ENSG00000222614	Y_RNA	19:47222763-47291851	NOTEST	0	0	0	0	1	1
ENSG00000222615	ENSG00000222615	AC134025.1	3:70246044-70361877	NOTEST	0	0	0	0	1	1
ENSG00000222616	ENSG00000222616	RN7SKP27	2:23084423-23084756	NOTEST	0	0	0	0	1	1
ENSG00000222617	ENSG00000222617	RN7SKP254	15:97029811-97030121	NOTEST	0	0	0	0	1	1
ENSG00000222623	ENSG00000222623	RNU6-1100P	1:141473-173862	NOTEST	0	0	0	0	1	1
ENSG00000222624	ENSG00000222624	RNU2-15P	1:65713901-65881689	NOTEST	0	0	0	0	1	1
ENSG00000222626	ENSG00000222626	RNU2-48P	5:157403773-157403964	NOTEST	0	0	0	0	1	1
ENSG00000222627	ENSG00000222627	RNU2-37P	3:127770483-128127485	NOTEST	0	0	0	0	1	1

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ENSG00000222630	ENSG00000222630	RN7SKP41	8:43236786-43237091	NOTEST	0	0	0	0	1	1
ENSG00000222631	ENSG00000222631	AC025426.1	10:71561643-71724031	NOTEST	0	0	0	0	1	1
ENSG00000222635	ENSG00000222635	RNU6-1203P	12:48436680-48540187	NOTEST	0	0	0	0	1	1
ENSG00000222636	ENSG00000222636	RN7SKP54	7:100663352-100702020	NOTEST	0	0	0	0	1	1
ENSG00000222640	ENSG00000222640	RNU2-51P	14:70791797-70883778	NOTEST	0	0	0	0	1	1
ENSG00000222643	ENSG00000222643	AL603632.1	13:106780719-106780837	NOTEST	0	0	0	0	1	1
ENSG00000222644	ENSG00000222644	RNU2-16P	4:76750606-76750742	NOTEST	0	0	0	0	1	1
ENSG00000222647	ENSG00000222647	AC002070.1	12:119772516-120119435	NOTEST	0	0	0	0	1	1
ENSG00000222649	ENSG00000222649	Y_RNA	6:119134604-119470552	NOTEST	0	0	0	0	1	1
ENSG00000222650	ENSG00000222650	RNU2-70P	1:236305831-236445319	NOTEST	0	0	0	0	1	1
ENSG00000222651	ENSG00000222651	MIR1469	15:96670597-96883492	NOTEST	0	0	0	0	1	1
ENSG00000222652	ENSG00000222652	RNU6-248P	6:76802550-76802657	NOTEST	0	0	0	0	1	1
ENSG00000222658	ENSG00000222658	Y_RNA	9:12885319-12885416	NOTEST	0	0	0	0	1	1
ENSG00000222659	ENSG00000222659	RNU2-8P	6:121901477-121901667	NOTEST	0	0	0	0	1	1
ENSG00000222663	ENSG00000222663	RNU4-55P	11:105480720-105852819	NOTEST	0	0	0	0	1	1
ENSG00000222664	ENSG00000222664	RN7SKP123	1:93491808-93492099	NOTEST	0	0	0	0	1	1
ENSG00000222666	ENSG00000222666	U3	10:28696968-28697180	NOTEST	0	0	0	0	1	1
ENSG00000222667	ENSG00000222667	RNU6-394P	X:65896099-65896206	NOTEST	0	0	0	0	1	1
ENSG00000222670	ENSG00000222670	CU459211.1	GL000241.1:11450-11589	NOTEST	0	0	0	0	1	1
ENSG00000222675	ENSG00000222675	RNA5SP146	3:156891706-156891829	NOTEST	0	0	0	0	1	1
ENSG00000222677	ENSG00000222677	AL513123.1	6:113836188-113836285	NOTEST	0	0	0	0	1	1
ENSG00000222678	ENSG00000222678	RN7SKP213	2:220455408-220455706	NOTEST	0	0	0	0	1	1
ENSG00000222679	ENSG00000222679	RNU6-1267P	17:28565758-28619074	NOTEST	0	0	0	0	1	1
ENSG00000222682	ENSG00000222682	RNA5SP38	13:106807720-106807839	NOTEST	0	0	0	0	1	1
ENSG00000222683	ENSG00000222683	AC093004.1	3:130064358-130203688	NOTEST	0	0	0	0	1	1
ENSG00000222685	ENSG00000222685	RN7SKP119	2:47572296-47614740	NOTEST	0	0	0	0	1	1
ENSG00000222686	ENSG00000222686	RNU4-72P	6:86461298-86461471	NOTEST	0	0	0	0	1	1
ENSG00000222691	ENSG00000222691	RNU6-733P	4:108745718-108899955	NOTEST	0	0	0	0	1	1
ENSG00000222692	ENSG00000222692	AC007402.1	2:51259738-52635055	NOTEST	0	0	0	0	1	1
ENSG00000222693	ENSG00000222693	RN7SKP120	9:25088808-25089149	NOTEST	0	0	0	0	1	1
ENSG00000222698	ENSG00000222698	Y_RNA	22:41441500-41441595	NOTEST	0	0	0	0	1	1
ENSG00000222701	ENSG00000222701	Y_RNA	16:30482907-30483024	NOTEST	0	0	0	0	1	1
ENSG00000222704	ENSG00000222704	RN7SKP182	18:36596010-36596308	NOTEST	0	0	0	0	1	1
ENSG00000222705	ENSG00000222705	RN7SKP39	10:28721936-28784742	NOTEST	0	0	0	0	1	1
ENSG00000222706	ENSG00000222706	RN7SKP89	5:113589209-113589451	NOTEST	0	0	0	0	1	1
ENSG00000222713	ENSG00000222713	RN7SKP51	6:117609462-117923691	NOTEST	0	0	0	0	1	1
ENSG00000222714	ENSG00000222714	RN7SKP38	2:219283814-219433084	NOTEST	0	0	0	0	1	1
ENSG00000222715	ENSG00000222715	MIR1911	X:113818550-114144624	NOTEST	0	0	0	0	1	1
ENSG00000222717	ENSG00000222717	AC016553.1	5:13174876-13174960	NOTEST	0	0	0	0	1	1
ENSG00000222719	ENSG00000222719	AC116038.2	3:38841786-38841885	NOTEST	0	0	0	0	1	1
ENSG00000222720	ENSG00000222720	AC027307.1	19:1554667-1568057	NOTEST	0	0	0	0	1	1
ENSG00000222721	ENSG00000222721	RN7SKP188	4:168584136-168584453	NOTEST	0	0	0	0	1	1
ENSG00000222722	ENSG00000222722	AL161790.1	9:126118448-126692431	NOTEST	0	0	0	0	1	1
ENSG00000222724	ENSG00000222724	RNU2-63P	2:88315872-88316066	NOTEST	0	0	0	0	1	1

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ENSG00000222727	ENSG00000222727	RNU4-64P	4:186947609-186947740	NOTEST	0	0	0	0	1	1
ENSG00000222729	ENSG00000222729	RNU2-67P	8:110886141-110886247	NOTEST	0	0	0	0	1	1
ENSG00000222730	ENSG00000222730	AC092296.1	19:36803968-36822620	NOTEST	0	0	0	0	1	1
ENSG00000222732	ENSG00000222732	AC008671.1	5:171636643-171711075	NOTEST	0	0	0	0	1	1
ENSG00000222733	ENSG00000222733	RNY4P29	13:59101788-59101885	NOTEST	0	0	0	0	1	1
ENSG00000222736	ENSG00000222736	RNU4-6P	X:16893268-16893390	NOTEST	0	0	0	0	1	1
ENSG00000222740	ENSG00000222740	RNA5SP328	10:127700949-128077024	NOTEST	0	0	0	0	1	1
ENSG00000222741	ENSG00000222741	RNA5SP229	7:33168855-33645680	NOTEST	0	0	0	0	1	1
ENSG00000222743	ENSG00000222743	RNU6-1190P	5:37379313-37753537	NOTEST	0	0	0	0	1	1
ENSG00000222744	ENSG00000222744	RN7SKP166	12:66686462-66686767	NOTEST	0	0	0	0	1	1
ENSG00000222747	ENSG00000222747	RNA5SP25	13:21943928-21944038	NOTEST	0	0	0	0	1	1
ENSG00000222749	ENSG00000222749	AL021398.1	1:177140632-177251558	NOTEST	0	0	0	0	1	1
ENSG00000222750	ENSG00000222750	RNU4-46P	16:19421817-19510435	NOTEST	0	0	0	0	1	1
ENSG00000222755	ENSG00000222755	RN7SKP206	8:130303228-130303521	NOTEST	0	0	0	0	1	1
ENSG00000222760	ENSG00000222760	RNU4-53P	9:36190852-36304921	NOTEST	0	0	0	0	1	1
ENSG00000222761	ENSG00000222761	RNU6-684P	14:104867279-104867385	NOTEST	0	0	0	0	1	1
ENSG00000222764	ENSG00000222764	RN7SKP106	6:141807277-141807549	NOTEST	0	0	0	0	1	1
ENSG00000222765	ENSG00000222765	RNU2-40P	4:66672957-66673153	NOTEST	0	0	0	0	1	1
ENSG00000222767	ENSG00000222767	Y_RNA	16:47178233-47735434	NOTEST	0	0	0	0	1	1
ENSG00000222770	ENSG00000222770	AC138761.1	17:21821898-21821986	NOTEST	0	0	0	0	1	1
ENSG00000222774	ENSG00000222774	RN7SKP121	11:127275922-127276227	NOTEST	0	0	0	0	1	1
ENSG00000222776	ENSG00000222776	AE000659.1	14:22248784-22248866	NOTEST	0	0	0	0	1	1
ENSG00000222777	ENSG00000222777	RNU6-233P	17:37617763-37721160	NOTEST	0	0	0	0	1	1
ENSG00000222778	ENSG00000222778	RNA5SP144	3:143905746-143905862	NOTEST	0	0	0	0	1	1
ENSG00000222783	ENSG00000222783	RN7SKP212	3:130530611-130530939	NOTEST	0	0	0	0	1	1
ENSG00000222784	ENSG00000222784	RN7SKP91	1:31316669-31316957	NOTEST	0	0	0	0	1	1
ENSG00000222787	ENSG00000222787	AL645944.1	1:30357748-30357852	NOTEST	0	0	0	0	1	1
ENSG00000222788	ENSG00000222788	RNU2-38P	1:144836156-145076186	NOTEST	0	0	0	0	1	1
ENSG00000222790	ENSG00000222790	RNU4-14P	5:139739786-139780952	NOTEST	0	0	0	0	1	1
ENSG00000222791	ENSG00000222791	RNU6-67P	13:83872205-83872302	NOTEST	0	0	0	0	1	1
ENSG00000222792	ENSG00000222792	RNU6-860P	3:197879236-197925886	NOTEST	0	0	0	0	1	1
ENSG00000222795	ENSG00000222795	RNU4-83P	8:101843955-101844088	NOTEST	0	0	0	0	1	1
ENSG00000222796	ENSG00000222796	RNU6-383P	X:150123966-150124060	NOTEST	0	0	0	0	1	1
ENSG00000222800	ENSG00000222800	RNU2-62P	6:27077568-27077759	NOTEST	0	0	0	0	1	1
ENSG00000222805	ENSG00000222805	AC010319.1	19:17546317-17571763	NOTEST	0	0	0	0	1	1
ENSG00000222806	ENSG00000222806	RNA5SP225	6:153741572-153741707	NOTEST	0	0	0	0	1	1
ENSG00000222808	ENSG00000222808	RNU4-47P	17:75082797-75213179	NOTEST	0	0	0	0	1	1
ENSG00000222810	ENSG00000222810	RNU2-68P	X:71549365-71792953	NOTEST	0	0	0	0	1	1
ENSG00000222821	ENSG00000222821	RNU4-27P	1:36868321-36868460	NOTEST	0	0	0	0	1	1
ENSG00000222826	ENSG00000222826	RN7SKP286	2:139621166-139621465	NOTEST	0	0	0	0	1	1
ENSG00000222831	ENSG00000222831	MIR1537	1:235824340-236046940	NOTEST	0	0	0	0	1	1
ENSG00000222832	ENSG00000222832	RNA5SP120	2:217536827-217858802	NOTEST	0	0	0	0	1	1
ENSG00000222833	ENSG00000222833	AC069067.1	3:151352137-151352251	NOTEST	0	0	0	0	1	1
ENSG00000222834	ENSG00000222834	AC074035.1	X:4636833-4636955	NOTEST	0	0	0	0	1	1

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ENSG00000222838	ENSG00000222838	RNA5SP136	3:72740855-72740962	NOTEST	0	0	0	0	1	1
ENSG00000222842	ENSG00000222842	RN7SKP168	2:17304107-17304407	NOTEST	0	0	0	0	1	1
ENSG00000222844	ENSG00000222844	RNU6-321P	11:125034582-125303285	NOTEST	0	0	0	0	1	1
ENSG00000222845	ENSG00000222845	RN7SKP42	2:187866602-188430487	NOTEST	0	0	0	0	1	1
ENSG00000222849	ENSG00000222849	RNA5SP21	1:78245308-78344106	NOTEST	0	0	0	0	1	1
ENSG00000222852	ENSG00000222852	Y_RNA	5:180326076-180377906	NOTEST	0	0	0	0	1	1
ENSG00000222854	ENSG00000222854	RNA5SP59	1:148913272-148913382	NOTEST	0	0	0	0	1	1
ENSG00000222858	ENSG00000222858	RNU6-920P	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000222859	ENSG00000222859	RN7SKP136	4:178102595-178102895	NOTEST	0	0	0	0	1	1
ENSG00000222861	ENSG00000222861	RNY5P4	4:130692813-130876523	NOTEST	0	0	0	0	1	1
ENSG00000222862	ENSG00000222862	RNU6-1086P	8:27537348-27537452	NOTEST	0	0	0	0	1	1
ENSG00000222864	ENSG00000222864	AL596268.1	X:35074447-35074575	NOTEST	0	0	0	0	1	1
ENSG00000222869	ENSG00000222869	RNU6-565P	7:36893960-37488852	NOTEST	0	0	0	0	1	1
ENSG00000222870	ENSG00000222870	RNU6-1328P	7:94124610-94124716	NOTEST	0	0	0	0	1	1
ENSG00000222872	ENSG00000222872	RNU4-78P	3:42055293-42267381	NOTEST	0	0	0	0	1	1
ENSG00000222874	ENSG00000222874	RN7SKP33	20:45487971-45488311	NOTEST	0	0	0	0	1	1
ENSG00000222880	ENSG00000222880	RN7SKP261	12:80603232-80772870	NOTEST	0	0	0	0	1	1
ENSG00000222881	ENSG00000222881	Y_RNA	17:38544767-38574202	NOTEST	0	0	0	0	1	1
ENSG00000222883	ENSG00000222883	Y_RNA	3:75955845-77699115	NOTEST	0	0	0	0	1	1
ENSG00000222884	ENSG00000222884	AC023513.1	12:42473562-42473684	NOTEST	0	0	0	0	1	1
ENSG00000222888	ENSG00000222888	AC012467.1	3:53901092-53916296	NOTEST	0	0	0	0	1	1
ENSG00000222889	ENSG00000222889	RN7SKP29	8:70579281-70767206	NOTEST	0	0	0	0	1	1
ENSG00000222890	ENSG00000222890	RNU6-1068P	12:101805134-101805237	NOTEST	0	0	0	0	1	1
ENSG00000222894	ENSG00000222894	AL662800.1	6:30568176-30594172	NOTEST	0	0	0	0	1	1
ENSG00000222895	ENSG00000222895	RNU6-1133P	6:31050786-31050886	NOTEST	0	0	0	0	1	1
ENSG00000222898	ENSG00000222898	RN7SKP97	8:61969716-62627155	NOTEST	0.0910187	0.291744	1.68047	0	1	1
ENSG00000222899	ENSG00000222899	AL110292.1	14:27305933-27629626	NOTEST	0	0	0	0	1	1
ENSG00000222909	ENSG00000222909	RNU6-193P	10:35231896-35232003	NOTEST	0	0	0	0	1	1
ENSG00000222915	ENSG00000222915	RNU6-564P	22:30727976-30825045	NOTEST	0	0	0	0	1	1
ENSG00000222920	ENSG00000222920	RNA5SP29	13:51568646-51654998	NOTEST	0	0	0	0	1	1
ENSG00000222921	ENSG00000222921	RNA5SP104	2:134877553-135212192	NOTEST	0	0	0	0	1	1
ENSG00000222922	ENSG00000222922	RNA5SP501	X:31115793-33357558	NOTEST	0	0	0	0	1	1
ENSG00000222923	ENSG00000222923	RNU2-41P	2:115177701-115177879	NOTEST	0	0	0	0	1	1
ENSG00000222924	ENSG00000222924	RNU6-1148P	5:137405043-137405147	NOTEST	0	0	0	0	1	1
ENSG00000222931	ENSG00000222931	RN7SKP205	14:24261138-24261445	NOTEST	0	0	0	0	1	1
ENSG00000222932	ENSG00000222932	RNU6-172P	12:102139274-102224716	NOTEST	0	0	0	0	1	1
ENSG00000222934	ENSG00000222934	RN7SKP284	3:86411281-86411624	NOTEST	0	0	0	0	1	1
ENSG00000222937	ENSG00000222937	SNORD63	5:137890570-137911133	NOTEST	0	0	0	0	1	1
ENSG00000222939	ENSG00000222939	AC079467.1	5:66675205-67198428	NOTEST	0	0	0	0	1	1
ENSG00000222940	ENSG00000222940	RNU6-370P	2:24232950-24286551	NOTEST	0	0	0	0	1	1
ENSG00000222941	ENSG00000222941	Y_RNA	7:151613411-151613503	NOTEST	0	0	0	0	1	1
ENSG00000222942	ENSG00000222942	RN7SKP58	3:41236327-42003922	NOTEST	0	0	0	0	1	1
ENSG00000222945	ENSG00000222945	AC091866.1	5:50357302-50357391	NOTEST	0	0	0	0	1	1
ENSG00000222950	ENSG00000222950	RN7SKP262	12:25932220-25932503	NOTEST	0	0	0	0	1	1

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ENSG00000222954	ENSG00000222954	AC110611.1	4:56796147-56796239	NOTEST	0	0	0	0	1	1
ENSG00000222955	ENSG00000222955	RNA5SP265	8:56608982-56738007	NOTEST	0	0	0	0	1	1
ENSG00000222958	ENSG00000222958	MIR1913	6:166822851-167370679	NOTEST	0	0	0	0	1	1
ENSG00000222960	ENSG00000222960	RNU6-272P	5:53179774-53606412	NOTEST	0	0	0	0	1	1
ENSG00000222961	ENSG00000222961	AC008949.1	5:32354455-32444867	NOTEST	0	0	0	0	1	1
ENSG00000222966	ENSG00000222966	SNORA40	7:99549655-99549781	NOTEST	0	0	0	0	1	1
ENSG00000222969	ENSG00000222969	RN7SKP8	13:98794815-99102027	NOTEST	0	0	0	0	1	1
ENSG00000222971	ENSG00000222971	RNA5SP222	6:146348781-146758734	NOTEST	0	0	0	0	1	1
ENSG00000222972	ENSG00000222972	RNU6-651P	2:202509592-202563417	NOTEST	0	0	0	0	1	1
ENSG00000222973	ENSG00000222973	RNU2-25P	9:2015341-2193624	NOTEST	0	0	0	0	1	1
ENSG00000222974	ENSG00000222974	RN7SKP228	7:12916308-12916571	NOTEST	0	0	0	0	1	1
ENSG00000222976	ENSG00000222976	RN7SKP94	17:55849306-55912110	NOTEST	0	0	0	0	1	1
ENSG00000222978	ENSG00000222978	Y_RNA	12:7965107-8043744	NOTEST	0	0	0	0	1	1
ENSG00000222979	ENSG00000222979	RN7SKP167	10:123170429-123170714	NOTEST	0	0	0	0	1	1
ENSG00000222982	ENSG00000222982	RN7SKP216	12:114942680-114942992	NOTEST	0	0	0	0	1	1
ENSG00000222983	ENSG00000222983	RNA5SP127	3:31270206-31270339	NOTEST	0	0	0	0	1	1
ENSG00000222985	ENSG00000222985	RNU2-14P	14:65591069-65591260	NOTEST	0	0	0	0	1	1
ENSG00000222986	ENSG00000222986	RNU5A-5P	1:231664398-232177018	NOTEST	0	0	0	0	1	1
ENSG00000222987	ENSG00000222987	RN7SKP68	5:101638207-101638514	NOTEST	0	0	0	0	1	1
ENSG00000222990	ENSG00000222990	RNU4-22P	14:88851267-89021077	NOTEST	0	0	0	0	1	1
ENSG00000222994	ENSG00000222994	AC006322.1	7:83548917-83549019	NOTEST	0	0	0	0	1	1
ENSG00000222997	ENSG00000222997	Y_RNA	10:132303369-132303465	NOTEST	0	0	0	0	1	1
ENSG00000222998	ENSG00000222998	RN7SKP259	11:57219162-57219495	NOTEST	0	0	0	0	1	1
ENSG00000222999	ENSG00000222999	AC105247.1	18:20714527-21017925	NOTEST	0	0	0	0	1	1
ENSG00000223001	ENSG00000223001	RNU2-61P	6:89773218-89773409	NOTEST	0	0	0	0	1	1
ENSG00000223003	ENSG00000223003	RNA5SP184	5:55395506-55529186	NOTEST	0	0	0	0	1	1
ENSG00000223004	ENSG00000223004	SNORD29	5:24811589-24811657	NOTEST	0	0	0	0	1	1
ENSG00000223006	ENSG00000223006	RN7SKP137	4:121956767-122001631	NOTEST	0	0	0	0	1	1
ENSG00000223007	ENSG00000223007	RN7SKP73	5:5126158-5126450	NOTEST	0	0	0	0	1	1
ENSG00000223009	ENSG00000223009	AL138930.1	1:160454819-160493052	NOTEST	0	0	0	0	1	1
ENSG00000223012	ENSG00000223012	RN7SKP264	9:88835179-88874572	NOTEST	0	0	0	0	1	1
ENSG00000223013	ENSG00000223013	RNA5SP344	11:75514475-75854239	NOTEST	0	0	0	0	1	1
ENSG00000223015	ENSG00000223015	RNU6-1135P	11:87317674-87317777	NOTEST	0	0	0	0	1	1
ENSG00000223018	ENSG00000223018	AL096700.1	X:18881681-18881826	NOTEST	0	0	0	0	1	1
ENSG00000223019	ENSG00000223019	RNA5SP306	10:26102739-26102846	NOTEST	0	0	0	0	1	1
ENSG00000223023	ENSG00000223023	Y_RNA	18:20279443-20606451	NOTEST	0	0	0	0	1	1
ENSG00000223024	ENSG00000223024	RNU6-55P	13:19390857-19446107	NOTEST	0	0	0	0	1	1
ENSG00000223026	ENSG00000223026	RN7SKP247	1:81717473-81717781	NOTEST	0	0	0	0	1	1
ENSG00000223027	ENSG00000223027	SNORA57	10:26986587-27150016	NOTEST	0	0	0	0	1	1
ENSG00000223029	ENSG00000223029	AC004969.1	7:89511666-89867451	NOTEST	0	0	0	0	1	1
ENSG00000223030	ENSG00000223030	AC091697.1	7:18126571-19042039	NOTEST	0	0	0	0	1	1
ENSG00000223036	ENSG00000223036	AC024158.1	3:3688139-3688262	NOTEST	0	0	0	0	1	1
ENSG00000223037	ENSG00000223037	RNU6-284P	4:165541883-165541989	NOTEST	0	0	0	0	1	1
ENSG00000223039	ENSG00000223039	RN7SKP268	6:151561133-151679692	NOTEST	0	0.229672	inf	0	1	1

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ENSG00000223040	ENSG00000223040	RN7SKP144	3:2130616-2130895	NOTEST	0	0	0	0	1	1
ENSG00000223042	ENSG00000223042	RN7SKP161	12:10222152-10264226	NOTEST	0	0	0	0	1	1
ENSG00000223044	ENSG00000223044	RNU6-130P	6:82879699-82957471	NOTEST	0	0	0	0	1	1
ENSG00000223046	ENSG00000223046	RNA5SP369	12:102230597-102230705	NOTEST	0	0	0	0	1	1
ENSG00000223047	ENSG00000223047	RNU6-847P	10:35215702-35215810	NOTEST	0	0	0	0	1	1
ENSG00000223052	ENSG00000223052	AC007096.1	7:29019582-29603286	NOTEST	0	0	0	0	1	1
ENSG00000223053	ENSG00000223053	AC022142.1	5:97974800-97974935	NOTEST	0	0	0	0	1	1
ENSG00000223056	ENSG00000223056	RN7SKP169	22:26138110-26427007	NOTEST	0	0	0	0	1	1
ENSG00000223059	ENSG00000223059	AL354896.1	13:88795121-88888337	NOTEST	0	0	0	0	1	1
ENSG00000223060	ENSG00000223060	Y_RNA	19:56598731-56632649	NOTEST	0	0	0	0	1	1
ENSG00000223061	ENSG00000223061	AC145212.3	GL000194.1:84812-84895	NOTEST	0	0	0	0	1	1
ENSG00000223062	ENSG00000223062	RNU6-1245P	1:28151048-28151154	NOTEST	0	0	0	0	1	1
ENSG00000223063	ENSG00000223063	AL157823.1	6:35541361-35696360	NOTEST	0	0	0	0	1	1
ENSG00000223064	ENSG00000223064	RNU6-325P	10:87297135-87297240	NOTEST	0	0	0	0	1	1
ENSG00000223070	ENSG00000223070	AC006377.1	7:31790792-32338941	NOTEST	0	0	0	0	1	1
ENSG00000223075	ENSG00000223075	RN7SKP126	1:192844815-192845115	NOTEST	0	0	0	0	1	1
ENSG00000223076	ENSG00000223076	RNA5SP31	13:61187741-61187868	NOTEST	0	0	0	0	1	1
ENSG00000223078	ENSG00000223078	RNU2-55P	21:24654057-24654231	NOTEST	0	0	0	0	1	1
ENSG00000223080	ENSG00000223080	Y_RNA	11:8964926-8965014	NOTEST	0	0	0	0	1	1
ENSG00000223082	ENSG00000223082	AC121336.1	12:40019968-40499891	NOTEST	0	0	0	0	1	1
ENSG00000223086	ENSG00000223086	RNA5SP155	4:10075962-10118573	NOTEST	0	0	0	0	1	1
ENSG00000223087	ENSG00000223087	RNU6-602P	14:31959161-32330430	NOTEST	0	0	0	0	1	1
ENSG00000223088	ENSG00000223088	RMRPP5	9:24905466-24905733	NOTEST	0	0	0	0	1	1
ENSG00000223091	ENSG00000223091	RNU6-981P	17:37617763-37721160	NOTEST	0	0	0	0	1	1
ENSG00000223092	ENSG00000223092	RNA5SP115	2:201713760-201713867	NOTEST	0	0	0	0	1	1
ENSG00000223096	ENSG00000223096	RNU5E-9P	2:179007274-179007378	NOTEST	0	0	0	0	1	1
ENSG00000223099	ENSG00000223099	AC119751.4	4:49601444-49601526	NOTEST	0	0	0	0	1	1
ENSG00000223101	ENSG00000223101	AP002364.1	11:89984399-90648220	NOTEST	0	0	0	0	1	1
ENSG00000223107	ENSG00000223107	RNU2-72P	10:62629195-62761198	NOTEST	0	0	0	0	1	1
ENSG00000223109	ENSG00000223109	MIR1538	16:69598996-69738569	NOTEST	0	0	0	0	1	1
ENSG00000223111	ENSG00000223111	SNORA74	10:51592079-51623365	NOTEST	0	0	0	0	1	1
ENSG00000223113	ENSG00000223113	RNA5SP247	7:139993492-140126050	NOTEST	0	0	0	0	1	1
ENSG00000223116	ENSG00000223116	AL157931.1	13:23551993-23552136	NOTEST	0	0	0	0	1	1
ENSG00000223118	ENSG00000223118	RN7SKP102	2:124626832-124627147	NOTEST	0	0	0	0	1	1
ENSG00000223119	ENSG00000223119	RNU6-1139P	1:242187250-242187356	NOTEST	0	0	0	0	1	1
ENSG00000223120	ENSG00000223120	RN7SKP181	15:97385298-97385614	NOTEST	0	0	0	0	1	1
ENSG00000223123	ENSG00000223123	AC010546.1	16:62859864-62859952	NOTEST	0	0	0	0	1	1
ENSG00000223125	ENSG00000223125	RNU2-32P	17:39624207-39624398	NOTEST	0	0	0	0	1	1
ENSG00000223126	ENSG00000223126	RN7SKP263	12:94402514-94402823	NOTEST	0	0	0	0	1	1
ENSG00000223128	ENSG00000223128	RN7SKP140	20:21405395-21405679	NOTEST	0	0	0	0	1	1
ENSG00000223131	ENSG00000223131	RNA5SP304	10:23216952-23326518	NOTEST	0	0	0	0	1	1
ENSG00000223134	ENSG00000223134	AL122015.1	11:33278217-33378569	NOTEST	0	0	0	0	1	1
ENSG00000223136	ENSG00000223136	RN7SKP207	5:29948934-29949237	NOTEST	0	0	0	0	1	1
ENSG00000223138	ENSG00000223138	RNA5SP450	18:9913998-9960018	NOTEST	0	0	0	0	1	1
ENSG00000223142	ENSG00000223142	RN7SKP252	22:50132324-50132651	NOTEST	0	0	0	0	1	1

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ENSG00000223145	ENSG00000223145	RN7SKP112	2:7281357-7281675	NOTEST	0	0	0	0	1	1
ENSG00000223148	ENSG00000223148	AC011478.1	19:30710572-31204445	NOTEST	0	0	0	0	1	1
ENSG00000223149	ENSG00000223149	AC010376.1	5:67263272-67263379	NOTEST	0	0	0	0	1	1
ENSG00000223152	ENSG00000223152	RNU4-88P	1:66258196-66840259	NOTEST	0	0	0	0	1	1
ENSG00000223156	ENSG00000223156	RNU2-18P	10:16478941-16555736	NOTEST	0	0	0	0	1	1
ENSG00000223158	ENSG00000223158	RNY1P3	13:25946208-26599989	NOTEST	0	0	0	0	1	1
ENSG00000223162	ENSG00000223162	RNA5SP280	9:27109138-27230173	NOTEST	0	0	0	0	1	1
ENSG00000223164	ENSG00000223164	AL445384.1	14:28459210-28459321	NOTEST	0	0	0	0	1	1
ENSG00000223168	ENSG00000223168	RN7SKP142	16:51705146-51705474	NOTEST	0	0	0	0	1	1
ENSG00000223169	ENSG00000223169	RNA5SP209	6:76458908-76629254	NOTEST	0	0	0	0	1	1
ENSG00000223174	ENSG00000223174	RN7SKP17	14:77356605-77356956	NOTEST	0	0	0	0	1	1
ENSG00000223175	ENSG00000223175	RNU4-61P	1:48761043-48937845	NOTEST	0	0	0	0	1	1
ENSG00000223177	ENSG00000223177	RNA5SP39	13:108903587-108960832	NOTEST	0	0	0	0	1	1
ENSG00000223179	ENSG00000223179	RNU6-373P	5:118342041-118584833	NOTEST	0	0	0	0	1	1
ENSG00000223180	ENSG00000223180	AC087738.1	15:84115979-84287495	NOTEST	0	0	0	0	1	1
ENSG00000223181	ENSG00000223181	RNU6-1199P	1:693612-693716	NOTEST	0	0	0	0	1	1
ENSG00000223182	ENSG00000223182	SNORA74	10:51371389-51387768	NOTEST	0	0	0	0	1	1
ENSG00000223187	ENSG00000223187	Y_RNA	11:47636449-47636546	NOTEST	0	0	0	0	1	1
ENSG00000223188	ENSG00000223188	Y_RNA	9:132815704-132902448	NOTEST	0	0	0	0	1	1
ENSG00000223189	ENSG00000223189	RNU6-177P	7:128171751-128269512	NOTEST	0	0	0	0	1	1
ENSG00000223190	ENSG00000223190	RN7SKP100	20:40701391-41818610	NOTEST	0	0	0	0	1	1
ENSG00000223191	ENSG00000223191	RNU6-293P	6:159347497-159347603	NOTEST	0	0	0	0	1	1
ENSG00000223192	ENSG00000223192	Y_RNA	3:57685499-57685575	NOTEST	0	0	0	0	1	1
ENSG00000223197	ENSG00000223197	RNU6-1001P	2:155945950-155946050	NOTEST	0	0	0	0	1	1
ENSG00000223198	ENSG00000223198	RNU2-22P	2:232366700-232366912	NOTEST	0	0	0	0	1	1
ENSG00000223200	ENSG00000223200	AC008836.1	5:60853109-60853194	NOTEST	0	0	0	0	1	1
ENSG00000223201	ENSG00000223201	AC004699.1	19:15160194-15169104	NOTEST	0	0	0	0	1	1
ENSG00000223202	ENSG00000223202	RN7SKP297	11:74396268-74396550	NOTEST	0	0	0	0	1	1
ENSG00000223203	ENSG00000223203	RNA5SP221	6:143743968-143771810	NOTEST	0	0	0	0	1	1
ENSG00000223208	ENSG00000223208	RNU6-1217P	4:120355159-120355263	NOTEST	0	0	0	0	1	1
ENSG00000223211	ENSG00000223211	AL158150.1	9:18473891-18910948	NOTEST	0	0	0	0	1	1
ENSG00000223212	ENSG00000223212	RNU4-74P	7:140752048-140752209	NOTEST	0	0	0	0	1	1
ENSG00000223213	ENSG00000223213	SNORD81	12:54185088-54185131	NOTEST	0	0	0	0	1	1
ENSG00000223214	ENSG00000223214	AC091559.1	8:15274723-15624158	NOTEST	0	0	0	0	1	1
ENSG00000223215	ENSG00000223215	RNU6-607P	8:37483532-37531905	NOTEST	0	0	0	0	1	1
ENSG00000223217	ENSG00000223217	RNU6-938P	17:73405166-73405269	NOTEST	0	0	0	0	1	1
ENSG00000223220	ENSG00000223220	Y_RNA	8:71581599-71702606	NOTEST	0	0	0	0	1	1
ENSG00000223223	ENSG00000223223	RN7SKP192	11:59473529-59473856	NOTEST	0	0	0	0	1	1
ENSG00000223224	ENSG00000223224	SNORD71	16:71762912-71843104	NOTEST	0	0	0	0	1	1
ENSG00000223225	ENSG00000223225	RNU6-1054P	4:119512927-119555914	NOTEST	0	0	0	0	1	1
ENSG00000223229	ENSG00000223229	RN7SKP270	1:97161411-97161723	NOTEST	0	0	0	0	1	1
ENSG00000223231	ENSG00000223231	AL035706.1	1:84041458-84326706	NOTEST	0	0	0	0	1	1
ENSG00000223235	ENSG00000223235	AP003498.2	11:71417524-71417624	NOTEST	0	0	0	0	1	1
ENSG00000223238	ENSG00000223238	RNA5SP294	9:114122971-114247025	NOTEST	0	0	0	0	1	1
ENSG00000223243	ENSG00000223243	AC074323.1	10:80510358-80510454	NOTEST	0	0	0	0	1	1

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ENSG00000223244	ENSG00000223244	MIR1909	19:1815247-1848452	NOTEST	0	0	0	0	1	1
ENSG00000223245	ENSG00000223245	RNU4-63P	2:42098410-42098528	NOTEST	0	0	0	0	1	1
ENSG00000223247	ENSG00000223247	RNU2-64P	3:73160142-73160333	NOTEST	0	0	0	0	1	1
ENSG00000223249	ENSG00000223249	Y_RNA	2:190539015-190630282	NOTEST	0	0	0	0	1	1
ENSG00000223253	ENSG00000223253	AC022872.1	15:72110736-72447800	NOTEST	0	0	0	0	1	1
ENSG00000223254	ENSG00000223254	Y_RNA	1:85729978-85730085	NOTEST	0	0	0	0	1	1
ENSG00000223255	ENSG00000223255	RN7SKP274	17:34216561-34216808	NOTEST	0	0	0	0	1	1
ENSG00000223256	ENSG00000223256	RNU6-785P	9:141150044-141150148	NOTEST	0	0	0	0	1	1
ENSG00000223258	ENSG00000223258	RNU6-575P	7:43152197-43605600	NOTEST	0	0	0	0	1	1
ENSG00000223259	ENSG00000223259	RNA5SP508	X:75875409-75875528	NOTEST	0	0	0	0	1	1
ENSG00000223260	ENSG00000223260	RN7SKP194	X:95665430-95665781	NOTEST	0	0	0	0	1	1
ENSG00000223262	ENSG00000223262	RNA5SP492	21:43619798-43717354	NOTEST	0	0	0	0	1	1
ENSG00000223263	ENSG00000223263	RNU6-387P	1:67873492-67896098	NOTEST	0	0	0	0	1	1
ENSG00000223265	ENSG00000223265	RNU6-592P	11:122449912-122450015	NOTEST	0	0	0	0	1	1
ENSG00000223269	ENSG00000223269	RN7SKP53	11:98891682-100229616	NOTEST	0	0	0	0	1	1
ENSG00000223271	ENSG00000223271	Y_RNA	15:66628543-66679084	NOTEST	0	0	0	0	1	1
ENSG00000223273	ENSG00000223273	RN7SKP172	12:76709530-76709828	NOTEST	0	0	0	0	1	1
ENSG00000223274	ENSG00000223274	RNA5SP498	X:1387692-1429274	NOTEST	0	0	0	0	1	1
ENSG00000223275	ENSG00000223275	AC006026.1	7:23708895-23708973	NOTEST	0	0	0	0	1	1
ENSG00000223280	ENSG00000223280	RNU6-57P	13:41885340-41951166	NOTEST	0	0	0	0	1	1
ENSG00000223281	ENSG00000223281	RN7SKP85	8:99413630-99955055	NOTEST	0	0	0	0	1	1
ENSG00000223282	ENSG00000223282	RN7SKP165	1:226633637-226633993	NOTEST	0	0	0	0	1	1
ENSG00000223284	ENSG00000223284	RNU6-195P	19:41197433-41271294	NOTEST	0	0	0	0	1	1
ENSG00000223286	ENSG00000223286	AL121952.1	6:155054458-155635627	NOTEST	0	0	0	0	1	1
ENSG00000223287	ENSG00000223287	RNU6-954P	21:15281894-15352758	NOTEST	0	0	0	0	1	1
ENSG00000223290	ENSG00000223290	RNA5SP107	2:155446918-155447040	NOTEST	0	0	0	0	1	1
ENSG00000223291	ENSG00000223291	AL354680.1	6:12717892-13328815	NOTEST	0	0	0	0	1	1
ENSG00000223293	ENSG00000223293	RNA5SP270	8:70842139-70842257	NOTEST	0	0	0	0	1	1
ENSG00000223294	ENSG00000223294	SNORD83	12:64969444-64969521	NOTEST	0	0	0	0	1	1
ENSG00000223297	ENSG00000223297	AC116154.1	8:96216683-96822364	NOTEST	0	0	0	0	1	1
ENSG00000223298	ENSG00000223298	RNY3P8	13:95963083-95963209	NOTEST	0	0	0	0	1	1
ENSG00000223299	ENSG00000223299	RN7SKP108	14:97104523-97104851	NOTEST	0	0	0	0	1	1
ENSG00000223300	ENSG00000223300	Y_RNA	14:74318546-74551196	NOTEST	0	0	0	0	1	1
ENSG00000223302	ENSG00000223302	Y_RNA	10:112402435-112402543	NOTEST	0	0	0	0	1	1
ENSG00000223305	ENSG00000223305	RN7SKP30	4:56262123-56414056	NOTEST	0.174228	0	#NAME?	0	1	1
ENSG00000223306	ENSG00000223306	RNU6-1304P	1:225888305-225939945	NOTEST	0	0	0	0	1	1
ENSG00000223307	ENSG00000223307	AC119674.1	1:56843004-56843090	NOTEST	0	0	0	0	1	1
ENSG00000223308	ENSG00000223308	RN7SKP101	15:46985485-47097042	NOTEST	0	0	0	0	1	1
ENSG00000223309	ENSG00000223309	RNU6-722P	X:48816439-48816543	NOTEST	0	0	0	0	1	1
ENSG00000223313	ENSG00000223313	RNU6-516P	15:40780239-40857256	NOTEST	0	0	0	0	1	1
ENSG00000223315	ENSG00000223315	RN7SKP279	11:127277745-127278043	NOTEST	0	0	0	0	1	1
ENSG00000223316	ENSG00000223316	AC027281.1	16:70841280-71264625	NOTEST	0	0	0	0	1	1
ENSG00000223318	ENSG00000223318	RNA5SP111	2:165752186-165752287	NOTEST	0	0	0	0	1	1
ENSG00000223321	ENSG00000223321	RN7SKP293	6:12406717-12407013	NOTEST	0	0	0	0	1	1
ENSG00000223322	ENSG00000223322	AL033378.1	6:148558720-148873186	NOTEST	0	0	0	0	1	1

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ENSG00000223324	ENSG00000223324	RN7SKP273	11:111473114-111637151	NOTEST	0	0	0	0	1	1
ENSG00000223327	ENSG00000223327	RNU2-71P	8:81497819-81498008	NOTEST	0	0	0	0	1	1
ENSG00000223330	ENSG00000223330	RNU6-1052P	7:56469762-56469866	NOTEST	0	0	0	0	1	1
ENSG00000223335	ENSG00000223335	RNU6-603P	6:32256302-32339684	NOTEST	0	0	0	0	1	1
ENSG00000223336	ENSG00000223336	RNU2-6P	13:46916138-47012325	NOTEST	0	0	0	0	1	1
ENSG00000223341	ENSG00000223341	RN7SKP3	13:45513383-45657260	NOTEST	0	0	0	0	1	1
ENSG00000223342	ENSG00000223342	RP3-429O6.1	6:6901254-6918948	NOTEST	0	0	0	0	1	1
ENSG00000223343	ENSG00000223343	RP13-131K19.2	3:48955220-49060928	NOTEST	0	0.0317958	inf	0	1	1
ENSG00000223344	ENSG00000223344	RP11-541F9.1	1:191827836-191980390	NOTEST	0	0	0	0	1	1
ENSG00000223345	ENSG00000223345	HIST2H2BA	1:120906027-120935937	NOTEST	0.275155	0.105592	-1.38175	0	1	1
ENSG00000223349	ENSG00000223349	KLF2P3	2:131437622-131476404	NOTEST	0	0	0	0	1	1
ENSG00000223350	ENSG00000223350	IGLV9-49	22:22697538-22698084	NOTEST	0	0	0	0	1	1
ENSG00000223351	ENSG00000223351	ZNF385D-AS2	3:21459914-22414812	NOTEST	0	0	0	0	1	1
ENSG00000223352	ENSG00000223352	HLA-U	HSCHR6_MHC_COX:29891599-29891785	NOTEST	0	0	0	0	1	1
ENSG00000223353	ENSG00000223353	RP11-290P14.2	1:245132651-245290466	NOTEST	0.000345068	0.198179	9.16571	0	1	1
ENSG00000223355	ENSG00000223355	NOTCH4	HSCHR6_MHC_MCF:32234969-32268294	NOTEST	0	0	0	0	1	1
ENSG00000223356	ENSG00000223356	RP11-66D17.5	1:156682003-156682966	NOTEST	0	0	0	0	1	1
ENSG00000223358	ENSG00000223358	EHHADH-AS1	3:184880658-184999778	NOTEST	0	0	0	0	1	1
ENSG00000223359	ENSG00000223359	DASS-397D15.4	HSCHR6_MHC_MANN:32492183-32492279	NOTEST	0	0	0	0	1	1
ENSG00000223360	ENSG00000223360	AC096559.2	2:12739112-12745271	NOTEST	0	0	0	0	1	1
ENSG00000223362	ENSG00000223362	CDY15P	Y:26001668-26003238	NOTEST	0	0	0	0	1	1
ENSG00000223364	ENSG00000223364	PSORS1C3	HSCHR6_MHC_COX:31134077-31138243	NOTEST	0	0	0	0	1	1
ENSG00000223367	ENSG00000223367	RPS18	HSCHR6_MHC_DBB:33195233-33222212	NOTEST	0	0	0	0	1	1
ENSG00000223368	ENSG00000223368	RP11-401G5.1	9:76485811-76488213	NOTEST	0	0	0	0	1	1
ENSG00000223372	ENSG00000223372	HLA-DPB2	HSCHR6_MHC_MCF:33113648-33118417	NOTEST	0	0	0	0	1	1
ENSG00000223373	ENSG00000223373	AC108066.1	2:213446080-214017151	NOTEST	0	0	0	0	1	1
ENSG00000223375	ENSG00000223375	RP11-224O19.5	1:218511882-218512098	NOTEST	0	0	0	0	1	1
ENSG00000223376	ENSG00000223376	RPS17P1	HSCHR6_MHC_MCF:29456832-29457238	NOTEST	0	0	0	0	1	1
ENSG00000223377	ENSG00000223377	RP5-1014O16.1	X:148839681-148839956	NOTEST	0	0	0	0	1	1
ENSG00000223379	ENSG00000223379	RP11-374M1.4	9:45004878-45023236	NOTEST	0	0.111888	inf	0	1	1
ENSG00000223381	ENSG00000223381	RP11-655H13.2	10:110470275-110599121	NOTEST	0	0	0	0	1	1
ENSG00000223382	ENSG00000223382	RP1-65J11.1	1:31297074-31307131	NOTEST	0.287067	0.239718	-0.26005	0	1	1
ENSG00000223383	ENSG00000223383	HIST1H2APS6	13:37064214-37064578	NOTEST	0	0	0	0	1	1
ENSG00000223387	ENSG00000223387	RP11-408H1.3	3:172278677-172313397	NOTEST	0.00976697	0.00342823	-1.51045	0	1	1
ENSG00000223389	ENSG00000223389	SDCBP2P1	6:74032559-74033173	NOTEST	0	0	0	0	1	1
ENSG00000223390	ENSG00000223390	RP11-91A18.4	1:52485802-52556388	NOTEST	0	0.029813	inf	0	1	1
ENSG00000223391	ENSG00000223391	GS1-309P15.3	X:27535887-27535998	NOTEST	0	0	0	0	1	1
ENSG00000223392	ENSG00000223392	CLDN10-AS1	13:96085857-96296957	NOTEST	0.153575	0.0608462	-1.3357	0	1	1
ENSG00000223393	ENSG00000223393	RP5-858B6.3	1:231010591-231014761	NOTEST	0.0675523	0.0879994	0.38149	0	1	1
ENSG00000223394	ENSG00000223394	TRBV29OR9-2	9:33750514-33920402	NOTEST	0	0	0	0	1	1
ENSG00000223395	ENSG00000223395	RBM22P7	X:52245866-52246128	NOTEST	0	0	0	0	1	1
ENSG00000223396	ENSG00000223396	RPS10P7	1:201452657-201502736	NOTEST	0.264616	0.299064	0.176555	0	1	1
ENSG00000223398	ENSG00000223398	AC027124.2	3:13501923-13502389	NOTEST	0	0	0	0	1	1

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ENSG00000223400	ENSG00000223400	AP006748.1	21:42948061-42953246	NOTEST	0	0	0	0	1	1
ENSG00000223401	ENSG00000223401	RP11-211G3.2	3:187416046-187463515	NOTEST	0.11629	0.220388	0.922315	0	1	1
ENSG00000223402	ENSG00000223402	AC074121.4	7:98107862-98108537	NOTEST	0	0	0	0	1	1
ENSG00000223403	ENSG00000223403	MEG9	14:101536247-101539274	NOTEST	0	0	0	0	1	1
ENSG00000223404	ENSG00000223404	LINC00397	13:88453290-88456063	NOTEST	0	0	0	0	1	1
ENSG00000223405	ENSG00000223405	DDR1-AS1	HSCHR6_MHC_QBL:30824354-30833288	NOTEST	0	0	0	0	1	1
ENSG00000223406	ENSG00000223406	XKRYP5	Y:27898534-27899017	NOTEST	0	0	0	0	1	1
ENSG00000223407	ENSG00000223407	USP9YP18	Y:25805612-25813969	NOTEST	0	0	0	0	1	1
ENSG00000223408	ENSG00000223408	RP11-38P6.1	9:67579806-67583159	NOTEST	0	0	0	0	1	1
ENSG00000223409	ENSG00000223409	RPL17P17	3:65339199-66024509	NOTEST	0	0	0	0	1	1
ENSG00000223410	ENSG00000223410	RP1-191L6.2	20:38749681-38754998	NOTEST	0	0	0	0	1	1
ENSG00000223412	ENSG00000223412	SUCLA2P1	HSCHR6_MHC_COX:30426521-30427891	NOTEST	0	0	0	0	1	1
ENSG00000223416	ENSG00000223416	RPS26P15	1:57394882-59012474	NOTEST	0.159985	0.452548	1.50014	0	1	1
ENSG00000223417	ENSG00000223417	TRIM49D1	11:89644278-89654935	NOTEST	0	0	0	0	1	1
ENSG00000223418	ENSG00000223418	GS1-590J6.2	X:11722242-11723710	NOTEST	0	0	0	0	1	1
ENSG00000223419	ENSG00000223419	AC006022.4	7:30692199-30965131	NOTEST	0	0	0	0	1	1
ENSG00000223421	ENSG00000223421	RP11-572H4.1	9:31165615-31166978	NOTEST	0	0	0	0	1	1
ENSG00000223422	ENSG00000223422	AC007274.2	Y:7546939-7549069	NOTEST	0	0	0	0	1	1
ENSG00000223427	ENSG00000223427	AC016716.1	2:79384131-80875905	NOTEST	0	0	0	0	1	1
ENSG00000223428	ENSG00000223428	RP11-399K21.5	10:77029576-77171600	NOTEST	0	0	0	0	1	1
ENSG00000223429	ENSG00000223429	RP4-800M22.2	1:52608045-52831865	NOTEST	0	0.0172444	inf	0	1	1
ENSG00000223430	ENSG00000223430	AC011243.1	2:133429373-134326034	NOTEST	0	0	0	0	1	1
ENSG00000223431	ENSG00000223431	MTND6P21	21:45892777-45894980	NOTEST	0	0	0	0	1	1
ENSG00000223432	ENSG00000223432	RP11-62L18.3	10:123374938-123375353	NOTEST	0	0	0	0	1	1
ENSG00000223433	ENSG00000223433	AC079767.3	2:208519504-208519675	NOTEST	0	0	0	0	1	1
ENSG00000223436	ENSG00000223436	AC011625.1	7:131808090-132333447	NOTEST	0	0	0	0	1	1
ENSG00000223437	ENSG00000223437	TMSB4XP3	7:29638410-29782210	NOTEST	0	0	0	0	1	1
ENSG00000223438	ENSG00000223438	RP1-171K16.5	X:140590842-140738057	NOTEST	0	0	0	0	1	1
ENSG00000223439	ENSG00000223439	HLA-J	HSCHR6_MHC_MANN:29963963-30027881	NOTEST	0	0	0	0	1	1
ENSG00000223440	ENSG00000223440	RP11-555J4.4	9:32629451-32648683	NOTEST	0	0	0	0	1	1
ENSG00000223441	ENSG00000223441	OR2I1P	HSCHR6_MHC_MANN:29520599-29521547	NOTEST	0	0	0	0	1	1
ENSG00000223442	ENSG00000223442	AC004041.2	5:131877135-131999964	NOTEST	0	0	0	0	1	1
ENSG00000223443	ENSG00000223443	USP17L2	8:11973290-12008698	NOTEST	0	0	0	0	1	1
ENSG00000223445	ENSG00000223445	RPL6P21	7:14110159-14111005	NOTEST	0	0	0	0	1	1
ENSG00000223446	ENSG00000223446	RP11-274J16.5	9:95857220-95857811	NOTEST	0	0	0	0	1	1
ENSG00000223447	ENSG00000223447	HLA-DPA3	HSCHR6_MHC_SSTO:33238299-33238426	NOTEST	0	0	0	0	1	1
ENSG00000223448	ENSG00000223448	LTB	HSCHR6_MHC_MANN:31587818-31589786	NOTEST	0	0	0	0	1	1
ENSG00000223449	ENSG00000223449	RP11-93P10.2	9:66061967-66062463	NOTEST	0	0	0	0	1	1
ENSG00000223450	ENSG00000223450	RP11-52I18.1	1:179923872-180084015	NOTEST	0	0.0530312	inf	0	1	1
ENSG00000223452	ENSG00000223452	HMGN2P18	1:155121019-155121295	NOTEST	0	0	0	0	1	1
ENSG00000223454	ENSG00000223454	HCG21	HSCHR6_MHC_COX:30903455-30912338	NOTEST	0	0	0	0	1	1
ENSG00000223455	ENSG00000223455	RP11-781P14.3	10:121829491-121829671	NOTEST	0	0	0	0	1	1
ENSG00000223457	ENSG00000223457	HTATSF1P	6:33205575-33207467	NOTEST	0	0	0	0	1	1
ENSG00000223458	ENSG00000223458	RP11-332E3.2	13:76445186-76457947	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000223460	ENSG00000223460	GAPDHP69	13:29598747-30077892	NOTEST	0	0.0428114	inf	0	1	1
ENSG00000223461	ENSG00000223461	AC004471.9	22:19023794-19115962	NOTEST	0.2061	0.528578	1.35877	0	1	1
ENSG00000223462	ENSG00000223462	RP11-285G1.9	10:45306471-45491339	NOTEST	0	0.0416662	inf	0	1	1
ENSG00000223463	ENSG00000223463	HLA-H	HSCHR6_MHC_MANN:29845968-29849143	NOTEST	0	0	0	0	1	1
ENSG00000223465	ENSG00000223465	LST1	HSCHR6_MHC_DBB:31536046-31542910	NOTEST	0	0	0	0	1	1
ENSG00000223466	ENSG00000223466	AC064834.2	2:196397758-196403405	NOTEST	0	0	0	0	1	1
ENSG00000223467	ENSG00000223467	CALM1P1	X:94754602-94755035	NOTEST	0	0	0	0	1	1
ENSG00000223469	ENSG00000223469	RP11-344J7.2	6:43819493-43820070	NOTEST	0	0	0	0	1	1
ENSG00000223470	ENSG00000223470	RP11-490O24.2	10:34198165-34206723	NOTEST	0	0	0	0	1	1
ENSG00000223474	ENSG00000223474	AL020996.1	1:26126666-26185903	NOTEST	0.291416	0.156352	-0.898279	0	1	1
ENSG00000223475	ENSG00000223475	RP11-310H4.1	7:55640863-55656029	NOTEST	0	0	0	0	1	1
ENSG00000223476	ENSG00000223476	VN1R42P	7:64393650-64393994	NOTEST	0.576717	0.128048	-2.17118	0	1	1
ENSG00000223477	ENSG00000223477	LINC00842	10:47011752-47174093	NOTEST	0	0	0	0	1	1
ENSG00000223479	ENSG00000223479	RP4-788P17.1	1:74100898-74180897	NOTEST	0	0	0	0	1	1
ENSG00000223481	ENSG00000223481	TAP2	HSCHR6_MHC_DBB:32767738-32784536	NOTEST	0	0	0	0	1	1
ENSG00000223484	ENSG00000223484	TRPC6P	X:155215034-155215914	NOTEST	0	0.0505554	inf	0	1	1
ENSG00000223485	ENSG00000223485	RP11-417E7.1	6:169558186-169563019	NOTEST	0.266244	0.112596	-1.24159	0	1	1
ENSG00000223486	ENSG00000223486	AC092198.1	X:39868528-39871435	NOTEST	0.00589319	0	#NAME?	0	1	1
ENSG00000223487	ENSG00000223487	FRMPD4-AS1	X:12156584-12742642	NOTEST	0	0	0	0	1	1
ENSG00000223488	ENSG00000223488	MAPK6PS2	21:23808609-23810669	NOTEST	0	0	0	0	1	1
ENSG00000223489	ENSG00000223489	NEFHP1	1:117282602-117285231	NOTEST	0	0	0	0	1	1
ENSG00000223490	ENSG00000223490	CHCHD2P5	1:94386823-94387223	NOTEST	0	0	0	0	1	1
ENSG00000223491	ENSG00000223491	RP3-328E19.4	1:148000212-148000494	NOTEST	0.256678	0.298505	0.217795	0	1	1
ENSG00000223492	ENSG00000223492	RP11-15M15.1	20:51588945-52120853	NOTEST	0	0	0	0	1	1
ENSG00000223493	ENSG00000223493	SKIV2L	HSCHR6_MHC_DBB:31902054-31919714	NOTEST	0	0	0	0	1	1
ENSG00000223494	ENSG00000223494	VARS2	HSCHR6_MHC_MANN:30920642-30938920	NOTEST	0	0	0	0	1	1
ENSG00000223495	ENSG00000223495	RP11-763B22.7	1:148853802-148854120	NOTEST	0	0	0	0	1	1
ENSG00000223497	ENSG00000223497	AC063979.1	5:71982938-72058554	NOTEST	0	0	0	0	1	1
ENSG00000223498	ENSG00000223498	RP11-716A19.3	X:16915773-16916644	NOTEST	0	0	0	0	1	1
ENSG00000223500	ENSG00000223500	AC083862.6	7:134671258-134855547	NOTEST	0	0	0	0	1	1
ENSG00000223502	ENSG00000223502	RP11-96B5.3	10:52750944-54073888	NOTEST	0.111837	0.0463205	-1.27168	0	1	1
ENSG00000223503	ENSG00000223503	RP11-29H23.6	1:155556434-155571988	NOTEST	0	0	0	0	1	1
ENSG00000223504	ENSG00000223504	RP11-542F9.1	6:68765242-68770394	NOTEST	0	0.134694	inf	0	1	1
ENSG00000223505	ENSG00000223505	RP11-397P13.7	1:203764781-203823252	NOTEST	0	0.14684	inf	0	1	1
ENSG00000223506	ENSG00000223506	SLC20A1P1	14:107139411-107140367	NOTEST	0	0	0	0	1	1
ENSG00000223510	ENSG00000223510	CDRT15	17:14138989-14140179	NOTEST	0	0	0	0	1	1
ENSG00000223511	ENSG00000223511	RP13-297E16.4	X:1851476-1874878	NOTEST	0	0	0	0	1	1
ENSG00000223512	ENSG00000223512	BX649597.3	9:43403147-43403646	NOTEST	0	0	0	0	1	1
ENSG00000223513	ENSG00000223513	ATP6V0E1P2	3:41236327-42003922	NOTEST	0	0	0	0	1	1
ENSG00000223514	ENSG00000223514	AC004866.1	7:80964421-80964499	NOTEST	0	0	0	0	1	1
ENSG00000223516	ENSG00000223516	AFF2-IT1	X:147582138-148082193	NOTEST	0	0	0	0	1	1
ENSG00000223517	ENSG00000223517	AC010723.1	Y:16388091-16389369	NOTEST	0	0	0	0	1	1
ENSG00000223518	ENSG00000223518	CSNK1A1P1	15:36871811-37110660	NOTEST	0	0	0	0	1	1

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ENSG00000223519	ENSG00000223519	KIF28P	1:246935138-246993361	NOTEST	0.00515829	0	#NAME?	0	1	1
ENSG00000223522	ENSG00000223522	AC093690.1	2:27994583-28561768	NOTEST	0.148522	0.0380705	-1.96393	0	1	1
ENSG00000223523	ENSG00000223523	AC079613.1	2:189463517-189704171	NOTEST	0	0	0	0	1	1
ENSG00000223524	ENSG00000223524	REXO1L11P	8:86747542-86749570	NOTEST	0	0	0	0	1	1
ENSG00000223525	ENSG00000223525	RABGAP1L-IT1	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000223528	ENSG00000223528	RP11-223P11.3	10:128593977-129250781	NOTEST	0	0	0	0	1	1
ENSG00000223529	ENSG00000223529	EEF1A1P8	3:183744156-183745544	NOTEST	0	0	0	0	1	1
ENSG00000223530	ENSG00000223530	AC012506.1	2:23553534-23554915	NOTEST	0	0	0	0	1	1
ENSG00000223531	ENSG00000223531	TRIM31	HSCHR6_MHC_MCF:30149159-30160985	NOTEST	0	0	0	0	1	1
ENSG00000223532	ENSG00000223532	HLA-B	HSCHR6_MHC_COX:31312133-31315506	NOTEST	0	0	0	0	1	1
ENSG00000223533	ENSG00000223533	CCHCR1	HSCHR6_MHC_MANN:31155176-31170971	NOTEST	0	0	0	0	1	1
ENSG00000223534	ENSG00000223534	HLA-DQB1-AS1	6:32627243-32636160	NOTEST	0	0	0	0	1	1
ENSG00000223535	ENSG00000223535	FAM90A17P	8:7603555-7614766	NOTEST	0	0	0	0	1	1
ENSG00000223536	ENSG00000223536	AC008069.1	2:16909390-16948822	NOTEST	0	0	0	0	1	1
ENSG00000223537	ENSG00000223537	RP5-919F19.5	6:109809108-110012420	NOTEST	0	0	0	0	1	1
ENSG00000223538	ENSG00000223538	RP11-216P16.6	12:121545022-121545293	NOTEST	0	0	0	0	1	1
ENSG00000223539	ENSG00000223539	AC011431.1	5:135078150-135082045	NOTEST	0	0	0	0	1	1
ENSG00000223540	ENSG00000223540	RPS15AP5	10:123473120-123473508	NOTEST	0	0	0	0	1	1
ENSG00000223542	ENSG00000223542	RP1-283K11.3	6:133561735-134216691	NOTEST	0	0	0	0	1	1
ENSG00000223543	ENSG00000223543	TCEAL4P1	13:37316014-37316602	NOTEST	0	0.0277373	inf	0	1	1
ENSG00000223544	ENSG00000223544	AC005838.2	17:15468796-15587625	NOTEST	0	0	0	0	1	1
ENSG00000223547	ENSG00000223547	ZNF844	19:12175513-12192380	NOTEST	0.0752091	0.239073	1.66847	0	1	1
ENSG00000223548	ENSG00000223548	AC034228.3	5:131142682-131348892	NOTEST	0.0395025	0.0139264	-1.50412	0	1	1
ENSG00000223549	ENSG00000223549	MTND5P28	2:120770580-120974855	NOTEST	0	0.0251645	inf	0	1	1
ENSG00000223550	ENSG00000223550	SNRPBP1	7:79959507-80308593	NOTEST	0	0	0	0	1	1
ENSG00000223551	ENSG00000223551	TMSB4XP4	9:131102924-131123749	NOTEST	0.155974	0	#NAME?	0	1	1
ENSG00000223552	ENSG00000223552	RP11-24F11.2	3:46406445-46448550	NOTEST	0	0	0	0	1	1
ENSG00000223553	ENSG00000223553	SMPD4P1	22:20956881-21011201	NOTEST	0	0	0	0	1	1
ENSG00000223554	ENSG00000223554	AC078851.1	2:140582464-140583446	NOTEST	0	0	0	0	1	1
ENSG00000223555	ENSG00000223555	USP9YP23	Y:19894089-19896695	NOTEST	0	0	0	0	1	1
ENSG00000223557	ENSG00000223557	DAQB-331I12.5	HSCHR6_MHC_COX:31835085-31853014	NOTEST	0	0	0	0	1	1
ENSG00000223558	ENSG00000223558	TRIM60P17	7:63545937-63546954	NOTEST	0	0	0	0	1	1
ENSG00000223559	ENSG00000223559	RP11-700P18.1	7:56355922-56359118	NOTEST	0.0208429	0.0772855	1.89064	0	1	1
ENSG00000223560	ENSG00000223560	UBQLN1P1	HSCHR6_MHC_APD:30339125-30340294	NOTEST	0	0	0	0	1	1
ENSG00000223561	ENSG00000223561	AC003090.1	7:25632970-25790614	NOTEST	0.173174	0.137781	-0.329844	0	1	1
ENSG00000223562	ENSG00000223562	RP11-543B16.3	1:211355497-211356446	NOTEST	0	0	0	0	1	1
ENSG00000223563	ENSG00000223563	AP001601.2	21:28261694-28338832	NOTEST	0	0	0	0	1	1
ENSG00000223564	ENSG00000223564	CYP4F32P	2:95425003-95426024	NOTEST	0	0	0	0	1	1
ENSG00000223565	ENSG00000223565	RP11-344L13.1	10:85495261-85496249	NOTEST	0	0	0	0	1	1
ENSG00000223566	ENSG00000223566	TNRC18P2	7:63028120-63045453	NOTEST	0	0	0	0	1	1
ENSG00000223568	ENSG00000223568	RPL3P11	9:14040714-14041860	NOTEST	0	0	0	0	1	1
ENSG00000223569	ENSG00000223569	USP17L15	4:9236110-9237700	NOTEST	0	0	0	0	1	1
ENSG00000223570	ENSG00000223570	RP11-275I14.2	1:226376570-226376922	NOTEST	0	0	0	0	1	1
ENSG00000223571	ENSG00000223571	DHRSX-IT1	X:2137556-2420846	NOTEST	0.087998	0.147006	0.74033	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000223572	ENSG00000223572	CKMT1A	15:43885251-44010458	NOTEST	0.220942	0.288057	0.382683	0	1	1
ENSG00000223574	ENSG00000223574	TPMTP4	X:85383896-85384574	NOTEST	0	0	0	0	1	1
ENSG00000223575	ENSG00000223575	RBMX2P3	1:119573838-119869926	NOTEST	0.0188967	0	#NAME?	0	1	1
ENSG00000223576	ENSG00000223576	RP11-61K9.2	13:20397621-20437776	NOTEST	0.156524	0	#NAME?	0	1	1
ENSG00000223577	ENSG00000223577	HCG27	HSCHR6_MHC_MCF:31244105-31250362	NOTEST	0	0	0	0	1	1
ENSG00000223579	ENSG00000223579	AC011718.2	22:20632022-20661407	NOTEST	0	0	0	0	1	1
ENSG00000223581	ENSG00000223581	RP11-393K12.2	10:7139113-7139637	NOTEST	0	0	0	0	1	1
ENSG00000223583	ENSG00000223583	RP3-476K8.4	1:26758772-26797785	NOTEST	0.151614	0.0317916	-2.25368	0	1	1
ENSG00000223584	ENSG00000223584	TVP23CP1	7:89964536-90839905	NOTEST	0	0	0	0	1	1
ENSG00000223586	ENSG00000223586	RP4-662A9.2	6:133561735-134216691	NOTEST	0	0	0	0	1	1
ENSG00000223587	ENSG00000223587	AY269186.1	3:65430-66175	NOTEST	0	0	0	0	1	1
ENSG00000223588	ENSG00000223588	AC103564.9	2:132534139-132534601	NOTEST	0	0.036311	inf	0	1	1
ENSG00000223589	ENSG00000223589	RP5-884C9.3	1:38512985-38584697	NOTEST	0	0	0	0	1	1
ENSG00000223590	ENSG00000223590	C6orf205	HSCHR6_MHC_MANN:30996173-31002464	NOTEST	0	0	0	0	1	1
ENSG00000223591	ENSG00000223591	CENPVP1	X:51453886-51455227	NOTEST	0	0	0	0	1	1
ENSG00000223592	ENSG00000223592	FNDC3CP	X:77421192-77427919	NOTEST	0	0	0	0	1	1
ENSG00000223593	ENSG00000223593	AL356806.3	14:34393436-34931980	NOTEST	0	0	0	0	1	1
ENSG00000223595	ENSG00000223595	LYPLA1P1	7:122870173-122870795	NOTEST	0	0	0	0	1	1
ENSG00000223597	ENSG00000223597	CTD-2296D1.5	5:7373229-7379903	NOTEST	0	0	0	0	1	1
ENSG00000223598	ENSG00000223598	RP1-292B18.4	6:151186684-151549582	NOTEST	0	0	0	0	1	1
ENSG00000223599	ENSG00000223599	RP11-216N14.7	1:153777200-153895451	NOTEST	0.112712	0.0396175	-1.50843	0	1	1
ENSG00000223600	ENSG00000223600	EEF1A1P41	Y:2803111-2870667	NOTEST	0	0	0	0	1	1
ENSG00000223601	ENSG00000223601	EBLN1	10:22497742-22498950	NOTEST	0	0	0	0	1	1
ENSG00000223602	ENSG00000223602	AC125634.1	9:69891207-69901481	NOTEST	0	0	0	0	1	1
ENSG00000223603	ENSG00000223603	CRPP1	1:159674772-159675397	NOTEST	0	0	0	0	1	1
ENSG00000223604	ENSG00000223604	AC007394.3	2:150186498-150330662	NOTEST	0	0	0	0	1	1
ENSG00000223605	ENSG00000223605	AC107399.1	4:118171079-118171344	NOTEST	0	0	0	0	1	1
ENSG00000223606	ENSG00000223606	HLA-V	HSCHR6_MHC_DBB:29756032-29762814	NOTEST	0	0	0	0	1	1
ENSG00000223608	ENSG00000223608	DSCR4-IT1	21:39323727-39493454	NOTEST	0	0	0	0	1	1
ENSG00000223609	ENSG00000223609	HBD	11:5253907-5256600	NOTEST	0	0	0	0	1	1
ENSG00000223611	ENSG00000223611	SUPT20HL2	X:24328978-24331432	NOTEST	0	0	0	0	1	1
ENSG00000223614	ENSG00000223614	RP11-468B6.1	7:63667580-63680031	NOTEST	0	0	0	0	1	1
ENSG00000223615	ENSG00000223615	RP11-196I18.2	9:109878064-109878235	NOTEST	0	0	0	0	1	1
ENSG00000223617	ENSG00000223617	LINC00370	13:109934320-109940081	NOTEST	0	0	0	0	1	1
ENSG00000223618	ENSG00000223618	VPS52	HSCHR6_MHC_MANN:33371217-33376673	NOTEST	0	0	0	0	1	1
ENSG00000223619	ENSG00000223619	AC009960.1	2:203478936-203479427	NOTEST	0	0	0	0	1	1
ENSG00000223620	ENSG00000223620	RBM48P1	4:127484663-127485931	NOTEST	0	0	0	0	1	1
ENSG00000223621	ENSG00000223621	AK4P4	9:5855780-5856426	NOTEST	0	0.0243417	inf	0	1	1
ENSG00000223622	ENSG00000223622	GSTA6P	6:52670410-52678258	NOTEST	0	0	0	0	1	1
ENSG00000223623	ENSG00000223623	RP3-425P12.1	6:24797548-25057301	NOTEST	0	0	0	0	1	1
ENSG00000223624	ENSG00000223624	RP1-125I3.4	1:26210671-26233482	NOTEST	0	0	0	0	1	1
ENSG00000223625	ENSG00000223625	CYCSP32	13:19997016-20110903	NOTEST	0	0	0	0	1	1
ENSG00000223626	ENSG00000223626	LINC01044	13:112976880-112985539	NOTEST	0	0	0	0	1	1
ENSG00000223628	ENSG00000223628	AC023449.2	15:25826115-25826269	NOTEST	0	0	0	0	1	1

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ENSG00000223629	ENSG00000223629	DEFA8P	8:6808247-6809121	NOTEST	0	0	0	0	1	1
ENSG00000223631	ENSG00000223631	LINC01120	2:132160473-132166622	NOTEST	0	0	0	0	1	1
ENSG00000223633	ENSG00000223633	RP11-143A22.1	6:58488887-58513860	NOTEST	0	0	0	0	1	1
ENSG00000223634	ENSG00000223634	AC012506.3	2:23580386-23583247	NOTEST	0	0.0291128	inf	0	1	1
ENSG00000223635	ENSG00000223635	RP4-613A2.1	1:229644247-229650019	NOTEST	0.0654247	0.0783544	0.260179	0	1	1
ENSG00000223636	ENSG00000223636	UBE2Q2P5Y	Y:27577302-27583462	NOTEST	0	0	0	0	1	1
ENSG00000223637	ENSG00000223637	RBMY2EP	Y:23556876-23563471	NOTEST	0	0	0	0	1	1
ENSG00000223638	ENSG00000223638	RFPL4A	19:56270379-56274541	NOTEST	0	0	0	0	1	1
ENSG00000223639	ENSG00000223639	CLIC1	HSCHR6_MHC_SSTO:31684773-31697500	NOTEST	0	0	0	0	1	1
ENSG00000223640	ENSG00000223640	RPL30P3	2:9221523-9221856	NOTEST	0	0	0	0	1	1
ENSG00000223641	ENSG00000223641	TTTY17C	Y:27329789-27330920	NOTEST	0	0	0	0	1	1
ENSG00000223642	ENSG00000223642	AC008277.1	2:160175489-160473593	NOTEST	0	0.0254804	inf	0	1	1
ENSG00000223643	ENSG00000223643	RP11-108M9.1	1:17066767-17299474	NOTEST	0	0	0	0	1	1
ENSG00000223646	ENSG00000223646	AC002463.3	7:112262432-112348135	NOTEST	0	0	0	0	1	1
ENSG00000223647	ENSG00000223647	AL133249.1	2:32018891-32029049	NOTEST	0	0	0	0	1	1
ENSG00000223648	ENSG00000223648	IGHV3-64	14:107113740-107114274	NOTEST	0	0	0	0	1	1
ENSG00000223649	ENSG00000223649	RP11-359E8.3	1:211649863-211666259	NOTEST	0	0	0	0	1	1
ENSG00000223650	ENSG00000223650	UHRF2P1	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000223651	ENSG00000223651	RP5-1121H13.1	20:40619779-40692609	NOTEST	0	0	0	0	1	1
ENSG00000223652	ENSG00000223652	AC106786.1	5:122422942-122529960	NOTEST	0	0	0	0	1	1
ENSG00000223653	ENSG00000223653	RP11-131L23.1	1:85731930-86043933	NOTEST	0	0	0	0	1	1
ENSG00000223654	ENSG00000223654	FLOT1	HSCHR6_MHC_APD:30703730-30706525	NOTEST	0	0	0	0	1	1
ENSG00000223655	ENSG00000223655	RAB9AP3	Y:28064469-28065042	NOTEST	0	0	0	0	1	1
ENSG00000223656	ENSG00000223656	HMGB3P10	1:100163797-100164734	NOTEST	0	0	0	0	1	1
ENSG00000223657	ENSG00000223657	KRT8P51	7:136370305-136866854	NOTEST	0	0	0	0	1	1
ENSG00000223659	ENSG00000223659	RP5-857K21.5	1:536815-660283	NOTEST	0	0	0	0	1	1
ENSG00000223660	ENSG00000223660	AC012314.20	19:54703320-54703838	NOTEST	0	0	0	0	1	1
ENSG00000223661	ENSG00000223661	C4B-AS1	HSCHR6_MHC_MCF:31942046-31996308	NOTEST	0	0	0	0	1	1
ENSG00000223662	ENSG00000223662	SAMSN1-AS1	21:15857548-16031142	NOTEST	0	0	0	0	1	1
ENSG00000223663	ENSG00000223663	RP5-890O3.3	1:1314045-1314412	NOTEST	0	0	0	0	1	1
ENSG00000223664	ENSG00000223664	AL162415.4	9:44562092-44562588	NOTEST	0	0	0	0	1	1
ENSG00000223665	ENSG00000223665	CTB-111F10.1	7:91268161-91272827	NOTEST	0	0	0	0	1	1
ENSG00000223666	ENSG00000223666	FKBPL	HSCHR6_MHC_MCF:32172914-32174499	NOTEST	0	0	0	0	1	1
ENSG00000223668	ENSG00000223668	EEF1A1P24	3:39400035-39401413	NOTEST	0	0	0	0	1	1
ENSG00000223669	ENSG00000223669	RP11-93B14.4	20:61340188-61394123	NOTEST	0	0	0	0	1	1
ENSG00000223671	ENSG00000223671	RPL34P3	21:36160097-37376965	NOTEST	0	0	0	0	1	1
ENSG00000223672	ENSG00000223672	RP11-272P10.3	9:13322804-13323449	NOTEST	0	0	0	0	1	1
ENSG00000223675	ENSG00000223675	RP11-86H7.6	1:95051111-95057853	NOTEST	0	0	0	0	1	1
ENSG00000223676	ENSG00000223676	RPL34P26	13:50601268-51423190	NOTEST	0	0	0	0	1	1
ENSG00000223677	ENSG00000223677	OR2AD1P	6:28994456-28995384	NOTEST	0	0	0	0	1	1
ENSG00000223678	ENSG00000223678	RP11-311H10.4	9:33402854-33409946	NOTEST	0	0	0	0	1	1
ENSG00000223679	ENSG00000223679	AP000362.1	22:23332864-23350523	NOTEST	0	0	0	0	1	1
ENSG00000223680	ENSG00000223680	DDR1	HSCHR6_MHC_MCF:30927311-30938427	NOTEST	0	0	0	0	1	1
ENSG00000223683	ENSG00000223683	AL138935.1	1:63655659-63782902	NOTEST	0.0350353	0	#NAME?	0	1	1

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ENSG00000223685	ENSG00000223685	LINC00571	13:38624953-38717369	NOTEST	0.584334	0.154502	-1.91916	0	1	1
ENSG00000223687	ENSG00000223687	ZNF311	HSCHR6_MHC_COX:28959157-28969698	NOTEST	0	0	0	0	1	1
ENSG00000223688	ENSG00000223688	RPS24P14	11:3490548-3602441	NOTEST	0	0	0	0	1	1
ENSG00000223691	ENSG00000223691	AC068044.1	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000223692	ENSG00000223692	DIP2A-IT1	21:47878811-47989926	NOTEST	0	0	0	0	1	1
ENSG00000223693	ENSG00000223693	SUCLA2P1	HSCHR6_MHC_QBL:30426180-30427550	NOTEST	0	0	0	0	1	1
ENSG00000223694	ENSG00000223694	ADH5P3	1:240177647-240643504	NOTEST	0	0	0	0	1	1
ENSG00000223695	ENSG00000223695	RP4-633O19__A.1	22:36784670-36792562	NOTEST	0	0.0341397	inf	0	1	1
ENSG00000223696	ENSG00000223696	HLA-DPA3	HSCHR6_MHC_DBB:33076901-33089011	NOTEST	0	0	0	0	1	1
ENSG00000223697	ENSG00000223697	AF230666.2	8:133787617-133861052	NOTEST	0.265472	0.289199	0.123503	0	1	1
ENSG00000223698	ENSG00000223698	GOLGA6L11P	Y:26314333-26320641	NOTEST	0	0	0	0	1	1
ENSG00000223699	ENSG00000223699	COL11A2	HSCHR6_MHC_MANN:33284376-33314194	NOTEST	0	0	0	0	1	1
ENSG00000223700	ENSG00000223700	AC104395.1	2:84104850-84105677	NOTEST	0	0	0	0	1	1
ENSG00000223701	ENSG00000223701	RAET1E-AS1	6:150139933-150244257	NOTEST	0	0	0	0	1	1
ENSG00000223702	ENSG00000223702	ZDHHC20P2	6:31348187-31348616	NOTEST	0	0	0	0	1	1
ENSG00000223703	ENSG00000223703	AC027612.4	2:91924751-91955465	NOTEST	0	0.00469015	inf	0	1	1
ENSG00000223704	ENSG00000223704	RP1-90L6.2	22:27254596-27261749	NOTEST	0	0.00177416	inf	0	1	1
ENSG00000223707	ENSG00000223707	RP1-93L7.3	X:85104414-85105144	NOTEST	0.0265724	0	#NAME?	0	1	1
ENSG00000223708	ENSG00000223708	HCG4P5	HSCHR6_MHC_COX:29898586-29903209	NOTEST	0	0	0	0	1	1
ENSG00000223709	ENSG00000223709	TRIM64EP	11:89764273-89806558	NOTEST	0	0	0	0	1	1
ENSG00000223710	ENSG00000223710	CRYGGP	2:51259738-52635055	NOTEST	0	0	0	0	1	1
ENSG00000223711	ENSG00000223711	AC091633.3	3:195270870-195277400	NOTEST	0	0	0	0	1	1
ENSG00000223714	ENSG00000223714	RP5-1172N10.2	X:41134991-41136031	NOTEST	0.122892	0.0331837	-1.88884	0	1	1
ENSG00000223715	ENSG00000223715	RP11-71G7.1	3:176321930-176353320	NOTEST	0	0	0	0	1	1
ENSG00000223716	ENSG00000223716	RP11-113O24.3	9:38360423-38376427	NOTEST	0	0	0	0	1	1
ENSG00000223717	ENSG00000223717	DNAJA1P1	13:59325180-59326367	NOTEST	0	0	0	0	1	1
ENSG00000223718	ENSG00000223718	AC093107.7	7:135344786-135345401	NOTEST	0.0677699	0	#NAME?	0	1	1
ENSG00000223719	ENSG00000223719	AC024162.2	3:6532165-7783215	NOTEST	0	0	0	0	1	1
ENSG00000223720	ENSG00000223720	RP5-1024N4.2	1:48671636-48672515	NOTEST	0	0	0	0	1	1
ENSG00000223721	ENSG00000223721	UQCRFS1P2	7:138386351-138387807	NOTEST	0	0	0	0	1	1
ENSG00000223722	ENSG00000223722	RP11-467L13.5	12:31907650-31908055	NOTEST	0	0	0	0	1	1
ENSG00000223723	ENSG00000223723	BX842568.2	X:36980268-36981498	NOTEST	0	0.00987157	inf	0	1	1
ENSG00000223724	ENSG00000223724	RAD17P2	13:49550047-49783915	NOTEST	0	0	0	0	1	1
ENSG00000223725	ENSG00000223725	AC007879.5	2:208104373-208490652	NOTEST	0.0410346	0	#NAME?	0	1	1
ENSG00000223726	ENSG00000223726	CTA-929C8.7	22:27703443-27714499	NOTEST	0	0	0	0	1	1
ENSG00000223727	ENSG00000223727	AC026188.1	3:3292370-3668980	NOTEST	0	0	0	0	1	1
ENSG00000223728	ENSG00000223728	RP11-314N2.2	1:147313095-147314493	NOTEST	0	0	0	0	1	1
ENSG00000223729	ENSG00000223729	RP11-145E17.2	9:137185776-137187243	NOTEST	0	0	0	0	1	1
ENSG00000223730	ENSG00000223730	RP1-127B20.4	22:45277041-45405880	NOTEST	0	0	0	0	1	1
ENSG00000223731	ENSG00000223731	SUPT20HL1	X:24380877-24383541	NOTEST	0	0	0	0	1	1
ENSG00000223732	ENSG00000223732	RP11-321C24.1	13:45513383-45657260	NOTEST	0	0	0	0	1	1

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ENSG00000223734	ENSG00000223734	RP11-644K8.1	2:20251894-20254257	NOTEST	0.0369527	0.0287753	-0.360848	0	1	1
ENSG00000223735	ENSG00000223735	OR51B3P	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000223738	ENSG00000223738	RP11-781E19.1	3:74150499-74152704	NOTEST	0	0	0	0	1	1
ENSG00000223739	ENSG00000223739	AC007389.2	2:65663844-66311773	NOTEST	0	0	0	0	1	1
ENSG00000223740	ENSG00000223740	RP11-760D2.4	7:56593120-56593806	NOTEST	0	0	0	0	1	1
ENSG00000223741	ENSG00000223741	PSMD4P1	21:37802657-37948867	NOTEST	0.0158341	0	#NAME?	0	1	1
ENSG00000223742	ENSG00000223742	RP11-149B9.2	X:28589648-28604512	NOTEST	0	0	0	0	1	1
ENSG00000223744	ENSG00000223744	RBMY2GP	Y:6196092-6211364	NOTEST	0	0	0	0	1	1
ENSG00000223746	ENSG00000223746	TCEB1P30	10:44236884-44237798	NOTEST	0	0	0	0	1	1
ENSG00000223747	ENSG00000223747	C4B-AS1	HSCHR6_MHC_MANN:31927378-31957964	NOTEST	0	0	0	0	1	1
ENSG00000223750	ENSG00000223750	SIRPB3P	20:1645928-1688846	NOTEST	0	0	0	0	1	1
ENSG00000223751	ENSG00000223751	AC116609.2	2:741976-749856	NOTEST	0	0	0	0	1	1
ENSG00000223752	ENSG00000223752	ATAT1	HSCHR6_MHC_COX:30584467-30604447	NOTEST	0	0	0	0	1	1
ENSG00000223753	ENSG00000223753	GHc-602D8.2	X:100938778-100939448	NOTEST	0	0	0	0	1	1
ENSG00000223754	ENSG00000223754	AC008073.9	2:24299395-24424567	NOTEST	0	0	0	0	1	1
ENSG00000223756	ENSG00000223756	TSSC2	11:3402190-3430208	NOTEST	0	0.004816	inf	0	1	1
ENSG00000223757	ENSG00000223757	VWA7	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000223758	ENSG00000223758	RP11-347J14.4	9:39368375-39368790	NOTEST	0	0	0	0	1	1
ENSG00000223759	ENSG00000223759	RP11-353N4.4	1:149646784-149719362	NOTEST	0.257108	0.188476	-0.447994	0	1	1
ENSG00000223760	ENSG00000223760	MED15P9	2:130887193-130902707	NOTEST	0	0	0	0	1	1
ENSG00000223761	ENSG00000223761	RP11-57C13.4	10:89351363-89365781	NOTEST	0	0	0	0	1	1
ENSG00000223764	ENSG00000223764	RP11-54O7.3	1:852244-856396	NOTEST	0.00673428	0	#NAME?	0	1	1
ENSG00000223765	ENSG00000223765	RP1-288M22.2	6:72160536-72168577	NOTEST	0	0	0	0	1	1
ENSG00000223766	ENSG00000223766	PRR3	HSCHR6_MHC_MANN:30553828-30576175	NOTEST	0	0	0	0	1	1
ENSG00000223767	ENSG00000223767	RNF5	HSCHR6_MHC_APD:32157474-32159914	NOTEST	0	0	0	0	1	1
ENSG00000223769	ENSG00000223769	RPS17P1	HSCHR6_MHC_DBB:29456981-29457387	NOTEST	0	0	0	0	1	1
ENSG00000223770	ENSG00000223770	MIR1255B1	7:81575759-82073114	NOTEST	0	0	0	0	1	1
ENSG00000223771	ENSG00000223771	SUMO2P1	HSCHR6_MHC_COX:29600437-29600721	NOTEST	0	0	0	0	1	1
ENSG00000223772	ENSG00000223772	GEMIN8P3	X:85403461-86087607	NOTEST	0	0	0	0	1	1
ENSG00000223774	ENSG00000223774	RP11-307B6.3	1:201862969-201915715	NOTEST	0.0195028	0.0112862	-0.789113	0	1	1
ENSG00000223775	ENSG00000223775	MRPS18B	HSCHR6_MHC_SSTO:30559597-30585593	NOTEST	0	0	0	0	1	1
ENSG00000223776	ENSG00000223776	LGALS8-AS1	1:236681299-236767804	NOTEST	0.0662098	0.0707998	0.0966986	0	1	1
ENSG00000223777	ENSG00000223777	AC092162.2	2:177588995-177684038	NOTEST	0	0	0	0	1	1
ENSG00000223779	ENSG00000223779	RP11-403I13.4	1:149239530-149265510	NOTEST	0.286138	0.302353	0.0795258	0	1	1
ENSG00000223780	ENSG00000223780	MEP1AP2	9:70727364-70734146	NOTEST	0	0	0	0	1	1
ENSG00000223781	ENSG00000223781	RP11-95K23.6	9:41277732-41298538	NOTEST	0	0	0	0	1	1
ENSG00000223782	ENSG00000223782	RPS21P8	13:27551679-27551926	NOTEST	0	0	0	0	1	1
ENSG00000223783	ENSG00000223783	AC124944.5	3:195563063-195587275	NOTEST	0	0	0	0	1	1
ENSG00000223784	ENSG00000223784	RP11-554I8.2	10:6779343-6780988	NOTEST	0	0	0	0	1	1
ENSG00000223786	ENSG00000223786	RP11-554D15.1	6:74779166-75443995	NOTEST	0	0.195199	inf	0	1	1
ENSG00000223787	ENSG00000223787	RP4-593M8.1	1:92974252-93257961	NOTEST	0	0	0	0	1	1
ENSG00000223788	ENSG00000223788	DIS3L2P1	2:233306743-233312128	NOTEST	0	0	0	0	1	1
ENSG00000223791	ENSG00000223791	UBE2E1-AS1	3:23845514-23932807	NOTEST	0.0244706	0	#NAME?	0	1	1
ENSG00000223793	ENSG00000223793	HLA-DQA2	HSCHR6_MHC_DBB:32688300-32694153	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000223794	ENSG00000223794	COX5BP8	1:179224867-179225216	NOTEST	0	0	0	0	1	1
ENSG00000223795	ENSG00000223795	RP11-473E2.2	9:137397317-137413288	NOTEST	0	0	0	0	1	1
ENSG00000223798	ENSG00000223798	HCG4P3	HSCHR6_MHC_APD:29905241-29969520	NOTEST	0	0	0	0	1	1
ENSG00000223800	ENSG00000223800	RP11-598C10.2	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000223806	ENSG00000223806	LINC00114	21:40110944-40119384	NOTEST	0	0	0	0	1	1
ENSG00000223807	ENSG00000223807	RP11-562M8.4	9:32926048-32926448	NOTEST	0	0	0	0	1	1
ENSG00000223808	ENSG00000223808	RP11-428L9.2	10:9012087-9015431	NOTEST	0	0	0	0	1	1
ENSG00000223809	ENSG00000223809	RP11-85L21.6	X:134193714-134257880	NOTEST	0	0	0	0	1	1
ENSG00000223810	ENSG00000223810	KRT8P28	1:151921998-151923388	NOTEST	0	0	0	0	1	1
ENSG00000223811	ENSG00000223811	RP11-437J19.1	6:113678204-113689146	NOTEST	0	0	0	0	1	1
ENSG00000223812	ENSG00000223812	RP11-197K6.1	3:191275112-191308145	NOTEST	0.0203466	0	#NAME?	0	1	1
ENSG00000223813	ENSG00000223813	AC007255.8	7:29019582-29603286	NOTEST	0	0.0833622	inf	0	1	1
ENSG00000223814	ENSG00000223814	RP11-543D5.2	1:48226199-48462567	NOTEST	0	0	0	0	1	1
ENSG00000223815	ENSG00000223815	DIAPH3-AS2	13:60239716-60738121	NOTEST	0	0	0	0	1	1
ENSG00000223816	ENSG00000223816	IGKV1OR2-2	2:92222171-92223026	NOTEST	0	0	0	0	1	1
ENSG00000223817	ENSG00000223817	CDH23-AS1	10:73156690-73575702	NOTEST	0	0	0	0	1	1
ENSG00000223819	ENSG00000223819	RP3-347M6.1	X:100055291-100055773	NOTEST	0	0	0	0	1	1
ENSG00000223821	ENSG00000223821	RP11-505P4.6	6:74171300-74218959	NOTEST	0	0	0	0	1	1
ENSG00000223822	ENSG00000223822	EEF1A1P1	21:24762578-24763317	NOTEST	0	0	0	0	1	1
ENSG00000223823	ENSG00000223823	RP11-465B22.5	1:1072396-1079436	NOTEST	0	0	0	0	1	1
ENSG00000223824	ENSG00000223824	AC019178.3	2:190744334-191236391	NOTEST	0	0	0	0	1	1
ENSG00000223825	ENSG00000223825	DAZAP2P1	2:203066102-203066609	NOTEST	0.0980575	0.0705744	-0.474483	0	1	1
ENSG00000223826	ENSG00000223826	AC092570.2	2:102095851-102103284	NOTEST	0	0	0	0	1	1
ENSG00000223827	ENSG00000223827	XXbac-BPG249D20.9	HSCHR6_MHC_COX:30473890-30476845	NOTEST	0	0	0	0	1	1
ENSG00000223828	ENSG00000223828	BANF1P4	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000223829	ENSG00000223829	AC004870.4	7:46930222-47118726	NOTEST	0	0	0	0	1	1
ENSG00000223831	ENSG00000223831	RP1-56J10.8	22:30972611-31023265	NOTEST	0	0	0	0	1	1
ENSG00000223833	ENSG00000223833	NCR3	HSCHR6_MHC_SSTO:31543844-31550705	NOTEST	0	0	0	0	1	1
ENSG00000223834	ENSG00000223834	RP11-472N13.2	10:31893527-31895146	NOTEST	0	0	0	0	1	1
ENSG00000223836	ENSG00000223836	RP11-548K12.2	7:57879524-57880333	NOTEST	0	0	0	0	1	1
ENSG00000223838	ENSG00000223838	AC007091.1	7:19393156-19618229	NOTEST	0	0	0	0	1	1
ENSG00000223840	ENSG00000223840	TRIM26BP	HSCHR6_MHC_COX:30191706-30304467	NOTEST	0	0	0	0	1	1
ENSG00000223841	ENSG00000223841	RP11-448K10.1	10:59715054-59716938	NOTEST	0	0	0	0	1	1
ENSG00000223842	ENSG00000223842	RP11-135J2.3	1:219395589-219398839	NOTEST	0.144427	0.0463256	-1.64046	0	1	1
ENSG00000223843	ENSG00000223843	EFCAB6-AS1	22:43911996-44208217	NOTEST	0	0	0	0	1	1
ENSG00000223844	ENSG00000223844	FAM8A5P	HSCHR6_MHC_MANN:32647648-32666810	NOTEST	0	0	0	0	1	1
ENSG00000223845	ENSG00000223845	VN1R40P	7:63904179-63905120	NOTEST	0	0	0	0	1	1
ENSG00000223847	ENSG00000223847	RP5-925F19.1	1:187683373-187683866	NOTEST	0	0	0	0	1	1
ENSG00000223849	ENSG00000223849	RP11-80I15.1	9:97861335-98079991	NOTEST	0.159965	0.130583	-0.292791	0	1	1
ENSG00000223850	ENSG00000223850	MYCNUN	2:16060520-16087129	NOTEST	0	0	0	0	1	1
ENSG00000223851	ENSG00000223851	PTMAP1	HSCHR6_MHC_MANN:30639293-30659275	NOTEST	0	0	0	0	1	1
ENSG00000223852	ENSG00000223852	ZFP57	HSCHR6_MHC_DBB:29640125-29648836	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000223853	ENSG00000223853	OR2H5P	HSCHR6_MHC_MCF:29523203-29600766	NOTEST	0	0	0	0	1	1
ENSG00000223855	ENSG00000223855	AC147651.3	7:560027-564869	NOTEST	0	0	0	0	1	1
ENSG00000223856	ENSG00000223856	RAB9AP2	Y:27856054-27859704	NOTEST	0	0	0	0	1	1
ENSG00000223858	ENSG00000223858	ZFP57	HSCHR6_MHC_MCF:29639953-29648669	NOTEST	0	0	0	0	1	1
ENSG00000223859	ENSG00000223859	AC007403.3	2:67267677-67269098	NOTEST	0	0	0	0	1	1
ENSG00000223860	ENSG00000223860	MCCD1P1	HSCHR6_MHC_SSTO:29865949-29866812	NOTEST	0	0	0	0	1	1
ENSG00000223861	ENSG00000223861	RP11-74C1.2	1:151512780-151556059	NOTEST	0	0.0325701	inf	0	1	1
ENSG00000223863	ENSG00000223863	AC008074.4	2:64713486-64728038	NOTEST	0	0	0	0	1	1
ENSG00000223864	ENSG00000223864	NPM1P19	20:37590941-37668366	NOTEST	0.0274722	0.021389	-0.361109	0	1	1
ENSG00000223866	ENSG00000223866	AC002486.3	7:20654829-20816658	NOTEST	0	0	0	0	1	1
ENSG00000223867	ENSG00000223867	AC098592.7	7:16977848-16978181	NOTEST	0	0	0	0	1	1
ENSG00000223868	ENSG00000223868	XXbac-BPG299F13.14	HSCHR6_MHC_QBL:31157982-31164195	NOTEST	0	0	0	0	1	1
ENSG00000223869	ENSG00000223869	RP11-323K10.1	1:215116465-215116883	NOTEST	0	0	0	0	1	1
ENSG00000223870	ENSG00000223870	AP000233.3	21:26499781-26507561	NOTEST	0	0	0	0	1	1
ENSG00000223872	ENSG00000223872	AC006372.5	7:157294015-157296271	NOTEST	0	0	0	0	1	1
ENSG00000223873	ENSG00000223873	AC013733.5	2:182559168-182559627	NOTEST	0	0.0366938	inf	0	1	1
ENSG00000223874	ENSG00000223874	AC007557.1	2:217536827-217858802	NOTEST	0	0	0	0	1	1
ENSG00000223875	ENSG00000223875	NBEAP3	22:16100516-16124973	NOTEST	0.279778	0.0879008	-1.67033	0	1	1
ENSG00000223876	ENSG00000223876	RPS27P1	10:93304608-93304855	NOTEST	0	0	0	0	1	1
ENSG00000223877	ENSG00000223877	RP11-2F9.3	15:22440226-22440848	NOTEST	0	0.0795637	inf	0	1	1
ENSG00000223878	ENSG00000223878	AC005517.3	17:15339331-15466909	NOTEST	0.133863	0.389723	1.54169	0	1	1
ENSG00000223880	ENSG00000223880	LINC01078	13:75824615-75826148	NOTEST	0	0	0	0	1	1
ENSG00000223881	ENSG00000223881	RP11-553K8.2	1:198566853-198567998	NOTEST	0	0	0	0	1	1
ENSG00000223882	ENSG00000223882	ABCC5-AS1	3:183637721-183735803	NOTEST	0	0	0	0	1	1
ENSG00000223883	ENSG00000223883	RP11-424D14.1	1:69521580-69650686	NOTEST	0	0	0	0	1	1
ENSG00000223884	ENSG00000223884	AC019048.1	2:7052407-7218011	NOTEST	0	0.121213	inf	0	1	1
ENSG00000223885	ENSG00000223885	FAM90A13P	8:7137291-7140766	NOTEST	0.0158877	0	#NAME?	0	1	1
ENSG00000223886	ENSG00000223886	RP11-251G23.2	7:105170655-105171118	NOTEST	0.298627	0.0723702	-2.04488	0	1	1
ENSG00000223887	ENSG00000223887	PRR3	HSCHR6_MHC_DBB:30499387-30521735	NOTEST	0	0	0	0	1	1
ENSG00000223889	ENSG00000223889	RP11-73B2.3	7:62854126-62882424	NOTEST	0	0	0	0	1	1
ENSG00000223890	ENSG00000223890	AC008171.1	2:205410515-206484886	NOTEST	0	0	0	0	1	1
ENSG00000223892	ENSG00000223892	HCG4P3	HSCHR6_MHC_MCF:30047254-30111187	NOTEST	0	0	0	0	1	1
ENSG00000223893	ENSG00000223893	AC096568.3	7:49813256-50199426	NOTEST	0	0	0	0	1	1
ENSG00000223894	ENSG00000223894	HLA-DPA2	HSCHR6_MHC_DBB:33037463-33043006	NOTEST	0	0	0	0	1	1
ENSG00000223896	ENSG00000223896	CCNJP2	1:92974252-93257961	NOTEST	0	0.0329513	inf	0	1	1
ENSG00000223897	ENSG00000223897	AC069157.1	2:53713281-53713418	NOTEST	0	0	0	0	1	1
ENSG00000223898	ENSG00000223898	OR11A1	HSCHR6_MHC_SSTO:29323120-29424524	NOTEST	0	0	0	0	1	1
ENSG00000223899	ENSG00000223899	SEC13P1	3:33038099-33138722	NOTEST	0.0955782	0.10951	0.196305	0	1	1
ENSG00000223901	ENSG00000223901	AP001469.5	21:47604992-47648738	NOTEST	0	0	0	0	1	1
ENSG00000223903	ENSG00000223903	RPL23P4	2:220550102-220602659	NOTEST	0	0	0	0	1	1
ENSG00000223904	ENSG00000223904	HMGB1P12	X:110677654-110678252	NOTEST	0	0	0	0	1	1
ENSG00000223905	ENSG00000223905	RP11-335E14.1	1:76540403-77100286	NOTEST	0	0	0	0	1	1
ENSG00000223906	ENSG00000223906	RP5-837M10.2	1:100810032-100985833	NOTEST	0	0	0	0	1	1

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ENSG00000223907	ENSG00000223907	RP11-439L8.4	1:31984035-31989846	NOTEST	0	0	0	0	1	1
ENSG00000223908	ENSG00000223908	AC068657.2	5:159436119-159546430	NOTEST	0	0	0	0	1	1
ENSG00000223910	ENSG00000223910	ZNF32-AS3	10:44124264-44170151	NOTEST	0	0	0	0	1	1
ENSG00000223911	ENSG00000223911	AC009480.3	2:148602085-149275805	NOTEST	0	0	0	0	1	1
ENSG00000223912	ENSG00000223912	EEF1A1P36	6:132593120-132594471	NOTEST	0	0	0	0	1	1
ENSG00000223914	ENSG00000223914	AC079630.2	12:40550040-40561509	NOTEST	0	0	0	0	1	1
ENSG00000223915	ENSG00000223915	DPPA2P1	Y:15342764-15343320	NOTEST	0	0	0	0	1	1
ENSG00000223916	ENSG00000223916	RP11-353H3.1	3:43328003-43775863	NOTEST	0	0	0	0	1	1
ENSG00000223917	ENSG00000223917	AC009237.2	2:96152227-96154375	NOTEST	0	0	0	0	1	1
ENSG00000223918	ENSG00000223918	RP13-461N9.2	9:113431050-113563859	NOTEST	0	0	0	0	1	1
ENSG00000223919	ENSG00000223919	LTA	HSCHR6_MHC_DBB:31521972-31524245	NOTEST	0	0	0	0	1	1
ENSG00000223920	ENSG00000223920	RP11-430G17.1	1:62119865-62120580	NOTEST	0	0	0	0	1	1
ENSG00000223921	ENSG00000223921	MTND1P27	2:140978152-140979054	NOTEST	0	0	0	0	1	1
ENSG00000223922	ENSG00000223922	ASS1P2	2:39024870-39103075	NOTEST	0.133562	0.125563	-0.0890971	0	1	1
ENSG00000223923	ENSG00000223923	AC010136.2	2:218664511-218867718	NOTEST	0	0	0	0	1	1
ENSG00000223925	ENSG00000223925	SLC25A15P4	21:10899081-10900005	NOTEST	0	0	0	0	1	1
ENSG00000223927	ENSG00000223927	RPL3P2	HSCHR6_MHC_QBL:31237898-31239098	NOTEST	0	0	0	0	1	1
ENSG00000223928	ENSG00000223928	RP11-183E9.2	10:23983674-24836772	NOTEST	0	0	0	0	1	1
ENSG00000223929	ENSG00000223929	AC007381.2	2:60586350-60618510	NOTEST	0	0	0	0	1	1
ENSG00000223930	ENSG00000223930	RP11-33A14.1	3:177919837-178578193	NOTEST	0	0	0	0	1	1
ENSG00000223931	ENSG00000223931	AC142381.1	16:32019758-32096106	NOTEST	0	0	0	0	1	1
ENSG00000223932	ENSG00000223932	GPANK1	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000223933	ENSG00000223933	TMPOP1	HSCHR6_MHC_COX:30424153-30425681	NOTEST	0	0	0	0	1	1
ENSG00000223935	ENSG00000223935	AC008074.3	2:64622353-64680932	NOTEST	0.0494512	0.0190122	-1.37908	0	1	1
ENSG00000223939	ENSG00000223939	PPP1R2P1	HSCHR6_MHC_SSTO:32898408-32937507	NOTEST	0	0	0	0	1	1
ENSG00000223940	ENSG00000223940	KRT8P8	X:151648048-151649496	NOTEST	0	0	0	0	1	1
ENSG00000223941	ENSG00000223941	LINC01014	3:177919837-178578193	NOTEST	0	0	0	0	1	1
ENSG00000223942	ENSG00000223942	RP11-252P19.2	6:165740775-166401536	NOTEST	0	0	0	0	1	1
ENSG00000223944	ENSG00000223944	RP5-1180C18.1	1:37728339-37790701	NOTEST	0	0	0	0	1	1
ENSG00000223945	ENSG00000223945	RP11-458I7.1	1:150025845-150027020	NOTEST	0.399647	0.236667	-0.755868	0	1	1
ENSG00000223946	ENSG00000223946	RP11-533O20.2	6:41902670-42018095	NOTEST	0	0	0	0	1	1
ENSG00000223947	ENSG00000223947	AC016738.4	2:101436613-101886778	NOTEST	0.257493	0.285957	0.151266	0	1	1
ENSG00000223948	ENSG00000223948	RP11-421N10.1	7:67234615-67235455	NOTEST	0	0	0	0	1	1
ENSG00000223949	ENSG00000223949	RP11-24J23.2	1:64239692-64647181	NOTEST	0.0105856	0.050507	2.25439	0	1	1
ENSG00000223951	ENSG00000223951	AL133244.1	2:33172038-33624576	NOTEST	0	0	0	0	1	1
ENSG00000223952	ENSG00000223952	TNF	HSCHR6_MHC_MCF:31619652-31622422	NOTEST	0	0	0	0	1	1
ENSG00000223955	ENSG00000223955	MTND6P1	Y:8231576-8232000	NOTEST	0	0	0	0	1	1
ENSG00000223956	ENSG00000223956	RP4-710M16.2	1:56880634-56881638	NOTEST	0	0	0	0	1	1
ENSG00000223957	ENSG00000223957	NEU1	HSCHR6_MHC_MANN:31865097-31870345	NOTEST	0	0	0	0	1	1
ENSG00000223958	ENSG00000223958	RP11-552J9.12	X:52736651-52738983	NOTEST	0	0	0	0	1	1
ENSG00000223962	ENSG00000223962	UBBP3	2:149621132-149621373	NOTEST	0.195471	0	#NAME?	0	1	1
ENSG00000223963	ENSG00000223963	PRKRIRP8	1:240928856-241520530	NOTEST	0.00763946	0	#NAME?	0	1	1
ENSG00000223965	ENSG00000223965	ZNF587P1	3:31699381-32119072	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000223966	ENSG00000223966	RP11-141J10.2	9:73143978-74061820	NOTEST	0	0	0	0	1	1
ENSG00000223967	ENSG00000223967	RP11-505P4.5	6:74225472-74280319	NOTEST	0	0	0	0	1	1
ENSG00000223968	ENSG00000223968	AC098614.1	3:27665692-27665947	NOTEST	0	0	0	0	1	1
ENSG00000223969	ENSG00000223969	AC002456.2	7:89964536-90839905	NOTEST	0	0	0	0	1	1
ENSG00000223970	ENSG00000223970	RP11-598O8.1	7:53070112-53071122	NOTEST	0	0	0	0	1	1
ENSG00000223971	ENSG00000223971	FGFR3P	HSCHR6_MHC_COX:31335648-31336251	NOTEST	0	0	0	0	1	1
ENSG00000223972	ENSG00000223972	DDX11L1	1:11868-31109	NOTEST	0.0205459	0.0578738	1.49406	0	1	1
ENSG00000223973	ENSG00000223973	AC068491.3	2:111953539-112268567	NOTEST	0	0	0	0	1	1
ENSG00000223974	ENSG00000223974	RP11-561N12.4	7:63980261-64023484	NOTEST	0	0.0264512	inf	0	1	1
ENSG00000223975	ENSG00000223975	AP001048.4	21:44881973-44899414	NOTEST	0	0	0	0	1	1
ENSG00000223976	ENSG00000223976	EXTL2P1	2:176707614-176708030	NOTEST	0	0	0	0	1	1
ENSG00000223977	ENSG00000223977	AC138623.1	2:83446013-83446229	NOTEST	0	0	0	0	1	1
ENSG00000223978	ENSG00000223978	ZNF736P1Y	Y:27131347-27132623	NOTEST	0	0	0	0	1	1
ENSG00000223980	ENSG00000223980	HLA-A	HSCHR6_MHC_SSTO:29897512-29902154	NOTEST	0	0	0	0	1	1
ENSG00000223981	ENSG00000223981	PHBP6	7:74602782-74653438	NOTEST	0	0	0	0	1	1
ENSG00000223982	ENSG00000223982	SNRPD2P2	1:231611701-231612034	NOTEST	0	0	0	0	1	1
ENSG00000223983	ENSG00000223983	RP11-12A20.8	9:67864635-67864981	NOTEST	0	0	0	0	1	1
ENSG00000223984	ENSG00000223984	HNRNPRP1	10:21823093-22032559	NOTEST	0.0938214	0.134317	0.517656	0	1	1
ENSG00000223985	ENSG00000223985	AC093326.1	2:490943-492655	NOTEST	0	0.0341397	inf	0	1	1
ENSG00000223986	ENSG00000223986	RP11-528A4.3	3:193483469-193483792	NOTEST	0	0	0	0	1	1
ENSG00000223987	ENSG00000223987	RP11-445P17.5	10:5346393-5346828	NOTEST	0	0	0	0	1	1
ENSG00000223989	ENSG00000223989	RP11-84A14.5	1:9908333-9970394	NOTEST	0	0	0	0	1	1
ENSG00000223990	ENSG00000223990	HLA-DPA2	HSCHR6_MHC_COX:32981427-32987014	NOTEST	0	0	0	0	1	1
ENSG00000223991	ENSG00000223991	AC104809.2	2:241858201-241932728	NOTEST	0	0	0	0	1	1
ENSG00000223993	ENSG00000223993	RP11-475D12.1	10:87191698-87192271	NOTEST	0	0	0	0	1	1
ENSG00000223995	ENSG00000223995	RPL32P35	X:127972418-127972812	NOTEST	0	0	0	0	1	1
ENSG00000223996	ENSG00000223996	ETF1P1	HSCHR6_MHC_SSTO:29957256-30022268	NOTEST	0	0	0	0	1	1
ENSG00000223997	ENSG00000223997	TRDD1	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000223999	ENSG00000223999	LL22NC03-102D1.18	22:23035262-23035797	NOTEST	0	0	0	0	1	1
ENSG00000224000	ENSG00000224000	RP3-471M13.2	1:172745044-173033155	NOTEST	0	0	0	0	1	1
ENSG00000224001	ENSG00000224001	RP11-270F18.2	9:100961310-101017915	NOTEST	0	0	0	0	1	1
ENSG00000224002	ENSG00000224002	AC090099.2	11:18161732-18211168	NOTEST	0.0332504	0	#NAME?	0	1	1
ENSG00000224003	ENSG00000224003	CTA-407F11.6	22:25960815-26125261	NOTEST	0.0101932	0.0223996	1.13587	0	1	1
ENSG00000224004	ENSG00000224004	ATP5C1P1	14:54457818-54458713	NOTEST	0	0.0159556	inf	0	1	1
ENSG00000224005	ENSG00000224005	AC022400.1	10:75404638-75490272	NOTEST	0.165774	0.26058	0.652511	0	1	1
ENSG00000224006	ENSG00000224006	HCG4P3	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1
ENSG00000224007	ENSG00000224007	AC019070.1	2:148602085-149275805	NOTEST	0	0	0	0	1	1
ENSG00000224008	ENSG00000224008	RP5-1010E17.2	20:54036873-54084752	NOTEST	0	0	0	0	1	1
ENSG00000224011	ENSG00000224011	AC111155.1	17:58754813-59488916	NOTEST	0	0	0	0	1	1
ENSG00000224012	ENSG00000224012	RP11-756G12.1	5:163136215-163136520	NOTEST	0	0	0	0	1	1
ENSG00000224014	ENSG00000224014	RP11-488L18.6	1:247338557-247338827	NOTEST	0	0	0	0	1	1
ENSG00000224015	ENSG00000224015	AC063976.3	5:131514926-131516821	NOTEST	0	0	0	0	1	1
ENSG00000224017	ENSG00000224017	AC005022.1	7:41141201-41173105	NOTEST	0.0257641	0	#NAME?	0	1	1

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ENSG00000224018	ENSG00000224018	AP000470.2	21:25527483-25560655	NOTEST	0	0	0	0	1	1
ENSG00000224019	ENSG00000224019	RPL21P32	2:186821313-186821790	NOTEST	0	0	0	0	1	1
ENSG00000224020	ENSG00000224020	MIR181A2HG	9:127279553-127535206	NOTEST	0.055741	0.0449596	-0.31011	0	1	1
ENSG00000224025	ENSG00000224025	RP11-274B18.3	9:71155951-71259358	NOTEST	0	0	0	0	1	1
ENSG00000224027	ENSG00000224027	RP1-231P7P.1	22:27959799-27969534	NOTEST	0	0	0	0	1	1
ENSG00000224028	ENSG00000224028	AC073928.2	2:140861151-140889349	NOTEST	0	0	0	0	1	1
ENSG00000224029	ENSG00000224029	RP11-136K14.2	6:150920998-151164799	NOTEST	0.0317409	0	#NAME?	0	1	1
ENSG00000224031	ENSG00000224031	TCEAL3-AS1	X:102862378-102885881	NOTEST	0	0.0608641	inf	0	1	1
ENSG00000224033	ENSG00000224033	CDY8P	Y:20134178-20135788	NOTEST	0	0	0	0	1	1
ENSG00000224034	ENSG00000224034	RP11-445P17.8	10:5307995-5313199	NOTEST	0	0	0	0	1	1
ENSG00000224035	ENSG00000224035	SFPQP1	Y:15195703-15207719	NOTEST	0	0	0	0	1	1
ENSG00000224036	ENSG00000224036	CTSLP2	10:48157040-48158148	NOTEST	0	0	0	0	1	1
ENSG00000224037	ENSG00000224037	RP4-781K5.7	1:234845134-234855723	NOTEST	0	0	0	0	1	1
ENSG00000224038	ENSG00000224038	RP11-347J14.8	9:39384502-39405302	NOTEST	0	0	0	0	1	1
ENSG00000224039	ENSG00000224039	AC091493.1	3:16729492-16738986	NOTEST	0	0	0	0	1	1
ENSG00000224041	ENSG00000224041	IGKV3D-15	2:90153695-90154258	NOTEST	0	0	0	0	1	1
ENSG00000224042	ENSG00000224042	MTND4P6	7:116902971-116904942	NOTEST	0	0	0	0	1	1
ENSG00000224044	ENSG00000224044	UBDP1	HSCHR6_MHC_QBL:29432260-29437471	NOTEST	0	0	0	0	1	1
ENSG00000224045	ENSG00000224045	RP11-98L5.4	9:138479847-138483821	NOTEST	0	0	0	0	1	1
ENSG00000224048	ENSG00000224048	AC104777.4	2:151451615-151491862	NOTEST	0.113244	0	#NAME?	0	1	1
ENSG00000224049	ENSG00000224049	RP11-30O15.1	3:187513974-187523046	NOTEST	0	0	0	0	1	1
ENSG00000224050	ENSG00000224050	RP1-90G24.6	22:32669406-32673173	NOTEST	0.101039	0	#NAME?	0	1	1
ENSG00000224052	ENSG00000224052	HTATSF1P	HSCHR6_MHC_DBB:33183490-33185382	NOTEST	0	0	0	0	1	1
ENSG00000224053	ENSG00000224053	RPL13AP	HSCHR6_MHC_APD:29523503-29601074	NOTEST	0	0	0	0	1	1
ENSG00000224054	ENSG00000224054	RP4-551E13.2	X:44325936-44328201	NOTEST	0	0	0	0	1	1
ENSG00000224055	ENSG00000224055	GAPDHP55	15:44162961-44487450	NOTEST	0	0	0	0	1	1
ENSG00000224056	ENSG00000224056	PSORS1C3	HSCHR6_MHC_SSTO:31135605-31139772	NOTEST	0	0	0	0	1	1
ENSG00000224057	ENSG00000224057	EGFR-AS1	7:55086713-55324313	NOTEST	0	0	0	0	1	1
ENSG00000224058	ENSG00000224058	AC006509.7	2:47922668-48134949	NOTEST	0	0	0	0	1	1
ENSG00000224059	ENSG00000224059	HSPA8P16	7:84624868-84816171	NOTEST	0	0	0	0	1	1
ENSG00000224060	ENSG00000224060	ARSEP1	Y:14460539-14468226	NOTEST	0.0844095	0.109494	0.37538	0	1	1
ENSG00000224061	ENSG00000224061	AC092106.1	2:106869686-106870173	NOTEST	0.094003	0.0366312	-1.35963	0	1	1
ENSG00000224062	ENSG00000224062	TUBB4BP5	4:122372695-122373122	NOTEST	0	0	0	0	1	1
ENSG00000224063	ENSG00000224063	AC007319.1	2:187866602-188430487	NOTEST	0.065513	0	#NAME?	0	1	1
ENSG00000224064	ENSG00000224064	RP11-344H11.5	1:27310118-27310515	NOTEST	0	0	0	0	1	1
ENSG00000224065	ENSG00000224065	SRIP2	X:88622433-88622599	NOTEST	0	0	0	0	1	1
ENSG00000224066	ENSG00000224066	RP4-622L5.7	1:32665986-32674288	NOTEST	0.045566	0.0375784	-0.278052	0	1	1
ENSG00000224067	ENSG00000224067	RP11-430K21.2	9:114565259-114565715	NOTEST	0.0613132	0	#NAME?	0	1	1
ENSG00000224069	ENSG00000224069	CTD-2183H9.7	X:154064062-154288578	NOTEST	0	0	0	0	1	1
ENSG00000224070	ENSG00000224070	HMGN1P6	2:207124351-207124642	NOTEST	0	0	0	0	1	1
ENSG00000224071	ENSG00000224071	AC009474.1	2:67047815-67049702	NOTEST	0	0	0	0	1	1
ENSG00000224072	ENSG00000224072	RP11-75A9.3	X:46306291-46356857	NOTEST	0.0139581	0.0370097	1.4068	0	1	1
ENSG00000224074	ENSG00000224074	LINC00691	3:24137759-24144729	NOTEST	0	0	0	0	1	1
ENSG00000224075	ENSG00000224075	TTTY22	Y:9638761-9650854	NOTEST	0	0	0	0	1	1

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ENSG00000224076	ENSG00000224076	AC009487.4	2:162272604-162841792	NOTEST	0	0	0	0	1	1
ENSG00000224077	ENSG00000224077	AP000936.4	11:116969702-116978886	NOTEST	0	0	0	0	1	1
ENSG00000224078	ENSG00000224078	SNHG14	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000224079	ENSG00000224079	AC091729.7	7:1036621-1177896	NOTEST	0.0638389	0.016551	-1.94752	0	1	1
ENSG00000224082	ENSG00000224082	UBTFL8	3:5121896-5126114	NOTEST	0	0	0	0	1	1
ENSG00000224083	ENSG00000224083	RP11-39K24.4	9:4985032-5128183	NOTEST	0.0109444	0.0263916	1.26988	0	1	1
ENSG00000224085	ENSG00000224085	RP11-4H14.1	3:140621035-140621493	NOTEST	0	0	0	0	1	1
ENSG00000224086	ENSG00000224086	LL22NC0386G7.1	22:22273792-22307209	NOTEST	0.170128	0.213258	0.32598	0	1	1
ENSG00000224087	ENSG00000224087	AC018804.3	2:130831107-130886795	NOTEST	0	0	0	0	1	1
ENSG00000224089	ENSG00000224089	CT47A10	X:120072560-120075873	NOTEST	0	0	0	0	1	1
ENSG00000224090	ENSG00000224090	AC097468.4	2:219866936-219906249	NOTEST	0	0	0	0	1	1
ENSG00000224091	ENSG00000224091	AC104389.16	11:5226270-5228538	NOTEST	0	0	0	0	1	1
ENSG00000224092	ENSG00000224092	RP11-443B9.1	9:1977783-1978547	NOTEST	0	0	0	0	1	1
ENSG00000224093	ENSG00000224093	RP5-1033H22.2	1:94027346-94312706	NOTEST	0.0456363	0.0425727	-0.100254	0	1	1
ENSG00000224094	ENSG00000224094	RPS24P8	3:45201265-45201667	NOTEST	0.371223	0.552946	0.574851	0	1	1
ENSG00000224095	ENSG00000224095	AC108051.1	2:103583865-103600887	NOTEST	0	0	0	0	1	1
ENSG00000224096	ENSG00000224096	HCG25	HSCHR6_MHC_COX:33138932-33165893	NOTEST	0	0	0	0	1	1
ENSG00000224097	ENSG00000224097	RP11-472B18.1	4:39481874-39483525	NOTEST	0.0119945	0.00767391	-0.644337	0	1	1
ENSG00000224098	ENSG00000224098	RPL32P1	HSCHR6_MHC_SSTO:33171991-33194624	NOTEST	0	0	0	0	1	1
ENSG00000224099	ENSG00000224099	AC064834.1	2:196313255-196380423	NOTEST	0	0	0	0	1	1
ENSG00000224100	ENSG00000224100	AP001630.5	21:44384748-44385473	NOTEST	0	0	0	0	1	1
ENSG00000224101	ENSG00000224101	ELMO1-AS1	7:36893960-37488852	NOTEST	0	0	0	0	1	1
ENSG00000224103	ENSG00000224103	HLA-DPA1	HSCHR6_MHC_COX:32954321-32976889	NOTEST	0	0	0	0	1	1
ENSG00000224104	ENSG00000224104	AC079809.2	7:152841397-152841673	NOTEST	0	0	0	0	1	1
ENSG00000224105	ENSG00000224105	C6orf15	HSCHR6_MHC_MCF:31157527-31158864	NOTEST	0	0	0	0	1	1
ENSG00000224106	ENSG00000224106	CYP4F25P	9:69477880-69478916	NOTEST	0.0425621	0	#NAME?	0	1	1
ENSG00000224107	ENSG00000224107	LINC00633	X:134193714-134257880	NOTEST	0	0	0	0	1	1
ENSG00000224108	ENSG00000224108	ETF1P1	HSCHR6_MHC_MANN:29963963-30027881	NOTEST	0	0	0	0	1	1
ENSG00000224109	ENSG00000224109	CENPVP3	X:51360960-51361446	NOTEST	0	0	0	0	1	1
ENSG00000224110	ENSG00000224110	RP11-274M4.1	8:130740989-130742691	NOTEST	0	0	0	0	1	1
ENSG00000224116	ENSG00000224116	INHBA-AS1	7:41706765-41818986	NOTEST	0	0	0	0	1	1
ENSG00000224117	ENSG00000224117	PTPN2P2	13:31032883-31191734	NOTEST	0	0	0	0	1	1
ENSG00000224118	ENSG00000224118	MICF	HSCHR6_MHC_COX:29817321-29817471	NOTEST	0	0	0	0	1	1
ENSG00000224120	ENSG00000224120	C6orf136	HSCHR6_MHC_MCF:30693276-30719302	NOTEST	0	0	0	0	1	1
ENSG00000224121	ENSG00000224121	ATG12P2	2:223725651-223809357	NOTEST	0.0605962	0.094527	0.641499	0	1	1
ENSG00000224122	ENSG00000224122	POU6F2-AS1	7:39017597-39532694	NOTEST	0	0	0	0	1	1
ENSG00000224124	ENSG00000224124	POM121L10P	22:25028881-25055114	NOTEST	0.00443846	0.0038161	-0.217959	0	1	1
ENSG00000224127	ENSG00000224127	RP11-510C10.2	1:75593514-75627218	NOTEST	0	0	0	0	1	1
ENSG00000224128	ENSG00000224128	AC107057.2	2:5742636-5831620	NOTEST	0	0	0	0	1	1
ENSG00000224129	ENSG00000224129	DPPA2P2	1:26845844-26846741	NOTEST	0	0	0	0	1	1
ENSG00000224130	ENSG00000224130	AP001652.1	11:58672870-58826132	NOTEST	0	0	0	0	1	1
ENSG00000224131	ENSG00000224131	FGFR3P	HSCHR6_MHC_MANN:31388243-31388845	NOTEST	0	0	0	0	1	1
ENSG00000224132	ENSG00000224132	AC112715.2	2:238165733-238166319	NOTEST	0	0.18596	inf	0	1	1
ENSG00000224133	ENSG00000224133	HCG20	HSCHR6_MHC_QBL:30724116-30749533	NOTEST	0	0	0	0	1	1

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ENSG00000224134	ENSG00000224134	AC004866.3	7:81061046-81062112	NOTEST	0	0	0	0	1	1
ENSG00000224136	ENSG00000224136	AC007568.1	7:117522912-117523729	NOTEST	0	0	0	0	1	1
ENSG00000224137	ENSG00000224137	AC079767.4	2:208527098-208531748	NOTEST	0	0	0	0	1	1
ENSG00000224140	ENSG00000224140	TNXA	HSCHR6_MHC_MCF:32052837-32056696	NOTEST	0	0	0	0	1	1
ENSG00000224141	ENSG00000224141	AL109763.2	21:19933582-20132321	NOTEST	0	0.0153643	inf	0	1	1
ENSG00000224142	ENSG00000224142	AMMECR1-IT1	X:109437413-109699562	NOTEST	0	0.027	inf	0	1	1
ENSG00000224143	ENSG00000224143	EHMT2	HSCHR6_MHC_SSTO:31839420-31849264	NOTEST	0	0	0	0	1	1
ENSG00000224144	ENSG00000224144	ASH2LP1	22:22774662-22775647	NOTEST	0.0182466	0	#NAME?	0	1	1
ENSG00000224145	ENSG00000224145	TRIM15	HSCHR6_MHC_SSTO:30120576-30130067	NOTEST	0	0	0	0	1	1
ENSG00000224146	ENSG00000224146	RPL13AP	HSCHR6_MHC_MANN:29522993-29600557	NOTEST	0	0	0	0	1	1
ENSG00000224149	ENSG00000224149	RP11-510C10.3	1:75593514-75627218	NOTEST	0	0	0	0	1	1
ENSG00000224151	ENSG00000224151	USP9YP28	Y:20994887-21001199	NOTEST	0	0	0	0	1	1
ENSG00000224152	ENSG00000224152	AC009506.1	2:160175489-160473593	NOTEST	0.566931	0.387521	-0.548898	0	1	1
ENSG00000224153	ENSG00000224153	RP11-433C9.2	3:183851806-184402546	NOTEST	0	0	0	0	1	1
ENSG00000224156	ENSG00000224156	TUBB	HSCHR6_MHC_APD:30696222-30701448	NOTEST	0	0	0	0	1	1
ENSG00000224157	ENSG00000224157	HCG14	6:28864306-28865099	NOTEST	0	0	0	0	1	1
ENSG00000224158	ENSG00000224158	RPL13P	HSCHR6_MHC_DBB:28827414-28831140	NOTEST	0	0	0	0	1	1
ENSG00000224159	ENSG00000224159	HMGB1P9	2:219065156-219066111	NOTEST	0	0	0	0	1	1
ENSG00000224160	ENSG00000224160	CICP10	2:243030783-243102304	NOTEST	0	0.29456	inf	0	1	1
ENSG00000224161	ENSG00000224161	RPS26P54	18:57428789-57429137	NOTEST	0	0	0	0	1	1
ENSG00000224162	ENSG00000224162	UQCRHP3	10:44227781-44228032	NOTEST	0	0	0	0	1	1
ENSG00000224163	ENSG00000224163	RP11-309L24.6	7:128552713-128554117	NOTEST	0	0	0	0	1	1
ENSG00000224164	ENSG00000224164	RP3-369A17.4	6:24742529-24752149	NOTEST	0	0	0	0	1	1
ENSG00000224166	ENSG00000224166	PRYP1	Y:19841407-19856476	NOTEST	0	0	0	0	1	1
ENSG00000224168	ENSG00000224168	TRIM31	HSCHR6_MHC_SSTO:30060268-30072086	NOTEST	0	0	0	0	1	1
ENSG00000224169	ENSG00000224169	HSFY6P	Y:25803985-25805205	NOTEST	0	0	0	0	1	1
ENSG00000224172	ENSG00000224172	RP11-416N13.1	7:64196310-64197121	NOTEST	0	0	0	0	1	1
ENSG00000224173	ENSG00000224173	AC007422.1	2:67789198-67911209	NOTEST	0	0	0	0	1	1
ENSG00000224174	ENSG00000224174	RP4-798A10.4	1:16847188-16848291	NOTEST	0	0	0	0	1	1
ENSG00000224177	ENSG00000224177	LINC00570	2:11534106-11543203	NOTEST	0	0	0	0	1	1
ENSG00000224180	ENSG00000224180	CCHCR1	HSCHR6_MHC_MCF:31188754-31204550	NOTEST	0	0	0	0	1	1
ENSG00000224183	ENSG00000224183	SDHDP6	1:25568727-25756683	NOTEST	0	0	0	0	1	1
ENSG00000224185	ENSG00000224185	SNX18P9	9:69451763-69452598	NOTEST	0.409921	0.509115	0.312645	0	1	1
ENSG00000224187	ENSG00000224187	RP11-132N15.3	3:187676562-187694195	NOTEST	0	0	0	0	1	1
ENSG00000224188	ENSG00000224188	UBE2D3P4	13:84594461-84594897	NOTEST	0	0	0	0	1	1
ENSG00000224190	ENSG00000224190	RP11-442O18.2	10:130711142-130714535	NOTEST	0	0	0	0	1	1
ENSG00000224192	ENSG00000224192	RP11-259P1.1	22:26565439-26779562	NOTEST	0	0	0	0	1	1
ENSG00000224194	ENSG00000224194	AC008278.3	2:15808807-15820608	NOTEST	0	0	0	0	1	1
ENSG00000224195	ENSG00000224195	RP11-574K11.5	10:75572258-75634343	NOTEST	0.314314	0.250622	-0.326694	0	1	1
ENSG00000224196	ENSG00000224196	OR5AK4P	11:56804911-56805009	NOTEST	0	0	0	0	1	1
ENSG00000224197	ENSG00000224197	HLA-DQB3	HSCHR6_MHC_QBL:32624039-32628148	NOTEST	0	0	0	0	1	1
ENSG00000224198	ENSG00000224198	RP4-604K5.2	1:87380330-87634884	NOTEST	0	0	0	0	1	1
ENSG00000224199	ENSG00000224199	WI2-2994D6.1	1:13196269-13199067	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000224200	ENSG00000224200	FKBPL	HSCHR6_MHC_DBB:32072258-32073843	NOTEST	0	0	0	0	1	1
ENSG00000224201	ENSG00000224201	PNMA6A	X:152240818-152340864	NOTEST	0	0	0	0	1	1
ENSG00000224203	ENSG00000224203	RPS23P10	1:161475219-161648444	NOTEST	0	0	0	0	1	1
ENSG00000224204	ENSG00000224204	PHEX-AS1	X:22050558-22269427	NOTEST	0	0	0	0	1	1
ENSG00000224205	ENSG00000224205	AP000351.4	22:24329510-24333615	NOTEST	0	0	0	0	1	1
ENSG00000224207	ENSG00000224207	RP11-10L12.1	4:103552659-103682151	NOTEST	0	0	0	0	1	1
ENSG00000224208	ENSG00000224208	AL590762.6	X:70534761-70535729	NOTEST	0	0	0	0	1	1
ENSG00000224209	ENSG00000224209	LINC00466	1:63655659-63782902	NOTEST	0.341368	0.270293	-0.336804	0	1	1
ENSG00000224210	ENSG00000224210	TRIM60P5Y	Y:26640855-26641730	NOTEST	0	0	0	0	1	1
ENSG00000224212	ENSG00000224212	TAP1	HSCHR6_MHC_DBB:32786474-32825559	NOTEST	0	0	0	0	1	1
ENSG00000224215	ENSG00000224215	RP11-371A19.2	10:23556123-23634110	NOTEST	0	0.0774651	inf	0	1	1
ENSG00000224216	ENSG00000224216	RP13-228J13.1	X:154564166-154581271	NOTEST	0	0	0	0	1	1
ENSG00000224217	ENSG00000224217	RP11-232D9.1	X:115882497-115882845	NOTEST	0	0	0	0	1	1
ENSG00000224218	ENSG00000224218	RP11-359D14.3	4:77356252-77723117	NOTEST	0	0	0	0	1	1
ENSG00000224219	ENSG00000224219	AC074290.1	2:194595278-194595413	NOTEST	0	0	0	0	1	1
ENSG00000224220	ENSG00000224220	AC104699.1	2:25600066-25896503	NOTEST	0	0	0	0	1	1
ENSG00000224221	ENSG00000224221	RPS6P8	6:74078277-74161999	NOTEST	0	0	0	0	1	1
ENSG00000224222	ENSG00000224222	RP11-262I2.2	10:71754381-71767592	NOTEST	0	0	0	0	1	1
ENSG00000224223	ENSG00000224223	GS1-18A18.1	7:54610017-54639419	NOTEST	0	0	0	0	1	1
ENSG00000224224	ENSG00000224224	HAUS1P2	X:18883888-18884672	NOTEST	0	0	0	0	1	1
ENSG00000224226	ENSG00000224226	TBC1D3B	17:34443569-34504870	NOTEST	0.0990006	0.154954	0.646335	0	1	1
ENSG00000224227	ENSG00000224227	OR2L1P	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000224228	ENSG00000224228	RP1-15D23.2	1:172745044-173033155	NOTEST	0	0	0	0	1	1
ENSG00000224229	ENSG00000224229	XXbac-BCX196D17.5	HSCHR6_MHC_APD:29092025-29096724	NOTEST	0	0	0	0	1	1
ENSG00000224230	ENSG00000224230	DASS-397D15.5	HSCHR6_MHC_MANN:32523181-32523277	NOTEST	0	0	0	0	1	1
ENSG00000224231	ENSG00000224231	AC069394.1	2:138859453-138863475	NOTEST	0	0	0	0	1	1
ENSG00000224232	ENSG00000224232	AC110299.5	2:242295657-242449145	NOTEST	0.0878959	0.112204	0.352261	0	1	1
ENSG00000224233	ENSG00000224233	OR2J4P	6:29149286-29150222	NOTEST	0	0	0	0	1	1
ENSG00000224234	ENSG00000224234	OR10C1	HSCHR6_MHC_COX:29319721-29421426	NOTEST	0	0	0	0	1	1
ENSG00000224235	ENSG00000224235	RP5-1027O11.1	1:88365591-88371397	NOTEST	0	0	0	0	1	1
ENSG00000224236	ENSG00000224236	MRRFP1	X:122249959-122251634	NOTEST	0	0	0	0	1	1
ENSG00000224237	ENSG00000224237	MINOS1P3	3:27151575-27410951	NOTEST	0	0	0	0	1	1
ENSG00000224238	ENSG00000224238	WARS2-IT1	1:119573838-119869926	NOTEST	0	0.00610883	inf	0	1	1
ENSG00000224239	ENSG00000224239	AC090044.2	3:898806-899774	NOTEST	0	0.145673	inf	0	1	1
ENSG00000224240	ENSG00000224240	CYCSP49	Y:28654359-28725837	NOTEST	0	0	0	0	1	1
ENSG00000224241	ENSG00000224241	TMEM183AP1	HSCHR6_MHC_MANN:29522993-29600557	NOTEST	0	0	0	0	1	1
ENSG00000224242	ENSG00000224242	BTNL2	HSCHR6_MHC_SSTO:32364870-32381497	NOTEST	0	0	0	0	1	1
ENSG00000224243	ENSG00000224243	LINC00403	13:112761432-112762329	NOTEST	0	0	0	0	1	1
ENSG00000224244	ENSG00000224244	AC090283.3	17:38843289-38845612	NOTEST	0	0	0	0	1	1
ENSG00000224245	ENSG00000224245	RP11-533K9.3	9:97258556-97275161	NOTEST	0	0	0	0	1	1
ENSG00000224246	ENSG00000224246	SFTA2	HSCHR6_MHC_COX:30888848-30889671	NOTEST	0	0	0	0	1	1
ENSG00000224247	ENSG00000224247	AJ009632.3	21:16866250-16868443	NOTEST	0	0	0	0	1	1
ENSG00000224250	ENSG00000224250	RP11-78A18.2	10:123495817-123499245	NOTEST	0	0	0	0	1	1
ENSG00000224251	ENSG00000224251	RP11-499O7.7	10:5029966-5060223	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000224252	ENSG00000224252	AC113618.2	2:239628964-239649421	NOTEST	0	0	0	0	1	1
ENSG00000224253	ENSG00000224253	HCG9P5	HSCHR6_MHC_COX:29684536-29710797	NOTEST	0	0	0	0	1	1
ENSG00000224254	ENSG00000224254	AC025627.4	17:19508766-19509246	NOTEST	0	0	0	0	1	1
ENSG00000224255	ENSG00000224255	PDCL3P6	1:52608045-52831865	NOTEST	0	0	0	0	1	1
ENSG00000224256	ENSG00000224256	CTA-292E10.7	22:29196670-29244547	NOTEST	0	0	0	0	1	1
ENSG00000224257	ENSG00000224257	VWC2L-IT1	2:214149112-215548970	NOTEST	0	0	0	0	1	1
ENSG00000224259	ENSG00000224259	LINC01133	1:159931007-159948851	NOTEST	0	0.0517843	inf	0	1	1
ENSG00000224261	ENSG00000224261	RP11-179G5.1	1:160185504-160256138	NOTEST	0.245731	0.388026	0.659075	0	1	1
ENSG00000224263	ENSG00000224263	CYCSP12	3:11901147-11932646	NOTEST	0	0	0	0	1	1
ENSG00000224264	ENSG00000224264	VARS	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000224265	ENSG00000224265	RP11-168L22.2	10:43819112-43823380	NOTEST	0	0	0	0	1	1
ENSG00000224267	ENSG00000224267	RP11-149F8.5	9:68324610-68340644	NOTEST	0	0	0	0	1	1
ENSG00000224269	ENSG00000224269	AP000697.6	21:38071072-38122218	NOTEST	0	0	0	0	1	1
ENSG00000224272	ENSG00000224272	AC114730.3	2:242749406-242758739	NOTEST	0.0255671	0.233283	3.18972	0	1	1
ENSG00000224273	ENSG00000224273	AC005077.7	7:75747042-75761505	NOTEST	0	0.0251376	inf	0	1	1
ENSG00000224274	ENSG00000224274	ENSAP1	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000224276	ENSG00000224276	RP11-336K24.5	1:155916629-155976861	NOTEST	0	0	0	0	1	1
ENSG00000224277	ENSG00000224277	AP000345.2	22:23909250-23922495	NOTEST	0	0	0	0	1	1
ENSG00000224278	ENSG00000224278	RP11-405P11.1	1:188211269-188211809	NOTEST	0	0	0	0	1	1
ENSG00000224279	ENSG00000224279	RP1-199H16.6	22:38970935-38971436	NOTEST	0	0	0	0	1	1
ENSG00000224280	ENSG00000224280	AC005014.5	7:16623406-16626382	NOTEST	0.00529438	0	#NAME?	0	1	1
ENSG00000224281	ENSG00000224281	SLC25A5-AS1	X:118599996-118605282	NOTEST	0.399315	0.360138	-0.148976	0	1	1
ENSG00000224282	ENSG00000224282	CTD-2290C23.1	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000224286	ENSG00000224286	LINC01142	1:170240743-170253349	NOTEST	0	0	0	0	1	1
ENSG00000224288	ENSG00000224288	AC013437.2	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000224289	ENSG00000224289	IFIT6P	10:90973325-91174314	NOTEST	0	0	0	0	1	1
ENSG00000224290	ENSG00000224290	APOM	HSCHR6_MHC_COX:31594211-31613401	NOTEST	0	0	0	0	1	1
ENSG00000224291	ENSG00000224291	AC012671.2	2:88727596-88728134	NOTEST	0	0	0	0	1	1
ENSG00000224292	ENSG00000224292	AF196972.9	X:48364910-48367226	NOTEST	0.118444	0.19058	0.686185	0	1	1
ENSG00000224293	ENSG00000224293	TMEM183AP1	HSCHR6_MHC_MCF:29523203-29600766	NOTEST	0	0	0	0	1	1
ENSG00000224294	ENSG00000224294	RP3-326I13.1	X:43036242-43085847	NOTEST	0	0	0	0	1	1
ENSG00000224295	ENSG00000224295	AC087380.14	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000224296	ENSG00000224296	MRPL49P1	5:63970679-63971214	NOTEST	0	0	0	0	1	1
ENSG00000224297	ENSG00000224297	RP11-197P3.1	9:77550091-77550612	NOTEST	0	0	0	0	1	1
ENSG00000224298	ENSG00000224298	AC069363.1	17:34400225-34417515	NOTEST	0	0	0	0	1	1
ENSG00000224299	ENSG00000224299	AC007282.6	2:202352147-202483901	NOTEST	0.161476	0.155194	-0.0572506	0	1	1
ENSG00000224300	ENSG00000224300	OR51P1P	11:5036367-5037309	NOTEST	0	0	0	0	1	1
ENSG00000224301	ENSG00000224301	RP11-144G16.1	10:64883697-64885297	NOTEST	0	0	0	0	1	1
ENSG00000224302	ENSG00000224302	RP11-302K17.3	10:103845232-103845487	NOTEST	0	0	0	0	1	1
ENSG00000224303	ENSG00000224303	RP11-327I22.5	9:43144979-43160008	NOTEST	0	0	0	0	1	1
ENSG00000224305	ENSG00000224305	HLA-DQB2	HSCHR6_MHC_COX:32647572-32655029	NOTEST	0	0	0	0	1	1
ENSG00000224307	ENSG00000224307	RP11-344B5.2	9:132044736-132048007	NOTEST	0	0	0	0	1	1
ENSG00000224308	ENSG00000224308	RP1-13P20.6	1:152902515-152921686	NOTEST	0	0	0	0	1	1

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ENSG00000224309	ENSG00000224309	ANKRD30BP2	21:14410480-14439354	NOTEST	0	0	0	0	1	1
ENSG00000224310	ENSG00000224310	AC012317.1	16:24672742-24682383	NOTEST	0	0	0	0	1	1
ENSG00000224311	ENSG00000224311	RP11-40H20.4	1:27555596-27560843	NOTEST	0	0	0	0	1	1
ENSG00000224312	ENSG00000224312	MCCD1P2	6:29962213-29963091	NOTEST	0.173039	0.0646267	-1.4209	0	1	1
ENSG00000224313	ENSG00000224313	DXO	HSCHR6_MHC_MCF:32014033-32025671	NOTEST	0	0	0	0	1	1
ENSG00000224314	ENSG00000224314	RP3-378P9.2	X:116533414-116534044	NOTEST	0	0	0	0	1	1
ENSG00000224315	ENSG00000224315	RPL7P7	1:8412456-8877702	NOTEST	0	0	0	0	1	1
ENSG00000224316	ENSG00000224316	RP11-479O9.2	7:65238606-65267054	NOTEST	0	0	0	0	1	1
ENSG00000224319	ENSG00000224319	OR2H2	HSCHR6_MHC_APD:29523503-29601074	NOTEST	0	0	0	0	1	1
ENSG00000224320	ENSG00000224320	HLA-A	HSCHR6_MHC_COX:29898586-29903209	NOTEST	0	0	0	0	1	1
ENSG00000224321	ENSG00000224321	RP11-169K16.6	1:16119290-16119780	NOTEST	0	0	0	0	1	1
ENSG00000224322	ENSG00000224322	AC004009.3	7:27401461-27449557	NOTEST	0	0	0	0	1	1
ENSG00000224323	ENSG00000224323	DPRXP1	2:187350882-187374090	NOTEST	0	0.0365653	inf	0	1	1
ENSG00000224324	ENSG00000224324	THAP5P1	7:158415879-158416141	NOTEST	0.156119	0.339928	1.12258	0	1	1
ENSG00000224326	ENSG00000224326	RP11-115A15.1	1:81000662-81112473	NOTEST	0	0	0	0	1	1
ENSG00000224328	ENSG00000224328	MDC1-AS1	6:30667583-30685666	NOTEST	0.0152229	0	#NAME?	0	1	1
ENSG00000224329	ENSG00000224329	LINC00297	13:30446749-30462542	NOTEST	0.0800701	0	#NAME?	0	1	1
ENSG00000224330	ENSG00000224330	AC005019.3	7:13893979-13898650	NOTEST	0.229001	0.0615044	-1.89659	0	1	1
ENSG00000224331	ENSG00000224331	AC019181.3	2:165510133-165705844	NOTEST	0	0.082625	inf	0	1	1
ENSG00000224333	ENSG00000224333	GAPDHP20	1:32867709-32868716	NOTEST	0	0	0	0	1	1
ENSG00000224334	ENSG00000224334	AP000357.4	22:25082889-25084054	NOTEST	0	0	0	0	1	1
ENSG00000224335	ENSG00000224335	RP11-301M17.2	1:147706572-147706607	NOTEST	0	0	0	0	1	1
ENSG00000224336	ENSG00000224336	FAM197Y1	Y:9374240-9384693	NOTEST	0	0	0	0	1	1
ENSG00000224337	ENSG00000224337	FAM8A3P	2:150177106-150177950	NOTEST	0	0	0	0	1	1
ENSG00000224338	ENSG00000224338	RP11-149P14.1	1:11485313-11485878	NOTEST	0	0	0	0	1	1
ENSG00000224339	ENSG00000224339	AL121578.5	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000224340	ENSG00000224340	RP11-496H15.2	1:10092889-10241297	NOTEST	0.170896	0	#NAME?	0	1	1
ENSG00000224341	ENSG00000224341	RP4-562J12.1	X:117973518-118015978	NOTEST	0	0	0	0	1	1
ENSG00000224342	ENSG00000224342	AC007879.1	2:208038357-208102599	NOTEST	0	0	0	0	1	1
ENSG00000224344	ENSG00000224344	KNOP1P3	2:51259738-52635055	NOTEST	0	0	0	0	1	1
ENSG00000224346	ENSG00000224346	AC005037.1	2:201708962-201710184	NOTEST	0	0	0	0	1	1
ENSG00000224347	ENSG00000224347	SCEL-AS1	13:78109808-78219398	NOTEST	0	0	0	0	1	1
ENSG00000224348	ENSG00000224348	RP11-306K13.1	1:240928856-241520530	NOTEST	0	0	0	0	1	1
ENSG00000224349	ENSG00000224349	RP11-462G2.2	6:71122530-71270877	NOTEST	0.0830442	0.0595733	-0.479212	0	1	1
ENSG00000224351	ENSG00000224351	CDKN2AIPNLP3	13:40391877-40392186	NOTEST	0	0	0	0	1	1
ENSG00000224352	ENSG00000224352	AC132479.4	2:131087714-131087858	NOTEST	0	0	0	0	1	1
ENSG00000224353	ENSG00000224353	ACE3P	17:61554421-61599209	NOTEST	0	0	0	0	1	1
ENSG00000224354	ENSG00000224354	MTND2P5	7:141502281-141503287	NOTEST	0	0	0	0	1	1
ENSG00000224355	ENSG00000224355	MICG	HSCHR6_MHC_QBL:29777532-29777664	NOTEST	0	0	0	0	1	1
ENSG00000224356	ENSG00000224356	RP11-151A6.4	13:101183809-101241782	NOTEST	0.0269895	0.0680496	1.33419	0	1	1
ENSG00000224357	ENSG00000224357	ATG3P1	20:37957656-37958567	NOTEST	0	0	0	0	1	1
ENSG00000224358	ENSG00000224358	RP11-466F5.8	1:165696031-165880855	NOTEST	0.110291	0.108704	-0.0209135	0	1	1
ENSG00000224359	ENSG00000224359	RP11-467I20.2	1:240652872-240775449	NOTEST	0	0	0	0	1	1
ENSG00000224360	ENSG00000224360	DDR1-AS1	HSCHR6_MHC_COX:30824630-30833593	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000224361	ENSG00000224361	AC011239.1	2:23608087-23931481	NOTEST	0	0	0	0	1	1
ENSG00000224362	ENSG00000224362	DDX39BP2	HSCHR6_MHC_MANN:29956157-29956554	NOTEST	0	0	0	0	1	1
ENSG00000224363	ENSG00000224363	RP11-289H16.1	1:143913614-144094424	NOTEST	0	0	0	0	1	1
ENSG00000224365	ENSG00000224365	RP11-252P18.1	7:65469003-65469124	NOTEST	0	0	0	0	1	1
ENSG00000224366	ENSG00000224366	AC138472.4	19:45041044-45222031	NOTEST	0	0	0	0	1	1
ENSG00000224367	ENSG00000224367	OACYLP	18:56663965-56736570	NOTEST	0.0236866	0	#NAME?	0	1	1
ENSG00000224368	ENSG00000224368	RP11-73B2.5	7:62854126-62882424	NOTEST	0	0	0	0	1	1
ENSG00000224370	ENSG00000224370	RP11-814E24.3	7:56448668-56449005	NOTEST	0	0	0	0	1	1
ENSG00000224371	ENSG00000224371	RP11-235G24.1	6:161293919-161339681	NOTEST	0	0	0	0	1	1
ENSG00000224372	ENSG00000224372	HLA-N	6:30319192-30319327	NOTEST	0	0	0	0	1	1
ENSG00000224373	ENSG00000224373	IGHV4-59	14:107081805-107083830	NOTEST	0	0	0	0	1	1
ENSG00000224374	ENSG00000224374	RP1-32B1.4	6:135581133-135582071	NOTEST	0	0	0	0	1	1
ENSG00000224375	ENSG00000224375	AC009276.4	7:134368895-134372742	NOTEST	0	0	0	0	1	1
ENSG00000224378	ENSG00000224378	MICB	HSCHR6_MHC_DBB:31447881-31461098	NOTEST	0	0	0	0	1	1
ENSG00000224379	ENSG00000224379	TCF19	HSCHR6_MHC_COX:31118871-31131037	NOTEST	0	0	0	0	1	1
ENSG00000224382	ENSG00000224382	LINC00703	10:4426437-4452804	NOTEST	0	0.0315609	inf	0	1	1
ENSG00000224383	ENSG00000224383	C17orf72	17:62073430-62097994	NOTEST	0.0516335	0.0404419	-0.352458	0	1	1
ENSG00000224384	ENSG00000224384	RP3-417O22.3	6:97233012-97285353	NOTEST	0	0	0	0	1	1
ENSG00000224387	ENSG00000224387	RP3-395M20.2	1:2357418-2436969	NOTEST	0	0	0	0	1	1
ENSG00000224388	ENSG00000224388	BACE2-IT1	21:42539727-42654445	NOTEST	0	0	0	0	1	1
ENSG00000224389	ENSG00000224389	C4B	6:31982538-32004035	NOTEST	0	0.013277	inf	0	1	1
ENSG00000224391	ENSG00000224391	AC073321.3	2:217455148-217475925	NOTEST	0	0	0	0	1	1
ENSG00000224392	ENSG00000224392	OR2G1P	HSCHR6_MHC_QBL:29197049-29197980	NOTEST	0	0	0	0	1	1
ENSG00000224393	ENSG00000224393	C6orf25	HSCHR6_MHC_DBB:31668543-31676660	NOTEST	0	0	0	0	1	1
ENSG00000224394	ENSG00000224394	GPC6-AS2	13:93879094-95059655	NOTEST	0	0	0	0	1	1
ENSG00000224395	ENSG00000224395	OR2H1	HSCHR6_MHC_MANN:29424527-29431676	NOTEST	0	0	0	0	1	1
ENSG00000224396	ENSG00000224396	METTL15P3	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000224398	ENSG00000224398	CSNK2B	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000224399	ENSG00000224399	SLC39A7	HSCHR6_MHC_MCF:33331731-33342580	NOTEST	0	0	0	0	1	1
ENSG00000224400	ENSG00000224400	AC010880.1	2:16535523-16613970	NOTEST	0	0	0	0	1	1
ENSG00000224401	ENSG00000224401	RPL7P57	X:47696300-47931025	NOTEST	0.152371	0.158966	0.0611379	0	1	1
ENSG00000224402	ENSG00000224402	OR6D1P	10:45753632-45754571	NOTEST	0	0	0	0	1	1
ENSG00000224403	ENSG00000224403	DPPA2P3	3:193675160-193788759	NOTEST	0.030692	0	#NAME?	0	1	1
ENSG00000224404	ENSG00000224404	LL22NC03-13G6.2	22:34604129-34605251	NOTEST	0	0	0	0	1	1
ENSG00000224405	ENSG00000224405	LINC00572	13:30492783-30500788	NOTEST	0	0	0	0	1	1
ENSG00000224406	ENSG00000224406	RP11-48F14.1	3:186172770-186211450	NOTEST	0	0	0	0	1	1
ENSG00000224407	ENSG00000224407	RP5-956O18.3	1:230193535-230417870	NOTEST	0	0	0	0	1	1
ENSG00000224408	ENSG00000224408	USP9YP22	Y:9021302-9023412	NOTEST	0	0	0	0	1	1
ENSG00000224409	ENSG00000224409	RP11-114B7.6	1:33183334-33190838	NOTEST	0	0	0	0	1	1
ENSG00000224410	ENSG00000224410	AC097499.2	2:126580684-126580892	NOTEST	0	0	0	0	1	1
ENSG00000224412	ENSG00000224412	RP11-351O1.3	10:65249220-65249398	NOTEST	0	0	0	0	1	1
ENSG00000224413	ENSG00000224413	AP001476.2	21:47456965-47459721	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000224414	ENSG00000224414	AC010886.2	2:218147461-218621316	NOTEST	0	0	0	0	1	1
ENSG00000224415	ENSG00000224415	RPL19P12	7:102740222-102790007	NOTEST	0.100794	0.249262	1.30626	0	1	1
ENSG00000224416	ENSG00000224416	IFNA22P	9:21278048-21278618	NOTEST	0.0689675	0	#NAME?	0	1	1
ENSG00000224417	ENSG00000224417	RP11-503C24.6	6:168693509-168720434	NOTEST	0	0	0	0	1	1
ENSG00000224418	ENSG00000224418	STK24-AS1	13:99102454-99231084	NOTEST	0.0134393	0.0389548	1.53534	0	1	1
ENSG00000224419	ENSG00000224419	KRT18P27	13:90882637-90883936	NOTEST	0	0	0	0	1	1
ENSG00000224420	ENSG00000224420	ADM5	19:50179042-50193832	NOTEST	0.346234	0.338013	-0.0346691	0	1	1
ENSG00000224421	ENSG00000224421	ATP5J2LP	21:37692089-37791313	NOTEST	0	0	0	0	1	1
ENSG00000224425	ENSG00000224425	AC073869.2	2:131862419-132111282	NOTEST	0	0	0	0	1	1
ENSG00000224426	ENSG00000224426	SLC31A1P1	3:172321229-172321796	NOTEST	0	0	0	0	1	1
ENSG00000224427	ENSG00000224427	AP000281.1	21:34144410-34266043	NOTEST	0	0	0	0	1	1
ENSG00000224429	ENSG00000224429	LINC00422	13:21872277-21922860	NOTEST	0.0188249	0.0693899	1.88209	0	1	1
ENSG00000224430	ENSG00000224430	MKRN5P	X:73164158-73513409	NOTEST	0.0208125	0	#NAME?	0	1	1
ENSG00000224431	ENSG00000224431	AC063976.7	5:131520568-131731306	NOTEST	0.121411	0.102007	-0.25123	0	1	1
ENSG00000224435	ENSG00000224435	NF1P6	22:16345911-16355362	NOTEST	0	0.00780899	inf	0	1	1
ENSG00000224436	ENSG00000224436	RP11-284L19.1	1:232357683-232357920	NOTEST	0	0	0	0	1	1
ENSG00000224438	ENSG00000224438	RP4-816N1.1	12:2891069-2891537	NOTEST	0	0	0	0	1	1
ENSG00000224439	ENSG00000224439	RP11-351M16.1	10:28721936-28784742	NOTEST	0	0	0	0	1	1
ENSG00000224440	ENSG00000224440	CXorf51A	X:145895623-145896244	NOTEST	0	0	0	0	1	1
ENSG00000224441	ENSG00000224441	AC068831.3	15:91473409-91506349	NOTEST	0	0.169714	inf	0	1	1
ENSG00000224442	ENSG00000224442	AC017035.2	2:197831740-198175897	NOTEST	0.0286649	0	#NAME?	0	1	1
ENSG00000224443	ENSG00000224443	AC006509.4	2:47922668-48134949	NOTEST	0	0	0	0	1	1
ENSG00000224444	ENSG00000224444	MAS1LP1	HSCHR6_MHC_COX:29439378-29440425	NOTEST	0	0	0	0	1	1
ENSG00000224445	ENSG00000224445	RP11-413P11.1	1:99937970-99999571	NOTEST	0	0	0	0	1	1
ENSG00000224446	ENSG00000224446	LINC01015	HSCHR6_MHC_DBB:29497134-29501283	NOTEST	0	0	0	0	1	1
ENSG00000224447	ENSG00000224447	HIST1H1PS2	6:26016606-26016829	NOTEST	0	0	0	0	1	1
ENSG00000224448	ENSG00000224448	GS1-259H13.7	7:99235864-99236390	NOTEST	0.239266	0.125492	-0.931024	0	1	1
ENSG00000224451	ENSG00000224451	ATP5F1P1	13:52158643-52336171	NOTEST	0	0	0	0	1	1
ENSG00000224452	ENSG00000224452	RSL24D1P6	20:30758192-30758593	NOTEST	0.566337	0.19035	-1.57301	0	1	1
ENSG00000224455	ENSG00000224455	VPS52	HSCHR6_MHC_MCF:33387703-33414664	NOTEST	0	0	0	0	1	1
ENSG00000224458	ENSG00000224458	GUSBP6	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000224459	ENSG00000224459	RP11-169K16.4	1:16010826-16076391	NOTEST	0	0	0	0	1	1
ENSG00000224460	ENSG00000224460	RP11-439L18.2	6:143267183-143277835	NOTEST	0	0.0501202	inf	0	1	1
ENSG00000224462	ENSG00000224462	C4BPAP1	1:207338840-207357407	NOTEST	0	0.0213807	inf	0	1	1
ENSG00000224463	ENSG00000224463	AC079354.6	2:203070902-203103331	NOTEST	0	0	0	0	1	1
ENSG00000224464	ENSG00000224464	PGAM1P6	2:23971533-24149984	NOTEST	0.025788	0	#NAME?	0	1	1
ENSG00000224465	ENSG00000224465	SOCS2P2	22:22525368-22525942	NOTEST	0	0	0	0	1	1
ENSG00000224466	ENSG00000224466	RP4-651E10.3	1:87012760-87158886	NOTEST	0	0	0	0	1	1
ENSG00000224467	ENSG00000224467	AC009313.1	2:161952741-162111179	NOTEST	0	0	0	0	1	1
ENSG00000224468	ENSG00000224468	RP11-181K3.4	1:182992594-183114727	NOTEST	0.0482239	0.141566	1.55365	0	1	1
ENSG00000224469	ENSG00000224469	AC009517.2	7:136370305-136866854	NOTEST	0	0	0	0	1	1
ENSG00000224471	ENSG00000224471	RP11-522L3.6	X:102024088-102161086	NOTEST	0	0	0	0	1	1
ENSG00000224472	ENSG00000224472	TCF19	HSCHR6_MHC_MCF:31204888-31232984	NOTEST	0	0	0	0	1	1
ENSG00000224473	ENSG00000224473	RP11-449I17.5	10:30692125-30692705	NOTEST	0	0	0	0	1	1

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ENSG00000224474	ENSG00000224474	AL355490.1	10:99116114-99185831	NOTEST	0.422841	0	#NAME?	0	1	1
ENSG00000224475	ENSG00000224475	AC073900.4	7:96830019-96830795	NOTEST	0	0	0	0	1	1
ENSG00000224476	ENSG00000224476	RPL36P16	19:41675765-41676071	NOTEST	0	0	0	0	1	1
ENSG00000224477	ENSG00000224477	RP1-81D8.3	6:161119319-161121664	NOTEST	0	0	0	0	1	1
ENSG00000224478	ENSG00000224478	RP11-13P5.1	6:159528822-159537085	NOTEST	0	0	0	0	1	1
ENSG00000224479	ENSG00000224479	AC136289.1	3:63727968-63849579	NOTEST	0.0276614	0.0195477	-0.500872	0	1	1
ENSG00000224481	ENSG00000224481	RP11-495P10.3	1:147801123-147816764	NOTEST	0	0.0488941	inf	0	1	1
ENSG00000224482	ENSG00000224482	HSFY4P	Y:22970661-22973695	NOTEST	0	0	0	0	1	1
ENSG00000224484	ENSG00000224484	RP11-548K12.4	7:57836677-57837227	NOTEST	0	0	0	0	1	1
ENSG00000224485	ENSG00000224485	USP9YP7	Y:20020634-20022686	NOTEST	0	0	0	0	1	1
ENSG00000224486	ENSG00000224486	HCG19P	6:30327054-30327688	NOTEST	0	0	0	0	1	1
ENSG00000224487	ENSG00000224487	OR12D3	HSCHR6_MHC_MANN:29323056-29424418	NOTEST	0	0	0	0	1	1
ENSG00000224488	ENSG00000224488	RP11-492A12.2	9:17134979-17503921	NOTEST	0	0	0	0	1	1
ENSG00000224490	ENSG00000224490	TTC21B-AS1	2:166713984-166810353	NOTEST	0.00712988	0.0310302	2.12172	0	1	1
ENSG00000224493	ENSG00000224493	RP11-87O11.1	1:75667815-76076801	NOTEST	0	0	0	0	1	1
ENSG00000224494	ENSG00000224494	HNRNPA3P14	1:81771844-82458120	NOTEST	0	0	0	0	1	1
ENSG00000224496	ENSG00000224496	TRIM40	HSCHR6_MHC_APD:30040742-30053350	NOTEST	0	0	0	0	1	1
ENSG00000224497	ENSG00000224497	RPL36P4	20:34129769-34145405	NOTEST	0.190205	0.255562	0.42612	0	1	1
ENSG00000224498	ENSG00000224498	MAPKAPK5P1	10:110607943-110609319	NOTEST	0	0	0	0	1	1
ENSG00000224500	ENSG00000224500	RP11-328K22.1	10:78629358-79398353	NOTEST	0	0	0	0	1	1
ENSG00000224501	ENSG00000224501	HSPA1B	HSCHR6_MHC_COX:31782889-31785413	NOTEST	0	0	0	0	1	1
ENSG00000224503	ENSG00000224503	AC104438.1	3:65339199-66024509	NOTEST	0	0	0	0	1	1
ENSG00000224504	ENSG00000224504	RP11-475D12.2	10:87192618-87208718	NOTEST	0	0	0	0	1	1
ENSG00000224505	ENSG00000224505	AC002117.1	17:43224683-43248951	NOTEST	0.0718027	0	#NAME?	0	1	1
ENSG00000224506	ENSG00000224506	RP1-293L8.2	6:125899703-126082415	NOTEST	0	0	0	0	1	1
ENSG00000224507	ENSG00000224507	HCG23	HSCHR6_MHC_SSTO:32364870-32381497	NOTEST	0	0	0	0	1	1
ENSG00000224508	ENSG00000224508	MDC1-AS1	HSCHR6_MHC_MANN:30712281-30730363	NOTEST	0	0	0	0	1	1
ENSG00000224509	ENSG00000224509	AC010884.1	2:105552868-105719402	NOTEST	0	0	0	0	1	1
ENSG00000224510	ENSG00000224510	POLR2KP2	13:48708493-48708670	NOTEST	0	0	0	0	1	1
ENSG00000224511	ENSG00000224511	LINC00365	13:30677314-30683012	NOTEST	0.0590401	0.0773187	0.389122	0	1	1
ENSG00000224512	ENSG00000224512	AC021593.1	17:76000248-76139049	NOTEST	0.173184	0.0427816	-2.01724	0	1	1
ENSG00000224513	ENSG00000224513	AC109309.4	11:3247290-3254068	NOTEST	0	0	0	0	1	1
ENSG00000224514	ENSG00000224514	LINC00620	3:13692195-13788132	NOTEST	0	0	0	0	1	1
ENSG00000224515	ENSG00000224515	RP11-5K23.5	1:161475219-161648444	NOTEST	0	0	0	0	1	1
ENSG00000224516	ENSG00000224516	AC068134.8	2:233243243-233247599	NOTEST	0	0	0	0	1	1
ENSG00000224517	ENSG00000224517	HTR2A-AS1	13:47405684-47471169	NOTEST	0	0	0	0	1	1
ENSG00000224518	ENSG00000224518	AC006989.2	Y:17053426-17054595	NOTEST	0	0	0	0	1	1
ENSG00000224519	ENSG00000224519	HMGN1P19	7:46674211-46674544	NOTEST	0	0	0	0	1	1
ENSG00000224520	ENSG00000224520	KRT8P45	1:157043048-157044495	NOTEST	0.0349178	0.0617749	0.823056	0	1	1
ENSG00000224521	ENSG00000224521	RP11-438F14.3	1:248712056-248727140	NOTEST	0	0	0	0	1	1
ENSG00000224523	ENSG00000224523	RP13-52K8.1	X:80664436-80682775	NOTEST	0	0	0	0	1	1
ENSG00000224524	ENSG00000224524	CYCSP42	21:16862848-16863086	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000224526	ENSG00000224526	HLA-K	HSCHR6_MHC_QBL:29883749-29888221	NOTEST	0	0	0	0	1	1
ENSG00000224529	ENSG00000224529	AC093698.4	2:209000117-209002421	NOTEST	0.0163753	0	#NAME?	0	1	1
ENSG00000224530	ENSG00000224530	PPIAP10	20:51588945-52120853	NOTEST	0	0	0	0	1	1
ENSG00000224532	ENSG00000224532	RP3-470L22.1	6:6758508-6759524	NOTEST	0	0	0	0	1	1
ENSG00000224533	ENSG00000224533	TMLHE-AS1	X:154695630-154899605	NOTEST	0.0549817	0.0136881	-2.00602	0	1	1
ENSG00000224535	ENSG00000224535	RP11-61J19.2	1:212640157-212641085	NOTEST	0	0	0	0	1	1
ENSG00000224536	ENSG00000224536	RP11-134G8.7	1:201452657-201502736	NOTEST	0.174694	0	#NAME?	0	1	1
ENSG00000224537	ENSG00000224537	MEP1AP4	9:44147905-44154014	NOTEST	0	0	0	0	1	1
ENSG00000224538	ENSG00000224538	MCCD1P1	HSCHR6_MHC_APD:29814009-29814872	NOTEST	0	0	0	0	1	1
ENSG00000224539	ENSG00000224539	RP11-432N13.3	X:134732851-134749356	NOTEST	0	0	0	0	1	1
ENSG00000224540	ENSG00000224540	RP11-385M4.3	1:209405540-209406764	NOTEST	0	0	0	0	1	1
ENSG00000224541	ENSG00000224541	AP001439.2	21:27252860-27589700	NOTEST	0	0	0	0	1	1
ENSG00000224542	ENSG00000224542	TRIM31	HSCHR6_MHC_APD:30015057-30019333	NOTEST	0	0	0	0	1	1
ENSG00000224544	ENSG00000224544	PSORS1C2	HSCHR6_MHC_COX:31075026-31100333	NOTEST	0	0	0	0	1	1
ENSG00000224545	ENSG00000224545	AC008264.4	7:131185020-131242976	NOTEST	0	0.24193	inf	0	1	1
ENSG00000224547	ENSG00000224547	AC023669.2	7:46184534-46185286	NOTEST	0	0	0	0	1	1
ENSG00000224548	ENSG00000224548	RP1-107N3.2	X:126930104-126930714	NOTEST	0	0	0	0	1	1
ENSG00000224549	ENSG00000224549	RP11-370B11.3	9:22646198-22824212	NOTEST	0.0537949	0.0383086	-0.489803	0	1	1
ENSG00000224551	ENSG00000224551	HMGB3P21	7:96745901-96811075	NOTEST	0	0	0	0	1	1
ENSG00000224552	ENSG00000224552	ABHD16A	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000224553	ENSG00000224553	AC008065.1	2:172173918-172341562	NOTEST	0	0	0	0	1	1
ENSG00000224554	ENSG00000224554	RANP1	HSCHR6_MHC_MANN:30498397-30499048	NOTEST	0	0	0	0	1	1
ENSG00000224555	ENSG00000224555	RP11-438N5.2	11:3875547-4114439	NOTEST	0	0	0	0	1	1
ENSG00000224556	ENSG00000224556	RP11-485B17.3	X:52164595-52202209	NOTEST	0	0	0	0	1	1
ENSG00000224557	ENSG00000224557	HLA-DPB2	6:33080227-33111102	NOTEST	0.292852	0.458425	0.646514	0	1	1
ENSG00000224559	ENSG00000224559	LINC01087	2:132394597-132407188	NOTEST	0	0.0141481	inf	0	1	1
ENSG00000224560	ENSG00000224560	RP11-270L13.1	4:45416353-45416927	NOTEST	0	0	0	0	1	1
ENSG00000224563	ENSG00000224563	LPP-AS1	3:187868993-188608460	NOTEST	0	0	0	0	1	1
ENSG00000224564	ENSG00000224564	HCG4	HSCHR6_MHC_MCF:29755698-29762471	NOTEST	0	0	0	0	1	1
ENSG00000224565	ENSG00000224565	RP1-148H17.1	20:46020672-46041071	NOTEST	0	0	0	0	1	1
ENSG00000224566	ENSG00000224566	FAM96AP2	1:228302697-228303174	NOTEST	0.411317	0.0756623	-2.4426	0	1	1
ENSG00000224567	ENSG00000224567	AC129778.5	9:42779313-42779707	NOTEST	0	0	0	0	1	1
ENSG00000224568	ENSG00000224568	AC096669.3	2:107871146-108172782	NOTEST	0	0	0	0	1	1
ENSG00000224569	ENSG00000224569	RP11-341G5.2	4:13978789-13979652	NOTEST	0.0392787	0	#NAME?	0	1	1
ENSG00000224570	ENSG00000224570	RP11-430H12.2	1:65886247-66107242	NOTEST	0	0	0	0	1	1
ENSG00000224571	ENSG00000224571	USP9YP13	Y:26066051-26067657	NOTEST	0	0	0	0	1	1
ENSG00000224573	ENSG00000224573	AC083863.5	7:32535037-33102409	NOTEST	0	0	0	0	1	1
ENSG00000224574	ENSG00000224574	COL18A1-AS2	21:46825051-46964325	NOTEST	0	0	0	0	1	1
ENSG00000224579	ENSG00000224579	AC012314.19	19:54704609-54752862	NOTEST	0	0	0	0	1	1
ENSG00000224581	ENSG00000224581	XX-FW84067D5.2	1:13632347-13635279	NOTEST	0	0	0	0	1	1
ENSG00000224582	ENSG00000224582	LINC01015	6:29497196-29501345	NOTEST	0	0	0	0	1	1
ENSG00000224583	ENSG00000224583	RP11-554D15.4	6:74779166-75443995	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000224584	ENSG00000224584	RP11-365D23.2	1:214776537-214837931	NOTEST	0	0.0432046	inf	0	1	1
ENSG00000224585	ENSG00000224585	AC103563.5	2:95637698-95637912	NOTEST	0	0	0	0	1	1
ENSG00000224586	ENSG00000224586	GPX5	6:28471072-28502729	NOTEST	0	0	0	0	1	1
ENSG00000224587	ENSG00000224587	MDC1	HSCHR6_MHC_COX:30657448-30675531	NOTEST	0	0	0	0	1	1
ENSG00000224589	ENSG00000224589	RP11-12D5.6	X:27911464-27912176	NOTEST	0	0	0	0	1	1
ENSG00000224590	ENSG00000224590	AC007163.10	2:202352147-202483901	NOTEST	0	0	0	0	1	1
ENSG00000224592	ENSG00000224592	RP5-884C9.2	1:38512985-38584697	NOTEST	0.609366	0.410872	-0.568621	0	1	1
ENSG00000224593	ENSG00000224593	RP11-30B1.1	7:3303663-4308632	NOTEST	0	0	0	0	1	1
ENSG00000224594	ENSG00000224594	RPL29P19	8:49297149-49297609	NOTEST	0	0	0	0	1	1
ENSG00000224595	ENSG00000224595	AC073626.2	7:113726381-114333827	NOTEST	0.0668975	0	#NAME?	0	1	1
ENSG00000224596	ENSG00000224596	ZMIZ1-AS1	10:80703084-80827652	NOTEST	0.0717819	0.0709379	-0.0170652	0	1	1
ENSG00000224598	ENSG00000224598	RPS5P2	21:35445523-35732332	NOTEST	0	0.022411	inf	0	1	1
ENSG00000224599	ENSG00000224599	BMS1P12	9:70083600-70087216	NOTEST	0.0510568	0.0216054	-1.24071	0	1	1
ENSG00000224600	ENSG00000224600	RP4-612B18.1	1:171793749-171794101	NOTEST	0	0	0	0	1	1
ENSG00000224602	ENSG00000224602	RPS26P5	21:17442841-17999716	NOTEST	0	0	0	0	1	1
ENSG00000224603	ENSG00000224603	RP11-96J15.1	9:46755556-46755935	NOTEST	0	0	0	0	1	1
ENSG00000224604	ENSG00000224604	AC008069.2	2:17035086-17036551	NOTEST	0	0	0	0	1	1
ENSG00000224605	ENSG00000224605	RP1-177I10.1	6:92100030-92102718	NOTEST	0	0	0	0	1	1
ENSG00000224606	ENSG00000224606	TGFA-IT1	2:70674411-70781325	NOTEST	0	0	0	0	1	1
ENSG00000224607	ENSG00000224607	IGKV1D-27	2:90007676-90008154	NOTEST	0	0	0	0	1	1
ENSG00000224608	ENSG00000224608	HLA-B	HSCHR6_MHC_MANN:31364706-31368080	NOTEST	0	0	0	0	1	1
ENSG00000224609	ENSG00000224609	RP11-470E16.1	1:59597607-59664293	NOTEST	0	0	0	0	1	1
ENSG00000224610	ENSG00000224610	RP11-265P11.1	X:39085355-39159040	NOTEST	0	0	0	0	1	1
ENSG00000224611	ENSG00000224611	AC007919.18	3:172223297-172241297	NOTEST	0	0	0	0	1	1
ENSG00000224612	ENSG00000224612	AC011901.2	2:154028500-154058240	NOTEST	0	0	0	0	1	1
ENSG00000224613	ENSG00000224613	RP11-153F1.1	1:103957500-104068105	NOTEST	0	0	0	0	1	1
ENSG00000224614	ENSG00000224614	TNK2-AS1	3:195590234-195638816	NOTEST	0.132212	0.049139	-1.42791	0	1	1
ENSG00000224617	ENSG00000224617	RP11-402P6.5	X:71009235-71009486	NOTEST	0	0	0	0	1	1
ENSG00000224618	ENSG00000224618	AC096921.2	3:30647993-30735634	NOTEST	0	0	0	0	1	1
ENSG00000224619	ENSG00000224619	HCG18	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000224620	ENSG00000224620	MEF2AP1	1:179334854-179545087	NOTEST	0	0	0	0	1	1
ENSG00000224621	ENSG00000224621	RP11-276H7.3	1:16485760-16488378	NOTEST	0	0	0	0	1	1
ENSG00000224622	ENSG00000224622	OR9R1P	12:55552630-55553507	NOTEST	0	0	0	0	1	1
ENSG00000224625	ENSG00000224625	TUBB8P6	1:242220386-242223544	NOTEST	0	0	0	0	1	1
ENSG00000224626	ENSG00000224626	AC106053.1	2:18966072-18969018	NOTEST	0	0	0	0	1	1
ENSG00000224627	ENSG00000224627	RPL37P10	2:83822079-83822367	NOTEST	0	0	0	0	1	1
ENSG00000224628	ENSG00000224628	RP5-854E16.2	20:29873119-29874638	NOTEST	0	0.00774816	inf	0	1	1
ENSG00000224630	ENSG00000224630	RP1-169P22.2	X:143391958-143392205	NOTEST	0	0	0	0	1	1
ENSG00000224632	ENSG00000224632	LL0XNC01-73E8.1	X:102262388-102263000	NOTEST	0	0	0	0	1	1
ENSG00000224633	ENSG00000224633	OR2B4P	HSCHR6_MHC_MCF:29258647-29259590	NOTEST	0	0	0	0	1	1
ENSG00000224634	ENSG00000224634	ZNF736P6Y	Y:8218971-8220184	NOTEST	0	0	0	0	1	1
ENSG00000224635	ENSG00000224635	RP4-564F22.5	20:37034657-37045444	NOTEST	0.0779633	0.0455444	-0.775522	0	1	1
ENSG00000224637	ENSG00000224637	AC019129.2	2:44393404-44394082	NOTEST	0.0539415	0	#NAME?	0	1	1

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ENSG00000224638	ENSG00000224638	AC106900.6	2:174745592-174764156	NOTEST	0.195252	0	#NAME?	0	1	1
ENSG00000224639	ENSG00000224639	C4B	HSCHR6_MHC_MCF:32026248-32026275	NOTEST	0	0	0	0	1	1
ENSG00000224640	ENSG00000224640	SRSF1P1	13:69982347-69982867	NOTEST	0	0	0	0	1	1
ENSG00000224641	ENSG00000224641	HCG20	HSCHR6_MHC_COX:30724440-30749869	NOTEST	0	0	0	0	1	1
ENSG00000224642	ENSG00000224642	HCG15	HSCHR6_MHC_APD:28953984-28956357	NOTEST	0	0	0	0	1	1
ENSG00000224643	ENSG00000224643	AC064871.3	2:183943286-183973247	NOTEST	0	0	0	0	1	1
ENSG00000224644	ENSG00000224644	RP11-16L21.7	9:114287438-114393569	NOTEST	0	0	0	0	1	1
ENSG00000224645	ENSG00000224645	RP11-126K1.8	1:151313115-151320503	NOTEST	0	0	0	0	1	1
ENSG00000224646	ENSG00000224646	AC007387.2	2:74981796-74981946	NOTEST	0	0	0	0	1	1
ENSG00000224647	ENSG00000224647	AC026954.6	17:7233770-7238732	NOTEST	0.013237	0	#NAME?	0	1	1
ENSG00000224648	ENSG00000224648	RP11-397D12.4	9:37383174-37384431	NOTEST	0	0	0	0	1	1
ENSG00000224649	ENSG00000224649	AF124730.4	21:30554347-30560116	NOTEST	0	0	0	0	1	1
ENSG00000224650	ENSG00000224650	IGHV3-74	14:107218675-107219365	NOTEST	0	0	0	0	1	1
ENSG00000224652	ENSG00000224652	LINC00885	3:195869506-195887761	NOTEST	0	0	0	0	1	1
ENSG00000224653	ENSG00000224653	RP11-548K12.10	7:57879524-57880333	NOTEST	0	0	0	0	1	1
ENSG00000224654	ENSG00000224654	UBD	HSCHR6_MHC_MANN:29522993-29600557	NOTEST	0	0	0	0	1	1
ENSG00000224655	ENSG00000224655	AC018737.3	2:122548019-122554278	NOTEST	0.0825749	0	#NAME?	0	1	1
ENSG00000224656	ENSG00000224656	RP1-212G6.4	X:47566589-47612855	NOTEST	0	0	0	0	1	1
ENSG00000224657	ENSG00000224657	RBMY2BP	Y:24795391-24805025	NOTEST	0	0	0	0	1	1
ENSG00000224658	ENSG00000224658	RP11-631F7.1	6:148558720-148873186	NOTEST	0	0	0	0	1	1
ENSG00000224659	ENSG00000224659	GAGE12J	X:49178535-49185863	NOTEST	0	0	0	0	1	1
ENSG00000224661	ENSG00000224661	AC010907.5	2:3705784-3836122	NOTEST	0	0	0	0	1	1
ENSG00000224662	ENSG00000224662	ATP6V1G1P3	9:139674390-139674670	NOTEST	0	0	0	0	1	1
ENSG00000224664	ENSG00000224664	RPL36AP53	X:113818550-114144624	NOTEST	0	0	0	0	1	1
ENSG00000224666	ENSG00000224666	RP1-50J22.4	6:36322418-36458920	NOTEST	0	0	0	0	1	1
ENSG00000224667	ENSG00000224667	AC013470.8	7:12536054-12581536	NOTEST	0	0	0	0	1	1
ENSG00000224668	ENSG00000224668	IPO8P1	1:210856554-211307457	NOTEST	0.0637609	0.0672281	0.076392	0	1	1
ENSG00000224669	ENSG00000224669	RP11-561N12.1	7:64043110-64043585	NOTEST	0	0	0	0	1	1
ENSG00000224670	ENSG00000224670	AC068135.1	2:194892642-194892888	NOTEST	0	0	0	0	1	1
ENSG00000224671	ENSG00000224671	RP11-335O13.8	1:203059781-203136533	NOTEST	0	0	0	0	1	1
ENSG00000224672	ENSG00000224672	AC007272.3	2:201966104-201967859	NOTEST	0.0386846	0	#NAME?	0	1	1
ENSG00000224674	ENSG00000224674	EIF3EP2	2:162944768-162946582	NOTEST	0	0.00702417	inf	0	1	1
ENSG00000224675	ENSG00000224675	AC009227.2	2:154728425-155313950	NOTEST	0	0	0	0	1	1
ENSG00000224676	ENSG00000224676	AP000351.8	22:24350067-24352081	NOTEST	0	0	0	0	1	1
ENSG00000224677	ENSG00000224677	PDIA3P2	15:43885251-44010458	NOTEST	0	0.869542	inf	0	1	1
ENSG00000224678	ENSG00000224678	GAPDHP46	1:92545861-92613393	NOTEST	0	0	0	0	1	1
ENSG00000224679	ENSG00000224679	MED15P4	2:132292759-132294561	NOTEST	0	0	0	0	1	1
ENSG00000224681	ENSG00000224681	RP11-146D12.5	9:42478012-42478478	NOTEST	0	0	0	0	1	1
ENSG00000224682	ENSG00000224682	SOCS5P2	9:138339291-138342000	NOTEST	0	0	0	0	1	1
ENSG00000224683	ENSG00000224683	RPL36AP29	7:16130816-16460947	NOTEST	0	0	0	0	1	1
ENSG00000224685	ENSG00000224685	RP11-84O12.3	1:101117502-101117823	NOTEST	0	0	0	0	1	1
ENSG00000224686	ENSG00000224686	TCEB1P23	13:78469615-79233314	NOTEST	0	0	0	0	1	1
ENSG00000224688	ENSG00000224688	KB-1592A4.13	22:21495912-21496660	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000224689	ENSG00000224689	ZNF812	19:9800599-9811452	NOTEST	0.103941	0.0432306	-1.26564	0	1	1
ENSG00000224690	ENSG00000224690	UBE2D3P3	1:150768683-150780799	NOTEST	0.0584331	0.0416662	-0.487909	0	1	1
ENSG00000224691	ENSG00000224691	GS1-174L6.4	1:185703682-186160085	NOTEST	0.480398	0.545778	0.184086	0	1	1
ENSG00000224692	ENSG00000224692	LL0XNC01-177E8.2	X:102513499-102514509	NOTEST	0	0	0	0	1	1
ENSG00000224693	ENSG00000224693	HLA-T	HSCHR6_MHC_SSTO:29854816-29855948	NOTEST	0	0	0	0	1	1
ENSG00000224695	ENSG00000224695	MTND6P7	2:83044661-83045185	NOTEST	0	0	0	0	1	1
ENSG00000224697	ENSG00000224697	NEFMP1	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000224698	ENSG00000224698	RP11-131J3.1	1:108803817-109013624	NOTEST	0	0	0	0	1	1
ENSG00000224700	ENSG00000224700	RP11-697E14.2	11:131240372-132206716	NOTEST	0	0	0	0	1	1
ENSG00000224701	ENSG00000224701	MED28P4	X:45811196-45811768	NOTEST	0	0	0	0	1	1
ENSG00000224702	ENSG00000224702	RP11-38C18.2	1:165171103-165325952	NOTEST	0	0	0	0	1	1
ENSG00000224705	ENSG00000224705	HCG18	HSCHR6_MHC_DBB:30192096-30304918	NOTEST	0	0	0	0	1	1
ENSG00000224706	ENSG00000224706	RPS17P13	7:36893960-37488852	NOTEST	0	0	0	0	1	1
ENSG00000224707	ENSG00000224707	E2F3-IT1	6:20402397-20493941	NOTEST	0	0	0	0	1	1
ENSG00000224708	ENSG00000224708	LY6G6E	HSCHR6_MHC_COX:31662076-31673108	NOTEST	0	0	0	0	1	1
ENSG00000224709	ENSG00000224709	OR11M1P	12:49021670-49022565	NOTEST	0	0	0	0	1	1
ENSG00000224710	ENSG00000224710	FAM90A8P	8:7595908-7598918	NOTEST	0	0	0	0	1	1
ENSG00000224711	ENSG00000224711	RP5-988G17.1	20:7328113-7348279	NOTEST	0	0	0	0	1	1
ENSG00000224712	ENSG00000224712	NPIPA3	16:14802800-14820195	NOTEST	0.101998	0.0777175	-0.392234	0	1	1
ENSG00000224713	ENSG00000224713	AC025165.8	12:58003962-58027138	NOTEST	0.225031	0.192348	-0.226405	0	1	1
ENSG00000224714	ENSG00000224714	RP11-179K3.2	10:66660893-66684276	NOTEST	0	0	0	0	1	1
ENSG00000224715	ENSG00000224715	CITF22-49D8.1	22:47741318-47769291	NOTEST	0	0	0	0	1	1
ENSG00000224717	ENSG00000224717	RP11-576D8.4	1:205342379-205438152	NOTEST	0	0.00425102	inf	0	1	1
ENSG00000224718	ENSG00000224718	RP11-222A5.1	1:175846478-175849604	NOTEST	0	0	0	0	1	1
ENSG00000224719	ENSG00000224719	AC009237.6	2:96168538-96170807	NOTEST	0	0	0	0	1	1
ENSG00000224721	ENSG00000224721	AC007182.6	14:76041230-76550928	NOTEST	0.029952	0.0119388	-1.327	0	1	1
ENSG00000224723	ENSG00000224723	GUSBP10	7:57245115-57247759	NOTEST	0	0	0	0	1	1
ENSG00000224725	ENSG00000224725	CEP57L1P1	10:72149181-72150382	NOTEST	0.0288459	0.106399	1.88305	0	1	1
ENSG00000224727	ENSG00000224727	FCF1P7	1:243419319-244014381	NOTEST	0.0383847	0	#NAME?	0	1	1
ENSG00000224728	ENSG00000224728	AC090945.1	3:15919553-15921078	NOTEST	0.500156	0.139527	-1.84184	0	1	1
ENSG00000224729	ENSG00000224729	PCOLCE-AS1	7:100169854-100205798	NOTEST	0.054927	0.0499644	-0.136615	0	1	1
ENSG00000224730	ENSG00000224730	AC009892.10	19:55084386-55150343	NOTEST	0	0	0	0	1	1
ENSG00000224731	ENSG00000224731	AC016716.2	2:79384131-80875905	NOTEST	0	0.0367478	inf	0	1	1
ENSG00000224732	ENSG00000224732	MAGEA7P	X:148889875-148890817	NOTEST	0	0	0	0	1	1
ENSG00000224733	ENSG00000224733	RP1-86D1.5	6:128289923-128841870	NOTEST	0	0	0	0	1	1
ENSG00000224735	ENSG00000224735	RP11-272G22.1	X:53785523-53785702	NOTEST	0	0	0	0	1	1
ENSG00000224736	ENSG00000224736	HLA-V	HSCHR6_MHC_MANN:29755658-29762533	NOTEST	0	0	0	0	1	1
ENSG00000224738	ENSG00000224738	AC099850.1	17:57059998-57232630	NOTEST	0.351238	0.310544	-0.177651	0	1	1
ENSG00000224739	ENSG00000224739	AC016735.1	2:43228494-43233200	NOTEST	0	0	0	0	1	1
ENSG00000224740	ENSG00000224740	FLOT1	HSCHR6_MHC_MCF:30773971-30787802	NOTEST	0	0	0	0	1	1
ENSG00000224743	ENSG00000224743	TEX26-AS1	13:31456069-31551760	NOTEST	0	0	0	0	1	1
ENSG00000224744	ENSG00000224744	PSORS1C3	HSCHR6_MHC_QBL:31133983-31138149	NOTEST	0	0	0	0	1	1
ENSG00000224745	ENSG00000224745	RP11-380G5.2	10:89618917-89731687	NOTEST	0.25939	0.421359	0.699923	0	1	1
ENSG00000224746	ENSG00000224746	AC015987.1	7:135611202-135662101	NOTEST	0	0	0	0	1	1

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ENSG00000224747	ENSG00000224747	AP001065.7	21:45889811-45892399	NOTEST	0	0	0	0	1	1
ENSG00000224748	ENSG00000224748	TAP1	HSCHR6_MHC_SSTO:32898408-32937507	NOTEST	0	0	0	0	1	1
ENSG00000224750	ENSG00000224750	RP11-94M14.2	10:92162277-92300562	NOTEST	0	0	0	0	1	1
ENSG00000224751	ENSG00000224751	SHMT1P1	1:44115828-44396831	NOTEST	0	0	0	0	1	1
ENSG00000224752	ENSG00000224752	VN1R21P	3:14130606-14131371	NOTEST	0	0	0	0	1	1
ENSG00000224753	ENSG00000224753	XXbac-BPG13B8.10	HSCHR6_MHC_APD:29465367-29478414	NOTEST	0	0	0	0	1	1
ENSG00000224755	ENSG00000224755	HMGN1P34	X:77775089-77775683	NOTEST	0	0	0	0	1	1
ENSG00000224758	ENSG00000224758	LINC01167	10:134757470-134778793	NOTEST	0	0	0	0	1	1
ENSG00000224760	ENSG00000224760	C1DP3	10:81784492-81784918	NOTEST	0	0	0	0	1	1
ENSG00000224761	ENSG00000224761	RP11-508N22.8	10:38453575-38501285	NOTEST	0	0	0	0	1	1
ENSG00000224762	ENSG00000224762	CR769776.3	9:69485457-69486244	NOTEST	0	0	0	0	1	1
ENSG00000224763	ENSG00000224763	FDPSP8	1:211833530-211834619	NOTEST	0.0161791	0.0125791	-0.3631	0	1	1
ENSG00000224764	ENSG00000224764	RP11-54O15.3	9:97488982-97849441	NOTEST	0.0470015	0.0366345	-0.359504	0	1	1
ENSG00000224765	ENSG00000224765	RP1-137H15.2	X:136638349-136646546	NOTEST	0	0	0	0	1	1
ENSG00000224766	ENSG00000224766	DASS-36P22.4	HSCHR6_MHC_SSTO:31839420-31849264	NOTEST	0	0	0	0	1	1
ENSG00000224769	ENSG00000224769	AC069213.1	3:195341817-195347104	NOTEST	0.0590515	0.0291349	-1.01922	0	1	1
ENSG00000224770	ENSG00000224770	BTNL2	HSCHR6_MHC_COX:32306511-32323110	NOTEST	0	0	0	0	1	1
ENSG00000224771	ENSG00000224771	ATP2B2-IT2	3:10365706-10749716	NOTEST	0	0	0	0	1	1
ENSG00000224773	ENSG00000224773	HSPA8P7	X:113818550-114144624	NOTEST	0.0151408	0.0117458	-0.366292	0	1	1
ENSG00000224774	ENSG00000224774	CSNK2B	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000224775	ENSG00000224775	BRAFP1	X:74802510-74805341	NOTEST	0	0	0	0	1	1
ENSG00000224776	ENSG00000224776	RP11-361A21.1	11:109852917-109853769	NOTEST	0.101659	0.26388	1.37615	0	1	1
ENSG00000224777	ENSG00000224777	OR4F2P	11:86648-87586	NOTEST	0	0	0	0	1	1
ENSG00000224778	ENSG00000224778	CENPIP1	13:19700538-19713751	NOTEST	0	0	0	0	1	1
ENSG00000224781	ENSG00000224781	EIF4A2P4	X:52861753-52862949	NOTEST	0.0289798	0.0225288	-0.363279	0	1	1
ENSG00000224782	ENSG00000224782	PFDN6	HSCHR6_MHC_DBB:33224809-33245105	NOTEST	0	0	0	0	1	1
ENSG00000224783	ENSG00000224783	MIPEPP2	1:238940348-238942500	NOTEST	0	0	0	0	1	1
ENSG00000224784	ENSG00000224784	AL591704.7	1:153369066-153369247	NOTEST	0	0	0	0	1	1
ENSG00000224785	ENSG00000224785	AC006026.9	7:23602077-23603880	NOTEST	0	0.0410785	inf	0	1	1
ENSG00000224786	ENSG00000224786	CETN4P	4:123651702-123653348	NOTEST	0.0498347	0	#NAME?	0	1	1
ENSG00000224788	ENSG00000224788	RP5-933E2.1	10:10100684-10105465	NOTEST	0	0	0	0	1	1
ENSG00000224789	ENSG00000224789	AC012363.4	2:120770580-120974855	NOTEST	0	0	0	0	1	1
ENSG00000224791	ENSG00000224791	KRT18P39	2:204629017-204630316	NOTEST	0	0	0	0	1	1
ENSG00000224792	ENSG00000224792	RP11-314A5.3	3:51851618-51864876	NOTEST	0	0	0	0	1	1
ENSG00000224793	ENSG00000224793	HLA-DQB3	HSCHR6_MHC_COX:32618751-32622852	NOTEST	0	0	0	0	1	1
ENSG00000224794	ENSG00000224794	RP3-333H23.8	22:39688992-39691568	NOTEST	0	0	0	0	1	1
ENSG00000224795	ENSG00000224795	AP003039.3	11:131240372-132206716	NOTEST	0	0	0	0	1	1
ENSG00000224796	ENSG00000224796	RPL32P1	6:33032345-33054978	NOTEST	0	0	0	0	1	1
ENSG00000224797	ENSG00000224797	RP11-57C19.6	9:133589332-133763062	NOTEST	0	0	0	0	1	1
ENSG00000224799	ENSG00000224799	RP11-445O16.3	X:56999942-57001229	NOTEST	0	0.0222178	inf	0	1	1
ENSG00000224800	ENSG00000224800	RP11-235D19.2	1:150853711-150854159	NOTEST	0.0536014	0	#NAME?	0	1	1
ENSG00000224801	ENSG00000224801	HCG4P8	HSCHR6_MHC_MANN:29791676-29795834	NOTEST	0	0	0	0	1	1
ENSG00000224802	ENSG00000224802	TUBB4BP2	9:34084329-34127397	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000224804	ENSG00000224804	AC004878.2	7:74807498-74867509	NOTEST	0	0	0	0	1	1
ENSG00000224805	ENSG00000224805	LINC00853	1:47533159-47646011	NOTEST	0.31915	0.0922238	-1.79102	0	1	1
ENSG00000224806	ENSG00000224806	ARL5AP4	22:25082134-25082646	NOTEST	0	0	0	0	1	1
ENSG00000224807	ENSG00000224807	DUX4L9	4:190942561-190943820	NOTEST	0	0	0	0	1	1
ENSG00000224808	ENSG00000224808	SRGAP3-AS1	3:9022274-9520924	NOTEST	0	0	0	0	1	1
ENSG00000224809	ENSG00000224809	BEND3P2	9:94933522-94935776	NOTEST	0.215953	0.519355	1.266	0	1	1
ENSG00000224810	ENSG00000224810	RP11-538D16.2	1:182031811-182038388	NOTEST	0.108914	0.271505	1.31779	0	1	1
ENSG00000224812	ENSG00000224812	TMEM72-AS1	10:45306471-45491339	NOTEST	0	0	0	0	1	1
ENSG00000224813	ENSG00000224813	RP4-669L17.4	1:317719-461954	NOTEST	0	0	0	0	1	1
ENSG00000224814	ENSG00000224814	AC114812.8	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000224815	ENSG00000224815	RP11-307E17.9	9:97094757-97123230	NOTEST	0	0	0	0	1	1
ENSG00000224816	ENSG00000224816	NAP1L4P2	X:105709771-105710670	NOTEST	0	0	0	0	1	1
ENSG00000224817	ENSG00000224817	RP11-190J1.3	10:103464408-103468158	NOTEST	0	0	0	0	1	1
ENSG00000224819	ENSG00000224819	AC093843.1	2:221655797-221662613	NOTEST	0	0	0	0	1	1
ENSG00000224820	ENSG00000224820	BTF3P4	9:74722733-74723228	NOTEST	0	0	0	0	1	1
ENSG00000224821	ENSG00000224821	COL4A2-AS2	13:110801317-111165374	NOTEST	0.0199586	0	#NAME?	0	1	1
ENSG00000224822	ENSG00000224822	THRB-IT1	3:24158650-24541833	NOTEST	0	0	0	0	1	1
ENSG00000224825	ENSG00000224825	RP11-171A24.3	9:77100466-77308093	NOTEST	0	0	0	0	1	1
ENSG00000224826	ENSG00000224826	AC019109.1	2:225034380-225036254	NOTEST	0	0	0	0	1	1
ENSG00000224827	ENSG00000224827	LINC00265-2P	Y:26422391-26423173	NOTEST	0	0	0	0	1	1
ENSG00000224828	ENSG00000224828	RP11-186G6.5	9:43318618-43319576	NOTEST	0	0	0	0	1	1
ENSG00000224829	ENSG00000224829	CTD-2589O24.1	11:77024650-77025077	NOTEST	0	0.0452308	inf	0	1	1
ENSG00000224830	ENSG00000224830	OR2X1P	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000224832	ENSG00000224832	AP000469.2	21:25676862-25693690	NOTEST	0	0	0	0	1	1
ENSG00000224834	ENSG00000224834	BTF3P9	1:227621764-227622047	NOTEST	0	0	0	0	1	1
ENSG00000224835	ENSG00000224835	C6orf47-AS1	HSCHR6_MHC_QBL:31616314-31618789	NOTEST	0	0	0	0	1	1
ENSG00000224836	ENSG00000224836	RP11-341G2.3	9:1151806-1152140	NOTEST	0	0	0	0	1	1
ENSG00000224838	ENSG00000224838	FKSG52	5:58264864-59843484	NOTEST	0	0	0	0	1	1
ENSG00000224839	ENSG00000224839	AC093698.2	2:208921971-208922469	NOTEST	0.0454227	0.145227	1.67683	0	1	1
ENSG00000224841	ENSG00000224841	RGL2	HSCHR6_MHC_COX:33168490-33188786	NOTEST	0	0	0	0	1	1
ENSG00000224843	ENSG00000224843	LINC00240	6:26924770-26991703	NOTEST	0.0905858	0.200134	1.14361	0	1	1
ENSG00000224844	ENSG00000224844	AC107079.1	2:238031552-238032740	NOTEST	0	0	0	0	1	1
ENSG00000224846	ENSG00000224846	RP1-90J20.8	6:2988200-3019996	NOTEST	0.105271	0.174662	0.730461	0	1	1
ENSG00000224848	ENSG00000224848	RP11-535M15.1	9:99449337-99483403	NOTEST	0.175299	0.176051	0.0061739	0	1	1
ENSG00000224849	ENSG00000224849	RP1-104O17.1	6:98150156-98180588	NOTEST	0	0	0	0	1	1
ENSG00000224850	ENSG00000224850	AC108051.3	2:103628236-103636356	NOTEST	0	0.107637	inf	0	1	1
ENSG00000224851	ENSG00000224851	LINC00502	10:92806922-92821916	NOTEST	0	0	0	0	1	1
ENSG00000224852	ENSG00000224852	MTND5P24	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000224853	ENSG00000224853	LINC00393	13:73987609-74222390	NOTEST	0	0.210406	inf	0	1	1
ENSG00000224854	ENSG00000224854	C9orf53	9:21802541-22121096	NOTEST	0.132713	0.0512467	-1.37278	0	1	1
ENSG00000224855	ENSG00000224855	OPA1-AS1	3:193310932-193415612	NOTEST	0.0618208	0.149638	1.27531	0	1	1
ENSG00000224856	ENSG00000224856	RP4-796I17.5	22:44319618-44568829	NOTEST	0	0.220582	inf	0	1	1
ENSG00000224857	ENSG00000224857	RP11-344P13.1	1:121315743-121322322	NOTEST	0	0	0	0	1	1
ENSG00000224859	ENSG00000224859	ZNRD1	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1

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ENSG00000224862	ENSG00000224862	XXbac-BPG27H4.8	HSCHR6_MHC_MCF:30885788-30894426	NOTEST	0	0	0	0	1	1
ENSG00000224863	ENSG00000224863	RP5-1109J22.2	1:46912344-46915376	NOTEST	0	0.0109172	inf	0	1	1
ENSG00000224865	ENSG00000224865	AC009518.4	7:131582399-131633712	NOTEST	0	0	0	0	1	1
ENSG00000224866	ENSG00000224866	USP9YP25	Y:25880339-25882396	NOTEST	0	0	0	0	1	1
ENSG00000224867	ENSG00000224867	AC096644.1	1:220603285-220608023	NOTEST	0	0	0	0	1	1
ENSG00000224869	ENSG00000224869	AC062016.1	2:117484028-117484347	NOTEST	0	0	0	0	1	1
ENSG00000224871	ENSG00000224871	XX-FW81066F1.2	X:149097744-149392815	NOTEST	0.0445232	0.0875462	0.975488	0	1	1
ENSG00000224873	ENSG00000224873	CDY13P	Y:24666827-24667842	NOTEST	0	0	0	0	1	1
ENSG00000224874	ENSG00000224874	MYL8P	HSCHR6_MHC_MCF:33477103-33477621	NOTEST	0	0	0	0	1	1
ENSG00000224875	ENSG00000224875	AC083949.1	2:42370377-42559688	NOTEST	0	0	0	0	1	1
ENSG00000224876	ENSG00000224876	RP11-49G10.3	20:31802725-31804873	NOTEST	0	0	0	0	1	1
ENSG00000224879	ENSG00000224879	AC011754.1	2:79384131-80875905	NOTEST	0	0	0	0	1	1
ENSG00000224880	ENSG00000224880	RP11-1217F2.7	7:57241063-57242069	NOTEST	0	0	0	0	1	1
ENSG00000224881	ENSG00000224881	AC068279.3	2:87607002-87607890	NOTEST	0	0.0146096	inf	0	1	1
ENSG00000224882	ENSG00000224882	IKBKGP1	X:153868250-153876549	NOTEST	0	0	0	0	1	1
ENSG00000224883	ENSG00000224883	CTA-250D10.19	22:42372275-42394225	NOTEST	0	0	0	0	1	1
ENSG00000224884	ENSG00000224884	AC034187.2	3:7994491-8653610	NOTEST	0	0	0	0	1	1
ENSG00000224885	ENSG00000224885	TSSC1-IT1	2:3192695-3381653	NOTEST	0	0.0191898	inf	0	1	1
ENSG00000224887	ENSG00000224887	RP11-276H19.4	9:89699075-89700066	NOTEST	0.470939	0.365695	-0.364901	0	1	1
ENSG00000224888	ENSG00000224888	RP5-1142A6.2	16:88772870-88851619	NOTEST	0.0340545	0.0203949	-0.739635	0	1	1
ENSG00000224889	ENSG00000224889	PTMAP1	HSCHR6_MHC_SSTO:30586039-30606022	NOTEST	0	0	0	0	1	1
ENSG00000224891	ENSG00000224891	AC007899.3	2:37311593-37384208	NOTEST	0	0	0	0	1	1
ENSG00000224892	ENSG00000224892	RPS4XP16	13:51909908-52126500	NOTEST	0.0479148	0.24594	2.35976	0	1	1
ENSG00000224893	ENSG00000224893	RP1-200K18.1	6:153115630-153153048	NOTEST	0	0	0	0	1	1
ENSG00000224894	ENSG00000224894	GPR53P	HSCHR6_MHC_QBL:29505443-29506234	NOTEST	0	0	0	0	1	1
ENSG00000224895	ENSG00000224895	VPS26BP1	3:47892181-48130769	NOTEST	0	0	0	0	1	1
ENSG00000224896	ENSG00000224896	SIGLEC30P	1:170084776-170085717	NOTEST	0	0	0	0	1	1
ENSG00000224899	ENSG00000224899	RP11-3B12.5	7:124462439-125019375	NOTEST	0.394573	0.447483	0.181542	0	1	1
ENSG00000224901	ENSG00000224901	RP11-448G4.4	1:197473877-197744826	NOTEST	0	0	0	0	1	1
ENSG00000224902	ENSG00000224902	GAGE12H	X:49344585-49351904	NOTEST	0	0	0	0	1	1
ENSG00000224903	ENSG00000224903	AC005534.8	7:156264889-156685924	NOTEST	0.0780421	0.158879	1.02561	0	1	1
ENSG00000224904	ENSG00000224904	RP5-934G17.6	1:11937826-11940463	NOTEST	0	0	0	0	1	1
ENSG00000224905	ENSG00000224905	AP001347.6	21:15399741-15583166	NOTEST	0.248478	0.210664	-0.238174	0	1	1
ENSG00000224906	ENSG00000224906	RP1-102E24.9	12:6547663-6548018	NOTEST	0	0	0	0	1	1
ENSG00000224907	ENSG00000224907	RP11-451M19.2	10:111567408-111567887	NOTEST	0	0	0	0	1	1
ENSG00000224908	ENSG00000224908	TIMM8BP2	X:133300711-133300962	NOTEST	0	0	0	0	1	1
ENSG00000224910	ENSG00000224910	AC002115.5	19:36088808-36092403	NOTEST	0	0	0	0	1	1
ENSG00000224911	ENSG00000224911	AC015936.3	17:42923720-42994305	NOTEST	0.195632	0.182095	-0.103453	0	1	1
ENSG00000224914	ENSG00000224914	LINC00863	10:89102492-89130452	NOTEST	0.421883	0.475855	0.173679	0	1	1
ENSG00000224916	ENSG00000224916	APOC4-APOC2	19:45445494-45452822	NOTEST	0.081235	0	#NAME?	0	1	1

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ENSG00000224917	ENSG00000224917	AC016694.2	Y:24816762-24819006	NOTEST	0	0	0	0	1	1
ENSG00000224918	ENSG00000224918	AY269186.2	3:95030-96029	NOTEST	0	0	0	0	1	1
ENSG00000224919	ENSG00000224919	RP11-144G6.4	10:47186202-47243502	NOTEST	0	0	0	0	1	1
ENSG00000224920	ENSG00000224920	TACC1P1	10:37811938-37833629	NOTEST	0	0	0	0	1	1
ENSG00000224921	ENSG00000224921	HCG4P11	HSCHR6_MHC_QBL:29688013-29714292	NOTEST	0	0	0	0	1	1
ENSG00000224922	ENSG00000224922	AL050303.7	21:15142252-15144061	NOTEST	0	0	0	0	1	1
ENSG00000224923	ENSG00000224923	HCG20	HSCHR6_MHC_DBB:30724986-30750718	NOTEST	0	0	0	0	1	1
ENSG00000224924	ENSG00000224924	LINC00320	21:22114907-22175534	NOTEST	0	0	0	0	1	1
ENSG00000224925	ENSG00000224925	OR2N1P	HSCHR6_MHC_COX:29102325-29103262	NOTEST	0	0	0	0	1	1
ENSG00000224927	ENSG00000224927	NDUFA5P10	1:110353263-110353620	NOTEST	0	0	0	0	1	1
ENSG00000224928	ENSG00000224928	KRT8P30	2:219809350-219826876	NOTEST	0.0310118	0	#NAME?	0	1	1
ENSG00000224929	ENSG00000224929	HLA-DPA3	HSCHR6_MHC_QBL:33027764-33039900	NOTEST	0	0	0	0	1	1
ENSG00000224930	ENSG00000224930	LINC00162	21:46419121-46424642	NOTEST	0	0	0	0	1	1
ENSG00000224931	ENSG00000224931	AC152010.1	X:152537077-152543260	NOTEST	0	0	0	0	1	1
ENSG00000224932	ENSG00000224932	AC107399.2	4:118235752-118294008	NOTEST	0	0	0	0	1	1
ENSG00000224933	ENSG00000224933	LINC01034	13:76587158-76588637	NOTEST	0.404605	0	#NAME?	0	1	1
ENSG00000224935	ENSG00000224935	RP11-74C3.1	9:12098659-12159147	NOTEST	0	0	0	0	1	1
ENSG00000224936	ENSG00000224936	SUCLA2P1	6:30436658-30438028	NOTEST	0.0371605	0.0279706	-0.409861	0	1	1
ENSG00000224937	ENSG00000224937	RP11-34H11.6	9:46334291-46334508	NOTEST	0	0	0	0	1	1
ENSG00000224939	ENSG00000224939	LINC00184	1:234765056-234770526	NOTEST	0.0128054	0.0159646	0.318129	0	1	1
ENSG00000224941	ENSG00000224941	TCF19	HSCHR6_MHC_MANN:31171309-31199405	NOTEST	0	0	0	0	1	1
ENSG00000224942	ENSG00000224942	RP11-51C14.1	X:139479226-139480476	NOTEST	0	0	0	0	1	1
ENSG00000224943	ENSG00000224943	RP11-180D21.3	1:159315955-159453166	NOTEST	0	0	0	0	1	1
ENSG00000224944	ENSG00000224944	CASC6	6:92339632-92400146	NOTEST	0	0	0	0	1	1
ENSG00000224945	ENSG00000224945	RP11-82L18.2	9:91628059-91793682	NOTEST	0	0	0	0	1	1
ENSG00000224946	ENSG00000224946	AC007312.3	7:33168855-33645680	NOTEST	0	0	0	0	1	1
ENSG00000224947	ENSG00000224947	VN1R25P	7:56626913-56627651	NOTEST	0	0	0	0	1	1
ENSG00000224948	ENSG00000224948	ATP5G1P8	10:78596325-78596619	NOTEST	0	0	0	0	1	1
ENSG00000224949	ENSG00000224949	RP11-161N3.3	X:54094756-54209714	NOTEST	0	0	0	0	1	1
ENSG00000224952	ENSG00000224952	PBX2	HSCHR6_MHC_SSTO:32159379-32164831	NOTEST	0	0	0	0	1	1
ENSG00000224953	ENSG00000224953	SRIP3	Y:6587002-6587221	NOTEST	0	0	0	0	1	1
ENSG00000224954	ENSG00000224954	PAIP1P1	HSCHR6_MHC_SSTO:30141781-30170758	NOTEST	0	0	0	0	1	1
ENSG00000224955	ENSG00000224955	RP11-32I2.1	9:27948075-28670283	NOTEST	0	0	0	0	1	1
ENSG00000224956	ENSG00000224956	RP11-206L10.1	1:661610-663527	NOTEST	0.412167	0.303578	-0.44116	0	1	1
ENSG00000224957	ENSG00000224957	AC090044.1	3:577913-887698	NOTEST	0	0	0	0	1	1
ENSG00000224958	ENSG00000224958	PGM5-AS1	9:70921443-71145977	NOTEST	0	0	0	0	1	1
ENSG00000224959	ENSG00000224959	AC017002.2	2:111953539-112268567	NOTEST	0.0801067	0.121069	0.595836	0	1	1
ENSG00000224960	ENSG00000224960	SMEK3P	X:27478920-27481413	NOTEST	0	0	0	0	1	1
ENSG00000224961	ENSG00000224961	RP1-278O22.1	20:10618331-10975572	NOTEST	0	0	0	0	1	1
ENSG00000224962	ENSG00000224962	PSAT1P4	3:166408974-166409503	NOTEST	0	0	0	0	1	1
ENSG00000224963	ENSG00000224963	U82695.9	X:152710177-152775012	NOTEST	0	0	0	0	1	1
ENSG00000224964	ENSG00000224964	TRAPPC2P3	Y:19909862-19912576	NOTEST	0	0	0	0	1	1
ENSG00000224965	ENSG00000224965	KCNC4-AS1	1:110751455-110752609	NOTEST	0.0514866	0.018182	-1.50168	0	1	1
ENSG00000224966	ENSG00000224966	TBC1D3P6	1:16316365-16321246	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000224967	ENSG00000224967	AC009303.3	2:118617002-118771709	NOTEST	0	0	0	0	1	1
ENSG00000224968	ENSG00000224968	RP1-35C21.1	1:177320721-177335408	NOTEST	0	0	0	0	1	1
ENSG00000224969	ENSG00000224969	RP11-54O7.11	1:947376-948573	NOTEST	0	0	0	0	1	1
ENSG00000224970	ENSG00000224970	RP11-114L10.2	7:142568955-142590199	NOTEST	0	0	0	0	1	1
ENSG00000224971	ENSG00000224971	SUMO2P3	7:55799836-55800124	NOTEST	0	0	0	0	1	1
ENSG00000224972	ENSG00000224972	RP11-403H13.1	9:6716547-7175648	NOTEST	0	0	0	0	1	1
ENSG00000224973	ENSG00000224973	LARGE-AS1	22:33558211-34318829	NOTEST	0	0	0	0	1	1
ENSG00000224976	ENSG00000224976	PARP4P2	13:19923276-19982102	NOTEST	0	0.00330419	inf	0	1	1
ENSG00000224977	ENSG00000224977	RP11-160H22.3	1:173991646-173992123	NOTEST	0	0	0	0	1	1
ENSG00000224978	ENSG00000224978	RP13-228J13.9	X:154425283-154468098	NOTEST	0	0	0	0	1	1
ENSG00000224979	ENSG00000224979	LSM2	HSCHR6_MHC_APD:31776525-31786115	NOTEST	0	0	0	0	1	1
ENSG00000224980	ENSG00000224980	RP11-377K22.3	1:56960418-57110974	NOTEST	0	0	0	0	1	1
ENSG00000224981	ENSG00000224981	AC000367.1	7:126078651-126893348	NOTEST	0	0	0	0	1	1
ENSG00000224982	ENSG00000224982	TMEM233	12:119772516-120119435	NOTEST	0	0	0	0	1	1
ENSG00000224984	ENSG00000224984	RP11-524H19.2	6:54704915-54705653	NOTEST	0	0	0	0	1	1
ENSG00000224985	ENSG00000224985	RP11-297K8.2	1:161122565-161129139	NOTEST	0	0	0	0	1	1
ENSG00000224986	ENSG00000224986	PPP1R8P1	1:48761043-48937845	NOTEST	0.0170132	0.0494537	1.53942	0	1	1
ENSG00000224987	ENSG00000224987	RP1-191J18.65	6:108306292-108306983	NOTEST	0	0	0	0	1	1
ENSG00000224988	ENSG00000224988	RP11-409K20.7	9:132645971-132646449	NOTEST	0	0	0	0	1	1
ENSG00000224989	ENSG00000224989	FAM41AY1	Y:19612837-19626898	NOTEST	0	0	0	0	1	1
ENSG00000224990	ENSG00000224990	OR2G1P	HSCHR6_MHC_DBB:29191798-29234885	NOTEST	0	0	0	0	1	1
ENSG00000224992	ENSG00000224992	RP11-295G24.5	9:135600964-135765588	NOTEST	0	0	0	0	1	1
ENSG00000224993	ENSG00000224993	RPL29P12	5:43571695-43707507	NOTEST	0.100195	0.232827	1.21645	0	1	1
ENSG00000224994	ENSG00000224994	TRIM39	HSCHR6_MHC_COX:30191706-30304467	NOTEST	0	0	0	0	1	1
ENSG00000224995	ENSG00000224995	RP5-991C6.3	6:82523002-82523874	NOTEST	0.0791703	0.0302102	-1.38992	0	1	1
ENSG00000224997	ENSG00000224997	AL049840.1	14:104019757-104181841	NOTEST	0.26678	0.309249	0.213121	0	1	1
ENSG00000224999	ENSG00000224999	XXyac-YX65C7_A.4	6:169696565-169698054	NOTEST	0	0	0	0	1	1
ENSG00000225000	ENSG00000225000	AC010082.2	7:18126571-19042039	NOTEST	0	0	0	0	1	1
ENSG00000225002	ENSG00000225002	RP11-6F6.1	9:108823634-108827106	NOTEST	0	0	0	0	1	1
ENSG00000225003	ENSG00000225003	OR51A5P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000225005	ENSG00000225005	RP11-483G21.3	7:72726534-72742085	NOTEST	0	0	0	0	1	1
ENSG00000225006	ENSG00000225006	RP11-669M2.1	1:188477668-188505596	NOTEST	0	0	0	0	1	1
ENSG00000225007	ENSG00000225007	AC000067.1	22:19654545-19655078	NOTEST	0	0	0	0	1	1
ENSG00000225008	ENSG00000225008	RP13-228J13.6	X:154505499-154563966	NOTEST	0	0	0	0	1	1
ENSG00000225010	ENSG00000225010	RP11-435B5.1	1:143342843-143343247	NOTEST	0	0.0909224	inf	0	1	1
ENSG00000225011	ENSG00000225011	RP11-810H18.1	1:29814704-29823405	NOTEST	0	0	0	0	1	1
ENSG00000225012	ENSG00000225012	RP13-348B13.2	X:88678736-88701982	NOTEST	0	0	0	0	1	1
ENSG00000225014	ENSG00000225014	KCTD9P1	17:19912656-20306870	NOTEST	0.0596475	0.0568706	-0.0687774	0	1	1
ENSG00000225015	ENSG00000225015	SNX18P15	1:142618768-142729975	NOTEST	0.299937	0.259058	-0.211383	0	1	1
ENSG00000225016	ENSG00000225016	LINC00328-2P	13:19383969-19384188	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000225017	ENSG00000225017	AP004289.1	8:100025493-100906290	NOTEST	0	0	0	0	1	1
ENSG00000225018	ENSG00000225018	RP11-419M24.5	7:55944430-55944717	NOTEST	0	0	0	0	1	1
ENSG00000225022	ENSG00000225022	UBE2D3P1	20:5273033-5273477	NOTEST	0	0.173995	inf	0	1	1
ENSG00000225023	ENSG00000225023	HCG4P8	HSCHR6_MHC_QBL:29791931-29796106	NOTEST	0	0	0	0	1	1
ENSG00000225024	ENSG00000225024	AC015977.5	2:26901086-26901378	NOTEST	0	0	0	0	1	1
ENSG00000225025	ENSG00000225025	KIF4CP	X:78578942-78580714	NOTEST	0	0	0	0	1	1
ENSG00000225026	ENSG00000225026	AC091492.2	3:12328866-12475855	NOTEST	0	0	0	0	1	1
ENSG00000225027	ENSG00000225027	IFNWP4	9:21106541-21106835	NOTEST	0	0	0	0	1	1
ENSG00000225028	ENSG00000225028	RP11-330M19.1	1:48226199-48462567	NOTEST	0	0	0	0	1	1
ENSG00000225029	ENSG00000225029	USP8P1	HSCHR6_MHC_SSTO:31235930-31239103	NOTEST	0	0	0	0	1	1
ENSG00000225030	ENSG00000225030	RP4-784A16.3	1:53711216-53793742	NOTEST	0	0	0	0	1	1
ENSG00000225034	ENSG00000225034	OR2H5P	HSCHR6_MHC_MANN:29522993-29600557	NOTEST	0	0	0	0	1	1
ENSG00000225036	ENSG00000225036	RP11-414B7.1	1:105976615-105977443	NOTEST	0	0	0	0	1	1
ENSG00000225037	ENSG00000225037	EIF1AX-AS1	X:20142635-20159962	NOTEST	0	0	0	0	1	1
ENSG00000225038	ENSG00000225038	TRIM31-AS1	HSCHR6_MHC_MCF:30149159-30160985	NOTEST	0	0	0	0	1	1
ENSG00000225039	ENSG00000225039	LINC01058	13:30993655-30996374	NOTEST	0.10055	0	#NAME?	0	1	1
ENSG00000225043	ENSG00000225043	RPL18AP2	21:47744035-47865682	NOTEST	0	0	0	0	1	1
ENSG00000225044	ENSG00000225044	RP11-204C23.1	3:2004064-2029154	NOTEST	0	0	0	0	1	1
ENSG00000225045	ENSG00000225045	MTND5P27	2:83042932-83044652	NOTEST	0	0	0	0	1	1
ENSG00000225046	ENSG00000225046	RP1-20I3.3	X:129464830-129465043	NOTEST	0	0	0	0	1	1
ENSG00000225048	ENSG00000225048	OR2AD1P	HSCHR6_MHC_DBB:28994470-28995398	NOTEST	0	0	0	0	1	1
ENSG00000225049	ENSG00000225049	AC068279.2	2:87586176-87586367	NOTEST	0	0	0	0	1	1
ENSG00000225050	ENSG00000225050	RP11-349E4.1	9:121450029-121468238	NOTEST	0	0	0	0	1	1
ENSG00000225051	ENSG00000225051	HMGB3P22	5:179105583-179157926	NOTEST	0.105659	0.103489	-0.0299271	0	1	1
ENSG00000225053	ENSG00000225053	PRPF38AP1	10:8203222-8204155	NOTEST	0	0	0	0	1	1
ENSG00000225055	ENSG00000225055	RP11-344N17.9	X:48216559-48218930	NOTEST	0	0	0	0	1	1
ENSG00000225056	ENSG00000225056	RP11-218C14.5	20:23635861-23637027	NOTEST	0	0	0	0	1	1
ENSG00000225057	ENSG00000225057	AC096574.4	2:239140324-239198743	NOTEST	0	0	0	0	1	1
ENSG00000225058	ENSG00000225058	RP11-132N15.1	3:187715209-187721778	NOTEST	0	0	0	0	1	1
ENSG00000225060	ENSG00000225060	PPP1R18	HSCHR6_MHC_MCF:30722653-30734160	NOTEST	0	0	0	0	1	1
ENSG00000225062	ENSG00000225062	AC021016.6	2:219135114-219232822	NOTEST	0.027259	0	#NAME?	0	1	1
ENSG00000225063	ENSG00000225063	RP11-383G10.5	1:205197303-205242471	NOTEST	0.0821959	0	#NAME?	0	1	1
ENSG00000225064	ENSG00000225064	AC007879.6	2:208104373-208490652	NOTEST	0	0	0	0	1	1
ENSG00000225066	ENSG00000225066	RP1-272E8.1	X:17951468-17952943	NOTEST	0	0	0	0	1	1
ENSG00000225067	ENSG00000225067	RPL23AP2	19:15722433-15722934	NOTEST	0	0.200067	inf	0	1	1
ENSG00000225069	ENSG00000225069	RP5-1025A1.2	20:25079740-25080564	NOTEST	0	0	0	0	1	1
ENSG00000225070	ENSG00000225070	LL22NC03-23C6.13	22:22345495-22398340	NOTEST	0	0	0	0	1	1
ENSG00000225071	ENSG00000225071	GS1-184P14.2	X:24447689-24448037	NOTEST	0.326943	0.250367	-0.384992	0	1	1
ENSG00000225072	ENSG00000225072	OR7E116P	9:92994466-92995423	NOTEST	0	0	0	0	1	1
ENSG00000225073	ENSG00000225073	DDX39B	HSCHR6_MHC_COX:31483951-31502076	NOTEST	0	0	0	0	1	1
ENSG00000225075	ENSG00000225075	RP11-426L16.3	1:113215762-113243368	NOTEST	0.0548667	0	#NAME?	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000225076	ENSG00000225076	WWC3-AS1	X:9983601-10112518	NOTEST	0.0367148	0	#NAME?	0	1	1
ENSG00000225077	ENSG00000225077	LINC00337	1:6296299-6299504	NOTEST	0.135065	0.252761	0.904119	0	1	1
ENSG00000225078	ENSG00000225078	RP11-123N4.4	9:125703111-125867145	NOTEST	0	0	0	0	1	1
ENSG00000225079	ENSG00000225079	FTH1P22	1:117317725-117318245	NOTEST	0	0	0	0	1	1
ENSG00000225080	ENSG00000225080	PFN1P4	1:147574427-147634886	NOTEST	0.0642176	0.150361	1.22739	0	1	1
ENSG00000225082	ENSG00000225082	DAP3P1	1:155556434-155571988	NOTEST	0	0	0	0	1	1
ENSG00000225083	ENSG00000225083	GRTP1-AS1	13:113978504-114018446	NOTEST	0.0213408	0.0185725	-0.200447	0	1	1
ENSG00000225084	ENSG00000225084	AL450226.2	17:1963132-2284352	NOTEST	0	0	0	0	1	1
ENSG00000225085	ENSG00000225085	RP11-15B24.1	9:84887670-85179347	NOTEST	0	0	0	0	1	1
ENSG00000225086	ENSG00000225086	HCG4P3	HSCHR6_MHC_MANN:29963963-30027881	NOTEST	0	0	0	0	1	1
ENSG00000225087	ENSG00000225087	RP4-660H19.1	1:73214603-73364823	NOTEST	0	0	0	0	1	1
ENSG00000225091	ENSG00000225091	SNORA71A	20:37049234-37063996	NOTEST	0	7.16596	inf	0	1	1
ENSG00000225092	ENSG00000225092	RP11-405O10.2	6:7107829-7252213	NOTEST	0	0	0	0	1	1
ENSG00000225093	ENSG00000225093	RPL3P7	6:108325560-108326772	NOTEST	0.0804628	0.0758468	-0.0852347	0	1	1
ENSG00000225094	ENSG00000225094	SETP20	4:110474398-110475250	NOTEST	0	0	0	0	1	1
ENSG00000225098	ENSG00000225098	BCRP1	22:24647795-24661493	NOTEST	0	0	0	0	1	1
ENSG00000225099	ENSG00000225099	ATP6V1E1P1	1:43368902-43369583	NOTEST	0	0	0	0	1	1
ENSG00000225100	ENSG00000225100	RP11-479O17.7	10:81742665-81742996	NOTEST	0	0	0	0	1	1
ENSG00000225101	ENSG00000225101	OR52K3P	11:4496042-4497123	NOTEST	0	0	0	0	1	1
ENSG00000225102	ENSG00000225102	RP11-456H18.1	6:11990575-11992245	NOTEST	0	0	0	0	1	1
ENSG00000225103	ENSG00000225103	HLA-DQA2	HSCHR6_MHC_QBL:32637804-32643664	NOTEST	0	0	0	0	1	1
ENSG00000225105	ENSG00000225105	LINC01076	13:25767244-25784433	NOTEST	0	0	0	0	1	1
ENSG00000225107	ENSG00000225107	AC092484.1	2:146326861-146345592	NOTEST	0	0	0	0	1	1
ENSG00000225108	ENSG00000225108	ZBTB45P1	2:110744515-110753717	NOTEST	0	0	0	0	1	1
ENSG00000225109	ENSG00000225109	PAIP1P1	HSCHR6_MHC_DBB:30142514-30171491	NOTEST	0	0	0	0	1	1
ENSG00000225110	ENSG00000225110	LL0XNC01-16G2.1	X:152583140-152586144	NOTEST	0	0.0182314	inf	0	1	1
ENSG00000225111	ENSG00000225111	AC083900.1	2:208693026-208890284	NOTEST	0.0996695	0	#NAME?	0	1	1
ENSG00000225112	ENSG00000225112	RP11-295P9.6	10:13628926-14504141	NOTEST	0	0	0	0	1	1
ENSG00000225113	ENSG00000225113	RP5-1160K1.3	1:110138846-110140403	NOTEST	0.199174	0.213133	0.0977279	0	1	1
ENSG00000225114	ENSG00000225114	HCG4P5	HSCHR6_MHC_DBB:29898999-29903640	NOTEST	0	0	0	0	1	1
ENSG00000225116	ENSG00000225116	RP11-137F15.1	20:3445823-3446091	NOTEST	0	0	0	0	1	1
ENSG00000225117	ENSG00000225117	ARSDP1	Y:14474826-14532255	NOTEST	0	0	0	0	1	1
ENSG00000225118	ENSG00000225118	RP11-477L16.2	10:94590934-94819250	NOTEST	0	0	0	0	1	1
ENSG00000225119	ENSG00000225119	LINC00999	10:38717073-38736820	NOTEST	0.243788	0.12529	-0.96036	0	1	1
ENSG00000225120	ENSG00000225120	HCG4P7	HSCHR6_MHC_MCF:29846326-29992167	NOTEST	0	0	0	0	1	1
ENSG00000225121	ENSG00000225121	EEF1B2P5	6:64190038-64191781	NOTEST	0	0	0	0	1	1
ENSG00000225122	ENSG00000225122	RP11-408E1.1	1:163392194-163392954	NOTEST	0	0	0	0	1	1
ENSG00000225123	ENSG00000225123	RP11-255A11.4	9:33574358-33574586	NOTEST	0	0	0	0	1	1
ENSG00000225124	ENSG00000225124	AC023271.2	2:203879601-204091101	NOTEST	0	0	0	0	1	1
ENSG00000225125	ENSG00000225125	RANP4	X:135889381-135890036	NOTEST	0.113133	0.0678883	-0.736786	0	1	1
ENSG00000225126	ENSG00000225126	RP4-549F15.1	1:6845383-7829766	NOTEST	0	0	0	0	1	1
ENSG00000225127	ENSG00000225127	LINC00237	20:21068244-21086999	NOTEST	0	0	0	0	1	1
ENSG00000225128	ENSG00000225128	LINC00972	7:85050437-85118609	NOTEST	0	0	0	0	1	1
ENSG00000225129	ENSG00000225129	RP4-614C15.2	20:57927249-57932829	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000225130	ENSG00000225130	TRIM31	HSCHR6_MHC_MANN:30065836-30077657	NOTEST	0	0	0	0	1	1
ENSG00000225132	ENSG00000225132	HLA-DPB2	HSCHR6_MHC_COX:33002123-33018445	NOTEST	0	0	0	0	1	1
ENSG00000225133	ENSG00000225133	MORF4L1P4	13:41773967-41774943	NOTEST	0	0	0	0	1	1
ENSG00000225136	ENSG00000225136	PGBD4P5	2:89221843-89222269	NOTEST	0	0	0	0	1	1
ENSG00000225140	ENSG00000225140	RP11-809C18.3	10:320129-735683	NOTEST	0.00999426	0.0928256	3.21535	0	1	1
ENSG00000225141	ENSG00000225141	PRRT1	HSCHR6_MHC_DBB:32091909-32101885	NOTEST	0	0	0	0	1	1
ENSG00000225142	ENSG00000225142	RP11-490K7.1	1:31581034-31581470	NOTEST	0	0	0	0	1	1
ENSG00000225144	ENSG00000225144	AC018643.4	7:131808090-132333447	NOTEST	0	0	0	0	1	1
ENSG00000225145	ENSG00000225145	HLA-S	HSCHR6_MHC_COX:31340323-31340538	NOTEST	0	0	0	0	1	1
ENSG00000225146	ENSG00000225146	AC073957.15	7:1036621-1177896	NOTEST	0	0	0	0	1	1
ENSG00000225147	ENSG00000225147	RPS12P10	5:141689991-142077617	NOTEST	0	0	0	0	1	1
ENSG00000225148	ENSG00000225148	RP5-899B16.2	6:140175986-140198528	NOTEST	0	0	0	0	1	1
ENSG00000225150	ENSG00000225150	OR2G1P	HSCHR6_MHC_COX:29188440-29231555	NOTEST	0	0	0	0	1	1
ENSG00000225152	ENSG00000225152	RP11-338O1.2	10:125115965-125277224	NOTEST	0	0	0	0	1	1
ENSG00000225154	ENSG00000225154	RP11-184J23.2	1:47533159-47646011	NOTEST	0	0	0	0	1	1
ENSG00000225155	ENSG00000225155	TOMM22P5	10:120403271-120403710	NOTEST	0	0	0	0	1	1
ENSG00000225156	ENSG00000225156	AC012354.6	2:45181802-45195901	NOTEST	0	0	0	0	1	1
ENSG00000225157	ENSG00000225157	AC005779.1	19:45574757-45808541	NOTEST	0	0	0	0	1	1
ENSG00000225158	ENSG00000225158	HSPE1P24	1:10955817-10956055	NOTEST	0	0	0	0	1	1
ENSG00000225164	ENSG00000225164	PRRC2A	HSCHR6_MHC_COX:31575862-31592960	NOTEST	0	0	0	0	1	1
ENSG00000225165	ENSG00000225165	CTD-2538A21.1	5:94727047-94786158	NOTEST	0	0.0222178	inf	0	1	1
ENSG00000225166	ENSG00000225166	AC012462.2	2:216318429-216328594	NOTEST	0	0	0	0	1	1
ENSG00000225167	ENSG00000225167	TXNP2	1:68939834-69004310	NOTEST	0	0	0	0	1	1
ENSG00000225169	ENSG00000225169	BRI3P1	1:100652474-100715390	NOTEST	0.272077	0	#NAME?	0	1	1
ENSG00000225170	ENSG00000225170	RP5-828K20.1	20:22252689-22254092	NOTEST	0	0	0	0	1	1
ENSG00000225171	ENSG00000225171	DUTP6	1:166825746-166845564	NOTEST	0	0.149955	inf	0	1	1
ENSG00000225172	ENSG00000225172	RP11-16L9.2	1:198952449-198954529	NOTEST	0	0	0	0	1	1
ENSG00000225173	ENSG00000225173	XXbac-BPG308K3.5	6:28805645-28806783	NOTEST	0.02761	0.0195111	-0.500894	0	1	1
ENSG00000225174	ENSG00000225174	OSTM1-AS1	6:108362612-108487058	NOTEST	0	0	0	0	1	1
ENSG00000225175	ENSG00000225175	RP11-795A2.2	3:186405117-186410295	NOTEST	0	0	0	0	1	1
ENSG00000225176	ENSG00000225176	ATP5LP4	4:149624677-149624984	NOTEST	0	0	0	0	1	1
ENSG00000225178	ENSG00000225178	RPSAP56	16:73974537-73975423	NOTEST	0	0	0	0	1	1
ENSG00000225179	ENSG00000225179	LINC00457	13:34922179-35245319	NOTEST	0	0	0	0	1	1
ENSG00000225180	ENSG00000225180	AATK-AS1	17:79008947-79156964	NOTEST	0	0.00793117	inf	0	1	1
ENSG00000225181	ENSG00000225181	RP11-388K2.1	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000225182	ENSG00000225182	AC092601.1	2:167744996-168116263	NOTEST	0	0	0	0	1	1
ENSG00000225183	ENSG00000225183	RP4-758J24.4	1:54519259-54578192	NOTEST	0	0	0	0	1	1
ENSG00000225184	ENSG00000225184	XXbac-BCX196D17.5	HSCHR6_MHC_QBL:29091992-29096691	NOTEST	0	0	0	0	1	1
ENSG00000225185	ENSG00000225185	RP11-481K9.4	12:98984500-98984992	NOTEST	0	0	0	0	1	1
ENSG00000225187	ENSG00000225187	AC073283.7	2:47126413-47403740	NOTEST	0.0215807	0.062778	1.54051	0	1	1
ENSG00000225188	ENSG00000225188	XXbac-BPG308J9.3	HSCHR6_MHC_MANN:29191795-29234882	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000225189	ENSG00000225189	REREP1Y	Y:25608611-25618427	NOTEST	0	0	0	0	1	1
ENSG00000225191	ENSG00000225191	RP11-97C18.1	1:104469188-104470428	NOTEST	0	0	0	0	1	1
ENSG00000225192	ENSG00000225192	ZNF33BP1	10:38083203-38085037	NOTEST	0	0	0	0	1	1
ENSG00000225193	ENSG00000225193	RPS12P26	15:90703835-90772911	NOTEST	0.131817	0.0514676	-1.3568	0	1	1
ENSG00000225194	ENSG00000225194	LINC00092	9:98782013-98790247	NOTEST	0	0.007422	inf	0	1	1
ENSG00000225195	ENSG00000225195	RP11-338E21.2	12:65004292-65091347	NOTEST	0	0	0	0	1	1
ENSG00000225196	ENSG00000225196	RP5-1118D24.2	1:12280850-12281166	NOTEST	0	0	0	0	1	1
ENSG00000225198	ENSG00000225198	SSXP3	X:48015794-48025778	NOTEST	0	0	0	0	1	1
ENSG00000225201	ENSG00000225201	HLA-E	HSCHR6_MHC_MCF:30535710-30540449	NOTEST	0	0	0	0	1	1
ENSG00000225203	ENSG00000225203	TBC1D4-AS1	13:75858807-76056250	NOTEST	0	0	0	0	1	1
ENSG00000225205	ENSG00000225205	AC093818.1	2:173292081-173489823	NOTEST	0.276746	0.305453	0.142387	0	1	1
ENSG00000225206	ENSG00000225206	MIR137HG	1:98453555-98515419	NOTEST	0	0.0663388	inf	0	1	1
ENSG00000225208	ENSG00000225208	RP11-107I14.2	10:103070774-103071262	NOTEST	0	0	0	0	1	1
ENSG00000225209	ENSG00000225209	RP11-358M3.1	7:67485239-67497677	NOTEST	0	0	0	0	1	1
ENSG00000225211	ENSG00000225211	NCR3	HSCHR6_MHC_MCF:31630206-31637066	NOTEST	0	0	0	0	1	1
ENSG00000225212	ENSG00000225212	AKR1B1P6	18:8545632-8546815	NOTEST	0	0	0	0	1	1
ENSG00000225213	ENSG00000225213	RP11-197M22.2	10:16632609-16859527	NOTEST	0	0.110129	inf	0	1	1
ENSG00000225214	ENSG00000225214	AC079790.2	2:152689289-152965716	NOTEST	0	0	0	0	1	1
ENSG00000225215	ENSG00000225215	SMARCE1P1	11:107197070-107328572	NOTEST	0	0	0	0	1	1
ENSG00000225216	ENSG00000225216	AC007362.3	2:206546713-206662857	NOTEST	0.0730212	0.0880103	0.269357	0	1	1
ENSG00000225217	ENSG00000225217	HSPA7	1:161475219-161648444	NOTEST	0.0729346	0.0322762	-1.17613	0	1	1
ENSG00000225218	ENSG00000225218	AP001628.6	21:44251149-44256587	NOTEST	0	0	0	0	1	1
ENSG00000225221	ENSG00000225221	PLA2G12AP2	13:39476523-39476787	NOTEST	0	0	0	0	1	1
ENSG00000225222	ENSG00000225222	CHCHD4P5	1:245912641-246670614	NOTEST	0	0	0	0	1	1
ENSG00000225224	ENSG00000225224	RP4-814D15.2	7:156931606-157062066	NOTEST	0	0	0	0	1	1
ENSG00000225225	ENSG00000225225	ARL2BPP10	22:18559292-18629321	NOTEST	0	0	0	0	1	1
ENSG00000225226	ENSG00000225226	AC007250.4	2:58503011-58523683	NOTEST	0.0231363	0	#NAME?	0	1	1
ENSG00000225228	ENSG00000225228	MCCD1	HSCHR6_MHC_APD:31507784-31518252	NOTEST	0	0	0	0	1	1
ENSG00000225230	ENSG00000225230	AC008937.3	5:56195867-56267502	NOTEST	0.167208	0.0483238	-1.79084	0	1	1
ENSG00000225231	ENSG00000225231	AC091814.2	12:10089177-10096094	NOTEST	0	0	0	0	1	1
ENSG00000225233	ENSG00000225233	RP11-554K11.2	1:213665643-213719790	NOTEST	0	0	0	0	1	1
ENSG00000225234	ENSG00000225234	TRAPPC12-AS1	2:3383445-3488865	NOTEST	0	0.0757756	inf	0	1	1
ENSG00000225235	ENSG00000225235	DDX26B-AS1	X:134654007-134716435	NOTEST	0	0.0510045	inf	0	1	1
ENSG00000225236	ENSG00000225236	AP000936.5	11:116988509-116989897	NOTEST	0	0	0	0	1	1
ENSG00000225237	ENSG00000225237	HNRNPA1P2	HSCHR6_MHC_MCF:32360674-32415872	NOTEST	0	0	0	0	1	1
ENSG00000225238	ENSG00000225238	RP1-169I5.4	X:41306686-41334963	NOTEST	0	0	0	0	1	1
ENSG00000225239	ENSG00000225239	RPL21P107	13:111415020-111415480	NOTEST	0	0.124296	inf	0	1	1
ENSG00000225240	ENSG00000225240	AC117490.2	3:196179866-196179926	NOTEST	0	0	0	0	1	1
ENSG00000225242	ENSG00000225242	COX6B1P7	1:68748070-68748305	NOTEST	0	0	0	0	1	1
ENSG00000225243	ENSG00000225243	RP1-127D3.4	1:171154346-171196927	NOTEST	0	0	0	0	1	1
ENSG00000225244	ENSG00000225244	RP11-220H4.2	7:57008047-57012060	NOTEST	0	0	0	0	1	1
ENSG00000225246	ENSG00000225246	RPS2P1	20:32710275-32711096	NOTEST	0	0	0	0	1	1
ENSG00000225247	ENSG00000225247	OR12D2	HSCHR6_MHC_SSTO:29323120-29424524	NOTEST	0	0	0	0	1	1
ENSG00000225248	ENSG00000225248	TMEM183AP1	HSCHR6_MHC_COX:29519994-29597568	NOTEST	0	0	0	0	1	1

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ENSG00000225249	ENSG00000225249	LINC00378	13:61259332-61268662	NOTEST	0	0	0	0	1	1
ENSG00000225251	ENSG00000225251	RPL5P25	10:12938626-13180291	NOTEST	0	0	0	0	1	1
ENSG00000225253	ENSG00000225253	AC011225.1	18:39399017-39399386	NOTEST	0	0.0584278	inf	0	1	1
ENSG00000225254	ENSG00000225254	RP11-403F21.1	9:38452778-38454067	NOTEST	0	0	0	0	1	1
ENSG00000225255	ENSG00000225255	LA16c-83F12.6	22:16199665-16231333	NOTEST	0	0	0	0	1	1
ENSG00000225256	ENSG00000225256	TRAPPC2P5	Y:27845597-27848709	NOTEST	0	0	0	0	1	1
ENSG00000225258	ENSG00000225258	AC009478.1	2:181436438-181557181	NOTEST	0	0	0	0	1	1
ENSG00000225261	ENSG00000225261	RP5-937E21.8	X:148558520-148632055	NOTEST	0.0149146	0	#NAME?	0	1	1
ENSG00000225263	ENSG00000225263	PCDH9-AS3	13:66876966-67804468	NOTEST	0	0	0	0	1	1
ENSG00000225267	ENSG00000225267	RPL8P2	21:31635697-31636199	NOTEST	0	0	0	0	1	1
ENSG00000225269	ENSG00000225269	LINC00705	10:4692376-4720346	NOTEST	0.00943544	0.0219969	1.22114	0	1	1
ENSG00000225270	ENSG00000225270	CICP12	7:55861236-55930482	NOTEST	0	0	0	0	1	1
ENSG00000225271	ENSG00000225271	RP11-66N5.2	X:8948465-8950546	NOTEST	0	0	0	0	1	1
ENSG00000225272	ENSG00000225272	RP11-466F5.4	1:165631452-165679205	NOTEST	0	0	0	0	1	1
ENSG00000225273	ENSG00000225273	UBE2Q2P2	15:82647359-82748784	NOTEST	0.411652	0.26692	-0.625019	0	1	1
ENSG00000225274	ENSG00000225274	GPR53P	HSCHR6_MHC_DBB:29505418-29506502	NOTEST	0	0	0	0	1	1
ENSG00000225275	ENSG00000225275	NUP210P2	3:11941484-11942719	NOTEST	0	0	0	0	1	1
ENSG00000225276	ENSG00000225276	MTND1P18	10:37889723-37890296	NOTEST	0	0	0	0	1	1
ENSG00000225279	ENSG00000225279	RP11-536C5.2	1:160007256-160049611	NOTEST	0	0	0	0	1	1
ENSG00000225280	ENSG00000225280	RP11-227D2.3	20:21376004-21381029	NOTEST	0	0	0	0	1	1
ENSG00000225282	ENSG00000225282	AP000350.6	22:24269086-24271761	NOTEST	0.0169129	0.00655729	-1.36696	0	1	1
ENSG00000225284	ENSG00000225284	AC018693.6	2:39024870-39103075	NOTEST	0.0392528	0	#NAME?	0	1	1
ENSG00000225285	ENSG00000225285	RP4-758J18.10	1:1365918-1369953	NOTEST	0.113046	0.0424125	-1.41434	0	1	1
ENSG00000225286	ENSG00000225286	AC005105.2	7:28338939-28865511	NOTEST	0	0	0	0	1	1
ENSG00000225287	ENSG00000225287	OFD1P13Y	Y:27821206-27843493	NOTEST	0	0	0	0	1	1
ENSG00000225289	ENSG00000225289	RPL29P29	13:88888801-88889224	NOTEST	0	0	0	0	1	1
ENSG00000225291	ENSG00000225291	OR14J1	HSCHR6_MHC_COX:29271117-29272234	NOTEST	0	0	0	0	1	1
ENSG00000225292	ENSG00000225292	RP11-57H14.3	10:114648493-114665870	NOTEST	0	0.0798533	inf	0	1	1
ENSG00000225293	ENSG00000225293	ABCD1P4	22:16868419-16871613	NOTEST	0	0	0	0	1	1
ENSG00000225294	ENSG00000225294	OSTCP2	1:27312387-27312831	NOTEST	0	0	0	0	1	1
ENSG00000225295	ENSG00000225295	MTND4P4	7:57237112-57238478	NOTEST	0	0	0	0	1	1
ENSG00000225297	ENSG00000225297	RP4-612C19.2	1:93615298-93835055	NOTEST	0	0	0	0	1	1
ENSG00000225298	ENSG00000225298	LINC00113	21:29094697-29123552	NOTEST	0	0	0	0	1	1
ENSG00000225299	ENSG00000225299	RP11-344A5.1	10:67672275-69455927	NOTEST	0	0	0	0	1	1
ENSG00000225300	ENSG00000225300	RP11-439E19.1	1:246729745-246831886	NOTEST	0.0300775	0.0129013	-1.22117	0	1	1
ENSG00000225303	ENSG00000225303	RP11-512N4.2	10:52065359-52401211	NOTEST	0	0	0	0	1	1
ENSG00000225304	ENSG00000225304	AC106901.1	2:205243817-205244515	NOTEST	0	0	0	0	1	1
ENSG00000225305	ENSG00000225305	TMEM183AP1	HSCHR6_MHC_APD:29523503-29601074	NOTEST	0	0	0	0	1	1
ENSG00000225308	ENSG00000225308	ASS1P11	7:21259831-21261047	NOTEST	0	0	0	0	1	1
ENSG00000225310	ENSG00000225310	DNAJC19P4	3:2140496-3102829	NOTEST	0	0	0	0	1	1
ENSG00000225311	ENSG00000225311	RP1-91J24.3	6:144606836-145174170	NOTEST	0	0	0	0	1	1
ENSG00000225312	ENSG00000225312	HSD17B8	HSCHR6_MHC_DBB:33150328-33152518	NOTEST	0	0	0	0	1	1
ENSG00000225314	ENSG00000225314	AC018634.9	7:37723398-38065297	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000225315	ENSG00000225315	RP11-293P20.2	1:24367324-24438665	NOTEST	0	0	0	0	1	1
ENSG00000225316	ENSG00000225316	LINC00350	13:20161257-20162490	NOTEST	0	0	0	0	1	1
ENSG00000225317	ENSG00000225317	PPIAP9	HSCHR6_MHC_QBL:31477554-31478366	NOTEST	0	0	0	0	1	1
ENSG00000225321	ENSG00000225321	RP5-828K20.2	20:22260865-22263310	NOTEST	0	0	0	0	1	1
ENSG00000225322	ENSG00000225322	RP11-472D17.1	X:52293396-52297093	NOTEST	0	0	0	0	1	1
ENSG00000225323	ENSG00000225323	Z84721.4	16:218677-219333	NOTEST	0	0	0	0	1	1
ENSG00000225325	ENSG00000225325	RP11-479J7.1	1:166356963-166421869	NOTEST	0	0	0	0	1	1
ENSG00000225326	ENSG00000225326	USP9YP19	Y:27894742-27896353	NOTEST	0	0	0	0	1	1
ENSG00000225327	ENSG00000225327	USP17L3	8:7812535-7866277	NOTEST	0	0	0	0	1	1
ENSG00000225328	ENSG00000225328	AC019100.3	2:108784203-108834297	NOTEST	0.293551	0.398714	0.441741	0	1	1
ENSG00000225329	ENSG00000225329	RP11-325F22.5	7:104558006-104567077	NOTEST	0.0584207	0	#NAME?	0	1	1
ENSG00000225330	ENSG00000225330	AF064860.5	21:40928368-41098012	NOTEST	0	0	0	0	1	1
ENSG00000225331	ENSG00000225331	AP001055.6	21:45578622-45579959	NOTEST	0.0392787	0.0166947	-1.23435	0	1	1
ENSG00000225333	ENSG00000225333	RP1-144F13.4	1:40157853-40254533	NOTEST	0	0	0	0	1	1
ENSG00000225334	ENSG00000225334	RP11-449J1.1	1:224954601-224961043	NOTEST	0	0.0879492	inf	0	1	1
ENSG00000225336	ENSG00000225336	HMGB3P1	20:33421377-33422265	NOTEST	0	0	0	0	1	1
ENSG00000225337	ENSG00000225337	RP11-561O23.7	9:70921443-71145977	NOTEST	0	0	0	0	1	1
ENSG00000225338	ENSG00000225338	RP11-384C4.3	1:212458878-212535200	NOTEST	0	0.0745486	inf	0	1	1
ENSG00000225339	ENSG00000225339	RP11-513I15.6	6:34247455-34393902	NOTEST	0.292589	0	#NAME?	0	1	1
ENSG00000225341	ENSG00000225341	AC013269.4	2:131287847-131294755	NOTEST	0	0	0	0	1	1
ENSG00000225342	ENSG00000225342	AC079630.4	12:40579810-40763087	NOTEST	0	0	0	0	1	1
ENSG00000225343	ENSG00000225343	RPL21P66	6:132839968-132840434	NOTEST	0	0	0	0	1	1
ENSG00000225344	ENSG00000225344	RP4-738P15.4	20:25141802-25142697	NOTEST	0	0.028935	inf	0	1	1
ENSG00000225346	ENSG00000225346	HCG4	HSCHR6_MHC_COX:29753036-29759260	NOTEST	0	0	0	0	1	1
ENSG00000225347	ENSG00000225347	SLC25A5P8	9:32333454-32334352	NOTEST	0	0	0	0	1	1
ENSG00000225349	ENSG00000225349	RP11-820K3.2	12:31535156-31768600	NOTEST	0	0	0	0	1	1
ENSG00000225350	ENSG00000225350	FREM2-AS1	13:39261265-39460074	NOTEST	0	0	0	0	1	1
ENSG00000225351	ENSG00000225351	ZNF311	HSCHR6_MHC_APD:28962605-28973138	NOTEST	0	0	0	0	1	1
ENSG00000225352	ENSG00000225352	RPL31P53	13:57965304-57965652	NOTEST	0	0	0	0	1	1
ENSG00000225354	ENSG00000225354	RP11-400G3.3	10:96642310-96643100	NOTEST	0	0	0	0	1	1
ENSG00000225355	ENSG00000225355	ARL6IP1P2	10:37283950-37284513	NOTEST	0	0	0	0	1	1
ENSG00000225356	ENSG00000225356	RP11-433O3.1	4:182443812-182444154	NOTEST	0	0	0	0	1	1
ENSG00000225357	ENSG00000225357	RPF2P1	20:34340735-34341641	NOTEST	0	0.0142497	inf	0	1	1
ENSG00000225358	ENSG00000225358	MIPEPP1	7:112375220-112378748	NOTEST	0	0	0	0	1	1
ENSG00000225359	ENSG00000225359	RP11-540K16.2	1:181159606-181160285	NOTEST	0	0	0	0	1	1
ENSG00000225360	ENSG00000225360	RP11-149F8.4	9:68324610-68340644	NOTEST	0	0	0	0	1	1
ENSG00000225362	ENSG00000225362	CT62	15:71389290-72075722	NOTEST	0	0	0	0	1	1
ENSG00000225364	ENSG00000225364	ATP6V0E1P1	5:132211070-132299326	NOTEST	0	0	0	0	1	1
ENSG00000225365	ENSG00000225365	AC078942.1	7:157331749-158380480	NOTEST	0	0	0	0	1	1
ENSG00000225366	ENSG00000225366	TDGF1P3	X:109763539-109766249	NOTEST	0	0	0	0	1	1
ENSG00000225368	ENSG00000225368	HCG15	HSCHR6_MHC_QBL:28953979-28956313	NOTEST	0	0	0	0	1	1
ENSG00000225369	ENSG00000225369	AC009506.2	2:160175489-160473593	NOTEST	0.0406526	0	#NAME?	0	1	1
ENSG00000225370	ENSG00000225370	AC011515.2	19:55182681-55184042	NOTEST	0	0	0	0	1	1

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ENSG00000225373	ENSG00000225373	WASH5P	19:60104-72719	NOTEST	0	0.0108263	inf	0	1	1
ENSG00000225376	ENSG00000225376	RP11-490D19.6	9:104230720-104295819	NOTEST	0	0.0475176	inf	0	1	1
ENSG00000225378	ENSG00000225378	AC015977.6	2:26894121-26897332	NOTEST	0	0	0	0	1	1
ENSG00000225380	ENSG00000225380	IGKV1OR9-2	9:42751726-42752381	NOTEST	0	0	0	0	1	1
ENSG00000225381	ENSG00000225381	RPS5P7	X:109096540-109097148	NOTEST	0	0	0	0	1	1
ENSG00000225382	ENSG00000225382	XXbac-BPG249D20.9	HSCHR6_MHC_APD:30492288-30495243	NOTEST	0	0	0	0	1	1
ENSG00000225383	ENSG00000225383	SFTA1P	10:10826399-10836943	NOTEST	0	0	0	0	1	1
ENSG00000225384	ENSG00000225384	RP13-643D4.1	X:34735556-34736109	NOTEST	0	0	0	0	1	1
ENSG00000225385	ENSG00000225385	RP11-350E12.4	9:90681829-90682952	NOTEST	0	0	0	0	1	1
ENSG00000225386	ENSG00000225386	AC099754.1	3:26660820-26664181	NOTEST	0	0	0	0	1	1
ENSG00000225387	ENSG00000225387	RP11-422P22.1	1:18712322-18715008	NOTEST	0	0	0	0	1	1
ENSG00000225390	ENSG00000225390	C6orf47-AS1	HSCHR6_MHC_MCF:31702357-31704832	NOTEST	0	0	0	0	1	1
ENSG00000225391	ENSG00000225391	RP11-55K22.5	6:137303301-137314371	NOTEST	0	0	0	0	1	1
ENSG00000225392	ENSG00000225392	AC016700.4	2:70316852-70330352	NOTEST	0	0	0	0	1	1
ENSG00000225394	ENSG00000225394	AC106883.1	2:195319304-195319866	NOTEST	0	0	0	0	1	1
ENSG00000225396	ENSG00000225396	RP11-69A21.2	X:71996832-72068636	NOTEST	0	0	0	0	1	1
ENSG00000225397	ENSG00000225397	RP11-552J9.13	X:52751386-52751573	NOTEST	0	0	0	0	1	1
ENSG00000225398	ENSG00000225398	RP11-395L14.5	2:114285144-114320875	NOTEST	0	0	0	0	1	1
ENSG00000225399	ENSG00000225399	RP11-3B7.1	3:49297517-49298744	NOTEST	0	0.0339214	inf	0	1	1
ENSG00000225400	ENSG00000225400	RP11-1114A5.5	X:135923089-135962923	NOTEST	0.373329	0.306865	-0.282845	0	1	1
ENSG00000225401	ENSG00000225401	TGIF2P1	1:244515936-244615436	NOTEST	0	0.0697865	inf	0	1	1
ENSG00000225402	ENSG00000225402	AC010878.3	2:38044057-38045104	NOTEST	0.0169549	0.0119443	-0.50538	0	1	1
ENSG00000225403	ENSG00000225403	WASF5P	HSCHR6_MHC_SSTO:31248141-31249593	NOTEST	0	0	0	0	1	1
ENSG00000225404	ENSG00000225404	RPL26P34	13:25254548-25285921	NOTEST	0	0	0	0	1	1
ENSG00000225405	ENSG00000225405	RP11-84A1.1	4:62066975-63031272	NOTEST	0	0	0	0	1	1
ENSG00000225406	ENSG00000225406	AC080125.1	2:186411861-186412545	NOTEST	0	0	0	0	1	1
ENSG00000225407	ENSG00000225407	CTD-2384B11.2	5:75699073-76031606	NOTEST	0	0.083656	inf	0	1	1
ENSG00000225408	ENSG00000225408	RP11-207C16.4	9:5629024-5833117	NOTEST	0	0	0	0	1	1
ENSG00000225411	ENSG00000225411	RP11-764K9.1	9:68397877-68409893	NOTEST	0.00548606	0	#NAME?	0	1	1
ENSG00000225412	ENSG00000225412	BTNL2	HSCHR6_MHC_MANN:32397724-32414370	NOTEST	0	0	0	0	1	1
ENSG00000225413	ENSG00000225413	AP000345.4	22:23854680-23855789	NOTEST	0	0	0	0	1	1
ENSG00000225414	ENSG00000225414	RP11-746P2.1	7:64721414-64721774	NOTEST	0	0	0	0	1	1
ENSG00000225415	ENSG00000225415	RP3-509I19.1	6:139117062-139309398	NOTEST	0.0227116	0	#NAME?	0	1	1
ENSG00000225416	ENSG00000225416	AC104843.3	7:152299297-152299977	NOTEST	0	0.0715115	inf	0	1	1
ENSG00000225417	ENSG00000225417	RP5-1178H5.2	20:20015011-20341346	NOTEST	0.130401	0	#NAME?	0	1	1
ENSG00000225418	ENSG00000225418	AKR1C5P	10:5164278-5177418	NOTEST	0	0	0	0	1	1
ENSG00000225419	ENSG00000225419	RPL21P3	20:18465908-18466696	NOTEST	0	0.183052	inf	0	1	1
ENSG00000225420	ENSG00000225420	AC104134.2	2:88838237-88931339	NOTEST	0.0170051	0	#NAME?	0	1	1
ENSG00000225421	ENSG00000225421	AC019330.1	2:199164086-199637080	NOTEST	0	0	0	0	1	1
ENSG00000225423	ENSG00000225423	TNPO1P1	10:86088341-86278273	NOTEST	0	0	0	0	1	1
ENSG00000225424	ENSG00000225424	RP11-168C9.1	10:131076514-131089986	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000225426	ENSG00000225426	LINC01015	HSCHR6_MHC_MANN:29496773-29500922	NOTEST	0	0	0	0	1	1
ENSG00000225427	ENSG00000225427	LINC00331	13:79361453-79366442	NOTEST	0	0	0	0	1	1
ENSG00000225428	ENSG00000225428	AC108479.1	2:88047605-88285309	NOTEST	0	0	0	0	1	1
ENSG00000225429	ENSG00000225429	HLA-DPB2	HSCHR6_MHC_DBB:33073503-33074770	NOTEST	0	0	0	0	1	1
ENSG00000225431	ENSG00000225431	AP001626.1	21:44019389-44035168	NOTEST	0	0	0	0	1	1
ENSG00000225432	ENSG00000225432	XXbac-BPG13B8.10	HSCHR6_MHC_SSTO:29464959-29478007	NOTEST	0	0	0	0	1	1
ENSG00000225433	ENSG00000225433	MTND1P12	9:42779842-42779998	NOTEST	0	0	0	0	1	1
ENSG00000225434	ENSG00000225434	RP11-63P12.6	9:74920345-74958126	NOTEST	0.0218901	0	#NAME?	0	1	1
ENSG00000225437	ENSG00000225437	RP1-257A15.1	6:161768451-163736524	NOTEST	0	0	0	0	1	1
ENSG00000225438	ENSG00000225438	KRT41P	17:39558667-39581301	NOTEST	0	0	0	0	1	1
ENSG00000225441	ENSG00000225441	OR2J1	HSCHR6_MHC_MANN:29068730-29069669	NOTEST	0	0	0	0	1	1
ENSG00000225442	ENSG00000225442	MPRIP-AS1	17:16945858-17140502	NOTEST	0.0167447	0.0903014	2.43105	0	1	1
ENSG00000225443	ENSG00000225443	AC004938.5	7:44550623-44550931	NOTEST	0	0	0	0	1	1
ENSG00000225444	ENSG00000225444	AC087073.1	2:51259738-52635055	NOTEST	0	0	0	0	1	1
ENSG00000225446	ENSG00000225446	RP4-665J23.2	1:91317315-91319843	NOTEST	0	0.0565628	inf	0	1	1
ENSG00000225447	ENSG00000225447	RPS15AP10	1:46092975-46216322	NOTEST	0	0.367655	inf	0	1	1
ENSG00000225448	ENSG00000225448	AC009477.7	2:131862419-132111282	NOTEST	0	0	0	0	1	1
ENSG00000225449	ENSG00000225449	RAB6C-AS1	2:130724164-130740311	NOTEST	0	3.10E-07	inf	0	1	1
ENSG00000225450	ENSG00000225450	RP3-508I15.14	22:39101727-39190203	NOTEST	0.0903915	0.0320694	-1.49499	0	1	1
ENSG00000225451	ENSG00000225451	RP11-340I6.5	7:63336718-63337728	NOTEST	0	0	0	0	1	1
ENSG00000225452	ENSG00000225452	RNF5	HSCHR6_MHC_MCF:32222562-32225000	NOTEST	0	0	0	0	1	1
ENSG00000225453	ENSG00000225453	PTMAP1	HSCHR6_MHC_COX:30584467-30604447	NOTEST	0	0	0	0	1	1
ENSG00000225454	ENSG00000225454	SFTA2	HSCHR6_MHC_DBB:30889842-30890665	NOTEST	0	0	0	0	1	1
ENSG00000225455	ENSG00000225455	TPI1P4	4:48988263-49064098	NOTEST	0	0	0	0	1	1
ENSG00000225457	ENSG00000225457	RP11-736E3.1	7:112740717-112786385	NOTEST	0	0	0	0	1	1
ENSG00000225458	ENSG00000225458	RP5-1121H13.4	20:40619779-40692609	NOTEST	0	0	0	0	1	1
ENSG00000225459	ENSG00000225459	HLA-Z	HSCHR6_MHC_MANN:33017987-33018062	NOTEST	0	0	0	0	1	1
ENSG00000225460	ENSG00000225460	RP13-93L13.1	9:91975701-92113045	NOTEST	0	0	0	0	1	1
ENSG00000225462	ENSG00000225462	FDPSP1	1:187532192-187533263	NOTEST	0.046587	0.0128311	-1.86029	0	1	1
ENSG00000225463	ENSG00000225463	ZNF70P1	6:33183481-33184105	NOTEST	0	0	0	0	1	1
ENSG00000225465	ENSG00000225465	RFPL1S	22:29832817-29874164	NOTEST	0.018331	0	#NAME?	0	1	1
ENSG00000225466	ENSG00000225466	OFD1P10Y	Y:25727741-25760787	NOTEST	0	0	0	0	1	1
ENSG00000225469	ENSG00000225469	RP3-406C18.2	X:141260651-141261775	NOTEST	0	0	0	0	1	1
ENSG00000225471	ENSG00000225471	RP11-262D11.2	X:71364033-71381600	NOTEST	0	0	0	0	1	1
ENSG00000225472	ENSG00000225472	RP11-120J1.1	9:14081841-14398982	NOTEST	0	0	0	0	1	1
ENSG00000225473	ENSG00000225473	ATP13A4-AS1	3:193119865-193310900	NOTEST	0	0	0	0	1	1
ENSG00000225475	ENSG00000225475	RP11-377K22.2	1:56960418-57110974	NOTEST	0	0	0	0	1	1
ENSG00000225476	ENSG00000225476	AC013437.6	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000225477	ENSG00000225477	CTD-2302A16.2	11:20691116-21597227	NOTEST	0	0	0	0	1	1
ENSG00000225478	ENSG00000225478	RP1-8B22.2	1:18921907-18922130	NOTEST	0	0	0	0	1	1
ENSG00000225479	ENSG00000225479	PLCB1-IT1	20:8112823-8949003	NOTEST	0	0	0	0	1	1
ENSG00000225480	ENSG00000225480	AC006548.19	22:17378334-17378436	NOTEST	0	0	0	0	1	1

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ENSG00000225483	ENSG00000225483	RP11-38J22.2	1:206180053-206180443	NOTEST	0	0	0	0	1	1
ENSG00000225486	ENSG00000225486	RP11-301G21.1	1:233971825-233972178	NOTEST	0	0	0	0	1	1
ENSG00000225487	ENSG00000225487	RP11-403P14.1	1:164890554-164890866	NOTEST	0	0	0	0	1	1
ENSG00000225488	ENSG00000225488	RP11-760D2.1	7:56549797-56550988	NOTEST	0	0	0	0	1	1
ENSG00000225489	ENSG00000225489	RP11-390F4.3	9:6716547-7175648	NOTEST	0.134877	0.106544	-0.340189	0	1	1
ENSG00000225490	ENSG00000225490	RP4-610C12.3	20:29521636-29522987	NOTEST	0.116661	0.180228	0.627497	0	1	1
ENSG00000225491	ENSG00000225491	UBE2Q2P4Y	Y:26378972-26385131	NOTEST	0	0	0	0	1	1
ENSG00000225492	ENSG00000225492	GBP1P1	1:89873237-89891802	NOTEST	0	0	0	0	1	1
ENSG00000225493	ENSG00000225493	LINC01107	2:239419330-239463695	NOTEST	0	0	0	0	1	1
ENSG00000225496	ENSG00000225496	AC104651.2	2:112656055-112787138	NOTEST	0	0.0186045	inf	0	1	1
ENSG00000225497	ENSG00000225497	RP11-180I22.2	10:78629358-79398353	NOTEST	0	0	0	0	1	1
ENSG00000225498	ENSG00000225498	AC002064.5	7:89941809-89951906	NOTEST	0	0	0	0	1	1
ENSG00000225499	ENSG00000225499	RPL15P4	6:31495890-31496470	NOTEST	0	0	0	0	1	1
ENSG00000225501	ENSG00000225501	SNRPFP3	13:69675963-69676188	NOTEST	0	0	0	0	1	1
ENSG00000225502	ENSG00000225502	GAPDHP16	21:16146621-16147583	NOTEST	0	0	0	0	1	1
ENSG00000225505	ENSG00000225505	RP11-330C7.3	1:92974252-93257961	NOTEST	0.0237277	0	#NAME?	0	1	1
ENSG00000225506	ENSG00000225506	CYP4A22-AS1	1:47533159-47646011	NOTEST	0	0.013963	inf	0	1	1
ENSG00000225508	ENSG00000225508	SSXP5	X:52701767-52706101	NOTEST	0	0	0	0	1	1
ENSG00000225509	ENSG00000225509	AIFM1P1	10:19024673-19027560	NOTEST	0	0	0	0	1	1
ENSG00000225510	ENSG00000225510	PCDH8P1	13:53774115-53776547	NOTEST	0.00656831	0	#NAME?	0	1	1
ENSG00000225511	ENSG00000225511	LINC00475	9:94903579-94922396	NOTEST	0.489988	0.605181	0.304622	0	1	1
ENSG00000225512	ENSG00000225512	XXbac-BPG116M5.15	HSCHR6_MHC_DBB:31964724-31979854	NOTEST	0	0	0	0	1	1
ENSG00000225513	ENSG00000225513	RP11-165N19.2	9:114803064-114937688	NOTEST	0.0532198	0.0414993	-0.358877	0	1	1
ENSG00000225514	ENSG00000225514	MTND1P34	1:47533159-47646011	NOTEST	0	0	0	0	1	1
ENSG00000225516	ENSG00000225516	AC006156.1	Y:9236029-9344176	NOTEST	0	0	0	0	1	1
ENSG00000225519	ENSG00000225519	RP11-236B18.2	10:92754376-92766147	NOTEST	0	0	0	0	1	1
ENSG00000225520	ENSG00000225520	TTTY16	Y:7567397-7569288	NOTEST	0	0	0	0	1	1
ENSG00000225521	ENSG00000225521	AC005237.4	2:241938254-242041747	NOTEST	0	0	0	0	1	1
ENSG00000225522	ENSG00000225522	RP11-203F10.1	1:204152133-204152665	NOTEST	0	0	0	0	1	1
ENSG00000225523	ENSG00000225523	IGKV6D-21	2:90060376-90060995	NOTEST	0	0	0	0	1	1
ENSG00000225526	ENSG00000225526	C3orf83	3:12525930-12705725	NOTEST	0.0610399	0	#NAME?	0	1	1
ENSG00000225527	ENSG00000225527	RP11-383B4.4	10:18429605-18948214	NOTEST	0	0	0	0	1	1
ENSG00000225528	ENSG00000225528	RP3-370M22.8	22:40297085-40369725	NOTEST	0	0	0	0	1	1
ENSG00000225529	ENSG00000225529	BX088645.3	9:39722429-39817308	NOTEST	0	0	0	0	1	1
ENSG00000225530	ENSG00000225530	SP3P	13:90013413-90015478	NOTEST	0	0	0	0	1	1
ENSG00000225531	ENSG00000225531	RP11-196I18.3	9:109879109-109883986	NOTEST	0.177677	0.188771	0.0873836	0	1	1
ENSG00000225532	ENSG00000225532	XX-C2158C6.3	6:171044838-171046865	NOTEST	0	0	0	0	1	1
ENSG00000225533	ENSG00000225533	PAWRP1	10:96943409-96943974	NOTEST	0	0	0	0	1	1
ENSG00000225535	ENSG00000225535	AC068610.3	7:114701590-114871409	NOTEST	0.0288958	0.209041	2.85485	0	1	1
ENSG00000225536	ENSG00000225536	RP6-145B8.3	X:85339719-85341343	NOTEST	0.028765	0	#NAME?	0	1	1
ENSG00000225537	ENSG00000225537	AC073325.1	7:45500310-45581781	NOTEST	0	0	0	0	1	1
ENSG00000225538	ENSG00000225538	OR5BE1P	11:55850276-55851215	NOTEST	0	0	0	0	1	1

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ENSG00000225539	ENSG00000225539	AC018799.1	2:195208992-195284369	NOTEST	0	0	0	0	1	1
ENSG00000225540	ENSG00000225540	C4A-AS1	HSCHR6_MHC_MCF:32058985-32080483	NOTEST	0	0	0	0	1	1
ENSG00000225541	ENSG00000225541	AC002480.5	7:22459062-22705152	NOTEST	0	0.0103915	inf	0	1	1
ENSG00000225542	ENSG00000225542	ZNF385D-AS1	3:21459914-22414812	NOTEST	0	0	0	0	1	1
ENSG00000225543	ENSG00000225543	C6orf15	HSCHR6_MHC_DBB:31072774-31074111	NOTEST	0	0	0	0	1	1
ENSG00000225545	ENSG00000225545	RP11-545I10.2	1:170556389-170557377	NOTEST	0	0	0	0	1	1
ENSG00000225546	ENSG00000225546	RP11-328J2.1	7:119344609-119547429	NOTEST	0	0	0	0	1	1
ENSG00000225548	ENSG00000225548	AC098973.2	3:27844252-27932792	NOTEST	0	0	0	0	1	1
ENSG00000225549	ENSG00000225549	RP11-210H10__A.1	6:119078680-119104583	NOTEST	0	0	0	0	1	1
ENSG00000225550	ENSG00000225550	OR2J2	HSCHR6_MHC_APD:29141356-29142397	NOTEST	0	0	0	0	1	1
ENSG00000225551	ENSG00000225551	RP11-19J3.5	9:95059639-95432547	NOTEST	0	0	0	0	1	1
ENSG00000225552	ENSG00000225552	NAALADL2-AS1	3:174156362-175523428	NOTEST	0	0	0	0	1	1
ENSG00000225553	ENSG00000225553	PHF1	HSCHR6_MHC_SSTO:33517536-33525482	NOTEST	0	0	0	0	1	1
ENSG00000225554	ENSG00000225554	RP11-527D7.1	1:241587591-241596792	NOTEST	0	0	0	0	1	1
ENSG00000225555	ENSG00000225555	AP000320.6	21:35736322-35747647	NOTEST	0.498692	0.286756	-0.798326	0	1	1
ENSG00000225557	ENSG00000225557	Z95114.6	22:36571214-36571902	NOTEST	0	0	0	0	1	1
ENSG00000225558	ENSG00000225558	UBE2D3P2	3:37034822-37225180	NOTEST	0	0	0	0	1	1
ENSG00000225559	ENSG00000225559	AC083867.4	7:137848185-137849383	NOTEST	0	0.0369535	inf	0	1	1
ENSG00000225560	ENSG00000225560	FAM197Y8	Y:9185119-9193010	NOTEST	0	0	0	0	1	1
ENSG00000225561	ENSG00000225561	RP11-412H9.2	1:219086098-219089526	NOTEST	0	0	0	0	1	1
ENSG00000225563	ENSG00000225563	AC006076.1	20:52416361-52417857	NOTEST	0	0	0	0	1	1
ENSG00000225564	ENSG00000225564	RP11-341A22.2	9:105902804-106087316	NOTEST	0	0	0	0	1	1
ENSG00000225567	ENSG00000225567	OR2AD1P	HSCHR6_MHC_MCF:28994614-28995542	NOTEST	0	0	0	0	1	1
ENSG00000225568	ENSG00000225568	RP11-384B12.3	1:87380330-87634884	NOTEST	0	0	0	0	1	1
ENSG00000225569	ENSG00000225569	CCT4P2	X:64490792-64492899	NOTEST	0	0	0	0	1	1
ENSG00000225570	ENSG00000225570	AC013733.4	2:182555106-182558142	NOTEST	0	0	0	0	1	1
ENSG00000225571	ENSG00000225571	XXbac-BPG248L24.10	HSCHR6_MHC_QBL:31265711-31266446	NOTEST	0	0	0	0	1	1
ENSG00000225572	ENSG00000225572	DOCK4-AS1	7:111366165-111846466	NOTEST	0.0115653	0	#NAME?	0	1	1
ENSG00000225574	ENSG00000225574	DRAXINP1	X:8751554-8752502	NOTEST	0	0	0	0	1	1
ENSG00000225578	ENSG00000225578	NCBP2-AS1	3:196662272-196669468	NOTEST	0.0796698	0.292816	1.87789	0	1	1
ENSG00000225579	ENSG00000225579	EDNRB-AS1	13:78402356-78408085	NOTEST	0.0638623	0	#NAME?	0	1	1
ENSG00000225581	ENSG00000225581	TRIM53AP	11:89726703-89732909	NOTEST	0	0	0	0	1	1
ENSG00000225582	ENSG00000225582	AC011193.1	17:32806330-32806976	NOTEST	0	0	0	0	1	1
ENSG00000225583	ENSG00000225583	RP4-630C24.1	7:123565285-123611468	NOTEST	0	0	0	0	1	1
ENSG00000225585	ENSG00000225585	IPPKP1	13:21677141-21678510	NOTEST	0	0	0	0	1	1
ENSG00000225588	ENSG00000225588	AC096669.1	2:107871146-108172782	NOTEST	0.0993366	0	#NAME?	0	1	1
ENSG00000225589	ENSG00000225589	MDC1	HSCHR6_MHC_DBB:30657846-30675928	NOTEST	0	0	0	0	1	1
ENSG00000225590	ENSG00000225590	VPS52	HSCHR6_MHC_COX:33138932-33165893	NOTEST	0	0	0	0	1	1
ENSG00000225591	ENSG00000225591	RP11-360D2.2	1:173684079-173755840	NOTEST	0.167491	0.516657	1.62513	0	1	1
ENSG00000225592	ENSG00000225592	OR2H4P	HSCHR6_MHC_SSTO:29183091-29184029	NOTEST	0	0	0	0	1	1
ENSG00000225594	ENSG00000225594	AC098826.4	2:132844861-132860137	NOTEST	0	0	0	0	1	1
ENSG00000225595	ENSG00000225595	XXbac-BPG308K3.6	6:28827401-28832407	NOTEST	0	0	0	0	1	1

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ENSG00000225598	ENSG00000225598	RP11-339D23.1	1:80839048-80840306	NOTEST	0	0	0	0	1	1
ENSG00000225602	ENSG00000225602	MTOR-AS1	1:11166591-11322564	NOTEST	0	0	0	0	1	1
ENSG00000225603	ENSG00000225603	RP11-325P15.1	1:146490894-146596107	NOTEST	0	0.00772529	inf	0	1	1
ENSG00000225604	ENSG00000225604	XXbac-BPG308K3.6	HSCHR6_MHC_DBB:28827414-28831140	NOTEST	0	0	0	0	1	1
ENSG00000225605	ENSG00000225605	RP11-550H2.1	1:76477008-76485041	NOTEST	0	0.0535539	inf	0	1	1
ENSG00000225606	ENSG00000225606	AC005281.2	7:12609750-12693228	NOTEST	0.0928135	0.288634	1.63684	0	1	1
ENSG00000225609	ENSG00000225609	CDY20P	Y:27764790-27766400	NOTEST	0	0	0	0	1	1
ENSG00000225610	ENSG00000225610	AC007679.3	2:206854308-206951288	NOTEST	0	0.0967979	inf	0	1	1
ENSG00000225611	ENSG00000225611	RP11-70C1.1	3:42734154-42846023	NOTEST	0	0	0	0	1	1
ENSG00000225612	ENSG00000225612	AC099552.2	7:155059008-155059762	NOTEST	0	0	0	0	1	1
ENSG00000225613	ENSG00000225613	MIR133BHG	6:52011611-52015917	NOTEST	0	0	0	0	1	1
ENSG00000225614	ENSG00000225614	ZNF469	16:88493878-88507165	NOTEST	0.00113624	0	#NAME?	0	1	1
ENSG00000225615	ENSG00000225615	RBMY2UP	Y:24344575-24349859	NOTEST	0	0	0	0	1	1
ENSG00000225616	ENSG00000225616	RP4-604A21.1	1:29213602-29450447	NOTEST	0	0	0	0	1	1
ENSG00000225618	ENSG00000225618	NCRNA00171	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000225619	ENSG00000225619	MYT1L-AS1	2:1792884-2335032	NOTEST	0	0	0	0	1	1
ENSG00000225620	ENSG00000225620	RP11-569A11.2	1:202317826-202679545	NOTEST	0	0	0	0	1	1
ENSG00000225622	ENSG00000225622	PPIAP17	20:16204394-16205180	NOTEST	0	0	0	0	1	1
ENSG00000225623	ENSG00000225623	AGBL4-IT1	1:48998526-50489585	NOTEST	0	0	0	0	1	1
ENSG00000225624	ENSG00000225624	TBL1YP1	Y:22889139-22904786	NOTEST	0	0	0	0	1	1
ENSG00000225625	ENSG00000225625	RP11-31H5.1	15:56922378-57210769	NOTEST	0	0	0	0	1	1
ENSG00000225626	ENSG00000225626	C9orf135-AS1	9:72433898-72435655	NOTEST	0	0	0	0	1	1
ENSG00000225629	ENSG00000225629	HCG22	HSCHR6_MHC_MCF:31100519-31106180	NOTEST	0	0	0	0	1	1
ENSG00000225632	ENSG00000225632	RP5-997D24.3	1:54598746-54879152	NOTEST	0	0	0	0	1	1
ENSG00000225635	ENSG00000225635	DDAH2	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000225636	ENSG00000225636	HNRNPA3P15	2:197831740-198175897	NOTEST	0.017372	0	#NAME?	0	1	1
ENSG00000225637	ENSG00000225637	AP001046.6	21:44783211-44786446	NOTEST	0.016844	0.0130859	-0.364223	0	1	1
ENSG00000225638	ENSG00000225638	PABPC1P12	10:38929038-38931213	NOTEST	0	0	0	0	1	1
ENSG00000225639	ENSG00000225639	PGAM1P2	9:35943206-35943931	NOTEST	0	0	0	0	1	1
ENSG00000225640	ENSG00000225640	RP5-1022P6.4	20:5488520-5490648	NOTEST	0	0	0	0	1	1
ENSG00000225642	ENSG00000225642	SNRPEP5	2:8741021-8763072	NOTEST	0	0	0	0	1	1
ENSG00000225643	ENSG00000225643	RP11-70P17.1	1:25907968-25916847	NOTEST	0.136494	0.115122	-0.245679	0	1	1
ENSG00000225644	ENSG00000225644	RPL35AP4	6:33357150-33357252	NOTEST	0	0	0	0	1	1
ENSG00000225646	ENSG00000225646	AC015815.7	17:75082797-75213179	NOTEST	0	0	0	0	1	1
ENSG00000225647	ENSG00000225647	AC005487.2	7:108238818-108254711	NOTEST	0.0300699	0.0877651	1.54533	0	1	1
ENSG00000225650	ENSG00000225650	EIF2S2P5	1:114935398-115053781	NOTEST	0	0	0	0	1	1
ENSG00000225652	ENSG00000225652	RP11-619F23.2	10:78629358-79398353	NOTEST	0	0	0	0	1	1
ENSG00000225653	ENSG00000225653	RNF19BPY	Y:3646037-3647587	NOTEST	0	0	0	0	1	1
ENSG00000225655	ENSG00000225655	RP11-143M1.2	9:52451-88826	NOTEST	0.132988	0	#NAME?	0	1	1
ENSG00000225656	ENSG00000225656	RP5-858B6.1	1:230959386-230960453	NOTEST	0.104781	0.0755062	-0.472705	0	1	1
ENSG00000225657	ENSG00000225657	RP5-843L14.1	20:55171365-55173677	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000225658	ENSG00000225658	TAF13P2	2:74425688-74621009	NOTEST	0	0	0	0	1	1
ENSG00000225659	ENSG00000225659	TRIM26BP	HSCHR6_MHC_DBB:30192096-30304918	NOTEST	0	0	0	0	1	1
ENSG00000225660	ENSG00000225660	RP1-73A14.1	X:146036592-146036727	NOTEST	0	0	0	0	1	1
ENSG00000225661	ENSG00000225661	RPL14P5	X:969237-970836	NOTEST	0	0	0	0	1	1
ENSG00000225662	ENSG00000225662	RP11-1036F1.1	3:62384021-62861054	NOTEST	0	0	0	0	1	1
ENSG00000225664	ENSG00000225664	YWHAZP8	X:72494620-72495351	NOTEST	0	0	0	0	1	1
ENSG00000225665	ENSG00000225665	SAR1P3	4:120976762-121337921	NOTEST	0	0	0	0	1	1
ENSG00000225667	ENSG00000225667	LINC00505	1:46921494-46948147	NOTEST	0.161614	0.302974	0.906644	0	1	1
ENSG00000225669	ENSG00000225669	AC068535.5	2:105294680-105295131	NOTEST	0	0	0	0	1	1
ENSG00000225670	ENSG00000225670	CTA-134P22.2	1:159141398-159177763	NOTEST	0.00588531	0.00809422	0.459773	0	1	1
ENSG00000225671	ENSG00000225671	FCF1P6	1:50871101-50871696	NOTEST	0	0	0	0	1	1
ENSG00000225672	ENSG00000225672	CCNT2P1	1:111550321-111558152	NOTEST	0	0	0	0	1	1
ENSG00000225673	ENSG00000225673	RP11-641C17.3	3:59735035-61237133	NOTEST	0	0	0	0	1	1
ENSG00000225674	ENSG00000225674	IPO7P2	13:24553838-24896673	NOTEST	0.508	0.557196	0.133357	0	1	1
ENSG00000225675	ENSG00000225675	RP4-784A16.5	1:53793904-53802181	NOTEST	0.112538	0.0265863	-2.08165	0	1	1
ENSG00000225676	ENSG00000225676	RP3-438O4.4	22:30580632-30603098	NOTEST	0	0	0	0	1	1
ENSG00000225678	ENSG00000225678	AP000619.5	11:102617698-102714534	NOTEST	0	0	0	0	1	1
ENSG00000225679	ENSG00000225679	RP11-216M21.6	9:42312409-42316345	NOTEST	0	0	0	0	1	1
ENSG00000225680	ENSG00000225680	AL163953.2	14:53635771-54153976	NOTEST	0	0	0	0	1	1
ENSG00000225681	ENSG00000225681	AC005730.2	17:19912656-20306870	NOTEST	0	0	0	0	1	1
ENSG00000225682	ENSG00000225682	DXO	HSCHR6_MHC_COX:31925138-31936775	NOTEST	0	0	0	0	1	1
ENSG00000225683	ENSG00000225683	AL078585.1	6:161768451-163736524	NOTEST	0	0	0	0	1	1
ENSG00000225684	ENSG00000225684	FAM225B	9:115865617-115873780	NOTEST	0.0136538	0.0190208	0.478282	0	1	1
ENSG00000225685	ENSG00000225685	TSPY5P	Y:9904162-9906760	NOTEST	0	0	0	0	1	1
ENSG00000225689	ENSG00000225689	RP1-30E17.2	X:127457597-127734446	NOTEST	0	0	0	0	1	1
ENSG00000225690	ENSG00000225690	TREML5P	6:41215106-41217387	NOTEST	0	0	0	0	1	1
ENSG00000225691	ENSG00000225691	HLA-C	HSCHR6_MHC_MCF:31313665-31317037	NOTEST	0	0	0	0	1	1
ENSG00000225693	ENSG00000225693	RP11-54K16.2	9:32972603-33025166	NOTEST	0.278409	0.18872	-0.560961	0	1	1
ENSG00000225695	ENSG00000225695	HNRNPA1P35	2:201773695-201950473	NOTEST	0.0342467	0.0264366	-0.373426	0	1	1
ENSG00000225696	ENSG00000225696	ZNF70P1	HSCHR6_MHC_SSTO:33322790-33323414	NOTEST	0	0	0	0	1	1
ENSG00000225698	ENSG00000225698	IGHV3-72	14:107198931-107199471	NOTEST	0	0	0	0	1	1
ENSG00000225701	ENSG00000225701	EIF4A1P13	7:88078102-88078332	NOTEST	0	0	0	0	1	1
ENSG00000225703	ENSG00000225703	AC005522.7	7:76139744-77045717	NOTEST	0	0	0	0	1	1
ENSG00000225704	ENSG00000225704	RP4-798A17.5	1:171314227-171314459	NOTEST	0.218376	2.19E-05	-13.2861	0	1	1
ENSG00000225705	ENSG00000225705	AC004899.3	7:48886021-48892494	NOTEST	0	0	0	0	1	1
ENSG00000225706	ENSG00000225706	RP11-75C9.1	9:8314245-10612723	NOTEST	0.101745	0.101011	-0.0104515	0	1	1
ENSG00000225708	ENSG00000225708	RP13-379L11.1	20:56644109-56647126	NOTEST	0	0	0	0	1	1
ENSG00000225710	ENSG00000225710	RP5-875O13.6	1:16875145-16879026	NOTEST	0	0.0162478	inf	0	1	1
ENSG00000225711	ENSG00000225711	RP11-345I18.4	1:179068461-179198819	NOTEST	0	0	0	0	1	1
ENSG00000225712	ENSG00000225712	ATP5G2P1	1:209441142-209441568	NOTEST	0	0	0	0	1	1
ENSG00000225713	ENSG00000225713	RPL30P1	1:174059273-174059612	NOTEST	0	0	0	0	1	1
ENSG00000225714	ENSG00000225714	POLR2LP	HSCHR6_MHC_MANN:31153466-31153653	NOTEST	0	0	0	0	1	1
ENSG00000225715	ENSG00000225715	RP11-325E14.5	X:79926352-80065187	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000225716	ENSG00000225716	TCEB1P13	Y:20602682-20603011	NOTEST	0	0	0	0	1	1
ENSG00000225718	ENSG00000225718	RP11-3P22.2	7:68689682-68895909	NOTEST	0	0	0	0	1	1
ENSG00000225719	ENSG00000225719	NMNAT1P2	1:164312241-164313101	NOTEST	0	0	0	0	1	1
ENSG00000225720	ENSG00000225720	RP4-742C19.12	22:39487590-39488860	NOTEST	0	0	0	0	1	1
ENSG00000225721	ENSG00000225721	RP11-269F19.2	1:45205489-45244451	NOTEST	0.0737102	0.168657	1.19416	0	1	1
ENSG00000225722	ENSG00000225722	RP11-706O15.8	X:3871096-3871602	NOTEST	0	0	0	0	1	1
ENSG00000225723	ENSG00000225723	MTND6P15	1:238112513-238113034	NOTEST	0	0	0	0	1	1
ENSG00000225724	ENSG00000225724	LL22NC03-80A10.11	22:22693925-22695567	NOTEST	0	0.00784618	inf	0	1	1
ENSG00000225725	ENSG00000225725	FAM66E	8:7812535-7866277	NOTEST	0.0331435	0.0169149	-0.970432	0	1	1
ENSG00000225726	ENSG00000225726	AC007000.10	7:76139744-77045717	NOTEST	0	0.0334133	inf	0	1	1
ENSG00000225727	ENSG00000225727	RP11-71C5.2	13:45007654-45151283	NOTEST	0	0	0	0	1	1
ENSG00000225728	ENSG00000225728	RP6-191P20.3	X:107182492-107182872	NOTEST	0	0	0	0	1	1
ENSG00000225730	ENSG00000225730	RP3-365O12.2	6:46820248-46922680	NOTEST	0	0	0	0	1	1
ENSG00000225731	ENSG00000225731	AP001627.1	21:44073745-44195619	NOTEST	0	0	0	0	1	1
ENSG00000225732	ENSG00000225732	TRIM31-AS1	HSCHR6_MHC_SSTO:30060268-30072086	NOTEST	0	0	0	0	1	1
ENSG00000225735	ENSG00000225735	NEK4P1	21:18582786-18583665	NOTEST	0	0	0	0	1	1
ENSG00000225736	ENSG00000225736	OR2B3	HSCHR6_MHC_DBB:29053996-29055102	NOTEST	0	0	0	0	1	1
ENSG00000225737	ENSG00000225737	SKIV2L	HSCHR6_MHC_COX:31907415-31925080	NOTEST	0	0	0	0	1	1
ENSG00000225738	ENSG00000225738	NRG3-AS1	10:83635069-84746935	NOTEST	0	0	0	0	1	1
ENSG00000225739	ENSG00000225739	NPM1P18	7:36858563-36859295	NOTEST	0	0	0	0	1	1
ENSG00000225740	ENSG00000225740	TCEB1P6	Y:19949080-19949408	NOTEST	0	0	0	0	1	1
ENSG00000225741	ENSG00000225741	LL22NC03-88E1.17	22:22457628-22459267	NOTEST	0	0	0	0	1	1
ENSG00000225742	ENSG00000225742	RP11-513G11.4	3:193920804-193975561	NOTEST	0.194075	0.118418	-0.712732	0	1	1
ENSG00000225744	ENSG00000225744	AC017002.4	2:112365417-112370095	NOTEST	0	0	0	0	1	1
ENSG00000225745	ENSG00000225745	PLAC4	21:42539727-42654445	NOTEST	0.0176817	0.0706968	1.99939	0	1	1
ENSG00000225746	ENSG00000225746	AL132709.5	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000225748	ENSG00000225748	PRRC2A	HSCHR6_MHC_MCF:31664742-31681839	NOTEST	0	0	0	0	1	1
ENSG00000225750	ENSG00000225750	RP11-242O24.3	1:29471005-29473506	NOTEST	0	0	0	0	1	1
ENSG00000225751	ENSG00000225751	AC087501.1	17:9153787-9479908	NOTEST	0	0	0	0	1	1
ENSG00000225752	ENSG00000225752	RP1-45I4.2	6:143381632-143661441	NOTEST	0	0	0	0	1	1
ENSG00000225755	ENSG00000225755	RP11-267N12.2	1:163080910-163325554	NOTEST	0.0154391	0	#NAME?	0	1	1
ENSG00000225756	ENSG00000225756	DBH-AS1	9:136501481-136524466	NOTEST	0	0.00530163	inf	0	1	1
ENSG00000225758	ENSG00000225758	RPS17P17	X:139553030-139553439	NOTEST	0	0	0	0	1	1
ENSG00000225759	ENSG00000225759	LINC00489	20:36247699-36251521	NOTEST	0	0	0	0	1	1
ENSG00000225761	ENSG00000225761	RP11-417O11.5	10:75757871-75879918	NOTEST	0	0	0	0	1	1
ENSG00000225762	ENSG00000225762	RP11-511I2.2	1:47846599-47874149	NOTEST	0	0	0	0	1	1
ENSG00000225763	ENSG00000225763	MICG	HSCHR6_MHC_DBB:29777569-29777701	NOTEST	0	0	0	0	1	1
ENSG00000225764	ENSG00000225764	LEPREL1-AS1	3:189674516-189862635	NOTEST	0.128536	0.0808027	-0.669701	0	1	1
ENSG00000225765	ENSG00000225765	AC068535.3	2:105027658-105032070	NOTEST	0	0	0	0	1	1
ENSG00000225766	ENSG00000225766	RP11-468E2.9	14:24505661-24520580	NOTEST	0.0430679	0.0516239	0.261424	0	1	1
ENSG00000225767	ENSG00000225767	RP5-850O15.3	1:50905149-51425935	NOTEST	0	0	0	0	1	1

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ENSG00000225769	ENSG00000225769	CROCCP1	X:134566884-134572559	NOTEST	0	0	0	0	1	1
ENSG00000225770	ENSG00000225770	AC092933.3	3:196263402-196263573	NOTEST	0	0	0	0	1	1
ENSG00000225773	ENSG00000225773	C4B-AS1	HSCHR6_MHC_SSTO:31879618-31911713	NOTEST	0	0	0	0	1	1
ENSG00000225774	ENSG00000225774	SIRPAP1	22:30918785-30942669	NOTEST	0	0	0	0	1	1
ENSG00000225775	ENSG00000225775	RP11-354I10.1	6:9124453-9162010	NOTEST	0.0303154	0.0214399	-0.499752	0	1	1
ENSG00000225777	ENSG00000225777	DDX39AP1	13:23278877-23280345	NOTEST	0	0	0	0	1	1
ENSG00000225778	ENSG00000225778	PROSER2-AS1	10:11865337-11936699	NOTEST	0.00500024	0.00351031	-0.510397	0	1	1
ENSG00000225779	ENSG00000225779	RP4-603I14.3	1:46836257-46836627	NOTEST	0	0	0	0	1	1
ENSG00000225781	ENSG00000225781	OR6V1	7:142749416-142750444	NOTEST	0	0	0	0	1	1
ENSG00000225782	ENSG00000225782	RP11-322F10.2	1:220701567-220837803	NOTEST	0.203172	0.33261	0.711131	0	1	1
ENSG00000225783	ENSG00000225783	MIAT	22:27042391-27176170	NOTEST	0.0539892	0.0698143	0.37085	0	1	1
ENSG00000225784	ENSG00000225784	RP11-592B15.4	10:51224680-51371338	NOTEST	0.152921	0.242385	0.664509	0	1	1
ENSG00000225785	ENSG00000225785	RP4-583K8.1	20:50827183-51266970	NOTEST	0	0	0	0	1	1
ENSG00000225786	ENSG00000225786	AL590639.1	1:10078084-10078592	NOTEST	0	0	0	0	1	1
ENSG00000225787	ENSG00000225787	LSM3P3	2:85329511-85329817	NOTEST	0	0	0	0	1	1
ENSG00000225788	ENSG00000225788	BRD2-IT1	HSCHR6_MHC_SSTO:32992301-33089202	NOTEST	0	0	0	0	1	1
ENSG00000225790	ENSG00000225790	RP11-2L8.1	3:177652610-177655450	NOTEST	0	0	0	0	1	1
ENSG00000225792	ENSG00000225792	AC004540.4	7:26331540-26416321	NOTEST	0.332631	0.0501845	-2.72861	0	1	1
ENSG00000225794	ENSG00000225794	AC073321.4	2:217455148-217475925	NOTEST	0.0307549	0	#NAME?	0	1	1
ENSG00000225795	ENSG00000225795	RP11-395G17.1	7:121958480-122526813	NOTEST	0	0	0	0	1	1
ENSG00000225796	ENSG00000225796	MTND4P23	2:202047603-202094129	NOTEST	0.0124596	0	#NAME?	0	1	1
ENSG00000225797	ENSG00000225797	UBDP1	6:29432372-29437583	NOTEST	0	0	0	0	1	1
ENSG00000225798	ENSG00000225798	AC025918.2	15:59063390-59389618	NOTEST	0	0	0	0	1	1
ENSG00000225801	ENSG00000225801	RABEPKP1	13:71870341-71871367	NOTEST	0	0	0	0	1	1
ENSG00000225802	ENSG00000225802	RP11-1036E20.10	11:59022832-59026959	NOTEST	0	0	0	0	1	1
ENSG00000225803	ENSG00000225803	MRPS11P1	20:20834763-20835285	NOTEST	0	0	0	0	1	1
ENSG00000225805	ENSG00000225805	CTD-2313N18.7	11:71576554-71639700	NOTEST	0	0	0	0	1	1
ENSG00000225806	ENSG00000225806	RP1-309F20.3	20:57393973-57486247	NOTEST	0.0677954	0.0972277	0.52018	0	1	1
ENSG00000225807	ENSG00000225807	RP11-44M6.1	7:100107339-100117549	NOTEST	0	0	0	0	1	1
ENSG00000225808	ENSG00000225808	DNAJC19P5	2:178092322-178408564	NOTEST	0.494028	0.459344	-0.105018	0	1	1
ENSG00000225809	ENSG00000225809	RBMY2KP	Y:8132489-8145229	NOTEST	0	0	0	0	1	1
ENSG00000225811	ENSG00000225811	RP11-547I7.1	1:190066791-190446759	NOTEST	0	0	0	0	1	1
ENSG00000225812	ENSG00000225812	RP11-157L3.3	9:46042424-46042722	NOTEST	0	0	0	0	1	1
ENSG00000225813	ENSG00000225813	AC009299.4	2:162138412-162139129	NOTEST	0	0.06011	inf	0	1	1
ENSG00000225814	ENSG00000225814	GRPEL2P2	X:63917757-63918427	NOTEST	0	0	0	0	1	1
ENSG00000225815	ENSG00000225815	AC092669.6	2:66554480-66556116	NOTEST	0	0	0	0	1	1
ENSG00000225816	ENSG00000225816	AC006045.3	7:15025002-15025699	NOTEST	0	0	0	0	1	1
ENSG00000225818	ENSG00000225818	AC118653.2	17:69592478-69593420	NOTEST	0	0	0	0	1	1
ENSG00000225819	ENSG00000225819	AC013269.3	2:131273569-131285579	NOTEST	0	0	0	0	1	1
ENSG00000225822	ENSG00000225822	UBXN7-AS1	3:196074532-196160242	NOTEST	0.0161689	0.0416647	1.3656	0	1	1
ENSG00000225823	ENSG00000225823	RPL7P45	13:105466677-105467420	NOTEST	0	0	0	0	1	1
ENSG00000225824	ENSG00000225824	HLA-DQB1	HSCHR6_MHC_MANN:32779139-32788434	NOTEST	0	0	0	0	1	1
ENSG00000225825	ENSG00000225825	IGHD6-25	14:106347396-106347414	NOTEST	0	0	0	0	1	1

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ENSG00000225826	ENSG00000225826	LINC00626	1:168756176-168762124	NOTEST	0	0.013354	inf	0	1	1
ENSG00000225827	ENSG00000225827	SFTPA3P	10:81355049-81355416	NOTEST	0	0	0	0	1	1
ENSG00000225831	ENSG00000225831	RPS18P1	20:5513523-5513981	NOTEST	0	0	0	0	1	1
ENSG00000225832	ENSG00000225832	RP3-348I23.3	6:20534687-21232635	NOTEST	0	0	0	0	1	1
ENSG00000225833	ENSG00000225833	GS1-594A7.3	X:15621003-15639607	NOTEST	0	0	0	0	1	1
ENSG00000225834	ENSG00000225834	HCG23	HSCHR6_MHC_COX:32306511-32323110	NOTEST	0	0	0	0	1	1
ENSG00000225836	ENSG00000225836	RP11-80H5.6	10:91342744-91410579	NOTEST	0	0.0538281	inf	0	1	1
ENSG00000225838	ENSG00000225838	OR2P1P	HSCHR6_MHC_COX:29036211-29036984	NOTEST	0	0	0	0	1	1
ENSG00000225839	ENSG00000225839	TRMT2B-AS1	X:100264334-100351353	NOTEST	0	0	0	0	1	1
ENSG00000225840	ENSG00000225840	AC010970.2	Y:10036112-10036711	NOTEST	0	0	0	0	1	1
ENSG00000225842	ENSG00000225842	AC139712.1	2:52701210-52701549	NOTEST	0	0	0	0	1	1
ENSG00000225843	ENSG00000225843	NIPA2P1	7:90940682-91186163	NOTEST	0	0	0	0	1	1
ENSG00000225845	ENSG00000225845	BTNL2	HSCHR6_MHC_MCF:32434446-32451073	NOTEST	0	0	0	0	1	1
ENSG00000225846	ENSG00000225846	RP11-630D6.1	4:76932336-77033955	NOTEST	0	0	0	0	1	1
ENSG00000225849	ENSG00000225849	MKRN7P	20:45092540-45093763	NOTEST	0	0	0	0	1	1
ENSG00000225850	ENSG00000225850	RP11-452K12.4	10:99092254-99102770	NOTEST	0.494872	0.103882	-2.25211	0	1	1
ENSG00000225851	ENSG00000225851	HLA-S	6:31349850-31350065	NOTEST	0	0	0	0	1	1
ENSG00000225854	ENSG00000225854	RP11-569G9.7	1:26648349-26680621	NOTEST	0	0	0	0	1	1
ENSG00000225856	ENSG00000225856	PCNPP2	9:91585801-91586256	NOTEST	0	0	0	0	1	1
ENSG00000225857	ENSG00000225857	RP11-46A10.2	1:180875786-180878302	NOTEST	0	0	0	0	1	1
ENSG00000225858	ENSG00000225858	RP1-172N19.3	X:71798663-71934167	NOTEST	0	0	0	0	1	1
ENSG00000225859	ENSG00000225859	DDX39B	HSCHR6_MHC_MANN:31536012-31554120	NOTEST	0	0	0	0	1	1
ENSG00000225860	ENSG00000225860	RP11-1018N14.2	17:49414075-49419932	NOTEST	0	0	0	0	1	1
ENSG00000225864	ENSG00000225864	HCG4P11	6:29690551-29716826	NOTEST	0.0524664	0.0923811	0.816204	0	1	1
ENSG00000225867	ENSG00000225867	RP5-1177I5.3	22:37946032-37947742	NOTEST	0	0	0	0	1	1
ENSG00000225868	ENSG00000225868	AC016582.2	19:38307998-38345855	NOTEST	0	0	0	0	1	1
ENSG00000225869	ENSG00000225869	CTB-70D19.1	5:142985192-143208337	NOTEST	0	0	0	0	1	1
ENSG00000225870	ENSG00000225870	LINC00368	13:111748184-111755444	NOTEST	0	0	0	0	1	1
ENSG00000225871	ENSG00000225871	RP11-495P10.10	1:147835126-147931933	NOTEST	0.0554213	0.035487	-0.64315	0	1	1
ENSG00000225872	ENSG00000225872	AC002398.5	19:36279777-36288787	NOTEST	0	0	0	0	1	1
ENSG00000225873	ENSG00000225873	LINC00694	3:44462618-44465499	NOTEST	0	0	0	0	1	1
ENSG00000225876	ENSG00000225876	AC024067.1	Y:28390497-28390720	NOTEST	0	0	0	0	1	1
ENSG00000225877	ENSG00000225877	AC004603.4	19:43256837-43359870	NOTEST	0	0	0	0	1	1
ENSG00000225878	ENSG00000225878	SERBP1P2	Y:4669725-4670889	NOTEST	0	0	0	0	1	1
ENSG00000225879	ENSG00000225879	RP3-495K2.3	6:169362704-169364436	NOTEST	0	0	0	0	1	1
ENSG00000225881	ENSG00000225881	AC009365.4	7:132443729-132445392	NOTEST	0	0	0	0	1	1
ENSG00000225882	ENSG00000225882	RP3-410B11.1	X:17988316-18122764	NOTEST	0	0	0	0	1	1
ENSG00000225883	ENSG00000225883	BMS1P11	9:69718151-69721729	NOTEST	0.0416054	0.126574	1.60514	0	1	1
ENSG00000225884	ENSG00000225884	AC098872.3	2:192658150-192684976	NOTEST	0	0	0	0	1	1
ENSG00000225885	ENSG00000225885	AC023590.1	8:119201697-119634234	NOTEST	0	0	0	0	1	1
ENSG00000225886	ENSG00000225886	RP11-288L9.4	1:27992571-27998729	NOTEST	0	0.0364003	inf	0	1	1
ENSG00000225888	ENSG00000225888	XXbac-BPG27H4.8	HSCHR6_MHC_QBL:30796823-30805462	NOTEST	0	0	0	0	1	1
ENSG00000225889	ENSG00000225889	AC074289.1	2:64319785-64479993	NOTEST	0.212547	0.329172	0.631059	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000225891	ENSG00000225891	RP3-476K8.3	1:26758772-26797785	NOTEST	0	0	0	0	1	1
ENSG00000225893	ENSG00000225893	RP11-6J24.3	9:4490443-4666674	NOTEST	0	0	0	0	1	1
ENSG00000225894	ENSG00000225894	PPP1R26P2	22:20499889-20503484	NOTEST	0	0	0	0	1	1
ENSG00000225895	ENSG00000225895	TRAPPC2P8	Y:20267199-20269988	NOTEST	0	0	0	0	1	1
ENSG00000225896	ENSG00000225896	AC007742.3	Y:19838631-19838960	NOTEST	0	0	0	0	1	1
ENSG00000225898	ENSG00000225898	AC002075.3	7:93220884-93540577	NOTEST	0	0.0918382	inf	0	1	1
ENSG00000225899	ENSG00000225899	FRG2B	10:135437398-135440299	NOTEST	0.0417701	0.0616147	0.560805	0	1	1
ENSG00000225900	ENSG00000225900	HSPE1P13	2:39208536-39351486	NOTEST	0	0	0	0	1	1
ENSG00000225901	ENSG00000225901	MTND2P9	9:83179946-83180877	NOTEST	0	0	0	0	1	1
ENSG00000225903	ENSG00000225903	RP1-144F13.3	1:40089824-40105617	NOTEST	0	0	0	0	1	1
ENSG00000225904	ENSG00000225904	MORF4L1P7	1:176336834-176337537	NOTEST	0	0	0	0	1	1
ENSG00000225905	ENSG00000225905	RP4-758J18.7	1:1353799-1358071	NOTEST	0	0	0	0	1	1
ENSG00000225906	ENSG00000225906	AP000949.1	21:24254902-24256321	NOTEST	0	0	0	0	1	1
ENSG00000225907	ENSG00000225907	RPS27P16	7:30207419-30207620	NOTEST	0	0	0	0	1	1
ENSG00000225911	ENSG00000225911	AC009310.1	2:220913542-220913993	NOTEST	0	0	0	0	1	1
ENSG00000225913	ENSG00000225913	RP11-57C13.6	10:89367741-89507462	NOTEST	0	0	0	0	1	1
ENSG00000225914	ENSG00000225914	XXbac-BPG154L12.4	6:32223487-32233615	NOTEST	0.017197	0.0130817	-0.394613	0	1	1
ENSG00000225916	ENSG00000225916	AC007879.4	2:208038357-208102599	NOTEST	0	0.0304463	inf	0	1	1
ENSG00000225918	ENSG00000225918	RPL7P59	7:144737091-144738034	NOTEST	0	0	0	0	1	1
ENSG00000225919	ENSG00000225919	RP11-66A2.1	1:232853816-232857996	NOTEST	0	0	0	0	1	1
ENSG00000225920	ENSG00000225920	RIMKLBP2	1:219259943-219386207	NOTEST	0.550592	0.319109	-0.786937	0	1	1
ENSG00000225922	ENSG00000225922	RP11-57G10.1	10:69553527-69554003	NOTEST	0	0	0	0	1	1
ENSG00000225923	ENSG00000225923	RP4-736I12.1	1:96856207-96856949	NOTEST	0	0	0	0	1	1
ENSG00000225924	ENSG00000225924	RP1-111D6.2	6:149539061-149732749	NOTEST	0	0	0	0	1	1
ENSG00000225925	ENSG00000225925	RP13-313G19.2	X:67694551-67696716	NOTEST	0	0	0	0	1	1
ENSG00000225926	ENSG00000225926	DDX39BP1	HSCHR6_MHC_MANN:29865099-29865466	NOTEST	0	0	0	0	1	1
ENSG00000225927	ENSG00000225927	DDX6P1	HSCHR6_MHC_MANN:29297451-29298887	NOTEST	0	0	0	0	1	1
ENSG00000225928	ENSG00000225928	CACYBPP1	10:86088341-86278273	NOTEST	0	0	0	0	1	1
ENSG00000225929	ENSG00000225929	AC000036.4	22:51174252-51176567	NOTEST	0	0	0	0	1	1
ENSG00000225930	ENSG00000225930	AC026150.5	15:30488238-30506743	NOTEST	0.0932302	0.0540055	-0.787691	0	1	1
ENSG00000225932	ENSG00000225932	CTAGE4	7:143880547-143883173	NOTEST	0.0286111	0.0316978	0.147807	0	1	1
ENSG00000225933	ENSG00000225933	AC133965.1	2:87954408-87954762	NOTEST	0	0	0	0	1	1
ENSG00000225934	ENSG00000225934	RP4-566D2.1	1:227751243-227865144	NOTEST	0	0	0	0	1	1
ENSG00000225935	ENSG00000225935	BANF1P5	7:107283209-107283468	NOTEST	0	0.116775	inf	0	1	1
ENSG00000225936	ENSG00000225936	RP11-501J20.5	10:118999110-119038941	NOTEST	0	0	0	0	1	1
ENSG00000225937	ENSG00000225937	PCA3	9:79226291-79521003	NOTEST	0.00714846	0	#NAME?	0	1	1
ENSG00000225938	ENSG00000225938	RP4-575N6.4	1:101701238-101702084	NOTEST	0	0	0	0	1	1
ENSG00000225939	ENSG00000225939	XXbac-BPG248L24.10	HSCHR6_MHC_COX:31266626-31267361	NOTEST	0	0	0	0	1	1
ENSG00000225940	ENSG00000225940	AC022431.2	5:55807393-55902059	NOTEST	0	0.0552124	inf	0	1	1
ENSG00000225942	ENSG00000225942	AC093326.2	2:545804-546667	NOTEST	0	0	0	0	1	1
ENSG00000225943	ENSG00000225943	AC016907.2	2:30273931-30366670	NOTEST	0	0	0	0	1	1
ENSG00000225944	ENSG00000225944	RIOK3P1	13:75402689-75404217	NOTEST	0	0	0	0	1	1
ENSG00000225945	ENSG00000225945	RP3-441A12.1	6:37783552-37786994	NOTEST	0	0	0	0	1	1

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ENSG00000225947	ENSG00000225947	RP11-313E4.1	9:75085289-75085992	NOTEST	0	0	0	0	1	1
ENSG00000225948	ENSG00000225948	RP11-554I8.1	10:6660677-6667308	NOTEST	0	0	0	0	1	1
ENSG00000225949	ENSG00000225949	RP3-358H7.1	X:132275327-132277968	NOTEST	0	0	0	0	1	1
ENSG00000225950	ENSG00000225950	NTF4	19:49557530-49568333	NOTEST	0.146015	0.194254	0.411829	0	1	1
ENSG00000225951	ENSG00000225951	ODF2-AS1	9:131217464-131263571	NOTEST	0.308937	0.283574	-0.123588	0	1	1
ENSG00000225952	ENSG00000225952	RP11-69E9.1	1:23037331-23241818	NOTEST	0	0	0	0	1	1
ENSG00000225953	ENSG00000225953	SATB2-AS1	2:200134222-200341658	NOTEST	0.00490349	0.00344525	-0.509198	0	1	1
ENSG00000225954	ENSG00000225954	WASF5P	HSCHR6_MHC_QBL:31245374-31246826	NOTEST	0	0	0	0	1	1
ENSG00000225955	ENSG00000225955	OR2H5P	HSCHR6_MHC_DBB:29523342-29600923	NOTEST	0	0	0	0	1	1
ENSG00000225956	ENSG00000225956	RP5-1077I2.3	20:13202417-13619587	NOTEST	0	0.130625	inf	0	1	1
ENSG00000225957	ENSG00000225957	CTD-2267G17.2	X:52125195-52128757	NOTEST	0	0	0	0	1	1
ENSG00000225959	ENSG00000225959	MTND4P3	7:67615269-67753220	NOTEST	0	0	0	0	1	1
ENSG00000225960	ENSG00000225960	RP11-360A18.1	9:122735371-122736600	NOTEST	0	0	0	0	1	1
ENSG00000225962	ENSG00000225962	RP11-459A10.2	X:6299514-6299685	NOTEST	0	0	0	0	1	1
ENSG00000225963	ENSG00000225963	AC009950.2	2:230990025-231268447	NOTEST	0.0763475	0.123545	0.694378	0	1	1
ENSG00000225964	ENSG00000225964	AC017076.5	2:6968644-6980595	NOTEST	0	0	0	0	1	1
ENSG00000225965	ENSG00000225965	RP11-508N22.6	10:38450497-38450677	NOTEST	0	0.40877	inf	0	1	1
ENSG00000225967	ENSG00000225967	TAP2	HSCHR6_MHC_APD:32773365-32790162	NOTEST	0	0	0	0	1	1
ENSG00000225968	ENSG00000225968	ELFN1	7:1727754-1787590	NOTEST	0.0555276	0.111428	1.00483	0	1	1
ENSG00000225970	ENSG00000225970	RP3-526F5.2	X:142840831-142911228	NOTEST	0	0	0	0	1	1
ENSG00000225971	ENSG00000225971	CTA-85E5.6	22:30279143-30573064	NOTEST	0	0	0	0	1	1
ENSG00000225972	ENSG00000225972	MTND1P23	1:536815-660283	NOTEST	0.221053	0.167877	-0.396988	0	1	1
ENSG00000225974	ENSG00000225974	AC005550.5	7:15728002-15735116	NOTEST	0	0	0	0	1	1
ENSG00000225976	ENSG00000225976	RP11-192N10.2	10:29698330-30025710	NOTEST	0	0.155661	inf	0	1	1
ENSG00000225978	ENSG00000225978	HAR1A	20:61726844-61735738	NOTEST	0.0157287	0	#NAME?	0	1	1
ENSG00000225979	ENSG00000225979	AC010746.3	2:198176116-198177464	NOTEST	0	0	0	0	1	1
ENSG00000225980	ENSG00000225980	OR7E19P	19:9376065-9377015	NOTEST	0	0	0	0	1	1
ENSG00000225981	ENSG00000225981	AC102953.4	7:1499572-1503644	NOTEST	0.0846777	0	#NAME?	0	1	1
ENSG00000225982	ENSG00000225982	RP11-538D16.3	1:182055685-182059247	NOTEST	0	0	0	0	1	1
ENSG00000225984	ENSG00000225984	HMGB1P26	1:229840980-229841608	NOTEST	0	0	0	0	1	1
ENSG00000225986	ENSG00000225986	UBXN10-AS1	1:20510734-20522541	NOTEST	0	0	0	0	1	1
ENSG00000225987	ENSG00000225987	PBX2	HSCHR6_MHC_APD:32163853-32169304	NOTEST	0	0	0	0	1	1
ENSG00000225988	ENSG00000225988	RP5-1119D9.4	20:9485826-9511171	NOTEST	0	0.020377	inf	0	1	1
ENSG00000225989	ENSG00000225989	ABCF1	HSCHR6_MHC_SSTO:30530572-30556377	NOTEST	0	0	0	0	1	1
ENSG00000225990	ENSG00000225990	SNRPEP7	1:27537755-27537975	NOTEST	0	0	0	0	1	1
ENSG00000225991	ENSG00000225991	RP11-731I19.1	2:27994583-28561768	NOTEST	0.0176118	0.0784778	2.15574	0	1	1
ENSG00000225992	ENSG00000225992	TRGVA	7:38362046-38362331	NOTEST	0	0	0	0	1	1
ENSG00000225993	ENSG00000225993	LY6G6D	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000225995	ENSG00000225995	ATP5A1P9	9:39654197-39655518	NOTEST	0	0	0	0	1	1
ENSG00000225996	ENSG00000225996	AL356356.1	1:150521039-150533413	NOTEST	0.0775638	0.0588698	-0.397856	0	1	1
ENSG00000225997	ENSG00000225997	OR4A8P	11:51435458-51436403	NOTEST	0	0	0	0	1	1

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ENSG00000225998	ENSG00000225998	LSM2	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000225999	ENSG00000225999	NDUFA12P1	13:100680022-100680428	NOTEST	0	0	0	0	1	1
ENSG00000226000	ENSG00000226000	OR2J2	HSCHR6_MHC_SSTO:29141341-29142382	NOTEST	0	0	0	0	1	1
ENSG00000226002	ENSG00000226002	RP11-460N20.5	7:64544480-64560610	NOTEST	0	0	0	0	1	1
ENSG00000226003	ENSG00000226003	RP11-312J18.3	1:160799949-160832692	NOTEST	0	0	0	0	1	1
ENSG00000226004	ENSG00000226004	RP11-10J5.1	6:138264215-138293659	NOTEST	0	0	0	0	1	1
ENSG00000226005	ENSG00000226005	RP11-464C19.3	10:3976710-3978005	NOTEST	0.403175	0.0801284	-2.33102	0	1	1
ENSG00000226007	ENSG00000226007	RP11-211N8.2	9:46842615-46846025	NOTEST	0.0730359	0.0373808	-0.966307	0	1	1
ENSG00000226008	ENSG00000226008	AC073135.7	3:197955064-197955247	NOTEST	0	0	0	0	1	1
ENSG00000226009	ENSG00000226009	KCNIP2-AS1	10:103578834-103603677	NOTEST	0.22411	0.231503	0.0468221	0	1	1
ENSG00000226010	ENSG00000226010	RP11-403E24.1	X:63364751-63366932	NOTEST	0	0	0	0	1	1
ENSG00000226011	ENSG00000226011	OFD1P1Y	Y:19921686-19937209	NOTEST	0	0	0	0	1	1
ENSG00000226012	ENSG00000226012	AP001434.2	21:39493544-39679279	NOTEST	0	0	0	0	1	1
ENSG00000226013	ENSG00000226013	MRPS18BP1	1:215796235-216596738	NOTEST	0	0	0	0	1	1
ENSG00000226014	ENSG00000226014	RP11-467I20.4	1:240652872-240775449	NOTEST	0	0	0	0	1	1
ENSG00000226015	ENSG00000226015	CCT8P1	1:146644349-146767443	NOTEST	0.192472	0.52026	1.43459	0	1	1
ENSG00000226016	ENSG00000226016	RPL36AP55	10:28064114-28287977	NOTEST	0	0	0	0	1	1
ENSG00000226017	ENSG00000226017	PRICKLE2-AS3	3:64053639-64440508	NOTEST	0	0	0	0	1	1
ENSG00000226020	ENSG00000226020	CDK2AP2P3	9:68370603-68370975	NOTEST	0	0	0	0	1	1
ENSG00000226022	ENSG00000226022	AC026167.1	3:6190170-6407572	NOTEST	0	0	0	0	1	1
ENSG00000226023	ENSG00000226023	CT47A6	X:120092018-120100198	NOTEST	0	0	0	0	1	1
ENSG00000226024	ENSG00000226024	COX5BP7	22:39516171-39548679	NOTEST	0	0	0	0	1	1
ENSG00000226025	ENSG00000226025	LGALS17A	19:40170013-40186898	NOTEST	0	0	0	0	1	1
ENSG00000226026	ENSG00000226026	RP11-57H12.3	1:95582893-95729610	NOTEST	0.121034	0	#NAME?	0	1	1
ENSG00000226027	ENSG00000226027	HLA-S	HSCHR6_MHC_SSTO:31342776-31342994	NOTEST	0	0	0	0	1	1
ENSG00000226028	ENSG00000226028	PFN1P12	1:149089874-149130302	NOTEST	0	0	0	0	1	1
ENSG00000226029	ENSG00000226029	RP4-798A10.2	1:16787442-16825752	NOTEST	0.349086	0.29153	-0.259941	0	1	1
ENSG00000226030	ENSG00000226030	HLA-DQB3	6:32698534-32699472	NOTEST	0	0	0	0	1	1
ENSG00000226031	ENSG00000226031	FGF13-AS1	X:137713734-138304939	NOTEST	0.2497	0.0618223	-2.014	0	1	1
ENSG00000226032	ENSG00000226032	RP1-111C20.3	6:159393902-159486305	NOTEST	0	0	0	0	1	1
ENSG00000226033	ENSG00000226033	STK19	HSCHR6_MHC_MCF:32014033-32025671	NOTEST	0	0	0	0	1	1
ENSG00000226034	ENSG00000226034	NANOGNBP1	2:101276660-101277140	NOTEST	0	0	0	0	1	1
ENSG00000226035	ENSG00000226035	HLA-DRB9	HSCHR6_MHC_QBL:32385107-32398790	NOTEST	0	0	0	0	1	1
ENSG00000226036	ENSG00000226036	RP11-338C15.2	1:212820637-212821097	NOTEST	0	0	0	0	1	1
ENSG00000226037	ENSG00000226037	LINC01040	13:90129861-90152763	NOTEST	0	0	0	0	1	1
ENSG00000226038	ENSG00000226038	PPIAP21	20:41859399-41859900	NOTEST	0	0	0	0	1	1
ENSG00000226040	ENSG00000226040	AC005740.3	5:141275732-141276254	NOTEST	0.0438034	0.0310959	-0.494319	0	1	1
ENSG00000226041	ENSG00000226041	AC010745.1	2:16383697-16385494	NOTEST	0	0	0	0	1	1
ENSG00000226042	ENSG00000226042	CDY10P	Y:23799360-23800927	NOTEST	0	0	0	0	1	1
ENSG00000226043	ENSG00000226043	AP000705.7	21:23582257-23793139	NOTEST	0	0	0	0	1	1
ENSG00000226044	ENSG00000226044	RP11-463P17.1	10:48324787-48332197	NOTEST	0	0	0	0	1	1
ENSG00000226045	ENSG00000226045	AC009274.6	7:130295819-130372268	NOTEST	0	0	0	0	1	1
ENSG00000226046	ENSG00000226046	AC007316.3	7:97066829-97067208	NOTEST	0	0	0	0	1	1

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ENSG00000226047	ENSG00000226047	RP11-196I18.4	9:109879109-109883986	NOTEST	0	0	0	0	1	1
ENSG00000226048	ENSG00000226048	YBX1P8	X:46464752-46618490	NOTEST	0	0	0	0	1	1
ENSG00000226050	ENSG00000226050	USP8P1	HSCHR6_MHC_MCF:31320464-31323637	NOTEST	0	0	0	0	1	1
ENSG00000226051	ENSG00000226051	ZNF503-AS1	10:77029576-77171600	NOTEST	0.0911444	0.0753799	-0.273974	0	1	1
ENSG00000226053	ENSG00000226053	RP5-1070A16.1	1:98676302-98738214	NOTEST	0.00721625	0.00506928	-0.509468	0	1	1
ENSG00000226055	ENSG00000226055	PAICSP1	9:37510888-38069210	NOTEST	0.219516	0.194083	-0.17765	0	1	1
ENSG00000226056	ENSG00000226056	MTND4P32	X:102024088-102161086	NOTEST	0	0	0	0	1	1
ENSG00000226057	ENSG00000226057	PHF2P2	13:19520894-19636858	NOTEST	0	0	0	0	1	1
ENSG00000226058	ENSG00000226058	AC092570.1	2:101962012-102004057	NOTEST	0	0	0	0	1	1
ENSG00000226059	ENSG00000226059	HMGB3P20	7:26706680-27034858	NOTEST	0	0	0	0	1	1
ENSG00000226060	ENSG00000226060	TRIM26	HSCHR6_MHC_DBB:30142514-30171491	NOTEST	0	0	0	0	1	1
ENSG00000226061	ENSG00000226061	PCMTD1P1	Y:10011461-10011816	NOTEST	0	0	0	0	1	1
ENSG00000226063	ENSG00000226063	AC009531.2	7:35297991-35299340	NOTEST	0	0	0	0	1	1
ENSG00000226064	ENSG00000226064	PGBD4P6	X:142372753-142605303	NOTEST	0	0	0	0	1	1
ENSG00000226065	ENSG00000226065	ZBTB45P2	2:111132714-111142219	NOTEST	0.0198225	0.101163	2.35147	0	1	1
ENSG00000226066	ENSG00000226066	AC009541.1	7:136170403-136173065	NOTEST	0	0	0	0	1	1
ENSG00000226068	ENSG00000226068	HNRNPA3P4	6:48116938-48117741	NOTEST	0	0	0	0	1	1
ENSG00000226070	ENSG00000226070	RP11-552E20.4	6:40302692-40347624	NOTEST	0	0	0	0	1	1
ENSG00000226071	ENSG00000226071	HLA-DPB2	HSCHR6_MHC_APD:33063594-33080224	NOTEST	0	0	0	0	1	1
ENSG00000226072	ENSG00000226072	AC016772.4	2:170501934-170550943	NOTEST	0	0	0	0	1	1
ENSG00000226074	ENSG00000226074	PRSS44	3:46753604-46854064	NOTEST	0	0	0	0	1	1
ENSG00000226075	ENSG00000226075	PHKG1P1	7:62693412-62708699	NOTEST	0	0	0	0	1	1
ENSG00000226078	ENSG00000226078	RP11-205K6.2	9:129289896-129292622	NOTEST	0	0	0	0	1	1
ENSG00000226079	ENSG00000226079	RP3-399L15.2	6:114844614-114857039	NOTEST	0	0	0	0	1	1
ENSG00000226080	ENSG00000226080	RP11-345J13.1	2:11239976-11272947	NOTEST	0	0.0152966	inf	0	1	1
ENSG00000226081	ENSG00000226081	USP12PX	X:89367648-89368705	NOTEST	0	0	0	0	1	1
ENSG00000226082	ENSG00000226082	RP11-24H1.1	3:62912045-62912557	NOTEST	0	0	0	0	1	1
ENSG00000226083	ENSG00000226083	SLC39A12-AS1	10:18240767-18332221	NOTEST	0	0	0	0	1	1
ENSG00000226086	ENSG00000226086	EIF3LP3	10:38368983-38369805	NOTEST	0.0417967	0	#NAME?	0	1	1
ENSG00000226087	ENSG00000226087	AC106869.2	2:47419543-47572213	NOTEST	0	0	0	0	1	1
ENSG00000226088	ENSG00000226088	RP11-180O5.2	1:70820487-70851022	NOTEST	0.0367698	0.0546869	0.572676	0	1	1
ENSG00000226089	ENSG00000226089	RP1-300G12.2	6:82201155-82462491	NOTEST	0	0	0	0	1	1
ENSG00000226092	ENSG00000226092	RBMY2AP	Y:24073667-24083297	NOTEST	0	0	0	0	1	1
ENSG00000226093	ENSG00000226093	RPS28P8	13:42577565-42577773	NOTEST	0	0	0	0	1	1
ENSG00000226094	ENSG00000226094	RPL7P3	20:61169877-61170591	NOTEST	0	0	0	0	1	1
ENSG00000226096	ENSG00000226096	AC087499.9	17:20512774-20512923	NOTEST	0	0	0	0	1	1
ENSG00000226097	ENSG00000226097	AC099342.1	7:20336330-20351335	NOTEST	0	0	0	0	1	1
ENSG00000226098	ENSG00000226098	RP11-53M11.2	8:55435338-55435875	NOTEST	0	0.10949	inf	0	1	1
ENSG00000226101	ENSG00000226101	AC007461.2	17:70017991-70216859	NOTEST	0.0299143	0	#NAME?	0	1	1
ENSG00000226102	ENSG00000226102	SEPT7P3	7:35985903-36013282	NOTEST	0.25058	0.0805377	-1.63753	0	1	1
ENSG00000226103	ENSG00000226103	C6orf47	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000226104	ENSG00000226104	AC011475.1	19:10713132-10755235	NOTEST	0	0	0	0	1	1
ENSG00000226107	ENSG00000226107	AC004383.3	X:133656731-133657020	NOTEST	0.123179	0	#NAME?	0	1	1
ENSG00000226108	ENSG00000226108	RP11-104G3.5	9:41879687-41880646	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226109	ENSG00000226109	HCG4P5	HSCHR6_MHC_MANN:29898023-29902665	NOTEST	0	0	0	0	1	1
ENSG00000226110	ENSG00000226110	RP11-272G22.2	X:53795483-53795717	NOTEST	0	0	0	0	1	1
ENSG00000226111	ENSG00000226111	MRPS18B	HSCHR6_MHC_MANN:30612851-30638847	NOTEST	0	0	0	0	1	1
ENSG00000226112	ENSG00000226112	FCF1P4	X:110187512-110470589	NOTEST	0	0	0	0	1	1
ENSG00000226113	ENSG00000226113	RP11-672F9.1	10:38536849-38622083	NOTEST	0	0	0	0	1	1
ENSG00000226114	ENSG00000226114	AC111200.8	2:87098423-87248975	NOTEST	0	0	0	0	1	1
ENSG00000226115	ENSG00000226115	AP001476.3	21:47476429-47477481	NOTEST	0	0	0	0	1	1
ENSG00000226116	ENSG00000226116	USP9YP6	Y:20024578-20033510	NOTEST	0	0	0	0	1	1
ENSG00000226117	ENSG00000226117	AC079199.2	17:37921197-38020441	NOTEST	0	0	0	0	1	1
ENSG00000226118	ENSG00000226118	MTND3P1	13:22687257-22687477	NOTEST	0	0	0	0	1	1
ENSG00000226119	ENSG00000226119	RP1-197J16.2	X:101261855-101262267	NOTEST	0	0	0	0	1	1
ENSG00000226122	ENSG00000226122	AC018705.5	7:50526133-50633154	NOTEST	0	0	0	0	1	1
ENSG00000226125	ENSG00000226125	AC098823.3	2:231555635-231565244	NOTEST	0	0	0	0	1	1
ENSG00000226126	ENSG00000226126	PSMC1P12	1:119156955-119158269	NOTEST	0	0	0	0	1	1
ENSG00000226127	ENSG00000226127	BTNL2	HSCHR6_MHC_APD:32369259-32385878	NOTEST	0	0	0	0	1	1
ENSG00000226128	ENSG00000226128	RPL26P9	1:97543298-98386605	NOTEST	0	0	0	0	1	1
ENSG00000226129	ENSG00000226129	RP11-157L3.5	9:46117171-46117907	NOTEST	0.0873472	0	#NAME?	0	1	1
ENSG00000226130	ENSG00000226130	AC013248.2	17:14629045-14633003	NOTEST	0	0	0	0	1	1
ENSG00000226131	ENSG00000226131	AC073465.3	2:174350592-174351090	NOTEST	0	0	0	0	1	1
ENSG00000226132	ENSG00000226132	RPS3AP46	14:53635771-54153976	NOTEST	0	0	0	0	1	1
ENSG00000226133	ENSG00000226133	RP4-683M8.2	1:48519216-48532873	NOTEST	0	0	0	0	1	1
ENSG00000226134	ENSG00000226134	RP11-120E13.1	13:98327264-98330217	NOTEST	0	0	0	0	1	1
ENSG00000226138	ENSG00000226138	RP1-228P16.7	12:48436680-48540187	NOTEST	0	0	0	0	1	1
ENSG00000226139	ENSG00000226139	XXbac-BPG254F23.7	HSCHR6_MHC_MANN:32839530-32840361	NOTEST	0	0	0	0	1	1
ENSG00000226140	ENSG00000226140	RP11-461K13.1	10:16320699-16337857	NOTEST	0	0	0	0	1	1
ENSG00000226141	ENSG00000226141	AF277315.13	X:153882819-153883599	NOTEST	0	0	0	0	1	1
ENSG00000226142	ENSG00000226142	RPL35P8	22:49609836-49610173	NOTEST	0	0	0	0	1	1
ENSG00000226143	ENSG00000226143	RP1-138B7.5	20:42136319-42179590	NOTEST	0	0.00214144	inf	0	1	1
ENSG00000226144	ENSG00000226144	RPS27AP3	20:35624751-35725581	NOTEST	0	0	0	0	1	1
ENSG00000226145	ENSG00000226145	AC022596.6	17:16721296-16725893	NOTEST	0	0.0454342	inf	0	1	1
ENSG00000226147	ENSG00000226147	TUBBP10	1:53392900-53517375	NOTEST	0.0716952	0.235968	1.71864	0	1	1
ENSG00000226148	ENSG00000226148	SLC25A39P1	1:202696525-202778598	NOTEST	0.0166135	0	#NAME?	0	1	1
ENSG00000226149	ENSG00000226149	RP1-69D17.4	6:129847770-129873732	NOTEST	0.0533358	0	#NAME?	0	1	1
ENSG00000226152	ENSG00000226152	HCG4P7	HSCHR6_MHC_COX:29846610-29849789	NOTEST	0	0	0	0	1	1
ENSG00000226153	ENSG00000226153	RP3-389A20.5	X:17393542-17754114	NOTEST	0	0	0	0	1	1
ENSG00000226155	ENSG00000226155	AC124944.3	3:195638919-195640857	NOTEST	0	0.0254707	inf	0	1	1
ENSG00000226156	ENSG00000226156	RPL23AP76	17:14851057-14851515	NOTEST	0	0	0	0	1	1
ENSG00000226157	ENSG00000226157	OR52E3P	11:5113905-5114841	NOTEST	0	0	0	0	1	1
ENSG00000226158	ENSG00000226158	CLCP2	13:115072120-115072541	NOTEST	0	0.0423401	inf	0	1	1
ENSG00000226159	ENSG00000226159	RP11-478K7.2	10:91675245-91717130	NOTEST	0	0	0	0	1	1
ENSG00000226160	ENSG00000226160	LA16c-17H1.3	22:16886055-16886143	NOTEST	0	0	0	0	1	1
ENSG00000226161	ENSG00000226161	EIF4A1P5	13:37512536-37513631	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226163	ENSG00000226163	RP11-167P22.3	10:74127097-74385899	NOTEST	0	0	0	0	1	1
ENSG00000226164	ENSG00000226164	FGFR3P6	1:247282970-247283580	NOTEST	0	0	0	0	1	1
ENSG00000226165	ENSG00000226165	HLA-DQB2	HSCHR6_MHC_SSTO:32814682-32822138	NOTEST	0	0	0	0	1	1
ENSG00000226166	ENSG00000226166	RP11-474O21.2	1:12752924-12753036	NOTEST	0	0	0	0	1	1
ENSG00000226167	ENSG00000226167	AP4B1-AS1	1:114304453-114456708	NOTEST	0.173786	0.067862	-1.35663	0	1	1
ENSG00000226168	ENSG00000226168	RP11-564C4.4	10:52455351-52455741	NOTEST	0	0	0	0	1	1
ENSG00000226169	ENSG00000226169	RP11-375H17.1	22:28112467-28117665	NOTEST	0	0	0	0	1	1
ENSG00000226170	ENSG00000226170	U82671.12	X:151953176-151953993	NOTEST	0	0	0	0	1	1
ENSG00000226171	ENSG00000226171	DHX16	HSCHR6_MHC_SSTO:30606237-30632260	NOTEST	0	0	0	0	1	1
ENSG00000226172	ENSG00000226172	RP4-712E4.1	1:119542966-119544028	NOTEST	0	0	0	0	1	1
ENSG00000226173	ENSG00000226173	TAP1	HSCHR6_MHC_MANN:32962292-33001424	NOTEST	0	0	0	0	1	1
ENSG00000226174	ENSG00000226174	TEX22	14:105864915-105937066	NOTEST	0.304681	0.222892	-0.450958	0	1	1
ENSG00000226175	ENSG00000226175	PAIP1P1	HSCHR6_MHC_MANN:30197333-30226303	NOTEST	0	0	0	0	1	1
ENSG00000226179	ENSG00000226179	LINC00685	X:281724-282586	NOTEST	0.0577545	0.173973	1.59086	0	1	1
ENSG00000226180	ENSG00000226180	AC010536.1	16:87634131-87799598	NOTEST	0.0658124	0.0805382	0.291315	0	1	1
ENSG00000226181	ENSG00000226181	RP1-92C8.3	6:117609462-117923691	NOTEST	0	0	0	0	1	1
ENSG00000226182	ENSG00000226182	LST1	HSCHR6_MHC_COX:31541312-31548170	NOTEST	0	0	0	0	1	1
ENSG00000226183	ENSG00000226183	RANP7	3:22945625-22946642	NOTEST	0	0	0	0	1	1
ENSG00000226185	ENSG00000226185	TRIM64FP	2:96180574-96185855	NOTEST	0	0	0	0	1	1
ENSG00000226186	ENSG00000226186	TCEB1P21	2:71163011-71306935	NOTEST	0	0	0	0	1	1
ENSG00000226187	ENSG00000226187	LY6G6E	HSCHR6_MHC_SSTO:31664594-31675654	NOTEST	0	0	0	0	1	1
ENSG00000226188	ENSG00000226188	HNRNPA1P3	20:44374375-44374926	NOTEST	0	0	0	0	1	1
ENSG00000226191	ENSG00000226191	RP11-438H8.8	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000226192	ENSG00000226192	OR2J1	HSCHR6_MHC_DBB:29068738-29069677	NOTEST	0	0	0	0	1	1
ENSG00000226193	ENSG00000226193	RP3-398G3.5	6:151977825-152958936	NOTEST	0	0	0	0	1	1
ENSG00000226194	ENSG00000226194	RP1-137D17.1	6:169770092-169788480	NOTEST	0.0324994	0.032679	0.00795004	0	1	1
ENSG00000226196	ENSG00000226196	RP11-373J16.2	1:189101480-189102423	NOTEST	0	0	0	0	1	1
ENSG00000226197	ENSG00000226197	RP11-536O18.1	9:13446489-13487510	NOTEST	0	0	0	0	1	1
ENSG00000226199	ENSG00000226199	RP11-12D5.2	X:27850291-27851321	NOTEST	0	0	0	0	1	1
ENSG00000226200	ENSG00000226200	RP11-50E11.3	10:52065359-52401211	NOTEST	0.113236	0.0638977	-0.825494	0	1	1
ENSG00000226201	ENSG00000226201	PSMB8	HSCHR6_MHC_MCF:32841973-32881069	NOTEST	0	0	0	0	1	1
ENSG00000226202	ENSG00000226202	RP11-328D5.1	1:208047139-208052418	NOTEST	0	0	0	0	1	1
ENSG00000226203	ENSG00000226203	RP4-760C5.5	20:25936447-25949924	NOTEST	0.0221416	0.0120469	-0.878104	0	1	1
ENSG00000226204	ENSG00000226204	AL157359.3	21:20325581-20339376	NOTEST	0	0	0	0	1	1
ENSG00000226205	ENSG00000226205	AC007790.4	7:132937828-133751342	NOTEST	0	0	0	0	1	1
ENSG00000226206	ENSG00000226206	RP5-1050E16.2	9:92501141-92523200	NOTEST	0	0	0	0	1	1
ENSG00000226207	ENSG00000226207	RP1-104O17.3	6:98150156-98180588	NOTEST	0	0	0	0	1	1
ENSG00000226208	ENSG00000226208	RP11-99H8.1	1:71172135-71252151	NOTEST	0	0	0	0	1	1
ENSG00000226209	ENSG00000226209	AL138764.1	10:13350144-13350447	NOTEST	0	0	0	0	1	1
ENSG00000226211	ENSG00000226211	RP11-453O22.1	1:221307206-221307563	NOTEST	0	0	0	0	1	1
ENSG00000226212	ENSG00000226212	TRGV6	7:38380300-38380599	NOTEST	0	0	0	0	1	1
ENSG00000226213	ENSG00000226213	UBQLN4P2	2:153733333-153734281	NOTEST	0	0	0	0	1	1
ENSG00000226215	ENSG00000226215	APOM	HSCHR6_MHC_MCF:31683094-31702270	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226216	ENSG00000226216	RPS12P5	3:29305684-30051886	NOTEST	0	0	0	0	1	1
ENSG00000226217	ENSG00000226217	RPL19P1	20:2761259-2761687	NOTEST	0	0	0	0	1	1
ENSG00000226218	ENSG00000226218	AC079163.1	2:146358474-146360991	NOTEST	0	0	0	0	1	1
ENSG00000226220	ENSG00000226220	CICP22	7:39836191-39837510	NOTEST	0.0858515	0.107076	0.318726	0	1	1
ENSG00000226222	ENSG00000226222	RP11-753E22.3	X:24576203-24690794	NOTEST	0	0	0	0	1	1
ENSG00000226223	ENSG00000226223	TSPY16P	Y:9477857-9478325	NOTEST	0	0	0	0	1	1
ENSG00000226225	ENSG00000226225	RPS18	HSCHR6_MHC_MCF:33387703-33414664	NOTEST	0	0	0	0	1	1
ENSG00000226226	ENSG00000226226	SLMO2P1	1:220641295-220642150	NOTEST	0	0	0	0	1	1
ENSG00000226227	ENSG00000226227	DASS-397D15.5	HSCHR6_MHC_SSTO:32490428-32490524	NOTEST	0	0	0	0	1	1
ENSG00000226228	ENSG00000226228	HCG23	HSCHR6_MHC_DBB:32333788-32350396	NOTEST	0	0	0	0	1	1
ENSG00000226229	ENSG00000226229	RPLP0P1	20:16566977-16567338	NOTEST	0	0	0	0	1	1
ENSG00000226230	ENSG00000226230	AC007237.2	7:77646392-79100524	NOTEST	0.0844319	0	#NAME?	0	1	1
ENSG00000226233	ENSG00000226233	RP1-151B14.9	22:37611777-37611931	NOTEST	0	0	0	0	1	1
ENSG00000226234	ENSG00000226234	KRT18P24	9:81651328-81652484	NOTEST	0	0	0	0	1	1
ENSG00000226235	ENSG00000226235	LEMD1-AS1	1:205342379-205438152	NOTEST	0.0102874	0	#NAME?	0	1	1
ENSG00000226237	ENSG00000226237	RP11-276H19.1	9:89563613-89616948	NOTEST	0.0909835	0.0450033	-1.01557	0	1	1
ENSG00000226238	ENSG00000226238	AC132807.1	3:17198653-18959184	NOTEST	0	0	0	0	1	1
ENSG00000226239	ENSG00000226239	RP1-310O13.7	20:30598244-30619984	NOTEST	0	0	0	0	1	1
ENSG00000226240	ENSG00000226240	LINC00381	13:74993309-75009296	NOTEST	0	0	0	0	1	1
ENSG00000226241	ENSG00000226241	LL0XNC01-221F2.2	X:102330737-102348157	NOTEST	0	0	0	0	1	1
ENSG00000226242	ENSG00000226242	RPS17P8	2:193614570-193641625	NOTEST	0	0	0	0	1	1
ENSG00000226243	ENSG00000226243	RPL37AP1	20:43095203-43095482	NOTEST	0	0	0	0	1	1
ENSG00000226245	ENSG00000226245	ZNF32-AS1	10:44124264-44170151	NOTEST	0	0	0	0	1	1
ENSG00000226246	ENSG00000226246	KRT18P36	9:30799468-30800744	NOTEST	0	0	0	0	1	1
ENSG00000226247	ENSG00000226247	AC005034.3	2:75873908-75938115	NOTEST	0.0873472	0	#NAME?	0	1	1
ENSG00000226248	ENSG00000226248	CLIC1	HSCHR6_MHC_DBB:31676986-31689717	NOTEST	0	0	0	0	1	1
ENSG00000226249	ENSG00000226249	RP11-307P5.2	6:147830062-148275073	NOTEST	0	0	0	0	1	1
ENSG00000226250	ENSG00000226250	LINC00408	13:19479578-19481950	NOTEST	0	0	0	0	1	1
ENSG00000226252	ENSG00000226252	RP1-18D14.7	1:47681961-47697892	NOTEST	0	0	0	0	1	1
ENSG00000226253	ENSG00000226253	MRPL35P3	10:75910959-76469061	NOTEST	0.0766922	0	#NAME?	0	1	1
ENSG00000226254	ENSG00000226254	PTP4A1P3	7:89964536-90839905	NOTEST	0	0	0	0	1	1
ENSG00000226255	ENSG00000226255	UBE2V2P1	10:19340383-19341099	NOTEST	0	0	0	0	1	1
ENSG00000226257	ENSG00000226257	STK19	HSCHR6_MHC_DBB:31919772-31953483	NOTEST	0	0	0	0	1	1
ENSG00000226258	ENSG00000226258	GRM7-AS3	3:6532165-7783215	NOTEST	0	0	0	0	1	1
ENSG00000226260	ENSG00000226260	HLA-DRA	HSCHR6_MHC_MANN:32446281-32451493	NOTEST	0	0	0	0	1	1
ENSG00000226261	ENSG00000226261	AC064836.3	2:203200746-203201450	NOTEST	0	0	0	0	1	1
ENSG00000226262	ENSG00000226262	PHKBP1	20:8078470-8080421	NOTEST	0	0	0	0	1	1
ENSG00000226263	ENSG00000226263	ISM1-AS1	20:13202417-13619587	NOTEST	0	0	0	0	1	1
ENSG00000226264	ENSG00000226264	HLA-DMB	HSCHR6_MHC_DBB:32880345-32898843	NOTEST	0	0	0	0	1	1
ENSG00000226267	ENSG00000226267	HCG9P5	HSCHR6_MHC_SSTO:29687513-29713718	NOTEST	0	0	0	0	1	1
ENSG00000226270	ENSG00000226270	ZNF736P2Y	Y:26829803-26831082	NOTEST	0	0	0	0	1	1
ENSG00000226271	ENSG00000226271	OR2J3	HSCHR6_MHC_APD:29079707-29080643	NOTEST	0	0	0	0	1	1
ENSG00000226272	ENSG00000226272	ARHGAP26-AS1	5:142149948-142608576	NOTEST	0	0	0	0	1	1
ENSG00000226273	ENSG00000226273	AC079305.5	2:177855235-178088686	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226275	ENSG00000226275	LTA	HSCHR6_MHC_MCF:31616137-31618410	NOTEST	0	0	0	0	1	1
ENSG00000226277	ENSG00000226277	AC105393.2	2:421056-422303	NOTEST	0	0	0	0	1	1
ENSG00000226278	ENSG00000226278	PSPHP1	7:55832489-55840981	NOTEST	0	0	0	0	1	1
ENSG00000226279	ENSG00000226279	AC005682.7	7:22921511-22922009	NOTEST	0	0	0	0	1	1
ENSG00000226280	ENSG00000226280	RP6-22P16.1	X:66593414-66595362	NOTEST	0	0	0	0	1	1
ENSG00000226281	ENSG00000226281	RP1-80N2.2	6:6692976-6711235	NOTEST	0	0	0	0	1	1
ENSG00000226284	ENSG00000226284	ARPC3P1	20:47729877-47804904	NOTEST	0.158725	0.276848	0.802563	0	1	1
ENSG00000226285	ENSG00000226285	AC091813.2	7:79173226-79174169	NOTEST	0	0	0	0	1	1
ENSG00000226286	ENSG00000226286	RP1-163G9.2	1:2985731-3355185	NOTEST	0	0	0	0	1	1
ENSG00000226288	ENSG00000226288	OR52I2	11:4608020-4609135	NOTEST	0	0	0	0	1	1
ENSG00000226289	ENSG00000226289	RP11-57I17.3	1:207818457-207911761	NOTEST	0	0	0	0	1	1
ENSG00000226291	ENSG00000226291	AC091729.8	7:1036621-1177896	NOTEST	0	0	0	0	1	1
ENSG00000226292	ENSG00000226292	RP11-7G12.1	1:165991451-165992264	NOTEST	0	0	0	0	1	1
ENSG00000226296	ENSG00000226296	RP11-71J2.1	10:55050831-55070825	NOTEST	0	0	0	0	1	1
ENSG00000226297	ENSG00000226297	AC007677.2	2:229715241-230136001	NOTEST	0	0	0	0	1	1
ENSG00000226298	ENSG00000226298	RAD23BLP	21:17066618-17068900	NOTEST	0	0	0	0	1	1
ENSG00000226299	ENSG00000226299	RP6-29D12.4	X:53352186-53353019	NOTEST	0	0	0	0	1	1
ENSG00000226301	ENSG00000226301	PDCL3P1	8:61297146-61429354	NOTEST	0	0	0	0	1	1
ENSG00000226302	ENSG00000226302	RP11-528N21.1	3:40644615-40646918	NOTEST	0	0	0	0	1	1
ENSG00000226303	ENSG00000226303	ZDHHC20P1	HSCHR6_MHC_MANN:29675446-29675869	NOTEST	0	0	0	0	1	1
ENSG00000226304	ENSG00000226304	RP11-435M3.2	10:26213376-26222639	NOTEST	0	0	0	0	1	1
ENSG00000226306	ENSG00000226306	NPY6R	5:137136881-137146440	NOTEST	0.0735499	0.0926875	0.333652	0	1	1
ENSG00000226307	ENSG00000226307	HNRNPDLP1	X:94893373-94893923	NOTEST	0	0	0	0	1	1
ENSG00000226308	ENSG00000226308	RP4-813D12.3	20:55841852-55858054	NOTEST	0	0	0	0	1	1
ENSG00000226309	ENSG00000226309	SMARCE1P2	6:85130745-85265870	NOTEST	0.0141719	0	#NAME?	0	1	1
ENSG00000226310	ENSG00000226310	RP3-323P24.3	X:57148094-57153676	NOTEST	0.0601398	0.134571	1.16198	0	1	1
ENSG00000226312	ENSG00000226312	CFLAR-AS1	2:201980826-202041410	NOTEST	0.266164	0.0885139	-1.58834	0	1	1
ENSG00000226313	ENSG00000226313	RP11-585K14.2	X:5087552-5088686	NOTEST	0	0	0	0	1	1
ENSG00000226314	ENSG00000226314	ZNF192P1	6:28129558-28137372	NOTEST	0.456314	0.4655	0.0287541	0	1	1
ENSG00000226317	ENSG00000226317	LINC00351	13:85937735-86118705	NOTEST	0	0	0	0	1	1
ENSG00000226318	ENSG00000226318	RP11-474D14.2	10:69681664-69835105	NOTEST	0.468717	0.276124	-0.763402	0	1	1
ENSG00000226320	ENSG00000226320	AC018359.1	3:34200825-34604369	NOTEST	0	0	0	0	1	1
ENSG00000226321	ENSG00000226321	AC104809.3	2:241858201-241932728	NOTEST	0	0	0	0	1	1
ENSG00000226323	ENSG00000226323	AC006150.1	7:14184673-15014402	NOTEST	0	0	0	0	1	1
ENSG00000226324	ENSG00000226324	RP11-115M14.1	1:71547006-72748417	NOTEST	0	0	0	0	1	1
ENSG00000226327	ENSG00000226327	RP11-350G13.1	9:90939368-90940254	NOTEST	0	0	0	0	1	1
ENSG00000226329	ENSG00000226329	AC005682.6	7:22903492-22920969	NOTEST	0.0458385	0.0339336	-0.433847	0	1	1
ENSG00000226330	ENSG00000226330	RP11-739N20.2	1:204346977-204463852	NOTEST	0	0.114024	inf	0	1	1
ENSG00000226331	ENSG00000226331	AC009302.4	2:222909243-222909713	NOTEST	0	0	0	0	1	1
ENSG00000226334	ENSG00000226334	RP11-217B7.2	9:107543282-107691173	NOTEST	0.192906	0.18064	-0.0947791	0	1	1
ENSG00000226335	ENSG00000226335	XXyac-YX155B6.6	1:147634988-147700929	NOTEST	0	0	0	0	1	1
ENSG00000226336	ENSG00000226336	MRPS16P3	22:36099849-36100223	NOTEST	0	0	0	0	1	1

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ENSG00000226337	ENSG00000226337	RP11-274B18.4	9:71155951-71259358	NOTEST	0	0	0	0	1	1
ENSG00000226338	ENSG00000226338	AC079150.2	2:154064599-154064677	NOTEST	0	0	0	0	1	1
ENSG00000226339	ENSG00000226339	RPS26P56	X:128542358-128542598	NOTEST	0	0	0	0	1	1
ENSG00000226340	ENSG00000226340	AC105402.3	2:149624038-149883273	NOTEST	0	0	0	0	1	1
ENSG00000226341	ENSG00000226341	AC062016.2	2:117508733-117509224	NOTEST	0	0	0	0	1	1
ENSG00000226342	ENSG00000226342	NMD3P1	7:63361200-63378372	NOTEST	0	0.00793116	inf	0	1	1
ENSG00000226343	ENSG00000226343	HLA-DQB3	HSCHR6_MHC_APD:32679934-32684035	NOTEST	0	0	0	0	1	1
ENSG00000226344	ENSG00000226344	CST12P	20:23456336-23460435	NOTEST	0	0	0	0	1	1
ENSG00000226345	ENSG00000226345	AC083822.2	3:196074532-196160242	NOTEST	0	0	0	0	1	1
ENSG00000226347	ENSG00000226347	OR2J2	HSCHR6_MHC_MANN:29141319-29142360	NOTEST	0	0	0	0	1	1
ENSG00000226348	ENSG00000226348	VN2R10P	16:77224731-77478233	NOTEST	0	0	0	0	1	1
ENSG00000226349	ENSG00000226349	RP11-145A3.2	1:225888305-225939945	NOTEST	0	0.0290317	inf	0	1	1
ENSG00000226352	ENSG00000226352	RP11-523H24.3	13:20248763-20357142	NOTEST	0.491634	0.334866	-0.553999	0	1	1
ENSG00000226353	ENSG00000226353	TAF9P1	Y:19740392-19741282	NOTEST	0	0	0	0	1	1
ENSG00000226354	ENSG00000226354	HLA-U	HSCHR6_MHC_MANN:29890930-29891116	NOTEST	0	0	0	0	1	1
ENSG00000226355	ENSG00000226355	RP11-65J3.2	9:132192930-132213701	NOTEST	0.0432856	0	#NAME?	0	1	1
ENSG00000226356	ENSG00000226356	RPS6P20	12:131776612-131777721	NOTEST	0	0	0	0	1	1
ENSG00000226358	ENSG00000226358	KRT8P38	10:90484300-90512543	NOTEST	0	0	0	0	1	1
ENSG00000226359	ENSG00000226359	AC055811.5	17:17145323-17146200	NOTEST	0.0805639	0	#NAME?	0	1	1
ENSG00000226361	ENSG00000226361	TERF1P5	13:19254633-19255846	NOTEST	0.178477	0.107308	-0.733983	0	1	1
ENSG00000226362	ENSG00000226362	FAM41AY2	Y:20552879-20566932	NOTEST	0	0	0	0	1	1
ENSG00000226364	ENSG00000226364	AC102948.2	17:50939480-50976948	NOTEST	0	0	0	0	1	1
ENSG00000226365	ENSG00000226365	UBDP1	HSCHR6_MHC_MANN:29431943-29437154	NOTEST	0	0	0	0	1	1
ENSG00000226366	ENSG00000226366	AC097463.1	2:51259738-52635055	NOTEST	0	0	0	0	1	1
ENSG00000226367	ENSG00000226367	ST7-AS2	7:116592499-116870157	NOTEST	0	0	0	0	1	1
ENSG00000226368	ENSG00000226368	BX088645.2	9:39860051-39860359	NOTEST	0	0	0	0	1	1
ENSG00000226369	ENSG00000226369	USP9YP11	Y:26081099-26086248	NOTEST	0	0	0	0	1	1
ENSG00000226370	ENSG00000226370	LINC00375	13:85639221-85653055	NOTEST	0	0	0	0	1	1
ENSG00000226372	ENSG00000226372	DCAF8L1	X:27996109-27999566	NOTEST	0	0	0	0	1	1
ENSG00000226374	ENSG00000226374	RP13-614K11.2	1:4000672-4015322	NOTEST	0	0	0	0	1	1
ENSG00000226375	ENSG00000226375	RP3-395P12.2	1:173143438-173144642	NOTEST	0	0	0	0	1	1
ENSG00000226376	ENSG00000226376	RP11-29B9.1	9:7930826-7935137	NOTEST	0	0	0	0	1	1
ENSG00000226377	ENSG00000226377	AC084809.2	17:30819539-31205655	NOTEST	0.354722	0.254049	-0.481582	0	1	1
ENSG00000226378	ENSG00000226378	DAQB-335A13.8	HSCHR6_MHC_MANN:29687659-29713937	NOTEST	0	0	0	0	1	1
ENSG00000226379	ENSG00000226379	HCG4	HSCHR6_MHC_MANN:29755658-29762533	NOTEST	0	0	0	0	1	1
ENSG00000226383	ENSG00000226383	AC093375.1	2:156868128-156881125	NOTEST	0.372024	0.338588	-0.135863	0	1	1
ENSG00000226384	ENSG00000226384	GTF2H4	HSCHR6_MHC_DBB:30866675-30884964	NOTEST	0	0	0	0	1	1
ENSG00000226386	ENSG00000226386	PARD3-AS1	10:35104694-35105314	NOTEST	0.217569	0.0874632	-1.31473	0	1	1
ENSG00000226387	ENSG00000226387	SORCS3-AS1	10:106400858-107024993	NOTEST	0	0	0	0	1	1
ENSG00000226388	ENSG00000226388	ELL2P4	X:145635245-145637283	NOTEST	0	0	0	0	1	1
ENSG00000226389	ENSG00000226389	RP11-507K13.4	10:50979886-50981345	NOTEST	0	0	0	0	1	1
ENSG00000226390	ENSG00000226390	RP11-358D14.2	20:62037541-62103993	NOTEST	0	0	0	0	1	1
ENSG00000226392	ENSG00000226392	RP4-736H5.1	7:67092817-67093006	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226393	ENSG00000226393	IFNA20P	9:21321298-21321826	NOTEST	0.160558	0.0914643	-0.811816	0	1	1
ENSG00000226394	ENSG00000226394	RP11-413E1.2	1:89990394-90402170	NOTEST	0	0	0	0	1	1
ENSG00000226395	ENSG00000226395	RP11-218D6.3	10:28288716-28338544	NOTEST	0	0	0	0	1	1
ENSG00000226397	ENSG00000226397	C12orf77	12:25146357-25150453	NOTEST	0	0	0	0	1	1
ENSG00000226398	ENSG00000226398	AC013480.2	2:42242764-42252442	NOTEST	0	0	0	0	1	1
ENSG00000226400	ENSG00000226400	CTD-2269E23.2	5:28925706-28927696	NOTEST	0	0	0	0	1	1
ENSG00000226401	ENSG00000226401	RP5-965K10.3	7:63092985-63096995	NOTEST	0	0	0	0	1	1
ENSG00000226402	ENSG00000226402	TRIM31	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1
ENSG00000226403	ENSG00000226403	RP11-31F19.1	9:213107-746105	NOTEST	0.438998	0.598079	0.446121	0	1	1
ENSG00000226404	ENSG00000226404	LY6G5C	HSCHR6_MHC_DBB:31611187-31653368	NOTEST	0	0	0	0	1	1
ENSG00000226405	ENSG00000226405	RP5-984P4.1	20:21468881-21469263	NOTEST	0	0	0	0	1	1
ENSG00000226406	ENSG00000226406	RBMX2P1	21:16191163-16254296	NOTEST	0	0	0	0	1	1
ENSG00000226407	ENSG00000226407	RPL23P11	10:34153240-34153651	NOTEST	0	0	0	0	1	1
ENSG00000226408	ENSG00000226408	XXbac-BPG299F13.14	HSCHR6_MHC_MCF:31244105-31250362	NOTEST	0	0	0	0	1	1
ENSG00000226409	ENSG00000226409	RP11-735G4.1	6:125691356-125695470	NOTEST	0.129427	0.0859708	-0.590221	0	1	1
ENSG00000226410	ENSG00000226410	AC104058.1	2:187027675-187027972	NOTEST	0	0	0	0	1	1
ENSG00000226411	ENSG00000226411	CTD-2526L21.2	7:63159767-63160819	NOTEST	0	0	0	0	1	1
ENSG00000226412	ENSG00000226412	RP11-476F14.1	10:33867858-33888968	NOTEST	0	0	0	0	1	1
ENSG00000226413	ENSG00000226413	OR8T1P	12:48733790-48836730	NOTEST	0	0	0	0	1	1
ENSG00000226414	ENSG00000226414	RP11-375A20.1	X:125863086-125864209	NOTEST	0	0	0	0	1	1
ENSG00000226416	ENSG00000226416	MRPL23-AS1	11:1968507-2011150	NOTEST	0.0805818	0.0647067	-0.316539	0	1	1
ENSG00000226417	ENSG00000226417	CLIC1	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000226420	ENSG00000226420	IGLV3-4	22:23200199-23200443	NOTEST	0	0	0	0	1	1
ENSG00000226421	ENSG00000226421	SLC25A5P5	7:32511124-32512021	NOTEST	0	0	0	0	1	1
ENSG00000226422	ENSG00000226422	PSORS1C3	HSCHR6_MHC_MANN:3117 1309-31199405	NOTEST	0	0	0	0	1	1
ENSG00000226423	ENSG00000226423	AC093642.4	2:242823513-243026289	NOTEST	0	0	0	0	1	1
ENSG00000226425	ENSG00000226425	RP11-348J12.2	10:94819419-94820183	NOTEST	0	0	0	0	1	1
ENSG00000226426	ENSG00000226426	RP11-174J11.1	10:65796104-65797040	NOTEST	0	0	0	0	1	1
ENSG00000226427	ENSG00000226427	HMGN2P7	3:15416879-15417152	NOTEST	0	0	0	0	1	1
ENSG00000226428	ENSG00000226428	RP11-106M7.4	10:116660480-116661125	NOTEST	0	0	0	0	1	1
ENSG00000226429	ENSG00000226429	RP11-111F5.6	9:46685428-46746500	NOTEST	0	0	0	0	1	1
ENSG00000226430	ENSG00000226430	USP17L7	8:11973290-12008698	NOTEST	0	0	0	0	1	1
ENSG00000226431	ENSG00000226431	RP11-416N2.3	10:105239359-105615301	NOTEST	0	0	0	0	1	1
ENSG00000226433	ENSG00000226433	AP000290.7	21:34528937-34531416	NOTEST	0	0	0	0	1	1
ENSG00000226434	ENSG00000226434	RP11-1L9.1	X:13395306-13421138	NOTEST	0	0	0	0	1	1
ENSG00000226435	ENSG00000226435	ANKRD18DP	3:197780392-197807591	NOTEST	0.0313743	0.0387013	0.302797	0	1	1
ENSG00000226436	ENSG00000226436	RP1-22N22.1	X:28605515-29974840	NOTEST	0	0	0	0	1	1
ENSG00000226437	ENSG00000226437	TRIM39	HSCHR6_MHC_MANN:3024 6906-30359341	NOTEST	0	0	0	0	1	1
ENSG00000226438	ENSG00000226438	RP11-420K8.1	1:39546987-39952849	NOTEST	0	0	0	0	1	1
ENSG00000226439	ENSG00000226439	RP11-621K7.1	4:62066975-63031272	NOTEST	0	0.0458584	inf	0	1	1
ENSG00000226440	ENSG00000226440	RP11-506B6.6	6:112429962-112672498	NOTEST	0	0	0	0	1	1
ENSG00000226441	ENSG00000226441	PLCL2-AS1	3:16844158-17132086	NOTEST	0	0	0	0	1	1

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ENSG00000226442	ENSG00000226442	AC006037.2	2:235017724-235018125	NOTEST	0	0	0	0	1	1
ENSG00000226443	ENSG00000226443	GAPDHP32	1:120076371-120077369	NOTEST	0.457525	0.447514	-0.0319202	0	1	1
ENSG00000226444	ENSG00000226444	ACTR3BP6	22:16967409-16969212	NOTEST	0	0	0	0	1	1
ENSG00000226446	ENSG00000226446	NOTCH2P1	1:120428926-120429550	NOTEST	0	0	0	0	1	1
ENSG00000226447	ENSG00000226447	RP11-393J16.4	10:38265752-38281395	NOTEST	0	0	0	0	1	1
ENSG00000226448	ENSG00000226448	RP11-93L14.1	10:67672275-69455927	NOTEST	0	0	0	0	1	1
ENSG00000226449	ENSG00000226449	CDY5P	Y:19833477-19835057	NOTEST	0	0	0	0	1	1
ENSG00000226450	ENSG00000226450	CYP2D8P	22:42545876-42551007	NOTEST	0.169779	0.138583	-0.292913	0	1	1
ENSG00000226453	ENSG00000226453	RP11-379B8.1	6:82554901-82643197	NOTEST	0	0.016101	inf	0	1	1
ENSG00000226454	ENSG00000226454	RP3-462C17.1	6:40359324-40555204	NOTEST	0	0	0	0	1	1
ENSG00000226455	ENSG00000226455	RP3-512E2.2	6:90636247-91006627	NOTEST	0	0	0	0	1	1
ENSG00000226457	ENSG00000226457	RP11-430L17.1	1:16679069-16763919	NOTEST	0	0	0	0	1	1
ENSG00000226461	ENSG00000226461	OR10G5P	11:123880361-123880719	NOTEST	0	0	0	0	1	1
ENSG00000226462	ENSG00000226462	KRT18P1	HSCHR6_MHC_MANN:28936914-28938245	NOTEST	0	0	0	0	1	1
ENSG00000226463	ENSG00000226463	OR2W1	HSCHR6_MHC_APD:29012034-29013062	NOTEST	0	0	0	0	1	1
ENSG00000226465	ENSG00000226465	RP13-401N8.1	20:25731853-25733397	NOTEST	0.197388	0.300785	0.607694	0	1	1
ENSG00000226466	ENSG00000226466	RPA2P2	10:82896295-82897091	NOTEST	0	0	0	0	1	1
ENSG00000226467	ENSG00000226467	AGPAT1	HSCHR6_MHC_COX:32064597-32094350	NOTEST	0	0	0	0	1	1
ENSG00000226468	ENSG00000226468	AC018641.7	7:32496574-32497370	NOTEST	0	0	0	0	1	1
ENSG00000226469	ENSG00000226469	ADAM1B	12:112364821-112366821	NOTEST	0.0405992	0.0177204	-1.19604	0	1	1
ENSG00000226470	ENSG00000226470	RP11-132E11.3	9:17048916-17112813	NOTEST	0	0	0	0	1	1
ENSG00000226471	ENSG00000226471	CTA-292E10.6	22:29196670-29244547	NOTEST	0.323198	0.062148	-2.37864	0	1	1
ENSG00000226472	ENSG00000226472	RP11-551L14.4	12:31149972-31158938	NOTEST	0.222664	0.198434	-0.166212	0	1	1
ENSG00000226473	ENSG00000226473	AC079807.1	2:48166876-48167357	NOTEST	0	0	0	0	1	1
ENSG00000226474	ENSG00000226474	LA16c-2F2.5	22:16362384-16362561	NOTEST	0	0	0	0	1	1
ENSG00000226476	ENSG00000226476	RP11-776H12.1	1:61005920-61106163	NOTEST	0	0	0	0	1	1
ENSG00000226477	ENSG00000226477	LL22NC03-84E4.11	22:23157167-23157423	NOTEST	0	0	0	0	1	1
ENSG00000226480	ENSG00000226480	OR7H1P	19:9389123-9390045	NOTEST	0	0	0	0	1	1
ENSG00000226481	ENSG00000226481	ACTR3BP2	2:92128693-92130496	NOTEST	0	0	0	0	1	1
ENSG00000226482	ENSG00000226482	ADIPOQ-AS1	3:186560462-186576252	NOTEST	0.00819778	0.00705112	-0.217379	0	1	1
ENSG00000226483	ENSG00000226483	RP5-964H19.2	1:109051195-109051865	NOTEST	0	0	0	0	1	1
ENSG00000226484	ENSG00000226484	RP11-87M18.2	X:36246734-36458375	NOTEST	0	0	0	0	1	1
ENSG00000226485	ENSG00000226485	RBM22P3	7:56558374-56559328	NOTEST	0	0	0	0	1	1
ENSG00000226486	ENSG00000226486	LINC01035	1:188874818-189006393	NOTEST	0	0	0	0	1	1
ENSG00000226487	ENSG00000226487	RP4-749H3.2	1:20687071-20757727	NOTEST	0	0	0	0	1	1
ENSG00000226488	ENSG00000226488	AC021021.2	2:6636008-6643938	NOTEST	0	0	0	0	1	1
ENSG00000226489	ENSG00000226489	AC104308.2	3:35913357-35913690	NOTEST	0	0	0	0	1	1
ENSG00000226490	ENSG00000226490	AC138647.1	8:142524737-142528837	NOTEST	0	0	0	0	1	1
ENSG00000226491	ENSG00000226491	FTOP1	2:43024364-43025852	NOTEST	0	0	0	0	1	1
ENSG00000226492	ENSG00000226492	CUTA	HSCHR6_MHC_SSTO:33517536-33525482	NOTEST	0	0	0	0	1	1
ENSG00000226493	ENSG00000226493	RP11-524O24.2	10:70237755-70287231	NOTEST	0	0.259534	inf	0	1	1
ENSG00000226494	ENSG00000226494	RPL7P4	HSCHR6_MHC_MANN:30709280-30710010	NOTEST	0	0	0	0	1	1
ENSG00000226496	ENSG00000226496	LINC00323	21:42513426-42520060	NOTEST	0.178852	0.382674	1.09735	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226497	ENSG00000226497	RP11-406O16.1	6:68936863-69039791	NOTEST	0	0	0	0	1	1
ENSG00000226498	ENSG00000226498	RP11-182B22.2	1:236958609-237067281	NOTEST	0	0	0	0	1	1
ENSG00000226499	ENSG00000226499	RP5-882O7.1	1:45309592-45309754	NOTEST	0	0	0	0	1	1
ENSG00000226500	ENSG00000226500	RP11-196G18.1	1:149725850-149726260	NOTEST	0	0	0	0	1	1
ENSG00000226501	ENSG00000226501	USF1P1	21:34696733-34732168	NOTEST	0.0777899	0	#NAME?	0	1	1
ENSG00000226502	ENSG00000226502	KRT8P27	X:63842996-63844453	NOTEST	0	0	0	0	1	1
ENSG00000226504	ENSG00000226504	TMEM167AP1	Y:23069229-23069448	NOTEST	0	0	0	0	1	1
ENSG00000226505	ENSG00000226505	AC016700.3	2:70316852-70330352	NOTEST	0.218911	0.187035	-0.227037	0	1	1
ENSG00000226506	ENSG00000226506	AC007463.2	2:8026900-8039786	NOTEST	0	0	0	0	1	1
ENSG00000226507	ENSG00000226507	IPMKP1	13:23411164-23412019	NOTEST	0	0	0	0	1	1
ENSG00000226509	ENSG00000226509	AC005588.2	7:153584181-154685995	NOTEST	0	0	0	0	1	1
ENSG00000226513	ENSG00000226513	COL11A2P1	HSCHR6_MHC_SSTO:33211190-33214727	NOTEST	0	0	0	0	1	1
ENSG00000226515	ENSG00000226515	AC004386.3	X:73562547-73562695	NOTEST	0	0	0	0	1	1
ENSG00000226516	ENSG00000226516	FAM138B	2:114334958-114336429	NOTEST	0	0	0	0	1	1
ENSG00000226517	ENSG00000226517	HCG4P7	HSCHR6_MHC_DBB:29846689-29849870	NOTEST	0	0	0	0	1	1
ENSG00000226519	ENSG00000226519	LINC00390	13:44680513-44711372	NOTEST	0	0	0	0	1	1
ENSG00000226521	ENSG00000226521	AC126365.1	17:20619793-20640440	NOTEST	0.0269865	0	#NAME?	0	1	1
ENSG00000226522	ENSG00000226522	AC004744.3	7:18126571-19042039	NOTEST	0	0	0	0	1	1
ENSG00000226523	ENSG00000226523	AC074375.1	2:42721708-42984087	NOTEST	0	0	0	0	1	1
ENSG00000226524	ENSG00000226524	RP1-102H19.8	6:87992695-88109467	NOTEST	0.047904	0.0442318	-0.11506	0	1	1
ENSG00000226526	ENSG00000226526	RP1-37C10.3	1:17300996-17338423	NOTEST	0	0	0	0	1	1
ENSG00000226527	ENSG00000226527	AP000289.6	21:34484004-34496009	NOTEST	0.0124805	0.00878078	-0.50726	0	1	1
ENSG00000226529	ENSG00000226529	MTND1P1	Y:8239703-8240071	NOTEST	0	0	0	0	1	1
ENSG00000226530	ENSG00000226530	RP11-348F1.2	X:51139362-51208513	NOTEST	0.0357952	0	#NAME?	0	1	1
ENSG00000226531	ENSG00000226531	C6orf47	HSCHR6_MHC_MCF:31702357-31704832	NOTEST	0	0	0	0	1	1
ENSG00000226532	ENSG00000226532	RP5-1052M9.1	X:123093082-124097666	NOTEST	0	0	0	0	1	1
ENSG00000226533	ENSG00000226533	BTBD9-AS1	6:38136226-38607924	NOTEST	0	0.0568392	inf	0	1	1
ENSG00000226534	ENSG00000226534	KB-1183D5.16	22:21724352-21726234	NOTEST	0	0	0	0	1	1
ENSG00000226535	ENSG00000226535	RP11-417L14.1	9:109931849-109933429	NOTEST	0.0402085	0.0230151	-0.804923	0	1	1
ENSG00000226536	ENSG00000226536	SETP15	X:15935670-15936754	NOTEST	0	0	0	0	1	1
ENSG00000226537	ENSG00000226537	OR7E33P	13:68485218-68486080	NOTEST	0	0	0	0	1	1
ENSG00000226538	ENSG00000226538	RPL35AP4	HSCHR6_MHC_SSTO:33496509-33496611	NOTEST	0	0	0	0	1	1
ENSG00000226540	ENSG00000226540	GAPDHP73	6:135604669-136037193	NOTEST	0	0	0	0	1	1
ENSG00000226541	ENSG00000226541	RP11-795J1.2	6:46188474-46459709	NOTEST	0	0	0	0	1	1
ENSG00000226542	ENSG00000226542	AC114814.4	2:235993465-235997230	NOTEST	0	0	0	0	1	1
ENSG00000226543	ENSG00000226543	MYL6P1	21:45275770-45276223	NOTEST	0	0	0	0	1	1
ENSG00000226544	ENSG00000226544	RPL7P22	5:71982938-72058554	NOTEST	0.255689	0.318376	0.316341	0	1	1
ENSG00000226545	ENSG00000226545	RP4-633I8.3	1:8412456-8877702	NOTEST	0	0	0	0	1	1
ENSG00000226546	ENSG00000226546	RP11-34H11.5	9:46382964-46383307	NOTEST	0.164762	0.207908	0.335562	0	1	1
ENSG00000226547	ENSG00000226547	SSU72P1	X:113625126-113625709	NOTEST	0	0	0	0	1	1
ENSG00000226548	ENSG00000226548	AC016722.3	2:47043806-47086146	NOTEST	0	0	0	0	1	1
ENSG00000226549	ENSG00000226549	SCDP1	17:20687957-20689038	NOTEST	0.138213	0.0359365	-1.94337	0	1	1
ENSG00000226550	ENSG00000226550	XXbac-BPG254F23.7	HSCHR6_MHC_MCF:32718926-32719761	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226552	ENSG00000226552	RP5-1092L12.2	1:171052705-171054346	NOTEST	0	0	0	0	1	1
ENSG00000226553	ENSG00000226553	AC018735.1	2:187866602-188430487	NOTEST	0	0	0	0	1	1
ENSG00000226554	ENSG00000226554	SOGA2P1	13:71497795-71498587	NOTEST	0	0	0	0	1	1
ENSG00000226555	ENSG00000226555	AGKP1	Y:16634517-16957530	NOTEST	0	0	0	0	1	1
ENSG00000226556	ENSG00000226556	NPM1P49	X:47298134-47299173	NOTEST	0	0	0	0	1	1
ENSG00000226557	ENSG00000226557	TRAF6P1	10:60896384-60897942	NOTEST	0	0	0	0	1	1
ENSG00000226558	ENSG00000226558	RP11-213N20.1	6:43263431-43337216	NOTEST	0	0	0	0	1	1
ENSG00000226560	ENSG00000226560	C2	HSCHR6_MHC_MCF:31942046-31996308	NOTEST	0	0	0	0	1	1
ENSG00000226563	ENSG00000226563	HCG4B	HSCHR6_MHC_MANN:29884569-29887819	NOTEST	0	0	0	0	1	1
ENSG00000226565	ENSG00000226565	RP11-164O23.5	1:207323521-207323626	NOTEST	0	0	0	0	1	1
ENSG00000226566	ENSG00000226566	RP11-436F21.1	9:106124233-106192174	NOTEST	0	0	0	0	1	1
ENSG00000226567	ENSG00000226567	LINC00606	3:10801168-10805877	NOTEST	0	0	0	0	1	1
ENSG00000226570	ENSG00000226570	RP11-505O17.1	1:182924524-182925283	NOTEST	0	0	0	0	1	1
ENSG00000226571	ENSG00000226571	RP11-445F6.2	6:139456248-139613276	NOTEST	0	0	0	0	1	1
ENSG00000226572	ENSG00000226572	SNORD57	20:2632790-2639039	NOTEST	0	0	0	0	1	1
ENSG00000226573	ENSG00000226573	CTA-85E5.7	22:30279143-30573064	NOTEST	0	0	0	0	1	1
ENSG00000226574	ENSG00000226574	SPANXA2-OT1	X:140590842-140738057	NOTEST	0	0.0150867	inf	0	1	1
ENSG00000226575	ENSG00000226575	MYL8P	HSCHR6_MHC_COX:33228366-33228884	NOTEST	0	0	0	0	1	1
ENSG00000226576	ENSG00000226576	RP11-523O18.1	10:49892920-50323554	NOTEST	0	0	0	0	1	1
ENSG00000226577	ENSG00000226577	MICC	6:30382491-30387096	NOTEST	0	0	0	0	1	1
ENSG00000226578	ENSG00000226578	RP11-258F22.1	10:38064298-38073059	NOTEST	0.187762	0.0800726	-1.22953	0	1	1
ENSG00000226579	ENSG00000226579	RP11-351K23.3	X:69340202-69341324	NOTEST	0	0	0	0	1	1
ENSG00000226580	ENSG00000226580	RPL39P40	21:18872996-18873142	NOTEST	0	0	0	0	1	1
ENSG00000226581	ENSG00000226581	RP11-340I6.8	7:63361200-63378372	NOTEST	0	0	0	0	1	1
ENSG00000226582	ENSG00000226582	UBE2V1P5	10:115876905-115877310	NOTEST	0	0	0	0	1	1
ENSG00000226586	ENSG00000226586	HLA-J	HSCHR6_MHC_MCF:30047254-30111187	NOTEST	0	0	0	0	1	1
ENSG00000226587	ENSG00000226587	RP5-905H7.9	7:62787051-62814743	NOTEST	0	0	0	0	1	1
ENSG00000226589	ENSG00000226589	VARS	HSCHR6_MHC_COX:31732661-31751095	NOTEST	0	0	0	0	1	1
ENSG00000226590	ENSG00000226590	UBE2V1P10	9:87774596-87774865	NOTEST	0	0	0	0	1	1
ENSG00000226591	ENSG00000226591	COL11A2P1	HSCHR6_MHC_MANN:33225721-33229258	NOTEST	0	0	0	0	1	1
ENSG00000226592	ENSG00000226592	AC004911.2	7:144966606-144967477	NOTEST	0	0	0	0	1	1
ENSG00000226594	ENSG00000226594	RP11-550C4.6	6:47697562-47708477	NOTEST	0	0	0	0	1	1
ENSG00000226595	ENSG00000226595	KB-288A10.19	22:22819995-22820323	NOTEST	0	0	0	0	1	1
ENSG00000226597	ENSG00000226597	IFNWP9	9:21190652-21191243	NOTEST	0.035369	0	#NAME?	0	1	1
ENSG00000226598	ENSG00000226598	AC017060.1	7:17414490-17598533	NOTEST	0	0	0	0	1	1
ENSG00000226599	ENSG00000226599	RP11-136K14.3	6:150920998-151164799	NOTEST	0	0	0	0	1	1
ENSG00000226600	ENSG00000226600	CT47A9	X:120077420-120080733	NOTEST	0	0	0	0	1	1
ENSG00000226601	ENSG00000226601	RP11-239E10.3	1:223354485-223361496	NOTEST	0	0	0	0	1	1
ENSG00000226603	ENSG00000226603	LY6G6D	HSCHR6_MHC_COX:31662076-31673108	NOTEST	0	0	0	0	1	1
ENSG00000226604	ENSG00000226604	PAPPA-AS2	9:118916082-119164601	NOTEST	0	0	0	0	1	1
ENSG00000226605	ENSG00000226605	AC007098.1	2:62900985-63275775	NOTEST	0	0	0	0	1	1
ENSG00000226609	ENSG00000226609	RP11-276E15.4	9:115511181-115512736	NOTEST	0.112304	0.144243	0.361102	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226610	ENSG00000226610	OR2J4P	HSCHR6_MHC_COX:29145973-29146909	NOTEST	0	0	0	0	1	1
ENSG00000226611	ENSG00000226611	OFD1P2Y	Y:20242566-20258088	NOTEST	0	0	0	0	1	1
ENSG00000226613	ENSG00000226613	GHc-1077H7.2	X:101470279-101581634	NOTEST	0	0	0	0	1	1
ENSG00000226614	ENSG00000226614	SLC39A7	HSCHR6_MHC_COX:33082996-33093846	NOTEST	0	0	0	0	1	1
ENSG00000226615	ENSG00000226615	AC018696.1	2:91635930-91636149	NOTEST	0	0	0	0	1	1
ENSG00000226616	ENSG00000226616	OR52M2P	11:4536195-4537154	NOTEST	0	0	0	0	1	1
ENSG00000226617	ENSG00000226617	RPL21P110	13:73277830-73278276	NOTEST	0	0	0	0	1	1
ENSG00000226618	ENSG00000226618	PRRC2A	HSCHR6_MHC_MANN:31627936-31645035	NOTEST	0	0	0	0	1	1
ENSG00000226619	ENSG00000226619	RP11-301J16.7	13:19520894-19636858	NOTEST	0	0	0	0	1	1
ENSG00000226620	ENSG00000226620	LINC00343	13:106356628-106416789	NOTEST	0	0	0	0	1	1
ENSG00000226621	ENSG00000226621	AC083855.5	3:11313994-11766453	NOTEST	0	0	0	0	1	1
ENSG00000226622	ENSG00000226622	AC092155.4	2:62817389-62889789	NOTEST	0	0.0430181	inf	0	1	1
ENSG00000226624	ENSG00000226624	CTA-351J1.1	7:105245513-105517050	NOTEST	0	0	0	0	1	1
ENSG00000226625	ENSG00000226625	RP11-290L7.2	9:39072763-39288312	NOTEST	0.0556816	0.0113308	-2.29695	0	1	1
ENSG00000226626	ENSG00000226626	RP11-315I14.5	9:23681891-23682660	NOTEST	0	0	0	0	1	1
ENSG00000226627	ENSG00000226627	SHANK2-AS1	11:70313960-70963623	NOTEST	0	0	0	0	1	1
ENSG00000226629	ENSG00000226629	LINC00974	17:39705857-39710747	NOTEST	0	0	0	0	1	1
ENSG00000226631	ENSG00000226631	SLC9A3P3	10:51780941-51827563	NOTEST	0	0	0	0	1	1
ENSG00000226632	ENSG00000226632	UBE2V1P1	20:3229950-3388272	NOTEST	0	0.084515	inf	0	1	1
ENSG00000226633	ENSG00000226633	PPIAP28	13:20753116-20753601	NOTEST	0	0	0	0	1	1
ENSG00000226634	ENSG00000226634	DDAH2	HSCHR6_MHC_COX:31682227-31694945	NOTEST	0	0	0	0	1	1
ENSG00000226636	ENSG00000226636	RP5-1049N15.2	7:121799353-121802297	NOTEST	0.0176486	0	#NAME?	0	1	1
ENSG00000226640	ENSG00000226640	RP11-21J7.1	1:193648023-193696165	NOTEST	0	0	0	0	1	1
ENSG00000226641	ENSG00000226641	RP13-13A3.1	X:41181853-41182364	NOTEST	0	0	0	0	1	1
ENSG00000226642	ENSG00000226642	ACTG1P12	3:12045875-12232900	NOTEST	0	0	0	0	1	1
ENSG00000226643	ENSG00000226643	RP11-358H9.1	1:222626081-222628047	NOTEST	0	0	0	0	1	1
ENSG00000226644	ENSG00000226644	RP11-128M1.1	20:2187862-2193797	NOTEST	0	0.060572	inf	0	1	1
ENSG00000226645	ENSG00000226645	AP006216.10	11:116644104-116644921	NOTEST	0	0	0	0	1	1
ENSG00000226646	ENSG00000226646	RPL7P37	10:35986227-35986965	NOTEST	0	0	0	0	1	1
ENSG00000226647	ENSG00000226647	RP11-336A10.2	10:5726800-5805703	NOTEST	0.124307	0.0667694	-0.896645	0	1	1
ENSG00000226648	ENSG00000226648	RP1-1J6.2	20:39657457-39946312	NOTEST	0.121293	0.0509347	-1.25177	0	1	1
ENSG00000226649	ENSG00000226649	AC019118.4	2:3160526-3161568	NOTEST	0	0	0	0	1	1
ENSG00000226650	ENSG00000226650	KIF4B	5:154393259-154397685	NOTEST	0.080359	0.0842828	0.0687791	0	1	1
ENSG00000226651	ENSG00000226651	CLIC1	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000226652	ENSG00000226652	PSMD10P2	3:186478892-186479564	NOTEST	0.0546025	0	#NAME?	0	1	1
ENSG00000226653	ENSG00000226653	OR13Z1P	1:146890776-146891610	NOTEST	0	0	0	0	1	1
ENSG00000226655	ENSG00000226655	AC096732.2	4:124571421-124851561	NOTEST	0	0	0	0	1	1
ENSG00000226657	ENSG00000226657	SAR1P1	HSCHR6_MHC_COX:29040960-29041556	NOTEST	0	0	0	0	1	1
ENSG00000226658	ENSG00000226658	AC005037.4	2:201773695-201950473	NOTEST	0	0	0	0	1	1
ENSG00000226660	ENSG00000226660	TRBV2	7:142000746-142001255	NOTEST	0	0	0	0	1	1
ENSG00000226661	ENSG00000226661	RP5-1139I1.2	X:118490263-118527558	NOTEST	0	0	0	0	1	1
ENSG00000226662	ENSG00000226662	CHMP1AP1	1:28013320-28013982	NOTEST	0	0	0	0	1	1
ENSG00000226663	ENSG00000226663	MTND4P10	1:235703352-235705006	NOTEST	0	0	0	0	1	1
ENSG00000226664	ENSG00000226664	RP4-745E8.2	1:20617411-20681387	NOTEST	0	0	0	0	1	1

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ENSG00000226665	ENSG00000226665	SSR1P2	13:75710290-75711077	NOTEST	0	0	0	0	1	1
ENSG00000226666	ENSG00000226666	HSPA9P1	2:222826455-222828484	NOTEST	0.0369464	0.0615967	0.737421	0	1	1
ENSG00000226667	ENSG00000226667	RP11-292F22.5	10:47570512-47573872	NOTEST	0	0	0	0	1	1
ENSG00000226668	ENSG00000226668	RP11-526D8.7	9:95571669-95661890	NOTEST	0	0	0	0	1	1
ENSG00000226669	ENSG00000226669	RP11-509J21.4	9:3674545-3691814	NOTEST	0	0	0	0	1	1
ENSG00000226670	ENSG00000226670	BCAS2P3	13:79740253-79741020	NOTEST	0	0	0	0	1	1
ENSG00000226671	ENSG00000226671	AC005008.3	7:80804823-80828431	NOTEST	0	0	0	0	1	1
ENSG00000226673	ENSG00000226673	LINC01108	6:14280357-14285376	NOTEST	0	0	0	0	1	1
ENSG00000226675	ENSG00000226675	RP11-666A1.3	1:148598397-148599531	NOTEST	0.58397	0.34032	-0.779	0	1	1
ENSG00000226676	ENSG00000226676	RP11-589B3.6	10:81388512-81391944	NOTEST	0	0	0	0	1	1
ENSG00000226677	ENSG00000226677	IGBP1P1	14:35390063-35498773	NOTEST	0	0	0	0	1	1
ENSG00000226679	ENSG00000226679	RP13-43E11.1	X:37208527-38548169	NOTEST	0.20536	0.227558	0.148079	0	1	1
ENSG00000226680	ENSG00000226680	RP11-61D3.1	7:122709302-122743643	NOTEST	0	0	0	0	1	1
ENSG00000226681	ENSG00000226681	AC020595.1	2:182286880-182290476	NOTEST	0	0	0	0	1	1
ENSG00000226683	ENSG00000226683	PWWP2AP1	13:81228889-81231162	NOTEST	0	0	0	0	1	1
ENSG00000226684	ENSG00000226684	RP3-418C23.2	6:97731178-97757924	NOTEST	0	0	0	0	1	1
ENSG00000226685	ENSG00000226685	CT47A12	X:120011343-120066151	NOTEST	0	0	0	0	1	1
ENSG00000226686	ENSG00000226686	AC012309.5	19:37742813-37756437	NOTEST	0.205727	0.164107	-0.326096	0	1	1
ENSG00000226687	ENSG00000226687	LINC01015	HSCHR6_MHC_QBL:29497089-29501238	NOTEST	0	0	0	0	1	1
ENSG00000226691	ENSG00000226691	HLA-Z	HSCHR6_MHC_MCF:32897629-32897704	NOTEST	0	0	0	0	1	1
ENSG00000226693	ENSG00000226693	RP11-412H9.1	1:219054941-219055992	NOTEST	0	0	0	0	1	1
ENSG00000226694	ENSG00000226694	RP11-69C17.2	10:2114038-2123291	NOTEST	0	0	0	0	1	1
ENSG00000226695	ENSG00000226695	ANKRD20A10P	13:25324794-25326309	NOTEST	0.0421612	0.0804817	0.932747	0	1	1
ENSG00000226698	ENSG00000226698	RP1-50O24.6	1:27202623-27216788	NOTEST	0	0	0	0	1	1
ENSG00000226699	ENSG00000226699	RP11-122K13.7	10:135093134-135166187	NOTEST	0	0	0	0	1	1
ENSG00000226700	ENSG00000226700	MTND4P25	2:83042107-83042640	NOTEST	0	0	0	0	1	1
ENSG00000226701	ENSG00000226701	RP11-570G20.1	10:73856277-73995618	NOTEST	0.0319825	0.102051	1.67394	0	1	1
ENSG00000226702	ENSG00000226702	AC011306.2	2:56179292-56613308	NOTEST	0	0	0	0	1	1
ENSG00000226703	ENSG00000226703	NPM1P4	13:28270529-28271341	NOTEST	0	0	0	0	1	1
ENSG00000226704	ENSG00000226704	HSPA1L	HSCHR6_MHC_APD:31788759-31794206	NOTEST	0	0	0	0	1	1
ENSG00000226705	ENSG00000226705	SDCBPP1	10:6319649-6377944	NOTEST	0	0	0	0	1	1
ENSG00000226706	ENSG00000226706	RP11-426A6.5	9:138387026-138398293	NOTEST	0.410977	0.280551	-0.550796	0	1	1
ENSG00000226707	ENSG00000226707	RP11-719J20.1	6:49791424-49792495	NOTEST	0	0	0	0	1	1
ENSG00000226708	ENSG00000226708	AC073409.1	2:124200841-124202021	NOTEST	0	0.105918	inf	0	1	1
ENSG00000226709	ENSG00000226709	FGF12-AS3	3:191857183-192485553	NOTEST	0	0	0	0	1	1
ENSG00000226710	ENSG00000226710	C6orf48	HSCHR6_MHC_COX:31789756-31794910	NOTEST	0	0	0	0	1	1
ENSG00000226713	ENSG00000226713	MICD	HSCHR6_MHC_DBB:29928529-29930192	NOTEST	0	0	0	0	1	1
ENSG00000226714	ENSG00000226714	RPL13P	HSCHR6_MHC_COX:28828043-28831792	NOTEST	0	0	0	0	1	1
ENSG00000226715	ENSG00000226715	RP11-411H5.1	1:102189297-102195170	NOTEST	0	0	0	0	1	1
ENSG00000226716	ENSG00000226716	AL589986.2	1:152095009-152097556	NOTEST	0	0	0	0	1	1
ENSG00000226717	ENSG00000226717	RP11-87N24.2	9:10613201-10620420	NOTEST	0	0	0	0	1	1
ENSG00000226718	ENSG00000226718	SNRPGP8	2:228643225-228643451	NOTEST	0	0	0	0	1	1
ENSG00000226721	ENSG00000226721	EEF1DP2	9:95571669-95661890	NOTEST	0.0417938	0.128948	1.62543	0	1	1
ENSG00000226722	ENSG00000226722	LINC00424	13:22446908-22449705	NOTEST	0	0	0	0	1	1

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ENSG00000226723	ENSG00000226723	RP11-142L4.3	1:192215837-192216617	NOTEST	0.589525	0.545918	-0.11087	0	1	1
ENSG00000226724	ENSG00000226724	RP11-795A2.3	3:186416308-186426363	NOTEST	0	0	0	0	1	1
ENSG00000226725	ENSG00000226725	RP11-493K23.1	X:72218226-72222695	NOTEST	0	0	0	0	1	1
ENSG00000226726	ENSG00000226726	TMEM256P2	2:222282746-222439174	NOTEST	0	0	0	0	1	1
ENSG00000226727	ENSG00000226727	HLA-T	HSCHR6_MHC_MANN:29855210-29856342	NOTEST	0	0	0	0	1	1
ENSG00000226729	ENSG00000226729	RPL35AP30	12:120397227-120397558	NOTEST	0	0	0	0	1	1
ENSG00000226732	ENSG00000226732	ZDHHC20P2	HSCHR6_MHC_MANN:31391240-31391669	NOTEST	0	0	0	0	1	1
ENSG00000226733	ENSG00000226733	RP11-397G17.1	6:50061423-50066995	NOTEST	0	0	0	0	1	1
ENSG00000226734	ENSG00000226734	SNRPGP12	10:111898971-111899184	NOTEST	0	0	0	0	1	1
ENSG00000226736	ENSG00000226736	HCG4P7	HSCHR6_MHC_SSTO:29845569-29848744	NOTEST	0	0	0	0	1	1
ENSG00000226738	ENSG00000226738	CTA-384D8.31	22:50984843-50986081	NOTEST	0	0	0	0	1	1
ENSG00000226739	ENSG00000226739	RP11-347L18.1	6:164767521-164769677	NOTEST	0	0	0	0	1	1
ENSG00000226740	ENSG00000226740	RP11-31L23.3	10:102849077-102899468	NOTEST	0	0	0	0	1	1
ENSG00000226741	ENSG00000226741	CTA-929C8.6	22:27703443-27714499	NOTEST	0	0	0	0	1	1
ENSG00000226744	ENSG00000226744	AC079781.5	7:97481429-97501854	NOTEST	0	0	0	0	1	1
ENSG00000226745	ENSG00000226745	RP11-115D7.3	1:40598435-40599120	NOTEST	0	0	0	0	1	1
ENSG00000226746	ENSG00000226746	SMCR5	17:17584786-17740325	NOTEST	0.0423111	0.0160921	-1.39469	0	1	1
ENSG00000226747	ENSG00000226747	AC007966.1	2:186584600-186698017	NOTEST	0	0	0	0	1	1
ENSG00000226750	ENSG00000226750	RP11-513D4.3	1:242246287-242687998	NOTEST	0	0	0	0	1	1
ENSG00000226751	ENSG00000226751	AF127936.5	21:16134030-16135411	NOTEST	0	0	0	0	1	1
ENSG00000226753	ENSG00000226753	RP11-212D3.2	X:75108534-75108723	NOTEST	0	0	0	0	1	1
ENSG00000226755	ENSG00000226755	VPS25P1	1:118092036-118092544	NOTEST	0.0440763	0	#NAME?	0	1	1
ENSG00000226756	ENSG00000226756	AC007365.3	2:64858754-64978139	NOTEST	0.0325764	0.101748	1.64311	0	1	1
ENSG00000226757	ENSG00000226757	AC079341.1	4:122680087-122687962	NOTEST	0	0	0	0	1	1
ENSG00000226758	ENSG00000226758	DISC1-IT1	1:231664398-232177018	NOTEST	0	0.0750489	inf	0	1	1
ENSG00000226759	ENSG00000226759	DAB1-AS1	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000226761	ENSG00000226761	TAS2R46	12:10977558-11324212	NOTEST	0	0	0	0	1	1
ENSG00000226762	ENSG00000226762	RP11-298E9.6	10:3282562-3299402	NOTEST	0	0	0	0	1	1
ENSG00000226763	ENSG00000226763	SRRM5	19:44100543-44124026	NOTEST	0.26206	0.141235	-0.891797	0	1	1
ENSG00000226764	ENSG00000226764	AC010145.4	2:16137170-16245963	NOTEST	0	0	0	0	1	1
ENSG00000226765	ENSG00000226765	RP11-694D5.1	3:167967309-168548387	NOTEST	0	0.015097	inf	0	1	1
ENSG00000226766	ENSG00000226766	FABP7P1	1:243419319-244014381	NOTEST	0	0	0	0	1	1
ENSG00000226767	ENSG00000226767	RP11-328P23.3	7:64973685-64973857	NOTEST	0	0	0	0	1	1
ENSG00000226768	ENSG00000226768	LINC01149	HSCHR6_MHC_SSTO:31402325-31407629	NOTEST	0	0	0	0	1	1
ENSG00000226769	ENSG00000226769	GAPDHP54	20:45523262-45817492	NOTEST	0	0	0	0	1	1
ENSG00000226770	ENSG00000226770	AC000124.1	7:127116936-127125858	NOTEST	0	0	0	0	1	1
ENSG00000226771	ENSG00000226771	AP001136.2	21:22370632-22915650	NOTEST	0	0	0	0	1	1
ENSG00000226772	ENSG00000226772	CTA-747E2.10	22:29469065-29564321	NOTEST	0	0.031442	inf	0	1	1
ENSG00000226773	ENSG00000226773	RP4-775D17.1	1:92668704-92669548	NOTEST	0	0	0	0	1	1
ENSG00000226774	ENSG00000226774	RP11-654E17.2	X:23352132-23422489	NOTEST	0	0	0	0	1	1
ENSG00000226776	ENSG00000226776	KRTAP3-4P	17:39160732-39161012	NOTEST	0	0	0	0	1	1
ENSG00000226777	ENSG00000226777	KIAA0125	14:106383837-106391825	NOTEST	0	0	0	0	1	1
ENSG00000226779	ENSG00000226779	NAALADL2-AS2	3:174156362-175523428	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226780	ENSG00000226780	RP11-38J22.3	1:206214525-206223548	NOTEST	0	0	0	0	1	1
ENSG00000226781	ENSG00000226781	TBCAP1	X:31115793-33357558	NOTEST	0	0.28739	inf	0	1	1
ENSG00000226782	ENSG00000226782	RP11-706D8.3	3:177055415-177066954	NOTEST	0	0	0	0	1	1
ENSG00000226783	ENSG00000226783	TLK1P1	9:125448211-125450651	NOTEST	0	0	0	0	1	1
ENSG00000226785	ENSG00000226785	AC073218.1	2:34608854-34860407	NOTEST	0	0	0	0	1	1
ENSG00000226786	ENSG00000226786	RP1-167F1.2	6:19535174-19840915	NOTEST	0.0476841	0.0336598	-0.50248	0	1	1
ENSG00000226788	ENSG00000226788	RING1	HSCHR6_MHC_COX:33097899-33102125	NOTEST	0	0	0	0	1	1
ENSG00000226789	ENSG00000226789	AC110926.4	2:128004833-128007658	NOTEST	0.010116	0	#NAME?	0	1	1
ENSG00000226790	ENSG00000226790	HNRNPA3P1	10:44282859-44285865	NOTEST	0.0693001	0.0558694	-0.310799	0	1	1
ENSG00000226791	ENSG00000226791	AC109826.1	2:99378400-99388543	NOTEST	0.0645925	0.0980815	0.602613	0	1	1
ENSG00000226792	ENSG00000226792	LINC00371	13:51656983-51746524	NOTEST	0.0235996	0	#NAME?	0	1	1
ENSG00000226794	ENSG00000226794	MTND1P20	10:71355242-71356192	NOTEST	0	0	0	0	1	1
ENSG00000226795	ENSG00000226795	SAR1P1	HSCHR6_MHC_QBL:29044351-29044947	NOTEST	0	0	0	0	1	1
ENSG00000226796	ENSG00000226796	OR2H5P	HSCHR6_MHC_COX:29519994-29597568	NOTEST	0	0	0	0	1	1
ENSG00000226797	ENSG00000226797	AC015923.1	17:61086916-61509572	NOTEST	0	0	0	0	1	1
ENSG00000226798	ENSG00000226798	RP11-289F5.1	9:83484672-83486210	NOTEST	0.0678831	0.0338238	-1.00501	0	1	1
ENSG00000226799	ENSG00000226799	XXbac-BPG308J9.3	HSCHR6_MHC_APD:29234761-29234916	NOTEST	0	0	0	0	1	1
ENSG00000226800	ENSG00000226800	CACTIN-AS1	19:3607244-3626813	NOTEST	0.344371	0.272086	-0.339904	0	1	1
ENSG00000226801	ENSG00000226801	OSTCP8	9:33921690-34048947	NOTEST	0	0.0763881	inf	0	1	1
ENSG00000226802	ENSG00000226802	RP11-72I18.1	X:127457597-127734446	NOTEST	0	0	0	0	1	1
ENSG00000226803	ENSG00000226803	RP11-203B9.4	6:56951641-57087078	NOTEST	0.110216	0.160863	0.545501	0	1	1
ENSG00000226804	ENSG00000226804	RP4-675G8.3	1:44616265-44617425	NOTEST	0	0	0	0	1	1
ENSG00000226806	ENSG00000226806	AC011893.3	2:136545409-136594750	NOTEST	0	0	0	0	1	1
ENSG00000226807	ENSG00000226807	MROH5	8:142443928-142517330	NOTEST	0	0	0	0	1	1
ENSG00000226808	ENSG00000226808	LINC00840	10:44354858-44390881	NOTEST	0	0	0	0	1	1
ENSG00000226810	ENSG00000226810	RP11-45H22.1	5:54104037-54168379	NOTEST	0	0	0	0	1	1
ENSG00000226812	ENSG00000226812	RP5-881L22.5	20:42965625-42983825	NOTEST	0.437756	0.350013	-0.322717	0	1	1
ENSG00000226813	ENSG00000226813	AC114813.1	2:126867675-126875562	NOTEST	0	0	0	0	1	1
ENSG00000226814	ENSG00000226814	RP3-419C19.2	1:192769700-192770271	NOTEST	0	0	0	0	1	1
ENSG00000226816	ENSG00000226816	AC005082.12	7:23245631-23247664	NOTEST	0	0	0	0	1	1
ENSG00000226818	ENSG00000226818	SLC6A6P1	21:20616859-20618709	NOTEST	0	0	0	0	1	1
ENSG00000226819	ENSG00000226819	MEIS1-AS3	2:66653866-66801001	NOTEST	0	0	0	0	1	1
ENSG00000226820	ENSG00000226820	RP11-747I9.1	X:65657186-65660510	NOTEST	0	0	0	0	1	1
ENSG00000226822	ENSG00000226822	RP11-356N1.2	1:108614103-108617141	NOTEST	0	0	0	0	1	1
ENSG00000226823	ENSG00000226823	SUGT1P	9:33503652-33510709	NOTEST	0.0486935	0.107204	1.13856	0	1	1
ENSG00000226824	ENSG00000226824	RP4-756H11.3	7:66093867-66309813	NOTEST	0.46632	0.247255	-0.915323	0	1	1
ENSG00000226825	ENSG00000226825	RP11-363D24.1	9:110182564-110193083	NOTEST	0	0	0	0	1	1
ENSG00000226826	ENSG00000226826	HLA-DPB1	HSCHR6_MHC_SSTO:33171991-33194624	NOTEST	0	0	0	0	1	1
ENSG00000226827	ENSG00000226827	NPM1P11	7:11221358-11871824	NOTEST	0	0	0	0	1	1
ENSG00000226828	ENSG00000226828	RP11-278H7.1	1:244080703-244210619	NOTEST	0	0	0	0	1	1
ENSG00000226829	ENSG00000226829	RP5-945F2.3	7:67615269-67753220	NOTEST	0	0	0	0	1	1
ENSG00000226831	ENSG00000226831	MED15P3	2:132152789-132153115	NOTEST	0	0	0	0	1	1
ENSG00000226832	ENSG00000226832	OR2B3	HSCHR6_MHC_SSTO:29054010-29055116	NOTEST	0	0	0	0	1	1
ENSG00000226833	ENSG00000226833	AC097724.3	2:28931818-28959071	NOTEST	0.309665	0.102766	-1.59134	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226834	ENSG00000226834	XXbac-BPG248L24.10	HSCHR6_MHC_SSTO:31268478-31269213	NOTEST	0	0	0	0	1	1
ENSG00000226835	ENSG00000226835	RP11-148B18.3	1:94798822-94800404	NOTEST	0	0	0	0	1	1
ENSG00000226836	ENSG00000226836	RP11-77B22.1	8:15800633-15801041	NOTEST	0	0	0	0	1	1
ENSG00000226837	ENSG00000226837	HMGB1P32	X:97677135-97677807	NOTEST	0	0	0	0	1	1
ENSG00000226838	ENSG00000226838	AC096582.8	7:45855814-45860663	NOTEST	0	0	0	0	1	1
ENSG00000226839	ENSG00000226839	MTND6P11	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000226840	ENSG00000226840	PAICSP3	6:74037246-74038740	NOTEST	0	0	0	0	1	1
ENSG00000226841	ENSG00000226841	MCCD1	HSCHR6_MHC_SSTO:31486440-31504572	NOTEST	0	0	0	0	1	1
ENSG00000226842	ENSG00000226842	RP11-166N17.3	10:32555216-32667726	NOTEST	0	0.023775	inf	0	1	1
ENSG00000226843	ENSG00000226843	RP11-2P2.1	1:208428634-208428721	NOTEST	0	0	0	0	1	1
ENSG00000226844	ENSG00000226844	OR2U2P	HSCHR6_MHC_COX:29232931-29233891	NOTEST	0	0	0	0	1	1
ENSG00000226845	ENSG00000226845	EEF1GP3	3:40637697-40638985	NOTEST	0	0	0	0	1	1
ENSG00000226846	ENSG00000226846	LINC00348	13:71589272-71742549	NOTEST	0	0	0	0	1	1
ENSG00000226847	ENSG00000226847	PRPS1P1	2:164606082-165208733	NOTEST	0	0	0	0	1	1
ENSG00000226849	ENSG00000226849	RP4-635E18.7	1:11126674-11162157	NOTEST	0.163457	0.18311	0.163801	0	1	1
ENSG00000226850	ENSG00000226850	ATP6V1G2	HSCHR6_MHC_MANN:31536012-31554120	NOTEST	0	0	0	0	1	1
ENSG00000226851	ENSG00000226851	AC004112.4	7:111846642-112049678	NOTEST	0	0	0	0	1	1
ENSG00000226854	ENSG00000226854	RP11-212D3.4	X:75122939-75124693	NOTEST	0	0	0	0	1	1
ENSG00000226855	ENSG00000226855	RP11-350G8.3	1:154349441-154351749	NOTEST	0.0208611	0.0769368	1.88286	0	1	1
ENSG00000226856	ENSG00000226856	AC093901.1	2:118889703-118943962	NOTEST	0	0	0	0	1	1
ENSG00000226857	ENSG00000226857	DUTP3	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000226858	ENSG00000226858	ZFP57	HSCHR6_MHC_COX:29636766-29645520	NOTEST	0	0	0	0	1	1
ENSG00000226859	ENSG00000226859	RP11-48F14.2	3:186172770-186211450	NOTEST	0	0.0893436	inf	0	1	1
ENSG00000226860	ENSG00000226860	AC109638.1	2:82836775-82837101	NOTEST	0	0	0	0	1	1
ENSG00000226861	ENSG00000226861	RP5-1119O21.2	10:8340859-8343630	NOTEST	0	0	0	0	1	1
ENSG00000226862	ENSG00000226862	RP11-569A11.1	1:202317826-202679545	NOTEST	0.102822	0	#NAME?	0	1	1
ENSG00000226863	ENSG00000226863	SHROOM2P1	Y:14649707-14656818	NOTEST	0	0	0	0	1	1
ENSG00000226864	ENSG00000226864	ATE1-AS1	10:123499938-123711480	NOTEST	0.0380842	0.0235904	-0.690991	0	1	1
ENSG00000226867	ENSG00000226867	RP13-77O11.8	X:52810500-52814830	NOTEST	0	0	0	0	1	1
ENSG00000226868	ENSG00000226868	RP11-122M14.3	1:211889269-211898744	NOTEST	0	0	0	0	1	1
ENSG00000226870	ENSG00000226870	BX276092.2	X:70938991-70939460	NOTEST	0	0	0	0	1	1
ENSG00000226871	ENSG00000226871	AC135178.7	17:8213558-8225829	NOTEST	0	0	0	0	1	1
ENSG00000226872	ENSG00000226872	AC002472.11	22:21353392-21399306	NOTEST	0	0	0	0	1	1
ENSG00000226873	ENSG00000226873	CDY14P	Y:25820525-25821539	NOTEST	0	0	0	0	1	1
ENSG00000226874	ENSG00000226874	AC005154.8	7:30536236-30673649	NOTEST	0.142473	0.0510748	-1.48001	0	1	1
ENSG00000226875	ENSG00000226875	ZNF877P	20:21246491-21247103	NOTEST	0	0	0	0	1	1
ENSG00000226876	ENSG00000226876	RP11-36N20.1	1:245912641-246670614	NOTEST	0	0	0	0	1	1
ENSG00000226877	ENSG00000226877	RP11-575L7.2	9:86444570-86536342	NOTEST	0	0	0	0	1	1
ENSG00000226878	ENSG00000226878	GSTM3P2	2:159825145-160089170	NOTEST	0	0	0	0	1	1
ENSG00000226879	ENSG00000226879	RPL32P1	HSCHR6_MHC_DBB:33010287-33032912	NOTEST	0	0	0	0	1	1
ENSG00000226880	ENSG00000226880	XX-2136C48.7	10:135505634-135505917	NOTEST	0	0	0	0	1	1
ENSG00000226881	ENSG00000226881	H3F3AP5	X:50648437-50648866	NOTEST	0	0	0	0	1	1
ENSG00000226882	ENSG00000226882	GNL1	HSCHR6_MHC_SSTO:30500572-30522918	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226883	ENSG00000226883	RP4-782L23.2	1:59762309-60254854	NOTEST	0	0	0	0	1	1
ENSG00000226884	ENSG00000226884	AC016727.3	2:61816632-61816798	NOTEST	0	0	0	0	1	1
ENSG00000226885	ENSG00000226885	KB-1183D5.9	22:21622449-21623192	NOTEST	0	0.062693	inf	0	1	1
ENSG00000226886	ENSG00000226886	AC093787.1	2:132795359-132795566	NOTEST	0	0	0	0	1	1
ENSG00000226887	ENSG00000226887	ERVMER34-1	4:53588784-53617807	NOTEST	0.129225	0.275906	1.0943	0	1	1
ENSG00000226888	ENSG00000226888	RP11-561G1.3	10:60848460-60848799	NOTEST	0	0	0	0	1	1
ENSG00000226889	ENSG00000226889	RP11-474I16.8	1:161735114-161736017	NOTEST	0.0367698	0	#NAME?	0	1	1
ENSG00000226890	ENSG00000226890	LA16c-395F10.1	16:1662325-1752281	NOTEST	0	0	0	0	1	1
ENSG00000226891	ENSG00000226891	RP11-182I10.3	1:65437907-65468159	NOTEST	0.0608667	0	#NAME?	0	1	1
ENSG00000226892	ENSG00000226892	C6orf10	HSCHR6_MHC_DBB:32236324-32315209	NOTEST	0	0	0	0	1	1
ENSG00000226893	ENSG00000226893	HLA-H	HSCHR6_MHC_COX:29846610-29849789	NOTEST	0	0	0	0	1	1
ENSG00000226896	ENSG00000226896	OR2I1P	HSCHR6_MHC_APD:29521109-29522057	NOTEST	0	0	0	0	1	1
ENSG00000226897	ENSG00000226897	RP11-435B5.6	1:143498343-143517299	NOTEST	0	0	0	0	1	1
ENSG00000226898	ENSG00000226898	UBD	HSCHR6_MHC_APD:29523503-29601074	NOTEST	0	0	0	0	1	1
ENSG00000226899	ENSG00000226899	RP11-298J20.3	10:126605711-126849739	NOTEST	0	0	0	0	1	1
ENSG00000226900	ENSG00000226900	RP11-432J24.5	10:134325129-134331695	NOTEST	0	0.0710003	inf	0	1	1
ENSG00000226902	ENSG00000226902	CHCHD2P1	X:122918858-122919301	NOTEST	0	0	0	0	1	1
ENSG00000226903	ENSG00000226903	LINC00354	13:112554298-112555490	NOTEST	0	0	0	0	1	1
ENSG00000226904	ENSG00000226904	RP11-561O23.8	9:70843566-70844228	NOTEST	0	0.211505	inf	0	1	1
ENSG00000226905	ENSG00000226905	AC005040.3	2:107579648-107580130	NOTEST	0	0	0	0	1	1
ENSG00000226906	ENSG00000226906	TTTY4	Y:25082601-25119431	NOTEST	0	0	0	0	1	1
ENSG00000226907	ENSG00000226907	CT45A6	X:134962848-134971244	NOTEST	0	0	0	0	1	1
ENSG00000226908	ENSG00000226908	HIST1H2BPS3	13:22057972-22058313	NOTEST	0	0	0	0	1	1
ENSG00000226912	ENSG00000226912	ISCA2P1	22:27040852-27041300	NOTEST	0	0	0	0	1	1
ENSG00000226913	ENSG00000226913	BSN-AS2	3:49586738-49591799	NOTEST	0.00610644	0.0533086	3.12596	0	1	1
ENSG00000226914	ENSG00000226914	PPP1R2P1	HSCHR6_MHC_QBL:32737203-32776334	NOTEST	0	0	0	0	1	1
ENSG00000226915	ENSG00000226915	AC068137.13	2:131051394-131051978	NOTEST	0	0	0	0	1	1
ENSG00000226916	ENSG00000226916	WDR46	HSCHR6_MHC_DBB:33224809-33245105	NOTEST	0	0	0	0	1	1
ENSG00000226917	ENSG00000226917	RP11-328M4.3	6:41462590-41570122	NOTEST	0	0	0	0	1	1
ENSG00000226918	ENSG00000226918	AC010086.1	Y:23473153-23480781	NOTEST	0	0	0	0	1	1
ENSG00000226919	ENSG00000226919	RP11-80B9.1	1:240928856-241520530	NOTEST	0	0	0	0	1	1
ENSG00000226920	ENSG00000226920	RP5-1068B5.3	1:229576030-229576767	NOTEST	0.422664	0.150831	-1.48658	0	1	1
ENSG00000226921	ENSG00000226921	LINC00454	13:114580580-114586624	NOTEST	0	0	0	0	1	1
ENSG00000226923	ENSG00000226923	MCCD1	HSCHR6_MHC_COX:31483951-31502076	NOTEST	0	0	0	0	1	1
ENSG00000226925	ENSG00000226925	AC007271.3	2:102681003-102798568	NOTEST	0	0	0	0	1	1
ENSG00000226926	ENSG00000226926	AC010423.1	5:102766106-102862319	NOTEST	0.264055	0.343834	0.380872	0	1	1
ENSG00000226927	ENSG00000226927	RP11-302I18.3	1:220533072-220533525	NOTEST	0	0	0	0	1	1
ENSG00000226928	ENSG00000226928	RPS14P4	2:111953539-112268567	NOTEST	0.113248	0	#NAME?	0	1	1
ENSG00000226929	ENSG00000226929	CT47A11	X:120067699-120071012	NOTEST	0	0	0	0	1	1
ENSG00000226930	ENSG00000226930	GTF2IP2	21:14815693-14861497	NOTEST	0	0	0	0	1	1
ENSG00000226931	ENSG00000226931	OR2J1	HSCHR6_MHC_MCF:29068533-29069806	NOTEST	0	0	0	0	1	1
ENSG00000226932	ENSG00000226932	OR2U2P	HSCHR6_MHC_SSTO:29236302-29237262	NOTEST	0	0	0	0	1	1

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ENSG00000226933	ENSG00000226933	NRBF2P2	3:46058515-46069234	NOTEST	0	0	0	0	1	1
ENSG00000226935	ENSG00000226935	LINC00161	21:29811666-30047170	NOTEST	0	0	0	0	1	1
ENSG00000226936	ENSG00000226936	B3GALT4	HSCHR6_MHC_COX:33166522-33168208	NOTEST	0	0	0	0	1	1
ENSG00000226937	ENSG00000226937	CEP164P1	10:45493145-45676875	NOTEST	0	0.00876433	inf	0	1	1
ENSG00000226938	ENSG00000226938	RP11-117D22.1	1:53814159-53814905	NOTEST	0	0	0	0	1	1
ENSG00000226939	ENSG00000226939	AC062021.1	2:140123734-140136717	NOTEST	0	0	0	0	1	1
ENSG00000226940	ENSG00000226940	MCCD1P1	HSCHR6_MHC_MANN:29866339-29867202	NOTEST	0	0	0	0	1	1
ENSG00000226941	ENSG00000226941	RBMY1J	Y:24454969-24564028	NOTEST	0	0	0	0	1	1
ENSG00000226942	ENSG00000226942	IL9RP3	16:61552-88321	NOTEST	0.0457259	0.0378658	-0.272118	0	1	1
ENSG00000226943	ENSG00000226943	ALG1L5P	7:6963434-6970466	NOTEST	0	0	0	0	1	1
ENSG00000226945	ENSG00000226945	RP11-564A8.4	1:207077730-207096592	NOTEST	0.0337612	0.432141	3.67806	0	1	1
ENSG00000226946	ENSG00000226946	AC062022.1	2:162272604-162841792	NOTEST	0	0	0	0	1	1
ENSG00000226947	ENSG00000226947	RP1-52J10.9	1:152616868-152617193	NOTEST	0	0	0	0	1	1
ENSG00000226948	ENSG00000226948	RPS4XP2	20:4610072-4610865	NOTEST	0	0	0	0	1	1
ENSG00000226949	ENSG00000226949	OR6K5P	1:158711935-158713205	NOTEST	0	0	0	0	1	1
ENSG00000226952	ENSG00000226952	RP4-714D9.4	1:100503652-100598511	NOTEST	0	0	0	0	1	1
ENSG00000226953	ENSG00000226953	AC010890.1	2:133429373-134326034	NOTEST	0	0.0708956	inf	0	1	1
ENSG00000226954	ENSG00000226954	RP5-983L19.2	22:50111700-50118154	NOTEST	0	0	0	0	1	1
ENSG00000226955	ENSG00000226955	AC104306.4	3:32634463-32634804	NOTEST	0	0	0	0	1	1
ENSG00000226956	ENSG00000226956	AP000432.2	21:19031593-19032702	NOTEST	0	0	0	0	1	1
ENSG00000226957	ENSG00000226957	RP4-533D7.4	1:46505811-46651630	NOTEST	0.057295	0.0751261	0.390906	0	1	1
ENSG00000226960	ENSG00000226960	RP5-837O21.1	1:94393269-94393858	NOTEST	0	0	0	0	1	1
ENSG00000226961	ENSG00000226961	AC018463.5	2:11491752-11492250	NOTEST	0	0	0	0	1	1
ENSG00000226962	ENSG00000226962	RAC1P6	7:114701590-114871409	NOTEST	0	0	0	0	1	1
ENSG00000226963	ENSG00000226963	AC078883.4	2:173292081-173489823	NOTEST	0	0	0	0	1	1
ENSG00000226964	ENSG00000226964	RHEBP2	10:47379726-47420712	NOTEST	0	0.0245203	inf	0	1	1
ENSG00000226965	ENSG00000226965	AC003088.1	7:110072295-110174811	NOTEST	0.0854884	0	#NAME?	0	1	1
ENSG00000226967	ENSG00000226967	HAUS4P1	1:170338363-170339508	NOTEST	0	0	0	0	1	1
ENSG00000226968	ENSG00000226968	LINC00423	13:33451568-33485788	NOTEST	0	0	0	0	1	1
ENSG00000226969	ENSG00000226969	RP11-547D24.3	1:1980641-1981509	NOTEST	0	0	0	0	1	1
ENSG00000226970	ENSG00000226970	RP11-82H13.2	1:84710016-84710260	NOTEST	0	0	0	0	1	1
ENSG00000226971	ENSG00000226971	AF196972.4	X:48305272-48307251	NOTEST	0	0	0	0	1	1
ENSG00000226972	ENSG00000226972	AC013717.3	2:44497759-44498245	NOTEST	0	0.0335121	inf	0	1	1
ENSG00000226973	ENSG00000226973	RP4-663N10.2	1:116014561-116018648	NOTEST	0	0	0	0	1	1
ENSG00000226974	ENSG00000226974	AL445989.1	13:64320933-64321323	NOTEST	0	0	0	0	1	1
ENSG00000226975	ENSG00000226975	AC006987.6	Y:10007396-10007923	NOTEST	0	0	0	0	1	1
ENSG00000226977	ENSG00000226977	HMGN1P24	13:96453833-96705736	NOTEST	0	0	0	0	1	1
ENSG00000226978	ENSG00000226978	MAGI2-AS2	7:77646392-79100524	NOTEST	0	0	0	0	1	1
ENSG00000226979	ENSG00000226979	LTA	6:31539830-31542101	NOTEST	0	0	0	0	1	1
ENSG00000226981	ENSG00000226981	ABHD17AP6	17:20717932-20947073	NOTEST	0.0480403	0	#NAME?	0	1	1
ENSG00000226982	ENSG00000226982	CENPCP1	12:89813494-89934079	NOTEST	0	0.013541	inf	0	1	1
ENSG00000226983	ENSG00000226983	AP000235.2	21:26212863-26442219	NOTEST	0	0	0	0	1	1
ENSG00000226984	ENSG00000226984	RP4-591B8.2	1:114935398-115053781	NOTEST	0	0	0	0	1	1
ENSG00000226985	ENSG00000226985	RP11-142G7.2	X:13353359-13391753	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000226986	ENSG00000226986	RP11-543B16.2	1:211380388-211381286	NOTEST	0	0.155602	inf	0	1	1
ENSG00000226987	ENSG00000226987	RP11-544A12.5	9:134116073-134117111	NOTEST	0	0	0	0	1	1
ENSG00000226989	ENSG00000226989	AL049758.2	22:43192507-43411151	NOTEST	0.0656195	0	#NAME?	0	1	1
ENSG00000226990	ENSG00000226990	RP11-543F8.2	10:8442822-8503826	NOTEST	0	0	0	0	1	1
ENSG00000226991	ENSG00000226991	AC112229.6	2:111116366-111116703	NOTEST	0	0	0	0	1	1
ENSG00000226992	ENSG00000226992	AC144525.1	2:239697288-239698357	NOTEST	0	0	0	0	1	1
ENSG00000226993	ENSG00000226993	POLR2LP	HSCHR6_MHC_COX:31101018-31101205	NOTEST	0	0	0	0	1	1
ENSG00000226994	ENSG00000226994	AC012593.1	2:35024916-35410755	NOTEST	0	0	0	0	1	1
ENSG00000226995	ENSG00000226995	LINC00658	20:5407540-5451740	NOTEST	0	0	0	0	1	1
ENSG00000226996	ENSG00000226996	AP000477.3	21:25415571-25422601	NOTEST	0	0	0	0	1	1
ENSG00000226998	ENSG00000226998	RP11-291J9.1	9:31505277-31505941	NOTEST	0	0	0	0	1	1
ENSG00000226999	ENSG00000226999	AC073325.2	7:45500310-45581781	NOTEST	0	0	0	0	1	1
ENSG00000227000	ENSG00000227000	HSPD1P14	1:33979608-34631443	NOTEST	0	0	0	0	1	1
ENSG00000227002	ENSG00000227002	SNRPEP10	1:223711348-223853436	NOTEST	0	0	0	0	1	1
ENSG00000227004	ENSG00000227004	AC108032.1	2:200732118-200775882	NOTEST	0	0	0	0	1	1
ENSG00000227005	ENSG00000227005	AC011718.3	22:20632022-20661407	NOTEST	0	0	0	0	1	1
ENSG00000227006	ENSG00000227006	RP5-956O18.2	1:230193535-230417870	NOTEST	0.358633	0.193128	-0.892953	0	1	1
ENSG00000227007	ENSG00000227007	AC105253.1	2:6506141-6515554	NOTEST	0	0	0	0	1	1
ENSG00000227009	ENSG00000227009	FUNDC2P4	22:39551529-39551950	NOTEST	0	0	0	0	1	1
ENSG00000227011	ENSG00000227011	C17orf112	17:51062879-51065012	NOTEST	0	0	0	0	1	1
ENSG00000227012	ENSG00000227012	RP1-97J1.2	6:112221691-112223054	NOTEST	0	0	0	0	1	1
ENSG00000227013	ENSG00000227013	OR7E96P	8:7897499-7898475	NOTEST	0	0	0	0	1	1
ENSG00000227014	ENSG00000227014	AC007285.6	7:29959718-30066300	NOTEST	0.12683	0.17481	0.462897	0	1	1
ENSG00000227015	ENSG00000227015	RP11-548K12.6	7:57830324-57830652	NOTEST	0	0	0	0	1	1
ENSG00000227016	ENSG00000227016	RP11-262K1.1	1:73214603-73364823	NOTEST	0	0	0	0	1	1
ENSG00000227017	ENSG00000227017	AC007036.6	7:30216002-30218630	NOTEST	0.0295317	0.109163	1.88615	0	1	1
ENSG00000227018	ENSG00000227018	IL6STP1	17:15686601-15687621	NOTEST	0	0.0558083	inf	0	1	1
ENSG00000227021	ENSG00000227021	AC007557.3	2:217536827-217858802	NOTEST	0	0	0	0	1	1
ENSG00000227023	ENSG00000227023	OR51A3P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000227025	ENSG00000227025	HCG4P3	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000227027	ENSG00000227027	HLA-T	HSCHR6_MHC_COX:29855862-29856994	NOTEST	0	0	0	0	1	1
ENSG00000227028	ENSG00000227028	SLC8A1-AS1	2:40013592-40838193	NOTEST	0	0.0540386	inf	0	1	1
ENSG00000227029	ENSG00000227029	RP11-168P8.3	10:44407891-44409684	NOTEST	0	0	0	0	1	1
ENSG00000227030	ENSG00000227030	RPL7AP7	HSCHR6_MHC_DBB:29768197-29768994	NOTEST	0	0	0	0	1	1
ENSG00000227032	ENSG00000227032	RP11-34E5.4	10:98353068-98480271	NOTEST	0	0	0	0	1	1
ENSG00000227033	ENSG00000227033	AC105461.1	2:232825954-233209060	NOTEST	0	0	0	0	1	1
ENSG00000227034	ENSG00000227034	RP11-234N17.1	1:99355805-99614408	NOTEST	0	0	0	0	1	1
ENSG00000227035	ENSG00000227035	RP11-3N2.8	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000227038	ENSG00000227038	AC005077.12	7:75719748-75738097	NOTEST	0.0241203	0.00986053	-1.29051	0	1	1
ENSG00000227039	ENSG00000227039	ITGB2-AS1	21:46305867-46351904	NOTEST	0	0.0104078	inf	0	1	1
ENSG00000227040	ENSG00000227040	RP11-533F5.2	4:57627084-57627651	NOTEST	0	0	0	0	1	1
ENSG00000227042	ENSG00000227042	RP6-1O2.1	X:10210378-10333363	NOTEST	0	0	0	0	1	1
ENSG00000227043	ENSG00000227043	RP11-286M16.1	1:230011296-230021499	NOTEST	0	0	0	0	1	1

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ENSG00000227044	ENSG00000227044	OR2H2	HSCHR6_MHC_MANN:29522993-29600557	NOTEST	0	0	0	0	1	1
ENSG00000227045	ENSG00000227045	RP11-98D18.1	1:151673501-151702281	NOTEST	0	0	0	0	1	1
ENSG00000227046	ENSG00000227046	DAXX	HSCHR6_MHC_COX:33207944-33218656	NOTEST	0	0	0	0	1	1
ENSG00000227047	ENSG00000227047	AC012065.4	2:20699330-20701071	NOTEST	0	0	0	0	1	1
ENSG00000227048	ENSG00000227048	RP11-134G8.2	1:201373624-201398994	NOTEST	0	0	0	0	1	1
ENSG00000227050	ENSG00000227050	RP11-460I13.2	1:28261503-28294607	NOTEST	0	0	0	0	1	1
ENSG00000227051	ENSG00000227051	C14orf132	14:96505660-96560417	NOTEST	0.0203299	0.0605624	1.57482	0	1	1
ENSG00000227053	ENSG00000227053	RP11-395B7.4	7:100612903-100662230	NOTEST	0	0	0	0	1	1
ENSG00000227054	ENSG00000227054	FDX1P2	21:27011583-27144771	NOTEST	0	0	0	0	1	1
ENSG00000227055	ENSG00000227055	AC009961.5	2:160568999-160761260	NOTEST	0	0	0	0	1	1
ENSG00000227056	ENSG00000227056	RPL6P2	1:119573838-119869926	NOTEST	0	0	0	0	1	1
ENSG00000227058	ENSG00000227058	RP13-34L8.7	X:52574162-52576707	NOTEST	0	0	0	0	1	1
ENSG00000227059	ENSG00000227059	ANHX	12:133794897-133812681	NOTEST	0	0	0	0	1	1
ENSG00000227060	ENSG00000227060	LINC00629	X:133684002-133693953	NOTEST	0.0268583	0.116273	2.11407	0	1	1
ENSG00000227061	ENSG00000227061	AC079779.7	2:197568-202605	NOTEST	0	0	0	0	1	1
ENSG00000227062	ENSG00000227062	RP11-115A15.4	1:80929985-80930403	NOTEST	0	0	0	0	1	1
ENSG00000227064	ENSG00000227064	RP3-363L9.1	X:131760043-132095423	NOTEST	0	0	0	0	1	1
ENSG00000227066	ENSG00000227066	RP3-340N1.2	1:20480830-20487061	NOTEST	0	0	0	0	1	1
ENSG00000227067	ENSG00000227067	DPPA3P1	X:103172004-103229570	NOTEST	0	0	0	0	1	1
ENSG00000227068	ENSG00000227068	RP11-12A16.3	9:128199671-128469513	NOTEST	0	0	0	0	1	1
ENSG00000227069	ENSG00000227069	CNN2P2	9:42491161-42492070	NOTEST	0.020126	0	#NAME?	0	1	1
ENSG00000227070	ENSG00000227070	RP11-191G24.1	1:51819934-52027301	NOTEST	0.167491	0	#NAME?	0	1	1
ENSG00000227071	ENSG00000227071	RP11-4E23.2	9:20658307-21031635	NOTEST	0	0	0	0	1	1
ENSG00000227072	ENSG00000227072	RP3-466I7.1	6:108616097-108847999	NOTEST	0	0	0	0	1	1
ENSG00000227073	ENSG00000227073	SDHDP2	7:135046546-135194875	NOTEST	0.0505111	0.035936	-0.491172	0	1	1
ENSG00000227074	ENSG00000227074	SAPCD1	HSCHR6_MHC_DBB:31689901-31715550	NOTEST	0	0	0	0	1	1
ENSG00000227075	ENSG00000227075	AP000472.3	21:23305634-23348000	NOTEST	0	0	0	0	1	1
ENSG00000227076	ENSG00000227076	RP11-4C20.4	10:129705324-129884119	NOTEST	0	0	0	0	1	1
ENSG00000227078	ENSG00000227078	AC004448.2	17:19322347-19327670	NOTEST	0	0	0	0	1	1
ENSG00000227080	ENSG00000227080	CTD-2021A8.3	7:51456126-51456811	NOTEST	0	0	0	0	1	1
ENSG00000227082	ENSG00000227082	AL592494.5	1:121102016-121204983	NOTEST	0.00850793	0.00298576	-1.51071	0	1	1
ENSG00000227083	ENSG00000227083	L29074.3	X:146981695-146982977	NOTEST	0	0.13079	inf	0	1	1
ENSG00000227084	ENSG00000227084	RP11-144A16.5	9:41529582-41550381	NOTEST	0	0	0	0	1	1
ENSG00000227087	ENSG00000227087	RBMX2P5	5:79627391-79628360	NOTEST	0.0194818	0.0470277	1.27138	0	1	1
ENSG00000227088	ENSG00000227088	AC084149.2	2:77879538-77881794	NOTEST	0	0	0	0	1	1
ENSG00000227089	ENSG00000227089	RP1-135L22.1	6:21354641-21355527	NOTEST	0	0	0	0	1	1
ENSG00000227090	ENSG00000227090	AP000402.3	21:26212863-26442219	NOTEST	0	0	0	0	1	1
ENSG00000227091	ENSG00000227091	RP5-1028L10.1	1:110693107-110744824	NOTEST	0.0540015	0.0472179	-0.193665	0	1	1
ENSG00000227094	ENSG00000227094	RP11-565P22.2	1:162039563-162356600	NOTEST	0	0	0	0	1	1
ENSG00000227096	ENSG00000227096	HMGB3P8	10:118187378-118237469	NOTEST	0	0.1169	inf	0	1	1
ENSG00000227098	ENSG00000227098	AC073636.1	2:177710720-177714156	NOTEST	0	0	0	0	1	1
ENSG00000227099	ENSG00000227099	HLA-DRB7	HSCHR6_MHC_SSTO:32594076-32613256	NOTEST	0	0	0	0	1	1
ENSG00000227100	ENSG00000227100	HCG19P	HSCHR6_MHC_QBL:30316558-30317192	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000227101	ENSG00000227101	RP11-433J20.2	10:4067131-4070586	NOTEST	0	0	0	0	1	1
ENSG00000227102	ENSG00000227102	OR2AS1P	1:248712056-248727140	NOTEST	0	0	0	0	1	1
ENSG00000227104	ENSG00000227104	PIGQP1	1:56381281-56410636	NOTEST	0	0	0	0	1	1
ENSG00000227105	ENSG00000227105	PARP1P1	13:111589105-111592131	NOTEST	0	0.00404098	inf	0	1	1
ENSG00000227107	ENSG00000227107	AC096574.5	2:238521619-238535168	NOTEST	0.0393721	0.0171839	-1.19611	0	1	1
ENSG00000227108	ENSG00000227108	IGHD1-14	14:106366495-106366512	NOTEST	0	0	0	0	1	1
ENSG00000227109	ENSG00000227109	CRIP1P3	1:202065886-202066106	NOTEST	0	0	0	0	1	1
ENSG00000227110	ENSG00000227110	LMCD1-AS1	3:7994491-8653610	NOTEST	0.469892	0.443358	-0.083858	0	1	1
ENSG00000227112	ENSG00000227112	RP1-86D1.4	6:128289923-128841870	NOTEST	0	0	0	0	1	1
ENSG00000227114	ENSG00000227114	AC018696.3	2:91685385-91685524	NOTEST	0	0	0	0	1	1
ENSG00000227115	ENSG00000227115	RP11-267C16.1	18:48872618-49088939	NOTEST	0.0165363	0	#NAME?	0	1	1
ENSG00000227116	ENSG00000227116	RP3-471C18.1	6:19535174-19840915	NOTEST	0	0	0	0	1	1
ENSG00000227117	ENSG00000227117	CTA-85E5.10	22:30279143-30573064	NOTEST	0	0.0143298	inf	0	1	1
ENSG00000227118	ENSG00000227118	BTF3P13	4:99661892-99662382	NOTEST	0	0	0	0	1	1
ENSG00000227120	ENSG00000227120	AC009238.7	2:96101880-96102304	NOTEST	0	0	0	0	1	1
ENSG00000227121	ENSG00000227121	RP11-319F12.2	10:54733247-54735575	NOTEST	0	0	0	0	1	1
ENSG00000227122	ENSG00000227122	PRRT1	HSCHR6_MHC_MCF:32192561-32222305	NOTEST	0	0	0	0	1	1
ENSG00000227123	ENSG00000227123	RPL12P44	3:44956748-45077563	NOTEST	0	0.0318769	inf	0	1	1
ENSG00000227125	ENSG00000227125	AP002856.6	11:131074893-131085058	NOTEST	0	0	0	0	1	1
ENSG00000227128	ENSG00000227128	LBX1-AS1	10:102986732-103029905	NOTEST	0	0.0406231	inf	0	1	1
ENSG00000227129	ENSG00000227129	NEU1	HSCHR6_MHC_MCF:31901916-31907164	NOTEST	0	0	0	0	1	1
ENSG00000227131	ENSG00000227131	RP11-552E20.1	6:40239304-40243976	NOTEST	0	0	0	0	1	1
ENSG00000227132	ENSG00000227132	XXbac-BPG118E17.9	HSCHR6_MHC_MCF:31076238-31081035	NOTEST	0	0	0	0	1	1
ENSG00000227133	ENSG00000227133	AC011742.5	2:26382891-26384005	NOTEST	0	0	0	0	1	1
ENSG00000227134	ENSG00000227134	AC093084.1	2:147234994-147235681	NOTEST	0	0	0	0	1	1
ENSG00000227135	ENSG00000227135	GCSAML-AS1	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000227136	ENSG00000227136	LINC00595	10:80008504-80115857	NOTEST	0.272851	0.166326	-0.714098	0	1	1
ENSG00000227137	ENSG00000227137	OR5V1	HSCHR6_MHC_SSTO:29323120-29424524	NOTEST	0	0	0	0	1	1
ENSG00000227138	ENSG00000227138	RP11-421B23.2	9:10777356-10777525	NOTEST	0	0	0	0	1	1
ENSG00000227139	ENSG00000227139	RP11-533N14.3	1:147169913-147171461	NOTEST	0	0	0	0	1	1
ENSG00000227140	ENSG00000227140	USP17L5	4:9341128-9342721	NOTEST	0	0	0	0	1	1
ENSG00000227141	ENSG00000227141	RP11-545A16.3	1:179555839-179558310	NOTEST	0	0.00453487	inf	0	1	1
ENSG00000227143	ENSG00000227143	LINC01153	10:122938213-122945480	NOTEST	0	0	0	0	1	1
ENSG00000227144	ENSG00000227144	VWA7	HSCHR6_MHC_COX:31720749-31732475	NOTEST	0	0	0	0	1	1
ENSG00000227145	ENSG00000227145	IL21-AS1	4:123533782-123610311	NOTEST	0.00415168	0.0123308	1.5705	0	1	1
ENSG00000227147	ENSG00000227147	TRIM15	HSCHR6_MHC_COX:30120905-30130396	NOTEST	0	0	0	0	1	1
ENSG00000227148	ENSG00000227148	RP11-196D18.1	7:62505204-62514809	NOTEST	0	0	0	0	1	1
ENSG00000227149	ENSG00000227149	AC092156.3	2:140974565-140974808	NOTEST	0	0	0	0	1	1
ENSG00000227150	ENSG00000227150	RP11-473E2.3	9:137444583-137445743	NOTEST	0	0	0	0	1	1
ENSG00000227151	ENSG00000227151	PRR20D	13:57734765-57737787	NOTEST	0	0	0	0	1	1
ENSG00000227152	ENSG00000227152	OR2T7	1:248604507-248605434	NOTEST	0	0	0	0	1	1
ENSG00000227154	ENSG00000227154	MKRNP2	6:35410820-35417643	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000227155	ENSG00000227155	RP11-165F24.3	9:213107-746105	NOTEST	0.0141058	0.014585	0.0481921	0	1	1
ENSG00000227157	ENSG00000227157	AC068535.2	2:105027658-105032070	NOTEST	0	0	0	0	1	1
ENSG00000227158	ENSG00000227158	AC073621.2	17:17325994-17327018	NOTEST	0	0	0	0	1	1
ENSG00000227159	ENSG00000227159	DDX11L16	X:155227245-155257848	NOTEST	0	0.0221706	inf	0	1	1
ENSG00000227160	ENSG00000227160	RP1-65P5.1	11:32133594-32364955	NOTEST	0	0	0	0	1	1
ENSG00000227161	ENSG00000227161	AC092755.4	15:59887073-59981733	NOTEST	0	0	0	0	1	1
ENSG00000227163	ENSG00000227163	RP5-1198O20.5	1:44501797-44570647	NOTEST	0	0	0	0	1	1
ENSG00000227164	ENSG00000227164	AL354993.1	20:51588945-52120853	NOTEST	0	0	0	0	1	1
ENSG00000227165	ENSG00000227165	WDR11-AS1	10:122521323-122669036	NOTEST	0	0	0	0	1	1
ENSG00000227166	ENSG00000227166	STSP1	Y:17659095-17705211	NOTEST	0	0	0	0	1	1
ENSG00000227167	ENSG00000227167	RP11-570H19.2	9:18360594-18362218	NOTEST	0	0	0	0	1	1
ENSG00000227168	ENSG00000227168	RPL35AP4	HSCHR6_MHC_QBL:33285980-33286082	NOTEST	0	0	0	0	1	1
ENSG00000227169	ENSG00000227169	RP1-37J18.1	1:4611794-4612205	NOTEST	0	0	0	0	1	1
ENSG00000227170	ENSG00000227170	AF178030.2	8:116420723-116821899	NOTEST	0	0	0	0	1	1
ENSG00000227171	ENSG00000227171	RNF39	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1
ENSG00000227172	ENSG00000227172	AC011290.4	7:39585244-39605838	NOTEST	0.122125	0	#NAME?	0	1	1
ENSG00000227173	ENSG00000227173	MYL6P3	10:66929195-66929627	NOTEST	0.327647	0.044364	-2.88468	0	1	1
ENSG00000227175	ENSG00000227175	RP11-214D15.2	10:13480483-13572262	NOTEST	0	0	0	0	1	1
ENSG00000227176	ENSG00000227176	AC092641.2	2:170683967-170940641	NOTEST	0	0	0	0	1	1
ENSG00000227177	ENSG00000227177	AIMP1P2	1:172745044-173033155	NOTEST	0	0	0	0	1	1
ENSG00000227178	ENSG00000227178	OR2B4P	HSCHR6_MHC_MANN:29258525-29259468	NOTEST	0	0	0	0	1	1
ENSG00000227179	ENSG00000227179	PGCP1	1:111925481-111934441	NOTEST	0	0	0	0	1	1
ENSG00000227180	ENSG00000227180	AC013467.1	2:175164051-175165684	NOTEST	0	0	0	0	1	1
ENSG00000227181	ENSG00000227181	RP11-317P15.3	1:182681996-182683679	NOTEST	0	0	0	0	1	1
ENSG00000227182	ENSG00000227182	VN1R28P	7:57482533-57483429	NOTEST	0	0	0	0	1	1
ENSG00000227183	ENSG00000227183	HDGFP1	X:130780647-130780899	NOTEST	0	0	0	0	1	1
ENSG00000227184	ENSG00000227184	EPPK1	8:144939496-144952632	NOTEST	0.00189755	0.00696359	1.87569	0	1	1
ENSG00000227185	ENSG00000227185	RP11-544D21.1	1:239433024-239439761	NOTEST	0	0	0	0	1	1
ENSG00000227186	ENSG00000227186	RP11-77G23.5	10:76585339-76792380	NOTEST	0	0	0	0	1	1
ENSG00000227187	ENSG00000227187	RP11-6C10.1	2:175898505-175898920	NOTEST	0	0	0	0	1	1
ENSG00000227188	ENSG00000227188	RP5-1104E15.6	22:39853348-39888199	NOTEST	0	0	0	0	1	1
ENSG00000227189	ENSG00000227189	AC092535.3	4:1107426-1147514	NOTEST	0	0.00578695	inf	0	1	1
ENSG00000227191	ENSG00000227191	TRGC2	7:38279180-38289173	NOTEST	0	0	0	0	1	1
ENSG00000227192	ENSG00000227192	RP1-45I4.3	6:143360561-143363461	NOTEST	0	0.0552896	inf	0	1	1
ENSG00000227193	ENSG00000227193	RP11-439A17.4	1:120876494-120905159	NOTEST	0	0	0	0	1	1
ENSG00000227194	ENSG00000227194	GLUD1P7	10:46772793-46778894	NOTEST	0	0	0	0	1	1
ENSG00000227195	ENSG00000227195	MIR663A	20:26167555-26232162	NOTEST	0.015501	0.0911605	2.55605	0	1	1
ENSG00000227196	ENSG00000227196	IGHD4-23	14:106350727-106350746	NOTEST	0	0	0	0	1	1
ENSG00000227197	ENSG00000227197	AC009518.8	7:132469628-132766848	NOTEST	0	0	0	0	1	1
ENSG00000227198	ENSG00000227198	C6orf47-AS1	6:31626074-31628549	NOTEST	0	0	0	0	1	1
ENSG00000227199	ENSG00000227199	ST7-AS1	7:116592499-116870157	NOTEST	0.288779	0.33116	0.197561	0	1	1
ENSG00000227200	ENSG00000227200	RP11-121A14.3	9:127019884-127115586	NOTEST	0.0735921	0.177633	1.27128	0	1	1
ENSG00000227201	ENSG00000227201	CNN2P1	22:30279143-30573064	NOTEST	0	0.04383	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000227203	ENSG00000227203	SUB1P1	8:11647513-11647897	NOTEST	0	0	0	0	1	1
ENSG00000227204	ENSG00000227204	RBMY2JP	Y:7995170-8012244	NOTEST	0	0	0	0	1	1
ENSG00000227205	ENSG00000227205	PFN1P9	1:120395938-120396371	NOTEST	0	0	0	0	1	1
ENSG00000227206	ENSG00000227206	XXbac-BCX196D17.5	6:29091986-29096685	NOTEST	0	0	0	0	1	1
ENSG00000227207	ENSG00000227207	RPL31P12	1:72767154-72767512	NOTEST	0	0	0	0	1	1
ENSG00000227208	ENSG00000227208	LINC00552	13:114451483-114454062	NOTEST	0	0	0	0	1	1
ENSG00000227209	ENSG00000227209	WARS2P1	10:82700420-82700957	NOTEST	0	0	0	0	1	1
ENSG00000227210	ENSG00000227210	AC079145.4	2:20189977-20212455	NOTEST	0	0	0	0	1	1
ENSG00000227211	ENSG00000227211	RP5-1100E15.4	X:101854095-101973607	NOTEST	0	0.0652786	inf	0	1	1
ENSG00000227213	ENSG00000227213	SPATA13-AS1	13:24553838-24896673	NOTEST	0	0	0	0	1	1
ENSG00000227214	ENSG00000227214	HCG15	6:28953979-28956313	NOTEST	0.218184	0.296842	0.444151	0	1	1
ENSG00000227215	ENSG00000227215	RP11-445L13__B.3	6:83602116-83775560	NOTEST	0.0480644	0	#NAME?	0	1	1
ENSG00000227216	ENSG00000227216	PFN1P5	1:146032646-146253110	NOTEST	0.286575	0.136617	-1.06878	0	1	1
ENSG00000227217	ENSG00000227217	RP11-367J7.3	1:157644110-157670647	NOTEST	0	0	0	0	1	1
ENSG00000227218	ENSG00000227218	RP11-203J24.8	9:130696781-130742792	NOTEST	0.160314	0.421547	1.39479	0	1	1
ENSG00000227220	ENSG00000227220	RP11-69I8.3	6:132269315-132398533	NOTEST	0.412073	0.104019	-1.98605	0	1	1
ENSG00000227222	ENSG00000227222	DHX16	HSCHR6_MHC_APD:30635496-30649062	NOTEST	0	0	0	0	1	1
ENSG00000227224	ENSG00000227224	RP11-72H11.1	3:53508726-53509116	NOTEST	0	0	0	0	1	1
ENSG00000227225	ENSG00000227225	MTND1P14	17:19505571-19506521	NOTEST	0	0	0	0	1	1
ENSG00000227227	ENSG00000227227	AC017101.10	2:187454791-187630685	NOTEST	0.0814697	0.030163	-1.43348	0	1	1
ENSG00000227228	ENSG00000227228	UBDP1	HSCHR6_MHC_COX:29428949-29434162	NOTEST	0	0	0	0	1	1
ENSG00000227230	ENSG00000227230	RP11-261C10.5	1:243287729-243418650	NOTEST	0.454152	0.219	-1.05224	0	1	1
ENSG00000227231	ENSG00000227231	IER3	HSCHR6_MHC_DBB:30701237-30702593	NOTEST	0	0	0	0	1	1
ENSG00000227233	ENSG00000227233	CICP17	7:51449980-51452357	NOTEST	0.0916829	0.0656099	-0.482737	0	1	1
ENSG00000227234	ENSG00000227234	SPANXB2	X:140084755-140085871	NOTEST	0	0	0	0	1	1
ENSG00000227236	ENSG00000227236	RP11-365D9.1	1:235710986-235814054	NOTEST	0.00956304	0.0141552	0.565793	0	1	1
ENSG00000227237	ENSG00000227237	AL672294.1	1:249153362-249158995	NOTEST	0	0	0	0	1	1
ENSG00000227238	ENSG00000227238	TTC39DP	2:38978675-39012142	NOTEST	0	0	0	0	1	1
ENSG00000227239	ENSG00000227239	AL121985.1	1:160639937-160681641	NOTEST	0	0	0	0	1	1
ENSG00000227240	ENSG00000227240	RP11-563D10.1	1:194118602-194167824	NOTEST	0	0	0	0	1	1
ENSG00000227241	ENSG00000227241	AC011998.4	2:178487979-178973066	NOTEST	0	0	0	0	1	1
ENSG00000227243	ENSG00000227243	SLAMF6P1	1:162415338-162415676	NOTEST	0	0	0	0	1	1
ENSG00000227244	ENSG00000227244	LINC00845	10:62776032-62786178	NOTEST	0.052051	0	#NAME?	0	1	1
ENSG00000227245	ENSG00000227245	RP11-136C24.2	3:43120723-43147568	NOTEST	0.043946	0	#NAME?	0	1	1
ENSG00000227246	ENSG00000227246	PSORS1C2	HSCHR6_MHC_MCF:31161054-31186363	NOTEST	0	0	0	0	1	1
ENSG00000227247	ENSG00000227247	TRIM60P13	13:89901071-89902354	NOTEST	0	0	0	0	1	1
ENSG00000227248	ENSG00000227248	FAM155A-IT1	13:107820882-108519083	NOTEST	0.0419936	0	#NAME?	0	1	1
ENSG00000227249	ENSG00000227249	AC000374.1	7:126078651-126893348	NOTEST	0	0	0	0	1	1
ENSG00000227251	ENSG00000227251	TRIM60P9Y	Y:25204176-25205333	NOTEST	0	0	0	0	1	1
ENSG00000227252	ENSG00000227252	AC105760.2	2:237968076-238009109	NOTEST	0.227834	0.244974	0.104646	0	1	1
ENSG00000227253	ENSG00000227253	RP11-166N17.1	10:32555216-32667726	NOTEST	0	0	0	0	1	1
ENSG00000227254	ENSG00000227254	VDAC1P12	13:34656565-34657447	NOTEST	0	0	0	0	1	1
ENSG00000227255	ENSG00000227255	CDRT15P2	17:15668016-15668978	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000227256	ENSG00000227256	MIS18A-AS1	21:33640529-33653299	NOTEST	0.024839	0.0175393	-0.50202	0	1	1
ENSG00000227257	ENSG00000227257	RP11-330M2.3	9:99660347-99775862	NOTEST	0	0	0	0	1	1
ENSG00000227259	ENSG00000227259	HMGN2P22	2:101207611-101207786	NOTEST	0	0	0	0	1	1
ENSG00000227260	ENSG00000227260	AC116035.1	3:30566236-30568677	NOTEST	0	0	0	0	1	1
ENSG00000227261	ENSG00000227261	YWHAZP7	X:63832511-63833142	NOTEST	0	0	0	0	1	1
ENSG00000227262	ENSG00000227262	HCG4B	6:29893759-29897009	NOTEST	0.117295	0.0924093	-0.344037	0	1	1
ENSG00000227264	ENSG00000227264	ACTR3BP5	10:38989554-38991356	NOTEST	0	0	0	0	1	1
ENSG00000227265	ENSG00000227265	AC073464.4	2:95400399-95401589	NOTEST	0	0	0	0	1	1
ENSG00000227267	ENSG00000227267	RP11-305O4.2	3:135684514-135866733	NOTEST	0	0	0	0	1	1
ENSG00000227268	ENSG00000227268	KLLN	10:89618917-89731687	NOTEST	0.0928467	0.0528436	-0.813123	0	1	1
ENSG00000227269	ENSG00000227269	RP11-96L7.2	9:101945654-101947173	NOTEST	0	0	0	0	1	1
ENSG00000227270	ENSG00000227270	AC009963.4	2:108520419-108520697	NOTEST	0	0	0	0	1	1
ENSG00000227271	ENSG00000227271	RPL39P25	10:77029149-77029303	NOTEST	0	0	0	0	1	1
ENSG00000227274	ENSG00000227274	AC005358.3	17:12569206-12894960	NOTEST	0	0	0	0	1	1
ENSG00000227275	ENSG00000227275	MTND6P10	2:132127357-132127874	NOTEST	0	0	0	0	1	1
ENSG00000227277	ENSG00000227277	RNF5	HSCHR6_MHC_SSTO:32153000-32155440	NOTEST	0	0	0	0	1	1
ENSG00000227278	ENSG00000227278	RP11-656D10.5	1:40974412-40982846	NOTEST	0	0	0	0	1	1
ENSG00000227279	ENSG00000227279	AC015933.2	18:25530929-25757410	NOTEST	0.465118	0.330651	-0.492288	0	1	1
ENSG00000227282	ENSG00000227282	RP11-164D18.2	20:58090245-58091094	NOTEST	0	0	0	0	1	1
ENSG00000227283	ENSG00000227283	RPL35AP12	4:164303330-164303668	NOTEST	0	0	0	0	1	1
ENSG00000227284	ENSG00000227284	MARK2P10	7:96487493-96488930	NOTEST	0	0	0	0	1	1
ENSG00000227285	ENSG00000227285	RP3-327A19.5	X:119055223-119056803	NOTEST	0.0697347	0.105322	0.594858	0	1	1
ENSG00000227286	ENSG00000227286	HLA-DPA2	HSCHR6_MHC_QBL:32988585-32994128	NOTEST	0	0	0	0	1	1
ENSG00000227288	ENSG00000227288	RP5-837I24.1	1:81771844-82458120	NOTEST	0.0950681	0.0230218	-2.04596	0	1	1
ENSG00000227289	ENSG00000227289	HSFY3P	Y:2709526-2800041	NOTEST	0	0	0	0	1	1
ENSG00000227290	ENSG00000227290	RP4-544H6.2	1:87819206-87837338	NOTEST	0	0	0	0	1	1
ENSG00000227291	ENSG00000227291	AC092170.1	2:117938467-117939138	NOTEST	0	0	0	0	1	1
ENSG00000227292	ENSG00000227292	AC009229.5	2:38430504-38466732	NOTEST	0	0	0	0	1	1
ENSG00000227293	ENSG00000227293	AC118345.1	2:66462508-66463345	NOTEST	0	0	0	0	1	1
ENSG00000227294	ENSG00000227294	AC016994.2	2:107418055-107503564	NOTEST	0	0	0	0	1	1
ENSG00000227295	ENSG00000227295	ELL2P1	1:158145639-158147545	NOTEST	0.0256794	0.0514669	1.00303	0	1	1
ENSG00000227296	ENSG00000227296	HLA-H	HSCHR6_MHC_QBL:29846366-29849546	NOTEST	0	0	0	0	1	1
ENSG00000227298	ENSG00000227298	RP5-905H7.5	7:62787051-62814743	NOTEST	0	0	0	0	1	1
ENSG00000227300	ENSG00000227300	KRT16P2	17:16733312-16736147	NOTEST	0	0	0	0	1	1
ENSG00000227301	ENSG00000227301	RP11-384P7.5	9:33719687-33722553	NOTEST	0	0	0	0	1	1
ENSG00000227302	ENSG00000227302	SSXP9	X:48181783-48186118	NOTEST	0	0	0	0	1	1
ENSG00000227303	ENSG00000227303	GS1-256O22.5	X:142372753-142605303	NOTEST	0	0	0	0	1	1
ENSG00000227304	ENSG00000227304	RP11-791G16.2	4:83404322-83483510	NOTEST	0	0	0	0	1	1
ENSG00000227305	ENSG00000227305	RP11-340I6.3	7:62854126-62882424	NOTEST	0	0	0	0	1	1
ENSG00000227306	ENSG00000227306	AP006285.6	11:1709526-1710286	NOTEST	0	0	0	0	1	1
ENSG00000227307	ENSG00000227307	RP11-95I16.2	10:122685058-122740213	NOTEST	0	0	0	0	1	1
ENSG00000227308	ENSG00000227308	AC009502.4	2:220550102-220602659	NOTEST	0.148666	0.330187	1.15121	0	1	1
ENSG00000227309	ENSG00000227309	AC140076.1	3:17198653-18959184	NOTEST	0	0	0	0	1	1

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ENSG00000227311	ENSG00000227311	RP1-228H13.1	1:40798747-40799230	NOTEST	0	0	0	0	1	1
ENSG00000227312	ENSG00000227312	RP11-496D1.2	1:24882601-24935819	NOTEST	0	0	0	0	1	1
ENSG00000227313	ENSG00000227313	RP11-309N24.1	10:36185801-36187891	NOTEST	0	0	0	0	1	1
ENSG00000227314	ENSG00000227314	MSH5	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000227315	ENSG00000227315	NEU1	HSCHR6_MHC_COX:31812977-31818226	NOTEST	0	0	0	0	1	1
ENSG00000227317	ENSG00000227317	DDAH2	HSCHR6_MHC_DBB:31676986-31689717	NOTEST	0	0	0	0	1	1
ENSG00000227318	ENSG00000227318	RP11-282E4.1	9:66664324-66665950	NOTEST	0.0574505	0.0468963	-0.292847	0	1	1
ENSG00000227319	ENSG00000227319	RBM22P6	X:52228191-52229056	NOTEST	0	0	0	0	1	1
ENSG00000227321	ENSG00000227321	MTND4P15	9:94794280-94877666	NOTEST	0.0314518	0.026795	-0.231176	0	1	1
ENSG00000227322	ENSG00000227322	RXRB	HSCHR6_MHC_COX:33082996-33093846	NOTEST	0	0	0	0	1	1
ENSG00000227325	ENSG00000227325	AC021106.1	4:37892707-38140796	NOTEST	0	0	0	0	1	1
ENSG00000227326	ENSG00000227326	RPL7AP7	HSCHR6_MHC_SSTO:29767669-29768466	NOTEST	0	0	0	0	1	1
ENSG00000227330	ENSG00000227330	AP000998.2	21:19273579-19639690	NOTEST	0	0	0	0	1	1
ENSG00000227331	ENSG00000227331	AC005042.2	2:159313475-159610287	NOTEST	0	0.0166682	inf	0	1	1
ENSG00000227332	ENSG00000227332	RP11-38M15.11	13:19390857-19446107	NOTEST	0	0	0	0	1	1
ENSG00000227333	ENSG00000227333	EHMT2	HSCHR6_MHC_DBB:31829720-31847649	NOTEST	0	0	0	0	1	1
ENSG00000227334	ENSG00000227334	HLA-N	HSCHR6_MHC_COX:30308998-30309133	NOTEST	0	0	0	0	1	1
ENSG00000227335	ENSG00000227335	IGHJ1P	14:106331833-106331888	NOTEST	0	0	0	0	1	1
ENSG00000227336	ENSG00000227336	LINC00434	13:60788485-60789080	NOTEST	0	0	0	0	1	1
ENSG00000227337	ENSG00000227337	AC139452.2	3:32827137-32827608	NOTEST	0	0.0352086	inf	0	1	1
ENSG00000227338	ENSG00000227338	RP11-195B3.1	10:3308194-3309207	NOTEST	0	0	0	0	1	1
ENSG00000227339	ENSG00000227339	THRAP3P1	3:31494323-31497386	NOTEST	0	0	0	0	1	1
ENSG00000227342	ENSG00000227342	LINC00307	21:31581468-31584101	NOTEST	0	0	0	0	1	1
ENSG00000227343	ENSG00000227343	RPL15P1	20:18070759-18071359	NOTEST	0	0	0	0	1	1
ENSG00000227347	ENSG00000227347	HNRNPKP2	2:136956683-136958073	NOTEST	0.0365508	0	#NAME?	0	1	1
ENSG00000227348	ENSG00000227348	MTND5P25	2:202047603-202094129	NOTEST	0	0	0	0	1	1
ENSG00000227349	ENSG00000227349	CEACAMP7	19:43453654-43454539	NOTEST	0	0	0	0	1	1
ENSG00000227350	ENSG00000227350	RP11-438P9.2	9:110305431-110305897	NOTEST	0	0	0	0	1	1
ENSG00000227351	ENSG00000227351	NANOGP6	10:101542488-101611949	NOTEST	0	0.114023	inf	0	1	1
ENSG00000227352	ENSG00000227352	ARHGEF7-AS1	13:111766158-111958084	NOTEST	0	0	0	0	1	1
ENSG00000227353	ENSG00000227353	RP11-475I24.6	9:44477548-44478456	NOTEST	0	0	0	0	1	1
ENSG00000227354	ENSG00000227354	RBM26-AS1	13:79885961-79998463	NOTEST	0.591372	0.481539	-0.296412	0	1	1
ENSG00000227355	ENSG00000227355	RP11-162D16.2	9:124137518-124262306	NOTEST	0	0	0	0	1	1
ENSG00000227356	ENSG00000227356	LINC00866	10:99588234-99609555	NOTEST	0	0.0428599	inf	0	1	1
ENSG00000227357	ENSG00000227357	HLA-DRB4	HSCHR6_MHC_SSTO:32509572-32524536	NOTEST	0	0	0	0	1	1
ENSG00000227358	ENSG00000227358	RP11-180I4.1	9:98412435-98478000	NOTEST	0	0	0	0	1	1
ENSG00000227360	ENSG00000227360	RP11-518I13.1	6:156814359-156820905	NOTEST	0	0	0	0	1	1
ENSG00000227361	ENSG00000227361	RPS24P7	2:62030277-62030523	NOTEST	0	0	0	0	1	1
ENSG00000227363	ENSG00000227363	AC019172.2	2:3891773-3895001	NOTEST	0	0	0	0	1	1
ENSG00000227364	ENSG00000227364	AC018685.2	2:2733679-2734729	NOTEST	0	0	0	0	1	1
ENSG00000227365	ENSG00000227365	AC008060.5	7:155266900-155326557	NOTEST	0	0	0	0	1	1
ENSG00000227366	ENSG00000227366	HLA-U	HSCHR6_MHC_APD:29838542-29838728	NOTEST	0	0	0	0	1	1
ENSG00000227367	ENSG00000227367	SLC9B1P4	22:16909689-16957613	NOTEST	0	0	0	0	1	1

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ENSG00000227368	ENSG00000227368	AC079753.5	2:113690201-113690748	NOTEST	0	0	0	0	1	1
ENSG00000227370	ENSG00000227370	RP4-669P10.19	22:42481528-42535938	NOTEST	0.559965	0.325625	-0.782124	0	1	1
ENSG00000227371	ENSG00000227371	RP11-3L10.2	7:121059125-121059899	NOTEST	0	0	0	0	1	1
ENSG00000227373	ENSG00000227373	RP11-160H22.5	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000227374	ENSG00000227374	RP11-109A6.3	10:131567107-131567699	NOTEST	0	0	0	0	1	1
ENSG00000227375	ENSG00000227375	DLG1-AS1	3:196769430-197030618	NOTEST	0.027492	0.0586638	1.09346	0	1	1
ENSG00000227379	ENSG00000227379	PPIAP2	20:25228704-25371619	NOTEST	0	0	0	0	1	1
ENSG00000227380	ENSG00000227380	HCG15	HSCHR6_MHC_COX:28950577-28952911	NOTEST	0	0	0	0	1	1
ENSG00000227382	ENSG00000227382	EIF4A2P2	10:74870216-75118617	NOTEST	0	0.0128581	inf	0	1	1
ENSG00000227383	ENSG00000227383	RP11-571F15.2	9:34179002-34329198	NOTEST	0	0	0	0	1	1
ENSG00000227384	ENSG00000227384	HLA-DRB9	HSCHR6_MHC_APD:32438581-32452263	NOTEST	0	0	0	0	1	1
ENSG00000227386	ENSG00000227386	AC091705.1	7:25587381-25590682	NOTEST	0	0	0	0	1	1
ENSG00000227388	ENSG00000227388	RP11-112J3.16	9:35772159-35790429	NOTEST	0.141595	0.0631824	-1.16417	0	1	1
ENSG00000227389	ENSG00000227389	DDX39BP2	HSCHR6_MHC_MCF:30039452-30039849	NOTEST	0	0	0	0	1	1
ENSG00000227391	ENSG00000227391	SALL1P1	X:49429446-49433283	NOTEST	0	0	0	0	1	1
ENSG00000227392	ENSG00000227392	HPN-AS1	19:35531409-35598141	NOTEST	0.0155848	0.0121165	-0.363163	0	1	1
ENSG00000227393	ENSG00000227393	RP6-127F18.2	X:28605515-29974840	NOTEST	0	0	0	0	1	1
ENSG00000227394	ENSG00000227394	AC007386.3	2:65187186-65187768	NOTEST	0.242226	0.13384	-0.855847	0	1	1
ENSG00000227395	ENSG00000227395	EIF2AP4	10:45301890-45303671	NOTEST	0	0	0	0	1	1
ENSG00000227397	ENSG00000227397	CTD-2526L21.3	7:63250286-63250476	NOTEST	0	0	0	0	1	1
ENSG00000227398	ENSG00000227398	KIF9-AS1	3:47205986-47388306	NOTEST	0.042141	0.0513791	0.285957	0	1	1
ENSG00000227399	ENSG00000227399	RP11-118F2.2	9:94768343-94768826	NOTEST	0	0	0	0	1	1
ENSG00000227400	ENSG00000227400	AC012501.2	2:154277190-154449801	NOTEST	0	0	0	0	1	1
ENSG00000227401	ENSG00000227401	RPL37P1	20:34146506-34195484	NOTEST	0	0	0	0	1	1
ENSG00000227402	ENSG00000227402	SLC39A7	HSCHR6_MHC_MANN:33315283-33326135	NOTEST	0	0	0	0	1	1
ENSG00000227403	ENSG00000227403	AC009299.3	2:161952741-162111179	NOTEST	0	0	0	0	1	1
ENSG00000227404	ENSG00000227404	KRT8P20	7:38694804-38696213	NOTEST	0	0	0	0	1	1
ENSG00000227405	ENSG00000227405	ZDHHC20P2	HSCHR6_MHC_SSTO:31341098-31341525	NOTEST	0	0	0	0	1	1
ENSG00000227406	ENSG00000227406	RNF6P1	21:40745688-40748992	NOTEST	0	0	0	0	1	1
ENSG00000227407	ENSG00000227407	AC008746.3	19:54926392-54948080	NOTEST	0	0	0	0	1	1
ENSG00000227408	ENSG00000227408	AMYP1	1:104256344-104262493	NOTEST	0	0	0	0	1	1
ENSG00000227409	ENSG00000227409	ZMYM4-AS1	1:35734567-35887659	NOTEST	0	0	0	0	1	1
ENSG00000227411	ENSG00000227411	BAATP1	9:104096365-104101629	NOTEST	0	0	0	0	1	1
ENSG00000227412	ENSG00000227412	STK33P1	9:88107493-88109009	NOTEST	0	0	0	0	1	1
ENSG00000227413	ENSG00000227413	RP5-1042K10.12	22:40742506-41032706	NOTEST	0.0804073	0	#NAME?	0	1	1
ENSG00000227415	ENSG00000227415	RP1-91G5.3	1:152346429-152417932	NOTEST	0	0	0	0	1	1
ENSG00000227416	ENSG00000227416	RP11-109P14.2	1:38248128-38248557	NOTEST	0	0	0	0	1	1
ENSG00000227417	ENSG00000227417	RP11-397P13.6	1:203764781-203823252	NOTEST	0	0.0918977	inf	0	1	1
ENSG00000227418	ENSG00000227418	PCGEM1	2:193614570-193641625	NOTEST	0	0	0	0	1	1
ENSG00000227420	ENSG00000227420	MRPS18B	HSCHR6_MHC_COX:30558025-30584021	NOTEST	0	0	0	0	1	1
ENSG00000227421	ENSG00000227421	RP11-476B1.1	1:196014125-196030203	NOTEST	0	0	0	0	1	1
ENSG00000227422	ENSG00000227422	DDR1-AS1	HSCHR6_MHC_MCF:30913329-30922258	NOTEST	0	0	0	0	1	1
ENSG00000227423	ENSG00000227423	OR10U1P	12:55587665-55588570	NOTEST	0	0	0	0	1	1

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ENSG00000227425	ENSG00000227425	MRPS21P2	1:157800703-157868046	NOTEST	0	0	0	0	1	1
ENSG00000227426	ENSG00000227426	VN1R33P	7:62854126-62882424	NOTEST	0	0	0	0	1	1
ENSG00000227427	ENSG00000227427	RP1-49C23.1	X:57792752-57793725	NOTEST	0	0	0	0	1	1
ENSG00000227429	ENSG00000227429	HCP5	HSCHR6_MHC_MCF:31508506-31509970	NOTEST	0	0	0	0	1	1
ENSG00000227430	ENSG00000227430	AC019185.2	2:209224437-209719227	NOTEST	0	0	0	0	1	1
ENSG00000227431	ENSG00000227431	RP1-155G6.4	20:47656999-47662581	NOTEST	0.0910187	0	#NAME?	0	1	1
ENSG00000227432	ENSG00000227432	AC053503.11	2:220299567-220403494	NOTEST	0	0	0	0	1	1
ENSG00000227433	ENSG00000227433	AC069213.4	3:194995464-195163807	NOTEST	0	0	0	0	1	1
ENSG00000227434	ENSG00000227434	RNF19BPX	X:89464794-89465419	NOTEST	0	0	0	0	1	1
ENSG00000227435	ENSG00000227435	PPP1R2P1	HSCHR6_MHC_DBB:32786474-32825559	NOTEST	0	0	0	0	1	1
ENSG00000227436	ENSG00000227436	FCF1P1	7:23636997-23684327	NOTEST	0.0687902	0	#NAME?	0	1	1
ENSG00000227437	ENSG00000227437	RP11-179H18.5	10:121397967-121398594	NOTEST	0	0.0230543	inf	0	1	1
ENSG00000227438	ENSG00000227438	AP001471.1	21:47513177-47517444	NOTEST	0	0	0	0	1	1
ENSG00000227439	ENSG00000227439	TTTY17B	Y:26631478-26632610	NOTEST	0	0	0	0	1	1
ENSG00000227440	ENSG00000227440	ATP5G1P4	3:172546525-172546966	NOTEST	0.598127	0.242448	-1.30277	0	1	1
ENSG00000227442	ENSG00000227442	HLA-DRB2	HSCHR6_MHC_QBL:32456256-32470744	NOTEST	0	0	0	0	1	1
ENSG00000227443	ENSG00000227443	RP11-344A7.1	9:21638283-21638675	NOTEST	0	0	0	0	1	1
ENSG00000227444	ENSG00000227444	AC007322.5	Y:24065081-24067253	NOTEST	0	0	0	0	1	1
ENSG00000227445	ENSG00000227445	OR10R1P	1:158484574-158485715	NOTEST	0	0	0	0	1	1
ENSG00000227446	ENSG00000227446	OR12D2	HSCHR6_MHC_DBB:29341258-29424782	NOTEST	0	0	0	0	1	1
ENSG00000227447	ENSG00000227447	XGPY	Y:14551844-14619171	NOTEST	0	0	0	0	1	1
ENSG00000227448	ENSG00000227448	XXbac-BCX196D17.5	HSCHR6_MHC_DBB:29091998-29096697	NOTEST	0	0	0	0	1	1
ENSG00000227449	ENSG00000227449	RP11-111F5.5	9:46685428-46746500	NOTEST	0.23698	0.344182	0.538406	0	1	1
ENSG00000227450	ENSG00000227450	CTB-58E17.5	17:36886487-36906969	NOTEST	0.141799	0	#NAME?	0	1	1
ENSG00000227453	ENSG00000227453	HNRNPA1P63	1:55002468-55003431	NOTEST	0	0	0	0	1	1
ENSG00000227454	ENSG00000227454	MTND4P30	2:203482417-203483604	NOTEST	0	0	0	0	1	1
ENSG00000227455	ENSG00000227455	RP11-300M24.1	6:165241238-165245119	NOTEST	0.0120085	0.0115882	-0.0513984	0	1	1
ENSG00000227456	ENSG00000227456	LINC00310	21:35445523-35732332	NOTEST	0.121682	0.156186	0.360148	0	1	1
ENSG00000227458	ENSG00000227458	TRIM40	HSCHR6_MHC_DBB:30094213-30106840	NOTEST	0	0	0	0	1	1
ENSG00000227459	ENSG00000227459	AC079612.2	2:240547391-240552533	NOTEST	0	0	0	0	1	1
ENSG00000227460	ENSG00000227460	SYNGAP1	HSCHR6_MHC_SSTO:33527234-33560852	NOTEST	0	0	0	0	1	1
ENSG00000227462	ENSG00000227462	RP11-108B14.4	10:22514626-22514953	NOTEST	0	0.213511	inf	0	1	1
ENSG00000227463	ENSG00000227463	RP11-158D2.2	9:86678357-86709492	NOTEST	0	0	0	0	1	1
ENSG00000227465	ENSG00000227465	GPN3P1	10:25936498-25937033	NOTEST	0	0	0	0	1	1
ENSG00000227466	ENSG00000227466	RP11-397C12.1	1:66258196-66840259	NOTEST	0	0	0	0	1	1
ENSG00000227467	ENSG00000227467	RP11-169D4.1	11:72281703-72284273	NOTEST	0	0.0202837	inf	0	1	1
ENSG00000227468	ENSG00000227468	AL928742.12	14:106064027-106071694	NOTEST	0	0	0	0	1	1
ENSG00000227469	ENSG00000227469	RBM22P8	X:52501126-52501685	NOTEST	0	0	0	0	1	1
ENSG00000227470	ENSG00000227470	AC073415.2	2:109403212-109501933	NOTEST	0	0	0	0	1	1
ENSG00000227471	ENSG00000227471	AKR1B15	7:134233887-134264627	NOTEST	0.0643244	0.0215597	-1.57703	0	1	1
ENSG00000227472	ENSG00000227472	TRIM10	HSCHR6_MHC_DBB:30110049-30119038	NOTEST	0	0	0	0	1	1
ENSG00000227473	ENSG00000227473	TSSK5P1	8:145196116-145198567	NOTEST	0.121084	0.101076	-0.26057	0	1	1
ENSG00000227474	ENSG00000227474	RP11-295P9.2	10:13628926-14504141	NOTEST	0	0	0	0	1	1

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ENSG00000227477	ENSG00000227477	STK4-AS1	20:43592434-43595043	NOTEST	0.367086	0.276695	-0.407823	0	1	1
ENSG00000227479	ENSG00000227479	AC124861.1	2:241166976-241195452	NOTEST	0	0	0	0	1	1
ENSG00000227480	ENSG00000227480	CCDC148-AS1	2:159023161-159313265	NOTEST	0	0	0	0	1	1
ENSG00000227481	ENSG00000227481	RP11-89N17.2	7:33769903-33771676	NOTEST	0	0	0	0	1	1
ENSG00000227482	ENSG00000227482	RP11-18B16.2	9:116413235-116445135	NOTEST	0.014118	0.00993753	-0.506572	0	1	1
ENSG00000227484	ENSG00000227484	XX-C283C717.1	22:50747458-50765489	NOTEST	0	0	0	0	1	1
ENSG00000227485	ENSG00000227485	RP11-5P4.2	1:63489877-63491329	NOTEST	0	0	0	0	1	1
ENSG00000227486	ENSG00000227486	RP13-188A5.1	X:55934555-56041606	NOTEST	0	0	0	0	1	1
ENSG00000227487	ENSG00000227487	NCAM1-AS1	11:112830001-113149158	NOTEST	0.0845943	0	#NAME?	0	1	1
ENSG00000227488	ENSG00000227488	GAGE12D	X:49306369-49313697	NOTEST	0	0	0	0	1	1
ENSG00000227489	ENSG00000227489	AC006458.3	7:15105831-15108276	NOTEST	0	0	0	0	1	1
ENSG00000227490	ENSG00000227490	RP11-157L3.6	9:46169972-46170336	NOTEST	0	0	0	0	1	1
ENSG00000227491	ENSG00000227491	CCNJP1	7:56296326-56297475	NOTEST	0	0	0	0	1	1
ENSG00000227492	ENSG00000227492	RP11-316M21.6	10:101989423-102027437	NOTEST	0.0633759	0	#NAME?	0	1	1
ENSG00000227493	ENSG00000227493	RP11-104D21.1	X:50773421-50774357	NOTEST	0	0	0	0	1	1
ENSG00000227494	ENSG00000227494	USP9YP14	Y:20642972-20649286	NOTEST	0	0	0	0	1	1
ENSG00000227495	ENSG00000227495	AC109333.10	17:4901242-4931696	NOTEST	0.0360558	0.0536177	0.572478	0	1	1
ENSG00000227496	ENSG00000227496	RP11-145A3.1	1:225888305-225939945	NOTEST	0.0526222	0.205406	1.96473	0	1	1
ENSG00000227497	ENSG00000227497	PABPC1P6	2:92065994-92068221	NOTEST	0	0	0	0	1	1
ENSG00000227498	ENSG00000227498	AC018359.3	3:34200825-34604369	NOTEST	0	0	0	0	1	1
ENSG00000227499	ENSG00000227499	RP11-419M24.4	7:55945604-55945857	NOTEST	0	0	0	0	1	1
ENSG00000227502	ENSG00000227502	RP1-249H1.4	6:114189177-114194516	NOTEST	0.0161384	0	#NAME?	0	1	1
ENSG00000227505	ENSG00000227505	RP11-434J24.2	X:146882522-146882820	NOTEST	0	0.0829831	inf	0	1	1
ENSG00000227506	ENSG00000227506	C6orf205	HSCHR6_MHC_MCF:31030033-31036234	NOTEST	0	0	0	0	1	1
ENSG00000227507	ENSG00000227507	LTB	6:31548301-31550299	NOTEST	0.360255	0.295831	-0.284244	0	1	1
ENSG00000227508	ENSG00000227508	RP5-894D12.3	6:170575756-170588975	NOTEST	0	0	0	0	1	1
ENSG00000227509	ENSG00000227509	EIF2B5-IT1	3:183851806-184402546	NOTEST	0	0	0	0	1	1
ENSG00000227510	ENSG00000227510	RP11-196P2.1	13:61491175-61494141	NOTEST	0	0	0	0	1	1
ENSG00000227511	ENSG00000227511	GS1-466O4.2	X:26188168-26189030	NOTEST	0	0	0	0	1	1
ENSG00000227512	ENSG00000227512	RP11-413M3.4	9:139388895-139440314	NOTEST	0.0392212	0	#NAME?	0	1	1
ENSG00000227513	ENSG00000227513	AC114755.3	2:106961021-106961889	NOTEST	0	0	0	0	1	1
ENSG00000227514	ENSG00000227514	RP11-709P2.1	8:113235156-114449328	NOTEST	0	0	0	0	1	1
ENSG00000227515	ENSG00000227515	C1DP4	10:81800376-81800800	NOTEST	0	0	0	0	1	1
ENSG00000227516	ENSG00000227516	RP5-973N23.4	6:41737913-41863099	NOTEST	0	0.0913478	inf	0	1	1
ENSG00000227517	ENSG00000227517	AC003051.1	17:67573391-67899141	NOTEST	0.477086	0.500516	0.0691659	0	1	1
ENSG00000227518	ENSG00000227518	MIR1302-9	9:11986-30891	NOTEST	0.0983768	0.0853356	-0.205171	0	1	1
ENSG00000227519	ENSG00000227519	CTA-342B11.1	22:32359343-32366387	NOTEST	0	0	0	0	1	1
ENSG00000227521	ENSG00000227521	RP13-213K19.1	X:93574036-93575024	NOTEST	0	0	0	0	1	1
ENSG00000227523	ENSG00000227523	RPS20P15	3:27414213-27525911	NOTEST	0	0	0	0	1	1
ENSG00000227525	ENSG00000227525	RPL7P6	12:19241973-19242825	NOTEST	0.0261917	0	#NAME?	0	1	1
ENSG00000227526	ENSG00000227526	HLA-DRB9	HSCHR6_MHC_COX:32375802-32389501	NOTEST	0	0	0	0	1	1

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ENSG00000227527	ENSG00000227527	RP11-223A3.1	1:42642209-42804047	NOTEST	0.0558575	0.0968084	0.793382	0	1	1
ENSG00000227528	ENSG00000227528	DIAPH3-AS1	13:60239716-60738121	NOTEST	0	0	0	0	1	1
ENSG00000227529	ENSG00000227529	SAR1P1	HSCHR6_MHC_MANN:29044352-29044948	NOTEST	0	0	0	0	1	1
ENSG00000227531	ENSG00000227531	RP11-202G18.1	9:113901525-114047116	NOTEST	0	0	0	0	1	1
ENSG00000227532	ENSG00000227532	AC002542.2	7:116592499-116870157	NOTEST	0	0	0	0	1	1
ENSG00000227534	ENSG00000227534	RP3-323B6.1	X:64688966-64690260	NOTEST	0	0	0	0	1	1
ENSG00000227535	ENSG00000227535	RP11-809N15.2	6:105175967-105307794	NOTEST	0	0.133036	inf	0	1	1
ENSG00000227536	ENSG00000227536	SOCS5P4	X:70263063-70265320	NOTEST	0.183747	0.0805893	-1.18906	0	1	1
ENSG00000227537	ENSG00000227537	RP11-215C7.3	10:23547139-23547474	NOTEST	0.0899395	0	#NAME?	0	1	1
ENSG00000227538	ENSG00000227538	HNRNPFP1	1:42506267-42507400	NOTEST	0	0	0	0	1	1
ENSG00000227541	ENSG00000227541	RP3-525N14.2	X:119170200-119379122	NOTEST	0.0287318	0.0223604	-0.361703	0	1	1
ENSG00000227542	ENSG00000227542	AC092614.2	2:192093890-192290115	NOTEST	0.231132	0.363282	0.652371	0	1	1
ENSG00000227544	ENSG00000227544	AC018647.3	7:35754643-35774497	NOTEST	0.0506693	0	#NAME?	0	1	1
ENSG00000227545	ENSG00000227545	RP5-905H7.10	7:62787051-62814743	NOTEST	0	0	0	0	1	1
ENSG00000227547	ENSG00000227547	OR4A2P	11:51451069-51451982	NOTEST	0	0	0	0	1	1
ENSG00000227549	ENSG00000227549	AC116035.2	3:30566236-30568677	NOTEST	0	0	0	0	1	1
ENSG00000227550	ENSG00000227550	TRBV7-5	7:142157377-142157849	NOTEST	0	0	0	0	1	1
ENSG00000227551	ENSG00000227551	USP17L12	4:9212382-9228214	NOTEST	0	0	0	0	1	1
ENSG00000227552	ENSG00000227552	RP11-417J8.1	1:142553292-142559170	NOTEST	0	0	0	0	1	1
ENSG00000227554	ENSG00000227554	RP11-444D13.1	1:183605219-183897665	NOTEST	0	0	0	0	1	1
ENSG00000227555	ENSG00000227555	RP11-406A20.4	9:92782935-92803781	NOTEST	0	0	0	0	1	1
ENSG00000227556	ENSG00000227556	RP11-472F19.1	1:78695282-79005434	NOTEST	0	0	0	0	1	1
ENSG00000227557	ENSG00000227557	MTND3P9	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000227558	ENSG00000227558	PGM5P2	9:69065654-69149621	NOTEST	0.127874	0.0797469	-0.681227	0	1	1
ENSG00000227559	ENSG00000227559	HCG14	HSCHR6_MHC_QBL:28864310-28865103	NOTEST	0	0	0	0	1	1
ENSG00000227560	ENSG00000227560	RP11-139K1.2	10:114710008-114927437	NOTEST	0	0	0	0	1	1
ENSG00000227562	ENSG00000227562	RP11-796I2.1	7:151647470-151652070	NOTEST	0	0	0	0	1	1
ENSG00000227563	ENSG00000227563	RNF11B	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000227564	ENSG00000227564	LINC00376	13:63757233-63801189	NOTEST	0	0	0	0	1	1
ENSG00000227565	ENSG00000227565	NFKBIL1	HSCHR6_MHC_MANN:31554141-31566099	NOTEST	0	0	0	0	1	1
ENSG00000227567	ENSG00000227567	APOM	HSCHR6_MHC_DBB:31588978-31608169	NOTEST	0	0	0	0	1	1
ENSG00000227568	ENSG00000227568	SNX18P26	13:19381418-19382158	NOTEST	0.0261053	0	#NAME?	0	1	1
ENSG00000227569	ENSG00000227569	RP11-266E16.1	9:45656240-45656586	NOTEST	0	0	0	0	1	1
ENSG00000227573	ENSG00000227573	RP5-1166A24.1	7:121958480-122526813	NOTEST	0	0	0	0	1	1
ENSG00000227574	ENSG00000227574	RP13-1039J1.3	2:111143953-111230652	NOTEST	0	0	0	0	1	1
ENSG00000227576	ENSG00000227576	GPR53P	HSCHR6_MHC_APD:29505567-29506651	NOTEST	0	0	0	0	1	1
ENSG00000227577	ENSG00000227577	COL11A2P1	HSCHR6_MHC_APD:33054937-33058474	NOTEST	0	0	0	0	1	1
ENSG00000227578	ENSG00000227578	RPS3AP53	3:15182886-15183664	NOTEST	0	0	0	0	1	1
ENSG00000227579	ENSG00000227579	RP1-35C21.2	1:177362422-177566844	NOTEST	0	0	0	0	1	1
ENSG00000227581	ENSG00000227581	RP13-140E4.1	X:89294211-89294833	NOTEST	0	0	0	0	1	1
ENSG00000227582	ENSG00000227582	RP11-262H14.7	9:66513031-66555928	NOTEST	0	0	0	0	1	1
ENSG00000227583	ENSG00000227583	RP11-119F7.3	10:70320412-70454239	NOTEST	0	0.0201342	inf	0	1	1

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ENSG00000227584	ENSG00000227584	MTND4P5	7:57260400-57261775	NOTEST	0	0	0	0	1	1
ENSG00000227585	ENSG00000227585	RP11-103C3.2	1:221723127-221723985	NOTEST	0	0	0	0	1	1
ENSG00000227586	ENSG00000227586	RP11-162A23.5	10:124931047-124931395	NOTEST	0	0	0	0	1	1
ENSG00000227587	ENSG00000227587	ATP6V1G2	HSCHR6_MHC_COX:31483951-31502076	NOTEST	0	0	0	0	1	1
ENSG00000227588	ENSG00000227588	CNTN4-AS2	3:2140496-3102829	NOTEST	0	0	0	0	1	1
ENSG00000227589	ENSG00000227589	RP5-1092A11.5	1:3547330-3663900	NOTEST	0	0	0	0	1	1
ENSG00000227590	ENSG00000227590	ATP5G1P5	13:107306263-107324511	NOTEST	0	0	0	0	1	1
ENSG00000227591	ENSG00000227591	RP1-28O10.1	1:209834708-209908295	NOTEST	0	0	0	0	1	1
ENSG00000227592	ENSG00000227592	PIGFP3	X:30035276-30035998	NOTEST	0	0	0	0	1	1
ENSG00000227593	ENSG00000227593	RP11-715G18.3	11:93754526-93846917	NOTEST	0	0	0	0	1	1
ENSG00000227596	ENSG00000227596	LINC00243	HSCHR6_MHC_DBB:30757110-30789111	NOTEST	0	0	0	0	1	1
ENSG00000227597	ENSG00000227597	AC019100.7	2:108893267-108894398	NOTEST	0	0	0	0	1	1
ENSG00000227598	ENSG00000227598	RP1-167A14.2	6:167383113-167412553	NOTEST	0.131425	0.16769	0.351556	0	1	1
ENSG00000227599	ENSG00000227599	RP4-753D4.2	20:40701391-41818610	NOTEST	0	0	0	0	1	1
ENSG00000227600	ENSG00000227600	PPT2	HSCHR6_MHC_SSTO:32123002-32152743	NOTEST	0	0	0	0	1	1
ENSG00000227602	ENSG00000227602	RP3-445N2.1	6:55921387-56258892	NOTEST	0	0	0	0	1	1
ENSG00000227603	ENSG00000227603	RP11-165J3.6	9:96197613-96199403	NOTEST	0.0811287	0.153824	0.922994	0	1	1
ENSG00000227604	ENSG00000227604	TOMM22P3	13:33528194-33528539	NOTEST	0	0	0	0	1	1
ENSG00000227606	ENSG00000227606	AC005392.13	19:43657430-43665014	NOTEST	0	0	0	0	1	1
ENSG00000227607	ENSG00000227607	SUMO2P2	9:23632103-23632358	NOTEST	0	0	0	0	1	1
ENSG00000227609	ENSG00000227609	TMEM183AP1	6:29523291-29601753	NOTEST	0	0	0	0	1	1
ENSG00000227610	ENSG00000227610	FRMPD3-AS1	X:106756212-106848481	NOTEST	0	0	0	0	1	1
ENSG00000227611	ENSG00000227611	LINC01074	13:62895437-62896531	NOTEST	0	0	0	0	1	1
ENSG00000227613	ENSG00000227613	QRSL1P2	1:222262510-222560776	NOTEST	0	0	0	0	1	1
ENSG00000227616	ENSG00000227616	AC063976.1	5:131483183-131485252	NOTEST	0	0	0	0	1	1
ENSG00000227617	ENSG00000227617	CERS6-AS1	2:169312371-169769881	NOTEST	0.0337951	0	#NAME?	0	1	1
ENSG00000227619	ENSG00000227619	RP11-492E3.2	9:132337687-132346835	NOTEST	0	0	0	0	1	1
ENSG00000227620	ENSG00000227620	ALG1L8P	11:67552743-67572807	NOTEST	0	0	0	0	1	1
ENSG00000227621	ENSG00000227621	PHBP11	1:224044280-224045089	NOTEST	0	0	0	0	1	1
ENSG00000227623	ENSG00000227623	AC073987.2	2:103892361-103892596	NOTEST	0	0	0	0	1	1
ENSG00000227624	ENSG00000227624	SNRPEP3	16:20250293-20250569	NOTEST	0	0	0	0	1	1
ENSG00000227625	ENSG00000227625	RP11-520H14.1	1:228322485-228322693	NOTEST	0	0	0	0	1	1
ENSG00000227626	ENSG00000227626	OR2AD1P	HSCHR6_MHC_COX:28991068-28991996	NOTEST	0	0	0	0	1	1
ENSG00000227627	ENSG00000227627	RP1-101K10.6	6:153304884-153323820	NOTEST	0.31907	0	#NAME?	0	1	1
ENSG00000227628	ENSG00000227628	RP11-472D17.3	X:52333856-52334578	NOTEST	0	0	0	0	1	1
ENSG00000227629	ENSG00000227629	SLC25A15P1	Y:28732788-28737748	NOTEST	0	0	0	0	1	1
ENSG00000227630	ENSG00000227630	LINC01132	1:234859788-234867390	NOTEST	0.011504	0.0159434	0.470824	0	1	1
ENSG00000227632	ENSG00000227632	AC018804.6	2:130959884-130970201	NOTEST	0.155974	0.0235231	-2.72915	0	1	1
ENSG00000227633	ENSG00000227633	RBMY2YP	Y:27412730-27419678	NOTEST	0	0	0	0	1	1
ENSG00000227634	ENSG00000227634	RP11-431K24.3	1:8268731-8275270	NOTEST	0	0	0	0	1	1
ENSG00000227635	ENSG00000227635	USP9YP21	Y:28079979-28082028	NOTEST	0	0	0	0	1	1
ENSG00000227637	ENSG00000227637	RP11-242O24.5	1:29474254-29508499	NOTEST	0.191002	0.300822	0.655323	0	1	1
ENSG00000227638	ENSG00000227638	HNRNPA1P14	9:91003333-91093609	NOTEST	0.0710445	0.0137059	-2.37392	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000227639	ENSG00000227639	OR2W1	HSCHR6_MHC_SSTO:29012009-29013037	NOTEST	0	0	0	0	1	1
ENSG00000227640	ENSG00000227640	SOX21-AS1	13:95364969-95368500	NOTEST	0	0.0103936	inf	0	1	1
ENSG00000227642	ENSG00000227642	AGPAT1	HSCHR6_MHC_MANN:32155582-32185300	NOTEST	0	0	0	0	1	1
ENSG00000227644	ENSG00000227644	HIGD1AP11	1:53527853-53551174	NOTEST	0	0	0	0	1	1
ENSG00000227645	ENSG00000227645	RPL7P54	X:78018722-78019396	NOTEST	0	0	0	0	1	1
ENSG00000227646	ENSG00000227646	STEAP2-AS1	7:89511666-89867451	NOTEST	0	0.0392357	inf	0	1	1
ENSG00000227647	ENSG00000227647	HCG9	HSCHR6_MHC_MANN:29938074-29941369	NOTEST	0	0	0	0	1	1
ENSG00000227649	ENSG00000227649	RP11-522L3.9	X:102024088-102161086	NOTEST	0	0	0	0	1	1
ENSG00000227650	ENSG00000227650	UQCRHP1	HSCHR6_MHC_COX:31566273-31566547	NOTEST	0	0	0	0	1	1
ENSG00000227652	ENSG00000227652	RANP1	HSCHR6_MHC_DBB:30443963-30444614	NOTEST	0	0	0	0	1	1
ENSG00000227653	ENSG00000227653	ISCA1P6	2:129276361-129276751	NOTEST	0.128313	0	#NAME?	0	1	1
ENSG00000227655	ENSG00000227655	PTMAP1	HSCHR6_MHC_MCF:30673077-30693061	NOTEST	0	0	0	0	1	1
ENSG00000227656	ENSG00000227656	RPL3P2	HSCHR6_MHC_MCF:31325199-31326399	NOTEST	0	0	0	0	1	1
ENSG00000227657	ENSG00000227657	RP13-483F6.1	X:105806003-105806634	NOTEST	0	0	0	0	1	1
ENSG00000227658	ENSG00000227658	AC005160.3	7:40174574-40900362	NOTEST	0	0	0	0	1	1
ENSG00000227659	ENSG00000227659	CLYBL-AS2	13:100258918-100549387	NOTEST	0.0805007	0	#NAME?	0	1	1
ENSG00000227660	ENSG00000227660	RP11-162J8.2	6:149068463-149398126	NOTEST	0	0	0	0	1	1
ENSG00000227661	ENSG00000227661	AC073869.10	2:132137725-132138486	NOTEST	0	0	0	0	1	1
ENSG00000227663	ENSG00000227663	RPL7P2	20:2056200-2056468	NOTEST	0	0	0	0	1	1
ENSG00000227665	ENSG00000227665	C6orf47-AS1	HSCHR6_MHC_DBB:31608256-31610731	NOTEST	0	0	0	0	1	1
ENSG00000227667	ENSG00000227667	RP11-331H2.3	1:162949340-162949583	NOTEST	0	0	0	0	1	1
ENSG00000227668	ENSG00000227668	MAS1LP1	HSCHR6_MHC_MCF:29442586-29443633	NOTEST	0	0	0	0	1	1
ENSG00000227669	ENSG00000227669	HLA-H	HSCHR6_MHC_DBB:29846689-29849870	NOTEST	0	0	0	0	1	1
ENSG00000227672	ENSG00000227672	RPL3P2	HSCHR6_MHC_SSTO:31240665-31241865	NOTEST	0	0	0	0	1	1
ENSG00000227673	ENSG00000227673	RP11-243J18.2	1:155579566-155829191	NOTEST	0	0	0	0	1	1
ENSG00000227675	ENSG00000227675	GS1-256O22.1	X:142627591-142631882	NOTEST	0	0	0	0	1	1
ENSG00000227676	ENSG00000227676	LINC01068	13:80140880-80144983	NOTEST	0	0.0599085	inf	0	1	1
ENSG00000227678	ENSG00000227678	RP11-73O6.3	6:130334843-130686570	NOTEST	0.0192146	0	#NAME?	0	1	1
ENSG00000227679	ENSG00000227679	RP11-453N3.1	10:39055225-39055622	NOTEST	0	0	0	0	1	1
ENSG00000227680	ENSG00000227680	AC108051.2	2:103603780-103605023	NOTEST	0	0	0	0	1	1
ENSG00000227681	ENSG00000227681	RP11-307P5.1	6:147830062-148275073	NOTEST	0	0.154268	inf	0	1	1
ENSG00000227682	ENSG00000227682	ATP5A1P2	2:156126144-156126399	NOTEST	0	0	0	0	1	1
ENSG00000227683	ENSG00000227683	RP11-445N18.5	10:45493145-45676875	NOTEST	0	0	0	0	1	1
ENSG00000227684	ENSG00000227684	CROCCP4	1:17066767-17299474	NOTEST	0	0.0707926	inf	0	1	1
ENSG00000227685	ENSG00000227685	AC087499.10	17:20515979-20536572	NOTEST	0	0.0257551	inf	0	1	1
ENSG00000227686	ENSG00000227686	VARS	HSCHR6_MHC_QBL:31749635-31753979	NOTEST	0	0	0	0	1	1
ENSG00000227687	ENSG00000227687	RP4-681L3.2	1:205882175-205912588	NOTEST	0	0	0	0	1	1
ENSG00000227688	ENSG00000227688	HNRNPA3P2	20:34894257-35274619	NOTEST	0	0	0	0	1	1
ENSG00000227689	ENSG00000227689	SRP68P2	17:18414534-18528930	NOTEST	0.00782717	0.123001	3.97403	0	1	1
ENSG00000227691	ENSG00000227691	CYCSP41	21:10906200-11098980	NOTEST	0	0	0	0	1	1
ENSG00000227692	ENSG00000227692	MED28P3	2:187229324-187229855	NOTEST	0.16505	0.0906956	-0.863796	0	1	1
ENSG00000227693	ENSG00000227693	GSTM3P1	20:21482032-21482606	NOTEST	0.420498	0.225592	-0.898382	0	1	1
ENSG00000227695	ENSG00000227695	DNMBP-AS1	10:101635333-101769676	NOTEST	0	0	0	0	1	1
ENSG00000227698	ENSG00000227698	AP001619.2	21:43218384-43299591	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000227700	ENSG00000227700	RP11-301M17.1	1:147718439-147718956	NOTEST	0	0	0	0	1	1
ENSG00000227702	ENSG00000227702	LINC00111	21:43099340-43117496	NOTEST	0	0	0	0	1	1
ENSG00000227703	ENSG00000227703	RANP1	HSCHR6_MHC_COX:30443577-30444228	NOTEST	0	0	0	0	1	1
ENSG00000227704	ENSG00000227704	RP1-266L20.4	6:170125186-170139088	NOTEST	0	0	0	0	1	1
ENSG00000227705	ENSG00000227705	RP11-15M15.2	20:51588945-52120853	NOTEST	0	0	0	0	1	1
ENSG00000227706	ENSG00000227706	RP11-301G19.1	6:68597537-68599231	NOTEST	0	0.00728204	inf	0	1	1
ENSG00000227707	ENSG00000227707	SDAD1P3	3:33813454-33813787	NOTEST	0	0	0	0	1	1
ENSG00000227708	ENSG00000227708	AC079150.3	2:154194218-154213936	NOTEST	0	0	0	0	1	1
ENSG00000227709	ENSG00000227709	RP11-118D22.3	3:155755489-156256545	NOTEST	0	0	0	0	1	1
ENSG00000227710	ENSG00000227710	LL22NC03-30E12.13	22:22522681-22523027	NOTEST	0	0	0	0	1	1
ENSG00000227711	ENSG00000227711	RP11-275O4.3	1:227698296-227708178	NOTEST	0	0	0	0	1	1
ENSG00000227712	ENSG00000227712	RP11-418J17.3	1:119573838-119869926	NOTEST	0.0782241	0.0317793	-1.29953	0	1	1
ENSG00000227713	ENSG00000227713	AC116609.1	2:724965-731224	NOTEST	0	0	0	0	1	1
ENSG00000227714	ENSG00000227714	MTND6P18	13:96329392-96447243	NOTEST	0	0	0	0	1	1
ENSG00000227715	ENSG00000227715	HLA-A	HSCHR6_MHC_MCF:29846326-29992167	NOTEST	0	0	0	0	1	1
ENSG00000227716	ENSG00000227716	AP000459.7	21:24849959-24863043	NOTEST	0	0	0	0	1	1
ENSG00000227717	ENSG00000227717	RP11-578F21.4	15:28798717-28806525	NOTEST	0	0	0	0	1	1
ENSG00000227718	ENSG00000227718	AC016730.1	2:13850655-14541087	NOTEST	0	0	0	0	1	1
ENSG00000227719	ENSG00000227719	AC006042.6	7:8152813-8384146	NOTEST	0.120325	0.0597277	-1.01046	0	1	1
ENSG00000227720	ENSG00000227720	PPP1R11	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000227721	ENSG00000227721	RPSAP64	21:40249214-40328392	NOTEST	0	0	0	0	1	1
ENSG00000227722	ENSG00000227722	RP5-1059H15.1	1:168338291-168338839	NOTEST	0	0	0	0	1	1
ENSG00000227723	ENSG00000227723	CTA-31J9.2	6:134846451-134980974	NOTEST	0	0	0	0	1	1
ENSG00000227726	ENSG00000227726	AP001271.3	11:70313960-70963623	NOTEST	0	0	0	0	1	1
ENSG00000227728	ENSG00000227728	RP11-690C23.4	1:246672339-246687589	NOTEST	0	0	0	0	1	1
ENSG00000227729	ENSG00000227729	RD3L	14:104394798-104519004	NOTEST	0	0	0	0	1	1
ENSG00000227730	ENSG00000227730	MTND6P5	9:4985032-5128183	NOTEST	0	0	0	0	1	1
ENSG00000227733	ENSG00000227733	RP4-565E6.1	1:146032646-146253110	NOTEST	0.085006	0.0720345	-0.238877	0	1	1
ENSG00000227734	ENSG00000227734	RP11-49L2.1	10:19492778-20079330	NOTEST	0	0	0	0	1	1
ENSG00000227735	ENSG00000227735	CYCSP5	1:244617678-244804479	NOTEST	0	0	0	0	1	1
ENSG00000227736	ENSG00000227736	AC007163.9	2:202352147-202483901	NOTEST	0	0	0	0	1	1
ENSG00000227737	ENSG00000227737	OR8B1P	11:124235529-124236447	NOTEST	0	0	0	0	1	1
ENSG00000227738	ENSG00000227738	AC092646.2	2:124519746-124520647	NOTEST	0	0	0	0	1	1
ENSG00000227739	ENSG00000227739	TUBB	HSCHR6_MHC_COX:30677841-30683067	NOTEST	0	0	0	0	1	1
ENSG00000227740	ENSG00000227740	RP11-318C24.2	1:175873897-175889649	NOTEST	0	0	0	0	1	1
ENSG00000227741	ENSG00000227741	RP11-536C5.7	1:160171988-160185166	NOTEST	0.406662	0.576843	0.504347	0	1	1
ENSG00000227742	ENSG00000227742	CALR4P	1:52027537-52344477	NOTEST	0.0733392	0	#NAME?	0	1	1
ENSG00000227743	ENSG00000227743	RP4-745K6.1	7:121283387-121290414	NOTEST	0	0	0	0	1	1
ENSG00000227744	ENSG00000227744	AC114788.2	2:239840997-239847965	NOTEST	0	0	0	0	1	1
ENSG00000227745	ENSG00000227745	AC098826.5	2:132890428-132897002	NOTEST	0	0	0	0	1	1
ENSG00000227746	ENSG00000227746	C4A	HSCHR6_MHC_MCF:32058985-32080483	NOTEST	0	0	0	0	1	1
ENSG00000227747	ENSG00000227747	RP11-16L9.1	1:198918144-198918934	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000227748	ENSG00000227748	RP11-497D6.3	6:147163036-147706866	NOTEST	0.0979961	0	#NAME?	0	1	1
ENSG00000227750	ENSG00000227750	HTATSF1P	HSCHR6_MHC_MCF:33375920-33377819	NOTEST	0	0	0	0	1	1
ENSG00000227751	ENSG00000227751	RP1-20B21.4	1:17733255-17766220	NOTEST	0	0	0	0	1	1
ENSG00000227753	ENSG00000227753	RP11-216N21.1	8:86999551-87166457	NOTEST	0	0	0	0	1	1
ENSG00000227754	ENSG00000227754	SUCLA2P1	HSCHR6_MHC_MANN:30481339-30482709	NOTEST	0	0	0	0	1	1
ENSG00000227755	ENSG00000227755	AP000344.4	22:23788784-23803020	NOTEST	0	0.725375	inf	0	1	1
ENSG00000227757	ENSG00000227757	AP000282.2	21:34285956-34444726	NOTEST	0	0	0	0	1	1
ENSG00000227759	ENSG00000227759	VTI1BP4	9:131314865-131419066	NOTEST	0	0	0	0	1	1
ENSG00000227760	ENSG00000227760	RP11-298E10.1	12:14344935-14345218	NOTEST	0	0	0	0	1	1
ENSG00000227761	ENSG00000227761	BAG6	HSCHR6_MHC_DBB:31588978-31608169	NOTEST	0	0	0	0	1	1
ENSG00000227762	ENSG00000227762	GUSBP8	5:98868331-98870315	NOTEST	0.029241	0	#NAME?	0	1	1
ENSG00000227764	ENSG00000227764	RP11-354K1.1	1:211809247-211827923	NOTEST	0	0	0	0	1	1
ENSG00000227765	ENSG00000227765	RP11-162O12.2	4:185220281-185220800	NOTEST	0	0	0	0	1	1
ENSG00000227766	ENSG00000227766	HCG4P5	6:29909036-29913661	NOTEST	0.139096	0.0793076	-0.810552	0	1	1
ENSG00000227769	ENSG00000227769	AC072062.3	2:215674952-216003151	NOTEST	0	0	0	0	1	1
ENSG00000227770	ENSG00000227770	RPL7P12	2:38430504-38466732	NOTEST	0	0	0	0	1	1
ENSG00000227772	ENSG00000227772	MICB	HSCHR6_MHC_SSTO:31455820-31468850	NOTEST	0	0	0	0	1	1
ENSG00000227773	ENSG00000227773	ASH1L-IT1	1:155305058-155533775	NOTEST	0	0	0	0	1	1
ENSG00000227776	ENSG00000227776	AKR1D1P1	1:167488772-167489823	NOTEST	0	0	0	0	1	1
ENSG00000227777	ENSG00000227777	RP4-738P11.3	1:168510002-168513235	NOTEST	0	0	0	0	1	1
ENSG00000227778	ENSG00000227778	XXyac-YX155B6.2	1:147552867-147566198	NOTEST	0	0.0504197	inf	0	1	1
ENSG00000227779	ENSG00000227779	GS1-164F24.1	X:140474986-140475271	NOTEST	0	0	0	0	1	1
ENSG00000227780	ENSG00000227780	ZBTB22	HSCHR6_MHC_DBB:33260108-33263646	NOTEST	0	0	0	0	1	1
ENSG00000227781	ENSG00000227781	GLUD1P2	10:48952490-48981273	NOTEST	0	0.0608971	inf	0	1	1
ENSG00000227782	ENSG00000227782	AC002553.1	17:15879873-16256970	NOTEST	0	0	0	0	1	1
ENSG00000227784	ENSG00000227784	ZNF965P	13:19308219-19309036	NOTEST	0	0	0	0	1	1
ENSG00000227785	ENSG00000227785	AC092013.1	7:85265328-85265660	NOTEST	0	0	0	0	1	1
ENSG00000227788	ENSG00000227788	AC012363.8	2:120770580-120974855	NOTEST	0	0.0174799	inf	0	1	1
ENSG00000227789	ENSG00000227789	AC098817.3	2:83045254-83046388	NOTEST	0	0	0	0	1	1
ENSG00000227790	ENSG00000227790	AC015922.5	17:15732682-15767467	NOTEST	0	0	0	0	1	1
ENSG00000227791	ENSG00000227791	AC007365.4	2:64858754-64978139	NOTEST	0	0	0	0	1	1
ENSG00000227792	ENSG00000227792	RP13-210D15.6	X:134370739-134371295	NOTEST	0	0	0	0	1	1
ENSG00000227794	ENSG00000227794	RPS18	HSCHR6_MHC_SSTO:33382445-33382651	NOTEST	0	0	0	0	1	1
ENSG00000227795	ENSG00000227795	AC092796.1	3:29305684-30051886	NOTEST	0	0	0	0	1	1
ENSG00000227799	ENSG00000227799	AC012358.4	2:55401926-55462989	NOTEST	0.323841	0.145567	-1.1536	0	1	1
ENSG00000227800	ENSG00000227800	IGHD4-17	14:106355941-106362435	NOTEST	0	0	0	0	1	1
ENSG00000227801	ENSG00000227801	COL11A2	HSCHR6_MHC_COX:33052090-33081908	NOTEST	0	0	0	0	1	1
ENSG00000227802	ENSG00000227802	DNAJB3	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000227803	ENSG00000227803	RP11-239H6.2	6:20100934-20317970	NOTEST	0	0	0	0	1	1
ENSG00000227804	ENSG00000227804	PPP1R10	HSCHR6_MHC_DBB:30558417-30584413	NOTEST	0	0	0	0	1	1
ENSG00000227805	ENSG00000227805	RP11-248J23.5	10:97471535-97849995	NOTEST	0	0	0	0	1	1
ENSG00000227806	ENSG00000227806	OR5W1P	11:55670816-55671754	NOTEST	0	0	0	0	1	1
ENSG00000227809	ENSG00000227809	RP11-171A24.2	9:76986446-76998446	NOTEST	0	0	0	0	1	1
ENSG00000227811	ENSG00000227811	FAM212B-AS1	1:112025969-112310638	NOTEST	0.321494	0.239991	-0.421807	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000227813	ENSG00000227813	RP1-180M12.1	22:32149943-32303012	NOTEST	0	0	0	0	1	1
ENSG00000227814	ENSG00000227814	MRPS17P9	X:118490263-118527558	NOTEST	0	0	0	0	1	1
ENSG00000227815	ENSG00000227815	RP11-195C7.3	1:176241618-176242538	NOTEST	0	0	0	0	1	1
ENSG00000227816	ENSG00000227816	TAP1	HSCHR6_MHC_APD:32792100-32831197	NOTEST	0	0	0	0	1	1
ENSG00000227817	ENSG00000227817	ARHGAP42P1	2:131862419-132111282	NOTEST	0	0	0	0	1	1
ENSG00000227818	ENSG00000227818	RP11-227F8.2	1:162008805-162009357	NOTEST	0	0	0	0	1	1
ENSG00000227821	ENSG00000227821	AL392086.1	10:6821559-6884868	NOTEST	0	0	0	0	1	1
ENSG00000227824	ENSG00000227824	AC122136.2	2:216734645-216735241	NOTEST	0	0	0	0	1	1
ENSG00000227825	ENSG00000227825	SLC9A7P1	12:98847612-98850923	NOTEST	0	0	0	0	1	1
ENSG00000227826	ENSG00000227826	DRB4	HSCHR6_MHC_MANN:32542661-32557610	NOTEST	0	0	0	0	1	1
ENSG00000227827	ENSG00000227827	RP11-958N24.2	16:16450080-16471364	NOTEST	0.0203967	0.023108	0.180058	0	1	1
ENSG00000227830	ENSG00000227830	TRIM60P3Y	Y:8281077-8282095	NOTEST	0	0	0	0	1	1
ENSG00000227832	ENSG00000227832	ST13P21	1:109044979-109046077	NOTEST	0	0	0	0	1	1
ENSG00000227834	ENSG00000227834	AP003385.2	11:67419046-67420875	NOTEST	0	0	0	0	1	1
ENSG00000227835	ENSG00000227835	CARM1P1	9:2907072-3053408	NOTEST	0	0	0	0	1	1
ENSG00000227836	ENSG00000227836	AC008850.3	5:96149730-96373219	NOTEST	0	0	0	0	1	1
ENSG00000227837	ENSG00000227837	TRIM60P11Y	Y:26837937-26839079	NOTEST	0	0	0	0	1	1
ENSG00000227838	ENSG00000227838	RP1-213J1P__B.1	22:28072555-28110959	NOTEST	0	0	0	0	1	1
ENSG00000227839	ENSG00000227839	AL645730.2	1:48998526-50489585	NOTEST	0	0	0	0	1	1
ENSG00000227840	ENSG00000227840	KRTAP8-3P	21:32179249-32179437	NOTEST	0	0	0	0	1	1
ENSG00000227841	ENSG00000227841	MTND5P31	2:202352147-202483901	NOTEST	0	0.00868805	inf	0	1	1
ENSG00000227842	ENSG00000227842	AC093166.2	2:112475084-112475414	NOTEST	0	0	0	0	1	1
ENSG00000227843	ENSG00000227843	DDX6P1	HSCHR6_MHC_SSTO:29297504-29298940	NOTEST	0	0	0	0	1	1
ENSG00000227844	ENSG00000227844	RP13-143G15.3	6:136172833-136546733	NOTEST	0.0408614	0.0781162	0.934885	0	1	1
ENSG00000227845	ENSG00000227845	RP11-184B22.2	9:128134603-128135045	NOTEST	0	0	0	0	1	1
ENSG00000227846	ENSG00000227846	UGT1A11P	2:234512198-234513047	NOTEST	0	0	0	0	1	1
ENSG00000227847	ENSG00000227847	RP11-420H19.2	7:124462439-125019375	NOTEST	0	0	0	0	1	1
ENSG00000227848	ENSG00000227848	SUCLA2-AS1	13:48510621-48621358	NOTEST	0.0723244	0.23015	1.67002	0	1	1
ENSG00000227850	ENSG00000227850	SEPT2P1	1:106240660-106240840	NOTEST	0	0	0	0	1	1
ENSG00000227851	ENSG00000227851	RP11-381K7.1	10:113109696-113111861	NOTEST	0	0	0	0	1	1
ENSG00000227852	ENSG00000227852	RP11-156G14.6	9:35592782-35592948	NOTEST	0	0	0	0	1	1
ENSG00000227853	ENSG00000227853	C6orf47-AS1	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000227854	ENSG00000227854	RP11-307O1.1	1:239216047-239216203	NOTEST	0	0	0	0	1	1
ENSG00000227856	ENSG00000227856	SAPCD1-AS1	HSCHR6_MHC_DBB:31689901-31715550	NOTEST	0	0	0	0	1	1
ENSG00000227857	ENSG00000227857	RP4-533D7.5	1:46505811-46651630	NOTEST	0	0.0687946	inf	0	1	1
ENSG00000227858	ENSG00000227858	ZFP57	HSCHR6_MHC_APD:29640387-29641038	NOTEST	0	0	0	0	1	1
ENSG00000227859	ENSG00000227859	MAS1LP1	HSCHR6_MHC_QBL:29442689-29443736	NOTEST	0	0	0	0	1	1
ENSG00000227860	ENSG00000227860	MTND5P18	1:238113035-238114836	NOTEST	0	0	0	0	1	1
ENSG00000227861	ENSG00000227861	SAPCD1	HSCHR6_MHC_APD:31735722-31744719	NOTEST	0	0	0	0	1	1
ENSG00000227862	ENSG00000227862	HNRNPA1P31	13:81193232-81194202	NOTEST	0	0	0	0	1	1
ENSG00000227863	ENSG00000227863	AC002383.2	7:89073287-89123576	NOTEST	0	0	0	0	1	1
ENSG00000227864	ENSG00000227864	ARL5AP1	X:118320404-118320792	NOTEST	0	0	0	0	1	1
ENSG00000227867	ENSG00000227867	TCEB1P11	Y:28137387-28137719	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000227868	ENSG00000227868	C1orf234	1:23337326-23342343	NOTEST	0.0878921	0.160042	0.864649	0	1	1
ENSG00000227869	ENSG00000227869	RP11-807H17.1	7:125071400-125106455	NOTEST	0	0	0	0	1	1
ENSG00000227871	ENSG00000227871	USP9YP12	Y:26092073-26098440	NOTEST	0	0	0	0	1	1
ENSG00000227873	ENSG00000227873	RP3-389A20.2	X:17787124-17787518	NOTEST	0	0	0	0	1	1
ENSG00000227874	ENSG00000227874	GRAMD4P1	21:15038188-15039867	NOTEST	0	0	0	0	1	1
ENSG00000227875	ENSG00000227875	RP11-426M1.2	1:12123433-12204264	NOTEST	0	0	0	0	1	1
ENSG00000227877	ENSG00000227877	LINC00948	10:61496752-61513203	NOTEST	0	0	0	0	1	1
ENSG00000227878	ENSG00000227878	AC114760.1	2:196602426-196933536	NOTEST	0	0	0	0	1	1
ENSG00000227880	ENSG00000227880	RP11-46E17.6	22:27853207-27856021	NOTEST	0	0	0	0	1	1
ENSG00000227881	ENSG00000227881	ASS1P5	X:114899214-114900453	NOTEST	0	0	0	0	1	1
ENSG00000227882	ENSG00000227882	PRKRIRP6	13:26808349-26811266	NOTEST	0	0	0	0	1	1
ENSG00000227883	ENSG00000227883	ATP6V0E1P4	1:48015867-48016425	NOTEST	0	0	0	0	1	1
ENSG00000227884	ENSG00000227884	C4B-AS1	HSCHR6_MHC_COX:31853113-31907413	NOTEST	0	0	0	0	1	1
ENSG00000227885	ENSG00000227885	RP11-79N23.1	6:53605546-53611820	NOTEST	0.0218752	0	#NAME?	0	1	1
ENSG00000227886	ENSG00000227886	XXbac-BPG13B8.10	HSCHR6_MHC_MCF:29465071-29478119	NOTEST	0	0	0	0	1	1
ENSG00000227887	ENSG00000227887	RPS26P13	1:208870713-208871043	NOTEST	0	0	0	0	1	1
ENSG00000227888	ENSG00000227888	FAM66A	8:12219526-12268510	NOTEST	0.217782	0.170211	-0.355559	0	1	1
ENSG00000227890	ENSG00000227890	PSMA2P3	2:202937977-203062585	NOTEST	0	0	0	0	1	1
ENSG00000227892	ENSG00000227892	OR5P4P	11:7710668-7927502	NOTEST	0	0	0	0	1	1
ENSG00000227893	ENSG00000227893	LINC00352	13:24072934-24077013	NOTEST	0	0	0	0	1	1
ENSG00000227895	ENSG00000227895	RP1-272J12.1	22:35318598-35483380	NOTEST	0	0	0	0	1	1
ENSG00000227896	ENSG00000227896	RP11-77P6.2	10:88281701-88284858	NOTEST	0.304052	0.355035	0.223643	0	1	1
ENSG00000227899	ENSG00000227899	MDC1-AS1	HSCHR6_MHC_QBL:30657118-30675200	NOTEST	0	0	0	0	1	1
ENSG00000227902	ENSG00000227902	AC062032.1	2:147637476-147655786	NOTEST	0	0	0	0	1	1
ENSG00000227905	ENSG00000227905	MED6P1	10:89807891-89809580	NOTEST	0	0	0	0	1	1
ENSG00000227906	ENSG00000227906	SNAP25-AS1	20:9966735-10349424	NOTEST	0	0	0	0	1	1
ENSG00000227907	ENSG00000227907	RP11-102C16.3	1:167021787-167059868	NOTEST	0	0	0	0	1	1
ENSG00000227908	ENSG00000227908	CTD-2031P19.3	5:55290994-55299477	NOTEST	0.0337253	0.0312141	-0.111632	0	1	1
ENSG00000227910	ENSG00000227910	RP11-73B2.6	7:63385164-63386684	NOTEST	0	0	0	0	1	1
ENSG00000227911	ENSG00000227911	RP11-141M1.1	13:33677271-33924767	NOTEST	0.0893198	0.120288	0.429446	0	1	1
ENSG00000227912	ENSG00000227912	RP11-69C17.3	10:2208525-2231668	NOTEST	0	0	0	0	1	1
ENSG00000227913	ENSG00000227913	KRT8P44	6:161768451-163736524	NOTEST	0	0	0	0	1	1
ENSG00000227914	ENSG00000227914	RP11-130C19.3	9:213107-746105	NOTEST	0.0156519	0	#NAME?	0	1	1
ENSG00000227915	ENSG00000227915	TCEB1P16	Y:25824650-25824982	NOTEST	0	0	0	0	1	1
ENSG00000227917	ENSG00000227917	RP11-143M1.3	9:100803-102941	NOTEST	0	0	0	0	1	1
ENSG00000227919	ENSG00000227919	AL353997.11	17:18353557-18379234	NOTEST	0	0	0	0	1	1
ENSG00000227920	ENSG00000227920	RP1-153P14.5	6:37511328-37518636	NOTEST	0	0	0	0	1	1
ENSG00000227922	ENSG00000227922	SPTLC1P5	13:78233547-78233799	NOTEST	0	0	0	0	1	1
ENSG00000227923	ENSG00000227923	RP5-905H7.7	7:62787051-62814743	NOTEST	0	0	0	0	1	1
ENSG00000227924	ENSG00000227924	RBPJP6	9:44471984-44473415	NOTEST	0	0	0	0	1	1
ENSG00000227925	ENSG00000227925	RP11-191N8.2	1:222001007-222014008	NOTEST	0	0	0	0	1	1
ENSG00000227927	ENSG00000227927	MACROD2-IT1	20:13829892-16033842	NOTEST	0	0.0726194	inf	0	1	1
ENSG00000227929	ENSG00000227929	SRGAP3-AS3	3:9022274-9520924	NOTEST	0	0	0	0	1	1

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ENSG00000227932	ENSG00000227932	RP13-16H11.2	10:26953134-26965088	NOTEST	0.192227	0	#NAME?	0	1	1
ENSG00000227933	ENSG00000227933	RP11-331F9.4	9:35605366-35647096	NOTEST	0.036861	0	#NAME?	0	1	1
ENSG00000227934	ENSG00000227934	RP11-423F24.3	1:231154703-231175992	NOTEST	0.432513	0.594964	0.46006	0	1	1
ENSG00000227935	ENSG00000227935	RP6-102O10.1	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000227936	ENSG00000227936	HLA-DPA3	HSCHR6_MHC_COX:33020574-33032712	NOTEST	0	0	0	0	1	1
ENSG00000227937	ENSG00000227937	MTND2P30	1:8146474-81546856	NOTEST	0	0	0	0	1	1
ENSG00000227938	ENSG00000227938	AC104695.4	2:28671033-28673051	NOTEST	0	0	0	0	1	1
ENSG00000227939	ENSG00000227939	RPL3P2	6:31248093-31249296	NOTEST	0.0287832	0.031668	0.1378	0	1	1
ENSG00000227940	ENSG00000227940	RP11-372M18.1	1:209498800-209501877	NOTEST	0	0	0	0	1	1
ENSG00000227941	ENSG00000227941	UQCRBP2	1:162511121-162511418	NOTEST	0	0	0	0	1	1
ENSG00000227942	ENSG00000227942	FRMD8P1	X:64770777-64772301	NOTEST	0	0	0	0	1	1
ENSG00000227945	ENSG00000227945	RP11-103C16.2	6:128289923-128841870	NOTEST	0.0511326	0	#NAME?	0	1	1
ENSG00000227947	ENSG00000227947	RP11-543D5.1	1:48154134-48169055	NOTEST	0	0	0	0	1	1
ENSG00000227948	ENSG00000227948	AC003989.4	7:110303109-111202573	NOTEST	0	0	0	0	1	1
ENSG00000227949	ENSG00000227949	CYCSP46	Y:17053426-17054595	NOTEST	0	0	0	0	1	1
ENSG00000227950	ENSG00000227950	RP11-312B8.2	1:6845383-7829766	NOTEST	0	0	0	0	1	1
ENSG00000227952	ENSG00000227952	RPL18AP17	13:73034269-73034467	NOTEST	0	0	0	0	1	1
ENSG00000227953	ENSG00000227953	RP11-439E19.3	1:246935138-246993361	NOTEST	0.0758662	0.131897	0.797887	0	1	1
ENSG00000227954	ENSG00000227954	RP3-323P13.2	6:133561735-134216691	NOTEST	0.33522	0.44851	0.420034	0	1	1
ENSG00000227956	ENSG00000227956	HCG4B	HSCHR6_MHC_COX:29885237-29888489	NOTEST	0	0	0	0	1	1
ENSG00000227958	ENSG00000227958	RP11-399H11.3	9:138096567-138129443	NOTEST	0	0	0	0	1	1
ENSG00000227959	ENSG00000227959	RP11-276H7.2	1:16450831-16483824	NOTEST	0.0370475	0.0932608	1.33189	0	1	1
ENSG00000227960	ENSG00000227960	RP5-837I24.6	1:81771844-82458120	NOTEST	0	0	0	0	1	1
ENSG00000227961	ENSG00000227961	RPL13AP	HSCHR6_MHC_DBB:29523342-29600923	NOTEST	0	0	0	0	1	1
ENSG00000227962	ENSG00000227962	RP11-382D8.3	1:235294497-235507847	NOTEST	0.256804	0.0943852	-1.44403	0	1	1
ENSG00000227963	ENSG00000227963	RP5-1074L1.1	1:110828996-110889299	NOTEST	0.0532169	0.0184601	-1.52748	0	1	1
ENSG00000227964	ENSG00000227964	RP5-1112F19.2	20:50448335-50479451	NOTEST	0	0	0	0	1	1
ENSG00000227965	ENSG00000227965	AC098592.6	7:16928244-16928509	NOTEST	0	0	0	0	1	1
ENSG00000227966	ENSG00000227966	XXbac-BPG308K3.6	HSCHR6_MHC_COX:28828043-28831792	NOTEST	0	0	0	0	1	1
ENSG00000227968	ENSG00000227968	AC004014.4	7:108634087-108635086	NOTEST	0	0	0	0	1	1
ENSG00000227969	ENSG00000227969	NPM1P22	13:68406007-68406959	NOTEST	0	0	0	0	1	1
ENSG00000227970	ENSG00000227970	NR1H5P	1:115379847-115394074	NOTEST	0	0	0	0	1	1
ENSG00000227971	ENSG00000227971	RP11-600G3.1	3:189349204-189615068	NOTEST	0	0	0	0	1	1
ENSG00000227972	ENSG00000227972	PRKRIRP3	10:54170894-54173252	NOTEST	0.00708879	0	#NAME?	0	1	1
ENSG00000227973	ENSG00000227973	PIN4P1	15:44162961-44487450	NOTEST	0.131817	0.30519	1.21117	0	1	1
ENSG00000227974	ENSG00000227974	HCG22	HSCHR6_MHC_QBL:31014737-31020038	NOTEST	0	0	0	0	1	1
ENSG00000227979	ENSG00000227979	AC002127.2	7:88339944-88386039	NOTEST	0	0	0	0	1	1
ENSG00000227981	ENSG00000227981	AC012668.3	2:216395169-216708445	NOTEST	0	0	0	0	1	1
ENSG00000227982	ENSG00000227982	RPL7P30	7:84157437-84158146	NOTEST	0	0	0	0	1	1
ENSG00000227983	ENSG00000227983	BRK1P2	13:91675985-91676208	NOTEST	0	0	0	0	1	1
ENSG00000227986	ENSG00000227986	TRIM60P18	7:63815455-63816577	NOTEST	0	0	0	0	1	1

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ENSG00000227988	ENSG00000227988	TDGF1P1	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000227989	ENSG00000227989	AC010141.8	Y:23717737-23719956	NOTEST	0	0	0	0	1	1
ENSG00000227993	ENSG00000227993	HLA-DRA	HSCHR6_MHC_COX:32355869-32361037	NOTEST	0	0	0	0	1	1
ENSG00000227994	ENSG00000227994	RP5-891H21.1	1:44638177-44638391	NOTEST	0	0	0	0	1	1
ENSG00000227995	ENSG00000227995	RAB11AP1	10:95641049-95641695	NOTEST	0	0	0	0	1	1
ENSG00000227997	ENSG00000227997	CENPVP2	X:51424999-51425485	NOTEST	0	0	0	0	1	1
ENSG00000227999	ENSG00000227999	MTND5P1	21:45892777-45894980	NOTEST	0.0123354	0	#NAME?	0	1	1
ENSG00000228000	ENSG00000228000	RPL7AP65	17:18174741-18218321	NOTEST	0	0	0	0	1	1
ENSG00000228001	ENSG00000228001	TRIM40	HSCHR6_MHC_COX:30093814-30106445	NOTEST	0	0	0	0	1	1
ENSG00000228002	ENSG00000228002	DHX9P1	13:77559002-77562078	NOTEST	0	0.00717795	inf	0	1	1
ENSG00000228004	ENSG00000228004	MYCLP2	X:57960270-57961237	NOTEST	0	0	0	0	1	1
ENSG00000228005	ENSG00000228005	AC020743.2	7:49813256-50199426	NOTEST	0	0	0	0	1	1
ENSG00000228007	ENSG00000228007	AC011933.2	17:73314156-73401790	NOTEST	0	0.237387	inf	0	1	1
ENSG00000228008	ENSG00000228008	CTD-2330K9.3	3:49924434-49967606	NOTEST	0.0692691	0.393568	2.50633	0	1	1
ENSG00000228010	ENSG00000228010	AC073343.13	7:6703604-6748532	NOTEST	0.384208	0.346191	-0.150319	0	1	1
ENSG00000228012	ENSG00000228012	RP11-393M18.1	1:187505232-187505431	NOTEST	0	0	0	0	1	1
ENSG00000228014	ENSG00000228014	RP11-321E8.5	7:63929562-63931031	NOTEST	0	0	0	0	1	1
ENSG00000228015	ENSG00000228015	AC074338.5	7:33168599-33168755	NOTEST	0	0	0	0	1	1
ENSG00000228016	ENSG00000228016	RAPGEF4-AS1	2:173541868-173917621	NOTEST	0	0.00803448	inf	0	1	1
ENSG00000228019	ENSG00000228019	RP11-166O4.4	7:66752527-66786513	NOTEST	0	0	0	0	1	1
ENSG00000228020	ENSG00000228020	HNRNPA1P46	1:191115154-191116091	NOTEST	0	0	0	0	1	1
ENSG00000228021	ENSG00000228021	RP11-383C5.3	10:127371797-127452712	NOTEST	0.0101094	0.0272007	1.42794	0	1	1
ENSG00000228024	ENSG00000228024	CYP1D1P	9:75515577-75695358	NOTEST	0.0427552	0	#NAME?	0	1	1
ENSG00000228025	ENSG00000228025	MTCO3P1	HSCHR6_MHC_MCF:32707549-32708382	NOTEST	0	0	0	0	1	1
ENSG00000228027	ENSG00000228027	RP1-251M9.3	10:11047258-11378674	NOTEST	0	0	0	0	1	1
ENSG00000228028	ENSG00000228028	AC069257.8	3:195938357-196065374	NOTEST	0.983407	2.1631	1.13724	0	1	1
ENSG00000228029	ENSG00000228029	HLA-W	HSCHR6_MHC_QBL:29913777-29915752	NOTEST	0	0	0	0	1	1
ENSG00000228030	ENSG00000228030	AC019084.7	7:158512420-158512852	NOTEST	0	0	0	0	1	1
ENSG00000228031	ENSG00000228031	AC078842.3	7:137029675-137039229	NOTEST	0	0.0551433	inf	0	1	1
ENSG00000228032	ENSG00000228032	C14orf144	14:104689920-104754406	NOTEST	0	0	0	0	1	1
ENSG00000228034	ENSG00000228034	HMGN2P21	2:71030288-71030558	NOTEST	0.144768	0	#NAME?	0	1	1
ENSG00000228035	ENSG00000228035	RP4-663N10.1	1:115825654-115910693	NOTEST	0	0	0	0	1	1
ENSG00000228036	ENSG00000228036	HSPD1P9	13:38567221-38568857	NOTEST	0	0	0	0	1	1
ENSG00000228037	ENSG00000228037	RP3-395M20.9	1:2512998-2515972	NOTEST	0.097944	0.432976	2.14426	0	1	1
ENSG00000228038	ENSG00000228038	VN1R51P	9:99855975-99856920	NOTEST	0	0	0	0	1	1
ENSG00000228039	ENSG00000228039	KB-1125A3.10	22:24305941-24306644	NOTEST	0	0	0	0	1	1
ENSG00000228040	ENSG00000228040	RP3-522D1.2	1:113433388-113433544	NOTEST	0	0	0	0	1	1
ENSG00000228041	ENSG00000228041	RP4-581F12.1	X:81753117-81753373	NOTEST	0	0	0	0	1	1
ENSG00000228042	ENSG00000228042	RP11-441A11.1	X:109880068-109880900	NOTEST	0	0	0	0	1	1
ENSG00000228043	ENSG00000228043	AC097721.2	2:139175853-139259268	NOTEST	0.163452	0.175367	0.101513	0	1	1
ENSG00000228044	ENSG00000228044	RP4-781K5.4	1:234780411-234831900	NOTEST	0	0	0	0	1	1
ENSG00000228045	ENSG00000228045	DNAJA1P6	22:17840836-18037850	NOTEST	0	0.0579487	inf	0	1	1

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ENSG00000228048	ENSG00000228048	RP11-598C10.1	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000228049	ENSG00000228049	POLR2J2	7:102122891-102312088	NOTEST	0.097808	0.0570364	-0.778068	0	1	1
ENSG00000228050	ENSG00000228050	TOP3BP1	22:22577579-22578959	NOTEST	0.375125	0.24126	-0.636783	0	1	1
ENSG00000228051	ENSG00000228051	RP11-325E14.2	X:79815644-79817553	NOTEST	0	0	0	0	1	1
ENSG00000228053	ENSG00000228053	RP11-151F5.2	9:112403067-112934792	NOTEST	0	0	0	0	1	1
ENSG00000228054	ENSG00000228054	RANP5	1:109589449-109590104	NOTEST	0	0	0	0	1	1
ENSG00000228055	ENSG00000228055	LINC00864	10:89156779-89184549	NOTEST	0	0	0	0	1	1
ENSG00000228056	ENSG00000228056	CFL1P3	1:64239692-64647181	NOTEST	0	0	0	0	1	1
ENSG00000228057	ENSG00000228057	SEC63P1	1:97543298-98386605	NOTEST	0.244767	0.18532	-0.401387	0	1	1
ENSG00000228058	ENSG00000228058	RP11-552D4.1	1:230138476-230142909	NOTEST	0	0	0	0	1	1
ENSG00000228060	ENSG00000228060	RP11-69E11.8	1:40026487-40042462	NOTEST	0	0	0	0	1	1
ENSG00000228061	ENSG00000228061	Z83001.1	11:31531296-31805546	NOTEST	0	0	0	0	1	1
ENSG00000228063	ENSG00000228063	RP11-135J2.4	1:219259943-219386207	NOTEST	0.0537255	0.116275	1.11386	0	1	1
ENSG00000228064	ENSG00000228064	AC023469.2	2:151839019-151905288	NOTEST	0	0	0	0	1	1
ENSG00000228065	ENSG00000228065	RP11-222A11.1	10:67330095-67526299	NOTEST	0	0	0	0	1	1
ENSG00000228067	ENSG00000228067	RP11-61J19.3	1:212719035-212729407	NOTEST	0.0915677	0	#NAME?	0	1	1
ENSG00000228069	ENSG00000228069	RP11-100G15.3	9:94794280-94877666	NOTEST	0	0.0552618	inf	0	1	1
ENSG00000228071	ENSG00000228071	RPL7P47	16:18026576-18266920	NOTEST	0.0385841	0	#NAME?	0	1	1
ENSG00000228072	ENSG00000228072	RP11-255A11.2	9:33512956-33514771	NOTEST	0	0	0	0	1	1
ENSG00000228073	ENSG00000228073	AC133106.2	2:189896621-190044605	NOTEST	0	0	0	0	1	1
ENSG00000228074	ENSG00000228074	UBBP5	13:87871258-87871524	NOTEST	0	0	0	0	1	1
ENSG00000228075	ENSG00000228075	BOD1L2	18:54814292-54817531	NOTEST	0	0	0	0	1	1
ENSG00000228076	ENSG00000228076	RP11-475E11.2	1:109289295-109352148	NOTEST	0	0	0	0	1	1
ENSG00000228078	ENSG00000228078	HLA-U	6:29901877-29902063	NOTEST	0	0	0	0	1	1
ENSG00000228079	ENSG00000228079	AC012368.1	2:64313483-64315380	NOTEST	0	0	0	0	1	1
ENSG00000228080	ENSG00000228080	HLA-DRB1	HSCHR6_MHC_SSTO:32637567-32670792	NOTEST	0	0	0	0	1	1
ENSG00000228081	ENSG00000228081	RP11-385M4.2	1:209346358-209346720	NOTEST	0	0	0	0	1	1
ENSG00000228082	ENSG00000228082	RP1-121G13.2	6:100832890-100912805	NOTEST	0	0	0	0	1	1
ENSG00000228083	ENSG00000228083	IFNA14	9:21239200-21239978	NOTEST	0.0978825	0.0590699	-0.728629	0	1	1
ENSG00000228084	ENSG00000228084	RP5-884G6.2	1:100433938-100492535	NOTEST	0.287675	0.390714	0.441674	0	1	1
ENSG00000228085	ENSG00000228085	AC004920.2	7:50911274-50911429	NOTEST	0	0	0	0	1	1
ENSG00000228086	ENSG00000228086	RP5-837M10.4	1:100810032-100985833	NOTEST	0	0	0	0	1	1
ENSG00000228089	ENSG00000228089	RP1-197O17.2	X:130836677-130964671	NOTEST	0	0	0	0	1	1
ENSG00000228090	ENSG00000228090	C6orf25	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000228092	ENSG00000228092	COX6CP15	10:78629358-79398353	NOTEST	0	0	0	0	1	1
ENSG00000228095	ENSG00000228095	RP11-361M4.1	9:87219025-87219344	NOTEST	0	0	0	0	1	1
ENSG00000228097	ENSG00000228097	RP11-39K24.12	9:4985032-5128183	NOTEST	0	0	0	0	1	1
ENSG00000228098	ENSG00000228098	AC110620.1	2:135493033-135716912	NOTEST	0	0	0	0	1	1
ENSG00000228099	ENSG00000228099	RPL12P1	HSCHR6_MHC_QBL:33288142-33306509	NOTEST	0	0	0	0	1	1
ENSG00000228100	ENSG00000228100	AC016912.3	2:46619435-46621306	NOTEST	0	0	0	0	1	1
ENSG00000228102	ENSG00000228102	IFITM4P	HSCHR6_MHC_DBB:29715983-29716404	NOTEST	0	0	0	0	1	1
ENSG00000228104	ENSG00000228104	BRD2-IT1	HSCHR6_MHC_QBL:32831135-32878022	NOTEST	0	0	0	0	1	1

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ENSG00000228107	ENSG00000228107	AP000692.9	21:37692089-37791313	NOTEST	0.153882	0.262997	0.773225	0	1	1
ENSG00000228108	ENSG00000228108	AC092839.3	2:54683421-54896812	NOTEST	0	0.0468557	inf	0	1	1
ENSG00000228111	ENSG00000228111	TPT1P2	2:209079447-209087349	NOTEST	0	0	0	0	1	1
ENSG00000228112	ENSG00000228112	AC112220.2	3:33768741-33769096	NOTEST	0	0	0	0	1	1
ENSG00000228113	ENSG00000228113	AC003991.3	7:87834432-87936206	NOTEST	0	0	0	0	1	1
ENSG00000228115	ENSG00000228115	RP11-165F24.5	9:213107-746105	NOTEST	0	0	0	0	1	1
ENSG00000228116	ENSG00000228116	PPT2	HSCHR6_MHC_DBB:32091909-32101885	NOTEST	0	0	0	0	1	1
ENSG00000228118	ENSG00000228118	LOC124685	17:69617118-69617577	NOTEST	0	0	0	0	1	1
ENSG00000228120	ENSG00000228120	AP001631.10	21:44579175-44582387	NOTEST	0	0	0	0	1	1
ENSG00000228121	ENSG00000228121	PHBP3	1:59465347-59466166	NOTEST	0	0	0	0	1	1
ENSG00000228122	ENSG00000228122	MTND1P17	22:17357107-17357311	NOTEST	0	0	0	0	1	1
ENSG00000228123	ENSG00000228123	RP11-15B24.3	9:84887670-85179347	NOTEST	0	0	0	0	1	1
ENSG00000228124	ENSG00000228124	RP1-122O8.7	6:90352217-90529442	NOTEST	0.197357	0.301877	0.613155	0	1	1
ENSG00000228125	ENSG00000228125	RP11-516A11.3	X:67262185-67653755	NOTEST	0	0	0	0	1	1
ENSG00000228126	ENSG00000228126	LINC00568	1:150488232-150490508	NOTEST	0.144901	0.0833745	-0.797392	0	1	1
ENSG00000228127	ENSG00000228127	RP11-12L8.1	1:116461996-116468529	NOTEST	0	0	0	0	1	1
ENSG00000228128	ENSG00000228128	DDAH2	HSCHR6_MHC_SSTO:31684773-31697500	NOTEST	0	0	0	0	1	1
ENSG00000228130	ENSG00000228130	SUMO2P1	HSCHR6_MHC_MANN:29603404-29603688	NOTEST	0	0	0	0	1	1
ENSG00000228131	ENSG00000228131	IGHD6-6	14:106376268-106376286	NOTEST	0	0	0	0	1	1
ENSG00000228132	ENSG00000228132	RP11-279E1.1	9:6276639-6276974	NOTEST	0	0	0	0	1	1
ENSG00000228133	ENSG00000228133	AC099684.1	17:1837970-1928639	NOTEST	0.0170859	0.0139471	-0.292844	0	1	1
ENSG00000228134	ENSG00000228134	AC092578.1	2:143300986-143301544	NOTEST	0	0	0	0	1	1
ENSG00000228135	ENSG00000228135	AC073128.10	2:219765532-219795358	NOTEST	0.0176817	0	#NAME?	0	1	1
ENSG00000228136	ENSG00000228136	RP11-216M21.5	9:42275938-42298165	NOTEST	0	0	0	0	1	1
ENSG00000228137	ENSG00000228137	AP001469.7	21:47649130-47706211	NOTEST	0.203091	0.193569	-0.0692761	0	1	1
ENSG00000228139	ENSG00000228139	GS1-421I3.4	X:119170200-119379122	NOTEST	0	0	0	0	1	1
ENSG00000228140	ENSG00000228140	RP3-467K16.4	1:15729474-15735929	NOTEST	0.0083171	0.00208094	-1.99885	0	1	1
ENSG00000228141	ENSG00000228141	AC105339.1	15:83379222-83382778	NOTEST	0	0	0	0	1	1
ENSG00000228142	ENSG00000228142	RP11-180I4.2	9:98412435-98478000	NOTEST	0	0	0	0	1	1
ENSG00000228143	ENSG00000228143	RP11-308N19.5	9:109484630-109485211	NOTEST	0	0	0	0	1	1
ENSG00000228144	ENSG00000228144	TMBIM4	12:66516841-66563852	NOTEST	0.177657	0.000926319	-7.58337	0	1	1
ENSG00000228146	ENSG00000228146	CASP16	16:3194219-3199964	NOTEST	0.0135108	0	#NAME?	0	1	1
ENSG00000228147	ENSG00000228147	HCG22	HSCHR6_MHC_APD:31033295-31038966	NOTEST	0	0	0	0	1	1
ENSG00000228149	ENSG00000228149	RPL3P1	21:37529079-37666572	NOTEST	0	0	0	0	1	1
ENSG00000228150	ENSG00000228150	RP11-84A14.4	1:9982172-10045559	NOTEST	0.476525	0.244774	-0.961102	0	1	1
ENSG00000228151	ENSG00000228151	AC004941.3	7:149095294-149098547	NOTEST	0	0.00391212	inf	0	1	1
ENSG00000228153	ENSG00000228153	RP11-23I7.1	1:204586297-204654861	NOTEST	0	0	0	0	1	1
ENSG00000228154	ENSG00000228154	RP11-302F12.2	4:25624398-25625223	NOTEST	0	0	0	0	1	1
ENSG00000228155	ENSG00000228155	AL589685.1	1:156278758-156337664	NOTEST	0	0	0	0	1	1
ENSG00000228156	ENSG00000228156	RP11-410N8.1	20:31030861-31196695	NOTEST	0	0	0	0	1	1
ENSG00000228157	ENSG00000228157	AC007952.5	17:18996286-19000150	NOTEST	0.0405813	0.0104096	-1.96291	0	1	1
ENSG00000228159	ENSG00000228159	AP001465.5	21:14918353-14930782	NOTEST	0	0	0	0	1	1

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ENSG00000228160	ENSG00000228160	RP13-57D9.3	X:68789511-68790200	NOTEST	0	0.116487	inf	0	1	1
ENSG00000228161	ENSG00000228161	LL22NC03-23C6.15	22:22400827-22400989	NOTEST	0	0	0	0	1	1
ENSG00000228162	ENSG00000228162	AC097713.3	2:235346971-235370771	NOTEST	0	0	0	0	1	1
ENSG00000228163	ENSG00000228163	HLA-DPA1	HSCHR6_MHC_MANN:33186488-33209127	NOTEST	0	0	0	0	1	1
ENSG00000228164	ENSG00000228164	COL11A2P1	HSCHR6_MHC_QBL:33000628-33004165	NOTEST	0	0	0	0	1	1
ENSG00000228165	ENSG00000228165	RP11-125K10.5	9:4792868-4885917	NOTEST	0	0	0	0	1	1
ENSG00000228166	ENSG00000228166	MTND1P11	9:4985032-5128183	NOTEST	0	0	0	0	1	1
ENSG00000228167	ENSG00000228167	RP11-489C13.1	1:194687924-194688366	NOTEST	0	0	0	0	1	1
ENSG00000228168	ENSG00000228168	HNRNPA1P21	3:39376469-39377430	NOTEST	0	0	0	0	1	1
ENSG00000228169	ENSG00000228169	PPIAP19	10:116449901-116450393	NOTEST	0	0.0360592	inf	0	1	1
ENSG00000228170	ENSG00000228170	RP1-40E16.11	6:3118607-3153812	NOTEST	0	0	0	0	1	1
ENSG00000228171	ENSG00000228171	AC121251.1	3:23244510-23633284	NOTEST	0	0	0	0	1	1
ENSG00000228172	ENSG00000228172	RP1-317E23.3	1:26126666-26185903	NOTEST	0.0853924	0	#NAME?	0	1	1
ENSG00000228173	ENSG00000228173	AC091770.3	7:48700170-48702901	NOTEST	0	0	0	0	1	1
ENSG00000228174	ENSG00000228174	RP11-244N9.6	9:100263461-100436030	NOTEST	0	0	0	0	1	1
ENSG00000228176	ENSG00000228176	RP4-656G21.1	1:30181697-30182394	NOTEST	0	0	0	0	1	1
ENSG00000228177	ENSG00000228177	C6orf47	HSCHR6_MHC_MANN:31665566-31668042	NOTEST	0	0	0	0	1	1
ENSG00000228179	ENSG00000228179	HLA-S	HSCHR6_MHC_MANN:31392903-31393118	NOTEST	0	0	0	0	1	1
ENSG00000228181	ENSG00000228181	RP11-455B2.9	10:15213034-15213277	NOTEST	0	0	0	0	1	1
ENSG00000228182	ENSG00000228182	MTND2P25	X:62063166-62063776	NOTEST	0	0	0	0	1	1
ENSG00000228184	ENSG00000228184	SNX19P1	21:14897919-14900900	NOTEST	0	0	0	0	1	1
ENSG00000228186	ENSG00000228186	PRR3	HSCHR6_MHC_COX:30498997-30521345	NOTEST	0	0	0	0	1	1
ENSG00000228187	ENSG00000228187	RP11-363H12.1	1:77554674-77685115	NOTEST	0	0	0	0	1	1
ENSG00000228189	ENSG00000228189	RP13-60M5.2	9:91242103-91267075	NOTEST	0	0	0	0	1	1
ENSG00000228190	ENSG00000228190	RP11-104D3.1	1:199117725-199362435	NOTEST	0	0	0	0	1	1
ENSG00000228191	ENSG00000228191	RP11-345I18.6	1:179240250-179240401	NOTEST	0	0	0	0	1	1
ENSG00000228193	ENSG00000228193	TCEB1P14	Y:20835918-20991373	NOTEST	0	0	0	0	1	1
ENSG00000228194	ENSG00000228194	CTA-415G2.2	22:32908538-33454358	NOTEST	0	0	0	0	1	1
ENSG00000228195	ENSG00000228195	RPL5P27	10:118509415-118510772	NOTEST	0	0	0	0	1	1
ENSG00000228196	ENSG00000228196	PTPN2P1	1:178693440-178889238	NOTEST	0.0601009	0	#NAME?	0	1	1
ENSG00000228197	ENSG00000228197	DDX6P1	HSCHR6_MHC_DBB:29297457-29298893	NOTEST	0	0	0	0	1	1
ENSG00000228198	ENSG00000228198	OR2M3	1:248366331-248367392	NOTEST	0	0	0	0	1	1
ENSG00000228199	ENSG00000228199	PAIP1P1	HSCHR6_MHC_COX:30142136-30171100	NOTEST	0	0	0	0	1	1
ENSG00000228201	ENSG00000228201	AL022341.3	16:691812-699200	NOTEST	0.128926	0.0530988	-1.27979	0	1	1
ENSG00000228202	ENSG00000228202	HCG9P5	HSCHR6_MHC_MCF:29706643-29713963	NOTEST	0	0	0	0	1	1
ENSG00000228204	ENSG00000228204	RP4-724E13.2	7:50934443-51384515	NOTEST	0	0	0	0	1	1
ENSG00000228205	ENSG00000228205	RP11-778D9.4	3:183851806-184402546	NOTEST	0.150299	0.31069	1.04764	0	1	1
ENSG00000228206	ENSG00000228206	AC016717.1	2:226562969-226568370	NOTEST	0	0.304978	inf	0	1	1
ENSG00000228207	ENSG00000228207	AC007967.2	Y:8769243-8771317	NOTEST	0	0	0	0	1	1
ENSG00000228208	ENSG00000228208	C1orf143	1:218683437-218699320	NOTEST	0	0	0	0	1	1
ENSG00000228209	ENSG00000228209	AC073091.2	2:76485159-76486023	NOTEST	0	0	0	0	1	1
ENSG00000228210	ENSG00000228210	RPL7AL2	20:4571638-4571946	NOTEST	0	0	0	0	1	1
ENSG00000228211	ENSG00000228211	HYALP1	7:123454192-123517532	NOTEST	0	0	0	0	1	1

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ENSG00000228212	ENSG00000228212	OFD1P17	5:37106329-37249530	NOTEST	0.0188549	0.0402257	1.09318	0	1	1
ENSG00000228213	ENSG00000228213	NLGN1-AS1	3:173114073-174004434	NOTEST	0	0	0	0	1	1
ENSG00000228214	ENSG00000228214	LINC00693	3:28616281-28799831	NOTEST	0.0658469	0.0503956	-0.385819	0	1	1
ENSG00000228215	ENSG00000228215	RP11-541F9.2	1:191827836-191980390	NOTEST	0	0	0	0	1	1
ENSG00000228216	ENSG00000228216	RP11-367F23.1	9:93719541-93727675	NOTEST	0	0	0	0	1	1
ENSG00000228217	ENSG00000228217	AL390877.1	1:118320708-118321128	NOTEST	0	0	0	0	1	1
ENSG00000228218	ENSG00000228218	ATF4P3	17:74132413-74236454	NOTEST	0.0167825	0.0759526	2.17814	0	1	1
ENSG00000228219	ENSG00000228219	NPM1P30	10:21068901-21463977	NOTEST	0	0	0	0	1	1
ENSG00000228220	ENSG00000228220	HLA-J	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1
ENSG00000228221	ENSG00000228221	LINC00578	3:177159708-177470093	NOTEST	0	0.248983	inf	0	1	1
ENSG00000228222	ENSG00000228222	AC074363.1	2:168149680-168414843	NOTEST	0	0.352967	inf	0	1	1
ENSG00000228223	ENSG00000228223	HCG11	6:26522075-26526807	NOTEST	0.214408	0.385729	0.847232	0	1	1
ENSG00000228224	ENSG00000228224	NACAP1	8:102374021-102384935	NOTEST	0	0	0	0	1	1
ENSG00000228225	ENSG00000228225	AC016908.1	2:84258263-84259482	NOTEST	0	0	0	0	1	1
ENSG00000228226	ENSG00000228226	AC074019.1	2:229548252-229549296	NOTEST	0	0	0	0	1	1
ENSG00000228227	ENSG00000228227	PAIP1P1	HSCHR6_MHC_QBL:30141749-30170728	NOTEST	0	0	0	0	1	1
ENSG00000228229	ENSG00000228229	RP11-219C24.10	1:13429633-13430113	NOTEST	0	0	0	0	1	1
ENSG00000228231	ENSG00000228231	RP11-124I4.2	6:54172656-54254950	NOTEST	0	0	0	0	1	1
ENSG00000228234	ENSG00000228234	GLRXP	20:36231253-36231587	NOTEST	0	0	0	0	1	1
ENSG00000228235	ENSG00000228235	AP001476.4	21:47472509-47473019	NOTEST	0	0	0	0	1	1
ENSG00000228236	ENSG00000228236	TXNP5	2:149894620-150071776	NOTEST	0	0	0	0	1	1
ENSG00000228237	ENSG00000228237	EFCAB14-AS1	1:47098408-47184824	NOTEST	0	0.0361722	inf	0	1	1
ENSG00000228238	ENSG00000228238	GS1-304P7.2	1:186547410-186548431	NOTEST	0	0	0	0	1	1
ENSG00000228239	ENSG00000228239	RP11-85G21.1	1:157202020-157206926	NOTEST	0	0	0	0	1	1
ENSG00000228240	ENSG00000228240	TTTY17A	Y:24997730-24998862	NOTEST	0	0	0	0	1	1
ENSG00000228241	ENSG00000228241	MOB1AP1	13:86543133-86543668	NOTEST	0	0	0	0	1	1
ENSG00000228242	ENSG00000228242	AC093495.4	3:14166439-14242619	NOTEST	0.0372369	0.0955967	1.36023	0	1	1
ENSG00000228243	ENSG00000228243	RP11-436G20.1	9:45949231-45949823	NOTEST	0.135835	0.112723	-0.26907	0	1	1
ENSG00000228245	ENSG00000228245	DDX39B-AS1	HSCHR6_MHC_SSTO:31486440-31504572	NOTEST	0	0	0	0	1	1
ENSG00000228247	ENSG00000228247	UBBP2	1:217804665-218045038	NOTEST	0	0	0	0	1	1
ENSG00000228248	ENSG00000228248	RP11-111E2.1	9:80037994-80263223	NOTEST	0	0	0	0	1	1
ENSG00000228250	ENSG00000228250	LY6G6C	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000228251	ENSG00000228251	AC012442.6	2:113341816-113372008	NOTEST	0.160103	0	#NAME?	0	1	1
ENSG00000228252	ENSG00000228252	COL6A4P2	3:129992143-129992649	NOTEST	0.00608393	0	#NAME?	0	1	1
ENSG00000228254	ENSG00000228254	HLA-DQB2	HSCHR6_MHC_MCF:32757660-32765119	NOTEST	0	0	0	0	1	1
ENSG00000228255	ENSG00000228255	RP11-323I1.1	1:213904758-213967930	NOTEST	0	0	0	0	1	1
ENSG00000228257	ENSG00000228257	AC010141.6	Y:23673223-23711212	NOTEST	0	0	0	0	1	1
ENSG00000228259	ENSG00000228259	AC136604.1	5:179078297-179079445	NOTEST	0	0	0	0	1	1
ENSG00000228260	ENSG00000228260	HLA-DRB9	HSCHR6_MHC_MCF:32502892-32516548	NOTEST	0	0	0	0	1	1
ENSG00000228261	ENSG00000228261	RP11-127L20.3	10:106071893-106098162	NOTEST	0	0	0	0	1	1
ENSG00000228263	ENSG00000228263	SLC44A4	HSCHR6_MHC_DBB:31813157-31829008	NOTEST	0	0	0	0	1	1
ENSG00000228264	ENSG00000228264	RP11-350G8.7	1:154374803-154441926	NOTEST	0.024862	0	#NAME?	0	1	1
ENSG00000228267	ENSG00000228267	C4B	HSCHR6_MHC_COX:31937352-31952482	NOTEST	0	0	0	0	1	1
ENSG00000228271	ENSG00000228271	RP11-513G11.2	3:193994470-194005157	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000228272	ENSG00000228272	AC106874.1	2:84542231-84577898	NOTEST	0	0	0	0	1	1
ENSG00000228273	ENSG00000228273	MUC3A	7:100547186-100611410	NOTEST	0	0	0	0	1	1
ENSG00000228275	ENSG00000228275	ARMCX3-AS1	X:100877786-100882833	NOTEST	0	0	0	0	1	1
ENSG00000228277	ENSG00000228277	AC112518.3	4:74576018-74580244	NOTEST	0.0735395	0.0260541	-1.49701	0	1	1
ENSG00000228278	ENSG00000228278	ORM2	9:117092148-117095532	NOTEST	0	0	0	0	1	1
ENSG00000228280	ENSG00000228280	RP11-367B6.2	10:77360997-78320752	NOTEST	0.219012	0.0880548	-1.31453	0	1	1
ENSG00000228283	ENSG00000228283	KATNBL1P6	6:146920100-147136598	NOTEST	0.0950259	0.136072	0.517977	0	1	1
ENSG00000228284	ENSG00000228284	HLA-DQA1	HSCHR6_MHC_MCF:32631438-32652184	NOTEST	0	0	0	0	1	1
ENSG00000228286	ENSG00000228286	AP000593.5	11:71960899-71962332	NOTEST	0	0	0	0	1	1
ENSG00000228289	ENSG00000228289	RP4-640E24.1	1:163738575-163738928	NOTEST	0	0	0	0	1	1
ENSG00000228290	ENSG00000228290	RP11-132M7.3	6:85397068-85474237	NOTEST	0	0	0	0	1	1
ENSG00000228291	ENSG00000228291	RP11-445P17.6	10:5202774-5260912	NOTEST	0	0	0	0	1	1
ENSG00000228292	ENSG00000228292	RP11-220I1.4	9:37120535-37358146	NOTEST	0	0	0	0	1	1
ENSG00000228293	ENSG00000228293	RP4-686C3.7	20:2644997-2646520	NOTEST	0	0.0978593	inf	0	1	1
ENSG00000228294	ENSG00000228294	BMS1P17	14:19650017-19718563	NOTEST	0	0	0	0	1	1
ENSG00000228295	ENSG00000228295	LINC00392	13:73987609-74222390	NOTEST	0	0	0	0	1	1
ENSG00000228296	ENSG00000228296	TTTY4C	Y:27209229-27246039	NOTEST	0	0	0	0	1	1
ENSG00000228299	ENSG00000228299	HLA-C	HSCHR6_MHC_DBB:31228736-31232108	NOTEST	0	0	0	0	1	1
ENSG00000228301	ENSG00000228301	RPL7P55	X:92828832-92829578	NOTEST	0	0	0	0	1	1
ENSG00000228302	ENSG00000228302	RP11-186N15.3	10:12171635-12292588	NOTEST	0.215815	0.212671	-0.0211771	0	1	1
ENSG00000228303	ENSG00000228303	RP11-10F11.2	7:56706635-56718389	NOTEST	0	0	0	0	1	1
ENSG00000228304	ENSG00000228304	OR4K6P	14:20315525-20316422	NOTEST	0	0	0	0	1	1
ENSG00000228307	ENSG00000228307	OR2S1P	9:36013180-36014130	NOTEST	0	0	0	0	1	1
ENSG00000228308	ENSG00000228308	RP11-255G21.1	3:176361728-176585626	NOTEST	0	0	0	0	1	1
ENSG00000228309	ENSG00000228309	GS1-204I12.1	1:185527503-185597659	NOTEST	0	0	0	0	1	1
ENSG00000228312	ENSG00000228312	GAPDHP45	10:15135261-15135610	NOTEST	0	0	0	0	1	1
ENSG00000228313	ENSG00000228313	CTD-2555K7.4	14:23064714-23081265	NOTEST	0	0.00922393	inf	0	1	1
ENSG00000228314	ENSG00000228314	CYP4F29P	21:15215453-15220685	NOTEST	0.0268086	0.193051	2.84822	0	1	1
ENSG00000228316	ENSG00000228316	RP11-522L3.5	X:102024088-102161086	NOTEST	0	0	0	0	1	1
ENSG00000228317	ENSG00000228317	RP11-235C23.5	9:108316315-108320310	NOTEST	0.032293	0	#NAME?	0	1	1
ENSG00000228318	ENSG00000228318	AP001610.5	21:42792230-42831141	NOTEST	0	0	0	0	1	1
ENSG00000228319	ENSG00000228319	SPATA2P1	13:56788506-56791076	NOTEST	0	0	0	0	1	1
ENSG00000228321	ENSG00000228321	TNF	HSCHR6_MHC_MANN:31582830-31585600	NOTEST	0	0	0	0	1	1
ENSG00000228322	ENSG00000228322	RP11-358M14.2	9:3824126-4348392	NOTEST	0	0	0	0	1	1
ENSG00000228323	ENSG00000228323	AC008753.6	19:54357834-54379691	NOTEST	0	0	0	0	1	1
ENSG00000228325	ENSG00000228325	RP11-685N3.1	2:90537838-90538397	NOTEST	0	0	0	0	1	1
ENSG00000228326	ENSG00000228326	RP11-109G10.2	10:51532101-51532572	NOTEST	0	0	0	0	1	1
ENSG00000228328	ENSG00000228328	RP11-516A11.1	X:67262185-67653755	NOTEST	0.132917	0.167156	0.330672	0	1	1
ENSG00000228329	ENSG00000228329	AC097495.3	2:69059175-69064856	NOTEST	0	0	0	0	1	1
ENSG00000228330	ENSG00000228330	RP11-730A19.5	10:13184184-13184977	NOTEST	0	0	0	0	1	1
ENSG00000228331	ENSG00000228331	RPL17P43	17:19398697-19501235	NOTEST	0.102041	0.158619	0.636417	0	1	1
ENSG00000228333	ENSG00000228333	RXRB	HSCHR6_MHC_DBB:33139274-33150126	NOTEST	0	0	0	0	1	1
ENSG00000228334	ENSG00000228334	AC024028.1	7:3122885-3126055	NOTEST	0	0	0	0	1	1

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ENSG00000228336	ENSG00000228336	OR9H1P	1:247938211-247939138	NOTEST	0	0	0	0	1	1
ENSG00000228337	ENSG00000228337	RP11-804H8.5	3:50712671-51421629	NOTEST	0	0	0	0	1	1
ENSG00000228338	ENSG00000228338	RP5-845O24.8	1:12882548-12883022	NOTEST	0	0	0	0	1	1
ENSG00000228339	ENSG00000228339	AMD1P1	10:20638977-20640029	NOTEST	0	0	0	0	1	1
ENSG00000228340	ENSG00000228340	RP5-1043L13.1	20:58662894-59102516	NOTEST	0.0302343	0.0179028	-0.755999	0	1	1
ENSG00000228341	ENSG00000228341	CTB-20D2.1	7:106809405-107218906	NOTEST	0	0	0	0	1	1
ENSG00000228345	ENSG00000228345	RP11-12D5.4	X:27872439-27873470	NOTEST	0	0	0	0	1	1
ENSG00000228347	ENSG00000228347	FTLP17	1:104695927-104696452	NOTEST	0	0	0	0	1	1
ENSG00000228349	ENSG00000228349	RPS26P4	21:40817780-40887433	NOTEST	0	0	0	0	1	1
ENSG00000228350	ENSG00000228350	RP11-148G20.1	3:48701208-48723797	NOTEST	0	0	0	0	1	1
ENSG00000228351	ENSG00000228351	AC018832.1	3:7994491-8653610	NOTEST	0	0	0	0	1	1
ENSG00000228352	ENSG00000228352	RP11-537H15.3	9:34084329-34127397	NOTEST	0.0640292	0.166027	1.37462	0	1	1
ENSG00000228353	ENSG00000228353	RP11-184A2.2	10:3810106-3810943	NOTEST	0	0	0	0	1	1
ENSG00000228354	ENSG00000228354	RP11-552J9.9	X:52684256-52686304	NOTEST	0	0	0	0	1	1
ENSG00000228355	ENSG00000228355	BX322559.3	21:46798115-46799550	NOTEST	0	0	0	0	1	1
ENSG00000228357	ENSG00000228357	HSD17B8	HSCHR6_MHC_MANN:33326337-33328531	NOTEST	0	0	0	0	1	1
ENSG00000228358	ENSG00000228358	AC113617.1	4:118235752-118294008	NOTEST	0	0	0	0	1	1
ENSG00000228360	ENSG00000228360	RP11-365F18.1	7:138912282-138912574	NOTEST	0	0	0	0	1	1
ENSG00000228361	ENSG00000228361	RP11-503C24.3	6:168630411-168641395	NOTEST	0	0	0	0	1	1
ENSG00000228363	ENSG00000228363	AC015971.2	2:86730553-87005164	NOTEST	0.110234	0.248553	1.17299	0	1	1
ENSG00000228364	ENSG00000228364	SAR1P1	6:29044349-29044945	NOTEST	0	0	0	0	1	1
ENSG00000228365	ENSG00000228365	RP1-90J20.2	6:2917127-2917967	NOTEST	0	0	0	0	1	1
ENSG00000228366	ENSG00000228366	RP11-18B3.3	9:108456824-108538893	NOTEST	0	0.0360606	inf	0	1	1
ENSG00000228367	ENSG00000228367	RP11-524L6.2	5:75216494-75217485	NOTEST	0	0	0	0	1	1
ENSG00000228368	ENSG00000228368	AC106873.4	7:116592499-116870157	NOTEST	0	0	0	0	1	1
ENSG00000228369	ENSG00000228369	TXNDC12-AS1	1:52485802-52556388	NOTEST	0	0.0526186	inf	0	1	1
ENSG00000228370	ENSG00000228370	XXbac-BPG13B8.10	HSCHR6_MHC_MANN:29464857-29477904	NOTEST	0	0	0	0	1	1
ENSG00000228371	ENSG00000228371	ZDHHC20P1	HSCHR6_MHC_QBL:29675808-29676231	NOTEST	0	0	0	0	1	1
ENSG00000228372	ENSG00000228372	RP11-85L21.4	X:134193714-134257880	NOTEST	0	0	0	0	1	1
ENSG00000228373	ENSG00000228373	RP11-497K15.1	9:90038548-90038808	NOTEST	0	0	0	0	1	1
ENSG00000228374	ENSG00000228374	AC012497.2	2:140490276-140490851	NOTEST	0	0	0	0	1	1
ENSG00000228375	ENSG00000228375	RPS20P25	9:84025193-84025545	NOTEST	0	0	0	0	1	1
ENSG00000228376	ENSG00000228376	RP11-520B13.4	9:99837952-99844227	NOTEST	0	0	0	0	1	1
ENSG00000228377	ENSG00000228377	MAS1L	HSCHR6_MHC_MANN:29454044-29455309	NOTEST	0	0	0	0	1	1
ENSG00000228379	ENSG00000228379	AC010891.2	Y:9650923-9655122	NOTEST	0	0	0	0	1	1
ENSG00000228380	ENSG00000228380	AC016697.2	2:209130990-209223475	NOTEST	0	0	0	0	1	1
ENSG00000228382	ENSG00000228382	ITPKB-IT1	1:226819390-226927024	NOTEST	0.0271058	0.0654455	1.27169	0	1	1
ENSG00000228383	ENSG00000228383	FAM197Y7	Y:9195405-9235047	NOTEST	0	0	0	0	1	1
ENSG00000228384	ENSG00000228384	AC007040.6	2:71163011-71306935	NOTEST	0.0942025	0.218204	1.21184	0	1	1
ENSG00000228386	ENSG00000228386	RP5-1125A11.4	20:32570857-32700138	NOTEST	0	0	0	0	1	1
ENSG00000228389	ENSG00000228389	AC068039.4	2:172629991-172632354	NOTEST	0.00769089	0.0849653	3.46565	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000228391	ENSG00000228391	AC011995.3	2:2874329-2875003	NOTEST	0	0	0	0	1	1
ENSG00000228392	ENSG00000228392	RP11-343J18.1	9:129032399-129038197	NOTEST	0	0	0	0	1	1
ENSG00000228397	ENSG00000228397	RP1-224A6.3	1:22350486-22351461	NOTEST	0.314099	0.0497296	-2.65904	0	1	1
ENSG00000228398	ENSG00000228398	HMGN2P25	3:141583848-141584121	NOTEST	0	0	0	0	1	1
ENSG00000228399	ENSG00000228399	RP4-575N6.2	1:101721829-101722172	NOTEST	0.0858605	0.0616422	-0.478074	0	1	1
ENSG00000228400	ENSG00000228400	AC079154.1	2:124774434-124782750	NOTEST	0	0	0	0	1	1
ENSG00000228401	ENSG00000228401	RP11-251M1.1	9:139543061-139567130	NOTEST	0	0	0	0	1	1
ENSG00000228403	ENSG00000228403	RP11-563N6.6	10:49892920-50323554	NOTEST	0	0	0	0	1	1
ENSG00000228404	ENSG00000228404	AP001468.58	21:47604992-47648738	NOTEST	0	0.185954	inf	0	1	1
ENSG00000228405	ENSG00000228405	RNF5	HSCHR6_MHC_COX:32094613-32097047	NOTEST	0	0	0	0	1	1
ENSG00000228407	ENSG00000228407	RP4-800M22.1	1:52608045-52831865	NOTEST	0.174706	0.416446	1.2532	0	1	1
ENSG00000228408	ENSG00000228408	RP1-111D6.3	6:149539061-149732749	NOTEST	0	0	0	0	1	1
ENSG00000228410	ENSG00000228410	TCEB1P24	X:155208656-155208990	NOTEST	0	0	0	0	1	1
ENSG00000228411	ENSG00000228411	CDY4P	Y:14813159-14972764	NOTEST	0	0	0	0	1	1
ENSG00000228413	ENSG00000228413	AC024937.2	3:195754053-195809060	NOTEST	0	0	0	0	1	1
ENSG00000228414	ENSG00000228414	AC010733.4	2:61052266-61108449	NOTEST	0	0	0	0	1	1
ENSG00000228415	ENSG00000228415	PTMAP1	6:30594618-30614600	NOTEST	0.593331	0.901448	0.603407	0	1	1
ENSG00000228417	ENSG00000228417	RP11-549L6.3	10:111967362-112047123	NOTEST	0	0	0	0	1	1
ENSG00000228418	ENSG00000228418	CTSLP3	10:48952490-48981273	NOTEST	0	0	0	0	1	1
ENSG00000228420	ENSG00000228420	RP4-735C1.6	1:110370976-110414058	NOTEST	0	0	0	0	1	1
ENSG00000228421	ENSG00000228421	AC005013.5	7:28992973-28998961	NOTEST	0	0	0	0	1	1
ENSG00000228422	ENSG00000228422	LINC00687	20:11781110-11851363	NOTEST	0	0	0	0	1	1
ENSG00000228423	ENSG00000228423	RP4-633I8.4	1:8412456-8877702	NOTEST	0	0	0	0	1	1
ENSG00000228425	ENSG00000228425	VPS52	HSCHR6_MHC_DBB:33195233-33222212	NOTEST	0	0	0	0	1	1
ENSG00000228426	ENSG00000228426	RP11-402L1.11	10:44124264-44170151	NOTEST	0	0	0	0	1	1
ENSG00000228427	ENSG00000228427	RP5-1091N2.9	X:70403408-70418025	NOTEST	0	0	0	0	1	1
ENSG00000228429	ENSG00000228429	RP5-859M6.1	7:68105784-68106571	NOTEST	0	0	0	0	1	1
ENSG00000228430	ENSG00000228430	RP11-15B24.5	9:84887670-85179347	NOTEST	0.0309077	0	#NAME?	0	1	1
ENSG00000228431	ENSG00000228431	ARL5AP3	1:68167148-68698803	NOTEST	0	0	0	0	1	1
ENSG00000228432	ENSG00000228432	DHFRP2	6:31334128-31334675	NOTEST	0	0	0	0	1	1
ENSG00000228433	ENSG00000228433	OR7E23P	21:33993358-33994406	NOTEST	0	0	0	0	1	1
ENSG00000228434	ENSG00000228434	AC004951.6	7:43966036-44058774	NOTEST	0.418346	0.362318	-0.207441	0	1	1
ENSG00000228435	ENSG00000228435	C6orf47	HSCHR6_MHC_DBB:31608256-31610731	NOTEST	0	0	0	0	1	1
ENSG00000228437	ENSG00000228437	RP11-400N13.2	1:222054322-222158306	NOTEST	0	0	0	0	1	1
ENSG00000228438	ENSG00000228438	RP5-859I17.2	20:8112823-8949003	NOTEST	0	0	0	0	1	1
ENSG00000228440	ENSG00000228440	MTND5P6	7:57238680-57240478	NOTEST	0	0	0	0	1	1
ENSG00000228444	ENSG00000228444	RP11-173B14.4	13:76123618-76434004	NOTEST	0.0214069	0.0317508	0.568713	0	1	1
ENSG00000228445	ENSG00000228445	UGT1A2P	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000228446	ENSG00000228446	AC073052.1	2:225334866-225450110	NOTEST	0.0820691	0.0580185	-0.500327	0	1	1
ENSG00000228448	ENSG00000228448	HCG21	HSCHR6_MHC_MCF:30987292-30997453	NOTEST	0	0	0	0	1	1
ENSG00000228450	ENSG00000228450	RP1-154J13.3	X:130626252-130626860	NOTEST	0	0	0	0	1	1
ENSG00000228453	ENSG00000228453	RPS15AP9	1:117680850-117681231	NOTEST	0	0.0551114	inf	0	1	1
ENSG00000228454	ENSG00000228454	C4B	HSCHR6_MHC_SSTO:31965199-32027628	NOTEST	0	0	0	0	1	1
ENSG00000228458	ENSG00000228458	DDX39BP2	HSCHR6_MHC_DBB:29950934-29951331	NOTEST	0	0	0	0	1	1

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ENSG00000228459	ENSG00000228459	CXorf28	X:3189860-3202694	NOTEST	0	0	0	0	1	1
ENSG00000228460	ENSG00000228460	CYP2C59P	10:96766882-96767313	NOTEST	0	0	0	0	1	1
ENSG00000228461	ENSG00000228461	RPL3P2	HSCHR6_MHC_COX:31239128-31240331	NOTEST	0	0	0	0	1	1
ENSG00000228462	ENSG00000228462	RP11-445N18.3	10:45493145-45676875	NOTEST	0	0	0	0	1	1
ENSG00000228464	ENSG00000228464	RP11-617O8.1	X:26363352-26364359	NOTEST	0	0	0	0	1	1
ENSG00000228465	ENSG00000228465	TRAPPC2P10	Y:26113710-26116841	NOTEST	0	0	0	0	1	1
ENSG00000228466	ENSG00000228466	TUBB4AP1	X:122695492-122696817	NOTEST	0	0	0	0	1	1
ENSG00000228467	ENSG00000228467	RP11-402N8.1	9:38804003-38851913	NOTEST	0	0	0	0	1	1
ENSG00000228469	ENSG00000228469	XXbac-BPG299F13.14	HSCHR6_MHC_DBB:31159279-31165485	NOTEST	0	0	0	0	1	1
ENSG00000228470	ENSG00000228470	RP11-176D17.3	1:214517514-214725792	NOTEST	0.132298	0.0965971	-0.453737	0	1	1
ENSG00000228471	ENSG00000228471	AC018865.11	2:130831107-130886795	NOTEST	0	0	0	0	1	1
ENSG00000228473	ENSG00000228473	LIN28AP2	13:88031726-88032513	NOTEST	0	0	0	0	1	1
ENSG00000228476	ENSG00000228476	CSTP1	20:23899407-23902806	NOTEST	0	0	0	0	1	1
ENSG00000228477	ENSG00000228477	RP3-342P20.2	1:40420801-40435638	NOTEST	0.599941	0.529972	-0.178903	0	1	1
ENSG00000228478	ENSG00000228478	RP1-290I10.3	6:10423372-10426409	NOTEST	0	0	0	0	1	1
ENSG00000228480	ENSG00000228480	AC130464.1	16:26366116-26369676	NOTEST	0	0	0	0	1	1
ENSG00000228481	ENSG00000228481	U51244.2	2:45878483-46415129	NOTEST	0	0	0	0	1	1
ENSG00000228482	ENSG00000228482	RP5-859D4.3	20:6711904-6716783	NOTEST	0	0	0	0	1	1
ENSG00000228483	ENSG00000228483	OR2J4P	HSCHR6_MHC_DBB:29149312-29150248	NOTEST	0	0	0	0	1	1
ENSG00000228484	ENSG00000228484	RP11-106M7.1	10:116524546-116539662	NOTEST	0.00672903	0	#NAME?	0	1	1
ENSG00000228485	ENSG00000228485	GRK5-IT1	10:120967100-121215131	NOTEST	0	0	0	0	1	1
ENSG00000228487	ENSG00000228487	RP13-225O21.2	9:129677052-129985445	NOTEST	0	0	0	0	1	1
ENSG00000228488	ENSG00000228488	AC092168.4	2:101338682-101339344	NOTEST	0	0	0	0	1	1
ENSG00000228489	ENSG00000228489	RPL21P50	4:124571421-124851561	NOTEST	0	0	0	0	1	1
ENSG00000228490	ENSG00000228490	HCG4P7	HSCHR6_MHC_APD:29793553-29796732	NOTEST	0	0	0	0	1	1
ENSG00000228491	ENSG00000228491	MICE	HSCHR6_MHC_MCF:29706643-29713963	NOTEST	0	0	0	0	1	1
ENSG00000228492	ENSG00000228492	RAB11FIP1P1	X:73164158-73513409	NOTEST	0.525936	0.39103	-0.427608	0	1	1
ENSG00000228496	ENSG00000228496	AC106875.1	2:11817720-11967535	NOTEST	0	0.0130127	inf	0	1	1
ENSG00000228498	ENSG00000228498	HLA-Z	HSCHR6_MHC_SSTO:32954062-32954137	NOTEST	0	0	0	0	1	1
ENSG00000228499	ENSG00000228499	TMSB10P1	2:236402732-237040444	NOTEST	0	0	0	0	1	1
ENSG00000228501	ENSG00000228501	RPL15P18	13:100741268-101182686	NOTEST	0.0673692	0	#NAME?	0	1	1
ENSG00000228503	ENSG00000228503	RP11-347D21.2	20:46586765-46587347	NOTEST	0	0	0	0	1	1
ENSG00000228504	ENSG00000228504	RP4-586O15.1	1:95776483-95783819	NOTEST	0.140471	0	#NAME?	0	1	1
ENSG00000228505	ENSG00000228505	AC011897.2	2:14756551-14770316	NOTEST	0	0	0	0	1	1
ENSG00000228507	ENSG00000228507	DAP3P2	2:172347931-172348441	NOTEST	0.250798	0.230383	-0.122493	0	1	1
ENSG00000228509	ENSG00000228509	AC006460.2	2:191511471-191573442	NOTEST	0.0237526	0.0211801	-0.165373	0	1	1
ENSG00000228510	ENSG00000228510	RP11-339B21.8	9:131206865-131208907	NOTEST	0	0	0	0	1	1
ENSG00000228512	ENSG00000228512	RP11-281A20.2	9:120545725-120659534	NOTEST	0	0	0	0	1	1
ENSG00000228513	ENSG00000228513	AC023271.1	2:203879601-204091101	NOTEST	0.0161738	0.106748	2.72248	0	1	1
ENSG00000228515	ENSG00000228515	MAS1L	HSCHR6_MHC_DBB:29454407-29455672	NOTEST	0	0	0	0	1	1
ENSG00000228517	ENSG00000228517	CT47A7	X:120087141-120090454	NOTEST	0	0	0	0	1	1
ENSG00000228518	ENSG00000228518	SURF6P1	Y:19304705-19305532	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000228520	ENSG00000228520	RING1	HSCHR6_MHC_DBB:33154181-33158409	NOTEST	0	0	0	0	1	1
ENSG00000228521	ENSG00000228521	AC099552.3	7:154995856-154996899	NOTEST	0	0	0	0	1	1
ENSG00000228522	ENSG00000228522	RP11-236F9.2	9:67272037-67298632	NOTEST	0.0442896	0.0358396	-0.305413	0	1	1
ENSG00000228523	ENSG00000228523	RP4-763G1.1	1:67743734-67744462	NOTEST	0	0	0	0	1	1
ENSG00000228524	ENSG00000228524	HLA-J	HSCHR6_MHC_APD:29905241-29969520	NOTEST	0	0	0	0	1	1
ENSG00000228525	ENSG00000228525	RP5-1087E8.2	1:227085236-227175246	NOTEST	0	0	0	0	1	1
ENSG00000228526	ENSG00000228526	RP3-510D11.1	1:9242065-9262678	NOTEST	0.412479	0.0757836	-2.44436	0	1	1
ENSG00000228527	ENSG00000228527	RP11-179B15.5	10:60064312-60065381	NOTEST	0	0.0734199	inf	0	1	1
ENSG00000228528	ENSG00000228528	AC068057.1	2:105320215-105321967	NOTEST	0	0.061012	inf	0	1	1
ENSG00000228530	ENSG00000228530	RP11-567B20.1	1:199846105-199846686	NOTEST	0	0	0	0	1	1
ENSG00000228534	ENSG00000228534	RP11-95H8.5	9:39925025-39926970	NOTEST	0	0	0	0	1	1
ENSG00000228536	ENSG00000228536	RP11-392O17.1	1:219583022-219585283	NOTEST	0.0232086	0.0180538	-0.362352	0	1	1
ENSG00000228537	ENSG00000228537	AL353608.1	9:70856396-70914929	NOTEST	0	0	0	0	1	1
ENSG00000228538	ENSG00000228538	AC009411.1	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000228539	ENSG00000228539	RP11-526K17.2	20:24449834-24647252	NOTEST	0	0	0	0	1	1
ENSG00000228541	ENSG00000228541	AC093159.1	2:62690261-62691205	NOTEST	0.117326	0	#NAME?	0	1	1
ENSG00000228543	ENSG00000228543	GS1-519E5.1	X:9217959-9243246	NOTEST	0	0	0	0	1	1
ENSG00000228544	ENSG00000228544	CCDC183-AS1	9:139685806-139735639	NOTEST	0.498686	0.451753	-0.142599	0	1	1
ENSG00000228546	ENSG00000228546	CTA-313A17.3	7:101977726-101979559	NOTEST	0	0	0	0	1	1
ENSG00000228547	ENSG00000228547	OR7E26P	10:15041048-15042054	NOTEST	0	0	0	0	1	1
ENSG00000228548	ENSG00000228548	ITPKB-AS1	1:226819390-226927024	NOTEST	0	0	0	0	1	1
ENSG00000228549	ENSG00000228549	U1	1:17066767-17299474	NOTEST	0.0189683	0.00935211	-1.02022	0	1	1
ENSG00000228550	ENSG00000228550	RP11-483M24.2	X:6966960-7066231	NOTEST	0	0	0	0	1	1
ENSG00000228551	ENSG00000228551	SNRPGP9	2:109745803-110262207	NOTEST	0	0	0	0	1	1
ENSG00000228553	ENSG00000228553	RP11-391J2.3	10:95753745-96122716	NOTEST	0	0	0	0	1	1
ENSG00000228554	ENSG00000228554	AC004837.5	7:39663081-39747723	NOTEST	0.04873	0.137827	1.49997	0	1	1
ENSG00000228557	ENSG00000228557	HSPA8P17	9:30988082-30990570	NOTEST	0	0	0	0	1	1
ENSG00000228559	ENSG00000228559	RP3-340B19.3	6:35512408-35513446	NOTEST	0	0	0	0	1	1
ENSG00000228560	ENSG00000228560	RP11-550P17.5	1:159315955-159453166	NOTEST	0.0470084	0.0718527	0.612125	0	1	1
ENSG00000228561	ENSG00000228561	RP11-114M1.1	3:177159708-177470093	NOTEST	0	0	0	0	1	1
ENSG00000228563	ENSG00000228563	AL133247.2	2:31747549-31806136	NOTEST	0	0	0	0	1	1
ENSG00000228564	ENSG00000228564	LINC01005	7:63488229-63490483	NOTEST	0	0	0	0	1	1
ENSG00000228566	ENSG00000228566	RP11-170M17.1	10:65424423-65750328	NOTEST	0	0	0	0	1	1
ENSG00000228567	ENSG00000228567	VN1R4	19:53769928-53770972	NOTEST	0	0	0	0	1	1
ENSG00000228568	ENSG00000228568	AC006461.2	2:72403112-73053170	NOTEST	0	0	0	0	1	1
ENSG00000228569	ENSG00000228569	AC073133.2	7:156225216-156228527	NOTEST	0	0	0	0	1	1
ENSG00000228570	ENSG00000228570	NUTM2E	10:81601113-81610632	NOTEST	0.0129145	0.0209164	0.69565	0	1	1
ENSG00000228571	ENSG00000228571	HSFY7P	Y:24683193-24683996	NOTEST	0	0	0	0	1	1
ENSG00000228572	ENSG00000228572	LL0YNC03-29C1.1	X:170409-171758	NOTEST	0	0	0	0	1	1
ENSG00000228573	ENSG00000228573	RP11-279N8.1	13:48399464-48410091	NOTEST	0	0.0482442	inf	0	1	1
ENSG00000228575	ENSG00000228575	MDC1	HSCHR6_MHC_MANN:30712281-30730363	NOTEST	0	0	0	0	1	1
ENSG00000228577	ENSG00000228577	AC010731.2	2:207308262-207485851	NOTEST	0.0551894	0.123153	1.15799	0	1	1
ENSG00000228578	ENSG00000228578	TUBB1P2	Y:19628715-19630918	NOTEST	0	0	0	0	1	1

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ENSG00000228579	ENSG00000228579	RPL32P1	HSCHR6_MHC_COX:32954321-32976889	NOTEST	0	0	0	0	1	1
ENSG00000228581	ENSG00000228581	GNL1	HSCHR6_MHC_MCF:30587610-30609957	NOTEST	0	0	0	0	1	1
ENSG00000228582	ENSG00000228582	TAP2	HSCHR6_MHC_COX:32711935-32728881	NOTEST	0	0	0	0	1	1
ENSG00000228583	ENSG00000228583	XXbac-BPG299F13.14	HSCHR6_MHC_COX:31158105-31164310	NOTEST	0	0	0	0	1	1
ENSG00000228585	ENSG00000228585	AC073143.1	2:5453872-5454267	NOTEST	0	0	0	0	1	1
ENSG00000228586	ENSG00000228586	AC005042.5	2:159313475-159610287	NOTEST	0	0	0	0	1	1
ENSG00000228587	ENSG00000228587	RP1-41P2.7	22:36081986-36085420	NOTEST	0	0	0	0	1	1
ENSG00000228590	ENSG00000228590	AC007381.3	2:60577729-60580151	NOTEST	0	0	0	0	1	1
ENSG00000228592	ENSG00000228592	AP000459.4	21:24733425-24757182	NOTEST	0	0	0	0	1	1
ENSG00000228593	ENSG00000228593	CFTRP1	20:25900134-25900317	NOTEST	0	0	0	0	1	1
ENSG00000228595	ENSG00000228595	PAICSP2	9:94325372-94712444	NOTEST	0	0	0	0	1	1
ENSG00000228596	ENSG00000228596	AC013436.6	7:44824648-44826939	NOTEST	0	0	0	0	1	1
ENSG00000228597	ENSG00000228597	MTND4P1	13:85094237-85095703	NOTEST	0	0	0	0	1	1
ENSG00000228598	ENSG00000228598	MACC1-AS1	7:19958603-20257027	NOTEST	0	0	0	0	1	1
ENSG00000228599	ENSG00000228599	RPL7P52	22:40440820-40731812	NOTEST	0	0.0202402	inf	0	1	1
ENSG00000228600	ENSG00000228600	POLR2CP	21:16129908-16130673	NOTEST	0	0	0	0	1	1
ENSG00000228601	ENSG00000228601	RPL39P	20:55034483-55034639	NOTEST	0	0	0	0	1	1
ENSG00000228604	ENSG00000228604	RP5-872K7.7	20:21106623-21227260	NOTEST	0	0	0	0	1	1
ENSG00000228605	ENSG00000228605	GPANK1	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000228606	ENSG00000228606	RP11-574F21.2	1:160185504-160256138	NOTEST	0.444983	0.353205	-0.333243	0	1	1
ENSG00000228607	ENSG00000228607	CLDN25	11:113650468-113651222	NOTEST	0	0	0	0	1	1
ENSG00000228610	ENSG00000228610	GS1-590J15.1	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000228611	ENSG00000228611	HNF4GP1	13:56573333-56574582	NOTEST	0	0	0	0	1	1
ENSG00000228613	ENSG00000228613	AC144450.1	2:1550436-1623885	NOTEST	0	0	0	0	1	1
ENSG00000228614	ENSG00000228614	RP13-476E20.1	6:53655672-53659072	NOTEST	0	0	0	0	1	1
ENSG00000228615	ENSG00000228615	AC093166.3	2:112500162-112502239	NOTEST	0	0	0	0	1	1
ENSG00000228616	ENSG00000228616	RP11-66N11.7	X:152876148-152878380	NOTEST	0	0	0	0	1	1
ENSG00000228617	ENSG00000228617	RP11-157L3.2	9:46117171-46117907	NOTEST	0	0	0	0	1	1
ENSG00000228618	ENSG00000228618	AC012462.3	2:216341389-216344971	NOTEST	0	0	0	0	1	1
ENSG00000228620	ENSG00000228620	RP3-434P1.6	22:38820292-38851205	NOTEST	0	0	0	0	1	1
ENSG00000228622	ENSG00000228622	RP1-302D9.1	22:33501368-33502045	NOTEST	0	0	0	0	1	1
ENSG00000228624	ENSG00000228624	RP3-399L15.3	6:114254191-114792869	NOTEST	0.075522	0.0415169	-0.863199	0	1	1
ENSG00000228625	ENSG00000228625	RP11-1B20.1	1:227177565-227506175	NOTEST	0	0	0	0	1	1
ENSG00000228626	ENSG00000228626	RP11-495P10.9	1:147760106-147761057	NOTEST	0	0	0	0	1	1
ENSG00000228627	ENSG00000228627	GS1-278J22.2	7:53626906-53635942	NOTEST	0	0	0	0	1	1
ENSG00000228628	ENSG00000228628	ATF6B	HSCHR6_MHC_MCF:32082522-32172461	NOTEST	0	0	0	0	1	1
ENSG00000228629	ENSG00000228629	AC092295.4	19:37001596-37119499	NOTEST	0	0	0	0	1	1
ENSG00000228630	ENSG00000228630	HOTAIR	12:54356091-54371427	NOTEST	0.419369	0.15759	-1.41205	0	1	1
ENSG00000228634	ENSG00000228634	RP4-534N18.2	1:32307619-32410457	NOTEST	0	0	0	0	1	1
ENSG00000228635	ENSG00000228635	OR2P1P	HSCHR6_MHC_MCF:29039753-29040529	NOTEST	0	0	0	0	1	1
ENSG00000228636	ENSG00000228636	RP5-1051H14.2	10:9800745-9801200	NOTEST	0	0	0	0	1	1
ENSG00000228639	ENSG00000228639	AC005152.3	17:70017991-70216859	NOTEST	0	0.190243	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000228643	ENSG00000228643	AC079779.4	2:279557-301515	NOTEST	0	0	0	0	1	1
ENSG00000228645	ENSG00000228645	PHKG1P2	7:62969680-62970543	NOTEST	0	0	0	0	1	1
ENSG00000228646	ENSG00000228646	RPL31P13	1:213602050-213602420	NOTEST	0	0	0	0	1	1
ENSG00000228648	ENSG00000228648	RP11-568A7.2	6:167655378-167659404	NOTEST	0	0	0	0	1	1
ENSG00000228650	ENSG00000228650	AC008940.1	5:56066625-56068130	NOTEST	0	0	0	0	1	1
ENSG00000228651	ENSG00000228651	RP11-556E13.1	10:54316461-54515169	NOTEST	0	0	0	0	1	1
ENSG00000228652	ENSG00000228652	OR2W1	HSCHR6_MHC_MANN:29011993-29013021	NOTEST	0	0	0	0	1	1
ENSG00000228653	ENSG00000228653	HNRNPCP7	7:63961202-63962107	NOTEST	0.101179	0.156206	0.626544	0	1	1
ENSG00000228655	ENSG00000228655	AC096558.1	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000228656	ENSG00000228656	MYO5BP3	9:68357279-68358558	NOTEST	0	0	0	0	1	1
ENSG00000228657	ENSG00000228657	RP11-170J3.2	10:104263743-104393292	NOTEST	0	0	0	0	1	1
ENSG00000228658	ENSG00000228658	RP11-791O21.5	9:91586552-91591213	NOTEST	0	0	0	0	1	1
ENSG00000228659	ENSG00000228659	RP1-23K20.2	X:130115563-130192120	NOTEST	0	0	0	0	1	1
ENSG00000228660	ENSG00000228660	VN1R35P	7:63423808-63424501	NOTEST	0	0	0	0	1	1
ENSG00000228661	ENSG00000228661	AC090587.5	11:3875547-4114439	NOTEST	0.0919752	0.386342	2.07056	0	1	1
ENSG00000228662	ENSG00000228662	MCCD1	HSCHR6_MHC_MCF:31572847-31602942	NOTEST	0	0	0	0	1	1
ENSG00000228663	ENSG00000228663	PSMD10P1	20:49505584-49575092	NOTEST	0.140996	0.109728	-0.361717	0	1	1
ENSG00000228664	ENSG00000228664	RP11-416K24.1	1:182297631-182298142	NOTEST	0	0	0	0	1	1
ENSG00000228666	ENSG00000228666	KRT18P1	6:28936906-28938237	NOTEST	0	0	0	0	1	1
ENSG00000228667	ENSG00000228667	RP11-129O7.2	10:25137535-25241533	NOTEST	0	0	0	0	1	1
ENSG00000228668	ENSG00000228668	TRGV5P	7:38384630-38385100	NOTEST	0	0	0	0	1	1
ENSG00000228669	ENSG00000228669	LINC00448	13:63246417-63306492	NOTEST	0	0	0	0	1	1
ENSG00000228670	ENSG00000228670	NANOGP2	2:223289235-223425667	NOTEST	0	0	0	0	1	1
ENSG00000228672	ENSG00000228672	PROB1	5:138727634-138730885	NOTEST	0.111061	0.0919467	-0.272484	0	1	1
ENSG00000228674	ENSG00000228674	CTB-147C22.3	19:51430333-51430831	NOTEST	0	0	0	0	1	1
ENSG00000228675	ENSG00000228675	AC006482.1	7:17719172-17720283	NOTEST	0	0	0	0	1	1
ENSG00000228677	ENSG00000228677	TTC3-AS1	21:38445525-38575413	NOTEST	0	0	0	0	1	1
ENSG00000228679	ENSG00000228679	RP4-676J13.2	6:84693446-84717042	NOTEST	0	0	0	0	1	1
ENSG00000228680	ENSG00000228680	AC004692.4	7:43152197-43605600	NOTEST	0	0	0	0	1	1
ENSG00000228681	ENSG00000228681	AC008072.1	2:225159646-225160470	NOTEST	0	0	0	0	1	1
ENSG00000228682	ENSG00000228682	RP11-439L8.3	1:31971840-31974167	NOTEST	0	0	0	0	1	1
ENSG00000228683	ENSG00000228683	RP11-31E13.2	10:80455818-80456779	NOTEST	0	0	0	0	1	1
ENSG00000228684	ENSG00000228684	HLA-DQB3	HSCHR6_MHC_MANN:32849114-32853223	NOTEST	0	0	0	0	1	1
ENSG00000228685	ENSG00000228685	RP11-336A10.7	10:5666893-5667089	NOTEST	0	0	0	0	1	1
ENSG00000228686	ENSG00000228686	RP11-492I21.1	1:175913966-176176629	NOTEST	0.184591	0.147532	-0.323308	0	1	1
ENSG00000228687	ENSG00000228687	RP3-419C19.3	1:192765662-192766335	NOTEST	0	0	0	0	1	1
ENSG00000228688	ENSG00000228688	COL11A2P1	6:33071570-33075107	NOTEST	0	0	0	0	1	1
ENSG00000228689	ENSG00000228689	RP3-335N17.2	6:51464520-51952423	NOTEST	0	0	0	0	1	1
ENSG00000228691	ENSG00000228691	NEU1	HSCHR6_MHC_APD:31836793-31842041	NOTEST	0	0	0	0	1	1
ENSG00000228692	ENSG00000228692	RP5-826L7.1	6:164007614-164009197	NOTEST	0	0	0	0	1	1
ENSG00000228694	ENSG00000228694	MTND4P18	10:36723637-36724102	NOTEST	0	0	0	0	1	1
ENSG00000228695	ENSG00000228695	CES1P1	16:55794459-55828070	NOTEST	0	0	0	0	1	1
ENSG00000228697	ENSG00000228697	RP5-968D22.1	1:168370066-168391894	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000228698	ENSG00000228698	OR2N1P	HSCHR6_MHC_MCF:29105803-29106740	NOTEST	0	0	0	0	1	1
ENSG00000228700	ENSG00000228700	RP11-155G14.1	7:128073475-128073767	NOTEST	0	0	0	0	1	1
ENSG00000228702	ENSG00000228702	RP11-671E7.1	10:46201878-46288409	NOTEST	0	0	0	0	1	1
ENSG00000228703	ENSG00000228703	RP5-1160K1.6	1:110158725-110174673	NOTEST	0.41099	0.309552	-0.408918	0	1	1
ENSG00000228704	ENSG00000228704	RP11-138M12.1	6:125746772-125766329	NOTEST	0	0	0	0	1	1
ENSG00000228705	ENSG00000228705	LINC00659	20:61405479-61406764	NOTEST	0	0.0893253	inf	0	1	1
ENSG00000228706	ENSG00000228706	HCG4	HSCHR6_MHC_SSTO:29755629-29762282	NOTEST	0	0	0	0	1	1
ENSG00000228707	ENSG00000228707	RP11-787B4.2	9:118774639-118775244	NOTEST	0	0.0624104	inf	0	1	1
ENSG00000228708	ENSG00000228708	AL109763.1	21:19641432-19858917	NOTEST	0	0	0	0	1	1
ENSG00000228709	ENSG00000228709	AP001065.15	21:45905459-45910171	NOTEST	0	0.0721233	inf	0	1	1
ENSG00000228711	ENSG00000228711	AC004006.2	7:82286350-82286727	NOTEST	0	0	0	0	1	1
ENSG00000228712	ENSG00000228712	HSD17B8	HSCHR6_MHC_COX:33094048-33096234	NOTEST	0	0	0	0	1	1
ENSG00000228713	ENSG00000228713	XXbac-BPG248L24.10	HSCHR6_MHC_MCF:31352705-31353440	NOTEST	0	0	0	0	1	1
ENSG00000228714	ENSG00000228714	RP11-284G10.1	9:118501941-118506518	NOTEST	0	0	0	0	1	1
ENSG00000228717	ENSG00000228717	AF013593.1	X:150394700-150396187	NOTEST	0	0	0	0	1	1
ENSG00000228718	ENSG00000228718	RP11-145H9.3	6:2637169-2640235	NOTEST	0.108237	0	#NAME?	0	1	1
ENSG00000228719	ENSG00000228719	RP5-1119A7.14	22:36841444-36850991	NOTEST	0	0	0	0	1	1
ENSG00000228721	ENSG00000228721	AC016909.2	2:133429373-134326034	NOTEST	0	0	0	0	1	1
ENSG00000228723	ENSG00000228723	SRGAP3-AS2	3:9022274-9520924	NOTEST	0	0	0	0	1	1
ENSG00000228725	ENSG00000228725	MTND2P12	17:19507109-19508361	NOTEST	0	0	0	0	1	1
ENSG00000228728	ENSG00000228728	RP11-316K19.3	X:149934809-150067289	NOTEST	0	0	0	0	1	1
ENSG00000228729	ENSG00000228729	RP11-211A18.2	1:227177565-227506175	NOTEST	0	0	0	0	1	1
ENSG00000228730	ENSG00000228730	RP11-95L3.2	3:190415711-190416637	NOTEST	0	0	0	0	1	1
ENSG00000228733	ENSG00000228733	AC015815.8	17:75082797-75213179	NOTEST	0	0	0	0	1	1
ENSG00000228734	ENSG00000228734	RP11-335E6.3	1:63655659-63782902	NOTEST	0.043178	0.171534	1.99013	0	1	1
ENSG00000228735	ENSG00000228735	GS1-18A18.2	7:54643744-54646487	NOTEST	0	0	0	0	1	1
ENSG00000228736	ENSG00000228736	RGL2	HSCHR6_MHC_MCF:33417261-33437523	NOTEST	0	0	0	0	1	1
ENSG00000228737	ENSG00000228737	AC008781.7	5:140894582-141016437	NOTEST	0.0874315	0	#NAME?	0	1	1
ENSG00000228738	ENSG00000228738	HCG23	HSCHR6_MHC_QBL:32315748-32332375	NOTEST	0	0	0	0	1	1
ENSG00000228739	ENSG00000228739	RP11-218I7.2	9:6047359-6066714	NOTEST	0.0452843	0.171226	1.91882	0	1	1
ENSG00000228740	ENSG00000228740	AC136896.1	15:27216428-27787137	NOTEST	0	0	0	0	1	1
ENSG00000228741	ENSG00000228741	RP11-309I15.1	13:24553838-24896673	NOTEST	0.0461295	0.0689817	0.580524	0	1	1
ENSG00000228742	ENSG00000228742	RP5-884M6.1	7:106415456-106436010	NOTEST	0	0.0124363	inf	0	1	1
ENSG00000228744	ENSG00000228744	RPS3AP30	8:6980378-6981226	NOTEST	0	0	0	0	1	1
ENSG00000228745	ENSG00000228745	CTSLP5	10:46790403-46791522	NOTEST	0	0	0	0	1	1
ENSG00000228748	ENSG00000228748	RP13-39P12.3	10:79542623-79686378	NOTEST	0.190732	0.21845	0.195754	0	1	1
ENSG00000228750	ENSG00000228750	RP11-242F24.1	1:6784696-6790072	NOTEST	0	0	0	0	1	1
ENSG00000228751	ENSG00000228751	AC004022.8	7:94926987-95025680	NOTEST	0	0	0	0	1	1
ENSG00000228753	ENSG00000228753	EIF4BP2	10:21068901-21463977	NOTEST	0.00915055	0	#NAME?	0	1	1
ENSG00000228754	ENSG00000228754	RP11-534L6.3	10:49892920-50323554	NOTEST	0	0	0	0	1	1
ENSG00000228755	ENSG00000228755	PABPC1P8	10:42775181-42777267	NOTEST	0	0	0	0	1	1
ENSG00000228757	ENSG00000228757	AB019438.66	14:106892324-106892465	NOTEST	0	0	0	0	1	1
ENSG00000228759	ENSG00000228759	FAF2P1	10:93525655-93526953	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000228760	ENSG00000228760	BAG6	HSCHR6_MHC_MANN:31646290-31665479	NOTEST	0	0	0	0	1	1
ENSG00000228762	ENSG00000228762	HCG20	HSCHR6_MHC_MANN:30779289-30804715	NOTEST	0	0	0	0	1	1
ENSG00000228763	ENSG00000228763	AC010095.5	2:109150856-109303702	NOTEST	0	0	0	0	1	1
ENSG00000228764	ENSG00000228764	ZNF885P	Y:22551936-22558682	NOTEST	0	0	0	0	1	1
ENSG00000228765	ENSG00000228765	ETF1P1	HSCHR6_MHC_MCF:30047254-30111187	NOTEST	0	0	0	0	1	1
ENSG00000228766	ENSG00000228766	RPL7L1P8	3:182328461-182329202	NOTEST	0.204215	0.284513	0.47841	0	1	1
ENSG00000228767	ENSG00000228767	KRT8P18	3:35257196-35258641	NOTEST	0	0	0	0	1	1
ENSG00000228768	ENSG00000228768	AC003101.1	17:29898160-29902678	NOTEST	0	0	0	0	1	1
ENSG00000228769	ENSG00000228769	ABCF2P2	7:71244475-71912136	NOTEST	0	0	0	0	1	1
ENSG00000228770	ENSG00000228770	AC007327.6	7:36192757-36341152	NOTEST	0	0	0	0	1	1
ENSG00000228771	ENSG00000228771	RP11-552J9.1	X:52613038-52615362	NOTEST	0	0	0	0	1	1
ENSG00000228772	ENSG00000228772	RP1-309H15.2	6:22589365-22594062	NOTEST	0	0	0	0	1	1
ENSG00000228775	ENSG00000228775	WEE2-AS1	7:141404137-141488440	NOTEST	0.309766	0.489048	0.658796	0	1	1
ENSG00000228776	ENSG00000228776	RP11-319C21.1	1:42606305-42607062	NOTEST	0	0	0	0	1	1
ENSG00000228777	ENSG00000228777	RP11-282C5.1	6:115954705-115955355	NOTEST	0	0	0	0	1	1
ENSG00000228778	ENSG00000228778	RP11-129J12.1	10:101286106-101290934	NOTEST	0	0	0	0	1	1
ENSG00000228779	ENSG00000228779	Z69666.2	16:127005-188859	NOTEST	0.0471544	0	#NAME?	0	1	1
ENSG00000228780	ENSG00000228780	RP1-50A13.1	X:42009763-42009997	NOTEST	0	0	0	0	1	1
ENSG00000228781	ENSG00000228781	RP11-336N8.3	9:80795129-80795609	NOTEST	0	0	0	0	1	1
ENSG00000228783	ENSG00000228783	RP11-147I11.1	9:1011084-1011799	NOTEST	0	0	0	0	1	1
ENSG00000228784	ENSG00000228784	LINC00954	2:20068620-20084808	NOTEST	0	0.0254806	inf	0	1	1
ENSG00000228785	ENSG00000228785	HLA-Z	HSCHR6_MHC_COX:32786512-32786587	NOTEST	0	0	0	0	1	1
ENSG00000228786	ENSG00000228786	LINC00266-4P	Y:27524446-27540866	NOTEST	0.0405293	0.0172182	-1.23503	0	1	1
ENSG00000228787	ENSG00000228787	NLGN4Y-AS1	Y:16634517-16957530	NOTEST	0	0	0	0	1	1
ENSG00000228789	ENSG00000228789	HCG22	6:31021226-31027667	NOTEST	0	0	0	0	1	1
ENSG00000228790	ENSG00000228790	AC098784.1	19:55215729-55216013	NOTEST	0	0	0	0	1	1
ENSG00000228791	ENSG00000228791	THRB-AS1	3:24158650-24541833	NOTEST	0.0142125	0	#NAME?	0	1	1
ENSG00000228792	ENSG00000228792	RP11-354K1.2	1:211809247-211827923	NOTEST	0	0	0	0	1	1
ENSG00000228793	ENSG00000228793	RP1-223B1.1	6:3594480-3624981	NOTEST	0	0.016967	inf	0	1	1
ENSG00000228798	ENSG00000228798	AP000473.5	21:18003145-18013002	NOTEST	0	0	0	0	1	1
ENSG00000228799	ENSG00000228799	AC113607.2	2:895901-901137	NOTEST	0	0	0	0	1	1
ENSG00000228800	ENSG00000228800	RP11-253D19.1	10:30842782-30843412	NOTEST	0	0	0	0	1	1
ENSG00000228802	ENSG00000228802	AC073641.2	2:224822120-224832431	NOTEST	0	0	0	0	1	1
ENSG00000228803	ENSG00000228803	AC073072.6	7:22787293-22788423	NOTEST	0	0	0	0	1	1
ENSG00000228804	ENSG00000228804	RP11-211G3.3	3:187416046-187463515	NOTEST	0	0	0	0	1	1
ENSG00000228806	ENSG00000228806	AC092628.3	7:154898109-154898361	NOTEST	0	0	0	0	1	1
ENSG00000228807	ENSG00000228807	MRPS18CP6	22:44879374-44879597	NOTEST	0	0	0	0	1	1
ENSG00000228808	ENSG00000228808	HMGB3P4	13:99853027-100038688	NOTEST	0.167218	0.131967	-0.341554	0	1	1
ENSG00000228809	ENSG00000228809	RP4-705D16.3	20:16695488-16722421	NOTEST	0.0159703	0	#NAME?	0	1	1
ENSG00000228810	ENSG00000228810	PABPC1P11	9:17579079-17797127	NOTEST	0	0	0	0	1	1
ENSG00000228812	ENSG00000228812	RP11-157P1.5	20:60877148-60942368	NOTEST	0	0	0	0	1	1
ENSG00000228813	ENSG00000228813	HLA-DQB2	HSCHR6_MHC_DBB:32703041-32710500	NOTEST	0	0	0	0	1	1
ENSG00000228814	ENSG00000228814	RP11-119H12.5	4:113739264-114304896	NOTEST	0	0	0	0	1	1
ENSG00000228815	ENSG00000228815	MARK2P13	7:36148633-36150482	NOTEST	0	0	0	0	1	1

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ENSG00000228817	ENSG00000228817	BACH1-IT2	21:30565800-31312351	NOTEST	0.028566	0	#NAME?	0	1	1
ENSG00000228819	ENSG00000228819	RP1-305B16.3	X:131264118-131265380	NOTEST	0	0	0	0	1	1
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ENSG00000228823	ENSG00000228823	RP11-293F5.8	1:21737952-21739786	NOTEST	0	0	0	0	1	1
ENSG00000228824	ENSG00000228824	MIR4500HG	13:88079454-88323514	NOTEST	0	0	0	0	1	1
ENSG00000228825	ENSG00000228825	LAMTOR3P1	13:37496675-37497045	NOTEST	0	0	0	0	1	1
ENSG00000228826	ENSG00000228826	RP11-344P13.4	1:121236176-121252181	NOTEST	0	0	0	0	1	1
ENSG00000228827	ENSG00000228827	RP11-234P3.2	X:51646433-51646946	NOTEST	0	0	0	0	1	1
ENSG00000228828	ENSG00000228828	RP11-162G10.1	10:38091750-38148038	NOTEST	0.0143558	0.00504262	-1.50939	0	1	1
ENSG00000228829	ENSG00000228829	AC005077.5	7:75803050-75806523	NOTEST	0	0	0	0	1	1
ENSG00000228833	ENSG00000228833	RP5-1014O16.9	X:148839457-148839556	NOTEST	0	0	0	0	1	1
ENSG00000228834	ENSG00000228834	RP11-249L21.4	6:109169618-109295186	NOTEST	0	0	0	0	1	1
ENSG00000228835	ENSG00000228835	AC012123.1	18:30252633-30354376	NOTEST	0.076904	0.0225003	-1.77311	0	1	1
ENSG00000228836	ENSG00000228836	CT45A4	X:134928330-134953994	NOTEST	0	0	0	0	1	1
ENSG00000228837	ENSG00000228837	CBX3P6	2:155797052-155797579	NOTEST	0	0	0	0	1	1
ENSG00000228838	ENSG00000228838	RP4-784A16.2	1:53711216-53793742	NOTEST	0.038239	0	#NAME?	0	1	1
ENSG00000228839	ENSG00000228839	RP3-400N23.6	22:31677578-31742218	NOTEST	0.22275	0.501895	1.17196	0	1	1
ENSG00000228840	ENSG00000228840	RPS17P1	HSCHR6_MHC_MANN:29456619-29457025	NOTEST	0	0	0	0	1	1
ENSG00000228842	ENSG00000228842	PCDH9-AS2	13:66876966-67804468	NOTEST	0	0	0	0	1	1
ENSG00000228843	ENSG00000228843	RP11-112J3.15	9:35696944-35758572	NOTEST	0.040645	0	#NAME?	0	1	1
ENSG00000228844	ENSG00000228844	RP11-467I20.3	1:240799898-240800352	NOTEST	0.0983409	0	#NAME?	0	1	1
ENSG00000228845	ENSG00000228845	MTCO3P1	HSCHR6_MHC_COX:32597336-32598168	NOTEST	0	0	0	0	1	1
ENSG00000228846	ENSG00000228846	OR2N1P	HSCHR6_MHC_MANN:29105656-29106593	NOTEST	0	0	0	0	1	1
ENSG00000228847	ENSG00000228847	ATP5G2P4	X:41958006-41958426	NOTEST	0	0	0	0	1	1
ENSG00000228848	ENSG00000228848	AC105402.2	2:149624038-149883273	NOTEST	0	0	0	0	1	1
ENSG00000228849	ENSG00000228849	TNF	HSCHR6_MHC_DBB:31525487-31528257	NOTEST	0	0	0	0	1	1
ENSG00000228850	ENSG00000228850	CDY12P	Y:24210844-24211859	NOTEST	0	0	0	0	1	1
ENSG00000228851	ENSG00000228851	RP11-1217F2.10	7:57258847-57259634	NOTEST	0	0	0	0	1	1
ENSG00000228853	ENSG00000228853	NEGR1-IT1	1:71547006-72748417	NOTEST	0	0	0	0	1	1
ENSG00000228854	ENSG00000228854	NRM	HSCHR6_MHC_APD:30664072-30667446	NOTEST	0	0	0	0	1	1
ENSG00000228855	ENSG00000228855	RP3-433G13.1	X:146673129-146673427	NOTEST	0	0	0	0	1	1
ENSG00000228856	ENSG00000228856	USP17L30	4:9364854-9366447	NOTEST	0	0	0	0	1	1
ENSG00000228857	ENSG00000228857	AC104653.1	2:114586966-114600933	NOTEST	0	0.02586	inf	0	1	1
ENSG00000228858	ENSG00000228858	RP11-95K23.5	9:41277732-41298538	NOTEST	0	0	0	0	1	1
ENSG00000228859	ENSG00000228859	LY6G6C	HSCHR6_MHC_DBB:31668543-31676660	NOTEST	0	0	0	0	1	1
ENSG00000228860	ENSG00000228860	RP11-565H13.3	10:21506819-21507208	NOTEST	0	0	0	0	1	1
ENSG00000228861	ENSG00000228861	RPL23AP12	21:40499493-40499966	NOTEST	0	0	0	0	1	1
ENSG00000228862	ENSG00000228862	RP11-91I20.3	8:61544067-61548830	NOTEST	0	0.00307211	inf	0	1	1
ENSG00000228863	ENSG00000228863	RP11-404F10.2	1:160639937-160681641	NOTEST	0.0467137	0	#NAME?	0	1	1

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ENSG00000228867	ENSG00000228867	NRM	HSCHR6_MHC_MANN:30700522-30703896	NOTEST	0	0	0	0	1	1
ENSG00000228868	ENSG00000228868	MYLKP1	3:75377699-75388222	NOTEST	0	0	0	0	1	1
ENSG00000228869	ENSG00000228869	COX4I1P2	13:46245979-46246526	NOTEST	0	0	0	0	1	1
ENSG00000228871	ENSG00000228871	MEP1AP1	9:42332814-42338938	NOTEST	0	0	0	0	1	1
ENSG00000228872	ENSG00000228872	AC096664.2	2:63348517-64054977	NOTEST	0	0	0	0	1	1
ENSG00000228873	ENSG00000228873	AC012307.2	2:96811340-96812751	NOTEST	0	0	0	0	1	1
ENSG00000228874	ENSG00000228874	AC090954.5	3:15173354-15173715	NOTEST	0	0	0	0	1	1
ENSG00000228875	ENSG00000228875	CSNK2B	HSCHR6_MHC_COX:31616420-31658607	NOTEST	0	0	0	0	1	1
ENSG00000228876	ENSG00000228876	AC010745.2	2:16405314-16410408	NOTEST	0	0	0	0	1	1
ENSG00000228877	ENSG00000228877	RP11-473E2.4	9:137419027-137437090	NOTEST	0	0	0	0	1	1
ENSG00000228878	ENSG00000228878	AC007551.3	7:35791465-35840226	NOTEST	0.102456	0.0149847	-2.77344	0	1	1
ENSG00000228879	ENSG00000228879	RP11-439E19.6	1:246887348-246931439	NOTEST	0.0974331	0.290692	1.57701	0	1	1
ENSG00000228881	ENSG00000228881	TRIM26	HSCHR6_MHC_APD:30089024-30118001	NOTEST	0	0	0	0	1	1
ENSG00000228882	ENSG00000228882	CICP9	10:38741914-38755104	NOTEST	0.0170508	0	#NAME?	0	1	1
ENSG00000228883	ENSG00000228883	LY6G5C	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000228884	ENSG00000228884	AC104634.2	2:232450574-232451038	NOTEST	0	0	0	0	1	1
ENSG00000228886	ENSG00000228886	RP11-290D2.3	13:45911007-45965872	NOTEST	0.310926	0.152071	-1.03183	0	1	1
ENSG00000228887	ENSG00000228887	EEF1DP1	19:14181153-14182052	NOTEST	0.040461	0.0288949	-0.485716	0	1	1
ENSG00000228888	ENSG00000228888	RP4-764O22.2	20:7050260-7234849	NOTEST	0	0	0	0	1	1
ENSG00000228890	ENSG00000228890	TTTY21	Y:9555261-9558905	NOTEST	0	0	0	0	1	1
ENSG00000228891	ENSG00000228891	DDX39BP1	HSCHR6_MHC_DBB:29865924-29866291	NOTEST	0	0	0	0	1	1
ENSG00000228892	ENSG00000228892	AGPAT1	HSCHR6_MHC_SSTO:32123002-32152743	NOTEST	0	0	0	0	1	1
ENSG00000228894	ENSG00000228894	HCG18	HSCHR6_MHC_COX:30191706-30304467	NOTEST	0	0	0	0	1	1
ENSG00000228896	ENSG00000228896	SKIV2L	HSCHR6_MHC_SSTO:31911715-31929380	NOTEST	0	0	0	0	1	1
ENSG00000228897	ENSG00000228897	CTD-2021A8.2	7:51454059-51454798	NOTEST	0	0	0	0	1	1
ENSG00000228898	ENSG00000228898	AC012365.3	2:117784112-117784600	NOTEST	0	0	0	0	1	1
ENSG00000228900	ENSG00000228900	HCG9P5	HSCHR6_MHC_MANN:29687659-29713937	NOTEST	0	0	0	0	1	1
ENSG00000228901	ENSG00000228901	HMGN2P36	11:13631909-13632318	NOTEST	0	0	0	0	1	1
ENSG00000228902	ENSG00000228902	ST6GALNAC2P1	2:84267008-84267844	NOTEST	0	0	0	0	1	1
ENSG00000228903	ENSG00000228903	RASA4CP	7:44066549-44081905	NOTEST	0.483634	0.505554	0.0639485	0	1	1
ENSG00000228904	ENSG00000228904	USP8P1	HSCHR6_MHC_QBL:31233163-31236336	NOTEST	0	0	0	0	1	1
ENSG00000228906	ENSG00000228906	RP13-216E22.4	X:73164158-73513409	NOTEST	0.510427	0.0755108	-2.75695	0	1	1
ENSG00000228907	ENSG00000228907	RNF5	HSCHR6_MHC_MANN:32185557-32187997	NOTEST	0	0	0	0	1	1
ENSG00000228909	ENSG00000228909	AC008281.1	2:220768771-220769610	NOTEST	0	0	0	0	1	1
ENSG00000228912	ENSG00000228912	IFITM4P	HSCHR6_MHC_COX:29712473-29712894	NOTEST	0	0	0	0	1	1
ENSG00000228913	ENSG00000228913	UBD	HSCHR6_MHC_COX:29519994-29597568	NOTEST	0	0	0	0	1	1
ENSG00000228914	ENSG00000228914	OR1H1P	9:125370314-125371079	NOTEST	0	0	0	0	1	1
ENSG00000228915	ENSG00000228915	OR7E128P	11:71576554-71639700	NOTEST	0.0317647	0.0665435	1.06687	0	1	1
ENSG00000228917	ENSG00000228917	RP11-544M22.8	1:161040784-161059389	NOTEST	0	0.0111514	inf	0	1	1
ENSG00000228918	ENSG00000228918	GS1-122H1.2	1:182098444-182283196	NOTEST	0	0	0	0	1	1
ENSG00000228919	ENSG00000228919	AC097381.1	4:7755816-7942022	NOTEST	0	0	0	0	1	1

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ENSG00000228921	ENSG00000228921	HCG4P5	HSCHR6_MHC_MCF:29846326-29992167	NOTEST	0	0	0	0	1	1
ENSG00000228922	ENSG00000228922	RP13-210D15.1	X:134335661-134349163	NOTEST	0	0	0	0	1	1
ENSG00000228923	ENSG00000228923	AP000355.2	22:24666785-24924358	NOTEST	0	0.10697	inf	0	1	1
ENSG00000228925	ENSG00000228925	AC016722.4	2:47126413-47403740	NOTEST	0.358945	0.331176	-0.116165	0	1	1
ENSG00000228926	ENSG00000228926	UQCRHP1	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000228927	ENSG00000228927	TSPY3	Y:9236029-9344176	NOTEST	0	0	0	0	1	1
ENSG00000228928	ENSG00000228928	AC002069.5	7:88194107-88195596	NOTEST	0	0	0	0	1	1
ENSG00000228929	ENSG00000228929	RP11-159C21.4	1:53192125-53293014	NOTEST	0.156854	0.230456	0.555075	0	1	1
ENSG00000228930	ENSG00000228930	MTCO1P3	21:46796105-46796297	NOTEST	0	0	0	0	1	1
ENSG00000228935	ENSG00000228935	RP11-189G24.2	20:22941170-22946700	NOTEST	0	0	0	0	1	1
ENSG00000228937	ENSG00000228937	AC005539.2	2:158733213-158992666	NOTEST	0	0	0	0	1	1
ENSG00000228938	ENSG00000228938	SNRPD2P1	10:91738473-91738827	NOTEST	0	0	0	0	1	1
ENSG00000228939	ENSG00000228939	AKT3-IT1	1:243419319-244014381	NOTEST	0.0429308	0	#NAME?	0	1	1
ENSG00000228940	ENSG00000228940	RP11-348A7.1	1:41403775-41405435	NOTEST	0	0	0	0	1	1
ENSG00000228941	ENSG00000228941	UBE3AP2	21:32432918-32435487	NOTEST	0	0	0	0	1	1
ENSG00000228943	ENSG00000228943	RP5-1053E7.2	1:28436249-28436809	NOTEST	0	0	0	0	1	1
ENSG00000228944	ENSG00000228944	AC004485.3	7:24236280-24295338	NOTEST	0	0	0	0	1	1
ENSG00000228945	ENSG00000228945	CLUHP2	Y:20442063-20446647	NOTEST	0	0	0	0	1	1
ENSG00000228948	ENSG00000228948	SLC25A6P5	9:108611990-108613706	NOTEST	0	0.0495739	inf	0	1	1
ENSG00000228949	ENSG00000228949	UGT1A12P	2:234494084-234494937	NOTEST	0	0	0	0	1	1
ENSG00000228950	ENSG00000228950	AC023137.2	2:20650802-20652708	NOTEST	0	0	0	0	1	1
ENSG00000228951	ENSG00000228951	RP11-336A10.4	10:5658824-5660124	NOTEST	0	0	0	0	1	1
ENSG00000228952	ENSG00000228952	RP11-567G11.1	3:187166632-187167238	NOTEST	0.184553	0.712328	1.94851	0	1	1
ENSG00000228953	ENSG00000228953	AC006026.12	7:23695300-23695480	NOTEST	0	0	0	0	1	1
ENSG00000228954	ENSG00000228954	XXbac-BPG248L24.10	HSCHR6_MHC_MANN:31319021-31319755	NOTEST	0	0	0	0	1	1
ENSG00000228955	ENSG00000228955	RP11-452J6.2	1:246729745-246831886	NOTEST	0.250165	0.596861	1.25452	0	1	1
ENSG00000228956	ENSG00000228956	AC144521.1	3:17198653-18959184	NOTEST	0.0285478	0.0255433	-0.160436	0	1	1
ENSG00000228957	ENSG00000228957	RP11-23J9.3	9:100148521-100158394	NOTEST	0	0	0	0	1	1
ENSG00000228958	ENSG00000228958	PIGPP3	20:32552967-32553382	NOTEST	0	0	0	0	1	1
ENSG00000228959	ENSG00000228959	RP5-1121H13.3	20:40619779-40692609	NOTEST	0	0	0	0	1	1
ENSG00000228960	ENSG00000228960	OR2A9P	7:143883175-144077725	NOTEST	0.045907	0.110748	1.27049	0	1	1
ENSG00000228961	ENSG00000228961	AP000282.3	21:34285956-34444726	NOTEST	0	0	0	0	1	1
ENSG00000228962	ENSG00000228962	HCG23	6:32358286-32361463	NOTEST	0.158875	0.180299	0.182498	0	1	1
ENSG00000228963	ENSG00000228963	OR7E93P	3:125443381-125444288	NOTEST	0	0	0	0	1	1
ENSG00000228964	ENSG00000228964	HLA-B	HSCHR6_MHC_SSTO:31314549-31317907	NOTEST	0	0	0	0	1	1
ENSG00000228965	ENSG00000228965	RP11-1007I13.2	X:151213785-151214665	NOTEST	0	0	0	0	1	1
ENSG00000228966	ENSG00000228966	HOMER2P1	14:106916016-106916980	NOTEST	0.124595	0.141996	0.188595	0	1	1
ENSG00000228968	ENSG00000228968	AC096554.1	2:104741725-104763687	NOTEST	0	0	0	0	1	1
ENSG00000228970	ENSG00000228970	UBTFL6	2:98253059-98254266	NOTEST	0	0	0	0	1	1
ENSG00000228971	ENSG00000228971	RP11-286B14.1	1:95975671-96247898	NOTEST	0	0.0638284	inf	0	1	1
ENSG00000228972	ENSG00000228972	RP1-86D1.2	6:128289923-128841870	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000228973	ENSG00000228973	AC009955.8	2:220489780-220491415	NOTEST	0	0	0	0	1	1
ENSG00000228974	ENSG00000228974	AC006483.5	7:5566781-5603415	NOTEST	0	0	0	0	1	1
ENSG00000228976	ENSG00000228976	SUMO2P8	6:108881037-109005977	NOTEST	0	0	0	0	1	1
ENSG00000228977	ENSG00000228977	OR2W1	HSCHR6_MHC_MCF:29012142-29013170	NOTEST	0	0	0	0	1	1
ENSG00000228978	ENSG00000228978	TNF	HSCHR6_MHC_APD:31555631-31557434	NOTEST	0	0	0	0	1	1
ENSG00000228979	ENSG00000228979	CTD-2501B8.5	17:61548964-61549456	NOTEST	0	0	0	0	1	1
ENSG00000228980	ENSG00000228980	RP11-702L6.4	3:109128524-109214014	NOTEST	0	0	0	0	1	1
ENSG00000228981	ENSG00000228981	RP11-364L4.1	4:144256417-144395721	NOTEST	0	0.0171925	inf	0	1	1
ENSG00000228982	ENSG00000228982	RP11-107G24.3	1:247248690-247249369	NOTEST	0	0	0	0	1	1
ENSG00000228983	ENSG00000228983	AC025627.7	17:19398697-19501235	NOTEST	0	0	0	0	1	1
ENSG00000228984	ENSG00000228984	RP11-101E19.8	8:47696421-47697550	NOTEST	0	0	0	0	1	1
ENSG00000228985	ENSG00000228985	TRDD3	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000228986	ENSG00000228986	RP13-228J13.8	X:154505499-154563966	NOTEST	0	0	0	0	1	1
ENSG00000228987	ENSG00000228987	HLA-DRA	HSCHR6_MHC_DBB:32382334-32387545	NOTEST	0	0	0	0	1	1
ENSG00000228988	ENSG00000228988	RP4-677H15.4	1:70671364-70718735	NOTEST	0.05192	0	#NAME?	0	1	1
ENSG00000228990	ENSG00000228990	KRT18P1	HSCHR6_MHC_SSTO:28936954-28938285	NOTEST	0	0	0	0	1	1
ENSG00000228991	ENSG00000228991	RP11-318K12.1	9:66693276-66759372	NOTEST	0	0	0	0	1	1
ENSG00000228992	ENSG00000228992	RPL5P32	15:28000020-28344504	NOTEST	0	0	0	0	1	1
ENSG00000228993	ENSG00000228993	GPR53P	HSCHR6_MHC_MCF:29505273-29506357	NOTEST	0	0	0	0	1	1
ENSG00000228995	ENSG00000228995	MTND1P9	20:55926065-55954267	NOTEST	0.0192164	0	#NAME?	0	1	1
ENSG00000228997	ENSG00000228997	RP1-186E20.1	10:10818185-10818624	NOTEST	0	0	0	0	1	1
ENSG00000228999	ENSG00000228999	AC068490.1	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000229000	ENSG00000229000	SEPT7P8	19:54275759-54276534	NOTEST	0	0	0	0	1	1
ENSG00000229001	ENSG00000229001	ACTBP14	10:70782533-70783622	NOTEST	0	0	0	0	1	1
ENSG00000229002	ENSG00000229002	RP11-666A1.4	1:148542872-148545128	NOTEST	0	0	0	0	1	1
ENSG00000229005	ENSG00000229005	HNF4A-AS1	20:42984339-43061485	NOTEST	0	0	0	0	1	1
ENSG00000229006	ENSG00000229006	TRIM27	HSCHR6_MHC_SSTO:28870843-28891821	NOTEST	0	0	0	0	1	1
ENSG00000229007	ENSG00000229007	EXOSC3P1	21:33784313-33887707	NOTEST	0.0902943	0.163457	0.856205	0	1	1
ENSG00000229009	ENSG00000229009	TMPRSS11GP	4:68566997-68995598	NOTEST	0	0	0	0	1	1
ENSG00000229010	ENSG00000229010	RP5-979D14.1	1:23345940-23504301	NOTEST	0	0	0	0	1	1
ENSG00000229011	ENSG00000229011	LINC01038	13:80378552-80379820	NOTEST	0	0	0	0	1	1
ENSG00000229012	ENSG00000229012	GS1-542M4.4	X:8831901-8835642	NOTEST	0	0	0	0	1	1
ENSG00000229013	ENSG00000229013	AC083939.1	2:35696781-35696907	NOTEST	0	0	0	0	1	1
ENSG00000229014	ENSG00000229014	RPL30P13	12:40019968-40499891	NOTEST	0	0	0	0	1	1
ENSG00000229015	ENSG00000229015	RP11-265D19.6	X:134530353-134531689	NOTEST	0	0	0	0	1	1
ENSG00000229016	ENSG00000229016	RP11-224O19.4	1:218458628-218511325	NOTEST	0	0	0	0	1	1
ENSG00000229017	ENSG00000229017	RP11-439L18.3	6:143287557-143359214	NOTEST	0	0	0	0	1	1
ENSG00000229019	ENSG00000229019	RP11-88I18.3	9:70921443-71145977	NOTEST	0.0369968	0.0446111	0.270001	0	1	1
ENSG00000229020	ENSG00000229020	AKR7A2P1	1:113454468-113542118	NOTEST	0.0598911	0.102142	0.770167	0	1	1
ENSG00000229021	ENSG00000229021	NBPF18P	1:151967006-152020383	NOTEST	0.013616	0.00908776	-0.583312	0	1	1
ENSG00000229022	ENSG00000229022	RP11-553N16.1	1:241995236-241996089	NOTEST	0	0	0	0	1	1
ENSG00000229023	ENSG00000229023	AC067945.3	2:191745522-191885686	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229025	ENSG00000229025	AP001595.1	21:27722098-27722953	NOTEST	0	0	0	0	1	1
ENSG00000229027	ENSG00000229027	HSFY1P1	22:17308363-17310225	NOTEST	0	0	0	0	1	1
ENSG00000229028	ENSG00000229028	KRT223P	17:38873486-38878184	NOTEST	0	0	0	0	1	1
ENSG00000229029	ENSG00000229029	RP11-408A13.1	9:14593574-14594198	NOTEST	0.121074	0.0255271	-2.24579	0	1	1
ENSG00000229030	ENSG00000229030	RP11-402P6.6	X:71068624-71068854	NOTEST	0	0	0	0	1	1
ENSG00000229031	ENSG00000229031	RP11-666G4.1	7:68689682-68895909	NOTEST	0	0	0	0	1	1
ENSG00000229032	ENSG00000229032	RP11-91A18.1	1:52373627-52456436	NOTEST	0	0	0	0	1	1
ENSG00000229034	ENSG00000229034	MCCD1P2	HSCHR6_MHC_SSTO:29950682-29951560	NOTEST	0	0	0	0	1	1
ENSG00000229035	ENSG00000229035	SPRR2C	1:153042699-153113927	NOTEST	0	0	0	0	1	1
ENSG00000229036	ENSG00000229036	RP1-20N2.6	6:143771943-143832827	NOTEST	0.583073	0.503196	-0.212556	0	1	1
ENSG00000229037	ENSG00000229037	RP11-272G22.3	X:53834273-53835121	NOTEST	0	0	0	0	1	1
ENSG00000229038	ENSG00000229038	RANP1	HSCHR6_MHC_QBL:30443237-30443888	NOTEST	0	0	0	0	1	1
ENSG00000229040	ENSG00000229040	OR2N1P	HSCHR6_MHC_APD:29105692-29106629	NOTEST	0	0	0	0	1	1
ENSG00000229042	ENSG00000229042	RP1-232N11.2	20:40701391-41818610	NOTEST	0	0	0	0	1	1
ENSG00000229044	ENSG00000229044	RP11-266K22.2	1:31769841-31837783	NOTEST	0	0	0	0	1	1
ENSG00000229045	ENSG00000229045	DDX6P1	HSCHR6_MHC_COX:29294119-29295554	NOTEST	0	0	0	0	1	1
ENSG00000229046	ENSG00000229046	HMGN1P2	21:33043345-33104388	NOTEST	0	0.082625	inf	0	1	1
ENSG00000229047	ENSG00000229047	AF127577.10	21:16333555-16437321	NOTEST	0	0	0	0	1	1
ENSG00000229048	ENSG00000229048	DUTP1	3:124801479-125094198	NOTEST	0	0	0	0	1	1
ENSG00000229051	ENSG00000229051	RP5-952N6.1	1:71172135-71252151	NOTEST	0	0	0	0	1	1
ENSG00000229052	ENSG00000229052	RP11-386I23.1	1:93307723-93427057	NOTEST	0	0.0367888	inf	0	1	1
ENSG00000229054	ENSG00000229054	AC074338.4	7:32535037-33102409	NOTEST	0	0	0	0	1	1
ENSG00000229055	ENSG00000229055	AC034110.1	18:74401985-74405592	NOTEST	0	0	0	0	1	1
ENSG00000229056	ENSG00000229056	AC020571.3	2:197059093-197458416	NOTEST	0.0802852	0.131827	0.715437	0	1	1
ENSG00000229057	ENSG00000229057	RP11-106A1.3	9:6645955-6670635	NOTEST	0.0263836	0	#NAME?	0	1	1
ENSG00000229058	ENSG00000229058	AGER	HSCHR6_MHC_MANN:32188171-32191528	NOTEST	0	0	0	0	1	1
ENSG00000229060	ENSG00000229060	RP11-20P5.2	9:27948075-28670283	NOTEST	0	0	0	0	1	1
ENSG00000229061	ENSG00000229061	ATAT1	HSCHR6_MHC_DBB:30584859-30604840	NOTEST	0	0	0	0	1	1
ENSG00000229063	ENSG00000229063	TRBV23OR9-2	9:33638032-33638492	NOTEST	0	0	0	0	1	1
ENSG00000229064	ENSG00000229064	RP11-746P2.5	7:64707971-64708122	NOTEST	0	0	0	0	1	1
ENSG00000229065	ENSG00000229065	RP11-80I15.4	9:97861335-98079991	NOTEST	0.154235	0.199351	0.370183	0	1	1
ENSG00000229066	ENSG00000229066	AC096649.3	2:176121977-176319368	NOTEST	0	0	0	0	1	1
ENSG00000229067	ENSG00000229067	RP11-91I11.1	1:92065727-92065878	NOTEST	0	0	0	0	1	1
ENSG00000229068	ENSG00000229068	TMPOP1	6:30434228-30435771	NOTEST	0.0381987	0.0911033	1.25398	0	1	1
ENSG00000229069	ENSG00000229069	OR2J4P	HSCHR6_MHC_SSTO:29149333-29150269	NOTEST	0	0	0	0	1	1
ENSG00000229071	ENSG00000229071	PRRT1	HSCHR6_MHC_COX:32064597-32094350	NOTEST	0	0	0	0	1	1
ENSG00000229072	ENSG00000229072	HMGN2P24	3:40740556-40740829	NOTEST	0	0	0	0	1	1
ENSG00000229074	ENSG00000229074	HLA-DRB1	HSCHR6_MHC_MANN:32691165-32725266	NOTEST	0	0	0	0	1	1
ENSG00000229075	ENSG00000229075	XXbac-BPG299F13.14	HSCHR6_MHC_SSTO:31159623-31165828	NOTEST	0	0	0	0	1	1
ENSG00000229077	ENSG00000229077	SLC44A4	HSCHR6_MHC_MCF:31907449-31923299	NOTEST	0	0	0	0	1	1
ENSG00000229079	ENSG00000229079	CR848007.5	9:44011052-44011839	NOTEST	0	0	0	0	1	1
ENSG00000229080	ENSG00000229080	RP11-291J9.2	9:31505943-31506613	NOTEST	0	0	0	0	1	1
ENSG00000229081	ENSG00000229081	LINC01165	10:134334330-134335953	NOTEST	0.0185566	0.0398018	1.1009	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229082	ENSG00000229082	OR5AW1P	X:130407479-130533677	NOTEST	0	0	0	0	1	1
ENSG00000229084	ENSG00000229084	LINC00226	14:106744268-106744975	NOTEST	0	0	0	0	1	1
ENSG00000229086	ENSG00000229086	C21orf54	21:34537775-34542541	NOTEST	0	0	0	0	1	1
ENSG00000229087	ENSG00000229087	RP11-32P22.1	2:15307031-15701454	NOTEST	0	0.0599085	inf	0	1	1
ENSG00000229088	ENSG00000229088	MTND1P10	22:36574601-36575433	NOTEST	0	0	0	0	1	1
ENSG00000229089	ENSG00000229089	ANKRD20A8P	2:95476790-95523027	NOTEST	0.00640655	0.00497751	-0.364124	0	1	1
ENSG00000229090	ENSG00000229090	RP1-232L22__A.1	X:100975312-100976682	NOTEST	0	0	0	0	1	1
ENSG00000229091	ENSG00000229091	HSPA8P8	7:10490937-10492153	NOTEST	0.0142125	0.0100044	-0.506532	0	1	1
ENSG00000229092	ENSG00000229092	IGHV3-47	14:106938444-106977000	NOTEST	0	0	0	0	1	1
ENSG00000229093	ENSG00000229093	OR51AB1P	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000229094	ENSG00000229094	POU5F1	HSCHR6_MHC_DBB:31120049-31132215	NOTEST	0	0	0	0	1	1
ENSG00000229099	ENSG00000229099	HLA-DRB7	HSCHR6_MHC_MANN:32647648-32666810	NOTEST	0	0	0	0	1	1
ENSG00000229100	ENSG00000229100	OR2P1P	HSCHR6_MHC_SSTO:29039626-29040402	NOTEST	0	0	0	0	1	1
ENSG00000229101	ENSG00000229101	TCEB1P20	1:116099446-116100096	NOTEST	0	0	0	0	1	1
ENSG00000229102	ENSG00000229102	RP11-360P21.2	3:178819153-178865761	NOTEST	0	0	0	0	1	1
ENSG00000229103	ENSG00000229103	WASF5P	HSCHR6_MHC_DBB:31247437-31248892	NOTEST	0	0	0	0	1	1
ENSG00000229104	ENSG00000229104	YY1P2	2:139654720-139655668	NOTEST	0	0	0	0	1	1
ENSG00000229105	ENSG00000229105	RP11-264C15.2	9:119187503-120177348	NOTEST	0	0	0	0	1	1
ENSG00000229106	ENSG00000229106	RP11-4M23.2	1:24197015-24285549	NOTEST	0	0	0	0	1	1
ENSG00000229107	ENSG00000229107	ABHD17AP4	22:21022123-21025272	NOTEST	0.29151	0.230882	-0.336389	0	1	1
ENSG00000229108	ENSG00000229108	AC005550.4	7:15728002-15735116	NOTEST	0	0	0	0	1	1
ENSG00000229109	ENSG00000229109	RP11-439K3.1	9:85834245-85849157	NOTEST	0.108768	0.0424125	-1.35869	0	1	1
ENSG00000229110	ENSG00000229110	AC006355.3	7:77646392-79100524	NOTEST	0	0	0	0	1	1
ENSG00000229111	ENSG00000229111	MED4-AS1	13:48627458-48669267	NOTEST	0.0426863	0.161057	1.91572	0	1	1
ENSG00000229112	ENSG00000229112	RP11-690C23.3	1:246691863-246692143	NOTEST	0	0	0	0	1	1
ENSG00000229115	ENSG00000229115	RP11-417B4.3	9:126118448-126692431	NOTEST	0	0	0	0	1	1
ENSG00000229116	ENSG00000229116	RP11-20J15.3	10:44787705-44789157	NOTEST	0	0	0	0	1	1
ENSG00000229118	ENSG00000229118	AC068491.2	2:111953539-112268567	NOTEST	0.0615122	0.307735	2.32274	0	1	1
ENSG00000229120	ENSG00000229120	CYCSP4	1:202317826-202679545	NOTEST	0	0	0	0	1	1
ENSG00000229122	ENSG00000229122	AGBL5-IT1	2:27265231-27294641	NOTEST	0	0.189301	inf	0	1	1
ENSG00000229125	ENSG00000229125	OR2H1	HSCHR6_MHC_APD:29425037-29432186	NOTEST	0	0	0	0	1	1
ENSG00000229126	ENSG00000229126	XXbac-BPG118E17.9	HSCHR6_MHC_SSTO:30978725-30994957	NOTEST	0	0	0	0	1	1
ENSG00000229127	ENSG00000229127	AC007038.7	2:210867288-211036115	NOTEST	0.297844	0.357409	0.263018	0	1	1
ENSG00000229129	ENSG00000229129	ACTG1P2	Y:19868880-19870005	NOTEST	0	0	0	0	1	1
ENSG00000229131	ENSG00000229131	AC016710.1	2:140227344-140235317	NOTEST	0.0941995	0	#NAME?	0	1	1
ENSG00000229133	ENSG00000229133	RPS7P4	1:68708156-68708738	NOTEST	0.103041	0	#NAME?	0	1	1
ENSG00000229136	ENSG00000229136	MAS1LP1	HSCHR6_MHC_APD:29442882-29443929	NOTEST	0	0	0	0	1	1
ENSG00000229137	ENSG00000229137	RP11-101P17.1	13:21834153-21868998	NOTEST	0.0539415	0.0647787	0.264124	0	1	1
ENSG00000229138	ENSG00000229138	CDY6P	Y:19993978-19995588	NOTEST	0	0	0	0	1	1
ENSG00000229140	ENSG00000229140	CCDC26	8:130363936-130695925	NOTEST	0.34979	0.37008	0.0813492	0	1	1
ENSG00000229143	ENSG00000229143	AC009480.4	2:148567914-148568346	NOTEST	0	0	0	0	1	1
ENSG00000229145	ENSG00000229145	ACTBP1	X:46147450-46148563	NOTEST	0	0	0	0	1	1
ENSG00000229146	ENSG00000229146	SNX18P5	9:44046988-44047817	NOTEST	0.0225735	0.017559	-0.36242	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229147	ENSG00000229147	SMPD4P2	13:19726706-19745334	NOTEST	0	0	0	0	1	1
ENSG00000229149	ENSG00000229149	HCG19P	HSCHR6_MHC_APD:30335293-30335927	NOTEST	0	0	0	0	1	1
ENSG00000229150	ENSG00000229150	CRYGEP	2:208972956-208977235	NOTEST	0	0	0	0	1	1
ENSG00000229151	ENSG00000229151	RP11-348F1.3	X:51099795-51139314	NOTEST	0	0	0	0	1	1
ENSG00000229153	ENSG00000229153	EPHA1-AS1	7:143078172-143220542	NOTEST	0	0	0	0	1	1
ENSG00000229154	ENSG00000229154	KCNQ5-AS1	6:73331519-73908574	NOTEST	0.0582035	0.0703407	0.273254	0	1	1
ENSG00000229155	ENSG00000229155	RP11-528A4.2	3:193560348-193561813	NOTEST	0	0	0	0	1	1
ENSG00000229159	ENSG00000229159	TSPY23P	Y:24329996-24332168	NOTEST	0	0	0	0	1	1
ENSG00000229160	ENSG00000229160	AC009229.6	2:38150329-38408997	NOTEST	0	0	0	0	1	1
ENSG00000229161	ENSG00000229161	TCP1P1	7:42834504-42842093	NOTEST	0	0	0	0	1	1
ENSG00000229162	ENSG00000229162	RP11-84D1.1	1:25226001-25291612	NOTEST	0.0648144	0.173259	1.41855	0	1	1
ENSG00000229163	ENSG00000229163	NAP1L1P2	Y:2709526-2800041	NOTEST	0	0	0	0	1	1
ENSG00000229164	ENSG00000229164	TRAC	14:23016446-23021097	NOTEST	0.215514	0.278796	0.371426	0	1	1
ENSG00000229165	ENSG00000229165	GDI2P1	7:48942151-48943487	NOTEST	0	0	0	0	1	1
ENSG00000229167	ENSG00000229167	RP11-73M7.1	1:32037185-32041174	NOTEST	0	0	0	0	1	1
ENSG00000229168	ENSG00000229168	RPL19P20	X:44508374-44508965	NOTEST	0	0	0	0	1	1
ENSG00000229169	ENSG00000229169	RP11-247I13.6	22:31795508-32058418	NOTEST	0	0	0	0	1	1
ENSG00000229170	ENSG00000229170	LINC00243	HSCHR6_MHC_MANN:30811118-30843127	NOTEST	0	0	0	0	1	1
ENSG00000229172	ENSG00000229172	AC073065.3	2:228666555-228669421	NOTEST	0	0	0	0	1	1
ENSG00000229173	ENSG00000229173	AC108059.4	2:128848773-128953251	NOTEST	0	0	0	0	1	1
ENSG00000229175	ENSG00000229175	LINC00382	13:80446720-80492079	NOTEST	0	0	0	0	1	1
ENSG00000229176	ENSG00000229176	SAPCD1	HSCHR6_MHC_COX:31695129-31720748	NOTEST	0	0	0	0	1	1
ENSG00000229177	ENSG00000229177	AC008154.5	7:134030822-134035543	NOTEST	0	0	0	0	1	1
ENSG00000229178	ENSG00000229178	AC069513.4	3:195382435-195384798	NOTEST	0.209304	0.167309	-0.323084	0	1	1
ENSG00000229179	ENSG00000229179	SAR1P1	HSCHR6_MHC_DBB:29044361-29044957	NOTEST	0	0	0	0	1	1
ENSG00000229180	ENSG00000229180	GS1-124K5.11	7:65976542-66010053	NOTEST	0.602979	0.361473	-0.738221	0	1	1
ENSG00000229181	ENSG00000229181	OR12D3	HSCHR6_MHC_APD:29390470-29424928	NOTEST	0	0	0	0	1	1
ENSG00000229182	ENSG00000229182	MRPS16P1	8:92929734-92930146	NOTEST	0	0	0	0	1	1
ENSG00000229183	ENSG00000229183	PGA4	11:60989687-61018929	NOTEST	0	0	0	0	1	1
ENSG00000229184	ENSG00000229184	RP11-255J3.3	9:2900319-2900804	NOTEST	0	0	0	0	1	1
ENSG00000229185	ENSG00000229185	OR2H2	HSCHR6_MHC_COX:29519994-29597568	NOTEST	0	0	0	0	1	1
ENSG00000229187	ENSG00000229187	MICC	HSCHR6_MHC_MANN:30427174-30431779	NOTEST	0	0	0	0	1	1
ENSG00000229188	ENSG00000229188	RP4-553F4.2	20:32316736-32398903	NOTEST	0	0	0	0	1	1
ENSG00000229189	ENSG00000229189	UQCRHP1	HSCHR6_MHC_QBL:31569104-31569378	NOTEST	0	0	0	0	1	1
ENSG00000229190	ENSG00000229190	RP11-390B4.3	10:17686123-17757913	NOTEST	0	0.152953	inf	0	1	1
ENSG00000229191	ENSG00000229191	RP11-168O16.1	1:200993076-200997920	NOTEST	0	0	0	0	1	1
ENSG00000229192	ENSG00000229192	AC004870.3	7:46930222-47118726	NOTEST	0	0	0	0	1	1
ENSG00000229194	ENSG00000229194	HLA-V	HSCHR6_MHC_MCF:29755698-29762471	NOTEST	0	0	0	0	1	1
ENSG00000229196	ENSG00000229196	RP11-775D22.2	7:129781570-129782455	NOTEST	0	0	0	0	1	1
ENSG00000229197	ENSG00000229197	RP11-227H15.7	10:71029739-71161638	NOTEST	0	0	0	0	1	1
ENSG00000229198	ENSG00000229198	RP11-12A20.4	9:67789325-67789530	NOTEST	0	0	0	0	1	1
ENSG00000229199	ENSG00000229199	XXbac-BPG118E17.9	HSCHR6_MHC_QBL:30964800-30993617	NOTEST	0	0	0	0	1	1
ENSG00000229200	ENSG00000229200	TRBV7-8	7:142099454-142099977	NOTEST	0	0	0	0	1	1
ENSG00000229201	ENSG00000229201	RP5-827O9.1	1:90976466-90999029	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229202	ENSG00000229202	PRR3	HSCHR6_MHC_SSTO:30500572-30522918	NOTEST	0	0	0	0	1	1
ENSG00000229203	ENSG00000229203	AC103564.7	2:132587373-132589604	NOTEST	0.108412	0.0842379	-0.363985	0	1	1
ENSG00000229204	ENSG00000229204	PTGES3P3	4:170712370-170712853	NOTEST	0.0953595	0.0338936	-1.49236	0	1	1
ENSG00000229205	ENSG00000229205	LINC00200	10:1205707-1210612	NOTEST	0	0.00509868	inf	0	1	1
ENSG00000229206	ENSG00000229206	RP11-397O4.1	10:11047258-11378674	NOTEST	0	0	0	0	1	1
ENSG00000229207	ENSG00000229207	SERPINH1P1	9:34179002-34329198	NOTEST	0.228063	0.209943	-0.119439	0	1	1
ENSG00000229208	ENSG00000229208	RBMY2NP	Y:9669026-9684305	NOTEST	0	0	0	0	1	1
ENSG00000229209	ENSG00000229209	AC073987.1	2:103726216-103792718	NOTEST	0	0	0	0	1	1
ENSG00000229210	ENSG00000229210	SUMO2P1	HSCHR6_MHC_DBB:29603794-29604078	NOTEST	0	0	0	0	1	1
ENSG00000229211	ENSG00000229211	RP11-363L24.2	8:31077409-31078500	NOTEST	0	0.0134402	inf	0	1	1
ENSG00000229213	ENSG00000229213	RP1-118J21.24	1:40261514-40261668	NOTEST	0	0	0	0	1	1
ENSG00000229214	ENSG00000229214	LINC00242	6:170188885-170202969	NOTEST	0.0119576	0.0191493	0.679358	0	1	1
ENSG00000229215	ENSG00000229215	HLA-A	HSCHR6_MHC_APD:29845528-29850151	NOTEST	0	0	0	0	1	1
ENSG00000229216	ENSG00000229216	PPIAP9	HSCHR6_MHC_MANN:31526784-31527596	NOTEST	0	0	0	0	1	1
ENSG00000229217	ENSG00000229217	CYCSP11	3:10068097-10149915	NOTEST	0	0	0	0	1	1
ENSG00000229220	ENSG00000229220	RP11-47A17.2	1:199996729-200146552	NOTEST	0	0	0	0	1	1
ENSG00000229221	ENSG00000229221	HNRNPA1P66	2:63348517-64054977	NOTEST	0	0	0	0	1	1
ENSG00000229222	ENSG00000229222	KRT18P4	20:48573281-48574569	NOTEST	0.0664815	0.261536	1.97599	0	1	1
ENSG00000229223	ENSG00000229223	TRIM31-AS1	HSCHR6_MHC_QBL:30060242-30072064	NOTEST	0	0	0	0	1	1
ENSG00000229224	ENSG00000229224	AC105398.3	2:29319708-29320391	NOTEST	0	0	0	0	1	1
ENSG00000229225	ENSG00000229225	RP11-5P4.3	1:63543751-63544702	NOTEST	0	0	0	0	1	1
ENSG00000229226	ENSG00000229226	BTF3L4P4	4:169277885-169931426	NOTEST	0	0	0	0	1	1
ENSG00000229227	ENSG00000229227	RP11-38L15.2	10:46897591-46971400	NOTEST	0.0701934	0.12155	0.792137	0	1	1
ENSG00000229228	ENSG00000229228	LINC00582	1:231664398-232177018	NOTEST	0	0	0	0	1	1
ENSG00000229229	ENSG00000229229	AC022201.4	2:70630065-70649810	NOTEST	0	0	0	0	1	1
ENSG00000229230	ENSG00000229230	MT1P3	20:33703166-33872788	NOTEST	0	0	0	0	1	1
ENSG00000229231	ENSG00000229231	FEM1AP1	21:15134658-15136653	NOTEST	0	0.00572121	inf	0	1	1
ENSG00000229232	ENSG00000229232	KRT18P53	X:505970-506087	NOTEST	0	0	0	0	1	1
ENSG00000229234	ENSG00000229234	RBMY1KP	Y:24355477-24362727	NOTEST	0	0	0	0	1	1
ENSG00000229235	ENSG00000229235	RP11-8L18.3	10:34398487-35104253	NOTEST	0	0	0	0	1	1
ENSG00000229236	ENSG00000229236	TTTY10	Y:22627553-22681114	NOTEST	0	0	0	0	1	1
ENSG00000229237	ENSG00000229237	HMGN1P37	X:154006958-154049282	NOTEST	0	0	0	0	1	1
ENSG00000229238	ENSG00000229238	PPP1R12BP1	Y:28424069-28500565	NOTEST	0	0	0	0	1	1
ENSG00000229239	ENSG00000229239	RP11-223J15.2	1:23996783-24006749	NOTEST	0	0	0	0	1	1
ENSG00000229240	ENSG00000229240	LINC00710	10:10969020-10994197	NOTEST	0	0	0	0	1	1
ENSG00000229241	ENSG00000229241	PNPT1P1	3:3742497-4508965	NOTEST	0	0.00538185	inf	0	1	1
ENSG00000229242	ENSG00000229242	RP5-1111A8.3	1:215796235-216596738	NOTEST	0	0.00484663	inf	0	1	1
ENSG00000229243	ENSG00000229243	AC098973.1	3:27844252-27932792	NOTEST	0	0	0	0	1	1
ENSG00000229245	ENSG00000229245	RP11-542K23.7	9:125165685-125211256	NOTEST	0	0	0	0	1	1
ENSG00000229246	ENSG00000229246	RP11-521J24.1	13:81617804-81618577	NOTEST	0	0.0976074	inf	0	1	1
ENSG00000229247	ENSG00000229247	RP11-492M19.3	1:26966867-26967105	NOTEST	0	0	0	0	1	1
ENSG00000229248	ENSG00000229248	WBP2P1	18:22596397-22597168	NOTEST	0	0	0	0	1	1
ENSG00000229249	ENSG00000229249	LINC00446	13:78469615-79233314	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229250	ENSG00000229250	USP9YP31	Y:26227850-26236493	NOTEST	0	0	0	0	1	1
ENSG00000229251	ENSG00000229251	HNRNPA1P8	7:84612862-84613825	NOTEST	0	0.055354	inf	0	1	1
ENSG00000229252	ENSG00000229252	HLA-E	HSCHR6_MHC_DBB:30447486-30452225	NOTEST	0	0	0	0	1	1
ENSG00000229253	ENSG00000229253	ZBTB22	HSCHR6_MHC_COX:33203790-33207330	NOTEST	0	0	0	0	1	1
ENSG00000229254	ENSG00000229254	OR8C1P	11:124246772-124247697	NOTEST	0	0	0	0	1	1
ENSG00000229255	ENSG00000229255	RP11-407H12.8	1:248647545-248648785	NOTEST	0	0	0	0	1	1
ENSG00000229256	ENSG00000229256	ST13P13	10:104975465-104976557	NOTEST	0.0161264	0.0502589	1.63996	0	1	1
ENSG00000229257	ENSG00000229257	RP11-229P13.22	9:139952114-139965040	NOTEST	0	0	0	0	1	1
ENSG00000229258	ENSG00000229258	RP11-552D8.1	1:211916798-212027045	NOTEST	0	0	0	0	1	1
ENSG00000229259	ENSG00000229259	LRRC37A12P	1:32888814-32892390	NOTEST	0	0	0	0	1	1
ENSG00000229261	ENSG00000229261	RP11-227H15.4	10:70975088-71027904	NOTEST	0.00842862	0	#NAME?	0	1	1
ENSG00000229262	ENSG00000229262	RP4-726N1.2	20:18040136-18051652	NOTEST	0	0	0	0	1	1
ENSG00000229263	ENSG00000229263	AC004691.5	7:30692199-30965131	NOTEST	0	0.0307711	inf	0	1	1
ENSG00000229265	ENSG00000229265	USP8P1	HSCHR6_MHC_MANN:31286805-31289978	NOTEST	0	0	0	0	1	1
ENSG00000229266	ENSG00000229266	POM121L8P	22:21637169-21638450	NOTEST	0	0	0	0	1	1
ENSG00000229267	ENSG00000229267	AC072062.1	2:215674952-216003151	NOTEST	0.345594	0.116496	-1.5688	0	1	1
ENSG00000229268	ENSG00000229268	PES1P2	9:13986173-13987908	NOTEST	0	0	0	0	1	1
ENSG00000229269	ENSG00000229269	RP11-298A8.2	X:140013902-140079613	NOTEST	0	0	0	0	1	1
ENSG00000229271	ENSG00000229271	AC091493.2	3:16729492-16738986	NOTEST	0	0	0	0	1	1
ENSG00000229272	ENSG00000229272	RP11-498J9.2	10:120763047-120763396	NOTEST	0	0	0	0	1	1
ENSG00000229274	ENSG00000229274	XXbac-BPG13B8.10	6:29465285-29478333	NOTEST	0	0	0	0	1	1
ENSG00000229275	ENSG00000229275	LL22NC03-121E8.3	22:48537358-48539046	NOTEST	0	0	0	0	1	1
ENSG00000229276	ENSG00000229276	REV3L-IT1	6:111620233-111927481	NOTEST	0	0	0	0	1	1
ENSG00000229278	ENSG00000229278	RP11-483F11.7	10:101411745-101413662	NOTEST	0.332484	0.332019	-0.00201704	0	1	1
ENSG00000229280	ENSG00000229280	RP11-374C13.1	1:4235587-4235959	NOTEST	0	0	0	0	1	1
ENSG00000229281	ENSG00000229281	GPR53P	6:29505480-29506564	NOTEST	0	0	0	0	1	1
ENSG00000229282	ENSG00000229282	RP1-40E16.2	6:3056123-3056995	NOTEST	0	0	0	0	1	1
ENSG00000229283	ENSG00000229283	RP5-1125M8.2	1:111833483-111866697	NOTEST	0	0	0	0	1	1
ENSG00000229284	ENSG00000229284	DPCR1	HSCHR6_MHC_QBL:30898352-30912213	NOTEST	0	0	0	0	1	1
ENSG00000229286	ENSG00000229286	LA16c-4G1.4	22:16076051-16076172	NOTEST	0	0	0	0	1	1
ENSG00000229287	ENSG00000229287	FABP5P4	13:92050928-93519490	NOTEST	0	0	0	0	1	1
ENSG00000229288	ENSG00000229288	RP11-1E11.2	9:90802649-90805117	NOTEST	0	0	0	0	1	1
ENSG00000229289	ENSG00000229289	AP000431.2	21:20502840-20506741	NOTEST	0	0	0	0	1	1
ENSG00000229291	ENSG00000229291	RP4-580N22.2	1:236121178-236135125	NOTEST	0.438829	1.42235	1.69655	0	1	1
ENSG00000229292	ENSG00000229292	RFPL4AL1	19:56280506-56284545	NOTEST	0	0	0	0	1	1
ENSG00000229293	ENSG00000229293	HLA-T	HSCHR6_MHC_DBB:29855953-29857085	NOTEST	0	0	0	0	1	1
ENSG00000229294	ENSG00000229294	RP5-1044H5.1	1:65713901-65881689	NOTEST	0	0	0	0	1	1
ENSG00000229295	ENSG00000229295	HLA-DPB1	HSCHR6_MHC_MANN:33186488-33209127	NOTEST	0	0	0	0	1	1
ENSG00000229297	ENSG00000229297	RP11-540H22.2	9:109040672-109367076	NOTEST	0	0	0	0	1	1
ENSG00000229298	ENSG00000229298	TUBB8P1	9:21802541-22121096	NOTEST	0.361045	0.409041	0.180067	0	1	1
ENSG00000229299	ENSG00000229299	RP4-583P15.10	20:62375018-62462597	NOTEST	0	0.0672931	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229300	ENSG00000229300	C6orf48	HSCHR6_MHC_DBB:31784574-31789730	NOTEST	0	0	0	0	1	1
ENSG00000229301	ENSG00000229301	RP5-905H7.8	7:62814834-62819684	NOTEST	0	0	0	0	1	1
ENSG00000229302	ENSG00000229302	TAF9P2	Y:20438492-20439381	NOTEST	0	0	0	0	1	1
ENSG00000229303	ENSG00000229303	PPIAP25	13:46010255-46010795	NOTEST	0	0	0	0	1	1
ENSG00000229305	ENSG00000229305	RP11-431K24.2	1:8249883-8252830	NOTEST	0	0	0	0	1	1
ENSG00000229306	ENSG00000229306	AP001464.4	21:14371996-14389013	NOTEST	0	0	0	0	1	1
ENSG00000229307	ENSG00000229307	LINC00459	13:62897789-62902966	NOTEST	0	0	0	0	1	1
ENSG00000229308	ENSG00000229308	AC010084.1	Y:3904537-3968361	NOTEST	0	0	0	0	1	1
ENSG00000229309	ENSG00000229309	RP11-452B18.2	13:81824572-81876542	NOTEST	0	0	0	0	1	1
ENSG00000229310	ENSG00000229310	RPP40P1	X:25609469-25609925	NOTEST	0	0	0	0	1	1
ENSG00000229311	ENSG00000229311	RP11-475I24.8	9:44384584-44391705	NOTEST	0	0	0	0	1	1
ENSG00000229312	ENSG00000229312	RP11-470P21.2	9:72042445-72287222	NOTEST	0	0	0	0	1	1
ENSG00000229313	ENSG00000229313	RP3-425P12.5	6:24797548-25057301	NOTEST	0	0	0	0	1	1
ENSG00000229314	ENSG00000229314	ORM1	9:117085335-117088755	NOTEST	0	0	0	0	1	1
ENSG00000229315	ENSG00000229315	MCHR2-AS1	6:100367785-100524289	NOTEST	0	0	0	0	1	1
ENSG00000229316	ENSG00000229316	HMGB1P45	1:50864496-50865445	NOTEST	0	0	0	0	1	1
ENSG00000229321	ENSG00000229321	AC008269.2	2:207731518-207733013	NOTEST	0	0	0	0	1	1
ENSG00000229322	ENSG00000229322	RP5-937E21.1	X:148730842-148731793	NOTEST	0	0	0	0	1	1
ENSG00000229323	ENSG00000229323	RP11-175B12.2	13:50601268-51423190	NOTEST	0	0	0	0	1	1
ENSG00000229324	ENSG00000229324	RP5-1091N2.3	X:70236380-70236755	NOTEST	0	0	0	0	1	1
ENSG00000229325	ENSG00000229325	ACAP2-IT1	3:194995464-195163807	NOTEST	0.325247	0.172602	-0.914086	0	1	1
ENSG00000229326	ENSG00000229326	AC069154.4	2:120456198-120457733	NOTEST	0	0	0	0	1	1
ENSG00000229327	ENSG00000229327	RP11-135A24.2	10:32555216-32667726	NOTEST	0	0	0	0	1	1
ENSG00000229328	ENSG00000229328	OR2W1	HSCHR6_MHC_DBB:29012003-29013031	NOTEST	0	0	0	0	1	1
ENSG00000229330	ENSG00000229330	AC006947.1	17:64298753-64806861	NOTEST	0	0	0	0	1	1
ENSG00000229331	ENSG00000229331	GK-IT1	X:30671475-30748725	NOTEST	0	0	0	0	1	1
ENSG00000229332	ENSG00000229332	PGBD4P8	1:60563086-60563648	NOTEST	0	0	0	0	1	1
ENSG00000229334	ENSG00000229334	AC046143.3	3:194304739-194393206	NOTEST	0.552222	0.35509	-0.637062	0	1	1
ENSG00000229335	ENSG00000229335	RP1-241P17.1	X:114957296-114959383	NOTEST	0	0	0	0	1	1
ENSG00000229336	ENSG00000229336	AP000568.2	21:21112022-21112464	NOTEST	0	0	0	0	1	1
ENSG00000229337	ENSG00000229337	AC079305.8	2:177855235-178088686	NOTEST	0	0	0	0	1	1
ENSG00000229338	ENSG00000229338	RP11-92C4.4	9:101652871-101654219	NOTEST	0	0	0	0	1	1
ENSG00000229339	ENSG00000229339	RP11-193I22.2	3:42055293-42267381	NOTEST	0	0	0	0	1	1
ENSG00000229341	ENSG00000229341	TNXB	HSCHR6_MHC_APD:32052786-32065237	NOTEST	0	0	0	0	1	1
ENSG00000229342	ENSG00000229342	MYL8P	HSCHR6_MHC_DBB:33284681-33285199	NOTEST	0	0	0	0	1	1
ENSG00000229343	ENSG00000229343	CDY22P	Y:27959159-27960713	NOTEST	0	0	0	0	1	1
ENSG00000229345	ENSG00000229345	RP11-332M4.1	9:98361826-98368568	NOTEST	0	0	0	0	1	1
ENSG00000229346	ENSG00000229346	TRIM10	HSCHR6_MHC_SSTO:30109309-30118301	NOTEST	0	0	0	0	1	1
ENSG00000229347	ENSG00000229347	RP11-504E21.1	X:35077043-35078091	NOTEST	0	0	0	0	1	1
ENSG00000229348	ENSG00000229348	HYI-AS1	1:43855552-43922666	NOTEST	0	0.0281683	inf	0	1	1
ENSG00000229349	ENSG00000229349	ACTG1P9	6:46172465-46175123	NOTEST	0	0	0	0	1	1
ENSG00000229351	ENSG00000229351	KRTAP9-11P	17:39427562-39428087	NOTEST	0	0	0	0	1	1
ENSG00000229352	ENSG00000229352	AC007563.3	2:217536827-217858802	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229353	ENSG00000229353	TNXB	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000229356	ENSG00000229356	LRRC3-AS1	21:45870868-45875167	NOTEST	0.0242311	0	#NAME?	0	1	1
ENSG00000229357	ENSG00000229357	CYCSP51	1:150876371-150876689	NOTEST	0	0	0	0	1	1
ENSG00000229359	ENSG00000229359	PIN1P1	1:70034080-70671303	NOTEST	0	0	0	0	1	1
ENSG00000229360	ENSG00000229360	PPP1R2P5	2:107557335-107557938	NOTEST	0	0	0	0	1	1
ENSG00000229361	ENSG00000229361	UBTFL7	11:49103458-49104649	NOTEST	0	0	0	0	1	1
ENSG00000229363	ENSG00000229363	NELFE	HSCHR6_MHC_MCF:31996310-32013975	NOTEST	0	0	0	0	1	1
ENSG00000229364	ENSG00000229364	DDX39BP1	HSCHR6_MHC_SSTO:29864709-29865076	NOTEST	0	0	0	0	1	1
ENSG00000229365	ENSG00000229365	RP4-639J15.2	7:156880648-156881237	NOTEST	0	0	0	0	1	1
ENSG00000229367	ENSG00000229367	HMGN2P19	1:229706278-229706543	NOTEST	0	0	0	0	1	1
ENSG00000229368	ENSG00000229368	AC090587.4	11:3875547-4114439	NOTEST	0.399602	0.502137	0.329516	0	1	1
ENSG00000229369	ENSG00000229369	RP13-225O21.5	9:129986543-130155939	NOTEST	0	0	0	0	1	1
ENSG00000229370	ENSG00000229370	AC092635.1	2:13677797-13749293	NOTEST	0	0	0	0	1	1
ENSG00000229372	ENSG00000229372	SZT2-AS1	1:43855552-43922666	NOTEST	0	0.0237045	inf	0	1	1
ENSG00000229373	ENSG00000229373	LINC00452	13:114591278-114626485	NOTEST	0	0	0	0	1	1
ENSG00000229375	ENSG00000229375	USP24P1	13:19520894-19636858	NOTEST	0	0	0	0	1	1
ENSG00000229376	ENSG00000229376	CICP3	1:536815-660283	NOTEST	0.106813	0.0602005	-0.827235	0	1	1
ENSG00000229379	ENSG00000229379	AC006041.1	7:15880921-15881985	NOTEST	0	0	0	0	1	1
ENSG00000229380	ENSG00000229380	AC147651.5	7:588833-829190	NOTEST	0	0	0	0	1	1
ENSG00000229381	ENSG00000229381	TRIM10	HSCHR6_MHC_MCF:30198207-30207199	NOTEST	0	0	0	0	1	1
ENSG00000229382	ENSG00000229382	BX322557.13	21:46756621-46761905	NOTEST	0	0	0	0	1	1
ENSG00000229383	ENSG00000229383	LINC01015	HSCHR6_MHC_SSTO:29496875-29501024	NOTEST	0	0	0	0	1	1
ENSG00000229384	ENSG00000229384	HMGB1P16	X:36229212-36229752	NOTEST	0	0	0	0	1	1
ENSG00000229385	ENSG00000229385	AC010975.1	2:79384131-80875905	NOTEST	0.174252	0.116342	-0.582812	0	1	1
ENSG00000229386	ENSG00000229386	OR8B9P	11:124350894-124351819	NOTEST	0	0	0	0	1	1
ENSG00000229388	ENSG00000229388	RP11-442N24__B.1	1:28969739-28975093	NOTEST	0.0856667	0.102418	0.257667	0	1	1
ENSG00000229389	ENSG00000229389	CTD-2022H16.1	15:30345144-30365267	NOTEST	0	0	0	0	1	1
ENSG00000229390	ENSG00000229390	MICD	6:29938577-29940241	NOTEST	0	0	0	0	1	1
ENSG00000229391	ENSG00000229391	HLA-DRB6	6:32520489-32527799	NOTEST	0	0	0	0	1	1
ENSG00000229393	ENSG00000229393	RP3-395M20.3	1:2357418-2436969	NOTEST	0	0	0	0	1	1
ENSG00000229394	ENSG00000229394	ZNF70P1	HSCHR6_MHC_DBB:33161391-33162015	NOTEST	0	0	0	0	1	1
ENSG00000229395	ENSG00000229395	AC013401.1	2:193494644-193510432	NOTEST	0	0	0	0	1	1
ENSG00000229396	ENSG00000229396	DAXX	HSCHR6_MHC_SSTO:33436113-33436396	NOTEST	0	0	0	0	1	1
ENSG00000229398	ENSG00000229398	RP4-620E11.5	20:40011022-40011747	NOTEST	0	0	0	0	1	1
ENSG00000229399	ENSG00000229399	RP11-378J18.6	1:222791427-222841354	NOTEST	0.257569	0	#NAME?	0	1	1
ENSG00000229402	ENSG00000229402	AL162151.4	14:99624752-99626006	NOTEST	0	0.0269998	inf	0	1	1
ENSG00000229403	ENSG00000229403	RP4-718N17.2	7:51681946-51698566	NOTEST	0	0	0	0	1	1
ENSG00000229404	ENSG00000229404	LINC00858	10:86039735-86054415	NOTEST	0.0838508	0.167884	1.00157	0	1	1
ENSG00000229405	ENSG00000229405	AC092580.1	2:7876568-7877226	NOTEST	0	0	0	0	1	1
ENSG00000229406	ENSG00000229406	OFD1P4Y	Y:20615035-20634023	NOTEST	0	0	0	0	1	1
ENSG00000229407	ENSG00000229407	RP11-12M5.3	1:179712297-179787326	NOTEST	0	0.0460582	inf	0	1	1
ENSG00000229408	ENSG00000229408	OR2H1	HSCHR6_MHC_SSTO:29424633-29431781	NOTEST	0	0	0	0	1	1
ENSG00000229409	ENSG00000229409	RP11-494O16.3	22:50239576-50239738	NOTEST	0	0	0	0	1	1

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ENSG00000229411	ENSG00000229411	MCCD1P1	HSCHR6_MHC_QBL:29866822-29867682	NOTEST	0	0	0	0	1	1
ENSG00000229412	ENSG00000229412	OR10C1	HSCHR6_MHC_DBB:29341258-29424782	NOTEST	0	0	0	0	1	1
ENSG00000229414	ENSG00000229414	KCNQ1-AS1	11:2465913-2882798	NOTEST	0	0	0	0	1	1
ENSG00000229415	ENSG00000229415	SFTA3	14:36942411-36992221	NOTEST	0	0	0	0	1	1
ENSG00000229416	ENSG00000229416	USP9YP8	Y:23839131-23843004	NOTEST	0	0	0	0	1	1
ENSG00000229417	ENSG00000229417	NPM1P25	10:97889471-98031344	NOTEST	0	0	0	0	1	1
ENSG00000229418	ENSG00000229418	RP11-35J23.1	10:98052441-98098321	NOTEST	0	0	0	0	1	1
ENSG00000229420	ENSG00000229420	RP11-782C8.7	1:143245163-143245590	NOTEST	0.167097	0.0826742	-1.01518	0	1	1
ENSG00000229421	ENSG00000229421	AC133141.1	3:25215822-25639423	NOTEST	0	0	0	0	1	1
ENSG00000229423	ENSG00000229423	RPL27AP8	13:48340774-48341220	NOTEST	0	0	0	0	1	1
ENSG00000229424	ENSG00000229424	AC007349.4	7:36790291-36802686	NOTEST	0	0	0	0	1	1
ENSG00000229425	ENSG00000229425	AJ006998.2	21:16742840-16774624	NOTEST	0	0	0	0	1	1
ENSG00000229427	ENSG00000229427	ANKRD26P4	13:31774072-31906413	NOTEST	0.0729599	0.0823384	0.174461	0	1	1
ENSG00000229428	ENSG00000229428	HLA-U	HSCHR6_MHC_QBL:29891331-29891516	NOTEST	0	0	0	0	1	1
ENSG00000229430	ENSG00000229430	RPL3P2	HSCHR6_MHC_DBB:31240244-31241447	NOTEST	0	0	0	0	1	1
ENSG00000229431	ENSG00000229431	RP1-92O14.6	1:43849587-43855479	NOTEST	0.213561	0.142408	-0.584624	0	1	1
ENSG00000229432	ENSG00000229432	C6orf15	HSCHR6_MHC_COX:31071499-31072836	NOTEST	0	0	0	0	1	1
ENSG00000229433	ENSG00000229433	RP11-329B9.1	3:184474176-184490943	NOTEST	0	0	0	0	1	1
ENSG00000229434	ENSG00000229434	AC017048.1	2:177370972-177372430	NOTEST	0	0	0	0	1	1
ENSG00000229435	ENSG00000229435	PIP5K1P2	7:159024124-159026067	NOTEST	0	0	0	0	1	1
ENSG00000229436	ENSG00000229436	AC073850.6	7:79959507-80308593	NOTEST	0	0	0	0	1	1
ENSG00000229437	ENSG00000229437	LINC00366	13:39150776-39153131	NOTEST	0	0	0	0	1	1
ENSG00000229439	ENSG00000229439	RPS17P1	HSCHR6_MHC_QBL:29456936-29457342	NOTEST	0	0	0	0	1	1
ENSG00000229440	ENSG00000229440	RP5-1033K19.2	1:68847123-68847340	NOTEST	0	0	0	0	1	1
ENSG00000229441	ENSG00000229441	OR2H4P	HSCHR6_MHC_DBB:29183061-29184005	NOTEST	0	0	0	0	1	1
ENSG00000229442	ENSG00000229442	THEMIS3P	18:8486994-8513847	NOTEST	0	0	0	0	1	1
ENSG00000229443	ENSG00000229443	LINC00433	13:89193118-89197764	NOTEST	0	0	0	0	1	1
ENSG00000229444	ENSG00000229444	RP11-184I16.4	1:44115828-44396831	NOTEST	0	0	0	0	1	1
ENSG00000229447	ENSG00000229447	RP11-490K7.4	1:31732416-31769662	NOTEST	0.216484	0.211552	-0.0332477	0	1	1
ENSG00000229452	ENSG00000229452	AC005162.4	7:29019582-29603286	NOTEST	0	0	0	0	1	1
ENSG00000229453	ENSG00000229453	SPINK8	3:48348335-48369831	NOTEST	0	0	0	0	1	1
ENSG00000229454	ENSG00000229454	RP11-202I11.2	9:88368220-88408395	NOTEST	0	0	0	0	1	1
ENSG00000229455	ENSG00000229455	RPS10P18	10:126150402-126480439	NOTEST	0.045847	0	#NAME?	0	1	1
ENSG00000229456	ENSG00000229456	RLIMP1	13:41129803-41240734	NOTEST	0	0	0	0	1	1
ENSG00000229457	ENSG00000229457	AC006227.1	2:107871146-108172782	NOTEST	0	0	0	0	1	1
ENSG00000229458	ENSG00000229458	RP11-202D18.2	10:83635069-84746935	NOTEST	0	0	0	0	1	1
ENSG00000229459	ENSG00000229459	AC023669.1	7:46300661-46334067	NOTEST	0	0	0	0	1	1
ENSG00000229461	ENSG00000229461	MICG	HSCHR6_MHC_MANN:29777285-29777417	NOTEST	0	0	0	0	1	1
ENSG00000229462	ENSG00000229462	AC127383.1	2:68672841-68676306	NOTEST	0	0	0	0	1	1
ENSG00000229463	ENSG00000229463	LYST-AS1	1:235824340-236046940	NOTEST	0.279251	0.165795	-0.752163	0	1	1
ENSG00000229464	ENSG00000229464	RP11-481A12.6	10:51623416-51741813	NOTEST	0	0	0	0	1	1
ENSG00000229465	ENSG00000229465	ACTG1P11	Y:20309769-20310894	NOTEST	0	0	0	0	1	1
ENSG00000229466	ENSG00000229466	RP11-56I23.1	10:107568532-107578955	NOTEST	0	0	0	0	1	1
ENSG00000229467	ENSG00000229467	OR2I1P	HSCHR6_MHC_COX:29517601-29518549	NOTEST	0	0	0	0	1	1

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ENSG00000229468	ENSG00000229468	AC097635.5	3:20053943-20054098	NOTEST	0	0	0	0	1	1
ENSG00000229469	ENSG00000229469	OR2H5P	HSCHR6_MHC_APD:29523503-29601074	NOTEST	0	0	0	0	1	1
ENSG00000229470	ENSG00000229470	GNL1	HSCHR6_MHC_DBB:30499387-30521735	NOTEST	0	0	0	0	1	1
ENSG00000229471	ENSG00000229471	RP11-95K23.7	9:41214066-41217717	NOTEST	0	0	0	0	1	1
ENSG00000229473	ENSG00000229473	RGS17P1	13:41506055-41658137	NOTEST	0.038887	0.149151	1.93941	0	1	1
ENSG00000229474	ENSG00000229474	PATL2	15:44957929-45003514	NOTEST	0	0	0	0	1	1
ENSG00000229477	ENSG00000229477	FAM90A16P	8:7580612-7591823	NOTEST	0	0	0	0	1	1
ENSG00000229478	ENSG00000229478	ROBO2P1	7:51667981-51668269	NOTEST	0	0	0	0	1	1
ENSG00000229481	ENSG00000229481	CTD-2554C21.3	19:38307998-38345855	NOTEST	0	0	0	0	1	1
ENSG00000229483	ENSG00000229483	LINC00362	13:23743973-23744736	NOTEST	0	0	0	0	1	1
ENSG00000229484	ENSG00000229484	RP5-888M10.2	1:12587765-12588462	NOTEST	0	0	0	0	1	1
ENSG00000229485	ENSG00000229485	KSR1P1	10:42644757-42644997	NOTEST	0	0	0	0	1	1
ENSG00000229486	ENSG00000229486	RP4-552O12.1	1:84481547-84484054	NOTEST	0	0	0	0	1	1
ENSG00000229487	ENSG00000229487	ALG13-AS1	X:110909042-111003877	NOTEST	0	0	0	0	1	1
ENSG00000229488	ENSG00000229488	PRRT1	HSCHR6_MHC_MANN:32155582-32185300	NOTEST	0	0	0	0	1	1
ENSG00000229489	ENSG00000229489	ATP5A1P5	9:43399986-43401315	NOTEST	0	0	0	0	1	1
ENSG00000229491	ENSG00000229491	RP11-342D14.1	X:45007618-45193162	NOTEST	0	0	0	0	1	1
ENSG00000229492	ENSG00000229492	AC004019.10	22:17840836-18037850	NOTEST	0	0	0	0	1	1
ENSG00000229493	ENSG00000229493	HLA-DQB2	HSCHR6_MHC_MANN:32877672-32885131	NOTEST	0	0	0	0	1	1
ENSG00000229494	ENSG00000229494	AC012494.1	2:78315855-78354932	NOTEST	0	0	0	0	1	1
ENSG00000229495	ENSG00000229495	RP11-173D14.3	6:79519431-79523020	NOTEST	0	0	0	0	1	1
ENSG00000229496	ENSG00000229496	DDX39B	HSCHR6_MHC_MCF:31572847-31602942	NOTEST	0	0	0	0	1	1
ENSG00000229497	ENSG00000229497	AC005189.6	7:43798278-43846939	NOTEST	0	0	0	0	1	1
ENSG00000229498	ENSG00000229498	AC105053.3	2:86042252-86052514	NOTEST	0.0174883	0.0279679	0.677381	0	1	1
ENSG00000229499	ENSG00000229499	MICG	HSCHR6_MHC_SSTO:29777039-29777171	NOTEST	0	0	0	0	1	1
ENSG00000229500	ENSG00000229500	RPL17P1	20:20015011-20341346	NOTEST	0	0	0	0	1	1
ENSG00000229501	ENSG00000229501	HCG22	HSCHR6_MHC_DBB:31015765-31021436	NOTEST	0	0	0	0	1	1
ENSG00000229502	ENSG00000229502	RP11-52J3.2	6:158244295-158366109	NOTEST	0	0	0	0	1	1
ENSG00000229503	ENSG00000229503	AC092155.1	2:62759717-62760194	NOTEST	0.13923	0.214845	0.625822	0	1	1
ENSG00000229505	ENSG00000229505	RP4-682E18.1	1:86194915-86622626	NOTEST	0	0	0	0	1	1
ENSG00000229508	ENSG00000229508	PHKG1P4	7:57128296-57129008	NOTEST	0	0	0	0	1	1
ENSG00000229509	ENSG00000229509	RP11-421E17.4	1:206506677-206506789	NOTEST	0	0	0	0	1	1
ENSG00000229510	ENSG00000229510	AC018692.2	GL000193.1:49251-88375	NOTEST	0	0	0	0	1	1
ENSG00000229511	ENSG00000229511	RP11-392E22.1	9:38486855-38488335	NOTEST	0	0.00881814	inf	0	1	1
ENSG00000229513	ENSG00000229513	EIF4EBP1P2	22:24347903-24349416	NOTEST	0	0	0	0	1	1
ENSG00000229515	ENSG00000229515	FLT1P1	3:46183849-46185169	NOTEST	0	0	0	0	1	1
ENSG00000229518	ENSG00000229518	UBE2V1P3	Y:3734346-3734763	NOTEST	0	0	0	0	1	1
ENSG00000229519	ENSG00000229519	RP11-58A11.2	1:6581406-6614595	NOTEST	0.064488	0	#NAME?	0	1	1
ENSG00000229520	ENSG00000229520	LINC00404	13:112760408-112761196	NOTEST	0	0	0	0	1	1
ENSG00000229521	ENSG00000229521	MYCBP2-AS2	13:77618791-77901185	NOTEST	0	0	0	0	1	1
ENSG00000229522	ENSG00000229522	RP11-347D21.4	20:46609231-46617488	NOTEST	0	0	0	0	1	1
ENSG00000229523	ENSG00000229523	RP11-7G23.4	9:45729708-45730417	NOTEST	0.403433	0.912205	1.17703	0	1	1
ENSG00000229524	ENSG00000229524	BAG6	HSCHR6_MHC_COX:31594211-31613401	NOTEST	0	0	0	0	1	1

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ENSG00000229525	ENSG00000229525	AC053503.4	2:220238267-220268355	NOTEST	0.0585859	0.0544551	-0.105488	0	1	1
ENSG00000229526	ENSG00000229526	KRT16P4	17:18353557-18379234	NOTEST	0	0	0	0	1	1
ENSG00000229528	ENSG00000229528	RP5-1066H13.4	1:41329585-41342342	NOTEST	0	0	0	0	1	1
ENSG00000229529	ENSG00000229529	HLA-V	HSCHR6_MHC_SSTO:29755629-29762282	NOTEST	0	0	0	0	1	1
ENSG00000229530	ENSG00000229530	RP11-62C3.8	9:95059639-95432547	NOTEST	0.0200175	0	#NAME?	0	1	1
ENSG00000229531	ENSG00000229531	RP1-102G20.5	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000229532	ENSG00000229532	AC105443.2	7:131771024-131772751	NOTEST	0	0	0	0	1	1
ENSG00000229533	ENSG00000229533	AC003986.5	7:19183915-19185876	NOTEST	0	0	0	0	1	1
ENSG00000229534	ENSG00000229534	HNRNPA1P53	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000229535	ENSG00000229535	RPL15P4	HSCHR6_MHC_DBB:31478074-31478654	NOTEST	0	0	0	0	1	1
ENSG00000229536	ENSG00000229536	AC079776.1	2:130626765-130635126	NOTEST	0	0	0	0	1	1
ENSG00000229537	ENSG00000229537	RP11-5P4.1	1:63466167-63478142	NOTEST	0	0	0	0	1	1
ENSG00000229539	ENSG00000229539	RP11-119B16.2	20:3868885-3907605	NOTEST	0.268218	0.160394	-0.741787	0	1	1
ENSG00000229541	ENSG00000229541	GAPDHP26	9:103737949-103738964	NOTEST	0	0	0	0	1	1
ENSG00000229542	ENSG00000229542	SSU72P7	11:4359892-4360475	NOTEST	0	0	0	0	1	1
ENSG00000229544	ENSG00000229544	NKX1-2	10:126135591-126138753	NOTEST	0.0484311	0.0365007	-0.408011	0	1	1
ENSG00000229546	ENSG00000229546	LINC00428	13:43416549-43417023	NOTEST	0	0	0	0	1	1
ENSG00000229547	ENSG00000229547	UBE2DNL	X:84189156-84189896	NOTEST	0	0	0	0	1	1
ENSG00000229549	ENSG00000229549	TSPY8	Y:9195405-9235047	NOTEST	0	0	0	0	1	1
ENSG00000229550	ENSG00000229550	AC012445.1	2:4184233-4188321	NOTEST	0	0	0	0	1	1
ENSG00000229551	ENSG00000229551	GAPDHP17	Y:23023222-23024223	NOTEST	0	0	0	0	1	1
ENSG00000229552	ENSG00000229552	HLA-T	HSCHR6_MHC_QBL:29855620-29856752	NOTEST	0	0	0	0	1	1
ENSG00000229553	ENSG00000229553	USP9YP17	Y:24195901-24204260	NOTEST	0	0	0	0	1	1
ENSG00000229554	ENSG00000229554	RPL21P24	1:47963565-47964013	NOTEST	0	0	0	0	1	1
ENSG00000229556	ENSG00000229556	RP11-363G2.4	13:23425911-23428277	NOTEST	0	0	0	0	1	1
ENSG00000229557	ENSG00000229557	LINC00379	13:91779866-91783661	NOTEST	0	0	0	0	1	1
ENSG00000229558	ENSG00000229558	SACS-AS1	13:23902964-24007841	NOTEST	0.112943	0.168788	0.579612	0	1	1
ENSG00000229559	ENSG00000229559	RP1-153P14.3	6:37511328-37518636	NOTEST	0	0	0	0	1	1
ENSG00000229560	ENSG00000229560	AC105761.1	2:82495550-82497051	NOTEST	0	0	0	0	1	1
ENSG00000229562	ENSG00000229562	ZFYVE9P1	X:136742677-136744401	NOTEST	0	0	0	0	1	1
ENSG00000229563	ENSG00000229563	RP11-245M24.1	X:45364632-45489447	NOTEST	0	0	0	0	1	1
ENSG00000229565	ENSG00000229565	AC108056.1	4:118755555-118791103	NOTEST	0	0	0	0	1	1
ENSG00000229567	ENSG00000229567	RP4-717I23.2	1:93615298-93835055	NOTEST	0	0	0	0	1	1
ENSG00000229568	ENSG00000229568	AC010146.1	2:137302281-137303112	NOTEST	0	0	0	0	1	1
ENSG00000229569	ENSG00000229569	RP11-481G8.2	10:80703084-80827652	NOTEST	0	0	0	0	1	1
ENSG00000229570	ENSG00000229570	GAPDHP58	1:120038458-120039464	NOTEST	0.17476	0.30247	0.79142	0	1	1
ENSG00000229571	ENSG00000229571	PRAMEF26	1:13216355-13219581	NOTEST	0	0	0	0	1	1
ENSG00000229572	ENSG00000229572	EIF4BP4	3:42382079-42383859	NOTEST	0	0	0	0	1	1
ENSG00000229573	ENSG00000229573	HCG4P11	HSCHR6_MHC_MANN:29687659-29713937	NOTEST	0	0	0	0	1	1
ENSG00000229575	ENSG00000229575	RPL7P4	HSCHR6_MHC_MCF:30743069-30743799	NOTEST	0	0	0	0	1	1
ENSG00000229578	ENSG00000229578	LINC00358	13:62578225-62603681	NOTEST	0	0	0	0	1	1
ENSG00000229579	ENSG00000229579	USP17L26	4:9336383-9337976	NOTEST	0	0	0	0	1	1
ENSG00000229582	ENSG00000229582	RP11-423C15.3	9:128506032-128508831	NOTEST	0.0658395	0	#NAME?	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229583	ENSG00000229583	RP1-172N19.1	X:71996832-72068636	NOTEST	0	0	0	0	1	1
ENSG00000229585	ENSG00000229585	RPL21P44	4:54243809-55164414	NOTEST	0	0.0350992	inf	0	1	1
ENSG00000229586	ENSG00000229586	RP11-434D2.6	17:20384642-20387304	NOTEST	0	0.0143694	inf	0	1	1
ENSG00000229587	ENSG00000229587	RP11-197P3.5	9:77567883-77643339	NOTEST	0.114365	0.152706	0.417109	0	1	1
ENSG00000229588	ENSG00000229588	RP11-479J7.2	1:166304120-166304999	NOTEST	0	0	0	0	1	1
ENSG00000229589	ENSG00000229589	ACVR2B-AS1	3:38492517-38534633	NOTEST	0.150997	0.192039	0.346879	0	1	1
ENSG00000229590	ENSG00000229590	MSX2P1	17:56234388-56235161	NOTEST	0	0	0	0	1	1
ENSG00000229591	ENSG00000229591	RP5-981O7.2	7:151722758-151819425	NOTEST	0.315025	0.182851	-0.784797	0	1	1
ENSG00000229593	ENSG00000229593	SUCLA2P3	2:25264998-25378243	NOTEST	0.0125226	0	#NAME?	0	1	1
ENSG00000229594	ENSG00000229594	RP11-167P23.4	X:55659463-55662089	NOTEST	0	0	0	0	1	1
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ENSG00000229596	ENSG00000229596	MYL8P	6:33306754-33307272	NOTEST	0	0	0	0	1	1
ENSG00000229597	ENSG00000229597	BTNL2	HSCHR6_MHC_QBL:32315748-32332375	NOTEST	0	0	0	0	1	1
ENSG00000229598	ENSG00000229598	PRDX3P1	22:39101727-39190203	NOTEST	0.213459	0.170722	-0.32231	0	1	1
ENSG00000229599	ENSG00000229599	LINC00411	13:101360578-102068843	NOTEST	0	0	0	0	1	1
ENSG00000229600	ENSG00000229600	RP11-524K14.1	6:94596617-94599128	NOTEST	0	0	0	0	1	1
ENSG00000229601	ENSG00000229601	AL590762.10	X:70586113-70752224	NOTEST	0.342051	0.124319	-1.46016	0	1	1
ENSG00000229603	ENSG00000229603	AC004014.3	7:108549509-108592723	NOTEST	0	0	0	0	1	1
ENSG00000229604	ENSG00000229604	MTATP8P2	2:88047605-88285309	NOTEST	0	0	0	0	1	1
ENSG00000229605	ENSG00000229605	RP11-492M23.2	10:29187924-29188422	NOTEST	0.273677	0.352583	0.365487	0	1	1
ENSG00000229606	ENSG00000229606	RP5-827L5.1	20:59654195-59655235	NOTEST	0	0	0	0	1	1
ENSG00000229607	ENSG00000229607	RP5-1125N11.1	1:31283224-31288400	NOTEST	0	0.0387345	inf	0	1	1
ENSG00000229608	ENSG00000229608	GOLGA2P4	22:43180467-43183106	NOTEST	0	0	0	0	1	1
ENSG00000229609	ENSG00000229609	LINC01079	13:27947484-27948503	NOTEST	0	0	0	0	1	1
ENSG00000229611	ENSG00000229611	RP11-390F4.10	9:6704470-6707780	NOTEST	0.0591278	0	#NAME?	0	1	1
ENSG00000229612	ENSG00000229612	SUMO1P2	1:168867373-168867677	NOTEST	0	0	0	0	1	1
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ENSG00000229615	ENSG00000229615	AC111200.1	2:87042461-87092827	NOTEST	0	0	0	0	1	1
ENSG00000229616	ENSG00000229616	RP11-369J21.11	10:81777468-81777667	NOTEST	0	0	0	0	1	1
ENSG00000229618	ENSG00000229618	AC011288.2	7:13141015-13743774	NOTEST	0	0	0	0	1	1
ENSG00000229619	ENSG00000229619	MBNL1-AS1	3:151961616-152214602	NOTEST	0.154038	0.115873	-0.410737	0	1	1
ENSG00000229620	ENSG00000229620	AF196972.2	X:48271747-48274761	NOTEST	0	0	0	0	1	1
ENSG00000229621	ENSG00000229621	AC018742.1	2:21444046-22753977	NOTEST	0.021662	0.0299811	0.468884	0	1	1
ENSG00000229622	ENSG00000229622	MTND5P2	13:96329392-96447243	NOTEST	0	0	0	0	1	1
ENSG00000229623	ENSG00000229623	METTL21AP1	21:40556101-40695144	NOTEST	0	0	0	0	1	1
ENSG00000229625	ENSG00000229625	RP11-44N12.2	8:99973655-99980512	NOTEST	0	0	0	0	1	1
ENSG00000229626	ENSG00000229626	PIGCP2	7:107449178-107450013	NOTEST	0	0	0	0	1	1
ENSG00000229627	ENSG00000229627	RP11-368M16.4	7:57688184-57704895	NOTEST	0	0	0	0	1	1
ENSG00000229628	ENSG00000229628	AC073115.7	7:46030503-46040497	NOTEST	0	0.0291944	inf	0	1	1
ENSG00000229629	ENSG00000229629	RP11-302K17.4	10:103849724-103849819	NOTEST	0	0	0	0	1	1
ENSG00000229630	ENSG00000229630	RP11-124O11.2	10:43474464-43476955	NOTEST	0	0	0	0	1	1
ENSG00000229631	ENSG00000229631	AL603926.1	GL000223.1:149786-180454	NOTEST	0	0	0	0	1	1

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ENSG00000229636	ENSG00000229636	KRT8P21	1:73570474-73571965	NOTEST	0	0	0	0	1	1
ENSG00000229639	ENSG00000229639	RP3-380B4.1	1:69898937-69901092	NOTEST	0	0	0	0	1	1
ENSG00000229641	ENSG00000229641	CYP2C56P	2:164606082-165208733	NOTEST	0	0	0	0	1	1
ENSG00000229642	ENSG00000229642	AC027119.1	3:6004528-6165807	NOTEST	0	0	0	0	1	1
ENSG00000229643	ENSG00000229643	LINC00280	Y:6225259-6229454	NOTEST	0	0	0	0	1	1
ENSG00000229646	ENSG00000229646	RP11-330A16.1	6:14597744-14599921	NOTEST	0	0	0	0	1	1
ENSG00000229647	ENSG00000229647	AC007879.7	2:208104373-208490652	NOTEST	0	0	0	0	1	1
ENSG00000229648	ENSG00000229648	AC016753.7	2:85718052-85718903	NOTEST	0	0.0169899	inf	0	1	1
ENSG00000229649	ENSG00000229649	RP11-107I14.4	10:102986732-103029905	NOTEST	0	0	0	0	1	1
ENSG00000229651	ENSG00000229651	MICC	HSCHR6_MHC_DBB:30372752-30377357	NOTEST	0	0	0	0	1	1
ENSG00000229652	ENSG00000229652	RP11-435P24.2	1:203322492-203322779	NOTEST	0	0	0	0	1	1
ENSG00000229653	ENSG00000229653	NCRNA00171	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1
ENSG00000229654	ENSG00000229654	RP1-60O19.2	6:107143409-107147869	NOTEST	0	0	0	0	1	1
ENSG00000229656	ENSG00000229656	RP11-462L8.1	10:33189246-33371030	NOTEST	0	0	0	0	1	1
ENSG00000229657	ENSG00000229657	RP11-494K3.2	1:204797778-204991950	NOTEST	0	0	0	0	1	1
ENSG00000229658	ENSG00000229658	PABPC1P9	22:16904667-16906756	NOTEST	0	0	0	0	1	1
ENSG00000229659	ENSG00000229659	RP11-345K20.2	10:75182016-75182454	NOTEST	0.160059	0.296749	0.890641	0	1	1
ENSG00000229660	ENSG00000229660	RP5-1142J19.1	7:157074229-157075380	NOTEST	0	0	0	0	1	1
ENSG00000229661	ENSG00000229661	RP11-145B3.2	X:74421325-74421625	NOTEST	0	0	0	0	1	1
ENSG00000229662	ENSG00000229662	RP11-552E4.5	X:48104328-48105180	NOTEST	0	0	0	0	1	1
ENSG00000229663	ENSG00000229663	AL672296.1	1:249065833-249067991	NOTEST	0	0	0	0	1	1
ENSG00000229664	ENSG00000229664	RP11-536K7.5	10:6052651-6104288	NOTEST	0	0	0	0	1	1
ENSG00000229665	ENSG00000229665	PRR20C	13:57728194-57731216	NOTEST	0	0	0	0	1	1
ENSG00000229666	ENSG00000229666	MAST4-AS1	5:65892175-66465423	NOTEST	0.024511	0.150787	2.62101	0	1	1
ENSG00000229667	ENSG00000229667	UBE2V1P9	X:89544534-89544902	NOTEST	0	0	0	0	1	1
ENSG00000229668	ENSG00000229668	RP11-317F20.2	10:116190871-116444762	NOTEST	0	0	0	0	1	1
ENSG00000229670	ENSG00000229670	PKP4P1	2:210043527-210046742	NOTEST	0	0.0164102	inf	0	1	1
ENSG00000229671	ENSG00000229671	LINC01150	11:1923876-1929145	NOTEST	0	0	0	0	1	1
ENSG00000229672	ENSG00000229672	RP11-184A2.3	10:3793258-3805418	NOTEST	0	0	0	0	1	1
ENSG00000229673	ENSG00000229673	LL22NC01116C6.1	22:32908538-33454358	NOTEST	0	0	0	0	1	1
ENSG00000229674	ENSG00000229674	AL121578.7	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000229676	ENSG00000229676	ZNF492	19:22817125-22899793	NOTEST	0.027741	0.0486221	0.809593	0	1	1
ENSG00000229677	ENSG00000229677	RP11-383F6.1	7:138728265-138794465	NOTEST	0	0.0867071	inf	0	1	1
ENSG00000229679	ENSG00000229679	AC007327.5	7:36192757-36341152	NOTEST	0	0	0	0	1	1
ENSG00000229680	ENSG00000229680	OR2H2	HSCHR6_MHC_DBB:29523342-29600923	NOTEST	0	0	0	0	1	1
ENSG00000229681	ENSG00000229681	MDC1-AS1	HSCHR6_MHC_DBB:30657846-30675928	NOTEST	0	0	0	0	1	1
ENSG00000229682	ENSG00000229682	AC114755.5	2:106984664-106985332	NOTEST	0	0	0	0	1	1
ENSG00000229683	ENSG00000229683	ASNSP5	1:142799586-142799739	NOTEST	0	0	0	0	1	1
ENSG00000229684	ENSG00000229684	TUBB	HSCHR6_MHC_MCF:30766463-30771689	NOTEST	0	0	0	0	1	1
ENSG00000229685	ENSG00000229685	HLA-DPA1	HSCHR6_MHC_DBB:33010287-33032912	NOTEST	0	0	0	0	1	1
ENSG00000229686	ENSG00000229686	SNORD56	20:2632790-2639039	NOTEST	0	0	0	0	1	1

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ENSG00000229688	ENSG00000229688	ISPD-AS1	7:16130816-16460947	NOTEST	0.0691908	0.0674659	-0.0364204	0	1	1
ENSG00000229689	ENSG00000229689	AC009237.8	2:96190856-96198153	NOTEST	0.468358	0.607353	0.374926	0	1	1
ENSG00000229690	ENSG00000229690	MTCO2P1	20:58662894-59102516	NOTEST	0	0	0	0	1	1
ENSG00000229693	ENSG00000229693	RP11-25C15.1	X:95875652-95876902	NOTEST	0	0	0	0	1	1
ENSG00000229694	ENSG00000229694	RP11-305L7.6	9:93881343-93945044	NOTEST	0.0983409	0.0539997	-0.864841	0	1	1
ENSG00000229695	ENSG00000229695	AC011242.5	2:43864411-43995126	NOTEST	0	0	0	0	1	1
ENSG00000229696	ENSG00000229696	KARSP1	13:42140972-42535256	NOTEST	0	0	0	0	1	1
ENSG00000229697	ENSG00000229697	RP11-374M1.3	9:45034956-45047145	NOTEST	0	0	0	0	1	1
ENSG00000229698	ENSG00000229698	HLA-F	HSCHR6_MHC_SSTO:29687513-29713718	NOTEST	0	0	0	0	1	1
ENSG00000229699	ENSG00000229699	RP1-140J1.1	1:153146993-153164152	NOTEST	0	0	0	0	1	1
ENSG00000229700	ENSG00000229700	RP1-130G2.1	6:20042685-20043171	NOTEST	0	0	0	0	1	1
ENSG00000229701	ENSG00000229701	MTND2P20	2:156120674-156121335	NOTEST	0	0	0	0	1	1
ENSG00000229702	ENSG00000229702	RP1-274L7.1	X:129611042-129658231	NOTEST	0.0100688	0	#NAME?	0	1	1
ENSG00000229703	ENSG00000229703	XX-CR54.1	1:248855491-248862411	NOTEST	0	0	0	0	1	1
ENSG00000229704	ENSG00000229704	EIF2S2P2	3:184880658-184999778	NOTEST	0	0	0	0	1	1
ENSG00000229706	ENSG00000229706	PPIAP9	HSCHR6_MHC_MCF:31563619-31564431	NOTEST	0	0	0	0	1	1
ENSG00000229707	ENSG00000229707	RP11-100J16.4	9:41630396-41630883	NOTEST	0	0	0	0	1	1
ENSG00000229708	ENSG00000229708	MARK2P12	13:73981904-73982489	NOTEST	0	0	0	0	1	1
ENSG00000229709	ENSG00000229709	USP9YP36	Y:27725936-27734591	NOTEST	0	0	0	0	1	1
ENSG00000229710	ENSG00000229710	MTCO3P1	HSCHR6_MHC_QBL:32602597-32603429	NOTEST	0	0	0	0	1	1
ENSG00000229711	ENSG00000229711	RP11-449O16.2	10:52499077-52645435	NOTEST	0	0	0	0	1	1
ENSG00000229713	ENSG00000229713	RP1-43O17.1	1:152709993-152710344	NOTEST	0	0	0	0	1	1
ENSG00000229714	ENSG00000229714	ZNF90P2	HSCHR6_MHC_QBL:28856612-28857687	NOTEST	0	0	0	0	1	1
ENSG00000229715	ENSG00000229715	EEF1DP3	13:32420977-32527609	NOTEST	0.146056	0.138482	-0.0768256	0	1	1
ENSG00000229716	ENSG00000229716	RP11-185B14.1	1:8891065-8891434	NOTEST	0	0	0	0	1	1
ENSG00000229717	ENSG00000229717	RP11-556N4.1	4:76751903-76753858	NOTEST	0	0	0	0	1	1
ENSG00000229719	ENSG00000229719	MIR194-2	11:64658826-64660921	NOTEST	0	0	0	0	1	1
ENSG00000229720	ENSG00000229720	RP3-495K2.2	6:169434291-169435737	NOTEST	0	0	0	0	1	1
ENSG00000229721	ENSG00000229721	RP11-252I14.1	5:179653377-179654000	NOTEST	0	0	0	0	1	1
ENSG00000229722	ENSG00000229722	RP11-557H15.5	6:134846451-134980974	NOTEST	0	0	0	0	1	1
ENSG00000229723	ENSG00000229723	LINC01054	13:115095033-115099423	NOTEST	0	0	0	0	1	1
ENSG00000229724	ENSG00000229724	OR2AQ1P	1:158765803-158766003	NOTEST	0	0	0	0	1	1
ENSG00000229725	ENSG00000229725	AC007322.1	Y:24017477-24019697	NOTEST	0	0	0	0	1	1
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ENSG00000229730	ENSG00000229730	AC013268.4	2:110769841-110770178	NOTEST	0	0	0	0	1	1
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ENSG00000229732	ENSG00000229732	AC019349.5	17:39657232-39661957	NOTEST	0	0	0	0	1	1
ENSG00000229733	ENSG00000229733	RP5-1189B24.1	X:122692200-122692435	NOTEST	0	0	0	0	1	1
ENSG00000229735	ENSG00000229735	FTLP16	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000229737	ENSG00000229737	TMEM183AP1	HSCHR6_MHC_QBL:29523309-29600897	NOTEST	0	0	0	0	1	1
ENSG00000229738	ENSG00000229738	AC010240.3	5:132323343-132323802	NOTEST	0	0	0	0	1	1
ENSG00000229739	ENSG00000229739	RP11-295K2.3	1:186412697-186430254	NOTEST	0	0	0	0	1	1

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ENSG00000229742	ENSG00000229742	RP11-365O16.5	1:224407314-224518089	NOTEST	0.0490142	0	#NAME?	0	1	1
ENSG00000229743	ENSG00000229743	LINC01159	2:105469742-105542510	NOTEST	0.0294132	0.00355588	-3.04819	0	1	1
ENSG00000229744	ENSG00000229744	AC011998.2	2:178487979-178973066	NOTEST	0	0	0	0	1	1
ENSG00000229745	ENSG00000229745	BPY2DP	Y:7801037-7805681	NOTEST	0	0	0	0	1	1
ENSG00000229746	ENSG00000229746	FAM74A4	9:65487272-65494248	NOTEST	0	0	0	0	1	1
ENSG00000229747	ENSG00000229747	RP11-567B20.2	1:199878048-199878776	NOTEST	0	0	0	0	1	1
ENSG00000229749	ENSG00000229749	COTL1P1	17:16757248-16757623	NOTEST	0	0	0	0	1	1
ENSG00000229750	ENSG00000229750	AC096649.2	2:175936977-176033250	NOTEST	0.0849462	0.0337486	-1.33172	0	1	1
ENSG00000229751	ENSG00000229751	RP11-142M10.2	10:13628926-14504141	NOTEST	0.0689765	0.116358	0.754397	0	1	1
ENSG00000229752	ENSG00000229752	RPL7P10	1:81563951-81564690	NOTEST	0	0	0	0	1	1
ENSG00000229753	ENSG00000229753	RP11-28P17.3	9:75136716-75451267	NOTEST	0	0	0	0	1	1
ENSG00000229754	ENSG00000229754	CXCR2P1	2:218899682-218955304	NOTEST	0	0	0	0	1	1
ENSG00000229755	ENSG00000229755	RP5-827L5.2	20:59652279-59652872	NOTEST	0	0	0	0	1	1
ENSG00000229756	ENSG00000229756	RPL31P20	3:24158650-24541833	NOTEST	0	0	0	0	1	1
ENSG00000229757	ENSG00000229757	RP4-738P11.4	1:168545710-168551315	NOTEST	0	0	0	0	1	1
ENSG00000229758	ENSG00000229758	DYNLT3P2	2:128957474-128957769	NOTEST	0.11758	0	#NAME?	0	1	1
ENSG00000229759	ENSG00000229759	MRPS18AP1	3:48282589-48343175	NOTEST	0.160491	0.291887	0.862915	0	1	1
ENSG00000229760	ENSG00000229760	RP11-266I3.5	X:55204639-55205170	NOTEST	0	0	0	0	1	1
ENSG00000229761	ENSG00000229761	RPS20P1	21:36160097-37376965	NOTEST	0	0	0	0	1	1
ENSG00000229762	ENSG00000229762	RP11-419M24.1	7:55861236-55930482	NOTEST	0	0	0	0	1	1
ENSG00000229765	ENSG00000229765	RP11-339A7.1	6:10214113-10214595	NOTEST	0	0	0	0	1	1
ENSG00000229766	ENSG00000229766	RP5-971N18.3	20:7957994-8024159	NOTEST	0.0169136	0	#NAME?	0	1	1
ENSG00000229767	ENSG00000229767	DDR1	HSCHR6_MHC_APD:30861247-30865452	NOTEST	0	0	0	0	1	1
ENSG00000229769	ENSG00000229769	TRBV10-2	7:142206510-142207011	NOTEST	0	0	0	0	1	1
ENSG00000229770	ENSG00000229770	CTA-796E4.4	22:26557799-26560269	NOTEST	0	0	0	0	1	1
ENSG00000229771	ENSG00000229771	RP4-644L1.2	20:39326534-39327256	NOTEST	0	0	0	0	1	1
ENSG00000229773	ENSG00000229773	XXbac-BPG308K3.6	HSCHR6_MHC_SSTO:28827312-28831035	NOTEST	0	0	0	0	1	1
ENSG00000229774	ENSG00000229774	AC018866.1	2:121444210-121468093	NOTEST	0	0	0	0	1	1
ENSG00000229775	ENSG00000229775	RP11-298H24.1	10:107900021-107948480	NOTEST	0	0	0	0	1	1
ENSG00000229776	ENSG00000229776	C4B-AS1	6:31982538-32004035	NOTEST	0	0	0	0	1	1
ENSG00000229779	ENSG00000229779	AC016751.2	2:176769098-176770230	NOTEST	0	0	0	0	1	1
ENSG00000229780	ENSG00000229780	UBE2Q1-AS1	1:154521052-154531504	NOTEST	0	0.0443653	inf	0	1	1
ENSG00000229781	ENSG00000229781	AC013444.1	2:143611663-143613567	NOTEST	0	0	0	0	1	1
ENSG00000229782	ENSG00000229782	AC118754.4	17:4400688-4458926	NOTEST	0	0	0	0	1	1
ENSG00000229785	ENSG00000229785	SLC25A38P1	1:172717699-172718642	NOTEST	0	0.0848024	inf	0	1	1
ENSG00000229786	ENSG00000229786	SNRPFP2	1:26210671-26233482	NOTEST	0	0	0	0	1	1
ENSG00000229788	ENSG00000229788	LINC00388	13:19184437-19185815	NOTEST	0.055625	0	#NAME?	0	1	1
ENSG00000229789	ENSG00000229789	RP11-391M20.1	9:68726628-68809906	NOTEST	0.0584331	0.13284	1.18483	0	1	1
ENSG00000229791	ENSG00000229791	RP11-385E5.5	13:19982181-19983669	NOTEST	0	0	0	0	1	1
ENSG00000229792	ENSG00000229792	LINC00399	13:110053042-110053988	NOTEST	0	0	0	0	1	1

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ENSG00000229794	ENSG00000229794	RP11-522L3.11	X:102024088-102161086	NOTEST	0	0	0	0	1	1
ENSG00000229795	ENSG00000229795	RPS21P1	1:235530674-235612283	NOTEST	0.550298	0	#NAME?	0	1	1
ENSG00000229796	ENSG00000229796	RP5-1077H22.1	6:958562-962511	NOTEST	0	0	0	0	1	1
ENSG00000229797	ENSG00000229797	AC140481.8	2:131501110-131525707	NOTEST	0	0	0	0	1	1
ENSG00000229798	ENSG00000229798	KRT18P26	2:74425688-74621009	NOTEST	0	0	0	0	1	1
ENSG00000229800	ENSG00000229800	ATP8A2P2	13:32974860-33112970	NOTEST	0.0618174	0.0405862	-0.607023	0	1	1
ENSG00000229801	ENSG00000229801	RP11-353N4.1	1:149575344-149637707	NOTEST	0	0	0	0	1	1
ENSG00000229802	ENSG00000229802	SLC39A7	HSCHR6_MHC_DBB:33139274-33150126	NOTEST	0	0	0	0	1	1
ENSG00000229805	ENSG00000229805	AC011306.1	2:56179292-56613308	NOTEST	0	0	0	0	1	1
ENSG00000229806	ENSG00000229806	RPS15P5	3:54156573-55108584	NOTEST	0	0	0	0	1	1
ENSG00000229807	ENSG00000229807	XIST	X:73012039-73072588	NOTEST	0	0.00429054	inf	0	1	1
ENSG00000229808	ENSG00000229808	RP11-456P18.2	1:161736083-161933860	NOTEST	0.146085	0.189662	0.37662	0	1	1
ENSG00000229814	ENSG00000229814	RPL35AP21	9:74204516-74204849	NOTEST	0	0	0	0	1	1
ENSG00000229815	ENSG00000229815	CCNB1IP1P1	1:45316449-45452282	NOTEST	0	0	0	0	1	1
ENSG00000229816	ENSG00000229816	DDX50P1	2:32390932-32449448	NOTEST	0.0923161	0.0554508	-0.735375	0	1	1
ENSG00000229817	ENSG00000229817	RP11-78H18.2	9:117607873-117610865	NOTEST	0	0	0	0	1	1
ENSG00000229818	ENSG00000229818	RP11-459A10.3	X:6299195-6299350	NOTEST	0	0	0	0	1	1
ENSG00000229820	ENSG00000229820	RP1-308E4.1	1:28696113-28826881	NOTEST	0	0	0	0	1	1
ENSG00000229821	ENSG00000229821	RP11-567E21.3	1:201159952-201198080	NOTEST	0.0454183	0	#NAME?	0	1	1
ENSG00000229822	ENSG00000229822	RP5-1174J21.2	X:41374186-41782716	NOTEST	0	0	0	0	1	1
ENSG00000229823	ENSG00000229823	XXbac-BPG299F13.14	HSCHR6_MHC_MANN:31212936-31213410	NOTEST	0	0	0	0	1	1
ENSG00000229824	ENSG00000229824	RPL12P34	13:69228703-69229182	NOTEST	0	0	0	0	1	1
ENSG00000229825	ENSG00000229825	RP5-1052M9.4	X:123093082-124097666	NOTEST	0	0	0	0	1	1
ENSG00000229826	ENSG00000229826	RP11-552J9.14	X:52764989-52765196	NOTEST	0	0	0	0	1	1
ENSG00000229827	ENSG00000229827	AC093899.3	2:170433880-170434256	NOTEST	0	0	0	0	1	1
ENSG00000229828	ENSG00000229828	RP11-94I2.1	1:146011090-146025308	NOTEST	0.0633834	0.0713083	0.169965	0	1	1
ENSG00000229829	ENSG00000229829	DUTP4	X:148898831-148899306	NOTEST	0	0	0	0	1	1
ENSG00000229830	ENSG00000229830	RP11-341A22.1	9:105827697-105827880	NOTEST	0	0	0	0	1	1
ENSG00000229831	ENSG00000229831	AC108039.3	2:62047342-62047701	NOTEST	0	0	0	0	1	1
ENSG00000229832	ENSG00000229832	RP11-384C4.2	1:212458878-212535200	NOTEST	0.0914036	0.17178	0.910241	0	1	1
ENSG00000229834	ENSG00000229834	RP11-48L13.1	9:29636483-29636851	NOTEST	0	0	0	0	1	1
ENSG00000229835	ENSG00000229835	KHSRPP1	9:21695174-21696942	NOTEST	0.0278986	0.028957	0.0537207	0	1	1
ENSG00000229836	ENSG00000229836	XXbac-BPG248L24.10	6:31275591-31276326	NOTEST	0	0	0	0	1	1
ENSG00000229839	ENSG00000229839	AC018462.2	2:62095223-62374382	NOTEST	0.0355383	0	#NAME?	0	1	1
ENSG00000229840	ENSG00000229840	ISCA1P2	1:229177917-229178338	NOTEST	0	0	0	0	1	1
ENSG00000229841	ENSG00000229841	RP11-361K17.2	1:217600333-217804424	NOTEST	0.0813133	0.229068	1.49421	0	1	1
ENSG00000229842	ENSG00000229842	RP5-837O21.4	1:94390961-94391744	NOTEST	0	0	0	0	1	1
ENSG00000229846	ENSG00000229846	RP11-141A19.1	1:48998526-50489585	NOTEST	0	0	0	0	1	1
ENSG00000229847	ENSG00000229847	EMX2OS	10:119184704-119309056	NOTEST	0	0	0	0	1	1
ENSG00000229848	ENSG00000229848	RP13-766D20.2	17:79476996-79494802	NOTEST	0	0.0878447	inf	0	1	1

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ENSG00000229849	ENSG00000229849	RP11-393K10.1	1:158848535-158853290	NOTEST	0	0	0	0	1	1
ENSG00000229851	ENSG00000229851	ARSD-AS1	X:2822010-2847392	NOTEST	0	0	0	0	1	1
ENSG00000229853	ENSG00000229853	RP5-1049G16.4	20:46130600-46415360	NOTEST	0.0394526	0.0167717	-1.23409	0	1	1
ENSG00000229854	ENSG00000229854	RP11-524G24.2	9:124329335-124547809	NOTEST	0	0	0	0	1	1
ENSG00000229855	ENSG00000229855	CTC-546K23.1	5:120535398-120693093	NOTEST	0	0	0	0	1	1
ENSG00000229856	ENSG00000229856	CYP21A1P	HSCHR6_MHC_MCF:32052156-32052675	NOTEST	0	0	0	0	1	1
ENSG00000229857	ENSG00000229857	RP11-159H20.3	9:79607014-79608024	NOTEST	0	0	0	0	1	1
ENSG00000229858	ENSG00000229858	AC016831.5	7:130507626-130508270	NOTEST	0	0	0	0	1	1
ENSG00000229859	ENSG00000229859	PGA3	11:60970778-60980570	NOTEST	0	0	0	0	1	1
ENSG00000229861	ENSG00000229861	MRPS18B	HSCHR6_MHC_MCF:30646634-30672631	NOTEST	0	0	0	0	1	1
ENSG00000229862	ENSG00000229862	RP11-505P4.7	6:74225472-74280319	NOTEST	0	0.149764	inf	0	1	1
ENSG00000229863	ENSG00000229863	RP11-157F20.1	3:57124009-57204334	NOTEST	0	0	0	0	1	1
ENSG00000229865	ENSG00000229865	RPL31P54	13:78469615-79233314	NOTEST	0	0	0	0	1	1
ENSG00000229866	ENSG00000229866	OR2J3	HSCHR6_MHC_DBB:29079680-29080616	NOTEST	0	0	0	0	1	1
ENSG00000229867	ENSG00000229867	STEAP3-AS1	2:119981383-120023228	NOTEST	0.0213614	0.00788671	-1.43751	0	1	1
ENSG00000229869	ENSG00000229869	RP11-363N22.2	10:978965-988683	NOTEST	0	0	0	0	1	1
ENSG00000229870	ENSG00000229870	RP11-507K13.6	10:51023141-51023608	NOTEST	0.100341	0	#NAME?	0	1	1
ENSG00000229871	ENSG00000229871	RP4-710M16.1	1:56673238-56674128	NOTEST	0	0	0	0	1	1
ENSG00000229873	ENSG00000229873	OGFR-AS1	20:61431978-61445352	NOTEST	0.0550523	0.112618	1.03256	0	1	1
ENSG00000229875	ENSG00000229875	RP11-130C19.1	9:213107-746105	NOTEST	0	0	0	0	1	1
ENSG00000229876	ENSG00000229876	CASC20	20:6427369-6509106	NOTEST	0	0	0	0	1	1
ENSG00000229877	ENSG00000229877	PAICSP5	7:143242278-143243828	NOTEST	0	0	0	0	1	1
ENSG00000229878	ENSG00000229878	RP11-479G22.7	10:33189246-33371030	NOTEST	0	0	0	0	1	1
ENSG00000229880	ENSG00000229880	IMMTP1	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000229881	ENSG00000229881	RP11-321E8.4	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000229882	ENSG00000229882	RP13-30A9.2	20:61265032-61267214	NOTEST	0	0	0	0	1	1
ENSG00000229885	ENSG00000229885	RP13-77O11.12	X:52830423-52830553	NOTEST	0	0	0	0	1	1
ENSG00000229886	ENSG00000229886	RP5-1132H15.3	7:65490112-65496531	NOTEST	0	0	0	0	1	1
ENSG00000229887	ENSG00000229887	HNRNPA1P6	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000229889	ENSG00000229889	MAS1LP1	HSCHR6_MHC_DBB:29442735-29443782	NOTEST	0	0	0	0	1	1
ENSG00000229890	ENSG00000229890	AC023672.1	2:108715565-108715948	NOTEST	0	0	0	0	1	1
ENSG00000229892	ENSG00000229892	RP4-730D4.1	20:40701391-41818610	NOTEST	0	0	0	0	1	1
ENSG00000229893	ENSG00000229893	AC004549.6	7:27773013-28283536	NOTEST	0.0613978	0.0168095	-1.86891	0	1	1
ENSG00000229894	ENSG00000229894	GK3P	4:165995573-166244308	NOTEST	0.345615	0.355745	0.0416788	0	1	1
ENSG00000229896	ENSG00000229896	RP11-456H18.2	6:12007902-12165232	NOTEST	0	0.0584904	inf	0	1	1
ENSG00000229897	ENSG00000229897	SEPT7P7	9:101050390-101471479	NOTEST	0.050185	0.0389308	-0.366345	0	1	1
ENSG00000229898	ENSG00000229898	ZDHHC20P1	HSCHR6_MHC_SSTO:29675601-29676024	NOTEST	0	0	0	0	1	1
ENSG00000229899	ENSG00000229899	AC084290.2	12:40579810-40763087	NOTEST	0	0	0	0	1	1
ENSG00000229900	ENSG00000229900	HSPD1P21	20:44162834-44176391	NOTEST	0	0	0	0	1	1
ENSG00000229901	ENSG00000229901	RP11-399E6.4	1:41827593-41849262	NOTEST	0	0	0	0	1	1
ENSG00000229903	ENSG00000229903	HCG23	HSCHR6_MHC_MANN:32397724-32414370	NOTEST	0	0	0	0	1	1

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ENSG00000229906	ENSG00000229906	SNRPGP11	13:51909908-52126500	NOTEST	0	0	0	0	1	1
ENSG00000229907	ENSG00000229907	DEFB108P1	8:7783858-7812271	NOTEST	0	0	0	0	1	1
ENSG00000229909	ENSG00000229909	TRIM60P16	7:56699431-56700420	NOTEST	0	0	0	0	1	1
ENSG00000229910	ENSG00000229910	HNRNPA1P18	13:68875736-68877434	NOTEST	0	0	0	0	1	1
ENSG00000229911	ENSG00000229911	RP4-630J13.1	1:119255621-119256301	NOTEST	0	0	0	0	1	1
ENSG00000229912	ENSG00000229912	AC128709.4	3:197171931-197185194	NOTEST	0.0986422	0.150253	0.607115	0	1	1
ENSG00000229913	ENSG00000229913	RP11-378I13.1	1:57289351-57292593	NOTEST	0	0	0	0	1	1
ENSG00000229914	ENSG00000229914	RP11-404O13.4	1:158165422-158165921	NOTEST	0	0	0	0	1	1
ENSG00000229915	ENSG00000229915	AC016999.2	2:239335382-239360891	NOTEST	0	0	0	0	1	1
ENSG00000229917	ENSG00000229917	RPL7P46	16:11038344-11276046	NOTEST	0	0	0	0	1	1
ENSG00000229918	ENSG00000229918	DOCK9-AS1	13:99445740-99738879	NOTEST	0	0	0	0	1	1
ENSG00000229919	ENSG00000229919	TCEB1P3	10:10216192-10216540	NOTEST	0	0	0	0	1	1
ENSG00000229920	ENSG00000229920	RPS4XP5	2:63348517-64054977	NOTEST	0	0	0	0	1	1
ENSG00000229921	ENSG00000229921	KIF25-AS1	6:168393501-168445769	NOTEST	0	0	0	0	1	1
ENSG00000229922	ENSG00000229922	RP11-240M16.1	6:138264215-138293659	NOTEST	0	0	0	0	1	1
ENSG00000229923	ENSG00000229923	RP11-102N11.1	6:131018456-131018923	NOTEST	0	0	0	0	1	1
ENSG00000229924	ENSG00000229924	FAM90A26	4:9172134-9178453	NOTEST	0	0	0	0	1	1
ENSG00000229925	ENSG00000229925	AP001043.1	21:40249214-40328392	NOTEST	0	0	0	0	1	1
ENSG00000229926	ENSG00000229926	RP11-424E7.3	9:141031546-141038316	NOTEST	0	0	0	0	1	1
ENSG00000229927	ENSG00000229927	RHEBP1	10:46897591-46971400	NOTEST	0	0	0	0	1	1
ENSG00000229928	ENSG00000229928	LINC00400	13:43732766-43733602	NOTEST	0	0	0	0	1	1
ENSG00000229929	ENSG00000229929	TRIM39	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000229930	ENSG00000229930	RP11-504P24.5	1:224218405-224222758	NOTEST	0	0	0	0	1	1
ENSG00000229935	ENSG00000229935	AC092662.6	2:156170577-156170880	NOTEST	0	0	0	0	1	1
ENSG00000229936	ENSG00000229936	RBM22P9	X:52518792-52519069	NOTEST	0	0	0	0	1	1
ENSG00000229937	ENSG00000229937	PRPS1L1	7:18066404-18067486	NOTEST	0	0	0	0	1	1
ENSG00000229938	ENSG00000229938	MYO16-AS2	13:109248499-109860355	NOTEST	0	0	0	0	1	1
ENSG00000229939	ENSG00000229939	RP11-111F16.2	X:110862035-110862322	NOTEST	0	0	0	0	1	1
ENSG00000229940	ENSG00000229940	TSPY22P	Y:24452071-24454098	NOTEST	0	0	0	0	1	1
ENSG00000229941	ENSG00000229941	AC012499.1	2:178487979-178973066	NOTEST	0	0	0	0	1	1
ENSG00000229942	ENSG00000229942	IFITM4P	HSCHR6_MHC_SSTO:29715394-29715815	NOTEST	0	0	0	0	1	1
ENSG00000229943	ENSG00000229943	RP11-93N20.1	1:75428997-75430802	NOTEST	0.087854	0	#NAME?	0	1	1
ENSG00000229946	ENSG00000229946	RP11-368G3.1	X:99141737-99142689	NOTEST	0	0	0	0	1	1
ENSG00000229947	ENSG00000229947	RP13-766D20.1	17:79476996-79494802	NOTEST	0	0	0	0	1	1
ENSG00000229948	ENSG00000229948	AC092431.2	2:69685128-70053596	NOTEST	0	0	0	0	1	1
ENSG00000229949	ENSG00000229949	AC005094.2	7:21440537-21441231	NOTEST	0	0	0	0	1	1
ENSG00000229951	ENSG00000229951	AC104695.3	2:28607275-28640179	NOTEST	0	0.00389225	inf	0	1	1
ENSG00000229952	ENSG00000229952	RP6-74O6.3	1:147494089-147498172	NOTEST	0.104047	0.0394616	-1.39871	0	1	1
ENSG00000229954	ENSG00000229954	MTND2P2	X:102024088-102161086	NOTEST	0	0	0	0	1	1
ENSG00000229955	ENSG00000229955	RP1-5O6.4	22:38686696-38794934	NOTEST	0	0.089095	inf	0	1	1
ENSG00000229957	ENSG00000229957	RP5-998H6.2	20:44797042-44799876	NOTEST	0	0	0	0	1	1
ENSG00000229959	ENSG00000229959	HLA-K	HSCHR6_MHC_SSTO:29884112-29887366	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000229960	ENSG00000229960	RP11-278H7.4	1:244232121-244256328	NOTEST	0	0	0	0	1	1
ENSG00000229961	ENSG00000229961	RP11-71G12.1	1:157155177-157157195	NOTEST	0	0	0	0	1	1
ENSG00000229962	ENSG00000229962	AP000221.1	21:26887784-26890650	NOTEST	0	0.0409493	inf	0	1	1
ENSG00000229964	ENSG00000229964	RP11-135A1.3	3:193809349-193826963	NOTEST	0	0	0	0	1	1
ENSG00000229965	ENSG00000229965	RP11-118H4.1	1:226626264-226627045	NOTEST	0	0	0	0	1	1
ENSG00000229967	ENSG00000229967	RP11-366F6.2	X:151072902-151093642	NOTEST	0	0	0	0	1	1
ENSG00000229968	ENSG00000229968	RP3-393P12.1	X:47636225-47638096	NOTEST	0	0	0	0	1	1
ENSG00000229969	ENSG00000229969	RP11-96C23.10	10:88695296-88784489	NOTEST	0	0	0	0	1	1
ENSG00000229970	ENSG00000229970	AC007128.1	7:8152813-8384146	NOTEST	0	0	0	0	1	1
ENSG00000229971	ENSG00000229971	RP5-1119A7.10	22:36948211-36948747	NOTEST	0	0	0	0	1	1
ENSG00000229972	ENSG00000229972	IQCF3	3:51851618-51864876	NOTEST	0	0	0	0	1	1
ENSG00000229974	ENSG00000229974	AC083862.1	7:134671258-134855547	NOTEST	0	0	0	0	1	1
ENSG00000229975	ENSG00000229975	LIPT1P1	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000229976	ENSG00000229976	RP5-1031J8.1	20:38414362-38441871	NOTEST	0	0	0	0	1	1
ENSG00000229977	ENSG00000229977	AC073264.10	7:143229841-143230257	NOTEST	0	0	0	0	1	1
ENSG00000229978	ENSG00000229978	RP13-221M14.3	1:13162644-13165443	NOTEST	0	0	0	0	1	1
ENSG00000229979	ENSG00000229979	U82670.9	X:152220508-152220772	NOTEST	0	0	0	0	1	1
ENSG00000229980	ENSG00000229980	TOB1-AS1	17:48939583-48987593	NOTEST	0.16903	0.485587	1.52245	0	1	1
ENSG00000229981	ENSG00000229981	RP11-215N21.1	10:109517590-109871360	NOTEST	0	0	0	0	1	1
ENSG00000229982	ENSG00000229982	RP11-515K14.1	7:118520156-118521342	NOTEST	0	0	0	0	1	1
ENSG00000229983	ENSG00000229983	RP11-15I11.2	1:212341548-212363601	NOTEST	0.0438165	0	#NAME?	0	1	1
ENSG00000229985	ENSG00000229985	RP11-40H20.5	1:27503241-27503768	NOTEST	0	0	0	0	1	1
ENSG00000229986	ENSG00000229986	AP001042.1	21:40218170-40220568	NOTEST	0	0	0	0	1	1
ENSG00000229988	ENSG00000229988	HBBP1	11:5263183-5264767	NOTEST	0	0	0	0	1	1
ENSG00000229989	ENSG00000229989	MIR181A1HG	1:198776621-198906558	NOTEST	0.0391381	0.0595809	0.606275	0	1	1
ENSG00000229990	ENSG00000229990	RP11-574K11.8	10:75572258-75634343	NOTEST	0	0	0	0	1	1
ENSG00000229991	ENSG00000229991	AKR1B1P1	1:224572844-224928251	NOTEST	0.0567624	0.0950421	0.743631	0	1	1
ENSG00000229992	ENSG00000229992	HMGB3P9	1:92974252-93257961	NOTEST	0.0667306	0	#NAME?	0	1	1
ENSG00000229995	ENSG00000229995	MICG	HSCHR6_MHC_COX:29774036-29774168	NOTEST	0	0	0	0	1	1
ENSG00000229996	ENSG00000229996	AC093585.6	2:241938254-242041747	NOTEST	0	0	0	0	1	1
ENSG00000229998	ENSG00000229998	PPP1R18	HSCHR6_MHC_MANN:30688864-30700371	NOTEST	0	0	0	0	1	1
ENSG00000229999	ENSG00000229999	RP5-1042K10.10	22:40742506-41032706	NOTEST	0	0	0	0	1	1
ENSG00000230000	ENSG00000230000	AC006455.1	7:62787051-62814743	NOTEST	0	0	0	0	1	1
ENSG00000230001	ENSG00000230001	RP11-70J12.1	9:3824126-4348392	NOTEST	0	0	0	0	1	1
ENSG00000230002	ENSG00000230002	ALMS1-IT1	2:73612885-73837920	NOTEST	0.234267	0.278786	0.251005	0	1	1
ENSG00000230003	ENSG00000230003	RP11-217F16.1	9:75060669-75060885	NOTEST	0	0	0	0	1	1
ENSG00000230004	ENSG00000230004	HCG14	HSCHR6_MHC_COX:28865130-28865921	NOTEST	0	0	0	0	1	1
ENSG00000230005	ENSG00000230005	SNAP47-AS1	1:227916239-227968927	NOTEST	0.0271984	0.0308177	0.180236	0	1	1
ENSG00000230006	ENSG00000230006	ANKRD36BP2	2:89065323-89106126	NOTEST	0.554357	0.305348	-0.860359	0	1	1
ENSG00000230009	ENSG00000230009	MTCO2P3	13:57778512-57778933	NOTEST	0	0	0	0	1	1
ENSG00000230010	ENSG00000230010	RP4-568F9.6	20:18303195-18339944	NOTEST	0	0.0154358	inf	0	1	1
ENSG00000230011	ENSG00000230011	CTSLP4	10:52465139-52468666	NOTEST	0	0	0	0	1	1
ENSG00000230012	ENSG00000230012	HTATSF1P	HSCHR6_MHC_MANN:33355727-33367637	NOTEST	0	0	0	0	1	1

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ENSG00000230013	ENSG00000230013	RP11-217B7.3	9:107753076-107754062	NOTEST	0	0.0241786	inf	0	1	1
ENSG00000230014	ENSG00000230014	LINC00709	10:9317795-9329020	NOTEST	0	0	0	0	1	1
ENSG00000230015	ENSG00000230015	RP11-80B9.4	1:240902718-240906911	NOTEST	0	0	0	0	1	1
ENSG00000230016	ENSG00000230016	DHFRP2	HSCHR6_MHC_COX:31324607-31325154	NOTEST	0	0	0	0	1	1
ENSG00000230017	ENSG00000230017	DAQB-335A13.8	HSCHR6_MHC_DBB:29688036-29714307	NOTEST	0	0	0	0	1	1
ENSG00000230018	ENSG00000230018	RP11-481H12.1	10:115242374-115242872	NOTEST	0	0	0	0	1	1
ENSG00000230019	ENSG00000230019	YWHAQP9	1:238271035-238271867	NOTEST	0	0	0	0	1	1
ENSG00000230020	ENSG00000230020	NHS-AS1	X:17393542-17754114	NOTEST	0	0	0	0	1	1
ENSG00000230021	ENSG00000230021	RP5-857K21.4	1:536815-660283	NOTEST	0.382222	0.183199	-1.061	0	1	1
ENSG00000230022	ENSG00000230022	FNTAP2	13:22066835-22178353	NOTEST	0.0320885	0	#NAME?	0	1	1
ENSG00000230023	ENSG00000230023	RP11-10N16.2	1:24526729-24538183	NOTEST	0	0	0	0	1	1
ENSG00000230024	ENSG00000230024	RP11-95P13.1	1:219608493-219615984	NOTEST	0	0.118176	inf	0	1	1
ENSG00000230025	ENSG00000230025	AC007967.4	Y:8839791-8842136	NOTEST	0	0	0	0	1	1
ENSG00000230026	ENSG00000230026	RP11-382D8.5	1:235524467-235525855	NOTEST	0	0.00858525	inf	0	1	1
ENSG00000230027	ENSG00000230027	RP11-550H2.2	1:76507375-76531913	NOTEST	0.246118	0.238509	-0.0453116	0	1	1
ENSG00000230029	ENSG00000230029	CDY11P	Y:23858455-23860106	NOTEST	0	0	0	0	1	1
ENSG00000230030	ENSG00000230030	RP11-505C13.1	9:111014433-111017100	NOTEST	0	0	0	0	1	1
ENSG00000230031	ENSG00000230031	POTEB2	15:21040700-21071643	NOTEST	0	0	0	0	1	1
ENSG00000230033	ENSG00000230033	RP5-1121A15.3	7:156737414-156738339	NOTEST	0	0	0	0	1	1
ENSG00000230034	ENSG00000230034	PSMB8	HSCHR6_MHC_DBB:32786474-32825559	NOTEST	0	0	0	0	1	1
ENSG00000230035	ENSG00000230035	RP11-174G17	1:18434239-18704977	NOTEST	0	0	0	0	1	1
ENSG00000230036	ENSG00000230036	AL596137.1	10:52065359-52401211	NOTEST	0	0	0	0	1	1
ENSG00000230037	ENSG00000230037	UBBP1	2:137087010-137087483	NOTEST	0	0.0699452	inf	0	1	1
ENSG00000230039	ENSG00000230039	RP11-314A15.2	X:65041096-65042091	NOTEST	0	0	0	0	1	1
ENSG00000230040	ENSG00000230040	LINC00364	13:67946518-67954108	NOTEST	0	0	0	0	1	1
ENSG00000230043	ENSG00000230043	TMSB4XP6	20:49411430-49493714	NOTEST	0	1.36138	inf	0	1	1
ENSG00000230044	ENSG00000230044	AC110754.3	2:11798303-11810290	NOTEST	0	0	0	0	1	1
ENSG00000230045	ENSG00000230045	FAM90A15P	8:7114425-7117436	NOTEST	0	0	0	0	1	1
ENSG00000230046	ENSG00000230046	BIRC6-AS1	2:32582095-32843966	NOTEST	0	0	0	0	1	1
ENSG00000230047	ENSG00000230047	AC017104.4	2:232301811-232302132	NOTEST	0	0	0	0	1	1
ENSG00000230048	ENSG00000230048	VWA7	HSCHR6_MHC_DBB:31715551-31727293	NOTEST	0	0	0	0	1	1
ENSG00000230051	ENSG00000230051	CTA-929C8.8	22:27727747-27775226	NOTEST	0	0	0	0	1	1
ENSG00000230052	ENSG00000230052	MTND3P2	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000230053	ENSG00000230053	RP11-76N22.1	1:88963991-88964359	NOTEST	0	0	0	0	1	1
ENSG00000230054	ENSG00000230054	RP11-402G3.5	9:117418583-117424654	NOTEST	0.176325	0.0496855	-1.82734	0	1	1
ENSG00000230056	ENSG00000230056	DDX6P1	6:29297402-29298838	NOTEST	0	0	0	0	1	1
ENSG00000230058	ENSG00000230058	RP11-172E9.2	13:40918093-40924440	NOTEST	0	0	0	0	1	1
ENSG00000230060	ENSG00000230060	C6orf25	HSCHR6_MHC_COX:31673783-31681900	NOTEST	0	0	0	0	1	1
ENSG00000230061	ENSG00000230061	AP001065.2	21:45770045-45862964	NOTEST	0.392669	0.532246	0.438777	0	1	1
ENSG00000230062	ENSG00000230062	ANKRD66	6:46714653-46728895	NOTEST	0	0	0	0	1	1
ENSG00000230063	ENSG00000230063	RP11-384C4.6	1:212458878-212535200	NOTEST	0	0	0	0	1	1
ENSG00000230064	ENSG00000230064	RP11-244N20.7	9:136205159-136214986	NOTEST	0.00201301	0.256468	6.99328	0	1	1
ENSG00000230065	ENSG00000230065	AC010974.3	2:133174146-133429152	NOTEST	0	0.0522311	inf	0	1	1
ENSG00000230066	ENSG00000230066	FAM197Y3	Y:9236029-9344176	NOTEST	0	0	0	0	1	1

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ENSG00000230067	ENSG00000230067	HSPD1P6	3:36808607-36825658	NOTEST	0.0730886	0.0966512	0.403141	0	1	1
ENSG00000230068	ENSG00000230068	CDC42-IT1	1:22379119-22419437	NOTEST	0.0285111	0	#NAME?	0	1	1
ENSG00000230069	ENSG00000230069	LRRC37A15P	4:103552659-103682151	NOTEST	0.181312	0.250292	0.465138	0	1	1
ENSG00000230071	ENSG00000230071	RPL4P6	22:40742506-41032706	NOTEST	0.0762745	0.134392	0.81717	0	1	1
ENSG00000230072	ENSG00000230072	SFTA2	HSCHR6_MHC_MANN:30943813-30944636	NOTEST	0	0	0	0	1	1
ENSG00000230073	ENSG00000230073	AC009947.2	Y:25669467-25671516	NOTEST	0	0	0	0	1	1
ENSG00000230075	ENSG00000230075	C4A-AS1	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000230076	ENSG00000230076	AC016708.2	2:215674952-216003151	NOTEST	0.387124	0.143977	-1.42695	0	1	1
ENSG00000230077	ENSG00000230077	MTAPP2	3:189674516-189862635	NOTEST	0	0	0	0	1	1
ENSG00000230079	ENSG00000230079	RP11-535K18.2	X:135377848-135382457	NOTEST	0	0.0103079	inf	0	1	1
ENSG00000230080	ENSG00000230080	AC139143.2	11:1824118-1825325	NOTEST	0	0.0315452	inf	0	1	1
ENSG00000230081	ENSG00000230081	HSPE1P28	9:114980714-115095947	NOTEST	0	0	0	0	1	1
ENSG00000230083	ENSG00000230083	AC009237.13	2:96256716-96256954	NOTEST	0	0	0	0	1	1
ENSG00000230084	ENSG00000230084	RP4-613B23.1	3:42589460-42709072	NOTEST	0.191706	0.351511	0.874673	0	1	1
ENSG00000230086	ENSG00000230086	VN1R96P	19:40627217-40628075	NOTEST	0	0	0	0	1	1
ENSG00000230087	ENSG00000230087	AC104389.31	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000230088	ENSG00000230088	KRT16P5	17:20396946-20397468	NOTEST	0	0.030036	inf	0	1	1
ENSG00000230089	ENSG00000230089	XXbac-BPG308J9.3	HSCHR6_MHC_SSTO:29191822-29234926	NOTEST	0	0	0	0	1	1
ENSG00000230090	ENSG00000230090	AC108025.2	2:5742636-5831620	NOTEST	0	0	0	0	1	1
ENSG00000230091	ENSG00000230091	TMEM254-AS1	10:81806615-81852313	NOTEST	0.0792411	0.12184	0.620662	0	1	1
ENSG00000230092	ENSG00000230092	RP11-206L10.8	1:714149-755214	NOTEST	0.0843992	0.0657508	-0.360222	0	1	1
ENSG00000230096	ENSG00000230096	RP11-34C15.2	10:4457496-4468371	NOTEST	0	0	0	0	1	1
ENSG00000230097	ENSG00000230097	RP11-460C6.1	9:29824739-29826709	NOTEST	0	0	0	0	1	1
ENSG00000230098	ENSG00000230098	TCERG1L-AS1	10:132890653-133109984	NOTEST	0	0	0	0	1	1
ENSG00000230099	ENSG00000230099	TRBV5-4	7:142168379-142169045	NOTEST	0	0	0	0	1	1
ENSG00000230100	ENSG00000230100	RP11-344N17.8	X:48193109-48193874	NOTEST	0	0	0	0	1	1
ENSG00000230101	ENSG00000230101	TUBB3P2	7:134419648-134419945	NOTEST	0	0	0	0	1	1
ENSG00000230102	ENSG00000230102	RP11-407B7.1	3:193675160-193788759	NOTEST	0.509407	0.548573	0.106866	0	1	1
ENSG00000230104	ENSG00000230104	AC018712.2	2:173538939-173539626	NOTEST	0	0.0224029	inf	0	1	1
ENSG00000230105	ENSG00000230105	RP11-431N15.2	X:56644823-56650891	NOTEST	0.0274061	0.0213257	-0.361906	0	1	1
ENSG00000230106	ENSG00000230106	AF228730.7	8:7028071-7028263	NOTEST	0	0	0	0	1	1
ENSG00000230107	ENSG00000230107	CTA-126B4.7	22:42834028-42842201	NOTEST	0.0686137	0	#NAME?	0	1	1
ENSG00000230108	ENSG00000230108	TNF	HSCHR6_MHC_SSTO:31533286-31536056	NOTEST	0	0	0	0	1	1
ENSG00000230109	ENSG00000230109	RP11-275N1.1	10:21629161-21661879	NOTEST	0	0	0	0	1	1
ENSG00000230110	ENSG00000230110	AC005086.1	7:101458958-101927249	NOTEST	0	0	0	0	1	1
ENSG00000230111	ENSG00000230111	AC115283.1	3:31310498-31310898	NOTEST	0	0	0	0	1	1
ENSG00000230112	ENSG00000230112	RP11-56H7.2	10:21068901-21463977	NOTEST	0	0	0	0	1	1
ENSG00000230113	ENSG00000230113	AC091177.1	17:29224353-29286340	NOTEST	0	0	0	0	1	1
ENSG00000230114	ENSG00000230114	RP11-141A19.2	1:48998526-50489585	NOTEST	0	0	0	0	1	1
ENSG00000230115	ENSG00000230115	TPRG1-AS2	3:188659503-189043093	NOTEST	0	0	0	0	1	1
ENSG00000230116	ENSG00000230116	RP11-163G10.2	1:42895999-43120335	NOTEST	0	0	0	0	1	1
ENSG00000230118	ENSG00000230118	AC092569.2	2:30945636-31043408	NOTEST	0	0	0	0	1	1
ENSG00000230119	ENSG00000230119	AC123900.2	3:33191536-33260707	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000230121	ENSG00000230121	RP11-385N23.1	10:7575168-7578527	NOTEST	0	0	0	0	1	1
ENSG00000230122	ENSG00000230122	ECEL1P3	2:233214463-233216019	NOTEST	0	0	0	0	1	1
ENSG00000230123	ENSG00000230123	DLEC1P1	3:38366727-38370561	NOTEST	0	0	0	0	1	1
ENSG00000230125	ENSG00000230125	EEF1A1P39	10:30590751-30591001	NOTEST	0	0	0	0	1	1
ENSG00000230126	ENSG00000230126	FGF12-AS2	3:191857183-192485553	NOTEST	0	0	0	0	1	1
ENSG00000230128	ENSG00000230128	IER3	HSCHR6_MHC_MANN:30755672-30757028	NOTEST	0	0	0	0	1	1
ENSG00000230130	ENSG00000230130	RP5-1189K21.2	X:142372753-142605303	NOTEST	0	0	0	0	1	1
ENSG00000230131	ENSG00000230131	RP11-282I1.1	10:125115965-125277224	NOTEST	0	0	0	0	1	1
ENSG00000230132	ENSG00000230132	RP5-1193P9.2	7:62940975-62941367	NOTEST	0	0	0	0	1	1
ENSG00000230133	ENSG00000230133	RP5-1100I6.2	20:24180402-24205224	NOTEST	0	0	0	0	1	1
ENSG00000230134	ENSG00000230134	HCG24	HSCHR6_MHC_DBB:33090472-33093457	NOTEST	0	0	0	0	1	1
ENSG00000230136	ENSG00000230136	OR2J4P	HSCHR6_MHC_MANN:29149307-29150243	NOTEST	0	0	0	0	1	1
ENSG00000230137	ENSG00000230137	RP4-539M6.18	22:30835823-30836305	NOTEST	0	0	0	0	1	1
ENSG00000230138	ENSG00000230138	RP11-117D22.2	1:53832339-53833917	NOTEST	0	0	0	0	1	1
ENSG00000230140	ENSG00000230140	AC016738.3	2:101436613-101886778	NOTEST	0.174348	0.14947	-0.222111	0	1	1
ENSG00000230141	ENSG00000230141	HLA-DOA	HSCHR6_MHC_MCF:33005420-33010855	NOTEST	0	0	0	0	1	1
ENSG00000230142	ENSG00000230142	LINC01075	13:62798229-62824080	NOTEST	0	0	0	0	1	1
ENSG00000230143	ENSG00000230143	FLOT1	HSCHR6_MHC_SSTO:30686934-30701969	NOTEST	0	0	0	0	1	1
ENSG00000230146	ENSG00000230146	SEPHS1P4	X:72989082-72990258	NOTEST	0	0.0356451	inf	0	1	1
ENSG00000230147	ENSG00000230147	RP11-305L7.5	9:93881343-93945044	NOTEST	0	0	0	0	1	1
ENSG00000230148	ENSG00000230148	HOXB-AS1	17:46618255-46683776	NOTEST	0.0675736	0.0476515	-0.503938	0	1	1
ENSG00000230149	ENSG00000230149	RP3-508I15.19	22:39101727-39190203	NOTEST	0.335903	0.219198	-0.61581	0	1	1
ENSG00000230150	ENSG00000230150	XXbac-BPG254F23.7	HSCHR6_MHC_QBL:32614455-32615286	NOTEST	0	0	0	0	1	1
ENSG00000230153	ENSG00000230153	AF003626.1	X:150084285-150089411	NOTEST	0	0	0	0	1	1
ENSG00000230155	ENSG00000230155	RP3-477O4.14	20:34042984-34099804	NOTEST	0	0	0	0	1	1
ENSG00000230156	ENSG00000230156	LINC00443	13:107306263-107324511	NOTEST	0	0	0	0	1	1
ENSG00000230157	ENSG00000230157	ATP5G1P1	14:106003197-106003576	NOTEST	0	0	0	0	1	1
ENSG00000230158	ENSG00000230158	MTND1P28	2:117781493-117782443	NOTEST	0	0	0	0	1	1
ENSG00000230159	ENSG00000230159	RP11-232D9.3	X:115826877-115828156	NOTEST	0.0435598	0.0309274	-0.49411	0	1	1
ENSG00000230160	ENSG00000230160	AC004854.5	7:44959267-44959928	NOTEST	0	0	0	0	1	1
ENSG00000230161	ENSG00000230161	RP11-62L10.1	9:103674601-103675023	NOTEST	0	0	0	0	1	1
ENSG00000230162	ENSG00000230162	RP11-97N5.2	X:135024636-135029298	NOTEST	0.0154229	0	#NAME?	0	1	1
ENSG00000230163	ENSG00000230163	RP5-997D16.2	1:35178337-35325417	NOTEST	0.288851	0.482994	0.741681	0	1	1
ENSG00000230164	ENSG00000230164	MAS1LP1	6:29442801-29443848	NOTEST	0	0	0	0	1	1
ENSG00000230165	ENSG00000230165	CTB-1144G6.5	10:115999017-116051272	NOTEST	0	0	0	0	1	1
ENSG00000230166	ENSG00000230166	RP11-526K21.2	10:51026324-51130715	NOTEST	0	0	0	0	1	1
ENSG00000230169	ENSG00000230169	RPL30P16	8:113235156-114449328	NOTEST	0	0	0	0	1	1
ENSG00000230170	ENSG00000230170	HNRNPA1P28	X:118354744-118355705	NOTEST	0	0.013252	inf	0	1	1
ENSG00000230171	ENSG00000230171	RPL22P18	10:81885696-81886073	NOTEST	0	0	0	0	1	1
ENSG00000230172	ENSG00000230172	AC090957.2	3:14716605-14814541	NOTEST	0	0	0	0	1	1
ENSG00000230173	ENSG00000230173	AC006196.1	2:195595318-195626159	NOTEST	0	0	0	0	1	1

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ENSG00000230174	ENSG00000230174	LINC01149	6:31368478-31445283	NOTEST	0	0.0181723	inf	0	1	1
ENSG00000230175	ENSG00000230175	RP11-466F5.3	1:165631452-165679205	NOTEST	0	0	0	0	1	1
ENSG00000230176	ENSG00000230176	RP4-779E11.3	20:4173711-4176590	NOTEST	0	0	0	0	1	1
ENSG00000230177	ENSG00000230177	RP5-1112D6.4	6:111599134-111599945	NOTEST	0.406498	0.204823	-0.988869	0	1	1
ENSG00000230178	ENSG00000230178	OR4F3	5:180794268-180795263	NOTEST	0	0	0	0	1	1
ENSG00000230180	ENSG00000230180	CTD-2542O7.2	X:16804549-16888537	NOTEST	0	0	0	0	1	1
ENSG00000230181	ENSG00000230181	RPL13AP	HSCHR6_MHC_COX:29519994-29597568	NOTEST	0	0	0	0	1	1
ENSG00000230182	ENSG00000230182	RNF10P1	3:5110360-5110729	NOTEST	0	0	0	0	1	1
ENSG00000230183	ENSG00000230183	CNOT6LP1	15:56297910-56299374	NOTEST	0.0464571	0.0614821	0.404267	0	1	1
ENSG00000230184	ENSG00000230184	SMYD3-IT1	1:245912641-246670614	NOTEST	0	0	0	0	1	1
ENSG00000230185	ENSG00000230185	C9orf147	9:115142216-115431677	NOTEST	0.0607429	0.18545	1.61024	0	1	1
ENSG00000230186	ENSG00000230186	RP5-998N21.7	1:149369293-149429348	NOTEST	0	0	0	0	1	1
ENSG00000230187	ENSG00000230187	RP11-291O7.1	X:69748789-70128581	NOTEST	0	0	0	0	1	1
ENSG00000230188	ENSG00000230188	RP11-405L18.4	9:37485931-37503694	NOTEST	0.0491762	0.0699452	0.508267	0	1	1
ENSG00000230190	ENSG00000230190	AC005518.2	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000230191	ENSG00000230191	RP4-725G10.3	7:56230837-56231226	NOTEST	0	0	0	0	1	1
ENSG00000230192	ENSG00000230192	AC073387.2	7:109300150-109300859	NOTEST	0	0	0	0	1	1
ENSG00000230193	ENSG00000230193	MYL8P	HSCHR6_MHC_QBL:33235604-33236122	NOTEST	0	0	0	0	1	1
ENSG00000230194	ENSG00000230194	AC000081.2	22:19166985-19279239	NOTEST	0	0	0	0	1	1
ENSG00000230196	ENSG00000230196	AC010091.4	7:81205701-81255532	NOTEST	0	0	0	0	1	1
ENSG00000230197	ENSG00000230197	RP11-160E2.17	17:18981087-18991191	NOTEST	0	0	0	0	1	1
ENSG00000230198	ENSG00000230198	RPL37P4	21:20966154-20966422	NOTEST	0	0	0	0	1	1
ENSG00000230199	ENSG00000230199	RP11-331N16.1	1:243138306-243138386	NOTEST	0	0	0	0	1	1
ENSG00000230201	ENSG00000230201	ATP6V0CP1	17:4736682-4806369	NOTEST	0.0332324	0	#NAME?	0	1	1
ENSG00000230203	ENSG00000230203	CTB-1048E9.7	22:26818036-26819159	NOTEST	0	0	0	0	1	1
ENSG00000230205	ENSG00000230205	RP11-631F7.2	6:148454944-148458540	NOTEST	0	0	0	0	1	1
ENSG00000230208	ENSG00000230208	IFNNP1	9:21058769-21059322	NOTEST	0	0	0	0	1	1
ENSG00000230209	ENSG00000230209	HNRNPA1P2	HSCHR6_MHC_DBB:32236324-32315209	NOTEST	0	0	0	0	1	1
ENSG00000230210	ENSG00000230210	FAM35EP	10:49087397-49094515	NOTEST	0	0	0	0	1	1
ENSG00000230211	ENSG00000230211	RPL15P4	HSCHR6_MHC_COX:31483348-31483928	NOTEST	0	0	0	0	1	1
ENSG00000230212	ENSG00000230212	AP000688.14	21:37402367-37498938	NOTEST	0.0697034	0.0534408	-0.383287	0	1	1
ENSG00000230213	ENSG00000230213	OR8V1P	11:55955854-55956727	NOTEST	0	0	0	0	1	1
ENSG00000230214	ENSG00000230214	FTLP18	1:37095935-37096458	NOTEST	0	0	0	0	1	1
ENSG00000230215	ENSG00000230215	EIF2B5-AS1	3:183851806-184402546	NOTEST	0	0	0	0	1	1
ENSG00000230216	ENSG00000230216	HSPB1P2	X:49090414-49090960	NOTEST	0.113129	0.0280922	-2.00973	0	1	1
ENSG00000230219	ENSG00000230219	FAM92A1P2	4:183958817-183961272	NOTEST	0	0	0	0	1	1
ENSG00000230221	ENSG00000230221	RP11-173G21.1	9:97861335-98079991	NOTEST	0	0.010027	inf	0	1	1
ENSG00000230223	ENSG00000230223	ATXN8OS	13:70274725-70713561	NOTEST	0	0	0	0	1	1
ENSG00000230225	ENSG00000230225	MTND5P14	9:4985032-5128183	NOTEST	0	0	0	0	1	1
ENSG00000230226	ENSG00000230226	RP4-697K14.3	20:62133639-62136464	NOTEST	0	0	0	0	1	1
ENSG00000230227	ENSG00000230227	SIAH1P1	X:35644246-35645181	NOTEST	0.0402805	0	#NAME?	0	1	1
ENSG00000230228	ENSG00000230228	RP11-4M23.4	1:24197015-24285549	NOTEST	0	0.0538266	inf	0	1	1
ENSG00000230229	ENSG00000230229	RP11-90J7.4	10:80008504-80115857	NOTEST	0	0	0	0	1	1

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ENSG00000230231	ENSG00000230231	FMO7P	1:166443981-166459276	NOTEST	0	0	0	0	1	1
ENSG00000230233	ENSG00000230233	AF240627.2	21:19933582-20132321	NOTEST	0	0	0	0	1	1
ENSG00000230234	ENSG00000230234	RP1-276N6.2	6:160592092-160698670	NOTEST	0	0	0	0	1	1
ENSG00000230237	ENSG00000230237	AC010975.2	2:79384131-80875905	NOTEST	0.0356235	0	#NAME?	0	1	1
ENSG00000230238	ENSG00000230238	HLA-V	HSCHR6_MHC_COX:29753036-29759260	NOTEST	0	0	0	0	1	1
ENSG00000230239	ENSG00000230239	RP11-108M9.2	1:17066767-17299474	NOTEST	0	0	0	0	1	1
ENSG00000230240	ENSG00000230240	RP11-241I20.1	10:32272812-32273482	NOTEST	0	0	0	0	1	1
ENSG00000230241	ENSG00000230241	RP11-38O23.3	X:47995035-47995537	NOTEST	0	0	0	0	1	1
ENSG00000230243	ENSG00000230243	FKBP1AP3	13:47079252-47079571	NOTEST	0	0	0	0	1	1
ENSG00000230244	ENSG00000230244	RAD23BP2	7:83292734-83293941	NOTEST	0	0	0	0	1	1
ENSG00000230245	ENSG00000230245	RP11-475I24.7	9:44333922-44334382	NOTEST	0	0	0	0	1	1
ENSG00000230246	ENSG00000230246	SPATA31C1	9:90529407-90538572	NOTEST	0	0	0	0	1	1
ENSG00000230247	ENSG00000230247	HNRNPH3P1	X:79784535-79785526	NOTEST	0	0	0	0	1	1
ENSG00000230248	ENSG00000230248	RP1-128O3.4	6:108596845-108597750	NOTEST	0	0	0	0	1	1
ENSG00000230249	ENSG00000230249	RP13-824C8.2	X:3030940-3031637	NOTEST	0	0	0	0	1	1
ENSG00000230250	ENSG00000230250	RP11-90C4.2	1:56381281-56410636	NOTEST	0	0	0	0	1	1
ENSG00000230251	ENSG00000230251	PHBP4	2:154728425-155313950	NOTEST	0	0	0	0	1	1
ENSG00000230252	ENSG00000230252	MTND2P4	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000230254	ENSG00000230254	HLA-E	HSCHR6_MHC_SSTO:30448675-30453414	NOTEST	0	0	0	0	1	1
ENSG00000230255	ENSG00000230255	RP11-423O2.1	1:142791487-142792556	NOTEST	0.156614	0.152118	-0.0420256	0	1	1
ENSG00000230256	ENSG00000230256	FGFR1OP2P1	13:27479498-27479998	NOTEST	0	0	0	0	1	1
ENSG00000230257	ENSG00000230257	NFE4	7:102453307-102715286	NOTEST	0	0	0	0	1	1
ENSG00000230258	ENSG00000230258	AC002539.1	17:68013464-68131749	NOTEST	0	0	0	0	1	1
ENSG00000230259	ENSG00000230259	AC008738.1	19:33790839-33793470	NOTEST	0.0150283	0.0937462	2.64108	0	1	1
ENSG00000230260	ENSG00000230260	RP11-75C23.1	1:197170591-197447585	NOTEST	0	0	0	0	1	1
ENSG00000230261	ENSG00000230261	OR52J2P	11:5058242-5059181	NOTEST	0	0	0	0	1	1
ENSG00000230262	ENSG00000230262	MIRLET7DHG	9:96928570-96966850	NOTEST	0.000510171	0.492038	9.91357	0	1	1
ENSG00000230265	ENSG00000230265	RP11-702C7.1	X:26575791-26576447	NOTEST	0	0	0	0	1	1
ENSG00000230268	ENSG00000230268	SSU72P8	7:124116424-124117009	NOTEST	0	0	0	0	1	1
ENSG00000230271	ENSG00000230271	RP11-548K12.5	7:57832289-57833087	NOTEST	0	0	0	0	1	1
ENSG00000230273	ENSG00000230273	AC087163.3	17:17876126-17942523	NOTEST	0	0.0551114	inf	0	1	1
ENSG00000230274	ENSG00000230274	PGAM1P3	3:40355292-40494820	NOTEST	0	0	0	0	1	1
ENSG00000230275	ENSG00000230275	SERBP1P4	X:90815434-90816596	NOTEST	0	0	0	0	1	1
ENSG00000230276	ENSG00000230276	RP11-373A6.1	9:29254072-29254424	NOTEST	0	0	0	0	1	1
ENSG00000230279	ENSG00000230279	LTA	HSCHR6_MHC_SSTO:31529773-31532044	NOTEST	0	0	0	0	1	1
ENSG00000230281	ENSG00000230281	AL590812.3	9:39651896-39652392	NOTEST	0	0	0	0	1	1
ENSG00000230282	ENSG00000230282	RPL7P61	2:164008760-164009817	NOTEST	0	0	0	0	1	1
ENSG00000230283	ENSG00000230283	RPS12P24	13:37794996-37795383	NOTEST	0	0	0	0	1	1
ENSG00000230284	ENSG00000230284	RP11-402G3.4	9:117458201-117458595	NOTEST	0	0	0	0	1	1
ENSG00000230285	ENSG00000230285	RP11-290M5.2	1:86064813-86066417	NOTEST	0	0	0	0	1	1
ENSG00000230286	ENSG00000230286	AC013472.4	2:27070614-27250064	NOTEST	0	0	0	0	1	1
ENSG00000230287	ENSG00000230287	RP11-305E17.4	1:100652474-100715390	NOTEST	0	0	0	0	1	1
ENSG00000230289	ENSG00000230289	RP11-334J6.6	9:134378288-134406655	NOTEST	0	0.0383333	inf	0	1	1
ENSG00000230290	ENSG00000230290	ARMC2-AS1	6:109169618-109295186	NOTEST	0	0	0	0	1	1

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ENSG00000230292	ENSG00000230292	NAALADL2-AS3	3:174156362-175523428	NOTEST	0	0	0	0	1	1
ENSG00000230293	ENSG00000230293	MSH5	HSCHR6_MHC_DBB:31689901-31715550	NOTEST	0	0	0	0	1	1
ENSG00000230294	ENSG00000230294	RP13-507P19.2	12:131832014-131855604	NOTEST	0	0	0	0	1	1
ENSG00000230295	ENSG00000230295	RP11-458F8.2	7:66345694-66347968	NOTEST	0	0	0	0	1	1
ENSG00000230298	ENSG00000230298	RP11-253D19.2	10:30865627-30869111	NOTEST	0	0	0	0	1	1
ENSG00000230299	ENSG00000230299	AC093162.3	2:85360532-85537511	NOTEST	0	0	0	0	1	1
ENSG00000230300	ENSG00000230300	STARD13-IT1	13:33677271-33924767	NOTEST	0	0.0412035	inf	0	1	1
ENSG00000230301	ENSG00000230301	OR5H6	3:97952494-98176742	NOTEST	0	0	0	0	1	1
ENSG00000230302	ENSG00000230302	MTND3P4	9:104555735-104556038	NOTEST	0	0	0	0	1	1
ENSG00000230303	ENSG00000230303	RP11-213G2.2	9:88368220-88408395	NOTEST	0	0.0853705	inf	0	1	1
ENSG00000230304	ENSG00000230304	CICP6	3:197950367-197953181	NOTEST	0	0	0	0	1	1
ENSG00000230305	ENSG00000230305	AC004980.9	7:76139744-77045717	NOTEST	0	0	0	0	1	1
ENSG00000230306	ENSG00000230306	BANF1P2	10:135093134-135166187	NOTEST	0.153218	0	#NAME?	0	1	1
ENSG00000230307	ENSG00000230307	OR6C5P	12:55677533-55706860	NOTEST	0	0	0	0	1	1
ENSG00000230308	ENSG00000230308	TRIM39	HSCHR6_MHC_APD:30266816-30322899	NOTEST	0	0	0	0	1	1
ENSG00000230309	ENSG00000230309	RP3-390M24.1	6:79314183-79315753	NOTEST	0	0	0	0	1	1
ENSG00000230310	ENSG00000230310	CTD-2192J16.11	19:12490002-12750912	NOTEST	0	0	0	0	1	1
ENSG00000230311	ENSG00000230311	AC004074.3	X:72442959-72443394	NOTEST	0.105689	0.124001	0.23052	0	1	1
ENSG00000230312	ENSG00000230312	LL0XNC01-116E7.4	X:103172004-103229570	NOTEST	0	0	0	0	1	1
ENSG00000230313	ENSG00000230313	HCG24	6:33112559-33115544	NOTEST	0	0	0	0	1	1
ENSG00000230314	ENSG00000230314	ELOVL2-AS1	6:10980991-11078459	NOTEST	0.0473233	0.0192504	-1.29766	0	1	1
ENSG00000230316	ENSG00000230316	FEZF1-AS1	7:121941447-121950745	NOTEST	0.141379	0.180498	0.352416	0	1	1
ENSG00000230317	ENSG00000230317	RP11-104D21.3	X:50838689-50914232	NOTEST	0	0	0	0	1	1
ENSG00000230318	ENSG00000230318	XRCC6P3	1:220487286-220488907	NOTEST	0	0	0	0	1	1
ENSG00000230319	ENSG00000230319	AL022476.2	22:43434590-43485434	NOTEST	0.0101085	0.011769	0.219426	0	1	1
ENSG00000230320	ENSG00000230320	RP4-769N13.2	X:101854095-101973607	NOTEST	0	0	0	0	1	1
ENSG00000230321	ENSG00000230321	CTD-3105H18.9	19:12490002-12750912	NOTEST	0.0577545	0.139764	1.27499	0	1	1
ENSG00000230322	ENSG00000230322	RP3-323N1.2	10:11047258-11378674	NOTEST	0	0	0	0	1	1
ENSG00000230323	ENSG00000230323	LINC00159	21:33452628-33570125	NOTEST	0	0	0	0	1	1
ENSG00000230324	ENSG00000230324	RP4-705O1.1	20:37842419-37853391	NOTEST	0	0	0	0	1	1
ENSG00000230325	ENSG00000230325	RP11-385F5.4	1:236681299-236767804	NOTEST	0.584639	0.391147	-0.579836	0	1	1
ENSG00000230326	ENSG00000230326	HMGN1P33	X:9754495-9917483	NOTEST	0	0	0	0	1	1
ENSG00000230327	ENSG00000230327	AC009234.1	2:50145642-51259674	NOTEST	0	0	0	0	1	1
ENSG00000230328	ENSG00000230328	RP11-35N6.6	9:104121213-104145801	NOTEST	0	0	0	0	1	1
ENSG00000230330	ENSG00000230330	HMGN2P3	16:25703346-26149009	NOTEST	0	0	0	0	1	1
ENSG00000230331	ENSG00000230331	RP5-1068B5.1	1:229560766-229561397	NOTEST	0	0	0	0	1	1
ENSG00000230332	ENSG00000230332	RNF39	HSCHR6_MHC_MCF:30112986-30122165	NOTEST	0	0	0	0	1	1
ENSG00000230333	ENSG00000230333	AC004538.3	7:11221358-11871824	NOTEST	0.0404678	0	#NAME?	0	1	1
ENSG00000230335	ENSG00000230335	RP11-159H20.1	9:79546176-79546982	NOTEST	0	0	0	0	1	1
ENSG00000230336	ENSG00000230336	POU5F1	HSCHR6_MHC_MANN:31171309-31199405	NOTEST	0	0	0	0	1	1

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ENSG00000230338	ENSG00000230338	MTND4P19	10:96443250-96613017	NOTEST	0	0	0	0	1	1
ENSG00000230339	ENSG00000230339	RP11-434D2.8	17:20457449-20457693	NOTEST	0	0	0	0	1	1
ENSG00000230341	ENSG00000230341	PPP1R18	HSCHR6_MHC_APD:30652414-30663921	NOTEST	0	0	0	0	1	1
ENSG00000230342	ENSG00000230342	FANCD2P2	3:11901147-11932646	NOTEST	0	0	0	0	1	1
ENSG00000230343	ENSG00000230343	AC018892.8	2:97700178-97700443	NOTEST	0	0	0	0	1	1
ENSG00000230345	ENSG00000230345	RP13-455A7.1	22:48256419-48257811	NOTEST	0	0	0	0	1	1
ENSG00000230347	ENSG00000230347	CT47A8	X:120082281-120085594	NOTEST	0	0	0	0	1	1
ENSG00000230350	ENSG00000230350	RPL35AP3	6:137295066-137295354	NOTEST	0	0	0	0	1	1
ENSG00000230352	ENSG00000230352	RP4-614C15.3	20:57935981-57939828	NOTEST	0	0	0	0	1	1
ENSG00000230353	ENSG00000230353	AC114755.2	2:106905258-106905509	NOTEST	0	0	0	0	1	1
ENSG00000230354	ENSG00000230354	STK19P	HSCHR6_MHC_MCF:32057493-32058011	NOTEST	0	0	0	0	1	1
ENSG00000230355	ENSG00000230355	AC009474.2	2:67108218-67108354	NOTEST	0	0	0	0	1	1
ENSG00000230356	ENSG00000230356	NCAPD2P1	7:34386123-34917944	NOTEST	0	0	0	0	1	1
ENSG00000230357	ENSG00000230357	MCCD1P1	HSCHR6_MHC_DBB:29867163-29868026	NOTEST	0	0	0	0	1	1
ENSG00000230358	ENSG00000230358	RP11-166O4.1	7:66744764-66751606	NOTEST	0.086754	0.069658	-0.316643	0	1	1
ENSG00000230359	ENSG00000230359	TPI1P2	7:128696072-128696824	NOTEST	0.243064	0.199228	-0.286918	0	1	1
ENSG00000230360	ENSG00000230360	DDX10P2	9:84701069-84703683	NOTEST	0	0	0	0	1	1
ENSG00000230361	ENSG00000230361	VN1R32P	7:62837706-62838611	NOTEST	0	0	0	0	1	1
ENSG00000230362	ENSG00000230362	RP11-809F4.2	3:175695284-175696358	NOTEST	0	0	0	0	1	1
ENSG00000230364	ENSG00000230364	RPL4P3	1:171652267-171653578	NOTEST	0.026056	0.0387819	0.573765	0	1	1
ENSG00000230365	ENSG00000230365	RP11-23D5.1	9:11275313-11276314	NOTEST	0	0	0	0	1	1
ENSG00000230366	ENSG00000230366	DSCR9	21:38580803-38640785	NOTEST	0.0749325	0.164728	1.13642	0	1	1
ENSG00000230368	ENSG00000230368	FAM41C	1:803450-812283	NOTEST	0.0704447	0.130622	0.89083	0	1	1
ENSG00000230370	ENSG00000230370	AC005007.3	7:11013498-11209250	NOTEST	0	0	0	0	1	1
ENSG00000230371	ENSG00000230371	KARSP2	13:113777127-113803843	NOTEST	0	0.00786223	inf	0	1	1
ENSG00000230372	ENSG00000230372	RP3-425P12.2	6:25061852-25063735	NOTEST	0	0	0	0	1	1
ENSG00000230375	ENSG00000230375	RP11-392A23.4	6:52712707-52735127	NOTEST	0	0	0	0	1	1
ENSG00000230376	ENSG00000230376	MEMO1P4	X:122899150-122899536	NOTEST	0	0	0	0	1	1
ENSG00000230377	ENSG00000230377	TCEB1P7	Y:20652800-20790963	NOTEST	0	0	0	0	1	1
ENSG00000230379	ENSG00000230379	AP000146.2	21:26212863-26442219	NOTEST	0	0	0	0	1	1
ENSG00000230381	ENSG00000230381	RP4-655J12.5	1:116966345-117021464	NOTEST	0.129541	0.0336421	-1.94507	0	1	1
ENSG00000230383	ENSG00000230383	AC009245.3	7:137065782-137531838	NOTEST	0.250645	0.324538	0.372742	0	1	1
ENSG00000230384	ENSG00000230384	AC016739.1	2:177106838-177107721	NOTEST	0	0	0	0	1	1
ENSG00000230385	ENSG00000230385	AC012507.4	2:231772032-231825781	NOTEST	0.219358	0.0448841	-2.28901	0	1	1
ENSG00000230386	ENSG00000230386	RP13-157F18.2	7:65081989-65084127	NOTEST	0	0	0	0	1	1
ENSG00000230387	ENSG00000230387	RP4-737E23.2	20:23168764-23170944	NOTEST	0	0	0	0	1	1
ENSG00000230389	ENSG00000230389	HCP5	HSCHR6_MHC_SSTO:31420863-31423498	NOTEST	0	0	0	0	1	1
ENSG00000230390	ENSG00000230390	LINC01048	13:38055603-38058906	NOTEST	0	0	0	0	1	1
ENSG00000230391	ENSG00000230391	RPSAP23	2:115199875-116603328	NOTEST	0	0	0	0	1	1
ENSG00000230392	ENSG00000230392	RP5-1139I1.1	X:118425491-118469573	NOTEST	0	0.0119098	inf	0	1	1
ENSG00000230393	ENSG00000230393	AC092667.2	2:100162322-100759201	NOTEST	0.0936828	0.0399633	-1.22911	0	1	1
ENSG00000230394	ENSG00000230394	RP11-692P14.1	X:7975418-7986201	NOTEST	0	0	0	0	1	1
ENSG00000230398	ENSG00000230398	AC026882.1	3:2140496-3102829	NOTEST	0	0	0	0	1	1
ENSG00000230399	ENSG00000230399	RBBP8P1	X:117629860-117820126	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000230400	ENSG00000230400	RP11-359G22.2	20:22656709-22665982	NOTEST	0	0	0	0	1	1
ENSG00000230401	ENSG00000230401	AC090505.4	3:194429149-194502897	NOTEST	0	0	0	0	1	1
ENSG00000230402	ENSG00000230402	RP11-84O12.4	1:101092604-101106169	NOTEST	0	0	0	0	1	1
ENSG00000230403	ENSG00000230403	LINC01066	13:31569298-31570275	NOTEST	0	0.0507779	inf	0	1	1
ENSG00000230404	ENSG00000230404	RP5-855F14.2	1:234701043-234705834	NOTEST	0	0	0	0	1	1
ENSG00000230405	ENSG00000230405	RPS3AP52	13:69208321-69208618	NOTEST	0	0	0	0	1	1
ENSG00000230406	ENSG00000230406	AC079834.1	2:222457160-222457581	NOTEST	0	0	0	0	1	1
ENSG00000230407	ENSG00000230407	AC018717.2	2:199973306-199974811	NOTEST	0	0	0	0	1	1
ENSG00000230408	ENSG00000230408	AC007163.6	2:201542955-201688569	NOTEST	0	0	0	0	1	1
ENSG00000230410	ENSG00000230410	XXbac-B33L19.6	22:20326327-20350457	NOTEST	0	0	0	0	1	1
ENSG00000230411	ENSG00000230411	OR3D1P	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000230412	ENSG00000230412	TCEB1P12	Y:20230368-20230696	NOTEST	0	0	0	0	1	1
ENSG00000230413	ENSG00000230413	HLA-G	HSCHR6_MHC_COX:29788430-29792600	NOTEST	0	0	0	0	1	1
ENSG00000230414	ENSG00000230414	HLA-DQB1-AS1	HSCHR6_MHC_SSTO:32697727-32726026	NOTEST	0	0	0	0	1	1
ENSG00000230415	ENSG00000230415	RP5-902P8.10	1:1210602-1215800	NOTEST	0.38677	0.669888	0.792442	0	1	1
ENSG00000230416	ENSG00000230416	OR5M4P	11:56216143-56217068	NOTEST	0	0	0	0	1	1
ENSG00000230417	ENSG00000230417	LINC00856	10:80008504-80115857	NOTEST	0	0	0	0	1	1
ENSG00000230418	ENSG00000230418	ARL2BPP7	9:104817533-104818023	NOTEST	0	0	0	0	1	1
ENSG00000230419	ENSG00000230419	HCG4P7	HSCHR6_MHC_QBL:29846366-29849546	NOTEST	0	0	0	0	1	1
ENSG00000230422	ENSG00000230422	TMPOP1	HSCHR6_MHC_SSTO:30423331-30424869	NOTEST	0	0	0	0	1	1
ENSG00000230423	ENSG00000230423	XX-C2158C6.1	6:171044838-171046865	NOTEST	0	0	0	0	1	1
ENSG00000230424	ENSG00000230424	RP1-43E13.2	1:19536994-19586622	NOTEST	0.208842	0.11693	-0.836763	0	1	1
ENSG00000230425	ENSG00000230425	RSU1P1	10:43221304-43232607	NOTEST	0	0	0	0	1	1
ENSG00000230426	ENSG00000230426	ERVMER61-1	1:187610357-187612992	NOTEST	0	0	0	0	1	1
ENSG00000230427	ENSG00000230427	RP11-313A24.1	1:95439962-95538501	NOTEST	0	0	0	0	1	1
ENSG00000230428	ENSG00000230428	RP1-196A12.1	16:475618-573011	NOTEST	0	0	0	0	1	1
ENSG00000230430	ENSG00000230430	USP17L25	4:9331636-9333229	NOTEST	0	0	0	0	1	1
ENSG00000230432	ENSG00000230432	AC114803.3	2:220154344-220174370	NOTEST	0.203418	0.082056	-1.30976	0	1	1
ENSG00000230433	ENSG00000230433	RP1-20B11.2	6:485132-693117	NOTEST	0.0436861	0.0169899	-1.3625	0	1	1
ENSG00000230434	ENSG00000230434	RP11-14O19.1	1:95816806-95817810	NOTEST	0	0	0	0	1	1
ENSG00000230435	ENSG00000230435	AC004160.4	7:11221358-11871824	NOTEST	0	0	0	0	1	1
ENSG00000230437	ENSG00000230437	RP11-102J14.1	20:12286260-12297133	NOTEST	0	0	0	0	1	1
ENSG00000230438	ENSG00000230438	RP11-420G6.4	6:2854895-2881641	NOTEST	0	0.00871462	inf	0	1	1
ENSG00000230439	ENSG00000230439	RP11-488P3.1	1:94027346-94312706	NOTEST	0.168999	0.208701	0.304422	0	1	1
ENSG00000230440	ENSG00000230440	RP13-329D4.3	20:26113522-26114834	NOTEST	0	0	0	0	1	1
ENSG00000230441	ENSG00000230441	UBQLN1P1	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000230442	ENSG00000230442	RP11-390E23.3	7:123207063-123277951	NOTEST	0	0	0	0	1	1
ENSG00000230444	ENSG00000230444	TFAMP1	7:1654225-1654961	NOTEST	0	0	0	0	1	1
ENSG00000230445	ENSG00000230445	LRRC37A6P	10:27532058-27577753	NOTEST	0.100946	0.195248	0.951729	0	1	1
ENSG00000230446	ENSG00000230446	RP11-423O2.3	1:142790232-142790520	NOTEST	0.124161	0.089753	-0.468185	0	1	1
ENSG00000230447	ENSG00000230447	CTF2P	16:30915668-30921529	NOTEST	0	0	0	0	1	1
ENSG00000230448	ENSG00000230448	LINC00276	2:13850655-14541087	NOTEST	0	0	0	0	1	1

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ENSG00000230449	ENSG00000230449	RPL7P4	6:30664582-30665312	NOTEST	0	0	0	0	1	1
ENSG00000230450	ENSG00000230450	NEK2P4	2:131862419-132111282	NOTEST	0	0.00997479	inf	0	1	1
ENSG00000230451	ENSG00000230451	RPS29P6	1:37796452-37796597	NOTEST	0	0	0	0	1	1
ENSG00000230452	ENSG00000230452	AC012457.2	2:25427181-25432071	NOTEST	0	0	0	0	1	1
ENSG00000230455	ENSG00000230455	BMS1P14	9:42808659-42812274	NOTEST	0	0	0	0	1	1
ENSG00000230456	ENSG00000230456	DDR1	HSCHR6_MHC_DBB:30839457-30858654	NOTEST	0	0	0	0	1	1
ENSG00000230457	ENSG00000230457	PA2G4P4	3:156465134-156534851	NOTEST	0.200393	0.108908	-0.879724	0	1	1
ENSG00000230458	ENSG00000230458	GPM6BP1	Y:20652800-20790963	NOTEST	0	0	0	0	1	1
ENSG00000230459	ENSG00000230459	RP11-741G21.1	15:77400470-77712486	NOTEST	0	0	0	0	1	1
ENSG00000230461	ENSG00000230461	PROX1-AS1	1:213991093-214214595	NOTEST	0.00534369	0	#NAME?	0	1	1
ENSG00000230463	ENSG00000230463	HLA-DRB3$0301	HSCHR6_MHC_APD:32470407-32484153	NOTEST	0	0	0	0	1	1
ENSG00000230465	ENSG00000230465	VENTXP4	3:26388171-26389129	NOTEST	0	0	0	0	1	1
ENSG00000230467	ENSG00000230467	RNF39	HSCHR6_MHC_SSTO:30024067-30033246	NOTEST	0	0	0	0	1	1
ENSG00000230468	ENSG00000230468	CLUHP5	10:135470738-135474139	NOTEST	0	0	0	0	1	1
ENSG00000230469	ENSG00000230469	RPL5P26	10:71538717-71539594	NOTEST	0	0	0	0	1	1
ENSG00000230470	ENSG00000230470	GS1-115G20.1	1:184356191-184598154	NOTEST	0	0	0	0	1	1
ENSG00000230471	ENSG00000230471	LA16c-2F2.8	22:16373080-16377055	NOTEST	0	0	0	0	1	1
ENSG00000230472	ENSG00000230472	RP1-28O17.1	6:50555319-50604918	NOTEST	0	0	0	0	1	1
ENSG00000230474	ENSG00000230474	ATP6V1G1P7	13:104096969-104097318	NOTEST	0	0	0	0	1	1
ENSG00000230475	ENSG00000230475	ABHD16A	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000230476	ENSG00000230476	OFD1P9Y	Y:24727135-24760228	NOTEST	0	0	0	0	1	1
ENSG00000230477	ENSG00000230477	AC005034.2	2:75825196-75825685	NOTEST	0	0	0	0	1	1
ENSG00000230478	ENSG00000230478	RP1-52D1.1	X:86680585-86680693	NOTEST	0	0	0	0	1	1
ENSG00000230479	ENSG00000230479	AP000695.6	21:37802657-37948867	NOTEST	0	0	0	0	1	1
ENSG00000230480	ENSG00000230480	AC093142.2	3:28390636-28579613	NOTEST	0	0	0	0	1	1
ENSG00000230481	ENSG00000230481	IGKV1OR22-5	22:17385108-17385586	NOTEST	0	0	0	0	1	1
ENSG00000230482	ENSG00000230482	ATP5G2P3	2:197831740-198175897	NOTEST	0	0	0	0	1	1
ENSG00000230483	ENSG00000230483	AC124057.5	11:2425744-2444275	NOTEST	0	0	0	0	1	1
ENSG00000230484	ENSG00000230484	OR51A10P	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000230485	ENSG00000230485	AC000077.2	22:19618272-19621097	NOTEST	0	0	0	0	1	1
ENSG00000230489	ENSG00000230489	VAV3-AS1	1:108113781-108537229	NOTEST	0	0	0	0	1	1
ENSG00000230491	ENSG00000230491	RP13-228J13.10	X:154505499-154563966	NOTEST	0	0	0	0	1	1
ENSG00000230492	ENSG00000230492	RP4-753D10.5	20:22990845-23011422	NOTEST	0	0	0	0	1	1
ENSG00000230493	ENSG00000230493	AC106017.1	17:19118927-19240028	NOTEST	0	0	0	0	1	1
ENSG00000230495	ENSG00000230495	RP11-462D18.2	20:17550507-17590564	NOTEST	0	0	0	0	1	1
ENSG00000230496	ENSG00000230496	AC068137.6	2:131033164-131033830	NOTEST	0	0	0	0	1	1
ENSG00000230497	ENSG00000230497	RP11-432A8.2	3:174156362-175523428	NOTEST	0	0	0	0	1	1
ENSG00000230498	ENSG00000230498	RP4-564M11.2	1:77533604-77544167	NOTEST	0	0	0	0	1	1
ENSG00000230500	ENSG00000230500	RP11-360I20.2	10:27961803-28056723	NOTEST	0	0	0	0	1	1
ENSG00000230501	ENSG00000230501	ANKRD30BP3	10:45493145-45676875	NOTEST	0	0	0	0	1	1
ENSG00000230502	ENSG00000230502	CTD-2230M5.1	X:113623440-113624407	NOTEST	0	0	0	0	1	1
ENSG00000230504	ENSG00000230504	HCG4P8	HSCHR6_MHC_SSTO:29791437-29795610	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000230505	ENSG00000230505	OR10C1	HSCHR6_MHC_APD:29390470-29424928	NOTEST	0	0	0	0	1	1
ENSG00000230506	ENSG00000230506	RP11-416N4.4	20:9966735-10349424	NOTEST	0	0	0	0	1	1
ENSG00000230507	ENSG00000230507	RPL7AP8	10:88390581-88391385	NOTEST	0	0	0	0	1	1
ENSG00000230508	ENSG00000230508	RPL19P21	X:150161973-150162564	NOTEST	0	0	0	0	1	1
ENSG00000230509	ENSG00000230509	HLA-N	HSCHR6_MHC_DBB:30309449-30309584	NOTEST	0	0	0	0	1	1
ENSG00000230510	ENSG00000230510	PPP5D1	19:46984052-47114050	NOTEST	0.383128	0.210255	-0.865687	0	1	1
ENSG00000230511	ENSG00000230511	NOL5BP	HSCHR6_MHC_DBB:28751413-28751785	NOTEST	0	0	0	0	1	1
ENSG00000230513	ENSG00000230513	THAP7-AS1	22:21353392-21399306	NOTEST	0.598588	0.333665	-0.843161	0	1	1
ENSG00000230514	ENSG00000230514	AGER	HSCHR6_MHC_MCF:32225174-32228531	NOTEST	0	0	0	0	1	1
ENSG00000230515	ENSG00000230515	AC092580.3	2:7811734-7812377	NOTEST	0	0	0	0	1	1
ENSG00000230516	ENSG00000230516	RP11-555J4.3	9:32629451-32648683	NOTEST	0	0	0	0	1	1
ENSG00000230519	ENSG00000230519	RP11-1060J15.5	12:27849320-27863703	NOTEST	0	0.0264518	inf	0	1	1
ENSG00000230520	ENSG00000230520	RP11-533K11.1	7:118590439-118591313	NOTEST	0	0	0	0	1	1
ENSG00000230521	ENSG00000230521	HCG4P7	6:29855070-29858259	NOTEST	0.0783817	0.0724657	-0.113218	0	1	1
ENSG00000230522	ENSG00000230522	MBD3L2	19:7049331-7051746	NOTEST	0	0	0	0	1	1
ENSG00000230523	ENSG00000230523	RP3-437I16.1	1:29656131-29676626	NOTEST	0	0	0	0	1	1
ENSG00000230524	ENSG00000230524	COL6A4P1	3:15193339-15247466	NOTEST	0	0	0	0	1	1
ENSG00000230525	ENSG00000230525	AC007403.2	2:67131567-67198594	NOTEST	0.130789	0	#NAME?	0	1	1
ENSG00000230526	ENSG00000230526	RP11-472G21.2	10:73638113-73638865	NOTEST	0.401895	0.187403	-1.10068	0	1	1
ENSG00000230528	ENSG00000230528	NOS2P3	17:20339649-20350557	NOTEST	0	0	0	0	1	1
ENSG00000230529	ENSG00000230529	CEACAMP9	19:43600607-43601512	NOTEST	0	0.138843	inf	0	1	1
ENSG00000230531	ENSG00000230531	MTND5P7	7:57261963-57263761	NOTEST	0	0	0	0	1	1
ENSG00000230532	ENSG00000230532	AC091133.1	17:47006677-47022479	NOTEST	0	0	0	0	1	1
ENSG00000230533	ENSG00000230533	RP11-95M15.1	6:137994596-137995691	NOTEST	0	0	0	0	1	1
ENSG00000230534	ENSG00000230534	RP11-297A16.2	10:35386933-35501886	NOTEST	0	0	0	0	1	1
ENSG00000230535	ENSG00000230535	BASP1P1	13:23468794-23490662	NOTEST	0	0	0	0	1	1
ENSG00000230536	ENSG00000230536	RP11-379C10.4	9:130823511-130871604	NOTEST	0.141785	0.0371368	-1.93278	0	1	1
ENSG00000230537	ENSG00000230537	RP11-305L7.1	9:93867238-93869586	NOTEST	0.111452	0.0162773	-2.7755	0	1	1
ENSG00000230538	ENSG00000230538	RP3-428A13.1	X:126524323-126526508	NOTEST	0	0.0058754	inf	0	1	1
ENSG00000230539	ENSG00000230539	AOAH-IT1	7:36552455-36764154	NOTEST	0	0	0	0	1	1
ENSG00000230541	ENSG00000230541	HCG21	HSCHR6_MHC_QBL:30898352-30912213	NOTEST	0	0	0	0	1	1
ENSG00000230542	ENSG00000230542	LINC00102	X:2527388-2575270	NOTEST	0	0	0	0	1	1
ENSG00000230543	ENSG00000230543	SNX3P1X	X:91034259-91878229	NOTEST	0	0	0	0	1	1
ENSG00000230545	ENSG00000230545	DAQB-335A13.8	HSCHR6_MHC_SSTO:29687513-29713718	NOTEST	0	0	0	0	1	1
ENSG00000230546	ENSG00000230546	RP11-393I23.3	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000230547	ENSG00000230547	HMGB1P11	1:171216718-171255117	NOTEST	0	0	0	0	1	1
ENSG00000230548	ENSG00000230548	MTND4P27	2:131036329-131037683	NOTEST	0	0	0	0	1	1
ENSG00000230549	ENSG00000230549	USP17L1P	8:7159132-7212876	NOTEST	0	0	0	0	1	1
ENSG00000230550	ENSG00000230550	RP11-74C13.3	1:204100189-204121307	NOTEST	0.0466565	0.0109517	-2.09093	0	1	1
ENSG00000230552	ENSG00000230552	AC092162.1	2:177588995-177684038	NOTEST	0.00925159	0	#NAME?	0	1	1
ENSG00000230553	ENSG00000230553	RP11-481A12.2	10:51535125-51535474	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000230555	ENSG00000230555	RP11-517P14.2	10:43916185-43917548	NOTEST	0.222814	0.167732	-0.409681	0	1	1
ENSG00000230556	ENSG00000230556	AC073264.6	7:143275999-143276165	NOTEST	0	0	0	0	1	1
ENSG00000230558	ENSG00000230558	CEACAMP2	19:42901279-43156507	NOTEST	0	0	0	0	1	1
ENSG00000230559	ENSG00000230559	RPL17P12	2:146951863-146952389	NOTEST	0	0	0	0	1	1
ENSG00000230561	ENSG00000230561	CTC-228N24.1	5:127039081-127418864	NOTEST	0	0	0	0	1	1
ENSG00000230563	ENSG00000230563	RP5-828H9.1	20:5451852-5455828	NOTEST	0	0	0	0	1	1
ENSG00000230564	ENSG00000230564	CALM1P2	7:55327501-55327949	NOTEST	0	0	0	0	1	1
ENSG00000230565	ENSG00000230565	ZNF32-AS2	10:44124264-44170151	NOTEST	0.144627	0.142272	-0.0236865	0	1	1
ENSG00000230567	ENSG00000230567	FAM203B	8:145437879-145440835	NOTEST	0	0	0	0	1	1
ENSG00000230568	ENSG00000230568	SF3A3P1	20:3451686-3631769	NOTEST	0	0	0	0	1	1
ENSG00000230569	ENSG00000230569	AC114763.1	2:139175853-139259268	NOTEST	0	0	0	0	1	1
ENSG00000230570	ENSG00000230570	RP11-69L16.6	6:7268538-7418270	NOTEST	0	0	0	0	1	1
ENSG00000230571	ENSG00000230571	CTD-2533K21.3	5:26669454-26670098	NOTEST	0	0	0	0	1	1
ENSG00000230572	ENSG00000230572	AC027612.3	2:91872472-91902771	NOTEST	0	0	0	0	1	1
ENSG00000230573	ENSG00000230573	RP11-464C19.2	10:3876141-3876920	NOTEST	0	0	0	0	1	1
ENSG00000230574	ENSG00000230574	NOL5BP	HSCHR6_MHC_COX:28752232-28752604	NOTEST	0	0	0	0	1	1
ENSG00000230575	ENSG00000230575	RP11-369F10.2	10:77360997-78320752	NOTEST	0	0	0	0	1	1
ENSG00000230576	ENSG00000230576	OR6R1P	1:247996650-247997590	NOTEST	0	0	0	0	1	1
ENSG00000230578	ENSG00000230578	RP13-228J13.5	X:154564166-154581271	NOTEST	0.11641	0.216592	0.895759	0	1	1
ENSG00000230580	ENSG00000230580	AC021016.7	2:219135114-219232822	NOTEST	0	0	0	0	1	1
ENSG00000230581	ENSG00000230581	RP11-390F4.8	9:6716547-7175648	NOTEST	0.0440815	0.04867	0.142859	0	1	1
ENSG00000230582	ENSG00000230582	PPIAL4F	1:148806014-148806799	NOTEST	0	0	0	0	1	1
ENSG00000230583	ENSG00000230583	GTF2IRD1P1	7:66093867-66309813	NOTEST	0.015046	0.0127695	-0.236684	0	1	1
ENSG00000230584	ENSG00000230584	CCT5P2	13:79483053-79484677	NOTEST	0	0.00794347	inf	0	1	1
ENSG00000230585	ENSG00000230585	PHBP12	1:50905149-51425935	NOTEST	0.108388	0.0525509	-1.04442	0	1	1
ENSG00000230587	ENSG00000230587	AC093609.1	2:43324883-43329829	NOTEST	0	0	0	0	1	1
ENSG00000230589	ENSG00000230589	IMP3P1	9:10829751-10830308	NOTEST	0	0	0	0	1	1
ENSG00000230593	ENSG00000230593	AC090804.1	11:3875547-4114439	NOTEST	0	0.0328278	inf	0	1	1
ENSG00000230594	ENSG00000230594	CT47A4	X:120101745-120105058	NOTEST	0	0	0	0	1	1
ENSG00000230595	ENSG00000230595	RSL24D1P2	2:62788192-62788558	NOTEST	0	0	0	0	1	1
ENSG00000230596	ENSG00000230596	AC112229.4	2:111143953-111230652	NOTEST	0.0197768	0	#NAME?	0	1	1
ENSG00000230597	ENSG00000230597	RP3-331H24.4	6:71931159-72130472	NOTEST	0	0	0	0	1	1
ENSG00000230598	ENSG00000230598	OR2H4P	6:29183012-29183956	NOTEST	0	0	0	0	1	1
ENSG00000230599	ENSG00000230599	AC018495.3	3:10809148-10813403	NOTEST	0	0	0	0	1	1
ENSG00000230600	ENSG00000230600	RP11-73B2.2	7:62840843-62846167	NOTEST	0	0	0	0	1	1
ENSG00000230601	ENSG00000230601	RP11-402G3.3	9:117428715-117434029	NOTEST	0	0	0	0	1	1
ENSG00000230602	ENSG00000230602	HCG23	HSCHR6_MHC_MCF:32434446-32451073	NOTEST	0	0	0	0	1	1
ENSG00000230603	ENSG00000230603	AC011753.6	2:110422785-110423319	NOTEST	0	0	0	0	1	1
ENSG00000230604	ENSG00000230604	TSEN15P2	1:52027537-52344477	NOTEST	0	0	0	0	1	1
ENSG00000230605	ENSG00000230605	AC006326.5	7:116902971-116904942	NOTEST	0	0	0	0	1	1
ENSG00000230607	ENSG00000230607	AC005722.4	17:19658556-19659520	NOTEST	0	0	0	0	1	1
ENSG00000230609	ENSG00000230609	RP11-167P22.4	10:74127097-74385899	NOTEST	0	0	0	0	1	1

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ENSG00000230611	ENSG00000230611	HMGB1P27	2:192038958-192039561	NOTEST	0	0	0	0	1	1
ENSG00000230612	ENSG00000230612	AC004237.1	5:132024372-132073330	NOTEST	0	0	0	0	1	1
ENSG00000230613	ENSG00000230613	HM13-AS1	20:30102230-30161066	NOTEST	0.165129	0.290418	0.814533	0	1	1
ENSG00000230614	ENSG00000230614	AC073958.2	7:85010433-85010691	NOTEST	0	0	0	0	1	1
ENSG00000230615	ENSG00000230615	RP5-1198O20.4	1:44501797-44570647	NOTEST	0.583477	0.458729	-0.347033	0	1	1
ENSG00000230616	ENSG00000230616	PPIAP9	HSCHR6_MHC_APD:31498548-31499360	NOTEST	0	0	0	0	1	1
ENSG00000230617	ENSG00000230617	AC079987.2	7:82993221-83278326	NOTEST	0	0	0	0	1	1
ENSG00000230618	ENSG00000230618	H3F3AP3	3:109128524-109214014	NOTEST	0	0	0	0	1	1
ENSG00000230621	ENSG00000230621	AC080002.1	2:226857696-226857913	NOTEST	0	0	0	0	1	1
ENSG00000230622	ENSG00000230622	UQCRHP1	6:31578859-31579133	NOTEST	0	0	0	0	1	1
ENSG00000230623	ENSG00000230623	RP11-469A15.2	1:200443047-200447421	NOTEST	0	0	0	0	1	1
ENSG00000230624	ENSG00000230624	DDX39B	HSCHR6_MHC_DBB:31478677-31496802	NOTEST	0	0	0	0	1	1
ENSG00000230627	ENSG00000230627	RP1-155D22.1	6:164529651-164530726	NOTEST	0	0	0	0	1	1
ENSG00000230628	ENSG00000230628	RP4-781K5.6	1:234780411-234831900	NOTEST	0	0	0	0	1	1
ENSG00000230630	ENSG00000230630	DNM3OS	1:171810620-172437971	NOTEST	0.037418	0	#NAME?	0	1	1
ENSG00000230631	ENSG00000230631	RP11-359N11.1	6:14230005-14231801	NOTEST	0	0	0	0	1	1
ENSG00000230633	ENSG00000230633	RP11-37E23.5	13:32872290-32872849	NOTEST	0.0558093	0	#NAME?	0	1	1
ENSG00000230634	ENSG00000230634	RP5-996D20.3	22:46756730-46933067	NOTEST	0.0569128	0	#NAME?	0	1	1
ENSG00000230635	ENSG00000230635	CYP4F60P	9:44019595-44020591	NOTEST	0.0480644	0.037463	-0.3595	0	1	1
ENSG00000230636	ENSG00000230636	RPL36P1	20:51506700-51506925	NOTEST	0	0	0	0	1	1
ENSG00000230637	ENSG00000230637	CTA-246H3.8	22:25723218-25735942	NOTEST	0	0	0	0	1	1
ENSG00000230638	ENSG00000230638	RP11-486B10.4	1:41972035-42501596	NOTEST	0.00717243	0.0329323	2.19897	0	1	1
ENSG00000230639	ENSG00000230639	VN1R36P	7:63426211-63426502	NOTEST	0	0	0	0	1	1
ENSG00000230641	ENSG00000230641	USP12-AS2	13:27746395-27757135	NOTEST	0	0	0	0	1	1
ENSG00000230643	ENSG00000230643	LA16c-60G3.5	22:16389484-16389602	NOTEST	0	0	0	0	1	1
ENSG00000230645	ENSG00000230645	AC016682.1	2:151027936-151157594	NOTEST	0	0	0	0	1	1
ENSG00000230646	ENSG00000230646	KLF2P2	2:131174327-131199048	NOTEST	0	0	0	0	1	1
ENSG00000230647	ENSG00000230647	AC022816.2	17:14277455-14324343	NOTEST	0	0	0	0	1	1
ENSG00000230648	ENSG00000230648	RP3-406P24.3	6:4018946-4021449	NOTEST	0.305867	0	#NAME?	0	1	1
ENSG00000230649	ENSG00000230649	AC024084.1	7:135710508-135769416	NOTEST	0	0	0	0	1	1
ENSG00000230650	ENSG00000230650	AC112229.1	2:111118184-111121314	NOTEST	0.00501883	0	#NAME?	0	1	1
ENSG00000230651	ENSG00000230651	RGPD4-AS1	2:108439518-108443347	NOTEST	0	0	0	0	1	1
ENSG00000230654	ENSG00000230654	RP11-666G4.2	7:68689682-68895909	NOTEST	0	0	0	0	1	1
ENSG00000230655	ENSG00000230655	OR7E55P	3:75419598-75420493	NOTEST	0	0	0	0	1	1
ENSG00000230657	ENSG00000230657	PRB4	12:11460016-11463369	NOTEST	0	0	0	0	1	1
ENSG00000230659	ENSG00000230659	RP11-466F5.9	1:165696031-165880855	NOTEST	0	0	0	0	1	1
ENSG00000230660	ENSG00000230660	HCG18	HSCHR6_MHC_MANN:30246906-30359341	NOTEST	0	0	0	0	1	1
ENSG00000230661	ENSG00000230661	YY1P1	10:72238576-72328205	NOTEST	0	0	0	0	1	1
ENSG00000230662	ENSG00000230662	TNPO1P2	17:18353557-18379234	NOTEST	0	0	0	0	1	1
ENSG00000230663	ENSG00000230663	FAM224B	Y:19664679-19691634	NOTEST	0	0	0	0	1	1
ENSG00000230665	ENSG00000230665	PRKRIRP1	X:73616705-73619385	NOTEST	0	0.00513429	inf	0	1	1
ENSG00000230666	ENSG00000230666	CEACAM22P	19:45041044-45222031	NOTEST	0	0.0125806	inf	0	1	1

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ENSG00000230667	ENSG00000230667	SETSIP	1:92540089-92540968	NOTEST	0.0210239	0.0148284	-0.50367	0	1	1
ENSG00000230668	ENSG00000230668	XXyac-YR29IB3.1	X:139763270-139769870	NOTEST	0	0	0	0	1	1
ENSG00000230669	ENSG00000230669	PSMB8	HSCHR6_MHC_APD:32792100-32831197	NOTEST	0	0	0	0	1	1
ENSG00000230671	ENSG00000230671	NDUFS5P5	4:119321668-119321989	NOTEST	0	0	0	0	1	1
ENSG00000230673	ENSG00000230673	PABPC1P3	X:73802922-73803381	NOTEST	0.148133	0.346786	1.22715	0	1	1
ENSG00000230674	ENSG00000230674	LINC01015	HSCHR6_MHC_COX:29493784-29497933	NOTEST	0	0	0	0	1	1
ENSG00000230675	ENSG00000230675	HLA-DQB2	HSCHR6_MHC_APD:32708755-32716212	NOTEST	0	0	0	0	1	1
ENSG00000230676	ENSG00000230676	RP11-65J3.3	9:132192930-132213701	NOTEST	0.0515605	0	#NAME?	0	1	1
ENSG00000230678	ENSG00000230678	BRD2	HSCHR6_MHC_DBB:32923567-32927227	NOTEST	0	0	0	0	1	1
ENSG00000230679	ENSG00000230679	ENO1-AS1	1:8921060-8939953	NOTEST	0.201832	0.329794	0.708409	0	1	1
ENSG00000230680	ENSG00000230680	AC004869.2	7:46516054-46521176	NOTEST	0	0	0	0	1	1
ENSG00000230681	ENSG00000230681	CEACAMP4	19:43807322-43808675	NOTEST	0	0	0	0	1	1
ENSG00000230682	ENSG00000230682	GRPEL2P3	7:94412197-94412837	NOTEST	0	0	0	0	1	1
ENSG00000230683	ENSG00000230683	DDTP1	3:38537617-38583652	NOTEST	0.139824	0.0545967	-1.35673	0	1	1
ENSG00000230684	ENSG00000230684	RP11-409K20.6	9:132649465-132805473	NOTEST	0	0	0	0	1	1
ENSG00000230685	ENSG00000230685	CLIC1	HSCHR6_MHC_COX:31682227-31694945	NOTEST	0	0	0	0	1	1
ENSG00000230686	ENSG00000230686	AC067945.2	2:191745522-191885686	NOTEST	0	0	0	0	1	1
ENSG00000230687	ENSG00000230687	RP5-1114G22.2	1:175172363-175173985	NOTEST	0	0	0	0	1	1
ENSG00000230690	ENSG00000230690	AC013402.5	2:105275794-105281295	NOTEST	0	0.119047	inf	0	1	1
ENSG00000230691	ENSG00000230691	MRPL35P4	X:12862983-12863549	NOTEST	0	0	0	0	1	1
ENSG00000230694	ENSG00000230694	RP11-62F24.1	9:16409500-16870841	NOTEST	0	0	0	0	1	1
ENSG00000230695	ENSG00000230695	AC012462.1	2:216300975-216301715	NOTEST	0	0	0	0	1	1
ENSG00000230696	ENSG00000230696	AC011753.5	2:110300558-110371783	NOTEST	0	0	0	0	1	1
ENSG00000230697	ENSG00000230697	AC097635.4	3:19988570-20053822	NOTEST	0.25658	0.0470919	-2.44586	0	1	1
ENSG00000230698	ENSG00000230698	CTD-2330K9.2	3:49924434-49967606	NOTEST	0	0.00159776	inf	0	1	1
ENSG00000230699	ENSG00000230699	RP11-54O7.1	1:840213-851356	NOTEST	0.00517087	0.0430759	3.0584	0	1	1
ENSG00000230700	ENSG00000230700	CSNK2B	HSCHR6_MHC_DBB:31611187-31653368	NOTEST	0	0	0	0	1	1
ENSG00000230701	ENSG00000230701	FBXW4P1	22:23521890-23660224	NOTEST	0.0141719	0.0532162	1.90884	0	1	1
ENSG00000230702	ENSG00000230702	RP11-681L4.1	2:62083829-62084190	NOTEST	0.0778829	0	#NAME?	0	1	1
ENSG00000230703	ENSG00000230703	RP11-293P20.4	1:24367324-24438665	NOTEST	0	0	0	0	1	1
ENSG00000230704	ENSG00000230704	RP1-117P20.3	1:169631244-169863408	NOTEST	0	0	0	0	1	1
ENSG00000230705	ENSG00000230705	TAP1	HSCHR6_MHC_MCF:32841973-32881069	NOTEST	0	0	0	0	1	1
ENSG00000230706	ENSG00000230706	RP5-998G20.1	X:87316590-87317845	NOTEST	0	0	0	0	1	1
ENSG00000230707	ENSG00000230707	RP11-364B14.3	X:139173901-139174720	NOTEST	0	0	0	0	1	1
ENSG00000230708	ENSG00000230708	HLA-DPB1	HSCHR6_MHC_COX:32954321-32976889	NOTEST	0	0	0	0	1	1
ENSG00000230709	ENSG00000230709	AC104024.1	17:16879312-16884667	NOTEST	0	0	0	0	1	1
ENSG00000230710	ENSG00000230710	LINC00332	13:40755945-40763165	NOTEST	0	0	0	0	1	1
ENSG00000230711	ENSG00000230711	CTAGE13P	6:168687584-168690030	NOTEST	0	0	0	0	1	1
ENSG00000230712	ENSG00000230712	AP000354.4	22:24644041-24645434	NOTEST	0	0	0	0	1	1
ENSG00000230714	ENSG00000230714	RP11-152L7.1	1:218205176-218207002	NOTEST	0	0	0	0	1	1
ENSG00000230716	ENSG00000230716	KRT8P7	11:119473586-119475018	NOTEST	0	0	0	0	1	1
ENSG00000230718	ENSG00000230718	RP11-272L13.2	1:97543298-98386605	NOTEST	0	0	0	0	1	1

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ENSG00000230721	ENSG00000230721	RP4-612B15.2	1:87250595-87251150	NOTEST	0.325652	0.244533	-0.413301	0	1	1
ENSG00000230722	ENSG00000230722	IFITM4P	HSCHR6_MHC_QBL:29715968-29716389	NOTEST	0	0	0	0	1	1
ENSG00000230725	ENSG00000230725	RP4-738P15.1	20:25121424-25129894	NOTEST	0	0	0	0	1	1
ENSG00000230726	ENSG00000230726	HLA-DRA	HSCHR6_MHC_MCF:32482995-32488206	NOTEST	0	0	0	0	1	1
ENSG00000230727	ENSG00000230727	RBMY2WP	Y:24908997-24915934	NOTEST	0	0	0	0	1	1
ENSG00000230728	ENSG00000230728	RP11-240D10.4	1:55007929-55104865	NOTEST	0	0	0	0	1	1
ENSG00000230729	ENSG00000230729	RP11-296L22.8	9:34521037-34524239	NOTEST	0	0	0	0	1	1
ENSG00000230730	ENSG00000230730	AC074011.2	2:28680011-28887406	NOTEST	0	0	0	0	1	1
ENSG00000230731	ENSG00000230731	RP11-478K15.6	13:44716681-44817328	NOTEST	0.00469216	0.00364502	-0.364325	0	1	1
ENSG00000230732	ENSG00000230732	AC127904.2	3:196594726-196661585	NOTEST	0.102391	0.155503	0.602857	0	1	1
ENSG00000230734	ENSG00000230734	RPL10P3	9:119187503-120177348	NOTEST	0.0500021	0	#NAME?	0	1	1
ENSG00000230735	ENSG00000230735	RP11-413E1.4	1:89990394-90402170	NOTEST	0	0	0	0	1	1
ENSG00000230736	ENSG00000230736	RP1-149A16.3	22:32750871-32781618	NOTEST	0.0777338	0.155219	0.997689	0	1	1
ENSG00000230737	ENSG00000230737	AC106870.1	2:29415639-30144432	NOTEST	0	0	0	0	1	1
ENSG00000230739	ENSG00000230739	RP11-331H2.4	1:162794247-162838605	NOTEST	0	0	0	0	1	1
ENSG00000230741	ENSG00000230741	SC22CB-1D7.1	22:33558211-34318829	NOTEST	0	0	0	0	1	1
ENSG00000230742	ENSG00000230742	OR5V1	HSCHR6_MHC_DBB:29341258-29424782	NOTEST	0	0	0	0	1	1
ENSG00000230745	ENSG00000230745	MICD	HSCHR6_MHC_MANN:29933757-29935421	NOTEST	0	0	0	0	1	1
ENSG00000230746	ENSG00000230746	AC006007.1	7:145372974-145378462	NOTEST	0	0	0	0	1	1
ENSG00000230747	ENSG00000230747	AC021188.4	2:96973000-96987469	NOTEST	0.0522106	0.0184397	-1.50153	0	1	1
ENSG00000230748	ENSG00000230748	RP11-541H12.1	1:165446077-165551713	NOTEST	0	0.0790364	inf	0	1	1
ENSG00000230749	ENSG00000230749	MEIS1-AS2	2:66653866-66801001	NOTEST	0	0.0632668	inf	0	1	1
ENSG00000230750	ENSG00000230750	SDAD1P2	20:10366426-10368454	NOTEST	0	0	0	0	1	1
ENSG00000230751	ENSG00000230751	AC007036.4	7:30174425-30202378	NOTEST	0	0	0	0	1	1
ENSG00000230752	ENSG00000230752	OR2U1P	HSCHR6_MHC_SSTO:29191822-29234926	NOTEST	0	0	0	0	1	1
ENSG00000230753	ENSG00000230753	RP4-553F4.6	20:32316736-32398903	NOTEST	0.0948656	0	#NAME?	0	1	1
ENSG00000230754	ENSG00000230754	OR2U2P	HSCHR6_MHC_APD:29236292-29237252	NOTEST	0	0	0	0	1	1
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ENSG00000230757	ENSG00000230757	NFU1P1	3:39685128-39686196	NOTEST	0	0	0	0	1	1
ENSG00000230758	ENSG00000230758	SNAP23P	20:47654893-47655139	NOTEST	0	0	0	0	1	1
ENSG00000230759	ENSG00000230759	RP11-153F1.2	1:103957500-104068105	NOTEST	0	0	0	0	1	1
ENSG00000230761	ENSG00000230761	RP11-342C24.8	10:46797867-46809021	NOTEST	0	0	0	0	1	1
ENSG00000230763	ENSG00000230763	HLA-DPB1	HSCHR6_MHC_MCF:33065821-33088426	NOTEST	0	0	0	0	1	1
ENSG00000230764	ENSG00000230764	MTND1P4	7:57253494-57253909	NOTEST	0	0	0	0	1	1
ENSG00000230768	ENSG00000230768	RP11-251P6.1	1:106130196-106161580	NOTEST	0	0	0	0	1	1
ENSG00000230769	ENSG00000230769	RP3-408N23.4	22:41165633-41215403	NOTEST	0	0.072345	inf	0	1	1
ENSG00000230772	ENSG00000230772	VN1R108P	20:25714899-25715729	NOTEST	0.349234	0.188357	-0.890727	0	1	1
ENSG00000230773	ENSG00000230773	AC079807.4	2:48168834-48468122	NOTEST	0	0	0	0	1	1
ENSG00000230777	ENSG00000230777	RP11-318C24.1	1:175891110-175891281	NOTEST	0	0	0	0	1	1
ENSG00000230778	ENSG00000230778	ANKRD63	15:40570376-40600136	NOTEST	0	0	0	0	1	1
ENSG00000230779	ENSG00000230779	RP1-140J1.4	1:153197555-153198482	NOTEST	0	0	0	0	1	1

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ENSG00000230781	ENSG00000230781	RP1-215K18.4	X:84228222-84232835	NOTEST	0	0	0	0	1	1
ENSG00000230782	ENSG00000230782	RP11-508N12.2	9:109625377-109865269	NOTEST	0	0.00495524	inf	0	1	1
ENSG00000230783	ENSG00000230783	AC009961.2	2:160527218-160568946	NOTEST	0	0	0	0	1	1
ENSG00000230785	ENSG00000230785	AC006326.3	7:116902971-116904942	NOTEST	0	0	0	0	1	1
ENSG00000230787	ENSG00000230787	PSAT1P3	1:79520629-79521740	NOTEST	0	0	0	0	1	1
ENSG00000230788	ENSG00000230788	RP11-560L11.1	X:105314471-105317193	NOTEST	0	0	0	0	1	1
ENSG00000230789	ENSG00000230789	ARHGAP26-IT1	5:142149948-142608576	NOTEST	0	0	0	0	1	1
ENSG00000230790	ENSG00000230790	AC012456.4	2:11817720-11967535	NOTEST	0.0706371	0	#NAME?	0	1	1
ENSG00000230791	ENSG00000230791	LST1	HSCHR6_MHC_SSTO:31543844-31550705	NOTEST	0	0	0	0	1	1
ENSG00000230793	ENSG00000230793	SMARCE1P5	13:45168993-45170218	NOTEST	0	0	0	0	1	1
ENSG00000230794	ENSG00000230794	AF015720.3	21:36160097-37376965	NOTEST	0	0	0	0	1	1
ENSG00000230795	ENSG00000230795	HLA-K	6:29893759-29897009	NOTEST	0.114015	0.22097	0.954633	0	1	1
ENSG00000230796	ENSG00000230796	RP11-368M16.9	7:57710086-57710825	NOTEST	0	0	0	0	1	1
ENSG00000230799	ENSG00000230799	AC007279.2	2:202565276-202645912	NOTEST	0.185659	0.233751	0.332319	0	1	1
ENSG00000230801	ENSG00000230801	RP11-243J16.8	20:30396305-30396552	NOTEST	0	0	0	0	1	1
ENSG00000230803	ENSG00000230803	AC097532.2	2:133043367-133051950	NOTEST	0	0	0	0	1	1
ENSG00000230804	ENSG00000230804	RP11-216M21.2	9:42266979-42267558	NOTEST	0	0	0	0	1	1
ENSG00000230805	ENSG00000230805	AL132709.1	14:101540205-101544247	NOTEST	0	0	0	0	1	1
ENSG00000230806	ENSG00000230806	RP11-343N15.1	1:121102016-121204983	NOTEST	0.124577	0.0139714	-3.1565	0	1	1
ENSG00000230807	ENSG00000230807	AC099535.4	3:27527737-27528108	NOTEST	0	0	0	0	1	1
ENSG00000230809	ENSG00000230809	RP11-309P22.1	10:113257948-113258699	NOTEST	0	0	0	0	1	1
ENSG00000230812	ENSG00000230812	RP4-794H19.4	1:59486058-59510286	NOTEST	0.108483	0	#NAME?	0	1	1
ENSG00000230813	ENSG00000230813	RP11-690C23.5	1:246690331-246691457	NOTEST	0	0	0	0	1	1
ENSG00000230814	ENSG00000230814	USP9YP24	Y:24674427-24682786	NOTEST	0	0	0	0	1	1
ENSG00000230815	ENSG00000230815	RP11-49O14.3	9:97488982-97849441	NOTEST	0	0	0	0	1	1
ENSG00000230816	ENSG00000230816	COL11A2P1	HSCHR6_MHC_COX:32993450-32997006	NOTEST	0	0	0	0	1	1
ENSG00000230817	ENSG00000230817	RP4-601K24.1	1:83368865-83632498	NOTEST	0	0	0	0	1	1
ENSG00000230818	ENSG00000230818	MTND2P16	10:19492778-20079330	NOTEST	0	0	0	0	1	1
ENSG00000230819	ENSG00000230819	ZNF736P5Y	Y:27164645-27165450	NOTEST	0	0	0	0	1	1
ENSG00000230820	ENSG00000230820	AC000362.1	7:126078651-126893348	NOTEST	0	0	0	0	1	1
ENSG00000230821	ENSG00000230821	KB-288A10.17	22:22801023-22802674	NOTEST	0	0	0	0	1	1
ENSG00000230823	ENSG00000230823	CBX1P1	X:62519125-62519552	NOTEST	0	0	0	0	1	1
ENSG00000230825	ENSG00000230825	AC005532.5	7:7294784-7317410	NOTEST	0.131655	0.207171	0.654067	0	1	1
ENSG00000230826	ENSG00000230826	RP11-417B4.2	9:126118448-126692431	NOTEST	0	0	0	0	1	1
ENSG00000230828	ENSG00000230828	RP11-492I2.1	1:50513685-50669458	NOTEST	0	0	0	0	1	1
ENSG00000230829	ENSG00000230829	CTD-2186M15.1	5:32222037-32222453	NOTEST	0	0	0	0	1	1
ENSG00000230830	ENSG00000230830	ARPP21-AS1	3:35680436-35835988	NOTEST	0	0	0	0	1	1
ENSG00000230831	ENSG00000230831	AC007349.7	7:36878576-36880978	NOTEST	0	0	0	0	1	1
ENSG00000230832	ENSG00000230832	RP11-325P15.2	1:146490894-146596107	NOTEST	0.0643864	0.00976966	-2.72037	0	1	1
ENSG00000230833	ENSG00000230833	RPEP3	1:28052489-28089633	NOTEST	0	0	0	0	1	1

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ENSG00000230835	ENSG00000230835	AP001187.11	11:64619113-64655768	NOTEST	0	0	0	0	1	1
ENSG00000230837	ENSG00000230837	RPL31P2	20:32316736-32398903	NOTEST	0	0.168525	inf	0	1	1
ENSG00000230838	ENSG00000230838	AC093850.2	2:216395169-216708445	NOTEST	0	0	0	0	1	1
ENSG00000230839	ENSG00000230839	RP5-968J1.1	20:1784661-1798252	NOTEST	0	0	0	0	1	1
ENSG00000230840	ENSG00000230840	AC097463.2	2:51259738-52635055	NOTEST	0	0	0	0	1	1
ENSG00000230841	ENSG00000230841	RP5-915N17.3	1:228636863-228637322	NOTEST	0	0	0	0	1	1
ENSG00000230843	ENSG00000230843	RP11-380D15.3	20:54871022-54874216	NOTEST	0	0	0	0	1	1
ENSG00000230845	ENSG00000230845	RP11-392A23.5	6:52737811-52744738	NOTEST	0	0	0	0	1	1
ENSG00000230846	ENSG00000230846	RP11-383M4.2	9:84542935-84592004	NOTEST	0	0	0	0	1	1
ENSG00000230847	ENSG00000230847	RP11-195E2.1	5:70370051-70389020	NOTEST	0.395426	0.15539	-1.34752	0	1	1
ENSG00000230848	ENSG00000230848	RP11-379C10.1	9:130801413-130819641	NOTEST	0	0	0	0	1	1
ENSG00000230849	ENSG00000230849	GOT2P2	1:173110238-173111489	NOTEST	0.0250166	0	#NAME?	0	1	1
ENSG00000230851	ENSG00000230851	AP006294.2	11:3612506-3612845	NOTEST	0	0	0	0	1	1
ENSG00000230852	ENSG00000230852	RP11-51G5.1	6:84732773-84734272	NOTEST	0	0	0	0	1	1
ENSG00000230853	ENSG00000230853	AC004159.1	7:79725915-79726531	NOTEST	0	0	0	0	1	1
ENSG00000230854	ENSG00000230854	USP9YP20	Y:28069534-28075973	NOTEST	0	0	0	0	1	1
ENSG00000230855	ENSG00000230855	OR2J3	HSCHR6_MHC_MCF:29079817-29080591	NOTEST	0	0	0	0	1	1
ENSG00000230856	ENSG00000230856	AC138649.1	15:23157870-23158157	NOTEST	0	0	0	0	1	1
ENSG00000230857	ENSG00000230857	RP11-318K12.2	9:66693276-66759372	NOTEST	0	0	0	0	1	1
ENSG00000230859	ENSG00000230859	YRDCP3	21:42235919-42236399	NOTEST	0	0	0	0	1	1
ENSG00000230860	ENSG00000230860	CCNB1IP1P2	20:44179791-44207965	NOTEST	0	0	0	0	1	1
ENSG00000230863	ENSG00000230863	RP4-595K12.2	1:76107030-76107772	NOTEST	0	0.0367492	inf	0	1	1
ENSG00000230864	ENSG00000230864	RP5-936J12.1	1:103228877-103319398	NOTEST	0	0	0	0	1	1
ENSG00000230865	ENSG00000230865	TSEN15P1	17:17359740-17360573	NOTEST	0	0	0	0	1	1
ENSG00000230866	ENSG00000230866	CTA-342B11.2	22:32366809-32369462	NOTEST	0	0	0	0	1	1
ENSG00000230867	ENSG00000230867	RP11-462B18.1	9:32727066-32727520	NOTEST	0	0	0	0	1	1
ENSG00000230869	ENSG00000230869	CTGLF10P	10:46174139-46195980	NOTEST	0.128707	0.0330754	-1.96026	0	1	1
ENSG00000230870	ENSG00000230870	FBXW11P1	21:32999439-33000913	NOTEST	0.098385	0.0160333	-2.61736	0	1	1
ENSG00000230871	ENSG00000230871	RPS6P23	13:99825846-99826744	NOTEST	0	0	0	0	1	1
ENSG00000230872	ENSG00000230872	AC092338.5	16:22357256-22547842	NOTEST	0.03982	0.0289995	-0.457465	0	1	1
ENSG00000230873	ENSG00000230873	STMND1	6:17102488-17131603	NOTEST	0	0	0	0	1	1
ENSG00000230874	ENSG00000230874	OR2G1P	HSCHR6_MHC_SSTO:29191822-29234926	NOTEST	0	0	0	0	1	1
ENSG00000230876	ENSG00000230876	LINC00486	2:33050509-33151760	NOTEST	0	0	0	0	1	1
ENSG00000230878	ENSG00000230878	HLA-DPA2	HSCHR6_MHC_MCF:33092977-33098520	NOTEST	0	0	0	0	1	1
ENSG00000230879	ENSG00000230879	RBMX2P4	7:12962169-12962545	NOTEST	0	0	0	0	1	1
ENSG00000230881	ENSG00000230881	RP11-486B10.3	1:41972035-42501596	NOTEST	0	0	0	0	1	1
ENSG00000230882	ENSG00000230882	AC005077.14	7:75700786-75704281	NOTEST	0.0537527	0.0602063	0.163577	0	1	1
ENSG00000230885	ENSG00000230885	MOG	HSCHR6_MHC_MANN:29624320-29639709	NOTEST	0	0	0	0	1	1
ENSG00000230886	ENSG00000230886	HMGB1P25	2:9158421-9159028	NOTEST	0	0	0	0	1	1
ENSG00000230887	ENSG00000230887	MICC	HSCHR6_MHC_MCF:30460940-30465545	NOTEST	0	0	0	0	1	1
ENSG00000230888	ENSG00000230888	SUMO2P1	HSCHR6_MHC_MCF:29603635-29603919	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000230891	ENSG00000230891	LINC00692	3:25900023-25915191	NOTEST	0	0	0	0	1	1
ENSG00000230894	ENSG00000230894	RP11-67K19.3	9:119187503-120177348	NOTEST	0.00555351	0.00216093	-1.36174	0	1	1
ENSG00000230897	ENSG00000230897	RPS18P12	17:14608392-14608851	NOTEST	0.444398	0.520339	0.227598	0	1	1
ENSG00000230898	ENSG00000230898	RP11-9L18.3	1:166026673-166136206	NOTEST	0	0	0	0	1	1
ENSG00000230899	ENSG00000230899	MAGEA8-AS1	X:149007635-149009870	NOTEST	0	0	0	0	1	1
ENSG00000230900	ENSG00000230900	ATP6V1G2	HSCHR6_MHC_MCF:31572847-31602942	NOTEST	0	0	0	0	1	1
ENSG00000230902	ENSG00000230902	FAM204CP	13:76123618-76434004	NOTEST	0	0	0	0	1	1
ENSG00000230904	ENSG00000230904	XKRYP2	Y:20835918-20991373	NOTEST	0	0	0	0	1	1
ENSG00000230906	ENSG00000230906	AC023115.1	2:67313577-67523207	NOTEST	0	0.0166949	inf	0	1	1
ENSG00000230907	ENSG00000230907	FKBPL	HSCHR6_MHC_COX:32044939-32046524	NOTEST	0	0	0	0	1	1
ENSG00000230908	ENSG00000230908	XXyac-YX60D10.1	20:23778777-23786300	NOTEST	0	0	0	0	1	1
ENSG00000230910	ENSG00000230910	RP3-525N10.2	6:69339853-69344919	NOTEST	0.446718	0.512018	0.19683	0	1	1
ENSG00000230911	ENSG00000230911	PPIHP1	11:111895537-112095422	NOTEST	0.0816129	0.137087	0.748222	0	1	1
ENSG00000230912	ENSG00000230912	RP3-508I15.10	22:39052640-39077825	NOTEST	0.0620776	0.0927551	0.579354	0	1	1
ENSG00000230913	ENSG00000230913	NPM1P51	6:41634643-41635387	NOTEST	0	0	0	0	1	1
ENSG00000230914	ENSG00000230914	AC004840.8	7:2423755-2428232	NOTEST	0	0	0	0	1	1
ENSG00000230915	ENSG00000230915	HLA-W	HSCHR6_MHC_MANN:29919577-29921543	NOTEST	0	0	0	0	1	1
ENSG00000230916	ENSG00000230916	RP11-10B2.1	X:125605687-125606386	NOTEST	0	0	0	0	1	1
ENSG00000230918	ENSG00000230918	AC008063.2	2:162848750-162931679	NOTEST	0	0	0	0	1	1
ENSG00000230920	ENSG00000230920	RP11-527D15.1	9:8314245-10612723	NOTEST	0	0	0	0	1	1
ENSG00000230921	ENSG00000230921	HAO2-IT1	1:119911401-119936753	NOTEST	0	0	0	0	1	1
ENSG00000230922	ENSG00000230922	RP4-753M9.1	22:45277041-45405880	NOTEST	0	0	0	0	1	1
ENSG00000230923	ENSG00000230923	LINC00309	2:64319785-64479993	NOTEST	0	0	0	0	1	1
ENSG00000230925	ENSG00000230925	RP11-176F3.7	9:33750514-33920402	NOTEST	0	0.0169119	inf	0	1	1
ENSG00000230926	ENSG00000230926	RP11-104D21.2	X:50825663-50834074	NOTEST	0	0	0	0	1	1
ENSG00000230927	ENSG00000230927	TMBIM7P	7:92042289-92068876	NOTEST	0	0	0	0	1	1
ENSG00000230928	ENSG00000230928	RP11-34A14.3	10:100007446-100028007	NOTEST	0.0608263	0.0325575	-0.901703	0	1	1
ENSG00000230929	ENSG00000230929	RP11-395C3.1	5:125963708-125964011	NOTEST	0	0.0810847	inf	0	1	1
ENSG00000230930	ENSG00000230930	COL11A2	HSCHR6_MHC_DBB:33108367-33138186	NOTEST	0	0	0	0	1	1
ENSG00000230931	ENSG00000230931	GXYLT1P1	13:19298554-19299044	NOTEST	0	0	0	0	1	1
ENSG00000230932	ENSG00000230932	RP5-947P14.2	1:106615868-106627121	NOTEST	0	0	0	0	1	1
ENSG00000230934	ENSG00000230934	RP11-402P6.2	X:70911781-70912029	NOTEST	0	0	0	0	1	1
ENSG00000230935	ENSG00000230935	RPS3P1	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000230936	ENSG00000230936	RP11-775L16.1	7:55410008-55412651	NOTEST	0	0.00466738	inf	0	1	1
ENSG00000230937	ENSG00000230937	MIR205HG	1:209602164-209606183	NOTEST	0	0	0	0	1	1
ENSG00000230940	ENSG00000230940	RP11-32B11.2	9:134735493-134955295	NOTEST	0	0	0	0	1	1
ENSG00000230941	ENSG00000230941	AC002386.1	7:108962376-108966372	NOTEST	0	0	0	0	1	1
ENSG00000230942	ENSG00000230942	HMGN1P5	1:158236542-158237110	NOTEST	0	0	0	0	1	1
ENSG00000230943	ENSG00000230943	RP11-367G18.1	6:113944736-113971276	NOTEST	0.296576	0.196059	-0.597109	0	1	1
ENSG00000230944	ENSG00000230944	AC026202.5	3:5297219-5298446	NOTEST	0	0	0	0	1	1
ENSG00000230945	ENSG00000230945	RP11-394O9.1	9:82645493-82649470	NOTEST	0	0	0	0	1	1
ENSG00000230946	ENSG00000230946	HNRNPA1P68	1:101361631-101447309	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000230947	ENSG00000230947	AP000356.2	22:24936405-25024972	NOTEST	0	0	0	0	1	1
ENSG00000230948	ENSG00000230948	AP001331.1	8:109143327-109144342	NOTEST	0	0	0	0	1	1
ENSG00000230949	ENSG00000230949	ZNF70P1	HSCHR6_MHC_COX:33105107-33105731	NOTEST	0	0	0	0	1	1
ENSG00000230950	ENSG00000230950	MTND2P21	2:117782652-117783694	NOTEST	0	0	0	0	1	1
ENSG00000230951	ENSG00000230951	RP11-573D15.6	3:186490377-186491265	NOTEST	0.037887	0.0760522	1.00529	0	1	1
ENSG00000230952	ENSG00000230952	AC099344.2	2:11497640-11505762	NOTEST	0	0	0	0	1	1
ENSG00000230953	ENSG00000230953	RP4-631H13.6	1:53361655-53392884	NOTEST	0	0	0	0	1	1
ENSG00000230955	ENSG00000230955	RP11-109P14.10	1:38326368-38412729	NOTEST	0	0.0130783	inf	0	1	1
ENSG00000230956	ENSG00000230956	RP3-452M16.1	X:87351393-87352226	NOTEST	0	0	0	0	1	1
ENSG00000230957	ENSG00000230957	MAS1LP1	HSCHR6_MHC_MANN:29442372-29443419	NOTEST	0	0	0	0	1	1
ENSG00000230958	ENSG00000230958	AC093166.4	2:112523847-112642267	NOTEST	0	0	0	0	1	1
ENSG00000230960	ENSG00000230960	RP5-1086L22.1	6:170563421-170571657	NOTEST	0	0	0	0	1	1
ENSG00000230961	ENSG00000230961	MSH5	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000230962	ENSG00000230962	RP11-113E21.1	10:87209348-87251753	NOTEST	0	0	0	0	1	1
ENSG00000230964	ENSG00000230964	AC018696.4	2:91766536-91766632	NOTEST	0	0	0	0	1	1
ENSG00000230965	ENSG00000230965	SNX18P13	21:15278280-15278809	NOTEST	0	0.0921063	inf	0	1	1
ENSG00000230967	ENSG00000230967	RP11-107I14.5	10:103082241-103083151	NOTEST	0	0	0	0	1	1
ENSG00000230968	ENSG00000230968	AC084149.1	2:77899340-77900918	NOTEST	0	0	0	0	1	1
ENSG00000230969	ENSG00000230969	AC104024.2	17:16891642-16893491	NOTEST	0	0	0	0	1	1
ENSG00000230970	ENSG00000230970	HHATL-AS1	3:42734154-42846023	NOTEST	0	0	0	0	1	1
ENSG00000230971	ENSG00000230971	AC005703.3	17:15170777-15175607	NOTEST	0	0.00651625	inf	0	1	1
ENSG00000230972	ENSG00000230972	AP001255.2	21:24437812-24503528	NOTEST	0	0	0	0	1	1
ENSG00000230973	ENSG00000230973	RP1-154J13.2	X:130571028-130571644	NOTEST	0	0	0	0	1	1
ENSG00000230975	ENSG00000230975	AC084193.1	2:80926512-81097315	NOTEST	0	0	0	0	1	1
ENSG00000230977	ENSG00000230977	AC023274.6	Y:26325462-26338017	NOTEST	0	0	0	0	1	1
ENSG00000230978	ENSG00000230978	LINC00160	21:36096104-36109478	NOTEST	0	0	0	0	1	1
ENSG00000230980	ENSG00000230980	RPL36AP39	11:1813782-1814100	NOTEST	0	0	0	0	1	1
ENSG00000230981	ENSG00000230981	AC006035.1	7:16127151-16129275	NOTEST	0	0	0	0	1	1
ENSG00000230983	ENSG00000230983	PSORS1C3	HSCHR6_MHC_MCF:31204888-31232984	NOTEST	0	0	0	0	1	1
ENSG00000230985	ENSG00000230985	VARSL	HSCHR6_MHC_DBB:30866675-30884964	NOTEST	0	0	0	0	1	1
ENSG00000230986	ENSG00000230986	DDX3YP2	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000230987	ENSG00000230987	RP11-113I24.1	1:189958699-189962227	NOTEST	0	0	0	0	1	1
ENSG00000230988	ENSG00000230988	RP11-661D19.1	14:103058997-103196913	NOTEST	0	0	0	0	1	1
ENSG00000230990	ENSG00000230990	RP4-734C18.1	20:11214817-11282173	NOTEST	0	0	0	0	1	1
ENSG00000230991	ENSG00000230991	AC092625.1	2:155822024-155824515	NOTEST	0	0	0	0	1	1
ENSG00000230992	ENSG00000230992	FAM201B	2:133110239-133112412	NOTEST	0.266205	0.234986	-0.179962	0	1	1
ENSG00000230993	ENSG00000230993	RPL12P15	2:122407225-122494499	NOTEST	0.168822	0.0352877	-2.25826	0	1	1
ENSG00000230994	ENSG00000230994	FGFR3P1	6:31345195-31345796	NOTEST	0	0	0	0	1	1
ENSG00000230995	ENSG00000230995	PPP1R10	HSCHR6_MHC_COX:30558025-30584021	NOTEST	0	0	0	0	1	1
ENSG00000230997	ENSG00000230997	RAB42P1	14:89591214-90421121	NOTEST	0	0	0	0	1	1
ENSG00000230998	ENSG00000230998	RP11-14C22.3	10:30944417-30946464	NOTEST	0	0	0	0	1	1
ENSG00000230999	ENSG00000230999	MTND5P8	7:111846642-112049678	NOTEST	0	0	0	0	1	1
ENSG00000231000	ENSG00000231000	RPS17P1	HSCHR6_MHC_SSTO:29456721-29457127	NOTEST	0	0	0	0	1	1
ENSG00000231001	ENSG00000231001	CCNB1IP1P3	X:94031737-94032566	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231002	ENSG00000231002	TRIM26	HSCHR6_MHC_MANN:30197333-30226303	NOTEST	0	0	0	0	1	1
ENSG00000231003	ENSG00000231003	C6orf25	HSCHR6_MHC_SSTO:31676329-31684446	NOTEST	0	0	0	0	1	1
ENSG00000231004	ENSG00000231004	CECR9	22:17809923-17810122	NOTEST	0	0	0	0	1	1
ENSG00000231005	ENSG00000231005	RP3-481F12.1	20:55903601-55903752	NOTEST	0	0	0	0	1	1
ENSG00000231006	ENSG00000231006	RPL7P32	7:108110865-108215294	NOTEST	0.0735586	0.156526	1.08943	0	1	1
ENSG00000231007	ENSG00000231007	CDC20P1	9:89623369-89657041	NOTEST	0.0596155	0.0174134	-1.77549	0	1	1
ENSG00000231009	ENSG00000231009	CUBNP1	10:43189818-43210023	NOTEST	0	0	0	0	1	1
ENSG00000231010	ENSG00000231010	RP6-109B7.2	22:46445357-46509808	NOTEST	0.0950161	0.076786	-0.307329	0	1	1
ENSG00000231011	ENSG00000231011	RP11-494I9.1	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000231013	ENSG00000231013	AC013275.2	2:120197418-120282070	NOTEST	0	0	0	0	1	1
ENSG00000231015	ENSG00000231015	RP5-860P4.2	20:24660182-24661627	NOTEST	0	0	0	0	1	1
ENSG00000231017	ENSG00000231017	AC013404.1	2:212163665-212163914	NOTEST	0	0	0	0	1	1
ENSG00000231018	ENSG00000231018	EIF4A1P3	9:134657956-134658200	NOTEST	0	0	0	0	1	1
ENSG00000231019	ENSG00000231019	RP11-545P6.2	13:88795121-88888337	NOTEST	0	0	0	0	1	1
ENSG00000231020	ENSG00000231020	RP11-357J22.1	1:176274807-176275231	NOTEST	0	0	0	0	1	1
ENSG00000231021	ENSG00000231021	DRB4	HSCHR6_MHC_MCF:32578923-32593887	NOTEST	0	0	0	0	1	1
ENSG00000231022	ENSG00000231022	RPS3AP9	1:188663450-188664242	NOTEST	0	0	0	0	1	1
ENSG00000231024	ENSG00000231024	AC092431.3	2:69685128-70053596	NOTEST	0	0	0	0	1	1
ENSG00000231026	ENSG00000231026	XKRYP4	Y:26063387-26063870	NOTEST	0	0	0	0	1	1
ENSG00000231027	ENSG00000231027	AC079325.6	17:72556854-72563482	NOTEST	0	0	0	0	1	1
ENSG00000231028	ENSG00000231028	LINC00271	6:135604669-136037193	NOTEST	0.0656195	0.0618754	-0.0847587	0	1	1
ENSG00000231029	ENSG00000231029	RP3-455J7.3	1:167560628-167561083	NOTEST	0	0	0	0	1	1
ENSG00000231030	ENSG00000231030	ZNF70P1	HSCHR6_MHC_QBL:33112311-33112935	NOTEST	0	0	0	0	1	1
ENSG00000231031	ENSG00000231031	AC008271.1	2:15830905-15884463	NOTEST	0.0158312	0.00678848	-1.22161	0	1	1
ENSG00000231032	ENSG00000231032	AC114814.2	2:236055659-236056144	NOTEST	0	0	0	0	1	1
ENSG00000231034	ENSG00000231034	RP11-346K17.3	20:33276491-33276782	NOTEST	0	0	0	0	1	1
ENSG00000231035	ENSG00000231035	RPL7L1P9	2:218625269-218626014	NOTEST	0	0.0182778	inf	0	1	1
ENSG00000231037	ENSG00000231037	HCG25	HSCHR6_MHC_MANN:33371217-33376673	NOTEST	0	0	0	0	1	1
ENSG00000231039	ENSG00000231039	RP11-445P17.3	10:5276320-5305371	NOTEST	0	0	0	0	1	1
ENSG00000231040	ENSG00000231040	AC103881.1	2:147595316-147607878	NOTEST	0	0	0	0	1	1
ENSG00000231041	ENSG00000231041	C6orf100	HSCHR6_MHC_MANN:28911661-28912322	NOTEST	0	0	0	0	1	1
ENSG00000231044	ENSG00000231044	NELFE	HSCHR6_MHC_COX:31907415-31925080	NOTEST	0	0	0	0	1	1
ENSG00000231046	ENSG00000231046	RP11-428F8.2	6:111408780-111580237	NOTEST	0	0	0	0	1	1
ENSG00000231047	ENSG00000231047	GCNT1P3	3:190231839-190375843	NOTEST	0.487528	0.495196	0.0225158	0	1	1
ENSG00000231048	ENSG00000231048	LST1	HSCHR6_MHC_MANN:31593387-31600249	NOTEST	0	0	0	0	1	1
ENSG00000231049	ENSG00000231049	OR52B5P	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000231050	ENSG00000231050	RP1-140A9.1	1:1822909-1824097	NOTEST	0.0571527	0.133316	1.22195	0	1	1
ENSG00000231051	ENSG00000231051	USP17L28	4:9350618-9352211	NOTEST	0	0	0	0	1	1
ENSG00000231052	ENSG00000231052	RP11-91N2.3	9:2422701-2660053	NOTEST	0	0	0	0	1	1
ENSG00000231053	ENSG00000231053	RP13-26D14.2	X:69506444-69640682	NOTEST	0.0830301	0	#NAME?	0	1	1
ENSG00000231054	ENSG00000231054	AC009236.2	2:45392008-45550434	NOTEST	0	0	0	0	1	1
ENSG00000231056	ENSG00000231056	RP1-290I10.5	6:10474732-10478735	NOTEST	0	0	0	0	1	1
ENSG00000231057	ENSG00000231057	RP11-122M14.1	1:211849103-211863445	NOTEST	0.00886644	0	#NAME?	0	1	1
ENSG00000231058	ENSG00000231058	MSANTD2P1	21:24437812-24503528	NOTEST	0	0	0	0	1	1

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ENSG00000231060	ENSG00000231060	FARSBP1	10:82535920-82537844	NOTEST	0	0	0	0	1	1
ENSG00000231061	ENSG00000231061	LINC00395	13:64241813-64312151	NOTEST	0	0	0	0	1	1
ENSG00000231062	ENSG00000231062	AC103563.9	2:95690937-95719737	NOTEST	0	0	0	0	1	1
ENSG00000231063	ENSG00000231063	AC006994.1	2:210867288-211036115	NOTEST	0.02225	0.0156938	-0.50361	0	1	1
ENSG00000231066	ENSG00000231066	NPM1P9	X:14852597-14853441	NOTEST	0.253642	0.265434	0.0655572	0	1	1
ENSG00000231067	ENSG00000231067	HCG4P5	HSCHR6_MHC_SSTO:29897512-29902154	NOTEST	0	0	0	0	1	1
ENSG00000231068	ENSG00000231068	KRTAP21-3	21:32090842-32091095	NOTEST	0	0	0	0	1	1
ENSG00000231069	ENSG00000231069	BX842568.4	X:37003595-37004166	NOTEST	0	0	0	0	1	1
ENSG00000231070	ENSG00000231070	OR52Y1P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000231071	ENSG00000231071	RP5-1068H6.1	20:4711927-4721314	NOTEST	0	0	0	0	1	1
ENSG00000231072	ENSG00000231072	GAPDHP64	1:117256454-117257457	NOTEST	0	0	0	0	1	1
ENSG00000231073	ENSG00000231073	RP11-316M1.3	1:150898738-150948010	NOTEST	0	0	0	0	1	1
ENSG00000231078	ENSG00000231078	RP11-560A15.4	20:55680796-55682184	NOTEST	0	0	0	0	1	1
ENSG00000231079	ENSG00000231079	AC105402.4	2:149624038-149883273	NOTEST	0	0	0	0	1	1
ENSG00000231080	ENSG00000231080	RP11-342H21.2	1:67278567-67390570	NOTEST	0	0	0	0	1	1
ENSG00000231081	ENSG00000231081	RP4-760C5.3	20:25989426-25991167	NOTEST	0.0800792	0.32954	2.04095	0	1	1
ENSG00000231082	ENSG00000231082	RP11-514F8.2	10:82409552-82413488	NOTEST	0	0	0	0	1	1
ENSG00000231083	ENSG00000231083	AC011747.6	2:8741021-8763072	NOTEST	0	0	0	0	1	1
ENSG00000231086	ENSG00000231086	TSSK1A	22:19023794-19115962	NOTEST	0.0248806	0.0175684	-0.502044	0	1	1
ENSG00000231087	ENSG00000231087	FDPSP7	7:76139744-77045717	NOTEST	0	0	0	0	1	1
ENSG00000231090	ENSG00000231090	RP11-101C11.1	1:55683533-55699850	NOTEST	0	0	0	0	1	1
ENSG00000231091	ENSG00000231091	AC138783.13	7:74602782-74653438	NOTEST	0	0	0	0	1	1
ENSG00000231092	ENSG00000231092	AC012513.6	2:217122587-217236750	NOTEST	0	0	0	0	1	1
ENSG00000231093	ENSG00000231093	RP13-150K15.1	X:144711735-144713893	NOTEST	0	0	0	0	1	1
ENSG00000231094	ENSG00000231094	PSORS1C1	HSCHR6_MHC_MANN:31127486-31152786	NOTEST	0	0	0	0	1	1
ENSG00000231095	ENSG00000231095	GYG1P3	1:55683533-55699850	NOTEST	0	0	0	0	1	1
ENSG00000231096	ENSG00000231096	AC015726.1	17:19674141-19771249	NOTEST	0	0	0	0	1	1
ENSG00000231098	ENSG00000231098	AC008154.4	7:133969251-133970807	NOTEST	0.0610625	0	#NAME?	0	1	1
ENSG00000231099	ENSG00000231099	BMS1P19	2:110424704-110425579	NOTEST	0	0	0	0	1	1
ENSG00000231100	ENSG00000231100	RP11-740C1.2	1:159527157-159527990	NOTEST	0	0.0233557	inf	0	1	1
ENSG00000231102	ENSG00000231102	RP11-298J23.5	6:41651715-41703997	NOTEST	0	0	0	0	1	1
ENSG00000231103	ENSG00000231103	RP5-845O24.3	1:12897977-12901210	NOTEST	0	0	0	0	1	1
ENSG00000231104	ENSG00000231104	RP11-354M20.3	10:119764426-119969663	NOTEST	0.0730513	0.427209	2.54796	0	1	1
ENSG00000231105	ENSG00000231105	RP5-1071N3.1	1:21543739-21671997	NOTEST	0	0	0	0	1	1
ENSG00000231106	ENSG00000231106	AP000688.8	21:37377635-37380136	NOTEST	0.0478193	0.152478	1.67293	0	1	1
ENSG00000231107	ENSG00000231107	RP11-389K14.3	9:93063183-93195787	NOTEST	0	0	0	0	1	1
ENSG00000231108	ENSG00000231108	RP11-390F4.9	9:6716547-7175648	NOTEST	0	0	0	0	1	1
ENSG00000231110	ENSG00000231110	AC004070.1	X:139298186-139298956	NOTEST	0	0	0	0	1	1
ENSG00000231112	ENSG00000231112	MTHFD2P3	6:108307014-108307235	NOTEST	0	0	0	0	1	1
ENSG00000231113	ENSG00000231113	RP3-475N16.1	6:42908101-42916098	NOTEST	0.337919	0.261533	-0.369685	0	1	1
ENSG00000231114	ENSG00000231114	AC078842.4	7:136912087-137028611	NOTEST	0	0	0	0	1	1
ENSG00000231115	ENSG00000231115	RING1	HSCHR6_MHC_MCF:33346635-33350863	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231116	ENSG00000231116	VARS	HSCHR6_MHC_APD:31756647-31775083	NOTEST	0	0	0	0	1	1
ENSG00000231118	ENSG00000231118	PPIAP9	HSCHR6_MHC_DBB:31469456-31470268	NOTEST	0	0	0	0	1	1
ENSG00000231119	ENSG00000231119	RP4-569M23.2	20:45837858-45985567	NOTEST	0.0691363	0.0919577	0.411528	0	1	1
ENSG00000231120	ENSG00000231120	BTF3P10	6:150298606-150300241	NOTEST	0.045635	0.22162	2.27987	0	1	1
ENSG00000231122	ENSG00000231122	FAM25E	10:46310875-46313036	NOTEST	0	0	0	0	1	1
ENSG00000231123	ENSG00000231123	SPATA20P1	21:39493544-39679279	NOTEST	0	0	0	0	1	1
ENSG00000231124	ENSG00000231124	UBE2V1P11	2:202655183-202760273	NOTEST	0	0	0	0	1	1
ENSG00000231125	ENSG00000231125	AF129075.5	21:30428125-30446118	NOTEST	0.0477179	0.0712201	0.577752	0	1	1
ENSG00000231128	ENSG00000231128	RP5-1073O3.2	1:114304453-114456708	NOTEST	0	0	0	0	1	1
ENSG00000231129	ENSG00000231129	ABCF1	HSCHR6_MHC_MANN:30583827-30609632	NOTEST	0	0	0	0	1	1
ENSG00000231130	ENSG00000231130	HLA-T	6:29864430-29865563	NOTEST	0	0	0	0	1	1
ENSG00000231131	ENSG00000231131	RP11-346D6.6	10:54210633-54230293	NOTEST	0	0	0	0	1	1
ENSG00000231132	ENSG00000231132	RP11-40C11.2	10:52750944-54073888	NOTEST	0	0	0	0	1	1
ENSG00000231133	ENSG00000231133	HAR1B	20:61726844-61735738	NOTEST	0	0	0	0	1	1
ENSG00000231134	ENSG00000231134	TCF7L1-IT1	2:85360532-85537511	NOTEST	0	0	0	0	1	1
ENSG00000231135	ENSG00000231135	MDC1	HSCHR6_MHC_SSTO:30659032-30677115	NOTEST	0	0	0	0	1	1
ENSG00000231136	ENSG00000231136	AP000705.6	21:23526269-23526619	NOTEST	0	0	0	0	1	1
ENSG00000231137	ENSG00000231137	RBM22P5	9:78505559-78977255	NOTEST	0	0	0	0	1	1
ENSG00000231138	ENSG00000231138	RP11-391M7.3	10:125465722-125699783	NOTEST	0	0	0	0	1	1
ENSG00000231139	ENSG00000231139	AC104843.4	7:152287725-152288026	NOTEST	0	0	0	0	1	1
ENSG00000231140	ENSG00000231140	RP11-347J14.7	9:39384502-39405302	NOTEST	0	0	0	0	1	1
ENSG00000231141	ENSG00000231141	TTTY3	Y:27874636-27881307	NOTEST	0	0	0	0	1	1
ENSG00000231143	ENSG00000231143	RP3-463P15.1	6:94873637-94904376	NOTEST	0	0	0	0	1	1
ENSG00000231144	ENSG00000231144	EEF1A1P40	X:106275477-106276050	NOTEST	0	0	0	0	1	1
ENSG00000231145	ENSG00000231145	AC013468.1	2:190635048-190649097	NOTEST	0	0	0	0	1	1
ENSG00000231147	ENSG00000231147	ARHGAP42P2	2:130748028-130808704	NOTEST	0	0	0	0	1	1
ENSG00000231148	ENSG00000231148	HMGB1P7	10:32094364-32217742	NOTEST	0	0	0	0	1	1
ENSG00000231149	ENSG00000231149	RP11-10J18.3	9:127277216-127278335	NOTEST	0	0	0	0	1	1
ENSG00000231150	ENSG00000231150	RP1-207H1.3	6:38683116-38998301	NOTEST	0	0	0	0	1	1
ENSG00000231152	ENSG00000231152	MTND2P15	10:71353796-71354688	NOTEST	0	0	0	0	1	1
ENSG00000231153	ENSG00000231153	AC002429.4	7:94536513-94925727	NOTEST	0	0	0	0	1	1
ENSG00000231154	ENSG00000231154	MORF4L2-AS1	X:102930423-102946700	NOTEST	0.109247	0.129526	0.245649	0	1	1
ENSG00000231156	ENSG00000231156	AC093702.1	2:45240352-45240807	NOTEST	0	0	0	0	1	1
ENSG00000231157	ENSG00000231157	SUCLA2P1	HSCHR6_MHC_DBB:30426943-30428313	NOTEST	0	0	0	0	1	1
ENSG00000231158	ENSG00000231158	PTP4A1P1	2:158733213-158992666	NOTEST	0	0	0	0	1	1
ENSG00000231159	ENSG00000231159	OFD1P8Y	Y:24118459-24151496	NOTEST	0	0	0	0	1	1
ENSG00000231160	ENSG00000231160	RP11-617D20.1	4:38614321-38702663	NOTEST	0.064166	0.104195	0.699398	0	1	1
ENSG00000231162	ENSG00000231162	COX11P1	6:28414749-28415584	NOTEST	0.0861092	0.104088	0.273564	0	1	1
ENSG00000231163	ENSG00000231163	RP5-1007G16.1	1:33979608-34631443	NOTEST	0	0	0	0	1	1
ENSG00000231164	ENSG00000231164	RPL7P56	X:135873222-135873939	NOTEST	0	0	0	0	1	1
ENSG00000231165	ENSG00000231165	TRBV26OR9-2	9:33695764-33696057	NOTEST	0.238783	0.655742	1.45743	0	1	1
ENSG00000231166	ENSG00000231166	TUBB4BP6	9:121526144-121526623	NOTEST	0	0	0	0	1	1
ENSG00000231167	ENSG00000231167	YBX1P2	7:105172531-105241322	NOTEST	0.405399	0.381937	-0.0860095	0	1	1
ENSG00000231169	ENSG00000231169	EEF1B2P1	15:52599479-52821247	NOTEST	0	0	0	0	1	1

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ENSG00000231170	ENSG00000231170	AC002451.3	7:95225993-95243031	NOTEST	0.0711682	0.0272108	-1.38706	0	1	1
ENSG00000231171	ENSG00000231171	LINC01098	4:178649910-178911904	NOTEST	0	0	0	0	1	1
ENSG00000231172	ENSG00000231172	AC007099.1	2:75696427-75796848	NOTEST	0.135948	0.0425445	-1.67601	0	1	1
ENSG00000231173	ENSG00000231173	AC116609.3	2:741976-749856	NOTEST	0	0	0	0	1	1
ENSG00000231175	ENSG00000231175	RP11-463J7.2	1:190594019-190770788	NOTEST	0	0	0	0	1	1
ENSG00000231177	ENSG00000231177	LINC00852	3:10289706-10362862	NOTEST	0.126155	0.10055	-0.32728	0	1	1
ENSG00000231178	ENSG00000231178	RP11-125D12.1	6:159774953-159775705	NOTEST	0	0	0	0	1	1
ENSG00000231179	ENSG00000231179	MICB	HSCHR6_MHC_APD:31477172-31490193	NOTEST	0	0	0	0	1	1
ENSG00000231182	ENSG00000231182	RP11-423O2.7	1:142950984-142956716	NOTEST	0.0231003	0	#NAME?	0	1	1
ENSG00000231183	ENSG00000231183	AC007003.1	7:76139744-77045717	NOTEST	0	0	0	0	1	1
ENSG00000231184	ENSG00000231184	FAM58DP	13:19923276-19982102	NOTEST	0	0	0	0	1	1
ENSG00000231187	ENSG00000231187	RP11-38L15.3	10:46897591-46971400	NOTEST	0.435101	0.380354	-0.194007	0	1	1
ENSG00000231188	ENSG00000231188	RP11-34D15.2	10:102095319-102106147	NOTEST	0.0495033	0	#NAME?	0	1	1
ENSG00000231189	ENSG00000231189	AC013448.1	2:224363490-224369329	NOTEST	0	0	0	0	1	1
ENSG00000231190	ENSG00000231190	RPL13AP	HSCHR6_MHC_MCF:29523203-29600766	NOTEST	0	0	0	0	1	1
ENSG00000231192	ENSG00000231192	OR5H1	3:97818751-97866978	NOTEST	0	0	0	0	1	1
ENSG00000231193	ENSG00000231193	RP11-462B18.2	9:32836572-32869593	NOTEST	0	0	0	0	1	1
ENSG00000231194	ENSG00000231194	FARP1-AS1	13:98794815-99102027	NOTEST	0.0970217	0	#NAME?	0	1	1
ENSG00000231195	ENSG00000231195	IFNA11P	9:21398612-21399138	NOTEST	0	0	0	0	1	1
ENSG00000231196	ENSG00000231196	RP11-495P10.8	1:147762995-147769663	NOTEST	0.06113	0.0432361	-0.499646	0	1	1
ENSG00000231197	ENSG00000231197	HCG4P7	HSCHR6_MHC_MANN:29845968-29849143	NOTEST	0	0	0	0	1	1
ENSG00000231198	ENSG00000231198	AC004987.10	7:39856147-39907739	NOTEST	0	0	0	0	1	1
ENSG00000231199	ENSG00000231199	MTND5P19	1:235701351-235703145	NOTEST	0	0	0	0	1	1
ENSG00000231200	ENSG00000231200	AC068490.2	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000231201	ENSG00000231201	AF127577.11	21:16333555-16437321	NOTEST	0	0	0	0	1	1
ENSG00000231202	ENSG00000231202	TRGVB	7:38335363-38335834	NOTEST	0	0	0	0	1	1
ENSG00000231203	ENSG00000231203	KRT8P10	2:183935767-183937214	NOTEST	0	0	0	0	1	1
ENSG00000231204	ENSG00000231204	AC011752.1	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000231205	ENSG00000231205	ZNF826P	19:20451077-20607775	NOTEST	0	0	0	0	1	1
ENSG00000231206	ENSG00000231206	HNRNPA1P25	X:73641084-73753752	NOTEST	0	0	0	0	1	1
ENSG00000231207	ENSG00000231207	RP1-144C9.2	1:27715971-27716649	NOTEST	0	0	0	0	1	1
ENSG00000231208	ENSG00000231208	RP4-583P15.11	20:62375018-62462597	NOTEST	0	0	0	0	1	1
ENSG00000231209	ENSG00000231209	GLUD1P6	10:48169664-48175810	NOTEST	0	0	0	0	1	1
ENSG00000231210	ENSG00000231210	AC006159.3	7:116203647-116254874	NOTEST	0	0	0	0	1	1
ENSG00000231211	ENSG00000231211	RPL17P49	X:12156584-12742642	NOTEST	0	0	0	0	1	1
ENSG00000231212	ENSG00000231212	RP11-111F5.3	9:46661241-46662837	NOTEST	0	0.0651403	inf	0	1	1
ENSG00000231213	ENSG00000231213	PLSCR5	3:146294341-146324003	NOTEST	0	0	0	0	1	1
ENSG00000231216	ENSG00000231216	GS1-600G8.3	X:13328770-13338518	NOTEST	0	0	0	0	1	1
ENSG00000231217	ENSG00000231217	RP11-1M18.1	X:6585905-6639585	NOTEST	0	0	0	0	1	1
ENSG00000231219	ENSG00000231219	RP11-219C24.8	1:13379148-13381237	NOTEST	0	0	0	0	1	1
ENSG00000231221	ENSG00000231221	AC023672.2	2:108665655-108669211	NOTEST	0.0683144	0	#NAME?	0	1	1
ENSG00000231222	ENSG00000231222	ARF4P4	13:81462482-81463002	NOTEST	0	0	0	0	1	1
ENSG00000231225	ENSG00000231225	MICA	HSCHR6_MHC_SSTO:31360500-31376956	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231226	ENSG00000231226	TRIM31-AS1	6:30070673-30082501	NOTEST	0.0729151	0.0557334	-0.387674	0	1	1
ENSG00000231227	ENSG00000231227	RP11-85O21.4	9:126763948-126795580	NOTEST	0	0	0	0	1	1
ENSG00000231228	ENSG00000231228	CTD-2593A12.4	5:180409242-180409611	NOTEST	0	0	0	0	1	1
ENSG00000231231	ENSG00000231231	AP001422.3	21:39695556-39705343	NOTEST	0	0	0	0	1	1
ENSG00000231232	ENSG00000231232	RP11-548K12.1	7:57881906-57882648	NOTEST	0	0	0	0	1	1
ENSG00000231233	ENSG00000231233	CCDC147-AS1	10:106111348-106113333	NOTEST	0.0674427	0.0336054	-1.00497	0	1	1
ENSG00000231234	ENSG00000231234	SKP1P1	7:65670185-65955095	NOTEST	0.314433	0.218939	-0.522222	0	1	1
ENSG00000231235	ENSG00000231235	RP11-75A9.1	X:46277884-46279514	NOTEST	0	0	0	0	1	1
ENSG00000231236	ENSG00000231236	AP001604.3	21:28731203-28820898	NOTEST	0	0.00428828	inf	0	1	1
ENSG00000231237	ENSG00000231237	OR6K1P	1:158664328-158665299	NOTEST	0	0	0	0	1	1
ENSG00000231238	ENSG00000231238	LINC00349	13:19114636-19124837	NOTEST	0	0	0	0	1	1
ENSG00000231240	ENSG00000231240	KLF2P1	2:130748028-130808704	NOTEST	0	0	0	0	1	1
ENSG00000231241	ENSG00000231241	RPS3AP3	20:35624751-35725581	NOTEST	0	0	0	0	1	1
ENSG00000231242	ENSG00000231242	RP11-87H9.3	9:69065654-69149621	NOTEST	0.0303972	0.0254246	-0.25771	0	1	1
ENSG00000231243	ENSG00000231243	RP11-134J21.1	3:38865392-38866793	NOTEST	0	0	0	0	1	1
ENSG00000231244	ENSG00000231244	PSMC1P3	7:136370305-136866854	NOTEST	0	0	0	0	1	1
ENSG00000231246	ENSG00000231246	RP5-965F6.2	1:112719855-112903150	NOTEST	0	0	0	0	1	1
ENSG00000231247	ENSG00000231247	PPP1R18	HSCHR6_MHC_COX:30634034-30645541	NOTEST	0	0	0	0	1	1
ENSG00000231248	ENSG00000231248	RP11-160N1.9	9:44823713-44835521	NOTEST	0	0	0	0	1	1
ENSG00000231249	ENSG00000231249	ITPR1-AS1	3:4532574-4534847	NOTEST	0.201519	0.0488847	-2.04346	0	1	1
ENSG00000231251	ENSG00000231251	RP3-357I16.1	1:30699369-30699462	NOTEST	0	0	0	0	1	1
ENSG00000231252	ENSG00000231252	RP11-436K8.1	1:61125302-61291256	NOTEST	0.0136686	0.0251128	0.877554	0	1	1
ENSG00000231253	ENSG00000231253	RP1-302D9.2	22:33504514-33512280	NOTEST	0	0	0	0	1	1
ENSG00000231254	ENSG00000231254	PCED1CP	2:213446080-214017151	NOTEST	0	0	0	0	1	1
ENSG00000231255	ENSG00000231255	AC005009.1	7:86273229-86494200	NOTEST	0	0	0	0	1	1
ENSG00000231256	ENSG00000231256	C17orf105	17:41857802-41864980	NOTEST	0.0282162	0.065398	1.21272	0	1	1
ENSG00000231257	ENSG00000231257	ATAT1	HSCHR6_MHC_MCF:30673077-30693061	NOTEST	0	0	0	0	1	1
ENSG00000231258	ENSG00000231258	ZSWIM5P2	17:20487070-20494493	NOTEST	0	0	0	0	1	1
ENSG00000231261	ENSG00000231261	HMGN2P10	22:42095502-42195460	NOTEST	0	0.110028	inf	0	1	1
ENSG00000231264	ENSG00000231264	RP11-73B2.7	7:63398282-63398887	NOTEST	0	0	0	0	1	1
ENSG00000231265	ENSG00000231265	TRERNA1	20:48657252-48658041	NOTEST	0	0	0	0	1	1
ENSG00000231266	ENSG00000231266	AC010745.3	2:16405314-16410408	NOTEST	0	0	0	0	1	1
ENSG00000231267	ENSG00000231267	PPIAL4E	1:148644010-148644795	NOTEST	0	0	0	0	1	1
ENSG00000231268	ENSG00000231268	AGER	HSCHR6_MHC_APD:32160088-32163445	NOTEST	0	0	0	0	1	1
ENSG00000231270	ENSG00000231270	RP13-347D8.1	X:118072115-118073097	NOTEST	0	0	0	0	1	1
ENSG00000231271	ENSG00000231271	AP000350.8	22:24292104-24296229	NOTEST	0	0	0	0	1	1
ENSG00000231272	ENSG00000231272	RP4-799P18.4	1:234040678-234460262	NOTEST	0	0	0	0	1	1
ENSG00000231274	ENSG00000231274	SBK3	19:56052022-56056909	NOTEST	0	0	0	0	1	1
ENSG00000231275	ENSG00000231275	HNRNPA1P2	HSCHR6_MHC_COX:32209048-32287940	NOTEST	0	0	0	0	1	1
ENSG00000231276	ENSG00000231276	E2F4P1	6:39297765-39693181	NOTEST	0	0	0	0	1	1
ENSG00000231278	ENSG00000231278	OR9S24P	2:241018849-241019779	NOTEST	0	0	0	0	1	1
ENSG00000231279	ENSG00000231279	OR2B4P	HSCHR6_MHC_COX:29255201-29256144	NOTEST	0	0	0	0	1	1
ENSG00000231280	ENSG00000231280	SALL4P6	3:42362496-42364187	NOTEST	0	0	0	0	1	1
ENSG00000231281	ENSG00000231281	HCG27	HSCHR6_MHC_SSTO:31159623-31165828	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231283	ENSG00000231283	RP11-472D17.6	X:52345598-52346259	NOTEST	0	0	0	0	1	1
ENSG00000231286	ENSG00000231286	HLA-DQB1	HSCHR6_MHC_MCF:32658021-32667070	NOTEST	0	0	0	0	1	1
ENSG00000231287	ENSG00000231287	HCG4B	HSCHR6_MHC_APD:29832178-29835432	NOTEST	0	0	0	0	1	1
ENSG00000231288	ENSG00000231288	RPL32P1	HSCHR6_MHC_MCF:33065821-33088426	NOTEST	0	0	0	0	1	1
ENSG00000231289	ENSG00000231289	RP11-782C8.6	1:143243808-143244859	NOTEST	0.112188	0.104131	-0.107515	0	1	1
ENSG00000231290	ENSG00000231290	APCDD1L-AS1	20:57090434-57194944	NOTEST	0.00603939	0.0386243	2.67704	0	1	1
ENSG00000231291	ENSG00000231291	RP11-445O3.1	5:4452042-4866334	NOTEST	0	0	0	0	1	1
ENSG00000231292	ENSG00000231292	IGKV1OR2-108	2:114163972-114164486	NOTEST	0	0	0	0	1	1
ENSG00000231293	ENSG00000231293	RPL36AP6	9:110596789-110597110	NOTEST	0	0	0	0	1	1
ENSG00000231294	ENSG00000231294	AC006994.2	2:211036241-211095107	NOTEST	0	0	0	0	1	1
ENSG00000231295	ENSG00000231295	RP4-797C5.2	7:119913721-120392568	NOTEST	0	0	0	0	1	1
ENSG00000231296	ENSG00000231296	RP1-39G22.4	1:40723778-40759856	NOTEST	0	0.0809492	inf	0	1	1
ENSG00000231297	ENSG00000231297	SNORD45	6:166513152-166526761	NOTEST	0	0.0121111	inf	0	1	1
ENSG00000231298	ENSG00000231298	LINC00704	10:4692376-4720346	NOTEST	0.0319966	0.0733225	1.19634	0	1	1
ENSG00000231299	ENSG00000231299	RP11-419M24.6	7:56428054-56428234	NOTEST	0	0	0	0	1	1
ENSG00000231300	ENSG00000231300	EZH2P1	21:36160097-37376965	NOTEST	0	0	0	0	1	1
ENSG00000231301	ENSG00000231301	RPL13AP	6:29523291-29601753	NOTEST	0	0.0950656	inf	0	1	1
ENSG00000231302	ENSG00000231302	RPL36P2	20:49202644-49308065	NOTEST	0	0	0	0	1	1
ENSG00000231304	ENSG00000231304	AC107622.1	3:20383959-20392420	NOTEST	0	0	0	0	1	1
ENSG00000231305	ENSG00000231305	RP11-723O4.2	3:128580155-128590383	NOTEST	0.111821	0.234236	1.06678	0	1	1
ENSG00000231307	ENSG00000231307	RPS3P2	20:37101458-37207504	NOTEST	0.107605	0.196829	0.8712	0	1	1
ENSG00000231309	ENSG00000231309	WASF5P	HSCHR6_MHC_MCF:31332381-31333836	NOTEST	0	0	0	0	1	1
ENSG00000231310	ENSG00000231310	TBL1XR1-AS1	3:176737142-176915261	NOTEST	0	0	0	0	1	1
ENSG00000231311	ENSG00000231311	PRYP2	Y:20323251-20338370	NOTEST	0	0	0	0	1	1
ENSG00000231313	ENSG00000231313	CLIC1P1	12:121352202-121352926	NOTEST	0.0268608	0.0607786	1.17806	0	1	1
ENSG00000231314	ENSG00000231314	LTB	HSCHR6_MHC_APD:31559652-31561620	NOTEST	0	0	0	0	1	1
ENSG00000231315	ENSG00000231315	AC107613.1	X:27608498-27766908	NOTEST	0	0	0	0	1	1
ENSG00000231316	ENSG00000231316	RP11-134L4.2	6:154926749-154927088	NOTEST	0	0	0	0	1	1
ENSG00000231317	ENSG00000231317	RP11-310H4.6	7:55724460-55746183	NOTEST	0.0454223	0	#NAME?	0	1	1
ENSG00000231319	ENSG00000231319	OR2B3	HSCHR6_MHC_MANN:29053988-29055094	NOTEST	0	0	0	0	1	1
ENSG00000231320	ENSG00000231320	OR2G1P	HSCHR6_MHC_MANN:29191795-29234882	NOTEST	0	0	0	0	1	1
ENSG00000231321	ENSG00000231321	RXRB	HSCHR6_MHC_MANN:33315283-33326135	NOTEST	0	0	0	0	1	1
ENSG00000231322	ENSG00000231322	RPL13AP17	7:77646392-79100524	NOTEST	0	0.00669391	inf	0	1	1
ENSG00000231324	ENSG00000231324	AP000696.2	21:38004978-38009331	NOTEST	0	0	0	0	1	1
ENSG00000231325	ENSG00000231325	LY6G5C	HSCHR6_MHC_COX:31616420-31658607	NOTEST	0	0	0	0	1	1
ENSG00000231326	ENSG00000231326	RP11-69C17.4	10:2208525-2231668	NOTEST	0	0	0	0	1	1
ENSG00000231327	ENSG00000231327	AC016700.5	2:70351167-70352449	NOTEST	0.383765	0.165099	-1.21689	0	1	1
ENSG00000231328	ENSG00000231328	TPT1P7	7:23749785-23872132	NOTEST	0	0	0	0	1	1
ENSG00000231329	ENSG00000231329	RP1-225E12.2	6:139456248-139613276	NOTEST	0	0	0	0	1	1
ENSG00000231331	ENSG00000231331	AC103563.2	2:95618905-95619338	NOTEST	0	0	0	0	1	1
ENSG00000231332	ENSG00000231332	OOEP-AS1	6:74078277-74161999	NOTEST	0	0	0	0	1	1
ENSG00000231333	ENSG00000231333	RPL34P6	1:200832935-200833280	NOTEST	0	0	0	0	1	1
ENSG00000231334	ENSG00000231334	AC104781.1	2:54950635-55199157	NOTEST	0	0	0	0	1	1
ENSG00000231335	ENSG00000231335	AC107072.2	4:77356252-77723117	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231336	ENSG00000231336	AC017006.3	2:45878483-46415129	NOTEST	0.0767147	0.227296	1.56699	0	1	1
ENSG00000231340	ENSG00000231340	ACTG1P10	X:53122891-53196196	NOTEST	0.302913	0.0704648	-2.10393	0	1	1
ENSG00000231341	ENSG00000231341	VDAC1P6	Y:4868266-5610265	NOTEST	0	0	0	0	1	1
ENSG00000231342	ENSG00000231342	ATF4P2	X:153809188-153810261	NOTEST	0	0	0	0	1	1
ENSG00000231343	ENSG00000231343	HCG25	HSCHR6_MHC_QBL:33146132-33173129	NOTEST	0	0	0	0	1	1
ENSG00000231344	ENSG00000231344	RP3-426I6.2	1:28052489-28089633	NOTEST	0	0.330906	inf	0	1	1
ENSG00000231345	ENSG00000231345	RP11-564C4.6	10:52415726-52420232	NOTEST	0.0993004	0.185235	0.899484	0	1	1
ENSG00000231346	ENSG00000231346	LINC01160	1:112025969-112310638	NOTEST	0.045651	0.11814	1.37177	0	1	1
ENSG00000231349	ENSG00000231349	RP11-444C12.1	1:86869858-86870549	NOTEST	0	0	0	0	1	1
ENSG00000231350	ENSG00000231350	C6orf205	HSCHR6_MHC_APD:30959726-30965917	NOTEST	0	0	0	0	1	1
ENSG00000231353	ENSG00000231353	RP11-5P18.3	1:16314676-16314936	NOTEST	0	0	0	0	1	1
ENSG00000231355	ENSG00000231355	AP000302.58	21:34854805-34856565	NOTEST	0	0	0	0	1	1
ENSG00000231356	ENSG00000231356	RP13-238N7.2	X:65580607-65581618	NOTEST	0	0	0	0	1	1
ENSG00000231357	ENSG00000231357	AC006028.11	7:2719155-2883958	NOTEST	0	0.0458584	inf	0	1	1
ENSG00000231358	ENSG00000231358	RP11-442J17.3	13:19496028-19497905	NOTEST	0	0	0	0	1	1
ENSG00000231359	ENSG00000231359	AC072052.7	7:6530423-6530729	NOTEST	0	0	0	0	1	1
ENSG00000231360	ENSG00000231360	AL592284.1	1:144275917-144521970	NOTEST	0.270355	0.195388	-0.468517	0	1	1
ENSG00000231361	ENSG00000231361	CTD-3105H18.5	19:12484422-12484545	NOTEST	0	0	0	0	1	1
ENSG00000231362	ENSG00000231362	RP11-715I4.1	3:12938718-13114617	NOTEST	0	0	0	0	1	1
ENSG00000231363	ENSG00000231363	RP11-148B18.1	1:94614543-94740624	NOTEST	0	0	0	0	1	1
ENSG00000231364	ENSG00000231364	RP11-413G15.1	1:83911735-83920454	NOTEST	0	0	0	0	1	1
ENSG00000231366	ENSG00000231366	RP11-399N22.3	10:72553985-72554279	NOTEST	0	0	0	0	1	1
ENSG00000231367	ENSG00000231367	AC016995.3	2:38633860-38742882	NOTEST	0.121137	0.14149	0.224071	0	1	1
ENSG00000231368	ENSG00000231368	RP11-461H3.2	6:148968842-148969733	NOTEST	0	0	0	0	1	1
ENSG00000231369	ENSG00000231369	RP1-40G4P.1	22:27282871-27283511	NOTEST	0.104072	0.111122	0.0945624	0	1	1
ENSG00000231370	ENSG00000231370	PRRC2A	HSCHR6_MHC_DBB:31570624-31587723	NOTEST	0	0	0	0	1	1
ENSG00000231371	ENSG00000231371	AKR1B1P8	X:115174735-115175671	NOTEST	0	0	0	0	1	1
ENSG00000231372	ENSG00000231372	MICB	HSCHR6_MHC_MANN:31512917-31518423	NOTEST	0	0	0	0	1	1
ENSG00000231373	ENSG00000231373	RP11-466A17.1	9:80037994-80263223	NOTEST	0	0	0	0	1	1
ENSG00000231375	ENSG00000231375	CDY17P	Y:26196024-26197634	NOTEST	0	0	0	0	1	1
ENSG00000231376	ENSG00000231376	HMGN2P16	9:15552894-16061661	NOTEST	0	0	0	0	1	1
ENSG00000231377	ENSG00000231377	DHX16	HSCHR6_MHC_MCF:30693276-30719302	NOTEST	0	0	0	0	1	1
ENSG00000231378	ENSG00000231378	NDUFAF4P4	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000231379	ENSG00000231379	RP11-237M21.1	9:65696701-65725786	NOTEST	0	0	0	0	1	1
ENSG00000231381	ENSG00000231381	RNF2P1	9:6645955-6670635	NOTEST	0	0	0	0	1	1
ENSG00000231382	ENSG00000231382	NBPF21P	3:36657497-36678949	NOTEST	0	0	0	0	1	1
ENSG00000231383	ENSG00000231383	FGF12-AS1	3:191857183-192485553	NOTEST	0	0	0	0	1	1
ENSG00000231384	ENSG00000231384	AC007919.19	3:172348038-172429008	NOTEST	0	0	0	0	1	1
ENSG00000231385	ENSG00000231385	HCG4P3	HSCHR6_MHC_SSTO:29957256-30022268	NOTEST	0	0	0	0	1	1
ENSG00000231386	ENSG00000231386	AC007395.4	2:71035774-71047732	NOTEST	0	0	0	0	1	1
ENSG00000231388	ENSG00000231388	RP11-702C7.2	X:26515052-26523720	NOTEST	0.0102213	0	#NAME?	0	1	1
ENSG00000231390	ENSG00000231390	SNX18P8	9:42368302-42474239	NOTEST	0.0633848	0.0149024	-2.08859	0	1	1
ENSG00000231391	ENSG00000231391	RP11-95K23.3	9:41313944-41327364	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231392	ENSG00000231392	LL22NC03-24A12.8	22:23117021-23117184	NOTEST	0	0	0	0	1	1
ENSG00000231393	ENSG00000231393	RP11-331F9.3	9:35605366-35647096	NOTEST	0	0	0	0	1	1
ENSG00000231394	ENSG00000231394	RP11-310H4.3	7:55661469-55662699	NOTEST	0	0	0	0	1	1
ENSG00000231395	ENSG00000231395	AC124914.3	3:23845514-23932807	NOTEST	0	0.318547	inf	0	1	1
ENSG00000231396	ENSG00000231396	USP17L10	4:9212382-9228214	NOTEST	0	0	0	0	1	1
ENSG00000231397	ENSG00000231397	AC004941.5	7:149018955-149019183	NOTEST	0	0	0	0	1	1
ENSG00000231398	ENSG00000231398	RP11-375N9.2	10:98757794-99052413	NOTEST	0	0	0	0	1	1
ENSG00000231399	ENSG00000231399	SNRPEP8	10:54798044-54798304	NOTEST	0	0	0	0	1	1
ENSG00000231401	ENSG00000231401	AC023481.1	3:7994491-8653610	NOTEST	0	0	0	0	1	1
ENSG00000231402	ENSG00000231402	WASF5P	6:31255286-31256741	NOTEST	0	0	0	0	1	1
ENSG00000231403	ENSG00000231403	AC099344.3	2:11528148-11530493	NOTEST	0	0	0	0	1	1
ENSG00000231404	ENSG00000231404	RAC1P3	13:41861876-41862456	NOTEST	0	0	0	0	1	1
ENSG00000231405	ENSG00000231405	CTA-992D9.7	22:27539438-27555840	NOTEST	0	0	0	0	1	1
ENSG00000231407	ENSG00000231407	RP11-576I22.2	1:170429593-170522587	NOTEST	0.517023	0.416547	-0.31175	0	1	1
ENSG00000231408	ENSG00000231408	LTA	HSCHR6_MHC_MANN:31579317-31581588	NOTEST	0	0	0	0	1	1
ENSG00000231409	ENSG00000231409	RP11-83J16.1	15:35147731-35262040	NOTEST	0.395348	0.0799084	-2.30671	0	1	1
ENSG00000231411	ENSG00000231411	AC006987.7	Y:10009198-10010334	NOTEST	0	0	0	0	1	1
ENSG00000231412	ENSG00000231412	CTC-490G23.2	19:43833446-43835582	NOTEST	0	0.352425	inf	0	1	1
ENSG00000231413	ENSG00000231413	RP11-193P11.3	1:48544458-48547868	NOTEST	0	0	0	0	1	1
ENSG00000231414	ENSG00000231414	AC016700.6	2:70480986-70481142	NOTEST	0	2.69823	inf	0	1	1
ENSG00000231416	ENSG00000231416	RP11-422P24.9	1:153965160-154127592	NOTEST	0	0	0	0	1	1
ENSG00000231417	ENSG00000231417	IRX1P1	13:25316814-25320322	NOTEST	0	0	0	0	1	1
ENSG00000231418	ENSG00000231418	AC006380.3	7:31454258-31460900	NOTEST	0	0	0	0	1	1
ENSG00000231419	ENSG00000231419	LINC00689	7:158799212-158937649	NOTEST	0.0146811	0.0817413	2.47711	0	1	1
ENSG00000231420	ENSG00000231420	AC113610.1	2:151027936-151157594	NOTEST	0	0	0	0	1	1
ENSG00000231421	ENSG00000231421	AC006050.2	17:28900488-28999807	NOTEST	0	0	0	0	1	1
ENSG00000231422	ENSG00000231422	RP11-80K21.3	10:25401986-25891155	NOTEST	0.11094	0.0783739	-0.501333	0	1	1
ENSG00000231423	ENSG00000231423	RAB9AP5	Y:26102715-26106365	NOTEST	0	0	0	0	1	1
ENSG00000231424	ENSG00000231424	RP1-45C12.1	1:171216718-171255117	NOTEST	0	0	0	0	1	1
ENSG00000231426	ENSG00000231426	RP5-899B16.1	6:140175986-140198528	NOTEST	0	0	0	0	1	1
ENSG00000231427	ENSG00000231427	RP11-436F9.1	7:54398389-54417542	NOTEST	0	0	0	0	1	1
ENSG00000231428	ENSG00000231428	LINC00396	13:110705631-110707299	NOTEST	0	0	0	0	1	1
ENSG00000231429	ENSG00000231429	RP11-343N15.2	1:121102016-121204983	NOTEST	0	0	0	0	1	1
ENSG00000231430	ENSG00000231430	HCG4P8	HSCHR6_MHC_DBB:29791967-29796126	NOTEST	0	0	0	0	1	1
ENSG00000231431	ENSG00000231431	FAR2P4	2:131862419-132111282	NOTEST	0	0.0108204	inf	0	1	1
ENSG00000231433	ENSG00000231433	WASF5P	HSCHR6_MHC_COX:31246322-31247777	NOTEST	0	0	0	0	1	1
ENSG00000231434	ENSG00000231434	RP11-144L1.8	1:158493461-158495628	NOTEST	0.0283508	0.0278983	-0.0232129	0	1	1
ENSG00000231435	ENSG00000231435	AC011747.3	2:8683721-8723922	NOTEST	0	0	0	0	1	1
ENSG00000231436	ENSG00000231436	RBMY3AP	Y:9448179-9458885	NOTEST	0	0	0	0	1	1
ENSG00000231437	ENSG00000231437	RP11-88H9.2	1:112532391-112541464	NOTEST	0	0	0	0	1	1
ENSG00000231439	ENSG00000231439	WASIR2	16:61552-88321	NOTEST	0.390803	0.264204	-0.564789	0	1	1
ENSG00000231440	ENSG00000231440	RP11-467I20.6	1:240652872-240775449	NOTEST	0	0	0	0	1	1

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ENSG00000231442	ENSG00000231442	LARP1BP1	4:64215831-64217190	NOTEST	0	0	0	0	1	1
ENSG00000231443	ENSG00000231443	AC024937.6	3:195664113-195665610	NOTEST	0.267326	0.326491	0.288444	0	1	1
ENSG00000231444	ENSG00000231444	DDR1-AS1	HSCHR6_MHC_MANN:30879449-30888383	NOTEST	0	0	0	0	1	1
ENSG00000231445	ENSG00000231445	TIMM8AP1	2:162933866-162934161	NOTEST	0.235159	0.454193	0.949668	0	1	1
ENSG00000231447	ENSG00000231447	RP1-14D6.7	X:151889194-151890140	NOTEST	0.124208	0.122965	-0.0145056	0	1	1
ENSG00000231448	ENSG00000231448	RP11-763B22.9	1:148854137-148891740	NOTEST	0	0	0	0	1	1
ENSG00000231449	ENSG00000231449	AC097359.2	3:37237694-37238157	NOTEST	0	0.113249	inf	0	1	1
ENSG00000231450	ENSG00000231450	PSORS1C3	HSCHR6_MHC_DBB:31135255-31139421	NOTEST	0	0	0	0	1	1
ENSG00000231453	ENSG00000231453	AC018470.4	2:175190754-175195371	NOTEST	0	0.00713236	inf	0	1	1
ENSG00000231454	ENSG00000231454	RP11-160N1.8	9:44873416-44874226	NOTEST	0	0	0	0	1	1
ENSG00000231457	ENSG00000231457	RBM22P1	X:52555980-52556851	NOTEST	0	0	0	0	1	1
ENSG00000231458	ENSG00000231458	RNASEH1P2	17:16586751-16587541	NOTEST	0.203982	0.0748616	-1.44615	0	1	1
ENSG00000231459	ENSG00000231459	LINC00032	9:27245681-27282791	NOTEST	0.00541603	0.0429629	2.98778	0	1	1
ENSG00000231460	ENSG00000231460	RP11-321L2.1	9:23829667-23849912	NOTEST	0	0	0	0	1	1
ENSG00000231461	ENSG00000231461	HLA-DPA2	6:33059529-33065072	NOTEST	0	0	0	0	1	1
ENSG00000231464	ENSG00000231464	AC024937.4	3:195723608-195725104	NOTEST	0.0277349	0.0305096	0.137559	0	1	1
ENSG00000231465	ENSG00000231465	RP11-542K23.9	9:125233636-125238096	NOTEST	0	0	0	0	1	1
ENSG00000231466	ENSG00000231466	CTA-246H3.11	22:25745509-25746289	NOTEST	0.47162	0.271204	-0.798248	0	1	1
ENSG00000231467	ENSG00000231467	RP5-1170K4.7	22:37461475-37505603	NOTEST	0	0	0	0	1	1
ENSG00000231468	ENSG00000231468	PRDX3P2	1:28832454-28865812	NOTEST	0.0337678	0.0262844	-0.36144	0	1	1
ENSG00000231470	ENSG00000231470	HMGB3P2	20:34660362-34673182	NOTEST	0	0	0	0	1	1
ENSG00000231471	ENSG00000231471	HMGN2P34	10:74396254-74396523	NOTEST	0	0.105918	inf	0	1	1
ENSG00000231473	ENSG00000231473	LINC00441	13:48870648-48877797	NOTEST	0.0583895	0.0455121	-0.35946	0	1	1
ENSG00000231474	ENSG00000231474	XXbac-BPG118E17.9	HSCHR6_MHC_MANN:31042649-31047446	NOTEST	0	0	0	0	1	1
ENSG00000231475	ENSG00000231475	IGHV4-31	14:106805208-106805716	NOTEST	0	0	0	0	1	1
ENSG00000231476	ENSG00000231476	AC074389.5	7:1660289-1661041	NOTEST	0	0	0	0	1	1
ENSG00000231477	ENSG00000231477	CTB-187M2.1	17:19342455-19364308	NOTEST	0	0	0	0	1	1
ENSG00000231478	ENSG00000231478	FCF1P9	X:85403461-86087607	NOTEST	0	0	0	0	1	1
ENSG00000231479	ENSG00000231479	SLC44A4	HSCHR6_MHC_COX:31818511-31834373	NOTEST	0	0	0	0	1	1
ENSG00000231480	ENSG00000231480	SNRPGP13	21:39751948-40033704	NOTEST	0	0	0	0	1	1
ENSG00000231481	ENSG00000231481	RP11-292F9.2	9:46359241-46380257	NOTEST	0	0	0	0	1	1
ENSG00000231482	ENSG00000231482	AC141930.2	2:1550436-1623885	NOTEST	0	0	0	0	1	1
ENSG00000231483	ENSG00000231483	RP11-336A10.5	10:5650437-5652756	NOTEST	0	0	0	0	1	1
ENSG00000231484	ENSG00000231484	RP11-548K12.12	7:57888036-57896752	NOTEST	0	0	0	0	1	1
ENSG00000231485	ENSG00000231485	RP4-535B20.1	1:65532309-65533420	NOTEST	0	0	0	0	1	1
ENSG00000231486	ENSG00000231486	AC096579.7	2:89109983-89165653	NOTEST	0	0	0	0	1	1
ENSG00000231487	ENSG00000231487	AP006285.7	11:1683813-1684573	NOTEST	0	0	0	0	1	1
ENSG00000231488	ENSG00000231488	ABHD16A	HSCHR6_MHC_DBB:31611187-31653368	NOTEST	0	0	0	0	1	1
ENSG00000231489	ENSG00000231489	AF196972.10	X:48281726-48281853	NOTEST	0	0	0	0	1	1
ENSG00000231490	ENSG00000231490	RPL7L1P2	7:50934443-51384515	NOTEST	0	0	0	0	1	1
ENSG00000231491	ENSG00000231491	RP11-71E22.1	9:12287319-12288238	NOTEST	0	0	0	0	1	1

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ENSG00000231494	ENSG00000231494	AC104634.3	2:232424613-232425075	NOTEST	0	0	0	0	1	1
ENSG00000231495	ENSG00000231495	RP1-213J1P__B.2	22:28072555-28110959	NOTEST	0	0	0	0	1	1
ENSG00000231496	ENSG00000231496	RP1-251M9.2	10:11002113-11012779	NOTEST	0	0	0	0	1	1
ENSG00000231501	ENSG00000231501	MTND4LP1	X:125606710-125606867	NOTEST	0	0	0	0	1	1
ENSG00000231502	ENSG00000231502	LSM2	HSCHR6_MHC_DBB:31747357-31756947	NOTEST	0	0	0	0	1	1
ENSG00000231503	ENSG00000231503	PTMAP4	12:9381128-9428413	NOTEST	0.0925512	0.246857	1.41535	0	1	1
ENSG00000231504	ENSG00000231504	NMD3P2	7:56569976-56570737	NOTEST	0	0	0	0	1	1
ENSG00000231505	ENSG00000231505	AC108868.5	2:107138358-107154535	NOTEST	0	0	0	0	1	1
ENSG00000231507	ENSG00000231507	RP11-134P9.3	1:203256279-203257929	NOTEST	0	0	0	0	1	1
ENSG00000231508	ENSG00000231508	RP11-452K12.6	10:99116114-99185831	NOTEST	0	0	0	0	1	1
ENSG00000231509	ENSG00000231509	RP11-574F11.3	9:5584489-5588994	NOTEST	0.0464441	0	#NAME?	0	1	1
ENSG00000231510	ENSG00000231510	RP11-542C10.1	1:5146518-5150959	NOTEST	0	0	0	0	1	1
ENSG00000231511	ENSG00000231511	RP11-45O22.3	9:41796923-41797395	NOTEST	0	0	0	0	1	1
ENSG00000231512	ENSG00000231512	RP11-261C10.2	1:243192813-243215554	NOTEST	0.060537	0	#NAME?	0	1	1
ENSG00000231513	ENSG00000231513	RP11-274K13.5	X:135179993-135180507	NOTEST	0	0	0	0	1	1
ENSG00000231514	ENSG00000231514	FAM58CP	Y:28740997-28780799	NOTEST	0	0	0	0	1	1
ENSG00000231515	ENSG00000231515	AC006003.3	7:157331749-158380480	NOTEST	0	0	0	0	1	1
ENSG00000231516	ENSG00000231516	CBX1P5	3:166528796-166529355	NOTEST	0	0	0	0	1	1
ENSG00000231517	ENSG00000231517	RP11-7G23.5	9:45737472-45738490	NOTEST	0	0	0	0	1	1
ENSG00000231518	ENSG00000231518	RP11-327L3.3	9:35930008-35937148	NOTEST	0	0	0	0	1	1
ENSG00000231519	ENSG00000231519	AC007285.7	7:30067019-30170096	NOTEST	0.20209	0.453501	1.16611	0	1	1
ENSG00000231521	ENSG00000231521	RP11-244N9.4	9:100263461-100436030	NOTEST	0	0	0	0	1	1
ENSG00000231522	ENSG00000231522	XXbac-BPG27H4.8	HSCHR6_MHC_COX:30797161-30805800	NOTEST	0	0	0	0	1	1
ENSG00000231523	ENSG00000231523	RP11-196D18.5	7:62577878-62615312	NOTEST	0	0	0	0	1	1
ENSG00000231525	ENSG00000231525	AC002486.2	7:20628612-20629708	NOTEST	0.313759	0.36225	0.207329	0	1	1
ENSG00000231526	ENSG00000231526	HLA-DQA2	HSCHR6_MHC_SSTO:32795637-32805799	NOTEST	0	0	0	0	1	1
ENSG00000231528	ENSG00000231528	FAM225A	9:115875352-115882208	NOTEST	0.50863	0.479626	-0.0847076	0	1	1
ENSG00000231529	ENSG00000231529	RP11-410C4.4	1:220658445-220660385	NOTEST	0	0	0	0	1	1
ENSG00000231530	ENSG00000231530	RP11-187A9.3	13:42614175-42830714	NOTEST	0	0	0	0	1	1
ENSG00000231531	ENSG00000231531	HINT1P1	7:143009773-143010154	NOTEST	0	0	0	0	1	1
ENSG00000231532	ENSG00000231532	AC022311.1	2:4675811-4703805	NOTEST	0	0	0	0	1	1
ENSG00000231533	ENSG00000231533	RP1-232L24.3	6:80130013-80131022	NOTEST	0	0.143935	inf	0	1	1
ENSG00000231534	ENSG00000231534	FBXO36-IT1	2:230628553-230877825	NOTEST	0	0	0	0	1	1
ENSG00000231535	ENSG00000231535	LINC00278	Y:2870952-2970313	NOTEST	0	0	0	0	1	1
ENSG00000231536	ENSG00000231536	AC123886.2	2:111368492-111369981	NOTEST	0	0	0	0	1	1
ENSG00000231537	ENSG00000231537	RP11-1217F2.3	7:57235586-57236358	NOTEST	0	0	0	0	1	1
ENSG00000231538	ENSG00000231538	DPP10-AS3	2:115199875-116603328	NOTEST	0	0	0	0	1	1
ENSG00000231539	ENSG00000231539	AC010132.10	7:42869270-42884037	NOTEST	0	0	0	0	1	1
ENSG00000231540	ENSG00000231540	TCEB1P9	Y:25954967-25955206	NOTEST	0	0	0	0	1	1
ENSG00000231541	ENSG00000231541	RPS6P2	2:179385909-179914813	NOTEST	0	0	0	0	1	1
ENSG00000231542	ENSG00000231542	TAB3-AS1	X:30845558-30993201	NOTEST	0	0	0	0	1	1
ENSG00000231543	ENSG00000231543	C2	HSCHR6_MHC_DBB:31847748-31902052	NOTEST	0	0	0	0	1	1

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ENSG00000231544	ENSG00000231544	RSL24D1P11	18:55505707-55506198	NOTEST	0	0.0330881	inf	0	1	1
ENSG00000231546	ENSG00000231546	RPL3P5	2:237232793-237416185	NOTEST	0	0	0	0	1	1
ENSG00000231547	ENSG00000231547	RP11-38O14.6	1:202968865-202969480	NOTEST	0	0	0	0	1	1
ENSG00000231548	ENSG00000231548	OR55B1P	11:4167511-4168525	NOTEST	0	0	0	0	1	1
ENSG00000231549	ENSG00000231549	USMG5P1	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000231550	ENSG00000231550	PTCHD3P2	2:170550974-170633499	NOTEST	0.0261443	0	#NAME?	0	1	1
ENSG00000231551	ENSG00000231551	RP11-495P10.1	1:147835126-147931933	NOTEST	0.0436689	0.0127172	-1.77982	0	1	1
ENSG00000231552	ENSG00000231552	IGBP1P3	3:32662394-32663394	NOTEST	0	0	0	0	1	1
ENSG00000231553	ENSG00000231553	RNMTL1P1	10:21682961-21683521	NOTEST	0	0	0	0	1	1
ENSG00000231555	ENSG00000231555	HSPA1B	HSCHR6_MHC_DBB:31777701-31780222	NOTEST	0	0	0	0	1	1
ENSG00000231556	ENSG00000231556	RSL24D1P3	7:64800086-64800581	NOTEST	0	0	0	0	1	1
ENSG00000231557	ENSG00000231557	AC018717.1	2:199747296-199936514	NOTEST	0	0	0	0	1	1
ENSG00000231558	ENSG00000231558	HLA-DOA	HSCHR6_MHC_MANN:33125749-33131183	NOTEST	0	0	0	0	1	1
ENSG00000231559	ENSG00000231559	RP3-354J5.3	6:109138882-109139129	NOTEST	0	0	0	0	1	1
ENSG00000231560	ENSG00000231560	AC091814.3	12:10100735-10183205	NOTEST	0	0	0	0	1	1
ENSG00000231561	ENSG00000231561	CEACAMP5	19:43158351-43173228	NOTEST	0	0	0	0	1	1
ENSG00000231562	ENSG00000231562	RP11-508N12.3	9:109625377-109865269	NOTEST	0	0	0	0	1	1
ENSG00000231563	ENSG00000231563	RP11-245P10.4	1:228595081-228604562	NOTEST	0	0.10143	inf	0	1	1
ENSG00000231564	ENSG00000231564	EIF4A1P11	1:179068461-179198819	NOTEST	0	0	0	0	1	1
ENSG00000231565	ENSG00000231565	NEK2P2	22:16364866-16366204	NOTEST	0	0	0	0	1	1
ENSG00000231566	ENSG00000231566	RP5-1158E12.3	X:45707327-45710920	NOTEST	0.0726154	0	#NAME?	0	1	1
ENSG00000231567	ENSG00000231567	MTND2P19	2:140975219-140977937	NOTEST	0	0	0	0	1	1
ENSG00000231568	ENSG00000231568	RP11-552E4.4	X:48088267-48088394	NOTEST	0	0	0	0	1	1
ENSG00000231569	ENSG00000231569	RP11-399L7.3	10:89156779-89184549	NOTEST	0	0	0	0	1	1
ENSG00000231570	ENSG00000231570	AC008173.1	2:56977434-56977698	NOTEST	0	0	0	0	1	1
ENSG00000231573	ENSG00000231573	HCG25	HSCHR6_MHC_SSTO:33356677-33379847	NOTEST	0	0	0	0	1	1
ENSG00000231574	ENSG00000231574	RP11-91K9.1	3:177534652-177617012	NOTEST	0	0	0	0	1	1
ENSG00000231575	ENSG00000231575	RP11-162K11.4	10:95753745-96122716	NOTEST	0	0	0	0	1	1
ENSG00000231576	ENSG00000231576	Z95114.3	22:36568981-36569996	NOTEST	0	0	0	0	1	1
ENSG00000231580	ENSG00000231580	RPL32P1	HSCHR6_MHC_APD:33015767-33038372	NOTEST	0	0	0	0	1	1
ENSG00000231582	ENSG00000231582	RP11-293G6__B.4	1:235703352-235705006	NOTEST	0	0	0	0	1	1
ENSG00000231583	ENSG00000231583	AC108938.3	2:111257676-111257812	NOTEST	0	0	0	0	1	1
ENSG00000231585	ENSG00000231585	AC034228.2	5:131142682-131348892	NOTEST	0	0	0	0	1	1
ENSG00000231586	ENSG00000231586	RPS23P9	1:161475219-161648444	NOTEST	0	0	0	0	1	1
ENSG00000231587	ENSG00000231587	SNORD62B	9:134269479-134375584	NOTEST	0	0	0	0	1	1
ENSG00000231588	ENSG00000231588	RP11-50E11.2	10:52065359-52401211	NOTEST	0.172504	0.072994	-1.24078	0	1	1
ENSG00000231589	ENSG00000231589	AC009110.1	16:62630275-62632353	NOTEST	0	0	0	0	1	1
ENSG00000231590	ENSG00000231590	RP11-353J17.3	X:101615315-101726732	NOTEST	0	0	0	0	1	1
ENSG00000231591	ENSG00000231591	TAPSAR1	HSCHR6_MHC_MANN:32962292-33001424	NOTEST	0	0	0	0	1	1
ENSG00000231592	ENSG00000231592	SAR1P1	HSCHR6_MHC_SSTO:29044375-29044971	NOTEST	0	0	0	0	1	1
ENSG00000231593	ENSG00000231593	RP13-34L8.8	X:52590780-52591313	NOTEST	0	0	0	0	1	1
ENSG00000231595	ENSG00000231595	AC005224.2	17:14113804-14121239	NOTEST	0.191682	0.179536	-0.0944432	0	1	1
ENSG00000231596	ENSG00000231596	HLA-DQB3	HSCHR6_MHC_DBB:32674533-32678642	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231597	ENSG00000231597	AC007557.4	2:217536827-217858802	NOTEST	0	0	0	0	1	1
ENSG00000231599	ENSG00000231599	LINC01037	1:187412737-187446354	NOTEST	0	0	0	0	1	1
ENSG00000231600	ENSG00000231600	AC151960.1	X:152415691-152416269	NOTEST	0	0	0	0	1	1
ENSG00000231601	ENSG00000231601	RP11-164C1.2	10:789931-790898	NOTEST	0	0	0	0	1	1
ENSG00000231602	ENSG00000231602	RPL35AP4	HSCHR6_MHC_MCF:33527510-33527612	NOTEST	0	0	0	0	1	1
ENSG00000231603	ENSG00000231603	RP11-344N17.12	X:48239581-48242564	NOTEST	0	0	0	0	1	1
ENSG00000231604	ENSG00000231604	RP5-897D18.1	20:55305452-55306516	NOTEST	0	0	0	0	1	1
ENSG00000231605	ENSG00000231605	RP11-277B15.2	1:167145153-167165029	NOTEST	0	0	0	0	1	1
ENSG00000231606	ENSG00000231606	RP11-344F13.1	1:14548385-14549613	NOTEST	0	0	0	0	1	1
ENSG00000231608	ENSG00000231608	TNXB	HSCHR6_MHC_DBB:31981893-32071805	NOTEST	0	0	0	0	1	1
ENSG00000231609	ENSG00000231609	AC009501.4	2:62900985-63275775	NOTEST	0.343073	0.397323	0.211798	0	1	1
ENSG00000231610	ENSG00000231610	AC021021.1	2:6636008-6643938	NOTEST	0	0	0	0	1	1
ENSG00000231611	ENSG00000231611	AP006216.11	11:116645825-116646592	NOTEST	0.139157	0.126328	-0.139538	0	1	1
ENSG00000231612	ENSG00000231612	RP11-522M21.3	1:245318286-245872733	NOTEST	0	0	0	0	1	1
ENSG00000231613	ENSG00000231613	RP5-943J3.1	1:89990394-90402170	NOTEST	0	0.0312052	inf	0	1	1
ENSG00000231615	ENSG00000231615	RP11-296O14.2	1:173331535-173332872	NOTEST	0	0	0	0	1	1
ENSG00000231616	ENSG00000231616	RP11-575L7.4	9:86444570-86536342	NOTEST	0.0349177	0.067688	0.954941	0	1	1
ENSG00000231617	ENSG00000231617	DAXX	HSCHR6_MHC_MCF:33456680-33468861	NOTEST	0	0	0	0	1	1
ENSG00000231618	ENSG00000231618	PPT2	HSCHR6_MHC_MCF:32192561-32222305	NOTEST	0	0	0	0	1	1
ENSG00000231619	ENSG00000231619	GS1-542M4.3	X:8824705-8825100	NOTEST	0	0	0	0	1	1
ENSG00000231620	ENSG00000231620	AP000855.4	21:20673929-20676056	NOTEST	0	0	0	0	1	1
ENSG00000231621	ENSG00000231621	AC013264.2	2:197831740-198175897	NOTEST	0	0	0	0	1	1
ENSG00000231622	ENSG00000231622	RP4-700A9.1	1:65613231-65697828	NOTEST	0	0	0	0	1	1
ENSG00000231623	ENSG00000231623	RPL15P4	HSCHR6_MHC_SSTO:31485837-31486417	NOTEST	0	0	0	0	1	1
ENSG00000231624	ENSG00000231624	C6orf15	HSCHR6_MHC_MANN:31123948-31125285	NOTEST	0	0	0	0	1	1
ENSG00000231625	ENSG00000231625	CTD-2104P17.1	17:19519101-19537138	NOTEST	0.0303417	0.0924604	1.60753	0	1	1
ENSG00000231626	ENSG00000231626	AC013402.4	2:105197278-105198348	NOTEST	0	0	0	0	1	1
ENSG00000231628	ENSG00000231628	RP3-355L5.4	6:105725439-105850959	NOTEST	0.180198	0.588195	1.70671	0	1	1
ENSG00000231630	ENSG00000231630	RP11-740P5.3	1:2730996-2731563	NOTEST	0	0	0	0	1	1
ENSG00000231631	ENSG00000231631	PSMB8	HSCHR6_MHC_SSTO:32898408-32937507	NOTEST	0	0	0	0	1	1
ENSG00000231632	ENSG00000231632	RP11-82L18.4	9:91624948-91625393	NOTEST	0	0	0	0	1	1
ENSG00000231633	ENSG00000231633	LINC00283	13:103395339-103397574	NOTEST	0.00836217	0	#NAME?	0	1	1
ENSG00000231635	ENSG00000231635	ATP5BP1	2:98703578-98929762	NOTEST	0	0	0	0	1	1
ENSG00000231636	ENSG00000231636	AGBL5-AS1	2:27265231-27294641	NOTEST	0	0	0	0	1	1
ENSG00000231637	ENSG00000231637	USP17L29	4:9355363-9356956	NOTEST	0	0	0	0	1	1
ENSG00000231638	ENSG00000231638	AC011738.4	7:43152197-43605600	NOTEST	0	0.0080015	inf	0	1	1
ENSG00000231641	ENSG00000231641	TRIM26	HSCHR6_MHC_MCF:30230671-30259555	NOTEST	0	0	0	0	1	1
ENSG00000231643	ENSG00000231643	GHc-210E9.2	X:100446103-100446398	NOTEST	0	0	0	0	1	1
ENSG00000231645	ENSG00000231645	AC025627.9	17:20415872-20420792	NOTEST	0	0	0	0	1	1
ENSG00000231646	ENSG00000231646	AC008174.3	2:186584600-186698017	NOTEST	0	0	0	0	1	1
ENSG00000231647	ENSG00000231647	DDX39B-AS1	HSCHR6_MHC_MANN:31536012-31554120	NOTEST	0	0	0	0	1	1
ENSG00000231648	ENSG00000231648	RP11-372M18.2	1:209541006-209553035	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231649	ENSG00000231649	SPATA31B1	9:84672561-84678597	NOTEST	0	0	0	0	1	1
ENSG00000231650	ENSG00000231650	RFESDP1	13:23424239-23424700	NOTEST	0	0	0	0	1	1
ENSG00000231651	ENSG00000231651	DLG3-AS1	X:69664710-69725337	NOTEST	0	0.0516821	inf	0	1	1
ENSG00000231652	ENSG00000231652	RP11-553A21.3	6:74403625-74538040	NOTEST	0.125315	0.0726137	-0.787243	0	1	1
ENSG00000231653	ENSG00000231653	AC010731.3	2:207504796-207506006	NOTEST	0	0	0	0	1	1
ENSG00000231654	ENSG00000231654	RPS6KA2-AS1	6:166822851-167370679	NOTEST	0	0	0	0	1	1
ENSG00000231655	ENSG00000231655	AC011742.3	2:26363131-26364133	NOTEST	0	0	0	0	1	1
ENSG00000231656	ENSG00000231656	FAM90A18P	8:7580612-7591823	NOTEST	0	0	0	0	1	1
ENSG00000231659	ENSG00000231659	UBQLN1P1	HSCHR6_MHC_MANN:30375567-30376736	NOTEST	0	0	0	0	1	1
ENSG00000231660	ENSG00000231660	RPS8P6	3:237440-451090	NOTEST	0	0	0	0	1	1
ENSG00000231662	ENSG00000231662	RP11-686D16.1	6:19290549-19321252	NOTEST	0.204589	0	#NAME?	0	1	1
ENSG00000231665	ENSG00000231665	OGFOD1P1	13:49784557-49786430	NOTEST	0	0.00734887	inf	0	1	1
ENSG00000231666	ENSG00000231666	RP11-404O13.1	1:158101833-158110429	NOTEST	0	0	0	0	1	1
ENSG00000231667	ENSG00000231667	OR7E111P	13:68476486-68477374	NOTEST	0	0	0	0	1	1
ENSG00000231668	ENSG00000231668	PPP2R2DP1	3:38080695-38178733	NOTEST	0	0	0	0	1	1
ENSG00000231670	ENSG00000231670	OR2N1P	HSCHR6_MHC_SSTO:29105678-29106615	NOTEST	0	0	0	0	1	1
ENSG00000231671	ENSG00000231671	RP11-157N3.1	1:101788892-101855859	NOTEST	0	0	0	0	1	1
ENSG00000231672	ENSG00000231672	DIRC3	2:218147461-218621316	NOTEST	0.442792	0.196872	-1.16937	0	1	1
ENSG00000231674	ENSG00000231674	LINC00410	13:91543207-91578851	NOTEST	0	0	0	0	1	1
ENSG00000231675	ENSG00000231675	AC005042.3	2:159313475-159610287	NOTEST	0	0	0	0	1	1
ENSG00000231676	ENSG00000231676	OR2J2	HSCHR6_MHC_COX:29137978-29139019	NOTEST	0	0	0	0	1	1
ENSG00000231677	ENSG00000231677	HLA-DQB1-AS1	HSCHR6_MHC_COX:32542404-32557884	NOTEST	0	0	0	0	1	1
ENSG00000231678	ENSG00000231678	RP11-339N8.1	9:111463649-111465372	NOTEST	0	0	0	0	1	1
ENSG00000231679	ENSG00000231679	HLA-DRB3$0301	HSCHR6_MHC_COX:32411910-32425028	NOTEST	0	0	0	0	1	1
ENSG00000231680	ENSG00000231680	AP003774.6	11:64161813-64163303	NOTEST	0	0	0	0	1	1
ENSG00000231681	ENSG00000231681	AC020743.3	7:50241834-50243914	NOTEST	0	0	0	0	1	1
ENSG00000231682	ENSG00000231682	AC097713.4	2:235346971-235370771	NOTEST	0	0	0	0	1	1
ENSG00000231683	ENSG00000231683	RP1-27K12.2	6:53362138-53481969	NOTEST	0	0	0	0	1	1
ENSG00000231688	ENSG00000231688	RPL21P43	3:168576446-168576918	NOTEST	0.0493392	0	#NAME?	0	1	1
ENSG00000231689	ENSG00000231689	LINC01090	2:188577542-189152418	NOTEST	0	0	0	0	1	1
ENSG00000231690	ENSG00000231690	LINC00574	6:170188885-170202969	NOTEST	0	0	0	0	1	1
ENSG00000231691	ENSG00000231691	RP11-203F10.5	1:204187978-204346793	NOTEST	0	0	0	0	1	1
ENSG00000231694	ENSG00000231694	RP5-1014O16.10	X:148842439-148842535	NOTEST	0	0	0	0	1	1
ENSG00000231697	ENSG00000231697	NANOGP5	9:102861537-103063282	NOTEST	0	0	0	0	1	1
ENSG00000231698	ENSG00000231698	AP002856.5	11:131123316-131220812	NOTEST	0	0	0	0	1	1
ENSG00000231699	ENSG00000231699	AC020550.7	2:198351304-198418423	NOTEST	0	0	0	0	1	1
ENSG00000231700	ENSG00000231700	RP11-367J7.4	1:157678875-157679433	NOTEST	0	0	0	0	1	1
ENSG00000231701	ENSG00000231701	BMS1P13	9:70334348-70337925	NOTEST	0	0	0	0	1	1
ENSG00000231702	ENSG00000231702	RP11-54O7.10	1:943455-943609	NOTEST	0	0	0	0	1	1
ENSG00000231703	ENSG00000231703	RP4-669H2.1	20:51588945-52120853	NOTEST	0	0	0	0	1	1
ENSG00000231704	ENSG00000231704	AC004895.4	7:6120733-6132716	NOTEST	0	0.101715	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231705	ENSG00000231705	RP11-432J24.2	10:134232586-134234457	NOTEST	0	0	0	0	1	1
ENSG00000231706	ENSG00000231706	CYCSP43	X:68705185-68705495	NOTEST	0	0	0	0	1	1
ENSG00000231707	ENSG00000231707	PABPC1P1	4:39824482-39979576	NOTEST	0	0	0	0	1	1
ENSG00000231709	ENSG00000231709	RP5-857K21.1	1:521368-532878	NOTEST	0.357599	0.33446	-0.0965099	0	1	1
ENSG00000231710	ENSG00000231710	XXbac-BPG248L24.10	HSCHR6_MHC_DBB:31267736-31268471	NOTEST	0	0	0	0	1	1
ENSG00000231711	ENSG00000231711	LINC00899	22:46435786-46440733	NOTEST	0.0640254	0.022861	-1.48576	0	1	1
ENSG00000231712	ENSG00000231712	AC104698.2	2:30432860-30433173	NOTEST	0	0	0	0	1	1
ENSG00000231713	ENSG00000231713	AF064860.7	21:41099681-41102607	NOTEST	0	0	0	0	1	1
ENSG00000231714	ENSG00000231714	RP11-476H20.1	1:194320072-194321556	NOTEST	0	0	0	0	1	1
ENSG00000231715	ENSG00000231715	COX6CP2	20:49096303-49096528	NOTEST	0	0.188993	inf	0	1	1
ENSG00000231716	ENSG00000231716	CDY23P	Y:28140830-28141844	NOTEST	0	0	0	0	1	1
ENSG00000231718	ENSG00000231718	RP11-382E9.1	1:199117725-199362435	NOTEST	0	0	0	0	1	1
ENSG00000231719	ENSG00000231719	MCCD1P2	HSCHR6_MHC_DBB:29952162-29953040	NOTEST	0	0	0	0	1	1
ENSG00000231720	ENSG00000231720	RP11-568A7.3	6:167650995-167653968	NOTEST	0	0	0	0	1	1
ENSG00000231722	ENSG00000231722	AC012075.1	2:81645846-81646426	NOTEST	0	0	0	0	1	1
ENSG00000231723	ENSG00000231723	AC018880.2	2:104240087-104240288	NOTEST	0	0	0	0	1	1
ENSG00000231724	ENSG00000231724	RP11-573D15.3	3:186525480-186543310	NOTEST	0	0.0285542	inf	0	1	1
ENSG00000231725	ENSG00000231725	VN1R110P	X:48494552-48495523	NOTEST	0	0	0	0	1	1
ENSG00000231726	ENSG00000231726	HMGN2P38	11:73111531-73309234	NOTEST	0	0	0	0	1	1
ENSG00000231728	ENSG00000231728	LL0XNC01-116E7.2	X:103172004-103229570	NOTEST	0.0676571	0.126305	0.900595	0	1	1
ENSG00000231729	ENSG00000231729	ARHGEF9-IT1	X:62854846-63005426	NOTEST	0	0	0	0	1	1
ENSG00000231731	ENSG00000231731	AC010976.2	2:128193782-128284462	NOTEST	0	0.040078	inf	0	1	1
ENSG00000231733	ENSG00000231733	XXbac-BPG27H4.8	HSCHR6_MHC_DBB:30797974-30806609	NOTEST	0	0	0	0	1	1
ENSG00000231734	ENSG00000231734	RP6-206I17.2	1:143647637-143745417	NOTEST	0.261699	0.218086	-0.26301	0	1	1
ENSG00000231735	ENSG00000231735	RP11-1O7.1	2:174162356-174163240	NOTEST	0	0	0	0	1	1
ENSG00000231737	ENSG00000231737	PPP1R10	HSCHR6_MHC_MANN:30612851-30638847	NOTEST	0	0	0	0	1	1
ENSG00000231739	ENSG00000231739	GAPDHP59	2:187866602-188430487	NOTEST	0	0	0	0	1	1
ENSG00000231740	ENSG00000231740	RP11-63G10.2	1:59250822-59365384	NOTEST	0	0	0	0	1	1
ENSG00000231741	ENSG00000231741	RP11-213G2.5	9:88549502-88551514	NOTEST	0	0	0	0	1	1
ENSG00000231743	ENSG00000231743	RP11-89K18.1	10:2978212-2978633	NOTEST	0	0	0	0	1	1
ENSG00000231744	ENSG00000231744	RP11-164H5.1	9:127279553-127535206	NOTEST	0	0	0	0	1	1
ENSG00000231745	ENSG00000231745	MCCD1P2	HSCHR6_MHC_MANN:29957385-29958263	NOTEST	0	0	0	0	1	1
ENSG00000231746	ENSG00000231746	RPL13P	HSCHR6_MHC_SSTO:28827312-28831035	NOTEST	0	0	0	0	1	1
ENSG00000231747	ENSG00000231747	AC079922.2	2:113379385-113379744	NOTEST	0	0	0	0	1	1
ENSG00000231748	ENSG00000231748	RP11-227H15.5	10:70975088-71027904	NOTEST	0	0	0	0	1	1
ENSG00000231749	ENSG00000231749	ABCA9-AS1	17:66970628-67057205	NOTEST	0	0	0	0	1	1
ENSG00000231750	ENSG00000231750	NANOGP10	X:43266913-43267808	NOTEST	0	0	0	0	1	1
ENSG00000231752	ENSG00000231752	EMBP1	1:121261142-121310591	NOTEST	0.155361	0.136474	-0.186994	0	1	1
ENSG00000231754	ENSG00000231754	RP11-204E9.1	6:21522706-21524003	NOTEST	0	0	0	0	1	1
ENSG00000231755	ENSG00000231755	CHODL-AS1	21:19207332-19257925	NOTEST	0.0600038	0.0578245	-0.0533737	0	1	1
ENSG00000231756	ENSG00000231756	RP11-183I6.2	9:16409500-16870841	NOTEST	0	0	0	0	1	1
ENSG00000231757	ENSG00000231757	FAM74A2	9:41306132-41311985	NOTEST	0	0	0	0	1	1
ENSG00000231758	ENSG00000231758	AC092652.1	2:143848930-144533642	NOTEST	0.0660677	0.0645217	-0.0341596	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231759	ENSG00000231759	CYP21A1P	HSCHR6_MHC_DBB:31955598-31958414	NOTEST	0	0	0	0	1	1
ENSG00000231760	ENSG00000231760	RP11-350J20.5	6:150045450-150132556	NOTEST	0.0286035	0.0122229	-1.22661	0	1	1
ENSG00000231762	ENSG00000231762	RP11-354K4.1	6:77370202-77372487	NOTEST	0	0	0	0	1	1
ENSG00000231763	ENSG00000231763	PQLC1P1	7:88239554-88239983	NOTEST	0	0	0	0	1	1
ENSG00000231765	ENSG00000231765	PPP1R11P2	X:57255466-57255848	NOTEST	0	0	0	0	1	1
ENSG00000231766	ENSG00000231766	AC013437.7	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000231768	ENSG00000231768	RP5-855F14.1	1:234663636-234667525	NOTEST	0.0409968	0.0608394	0.569495	0	1	1
ENSG00000231769	ENSG00000231769	RP1-8B1.4	6:46064829-46097443	NOTEST	0	0	0	0	1	1
ENSG00000231772	ENSG00000231772	RP1-154K9.2	X:42111711-42558636	NOTEST	0	0	0	0	1	1
ENSG00000231773	ENSG00000231773	ZDHHC20P2	HSCHR6_MHC_QBL:31338301-31338728	NOTEST	0	0	0	0	1	1
ENSG00000231774	ENSG00000231774	RP11-402P6.11	X:70980624-70981509	NOTEST	0	0	0	0	1	1
ENSG00000231775	ENSG00000231775	RP11-472D17.4	X:52370416-52373978	NOTEST	0	0	0	0	1	1
ENSG00000231776	ENSG00000231776	RP1-90L14.1	6:85130745-85265870	NOTEST	0	0.138191	inf	0	1	1
ENSG00000231777	ENSG00000231777	MTND4P21	2:132129866-132131223	NOTEST	0	0	0	0	1	1
ENSG00000231780	ENSG00000231780	AC090960.1	3:17198653-18959184	NOTEST	0	0	0	0	1	1
ENSG00000231781	ENSG00000231781	AC079896.1	2:82210395-82232824	NOTEST	0	0	0	0	1	1
ENSG00000231782	ENSG00000231782	LINC00575	4:83534265-83542590	NOTEST	0	0	0	0	1	1
ENSG00000231784	ENSG00000231784	DBIL5P	17:647653-658576	NOTEST	0.0874582	0.229045	1.38897	0	1	1
ENSG00000231785	ENSG00000231785	MICC	HSCHR6_MHC_SSTO:30371600-30376206	NOTEST	0	0	0	0	1	1
ENSG00000231787	ENSG00000231787	RP11-370B6.1	X:103159242-103159675	NOTEST	0	0	0	0	1	1
ENSG00000231788	ENSG00000231788	RPL31P50	12:31535156-31768600	NOTEST	0	0	0	0	1	1
ENSG00000231791	ENSG00000231791	RP11-382D12.1	1:184298204-184301960	NOTEST	0	0	0	0	1	1
ENSG00000231793	ENSG00000231793	DOC2GP	11:67380123-67383728	NOTEST	0.021652	0.0762355	1.81596	0	1	1
ENSG00000231794	ENSG00000231794	AC009542.2	7:134868589-134896316	NOTEST	0.24582	0.238449	-0.0439251	0	1	1
ENSG00000231795	ENSG00000231795	ITCH-IT1	20:32951040-33099198	NOTEST	0	0	0	0	1	1
ENSG00000231799	ENSG00000231799	RP13-93L13.2	9:91975701-92113045	NOTEST	0	0	0	0	1	1
ENSG00000231801	ENSG00000231801	ANP32BP2	22:45047714-45048259	NOTEST	0	0	0	0	1	1
ENSG00000231802	ENSG00000231802	AC009502.1	2:220548751-220549517	NOTEST	0	0.0176279	inf	0	1	1
ENSG00000231804	ENSG00000231804	RP11-317B17.3	9:91099766-91100240	NOTEST	0	0	0	0	1	1
ENSG00000231806	ENSG00000231806	PCAT7	9:97317350-97356075	NOTEST	0.119655	0.369603	1.62709	0	1	1
ENSG00000231808	ENSG00000231808	RP11-143M1.4	9:112715-113754	NOTEST	0	0	0	0	1	1
ENSG00000231809	ENSG00000231809	NANOGP9	X:64992582-64993474	NOTEST	0	0	0	0	1	1
ENSG00000231810	ENSG00000231810	RPL36AP35	9:111583976-111584284	NOTEST	0	0	0	0	1	1
ENSG00000231812	ENSG00000231812	AC005326.2	7:97515179-97515386	NOTEST	0	0	0	0	1	1
ENSG00000231814	ENSG00000231814	LINC00210	1:218066241-218094146	NOTEST	0	0	0	0	1	1
ENSG00000231815	ENSG00000231815	AC007179.1	2:59444842-60327335	NOTEST	0	0	0	0	1	1
ENSG00000231816	ENSG00000231816	RP4-782L23.1	1:59762309-60254854	NOTEST	0	0.0587888	inf	0	1	1
ENSG00000231821	ENSG00000231821	NPM1P48	2:4561793-4562646	NOTEST	0	0	0	0	1	1
ENSG00000231823	ENSG00000231823	HLA-DQA2	HSCHR6_MHC_MANN:32862879-32868441	NOTEST	0	0	0	0	1	1
ENSG00000231824	ENSG00000231824	C18orf42	18:5145283-5197502	NOTEST	0	0.0299461	inf	0	1	1
ENSG00000231825	ENSG00000231825	PRRC2A	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000231826	ENSG00000231826	AC016735.2	2:43254991-43266686	NOTEST	0	0	0	0	1	1
ENSG00000231827	ENSG00000231827	RP11-216N14.5	1:153767648-153774567	NOTEST	0	0	0	0	1	1

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ENSG00000231829	ENSG00000231829	RP11-310E22.5	10:96901681-96928182	NOTEST	0	0	0	0	1	1
ENSG00000231830	ENSG00000231830	XX-FW83128A1.2	X:153562309-153563387	NOTEST	0.0868461	0	#NAME?	0	1	1
ENSG00000231831	ENSG00000231831	MTHFD1P1	X:57313138-57515629	NOTEST	0.150238	0.152482	0.021387	0	1	1
ENSG00000231834	ENSG00000231834	HLA-A	HSCHR6_MHC_MANN:29898023-29902665	NOTEST	0	0	0	0	1	1
ENSG00000231836	ENSG00000231836	LINC01149	HSCHR6_MHC_MANN:31451928-31457226	NOTEST	0	0	0	0	1	1
ENSG00000231837	ENSG00000231837	RPS7P2	1:153965160-154127592	NOTEST	0	0	0	0	1	1
ENSG00000231838	ENSG00000231838	RP11-449H15.2	9:45164577-45212501	NOTEST	0	0	0	0	1	1
ENSG00000231839	ENSG00000231839	AC073055.2	7:145280289-145281910	NOTEST	0	0	0	0	1	1
ENSG00000231840	ENSG00000231840	AC073342.12	7:142941185-142985141	NOTEST	0.49496	0.39444	-0.327504	0	1	1
ENSG00000231841	ENSG00000231841	RP11-206F17.2	4:153848597-153849359	NOTEST	0.121523	0.184233	0.600297	0	1	1
ENSG00000231842	ENSG00000231842	RP11-527F13.1	6:126498338-126523385	NOTEST	0	0	0	0	1	1
ENSG00000231845	ENSG00000231845	HMGB3P14	3:133784146-133969689	NOTEST	0.0347079	0.0245782	-0.497886	0	1	1
ENSG00000231846	ENSG00000231846	RP11-494I9.2	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000231848	ENSG00000231848	AC012354.8	2:45223551-45224012	NOTEST	0.0512059	0	#NAME?	0	1	1
ENSG00000231849	ENSG00000231849	UBE2V2P4	1:36690016-36770958	NOTEST	0	0	0	0	1	1
ENSG00000231850	ENSG00000231850	GAGE2B	X:49235707-49242997	NOTEST	0	0	0	0	1	1
ENSG00000231851	ENSG00000231851	AC104655.2	2:105552868-105719402	NOTEST	0.169582	0	#NAME?	0	1	1
ENSG00000231852	ENSG00000231852	CYP21A2	6:32006041-32096030	NOTEST	0	0	0	0	1	1
ENSG00000231854	ENSG00000231854	XXbac-BPG27H4.8	HSCHR6_MHC_MANN:30851992-30860627	NOTEST	0	0	0	0	1	1
ENSG00000231855	ENSG00000231855	GLUDP5	10:31917467-31917527	NOTEST	0	0	0	0	1	1
ENSG00000231856	ENSG00000231856	RP11-327P2.5	13:52378432-52387356	NOTEST	0.367738	0.0819678	-2.16555	0	1	1
ENSG00000231857	ENSG00000231857	MORF4L1P5	X:64547867-64551113	NOTEST	0	0	0	0	1	1
ENSG00000231858	ENSG00000231858	AC067945.4	2:191886251-192016322	NOTEST	0	0	0	0	1	1
ENSG00000231859	ENSG00000231859	AC007875.2	7:97535740-97536134	NOTEST	0	0	0	0	1	1
ENSG00000231860	ENSG00000231860	MDC1-AS1	HSCHR6_MHC_APD:30675830-30693912	NOTEST	0	0	0	0	1	1
ENSG00000231861	ENSG00000231861	OR5K2	3:98216447-98312567	NOTEST	0	0	0	0	1	1
ENSG00000231863	ENSG00000231863	RP3-428L16.1	6:161352111-161390803	NOTEST	0	0	0	0	1	1
ENSG00000231865	ENSG00000231865	SIK3-IT1	11:116706466-116969153	NOTEST	0.0129083	0.0191815	0.571418	0	1	1
ENSG00000231866	ENSG00000231866	RP4-631H13.4	1:53361655-53392884	NOTEST	0	0	0	0	1	1
ENSG00000231867	ENSG00000231867	AP001625.5	21:43892595-44001550	NOTEST	0	0	0	0	1	1
ENSG00000231868	ENSG00000231868	RP1-202O8.2	1:6484847-6580121	NOTEST	0	0	0	0	1	1
ENSG00000231869	ENSG00000231869	DAQB-331I12.5	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000231870	ENSG00000231870	KRT17P3	17:28894717-28898766	NOTEST	0	0	0	0	1	1
ENSG00000231871	ENSG00000231871	IPO9-AS1	1:201592012-201853422	NOTEST	0.10384	0.190501	0.875434	0	1	1
ENSG00000231873	ENSG00000231873	RP11-761N21.1	3:40807697-40904117	NOTEST	0	0	0	0	1	1
ENSG00000231874	ENSG00000231874	TSPY18P	Y:9707272-9708390	NOTEST	0	0	0	0	1	1
ENSG00000231875	ENSG00000231875	RP11-346E8.1	X:80618766-80619669	NOTEST	0.020291	0	#NAME?	0	1	1
ENSG00000231876	ENSG00000231876	AC009158.1	16:26329427-26345749	NOTEST	0	0	0	0	1	1
ENSG00000231877	ENSG00000231877	RP11-177F15.1	1:238643683-238701605	NOTEST	0	0.00382082	inf	0	1	1
ENSG00000231878	ENSG00000231878	SNRPFP1	20:48346127-48346379	NOTEST	0	0.251328	inf	0	1	1
ENSG00000231879	ENSG00000231879	TXNL1P1	13:87377754-87378308	NOTEST	0	0	0	0	1	1
ENSG00000231880	ENSG00000231880	KBTBD4	11:47487495-47606114	NOTEST	0.0871488	0.130254	0.579776	0	1	1

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ENSG00000231881	ENSG00000231881	RP5-1120P11.3	6:43963459-44045689	NOTEST	0.0187519	0	#NAME?	0	1	1
ENSG00000231882	ENSG00000231882	F10-AS1	13:113777127-113803843	NOTEST	0	0	0	0	1	1
ENSG00000231883	ENSG00000231883	RP1-297M16.2	6:151186684-151549582	NOTEST	0	0	0	0	1	1
ENSG00000231884	ENSG00000231884	NDUFB1P1	3:48198635-48229892	NOTEST	0	0	0	0	1	1
ENSG00000231887	ENSG00000231887	PRH1	12:10977558-11324212	NOTEST	0.160505	0	#NAME?	0	1	1
ENSG00000231888	ENSG00000231888	MTND5P15	3:176728506-176728855	NOTEST	0	0	0	0	1	1
ENSG00000231890	ENSG00000231890	AC093391.2	2:136664246-136779888	NOTEST	0.367926	0.253828	-0.535569	0	1	1
ENSG00000231892	ENSG00000231892	AC073316.2	7:3236257-3237888	NOTEST	0	0	0	0	1	1
ENSG00000231894	ENSG00000231894	WDR95P	13:31651390-31689836	NOTEST	0	0	0	0	1	1
ENSG00000231895	ENSG00000231895	HLA-DPA3	HSCHR6_MHC_APD:33082355-33082482	NOTEST	0	0	0	0	1	1
ENSG00000231896	ENSG00000231896	AC019185.4	2:209224437-209719227	NOTEST	0	0	0	0	1	1
ENSG00000231897	ENSG00000231897	MARK2P14	3:11948000-11953787	NOTEST	0	0	0	0	1	1
ENSG00000231898	ENSG00000231898	AC012594.1	2:171034654-171551884	NOTEST	0	0	0	0	1	1
ENSG00000231900	ENSG00000231900	GOT2P1	1:55833138-55834447	NOTEST	0	0	0	0	1	1
ENSG00000231901	ENSG00000231901	RP11-281A20.1	9:120545725-120659534	NOTEST	0	0	0	0	1	1
ENSG00000231902	ENSG00000231902	RP11-29B9.2	9:7960412-7961080	NOTEST	0	0	0	0	1	1
ENSG00000231903	ENSG00000231903	AC079354.5	2:202937977-203062585	NOTEST	0.203417	0	#NAME?	0	1	1
ENSG00000231904	ENSG00000231904	HLA-H	HSCHR6_MHC_APD:29793553-29796732	NOTEST	0	0	0	0	1	1
ENSG00000231905	ENSG00000231905	SETP10	1:179068461-179198819	NOTEST	0	0	0	0	1	1
ENSG00000231906	ENSG00000231906	RP11-541M12.3	10:49654076-49864310	NOTEST	0	0	0	0	1	1
ENSG00000231907	ENSG00000231907	GAPDHP37	22:41069487-41070455	NOTEST	0	0.0144919	inf	0	1	1
ENSG00000231909	ENSG00000231909	RP11-363E7.3	9:19460923-19464522	NOTEST	0	0	0	0	1	1
ENSG00000231910	ENSG00000231910	GAMTP2	13:34922179-35245319	NOTEST	0	0	0	0	1	1
ENSG00000231911	ENSG00000231911	TPRKBP1	10:28947915-28948396	NOTEST	0	0	0	0	1	1
ENSG00000231912	ENSG00000231912	RP1-249H1.2	6:114113031-114158556	NOTEST	0	0	0	0	1	1
ENSG00000231913	ENSG00000231913	RARRES2P3	X:21392535-21672813	NOTEST	0	0	0	0	1	1
ENSG00000231914	ENSG00000231914	LINC00387	13:19246966-19250303	NOTEST	0	0	0	0	1	1
ENSG00000231915	ENSG00000231915	SALL4P5	3:23031313-23033073	NOTEST	0	0	0	0	1	1
ENSG00000231916	ENSG00000231916	AC006033.22	7:38350983-38351409	NOTEST	0	0	0	0	1	1
ENSG00000231918	ENSG00000231918	AC007682.1	2:51259738-52635055	NOTEST	0	0	0	0	1	1
ENSG00000231919	ENSG00000231919	OR2H4P	HSCHR6_MHC_MANN:29183058-29184002	NOTEST	0	0	0	0	1	1
ENSG00000231920	ENSG00000231920	NEBL-AS1	10:21068901-21463977	NOTEST	0	0	0	0	1	1
ENSG00000231922	ENSG00000231922	AL138479.3	14:54383987-54384471	NOTEST	0	0	0	0	1	1
ENSG00000231923	ENSG00000231923	AC024082.3	7:137687069-137802732	NOTEST	0	0	0	0	1	1
ENSG00000231926	ENSG00000231926	SEPHS1P7	2:115017626-115018803	NOTEST	0	0	0	0	1	1
ENSG00000231927	ENSG00000231927	AC102953.6	7:1548290-1549063	NOTEST	0	0	0	0	1	1
ENSG00000231928	ENSG00000231928	TRIM26BP	HSCHR6_MHC_MANN:30246906-30359341	NOTEST	0	0	0	0	1	1
ENSG00000231929	ENSG00000231929	HMGB3P31	X:134095740-134096335	NOTEST	0	0	0	0	1	1
ENSG00000231930	ENSG00000231930	AF228730.5	8:7058277-7058379	NOTEST	0	0	0	0	1	1
ENSG00000231931	ENSG00000231931	AC024082.4	7:137687069-137802732	NOTEST	0	0	0	0	1	1
ENSG00000231933	ENSG00000231933	CTA-125H2.2	22:26138110-26427007	NOTEST	0	0	0	0	1	1
ENSG00000231934	ENSG00000231934	RP4-610C12.1	20:29558487-29596406	NOTEST	0.0996397	0	#NAME?	0	1	1
ENSG00000231937	ENSG00000231937	RP11-329E24.6	X:151307354-151619830	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231939	ENSG00000231939	HLA-DQB1	HSCHR6_MHC_SSTO:32697727-32726026	NOTEST	0	0	0	0	1	1
ENSG00000231940	ENSG00000231940	RPS7P3	1:233086350-233431473	NOTEST	0	0.0540203	inf	0	1	1
ENSG00000231941	ENSG00000231941	HCG4B	HSCHR6_MHC_DBB:29885324-29888576	NOTEST	0	0	0	0	1	1
ENSG00000231942	ENSG00000231942	HNRNPA1P36	8:82704057-82755101	NOTEST	0.0881589	0.0845684	-0.0599889	0	1	1
ENSG00000231943	ENSG00000231943	RP11-395L14.4	2:114285144-114320875	NOTEST	0.031339	0.0756923	1.27219	0	1	1
ENSG00000231944	ENSG00000231944	PHKA1-AS1	X:71798663-71934167	NOTEST	0	0	0	0	1	1
ENSG00000231945	ENSG00000231945	VARS	HSCHR6_MHC_SSTO:31735248-31822599	NOTEST	0	0	0	0	1	1
ENSG00000231947	ENSG00000231947	MTND2P24	X:55205626-55206432	NOTEST	0	0	0	0	1	1
ENSG00000231948	ENSG00000231948	HS1BP3-IT1	2:20760207-20850849	NOTEST	0.103881	0.0245235	-2.08269	0	1	1
ENSG00000231949	ENSG00000231949	RP4-591L5.2	1:30888671-30893955	NOTEST	0	0	0	0	1	1
ENSG00000231951	ENSG00000231951	AC004837.4	7:39605974-39649919	NOTEST	0	0	0	0	1	1
ENSG00000231952	ENSG00000231952	DPY19L1P2	7:32535037-33102409	NOTEST	0.435108	0.590367	0.440238	0	1	1
ENSG00000231953	ENSG00000231953	RP4-706G24.1	1:25534629-25535360	NOTEST	0	0	0	0	1	1
ENSG00000231954	ENSG00000231954	MTND2P22	2:131030051-131031084	NOTEST	0	0	0	0	1	1
ENSG00000231955	ENSG00000231955	AC007383.4	2:206979540-207027652	NOTEST	0	0	0	0	1	1
ENSG00000231956	ENSG00000231956	HNRNPA1P9	7:87133174-87461611	NOTEST	0	0	0	0	1	1
ENSG00000231957	ENSG00000231957	GNAI2P2	10:79828380-79829296	NOTEST	0	0	0	0	1	1
ENSG00000231960	ENSG00000231960	XXbac-BCX196D17.5	HSCHR6_MHC_MANN:29091991-29096689	NOTEST	0	0	0	0	1	1
ENSG00000231961	ENSG00000231961	RP5-967N21.7	20:5931297-5975852	NOTEST	0	0	0	0	1	1
ENSG00000231962	ENSG00000231962	VN1R7P	21:11153836-11155057	NOTEST	0	0	0	0	1	1
ENSG00000231963	ENSG00000231963	RP11-493K23.4	X:72300005-72304474	NOTEST	0	0	0	0	1	1
ENSG00000231964	ENSG00000231964	RP11-67C2.2	10:45869660-45948569	NOTEST	0	0	0	0	1	1
ENSG00000231965	ENSG00000231965	AF131215.1	8:10753554-11058875	NOTEST	0	0	0	0	1	1
ENSG00000231966	ENSG00000231966	RP11-12M5.4	1:179798743-179805259	NOTEST	0	0	0	0	1	1
ENSG00000231967	ENSG00000231967	RP11-12D24.6	9:5356311-5356525	NOTEST	0	0	0	0	1	1
ENSG00000231968	ENSG00000231968	UBD	HSCHR6_MHC_DBB:29523342-29600923	NOTEST	0	0	0	0	1	1
ENSG00000231969	ENSG00000231969	AC144449.1	2:150426147-150715705	NOTEST	0.0592128	0.0687081	0.21457	0	1	1
ENSG00000231970	ENSG00000231970	RP11-452K12.7	10:99116114-99185831	NOTEST	0.392634	0.251119	-0.644815	0	1	1
ENSG00000231971	ENSG00000231971	RP11-557H15.3	6:134749377-134841723	NOTEST	0.0476832	0.089384	0.906535	0	1	1
ENSG00000231973	ENSG00000231973	OR2I1P	HSCHR6_MHC_QBL:29520915-29521863	NOTEST	0	0	0	0	1	1
ENSG00000231974	ENSG00000231974	APOM	HSCHR6_MHC_MANN:31646290-31665479	NOTEST	0	0	0	0	1	1
ENSG00000231975	ENSG00000231975	MCCD1	HSCHR6_MHC_DBB:31478677-31496802	NOTEST	0	0	0	0	1	1
ENSG00000231976	ENSG00000231976	LINC00202-2	10:26932097-26942383	NOTEST	0.0613132	0.00554963	-3.46573	0	1	1
ENSG00000231977	ENSG00000231977	RP5-963E22.4	20:61798148-61812255	NOTEST	0	0	0	0	1	1
ENSG00000231978	ENSG00000231978	RP11-132G19.3	1:22004790-22110099	NOTEST	0	0	0	0	1	1
ENSG00000231979	ENSG00000231979	RP11-35L17.3	1:239549864-240080255	NOTEST	0	0	0	0	1	1
ENSG00000231980	ENSG00000231980	AC011899.10	7:157331749-158380480	NOTEST	0	0	0	0	1	1
ENSG00000231981	ENSG00000231981	RPL7L1P12	13:99445740-99738879	NOTEST	0	0	0	0	1	1
ENSG00000231982	ENSG00000231982	RP11-573D15.1	3:186544337-186545126	NOTEST	0	0.296929	inf	0	1	1
ENSG00000231983	ENSG00000231983	LINC00415	13:26626413-26627523	NOTEST	0	0	0	0	1	1
ENSG00000231984	ENSG00000231984	RP11-2L13.1	1:199721618-199722018	NOTEST	0	0	0	0	1	1
ENSG00000231985	ENSG00000231985	RP11-82L20.1	1:71547006-72748417	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000231986	ENSG00000231986	AP000474.1	21:25261113-25262857	NOTEST	0	0	0	0	1	1
ENSG00000231987	ENSG00000231987	RP5-898J17.1	1:96719624-96839681	NOTEST	0	0	0	0	1	1
ENSG00000231988	ENSG00000231988	OFD1P3Y	Y:8898634-8908029	NOTEST	0	0	0	0	1	1
ENSG00000231990	ENSG00000231990	RP11-53B5.1	9:96619364-96620615	NOTEST	0	0	0	0	1	1
ENSG00000231992	ENSG00000231992	RP11-57H12.2	1:95582893-95729610	NOTEST	0	0	0	0	1	1
ENSG00000231993	ENSG00000231993	RP1-85F18.5	22:41487789-41593460	NOTEST	0.557984	0.162554	-1.7793	0	1	1
ENSG00000231995	ENSG00000231995	RP11-111F5.2	9:46577619-46578220	NOTEST	0.202048	0.336768	0.737058	0	1	1
ENSG00000231996	ENSG00000231996	RP4-581O6.1	1:100308165-100308317	NOTEST	0	0	0	0	1	1
ENSG00000231997	ENSG00000231997	FAM27D1	9:46389109-46391556	NOTEST	0.43547	0.369516	-0.236937	0	1	1
ENSG00000231998	ENSG00000231998	MCCD1P1	HSCHR6_MHC_COX:29867066-29867931	NOTEST	0	0	0	0	1	1
ENSG00000232000	ENSG00000232000	RP11-54D18.3	9:14987299-15146399	NOTEST	0.00837632	0.00650878	-0.363929	0	1	1
ENSG00000232001	ENSG00000232001	AC108868.6	2:107159469-107160753	NOTEST	0	0	0	0	1	1
ENSG00000232002	ENSG00000232002	AC093642.6	2:242823513-243026289	NOTEST	0	0	0	0	1	1
ENSG00000232003	ENSG00000232003	ZNF736P12Y	Y:26646409-26647652	NOTEST	0	0	0	0	1	1
ENSG00000232004	ENSG00000232004	CAP1P2	10:44100290-44101699	NOTEST	0	0	0	0	1	1
ENSG00000232005	ENSG00000232005	PBX2	HSCHR6_MHC_MANN:32191944-32197387	NOTEST	0	0	0	0	1	1
ENSG00000232006	ENSG00000232006	AC005537.2	7:42993733-43099149	NOTEST	0	0	0	0	1	1
ENSG00000232007	ENSG00000232007	POLR2LP	HSCHR6_MHC_DBB:31102241-31102428	NOTEST	0	0	0	0	1	1
ENSG00000232009	ENSG00000232009	RP11-571E6.4	X:47229981-47273704	NOTEST	0	0	0	0	1	1
ENSG00000232010	ENSG00000232010	AP001059.5	21:45666221-45682099	NOTEST	0	0	0	0	1	1
ENSG00000232011	ENSG00000232011	HLA-W	HSCHR6_MHC_COX:29913885-29915860	NOTEST	0	0	0	0	1	1
ENSG00000232013	ENSG00000232013	AC107021.1	3:145781828-145881440	NOTEST	0.0769762	0.0135008	-2.51136	0	1	1
ENSG00000232014	ENSG00000232014	MTND1P13	22:24347903-24349416	NOTEST	0	0	0	0	1	1
ENSG00000232015	ENSG00000232015	HSPE1P25	1:78245308-78344106	NOTEST	0	0	0	0	1	1
ENSG00000232017	ENSG00000232017	ZNF90P2	HSCHR6_MHC_MCF:28856779-28857854	NOTEST	0	0	0	0	1	1
ENSG00000232018	ENSG00000232018	AL132709.8	14:101426845-101433377	NOTEST	0	0	0	0	1	1
ENSG00000232019	ENSG00000232019	AC074183.4	7:84568664-84569561	NOTEST	0.393098	0.343186	-0.1959	0	1	1
ENSG00000232021	ENSG00000232021	LEF1-AS1	4:108968700-109177992	NOTEST	0.411538	0.282825	-0.541114	0	1	1
ENSG00000232023	ENSG00000232023	AC009410.1	2:229347976-229476111	NOTEST	0	0	0	0	1	1
ENSG00000232025	ENSG00000232025	RP1-218B13.1	X:112160863-112160989	NOTEST	0	0	0	0	1	1
ENSG00000232026	ENSG00000232026	XXbac-BPG254F23.7	HSCHR6_MHC_COX:32609186-32610017	NOTEST	0	0	0	0	1	1
ENSG00000232027	ENSG00000232027	RP11-275F13.3	1:51819934-52027301	NOTEST	0.195297	0.0695387	-1.48978	0	1	1
ENSG00000232028	ENSG00000232028	AC007391.2	2:37552482-37553940	NOTEST	0.0831015	0.139527	0.747601	0	1	1
ENSG00000232029	ENSG00000232029	TCEB1P15	Y:24214966-24215298	NOTEST	0	0	0	0	1	1
ENSG00000232030	ENSG00000232030	MAGEB6P1	X:26178717-26180013	NOTEST	0	0	0	0	1	1
ENSG00000232031	ENSG00000232031	RP5-991C6.4	6:82201155-82462491	NOTEST	0	0	0	0	1	1
ENSG00000232032	ENSG00000232032	AC079781.7	7:97537567-97537736	NOTEST	0	0	0	0	1	1
ENSG00000232034	ENSG00000232034	AC092168.2	2:101436613-101886778	NOTEST	0.0544111	0.102449	0.91293	0	1	1
ENSG00000232035	ENSG00000232035	RP11-87N24.3	9:10631749-10632203	NOTEST	0	0	0	0	1	1
ENSG00000232036	ENSG00000232036	GS1-115G20.2	1:184356191-184598154	NOTEST	0.0128699	0.00905576	-0.507097	0	1	1
ENSG00000232037	ENSG00000232037	RP11-26H16.1	1:22138757-22263790	NOTEST	0	0.115142	inf	0	1	1
ENSG00000232039	ENSG00000232039	DEFT1P2	8:6854287-6875823	NOTEST	0	0	0	0	1	1
ENSG00000232040	ENSG00000232040	SCAND3	6:28539406-28583989	NOTEST	0.122719	0.158673	0.370698	0	1	1
ENSG00000232041	ENSG00000232041	PSMD10P3	13:73610538-73610986	NOTEST	0	0	0	0	1	1
ENSG00000232042	ENSG00000232042	RP11-45J1.1	X:119392504-119445411	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232043	ENSG00000232043	RP4-530I15.9	20:49126890-49201299	NOTEST	0.117519	0.262386	1.15879	0	1	1
ENSG00000232044	ENSG00000232044	LINC01105	2:6072818-6141407	NOTEST	0	0	0	0	1	1
ENSG00000232045	ENSG00000232045	EHMT2	HSCHR6_MHC_APD:31858892-31876828	NOTEST	0	0	0	0	1	1
ENSG00000232046	ENSG00000232046	AC007392.3	2:66801161-66957289	NOTEST	0	0	0	0	1	1
ENSG00000232048	ENSG00000232048	HNRNPCP9	1:68125837-68126696	NOTEST	0	0	0	0	1	1
ENSG00000232049	ENSG00000232049	OR2I1P	HSCHR6_MHC_MCF:29520810-29521758	NOTEST	0	0	0	0	1	1
ENSG00000232050	ENSG00000232050	CTA-125H2.3	22:26138110-26427007	NOTEST	0	0	0	0	1	1
ENSG00000232054	ENSG00000232054	NPM1P34	X:123093082-124097666	NOTEST	0	0	0	0	1	1
ENSG00000232056	ENSG00000232056	AC092687.4	2:10987702-10995081	NOTEST	0	0	0	0	1	1
ENSG00000232057	ENSG00000232057	AC093390.1	2:1792884-2335032	NOTEST	0	0	0	0	1	1
ENSG00000232058	ENSG00000232058	AC005772.2	17:14918121-14955593	NOTEST	0	0	0	0	1	1
ENSG00000232059	ENSG00000232059	RP11-173A6.2	1:244816236-244872335	NOTEST	0	0.363538	inf	0	1	1
ENSG00000232062	ENSG00000232062	HLA-DQA1	HSCHR6_MHC_SSTO:32697727-32726026	NOTEST	0	0	0	0	1	1
ENSG00000232064	ENSG00000232064	USP9YP33	Y:27736469-27738492	NOTEST	0	0	0	0	1	1
ENSG00000232065	ENSG00000232065	LINC01063	3:196358368-196359458	NOTEST	0.166978	0.441431	1.40253	0	1	1
ENSG00000232068	ENSG00000232068	AF003529.2	X:133123469-133124113	NOTEST	0	0	0	0	1	1
ENSG00000232069	ENSG00000232069	RPS29P28	X:95450475-95450616	NOTEST	0	0	0	0	1	1
ENSG00000232070	ENSG00000232070	TMEM253	14:21484921-21572881	NOTEST	0.129808	0.137046	0.0782819	0	1	1
ENSG00000232072	ENSG00000232072	AC004901.1	7:46930222-47118726	NOTEST	0	0	0	0	1	1
ENSG00000232073	ENSG00000232073	RP1-302D9.3	22:33558211-34318829	NOTEST	0.0441221	0	#NAME?	0	1	1
ENSG00000232075	ENSG00000232075	MRPL35P2	10:65394076-65394587	NOTEST	0.0813348	0.0310195	-1.3907	0	1	1
ENSG00000232077	ENSG00000232077	LINC01031	1:193273874-193335083	NOTEST	0	0	0	0	1	1
ENSG00000232079	ENSG00000232079	AL035610.1	21:29420732-29600986	NOTEST	0	0	0	0	1	1
ENSG00000232080	ENSG00000232080	XXbac-BPG254F23.7	6:32685781-32686612	NOTEST	0	0	0	0	1	1
ENSG00000232081	ENSG00000232081	LARGE-IT1	22:33558211-34318829	NOTEST	0	0	0	0	1	1
ENSG00000232082	ENSG00000232082	RPS6KA2-IT1	6:166822851-167370679	NOTEST	0	0.0257985	inf	0	1	1
ENSG00000232083	ENSG00000232083	RPL31P7	17:78518618-78945013	NOTEST	0	0	0	0	1	1
ENSG00000232084	ENSG00000232084	LINC01104	2:100824715-100867946	NOTEST	0	0	0	0	1	1
ENSG00000232085	ENSG00000232085	RP11-261C10.4	1:243287729-243418650	NOTEST	0	0	0	0	1	1
ENSG00000232086	ENSG00000232086	RP11-141J10.1	9:73143978-74061820	NOTEST	0	0	0	0	1	1
ENSG00000232087	ENSG00000232087	HCFC2P1	13:109132573-109134165	NOTEST	0	0	0	0	1	1
ENSG00000232089	ENSG00000232089	AC011233.2	2:222027490-222027773	NOTEST	0	0	0	0	1	1
ENSG00000232090	ENSG00000232090	AC016724.6	2:113753093-113753514	NOTEST	0	0	0	0	1	1
ENSG00000232091	ENSG00000232091	PNLIPP1	10:118336819-118342829	NOTEST	0	0	0	0	1	1
ENSG00000232095	ENSG00000232095	UBQLN1P1	HSCHR6_MHC_COX:30320703-30321872	NOTEST	0	0	0	0	1	1
ENSG00000232096	ENSG00000232096	GS1-122H1.3	1:182098444-182283196	NOTEST	0	0	0	0	1	1
ENSG00000232097	ENSG00000232097	AC079781.8	7:97567750-97568106	NOTEST	0	0	0	0	1	1
ENSG00000232099	ENSG00000232099	ZFP57	HSCHR6_MHC_MANN:29639728-29648438	NOTEST	0	0	0	0	1	1
ENSG00000232100	ENSG00000232100	RP11-152L7.2	1:218216846-218232482	NOTEST	0	0	0	0	1	1
ENSG00000232101	ENSG00000232101	AC108059.2	2:128848773-128953251	NOTEST	0	0	0	0	1	1
ENSG00000232102	ENSG00000232102	MTCO3P2	13:24304327-24476794	NOTEST	0	0	0	0	1	1
ENSG00000232104	ENSG00000232104	RP11-509J21.1	9:3526722-3671646	NOTEST	0	0.110508	inf	0	1	1
ENSG00000232105	ENSG00000232105	RPL32P28	13:62897789-62902966	NOTEST	0	0	0	0	1	1
ENSG00000232106	ENSG00000232106	C6orf10	HSCHR6_MHC_SSTO:32267411-32346296	NOTEST	0	0	0	0	1	1

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ENSG00000232109	ENSG00000232109	AL022344.2	10:43156175-43157224	NOTEST	0	0.013153	inf	0	1	1
ENSG00000232110	ENSG00000232110	RP11-149I23.3	10:90973325-91174314	NOTEST	0	0	0	0	1	1
ENSG00000232111	ENSG00000232111	RP11-126O22.1	X:9370790-9382606	NOTEST	0	0	0	0	1	1
ENSG00000232113	ENSG00000232113	RP11-360D2.1	1:173469602-173639001	NOTEST	0	0	0	0	1	1
ENSG00000232114	ENSG00000232114	AC018693.5	2:38978675-39012142	NOTEST	0	0	0	0	1	1
ENSG00000232115	ENSG00000232115	RP11-123G9.1	10:59866183-59866640	NOTEST	0	0	0	0	1	1
ENSG00000232117	ENSG00000232117	LINC00384	13:30726022-30733758	NOTEST	0.00623085	0	#NAME?	0	1	1
ENSG00000232118	ENSG00000232118	BACH1-AS1	21:30565800-31312351	NOTEST	0	0	0	0	1	1
ENSG00000232120	ENSG00000232120	RP11-349P19.1	6:64345724-66417118	NOTEST	0	0	0	0	1	1
ENSG00000232121	ENSG00000232121	RP13-30A9.1	20:61265032-61267214	NOTEST	0	0	0	0	1	1
ENSG00000232122	ENSG00000232122	HCG4P8	HSCHR6_MHC_MCF:29791625-29795784	NOTEST	0	0	0	0	1	1
ENSG00000232124	ENSG00000232124	AP001057.1	21:45621172-45622579	NOTEST	0	0	0	0	1	1
ENSG00000232125	ENSG00000232125	DYTN	2:207516344-207583120	NOTEST	0	0	0	0	1	1
ENSG00000232126	ENSG00000232126	HLA-B	HSCHR6_MHC_MCF:31398031-31401418	NOTEST	0	0	0	0	1	1
ENSG00000232127	ENSG00000232127	PSORS1C2	HSCHR6_MHC_DBB:31076301-31101556	NOTEST	0	0	0	0	1	1
ENSG00000232128	ENSG00000232128	AC097374.4	2:95533230-95613086	NOTEST	0	0	0	0	1	1
ENSG00000232129	ENSG00000232129	AC011385.2	5:137887849-137888050	NOTEST	0	0	0	0	1	1
ENSG00000232130	ENSG00000232130	RP11-143P4.2	3:192862252-192894653	NOTEST	0	0	0	0	1	1
ENSG00000232131	ENSG00000232131	NCOA7-AS1	6:126102306-126252266	NOTEST	0.0450102	0	#NAME?	0	1	1
ENSG00000232132	ENSG00000232132	NDFIP2-AS1	13:80051498-80130210	NOTEST	0	0	0	0	1	1
ENSG00000232133	ENSG00000232133	IMPDH1P10	2:201980826-202041410	NOTEST	0.264839	0.225008	-0.235139	0	1	1
ENSG00000232134	ENSG00000232134	RPS15AP12	1:220267443-220321380	NOTEST	0.0683144	0.0533424	-0.356907	0	1	1
ENSG00000232135	ENSG00000232135	RP3-461P17.6	20:44162834-44176391	NOTEST	0	0	0	0	1	1
ENSG00000232136	ENSG00000232136	DUXAP7	20:18568536-18744561	NOTEST	0	0	0	0	1	1
ENSG00000232138	ENSG00000232138	IFNWP5	9:21231264-21231852	NOTEST	0.172779	0	#NAME?	0	1	1
ENSG00000232139	ENSG00000232139	LINC00867	10:120116619-120124615	NOTEST	0	0	0	0	1	1
ENSG00000232140	ENSG00000232140	AC073257.1	2:121311318-121315685	NOTEST	0	0	0	0	1	1
ENSG00000232141	ENSG00000232141	ETF1P1	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1
ENSG00000232142	ENSG00000232142	RP11-367H5.8	10:71958743-71958995	NOTEST	0	0	0	0	1	1
ENSG00000232143	ENSG00000232143	GNL1	HSCHR6_MHC_MANN:30553828-30576175	NOTEST	0	0	0	0	1	1
ENSG00000232144	ENSG00000232144	PSAT1P2	2:62779597-62780569	NOTEST	0	0	0	0	1	1
ENSG00000232145	ENSG00000232145	RP11-307I2.1	7:143318042-143534026	NOTEST	0	0	0	0	1	1
ENSG00000232146	ENSG00000232146	OR2B4P	HSCHR6_MHC_SSTO:29258569-29259512	NOTEST	0	0	0	0	1	1
ENSG00000232148	ENSG00000232148	FMO11P	1:166732570-166762004	NOTEST	0	0	0	0	1	1
ENSG00000232151	ENSG00000232151	RP11-353N4.8	1:149575344-149637707	NOTEST	0.117147	0.0548401	-1.09502	0	1	1
ENSG00000232153	ENSG00000232153	AC073218.3	2:34902645-34963298	NOTEST	0	0	0	0	1	1
ENSG00000232154	ENSG00000232154	RP11-193H5.5	1:238111316-238112443	NOTEST	0	0	0	0	1	1
ENSG00000232155	ENSG00000232155	AF277315.19	X:153834110-153834203	NOTEST	0	0	0	0	1	1
ENSG00000232156	ENSG00000232156	HLA-DRB2	HSCHR6_MHC_COX:32450946-32465488	NOTEST	0	0	0	0	1	1
ENSG00000232158	ENSG00000232158	RP11-252O2.2	9:19507449-19786926	NOTEST	0	0	0	0	1	1
ENSG00000232159	ENSG00000232159	RAB9BP1	5:103718998-104728671	NOTEST	0	0	0	0	1	1
ENSG00000232161	ENSG00000232161	RP11-548K12.7	7:57830671-57830879	NOTEST	0	0	0	0	1	1
ENSG00000232162	ENSG00000232162	USP12-AS1	13:27640292-27746033	NOTEST	0	0	0	0	1	1
ENSG00000232163	ENSG00000232163	RPLP1P13	13:23902964-24007841	NOTEST	0	0	0	0	1	1
ENSG00000232164	ENSG00000232164	AC092669.3	2:66610437-66619582	NOTEST	0	0.00765351	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232165	ENSG00000232165	RP5-905H7.6	7:62787051-62814743	NOTEST	0	0	0	0	1	1
ENSG00000232166	ENSG00000232166	RP4-799P18.5	1:234040678-234460262	NOTEST	0	0	0	0	1	1
ENSG00000232167	ENSG00000232167	AC137675.1	3:27566843-27566885	NOTEST	0	0	0	0	1	1
ENSG00000232168	ENSG00000232168	RP11-180D15.1	X:78340432-78341345	NOTEST	0	0	0	0	1	1
ENSG00000232169	ENSG00000232169	ABCF1	HSCHR6_MHC_DBB:30529390-30555197	NOTEST	0	0	0	0	1	1
ENSG00000232170	ENSG00000232170	LINC00708	10:8301293-8310268	NOTEST	0	0	0	0	1	1
ENSG00000232172	ENSG00000232172	RP11-57C19.2	9:133527185-133527770	NOTEST	0	0	0	0	1	1
ENSG00000232173	ENSG00000232173	OR2H5P	6:29523291-29601753	NOTEST	0	0.0305178	inf	0	1	1
ENSG00000232174	ENSG00000232174	CTB-164L20.1	5:137946655-138270723	NOTEST	0	0	0	0	1	1
ENSG00000232175	ENSG00000232175	RP4-659I19.1	1:233052980-233053764	NOTEST	0	0	0	0	1	1
ENSG00000232176	ENSG00000232176	RP11-146N23.1	9:19200332-19201044	NOTEST	0.0504784	0.0213652	-1.2404	0	1	1
ENSG00000232177	ENSG00000232177	MTND4P24	X:125606867-125607264	NOTEST	0	0	0	0	1	1
ENSG00000232178	ENSG00000232178	OR2J3	HSCHR6_MHC_COX:29076340-29077276	NOTEST	0	0	0	0	1	1
ENSG00000232179	ENSG00000232179	RP11-100G15.2	9:94794280-94877666	NOTEST	0	0	0	0	1	1
ENSG00000232180	ENSG00000232180	SLC44A4	HSCHR6_MHC_SSTO:31822858-31838708	NOTEST	0	0	0	0	1	1
ENSG00000232183	ENSG00000232183	RP6-27P15.2	X:137709237-137709504	NOTEST	0	0	0	0	1	1
ENSG00000232184	ENSG00000232184	RP11-370K11.1	1:243419319-244014381	NOTEST	0	0	0	0	1	1
ENSG00000232185	ENSG00000232185	CNOT7P2	1:116107221-116108053	NOTEST	0	0	0	0	1	1
ENSG00000232186	ENSG00000232186	RP11-311P8.2	X:74546606-74547834	NOTEST	0.13037	0.136314	0.0643243	0	1	1
ENSG00000232188	ENSG00000232188	RP11-312J18.6	1:160901528-160924589	NOTEST	0	0.0572649	inf	0	1	1
ENSG00000232189	ENSG00000232189	TMEM183AP1	HSCHR6_MHC_DBB:29523342-29600923	NOTEST	0	0	0	0	1	1
ENSG00000232190	ENSG00000232190	RP11-134D3.1	16:87091389-87097597	NOTEST	0	0	0	0	1	1
ENSG00000232192	ENSG00000232192	RP11-62I21.1	1:245318286-245872733	NOTEST	0	0	0	0	1	1
ENSG00000232193	ENSG00000232193	AL157359.4	21:20290251-20308177	NOTEST	0	0	0	0	1	1
ENSG00000232194	ENSG00000232194	RP1-313L4.3	1:167778624-167883453	NOTEST	0.0543116	0	#NAME?	0	1	1
ENSG00000232195	ENSG00000232195	TOMM22P2	Y:2696022-2696259	NOTEST	0	0	0	0	1	1
ENSG00000232196	ENSG00000232196	MTRNR2L4	16:3415098-3627401	NOTEST	0.0140189	0.0604218	2.10769	0	1	1
ENSG00000232197	ENSG00000232197	RP11-302L19.1	6:170477740-170478251	NOTEST	0	0	0	0	1	1
ENSG00000232198	ENSG00000232198	RP4-633H17.2	1:55838382-55838989	NOTEST	0	0	0	0	1	1
ENSG00000232199	ENSG00000232199	RPL3P8	7:109638490-109639681	NOTEST	0	0.0351202	inf	0	1	1
ENSG00000232200	ENSG00000232200	RP4-564O4.1	20:24278220-24298722	NOTEST	0	0	0	0	1	1
ENSG00000232202	ENSG00000232202	AC098824.6	2:43053461-43054757	NOTEST	0.0550782	0.114469	1.05541	0	1	1
ENSG00000232203	ENSG00000232203	SLC25A6P2	9:31253898-31254775	NOTEST	0	0	0	0	1	1
ENSG00000232204	ENSG00000232204	TET1P1	13:88542426-88544727	NOTEST	0	0	0	0	1	1
ENSG00000232205	ENSG00000232205	CDY18P	Y:26250253-26252165	NOTEST	0	0	0	0	1	1
ENSG00000232208	ENSG00000232208	RP3-477M7.5	1:8967451-8967803	NOTEST	0	0	0	0	1	1
ENSG00000232210	ENSG00000232210	PHBP15	7:74071993-74306731	NOTEST	0.0902097	0.140697	0.641241	0	1	1
ENSG00000232211	ENSG00000232211	RP11-395D3.1	9:89247061-89311411	NOTEST	0	0	0	0	1	1
ENSG00000232212	ENSG00000232212	RP11-398M15.1	1:189744594-189784048	NOTEST	0	0	0	0	1	1
ENSG00000232215	ENSG00000232215	OR2L6P	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000232216	ENSG00000232216	IGHV3-43	14:106926187-106926724	NOTEST	0.318319	0.088053	-1.85403	0	1	1
ENSG00000232217	ENSG00000232217	FTLP8	13:98605911-98676551	NOTEST	0	0	0	0	1	1
ENSG00000232218	ENSG00000232218	RP1-149A16.16	22:32782654-32782855	NOTEST	0	1.10911	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232220	ENSG00000232220	AC008440.5	19:54357834-54379691	NOTEST	0	0	0	0	1	1
ENSG00000232222	ENSG00000232222	RP3-434O14.8	1:209959035-209979465	NOTEST	0	0	0	0	1	1
ENSG00000232223	ENSG00000232223	CNN2P10	1:166765502-166766420	NOTEST	0	0	0	0	1	1
ENSG00000232224	ENSG00000232224	LINC00202-1	10:27220134-27230930	NOTEST	0.102672	0.0373287	-1.45968	0	1	1
ENSG00000232225	ENSG00000232225	LINC01047	13:89867100-89889144	NOTEST	0	0	0	0	1	1
ENSG00000232226	ENSG00000232226	ARSFP1	Y:14373024-14378737	NOTEST	0	0	0	0	1	1
ENSG00000232227	ENSG00000232227	AC013401.2	2:193494644-193510432	NOTEST	0	0	0	0	1	1
ENSG00000232228	ENSG00000232228	RP11-77O7.1	2:69685128-70053596	NOTEST	0	0.0782932	inf	0	1	1
ENSG00000232229	ENSG00000232229	LINC00865	10:91589266-91600618	NOTEST	0	0.00961996	inf	0	1	1
ENSG00000232230	ENSG00000232230	TPM4P1	10:101874173-101874980	NOTEST	0	0	0	0	1	1
ENSG00000232232	ENSG00000232232	HLA-N	HSCHR6_MHC_APD:30327430-30327565	NOTEST	0	0	0	0	1	1
ENSG00000232233	ENSG00000232233	RP11-573D15.2	3:186525480-186543310	NOTEST	0.0268235	0.0544283	1.02086	0	1	1
ENSG00000232234	ENSG00000232234	RP11-203H2.1	6:8329887-8343254	NOTEST	0	0.0462614	inf	0	1	1
ENSG00000232235	ENSG00000232235	CDY3P	Y:9003693-9005311	NOTEST	0	0	0	0	1	1
ENSG00000232237	ENSG00000232237	ASCL5	1:201083080-201096312	NOTEST	0.0649119	0.0586894	-0.145382	0	1	1
ENSG00000232238	ENSG00000232238	AC017080.1	2:149352726-149352897	NOTEST	0	0	0	0	1	1
ENSG00000232239	ENSG00000232239	RBPJP5	9:41884764-41886211	NOTEST	0	0	0	0	1	1
ENSG00000232240	ENSG00000232240	RP5-1125M8.3	1:111833483-111866697	NOTEST	0	0	0	0	1	1
ENSG00000232241	ENSG00000232241	DYNLT3P1	20:17206751-17465223	NOTEST	0	0	0	0	1	1
ENSG00000232242	ENSG00000232242	ZYG11AP1	9:105281917-105419796	NOTEST	0.15235	0.270987	0.830829	0	1	1
ENSG00000232243	ENSG00000232243	RP11-408E5.5	13:19836936-19838013	NOTEST	0	0	0	0	1	1
ENSG00000232244	ENSG00000232244	FGFR3P	HSCHR6_MHC_SSTO:31338076-31338679	NOTEST	0	0	0	0	1	1
ENSG00000232245	ENSG00000232245	RP4-705F19.1	1:54881928-54886533	NOTEST	0	0	0	0	1	1
ENSG00000232249	ENSG00000232249	LL0XNC01-37G1.2	X:152599612-152625568	NOTEST	0	0	0	0	1	1
ENSG00000232251	ENSG00000232251	DPCR1	HSCHR6_MHC_DBB:30899495-30913356	NOTEST	0	0	0	0	1	1
ENSG00000232252	ENSG00000232252	RP11-30L8.1	13:86634947-86745025	NOTEST	0	0	0	0	1	1
ENSG00000232253	ENSG00000232253	MICF	HSCHR6_MHC_QBL:29817100-29817229	NOTEST	0	0	0	0	1	1
ENSG00000232254	ENSG00000232254	CSF2RBP1	22:37346570-37349764	NOTEST	0	0	0	0	1	1
ENSG00000232256	ENSG00000232256	DDX39B-AS1	HSCHR6_MHC_COX:31483951-31502076	NOTEST	0	0	0	0	1	1
ENSG00000232258	ENSG00000232258	TMEM114	16:8619501-8622304	NOTEST	0	0	0	0	1	1
ENSG00000232259	ENSG00000232259	RP11-4C20.3	10:129705324-129884119	NOTEST	0	0	0	0	1	1
ENSG00000232260	ENSG00000232260	BTF3L4P1	21:18884699-18965897	NOTEST	0	0	0	0	1	1
ENSG00000232261	ENSG00000232261	RP4-560B9.5	1:171720682-171721165	NOTEST	0	0	0	0	1	1
ENSG00000232263	ENSG00000232263	KRTAP25-1	21:31661462-31661832	NOTEST	0	0	0	0	1	1
ENSG00000232264	ENSG00000232264	USP17L24	4:9326890-9328483	NOTEST	0	0	0	0	1	1
ENSG00000232265	ENSG00000232265	XXyac-YX155B6.5	1:147634988-147700929	NOTEST	0	0	0	0	1	1
ENSG00000232266	ENSG00000232266	DAQB-331I12.5	HSCHR6_MHC_APD:31858892-31876828	NOTEST	0	0	0	0	1	1
ENSG00000232267	ENSG00000232267	ACTR3P2	X:67991164-67992421	NOTEST	0	0	0	0	1	1
ENSG00000232268	ENSG00000232268	OR52I1	11:4615036-4616243	NOTEST	0	0	0	0	1	1
ENSG00000232270	ENSG00000232270	INTS4L2	7:65112080-65180636	NOTEST	0.257322	0.206846	-0.315018	0	1	1
ENSG00000232271	ENSG00000232271	RP4-764O22.1	20:7050260-7234849	NOTEST	0	0	0	0	1	1
ENSG00000232272	ENSG00000232272	XXbac-BCX196D17.5	HSCHR6_MHC_COX:29088660-29093357	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232273	ENSG00000232273	FTH1P1	1:38000049-38019903	NOTEST	0	0	0	0	1	1
ENSG00000232276	ENSG00000232276	FGFR3P	HSCHR6_MHC_QBL:31335307-31335905	NOTEST	0	0	0	0	1	1
ENSG00000232277	ENSG00000232277	AC104651.3	2:112656055-112787138	NOTEST	0	0	0	0	1	1
ENSG00000232280	ENSG00000232280	FLOT1	HSCHR6_MHC_COX:30685347-30700375	NOTEST	0	0	0	0	1	1
ENSG00000232281	ENSG00000232281	IFNWP15	9:21178587-21179187	NOTEST	0	0	0	0	1	1
ENSG00000232282	ENSG00000232282	MTND1P32	X:102024088-102161086	NOTEST	0	0	0	0	1	1
ENSG00000232283	ENSG00000232283	RP11-240L7.4	9:98997587-99064434	NOTEST	0.0300505	0	#NAME?	0	1	1
ENSG00000232285	ENSG00000232285	TCEB2P3	2:49007740-49008034	NOTEST	0	0	0	0	1	1
ENSG00000232286	ENSG00000232286	RP11-80K6.2	20:51474876-51479394	NOTEST	0	0	0	0	1	1
ENSG00000232287	ENSG00000232287	SLC6A1-AS1	3:11034409-11080933	NOTEST	0	0	0	0	1	1
ENSG00000232289	ENSG00000232289	OR11A1	HSCHR6_MHC_APD:29390470-29424928	NOTEST	0	0	0	0	1	1
ENSG00000232290	ENSG00000232290	RP1-292B18.3	6:151186684-151549582	NOTEST	0	0	0	0	1	1
ENSG00000232292	ENSG00000232292	ALDH7A1P2	2:173541868-173917621	NOTEST	0	0	0	0	1	1
ENSG00000232293	ENSG00000232293	PAICSP7	X:93891661-93894569	NOTEST	0	0	0	0	1	1
ENSG00000232294	ENSG00000232294	RP4-715N11.2	20:51288455-51307468	NOTEST	0	0	0	0	1	1
ENSG00000232295	ENSG00000232295	RP11-154D6.1	6:71931159-72130472	NOTEST	0	0	0	0	1	1
ENSG00000232296	ENSG00000232296	RP11-510N19.2	1:201997733-201997820	NOTEST	0	0	0	0	1	1
ENSG00000232298	ENSG00000232298	RP11-10N16.3	1:24634045-24799466	NOTEST	0	0	0	0	1	1
ENSG00000232299	ENSG00000232299	RP1-105O18.1	6:112797739-112802838	NOTEST	0	0	0	0	1	1
ENSG00000232300	ENSG00000232300	FAM215B	17:44588876-44657088	NOTEST	0.0207435	0.0229798	0.147704	0	1	1
ENSG00000232301	ENSG00000232301	RP11-132A1.3	7:100942893-100944551	NOTEST	0	0	0	0	1	1
ENSG00000232302	ENSG00000232302	RPS17P1	HSCHR6_MHC_COX:29453624-29454030	NOTEST	0	0	0	0	1	1
ENSG00000232303	ENSG00000232303	RP11-205M20.7	9:32540541-32573160	NOTEST	0.536635	0.280945	-0.933654	0	1	1
ENSG00000232305	ENSG00000232305	CLCP1	22:17840836-18037850	NOTEST	0	0	0	0	1	1
ENSG00000232306	ENSG00000232306	AC012485.2	2:239207350-239209261	NOTEST	0.0378952	0	#NAME?	0	1	1
ENSG00000232307	ENSG00000232307	DAOA-AS1	13:106111403-106158030	NOTEST	0	0	0	0	1	1
ENSG00000232308	ENSG00000232308	DPCR1	HSCHR6_MHC_COX:30903455-30912338	NOTEST	0	0	0	0	1	1
ENSG00000232309	ENSG00000232309	GS1-122H1.1	1:182096431-182097800	NOTEST	0	0	0	0	1	1
ENSG00000232311	ENSG00000232311	RP1-249I4.2	6:110147724-110149988	NOTEST	0	0	0	0	1	1
ENSG00000232312	ENSG00000232312	GPANK1	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000232314	ENSG00000232314	PSMC1P13	13:70274725-70713561	NOTEST	0	0	0	0	1	1
ENSG00000232316	ENSG00000232316	RP1-124C6.1	6:113749741-113754623	NOTEST	0	0	0	0	1	1
ENSG00000232324	ENSG00000232324	AC008440.10	19:54357834-54379691	NOTEST	0	0	0	0	1	1
ENSG00000232325	ENSG00000232325	AC093627.7	7:70971-71835	NOTEST	0	0	0	0	1	1
ENSG00000232326	ENSG00000232326	TAP2	HSCHR6_MHC_SSTO:32879674-32896470	NOTEST	0	0	0	0	1	1
ENSG00000232327	ENSG00000232327	RP11-395C17.1	4:81187752-81884910	NOTEST	0	0	0	0	1	1
ENSG00000232328	ENSG00000232328	AC011286.1	2:237642024-237663006	NOTEST	0	0	0	0	1	1
ENSG00000232331	ENSG00000232331	HLA-K	HSCHR6_MHC_COX:29885237-29888489	NOTEST	0	0	0	0	1	1
ENSG00000232332	ENSG00000232332	RP3-481A17.1	X:75249729-75250165	NOTEST	0	0	0	0	1	1
ENSG00000232333	ENSG00000232333	RPS27AP2	20:17474549-17549865	NOTEST	0.0505111	0.0393786	-0.35919	0	1	1
ENSG00000232334	ENSG00000232334	RP11-47G11.2	10:125763819-125764344	NOTEST	0	0	0	0	1	1
ENSG00000232335	ENSG00000232335	RP11-435D7.3	1:36185818-36235568	NOTEST	0.0403671	0	#NAME?	0	1	1
ENSG00000232337	ENSG00000232337	AC009313.2	2:161905116-161907057	NOTEST	0	0	0	0	1	1
ENSG00000232339	ENSG00000232339	NOTCH4	HSCHR6_MHC_MANN:32197966-32231292	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232341	ENSG00000232341	RPL4P2	1:166716615-166717897	NOTEST	0	0	0	0	1	1
ENSG00000232342	ENSG00000232342	RP11-46O21.2	10:75910959-76469061	NOTEST	0.100287	0.151087	0.591243	0	1	1
ENSG00000232343	ENSG00000232343	XXbac-BPG254F23.7	HSCHR6_MHC_SSTO:32776587-32777418	NOTEST	0	0	0	0	1	1
ENSG00000232344	ENSG00000232344	AC087163.2	17:17876126-17942523	NOTEST	0.043558	0.130958	1.5881	0	1	1
ENSG00000232345	ENSG00000232345	MICD	HSCHR6_MHC_QBL:29927982-29929646	NOTEST	0	0	0	0	1	1
ENSG00000232347	ENSG00000232347	RP11-488L18.8	1:247353152-247405125	NOTEST	0.129047	0.0226149	-2.51255	0	1	1
ENSG00000232348	ENSG00000232348	LINC00279	Y:8506334-8512883	NOTEST	0	0	0	0	1	1
ENSG00000232349	ENSG00000232349	YBX1P7	2:133174146-133429152	NOTEST	0	0	0	0	1	1
ENSG00000232350	ENSG00000232350	LL22NC03-102D1.16	22:23032314-23032462	NOTEST	0	0	0	0	1	1
ENSG00000232351	ENSG00000232351	HLA-DQB1-AS1	HSCHR6_MHC_MCF:32658021-32667070	NOTEST	0	0	0	0	1	1
ENSG00000232352	ENSG00000232352	SEMA3B-AS1	3:50304072-50304803	NOTEST	0.169843	0	#NAME?	0	1	1
ENSG00000232353	ENSG00000232353	RP11-655G22.1	3:191747668-191754346	NOTEST	0	0	0	0	1	1
ENSG00000232354	ENSG00000232354	VIPR1-AS1	3:42530790-42579059	NOTEST	0	0	0	0	1	1
ENSG00000232355	ENSG00000232355	RP11-263F14.3	9:137760081-137760321	NOTEST	0	0	0	0	1	1
ENSG00000232356	ENSG00000232356	XXbac-BPG13B8.10	HSCHR6_MHC_DBB:29465219-29478267	NOTEST	0	0	0	0	1	1
ENSG00000232357	ENSG00000232357	HSD17B8	HSCHR6_MHC_MCF:33342782-33344972	NOTEST	0	0	0	0	1	1
ENSG00000232358	ENSG00000232358	RP5-955M13.4	20:49615906-49639666	NOTEST	0	0.0519484	inf	0	1	1
ENSG00000232359	ENSG00000232359	AC104777.1	2:151451615-151491862	NOTEST	0	0	0	0	1	1
ENSG00000232360	ENSG00000232360	AP000281.2	21:34144410-34266043	NOTEST	0	0	0	0	1	1
ENSG00000232361	ENSG00000232361	RP11-632K21.3	7:150311148-150311852	NOTEST	0	0	0	0	1	1
ENSG00000232362	ENSG00000232362	ATP5LP2	6:123180822-123181133	NOTEST	0	0	0	0	1	1
ENSG00000232363	ENSG00000232363	RP1-102D24.5	22:45831743-45844624	NOTEST	0	0	0	0	1	1
ENSG00000232366	ENSG00000232366	VDAC1P9	1:157693969-157694810	NOTEST	0	0	0	0	1	1
ENSG00000232367	ENSG00000232367	TAP1	HSCHR6_MHC_COX:32730816-32769949	NOTEST	0	0	0	0	1	1
ENSG00000232368	ENSG00000232368	FTLP2	X:30648414-30648942	NOTEST	0.0773404	0	#NAME?	0	1	1
ENSG00000232369	ENSG00000232369	RP5-882O7.4	1:45453905-45457506	NOTEST	0	0	0	0	1	1
ENSG00000232370	ENSG00000232370	AF241726.2	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000232373	ENSG00000232373	MTCYBP3	13:96329392-96447243	NOTEST	0	0	0	0	1	1
ENSG00000232374	ENSG00000232374	GPR79	3:158558787-158559873	NOTEST	0.138284	0.0228657	-2.59638	0	1	1
ENSG00000232375	ENSG00000232375	RP11-136C24.1	3:42846243-43101703	NOTEST	0	0	0	0	1	1
ENSG00000232376	ENSG00000232376	LYPLA2P1	HSCHR6_MHC_QBL:33262069-33262864	NOTEST	0	0	0	0	1	1
ENSG00000232377	ENSG00000232377	AC016910.1	2:144694639-145090135	NOTEST	0	0.0119581	inf	0	1	1
ENSG00000232378	ENSG00000232378	RPL29P28	13:37500574-37501356	NOTEST	0	0	0	0	1	1
ENSG00000232379	ENSG00000232379	RP11-308D16.1	X:135991553-136103789	NOTEST	0	0	0	0	1	1
ENSG00000232381	ENSG00000232381	OR52U1P	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000232382	ENSG00000232382	OR5K1	3:98188323-98189420	NOTEST	0	0	0	0	1	1
ENSG00000232383	ENSG00000232383	AC010677.5	7:26315814-26316226	NOTEST	0	0	0	0	1	1
ENSG00000232384	ENSG00000232384	RP11-204I15.1	X:52464669-52467221	NOTEST	0	0	0	0	1	1
ENSG00000232386	ENSG00000232386	RP11-66B24.2	15:101389765-101626271	NOTEST	0.146438	0.364547	1.31581	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232389	ENSG00000232389	RP11-134K13.2	6:71317936-71319037	NOTEST	0.0319406	0.101881	1.67342	0	1	1
ENSG00000232390	ENSG00000232390	NDUFA5P1	11:3343091-3343432	NOTEST	0	0	0	0	1	1
ENSG00000232391	ENSG00000232391	RANP2	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000232392	ENSG00000232392	AC002366.3	X:11129420-11683821	NOTEST	0	0	0	0	1	1
ENSG00000232393	ENSG00000232393	RPL5P6	1:91489475-91490361	NOTEST	0	0	0	0	1	1
ENSG00000232394	ENSG00000232394	AC090696.2	15:28000020-28344504	NOTEST	0	0	0	0	1	1
ENSG00000232395	ENSG00000232395	RP3-399L15.1	6:114798513-114809916	NOTEST	0	0	0	0	1	1
ENSG00000232396	ENSG00000232396	RP1-76B20.11	22:30101244-30115848	NOTEST	0	0	0	0	1	1
ENSG00000232397	ENSG00000232397	OR10C1	HSCHR6_MHC_MANN:29323056-29424418	NOTEST	0	0	0	0	1	1
ENSG00000232398	ENSG00000232398	TMPRSS11CP	4:68566997-68995598	NOTEST	0	0	0	0	1	1
ENSG00000232399	ENSG00000232399	USP17L13	4:9212382-9228214	NOTEST	0	0	0	0	1	1
ENSG00000232400	ENSG00000232400	RAD17P1	7:16899028-16921611	NOTEST	0.00793755	0	#NAME?	0	1	1
ENSG00000232401	ENSG00000232401	LINC00112	21:43136595-43137740	NOTEST	0	0	0	0	1	1
ENSG00000232403	ENSG00000232403	RP11-511I11.1	2:63335252-63335564	NOTEST	0	0.0749839	inf	0	1	1
ENSG00000232406	ENSG00000232406	RP11-234K24.3	20:34679425-34820721	NOTEST	0	0	0	0	1	1
ENSG00000232407	ENSG00000232407	RP11-641C17.2	3:59735035-61237133	NOTEST	0	0	0	0	1	1
ENSG00000232408	ENSG00000232408	AC140481.4	2:131328401-131348036	NOTEST	0	0	0	0	1	1
ENSG00000232409	ENSG00000232409	AC019185.3	2:209224437-209719227	NOTEST	0	0	0	0	1	1
ENSG00000232412	ENSG00000232412	RP1-315G1.3	X:123093082-124097666	NOTEST	0.0950019	0	#NAME?	0	1	1
ENSG00000232413	ENSG00000232413	RP11-343J18.2	9:128819858-128921892	NOTEST	0	0	0	0	1	1
ENSG00000232414	ENSG00000232414	CYP21A2	HSCHR6_MHC_DBB:31981893-32071805	NOTEST	0	0	0	0	1	1
ENSG00000232415	ENSG00000232415	CTB-51J22.1	7:73442118-73484237	NOTEST	0	0	0	0	1	1
ENSG00000232416	ENSG00000232416	BPESC1	3:138722803-139108574	NOTEST	0	0	0	0	1	1
ENSG00000232417	ENSG00000232417	CT45A3	X:134883487-134891885	NOTEST	0	0.0389954	inf	0	1	1
ENSG00000232418	ENSG00000232418	RP11-678B3.1	7:53723201-53879624	NOTEST	0	0	0	0	1	1
ENSG00000232419	ENSG00000232419	TTTY19	Y:8572512-8573324	NOTEST	0	0	0	0	1	1
ENSG00000232420	ENSG00000232420	IL9RP2	10:126333-132205	NOTEST	0	0	0	0	1	1
ENSG00000232421	ENSG00000232421	TUBB	HSCHR6_MHC_SSTO:30679426-30684652	NOTEST	0	0	0	0	1	1
ENSG00000232422	ENSG00000232422	KNOP1P4	6:73331519-73908574	NOTEST	0	0.00824526	inf	0	1	1
ENSG00000232423	ENSG00000232423	PRAMEF6	1:12998180-13117751	NOTEST	0	0	0	0	1	1
ENSG00000232424	ENSG00000232424	USP9YP29	Y:25886404-25892840	NOTEST	0	0	0	0	1	1
ENSG00000232426	ENSG00000232426	RP11-508M1.7	10:48988120-48998766	NOTEST	0	0	0	0	1	1
ENSG00000232429	ENSG00000232429	RPL21P131	19:34080111-34080594	NOTEST	0	0	0	0	1	1
ENSG00000232430	ENSG00000232430	RPL31P15	2:183580998-183659191	NOTEST	0	0	0	0	1	1
ENSG00000232431	ENSG00000232431	RP11-578F21.10	15:29033388-29101361	NOTEST	0	0	0	0	1	1
ENSG00000232433	ENSG00000232433	RP11-341A11.2	9:42493616-42494809	NOTEST	0.134875	0.0565794	-1.25327	0	1	1
ENSG00000232435	ENSG00000232435	DDX6P1	HSCHR6_MHC_MCF:29297637-29299073	NOTEST	0	0	0	0	1	1
ENSG00000232436	ENSG00000232436	RP11-103C3.1	1:221681900-221684321	NOTEST	0	0	0	0	1	1
ENSG00000232437	ENSG00000232437	RP11-487I5.4	10:76854191-76941881	NOTEST	0	0	0	0	1	1
ENSG00000232438	ENSG00000232438	CTSLP7	10:47271221-47272342	NOTEST	0	0	0	0	1	1
ENSG00000232441	ENSG00000232441	DASS-397D15.4	HSCHR6_MHC_MCF:32528785-32528881	NOTEST	0	0	0	0	1	1
ENSG00000232444	ENSG00000232444	AC010745.4	2:16497591-16500834	NOTEST	0	0	0	0	1	1
ENSG00000232446	ENSG00000232446	RP13-60P5.2	X:26165890-26166398	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232447	ENSG00000232447	MTND5P3	13:85095859-85098050	NOTEST	0	0	0	0	1	1
ENSG00000232448	ENSG00000232448	RP11-416N4.1	20:9966735-10349424	NOTEST	0	0	0	0	1	1
ENSG00000232450	ENSG00000232450	RP4-730K3.3	1:114239452-114302111	NOTEST	0.171779	0.25942	0.594732	0	1	1
ENSG00000232451	ENSG00000232451	AC016768.1	2:23240996-23421927	NOTEST	0	0	0	0	1	1
ENSG00000232453	ENSG00000232453	RP4-794H19.1	1:59250822-59365384	NOTEST	0.226309	0.041476	-2.44794	0	1	1
ENSG00000232454	ENSG00000232454	RP11-3J10.7	9:37510888-38069210	NOTEST	0.0821829	0.0642214	-0.355784	0	1	1
ENSG00000232455	ENSG00000232455	LARS2-AS1	3:45429997-45590913	NOTEST	0	0	0	0	1	1
ENSG00000232456	ENSG00000232456	RP11-5P18.10	1:16361672-16366524	NOTEST	0	0	0	0	1	1
ENSG00000232457	ENSG00000232457	SLC16A6P1	17:62936699-62952664	NOTEST	0.47182	0.175287	-1.42852	0	1	1
ENSG00000232458	ENSG00000232458	AC005029.1	7:41004265-41019537	NOTEST	0.00867767	0	#NAME?	0	1	1
ENSG00000232459	ENSG00000232459	OR4F14P	15:102368943-102369882	NOTEST	0	0	0	0	1	1
ENSG00000232461	ENSG00000232461	RP11-644C3.1	3:176361728-176585626	NOTEST	0	0	0	0	1	1
ENSG00000232462	ENSG00000232462	RP11-13E1.5	10:49363367-49364177	NOTEST	0.0593629	0	#NAME?	0	1	1
ENSG00000232463	ENSG00000232463	RP11-195C7.2	1:176200335-176200966	NOTEST	0	0	0	0	1	1
ENSG00000232464	ENSG00000232464	CTA-125H2.1	22:26138110-26427007	NOTEST	0	0	0	0	1	1
ENSG00000232465	ENSG00000232465	RP5-1022J11.2	20:50827183-51266970	NOTEST	0	0	0	0	1	1
ENSG00000232466	ENSG00000232466	RP11-337A23.5	9:26840682-26892802	NOTEST	0	0.0527839	inf	0	1	1
ENSG00000232467	ENSG00000232467	TMA16P2	1:46252658-46501796	NOTEST	0	0	0	0	1	1
ENSG00000232469	ENSG00000232469	OR2B4P	HSCHR6_MHC_DBB:29258527-29259470	NOTEST	0	0	0	0	1	1
ENSG00000232470	ENSG00000232470	RP11-313D6.3	10:112629500-112679032	NOTEST	0	0.0460595	inf	0	1	1
ENSG00000232471	ENSG00000232471	RP11-241F15.7	4:49552048-49559417	NOTEST	0	0	0	0	1	1
ENSG00000232473	ENSG00000232473	UBQLN1P1	HSCHR6_MHC_DBB:30321144-30322313	NOTEST	0	0	0	0	1	1
ENSG00000232474	ENSG00000232474	NCKAP5-IT1	2:133429373-134326034	NOTEST	0	0	0	0	1	1
ENSG00000232475	ENSG00000232475	HSFY5P	Y:24194700-24195494	NOTEST	0	0	0	0	1	1
ENSG00000232478	ENSG00000232478	CT45A1	X:134847184-134857354	NOTEST	0	0.104051	inf	0	1	1
ENSG00000232479	ENSG00000232479	AC010900.2	2:203739504-203879521	NOTEST	0	0.0421036	inf	0	1	1
ENSG00000232480	ENSG00000232480	RP11-224O19.2	1:218517537-218519020	NOTEST	0	0.0299716	inf	0	1	1
ENSG00000232482	ENSG00000232482	RP4-654C18.1	1:23707553-23751233	NOTEST	0	0	0	0	1	1
ENSG00000232485	ENSG00000232485	AC098820.3	2:217250010-217443903	NOTEST	0.208694	0.15754	-0.405671	0	1	1
ENSG00000232486	ENSG00000232486	RP11-18B3.2	9:108456824-108538893	NOTEST	0.0421809	0	#NAME?	0	1	1
ENSG00000232487	ENSG00000232487	RASA3-IT1	13:114747193-114898086	NOTEST	0	0	0	0	1	1
ENSG00000232489	ENSG00000232489	MFAP1P1	13:31032883-31191734	NOTEST	0	0	0	0	1	1
ENSG00000232490	ENSG00000232490	OSBPL10-AS1	3:31699381-32119072	NOTEST	0	0	0	0	1	1
ENSG00000232491	ENSG00000232491	RP4-756H11.1	7:66010633-66057373	NOTEST	0.0218752	0.16631	2.9265	0	1	1
ENSG00000232492	ENSG00000232492	NPM1P13	7:18126571-19042039	NOTEST	0	0	0	0	1	1
ENSG00000232493	ENSG00000232493	RPL12P11	20:40030740-40247133	NOTEST	0	0.108839	inf	0	1	1
ENSG00000232494	ENSG00000232494	RP11-403N16.2	9:82489610-82501593	NOTEST	0	0	0	0	1	1
ENSG00000232496	ENSG00000232496	RPL3P12	X:121672105-121673313	NOTEST	0	0	0	0	1	1
ENSG00000232497	ENSG00000232497	ADIPOR1P1	10:22451920-22454723	NOTEST	0	0	0	0	1	1
ENSG00000232498	ENSG00000232498	RP5-1011O1.2	1:192486768-192536347	NOTEST	0	0	0	0	1	1
ENSG00000232500	ENSG00000232500	AP005273.1	11:64268324-64272858	NOTEST	0	0	0	0	1	1
ENSG00000232502	ENSG00000232502	AC073464.7	2:95426518-95426861	NOTEST	0	0	0	0	1	1
ENSG00000232503	ENSG00000232503	CYCSP8	2:131534218-131534530	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232505	ENSG00000232505	XXbac-BPG308J9.3	6:29191749-29258217	NOTEST	0	0	0	0	1	1
ENSG00000232508	ENSG00000232508	MRPL45P1	2:88664213-88665127	NOTEST	0	0	0	0	1	1
ENSG00000232510	ENSG00000232510	TRIM31-AS1	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000232511	ENSG00000232511	OR2AH1P	11:56436492-56437420	NOTEST	0	0	0	0	1	1
ENSG00000232512	ENSG00000232512	7SK	21:26467334-26475983	NOTEST	0	0	0	0	1	1
ENSG00000232514	ENSG00000232514	RP11-329A14.2	1:48962934-48963408	NOTEST	0	0	0	0	1	1
ENSG00000232515	ENSG00000232515	LL22NC03-75A1.9	22:22702156-22702514	NOTEST	0	0	0	0	1	1
ENSG00000232516	ENSG00000232516	ETF1P1	HSCHR6_MHC_QBL:29958304-30022269	NOTEST	0	0	0	0	1	1
ENSG00000232517	ENSG00000232517	AC112198.1	5:54104037-54168379	NOTEST	0.00217586	0	#NAME?	0	1	1
ENSG00000232518	ENSG00000232518	AC074366.3	2:38893051-38968379	NOTEST	0	0	0	0	1	1
ENSG00000232519	ENSG00000232519	RP11-29H23.4	1:155579566-155829191	NOTEST	0	0	0	0	1	1
ENSG00000232520	ENSG00000232520	AC012507.3	2:231751214-231761806	NOTEST	0	0.0308359	inf	0	1	1
ENSG00000232522	ENSG00000232522	ZNF886P	Y:22163070-22174090	NOTEST	0	0	0	0	1	1
ENSG00000232523	ENSG00000232523	XXbac-BPG249D20.9	HSCHR6_MHC_SSTO:30475462-30478417	NOTEST	0	0	0	0	1	1
ENSG00000232524	ENSG00000232524	RP11-332K15.1	7:123092453-123175131	NOTEST	0	0	0	0	1	1
ENSG00000232525	ENSG00000232525	SS18L2P1	10:35164137-35164350	NOTEST	0	0	0	0	1	1
ENSG00000232526	ENSG00000232526	AC025750.6	2:42669156-42721237	NOTEST	0	0.0152295	inf	0	1	1
ENSG00000232528	ENSG00000232528	RP4-673D20.3	20:1748602-1760641	NOTEST	0.0473488	0.0402859	-0.233051	0	1	1
ENSG00000232529	ENSG00000232529	RP1-257I9.2	6:155701644-155702317	NOTEST	0	0	0	0	1	1
ENSG00000232530	ENSG00000232530	RP1-102K2.6	22:30635182-30642987	NOTEST	0	0	0	0	1	1
ENSG00000232531	ENSG00000232531	AC027612.1	2:91924751-91955465	NOTEST	0.391891	0.478407	0.287787	0	1	1
ENSG00000232532	ENSG00000232532	RP11-63K6.7	6:90629914-90631479	NOTEST	0	0	0	0	1	1
ENSG00000232533	ENSG00000232533	AC093673.5	7:143076784-143077588	NOTEST	0.27541	0.287027	0.0596075	0	1	1
ENSG00000232535	ENSG00000232535	OR5H8P	3:97952494-98176742	NOTEST	0	0	0	0	1	1
ENSG00000232536	ENSG00000232536	RP11-74C1.4	1:151512780-151556059	NOTEST	0	0	0	0	1	1
ENSG00000232537	ENSG00000232537	RP11-385M4.1	1:209320611-209328446	NOTEST	0	0	0	0	1	1
ENSG00000232539	ENSG00000232539	LINC00945	21:34285956-34444726	NOTEST	0	0	0	0	1	1
ENSG00000232540	ENSG00000232540	RPL36P19	13:43787653-44361044	NOTEST	0	0	0	0	1	1
ENSG00000232541	ENSG00000232541	COL11A2	HSCHR6_MHC_SSTO:33269766-33296554	NOTEST	0	0	0	0	1	1
ENSG00000232542	ENSG00000232542	DPYD-IT1	1:97543298-98386605	NOTEST	0	0	0	0	1	1
ENSG00000232543	ENSG00000232543	IGHD4-11	14:106369473-106369489	NOTEST	0	0	0	0	1	1
ENSG00000232546	ENSG00000232546	RP11-458F8.1	7:66313482-66323123	NOTEST	0	0	0	0	1	1
ENSG00000232548	ENSG00000232548	AC010744.1	2:83749937-83750626	NOTEST	0	0	0	0	1	1
ENSG00000232549	ENSG00000232549	SRD5A1P1	X:138529049-138529835	NOTEST	0	0	0	0	1	1
ENSG00000232551	ENSG00000232551	RP11-233E12.2	1:107347095-107348654	NOTEST	0	0	0	0	1	1
ENSG00000232553	ENSG00000232553	AC006026.10	7:23624680-23625974	NOTEST	0.0240489	0.0290907	0.274587	0	1	1
ENSG00000232554	ENSG00000232554	RSU1P2	10:45493145-45676875	NOTEST	0	0	0	0	1	1
ENSG00000232555	ENSG00000232555	AC104088.1	2:173180014-173188465	NOTEST	0	0	0	0	1	1
ENSG00000232556	ENSG00000232556	AC092570.4	2:102137295-102138438	NOTEST	0	0	0	0	1	1
ENSG00000232557	ENSG00000232557	RP11-4M23.3	1:24197015-24285549	NOTEST	0	0	0	0	1	1
ENSG00000232558	ENSG00000232558	KCND3-IT1	1:112313283-112531777	NOTEST	0	0	0	0	1	1
ENSG00000232560	ENSG00000232560	C21orf37	21:18811207-18821503	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232562	ENSG00000232562	TPMTP3	X:51722318-51723108	NOTEST	0	0	0	0	1	1
ENSG00000232563	ENSG00000232563	AC026214.2	3:1134259-1445901	NOTEST	0	0	0	0	1	1
ENSG00000232564	ENSG00000232564	RP4-591N18.2	22:40742506-41032706	NOTEST	0.0152798	0	#NAME?	0	1	1
ENSG00000232565	ENSG00000232565	C4A-AS1	HSCHR6_MHC_DBB:31919772-31953483	NOTEST	0	0	0	0	1	1
ENSG00000232567	ENSG00000232567	GLUD1P8	10:47253594-47259683	NOTEST	0	0	0	0	1	1
ENSG00000232568	ENSG00000232568	RPL23AP35	2:187126145-187126646	NOTEST	0	0	0	0	1	1
ENSG00000232569	ENSG00000232569	GABBR1	HSCHR6_MHC_APD:29523503-29601074	NOTEST	0	0	0	0	1	1
ENSG00000232571	ENSG00000232571	RP11-435B5.2	1:143343558-143344609	NOTEST	0.0506336	0.0250128	-1.01743	0	1	1
ENSG00000232572	ENSG00000232572	RPL15P4	HSCHR6_MHC_QBL:31486174-31486754	NOTEST	0	0	0	0	1	1
ENSG00000232575	ENSG00000232575	TUBB	HSCHR6_MHC_MANN:30732674-30737900	NOTEST	0	0	0	0	1	1
ENSG00000232576	ENSG00000232576	RP11-137D19.1	X:88163403-88163764	NOTEST	0	0	0	0	1	1
ENSG00000232577	ENSG00000232577	XXbac-BPG116M5.15	HSCHR6_MHC_SSTO:31941652-31963150	NOTEST	0	0	0	0	1	1
ENSG00000232578	ENSG00000232578	CTC-303L1.1	5:93488670-94620279	NOTEST	0	0	0	0	1	1
ENSG00000232579	ENSG00000232579	CTD-3105H18.10	19:12490002-12750912	NOTEST	0	0	0	0	1	1
ENSG00000232581	ENSG00000232581	AC079742.4	7:6617064-6629005	NOTEST	0	0	0	0	1	1
ENSG00000232582	ENSG00000232582	RP11-85L21.5	X:134269076-134269698	NOTEST	0	0	0	0	1	1
ENSG00000232583	ENSG00000232583	GPR143P	Y:6968773-6974543	NOTEST	0	0	0	0	1	1
ENSG00000232585	ENSG00000232585	OFD1P12Y	Y:26118926-26141228	NOTEST	0	0	0	0	1	1
ENSG00000232587	ENSG00000232587	EEF1A1P3	13:28712642-28869475	NOTEST	0.0122338	0.00860655	-0.507363	0	1	1
ENSG00000232590	ENSG00000232590	RP11-128I7.1	9:76188530-76194414	NOTEST	0	0	0	0	1	1
ENSG00000232591	ENSG00000232591	RP5-1031D4.2	10:7487519-7513904	NOTEST	0	0	0	0	1	1
ENSG00000232594	ENSG00000232594	AC103563.3	2:95626791-95627248	NOTEST	0	0	0	0	1	1
ENSG00000232595	ENSG00000232595	CST2P1	20:23691956-23692043	NOTEST	0	0	0	0	1	1
ENSG00000232596	ENSG00000232596	RP1-37J18.2	1:4631607-4643481	NOTEST	0	0	0	0	1	1
ENSG00000232597	ENSG00000232597	AC013727.1	2:104473427-104694236	NOTEST	0	0	0	0	1	1
ENSG00000232598	ENSG00000232598	RP1-90K10.4	6:36907846-36912451	NOTEST	0	0	0	0	1	1
ENSG00000232599	ENSG00000232599	RP1-161N10.1	X:124337653-124338187	NOTEST	0	0	0	0	1	1
ENSG00000232600	ENSG00000232600	AC084125.4	8:145654164-145669827	NOTEST	0.148289	0.0689738	-1.10429	0	1	1
ENSG00000232601	ENSG00000232601	RP11-393N4.1	3:174020733-174021077	NOTEST	0	0	0	0	1	1
ENSG00000232603	ENSG00000232603	LL22NC03-22A12.12	22:22725196-22725488	NOTEST	0	0	0	0	1	1
ENSG00000232604	ENSG00000232604	AC010967.3	2:52949814-53137158	NOTEST	0	0	0	0	1	1
ENSG00000232605	ENSG00000232605	HMGN2P11	7:84505869-84506272	NOTEST	0	0	0	0	1	1
ENSG00000232606	ENSG00000232606	AC010090.1	2:145324001-145337001	NOTEST	0	0	0	0	1	1
ENSG00000232608	ENSG00000232608	TIMM9P2	21:40556101-40695144	NOTEST	0	0	0	0	1	1
ENSG00000232610	ENSG00000232610	CCT6P4	3:190432599-190434188	NOTEST	0	0	0	0	1	1
ENSG00000232611	ENSG00000232611	RP11-1114A5.4	X:135923089-135962923	NOTEST	0.316145	0.300044	-0.075412	0	1	1
ENSG00000232612	ENSG00000232612	RPL31P35	7:54724050-54724427	NOTEST	0	0	0	0	1	1
ENSG00000232613	ENSG00000232613	AC007386.4	2:65257860-65264631	NOTEST	0.0854884	0.071449	-0.258814	0	1	1
ENSG00000232614	ENSG00000232614	USP9YP9	Y:27874636-27881307	NOTEST	0	0	0	0	1	1
ENSG00000232615	ENSG00000232615	CTD-2012J19.1	5:1594740-1634120	NOTEST	0.22899	0.194199	-0.237746	0	1	1
ENSG00000232616	ENSG00000232616	SKIV2L	HSCHR6_MHC_MCF:31996310-32013975	NOTEST	0	0	0	0	1	1
ENSG00000232617	ENSG00000232617	AC017019.1	Y:9502837-9506619	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232618	ENSG00000232618	RP11-439L18.1	6:143267183-143277835	NOTEST	0	0	0	0	1	1
ENSG00000232620	ENSG00000232620	TSPY17P	Y:6388503-6388970	NOTEST	0	0	0	0	1	1
ENSG00000232621	ENSG00000232621	C4BPAP2	1:207399142-207402547	NOTEST	0	0	0	0	1	1
ENSG00000232622	ENSG00000232622	RP11-484D4.3	1:85101840-85102789	NOTEST	0	0	0	0	1	1
ENSG00000232623	ENSG00000232623	AP000266.7	21:33664123-33765335	NOTEST	0	0.105697	inf	0	1	1
ENSG00000232624	ENSG00000232624	RP11-478H13.3	10:29078116-29102387	NOTEST	0	0	0	0	1	1
ENSG00000232625	ENSG00000232625	AC009974.11	2:219706321-219706788	NOTEST	0.0501707	0.039112	-0.359234	0	1	1
ENSG00000232626	ENSG00000232626	RP11-175B9.2	1:202317826-202679545	NOTEST	0	0.0612776	inf	0	1	1
ENSG00000232627	ENSG00000232627	AC021876.4	7:23338357-23510086	NOTEST	0.150342	0.17949	0.255651	0	1	1
ENSG00000232628	ENSG00000232628	RP11-365O16.3	1:224396448-224400981	NOTEST	0	0	0	0	1	1
ENSG00000232629	ENSG00000232629	HLA-DQB2	6:32723874-32731311	NOTEST	0.225545	0.221346	-0.0271143	0	1	1
ENSG00000232631	ENSG00000232631	MTND2P23	2:212240445-213403565	NOTEST	0	0	0	0	1	1
ENSG00000232632	ENSG00000232632	GABBR1	HSCHR6_MHC_COX:29519994-29597568	NOTEST	0	0	0	0	1	1
ENSG00000232633	ENSG00000232633	CTD-2201G3.1	5:112357795-112824527	NOTEST	0	0	0	0	1	1
ENSG00000232634	ENSG00000232634	NEFLP1	Y:23382991-23383975	NOTEST	0	0	0	0	1	1
ENSG00000232636	ENSG00000232636	RP11-342C20.2	13:88079454-88323514	NOTEST	0	0	0	0	1	1
ENSG00000232638	ENSG00000232638	RP11-379F12.4	10:8092412-8095447	NOTEST	0	0	0	0	1	1
ENSG00000232639	ENSG00000232639	LYPLA2P1	HSCHR6_MHC_COX:33254835-33255630	NOTEST	0	0	0	0	1	1
ENSG00000232640	ENSG00000232640	RP1-266L20.2	6:170125186-170139088	NOTEST	0.120857	0.143028	0.242996	0	1	1
ENSG00000232641	ENSG00000232641	MOG	HSCHR6_MHC_MCF:29624567-29639934	NOTEST	0	0	0	0	1	1
ENSG00000232642	ENSG00000232642	AC008073.7	2:24299395-24424567	NOTEST	0	0	0	0	1	1
ENSG00000232643	ENSG00000232643	LINC00385	13:30726022-30733758	NOTEST	0	0	0	0	1	1
ENSG00000232644	ENSG00000232644	GS1-466O4.3	X:26218158-26218764	NOTEST	0	0	0	0	1	1
ENSG00000232645	ENSG00000232645	RP3-322G13.5	20:23337230-23338753	NOTEST	0.206751	0	#NAME?	0	1	1
ENSG00000232646	ENSG00000232646	RP11-344N10.4	10:74766974-74856732	NOTEST	0	0	0	0	1	1
ENSG00000232647	ENSG00000232647	POLR3KP1	13:59645595-59645937	NOTEST	0	0	0	0	1	1
ENSG00000232648	ENSG00000232648	RP11-367N14.2	4:184416090-184425647	NOTEST	0.147552	0.0596334	-1.30703	0	1	1
ENSG00000232649	ENSG00000232649	MCCD1P1	HSCHR6_MHC_MCF:29846326-29992167	NOTEST	0	0	0	0	1	1
ENSG00000232652	ENSG00000232652	XXbac-BPG13B8.10	HSCHR6_MHC_COX:29461862-29474910	NOTEST	0	0	0	0	1	1
ENSG00000232653	ENSG00000232653	GOLGA8N	15:32885656-32896179	NOTEST	0.163567	0.114439	-0.515305	0	1	1
ENSG00000232654	ENSG00000232654	FAM136BP	6:3045617-3046034	NOTEST	0	0	0	0	1	1
ENSG00000232655	ENSG00000232655	CTA-397C4.2	22:44839206-44840668	NOTEST	0	0	0	0	1	1
ENSG00000232658	ENSG00000232658	AC092638.1	2:194121207-194122482	NOTEST	0	0	0	0	1	1
ENSG00000232659	ENSG00000232659	ZDHHC20P2	HSCHR6_MHC_COX:31338653-31339080	NOTEST	0	0	0	0	1	1
ENSG00000232661	ENSG00000232661	AC000111.3	7:117105837-117514193	NOTEST	0	0	0	0	1	1
ENSG00000232662	ENSG00000232662	LDHBP1	13:113930930-113932049	NOTEST	0	0.0110329	inf	0	1	1
ENSG00000232663	ENSG00000232663	RP3-477M7.6	1:8969800-8969963	NOTEST	0	0	0	0	1	1
ENSG00000232664	ENSG00000232664	LARP1BP3	X:133338382-133339946	NOTEST	0	0	0	0	1	1
ENSG00000232665	ENSG00000232665	PHBP10	X:103810995-105011822	NOTEST	0	0	0	0	1	1
ENSG00000232667	ENSG00000232667	AC004862.6	7:79959507-80308593	NOTEST	0	0	0	0	1	1

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ENSG00000232668	ENSG00000232668	AC010967.1	2:52949814-53137158	NOTEST	0	0	0	0	1	1
ENSG00000232672	ENSG00000232672	RP4-706L14.2	1:78239549-78240549	NOTEST	0	0	0	0	1	1
ENSG00000232675	ENSG00000232675	RP4-718D20.3	20:19193289-19703581	NOTEST	0	0	0	0	1	1
ENSG00000232676	ENSG00000232676	ADH5P2	1:79986764-79987888	NOTEST	0	0	0	0	1	1
ENSG00000232678	ENSG00000232678	SPTLC1P4	1:152050427-152050687	NOTEST	0	0	0	0	1	1
ENSG00000232679	ENSG00000232679	RP11-400N13.3	1:222215046-222238105	NOTEST	0.21126	0.0861045	-1.29486	0	1	1
ENSG00000232680	ENSG00000232680	AC002511.3	19:35923858-35925544	NOTEST	0.0326969	0	#NAME?	0	1	1
ENSG00000232682	ENSG00000232682	RP11-388P9.2	10:61786055-62493248	NOTEST	0	0	0	0	1	1
ENSG00000232683	ENSG00000232683	UQCRHP1	HSCHR6_MHC_DBB:31561041-31561315	NOTEST	0	0	0	0	1	1
ENSG00000232684	ENSG00000232684	ATP11A-AS1	13:113344642-113541482	NOTEST	0	0	0	0	1	1
ENSG00000232685	ENSG00000232685	LINC00442	13:19520894-19636858	NOTEST	0	0	0	0	1	1
ENSG00000232686	ENSG00000232686	ARID4B-IT1	1:235294497-235507847	NOTEST	0	0.228819	inf	0	1	1
ENSG00000232687	ENSG00000232687	RPL12P9	21:30449791-30548210	NOTEST	0	0	0	0	1	1
ENSG00000232688	ENSG00000232688	AC007403.1	2:67131567-67198594	NOTEST	0	0	0	0	1	1
ENSG00000232690	ENSG00000232690	HSPE1P9	2:235346971-235370771	NOTEST	0	0	0	0	1	1
ENSG00000232691	ENSG00000232691	NCRNA00171	HSCHR6_MHC_MCF:30047254-30111187	NOTEST	0	0	0	0	1	1
ENSG00000232692	ENSG00000232692	AP001596.6	21:27750870-27945603	NOTEST	0.0625998	0.134391	1.10221	0	1	1
ENSG00000232693	ENSG00000232693	AC012370.2	2:65537984-65659771	NOTEST	0	0	0	0	1	1
ENSG00000232694	ENSG00000232694	XX-CR54.3	1:248881946-248885506	NOTEST	0.486251	0.34774	-0.483691	0	1	1
ENSG00000232695	ENSG00000232695	TCEB1P17	Y:28007089-28007415	NOTEST	0	0	0	0	1	1
ENSG00000232696	ENSG00000232696	AC017006.2	2:45878483-46415129	NOTEST	0	0	0	0	1	1
ENSG00000232698	ENSG00000232698	AP001058.3	21:45626407-45627282	NOTEST	0	0	0	0	1	1
ENSG00000232699	ENSG00000232699	BDH2P1	6:99622619-99623357	NOTEST	0.0262441	0.0579682	1.14327	0	1	1
ENSG00000232701	ENSG00000232701	RPL21P108	13:74951299-74952088	NOTEST	0	0	0	0	1	1
ENSG00000232705	ENSG00000232705	HLA-DRB9	HSCHR6_MHC_SSTO:32433543-32447199	NOTEST	0	0	0	0	1	1
ENSG00000232706	ENSG00000232706	NUTM2HP	10:52436502-52446086	NOTEST	0	0	0	0	1	1
ENSG00000232707	ENSG00000232707	AP1B1P2	22:32530014-32530120	NOTEST	0	0	0	0	1	1
ENSG00000232708	ENSG00000232708	HLA-K	HSCHR6_MHC_DBB:29885324-29888576	NOTEST	0	0	0	0	1	1
ENSG00000232709	ENSG00000232709	MARK2P9	10:94178423-94180632	NOTEST	0	0	0	0	1	1
ENSG00000232710	ENSG00000232710	RP4-669P10.16	22:42481528-42535938	NOTEST	0.089847	0	#NAME?	0	1	1
ENSG00000232712	ENSG00000232712	RP4-777D9.2	20:21106623-21227260	NOTEST	0	0	0	0	1	1
ENSG00000232713	ENSG00000232713	AC010733.5	2:61165338-61165739	NOTEST	0.064488	0.146735	1.18611	0	1	1
ENSG00000232714	ENSG00000232714	MTND3P8	1:235705058-235705397	NOTEST	0	0	0	0	1	1
ENSG00000232715	ENSG00000232715	LINC01022	7:158383320-158383812	NOTEST	0	0	0	0	1	1
ENSG00000232716	ENSG00000232716	AC016831.6	7:130524962-130528484	NOTEST	0	0	0	0	1	1
ENSG00000232717	ENSG00000232717	TRIM51JP	2:96240646-96246512	NOTEST	0	0	0	0	1	1
ENSG00000232718	ENSG00000232718	GAPDHP48	2:3705784-3836122	NOTEST	0	0	0	0	1	1
ENSG00000232719	ENSG00000232719	RP11-13J8.1	2:201966104-201967859	NOTEST	0	0	0	0	1	1
ENSG00000232721	ENSG00000232721	RP11-403I13.5	1:149230715-149232554	NOTEST	0.0300167	0.0231966	-0.37185	0	1	1
ENSG00000232722	ENSG00000232722	MROH4P	8:143648620-143653366	NOTEST	0	0	0	0	1	1
ENSG00000232723	ENSG00000232723	AC013399.3	2:122067570-122067988	NOTEST	0	0	0	0	1	1
ENSG00000232724	ENSG00000232724	AC111186.1	17:73070400-73075644	NOTEST	0	0	0	0	1	1
ENSG00000232725	ENSG00000232725	U52111.14	X:152990322-153051187	NOTEST	0.366058	0.271698	-0.430072	0	1	1
ENSG00000232727	ENSG00000232727	YWHAEP1	7:63894207-63894970	NOTEST	0	0	0	0	1	1

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ENSG00000232728	ENSG00000232728	PHB2P1	10:111287876-111288766	NOTEST	0	0	0	0	1	1
ENSG00000232729	ENSG00000232729	AC083884.8	7:74071993-74306731	NOTEST	0.235734	0.282502	0.261098	0	1	1
ENSG00000232730	ENSG00000232730	FAM8A4P	Y:14442349-14443562	NOTEST	0	0	0	0	1	1
ENSG00000232732	ENSG00000232732	AC073043.1	2:200732118-200775882	NOTEST	0	0.121261	inf	0	1	1
ENSG00000232733	ENSG00000232733	RPL12P1	HSCHR6_MHC_SSTO:33498670-33517062	NOTEST	0	0	0	0	1	1
ENSG00000232734	ENSG00000232734	ATP5G1P7	10:71192727-71193127	NOTEST	0	0	0	0	1	1
ENSG00000232735	ENSG00000232735	ATG4AP1	X:82253706-82254244	NOTEST	0	0	0	0	1	1
ENSG00000232736	ENSG00000232736	AC007551.2	7:35791465-35840226	NOTEST	0	0	0	0	1	1
ENSG00000232738	ENSG00000232738	RP5-986I17.2	20:9518035-9819689	NOTEST	0	0	0	0	1	1
ENSG00000232739	ENSG00000232739	RP11-25G10.2	10:15253641-15413061	NOTEST	0	0	0	0	1	1
ENSG00000232740	ENSG00000232740	AC062020.1	2:123822896-123831057	NOTEST	0	0	0	0	1	1
ENSG00000232743	ENSG00000232743	XXyac-YM21GA2.1	9:90431379-90432885	NOTEST	0	0	0	0	1	1
ENSG00000232744	ENSG00000232744	USP9YP16	Y:20283080-20285685	NOTEST	0	0	0	0	1	1
ENSG00000232745	ENSG00000232745	ANKRD20A14P	1:142803223-142827235	NOTEST	0.450328	0.303183	-0.570787	0	1	1
ENSG00000232746	ENSG00000232746	RP11-767C1.1	3:12919020-12926710	NOTEST	0	0	0	0	1	1
ENSG00000232747	ENSG00000232747	IGKV1D-35	2:89934311-89934582	NOTEST	0	0	0	0	1	1
ENSG00000232748	ENSG00000232748	ZNF668	16:31072163-31085641	NOTEST	0.294729	0.564909	0.938631	0	1	1
ENSG00000232749	ENSG00000232749	RP11-15B24.4	9:84887670-85179347	NOTEST	0	0	0	0	1	1
ENSG00000232750	ENSG00000232750	RP11-177A2.5	1:178994938-179045697	NOTEST	0.249156	0	#NAME?	0	1	1
ENSG00000232751	ENSG00000232751	RP11-296O14.1	1:173320827-173321143	NOTEST	0	0	0	0	1	1
ENSG00000232752	ENSG00000232752	RP5-837O21.5	1:94390298-94390941	NOTEST	0	0	0	0	1	1
ENSG00000232753	ENSG00000232753	RP11-347K2.1	1:103817768-103835986	NOTEST	0	0	0	0	1	1
ENSG00000232754	ENSG00000232754	RP1-85F18.6	22:41487789-41593460	NOTEST	0	0	0	0	1	1
ENSG00000232756	ENSG00000232756	RP5-1185I7.1	7:77619700-77624488	NOTEST	0.0383847	0.0865153	1.17242	0	1	1
ENSG00000232757	ENSG00000232757	ETF1P1	6:29968787-30032686	NOTEST	0	0	0	0	1	1
ENSG00000232758	ENSG00000232758	HCG27	HSCHR6_MHC_COX:31158105-31164310	NOTEST	0	0	0	0	1	1
ENSG00000232759	ENSG00000232759	AC002480.3	7:22459062-22705152	NOTEST	0.0315881	0.00461324	-2.77553	0	1	1
ENSG00000232760	ENSG00000232760	AC103564.6	2:132591355-132594105	NOTEST	0	0	0	0	1	1
ENSG00000232762	ENSG00000232762	RP4-784A16.4	1:53711216-53793742	NOTEST	0	0.0180566	inf	0	1	1
ENSG00000232764	ENSG00000232764	TRIM60P8Y	Y:25171740-25172810	NOTEST	0	0	0	0	1	1
ENSG00000232765	ENSG00000232765	RP11-382F24.2	X:55306271-55315218	NOTEST	0	0	0	0	1	1
ENSG00000232766	ENSG00000232766	AC098614.3	3:27744619-27745059	NOTEST	0	0	0	0	1	1
ENSG00000232767	ENSG00000232767	RP11-498B4.5	10:118423206-118502085	NOTEST	0	0	0	0	1	1
ENSG00000232768	ENSG00000232768	RP11-201O14.2	1:31404352-31538838	NOTEST	0	0	0	0	1	1
ENSG00000232771	ENSG00000232771	PPP1R26P5	22:21695883-21699547	NOTEST	0	0	0	0	1	1
ENSG00000232772	ENSG00000232772	MTND4P22	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000232773	ENSG00000232773	RP11-1396O13.15	4:9424038-9431428	NOTEST	0	0	0	0	1	1
ENSG00000232774	ENSG00000232774	RP11-47I22.3	14:61654276-62125414	NOTEST	0.102183	0.0949271	-0.106256	0	1	1
ENSG00000232777	ENSG00000232777	MRPL51P2	21:44535443-44535819	NOTEST	0	0	0	0	1	1
ENSG00000232778	ENSG00000232778	RPL23AP50	6:108188959-108281190	NOTEST	0	0	0	0	1	1
ENSG00000232780	ENSG00000232780	RP5-871G17.5	1:119977078-119977703	NOTEST	0.1636	0.176291	0.107794	0	1	1
ENSG00000232781	ENSG00000232781	OR2AD1P	HSCHR6_MHC_MANN:28994460-28995388	NOTEST	0	0	0	0	1	1

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ENSG00000232783	ENSG00000232783	AC073135.3	3:197836982-197838749	NOTEST	0	0.123092	inf	0	1	1
ENSG00000232784	ENSG00000232784	AC067961.1	2:226264425-226265304	NOTEST	0	0	0	0	1	1
ENSG00000232786	ENSG00000232786	TIMM9P3	13:46039059-46189874	NOTEST	0	0	0	0	1	1
ENSG00000232787	ENSG00000232787	OR7L1P	X:130730112-130730812	NOTEST	0	0	0	0	1	1
ENSG00000232788	ENSG00000232788	AC078883.3	2:173292081-173489823	NOTEST	0.0255321	0	#NAME?	0	1	1
ENSG00000232789	ENSG00000232789	AC053503.2	2:220223591-220223705	NOTEST	0	0	0	0	1	1
ENSG00000232790	ENSG00000232790	LINC01162	7:20875049-21062767	NOTEST	0	0	0	0	1	1
ENSG00000232791	ENSG00000232791	OR11I1P	1:111396559-111397513	NOTEST	0	0	0	0	1	1
ENSG00000232792	ENSG00000232792	FTH1P25	1:185014495-185071740	NOTEST	0	0	0	0	1	1
ENSG00000232793	ENSG00000232793	DNAJC19P8	1:245318286-245872733	NOTEST	0	0	0	0	1	1
ENSG00000232794	ENSG00000232794	HNRNPDP1	X:63264184-63264938	NOTEST	0	0	0	0	1	1
ENSG00000232795	ENSG00000232795	SCAND3P1	13:35516423-36247159	NOTEST	0.0334327	0	#NAME?	0	1	1
ENSG00000232797	ENSG00000232797	FAM207CP	21:15164955-15165462	NOTEST	0	0	0	0	1	1
ENSG00000232798	ENSG00000232798	RP11-204M4.1	9:42037567-42037913	NOTEST	0	0	0	0	1	1
ENSG00000232799	ENSG00000232799	CRYGFP	2:210009964-210012411	NOTEST	0	0	0	0	1	1
ENSG00000232800	ENSG00000232800	SLC7A15P	2:20586146-20596349	NOTEST	0	0	0	0	1	1
ENSG00000232801	ENSG00000232801	SDCBPP3	X:40749899-40750790	NOTEST	0.0618879	0.346822	2.48647	0	1	1
ENSG00000232802	ENSG00000232802	COL11A2P1	HSCHR6_MHC_DBB:33049478-33049682	NOTEST	0	0	0	0	1	1
ENSG00000232804	ENSG00000232804	HSPA1B	HSCHR6_MHC_APD:31806878-31809393	NOTEST	0	0	0	0	1	1
ENSG00000232805	ENSG00000232805	NIP7P1	10:94866628-94867140	NOTEST	0	0	0	0	1	1
ENSG00000232806	ENSG00000232806	AP001610.9	21:42931051-42934885	NOTEST	0	0	0	0	1	1
ENSG00000232807	ENSG00000232807	RP11-536K7.3	10:5903579-5987863	NOTEST	0.0640251	0.0425585	-0.58919	0	1	1
ENSG00000232808	ENSG00000232808	TTTY20	Y:9167488-9172441	NOTEST	0	0	0	0	1	1
ENSG00000232809	ENSG00000232809	VDAC1P10	1:215549826-215550717	NOTEST	0	0	0	0	1	1
ENSG00000232811	ENSG00000232811	RP11-96K19.2	1:111486088-111507271	NOTEST	0.097039	0.0814526	-0.252604	0	1	1
ENSG00000232812	ENSG00000232812	RP11-459K23.2	1:208902032-208906529	NOTEST	0	0	0	0	1	1
ENSG00000232813	ENSG00000232813	RP11-344N17.2	X:48134338-48134482	NOTEST	0	0	0	0	1	1
ENSG00000232814	ENSG00000232814	COL4A2-AS1	13:110801317-111165374	NOTEST	0	0.0973039	inf	0	1	1
ENSG00000232815	ENSG00000232815	LINC00537	9:68413481-68414196	NOTEST	0.0273053	0.0796271	1.54408	0	1	1
ENSG00000232816	ENSG00000232816	HLA-K	HSCHR6_MHC_MANN:29884569-29887819	NOTEST	0	0	0	0	1	1
ENSG00000232817	ENSG00000232817	RP11-73B2.4	7:62849185-62854035	NOTEST	0	0	0	0	1	1
ENSG00000232818	ENSG00000232818	RPS2P32	7:23530091-23530983	NOTEST	0.0582741	0.125683	1.10887	0	1	1
ENSG00000232821	ENSG00000232821	AC003986.6	7:19060613-19157295	NOTEST	0.35027	0.371081	0.0832664	0	1	1
ENSG00000232823	ENSG00000232823	TXNP1	10:121442638-121443335	NOTEST	0.140977	0	#NAME?	0	1	1
ENSG00000232824	ENSG00000232824	RP11-401A10.2	1:198126092-198291550	NOTEST	0	0	0	0	1	1
ENSG00000232825	ENSG00000232825	RP5-896L10.1	1:99355805-99614408	NOTEST	0	0	0	0	1	1
ENSG00000232827	ENSG00000232827	RP11-211N8.7	9:46826491-46833319	NOTEST	0	0	0	0	1	1
ENSG00000232828	ENSG00000232828	AF196970.3	X:48553944-48595570	NOTEST	0	0	0	0	1	1
ENSG00000232829	ENSG00000232829	GSTO3P	3:130546502-130547220	NOTEST	0	0.0655655	inf	0	1	1
ENSG00000232830	ENSG00000232830	RP11-144C15.1	3:101043048-101232085	NOTEST	0	0	0	0	1	1
ENSG00000232832	ENSG00000232832	LMLN-AS1	3:197687070-197770591	NOTEST	0.0406023	0	#NAME?	0	1	1
ENSG00000232834	ENSG00000232834	RP11-12D5.3	X:27865704-27866056	NOTEST	0	0	0	0	1	1
ENSG00000232835	ENSG00000232835	AC107057.1	2:5689911-5696163	NOTEST	0	0	0	0	1	1
ENSG00000232837	ENSG00000232837	AF064858.7	21:40346354-40349700	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000232839	ENSG00000232839	TRIM39	HSCHR6_MHC_DBB:30192096-30304918	NOTEST	0	0	0	0	1	1
ENSG00000232841	ENSG00000232841	AC098592.8	7:17072712-17073102	NOTEST	0	0	0	0	1	1
ENSG00000232842	ENSG00000232842	RP5-961K14.1	X:95228326-95229314	NOTEST	0	0.0141366	inf	0	1	1
ENSG00000232843	ENSG00000232843	SNX18P2	9:95571669-95661890	NOTEST	0	0	0	0	1	1
ENSG00000232845	ENSG00000232845	TRAPPC2P9	Y:25908984-25911730	NOTEST	0	0	0	0	1	1
ENSG00000232846	ENSG00000232846	SLC25A6P3	1:52027537-52344477	NOTEST	0	0	0	0	1	1
ENSG00000232848	ENSG00000232848	CTA-215D11.4	1:8086797-8182762	NOTEST	0	0	0	0	1	1
ENSG00000232849	ENSG00000232849	LINC00363	13:93708909-93710179	NOTEST	0	0	0	0	1	1
ENSG00000232850	ENSG00000232850	AL590708.2	9:130882971-130891481	NOTEST	0.189146	0.0840389	-1.17037	0	1	1
ENSG00000232851	ENSG00000232851	ATP5J2P3	9:79655316-79655589	NOTEST	0	0	0	0	1	1
ENSG00000232852	ENSG00000232852	CICP4	20:62887093-62944485	NOTEST	0.0382818	0.0384593	0.00667064	0	1	1
ENSG00000232853	ENSG00000232853	LUZP4P1	10:21536680-21537024	NOTEST	0	0	0	0	1	1
ENSG00000232855	ENSG00000232855	AF131217.1	21:29811666-30047170	NOTEST	0	0.00603217	inf	0	1	1
ENSG00000232857	ENSG00000232857	KATNBL1P2	1:95104016-95285837	NOTEST	0	0	0	0	1	1
ENSG00000232858	ENSG00000232858	RPL34P27	13:25562714-25563063	NOTEST	0	0	0	0	1	1
ENSG00000232860	ENSG00000232860	SMG7-AS1	1:183430008-183440881	NOTEST	0.0973424	0.0916486	-0.0869551	0	1	1
ENSG00000232862	ENSG00000232862	RP4-665N4.4	1:36545666-36547923	NOTEST	0	0	0	0	1	1
ENSG00000232863	ENSG00000232863	RP11-327I22.1	9:43064965-43133544	NOTEST	0	0	0	0	1	1
ENSG00000232864	ENSG00000232864	CTD-2090I13.2	1:227581291-227618736	NOTEST	0	0	0	0	1	1
ENSG00000232866	ENSG00000232866	AL513478.1	9:43135094-43135514	NOTEST	0	0	0	0	1	1
ENSG00000232867	ENSG00000232867	RP11-179D22.1	9:27109138-27230173	NOTEST	0	0	0	0	1	1
ENSG00000232869	ENSG00000232869	TRBV29-1	7:142448052-142448741	NOTEST	0	0	0	0	1	1
ENSG00000232871	ENSG00000232871	SEC1P	19:49141198-49184461	NOTEST	0	0.0425673	inf	0	1	1
ENSG00000232872	ENSG00000232872	CTAGE3P	13:52482353-52484757	NOTEST	0.0706207	0.0244368	-1.53103	0	1	1
ENSG00000232873	ENSG00000232873	AC046143.6	3:194283706-194284730	NOTEST	0	0	0	0	1	1
ENSG00000232874	ENSG00000232874	RP11-135A1.2	3:193848404-193848990	NOTEST	0	0	0	0	1	1
ENSG00000232875	ENSG00000232875	HMGN2P35	10:98592016-98740800	NOTEST	0	0	0	0	1	1
ENSG00000232876	ENSG00000232876	CTA-212D2.2	6:135281515-135424194	NOTEST	0.0919912	0.0935361	0.0240274	0	1	1
ENSG00000232878	ENSG00000232878	DPYD-AS1	1:97543298-98386605	NOTEST	0	0	0	0	1	1
ENSG00000232879	ENSG00000232879	RP11-544M22.3	1:160965000-161008780	NOTEST	0	0	0	0	1	1
ENSG00000232880	ENSG00000232880	RP3-453C12.8	20:43990576-44039250	NOTEST	0	0	0	0	1	1
ENSG00000232881	ENSG00000232881	RPS10P21	13:72487841-72488316	NOTEST	0	0	0	0	1	1
ENSG00000232882	ENSG00000232882	PHKA1P1	1:91358548-91359169	NOTEST	0.154913	0.300334	0.955112	0	1	1
ENSG00000232883	ENSG00000232883	RP11-302I18.1	1:220490008-220490941	NOTEST	0	0	0	0	1	1
ENSG00000232884	ENSG00000232884	AF127936.3	21:16119082-16126184	NOTEST	0	0	0	0	1	1
ENSG00000232885	ENSG00000232885	GPC5-AS2	13:92050928-93519490	NOTEST	0	0	0	0	1	1
ENSG00000232886	ENSG00000232886	AF212831.2	21:18235194-18246011	NOTEST	0	0	0	0	1	1
ENSG00000232887	ENSG00000232887	AC006466.5	7:31158897-31159186	NOTEST	0	0	0	0	1	1
ENSG00000232889	ENSG00000232889	AC087499.4	17:20498843-20499021	NOTEST	0	0	0	0	1	1
ENSG00000232891	ENSG00000232891	RP11-136K14.1	6:150920998-151164799	NOTEST	0	0	0	0	1	1
ENSG00000232892	ENSG00000232892	RP11-267N12.1	1:163080910-163325554	NOTEST	0	0.0145395	inf	0	1	1
ENSG00000232893	ENSG00000232893	AC019068.2	2:237232793-237416185	NOTEST	0	0	0	0	1	1
ENSG00000232894	ENSG00000232894	MRPS31P2	13:20126710-20144428	NOTEST	0	0	0	0	1	1
ENSG00000232895	ENSG00000232895	RP4-543J13.1	1:114749048-114804900	NOTEST	0	0	0	0	1	1

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ENSG00000232897	ENSG00000232897	RP11-191L9.5	22:48027422-48251349	NOTEST	0	0	0	0	1	1
ENSG00000232899	ENSG00000232899	CDY9P	Y:20344720-20346300	NOTEST	0	0	0	0	1	1
ENSG00000232900	ENSG00000232900	RP4-697P8.3	20:10618331-10975572	NOTEST	0	0	0	0	1	1
ENSG00000232901	ENSG00000232901	CYCSP10	3:10000400-10052893	NOTEST	0	0.798213	inf	0	1	1
ENSG00000232902	ENSG00000232902	XXbac-BPG13B8.10	HSCHR6_MHC_QBL:29465174-29478221	NOTEST	0	0	0	0	1	1
ENSG00000232903	ENSG00000232903	LINC01166	10:134757470-134778793	NOTEST	0	0	0	0	1	1
ENSG00000232905	ENSG00000232905	RP11-534I8.1	9:116612966-116613912	NOTEST	0	0	0	0	1	1
ENSG00000232906	ENSG00000232906	RP11-746P2.3	7:64820846-64822089	NOTEST	0	0	0	0	1	1
ENSG00000232907	ENSG00000232907	RP5-977B1.7	20:34894257-35274619	NOTEST	0.163022	0.119863	-0.443678	0	1	1
ENSG00000232908	ENSG00000232908	HSD17B7P1	1:247990787-247991804	NOTEST	0	0	0	0	1	1
ENSG00000232909	ENSG00000232909	RP3-510O8.4	6:35701643-35704724	NOTEST	0	0.065961	inf	0	1	1
ENSG00000232910	ENSG00000232910	RAB9AP1	Y:25897334-25897907	NOTEST	0	0	0	0	1	1
ENSG00000232912	ENSG00000232912	RP5-1115A15.	1:8412456-8877702	NOTEST	0.0430552	0	#NAME?	0	1	1
ENSG00000232913	ENSG00000232913	RP11-429H9.4	10:95753745-96122716	NOTEST	0	0	0	0	1	1
ENSG00000232914	ENSG00000232914	TRAPPC2P4	Y:28050664-28053397	NOTEST	0	0	0	0	1	1
ENSG00000232915	ENSG00000232915	AC097721.1	2:139169635-139170888	NOTEST	0	0	0	0	1	1
ENSG00000232916	ENSG00000232916	HMGN2P27	5:115419503-115748459	NOTEST	0	0	0	0	1	1
ENSG00000232917	ENSG00000232917	HSPE1P6	1:203872850-203873147	NOTEST	0	0	0	0	1	1
ENSG00000232918	ENSG00000232918	RP11-366L18.1	1:94871950-94872438	NOTEST	0	0	0	0	1	1
ENSG00000232920	ENSG00000232920	RP11-465M18.1	9:37073527-37075789	NOTEST	0	0	0	0	1	1
ENSG00000232922	ENSG00000232922	AC004112.5	7:111846642-112049678	NOTEST	0	0	0	0	1	1
ENSG00000232924	ENSG00000232924	TCEB1P4	Y:9068523-9068856	NOTEST	0	0	0	0	1	1
ENSG00000232925	ENSG00000232925	MRPS16P2	20:57688278-57688686	NOTEST	0	0	0	0	1	1
ENSG00000232926	ENSG00000232926	AC000078.5	22:19863039-20004331	NOTEST	0.252393	0.402051	0.671707	0	1	1
ENSG00000232927	ENSG00000232927	USP12PY	Y:3550845-3551909	NOTEST	0	0	0	0	1	1
ENSG00000232928	ENSG00000232928	DDX3YP1	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000232930	ENSG00000232930	AC083864.3	7:36069220-36095041	NOTEST	0	0	0	0	1	1
ENSG00000232934	ENSG00000232934	RP11-324O2.3	10:114133775-114188138	NOTEST	0	0	0	0	1	1
ENSG00000232935	ENSG00000232935	RP11-223P11.2	10:128593977-129250781	NOTEST	0	0	0	0	1	1
ENSG00000232936	ENSG00000232936	RP11-80H5.2	10:91342744-91410579	NOTEST	0.318455	0.0808501	-1.97777	0	1	1
ENSG00000232937	ENSG00000232937	RP11-98D18.2	1:151728016-151766878	NOTEST	0.183735	0.0520444	-1.81981	0	1	1
ENSG00000232939	ENSG00000232939	RP11-406O23.2	9:112403067-112934792	NOTEST	0	0	0	0	1	1
ENSG00000232943	ENSG00000232943	RP4-717M23.2	20:18200756-18201156	NOTEST	0	0	0	0	1	1
ENSG00000232944	ENSG00000232944	RP13-492C18.1	7:56476391-56476903	NOTEST	0	0	0	0	1	1
ENSG00000232945	ENSG00000232945	OR2J2	HSCHR6_MHC_DBB:29141328-29142369	NOTEST	0	0	0	0	1	1
ENSG00000232946	ENSG00000232946	RP11-390F4.2	9:6675283-6675614	NOTEST	0	0	0	0	1	1
ENSG00000232947	ENSG00000232947	RP11-401E14.2	6:15995174-16000028	NOTEST	0	0	0	0	1	1
ENSG00000232948	ENSG00000232948	DEFB130	8:12168470-12175825	NOTEST	0	0	0	0	1	1
ENSG00000232949	ENSG00000232949	AC002480.4	7:22459062-22705152	NOTEST	0	0	0	0	1	1
ENSG00000232950	ENSG00000232950	RP11-36D19.4	10:82057475-82059411	NOTEST	0	0	0	0	1	1
ENSG00000232951	ENSG00000232951	IPO7P1	X:51664959-51665595	NOTEST	0	0.0474703	inf	0	1	1
ENSG00000232952	ENSG00000232952	RP11-90H3.1	1:106434360-106436139	NOTEST	0.498199	0.495165	-0.00881405	0	1	1

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ENSG00000232953	ENSG00000232953	HSPA8P18	3:19920963-19988517	NOTEST	0	0	0	0	1	1
ENSG00000232954	ENSG00000232954	LINC00374	13:58785830-58807251	NOTEST	0	0	0	0	1	1
ENSG00000232957	ENSG00000232957	HLA-DOA	HSCHR6_MHC_SSTO:3311812-33117246	NOTEST	0	0	0	0	1	1
ENSG00000232958	ENSG00000232958	AC091069.1	3:6190170-6407572	NOTEST	0	0	0	0	1	1
ENSG00000232959	ENSG00000232959	RP11-332H17.1	1:169890466-170054349	NOTEST	0	0	0	0	1	1
ENSG00000232960	ENSG00000232960	CSNK2B	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000232962	ENSG00000232962	HLA-DOA	HSCHR6_MHC_COX:32894247-32899682	NOTEST	0	0	0	0	1	1
ENSG00000232963	ENSG00000232963	HMGN2P20	2:24425732-24583583	NOTEST	0	0	0	0	1	1
ENSG00000232964	ENSG00000232964	RP11-543E8.1	1:230728405-230731329	NOTEST	0	0	0	0	1	1
ENSG00000232965	ENSG00000232965	RPS12P18	10:81303842-81304112	NOTEST	0	0	0	0	1	1
ENSG00000232968	ENSG00000232968	AC008163.6	7:81092351-81092929	NOTEST	0	0	0	0	1	1
ENSG00000232969	ENSG00000232969	AP001062.9	21:45748826-45760353	NOTEST	0	0	0	0	1	1
ENSG00000232970	ENSG00000232970	POLHP1	2:216972186-217071026	NOTEST	0	0	0	0	1	1
ENSG00000232971	ENSG00000232971	RP11-293A10.3	1:109255278-109285365	NOTEST	0	0	0	0	1	1
ENSG00000232973	ENSG00000232973	CYP1B1-AS1	2:38150329-38408997	NOTEST	0	0	0	0	1	1
ENSG00000232974	ENSG00000232974	RPS17P1	HSCHR6_MHC_APD:29457129-29457535	NOTEST	0	0	0	0	1	1
ENSG00000232975	ENSG00000232975	RP5-945F2.1	7:67556209-67584196	NOTEST	0	0	0	0	1	1
ENSG00000232976	ENSG00000232976	TRIM60P10Y	Y:26805483-26806553	NOTEST	0	0	0	0	1	1
ENSG00000232978	ENSG00000232978	RP11-146N23.4	9:19230432-19374139	NOTEST	0	0.0973071	inf	0	1	1
ENSG00000232979	ENSG00000232979	AC092580.2	2:7875775-7875914	NOTEST	0	0	0	0	1	1
ENSG00000232981	ENSG00000232981	RP11-117O7.2	9:83178485-83179545	NOTEST	0	0	0	0	1	1
ENSG00000232982	ENSG00000232982	AC092662.2	2:156119969-156120236	NOTEST	0	0	0	0	1	1
ENSG00000232983	ENSG00000232983	RP11-296L22.7	9:34546521-34546994	NOTEST	0	0	0	0	1	1
ENSG00000232984	ENSG00000232984	OR2H1	HSCHR6_MHC_DBB:29424891-29432039	NOTEST	0	0	0	0	1	1
ENSG00000232985	ENSG00000232985	RP11-442O18.1	10:130757035-130758326	NOTEST	0	0	0	0	1	1
ENSG00000232986	ENSG00000232986	RP11-179A7.2	13:33929342-34250905	NOTEST	0.140471	0	#NAME?	0	1	1
ENSG00000232987	ENSG00000232987	AC051649.6	11:2012325-2014699	NOTEST	0	0.0209766	inf	0	1	1
ENSG00000232988	ENSG00000232988	HLA-T	HSCHR6_MHC_APD:29802805-29803937	NOTEST	0	0	0	0	1	1
ENSG00000232989	ENSG00000232989	RP11-136B18.1	1:238431793-238431895	NOTEST	0	0	0	0	1	1
ENSG00000232990	ENSG00000232990	MTATP6P7	2:131034079-131035530	NOTEST	0	0	0	0	1	1
ENSG00000232991	ENSG00000232991	GACAT1	2:108370567-108438585	NOTEST	0	0	0	0	1	1
ENSG00000232992	ENSG00000232992	AHCYP4	2:139659002-139660317	NOTEST	0	0	0	0	1	1
ENSG00000232993	ENSG00000232993	RP11-334A14.5	1:53527853-53551174	NOTEST	0	0	0	0	1	1
ENSG00000232994	ENSG00000232994	RPL7P14	2:203879601-204091101	NOTEST	0	0.0386979	inf	0	1	1
ENSG00000232997	ENSG00000232997	ZNF90P2	HSCHR6_MHC_SSTO:28856682-28857757	NOTEST	0	0	0	0	1	1
ENSG00000232998	ENSG00000232998	VPS13A-AS1	9:79791671-80036457	NOTEST	0	0	0	0	1	1
ENSG00000232999	ENSG00000232999	RP1-90J20.10	6:2910846-2912347	NOTEST	0	0	0	0	1	1
ENSG00000233002	ENSG00000233002	AC005324.6	17:15602890-15652629	NOTEST	0	0	0	0	1	1
ENSG00000233005	ENSG00000233005	AC067959.1	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000233007	ENSG00000233007	AF241726.4	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000233009	ENSG00000233009	NALCN-AS1	13:101360578-102068843	NOTEST	0	0.0160799	inf	0	1	1
ENSG00000233010	ENSG00000233010	RPEP4	22:29999544-30094587	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000233011	ENSG00000233011	SLC9A3P1	10:51910362-51912047	NOTEST	0	0	0	0	1	1
ENSG00000233012	ENSG00000233012	HDAC1P2	1:220701567-220837803	NOTEST	0.0816584	0.0722873	-0.175859	0	1	1
ENSG00000233013	ENSG00000233013	FAM157B	9:141106636-141143444	NOTEST	0	0.00710641	inf	0	1	1
ENSG00000233014	ENSG00000233014	TBC1D3P7	17:39479678-39485797	NOTEST	0	0	0	0	1	1
ENSG00000233015	ENSG00000233015	SLC25A6P1	20:21722940-21723715	NOTEST	0	0	0	0	1	1
ENSG00000233017	ENSG00000233017	RP5-908M14.5	20:61004603-61006568	NOTEST	0	0	0	0	1	1
ENSG00000233018	ENSG00000233018	RP4-597N16.1	1:235260501-235260727	NOTEST	0	0	0	0	1	1
ENSG00000233019	ENSG00000233019	OR2P1P	HSCHR6_MHC_MANN:29039603-29040379	NOTEST	0	0	0	0	1	1
ENSG00000233020	ENSG00000233020	RP11-42O15.2	1:70996208-70997175	NOTEST	0	0	0	0	1	1
ENSG00000233021	ENSG00000233021	RP11-490E15.2	10:320129-735683	NOTEST	0	0	0	0	1	1
ENSG00000233022	ENSG00000233022	RP11-118H15.1	9:65880532-65883885	NOTEST	0	0	0	0	1	1
ENSG00000233023	ENSG00000233023	IFITM4P	HSCHR6_MHC_MANN:29715613-29716034	NOTEST	0	0	0	0	1	1
ENSG00000233026	ENSG00000233026	AC026166.2	3:12045875-12232900	NOTEST	0	0	0	0	1	1
ENSG00000233028	ENSG00000233028	RP4-725G10.4	7:56243326-56244105	NOTEST	0.0448093	0	#NAME?	0	1	1
ENSG00000233029	ENSG00000233029	RP11-439A17.9	1:120906027-120935937	NOTEST	0	0	0	0	1	1
ENSG00000233030	ENSG00000233030	RP11-196G18.3	1:149754226-149783928	NOTEST	0.0387833	0.0198874	-0.96358	0	1	1
ENSG00000233031	ENSG00000233031	AC125238.3	2:204536897-204537146	NOTEST	0	0	0	0	1	1
ENSG00000233033	ENSG00000233033	CASK-AS1	X:41374186-41782716	NOTEST	0	0	0	0	1	1
ENSG00000233035	ENSG00000233035	HCG15	HSCHR6_MHC_MANN:28953984-28956318	NOTEST	0	0	0	0	1	1
ENSG00000233036	ENSG00000233036	KRTAP8-2P	21:32174559-32174745	NOTEST	0	0	0	0	1	1
ENSG00000233037	ENSG00000233037	AC009237.10	2:96208477-96208978	NOTEST	0	0	0	0	1	1
ENSG00000233038	ENSG00000233038	AC011899.9	7:157331749-158380480	NOTEST	0	0	0	0	1	1
ENSG00000233039	ENSG00000233039	MTND5P30	2:156168208-156169939	NOTEST	0	0	0	0	1	1
ENSG00000233040	ENSG00000233040	FAM204BP	1:197473877-197744826	NOTEST	0	0	0	0	1	1
ENSG00000233041	ENSG00000233041	PHGR1	15:40643233-40648635	NOTEST	0	0	0	0	1	1
ENSG00000233043	ENSG00000233043	HCG24	HSCHR6_MHC_MANN:33266457-33269442	NOTEST	0	0	0	0	1	1
ENSG00000233044	ENSG00000233044	RP1-137K2.2	6:157099062-157531913	NOTEST	0	0.0880605	inf	0	1	1
ENSG00000233045	ENSG00000233045	AC097523.1	2:139036143-139036780	NOTEST	0.0956315	0.0705384	-0.439077	0	1	1
ENSG00000233046	ENSG00000233046	OR5V1	HSCHR6_MHC_COX:29319721-29421426	NOTEST	0	0	0	0	1	1
ENSG00000233047	ENSG00000233047	RP11-24P14.1	1:106470245-106565834	NOTEST	0	0	0	0	1	1
ENSG00000233048	ENSG00000233048	RP5-1069C8.2	20:12845849-12933167	NOTEST	0.0103779	0	#NAME?	0	1	1
ENSG00000233049	ENSG00000233049	DHX16	HSCHR6_MHC_MANN:30659490-30685513	NOTEST	0	0	0	0	1	1
ENSG00000233050	ENSG00000233050	DEFB130	8:11921897-11929256	NOTEST	0	0	0	0	1	1
ENSG00000233051	ENSG00000233051	MICA	HSCHR6_MHC_COX:31358052-31374512	NOTEST	0	0	0	0	1	1
ENSG00000233052	ENSG00000233052	RP11-398B16.2	10:1228072-1779670	NOTEST	0	0	0	0	1	1
ENSG00000233053	ENSG00000233053	HLA-Z	HSCHR6_MHC_QBL:32792897-32792972	NOTEST	0	0	0	0	1	1
ENSG00000233054	ENSG00000233054	OR2B3	HSCHR6_MHC_APD:29054027-29055133	NOTEST	0	0	0	0	1	1
ENSG00000233055	ENSG00000233055	RP11-490D19.8	9:104230720-104295819	NOTEST	0	0	0	0	1	1
ENSG00000233056	ENSG00000233056	ERVH48-1	21:44336912-44345756	NOTEST	0.0159222	0	#NAME?	0	1	1
ENSG00000233057	ENSG00000233057	EEF1A1P14	1:194118602-194167824	NOTEST	0	0	0	0	1	1
ENSG00000233058	ENSG00000233058	LINC00884	3:194123400-194239008	NOTEST	0.11373	0.0878207	-0.372985	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000233060	ENSG00000233060	AC016700.2	2:70316852-70330352	NOTEST	0	0	0	0	1	1
ENSG00000233061	ENSG00000233061	TTLL7-IT1	1:84330710-84464833	NOTEST	0	0	0	0	1	1
ENSG00000233063	ENSG00000233063	SAR1AP4	X:75104380-75104971	NOTEST	0	0	0	0	1	1
ENSG00000233064	ENSG00000233064	RP3-380B8.4	6:5851738-5870453	NOTEST	0	0	0	0	1	1
ENSG00000233067	ENSG00000233067	RP11-40F8.2	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000233068	ENSG00000233068	RP1-140K8.1	6:3893359-3894524	NOTEST	0	0	0	0	1	1
ENSG00000233069	ENSG00000233069	RP5-930J4.2	1:21059372-21060445	NOTEST	0	0	0	0	1	1
ENSG00000233070	ENSG00000233070	ZFY-AS1	Y:2803111-2870667	NOTEST	0	0	0	0	1	1
ENSG00000233071	ENSG00000233071	RP4-635G19.1	X:102460937-102461827	NOTEST	0	0	0	0	1	1
ENSG00000233072	ENSG00000233072	RPS15AP6	1:21132962-21503377	NOTEST	0	0	0	0	1	1
ENSG00000233073	ENSG00000233073	AC005009.2	7:86273229-86494200	NOTEST	0.0291665	0	#NAME?	0	1	1
ENSG00000233074	ENSG00000233074	RP11-327I22.6	9:43140536-43142739	NOTEST	0	0	0	0	1	1
ENSG00000233075	ENSG00000233075	AL023583.1	6:13817712-13817966	NOTEST	0	0	0	0	1	1
ENSG00000233076	ENSG00000233076	DDAH2	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000233077	ENSG00000233077	RP11-290F20.2	20:48909256-48937879	NOTEST	0.19993	0.305868	0.613416	0	1	1
ENSG00000233078	ENSG00000233078	RP11-5P18.5	1:16330730-16335302	NOTEST	0	0.0676219	inf	0	1	1
ENSG00000233079	ENSG00000233079	RP11-90C4.3	1:56410759-56415792	NOTEST	0	0	0	0	1	1
ENSG00000233080	ENSG00000233080	CTA-714B7.5	22:35515816-35627049	NOTEST	0.119701	0.299223	1.32179	0	1	1
ENSG00000233081	ENSG00000233081	RP11-440G5.2	9:94188519-94189426	NOTEST	0	0.0348558	inf	0	1	1
ENSG00000233082	ENSG00000233082	AC073094.4	7:1306988-1308903	NOTEST	0	0	0	0	1	1
ENSG00000233083	ENSG00000233083	FTH1P6	2:52856880-52857216	NOTEST	0	0	0	0	1	1
ENSG00000233084	ENSG00000233084	AL672183.2	1:249230779-249231242	NOTEST	0.190404	0	#NAME?	0	1	1
ENSG00000233085	ENSG00000233085	XXyac-YX65C7_A.3	6:169686628-169689311	NOTEST	0.153776	0.045691	-1.75085	0	1	1
ENSG00000233086	ENSG00000233086	RP11-375O18.2	9:82120718-82147257	NOTEST	0	0	0	0	1	1
ENSG00000233087	ENSG00000233087	AC073869.1	2:132118065-132121731	NOTEST	0.0119229	0.0102399	-0.219526	0	1	1
ENSG00000233089	ENSG00000233089	TAPSAR1	HSCHR6_MHC_APD:32792100-32831197	NOTEST	0	0	0	0	1	1
ENSG00000233090	ENSG00000233090	AC015922.7	17:15696175-15696359	NOTEST	0	0	0	0	1	1
ENSG00000233091	ENSG00000233091	RPL7P4	HSCHR6_MHC_DBB:30654845-30655575	NOTEST	0	0	0	0	1	1
ENSG00000233093	ENSG00000233093	LINC00892	X:135721701-135724588	NOTEST	0	0	0	0	1	1
ENSG00000233094	ENSG00000233094	AL592170.1	GL000222.1:129788-134090	NOTEST	0	0	0	0	1	1
ENSG00000233095	ENSG00000233095	HLA-G	HSCHR6_MHC_SSTO:29791437-29795610	NOTEST	0	0	0	0	1	1
ENSG00000233096	ENSG00000233096	RP11-520A21.1	3:41012031-41013069	NOTEST	0	0	0	0	1	1
ENSG00000233098	ENSG00000233098	RP11-344E13.3	17:20717932-20947073	NOTEST	0	0.119116	inf	0	1	1
ENSG00000233099	ENSG00000233099	RP11-375A5.1	1:77747735-78025651	NOTEST	0	0	0	0	1	1
ENSG00000233101	ENSG00000233101	HOXB-AS3	17:46618255-46683776	NOTEST	0.135315	0.259577	0.939847	0	1	1
ENSG00000233103	ENSG00000233103	RP11-524P6.1	X:41907135-41914089	NOTEST	0	0	0	0	1	1
ENSG00000233105	ENSG00000233105	AC103563.4	2:95630217-95630581	NOTEST	0	0	0	0	1	1
ENSG00000233106	ENSG00000233106	RPL12P3	20:31860067-31860463	NOTEST	0	0	0	0	1	1
ENSG00000233107	ENSG00000233107	SUCLA2P2	2:76333141-76334450	NOTEST	0	0	0	0	1	1
ENSG00000233108	ENSG00000233108	AC006042.7	7:7676148-8133902	NOTEST	0	0	0	0	1	1
ENSG00000233109	ENSG00000233109	RP11-22C8.1	8:49826418-49826939	NOTEST	0.120313	0	#NAME?	0	1	1
ENSG00000233110	ENSG00000233110	RP11-301L8.2	4:186506597-186877806	NOTEST	0.0516364	0.0479366	-0.107261	0	1	1
ENSG00000233111	ENSG00000233111	RAB1C	9:37510888-38069210	NOTEST	0	0	0	0	1	1

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ENSG00000233113	ENSG00000233113	RPL7AP7	HSCHR6_MHC_QBL:29768167-29768964	NOTEST	0	0	0	0	1	1
ENSG00000233114	ENSG00000233114	RP4-533D7.3	1:46505811-46651630	NOTEST	0	0	0	0	1	1
ENSG00000233115	ENSG00000233115	FAM90A11P	8:7869303-7874533	NOTEST	0	0	0	0	1	1
ENSG00000233118	ENSG00000233118	UBE2V1P8	1:41407922-41408187	NOTEST	0	0	0	0	1	1
ENSG00000233119	ENSG00000233119	XXbac-BCX196D17.5	HSCHR6_MHC_SSTO:29092012-29096710	NOTEST	0	0	0	0	1	1
ENSG00000233120	ENSG00000233120	USP9YP15	Y:20278412-20279581	NOTEST	0	0	0	0	1	1
ENSG00000233121	ENSG00000233121	VN1R20P	3:13968309-13969275	NOTEST	0	0	0	0	1	1
ENSG00000233122	ENSG00000233122	CTAGE7P	10:131864637-131909081	NOTEST	0.0590096	0.0323133	-0.868821	0	1	1
ENSG00000233123	ENSG00000233123	LINC01007	7:101206058-101212286	NOTEST	0	0	0	0	1	1
ENSG00000233124	ENSG00000233124	LINC00456	13:97824722-97831876	NOTEST	0.137993	0.242804	0.8152	0	1	1
ENSG00000233125	ENSG00000233125	ACTBP12	1:92683496-92711370	NOTEST	0	0	0	0	1	1
ENSG00000233126	ENSG00000233126	ZNF736P3Y	Y:25195393-25197342	NOTEST	0	0	0	0	1	1
ENSG00000233128	ENSG00000233128	AC007317.1	2:40973626-40994592	NOTEST	0	0	0	0	1	1
ENSG00000233129	ENSG00000233129	RP5-837O21.2	1:94400034-94400800	NOTEST	0	0	0	0	1	1
ENSG00000233131	ENSG00000233131	AC096649.1	2:176040985-176049335	NOTEST	0	0	0	0	1	1
ENSG00000233132	ENSG00000233132	FAM90A3P	8:7122047-7132680	NOTEST	0	0	0	0	1	1
ENSG00000233133	ENSG00000233133	AC104451.2	3:17198653-18959184	NOTEST	0	0	0	0	1	1
ENSG00000233134	ENSG00000233134	AC009960.7	2:203482006-203482350	NOTEST	0	0	0	0	1	1
ENSG00000233135	ENSG00000233135	RPS27P18	10:127162254-127162501	NOTEST	0	0	0	0	1	1
ENSG00000233136	ENSG00000233136	USP17L11	4:9212382-9228214	NOTEST	0	0	0	0	1	1
ENSG00000233138	ENSG00000233138	RP1-67K17.3	6:143069579-143266338	NOTEST	0	0.127102	inf	0	1	1
ENSG00000233139	ENSG00000233139	RP11-38O23.4	X:48013295-48015369	NOTEST	0	0	0	0	1	1
ENSG00000233140	ENSG00000233140	TAPSAR1	HSCHR6_MHC_SSTO:32898408-32937507	NOTEST	0	0	0	0	1	1
ENSG00000233141	ENSG00000233141	MAS1L	HSCHR6_MHC_COX:29451050-29452315	NOTEST	0	0	0	0	1	1
ENSG00000233143	ENSG00000233143	AC009492.1	2:218147461-218621316	NOTEST	0	0	0	0	1	1
ENSG00000233144	ENSG00000233144	RP11-537A6.9	10:75134858-75173834	NOTEST	0	0	0	0	1	1
ENSG00000233145	ENSG00000233145	RP11-364B14.1	X:139099426-139100196	NOTEST	0	0	0	0	1	1
ENSG00000233146	ENSG00000233146	BPIFB5P	20:31904674-31917775	NOTEST	0	0	0	0	1	1
ENSG00000233147	ENSG00000233147	RP11-90C4.1	1:56289479-56333921	NOTEST	0	0	0	0	1	1
ENSG00000233148	ENSG00000233148	SYF2P2	9:35010699-35011282	NOTEST	0	0	0	0	1	1
ENSG00000233149	ENSG00000233149	GTF2H4	HSCHR6_MHC_MANN:30920642-30938920	NOTEST	0	0	0	0	1	1
ENSG00000233151	ENSG00000233151	CYP21A2	HSCHR6_MHC_COX:31954521-32044486	NOTEST	0	0	0	0	1	1
ENSG00000233153	ENSG00000233153	UBE2E2-AS1	3:23236560-23244069	NOTEST	0	0.0700063	inf	0	1	1
ENSG00000233155	ENSG00000233155	HMGA1P8	2:74641303-74648718	NOTEST	0.38573	0	#NAME?	0	1	1
ENSG00000233156	ENSG00000233156	HSFY8P	Y:28157581-28158384	NOTEST	0	0	0	0	1	1
ENSG00000233157	ENSG00000233157	RP3-388M5.8	22:43911996-44208217	NOTEST	0	0	0	0	1	1
ENSG00000233158	ENSG00000233158	RPS24P6	2:95533230-95613086	NOTEST	0	0	0	0	1	1
ENSG00000233159	ENSG00000233159	AC007390.4	2:37394962-37551951	NOTEST	0	0	0	0	1	1
ENSG00000233160	ENSG00000233160	HNRNPA1P2	HSCHR6_MHC_MANN:32299913-32391764	NOTEST	0	0	0	0	1	1
ENSG00000233161	ENSG00000233161	DHFRP2	HSCHR6_MHC_SSTO:31327026-31327573	NOTEST	0	0	0	0	1	1
ENSG00000233162	ENSG00000233162	MORF4L1P6	X:72694398-72694666	NOTEST	0	0	0	0	1	1
ENSG00000233163	ENSG00000233163	RP11-259F16.3	10:70883267-70932617	NOTEST	0	0	0	0	1	1
ENSG00000233164	ENSG00000233164	C6orf136	HSCHR6_MHC_MANN:30659490-30685513	NOTEST	0	0	0	0	1	1

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ENSG00000233167	ENSG00000233167	EEF1A1P26	7:14184673-15014402	NOTEST	0	0	0	0	1	1
ENSG00000233168	ENSG00000233168	OR2U1P	HSCHR6_MHC_DBB:29191798-29234885	NOTEST	0	0	0	0	1	1
ENSG00000233169	ENSG00000233169	C6orf47-AS1	HSCHR6_MHC_MANN:31665566-31668042	NOTEST	0	0	0	0	1	1
ENSG00000233171	ENSG00000233171	RP11-459O16.3	9:66358547-66359282	NOTEST	0	0	0	0	1	1
ENSG00000233172	ENSG00000233172	RP11-12A20.6	9:67789673-67789866	NOTEST	0	0	0	0	1	1
ENSG00000233173	ENSG00000233173	VN1R34P	7:63394826-63395709	NOTEST	0	0	0	0	1	1
ENSG00000233175	ENSG00000233175	CTD-2020K17.3	17:43268297-43394414	NOTEST	0.0866416	0.158835	0.874393	0	1	1
ENSG00000233176	ENSG00000233176	OR7E157P	8:7449527-7450438	NOTEST	0	0	0	0	1	1
ENSG00000233178	ENSG00000233178	RP11-88I18.2	9:70921443-71145977	NOTEST	0.191198	0.133772	-0.515296	0	1	1
ENSG00000233179	ENSG00000233179	RP11-536P6.3	22:48844701-48847029	NOTEST	0	0	0	0	1	1
ENSG00000233180	ENSG00000233180	OR2B3	HSCHR6_MHC_COX:29050653-29051759	NOTEST	0	0	0	0	1	1
ENSG00000233182	ENSG00000233182	OR2H4P	HSCHR6_MHC_MCF:29183172-29184116	NOTEST	0	0	0	0	1	1
ENSG00000233183	ENSG00000233183	RP3-468B3.2	6:33835282-33895408	NOTEST	0	0.00162211	inf	0	1	1
ENSG00000233186	ENSG00000233186	RP11-307I14.3	9:4792868-4885917	NOTEST	0	0	0	0	1	1
ENSG00000233189	ENSG00000233189	RPL12P29	10:86088341-86278273	NOTEST	0	0	0	0	1	1
ENSG00000233190	ENSG00000233190	RPS24P13	10:32520776-32521173	NOTEST	0	0	0	0	1	1
ENSG00000233191	ENSG00000233191	AC006372.6	7:157305987-157309535	NOTEST	0	0	0	0	1	1
ENSG00000233192	ENSG00000233192	HLA-DQA2	HSCHR6_MHC_APD:32694038-32700103	NOTEST	0	0	0	0	1	1
ENSG00000233193	ENSG00000233193	AC005324.7	17:15664927-15667083	NOTEST	0	0	0	0	1	1
ENSG00000233194	ENSG00000233194	RPL32P1	HSCHR6_MHC_QBL:32961399-32984034	NOTEST	0	0	0	0	1	1
ENSG00000233196	ENSG00000233196	GS1-304P7.1	1:186549646-186550323	NOTEST	0	0	0	0	1	1
ENSG00000233197	ENSG00000233197	TMEM256P1	10:71283066-71283406	NOTEST	0	0	0	0	1	1
ENSG00000233198	ENSG00000233198	RNF224	9:140122017-140124090	NOTEST	0.166056	0.126026	-0.397957	0	1	1
ENSG00000233200	ENSG00000233200	RP11-324I22.2	10:35508821-35519526	NOTEST	0	0	0	0	1	1
ENSG00000233203	ENSG00000233203	RP11-67L3.4	1:55315305-55354523	NOTEST	0.300083	0	#NAME?	0	1	1
ENSG00000233204	ENSG00000233204	MAPRE1P3	2:166095911-166248818	NOTEST	0	0	0	0	1	1
ENSG00000233206	ENSG00000233206	RPS3AP1	21:21802754-21803074	NOTEST	0	0	0	0	1	1
ENSG00000233207	ENSG00000233207	RP11-216M21.7	9:42363047-42367092	NOTEST	0.00490283	0.011816	1.26906	0	1	1
ENSG00000233208	ENSG00000233208	LINC00642	14:90921573-90925249	NOTEST	0	0	0	0	1	1
ENSG00000233209	ENSG00000233209	HLA-DQB1	HSCHR6_MHC_DBB:32602483-32612425	NOTEST	0	0	0	0	1	1
ENSG00000233210	ENSG00000233210	GPANK1	HSCHR6_MHC_DBB:31611187-31653368	NOTEST	0	0	0	0	1	1
ENSG00000233211	ENSG00000233211	GRPEL2P1	13:89630700-89631039	NOTEST	0	0	0	0	1	1
ENSG00000233213	ENSG00000233213	KCNJ6-IT1	21:38979677-39288749	NOTEST	0	0	0	0	1	1
ENSG00000233214	ENSG00000233214	AC002511.2	19:35914963-35915554	NOTEST	0	0	0	0	1	1
ENSG00000233215	ENSG00000233215	AP000472.2	21:23381262-23470778	NOTEST	0	0.0393783	inf	0	1	1
ENSG00000233216	ENSG00000233216	RP11-414C16.1	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000233217	ENSG00000233217	MROH3P	1:200890121-200935658	NOTEST	0	0	0	0	1	1
ENSG00000233219	ENSG00000233219	RP11-89N17.3	7:33908112-33913843	NOTEST	0	0	0	0	1	1
ENSG00000233220	ENSG00000233220	LINC00167	11:129872832-129874251	NOTEST	0.0238009	0	#NAME?	0	1	1
ENSG00000233221	ENSG00000233221	AC133785.1	2:131588550-131804836	NOTEST	0	0.0350426	inf	0	1	1
ENSG00000233222	ENSG00000233222	RP11-216N14.9	1:153700542-153746555	NOTEST	0	0	0	0	1	1
ENSG00000233224	ENSG00000233224	HIST1H2AM	6:27858092-27860963	NOTEST	0.416655	0.479861	0.203762	0	1	1
ENSG00000233228	ENSG00000233228	LPCAT2BP	1:92531862-92533396	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000233229	ENSG00000233229	CNOT7P1	X:68835910-69259319	NOTEST	0	0	0	0	1	1
ENSG00000233230	ENSG00000233230	AC079807.2	2:47922668-48134949	NOTEST	0.309987	0.459529	0.567951	0	1	1
ENSG00000233231	ENSG00000233231	HNRNPA1P49	6:166733215-166756079	NOTEST	0.13489	0.226257	0.746177	0	1	1
ENSG00000233232	ENSG00000233232	NPIPB7	16:28467692-28510291	NOTEST	0	0	0	0	1	1
ENSG00000233234	ENSG00000233234	RP11-740P5.2	1:2728414-2729257	NOTEST	0	0	0	0	1	1
ENSG00000233235	ENSG00000233235	RP5-908D6.1	1:89790204-89800563	NOTEST	0	0	0	0	1	1
ENSG00000233236	ENSG00000233236	AP001171.1	21:21629064-21631133	NOTEST	0	0	0	0	1	1
ENSG00000233238	ENSG00000233238	DEFA9P	8:6816810-6817683	NOTEST	0	0	0	0	1	1
ENSG00000233239	ENSG00000233239	HLA-U	HSCHR6_MHC_DBB:29891685-29891871	NOTEST	0	0	0	0	1	1
ENSG00000233240	ENSG00000233240	HLA-DRB7	HSCHR6_MHC_DBB:32472043-32491190	NOTEST	0	0	0	0	1	1
ENSG00000233241	ENSG00000233241	DDX39BP1	HSCHR6_MHC_COX:29865827-29866194	NOTEST	0	0	0	0	1	1
ENSG00000233242	ENSG00000233242	RP11-220I1.2	9:37112544-37115487	NOTEST	0	0	0	0	1	1
ENSG00000233243	ENSG00000233243	RP11-12D5.5	X:27882009-27882466	NOTEST	0	0	0	0	1	1
ENSG00000233244	ENSG00000233244	CYP4F59P	9:43027747-43032877	NOTEST	0.117323	0.125183	0.093554	0	1	1
ENSG00000233246	ENSG00000233246	RP11-415J8.5	1:33772366-33896653	NOTEST	0	0.0362859	inf	0	1	1
ENSG00000233247	ENSG00000233247	GS1-257G1.1	X:14262324-14263544	NOTEST	0.0799993	0.0956903	0.258384	0	1	1
ENSG00000233248	ENSG00000233248	MTND6P9	2:156169951-156170470	NOTEST	0	0	0	0	1	1
ENSG00000233250	ENSG00000233250	RP3-339A18.6	X:53458205-53461320	NOTEST	0	0	0	0	1	1
ENSG00000233251	ENSG00000233251	AC007743.1	2:56179292-56613308	NOTEST	0	0	0	0	1	1
ENSG00000233252	ENSG00000233252	CRIP1P1	3:12715197-12715382	NOTEST	0	0	0	0	1	1
ENSG00000233254	ENSG00000233254	RPL21P134	X:74588261-74743337	NOTEST	0.0476031	0	#NAME?	0	1	1
ENSG00000233255	ENSG00000233255	AC019181.2	2:165510133-165705844	NOTEST	0.385038	0.36596	-0.0733167	0	1	1
ENSG00000233256	ENSG00000233256	RP11-445K13.2	10:13457201-13465133	NOTEST	0	0	0	0	1	1
ENSG00000233258	ENSG00000233258	RP11-219F10.1	10:85671409-85672678	NOTEST	0	0	0	0	1	1
ENSG00000233259	ENSG00000233259	FABP3P2	13:42943373-42943793	NOTEST	0	0	0	0	1	1
ENSG00000233260	ENSG00000233260	RPSAP63	X:132669772-133119922	NOTEST	0	0	0	0	1	1
ENSG00000233261	ENSG00000233261	LINC00264	10:26878793-26883253	NOTEST	0	0	0	0	1	1
ENSG00000233262	ENSG00000233262	RP11-380F14.2	9:86890371-86955672	NOTEST	0.0733248	0	#NAME?	0	1	1
ENSG00000233263	ENSG00000233263	AC009518.2	7:131577374-131578374	NOTEST	0	0	0	0	1	1
ENSG00000233264	ENSG00000233264	AC006042.8	7:7676148-8133902	NOTEST	0	0.0503077	inf	0	1	1
ENSG00000233265	ENSG00000233265	MICF	6:29820139-29820268	NOTEST	0	0	0	0	1	1
ENSG00000233266	ENSG00000233266	HMGB1P31	2:54091203-54532437	NOTEST	0	0.0413371	inf	0	1	1
ENSG00000233268	ENSG00000233268	RP11-558F24.2	1:9711789-9884584	NOTEST	0	0	0	0	1	1
ENSG00000233271	ENSG00000233271	RP11-12C17.2	1:55446464-55457966	NOTEST	0	0	0	0	1	1
ENSG00000233272	ENSG00000233272	PNPT1P2	7:121482421-121485185	NOTEST	0	0	0	0	1	1
ENSG00000233273	ENSG00000233273	AMMECR1LP1	13:96743092-97485671	NOTEST	0	0	0	0	1	1
ENSG00000233275	ENSG00000233275	AC009238.8	2:96100506-96100861	NOTEST	0	0	0	0	1	1
ENSG00000233277	ENSG00000233277	RP5-1030M6.3	20:42523359-42524108	NOTEST	0	0	0	0	1	1
ENSG00000233278	ENSG00000233278	RPS26P2	9:30831875-30832223	NOTEST	0	0	0	0	1	1
ENSG00000233285	ENSG00000233285	AC073869.13	2:132126634-132127284	NOTEST	0	0	0	0	1	1
ENSG00000233286	ENSG00000233286	MTND3P10	2:120770580-120974855	NOTEST	0	0	0	0	1	1
ENSG00000233287	ENSG00000233287	AC009362.2	7:130626518-131182453	NOTEST	0	0	0	0	1	1
ENSG00000233288	ENSG00000233288	RP11-760D2.5	7:56601922-56605823	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000233291	ENSG00000233291	RPL7AP61	13:98553906-98554542	NOTEST	0	0	0	0	1	1
ENSG00000233292	ENSG00000233292	RP11-341B24.3	10:90898800-90899215	NOTEST	0	0	0	0	1	1
ENSG00000233293	ENSG00000233293	RP11-410N8.3	20:31030861-31196695	NOTEST	0	0	0	0	1	1
ENSG00000233295	ENSG00000233295	FAM90A20P	8:7152535-7155546	NOTEST	0	0	0	0	1	1
ENSG00000233296	ENSG00000233296	AC092159.2	2:667334-697371	NOTEST	0.0406151	0.0245861	-0.72417	0	1	1
ENSG00000233297	ENSG00000233297	RASA4DP	7:102322282-102330916	NOTEST	0.105185	0.130753	0.313916	0	1	1
ENSG00000233298	ENSG00000233298	IFITM4P	HSCHR6_MHC_MCF:29715642-29716062	NOTEST	0	0	0	0	1	1
ENSG00000233299	ENSG00000233299	HIGD1AP4	2:224262984-224263264	NOTEST	0	0	0	0	1	1
ENSG00000233300	ENSG00000233300	EIF4A1P1	21:28731203-28820898	NOTEST	0	0	0	0	1	1
ENSG00000233301	ENSG00000233301	OR4C14P	11:55304477-55305400	NOTEST	0	0	0	0	1	1
ENSG00000233303	ENSG00000233303	XXYLT1-AS1	3:194789007-194991896	NOTEST	0	0	0	0	1	1
ENSG00000233304	ENSG00000233304	RP13-614K11.1	1:4000672-4015322	NOTEST	0	0	0	0	1	1
ENSG00000233306	ENSG00000233306	TRGV2	7:38402464-38403119	NOTEST	0	0	0	0	1	1
ENSG00000233307	ENSG00000233307	AC109815.2	2:110490307-110490713	NOTEST	0	0	0	0	1	1
ENSG00000233308	ENSG00000233308	OSTN-AS1	3:190917029-190983404	NOTEST	0	0	0	0	1	1
ENSG00000233309	ENSG00000233309	RPS6P12	9:85358981-85359707	NOTEST	0	0	0	0	1	1
ENSG00000233311	ENSG00000233311	AC009960.3	2:203483907-203484619	NOTEST	0	0	0	0	1	1
ENSG00000233312	ENSG00000233312	C4B_2	HSCHR6_MHC_SSTO:31941652-31963150	NOTEST	0	0	0	0	1	1
ENSG00000233313	ENSG00000233313	HMGA1P5	10:77029576-77171600	NOTEST	0	0	0	0	1	1
ENSG00000233314	ENSG00000233314	PPP1R11	HSCHR6_MHC_APD:29971319-29980498	NOTEST	0	0	0	0	1	1
ENSG00000233315	ENSG00000233315	XXbac-BPG249D20.9	HSCHR6_MHC_DBB:30474277-30477232	NOTEST	0	0	0	0	1	1
ENSG00000233316	ENSG00000233316	DSCR10	21:39493544-39679279	NOTEST	0	0	0	0	1	1
ENSG00000233317	ENSG00000233317	MTCO3P1	HSCHR6_MHC_SSTO:32765193-32766025	NOTEST	0	0	0	0	1	1
ENSG00000233318	ENSG00000233318	RP11-573G6.2	10:22555919-22556275	NOTEST	0	0	0	0	1	1
ENSG00000233319	ENSG00000233319	PPIAP32	10:131930033-131930505	NOTEST	0	0	0	0	1	1
ENSG00000233320	ENSG00000233320	H2BFXP	X:103230534-103230898	NOTEST	0	0	0	0	1	1
ENSG00000233321	ENSG00000233321	RP11-482E14.1	10:3529085-3545030	NOTEST	0	0	0	0	1	1
ENSG00000233323	ENSG00000233323	TNXB	HSCHR6_MHC_COX:31954521-32044486	NOTEST	0	0	0	0	1	1
ENSG00000233324	ENSG00000233324	EEF1A1P34	20:18763067-18764334	NOTEST	0	0	0	0	1	1
ENSG00000233329	ENSG00000233329	AC068287.1	2:140988991-142895399	NOTEST	0	0	0	0	1	1
ENSG00000233332	ENSG00000233332	RP4-799P18.2	1:234040678-234460262	NOTEST	0	0	0	0	1	1
ENSG00000233333	ENSG00000233333	RNFT1P2	1:78636164-78636921	NOTEST	0	0	0	0	1	1
ENSG00000233334	ENSG00000233334	FAM53B-AS1	10:126150402-126480439	NOTEST	0	0.00874557	inf	0	1	1
ENSG00000233335	ENSG00000233335	AC016696.1	2:46483998-46484316	NOTEST	0	0	0	0	1	1
ENSG00000233336	ENSG00000233336	RP13-221M14.2	1:13146776-13147256	NOTEST	0	0	0	0	1	1
ENSG00000233338	ENSG00000233338	TLR8-AS1	X:12920935-12941288	NOTEST	0	0	0	0	1	1
ENSG00000233339	ENSG00000233339	AC018878.3	2:106709758-106810795	NOTEST	0	0	0	0	1	1
ENSG00000233340	ENSG00000233340	RP11-25C19.3	10:114206755-114578503	NOTEST	0	0	0	0	1	1
ENSG00000233342	ENSG00000233342	RP11-235G24.3	6:161347400-161348194	NOTEST	0	0	0	0	1	1
ENSG00000233343	ENSG00000233343	ATP6V1G1P4	10:35386933-35501886	NOTEST	0.0900186	0	#NAME?	0	1	1
ENSG00000233345	ENSG00000233345	MSH5	HSCHR6_MHC_APD:31735722-31744719	NOTEST	0	0	0	0	1	1
ENSG00000233347	ENSG00000233347	ERP29P1	20:50668201-50820847	NOTEST	0.532933	0.435132	-0.292502	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000233348	ENSG00000233348	BAG6	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000233349	ENSG00000233349	LINC00333	13:85136498-85137371	NOTEST	0	0	0	0	1	1
ENSG00000233350	ENSG00000233350	TRIM26BP	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000233351	ENSG00000233351	RP1-69D17.3	6:129204341-129837714	NOTEST	0	0.100789	inf	0	1	1
ENSG00000233352	ENSG00000233352	RP1-300I2.3	20:43858457-43858832	NOTEST	0	0	0	0	1	1
ENSG00000233353	ENSG00000233353	RPS7P9	10:82476238-82476824	NOTEST	0	0	0	0	1	1
ENSG00000233354	ENSG00000233354	LINC00028	20:30073580-30075377	NOTEST	0	0	0	0	1	1
ENSG00000233355	ENSG00000233355	CHRM3-AS2	1:239549864-240080255	NOTEST	0	0	0	0	1	1
ENSG00000233357	ENSG00000233357	RPL30P15	X:13587723-13651694	NOTEST	0	0	0	0	1	1
ENSG00000233358	ENSG00000233358	RP1-209A6.1	6:22744623-23032009	NOTEST	0	0.0149667	inf	0	1	1
ENSG00000233359	ENSG00000233359	RP11-202K23.1	1:102665294-102855186	NOTEST	0	0	0	0	1	1
ENSG00000233360	ENSG00000233360	Z83844.1	22:38030660-38062941	NOTEST	0.0240866	0.0132814	-0.858817	0	1	1
ENSG00000233363	ENSG00000233363	AC006019.4	7:153584181-154685995	NOTEST	0	0	0	0	1	1
ENSG00000233365	ENSG00000233365	RP4-655C5.4	6:166650456-166657197	NOTEST	0	0	0	0	1	1
ENSG00000233366	ENSG00000233366	ZNF90P2	6:28856608-28857683	NOTEST	0	0	0	0	1	1
ENSG00000233367	ENSG00000233367	RP11-307L3.4	9:6413150-6507054	NOTEST	0	0	0	0	1	1
ENSG00000233368	ENSG00000233368	RP11-277L2.3	1:149575344-149637707	NOTEST	0.153539	0.19933	0.376554	0	1	1
ENSG00000233370	ENSG00000233370	AC092664.1	2:110879887-110962643	NOTEST	0	0	0	0	1	1
ENSG00000233372	ENSG00000233372	RP5-893G23.1	1:30613109-30614454	NOTEST	0	0	0	0	1	1
ENSG00000233373	ENSG00000233373	AC106874.3	2:84542231-84577898	NOTEST	0	0	0	0	1	1
ENSG00000233376	ENSG00000233376	RP5-881L22.6	20:42984339-43061485	NOTEST	0	0	0	0	1	1
ENSG00000233377	ENSG00000233377	MTND4P20	10:96698414-96749147	NOTEST	0	0	0	0	1	1
ENSG00000233378	ENSG00000233378	USP9YP34	Y:20096228-20105140	NOTEST	0	0	0	0	1	1
ENSG00000233379	ENSG00000233379	RP11-318G21.4	13:78469615-79233314	NOTEST	0.0406605	0.0158025	-1.36347	0	1	1
ENSG00000233380	ENSG00000233380	RPS2P48	17:51834349-51835231	NOTEST	0.156417	0.0649913	-1.26708	0	1	1
ENSG00000233381	ENSG00000233381	AK4P3	12:31768701-31769373	NOTEST	0	0.0719842	inf	0	1	1
ENSG00000233383	ENSG00000233383	RP11-324F21.1	7:66452663-66704501	NOTEST	0	0	0	0	1	1
ENSG00000233385	ENSG00000233385	RP11-3N2.9	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000233387	ENSG00000233387	RP11-342D11.3	10:33385184-33405600	NOTEST	0	0	0	0	1	1
ENSG00000233388	ENSG00000233388	RP4-569D19.5	22:35897907-35899633	NOTEST	0.00955074	0.00671377	-0.508489	0	1	1
ENSG00000233392	ENSG00000233392	AC104809.4	2:241858201-241932728	NOTEST	0	0.0252334	inf	0	1	1
ENSG00000233393	ENSG00000233393	AP000688.29	21:37402367-37498938	NOTEST	0	0	0	0	1	1
ENSG00000233394	ENSG00000233394	RP11-248D7.2	1:13351481-13354323	NOTEST	0	0	0	0	1	1
ENSG00000233395	ENSG00000233395	LINC00841	10:44434450-44439914	NOTEST	0	0	0	0	1	1
ENSG00000233396	ENSG00000233396	RP11-458D21.1	1:145373053-145382434	NOTEST	0.137727	0.0277667	-2.31038	0	1	1
ENSG00000233397	ENSG00000233397	AC008063.3	2:162949938-162951364	NOTEST	0	0	0	0	1	1
ENSG00000233399	ENSG00000233399	RP11-111I12.1	1:30486798-30510459	NOTEST	0	0	0	0	1	1
ENSG00000233401	ENSG00000233401	PRKAR1AP	1:92545861-92613393	NOTEST	0.0272895	0	#NAME?	0	1	1
ENSG00000233402	ENSG00000233402	TARDBPP1	20:6181635-6182838	NOTEST	0	0	0	0	1	1
ENSG00000233403	ENSG00000233403	RP11-86A5.1	X:25896455-25911661	NOTEST	0	0	0	0	1	1
ENSG00000233405	ENSG00000233405	LINC01046	13:21808706-21809343	NOTEST	0	0	0	0	1	1
ENSG00000233406	ENSG00000233406	RP11-296A18.5	1:51701942-51739127	NOTEST	0.0214955	0.153865	2.83956	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000233407	ENSG00000233407	RP11-567C20.3	1:50671755-50688799	NOTEST	0	0	0	0	1	1
ENSG00000233408	ENSG00000233408	LA16c-23H5.4	22:16399956-16436527	NOTEST	0	0	0	0	1	1
ENSG00000233409	ENSG00000233409	FANK1-AS1	10:127585107-127698161	NOTEST	0	0	0	0	1	1
ENSG00000233410	ENSG00000233410	RP11-16L9.3	1:198975168-199045864	NOTEST	0	0	0	0	1	1
ENSG00000233411	ENSG00000233411	RP11-104L21.2	1:167399876-167487847	NOTEST	0.215906	0.159895	-0.433276	0	1	1
ENSG00000233412	ENSG00000233412	OR5H15	3:97887543-97888485	NOTEST	0	0	0	0	1	1
ENSG00000233414	ENSG00000233414	CNN2P5	9:66345260-66346161	NOTEST	0	0	0	0	1	1
ENSG00000233415	ENSG00000233415	RP11-101E14.3	20:38660226-38672531	NOTEST	0	0	0	0	1	1
ENSG00000233416	ENSG00000233416	AC012065.5	2:20760207-20850849	NOTEST	0.290462	0.276398	-0.0716021	0	1	1
ENSG00000233417	ENSG00000233417	RP4-742N3.1	7:119781069-119783050	NOTEST	0	0	0	0	1	1
ENSG00000233418	ENSG00000233418	DHX16	HSCHR6_MHC_DBB:30605055-30631079	NOTEST	0	0	0	0	1	1
ENSG00000233419	ENSG00000233419	RP4-781L3.1	1:25451543-25451945	NOTEST	0	0	0	0	1	1
ENSG00000233420	ENSG00000233420	AC002127.4	7:88339944-88386039	NOTEST	0	0	0	0	1	1
ENSG00000233421	ENSG00000233421	U1	1:16860380-16862144	NOTEST	0	0	0	0	1	1
ENSG00000233423	ENSG00000233423	RP4-736H5.3	7:67156044-67162016	NOTEST	0	0	0	0	1	1
ENSG00000233424	ENSG00000233424	RP11-175I6.5	9:44256579-44263319	NOTEST	0	0.0037788	inf	0	1	1
ENSG00000233425	ENSG00000233425	KRT18P67	9:125599835-125601099	NOTEST	0	0	0	0	1	1
ENSG00000233427	ENSG00000233427	RP1-212P9.3	1:29194086-29203848	NOTEST	0.12865	0.0211712	-2.60327	0	1	1
ENSG00000233428	ENSG00000233428	AC019050.1	2:130253869-130254361	NOTEST	0	0	0	0	1	1
ENSG00000233430	ENSG00000233430	RP11-403I13.9	1:149305909-149313076	NOTEST	0	0	0	0	1	1
ENSG00000233431	ENSG00000233431	RP11-63N8.3	1:21912964-21917680	NOTEST	0	0	0	0	1	1
ENSG00000233432	ENSG00000233432	RP11-344P13.3	1:121236176-121252181	NOTEST	0	0	0	0	1	1
ENSG00000233433	ENSG00000233433	RP1-296G17.3	X:120158817-120160417	NOTEST	0	0.0073076	inf	0	1	1
ENSG00000233434	ENSG00000233434	BX649567.1	9:67924790-67925210	NOTEST	0	0	0	0	1	1
ENSG00000233435	ENSG00000233435	AGGF1P2	10:135455589-135456398	NOTEST	0.159071	0.0726249	-1.13113	0	1	1
ENSG00000233436	ENSG00000233436	BTBD18	11:57480071-57587018	NOTEST	0.0321	0.0150373	-1.09403	0	1	1
ENSG00000233437	ENSG00000233437	RP13-580B18.1	7:56943077-56949839	NOTEST	0	0	0	0	1	1
ENSG00000233438	ENSG00000233438	AC109829.1	2:27760252-27790011	NOTEST	0	0.0176666	inf	0	1	1
ENSG00000233439	ENSG00000233439	PSORS1C1	HSCHR6_MHC_DBB:31076301-31101556	NOTEST	0	0	0	0	1	1
ENSG00000233440	ENSG00000233440	HMGA1P6	13:23708312-23708703	NOTEST	0	0	0	0	1	1
ENSG00000233441	ENSG00000233441	CYP2AB1P	3:183613687-183628724	NOTEST	0	0	0	0	1	1
ENSG00000233442	ENSG00000233442	PPP6R2P1	21:15379454-15387201	NOTEST	0	0	0	0	1	1
ENSG00000233444	ENSG00000233444	AC013262.1	2:81893600-81893852	NOTEST	0	0.13589	inf	0	1	1
ENSG00000233445	ENSG00000233445	RPL17P11	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000233446	ENSG00000233446	XXyac-YR12DB5.1	X:80855570-80856805	NOTEST	0	0	0	0	1	1
ENSG00000233447	ENSG00000233447	AC103563.6	2:95640288-95640583	NOTEST	0	0	0	0	1	1
ENSG00000233448	ENSG00000233448	PMS2P9	7:76139744-77045717	NOTEST	0.0964502	0.0306623	-1.65332	0	1	1
ENSG00000233449	ENSG00000233449	RP11-233E12.4	1:107345376-107346049	NOTEST	0	0	0	0	1	1
ENSG00000233450	ENSG00000233450	KIFC1	HSCHR6_MHC_SSTO:33498670-33517062	NOTEST	0	0	0	0	1	1
ENSG00000233451	ENSG00000233451	RP11-301N24.3	10:22634398-22743153	NOTEST	0	0	0	0	1	1
ENSG00000233452	ENSG00000233452	STXBP5-AS1	6:147163036-147706866	NOTEST	0.466623	0.166759	-1.48449	0	1	1
ENSG00000233454	ENSG00000233454	RP11-196D18.2	7:62517830-62520462	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000233455	ENSG00000233455	RP4-667H12.4	1:210477028-210477885	NOTEST	0	0	0	0	1	1
ENSG00000233456	ENSG00000233456	LINC01077	13:49144774-49147453	NOTEST	0	0	0	0	1	1
ENSG00000233457	ENSG00000233457	RP11-336N8.1	9:80765447-80766109	NOTEST	0	0	0	0	1	1
ENSG00000233459	ENSG00000233459	AC125238.2	2:204499299-204500739	NOTEST	0	0	0	0	1	1
ENSG00000233460	ENSG00000233460	RPL35AP31	13:72012097-72441330	NOTEST	0	0	0	0	1	1
ENSG00000233462	ENSG00000233462	RPL7AP7	HSCHR6_MHC_COX:29764668-29765465	NOTEST	0	0	0	0	1	1
ENSG00000233464	ENSG00000233464	RP11-133I21.2	6:151977825-152958936	NOTEST	0	0	0	0	1	1
ENSG00000233465	ENSG00000233465	RPL7AP7	HSCHR6_MHC_MANN:29767916-29768713	NOTEST	0	0	0	0	1	1
ENSG00000233466	ENSG00000233466	MICC	HSCHR6_MHC_COX:30372299-30376905	NOTEST	0	0	0	0	1	1
ENSG00000233467	ENSG00000233467	U40455.1	X:147279533-147280398	NOTEST	0	0	0	0	1	1
ENSG00000233469	ENSG00000233469	ST6GALNAC4P1	13:20392260-20392759	NOTEST	0.0844109	0	#NAME?	0	1	1
ENSG00000233470	ENSG00000233470	RP11-524K22.1	6:50481747-50488817	NOTEST	0	0	0	0	1	1
ENSG00000233471	ENSG00000233471	KRT18P62	22:19166985-19279239	NOTEST	0	0.029274	inf	0	1	1
ENSG00000233472	ENSG00000233472	RP11-218D6.4	10:28288716-28338544	NOTEST	0	0	0	0	1	1
ENSG00000233473	ENSG00000233473	RAD1P2	1:159032273-159116886	NOTEST	0.0301923	0.042704	0.500191	0	1	1
ENSG00000233477	ENSG00000233477	RP11-45P22.2	10:107445140-107445623	NOTEST	0	0	0	0	1	1
ENSG00000233478	ENSG00000233478	RP1-187B23.1	1:25943958-26112698	NOTEST	0	0	0	0	1	1
ENSG00000233479	ENSG00000233479	AC017074.1	2:114426742-114430768	NOTEST	0	0	0	0	1	1
ENSG00000233480	ENSG00000233480	AP000946.2	21:21265592-21272069	NOTEST	0	0	0	0	1	1
ENSG00000233481	ENSG00000233481	OR12D2	HSCHR6_MHC_MANN:29323056-29424418	NOTEST	0	0	0	0	1	1
ENSG00000233482	ENSG00000233482	RP11-78O9.1	1:94610666-94611175	NOTEST	0	0	0	0	1	1
ENSG00000233483	ENSG00000233483	CTD-2020K17.4	17:43268297-43394414	NOTEST	0.0674033	0.0283509	-1.24942	0	1	1
ENSG00000233484	ENSG00000233484	RP11-74B21.1	X:83572881-83757487	NOTEST	0	0	0	0	1	1
ENSG00000233485	ENSG00000233485	RP3-467K16.2	1:15573767-15726779	NOTEST	0.00584234	0.00355345	-0.717326	0	1	1
ENSG00000233486	ENSG00000233486	USP8P1	HSCHR6_MHC_COX:31234394-31237566	NOTEST	0	0	0	0	1	1
ENSG00000233487	ENSG00000233487	AC011322.1	3:196710760-196714429	NOTEST	0.0208611	0.0441392	1.08124	0	1	1
ENSG00000233489	ENSG00000233489	AC091652.2	7:153146513-153146960	NOTEST	0	0	0	0	1	1
ENSG00000233490	ENSG00000233490	GPSM3	HSCHR6_MHC_COX:32107016-32140316	NOTEST	0	0	0	0	1	1
ENSG00000233491	ENSG00000233491	AC010091.1	7:81205701-81255532	NOTEST	0	0	0	0	1	1
ENSG00000233492	ENSG00000233492	RP5-984P4.4	20:21510839-21511382	NOTEST	0	0	0	0	1	1
ENSG00000233493	ENSG00000233493	TMEM238	19:55890612-55895966	NOTEST	0.0179164	0.0265568	0.567802	0	1	1
ENSG00000233494	ENSG00000233494	AC009963.3	2:108519452-108519590	NOTEST	0	0	0	0	1	1
ENSG00000233496	ENSG00000233496	SYNJ2-IT1	6:158402887-158520208	NOTEST	0	0	0	0	1	1
ENSG00000233497	ENSG00000233497	HNRNPA1P60	11:110658748-110659735	NOTEST	0	0	0	0	1	1
ENSG00000233498	ENSG00000233498	PPP1R2P1	HSCHR6_MHC_MCF:32841973-32881069	NOTEST	0	0	0	0	1	1
ENSG00000233499	ENSG00000233499	OR5B1P	11:58133308-58134236	NOTEST	0	0.0473439	inf	0	1	1
ENSG00000233501	ENSG00000233501	SRGAP2-AS1	1:206516199-206637783	NOTEST	0	0.00575973	inf	0	1	1
ENSG00000233502	ENSG00000233502	AC104794.4	2:10223907-10226228	NOTEST	0	0	0	0	1	1
ENSG00000233503	ENSG00000233503	HNRNPLP1	6:7481326-7482827	NOTEST	0	0	0	0	1	1
ENSG00000233504	ENSG00000233504	POLR2LP	HSCHR6_MHC_MCF:31187043-31187230	NOTEST	0	0	0	0	1	1
ENSG00000233505	ENSG00000233505	KRT18P1	HSCHR6_MHC_COX:28933440-28934771	NOTEST	0	0	0	0	1	1
ENSG00000233506	ENSG00000233506	OR2N1P	HSCHR6_MHC_QBL:29105659-29106596	NOTEST	0	0	0	0	1	1
ENSG00000233508	ENSG00000233508	RP1-269M15.3	20:41818861-41830011	NOTEST	0	0	0	0	1	1

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ENSG00000233511	ENSG00000233511	RP1-128O3.5	6:108532425-108582464	NOTEST	0	0	0	0	1	1
ENSG00000233514	ENSG00000233514	RP11-570P14.1	1:44584521-44600812	NOTEST	0.377251	0.595117	0.657646	0	1	1
ENSG00000233515	ENSG00000233515	AL022344.4	10:43169644-43187171	NOTEST	0	0	0	0	1	1
ENSG00000233516	ENSG00000233516	RP11-388N2.1	9:120224571-120228538	NOTEST	0	0	0	0	1	1
ENSG00000233517	ENSG00000233517	AC005162.5	7:29019582-29603286	NOTEST	0	0	0	0	1	1
ENSG00000233518	ENSG00000233518	RPL7P35	10:112309872-112310612	NOTEST	0	0	0	0	1	1
ENSG00000233519	ENSG00000233519	RP11-177F11.1	1:240177647-240643504	NOTEST	0	0	0	0	1	1
ENSG00000233521	ENSG00000233521	RP5-1172A22.1	22:27617309-27620688	NOTEST	0	0	0	0	1	1
ENSG00000233522	ENSG00000233522	FAM224A	Y:20488138-20515096	NOTEST	0	0	0	0	1	1
ENSG00000233523	ENSG00000233523	PHBP5	7:72569032-72619657	NOTEST	0	0	0	0	1	1
ENSG00000233524	ENSG00000233524	RANP8	13:21302869-21348097	NOTEST	0	0	0	0	1	1
ENSG00000233526	ENSG00000233526	RP11-490H9.1	9:79687015-79688211	NOTEST	0	0	0	0	1	1
ENSG00000233528	ENSG00000233528	LINC00430	13:87564172-87589271	NOTEST	0	0	0	0	1	1
ENSG00000233529	ENSG00000233529	HCG21	6:30908748-30922639	NOTEST	0	0	0	0	1	1
ENSG00000233531	ENSG00000233531	DEFA10P	8:6825662-6826635	NOTEST	0	0	0	0	1	1
ENSG00000233532	ENSG00000233532	LINC00460	13:107028910-107030565	NOTEST	0	0.110169	inf	0	1	1
ENSG00000233533	ENSG00000233533	MKNK2P1	10:37233038-37233666	NOTEST	0	0	0	0	1	1
ENSG00000233534	ENSG00000233534	RP1-38C16.2	6:135604669-136037193	NOTEST	0	0	0	0	1	1
ENSG00000233535	ENSG00000233535	RP1-122K4.2	X:13973511-13982023	NOTEST	0	0	0	0	1	1
ENSG00000233536	ENSG00000233536	RP11-867G2.5	11:94277005-94658686	NOTEST	0	0	0	0	1	1
ENSG00000233537	ENSG00000233537	TEDDM1P1	1:182410711-182411497	NOTEST	0	0	0	0	1	1
ENSG00000233538	ENSG00000233538	AC017104.2	2:232316905-232317864	NOTEST	0	0	0	0	1	1
ENSG00000233540	ENSG00000233540	DNM3-IT1	1:171810620-172437971	NOTEST	0	0	0	0	1	1
ENSG00000233541	ENSG00000233541	RPL31P47	11:122921868-122922109	NOTEST	0	0	0	0	1	1
ENSG00000233542	ENSG00000233542	RP11-547D24.1	1:1944651-1946969	NOTEST	0	0	0	0	1	1
ENSG00000233543	ENSG00000233543	CHTF8P1	X:44492937-44494478	NOTEST	0	0	0	0	1	1
ENSG00000233544	ENSG00000233544	EIF3KP2	3:24597324-24597950	NOTEST	0	0.0788622	inf	0	1	1
ENSG00000233545	ENSG00000233545	CYCSP33	13:24974840-24975167	NOTEST	0	0	0	0	1	1
ENSG00000233546	ENSG00000233546	PRYP5	Y:20652800-20790963	NOTEST	0	0	0	0	1	1
ENSG00000233547	ENSG00000233547	RP11-57H14.2	10:114710008-114927437	NOTEST	0	0	0	0	1	1
ENSG00000233548	ENSG00000233548	CYCSP44	X:144258101-144258414	NOTEST	0	0	0	0	1	1
ENSG00000233549	ENSG00000233549	CYCSP35	13:99281939-99282243	NOTEST	0	0	0	0	1	1
ENSG00000233550	ENSG00000233550	AC068137.11	2:131040251-131040902	NOTEST	0	0	0	0	1	1
ENSG00000233551	ENSG00000233551	RP11-335H2.2	9:16409500-16870841	NOTEST	0	0	0	0	1	1
ENSG00000233553	ENSG00000233553	AC108462.1	2:946553-1371385	NOTEST	0	0	0	0	1	1
ENSG00000233555	ENSG00000233555	RP11-452D2.1	9:68176987-68177568	NOTEST	0.134131	0	#NAME?	0	1	1
ENSG00000233557	ENSG00000233557	NFU1P2	1:98542555-98543024	NOTEST	0	0	0	0	1	1
ENSG00000233558	ENSG00000233558	RP3-486I3.4	6:116575335-116762424	NOTEST	0.546431	0.307643	-0.828781	0	1	1
ENSG00000233560	ENSG00000233560	KRT8P39	12:69068150-69136785	NOTEST	0.238493	0.0989468	-1.26922	0	1	1
ENSG00000233561	ENSG00000233561	DHX16	HSCHR6_MHC_COX:30604662-30630683	NOTEST	0	0	0	0	1	1
ENSG00000233562	ENSG00000233562	RP11-548N1.1	1:183217371-183387737	NOTEST	0	0	0	0	1	1
ENSG00000233563	ENSG00000233563	OR52E7P	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000233564	ENSG00000233564	PRR3	HSCHR6_MHC_MCF:30587610-30609957	NOTEST	0	0	0	0	1	1

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ENSG00000233566	ENSG00000233566	C6orf100	HSCHR6_MHC_SSTO:28911712-28912373	NOTEST	0	0	0	0	1	1
ENSG00000233569	ENSG00000233569	RP11-500B12.1	9:120410883-120419305	NOTEST	0	0	0	0	1	1
ENSG00000233570	ENSG00000233570	LINC00690	3:16577826-16582880	NOTEST	0	0	0	0	1	1
ENSG00000233571	ENSG00000233571	RP11-545D19.1	X:34224841-34433654	NOTEST	0	0	0	0	1	1
ENSG00000233573	ENSG00000233573	TRIM31	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000233574	ENSG00000233574	CTA-929C8.5	22:27672200-27682310	NOTEST	0	0	0	0	1	1
ENSG00000233575	ENSG00000233575	RP11-459D20.1	9:1328663-1328987	NOTEST	0	0	0	0	1	1
ENSG00000233576	ENSG00000233576	RP11-778D9.9	3:183794566-183802007	NOTEST	0	0	0	0	1	1
ENSG00000233577	ENSG00000233577	RP3-462D8.2	22:25675495-25678641	NOTEST	0	0	0	0	1	1
ENSG00000233578	ENSG00000233578	RP5-1022P6.3	20:5525084-5591672	NOTEST	0	0.0245529	inf	0	1	1
ENSG00000233579	ENSG00000233579	KRT8P15	2:203640689-203736708	NOTEST	0.0210726	0.00816126	-1.3685	0	1	1
ENSG00000233581	ENSG00000233581	AC069155.1	2:217122587-217236750	NOTEST	0	0	0	0	1	1
ENSG00000233583	ENSG00000233583	RP4-635A23.3	1:185126211-185260897	NOTEST	0	0.0117703	inf	0	1	1
ENSG00000233584	ENSG00000233584	HLA-DPB2	HSCHR6_MHC_MANN:33234378-33250727	NOTEST	0	0	0	0	1	1
ENSG00000233585	ENSG00000233585	AC115617.2	X:48634407-48635486	NOTEST	0	0.0808056	inf	0	1	1
ENSG00000233586	ENSG00000233586	RP11-763B22.3	1:148760503-148761583	NOTEST	0	0	0	0	1	1
ENSG00000233587	ENSG00000233587	AC096570.1	2:22759350-22761160	NOTEST	0	0	0	0	1	1
ENSG00000233589	ENSG00000233589	RP4-694A7.2	1:68939834-69004310	NOTEST	0.282114	0.127257	-1.14853	0	1	1
ENSG00000233590	ENSG00000233590	RP11-153K11.3	10:69993007-70002136	NOTEST	0	0	0	0	1	1
ENSG00000233592	ENSG00000233592	MICG	HSCHR6_MHC_MCF:29777226-29777358	NOTEST	0	0	0	0	1	1
ENSG00000233594	ENSG00000233594	BTF3P5	2:55662291-55662758	NOTEST	0	0	0	0	1	1
ENSG00000233595	ENSG00000233595	MTND2P29	1:48998526-50489585	NOTEST	0	0	0	0	1	1
ENSG00000233597	ENSG00000233597	RP11-343B5.1	3:141663269-141868386	NOTEST	0.0679327	0.0545507	-0.316509	0	1	1
ENSG00000233599	ENSG00000233599	TRIM15	HSCHR6_MHC_MANN:30176130-30185621	NOTEST	0	0	0	0	1	1
ENSG00000233601	ENSG00000233601	NCOR1P3	7:57659499-57669810	NOTEST	0	0	0	0	1	1
ENSG00000233602	ENSG00000233602	ERI3-IT1	1:44686741-44820932	NOTEST	0.44387	0.310073	-0.517527	0	1	1
ENSG00000233603	ENSG00000233603	JTBP1	22:41165633-41215403	NOTEST	0	0	0	0	1	1
ENSG00000233604	ENSG00000233604	DHFRP2	HSCHR6_MHC_MANN:31377182-31377729	NOTEST	0	0	0	0	1	1
ENSG00000233605	ENSG00000233605	AC073628.1	2:78143059-78145135	NOTEST	0	0	0	0	1	1
ENSG00000233606	ENSG00000233606	OR6C66P	12:55782228-55783158	NOTEST	0	0	0	0	1	1
ENSG00000233607	ENSG00000233607	AC068610.5	7:114701590-114871409	NOTEST	0	0	0	0	1	1
ENSG00000233608	ENSG00000233608	TWIST2	2:239756672-239795893	NOTEST	0	0	0	0	1	1
ENSG00000233609	ENSG00000233609	RP11-62H7.2	8:8818709-8836535	NOTEST	0	0	0	0	1	1
ENSG00000233610	ENSG00000233610	LINC00462	13:49151109-49152224	NOTEST	0.0187773	0.0132351	-0.504614	0	1	1
ENSG00000233611	ENSG00000233611	AC079135.1	2:237073878-237203570	NOTEST	0.0744638	0.0659944	-0.174194	0	1	1
ENSG00000233613	ENSG00000233613	DCUN1D2-AS	13:114110133-114145267	NOTEST	0.291548	0.240465	-0.277907	0	1	1
ENSG00000233614	ENSG00000233614	DDX11L10	16:61552-88321	NOTEST	0	0	0	0	1	1
ENSG00000233615	ENSG00000233615	HNRNPA1P42	1:240928856-241520530	NOTEST	0	0	0	0	1	1
ENSG00000233616	ENSG00000233616	RP11-542K23.10	9:125163248-125165185	NOTEST	0	0	0	0	1	1
ENSG00000233617	ENSG00000233617	HCG4P11	HSCHR6_MHC_DBB:29688036-29714307	NOTEST	0	0	0	0	1	1
ENSG00000233618	ENSG00000233618	OR2J3	HSCHR6_MHC_SSTO:29079694-29080630	NOTEST	0	0	0	0	1	1
ENSG00000233619	ENSG00000233619	AC006328.9	Y:27624415-27633809	NOTEST	0	0	0	0	1	1

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ENSG00000233622	ENSG00000233622	CYP2T2P	19:41277552-41406413	NOTEST	0.126115	0.0604453	-1.06103	0	1	1
ENSG00000233623	ENSG00000233623	PGAM1P11	1:10092889-10241297	NOTEST	0.0291835	0	#NAME?	0	1	1
ENSG00000233625	ENSG00000233625	RP5-905G11.3	20:17868006-17868804	NOTEST	0	0	0	0	1	1
ENSG00000233626	ENSG00000233626	RP11-565J7.1	1:212109590-212109976	NOTEST	0.20683	0.0538363	-1.94179	0	1	1
ENSG00000233627	ENSG00000233627	C4A-AS1	6:31937586-31971298	NOTEST	0	0	0	0	1	1
ENSG00000233628	ENSG00000233628	VN2R5P	9:40371837-40394460	NOTEST	0	0	0	0	1	1
ENSG00000233630	ENSG00000233630	FAM138F	19:76219-77690	NOTEST	0	0	0	0	1	1
ENSG00000233631	ENSG00000233631	RP11-457M11.2	6:26634610-26659980	NOTEST	0.0413774	0.0644651	0.639676	0	1	1
ENSG00000233632	ENSG00000233632	RP1-302D9.5	22:33533125-33533324	NOTEST	0	0	0	0	1	1
ENSG00000233633	ENSG00000233633	AC093326.3	2:558203-578145	NOTEST	0	0	0	0	1	1
ENSG00000233634	ENSG00000233634	GOT2P5	Y:6705747-6706293	NOTEST	0	0	0	0	1	1
ENSG00000233635	ENSG00000233635	AC037445.1	17:61086916-61509572	NOTEST	0	0	0	0	1	1
ENSG00000233636	ENSG00000233636	OR2J3	HSCHR6_MHC_MANN:29079672-29080608	NOTEST	0	0	0	0	1	1
ENSG00000233640	ENSG00000233640	KRTAP13-5P	21:31808783-31809282	NOTEST	0	0	0	0	1	1
ENSG00000233641	ENSG00000233641	C6orf136	HSCHR6_MHC_COX:30604662-30630683	NOTEST	0	0	0	0	1	1
ENSG00000233642	ENSG00000233642	GPR158-AS1	10:25401986-25891155	NOTEST	0.0080387	0.0172316	1.10002	0	1	1
ENSG00000233643	ENSG00000233643	RP11-491H19.1	10:63541502-63581004	NOTEST	0	0.0311121	inf	0	1	1
ENSG00000233644	ENSG00000233644	ARHGEF7-IT1	13:111766158-111958084	NOTEST	0	0	0	0	1	1
ENSG00000233645	ENSG00000233645	RP11-431K24.4	1:8278249-8280589	NOTEST	0	0	0	0	1	1
ENSG00000233646	ENSG00000233646	OR52T1P	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000233647	ENSG00000233647	RP11-8J9.1	1:47098408-47184824	NOTEST	0	0	0	0	1	1
ENSG00000233648	ENSG00000233648	AC010095.6	2:109311205-109311349	NOTEST	0	0	0	0	1	1
ENSG00000233649	ENSG00000233649	DAQB-331I12.5	HSCHR6_MHC_MCF:31924011-31941947	NOTEST	0	0	0	0	1	1
ENSG00000233650	ENSG00000233650	OR2AD1P	HSCHR6_MHC_SSTO:28994478-28995406	NOTEST	0	0	0	0	1	1
ENSG00000233651	ENSG00000233651	RP11-111F5.8	9:46685428-46746500	NOTEST	0	0	0	0	1	1
ENSG00000233652	ENSG00000233652	CICP1	Y:27524446-27540866	NOTEST	0	0	0	0	1	1
ENSG00000233653	ENSG00000233653	CICP7	1:317719-461954	NOTEST	0.0852415	0.0331028	-1.3646	0	1	1
ENSG00000233654	ENSG00000233654	AC093388.3	2:191399580-191432828	NOTEST	0.0636642	0	#NAME?	0	1	1
ENSG00000233655	ENSG00000233655	IGHD4-4	14:106379080-106379096	NOTEST	0	0	0	0	1	1
ENSG00000233656	ENSG00000233656	RP11-716O23.1	6:11417582-11481472	NOTEST	0	0	0	0	1	1
ENSG00000233659	ENSG00000233659	NDUFA5P4	9:35874806-35875191	NOTEST	0	0	0	0	1	1
ENSG00000233661	ENSG00000233661	SPIN4-AS1	X:62563105-62780951	NOTEST	0	0	0	0	1	1
ENSG00000233662	ENSG00000233662	CALM2P4	13:99293067-99293493	NOTEST	0	0	0	0	1	1
ENSG00000233663	ENSG00000233663	RP11-497J7.1	X:35729027-35730059	NOTEST	0	0	0	0	1	1
ENSG00000233664	ENSG00000233664	NDUFS5P3	1:53174793-53175114	NOTEST	0	0	0	0	1	1
ENSG00000233665	ENSG00000233665	RP11-523O18.5	10:49892920-50323554	NOTEST	0	0	0	0	1	1
ENSG00000233668	ENSG00000233668	RP11-571F15.3	9:34179002-34329198	NOTEST	0.178257	0.0221705	-3.00724	0	1	1
ENSG00000233670	ENSG00000233670	PIRT	17:10725791-10741762	NOTEST	0	0	0	0	1	1
ENSG00000233671	ENSG00000233671	AC083899.1	2:87448235-87449611	NOTEST	0	0	0	0	1	1
ENSG00000233672	ENSG00000233672	RNASEH2B-AS1	13:51450821-51544592	NOTEST	0.183025	0.0784359	-1.22246	0	1	1
ENSG00000233673	ENSG00000233673	ANAPC1P1	2:87098423-87248975	NOTEST	0.0900983	0.0736429	-0.290954	0	1	1
ENSG00000233674	ENSG00000233674	RP11-184I16.3	1:44115828-44396831	NOTEST	0	0	0	0	1	1
ENSG00000233676	ENSG00000233676	FDPSP6	21:21760645-21761157	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000233680	ENSG00000233680	HNRNPA1P27	X:100142624-100143579	NOTEST	0.0346013	0	#NAME?	0	1	1
ENSG00000233681	ENSG00000233681	CEACAMP1	19:42901279-43156507	NOTEST	0	0	0	0	1	1
ENSG00000233682	ENSG00000233682	RP11-13P5.2	6:159586940-159693141	NOTEST	0	0	0	0	1	1
ENSG00000233683	ENSG00000233683	RP5-1106H14.1	7:101006100-101202304	NOTEST	0	0	0	0	1	1
ENSG00000233684	ENSG00000233684	AC079779.6	2:317911-342118	NOTEST	0	0	0	0	1	1
ENSG00000233685	ENSG00000233685	OR6L1P	10:135388625-135389535	NOTEST	0	0	0	0	1	1
ENSG00000233686	ENSG00000233686	PIEZO1P1	20:58035673-58035892	NOTEST	0	0	0	0	1	1
ENSG00000233687	ENSG00000233687	OR2B3	HSCHR6_MHC_MCF:29054125-29055231	NOTEST	0	0	0	0	1	1
ENSG00000233688	ENSG00000233688	CTD-2183H9.3	X:154064062-154288578	NOTEST	0	0	0	0	1	1
ENSG00000233689	ENSG00000233689	RP11-123O1.1	7:68505138-68511790	NOTEST	0	0	0	0	1	1
ENSG00000233690	ENSG00000233690	EBAG9P1	10:101419262-101515891	NOTEST	0	0.124836	inf	0	1	1
ENSG00000233691	ENSG00000233691	RP11-312J18.7	1:160901528-160924589	NOTEST	0	0	0	0	1	1
ENSG00000233692	ENSG00000233692	C4B-AS1	HSCHR6_MHC_DBB:31847748-31902052	NOTEST	0	0	0	0	1	1
ENSG00000233693	ENSG00000233693	RP11-506O24.1	1:164524820-164868533	NOTEST	0	0	0	0	1	1
ENSG00000233694	ENSG00000233694	AC007365.1	2:64834108-64843616	NOTEST	0	0	0	0	1	1
ENSG00000233697	ENSG00000233697	HLA-DRB8	HSCHR6_MHC_SSTO:32556189-32558727	NOTEST	0	0	0	0	1	1
ENSG00000233699	ENSG00000233699	TTTY18	Y:8551410-8551919	NOTEST	0	0	0	0	1	1
ENSG00000233700	ENSG00000233700	TMPOP1	HSCHR6_MHC_MANN:30478909-30480452	NOTEST	0	0	0	0	1	1
ENSG00000233701	ENSG00000233701	PRR23C	3:138722803-139108574	NOTEST	0	0	0	0	1	1
ENSG00000233702	ENSG00000233702	AC107083.1	2:62727355-62739029	NOTEST	0.133721	0	#NAME?	0	1	1
ENSG00000233703	ENSG00000233703	RP11-20E23.1	10:82509387-82510987	NOTEST	0	0	0	0	1	1
ENSG00000233705	ENSG00000233705	SLC26A4-AS1	7:107294420-107358254	NOTEST	0.670873	0.151089	-2.15064	0	1	1
ENSG00000233706	ENSG00000233706	RP5-1087E8.3	1:227177565-227506175	NOTEST	0	0	0	0	1	1
ENSG00000233707	ENSG00000233707	RPL22P11	2:110494712-110495100	NOTEST	0	0	0	0	1	1
ENSG00000233708	ENSG00000233708	RP11-342M1.7	1:43352267-43354438	NOTEST	0	0	0	0	1	1
ENSG00000233709	ENSG00000233709	MTND4P28	2:156167534-156167921	NOTEST	0	0	0	0	1	1
ENSG00000233710	ENSG00000233710	RP4-808O4.2	X:66753004-66753829	NOTEST	0	0	0	0	1	1
ENSG00000233711	ENSG00000233711	EIF4EBP2P1	20:42051835-42052178	NOTEST	0	0.207908	inf	0	1	1
ENSG00000233712	ENSG00000233712	RP4-801G22.3	1:157606089-157610091	NOTEST	0	0	0	0	1	1
ENSG00000233713	ENSG00000233713	RP11-379P1.4	9:88747536-88747766	NOTEST	0	0	0	0	1	1
ENSG00000233714	ENSG00000233714	AC012506.2	2:23570524-23574735	NOTEST	0	0.0160221	inf	0	1	1
ENSG00000233716	ENSG00000233716	AC074367.1	2:63348517-64054977	NOTEST	0	0	0	0	1	1
ENSG00000233717	ENSG00000233717	RP11-68I18.2	1:151043053-151098018	NOTEST	0	0	0	0	1	1
ENSG00000233718	ENSG00000233718	MYCNOS	2:16060520-16087129	NOTEST	0	0	0	0	1	1
ENSG00000233719	ENSG00000233719	GOT2P3	12:9787187-9811008	NOTEST	0	0	0	0	1	1
ENSG00000233720	ENSG00000233720	LL22NC03-30E12.11	22:22511774-22512024	NOTEST	0	0	0	0	1	1
ENSG00000233721	ENSG00000233721	RP11-205K6.1	9:129278695-129281087	NOTEST	0	0	0	0	1	1
ENSG00000233723	ENSG00000233723	LINC01122	2:58654933-59290901	NOTEST	0.314005	0.105317	-1.57604	0	1	1
ENSG00000233724	ENSG00000233724	RP11-252C24.2	10:67007789-67008550	NOTEST	0	0	0	0	1	1
ENSG00000233725	ENSG00000233725	LINC00284	13:44482849-44604597	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000233727	ENSG00000233727	RP11-380I20.2	9:110616063-110616539	NOTEST	0	0	0	0	1	1
ENSG00000233728	ENSG00000233728	RP11-109P14.9	1:38259473-38266809	NOTEST	0	0	0	0	1	1
ENSG00000233729	ENSG00000233729	AC016909.1	2:133429373-134326034	NOTEST	0	0	0	0	1	1
ENSG00000233730	ENSG00000233730	RP4-666F24.3	1:115642292-115645279	NOTEST	0	0	0	0	1	1
ENSG00000233732	ENSG00000233732	IGHV3OR16-10	16:32963313-33039358	NOTEST	0	0	0	0	1	1
ENSG00000233733	ENSG00000233733	H2AFZP6	22:31795508-32058418	NOTEST	0	0	0	0	1	1
ENSG00000233734	ENSG00000233734	PSORS1C1	HSCHR6_MHC_MCF:31161054-31186363	NOTEST	0	0	0	0	1	1
ENSG00000233735	ENSG00000233735	RP11-567G24.3	1:240177647-240643504	NOTEST	0	0	0	0	1	1
ENSG00000233737	ENSG00000233737	RP11-573M3.4	11:92954651-92954796	NOTEST	0	0	0	0	1	1
ENSG00000233739	ENSG00000233739	RP5-1039K5.13	22:38452317-38471708	NOTEST	0	0.0476689	inf	0	1	1
ENSG00000233740	ENSG00000233740	CICP2	Y:26424483-26437493	NOTEST	0	0	0	0	1	1
ENSG00000233741	ENSG00000233741	AC016691.2	2:120750774-120751187	NOTEST	0	0	0	0	1	1
ENSG00000233742	ENSG00000233742	RP11-472D17.2	X:52304892-52307444	NOTEST	0	0	0	0	1	1
ENSG00000233744	ENSG00000233744	HLA-DQB1-AS1	HSCHR6_MHC_QBL:32547664-32563145	NOTEST	0	0	0	0	1	1
ENSG00000233746	ENSG00000233746	LINC00656	20:23105704-23113258	NOTEST	0	0	0	0	1	1
ENSG00000233747	ENSG00000233747	RPL36AP13	2:24425732-24583583	NOTEST	0	0	0	0	1	1
ENSG00000233750	ENSG00000233750	CICP27	1:89294-134836	NOTEST	0	0	0	0	1	1
ENSG00000233751	ENSG00000233751	AC104772.1	2:223536504-223574649	NOTEST	0	0	0	0	1	1
ENSG00000233752	ENSG00000233752	AC009414.1	2:36526530-36526973	NOTEST	0	0	0	0	1	1
ENSG00000233754	ENSG00000233754	AP001628.7	21:44201183-44202343	NOTEST	0	0	0	0	1	1
ENSG00000233755	ENSG00000233755	RP4-799D16.1	1:25370197-25439611	NOTEST	0.0335325	0	#NAME?	0	1	1
ENSG00000233756	ENSG00000233756	DSCAM-IT1	21:41382925-42219065	NOTEST	0	0	0	0	1	1
ENSG00000233757	ENSG00000233757	AC092835.2	2:95873282-95881351	NOTEST	0.285135	0.381462	0.419894	0	1	1
ENSG00000233760	ENSG00000233760	AC004947.2	7:26591440-26596819	NOTEST	0.0113799	0.00399532	-1.51011	0	1	1
ENSG00000233764	ENSG00000233764	Z95114.4	22:36568469-36568827	NOTEST	0	0	0	0	1	1
ENSG00000233765	ENSG00000233765	RP11-154P18.2	9:70662043-70663084	NOTEST	0	0.0226529	inf	0	1	1
ENSG00000233766	ENSG00000233766	AC098617.1	2:192699027-193060435	NOTEST	0	0	0	0	1	1
ENSG00000233767	ENSG00000233767	PSMA6P3	21:47491998-47492162	NOTEST	0	0	0	0	1	1
ENSG00000233771	ENSG00000233771	CICP5	1:224135306-224138118	NOTEST	0.390324	0.247248	-0.658715	0	1	1
ENSG00000233772	ENSG00000233772	HCG25	HSCHR6_MHC_DBB:33195233-33222212	NOTEST	0	0	0	0	1	1
ENSG00000233774	ENSG00000233774	MED14P1	Y:14730914-14746333	NOTEST	0	0	0	0	1	1
ENSG00000233775	ENSG00000233775	RP4-811H24.9	1:32814794-32816264	NOTEST	0.0575749	0.0203502	-1.5004	0	1	1
ENSG00000233776	ENSG00000233776	RP11-384P7.6	9:33732972-33738414	NOTEST	0	0	0	0	1	1
ENSG00000233778	ENSG00000233778	RP11-777J24.1	8:93156315-93156663	NOTEST	0	0	0	0	1	1
ENSG00000233780	ENSG00000233780	HNRNPA1P30	13:21512702-21523738	NOTEST	0	0.0126713	inf	0	1	1
ENSG00000233782	ENSG00000233782	ZNF90P3	7:62547447-62548639	NOTEST	0	0	0	0	1	1
ENSG00000233783	ENSG00000233783	AP001442.2	21:27252860-27589700	NOTEST	0	0	0	0	1	1
ENSG00000233785	ENSG00000233785	RP13-314C10.5	X:23791108-23801073	NOTEST	0.198154	0.208209	0.071411	0	1	1
ENSG00000233786	ENSG00000233786	CDC27P1	2:133019900-133020615	NOTEST	0	0	0	0	1	1
ENSG00000233787	ENSG00000233787	CTD-2057J6.1	5:29881815-29883052	NOTEST	0	0	0	0	1	1
ENSG00000233788	ENSG00000233788	SPATA31A5	9:41500678-41514094	NOTEST	0	0	0	0	1	1
ENSG00000233791	ENSG00000233791	LINC01136	1:203267885-203274437	NOTEST	0.012543	0	#NAME?	0	1	1

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ENSG00000233795	ENSG00000233795	ZNRD1	HSCHR6_MHC_SSTO:29957256-30022268	NOTEST	0	0	0	0	1	1
ENSG00000233797	ENSG00000233797	UFL1-AS1	6:96806249-97003152	NOTEST	0	0	0	0	1	1
ENSG00000233798	ENSG00000233798	RP11-417J8.2	1:142569265-142588233	NOTEST	0	0	0	0	1	1
ENSG00000233799	ENSG00000233799	AC139887.4	4:699536-775637	NOTEST	0.247848	0.182502	-0.441548	0	1	1
ENSG00000233800	ENSG00000233800	RP11-295G24.4	9:135820931-135867083	NOTEST	0.0777899	0.0593876	-0.38942	0	1	1
ENSG00000233801	ENSG00000233801	NELFE	HSCHR6_MHC_SSTO:31911715-31929380	NOTEST	0	0	0	0	1	1
ENSG00000233802	ENSG00000233802	TRIM49D2P	11:89657231-89666218	NOTEST	0	0	0	0	1	1
ENSG00000233803	ENSG00000233803	TSPY4	Y:9175072-9177893	NOTEST	0	0	0	0	1	1
ENSG00000233805	ENSG00000233805	RP11-449J3.3	10:55526159-55526374	NOTEST	0	0	0	0	1	1
ENSG00000233806	ENSG00000233806	AC131097.3	2:242823513-243026289	NOTEST	0.124902	0.301187	1.26986	0	1	1
ENSG00000233807	ENSG00000233807	RP11-268G12.2	X:27061023-27417114	NOTEST	0.0731143	0	#NAME?	0	1	1
ENSG00000233810	ENSG00000233810	MOB1AP2	X:37150419-37151479	NOTEST	0	0	0	0	1	1
ENSG00000233812	ENSG00000233812	AC139426.2	15:32684982-32727434	NOTEST	0	0	0	0	1	1
ENSG00000233813	ENSG00000233813	MRPS18B	HSCHR6_MHC_DBB:30558417-30584413	NOTEST	0	0	0	0	1	1
ENSG00000233814	ENSG00000233814	RP11-66C24.1	9:79034751-79122332	NOTEST	0	0	0	0	1	1
ENSG00000233816	ENSG00000233816	IFNA13	9:21367370-21368075	NOTEST	0	0	0	0	1	1
ENSG00000233817	ENSG00000233817	RP11-168K11.3	9:116381507-116384914	NOTEST	0.00517087	0.00363028	-0.510325	0	1	1
ENSG00000233818	ENSG00000233818	AP000695.4	21:37802657-37948867	NOTEST	0.0310767	0	#NAME?	0	1	1
ENSG00000233819	ENSG00000233819	RP1-43O17.2	1:152716774-152717082	NOTEST	0	0	0	0	1	1
ENSG00000233820	ENSG00000233820	RP11-535M15.2	9:99488171-99489751	NOTEST	0	0.00958084	inf	0	1	1
ENSG00000233821	ENSG00000233821	ENOX1-AS1	13:43787653-44361044	NOTEST	0	0	0	0	1	1
ENSG00000233823	ENSG00000233823	RP3-443C4.2	6:151977825-152958936	NOTEST	0	0	0	0	1	1
ENSG00000233824	ENSG00000233824	AC003985.1	7:25360920-25366434	NOTEST	0	0	0	0	1	1
ENSG00000233825	ENSG00000233825	RP11-135A24.4	10:32555216-32667726	NOTEST	0	0	0	0	1	1
ENSG00000233826	ENSG00000233826	XXbac-BPG308K3.5	HSCHR6_MHC_SSTO:28805556-28806694	NOTEST	0	0	0	0	1	1
ENSG00000233827	ENSG00000233827	FAM58BP	1:200182655-200183643	NOTEST	0	0	0	0	1	1
ENSG00000233828	ENSG00000233828	AC008394.1	5:86512422-86534822	NOTEST	0	0	0	0	1	1
ENSG00000233829	ENSG00000233829	AC017078.1	2:45878483-46415129	NOTEST	0	0	0	0	1	1
ENSG00000233831	ENSG00000233831	ZNF311	HSCHR6_MHC_SSTO:28962689-28973114	NOTEST	0	0	0	0	1	1
ENSG00000233832	ENSG00000233832	RP11-96F8.1	10:39076134-39076239	NOTEST	0	0	0	0	1	1
ENSG00000233833	ENSG00000233833	ETF1P3	X:65014186-65015677	NOTEST	0	0	0	0	1	1
ENSG00000233834	ENSG00000233834	AC005083.1	7:20257199-20261323	NOTEST	0	0.0415949	inf	0	1	1
ENSG00000233835	ENSG00000233835	RP1-92C4.2	6:80581589-80584327	NOTEST	0	0	0	0	1	1
ENSG00000233836	ENSG00000233836	RP11-255H23.2	19:23945745-24057503	NOTEST	0	0.0126099	inf	0	1	1
ENSG00000233837	ENSG00000233837	EIF3LP2	10:43062124-43062931	NOTEST	0.066155	0	#NAME?	0	1	1
ENSG00000233839	ENSG00000233839	RP11-389O22.4	1:113711615-113712025	NOTEST	0	0	0	0	1	1
ENSG00000233840	ENSG00000233840	PCDH9-AS4	13:66876966-67804468	NOTEST	0	0	0	0	1	1
ENSG00000233841	ENSG00000233841	HLA-C	HSCHR6_MHC_COX:31227576-31230958	NOTEST	0	0	0	0	1	1
ENSG00000233842	ENSG00000233842	AC062031.1	2:146672657-146688714	NOTEST	0	0	0	0	1	1
ENSG00000233843	ENSG00000233843	CYCSP48	Y:28546757-28547377	NOTEST	0	0	0	0	1	1
ENSG00000233845	ENSG00000233845	AC093732.1	2:47126413-47403740	NOTEST	0.044653	0.0347596	-0.361345	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000233846	ENSG00000233846	RP11-307L3.2	9:6278666-6279153	NOTEST	0.376012	0.465471	0.307913	0	1	1
ENSG00000233847	ENSG00000233847	AC104113.3	5:60169657-60240900	NOTEST	0	0	0	0	1	1
ENSG00000233848	ENSG00000233848	RP3-348I23.2	6:20534687-21232635	NOTEST	0	0	0	0	1	1
ENSG00000233849	ENSG00000233849	AC022201.5	2:70523106-70529222	NOTEST	0	0	0	0	1	1
ENSG00000233850	ENSG00000233850	AC103563.8	2:95690937-95719737	NOTEST	0	0	0	0	1	1
ENSG00000233851	ENSG00000233851	LATS2-AS1	13:21547170-21635686	NOTEST	0	0.0778977	inf	0	1	1
ENSG00000233852	ENSG00000233852	AC005304.1	17:13659794-13972812	NOTEST	0	0	0	0	1	1
ENSG00000233853	ENSG00000233853	HLA-DRB8	HSCHR6_MHC_MANN:32589232-32591694	NOTEST	0	0	0	0	1	1
ENSG00000233854	ENSG00000233854	POU6F2-AS2	7:39017597-39532694	NOTEST	0.0433062	0	#NAME?	0	1	1
ENSG00000233857	ENSG00000233857	LINC01015	HSCHR6_MHC_MCF:29496989-29501138	NOTEST	0	0	0	0	1	1
ENSG00000233858	ENSG00000233858	AC026904.1	8:49464126-49611069	NOTEST	0	0	0	0	1	1
ENSG00000233859	ENSG00000233859	ADH5P4	6:66546822-66547947	NOTEST	0.150562	0.049542	-1.60363	0	1	1
ENSG00000233860	ENSG00000233860	RP11-359D14.2	4:77356252-77723117	NOTEST	0.0717419	0.0301293	-1.25165	0	1	1
ENSG00000233861	ENSG00000233861	RP13-36C9.4	X:134899165-134900630	NOTEST	0	0	0	0	1	1
ENSG00000233862	ENSG00000233862	AC016907.3	2:30273931-30366670	NOTEST	0.0122857	0.0269	1.13063	0	1	1
ENSG00000233863	ENSG00000233863	AC012215.1	8:35092974-35654068	NOTEST	0	0	0	0	1	1
ENSG00000233864	ENSG00000233864	TTTY15	Y:14774264-14804162	NOTEST	0	0	0	0	1	1
ENSG00000233866	ENSG00000233866	LA16c-4G1.3	22:16062156-16063236	NOTEST	0	0	0	0	1	1
ENSG00000233867	ENSG00000233867	SLC9B1P3	10:38934101-38982199	NOTEST	0	0	0	0	1	1
ENSG00000233869	ENSG00000233869	AC016697.1	2:209072858-209073708	NOTEST	0	0	0	0	1	1
ENSG00000233870	ENSG00000233870	AC007881.4	2:71405716-71405903	NOTEST	0	0	0	0	1	1
ENSG00000233871	ENSG00000233871	DLG5-AS1	10:79687129-79689582	NOTEST	0.235007	0.210108	-0.161575	0	1	1
ENSG00000233872	ENSG00000233872	AC005033.6	2:74785009-74875465	NOTEST	0	0	0	0	1	1
ENSG00000233873	ENSG00000233873	RPL7P44	13:77555309-77556051	NOTEST	0	0	0	0	1	1
ENSG00000233874	ENSG00000233874	RP1-136J15.5	X:108811706-108813518	NOTEST	0	0	0	0	1	1
ENSG00000233875	ENSG00000233875	RP11-61L14.6	1:154540256-154552502	NOTEST	0.139252	0.0468392	-1.57191	0	1	1
ENSG00000233876	ENSG00000233876	GAPDHP68	7:9654607-9655615	NOTEST	0	0	0	0	1	1
ENSG00000233877	ENSG00000233877	RP11-182I10.2	1:65210777-65432187	NOTEST	0	0	0	0	1	1
ENSG00000233878	ENSG00000233878	AC073133.1	7:156230482-156238282	NOTEST	0	0	0	0	1	1
ENSG00000233880	ENSG00000233880	RP11-497J7.2	X:35779615-35780596	NOTEST	0	0	0	0	1	1
ENSG00000233882	ENSG00000233882	RP11-309H21.2	1:191190288-191197597	NOTEST	0	0	0	0	1	1
ENSG00000233883	ENSG00000233883	MDC1-AS1	HSCHR6_MHC_MCF:30746070-30764152	NOTEST	0	0	0	0	1	1
ENSG00000233884	ENSG00000233884	XXyac-YM21GA2.3	9:90463027-90468357	NOTEST	0	0	0	0	1	1
ENSG00000233887	ENSG00000233887	ERVWE2	X:97102260-97104015	NOTEST	0	0	0	0	1	1
ENSG00000233888	ENSG00000233888	AC009960.2	2:203479575-203480252	NOTEST	0	0	0	0	1	1
ENSG00000233889	ENSG00000233889	AL353698.1	X:56100756-56102014	NOTEST	0	0	0	0	1	1
ENSG00000233890	ENSG00000233890	TCF19	HSCHR6_MHC_DBB:31120049-31132215	NOTEST	0	0	0	0	1	1
ENSG00000233891	ENSG00000233891	AC007131.2	2:59444842-60327335	NOTEST	0	0	0	0	1	1
ENSG00000233892	ENSG00000233892	PAIP1P1	6:30152231-30181204	NOTEST	0.069368	0.0958428	0.466399	0	1	1
ENSG00000233893	ENSG00000233893	EZR-AS1	6:159186772-159241625	NOTEST	0	0	0	0	1	1
ENSG00000233894	ENSG00000233894	RP4-650F12.2	1:74663895-75010112	NOTEST	0	0	0	0	1	1
ENSG00000233895	ENSG00000233895	RP1-122P22.2	20:19738295-19790319	NOTEST	0	0.0433923	inf	0	1	1

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ENSG00000233896	ENSG00000233896	RP4-684O24.5	20:1927891-1988163	NOTEST	0	0	0	0	1	1
ENSG00000233900	ENSG00000233900	RPL17P35	10:66380130-66380679	NOTEST	0	0	0	0	1	1
ENSG00000233902	ENSG00000233902	XXbac-BPG181B23.6	6:31368478-31445283	NOTEST	0	0	0	0	1	1
ENSG00000233903	ENSG00000233903	Z83851.4	22:42556018-42739622	NOTEST	0.192874	0.124164	-0.635409	0	1	1
ENSG00000233904	ENSG00000233904	HLA-E	HSCHR6_MHC_COX:30447103-30451842	NOTEST	0	0	0	0	1	1
ENSG00000233905	ENSG00000233905	LONRF2P2	13:19183271-19183842	NOTEST	0	0.0263175	inf	0	1	1
ENSG00000233906	ENSG00000233906	RP11-315I14.2	9:23671785-23672397	NOTEST	0	0	0	0	1	1
ENSG00000233907	ENSG00000233907	RP4-617C6.1	1:95940292-95944912	NOTEST	0	0	0	0	1	1
ENSG00000233908	ENSG00000233908	RP11-425D10.1	6:109609642-109609765	NOTEST	0	0	0	0	1	1
ENSG00000233909	ENSG00000233909	UBE2V1P4	9:132553474-132554116	NOTEST	0	0	0	0	1	1
ENSG00000233910	ENSG00000233910	GTF2F2P2	1:41059304-41060025	NOTEST	0	0	0	0	1	1
ENSG00000233911	ENSG00000233911	POU5F1	HSCHR6_MHC_COX:31118871-31131037	NOTEST	0	0	0	0	1	1
ENSG00000233912	ENSG00000233912	AC026202.3	3:5163904-5229014	NOTEST	0.257824	0.137164	-0.910482	0	1	1
ENSG00000233915	ENSG00000233915	UBE2Q2P10	8:87345502-87777251	NOTEST	0	0	0	0	1	1
ENSG00000233916	ENSG00000233916	ZDHHC20P1	6:29675901-29676324	NOTEST	0.169811	0.133898	-0.342795	0	1	1
ENSG00000233917	ENSG00000233917	POTEB	15:22051852-22083227	NOTEST	0	0	0	0	1	1
ENSG00000233918	ENSG00000233918	RP11-715L17.1	7:61821868-61822186	NOTEST	0	0	0	0	1	1
ENSG00000233919	ENSG00000233919	RP11-372H2.1	3:41203777-41210038	NOTEST	0	0	0	0	1	1
ENSG00000233920	ENSG00000233920	RP5-1061H20.5	1:229359207-229363309	NOTEST	0	0	0	0	1	1
ENSG00000233921	ENSG00000233921	RPS15AP40	X:36246734-36458375	NOTEST	0	0	0	0	1	1
ENSG00000233924	ENSG00000233924	AL160471.6	14:55405667-55493823	NOTEST	0.0597352	0.0164097	-1.86404	0	1	1
ENSG00000233926	ENSG00000233926	RP11-154D17.1	9:84304627-84391815	NOTEST	0	0	0	0	1	1
ENSG00000233928	ENSG00000233928	RP11-305F18.1	X:33744624-33960397	NOTEST	0	0	0	0	1	1
ENSG00000233929	ENSG00000233929	MT1XP1	1:16567707-16567893	NOTEST	0	0	0	0	1	1
ENSG00000233930	ENSG00000233930	KRTAP5-AS1	11:1575273-1620414	NOTEST	0.0211634	0.11327	2.42012	0	1	1
ENSG00000233931	ENSG00000233931	TRIM40	HSCHR6_MHC_SSTO:30093486-30106107	NOTEST	0	0	0	0	1	1
ENSG00000233932	ENSG00000233932	CTXN2	15:48481233-48596275	NOTEST	0.0101045	0.0771677	2.933	0	1	1
ENSG00000233933	ENSG00000233933	RP11-63P12.2	9:74890368-74890889	NOTEST	0	0	0	0	1	1
ENSG00000233934	ENSG00000233934	RPL21P38	2:172443602-172443769	NOTEST	0	0	0	0	1	1
ENSG00000233935	ENSG00000233935	HCG4P11	HSCHR6_MHC_COX:29684536-29710797	NOTEST	0	0	0	0	1	1
ENSG00000233936	ENSG00000233936	RP11-399H11.2	9:138137541-138144554	NOTEST	0	0	0	0	1	1
ENSG00000233938	ENSG00000233938	PPP1R26P3	22:20670708-20674508	NOTEST	0	0	0	0	1	1
ENSG00000233939	ENSG00000233939	AC114755.4	2:106921210-106921653	NOTEST	0	0	0	0	1	1
ENSG00000233940	ENSG00000233940	RP11-248I9.2	1:35519068-35524872	NOTEST	0	0	0	0	1	1
ENSG00000233941	ENSG00000233941	RP11-404H14.1	6:106806440-106807592	NOTEST	0	0	0	0	1	1
ENSG00000233942	ENSG00000233942	AC004012.1	7:95101146-95103310	NOTEST	0	0	0	0	1	1
ENSG00000233943	ENSG00000233943	AC114973.1	5:56271419-56272051	NOTEST	0	0	0	0	1	1
ENSG00000233944	ENSG00000233944	LINC00265-3P	Y:27524446-27540866	NOTEST	0	0	0	0	1	1
ENSG00000233945	ENSG00000233945	RP11-344L13.2	10:85432161-85435195	NOTEST	0	0	0	0	1	1
ENSG00000233946	ENSG00000233946	RP5-1114G22.1	1:175266215-175266376	NOTEST	0	0	0	0	1	1
ENSG00000233947	ENSG00000233947	RP11-336N8.2	9:80793178-80794428	NOTEST	0	0	0	0	1	1
ENSG00000233948	ENSG00000233948	TRIM27	HSCHR6_MHC_MCF:28887955-28891932	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000233950	ENSG00000233950	XXbac-BPG308J9.3	HSCHR6_MHC_COX:29188440-29231555	NOTEST	0	0	0	0	1	1
ENSG00000233951	ENSG00000233951	RCC2P3	7:137806947-137809341	NOTEST	0	0	0	0	1	1
ENSG00000233952	ENSG00000233952	FTLP15	7:46030503-46040497	NOTEST	0	0	0	0	1	1
ENSG00000233953	ENSG00000233953	AC009970.1	2:60678301-60780702	NOTEST	0	0	0	0	1	1
ENSG00000233955	ENSG00000233955	AHCYP3	2:105011459-105012738	NOTEST	0	0	0	0	1	1
ENSG00000233956	ENSG00000233956	BTF3P6	21:34876237-35349992	NOTEST	0.0453995	0	#NAME?	0	1	1
ENSG00000233960	ENSG00000233960	RP11-153N17.1	7:52232930-52260609	NOTEST	0	0	0	0	1	1
ENSG00000233961	ENSG00000233961	RP11-87H9.2	9:69065654-69149621	NOTEST	0.201112	0.189568	-0.0852878	0	1	1
ENSG00000233962	ENSG00000233962	RP11-368M16.8	7:57712441-57713165	NOTEST	0	0	0	0	1	1
ENSG00000233963	ENSG00000233963	ATP8A2P3	13:26688546-26796791	NOTEST	0	0	0	0	1	1
ENSG00000233964	ENSG00000233964	HLA-K	HSCHR6_MHC_APD:29832178-29835432	NOTEST	0	0	0	0	1	1
ENSG00000233965	ENSG00000233965	RPL15P4	HSCHR6_MHC_APD:31507181-31507761	NOTEST	0	0	0	0	1	1
ENSG00000233967	ENSG00000233967	RP11-250B2.3	6:81153060-81175644	NOTEST	0.446187	0.359582	-0.311327	0	1	1
ENSG00000233968	ENSG00000233968	RP11-354E11.2	10:19492778-20079330	NOTEST	0	0	0	0	1	1
ENSG00000233969	ENSG00000233969	RP5-1006K12.1	7:119808398-119826118	NOTEST	0	0	0	0	1	1
ENSG00000233970	ENSG00000233970	AC092159.3	2:667334-697371	NOTEST	0	0	0	0	1	1
ENSG00000233971	ENSG00000233971	RPS20P10	2:72211311-72211564	NOTEST	0	0.124319	inf	0	1	1
ENSG00000233972	ENSG00000233972	RPL32P1	HSCHR6_MHC_MANN:33186488-33209127	NOTEST	0	0	0	0	1	1
ENSG00000233973	ENSG00000233973	RP4-598G3.1	1:73771852-73820934	NOTEST	0	0	0	0	1	1
ENSG00000233974	ENSG00000233974	RP11-823P9.3	5:21341941-21589481	NOTEST	0.0224965	0.0266824	0.246187	0	1	1
ENSG00000233975	ENSG00000233975	RP11-288L9.1	1:27986838-27989233	NOTEST	0.103254	0	#NAME?	0	1	1
ENSG00000233977	ENSG00000233977	RP11-310H4.2	7:55659766-55660886	NOTEST	0	0	0	0	1	1
ENSG00000233978	ENSG00000233978	AC016735.3	2:43268331-43270921	NOTEST	0	0	0	0	1	1
ENSG00000233979	ENSG00000233979	AC002553.4	17:15879873-16256970	NOTEST	0	0	0	0	1	1
ENSG00000233980	ENSG00000233980	FDPSP2	7:76090992-76135312	NOTEST	0	0	0	0	1	1
ENSG00000233981	ENSG00000233981	RP3-380E11.2	6:14005150-14007132	NOTEST	0	0	0	0	1	1
ENSG00000233982	ENSG00000233982	RPL7AP7	HSCHR6_MHC_MCF:29767854-29768651	NOTEST	0	0	0	0	1	1
ENSG00000233983	ENSG00000233983	RP4-735N21.1	1:99929933-99930332	NOTEST	0	0	0	0	1	1
ENSG00000233985	ENSG00000233985	RP11-297H3.3	1:170143543-170210428	NOTEST	0	0.0196204	inf	0	1	1
ENSG00000233987	ENSG00000233987	AC106706.1	3:194426276-194427693	NOTEST	0.0771682	0.200375	1.37663	0	1	1
ENSG00000233988	ENSG00000233988	ADAM6	14:106435818-106438358	NOTEST	0	0	0	0	1	1
ENSG00000233989	ENSG00000233989	UBDP1	HSCHR6_MHC_DBB:29432306-29437517	NOTEST	0	0	0	0	1	1
ENSG00000233990	ENSG00000233990	RP11-401E9.3	10:7860466-8058590	NOTEST	0	0	0	0	1	1
ENSG00000233991	ENSG00000233991	AC116050.1	2:91777535-91847998	NOTEST	0.0255798	0	#NAME?	0	1	1
ENSG00000233993	ENSG00000233993	RP11-379J5.5	20:18568536-18744561	NOTEST	0	0.00685074	inf	0	1	1
ENSG00000233995	ENSG00000233995	KB-67B5.12	22:17052916-17055527	NOTEST	0	0	0	0	1	1
ENSG00000233996	ENSG00000233996	AC013439.4	2:190351205-190352718	NOTEST	0	0	0	0	1	1
ENSG00000233997	ENSG00000233997	AP000475.2	21:23119292-23169735	NOTEST	0	0	0	0	1	1
ENSG00000233998	ENSG00000233998	SETP5	9:140513443-141019076	NOTEST	0	0	0	0	1	1
ENSG00000233999	ENSG00000233999	IGKV3OR2-268	2:87565633-87566158	NOTEST	0	0	0	0	1	1
ENSG00000234000	ENSG00000234000	PPP1R18	HSCHR6_MHC_DBB:30634430-30645937	NOTEST	0	0	0	0	1	1
ENSG00000234001	ENSG00000234001	AC000111.5	7:117105837-117514193	NOTEST	0	0	0	0	1	1
ENSG00000234003	ENSG00000234003	CTD-3105H18.11	19:12490002-12750912	NOTEST	0	0	0	0	1	1

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ENSG00000234004	ENSG00000234004	RP11-543B16.1	1:211346818-211347193	NOTEST	0.077438	0.0605274	-0.355453	0	1	1
ENSG00000234005	ENSG00000234005	GAPDHP22	13:99842832-99843245	NOTEST	0.115677	0.137033	0.244417	0	1	1
ENSG00000234006	ENSG00000234006	DDX39B-AS1	6:31496493-31526606	NOTEST	0.203409	0.126933	-0.680321	0	1	1
ENSG00000234007	ENSG00000234007	AC020601.1	2:138636323-138683977	NOTEST	0	0	0	0	1	1
ENSG00000234008	ENSG00000234008	PPP1R2P2	21:36160097-37376965	NOTEST	0	0	0	0	1	1
ENSG00000234011	ENSG00000234011	RP3-461P17.10	20:44074070-44077220	NOTEST	0.147169	0.266663	0.857545	0	1	1
ENSG00000234012	ENSG00000234012	MDC1	HSCHR6_MHC_APD:30675830-30693912	NOTEST	0	0	0	0	1	1
ENSG00000234015	ENSG00000234015	RP11-125M16.1	6:12583146-12585636	NOTEST	0	0	0	0	1	1
ENSG00000234016	ENSG00000234016	GNG10P1	10:127585107-127698161	NOTEST	0	0	0	0	1	1
ENSG00000234017	ENSG00000234017	RP11-214N15.5	10:114206755-114578503	NOTEST	0	0	0	0	1	1
ENSG00000234019	ENSG00000234019	RP11-236P24.3	X:53122891-53196196	NOTEST	0.0334575	0	#NAME?	0	1	1
ENSG00000234020	ENSG00000234020	CHIAP3	1:111895896-111910031	NOTEST	0	0	0	0	1	1
ENSG00000234021	ENSG00000234021	RP11-75C9.2	9:8314245-10612723	NOTEST	0	0	0	0	1	1
ENSG00000234022	ENSG00000234022	AC008278.2	2:15704293-15713992	NOTEST	0	0	0	0	1	1
ENSG00000234025	ENSG00000234025	RP11-257K9.3	6:73331519-73908574	NOTEST	0	0	0	0	1	1
ENSG00000234026	ENSG00000234026	RP11-310E22.4	10:96953956-96990901	NOTEST	0	0	0	0	1	1
ENSG00000234028	ENSG00000234028	AC062029.1	2:88838237-88931339	NOTEST	0.194583	0.217363	0.159722	0	1	1
ENSG00000234030	ENSG00000234030	TMEM97P1	21:45203003-45203454	NOTEST	0.0994332	0.169644	0.77071	0	1	1
ENSG00000234031	ENSG00000234031	RPS3AP44	13:27131839-27263085	NOTEST	0	0	0	0	1	1
ENSG00000234032	ENSG00000234032	VARS2	HSCHR6_MHC_MCF:30954518-30972803	NOTEST	0	0	0	0	1	1
ENSG00000234033	ENSG00000234033	RAC1P8	13:62379282-62379809	NOTEST	0	0	0	0	1	1
ENSG00000234034	ENSG00000234034	AP000959.2	21:23872923-23892377	NOTEST	0	0	0	0	1	1
ENSG00000234035	ENSG00000234035	AP001044.2	21:40249214-40328392	NOTEST	0	0	0	0	1	1
ENSG00000234036	ENSG00000234036	TXNP6	4:77870855-77961537	NOTEST	0	0	0	0	1	1
ENSG00000234037	ENSG00000234037	RP11-347K2.2	1:103817768-103835986	NOTEST	0	0.0576314	inf	0	1	1
ENSG00000234038	ENSG00000234038	AC123768.3	15:32885656-32896179	NOTEST	0.0775645	0	#NAME?	0	1	1
ENSG00000234039	ENSG00000234039	NDUFA5P7	X:85321230-85321472	NOTEST	0	0	0	0	1	1
ENSG00000234040	ENSG00000234040	RP11-254B13.4	12:69004618-69054372	NOTEST	0	0	0	0	1	1
ENSG00000234041	ENSG00000234041	RP11-345I18.1	1:179068461-179198819	NOTEST	0	0	0	0	1	1
ENSG00000234042	ENSG00000234042	RP11-452D2.2	9:68298798-68299489	NOTEST	0.247955	0.259112	0.0634936	0	1	1
ENSG00000234043	ENSG00000234043	RP11-56M3.1	10:92912361-92913106	NOTEST	0.215947	0.0566899	-1.92952	0	1	1
ENSG00000234044	ENSG00000234044	AC108059.1	2:128824767-128824981	NOTEST	0	0	0	0	1	1
ENSG00000234046	ENSG00000234046	TRIM26	HSCHR6_MHC_SSTO:30141781-30170758	NOTEST	0	0	0	0	1	1
ENSG00000234047	ENSG00000234047	AC113612.1	2:90300125-90300402	NOTEST	0	0	0	0	1	1
ENSG00000234048	ENSG00000234048	FAM96AP1	3:28390636-28579613	NOTEST	0	0	0	0	1	1
ENSG00000234050	ENSG00000234050	LL0XNC01-237H1.3	X:102192199-102195489	NOTEST	0	3.94E-05	inf	0	1	1
ENSG00000234052	ENSG00000234052	AP001607.1	21:29011011-29025810	NOTEST	0	0	0	0	1	1
ENSG00000234055	ENSG00000234055	RP11-247A12.1	9:131857088-131911225	NOTEST	0	0	0	0	1	1
ENSG00000234056	ENSG00000234056	AMER2-AS1	13:25746965-25754217	NOTEST	0	0	0	0	1	1
ENSG00000234057	ENSG00000234057	XXbac-BPG249D20.9	HSCHR6_MHC_MCF:30562496-30565448	NOTEST	0	0	0	0	1	1
ENSG00000234058	ENSG00000234058	PPP1R11	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1
ENSG00000234059	ENSG00000234059	CASKP1	Y:15042074-15060090	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000234061	ENSG00000234061	AC007969.4	2:172349414-172349605	NOTEST	0.429498	0	#NAME?	0	1	1
ENSG00000234062	ENSG00000234062	RP11-308D16.4	X:135991553-136103789	NOTEST	0.452866	0.295734	-0.614784	0	1	1
ENSG00000234063	ENSG00000234063	XXbac-BPG118E17.9	HSCHR6_MHC_COX:30964484-30993378	NOTEST	0	0	0	0	1	1
ENSG00000234064	ENSG00000234064	RP11-450I1.2	1:12985989-12988081	NOTEST	0	0	0	0	1	1
ENSG00000234065	ENSG00000234065	MTND4P26	2:120770580-120974855	NOTEST	0	0.00879562	inf	0	1	1
ENSG00000234066	ENSG00000234066	TAS2R62P	7:143078172-143220542	NOTEST	0	0	0	0	1	1
ENSG00000234067	ENSG00000234067	RPL5P10	3:40628025-40628919	NOTEST	0	0	0	0	1	1
ENSG00000234068	ENSG00000234068	PAGE2	X:55115440-55119275	NOTEST	0.0725198	0	#NAME?	0	1	1
ENSG00000234069	ENSG00000234069	GAPDHP53	20:24426026-24426950	NOTEST	0	0	0	0	1	1
ENSG00000234070	ENSG00000234070	SPATA17-AS1	1:217804665-218045038	NOTEST	0	0	0	0	1	1
ENSG00000234071	ENSG00000234071	RP11-420H19.1	7:124462439-125019375	NOTEST	0	0	0	0	1	1
ENSG00000234073	ENSG00000234073	AC011816.1	3:36868310-36986548	NOTEST	0	0	0	0	1	1
ENSG00000234074	ENSG00000234074	HLA-J	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000234075	ENSG00000234075	RPL35AP	20:46106957-46107754	NOTEST	0	0	0	0	1	1
ENSG00000234076	ENSG00000234076	TPRG1-AS1	3:188659503-189043093	NOTEST	0.16491	0.170527	0.0483203	0	1	1
ENSG00000234078	ENSG00000234078	DDR1	HSCHR6_MHC_MANN:30893439-30912617	NOTEST	0	0	0	0	1	1
ENSG00000234079	ENSG00000234079	HCG27	HSCHR6_MHC_DBB:31159279-31165485	NOTEST	0	0	0	0	1	1
ENSG00000234080	ENSG00000234080	RP11-183G22.1	1:50791802-50792682	NOTEST	0.0478558	0	#NAME?	0	1	1
ENSG00000234081	ENSG00000234081	TCEB1P10	Y:26153057-26153384	NOTEST	0	0	0	0	1	1
ENSG00000234082	ENSG00000234082	DDX39B-AS1	HSCHR6_MHC_MCF:31572847-31602942	NOTEST	0	0	0	0	1	1
ENSG00000234083	ENSG00000234083	AJ006995.3	21:29327239-29357614	NOTEST	0	0	0	0	1	1
ENSG00000234084	ENSG00000234084	RP3-388E23.2	6:135604669-136037193	NOTEST	0.0677495	0.0284928	-1.24961	0	1	1
ENSG00000234085	ENSG00000234085	RP11-368M16.7	7:57714527-57715098	NOTEST	0	0	0	0	1	1
ENSG00000234086	ENSG00000234086	AL391994.1	1:235294497-235507847	NOTEST	0	0	0	0	1	1
ENSG00000234087	ENSG00000234087	CTD-3216D2.4	20:32935476-32935591	NOTEST	0	0	0	0	1	1
ENSG00000234088	ENSG00000234088	RPS15AP7	1:62656193-62656598	NOTEST	0	0	0	0	1	1
ENSG00000234089	ENSG00000234089	RP11-1217F2.15	7:57277571-57289881	NOTEST	0	0	0	0	1	1
ENSG00000234091	ENSG00000234091	RP11-353M9.1	10:13628926-14504141	NOTEST	0	0	0	0	1	1
ENSG00000234092	ENSG00000234092	OR2H4P	HSCHR6_MHC_COX:29179709-29180647	NOTEST	0	0	0	0	1	1
ENSG00000234093	ENSG00000234093	RPS15AP11	1:45245997-45246387	NOTEST	0.128313	0.0494833	-1.37465	0	1	1
ENSG00000234095	ENSG00000234095	HLA-N	HSCHR6_MHC_MANN:30363872-30364007	NOTEST	0	0	0	0	1	1
ENSG00000234096	ENSG00000234096	MOG	HSCHR6_MHC_APD:29624886-29640277	NOTEST	0	0	0	0	1	1
ENSG00000234099	ENSG00000234099	MTND4P11	1:94388129-94389501	NOTEST	0	0	0	0	1	1
ENSG00000234100	ENSG00000234100	OR14J1	HSCHR6_MHC_MANN:29274450-29275567	NOTEST	0	0	0	0	1	1
ENSG00000234101	ENSG00000234101	OR2W1	HSCHR6_MHC_COX:29008602-29009630	NOTEST	0	0	0	0	1	1
ENSG00000234102	ENSG00000234102	KRT19P4	10:70020313-70021256	NOTEST	0	0	0	0	1	1
ENSG00000234104	ENSG00000234104	RP5-1177M21.1	20:20951088-20953203	NOTEST	0	0	0	0	1	1
ENSG00000234105	ENSG00000234105	GS1-278J22.1	7:53582684-53584809	NOTEST	0	0	0	0	1	1
ENSG00000234106	ENSG00000234106	RP11-288E14.2	11:93211637-93276674	NOTEST	0	0.0649143	inf	0	1	1
ENSG00000234107	ENSG00000234107	TPT1P1	21:33212652-33213170	NOTEST	0	0	0	0	1	1

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ENSG00000234110	ENSG00000234110	TSPY25P	Y:9461791-9463961	NOTEST	0	0	0	0	1	1
ENSG00000234111	ENSG00000234111	RP11-364P22.1	4:158493641-158497306	NOTEST	0	0	0	0	1	1
ENSG00000234112	ENSG00000234112	RP11-145A3.4	1:225990849-225991150	NOTEST	0	0	0	0	1	1
ENSG00000234113	ENSG00000234113	AC008163.4	7:81157718-81191099	NOTEST	0	0	0	0	1	1
ENSG00000234114	ENSG00000234114	CCHCR1	HSCHR6_MHC_COX:31102771-31118543	NOTEST	0	0	0	0	1	1
ENSG00000234115	ENSG00000234115	RP11-288G3.4	6:7516832-7518073	NOTEST	0	0	0	0	1	1
ENSG00000234116	ENSG00000234116	RP11-261C10.1	1:243169146-243170770	NOTEST	0	0	0	0	1	1
ENSG00000234117	ENSG00000234117	RP11-259P20.1	6:116813459-116880031	NOTEST	0	0	0	0	1	1
ENSG00000234118	ENSG00000234118	RPL13AP6	10:112679300-112773425	NOTEST	0	0.0763104	inf	0	1	1
ENSG00000234119	ENSG00000234119	AC079248.1	2:146583852-146585398	NOTEST	0	0	0	0	1	1
ENSG00000234120	ENSG00000234120	AF228730.8	8:6969835-6971250	NOTEST	0	0	0	0	1	1
ENSG00000234121	ENSG00000234121	GPM6BP3	22:17318411-17318556	NOTEST	0	0	0	0	1	1
ENSG00000234122	ENSG00000234122	TRBV22OR9-2	9:33634108-33634244	NOTEST	0	0	0	0	1	1
ENSG00000234123	ENSG00000234123	RHBDF1P1	3:14614358-14616299	NOTEST	0	0	0	0	1	1
ENSG00000234124	ENSG00000234124	CSN1S2AP	4:70933102-70951007	NOTEST	0.0451458	0.0172482	-1.38815	0	1	1
ENSG00000234125	ENSG00000234125	EEF1GP8	4:130692813-130876523	NOTEST	0	0	0	0	1	1
ENSG00000234130	ENSG00000234130	RP13-88F20.1	X:92477218-92480014	NOTEST	0.155373	0.251564	0.695196	0	1	1
ENSG00000234131	ENSG00000234131	TCEB1P8	Y:24663388-24663720	NOTEST	0	0	0	0	1	1
ENSG00000234132	ENSG00000234132	RP11-168O16.2	1:201004223-201081694	NOTEST	0	0	0	0	1	1
ENSG00000234134	ENSG00000234134	RP11-383C5.5	10:127371797-127452712	NOTEST	0.226542	0	#NAME?	0	1	1
ENSG00000234135	ENSG00000234135	RPL23AP83	X:56258853-56314322	NOTEST	0	0	0	0	1	1
ENSG00000234136	ENSG00000234136	AC055764.1	3:197518096-197615307	NOTEST	0.0491762	0.0383333	-0.35936	0	1	1
ENSG00000234137	ENSG00000234137	C6orf205	HSCHR6_MHC_COX:30941180-30947386	NOTEST	0	0	0	0	1	1
ENSG00000234138	ENSG00000234138	RP11-144A16.1	9:41418936-41433320	NOTEST	0	0	0	0	1	1
ENSG00000234139	ENSG00000234139	RP4-550H1.4	20:34660362-34673182	NOTEST	0	0	0	0	1	1
ENSG00000234140	ENSG00000234140	DDX39BP2	HSCHR6_MHC_QBL:29950407-29950803	NOTEST	0	0	0	0	1	1
ENSG00000234141	ENSG00000234141	AC009473.1	7:7676148-8133902	NOTEST	0.0285301	0.0201545	-0.501382	0	1	1
ENSG00000234142	ENSG00000234142	RP11-276E17.2	1:166443981-166459276	NOTEST	0	0	0	0	1	1
ENSG00000234143	ENSG00000234143	UGT1A13P	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000234144	ENSG00000234144	COX6CP13	1:65713901-65881689	NOTEST	0	0	0	0	1	1
ENSG00000234145	ENSG00000234145	NAP1L4P3	13:48337594-48338741	NOTEST	0.0277139	0	#NAME?	0	1	1
ENSG00000234146	ENSG00000234146	RP11-109M17.1	9:11011747-11013096	NOTEST	0	0	0	0	1	1
ENSG00000234147	ENSG00000234147	RP3-460G2.2	6:141167094-141174061	NOTEST	0.0987023	0.0374839	-1.39681	0	1	1
ENSG00000234148	ENSG00000234148	RP11-395L14.3	2:114270039-114273062	NOTEST	0	0	0	0	1	1
ENSG00000234149	ENSG00000234149	RP11-77G23.2	10:76585339-76792380	NOTEST	0	0	0	0	1	1
ENSG00000234152	ENSG00000234152	TCEB2P1	13:25939936-25940293	NOTEST	0	0	0	0	1	1
ENSG00000234154	ENSG00000234154	HLA-DMB	HSCHR6_MHC_COX:32824725-32871622	NOTEST	0	0	0	0	1	1
ENSG00000234155	ENSG00000234155	RP11-30P6.6	6:86096936-86099904	NOTEST	0.0190234	0.0311737	0.712557	0	1	1
ENSG00000234156	ENSG00000234156	RP11-64P14.7	9:125372193-125401964	NOTEST	0	0	0	0	1	1
ENSG00000234158	ENSG00000234158	RPEP2	3:26057159-26057860	NOTEST	0	0	0	0	1	1
ENSG00000234159	ENSG00000234159	RBPMSLP	21:17102343-17252377	NOTEST	0	0	0	0	1	1
ENSG00000234161	ENSG00000234161	PABPC5-AS1	X:90669876-90693583	NOTEST	0	0	0	0	1	1

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ENSG00000234163	ENSG00000234163	RP11-479G22.6	10:33189246-33371030	NOTEST	0	0	0	0	1	1
ENSG00000234164	ENSG00000234164	HLA-DRB9	HSCHR6_MHC_MANN:32466295-32479952	NOTEST	0	0	0	0	1	1
ENSG00000234165	ENSG00000234165	AC114877.3	3:26753797-26754855	NOTEST	0	0	0	0	1	1
ENSG00000234166	ENSG00000234166	ARHGEF19-AS1	1:16524348-16539104	NOTEST	0	0.0279484	inf	0	1	1
ENSG00000234167	ENSG00000234167	TCEB2P4	10:34398487-35104253	NOTEST	0	0	0	0	1	1
ENSG00000234168	ENSG00000234168	LINC01039	13:100229365-100232622	NOTEST	0	0	0	0	1	1
ENSG00000234169	ENSG00000234169	AC092168.3	2:101286353-101292500	NOTEST	0	0	0	0	1	1
ENSG00000234170	ENSG00000234170	RP11-446F3.2	10:2488446-2489546	NOTEST	0	0	0	0	1	1
ENSG00000234172	ENSG00000234172	AC093639.1	2:184769255-184813839	NOTEST	0	0	0	0	1	1
ENSG00000234173	ENSG00000234173	RP11-257I14.1	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000234174	ENSG00000234174	AC016683.5	2:113914901-113966973	NOTEST	0	0	0	0	1	1
ENSG00000234175	ENSG00000234175	RP11-730A19.9	10:13181195-13181533	NOTEST	0.0883665	0.138231	0.64551	0	1	1
ENSG00000234176	ENSG00000234176	HSPA8P1	X:120337035-120338868	NOTEST	0.0089358	0	#NAME?	0	1	1
ENSG00000234177	ENSG00000234177	LINC01114	2:105363095-105374177	NOTEST	0	0	0	0	1	1
ENSG00000234178	ENSG00000234178	DEFA11P	8:6886162-6887011	NOTEST	0	0	0	0	1	1
ENSG00000234179	ENSG00000234179	MTCYBP1	Y:8232072-8233191	NOTEST	0	0	0	0	1	1
ENSG00000234181	ENSG00000234181	RP11-182N22.8	9:35088684-35098138	NOTEST	0	0	0	0	1	1
ENSG00000234182	ENSG00000234182	RP11-118K6.2	10:3052722-3055303	NOTEST	0	0	0	0	1	1
ENSG00000234183	ENSG00000234183	AC004854.4	7:44888014-44889167	NOTEST	0	0	0	0	1	1
ENSG00000234184	ENSG00000234184	RP5-887A10.1	1:81000662-81112473	NOTEST	0	0	0	0	1	1
ENSG00000234185	ENSG00000234185	RP5-1132H15.	7:65540784-65629998	NOTEST	0	0	0	0	1	1
ENSG00000234186	ENSG00000234186	C16orf82	16:27078027-27080486	NOTEST	0	0	0	0	1	1
ENSG00000234187	ENSG00000234187	AIMP1P1	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000234188	ENSG00000234188	AL121963.1	6:116422011-116570660	NOTEST	0	0	0	0	1	1
ENSG00000234189	ENSG00000234189	AC099799.1	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000234190	ENSG00000234190	RP11-433J22.3	1:147249699-147261065	NOTEST	0	0	0	0	1	1
ENSG00000234191	ENSG00000234191	RP11-157D23.2	X:39260505-39294078	NOTEST	0	0	0	0	1	1
ENSG00000234192	ENSG00000234192	RP11-57C13.5	10:89367741-89507462	NOTEST	0	0	0	0	1	1
ENSG00000234193	ENSG00000234193	AC097461.4	2:223725651-223809357	NOTEST	0.539278	0.308583	-0.805368	0	1	1
ENSG00000234195	ENSG00000234195	OR14J1	HSCHR6_MHC_SSTO:29274498-29275615	NOTEST	0	0	0	0	1	1
ENSG00000234196	ENSG00000234196	ZBTB12	HSCHR6_MHC_MCF:31942046-31996308	NOTEST	0	0	0	0	1	1
ENSG00000234199	ENSG00000234199	AC010982.1	2:114737145-114764879	NOTEST	0.0220703	0.0844075	1.93527	0	1	1
ENSG00000234200	ENSG00000234200	U82671.8	X:152197129-152198791	NOTEST	0	0	0	0	1	1
ENSG00000234201	ENSG00000234201	RP11-383C12.2	X:67011796-67012737	NOTEST	0	0	0	0	1	1
ENSG00000234202	ENSG00000234202	RP11-330C7.4	1:92974252-93257961	NOTEST	0	0	0	0	1	1
ENSG00000234203	ENSG00000234203	RP5-1050D4.2	17:4871286-4890972	NOTEST	0	0	0	0	1	1
ENSG00000234204	ENSG00000234204	PIGPP2	1:62654802-62655625	NOTEST	0	0	0	0	1	1
ENSG00000234206	ENSG00000234206	RP1-67A8.3	6:107811161-107981357	NOTEST	0	0	0	0	1	1
ENSG00000234207	ENSG00000234207	AC096570.2	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000234208	ENSG00000234208	CTA-256D12.11	22:29901867-29977326	NOTEST	0	0	0	0	1	1

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ENSG00000234211	ENSG00000234211	RP11-25K21.1	1:161475219-161648444	NOTEST	0	0	0	0	1	1
ENSG00000234213	ENSG00000234213	FHP1	13:42614175-42830714	NOTEST	0	0	0	0	1	1
ENSG00000234214	ENSG00000234214	SPATA31A4	9:41313944-41327364	NOTEST	0	0	0	0	1	1
ENSG00000234215	ENSG00000234215	RP5-942I16.1	7:69060943-69062434	NOTEST	0.028566	0.0201923	-0.500491	0	1	1
ENSG00000234216	ENSG00000234216	HNRNPA1P2	HSCHR6_MHC_APD:32295496-32350672	NOTEST	0	0	0	0	1	1
ENSG00000234217	ENSG00000234217	RBPJP7	9:46912526-46913973	NOTEST	0	0	0	0	1	1
ENSG00000234218	ENSG00000234218	MICB	HSCHR6_MHC_COX:31453327-31466366	NOTEST	0	0	0	0	1	1
ENSG00000234219	ENSG00000234219	RP11-454L1.2	1:207925401-207968858	NOTEST	0	0.0227131	inf	0	1	1
ENSG00000234222	ENSG00000234222	RP11-315I20.1	1:145475981-145516076	NOTEST	0.628962	0.433021	-0.53394	0	1	1
ENSG00000234223	ENSG00000234223	AC003988.1	7:79875724-79941772	NOTEST	0	0	0	0	1	1
ENSG00000234224	ENSG00000234224	TMEM229A	7:123670972-124035172	NOTEST	0.0237659	0.0194221	-0.291194	0	1	1
ENSG00000234225	ENSG00000234225	RP4-704D21.2	1:146473489-146475177	NOTEST	0	0	0	0	1	1
ENSG00000234226	ENSG00000234226	NDUFS5P2	1:97049972-97050290	NOTEST	0	0	0	0	1	1
ENSG00000234227	ENSG00000234227	RPL7L1P1	13:90485410-90486195	NOTEST	0	0	0	0	1	1
ENSG00000234228	ENSG00000234228	NCLP2	X:134193714-134257880	NOTEST	0	0	0	0	1	1
ENSG00000234229	ENSG00000234229	RP11-308N19.4	9:109378338-109464943	NOTEST	0.249069	0.150956	-0.722415	0	1	1
ENSG00000234230	ENSG00000234230	ZFX-AS1	X:24164341-24234372	NOTEST	0	0	0	0	1	1
ENSG00000234232	ENSG00000234232	RP11-353N4.5	1:149646784-149719362	NOTEST	0	0.028791	inf	0	1	1
ENSG00000234234	ENSG00000234234	RP11-3N2.7	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000234235	ENSG00000234235	BOK-AS1	2:242483817-242513546	NOTEST	0	0	0	0	1	1
ENSG00000234237	ENSG00000234237	AL162431.1	1:180882289-180992047	NOTEST	0	0	0	0	1	1
ENSG00000234238	ENSG00000234238	RP11-430L16.1	3:187824883-187864808	NOTEST	0	0	0	0	1	1
ENSG00000234239	ENSG00000234239	CFL1P8	13:100234959-100235434	NOTEST	0	0.0347397	inf	0	1	1
ENSG00000234241	ENSG00000234241	RP4-775C13.1	20:6194345-6196028	NOTEST	0.350617	0.399969	0.189991	0	1	1
ENSG00000234242	ENSG00000234242	DDX39BP2	HSCHR6_MHC_COX:29950498-29950895	NOTEST	0	0	0	0	1	1
ENSG00000234243	ENSG00000234243	GPSM3	HSCHR6_MHC_MCF:32234969-32268294	NOTEST	0	0	0	0	1	1
ENSG00000234244	ENSG00000234244	RP11-139J15.5	10:19035361-19036782	NOTEST	0	0	0	0	1	1
ENSG00000234245	ENSG00000234245	RP11-94I2.4	1:145952371-145956451	NOTEST	0	0	0	0	1	1
ENSG00000234247	ENSG00000234247	RP11-100E13.3	1:224572844-224928251	NOTEST	0	0	0	0	1	1
ENSG00000234248	ENSG00000234248	RP11-799O21.2	10:6933418-6962434	NOTEST	0	0	0	0	1	1
ENSG00000234249	ENSG00000234249	COL11A2P1	HSCHR6_MHC_MCF:33104991-33108528	NOTEST	0	0	0	0	1	1
ENSG00000234251	ENSG00000234251	HTATSF1P	HSCHR6_MHC_SSTO:33344877-33346777	NOTEST	0	0	0	0	1	1
ENSG00000234252	ENSG00000234252	AC007308.6	22:21061978-21245506	NOTEST	0.146887	0.159258	0.116657	0	1	1
ENSG00000234253	ENSG00000234253	RPL7P13	2:50105760-50106501	NOTEST	0	0	0	0	1	1
ENSG00000234255	ENSG00000234255	AC012370.3	2:65663844-66311773	NOTEST	0	0	0	0	1	1
ENSG00000234256	ENSG00000234256	PTCD2P2	10:90636206-90637301	NOTEST	0	0	0	0	1	1
ENSG00000234257	ENSG00000234257	SOD2P1	1:103342022-103574052	NOTEST	0	0	0	0	1	1
ENSG00000234258	ENSG00000234258	HSPA1L	HSCHR6_MHC_DBB:31759585-31765032	NOTEST	0	0	0	0	1	1
ENSG00000234259	ENSG00000234259	CTC-507E12.1	5:119015891-119016775	NOTEST	0	0	0	0	1	1
ENSG00000234260	ENSG00000234260	HLA-DPA2	HSCHR6_MHC_APD:33042923-33048466	NOTEST	0	0	0	0	1	1
ENSG00000234261	ENSG00000234261	RP11-146I2.1	6:14977018-15090234	NOTEST	0	0	0	0	1	1
ENSG00000234262	ENSG00000234262	RP1-20N18.4	1:152996437-152996736	NOTEST	0	0	0	0	1	1

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ENSG00000234263	ENSG00000234263	RP3-325F22.3	6:136878184-137113656	NOTEST	0	0	0	0	1	1
ENSG00000234264	ENSG00000234264	RP4-694A7.4	1:68939834-69004310	NOTEST	0.0803227	0.00971595	-3.04738	0	1	1
ENSG00000234265	ENSG00000234265	RP11-157E14.1	20:12845849-12933167	NOTEST	0	0	0	0	1	1
ENSG00000234267	ENSG00000234267	TULP3P1	13:97593534-97636426	NOTEST	0	0	0	0	1	1
ENSG00000234269	ENSG00000234269	RP11-338N12.1	9:105684855-105685526	NOTEST	0	0	0	0	1	1
ENSG00000234270	ENSG00000234270	RPL36P20	3:41236327-42003922	NOTEST	0	0	0	0	1	1
ENSG00000234271	ENSG00000234271	RP1-138B7.4	20:42136319-42179590	NOTEST	0	0	0	0	1	1
ENSG00000234272	ENSG00000234272	RPL30P2	2:152973314-153032506	NOTEST	0	0	0	0	1	1
ENSG00000234273	ENSG00000234273	AC073071.1	7:109162037-109237223	NOTEST	0	0	0	0	1	1
ENSG00000234274	ENSG00000234274	COX7BP2	20:34359895-34538303	NOTEST	0	0	0	0	1	1
ENSG00000234275	ENSG00000234275	AC017053.1	2:6453085-6465778	NOTEST	0	0	0	0	1	1
ENSG00000234276	ENSG00000234276	BX664724.4	9:47001333-47001835	NOTEST	0	0	0	0	1	1
ENSG00000234277	ENSG00000234277	CTD-2090I13.1	1:227581291-227618736	NOTEST	0	0	0	0	1	1
ENSG00000234278	ENSG00000234278	PRR20E	13:57741330-57744352	NOTEST	0	0	0	0	1	1
ENSG00000234279	ENSG00000234279	AC113618.1	2:239628964-239649421	NOTEST	0	0	0	0	1	1
ENSG00000234280	ENSG00000234280	C6orf10	HSCHR6_MHC_COX:32209048-32287940	NOTEST	0	0	0	0	1	1
ENSG00000234281	ENSG00000234281	AC007970.1	2:211189482-211342376	NOTEST	0.0701267	0.0472725	-0.568961	0	1	1
ENSG00000234282	ENSG00000234282	RP4-673D20.4	20:1702690-1703183	NOTEST	0	0	0	0	1	1
ENSG00000234283	ENSG00000234283	RP11-495P10.6	1:147744013-147752855	NOTEST	0	0	0	0	1	1
ENSG00000234285	ENSG00000234285	GAPDHP49	2:223289235-223425667	NOTEST	0	0	0	0	1	1
ENSG00000234286	ENSG00000234286	AC006026.13	7:23719748-23742868	NOTEST	0	0	0	0	1	1
ENSG00000234288	ENSG00000234288	OR1AA1P	X:130558272-130559188	NOTEST	0	0	0	0	1	1
ENSG00000234289	ENSG00000234289	H2BFS	21:44949071-45079374	NOTEST	0	0.0551114	inf	0	1	1
ENSG00000234290	ENSG00000234290	AC116366.6	5:131746327-131811736	NOTEST	0.040221	0.0451939	0.168181	0	1	1
ENSG00000234292	ENSG00000234292	RP11-213H15.1	5:90575913-90576959	NOTEST	0.0818782	0.15008	0.874177	0	1	1
ENSG00000234293	ENSG00000234293	BACH1-IT3	21:30565800-31312351	NOTEST	0	0	0	0	1	1
ENSG00000234295	ENSG00000234295	AC109135.1	GL000192.1:222729-407630	NOTEST	0	0	0	0	1	1
ENSG00000234296	ENSG00000234296	RP13-16H11.7	10:26932097-26942383	NOTEST	0	0	0	0	1	1
ENSG00000234298	ENSG00000234298	TCEB3CL	18:44388352-44627658	NOTEST	0	0	0	0	1	1
ENSG00000234299	ENSG00000234299	CDK2AP2P1	9:45363480-45363852	NOTEST	0	0	0	0	1	1
ENSG00000234300	ENSG00000234300	LINC00229	22:45002818-45021299	NOTEST	0	0	0	0	1	1
ENSG00000234303	ENSG00000234303	CLYBL-AS1	13:100258918-100549387	NOTEST	0	0	0	0	1	1
ENSG00000234304	ENSG00000234304	RP11-398K14.1	7:52959529-52965500	NOTEST	0	0	0	0	1	1
ENSG00000234305	ENSG00000234305	OR2J1	HSCHR6_MHC_APD:29068769-29069708	NOTEST	0	0	0	0	1	1
ENSG00000234306	ENSG00000234306	RP11-271F18.1	10:10407142-10408450	NOTEST	0	0	0	0	1	1
ENSG00000234308	ENSG00000234308	AC093381.2	2:213446080-214017151	NOTEST	0	0	0	0	1	1
ENSG00000234309	ENSG00000234309	SLC25A18P1	10:120332382-120333132	NOTEST	0	0	0	0	1	1
ENSG00000234311	ENSG00000234311	RP11-432J24.3	10:134247236-134254988	NOTEST	0	0	0	0	1	1
ENSG00000234312	ENSG00000234312	RP11-196D18.4	7:62574012-62575183	NOTEST	0	0	0	0	1	1
ENSG00000234313	ENSG00000234313	HCG9	HSCHR6_MHC_DBB:29932825-29936125	NOTEST	0	0	0	0	1	1
ENSG00000234315	ENSG00000234315	OSTCP5	1:45482070-45771881	NOTEST	0	0	0	0	1	1
ENSG00000234318	ENSG00000234318	RP4-771M4.3	1:63361679-63367310	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000234319	ENSG00000234319	RPS12P2	10:81967465-81979413	NOTEST	0	0	0	0	1	1
ENSG00000234320	ENSG00000234320	RP11-381O7.6	9:66954106-66954749	NOTEST	0	0	0	0	1	1
ENSG00000234322	ENSG00000234322	ST13P18	X:92542731-92543758	NOTEST	0.0490027	0.0798009	0.703543	0	1	1
ENSG00000234324	ENSG00000234324	RPL9P2	17:15339331-15466909	NOTEST	0	0	0	0	1	1
ENSG00000234325	ENSG00000234325	MRPS10P2	3:3742497-4508965	NOTEST	0	0	0	0	1	1
ENSG00000234328	ENSG00000234328	TNXA	HSCHR6_MHC_SSTO:31965199-32027628	NOTEST	0	0	0	0	1	1
ENSG00000234329	ENSG00000234329	RP11-767N6.2	1:46092975-46216322	NOTEST	0.224721	0.411208	0.871731	0	1	1
ENSG00000234331	ENSG00000234331	XXbac-BPG254F23.7	HSCHR6_MHC_DBB:32664298-32665133	NOTEST	0	0	0	0	1	1
ENSG00000234332	ENSG00000234332	BCAS2P2	1:100810032-100985833	NOTEST	0.345014	0.186499	-0.887488	0	1	1
ENSG00000234333	ENSG00000234333	CYCSP53	1:171413837-171414102	NOTEST	0	0	0	0	1	1
ENSG00000234335	ENSG00000234335	RPS4XP11	10:32391449-32392221	NOTEST	0.024715	0.131676	2.41353	0	1	1
ENSG00000234336	ENSG00000234336	JAZF1-AS1	7:27773013-28283536	NOTEST	0.342339	0.16824	-1.02491	0	1	1
ENSG00000234337	ENSG00000234337	RP11-297L17.6	16:52689215-52689962	NOTEST	0.122102	0.0184446	-2.72682	0	1	1
ENSG00000234340	ENSG00000234340	AP000705.8	21:23507017-23508403	NOTEST	0	0	0	0	1	1
ENSG00000234343	ENSG00000234343	NEU1	HSCHR6_MHC_DBB:31807624-31812872	NOTEST	0	0	0	0	1	1
ENSG00000234344	ENSG00000234344	MEP1AP3	9:43162900-43169024	NOTEST	0	0	0	0	1	1
ENSG00000234345	ENSG00000234345	LL0XNC01-116E7.1	X:103165224-103166272	NOTEST	0.0478193	0.062395	0.383837	0	1	1
ENSG00000234347	ENSG00000234347	OR11A1	HSCHR6_MHC_DBB:29341258-29424782	NOTEST	0	0	0	0	1	1
ENSG00000234349	ENSG00000234349	GLUD1P9	X:110473116-110474289	NOTEST	0	0	0	0	1	1
ENSG00000234350	ENSG00000234350	AC007405.4	2:171579718-171627276	NOTEST	0.0610244	0.0174716	-1.80438	0	1	1
ENSG00000234351	ENSG00000234351	OR2U2P	HSCHR6_MHC_DBB:29236261-29237221	NOTEST	0	0	0	0	1	1
ENSG00000234352	ENSG00000234352	hsa-mir-490	7:136370305-136866854	NOTEST	0.0135177	0	#NAME?	0	1	1
ENSG00000234354	ENSG00000234354	RPS26P47	13:101183809-101241782	NOTEST	0.326295	0.400602	0.295993	0	1	1
ENSG00000234355	ENSG00000234355	FTH1P27	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000234356	ENSG00000234356	AC009945.4	7:10516207-10516505	NOTEST	0	0	0	0	1	1
ENSG00000234358	ENSG00000234358	AC003080.4	7:111366165-111846466	NOTEST	0	0	0	0	1	1
ENSG00000234359	ENSG00000234359	ELK1P1	7:45431224-45431804	NOTEST	0	0	0	0	1	1
ENSG00000234360	ENSG00000234360	RP11-87N24.1	9:8314245-10612723	NOTEST	0	0	0	0	1	1
ENSG00000234361	ENSG00000234361	RP11-52J3.3	6:158244295-158366109	NOTEST	0	0	0	0	1	1
ENSG00000234362	ENSG00000234362	AC104654.2	2:42158738-42160863	NOTEST	0.0704122	0.134125	0.929686	0	1	1
ENSG00000234363	ENSG00000234363	PPIAP27	13:21530317-21530582	NOTEST	0	0	0	0	1	1
ENSG00000234364	ENSG00000234364	MICF	HSCHR6_MHC_MCF:29816994-29817123	NOTEST	0	0	0	0	1	1
ENSG00000234365	ENSG00000234365	TAPSAR1	HSCHR6_MHC_MCF:32841973-32881069	NOTEST	0	0	0	0	1	1
ENSG00000234367	ENSG00000234367	PFN1P3	1:148349255-148349657	NOTEST	0.570878	0.381472	-0.581604	0	1	1
ENSG00000234369	ENSG00000234369	TATDN1P1	10:64926980-65226323	NOTEST	0.0206293	0.0497815	1.27092	0	1	1
ENSG00000234370	ENSG00000234370	GTF2H4	HSCHR6_MHC_MCF:30954518-30972803	NOTEST	0	0	0	0	1	1
ENSG00000234371	ENSG00000234371	RP11-315J22.5	3:183547172-183606237	NOTEST	0.0272602	0.0214862	-0.343384	0	1	1
ENSG00000234372	ENSG00000234372	HLA-DPA3	HSCHR6_MHC_MANN:33252857-33264993	NOTEST	0	0	0	0	1	1
ENSG00000234375	ENSG00000234375	VN2R4P	9:40063115-40085739	NOTEST	0	0	0	0	1	1
ENSG00000234376	ENSG00000234376	UBTFL2	11:89485952-89487143	NOTEST	0	0	0	0	1	1
ENSG00000234377	ENSG00000234377	RNF219-AS1	13:78469615-79233314	NOTEST	0.28147	0.183939	-0.613753	0	1	1
ENSG00000234378	ENSG00000234378	AC098828.2	2:20263616-20306590	NOTEST	0	0	0	0	1	1
ENSG00000234379	ENSG00000234379	HMGB1P48	1:45996598-45997811	NOTEST	0	0	0	0	1	1
ENSG00000234380	ENSG00000234380	AP000330.8	21:36118053-36157183	NOTEST	0.144634	0.0218357	-2.72765	0	1	1

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ENSG00000234381	ENSG00000234381	MED15P7	22:16333632-16342783	NOTEST	0	0	0	0	1	1
ENSG00000234382	ENSG00000234382	RP11-40F6.1	10:81993419-82005123	NOTEST	0	0	0	0	1	1
ENSG00000234383	ENSG00000234383	CTBP2P8	1:68167148-68698803	NOTEST	0.0489388	0.0280045	-0.805317	0	1	1
ENSG00000234384	ENSG00000234384	LINC01049	13:91145540-91187334	NOTEST	0	0	0	0	1	1
ENSG00000234385	ENSG00000234385	RCC2P1	Y:13901757-13903233	NOTEST	0	0	0	0	1	1
ENSG00000234386	ENSG00000234386	OR7E162P	4:3903292-3904321	NOTEST	0	0	0	0	1	1
ENSG00000234387	ENSG00000234387	RP11-340I6.1	7:62854126-62882424	NOTEST	0	0	0	0	1	1
ENSG00000234388	ENSG00000234388	TXNP3	1:112905902-112906203	NOTEST	0	0	0	0	1	1
ENSG00000234389	ENSG00000234389	AC007278.3	2:103035148-103069025	NOTEST	0	0	0	0	1	1
ENSG00000234390	ENSG00000234390	USP27X-AS1	X:49641326-49643844	NOTEST	0.408355	0.333129	-0.293746	0	1	1
ENSG00000234391	ENSG00000234391	RP11-344N17.6	X:48166203-48168490	NOTEST	0	0	0	0	1	1
ENSG00000234393	ENSG00000234393	RP11-211N11.5	10:115438941-115490662	NOTEST	0	0.0201532	inf	0	1	1
ENSG00000234394	ENSG00000234394	RP11-561O23.5	9:70921443-71145977	NOTEST	0.0078619	0	#NAME?	0	1	1
ENSG00000234396	ENSG00000234396	RP11-181G12.4	1:1981908-2152177	NOTEST	0	0	0	0	1	1
ENSG00000234397	ENSG00000234397	RP11-415K20.1	1:22649332-22649824	NOTEST	0	0	0	0	1	1
ENSG00000234398	ENSG00000234398	AC134915.1	2:131003543-131006343	NOTEST	0	0	0	0	1	1
ENSG00000234399	ENSG00000234399	RBMY2XP	Y:26542750-26549673	NOTEST	0	0	0	0	1	1
ENSG00000234402	ENSG00000234402	ELK2BP	14:106012946-106016031	NOTEST	0	0	0	0	1	1
ENSG00000234404	ENSG00000234404	BX682235.1	X:76594674-76601782	NOTEST	0	0	0	0	1	1
ENSG00000234406	ENSG00000234406	AC004129.7	7:25225241-25228343	NOTEST	0	0	0	0	1	1
ENSG00000234407	ENSG00000234407	FAM74A6	9:41516045-41523018	NOTEST	0	0	0	0	1	1
ENSG00000234409	ENSG00000234409	AC006547.14	22:20135949-20138399	NOTEST	0.0916138	0.101519	0.148119	0	1	1
ENSG00000234411	ENSG00000234411	HCG14	HSCHR6_MHC_APD:28864310-28865103	NOTEST	0	0	0	0	1	1
ENSG00000234413	ENSG00000234413	RP6-29D12.2	X:53370191-53370711	NOTEST	0	0	0	0	1	1
ENSG00000234414	ENSG00000234414	RBMY1A1	Y:23673223-23711212	NOTEST	0	0	0	0	1	1
ENSG00000234415	ENSG00000234415	RPL5P7	2:174736380-174737193	NOTEST	0	0	0	0	1	1
ENSG00000234416	ENSG00000234416	SNX18P4	9:43062928-43063757	NOTEST	0.105262	0.100849	-0.0617897	0	1	1
ENSG00000234417	ENSG00000234417	HCG19P	HSCHR6_MHC_COX:30316859-30317493	NOTEST	0	0	0	0	1	1
ENSG00000234418	ENSG00000234418	RP11-560I19.1	7:121856400-121858491	NOTEST	0.0493392	0	#NAME?	0	1	1
ENSG00000234419	ENSG00000234419	CICP13	1:222641435-222644224	NOTEST	0.555724	0.312938	-0.82849	0	1	1
ENSG00000234421	ENSG00000234421	SLC25A5P4	13:57888872-57890043	NOTEST	0	0	0	0	1	1
ENSG00000234422	ENSG00000234422	UBE2WP1	1:96884149-96884489	NOTEST	0	0	0	0	1	1
ENSG00000234423	ENSG00000234423	AC019118.2	2:2898819-3129798	NOTEST	0	0	0	0	1	1
ENSG00000234424	ENSG00000234424	RP11-213G2.1	9:88368220-88408395	NOTEST	0.0747229	0	#NAME?	0	1	1
ENSG00000234425	ENSG00000234425	RP11-528G1.2	1:160506862-160549306	NOTEST	0	0	0	0	1	1
ENSG00000234426	ENSG00000234426	RP11-459O1.2	6:89008668-89130752	NOTEST	0	0.0855868	inf	0	1	1
ENSG00000234427	ENSG00000234427	RP3-413H6.2	6:11810834-11811481	NOTEST	0	0	0	0	1	1
ENSG00000234428	ENSG00000234428	RP11-666F17.1	12:26272958-26986131	NOTEST	0.0210683	0.0464643	1.14105	0	1	1
ENSG00000234429	ENSG00000234429	AC105342.1	2:81421460-81428308	NOTEST	0	0	0	0	1	1
ENSG00000234430	ENSG00000234430	SNX18P6	9:66394411-66395279	NOTEST	0	0	0	0	1	1
ENSG00000234431	ENSG00000234431	AC007283.5	2:201980826-202041410	NOTEST	0.326454	0.270582	-0.270814	0	1	1
ENSG00000234432	ENSG00000234432	RP11-1275H24.1	7:5465400-5469303	NOTEST	0.00599798	0	#NAME?	0	1	1
ENSG00000234433	ENSG00000234433	VWA7	HSCHR6_MHC_SSTO:31723321-31735062	NOTEST	0	0	0	0	1	1
ENSG00000234435	ENSG00000234435	RP11-125P18.1	20:22034830-22055238	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000234436	ENSG00000234436	AC008984.7	19:54813046-54817309	NOTEST	0	0	0	0	1	1
ENSG00000234437	ENSG00000234437	RP1-206D15.3	1:169337207-169429907	NOTEST	0	0	0	0	1	1
ENSG00000234438	ENSG00000234438	KBTBD13	15:65369153-65372276	NOTEST	0	0	0	0	1	1
ENSG00000234439	ENSG00000234439	KRT18P2	21:21797260-21798518	NOTEST	0	0	0	0	1	1
ENSG00000234441	ENSG00000234441	RP5-1108M17.5	1:104210692-104210890	NOTEST	0	0	0	0	1	1
ENSG00000234442	ENSG00000234442	BX276092.3	X:70981814-70982283	NOTEST	0	0	0	0	1	1
ENSG00000234443	ENSG00000234443	LY6G6D	HSCHR6_MHC_DBB:31656814-31667868	NOTEST	0	0	0	0	1	1
ENSG00000234444	ENSG00000234444	ZNF736	7:63767836-63815238	NOTEST	0.152236	0.0857904	-0.827426	0	1	1
ENSG00000234445	ENSG00000234445	FGF14-AS1	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000234446	ENSG00000234446	AC068489.1	2:222502262-222506533	NOTEST	0	0	0	0	1	1
ENSG00000234448	ENSG00000234448	RP11-344N17.13	X:48231337-48231528	NOTEST	0	0	0	0	1	1
ENSG00000234449	ENSG00000234449	RP11-706O15.3	X:3771050-3800358	NOTEST	0	0.00525878	inf	0	1	1
ENSG00000234450	ENSG00000234450	AC005534.6	7:156264889-156685924	NOTEST	0	0.207181	inf	0	1	1
ENSG00000234451	ENSG00000234451	RP11-211N8.6	9:46921025-46922100	NOTEST	0	0	0	0	1	1
ENSG00000234452	ENSG00000234452	RP11-168O10.6	10:91190050-91316398	NOTEST	0	0	0	0	1	1
ENSG00000234453	ENSG00000234453	RP11-488L4.1	1:234040678-234460262	NOTEST	0	0	0	0	1	1
ENSG00000234454	ENSG00000234454	RP1-14D6.2	X:151851486-151852303	NOTEST	0	0	0	0	1	1
ENSG00000234455	ENSG00000234455	AC067960.1	2:121839012-121846302	NOTEST	0	0	0	0	1	1
ENSG00000234457	ENSG00000234457	AC006960.5	7:36345239-36345513	NOTEST	0	0	0	0	1	1
ENSG00000234458	ENSG00000234458	OR7E130P	3:125422192-125423156	NOTEST	0	0	0	0	1	1
ENSG00000234459	ENSG00000234459	AC002064.4	7:89874487-89940377	NOTEST	0	0	0	0	1	1
ENSG00000234460	ENSG00000234460	XXyac-YM21GA2.4	9:90479080-90481205	NOTEST	0	0	0	0	1	1
ENSG00000234461	ENSG00000234461	XXbac-BPG118E17.9	HSCHR6_MHC_DBB:30988742-30993542	NOTEST	0	0	0	0	1	1
ENSG00000234463	ENSG00000234463	COX6CP12	X:67865167-67865369	NOTEST	0	0	0	0	1	1
ENSG00000234464	ENSG00000234464	RP11-136B18.2	1:238439336-238450316	NOTEST	0	0	0	0	1	1
ENSG00000234465	ENSG00000234465	PINLYP	19:44047191-44100287	NOTEST	0.135224	0.330868	1.29091	0	1	1
ENSG00000234466	ENSG00000234466	RP11-266I3.1	X:55081377-55082271	NOTEST	0	0	0	0	1	1
ENSG00000234467	ENSG00000234467	SLC25A1P2	7:62854126-62882424	NOTEST	0	0	0	0	1	1
ENSG00000234469	ENSG00000234469	AC002365.1	X:9935391-9936134	NOTEST	0	0.0223131	inf	0	1	1
ENSG00000234470	ENSG00000234470	DASS-23B5.2	HSCHR6_MHC_DBB:32469328-32469736	NOTEST	0	0	0	0	1	1
ENSG00000234471	ENSG00000234471	AC147651.1	7:523743-535755	NOTEST	0	0	0	0	1	1
ENSG00000234473	ENSG00000234473	ZNF101P2	1:192962578-192963807	NOTEST	0.0255425	0.0437381	0.775991	0	1	1
ENSG00000234474	ENSG00000234474	RP11-501J20.2	10:118918166-118928570	NOTEST	0	0	0	0	1	1
ENSG00000234475	ENSG00000234475	HSPA1A	HSCHR6_MHC_DBB:31765430-31767913	NOTEST	0	0	0	0	1	1
ENSG00000234477	ENSG00000234477	AC004231.2	17:39077681-39132178	NOTEST	0	0	0	0	1	1
ENSG00000234478	ENSG00000234478	RP11-275I14.4	1:226332379-226374431	NOTEST	0.179565	0.260008	0.534049	0	1	1
ENSG00000234479	ENSG00000234479	AP1B1P1	22:32517963-32529456	NOTEST	0	0	0	0	1	1
ENSG00000234480	ENSG00000234480	AC073869.8	2:132139412-132140070	NOTEST	0	0	0	0	1	1
ENSG00000234481	ENSG00000234481	RP4-614N24.1	1:37238740-37241369	NOTEST	0	0	0	0	1	1
ENSG00000234482	ENSG00000234482	RP11-433J22.2	1:147228331-147245484	NOTEST	0	0	0	0	1	1

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ENSG00000234485	ENSG00000234485	OR7E46P	2:71163011-71306935	NOTEST	0	0	0	0	1	1
ENSG00000234487	ENSG00000234487	HLA-F	HSCHR6_MHC_MCF:29687667-29690477	NOTEST	0	0	0	0	1	1
ENSG00000234488	ENSG00000234488	AC096664.1	2:63348517-64054977	NOTEST	0	0	0	0	1	1
ENSG00000234489	ENSG00000234489	ALDH7A1P4	10:64500967-64501145	NOTEST	0	0	0	0	1	1
ENSG00000234491	ENSG00000234491	HNRNPA1P51	2:207284015-207284962	NOTEST	0	0	0	0	1	1
ENSG00000234492	ENSG00000234492	RPL34-AS1	4:109459345-109541616	NOTEST	0.0851397	0.083181	-0.0335781	0	1	1
ENSG00000234493	ENSG00000234493	GS1-421I3.2	X:119144674-119149501	NOTEST	0	0.0720146	inf	0	1	1
ENSG00000234495	ENSG00000234495	TRIM27	HSCHR6_MHC_APD:28870782-28891771	NOTEST	0	0	0	0	1	1
ENSG00000234496	ENSG00000234496	MRPS21P1	1:65558074-65558297	NOTEST	0	0	0	0	1	1
ENSG00000234497	ENSG00000234497	RP4-612J11.1	1:75033794-75139422	NOTEST	0	0	0	0	1	1
ENSG00000234498	ENSG00000234498	RPL13AP20	12:13028432-13029044	NOTEST	0.0962495	0.368768	1.93786	0	1	1
ENSG00000234500	ENSG00000234500	GS1-124K5.10	7:65976542-66010053	NOTEST	0	0	0	0	1	1
ENSG00000234502	ENSG00000234502	FYTTD1P1	9:104121213-104145801	NOTEST	0	0	0	0	1	1
ENSG00000234503	ENSG00000234503	KB-1592A4.14	22:21522046-21546445	NOTEST	0	0	0	0	1	1
ENSG00000234504	ENSG00000234504	RP11-285G1.2	10:45306471-45491339	NOTEST	0	0	0	0	1	1
ENSG00000234506	ENSG00000234506	RP11-274B18.2	9:71155951-71259358	NOTEST	0	0	0	0	1	1
ENSG00000234507	ENSG00000234507	BRD2	HSCHR6_MHC_COX:32824725-32871622	NOTEST	0	0	0	0	1	1
ENSG00000234508	ENSG00000234508	GPSM3	HSCHR6_MHC_SSTO:32165410-32198715	NOTEST	0	0	0	0	1	1
ENSG00000234509	ENSG00000234509	AP000253.1	21:33025905-33031813	NOTEST	0.0274409	0.011192	-1.29386	0	1	1
ENSG00000234510	ENSG00000234510	HLA-DQB3	HSCHR6_MHC_MCF:32729152-32733261	NOTEST	0	0	0	0	1	1
ENSG00000234511	ENSG00000234511	C5orf58	5:169659450-169725231	NOTEST	0	0	0	0	1	1
ENSG00000234512	ENSG00000234512	TLR12P	1:33931849-33934555	NOTEST	0	0	0	0	1	1
ENSG00000234513	ENSG00000234513	AC073072.7	7:22813264-22813612	NOTEST	0.0834891	0	#NAME?	0	1	1
ENSG00000234514	ENSG00000234514	LST1	HSCHR6_MHC_MCF:31630206-31637066	NOTEST	0	0	0	0	1	1
ENSG00000234515	ENSG00000234515	PPP1R2P1	6:32846947-32847625	NOTEST	0.0332276	0.0258684	-0.361193	0	1	1
ENSG00000234519	ENSG00000234519	RP3-495K2.1	6:169467912-169469519	NOTEST	0	0	0	0	1	1
ENSG00000234520	ENSG00000234520	AC018464.3	7:112594700-112635689	NOTEST	0	0	0	0	1	1
ENSG00000234521	ENSG00000234521	AC005041.11	2:74640146-74640608	NOTEST	0	0	0	0	1	1
ENSG00000234522	ENSG00000234522	RP11-572P18.2	10:122194494-122199888	NOTEST	0	0	0	0	1	1
ENSG00000234523	ENSG00000234523	NDUFB1P2	1:222988363-223179337	NOTEST	0	0	0	0	1	1
ENSG00000234524	ENSG00000234524	RPL12P43	X:117280025-117280524	NOTEST	0	0	0	0	1	1
ENSG00000234527	ENSG00000234527	PCDH9-AS1	13:66876966-67804468	NOTEST	0	0	0	0	1	1
ENSG00000234528	ENSG00000234528	SUMO2P1	HSCHR6_MHC_QBL:29603760-29604044	NOTEST	0	0	0	0	1	1
ENSG00000234529	ENSG00000234529	GAPDHP19	Y:21489454-21490459	NOTEST	0	0	0	0	1	1
ENSG00000234530	ENSG00000234530	NFKBIL1	HSCHR6_MHC_COX:31502097-31514044	NOTEST	0	0	0	0	1	1
ENSG00000234531	ENSG00000234531	RP11-288G11.3	10:134351323-134598269	NOTEST	0	0	0	0	1	1
ENSG00000234534	ENSG00000234534	RP11-39K24.2	9:4985032-5128183	NOTEST	0	0	0	0	1	1
ENSG00000234536	ENSG00000234536	AC096582.7	7:45813193-45822756	NOTEST	0.199734	0.156972	-0.347576	0	1	1
ENSG00000234537	ENSG00000234537	RP11-100G15.7	9:94894679-94900911	NOTEST	0.128901	0.153374	0.250793	0	1	1
ENSG00000234538	ENSG00000234538	ZNF114P1	21:15211438-15211730	NOTEST	0	0	0	0	1	1
ENSG00000234539	ENSG00000234539	ATF6B	HSCHR6_MHC_COX:31954521-32044486	NOTEST	0	0	0	0	1	1
ENSG00000234540	ENSG00000234540	RP3-448I9.1	6:14394556-14404520	NOTEST	0	0	0	0	1	1
ENSG00000234541	ENSG00000234541	CHEK2P5	10:39006325-39012360	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000234542	ENSG00000234542	RP11-282I1.2	10:125333742-125343283	NOTEST	0	0	0	0	1	1
ENSG00000234544	ENSG00000234544	PTGES3P5	10:110055856-110056290	NOTEST	0	0	0	0	1	1
ENSG00000234548	ENSG00000234548	RP11-78H24.1	3:186158133-186168485	NOTEST	0	0	0	0	1	1
ENSG00000234549	ENSG00000234549	ATAT1	HSCHR6_MHC_SSTO:30586039-30606022	NOTEST	0	0	0	0	1	1
ENSG00000234551	ENSG00000234551	RP11-123H22.1	13:104077549-104080035	NOTEST	0	0	0	0	1	1
ENSG00000234553	ENSG00000234553	AC022431.3	5:55807393-55902059	NOTEST	0.0406975	0	#NAME?	0	1	1
ENSG00000234556	ENSG00000234556	LINC00701	10:2347276-2357269	NOTEST	0	0	0	0	1	1
ENSG00000234557	ENSG00000234557	RP1-164F3.8	X:100673274-100788446	NOTEST	0	0	0	0	1	1
ENSG00000234559	ENSG00000234559	AC079776.4	2:130680434-130704276	NOTEST	0.0744145	0	#NAME?	0	1	1
ENSG00000234560	ENSG00000234560	OR10G8	11:123900296-123901341	NOTEST	0	0	0	0	1	1
ENSG00000234562	ENSG00000234562	TPMTP2	3:42055293-42267381	NOTEST	0	0	0	0	1	1
ENSG00000234564	ENSG00000234564	HSPA8P20	X:123093082-124097666	NOTEST	0	0	0	0	1	1
ENSG00000234565	ENSG00000234565	COX6B1P1	7:148751052-148751265	NOTEST	0	0	0	0	1	1
ENSG00000234566	ENSG00000234566	RPL7AP71	X:54219255-54385075	NOTEST	0	0	0	0	1	1
ENSG00000234567	ENSG00000234567	RP1-283K11.2	6:133561735-134216691	NOTEST	0	0	0	0	1	1
ENSG00000234568	ENSG00000234568	BIN2P1	4:83196223-83197753	NOTEST	0	0	0	0	1	1
ENSG00000234569	ENSG00000234569	RAD1P1	10:121380579-121381392	NOTEST	0	0	0	0	1	1
ENSG00000234570	ENSG00000234570	ZFRP1	X:62098280-62104312	NOTEST	0	0	0	0	1	1
ENSG00000234571	ENSG00000234571	RP5-998N21.4	1:149369293-149429348	NOTEST	0	0	0	0	1	1
ENSG00000234572	ENSG00000234572	AC007880.1	2:65073263-65090760	NOTEST	0	0	0	0	1	1
ENSG00000234573	ENSG00000234573	RP5-1116H23.1	20:4994165-4994370	NOTEST	0	0	0	0	1	1
ENSG00000234574	ENSG00000234574	PAIP1P1	HSCHR6_MHC_MCF:30230671-30259555	NOTEST	0	0	0	0	1	1
ENSG00000234575	ENSG00000234575	CTSLP8	9:90459066-90462229	NOTEST	0	0	0	0	1	1
ENSG00000234576	ENSG00000234576	MTND1P26	2:132143272-132143810	NOTEST	0	0	0	0	1	1
ENSG00000234577	ENSG00000234577	SYNE1-AS1	6:151977825-152958936	NOTEST	0.332691	0.47793	0.522618	0	1	1
ENSG00000234578	ENSG00000234578	RP4-784A16.1	1:53711216-53793742	NOTEST	0.0209377	0.122421	2.54768	0	1	1
ENSG00000234579	ENSG00000234579	AC009305.1	2:31133332-31378068	NOTEST	0	0	0	0	1	1
ENSG00000234580	ENSG00000234580	RP11-733D4.1	10:45086655-45097552	NOTEST	0	0	0	0	1	1
ENSG00000234583	ENSG00000234583	TSPY19P	Y:6171997-6173115	NOTEST	0	0	0	0	1	1
ENSG00000234584	ENSG00000234584	AC019186.1	2:158582219-158592517	NOTEST	0.272311	0.463377	0.766929	0	1	1
ENSG00000234586	ENSG00000234586	RP11-382H24.2	9:13021692-13022891	NOTEST	0	0	0	0	1	1
ENSG00000234587	ENSG00000234587	MRPL50P1	2:35949824-35950208	NOTEST	0	0	0	0	1	1
ENSG00000234588	ENSG00000234588	FABP5P14	2:217536827-217858802	NOTEST	0	0	0	0	1	1
ENSG00000234589	ENSG00000234589	RP11-253E3.1	12:3180697-3181314	NOTEST	0	0	0	0	1	1
ENSG00000234590	ENSG00000234590	GNG5P5	13:47881216-47881436	NOTEST	0	0	0	0	1	1
ENSG00000234592	ENSG00000234592	RP11-41L14.1	X:128175512-128177160	NOTEST	0	0	0	0	1	1
ENSG00000234593	ENSG00000234593	RP4-704D23.1	1:14675449-14677518	NOTEST	0	0	0	0	1	1
ENSG00000234594	ENSG00000234594	RP11-263C16.2	3:171252211-171252404	NOTEST	0	0	0	0	1	1
ENSG00000234595	ENSG00000234595	AC013733.3	2:182547839-182550434	NOTEST	0	0	0	0	1	1
ENSG00000234597	ENSG00000234597	AC010096.1	2:19657980-19668722	NOTEST	0	0	0	0	1	1
ENSG00000234599	ENSG00000234599	HCG9	HSCHR6_MHC_MCF:30021352-30024652	NOTEST	0	0	0	0	1	1
ENSG00000234601	ENSG00000234601	CHRM3-AS1	1:239549864-240080255	NOTEST	0	0	0	0	1	1

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ENSG00000234605	ENSG00000234605	PSORS1C2	HSCHR6_MHC_MANN:31127486-31152786	NOTEST	0	0	0	0	1	1
ENSG00000234607	ENSG00000234607	RP11-5P18.1	1:16268363-16302627	NOTEST	0	0	0	0	1	1
ENSG00000234610	ENSG00000234610	LINC00624	1:146986157-146989699	NOTEST	0	0	0	0	1	1
ENSG00000234611	ENSG00000234611	OR2AT2P	11:74782192-74783097	NOTEST	0	0	0	0	1	1
ENSG00000234612	ENSG00000234612	H2AFZP5	10:79713252-79713634	NOTEST	0	0	0	0	1	1
ENSG00000234613	ENSG00000234613	RP5-1158E12.	X:45772552-45776475	NOTEST	0	0	0	0	1	1
ENSG00000234614	ENSG00000234614	AL450992.2	1:151814352-151826173	NOTEST	0.558141	0.438379	-0.348453	0	1	1
ENSG00000234617	ENSG00000234617	SNRK-AS1	3:43328003-43775863	NOTEST	0.108048	0	#NAME?	0	1	1
ENSG00000234618	ENSG00000234618	RPSAP9	9:79013614-79014502	NOTEST	0.220783	0.491906	1.15575	0	1	1
ENSG00000234619	ENSG00000234619	RPL7P11	1:8412456-8877702	NOTEST	0	0.0674659	inf	0	1	1
ENSG00000234620	ENSG00000234620	HDHD1P1	Y:17460541-17567954	NOTEST	0	0	0	0	1	1
ENSG00000234622	ENSG00000234622	RP13-297E16.5	X:1886239-1887669	NOTEST	0	0	0	0	1	1
ENSG00000234623	ENSG00000234623	MOG	HSCHR6_MHC_DBB:29624713-29640106	NOTEST	0	0	0	0	1	1
ENSG00000234624	ENSG00000234624	AC016894.1	2:61404552-61697904	NOTEST	0	0	0	0	1	1
ENSG00000234625	ENSG00000234625	LINC00380	13:91739507-91741847	NOTEST	0	0	0	0	1	1
ENSG00000234626	ENSG00000234626	RP1-149A16.12	22:32723157-32739092	NOTEST	0	0	0	0	1	1
ENSG00000234627	ENSG00000234627	NUS1P3	13:24902348-24903210	NOTEST	0	0	0	0	1	1
ENSG00000234629	ENSG00000234629	WDR82P1	3:94655929-94656868	NOTEST	0.0193397	0	#NAME?	0	1	1
ENSG00000234630	ENSG00000234630	LL22NC03-2H8.4	22:22648097-22649159	NOTEST	0	0.224556	inf	0	1	1
ENSG00000234631	ENSG00000234631	AL162407.1	10:115614419-115676953	NOTEST	0	0	0	0	1	1
ENSG00000234632	ENSG00000234632	NECAP1P2	2:74425688-74621009	NOTEST	0	0	0	0	1	1
ENSG00000234634	ENSG00000234634	AC003664.1	17:13202500-13210077	NOTEST	0	0	0	0	1	1
ENSG00000234637	ENSG00000234637	RPS19P6	9:83397252-83397685	NOTEST	0	0	0	0	1	1
ENSG00000234638	ENSG00000234638	AC053503.6	2:220283098-220291461	NOTEST	0	0	0	0	1	1
ENSG00000234639	ENSG00000234639	AC009263.2	7:137687069-137802732	NOTEST	0	0	0	0	1	1
ENSG00000234640	ENSG00000234640	RP11-264E18.1	10:130114545-130118478	NOTEST	0	0	0	0	1	1
ENSG00000234642	ENSG00000234642	PPP1R2P1	HSCHR6_MHC_APD:32792100-32831197	NOTEST	0	0	0	0	1	1
ENSG00000234643	ENSG00000234643	EIF3FP1	21:11169719-11184046	NOTEST	0.112387	0.0611021	-0.879177	0	1	1
ENSG00000234644	ENSG00000234644	RP11-360J12.1	9:78339137-78339491	NOTEST	0	0	0	0	1	1
ENSG00000234645	ENSG00000234645	YWHAEP5	2:139045598-139046363	NOTEST	0	0	0	0	1	1
ENSG00000234646	ENSG00000234646	RP4-753D10.3	20:23012178-23019873	NOTEST	0	0	0	0	1	1
ENSG00000234647	ENSG00000234647	RP11-503C24.4	6:168643617-168663261	NOTEST	0	0	0	0	1	1
ENSG00000234650	ENSG00000234650	PCCA-AS1	13:100741268-101182686	NOTEST	0	0	0	0	1	1
ENSG00000234651	ENSG00000234651	BAG6	HSCHR6_MHC_MCF:31683094-31702270	NOTEST	0	0	0	0	1	1
ENSG00000234652	ENSG00000234652	AGPAT5P1	Y:3161848-3162867	NOTEST	0	0	0	0	1	1
ENSG00000234653	ENSG00000234653	AC079117.1	2:76974844-77820445	NOTEST	0	0	0	0	1	1
ENSG00000234654	ENSG00000234654	RP11-782C8.8	1:143245822-143246210	NOTEST	0	0	0	0	1	1
ENSG00000234655	ENSG00000234655	OR7E155P	13:42013951-42015035	NOTEST	0	0	0	0	1	1
ENSG00000234658	ENSG00000234658	AC013429.4	7:138279029-138386097	NOTEST	0	0	0	0	1	1
ENSG00000234660	ENSG00000234660	LINC00440	13:89925456-89932494	NOTEST	0	0	0	0	1	1
ENSG00000234661	ENSG00000234661	CHL1-AS1	3:237440-451090	NOTEST	0.21359	0.243169	0.187119	0	1	1
ENSG00000234663	ENSG00000234663	AC104820.2	2:181831974-182264286	NOTEST	0.0185642	0.00652442	-1.5086	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000234665	ENSG00000234665	RP11-262H14.3	9:66513031-66555928	NOTEST	0	0.0768671	inf	0	1	1
ENSG00000234667	ENSG00000234667	ACTBP13	3:49910779-49915413	NOTEST	0	0	0	0	1	1
ENSG00000234668	ENSG00000234668	ATP6V1G2	HSCHR6_MHC_DBB:31478677-31496802	NOTEST	0	0	0	0	1	1
ENSG00000234669	ENSG00000234669	ZFP57	HSCHR6_MHC_SSTO:29639863-29658187	NOTEST	0	0	0	0	1	1
ENSG00000234670	ENSG00000234670	OR6C64P	12:55828520-55979255	NOTEST	0	0	0	0	1	1
ENSG00000234671	ENSG00000234671	RP11-1217F2.13	7:57264344-57265479	NOTEST	0	0	0	0	1	1
ENSG00000234673	ENSG00000234673	BRD2-IT1	HSCHR6_MHC_COX:32824725-32871622	NOTEST	0	0	0	0	1	1
ENSG00000234674	ENSG00000234674	TCF19	HSCHR6_MHC_SSTO:31120396-31132565	NOTEST	0	0	0	0	1	1
ENSG00000234675	ENSG00000234675	RP11-242F11.2	6:148338557-148342110	NOTEST	0	0	0	0	1	1
ENSG00000234676	ENSG00000234676	RP11-337A23.3	9:26904080-27062928	NOTEST	0	0	0	0	1	1
ENSG00000234677	ENSG00000234677	RP11-285A18.2	10:125465722-125699783	NOTEST	0	0	0	0	1	1
ENSG00000234678	ENSG00000234678	RP11-465N4.4	1:201951499-201986316	NOTEST	0.333363	0.115195	-1.53302	0	1	1
ENSG00000234680	ENSG00000234680	VN2R3P	9:39016965-39039591	NOTEST	0	0	0	0	1	1
ENSG00000234681	ENSG00000234681	HCG4P8	HSCHR6_MHC_COX:29788430-29792600	NOTEST	0	0	0	0	1	1
ENSG00000234682	ENSG00000234682	AC110620.2	2:135493033-135716912	NOTEST	0	0.0194413	inf	0	1	1
ENSG00000234683	ENSG00000234683	RP5-837I24.5	1:81771844-82458120	NOTEST	0	0	0	0	1	1
ENSG00000234685	ENSG00000234685	NUS1P2	13:23468794-23490662	NOTEST	0	0	0	0	1	1
ENSG00000234686	ENSG00000234686	AC010971.1	7:49269732-49294412	NOTEST	0	0	0	0	1	1
ENSG00000234688	ENSG00000234688	RP1-293L6.1	22:37099962-37117517	NOTEST	0	0	0	0	1	1
ENSG00000234689	ENSG00000234689	LINC00444	13:48479463-48481492	NOTEST	0.277692	0	#NAME?	0	1	1
ENSG00000234690	ENSG00000234690	AC073283.4	2:47419543-47572213	NOTEST	0	0.0259244	inf	0	1	1
ENSG00000234692	ENSG00000234692	RP11-445L6.3	9:117904096-118164923	NOTEST	0	0	0	0	1	1
ENSG00000234693	ENSG00000234693	RP4-530I15.6	20:49202644-49308065	NOTEST	0	0	0	0	1	1
ENSG00000234695	ENSG00000234695	AC002076.10	7:93220884-93540577	NOTEST	0	0	0	0	1	1
ENSG00000234696	ENSG00000234696	GPR50-AS1	X:150343663-150349937	NOTEST	0	0	0	0	1	1
ENSG00000234698	ENSG00000234698	RP11-112L6.2	20:48782898-48788279	NOTEST	0	0	0	0	1	1
ENSG00000234699	ENSG00000234699	RP11-225H22.4	10:105206542-105222452	NOTEST	0	0.0216236	inf	0	1	1
ENSG00000234700	ENSG00000234700	RP11-3N2.5	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000234701	ENSG00000234701	PRDX3P3	13:39191555-39192077	NOTEST	0	0	0	0	1	1
ENSG00000234702	ENSG00000234702	VDAC1P3	X:91034259-91878229	NOTEST	0.0799674	0	#NAME?	0	1	1
ENSG00000234703	ENSG00000234703	AF015262.2	21:36160097-37376965	NOTEST	0	0.0219341	inf	0	1	1
ENSG00000234704	ENSG00000234704	BRD2	HSCHR6_MHC_MANN:33056219-33103106	NOTEST	0	0	0	0	1	1
ENSG00000234705	ENSG00000234705	HMGA1P4	9:131425412-131425857	NOTEST	0	0	0	0	1	1
ENSG00000234706	ENSG00000234706	PRUNEP1	13:26688546-26796791	NOTEST	0	0	0	0	1	1
ENSG00000234707	ENSG00000234707	RP11-745C15.2	7:54819942-54872621	NOTEST	0	0	0	0	1	1
ENSG00000234709	ENSG00000234709	UPF3AP3	9:102741460-102861322	NOTEST	0.149034	0.2698	0.85625	0	1	1
ENSG00000234710	ENSG00000234710	AC060834.3	7:9776950-9809142	NOTEST	0	0	0	0	1	1
ENSG00000234711	ENSG00000234711	TUBB8P11	1:803450-812283	NOTEST	0.0472756	0	#NAME?	0	1	1
ENSG00000234712	ENSG00000234712	RP11-143G3.1	X:144314448-144315139	NOTEST	0	0	0	0	1	1
ENSG00000234713	ENSG00000234713	RP11-726G23.10	8:43131412-43131966	NOTEST	0	0	0	0	1	1
ENSG00000234714	ENSG00000234714	AC009965.2	2:204955179-204974572	NOTEST	0	0	0	0	1	1
ENSG00000234715	ENSG00000234715	CTB-107G13.1	7:102937868-103629963	NOTEST	0.0058469	0	#NAME?	0	1	1

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ENSG00000234717	ENSG00000234717	TMEM212-AS1	3:171561138-171656505	NOTEST	0	0	0	0	1	1
ENSG00000234718	ENSG00000234718	AC007161.5	7:7676148-8133902	NOTEST	0	0	0	0	1	1
ENSG00000234720	ENSG00000234720	ATP5A1P8	9:41799258-41800556	NOTEST	0	0	0	0	1	1
ENSG00000234721	ENSG00000234721	AC125421.1	17:71733992-71824659	NOTEST	0	0	0	0	1	1
ENSG00000234722	ENSG00000234722	AC073236.3	7:153097004-153111048	NOTEST	0.206938	0.271628	0.392432	0	1	1
ENSG00000234723	ENSG00000234723	AC092421.1	3:22711691-22712202	NOTEST	0	0	0	0	1	1
ENSG00000234724	ENSG00000234724	HDAC1P1	10:95753745-96122716	NOTEST	0	0	0	0	1	1
ENSG00000234725	ENSG00000234725	RP11-157L3.1	9:46121005-46121348	NOTEST	0	0	0	0	1	1
ENSG00000234726	ENSG00000234726	LL22NC03-123E1.5	22:22583114-22584865	NOTEST	0	0	0	0	1	1
ENSG00000234728	ENSG00000234728	C6orf48	HSCHR6_MHC_APD:31813741-31818898	NOTEST	0	0	0	0	1	1
ENSG00000234729	ENSG00000234729	AGER	HSCHR6_MHC_COX:32097221-32100578	NOTEST	0	0	0	0	1	1
ENSG00000234730	ENSG00000234730	AF241725.4	21:22939083-22987758	NOTEST	0	0	0	0	1	1
ENSG00000234731	ENSG00000234731	AC007163.11	2:202352147-202483901	NOTEST	0	0	0	0	1	1
ENSG00000234732	ENSG00000234732	RPEP5	2:162272604-162841792	NOTEST	0	0	0	0	1	1
ENSG00000234734	ENSG00000234734	SPATA31A7	9:65503362-65509610	NOTEST	0.00366227	0.00771006	1.07401	0	1	1
ENSG00000234735	ENSG00000234735	AL022237.3	22:43488172-43488530	NOTEST	0	0	0	0	1	1
ENSG00000234736	ENSG00000234736	FAM170B-AS1	10:50329883-50359592	NOTEST	0	0	0	0	1	1
ENSG00000234737	ENSG00000234737	KRT18P15	3:32280170-32411817	NOTEST	0	0	0	0	1	1
ENSG00000234743	ENSG00000234743	EIF5AP4	10:82006974-82007439	NOTEST	0.0505111	0	#NAME?	0	1	1
ENSG00000234744	ENSG00000234744	USP9YP26	Y:28148400-28155003	NOTEST	0	0	0	0	1	1
ENSG00000234746	ENSG00000234746	OR2J2	HSCHR6_MHC_QBL:29141322-29142363	NOTEST	0	0	0	0	1	1
ENSG00000234748	ENSG00000234748	RP11-183K14.1	X:145619052-145619566	NOTEST	0	0	0	0	1	1
ENSG00000234749	ENSG00000234749	FAM90A21P	8:7421319-7440175	NOTEST	0	0	0	0	1	1
ENSG00000234750	ENSG00000234750	CTD-2666L21.2	19:12305829-12405702	NOTEST	0.0620123	0.0528716	-0.230061	0	1	1
ENSG00000234751	ENSG00000234751	AP002381.2	11:72525352-72853306	NOTEST	0	0.0808221	inf	0	1	1
ENSG00000234752	ENSG00000234752	RP11-428L9.1	10:8939951-8956559	NOTEST	0	0	0	0	1	1
ENSG00000234753	ENSG00000234753	RP11-328M4.2	6:41462590-41570122	NOTEST	0.507916	0.224557	-1.17751	0	1	1
ENSG00000234754	ENSG00000234754	RP11-421L10.1	1:221503421-221509638	NOTEST	0.0742012	0.172054	1.21335	0	1	1
ENSG00000234756	ENSG00000234756	RP11-120C12.3	10:64049279-64063792	NOTEST	0	0	0	0	1	1
ENSG00000234757	ENSG00000234757	CA15P2	22:20486311-20488882	NOTEST	0	0	0	0	1	1
ENSG00000234758	ENSG00000234758	AC034228.4	5:131142682-131348892	NOTEST	0	0	0	0	1	1
ENSG00000234761	ENSG00000234761	RP11-38O14.5	1:202955684-202957710	NOTEST	0	0	0	0	1	1
ENSG00000234763	ENSG00000234763	RP11-203H2.2	6:8329887-8343254	NOTEST	0	3.96E-07	inf	0	1	1
ENSG00000234765	ENSG00000234765	ELL2P3	13:68863810-68865412	NOTEST	0	0	0	0	1	1
ENSG00000234766	ENSG00000234766	RP11-56H2.2	X:51244941-51253857	NOTEST	0	0	0	0	1	1
ENSG00000234767	ENSG00000234767	LINC01052	13:66440305-66452351	NOTEST	0	0	0	0	1	1
ENSG00000234768	ENSG00000234768	RP11-503C24.1	6:168595037-168605181	NOTEST	0	0	0	0	1	1
ENSG00000234770	ENSG00000234770	GULOP	8:27417790-27446590	NOTEST	0	0	0	0	1	1
ENSG00000234771	ENSG00000234771	RP11-395P17.3	9:130873449-130881013	NOTEST	0.112134	0.137007	0.289019	0	1	1
ENSG00000234772	ENSG00000234772	LINC00412	13:27810418-27810948	NOTEST	0.0596	0.042512	-0.487442	0	1	1
ENSG00000234773	ENSG00000234773	CTD-2666L21.1	19:12305829-12405702	NOTEST	0	0.0154845	inf	0	1	1

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ENSG00000234776	ENSG00000234776	C11orf94	11:45928084-45928833	NOTEST	0	0	0	0	1	1
ENSG00000234777	ENSG00000234777	RP11-125D12.2	6:159804562-159817475	NOTEST	0	0	0	0	1	1
ENSG00000234779	ENSG00000234779	RP11-62F24.2	9:16409500-16870841	NOTEST	0.108678	0.173974	0.678815	0	1	1
ENSG00000234780	ENSG00000234780	RP11-552E4.2	X:48056656-48058867	NOTEST	0	0	0	0	1	1
ENSG00000234781	ENSG00000234781	LINC01103	2:105049724-105137290	NOTEST	0	0	0	0	1	1
ENSG00000234782	ENSG00000234782	TPT1P9	9:120845141-120845660	NOTEST	0.0603185	0	#NAME?	0	1	1
ENSG00000234784	ENSG00000234784	RP11-182I10.1	1:65210777-65432187	NOTEST	0	0	0	0	1	1
ENSG00000234785	ENSG00000234785	EEF1GP5	X:114937130-114938440	NOTEST	0	0	0	0	1	1
ENSG00000234786	ENSG00000234786	HLA-W	HSCHR6_MHC_SSTO:29912853-29914819	NOTEST	0	0	0	0	1	1
ENSG00000234787	ENSG00000234787	LINC00458	13:54689923-54707001	NOTEST	0	0	0	0	1	1
ENSG00000234788	ENSG00000234788	HSPA8P3	10:26986587-27150016	NOTEST	0.0447343	0	#NAME?	0	1	1
ENSG00000234789	ENSG00000234789	RP11-483H20.4	9:132399170-132404444	NOTEST	0.302622	0.400481	0.404216	0	1	1
ENSG00000234790	ENSG00000234790	RP11-426L16.7	1:113290716-113291097	NOTEST	0	0	0	0	1	1
ENSG00000234791	ENSG00000234791	AC108448.3	11:3210775-3211159	NOTEST	0	0	0	0	1	1
ENSG00000234792	ENSG00000234792	RP11-552J9.6	X:52641705-52642573	NOTEST	0	0	0	0	1	1
ENSG00000234793	ENSG00000234793	AC114730.7	2:242673993-242708231	NOTEST	0.550701	0.135851	-2.01924	0	1	1
ENSG00000234794	ENSG00000234794	HLA-DRA	HSCHR6_MHC_SSTO:32413424-32418635	NOTEST	0	0	0	0	1	1
ENSG00000234795	ENSG00000234795	RFTN1P1	Y:7581025-7678724	NOTEST	0	0	0	0	1	1
ENSG00000234796	ENSG00000234796	AC113607.3	2:906611-916810	NOTEST	0	0	0	0	1	1
ENSG00000234798	ENSG00000234798	DXO	HSCHR6_MHC_SSTO:31929438-31941075	NOTEST	0	0	0	0	1	1
ENSG00000234799	ENSG00000234799	HLA-N	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000234800	ENSG00000234800	PCMTD1P3	7:23749785-23872132	NOTEST	0	0	0	0	1	1
ENSG00000234801	ENSG00000234801	MORF4	4:174537086-174538057	NOTEST	0	0	0	0	1	1
ENSG00000234803	ENSG00000234803	FAM197Y2	Y:9355207-9364506	NOTEST	0	0	0	0	1	1
ENSG00000234804	ENSG00000234804	OR2J1	HSCHR6_MHC_COX:29065390-29066329	NOTEST	0	0	0	0	1	1
ENSG00000234805	ENSG00000234805	AC090505.5	3:194429149-194502897	NOTEST	0.0429772	0.0278064	-0.628154	0	1	1
ENSG00000234806	ENSG00000234806	RP11-9E13.4	10:70173820-70231879	NOTEST	0	0	0	0	1	1
ENSG00000234807	ENSG00000234807	LINC01135	1:59250822-59365384	NOTEST	0.0328982	0	#NAME?	0	1	1
ENSG00000234809	ENSG00000234809	NRM	HSCHR6_MHC_MCF:30734311-30737685	NOTEST	0	0	0	0	1	1
ENSG00000234810	ENSG00000234810	RP11-466L17.1	1:56046709-56200675	NOTEST	0	0.022043	inf	0	1	1
ENSG00000234811	ENSG00000234811	RP11-241I20.5	10:32398788-32400717	NOTEST	0	0	0	0	1	1
ENSG00000234812	ENSG00000234812	RP11-146D12.6	9:42368302-42474239	NOTEST	0	0	0	0	1	1
ENSG00000234813	ENSG00000234813	RP11-288D15.1	10:19229429-19229882	NOTEST	0	0	0	0	1	1
ENSG00000234816	ENSG00000234816	U91328.2	6:26044216-26044585	NOTEST	0	0	0	0	1	1
ENSG00000234817	ENSG00000234817	RP3-400B16.1	6:4021500-4157619	NOTEST	0.060784	0.0885471	0.542754	0	1	1
ENSG00000234818	ENSG00000234818	AC092687.5	2:10710891-10830101	NOTEST	0	0	0	0	1	1
ENSG00000234819	ENSG00000234819	RP11-336N8.4	9:80834035-80834273	NOTEST	0	0	0	0	1	1
ENSG00000234821	ENSG00000234821	MRPS33P4	20:50827183-51266970	NOTEST	0	0	0	0	1	1
ENSG00000234825	ENSG00000234825	XRCC6P2	X:149399290-149401116	NOTEST	0.473416	0.460547	-0.0397617	0	1	1
ENSG00000234826	ENSG00000234826	AC003084.2	7:117638911-117644099	NOTEST	0	0.0438596	inf	0	1	1
ENSG00000234828	ENSG00000234828	RP11-526A4.1	4:150273168-150817385	NOTEST	0	0	0	0	1	1
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ENSG00000234831	ENSG00000234831	HCG4P5	HSCHR6_MHC_APD:29845528-29850151	NOTEST	0	0	0	0	1	1
ENSG00000234832	ENSG00000234832	RP3-322G13.7	20:23327577-23335414	NOTEST	0	0.167267	inf	0	1	1
ENSG00000234834	ENSG00000234834	HLA-DPB2	HSCHR6_MHC_QBL:33009285-33025634	NOTEST	0	0	0	0	1	1
ENSG00000234835	ENSG00000234835	PHBP13	13:35516423-36247159	NOTEST	0.0462902	0.0196473	-1.23638	0	1	1
ENSG00000234836	ENSG00000234836	AIF1	HSCHR6_MHC_DBB:31565138-31566976	NOTEST	0	0	0	0	1	1
ENSG00000234837	ENSG00000234837	AC073464.6	2:95416326-95417038	NOTEST	0	0	0	0	1	1
ENSG00000234838	ENSG00000234838	RP11-5P22.1	5:65867884-65868374	NOTEST	0	0	0	0	1	1
ENSG00000234839	ENSG00000234839	RPS26P30	7:20875049-21062767	NOTEST	0	0	0	0	1	1
ENSG00000234840	ENSG00000234840	RP11-399D6.2	9:22646198-22824212	NOTEST	0.0656491	0.0345744	-0.925071	0	1	1
ENSG00000234841	ENSG00000234841	RP11-119H12.4	4:113739264-114304896	NOTEST	0.0560906	0	#NAME?	0	1	1
ENSG00000234842	ENSG00000234842	AC007163.8	2:202352147-202483901	NOTEST	0.137458	0.129273	-0.0885709	0	1	1
ENSG00000234844	ENSG00000234844	CDC42P2	7:55705966-55706535	NOTEST	0	0	0	0	1	1
ENSG00000234846	ENSG00000234846	NEU1	HSCHR6_MHC_SSTO:31735248-31822599	NOTEST	0	0	0	0	1	1
ENSG00000234848	ENSG00000234848	CTD-3105H18.7	19:12490002-12750912	NOTEST	0	0	0	0	1	1
ENSG00000234849	ENSG00000234849	HLA-W	HSCHR6_MHC_DBB:29914323-29916298	NOTEST	0	0	0	0	1	1
ENSG00000234850	ENSG00000234850	MTND2P3	Y:8240281-8240751	NOTEST	0	0	0	0	1	1
ENSG00000234852	ENSG00000234852	ZBTB12	HSCHR6_MHC_DBB:31847748-31902052	NOTEST	0	0	0	0	1	1
ENSG00000234853	ENSG00000234853	NDUFA5P3	9:19383214-19383885	NOTEST	0	0	0	0	1	1
ENSG00000234854	ENSG00000234854	LINC00676	13:110380628-110382354	NOTEST	0	0	0	0	1	1
ENSG00000234855	ENSG00000234855	RP11-453E2.2	10:98757794-99052413	NOTEST	0	0	0	0	1	1
ENSG00000234856	ENSG00000234856	UBDP1	HSCHR6_MHC_MCF:29432157-29437368	NOTEST	0	0	0	0	1	1
ENSG00000234858	ENSG00000234858	LINC01149	HSCHR6_MHC_COX:31399873-31405174	NOTEST	0	0	0	0	1	1
ENSG00000234859	ENSG00000234859	AC003958.2	17:39558667-39581301	NOTEST	0	0	0	0	1	1
ENSG00000234860	ENSG00000234860	RP11-547C13.1	9:102293977-102299206	NOTEST	0	0	0	0	1	1
ENSG00000234861	ENSG00000234861	ATP5A1P6	9:44558937-44560285	NOTEST	0	0	0	0	1	1
ENSG00000234862	ENSG00000234862	RP5-1097P24.1	20:22201191-22203921	NOTEST	0	0	0	0	1	1
ENSG00000234863	ENSG00000234863	RP11-410C4.2	1:220628495-220628654	NOTEST	0	0	0	0	1	1
ENSG00000234864	ENSG00000234864	AL022344.5	10:43189818-43210023	NOTEST	0	0	0	0	1	1
ENSG00000234865	ENSG00000234865	CTD-2138O14.1	5:23951456-24178372	NOTEST	0	0	0	0	1	1
ENSG00000234871	ENSG00000234871	LINC01032	1:192906429-192917387	NOTEST	0	0	0	0	1	1
ENSG00000234872	ENSG00000234872	RP11-467I20.5	1:240817540-240817925	NOTEST	0	0	0	0	1	1
ENSG00000234876	ENSG00000234876	NOTCH4	HSCHR6_MHC_SSTO:32165410-32198715	NOTEST	0	0	0	0	1	1
ENSG00000234877	ENSG00000234877	AC092660.1	2:78825036-78826532	NOTEST	0	0	0	0	1	1
ENSG00000234878	ENSG00000234878	HSPE1P1	20:38561563-38561881	NOTEST	0	0	0	0	1	1
ENSG00000234880	ENSG00000234880	LINC00163	21:46409778-46414001	NOTEST	0.0273643	0.0352654	0.365959	0	1	1
ENSG00000234881	ENSG00000234881	PIGFP2	9:126118448-126692431	NOTEST	0	0	0	0	1	1
ENSG00000234883	ENSG00000234883	MIR155HG	21:26934220-26947480	NOTEST	0.15011	0.274495	0.870762	0	1	1
ENSG00000234884	ENSG00000234884	CTA-407F11.8	22:25957083-25960429	NOTEST	0.0560139	0.0377549	-0.569122	0	1	1
ENSG00000234886	ENSG00000234886	MTND5P26	X:102024088-102161086	NOTEST	0	0	0	0	1	1
ENSG00000234888	ENSG00000234888	OFD1P15Y	Y:28201925-28234640	NOTEST	0	0	0	0	1	1
ENSG00000234889	ENSG00000234889	RP13-130D24.1	X:97230875-97233639	NOTEST	0	0	0	0	1	1
ENSG00000234890	ENSG00000234890	HNRNPDLP2	2:159023161-159313265	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000234891	ENSG00000234891	RP1-288L1.5	22:35099116-35100876	NOTEST	0	0	0	0	1	1
ENSG00000234892	ENSG00000234892	Z82214.2	22:43593288-43739394	NOTEST	0	0	0	0	1	1
ENSG00000234893	ENSG00000234893	HCG18	HSCHR6_MHC_QBL:30191333-30304165	NOTEST	0	0	0	0	1	1
ENSG00000234894	ENSG00000234894	RP11-408E5.6	13:19725693-19726447	NOTEST	0	0	0	0	1	1
ENSG00000234895	ENSG00000234895	OR52X1P	11:6088102-6089016	NOTEST	0	0	0	0	1	1
ENSG00000234896	ENSG00000234896	OR7E62P	2:71163011-71306935	NOTEST	0	0	0	0	1	1
ENSG00000234898	ENSG00000234898	CHEK2P3	2:92145461-92151636	NOTEST	0	0	0	0	1	1
ENSG00000234899	ENSG00000234899	SOX9-AS1	17:70017991-70216859	NOTEST	0	0	0	0	1	1
ENSG00000234900	ENSG00000234900	RP1-278O22.2	20:10618331-10975572	NOTEST	0	0	0	0	1	1
ENSG00000234901	ENSG00000234901	MTND6P13	X:101263496-101264019	NOTEST	0	0	0	0	1	1
ENSG00000234902	ENSG00000234902	AC007879.2	2:208038357-208102599	NOTEST	0	0	0	0	1	1
ENSG00000234903	ENSG00000234903	AC133104.2	2:96134610-96135526	NOTEST	0	0	0	0	1	1
ENSG00000234904	ENSG00000234904	RPL13P	HSCHR6_MHC_MCF:28827409-28831132	NOTEST	0	0	0	0	1	1
ENSG00000234907	ENSG00000234907	RP11-415H23.4	9:135820931-135867083	NOTEST	0	0	0	0	1	1
ENSG00000234910	ENSG00000234910	IL6RP1	9:92843578-92844851	NOTEST	0	0	0	0	1	1
ENSG00000234911	ENSG00000234911	TEX21P	14:64812888-64846036	NOTEST	0.0341418	0.0594596	0.800372	0	1	1
ENSG00000234913	ENSG00000234913	XXbac-B476C20.13	22:18270414-18507325	NOTEST	0.282016	0.258008	-0.128359	0	1	1
ENSG00000234915	ENSG00000234915	RP11-384C4.7	1:212458878-212535200	NOTEST	0	0.166196	inf	0	1	1
ENSG00000234917	ENSG00000234917	RP5-994D16.3	1:43144405-43147325	NOTEST	0.0699058	0.129389	0.888233	0	1	1
ENSG00000234918	ENSG00000234918	RP11-20F24.2	10:37414784-37673039	NOTEST	0	0	0	0	1	1
ENSG00000234919	ENSG00000234919	AC064834.3	2:196434351-196437694	NOTEST	0	0	0	0	1	1
ENSG00000234920	ENSG00000234920	ATP6V1G2	HSCHR6_MHC_SSTO:31486440-31504572	NOTEST	0	0	0	0	1	1
ENSG00000234921	ENSG00000234921	RP11-85O21.5	9:126763948-126795580	NOTEST	0	0	0	0	1	1
ENSG00000234922	ENSG00000234922	TSEN15P3	7:25305542-25305909	NOTEST	0	0	0	0	1	1
ENSG00000234925	ENSG00000234925	RP11-254B13.3	12:69004618-69054372	NOTEST	0.189082	0.0380806	-2.31189	0	1	1
ENSG00000234927	ENSG00000234927	HMGN1P18	7:120628730-120937498	NOTEST	0.000453746	0	#NAME?	0	1	1
ENSG00000234928	ENSG00000234928	AP000344.3	22:23775750-23777258	NOTEST	0	0	0	0	1	1
ENSG00000234929	ENSG00000234929	AC018685.1	2:2645760-2660402	NOTEST	0	0	0	0	1	1
ENSG00000234931	ENSG00000234931	MARK2P15	10:85071383-85074231	NOTEST	0	0	0	0	1	1
ENSG00000234932	ENSG00000234932	AC009969.1	2:153707166-153707338	NOTEST	0	0	0	0	1	1
ENSG00000234933	ENSG00000234933	CDC42P1	20:32951040-33099198	NOTEST	0	0	0	0	1	1
ENSG00000234934	ENSG00000234934	MTND5P29	2:131037871-131040179	NOTEST	0	0	0	0	1	1
ENSG00000234936	ENSG00000234936	AC010883.5	2:43393799-43823185	NOTEST	0.259031	0.209158	-0.308533	0	1	1
ENSG00000234937	ENSG00000234937	RP11-101O6.2	1:155579566-155829191	NOTEST	0	0.0615607	inf	0	1	1
ENSG00000234938	ENSG00000234938	AC012668.1	2:216395169-216708445	NOTEST	0	0	0	0	1	1
ENSG00000234939	ENSG00000234939	MTND2P18	2:132142033-132143063	NOTEST	0	0	0	0	1	1
ENSG00000234940	ENSG00000234940	AC023128.1	2:145425533-145940216	NOTEST	0	0	0	0	1	1
ENSG00000234941	ENSG00000234941	RP11-508N22.11	10:38536849-38622083	NOTEST	0	0	0	0	1	1
ENSG00000234942	ENSG00000234942	RP11-93H12.2	10:87359311-88126250	NOTEST	0	0	0	0	1	1
ENSG00000234943	ENSG00000234943	AC092839.4	2:54683421-54896812	NOTEST	0	0	0	0	1	1
ENSG00000234944	ENSG00000234944	RP11-124O11.1	10:43366968-43369508	NOTEST	0	0	0	0	1	1
ENSG00000234945	ENSG00000234945	AC109828.1	2:27548715-27593353	NOTEST	0.209475	0.439648	1.06957	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000234946	ENSG00000234946	SDHCP3	2:24150154-24227779	NOTEST	0	0	0	0	1	1
ENSG00000234947	ENSG00000234947	STK19	HSCHR6_MHC_COX:31925138-31936775	NOTEST	0	0	0	0	1	1
ENSG00000234948	ENSG00000234948	RP4-723E3.1	20:50827183-51266970	NOTEST	0.0258779	0	#NAME?	0	1	1
ENSG00000234950	ENSG00000234950	RBMY2OP	Y:9789161-9797032	NOTEST	0	0	0	0	1	1
ENSG00000234951	ENSG00000234951	SAPCD1	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000234952	ENSG00000234952	RP11-328K15.1	10:119494823-119495918	NOTEST	0	0	0	0	1	1
ENSG00000234953	ENSG00000234953	RP5-837I24.2	1:81771844-82458120	NOTEST	0	0	0	0	1	1
ENSG00000234954	ENSG00000234954	MAS1L	HSCHR6_MHC_APD:29454554-29455819	NOTEST	0	0	0	0	1	1
ENSG00000234956	ENSG00000234956	RP11-356I2.1	6:138051306-138060120	NOTEST	0	0	0	0	1	1
ENSG00000234958	ENSG00000234958	FABP5P13	X:484509-484837	NOTEST	0	0	0	0	1	1
ENSG00000234962	ENSG00000234962	LINC00700	10:2047666-2056542	NOTEST	0	0	0	0	1	1
ENSG00000234965	ENSG00000234965	SHISA8	22:42307296-42310570	NOTEST	0	0.104864	inf	0	1	1
ENSG00000234966	ENSG00000234966	XXbac-BPG308K3.6	HSCHR6_MHC_MCF:28827409-28831132	NOTEST	0	0	0	0	1	1
ENSG00000234967	ENSG00000234967	RP11-347D21.1	20:46579542-46580799	NOTEST	0	0	0	0	1	1
ENSG00000234968	ENSG00000234968	HLA-DQB3	HSCHR6_MHC_SSTO:32789344-32790282	NOTEST	0	0	0	0	1	1
ENSG00000234969	ENSG00000234969	RP13-33H18.1	X:73164158-73513409	NOTEST	0.0267466	0.0114179	-1.22805	0	1	1
ENSG00000234970	ENSG00000234970	MCCD1P2	HSCHR6_MHC_QBL:29951634-29952512	NOTEST	0	0	0	0	1	1
ENSG00000234972	ENSG00000234972	TBC1D3C	17:34580901-34808104	NOTEST	0.232559	0.326254	0.488397	0	1	1
ENSG00000234973	ENSG00000234973	RP11-272J7.4	10:44273009-44274273	NOTEST	0	0	0	0	1	1
ENSG00000234977	ENSG00000234977	AC074389.7	7:1727754-1787590	NOTEST	0	0	0	0	1	1
ENSG00000234979	ENSG00000234979	CITF22-24E5.1	22:37196727-37215780	NOTEST	0	0	0	0	1	1
ENSG00000234980	ENSG00000234980	WASF5P	HSCHR6_MHC_MANN:31298729-31300181	NOTEST	0	0	0	0	1	1
ENSG00000234981	ENSG00000234981	RP11-534L20.4	1:206680878-206785904	NOTEST	0.0239233	0	#NAME?	0	1	1
ENSG00000234982	ENSG00000234982	RP11-280O24.3	9:14081841-14398982	NOTEST	0	0	0	0	1	1
ENSG00000234983	ENSG00000234983	AC010132.11	7:42948324-42988557	NOTEST	0	0.208137	inf	0	1	1
ENSG00000234984	ENSG00000234984	FMO10P	1:166635121-166651433	NOTEST	0	0	0	0	1	1
ENSG00000234985	ENSG00000234985	RP11-3L10.3	7:121080887-121081315	NOTEST	0	0	0	0	1	1
ENSG00000234986	ENSG00000234986	XX-C2158C12.1	6:171004400-171006038	NOTEST	0	0	0	0	1	1
ENSG00000234988	ENSG00000234988	AC068538.4	2:101223489-101225820	NOTEST	0	0	0	0	1	1
ENSG00000234992	ENSG00000234992	GPR53P	HSCHR6_MHC_SSTO:29505159-29506243	NOTEST	0	0	0	0	1	1
ENSG00000234993	ENSG00000234993	CUBNP2	10:45727473-45742809	NOTEST	0	0	0	0	1	1
ENSG00000234995	ENSG00000234995	AC013429.5	7:138145078-138274738	NOTEST	0	0	0	0	1	1
ENSG00000234997	ENSG00000234997	AC016745.3	2:114182071-114182901	NOTEST	0	0.106565	inf	0	1	1
ENSG00000234998	ENSG00000234998	RP11-439A17.10	1:120906027-120935937	NOTEST	0	0	0	0	1	1
ENSG00000234999	ENSG00000234999	AC004016.2	7:24836157-25021253	NOTEST	0	0	0	0	1	1
ENSG00000235002	ENSG00000235002	RP11-157D18.2	1:42846465-42888249	NOTEST	0	0.146881	inf	0	1	1
ENSG00000235003	ENSG00000235003	RP11-459O16.7	9:66396885-66397113	NOTEST	0	0	0	0	1	1
ENSG00000235004	ENSG00000235004	USP9YP30	Y:27869162-27870333	NOTEST	0	0	0	0	1	1
ENSG00000235005	ENSG00000235005	RP11-195M16.1	1:110426797-110428886	NOTEST	0	0	0	0	1	1
ENSG00000235007	ENSG00000235007	RP11-344B5.4	9:132020632-132023860	NOTEST	0	0	0	0	1	1
ENSG00000235008	ENSG00000235008	RP3-497J21.1	6:166822851-167370679	NOTEST	0.00943479	0.00732802	-0.364567	0	1	1
ENSG00000235009	ENSG00000235009	AC093822.1	2:38633860-38742882	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235010	ENSG00000235010	RP11-140A10.3	10:133918174-133999466	NOTEST	0.137394	0	#NAME?	0	1	1
ENSG00000235011	ENSG00000235011	RP4-726F1.1	1:79789453-79790548	NOTEST	0	0	0	0	1	1
ENSG00000235012	ENSG00000235012	AF121897.4	21:40897509-40901782	NOTEST	0	0	0	0	1	1
ENSG00000235013	ENSG00000235013	COX20P2	2:231772032-231825781	NOTEST	0	0.0567098	inf	0	1	1
ENSG00000235014	ENSG00000235014	REREP2Y	Y:28344477-28354295	NOTEST	0	0	0	0	1	1
ENSG00000235015	ENSG00000235015	RP11-216N14.1	1:153689778-153690823	NOTEST	0	0	0	0	1	1
ENSG00000235016	ENSG00000235016	RP11-493K19.3	3:49977439-50226508	NOTEST	0.238994	0.549498	1.20114	0	1	1
ENSG00000235017	ENSG00000235017	C2	HSCHR6_MHC_COX:31853113-31907413	NOTEST	0	0	0	0	1	1
ENSG00000235018	ENSG00000235018	RP11-11M20.2	20:60528524-60640866	NOTEST	0.0416102	0	#NAME?	0	1	1
ENSG00000235020	ENSG00000235020	RP11-109I13.2	10:18429605-18948214	NOTEST	0	0	0	0	1	1
ENSG00000235021	ENSG00000235021	RP11-439E19.7	1:246853348-246855123	NOTEST	0	0	0	0	1	1
ENSG00000235022	ENSG00000235022	RNF39	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000235023	ENSG00000235023	AP001626.2	21:44068380-44071354	NOTEST	0	0.00430016	inf	0	1	1
ENSG00000235024	ENSG00000235024	AC097468.7	2:219809350-219826876	NOTEST	0	0	0	0	1	1
ENSG00000235025	ENSG00000235025	TRIM10	HSCHR6_MHC_MANN:30164889-30173878	NOTEST	0	0	0	0	1	1
ENSG00000235026	ENSG00000235026	DPP10-AS1	2:115199875-116603328	NOTEST	0	0	0	0	1	1
ENSG00000235028	ENSG00000235028	HMGN1P30	18:55686020-55686293	NOTEST	0	0	0	0	1	1
ENSG00000235029	ENSG00000235029	MNX1-AS2	7:156786744-156803345	NOTEST	0	0	0	0	1	1
ENSG00000235030	ENSG00000235030	IER3	HSCHR6_MHC_SSTO:30702434-30703790	NOTEST	0	0	0	0	1	1
ENSG00000235032	ENSG00000235032	RP4-813D12.2	20:55743803-55841685	NOTEST	0	0	0	0	1	1
ENSG00000235035	ENSG00000235035	AC007395.3	2:70834749-70995357	NOTEST	0	0	0	0	1	1
ENSG00000235036	ENSG00000235036	RP5-1099D15.1	20:10415950-10617477	NOTEST	0.337023	0.148606	-1.18136	0	1	1
ENSG00000235037	ENSG00000235037	RP11-187C18.5	9:45393844-45415976	NOTEST	0	0	0	0	1	1
ENSG00000235038	ENSG00000235038	RP11-393I23.4	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000235039	ENSG00000235039	MTND6P12	X:5086958-5087480	NOTEST	0	0	0	0	1	1
ENSG00000235040	ENSG00000235040	MTCO3P1	6:32673900-32674732	NOTEST	0	0	0	0	1	1
ENSG00000235042	ENSG00000235042	AC098820.2	2:217250010-217443903	NOTEST	0	0.0305109	inf	0	1	1
ENSG00000235044	ENSG00000235044	PPIAP3	20:36158440-36158945	NOTEST	0	0	0	0	1	1
ENSG00000235045	ENSG00000235045	RPL7P8	1:110193991-110194721	NOTEST	0	0.0586998	inf	0	1	1
ENSG00000235047	ENSG00000235047	AC016751.3	2:176762063-176768960	NOTEST	0	0	0	0	1	1
ENSG00000235049	ENSG00000235049	LINC00940	12:2038367-2045740	NOTEST	0.0902241	0.0414377	-1.12257	0	1	1
ENSG00000235050	ENSG00000235050	MLIP-AS1	6:53794779-54131078	NOTEST	0	0	0	0	1	1
ENSG00000235051	ENSG00000235051	RP11-637O19.2	6:10747991-10979553	NOTEST	0	0	0	0	1	1
ENSG00000235052	ENSG00000235052	RP1-150O5.3	1:23875629-23877406	NOTEST	0	0.0406243	inf	0	1	1
ENSG00000235054	ENSG00000235054	RP5-1166F10.1	1:4472110-4484747	NOTEST	0	0	0	0	1	1
ENSG00000235055	ENSG00000235055	RP4-609E1.2	1:68167148-68698803	NOTEST	0	0	0	0	1	1
ENSG00000235056	ENSG00000235056	AC010983.1	2:195868434-195891094	NOTEST	0	0.0122105	inf	0	1	1
ENSG00000235058	ENSG00000235058	ZMYND10-AS1	3:50378536-50384283	NOTEST	0	0	0	0	1	1
ENSG00000235059	ENSG00000235059	AC008175.1	Y:24585086-24631739	NOTEST	0	0	0	0	1	1
ENSG00000235060	ENSG00000235060	VDAC1P4	1:180199420-180472089	NOTEST	0	0	0	0	1	1
ENSG00000235061	ENSG00000235061	UBE2V1P7	X:77809908-77810248	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235062	ENSG00000235062	BCRP5	22:21044216-21053226	NOTEST	0	0	0	0	1	1
ENSG00000235064	ENSG00000235064	SLC25A5P2	2:33931952-34522820	NOTEST	0.0374177	0.0652844	0.803016	0	1	1
ENSG00000235066	ENSG00000235066	AC009303.1	2:118617002-118771709	NOTEST	0	0.0737463	inf	0	1	1
ENSG00000235067	ENSG00000235067	TUBB	HSCHR6_MHC_DBB:30678238-30683464	NOTEST	0	0	0	0	1	1
ENSG00000235068	ENSG00000235068	POU5F1	HSCHR6_MHC_MCF:31204888-31232984	NOTEST	0	0	0	0	1	1
ENSG00000235069	ENSG00000235069	RP4-785J1.1	1:26973937-26974172	NOTEST	0	0	0	0	1	1
ENSG00000235070	ENSG00000235070	AC068138.1	2:227044759-227050087	NOTEST	0	0.0448089	inf	0	1	1
ENSG00000235071	ENSG00000235071	RP11-759L5.2	X:16492464-16493463	NOTEST	0	0	0	0	1	1
ENSG00000235072	ENSG00000235072	AC012074.2	2:25592041-25598714	NOTEST	0.0598389	0.0426852	-0.487347	0	1	1
ENSG00000235073	ENSG00000235073	RBM22P10	X:52270114-52270985	NOTEST	0	0	0	0	1	1
ENSG00000235074	ENSG00000235074	DASS-397D15.5	HSCHR6_MHC_MCF:32559778-32559874	NOTEST	0	0	0	0	1	1
ENSG00000235076	ENSG00000235076	GAPDHP52	13:21932511-21933453	NOTEST	0.0385289	0.0149814	-1.36277	0	1	1
ENSG00000235077	ENSG00000235077	AC073842.19	7:99728586-99738305	NOTEST	0	0	0	0	1	1
ENSG00000235078	ENSG00000235078	AC142528.1	2:3500726-3526968	NOTEST	0.0739777	0.0929644	0.329588	0	1	1
ENSG00000235079	ENSG00000235079	ZRANB2-AS1	1:71514537-71546980	NOTEST	0	0.025588	inf	0	1	1
ENSG00000235080	ENSG00000235080	MTND5P23	2:132127993-132129648	NOTEST	0	0	0	0	1	1
ENSG00000235081	ENSG00000235081	AC010492.2	19:54704609-54752862	NOTEST	0	0.044912	inf	0	1	1
ENSG00000235083	ENSG00000235083	RP11-669M2.2	1:188640483-188640890	NOTEST	0	0.044878	inf	0	1	1
ENSG00000235084	ENSG00000235084	CHCHD2P6	1:15931076-15931538	NOTEST	0.215148	0.290623	0.433822	0	1	1
ENSG00000235085	ENSG00000235085	AC091153.4	17:4574678-4608824	NOTEST	0	0	0	0	1	1
ENSG00000235086	ENSG00000235086	FNDC1-IT1	6:159586940-159693141	NOTEST	0	0	0	0	1	1
ENSG00000235088	ENSG00000235088	RP4-620E11.4	20:40030740-40247133	NOTEST	0	0	0	0	1	1
ENSG00000235089	ENSG00000235089	RP3-445O10.1	1:81674252-81674895	NOTEST	0	0	0	0	1	1
ENSG00000235090	ENSG00000235090	RPL7L1P3	7:75528517-75623977	NOTEST	0.0814817	0.0223241	-1.86787	0	1	1
ENSG00000235091	ENSG00000235091	WI2-85898F10.1	22:46271878-46283628	NOTEST	0	0	0	0	1	1
ENSG00000235094	ENSG00000235094	AC006335.10	Y:6174082-6177628	NOTEST	0	0	0	0	1	1
ENSG00000235095	ENSG00000235095	RP11-1217F2.1	7:57215692-57218054	NOTEST	0	0	0	0	1	1
ENSG00000235096	ENSG00000235096	RP11-83A16.1	1:245912641-246670614	NOTEST	0	0	0	0	1	1
ENSG00000235097	ENSG00000235097	LINC00330	13:45373638-45383766	NOTEST	0	0	0	0	1	1
ENSG00000235098	ENSG00000235098	ANKRD65	1:1353799-1358071	NOTEST	0.0247148	0.0174494	-0.502192	0	1	1
ENSG00000235099	ENSG00000235099	RP1-23E21.2	6:93780104-93813102	NOTEST	0	0	0	0	1	1
ENSG00000235100	ENSG00000235100	RP11-80H5.9	10:91426937-91459428	NOTEST	0.0395349	0.0492785	0.317829	0	1	1
ENSG00000235101	ENSG00000235101	SETP9	1:160639937-160681641	NOTEST	0	0	0	0	1	1
ENSG00000235102	ENSG00000235102	RP3-450M14.1	20:39959762-39960300	NOTEST	0	0	0	0	1	1
ENSG00000235107	ENSG00000235107	RING1	HSCHR6_MHC_MANN:33330194-33334422	NOTEST	0	0	0	0	1	1
ENSG00000235108	ENSG00000235108	IFNA12P	9:21403079-21403650	NOTEST	0	0	0	0	1	1
ENSG00000235109	ENSG00000235109	ZSCAN31	6:28292469-28336947	NOTEST	0.607021	0.579066	-0.068017	0	1	1
ENSG00000235110	ENSG00000235110	RP11-8J23.1	3:143574580-143574985	NOTEST	0	0	0	0	1	1
ENSG00000235111	ENSG00000235111	RP1-29C18.8	22:49808175-50051190	NOTEST	0	0.00371846	inf	0	1	1
ENSG00000235112	ENSG00000235112	HSPE1P27	1:21132962-21503377	NOTEST	0	0	0	0	1	1
ENSG00000235113	ENSG00000235113	RP11-241I20.4	10:32398788-32400717	NOTEST	0	0	0	0	1	1
ENSG00000235115	ENSG00000235115	CHCHD2P8	13:28681567-28682014	NOTEST	0	0	0	0	1	1
ENSG00000235116	ENSG00000235116	DASS-23B5.2	HSCHR6_MHC_SSTO:32591349-32591757	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235117	ENSG00000235117	RP11-229P13.20	9:139931491-139932407	NOTEST	0	0	0	0	1	1
ENSG00000235118	ENSG00000235118	AC010731.4	2:207507141-207514173	NOTEST	0.282063	0.027103	-3.37949	0	1	1
ENSG00000235119	ENSG00000235119	RP11-9M16.2	9:117159003-117160783	NOTEST	0	1.68668	inf	0	1	1
ENSG00000235120	ENSG00000235120	BSN-AS1	3:49591921-49708978	NOTEST	0	0	0	0	1	1
ENSG00000235121	ENSG00000235121	RP11-90L20.2	1:201592012-201853422	NOTEST	0.112807	0.0382585	-1.56	0	1	1
ENSG00000235122	ENSG00000235122	RP3-417L20.4	6:49785142-49788155	NOTEST	0	0	0	0	1	1
ENSG00000235123	ENSG00000235123	DSCAM-AS1	21:41382925-42219065	NOTEST	0	0	0	0	1	1
ENSG00000235124	ENSG00000235124	KRT8P17	X:58011119-58012567	NOTEST	0	0	0	0	1	1
ENSG00000235125	ENSG00000235125	NFKBIL1	HSCHR6_MHC_MCF:31572847-31602942	NOTEST	0	0	0	0	1	1
ENSG00000235126	ENSG00000235126	AC128709.3	3:197171931-197185194	NOTEST	0.0711694	0.0851194	0.258231	0	1	1
ENSG00000235127	ENSG00000235127	AC068286.1	2:15026770-15047788	NOTEST	0	0	0	0	1	1
ENSG00000235128	ENSG00000235128	AC013474.4	2:127413508-127454246	NOTEST	0.252277	0.417342	0.726225	0	1	1
ENSG00000235129	ENSG00000235129	FABP7P2	2:95963051-96051825	NOTEST	0	0.215412	inf	0	1	1
ENSG00000235130	ENSG00000235130	MYO5BP1	9:45375909-45377188	NOTEST	0	0	0	0	1	1
ENSG00000235131	ENSG00000235131	RP5-1092A11.2	1:3547330-3663900	NOTEST	0	0	0	0	1	1
ENSG00000235132	ENSG00000235132	OR2H1	HSCHR6_MHC_COX:29421535-29428682	NOTEST	0	0	0	0	1	1
ENSG00000235133	ENSG00000235133	RPL35AP22	9:120447531-120447866	NOTEST	0	0	0	0	1	1
ENSG00000235134	ENSG00000235134	CYP21A2	HSCHR6_MHC_MCF:32082522-32172461	NOTEST	0	0	0	0	1	1
ENSG00000235135	ENSG00000235135	HCG23	HSCHR6_MHC_APD:32369259-32385878	NOTEST	0	0	0	0	1	1
ENSG00000235136	ENSG00000235136	RP13-146A14.1	X:55626095-55626539	NOTEST	0	0	0	0	1	1
ENSG00000235137	ENSG00000235137	HSP90AB6P	13:97536095-97542067	NOTEST	0	0	0	0	1	1
ENSG00000235138	ENSG00000235138	RP11-374P20.4	9:136890560-136933657	NOTEST	0.104221	0.213835	1.03686	0	1	1
ENSG00000235139	ENSG00000235139	AC003984.1	7:84161791-84213638	NOTEST	0	0	0	0	1	1
ENSG00000235140	ENSG00000235140	RP11-135D11.2	10:61348907-61371006	NOTEST	0	0	0	0	1	1
ENSG00000235141	ENSG00000235141	COX6CP17	10:7200585-7453450	NOTEST	0	0	0	0	1	1
ENSG00000235142	ENSG00000235142	RP1-60O19.1	6:107165326-107235416	NOTEST	0	0	0	0	1	1
ENSG00000235143	ENSG00000235143	RP1-65J11.5	1:31331004-31333101	NOTEST	0	0	0	0	1	1
ENSG00000235144	ENSG00000235144	HLA-W	HSCHR6_MHC_APD:29860827-29862802	NOTEST	0	0	0	0	1	1
ENSG00000235145	ENSG00000235145	RP11-533E19.3	1:179923872-180084015	NOTEST	0.0647707	0	#NAME?	0	1	1
ENSG00000235146	ENSG00000235146	RP5-857K21.2	1:521368-532878	NOTEST	0	0	0	0	1	1
ENSG00000235147	ENSG00000235147	AC128677.3	2:92194705-92195147	NOTEST	0	0	0	0	1	1
ENSG00000235148	ENSG00000235148	HMGB3P23	9:31644573-31645158	NOTEST	0	0	0	0	1	1
ENSG00000235149	ENSG00000235149	RP11-45I20.1	4:186506597-186877806	NOTEST	0	0	0	0	1	1
ENSG00000235150	ENSG00000235150	RCBTB2P1	10:90545356-90546818	NOTEST	0	0	0	0	1	1
ENSG00000235151	ENSG00000235151	AC114730.2	2:242786531-242787188	NOTEST	0	0	0	0	1	1
ENSG00000235152	ENSG00000235152	RP5-865N13.2	1:232295836-232321389	NOTEST	0	0	0	0	1	1
ENSG00000235154	ENSG00000235154	CTA-280A3__B.2	22:48440526-48444366	NOTEST	0	0	0	0	1	1
ENSG00000235155	ENSG00000235155	B3GALT4	HSCHR6_MHC_DBB:33222841-33224527	NOTEST	0	0	0	0	1	1
ENSG00000235156	ENSG00000235156	TMEM30C	3:99904530-99913035	NOTEST	0	0	0	0	1	1
ENSG00000235158	ENSG00000235158	AC087430.1	3:1049818-1054618	NOTEST	0	0	0	0	1	1
ENSG00000235159	ENSG00000235159	RP6-109B7.4	22:46445357-46509808	NOTEST	0.0603902	0	#NAME?	0	1	1
ENSG00000235160	ENSG00000235160	AC009878.2	15:26640218-26691921	NOTEST	0	0	0	0	1	1

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ENSG00000235163	ENSG00000235163	RP11-410C4.1	1:220621857-220622195	NOTEST	0	0	0	0	1	1
ENSG00000235165	ENSG00000235165	AC016405.1	8:123781512-123782389	NOTEST	0	0.0148387	inf	0	1	1
ENSG00000235166	ENSG00000235166	RP5-1010E17.	20:54036873-54084752	NOTEST	0	0	0	0	1	1
ENSG00000235168	ENSG00000235168	RP1-12G14.5	6:149882287-149885085	NOTEST	0	0	0	0	1	1
ENSG00000235170	ENSG00000235170	MTND1P31	X:62062011-62062972	NOTEST	0	0	0	0	1	1
ENSG00000235171	ENSG00000235171	HNRNPA1P2	HSCHR6_MHC_QBL:32218296-32297155	NOTEST	0	0	0	0	1	1
ENSG00000235175	ENSG00000235175	RPL26P37	Y:5661340-5661778	NOTEST	0	0	0	0	1	1
ENSG00000235176	ENSG00000235176	ZNRD1	HSCHR6_MHC_MANN:29963963-30027881	NOTEST	0	0	0	0	1	1
ENSG00000235178	ENSG00000235178	ZNF311	HSCHR6_MHC_DBB:28962575-28973107	NOTEST	0	0	0	0	1	1
ENSG00000235181	ENSG00000235181	AC009892.2	19:55063252-55063539	NOTEST	0	0	0	0	1	1
ENSG00000235182	ENSG00000235182	RP11-348H3.4	1:213025449-213031430	NOTEST	0	0	0	0	1	1
ENSG00000235183	ENSG00000235183	RP11-613C6.4	17:47778304-47906458	NOTEST	0	0	0	0	1	1
ENSG00000235184	ENSG00000235184	ZNF90P2	HSCHR6_MHC_COX:28857439-28858514	NOTEST	0	0	0	0	1	1
ENSG00000235185	ENSG00000235185	RP5-1056L3.1	1:19918295-19923326	NOTEST	0	0	0	0	1	1
ENSG00000235186	ENSG00000235186	AC103563.7	2:95657624-95660107	NOTEST	0	0	0	0	1	1
ENSG00000235189	ENSG00000235189	RP4-537K23.4	X:129003039-129091504	NOTEST	0	0.0929191	inf	0	1	1
ENSG00000235190	ENSG00000235190	RP1-197O17.3	X:131071697-131071881	NOTEST	0	0	0	0	1	1
ENSG00000235191	ENSG00000235191	NUCB1-AS1	19:49403306-49426629	NOTEST	0.0566575	0	#NAME?	0	1	1
ENSG00000235192	ENSG00000235192	AC009495.2	2:166651360-166702601	NOTEST	0.466633	0.576585	0.305245	0	1	1
ENSG00000235193	ENSG00000235193	AC006987.4	Y:9925634-9927195	NOTEST	0	0	0	0	1	1
ENSG00000235195	ENSG00000235195	OR2P1P	HSCHR6_MHC_QBL:29039602-29040378	NOTEST	0	0	0	0	1	1
ENSG00000235196	ENSG00000235196	RP1-3E10.2	X:101137261-101187004	NOTEST	0	0	0	0	1	1
ENSG00000235197	ENSG00000235197	ZNF33AP1	10:38183564-38185594	NOTEST	0	0	0	0	1	1
ENSG00000235198	ENSG00000235198	CTA-109P11.1	10:119321594-119331968	NOTEST	0	0	0	0	1	1
ENSG00000235199	ENSG00000235199	CYP2C58P	10:96625608-96632886	NOTEST	0	0	0	0	1	1
ENSG00000235200	ENSG00000235200	RP4-763G1.2	1:67995312-67998012	NOTEST	0	0	0	0	1	1
ENSG00000235201	ENSG00000235201	RP11-127L21.1	9:121502840-121507590	NOTEST	0	0	0	0	1	1
ENSG00000235202	ENSG00000235202	RP11-39H13.1	1:117838141-117863958	NOTEST	0	0	0	0	1	1
ENSG00000235203	ENSG00000235203	TBC1D3P3	17:20446286-20454276	NOTEST	0	0	0	0	1	1
ENSG00000235205	ENSG00000235205	TATDN2P3	13:23755090-23899304	NOTEST	0	0	0	0	1	1
ENSG00000235207	ENSG00000235207	TUBBP6	7:55713312-55714644	NOTEST	0.0465079	0	#NAME?	0	1	1
ENSG00000235208	ENSG00000235208	RPL7AL3	20:16664752-16665049	NOTEST	0	0	0	0	1	1
ENSG00000235209	ENSG00000235209	CTA-150C2.13	22:39317231-39320713	NOTEST	0	0	0	0	1	1
ENSG00000235211	ENSG00000235211	TMSB10P2	X:18257433-18372847	NOTEST	0	0	0	0	1	1
ENSG00000235213	ENSG00000235213	OR6E1P	14:23171351-23241007	NOTEST	0	0	0	0	1	1
ENSG00000235214	ENSG00000235214	FAM83C-AS1	20:33873053-33880204	NOTEST	0	0	0	0	1	1
ENSG00000235215	ENSG00000235215	RP11-145M4.2	1:59520068-59553867	NOTEST	0	0	0	0	1	1
ENSG00000235217	ENSG00000235217	TSPY26P	20:30774279-30778330	NOTEST	0.071632	0.0784062	0.130364	0	1	1
ENSG00000235218	ENSG00000235218	AC092638.2	2:194141392-194142339	NOTEST	0	0	0	0	1	1
ENSG00000235219	ENSG00000235219	CTC-233O10.1	X:152459851-152462342	NOTEST	0	0	0	0	1	1
ENSG00000235220	ENSG00000235220	HLA-F	HSCHR6_MHC_DBB:29688036-29714307	NOTEST	0	0	0	0	1	1
ENSG00000235221	ENSG00000235221	LINC00401	13:69885464-69896233	NOTEST	0	0	0	0	1	1
ENSG00000235222	ENSG00000235222	MSH5	HSCHR6_MHC_COX:31695129-31720748	NOTEST	0	0	0	0	1	1
ENSG00000235223	ENSG00000235223	TMPOP1	HSCHR6_MHC_QBL:30423832-30425362	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235224	ENSG00000235224	RP11-236P24.1	X:53122891-53196196	NOTEST	0	0	0	0	1	1
ENSG00000235225	ENSG00000235225	AC016712.2	2:223591175-223591553	NOTEST	0.143153	0.321112	1.16552	0	1	1
ENSG00000235226	ENSG00000235226	RP11-419N10.5	1:159728959-159729379	NOTEST	0	0	0	0	1	1
ENSG00000235227	ENSG00000235227	VN1R38P	7:63640383-63641270	NOTEST	0	0	0	0	1	1
ENSG00000235228	ENSG00000235228	DASS-397D15.4	HSCHR6_MHC_SSTO:32459436-32459532	NOTEST	0	0	0	0	1	1
ENSG00000235232	ENSG00000235232	MRPS18BP2	2:140426115-140426874	NOTEST	0	0	0	0	1	1
ENSG00000235233	ENSG00000235233	MICA	HSCHR6_MHC_MANN:31410599-31427049	NOTEST	0	0	0	0	1	1
ENSG00000235235	ENSG00000235235	IGKV1OR-1	2:92005796-92006650	NOTEST	0	0	0	0	1	1
ENSG00000235236	ENSG00000235236	RP13-131K19.1	3:48955220-49060928	NOTEST	0.0425621	0.0936182	1.13722	0	1	1
ENSG00000235237	ENSG00000235237	RP1-151B14.6	22:37521877-37595425	NOTEST	0	0	0	0	1	1
ENSG00000235239	ENSG00000235239	RP1-203C2.4	X:127261067-127262190	NOTEST	0	0	0	0	1	1
ENSG00000235240	ENSG00000235240	AC026185.1	3:11313994-11766453	NOTEST	0	0	0	0	1	1
ENSG00000235242	ENSG00000235242	AC010982.2	2:114879850-114880870	NOTEST	0	0	0	0	1	1
ENSG00000235243	ENSG00000235243	AC093716.1	7:84477192-84477569	NOTEST	0	0	0	0	1	1
ENSG00000235244	ENSG00000235244	RP11-761E20.1	X:115033603-115085422	NOTEST	0.0218786	0.0248112	0.181471	0	1	1
ENSG00000235246	ENSG00000235246	RP1-5O6.5	22:38615297-38669040	NOTEST	0	0	0	0	1	1
ENSG00000235248	ENSG00000235248	OR13C1P	9:107419034-107419997	NOTEST	0	0	0	0	1	1
ENSG00000235249	ENSG00000235249	OR4F29	1:317719-461954	NOTEST	0	0	0	0	1	1
ENSG00000235250	ENSG00000235250	C4B-AS1	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000235251	ENSG00000235251	RP11-384B12.2	1:87380330-87634884	NOTEST	0	0	0	0	1	1
ENSG00000235253	ENSG00000235253	AC010240.2	5:132211070-132299326	NOTEST	0	0	0	0	1	1
ENSG00000235254	ENSG00000235254	TMEM185AP1	X:148850557-148853029	NOTEST	0.113129	0.151924	0.425383	0	1	1
ENSG00000235256	ENSG00000235256	BX664724.1	9:47021336-47022699	NOTEST	0	0	0	0	1	1
ENSG00000235258	ENSG00000235258	AC115115.3	2:113033170-113097640	NOTEST	0	0	0	0	1	1
ENSG00000235259	ENSG00000235259	TRIM15	HSCHR6_MHC_APD:30067804-30077295	NOTEST	0	0	0	0	1	1
ENSG00000235262	ENSG00000235262	KDM5C-IT1	X:53220502-53254604	NOTEST	0.0254873	0	#NAME?	0	1	1
ENSG00000235263	ENSG00000235263	RP13-392I16.1	1:9561150-9563530	NOTEST	0	0	0	0	1	1
ENSG00000235264	ENSG00000235264	RPL5P28	10:134958115-134958808	NOTEST	0	0	0	0	1	1
ENSG00000235265	ENSG00000235265	LA16c-4G1.5	22:16084248-16084826	NOTEST	0	0	0	0	1	1
ENSG00000235266	ENSG00000235266	RP11-753C18.8	10:104613979-104661656	NOTEST	0	0	0	0	1	1
ENSG00000235267	ENSG00000235267	AC074117.13	2:27665232-27712656	NOTEST	0	0	0	0	1	1
ENSG00000235268	ENSG00000235268	KDM4E	11:94758421-94760760	NOTEST	0	0	0	0	1	1
ENSG00000235269	ENSG00000235269	AL162759.1	14:54235659-54317600	NOTEST	0	0	0	0	1	1
ENSG00000235271	ENSG00000235271	RP1-90L6.3	22:27299254-27316574	NOTEST	0	0	0	0	1	1
ENSG00000235273	ENSG00000235273	XXbac-BPG308J9.3	HSCHR6_MHC_DBB:29191798-29234885	NOTEST	0	0	0	0	1	1
ENSG00000235274	ENSG00000235274	RP1-107N3.1	X:126862714-126864839	NOTEST	0	0	0	0	1	1
ENSG00000235275	ENSG00000235275	KRT18P16	5:122971803-122973097	NOTEST	0	0	0	0	1	1
ENSG00000235277	ENSG00000235277	AF127577.8	21:16290854-16319417	NOTEST	0	0	0	0	1	1
ENSG00000235278	ENSG00000235278	ZNF652P1	3:50712671-51421629	NOTEST	0	0	0	0	1	1
ENSG00000235279	ENSG00000235279	RP11-539E19.2	10:52750944-54073888	NOTEST	0	0	0	0	1	1
ENSG00000235280	ENSG00000235280	MCF2L-AS1	13:113548691-113754053	NOTEST	0	0.0213652	inf	0	1	1
ENSG00000235281	ENSG00000235281	RP11-526P5.2	10:2543974-2609431	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235282	ENSG00000235282	RP1-8B22.1	1:18839611-18839881	NOTEST	0	0	0	0	1	1
ENSG00000235283	ENSG00000235283	RP11-395E19.5	9:40700290-40713709	NOTEST	0	0	0	0	1	1
ENSG00000235284	ENSG00000235284	SNORD62A	9:134269479-134375584	NOTEST	0	0	0	0	1	1
ENSG00000235285	ENSG00000235285	SMIM2-IT1	13:44716681-44817328	NOTEST	0	0	0	0	1	1
ENSG00000235286	ENSG00000235286	AP000925.2	11:111473114-111637151	NOTEST	0	0.0163524	inf	0	1	1
ENSG00000235288	ENSG00000235288	RP11-70C1.3	3:42846243-43101703	NOTEST	0.0874412	0	#NAME?	0	1	1
ENSG00000235289	ENSG00000235289	BRD7P6	2:70580141-70583047	NOTEST	0	0	0	0	1	1
ENSG00000235290	ENSG00000235290	HLA-W	6:29924372-29926347	NOTEST	0	0	0	0	1	1
ENSG00000235291	ENSG00000235291	PPP1R10	HSCHR6_MHC_MCF:30646634-30672631	NOTEST	0	0	0	0	1	1
ENSG00000235292	ENSG00000235292	RP4-796I8.1	20:12224542-12224944	NOTEST	0	0	0	0	1	1
ENSG00000235293	ENSG00000235293	AC114814.3	2:236086539-236087549	NOTEST	0	0	0	0	1	1
ENSG00000235294	ENSG00000235294	RPL7AP25	3:180701496-181554668	NOTEST	0	0	0	0	1	1
ENSG00000235295	ENSG00000235295	XXbac-B476C20.17	22:18512150-18520734	NOTEST	0.0121699	0	#NAME?	0	1	1
ENSG00000235296	ENSG00000235296	AC137723.5	17:79890259-79905477	NOTEST	0.0811763	0	#NAME?	0	1	1
ENSG00000235299	ENSG00000235299	MRPL53P1	1:113009162-113214241	NOTEST	0	0	0	0	1	1
ENSG00000235300	ENSG00000235300	AC090627.1	17:46210801-46507637	NOTEST	0	0	0	0	1	1
ENSG00000235301	ENSG00000235301	HLA-Z	6:32864192-32864267	NOTEST	0	0	0	0	1	1
ENSG00000235302	ENSG00000235302	LY6G6D	HSCHR6_MHC_SSTO:31664594-31675654	NOTEST	0	0	0	0	1	1
ENSG00000235303	ENSG00000235303	RP1-79C4.1	1:170567994-170616480	NOTEST	0	0.0186175	inf	0	1	1
ENSG00000235304	ENSG00000235304	RP11-265P11.2	X:39164209-39186616	NOTEST	0.0295906	0	#NAME?	0	1	1
ENSG00000235305	ENSG00000235305	DDX39BP2	HSCHR6_MHC_SSTO:29949454-29949851	NOTEST	0	0	0	0	1	1
ENSG00000235306	ENSG00000235306	GAPDHP34	13:37314177-37315000	NOTEST	0	0	0	0	1	1
ENSG00000235307	ENSG00000235307	BRD2	HSCHR6_MHC_SSTO:32992301-33089202	NOTEST	0	0	0	0	1	1
ENSG00000235308	ENSG00000235308	RP11-82K18.2	1:89389052-89389527	NOTEST	0.140167	0.0347397	-2.01248	0	1	1
ENSG00000235309	ENSG00000235309	HLA-J	HSCHR6_MHC_SSTO:29957256-30022268	NOTEST	0	0	0	0	1	1
ENSG00000235310	ENSG00000235310	RP11-250H24.4	9:69501017-69502204	NOTEST	0	0.0102912	inf	0	1	1
ENSG00000235312	ENSG00000235312	KRTAP19-10P	21:31886930-31887117	NOTEST	0	0	0	0	1	1
ENSG00000235315	ENSG00000235315	RPL23AP69	13:25767244-25784433	NOTEST	0	0	0	0	1	1
ENSG00000235316	ENSG00000235316	DUSP8P5	10:75490319-75497069	NOTEST	0.607528	0.512191	-0.246269	0	1	1
ENSG00000235317	ENSG00000235317	HCG4	HSCHR6_MHC_DBB:29756032-29762814	NOTEST	0	0	0	0	1	1
ENSG00000235318	ENSG00000235318	AC005037.6	2:202047603-202094129	NOTEST	0	0	0	0	1	1
ENSG00000235319	ENSG00000235319	AC012360.4	2:105880870-105946986	NOTEST	0.202039	0.0417617	-2.27438	0	1	1
ENSG00000235321	ENSG00000235321	AC007556.3	2:169957252-169957720	NOTEST	0	0	0	0	1	1
ENSG00000235323	ENSG00000235323	COTL1P2	17:20467850-20468202	NOTEST	0	0	0	0	1	1
ENSG00000235324	ENSG00000235324	DASS-23B5.1	HSCHR6_MHC_SSTO:32588903-32589843	NOTEST	0	0	0	0	1	1
ENSG00000235325	ENSG00000235325	AC009963.6	2:108537218-108537704	NOTEST	0	0	0	0	1	1
ENSG00000235326	ENSG00000235326	RP11-509J21.3	9:3674545-3691814	NOTEST	0.0811727	0	#NAME?	0	1	1
ENSG00000235327	ENSG00000235327	CYP4F61P	9:66366965-66367990	NOTEST	0	0	0	0	1	1
ENSG00000235328	ENSG00000235328	AC006946.12	22:17565843-17596583	NOTEST	0.180963	0.28557	0.658146	0	1	1
ENSG00000235329	ENSG00000235329	RP5-1168A5.1	X:112590639-112590846	NOTEST	0	0	0	0	1	1
ENSG00000235330	ENSG00000235330	RP11-165F24.2	9:213107-746105	NOTEST	0	0	0	0	1	1
ENSG00000235332	ENSG00000235332	RP11-366O20.5	9:127956927-127958100	NOTEST	0	0	0	0	1	1
ENSG00000235334	ENSG00000235334	RP1-203C2.3	X:127256711-127257474	NOTEST	0	0	0	0	1	1

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ENSG00000235335	ENSG00000235335	AC016723.4	2:168671283-168797654	NOTEST	0	0.0250285	inf	0	1	1
ENSG00000235336	ENSG00000235336	SLC44A4	HSCHR6_MHC_APD:31842326-31858180	NOTEST	0	0	0	0	1	1
ENSG00000235337	ENSG00000235337	AC114765.2	2:220970376-221569286	NOTEST	0	0	0	0	1	1
ENSG00000235338	ENSG00000235338	DUSP5P2	3:9642431-9644412	NOTEST	0	0	0	0	1	1
ENSG00000235339	ENSG00000235339	RP11-626A1.1	3:42018499-42019526	NOTEST	0	0	0	0	1	1
ENSG00000235340	ENSG00000235340	MCCD1P2	HSCHR6_MHC_COX:29951726-29952604	NOTEST	0	0	0	0	1	1
ENSG00000235342	ENSG00000235342	RPL7P4	HSCHR6_MHC_COX:30654449-30655179	NOTEST	0	0	0	0	1	1
ENSG00000235346	ENSG00000235346	HLA-G	HSCHR6_MHC_DBB:29791967-29796126	NOTEST	0	0	0	0	1	1
ENSG00000235347	ENSG00000235347	RP1-37M3.8	22:46067677-46241187	NOTEST	0	0	0	0	1	1
ENSG00000235349	ENSG00000235349	RP11-561N12.6	7:64027191-64027821	NOTEST	0	0	0	0	1	1
ENSG00000235350	ENSG00000235350	AF196972.3	X:48291579-48299998	NOTEST	0	0	0	0	1	1
ENSG00000235351	ENSG00000235351	AC114730.11	2:242641449-242668893	NOTEST	0.183056	0.12793	-0.51693	0	1	1
ENSG00000235352	ENSG00000235352	AC023128.2	2:145425533-145940216	NOTEST	0	0	0	0	1	1
ENSG00000235354	ENSG00000235354	CTA-276O3.4	7:102937868-103629963	NOTEST	1.58859	0.524917	-1.59758	0	1	1
ENSG00000235355	ENSG00000235355	RP11-381O7.4	9:66951141-66951845	NOTEST	0	0	0	0	1	1
ENSG00000235356	ENSG00000235356	RP11-428G2.1	10:67073542-67074728	NOTEST	0	0	0	0	1	1
ENSG00000235357	ENSG00000235357	RP1-159G19.1	6:80513299-80516942	NOTEST	0	0	0	0	1	1
ENSG00000235358	ENSG00000235358	RP11-399E6.1	1:41708044-41750533	NOTEST	0	0.218099	inf	0	1	1
ENSG00000235360	ENSG00000235360	C6orf47	HSCHR6_MHC_COX:31613488-31615961	NOTEST	0	0	0	0	1	1
ENSG00000235361	ENSG00000235361	AC016292.1	17:900356-1132315	NOTEST	0	0	0	0	1	1
ENSG00000235366	ENSG00000235366	LINC01055	13:46255224-46256554	NOTEST	0	0	0	0	1	1
ENSG00000235368	ENSG00000235368	RP11-114G11.2	7:57484206-57485380	NOTEST	0	0	0	0	1	1
ENSG00000235369	ENSG00000235369	RPL36AP15	2:47922668-48134949	NOTEST	0	0	0	0	1	1
ENSG00000235370	ENSG00000235370	DNM1P51	15:84953013-84966399	NOTEST	0.173204	0.209759	0.276255	0	1	1
ENSG00000235371	ENSG00000235371	RP4-764D2.1	1:236273360-236275670	NOTEST	0	0.0249021	inf	0	1	1
ENSG00000235372	ENSG00000235372	ETF1P1	HSCHR6_MHC_APD:29905241-29969520	NOTEST	0	0	0	0	1	1
ENSG00000235373	ENSG00000235373	RP11-206L10.3	1:677192-685396	NOTEST	0.00888205	0.00940412	0.082401	0	1	1
ENSG00000235376	ENSG00000235376	RPEL1	10:105005643-105007773	NOTEST	0.0895355	0.10698	0.256812	0	1	1
ENSG00000235377	ENSG00000235377	RP11-388B24.4	9:84745666-84746547	NOTEST	0	0	0	0	1	1
ENSG00000235378	ENSG00000235378	MRPS10P1	1:169890466-170054349	NOTEST	0	0	0	0	1	1
ENSG00000235379	ENSG00000235379	RPL7P31	7:34386123-34917944	NOTEST	0	0	0	0	1	1
ENSG00000235380	ENSG00000235380	MICD	HSCHR6_MHC_SSTO:29927035-29928699	NOTEST	0	0	0	0	1	1
ENSG00000235381	ENSG00000235381	RP11-477D19.2	6:155054458-155635627	NOTEST	0.328291	0.349317	0.0895614	0	1	1
ENSG00000235382	ENSG00000235382	MTND4P31	X:69344821-69348921	NOTEST	0	0	0	0	1	1
ENSG00000235385	ENSG00000235385	GS1-600G8.5	X:13284166-13321571	NOTEST	0	0.0422861	inf	0	1	1
ENSG00000235386	ENSG00000235386	RP11-397A15.4	1:246935138-246993361	NOTEST	0	0	0	0	1	1
ENSG00000235387	ENSG00000235387	LINC00961	9:35909479-35911683	NOTEST	0	0	0	0	1	1
ENSG00000235388	ENSG00000235388	AC018696.7	2:91740599-91740793	NOTEST	0.863427	0	#NAME?	0	1	1
ENSG00000235389	ENSG00000235389	RP11-134K1.3	9:8314245-10612723	NOTEST	0	0	0	0	1	1
ENSG00000235390	ENSG00000235390	CTD-2651B20.5	15:45613274-45613890	NOTEST	0	0	0	0	1	1
ENSG00000235391	ENSG00000235391	FAM8A5P	HSCHR6_MHC_DBB:32472043-32491190	NOTEST	0	0	0	0	1	1
ENSG00000235394	ENSG00000235394	NCRNA00171	HSCHR6_MHC_MANN:29963963-30027881	NOTEST	0	0	0	0	1	1
ENSG00000235396	ENSG00000235396	NOTCH4	HSCHR6_MHC_COX:32107016-32140316	NOTEST	0	0	0	0	1	1

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ENSG00000235399	ENSG00000235399	RP11-204P2.3	6:137316306-137320641	NOTEST	0	0	0	0	1	1
ENSG00000235400	ENSG00000235400	RP4-641G12.4	1:79214757-79216344	NOTEST	0.0190322	0	#NAME?	0	1	1
ENSG00000235401	ENSG00000235401	OR2H4P	HSCHR6_MHC_QBL:29183058-29184002	NOTEST	0	0	0	0	1	1
ENSG00000235403	ENSG00000235403	AC114808.3	2:946553-1371385	NOTEST	0	0	0	0	1	1
ENSG00000235405	ENSG00000235405	HCG15	HSCHR6_MHC_DBB:28953993-28956327	NOTEST	0	0	0	0	1	1
ENSG00000235407	ENSG00000235407	RP11-470L19.2	1:111023373-111033899	NOTEST	0	0	0	0	1	1
ENSG00000235408	ENSG00000235408	SNORA71B	20:37049234-37063996	NOTEST	0	0	0	0	1	1
ENSG00000235410	ENSG00000235410	RP11-397C18.2	10:13628926-14504141	NOTEST	0.0240019	0.0308135	0.360411	0	1	1
ENSG00000235411	ENSG00000235411	AC007041.2	2:20439652-20440807	NOTEST	0.160628	0.445669	1.47225	0	1	1
ENSG00000235412	ENSG00000235412	TTTY4B	Y:26716348-26753172	NOTEST	0	0	0	0	1	1
ENSG00000235413	ENSG00000235413	KRT18P63	4:17812524-18023499	NOTEST	0.0183993	0.101682	2.46634	0	1	1
ENSG00000235414	ENSG00000235414	AC016737.1	2:174907735-174908608	NOTEST	0	0	0	0	1	1
ENSG00000235415	ENSG00000235415	AC005808.3	20:52169308-52251129	NOTEST	0	0	0	0	1	1
ENSG00000235416	ENSG00000235416	RP3-339A18.3	X:53483219-53483976	NOTEST	0	0	0	0	1	1
ENSG00000235419	ENSG00000235419	AC010149.4	2:231280656-231444721	NOTEST	0	0	0	0	1	1
ENSG00000235420	ENSG00000235420	RPL29P30	15:71088935-71095027	NOTEST	0	0	0	0	1	1
ENSG00000235421	ENSG00000235421	RP11-667F9.1	7:64990541-65019657	NOTEST	0.0408092	0	#NAME?	0	1	1
ENSG00000235422	ENSG00000235422	KATNBL1P3	18:2571509-2616634	NOTEST	0	0	0	0	1	1
ENSG00000235424	ENSG00000235424	SUMO2P10	3:33038099-33138722	NOTEST	0	0	0	0	1	1
ENSG00000235425	ENSG00000235425	RPS7P13	X:94934128-94934626	NOTEST	0	0	0	0	1	1
ENSG00000235426	ENSG00000235426	RP11-342M3.5	10:81142080-81205383	NOTEST	0	0	0	0	1	1
ENSG00000235427	ENSG00000235427	AC006159.5	7:116164838-116201233	NOTEST	0	0.167115	inf	0	1	1
ENSG00000235428	ENSG00000235428	WI2-2998D17.2	1:223711348-223853436	NOTEST	0	0	0	0	1	1
ENSG00000235429	ENSG00000235429	AC083875.2	7:132937828-133751342	NOTEST	0	0	0	0	1	1
ENSG00000235430	ENSG00000235430	ZSWIM5P1	17:15672030-15674740	NOTEST	0	0	0	0	1	1
ENSG00000235431	ENSG00000235431	AC006373.1	7:10000650-10021444	NOTEST	0	0.0608641	inf	0	1	1
ENSG00000235432	ENSG00000235432	RP5-930J4.5	1:20990506-21044510	NOTEST	0	0	0	0	1	1
ENSG00000235433	ENSG00000235433	AC009960.4	2:203480491-203481163	NOTEST	0	0	0	0	1	1
ENSG00000235434	ENSG00000235434	RP11-91K11.2	1:20140522-20145995	NOTEST	0	0	0	0	1	1
ENSG00000235435	ENSG00000235435	AC064865.1	2:146051844-146089415	NOTEST	0	0	0	0	1	1
ENSG00000235438	ENSG00000235438	ESRRAP2	13:21834153-21868998	NOTEST	0	0	0	0	1	1
ENSG00000235439	ENSG00000235439	DDX39B	HSCHR6_MHC_SSTO:31486440-31504572	NOTEST	0	0	0	0	1	1
ENSG00000235440	ENSG00000235440	RP11-214J9.1	2:26256975-26360323	NOTEST	0	0.050498	inf	0	1	1
ENSG00000235441	ENSG00000235441	OR10C1	HSCHR6_MHC_SSTO:29323120-29424524	NOTEST	0	0	0	0	1	1
ENSG00000235443	ENSG00000235443	ZNRD1	HSCHR6_MHC_APD:29905241-29969520	NOTEST	0	0	0	0	1	1
ENSG00000235444	ENSG00000235444	PSMB3P2	2:217455148-217475925	NOTEST	0	0	0	0	1	1
ENSG00000235445	ENSG00000235445	XXbac-B476C20.14	22:18270414-18507325	NOTEST	0	0.0608682	inf	0	1	1
ENSG00000235446	ENSG00000235446	RP11-74K19.1	1:69709054-69715106	NOTEST	0	0	0	0	1	1
ENSG00000235447	ENSG00000235447	RP1-279N11.1	X:75875898-75876960	NOTEST	0	0	0	0	1	1
ENSG00000235449	ENSG00000235449	RP11-480I12.2	1:202696525-202778598	NOTEST	0.945474	0.670158	-0.496537	0	1	1
ENSG00000235450	ENSG00000235450	RP11-142A5.1	7:90940682-91186163	NOTEST	0	0	0	0	1	1

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ENSG00000235451	ENSG00000235451	PNPLA4P1	Y:16192954-16198480	NOTEST	0	0	0	0	1	1
ENSG00000235452	ENSG00000235452	LY6G6C	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000235455	ENSG00000235455	IQCF5-AS1	3:51907611-51909783	NOTEST	0	0	0	0	1	1
ENSG00000235458	ENSG00000235458	HCG9P5	HSCHR6_MHC_DBB:29688036-29714307	NOTEST	0	0	0	0	1	1
ENSG00000235459	ENSG00000235459	RPS26P31	7:121958480-122526813	NOTEST	0.28209	0.18411	-0.615587	0	1	1
ENSG00000235460	ENSG00000235460	XXbac-BPG308K3.5	HSCHR6_MHC_DBB:28805658-28806796	NOTEST	0	0	0	0	1	1
ENSG00000235461	ENSG00000235461	RP5-928E24.2	X:84465711-84474704	NOTEST	0	0	0	0	1	1
ENSG00000235462	ENSG00000235462	TAB3P1	Y:15265841-15274125	NOTEST	0	0	0	0	1	1
ENSG00000235463	ENSG00000235463	AC078974.2	2:85295931-85296154	NOTEST	0	0	0	0	1	1
ENSG00000235464	ENSG00000235464	AC007652.1	7:35535630-35549873	NOTEST	0	0	0	0	1	1
ENSG00000235467	ENSG00000235467	RP11-513D4.2	1:242246287-242687998	NOTEST	0	0	0	0	1	1
ENSG00000235469	ENSG00000235469	MRPL50P4	10:61311161-61311636	NOTEST	0	0	0	0	1	1
ENSG00000235470	ENSG00000235470	RP11-225H22.5	10:105239359-105615301	NOTEST	0	0	0	0	1	1
ENSG00000235472	ENSG00000235472	EIF4A1P7	13:29172969-29174189	NOTEST	0.108162	0.0951987	-0.184173	0	1	1
ENSG00000235475	ENSG00000235475	RP11-166O4.5	7:66800962-66805011	NOTEST	0.273982	0.285323	0.0585129	0	1	1
ENSG00000235476	ENSG00000235476	AF254982.2	21:10872118-10872429	NOTEST	0	0	0	0	1	1
ENSG00000235478	ENSG00000235478	AC006946.15	22:17602475-17612994	NOTEST	0.014793	0	#NAME?	0	1	1
ENSG00000235479	ENSG00000235479	RAB9AP4	Y:20811556-20812165	NOTEST	0	0	0	0	1	1
ENSG00000235480	ENSG00000235480	RP11-363D14.1	2:97193676-97198043	NOTEST	0	0	0	0	1	1
ENSG00000235481	ENSG00000235481	RP11-133O22.6	9:33750514-33920402	NOTEST	0	0	0	0	1	1
ENSG00000235482	ENSG00000235482	RPL21P135	3:37493605-37903271	NOTEST	0	0	0	0	1	1
ENSG00000235483	ENSG00000235483	GYG2-AS1	X:2746828-2800859	NOTEST	0	0	0	0	1	1
ENSG00000235485	ENSG00000235485	RP1-101G11.2	22:34985076-34987270	NOTEST	0	0	0	0	1	1
ENSG00000235486	ENSG00000235486	AC114755.7	2:106986179-106994703	NOTEST	0.491063	0.291826	-0.7508	0	1	1
ENSG00000235487	ENSG00000235487	PSORS1C1	HSCHR6_MHC_COX:31075026-31100333	NOTEST	0	0	0	0	1	1
ENSG00000235488	ENSG00000235488	JARID2-AS1	6:15246526-15522252	NOTEST	0	0.115201	inf	0	1	1
ENSG00000235491	ENSG00000235491	AC097499.1	2:126468545-126523419	NOTEST	0	0	0	0	1	1
ENSG00000235492	ENSG00000235492	RP11-16L9.4	1:198975168-199045864	NOTEST	0	0	0	0	1	1
ENSG00000235493	ENSG00000235493	AC092415.1	3:28038700-28070095	NOTEST	0	0	0	0	1	1
ENSG00000235494	ENSG00000235494	RP11-498P14.4	9:99918851-100140806	NOTEST	0	0	0	0	1	1
ENSG00000235495	ENSG00000235495	AC010987.5	2:67789198-67911209	NOTEST	0.802454	0	#NAME?	0	1	1
ENSG00000235496	ENSG00000235496	RP11-101E5.2	9:65496524-65496924	NOTEST	0	0	0	0	1	1
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ENSG00000235498	ENSG00000235498	MICF	HSCHR6_MHC_MANN:29816711-29816840	NOTEST	0	0	0	0	1	1
ENSG00000235500	ENSG00000235500	SNX19P2	13:19466399-19469370	NOTEST	0	0	0	0	1	1
ENSG00000235503	ENSG00000235503	AC079799.2	7:82984469-82991582	NOTEST	0	0	0	0	1	1
ENSG00000235504	ENSG00000235504	RP3-453D15.1	6:99006309-99006447	NOTEST	0	0	0	0	1	1
ENSG00000235505	ENSG00000235505	RP11-693N9.2	11:104772275-104789800	NOTEST	0.00884228	0.135791	3.94083	0	1	1
ENSG00000235506	ENSG00000235506	SLC20A1P2	14:106636401-106637113	NOTEST	0	0	0	0	1	1
ENSG00000235507	ENSG00000235507	ZDHHC20P1	HSCHR6_MHC_COX:29672539-29672962	NOTEST	0	0	0	0	1	1
ENSG00000235508	ENSG00000235508	RPS2P7	20:44269124-44270009	NOTEST	0.0380488	0.426441	3.48643	0	1	1
ENSG00000235510	ENSG00000235510	BX842568.1	X:36975985-36976212	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235511	ENSG00000235511	OFD1P18Y	Y:28018077-28044800	NOTEST	0	0	0	0	1	1
ENSG00000235512	ENSG00000235512	TAB3-AS2	X:30845558-30993201	NOTEST	0	0	0	0	1	1
ENSG00000235514	ENSG00000235514	AP000226.9	21:27011583-27144771	NOTEST	0	0	0	0	1	1
ENSG00000235516	ENSG00000235516	C6orf47-AS1	HSCHR6_MHC_COX:31613488-31615961	NOTEST	0	0	0	0	1	1
ENSG00000235518	ENSG00000235518	AC011196.3	15:26788692-27194354	NOTEST	0	0	0	0	1	1
ENSG00000235519	ENSG00000235519	AC012075.2	2:81689818-81694070	NOTEST	0	0	0	0	1	1
ENSG00000235521	ENSG00000235521	USP9YP27	Y:19900194-19901364	NOTEST	0	0	0	0	1	1
ENSG00000235522	ENSG00000235522	AC009505.2	2:106361353-106510730	NOTEST	0.252198	0	#NAME?	0	1	1
ENSG00000235523	ENSG00000235523	RP11-63P12.7	9:74872251-74872699	NOTEST	0	0	0	0	1	1
ENSG00000235524	ENSG00000235524	RP11-343J3.5	10:71351161-71352687	NOTEST	0	0	0	0	1	1
ENSG00000235525	ENSG00000235525	FTLP1	20:44603887-44604714	NOTEST	0	0	0	0	1	1
ENSG00000235527	ENSG00000235527	RP5-1073O3.7	1:114466621-114520426	NOTEST	0	0	0	0	1	1
ENSG00000235528	ENSG00000235528	HLA-DPA2	HSCHR6_MHC_MANN:33213678-33219221	NOTEST	0	0	0	0	1	1
ENSG00000235529	ENSG00000235529	AGAP1-IT1	2:236402732-237040444	NOTEST	0.287052	0.0916735	-1.64674	0	1	1
ENSG00000235530	ENSG00000235530	AC087294.2	17:21100592-21133348	NOTEST	0.42401	0.295181	-0.522497	0	1	1
ENSG00000235532	ENSG00000235532	LINC00402	13:74805593-74834113	NOTEST	0	0.01028	inf	0	1	1
ENSG00000235533	ENSG00000235533	RP11-284P20.3	9:14025969-14030114	NOTEST	0	0	0	0	1	1
ENSG00000235534	ENSG00000235534	FECHP1	3:34914132-34915346	NOTEST	0	0	0	0	1	1
ENSG00000235535	ENSG00000235535	RP11-532N4.2	6:123537482-123958238	NOTEST	0	0	0	0	1	1
ENSG00000235536	ENSG00000235536	MICF	HSCHR6_MHC_DBB:29817346-29817475	NOTEST	0	0	0	0	1	1
ENSG00000235537	ENSG00000235537	AC009411.2	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000235538	ENSG00000235538	RP1-230L10.1	6:164124935-164180873	NOTEST	0	0	0	0	1	1
ENSG00000235539	ENSG00000235539	MTND1P33	X:142372753-142605303	NOTEST	0	0	0	0	1	1
ENSG00000235540	ENSG00000235540	TAPSAR1	HSCHR6_MHC_COX:32730816-32769949	NOTEST	0	0	0	0	1	1
ENSG00000235541	ENSG00000235541	KRT18P1	HSCHR6_MHC_QBL:28936909-28938240	NOTEST	0	0	0	0	1	1
ENSG00000235544	ENSG00000235544	RPS11P1	20:11326030-11326503	NOTEST	0	0	0	0	1	1
ENSG00000235545	ENSG00000235545	RP11-230B22.1	1:63154152-63176365	NOTEST	0.065185	0.0208133	-1.64704	0	1	1
ENSG00000235546	ENSG00000235546	AC087499.5	17:20515979-20536572	NOTEST	0	0	0	0	1	1
ENSG00000235547	ENSG00000235547	NDUFB11P1	11:92069197-92069662	NOTEST	0	0	0	0	1	1
ENSG00000235548	ENSG00000235548	AC073551.1	2:156889758-156890592	NOTEST	0	0	0	0	1	1
ENSG00000235549	ENSG00000235549	RP11-781D11.1	1:39423946-39424597	NOTEST	0	0	0	0	1	1
ENSG00000235550	ENSG00000235550	ANKRD26P2	13:39496863-39510336	NOTEST	0	0	0	0	1	1
ENSG00000235555	ENSG00000235555	SUMO1P4	19:49778375-49778677	NOTEST	0	0.253968	inf	0	1	1
ENSG00000235558	ENSG00000235558	RP11-1198D22.1	5:70435715-70585611	NOTEST	0	0	0	0	1	1
ENSG00000235559	ENSG00000235559	NOL5BP	6:28751409-28751781	NOTEST	0	0	0	0	1	1
ENSG00000235560	ENSG00000235560	AC002310.12	16:30535324-30569819	NOTEST	0.528046	0.434776	-0.28039	0	1	1
ENSG00000235561	ENSG00000235561	HCG19P	HSCHR6_MHC_DBB:30317312-30317946	NOTEST	0	0	0	0	1	1
ENSG00000235563	ENSG00000235563	RP11-334A14.8	1:53552854-53608289	NOTEST	0	0	0	0	1	1
ENSG00000235564	ENSG00000235564	AP000477.2	21:25333219-25339588	NOTEST	0	0	0	0	1	1
ENSG00000235565	ENSG00000235565	RP11-86H7.7	1:95086706-95089740	NOTEST	0.26527	0.214842	-0.304186	0	1	1
ENSG00000235566	ENSG00000235566	RP11-435B5.7	1:143527554-143533272	NOTEST	0	0	0	0	1	1
ENSG00000235568	ENSG00000235568	NFAM1	22:42776415-42828401	NOTEST	0.0353215	0.00191834	-4.20261	0	1	1
ENSG00000235569	ENSG00000235569	MSH5	HSCHR6_MHC_QBL:31698008-31719779	NOTEST	0	0	0	0	1	1

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ENSG00000235570	ENSG00000235570	LINC00533	6:28616062-28616843	NOTEST	0	0.090067	inf	0	1	1
ENSG00000235571	ENSG00000235571	SNX18P14	2:95452432-95453006	NOTEST	0	0	0	0	1	1
ENSG00000235572	ENSG00000235572	RP11-555H7.2	9:138244529-138246066	NOTEST	0	0	0	0	1	1
ENSG00000235573	ENSG00000235573	RP3-412A9.12	22:31500757-31516055	NOTEST	0	0	0	0	1	1
ENSG00000235574	ENSG00000235574	AC073150.6	7:27531300-27532384	NOTEST	0.0296505	0	#NAME?	0	1	1
ENSG00000235575	ENSG00000235575	RP4-800F24.1	1:169074934-169337205	NOTEST	0	0	0	0	1	1
ENSG00000235576	ENSG00000235576	AC092580.4	2:7865931-7870836	NOTEST	0	0	0	0	1	1
ENSG00000235577	ENSG00000235577	DASS-397D15.4	HSCHR6_MHC_DBB:32428190-32428286	NOTEST	0	0	0	0	1	1
ENSG00000235578	ENSG00000235578	XXbac-B33L19.4	22:20326327-20350457	NOTEST	0	0	0	0	1	1
ENSG00000235579	ENSG00000235579	AC007283.4	2:201980826-202041410	NOTEST	0	0	0	0	1	1
ENSG00000235581	ENSG00000235581	GS1-111G14.1	7:71244475-71912136	NOTEST	0	0	0	0	1	1
ENSG00000235582	ENSG00000235582	RP11-448G4.2	1:197473877-197744826	NOTEST	0	0	0	0	1	1
ENSG00000235583	ENSG00000235583	AC007562.1	Y:27658447-27673933	NOTEST	0	0	0	0	1	1
ENSG00000235584	ENSG00000235584	AC008268.1	2:96331831-96334463	NOTEST	0	0	0	0	1	1
ENSG00000235586	ENSG00000235586	AC011247.3	2:38789119-38830728	NOTEST	0.215595	0	#NAME?	0	1	1
ENSG00000235588	ENSG00000235588	AIF1	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000235589	ENSG00000235589	ZNF311	HSCHR6_MHC_MANN:28962565-28973097	NOTEST	0	0	0	0	1	1
ENSG00000235590	ENSG00000235590	GNAS-AS1	20:57393973-57486247	NOTEST	0.0850971	0.151733	0.834351	0	1	1
ENSG00000235592	ENSG00000235592	GS1-600G8.4	X:13346055-13347986	NOTEST	0	0	0	0	1	1
ENSG00000235593	ENSG00000235593	RBMS3-AS1	3:29305684-30051886	NOTEST	0	0	0	0	1	1
ENSG00000235594	ENSG00000235594	RP11-380D15.2	20:54842927-54844287	NOTEST	0	0	0	0	1	1
ENSG00000235595	ENSG00000235595	GAPDHP23	1:120004651-120005644	NOTEST	0.300855	0.49701	0.724207	0	1	1
ENSG00000235596	ENSG00000235596	PPIAP9	HSCHR6_MHC_SSTO:31477202-31478014	NOTEST	0	0	0	0	1	1
ENSG00000235598	ENSG00000235598	RRM2P4	X:143392256-143392818	NOTEST	0	0	0	0	1	1
ENSG00000235600	ENSG00000235600	MICD	HSCHR6_MHC_MCF:30017031-30018695	NOTEST	0	0	0	0	1	1
ENSG00000235601	ENSG00000235601	RP11-231K24.2	9:96717878-96721422	NOTEST	0	0	0	0	1	1
ENSG00000235602	ENSG00000235602	POU5F1P3	12:8276227-8371507	NOTEST	0	0.238546	inf	0	1	1
ENSG00000235604	ENSG00000235604	SPANXB1	X:140096760-140097876	NOTEST	0	0	0	0	1	1
ENSG00000235605	ENSG00000235605	RP5-827C21.1	1:234492449-234501574	NOTEST	0	0	0	0	1	1
ENSG00000235606	ENSG00000235606	AK4P6	4:151948241-151948769	NOTEST	0	0	0	0	1	1
ENSG00000235608	ENSG00000235608	NKX1-1	4:1396719-1400119	NOTEST	0	0	0	0	1	1
ENSG00000235609	ENSG00000235609	AF127936.7	21:16191163-16254296	NOTEST	0.568608	0.363141	-0.646904	0	1	1
ENSG00000235610	ENSG00000235610	AC013448.2	2:224370193-224375651	NOTEST	0	0	0	0	1	1
ENSG00000235612	ENSG00000235612	RP1-158P9.1	1:56611392-56620896	NOTEST	0	0	0	0	1	1
ENSG00000235613	ENSG00000235613	NSRP1P1	1:78245308-78344106	NOTEST	0	0.00685976	inf	0	1	1
ENSG00000235615	ENSG00000235615	AJ239322.1	2:132715849-132737446	NOTEST	0	0	0	0	1	1
ENSG00000235616	ENSG00000235616	ST13P2	2:188577542-189152418	NOTEST	0	0	0	0	1	1
ENSG00000235617	ENSG00000235617	XXbac-B476C20.10	22:18559292-18629321	NOTEST	0	0	0	0	1	1
ENSG00000235618	ENSG00000235618	RP11-324H6.5	10:51780941-51827563	NOTEST	0.158114	0.0508059	-1.6379	0	1	1
ENSG00000235619	ENSG00000235619	RPL36AP33	9:35490123-35563896	NOTEST	0	0	0	0	1	1
ENSG00000235620	ENSG00000235620	AC020743.4	7:50314385-50315218	NOTEST	0	0	0	0	1	1
ENSG00000235621	ENSG00000235621	LINC00494	20:46988692-46999372	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000235625	ENSG00000235625	RP11-203P2.2	13:78469615-79233314	NOTEST	0	0	0	0	1	1
ENSG00000235626	ENSG00000235626	KRT18P66	9:30773461-30774730	NOTEST	0	0	0	0	1	1
ENSG00000235627	ENSG00000235627	SNRPFP4	3:48198635-48229892	NOTEST	0.193194	0	#NAME?	0	1	1
ENSG00000235628	ENSG00000235628	TNR-IT1	1:175276353-175712906	NOTEST	0	0	0	0	1	1
ENSG00000235629	ENSG00000235629	AC090952.5	3:14689700-14690939	NOTEST	0	0	0	0	1	1
ENSG00000235630	ENSG00000235630	OR2H5P	HSCHR6_MHC_QBL:29523309-29600897	NOTEST	0	0	0	0	1	1
ENSG00000235631	ENSG00000235631	RNF148	7:121958480-122526813	NOTEST	0.0393255	0.0694756	0.821039	0	1	1
ENSG00000235632	ENSG00000235632	OR2J1	HSCHR6_MHC_SSTO:29068752-29069691	NOTEST	0	0	0	0	1	1
ENSG00000235635	ENSG00000235635	AC016644.1	5:56195867-56267502	NOTEST	0	0	0	0	1	1
ENSG00000235637	ENSG00000235637	RP11-457D2.3	10:18098351-18200091	NOTEST	0	0	0	0	1	1
ENSG00000235638	ENSG00000235638	MTND6P14	1:235700819-235701341	NOTEST	0	0	0	0	1	1
ENSG00000235639	ENSG00000235639	AC002069.6	7:88141343-88142502	NOTEST	0	0	0	0	1	1
ENSG00000235640	ENSG00000235640	AC092646.1	2:124452877-124454972	NOTEST	0	0	0	0	1	1
ENSG00000235641	ENSG00000235641	LINC00484	9:93881343-93945044	NOTEST	0.127677	0.0494238	-1.36922	0	1	1
ENSG00000235642	ENSG00000235642	PTP4A1P5	X:27445893-27446348	NOTEST	0	0	0	0	1	1
ENSG00000235643	ENSG00000235643	RP1-69M21.2	1:11669587-11673412	NOTEST	0	0.0103634	inf	0	1	1
ENSG00000235644	ENSG00000235644	AC010095.7	2:109328717-109329356	NOTEST	0	0	0	0	1	1
ENSG00000235645	ENSG00000235645	RP11-242G20.1	10:71444654-71452208	NOTEST	0	0	0	0	1	1
ENSG00000235646	ENSG00000235646	MTND1P2	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000235647	ENSG00000235647	RP1-172B20.6	22:40139048-40289868	NOTEST	0	0	0	0	1	1
ENSG00000235649	ENSG00000235649	MXRA5P1	Y:14077913-14108092	NOTEST	0	0	0	0	1	1
ENSG00000235650	ENSG00000235650	RPS18	HSCHR6_MHC_COX:33138932-33165893	NOTEST	0	0	0	0	1	1
ENSG00000235651	ENSG00000235651	AC064850.4	2:135809834-136288806	NOTEST	0.0121069	0	#NAME?	0	1	1
ENSG00000235652	ENSG00000235652	RP11-545I5.3	6:146136047-146285559	NOTEST	0.422046	0.318758	-0.404937	0	1	1
ENSG00000235653	ENSG00000235653	AC007253.1	2:40013592-40838193	NOTEST	0	0	0	0	1	1
ENSG00000235656	ENSG00000235656	RPL36P18	X:114345184-114468635	NOTEST	0	0	0	0	1	1
ENSG00000235657	ENSG00000235657	HLA-A	HSCHR6_MHC_DBB:29898999-29903640	NOTEST	0	0	0	0	1	1
ENSG00000235658	ENSG00000235658	ATAT1	HSCHR6_MHC_MANN:30639293-30659275	NOTEST	0	0	0	0	1	1
ENSG00000235659	ENSG00000235659	RP11-374M1.5	9:45001906-45003117	NOTEST	0	0.0394657	inf	0	1	1
ENSG00000235660	ENSG00000235660	LINC00345	13:53058295-53058815	NOTEST	0	0	0	0	1	1
ENSG00000235661	ENSG00000235661	MIR670HG	11:43577985-43902276	NOTEST	0	0.0797083	inf	0	1	1
ENSG00000235663	ENSG00000235663	SAPCD1-AS1	6:31707724-31733365	NOTEST	0	0.0342914	inf	0	1	1
ENSG00000235664	ENSG00000235664	AC005682.8	7:22928989-22980809	NOTEST	0	0.0229376	inf	0	1	1
ENSG00000235665	ENSG00000235665	LINC00298	2:8062555-8523751	NOTEST	0	0	0	0	1	1
ENSG00000235666	ENSG00000235666	SUMO2P1	HSCHR6_MHC_SSTO:29603536-29603820	NOTEST	0	0	0	0	1	1
ENSG00000235668	ENSG00000235668	XXbac-BPG308K3.5	HSCHR6_MHC_MCF:28805654-28806792	NOTEST	0	0	0	0	1	1
ENSG00000235669	ENSG00000235669	AC004593.3	7:29019582-29603286	NOTEST	0.0671163	0.211103	1.65321	0	1	1
ENSG00000235670	ENSG00000235670	RPL21P40	3:31699381-32119072	NOTEST	0	0	0	0	1	1
ENSG00000235672	ENSG00000235672	AC090286.2	17:18739019-18834581	NOTEST	0.173211	0	#NAME?	0	1	1
ENSG00000235673	ENSG00000235673	RP11-109P14.8	1:38275238-38325292	NOTEST	0	0	0	0	1	1
ENSG00000235675	ENSG00000235675	AC151961.1	X:152387935-152393740	NOTEST	0	0	0	0	1	1
ENSG00000235676	ENSG00000235676	ABHD16A	HSCHR6_MHC_COX:31616420-31658607	NOTEST	0	0	0	0	1	1
ENSG00000235677	ENSG00000235677	NPM1P26	10:98277865-98347209	NOTEST	0.218667	0.195387	-0.162402	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235678	ENSG00000235678	OR5AN2P	11:59077153-59078049	NOTEST	0	0	0	0	1	1
ENSG00000235679	ENSG00000235679	RP11-449I17.9	10:30672328-30672551	NOTEST	0	0	0	0	1	1
ENSG00000235680	ENSG00000235680	HLA-G	HSCHR6_MHC_MANN:29791676-29795834	NOTEST	0	0	0	0	1	1
ENSG00000235681	ENSG00000235681	AC008746.5	19:54955990-54974894	NOTEST	1.06106	1.46905	0.469375	0	1	1
ENSG00000235683	ENSG00000235683	AC018442.1	8:100025493-100906290	NOTEST	0	0.00552095	inf	0	1	1
ENSG00000235684	ENSG00000235684	HTATSF1P	HSCHR6_MHC_QBL:33130641-33142541	NOTEST	0	0	0	0	1	1
ENSG00000235685	ENSG00000235685	RP11-126D17.1	X:40374146-40374760	NOTEST	0	0	0	0	1	1
ENSG00000235686	ENSG00000235686	PPIAP20	19:12490002-12750912	NOTEST	0	0	0	0	1	1
ENSG00000235687	ENSG00000235687	LINC00993	10:37414784-37673039	NOTEST	0	0	0	0	1	1
ENSG00000235688	ENSG00000235688	AC116614.1	2:945319-945960	NOTEST	0	0	0	0	1	1
ENSG00000235689	ENSG00000235689	AP000351.13	22:24402750-24404704	NOTEST	0	0	0	0	1	1
ENSG00000235690	ENSG00000235690	CUBNP3	10:45493145-45676875	NOTEST	0	0	0	0	1	1
ENSG00000235691	ENSG00000235691	AC006987.5	Y:9928410-9928816	NOTEST	0	0	0	0	1	1
ENSG00000235692	ENSG00000235692	PFDN6	HSCHR6_MHC_MCF:33417261-33437523	NOTEST	0	0	0	0	1	1
ENSG00000235695	ENSG00000235695	RP11-395P16.1	3:47626761-47823596	NOTEST	0	0	0	0	1	1
ENSG00000235696	ENSG00000235696	C2	HSCHR6_MHC_SSTO:31879618-31911713	NOTEST	0	0	0	0	1	1
ENSG00000235697	ENSG00000235697	DDX39BP1	HSCHR6_MHC_APD:29812770-29813137	NOTEST	0	0	0	0	1	1
ENSG00000235698	ENSG00000235698	PA2G4P2	20:12360703-12361903	NOTEST	0	0	0	0	1	1
ENSG00000235699	ENSG00000235699	CXorf51B	X:145891301-145891927	NOTEST	0	0	0	0	1	1
ENSG00000235700	ENSG00000235700	CYCSP52	1:157090982-157108266	NOTEST	0.415907	0.765983	0.881053	0	1	1
ENSG00000235701	ENSG00000235701	PCBP2P1	21:40543055-40544032	NOTEST	0	0	0	0	1	1
ENSG00000235702	ENSG00000235702	WI2-925H4.1	1:145827204-145833118	NOTEST	0	0	0	0	1	1
ENSG00000235704	ENSG00000235704	AC023490.2	22:20377668-20378803	NOTEST	0.0797289	0.0634013	-0.330591	0	1	1
ENSG00000235705	ENSG00000235705	AL133481.1	10:81266125-81270678	NOTEST	0.0104368	0.0162222	0.63629	0	1	1
ENSG00000235707	ENSG00000235707	RP11-323A7.1	9:78016804-78017908	NOTEST	0	0	0	0	1	1
ENSG00000235708	ENSG00000235708	COL11A2	HSCHR6_MHC_MCF:33300826-33330643	NOTEST	0	0	0	0	1	1
ENSG00000235710	ENSG00000235710	RP5-1097F14.3	1:231297857-231357302	NOTEST	0.0126184	0	#NAME?	0	1	1
ENSG00000235711	ENSG00000235711	ANKRD34C	15:79484048-79590580	NOTEST	0	0.0249191	inf	0	1	1
ENSG00000235712	ENSG00000235712	RXRB	HSCHR6_MHC_MCF:33331731-33342580	NOTEST	0	0	0	0	1	1
ENSG00000235713	ENSG00000235713	RP4-604G5.3	7:99590019-99590673	NOTEST	0	0	0	0	1	1
ENSG00000235714	ENSG00000235714	MICG	HSCHR6_MHC_APD:29780381-29780513	NOTEST	0	0	0	0	1	1
ENSG00000235715	ENSG00000235715	PSMB8	HSCHR6_MHC_COX:32730816-32769949	NOTEST	0	0	0	0	1	1
ENSG00000235716	ENSG00000235716	KRT18P46	2:162272604-162841792	NOTEST	0.0134043	0	#NAME?	0	1	1
ENSG00000235717	ENSG00000235717	DPP10-AS2	2:115199875-116603328	NOTEST	0	0	0	0	1	1
ENSG00000235718	ENSG00000235718	MFRP	11:119209651-119217383	NOTEST	0	0	0	0	1	1
ENSG00000235719	ENSG00000235719	AC010141.1	Y:23627269-23629049	NOTEST	0	0	0	0	1	1
ENSG00000235721	ENSG00000235721	AC013268.3	2:110765251-110768360	NOTEST	0	0.00484514	inf	0	1	1
ENSG00000235722	ENSG00000235722	TRIM31-AS1	HSCHR6_MHC_APD:30015057-30019333	NOTEST	0	0	0	0	1	1
ENSG00000235724	ENSG00000235724	AC009299.2	2:161952741-162111179	NOTEST	0	0	0	0	1	1
ENSG00000235725	ENSG00000235725	AC007389.3	2:65663844-66311773	NOTEST	0	0	0	0	1	1
ENSG00000235726	ENSG00000235726	AC010148.1	2:235742958-235822028	NOTEST	0	0	0	0	1	1
ENSG00000235727	ENSG00000235727	HCG18	HSCHR6_MHC_APD:30266816-30322899	NOTEST	0	0	0	0	1	1
ENSG00000235728	ENSG00000235728	AC007349.5	7:36820612-36822394	NOTEST	0	0	0	0	1	1
ENSG00000235729	ENSG00000235729	RP11-29O6.2	X:142840831-142911228	NOTEST	0	0	0	0	1	1
ENSG00000235730	ENSG00000235730	OR2AF1P	X:130753022-130753911	NOTEST	0	0	0	0	1	1

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ENSG00000235733	ENSG00000235733	RP3-522P13.3	6:25245583-25261959	NOTEST	0	0	0	0	1	1
ENSG00000235734	ENSG00000235734	HMGN1P36	2:98372798-98612388	NOTEST	0	0.27728	inf	0	1	1
ENSG00000235735	ENSG00000235735	RPL7AP72	X:127447258-127448026	NOTEST	0	0	0	0	1	1
ENSG00000235736	ENSG00000235736	RP1-10C16.1	1:168732602-168743728	NOTEST	0	0	0	0	1	1
ENSG00000235737	ENSG00000235737	TRIM60P19	13:66843128-66844590	NOTEST	0	0	0	0	1	1
ENSG00000235738	ENSG00000235738	RP11-419M24.2	7:55861236-55930482	NOTEST	0	0	0	0	1	1
ENSG00000235740	ENSG00000235740	RP11-436I24.1	6:143857981-144184949	NOTEST	0	0	0	0	1	1
ENSG00000235741	ENSG00000235741	RP5-866L20.1	1:54982084-54982932	NOTEST	0	0	0	0	1	1
ENSG00000235742	ENSG00000235742	RP11-5G18.2	10:118592511-118886097	NOTEST	0	0	0	0	1	1
ENSG00000235743	ENSG00000235743	RP11-439H9.1	6:23337938-23346788	NOTEST	0	0	0	0	1	1
ENSG00000235744	ENSG00000235744	HLA-DOA	HSCHR6_MHC_DBB:32949906-32955340	NOTEST	0	0	0	0	1	1
ENSG00000235746	ENSG00000235746	CTBP2P2	10:96406120-96407753	NOTEST	0.0127703	0	#NAME?	0	1	1
ENSG00000235747	ENSG00000235747	HCG21	HSCHR6_MHC_DBB:30899495-30913356	NOTEST	0	0	0	0	1	1
ENSG00000235748	ENSG00000235748	RP11-32D17.4	1:197053257-197115824	NOTEST	0.0707927	0.199098	1.4918	0	1	1
ENSG00000235749	ENSG00000235749	RP11-634B7.4	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000235751	ENSG00000235751	MAGI2-IT1	7:77646392-79100524	NOTEST	0.0682805	0	#NAME?	0	1	1
ENSG00000235754	ENSG00000235754	APOM	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000235756	ENSG00000235756	RP11-339A11.1	1:80557787-80558922	NOTEST	0	0	0	0	1	1
ENSG00000235757	ENSG00000235757	PTMAP1	HSCHR6_MHC_QBL:30584128-30604110	NOTEST	0	0	0	0	1	1
ENSG00000235758	ENSG00000235758	AGPAT1	HSCHR6_MHC_MCF:32192561-32222305	NOTEST	0	0	0	0	1	1
ENSG00000235759	ENSG00000235759	ARHGAP42P3	22:16399956-16436527	NOTEST	0	0	0	0	1	1
ENSG00000235760	ENSG00000235760	AC138655.4	2:47630107-47798078	NOTEST	0	0	0	0	1	1
ENSG00000235761	ENSG00000235761	RP11-293G6__B.2	1:235705458-235705690	NOTEST	0	0	0	0	1	1
ENSG00000235763	ENSG00000235763	SNRPGP5	10:12938626-13180291	NOTEST	0	0	0	0	1	1
ENSG00000235764	ENSG00000235764	ETF1P1	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000235765	ENSG00000235765	SAPCD1-AS1	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000235768	ENSG00000235768	BRD7P5	13:95409704-95411526	NOTEST	0	0.00699011	inf	0	1	1
ENSG00000235769	ENSG00000235769	LY6G6E	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000235770	ENSG00000235770	LINC00607	2:216395169-216708445	NOTEST	0.350228	0.138392	-1.33953	0	1	1
ENSG00000235772	ENSG00000235772	AP001625.6	21:43892595-44001550	NOTEST	0.0680947	0.143535	1.07579	0	1	1
ENSG00000235773	ENSG00000235773	NRM	HSCHR6_MHC_COX:30645692-30649066	NOTEST	0	0	0	0	1	1
ENSG00000235774	ENSG00000235774	AC023347.1	2:127066086-127101569	NOTEST	0.0343071	0.0759754	1.14703	0	1	1
ENSG00000235775	ENSG00000235775	AC063976.2	5:131499295-131499458	NOTEST	0	0	0	0	1	1
ENSG00000235776	ENSG00000235776	AC000089.3	22:19744225-19842462	NOTEST	0.0707311	0.113817	0.686303	0	1	1
ENSG00000235777	ENSG00000235777	DPYD-AS2	1:97543298-98386605	NOTEST	0	0	0	0	1	1
ENSG00000235778	ENSG00000235778	AC130360.8	8:7159132-7212876	NOTEST	0	0	0	0	1	1
ENSG00000235779	ENSG00000235779	AC079779.5	2:305110-314367	NOTEST	0	0	0	0	1	1
ENSG00000235780	ENSG00000235780	USP17L27	4:9345873-9347466	NOTEST	0	0	0	0	1	1
ENSG00000235781	ENSG00000235781	XXbac-BPG249D20.9	6:30484042-30486994	NOTEST	0.0836698	0.0663795	-0.333969	0	1	1
ENSG00000235782	ENSG00000235782	RP3-333A15.1	1:71318035-71513491	NOTEST	0	0.0181505	inf	0	1	1
ENSG00000235784	ENSG00000235784	HNRNPA1P29	13:93879094-95059655	NOTEST	0	0	0	0	1	1
ENSG00000235785	ENSG00000235785	AL109767.1	14:99635623-99737861	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235786	ENSG00000235786	ZNRF3-IT1	22:29279579-29453475	NOTEST	0.0295317	0	#NAME?	0	1	1
ENSG00000235787	ENSG00000235787	RP11-219I21.1	3:42511131-42511371	NOTEST	0	0	0	0	1	1
ENSG00000235788	ENSG00000235788	LINC01015	HSCHR6_MHC_APD:29497283-29501432	NOTEST	0	0	0	0	1	1
ENSG00000235790	ENSG00000235790	RP11-73M7.6	1:32083286-32169920	NOTEST	0	0.092588	inf	0	1	1
ENSG00000235794	ENSG00000235794	RP5-837O21.6	1:94389941-94390272	NOTEST	0	0	0	0	1	1
ENSG00000235795	ENSG00000235795	RP11-421L21.2	1:101455178-101552821	NOTEST	0.397121	0.543597	0.452956	0	1	1
ENSG00000235797	ENSG00000235797	RP11-402G3.6	9:117335180-117335651	NOTEST	0	0.0704172	inf	0	1	1
ENSG00000235801	ENSG00000235801	XXbac-BPG249D20.9	HSCHR6_MHC_MANN:30528709-30531661	NOTEST	0	0	0	0	1	1
ENSG00000235802	ENSG00000235802	HCFC1-AS1	X:153213003-153237258	NOTEST	0.0831085	0	#NAME?	0	1	1
ENSG00000235803	ENSG00000235803	RP11-343J3.6	10:71350338-71351018	NOTEST	0	0	0	0	1	1
ENSG00000235804	ENSG00000235804	RP4-535B20.2	1:65543095-65543814	NOTEST	0	0	0	0	1	1
ENSG00000235805	ENSG00000235805	SOCS5P3	3:44750802-44752378	NOTEST	0	0	0	0	1	1
ENSG00000235806	ENSG00000235806	RP4-646N3.1	X:38629583-38658911	NOTEST	0	0.0207258	inf	0	1	1
ENSG00000235808	ENSG00000235808	MYL6P2	21:40817780-40887433	NOTEST	0	0	0	0	1	1
ENSG00000235809	ENSG00000235809	DDX39BP2	HSCHR6_MHC_APD:29897439-29897836	NOTEST	0	0	0	0	1	1
ENSG00000235810	ENSG00000235810	RP11-550A9.1	10:59272916-59273185	NOTEST	0	0	0	0	1	1
ENSG00000235811	ENSG00000235811	RP11-510N19.3	1:202008978-202009062	NOTEST	0	0	0	0	1	1
ENSG00000235812	ENSG00000235812	ADAM21P1	14:70712207-70714518	NOTEST	0.00790528	0.0173638	1.1352	0	1	1
ENSG00000235813	ENSG00000235813	RP11-308B5.2	X:133699867-133898352	NOTEST	0	0	0	0	1	1
ENSG00000235814	ENSG00000235814	NCRNA00171	HSCHR6_MHC_QBL:29958304-30022269	NOTEST	0	0	0	0	1	1
ENSG00000235815	ENSG00000235815	RP1-125N5.2	6:169116744-169123604	NOTEST	0	0	0	0	1	1
ENSG00000235816	ENSG00000235816	PRELID1P3	10:64926980-65226323	NOTEST	0	0	0	0	1	1
ENSG00000235817	ENSG00000235817	RP11-543E8.2	1:230747754-230748158	NOTEST	0	0	0	0	1	1
ENSG00000235818	ENSG00000235818	VN1R17P	1:247353152-247405125	NOTEST	0	0	0	0	1	1
ENSG00000235819	ENSG00000235819	RP11-359J6.1	9:89029196-89029485	NOTEST	0	0	0	0	1	1
ENSG00000235820	ENSG00000235820	RP5-1022P6.5	20:5514273-5516535	NOTEST	0	0	0	0	1	1
ENSG00000235822	ENSG00000235822	LINC01073	13:32559821-32565134	NOTEST	0	0	0	0	1	1
ENSG00000235824	ENSG00000235824	LINC00837	10:29078116-29102387	NOTEST	0	0	0	0	1	1
ENSG00000235825	ENSG00000235825	FAM90A9P	8:7618851-7621862	NOTEST	0	0	0	0	1	1
ENSG00000235827	ENSG00000235827	TUBB8P9	1:227693882-227695993	NOTEST	0	0	0	0	1	1
ENSG00000235828	ENSG00000235828	RPL36AP26	7:15741056-15741377	NOTEST	0	0	0	0	1	1
ENSG00000235829	ENSG00000235829	TBCAP2	1:14925199-15478960	NOTEST	0	0	0	0	1	1
ENSG00000235830	ENSG00000235830	SRGAP3-AS4	3:9022274-9520924	NOTEST	0	0	0	0	1	1
ENSG00000235831	ENSG00000235831	BHLHE40-AS1	3:4938492-5027008	NOTEST	0.171247	0.256634	0.58363	0	1	1
ENSG00000235832	ENSG00000235832	CNN2P3	9:69498581-69499487	NOTEST	0	0	0	0	1	1
ENSG00000235833	ENSG00000235833	AC159540.14	2:98108977-98206428	NOTEST	0	0	0	0	1	1
ENSG00000235834	ENSG00000235834	RP1-60N8.1	X:17393542-17754114	NOTEST	0	0	0	0	1	1
ENSG00000235836	ENSG00000235836	AC124944.4	3:195563063-195587275	NOTEST	0	0	0	0	1	1
ENSG00000235837	ENSG00000235837	AC073333.8	7:16685755-16759523	NOTEST	0	0.0220965	inf	0	1	1
ENSG00000235838	ENSG00000235838	HSP90AB7P	10:9763925-9766379	NOTEST	0	0	0	0	1	1
ENSG00000235840	ENSG00000235840	AC012363.13	2:121076582-121083874	NOTEST	0	0	0	0	1	1
ENSG00000235843	ENSG00000235843	RP13-16H11.5	10:26986587-27150016	NOTEST	0.0946007	0	#NAME?	0	1	1
ENSG00000235844	ENSG00000235844	HLA-DPA1	HSCHR6_MHC_APD:33015767-33038372	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235845	ENSG00000235845	RP11-272D20.2	3:44916099-44956482	NOTEST	0	0	0	0	1	1
ENSG00000235847	ENSG00000235847	LDHAP7	2:84743578-85046713	NOTEST	0	0	0	0	1	1
ENSG00000235848	ENSG00000235848	RMDN2-AS1	2:38150329-38408997	NOTEST	0.021589	0	#NAME?	0	1	1
ENSG00000235849	ENSG00000235849	HS6ST2-AS1	X:131760043-132095423	NOTEST	0	0	0	0	1	1
ENSG00000235852	ENSG00000235852	AC005540.3	2:191745522-191885686	NOTEST	0	0.0206339	inf	0	1	1
ENSG00000235855	ENSG00000235855	RP11-655M14.6	11:67489953-67490926	NOTEST	0	0	0	0	1	1
ENSG00000235857	ENSG00000235857	CTBP2P1	Y:59001390-59001635	NOTEST	0	0	0	0	1	1
ENSG00000235858	ENSG00000235858	RP11-36D19.8	10:82093526-82094182	NOTEST	0	0	0	0	1	1
ENSG00000235861	ENSG00000235861	AC005237.2	2:242045513-242123067	NOTEST	0	0	0	0	1	1
ENSG00000235862	ENSG00000235862	RP11-338C15.5	1:212797625-212800120	NOTEST	0	0	0	0	1	1
ENSG00000235864	ENSG00000235864	HSPA8P6	2:209937320-209938872	NOTEST	0	0	0	0	1	1
ENSG00000235868	ENSG00000235868	GAPDHP31	12:7718964-7719978	NOTEST	0	0	0	0	1	1
ENSG00000235869	ENSG00000235869	RP1-102G20.4	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000235871	ENSG00000235871	AC062016.3	2:117575661-117576337	NOTEST	0	0	0	0	1	1
ENSG00000235875	ENSG00000235875	ARHGEF7-AS2	13:111766158-111958084	NOTEST	0	0	0	0	1	1
ENSG00000235876	ENSG00000235876	FEM1AP4	13:19239374-19241361	NOTEST	0	0	0	0	1	1
ENSG00000235877	ENSG00000235877	HCG19P	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000235878	ENSG00000235878	AP001468.1	21:47604992-47648738	NOTEST	0.179105	0.622462	1.79718	0	1	1
ENSG00000235879	ENSG00000235879	FAR1P1	13:90823119-90824053	NOTEST	0	0	0	0	1	1
ENSG00000235880	ENSG00000235880	RP11-59O6.3	9:213107-746105	NOTEST	0	0	0	0	1	1
ENSG00000235881	ENSG00000235881	AC114776.3	2:111467151-111474172	NOTEST	0	0	0	0	1	1
ENSG00000235884	ENSG00000235884	LINC00941	12:30947976-30955645	NOTEST	0.427676	0.553515	0.372104	0	1	1
ENSG00000235885	ENSG00000235885	AC023115.2	2:67313577-67523207	NOTEST	0.0549128	0.0617951	0.17035	0	1	1
ENSG00000235886	ENSG00000235886	RP4-672N11.1	3:43820452-43821474	NOTEST	0	0	0	0	1	1
ENSG00000235887	ENSG00000235887	RP11-763B22.6	1:148852392-148853717	NOTEST	0	0	0	0	1	1
ENSG00000235888	ENSG00000235888	AF064858.8	21:40360632-40378079	NOTEST	0	0	0	0	1	1
ENSG00000235890	ENSG00000235890	TSPEAR-AS1	21:45917774-46131495	NOTEST	0	0.0171705	inf	0	1	1
ENSG00000235892	ENSG00000235892	PKMP2	X:65717589-65719266	NOTEST	0	0	0	0	1	1
ENSG00000235893	ENSG00000235893	RP11-460E7.8	9:70348572-70349113	NOTEST	0	0	0	0	1	1
ENSG00000235895	ENSG00000235895	AC010154.2	Y:6361016-6364798	NOTEST	0	0	0	0	1	1
ENSG00000235896	ENSG00000235896	IGKV3D-7	2:90273678-90274235	NOTEST	0	0	0	0	1	1
ENSG00000235897	ENSG00000235897	TM4SF19-AS1	3:195938357-196065374	NOTEST	0.169375	0.538876	1.66973	0	1	1
ENSG00000235899	ENSG00000235899	RP11-345L23.1	6:53493177-53496192	NOTEST	0	0	0	0	1	1
ENSG00000235901	ENSG00000235901	RP11-342F21.1	9:105277485-105280590	NOTEST	0	0	0	0	1	1
ENSG00000235902	ENSG00000235902	RP11-626E13.1	4:186506597-186877806	NOTEST	0	0.160556	inf	0	1	1
ENSG00000235904	ENSG00000235904	RBMS3-AS3	3:29305684-30051886	NOTEST	0	0.0499563	inf	0	1	1
ENSG00000235905	ENSG00000235905	TRIM15	HSCHR6_MHC_MCF:30209466-30218957	NOTEST	0	0	0	0	1	1
ENSG00000235907	ENSG00000235907	RP4-580O19.2	1:33977607-33978343	NOTEST	0	0	0	0	1	1
ENSG00000235908	ENSG00000235908	RHOA-IT1	3:49396577-49453908	NOTEST	0.0858617	0.0974285	0.182328	0	1	1
ENSG00000235910	ENSG00000235910	APOA1-AS	11:116706466-116969153	NOTEST	0	0	0	0	1	1
ENSG00000235911	ENSG00000235911	AC019055.1	2:19911475-19917337	NOTEST	0	0	0	0	1	1
ENSG00000235914	ENSG00000235914	MACROD2-AS1	20:13829892-16033842	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000235915	ENSG00000235915	LST1	HSCHR6_MHC_APD:31565221-31572083	NOTEST	0	0	0	0	1	1
ENSG00000235916	ENSG00000235916	RP13-444K19.1	X:53852384-53852807	NOTEST	0	0	0	0	1	1
ENSG00000235917	ENSG00000235917	RP11-39K24.14	9:4985032-5128183	NOTEST	0	0	0	0	1	1
ENSG00000235920	ENSG00000235920	AC073109.2	7:11221358-11871824	NOTEST	0	0	0	0	1	1
ENSG00000235922	ENSG00000235922	RP11-323C15.1	20:45492201-45492743	NOTEST	0	0	0	0	1	1
ENSG00000235923	ENSG00000235923	TRIM26BP	HSCHR6_MHC_QBL:30191333-30304165	NOTEST	0	0	0	0	1	1
ENSG00000235924	ENSG00000235924	ZNRF2P3	10:81664653-81742370	NOTEST	0	0	0	0	1	1
ENSG00000235925	ENSG00000235925	LY6G6C	HSCHR6_MHC_SSTO:31676329-31684446	NOTEST	0	0	0	0	1	1
ENSG00000235926	ENSG00000235926	RP13-650G11.1	7:100525989-100526160	NOTEST	0	0	0	0	1	1
ENSG00000235927	ENSG00000235927	NEXN-AS1	1:78347032-78409580	NOTEST	0.0149105	0.00491843	-1.60006	0	1	1
ENSG00000235929	ENSG00000235929	TPT1P14	X:14996080-14996585	NOTEST	0	0	0	0	1	1
ENSG00000235930	ENSG00000235930	HSPE1P12	12:10902832-10930043	NOTEST	0	0	0	0	1	1
ENSG00000235931	ENSG00000235931	C10orf40	10:61715187-61720671	NOTEST	0	0.00701989	inf	0	1	1
ENSG00000235932	ENSG00000235932	RP11-250H24.6	9:69749820-69750173	NOTEST	0	0	0	0	1	1
ENSG00000235933	ENSG00000235933	RP5-1185H19.2	1:116706904-116708862	NOTEST	0	0	0	0	1	1
ENSG00000235934	ENSG00000235934	AC007405.8	2:171669722-171717661	NOTEST	0.131401	0.229026	0.801533	0	1	1
ENSG00000235937	ENSG00000235937	AC008280.1	2:54091203-54532437	NOTEST	0	0	0	0	1	1
ENSG00000235938	ENSG00000235938	RP11-157L3.4	9:46113698-46114039	NOTEST	0.0868461	0.0679181	-0.354664	0	1	1
ENSG00000235939	ENSG00000235939	RP11-123B3.2	10:50627322-50747584	NOTEST	0	0	0	0	1	1
ENSG00000235940	ENSG00000235940	MTND1P21	10:21068901-21463977	NOTEST	0	0	0	0	1	1
ENSG00000235941	ENSG00000235941	HSPA1A	HSCHR6_MHC_APD:31794604-31797087	NOTEST	0	0	0	0	1	1
ENSG00000235942	ENSG00000235942	LCE6A	1:152815343-152816459	NOTEST	0	0	0	0	1	1
ENSG00000235943	ENSG00000235943	TMEM212-IT1	3:171561138-171656505	NOTEST	0	0	0	0	1	1
ENSG00000235945	ENSG00000235945	AC002543.2	7:116451123-116562103	NOTEST	0.0150895	0	#NAME?	0	1	1
ENSG00000235946	ENSG00000235946	LL0XNC01-240C2.1	X:103317105-103317601	NOTEST	0	0	0	0	1	1
ENSG00000235947	ENSG00000235947	EGOT	3:4535031-4928977	NOTEST	0	0	0	0	1	1
ENSG00000235949	ENSG00000235949	AC061961.2	2:155552973-155554329	NOTEST	0	0	0	0	1	1
ENSG00000235950	ENSG00000235950	DUX4L15	10:135496887-135498492	NOTEST	0	0	0	0	1	1
ENSG00000235951	ENSG00000235951	AC009965.1	2:204930428-204932086	NOTEST	0	0	0	0	1	1
ENSG00000235952	ENSG00000235952	HCG4P5	HSCHR6_MHC_QBL:29898416-29903057	NOTEST	0	0	0	0	1	1
ENSG00000235955	ENSG00000235955	CICP20	7:45855814-45860663	NOTEST	0.102781	0.133053	0.372429	0	1	1
ENSG00000235956	ENSG00000235956	PRRT1	HSCHR6_MHC_SSTO:32123002-32152743	NOTEST	0	0	0	0	1	1
ENSG00000235958	ENSG00000235958	UBOX5-AS1	20:3087558-3140842	NOTEST	0	0	0	0	1	1
ENSG00000235959	ENSG00000235959	AC009237.17	2:96305928-96306352	NOTEST	0	0	0	0	1	1
ENSG00000235960	ENSG00000235960	TRIM15	HSCHR6_MHC_DBB:30121294-30130785	NOTEST	0	0	0	0	1	1
ENSG00000235962	ENSG00000235962	RP11-462L8.2	10:33189246-33371030	NOTEST	0	0	0	0	1	1
ENSG00000235963	ENSG00000235963	MCCD1P1	6:29875559-29876422	NOTEST	0	0	0	0	1	1
ENSG00000235964	ENSG00000235964	FXYD6P2	10:38380691-38380979	NOTEST	0	0	0	0	1	1
ENSG00000235965	ENSG00000235965	AP000431.1	21:20418628-20420003	NOTEST	0	0	0	0	1	1
ENSG00000235966	ENSG00000235966	OR12D2	HSCHR6_MHC_COX:29319721-29421426	NOTEST	0	0	0	0	1	1
ENSG00000235967	ENSG00000235967	COX5BP3	7:132937828-133751342	NOTEST	0	0	0	0	1	1
ENSG00000235968	ENSG00000235968	AC079112.1	2:68250825-68251898	NOTEST	0	0	0	0	1	1
ENSG00000235969	ENSG00000235969	CHEK2P4	22:16984193-16990365	NOTEST	0	0	0	0	1	1

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ENSG00000235974	ENSG00000235974	VN2R19P	19:58523956-58537294	NOTEST	0	0	0	0	1	1
ENSG00000235975	ENSG00000235975	RP1-106C24.1	X:137713734-138304939	NOTEST	0	0	0	0	1	1
ENSG00000235976	ENSG00000235976	RP1-197J16.1	X:101244453-101244845	NOTEST	0	0	0	0	1	1
ENSG00000235978	ENSG00000235978	AC018816.3	3:4535031-4928977	NOTEST	0	0	0	0	1	1
ENSG00000235979	ENSG00000235979	AC004448.5	17:19342455-19364308	NOTEST	0	0	0	0	1	1
ENSG00000235981	ENSG00000235981	AC023274.4	Y:26288504-26303990	NOTEST	0	0	0	0	1	1
ENSG00000235982	ENSG00000235982	AC007875.3	7:97512593-97513107	NOTEST	0	0	0	0	1	1
ENSG00000235984	ENSG00000235984	GPC5-AS1	13:92050928-93519490	NOTEST	0	0	0	0	1	1
ENSG00000235985	ENSG00000235985	AIF1	HSCHR6_MHC_MCF:31659257-31661095	NOTEST	0	0	0	0	1	1
ENSG00000235986	ENSG00000235986	GNL1	HSCHR6_MHC_COX:30498997-30521345	NOTEST	0	0	0	0	1	1
ENSG00000235988	ENSG00000235988	RP11-495P10.4	1:147789798-147790129	NOTEST	0	0	0	0	1	1
ENSG00000235989	ENSG00000235989	MORC2-AS1	22:31318294-31364284	NOTEST	0.0349675	0.0455879	0.382639	0	1	1
ENSG00000235990	ENSG00000235990	RP11-323D18.5	1:242079424-242079845	NOTEST	0	0.0846803	inf	0	1	1
ENSG00000235991	ENSG00000235991	RP11-143H17.1	X:154289896-154384778	NOTEST	0	0	0	0	1	1
ENSG00000235992	ENSG00000235992	GRAMD4P2	22:16199665-16231333	NOTEST	0	0	0	0	1	1
ENSG00000235993	ENSG00000235993	AC007559.1	2:230222344-230579274	NOTEST	0	0	0	0	1	1
ENSG00000235994	ENSG00000235994	RP3-470B24.5	6:168376603-168380456	NOTEST	0	0	0	0	1	1
ENSG00000235995	ENSG00000235995	UBE2V1P6	2:169971704-169972190	NOTEST	0	0	0	0	1	1
ENSG00000235996	ENSG00000235996	RP11-97N19.2	20:19193289-19703581	NOTEST	0	0	0	0	1	1
ENSG00000235997	ENSG00000235997	AC109642.1	2:30569524-30575297	NOTEST	0	0.00414855	inf	0	1	1
ENSG00000235998	ENSG00000235998	TAAR7P	6:132880162-132880404	NOTEST	0	0	0	0	1	1
ENSG00000236002	ENSG00000236002	CTB-75G16.1	17:34900736-34946278	NOTEST	0.246258	0.333171	0.436093	0	1	1
ENSG00000236003	ENSG00000236003	AC007050.17	22:20850199-20946505	NOTEST	0	0	0	0	1	1
ENSG00000236004	ENSG00000236004	RP4-800M22.4	1:52608045-52831865	NOTEST	0	0	0	0	1	1
ENSG00000236005	ENSG00000236005	RP11-438P9.1	9:110296670-110297443	NOTEST	0	0	0	0	1	1
ENSG00000236006	ENSG00000236006	LINC00243	HSCHR6_MHC_COX:30756279-30788292	NOTEST	0	0	0	0	1	1
ENSG00000236007	ENSG00000236007	AC105921.5	2:212240445-213403565	NOTEST	0	0	0	0	1	1
ENSG00000236008	ENSG00000236008	AC011747.4	2:8683721-8723922	NOTEST	0	0	0	0	1	1
ENSG00000236009	ENSG00000236009	RP11-293F5.1	1:21742390-21743985	NOTEST	0	0	0	0	1	1
ENSG00000236011	ENSG00000236011	GPANK1	HSCHR6_MHC_COX:31616420-31658607	NOTEST	0	0	0	0	1	1
ENSG00000236012	ENSG00000236012	HIGD1AP12	1:111922912-111923193	NOTEST	0	0	0	0	1	1
ENSG00000236014	ENSG00000236014	VPS52	HSCHR6_MHC_SSTO:33356677-33379847	NOTEST	0	0	0	0	1	1
ENSG00000236016	ENSG00000236016	RP1-3J17.3	6:86215213-86353510	NOTEST	0.0199369	0	#NAME?	0	1	1
ENSG00000236018	ENSG00000236018	RP4-814D15.1	7:156931606-157062066	NOTEST	0.0249793	0.0176279	-0.502874	0	1	1
ENSG00000236019	ENSG00000236019	DDX39B-AS1	HSCHR6_MHC_DBB:31478677-31496802	NOTEST	0	0	0	0	1	1
ENSG00000236021	ENSG00000236021	RP11-195C7.1	1:176176783-176198466	NOTEST	0.171216	0	#NAME?	0	1	1
ENSG00000236022	ENSG00000236022	RP11-160E2.16	17:19107137-19117358	NOTEST	0	0	0	0	1	1
ENSG00000236024	ENSG00000236024	RP11-483H20.6	9:132427919-132484875	NOTEST	0	0	0	0	1	1
ENSG00000236025	ENSG00000236025	RP11-463J7.1	1:190594019-190770788	NOTEST	0	0	0	0	1	1
ENSG00000236026	ENSG00000236026	AC009237.14	2:96272671-96282981	NOTEST	0	0	0	0	1	1
ENSG00000236027	ENSG00000236027	PATE3	11:125658005-125661495	NOTEST	0	0	0	0	1	1

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ENSG00000236029	ENSG00000236029	AL953854.2	9:47295854-47314322	NOTEST	0.0169243	0.0237833	0.490856	0	1	1
ENSG00000236030	ENSG00000236030	LINC01036	1:187061973-187329455	NOTEST	0	0	0	0	1	1
ENSG00000236031	ENSG00000236031	RP11-269F20.1	1:243419319-244014381	NOTEST	0.072626	0.0380128	-0.934002	0	1	1
ENSG00000236032	ENSG00000236032	OR5H14	3:97868169-97869249	NOTEST	0	0	0	0	1	1
ENSG00000236033	ENSG00000236033	HCG4B	HSCHR6_MHC_SSTO:29884112-29887366	NOTEST	0	0	0	0	1	1
ENSG00000236035	ENSG00000236035	RP11-90O23.1	1:203595688-203713209	NOTEST	0	0	0	0	1	1
ENSG00000236036	ENSG00000236036	LINC00445	13:36271660-36273393	NOTEST	0	0	0	0	1	1
ENSG00000236039	ENSG00000236039	AC019117.2	7:17414490-17598533	NOTEST	0	0	0	0	1	1
ENSG00000236040	ENSG00000236040	CHIAP1	1:111792875-111799337	NOTEST	0	0	0	0	1	1
ENSG00000236041	ENSG00000236041	COX6CP18	11:2465913-2882798	NOTEST	0	0	0	0	1	1
ENSG00000236042	ENSG00000236042	RP1-203C2.2	X:127232010-127232508	NOTEST	0	0	0	0	1	1
ENSG00000236044	ENSG00000236044	FABP5P2	13:52506808-52585630	NOTEST	0.118212	0.139968	0.24372	0	1	1
ENSG00000236045	ENSG00000236045	RP3-467K16.7	1:15573767-15726779	NOTEST	0	0	0	0	1	1
ENSG00000236046	ENSG00000236046	AC004920.3	7:50907059-50909689	NOTEST	0	0	0	0	1	1
ENSG00000236047	ENSG00000236047	AC073410.1	2:203241658-203432474	NOTEST	0.465555	0.57181	0.296586	0	1	1
ENSG00000236048	ENSG00000236048	AC013470.6	7:12510977-12512171	NOTEST	0	0	0	0	1	1
ENSG00000236049	ENSG00000236049	AC104777.2	2:151409045-151428735	NOTEST	0	0.0151868	inf	0	1	1
ENSG00000236051	ENSG00000236051	MYCBP2-AS1	13:77618791-77901185	NOTEST	0.0237078	0.0712048	1.58661	0	1	1
ENSG00000236052	ENSG00000236052	LL22NC03-86D4.1	22:34413461-34584414	NOTEST	0	0	0	0	1	1
ENSG00000236053	ENSG00000236053	LINC01067	13:109962482-109964121	NOTEST	0	0	0	0	1	1
ENSG00000236054	ENSG00000236054	LL22NC03-104C7.1	22:32908538-33454358	NOTEST	0	0	0	0	1	1
ENSG00000236055	ENSG00000236055	RP11-423O2.2	1:142790582-142791175	NOTEST	0.100308	0.345683	1.78502	0	1	1
ENSG00000236056	ENSG00000236056	GAPDHP14	21:30565800-31312351	NOTEST	0	0.0273458	inf	0	1	1
ENSG00000236060	ENSG00000236060	HSPB1P1	9:74622796-74623052	NOTEST	0.331788	0.631748	0.929087	0	1	1
ENSG00000236062	ENSG00000236062	GSTM5P1	3:12299299-12299959	NOTEST	0	0	0	0	1	1
ENSG00000236063	ENSG00000236063	ABHD16A	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000236064	ENSG00000236064	RP6-191P20.4	X:107068984-107179210	NOTEST	0	0	0	0	1	1
ENSG00000236065	ENSG00000236065	RP1-117O3.2	1:33452552-33546597	NOTEST	0.064176	0	#NAME?	0	1	1
ENSG00000236066	ENSG00000236066	RP11-389O22.1	1:113550875-113615727	NOTEST	0	0	0	0	1	1
ENSG00000236068	ENSG00000236068	AC016561.1	5:63700338-63782442	NOTEST	0	0	0	0	1	1
ENSG00000236069	ENSG00000236069	RP5-1011O1.3	1:192486768-192536347	NOTEST	0	0	0	0	1	1
ENSG00000236070	ENSG00000236070	OR2AD1P	HSCHR6_MHC_APD:28994501-28995429	NOTEST	0	0	0	0	1	1
ENSG00000236072	ENSG00000236072	RP11-281B1.2	X:34224841-34433654	NOTEST	0	0	0	0	1	1
ENSG00000236073	ENSG00000236073	RP11-487E1.2	1:21132962-21503377	NOTEST	0	0	0	0	1	1
ENSG00000236075	ENSG00000236075	RP11-121P10.1	6:40359324-40555204	NOTEST	0	0	0	0	1	1
ENSG00000236076	ENSG00000236076	LINC01072	13:20676839-20677369	NOTEST	0	0	0	0	1	1
ENSG00000236077	ENSG00000236077	RP11-232D9.2	X:115803777-115814271	NOTEST	0	0	0	0	1	1
ENSG00000236078	ENSG00000236078	AC095067.1	7:47661536-47669491	NOTEST	0	0	0	0	1	1
ENSG00000236079	ENSG00000236079	RP1-32I10.11	22:44809364-44810694	NOTEST	0	0	0	0	1	1
ENSG00000236080	ENSG00000236080	YAP1P2	X:114303799-114304409	NOTEST	0	0	0	0	1	1
ENSG00000236082	ENSG00000236082	RP11-217L21.1	11:131240372-132206716	NOTEST	0	0	0	0	1	1
ENSG00000236083	ENSG00000236083	OR13E1P	9:35859058-35859980	NOTEST	0.0395552	0.0293253	-0.431722	0	1	1

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ENSG00000236085	ENSG00000236085	ACTG1P4	1:104068312-104122156	NOTEST	0.0821297	0.0164806	-2.31713	0	1	1
ENSG00000236086	ENSG00000236086	HMGN2P28	6:2245981-2482256	NOTEST	0	0	0	0	1	1
ENSG00000236090	ENSG00000236090	LDHAP3	2:42046886-42047894	NOTEST	0	0	0	0	1	1
ENSG00000236091	ENSG00000236091	RP3-473B4.3	X:134083578-134087412	NOTEST	0.0343347	0	#NAME?	0	1	1
ENSG00000236093	ENSG00000236093	PPP1R2P1	HSCHR6_MHC_COX:32730816-32769949	NOTEST	0	0	0	0	1	1
ENSG00000236094	ENSG00000236094	LINC00545	13:31456069-31551760	NOTEST	0	0	0	0	1	1
ENSG00000236095	ENSG00000236095	RP11-49O14.2	9:97488982-97849441	NOTEST	0	0.0172482	inf	0	1	1
ENSG00000236097	ENSG00000236097	BNIP3P2	22:16627919-16628496	NOTEST	0	0	0	0	1	1
ENSG00000236098	ENSG00000236098	RP11-148B18.4	1:94784034-94790125	NOTEST	0.035285	0	#NAME?	0	1	1
ENSG00000236099	ENSG00000236099	AC013403.13	2:27381430-27382097	NOTEST	0	0	0	0	1	1
ENSG00000236100	ENSG00000236100	RPL7P4	HSCHR6_MHC_APD:30672829-30673559	NOTEST	0	0	0	0	1	1
ENSG00000236101	ENSG00000236101	RAC1P7	1:234040678-234460262	NOTEST	0	0	0	0	1	1
ENSG00000236102	ENSG00000236102	RP4-639J15.1	7:156850402-156851208	NOTEST	0	0	0	0	1	1
ENSG00000236105	ENSG00000236105	AC000110.1	7:126935673-126936257	NOTEST	0	0	0	0	1	1
ENSG00000236106	ENSG00000236106	AC010729.2	2:5866580-5870474	NOTEST	0	0	0	0	1	1
ENSG00000236107	ENSG00000236107	AC010127.3	2:166813908-167232503	NOTEST	0	0	0	0	1	1
ENSG00000236108	ENSG00000236108	RP11-383G10.1	1:205103773-205104078	NOTEST	0	0	0	0	1	1
ENSG00000236109	ENSG00000236109	AC013402.3	2:105199609-105201812	NOTEST	0	0	0	0	1	1
ENSG00000236110	ENSG00000236110	OR2AM1P	9:36021688-36022110	NOTEST	0	0	0	0	1	1
ENSG00000236111	ENSG00000236111	RP11-630I5.1	1:46246948-46247629	NOTEST	0.0574051	0	#NAME?	0	1	1
ENSG00000236113	ENSG00000236113	MCCD1P2	HSCHR6_MHC_MCF:30040680-30041558	NOTEST	0	0	0	0	1	1
ENSG00000236114	ENSG00000236114	RP11-517P14.7	10:44018703-44020665	NOTEST	0	0	0	0	1	1
ENSG00000236115	ENSG00000236115	RP11-62C3.6	9:94967637-94972440	NOTEST	0	0	0	0	1	1
ENSG00000236116	ENSG00000236116	AC064853.2	2:228474805-228513322	NOTEST	0	0	0	0	1	1
ENSG00000236117	ENSG00000236117	RP4-754E20__A.5	22:43796336-43805687	NOTEST	0	0	0	0	1	1
ENSG00000236118	ENSG00000236118	LL22NC0330E12.10	22:22509974-22510335	NOTEST	0	0	0	0	1	1
ENSG00000236119	ENSG00000236119	AP000688.15	21:37402367-37498938	NOTEST	0	0	0	0	1	1
ENSG00000236120	ENSG00000236120	RP11-733O18.1	X:5571461-5644346	NOTEST	0	0	0	0	1	1
ENSG00000236121	ENSG00000236121	HAUS6P2	20:29929173-29932274	NOTEST	0	0	0	0	1	1
ENSG00000236122	ENSG00000236122	UBQLN1P1	HSCHR6_MHC_QBL:30320388-30321557	NOTEST	0	0	0	0	1	1
ENSG00000236123	ENSG00000236123	CEACAMP11	19:43783084-43788470	NOTEST	0.241629	0.143268	-0.754077	0	1	1
ENSG00000236124	ENSG00000236124	HMGN2P23	2:113730779-113743242	NOTEST	0	0	0	0	1	1
ENSG00000236125	ENSG00000236125	USP17L4	8:7159132-7212876	NOTEST	0	0	0	0	1	1
ENSG00000236126	ENSG00000236126	CT47A3	X:120106605-120109918	NOTEST	0	0	0	0	1	1
ENSG00000236129	ENSG00000236129	AP002856.4	11:131056916-131059648	NOTEST	0	0	0	0	1	1
ENSG00000236130	ENSG00000236130	RP11-23B15.1	9:100568216-100572290	NOTEST	0	0	0	0	1	1
ENSG00000236131	ENSG00000236131	MED13P1	Y:17019777-17019948	NOTEST	0	0	0	0	1	1
ENSG00000236132	ENSG00000236132	CTA-440B3.1	22:32149943-32303012	NOTEST	0.0485347	0.269276	2.472	0	1	1
ENSG00000236133	ENSG00000236133	LINC01069	13:78469615-79233314	NOTEST	0.15279	0.0280922	-2.44331	0	1	1
ENSG00000236136	ENSG00000236136	ADORA2BP	1:209917717-209918559	NOTEST	0	0	0	0	1	1
ENSG00000236137	ENSG00000236137	RP11-27K13.3	1:117544381-117602112	NOTEST	0.0290503	0.0329506	0.181749	0	1	1
ENSG00000236138	ENSG00000236138	RP11-413E6.7	3:75718081-75719336	NOTEST	0	0	0	0	1	1
ENSG00000236140	ENSG00000236140	RP11-89F3.2	1:148246958-148248104	NOTEST	0.141132	0	#NAME?	0	1	1

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ENSG00000236141	ENSG00000236141	AC013727.2	2:104473427-104694236	NOTEST	0	0	0	0	1	1
ENSG00000236145	ENSG00000236145	AC079988.3	2:121935902-121940156	NOTEST	0	0	0	0	1	1
ENSG00000236146	ENSG00000236146	RP11-65J3.6	9:132142414-132142749	NOTEST	0	0	0	0	1	1
ENSG00000236148	ENSG00000236148	AC114752.2	2:64574326-64574875	NOTEST	0	0	0	0	1	1
ENSG00000236149	ENSG00000236149	ABCF1	HSCHR6_MHC_COX:30528999-30554805	NOTEST	0	0	0	0	1	1
ENSG00000236151	ENSG00000236151	RP5-1100I6.1	20:24123225-24125022	NOTEST	0	0	0	0	1	1
ENSG00000236153	ENSG00000236153	AC104076.3	2:181831974-182264286	NOTEST	0.151674	0	#NAME?	0	1	1
ENSG00000236154	ENSG00000236154	RP11-343J3.2	10:71335562-71336910	NOTEST	0.0447394	0.134282	1.58565	0	1	1
ENSG00000236155	ENSG00000236155	RP11-231P20.2	1:26536231-26556331	NOTEST	0	0	0	0	1	1
ENSG00000236156	ENSG00000236156	CHCHD4P3	9:37422662-37436987	NOTEST	0.406114	0.138779	-1.5491	0	1	1
ENSG00000236157	ENSG00000236157	RP11-187C18.4	9:45424049-45424634	NOTEST	0.0663993	0.0762545	0.199654	0	1	1
ENSG00000236158	ENSG00000236158	RFC3P1	3:36211258-36211940	NOTEST	0	0	0	0	1	1
ENSG00000236159	ENSG00000236159	RP3-343K2.4	20:35729628-35870022	NOTEST	0	0	0	0	1	1
ENSG00000236160	ENSG00000236160	GS1-541M1.2	X:26675407-26675624	NOTEST	0	0	0	0	1	1
ENSG00000236162	ENSG00000236162	AC092687.3	2:10857898-10861078	NOTEST	0	0	0	0	1	1
ENSG00000236164	ENSG00000236164	RP11-268F1.3	6:46714653-46728895	NOTEST	0	0	0	0	1	1
ENSG00000236165	ENSG00000236165	PRADC1P1	3:37017806-37018331	NOTEST	0	0.0297785	inf	0	1	1
ENSG00000236167	ENSG00000236167	GAPDHP57	2:75683119-75683704	NOTEST	0	0	0	0	1	1
ENSG00000236168	ENSG00000236168	RP5-831C21.1	20:23961221-23961371	NOTEST	0	0	0	0	1	1
ENSG00000236169	ENSG00000236169	LINC00418	13:19292906-19293869	NOTEST	0	0	0	0	1	1
ENSG00000236170	ENSG00000236170	IGHD1-1	14:106383837-106391825	NOTEST	0	0	0	0	1	1
ENSG00000236171	ENSG00000236171	RP11-501J20.3	10:118955678-118956165	NOTEST	0	0	0	0	1	1
ENSG00000236172	ENSG00000236172	hsa-mir-7515	2:6755721-6790667	NOTEST	0	0	0	0	1	1
ENSG00000236173	ENSG00000236173	RP1-182D15.2	6:170209413-170210198	NOTEST	0	0	0	0	1	1
ENSG00000236175	ENSG00000236175	SSU72P6	11:4299934-4300422	NOTEST	0	0	0	0	1	1
ENSG00000236176	ENSG00000236176	LINC00353	13:90200944-90206058	NOTEST	0	0	0	0	1	1
ENSG00000236177	ENSG00000236177	HLA-DPA1	HSCHR6_MHC_SSTO:33171991-33194624	NOTEST	0	0	0	0	1	1
ENSG00000236178	ENSG00000236178	VARSL	HSCHR6_MHC_COX:30865831-30883959	NOTEST	0	0	0	0	1	1
ENSG00000236179	ENSG00000236179	RP13-221M14.4	1:13171870-13173157	NOTEST	0	0	0	0	1	1
ENSG00000236180	ENSG00000236180	RP11-163G10.4	1:42895999-43120335	NOTEST	0	0	0	0	1	1
ENSG00000236182	ENSG00000236182	RP11-297K7.1	3:188659503-189043093	NOTEST	0	0	0	0	1	1
ENSG00000236183	ENSG00000236183	LY6G6C	HSCHR6_MHC_COX:31673783-31681900	NOTEST	0	0	0	0	1	1
ENSG00000236184	ENSG00000236184	TCEA1P4	9:32972603-33025166	NOTEST	0.257379	0.120338	-1.0968	0	1	1
ENSG00000236185	ENSG00000236185	HNRNPDLP3	X:94865576-94865956	NOTEST	0	0	0	0	1	1
ENSG00000236187	ENSG00000236187	GJA6P	X:18443702-18690229	NOTEST	0	0	0	0	1	1
ENSG00000236188	ENSG00000236188	PRKX-AS1	X:3522410-3631649	NOTEST	0	0	0	0	1	1
ENSG00000236189	ENSG00000236189	RPL18AP15	X:110867437-110867954	NOTEST	0	0	0	0	1	1
ENSG00000236190	ENSG00000236190	RP3-431C21.1	X:86143588-86143819	NOTEST	0	0	0	0	1	1
ENSG00000236191	ENSG00000236191	RPS15AP25	8:69215702-69731257	NOTEST	0	0	0	0	1	1
ENSG00000236193	ENSG00000236193	RP11-105N14.3	2:214020529-214032436	NOTEST	0	0	0	0	1	1
ENSG00000236194	ENSG00000236194	AC003104.1	17:40351185-40428725	NOTEST	0.029242	0	#NAME?	0	1	1
ENSG00000236195	ENSG00000236195	RNMTL1P2	7:18001701-18002652	NOTEST	0	0	0	0	1	1
ENSG00000236196	ENSG00000236196	NFKBIL1	HSCHR6_MHC_DBB:31496823-31508774	NOTEST	0	0	0	0	1	1
ENSG00000236197	ENSG00000236197	AC002429.5	7:94536513-94925727	NOTEST	0	0.00481149	inf	0	1	1

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ENSG00000236198	ENSG00000236198	AC104395.2	2:84101831-84103457	NOTEST	0	0	0	0	1	1
ENSG00000236199	ENSG00000236199	RP11-264I13.2	9:2015341-2193624	NOTEST	0.17889	0.396186	1.1471	0	1	1
ENSG00000236202	ENSG00000236202	GRM7-AS1	3:6532165-7783215	NOTEST	0	0	0	0	1	1
ENSG00000236203	ENSG00000236203	MCCD1P2	HSCHR6_MHC_APD:29898667-29899545	NOTEST	0	0	0	0	1	1
ENSG00000236204	ENSG00000236204	AC092594.1	2:19167728-19546509	NOTEST	0.0955132	0.217416	1.18668	0	1	1
ENSG00000236205	ENSG00000236205	RP3-406C18.1	X:141235647-141236652	NOTEST	0	0	0	0	1	1
ENSG00000236206	ENSG00000236206	RP11-306I1.2	1:165567699-165592568	NOTEST	0	0	0	0	1	1
ENSG00000236208	ENSG00000236208	C10orf71-AS1	10:50504156-50507063	NOTEST	0	0	0	0	1	1
ENSG00000236209	ENSG00000236209	AC104135.2	2:75145274-75165545	NOTEST	0.368087	0.42483	0.206836	0	1	1
ENSG00000236210	ENSG00000236210	LY6G6E	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000236211	ENSG00000236211	AC068137.5	2:131031480-131033022	NOTEST	0	0	0	0	1	1
ENSG00000236212	ENSG00000236212	AC009262.2	7:34249137-34295955	NOTEST	0	0	0	0	1	1
ENSG00000236213	ENSG00000236213	AC006369.2	2:37827278-37965611	NOTEST	0	0	0	0	1	1
ENSG00000236216	ENSG00000236216	PPP1R11P1	1:21724479-21724855	NOTEST	0	0	0	0	1	1
ENSG00000236217	ENSG00000236217	C1DP2	10:81791599-81792149	NOTEST	0	0.129945	inf	0	1	1
ENSG00000236221	ENSG00000236221	TNXB	HSCHR6_MHC_MANN:32072021-32105429	NOTEST	0	0	0	0	1	1
ENSG00000236222	ENSG00000236222	WDR46	HSCHR6_MHC_MCF:33417261-33437523	NOTEST	0	0	0	0	1	1
ENSG00000236225	ENSG00000236225	HCG4	HSCHR6_MHC_APD:29758889-29765609	NOTEST	0	0	0	0	1	1
ENSG00000236226	ENSG00000236226	RP11-645N11.3	7:102453307-102715286	NOTEST	0	0	0	0	1	1
ENSG00000236227	ENSG00000236227	BRD2	HSCHR6_MHC_MCF:32980790-32980956	NOTEST	0	0	0	0	1	1
ENSG00000236229	ENSG00000236229	VEZF1P1	3:192862252-192894653	NOTEST	0	0	0	0	1	1
ENSG00000236230	ENSG00000236230	RP11-400N13.1	1:222262510-222560776	NOTEST	0.167486	0	#NAME?	0	1	1
ENSG00000236231	ENSG00000236231	AC017048.2	2:177389606-177396411	NOTEST	0	0	0	0	1	1
ENSG00000236232	ENSG00000236232	AC004112.7	7:111846642-112049678	NOTEST	0	0	0	0	1	1
ENSG00000236234	ENSG00000236234	AC091132.1	17:43513265-43568115	NOTEST	0.0509998	0.0917218	0.846774	0	1	1
ENSG00000236235	ENSG00000236235	LA16c-13E4.3	22:16680766-16687245	NOTEST	0	0	0	0	1	1
ENSG00000236236	ENSG00000236236	TNXB	HSCHR6_MHC_SSTO:31965199-32027628	NOTEST	0	0	0	0	1	1
ENSG00000236237	ENSG00000236237	LTB	HSCHR6_MHC_MCF:31624640-31626608	NOTEST	0	0	0	0	1	1
ENSG00000236238	ENSG00000236238	AC093106.4	7:131350265-131350617	NOTEST	0	0	0	0	1	1
ENSG00000236240	ENSG00000236240	GPC5-IT1	13:92050928-93519490	NOTEST	0	0	0	0	1	1
ENSG00000236241	ENSG00000236241	RP11-744O11.2	3:174156362-175523428	NOTEST	0	0	0	0	1	1
ENSG00000236242	ENSG00000236242	MYO16-AS1	13:109248499-109860355	NOTEST	0	0	0	0	1	1
ENSG00000236243	ENSG00000236243	RPL6P29	X:97506676-97507541	NOTEST	0	0	0	0	1	1
ENSG00000236244	ENSG00000236244	RP4-799P18.3	1:234040678-234460262	NOTEST	0	0	0	0	1	1
ENSG00000236246	ENSG00000236246	AC073135.4	3:197848258-197850145	NOTEST	0	0	0	0	1	1
ENSG00000236247	ENSG00000236247	RP11-292B8.2	9:40479775-40481177	NOTEST	0	0	0	0	1	1
ENSG00000236248	ENSG00000236248	AC104389.32	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000236249	ENSG00000236249	GAGE2C	X:49226181-49233481	NOTEST	0	0.0953441	inf	0	1	1
ENSG00000236250	ENSG00000236250	STK19	HSCHR6_MHC_SSTO:31929438-31941075	NOTEST	0	0	0	0	1	1
ENSG00000236251	ENSG00000236251	HSPA1L	HSCHR6_MHC_COX:31764772-31770218	NOTEST	0	0	0	0	1	1
ENSG00000236252	ENSG00000236252	RP11-15J10.8	9:70113592-70124467	NOTEST	0	0	0	0	1	1
ENSG00000236253	ENSG00000236253	SLC25A3P1	1:53878820-53905693	NOTEST	0	0	0	0	1	1
ENSG00000236254	ENSG00000236254	MTND4P14	9:4985032-5128183	NOTEST	0.0228173	0	#NAME?	0	1	1
ENSG00000236256	ENSG00000236256	DIAPH2-AS1	X:95939661-96897588	NOTEST	0.0337708	0	#NAME?	0	1	1

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ENSG00000236258	ENSG00000236258	TIMM8BP1	13:30440095-30440306	NOTEST	0	0	0	0	1	1
ENSG00000236259	ENSG00000236259	AC017083.2	2:68350067-68488362	NOTEST	0	0	0	0	1	1
ENSG00000236261	ENSG00000236261	RP11-368M16.6	7:57712441-57713165	NOTEST	0	0	0	0	1	1
ENSG00000236262	ENSG00000236262	SHANK2-AS2	11:70313960-70963623	NOTEST	0	0	0	0	1	1
ENSG00000236263	ENSG00000236263	RP11-263K19.6	1:155165378-155183615	NOTEST	0	0	0	0	1	1
ENSG00000236265	ENSG00000236265	DDX39BP1	HSCHR6_MHC_MCF:29846326-29992167	NOTEST	0	0	0	0	1	1
ENSG00000236266	ENSG00000236266	RP3-467L1.4	1:7844379-7913572	NOTEST	0.225237	0.442224	0.973338	0	1	1
ENSG00000236267	ENSG00000236267	AP006216.5	11:116683919-116684719	NOTEST	0	0	0	0	1	1
ENSG00000236268	ENSG00000236268	RP11-170N11.1	1:83368865-83632498	NOTEST	0.07546	0.0845675	0.164391	0	1	1
ENSG00000236269	ENSG00000236269	ENO1-IT1	1:8921060-8939953	NOTEST	0.142807	0.428601	1.58557	0	1	1
ENSG00000236271	ENSG00000236271	FLOT1	HSCHR6_MHC_MANN:30752724-30755207	NOTEST	0	0	0	0	1	1
ENSG00000236272	ENSG00000236272	Z82214.3	22:43593288-43739394	NOTEST	0	0	0	0	1	1
ENSG00000236273	ENSG00000236273	RPL15P4	HSCHR6_MHC_MANN:31535409-31535989	NOTEST	0	0	0	0	1	1
ENSG00000236274	ENSG00000236274	RP4-728D4.3	1:35899090-36032875	NOTEST	0	0	0	0	1	1
ENSG00000236276	ENSG00000236276	NDP-AS1	X:43808021-43832750	NOTEST	0	0	0	0	1	1
ENSG00000236277	ENSG00000236277	NIPA2P5	13:79664917-79668254	NOTEST	0	0	0	0	1	1
ENSG00000236278	ENSG00000236278	PEBP1P3	1:198607800-198726545	NOTEST	0	0	0	0	1	1
ENSG00000236279	ENSG00000236279	CLEC2L	7:139208601-139229730	NOTEST	0	0	0	0	1	1
ENSG00000236280	ENSG00000236280	AC114737.3	7:76139744-77045717	NOTEST	0	1.51907	inf	0	1	1
ENSG00000236281	ENSG00000236281	AC093106.5	7:131438504-131439011	NOTEST	0	0	0	0	1	1
ENSG00000236283	ENSG00000236283	AC013463.2	2:165848493-166060577	NOTEST	0	0	0	0	1	1
ENSG00000236284	ENSG00000236284	VN1R31P	7:62827804-62828534	NOTEST	0	0	0	0	1	1
ENSG00000236285	ENSG00000236285	NPM1P8	X:31115793-33357558	NOTEST	0	0	0	0	1	1
ENSG00000236289	ENSG00000236289	AC130710.1	2:16137170-16245963	NOTEST	0	0	0	0	1	1
ENSG00000236290	ENSG00000236290	EEF1GP7	1:53038785-53039488	NOTEST	0.051351	0	#NAME?	0	1	1
ENSG00000236292	ENSG00000236292	RP5-1099E6.3	1:215796235-216596738	NOTEST	0	0	0	0	1	1
ENSG00000236294	ENSG00000236294	TSRM	7:113091126-113091457	NOTEST	0	0	0	0	1	1
ENSG00000236295	ENSG00000236295	AC007563.1	2:217536827-217858802	NOTEST	0	0	0	0	1	1
ENSG00000236297	ENSG00000236297	RP11-175P19.2	3:193119865-193310900	NOTEST	0.443026	0.38715	-0.194498	0	1	1
ENSG00000236299	ENSG00000236299	RP11-340I6.7	7:63348577-63361113	NOTEST	0	0	0	0	1	1
ENSG00000236300	ENSG00000236300	AC013437.4	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000236301	ENSG00000236301	MRGPRG-AS1	11:3239173-3244361	NOTEST	0	0	0	0	1	1
ENSG00000236303	ENSG00000236303	RP11-540N6.1	10:132237330-132281418	NOTEST	0	0	0	0	1	1
ENSG00000236304	ENSG00000236304	AP001189.4	11:76368099-76381791	NOTEST	0	0	0	0	1	1
ENSG00000236305	ENSG00000236305	RP11-126L15.4	7:100400186-100464631	NOTEST	0.509444	0	#NAME?	0	1	1
ENSG00000236306	ENSG00000236306	RP11-33G16.1	9:25780053-25784560	NOTEST	0	0	0	0	1	1
ENSG00000236307	ENSG00000236307	AC104651.1	2:112645490-112646318	NOTEST	0.107807	0	#NAME?	0	1	1
ENSG00000236308	ENSG00000236308	RP11-316M21.7	10:101909850-101989376	NOTEST	0.323067	0.432806	0.421887	0	1	1
ENSG00000236309	ENSG00000236309	RP11-508N22.10	10:38453575-38501285	NOTEST	0	0	0	0	1	1
ENSG00000236310	ENSG00000236310	AC005027.3	7:41706765-41818986	NOTEST	0	0	0	0	1	1
ENSG00000236311	ENSG00000236311	TLX1NB	10:102849077-102899468	NOTEST	0	0	0	0	1	1
ENSG00000236312	ENSG00000236312	RPL34P34	19:22551400-22551754	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000236313	ENSG00000236313	VN1R53P	10:37414784-37673039	NOTEST	0	0	0	0	1	1
ENSG00000236315	ENSG00000236315	NCR3	HSCHR6_MHC_APD:31565221-31572083	NOTEST	0	0	0	0	1	1
ENSG00000236316	ENSG00000236316	OR7E109P	9:93504807-93505662	NOTEST	0	0	0	0	1	1
ENSG00000236317	ENSG00000236317	RP11-348H3.5	1:213025449-213031430	NOTEST	0	0	0	0	1	1
ENSG00000236318	ENSG00000236318	AC019117.1	7:17414490-17598533	NOTEST	0	0	0	0	1	1
ENSG00000236319	ENSG00000236319	CTD-2033D24.2	17:53604324-53638938	NOTEST	0.109878	0	#NAME?	0	1	1
ENSG00000236320	ENSG00000236320	SLFN14	17:33875143-33885117	NOTEST	0	0	0	0	1	1
ENSG00000236322	ENSG00000236322	RP11-327I22.8	9:43184067-43189411	NOTEST	0	0	0	0	1	1
ENSG00000236323	ENSG00000236323	BMP6P1	22:22540330-22541009	NOTEST	0	0	0	0	1	1
ENSG00000236324	ENSG00000236324	RP3-403L10.3	6:158244295-158366109	NOTEST	0	0	0	0	1	1
ENSG00000236325	ENSG00000236325	AC005300.5	22:17660193-17702879	NOTEST	0	0	0	0	1	1
ENSG00000236326	ENSG00000236326	RP3-486I3.5	6:116422011-116570660	NOTEST	0.272955	0.00516333	-5.72422	0	1	1
ENSG00000236327	ENSG00000236327	RP11-759F5.1	1:153777200-153895451	NOTEST	0	0	0	0	1	1
ENSG00000236330	ENSG00000236330	RPL5P9	2:111490149-111875799	NOTEST	0	0	0	0	1	1
ENSG00000236332	ENSG00000236332	AP001605.4	21:28731203-28820898	NOTEST	0	0	0	0	1	1
ENSG00000236333	ENSG00000236333	TRHDE-AS1	12:72332625-73059422	NOTEST	0.0259474	0.00296704	-3.12849	0	1	1
ENSG00000236334	ENSG00000236334	PPIAL4G	1:143767143-143767881	NOTEST	0.0261974	0	#NAME?	0	1	1
ENSG00000236335	ENSG00000236335	RP4-591L5.1	1:30882406-30884485	NOTEST	0	0	0	0	1	1
ENSG00000236336	ENSG00000236336	RP3-430A16.1	6:4706392-4955785	NOTEST	0	0	0	0	1	1
ENSG00000236337	ENSG00000236337	FMR1-IT1	X:146993468-147032645	NOTEST	0.0858898	0.067142	-0.35527	0	1	1
ENSG00000236339	ENSG00000236339	POM121L13P	13:29352694-29353074	NOTEST	0	0	0	0	1	1
ENSG00000236340	ENSG00000236340	AC000099.1	7:126078651-126893348	NOTEST	0	0	0	0	1	1
ENSG00000236341	ENSG00000236341	RP5-1103B4.3	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000236342	ENSG00000236342	ABCF1	HSCHR6_MHC_MCF:30617609-30643414	NOTEST	0	0	0	0	1	1
ENSG00000236343	ENSG00000236343	EI24P4	7:144702150-144703228	NOTEST	0	0	0	0	1	1
ENSG00000236345	ENSG00000236345	RP11-59D5__B.2	6:64345724-66417118	NOTEST	0.032599	0.0588723	0.852762	0	1	1
ENSG00000236346	ENSG00000236346	NFKBIL1	HSCHR6_MHC_SSTO:3150459-31516550	NOTEST	0	0	0	0	1	1
ENSG00000236347	ENSG00000236347	RP11-346D19.1	6:113852319-113864995	NOTEST	0	0.0246948	inf	0	1	1
ENSG00000236348	ENSG00000236348	PSMC1P10	2:17566357-17567684	NOTEST	0	0	0	0	1	1
ENSG00000236352	ENSG00000236352	AC005220.3	20:52553315-52687304	NOTEST	0	0.115235	inf	0	1	1
ENSG00000236353	ENSG00000236353	PBX2	HSCHR6_MHC_MCF:32228947-32234390	NOTEST	0	0	0	0	1	1
ENSG00000236354	ENSG00000236354	LINC00437	13:39107479-39119436	NOTEST	0	0	0	0	1	1
ENSG00000236355	ENSG00000236355	RP3-503A6.2	6:38681826-38682993	NOTEST	0	0	0	0	1	1
ENSG00000236356	ENSG00000236356	AC079584.2	2:144557035-144577168	NOTEST	0	0	0	0	1	1
ENSG00000236357	ENSG00000236357	EI24P1	3:175785829-175786696	NOTEST	0	0	0	0	1	1
ENSG00000236358	ENSG00000236358	RP5-827C21.2	1:234492449-234501574	NOTEST	0	0	0	0	1	1
ENSG00000236359	ENSG00000236359	OR51B8P	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000236361	ENSG00000236361	RP11-395E19.7	9:40740775-40742447	NOTEST	0	0	0	0	1	1
ENSG00000236362	ENSG00000236362	GAGE12F	X:49325478-49332808	NOTEST	0	0	0	0	1	1
ENSG00000236365	ENSG00000236365	RP5-849L7.1	X:82130656-82130893	NOTEST	0	0	0	0	1	1
ENSG00000236366	ENSG00000236366	RP11-440G9.1	6:142847591-142959026	NOTEST	0.0139972	0.0157914	0.174004	0	1	1
ENSG00000236369	ENSG00000236369	TMPOP1	HSCHR6_MHC_DBB:30424509-30426052	NOTEST	0	0	0	0	1	1

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ENSG00000236371	ENSG00000236371	CT47A1	X:120111459-120119642	NOTEST	0	0	0	0	1	1
ENSG00000236372	ENSG00000236372	RP5-865N13.1	1:232295836-232321389	NOTEST	0	0	0	0	1	1
ENSG00000236373	ENSG00000236373	RP11-15K3.1	10:92162277-92300562	NOTEST	0	0	0	0	1	1
ENSG00000236374	ENSG00000236374	USP8P1	HSCHR6_MHC_DBB:31235516-31238689	NOTEST	0	0	0	0	1	1
ENSG00000236375	ENSG00000236375	POU5F1P5	10:69681664-69835105	NOTEST	0	0	0	0	1	1
ENSG00000236376	ENSG00000236376	RP11-470F18.1	9:78194584-78203464	NOTEST	0	0	0	0	1	1
ENSG00000236377	ENSG00000236377	AC084809.3	17:31232679-31233602	NOTEST	0.243266	0.357194	0.554177	0	1	1
ENSG00000236378	ENSG00000236378	RP11-394G3.2	6:136128285-136129604	NOTEST	0	0	0	0	1	1
ENSG00000236379	ENSG00000236379	ZNF736P4Y	Y:27314745-27315988	NOTEST	0	0	0	0	1	1
ENSG00000236380	ENSG00000236380	VENTXP7	3:21447217-21448175	NOTEST	0	0	0	0	1	1
ENSG00000236382	ENSG00000236382	KRTAP10-13P	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000236383	ENSG00000236383	LINC00854	17:41363853-41383338	NOTEST	0.195326	0.333604	0.772254	0	1	1
ENSG00000236384	ENSG00000236384	LINC00479	21:43131679-43135935	NOTEST	0.0144453	0.0891695	2.62595	0	1	1
ENSG00000236386	ENSG00000236386	AC009518.3	7:131578580-131578833	NOTEST	0	0	0	0	1	1
ENSG00000236387	ENSG00000236387	RP11-307O10.1	20:4411807-4412320	NOTEST	0	0	0	0	1	1
ENSG00000236388	ENSG00000236388	ITCH-AS1	20:32951040-33099198	NOTEST	0	0	0	0	1	1
ENSG00000236389	ENSG00000236389	RP1-287H17.1	6:135027197-135028487	NOTEST	0	0	0	0	1	1
ENSG00000236390	ENSG00000236390	RP11-25B7.1	1:201592012-201853422	NOTEST	0	0	0	0	1	1
ENSG00000236391	ENSG00000236391	AC092573.2	2:174202946-174233725	NOTEST	0	0	0	0	1	1
ENSG00000236392	ENSG00000236392	AC100848.1	18:61747242-62090836	NOTEST	0	0	0	0	1	1
ENSG00000236393	ENSG00000236393	RP11-320G24.1	X:40122169-40146973	NOTEST	0	0.0110566	inf	0	1	1
ENSG00000236394	ENSG00000236394	RP11-229P13.15	9:139942549-139948497	NOTEST	0	0	0	0	1	1
ENSG00000236395	ENSG00000236395	AC093106.6	7:131387027-131387412	NOTEST	0	0	0	0	1	1
ENSG00000236396	ENSG00000236396	RP11-677O4.3	18:11609543-11610687	NOTEST	0	0	0	0	1	1
ENSG00000236398	ENSG00000236398	TAS2R39	7:142880511-142881528	NOTEST	0	0	0	0	1	1
ENSG00000236399	ENSG00000236399	TRIM40	HSCHR6_MHC_MCF:30182384-30195005	NOTEST	0	0	0	0	1	1
ENSG00000236400	ENSG00000236400	KRTAP21-4P	21:32114097-32114913	NOTEST	0	0	0	0	1	1
ENSG00000236401	ENSG00000236401	RP11-393M18.4	1:187675691-187678029	NOTEST	0	0	0	0	1	1
ENSG00000236403	ENSG00000236403	RP11-447M12.2	9:137828996-137835041	NOTEST	0	0	0	0	1	1
ENSG00000236405	ENSG00000236405	UBQLN1P1	6:30330888-30332057	NOTEST	0	0	0	0	1	1
ENSG00000236407	ENSG00000236407	HMGB1P18	1:80749036-80749655	NOTEST	0	0	0	0	1	1
ENSG00000236408	ENSG00000236408	RP11-476H24.1	7:153584181-154685995	NOTEST	0	0	0	0	1	1
ENSG00000236409	ENSG00000236409	NRADDP	3:47053031-47054636	NOTEST	0	0.0222301	inf	0	1	1
ENSG00000236411	ENSG00000236411	NDUFAF4P3	3:37493605-37903271	NOTEST	0.167845	0.0297799	-2.49472	0	1	1
ENSG00000236412	ENSG00000236412	RP11-132N15.2	3:187715209-187721778	NOTEST	0	0	0	0	1	1
ENSG00000236413	ENSG00000236413	RP13-24G8.2	X:90669876-90693583	NOTEST	0	0	0	0	1	1
ENSG00000236414	ENSG00000236414	AC004535.2	7:10742302-10747033	NOTEST	0	0	0	0	1	1
ENSG00000236415	ENSG00000236415	PPIAP9	HSCHR6_MHC_COX:31474725-31475537	NOTEST	0	0	0	0	1	1
ENSG00000236417	ENSG00000236417	CTSLP1	10:89146441-89149960	NOTEST	0	0	0	0	1	1
ENSG00000236418	ENSG00000236418	HLA-DQA1	HSCHR6_MHC_DBB:32574290-32596644	NOTEST	0	0	0	0	1	1
ENSG00000236420	ENSG00000236420	CHCHD3P1	10:8661895-8662571	NOTEST	0	0	0	0	1	1
ENSG00000236422	ENSG00000236422	HCG19P	HSCHR6_MHC_MANN:30371735-30372369	NOTEST	0	0	0	0	1	1
ENSG00000236423	ENSG00000236423	LINC01134	1:3816935-3833789	NOTEST	0.0932095	0.0984818	0.0793796	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000236424	ENSG00000236424	TSPY10	Y:9365488-9368291	NOTEST	0	0	0	0	1	1
ENSG00000236425	ENSG00000236425	AC090018.1	3:195288084-195288450	NOTEST	0	0	0	0	1	1
ENSG00000236426	ENSG00000236426	RP11-79M19.2	10:120967100-121215131	NOTEST	0.0251759	0	#NAME?	0	1	1
ENSG00000236427	ENSG00000236427	RP11-107M16.2	1:152140600-152339163	NOTEST	0.517907	0.193763	-1.4184	0	1	1
ENSG00000236428	ENSG00000236428	PPP1R18	HSCHR6_MHC_SSTO:30635611-30638612	NOTEST	0	0	0	0	1	1
ENSG00000236429	ENSG00000236429	GPM6BP2	Y:20835918-20991373	NOTEST	0	0	0	0	1	1
ENSG00000236430	ENSG00000236430	KRT8P29	1:203841701-203843315	NOTEST	0	0.00870733	inf	0	1	1
ENSG00000236431	ENSG00000236431	AC009237.11	2:96201864-96202243	NOTEST	0.413193	0.152905	-1.43418	0	1	1
ENSG00000236433	ENSG00000236433	RPL37P21	13:68905469-68905745	NOTEST	0	0	0	0	1	1
ENSG00000236434	ENSG00000236434	RP11-296A18.6	1:51701942-51739127	NOTEST	0	0	0	0	1	1
ENSG00000236435	ENSG00000236435	TSPY12P	Y:7555779-7557589	NOTEST	0	0	0	0	1	1
ENSG00000236436	ENSG00000236436	AC012361.1	2:21059530-21061421	NOTEST	0	0	0	0	1	1
ENSG00000236437	ENSG00000236437	AP001891.1	11:116367615-116371347	NOTEST	0	0	0	0	1	1
ENSG00000236438	ENSG00000236438	FAM157A	3:197879236-197925886	NOTEST	0.0269264	0.0110027	-1.29116	0	1	1
ENSG00000236440	ENSG00000236440	AC117947.1	2:140988991-142895399	NOTEST	0	0	0	0	1	1
ENSG00000236441	ENSG00000236441	DDX39BP1	HSCHR6_MHC_QBL:29865580-29865947	NOTEST	0	0	0	0	1	1
ENSG00000236442	ENSG00000236442	ANKRD54P1	10:45493145-45676875	NOTEST	0	0	0	0	1	1
ENSG00000236443	ENSG00000236443	PSMB8	HSCHR6_MHC_MANN:32962292-33001424	NOTEST	0	0	0	0	1	1
ENSG00000236444	ENSG00000236444	UBE2L5P	13:31002083-31002656	NOTEST	0	0	0	0	1	1
ENSG00000236445	ENSG00000236445	LINC00608	2:219840320-219844382	NOTEST	0	0	0	0	1	1
ENSG00000236446	ENSG00000236446	CT47B1	X:120006456-120009779	NOTEST	0	0	0	0	1	1
ENSG00000236447	ENSG00000236447	ATG10-IT1	5:81267843-81574396	NOTEST	0	0	0	0	1	1
ENSG00000236450	ENSG00000236450	RP11-111F5.1	9:46669134-46669441	NOTEST	0	0	0	0	1	1
ENSG00000236451	ENSG00000236451	AC067956.1	2:220970376-221569286	NOTEST	0	0	0	0	1	1
ENSG00000236452	ENSG00000236452	AC123023.1	3:34200825-34604369	NOTEST	0	0	0	0	1	1
ENSG00000236456	ENSG00000236456	RP4-785G19.2	20:32782374-32899608	NOTEST	0.0717651	0	#NAME?	0	1	1
ENSG00000236457	ENSG00000236457	AC130689.5	17:1963132-2284352	NOTEST	0	0	0	0	1	1
ENSG00000236459	ENSG00000236459	HNRNPA1P22	3:42846243-43101703	NOTEST	0.019165	0	#NAME?	0	1	1
ENSG00000236460	ENSG00000236460	SNX2P2	7:31790792-32338941	NOTEST	0	0	0	0	1	1
ENSG00000236461	ENSG00000236461	RP11-523L1.2	9:117881817-117900688	NOTEST	0	0	0	0	1	1
ENSG00000236463	ENSG00000236463	LINC00427	13:30890496-30894040	NOTEST	0	0	0	0	1	1
ENSG00000236464	ENSG00000236464	CTA-796E4.3	22:26557799-26560269	NOTEST	0	0	0	0	1	1
ENSG00000236466	ENSG00000236466	RP11-795J1.1	6:46459788-46500495	NOTEST	0	0	0	0	1	1
ENSG00000236467	ENSG00000236467	RP11-443A13.5	10:78629358-79398353	NOTEST	0	0	0	0	1	1
ENSG00000236468	ENSG00000236468	RP11-104D3.2	1:199117725-199362435	NOTEST	0	0	0	0	1	1
ENSG00000236469	ENSG00000236469	AC007040.8	2:71163011-71306935	NOTEST	0	0	0	0	1	1
ENSG00000236471	ENSG00000236471	AF127577.12	21:16439390-16440158	NOTEST	0	0	0	0	1	1
ENSG00000236472	ENSG00000236472	AC002401.1	17:48211103-48227991	NOTEST	0	0	0	0	1	1
ENSG00000236473	ENSG00000236473	KRT43P	17:39604434-39610307	NOTEST	0	0	0	0	1	1
ENSG00000236474	ENSG00000236474	GCNT1P1	20:18364010-18465287	NOTEST	0.0132171	0.0102711	-0.363814	0	1	1
ENSG00000236475	ENSG00000236475	TRIM26BP	6:30201815-30314661	NOTEST	0	0	0	0	1	1
ENSG00000236476	ENSG00000236476	RP11-8J9.5	1:47208000-47208805	NOTEST	0	0	0	0	1	1
ENSG00000236477	ENSG00000236477	RPS24P1	Y:14365456-14366162	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000236478	ENSG00000236478	AC012513.4	2:216972186-217071026	NOTEST	0.015375	0.0216527	0.493956	0	1	1
ENSG00000236480	ENSG00000236480	PKMP1	1:115078615-115080461	NOTEST	0.0109849	0	#NAME?	0	1	1
ENSG00000236481	ENSG00000236481	AC002331.1	16:26596075-26606134	NOTEST	0	0	0	0	1	1
ENSG00000236483	ENSG00000236483	CTD-3105H18.8	19:12490002-12750912	NOTEST	0.103351	0.0156421	-2.72404	0	1	1
ENSG00000236484	ENSG00000236484	RRM2P2	1:161348496-161349148	NOTEST	0	0	0	0	1	1
ENSG00000236485	ENSG00000236485	RP1-156L9.1	2:132741509-132751734	NOTEST	0	0	0	0	1	1
ENSG00000236487	ENSG00000236487	RP11-753E22.2	X:24700025-24700751	NOTEST	0	0	0	0	1	1
ENSG00000236488	ENSG00000236488	PPP1R2P21	HSCHR6_MHC_MANN:32962292-33001424	NOTEST	0	0	0	0	1	1
ENSG00000236489	ENSG00000236489	RP11-537I16.2	3:185300283-185351339	NOTEST	0.228435	0.26122	0.193477	0	1	1
ENSG00000236490	ENSG00000236490	TAPBP	HSCHR6_MHC_DBB:33245399-33260090	NOTEST	0	0	0	0	1	1
ENSG00000236491	ENSG00000236491	RP13-565O16.2	X:134314178-134328610	NOTEST	0	0	0	0	1	1
ENSG00000236492	ENSG00000236492	DDR1-AS1	HSCHR6_MHC_DBB:30825442-30834387	NOTEST	0	0	0	0	1	1
ENSG00000236494	ENSG00000236494	RP11-89N17.4	7:33832779-33842768	NOTEST	0	0.00736447	inf	0	1	1
ENSG00000236495	ENSG00000236495	RP11-7C6.1	10:14560555-14816896	NOTEST	0	0	0	0	1	1
ENSG00000236496	ENSG00000236496	RP11-255J3.2	9:2875441-2876427	NOTEST	0.585489	0.429653	-0.446471	0	1	1
ENSG00000236497	ENSG00000236497	RP11-66A2.2	1:232862999-232878461	NOTEST	0	0	0	0	1	1
ENSG00000236498	ENSG00000236498	AC107081.5	2:62095223-62374382	NOTEST	0.205986	0.0996944	-1.04696	0	1	1
ENSG00000236499	ENSG00000236499	LINC00896	22:20193919-20196047	NOTEST	0.0943409	0.175937	0.899104	0	1	1
ENSG00000236500	ENSG00000236500	RP4-680D5.4	1:15941137-15941362	NOTEST	0	0	0	0	1	1
ENSG00000236501	ENSG00000236501	AC079305.11	2:177855235-178088686	NOTEST	0.0375125	0	#NAME?	0	1	1
ENSG00000236502	ENSG00000236502	SIX3-AS1	2:45167292-45173216	NOTEST	0	0.065851	inf	0	1	1
ENSG00000236503	ENSG00000236503	AC009784.4	7:135777672-136122174	NOTEST	0	0	0	0	1	1
ENSG00000236504	ENSG00000236504	AC087499.7	17:20550599-20585112	NOTEST	0	0	0	0	1	1
ENSG00000236505	ENSG00000236505	RP1-63P18.2	1:41029205-41029331	NOTEST	0	0	0	0	1	1
ENSG00000236507	ENSG00000236507	RP5-1050E16.1	9:92501141-92523200	NOTEST	0	0	0	0	1	1
ENSG00000236508	ENSG00000236508	ATP13A5-AS1	3:192958913-193096632	NOTEST	0	0	0	0	1	1
ENSG00000236509	ENSG00000236509	RPL21P133	X:133699867-133898352	NOTEST	0	0	0	0	1	1
ENSG00000236510	ENSG00000236510	AC011284.3	7:3303663-4308632	NOTEST	0	0	0	0	1	1
ENSG00000236511	ENSG00000236511	RP11-32F11.2	9:3181588-3198517	NOTEST	0	0	0	0	1	1
ENSG00000236512	ENSG00000236512	RP3-336K20__B.2	6:7620654-7621111	NOTEST	0.10384	0	#NAME?	0	1	1
ENSG00000236513	ENSG00000236513	RP11-707P20.1	X:4545240-4551613	NOTEST	0.0146616	0	#NAME?	0	1	1
ENSG00000236514	ENSG00000236514	RP11-162G10.5	10:38091750-38148038	NOTEST	0.0415447	0.0811696	0.966275	0	1	1
ENSG00000236515	ENSG00000236515	ZBTB9	HSCHR6_MHC_SSTO:3356741-33564711	NOTEST	0	0	0	0	1	1
ENSG00000236516	ENSG00000236516	KLF2P4	2:131862419-132111282	NOTEST	0	0.0177578	inf	0	1	1
ENSG00000236518	ENSG00000236518	RP13-77O11.7	X:52799879-52800150	NOTEST	0	0	0	0	1	1
ENSG00000236519	ENSG00000236519	AL773604.8	21:46222491-46224632	NOTEST	0.135125	0.0755282	-0.839207	0	1	1
ENSG00000236520	ENSG00000236520	GPC6-AS1	13:93879094-95059655	NOTEST	0	0	0	0	1	1
ENSG00000236521	ENSG00000236521	NPAP1P4	9:82971943-82975253	NOTEST	0	0	0	0	1	1
ENSG00000236522	ENSG00000236522	MDC1-AS1	HSCHR6_MHC_SSTO:30659032-30677115	NOTEST	0	0	0	0	1	1
ENSG00000236523	ENSG00000236523	NPM1P40	1:203181954-203242769	NOTEST	0	0	0	0	1	1
ENSG00000236524	ENSG00000236524	RP11-134F2.2	3:186353757-186396029	NOTEST	0	0	0	0	1	1
ENSG00000236525	ENSG00000236525	AC007278.2	2:103035148-103069025	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000236526	ENSG00000236526	RP4-742J24.2	20:11871370-11907257	NOTEST	0.0629417	0.0427907	-0.556717	0	1	1
ENSG00000236527	ENSG00000236527	ARF4P2	20:61503601-61504428	NOTEST	0.0836865	0.0593873	-0.494841	0	1	1
ENSG00000236530	ENSG00000236530	AC097711.1	4:80822302-81046608	NOTEST	0	0	0	0	1	1
ENSG00000236531	ENSG00000236531	RP5-945F2.2	7:67556209-67584196	NOTEST	0	0	0	0	1	1
ENSG00000236532	ENSG00000236532	AL035610.2	21:29420732-29600986	NOTEST	0	0.270317	inf	0	1	1
ENSG00000236533	ENSG00000236533	AC009413.2	2:42077342-42077741	NOTEST	0	0	0	0	1	1
ENSG00000236534	ENSG00000236534	H3F3BP1	13:72012097-72441330	NOTEST	0	0.049906	inf	0	1	1
ENSG00000236535	ENSG00000236535	RC3H1-IT1	1:173900351-173991435	NOTEST	0	0	0	0	1	1
ENSG00000236536	ENSG00000236536	AC003986.7	7:19159555-19161539	NOTEST	0	0.0688461	inf	0	1	1
ENSG00000236538	ENSG00000236538	ZNF863P	2:51259738-52635055	NOTEST	0	0	0	0	1	1
ENSG00000236539	ENSG00000236539	HNRNPA1P54	1:179334854-179545087	NOTEST	0	0.0033913	inf	0	1	1
ENSG00000236541	ENSG00000236541	VN2R9P	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000236542	ENSG00000236542	MED28P7	20:25593570-25677477	NOTEST	0	0.0497522	inf	0	1	1
ENSG00000236543	ENSG00000236543	RP11-98L5.5	9:138506141-138507354	NOTEST	0	0	0	0	1	1
ENSG00000236544	ENSG00000236544	AC008060.8	7:155213900-155249794	NOTEST	0.0409216	0.358677	3.13175	0	1	1
ENSG00000236545	ENSG00000236545	AP001619.3	21:43218384-43299591	NOTEST	0	0.106921	inf	0	1	1
ENSG00000236546	ENSG00000236546	RP1-118J21.5	1:40361097-40367928	NOTEST	0	0	0	0	1	1
ENSG00000236547	ENSG00000236547	RPL15P4	HSCHR6_MHC_MCF:31572244-31572824	NOTEST	0	0	0	0	1	1
ENSG00000236548	ENSG00000236548	RP11-510H23.1	6:125230238-125413779	NOTEST	0.0105236	0.0051787	-1.02296	0	1	1
ENSG00000236549	ENSG00000236549	AC079807.3	2:47922668-48134949	NOTEST	0	0	0	0	1	1
ENSG00000236550	ENSG00000236550	RP4-673D20.5	20:1645928-1688846	NOTEST	0	0	0	0	1	1
ENSG00000236554	ENSG00000236554	ASNSP3	13:100714549-100715855	NOTEST	0	0	0	0	1	1
ENSG00000236555	ENSG00000236555	AC115115.4	2:113103587-113103835	NOTEST	0	0	0	0	1	1
ENSG00000236556	ENSG00000236556	RP11-443O13.3	10:60936349-61122939	NOTEST	0	0	0	0	1	1
ENSG00000236558	ENSG00000236558	AC138655.6	2:47630107-47798078	NOTEST	0.0293024	0.011969	-1.29171	0	1	1
ENSG00000236559	ENSG00000236559	RP11-243J16.7	20:30252254-30311792	NOTEST	0	0	0	0	1	1
ENSG00000236560	ENSG00000236560	PPP1R11	HSCHR6_MHC_MANN:30029680-30038860	NOTEST	0	0	0	0	1	1
ENSG00000236561	ENSG00000236561	MOG	HSCHR6_MHC_SSTO:29624455-29639844	NOTEST	0	0	0	0	1	1
ENSG00000236562	ENSG00000236562	RP11-396M11.1	4:66864563-67015730	NOTEST	0	0	0	0	1	1
ENSG00000236564	ENSG00000236564	YWHAQP5	2:99235568-99347589	NOTEST	0	0	0	0	1	1
ENSG00000236567	ENSG00000236567	RP11-39K24.7	9:4985032-5128183	NOTEST	0.0152357	0	#NAME?	0	1	1
ENSG00000236569	ENSG00000236569	HNRNPA1P73	7:27368225-27369153	NOTEST	0	0	0	0	1	1
ENSG00000236570	ENSG00000236570	RAD23BP1	3:17198653-18959184	NOTEST	0	0	0	0	1	1
ENSG00000236571	ENSG00000236571	RP6-29D12.3	X:53366988-53367179	NOTEST	0	0	0	0	1	1
ENSG00000236572	ENSG00000236572	AC006369.3	2:37971475-37974189	NOTEST	0	0	0	0	1	1
ENSG00000236574	ENSG00000236574	RP11-340I6.4	7:63303691-63303883	NOTEST	0	0	0	0	1	1
ENSG00000236575	ENSG00000236575	ZNF26	GL000223.1:93510-119608	NOTEST	0	0	0	0	1	1
ENSG00000236576	ENSG00000236576	RP11-22B10.3	X:51546102-51645453	NOTEST	0	0	0	0	1	1
ENSG00000236577	ENSG00000236577	SNRPGP14	13:49882785-50069138	NOTEST	0	0	0	0	1	1
ENSG00000236579	ENSG00000236579	HCG9	HSCHR6_MHC_COX:29932390-29935687	NOTEST	0	0	0	0	1	1
ENSG00000236580	ENSG00000236580	RP11-95P9.1	7:113726381-114333827	NOTEST	0	0	0	0	1	1
ENSG00000236581	ENSG00000236581	STARD13-AS	13:33677271-33924767	NOTEST	0	0.350029	inf	0	1	1
ENSG00000236582	ENSG00000236582	PRPF38AP2	10:17619360-17620211	NOTEST	0	0	0	0	1	1

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ENSG00000236583	ENSG00000236583	AP004290.1	8:100025493-100906290	NOTEST	0	0	0	0	1	1
ENSG00000236584	ENSG00000236584	BX664726.3	9:39897659-39897987	NOTEST	0	0	0	0	1	1
ENSG00000236587	ENSG00000236587	XXbac-BPG116M5.15	HSCHR6_MHC_COX:31937352-31952482	NOTEST	0	0	0	0	1	1
ENSG00000236590	ENSG00000236590	MTATP6P4	2:132138488-132139163	NOTEST	0	0	0	0	1	1
ENSG00000236591	ENSG00000236591	RP11-162J8.3	6:149068463-149398126	NOTEST	0	0	0	0	1	1
ENSG00000236592	ENSG00000236592	S100A11P2	7:35119600-35225934	NOTEST	0	0	0	0	1	1
ENSG00000236594	ENSG00000236594	RPS27AP14	9:1164413-1164867	NOTEST	0	0	0	0	1	1
ENSG00000236595	ENSG00000236595	MED15P5	2:131009140-131010132	NOTEST	0	0	0	0	1	1
ENSG00000236596	ENSG00000236596	AC092568.1	2:104110698-104112300	NOTEST	0	0	0	0	1	1
ENSG00000236597	ENSG00000236597	IGHD7-27	14:106331760-106331771	NOTEST	0	0	0	0	1	1
ENSG00000236598	ENSG00000236598	NCRNA00171	HSCHR6_MHC_APD:29905241-29969520	NOTEST	0	0	0	0	1	1
ENSG00000236599	ENSG00000236599	TCEB1P26	Y:20340817-20341146	NOTEST	0	0	0	0	1	1
ENSG00000236601	ENSG00000236601	RP4-669L17.2	1:317719-461954	NOTEST	0	0	0	0	1	1
ENSG00000236604	ENSG00000236604	RP11-159H20.2	9:79585237-79585944	NOTEST	0	0	0	0	1	1
ENSG00000236605	ENSG00000236605	AC023115.4	2:67551758-67552436	NOTEST	0	0	0	0	1	1
ENSG00000236606	ENSG00000236606	RP11-93H12.3	10:87359311-88126250	NOTEST	0	0	0	0	1	1
ENSG00000236607	ENSG00000236607	RP11-691L4.2	11:61936764-61937300	NOTEST	0	0	0	0	1	1
ENSG00000236608	ENSG00000236608	EIF4A1P6	13:61211021-61212231	NOTEST	0	0	0	0	1	1
ENSG00000236609	ENSG00000236609	ZNF853	7:6655247-6663921	NOTEST	0.0444324	0.218311	2.2967	0	1	1
ENSG00000236610	ENSG00000236610	SOCS5P1	7:85846100-85847049	NOTEST	0	0	0	0	1	1
ENSG00000236611	ENSG00000236611	AP000343.2	22:23668802-23670680	NOTEST	0	0	0	0	1	1
ENSG00000236612	ENSG00000236612	KRTAP19-11P	21:31909596-31909700	NOTEST	0	0	0	0	1	1
ENSG00000236614	ENSG00000236614	ZNF90P2	HSCHR6_MHC_APD:28856612-28857687	NOTEST	0	0	0	0	1	1
ENSG00000236615	ENSG00000236615	AC010086.5	Y:23567655-23567881	NOTEST	0	0	0	0	1	1
ENSG00000236616	ENSG00000236616	BAK1P2	11:130416693-130417324	NOTEST	0	0	0	0	1	1
ENSG00000236617	ENSG00000236617	RP11-46H11.12	12:133345494-133532892	NOTEST	0.149111	0.0548563	-1.44266	0	1	1
ENSG00000236619	ENSG00000236619	HCG9P5	HSCHR6_MHC_QBL:29688013-29714292	NOTEST	0	0	0	0	1	1
ENSG00000236620	ENSG00000236620	XKRYP3	Y:25862068-25872955	NOTEST	0	0	0	0	1	1
ENSG00000236621	ENSG00000236621	OR52E1	11:5090801-5091727	NOTEST	0	0	0	0	1	1
ENSG00000236625	ENSG00000236625	C4B	HSCHR6_MHC_DBB:31964724-31979854	NOTEST	0	0	0	0	1	1
ENSG00000236626	ENSG00000236626	MTND5P17	10:36721809-36723412	NOTEST	0	0	0	0	1	1
ENSG00000236627	ENSG00000236627	RP11-252P19.1	6:165740775-166401536	NOTEST	0.0753041	0.0453771	-0.730763	0	1	1
ENSG00000236629	ENSG00000236629	MTCO3P1	HSCHR6_MHC_DBB:32652914-32653747	NOTEST	0	0	0	0	1	1
ENSG00000236632	ENSG00000236632	HLA-E	HSCHR6_MHC_MANN:30501924-30506663	NOTEST	0	0	0	0	1	1
ENSG00000236634	ENSG00000236634	AC016903.1	2:205334798-205338560	NOTEST	0	0	0	0	1	1
ENSG00000236635	ENSG00000236635	RP11-35J1.1	6:77232167-77303340	NOTEST	0	0	0	0	1	1
ENSG00000236636	ENSG00000236636	RP11-211A18.1	1:227177565-227506175	NOTEST	0	0	0	0	1	1
ENSG00000236637	ENSG00000236637	IFNA4	9:21186616-21187598	NOTEST	0	0	0	0	1	1
ENSG00000236638	ENSG00000236638	RP5-905H7.4	7:62723442-62723834	NOTEST	0	0	0	0	1	1
ENSG00000236641	ENSG00000236641	CTA-221G9.7	22:25608708-25609652	NOTEST	0	0	0	0	1	1
ENSG00000236642	ENSG00000236642	MICF	HSCHR6_MHC_SSTO:29816324-29816469	NOTEST	0	0	0	0	1	1
ENSG00000236643	ENSG00000236643	RP11-175D17.3	9:127279553-127535206	NOTEST	0	0	0	0	1	1
ENSG00000236646	ENSG00000236646	LAMTOR5P1	1:62208148-62629592	NOTEST	0	0	0	0	1	1
ENSG00000236647	ENSG00000236647	AC009947.5	Y:25695955-25697532	NOTEST	0	0	0	0	1	1

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ENSG00000236648	ENSG00000236648	RP11-473A10.2	1:18044181-18076473	NOTEST	0	0	0	0	1	1
ENSG00000236649	ENSG00000236649	PPT2	HSCHR6_MHC_APD:32127475-32157217	NOTEST	0	0	0	0	1	1
ENSG00000236651	ENSG00000236651	AC104801.1	2:172967733-172974710	NOTEST	0.114399	0.0702852	-0.702785	0	1	1
ENSG00000236653	ENSG00000236653	AC005235.1	2:199164086-199637080	NOTEST	0	0	0	0	1	1
ENSG00000236654	ENSG00000236654	AC079780.3	7:23520371-23520578	NOTEST	0	0	0	0	1	1
ENSG00000236655	ENSG00000236655	AC023347.2	2:127066086-127101569	NOTEST	0.0510305	0.22134	2.11683	0	1	1
ENSG00000236656	ENSG00000236656	RP11-144L1.4	1:158444243-158464676	NOTEST	0	0	0	0	1	1
ENSG00000236657	ENSG00000236657	BRD2-IT1	HSCHR6_MHC_MANN:33056219-33103106	NOTEST	0	0	0	0	1	1
ENSG00000236658	ENSG00000236658	RP11-83J21.3	9:133777824-133820907	NOTEST	0	0	0	0	1	1
ENSG00000236660	ENSG00000236660	FAM90A7P	8:7414221-7417234	NOTEST	0	0	0	0	1	1
ENSG00000236662	ENSG00000236662	RP11-108L7.4	10:102729214-102754158	NOTEST	0.105143	0	#NAME?	0	1	1
ENSG00000236663	ENSG00000236663	AP001631.9	21:44560632-44561202	NOTEST	0	0	0	0	1	1
ENSG00000236664	ENSG00000236664	AC011998.1	2:178487979-178973066	NOTEST	0	0	0	0	1	1
ENSG00000236665	ENSG00000236665	AC114808.2	2:946553-1371385	NOTEST	0	0	0	0	1	1
ENSG00000236666	ENSG00000236666	POTEH-AS1	22:16255354-16287937	NOTEST	0	0	0	0	1	1
ENSG00000236667	ENSG00000236667	AC104076.2	2:181803556-181804025	NOTEST	0	0	0	0	1	1
ENSG00000236668	ENSG00000236668	RP11-85O21.2	9:126763948-126795580	NOTEST	0	0	0	0	1	1
ENSG00000236669	ENSG00000236669	AC006372.1	7:157318476-157320019	NOTEST	0	0	0	0	1	1
ENSG00000236671	ENSG00000236671	PRKG1-AS1	10:52750944-54073888	NOTEST	0.0393396	0.0408272	0.0535512	0	1	1
ENSG00000236672	ENSG00000236672	C6orf10	HSCHR6_MHC_APD:32295496-32350672	NOTEST	0	0	0	0	1	1
ENSG00000236673	ENSG00000236673	RP11-691I8.2	6:132223102-132241705	NOTEST	0	0	0	0	1	1
ENSG00000236674	ENSG00000236674	RP4-792G4.3	1:63825493-63826850	NOTEST	0	0	0	0	1	1
ENSG00000236676	ENSG00000236676	RP5-837I24.4	1:81771844-82458120	NOTEST	0	0	0	0	1	1
ENSG00000236677	ENSG00000236677	AP000688.11	21:37402367-37498938	NOTEST	0	0	0	0	1	1
ENSG00000236678	ENSG00000236678	LINC00347	13:75117974-75139582	NOTEST	0	0	0	0	1	1
ENSG00000236679	ENSG00000236679	RP4-669L17.1	1:470970-471355	NOTEST	0.0692618	0.16769	1.27566	0	1	1
ENSG00000236680	ENSG00000236680	RP11-296P7.4	9:18927655-19033251	NOTEST	0.0139195	0	#NAME?	0	1	1
ENSG00000236681	ENSG00000236681	DSTNP5	2:205171564-205172087	NOTEST	0	0	0	0	1	1
ENSG00000236682	ENSG00000236682	AC068282.3	2:128146705-128158156	NOTEST	0.00589553	0.0271473	2.20312	0	1	1
ENSG00000236683	ENSG00000236683	HMGA1P1	X:26766145-26767207	NOTEST	0	0.0752902	inf	0	1	1
ENSG00000236684	ENSG00000236684	AL645728.3	1:1515135-1515379	NOTEST	0	0	0	0	1	1
ENSG00000236686	ENSG00000236686	BZW1P1	3:172143639-172144879	NOTEST	0	0	0	0	1	1
ENSG00000236687	ENSG00000236687	RP11-323H21.3	9:134691578-134696375	NOTEST	0	0	0	0	1	1
ENSG00000236688	ENSG00000236688	HLA-N	HSCHR6_MHC_QBL:30308696-30308831	NOTEST	0	0	0	0	1	1
ENSG00000236689	ENSG00000236689	RP5-837O21.3	1:94392170-94393125	NOTEST	0	0	0	0	1	1
ENSG00000236690	ENSG00000236690	AC007274.5	Y:7558551-7560719	NOTEST	0	0	0	0	1	1
ENSG00000236691	ENSG00000236691	NDUFA4P2	3:102959830-102960074	NOTEST	0	0	0	0	1	1
ENSG00000236692	ENSG00000236692	RP11-1217F2.9	7:57255598-57257847	NOTEST	0	0	0	0	1	1
ENSG00000236693	ENSG00000236693	HLA-DPB1	HSCHR6_MHC_APD:33015767-33038372	NOTEST	0	0	0	0	1	1
ENSG00000236695	ENSG00000236695	HNRNPA1P47	2:195052102-195053033	NOTEST	0	0	0	0	1	1
ENSG00000236697	ENSG00000236697	GPSM3	HSCHR6_MHC_MANN:32197966-32231292	NOTEST	0	0	0	0	1	1
ENSG00000236699	ENSG00000236699	ARHGEF38	4:106473776-106943635	NOTEST	0.0119552	0.208891	4.12705	0	1	1
ENSG00000236700	ENSG00000236700	LINC01010	6:134749377-134841723	NOTEST	0.183539	0.238745	0.379384	0	1	1
ENSG00000236701	ENSG00000236701	RP11-549A6.1	9:76263743-76264755	NOTEST	0	0.0389021	inf	0	1	1

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ENSG00000236703	ENSG00000236703	MYB-AS1	6:135502452-135540311	NOTEST	0	0	0	0	1	1
ENSG00000236704	ENSG00000236704	CNOT4P1	13:21495802-21497372	NOTEST	0	0	0	0	1	1
ENSG00000236706	ENSG00000236706	HLA-U	HSCHR6_MHC_SSTO:29890475-29890660	NOTEST	0	0	0	0	1	1
ENSG00000236708	ENSG00000236708	AC073316.1	7:3303663-4308632	NOTEST	0	0	0	0	1	1
ENSG00000236709	ENSG00000236709	DAPK1-IT1	9:90112142-90323548	NOTEST	0	0	0	0	1	1
ENSG00000236710	ENSG00000236710	AC108448.2	11:3105622-3106673	NOTEST	0.0265724	0.0206757	-0.361994	0	1	1
ENSG00000236711	ENSG00000236711	SMAD9-AS1	13:37418967-37494902	NOTEST	0	0.069513	inf	0	1	1
ENSG00000236712	ENSG00000236712	AC079448.1	7:7333138-7333511	NOTEST	0	0	0	0	1	1
ENSG00000236713	ENSG00000236713	RP11-363I22.3	1:150752747-150753120	NOTEST	0.0733247	0	#NAME?	0	1	1
ENSG00000236714	ENSG00000236714	AC005592.1	5:142125164-142140563	NOTEST	0.230747	0.20145	-0.195891	0	1	1
ENSG00000236716	ENSG00000236716	RP11-478H13.1	10:29032673-29033592	NOTEST	0	0	0	0	1	1
ENSG00000236717	ENSG00000236717	RP11-100G15.10	9:94903579-94922396	NOTEST	0	0	0	0	1	1
ENSG00000236718	ENSG00000236718	RBMY2QP	Y:9860097-9871796	NOTEST	0	0	0	0	1	1
ENSG00000236720	ENSG00000236720	RP11-63B19.1	1:177669658-177679465	NOTEST	0	0	0	0	1	1
ENSG00000236722	ENSG00000236722	RP11-359I18.1	3:58490862-58523046	NOTEST	0	0	0	0	1	1
ENSG00000236723	ENSG00000236723	RP5-1024G6.2	1:53662100-53686289	NOTEST	0	0	0	0	1	1
ENSG00000236724	ENSG00000236724	RP11-252M18.3	9:3824126-4348392	NOTEST	0	0	0	0	1	1
ENSG00000236727	ENSG00000236727	MICC	HSCHR6_MHC_APD:30390729-30395334	NOTEST	0	0	0	0	1	1
ENSG00000236729	ENSG00000236729	HCG17	HSCHR6_MHC_APD:30266816-30322899	NOTEST	0	0	0	0	1	1
ENSG00000236731	ENSG00000236731	RP4-801G22.2	1:157599728-157600518	NOTEST	0	0	0	0	1	1
ENSG00000236732	ENSG00000236732	AC094019.4	3:32147180-32210205	NOTEST	0.0986784	0.144904	0.554295	0	1	1
ENSG00000236733	ENSG00000236733	RP11-203L2.4	9:71320574-71624092	NOTEST	0	0	0	0	1	1
ENSG00000236734	ENSG00000236734	GRIFIN	7:2514359-2516528	NOTEST	0	0	0	0	1	1
ENSG00000236735	ENSG00000236735	RPL31P63	X:67819925-67820315	NOTEST	0	0	0	0	1	1
ENSG00000236736	ENSG00000236736	UQCRC2P1	3:46352081-46353413	NOTEST	0	0	0	0	1	1
ENSG00000236737	ENSG00000236737	GAGE12B	X:49294471-49294588	NOTEST	0	0	0	0	1	1
ENSG00000236740	ENSG00000236740	RP11-411K7.1	6:53794779-54131078	NOTEST	0	0	0	0	1	1
ENSG00000236741	ENSG00000236741	RP4-560B9.4	1:171731213-171731664	NOTEST	0	0	0	0	1	1
ENSG00000236742	ENSG00000236742	CTD-2340F8.3	9:41031935-41032439	NOTEST	0	0	0	0	1	1
ENSG00000236743	ENSG00000236743	RP5-857K21.15	1:317719-461954	NOTEST	0	0	0	0	1	1
ENSG00000236744	ENSG00000236744	RP11-168O22.1	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000236745	ENSG00000236745	YRDCP2	9:99660347-99775862	NOTEST	0	0.0468626	inf	0	1	1
ENSG00000236746	ENSG00000236746	HLA-W	HSCHR6_MHC_MCF:30002850-30004812	NOTEST	0	0	0	0	1	1
ENSG00000236747	ENSG00000236747	RP11-157D23.1	X:39226538-39251028	NOTEST	0	0	0	0	1	1
ENSG00000236748	ENSG00000236748	AC009500.2	7:8978416-8978999	NOTEST	0	0	0	0	1	1
ENSG00000236750	ENSG00000236750	AC009237.16	2:96307381-96307728	NOTEST	0	0	0	0	1	1
ENSG00000236751	ENSG00000236751	RP1-30G7.2	X:46185358-46187080	NOTEST	0.185824	0.206244	0.150417	0	1	1
ENSG00000236754	ENSG00000236754	AC004019.13	22:18043138-18073760	NOTEST	0.0161468	0.00692297	-1.22178	0	1	1
ENSG00000236756	ENSG00000236756	DNAJC9-AS1	10:74870216-75118617	NOTEST	0	0.00387891	inf	0	1	1
ENSG00000236757	ENSG00000236757	AC007251.2	2:103489797-103512180	NOTEST	0	0	0	0	1	1
ENSG00000236758	ENSG00000236758	MTUS2-AS2	13:29598747-30077892	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000236759	ENSG00000236759	EHMT2	HSCHR6_MHC_COX:31835085-31853014	NOTEST	0	0	0	0	1	1
ENSG00000236760	ENSG00000236760	AC019118.3	2:3135352-3149551	NOTEST	0	0.0211303	inf	0	1	1
ENSG00000236761	ENSG00000236761	CTAGE9	6:131949581-132068553	NOTEST	0.016989	0.0188283	0.148298	0	1	1
ENSG00000236762	ENSG00000236762	RP11-159H3.1	10:122892603-122893237	NOTEST	0	0	0	0	1	1
ENSG00000236763	ENSG00000236763	TRMT112P4	9:104118747-104119126	NOTEST	0	0	0	0	1	1
ENSG00000236764	ENSG00000236764	COX7A2P2	4:97823951-97824201	NOTEST	0	0	0	0	1	1
ENSG00000236765	ENSG00000236765	DXO	HSCHR6_MHC_DBB:31919772-31953483	NOTEST	0	0	0	0	1	1
ENSG00000236766	ENSG00000236766	MDC1-AS1	HSCHR6_MHC_COX:30657448-30675531	NOTEST	0	0	0	0	1	1
ENSG00000236768	ENSG00000236768	RP11-1029M24.1	3:48162158-48162705	NOTEST	0	0	0	0	1	1
ENSG00000236769	ENSG00000236769	RP11-168P8.5	10:44396812-44407774	NOTEST	0	0	0	0	1	1
ENSG00000236770	ENSG00000236770	AC079325.5	17:72545537-72548876	NOTEST	0	0	0	0	1	1
ENSG00000236771	ENSG00000236771	OR2N1P	HSCHR6_MHC_DBB:29105665-29106602	NOTEST	0	0	0	0	1	1
ENSG00000236772	ENSG00000236772	RP5-1184F4.5	20:31030861-31196695	NOTEST	0.0726168	0.0865041	0.252466	0	1	1
ENSG00000236775	ENSG00000236775	RP11-551G24.3	1:247108848-247242113	NOTEST	0	0	0	0	1	1
ENSG00000236776	ENSG00000236776	RPL21P23	1:56960418-57110974	NOTEST	0	0	0	0	1	1
ENSG00000236777	ENSG00000236777	RP11-108B14.1	10:22451920-22454723	NOTEST	0	0	0	0	1	1
ENSG00000236779	ENSG00000236779	RP11-430C7.2	1:204485510-204542871	NOTEST	0.0219399	0.017081	-0.361164	0	1	1
ENSG00000236780	ENSG00000236780	AC078941.1	2:67313577-67523207	NOTEST	0.0742749	0.0289198	-1.36082	0	1	1
ENSG00000236783	ENSG00000236783	RPS15AP27	9:110725983-110726326	NOTEST	0	0	0	0	1	1
ENSG00000236785	ENSG00000236785	AC007248.7	2:103027702-103028568	NOTEST	0	0	0	0	1	1
ENSG00000236786	ENSG00000236786	TSPY15P	Y:9385716-9388290	NOTEST	0	0	0	0	1	1
ENSG00000236787	ENSG00000236787	RP11-592B15.6	10:51224680-51371338	NOTEST	0	0	0	0	1	1
ENSG00000236790	ENSG00000236790	LINC00299	2:8062555-8523751	NOTEST	0	0	0	0	1	1
ENSG00000236791	ENSG00000236791	OR2AI1P	5:180119831-180120763	NOTEST	0	0	0	0	1	1
ENSG00000236792	ENSG00000236792	RP11-142L4.2	1:192216634-192217077	NOTEST	0.429965	0.490732	0.190715	0	1	1
ENSG00000236794	ENSG00000236794	BCRP8	22:23521890-23660224	NOTEST	0	0	0	0	1	1
ENSG00000236795	ENSG00000236795	AC006004.1	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000236796	ENSG00000236796	RP11-462B18.3	9:32836572-32869593	NOTEST	0	0	0	0	1	1
ENSG00000236797	ENSG00000236797	SPA17P1	10:77029576-77171600	NOTEST	0	0	0	0	1	1
ENSG00000236798	ENSG00000236798	PAIP1P1	HSCHR6_MHC_APD:30089024-30118001	NOTEST	0	0	0	0	1	1
ENSG00000236799	ENSG00000236799	RP11-383C6.2	10:116754415-116756352	NOTEST	0	0	0	0	1	1
ENSG00000236800	ENSG00000236800	RP11-534L6.2	10:49872243-49880469	NOTEST	0	0	0	0	1	1
ENSG00000236802	ENSG00000236802	B3GALT4	HSCHR6_MHC_MCF:33415293-33416979	NOTEST	0	0	0	0	1	1
ENSG00000236803	ENSG00000236803	SDAD1P4	13:23755090-23899304	NOTEST	0	0	0	0	1	1
ENSG00000236804	ENSG00000236804	RPS3AP12	1:119573838-119869926	NOTEST	0.0510441	0	#NAME?	0	1	1
ENSG00000236806	ENSG00000236806	RP11-337C18.7	1:146644349-146767443	NOTEST	0	0	0	0	1	1
ENSG00000236807	ENSG00000236807	AC092066.6	19:45268404-45268721	NOTEST	0	0	0	0	1	1
ENSG00000236808	ENSG00000236808	ZNRD1	HSCHR6_MHC_MCF:30047254-30111187	NOTEST	0	0	0	0	1	1
ENSG00000236809	ENSG00000236809	SNX25P1	1:211556144-211605878	NOTEST	0.0410269	0.033234	-0.303911	0	1	1
ENSG00000236811	ENSG00000236811	GAPDHP2	20:13202417-13619587	NOTEST	0.032777	0	#NAME?	0	1	1
ENSG00000236813	ENSG00000236813	BTF3P8	X:62854846-63005426	NOTEST	0	0	0	0	1	1
ENSG00000236816	ENSG00000236816	ANKRD20A7P	9:44076367-44118444	NOTEST	0.184432	0.175504	-0.071584	0	1	1
ENSG00000236817	ENSG00000236817	RP11-978I15.10	1:247670359-247910364	NOTEST	0	0	0	0	1	1

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ENSG00000236818	ENSG00000236818	ARL5AP2	10:100218874-100995619	NOTEST	0	0	0	0	1	1
ENSG00000236819	ENSG00000236819	AC087393.1	17:20978868-20993928	NOTEST	0.0470988	0	#NAME?	0	1	1
ENSG00000236822	ENSG00000236822	RP11-137J7.2	6:142379466-142410356	NOTEST	0	0	0	0	1	1
ENSG00000236823	ENSG00000236823	RP1-249F5.3	6:160320217-160323542	NOTEST	0	0	0	0	1	1
ENSG00000236824	ENSG00000236824	BCYRN1	2:47419543-47572213	NOTEST	0.0961549	0.136378	0.504176	0	1	1
ENSG00000236825	ENSG00000236825	RP11-211N8.5	9:46918097-46919049	NOTEST	0	0	0	0	1	1
ENSG00000236826	ENSG00000236826	LSM2	HSCHR6_MHC_COX:31752536-31762128	NOTEST	0	0	0	0	1	1
ENSG00000236827	ENSG00000236827	LINC00529	8:11105134-11125374	NOTEST	0	0	0	0	1	1
ENSG00000236828	ENSG00000236828	DMD-AS3	X:31115793-33357558	NOTEST	0	0	0	0	1	1
ENSG00000236831	ENSG00000236831	YME1L1P1	22:16485398-16487973	NOTEST	0	0	0	0	1	1
ENSG00000236832	ENSG00000236832	AC073465.2	2:174342723-174343128	NOTEST	0	0	0	0	1	1
ENSG00000236833	ENSG00000236833	AC024560.2	3:197387435-197392628	NOTEST	0	0.0329849	inf	0	1	1
ENSG00000236834	ENSG00000236834	LINC00421	13:19919188-19920889	NOTEST	0	0	0	0	1	1
ENSG00000236835	ENSG00000236835	HCG14	HSCHR6_MHC_MCF:28864473-28865264	NOTEST	0	0	0	0	1	1
ENSG00000236836	ENSG00000236836	PCYT1B-AS1	X:24576203-24690794	NOTEST	0	0	0	0	1	1
ENSG00000236837	ENSG00000236837	AC139712.4	2:52721825-52727890	NOTEST	0	0	0	0	1	1
ENSG00000236838	ENSG00000236838	AC090617.1	17:1963132-2284352	NOTEST	0	0	0	0	1	1
ENSG00000236839	ENSG00000236839	RP11-3P22.1	7:68652819-68654305	NOTEST	0	0	0	0	1	1
ENSG00000236841	ENSG00000236841	AC007750.5	2:163016271-163101661	NOTEST	0.0445114	0.0365693	-0.283544	0	1	1
ENSG00000236842	ENSG00000236842	RP11-399K21.10	10:77190328-77191346	NOTEST	0	0.1251	inf	0	1	1
ENSG00000236843	ENSG00000236843	NRM	HSCHR6_MHC_DBB:30646088-30649462	NOTEST	0	0	0	0	1	1
ENSG00000236844	ENSG00000236844	AC091633.2	3:195281427-195281901	NOTEST	0	0	0	0	1	1
ENSG00000236846	ENSG00000236846	RP11-239E10.2	1:223317390-223318296	NOTEST	0	0	0	0	1	1
ENSG00000236847	ENSG00000236847	AC018892.3	2:97701197-97703286	NOTEST	0	0	0	0	1	1
ENSG00000236848	ENSG00000236848	RP11-401L13.5	7:102792453-102792772	NOTEST	0	0.119126	inf	0	1	1
ENSG00000236851	ENSG00000236851	DHFRP2	HSCHR6_MHC_QBL:31324239-31324786	NOTEST	0	0	0	0	1	1
ENSG00000236852	ENSG00000236852	RP11-3D23.1	X:61998719-61999796	NOTEST	0	0	0	0	1	1
ENSG00000236853	ENSG00000236853	OR2R1P	7:143078172-143220542	NOTEST	0	0	0	0	1	1
ENSG00000236854	ENSG00000236854	AL121656.5	2:33152193-33153472	NOTEST	0	0	0	0	1	1
ENSG00000236856	ENSG00000236856	AC105393.1	2:388411-416885	NOTEST	0	0	0	0	1	1
ENSG00000236857	ENSG00000236857	RP11-503K16.2	9:18473891-18910948	NOTEST	0	0	0	0	1	1
ENSG00000236858	ENSG00000236858	CTA-992D9.6	22:27444105-27456480	NOTEST	0	0	0	0	1	1
ENSG00000236860	ENSG00000236860	RPL39P29	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000236861	ENSG00000236861	AC006378.2	7:93592073-93640425	NOTEST	0	0	0	0	1	1
ENSG00000236862	ENSG00000236862	RPS20P24	9:75136716-75451267	NOTEST	0	0	0	0	1	1
ENSG00000236863	ENSG00000236863	RPL23AP23	1:235294497-235507847	NOTEST	0	0	0	0	1	1
ENSG00000236864	ENSG00000236864	RP11-44H4.1	3:187650551-187664009	NOTEST	0	0	0	0	1	1
ENSG00000236866	ENSG00000236866	AL157902.3	1:118139453-118148392	NOTEST	0	0	0	0	1	1
ENSG00000236867	ENSG00000236867	RP3-522J7.5	22:50166930-50221160	NOTEST	0.0505111	0.295665	2.54929	0	1	1
ENSG00000236869	ENSG00000236869	RP11-944L7.4	3:44596684-44727145	NOTEST	0	0	0	0	1	1
ENSG00000236870	ENSG00000236870	RP1-223D17.1	X:82814903-82815320	NOTEST	0	0	0	0	1	1
ENSG00000236871	ENSG00000236871	LINC00106	X:1515319-1518295	NOTEST	0.154364	0.707575	2.19654	0	1	1
ENSG00000236872	ENSG00000236872	RP11-291L19.1	1:45794834-45956872	NOTEST	0	0	0	0	1	1
ENSG00000236873	ENSG00000236873	AGPAT1	HSCHR6_MHC_APD:32127475-32157217	NOTEST	0	0	0	0	1	1

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ENSG00000236875	ENSG00000236875	DDX11L5	9:11986-30891	NOTEST	0.0204754	0.00793116	-1.36829	0	1	1
ENSG00000236876	ENSG00000236876	TMSB4XP1	1:42895999-43120335	NOTEST	0	0	0	0	1	1
ENSG00000236877	ENSG00000236877	RP11-443K8.2	2:108842470-108842787	NOTEST	0	0	0	0	1	1
ENSG00000236878	ENSG00000236878	AC012363.7	2:120770580-120974855	NOTEST	0	0.0235464	inf	0	1	1
ENSG00000236880	ENSG00000236880	RP3-384D21.2	X:123093082-124097666	NOTEST	0	0	0	0	1	1
ENSG00000236881	ENSG00000236881	HCG4P11	HSCHR6_MHC_SSTO:29687513-29713718	NOTEST	0	0	0	0	1	1
ENSG00000236882	ENSG00000236882	C5orf27	5:95171646-95195837	NOTEST	0	0.0996635	inf	0	1	1
ENSG00000236883	ENSG00000236883	AP001615.9	21:43159528-43187266	NOTEST	0	0	0	0	1	1
ENSG00000236884	ENSG00000236884	HLA-DRB1	HSCHR6_MHC_DBB:32516730-32550833	NOTEST	0	0	0	0	1	1
ENSG00000236885	ENSG00000236885	AC018731.3	2:151974468-152043109	NOTEST	0	0	0	0	1	1
ENSG00000236886	ENSG00000236886	AC007563.5	2:217536827-217858802	NOTEST	0	0	0	0	1	1
ENSG00000236887	ENSG00000236887	RP11-389O22.5	1:113741446-113741880	NOTEST	0	0.0440265	inf	0	1	1
ENSG00000236888	ENSG00000236888	RPS20P5	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000236889	ENSG00000236889	RP11-38J22.1	1:206164083-206166270	NOTEST	0	0	0	0	1	1
ENSG00000236890	ENSG00000236890	XXbac-B476C20.11	22:18559292-18629321	NOTEST	0.300888	0.457935	0.605914	0	1	1
ENSG00000236892	ENSG00000236892	RP11-482E14.2	10:3574285-3579223	NOTEST	0	0	0	0	1	1
ENSG00000236893	ENSG00000236893	ASS1P7	3:177012229-177041206	NOTEST	0	0	0	0	1	1
ENSG00000236894	ENSG00000236894	RP11-128B16.3	10:26866604-26868024	NOTEST	0	0	0	0	1	1
ENSG00000236895	ENSG00000236895	GTF2H4	HSCHR6_MHC_COX:30865831-30883959	NOTEST	0	0	0	0	1	1
ENSG00000236896	ENSG00000236896	RP11-535C21.3	9:100745642-100778225	NOTEST	0	0	0	0	1	1
ENSG00000236897	ENSG00000236897	AC113331.9	11:5127291-5128760	NOTEST	0	0	0	0	1	1
ENSG00000236898	ENSG00000236898	HLA-DPA2	HSCHR6_MHC_SSTO:33199175-33204718	NOTEST	0	0	0	0	1	1
ENSG00000236900	ENSG00000236900	TIMM9P1	10:75910959-76469061	NOTEST	0	0	0	0	1	1
ENSG00000236902	ENSG00000236902	LY6G6D	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000236903	ENSG00000236903	DAQB-331I12.5	HSCHR6_MHC_DBB:31829720-31847649	NOTEST	0	0	0	0	1	1
ENSG00000236905	ENSG00000236905	RP11-348H3.2	1:212997368-212997847	NOTEST	0	0	0	0	1	1
ENSG00000236907	ENSG00000236907	RP11-548K12.3	7:57877306-57877903	NOTEST	0	0	0	0	1	1
ENSG00000236908	ENSG00000236908	RP5-1063M23.2	12:3427883-3434509	NOTEST	0	0	0	0	1	1
ENSG00000236909	ENSG00000236909	OR2P1P	6:29039600-29040376	NOTEST	0	0	0	0	1	1
ENSG00000236910	ENSG00000236910	ZNF70P1	HSCHR6_MHC_MANN:33337404-33338028	NOTEST	0	0	0	0	1	1
ENSG00000236911	ENSG00000236911	RP11-78B10.2	1:207669491-207813992	NOTEST	0	0	0	0	1	1
ENSG00000236912	ENSG00000236912	SAPCD1-AS1	HSCHR6_MHC_APD:31735722-31744719	NOTEST	0	0	0	0	1	1
ENSG00000236913	ENSG00000236913	AC025750.5	2:42669156-42721237	NOTEST	0	0.0378918	inf	0	1	1
ENSG00000236914	ENSG00000236914	RP11-1008C21.2	15:38361681-38365160	NOTEST	0.356428	0.102201	-1.8022	0	1	1
ENSG00000236915	ENSG00000236915	RP4-651E10.4	1:87012760-87158886	NOTEST	0	0	0	0	1	1
ENSG00000236917	ENSG00000236917	DNAJA1P2	2:154617962-154619159	NOTEST	0	0	0	0	1	1
ENSG00000236918	ENSG00000236918	OR2U1P	HSCHR6_MHC_MANN:29191795-29234882	NOTEST	0	0	0	0	1	1
ENSG00000236919	ENSG00000236919	RP11-347H15.6	11:50205724-50206932	NOTEST	0	0	0	0	1	1
ENSG00000236920	ENSG00000236920	RP11-111D3.2	6:98264584-98847748	NOTEST	0	0	0	0	1	1

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ENSG00000236922	ENSG00000236922	AC092661.1	4:118349551-118612343	NOTEST	0	0	0	0	1	1
ENSG00000236924	ENSG00000236924	RP11-390F4.6	9:6645955-6670635	NOTEST	0.0777899	0.0296936	-1.38943	0	1	1
ENSG00000236925	ENSG00000236925	LTB	HSCHR6_MHC_DBB:31530475-31532443	NOTEST	0	0	0	0	1	1
ENSG00000236926	ENSG00000236926	ZDHHC20P1	HSCHR6_MHC_MCF:29675657-29676080	NOTEST	0	0	0	0	1	1
ENSG00000236927	ENSG00000236927	OR14J1	HSCHR6_MHC_APD:29274488-29275605	NOTEST	0	0	0	0	1	1
ENSG00000236928	ENSG00000236928	RP11-792A8.1	7:65670185-65955095	NOTEST	0	0	0	0	1	1
ENSG00000236929	ENSG00000236929	RP11-699A7.1	X:15135558-15135890	NOTEST	0	0	0	0	1	1
ENSG00000236930	ENSG00000236930	RP11-852E15.1	3:45864807-45957534	NOTEST	0	0	0	0	1	1
ENSG00000236931	ENSG00000236931	BX664608.1	9:40760699-40836415	NOTEST	0	0	0	0	1	1
ENSG00000236932	ENSG00000236932	CEACAMP8	19:43540020-43545400	NOTEST	0	0	0	0	1	1
ENSG00000236934	ENSG00000236934	XXbac-BPG249D20.9	HSCHR6_MHC_QBL:30473551-30476506	NOTEST	0	0	0	0	1	1
ENSG00000236935	ENSG00000236935	AP003774.1	11:64092521-64096976	NOTEST	0	0	0	0	1	1
ENSG00000236936	ENSG00000236936	RP3-329E20.2	1:21543739-21671997	NOTEST	0	0	0	0	1	1
ENSG00000236937	ENSG00000236937	PTGES3P4	10:104605351-104605707	NOTEST	0	0	0	0	1	1
ENSG00000236938	ENSG00000236938	AC003092.2	7:93701070-93706469	NOTEST	0	0	0	0	1	1
ENSG00000236939	ENSG00000236939	C8orf56	8:104133259-104345094	NOTEST	0.118726	0	#NAME?	0	1	1
ENSG00000236940	ENSG00000236940	RP11-98D18.7	1:151728016-151766878	NOTEST	0	0	0	0	1	1
ENSG00000236941	ENSG00000236941	RP11-366M4.8	4:165869230-165899980	NOTEST	0	0	0	0	1	1
ENSG00000236942	ENSG00000236942	RP11-6B6.3	1:205577070-205601090	NOTEST	0.155429	0.058271	-1.41541	0	1	1
ENSG00000236944	ENSG00000236944	CCDC58P2	10:52722752-52723118	NOTEST	0	0	0	0	1	1
ENSG00000236946	ENSG00000236946	HNRNPA1P70	12:68383224-68628466	NOTEST	0	0	0	0	1	1
ENSG00000236948	ENSG00000236948	RP11-154H17.1	1:5647427-5728355	NOTEST	0	0	0	0	1	1
ENSG00000236949	ENSG00000236949	ZNRD1	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000236950	ENSG00000236950	RP5-1051D14.1	1:209145798-209148652	NOTEST	0	0	0	0	1	1
ENSG00000236951	ENSG00000236951	AC007359.6	Y:24246960-24293631	NOTEST	0	0	0	0	1	1
ENSG00000236953	ENSG00000236953	ZDHHC20-IT1	13:21950262-22033509	NOTEST	0	0.166181	inf	0	1	1
ENSG00000236956	ENSG00000236956	NF1P8	2:131862419-132111282	NOTEST	0	0	0	0	1	1
ENSG00000236957	ENSG00000236957	RP11-451O13.1	1:157894854-157918861	NOTEST	0	0	0	0	1	1
ENSG00000236958	ENSG00000236958	RP11-264A11.1	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000236959	ENSG00000236959	SULT1D1P	4:70657589-70725870	NOTEST	0	0	0	0	1	1
ENSG00000236960	ENSG00000236960	RP11-265G8.3	10:19492778-20079330	NOTEST	0	0	0	0	1	1
ENSG00000236961	ENSG00000236961	RP1-261G23.5	6:43690522-43705571	NOTEST	0	0	0	0	1	1
ENSG00000236963	ENSG00000236963	LINC01141	1:20687071-20757727	NOTEST	0	0	0	0	1	1
ENSG00000236965	ENSG00000236965	OR52N3P	11:5684424-5959849	NOTEST	0	0	0	0	1	1
ENSG00000236966	ENSG00000236966	RP11-216M21.4	9:42275938-42298165	NOTEST	0	0	0	0	1	1
ENSG00000236967	ENSG00000236967	RNF39	HSCHR6_MHC_APD:29971319-29980498	NOTEST	0	0	0	0	1	1
ENSG00000236968	ENSG00000236968	RP11-298E9.5	10:3266007-3269599	NOTEST	0	0.0246948	inf	0	1	1
ENSG00000236969	ENSG00000236969	GGT8P	2:91963969-91969195	NOTEST	0	0	0	0	1	1
ENSG00000236971	ENSG00000236971	SUMO2P1	HSCHR6_MHC_APD:29603969-29604253	NOTEST	0	0	0	0	1	1
ENSG00000236972	ENSG00000236972	FABP5P1	13:73674712-73675123	NOTEST	0	0.0445749	inf	0	1	1
ENSG00000236973	ENSG00000236973	GAPDHP51	1:52027537-52344477	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000236975	ENSG00000236975	RP5-1065P14.2	1:229228561-229230652	NOTEST	0	0	0	0	1	1
ENSG00000236976	ENSG00000236976	RP11-165H4.2	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000236977	ENSG00000236977	ANKRD44-IT1	2:197831740-198175897	NOTEST	0	0	0	0	1	1
ENSG00000236978	ENSG00000236978	RP11-575M4.1	7:70302723-70302999	NOTEST	0	0	0	0	1	1
ENSG00000236979	ENSG00000236979	NCR3	HSCHR6_MHC_MANN:31593387-31600249	NOTEST	0	0	0	0	1	1
ENSG00000236980	ENSG00000236980	C3orf84	3:49215064-49229291	NOTEST	0	0	0	0	1	1
ENSG00000236981	ENSG00000236981	OR10G9	11:123893719-123894655	NOTEST	0	0	0	0	1	1
ENSG00000236982	ENSG00000236982	RP13-100A9.2	X:63946627-63946928	NOTEST	0	0	0	0	1	1
ENSG00000236983	ENSG00000236983	LINC00614	10:27232251-27233347	NOTEST	0	0	0	0	1	1
ENSG00000236984	ENSG00000236984	XXbac-B33L19.10	22:20473205-20475156	NOTEST	0	0	0	0	1	1
ENSG00000236985	ENSG00000236985	RP5-1195D24.1	20:16838606-16844793	NOTEST	0.0224371	0.0174527	-0.362434	0	1	1
ENSG00000236986	ENSG00000236986	RP11-544A12.4	9:134000947-134110057	NOTEST	0	0	0	0	1	1
ENSG00000236987	ENSG00000236987	NDUFA5P8	11:3297274-3297620	NOTEST	0	0	0	0	1	1
ENSG00000236988	ENSG00000236988	RP11-402K9.1	X:99404780-99406338	NOTEST	0	0	0	0	1	1
ENSG00000236989	ENSG00000236989	AC142119.1	2:16137170-16245963	NOTEST	0	0	0	0	1	1
ENSG00000236990	ENSG00000236990	RP11-433J20.1	10:4093917-4131205	NOTEST	0.0745329	0.0600546	-0.311602	0	1	1
ENSG00000236991	ENSG00000236991	EDRF1-AS1	10:127371797-127452712	NOTEST	0.201128	0.0611925	-1.71669	0	1	1
ENSG00000236993	ENSG00000236993	GAPDHP21	10:57427100-57428110	NOTEST	0	0	0	0	1	1
ENSG00000236994	ENSG00000236994	YBX1P9	1:226505715-226506394	NOTEST	0	0	0	0	1	1
ENSG00000236996	ENSG00000236996	MLIP-IT1	6:53794779-54131078	NOTEST	0	0	0	0	1	1
ENSG00000236998	ENSG00000236998	RP11-203L2.3	9:71320574-71624092	NOTEST	0	0.0204261	inf	0	1	1
ENSG00000236999	ENSG00000236999	ATP2B2-IT1	3:10365706-10749716	NOTEST	0	0	0	0	1	1
ENSG00000237000	ENSG00000237000	PTMAP6	20:55275892-55276570	NOTEST	0	0	0	0	1	1
ENSG00000237001	ENSG00000237001	WASF3-AS1	13:27131839-27263085	NOTEST	0	0	0	0	1	1
ENSG00000237002	ENSG00000237002	SNORA40	10:36727543-36731320	NOTEST	0	0	0	0	1	1
ENSG00000237003	ENSG00000237003	RP4-612C19.1	1:93615298-93835055	NOTEST	0	0	0	0	1	1
ENSG00000237005	ENSG00000237005	HIGD1AP15	20:9966735-10349424	NOTEST	0	0	0	0	1	1
ENSG00000237006	ENSG00000237006	XXbac-BPG308K3.5	HSCHR6_MHC_COX:28806289-28807427	NOTEST	0	0	0	0	1	1
ENSG00000237007	ENSG00000237007	KRT18P52	2:32047659-32048886	NOTEST	0	0	0	0	1	1
ENSG00000237008	ENSG00000237008	AL591704.5	1:153352296-153353275	NOTEST	0	0	0	0	1	1
ENSG00000237009	ENSG00000237009	GLIS3-AS1	9:3824126-4348392	NOTEST	0	0	0	0	1	1
ENSG00000237010	ENSG00000237010	HCG14	HSCHR6_MHC_SSTO:28864372-28865163	NOTEST	0	0	0	0	1	1
ENSG00000237011	ENSG00000237011	RP11-98G13.1	1:193648023-193696165	NOTEST	0	0	0	0	1	1
ENSG00000237012	ENSG00000237012	C6orf136	HSCHR6_MHC_DBB:30605055-30631079	NOTEST	0	0	0	0	1	1
ENSG00000237013	ENSG00000237013	AC010987.6	2:68023185-68052694	NOTEST	0.0760812	0.0757721	-0.00587426	0	1	1
ENSG00000237014	ENSG00000237014	AC004074.4	X:72457482-72458545	NOTEST	0	0	0	0	1	1
ENSG00000237015	ENSG00000237015	CTA-984G1.5	22:29655840-29696515	NOTEST	0.415588	0.15778	-1.39724	0	1	1
ENSG00000237016	ENSG00000237016	AC013410.1	2:174439837-174441069	NOTEST	0	0	0	0	1	1
ENSG00000237017	ENSG00000237017	AC012314.8	19:54606035-54635140	NOTEST	0.140511	0.195114	0.473638	0	1	1
ENSG00000237019	ENSG00000237019	GS1-433O24.1	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000237020	ENSG00000237020	IGHD1-20	14:106355941-106362435	NOTEST	0	0	0	0	1	1
ENSG00000237021	ENSG00000237021	RP3-486I3.7	6:116575335-116762424	NOTEST	0.037408	0.0175475	-1.09208	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237022	ENSG00000237022	HLA-C	HSCHR6_MHC_MANN:31280023-31283395	NOTEST	0	0	0	0	1	1
ENSG00000237023	ENSG00000237023	USP9YP3	Y:23823811-23835894	NOTEST	0	0	0	0	1	1
ENSG00000237024	ENSG00000237024	AC010733.7	2:61052266-61108449	NOTEST	0	0	0	0	1	1
ENSG00000237025	ENSG00000237025	RP1-315G1.1	X:122993573-123047829	NOTEST	0.0509595	0.0195846	-1.37963	0	1	1
ENSG00000237026	ENSG00000237026	RP11-328P23.2	7:64696163-64697097	NOTEST	0	0	0	0	1	1
ENSG00000237027	ENSG00000237027	RP11-16C18.3	6:90142888-90348472	NOTEST	0	0	0	0	1	1
ENSG00000237031	ENSG00000237031	AC008067.2	2:79384131-80875905	NOTEST	0	0	0	0	1	1
ENSG00000237032	ENSG00000237032	RP11-398C13.2	10:14560555-14816896	NOTEST	0	0	0	0	1	1
ENSG00000237033	ENSG00000237033	CASP3P1	1:71126339-71126948	NOTEST	0	0	0	0	1	1
ENSG00000237034	ENSG00000237034	MICC	HSCHR6_MHC_QBL:30371998-30376604	NOTEST	0	0	0	0	1	1
ENSG00000237035	ENSG00000237035	AC109589.1	2:199052525-199056245	NOTEST	0	0	0	0	1	1
ENSG00000237036	ENSG00000237036	ZEB1-AS1	10:31476811-31818742	NOTEST	0.56982	0.494948	-0.203231	0	1	1
ENSG00000237038	ENSG00000237038	USP17L8	8:7812535-7866277	NOTEST	0	0	0	0	1	1
ENSG00000237039	ENSG00000237039	AC018738.2	2:232063259-232239548	NOTEST	0	0	0	0	1	1
ENSG00000237040	ENSG00000237040	DPH3P2	X:155105298-155105548	NOTEST	0	0	0	0	1	1
ENSG00000237041	ENSG00000237041	AC007679.4	2:206854308-206951288	NOTEST	0	0	0	0	1	1
ENSG00000237042	ENSG00000237042	MICG	6:29780341-29780473	NOTEST	0	0	0	0	1	1
ENSG00000237043	ENSG00000237043	OR2AD1P	HSCHR6_MHC_QBL:28994456-28995384	NOTEST	0	0	0	0	1	1
ENSG00000237046	ENSG00000237046	TRIM40	HSCHR6_MHC_MANN:30149052-30161680	NOTEST	0	0	0	0	1	1
ENSG00000237048	ENSG00000237048	TTTY12	Y:7581025-7678724	NOTEST	0	0	0	0	1	1
ENSG00000237049	ENSG00000237049	RPL34P1	1:168179853-168180207	NOTEST	0	0	0	0	1	1
ENSG00000237050	ENSG00000237050	TRIM31-AS1	HSCHR6_MHC_MANN:30065836-30077657	NOTEST	0	0	0	0	1	1
ENSG00000237051	ENSG00000237051	GABBR1	HSCHR6_MHC_MANN:29522993-29600557	NOTEST	0	0	0	0	1	1
ENSG00000237052	ENSG00000237052	GPSM3	HSCHR6_MHC_APD:32169883-32183518	NOTEST	0	0	0	0	1	1
ENSG00000237053	ENSG00000237053	FUCA1P1	2:177588995-177684038	NOTEST	0	0	0	0	1	1
ENSG00000237054	ENSG00000237054	PRMT5-AS1	14:23388664-23398794	NOTEST	0.143822	0.169864	0.240103	0	1	1
ENSG00000237055	ENSG00000237055	AC097374.3	2:95533230-95613086	NOTEST	0	0	0	0	1	1
ENSG00000237056	ENSG00000237056	ZBTB22	HSCHR6_MHC_MCF:33452527-33456065	NOTEST	0	0	0	0	1	1
ENSG00000237057	ENSG00000237057	AC015922.6	17:15709554-15721056	NOTEST	0	0	0	0	1	1
ENSG00000237058	ENSG00000237058	RP13-436F16.1	1:2517929-2718286	NOTEST	0	0	0	0	1	1
ENSG00000237061	ENSG00000237061	RP11-956J14.1	8:73976774-74036323	NOTEST	0	0	0	0	1	1
ENSG00000237062	ENSG00000237062	RP11-308N19.3	9:109377358-109378087	NOTEST	0.0644782	0	#NAME?	0	1	1
ENSG00000237063	ENSG00000237063	RP4-550H1.5	20:34674173-34676114	NOTEST	0	0	0	0	1	1
ENSG00000237064	ENSG00000237064	EIF3IP1	7:109599274-109600241	NOTEST	0	0	0	0	1	1
ENSG00000237065	ENSG00000237065	NANOGP4	7:29019582-29603286	NOTEST	0	0	0	0	1	1
ENSG00000237068	ENSG00000237068	RPL5P2	20:44119457-44120311	NOTEST	0	0	0	0	1	1
ENSG00000237069	ENSG00000237069	TTTY23B	Y:6109808-6113324	NOTEST	0	0	0	0	1	1
ENSG00000237070	ENSG00000237070	AC005550.3	7:15650836-15726437	NOTEST	0	0	0	0	1	1
ENSG00000237071	ENSG00000237071	TRIM27	HSCHR6_MHC_COX:28871598-28892590	NOTEST	0	0	0	0	1	1
ENSG00000237072	ENSG00000237072	RP11-232A1.2	9:84103222-84103752	NOTEST	0	0	0	0	1	1
ENSG00000237073	ENSG00000237073	RP11-168K11.2	9:116207010-116360018	NOTEST	0	0	0	0	1	1
ENSG00000237074	ENSG00000237074	RP11-6J21.2	1:207422411-207482466	NOTEST	0.135942	0.0421149	-1.69059	0	1	1
ENSG00000237075	ENSG00000237075	RP11-497H16.2	5:69783428-69786959	NOTEST	0.0256625	0.0336921	0.392752	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000237077	ENSG00000237077	AC105399.2	2:78015507-78020213	NOTEST	0	0	0	0	1	1
ENSG00000237078	ENSG00000237078	AC007272.1	2:201973423-201973553	NOTEST	0	0	0	0	1	1
ENSG00000237080	ENSG00000237080	EHMT2-AS1	6:31847535-31865464	NOTEST	0	0.180253	inf	0	1	1
ENSG00000237082	ENSG00000237082	COX5BP6	13:101256180-101327347	NOTEST	0.296045	0.467173	0.658141	0	1	1
ENSG00000237083	ENSG00000237083	RP11-132E11.4	9:17048916-17112813	NOTEST	0	0	0	0	1	1
ENSG00000237085	ENSG00000237085	AC127391.3	2:92047409-92047507	NOTEST	0	0	0	0	1	1
ENSG00000237086	ENSG00000237086	RBPJP2	9:65973176-65974604	NOTEST	0	0	0	0	1	1
ENSG00000237087	ENSG00000237087	AC068134.6	2:233285370-233286171	NOTEST	0	0	0	0	1	1
ENSG00000237088	ENSG00000237088	RP11-73E6.2	9:20341662-20622542	NOTEST	0.044144	0	#NAME?	0	1	1
ENSG00000237089	ENSG00000237089	PCNPP4	X:74757381-74758537	NOTEST	0	0	0	0	1	1
ENSG00000237090	ENSG00000237090	RP11-342M1.6	1:43356764-43358101	NOTEST	0	0	0	0	1	1
ENSG00000237092	ENSG00000237092	LINC01065	13:53720673-53725943	NOTEST	0	0	0	0	1	1
ENSG00000237093	ENSG00000237093	HCG22	HSCHR6_MHC_SSTO:31016107-31021766	NOTEST	0	0	0	0	1	1
ENSG00000237095	ENSG00000237095	MDC1	HSCHR6_MHC_MCF:30746070-30764152	NOTEST	0	0	0	0	1	1
ENSG00000237096	ENSG00000237096	RP4-782G3.1	1:166864947-166877317	NOTEST	0	0	0	0	1	1
ENSG00000237098	ENSG00000237098	HLA-T	HSCHR6_MHC_MCF:29846326-29992167	NOTEST	0	0	0	0	1	1
ENSG00000237099	ENSG00000237099	GYG1P2	13:83397265-83398271	NOTEST	0	0	0	0	1	1
ENSG00000237100	ENSG00000237100	C6orf136	HSCHR6_MHC_SSTO:30606237-30632260	NOTEST	0	0	0	0	1	1
ENSG00000237101	ENSG00000237101	RP11-365O16.6	1:224407314-224518089	NOTEST	0.0420928	0.0388078	-0.117227	0	1	1
ENSG00000237102	ENSG00000237102	AC040160.1	16:67241041-67260951	NOTEST	0.0244703	0.145957	2.57644	0	1	1
ENSG00000237103	ENSG00000237103	NCR3	HSCHR6_MHC_DBB:31536046-31542910	NOTEST	0	0	0	0	1	1
ENSG00000237104	ENSG00000237104	AC018890.4	2:175647773-175652656	NOTEST	0	0	0	0	1	1
ENSG00000237105	ENSG00000237105	HCP5	HSCHR6_MHC_COX:31418401-31421036	NOTEST	0	0	0	0	1	1
ENSG00000237106	ENSG00000237106	FABP5P15	X:76760355-77041702	NOTEST	0	0	0	0	1	1
ENSG00000237107	ENSG00000237107	RP11-256G5.1	6:42467447-42467760	NOTEST	0	0	0	0	1	1
ENSG00000237108	ENSG00000237108	XXbac-BPG118E17.9	HSCHR6_MHC_APD:31006268-31011068	NOTEST	0	0	0	0	1	1
ENSG00000237109	ENSG00000237109	RPL21P111	13:79335309-79335786	NOTEST	0	0	0	0	1	1
ENSG00000237110	ENSG00000237110	TAAR9	6:132859428-132860470	NOTEST	0.130408	0.0771774	-0.756779	0	1	1
ENSG00000237111	ENSG00000237111	IGHJ3P	14:106329625-106329675	NOTEST	0	0	0	0	1	1
ENSG00000237112	ENSG00000237112	GABBR1	HSCHR6_MHC_DBB:29523342-29600923	NOTEST	0	0	0	0	1	1
ENSG00000237114	ENSG00000237114	CDSN	HSCHR6_MHC_MANN:31127486-31152786	NOTEST	0	0	0	0	1	1
ENSG00000237115	ENSG00000237115	RP1-131F15.2	6:132129155-132216295	NOTEST	0.0131308	0.0195118	0.571389	0	1	1
ENSG00000237118	ENSG00000237118	CYP2F2P	19:41277552-41406413	NOTEST	0.0335894	0.0404859	0.269414	0	1	1
ENSG00000237119	ENSG00000237119	LINC01056	20:61640734-61716423	NOTEST	0	0	0	0	1	1
ENSG00000237120	ENSG00000237120	DASS-23B5.2	HSCHR6_MHC_MANN:32644921-32645329	NOTEST	0	0	0	0	1	1
ENSG00000237121	ENSG00000237121	PIEZO1P2	20:57315587-57358877	NOTEST	0	0	0	0	1	1
ENSG00000237122	ENSG00000237122	FAM90A19P	8:7603555-7614766	NOTEST	0	0	0	0	1	1
ENSG00000237123	ENSG00000237123	CDSN	HSCHR6_MHC_DBB:31076301-31101556	NOTEST	0	0	0	0	1	1
ENSG00000237124	ENSG00000237124	MTND2P11	9:111934254-112083244	NOTEST	0	0	0	0	1	1
ENSG00000237125	ENSG00000237125	HAND2-AS1	4:174446119-174512475	NOTEST	0.00498929	0	#NAME?	0	1	1
ENSG00000237126	ENSG00000237126	AC073254.1	2:233412778-233547491	NOTEST	0.313272	0.48059	0.617391	0	1	1
ENSG00000237127	ENSG00000237127	LL22NC03-84E4.8	22:23177040-23177293	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237128	ENSG00000237128	RP11-351M16.3	10:28721936-28784742	NOTEST	0	0	0	0	1	1
ENSG00000237129	ENSG00000237129	Z95114.7	22:36571904-36572574	NOTEST	0	0	0	0	1	1
ENSG00000237130	ENSG00000237130	MRPS6P2	1:50905149-51425935	NOTEST	0	0	0	0	1	1
ENSG00000237131	ENSG00000237131	RP1-69E11.3	1:168184642-168184890	NOTEST	0	0	0	0	1	1
ENSG00000237132	ENSG00000237132	VN2R6P	9:47249605-47264801	NOTEST	0	0	0	0	1	1
ENSG00000237133	ENSG00000237133	AC020594.5	2:33661390-33789817	NOTEST	0.51644	0	#NAME?	0	1	1
ENSG00000237135	ENSG00000237135	DDX10P1	10:31109135-31320866	NOTEST	0.00842898	0	#NAME?	0	1	1
ENSG00000237136	ENSG00000237136	C4orf51	4:146601355-146859787	NOTEST	0	0	0	0	1	1
ENSG00000237137	ENSG00000237137	RP11-408A13.2	9:14531913-14532040	NOTEST	0	0	0	0	1	1
ENSG00000237138	ENSG00000237138	HUNK-AS1	21:33245627-33416946	NOTEST	0	0	0	0	1	1
ENSG00000237139	ENSG00000237139	RP11-137L10.5	10:75196185-75385711	NOTEST	0	0	0	0	1	1
ENSG00000237140	ENSG00000237140	HSPE1P16	16:25703346-26149009	NOTEST	0	0	0	0	1	1
ENSG00000237141	ENSG00000237141	DNAJC19P1	10:69556426-69597924	NOTEST	0	0	0	0	1	1
ENSG00000237145	ENSG00000237145	MTCO3P1	HSCHR6_MHC_MANN:32828154-32828985	NOTEST	0	0	0	0	1	1
ENSG00000237148	ENSG00000237148	HIGD1AP2	13:81824572-81876542	NOTEST	0	0	0	0	1	1
ENSG00000237152	ENSG00000237152	DLEU7-AS1	13:50601268-51423190	NOTEST	0.0535521	0.0147338	-1.86181	0	1	1
ENSG00000237153	ENSG00000237153	RP11-132E11.2	9:17048916-17112813	NOTEST	0.170578	0.0848856	-1.00684	0	1	1
ENSG00000237154	ENSG00000237154	MCFD2P1	6:27375475-27375775	NOTEST	0	0	0	0	1	1
ENSG00000237155	ENSG00000237155	IER3	HSCHR6_MHC_COX:30700840-30702196	NOTEST	0	0	0	0	1	1
ENSG00000237156	ENSG00000237156	PTMAP1	HSCHR6_MHC_DBB:30584859-30604840	NOTEST	0	0	0	0	1	1
ENSG00000237158	ENSG00000237158	RP11-472F14.4	9:6532463-6645650	NOTEST	0	0	0	0	1	1
ENSG00000237159	ENSG00000237159	CNTFR-AS1	9:34551429-34590121	NOTEST	0	0	0	0	1	1
ENSG00000237160	ENSG00000237160	AC004022.7	7:94926987-95025680	NOTEST	0	0	0	0	1	1
ENSG00000237161	ENSG00000237161	RP11-32B5.1	15:21936559-21938111	NOTEST	0.226183	0.207166	-0.126701	0	1	1
ENSG00000237162	ENSG00000237162	RP11-443F16.1	2:62900985-63275775	NOTEST	0	0	0	0	1	1
ENSG00000237163	ENSG00000237163	RP4-771M4.2	1:63370850-63371153	NOTEST	0	0	0	0	1	1
ENSG00000237164	ENSG00000237164	SLC25A15P2	13:19985370-19990328	NOTEST	0	0	0	0	1	1
ENSG00000237165	ENSG00000237165	CDSN	HSCHR6_MHC_MCF:31161054-31186363	NOTEST	0	0	0	0	1	1
ENSG00000237166	ENSG00000237166	AC007163.3	2:201542955-201688569	NOTEST	0	0	0	0	1	1
ENSG00000237167	ENSG00000237167	AC128709.2	3:197185275-197193976	NOTEST	0	0	0	0	1	1
ENSG00000237169	ENSG00000237169	RP11-452K12.3	10:99068894-99069715	NOTEST	0	0	0	0	1	1
ENSG00000237170	ENSG00000237170	RPS7P15	4:4349866-4712665	NOTEST	0	0	0	0	1	1
ENSG00000237171	ENSG00000237171	GS1-466O4.5	X:26242019-26242775	NOTEST	0	0	0	0	1	1
ENSG00000237173	ENSG00000237173	RP5-866L20.2	1:54990496-54990604	NOTEST	0	0	0	0	1	1
ENSG00000237174	ENSG00000237174	RP11-415D17.3	6:75994729-76203454	NOTEST	0	0	0	0	1	1
ENSG00000237175	ENSG00000237175	NME1P1	13:22673301-22673683	NOTEST	0	0	0	0	1	1
ENSG00000237176	ENSG00000237176	RP11-813P10.2	12:60205882-60206357	NOTEST	0	0	0	0	1	1
ENSG00000237178	ENSG00000237178	AC019080.1	2:178092322-178408564	NOTEST	0.125925	0.0475176	-1.40602	0	1	1
ENSG00000237179	ENSG00000237179	AC007392.4	2:66801161-66957289	NOTEST	0	0	0	0	1	1
ENSG00000237180	ENSG00000237180	CYP46A4P	1:48555039-48555306	NOTEST	0	0	0	0	1	1
ENSG00000237181	ENSG00000237181	AC147651.4	7:588833-829190	NOTEST	0.0530734	0.287983	2.43992	0	1	1
ENSG00000237182	ENSG00000237182	RP11-402P6.3	X:70956303-70956553	NOTEST	0	0	0	0	1	1
ENSG00000237183	ENSG00000237183	KRTAP9-10P	17:39436855-39437062	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237184	ENSG00000237184	AC091199.1	17:36158868-36162759	NOTEST	0	0	0	0	1	1
ENSG00000237185	ENSG00000237185	VN1R66P	16:31659627-31660543	NOTEST	0	0	0	0	1	1
ENSG00000237186	ENSG00000237186	RP11-229A12.2	3:57327726-57530071	NOTEST	0	0	0	0	1	1
ENSG00000237189	ENSG00000237189	RP11-85G21.2	1:157257492-157257843	NOTEST	0	0	0	0	1	1
ENSG00000237191	ENSG00000237191	RP11-120E5.2	9:65978719-65979683	NOTEST	0	0	0	0	1	1
ENSG00000237192	ENSG00000237192	TRIM10	HSCHR6_MHC_COX:30109654-30118642	NOTEST	0	0	0	0	1	1
ENSG00000237193	ENSG00000237193	RP11-275O4.4	1:227669953-227670155	NOTEST	0	0	0	0	1	1
ENSG00000237194	ENSG00000237194	SNAI1P1	2:210636716-210864024	NOTEST	0	0	0	0	1	1
ENSG00000237195	ENSG00000237195	DLGAP5P1	Y:6026842-6027306	NOTEST	0	0	0	0	1	1
ENSG00000237196	ENSG00000237196	HCG24	HSCHR6_MHC_COX:33034176-33037170	NOTEST	0	0	0	0	1	1
ENSG00000237197	ENSG00000237197	IGHD1-7	14:106375765-106375782	NOTEST	0	0	0	0	1	1
ENSG00000237198	ENSG00000237198	FAM27E1	9:46385690-46387222	NOTEST	0.36118	0.13084	-1.46491	0	1	1
ENSG00000237200	ENSG00000237200	ZBTB40-IT1	1:22778343-22857650	NOTEST	0	0.434288	inf	0	1	1
ENSG00000237202	ENSG00000237202	AJ239321.3	21:14492564-14493128	NOTEST	0	0.0267915	inf	0	1	1
ENSG00000237205	ENSG00000237205	RPL7P34	10:90377979-90378691	NOTEST	0	0	0	0	1	1
ENSG00000237206	ENSG00000237206	IMPDH1P4	X:43137373-43138907	NOTEST	0	0	0	0	1	1
ENSG00000237207	ENSG00000237207	RP11-24B13.1	9:43684901-43924049	NOTEST	0	0	0	0	1	1
ENSG00000237208	ENSG00000237208	RP11-13E5.2	X:125243744-125249545	NOTEST	0	0	0	0	1	1
ENSG00000237210	ENSG00000237210	RP11-339F13.2	7:55086713-55324313	NOTEST	0	0	0	0	1	1
ENSG00000237211	ENSG00000237211	SETP4	X:84010143-84011011	NOTEST	0	0	0	0	1	1
ENSG00000237212	ENSG00000237212	RP11-569G13.2	9:98857492-98864194	NOTEST	0	0.0156368	inf	0	1	1
ENSG00000237213	ENSG00000237213	RPL23AP22	1:193725944-193726397	NOTEST	0	0	0	0	1	1
ENSG00000237214	ENSG00000237214	RP11-12M9.3	22:41460055-41460640	NOTEST	0.138764	0.0280421	-2.30696	0	1	1
ENSG00000237215	ENSG00000237215	ABC12-47043100G14.2	8:12147579-12153689	NOTEST	0	0	0	0	1	1
ENSG00000237216	ENSG00000237216	HLA-G	HSCHR6_MHC_MCF:29791625-29795784	NOTEST	0	0	0	0	1	1
ENSG00000237217	ENSG00000237217	AC008074.5	2:64622353-64680932	NOTEST	0	0	0	0	1	1
ENSG00000237218	ENSG00000237218	HLA-H	HSCHR6_MHC_SSTO:29845569-29848744	NOTEST	0	0	0	0	1	1
ENSG00000237220	ENSG00000237220	AC104777.3	2:151409045-151428735	NOTEST	0	0	0	0	1	1
ENSG00000237221	ENSG00000237221	PPEF1-AS1	X:18694028-18846039	NOTEST	0	0	0	0	1	1
ENSG00000237222	ENSG00000237222	AC090505.6	3:194429149-194502897	NOTEST	0.0119882	0	#NAME?	0	1	1
ENSG00000237223	ENSG00000237223	SULT1C2P1	2:108938693-108970255	NOTEST	0	0	0	0	1	1
ENSG00000237224	ENSG00000237224	RP11-109A6.2	10:131265447-131566271	NOTEST	0	0	0	0	1	1
ENSG00000237225	ENSG00000237225	OR13K1P	X:130696711-130697808	NOTEST	0	0	0	0	1	1
ENSG00000237226	ENSG00000237226	RPS3AP39	11:3490548-3602441	NOTEST	0	0	0	0	1	1
ENSG00000237227	ENSG00000237227	RP5-1155K23.4	1:62660502-62678000	NOTEST	0	0	0	0	1	1
ENSG00000237230	ENSG00000237230	KRTAP2-5P	17:39228197-39228593	NOTEST	0	0	0	0	1	1
ENSG00000237232	ENSG00000237232	ZNF295-AS1	21:43406939-43445060	NOTEST	0.0380355	0.133422	1.81058	0	1	1
ENSG00000237233	ENSG00000237233	RP11-809M12.1	10:63166400-63241714	NOTEST	0	0	0	0	1	1
ENSG00000237234	ENSG00000237234	RP1-142L7.5	6:112429962-112672498	NOTEST	0	0.0173055	inf	0	1	1
ENSG00000237235	ENSG00000237235	TRDD2	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000237236	ENSG00000237236	RP11-548K12.11	7:57881906-57882648	NOTEST	0	0	0	0	1	1
ENSG00000237242	ENSG00000237242	BTF3P15	10:111294412-111294748	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237243	ENSG00000237243	AC022173.2	7:137559724-137686813	NOTEST	0	0	0	0	1	1
ENSG00000237247	ENSG00000237247	MBD3L5	19:7030588-7033022	NOTEST	0	0	0	0	1	1
ENSG00000237248	ENSG00000237248	LINC00987	12:9381128-9428413	NOTEST	0.00709033	0.00504294	-0.491589	0	1	1
ENSG00000237249	ENSG00000237249	RP1-102G20.2	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000237250	ENSG00000237250	RP11-193H5.1	1:238025474-238091621	NOTEST	0	0	0	0	1	1
ENSG00000237251	ENSG00000237251	AC072061.2	7:39856147-39907739	NOTEST	0	0	0	0	1	1
ENSG00000237252	ENSG00000237252	RP11-322A17.1	X:75443035-75443496	NOTEST	0	0	0	0	1	1
ENSG00000237253	ENSG00000237253	RP11-666A1.5	1:148598397-148599531	NOTEST	0	0.231071	inf	0	1	1
ENSG00000237254	ENSG00000237254	TRBV30	7:142510270-142511084	NOTEST	0	0	0	0	1	1
ENSG00000237256	ENSG00000237256	PGAM3P	20:11601698-11602125	NOTEST	0	0	0	0	1	1
ENSG00000237257	ENSG00000237257	MTND2P8	9:81356635-81357660	NOTEST	0	0	0	0	1	1
ENSG00000237258	ENSG00000237258	OR11A1	HSCHR6_MHC_MANN:29323056-29424418	NOTEST	0	0	0	0	1	1
ENSG00000237259	ENSG00000237259	RP4-568F9.3	20:18269120-18297640	NOTEST	0	0	0	0	1	1
ENSG00000237260	ENSG00000237260	AC073069.2	2:177203364-177203805	NOTEST	0	0.297152	inf	0	1	1
ENSG00000237261	ENSG00000237261	AC233263.1	2:90532367-90532626	NOTEST	0	0	0	0	1	1
ENSG00000237262	ENSG00000237262	AC068492.1	2:136835461-136836083	NOTEST	0	0	0	0	1	1
ENSG00000237263	ENSG00000237263	MAPK6PS3	13:42614175-42830714	NOTEST	0	0	0	0	1	1
ENSG00000237265	ENSG00000237265	RP11-402P6.9	X:70882844-70885603	NOTEST	0	0	0	0	1	1
ENSG00000237266	ENSG00000237266	AC010729.3	2:5950772-5952728	NOTEST	0	0	0	0	1	1
ENSG00000237267	ENSG00000237267	RP11-181F12.1	10:86953176-86957714	NOTEST	0	0	0	0	1	1
ENSG00000237268	ENSG00000237268	RP13-492C18.2	7:56489549-56516068	NOTEST	0	0	0	0	1	1
ENSG00000237269	ENSG00000237269	RBMY2TP	Y:23592582-23599131	NOTEST	0	0	0	0	1	1
ENSG00000237271	ENSG00000237271	AC009498.1	2:205092859-205099708	NOTEST	0	0	0	0	1	1
ENSG00000237272	ENSG00000237272	OR51R1P	11:4439289-4440193	NOTEST	0	0	0	0	1	1
ENSG00000237273	ENSG00000237273	RSL24D1P8	19:12203077-12267546	NOTEST	0	0	0	0	1	1
ENSG00000237274	ENSG00000237274	RP11-575C20.1	9:6195933-6197248	NOTEST	0	0	0	0	1	1
ENSG00000237275	ENSG00000237275	RP11-552J9.11	X:52716412-52716683	NOTEST	0	0	0	0	1	1
ENSG00000237276	ENSG00000237276	ANO7P1	1:16542403-16554522	NOTEST	0.422071	0.377915	-0.159423	0	1	1
ENSG00000237278	ENSG00000237278	RLIMP2	1:113615830-113674882	NOTEST	0.0822095	0	#NAME?	0	1	1
ENSG00000237279	ENSG00000237279	RP4-631H13.5	1:53392900-53517375	NOTEST	0	0	0	0	1	1
ENSG00000237280	ENSG00000237280	RP11-96C23.9	10:88810242-88951225	NOTEST	0	0	0	0	1	1
ENSG00000237281	ENSG00000237281	AC021016.8	2:219135114-219232822	NOTEST	0	0	0	0	1	1
ENSG00000237282	ENSG00000237282	LINC00851	20:18359692-18362128	NOTEST	0	0	0	0	1	1
ENSG00000237283	ENSG00000237283	RP11-316I3.1	1:188674753-188680011	NOTEST	0	0	0	0	1	1
ENSG00000237284	ENSG00000237284	MAS1L	HSCHR6_MHC_SSTO:29454147-29455412	NOTEST	0	0	0	0	1	1
ENSG00000237285	ENSG00000237285	HNRNPA1P2	6:32256302-32339684	NOTEST	0	0	0	0	1	1
ENSG00000237286	ENSG00000237286	AC004906.3	7:2945774-3083579	NOTEST	0	0	0	0	1	1
ENSG00000237290	ENSG00000237290	RP11-214L19.1	1:38674705-38680439	NOTEST	0	0	0	0	1	1
ENSG00000237291	ENSG00000237291	RP11-782C8.4	1:143118703-143240439	NOTEST	0.131716	0.0757991	-0.79718	0	1	1
ENSG00000237292	ENSG00000237292	RP11-540K16.1	1:181143619-181151344	NOTEST	0.0400396	0.121999	1.60736	0	1	1
ENSG00000237293	ENSG00000237293	AC007099.2	2:75696427-75796848	NOTEST	0	0	0	0	1	1
ENSG00000237294	ENSG00000237294	EIF4BP9	X:65294676-65296189	NOTEST	0	0.0266849	inf	0	1	1
ENSG00000237295	ENSG00000237295	HNRNPA1P2	HSCHR6_MHC_SSTO:32267411-32346296	NOTEST	0	0	0	0	1	1
ENSG00000237297	ENSG00000237297	RP11-631M21.6	10:90651-92824	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237298	ENSG00000237298	TTN-AS1	2:179385909-179914813	NOTEST	0.119429	0.0327869	-1.86496	0	1	1
ENSG00000237299	ENSG00000237299	LA16c-60G3.6	22:16399956-16436527	NOTEST	0	0	0	0	1	1
ENSG00000237300	ENSG00000237300	RP11-522L3.3	X:102024088-102161086	NOTEST	0	0	0	0	1	1
ENSG00000237301	ENSG00000237301	RP4-680D5.2	1:15853307-15930121	NOTEST	0	0.00431464	inf	0	1	1
ENSG00000237302	ENSG00000237302	OFD1P11Y	Y:25917378-25944297	NOTEST	0	0	0	0	1	1
ENSG00000237303	ENSG00000237303	HIGD1AP8	12:11504756-11653975	NOTEST	0	0	0	0	1	1
ENSG00000237306	ENSG00000237306	HSPE1P22	9:94789779-94790106	NOTEST	0.0944123	0	#NAME?	0	1	1
ENSG00000237307	ENSG00000237307	SRRM1P3	X:135991553-136103789	NOTEST	0.010712	0	#NAME?	0	1	1
ENSG00000237308	ENSG00000237308	AC009237.5	2:96161769-96162279	NOTEST	0	0	0	0	1	1
ENSG00000237309	ENSG00000237309	MTND2P6	7:57254118-57255148	NOTEST	0	0	0	0	1	1
ENSG00000237311	ENSG00000237311	RP6-159A1.3	X:65219592-65220913	NOTEST	0	0	0	0	1	1
ENSG00000237312	ENSG00000237312	RP11-475C16.2	6:153552454-153668623	NOTEST	0	0	0	0	1	1
ENSG00000237313	ENSG00000237313	C6orf100	HSCHR6_MHC_MCF:28911819-28912480	NOTEST	0	0	0	0	1	1
ENSG00000237314	ENSG00000237314	RPL12P39	18:61739391-61739887	NOTEST	0	0	0	0	1	1
ENSG00000237316	ENSG00000237316	RP1-288L1.4	22:35107898-35120910	NOTEST	0	0	0	0	1	1
ENSG00000237317	ENSG00000237317	RP4-809F4.1	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000237319	ENSG00000237319	RP1-136J15.1	X:108866928-108976632	NOTEST	0	0	0	0	1	1
ENSG00000237320	ENSG00000237320	AC019064.1	2:35024916-35410755	NOTEST	0	0	0	0	1	1
ENSG00000237321	ENSG00000237321	RP11-374A22.1	6:124125285-125146803	NOTEST	0	0	0	0	1	1
ENSG00000237322	ENSG00000237322	RPL7L1P10	2:229618039-229618502	NOTEST	0	0	0	0	1	1
ENSG00000237323	ENSG00000237323	AC009892.9	19:55163534-55163680	NOTEST	0	0	0	0	1	1
ENSG00000237324	ENSG00000237324	RP11-439H8.4	1:74663895-75010112	NOTEST	0	0	0	0	1	1
ENSG00000237325	ENSG00000237325	AP000563.2	21:32490733-32932800	NOTEST	0	0	0	0	1	1
ENSG00000237326	ENSG00000237326	AC113608.1	2:15941870-15951001	NOTEST	0	0	0	0	1	1
ENSG00000237327	ENSG00000237327	UPP2-IT1	2:158733213-158992666	NOTEST	0	0	0	0	1	1
ENSG00000237328	ENSG00000237328	RAI1-AS1	17:17584786-17740325	NOTEST	0.0268616	0	#NAME?	0	1	1
ENSG00000237329	ENSG00000237329	RP11-201O14.1	1:31404352-31538838	NOTEST	0	0	0	0	1	1
ENSG00000237330	ENSG00000237330	RNF223	1:1006345-1009687	NOTEST	0.00857958	0.0133336	0.636092	0	1	1
ENSG00000237331	ENSG00000237331	XIAP-AS1	X:122993573-123047829	NOTEST	0	0.115493	inf	0	1	1
ENSG00000237332	ENSG00000237332	RP5-878I13.1	X:114658575-114660070	NOTEST	0	0	0	0	1	1
ENSG00000237333	ENSG00000237333	MSH5	HSCHR6_MHC_SSTO:31714323-31722583	NOTEST	0	0	0	0	1	1
ENSG00000237334	ENSG00000237334	HLA-Z	HSCHR6_MHC_APD:32847756-32847831	NOTEST	0	0	0	0	1	1
ENSG00000237335	ENSG00000237335	PFDN6	HSCHR6_MHC_COX:33168490-33188786	NOTEST	0	0	0	0	1	1
ENSG00000237336	ENSG00000237336	RP11-230L22.4	9:126118448-126692431	NOTEST	0	0	0	0	1	1
ENSG00000237337	ENSG00000237337	RP11-567C20.2	1:50513685-50669458	NOTEST	0	0	0	0	1	1
ENSG00000237338	ENSG00000237338	FTCD-AS1	21:47556175-47575481	NOTEST	0	0	0	0	1	1
ENSG00000237339	ENSG00000237339	RP11-98L5.2	9:138466780-138478958	NOTEST	0.0116807	0.0141722	0.278939	0	1	1
ENSG00000237341	ENSG00000237341	SYP-AS1	X:49044268-49058913	NOTEST	0	0	0	0	1	1
ENSG00000237342	ENSG00000237342	AL132796.1	14:99311232-99311934	NOTEST	0	0	0	0	1	1
ENSG00000237343	ENSG00000237343	RP11-763B22.4	1:148760503-148761583	NOTEST	0	0	0	0	1	1
ENSG00000237344	ENSG00000237344	PBX2	HSCHR6_MHC_COX:32100986-32106437	NOTEST	0	0	0	0	1	1
ENSG00000237345	ENSG00000237345	RP11-344N17.11	X:48138857-48141227	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237346	ENSG00000237346	RP3-448I9.2	6:14391461-14393519	NOTEST	0	0	0	0	1	1
ENSG00000237347	ENSG00000237347	AC004461.4	22:19023794-19115962	NOTEST	0	0	0	0	1	1
ENSG00000237348	ENSG00000237348	BRD2-IT1	HSCHR6_MHC_MCF:32935859-32980443	NOTEST	0	0	0	0	1	1
ENSG00000237349	ENSG00000237349	RP5-1065J22.2	1:109512835-109584850	NOTEST	0	0	0	0	1	1
ENSG00000237351	ENSG00000237351	CTD-2522E6.4	X:47001614-47046212	NOTEST	0.105335	0.0107199	-3.29662	0	1	1
ENSG00000237352	ENSG00000237352	RP11-145M4.3	1:59520068-59553867	NOTEST	0	0	0	0	1	1
ENSG00000237353	ENSG00000237353	PATE4	11:125703210-125709964	NOTEST	0.0720914	0.0179993	-2.00188	0	1	1
ENSG00000237354	ENSG00000237354	OR52S1P	11:5097359-5098296	NOTEST	0	0	0	0	1	1
ENSG00000237357	ENSG00000237357	RP11-475I24.3	9:44400716-44404440	NOTEST	0.0927759	0.105358	0.183473	0	1	1
ENSG00000237358	ENSG00000237358	AC007064.25	22:17357441-17357792	NOTEST	0	0	0	0	1	1
ENSG00000237359	ENSG00000237359	RP11-509J21.2	9:3526722-3671646	NOTEST	0	0	0	0	1	1
ENSG00000237360	ENSG00000237360	CHCHD4P2	9:110859711-110860131	NOTEST	0	0	0	0	1	1
ENSG00000237361	ENSG00000237361	LINC01071	13:44974385-44980120	NOTEST	0	0	0	0	1	1
ENSG00000237363	ENSG00000237363	AP006288.1	11:64298515-64300442	NOTEST	0	0	0	0	1	1
ENSG00000237365	ENSG00000237365	RP11-334N17.1	1:6845383-7829766	NOTEST	0	0.187016	inf	0	1	1
ENSG00000237366	ENSG00000237366	OR2U1P	HSCHR6_MHC_COX:29188440-29231555	NOTEST	0	0	0	0	1	1
ENSG00000237369	ENSG00000237369	UBDP1	HSCHR6_MHC_SSTO:29432048-29437257	NOTEST	0	0	0	0	1	1
ENSG00000237370	ENSG00000237370	AC010907.2	2:3642425-3692048	NOTEST	0	0	0	0	1	1
ENSG00000237371	ENSG00000237371	RP13-152O15.5	20:62681188-62703700	NOTEST	0	0	0	0	1	1
ENSG00000237372	ENSG00000237372	RP11-316P17.2	9:92316565-92334585	NOTEST	0.0228163	0	#NAME?	0	1	1
ENSG00000237373	ENSG00000237373	BRWD1-IT1	21:40556101-40695144	NOTEST	0	0	0	0	1	1
ENSG00000237374	ENSG00000237374	AC007680.2	2:51259738-52635055	NOTEST	0	0	0	0	1	1
ENSG00000237375	ENSG00000237375	BX072566.1	GL000213.1:108006-139339	NOTEST	0	0	0	0	1	1
ENSG00000237377	ENSG00000237377	AC005703.2	17:15179878-15182794	NOTEST	0	0	0	0	1	1
ENSG00000237378	ENSG00000237378	RP11-473M10.3	13:64322131-64325213	NOTEST	0	0	0	0	1	1
ENSG00000237379	ENSG00000237379	CBX1P3	1:203923767-203924908	NOTEST	0	0	0	0	1	1
ENSG00000237381	ENSG00000237381	RP3-455H14.1	X:92643073-92644496	NOTEST	0	0	0	0	1	1
ENSG00000237382	ENSG00000237382	RPL21P121	17:18174741-18218321	NOTEST	0	0.112468	inf	0	1	1
ENSG00000237383	ENSG00000237383	CNN2P11	2:95391418-95391680	NOTEST	0	0	0	0	1	1
ENSG00000237385	ENSG00000237385	RP11-165J3.5	9:96192623-96193581	NOTEST	0	0	0	0	1	1
ENSG00000237387	ENSG00000237387	CTA-407F11.7	22:25960815-26125261	NOTEST	0	0	0	0	1	1
ENSG00000237388	ENSG00000237388	OR4A47	11:48510268-48511332	NOTEST	0	0	0	0	1	1
ENSG00000237389	ENSG00000237389	RP11-402L1.4	10:44124264-44170151	NOTEST	0	0	0	0	1	1
ENSG00000237390	ENSG00000237390	RP11-139I14.2	1:156358017-156365401	NOTEST	0	0	0	0	1	1
ENSG00000237393	ENSG00000237393	SLC9A3P4	10:47965759-47967323	NOTEST	0	0	0	0	1	1
ENSG00000237395	ENSG00000237395	MICD	HSCHR6_MHC_COX:29928091-29929754	NOTEST	0	0	0	0	1	1
ENSG00000237396	ENSG00000237396	RP4-788L20.3	20:22568159-22588155	NOTEST	0	0	0	0	1	1
ENSG00000237398	ENSG00000237398	HLA-DPA3	6:33080227-33111102	NOTEST	0	0	0	0	1	1
ENSG00000237399	ENSG00000237399	PITRM1-AS1	10:3179919-3215003	NOTEST	0.0652943	0.103164	0.659918	0	1	1
ENSG00000237400	ENSG00000237400	AC006960.7	7:36502631-36544121	NOTEST	0	0	0	0	1	1
ENSG00000237401	ENSG00000237401	AC107070.1	2:4005244-4021660	NOTEST	0	0	0	0	1	1
ENSG00000237402	ENSG00000237402	CAMTA1-IT1	1:6845383-7829766	NOTEST	0	0.226141	inf	0	1	1
ENSG00000237403	ENSG00000237403	PPP1R11	HSCHR6_MHC_MCF:30112986-30122165	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237404	ENSG00000237404	RP3-471C18.2	6:19535174-19840915	NOTEST	0	0	0	0	1	1
ENSG00000237405	ENSG00000237405	AGER	HSCHR6_MHC_SSTO:32155614-32158971	NOTEST	0	0	0	0	1	1
ENSG00000237406	ENSG00000237406	NDUFA9P1	22:36134782-36424473	NOTEST	0.015407	0.0108576	-0.504886	0	1	1
ENSG00000237407	ENSG00000237407	KB-1183D5.14	22:21655278-21679331	NOTEST	0	0	0	0	1	1
ENSG00000237408	ENSG00000237408	AP005019.3	11:72189264-72190281	NOTEST	0	0	0	0	1	1
ENSG00000237409	ENSG00000237409	RP11-226L15.1	1:159990089-159990517	NOTEST	0	0	0	0	1	1
ENSG00000237410	ENSG00000237410	AP001092.4	11:64373645-64490660	NOTEST	0	0	0	0	1	1
ENSG00000237412	ENSG00000237412	PRSS56	2:233385172-233390422	NOTEST	0	0.082572	inf	0	1	1
ENSG00000237413	ENSG00000237413	RP11-183M13.1	1:78695282-79005434	NOTEST	0	0	0	0	1	1
ENSG00000237414	ENSG00000237414	RP11-321L2.2	9:23894987-23898052	NOTEST	0	0	0	0	1	1
ENSG00000237415	ENSG00000237415	NRBF2P3	1:111390698-111391563	NOTEST	0	0	0	0	1	1
ENSG00000237416	ENSG00000237416	RP11-465K1.2	1:95285897-95360802	NOTEST	0	0	0	0	1	1
ENSG00000237417	ENSG00000237417	XRCC6P1	10:94966613-94969384	NOTEST	0	0.00638829	inf	0	1	1
ENSG00000237418	ENSG00000237418	AC069257.6	3:195938357-196065374	NOTEST	0	0	0	0	1	1
ENSG00000237419	ENSG00000237419	RP11-885N19.6	9:141090382-141093775	NOTEST	0	0	0	0	1	1
ENSG00000237421	ENSG00000237421	UBDP1	HSCHR6_MHC_APD:29432453-29437664	NOTEST	0	0	0	0	1	1
ENSG00000237422	ENSG00000237422	RP11-305L7.3	9:93881343-93945044	NOTEST	0.0886784	0	#NAME?	0	1	1
ENSG00000237423	ENSG00000237423	RP11-347D21.3	20:46609231-46617488	NOTEST	0	0	0	0	1	1
ENSG00000237424	ENSG00000237424	FOXD2-AS1	1:47897804-47900313	NOTEST	0.608771	0.294411	-1.04807	0	1	1
ENSG00000237425	ENSG00000237425	RPSAP2	6:28699793-28700681	NOTEST	0	0.0146096	inf	0	1	1
ENSG00000237426	ENSG00000237426	ZIK1P1	X:123093082-124097666	NOTEST	0	0	0	0	1	1
ENSG00000237427	ENSG00000237427	TOMM22P1	Y:23292755-23293067	NOTEST	0	0	0	0	1	1
ENSG00000237428	ENSG00000237428	LL22NC03-22A12.9	22:22720577-22722138	NOTEST	0	0	0	0	1	1
ENSG00000237429	ENSG00000237429	RP1-159A19.4	1:27852315-27857072	NOTEST	0	0	0	0	1	1
ENSG00000237432	ENSG00000237432	RPS7P12	X:133699867-133898352	NOTEST	0	0	0	0	1	1
ENSG00000237433	ENSG00000237433	AC097639.8	3:32232238-32233119	NOTEST	0.0418398	0.106664	1.35012	0	1	1
ENSG00000237434	ENSG00000237434	RP11-15P13.1	9:20331443-20332275	NOTEST	0	0	0	0	1	1
ENSG00000237435	ENSG00000237435	RP11-147C23.1	1:96403456-96488436	NOTEST	0	0	0	0	1	1
ENSG00000237436	ENSG00000237436	RP11-312B8.1	1:6843951-6844903	NOTEST	0	0	0	0	1	1
ENSG00000237437	ENSG00000237437	ASS1P12	9:32945993-32947220	NOTEST	0.240473	0.26554	0.143055	0	1	1
ENSG00000237439	ENSG00000237439	RP1-127L4.10	22:32517963-32529456	NOTEST	0	0	0	0	1	1
ENSG00000237440	ENSG00000237440	ZNF737	19:20718630-20844402	NOTEST	0.064031	0.0851005	0.410396	0	1	1
ENSG00000237442	ENSG00000237442	HNRNPA1P57	2:41370919-41384695	NOTEST	0	0	0	0	1	1
ENSG00000237443	ENSG00000237443	OR13D2P	9:107352324-107353231	NOTEST	0	0.044489	inf	0	1	1
ENSG00000237444	ENSG00000237444	AP001342.1	21:26212863-26442219	NOTEST	0	0	0	0	1	1
ENSG00000237445	ENSG00000237445	CTA-520D8.2	1:13983805-13986405	NOTEST	0	0	0	0	1	1
ENSG00000237446	ENSG00000237446	RHEBP3	22:18270414-18507325	NOTEST	0	0	0	0	1	1
ENSG00000237447	ENSG00000237447	CDC27P2	Y:10027985-10029907	NOTEST	0	0	0	0	1	1
ENSG00000237448	ENSG00000237448	RPL3P2	HSCHR6_MHC_MANN:31291540-31292743	NOTEST	0	0	0	0	1	1
ENSG00000237449	ENSG00000237449	TAAR4P	6:132915536-132916575	NOTEST	0	0	0	0	1	1
ENSG00000237450	ENSG00000237450	RP11-671J11.1	14:34955184-34955653	NOTEST	0	0	0	0	1	1
ENSG00000237451	ENSG00000237451	CDK2AP2P2	9:66500641-66501008	NOTEST	0.143959	0.113121	-0.347795	0	1	1
ENSG00000237452	ENSG00000237452	AC074212.3	19:46236508-46267792	NOTEST	0	0.004045	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237453	ENSG00000237453	RP11-67L3.2	1:55245384-55266940	NOTEST	0	0	0	0	1	1
ENSG00000237455	ENSG00000237455	HLA-DQB1-AS1	HSCHR6_MHC_DBB:32602483-32612425	NOTEST	0	0	0	0	1	1
ENSG00000237456	ENSG00000237456	RP11-154D3.1	3:61547242-62355005	NOTEST	0	0	0	0	1	1
ENSG00000237457	ENSG00000237457	RP11-547I7.2	1:190447680-190463427	NOTEST	0.167373	0.133745	-0.323582	0	1	1
ENSG00000237458	ENSG00000237458	TUBB4BP3	X:117262710-117262981	NOTEST	0	0	0	0	1	1
ENSG00000237459	ENSG00000237459	C6orf25	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000237460	ENSG00000237460	RP11-233E12.1	1:107360860-107380789	NOTEST	0	0	0	0	1	1
ENSG00000237461	ENSG00000237461	RP11-554F20.1	9:102348067-102582171	NOTEST	0	0	0	0	1	1
ENSG00000237462	ENSG00000237462	TRIM27	HSCHR6_MHC_MANN:28882557-28891771	NOTEST	0	0	0	0	1	1
ENSG00000237463	ENSG00000237463	RP11-280O1.2	1:165446077-165551713	NOTEST	0	0	0	0	1	1
ENSG00000237464	ENSG00000237464	RP3-461P17.9	20:44116252-44118888	NOTEST	0	0	0	0	1	1
ENSG00000237466	ENSG00000237466	RP4-736H5.2	7:67093008-67093336	NOTEST	0	0	0	0	1	1
ENSG00000237467	ENSG00000237467	USP9YP35	Y:26223945-26225959	NOTEST	0	0	0	0	1	1
ENSG00000237468	ENSG00000237468	RP11-715G15.1	6:146915651-146920067	NOTEST	0	0	0	0	1	1
ENSG00000237469	ENSG00000237469	TUBB8P10	1:227680729-227682843	NOTEST	0	0	0	0	1	1
ENSG00000237470	ENSG00000237470	DCLRE1CP1	10:15057070-15130775	NOTEST	0	0	0	0	1	1
ENSG00000237471	ENSG00000237471	AC073115.6	7:46009255-46019790	NOTEST	0	0.0857927	inf	0	1	1
ENSG00000237472	ENSG00000237472	AP000361.2	22:23330437-23330756	NOTEST	0	0	0	0	1	1
ENSG00000237473	ENSG00000237473	RP11-324C10.1	3:172871526-173054755	NOTEST	0	0	0	0	1	1
ENSG00000237474	ENSG00000237474	AC233263.2	2:90512494-90512771	NOTEST	0	0	0	0	1	1
ENSG00000237475	ENSG00000237475	RPL7P53	X:72744110-72782921	NOTEST	0	0	0	0	1	1
ENSG00000237477	ENSG00000237477	AC093911.1	2:180138557-180150434	NOTEST	0	0	0	0	1	1
ENSG00000237478	ENSG00000237478	RP5-926E3.1	1:48998526-50489585	NOTEST	0	0	0	0	1	1
ENSG00000237479	ENSG00000237479	AC007557.2	2:217536827-217858802	NOTEST	0	0	0	0	1	1
ENSG00000237480	ENSG00000237480	RP5-947P14.1	1:106615868-106627121	NOTEST	0	0	0	0	1	1
ENSG00000237481	ENSG00000237481	RP4-803J11.2	1:229455149-229479041	NOTEST	0.15364	0.129221	-0.249709	0	1	1
ENSG00000237482	ENSG00000237482	LY6G6E	HSCHR6_MHC_DBB:31656814-31667868	NOTEST	0	0	0	0	1	1
ENSG00000237483	ENSG00000237483	RP11-423E7.1	3:171757417-172119455	NOTEST	0	0	0	0	1	1
ENSG00000237484	ENSG00000237484	AP000476.1	21:25801053-25920256	NOTEST	0	0	0	0	1	1
ENSG00000237485	ENSG00000237485	SGOL1-AS1	3:20202084-20227919	NOTEST	0	0	0	0	1	1
ENSG00000237487	ENSG00000237487	VN1R48P	9:38504443-38505479	NOTEST	0	0	0	0	1	1
ENSG00000237489	ENSG00000237489	LINC00959	10:131864637-131909081	NOTEST	0.00555793	0	#NAME?	0	1	1
ENSG00000237490	ENSG00000237490	RP13-926M18.1	X:6907369-6907824	NOTEST	0	0	0	0	1	1
ENSG00000237491	ENSG00000237491	RP11-206L10.9	1:714149-755214	NOTEST	0.612391	0.657887	0.103387	0	1	1
ENSG00000237492	ENSG00000237492	OR2L9P	1:248099362-248264224	NOTEST	0	0	0	0	1	1
ENSG00000237494	ENSG00000237494	RP11-753B14.1	6:142572983-142580769	NOTEST	0	0	0	0	1	1
ENSG00000237495	ENSG00000237495	LY6G5C	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000237498	ENSG00000237498	AC010105.1	2:82706251-82765835	NOTEST	0	0	0	0	1	1
ENSG00000237500	ENSG00000237500	RP11-526P5.1	10:2541912-2542762	NOTEST	0	0	0	0	1	1
ENSG00000237501	ENSG00000237501	RP11-816B4.1	3:172548770-172549019	NOTEST	0	0	0	0	1	1
ENSG00000237502	ENSG00000237502	RP1-12G14.6	6:149887429-149912884	NOTEST	0	0	0	0	1	1
ENSG00000237503	ENSG00000237503	RP5-998N21.3	1:149340658-149341066	NOTEST	0	0	0	0	1	1
ENSG00000237505	ENSG00000237505	RP11-76N22.2	1:89003195-89301938	NOTEST	0.0251333	0.0732607	1.54344	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237508	ENSG00000237508	HLA-F	HSCHR6_MHC_MANN:29687659-29713937	NOTEST	0	0	0	0	1	1
ENSG00000237510	ENSG00000237510	AC008268.2	2:96455401-96465914	NOTEST	0	0	0	0	1	1
ENSG00000237512	ENSG00000237512	UNC5B-AS1	10:72972326-73062621	NOTEST	0	0	0	0	1	1
ENSG00000237513	ENSG00000237513	RP11-325F22.2	7:104581509-104653491	NOTEST	0	0.0204301	inf	0	1	1
ENSG00000237514	ENSG00000237514	PTP4A1P7	1:176432306-176814735	NOTEST	0	0	0	0	1	1
ENSG00000237515	ENSG00000237515	SHISA9	16:12995476-13334272	NOTEST	0	0.0017596	inf	0	1	1
ENSG00000237520	ENSG00000237520	RP11-443B7.2	1:235092977-235105809	NOTEST	0	0	0	0	1	1
ENSG00000237521	ENSG00000237521	OR7E24	19:9361605-9362820	NOTEST	0	0	0	0	1	1
ENSG00000237522	ENSG00000237522	NONOP2	2:61163953-61165184	NOTEST	0.230607	0.272673	0.241737	0	1	1
ENSG00000237523	ENSG00000237523	LINC00857	10:81967465-81979413	NOTEST	0	0	0	0	1	1
ENSG00000237524	ENSG00000237524	AC114783.1	2:127656471-127659673	NOTEST	0	0	0	0	1	1
ENSG00000237525	ENSG00000237525	AC012668.2	2:216395169-216708445	NOTEST	0.0183151	0.0221857	0.276601	0	1	1
ENSG00000237527	ENSG00000237527	AF241725.6	21:23027358-23058649	NOTEST	0	0.0341708	inf	0	1	1
ENSG00000237528	ENSG00000237528	RP11-234P3.4	X:51666647-51666836	NOTEST	0	0	0	0	1	1
ENSG00000237529	ENSG00000237529	RP11-439K3.3	9:85857904-86153461	NOTEST	0	0.032505	inf	0	1	1
ENSG00000237530	ENSG00000237530	RP3-449H6.1	6:44492995-44494491	NOTEST	0	0	0	0	1	1
ENSG00000237531	ENSG00000237531	RP11-309M23.1	X:950955-955100	NOTEST	0	0	0	0	1	1
ENSG00000237532	ENSG00000237532	AC012451.1	2:129338064-129339150	NOTEST	0	0	0	0	1	1
ENSG00000237533	ENSG00000237533	PFN1P6	1:148736688-148737087	NOTEST	0	0	0	0	1	1
ENSG00000237534	ENSG00000237534	LINC00383	13:69796477-69866286	NOTEST	0	0	0	0	1	1
ENSG00000237536	ENSG00000237536	HTATSF1P	HSCHR6_MHC_COX:33127217-33129109	NOTEST	0	0	0	0	1	1
ENSG00000237539	ENSG00000237539	GS1-594A7.5	X:15645440-15683154	NOTEST	0	0	0	0	1	1
ENSG00000237540	ENSG00000237540	RP11-730A19.7	10:13201476-13201777	NOTEST	0	0	0	0	1	1
ENSG00000237541	ENSG00000237541	HLA-DQA2	6:32709118-32714992	NOTEST	0	0.00771943	inf	0	1	1
ENSG00000237542	ENSG00000237542	AC009960.5	2:203481422-203481935	NOTEST	0	0	0	0	1	1
ENSG00000237543	ENSG00000237543	RP11-58A12.3	9:69065654-69149621	NOTEST	0.0582703	0.0288696	-1.01321	0	1	1
ENSG00000237544	ENSG00000237544	MAS1LP1	HSCHR6_MHC_SSTO:29442475-29443522	NOTEST	0	0	0	0	1	1
ENSG00000237545	ENSG00000237545	POLR2LP	HSCHR6_MHC_QBL:31100957-31101144	NOTEST	0	0	0	0	1	1
ENSG00000237546	ENSG00000237546	XKRYP6	Y:28089414-28100299	NOTEST	0	0	0	0	1	1
ENSG00000237547	ENSG00000237547	IGHJ2P	14:106331002-106331062	NOTEST	0	0	0	0	1	1
ENSG00000237548	ENSG00000237548	TTLL11-IT1	9:124584206-124855885	NOTEST	0.0505761	0.0118779	-2.09017	0	1	1
ENSG00000237549	ENSG00000237549	AC092570.3	2:102125991-102126684	NOTEST	0	0	0	0	1	1
ENSG00000237550	ENSG00000237550	UBE2Q2P6	15:82647359-82748784	NOTEST	0.0364049	0.187165	2.3621	0	1	1
ENSG00000237551	ENSG00000237551	AC096775.2	7:95749531-95951459	NOTEST	0	0.0381686	inf	0	1	1
ENSG00000237552	ENSG00000237552	RP11-415A20.1	1:77223808-77244952	NOTEST	0	0	0	0	1	1
ENSG00000237553	ENSG00000237553	RP11-140C18.2	9:5193338-5193558	NOTEST	0	0	0	0	1	1
ENSG00000237554	ENSG00000237554	RPL7AP7	HSCHR6_MHC_APD:29771013-29771810	NOTEST	0	0	0	0	1	1
ENSG00000237555	ENSG00000237555	RP5-862K6.4	20:42017281-42017681	NOTEST	0	0	0	0	1	1
ENSG00000237556	ENSG00000237556	KCND3-AS1	1:112313283-112531777	NOTEST	0	0	0	0	1	1
ENSG00000237557	ENSG00000237557	RP13-198D9.3	9:38643038-38643765	NOTEST	0.049088	0.0188743	-1.37894	0	1	1
ENSG00000237558	ENSG00000237558	CDY7P	Y:20063468-20065380	NOTEST	0	0	0	0	1	1
ENSG00000237559	ENSG00000237559	HLA-S	HSCHR6_MHC_QBL:31339951-31340166	NOTEST	0	0	0	0	1	1
ENSG00000237560	ENSG00000237560	AC004562.1	17:67957847-67979679	NOTEST	0	0	0	0	1	1

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ENSG00000237565	ENSG00000237565	SSU72P5	11:4254515-4255099	NOTEST	0	0	0	0	1	1
ENSG00000237566	ENSG00000237566	AC090955.5	3:5141311-5141546	NOTEST	0	0	0	0	1	1
ENSG00000237567	ENSG00000237567	RP3-359N14.2	6:106060541-106080071	NOTEST	0	0	0	0	1	1
ENSG00000237568	ENSG00000237568	RP4-620F22.2	1:89724632-89738544	NOTEST	0	0	0	0	1	1
ENSG00000237569	ENSG00000237569	TUBAP	21:24779977-24781448	NOTEST	0	0	0	0	1	1
ENSG00000237571	ENSG00000237571	AC073284.4	2:216139714-216142670	NOTEST	0	0	0	0	1	1
ENSG00000237572	ENSG00000237572	RP11-373D7.1	7:62669596-62672200	NOTEST	0	0	0	0	1	1
ENSG00000237574	ENSG00000237574	AC079776.3	2:130680434-130704276	NOTEST	0	0	0	0	1	1
ENSG00000237575	ENSG00000237575	PYY2	17:26553588-26555091	NOTEST	0.138982	0.0988453	-0.491659	0	1	1
ENSG00000237576	ENSG00000237576	AC097495.2	2:69059175-69064856	NOTEST	0	0	0	0	1	1
ENSG00000237577	ENSG00000237577	XXbac-BPG254F23.7	HSCHR6_MHC_APD:32670371-32671202	NOTEST	0	0	0	0	1	1
ENSG00000237578	ENSG00000237578	RP11-174M13.1	12:129556269-130388211	NOTEST	0	0	0	0	1	1
ENSG00000237579	ENSG00000237579	RP11-324L3.1	10:102936079-102953904	NOTEST	0	0	0	0	1	1
ENSG00000237580	ENSG00000237580	GCSHP3	2:206979540-207027652	NOTEST	0	0.0496327	inf	0	1	1
ENSG00000237581	ENSG00000237581	AC005538.5	2:234826042-234928166	NOTEST	0	0	0	0	1	1
ENSG00000237582	ENSG00000237582	POU5F1	HSCHR6_MHC_SSTO:31120396-31132565	NOTEST	0	0	0	0	1	1
ENSG00000237583	ENSG00000237583	AC093166.1	2:112432602-112432920	NOTEST	0	0	0	0	1	1
ENSG00000237584	ENSG00000237584	RAC1P4	X:136523416-136523995	NOTEST	0	0	0	0	1	1
ENSG00000237585	ENSG00000237585	LINC00407	13:45225947-45275152	NOTEST	0	0	0	0	1	1
ENSG00000237586	ENSG00000237586	RP11-383J24.2	8:125313555-125314045	NOTEST	0.0868743	0	#NAME?	0	1	1
ENSG00000237587	ENSG00000237587	RP11-327I22.4	9:43064965-43133544	NOTEST	0	0	0	0	1	1
ENSG00000237588	ENSG00000237588	RP11-66D17.3	1:156657486-156661789	NOTEST	0	0	0	0	1	1
ENSG00000237589	ENSG00000237589	HMGN1P32	19:54271224-54271807	NOTEST	0	0	0	0	1	1
ENSG00000237590	ENSG00000237590	RP11-20J15.2	10:44755049-44757261	NOTEST	0	0	0	0	1	1
ENSG00000237591	ENSG00000237591	HLA-DRB9	HSCHR6_MHC_DBB:32402297-32415953	NOTEST	0	0	0	0	1	1
ENSG00000237592	ENSG00000237592	IGKV1OR10-1	10:42680786-42681239	NOTEST	0	0	0	0	1	1
ENSG00000237593	ENSG00000237593	RP11-317B3.2	6:154331630-154677926	NOTEST	0	0	0	0	1	1
ENSG00000237594	ENSG00000237594	AP000251.3	21:32490733-32932800	NOTEST	0	0	0	0	1	1
ENSG00000237595	ENSG00000237595	RP11-112L6.3	20:48780000-48782639	NOTEST	0.17209	0.0995139	-0.790191	0	1	1
ENSG00000237596	ENSG00000237596	RP13-143G15.4	6:136172833-136546733	NOTEST	0.0521783	0.0186309	-1.48575	0	1	1
ENSG00000237597	ENSG00000237597	GAGE13	X:49188093-49195366	NOTEST	0	0	0	0	1	1
ENSG00000237599	ENSG00000237599	TAP2	HSCHR6_MHC_MCF:32823108-32840035	NOTEST	0	0	0	0	1	1
ENSG00000237601	ENSG00000237601	AP000358.5	22:25099314-25099470	NOTEST	0	0	0	0	1	1
ENSG00000237603	ENSG00000237603	HMGB3P12	3:26257812-26258368	NOTEST	0.0715501	0	#NAME?	0	1	1
ENSG00000237604	ENSG00000237604	AP001056.1	21:45595371-45596336	NOTEST	0.0228514	0	#NAME?	0	1	1
ENSG00000237605	ENSG00000237605	RP11-343H5.6	1:206807993-206857764	NOTEST	0.151136	0.175249	0.213563	0	1	1
ENSG00000237606	ENSG00000237606	RP11-203P23.2	7:103969103-104549001	NOTEST	0.051206	0	#NAME?	0	1	1
ENSG00000237608	ENSG00000237608	OR2P1P	HSCHR6_MHC_DBB:29039612-29040388	NOTEST	0	0	0	0	1	1
ENSG00000237609	ENSG00000237609	AF064858.10	21:40400460-40401053	NOTEST	0	0	0	0	1	1
ENSG00000237610	ENSG00000237610	OR4C50P	11:51526870-51527800	NOTEST	0	0	0	0	1	1
ENSG00000237612	ENSG00000237612	AP002856.7	11:131104432-131121711	NOTEST	0	0	0	0	1	1
ENSG00000237613	ENSG00000237613	FAM138A	1:34553-36081	NOTEST	0.0146183	0	#NAME?	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237614	ENSG00000237614	AC073257.2	2:121300484-121301902	NOTEST	0	0	0	0	1	1
ENSG00000237616	ENSG00000237616	USP9YP32	Y:20107080-20109132	NOTEST	0	0	0	0	1	1
ENSG00000237617	ENSG00000237617	AC013410.2	2:174570675-174570876	NOTEST	0	0	0	0	1	1
ENSG00000237618	ENSG00000237618	BTBD7P2	10:113082535-113083155	NOTEST	0	0	0	0	1	1
ENSG00000237619	ENSG00000237619	OR3B1P	X:153887063-153887956	NOTEST	0	0	0	0	1	1
ENSG00000237620	ENSG00000237620	GCNT1P5	7:77090774-77091456	NOTEST	0	0	0	0	1	1
ENSG00000237621	ENSG00000237621	OR9A1P	7:141586947-141587892	NOTEST	0	0	0	0	1	1
ENSG00000237622	ENSG00000237622	TCEB1P18	1:68841009-68841346	NOTEST	0	0	0	0	1	1
ENSG00000237623	ENSG00000237623	RP11-571E6.1	X:47132764-47133789	NOTEST	0	0	0	0	1	1
ENSG00000237624	ENSG00000237624	OXCT2P1	1:39957317-40024379	NOTEST	0.0217765	0.015314	-0.507922	0	1	1
ENSG00000237625	ENSG00000237625	RP11-144A16.2	9:41475786-41476094	NOTEST	0	0	0	0	1	1
ENSG00000237626	ENSG00000237626	RP11-406A20.1	9:92740563-92749768	NOTEST	0	0	0	0	1	1
ENSG00000237628	ENSG00000237628	RP11-522L3.4	X:102024088-102161086	NOTEST	0	0	0	0	1	1
ENSG00000237629	ENSG00000237629	UQCRHP2	2:26217662-26217950	NOTEST	0	0	0	0	1	1
ENSG00000237630	ENSG00000237630	NIFKP9	2:127927586-127927807	NOTEST	0	0	0	0	1	1
ENSG00000237631	ENSG00000237631	RP11-72B4.2	9:98521512-98776842	NOTEST	0	0	0	0	1	1
ENSG00000237632	ENSG00000237632	S100A11P1	7:102815579-102920857	NOTEST	0	0	0	0	1	1
ENSG00000237633	ENSG00000237633	AC104623.2	2:16704443-16710655	NOTEST	0	0	0	0	1	1
ENSG00000237634	ENSG00000237634	C6orf100	HSCHR6_MHC_COX:28908183-28908844	NOTEST	0	0	0	0	1	1
ENSG00000237635	ENSG00000237635	XX-2136C48.8	10:135477930-135478609	NOTEST	0	0	0	0	1	1
ENSG00000237636	ENSG00000237636	ANKRD26P3	13:19864732-19918965	NOTEST	0	0	0	0	1	1
ENSG00000237637	ENSG00000237637	FRY-AS1	13:32599450-32870794	NOTEST	0	0	0	0	1	1
ENSG00000237638	ENSG00000237638	AC007386.2	2:65128973-65132271	NOTEST	0	0	0	0	1	1
ENSG00000237639	ENSG00000237639	RP11-368M16.5	7:57710086-57710825	NOTEST	0	0	0	0	1	1
ENSG00000237640	ENSG00000237640	RP4-604G5.1	7:99520891-99546243	NOTEST	0	0.0464061	inf	0	1	1
ENSG00000237642	ENSG00000237642	HMGB3P5	10:112188597-112255962	NOTEST	0	0	0	0	1	1
ENSG00000237643	ENSG00000237643	RP11-462G2.1	6:71104589-71109120	NOTEST	0	0	0	0	1	1
ENSG00000237645	ENSG00000237645	RP11-521A24.1	3:173114073-174004434	NOTEST	0	0	0	0	1	1
ENSG00000237646	ENSG00000237646	HLCS-IT1	21:38123188-38362536	NOTEST	0	0	0	0	1	1
ENSG00000237647	ENSG00000237647	ERICH1-AS1	8:564745-1212580	NOTEST	0	0	0	0	1	1
ENSG00000237650	ENSG00000237650	OR11Q1P	X:130338101-130338978	NOTEST	0	0	0	0	1	1
ENSG00000237653	ENSG00000237653	RP11-655G22.2	3:191670137-191670615	NOTEST	0	0	0	0	1	1
ENSG00000237654	ENSG00000237654	AP003025.2	11:131240372-132206716	NOTEST	0	0	0	0	1	1
ENSG00000237655	ENSG00000237655	AC073834.3	2:178467816-178483694	NOTEST	0	0	0	0	1	1
ENSG00000237658	ENSG00000237658	RP5-968D22.3	1:168433451-168464882	NOTEST	0	0	0	0	1	1
ENSG00000237659	ENSG00000237659	RNASEH2CP1	Y:2657867-2658369	NOTEST	0	0	0	0	1	1
ENSG00000237661	ENSG00000237661	RP11-169L17.5	X:40691096-40691815	NOTEST	0	0	0	0	1	1
ENSG00000237662	ENSG00000237662	SOCS2P1	20:31775196-31776098	NOTEST	0	0	0	0	1	1
ENSG00000237663	ENSG00000237663	DNAJC19P7	1:52608045-52831865	NOTEST	0	0	0	0	1	1
ENSG00000237664	ENSG00000237664	LINC00316	21:46756621-46761905	NOTEST	0	0	0	0	1	1
ENSG00000237665	ENSG00000237665	GRM7-AS2	3:6532165-7783215	NOTEST	0	0	0	0	1	1
ENSG00000237666	ENSG00000237666	AC108868.3	2:107087254-107094125	NOTEST	0.0413773	0	#NAME?	0	1	1

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ENSG00000237668	ENSG00000237668	RPS15AP38	22:36817317-36817689	NOTEST	0.147369	0.664229	2.17225	0	1	1
ENSG00000237670	ENSG00000237670	AC080094.1	2:17151300-17155764	NOTEST	0	0	0	0	1	1
ENSG00000237671	ENSG00000237671	GAGE12C	X:49296813-49304141	NOTEST	0	0	0	0	1	1
ENSG00000237672	ENSG00000237672	KRR1P1	13:20532809-20665968	NOTEST	0.0430763	0.156483	1.86104	0	1	1
ENSG00000237674	ENSG00000237674	GSTA7P	6:52604387-52609454	NOTEST	0	0.0417993	inf	0	1	1
ENSG00000237675	ENSG00000237675	TEX36-AS1	10:127262939-127371713	NOTEST	0	0	0	0	1	1
ENSG00000237676	ENSG00000237676	RPL30P4	3:32676713-32677046	NOTEST	0	0	0	0	1	1
ENSG00000237677	ENSG00000237677	AC113612.2	2:90294145-90294339	NOTEST	0	0	0	0	1	1
ENSG00000237679	ENSG00000237679	VDAC1P11	9:97021592-97063736	NOTEST	0	0.048108	inf	0	1	1
ENSG00000237682	ENSG00000237682	RP3-514P16.1	X:100792471-100794263	NOTEST	0.0773102	0.129507	0.744299	0	1	1
ENSG00000237683	ENSG00000237683	AL627309.1	1:134900-139379	NOTEST	0.0897117	0.0718849	-0.319608	0	1	1
ENSG00000237684	ENSG00000237684	RPSAP35	4:118334617-118335435	NOTEST	0	0	0	0	1	1
ENSG00000237685	ENSG00000237685	RP11-360O19.4	6:10492455-10629601	NOTEST	0.180947	0.198332	0.132352	0	1	1
ENSG00000237687	ENSG00000237687	LINC00686	20:61326375-61331832	NOTEST	0	0	0	0	1	1
ENSG00000237689	ENSG00000237689	AC007064.24	22:17350367-17352016	NOTEST	0	0.0351802	inf	0	1	1
ENSG00000237690	ENSG00000237690	OR2B4P	HSCHR6_MHC_APD:29258559-29259502	NOTEST	0	0	0	0	1	1
ENSG00000237691	ENSG00000237691	IFNWP2	9:21420232-21420812	NOTEST	0	0.0804868	inf	0	1	1
ENSG00000237693	ENSG00000237693	IRGM	5:150226084-150284545	NOTEST	0	0.00701698	inf	0	1	1
ENSG00000237697	ENSG00000237697	LINC00312	3:7994491-8653610	NOTEST	0.148612	0.248826	0.743586	0	1	1
ENSG00000237698	ENSG00000237698	GPR53P	HSCHR6_MHC_COX:29502068-29503152	NOTEST	0	0	0	0	1	1
ENSG00000237699	ENSG00000237699	RP11-199F6.4	13:114580580-114586624	NOTEST	0	0	0	0	1	1
ENSG00000237700	ENSG00000237700	RP11-219C24.6	1:13411550-13414482	NOTEST	0	0	0	0	1	1
ENSG00000237701	ENSG00000237701	ATP5JP1	Y:6768793-6769413	NOTEST	0	0	0	0	1	1
ENSG00000237702	ENSG00000237702	TRBV3-1	7:142008364-142008871	NOTEST	0	0	0	0	1	1
ENSG00000237703	ENSG00000237703	TRIM10	HSCHR6_MHC_APD:30056559-30065548	NOTEST	0	0	0	0	1	1
ENSG00000237704	ENSG00000237704	AP004289.2	8:100025493-100906290	NOTEST	0	0	0	0	1	1
ENSG00000237705	ENSG00000237705	AC008937.2	5:56111400-56191979	NOTEST	0	0	0	0	1	1
ENSG00000237706	ENSG00000237706	TRIM51EP	11:89714608-89724840	NOTEST	0	0	0	0	1	1
ENSG00000237707	ENSG00000237707	RP5-1018K9.1	1:169073361-169074145	NOTEST	0	0	0	0	1	1
ENSG00000237708	ENSG00000237708	RP11-445O16.2	X:57095346-57096118	NOTEST	0	0.0192278	inf	0	1	1
ENSG00000237709	ENSG00000237709	EEF1A1P28	7:88268327-88269730	NOTEST	0	0	0	0	1	1
ENSG00000237710	ENSG00000237710	HLA-DPB1	HSCHR6_MHC_DBB:33010287-33032912	NOTEST	0	0	0	0	1	1
ENSG00000237711	ENSG00000237711	RP11-39K24.13	9:4985032-5128183	NOTEST	0	0.0173922	inf	0	1	1
ENSG00000237713	ENSG00000237713	AC006000.5	7:13141015-13743774	NOTEST	0	0	0	0	1	1
ENSG00000237714	ENSG00000237714	P4HA2-AS1	5:131520568-131731306	NOTEST	0	0	0	0	1	1
ENSG00000237716	ENSG00000237716	RP3-400B16.3	6:4186857-4188343	NOTEST	0	0	0	0	1	1
ENSG00000237717	ENSG00000237717	RP11-402P6.4	X:70964677-70964927	NOTEST	0	0	0	0	1	1
ENSG00000237718	ENSG00000237718	AC009095.4	16:67583116-67673086	NOTEST	0	0.223024	inf	0	1	1
ENSG00000237719	ENSG00000237719	RP1-179N16.3	6:35995487-36079013	NOTEST	0.17897	0.178874	-0.000780207	0	1	1
ENSG00000237720	ENSG00000237720	AC011995.1	2:2838035-2842163	NOTEST	0	0	0	0	1	1
ENSG00000237721	ENSG00000237721	AF064858.11	21:40378573-40383255	NOTEST	0	0	0	0	1	1
ENSG00000237722	ENSG00000237722	MTND1P29	2:131028168-131029845	NOTEST	0	0	0	0	1	1

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ENSG00000237724	ENSG00000237724	HSPA1A	HSCHR6_MHC_COX:31770616-31773099	NOTEST	0	0	0	0	1	1
ENSG00000237725	ENSG00000237725	OR2I1P	HSCHR6_MHC_DBB:29520949-29521897	NOTEST	0	0	0	0	1	1
ENSG00000237726	ENSG00000237726	RP11-386O9.2	1:71547006-72748417	NOTEST	0	0	0	0	1	1
ENSG00000237727	ENSG00000237727	AIF1	HSCHR6_MHC_COX:31570374-31572212	NOTEST	0	0	0	0	1	1
ENSG00000237728	ENSG00000237728	RP3-453P22.2	1:6845383-7829766	NOTEST	0	0	0	0	1	1
ENSG00000237729	ENSG00000237729	AC002075.4	7:93220884-93540577	NOTEST	0.345718	0.648813	0.908207	0	1	1
ENSG00000237730	ENSG00000237730	RP11-459A10.1	X:6340132-6340742	NOTEST	0	0	0	0	1	1
ENSG00000237731	ENSG00000237731	RNGTTP1	21:27011583-27144771	NOTEST	0	0	0	0	1	1
ENSG00000237733	ENSG00000237733	RNF39	HSCHR6_MHC_MANN:30029680-30038860	NOTEST	0	0	0	0	1	1
ENSG00000237734	ENSG00000237734	RP11-298E2.2	9:27325206-27529779	NOTEST	0	0	0	0	1	1
ENSG00000237735	ENSG00000237735	AP000473.6	21:18126837-18188007	NOTEST	0	0	0	0	1	1
ENSG00000237736	ENSG00000237736	U82670.4	X:152435329-152439737	NOTEST	0	0	0	0	1	1
ENSG00000237737	ENSG00000237737	DCTN1-AS1	2:74425688-74621009	NOTEST	0.084176	0.032782	-1.36051	0	1	1
ENSG00000237738	ENSG00000237738	RNF216-IT1	7:5659677-5821370	NOTEST	0	0	0	0	1	1
ENSG00000237740	ENSG00000237740	NPAP1P3	10:89136652-89138238	NOTEST	0	0	0	0	1	1
ENSG00000237741	ENSG00000237741	AC002368.4	X:147579632-147582135	NOTEST	0	0	0	0	1	1
ENSG00000237742	ENSG00000237742	RP11-624M8.1	6:125899703-126082415	NOTEST	0.0420802	0	#NAME?	0	1	1
ENSG00000237743	ENSG00000237743	XXyac-YM21GA2.6	9:90441401-90452140	NOTEST	0	0	0	0	1	1
ENSG00000237745	ENSG00000237745	AC009963.5	2:108531403-108531742	NOTEST	0	0	0	0	1	1
ENSG00000237746	ENSG00000237746	ZNF101P1	10:28627482-28629871	NOTEST	0	0	0	0	1	1
ENSG00000237747	ENSG00000237747	RP11-65B23.3	9:90356147-90356868	NOTEST	0	0	0	0	1	1
ENSG00000237748	ENSG00000237748	UQCRBP1	X:56755691-56844813	NOTEST	0	0	0	0	1	1
ENSG00000237750	ENSG00000237750	AC007740.1	2:163175349-163695240	NOTEST	0	0	0	0	1	1
ENSG00000237751	ENSG00000237751	LINC01143	2:71115000-71117089	NOTEST	0.12584	0.0790364	-0.671002	0	1	1
ENSG00000237752	ENSG00000237752	RP13-75G22.1	X:97161641-97163088	NOTEST	0	0	0	0	1	1
ENSG00000237753	ENSG00000237753	AC079922.3	2:113399408-113403267	NOTEST	0.558434	0.284631	-0.972293	0	1	1
ENSG00000237754	ENSG00000237754	RP11-521C10.1	7:67615269-67753220	NOTEST	0	0	0	0	1	1
ENSG00000237756	ENSG00000237756	RP11-77M5.1	1:163080910-163325554	NOTEST	0	0	0	0	1	1
ENSG00000237757	ENSG00000237757	EEF1A1P30	X:119170200-119379122	NOTEST	0	0.0307704	inf	0	1	1
ENSG00000237758	ENSG00000237758	BANF1P3	2:231577559-231685790	NOTEST	0	0.123872	inf	0	1	1
ENSG00000237759	ENSG00000237759	RP11-278H7.3	1:244270666-244272313	NOTEST	0	0	0	0	1	1
ENSG00000237760	ENSG00000237760	AC092657.2	7:46341717-46383219	NOTEST	0	0	0	0	1	1
ENSG00000237761	ENSG00000237761	RP11-127O4.2	10:106375859-106376731	NOTEST	0	0	0	0	1	1
ENSG00000237763	ENSG00000237763	AMY1A	1:104197911-104207173	NOTEST	0	0	0	0	1	1
ENSG00000237764	ENSG00000237764	RP11-3B12.2	7:124462439-125019375	NOTEST	0.0210394	0	#NAME?	0	1	1
ENSG00000237766	ENSG00000237766	GGTA2P	12:67659621-67660746	NOTEST	0.0439292	0.0452337	0.0422173	0	1	1
ENSG00000237767	ENSG00000237767	RP11-101E14.2	20:38633118-38637171	NOTEST	0	0	0	0	1	1
ENSG00000237768	ENSG00000237768	RP11-344N10.2	10:74766974-74856732	NOTEST	0	0	0	0	1	1
ENSG00000237770	ENSG00000237770	SPATA31D2P	9:84542935-84592004	NOTEST	0	0	0	0	1	1
ENSG00000237772	ENSG00000237772	AC092620.3	2:139362079-139370737	NOTEST	0	0	0	0	1	1
ENSG00000237773	ENSG00000237773	AC003075.4	7:17319457-17385776	NOTEST	0.0966434	0.284613	1.55826	0	1	1
ENSG00000237774	ENSG00000237774	RP11-129B9.1	12:95470524-95611258	NOTEST	0	0	0	0	1	1
ENSG00000237775	ENSG00000237775	DDR1-AS1	6:30834758-30843695	NOTEST	0	0	0	0	1	1

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ENSG00000237777	ENSG00000237777	OR14J1	HSCHR6_MHC_DBB:29274456-29275573	NOTEST	0	0	0	0	1	1
ENSG00000237781	ENSG00000237781	RP11-54A4.2	1:150521039-150533413	NOTEST	0.11125	0.0729154	-0.609511	0	1	1
ENSG00000237782	ENSG00000237782	RP1-192P9.1	X:45240771-45241325	NOTEST	0	0	0	0	1	1
ENSG00000237783	ENSG00000237783	RP11-306I1.1	1:165446077-165551713	NOTEST	0	0	0	0	1	1
ENSG00000237784	ENSG00000237784	AC097713.5	2:235238126-235238482	NOTEST	0	0	0	0	1	1
ENSG00000237786	ENSG00000237786	GFOD1-AS1	6:13358061-13487894	NOTEST	0	0	0	0	1	1
ENSG00000237787	ENSG00000237787	C3orf79	3:153102722-153697975	NOTEST	0.0363203	0	#NAME?	0	1	1
ENSG00000237788	ENSG00000237788	RP5-1041C10.3	20:48429249-48508779	NOTEST	0.0382205	0.0241617	-0.661625	0	1	1
ENSG00000237790	ENSG00000237790	AC009499.2	2:33931952-34522820	NOTEST	0	0.156246	inf	0	1	1
ENSG00000237792	ENSG00000237792	RP11-203I2.1	9:65585691-65661972	NOTEST	0.224035	0.223559	-0.00306375	0	1	1
ENSG00000237793	ENSG00000237793	RPL18AP16	X:152927610-152928147	NOTEST	0	0	0	0	1	1
ENSG00000237797	ENSG00000237797	RP11-472N13.3	10:31982011-31996316	NOTEST	0.0839531	0.120495	0.521321	0	1	1
ENSG00000237798	ENSG00000237798	AC010894.5	2:175411868-175639555	NOTEST	0	0.036963	inf	0	1	1
ENSG00000237799	ENSG00000237799	CICP11	7:55804471-55807289	NOTEST	0	0.00829805	inf	0	1	1
ENSG00000237801	ENSG00000237801	AMDP1	X:155058247-155059239	NOTEST	0	0	0	0	1	1
ENSG00000237802	ENSG00000237802	FAM197Y6	Y:9195405-9235047	NOTEST	0	0	0	0	1	1
ENSG00000237803	ENSG00000237803	LINC00211	2:38053389-38103417	NOTEST	0.00847673	0.00595693	-0.50894	0	1	1
ENSG00000237804	ENSG00000237804	HNRNPA1P39	2:175174742-175175702	NOTEST	0.0343788	0	#NAME?	0	1	1
ENSG00000237805	ENSG00000237805	AC015849.2	17:34195970-34212867	NOTEST	0	0	0	0	1	1
ENSG00000237806	ENSG00000237806	FAUP2	3:180701496-181554668	NOTEST	0	0	0	0	1	1
ENSG00000237807	ENSG00000237807	RP11-400K9.4	8:54427729-54436491	NOTEST	0.135107	0.468016	1.79246	0	1	1
ENSG00000237808	ENSG00000237808	NCR3	HSCHR6_MHC_COX:31541312-31548170	NOTEST	0	0	0	0	1	1
ENSG00000237810	ENSG00000237810	CTD-2571E19.3	8:63055869-63057328	NOTEST	0.0324714	0	#NAME?	0	1	1
ENSG00000237811	ENSG00000237811	GPR53P	HSCHR6_MHC_MANN:29505057-29506141	NOTEST	0	0	0	0	1	1
ENSG00000237812	ENSG00000237812	HCG9	HSCHR6_MHC_SSTO:29931357-29934651	NOTEST	0	0	0	0	1	1
ENSG00000237813	ENSG00000237813	AC002066.1	7:115850546-116148595	NOTEST	0.47555	0.0198861	-4.57976	0	1	1
ENSG00000237814	ENSG00000237814	SFTA2	HSCHR6_MHC_MCF:30977671-30978494	NOTEST	0	0	0	0	1	1
ENSG00000237815	ENSG00000237815	AC007000.11	7:76139744-77045717	NOTEST	0	0	0	0	1	1
ENSG00000237816	ENSG00000237816	RPL21P109	13:72012097-72441330	NOTEST	0	0	0	0	1	1
ENSG00000237818	ENSG00000237818	RPS3AP29	7:97527658-97528427	NOTEST	0	0	0	0	1	1
ENSG00000237823	ENSG00000237823	CDY19P	Y:27710268-27712180	NOTEST	0	0	0	0	1	1
ENSG00000237824	ENSG00000237824	AC010747.2	2:185463092-185804219	NOTEST	0	0	0	0	1	1
ENSG00000237825	ENSG00000237825	RGL2	HSCHR6_MHC_DBB:33224809-33245105	NOTEST	0	0	0	0	1	1
ENSG00000237827	ENSG00000237827	RP11-332O19.2	10:104678049-104953056	NOTEST	0	0	0	0	1	1
ENSG00000237828	ENSG00000237828	PA2G4P1	X:120002464-120003661	NOTEST	0	0.0203809	inf	0	1	1
ENSG00000237829	ENSG00000237829	PPP1R11	HSCHR6_MHC_SSTO:30024067-30033246	NOTEST	0	0	0	0	1	1
ENSG00000237831	ENSG00000237831	RP11-499O7.4	10:5077545-5149878	NOTEST	0	0	0	0	1	1
ENSG00000237832	ENSG00000237832	RP5-974N19.1	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000237833	ENSG00000237833	RP11-432N13.2	X:134717575-134719085	NOTEST	0	0	0	0	1	1
ENSG00000237834	ENSG00000237834	MOG	HSCHR6_MHC_COX:29621354-29636747	NOTEST	0	0	0	0	1	1
ENSG00000237835	ENSG00000237835	AC007064.22	22:17336693-17337052	NOTEST	0	0	0	0	1	1
ENSG00000237836	ENSG00000237836	PHKA2-AS1	X:18908413-19002716	NOTEST	0.0619584	0.0616669	-0.00680311	0	1	1
ENSG00000237837	ENSG00000237837	AC159540.3	2:98069547-98071970	NOTEST	0	0	0	0	1	1

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ENSG00000237840	ENSG00000237840	FAM21FP	10:46201878-46288409	NOTEST	0.122482	0.209162	0.77205	0	1	1
ENSG00000237841	ENSG00000237841	KRTAP19-9P	21:31882624-31882815	NOTEST	0	0	0	0	1	1
ENSG00000237842	ENSG00000237842	RP11-110J1.2	1:157029023-157030554	NOTEST	0.0109203	0.0843452	2.94929	0	1	1
ENSG00000237843	ENSG00000237843	AC016903.2	2:205340078-205372395	NOTEST	0	0	0	0	1	1
ENSG00000237844	ENSG00000237844	AC092684.1	2:164606082-165208733	NOTEST	0	0	0	0	1	1
ENSG00000237845	ENSG00000237845	RP5-940F7.2	1:236105852-236107105	NOTEST	0	0.0368794	inf	0	1	1
ENSG00000237847	ENSG00000237847	FAM231A	1:16999497-17000007	NOTEST	0	0	0	0	1	1
ENSG00000237848	ENSG00000237848	RP11-739N20.3	1:204346977-204463852	NOTEST	0	0	0	0	1	1
ENSG00000237849	ENSG00000237849	NFYAP1	13:64549583-64550555	NOTEST	0.295852	0.479428	0.696437	0	1	1
ENSG00000237850	ENSG00000237850	RP11-483E23.2	15:28594196-28603226	NOTEST	0	0	0	0	1	1
ENSG00000237851	ENSG00000237851	RP1-67K17.4	6:143069579-143266338	NOTEST	0	0	0	0	1	1
ENSG00000237852	ENSG00000237852	RP4-630A11.3	1:65886247-66107242	NOTEST	0	0	0	0	1	1
ENSG00000237853	ENSG00000237853	RP5-833A20.1	1:61330930-61928465	NOTEST	0	0	0	0	1	1
ENSG00000237856	ENSG00000237856	AC062020.2	2:123822896-123831057	NOTEST	0	0	0	0	1	1
ENSG00000237857	ENSG00000237857	RP11-435O5.2	9:98177115-98189078	NOTEST	0.222238	0.23089	0.0550968	0	1	1
ENSG00000237859	ENSG00000237859	EEF1A1P31	X:154064062-154288578	NOTEST	0	0	0	0	1	1
ENSG00000237860	ENSG00000237860	RP11-232D9.4	X:115822837-115824153	NOTEST	0	0	0	0	1	1
ENSG00000237861	ENSG00000237861	RP11-332L8.1	1:197170591-197447585	NOTEST	0	0	0	0	1	1
ENSG00000237862	ENSG00000237862	RP1-63G5.7	22:37735623-37823505	NOTEST	0	0	0	0	1	1
ENSG00000237863	ENSG00000237863	RP6-24A23.3	X:107963178-107982133	NOTEST	0.375275	0.241557	-0.635583	0	1	1
ENSG00000237864	ENSG00000237864	LINC00322	21:44742296-44751919	NOTEST	0	0	0	0	1	1
ENSG00000237865	ENSG00000237865	SUCLA2P1	HSCHR6_MHC_SSTO:30425678-30427048	NOTEST	0	0	0	0	1	1
ENSG00000237869	ENSG00000237869	RP11-459O16.1	9:66342520-66343121	NOTEST	0.0984087	0.166922	0.762313	0	1	1
ENSG00000237870	ENSG00000237870	AC073130.1	7:115850546-116148595	NOTEST	0.0593629	0.086284	0.53953	0	1	1
ENSG00000237871	ENSG00000237871	HLA-Z	HSCHR6_MHC_DBB:32842121-32842196	NOTEST	0	0	0	0	1	1
ENSG00000237872	ENSG00000237872	POU5F1P4	1:155305058-155533775	NOTEST	0	0.0629189	inf	0	1	1
ENSG00000237873	ENSG00000237873	RP11-156J23.1	X:92297488-92297941	NOTEST	0	0	0	0	1	1
ENSG00000237874	ENSG00000237874	RP3-393K13.1	6:84437773-84446244	NOTEST	0	0	0	0	1	1
ENSG00000237875	ENSG00000237875	RP5-1174J21.1	X:41374186-41782716	NOTEST	0	0	0	0	1	1
ENSG00000237876	ENSG00000237876	AKR1B1P4	13:46261682-46262604	NOTEST	0	0	0	0	1	1
ENSG00000237877	ENSG00000237877	AC097500.2	2:186897617-186947960	NOTEST	0.604137	0.256674	-1.23494	0	1	1
ENSG00000237879	ENSG00000237879	LINC00398	13:31377342-31384782	NOTEST	0	0.0142497	inf	0	1	1
ENSG00000237880	ENSG00000237880	AC096669.2	2:107871146-108172782	NOTEST	0	0	0	0	1	1
ENSG00000237881	ENSG00000237881	C6orf10	HSCHR6_MHC_MCF:32360674-32415872	NOTEST	0	0	0	0	1	1
ENSG00000237882	ENSG00000237882	PPIAP13	10:76849005-76849483	NOTEST	0	0	0	0	1	1
ENSG00000237883	ENSG00000237883	DGUOK-AS1	2:74153952-74208568	NOTEST	0.473272	0.199451	-1.24663	0	1	1
ENSG00000237884	ENSG00000237884	HCG4P3	HSCHR6_MHC_QBL:29958304-30022269	NOTEST	0	0	0	0	1	1
ENSG00000237885	ENSG00000237885	RP11-208C17.4	10:96791396-96791805	NOTEST	0	0	0	0	1	1
ENSG00000237887	ENSG00000237887	RPL23AP32	2:54683421-54896812	NOTEST	0.0965723	0	#NAME?	0	1	1
ENSG00000237888	ENSG00000237888	AC087650.1	17:41553565-41554033	NOTEST	0	0	0	0	1	1
ENSG00000237889	ENSG00000237889	DDX39B	HSCHR6_MHC_APD:31507784-31518252	NOTEST	0	0	0	0	1	1
ENSG00000237890	ENSG00000237890	LINC00243	HSCHR6_MHC_SSTO:30757841-30789807	NOTEST	0	0	0	0	1	1

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ENSG00000237892	ENSG00000237892	KLF7-IT1	2:207938860-208031991	NOTEST	0	0	0	0	1	1
ENSG00000237894	ENSG00000237894	HCG22	HSCHR6_MHC_MANN:31066941-31072606	NOTEST	0	0	0	0	1	1
ENSG00000237896	ENSG00000237896	AC005008.2	7:80804823-80828431	NOTEST	0	0	0	0	1	1
ENSG00000237897	ENSG00000237897	RP11-90H3.2	1:106433314-106434052	NOTEST	0	0	0	0	1	1
ENSG00000237898	ENSG00000237898	HCG15	HSCHR6_MHC_SSTO:28954098-28956435	NOTEST	0	0	0	0	1	1
ENSG00000237899	ENSG00000237899	RP4-739H11.3	1:41134760-41153260	NOTEST	0	0	0	0	1	1
ENSG00000237900	ENSG00000237900	ZBTB12	HSCHR6_MHC_COX:31853113-31907413	NOTEST	0	0	0	0	1	1
ENSG00000237901	ENSG00000237901	AC009161.1	16:62391274-62391650	NOTEST	0	0	0	0	1	1
ENSG00000237902	ENSG00000237902	TSPY21P	Y:24454969-24564028	NOTEST	0	0	0	0	1	1
ENSG00000237903	ENSG00000237903	RP3-404F18.5	X:118533022-118588441	NOTEST	0.163184	0	#NAME?	0	1	1
ENSG00000237904	ENSG00000237904	RP11-460E7.9	9:70366920-70367319	NOTEST	0	0	0	0	1	1
ENSG00000237905	ENSG00000237905	HCG4	HSCHR6_MHC_QBL:29756043-29762764	NOTEST	0	0	0	0	1	1
ENSG00000237906	ENSG00000237906	MUPP	9:115721413-115724541	NOTEST	0	0	0	0	1	1
ENSG00000237907	ENSG00000237907	RP5-1013A22.2	20:43077416-43078732	NOTEST	0	0	0	0	1	1
ENSG00000237910	ENSG00000237910	AC073869.7	2:132140215-132141634	NOTEST	0	0	0	0	1	1
ENSG00000237911	ENSG00000237911	SRP68P3	17:20318859-20334321	NOTEST	0.00941235	0.0612873	2.70296	0	1	1
ENSG00000237913	ENSG00000237913	FTLP19	10:16113414-16113808	NOTEST	0	0	0	0	1	1
ENSG00000237914	ENSG00000237914	RP11-77C3.3	20:1609797-1638425	NOTEST	0	0	0	0	1	1
ENSG00000237916	ENSG00000237916	RP11-537E18.1	2:110300558-110371783	NOTEST	0.104858	0.633348	2.59457	0	1	1
ENSG00000237917	ENSG00000237917	PARP4P1	Y:28740997-28780799	NOTEST	0	0	0	0	1	1
ENSG00000237918	ENSG00000237918	SAPCD1	HSCHR6_MHC_SSTO:31714323-31722583	NOTEST	0	0	0	0	1	1
ENSG00000237919	ENSG00000237919	RP11-181B18.1	1:70034080-70671303	NOTEST	0	0	0	0	1	1
ENSG00000237920	ENSG00000237920	RP11-350G8.4	1:154349441-154351749	NOTEST	0	0	0	0	1	1
ENSG00000237921	ENSG00000237921	AC004543.2	7:19853307-19857713	NOTEST	0	0	0	0	1	1
ENSG00000237922	ENSG00000237922	RP11-478H16.1	1:236449275-236450260	NOTEST	0	0	0	0	1	1
ENSG00000237923	ENSG00000237923	XXbac-BPG27H4.8	6:30807302-30815936	NOTEST	0	0	0	0	1	1
ENSG00000237924	ENSG00000237924	RPL21P112	13:95412806-95413269	NOTEST	0	0	0	0	1	1
ENSG00000237926	ENSG00000237926	RP13-346H10.2	X:50838689-50914232	NOTEST	0	0	0	0	1	1
ENSG00000237927	ENSG00000237927	RP3-393E18.2	6:160007986-160010201	NOTEST	0	0.00630246	inf	0	1	1
ENSG00000237928	ENSG00000237928	RP4-668G5.1	1:61330930-61928465	NOTEST	0.0248861	0.0843185	1.76051	0	1	1
ENSG00000237929	ENSG00000237929	RPL31P3	20:29899105-29899765	NOTEST	0	0	0	0	1	1
ENSG00000237930	ENSG00000237930	AC007563.4	2:217536827-217858802	NOTEST	0	0	0	0	1	1
ENSG00000237931	ENSG00000237931	RP11-469E19.1	X:40936251-40937003	NOTEST	0	0.168919	inf	0	1	1
ENSG00000237934	ENSG00000237934	RP11-467D18.2	1:29519384-29557454	NOTEST	0.0369527	0	#NAME?	0	1	1
ENSG00000237936	ENSG00000237936	RP11-224P11.1	10:30179960-30180396	NOTEST	0	0	0	0	1	1
ENSG00000237937	ENSG00000237937	AP000770.1	11:116510138-116528969	NOTEST	0	0	0	0	1	1
ENSG00000237939	ENSG00000237939	AC097523.3	2:139064888-139065540	NOTEST	0	0	0	0	1	1
ENSG00000237940	ENSG00000237940	AC093642.3	2:242823513-243026289	NOTEST	0.0495664	0.230233	2.21566	0	1	1
ENSG00000237941	ENSG00000237941	KCNQ1DN	11:2891262-2893335	NOTEST	0	0	0	0	1	1
ENSG00000237943	ENSG00000237943	PRKCQ-AS1	10:6649248-6658414	NOTEST	0	0	0	0	1	1
ENSG00000237945	ENSG00000237945	LINC00649	21:34876237-35349992	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000237947	ENSG00000237947	RP11-570K4.1	6:40681149-40683102	NOTEST	0	0	0	0	1	1
ENSG00000237948	ENSG00000237948	Z95114.5	22:36570308-36570870	NOTEST	0	0	0	0	1	1
ENSG00000237949	ENSG00000237949	LINC00844	10:60759385-60761303	NOTEST	0	0	0	0	1	1
ENSG00000237951	ENSG00000237951	PPIL1P1	2:26384924-26385423	NOTEST	0	0	0	0	1	1
ENSG00000237952	ENSG00000237952	RPL7AP73	13:23377434-23377787	NOTEST	0	0	0	0	1	1
ENSG00000237953	ENSG00000237953	AC013267.1	2:25166504-25262563	NOTEST	0	0	0	0	1	1
ENSG00000237954	ENSG00000237954	RP11-14O19.2	1:95821784-95846556	NOTEST	0	0	0	0	1	1
ENSG00000237955	ENSG00000237955	AC008746.10	19:54891092-54891564	NOTEST	0	0	0	0	1	1
ENSG00000237956	ENSG00000237956	TRIAP1P1	10:27667066-27667291	NOTEST	0	0	0	0	1	1
ENSG00000237957	ENSG00000237957	CT47A5	X:120092018-120100198	NOTEST	0	0	0	0	1	1
ENSG00000237959	ENSG00000237959	RPL36AP10	1:89003195-89301938	NOTEST	0	0	0	0	1	1
ENSG00000237961	ENSG00000237961	RP11-1281K21.1	4:49239115-49247436	NOTEST	0	0	0	0	1	1
ENSG00000237962	ENSG00000237962	C6orf205	HSCHR6_MHC_DBB:30942198-30948389	NOTEST	0	0	0	0	1	1
ENSG00000237963	ENSG00000237963	RP11-151G12.2	X:64576769-64577427	NOTEST	0	0	0	0	1	1
ENSG00000237964	ENSG00000237964	AC068042.1	2:180264454-180265602	NOTEST	0	0	0	0	1	1
ENSG00000237968	ENSG00000237968	AC007322.7	Y:24086158-24087740	NOTEST	0	0	0	0	1	1
ENSG00000237970	ENSG00000237970	TMEM161BP1	10:37414784-37673039	NOTEST	0	0.044027	inf	0	1	1
ENSG00000237971	ENSG00000237971	RP11-231N9.1	X:64404897-64407145	NOTEST	0	0	0	0	1	1
ENSG00000237972	ENSG00000237972	TUBG1P	7:43906156-43966010	NOTEST	0.0750725	0.0753106	0.00456866	0	1	1
ENSG00000237974	ENSG00000237974	AC000111.4	7:117105837-117514193	NOTEST	0	0	0	0	1	1
ENSG00000237977	ENSG00000237977	EIF4HP2	22:31089768-31303811	NOTEST	0.0757905	0.118437	0.644027	0	1	1
ENSG00000237978	ENSG00000237978	RP11-385J1.2	3:177919837-178578193	NOTEST	0.539993	0.1432	-1.91491	0	1	1
ENSG00000237979	ENSG00000237979	AC007389.1	2:65663844-66311773	NOTEST	0.0955215	0	#NAME?	0	1	1
ENSG00000237980	ENSG00000237980	RP11-338C15.3	1:212827340-212838776	NOTEST	0	0	0	0	1	1
ENSG00000237982	ENSG00000237982	RP11-815I22.1	3:38307302-38319806	NOTEST	0	0	0	0	1	1
ENSG00000237986	ENSG00000237986	CELF2-AS2	10:11047258-11378674	NOTEST	0	0	0	0	1	1
ENSG00000237987	ENSG00000237987	RP11-503C24.2	6:168625958-168627197	NOTEST	0	0	0	0	1	1
ENSG00000237988	ENSG00000237988	OR2I1P	6:29520995-29521943	NOTEST	0.0358878	0.0138429	-1.37434	0	1	1
ENSG00000237990	ENSG00000237990	CNTN4-AS1	3:2140496-3102829	NOTEST	0	0	0	0	1	1
ENSG00000237991	ENSG00000237991	RPL35P1	1:237144636-237145008	NOTEST	0	0	0	0	1	1
ENSG00000237992	ENSG00000237992	AC010096.2	2:19675210-19688611	NOTEST	0	0	0	0	1	1
ENSG00000237993	ENSG00000237993	RP11-159M11.2	1:116519118-116612675	NOTEST	0	0	0	0	1	1
ENSG00000237994	ENSG00000237994	RP1-146A15.1	X:28605515-29974840	NOTEST	0	0	0	0	1	1
ENSG00000237997	ENSG00000237997	RCC2P2	Y:22148460-22149738	NOTEST	0	0	0	0	1	1
ENSG00000237998	ENSG00000237998	RP11-432J9.5	10:72575716-72640930	NOTEST	0.0208319	0.0162022	-0.362605	0	1	1
ENSG00000237999	ENSG00000237999	RP11-394D2.1	9:103493521-103494637	NOTEST	0	0	0	0	1	1
ENSG00000238000	ENSG00000238000	RP11-274E7.2	5:97549105-97549825	NOTEST	0.0497272	0.217031	2.1258	0	1	1
ENSG00000238001	ENSG00000238001	RP11-555J4.2	9:32676060-32676518	NOTEST	0	0.0368232	inf	0	1	1
ENSG00000238002	ENSG00000238002	NPAP1P6	9:82477933-82481790	NOTEST	0	0	0	0	1	1
ENSG00000238003	ENSG00000238003	RP11-465N4.2	1:201947769-201948077	NOTEST	0	0	0	0	1	1
ENSG00000238004	ENSG00000238004	AC009227.3	2:155316368-155317332	NOTEST	0	0	0	0	1	1
ENSG00000238005	ENSG00000238005	RP11-443B7.1	1:235092977-235105809	NOTEST	0.149506	0.113518	-0.397277	0	1	1
ENSG00000238007	ENSG00000238007	AC024619.2	17:27232267-27384234	NOTEST	0.0854884	0	#NAME?	0	1	1
ENSG00000238008	ENSG00000238008	COX6CP10	3:33537736-33759848	NOTEST	0	0.574509	inf	0	1	1

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ENSG00000238012	ENSG00000238012	AC114752.1	2:64557619-64559265	NOTEST	0	0	0	0	1	1
ENSG00000238013	ENSG00000238013	RP11-427P5.2	3:46753604-46854064	NOTEST	0	0	0	0	1	1
ENSG00000238015	ENSG00000238015	RP4-641G12.3	1:79131956-79132380	NOTEST	0	0	0	0	1	1
ENSG00000238017	ENSG00000238017	SAPCD1-AS1	HSCHR6_MHC_COX:31695129-31720748	NOTEST	0	0	0	0	1	1
ENSG00000238019	ENSG00000238019	RP11-732M18.2	6:158733691-158932860	NOTEST	0	0	0	0	1	1
ENSG00000238020	ENSG00000238020	HTR3E-AS1	3:183812905-183824783	NOTEST	0	0	0	0	1	1
ENSG00000238021	ENSG00000238021	ARMC4P1	10:27532058-27577753	NOTEST	0	0	0	0	1	1
ENSG00000238022	ENSG00000238022	RP11-38C18.3	1:165171103-165325952	NOTEST	0	0	0	0	1	1
ENSG00000238024	ENSG00000238024	DDX39BP2	6:29960985-29961382	NOTEST	0	0	0	0	1	1
ENSG00000238025	ENSG00000238025	ZDHHC4P1	13:43460523-43566407	NOTEST	0	0	0	0	1	1
ENSG00000238026	ENSG00000238026	RP11-78E6.1	3:175831489-175832325	NOTEST	0	0	0	0	1	1
ENSG00000238027	ENSG00000238027	TRIM31-AS1	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1
ENSG00000238029	ENSG00000238029	AC012493.1	2:101041809-101042569	NOTEST	0	0	0	0	1	1
ENSG00000238031	ENSG00000238031	AC090505.1	3:194548618-194553321	NOTEST	0	0	0	0	1	1
ENSG00000238032	ENSG00000238032	RP11-38O23.7	X:48037166-48037459	NOTEST	0	0	0	0	1	1
ENSG00000238033	ENSG00000238033	AC002480.2	7:22459062-22705152	NOTEST	0	0	0	0	1	1
ENSG00000238034	ENSG00000238034	RP5-1185K9.1	20:21928284-21951421	NOTEST	0	0	0	0	1	1
ENSG00000238035	ENSG00000238035	AC138035.2	5:180733502-180755068	NOTEST	0.077104	0	#NAME?	0	1	1
ENSG00000238037	ENSG00000238037	OOSP1P1	1:44620699-44620973	NOTEST	0	0	0	0	1	1
ENSG00000238038	ENSG00000238038	ATP6V0E1P3	2:33827107-33827353	NOTEST	0	0	0	0	1	1
ENSG00000238039	ENSG00000238039	AF011889.2	X:148558520-148632055	NOTEST	0.1697	0.217425	0.357531	0	1	1
ENSG00000238040	ENSG00000238040	SALL4P2	X:129003039-129091504	NOTEST	0	0	0	0	1	1
ENSG00000238041	ENSG00000238041	RP11-59K5.1	11:56457940-56458199	NOTEST	0	0.116775	inf	0	1	1
ENSG00000238042	ENSG00000238042	RP11-815M8.1	1:222054322-222158306	NOTEST	0.034225	0.0266464	-0.361111	0	1	1
ENSG00000238043	ENSG00000238043	RP11-699L21.2	3:193675160-193788759	NOTEST	0	0.0292868	inf	0	1	1
ENSG00000238046	ENSG00000238046	MTND5P22	2:124782863-125672864	NOTEST	0	0	0	0	1	1
ENSG00000238047	ENSG00000238047	MTND1P30	X:55206809-55207710	NOTEST	0	0	0	0	1	1
ENSG00000238048	ENSG00000238048	AP005019.4	11:72231029-72232777	NOTEST	0	0	0	0	1	1
ENSG00000238049	ENSG00000238049	LL0XNC01-105G4.3	X:102602389-102602657	NOTEST	0	0	0	0	1	1
ENSG00000238051	ENSG00000238051	ISCUP1	1:170143543-170210428	NOTEST	0	0	0	0	1	1
ENSG00000238053	ENSG00000238053	ZDHHC20P1	HSCHR6_MHC_DBB:29675842-29676265	NOTEST	0	0	0	0	1	1
ENSG00000238054	ENSG00000238054	RP11-316I3.2	1:188838607-188856565	NOTEST	0	0.112081	inf	0	1	1
ENSG00000238055	ENSG00000238055	RP1-128O3.6	6:108616097-108847999	NOTEST	0.183356	0	#NAME?	0	1	1
ENSG00000238056	ENSG00000238056	PRRT1	HSCHR6_MHC_APD:32127475-32157217	NOTEST	0	0	0	0	1	1
ENSG00000238057	ENSG00000238057	ZEB2-AS1	2:145141647-145282147	NOTEST	0.0818654	0.0666173	-0.297357	0	1	1
ENSG00000238058	ENSG00000238058	RP11-432J22.2	9:138799657-138805359	NOTEST	0.104781	0.0755062	-0.472705	0	1	1
ENSG00000238059	ENSG00000238059	HSPE1P21	6:133561735-134216691	NOTEST	0	0	0	0	1	1
ENSG00000238061	ENSG00000238061	RP4-635A23.4	1:185126211-185260897	NOTEST	0.126412	0.144573	0.193664	0	1	1
ENSG00000238062	ENSG00000238062	SPATA3-AS1	2:231849082-231860747	NOTEST	0.0383282	0.0228662	-0.745191	0	1	1
ENSG00000238063	ENSG00000238063	RP11-329N22.1	1:38940867-38942156	NOTEST	0	0	0	0	1	1
ENSG00000238064	ENSG00000238064	HCG25	HSCHR6_MHC_MCF:33387703-33414664	NOTEST	0	0	0	0	1	1

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ENSG00000238065	ENSG00000238065	AC010740.1	2:140988991-142895399	NOTEST	0	0	0	0	1	1
ENSG00000238066	ENSG00000238066	RP3-378P9.1	X:116531900-116532169	NOTEST	0	0	0	0	1	1
ENSG00000238067	ENSG00000238067	XKRYP1	Y:20652800-20790963	NOTEST	0	0	0	0	1	1
ENSG00000238068	ENSG00000238068	ZNF630-AS1	X:47696300-47931025	NOTEST	0.0659234	0	#NAME?	0	1	1
ENSG00000238069	ENSG00000238069	RPLP0P7	2:157634217-157634884	NOTEST	0	0	0	0	1	1
ENSG00000238070	ENSG00000238070	SAR1P1	HSCHR6_MHC_MCF:29044502-29045098	NOTEST	0	0	0	0	1	1
ENSG00000238071	ENSG00000238071	DDX39B-AS1	HSCHR6_MHC_QBL:31486777-31504899	NOTEST	0	0	0	0	1	1
ENSG00000238073	ENSG00000238073	RBMY2HP	Y:7539783-7544065	NOTEST	0	0	0	0	1	1
ENSG00000238074	ENSG00000238074	TSPY6P	Y:9236029-9344176	NOTEST	0	0	0	0	1	1
ENSG00000238075	ENSG00000238075	AC087431.1	3:577913-887698	NOTEST	0	0	0	0	1	1
ENSG00000238076	ENSG00000238076	MRPL48P1	6:10460138-10460774	NOTEST	0.0958372	0.0955582	-0.00420558	0	1	1
ENSG00000238077	ENSG00000238077	NMNAT1P3	3:189884552-189885440	NOTEST	0	0	0	0	1	1
ENSG00000238078	ENSG00000238078	RP11-295M18.2	1:221002596-221005771	NOTEST	0.124913	0.271477	1.11991	0	1	1
ENSG00000238079	ENSG00000238079	RP11-72I2.1	6:108616097-108847999	NOTEST	0	0	0	0	1	1
ENSG00000238081	ENSG00000238081	RP4-620F22.3	1:89755358-89756020	NOTEST	0	0	0	0	1	1
ENSG00000238082	ENSG00000238082	AC009948.7	2:179278665-179326117	NOTEST	0	0.0661729	inf	0	1	1
ENSG00000238084	ENSG00000238084	RP3-469D22.1	1:25568727-25756683	NOTEST	0.0904121	0	#NAME?	0	1	1
ENSG00000238085	ENSG00000238085	RP11-435F13.2	1:240928856-241520530	NOTEST	0	0	0	0	1	1
ENSG00000238086	ENSG00000238086	PPP1R26P1	13:48877886-49056122	NOTEST	0	0	0	0	1	1
ENSG00000238087	ENSG00000238087	FMO8P	1:166535414-166549942	NOTEST	0	0	0	0	1	1
ENSG00000238088	ENSG00000238088	OFD1P7Y	Y:21010149-21029166	NOTEST	0	0	0	0	1	1
ENSG00000238090	ENSG00000238090	AC006195.2	7:33168855-33645680	NOTEST	0.0721929	0.0307335	-1.23205	0	1	1
ENSG00000238091	ENSG00000238091	AC016745.1	2:114195267-114253766	NOTEST	0	0	0	0	1	1
ENSG00000238092	ENSG00000238092	CEACAMP6	19:43256837-43359870	NOTEST	0	0	0	0	1	1
ENSG00000238094	ENSG00000238094	AC009892.5	19:55084386-55150343	NOTEST	0	0	0	0	1	1
ENSG00000238097	ENSG00000238097	RP11-513G11.3	3:193920804-193975561	NOTEST	0.0145042	0	#NAME?	0	1	1
ENSG00000238099	ENSG00000238099	RP11-12A2.3	6:139791300-139794192	NOTEST	0	0	0	0	1	1
ENSG00000238100	ENSG00000238100	HCG24	HSCHR6_MHC_QBL:33041364-33044349	NOTEST	0	0	0	0	1	1
ENSG00000238101	ENSG00000238101	FAM8A5P	HSCHR6_MHC_SSTO:32594076-32613256	NOTEST	0	0	0	0	1	1
ENSG00000238102	ENSG00000238102	RP11-19D2.1	20:7237226-7238861	NOTEST	0	0	0	0	1	1
ENSG00000238104	ENSG00000238104	PPP1R10	HSCHR6_MHC_SSTO:30559597-30585593	NOTEST	0	0	0	0	1	1
ENSG00000238106	ENSG00000238106	RP11-402P6.7	X:70939765-70940650	NOTEST	0	0	0	0	1	1
ENSG00000238107	ENSG00000238107	RP11-495P10.5	1:147762995-147769663	NOTEST	0	0	0	0	1	1
ENSG00000238108	ENSG00000238108	RP11-463J7.3	1:190594019-190770788	NOTEST	0	0	0	0	1	1
ENSG00000238109	ENSG00000238109	AC004893.10	7:98475555-98741723	NOTEST	0.0342359	0.0447211	0.385446	0	1	1
ENSG00000238110	ENSG00000238110	RP11-350E12.5	9:90559190-90559938	NOTEST	0.0514866	0.0950644	0.884709	0	1	1
ENSG00000238111	ENSG00000238111	AC066692.3	2:23971533-24149984	NOTEST	0	0	0	0	1	1
ENSG00000238113	ENSG00000238113	RP11-262H14.1	9:66457284-66469310	NOTEST	0.155906	0.0792645	-0.975933	0	1	1
ENSG00000238114	ENSG00000238114	LTB	HSCHR6_MHC_SSTO:31538274-31540242	NOTEST	0	0	0	0	1	1
ENSG00000238116	ENSG00000238116	RP3-347M6.2	X:100056176-100058049	NOTEST	0	0.0210361	inf	0	1	1
ENSG00000238117	ENSG00000238117	AP004372.1	11:131240372-132206716	NOTEST	0	0	0	0	1	1
ENSG00000238118	ENSG00000238118	SLC25A24P2	1:108803817-109013624	NOTEST	0	0.0311121	inf	0	1	1
ENSG00000238120	ENSG00000238120	CTA-941F9.9	22:46000311-46001501	NOTEST	0	0	0	0	1	1

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ENSG00000238122	ENSG00000238122	RP11-483I13.2	1:108803817-109013624	NOTEST	0	0	0	0	1	1
ENSG00000238123	ENSG00000238123	MID1IP1-AS1	X:38660684-38665790	NOTEST	0.354376	0.630136	0.830385	0	1	1
ENSG00000238124	ENSG00000238124	RP11-667F9.2	7:64927983-64928351	NOTEST	0	0	0	0	1	1
ENSG00000238125	ENSG00000238125	SLC9A3P2	22:20956881-21011201	NOTEST	0	0	0	0	1	1
ENSG00000238126	ENSG00000238126	UQCRHP1	HSCHR6_MHC_APD:31590210-31590484	NOTEST	0	0	0	0	1	1
ENSG00000238127	ENSG00000238127	RP11-552J9.15	X:52777573-52779905	NOTEST	0	0	0	0	1	1
ENSG00000238129	ENSG00000238129	RP3-410C9.2	20:26167555-26232162	NOTEST	0	0	0	0	1	1
ENSG00000238130	ENSG00000238130	LTA	HSCHR6_MHC_COX:31527242-31529513	NOTEST	0	0	0	0	1	1
ENSG00000238131	ENSG00000238131	RP11-806J6.1	7:53994368-54015437	NOTEST	0	0	0	0	1	1
ENSG00000238132	ENSG00000238132	CASC4P1	13:20126710-20144428	NOTEST	0	0.00915935	inf	0	1	1
ENSG00000238133	ENSG00000238133	MLK7-AS1	2:173940162-174146764	NOTEST	0.024218	0.0249515	0.0430488	0	1	1
ENSG00000238134	ENSG00000238134	EHMT2	HSCHR6_MHC_MCF:31924011-31941947	NOTEST	0	0	0	0	1	1
ENSG00000238135	ENSG00000238135	USP9YP10	Y:20835918-20991373	NOTEST	0	0	0	0	1	1
ENSG00000238137	ENSG00000238137	ARPC3P2	1:211615615-211616148	NOTEST	0	0	0	0	1	1
ENSG00000238138	ENSG00000238138	AC027124.3	3:13501793-13501898	NOTEST	0	0	0	0	1	1
ENSG00000238139	ENSG00000238139	RP11-393N21.1	1:68026755-68027129	NOTEST	0	0	0	0	1	1
ENSG00000238140	ENSG00000238140	RP11-253A20.1	1:51819934-52027301	NOTEST	0	0	0	0	1	1
ENSG00000238141	ENSG00000238141	BRWD1-AS1	21:40556101-40695144	NOTEST	0	0	0	0	1	1
ENSG00000238143	ENSG00000238143	RP11-70K10.2	9:103790990-104087417	NOTEST	0	0	0	0	1	1
ENSG00000238145	ENSG00000238145	RP11-346M5.1	1:47308766-47366109	NOTEST	0	0	0	0	1	1
ENSG00000238148	ENSG00000238148	HCG27	HSCHR6_MHC_MANN:31210905-31210949	NOTEST	0	0	0	0	1	1
ENSG00000238149	ENSG00000238149	AC104978.1	11:28042166-28355054	NOTEST	0	0	0	0	1	1
ENSG00000238150	ENSG00000238150	AC008753.3	19:54278852-54279136	NOTEST	0	0.100591	inf	0	1	1
ENSG00000238152	ENSG00000238152	OR7E140P	12:8567375-8568401	NOTEST	0	0	0	0	1	1
ENSG00000238153	ENSG00000238153	CTA-714B7.4	22:35515816-35627049	NOTEST	0	0	0	0	1	1
ENSG00000238154	ENSG00000238154	USP9YP4	Y:9027237-9042220	NOTEST	0	0	0	0	1	1
ENSG00000238156	ENSG00000238156	RP11-415D17.4	6:75994729-76203454	NOTEST	0	0	0	0	1	1
ENSG00000238158	ENSG00000238158	RP11-420L9.4	6:3832166-3855971	NOTEST	0	0	0	0	1	1
ENSG00000238160	ENSG00000238160	AC116366.5	5:131746327-131811736	NOTEST	0	0	0	0	1	1
ENSG00000238161	ENSG00000238161	OR7E117P	11:3620824-3621936	NOTEST	0	0	0	0	1	1
ENSG00000238162	ENSG00000238162	AC009237.4	2:96151288-96151553	NOTEST	0	0	0	0	1	1
ENSG00000238165	ENSG00000238165	AC007560.1	2:50145642-51259674	NOTEST	0	0	0	0	1	1
ENSG00000238166	ENSG00000238166	RP11-160C18.4	15:79044448-79045715	NOTEST	0	0	0	0	1	1
ENSG00000238168	ENSG00000238168	RP11-686G8.1	12:111890017-112038060	NOTEST	0.066233	0	#NAME?	0	1	1
ENSG00000238169	ENSG00000238169	LINC01053	13:25755578-25763898	NOTEST	0	0	0	0	1	1
ENSG00000238170	ENSG00000238170	C4A-AS1	HSCHR6_MHC_SSTO:31965199-32027628	NOTEST	0	0	0	0	1	1
ENSG00000238171	ENSG00000238171	AC068196.1	2:181831974-182264286	NOTEST	0	0	0	0	1	1
ENSG00000238172	ENSG00000238172	RPS2P35	9:102861537-103063282	NOTEST	0	0	0	0	1	1
ENSG00000238173	ENSG00000238173	RPL39P6	1:11166591-11322564	NOTEST	0	0	0	0	1	1
ENSG00000238176	ENSG00000238176	RP11-322I2.1	10:37229036-37232860	NOTEST	0	0	0	0	1	1
ENSG00000238178	ENSG00000238178	RP11-431J24.2	X:16141678-16189587	NOTEST	0.179578	0.119172	-0.59156	0	1	1
ENSG00000238180	ENSG00000238180	AC017079.4	2:128975161-128975646	NOTEST	0	0	0	0	1	1
ENSG00000238181	ENSG00000238181	AHCYP2	9:123482950-123484250	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238183	ENSG00000238183	RPS27P5	1:226969201-226969445	NOTEST	0	0	0	0	1	1
ENSG00000238184	ENSG00000238184	CD81-AS1	11:2349978-2418649	NOTEST	0.181776	0.180546	-0.0097947	0	1	1
ENSG00000238185	ENSG00000238185	RP11-252M21.6	13:31456069-31551760	NOTEST	0	0	0	0	1	1
ENSG00000238186	ENSG00000238186	RP11-656D10.6	1:40974412-40982846	NOTEST	0	0.118065	inf	0	1	1
ENSG00000238188	ENSG00000238188	RP5-875H3.2	X:129757349-130037208	NOTEST	0.0979569	0	#NAME?	0	1	1
ENSG00000238189	ENSG00000238189	ENOX1-AS2	13:43787653-44361044	NOTEST	0	0	0	0	1	1
ENSG00000238190	ENSG00000238190	HMGB1P15	X:50674113-50674548	NOTEST	0	0	0	0	1	1
ENSG00000238191	ENSG00000238191	CLUHP1	Y:19733138-19737712	NOTEST	0	0	0	0	1	1
ENSG00000238192	ENSG00000238192	LL22NC03-121E8.4	22:48535277-48536818	NOTEST	0	0	0	0	1	1
ENSG00000238193	ENSG00000238193	RP11-555H23.1	X:5223754-5225169	NOTEST	0	0	0	0	1	1
ENSG00000238194	ENSG00000238194	RP4-719C8.1	20:58152563-58422766	NOTEST	0	0	0	0	1	1
ENSG00000238195	ENSG00000238195	CTA-503F6.2	22:27600172-27601088	NOTEST	0	0	0	0	1	1
ENSG00000238196	ENSG00000238196	NOTCH4	HSCHR6_MHC_APD:32169883-32183518	NOTEST	0	0	0	0	1	1
ENSG00000238197	ENSG00000238197	PAXBP1-AS1	21:34100425-34144169	NOTEST	0.216566	0.109571	-0.982936	0	1	1
ENSG00000238198	ENSG00000238198	RP11-31F15.2	1:113550875-113615727	NOTEST	0.0259632	0.0298054	0.199109	0	1	1
ENSG00000238199	ENSG00000238199	UBE2V2P3	1:11333262-11356106	NOTEST	0.111619	0	#NAME?	0	1	1
ENSG00000238200	ENSG00000238200	RP13-36C9.5	X:134919549-134921014	NOTEST	0	0	0	0	1	1
ENSG00000238201	ENSG00000238201	AC114752.3	2:64565200-64568781	NOTEST	0	0	0	0	1	1
ENSG00000238202	ENSG00000238202	AC002465.2	7:116916684-116963343	NOTEST	0	0	0	0	1	1
ENSG00000238203	ENSG00000238203	VWA7	HSCHR6_MHC_APD:31744720-31756461	NOTEST	0	0	0	0	1	1
ENSG00000238205	ENSG00000238205	MPC1L	X:40482835-40483112	NOTEST	0	0	0	0	1	1
ENSG00000238207	ENSG00000238207	AC009312.1	2:118515138-118561750	NOTEST	0	0	0	0	1	1
ENSG00000238208	ENSG00000238208	RP11-112N13.1	9:107944760-107949038	NOTEST	0.00413895	0	#NAME?	0	1	1
ENSG00000238210	ENSG00000238210	RP13-210D15.4	X:134382866-134478012	NOTEST	0	0	0	0	1	1
ENSG00000238211	ENSG00000238211	POLR2LP	6:31108503-31108690	NOTEST	0	0	0	0	1	1
ENSG00000238212	ENSG00000238212	AC005863.2	17:14737954-14803871	NOTEST	0	0	0	0	1	1
ENSG00000238213	ENSG00000238213	TARDBPP2	13:60848909-60850140	NOTEST	0	0	0	0	1	1
ENSG00000238215	ENSG00000238215	RP11-167P22.5	10:74402768-74404408	NOTEST	0	0	0	0	1	1
ENSG00000238216	ENSG00000238216	HCG20	HSCHR6_MHC_SSTO:30747882-30751451	NOTEST	0	0	0	0	1	1
ENSG00000238217	ENSG00000238217	AC093590.1	2:200472790-200523855	NOTEST	0.0763749	0.0568089	-0.426982	0	1	1
ENSG00000238220	ENSG00000238220	AP000275.64	21:33996725-33997406	NOTEST	0	0	0	0	1	1
ENSG00000238221	ENSG00000238221	RP11-69L16.4	6:7268538-7418270	NOTEST	0	0	0	0	1	1
ENSG00000238222	ENSG00000238222	MKRN4P	X:40693737-40695258	NOTEST	0	0	0	0	1	1
ENSG00000238223	ENSG00000238223	RP6-204F4.2	X:114298498-114299357	NOTEST	0	0	0	0	1	1
ENSG00000238224	ENSG00000238224	RP11-522M21.2	1:245318286-245872733	NOTEST	0	0	0	0	1	1
ENSG00000238225	ENSG00000238225	CRIP1P2	3:25728386-25728614	NOTEST	0	0	0	0	1	1
ENSG00000238226	ENSG00000238226	HLA-DQB1-AS1	HSCHR6_MHC_MANN:32779139-32788434	NOTEST	0	0	0	0	1	1
ENSG00000238228	ENSG00000238228	OR7E7P	7:97576298-97577310	NOTEST	0	0	0	0	1	1
ENSG00000238230	ENSG00000238230	LINC00391	13:95351947-95355116	NOTEST	0	0	0	0	1	1
ENSG00000238231	ENSG00000238231	RP11-460I13.6	1:28296854-28415207	NOTEST	0	0.118038	inf	0	1	1
ENSG00000238232	ENSG00000238232	RP11-95P13.2	1:219730533-219731043	NOTEST	0	0	0	0	1	1
ENSG00000238234	ENSG00000238234	HCG22	HSCHR6_MHC_COX:31014485-31020156	NOTEST	0	0	0	0	1	1
ENSG00000238235	ENSG00000238235	TSPY11P	Y:6134633-6137316	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238236	ENSG00000238236	RP4-534P7.2	1:235683268-235683983	NOTEST	0	0	0	0	1	1
ENSG00000238238	ENSG00000238238	MCCD1	HSCHR6_MHC_MANN:31536012-31554120	NOTEST	0	0	0	0	1	1
ENSG00000238240	ENSG00000238240	RP4-740C4.5	1:2252691-2323146	NOTEST	0.462143	0.225619	-1.03445	0	1	1
ENSG00000238241	ENSG00000238241	CCR12P	13:100060034-100061316	NOTEST	0	0	0	0	1	1
ENSG00000238242	ENSG00000238242	RP11-575B7.3	1:60580546-60615351	NOTEST	0	0	0	0	1	1
ENSG00000238243	ENSG00000238243	OR2W3	1:248020500-248060449	NOTEST	0	0.0600289	inf	0	1	1
ENSG00000238244	ENSG00000238244	GABARAPL3	15:90890818-90892669	NOTEST	0	0	0	0	1	1
ENSG00000238245	ENSG00000238245	MYO5BP2	9:66513031-66555928	NOTEST	0	0	0	0	1	1
ENSG00000238246	ENSG00000238246	RP11-575A19.2	10:20105167-20578785	NOTEST	0	0	0	0	1	1
ENSG00000238247	ENSG00000238247	GS1-309P15.4	X:27536000-27537876	NOTEST	0	0	0	0	1	1
ENSG00000238248	ENSG00000238248	DASS-23B5.1	HSCHR6_MHC_MANN:32642475-32643415	NOTEST	0	0	0	0	1	1
ENSG00000238249	ENSG00000238249	HMGN2P17	1:8953467-8954210	NOTEST	0	0	0	0	1	1
ENSG00000238250	ENSG00000238250	ST6GAL2-IT1	2:107418055-107503564	NOTEST	0	0	0	0	1	1
ENSG00000238251	ENSG00000238251	RP11-172F4.2	9:99148222-99180611	NOTEST	0.043306	0.138437	1.67659	0	1	1
ENSG00000238254	ENSG00000238254	CTC-431G16.3	5:79145374-79145669	NOTEST	0	0	0	0	1	1
ENSG00000238255	ENSG00000238255	RPL7P4	HSCHR6_MHC_QBL:30654117-30654847	NOTEST	0	0	0	0	1	1
ENSG00000238256	ENSG00000238256	MTND5P20	1:113933370-114228545	NOTEST	0	0	0	0	1	1
ENSG00000238257	ENSG00000238257	AP000244.11	21:32134999-32135200	NOTEST	0	0	0	0	1	1
ENSG00000238258	ENSG00000238258	RP11-342D11.2	10:33466419-33625190	NOTEST	0	0	0	0	1	1
ENSG00000238259	ENSG00000238259	AC067940.1	2:168810529-169104651	NOTEST	0	0	0	0	1	1
ENSG00000238260	ENSG00000238260	RP11-46F15.2	1:3539753-3541307	NOTEST	0.126688	0.198785	0.649932	0	1	1
ENSG00000238262	ENSG00000238262	NTM-IT	11:131240372-132206716	NOTEST	0	0	0	0	1	1
ENSG00000238263	ENSG00000238263	RP11-402L1.12	10:44124264-44170151	NOTEST	0	0	0	0	1	1
ENSG00000238265	ENSG00000238265	LINC00317	21:23095612-23109639	NOTEST	0	0	0	0	1	1
ENSG00000238266	ENSG00000238266	LINC00707	10:6821559-6884868	NOTEST	0	0	0	0	1	1
ENSG00000238267	ENSG00000238267	RP11-241K18.2	3:39379619-39380370	NOTEST	0	0	0	0	1	1
ENSG00000238268	ENSG00000238268	RP11-229P13.19	9:139869545-139871433	NOTEST	0	0	0	0	1	1
ENSG00000238269	ENSG00000238269	PAGE2B	X:55101495-55105342	NOTEST	0.0860374	0.156688	0.864862	0	1	1
ENSG00000238270	ENSG00000238270	RP11-445J9.1	1:189837130-189837658	NOTEST	0	0	0	0	1	1
ENSG00000238271	ENSG00000238271	IFNWP19	9:21455482-21559668	NOTEST	0.0752149	0.0878603	0.224191	0	1	1
ENSG00000238272	ENSG00000238272	RP3-436N22.3	1:173469602-173639001	NOTEST	0.0540218	0.0643445	0.252276	0	1	1
ENSG00000238273	ENSG00000238273	AC012360.6	2:105974168-106054970	NOTEST	0.112948	0.255162	1.17576	0	1	1
ENSG00000238275	ENSG00000238275	HOMER2P2	14:106743405-106744252	NOTEST	0	0	0	0	1	1
ENSG00000238276	ENSG00000238276	RP11-245J24.1	10:120001075-120027222	NOTEST	0	0	0	0	1	1
ENSG00000238277	ENSG00000238277	AC068483.1	2:129821418-129829298	NOTEST	0	0	0	0	1	1
ENSG00000238278	ENSG00000238278	ALG1L6P	3:75464220-75484261	NOTEST	0.0718968	0.0736628	0.0350086	0	1	1
ENSG00000238279	ENSG00000238279	BX470102.3	1:153506078-153508720	NOTEST	0.32425	0.433693	0.419566	0	1	1
ENSG00000238280	ENSG00000238280	RP11-436D10.3	10:64553321-64568238	NOTEST	0.112688	0.04213	-1.41941	0	1	1
ENSG00000238282	ENSG00000238282	RP5-1164C1.2	20:4456284-4505846	NOTEST	0	0	0	0	1	1
ENSG00000238283	ENSG00000238283	TBC1D3P1	17:57970446-58096413	NOTEST	0	0.00685976	inf	0	1	1
ENSG00000238284	ENSG00000238284	AC027269.2	7:42701324-42746046	NOTEST	0	0	0	0	1	1
ENSG00000238285	ENSG00000238285	MRPL50P2	2:204180112-204180594	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238286	ENSG00000238286	SLC35E1P1	13:21140584-21265503	NOTEST	0.146387	0.0317904	-2.20313	0	1	1
ENSG00000238287	ENSG00000238287	RP11-656D10.3	1:40942886-40974333	NOTEST	0.131714	0.109337	-0.268625	0	1	1
ENSG00000238288	ENSG00000238288	RP11-100G15.4	9:94794280-94877666	NOTEST	0	0.186142	inf	0	1	1
ENSG00000238289	ENSG00000238289	MICB	HSCHR6_MHC_MCF:31542227-31555259	NOTEST	0	0	0	0	1	1
ENSG00000238290	ENSG00000238290	RP11-431K24.1	1:8086797-8182762	NOTEST	0	0	0	0	1	1
ENSG00000238291	ENSG00000238291	RP11-94M14.3	10:92162277-92300562	NOTEST	0	0	0	0	1	1
ENSG00000238294	ENSG00000238294	snoU13	20:55043646-55101198	NOTEST	0	0	0	0	1	1
ENSG00000238295	ENSG00000238295	snoU13	2:178092322-178408564	NOTEST	0	0	0	0	1	1
ENSG00000238296	ENSG00000238296	snoU13	1:101694219-101694321	NOTEST	0	0	0	0	1	1
ENSG00000238297	ENSG00000238297	U3	7:107531414-107643700	NOTEST	0	0	0	0	1	1
ENSG00000238298	ENSG00000238298	snoU13	9:133320315-133376661	NOTEST	0	0	0	0	1	1
ENSG00000238300	ENSG00000238300	SNORD121B	9:33921690-34048947	NOTEST	0	0	0	0	1	1
ENSG00000238301	ENSG00000238301	snoU13	4:46920916-47428461	NOTEST	0	0	0	0	1	1
ENSG00000238302	ENSG00000238302	RNU7-120P	12:89441963-89703330	NOTEST	0	0	0	0	1	1
ENSG00000238303	ENSG00000238303	AL592183.2	GL000219.1:164277-164360	NOTEST	0	0	0	0	1	1
ENSG00000238304	ENSG00000238304	RNU7-50P	11:3686816-3847601	NOTEST	0	0	0	0	1	1
ENSG00000238305	ENSG00000238305	snoU13	13:100258918-100549387	NOTEST	0	0	0	0	1	1
ENSG00000238306	ENSG00000238306	snoU13	2:184814059-184814163	NOTEST	0	0	0	0	1	1
ENSG00000238309	ENSG00000238309	snoU13	18:12438888-12725739	NOTEST	0	0	0	0	1	1
ENSG00000238310	ENSG00000238310	RNU7-122P	1:109750415-109750470	NOTEST	0	0	0	0	1	1
ENSG00000238311	ENSG00000238311	snoU13	15:65903703-66184329	NOTEST	0	0	0	0	1	1
ENSG00000238312	ENSG00000238312	snoU13	3:100920675-100920779	NOTEST	0	0	0	0	1	1
ENSG00000238313	ENSG00000238313	snoU13	9:38190403-38190504	NOTEST	0	0	0	0	1	1
ENSG00000238314	ENSG00000238314	snoU13	21:26842420-26842513	NOTEST	0	0	0	0	1	1
ENSG00000238315	ENSG00000238315	AL360154.2	GL000192.1:112236-112366	NOTEST	0	0	0	0	1	1
ENSG00000238316	ENSG00000238316	snoU13	1:26968776-26968880	NOTEST	0	0	0	0	1	1
ENSG00000238317	ENSG00000238317	SNORD11	2:203130438-203168389	NOTEST	0	0	0	0	1	1
ENSG00000238318	ENSG00000238318	snoU13	4:71677962-71678063	NOTEST	0	0	0	0	1	1
ENSG00000238319	ENSG00000238319	snoU13	4:184020445-184241930	NOTEST	0	0	0	0	1	1
ENSG00000238320	ENSG00000238320	AC027612.2	2:91924751-91955465	NOTEST	0	0	0	0	1	1
ENSG00000238321	ENSG00000238321	snoU13	16:82487924-82488023	NOTEST	0	0	0	0	1	1
ENSG00000238322	ENSG00000238322	snoU13	6:25279305-25620758	NOTEST	0	0	0	0	1	1
ENSG00000238323	ENSG00000238323	AC068587.1	8:12493612-12493761	NOTEST	0	0	0	0	1	1
ENSG00000238324	ENSG00000238324	RN7SKP198	7:102453307-102715286	NOTEST	0	0	0	0	1	1
ENSG00000238325	ENSG00000238325	snoU13	1:167010671-167010773	NOTEST	0	0	0	0	1	1
ENSG00000238326	ENSG00000238326	snoU13	5:55290994-55299477	NOTEST	0	0	0	0	1	1
ENSG00000238327	ENSG00000238327	snoU13	X:23525327-23525430	NOTEST	0	0	0	0	1	1
ENSG00000238328	ENSG00000238328	snoU13	2:101193930-101194019	NOTEST	0	0	0	0	1	1
ENSG00000238329	ENSG00000238329	snoU13	16:18814404-18937776	NOTEST	0	0	0	0	1	1
ENSG00000238330	ENSG00000238330	snoU13	14:74181824-74269973	NOTEST	0	0	0	0	1	1
ENSG00000238331	ENSG00000238331	AC100791.2	17:77784477-77784573	NOTEST	0	0	0	0	1	1
ENSG00000238333	ENSG00000238333	RNU7-145P	18:38052784-38052846	NOTEST	0	0	0	0	1	1
ENSG00000238334	ENSG00000238334	snoU13	5:68462836-68474072	NOTEST	0	0	0	0	1	1
ENSG00000238335	ENSG00000238335	AC008869.1	5:37802072-37802167	NOTEST	0	0	0	0	1	1
ENSG00000238336	ENSG00000238336	snoU13	7:129932973-129964020	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238337	ENSG00000238337	snoU13	2:135809834-136288806	NOTEST	0	0	0	0	1	1
ENSG00000238339	ENSG00000238339	snoU13	2:179966418-180129517	NOTEST	0	0	0	0	1	1
ENSG00000238340	ENSG00000238340	AC055876.2	15:28947099-29002537	NOTEST	0	0	0	0	1	1
ENSG00000238341	ENSG00000238341	snoU13	2:122407225-122494499	NOTEST	0	0	0	0	1	1
ENSG00000238342	ENSG00000238342	snoU13	15:33057746-33486897	NOTEST	0	0	0	0	1	1
ENSG00000238343	ENSG00000238343	snoU13	16:68344876-68482591	NOTEST	0	0	0	0	1	1
ENSG00000238344	ENSG00000238344	SNORD126	14:20779526-20801471	NOTEST	0	0	0	0	1	1
ENSG00000238345	ENSG00000238345	snoU13	3:10182691-10193904	NOTEST	0	0	0	0	1	1
ENSG00000238347	ENSG00000238347	AC100757.1	15:23435095-23448420	NOTEST	0	0	0	0	1	1
ENSG00000238348	ENSG00000238348	snoU13	9:19230432-19374139	NOTEST	0	0	0	0	1	1
ENSG00000238349	ENSG00000238349	snoU13	19:11531271-11561783	NOTEST	0	0	0	0	1	1
ENSG00000238350	ENSG00000238350	snoU13	3:47455202-47518616	NOTEST	0	0	0	0	1	1
ENSG00000238351	ENSG00000238351	snoU13	4:40812043-41218731	NOTEST	0	0	0	0	1	1
ENSG00000238352	ENSG00000238352	snoU13	16:28797730-28797834	NOTEST	0	0	0	0	1	1
ENSG00000238354	ENSG00000238354	snoU13	7:54427584-54427688	NOTEST	0	0	0	0	1	1
ENSG00000238355	ENSG00000238355	snoU13	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000238357	ENSG00000238357	RNU7-148P	2:168487989-168488051	NOTEST	0	0	0	0	1	1
ENSG00000238358	ENSG00000238358	RP5-1121E10.2	7:89511666-89867451	NOTEST	0.126449	0	#NAME?	0	1	1
ENSG00000238359	ENSG00000238359	snoU13	3:171318194-171528740	NOTEST	0	0	0	0	1	1
ENSG00000238361	ENSG00000238361	snoU13	12:93659404-93659508	NOTEST	0	0	0	0	1	1
ENSG00000238362	ENSG00000238362	AL158147.1	9:4968096-4968185	NOTEST	0	0	0	0	1	1
ENSG00000238363	ENSG00000238363	SNORA13	5:111478137-111755013	NOTEST	0	0	0	0	1	1
ENSG00000238364	ENSG00000238364	RNU7-140P	19:10654570-10676713	NOTEST	0	0	0	0	1	1
ENSG00000238365	ENSG00000238365	RNU7-57P	1:154298028-154323783	NOTEST	0	0	0	0	1	1
ENSG00000238366	ENSG00000238366	Y_RNA	10:6287693-6287794	NOTEST	0	0	0	0	1	1
ENSG00000238367	ENSG00000238367	MIR2113	6:98264584-98847748	NOTEST	0	0	0	0	1	1
ENSG00000238368	ENSG00000238368	snoU13	2:120517206-120741394	NOTEST	0	0	0	0	1	1
ENSG00000238369	ENSG00000238369	snoU13	5:149340299-149432386	NOTEST	0	0	0	0	1	1
ENSG00000238370	ENSG00000238370	RNU7-103P	12:673461-772945	NOTEST	0	0	0	0	1	1
ENSG00000238371	ENSG00000238371	snoU13	2:16043791-16043895	NOTEST	0	0	0	0	1	1
ENSG00000238372	ENSG00000238372	snoU13	8:102698770-103137135	NOTEST	0	0	0	0	1	1
ENSG00000238374	ENSG00000238374	RNU7-180P	5:145583112-145756526	NOTEST	0	0	0	0	1	1
ENSG00000238375	ENSG00000238375	snoU13	6:37179955-37300746	NOTEST	0	0	0	0	1	1
ENSG00000238376	ENSG00000238376	snoU13	18:28645939-28742819	NOTEST	0	0	0	0	1	1
ENSG00000238377	ENSG00000238377	SNORD61	3:99940364-99940436	NOTEST	0	0	0	0	1	1
ENSG00000238379	ENSG00000238379	RNA5SP103	2:129202654-129202772	NOTEST	0	0	0	0	1	1
ENSG00000238380	ENSG00000238380	RNU7-165P	10:115113183-115113243	NOTEST	0	0	0	0	1	1
ENSG00000238382	ENSG00000238382	RNU6-1211P	1:232835949-232836054	NOTEST	0	0	0	0	1	1
ENSG00000238383	ENSG00000238383	snoU13	4:22346693-22517677	NOTEST	0	0	0	0	1	1
ENSG00000238384	ENSG00000238384	snoU13	7:94536513-94925727	NOTEST	0	0	0	0	1	1
ENSG00000238385	ENSG00000238385	AC004458.1	7:96097642-96097734	NOTEST	0	0	0	0	1	1
ENSG00000238386	ENSG00000238386	RNU7-48P	6:71122530-71270877	NOTEST	0	0	0	0	1	1
ENSG00000238387	ENSG00000238387	snoU13	11:9595227-9615004	NOTEST	0	0	0	0	1	1
ENSG00000238388	ENSG00000238388	snoU13	11:100554892-100862668	NOTEST	0	0	0	0	1	1
ENSG00000238389	ENSG00000238389	snoU13	1:94614543-94740624	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238390	ENSG00000238390	SNORA81	21:33031934-33041244	NOTEST	0	0	0	0	1	1
ENSG00000238391	ENSG00000238391	RNA5SP233	7:73868119-74016931	NOTEST	0	0	0	0	1	1
ENSG00000238392	ENSG00000238392	AC093668.1	7:102122891-102312088	NOTEST	0	0	0	0	1	1
ENSG00000238393	ENSG00000238393	AC009009.1	5:135048807-135048905	NOTEST	0	0	0	0	1	1
ENSG00000238394	ENSG00000238394	snoU13	7:5470965-5553429	NOTEST	0	0	0	0	1	1
ENSG00000238395	ENSG00000238395	snoU13	12:49354520-49354619	NOTEST	0	0	0	0	1	1
ENSG00000238397	ENSG00000238397	RNU6-368P	9:67926760-67987998	NOTEST	0	0	0	0	1	1
ENSG00000238398	ENSG00000238398	snoU13	3:162744183-163079351	NOTEST	0	0	0	0	1	1
ENSG00000238399	ENSG00000238399	MIR2053	8:113235156-114449328	NOTEST	0	0	0	0	1	1
ENSG00000238400	ENSG00000238400	snoU13	5:65526956-65527060	NOTEST	0	0	0	0	1	1
ENSG00000238401	ENSG00000238401	snoU13	1:207212038-207212145	NOTEST	0	0	0	0	1	1
ENSG00000238402	ENSG00000238402	snoU13	9:75136716-75451267	NOTEST	0	0	0	0	1	1
ENSG00000238403	ENSG00000238403	snoU13	17:80477588-80606429	NOTEST	0	0	0	0	1	1
ENSG00000238405	ENSG00000238405	RNA5SP311	10:46737611-46761205	NOTEST	0	0	0	0	1	1
ENSG00000238406	ENSG00000238406	RNU7-171P	9:131266978-131314689	NOTEST	0	0	0	0	1	1
ENSG00000238407	ENSG00000238407	snoU13	13:98538062-98538166	NOTEST	0	0	0	0	1	1
ENSG00000238408	ENSG00000238408	snoU13	13:39917028-40177665	NOTEST	0	0	0	0	1	1
ENSG00000238409	ENSG00000238409	snoU13	16:11343475-11445619	NOTEST	0	0	0	0	1	1
ENSG00000238410	ENSG00000238410	snoU109	2:75696427-75796848	NOTEST	0	0	0	0	1	1
ENSG00000238411	ENSG00000238411	CR381670.1	21:9683190-9683272	NOTEST	0	0	0	0	1	1
ENSG00000238412	ENSG00000238412	AL589947.1	6:93521758-93521852	NOTEST	0	0	0	0	1	1
ENSG00000238413	ENSG00000238413	Y_RNA	9:46141563-46141675	NOTEST	0	0	0	0	1	1
ENSG00000238414	ENSG00000238414	snoU13	10:27157093-27157193	NOTEST	0	0	0	0	1	1
ENSG00000238415	ENSG00000238415	RNU6-538P	9:43064965-43133544	NOTEST	0	0	0	0	1	1
ENSG00000238416	ENSG00000238416	snoU13	3:73131137-73131241	NOTEST	0	0	0	0	1	1
ENSG00000238417	ENSG00000238417	RNU7-63P	16:8768421-8962866	NOTEST	0	0	0	0	1	1
ENSG00000238418	ENSG00000238418	snoU13	17:74305566-74383941	NOTEST	0	0	0	0	1	1
ENSG00000238419	ENSG00000238419	RNU7-186P	17:45331211-45518678	NOTEST	0	0	0	0	1	1
ENSG00000238420	ENSG00000238420	RNU6-437P	6:108188959-108281190	NOTEST	0	0	0	0	1	1
ENSG00000238421	ENSG00000238421	U1	GL000192.1:544947-545107	NOTEST	0	0	0	0	1	1
ENSG00000238422	ENSG00000238422	snoU13	8:124232195-124287781	NOTEST	0	0	0	0	1	1
ENSG00000238423	ENSG00000238423	SNORD42B	17:27046410-27070473	NOTEST	0	0	0	0	1	1
ENSG00000238424	ENSG00000238424	AC190387.1	12:109425359-109425450	NOTEST	0	0	0	0	1	1
ENSG00000238425	ENSG00000238425	snoU13	18:2655736-2833063	NOTEST	0	0	0	0	1	1
ENSG00000238426	ENSG00000238426	Y_RNA	X:41175740-41175842	NOTEST	0	0	0	0	1	1
ENSG00000238427	ENSG00000238427	RNU7-136P	3:159943422-160203561	NOTEST	0	0	0	0	1	1
ENSG00000238428	ENSG00000238428	snoU13	2:219049701-219049805	NOTEST	0	0	0	0	1	1
ENSG00000238430	ENSG00000238430	snoU13	1:173469602-173639001	NOTEST	0	0	0	0	1	1
ENSG00000238431	ENSG00000238431	RNU7-157P	7:57294707-57294773	NOTEST	0	0	0	0	1	1
ENSG00000238432	ENSG00000238432	U6	GL000213.1:108006-139339	NOTEST	0	0	0	0	1	1
ENSG00000238433	ENSG00000238433	snoU13	8:59574799-59574903	NOTEST	0	0	0	0	1	1
ENSG00000238436	ENSG00000238436	snoU13	12:58062726-58062822	NOTEST	0	0	0	0	1	1
ENSG00000238437	ENSG00000238437	snoU13	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000238438	ENSG00000238438	snoU13	6:1186752-1186855	NOTEST	0	0	0	0	1	1
ENSG00000238440	ENSG00000238440	snoU13	12:64616116-64790845	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238441	ENSG00000238441	RNU7-130P	5:35617945-35827120	NOTEST	0	0	0	0	1	1
ENSG00000238442	ENSG00000238442	CR383657.1	14:19253847-19253930	NOTEST	0	0	0	0	1	1
ENSG00000238443	ENSG00000238443	Y_RNA	12:133815040-133815135	NOTEST	0	0	0	0	1	1
ENSG00000238444	ENSG00000238444	RNU6-893P	11:111895537-112095422	NOTEST	0	0	0	0	1	1
ENSG00000238445	ENSG00000238445	snoU13	18:3496029-4455335	NOTEST	0	0	0	0	1	1
ENSG00000238446	ENSG00000238446	RNU7-38P	10:73576054-73611126	NOTEST	0	0	0	0	1	1
ENSG00000238447	ENSG00000238447	RNU7-134P	17:55762889-55762953	NOTEST	0	0	0	0	1	1
ENSG00000238448	ENSG00000238448	AL121652.2	2:32035263-32035357	NOTEST	0	0	0	0	1	1
ENSG00000238449	ENSG00000238449	AC019131.1	4:99792834-99916145	NOTEST	0	0	0	0	1	1
ENSG00000238450	ENSG00000238450	snoU13	8:71485676-71520622	NOTEST	0	0	0	0	1	1
ENSG00000238451	ENSG00000238451	snoU13	5:70370051-70389020	NOTEST	0	0	0	0	1	1
ENSG00000238452	ENSG00000238452	RNU7-144P	20:47122479-47122555	NOTEST	0	0	0	0	1	1
ENSG00000238453	ENSG00000238453	snoU13	7:77045989-77054760	NOTEST	0	0	0	0	1	1
ENSG00000238455	ENSG00000238455	snoU13	13:57133757-57133859	NOTEST	0	0	0	0	1	1
ENSG00000238456	ENSG00000238456	RNU6-1014P	15:46952855-46952958	NOTEST	0	0	0	0	1	1
ENSG00000238457	ENSG00000238457	RNU7-169P	12:109038884-109125372	NOTEST	0	0	0	0	1	1
ENSG00000238458	ENSG00000238458	snoU13	6:18366966-18469105	NOTEST	0	0	0	0	1	1
ENSG00000238459	ENSG00000238459	snoU13	7:98475555-98741723	NOTEST	0	0	0	0	1	1
ENSG00000238460	ENSG00000238460	AC068587.2	8:12435513-12435661	NOTEST	0	0	0	0	1	1
ENSG00000238462	ENSG00000238462	snoU13	2:9613786-9695921	NOTEST	0	0	0	0	1	1
ENSG00000238463	ENSG00000238463	snoU13	13:95672082-95953687	NOTEST	0	0	0	0	1	1
ENSG00000238464	ENSG00000238464	snoU13	6:74078277-74161999	NOTEST	0	0	0	0	1	1
ENSG00000238465	ENSG00000238465	snoU13	2:70120691-70170077	NOTEST	0	0	0	0	1	1
ENSG00000238466	ENSG00000238466	snoU13	8:21881635-21894408	NOTEST	0	0	0	0	1	1
ENSG00000238468	ENSG00000238468	RNU7-14P	20:52285235-52285297	NOTEST	0	0	0	0	1	1
ENSG00000238469	ENSG00000238469	AC091487.1	10:86623020-86623118	NOTEST	0	0	0	0	1	1
ENSG00000238470	ENSG00000238470	AC097361.1	3:29052732-29052827	NOTEST	0	0	0	0	1	1
ENSG00000238471	ENSG00000238471	U2	GL000216.1:88882-88995	NOTEST	0	0	0	0	1	1
ENSG00000238472	ENSG00000238472	snoU13	10:101779350-101779456	NOTEST	0	0	0	0	1	1
ENSG00000238473	ENSG00000238473	snoU13	X:47941135-47941239	NOTEST	0	0	0	0	1	1
ENSG00000238474	ENSG00000238474	snoU13	6:109612230-109676266	NOTEST	0	0	0	0	1	1
ENSG00000238475	ENSG00000238475	snoU13	12:63037761-63328817	NOTEST	0	0	0	0	1	1
ENSG00000238476	ENSG00000238476	Y_RNA	GL000223.1:18463-18566	NOTEST	0	0	0	0	1	1
ENSG00000238477	ENSG00000238477	CU442762.1	GL000247.1:11985-12067	NOTEST	0	0	0	0	1	1
ENSG00000238478	ENSG00000238478	RNU6-498P	15:20935075-20961512	NOTEST	0	0	0	0	1	1
ENSG00000238480	ENSG00000238480	snoU13	3:122458845-122512671	NOTEST	0	0	0	0	1	1
ENSG00000238481	ENSG00000238481	snoU13	2:157278706-157278811	NOTEST	0	0	0	0	1	1
ENSG00000238482	ENSG00000238482	RNU6-1208P	1:25071847-25170815	NOTEST	0	0	0	0	1	1
ENSG00000238483	ENSG00000238483	snoU13	13:46786082-46851501	NOTEST	0	0	0	0	1	1
ENSG00000238484	ENSG00000238484	snoU13	6:34555064-34665247	NOTEST	0	0	0	0	1	1
ENSG00000238485	ENSG00000238485	snoU13	X:138663928-138790386	NOTEST	0	0	0	0	1	1
ENSG00000238486	ENSG00000238486	snoU13	19:52172657-52172761	NOTEST	0	0	0	0	1	1
ENSG00000238487	ENSG00000238487	RNU7-114P	12:114040595-114040658	NOTEST	0	0	0	0	1	1
ENSG00000238488	ENSG00000238488	snoU13	7:136370305-136866854	NOTEST	0	0	0	0	1	1
ENSG00000238489	ENSG00000238489	RNU6-749P	15:21040700-21071643	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238490	ENSG00000238490	Y_RNA	6:108362612-108487058	NOTEST	0	0	0	0	1	1
ENSG00000238491	ENSG00000238491	snoU13	3:197066327-197066422	NOTEST	0	0	0	0	1	1
ENSG00000238492	ENSG00000238492	snoU13	14:20187173-20296531	NOTEST	0	0	0	0	1	1
ENSG00000238493	ENSG00000238493	RNU6-221P	2:55683241-55683340	NOTEST	0	0	0	0	1	1
ENSG00000238494	ENSG00000238494	snoU13	15:43885251-44010458	NOTEST	0	0	0	0	1	1
ENSG00000238496	ENSG00000238496	snoU13	8:9789229-9789333	NOTEST	0	0	0	0	1	1
ENSG00000238498	ENSG00000238498	snoU13	22:42470254-42475445	NOTEST	0	0	0	0	1	1
ENSG00000238500	ENSG00000238500	RNU7-87P	13:66876966-67804468	NOTEST	0	0	0	0	1	1
ENSG00000238501	ENSG00000238501	snoU13	14:45036115-45036209	NOTEST	0	0	0	0	1	1
ENSG00000238502	ENSG00000238502	snoU13	15:102193800-102264807	NOTEST	0	0	0	0	1	1
ENSG00000238503	ENSG00000238503	SNORD18	2:11988747-12718474	NOTEST	0	0	0	0	1	1
ENSG00000238504	ENSG00000238504	AP005638.1	11:132284870-133402414	NOTEST	0	0	0	0	1	1
ENSG00000238506	ENSG00000238506	snoU13	7:52391493-52391585	NOTEST	0	0	0	0	1	1
ENSG00000238507	ENSG00000238507	snoU13	16:62438154-62438258	NOTEST	0	0	0	0	1	1
ENSG00000238508	ENSG00000238508	AC024569.1	5:52856462-52979168	NOTEST	0	0	0	0	1	1
ENSG00000238509	ENSG00000238509	RNU6-104P	8:43147625-43218661	NOTEST	0	0	0	0	1	1
ENSG00000238511	ENSG00000238511	snoU13	1:153700542-153746555	NOTEST	0	0	0	0	1	1
ENSG00000238512	ENSG00000238512	AC117401.1	3:123780840-123780931	NOTEST	0	0	0	0	1	1
ENSG00000238513	ENSG00000238513	snoU13	15:56119119-56285944	NOTEST	0	0	0	0	1	1
ENSG00000238514	ENSG00000238514	snoU13	19:29374336-29444152	NOTEST	0	0	0	0	1	1
ENSG00000238515	ENSG00000238515	snoU13	10:23688459-23688528	NOTEST	0	0	0	0	1	1
ENSG00000238516	ENSG00000238516	Y_RNA	17:27082995-27188085	NOTEST	0	0	0	0	1	1
ENSG00000238517	ENSG00000238517	MIR1270-1	19:20451077-20607775	NOTEST	0	0	0	0	1	1
ENSG00000238518	ENSG00000238518	AC020900.1	5:95220801-96143803	NOTEST	0	0	0	0	1	1
ENSG00000238519	ENSG00000238519	U8	15:30653442-30686052	NOTEST	0	0	0	0	1	1
ENSG00000238520	ENSG00000238520	snoU13	2:115038660-115038752	NOTEST	0	0	0	0	1	1
ENSG00000238521	ENSG00000238521	snoU13	2:75645971-75646075	NOTEST	0	0	0	0	1	1
ENSG00000238522	ENSG00000238522	snoU13	13:97709632-97709734	NOTEST	0	0	0	0	1	1
ENSG00000238523	ENSG00000238523	RNU7-107P	10:52065359-52401211	NOTEST	0	0	0	0	1	1
ENSG00000238524	ENSG00000238524	AL592170.2	GL000222.1:122778-122874	NOTEST	0	0	0	0	1	1
ENSG00000238525	ENSG00000238525	snoU13	3:101043048-101232085	NOTEST	0	0	0	0	1	1
ENSG00000238526	ENSG00000238526	snoU13	1:150227488-150237478	NOTEST	0	0	0	0	1	1
ENSG00000238528	ENSG00000238528	snoU13	12:66739498-66739602	NOTEST	0	0	0	0	1	1
ENSG00000238529	ENSG00000238529	RNU6-599P	9:44076367-44118444	NOTEST	0	0	0	0	1	1
ENSG00000238530	ENSG00000238530	snoU13	9:117327529-117327632	NOTEST	0	0	0	0	1	1
ENSG00000238531	ENSG00000238531	SNORD105B	19:10216898-10230596	NOTEST	0	0	0	0	1	1
ENSG00000238532	ENSG00000238532	AL355794.1	1:117117030-117210375	NOTEST	0	0	0	0	1	1
ENSG00000238533	ENSG00000238533	snoU13	8:103251621-103425069	NOTEST	0	0	0	0	1	1
ENSG00000238534	ENSG00000238534	Y_RNA	7:6201406-6312275	NOTEST	0	0	0	0	1	1
ENSG00000238535	ENSG00000238535	snoU13	15:43885251-44010458	NOTEST	0	0	0	0	1	1
ENSG00000238536	ENSG00000238536	snoU13	4:17530559-17530663	NOTEST	0	0	0	0	1	1
ENSG00000238537	ENSG00000238537	snoU13	18:20279443-20606451	NOTEST	0	0	0	0	1	1
ENSG00000238538	ENSG00000238538	snoU13	1:24197015-24285549	NOTEST	0	0	0	0	1	1
ENSG00000238540	ENSG00000238540	RNU7-93P	14:36874418-36874479	NOTEST	0	0	0	0	1	1
ENSG00000238541	ENSG00000238541	snoU13	4:57829535-58071676	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238542	ENSG00000238542	RNU7-104P	2:179385909-179914813	NOTEST	0	0	0	0	1	1
ENSG00000238543	ENSG00000238543	snoU13	2:157266655-157266758	NOTEST	0	0	0	0	1	1
ENSG00000238544	ENSG00000238544	snoU13	16:50280047-50405391	NOTEST	0	0	0	0	1	1
ENSG00000238545	ENSG00000238545	snoU13	1:226418849-226497570	NOTEST	0	0	0	0	1	1
ENSG00000238546	ENSG00000238546	snoU13	2:130184994-130185098	NOTEST	0	0	0	0	1	1
ENSG00000238549	ENSG00000238549	snoU13	20:34291530-34330234	NOTEST	0	0	0	0	1	1
ENSG00000238551	ENSG00000238551	RNU6-1193P	9:69381811-69425560	NOTEST	0	0	0	0	1	1
ENSG00000238552	ENSG00000238552	snoU13	10:16440653-16440758	NOTEST	0	0	0	0	1	1
ENSG00000238553	ENSG00000238553	AF213884.3	4:103422485-103538459	NOTEST	0	0	0	0	1	1
ENSG00000238554	ENSG00000238554	RNU1-88P	6:36607321-36607449	NOTEST	0	0	0	0	1	1
ENSG00000238556	ENSG00000238556	snoU13	21:40714240-40721573	NOTEST	0	0	0	0	1	1
ENSG00000238557	ENSG00000238557	snoU13	7:152293007-152293115	NOTEST	0	0	0	0	1	1
ENSG00000238558	ENSG00000238558	RNU7-21P	9:135820931-135867083	NOTEST	0	0	0	0	1	1
ENSG00000238559	ENSG00000238559	snoU13	15:40886217-40956540	NOTEST	0	0	0	0	1	1
ENSG00000238560	ENSG00000238560	Y_RNA	7:76139744-77045717	NOTEST	0	0	0	0	1	1
ENSG00000238561	ENSG00000238561	RNU6ATAC28P	14:84216727-84216845	NOTEST	0	0	0	0	1	1
ENSG00000238562	ENSG00000238562	RNU7-159P	11:102774621-102774683	NOTEST	0	0	0	0	1	1
ENSG00000238563	ENSG00000238563	snoU13	6:114162000-114162089	NOTEST	0	0	0	0	1	1
ENSG00000238564	ENSG00000238564	snoU13	15:40226346-40327797	NOTEST	0	0	0	0	1	1
ENSG00000238565	ENSG00000238565	snoU13	3:53317215-53317319	NOTEST	0	0	0	0	1	1
ENSG00000238566	ENSG00000238566	snoU13	8:85095021-85834079	NOTEST	0	0	0	0	1	1
ENSG00000238567	ENSG00000238567	snoU13	2:171847332-172087824	NOTEST	0	0	0	0	1	1
ENSG00000238568	ENSG00000238568	snoU13	3:72622115-72622219	NOTEST	0	0	0	0	1	1
ENSG00000238569	ENSG00000238569	snoU13	22:38181532-38181614	NOTEST	0	0	0	0	1	1
ENSG00000238570	ENSG00000238570	snoU13	2:162272604-162841792	NOTEST	0	0	0	0	1	1
ENSG00000238571	ENSG00000238571	snoU13	1:202163028-202288909	NOTEST	0	0	0	0	1	1
ENSG00000238572	ENSG00000238572	snoU13	2:173020756-173020848	NOTEST	0	0	0	0	1	1
ENSG00000238575	ENSG00000238575	snoU109	18:2537523-2571508	NOTEST	0	0	0	0	1	1
ENSG00000238576	ENSG00000238576	snoU13	1:220267443-220321380	NOTEST	0	0	0	0	1	1
ENSG00000238577	ENSG00000238577	snoU13	10:116190871-116444762	NOTEST	0	0	0	0	1	1
ENSG00000238578	ENSG00000238578	SNORD4A	17:27046410-27070473	NOTEST	0	0	0	0	1	1
ENSG00000238579	ENSG00000238579	snoU13	4:57829535-58071676	NOTEST	0	0	0	0	1	1
ENSG00000238581	ENSG00000238581	snoU13	21:39493544-39679279	NOTEST	0	0	0	0	1	1
ENSG00000238582	ENSG00000238582	snoU13	2:208938784-208938886	NOTEST	0	0	0	0	1	1
ENSG00000238583	ENSG00000238583	snoU13	15:45722726-45878488	NOTEST	0	0	0	0	1	1
ENSG00000238584	ENSG00000238584	RNU7-167P	22:35645764-35645826	NOTEST	0	0	0	0	1	1
ENSG00000238585	ENSG00000238585	Y_RNA	4:56262123-56414056	NOTEST	0	0	0	0	1	1
ENSG00000238587	ENSG00000238587	snoU13	7:87133174-87461611	NOTEST	0	0	0	0	1	1
ENSG00000238588	ENSG00000238588	snoU13	10:101361536-101361637	NOTEST	0	0	0	0	1	1
ENSG00000238590	ENSG00000238590	RNU7-54P	7:128083502-128083564	NOTEST	0	0	0	0	1	1
ENSG00000238591	ENSG00000238591	snoU13	21:17080977-17081077	NOTEST	0	0	0	0	1	1
ENSG00000238592	ENSG00000238592	snoU13	12:65153300-65173098	NOTEST	0	0	0	0	1	1
ENSG00000238593	ENSG00000238593	AC078785.1	3:112709293-112902148	NOTEST	0	0	0	0	1	1
ENSG00000238594	ENSG00000238594	snoU13	6:150464211-150571493	NOTEST	0	0	0	0	1	1
ENSG00000238595	ENSG00000238595	snoU13	8:76805034-76805139	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238596	ENSG00000238596	snoU13	4:184250450-184250554	NOTEST	0	0	0	0	1	1
ENSG00000238597	ENSG00000238597	SNORD4B	17:27046410-27070473	NOTEST	0	0	0	0	1	1
ENSG00000238598	ENSG00000238598	snoU13	9:78291822-78291928	NOTEST	0	0	0	0	1	1
ENSG00000238600	ENSG00000238600	AL592183.3	GL000219.1:168105-168180	NOTEST	0	0	0	0	1	1
ENSG00000238601	ENSG00000238601	AC040163.1	16:59448676-59448749	NOTEST	0	0	0	0	1	1
ENSG00000238602	ENSG00000238602	5S_rRNA	GL000192.1:415331-415454	NOTEST	0	0	0	0	1	1
ENSG00000238603	ENSG00000238603	RNVU1-1	1:143647013-143647177	NOTEST	0	0	0	0	1	1
ENSG00000238604	ENSG00000238604	Y_RNA	22:50781732-50913454	NOTEST	0	0	0	0	1	1
ENSG00000238605	ENSG00000238605	snoU13	5:137450865-137475132	NOTEST	0	0	0	0	1	1
ENSG00000238606	ENSG00000238606	RNU7-7P	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000238607	ENSG00000238607	AC138749.1	15:28764756-28778160	NOTEST	0	0	0	0	1	1
ENSG00000238608	ENSG00000238608	snoU13	9:85857904-86153461	NOTEST	0	0	0	0	1	1
ENSG00000238609	ENSG00000238609	RNU7-94P	12:106631654-106740793	NOTEST	0	0	0	0	1	1
ENSG00000238610	ENSG00000238610	RNU7-26P	6:27865281-27865344	NOTEST	0	0	0	0	1	1
ENSG00000238611	ENSG00000238611	snoU13	6:42473237-42473344	NOTEST	0	0	0	0	1	1
ENSG00000238612	ENSG00000238612	snoU13	17:65373574-65693372	NOTEST	0	0	0	0	1	1
ENSG00000238615	ENSG00000238615	snoU13	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000238616	ENSG00000238616	RNU6-300P	6:151186684-151549582	NOTEST	0	0	0	0	1	1
ENSG00000238617	ENSG00000238617	AL591856.1	GL000224.1:137251-137327	NOTEST	0	0	0	0	1	1
ENSG00000238618	ENSG00000238618	snoU13	1:51660766-51700768	NOTEST	0	0	0	0	1	1
ENSG00000238619	ENSG00000238619	RNU6-775P	2:55678139-55678235	NOTEST	0	0	0	0	1	1
ENSG00000238620	ENSG00000238620	snoU13	10:106113521-106214848	NOTEST	0	0	0	0	1	1
ENSG00000238621	ENSG00000238621	TRNAI2	6:26924770-26991703	NOTEST	0	0	0	0	1	1
ENSG00000238622	ENSG00000238622	SNORD97	11:10804859-10830657	NOTEST	0	4.23193	inf	0	1	1
ENSG00000238623	ENSG00000238623	AC073597.1	X:16393758-16393855	NOTEST	0	0	0	0	1	1
ENSG00000238624	ENSG00000238624	snoU13	8:27590834-27695612	NOTEST	0	0	0	0	1	1
ENSG00000238625	ENSG00000238625	snoU13	11:116191060-116191162	NOTEST	0	0	0	0	1	1
ENSG00000238626	ENSG00000238626	snoU13	X:123093082-124097666	NOTEST	0	0	0	0	1	1
ENSG00000238627	ENSG00000238627	RNA5SP489	21:26541744-26706139	NOTEST	0	0	0	0	1	1
ENSG00000238628	ENSG00000238628	snoU13	6:88430632-88430736	NOTEST	0	0	0	0	1	1
ENSG00000238629	ENSG00000238629	snoU13	13:110801317-111165374	NOTEST	0	0	0	0	1	1
ENSG00000238630	ENSG00000238630	snoU13	19:52616343-52680255	NOTEST	0	0	0	0	1	1
ENSG00000238631	ENSG00000238631	snoU13	6:134490383-134639250	NOTEST	0	0	0	0	1	1
ENSG00000238632	ENSG00000238632	RNU7-126P	4:25600185-25600247	NOTEST	0	0	0	0	1	1
ENSG00000238634	ENSG00000238634	AE000660.1	14:22610886-22610964	NOTEST	0	0	0	0	1	1
ENSG00000238638	ENSG00000238638	AL353626.1	9:66858536-66858612	NOTEST	0	0	0	0	1	1
ENSG00000238639	ENSG00000238639	snoU13	16:29262828-29519817	NOTEST	0	0	0	0	1	1
ENSG00000238641	ENSG00000238641	AC008122.1	2:190744334-191236391	NOTEST	0	0	0	0	1	1
ENSG00000238642	ENSG00000238642	snoU13	3:10175068-10175172	NOTEST	0	0	0	0	1	1
ENSG00000238643	ENSG00000238643	CT978678.1	GL000229.1:17284-17399	NOTEST	0	0	0	0	1	1
ENSG00000238644	ENSG00000238644	AL117380.1	20:55629845-55629897	NOTEST	0	0	0	0	1	1
ENSG00000238645	ENSG00000238645	snoU13	16:53368473-53368576	NOTEST	0	0	0	0	1	1
ENSG00000238646	ENSG00000238646	snoU13	3:32214147-32214252	NOTEST	0	0	0	0	1	1
ENSG00000238648	ENSG00000238648	TRNAI6	6:27599187-27599311	NOTEST	0	0	0	0	1	1
ENSG00000238649	ENSG00000238649	SNORD42A	17:27046410-27070473	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238650	ENSG00000238650	SNORD54	8:56979853-56987069	NOTEST	0	0	0	0	1	1
ENSG00000238651	ENSG00000238651	snoU13	13:41754116-41754223	NOTEST	0	0	0	0	1	1
ENSG00000238652	ENSG00000238652	snoU13	4:88689636-88689733	NOTEST	0	0	0	0	1	1
ENSG00000238653	ENSG00000238653	RNU7-62P	1:64850080-64850142	NOTEST	0	0	0	0	1	1
ENSG00000238654	ENSG00000238654	snoU13	9:5881595-6007904	NOTEST	0	0	0	0	1	1
ENSG00000238656	ENSG00000238656	snoU13	8:113235156-114449328	NOTEST	0	0	0	0	1	1
ENSG00000238657	ENSG00000238657	snoU13	9:135968438-135968538	NOTEST	0	0	0	0	1	1
ENSG00000238658	ENSG00000238658	RNU6-625P	17:76000248-76139049	NOTEST	0	0	0	0	1	1
ENSG00000238660	ENSG00000238660	AP001340.1	21:26711318-26711413	NOTEST	0	0	0	0	1	1
ENSG00000238661	ENSG00000238661	snoU13	12:31433517-31479992	NOTEST	0	0	0	0	1	1
ENSG00000238662	ENSG00000238662	snoU13	2:166813908-167232503	NOTEST	0	0	0	0	1	1
ENSG00000238663	ENSG00000238663	snoU13	2:216167488-216167587	NOTEST	0	0	0	0	1	1
ENSG00000238664	ENSG00000238664	AL592183.4	GL000219.1:173993-174069	NOTEST	0	0	0	0	1	1
ENSG00000238665	ENSG00000238665	snoU13	13:20449326-20449425	NOTEST	0	0	0	0	1	1
ENSG00000238666	ENSG00000238666	snoU13	11:85805233-85805337	NOTEST	0	0	0	0	1	1
ENSG00000238667	ENSG00000238667	CU442762.2	GL000247.1:11745-11828	NOTEST	0	0	0	0	1	1
ENSG00000238669	ENSG00000238669	RNU6-333P	12:53532328-53532435	NOTEST	0	0	0	0	1	1
ENSG00000238670	ENSG00000238670	snoU13	3:121310140-121310241	NOTEST	0	0	0	0	1	1
ENSG00000238672	ENSG00000238672	AC020626.1	3:23809101-23809195	NOTEST	0	0	0	0	1	1
ENSG00000238673	ENSG00000238673	snoU13	7:56168351-56168445	NOTEST	0	0	0	0	1	1
ENSG00000238674	ENSG00000238674	snoU13	5:18844005-18844109	NOTEST	0	0	0	0	1	1
ENSG00000238676	ENSG00000238676	snoU13	17:7937804-7937902	NOTEST	0	0	0	0	1	1
ENSG00000238677	ENSG00000238677	RNA5SP58	1:147634988-147700929	NOTEST	0	0	0	0	1	1
ENSG00000238679	ENSG00000238679	snoU13	1:119573838-119869926	NOTEST	0	0	0	0	1	1
ENSG00000238680	ENSG00000238680	RNU6-1037P	18:64613352-64613459	NOTEST	0	0	0	0	1	1
ENSG00000238683	ENSG00000238683	snoU13	16:69740898-69760854	NOTEST	0	0	0	0	1	1
ENSG00000238684	ENSG00000238684	snoU13	16:28671016-28752102	NOTEST	0	0	0	0	1	1
ENSG00000238685	ENSG00000238685	ACA64	16:12070593-12704901	NOTEST	0	0	0	0	1	1
ENSG00000238686	ENSG00000238686	snoU13	11:3686816-3847601	NOTEST	0	0	0	0	1	1
ENSG00000238687	ENSG00000238687	snoU13	8:104495625-105268322	NOTEST	0	0	0	0	1	1
ENSG00000238688	ENSG00000238688	snoU13	5:76079920-76080024	NOTEST	0	0	0	0	1	1
ENSG00000238689	ENSG00000238689	RNU7-166P	12:2904118-3050306	NOTEST	0	0	0	0	1	1
ENSG00000238690	ENSG00000238690	snoU13	2:57243195-57243299	NOTEST	0	0	0	0	1	1
ENSG00000238691	ENSG00000238691	snoU13	17:18012019-18113268	NOTEST	0	0	0	0	1	1
ENSG00000238692	ENSG00000238692	snoU13	11:57093076-57103351	NOTEST	0	0	0	0	1	1
ENSG00000238693	ENSG00000238693	snoU13	11:132284870-133402414	NOTEST	0	0	0	0	1	1
ENSG00000238694	ENSG00000238694	snoU13	4:34967862-34967966	NOTEST	0	0	0	0	1	1
ENSG00000238695	ENSG00000238695	snoU13	4:142218927-142219032	NOTEST	0	0	0	0	1	1
ENSG00000238696	ENSG00000238696	snoU13	2:65135720-65135820	NOTEST	0	0	0	0	1	1
ENSG00000238697	ENSG00000238697	RNU6-261P	6:77156704-77156806	NOTEST	0	0	0	0	1	1
ENSG00000238698	ENSG00000238698	RNU7-147P	2:200055781-200055843	NOTEST	0	0	0	0	1	1
ENSG00000238699	ENSG00000238699	snoU13	16:29065052-29231352	NOTEST	0	0	0	0	1	1
ENSG00000238701	ENSG00000238701	snoU13	3:131252398-132004254	NOTEST	0	0	0	0	1	1
ENSG00000238702	ENSG00000238702	snoU13	5:50617816-50617919	NOTEST	0	0	0	0	1	1
ENSG00000238703	ENSG00000238703	snoU13	16:28453986-28454090	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238704	ENSG00000238704	RNU7-97P	17:40592215-40592277	NOTEST	0	0	0	0	1	1
ENSG00000238705	ENSG00000238705	MIR1976	1:26856251-26901521	NOTEST	0	0	0	0	1	1
ENSG00000238707	ENSG00000238707	SNORD2	10:58355722-58355791	NOTEST	0	0	0	0	1	1
ENSG00000238708	ENSG00000238708	snoU13	2:69685128-70053596	NOTEST	0	0	0	0	1	1
ENSG00000238709	ENSG00000238709	RNU7-56P	X:16785966-16786028	NOTEST	0	0	0	0	1	1
ENSG00000238711	ENSG00000238711	RNY4P25	1:151375199-151431941	NOTEST	0	0	0	0	1	1
ENSG00000238712	ENSG00000238712	snoU13	16:21845889-21930477	NOTEST	0	0	0	0	1	1
ENSG00000238713	ENSG00000238713	Y_RNA	4:145888263-146101313	NOTEST	0	0	0	0	1	1
ENSG00000238714	ENSG00000238714	snoU13	8:42083150-42083252	NOTEST	0	0	0	0	1	1
ENSG00000238715	ENSG00000238715	snoU13	15:65822755-65870687	NOTEST	0	0	0	0	1	1
ENSG00000238716	ENSG00000238716	AL031905.1	6:38136226-38607924	NOTEST	0	0	0	0	1	1
ENSG00000238717	ENSG00000238717	snoU13	5:56111400-56191979	NOTEST	0	0	0	0	1	1
ENSG00000238718	ENSG00000238718	snoU13	14:36007557-36278510	NOTEST	0	0	0	0	1	1
ENSG00000238719	ENSG00000238719	RNU7-96P	2:98372798-98612388	NOTEST	0	0	0	0	1	1
ENSG00000238720	ENSG00000238720	CT476828.2	GL000228.1:65369-65465	NOTEST	0	0	0	0	1	1
ENSG00000238721	ENSG00000238721	RNU7-194P	4:150999425-151178609	NOTEST	0	0	0	0	1	1
ENSG00000238722	ENSG00000238722	snoU13	2:2898819-3129798	NOTEST	0	0	0	0	1	1
ENSG00000238723	ENSG00000238723	Y_RNA	17:44107281-44302733	NOTEST	0	0	0	0	1	1
ENSG00000238724	ENSG00000238724	snoU13	11:114392436-114430617	NOTEST	0	0	0	0	1	1
ENSG00000238726	ENSG00000238726	AC073648.1	4:9025058-9025206	NOTEST	0	0	0	0	1	1
ENSG00000238727	ENSG00000238727	AC099540.1	3:31437428-31437523	NOTEST	0	0	0	0	1	1
ENSG00000238728	ENSG00000238728	MIR1972-1	16:15068447-15248421	NOTEST	0	0	0	0	1	1
ENSG00000238729	ENSG00000238729	snoU13	X:47138525-47138629	NOTEST	0	0	0	0	1	1
ENSG00000238730	ENSG00000238730	RNU7-164P	X:40394753-40394815	NOTEST	0	0	0	0	1	1
ENSG00000238731	ENSG00000238731	RNU7-90P	16:72699068-73093597	NOTEST	0	0	0	0	1	1
ENSG00000238732	ENSG00000238732	snoU13	10:43278248-43330385	NOTEST	0	0	0	0	1	1
ENSG00000238733	ENSG00000238733	snoU13	7:128701584-128701688	NOTEST	0	0	0	0	1	1
ENSG00000238734	ENSG00000238734	snoU13	16:70253476-70279519	NOTEST	0	0	0	0	1	1
ENSG00000238735	ENSG00000238735	RNU7-113P	2:20446086-20446148	NOTEST	0	0	0	0	1	1
ENSG00000238736	ENSG00000238736	snoU13	2:219135114-219232822	NOTEST	0	0	0	0	1	1
ENSG00000238737	ENSG00000238737	AC100756.1	15:23599894-23612378	NOTEST	0	0	0	0	1	1
ENSG00000238738	ENSG00000238738	AC116345.1	5:72449937-72450011	NOTEST	0	0	0	0	1	1
ENSG00000238739	ENSG00000238739	snoU13	7:89964536-90839905	NOTEST	0	0	0	0	1	1
ENSG00000238740	ENSG00000238740	snoU13	5:68773298-69006341	NOTEST	0	0	0	0	1	1
ENSG00000238741	ENSG00000238741	SCARNA7	3:160212782-160287036	NOTEST	0	0.145036	inf	0	1	1
ENSG00000238742	ENSG00000238742	MIR2110	10:115880620-115933979	NOTEST	0	0	0	0	1	1
ENSG00000238744	ENSG00000238744	snoU13	4:169137443-169239958	NOTEST	0	0	0	0	1	1
ENSG00000238745	ENSG00000238745	snoU13	5:137946655-138270723	NOTEST	0	0	0	0	1	1
ENSG00000238746	ENSG00000238746	snoU13	9:97861335-98079991	NOTEST	0	0	0	0	1	1
ENSG00000238747	ENSG00000238747	snoU13	6:90533013-90533115	NOTEST	0	0	0	0	1	1
ENSG00000238748	ENSG00000238748	snoU13	12:100750856-100815837	NOTEST	0	0	0	0	1	1
ENSG00000238749	ENSG00000238749	Y_RNA	9:45004878-45023236	NOTEST	0	0	0	0	1	1
ENSG00000238750	ENSG00000238750	RNU7-27P	7:127984134-127984196	NOTEST	0	0	0	0	1	1
ENSG00000238752	ENSG00000238752	snoU13	11:65818199-65837090	NOTEST	0	0	0	0	1	1
ENSG00000238753	ENSG00000238753	snoU13	4:54243809-55164414	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238754	ENSG00000238754	snoU109	1:192981379-193060907	NOTEST	0	0	0	0	1	1
ENSG00000238755	ENSG00000238755	RP11-23D24.2	3:153102722-153697975	NOTEST	0.0332442	0.0835029	1.32873	0	1	1
ENSG00000238756	ENSG00000238756	snoU13	2:53759809-54087297	NOTEST	0	0	0	0	1	1
ENSG00000238758	ENSG00000238758	AL512791.1	14:90847541-90847596	NOTEST	0	0	0	0	1	1
ENSG00000238759	ENSG00000238759	RNU7-155P	17:69294296-69294359	NOTEST	0	0	0	0	1	1
ENSG00000238760	ENSG00000238760	snoU13	2:97541619-97684341	NOTEST	0	0	0	0	1	1
ENSG00000238761	ENSG00000238761	snoU13	1:112913625-112913729	NOTEST	0	0	0	0	1	1
ENSG00000238762	ENSG00000238762	5S_rRNA	GL000228.1:22672-22791	NOTEST	0	0	0	0	1	1
ENSG00000238763	ENSG00000238763	snoU13	11:65837833-66012218	NOTEST	0	0	0	0	1	1
ENSG00000238764	ENSG00000238764	snoU13	X:17376052-17376156	NOTEST	0	0	0	0	1	1
ENSG00000238765	ENSG00000238765	RNA5SP57	1:146032646-146253110	NOTEST	0	0	0	0	1	1
ENSG00000238766	ENSG00000238766	AL513185.1	10:74127097-74385899	NOTEST	0	0	0	0	1	1
ENSG00000238767	ENSG00000238767	snoU13	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000238768	ENSG00000238768	snoU13	11:71709586-71823826	NOTEST	0	0	0	0	1	1
ENSG00000238769	ENSG00000238769	snoU13	12:77556705-77556805	NOTEST	0	0	0	0	1	1
ENSG00000238770	ENSG00000238770	snoU13	2:202937977-203062585	NOTEST	0	0	0	0	1	1
ENSG00000238771	ENSG00000238771	snoU13	1:12799692-12799796	NOTEST	0	0	0	0	1	1
ENSG00000238772	ENSG00000238772	snoU13	7:36893960-37488852	NOTEST	0	0	0	0	1	1
ENSG00000238773	ENSG00000238773	AL137855.1	1:57394882-59012474	NOTEST	0	0	0	0	1	1
ENSG00000238774	ENSG00000238774	AC009121.1	16:11343475-11445619	NOTEST	0	0	0	0	1	1
ENSG00000238775	ENSG00000238775	snoU13	6:111279762-111289093	NOTEST	0	0	0	0	1	1
ENSG00000238776	ENSG00000238776	snoU13	14:96747594-96853625	NOTEST	0	0	0	0	1	1
ENSG00000238777	ENSG00000238777	RNU7-141P	20:58427721-58427783	NOTEST	0	0	0	0	1	1
ENSG00000238778	ENSG00000238778	RNU7-80P	1:68167148-68698803	NOTEST	0	0	0	0	1	1
ENSG00000238781	ENSG00000238781	snoU13	7:4683387-4811074	NOTEST	0	0	0	0	1	1
ENSG00000238782	ENSG00000238782	RNU7-9P	2:230222344-230579274	NOTEST	0	0	0	0	1	1
ENSG00000238783	ENSG00000238783	Y_RNA	15:30647638-30647743	NOTEST	0	0	0	0	1	1
ENSG00000238785	ENSG00000238785	RNU7-92P	20:46533091-46533167	NOTEST	0	0	0	0	1	1
ENSG00000238787	ENSG00000238787	AC093577.1	1:93447793-93447865	NOTEST	0	0	0	0	1	1
ENSG00000238788	ENSG00000238788	RNU7-182P	2:127774996-127775058	NOTEST	0	0	0	0	1	1
ENSG00000238789	ENSG00000238789	RNU7-152P	6:155976096-155976160	NOTEST	0	0	0	0	1	1
ENSG00000238790	ENSG00000238790	snoU13	18:3496029-4455335	NOTEST	0	0	0	0	1	1
ENSG00000238791	ENSG00000238791	snoU13	8:95825538-96128683	NOTEST	0	0	0	0	1	1
ENSG00000238792	ENSG00000238792	snoU13	9:96995759-96995863	NOTEST	0	0	0	0	1	1
ENSG00000238793	ENSG00000238793	SNORD124	17:38175349-38256978	NOTEST	0	0	0	0	1	1
ENSG00000238796	ENSG00000238796	snoU13	5:133186547-133186648	NOTEST	0	0	0	0	1	1
ENSG00000238797	ENSG00000238797	Y_RNA	4:39408472-39453156	NOTEST	0	0	0	0	1	1
ENSG00000238798	ENSG00000238798	snoU13	1:220141942-220220000	NOTEST	0	0	0	0	1	1
ENSG00000238799	ENSG00000238799	snoU13	17:58754813-59488916	NOTEST	0	0	0	0	1	1
ENSG00000238800	ENSG00000238800	snoU13	12:101673886-101780394	NOTEST	0	0	0	0	1	1
ENSG00000238801	ENSG00000238801	snoU13	6:4643995-4644088	NOTEST	0	0	0	0	1	1
ENSG00000238802	ENSG00000238802	snoU13	4:129677180-129677284	NOTEST	0	0	0	0	1	1
ENSG00000238803	ENSG00000238803	AL732479.1	10:87359311-88126250	NOTEST	0	0	0	0	1	1
ENSG00000238804	ENSG00000238804	snoU13	17:47034011-47034115	NOTEST	0	0	0	0	1	1
ENSG00000238805	ENSG00000238805	snoU13	1:155305058-155533775	NOTEST	0	0	0	0	1	1

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ENSG00000238806	ENSG00000238806	snoU13	17:15133094-15169024	NOTEST	0	0	0	0	1	1
ENSG00000238807	ENSG00000238807	snoU13	17:3907738-4046314	NOTEST	0	0	0	0	1	1
ENSG00000238808	ENSG00000238808	RNU7-102P	8:70022747-70022809	NOTEST	0	0	0	0	1	1
ENSG00000238809	ENSG00000238809	snoU13	2:62492129-62492233	NOTEST	0	0	0	0	1	1
ENSG00000238811	ENSG00000238811	snoU13	X:112244246-112244356	NOTEST	0	0	0	0	1	1
ENSG00000238812	ENSG00000238812	RNU7-127P	2:236402732-237040444	NOTEST	0	0	0	0	1	1
ENSG00000238813	ENSG00000238813	Y_RNA	2:166813908-167232503	NOTEST	0	0	0	0	1	1
ENSG00000238815	ENSG00000238815	snoU13	17:49039534-49198226	NOTEST	0	0	0	0	1	1
ENSG00000238816	ENSG00000238816	snoU13	4:79561253-79561356	NOTEST	0	0	0	0	1	1
ENSG00000238818	ENSG00000238818	snoU13	1:16160559-16266955	NOTEST	0	0	0	0	1	1
ENSG00000238819	ENSG00000238819	SNORD11	15:46643859-46643944	NOTEST	0	0	0	0	1	1
ENSG00000238821	ENSG00000238821	snoU13	1:28832454-28865812	NOTEST	0	0	0	0	1	1
ENSG00000238822	ENSG00000238822	snoU13	12:131274144-131323811	NOTEST	0	0	0	0	1	1
ENSG00000238823	ENSG00000238823	AC215219.1	12:73184-73322	NOTEST	0	0	0	0	1	1
ENSG00000238824	ENSG00000238824	snoU13	9:140017960-140018060	NOTEST	0	0	0	0	1	1
ENSG00000238825	ENSG00000238825	RNU1-13P	1:143647637-143745417	NOTEST	0	0	0	0	1	1
ENSG00000238826	ENSG00000238826	AL359253.1	9:78505559-78977255	NOTEST	0	0	0	0	1	1
ENSG00000238827	ENSG00000238827	AC093611.1	3:13692195-13788132	NOTEST	0	0	0	0	1	1
ENSG00000238829	ENSG00000238829	RNU7-45P	2:201980826-202041410	NOTEST	0	0	0	0	1	1
ENSG00000238830	ENSG00000238830	RNU7-46P	2:99410308-99552722	NOTEST	0	0	0	0	1	1
ENSG00000238831	ENSG00000238831	RNU7-189P	12:9362158-9362217	NOTEST	0	0	0	0	1	1
ENSG00000238832	ENSG00000238832	snoU109	7:107220001-107269943	NOTEST	0	0	0	0	1	1
ENSG00000238833	ENSG00000238833	RNU1-131P	20:17189704-17189865	NOTEST	0	0	0	0	1	1
ENSG00000238834	ENSG00000238834	snoU13	16:47111613-47177908	NOTEST	0	0	0	0	1	1
ENSG00000238835	ENSG00000238835	SCARNA18	5:82348664-82649606	NOTEST	0	0	0	0	1	1
ENSG00000238836	ENSG00000238836	AC074129.1	5:38025798-38184034	NOTEST	0	0	0	0	1	1
ENSG00000238837	ENSG00000238837	RP11-646E18.2	3:182362001-182373668	NOTEST	0	0	0	0	1	1
ENSG00000238838	ENSG00000238838	snoU13	19:38826414-38861589	NOTEST	0	0	0	0	1	1
ENSG00000238840	ENSG00000238840	U8	10:4934795-5025475	NOTEST	0	0	0	0	1	1
ENSG00000238841	ENSG00000238841	snoU13	7:66093867-66309813	NOTEST	0	0	0	0	1	1
ENSG00000238842	ENSG00000238842	RNU7-106P	12:80462470-80462537	NOTEST	0	0	0	0	1	1
ENSG00000238843	ENSG00000238843	snoU13	1:156495196-156542396	NOTEST	0	0	0	0	1	1
ENSG00000238844	ENSG00000238844	AC083875.1	7:132937828-133751342	NOTEST	0	0	0	0	1	1
ENSG00000238845	ENSG00000238845	Y_RNA	15:45118568-45176978	NOTEST	0	0	0	0	1	1
ENSG00000238849	ENSG00000238849	snoU13	7:23931322-23936954	NOTEST	0	0	0	0	1	1
ENSG00000238850	ENSG00000238850	U2	GL000225.1:183251-183364	NOTEST	0	0	0	0	1	1
ENSG00000238851	ENSG00000238851	snoU13	21:37529079-37666572	NOTEST	0	0	0	0	1	1
ENSG00000238852	ENSG00000238852	snoU13	2:223536504-223574649	NOTEST	0	0	0	0	1	1
ENSG00000238853	ENSG00000238853	snoU13	14:103243812-103377837	NOTEST	0	0	0	0	1	1
ENSG00000238854	ENSG00000238854	SNORD5	8:142443928-142517330	NOTEST	0	0	0	0	1	1
ENSG00000238855	ENSG00000238855	snoU13	11:126151551-126151649	NOTEST	0	0	0	0	1	1
ENSG00000238856	ENSG00000238856	snoU13	1:224524492-224524591	NOTEST	0	0	0	0	1	1
ENSG00000238857	ENSG00000238857	snoU13	7:2577510-2595361	NOTEST	0	0	0	0	1	1
ENSG00000238858	ENSG00000238858	snoU13	17:33332106-33448541	NOTEST	0	0	0	0	1	1
ENSG00000238859	ENSG00000238859	snoU13	1:171451045-171451148	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238860	ENSG00000238860	snoU13	2:148081538-148081643	NOTEST	0	0	0	0	1	1
ENSG00000238861	ENSG00000238861	AP003064.1	11:62201015-62323707	NOTEST	0	0	0	0	1	1
ENSG00000238862	ENSG00000238862	SNORD19B	3:52529353-52742182	NOTEST	0	0	0	0	1	1
ENSG00000238863	ENSG00000238863	snoU13	18:3411605-3458409	NOTEST	0	0	0	0	1	1
ENSG00000238864	ENSG00000238864	snoU13	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000238865	ENSG00000238865	snoU13	12:92938667-92938763	NOTEST	0	0	0	0	1	1
ENSG00000238867	ENSG00000238867	AL136967.1	6:41323186-41323246	NOTEST	0	0	0	0	1	1
ENSG00000238868	ENSG00000238868	snoU13	7:139993492-140126050	NOTEST	0	0	0	0	1	1
ENSG00000238869	ENSG00000238869	snoU13	13:103374151-103374255	NOTEST	0	0	0	0	1	1
ENSG00000238870	ENSG00000238870	AC009677.1	15:70023078-70023161	NOTEST	0	0	0	0	1	1
ENSG00000238871	ENSG00000238871	snoU13	1:38179551-38230805	NOTEST	0	0	0	0	1	1
ENSG00000238872	ENSG00000238872	snoU13	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000238874	ENSG00000238874	snoU13	3:128792937-128793045	NOTEST	0	0	0	0	1	1
ENSG00000238875	ENSG00000238875	RN7SKP210	22:40139048-40289868	NOTEST	0	0	0	0	1	1
ENSG00000238876	ENSG00000238876	AL391261.1	14:66478358-66478451	NOTEST	0	0	0	0	1	1
ENSG00000238878	ENSG00000238878	snoU13	13:22066835-22178353	NOTEST	0	0	0	0	1	1
ENSG00000238880	ENSG00000238880	RNU7-59P	11:77225980-77348850	NOTEST	0	0	0	0	1	1
ENSG00000238882	ENSG00000238882	RNU6-329P	9:105018885-105018992	NOTEST	0	0	0	0	1	1
ENSG00000238883	ENSG00000238883	AC114491.1	1:107682628-108026080	NOTEST	0	0	0	0	1	1
ENSG00000238884	ENSG00000238884	RNU7-85P	8:80680376-80783994	NOTEST	0	0	0	0	1	1
ENSG00000238885	ENSG00000238885	snoU13	18:48872618-49088939	NOTEST	0	0	0	0	1	1
ENSG00000238886	ENSG00000238886	SNORD121A	9:33921690-34048947	NOTEST	0	0	0	0	1	1
ENSG00000238887	ENSG00000238887	snoU13	22:41253080-41369313	NOTEST	0	0	0	0	1	1
ENSG00000238888	ENSG00000238888	snoU13	2:8992819-9143942	NOTEST	0	0	0	0	1	1
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ENSG00000238891	ENSG00000238891	snoU13	3:15295690-15382875	NOTEST	0	0	0	0	1	1
ENSG00000238892	ENSG00000238892	snoU13	11:66886739-67025558	NOTEST	0	0	0	0	1	1
ENSG00000238893	ENSG00000238893	snoU13	13:21543456-21543555	NOTEST	0	0	0	0	1	1
ENSG00000238895	ENSG00000238895	snoU13	12:128751947-129192460	NOTEST	0	0	0	0	1	1
ENSG00000238896	ENSG00000238896	snoU13	6:11079247-11079346	NOTEST	0	0	0	0	1	1
ENSG00000238898	ENSG00000238898	RNU1-80P	17:75916179-75916340	NOTEST	0	0	0	0	1	1
ENSG00000238899	ENSG00000238899	snoU13	5:57366014-57366118	NOTEST	0	0	0	0	1	1
ENSG00000238900	ENSG00000238900	snoU13	10:12171635-12292588	NOTEST	0	0	0	0	1	1
ENSG00000238901	ENSG00000238901	snoU13	8:123682623-123706345	NOTEST	0	0	0	0	1	1
ENSG00000238902	ENSG00000238902	snoU13	3:191857183-192485553	NOTEST	0	0	0	0	1	1
ENSG00000238904	ENSG00000238904	RNU7-34P	5:118093905-118093969	NOTEST	0	0	0	0	1	1
ENSG00000238905	ENSG00000238905	snoU13	3:57327726-57530071	NOTEST	0	0	0	0	1	1
ENSG00000238906	ENSG00000238906	snoU13	7:29846101-29956682	NOTEST	0	0	0	0	1	1
ENSG00000238907	ENSG00000238907	snoU13	18:19840538-19840640	NOTEST	0	0	0	0	1	1
ENSG00000238908	ENSG00000238908	RNA5SP484	20:39482758-39482869	NOTEST	0	0	0	0	1	1
ENSG00000238909	ENSG00000238909	AC068643.1	12:103631368-103889749	NOTEST	0	0	0	0	1	1
ENSG00000238910	ENSG00000238910	snoU13	22:32329506-32353590	NOTEST	0	0	0	0	1	1
ENSG00000238911	ENSG00000238911	AC026357.1	12:33194658-33194755	NOTEST	0	0	0	0	1	1
ENSG00000238912	ENSG00000238912	Y_RNA	3:27589247-27589349	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000238914	ENSG00000238914	snoU13	12:103981050-104162636	NOTEST	0	0	0	0	1	1
ENSG00000238917	ENSG00000238917	SNORD10	17:7465191-7536700	NOTEST	0	0	0	0	1	1
ENSG00000238918	ENSG00000238918	snoU13	10:73079014-73123142	NOTEST	0	0	0	0	1	1
ENSG00000238919	ENSG00000238919	AL353763.1	9:69001998-69002081	NOTEST	0	0	0	0	1	1
ENSG00000238920	ENSG00000238920	snoU13	X:40122169-40146973	NOTEST	0	0	0	0	1	1
ENSG00000238921	ENSG00000238921	AL360178.1	6:136172833-136546733	NOTEST	0	0	0	0	1	1
ENSG00000238922	ENSG00000238922	snoU13	7:110303109-111202573	NOTEST	0	0	0	0	1	1
ENSG00000238923	ENSG00000238923	RNU7-1	12:7052140-7055166	NOTEST	0	0	0	0	1	1
ENSG00000238924	ENSG00000238924	RNU7-163P	10:1034337-1095110	NOTEST	0	0	0	0	1	1
ENSG00000238925	ENSG00000238925	snoU13	4:58357555-58361399	NOTEST	0	0	0	0	1	1
ENSG00000238926	ENSG00000238926	Y_RNA	X:71401202-71527037	NOTEST	0	0	0	0	1	1
ENSG00000238929	ENSG00000238929	snoU13	3:37238231-37238335	NOTEST	0	0	0	0	1	1
ENSG00000238930	ENSG00000238930	Y_RNA	9:45755238-45755350	NOTEST	0	0	0	0	1	1
ENSG00000238931	ENSG00000238931	snoU13	1:65886247-66107242	NOTEST	0	0	0	0	1	1
ENSG00000238932	ENSG00000238932	snoU13	13:45202704-45202809	NOTEST	0	0	0	0	1	1
ENSG00000238933	ENSG00000238933	Y_RNA	9:44850220-44850332	NOTEST	0	0	0	0	1	1
ENSG00000238934	ENSG00000238934	ACA64	1:161110997-161111126	NOTEST	0	0	0	0	1	1
ENSG00000238935	ENSG00000238935	snoU13	7:75742115-75742214	NOTEST	0	0	0	0	1	1
ENSG00000238936	ENSG00000238936	SNORD65	8:41284173-41284246	NOTEST	0	0	0	0	1	1
ENSG00000238938	ENSG00000238938	snoU13	6:128934345-128934452	NOTEST	0	0	0	0	1	1
ENSG00000238939	ENSG00000238939	snoU13	6:151561133-151679692	NOTEST	0	0	0	0	1	1
ENSG00000238940	ENSG00000238940	snoU13	12:102139274-102224716	NOTEST	0	0	0	0	1	1
ENSG00000238941	ENSG00000238941	RNU6-953P	15:45646976-45647083	NOTEST	0	0	0	0	1	1
ENSG00000238942	ENSG00000238942	SNORD2	3:186499568-186524847	NOTEST	0	0	0	0	1	1
ENSG00000238943	ENSG00000238943	Y_RNA	12:8745071-8745181	NOTEST	0	0	0	0	1	1
ENSG00000238945	ENSG00000238945	snoU13	1:45794834-45956872	NOTEST	0	0	0	0	1	1
ENSG00000238946	ENSG00000238946	snoU13	17:1472560-1532180	NOTEST	0	0	0	0	1	1
ENSG00000238947	ENSG00000238947	snoU13	17:80059335-80170706	NOTEST	0	0	0	0	1	1
ENSG00000238948	ENSG00000238948	snoU13	4:103715539-103790053	NOTEST	0	0	0	0	1	1
ENSG00000238949	ENSG00000238949	RNU7-66P	6:67438735-67438797	NOTEST	0	0	0	0	1	1
ENSG00000238950	ENSG00000238950	RNU7-173P	20:46455712-46455788	NOTEST	0	0	0	0	1	1
ENSG00000238951	ENSG00000238951	snoU13	2:113028847-113028944	NOTEST	0	0	0	0	1	1
ENSG00000238952	ENSG00000238952	AC099757.1	1:244617678-244804479	NOTEST	0	0	0	0	1	1
ENSG00000238953	ENSG00000238953	U6atac	GL000192.1:91795-91912	NOTEST	0	0	0	0	1	1
ENSG00000238954	ENSG00000238954	snoU13	16:21413557-21531765	NOTEST	0	0	0	0	1	1
ENSG00000238957	ENSG00000238957	AL512640.1	10:44529987-44530059	NOTEST	0	0	0	0	1	1
ENSG00000238958	ENSG00000238958	AC098649.1	3:44803208-44914868	NOTEST	0	0	0	0	1	1
ENSG00000238959	ENSG00000238959	RNU7-19P	3:72937223-73118350	NOTEST	0	0	0	0	1	1
ENSG00000238960	ENSG00000238960	snoU13	15:22278009-22413497	NOTEST	0	0	0	0	1	1
ENSG00000238961	ENSG00000238961	SNORA47	5:76367896-76462734	NOTEST	0	0	0	0	1	1
ENSG00000238962	ENSG00000238962	RNU7-176P	2:10861774-10978103	NOTEST	0	0	0	0	1	1
ENSG00000238963	ENSG00000238963	U8	6:155054458-155635627	NOTEST	0	0	0	0	1	1
ENSG00000238964	ENSG00000238964	RNU7-125P	16:14726671-14763093	NOTEST	0	0	0	0	1	1
ENSG00000238965	ENSG00000238965	RNA5SP351	11:111797867-111893308	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000238966	ENSG00000238966	SNORD112	8:41786996-41909508	NOTEST	0	0	0	0	1	1
ENSG00000238969	ENSG00000238969	snoU13	X:31115793-33357558	NOTEST	0	0	0	0	1	1
ENSG00000238970	ENSG00000238970	snoU13	10:59951277-60027694	NOTEST	0	0	0	0	1	1
ENSG00000238971	ENSG00000238971	AC093766.1	4:139732831-139732920	NOTEST	0	0	0	0	1	1
ENSG00000238972	ENSG00000238972	snoU13	14:73376144-73376231	NOTEST	0	0	0	0	1	1
ENSG00000238974	ENSG00000238974	snoU13	6:108532425-108582464	NOTEST	0	0	0	0	1	1
ENSG00000238975	ENSG00000238975	snoU13	1:113009162-113214241	NOTEST	0	0	0	0	1	1
ENSG00000238976	ENSG00000238976	AC004016.1	7:24836157-25021253	NOTEST	0	0	0	0	1	1
ENSG00000238978	ENSG00000238978	snoU13	14:82928431-82928532	NOTEST	0	0	0	0	1	1
ENSG00000238979	ENSG00000238979	snoU13	2:88310620-88310721	NOTEST	0	0	0	0	1	1
ENSG00000238980	ENSG00000238980	AL354806.1	13:81778397-81778491	NOTEST	0	0	0	0	1	1
ENSG00000238981	ENSG00000238981	snoU13	15:92378608-92378706	NOTEST	0	0	0	0	1	1
ENSG00000238982	ENSG00000238982	snoU13	18:29598334-30050447	NOTEST	0	0	0	0	1	1
ENSG00000238983	ENSG00000238983	snoU13	10:74870216-75118617	NOTEST	0	0	0	0	1	1
ENSG00000238984	ENSG00000238984	snoU13	7:137860930-137861028	NOTEST	0	0	0	0	1	1
ENSG00000238985	ENSG00000238985	snoU13	1:231031177-231031250	NOTEST	0	0	0	0	1	1
ENSG00000238986	ENSG00000238986	snoU13	1:24958206-24999758	NOTEST	0	0	0	0	1	1
ENSG00000238987	ENSG00000238987	RNU7-133P	6:14156692-14156754	NOTEST	0	0	0	0	1	1
ENSG00000238988	ENSG00000238988	snoU13	18:60790578-60987361	NOTEST	0	0	0	0	1	1
ENSG00000238991	ENSG00000238991	snoU13	10:90820787-90820888	NOTEST	0	0	0	0	1	1
ENSG00000238992	ENSG00000238992	snoU13	3:125164904-125165007	NOTEST	0	0	0	0	1	1
ENSG00000238993	ENSG00000238993	AL356585.4	GL000212.1:111480-111574	NOTEST	0	0	0	0	1	1
ENSG00000238995	ENSG00000238995	snoU13	11:82534543-82782965	NOTEST	0	0	0	0	1	1
ENSG00000238996	ENSG00000238996	snoU13	9:94903579-94922396	NOTEST	0	0	0	0	1	1
ENSG00000238997	ENSG00000238997	AC105052.1	7:102122891-102312088	NOTEST	0	0	0	0	1	1
ENSG00000238998	ENSG00000238998	RNU7-187P	11:112830001-113149158	NOTEST	0	0	0	0	1	1
ENSG00000238999	ENSG00000238999	snoU13	6:101405035-101405139	NOTEST	0	0	0	0	1	1
ENSG00000239000	ENSG00000239000	snoU13	10:67672275-69455927	NOTEST	0	0	0	0	1	1
ENSG00000239001	ENSG00000239001	RNU6-420P	4:21950637-22331953	NOTEST	0	0	0	0	1	1
ENSG00000239003	ENSG00000239003	RNU7-88P	13:60054203-60054266	NOTEST	0	0	0	0	1	1
ENSG00000239004	ENSG00000239004	RNU7-76P	7:46009255-46019790	NOTEST	0	0	0	0	1	1
ENSG00000239005	ENSG00000239005	ACA64	4:140187316-140397763	NOTEST	0	0	0	0	1	1
ENSG00000239006	ENSG00000239006	AC105941.1	1:199117725-199362435	NOTEST	0	0	0	0	1	1
ENSG00000239007	ENSG00000239007	RNU7-95P	1:53971909-54199877	NOTEST	0	0	0	0	1	1
ENSG00000239008	ENSG00000239008	ACA64	X:80112574-80112701	NOTEST	0	0	0	0	1	1
ENSG00000239010	ENSG00000239010	RNU7-74P	4:40379468-40379530	NOTEST	0	0	0	0	1	1
ENSG00000239011	ENSG00000239011	snoU13	5:118342041-118584833	NOTEST	0	0	0	0	1	1
ENSG00000239012	ENSG00000239012	AL583842.1	1:142618768-142729975	NOTEST	0	0	0	0	1	1
ENSG00000239013	ENSG00000239013	snoU13	16:48526308-48526412	NOTEST	0	0	0	0	1	1
ENSG00000239014	ENSG00000239014	SNORD108	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000239015	ENSG00000239015	snoU13	6:111967529-111967630	NOTEST	0	0	0	0	1	1
ENSG00000239017	ENSG00000239017	snoU13	X:48397844-48420997	NOTEST	0	0	0	0	1	1
ENSG00000239018	ENSG00000239018	snoU13	2:75862266-75862370	NOTEST	0	0	0	0	1	1
ENSG00000239020	ENSG00000239020	snoU13	1:17776258-17776359	NOTEST	0	0	0	0	1	1
ENSG00000239021	ENSG00000239021	RNA5SP246	7:130287671-130287790	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000239022	ENSG00000239022	AC069082.1	15:79406634-79406701	NOTEST	0	0	0	0	1	1
ENSG00000239023	ENSG00000239023	RNU1-98P	21:18091316-18091476	NOTEST	0	0	0	0	1	1
ENSG00000239024	ENSG00000239024	snoU13	17:2496503-2588909	NOTEST	0	0	0	0	1	1
ENSG00000239025	ENSG00000239025	snoU13	15:42867856-43013179	NOTEST	0	0	0	0	1	1
ENSG00000239026	ENSG00000239026	snoU13	5:174877818-174877921	NOTEST	0	0	0	0	1	1
ENSG00000239027	ENSG00000239027	snoU13	1:19858663-19858768	NOTEST	0	0	0	0	1	1
ENSG00000239028	ENSG00000239028	AL359955.1	9:69821759-69821841	NOTEST	0	0	0	0	1	1
ENSG00000239030	ENSG00000239030	RNU6-956P	7:94341720-94341823	NOTEST	0	0	0	0	1	1
ENSG00000239031	ENSG00000239031	snoU13	18:10389894-10389997	NOTEST	0	0	0	0	1	1
ENSG00000239033	ENSG00000239033	snoU13	12:31535156-31768600	NOTEST	0	0	0	0	1	1
ENSG00000239034	ENSG00000239034	snoU13	4:186506597-186877806	NOTEST	0	0	0	0	1	1
ENSG00000239035	ENSG00000239035	snoU13	15:57210820-57591479	NOTEST	0	0	0	0	1	1
ENSG00000239036	ENSG00000239036	AC010209.1	12:101049499-101049582	NOTEST	0	0	0	0	1	1
ENSG00000239037	ENSG00000239037	snoU13	X:152599612-152625568	NOTEST	0	0	0	0	1	1
ENSG00000239038	ENSG00000239038	snoU13	16:48657346-48778553	NOTEST	0	0	0	0	1	1
ENSG00000239039	ENSG00000239039	SNORD13	8:33228341-33371119	NOTEST	0	0	0	0	1	1
ENSG00000239040	ENSG00000239040	Y_RNA	4:56262123-56414056	NOTEST	0	0	0	0	1	1
ENSG00000239041	ENSG00000239041	snoU13	2:173541868-173917621	NOTEST	0	0	0	0	1	1
ENSG00000239043	ENSG00000239043	SNORD127	14:45553301-45604522	NOTEST	0	0	0	0	1	1
ENSG00000239044	ENSG00000239044	snoU13	7:129984254-129984358	NOTEST	0	0	0	0	1	1
ENSG00000239045	ENSG00000239045	snoU13	7:151722758-151819425	NOTEST	0	0	0	0	1	1
ENSG00000239046	ENSG00000239046	snoU13	1:202163028-202288909	NOTEST	0	0	0	0	1	1
ENSG00000239048	ENSG00000239048	AC008706.1	5:159556216-159556280	NOTEST	0	0	0	0	1	1
ENSG00000239049	ENSG00000239049	snoU13	2:88606878-88606982	NOTEST	0	0	0	0	1	1
ENSG00000239050	ENSG00000239050	AL354741.1	13:107627285-107627374	NOTEST	0	0	0	0	1	1
ENSG00000239051	ENSG00000239051	AL591856.2	GL000224.1:166713-166794	NOTEST	0	0	0	0	1	1
ENSG00000239052	ENSG00000239052	snoU13	2:44394763-44471523	NOTEST	0	0	0	0	1	1
ENSG00000239053	ENSG00000239053	RNU7-138P	2:10861774-10978103	NOTEST	0	0	0	0	1	1
ENSG00000239054	ENSG00000239054	snoU13	1:222988363-223179337	NOTEST	0	0	0	0	1	1
ENSG00000239055	ENSG00000239055	snoU13	9:131486723-131534693	NOTEST	0	0	0	0	1	1
ENSG00000239056	ENSG00000239056	snoU13	22:37344521-37344599	NOTEST	0	0	0	0	1	1
ENSG00000239057	ENSG00000239057	MIR500B	X:49687224-49863892	NOTEST	0	0	0	0	1	1
ENSG00000239058	ENSG00000239058	snoU13	X:123093082-124097666	NOTEST	0	0	0	0	1	1
ENSG00000239059	ENSG00000239059	snoU13	6:34555064-34665247	NOTEST	0	0	0	0	1	1
ENSG00000239060	ENSG00000239060	AL592183.5	GL000219.1:171363-171439	NOTEST	0	0	0	0	1	1
ENSG00000239061	ENSG00000239061	snoU13	14:102783713-102829253	NOTEST	0	0	0	0	1	1
ENSG00000239063	ENSG00000239063	snoU13	1:52870235-53019159	NOTEST	0	0	0	0	1	1
ENSG00000239064	ENSG00000239064	snoU13	2:71127719-71160576	NOTEST	0	0	0	0	1	1
ENSG00000239065	ENSG00000239065	snoU13	8:9724416-9724520	NOTEST	0	0	0	0	1	1
ENSG00000239066	ENSG00000239066	snoU13	22:22868059-22874613	NOTEST	0	0	0	0	1	1
ENSG00000239067	ENSG00000239067	snoU13	5:118788137-118972894	NOTEST	0	0	0	0	1	1
ENSG00000239068	ENSG00000239068	snoU13	4:53376178-53376282	NOTEST	0	0	0	0	1	1
ENSG00000239069	ENSG00000239069	Y_RNA	7:74306893-74366314	NOTEST	0	0	0	0	1	1
ENSG00000239070	ENSG00000239070	MIR1299	9:69002238-69002321	NOTEST	0	0	0	0	1	1
ENSG00000239072	ENSG00000239072	snoU13	2:70182776-70182879	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000239073	ENSG00000239073	snoU13	12:93710910-93771512	NOTEST	0	0	0	0	1	1
ENSG00000239075	ENSG00000239075	RNU6-274P	7:89383933-89384040	NOTEST	0	0	0	0	1	1
ENSG00000239077	ENSG00000239077	snoU13	2:114605709-114605813	NOTEST	0	0	0	0	1	1
ENSG00000239078	ENSG00000239078	RNU7-55P	8:8859656-8974256	NOTEST	0	0	0	0	1	1
ENSG00000239079	ENSG00000239079	snoU13	11:122526382-122685181	NOTEST	0	0	0	0	1	1
ENSG00000239080	ENSG00000239080	snoU13	X:135216475-135216579	NOTEST	0	0	0	0	1	1
ENSG00000239081	ENSG00000239081	RNU7-24P	16:24411376-24411438	NOTEST	0	0	0	0	1	1
ENSG00000239082	ENSG00000239082	RNU7-170P	12:122326636-122441833	NOTEST	0	0	0	0	1	1
ENSG00000239083	ENSG00000239083	snoU13	15:20549988-20564419	NOTEST	0	0	0	0	1	1
ENSG00000239084	ENSG00000239084	snoU13	5:118788137-118972894	NOTEST	0	0	0	0	1	1
ENSG00000239086	ENSG00000239086	snoU13	11:92085261-92629618	NOTEST	0	0	0	0	1	1
ENSG00000239087	ENSG00000239087	snoU13	18:9102627-9285983	NOTEST	0	0	0	0	1	1
ENSG00000239089	ENSG00000239089	snoU13	20:34679425-34820721	NOTEST	0	0	0	0	1	1
ENSG00000239090	ENSG00000239090	Y_RNA	9:46359241-46380257	NOTEST	0	0	0	0	1	1
ENSG00000239091	ENSG00000239091	snoU13	10:103113819-103317078	NOTEST	0	0	0	0	1	1
ENSG00000239093	ENSG00000239093	snoU13	3:187141102-187141207	NOTEST	0	0	0	0	1	1
ENSG00000239094	ENSG00000239094	snoU13	1:226503761-226503865	NOTEST	0	0	0	0	1	1
ENSG00000239095	ENSG00000239095	snoU13	6:112797739-112802838	NOTEST	0	0	0	0	1	1
ENSG00000239096	ENSG00000239096	snoU13	3:179322477-179345435	NOTEST	0	0	0	0	1	1
ENSG00000239098	ENSG00000239098	snoU13	7:24301227-24301333	NOTEST	0	0	0	0	1	1
ENSG00000239099	ENSG00000239099	RNU7-23P	11:66615703-66725847	NOTEST	0	0	0	0	1	1
ENSG00000239100	ENSG00000239100	snoU13	15:58887402-59042177	NOTEST	0	0	0	0	1	1
ENSG00000239101	ENSG00000239101	AL162430.2	1:51654134-51654223	NOTEST	0	0	0	0	1	1
ENSG00000239102	ENSG00000239102	RNU7-185P	9:8314245-10612723	NOTEST	0	0	0	0	1	1
ENSG00000239103	ENSG00000239103	snoU13	5:122179133-122390362	NOTEST	0	0	0	0	1	1
ENSG00000239105	ENSG00000239105	RNU7-73P	3:37493605-37903271	NOTEST	0	0	0	0	1	1
ENSG00000239106	ENSG00000239106	Y_RNA	1:24951901-24952004	NOTEST	0	0	0	0	1	1
ENSG00000239107	ENSG00000239107	CR392039.1	21:9907189-9968585	NOTEST	0	0	0	0	1	1
ENSG00000239108	ENSG00000239108	RNU6-1132P	2:132905163-133015542	NOTEST	0	0	0	0	1	1
ENSG00000239111	ENSG00000239111	snoU13	1:112719855-112903150	NOTEST	0	0	0	0	1	1
ENSG00000239112	ENSG00000239112	SNORD123	5:9546311-9550721	NOTEST	0	0	0	0	1	1
ENSG00000239114	ENSG00000239114	snoU13	16:30234229-30346695	NOTEST	0	0	0	0	1	1
ENSG00000239115	ENSG00000239115	RNU7-67P	8:102319594-102319656	NOTEST	0	0	0	0	1	1
ENSG00000239116	ENSG00000239116	snoU13	4:184503347-184503454	NOTEST	0	0	0	0	1	1
ENSG00000239117	ENSG00000239117	AL161669.1	14:103669522-103669601	NOTEST	0	0	0	0	1	1
ENSG00000239118	ENSG00000239118	MIR1972-2	16:70010199-70099851	NOTEST	0	0	0	0	1	1
ENSG00000239119	ENSG00000239119	RNU7-119P	3:73431583-73675149	NOTEST	0	0	0	0	1	1
ENSG00000239120	ENSG00000239120	AL121761.1	20:19715459-19715553	NOTEST	0	0	0	0	1	1
ENSG00000239121	ENSG00000239121	snoU13	16:58549382-58663790	NOTEST	0	0	0	0	1	1
ENSG00000239122	ENSG00000239122	RNU2-11P	3:195655459-195655646	NOTEST	0	0.371144	inf	0	1	1
ENSG00000239123	ENSG00000239123	snoU13	7:138145078-138274738	NOTEST	0	0	0	0	1	1
ENSG00000239124	ENSG00000239124	AC091565.1	15:23255241-23268823	NOTEST	0	0	0	0	1	1
ENSG00000239125	ENSG00000239125	snoU13	10:112327448-112364394	NOTEST	0	0	0	0	1	1
ENSG00000239126	ENSG00000239126	snoU13	3:4535031-4928977	NOTEST	0	0	0	0	1	1
ENSG00000239127	ENSG00000239127	SNORD125	22:29723668-29819182	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000239128	ENSG00000239128	snoU13	3:47205986-47388306	NOTEST	0	0	0	0	1	1
ENSG00000239129	ENSG00000239129	snoU13	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000239130	ENSG00000239130	snoU13	10:15928356-15928464	NOTEST	0	0	0	0	1	1
ENSG00000239131	ENSG00000239131	AC016706.1	2:143070508-143070577	NOTEST	0	0	0	0	1	1
ENSG00000239132	ENSG00000239132	snoU13	6:76458908-76629254	NOTEST	0	0	0	0	1	1
ENSG00000239133	ENSG00000239133	snoU13	7:98923520-99063954	NOTEST	0	0	0	0	1	1
ENSG00000239134	ENSG00000239134	snoU13	8:92476262-92476367	NOTEST	0	0	0	0	1	1
ENSG00000239135	ENSG00000239135	snoU13	17:48322256-48322365	NOTEST	0	0	0	0	1	1
ENSG00000239136	ENSG00000239136	snoU13	6:161768451-163736524	NOTEST	0	0	0	0	1	1
ENSG00000239137	ENSG00000239137	snoU13	19:55663136-55691809	NOTEST	0	0	0	0	1	1
ENSG00000239138	ENSG00000239138	AC023818.1	16:48198862-48482313	NOTEST	0	0	0	0	1	1
ENSG00000239140	ENSG00000239140	snoU13	3:12525930-12705725	NOTEST	0	0	0	0	1	1
ENSG00000239141	ENSG00000239141	snoU13	3:172607147-172859058	NOTEST	0	0	0	0	1	1
ENSG00000239142	ENSG00000239142	U8	10:5077545-5149878	NOTEST	0	0	0	0	1	1
ENSG00000239143	ENSG00000239143	Y_RNA	2:85560017-85560119	NOTEST	0	0	0	0	1	1
ENSG00000239144	ENSG00000239144	snoU13	1:48998526-50489585	NOTEST	0	0	0	0	1	1
ENSG00000239145	ENSG00000239145	snoU13	7:137805833-137805937	NOTEST	0	0	0	0	1	1
ENSG00000239146	ENSG00000239146	snoU13	3:185000728-185216845	NOTEST	0	0	0	0	1	1
ENSG00000239148	ENSG00000239148	U8	10:5029966-5060223	NOTEST	0	0	0	0	1	1
ENSG00000239149	ENSG00000239149	SNORA59A	1:12290123-12572099	NOTEST	0	0	0	0	1	1
ENSG00000239150	ENSG00000239150	AL592183.6	GL000219.1:163852-163928	NOTEST	0	0	0	0	1	1
ENSG00000239151	ENSG00000239151	RNU7-195P	15:89630308-89745591	NOTEST	0	0	0	0	1	1
ENSG00000239152	ENSG00000239152	RNA5SP310	10:46349540-46411619	NOTEST	0	0	0	0	1	1
ENSG00000239153	ENSG00000239153	snoU13	11:115497799-115497903	NOTEST	0	0	0	0	1	1
ENSG00000239154	ENSG00000239154	snoU13	11:101918173-101955291	NOTEST	0	0	0	0	1	1
ENSG00000239155	ENSG00000239155	snoU13	9:30178472-30178575	NOTEST	0	0	0	0	1	1
ENSG00000239156	ENSG00000239156	5S_rRNA	GL000228.1:20112-20230	NOTEST	0	0	0	0	1	1
ENSG00000239157	ENSG00000239157	snoU13	20:48552947-48570429	NOTEST	0	0	0	0	1	1
ENSG00000239158	ENSG00000239158	AP001178.1	18:596987-712676	NOTEST	0	0	0	0	1	1
ENSG00000239159	ENSG00000239159	snoU13	5:79407049-79551898	NOTEST	0	0	0	0	1	1
ENSG00000239160	ENSG00000239160	AL109947.1	6:109711417-109765122	NOTEST	0	0	0	0	1	1
ENSG00000239161	ENSG00000239161	snoU13	2:197059093-197458416	NOTEST	0	0	0	0	1	1
ENSG00000239163	ENSG00000239163	AC007056.1	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000239164	ENSG00000239164	RNU7-184P	12:103474727-103572453	NOTEST	0	0	0	0	1	1
ENSG00000239166	ENSG00000239166	snoU13	1:6812778-6812881	NOTEST	0	0	0	0	1	1
ENSG00000239167	ENSG00000239167	AC090841.1	3:10365706-10749716	NOTEST	0	0	0	0	1	1
ENSG00000239168	ENSG00000239168	RNU7-197P	4:149912723-149912785	NOTEST	0	0	0	0	1	1
ENSG00000239169	ENSG00000239169	SNORD109B	15:25497371-25684128	NOTEST	0	0	0	0	1	1
ENSG00000239170	ENSG00000239170	snoU13	2:233412778-233547491	NOTEST	0	0	0	0	1	1
ENSG00000239171	ENSG00000239171	snoU13	21:30565800-31312351	NOTEST	0	0	0	0	1	1
ENSG00000239172	ENSG00000239172	snoU13	16:22357256-22547842	NOTEST	0	0	0	0	1	1
ENSG00000239173	ENSG00000239173	snoU13	17:77687492-77687588	NOTEST	0	0	0	0	1	1
ENSG00000239175	ENSG00000239175	RNU6-1218P	8:29901316-29901424	NOTEST	0	0	0	0	1	1
ENSG00000239176	ENSG00000239176	snoU13	1:89990394-90402170	NOTEST	0	0	0	0	1	1
ENSG00000239178	ENSG00000239178	RNU6-671P	12:45875653-46004403	NOTEST	0	0	0	0	1	1

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ENSG00000239179	ENSG00000239179	CR392039.2	21:9907189-9968585	NOTEST	0	0	0	0	1	1
ENSG00000239180	ENSG00000239180	Y_RNA	9:72873936-72969804	NOTEST	0	0	0	0	1	1
ENSG00000239181	ENSG00000239181	AC092048.1	3:42463637-42463730	NOTEST	0	0	0	0	1	1
ENSG00000239182	ENSG00000239182	SNORA35	X:117861534-117928502	NOTEST	0	0	0	0	1	1
ENSG00000239183	ENSG00000239183	SNORA84	9:94972488-95056038	NOTEST	4.04783	0	#NAME?	0	1	1
ENSG00000239184	ENSG00000239184	RNA5SP269	8:69215702-69731257	NOTEST	0	0	0	0	1	1
ENSG00000239185	ENSG00000239185	RNU7-190P	2:117897290-117897351	NOTEST	0	0	0	0	1	1
ENSG00000239186	ENSG00000239186	snoU13	16:87117167-87438385	NOTEST	0	0	0	0	1	1
ENSG00000239188	ENSG00000239188	snoU13	X:141961745-141961849	NOTEST	0	0	0	0	1	1
ENSG00000239189	ENSG00000239189	RNU6-634P	2:55727085-55727191	NOTEST	0	0	0	0	1	1
ENSG00000239190	ENSG00000239190	RNU6-717P	12:133814920-133815024	NOTEST	0	0	0	0	1	1
ENSG00000239191	ENSG00000239191	snoU13	5:149855093-149937773	NOTEST	0	0	0	0	1	1
ENSG00000239192	ENSG00000239192	AC011363.1	5:159990126-160279221	NOTEST	0	0	0	0	1	1
ENSG00000239193	ENSG00000239193	snoU13	16:29538888-29606395	NOTEST	0	0	0	0	1	1
ENSG00000239194	ENSG00000239194	RNU1-123P	16:67423711-67427438	NOTEST	0	0	0	0	1	1
ENSG00000239195	ENSG00000239195	SNORD5	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000239196	ENSG00000239196	AL591856.3	GL000224.1:43375-43458	NOTEST	0	0	0	0	1	1
ENSG00000239197	ENSG00000239197	snoU109	15:92937057-93011958	NOTEST	0	0	0	0	1	1
ENSG00000239198	ENSG00000239198	RPL5P22	8:28107579-28200872	NOTEST	0	0	0	0	1	1
ENSG00000239199	ENSG00000239199	RPL21P6	14:55880258-55923444	NOTEST	0	0	0	0	1	1
ENSG00000239200	ENSG00000239200	RP11-536C10.1	14:19468508-19468885	NOTEST	0	0	0	0	1	1
ENSG00000239201	ENSG00000239201	RPL21P106	12:92378755-92583436	NOTEST	0	0	0	0	1	1
ENSG00000239202	ENSG00000239202	RN7SL499P	2:232510710-232510984	NOTEST	0	0	0	0	1	1
ENSG00000239203	ENSG00000239203	AC093484.4	17:16317837-16340317	NOTEST	0.289223	0.511667	0.823025	0	1	1
ENSG00000239205	ENSG00000239205	RP11-747D18.1	3:164867793-164875850	NOTEST	0	0	0	0	1	1
ENSG00000239207	ENSG00000239207	GAPDHP39	3:138372859-138553780	NOTEST	0.0183875	0	#NAME?	0	1	1
ENSG00000239210	ENSG00000239210	RPS26P55	19:35024331-35024989	NOTEST	0	0	0	0	1	1
ENSG00000239211	ENSG00000239211	RN7SL563P	8:102409862-102410161	NOTEST	0	0	0	0	1	1
ENSG00000239212	ENSG00000239212	RPL6P7	3:155093368-155462856	NOTEST	0	0	0	0	1	1
ENSG00000239215	ENSG00000239215	RPL27P12	12:124196864-124246302	NOTEST	0	0	0	0	1	1
ENSG00000239216	ENSG00000239216	RP4-712E4.2	1:119542966-119544028	NOTEST	0	0	0	0	1	1
ENSG00000239218	ENSG00000239218	RPS20P22	8:38268655-38326352	NOTEST	0	0	0	0	1	1
ENSG00000239219	ENSG00000239219	RP11-379K17.4	3:169657140-169716161	NOTEST	0.0546261	0.00379421	-3.84772	0	1	1
ENSG00000239221	ENSG00000239221	RN7SL442P	17:15879873-16256970	NOTEST	0	0	0	0	1	1
ENSG00000239223	ENSG00000239223	RPL34P31	17:25601132-25601503	NOTEST	0	0	0	0	1	1
ENSG00000239224	ENSG00000239224	RN7SL546P	14:103049226-103049514	NOTEST	0	0	0	0	1	1
ENSG00000239225	ENSG00000239225	TTTY23	Y:9748406-9749571	NOTEST	0	0	0	0	1	1
ENSG00000239226	ENSG00000239226	MRPS17P3	3:78574250-78574635	NOTEST	0	0	0	0	1	1
ENSG00000239227	ENSG00000239227	RP11-12K11.1	3:166579731-166579898	NOTEST	0	0	0	0	1	1
ENSG00000239228	ENSG00000239228	RN7SL578P	X:2959511-3030767	NOTEST	0	0	0	0	1	1
ENSG00000239230	ENSG00000239230	RN7SL95P	2:169297415-169297715	NOTEST	0	0	0	0	1	1
ENSG00000239238	ENSG00000239238	MEMO1P3	3:167606201-167606503	NOTEST	0	0	0	0	1	1
ENSG00000239247	ENSG00000239247	RN7SL589P	4:2271308-2420390	NOTEST	0.207937	0.0771155	-1.43105	0	1	1
ENSG00000239249	ENSG00000239249	RN7SL757P	22:28247656-29075853	NOTEST	0	0	0	0	1	1
ENSG00000239250	ENSG00000239250	RN7SL271P	3:71876327-71876614	NOTEST	0	0	0	0	1	1

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ENSG00000239253	ENSG00000239253	RPS4XP23	19:34512563-34512800	NOTEST	0	0	0	0	1	1
ENSG00000239254	ENSG00000239254	RP11-365F18.3	7:138818489-138876732	NOTEST	0.0775689	0.0438779	-0.821983	0	1	1
ENSG00000239255	ENSG00000239255	RP11-145M9.2	3:179170182-179170207	NOTEST	0	0	0	0	1	1
ENSG00000239256	ENSG00000239256	RPL35AP35	17:27667499-27667840	NOTEST	0	0	0	0	1	1
ENSG00000239261	ENSG00000239261	RPL31P41	8:66067641-66068013	NOTEST	0	0	0	0	1	1
ENSG00000239263	ENSG00000239263	RBM43P1	3:69219140-69591734	NOTEST	0	0	0	0	1	1
ENSG00000239265	ENSG00000239265	CLRN1-AS1	3:150570270-150798513	NOTEST	0	0	0	0	1	1
ENSG00000239268	ENSG00000239268	RP11-384F7.2	3:115521234-117716439	NOTEST	0.0387855	0.112704	1.53894	0	1	1
ENSG00000239269	ENSG00000239269	RPSAP4	14:95192624-95193512	NOTEST	0.134377	0.108429	-0.309534	0	1	1
ENSG00000239272	ENSG00000239272	RPL21P10	14:78138746-78174363	NOTEST	0.0868743	0.036286	-1.25952	0	1	1
ENSG00000239275	ENSG00000239275	RP4-675G8.2	1:44603513-44604485	NOTEST	0	0	0	0	1	1
ENSG00000239279	ENSG00000239279	RN7SL184P	4:114340995-114341290	NOTEST	0	0	0	0	1	1
ENSG00000239280	ENSG00000239280	RP11-271C24.3	3:113435306-113465147	NOTEST	0.106974	0	#NAME?	0	1	1
ENSG00000239281	ENSG00000239281	RPS29P2	8:41119480-41167016	NOTEST	0	0	0	0	1	1
ENSG00000239285	ENSG00000239285	LY6G5B	HSCHR6_MHC_QBL:31619245-31631569	NOTEST	0	0	0	0	1	1
ENSG00000239288	ENSG00000239288	RP11-59E19.3	3:108960353-108961972	NOTEST	0	0	0	0	1	1
ENSG00000239291	ENSG00000239291	RP5-867C24.1	17:45195068-45266788	NOTEST	0.0430772	0	#NAME?	0	1	1
ENSG00000239293	ENSG00000239293	OR9P1P	7:142744313-142744681	NOTEST	0	0	0	0	1	1
ENSG00000239300	ENSG00000239300	RP11-400L8.2	2:9613786-9695921	NOTEST	0	0	0	0	1	1
ENSG00000239304	ENSG00000239304	DNM1P48	Y:27624415-27633809	NOTEST	0	0	0	0	1	1
ENSG00000239311	ENSG00000239311	RP11-615J4.3	3:111011565-111384597	NOTEST	0	0	0	0	1	1
ENSG00000239314	ENSG00000239314	MORC1-AS1	3:108677085-108836989	NOTEST	0	0	0	0	1	1
ENSG00000239315	ENSG00000239315	RPL19P13	8:11105134-11125374	NOTEST	0	0	0	0	1	1
ENSG00000239316	ENSG00000239316	RN7SL11P	6:90142888-90348472	NOTEST	0	0	0	0	1	1
ENSG00000239317	ENSG00000239317	RP11-449H3.2	5:145463948-145562223	NOTEST	0	0	0	0	1	1
ENSG00000239319	ENSG00000239319	RN7SL854P	1:66226742-66227035	NOTEST	0	0	0	0	1	1
ENSG00000239320	ENSG00000239320	RPS29P26	19:40088471-40088642	NOTEST	0	0	0	0	1	1
ENSG00000239323	ENSG00000239323	CTD-2213F21.1	14:31932000-31932577	NOTEST	0	0	0	0	1	1
ENSG00000239327	ENSG00000239327	RP11-14J7.1	14:21084802-21085150	NOTEST	0	0	0	0	1	1
ENSG00000239329	ENSG00000239329	HLA-DMB	HSCHR6_MHC_MANN:3305621933103106	NOTEST	0	0	0	0	1	1
ENSG00000239332	ENSG00000239332	LINC01119	2:47043806-47086146	NOTEST	0.0545578	0.0667233	0.290404	0	1	1
ENSG00000239333	ENSG00000239333	RN7SL658P	X:16557261-16557562	NOTEST	0	0	0	0	1	1
ENSG00000239334	ENSG00000239334	GSTTP2	22:24385937-24401899	NOTEST	0	0	0	0	1	1
ENSG00000239344	ENSG00000239344	RP11-771F20.1	8:104495625-105268322	NOTEST	0	0	0	0	1	1
ENSG00000239345	ENSG00000239345	HNRNPA1P26	X:100098312-100129334	NOTEST	0	0	0	0	1	1
ENSG00000239350	ENSG00000239350	RP11-398A8.2	3:72084450-72291716	NOTEST	0	0	0	0	1	1
ENSG00000239351	ENSG00000239351	NPM1P29	3:149478891-149942977	NOTEST	0	0	0	0	1	1
ENSG00000239353	ENSG00000239353	RP11-492E3.51	9:132245729-132275965	NOTEST	0.147439	0.157473	0.094983	0	1	1
ENSG00000239354	ENSG00000239354	RPS17P15	11:110976270-110976619	NOTEST	0	0	0	0	1	1
ENSG00000239356	ENSG00000239356	RN7SL309P	11:65463005-65463306	NOTEST	0	0	0	0	1	1
ENSG00000239365	ENSG00000239365	RPS26P49	14:105297174-105297508	NOTEST	0	0	0	0	1	1
ENSG00000239367	ENSG00000239367	RN7SL477P	19:1570573-1570859	NOTEST	0.126172	0	#NAME?	0	1	1
ENSG00000239373	ENSG00000239373	RN7SL425P	1:171454650-171562650	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000239374	ENSG00000239374	RP11-407P2.1	12:117176095-117291436	NOTEST	0	0	0	0	1	1
ENSG00000239377	ENSG00000239377	RP4-584D14.6	7:150060865-150109558	NOTEST	0.350708	0.404903	0.207308	0	1	1
ENSG00000239381	ENSG00000239381	RP11-4B14.3	3:180701496-181554668	NOTEST	0	0	0	0	1	1
ENSG00000239383	ENSG00000239383	RP11-413E6.2	3:75639448-75639800	NOTEST	0	0	0	0	1	1
ENSG00000239388	ENSG00000239388	ASB14	3:57261764-57326710	NOTEST	0.220044	0.222232	0.0142755	0	1	1
ENSG00000239389	ENSG00000239389	PCDHA13	5:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000239390	ENSG00000239390	RN7SL87P	5:143520443-143520729	NOTEST	0	0	0	0	1	1
ENSG00000239392	ENSG00000239392	RP11-537H15.4	9:34133154-34134694	NOTEST	0	0	0	0	1	1
ENSG00000239393	ENSG00000239393	CTD-2301A4.1	5:176758562-176778853	NOTEST	0	0	0	0	1	1
ENSG00000239395	ENSG00000239395	RP11-634B7.5	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000239396	ENSG00000239396	RN7SL414P	2:45615818-45839304	NOTEST	0	0	0	0	1	1
ENSG00000239397	ENSG00000239397	RP11-101K23.1	12:46397820-46398468	NOTEST	0	0	0	0	1	1
ENSG00000239398	ENSG00000239398	RN7SL342P	18:57640145-57640437	NOTEST	0	0	0	0	1	1
ENSG00000239402	ENSG00000239402	CYP4F62P	2:131174327-131199048	NOTEST	0	0	0	0	1	1
ENSG00000239405	ENSG00000239405	TMED10P2	3:128256862-128257474	NOTEST	0	0.0262236	inf	0	1	1
ENSG00000239408	ENSG00000239408	RP11-278L15.4	3:149182625-149182988	NOTEST	0	0	0	0	1	1
ENSG00000239412	ENSG00000239412	RPL21P71	3:146627471-147088443	NOTEST	0	0	0	0	1	1
ENSG00000239413	ENSG00000239413	RPS27P23	12:101818218-101818469	NOTEST	0	0	0	0	1	1
ENSG00000239419	ENSG00000239419	RN7SL535P	7:142985307-143004789	NOTEST	0.678803	0.0836188	-3.02109	0	1	1
ENSG00000239426	ENSG00000239426	OR8F1P	11:124077889-124078822	NOTEST	0	0	0	0	1	1
ENSG00000239428	ENSG00000239428	GM2AP2	1:171361367-171361929	NOTEST	0	0	0	0	1	1
ENSG00000239429	ENSG00000239429	RP11-45D17.1	X:150732093-150845211	NOTEST	0	0	0	0	1	1
ENSG00000239432	ENSG00000239432	GS1-388B5.8	3:125474928-125475305	NOTEST	0	0	0	0	1	1
ENSG00000239435	ENSG00000239435	KCNMB3P1	22:17061815-17063607	NOTEST	0.215446	0	#NAME?	0	1	1
ENSG00000239437	ENSG00000239437	RN7SL752P	3:129274017-129325661	NOTEST	0	0	0	0	1	1
ENSG00000239438	ENSG00000239438	RP11-332E19.1	14:78697623-78697962	NOTEST	0	0	0	0	1	1
ENSG00000239439	ENSG00000239439	RFKP2	3:111749777-111750496	NOTEST	0	0	0	0	1	1
ENSG00000239440	ENSG00000239440	RP11-260O18.1	3:82035288-82512826	NOTEST	0	0	0	0	1	1
ENSG00000239443	ENSG00000239443	PABPC1P10	3:155027215-155027596	NOTEST	0	0	0	0	1	1
ENSG00000239446	ENSG00000239446	RP1-76B20.12	22:30101244-30115848	NOTEST	0	0	0	0	1	1
ENSG00000239453	ENSG00000239453	SIDT1-AS1	3:113251142-113348425	NOTEST	0	0	0	0	1	1
ENSG00000239454	ENSG00000239454	RP11-508O18.1	3:74048955-74054760	NOTEST	0	0	0	0	1	1
ENSG00000239455	ENSG00000239455	RP11-561O4.1	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000239457	ENSG00000239457	HLA-DOB	HSCHR6_MHC_SSTO:32870614-32874900	NOTEST	0	0	0	0	1	1
ENSG00000239462	ENSG00000239462	CTD-2021J15.1	3:98621267-98737406	NOTEST	0	0.148212	inf	0	1	1
ENSG00000239463	ENSG00000239463	HLA-DMA	HSCHR6_MHC_MCF:32935859-32980443	NOTEST	0	0	0	0	1	1
ENSG00000239464	ENSG00000239464	RN7SL691P	4:43600558-43600854	NOTEST	0	0	0	0	1	1
ENSG00000239465	ENSG00000239465	RP11-330L19.2	15:64752940-64978264	NOTEST	0	0	0	0	1	1
ENSG00000239466	ENSG00000239466	RN7SL552P	4:85590703-85932430	NOTEST	0.121257	0	#NAME?	0	1	1
ENSG00000239468	ENSG00000239468	RN7SL569P	7:148587305-148587607	NOTEST	0	0	0	0	1	1
ENSG00000239470	ENSG00000239470	RP11-16F15.2	11:9681945-9682503	NOTEST	0.411041	0.316274	-0.378109	0	1	1
ENSG00000239471	ENSG00000239471	RN7SL584P	15:20300987-20301282	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000239472	ENSG00000239472	RN7SL221P	6:5918792-5919077	NOTEST	0	0	0	0	1	1
ENSG00000239473	ENSG00000239473	RPL7P38	12:80422672-80423411	NOTEST	0.0261513	0	#NAME?	0	1	1
ENSG00000239475	ENSG00000239475	HYDIN2	1:146310554-146349531	NOTEST	0	0	0	0	1	1
ENSG00000239480	ENSG00000239480	RP11-514P8.2	7:102067264-102105323	NOTEST	0.07454	0.0312716	-1.25316	0	1	1
ENSG00000239481	ENSG00000239481	RPS3AP41	11:71380565-71381343	NOTEST	0	0	0	0	1	1
ENSG00000239483	ENSG00000239483	RPS15AP16	3:128444964-128533639	NOTEST	0.382317	0.734956	0.94289	0	1	1
ENSG00000239486	ENSG00000239486	RP11-163E9.1	7:102004318-102067123	NOTEST	0	0	0	0	1	1
ENSG00000239490	ENSG00000239490	RPS4XP18	18:20166427-20167190	NOTEST	0	0	0	0	1	1
ENSG00000239492	ENSG00000239492	FAM25HP	10:47740329-47770871	NOTEST	0	0	0	0	1	1
ENSG00000239494	ENSG00000239494	RN7SL333P	1:169631244-169863408	NOTEST	0.115819	0.0836164	-0.470019	0	1	1
ENSG00000239497	ENSG00000239497	LY6G5B	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000239498	ENSG00000239498	AC114765.1	2:220970376-221569286	NOTEST	0	0	0	0	1	1
ENSG00000239500	ENSG00000239500	RP1-169K13.3	X:117031775-117251303	NOTEST	0	0	0	0	1	1
ENSG00000239503	ENSG00000239503	MARK2P8	3:128444964-128533639	NOTEST	0	0.0419143	inf	0	1	1
ENSG00000239504	ENSG00000239504	RN7SL583P	1:88943513-88943797	NOTEST	0	0	0	0	1	1
ENSG00000239510	ENSG00000239510	RPL9P5	14:59030863-59031334	NOTEST	0	0	0	0	1	1
ENSG00000239511	ENSG00000239511	POM121L7	22:21457304-21482352	NOTEST	0	0	0	0	1	1
ENSG00000239513	ENSG00000239513	RP11-2A4.3	3:137490790-137499720	NOTEST	0	0	0	0	1	1
ENSG00000239516	ENSG00000239516	FLYWCH1P1	3:180319917-180700541	NOTEST	0	0	0	0	1	1
ENSG00000239517	ENSG00000239517	CTD-2503O16.1	5:74213550-74319753	NOTEST	0	0	0	0	1	1
ENSG00000239519	ENSG00000239519	CADM2-AS1	3:85008131-86123579	NOTEST	0	0	0	0	1	1
ENSG00000239520	ENSG00000239520	RPL17P42	17:33901813-34053436	NOTEST	0	0	0	0	1	1
ENSG00000239524	ENSG00000239524	RPL32P34	19:5158505-5340814	NOTEST	0	0	0	0	1	1
ENSG00000239525	ENSG00000239525	RPL30P5	4:84377084-84444501	NOTEST	0	0	0	0	1	1
ENSG00000239527	ENSG00000239527	RPS23P7	17:60447578-60493837	NOTEST	0	0	0	0	1	1
ENSG00000239528	ENSG00000239528	CTB-118N6.1	5:115779311-115927094	NOTEST	0	0.0584813	inf	0	1	1
ENSG00000239532	ENSG00000239532	RP11-9D8.1	4:37822982-37823460	NOTEST	0.0483769	0.117	1.27412	0	1	1
ENSG00000239533	ENSG00000239533	GOLGA2P2Y	Y:26355713-26361728	NOTEST	0	0	0	0	1	1
ENSG00000239539	ENSG00000239539	HMGN1P20	10:19492778-20079330	NOTEST	0	0	0	0	1	1
ENSG00000239542	ENSG00000239542	RN7SL399P	17:39775688-39943183	NOTEST	0.40604	0	#NAME?	0	1	1
ENSG00000239544	ENSG00000239544	RP11-109N23.1	14:73430352-73430716	NOTEST	0	0	0	0	1	1
ENSG00000239545	ENSG00000239545	RN7SL822P	4:56081792-56082079	NOTEST	0	0	0	0	1	1
ENSG00000239547	ENSG00000239547	RN7SL843P	22:17833772-17834067	NOTEST	0	0	0	0	1	1
ENSG00000239552	ENSG00000239552	HOXB-AS2	17:46618255-46683776	NOTEST	0	0.0171422	inf	0	1	1
ENSG00000239553	ENSG00000239553	RN7SL12P	11:66452718-66496697	NOTEST	0	0	0	0	1	1
ENSG00000239555	ENSG00000239555	RN7SL841P	16:55293880-55367500	NOTEST	0	0	0	0	1	1
ENSG00000239556	ENSG00000239556	AC004951.5	7:43966036-44058774	NOTEST	0	0.0656909	inf	0	1	1
ENSG00000239559	ENSG00000239559	RPL37P2	11:67450242-67450529	NOTEST	0	0	0	0	1	1
ENSG00000239560	ENSG00000239560	RN7SL479P	1:44582771-44583069	NOTEST	0	0	0	0	1	1
ENSG00000239568	ENSG00000239568	RP11-654C22.1	3:72632520-72632686	NOTEST	0	0	0	0	1	1
ENSG00000239570	ENSG00000239570	SETP11	3:150803483-151176497	NOTEST	0	0	0	0	1	1
ENSG00000239571	ENSG00000239571	IGKV2D-30	2:89975668-89976489	NOTEST	0	0	0	0	1	1
ENSG00000239572	ENSG00000239572	RP11-451B8.1	3:87780551-87842779	NOTEST	0	0	0	0	1	1
ENSG00000239576	ENSG00000239576	COX6CP14	3:49761726-49823975	NOTEST	0	0	0	0	1	1

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ENSG00000239579	ENSG00000239579	RN7SL325P	X:136677423-136677710	NOTEST	0	0	0	0	1	1
ENSG00000239580	ENSG00000239580	RN7SL675P	8:70834988-70835281	NOTEST	0	0	0	0	1	1
ENSG00000239581	ENSG00000239581	RP11-19G24.1	17:35441922-35766909	NOTEST	0	0	0	0	1	1
ENSG00000239586	ENSG00000239586	MTND1P16	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000239587	ENSG00000239587	AC018730.4	2:105469742-105542510	NOTEST	0	0	0	0	1	1
ENSG00000239589	ENSG00000239589	LINC00879	3:94657015-94871353	NOTEST	0	0	0	0	1	1
ENSG00000239590	ENSG00000239590	OR1J4	9:125281419-125282361	NOTEST	0	0	0	0	1	1
ENSG00000239593	ENSG00000239593	RP11-477J21.6	9:123940414-124095121	NOTEST	0.0897107	0.0597032	-0.587473	0	1	1
ENSG00000239594	ENSG00000239594	MIR18B	X:133304063-133304146	NOTEST	0	0	0	0	1	1
ENSG00000239595	ENSG00000239595	RN7SL79P	17:29718641-29865236	NOTEST	0	0	0	0	1	1
ENSG00000239600	ENSG00000239600	AP000797.2	11:115821822-115822209	NOTEST	0	0	0	0	1	1
ENSG00000239602	ENSG00000239602	RP11-449H3.1	5:145463948-145562223	NOTEST	0	0	0	0	1	1
ENSG00000239605	ENSG00000239605	C2orf61	2:47126413-47403740	NOTEST	0.0204958	0.00721184	-1.50689	0	1	1
ENSG00000239607	ENSG00000239607	RN7SL573P	17:73028669-73061984	NOTEST	0	0.433004	inf	0	1	1
ENSG00000239608	ENSG00000239608	RUVBL1-AS1	3:127770483-128127485	NOTEST	0	0.0277603	inf	0	1	1
ENSG00000239610	ENSG00000239610	RN7SL13P	7:97653040-97653288	NOTEST	0	0	0	0	1	1
ENSG00000239614	ENSG00000239614	HMGN1P7	3:93698982-93847389	NOTEST	0	0	0	0	1	1
ENSG00000239615	ENSG00000239615	CTD-2410N18.1	5:133450401-133706738	NOTEST	0	0	0	0	1	1
ENSG00000239617	ENSG00000239617	RP11-302B13.1	12:49297200-49351334	NOTEST	0.190904	0.428114	1.16515	0	1	1
ENSG00000239618	ENSG00000239618	HLA-L	HSCHR6_MHC_MANN:30246906-30359341	NOTEST	0	0	0	0	1	1
ENSG00000239620	ENSG00000239620	RP11-88I21.1	3:127002923-127003524	NOTEST	0	0	0	0	1	1
ENSG00000239622	ENSG00000239622	CTA-242H14.1	7:25632970-25790614	NOTEST	0	0	0	0	1	1
ENSG00000239624	ENSG00000239624	CU013544.1	GL000233.1:28799-28881	NOTEST	0	0	0	0	1	1
ENSG00000239625	ENSG00000239625	RN7SL241P	10:30598729-30663377	NOTEST	0	0	0	0	1	1
ENSG00000239627	ENSG00000239627	RP11-124A7.1	4:41361623-41702061	NOTEST	0	0	0	0	1	1
ENSG00000239628	ENSG00000239628	RP11-543D10.2	3:170063465-170071749	NOTEST	0	0	0	0	1	1
ENSG00000239632	ENSG00000239632	RP11-52L11.9	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000239636	ENSG00000239636	RP4-728D4.2	1:36035413-36060929	NOTEST	0.039924	0.117711	1.55992	0	1	1
ENSG00000239640	ENSG00000239640	RN7SL62P	1:53180070-53180365	NOTEST	0	0	0	0	1	1
ENSG00000239641	ENSG00000239641	PLS1-AS1	3:142315228-142432506	NOTEST	0	0	0	0	1	1
ENSG00000239642	ENSG00000239642	AC034228.7	5:131142682-131348892	NOTEST	0	0	0	0	1	1
ENSG00000239648	ENSG00000239648	MTND1P3	7:141503500-141504452	NOTEST	0	0	0	0	1	1
ENSG00000239649	ENSG00000239649	MYADML	2:33931952-34522820	NOTEST	0.0501871	0.0803621	0.679199	0	1	1
ENSG00000239650	ENSG00000239650	GUSBP4	6:58246050-58256569	NOTEST	0.223107	0.180382	-0.306683	0	1	1
ENSG00000239653	ENSG00000239653	PSMD6-AS2	3:63989697-64009658	NOTEST	0.439005	0.484354	0.141826	0	1	1
ENSG00000239659	ENSG00000239659	RPL9P31	18:56298490-56299352	NOTEST	0	0	0	0	1	1
ENSG00000239661	ENSG00000239661	RP11-78O22.1	3:147561909-147564444	NOTEST	0	0	0	0	1	1
ENSG00000239664	ENSG00000239664	RP5-857K21.3	1:521368-532878	NOTEST	0	0	0	0	1	1
ENSG00000239670	ENSG00000239670	RP4-803A2.2	1:33452552-33546597	NOTEST	0.107321	0.0972224	-0.142571	0	1	1
ENSG00000239671	ENSG00000239671	CTD-3193K9.1	17:40852292-40897071	NOTEST	0	0	0	0	1	1
ENSG00000239674	ENSG00000239674	RP1-127L4.7	22:32537253-32539259	NOTEST	0.139654	0	#NAME?	0	1	1
ENSG00000239675	ENSG00000239675	HCG16	HSCHR6_MHC_DBB:28953993-28956327	NOTEST	0	0	0	0	1	1
ENSG00000239677	ENSG00000239677	PDZRN3-AS1	3:73431583-73675149	NOTEST	0.275232	0.504015	0.872817	0	1	1

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ENSG00000239679	ENSG00000239679	RN7SL193P	4:43865290-43865563	NOTEST	0	0	0	0	1	1
ENSG00000239683	ENSG00000239683	RP11-322E11.1	18:32963317-32963989	NOTEST	0	0	0	0	1	1
ENSG00000239684	ENSG00000239684	PTGER4P3	9:68371625-68371877	NOTEST	0	0.551947	inf	0	1	1
ENSG00000239686	ENSG00000239686	RP11-665C16.1	14:55729484-55828636	NOTEST	0.0834905	0	#NAME?	0	1	1
ENSG00000239689	ENSG00000239689	RPL17P46	18:48324573-48351772	NOTEST	0	0	0	0	1	1
ENSG00000239690	ENSG00000239690	RN7SL668P	1:235039932-235040233	NOTEST	0	0	0	0	1	1
ENSG00000239694	ENSG00000239694	CTD-2156G10.1	5:41951414-41952295	NOTEST	0	0	0	0	1	1
ENSG00000239696	ENSG00000239696	RP11-397J20.1	7:7117925-7119373	NOTEST	0	0	0	0	1	1
ENSG00000239699	ENSG00000239699	HNRNPA3P8	3:80265410-80266384	NOTEST	0	0	0	0	1	1
ENSG00000239701	ENSG00000239701	RP3-461F17.1	12:7072407-7178336	NOTEST	0.121257	0.0876159	-0.468805	0	1	1
ENSG00000239702	ENSG00000239702	RN7SL507P	17:42368225-42368519	NOTEST	0	0	0	0	1	1
ENSG00000239703	ENSG00000239703	RN7SL568P	15:56321885-56322179	NOTEST	0	0	0	0	1	1
ENSG00000239704	ENSG00000239704	CDRT4	17:15339331-15466909	NOTEST	0.357377	0.542427	0.601983	0	1	1
ENSG00000239705	ENSG00000239705	RP11-65N13.8	9:128003941-128019297	NOTEST	0	0	0	0	1	1
ENSG00000239706	ENSG00000239706	RP11-6F2.3	3:156543269-156763918	NOTEST	0	0.0272146	inf	0	1	1
ENSG00000239708	ENSG00000239708	RN7SL782P	5:107070475-107070767	NOTEST	0	0	0	0	1	1
ENSG00000239710	ENSG00000239710	RN7SL692P	1:93440385-93440680	NOTEST	0	0	0	0	1	1
ENSG00000239713	ENSG00000239713	APOBEC3G	22:39436608-39483748	NOTEST	0	0.0555553	inf	0	1	1
ENSG00000239715	ENSG00000239715	AC093627.11	7:174919-176013	NOTEST	0	0	0	0	1	1
ENSG00000239716	ENSG00000239716	RP11-290K4.1	3:157694349-157695925	NOTEST	0	0	0	0	1	1
ENSG00000239718	ENSG00000239718	HLTF-AS1	3:148747913-148820610	NOTEST	0	0	0	0	1	1
ENSG00000239719	ENSG00000239719	RP4-800G7.1	7:148888134-148888315	NOTEST	0	0	0	0	1	1
ENSG00000239722	ENSG00000239722	IMP3P2	7:128333503-128333978	NOTEST	0	0	0	0	1	1
ENSG00000239726	ENSG00000239726	RN7SL688P	11:118754474-118829269	NOTEST	0	0	0	0	1	1
ENSG00000239731	ENSG00000239731	RN7SL825P	10:32281017-32281309	NOTEST	0	0.0943241	inf	0	1	1
ENSG00000239732	ENSG00000239732	TLR9	3:52255095-52275113	NOTEST	0.00878457	0	#NAME?	0	1	1
ENSG00000239736	ENSG00000239736	CEACAMP3	19:42106089-42112339	NOTEST	0	0	0	0	1	1
ENSG00000239739	ENSG00000239739	RP11-373E16.4	3:170136652-170578169	NOTEST	0	0.494279	inf	0	1	1
ENSG00000239741	ENSG00000239741	LY6G6F	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000239742	ENSG00000239742	RN7SL672P	20:49126890-49201299	NOTEST	0	0	0	0	1	1
ENSG00000239744	ENSG00000239744	RN7SL63P	10:30844531-30844833	NOTEST	0	0	0	0	1	1
ENSG00000239745	ENSG00000239745	RN7SL790P	X:73610526-73610822	NOTEST	0	0	0	0	1	1
ENSG00000239748	ENSG00000239748	RN7SL795P	18:68179962-68180241	NOTEST	0	0	0	0	1	1
ENSG00000239754	ENSG00000239754	CFB	HSCHR6_MHC_COX:31853113-31907413	NOTEST	0	0	0	0	1	1
ENSG00000239756	ENSG00000239756	PHF1	HSCHR6_MHC_QBL:33306983-33307829	NOTEST	0	0	0	0	1	1
ENSG00000239763	ENSG00000239763	AC009120.3	16:74330672-74403724	NOTEST	0.0919606	0.378358	2.04066	0	1	1
ENSG00000239767	ENSG00000239767	RP11-789F5.1	3:86313704-86316511	NOTEST	0	0	0	0	1	1
ENSG00000239774	ENSG00000239774	RP11-496B10.3	3:180284505-180319723	NOTEST	0	0	0	0	1	1
ENSG00000239775	ENSG00000239775	AC017116.11	7:44084238-44109055	NOTEST	0.345764	0.325904	-0.0853379	0	1	1
ENSG00000239776	ENSG00000239776	AC079949.1	12:127650615-127650672	NOTEST	0	0	0	0	1	1
ENSG00000239780	ENSG00000239780	RPLP0P11	18:47984256-47985165	NOTEST	0	0	0	0	1	1
ENSG00000239783	ENSG00000239783	RP5-1050K3.3	20:45523262-45817492	NOTEST	0	0	0	0	1	1
ENSG00000239784	ENSG00000239784	RPL23AP1	HSCHR6_MHC_QBL:29688013-29714292	NOTEST	0	0	0	0	1	1

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ENSG00000239791	ENSG00000239791	AC002310.7	16:30580666-30597092	NOTEST	0.141822	0.0321106	-2.14296	0	1	1
ENSG00000239792	ENSG00000239792	RP11-255N24.1	9:30670961-30671964	NOTEST	0	0	0	0	1	1
ENSG00000239793	ENSG00000239793	RP11-109G23.1	4:79689652-79689904	NOTEST	0	0	0	0	1	1
ENSG00000239794	ENSG00000239794	RN7SL653P	1:92145901-92371892	NOTEST	0	0	0	0	1	1
ENSG00000239797	ENSG00000239797	RPL21P39	3:145542043-145542526	NOTEST	0.314277	0.0338383	-3.21531	0	1	1
ENSG00000239799	ENSG00000239799	ITIH4-AS1	3:52846990-52931612	NOTEST	0	0	0	0	1	1
ENSG00000239801	ENSG00000239801	RP11-755B10.2	3:57611183-57678816	NOTEST	0	0	0	0	1	1
ENSG00000239804	ENSG00000239804	RP11-379B18.1	3:125493556-125516796	NOTEST	0	0	0	0	1	1
ENSG00000239805	ENSG00000239805	RP11-252O18.2	3:181565313-181565673	NOTEST	0	0	0	0	1	1
ENSG00000239808	ENSG00000239808	RN7SL255P	5:103596233-103596527	NOTEST	0	0	0	0	1	1
ENSG00000239809	ENSG00000239809	RP11-51L5.2	17:60447578-60493837	NOTEST	0	0	0	0	1	1
ENSG00000239810	ENSG00000239810	WI2-3308P17.2	1:12998180-13117751	NOTEST	0	0	0	0	1	1
ENSG00000239815	ENSG00000239815	RP11-309L24.4	7:128470430-128550773	NOTEST	0.0572959	0	#NAME?	0	1	1
ENSG00000239819	ENSG00000239819	IGKV1D-8	2:90259592-90260248	NOTEST	0	0	0	0	1	1
ENSG00000239820	ENSG00000239820	RN7SL213P	14:68168602-68283307	NOTEST	0.101989	0	#NAME?	0	1	1
ENSG00000239821	ENSG00000239821	RN7SL513P	19:18444085-18444381	NOTEST	0	0	0	0	1	1
ENSG00000239822	ENSG00000239822	RN7SL754P	10:320129-735683	NOTEST	0	0	0	0	1	1
ENSG00000239823	ENSG00000239823	Y_RNA	HG183_PATCH:62399862-62491136	NOTEST	0	0	0	0	1	1
ENSG00000239825	ENSG00000239825	RN7SL549P	7:100503918-100504197	NOTEST	0	0	0	0	1	1
ENSG00000239827	ENSG00000239827	SUGT1P3	13:41396431-41495910	NOTEST	0.234535	0.302802	0.368571	0	1	1
ENSG00000239828	ENSG00000239828	RP11-446H18.5	3:106959538-107101007	NOTEST	0.110828	0.0218887	-2.34007	0	1	1
ENSG00000239829	ENSG00000239829	KRT8P25	3:87372417-87373873	NOTEST	0	0	0	0	1	1
ENSG00000239830	ENSG00000239830	RPS4XP22	19:9793969-9794749	NOTEST	0	0	0	0	1	1
ENSG00000239831	ENSG00000239831	RNF7P1	3:57327726-57530071	NOTEST	0	0	0	0	1	1
ENSG00000239835	ENSG00000239835	RP11-767L7.1	3:119540169-119813264	NOTEST	0	0.0120532	inf	0	1	1
ENSG00000239836	ENSG00000239836	PSMB9	HSCHR6_MHC_MANN:32962292-33001424	NOTEST	0	0	0	0	1	1
ENSG00000239839	ENSG00000239839	DEFA3	8:6854287-6875823	NOTEST	0	0	0	0	1	1
ENSG00000239840	ENSG00000239840	RPL23AP72	16:47178233-47735434	NOTEST	0	0	0	0	1	1
ENSG00000239855	ENSG00000239855	IGKV1-6	2:89265780-89266286	NOTEST	0	0	0	0	1	1
ENSG00000239856	ENSG00000239856	RN7SL225P	11:86013252-86056969	NOTEST	0	0.0914611	inf	0	1	1
ENSG00000239859	ENSG00000239859	RN7SL281P	1:36171625-36171875	NOTEST	0	0	0	0	1	1
ENSG00000239861	ENSG00000239861	RP11-690D19.1	11:102915965-102916441	NOTEST	0	0	0	0	1	1
ENSG00000239862	ENSG00000239862	IGKV1-37	2:89597020-89597542	NOTEST	0	0	0	0	1	1
ENSG00000239865	ENSG00000239865	RPP21	HSCHR6_MHC_MANN:30246906-30359341	NOTEST	0	0	0	0	1	1
ENSG00000239867	ENSG00000239867	BX088702.2	GL000199.1:4721-4804	NOTEST	0	0	0	0	1	1
ENSG00000239868	ENSG00000239868	RN7SL34P	19:41768400-41930910	NOTEST	0.13282	0.0960201	-0.468065	0	1	1
ENSG00000239870	ENSG00000239870	RP11-83M16.1	5:66675205-67198428	NOTEST	0	0	0	0	1	1
ENSG00000239872	ENSG00000239872	RPL35AP19	8:122392376-122392705	NOTEST	0	0	0	0	1	1
ENSG00000239877	ENSG00000239877	IGSF11-AS1	3:118619403-118864915	NOTEST	0	0	0	0	1	1
ENSG00000239880	ENSG00000239880	RP11-420J11.1	3:180040894-180042847	NOTEST	0	0	0	0	1	1
ENSG00000239881	ENSG00000239881	RPS27P25	12:120807242-120809491	NOTEST	0	0	0	0	1	1
ENSG00000239882	ENSG00000239882	CYP21A1P	HSCHR6_MHC_SSTO:31965199-32027628	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000239886	ENSG00000239886	KRTAP9-2	17:39382899-39383904	NOTEST	0	0	0	0	1	1
ENSG00000239888	ENSG00000239888	RN7SL792P	17:15283180-15321195	NOTEST	0	0	0	0	1	1
ENSG00000239891	ENSG00000239891	RN7SL341P	2:65044511-65044808	NOTEST	0	0	0	0	1	1
ENSG00000239893	ENSG00000239893	ZNF736P9Y	Y:7936936-7938764	NOTEST	0	0	0	0	1	1
ENSG00000239898	ENSG00000239898	RN7SL796P	15:30844182-30854704	NOTEST	0	0	0	0	1	1
ENSG00000239899	ENSG00000239899	RN7SL674P	2:11674241-11782914	NOTEST	0	0	0	0	1	1
ENSG00000239903	ENSG00000239903	RP11-353N4.2	1:149646784-149719362	NOTEST	0.0482018	0.0405511	-0.249344	0	1	1
ENSG00000239906	ENSG00000239906	RP11-34P13.14	1:139789-140339	NOTEST	0.187061	0	#NAME?	0	1	1
ENSG00000239908	ENSG00000239908	RN7SL75P	9:102861537-103063282	NOTEST	0.531203	0.314764	-0.754993	0	1	1
ENSG00000239910	ENSG00000239910	RN7SL530P	14:74551498-74667936	NOTEST	0	0	0	0	1	1
ENSG00000239911	ENSG00000239911	PRKAG2-AS1	7:151253196-151576299	NOTEST	0.0612718	0.556487	3.18305	0	1	1
ENSG00000239912	ENSG00000239912	RPL39P36	19:53868945-53930574	NOTEST	0	0.940147	inf	0	1	1
ENSG00000239917	ENSG00000239917	RPS10P16	8:118532951-118552501	NOTEST	0	0	0	0	1	1
ENSG00000239919	ENSG00000239919	SNRPGP3	7:129074273-129128240	NOTEST	0	0	0	0	1	1
ENSG00000239920	ENSG00000239920	AC015691.13	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000239921	ENSG00000239921	RP11-59J16.1	3:127199532-127255655	NOTEST	0	0	0	0	1	1
ENSG00000239922	ENSG00000239922	RP11-71N10.1	3:147657790-147724542	NOTEST	0	0	0	0	1	1
ENSG00000239923	ENSG00000239923	RN7SL864P	20:13829892-16033842	NOTEST	0	0	0	0	1	1
ENSG00000239924	ENSG00000239924	RPL29P22	11:62847411-63137190	NOTEST	0	0	0	0	1	1
ENSG00000239926	ENSG00000239926	PRDX3P4	3:64053639-64440508	NOTEST	0	0.0200735	inf	0	1	1
ENSG00000239927	ENSG00000239927	RPP21	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000239930	ENSG00000239930	AP001625.4	21:43892595-44001550	NOTEST	0	0	0	0	1	1
ENSG00000239932	ENSG00000239932	RN7SL606P	17:58754813-59488916	NOTEST	0	0	0	0	1	1
ENSG00000239939	ENSG00000239939	RPSAP34	4:109328998-109329734	NOTEST	0	0.0634716	inf	0	1	1
ENSG00000239940	ENSG00000239940	HCG16	HSCHR6_MHC_COX:28950577-28952911	NOTEST	0	0	0	0	1	1
ENSG00000239941	ENSG00000239941	RP11-246A10.1	3:151835961-151869513	NOTEST	0	0	0	0	1	1
ENSG00000239942	ENSG00000239942	RN7SL394P	10:69556426-69597924	NOTEST	0	0	0	0	1	1
ENSG00000239944	ENSG00000239944	TRBV8-2	7:142245302-142245572	NOTEST	0	0	0	0	1	1
ENSG00000239945	ENSG00000239945	RP11-34P13.8	1:89294-134836	NOTEST	0.566393	0.300738	-0.913295	0	1	1
ENSG00000239946	ENSG00000239946	ZBTB20-AS3	3:114056940-114866118	NOTEST	0	0	0	0	1	1
ENSG00000239948	ENSG00000239948	RN7SL368P	19:44150246-44174699	NOTEST	0	0	0	0	1	1
ENSG00000239951	ENSG00000239951	IGKV3-20	2:89442056-89442643	NOTEST	0	0	0	0	1	1
ENSG00000239953	ENSG00000239953	RN7SL273P	6:37321747-37362514	NOTEST	0	0	0	0	1	1
ENSG00000239955	ENSG00000239955	RN7SL673P	15:30375157-30385702	NOTEST	0	0	0	0	1	1
ENSG00000239958	ENSG00000239958	RN7SL51P	2:62489523-62489806	NOTEST	0	0	0	0	1	1
ENSG00000239959	ENSG00000239959	ENPP7P2	3:75484498-75540353	NOTEST	0.0928657	0.12137	0.386189	0	1	1
ENSG00000239961	ENSG00000239961	LILRA4	19:54818352-54850421	NOTEST	0	0	0	0	1	1
ENSG00000239964	ENSG00000239964	RN7SL748P	6:36461668-36515247	NOTEST	0	0	0	0	1	1
ENSG00000239967	ENSG00000239967	OR2A41P	7:143774813-143774918	NOTEST	0	0	0	0	1	1
ENSG00000239974	ENSG00000239974	EGFL8	HSCHR6_MHC_SSTO:32123002-32152743	NOTEST	0	0	0	0	1	1
ENSG00000239975	ENSG00000239975	IGKV1D-33	2:89952791-89953355	NOTEST	0	0	0	0	1	1
ENSG00000239978	ENSG00000239978	OR7E53P	3:125453137-125454041	NOTEST	0	0	0	0	1	1
ENSG00000239981	ENSG00000239981	OR2A15P	7:143815553-143816453	NOTEST	0	0	0	0	1	1
ENSG00000239983	ENSG00000239983	RP11-79E3.1	4:33777968-34041515	NOTEST	0	0	0	0	1	1
ENSG00000239984	ENSG00000239984	RN7SL420P	1:116149091-116149390	NOTEST	0	0	0	0	1	1

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ENSG00000239986	ENSG00000239986	RP11-366N18.2	9:43617726-43618056	NOTEST	0	0	0	0	1	1
ENSG00000239988	ENSG00000239988	RPL31P60	19:33369901-33462897	NOTEST	0	0	0	0	1	1
ENSG00000239989	ENSG00000239989	AC008132.14	22:18761177-18830912	NOTEST	0	0	0	0	1	1
ENSG00000239991	ENSG00000239991	RP11-889D3.1	3:55200937-55209760	NOTEST	0	0	0	0	1	1
ENSG00000239992	ENSG00000239992	TRBVA	7:142389236-142389691	NOTEST	0	0	0	0	1	1
ENSG00000239994	ENSG00000239994	RP11-169N13.4	3:119421868-119485949	NOTEST	0	0	0	0	1	1
ENSG00000239995	ENSG00000239995	TPT1P11	2:48756521-49003654	NOTEST	0	0	0	0	1	1
ENSG00000239997	ENSG00000239997	FCF1P3	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000239998	ENSG00000239998	LILRA2	19:55084386-55150343	NOTEST	0	0	0	0	1	1
ENSG00000240002	ENSG00000240002	YBX1P3	3:114056940-114866118	NOTEST	0	0	0	0	1	1
ENSG00000240003	ENSG00000240003	RPL7P24	5:79778111-79838382	NOTEST	0.0255688	0.154291	2.5932	0	1	1
ENSG00000240006	ENSG00000240006	RP11-200A1.1	3:134032417-134040013	NOTEST	0	0.286531	inf	0	1	1
ENSG00000240007	ENSG00000240007	RP6-206I17.4	1:143647637-143745417	NOTEST	0.0177909	0.0367999	1.04856	0	1	1
ENSG00000240008	ENSG00000240008	LY6G6F	HSCHR6_MHC_COX:31662076-31673108	NOTEST	0	0	0	0	1	1
ENSG00000240010	ENSG00000240010	CT867976.1	GL000230.1:40400-40482	NOTEST	0	0	0	0	1	1
ENSG00000240012	ENSG00000240012	SLC9A9-AS1	3:142984063-143567373	NOTEST	0	0	0	0	1	1
ENSG00000240014	ENSG00000240014	RN7SL254P	4:148653213-148993931	NOTEST	0	0	0	0	1	1
ENSG00000240015	ENSG00000240015	RP11-90P5.5	8:37962759-38070819	NOTEST	0.0330225	0	#NAME?	0	1	1
ENSG00000240021	ENSG00000240021	TEX35	1:178482211-178518024	NOTEST	0.0329746	0.0281419	-0.228633	0	1	1
ENSG00000240023	ENSG00000240023	RP11-561B11.1	14:35857326-35858275	NOTEST	0	0	0	0	1	1
ENSG00000240027	ENSG00000240027	RP11-415I12.1	12:63952692-64217675	NOTEST	0	0	0	0	1	1
ENSG00000240031	ENSG00000240031	OR9A3P	7:141562659-141563537	NOTEST	0	0	0	0	1	1
ENSG00000240032	ENSG00000240032	RP11-274H2.3	3:145781828-145881440	NOTEST	0.105986	0.0861762	-0.298511	0	1	1
ENSG00000240033	ENSG00000240033	RP11-12K11.2	3:166552808-166562744	NOTEST	0	0	0	0	1	1
ENSG00000240034	ENSG00000240034	MTND6P6	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000240040	ENSG00000240040	AC096579.13	2:89109983-89165653	NOTEST	0	0	0	0	1	1
ENSG00000240041	ENSG00000240041	IGHJ4	14:106330424-106330470	NOTEST	0	0	0	0	1	1
ENSG00000240042	ENSG00000240042	AC098789.1	19:54771857-54772899	NOTEST	0	0	0	0	1	1
ENSG00000240043	ENSG00000240043	RPS27P26	16:70478576-70478815	NOTEST	0	0	0	0	1	1
ENSG00000240045	ENSG00000240045	RP11-451G4.2	3:155008017-155011965	NOTEST	0	0	0	0	1	1
ENSG00000240047	ENSG00000240047	RPS3AP32	8:74964574-75012088	NOTEST	0	0	0	0	1	1
ENSG00000240048	ENSG00000240048	DDX50P2	3:154055460-154147504	NOTEST	0	0	0	0	1	1
ENSG00000240050	ENSG00000240050	RP1-93H18.1	6:116575335-116762424	NOTEST	0	0	0	0	1	1
ENSG00000240051	ENSG00000240051	RPL23AP10	14:96858447-96955764	NOTEST	0	0	0	0	1	1
ENSG00000240052	ENSG00000240052	RP11-289K10.1	5:52709333-52710090	NOTEST	0	0	0	0	1	1
ENSG00000240056	ENSG00000240056	RP11-349J5.2	6:135238527-135271260	NOTEST	0	0	0	0	1	1
ENSG00000240057	ENSG00000240057	RP11-572M11.4	3:112709293-112902148	NOTEST	0.379541	0.413118	0.122299	0	1	1
ENSG00000240058	ENSG00000240058	ARGFXP1	5:121964646-122066380	NOTEST	0	0	0	0	1	1
ENSG00000240063	ENSG00000240063	RP11-225N10.1	3:182501023-182511182	NOTEST	0.00870531	0.0135292	0.636106	0	1	1
ENSG00000240068	ENSG00000240068	RPL21P42	3:153741623-153742087	NOTEST	0	0	0	0	1	1
ENSG00000240069	ENSG00000240069	GPAA1P1	2:110690737-110742667	NOTEST	0	0	0	0	1	1
ENSG00000240074	ENSG00000240074	RPL9P30	17:27887564-28513493	NOTEST	0	0	0	0	1	1

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ENSG00000240084	ENSG00000240084	RP11-12N13.6	3:165878201-165878492	NOTEST	0	0	0	0	1	1
ENSG00000240089	ENSG00000240089	BMS1P3	10:88695296-88784489	NOTEST	0	0	0	0	1	1
ENSG00000240093	ENSG00000240093	AC093627.12	7:182934-300711	NOTEST	0	0	0	0	1	1
ENSG00000240095	ENSG00000240095	RP11-88H10.3	3:145679541-145681410	NOTEST	0	0	0	0	1	1
ENSG00000240096	ENSG00000240096	RP11-85G20.1	14:93651295-93695561	NOTEST	0.0802299	0.0284419	-1.49612	0	1	1
ENSG00000240097	ENSG00000240097	RP11-641C17.4	3:59735035-61237133	NOTEST	0	0	0	0	1	1
ENSG00000240098	ENSG00000240098	RN7SL351P	11:126071992-126148026	NOTEST	0	0	0	0	1	1
ENSG00000240100	ENSG00000240100	RP11-240G22.1	12:117346116-117346432	NOTEST	0	0	0	0	1	1
ENSG00000240103	ENSG00000240103	RP11-846F4.6	17:22026649-22028896	NOTEST	0	0	0	0	1	1
ENSG00000240106	ENSG00000240106	RN7SL146P	19:16589867-16771253	NOTEST	0.231661	0.0907708	-1.35172	0	1	1
ENSG00000240107	ENSG00000240107	RP11-628J14.1	3:103257478-103259331	NOTEST	0	0	0	0	1	1
ENSG00000240108	ENSG00000240108	NCOR1P1	20:26084051-26094664	NOTEST	0	0	0	0	1	1
ENSG00000240110	ENSG00000240110	XXbac-BPG254F23.6	HSCHR6_MHC_QBL:32547664-32563145	NOTEST	0	0	0	0	1	1
ENSG00000240111	ENSG00000240111	HCG16	HSCHR6_MHC_MANN:28953984-28956318	NOTEST	0	0	0	0	1	1
ENSG00000240116	ENSG00000240116	RN7SL303P	8:22545171-22941132	NOTEST	0	0	0	0	1	1
ENSG00000240118	ENSG00000240118	PSMB9	HSCHR6_MHC_DBB:32786474-32825559	NOTEST	0	0	0	0	1	1
ENSG00000240121	ENSG00000240121	RPS27P20	11:129407763-129408009	NOTEST	0	0	0	0	1	1
ENSG00000240122	ENSG00000240122	FABP5P11	22:17075978-17076375	NOTEST	0	0	0	0	1	1
ENSG00000240125	ENSG00000240125	RP11-58O9.1	17:38595718-38596169	NOTEST	0	0	0	0	1	1
ENSG00000240128	ENSG00000240128	KRT18P43	3:169620767-169622048	NOTEST	0	0	0	0	1	1
ENSG00000240130	ENSG00000240130	OR5V1	HSCHR6_MHC_QBL:29384950-29424735	NOTEST	0	0	0	0	1	1
ENSG00000240131	ENSG00000240131	RP11-124D2.1	14:23654524-23795394	NOTEST	0	0	0	0	1	1
ENSG00000240132	ENSG00000240132	ETF1P2	7:151163097-151217206	NOTEST	0.0781289	0.122532	0.649229	0	1	1
ENSG00000240135	ENSG00000240135	PSMD12P	3:72925887-72927253	NOTEST	0	0	0	0	1	1
ENSG00000240138	ENSG00000240138	EEF1GP4	3:161042700-161044007	NOTEST	0	0	0	0	1	1
ENSG00000240143	ENSG00000240143	RP4-753P9.3	X:128913954-128930939	NOTEST	0	0	0	0	1	1
ENSG00000240151	ENSG00000240151	RN7SL826P	8:117962511-118188953	NOTEST	0	0	0	0	1	1
ENSG00000240152	ENSG00000240152	RP11-16N2.1	4:62009373-62019680	NOTEST	0	0	0	0	1	1
ENSG00000240156	ENSG00000240156	COX6CP6	3:70800273-70800501	NOTEST	0	0	0	0	1	1
ENSG00000240159	ENSG00000240159	RP11-162O12.1	4:185175661-185176483	NOTEST	0	0	0	0	1	1
ENSG00000240160	ENSG00000240160	RN7SL263P	22:23521890-23660224	NOTEST	0	0.300181	inf	0	1	1
ENSG00000240163	ENSG00000240163	RP11-745A24.1	15:60639332-60695082	NOTEST	0	0.0814945	inf	0	1	1
ENSG00000240165	ENSG00000240165	RN7SL787P	9:67858946-67859228	NOTEST	0	0	0	0	1	1
ENSG00000240167	ENSG00000240167	RPS7P7	4:42410389-42659122	NOTEST	0	0	0	0	1	1
ENSG00000240173	ENSG00000240173	RN7SL771P	7:140218219-140624564	NOTEST	0	0	0	0	1	1
ENSG00000240174	ENSG00000240174	RP11-851M3.1	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000240175	ENSG00000240175	MAGI1-AS1	3:65339199-66024509	NOTEST	0	0	0	0	1	1
ENSG00000240179	ENSG00000240179	RPL26P3	14:28959115-28959568	NOTEST	0	0	0	0	1	1
ENSG00000240180	ENSG00000240180	RP11-318E3.4	10:5903579-5987863	NOTEST	0.219029	0.0381414	-2.52169	0	1	1
ENSG00000240183	ENSG00000240183	RN7SL297P	2:112656055-112787138	NOTEST	0	0	0	0	1	1
ENSG00000240186	ENSG00000240186	RN7SL633P	22:31455974-31456269	NOTEST	0	0	0	0	1	1
ENSG00000240189	ENSG00000240189	RN7SL621P	8:33437729-33438026	NOTEST	0	0	0	0	1	1
ENSG00000240194	ENSG00000240194	CYMP	1:111023373-111033899	NOTEST	0	0	0	0	1	1

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ENSG00000240198	ENSG00000240198	ARHGEF3-AS1	3:56761445-57114129	NOTEST	0	0	0	0	1	1
ENSG00000240199	ENSG00000240199	RN7SL520P	16:75661621-75795770	NOTEST	0	0	0	0	1	1
ENSG00000240201	ENSG00000240201	RP11-269C4.1	14:30045686-30766249	NOTEST	0	0	0	0	1	1
ENSG00000240202	ENSG00000240202	RN7SL223P	11:93290078-93290369	NOTEST	0	0	0	0	1	1
ENSG00000240203	ENSG00000240203	RN7SL567P	3:42717683-42717983	NOTEST	0	0	0	0	1	1
ENSG00000240205	ENSG00000240205	RN7SL865P	12:116155529-116155816	NOTEST	0	0	0	0	1	1
ENSG00000240207	ENSG00000240207	RP11-379F4.4	3:158414680-158547508	NOTEST	0.196321	0.101236	-0.955499	0	1	1
ENSG00000240210	ENSG00000240210	RP11-204K16.1	14:68286495-69196935	NOTEST	0.0243877	0	#NAME?	0	1	1
ENSG00000240211	ENSG00000240211	RP11-758P17.3	7:100032879-100036127	NOTEST	0	0	0	0	1	1
ENSG00000240215	ENSG00000240215	TRBV25OR9-2	9:33662163-33662661	NOTEST	0	0	0	0	1	1
ENSG00000240216	ENSG00000240216	CPHL1P	3:148947142-149052201	NOTEST	0	0.0328754	inf	0	1	1
ENSG00000240219	ENSG00000240219	RP11-430C7.5	1:204586297-204654861	NOTEST	0.0290059	0.00509409	-2.50945	0	1	1
ENSG00000240221	ENSG00000240221	RN7SL196P	15:30695942-30706463	NOTEST	0	0	0	0	1	1
ENSG00000240224	ENSG00000240224	UGT1A5	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000240231	ENSG00000240231	RPS27P29	19:23708432-23870022	NOTEST	0	0.400967	inf	0	1	1
ENSG00000240233	ENSG00000240233	RN7SL587P	14:77972339-78083116	NOTEST	0	0	0	0	1	1
ENSG00000240235	ENSG00000240235	RN7SL794P	9:101947867-101948148	NOTEST	0	0	0	0	1	1
ENSG00000240236	ENSG00000240236	HNRNPA1P23	3:122036455-122037588	NOTEST	0	0	0	0	1	1
ENSG00000240237	ENSG00000240237	CTD-2182N23.1	8:133879202-134147147	NOTEST	0	0	0	0	1	1
ENSG00000240238	ENSG00000240238	RP11-112N19.2	15:59844813-59845292	NOTEST	0	0	0	0	1	1
ENSG00000240240	ENSG00000240240	RP11-146D12.2	9:42368302-42474239	NOTEST	0.14342	0.045173	-1.66671	0	1	1
ENSG00000240241	ENSG00000240241	RP11-314M24.1	3:78316089-78343881	NOTEST	0	0	0	0	1	1
ENSG00000240244	ENSG00000240244	GAPDHP33	1:120138789-120139802	NOTEST	0.41407	0.530952	0.358707	0	1	1
ENSG00000240246	ENSG00000240246	RP11-167H9.1	3:149150830-149151061	NOTEST	0	0	0	0	1	1
ENSG00000240247	ENSG00000240247	DEFA1B	8:6854287-6875823	NOTEST	0	0	0	0	1	1
ENSG00000240250	ENSG00000240250	RN7SL541P	5:133853500-133853785	NOTEST	0	0	0	0	1	1
ENSG00000240253	ENSG00000240253	FAR2P3	2:131437622-131476404	NOTEST	0	0	0	0	1	1
ENSG00000240254	ENSG00000240254	B4GALT4-AS1	3:118930578-119009513	NOTEST	0	0.0310193	inf	0	1	1
ENSG00000240255	ENSG00000240255	PSMC1P6	3:87679450-87680769	NOTEST	0	0	0	0	1	1
ENSG00000240257	ENSG00000240257	GAGE2D	X:49207159-49214420	NOTEST	0.12281	0	#NAME?	0	1	1
ENSG00000240265	ENSG00000240265	RP11-62G11.1	3:69219140-69591734	NOTEST	0	0	0	0	1	1
ENSG00000240268	ENSG00000240268	MOXD2P	7:141940558-141946886	NOTEST	0	0	0	0	1	1
ENSG00000240270	ENSG00000240270	RPL12P37	17:78950253-78950748	NOTEST	0.0916853	0	#NAME?	0	1	1
ENSG00000240271	ENSG00000240271	RP11-200A13.2	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000240279	ENSG00000240279	AL353997.4	17:18319041-18328411	NOTEST	0	0	0	0	1	1
ENSG00000240281	ENSG00000240281	CTD-2062O1.1	5:41895169-41895701	NOTEST	0	0	0	0	1	1
ENSG00000240286	ENSG00000240286	MEAF6P1	2:210043527-210046742	NOTEST	0	0	0	0	1	1
ENSG00000240288	ENSG00000240288	GHRLOS	3:10289706-10362862	NOTEST	0.169067	0.223886	0.405175	0	1	1
ENSG00000240291	ENSG00000240291	RP11-499P20.2	10:18429605-18948214	NOTEST	0.272396	0.145941	-0.900322	0	1	1
ENSG00000240292	ENSG00000240292	RP11-298O21.2	3:167582560-167601170	NOTEST	0	0	0	0	1	1
ENSG00000240294	ENSG00000240294	RN7SKP241	10:25137535-25241533	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000240296	ENSG00000240296	AC010492.5	19:54771857-54772899	NOTEST	0	0	0	0	1	1
ENSG00000240298	ENSG00000240298	RPL36AP40	11:25610020-25610389	NOTEST	0.29417	0.288473	-0.0282164	0	1	1
ENSG00000240299	ENSG00000240299	RN7SL187P	9:124137518-124262306	NOTEST	0	0	0	0	1	1
ENSG00000240302	ENSG00000240302	RN7SL717P	2:200732118-200775882	NOTEST	0	0	0	0	1	1
ENSG00000240305	ENSG00000240305	RP11-1072C15.1	17:42785975-42829632	NOTEST	0.0222689	0.0664469	1.57717	0	1	1
ENSG00000240306	ENSG00000240306	RN7SL100P	9:26895675-26895968	NOTEST	0	0	0	0	1	1
ENSG00000240309	ENSG00000240309	RP11-91A15.1	3:89637863-89639247	NOTEST	0	0	0	0	1	1
ENSG00000240311	ENSG00000240311	LA16c-306E5.1	16:3415098-3627401	NOTEST	0.138666	0.0530474	-1.38626	0	1	1
ENSG00000240317	ENSG00000240317	RN7SL764P	2:219940038-220035549	NOTEST	0	0	0	0	1	1
ENSG00000240320	ENSG00000240320	AC006133.3	19:40188543-40188713	NOTEST	0	0	0	0	1	1
ENSG00000240322	ENSG00000240322	RN7SL481P	7:142985307-143004789	NOTEST	0.115843	0.787047	2.76428	0	1	1
ENSG00000240327	ENSG00000240327	RN7SL93P	X:113219602-113219893	NOTEST	0	0	0	0	1	1
ENSG00000240328	ENSG00000240328	RP11-841C19.1	12:19556978-19873735	NOTEST	0	0.0675279	inf	0	1	1
ENSG00000240338	ENSG00000240338	RP11-331F4.4	16:75259971-75262093	NOTEST	0	0	0	0	1	1
ENSG00000240341	ENSG00000240341	AL162853.1	13:23453263-23453338	NOTEST	0	0	0	0	1	1
ENSG00000240347	ENSG00000240347	RN7SL35P	7:79947568-79947857	NOTEST	0	0	0	0	1	1
ENSG00000240350	ENSG00000240350	AC017002.1	2:111953539-112268567	NOTEST	0	0.0555224	inf	0	1	1
ENSG00000240354	ENSG00000240354	RP11-774I5.1	3:161534696-161539696	NOTEST	0	0	0	0	1	1
ENSG00000240355	ENSG00000240355	AC004869.3	7:46516054-46521176	NOTEST	0	0	0	0	1	1
ENSG00000240359	ENSG00000240359	UBL5P3	3:63188893-63189124	NOTEST	0	0	0	0	1	1
ENSG00000240361	ENSG00000240361	OR4G11P	1:62947-63887	NOTEST	0	0	0	0	1	1
ENSG00000240364	ENSG00000240364	RPL31P59	18:3377913-3378245	NOTEST	0	0	0	0	1	1
ENSG00000240366	ENSG00000240366	RPL36AP45	15:75478991-75479309	NOTEST	0	0	0	0	1	1
ENSG00000240371	ENSG00000240371	RPS4XP13	11:57343764-57344553	NOTEST	0	0	0	0	1	1
ENSG00000240374	ENSG00000240374	RN7SL503P	1:35734567-35887659	NOTEST	0	0	0	0	1	1
ENSG00000240375	ENSG00000240375	VPS26AP1	3:113547028-113666417	NOTEST	0	0	0	0	1	1
ENSG00000240376	ENSG00000240376	RP11-36C20.1	5:32925744-33298016	NOTEST	0.119719	0.128839	0.105925	0	1	1
ENSG00000240382	ENSG00000240382	IGKV1-17	2:89416832-89417335	NOTEST	0	0	0	0	1	1
ENSG00000240385	ENSG00000240385	RPS29P20	11:3875547-4114439	NOTEST	0	0	0	0	1	1
ENSG00000240386	ENSG00000240386	LCE1F	1:152748847-152749445	NOTEST	0	0	0	0	1	1
ENSG00000240388	ENSG00000240388	CTD-2061E19.1	5:90650294-90650751	NOTEST	0	0	0	0	1	1
ENSG00000240389	ENSG00000240389	EGFL8	HSCHR6_MHC_APD:32127475-32157217	NOTEST	0	0	0	0	1	1
ENSG00000240392	ENSG00000240392	RPL9P3	14:35514112-35786699	NOTEST	0	0	0	0	1	1
ENSG00000240393	ENSG00000240393	RP11-768G7.1	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000240395	ENSG00000240395	RPL5P23	8:42195971-42229326	NOTEST	0.0639308	0.0830338	0.377187	0	1	1
ENSG00000240396	ENSG00000240396	CU459202.1	GL000243.1:4606-4688	NOTEST	0	0	0	0	1	1
ENSG00000240401	ENSG00000240401	AC012358.8	2:55514977-55647057	NOTEST	0.210619	0.0757693	-1.47495	0	1	1
ENSG00000240403	ENSG00000240403	KIR3DL2	19:55235968-55378662	NOTEST	0	0	0	0	1	1
ENSG00000240404	ENSG00000240404	RP11-142L1.3	3:81538849-81811312	NOTEST	0	0	0	0	1	1
ENSG00000240409	ENSG00000240409	MTATP8P1	1:536815-660283	NOTEST	0	0	0	0	1	1
ENSG00000240411	ENSG00000240411	RPL5P16	5:82073615-82074405	NOTEST	0	0	0	0	1	1
ENSG00000240412	ENSG00000240412	RPL5P15	5:57878047-58159241	NOTEST	0	0	0	0	1	1
ENSG00000240416	ENSG00000240416	CYCSP20	7:128757566-128757881	NOTEST	0	0	0	0	1	1
ENSG00000240418	ENSG00000240418	CTD-2013N17.1	19:16466049-16582896	NOTEST	0	0.0465075	inf	0	1	1

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ENSG00000240423	ENSG00000240423	LINC00636	3:107602094-107647754	NOTEST	0	0	0	0	1	1
ENSG00000240424	ENSG00000240424	RP11-158N24.1	12:12721134-12721710	NOTEST	0	0	0	0	1	1
ENSG00000240426	ENSG00000240426	RP11-356M17.1	4:77234153-77343021	NOTEST	0	0	0	0	1	1
ENSG00000240427	ENSG00000240427	RPS26P34	8:82517803-82543369	NOTEST	0	0	0	0	1	1
ENSG00000240429	ENSG00000240429	LRRFIP1P1	3:178865901-178984790	NOTEST	0.318338	0.564946	0.827553	0	1	1
ENSG00000240432	ENSG00000240432	KRTAP13-3	21:31797582-31798286	NOTEST	0	0	0	0	1	1
ENSG00000240433	ENSG00000240433	LY6G5B	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000240435	ENSG00000240435	RPS12P27	16:68021296-68272005	NOTEST	0.25987	0	#NAME?	0	1	1
ENSG00000240436	ENSG00000240436	RP11-95I19.1	5:61601988-61924409	NOTEST	0.0981779	0	#NAME?	0	1	1
ENSG00000240438	ENSG00000240438	OFD1P5Y	Y:20652800-20790963	NOTEST	0	0	0	0	1	1
ENSG00000240439	ENSG00000240439	RN7SL91P	X:25078767-25079056	NOTEST	0	0	0	0	1	1
ENSG00000240440	ENSG00000240440	AC007879.3	2:208038357-208102599	NOTEST	0	0	0	0	1	1
ENSG00000240441	ENSG00000240441	RP11-864J10.2	12:108113375-108113910	NOTEST	0.0408092	0	#NAME?	0	1	1
ENSG00000240443	ENSG00000240443	RPS10P20	12:48876285-48894744	NOTEST	0	0	0	0	1	1
ENSG00000240445	ENSG00000240445	FOXO3B	17:18538318-18585575	NOTEST	0.326968	0.428869	0.391391	0	1	1
ENSG00000240449	ENSG00000240449	RP4-584D14.5	7:150060865-150109558	NOTEST	0.0365901	0	#NAME?	0	1	1
ENSG00000240452	ENSG00000240452	RP11-567P17.1	3:120405527-120501916	NOTEST	0	0	0	0	1	1
ENSG00000240453	ENSG00000240453	RP11-206L10.10	1:714149-755214	NOTEST	0	0	0	0	1	1
ENSG00000240454	ENSG00000240454	RPL39P26	11:13690216-13753893	NOTEST	0	0	0	0	1	1
ENSG00000240455	ENSG00000240455	RN7SL671P	4:1870786-1871064	NOTEST	0	0	0	0	1	1
ENSG00000240457	ENSG00000240457	RN7SL472P	14:102543519-102543810	NOTEST	0	0	0	0	1	1
ENSG00000240458	ENSG00000240458	RP11-450H5.3	3:166439245-166439398	NOTEST	0	0	0	0	1	1
ENSG00000240459	ENSG00000240459	RP11-477G18.1	4:113037665-113038059	NOTEST	0	0	0	0	1	1
ENSG00000240466	ENSG00000240466	RN7SL331P	15:84867599-84898888	NOTEST	0	0	0	0	1	1
ENSG00000240470	ENSG00000240470	RN7SL346P	15:90703835-90772911	NOTEST	0	0	0	0	1	1
ENSG00000240471	ENSG00000240471	PHBP8	3:119499330-119537332	NOTEST	0	0	0	0	1	1
ENSG00000240474	ENSG00000240474	RN7SL116P	20:37434347-37551667	NOTEST	0	0	0	0	1	1
ENSG00000240476	ENSG00000240476	LINC00973	3:98621267-98737406	NOTEST	0.075109	0.397945	2.40551	0	1	1
ENSG00000240477	ENSG00000240477	RP11-63E16.1	3:149478891-149942977	NOTEST	0	0	0	0	1	1
ENSG00000240478	ENSG00000240478	RP11-416O18.2	3:181839671-181859925	NOTEST	0	0	0	0	1	1
ENSG00000240480	ENSG00000240480	RPL29P2	17:7620671-7737062	NOTEST	0	0	0	0	1	1
ENSG00000240481	ENSG00000240481	RN7SL38P	12:24857498-24927147	NOTEST	0	0	0	0	1	1
ENSG00000240484	ENSG00000240484	RP11-386M24.1	15:93146139-93353114	NOTEST	0	0	0	0	1	1
ENSG00000240486	ENSG00000240486	RPL23AP54	8:5334069-5334488	NOTEST	0	0	0	0	1	1
ENSG00000240487	ENSG00000240487	RP11-553L6.3	3:113933159-113956425	NOTEST	0	0	0	0	1	1
ENSG00000240490	ENSG00000240490	RN7SL277P	1:19665266-19812066	NOTEST	0	0	0	0	1	1
ENSG00000240499	ENSG00000240499	RP5-1101C3.1	7:121958480-122526813	NOTEST	0	0	0	0	1	1
ENSG00000240502	ENSG00000240502	RN7SL837P	1:231029886-231030173	NOTEST	0.245729	0	#NAME?	0	1	1
ENSG00000240505	ENSG00000240505	TNFRSF13B	17:16826228-16875432	NOTEST	0	0	0	0	1	1
ENSG00000240508	ENSG00000240508	PSMB9	HSCHR6_MHC_MCF:32841973-32881069	NOTEST	0	0	0	0	1	1
ENSG00000240509	ENSG00000240509	RPL34P18	8:94969565-94969919	NOTEST	0.470717	0.424087	-0.150501	0	1	1

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ENSG00000240511	ENSG00000240511	MED28P2	3:148747913-148820610	NOTEST	0	0	0	0	1	1
ENSG00000240513	ENSG00000240513	RP11-829H16.1	14:31091317-31291908	NOTEST	0	0	0	0	1	1
ENSG00000240518	ENSG00000240518	RP11-515C16.1	5:139988669-139988985	NOTEST	0	0	0	0	1	1
ENSG00000240519	ENSG00000240519	RP11-384C12.1	8:26605666-26724790	NOTEST	0	0	0	0	1	1
ENSG00000240520	ENSG00000240520	UOX	1:84764048-84863514	NOTEST	0.0323636	0	#NAME?	0	1	1
ENSG00000240521	ENSG00000240521	RP11-680B3.2	3:148508888-148677899	NOTEST	0	0	0	0	1	1
ENSG00000240524	ENSG00000240524	RP5-1061H20.3	1:229394027-229441641	NOTEST	0.0321859	0	#NAME?	0	1	1
ENSG00000240527	ENSG00000240527	RP11-429G19.3	10:97471535-97849995	NOTEST	0	0	0	0	1	1
ENSG00000240531	ENSG00000240531	RPL21P123	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000240533	ENSG00000240533	RN7SL69P	12:6058039-6233936	NOTEST	0	0	0	0	1	1
ENSG00000240534	ENSG00000240534	RPL34P17	8:53023398-53373519	NOTEST	0	0	0	0	1	1
ENSG00000240535	ENSG00000240535	CTD-2313F11.1	5:54273691-54338672	NOTEST	0	0	0	0	1	1
ENSG00000240540	ENSG00000240540	RPL3P9	8:80483387-80484570	NOTEST	0	0	0	0	1	1
ENSG00000240541	ENSG00000240541	TM4SF1-AS1	3:149086808-149104370	NOTEST	0	0	0	0	1	1
ENSG00000240542	ENSG00000240542	KRTAP9-1	17:39344696-39346891	NOTEST	0	0	0	0	1	1
ENSG00000240545	ENSG00000240545	RN7SL492P	4:57660515-57660808	NOTEST	0	0	0	0	1	1
ENSG00000240549	ENSG00000240549	THOC7-AS1	3:63727968-63849579	NOTEST	0.108982	0.0230292	-2.24256	0	1	1
ENSG00000240553	ENSG00000240553	RP1-184J9.2	1:23345940-23504301	NOTEST	0	0	0	0	1	1
ENSG00000240554	ENSG00000240554	RPL7AP58	11:29735455-29903261	NOTEST	0	0	0	0	1	1
ENSG00000240562	ENSG00000240562	RP11-59J16.2	3:127199532-127255655	NOTEST	0	0	0	0	1	1
ENSG00000240563	ENSG00000240563	L1TD1	1:62660502-62678000	NOTEST	0	0	0	0	1	1
ENSG00000240566	ENSG00000240566	AC010153.3	Y:26796954-26797681	NOTEST	0	0	0	0	1	1
ENSG00000240567	ENSG00000240567	RP11-3P17.4	3:161144214-161166030	NOTEST	0	0	0	0	1	1
ENSG00000240568	ENSG00000240568	RP11-1008M1.1	3:68053358-68594776	NOTEST	0	0	0	0	1	1
ENSG00000240571	ENSG00000240571	RP11-775D22.3	7:129804554-129847610	NOTEST	0	0.0286324	inf	0	1	1
ENSG00000240572	ENSG00000240572	RP11-121C1.1	3:99045220-99045396	NOTEST	0	0	0	0	1	1
ENSG00000240573	ENSG00000240573	RP11-354H21.2	3:78136554-78141421	NOTEST	0	0	0	0	1	1
ENSG00000240577	ENSG00000240577	RN7SL445P	10:5673425-5673716	NOTEST	0	0	0	0	1	1
ENSG00000240578	ENSG00000240578	TRBV22-1	7:142349248-142349699	NOTEST	0	0	0	0	1	1
ENSG00000240579	ENSG00000240579	RP11-20L24.1	7:127292233-127732661	NOTEST	0	0	0	0	1	1
ENSG00000240583	ENSG00000240583	AQP1	7:30692199-30965131	NOTEST	0.0875025	0.140079	0.678849	0	1	1
ENSG00000240584	ENSG00000240584	RN7SL547P	20:7614210-7614498	NOTEST	0	0	0	0	1	1
ENSG00000240589	ENSG00000240589	RN7SL258P	17:42472651-42580798	NOTEST	0	0	0	0	1	1
ENSG00000240590	ENSG00000240590	RP11-403P13.1	8:111117304-111118193	NOTEST	0	0	0	0	1	1
ENSG00000240591	ENSG00000240591	RP11-247I13.11	22:31795508-32058418	NOTEST	0.369621	0.162027	-1.18981	0	1	1
ENSG00000240592	ENSG00000240592	EGFL8	HSCHR6_MHC_MCF:32192561-32222305	NOTEST	0	0	0	0	1	1
ENSG00000240596	ENSG00000240596	KCNAB1-AS2	3:155755489-156256545	NOTEST	0	0	0	0	1	1
ENSG00000240601	ENSG00000240601	RPL9P15	3:154394376-154394908	NOTEST	0	0	0	0	1	1
ENSG00000240602	ENSG00000240602	RP11-64D22.2	3:151451703-151645963	NOTEST	0	0	0	0	1	1
ENSG00000240606	ENSG00000240606	RN7SL564P	6:123066418-123066693	NOTEST	0	0	0	0	1	1
ENSG00000240611	ENSG00000240611	CTB-49A3.1	5:132496129-132948255	NOTEST	0	0	0	0	1	1

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ENSG00000240621	ENSG00000240621	OR2AO1P	7:143873832-143874235	NOTEST	0	0	0	0	1	1
ENSG00000240622	ENSG00000240622	RPL7P15	3:123798869-124445172	NOTEST	0	0	0	0	1	1
ENSG00000240624	ENSG00000240624	RP11-45P15.2	14:103749269-103749805	NOTEST	0	0	0	0	1	1
ENSG00000240625	ENSG00000240625	RN7SL403P	6:43003935-43004238	NOTEST	0	0	0	0	1	1
ENSG00000240626	ENSG00000240626	RN7SL150P	19:34418267-34418530	NOTEST	0	0	0	0	1	1
ENSG00000240627	ENSG00000240627	CTD-2312P21.1	5:50571086-50571568	NOTEST	0	0	0	0	1	1
ENSG00000240631	ENSG00000240631	RPL30P12	12:107304534-107304887	NOTEST	0	0	0	0	1	1
ENSG00000240632	ENSG00000240632	SPATA31D5P	9:84528351-84534841	NOTEST	0	0	0	0	1	1
ENSG00000240634	ENSG00000240634	RP11-1348G14.1	16:28814096-28829149	NOTEST	0.0568041	0.0642801	0.178376	0	1	1
ENSG00000240637	ENSG00000240637	RN7SL808P	4:115720486-115720783	NOTEST	0	0	0	0	1	1
ENSG00000240639	ENSG00000240639	RN7SL666P	20:41850845-41851147	NOTEST	0	0	0	0	1	1
ENSG00000240641	ENSG00000240641	RN7SL580P	6:51464520-51952423	NOTEST	0	0	0	0	1	1
ENSG00000240647	ENSG00000240647	RN7SL305P	22:32377131-32377414	NOTEST	0	0	0	0	1	1
ENSG00000240651	ENSG00000240651	SEPT7P4	7:62693412-62708699	NOTEST	0	0	0	0	1	1
ENSG00000240652	ENSG00000240652	RP11-832N8.1	11:107661716-107799019	NOTEST	0.0848964	0.0609373	-0.478378	0	1	1
ENSG00000240654	ENSG00000240654	C1QTNF9	13:24553838-24896673	NOTEST	0	0.00623009	inf	0	1	1
ENSG00000240661	ENSG00000240661	RP11-174O3.3	3:120068356-120086845	NOTEST	0	0	0	0	1	1
ENSG00000240663	ENSG00000240663	RN7SL310P	18:47733369-47733648	NOTEST	0	0	0	0	1	1
ENSG00000240665	ENSG00000240665	LSP1P2	3:75444338-75444471	NOTEST	0	0	0	0	1	1
ENSG00000240666	ENSG00000240666	MME-AS1	3:154741912-154901497	NOTEST	0.0714645	0.164238	1.20049	0	1	1
ENSG00000240667	ENSG00000240667	AL450992.6	1:151967006-152020383	NOTEST	0	0	0	0	1	1
ENSG00000240668	ENSG00000240668	KRT8P36	3:137780831-137834660	NOTEST	0.0797747	0.124064	0.637082	0	1	1
ENSG00000240669	ENSG00000240669	RP11-555K12.2	4:153535026-153535485	NOTEST	0	0	0	0	1	1
ENSG00000240671	ENSG00000240671	IGKV1-8	2:89291927-89292450	NOTEST	0	0	0	0	1	1
ENSG00000240673	ENSG00000240673	AC006539.2	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000240677	ENSG00000240677	MYL6P4	7:141511604-141512057	NOTEST	0	0	0	0	1	1
ENSG00000240680	ENSG00000240680	AC016831.3	7:130507626-130508270	NOTEST	0	0	0	0	1	1
ENSG00000240684	ENSG00000240684	XXbac-BPG254F23.6	HSCHR6_MHC_DBB:32602483-32612425	NOTEST	0	0	0	0	1	1
ENSG00000240687	ENSG00000240687	RP11-521D12.1	2:9778900-9789568	NOTEST	0	0	0	0	1	1
ENSG00000240688	ENSG00000240688	CU013544.2	GL000233.1:35213-35296	NOTEST	0	0	0	0	1	1
ENSG00000240692	ENSG00000240692	RN7SL538P	1:70034080-70671303	NOTEST	0	0	0	0	1	1
ENSG00000240695	ENSG00000240695	RP11-102M11.1	3:135969147-136471220	NOTEST	0.128567	0	#NAME?	0	1	1
ENSG00000240698	ENSG00000240698	RPS2P39	11:108535751-108811657	NOTEST	0	0	0	0	1	1
ENSG00000240704	ENSG00000240704	KLF7P1	3:170670638-170671686	NOTEST	0	0	0	0	1	1
ENSG00000240707	ENSG00000240707	LINC01168	10:134779037-134789858	NOTEST	0	0	0	0	1	1
ENSG00000240708	ENSG00000240708	RP11-64C1.1	3:55330227-55334766	NOTEST	0	0	0	0	1	1
ENSG00000240710	ENSG00000240710	RP11-430C7.4	1:204572162-204585693	NOTEST	0	0	0	0	1	1
ENSG00000240713	ENSG00000240713	RN7SL860P	19:22779058-22791303	NOTEST	0	0	0	0	1	1
ENSG00000240718	ENSG00000240718	RN7SL851P	7:6048875-6098861	NOTEST	0	0	0	0	1	1
ENSG00000240720	ENSG00000240720	LRRD1	7:91741464-91810039	NOTEST	0.0119095	0	#NAME?	0	1	1
ENSG00000240721	ENSG00000240721	RPS4XP15	12:88338661-88344596	NOTEST	0	0	0	0	1	1
ENSG00000240723	ENSG00000240723	RN7SL382P	4:139936942-140098372	NOTEST	0	0.104104	inf	0	1	1
ENSG00000240724	ENSG00000240724	RPS12P15	8:103515980-103516365	NOTEST	0	0	0	0	1	1

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ENSG00000240730	ENSG00000240730	RN7SL710P	14:97925152-98047938	NOTEST	0	0	0	0	1	1
ENSG00000240733	ENSG00000240733	RN7SL502P	6:36322418-36458920	NOTEST	0.491457	0.0904889	-2.44125	0	1	1
ENSG00000240738	ENSG00000240738	RP1-273G13.1	8:33462373-33896526	NOTEST	0	0	0	0	1	1
ENSG00000240739	ENSG00000240739	RP11-69M1.1	12:8147365-8147680	NOTEST	0	0	0	0	1	1
ENSG00000240747	ENSG00000240747	KRBOX1	3:42846243-43101703	NOTEST	0	0	0	0	1	1
ENSG00000240750	ENSG00000240750	RN7SL559P	1:28296854-28415207	NOTEST	0.11758	0.0921612	-0.351407	0	1	1
ENSG00000240751	ENSG00000240751	RP11-553D4.2	3:112929849-113160457	NOTEST	0.0782541	0.0786754	0.00774621	0	1	1
ENSG00000240752	ENSG00000240752	RP11-588D3.1	3:78646389-79816965	NOTEST	0	0	0	0	1	1
ENSG00000240754	ENSG00000240754	RP11-38J22.6	1:206238871-206306131	NOTEST	0	0	0	0	1	1
ENSG00000240755	ENSG00000240755	ERLEC1P1	21:15399741-15583166	NOTEST	0	1.49E-06	inf	0	1	1
ENSG00000240758	ENSG00000240758	RP11-155G14.6	7:128095893-128146656	NOTEST	0.429618	0.537149	0.322269	0	1	1
ENSG00000240760	ENSG00000240760	RPL31P56	16:55386632-55387000	NOTEST	0	0	0	0	1	1
ENSG00000240761	ENSG00000240761	AC098831.4	2:203638747-203639083	NOTEST	0	0	0	0	1	1
ENSG00000240764	ENSG00000240764	PCDHGC5	5:140710251-140892546	NOTEST	0.144599	0.218993	0.59883	0	1	1
ENSG00000240766	ENSG00000240766	PLCXD2-AS1	3:111393522-111695364	NOTEST	0	0	0	0	1	1
ENSG00000240767	ENSG00000240767	RN7SL288P	13:46700054-46786006	NOTEST	0	0	0	0	1	1
ENSG00000240770	ENSG00000240770	C21orf91-OT1	21:19135631-19191703	NOTEST	0	0	0	0	1	1
ENSG00000240772	ENSG00000240772	RN7SL776P	4:168321647-168321905	NOTEST	0	0	0	0	1	1
ENSG00000240774	ENSG00000240774	RP11-359H3.4	3:120203017-120203374	NOTEST	0	0	0	0	1	1
ENSG00000240775	ENSG00000240775	RP11-170N16.2	4:123747862-123844123	NOTEST	0	0	0	0	1	1
ENSG00000240776	ENSG00000240776	RP11-435F17.1	3:113547028-113666417	NOTEST	0.0855006	0	#NAME?	0	1	1
ENSG00000240777	ENSG00000240777	RP11-58O15.1	3:55542335-56502391	NOTEST	0	0	0	0	1	1
ENSG00000240779	ENSG00000240779	CU463998.1	GL000240.1:3054-3137	NOTEST	0	0	0	0	1	1
ENSG00000240785	ENSG00000240785	RPL36AP21	5:18049658-18049981	NOTEST	0	0	0	0	1	1
ENSG00000240787	ENSG00000240787	RP11-615J4.4	3:111011565-111384597	NOTEST	0	0.0470689	inf	0	1	1
ENSG00000240790	ENSG00000240790	AC073934.6	7:127284738-127292066	NOTEST	0	0	0	0	1	1
ENSG00000240791	ENSG00000240791	RP11-100G15.5	9:94794280-94877666	NOTEST	0	0	0	0	1	1
ENSG00000240792	ENSG00000240792	RP11-418B12.1	3:163192854-163197153	NOTEST	0	0	0	0	1	1
ENSG00000240793	ENSG00000240793	UBA52P8	16:48198862-48482313	NOTEST	0.20197	0.155977	-0.37281	0	1	1
ENSG00000240796	ENSG00000240796	MTND2P14	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000240800	ENSG00000240800	ATP8A2P1	10:37414784-37673039	NOTEST	0	0	0	0	1	1
ENSG00000240801	ENSG00000240801	AC132217.4	11:2150341-2182571	NOTEST	0.376283	0.280482	-0.423907	0	1	1
ENSG00000240803	ENSG00000240803	RN7SL231P	19:14323863-14324131	NOTEST	0	0	0	0	1	1
ENSG00000240804	ENSG00000240804	NPM1P28	3:147308782-147309622	NOTEST	0	0	0	0	1	1
ENSG00000240808	ENSG00000240808	CTD-3236F5.1	11:17095935-17229530	NOTEST	0	0.0883176	inf	0	1	1
ENSG00000240809	ENSG00000240809	RP11-550F7.1	3:75955845-77699115	NOTEST	0.0457202	0.0915788	1.00218	0	1	1
ENSG00000240813	ENSG00000240813	RP11-963H4.2	17:10583653-10718481	NOTEST	0	0	0	0	1	1
ENSG00000240820	ENSG00000240820	RN7SL695P	18:48633123-48633416	NOTEST	0.119391	0.272339	1.18971	0	1	1
ENSG00000240821	ENSG00000240821	RPL9P25	15:66628543-66679084	NOTEST	0.166418	0.014062	-3.56494	0	1	1
ENSG00000240823	ENSG00000240823	RN7SL23P	11:61170120-61258403	NOTEST	0.339511	0.0829831	-2.03257	0	1	1
ENSG00000240824	ENSG00000240824	MTND3P7	3:165878564-165878907	NOTEST	0	0	0	0	1	1
ENSG00000240827	ENSG00000240827	RP11-227H4.1	3:98338908-98339462	NOTEST	0	0	0	0	1	1
ENSG00000240828	ENSG00000240828	RPL21P4	17:41196311-41277500	NOTEST	0	0.0375879	inf	0	1	1

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ENSG00000240834	ENSG00000240834	IGKV1D-12	2:90198534-90199190	NOTEST	0	0	0	0	1	1
ENSG00000240837	ENSG00000240837	RN7SL77P	14:71047973-71108015	NOTEST	0	0	0	0	1	1
ENSG00000240842	ENSG00000240842	RP11-62G11.2	3:69613256-69620273	NOTEST	0	0	0	0	1	1
ENSG00000240845	ENSG00000240845	RPL23AP1	HSCHR6_MHC_DBB:29688036-29714307	NOTEST	0	0	0	0	1	1
ENSG00000240846	ENSG00000240846	RPS15P9	19:1285889-1378430	NOTEST	0	0	0	0	1	1
ENSG00000240847	ENSG00000240847	RN7SL497P	15:41474922-41522941	NOTEST	0	0	0	0	1	1
ENSG00000240853	ENSG00000240853	RN7SL328P	9:134452156-134615461	NOTEST	0	0	0	0	1	1
ENSG00000240854	ENSG00000240854	RP11-64K7.1	3:131252398-132004254	NOTEST	0.0130394	0.0314465	1.27002	0	1	1
ENSG00000240859	ENSG00000240859	AC093627.10	7:149596-155465	NOTEST	0.274965	0.156234	-0.815542	0	1	1
ENSG00000240861	ENSG00000240861	RP11-572F4.1	16:74485855-74641012	NOTEST	0	0	0	0	1	1
ENSG00000240863	ENSG00000240863	RN7SL645P	16:58163432-58251709	NOTEST	0	0	0	0	1	1
ENSG00000240864	ENSG00000240864	IGKV1-16	2:89399351-89399854	NOTEST	0	0	0	0	1	1
ENSG00000240868	ENSG00000240868	C1QTNF9-AS1	13:24553838-24896673	NOTEST	0	0	0	0	1	1
ENSG00000240869	ENSG00000240869	RN7SL128P	6:20402397-20493941	NOTEST	0.107723	0	#NAME?	0	1	1
ENSG00000240870	ENSG00000240870	RPL19P14	8:99413630-99955055	NOTEST	0	0.0261286	inf	0	1	1
ENSG00000240871	ENSG00000240871	KRTAP4-7	17:39240458-39241396	NOTEST	0	0	0	0	1	1
ENSG00000240873	ENSG00000240873	RPS29P22	17:26368762-26523407	NOTEST	0	0	0	0	1	1
ENSG00000240874	ENSG00000240874	CTD-2515H24.1	15:57848148-57848577	NOTEST	0	0	0	0	1	1
ENSG00000240877	ENSG00000240877	RN7SL521P	7:148799875-148823438	NOTEST	0.355438	0	#NAME?	0	1	1
ENSG00000240881	ENSG00000240881	RP11-713P14.1	11:23541867-23542748	NOTEST	0	0	0	0	1	1
ENSG00000240882	ENSG00000240882	RP11-174O3.1	3:120025572-120026799	NOTEST	0.028129	0.00989973	-1.50659	0	1	1
ENSG00000240888	ENSG00000240888	RP13-635I23.3	3:142984063-143567373	NOTEST	0	0	0	0	1	1
ENSG00000240889	ENSG00000240889	NDUFB2-AS1	7:140218219-140624564	NOTEST	0.155014	0.183479	0.24322	0	1	1
ENSG00000240890	ENSG00000240890	RP11-65E22.2	3:132105365-132107918	NOTEST	0.00715368	0	#NAME?	0	1	1
ENSG00000240893	ENSG00000240893	RP11-572C15.5	3:112455293-112468166	NOTEST	0	0	0	0	1	1
ENSG00000240895	ENSG00000240895	RP11-119D18.1	3:110246328-110248429	NOTEST	0	0	0	0	1	1
ENSG00000240902	ENSG00000240902	APOOP2	3:87643987-87644526	NOTEST	0	0	0	0	1	1
ENSG00000240905	ENSG00000240905	RN7SL798P	8:56792371-56923940	NOTEST	0	0	0	0	1	1
ENSG00000240906	ENSG00000240906	AP000356.1	22:25028881-25055114	NOTEST	0.524629	0.233483	-1.16798	0	1	1
ENSG00000240907	ENSG00000240907	BX255923.3	9:69174212-69179458	NOTEST	0.0109884	0.00771526	-0.51019	0	1	1
ENSG00000240912	ENSG00000240912	RP11-274J15.2	3:113822095-113822475	NOTEST	0	0	0	0	1	1
ENSG00000240913	ENSG00000240913	RN7SL856P	2:25264998-25378243	NOTEST	0	0	0	0	1	1
ENSG00000240914	ENSG00000240914	RPL15P2	14:95267185-95267800	NOTEST	0	0.0236836	inf	0	1	1
ENSG00000240915	ENSG00000240915	RP11-659E9.2	8:63925626-63927240	NOTEST	0	0	0	0	1	1
ENSG00000240919	ENSG00000240919	RP11-400K9.1	8:54445467-54446264	NOTEST	0.0903899	0.117	0.372275	0	1	1
ENSG00000240922	ENSG00000240922	LSAMP-AS1	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000240924	ENSG00000240924	HCG17	HSCHR6_MHC_MANN:30246906-30359341	NOTEST	0	0	0	0	1	1
ENSG00000240925	ENSG00000240925	RPS20P31	12:120639093-120703574	NOTEST	0.091656	0	#NAME?	0	1	1
ENSG00000240927	ENSG00000240927	RN7SL209P	15:102291234-102334505	NOTEST	0	0	0	0	1	1
ENSG00000240929	ENSG00000240929	HIST2H2BB	1:149369293-149429348	NOTEST	0	0	0	0	1	1
ENSG00000240934	ENSG00000240934	RP11-925D8.1	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000240935	ENSG00000240935	PLGLA	2:106998561-107010027	NOTEST	0.00520348	0	#NAME?	0	1	1
ENSG00000240936	ENSG00000240936	RN7SL554P	6:6938834-6939130	NOTEST	0	0	0	0	1	1
ENSG00000240940	ENSG00000240940	RN7SL591P	10:64109767-64110048	NOTEST	0	0	0	0	1	1

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ENSG00000240951	ENSG00000240951	RP11-91A15.2	3:89637035-89637720	NOTEST	0	0	0	0	1	1
ENSG00000240954	ENSG00000240954	RPL4P1	14:22218552-22219830	NOTEST	0	0	0	0	1	1
ENSG00000240957	ENSG00000240957	LY6G6F	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000240959	ENSG00000240959	ST13P14	3:50712671-51421629	NOTEST	0	0	0	0	1	1
ENSG00000240960	ENSG00000240960	RP11-521D12.4	2:9886832-9886998	NOTEST	0	0	0	0	1	1
ENSG00000240961	ENSG00000240961	RN7SL415P	6:92449326-92449614	NOTEST	0	0	0	0	1	1
ENSG00000240963	ENSG00000240963	RP11-518L10.5	1:244515936-244615436	NOTEST	0	0	0	0	1	1
ENSG00000240964	ENSG00000240964	RN7SL751P	3:78646389-79816965	NOTEST	0	0	0	0	1	1
ENSG00000240966	ENSG00000240966	RN7SL681P	4:88224940-88312538	NOTEST	0	0	0	0	1	1
ENSG00000240970	ENSG00000240970	RPL23AP64	11:118868851-118901616	NOTEST	0.267642	0.211773	-0.337781	0	1	1
ENSG00000240973	ENSG00000240973	RP11-458K10.2	7:115319398-115322672	NOTEST	0	0	0	0	1	1
ENSG00000240974	ENSG00000240974	CTD-2024I7.1	5:140894582-141016437	NOTEST	0	0	0	0	1	1
ENSG00000240975	ENSG00000240975	RP11-313M3.1	11:39183002-39183517	NOTEST	0	0	0	0	1	1
ENSG00000240977	ENSG00000240977	RN7SL283P	2:140740252-140740553	NOTEST	0	0	0	0	1	1
ENSG00000240979	ENSG00000240979	RP11-79D8.2	9:82186687-82341658	NOTEST	0	0	0	0	1	1
ENSG00000240980	ENSG00000240980	RP11-734K21.4	2:9283294-9286235	NOTEST	0	0	0	0	1	1
ENSG00000240983	ENSG00000240983	RP11-742D12.1	18:44259080-44340307	NOTEST	0	0	0	0	1	1
ENSG00000240991	ENSG00000240991	RPL23AP67	12:133692277-133707059	NOTEST	0	0	0	0	1	1
ENSG00000240992	ENSG00000240992	RPS23P4	4:146190961-146191710	NOTEST	0	0	0	0	1	1
ENSG00000240993	ENSG00000240993	RN7SL459P	12:19282647-19529334	NOTEST	0	0	0	0	1	1
ENSG00000240994	ENSG00000240994	RN7SL61P	15:82751613-82798350	NOTEST	0	0	0	0	1	1
ENSG00000240995	ENSG00000240995	RP11-708H21.1	17:47209821-47247351	NOTEST	0	0	0	0	1	1
ENSG00000240996	ENSG00000240996	RP11-80H5.7	10:91426937-91459428	NOTEST	0.200178	0.183042	-0.129106	0	1	1
ENSG00000240997	ENSG00000240997	RN7SL183P	6:88555367-88555663	NOTEST	0	0	0	0	1	1
ENSG00000241000	ENSG00000241000	CU463998.2	GL000240.1:1480-1563	NOTEST	0	0	0	0	1	1
ENSG00000241002	ENSG00000241002	RP11-119H12.1	4:113659827-113660262	NOTEST	0	0	0	0	1	1
ENSG00000241003	ENSG00000241003	RP11-22C11.1	8:95653301-95719694	NOTEST	0	0	0	0	1	1
ENSG00000241007	ENSG00000241007	SEPT7P6	7:151832009-152133090	NOTEST	0.0583895	0.0118794	-2.29725	0	1	1
ENSG00000241008	ENSG00000241008	RP11-494M8.1	11:7710668-7927502	NOTEST	0	0	0	0	1	1
ENSG00000241011	ENSG00000241011	RP11-713C19.1	4:189012426-189030757	NOTEST	0	0	0	0	1	1
ENSG00000241014	ENSG00000241014	RP11-244H3.1	1:35439956-35497569	NOTEST	0.135597	0.0695706	-0.962775	0	1	1
ENSG00000241018	ENSG00000241018	RCC2P5	3:96472028-96473515	NOTEST	0	0	0	0	1	1
ENSG00000241022	ENSG00000241022	NIPA2P2	3:75133305-75134388	NOTEST	0	0	0	0	1	1
ENSG00000241026	ENSG00000241026	CTD-2036J7.1	8:22224761-22291642	NOTEST	0	0	0	0	1	1
ENSG00000241030	ENSG00000241030	RPL29P24	12:120941076-121015397	NOTEST	0.0526715	0	#NAME?	0	1	1
ENSG00000241032	ENSG00000241032	RN7SL709P	8:37766258-37766553	NOTEST	0	0	0	0	1	1
ENSG00000241034	ENSG00000241034	RN7SL545P	15:22704720-22715604	NOTEST	0	0	0	0	1	1
ENSG00000241035	ENSG00000241035	RP11-689J19.1	14:21853352-21924285	NOTEST	0	0	0	0	1	1
ENSG00000241037	ENSG00000241037	RN7SL335P	4:123008660-123008966	NOTEST	0	0	0	0	1	1
ENSG00000241042	ENSG00000241042	RP11-145M4.1	1:59520068-59553867	NOTEST	0	0	0	0	1	1
ENSG00000241043	ENSG00000241043	GVQW1	9:32540541-32573160	NOTEST	0.459222	0.411063	-0.159832	0	1	1
ENSG00000241045	ENSG00000241045	RPL7P43	12:77115313-77116066	NOTEST	0	0	0	0	1	1
ENSG00000241048	ENSG00000241048	RP11-167H9.5	3:149478891-149942977	NOTEST	0	0	0	0	1	1

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ENSG00000241053	ENSG00000241053	HCG17	HSCHR6_MHC_DBB:30192096-30304918	NOTEST	0	0	0	0	1	1
ENSG00000241054	ENSG00000241054	RP5-1002M8.4	20:20015011-20341346	NOTEST	0.213066	0.126422	-0.753059	0	1	1
ENSG00000241057	ENSG00000241057	AC004985.12	7:43966036-44058774	NOTEST	0	0	0	0	1	1
ENSG00000241059	ENSG00000241059	CTD-2061E19.6	5:90651196-90651843	NOTEST	0	0	0	0	1	1
ENSG00000241061	ENSG00000241061	RPL5P1	15:25068793-25492435	NOTEST	0.367625	0.145337	-1.33884	0	1	1
ENSG00000241064	ENSG00000241064	RN7SL110P	3:15422781-15563258	NOTEST	0	0	0	0	1	1
ENSG00000241067	ENSG00000241067	RPL17P40	16:16043433-16236931	NOTEST	0	0	0	0	1	1
ENSG00000241069	ENSG00000241069	CTD-3141N22.1	19:53868945-53930574	NOTEST	0.355317	0	#NAME?	0	1	1
ENSG00000241073	ENSG00000241073	RP4-714D9.2	1:100503652-100598511	NOTEST	0.0518037	0	#NAME?	0	1	1
ENSG00000241074	ENSG00000241074	RN7SL813P	2:169307833-169308136	NOTEST	0	0	0	0	1	1
ENSG00000241075	ENSG00000241075	RN7SL719P	15:28947099-29002537	NOTEST	0	0	0	0	1	1
ENSG00000241082	ENSG00000241082	RN7SL259P	11:62703455-62703706	NOTEST	0	0	0	0	1	1
ENSG00000241084	ENSG00000241084	RP11-344B5.3	9:132020632-132023860	NOTEST	0	0	0	0	1	1
ENSG00000241088	ENSG00000241088	RPL17P44	18:60082910-60083460	NOTEST	0	0	0	0	1	1
ENSG00000241095	ENSG00000241095	CYP51A1P1	3:82855665-82857172	NOTEST	0.278772	0.229405	-0.281191	0	1	1
ENSG00000241097	ENSG00000241097	RP11-864N7.1	11:74449522-74449841	NOTEST	0	0	0	0	1	1
ENSG00000241098	ENSG00000241098	RP11-139K4.1	3:182164757-182204152	NOTEST	0	0	0	0	1	1
ENSG00000241101	ENSG00000241101	PRICKLE2-AS2	3:64053639-64440508	NOTEST	0	0	0	0	1	1
ENSG00000241102	ENSG00000241102	RP11-286H14.2	7:128735354-128735865	NOTEST	0	0	0	0	1	1
ENSG00000241103	ENSG00000241103	RP11-398J16.1	4:95290983-95291314	NOTEST	0	0	0	0	1	1
ENSG00000241105	ENSG00000241105	RP11-333A23.2	8:71418485-71419053	NOTEST	0	0	0	0	1	1
ENSG00000241106	ENSG00000241106	HLA-DOB	6:32780539-32806599	NOTEST	0.102907	0.258262	1.32749	0	1	1
ENSG00000241111	ENSG00000241111	RP11-129B22.1	3:64053639-64440508	NOTEST	0	0	0	0	1	1
ENSG00000241112	ENSG00000241112	RPL29P14	5:148871759-148931007	NOTEST	0.166564	0.311558	0.903422	0	1	1
ENSG00000241114	ENSG00000241114	AC008280.3	2:54091203-54532437	NOTEST	0	0.12627	inf	0	1	1
ENSG00000241119	ENSG00000241119	UGT1A9	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000241120	ENSG00000241120	HMGN1P8	3:167401085-167452727	NOTEST	0.367858	0.373483	0.0218936	0	1	1
ENSG00000241123	ENSG00000241123	KRTAP10-5	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000241124	ENSG00000241124	HCG16	HSCHR6_MHC_SSTO:28954098-28956435	NOTEST	0	0	0	0	1	1
ENSG00000241125	ENSG00000241125	RP11-508N22.9	10:38453575-38501285	NOTEST	0	0	0	0	1	1
ENSG00000241128	ENSG00000241128	OR14A2	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000241129	ENSG00000241129	RPL22P19	12:125420000-125420441	NOTEST	0	0.0428842	inf	0	1	1
ENSG00000241130	ENSG00000241130	RP11-507J18.1	15:51090866-51091148	NOTEST	0	0	0	0	1	1
ENSG00000241131	ENSG00000241131	RP11-639B1.1	3:147795945-147805816	NOTEST	0	0	0	0	1	1
ENSG00000241132	ENSG00000241132	LY6G5B	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000241134	ENSG00000241134	RP5-1051J4.4	7:150413644-150487837	NOTEST	0	0	0	0	1	1
ENSG00000241136	ENSG00000241136	PAICSP6	7:143318042-143534026	NOTEST	0	0	0	0	1	1
ENSG00000241143	ENSG00000241143	RPL32P9	3:149478891-149942977	NOTEST	0.125722	0.250454	0.994308	0	1	1
ENSG00000241144	ENSG00000241144	RN7SL728P	4:103172197-103371167	NOTEST	0	0	0	0	1	1
ENSG00000241146	ENSG00000241146	RPL7P41	12:53279212-53280169	NOTEST	0	0	0	0	1	1
ENSG00000241149	ENSG00000241149	RP11-561N12.2	7:63465953-63476508	NOTEST	0	0	0	0	1	1

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ENSG00000241151	ENSG00000241151	RP11-454C18.1	3:151354961-151375754	NOTEST	0.0363203	0	#NAME?	0	1	1
ENSG00000241152	ENSG00000241152	RN7SL720P	9:17048916-17112813	NOTEST	0	0	0	0	1	1
ENSG00000241155	ENSG00000241155	ARHGAP31-AS1	3:119013219-119139561	NOTEST	0.0656206	0.10242	0.642275	0	1	1
ENSG00000241156	ENSG00000241156	RN7SL582P	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000241157	ENSG00000241157	RP11-3K24.1	17:58256454-58508782	NOTEST	0.455814	0.464514	0.027277	0	1	1
ENSG00000241158	ENSG00000241158	ADAMTS9-AS1	3:64501332-64997143	NOTEST	0	0	0	0	1	1
ENSG00000241159	ENSG00000241159	RN7SL160P	2:71163011-71306935	NOTEST	0	0	0	0	1	1
ENSG00000241162	ENSG00000241162	RN7SL617P	6:110745889-110797844	NOTEST	0	0	0	0	1	1
ENSG00000241163	ENSG00000241163	LINC00877	3:72084450-72291716	NOTEST	0	0	0	0	1	1
ENSG00000241166	ENSG00000241166	HLA-L	HSCHR6_MHC_DBB:30192096-30304918	NOTEST	0	0	0	0	1	1
ENSG00000241167	ENSG00000241167	RN7SL469P	15:30427351-30437770	NOTEST	0	0	0	0	1	1
ENSG00000241168	ENSG00000241168	RP11-10O22.1	3:162744183-163079351	NOTEST	0	0	0	0	1	1
ENSG00000241169	ENSG00000241169	RP4-752I6.1	1:27730729-27816669	NOTEST	0	0	0	0	1	1
ENSG00000241172	ENSG00000241172	RN7SL70P	19:19068768-19069067	NOTEST	0	0	0	0	1	1
ENSG00000241174	ENSG00000241174	RN7SL570P	9:72435708-72521148	NOTEST	0	0	0	0	1	1
ENSG00000241175	ENSG00000241175	RN7SL494P	15:50534143-50558223	NOTEST	0	0	0	0	1	1
ENSG00000241179	ENSG00000241179	CTB-2L9.1	5:134094468-134195427	NOTEST	0	0	0	0	1	1
ENSG00000241180	ENSG00000241180	RP11-54O7.2	1:840213-851356	NOTEST	0	0	0	0	1	1
ENSG00000241183	ENSG00000241183	RP11-106J23.1	16:70113031-70113527	NOTEST	0	0	0	0	1	1
ENSG00000241185	ENSG00000241185	RPL21P122	17:11901669-12047147	NOTEST	0	0	0	0	1	1
ENSG00000241186	ENSG00000241186	TDGF1	3:46556912-46668033	NOTEST	0	0	0	0	1	1
ENSG00000241187	ENSG00000241187	CTC-209L16.1	5:154092461-154197167	NOTEST	0	0	0	0	1	1
ENSG00000241188	ENSG00000241188	RN7SL165P	1:27141312-27141601	NOTEST	0	0	0	0	1	1
ENSG00000241198	ENSG00000241198	RN7SL191P	X:130268061-130268364	NOTEST	0	0	0	0	1	1
ENSG00000241200	ENSG00000241200	ZNF736P7Y	Y:7859027-7859847	NOTEST	0	0	0	0	1	1
ENSG00000241202	ENSG00000241202	ZIC4-AS1	3:147103832-147228080	NOTEST	0	0	0	0	1	1
ENSG00000241203	ENSG00000241203	HMGN2P26	3:167676531-167676870	NOTEST	0	0	0	0	1	1
ENSG00000241204	ENSG00000241204	RP11-333A23.1	8:71336359-71336811	NOTEST	0	0	0	0	1	1
ENSG00000241207	ENSG00000241207	RP11-344N17.3	X:48136138-48137013	NOTEST	0	0	0	0	1	1
ENSG00000241211	ENSG00000241211	IQCJ-SCHIP1-AS1	3:158680023-159615155	NOTEST	0	0	0	0	1	1
ENSG00000241213	ENSG00000241213	RP11-768G7.2	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000241216	ENSG00000241216	SNAPC5P1	6:6346697-6655216	NOTEST	0	0	0	0	1	1
ENSG00000241217	ENSG00000241217	RN7SL809P	12:57057126-57082159	NOTEST	0	0.276484	inf	0	1	1
ENSG00000241218	ENSG00000241218	RP11-446H18.1	3:106959538-107101007	NOTEST	0.0124076	0.00964415	-0.363498	0	1	1
ENSG00000241219	ENSG00000241219	RP11-572M11.1	3:112709293-112902148	NOTEST	0	0	0	0	1	1
ENSG00000241220	ENSG00000241220	RP11-292E2.1	3:153074895-153091975	NOTEST	0.0320838	0	#NAME?	0	1	1
ENSG00000241221	ENSG00000241221	AC009960.6	2:203482417-203483604	NOTEST	0	0	0	0	1	1
ENSG00000241223	ENSG00000241223	RN7SL39P	18:3496029-4455335	NOTEST	0	0	0	0	1	1
ENSG00000241224	ENSG00000241224	RP11-59E19.1	3:108855560-108868973	NOTEST	0.0166774	0.0532187	1.67404	0	1	1
ENSG00000241225	ENSG00000241225	TRNAS30P	17:22026649-22028896	NOTEST	0	0	0	0	1	1
ENSG00000241226	ENSG00000241226	RN7SL836P	19:46154767-46155060	NOTEST	0	0	0	0	1	1
ENSG00000241227	ENSG00000241227	RN7SL553P	3:5294612-5294908	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000241228	ENSG00000241228	RP5-916O11.1	11:35965530-36253686	NOTEST	0	0	0	0	1	1
ENSG00000241229	ENSG00000241229	RN7SL443P	20:42543503-42698256	NOTEST	0	0	0	0	1	1
ENSG00000241230	ENSG00000241230	RN7SL801P	5:53179774-53606412	NOTEST	0	0	0	0	1	1
ENSG00000241231	ENSG00000241231	RP11-275H4.1	3:180701496-181554668	NOTEST	0	0	0	0	1	1
ENSG00000241233	ENSG00000241233	KRTAP5-8	11:71249070-71250253	NOTEST	0.0146761	0	#NAME?	0	1	1
ENSG00000241241	ENSG00000241241	KRTAP4-16P	17:39257753-39258461	NOTEST	0	0	0	0	1	1
ENSG00000241243	ENSG00000241243	RN7SL629P	5:86563704-86708836	NOTEST	0	0	0	0	1	1
ENSG00000241244	ENSG00000241244	IGKV1D-16	2:90139077-90139580	NOTEST	0	0	0	0	1	1
ENSG00000241246	ENSG00000241246	RN7SL302P	9:127279553-127535206	NOTEST	0	0	0	0	1	1
ENSG00000241248	ENSG00000241248	RN7SL727P	X:139168013-139168307	NOTEST	0	0	0	0	1	1
ENSG00000241250	ENSG00000241250	RPL17P20	4:57576225-57576780	NOTEST	0	0	0	0	1	1
ENSG00000241251	ENSG00000241251	RP11-73B8.1	12:43954586-43955100	NOTEST	0	0	0	0	1	1
ENSG00000241253	ENSG00000241253	CFB	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000241254	ENSG00000241254	AC092669.2	2:66554480-66556116	NOTEST	0	0	0	0	1	1
ENSG00000241255	ENSG00000241255	RP1-89D4.1	11:33258553-33258955	NOTEST	0.121401	0	#NAME?	0	1	1
ENSG00000241257	ENSG00000241257	RP11-397K18.1	3:109082893-109083081	NOTEST	0	0	0	0	1	1
ENSG00000241261	ENSG00000241261	RPL17P19	4:62066975-63031272	NOTEST	0	0	0	0	1	1
ENSG00000241266	ENSG00000241266	RN7SL82P	15:31083775-31094062	NOTEST	0	0	0	0	1	1
ENSG00000241269	ENSG00000241269	AC093620.5	7:5313999-5465045	NOTEST	0.0667306	0.0255429	-1.38543	0	1	1
ENSG00000241273	ENSG00000241273	RN7SL238P	15:28623766-28637170	NOTEST	0	0	0	0	1	1
ENSG00000241278	ENSG00000241278	ENPP7P4	3:125546080-125629115	NOTEST	0.205259	0.145614	-0.495297	0	1	1
ENSG00000241281	ENSG00000241281	RP11-364M6.1	4:148347125-148347503	NOTEST	0	0	0	0	1	1
ENSG00000241282	ENSG00000241282	RPL34P33	19:22817125-22899793	NOTEST	0	0	0	0	1	1
ENSG00000241286	ENSG00000241286	RPL29P25	12:111269582-111283767	NOTEST	0	0	0	0	1	1
ENSG00000241287	ENSG00000241287	XXbac-BPG254F23.6	6:32627243-32636160	NOTEST	0	0.15314	inf	0	1	1
ENSG00000241291	ENSG00000241291	RN7SL791P	5:145942788-146464347	NOTEST	0	0	0	0	1	1
ENSG00000241293	ENSG00000241293	PPATP1	3:87100341-87101888	NOTEST	0.0971397	0.0419419	-1.21167	0	1	1
ENSG00000241294	ENSG00000241294	IGKV2-24	2:89475811-89476644	NOTEST	0	0	0	0	1	1
ENSG00000241295	ENSG00000241295	ZBTB20-AS2	3:114056940-114866118	NOTEST	0	0	0	0	1	1
ENSG00000241296	ENSG00000241296	HLA-DMB	HSCHR6_MHC_SSTO:32992301-33089202	NOTEST	0	0	0	0	1	1
ENSG00000241305	ENSG00000241305	ACTG1P13	3:98934067-98935110	NOTEST	0	0	0	0	1	1
ENSG00000241307	ENSG00000241307	RP11-674E16.1	3:155478405-155479006	NOTEST	0	0.0244627	inf	0	1	1
ENSG00000241317	ENSG00000241317	RP11-342M3.1	10:81263828-81266037	NOTEST	0	0	0	0	1	1
ENSG00000241318	ENSG00000241318	RP11-47K11.2	1:92000222-92001150	NOTEST	0	0.0152589	inf	0	1	1
ENSG00000241319	ENSG00000241319	SETP6	3:81538849-81811312	NOTEST	0	0	0	0	1	1
ENSG00000241322	ENSG00000241322	CDRT1	17:15468796-15587625	NOTEST	0.0513533	0.0134986	-1.92765	0	1	1
ENSG00000241324	ENSG00000241324	RP5-921G16.2	7:123670972-124035172	NOTEST	0	0	0	0	1	1
ENSG00000241326	ENSG00000241326	RP11-807G9.2	1:9982172-10045559	NOTEST	0.0196932	0.217341	3.46419	0	1	1
ENSG00000241328	ENSG00000241328	RP11-331K15.1	3:86531092-86546146	NOTEST	0	0	0	0	1	1
ENSG00000241333	ENSG00000241333	RN7SL385P	22:38065472-38065746	NOTEST	0	0	0	0	1	1
ENSG00000241334	ENSG00000241334	RPL35AP33	16:68511139-68511473	NOTEST	0	0	0	0	1	1
ENSG00000241335	ENSG00000241335	RNA5-8S5	GL000220.1:155996-156149	NOTEST	0	0	0	0	1	1
ENSG00000241336	ENSG00000241336	RP11-451G4.1	3:154958733-154960933	NOTEST	0	0.0157378	inf	0	1	1
ENSG00000241341	ENSG00000241341	RP11-395E19.2	9:40700290-40713709	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000241344	ENSG00000241344	RPL21P47	4:63114011-63114488	NOTEST	0	0	0	0	1	1
ENSG00000241345	ENSG00000241345	RP4-630C24.3	7:123634675-123667713	NOTEST	0	0	0	0	1	1
ENSG00000241346	ENSG00000241346	RP11-379B18.3	3:125534924-125535129	NOTEST	0	0	0	0	1	1
ENSG00000241347	ENSG00000241347	RN7SL466P	1:161705597-161705889	NOTEST	0	0	0	0	1	1
ENSG00000241350	ENSG00000241350	PMS2P11	7:76139744-77045717	NOTEST	0	0.0287037	inf	0	1	1
ENSG00000241351	ENSG00000241351	IGKV3-11	2:89326667-89327228	NOTEST	0	0	0	0	1	1
ENSG00000241352	ENSG00000241352	RP11-392P7.1	12:13003915-13004674	NOTEST	0	0	0	0	1	1
ENSG00000241353	ENSG00000241353	PPP1R2P4	13:46916138-47012325	NOTEST	0	0	0	0	1	1
ENSG00000241354	ENSG00000241354	RP11-1042B17.2	14:61068863-61069251	NOTEST	0	0	0	0	1	1
ENSG00000241356	ENSG00000241356	OR5G3	11:56569331-56587980	NOTEST	0	0	0	0	1	1
ENSG00000241357	ENSG00000241357	RP11-758P17.2	7:100032879-100036127	NOTEST	0.393509	0	#NAME?	0	1	1
ENSG00000241358	ENSG00000241358	RP11-758I14.3	3:146109149-146213778	NOTEST	0	0	0	0	1	1
ENSG00000241359	ENSG00000241359	SYNPR-AS1	3:63213990-63602597	NOTEST	0	0	0	0	1	1
ENSG00000241361	ENSG00000241361	SLC25A24P1	1:108803817-109013624	NOTEST	0.215232	0.253656	0.236986	0	1	1
ENSG00000241367	ENSG00000241367	RPL7AP23	3:82035288-82512826	NOTEST	0	0	0	0	1	1
ENSG00000241369	ENSG00000241369	CT64	3:162744183-163079351	NOTEST	0.0110175	0	#NAME?	0	1	1
ENSG00000241383	ENSG00000241383	RP11-152C17.1	3:168720861-168723254	NOTEST	0	0	0	0	1	1
ENSG00000241385	ENSG00000241385	RP11-25D10.1	8:110911474-110911991	NOTEST	0	0	0	0	1	1
ENSG00000241386	ENSG00000241386	HLA-DOB	HSCHR6_MHC_COX:32702865-32707151	NOTEST	0	0	0	0	1	1
ENSG00000241388	ENSG00000241388	HNF1A-AS1	12:121406415-121454305	NOTEST	0	0	0	0	1	1
ENSG00000241391	ENSG00000241391	RN7SL234P	6:149539061-149732749	NOTEST	0	0	0	0	1	1
ENSG00000241392	ENSG00000241392	RN7SL205P	4:132641416-132641698	NOTEST	0	0	0	0	1	1
ENSG00000241394	ENSG00000241394	HLA-DMA	HSCHR6_MHC_DBB:32880345-32898843	NOTEST	0	0	0	0	1	1
ENSG00000241395	ENSG00000241395	RN7SL344P	1:211916798-212027045	NOTEST	0	0	0	0	1	1
ENSG00000241397	ENSG00000241397	LINC00903	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000241400	ENSG00000241400	RP11-764I5.1	3:140947567-141168634	NOTEST	0	0	0	0	1	1
ENSG00000241406	ENSG00000241406	RN7SL515P	13:42140972-42535256	NOTEST	0	0	0	0	1	1
ENSG00000241408	ENSG00000241408	HCG16	HSCHR6_MHC_APD:28953984-28956357	NOTEST	0	0	0	0	1	1
ENSG00000241409	ENSG00000241409	AC064852.4	2:233562008-233880595	NOTEST	0	0	0	0	1	1
ENSG00000241411	ENSG00000241411	RP11-192C21.1	4:135873413-135874044	NOTEST	0	0	0	0	1	1
ENSG00000241413	ENSG00000241413	RN7SL441P	12:110288747-110318293	NOTEST	0	0	0	0	1	1
ENSG00000241416	ENSG00000241416	KRT8P13	3:170136652-170578169	NOTEST	0	0	0	0	1	1
ENSG00000241418	ENSG00000241418	RP11-512H23.2	X:130836677-130964671	NOTEST	0.381206	0.264974	-0.52472	0	1	1
ENSG00000241420	ENSG00000241420	RN7SL505P	7:32535037-33102409	NOTEST	0	0	0	0	1	1
ENSG00000241423	ENSG00000241423	RPL21P103	12:58638160-58638648	NOTEST	0	0	0	0	1	1
ENSG00000241429	ENSG00000241429	EEF1A1P25	3:138372859-138553780	NOTEST	0	0.0190739	inf	0	1	1
ENSG00000241431	ENSG00000241431	RP11-17A4.1	8:57500943-57501346	NOTEST	0.231787	0	#NAME?	0	1	1
ENSG00000241434	ENSG00000241434	CTD-2224J9.4	19:53970988-54015941	NOTEST	0	0	0	0	1	1
ENSG00000241438	ENSG00000241438	TDGF1P6	3:135867763-135916083	NOTEST	0	0	0	0	1	1
ENSG00000241439	ENSG00000241439	RP11-666A20.3	3:125677398-125677660	NOTEST	0	0	0	0	1	1
ENSG00000241449	ENSG00000241449	RP11-545G3.1	7:149737609-149773744	NOTEST	0	0	0	0	1	1
ENSG00000241451	ENSG00000241451	RPS27P22	12:22852792-23404433	NOTEST	0.195474	0.153817	-0.345761	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000241457	ENSG00000241457	PLSCR5-AS1	3:146294341-146324003	NOTEST	0	0	0	0	1	1
ENSG00000241459	ENSG00000241459	RN7SL185P	15:32684982-32727434	NOTEST	0	0	0	0	1	1
ENSG00000241461	ENSG00000241461	RN7SL182P	3:49067139-49131796	NOTEST	0	0	0	0	1	1
ENSG00000241462	ENSG00000241462	RP11-579O24.1	17:56833229-57058983	NOTEST	0	0	0	0	1	1
ENSG00000241464	ENSG00000241464	RPL39P38	19:18396152-18396305	NOTEST	0	0	0	0	1	1
ENSG00000241465	ENSG00000241465	GAGE12I	X:49216658-49223943	NOTEST	0	0	0	0	1	1
ENSG00000241469	ENSG00000241469	LINC00635	3:107559074-107600847	NOTEST	0	0	0	0	1	1
ENSG00000241473	ENSG00000241473	RP11-259P15.3	3:180319917-180700541	NOTEST	0	0	0	0	1	1
ENSG00000241475	ENSG00000241475	RP4-781K5.5	1:234780411-234831900	NOTEST	0	0	0	0	1	1
ENSG00000241476	ENSG00000241476	SSX2	X:52725945-52736239	NOTEST	0.0132467	0.00932213	-0.506901	0	1	1
ENSG00000241478	ENSG00000241478	HSPA8P9	3:137599136-137601079	NOTEST	0	0	0	0	1	1
ENSG00000241479	ENSG00000241479	RP11-641D5.2	3:168801286-169381406	NOTEST	0	0	0	0	1	1
ENSG00000241481	ENSG00000241481	AC159540.2	2:98081082-98100408	NOTEST	0.237129	0.0524645	-2.17626	0	1	1
ENSG00000241484	ENSG00000241484	ARHGAP8	22:45064592-45258665	NOTEST	0.0113996	0.0812615	2.83359	0	1	1
ENSG00000241487	ENSG00000241487	RN7SL586P	14:73507328-73507622	NOTEST	0	0	0	0	1	1
ENSG00000241490	ENSG00000241490	RP11-553L6.2	3:113933159-113956425	NOTEST	0	0	0	0	1	1
ENSG00000241493	ENSG00000241493	RP11-274B21.5	7:128309140-128309946	NOTEST	0	0	0	0	1	1
ENSG00000241494	ENSG00000241494	RP11-796G6.1	14:102100790-102198859	NOTEST	0.160059	0.0396152	-2.01448	0	1	1
ENSG00000241499	ENSG00000241499	RP11-85G20.2	14:93703895-93799438	NOTEST	0	0	0	0	1	1
ENSG00000241500	ENSG00000241500	RN7SL256P	15:82944772-82988374	NOTEST	0	0	0	0	1	1
ENSG00000241505	ENSG00000241505	RP11-161I10.1	1:190447680-190463427	NOTEST	0	0	0	0	1	1
ENSG00000241511	ENSG00000241511	RPS15AP24	8:29952913-30041156	NOTEST	0.0659087	0.0985457	0.580324	0	1	1
ENSG00000241520	ENSG00000241520	AC098820.4	2:217250010-217443903	NOTEST	0.0369029	0.0130037	-1.50482	0	1	1
ENSG00000241524	ENSG00000241524	RN7SL632P	2:61052266-61108449	NOTEST	0	0	0	0	1	1
ENSG00000241525	ENSG00000241525	AC108004.3	17:254325-273510	NOTEST	5.22E-05	0.618794	13.5342	0	1	1
ENSG00000241526	ENSG00000241526	RP11-144C9.1	3:141443266-141443368	NOTEST	0	0	0	0	1	1
ENSG00000241527	ENSG00000241527	CA15P1	22:19019076-19022077	NOTEST	0	0	0	0	1	1
ENSG00000241529	ENSG00000241529	RN7SL767P	3:113351550-113351827	NOTEST	0	0.106753	inf	0	1	1
ENSG00000241532	ENSG00000241532	AGGF1P3	3:75702711-75703924	NOTEST	0.0259391	0.0999025	1.94539	0	1	1
ENSG00000241534	ENSG00000241534	CFB	HSCHR6_MHC_DBB:31847748-31902052	NOTEST	0	0	0	0	1	1
ENSG00000241535	ENSG00000241535	CBX5P1	3:88101093-88217879	NOTEST	0	0	0	0	1	1
ENSG00000241536	ENSG00000241536	RP11-381G8.1	9:39485379-39485866	NOTEST	0	0	0	0	1	1
ENSG00000241537	ENSG00000241537	RP11-624D20.1	3:72798427-72911065	NOTEST	0.0194921	0	#NAME?	0	1	1
ENSG00000241539	ENSG00000241539	RP11-740N7.4	7:6963434-6970466	NOTEST	0	0	0	0	1	1
ENSG00000241541	ENSG00000241541	Y_RNA	HG1293_PATCH:206811540-206811653	NOTEST	0	0	0	0	1	1
ENSG00000241542	ENSG00000241542	RN7SL369P	14:68168602-68283307	NOTEST	0	0	0	0	1	1
ENSG00000241544	ENSG00000241544	RP11-6F2.5	3:156799455-156840793	NOTEST	0.00347612	0.0200746	2.52982	0	1	1
ENSG00000241546	ENSG00000241546	RP11-767L7.2	3:119540169-119813264	NOTEST	0	0	0	0	1	1
ENSG00000241550	ENSG00000241550	RN7SL41P	8:80830951-81143467	NOTEST	0	0	0	0	1	1
ENSG00000241552	ENSG00000241552	RN7SL58P	5:18547420-18547712	NOTEST	0	0	0	0	1	1
ENSG00000241559	ENSG00000241559	CU459202.2	GL000243.1:8049-8132	NOTEST	0	0	0	0	1	1
ENSG00000241560	ENSG00000241560	ZBTB20-AS1	3:114056940-114866118	NOTEST	0.028621	0	#NAME?	0	1	1
ENSG00000241562	ENSG00000241562	RPL7P5	15:100017369-100273766	NOTEST	0.0482922	0	#NAME?	0	1	1

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ENSG00000241566	ENSG00000241566	IGKV2D-24	2:90043606-90044439	NOTEST	0	0	0	0	1	1
ENSG00000241568	ENSG00000241568	RN7SL338P	9:35049267-35049558	NOTEST	0	0	0	0	1	1
ENSG00000241570	ENSG00000241570	RP11-372E1.6	3:142668005-142779567	NOTEST	0.432491	0.533266	0.302187	0	1	1
ENSG00000241571	ENSG00000241571	ATP5A1P7	9:46998212-46999491	NOTEST	0	0	0	0	1	1
ENSG00000241572	ENSG00000241572	PRICKLE2-AS1	3:64053639-64440508	NOTEST	0	0	0	0	1	1
ENSG00000241573	ENSG00000241573	RP11-286H14.1	7:128736080-128736789	NOTEST	0	0	0	0	1	1
ENSG00000241577	ENSG00000241577	RP11-523O18.7	10:49892920-50323554	NOTEST	0	0	0	0	1	1
ENSG00000241582	ENSG00000241582	RP11-434O22.2	14:35163375-35163850	NOTEST	0	0	0	0	1	1
ENSG00000241587	ENSG00000241587	RN7SL482P	3:66119284-66551687	NOTEST	0	0	0	0	1	1
ENSG00000241588	ENSG00000241588	RN7SL484P	15:100330360-100347132	NOTEST	0.15949	0.286096	0.84303	0	1	1
ENSG00000241590	ENSG00000241590	RPL17P37	12:119175768-119176316	NOTEST	0	0	0	0	1	1
ENSG00000241592	ENSG00000241592	RP11-372E1.7	3:142668005-142779567	NOTEST	0	0	0	0	1	1
ENSG00000241593	ENSG00000241593	RP11-520D19.2	3:81295729-81346496	NOTEST	0.0176188	0	#NAME?	0	1	1
ENSG00000241595	ENSG00000241595	KRTAP9-4	17:39405938-39406904	NOTEST	0	0	0	0	1	1
ENSG00000241596	ENSG00000241596	RP11-326J18.1	3:115342170-115440337	NOTEST	0	0	0	0	1	1
ENSG00000241597	ENSG00000241597	CTD-2007H13.1	5:98264874-98330717	NOTEST	0	0.025796	inf	0	1	1
ENSG00000241598	ENSG00000241598	KRTAP5-4	11:1642187-1643368	NOTEST	0	0	0	0	1	1
ENSG00000241599	ENSG00000241599	RP11-34P13.9	1:141473-173862	NOTEST	0	0	0	0	1	1
ENSG00000241601	ENSG00000241601	CT867976.2	GL000230.1:33985-34068	NOTEST	0	0	0	0	1	1
ENSG00000241604	ENSG00000241604	RN7SL340P	19:29723998-29724292	NOTEST	0	0	0	0	1	1
ENSG00000241607	ENSG00000241607	RP11-357K9.2	X:37208527-38548169	NOTEST	0	0.36793	inf	0	1	1
ENSG00000241612	ENSG00000241612	RP13-585F24.1	4:19173957-19911315	NOTEST	0.184097	0.468777	1.34843	0	1	1
ENSG00000241613	ENSG00000241613	RN7SL618P	13:53832211-53832505	NOTEST	0	0	0	0	1	1
ENSG00000241621	ENSG00000241621	GOLGA2P6	10:30598729-30663377	NOTEST	0	0	0	0	1	1
ENSG00000241622	ENSG00000241622	RARRES2P1	3:75707684-75708165	NOTEST	0.233214	0.24722	0.0841434	0	1	1
ENSG00000241625	ENSG00000241625	RN7SL18P	2:62718312-62718601	NOTEST	0	0	0	0	1	1
ENSG00000241631	ENSG00000241631	RN7SL316P	17:29029525-29029793	NOTEST	0	0	0	0	1	1
ENSG00000241635	ENSG00000241635	UGT1A8	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000241636	ENSG00000241636	RP11-71H9.2	3:164388665-164403864	NOTEST	0	0	0	0	1	1
ENSG00000241640	ENSG00000241640	RP11-59H7.1	15:59063390-59389618	NOTEST	0	0	0	0	1	1
ENSG00000241641	ENSG00000241641	RPS23P6	16:12070593-12704901	NOTEST	0	0	0	0	1	1
ENSG00000241644	ENSG00000241644	INMT	7:30692199-30965131	NOTEST	0	0	0	0	1	1
ENSG00000241648	ENSG00000241648	CADM2-AS2	3:85008131-86123579	NOTEST	0	0	0	0	1	1
ENSG00000241651	ENSG00000241651	RP11-214O14.1	4:128982422-129144086	NOTEST	0	0	0	0	1	1
ENSG00000241652	ENSG00000241652	RN7SL253P	4:174053078-174250845	NOTEST	0	0	0	0	1	1
ENSG00000241654	ENSG00000241654	RPL19P18	17:9479943-9633008	NOTEST	0	0	0	0	1	1
ENSG00000241656	ENSG00000241656	UBA52P7	12:116019865-116077539	NOTEST	0	0	0	0	1	1
ENSG00000241657	ENSG00000241657	TRBV11-2	7:142197569-142198069	NOTEST	0	0	0	0	1	1
ENSG00000241661	ENSG00000241661	PPP1R2P6	7:139992551-139993139	NOTEST	0	0	0	0	1	1
ENSG00000241665	ENSG00000241665	RN7SL418P	3:69788585-70017488	NOTEST	0	0	0	0	1	1
ENSG00000241666	ENSG00000241666	RP3-455J7.4	1:167596621-167675486	NOTEST	0	0	0	0	1	1
ENSG00000241667	ENSG00000241667	RP11-444P10.1	3:69640491-69642272	NOTEST	0	0	0	0	1	1

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ENSG00000241669	ENSG00000241669	RP11-576M8.2	3:167110583-167126307	NOTEST	0	0	0	0	1	1
ENSG00000241670	ENSG00000241670	AP006222.1	1:227614-267253	NOTEST	0	0	0	0	1	1
ENSG00000241671	ENSG00000241671	RP11-529G21.3	3:152846862-152847429	NOTEST	0	0	0	0	1	1
ENSG00000241673	ENSG00000241673	RPS27P12	3:128936935-128937193	NOTEST	0	0	0	0	1	1
ENSG00000241674	ENSG00000241674	HLA-DMB	HSCHR6_MHC_QBL:32831135-32878022	NOTEST	0	0	0	0	1	1
ENSG00000241678	ENSG00000241678	RP11-732A19.1	11:6707121-6707600	NOTEST	0	0	0	0	1	1
ENSG00000241679	ENSG00000241679	RP11-80H8.4	3:142842203-142850735	NOTEST	0.127705	0.052618	-1.27918	0	1	1
ENSG00000241680	ENSG00000241680	RPL31P49	12:110890288-110928190	NOTEST	0.276277	0	#NAME?	0	1	1
ENSG00000241684	ENSG00000241684	ADAMTS9-AS2	3:64501332-64997143	NOTEST	0.0121203	0	#NAME?	0	1	1
ENSG00000241693	ENSG00000241693	RN7SL704P	22:38615297-38669040	NOTEST	0	0	0	0	1	1
ENSG00000241695	ENSG00000241695	GM2AP1	3:145402358-145402879	NOTEST	0	0	0	0	1	1
ENSG00000241696	ENSG00000241696	RP11-420J11.2	3:180131961-180140294	NOTEST	0	0	0	0	1	1
ENSG00000241701	ENSG00000241701	HCG17	HSCHR6_MHC_COX:30191706-30304467	NOTEST	0	0	0	0	1	1
ENSG00000241708	ENSG00000241708	RN7SL129P	17:8316448-8534079	NOTEST	0	0	0	0	1	1
ENSG00000241709	ENSG00000241709	RN7SL265P	7:73146900-73147201	NOTEST	0	0	0	0	1	1
ENSG00000241710	ENSG00000241710	RN7SL10P	12:42632248-42984157	NOTEST	0	0	0	0	1	1
ENSG00000241713	ENSG00000241713	LY6G5B	HSCHR6_MHC_COX:31616420-31658607	NOTEST	0	0	0	0	1	1
ENSG00000241717	ENSG00000241717	VWFP1	22:17082776-17185367	NOTEST	0.0457183	0.0478322	0.0652099	0	1	1
ENSG00000241720	ENSG00000241720	RP4-735C1.4	1:110254863-110318050	NOTEST	0	0	0	0	1	1
ENSG00000241721	ENSG00000241721	SUMO1P1	20:52491790-52492096	NOTEST	0	0	0	0	1	1
ENSG00000241722	ENSG00000241722	RP11-255I10.1	4:112473009-112473329	NOTEST	0	0	0	0	1	1
ENSG00000241723	ENSG00000241723	RP11-113A11.1	3:157814947-158288855	NOTEST	0	0	0	0	1	1
ENSG00000241728	ENSG00000241728	AP001062.8	21:45748826-45760353	NOTEST	0.110629	0.131688	0.251395	0	1	1
ENSG00000241732	ENSG00000241732	RP11-38P22.2	3:152557178-152559228	NOTEST	0.142703	0.243162	0.768901	0	1	1
ENSG00000241735	ENSG00000241735	FABP5P3	7:152133979-152140272	NOTEST	0	0.0446868	inf	0	1	1
ENSG00000241737	ENSG00000241737	FAM90A23P	8:7421319-7440175	NOTEST	0	0	0	0	1	1
ENSG00000241738	ENSG00000241738	ZNF90P1	3:101043048-101232085	NOTEST	0	0	0	0	1	1
ENSG00000241739	ENSG00000241739	CTD-2290C23.2	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000241743	ENSG00000241743	RP5-964N17.1	X:112859586-113181506	NOTEST	0	0	0	0	1	1
ENSG00000241744	ENSG00000241744	RP11-399D15.1	12:101621918-101622654	NOTEST	0	0	0	0	1	1
ENSG00000241745	ENSG00000241745	RN7SL788P	1:52608045-52831865	NOTEST	0	0	0	0	1	1
ENSG00000241746	ENSG00000241746	RP11-941H19.1	8:81177762-81252075	NOTEST	0	0	0	0	1	1
ENSG00000241749	ENSG00000241749	RPSAP52	12:66151799-66360075	NOTEST	0.220346	0.129764	-0.763876	0	1	1
ENSG00000241754	ENSG00000241754	RP11-280H21.1	3:102382006-102392757	NOTEST	0	0	0	0	1	1
ENSG00000241755	ENSG00000241755	IGKV1-9	2:89309478-89310012	NOTEST	0	0	0	0	1	1
ENSG00000241756	ENSG00000241756	RN7SL83P	7:38423304-38671167	NOTEST	0	0	0	0	1	1
ENSG00000241757	ENSG00000241757	RN7SL714P	14:98817705-98818001	NOTEST	0	0	0	0	1	1
ENSG00000241765	ENSG00000241765	RP11-159A18.1	12:69816435-69816775	NOTEST	0.167775	0	#NAME?	0	1	1
ENSG00000241767	ENSG00000241767	RP11-71H9.1	3:164431882-164549268	NOTEST	0	0	0	0	1	1
ENSG00000241770	ENSG00000241770	RP11-555M1.3	3:156880451-156886922	NOTEST	0	0	0	0	1	1
ENSG00000241772	ENSG00000241772	AC092620.2	2:139259370-139332028	NOTEST	0.240629	0.218991	-0.135934	0	1	1
ENSG00000241774	ENSG00000241774	RN7SL438P	15:69452922-69564556	NOTEST	0	0	0	0	1	1
ENSG00000241776	ENSG00000241776	RP11-651J20.1	3:84687556-84930830	NOTEST	0	0	0	0	1	1

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ENSG00000241778	ENSG00000241778	AC005077.9	7:75719748-75738097	NOTEST	0	0	0	0	1	1
ENSG00000241779	ENSG00000241779	RPP21	HSCHR6_MHC_APD:30266816-30322899	NOTEST	0	0	0	0	1	1
ENSG00000241781	ENSG00000241781	AL161626.1	9:79186730-79186787	NOTEST	0	0	0	0	1	1
ENSG00000241782	ENSG00000241782	RP11-91P24.1	11:77532154-77705724	NOTEST	0.0490142	0.034856	-0.491793	0	1	1
ENSG00000241785	ENSG00000241785	RN7SL390P	12:54624723-54745633	NOTEST	0	0	0	0	1	1
ENSG00000241787	ENSG00000241787	MTND4P16	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000241788	ENSG00000241788	COX6B1P2	17:46791091-46791321	NOTEST	0	0	0	0	1	1
ENSG00000241789	ENSG00000241789	RN7SL504P	3:51906220-51906467	NOTEST	0	0	0	0	1	1
ENSG00000241790	ENSG00000241790	ENO1P4	2:202484906-202508293	NOTEST	0.170596	0.55961	1.71384	0	1	1
ENSG00000241791	ENSG00000241791	RN7SL817P	2:46656328-46711564	NOTEST	0	0	0	0	1	1
ENSG00000241792	ENSG00000241792	RP11-501O2.1	3:147810961-147845020	NOTEST	0	0	0	0	1	1
ENSG00000241794	ENSG00000241794	SPRR2A	1:153028588-153030013	NOTEST	0	0	0	0	1	1
ENSG00000241804	ENSG00000241804	RP11-719N22.1	3:59521588-59522141	NOTEST	0	0	0	0	1	1
ENSG00000241807	ENSG00000241807	RN7SL319P	15:76067893-76079239	NOTEST	0	0	0	0	1	1
ENSG00000241808	ENSG00000241808	RPS15AP34	16:63348167-63651950	NOTEST	0	0	0	0	1	1
ENSG00000241809	ENSG00000241809	CTD-2207L17.1	5:51971026-52390609	NOTEST	0	0	0	0	1	1
ENSG00000241810	ENSG00000241810	HMGN2P13	3:152785066-152785340	NOTEST	0	0	0	0	1	1
ENSG00000241811	ENSG00000241811	RN7SL651P	8:25038945-25039235	NOTEST	0	0	0	0	1	1
ENSG00000241815	ENSG00000241815	RP11-124D9.1	3:96285200-96285947	NOTEST	0	0	0	0	1	1
ENSG00000241818	ENSG00000241818	RP11-1000B6.2	15:32933876-32989299	NOTEST	0	0	0	0	1	1
ENSG00000241821	ENSG00000241821	RN7SL170P	20:55263456-55263749	NOTEST	0	0	0	0	1	1
ENSG00000241822	ENSG00000241822	LY6G6F	HSCHR6_MHC_SSTO:31664594-31675654	NOTEST	0	0	0	0	1	1
ENSG00000241825	ENSG00000241825	RPL7P42	12:69068150-69136785	NOTEST	0	0	0	0	1	1
ENSG00000241828	ENSG00000241828	RP11-277J24.1	12:7965107-8043744	NOTEST	0	0	0	0	1	1
ENSG00000241829	ENSG00000241829	RPL21P54	5:34837653-34899561	NOTEST	0	0	0	0	1	1
ENSG00000241832	ENSG00000241832	CECR3	22:17737748-17747623	NOTEST	0	0	0	0	1	1
ENSG00000241834	ENSG00000241834	RN7SL149P	8:41510738-41754280	NOTEST	0	0	0	0	1	1
ENSG00000241838	ENSG00000241838	LA16c-3G11.7	22:16255354-16287937	NOTEST	0	0	0	0	1	1
ENSG00000241840	ENSG00000241840	RN7SL194P	20:37981401-37981674	NOTEST	0	0	0	0	1	1
ENSG00000241846	ENSG00000241846	RP11-318G8.1	12:25562226-25801513	NOTEST	0	0	0	0	1	1
ENSG00000241847	ENSG00000241847	VDAC1P8	6:143771943-143832827	NOTEST	0.0282617	0	#NAME?	0	1	1
ENSG00000241850	ENSG00000241850	GSTTP1	22:24340827-24347258	NOTEST	0.0352014	0	#NAME?	0	1	1
ENSG00000241853	ENSG00000241853	RP11-147K6.1	4:89011415-89152474	NOTEST	0	0	0	0	1	1
ENSG00000241859	ENSG00000241859	KALP	Y:15863535-16027704	NOTEST	0	0	0	0	1	1
ENSG00000241860	ENSG00000241860	RP11-34P13.13	1:141473-173862	NOTEST	0.146294	0.0445807	-1.71438	0	1	1
ENSG00000241861	ENSG00000241861	GAPDHP50	3:89096591-89097584	NOTEST	0	0	0	0	1	1
ENSG00000241863	ENSG00000241863	RPP21	HSCHR6_MHC_COX:30191706-30304467	NOTEST	0	0	0	0	1	1
ENSG00000241866	ENSG00000241866	RN7SL401P	18:71412169-71412464	NOTEST	0	0	0	0	1	1
ENSG00000241868	ENSG00000241868	RN7SL434P	3:196074532-196160242	NOTEST	0	0.11612	inf	0	1	1
ENSG00000241869	ENSG00000241869	RN7SL363P	15:91399166-91399437	NOTEST	0	0	0	0	1	1
ENSG00000241870	ENSG00000241870	CTB-14A14.1	5:180492085-180492677	NOTEST	0	0	0	0	1	1
ENSG00000241874	ENSG00000241874	TOMM22P6	3:162204328-162204737	NOTEST	0	0	0	0	1	1
ENSG00000241877	ENSG00000241877	RP11-84H6.1	4:179207848-179208439	NOTEST	0	0	0	0	1	1

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ENSG00000241880	ENSG00000241880	RPL23AP1	HSCHR6_MHC_COX:29684536-29710797	NOTEST	0	0	0	0	1	1
ENSG00000241881	ENSG00000241881	U66059.58	7:141985578-141991423	NOTEST	0	0	0	0	1	1
ENSG00000241882	ENSG00000241882	RP11-637O11.2	3:167967309-168548387	NOTEST	0	0	0	0	1	1
ENSG00000241884	ENSG00000241884	RP11-85I21.1	3:67346723-67356783	NOTEST	0	0	0	0	1	1
ENSG00000241886	ENSG00000241886	RP11-242C19.2	X:30671475-30748725	NOTEST	0.580063	0.0538626	-3.42885	0	1	1
ENSG00000241888	ENSG00000241888	RPSAP37	5:125302469-125303778	NOTEST	0	0	0	0	1	1
ENSG00000241890	ENSG00000241890	RPL13P4	15:75648132-75748183	NOTEST	0	0.0591745	inf	0	1	1
ENSG00000241891	ENSG00000241891	RP11-228P1.1	14:82194123-82496693	NOTEST	0	0	0	0	1	1
ENSG00000241899	ENSG00000241899	TPT1P3	3:141382040-141439915	NOTEST	0	0	0	0	1	1
ENSG00000241905	ENSG00000241905	RP11-305O4.1	3:135678116-135678432	NOTEST	0	0	0	0	1	1
ENSG00000241907	ENSG00000241907	RPS20P4	5:149340299-149432386	NOTEST	0	0.0628253	inf	0	1	1
ENSG00000241910	ENSG00000241910	HLA-DOB	HSCHR6_MHC_MCF:32814043-32818329	NOTEST	0	0	0	0	1	1
ENSG00000241911	ENSG00000241911	TRBVB	7:142419211-142419752	NOTEST	0	0	0	0	1	1
ENSG00000241912	ENSG00000241912	RP11-292E2.2	3:153094619-153095351	NOTEST	0.133364	0.0502394	-1.40848	0	1	1
ENSG00000241913	ENSG00000241913	RP5-1073F15.1	17:57970446-58096413	NOTEST	0	0	0	0	1	1
ENSG00000241917	ENSG00000241917	RP11-512N21.1	12:102271128-102405908	NOTEST	0	0	0	0	1	1
ENSG00000241921	ENSG00000241921	AC000370.2	7:126019023-126064239	NOTEST	0	0	0	0	1	1
ENSG00000241923	ENSG00000241923	RP11-425I13.1	4:141178439-141306880	NOTEST	0.0988377	0.0729131	-0.438884	0	1	1
ENSG00000241926	ENSG00000241926	RP5-1154E9.7	7:141501114-141501859	NOTEST	0	0	0	0	1	1
ENSG00000241929	ENSG00000241929	RP11-278L15.3	3:149179968-149182617	NOTEST	0	0	0	0	1	1
ENSG00000241932	ENSG00000241932	RP11-14K2.1	16:12975026-12975350	NOTEST	0	0	0	0	1	1
ENSG00000241933	ENSG00000241933	RP11-755B10.3	3:57678931-57682323	NOTEST	0	0	0	0	1	1
ENSG00000241939	ENSG00000241939	RN7SL517P	3:43328003-43775863	NOTEST	0	0	0	0	1	1
ENSG00000241941	ENSG00000241941	RPL32P26	12:63037761-63328817	NOTEST	0	0	0	0	1	1
ENSG00000241942	ENSG00000241942	RPS20P20	8:72740401-73030628	NOTEST	0	0	0	0	1	1
ENSG00000241943	ENSG00000241943	RN7SL188P	11:15987994-16778428	NOTEST	0	0	0	0	1	1
ENSG00000241946	ENSG00000241946	RP11-496B10.1	3:180284505-180319723	NOTEST	0	0	0	0	1	1
ENSG00000241947	ENSG00000241947	HNRNPA1P24	3:149478891-149942977	NOTEST	0	0	0	0	1	1
ENSG00000241950	ENSG00000241950	RPL29P23	11:33060962-33213144	NOTEST	0	0.132553	inf	0	1	1
ENSG00000241954	ENSG00000241954	RP1-149A16.17	22:32750871-32781618	NOTEST	0	4.62E-06	inf	0	1	1
ENSG00000241956	ENSG00000241956	CTC-340A15.2	5:163723701-164598649	NOTEST	0	0	0	0	1	1
ENSG00000241959	ENSG00000241959	RN7SL76P	7:151161737-151162024	NOTEST	0.245729	0	#NAME?	0	1	1
ENSG00000241961	ENSG00000241961	RP11-7F18.1	8:68318749-68319307	NOTEST	0	0	0	0	1	1
ENSG00000241963	ENSG00000241963	RN7SL655P	5:153369687-153825410	NOTEST	0	0	0	0	1	1
ENSG00000241964	ENSG00000241964	RN7SL135P	8:64147194-64147469	NOTEST	0	0	0	0	1	1
ENSG00000241965	ENSG00000241965	RPS2P25	5:85058376-85058956	NOTEST	0	0	0	0	1	1
ENSG00000241981	ENSG00000241981	AF224669.3	4:103552659-103682151	NOTEST	0	0	0	0	1	1
ENSG00000241983	ENSG00000241983	RN7SL566P	19:39833035-39876350	NOTEST	0.118531	0.085621	-0.469225	0	1	1
ENSG00000241984	ENSG00000241984	RPL7AP2	14:39617014-39639736	NOTEST	0.0261055	0.0387566	0.570086	0	1	1
ENSG00000241985	ENSG00000241985	WWTR1-IT1	3:149235021-149454501	NOTEST	0	0.0413509	inf	0	1	1
ENSG00000241991	ENSG00000241991	RP11-95I19.2	5:61601988-61924409	NOTEST	0	0	0	0	1	1
ENSG00000241992	ENSG00000241992	RN7SL831P	1:97048764-97049081	NOTEST	0	0	0	0	1	1

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ENSG00000241997	ENSG00000241997	RN7SL323P	8:56934579-56934872	NOTEST	0	0	0	0	1	1
ENSG00000242001	ENSG00000242001	GS1-388B5.1	3:125400148-125400297	NOTEST	0	0	0	0	1	1
ENSG00000242009	ENSG00000242009	RP11-359D24.1	3:81889697-81972012	NOTEST	0	0	0	0	1	1
ENSG00000242012	ENSG00000242012	RP11-338L18.1	3:182082934-182086044	NOTEST	0	0	0	0	1	1
ENSG00000242014	ENSG00000242014	RN7SL26P	6:33508470-33508774	NOTEST	0	0	0	0	1	1
ENSG00000242017	ENSG00000242017	ALG1L15P	3:155755489-156256545	NOTEST	0.115236	0.284038	1.30149	0	1	1
ENSG00000242019	ENSG00000242019	KIR3DL3	19:55235968-55378662	NOTEST	0	0	0	0	1	1
ENSG00000242020	ENSG00000242020	RN7SL68P	5:140710251-140892546	NOTEST	0	0.0771169	inf	0	1	1
ENSG00000242022	ENSG00000242022	OR12D3	HSCHR6_MHC_DBB:29341258-29424782	NOTEST	0	0	0	0	1	1
ENSG00000242029	ENSG00000242029	RP11-457K10.1	3:109366953-109529708	NOTEST	0	0	0	0	1	1
ENSG00000242034	ENSG00000242034	RP11-1396O13.1	4:9555233-9555605	NOTEST	0	0	0	0	1	1
ENSG00000242036	ENSG00000242036	RP11-603B13.1	3:167674098-167674404	NOTEST	0	0	0	0	1	1
ENSG00000242037	ENSG00000242037	RN7SL585P	13:95351478-95351756	NOTEST	0	0	0	0	1	1
ENSG00000242038	ENSG00000242038	EGFL8	HSCHR6_MHC_COX:32064597-32094350	NOTEST	0	0	0	0	1	1
ENSG00000242039	ENSG00000242039	RPL23AP1	HSCHR6_MHC_MANN:29687659-29713937	NOTEST	0	0	0	0	1	1
ENSG00000242041	ENSG00000242041	RP11-70F11.2	12:50254989-50259528	NOTEST	0	0	0	0	1	1
ENSG00000242042	ENSG00000242042	RP11-690C23.2	1:246672339-246687589	NOTEST	0	0	0	0	1	1
ENSG00000242044	ENSG00000242044	XXbac-BPG254F23.6	HSCHR6_MHC_MCF:32658021-32667070	NOTEST	0	0	0	0	1	1
ENSG00000242048	ENSG00000242048	RP13-452N2.1	7:151253196-151576299	NOTEST	0	0	0	0	1	1
ENSG00000242049	ENSG00000242049	DNAJB8-AS1	3:128181281-128191160	NOTEST	0	0	0	0	1	1
ENSG00000242052	ENSG00000242052	RP11-190C22.1	3:119354372-119354997	NOTEST	0	0	0	0	1	1
ENSG00000242058	ENSG00000242058	RPS4XP19	18:9020026-9020762	NOTEST	0	0	0	0	1	1
ENSG00000242060	ENSG00000242060	RPS3AP49	18:57792264-57828428	NOTEST	0	0	0	0	1	1
ENSG00000242061	ENSG00000242061	CTD-2555K7.1	14:23163306-23163744	NOTEST	0	0	0	0	1	1
ENSG00000242062	ENSG00000242062	MARK2P6	3:128570954-128571851	NOTEST	0	0.0144274	inf	0	1	1
ENSG00000242065	ENSG00000242065	RN7SL291P	X:44632020-44632307	NOTEST	0	0	0	0	1	1
ENSG00000242066	ENSG00000242066	RN7SL214P	15:78206558-78219188	NOTEST	0	0	0	0	1	1
ENSG00000242067	ENSG00000242067	RPL9P28	17:46760728-46781844	NOTEST	0	0	0	0	1	1
ENSG00000242068	ENSG00000242068	RP11-259P15.4	3:180319917-180700541	NOTEST	0	0	0	0	1	1
ENSG00000242070	ENSG00000242070	NPM1P17	3:137442615-137443385	NOTEST	0	0	0	0	1	1
ENSG00000242072	ENSG00000242072	RP11-458K10.1	7:115287514-115316383	NOTEST	0	0	0	0	1	1
ENSG00000242076	ENSG00000242076	IGKV1-33	2:89567757-89568263	NOTEST	0	0	0	0	1	1
ENSG00000242078	ENSG00000242078	RP11-738B7.1	7:129423209-129425025	NOTEST	0	0	0	0	1	1
ENSG00000242079	ENSG00000242079	RN7SL318P	8:4999932-5000229	NOTEST	0	0	0	0	1	1
ENSG00000242080	ENSG00000242080	CTC-550M4.1	5:151875278-151875578	NOTEST	0	0	0	0	1	1
ENSG00000242082	ENSG00000242082	RP1-90G24.10	22:32601101-32669097	NOTEST	0	0.0672291	inf	0	1	1
ENSG00000242087	ENSG00000242087	RPL36AP41	12:64238072-64541637	NOTEST	0	0	0	0	1	1
ENSG00000242088	ENSG00000242088	AC090602.2	15:25068793-25492435	NOTEST	0	0.125664	inf	0	1	1
ENSG00000242092	ENSG00000242092	HLA-DMB	HSCHR6_MHC_APD:32885992-32904491	NOTEST	0	0	0	0	1	1
ENSG00000242094	ENSG00000242094	FOXP1-IT1	3:71003843-71633140	NOTEST	0.0079651	0	#NAME?	0	1	1
ENSG00000242095	ENSG00000242095	RN7SL113P	2:85569210-85618875	NOTEST	0.342172	0	#NAME?	0	1	1

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ENSG00000242100	ENSG00000242100	RPL9P32	19:30414550-30506611	NOTEST	0	0.0257551	inf	0	1	1
ENSG00000242101	ENSG00000242101	RN7SL416P	7:100127986-100128282	NOTEST	0	0.0914609	inf	0	1	1
ENSG00000242102	ENSG00000242102	RN7SL152P	4:141499078-141499374	NOTEST	0	0	0	0	1	1
ENSG00000242103	ENSG00000242103	RP11-10G15.4	3:120626918-121143608	NOTEST	0	0	0	0	1	1
ENSG00000242104	ENSG00000242104	RP11-340E6.1	3:141382040-141439915	NOTEST	0.0184506	0	#NAME?	0	1	1
ENSG00000242107	ENSG00000242107	LINC01100	3:159631188-159943086	NOTEST	0	0	0	0	1	1
ENSG00000242109	ENSG00000242109	NPM1P23	3:24137759-24144729	NOTEST	0	0	0	0	1	1
ENSG00000242111	ENSG00000242111	RP11-86L19.2	9:107032508-107049236	NOTEST	0	0	0	0	1	1
ENSG00000242113	ENSG00000242113	RN7SL124P	2:152214105-152236560	NOTEST	0	0	0	0	1	1
ENSG00000242115	ENSG00000242115	PRSS3P3	7:141985578-141991423	NOTEST	0	0	0	0	1	1
ENSG00000242118	ENSG00000242118	RN7SL201P	2:82194202-82194496	NOTEST	0	0	0	0	1	1
ENSG00000242119	ENSG00000242119	RP11-312P21.2	3:151217426-151217594	NOTEST	0	0	0	0	1	1
ENSG00000242120	ENSG00000242120	RP11-231I13.2	3:70246044-70361877	NOTEST	0	0	0	0	1	1
ENSG00000242121	ENSG00000242121	RN7SL267P	2:183004762-183387919	NOTEST	0	0	0	0	1	1
ENSG00000242123	ENSG00000242123	RP11-51L5.1	17:60397244-60397550	NOTEST	0	0	0	0	1	1
ENSG00000242134	ENSG00000242134	RPL5P13	4:142944312-143768585	NOTEST	0	0.143546	inf	0	1	1
ENSG00000242135	ENSG00000242135	RPL17P2	14:60679179-60679630	NOTEST	0	0	0	0	1	1
ENSG00000242136	ENSG00000242136	RP11-734K21.2	2:9243568-9245243	NOTEST	0	0	0	0	1	1
ENSG00000242137	ENSG00000242137	RPL11P5	12:121031817-121032351	NOTEST	0	0	0	0	1	1
ENSG00000242138	ENSG00000242138	XXbac-BPG254F23.6	HSCHR6_MHC_MANN:32779139-32788434	NOTEST	0	0	0	0	1	1
ENSG00000242140	ENSG00000242140	RP11-262M14.2	3:180701496-181554668	NOTEST	0	0	0	0	1	1
ENSG00000242142	ENSG00000242142	SERBP1P3	3:52937587-53164478	NOTEST	0	0	0	0	1	1
ENSG00000242145	ENSG00000242145	RP11-520D19.1	3:81257343-81258065	NOTEST	0	0	0	0	1	1
ENSG00000242147	ENSG00000242147	RP13-463N16.6	10:5636953-5638081	NOTEST	0	0	0	0	1	1
ENSG00000242150	ENSG00000242150	RP11-134G8.6	1:201452657-201502736	NOTEST	0.33854	0.247682	-0.450838	0	1	1
ENSG00000242151	ENSG00000242151	CTD-2501O3.3	3:154375082-154375352	NOTEST	0	0	0	0	1	1
ENSG00000242152	ENSG00000242152	RP11-639F1.3	3:155093368-155462856	NOTEST	0	0	0	0	1	1
ENSG00000242153	ENSG00000242153	OFD1P6Y	Y:20835918-20991373	NOTEST	0	0	0	0	1	1
ENSG00000242154	ENSG00000242154	RP4-778K6.3	7:104653871-105039755	NOTEST	0.186657	0.426309	1.19151	0	1	1
ENSG00000242158	ENSG00000242158	RN7SL361P	2:60867839-60868135	NOTEST	0	0	0	0	1	1
ENSG00000242159	ENSG00000242159	ABCF2P1	3:88366305-88368172	NOTEST	0	0.0211105	inf	0	1	1
ENSG00000242162	ENSG00000242162	RP11-128A6.3	7:128706074-128706516	NOTEST	0	0.171576	inf	0	1	1
ENSG00000242163	ENSG00000242163	RP11-299L17.1	14:81726999-81902809	NOTEST	0	0	0	0	1	1
ENSG00000242165	ENSG00000242165	RN7SL222P	11:100512708-100513004	NOTEST	0	0	0	0	1	1
ENSG00000242169	ENSG00000242169	RP11-219G10.1	4:189270529-189271178	NOTEST	0	0.0219832	inf	0	1	1
ENSG00000242170	ENSG00000242170	RN7SL329P	8:126036501-126379362	NOTEST	0	0	0	0	1	1
ENSG00000242173	ENSG00000242173	ARHGDIG	16:284544-333003	NOTEST	0.0883826	0	#NAME?	0	1	1
ENSG00000242175	ENSG00000242175	RN7SL127P	4:79697495-79860592	NOTEST	0.114958	0.458288	1.99515	0	1	1
ENSG00000242176	ENSG00000242176	RPL39P31	16:71963440-72033877	NOTEST	0	0	0	0	1	1
ENSG00000242178	ENSG00000242178	MTND4P17	3:165877808-165878158	NOTEST	0	0	0	0	1	1
ENSG00000242180	ENSG00000242180	OR51B5	11:5274419-5667019	NOTEST	0	0.0129034	inf	0	1	1
ENSG00000242182	ENSG00000242182	RN7SL745P	18:20279443-20606451	NOTEST	0	0	0	0	1	1

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ENSG00000242186	ENSG00000242186	AC002523.1	X:148138245-148138696	NOTEST	0	0	0	0	1	1
ENSG00000242188	ENSG00000242188	RN7SL428P	15:85734668-85778026	NOTEST	0	0	0	0	1	1
ENSG00000242190	ENSG00000242190	RP11-142L1.1	3:81811856-81813907	NOTEST	0	0	0	0	1	1
ENSG00000242195	ENSG00000242195	SRRM1P2	3:83986195-83987387	NOTEST	0	0	0	0	1	1
ENSG00000242197	ENSG00000242197	RP11-588L15.1	4:40425271-40632892	NOTEST	0	0	0	0	1	1
ENSG00000242199	ENSG00000242199	RP11-71H17.1	3:124449212-124464040	NOTEST	0.170948	0	#NAME?	0	1	1
ENSG00000242201	ENSG00000242201	RN7SL215P	3:193863462-193863756	NOTEST	0	0	0	0	1	1
ENSG00000242206	ENSG00000242206	RPS26P35	8:119774094-119774440	NOTEST	0.168844	0	#NAME?	0	1	1
ENSG00000242207	ENSG00000242207	HOXB-AS4	17:46684593-46712294	NOTEST	0	0	0	0	1	1
ENSG00000242208	ENSG00000242208	RPL5P29	11:56124803-56125697	NOTEST	0	0	0	0	1	1
ENSG00000242209	ENSG00000242209	AC006445.6	4:13649320-13650024	NOTEST	0	0	0	0	1	1
ENSG00000242214	ENSG00000242214	MTND3P6	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000242216	ENSG00000242216	RN7SL97P	18:23398199-23398496	NOTEST	0	0	0	0	1	1
ENSG00000242220	ENSG00000242220	TCP10L	21:33948861-33985176	NOTEST	0	0.12233	inf	0	1	1
ENSG00000242221	ENSG00000242221	PSG2	19:43568362-43587197	NOTEST	0.0238035	0	#NAME?	0	1	1
ENSG00000242222	ENSG00000242222	RP11-237P21.1	3:135644732-135645009	NOTEST	0	0	0	0	1	1
ENSG00000242227	ENSG00000242227	HLA-L	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000242229	ENSG00000242229	RPS3AP14	3:125493556-125516796	NOTEST	0	0	0	0	1	1
ENSG00000242236	ENSG00000242236	RN7SL594P	20:25593570-25677477	NOTEST	0	0	0	0	1	1
ENSG00000242241	ENSG00000242241	RN7SL306P	7:128594947-128695198	NOTEST	0.221062	0	#NAME?	0	1	1
ENSG00000242242	ENSG00000242242	PVRL3-AS1	3:110612554-110994410	NOTEST	0.354285	0.312465	-0.181214	0	1	1
ENSG00000242244	ENSG00000242244	ATP5G1P3	3:138608096-138608799	NOTEST	0	0	0	0	1	1
ENSG00000242246	ENSG00000242246	RP11-331O9.2	6:153987600-153989241	NOTEST	0	0	0	0	1	1
ENSG00000242248	ENSG00000242248	RPL7AP57	11:91894271-91895055	NOTEST	0	0	0	0	1	1
ENSG00000242251	ENSG00000242251	RN7SL20P	22:32149943-32303012	NOTEST	0	0	0	0	1	1
ENSG00000242252	ENSG00000242252	BGLAP	1:156182772-156213123	NOTEST	0.276595	0.441023	0.673077	0	1	1
ENSG00000242255	ENSG00000242255	RPL39P34	19:53030904-53090427	NOTEST	0	0.858437	inf	0	1	1
ENSG00000242256	ENSG00000242256	RN7SL57P	9:114980714-115095947	NOTEST	0	0	0	0	1	1
ENSG00000242258	ENSG00000242258	LINC00996	7:150130741-150145228	NOTEST	0	0	0	0	1	1
ENSG00000242262	ENSG00000242262	RP11-100N21.1	4:47596014-47840123	NOTEST	0	0.0519745	inf	0	1	1
ENSG00000242266	ENSG00000242266	RN7SL456P	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000242267	ENSG00000242267	SKINTL	1:48561763-48648100	NOTEST	0	0	0	0	1	1
ENSG00000242268	ENSG00000242268	RP11-368I23.2	3:168621153-168639784	NOTEST	0.0551174	0	#NAME?	0	1	1
ENSG00000242272	ENSG00000242272	AK2P2	2:32047659-32048886	NOTEST	0	0	0	0	1	1
ENSG00000242276	ENSG00000242276	RPL5P3	15:71355439-71356328	NOTEST	0	0	0	0	1	1
ENSG00000242278	ENSG00000242278	RP11-382N13.1	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000242279	ENSG00000242279	RP11-659G9.1	11:82534543-82782965	NOTEST	0.0238421	0.0336625	0.497632	0	1	1
ENSG00000242280	ENSG00000242280	SLC16A1P1	7:143651936-143694405	NOTEST	0	0	0	0	1	1
ENSG00000242281	ENSG00000242281	RN7SL159P	9:132132451-132132740	NOTEST	0	0	0	0	1	1
ENSG00000242284	ENSG00000242284	CT45A5	X:134928330-134953994	NOTEST	0	0	0	0	1	1
ENSG00000242285	ENSG00000242285	RPL6P8	3:160302732-160303575	NOTEST	0.0221031	0.0533446	1.27109	0	1	1
ENSG00000242289	ENSG00000242289	OR5V1	HSCHR6_MHC_APD:29390470-29424928	NOTEST	0	0	0	0	1	1
ENSG00000242290	ENSG00000242290	RP11-197K3.1	3:114056940-114866118	NOTEST	0	0	0	0	1	1

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ENSG00000242293	ENSG00000242293	RP11-226F19.1	14:69489866-69490025	NOTEST	0	0	0	0	1	1
ENSG00000242295	ENSG00000242295	RP11-522B15.1	15:96991383-96991723	NOTEST	0	0	0	0	1	1
ENSG00000242296	ENSG00000242296	DEFB109P1	8:12219526-12268510	NOTEST	0	0	0	0	1	1
ENSG00000242301	ENSG00000242301	RP11-93P10.3	9:66081971-66083332	NOTEST	0	0	0	0	1	1
ENSG00000242307	ENSG00000242307	RPS26P52	16:14014013-14046202	NOTEST	0.160039	0	#NAME?	0	1	1
ENSG00000242308	ENSG00000242308	RP11-572C15.3	3:112415754-112416553	NOTEST	0	0	0	0	1	1
ENSG00000242311	ENSG00000242311	RN7SL21P	10:104263743-104393292	NOTEST	0.132592	0.0959613	-0.466473	0	1	1
ENSG00000242314	ENSG00000242314	RP11-428G5.2	12:32101267-32101761	NOTEST	0	0	0	0	1	1
ENSG00000242315	ENSG00000242315	RN7SL685P	8:101970110-101970406	NOTEST	0	0.282243	inf	0	1	1
ENSG00000242317	ENSG00000242317	RP11-875H7.5	3:55527857-55539289	NOTEST	0.216261	0	#NAME?	0	1	1
ENSG00000242318	ENSG00000242318	RP11-810D13.1	4:99172838-99365012	NOTEST	0	0	0	0	1	1
ENSG00000242320	ENSG00000242320	RPL21P126	18:52889561-53332018	NOTEST	0	0	0	0	1	1
ENSG00000242321	ENSG00000242321	RPL23AP40	3:138372859-138553780	NOTEST	0	0	0	0	1	1
ENSG00000242324	ENSG00000242324	RP4-576H24.2	20:1497404-1600707	NOTEST	0	0	0	0	1	1
ENSG00000242325	ENSG00000242325	RPS12P31	19:33087912-33169206	NOTEST	0.130666	0.0976797	-0.419753	0	1	1
ENSG00000242326	ENSG00000242326	RP11-12N13.2	3:165899100-165899608	NOTEST	0	0	0	0	1	1
ENSG00000242327	ENSG00000242327	CTD-2184D3.1	15:52121824-52392720	NOTEST	0	0	0	0	1	1
ENSG00000242329	ENSG00000242329	RP11-59H1.1	12:12993737-12994013	NOTEST	0	0	0	0	1	1
ENSG00000242330	ENSG00000242330	RN7SL683P	14:71759441-72207946	NOTEST	0	0	0	0	1	1
ENSG00000242335	ENSG00000242335	CFB	HSCHR6_MHC_SSTO:31879618-31911713	NOTEST	0	0	0	0	1	1
ENSG00000242337	ENSG00000242337	TFP1	3:133380841-133497850	NOTEST	0	0.0280922	inf	0	1	1
ENSG00000242338	ENSG00000242338	BMS1P4	10:75404638-75490272	NOTEST	0.395333	0.37547	-0.074374	0	1	1
ENSG00000242339	ENSG00000242339	RP11-735B13.2	3:84934086-84942530	NOTEST	0	0	0	0	1	1
ENSG00000242341	ENSG00000242341	RN7SL646P	5:177664618-178017556	NOTEST	0	0	0	0	1	1
ENSG00000242348	ENSG00000242348	RN7SL561P	20:1645928-1688846	NOTEST	0	0	0	0	1	1
ENSG00000242352	ENSG00000242352	RP11-403I13.6	1:149239530-149265510	NOTEST	0.248714	0.194343	-0.355886	0	1	1
ENSG00000242353	ENSG00000242353	RP4-710M3.1	11:30389694-30390193	NOTEST	0.168822	0.0352877	-2.25826	0	1	1
ENSG00000242357	ENSG00000242357	RP11-809C18.5	10:320129-735683	NOTEST	0.0391948	0.117466	1.58351	0	1	1
ENSG00000242358	ENSG00000242358	RPS21P4	4:16162127-16321763	NOTEST	0.184698	0	#NAME?	0	1	1
ENSG00000242360	ENSG00000242360	RN7SL272P	13:28563434-28563721	NOTEST	0	0	0	0	1	1
ENSG00000242361	ENSG00000242361	HLA-DMA	HSCHR6_MHC_APD:32885992-32904491	NOTEST	0	0	0	0	1	1
ENSG00000242362	ENSG00000242362	CT47A2	X:120111459-120119642	NOTEST	0	0	0	0	1	1
ENSG00000242364	ENSG00000242364	RP11-451J24.1	3:73697549-73697958	NOTEST	0.117696	0.150885	0.358383	0	1	1
ENSG00000242365	ENSG00000242365	NDUFA5P5	3:88650210-88650552	NOTEST	0	0	0	0	1	1
ENSG00000242366	ENSG00000242366	UGT1A1	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000242370	ENSG00000242370	KCNAB1-AS1	3:155755489-156256545	NOTEST	0	0	0	0	1	1
ENSG00000242371	ENSG00000242371	IGKV1-39	2:89619382-89619904	NOTEST	0	0	0	0	1	1
ENSG00000242375	ENSG00000242375	RP11-498P14.3	9:99918851-100140806	NOTEST	0	0	0	0	1	1
ENSG00000242379	ENSG00000242379	RN7SL261P	1:147161374-147161681	NOTEST	0	0	0	0	1	1
ENSG00000242381	ENSG00000242381	RN7SL741P	13:25946208-26599989	NOTEST	0	0	0	0	1	1

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ENSG00000242385	ENSG00000242385	LINC00901	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000242386	ENSG00000242386	HLA-DMB	HSCHR6_MHC_MCF:32935859-32980443	NOTEST	0	0	0	0	1	1
ENSG00000242387	ENSG00000242387	HIST1H2APS2	6:25833293-25882623	NOTEST	0	0	0	0	1	1
ENSG00000242389	ENSG00000242389	RBMY1E	Y:24026222-24064214	NOTEST	0	0	0	0	1	1
ENSG00000242390	ENSG00000242390	RPL6P9	3:142299751-142301241	NOTEST	0	0.0152295	inf	0	1	1
ENSG00000242391	ENSG00000242391	RP4-631H13.2	1:53308182-53360670	NOTEST	0	0	0	0	1	1
ENSG00000242393	ENSG00000242393	AC010141.4	Y:23670184-23672356	NOTEST	0	0	0	0	1	1
ENSG00000242396	ENSG00000242396	RP11-67L3.5	1:55315305-55354523	NOTEST	0	0.0324741	inf	0	1	1
ENSG00000242398	ENSG00000242398	RN7SL800P	17:60019965-60142643	NOTEST	0	0	0	0	1	1
ENSG00000242399	ENSG00000242399	RPS20P23	8:101788739-101789093	NOTEST	0	0	0	0	1	1
ENSG00000242405	ENSG00000242405	RP11-267J23.1	12:12202777-12419946	NOTEST	0.0436878	0	#NAME?	0	1	1
ENSG00000242407	ENSG00000242407	CTD-2377D24.4	17:46810452-46811250	NOTEST	0	0	0	0	1	1
ENSG00000242411	ENSG00000242411	CTD-2086L14.1	19:56728536-56729146	NOTEST	0	0.0263434	inf	0	1	1
ENSG00000242412	ENSG00000242412	DBIL5P2	2:63344985-63346677	NOTEST	0	0.00758804	inf	0	1	1
ENSG00000242417	ENSG00000242417	RP11-286B5.1	14:48865710-48960970	NOTEST	0	0	0	0	1	1
ENSG00000242419	ENSG00000242419	PCDHGC4	5:140710251-140892546	NOTEST	0.12127	0.108048	-0.166551	0	1	1
ENSG00000242421	ENSG00000242421	RN7SL313P	2:97766320-97766609	NOTEST	0	0	0	0	1	1
ENSG00000242423	ENSG00000242423	RP11-451N19.1	16:58741034-59142878	NOTEST	0	0	0	0	1	1
ENSG00000242425	ENSG00000242425	RN7SL818P	Y:26355713-26361728	NOTEST	0	0	0	0	1	1
ENSG00000242428	ENSG00000242428	RP11-147N17.1	3:58703091-59035810	NOTEST	0	0.0160459	inf	0	1	1
ENSG00000242429	ENSG00000242429	RP11-19G24.2	17:35441922-35766909	NOTEST	0	0	0	0	1	1
ENSG00000242430	ENSG00000242430	RN7SL274P	16:14529557-14726585	NOTEST	0	0	0	0	1	1
ENSG00000242431	ENSG00000242431	RP11-731J8.1	4:47487304-47595503	NOTEST	0	0	0	0	1	1
ENSG00000242435	ENSG00000242435	UPK3BP1	7:76139744-77045717	NOTEST	0.103848	0.106249	0.0329809	0	1	1
ENSG00000242436	ENSG00000242436	RN7SL789P	19:33087912-33169206	NOTEST	0	0	0	0	1	1
ENSG00000242439	ENSG00000242439	CTD-2349P21.1	17:29157918-29158336	NOTEST	0	0	0	0	1	1
ENSG00000242440	ENSG00000242440	RP11-501O2.5	3:147998677-148117743	NOTEST	0	0	0	0	1	1
ENSG00000242441	ENSG00000242441	GTF2A1L	2:48756521-49003654	NOTEST	0	0	0	0	1	1
ENSG00000242443	ENSG00000242443	RN7SL759P	15:20767699-20781019	NOTEST	0	0	0	0	1	1
ENSG00000242444	ENSG00000242444	RP11-320N7.1	12:4218826-4227298	NOTEST	0	0	0	0	1	1
ENSG00000242456	ENSG00000242456	RP11-12N13.4	3:165878990-165879756	NOTEST	0	0	0	0	1	1
ENSG00000242457	ENSG00000242457	RBBP4P2	3:93698982-93847389	NOTEST	0.0790731	0.252276	1.67374	0	1	1
ENSG00000242461	ENSG00000242461	RPS15AP32	12:113491866-113492240	NOTEST	0	0	0	0	1	1
ENSG00000242463	ENSG00000242463	RN7SL500P	22:50781732-50913454	NOTEST	0	0	0	0	1	1
ENSG00000242472	ENSG00000242472	IGHJ5	14:106330023-106330072	NOTEST	0	0	0	0	1	1
ENSG00000242473	ENSG00000242473	KIR2DP1	19:55235968-55378662	NOTEST	0	0	0	0	1	1
ENSG00000242474	ENSG00000242474	AC093627.9	7:135852-149466	NOTEST	0.115064	0.0410131	-1.48827	0	1	1
ENSG00000242479	ENSG00000242479	RP11-383G6.4	3:142168076-142297668	NOTEST	0.0767274	0.0385208	-0.994106	0	1	1
ENSG00000242480	ENSG00000242480	RN7SL286P	15:32885656-32896179	NOTEST	0	0	0	0	1	1
ENSG00000242482	ENSG00000242482	RN7SL392P	1:68122515-68122812	NOTEST	0	0	0	0	1	1
ENSG00000242483	ENSG00000242483	RN7SL293P	8:11197145-11332224	NOTEST	0	0	0	0	1	1
ENSG00000242486	ENSG00000242486	RP1-104O17.2	6:98150156-98180588	NOTEST	0	0	0	0	1	1

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ENSG00000242493	ENSG00000242493	RN7SL37P	5:37106329-37249530	NOTEST	0	0	0	0	1	1
ENSG00000242502	ENSG00000242502	RN7SL536P	15:23599894-23612378	NOTEST	0	0	0	0	1	1
ENSG00000242507	ENSG00000242507	RP3-477O4.5	20:34108568-34117481	NOTEST	0	0	0	0	1	1
ENSG00000242509	ENSG00000242509	RN7SL156P	20:35498501-35498793	NOTEST	0	0	0	0	1	1
ENSG00000242510	ENSG00000242510	NDUFB4P1	3:67410883-67705038	NOTEST	0	0	0	0	1	1
ENSG00000242511	ENSG00000242511	RPL23AP1	HSCHR6_MHC_SSTO:29687513-29713718	NOTEST	0	0	0	0	1	1
ENSG00000242512	ENSG00000242512	RP11-416O18.1	3:181670130-181728466	NOTEST	0	0	0	0	1	1
ENSG00000242515	ENSG00000242515	UGT1A10	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000242516	ENSG00000242516	LINC00960	3:75721541-75728454	NOTEST	0.232256	0.337463	0.539014	0	1	1
ENSG00000242520	ENSG00000242520	MAGEA5	X:151282525-151307033	NOTEST	0	0.0214541	inf	0	1	1
ENSG00000242522	ENSG00000242522	KLHL6-AS1	3:183205318-183273477	NOTEST	0	0	0	0	1	1
ENSG00000242524	ENSG00000242524	OR2U2P	6:29191749-29258217	NOTEST	0	0	0	0	1	1
ENSG00000242525	ENSG00000242525	OR7E100P	3:112243033-112244048	NOTEST	0.0175979	0	#NAME?	0	1	1
ENSG00000242527	ENSG00000242527	RP11-159H22.1	11:27505396-27505675	NOTEST	0	0	0	0	1	1
ENSG00000242529	ENSG00000242529	AHCYP8	1:248881946-248885506	NOTEST	0.545188	0	#NAME?	0	1	1
ENSG00000242531	ENSG00000242531	RP11-299J3.6	3:122135053-122233792	NOTEST	0	0	0	0	1	1
ENSG00000242534	ENSG00000242534	IGKV2D-28	2:89998788-89999564	NOTEST	0	0	0	0	1	1
ENSG00000242536	ENSG00000242536	RP11-290K4.2	3:157734004-157806786	NOTEST	0	0	0	0	1	1
ENSG00000242537	ENSG00000242537	RP11-294L13.1	3:155755489-156256545	NOTEST	0	0	0	0	1	1
ENSG00000242540	ENSG00000242540	AC010729.1	2:5832798-5848227	NOTEST	0	0	0	0	1	1
ENSG00000242542	ENSG00000242542	RN7SL489P	15:75550939-75562540	NOTEST	0	0	0	0	1	1
ENSG00000242545	ENSG00000242545	RP11-719N22.2	3:59450055-59496404	NOTEST	0	0	0	0	1	1
ENSG00000242547	ENSG00000242547	RN7SL169P	5:63802083-63908139	NOTEST	0	0	0	0	1	1
ENSG00000242550	ENSG00000242550	SERPINB10	18:61538925-61609601	NOTEST	0.0909875	0.0148788	-2.61241	0	1	1
ENSG00000242551	ENSG00000242551	POU5F1P6	3:128338816-128399918	NOTEST	0.0181352	0	#NAME?	0	1	1
ENSG00000242552	ENSG00000242552	MRPL42P4	7:46930222-47118726	NOTEST	0	0	0	0	1	1
ENSG00000242553	ENSG00000242553	AP001432.14	21:38580803-38640785	NOTEST	0.480979	0.457276	-0.0729087	0	1	1
ENSG00000242559	ENSG00000242559	RN7SL144P	X:41374186-41782716	NOTEST	0	0	0	0	1	1
ENSG00000242560	ENSG00000242560	RN7SL797P	6:96730442-96730737	NOTEST	0	0	0	0	1	1
ENSG00000242561	ENSG00000242561	ATP5LP5	3:152518222-152518521	NOTEST	0	0	0	0	1	1
ENSG00000242562	ENSG00000242562	DCAF13P1	7:105765816-105767146	NOTEST	0.0594034	0.0309033	-0.942786	0	1	1
ENSG00000242565	ENSG00000242565	RN7SL372P	1:153676563-153676859	NOTEST	0	0	0	0	1	1
ENSG00000242568	ENSG00000242568	RP11-875H7.1	3:55369489-55384943	NOTEST	0	0	0	0	1	1
ENSG00000242569	ENSG00000242569	RP11-435B5.3	1:143347957-143467632	NOTEST	0.0982185	0.019733	-2.31538	0	1	1
ENSG00000242571	ENSG00000242571	RPL21P11	14:90833040-90833523	NOTEST	0.190412	0.0709403	-1.42445	0	1	1
ENSG00000242573	ENSG00000242573	ACTR3P3	3:100881937-100882830	NOTEST	0	0	0	0	1	1
ENSG00000242575	ENSG00000242575	AC012501.3	2:154277190-154449801	NOTEST	0	0	0	0	1	1
ENSG00000242576	ENSG00000242576	RNU2-38P	HG1287_PATCH:149575877-149719430	NOTEST	0	0	0	0	1	1
ENSG00000242578	ENSG00000242578	RP11-469J4.3	3:170128299-170136403	NOTEST	0.0301309	0	#NAME?	0	1	1
ENSG00000242580	ENSG00000242580	IGKV1D-43	2:90248738-90249395	NOTEST	0	0	0	0	1	1
ENSG00000242583	ENSG00000242583	RP11-379K17.9	3:169755716-169803191	NOTEST	0	0.0390906	inf	0	1	1
ENSG00000242586	ENSG00000242586	RP11-481N16.1	3:80491230-80491455	NOTEST	0	0	0	0	1	1
ENSG00000242590	ENSG00000242590	RP11-54O7.14	1:955502-991496	NOTEST	0	0	0	0	1	1

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ENSG00000242595	ENSG00000242595	RP11-648L3.1	8:58907067-59116838	NOTEST	0	0	0	0	1	1
ENSG00000242598	ENSG00000242598	MED28P8	1:81771844-82458120	NOTEST	0	0	0	0	1	1
ENSG00000242600	ENSG00000242600	MBL1P	10:81664653-81742370	NOTEST	0.33439	0.247069	-0.436618	0	1	1
ENSG00000242602	ENSG00000242602	CTD-2339M3.1	5:72090231-72212560	NOTEST	0	0	0	0	1	1
ENSG00000242607	ENSG00000242607	RPS3AP34	8:12427858-12428639	NOTEST	0	0.0171912	inf	0	1	1
ENSG00000242608	ENSG00000242608	RPS23P5	5:13250346-13250774	NOTEST	0	0	0	0	1	1
ENSG00000242609	ENSG00000242609	RP11-398A8.1	3:72084450-72291716	NOTEST	0	0	0	0	1	1
ENSG00000242610	ENSG00000242610	OR5BH1P	X:130407479-130533677	NOTEST	0	0	0	0	1	1
ENSG00000242611	ENSG00000242611	AC093627.8	7:77037-80418	NOTEST	0	0	0	0	1	1
ENSG00000242613	ENSG00000242613	RP11-174O3.4	3:120106875-120108162	NOTEST	0	0	0	0	1	1
ENSG00000242614	ENSG00000242614	RN7SL164P	13:96743092-97485671	NOTEST	0	0	0	0	1	1
ENSG00000242615	ENSG00000242615	CTC-359D24.3	19:12203077-12267546	NOTEST	0.188398	0.204271	0.1167	0	1	1
ENSG00000242618	ENSG00000242618	RP11-433A10.2	3:72084450-72291716	NOTEST	0	0	0	0	1	1
ENSG00000242620	ENSG00000242620	RN7SL736P	15:90835193-90838915	NOTEST	0	0	0	0	1	1
ENSG00000242628	ENSG00000242628	AC009228.1	2:24425732-24583583	NOTEST	0	0	0	0	1	1
ENSG00000242634	ENSG00000242634	RPS24P16	15:67493370-67819628	NOTEST	0	0	0	0	1	1
ENSG00000242635	ENSG00000242635	RPS14P7	4:161739573-161740021	NOTEST	0	0	0	0	1	1
ENSG00000242636	ENSG00000242636	RPL21P129	19:7815569-7816047	NOTEST	0	0	0	0	1	1
ENSG00000242638	ENSG00000242638	RN7SL294P	3:75231906-75232199	NOTEST	0	0	0	0	1	1
ENSG00000242640	ENSG00000242640	RP11-302F12.1	4:25680471-25680642	NOTEST	0	0	0	0	1	1
ENSG00000242641	ENSG00000242641	LINC00971	3:84687556-84930830	NOTEST	0	0	0	0	1	1
ENSG00000242650	ENSG00000242650	RN7SL292P	7:51784353-51784615	NOTEST	0	0	0	0	1	1
ENSG00000242651	ENSG00000242651	RN7SL862P	18:9708161-9862548	NOTEST	0	0	0	0	1	1
ENSG00000242653	ENSG00000242653	RN7SL132P	7:34386123-34917944	NOTEST	0	0	0	0	1	1
ENSG00000242654	ENSG00000242654	RPL32P14	5:18965969-19142455	NOTEST	0	0	0	0	1	1
ENSG00000242657	ENSG00000242657	RN7SL581P	X:69441857-69442164	NOTEST	0	0	0	0	1	1
ENSG00000242659	ENSG00000242659	RP11-271C24.2	3:113465718-113530903	NOTEST	0	0.0799475	inf	0	1	1
ENSG00000242660	ENSG00000242660	RP11-1094M14.1	17:33893535-33893691	NOTEST	0	0	0	0	1	1
ENSG00000242661	ENSG00000242661	RPS3AP43	12:8407122-8549399	NOTEST	0	0	0	0	1	1
ENSG00000242663	ENSG00000242663	RP11-196G18.21	1:149754226-149783928	NOTEST	0	0	0	0	1	1
ENSG00000242667	ENSG00000242667	RP11-745A24.2	15:60696661-60697159	NOTEST	0	0.142099	inf	0	1	1
ENSG00000242668	ENSG00000242668	RN7SL317P	19:54132966-54133246	NOTEST	0	0	0	0	1	1
ENSG00000242670	ENSG00000242670	RP11-601I15.1	4:54243809-55164414	NOTEST	0	0	0	0	1	1
ENSG00000242671	ENSG00000242671	RP11-232M24.1	3:146627471-147088443	NOTEST	0	0	0	0	1	1
ENSG00000242673	ENSG00000242673	RN7SL167P	11:130874024-130874324	NOTEST	0	0	0	0	1	1
ENSG00000242675	ENSG00000242675	RPS16P9	19:45835955-45836382	NOTEST	0	0	0	0	1	1
ENSG00000242683	ENSG00000242683	CTB-46B19.1	5:138282408-138667360	NOTEST	0	0	0	0	1	1
ENSG00000242685	ENSG00000242685	HLA-DMA	HSCHR6_MHC_QBL:32831135-32878022	NOTEST	0	0	0	0	1	1
ENSG00000242686	ENSG00000242686	RP11-1191J2.2	4:619372-664571	NOTEST	0	0	0	0	1	1
ENSG00000242688	ENSG00000242688	RN7SL304P	1:20297461-20297760	NOTEST	0	0	0	0	1	1

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ENSG00000242692	ENSG00000242692	RPS27AP1	17:10162078-10162549	NOTEST	0	0.119734	inf	0	1	1
ENSG00000242696	ENSG00000242696	RN7SL40P	2:203221843-203222140	NOTEST	0	0	0	0	1	1
ENSG00000242697	ENSG00000242697	RPL5P12	4:98105243-99064391	NOTEST	0	0	0	0	1	1
ENSG00000242699	ENSG00000242699	RN7SL516P	2:29415639-30144432	NOTEST	0	0	0	0	1	1
ENSG00000242703	ENSG00000242703	CCT4P1	7:140697751-140699600	NOTEST	0	0	0	0	1	1
ENSG00000242705	ENSG00000242705	NARG2P2	3:88997291-89000078	NOTEST	0	0	0	0	1	1
ENSG00000242706	ENSG00000242706	CTD-2015H6.2	5:79778111-79838382	NOTEST	0.0556071	0	#NAME?	0	1	1
ENSG00000242707	ENSG00000242707	RN7SL362P	18:13663345-13764557	NOTEST	0	0	0	0	1	1
ENSG00000242709	ENSG00000242709	RPL30P9	8:19936815-19975953	NOTEST	0	0	0	0	1	1
ENSG00000242711	ENSG00000242711	PSMB9	HSCHR6_MHC_APD:32792100-32831197	NOTEST	0	0	0	0	1	1
ENSG00000242712	ENSG00000242712	RN7SL529P	11:118865043-118865343	NOTEST	0.113271	0	#NAME?	0	1	1
ENSG00000242716	ENSG00000242716	RNA5-8S5	GL000220.1:112024-112177	NOTEST	0	0	0	0	1	1
ENSG00000242719	ENSG00000242719	RN7SL806P	8:42704779-42940931	NOTEST	0	0	0	0	1	1
ENSG00000242726	ENSG00000242726	RPP21	HSCHR6_MHC_QBL:30191333-30304165	NOTEST	0	0	0	0	1	1
ENSG00000242727	ENSG00000242727	RP11-123J14.1	4:77812186-77812598	NOTEST	0	0	0	0	1	1
ENSG00000242728	ENSG00000242728	UQCRHP4	3:70189367-70189639	NOTEST	0.568673	0	#NAME?	0	1	1
ENSG00000242729	ENSG00000242729	RP11-124G5.1	11:41540444-41735998	NOTEST	0	0	0	0	1	1
ENSG00000242731	ENSG00000242731	FAM86LP	7:6971314-6979234	NOTEST	0	0	0	0	1	1
ENSG00000242732	ENSG00000242732	RGAG4	X:71130937-71363424	NOTEST	0.164513	0.241543	0.55408	0	1	1
ENSG00000242735	ENSG00000242735	AC018462.3	2:62095223-62374382	NOTEST	0.34867	0.0934081	-1.90024	0	1	1
ENSG00000242736	ENSG00000242736	TRBV1	7:141999016-141999300	NOTEST	0	0	0	0	1	1
ENSG00000242737	ENSG00000242737	RP11-562A8.1	15:50716576-50838905	NOTEST	0.150304	0.0615044	-1.28912	0	1	1
ENSG00000242741	ENSG00000242741	RP11-20B7.1	3:73857751-73952017	NOTEST	0	0.0171628	inf	0	1	1
ENSG00000242747	ENSG00000242747	RP11-30K9.1	15:59063390-59389618	NOTEST	0	0	0	0	1	1
ENSG00000242748	ENSG00000242748	RPL23AP81	20:39657457-39946312	NOTEST	0.43895	0.596073	0.441432	0	1	1
ENSG00000242752	ENSG00000242752	TRNAQ41P	17:19506586-19506658	NOTEST	0	0	0	0	1	1
ENSG00000242753	ENSG00000242753	RP11-716O23.2	6:11487458-11516699	NOTEST	0.0288434	0	#NAME?	0	1	1
ENSG00000242756	ENSG00000242756	RHOT1P3	13:19390857-19446107	NOTEST	0	0	0	0	1	1
ENSG00000242757	ENSG00000242757	CTD-2090I13.3	1:227581291-227618736	NOTEST	0	0	0	0	1	1
ENSG00000242764	ENSG00000242764	RN7SL824P	1:92867947-92868242	NOTEST	0	0	0	0	1	1
ENSG00000242766	ENSG00000242766	IGKV1D-17	2:90121476-90122133	NOTEST	0	0	0	0	1	1
ENSG00000242767	ENSG00000242767	ZBTB20-AS4	3:114056940-114866118	NOTEST	0	0	0	0	1	1
ENSG00000242768	ENSG00000242768	RP11-556G22.1	4:20697904-21950422	NOTEST	0	0	0	0	1	1
ENSG00000242769	ENSG00000242769	RN7SL432P	1:115240249-115240545	NOTEST	0	0	0	0	1	1
ENSG00000242770	ENSG00000242770	RP11-180K7.1	3:112521324-112531666	NOTEST	0	0	0	0	1	1
ENSG00000242771	ENSG00000242771	TRBV5-2	7:142259058-142259331	NOTEST	0	0	0	0	1	1
ENSG00000242775	ENSG00000242775	RP11-875H7.2	3:55394470-55395857	NOTEST	0	0	0	0	1	1
ENSG00000242779	ENSG00000242779	ZNF702P	19:53430387-53541151	NOTEST	0.00827365	0.0116277	0.490975	0	1	1
ENSG00000242781	ENSG00000242781	RP11-47P18.2	3:80810192-80838505	NOTEST	0	0	0	0	1	1
ENSG00000242790	ENSG00000242790	RP11-451G4.3	3:155008017-155011965	NOTEST	0	0	0	0	1	1
ENSG00000242791	ENSG00000242791	RP11-651P23.5	3:149478891-149942977	NOTEST	0.058367	0.354257	2.60157	0	1	1
ENSG00000242793	ENSG00000242793	AC135999.2	15:26788692-27194354	NOTEST	0	0	0	0	1	1
ENSG00000242794	ENSG00000242794	RN7SL299P	1:232358611-232358891	NOTEST	0	0	0	0	1	1

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ENSG00000242797	ENSG00000242797	GLYCTK-AS1	3:52288436-52333083	NOTEST	0	0.0894017	inf	0	1	1
ENSG00000242807	ENSG00000242807	RPL26P31	11:92785560-92785993	NOTEST	0	0	0	0	1	1
ENSG00000242808	ENSG00000242808	SOX2-OT	3:180701496-181554668	NOTEST	0.145598	0.0624373	-1.22151	0	1	1
ENSG00000242810	ENSG00000242810	MRPL42P6	3:151193591-151193962	NOTEST	0	0	0	0	1	1
ENSG00000242811	ENSG00000242811	RN7SL229P	3:180319917-180700541	NOTEST	0	0	0	0	1	1
ENSG00000242814	ENSG00000242814	RP11-436H11.1	5:124144520-124144926	NOTEST	0	0.0450708	inf	0	1	1
ENSG00000242816	ENSG00000242816	RP11-768G7.3	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000242818	ENSG00000242818	RN7SL846P	10:121485608-121588652	NOTEST	0	0.0928731	inf	0	1	1
ENSG00000242822	ENSG00000242822	RN7SL575P	2:95669291-95669588	NOTEST	0	0	0	0	1	1
ENSG00000242828	ENSG00000242828	RP11-47P18.1	3:80810192-80838505	NOTEST	0	0	0	0	1	1
ENSG00000242829	ENSG00000242829	RPS26P21	3:119013219-119139561	NOTEST	0.0835815	0.262077	1.64874	0	1	1
ENSG00000242834	ENSG00000242834	RPL7AP56	11:37747215-37748006	NOTEST	0	0	0	0	1	1
ENSG00000242836	ENSG00000242836	RP11-52L11.7	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000242837	ENSG00000242837	RPL21P13	14:103707828-103708309	NOTEST	0	0	0	0	1	1
ENSG00000242841	ENSG00000242841	KRT8P35	3:62936104-63110738	NOTEST	0	0	0	0	1	1
ENSG00000242849	ENSG00000242849	ALDOAP1	3:52227185-52228801	NOTEST	0	0	0	0	1	1
ENSG00000242850	ENSG00000242850	RPL23AP68	12:87563761-87564206	NOTEST	0	0	0	0	1	1
ENSG00000242852	ENSG00000242852	ZNF709	19:12490002-12750912	NOTEST	0.351265	0.198589	-0.822772	0	1	1
ENSG00000242853	ENSG00000242853	RN7SL749P	10:120967100-121215131	NOTEST	0	0	0	0	1	1
ENSG00000242854	ENSG00000242854	DNM1P24	Y:26325462-26338017	NOTEST	0	0	0	0	1	1
ENSG00000242855	ENSG00000242855	RN7SL496P	7:39927971-39928261	NOTEST	0	0	0	0	1	1
ENSG00000242856	ENSG00000242856	VN1R105P	19:55155339-55161049	NOTEST	0	0	0	0	1	1
ENSG00000242858	ENSG00000242858	CTC-484M2.1	5:83042206-83042808	NOTEST	0	0	0	0	1	1
ENSG00000242860	ENSG00000242860	RN7SL180P	1:62208148-62629592	NOTEST	0	0	0	0	1	1
ENSG00000242863	ENSG00000242863	RN7SL677P	15:97815406-97975324	NOTEST	0	0	0	0	1	1
ENSG00000242865	ENSG00000242865	RN7SL244P	6:52866076-52965671	NOTEST	0	0	0	0	1	1
ENSG00000242866	ENSG00000242866	STRC	15:43885251-44010458	NOTEST	0.0707971	0.0210433	-1.75033	0	1	1
ENSG00000242871	ENSG00000242871	RN7SL109P	21:33664123-33765335	NOTEST	0	0	0	0	1	1
ENSG00000242875	ENSG00000242875	RBMY1B	Y:23673223-23711212	NOTEST	0	0	0	0	1	1
ENSG00000242879	ENSG00000242879	AC006335.11	Y:6174082-6177628	NOTEST	0	0	0	0	1	1
ENSG00000242880	ENSG00000242880	RP11-190P13.2	3:114970042-115004194	NOTEST	0.0410346	0	#NAME?	0	1	1
ENSG00000242882	ENSG00000242882	RPL5P11	4:174340395-174341288	NOTEST	0	0	0	0	1	1
ENSG00000242887	ENSG00000242887	IGHJ3	14:106330796-106330845	NOTEST	0	0	0	0	1	1
ENSG00000242888	ENSG00000242888	RP11-436M15.1	14:100437785-100610573	NOTEST	0	0.0509728	inf	0	1	1
ENSG00000242893	ENSG00000242893	RN7SL413P	13:52158643-52336171	NOTEST	0	0	0	0	1	1
ENSG00000242894	ENSG00000242894	RN7SL634P	14:104394798-104519004	NOTEST	0.240991	0.375145	0.638468	0	1	1
ENSG00000242899	ENSG00000242899	RPL7P16	3:131252398-132004254	NOTEST	0	0	0	0	1	1
ENSG00000242902	ENSG00000242902	RP11-309L24.2	7:128470430-128550773	NOTEST	0	0	0	0	1	1
ENSG00000242908	ENSG00000242908	RP11-454C18.2	3:151451703-151645963	NOTEST	0	0	0	0	1	1
ENSG00000242911	ENSG00000242911	RP11-118N24.2	3:94654603-94654964	NOTEST	0	0	0	0	1	1
ENSG00000242912	ENSG00000242912	RN7SL384P	10:116183530-116183826	NOTEST	0	0	0	0	1	1
ENSG00000242915	ENSG00000242915	SNRPGP7	2:28680011-28887406	NOTEST	0	0	0	0	1	1

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ENSG00000242924	ENSG00000242924	RP11-298O21.6	3:167582560-167601170	NOTEST	0	0	0	0	1	1
ENSG00000242925	ENSG00000242925	PLCH1-AS2	3:155093368-155462856	NOTEST	0.243407	0.237676	-0.0343779	0	1	1
ENSG00000242928	ENSG00000242928	RN7SL868P	5:149101632-149101933	NOTEST	0	0	0	0	1	1
ENSG00000242931	ENSG00000242931	RPL7P49	17:74385531-74449288	NOTEST	0.0508625	0	#NAME?	0	1	1
ENSG00000242936	ENSG00000242936	RPL30P6	4:96566102-96566444	NOTEST	0	0	0	0	1	1
ENSG00000242941	ENSG00000242941	CTD-2325P2.2	14:68286495-69196935	NOTEST	0.085762	0.138066	0.686948	0	1	1
ENSG00000242943	ENSG00000242943	NKAIN1P1	1:148854137-148891740	NOTEST	0	0	0	0	1	1
ENSG00000242945	ENSG00000242945	RPL29P32	18:51131623-51132095	NOTEST	0	0	0	0	1	1
ENSG00000242948	ENSG00000242948	EPS15P1	7:46820970-46823041	NOTEST	0.208915	0.339299	0.699644	0	1	1
ENSG00000242950	ENSG00000242950	ERVW-1	7:92076766-92157845	NOTEST	0.0150329	0.0252993	0.750976	0	1	1
ENSG00000242951	ENSG00000242951	RP11-507E23.1	14:76041230-76550928	NOTEST	0	0	0	0	1	1
ENSG00000242952	ENSG00000242952	RP11-187O7.1	14:76776956-77227731	NOTEST	0.0207446	0.0765046	1.88281	0	1	1
ENSG00000242953	ENSG00000242953	RP11-803B1.3	3:75444554-75444687	NOTEST	0	0	0	0	1	1
ENSG00000242958	ENSG00000242958	RP11-662B19.1	8:28625177-28747759	NOTEST	0	0.229672	inf	0	1	1
ENSG00000242962	ENSG00000242962	RN7SL106P	15:23435095-23448420	NOTEST	0	0	0	0	1	1
ENSG00000242963	ENSG00000242963	RP11-143E21.1	12:130701351-130701702	NOTEST	0	0	0	0	1	1
ENSG00000242968	ENSG00000242968	RP11-731C17.1	3:136527392-136528465	NOTEST	0	0	0	0	1	1
ENSG00000242970	ENSG00000242970	AC068522.4	8:59496062-59572403	NOTEST	0	0.0609373	inf	0	1	1
ENSG00000242971	ENSG00000242971	RN7SL233P	18:19284917-19450918	NOTEST	0	0	0	0	1	1
ENSG00000242973	ENSG00000242973	RP11-446F17.3	6:46620677-46703430	NOTEST	0	0	0	0	1	1
ENSG00000242976	ENSG00000242976	RN7SL177P	5:152869174-153193429	NOTEST	0	0	0	0	1	1
ENSG00000242978	ENSG00000242978	RP4-545C24.5	7:144131918-144132407	NOTEST	0	0	0	0	1	1
ENSG00000242979	ENSG00000242979	RPS15AP18	5:179338650-179499118	NOTEST	0	0	0	0	1	1
ENSG00000242983	ENSG00000242983	CABYRP1	3:54081775-54082820	NOTEST	0	0	0	0	1	1
ENSG00000242985	ENSG00000242985	RN7SL50P	18:8471828-8472124	NOTEST	0	0	0	0	1	1
ENSG00000242986	ENSG00000242986	RP11-1110J8.1	12:29653772-29937692	NOTEST	0	0	0	0	1	1
ENSG00000242989	ENSG00000242989	RN7SL332P	6:15113198-15113450	NOTEST	0	0	0	0	1	1
ENSG00000242990	ENSG00000242990	RP11-571M6.1	12:58068447-58069033	NOTEST	0	0	0	0	1	1
ENSG00000242991	ENSG00000242991	RPL7P40	12:17274649-17275394	NOTEST	0	0	0	0	1	1
ENSG00000242992	ENSG00000242992	FTH1P4	3:128444964-128533639	NOTEST	0.150187	0.380283	1.34031	0	1	1
ENSG00000242993	ENSG00000242993	RP11-697H10.1	11:95696382-95696788	NOTEST	0.126253	0	#NAME?	0	1	1
ENSG00000242995	ENSG00000242995	RP11-1085N6.1	14:56955071-57197253	NOTEST	0	0	0	0	1	1
ENSG00000242998	ENSG00000242998	RN7SL379P	X:95278358-95278644	NOTEST	0	0	0	0	1	1
ENSG00000242999	ENSG00000242999	RN7SL239P	11:74459912-74660245	NOTEST	0	0.0907708	inf	0	1	1
ENSG00000243000	ENSG00000243000	RP11-504P24.3	1:224183596-224198314	NOTEST	0	0	0	0	1	1
ENSG00000243003	ENSG00000243003	LY6G6F	HSCHR6_MHC_DBB:31656814-31667868	NOTEST	0	0	0	0	1	1
ENSG00000243004	ENSG00000243004	AC005062.2	7:19958603-20257027	NOTEST	0	0.075154	inf	0	1	1
ENSG00000243005	ENSG00000243005	RN7SL16P	4:24519063-24586173	NOTEST	0	0	0	0	1	1
ENSG00000243007	ENSG00000243007	RP11-106M3.1	15:72671555-72672051	NOTEST	0	0	0	0	1	1
ENSG00000243008	ENSG00000243008	RP11-556N21.1	13:24982294-25171814	NOTEST	0.149851	0.327675	1.12874	0	1	1
ENSG00000243009	ENSG00000243009	RPP21	HSCHR6_MHC_DBB:30192096-30304918	NOTEST	0	0	0	0	1	1

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ENSG00000243012	ENSG00000243012	RP11-292E2.4	3:153102722-153697975	NOTEST	0	0	0	0	1	1
ENSG00000243014	ENSG00000243014	PTMAP8	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000243015	ENSG00000243015	RN7SL737P	12:93903262-93903544	NOTEST	0.387062	0.68379	0.820989	0	1	1
ENSG00000243016	ENSG00000243016	RP11-305F5.2	3:126940036-126940724	NOTEST	0	0	0	0	1	1
ENSG00000243018	ENSG00000243018	RP5-1070G24.2	7:150929574-150974982	NOTEST	0	0	0	0	1	1
ENSG00000243020	ENSG00000243020	RPL7P39	12:65174588-65274812	NOTEST	0	0	0	0	1	1
ENSG00000243022	ENSG00000243022	RP11-221E20.4	3:128567515-128568242	NOTEST	0	0	0	0	1	1
ENSG00000243023	ENSG00000243023	UBA52P3	14:58466452-58764857	NOTEST	0.133365	0	#NAME?	0	1	1
ENSG00000243024	ENSG00000243024	RPS11P6	12:64616116-64790845	NOTEST	0.162643	0.0960171	-0.760345	0	1	1
ENSG00000243025	ENSG00000243025	MTAPP1	3:158327398-158328646	NOTEST	0	0	0	0	1	1
ENSG00000243027	ENSG00000243027	RN7SL354P	15:50981096-50981388	NOTEST	0	0	0	0	1	1
ENSG00000243029	ENSG00000243029	RN7SL635P	2:65663844-66311773	NOTEST	0.118479	0	#NAME?	0	1	1
ENSG00000243033	ENSG00000243033	GAPDHP47	3:142984063-143567373	NOTEST	0	0	0	0	1	1
ENSG00000243035	ENSG00000243035	RN7SL810P	13:78469615-79233314	NOTEST	0	0	0	0	1	1
ENSG00000243038	ENSG00000243038	RP11-58E21.1	14:50448429-50559361	NOTEST	0	0.0213261	inf	0	1	1
ENSG00000243039	ENSG00000243039	RN7SL210P	2:96670312-96670601	NOTEST	0	0	0	0	1	1
ENSG00000243040	ENSG00000243040	RBMY2FP	Y:24454969-24564028	NOTEST	0	0	0	0	1	1
ENSG00000243044	ENSG00000243044	RP13-526J3.1	3:162319414-162319580	NOTEST	0	0	0	0	1	1
ENSG00000243048	ENSG00000243048	FTH1P18	X:37061095-37061650	NOTEST	0	0	0	0	1	1
ENSG00000243049	ENSG00000243049	RN7SL33P	17:2461095-2461388	NOTEST	0	0	0	0	1	1
ENSG00000243050	ENSG00000243050	RPL30P10	8:58305104-58305441	NOTEST	0	0	0	0	1	1
ENSG00000243051	ENSG00000243051	RN7SL269P	1:169890466-170054349	NOTEST	0	0	0	0	1	1
ENSG00000243053	ENSG00000243053	RPL31P58	17:27082995-27188085	NOTEST	0	0	0	0	1	1
ENSG00000243055	ENSG00000243055	GK-AS1	X:30671475-30748725	NOTEST	0.180846	0.215469	0.252718	0	1	1
ENSG00000243058	ENSG00000243058	RPL39P33	17:54650400-54650556	NOTEST	0	0	0	0	1	1
ENSG00000243059	ENSG00000243059	RN7SL400P	15:21308173-21308467	NOTEST	0	0	0	0	1	1
ENSG00000243062	ENSG00000243062	RP11-12M5.1	1:179699351-179711832	NOTEST	0	0	0	0	1	1
ENSG00000243063	ENSG00000243063	IGKV3-7	2:89277986-89278600	NOTEST	0	0	0	0	1	1
ENSG00000243064	ENSG00000243064	ABCC13	21:15608526-15735075	NOTEST	0	0	0	0	1	1
ENSG00000243066	ENSG00000243066	RN7SL842P	19:14693895-14721969	NOTEST	0	0	0	0	1	1
ENSG00000243067	ENSG00000243067	PSMB9	HSCHR6_MHC_COX:32730816-32769949	NOTEST	0	0	0	0	1	1
ENSG00000243071	ENSG00000243071	RP11-613M5.2	12:77054184-77054664	NOTEST	0.503331	0.40061	-0.329308	0	1	1
ENSG00000243072	ENSG00000243072	GS1-388B5.2	3:125398416-125398625	NOTEST	0	0	0	0	1	1
ENSG00000243073	ENSG00000243073	PRAMEF4	1:12939044-12946025	NOTEST	0	0	0	0	1	1
ENSG00000243075	ENSG00000243075	RN7SL519P	12:51235282-51235612	NOTEST	0	0	0	0	1	1
ENSG00000243081	ENSG00000243081	RP11-231E6.1	3:112115493-112127981	NOTEST	0	0	0	0	1	1
ENSG00000243083	ENSG00000243083	LINC00870	3:72084450-72291716	NOTEST	0.0386846	0	#NAME?	0	1	1
ENSG00000243085	ENSG00000243085	RP11-392E22.3	9:38526827-38527029	NOTEST	0	0	0	0	1	1
ENSG00000243088	ENSG00000243088	RN7SL539P	15:32737306-32747835	NOTEST	0	0	0	0	1	1
ENSG00000243089	ENSG00000243089	RP11-779P15.2	3:99226030-99245957	NOTEST	0	0	0	0	1	1
ENSG00000243094	ENSG00000243094	RP11-1084A12.1	15:34376217-34394149	NOTEST	0	0.049691	inf	0	1	1
ENSG00000243095	ENSG00000243095	RPL3P10	8:38964508-39142430	NOTEST	0	0.0105306	inf	0	1	1

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ENSG00000243099	ENSG00000243099	AC020983.5	7:138279029-138386097	NOTEST	0	0	0	0	1	1
ENSG00000243101	ENSG00000243101	RPS3P7	16:78133309-79246564	NOTEST	0	0	0	0	1	1
ENSG00000243103	ENSG00000243103	RN7SL452P	14:50885218-51135049	NOTEST	0	0	0	0	1	1
ENSG00000243104	ENSG00000243104	AC012363.10	2:120770580-120974855	NOTEST	0	0	0	0	1	1
ENSG00000243107	ENSG00000243107	AC000120.7	7:91828282-91875480	NOTEST	0.137348	0.0501491	-1.45354	0	1	1
ENSG00000243115	ENSG00000243115	RN7SL849P	9:12685438-12822130	NOTEST	0	0	0	0	1	1
ENSG00000243116	ENSG00000243116	RP11-564C24.1	3:158680023-159615155	NOTEST	0	0	0	0	1	1
ENSG00000243122	ENSG00000243122	RP11-25H11.1	15:37657227-37783304	NOTEST	0	0	0	0	1	1
ENSG00000243124	ENSG00000243124	RN7SL643P	6:87145569-87145854	NOTEST	0	0	0	0	1	1
ENSG00000243125	ENSG00000243125	RN7SL807P	2:224113218-224113512	NOTEST	0	0	0	0	1	1
ENSG00000243129	ENSG00000243129	RP11-377D9.1	12:13080659-13193613	NOTEST	0	0	0	0	1	1
ENSG00000243130	ENSG00000243130	PSG11	19:43511807-43530664	NOTEST	0.152984	0.273899	0.840265	0	1	1
ENSG00000243135	ENSG00000243135	UGT1A3	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000243136	ENSG00000243136	RN7SL22P	9:35658300-35681156	NOTEST	0	0	0	0	1	1
ENSG00000243141	ENSG00000243141	RP11-757G14.1	12:12482197-12503475	NOTEST	0	0	0	0	1	1
ENSG00000243144	ENSG00000243144	RP11-115N4.1	7:90940682-91186163	NOTEST	0.0467063	0	#NAME?	0	1	1
ENSG00000243149	ENSG00000243149	RP11-543A18.1	3:65160632-65179174	NOTEST	0	0	0	0	1	1
ENSG00000243150	ENSG00000243150	RP11-538P18.2	3:157814947-158288855	NOTEST	0	0	0	0	1	1
ENSG00000243151	ENSG00000243151	AL592188.1	GL000220.1:151419-151533	NOTEST	0	0	0	0	1	1
ENSG00000243154	ENSG00000243154	CTD-2501O3.2	3:154369444-154370212	NOTEST	0	0	0	0	1	1
ENSG00000243155	ENSG00000243155	RP11-46A10.5	1:180882289-180992047	NOTEST	0.612662	0.466625	-0.392829	0	1	1
ENSG00000243160	ENSG00000243160	RP11-342F17.2	5:78825124-78825916	NOTEST	0	0	0	0	1	1
ENSG00000243164	ENSG00000243164	RP11-166B14.1	12:74042445-74042819	NOTEST	0	0	0	0	1	1
ENSG00000243165	ENSG00000243165	RP11-79M21.3	3:158344444-158344638	NOTEST	0	0	0	0	1	1
ENSG00000243167	ENSG00000243167	RPS10P28	19:43174156-43174968	NOTEST	0	0.0676636	inf	0	1	1
ENSG00000243171	ENSG00000243171	RP11-273P3.1	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000243173	ENSG00000243173	RN7SL861P	1:162601162-162757190	NOTEST	0	0	0	0	1	1
ENSG00000243175	ENSG00000243175	RP11-58H15.1	4:144256417-144395721	NOTEST	0	0.016551	inf	0	1	1
ENSG00000243176	ENSG00000243176	RP11-550I24.2	3:156893011-157251408	NOTEST	0.514091	0.309136	-0.733782	0	1	1
ENSG00000243179	ENSG00000243179	AC110769.3	2:114737145-114764879	NOTEST	0.0230644	0	#NAME?	0	1	1
ENSG00000243181	ENSG00000243181	RP11-734J24.1	8:34731676-34732151	NOTEST	0.0913133	0.225716	1.30561	0	1	1
ENSG00000243187	ENSG00000243187	CCDC39-AS1	3:180319917-180700541	NOTEST	0	0	0	0	1	1
ENSG00000243188	ENSG00000243188	HNRNPA1P17	3:108015375-108097132	NOTEST	0	0	0	0	1	1
ENSG00000243189	ENSG00000243189	HLA-DMA	HSCHR6_MHC_MANN:33056219-33103106	NOTEST	0	0	0	0	1	1
ENSG00000243193	ENSG00000243193	CTA-360L10.1	7:106685093-106802256	NOTEST	0	0	0	0	1	1
ENSG00000243195	ENSG00000243195	TUBBP11	3:103349504-103349756	NOTEST	0	0	0	0	1	1
ENSG00000243197	ENSG00000243197	TUSC7	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000243207	ENSG00000243207	PPAN-P2RY11	19:10216898-10230596	NOTEST	0.12692	0.00947074	-3.74429	0	1	1
ENSG00000243215	ENSG00000243215	HLA-DMA	HSCHR6_MHC_SSTO:32992301-33089202	NOTEST	0	0	0	0	1	1
ENSG00000243220	ENSG00000243220	AC006159.4	7:116203647-116254874	NOTEST	0	0	0	0	1	1
ENSG00000243224	ENSG00000243224	RP5-1157M23.2	3:52255095-52275113	NOTEST	0.183179	0.0484842	-1.91767	0	1	1
ENSG00000243225	ENSG00000243225	RP11-7F17.1	14:77435025-77435488	NOTEST	0	0	0	0	1	1
ENSG00000243227	ENSG00000243227	RN7SL55P	4:110268630-110462052	NOTEST	0	0	0	0	1	1

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ENSG00000243232	ENSG00000243232	PCDHAC2	5:140165875-140391936	NOTEST	0	0.00291738	inf	0	1	1
ENSG00000243234	ENSG00000243234	CTD-2583A14.1	19:58464525-58465127	NOTEST	0	0	0	0	1	1
ENSG00000243236	ENSG00000243236	RP1-214M20.2	6:52804523-52822319	NOTEST	0	0	0	0	1	1
ENSG00000243238	ENSG00000243238	IGKV2-30	2:89544263-89545079	NOTEST	0	0	0	0	1	1
ENSG00000243243	ENSG00000243243	AC073130.3	7:115850546-116148595	NOTEST	0.0892961	0.130211	0.544184	0	1	1
ENSG00000243245	ENSG00000243245	XXbac-BPG254F23.6	HSCHR6_MHC_SSTO:32697727-32726026	NOTEST	0	0	0	0	1	1
ENSG00000243250	ENSG00000243250	RPS6P16	11:112097087-112140678	NOTEST	0.0665246	0	#NAME?	0	1	1
ENSG00000243252	ENSG00000243252	XXbac-BPG254F23.6	HSCHR6_MHC_COX:32542404-32557884	NOTEST	0	0	0	0	1	1
ENSG00000243254	ENSG00000243254	RN7SL350P	8:100025493-100906290	NOTEST	0	0	0	0	1	1
ENSG00000243256	ENSG00000243256	RPL30P14	18:59000814-59223006	NOTEST	0	0	0	0	1	1
ENSG00000243257	ENSG00000243257	RP11-567P17.2	3:120405527-120501916	NOTEST	0	0	0	0	1	1
ENSG00000243260	ENSG00000243260	RN7SL558P	4:39699663-39784412	NOTEST	0	0.257957	inf	0	1	1
ENSG00000243264	ENSG00000243264	IGKV2D-29	2:89986321-89987079	NOTEST	0	0	0	0	1	1
ENSG00000243265	ENSG00000243265	RP11-1149O23.1	8:23046791-23088439	NOTEST	0	0.0412038	inf	0	1	1
ENSG00000243267	ENSG00000243267	RN7SL614P	1:10516578-10690815	NOTEST	0.266388	0	#NAME?	0	1	1
ENSG00000243268	ENSG00000243268	ATP5A1P1	9:41028803-41030086	NOTEST	0	0	0	0	1	1
ENSG00000243273	ENSG00000243273	RP11-166N6.2	3:150570270-150798513	NOTEST	0	0	0	0	1	1
ENSG00000243274	ENSG00000243274	RN7SL571P	13:76709066-76709360	NOTEST	0	0	0	0	1	1
ENSG00000243276	ENSG00000243276	RP11-384F7.1	3:117723665-118276515	NOTEST	0	0	0	0	1	1
ENSG00000243280	ENSG00000243280	RP11-477G18.2	4:113066552-113116412	NOTEST	0.200506	0	#NAME?	0	1	1
ENSG00000243284	ENSG00000243284	VSIG8	1:159796539-159869953	NOTEST	0.0597402	0.0529608	-0.173778	0	1	1
ENSG00000243286	ENSG00000243286	HCG16	HSCHR6_MHC_QBL:28953979-28956313	NOTEST	0	0	0	0	1	1
ENSG00000243287	ENSG00000243287	RPS17P14	8:109213444-109447562	NOTEST	0	0	0	0	1	1
ENSG00000243289	ENSG00000243289	CTGLF8P	10:46717126-46733073	NOTEST	0	0	0	0	1	1
ENSG00000243290	ENSG00000243290	IGKV1-12	2:89339720-89340242	NOTEST	0	0	0	0	1	1
ENSG00000243295	ENSG00000243295	CTD-2185K10.1	3:59050875-59105235	NOTEST	0	0	0	0	1	1
ENSG00000243296	ENSG00000243296	RP11-779P15.1	3:99219190-99224352	NOTEST	0	0	0	0	1	1
ENSG00000243297	ENSG00000243297	RPL31P61	19:37288419-37407193	NOTEST	0	0	0	0	1	1
ENSG00000243300	ENSG00000243300	LINC00359	13:97593534-97636426	NOTEST	0	0	0	0	1	1
ENSG00000243303	ENSG00000243303	RP11-268I9.1	18:19284917-19450918	NOTEST	0	0	0	0	1	1
ENSG00000243304	ENSG00000243304	CTC-428G20.1	5:114600365-114601161	NOTEST	0	0	0	0	1	1
ENSG00000243305	ENSG00000243305	RP11-362A9.3	3:151961616-152214602	NOTEST	0.0745294	0.234731	1.65513	0	1	1
ENSG00000243307	ENSG00000243307	RP11-239L20.3	6:26839262-26924333	NOTEST	0	0	0	0	1	1
ENSG00000243312	ENSG00000243312	RP11-397E7.1	4:87791343-87792557	NOTEST	0.0215264	0	#NAME?	0	1	1
ENSG00000243313	ENSG00000243313	RN7SL285P	6:37787274-38122400	NOTEST	0	0	0	0	1	1
ENSG00000243314	ENSG00000243314	RP11-538P18.1	3:157814947-158288855	NOTEST	0	0	0	0	1	1
ENSG00000243316	ENSG00000243316	GUCY2GP	10:114067938-114116332	NOTEST	0.116417	0.189137	0.700127	0	1	1
ENSG00000243319	ENSG00000243319	FGF14-IT1	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000243321	ENSG00000243321	snoU13	3:149478891-149942977	NOTEST	0	0.0414026	inf	0	1	1
ENSG00000243323	ENSG00000243323	PTPRVP	1:202137178-202158583	NOTEST	0.0147629	0.0145349	-0.0224566	0	1	1
ENSG00000243328	ENSG00000243328	RP11-520P18.1	8:144147331-144148004	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000243333	ENSG00000243333	RN7SL174P	5:118604386-118735383	NOTEST	0	0	0	0	1	1
ENSG00000243336	ENSG00000243336	HLA-J	HSCHR6_MHC_QBL:29958304-30022269	NOTEST	0	0	0	0	1	1
ENSG00000243338	ENSG00000243338	RN7SL307P	15:49398267-49913128	NOTEST	0	0	0	0	1	1
ENSG00000243345	ENSG00000243345	RP11-458K10.3	7:115429782-115431103	NOTEST	0	0	0	0	1	1
ENSG00000243346	ENSG00000243346	RN7SL601P	17:11060771-11061062	NOTEST	0	0	0	0	1	1
ENSG00000243347	ENSG00000243347	RP11-501O2.4	3:147878697-147997885	NOTEST	0	0	0	0	1	1
ENSG00000243349	ENSG00000243349	RP11-445N18.7	10:45493145-45676875	NOTEST	0	0	0	0	1	1
ENSG00000243350	ENSG00000243350	RP11-379F12.3	10:8092412-8095447	NOTEST	0	0	0	0	1	1
ENSG00000243352	ENSG00000243352	RN7SL8P	7:104552363-104552644	NOTEST	0	0.103148	inf	0	1	1
ENSG00000243353	ENSG00000243353	RP11-667M19.1	11:113603908-113644533	NOTEST	0	0	0	0	1	1
ENSG00000243355	ENSG00000243355	RP11-57G22.1	18:30359001-30359249	NOTEST	0	0	0	0	1	1
ENSG00000243359	ENSG00000243359	RN7SL815P	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000243365	ENSG00000243365	RN7SL278P	15:77269257-77269551	NOTEST	0.231789	0	#NAME?	0	1	1
ENSG00000243366	ENSG00000243366	RN7SL60P	13:99324233-99324529	NOTEST	0	0	0	0	1	1
ENSG00000243368	ENSG00000243368	MCCC1-AS1	3:182733005-182833863	NOTEST	0.308599	0.486696	0.657291	0	1	1
ENSG00000243370	ENSG00000243370	RN7SL775P	17:16945858-17140502	NOTEST	0	0	0	0	1	1
ENSG00000243373	ENSG00000243373	RN7SL173P	6:158733691-158932860	NOTEST	0	0	0	0	1	1
ENSG00000243374	ENSG00000243374	RN7SL72P	7:148135400-148135667	NOTEST	0	0	0	0	1	1
ENSG00000243378	ENSG00000243378	RP11-646E18.3	3:182409715-182410073	NOTEST	0	0	0	0	1	1
ENSG00000243382	ENSG00000243382	ATP5A1P10	9:66058842-66060121	NOTEST	0	0	0	0	1	1
ENSG00000243383	ENSG00000243383	RN7SL89P	4:106214814-106215100	NOTEST	0	0	0	0	1	1
ENSG00000243384	ENSG00000243384	RP11-475O23.2	3:58549843-58652575	NOTEST	0	0	0	0	1	1
ENSG00000243385	ENSG00000243385	CTD-2110K23.1	5:82348664-82649606	NOTEST	0	0	0	0	1	1
ENSG00000243388	ENSG00000243388	RPL3P3	14:57279900-57618895	NOTEST	0	0	0	0	1	1
ENSG00000243389	ENSG00000243389	AC012442.5	2:113341816-113372008	NOTEST	0.11001	0.086642	-0.344496	0	1	1
ENSG00000243396	ENSG00000243396	RP11-454H13.1	3:101318086-101318488	NOTEST	0	0.155434	inf	0	1	1
ENSG00000243398	ENSG00000243398	RN7SL141P	3:171757417-172119455	NOTEST	0	0	0	0	1	1
ENSG00000243402	ENSG00000243402	RP11-473O4.1	8:130844546-131029375	NOTEST	0	0.117493	inf	0	1	1
ENSG00000243403	ENSG00000243403	RP11-330L19.1	15:64752940-64978264	NOTEST	0	0	0	0	1	1
ENSG00000243404	ENSG00000243404	RPL35AP32	15:66679154-66790151	NOTEST	0	0	0	0	1	1
ENSG00000243410	ENSG00000243410	RP11-245J9.4	3:63989697-64009658	NOTEST	0	0.101116	inf	0	1	1
ENSG00000243414	ENSG00000243414	TICAM2	5:114914338-114968689	NOTEST	0.0493439	0.0907306	0.878717	0	1	1
ENSG00000243415	ENSG00000243415	RP11-274H2.2	3:145781828-145881440	NOTEST	0	0.120803	inf	0	1	1
ENSG00000243417	ENSG00000243417	RP11-555K12.1	4:153472428-153473516	NOTEST	0	0	0	0	1	1
ENSG00000243420	ENSG00000243420	RN7SL734P	12:75956981-76377795	NOTEST	0	0	0	0	1	1
ENSG00000243422	ENSG00000243422	RP11-413E6.1	3:75673836-75674304	NOTEST	0.33063	0.23226	-0.509477	0	1	1
ENSG00000243423	ENSG00000243423	RP5-837J1.1	17:33332106-33448541	NOTEST	0	0	0	0	1	1
ENSG00000243424	ENSG00000243424	RN7SL107P	8:81525778-81526061	NOTEST	0	0	0	0	1	1
ENSG00000243426	ENSG00000243426	RN7SL454P	17:76374720-76573476	NOTEST	0	0	0	0	1	1
ENSG00000243429	ENSG00000243429	OR7E29P	3:125430982-125431889	NOTEST	0	0	0	0	1	1
ENSG00000243430	ENSG00000243430	DAQB-335A13.8	HSCHR6_MHC_MCF:29706643-29713963	NOTEST	0	0	0	0	1	1

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ENSG00000243437	ENSG00000243437	RN7SL370P	1:78028100-78149104	NOTEST	0	0	0	0	1	1
ENSG00000243438	ENSG00000243438	LARP1BP2	7:105955670-105956189	NOTEST	0	0	0	0	1	1
ENSG00000243439	ENSG00000243439	RN7SL352P	6:1507556-1507851	NOTEST	0	0	0	0	1	1
ENSG00000243440	ENSG00000243440	AF165138.7	21:15857548-16031142	NOTEST	0	0	0	0	1	1
ENSG00000243441	ENSG00000243441	OR5V1	HSCHR6_MHC_MANN:29323056-29424418	NOTEST	0	0	0	0	1	1
ENSG00000243445	ENSG00000243445	RP11-715J22.1	16:2325881-2476700	NOTEST	0	0	0	0	1	1
ENSG00000243446	ENSG00000243446	RN7SL284P	10:79542623-79686378	NOTEST	0	0	0	0	1	1
ENSG00000243453	ENSG00000243453	COX7BP1	22:35515816-35627049	NOTEST	0	0.137445	inf	0	1	1
ENSG00000243455	ENSG00000243455	RPS18P13	19:18159446-18159900	NOTEST	0	0	0	0	1	1
ENSG00000243464	ENSG00000243464	RN7SL410P	15:83128127-83182928	NOTEST	0	0	0	0	1	1
ENSG00000243466	ENSG00000243466	IGKV1-5	2:89246818-89247475	NOTEST	0	0	0	0	1	1
ENSG00000243468	ENSG00000243468	INGX	X:70586113-70752224	NOTEST	0.0248767	0.0175588	-0.5026	0	1	1
ENSG00000243469	ENSG00000243469	RPL7P51	19:52152114-52152863	NOTEST	0	0	0	0	1	1
ENSG00000243478	ENSG00000243478	AOX2P	2:201542955-201688569	NOTEST	0.0241156	0	#NAME?	0	1	1
ENSG00000243479	ENSG00000243479	MNX1-AS1	7:156803498-156809120	NOTEST	0.0622709	0.0869536	0.481687	0	1	1
ENSG00000243480	ENSG00000243480	AMY2A	1:104159998-104168402	NOTEST	0	0.0291944	inf	0	1	1
ENSG00000243483	ENSG00000243483	RP11-572M11.2	3:112709293-112902148	NOTEST	0	0	0	0	1	1
ENSG00000243485	ENSG00000243485	MIR1302-10	1:11868-31109	NOTEST	0.0504862	0	#NAME?	0	1	1
ENSG00000243486	ENSG00000243486	RP11-217E22.5	3:153102722-153697975	NOTEST	0	0	0	0	1	1
ENSG00000243488	ENSG00000243488	RN7SL337P	19:14693895-14721969	NOTEST	0	0	0	0	1	1
ENSG00000243489	ENSG00000243489	KRTAP10-11	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000243491	ENSG00000243491	RP11-521D12.5	2:9897624-9910470	NOTEST	0	0	0	0	1	1
ENSG00000243492	ENSG00000243492	HLA-L	HSCHR6_MHC_COX:30191706-30304467	NOTEST	0	0	0	0	1	1
ENSG00000243494	ENSG00000243494	CTC-550B14.1	19:55434876-55512510	NOTEST	0	0	0	0	1	1
ENSG00000243495	ENSG00000243495	GMFBP1	3:100328432-100414323	NOTEST	0	0.0413371	inf	0	1	1
ENSG00000243496	ENSG00000243496	HLA-DOB	HSCHR6_MHC_DBB:32758668-32762954	NOTEST	0	0	0	0	1	1
ENSG00000243498	ENSG00000243498	UBA52P5	8:124232195-124287781	NOTEST	0	0	0	0	1	1
ENSG00000243499	ENSG00000243499	RPS6P21	12:132152036-132152791	NOTEST	0	0	0	0	1	1
ENSG00000243500	ENSG00000243500	RP11-364B6.2	1:104615631-104619709	NOTEST	0.309361	0.0295253	-3.38927	0	1	1
ENSG00000243501	ENSG00000243501	RP11-257K9.8	6:73918805-74020088	NOTEST	0	0.00953239	inf	0	1	1
ENSG00000243503	ENSG00000243503	AC090453.1	8:36845494-36845930	NOTEST	0	0	0	0	1	1
ENSG00000243504	ENSG00000243504	RPS23P1	8:98877281-98877713	NOTEST	0	0	0	0	1	1
ENSG00000243505	ENSG00000243505	RN7SL240P	11:29735455-29903261	NOTEST	0	0	0	0	1	1
ENSG00000243507	ENSG00000243507	RP11-476M19.1	12:3490514-3703139	NOTEST	0	0	0	0	1	1
ENSG00000243508	ENSG00000243508	RP11-775J23.2	3:124801479-125094198	NOTEST	0	0	0	0	1	1
ENSG00000243509	ENSG00000243509	TNFRSF6B	20:62289162-62374858	NOTEST	0	0	0	0	1	1
ENSG00000243510	ENSG00000243510	RN7SL111P	2:118773957-118774243	NOTEST	0	0	0	0	1	1
ENSG00000243514	ENSG00000243514	RPL32P33	17:70319263-70636611	NOTEST	0	0	0	0	1	1
ENSG00000243516	ENSG00000243516	RP11-19F9.1	18:35252651-35253139	NOTEST	0	0	0	0	1	1
ENSG00000243517	ENSG00000243517	RP11-627K11.1	12:31404925-31405531	NOTEST	0.0972581	0.158121	0.701138	0	1	1
ENSG00000243518	ENSG00000243518	RP11-639F1.2	3:155093368-155462856	NOTEST	0	0	0	0	1	1
ENSG00000243519	ENSG00000243519	IGLVIVOR22-2	22:32750871-32781618	NOTEST	0.17863	0	#NAME?	0	1	1
ENSG00000243521	ENSG00000243521	RPL5P33	17:48925310-48926631	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000243532	ENSG00000243532	RN7SL19P	8:71520811-71581409	NOTEST	0	0	0	0	1	1
ENSG00000243533	ENSG00000243533	TBCE-AS1	1:235530674-235612283	NOTEST	0.0888849	0	#NAME?	0	1	1
ENSG00000243536	ENSG00000243536	ANTXRLP1	10:47605210-47644793	NOTEST	0	0	0	0	1	1
ENSG00000243537	ENSG00000243537	CTC-458A3.1	8:134338239-134338647	NOTEST	0	0	0	0	1	1
ENSG00000243538	ENSG00000243538	CTB-55B8.1	5:16665394-16936372	NOTEST	0.167144	0	#NAME?	0	1	1
ENSG00000243539	ENSG00000243539	RN7SL649P	1:12096798-12097071	NOTEST	0	0	0	0	1	1
ENSG00000243541	ENSG00000243541	RN7SL104P	2:16090811-16091103	NOTEST	0	0	0	0	1	1
ENSG00000243543	ENSG00000243543	WFDC6	20:44162834-44176391	NOTEST	0	0	0	0	1	1
ENSG00000243544	ENSG00000243544	RN7SL172P	3:121350245-121379774	NOTEST	0	0	0	0	1	1
ENSG00000243546	ENSG00000243546	RN7SL108P	14:68286495-69196935	NOTEST	0	0	0	0	1	1
ENSG00000243547	ENSG00000243547	HNRNPKP4	3:96068397-96069783	NOTEST	0.0344343	0.0380767	0.145062	0	1	1
ENSG00000243548	ENSG00000243548	RN7SL101P	4:28712819-28713094	NOTEST	0	0	0	0	1	1
ENSG00000243549	ENSG00000243549	RN7SL705P	18:60317542-60317834	NOTEST	0	0	0	0	1	1
ENSG00000243550	ENSG00000243550	RP11-483E7.1	3:149983198-150005160	NOTEST	0	0	0	0	1	1
ENSG00000243554	ENSG00000243554	AC004967.7	7:97598316-97601566	NOTEST	0.369902	0.214054	-0.789168	0	1	1
ENSG00000243558	ENSG00000243558	RP11-181G12.5	1:1981908-2152177	NOTEST	0.157845	0.517633	1.71342	0	1	1
ENSG00000243560	ENSG00000243560	RN7SL364P	19:47150868-47220384	NOTEST	0	0	0	0	1	1
ENSG00000243562	ENSG00000243562	RN7SL838P	11:417932-442011	NOTEST	0	0	0	0	1	1
ENSG00000243566	ENSG00000243566	UPK3B	7:76139744-77045717	NOTEST	0.0782535	0.0298714	-1.38939	0	1	1
ENSG00000243568	ENSG00000243568	RP11-2I17.1	15:72110736-72447800	NOTEST	0	0.0524524	inf	0	1	1
ENSG00000243570	ENSG00000243570	CFB	HSCHR6_MHC_MCF:31942046-31996308	NOTEST	0	0	0	0	1	1
ENSG00000243572	ENSG00000243572	RP11-889D3.2	3:55212199-55223242	NOTEST	0	0	0	0	1	1
ENSG00000243574	ENSG00000243574	RP11-264K23.1	7:123670972-124035172	NOTEST	0	0	0	0	1	1
ENSG00000243581	ENSG00000243581	RPS29P25	19:40081620-40081791	NOTEST	0	0	0	0	1	1
ENSG00000243583	ENSG00000243583	RP4-669B10.3	7:143651936-143694405	NOTEST	0	0	0	0	1	1
ENSG00000243584	ENSG00000243584	RP11-14I2.2	3:183331407-183334530	NOTEST	0	0	0	0	1	1
ENSG00000243587	ENSG00000243587	C6orf183	6:109487035-109592217	NOTEST	0	0	0	0	1	1
ENSG00000243591	ENSG00000243591	RN7SL282P	18:6601538-6601834	NOTEST	0	0	0	0	1	1
ENSG00000243592	ENSG00000243592	RPL17P22	5:55395506-55529186	NOTEST	0	0	0	0	1	1
ENSG00000243593	ENSG00000243593	RP11-500K19.1	3:120552286-120555207	NOTEST	0	0	0	0	1	1
ENSG00000243594	ENSG00000243594	PSMB9	HSCHR6_MHC_QBL:32737203-32776334	NOTEST	0	0	0	0	1	1
ENSG00000243596	ENSG00000243596	RP11-758I14.2	3:146060782-146066267	NOTEST	0	0	0	0	1	1
ENSG00000243601	ENSG00000243601	RP11-152P17.1	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000243607	ENSG00000243607	RPL35AP26	11:126148151-126148472	NOTEST	0	0	0	0	1	1
ENSG00000243609	ENSG00000243609	RPS2P44	16:48572636-48654059	NOTEST	0	0	0	0	1	1
ENSG00000243612	ENSG00000243612	HLA-DOB	HSCHR6_MHC_APD:32764305-32768591	NOTEST	0	0	0	0	1	1
ENSG00000243613	ENSG00000243613	RP11-216N14.8	1:153700542-153746555	NOTEST	0	0	0	0	1	1
ENSG00000243620	ENSG00000243620	RP11-649A16.1	3:146627471-147088443	NOTEST	0.0372305	0	#NAME?	0	1	1
ENSG00000243621	ENSG00000243621	AC003989.3	7:110303109-111202573	NOTEST	0	0	0	0	1	1
ENSG00000243627	ENSG00000243627	AP000322.53	21:35791012-35796264	NOTEST	0	0	0	0	1	1
ENSG00000243629	ENSG00000243629	LINC00880	3:156799455-156840793	NOTEST	0.168327	0.0275325	-2.61206	0	1	1
ENSG00000243633	ENSG00000243633	RN7SL542P	7:21255158-21255449	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000243636	ENSG00000243636	RP11-164O23.7	1:207338840-207357407	NOTEST	0.0350551	0.0199179	-0.81556	0	1	1
ENSG00000243641	ENSG00000243641	OR13C7P	9:36002905-36003864	NOTEST	0	0	0	0	1	1
ENSG00000243642	ENSG00000243642	RN7SL526P	19:58570606-58629794	NOTEST	0	0	0	0	1	1
ENSG00000243643	ENSG00000243643	TSPY20P	Y:9873803-9875984	NOTEST	0	0	0	0	1	1
ENSG00000243644	ENSG00000243644	RNA5SP58	HG1287_PATCH:148880130-148880253	NOTEST	0	0	0	0	1	1
ENSG00000243648	ENSG00000243648	RP11-215P8.1	5:133758528-133759026	NOTEST	0	0	0	0	1	1
ENSG00000243649	ENSG00000243649	CFB	6:31865561-31919861	NOTEST	0.259078	0.197504	-0.391507	0	1	1
ENSG00000243650	ENSG00000243650	RN7SL834P	2:231280656-231444721	NOTEST	0.380478	0	#NAME?	0	1	1
ENSG00000243654	ENSG00000243654	RN7SL295P	5:159678658-159772403	NOTEST	0	0	0	0	1	1
ENSG00000243655	ENSG00000243655	RP11-846F4.12	17:22022436-22025022	NOTEST	0	0	0	0	1	1
ENSG00000243658	ENSG00000243658	MTND5P16	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000243659	ENSG00000243659	RP11-4K3__A.3	1:27637730-27638329	NOTEST	0	0	0	0	1	1
ENSG00000243660	ENSG00000243660	ZNF487	10:43932281-43991517	NOTEST	0.238611	0.276998	0.215214	0	1	1
ENSG00000243661	ENSG00000243661	WBP1LP1	7:142486451-142487347	NOTEST	0	0	0	0	1	1
ENSG00000243663	ENSG00000243663	RPS4XP14	12:1797739-1897844	NOTEST	0	0.0759712	inf	0	1	1
ENSG00000243664	ENSG00000243664	RPS29P12	5:180326076-180377906	NOTEST	0	0	0	0	1	1
ENSG00000243669	ENSG00000243669	RPL34P23	11:122906574-122906932	NOTEST	0	0	0	0	1	1
ENSG00000243671	ENSG00000243671	RN7SL761P	13:69267937-69268213	NOTEST	0	0	0	0	1	1
ENSG00000243672	ENSG00000243672	RPS3AP40	11:67693121-67693902	NOTEST	0	0	0	0	1	1
ENSG00000243674	ENSG00000243674	OR7E66P	3:75396983-75397938	NOTEST	0.0535463	0.103262	0.947455	0	1	1
ENSG00000243675	ENSG00000243675	RP11-379F4.1	3:158414680-158547508	NOTEST	0	0.145434	inf	0	1	1
ENSG00000243680	ENSG00000243680	RPL37P23	19:52616343-52680255	NOTEST	0	0	0	0	1	1
ENSG00000243686	ENSG00000243686	RPLP1P11	17:15879873-16256970	NOTEST	0.0972304	0.380945	1.9701	0	1	1
ENSG00000243687	ENSG00000243687	RP11-432B6.1	3:159943422-160203561	NOTEST	0	0	0	0	1	1
ENSG00000243694	ENSG00000243694	RP11-6B4.1	3:81043018-81144798	NOTEST	0	0	0	0	1	1
ENSG00000243695	ENSG00000243695	RP11-290L7.3	9:39072763-39288312	NOTEST	0.178517	0.247662	0.472313	0	1	1
ENSG00000243696	ENSG00000243696	RP5-966M1.6	3:52846990-52931612	NOTEST	0.147303	0.0568214	-1.37428	0	1	1
ENSG00000243697	ENSG00000243697	RP11-463O9.1	16:86559062-86559858	NOTEST	0	0.018488	inf	0	1	1
ENSG00000243700	ENSG00000243700	RN7SL598P	14:58466452-58764857	NOTEST	0	0	0	0	1	1
ENSG00000243702	ENSG00000243702	RN7SL638P	20:18568536-18744561	NOTEST	0	0	0	0	1	1
ENSG00000243704	ENSG00000243704	RN7SL105P	17:1472560-1532180	NOTEST	0	0	0	0	1	1
ENSG00000243705	ENSG00000243705	RP11-178L8.1	16:87117167-87438385	NOTEST	0	0	0	0	1	1
ENSG00000243708	ENSG00000243708	PLA2G4B	15:42120282-42190773	NOTEST	0.509606	0.42564	-0.259748	0	1	1
ENSG00000243709	ENSG00000243709	LEFTY1	1:226073981-226111978	NOTEST	0.0204169	0	#NAME?	0	1	1
ENSG00000243710	ENSG00000243710	WDR65	1:43629845-43739673	NOTEST	0.117484	0.0886771	-0.405833	0	1	1
ENSG00000243711	ENSG00000243711	RPL21P116	15:79051544-79190475	NOTEST	0	0	0	0	1	1
ENSG00000243714	ENSG00000243714	RN7SL696P	12:79918656-79918950	NOTEST	0	0	0	0	1	1
ENSG00000243715	ENSG00000243715	CACNA2D3-AS1	3:54156573-55108584	NOTEST	0	0	0	0	1	1
ENSG00000243719	ENSG00000243719	HLA-DMA	HSCHR6_MHC_COX:32824725-32871622	NOTEST	0	0	0	0	1	1
ENSG00000243720	ENSG00000243720	RPL21P127	18:3406339-3406816	NOTEST	0	0	0	0	1	1
ENSG00000243721	ENSG00000243721	RP11-472I20.1	11:43577985-43902276	NOTEST	0	0.190151	inf	0	1	1
ENSG00000243723	ENSG00000243723	RN7SL393P	2:159023161-159313265	NOTEST	0	0	0	0	1	1
ENSG00000243729	ENSG00000243729	OR5V1	6:29323006-29424848	NOTEST	0	0	0	0	1	1

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ENSG00000243733	ENSG00000243733	RP11-80H8.3	3:142830643-142831201	NOTEST	0	0	0	0	1	1
ENSG00000243738	ENSG00000243738	RN7SL181P	9:123940414-124095121	NOTEST	0	0.0993727	inf	0	1	1
ENSG00000243742	ENSG00000243742	RPLP0P2	11:61382507-61406921	NOTEST	0.537893	0.657984	0.290733	0	1	1
ENSG00000243744	ENSG00000243744	CTC-232H10.1	5:13638027-13638490	NOTEST	0	0	0	0	1	1
ENSG00000243745	ENSG00000243745	RN7SL844P	19:16466049-16582896	NOTEST	0.355445	0.0928716	-1.93632	0	1	1
ENSG00000243746	ENSG00000243746	EEF1A1P10	7:144149033-144533488	NOTEST	0	0	0	0	1	1
ENSG00000243758	ENSG00000243758	RPL35AP15	5:116636799-116637138	NOTEST	0	0	0	0	1	1
ENSG00000243761	ENSG00000243761	RP11-216N21.2	8:86999551-87166457	NOTEST	0	0	0	0	1	1
ENSG00000243762	ENSG00000243762	AC006547.8	22:20067754-20114878	NOTEST	0	0.0138437	inf	0	1	1
ENSG00000243766	ENSG00000243766	HOTTIP	7:27233121-27246878	NOTEST	0.0243496	0.027182	0.158752	0	1	1
ENSG00000243770	ENSG00000243770	RN7SL65P	2:174937174-175113426	NOTEST	0	0	0	0	1	1
ENSG00000243771	ENSG00000243771	CTD-3131K8.1	19:17700403-17700880	NOTEST	0	0	0	0	1	1
ENSG00000243772	ENSG00000243772	KIR2DL3	19:55235968-55378662	NOTEST	0	0	0	0	1	1
ENSG00000243775	ENSG00000243775	OSTCP1	6:159262148-159278664	NOTEST	0	0	0	0	1	1
ENSG00000243777	ENSG00000243777	RP11-864G5.1	11:102165790-102166537	NOTEST	0	0	0	0	1	1
ENSG00000243779	ENSG00000243779	RP11-681N23.1	18:13919601-13919922	NOTEST	0	0	0	0	1	1
ENSG00000243780	ENSG00000243780	RP11-112N19.1	15:59817620-59818080	NOTEST	0	0	0	0	1	1
ENSG00000243781	ENSG00000243781	RP11-193H5.2	1:238025474-238091621	NOTEST	0	0	0	0	1	1
ENSG00000243782	ENSG00000243782	RN7SL78P	10:89511268-89605369	NOTEST	0	0	0	0	1	1
ENSG00000243790	ENSG00000243790	RN7SL485P	15:72897523-72929260	NOTEST	0	0	0	0	1	1
ENSG00000243792	ENSG00000243792	OR7E89P	2:159651828-159719797	NOTEST	0	0	0	0	1	1
ENSG00000243794	ENSG00000243794	CTD-2026G6.2	3:75570953-75571163	NOTEST	0	0	0	0	1	1
ENSG00000243795	ENSG00000243795	RP11-572M11.3	3:112709293-112902148	NOTEST	0.0230492	0.0143765	-0.681008	0	1	1
ENSG00000243797	ENSG00000243797	CTB-111H14.1	7:106012696-106410653	NOTEST	0.117796	0	#NAME?	0	1	1
ENSG00000243799	ENSG00000243799	PEX5L-AS1	3:179512745-179754841	NOTEST	0	0	0	0	1	1
ENSG00000243801	ENSG00000243801	RN7SL461P	14:57279900-57618895	NOTEST	0	0	0	0	1	1
ENSG00000243802	ENSG00000243802	RP11-390K5.1	11:47212731-47213093	NOTEST	0	0	0	0	1	1
ENSG00000243804	ENSG00000243804	LY6G6F	HSCHR6_MHC_QBL:31664900-31675931	NOTEST	0	0	0	0	1	1
ENSG00000243806	ENSG00000243806	RPL7P18	5:93488670-94620279	NOTEST	0	0	0	0	1	1
ENSG00000243810	ENSG00000243810	RP5-1096J16.1	20:20015011-20341346	NOTEST	0	0	0	0	1	1
ENSG00000243813	ENSG00000243813	RP11-678L1.1	3:120626918-121143608	NOTEST	0	0	0	0	1	1
ENSG00000243817	ENSG00000243817	RN7SL189P	14:21431737-21432024	NOTEST	0	0	0	0	1	1
ENSG00000243818	ENSG00000243818	RP11-372E1.4	3:142645516-142661376	NOTEST	0	0	0	0	1	1
ENSG00000243819	ENSG00000243819	RN7SL832P	2:10830469-10832225	NOTEST	0.110036	0.0570431	-0.947858	0	1	1
ENSG00000243822	ENSG00000243822	RP11-2G17.1	3:149074955-149075332	NOTEST	0	0	0	0	1	1
ENSG00000243824	ENSG00000243824	RP11-434O22.1	14:35209541-35210039	NOTEST	0.136268	0.419526	1.62231	0	1	1
ENSG00000243828	ENSG00000243828	RP11-307F22.2	6:64345724-66417118	NOTEST	0	0	0	0	1	1
ENSG00000243829	ENSG00000243829	CTB-33G10.1	19:50222754-50223338	NOTEST	0.271631	0.25242	-0.105818	0	1	1
ENSG00000243830	ENSG00000243830	RP11-113C12.2	12:8608521-8630926	NOTEST	0.0617962	0	#NAME?	0	1	1
ENSG00000243831	ENSG00000243831	RP1-81D8.4	6:160952514-161097555	NOTEST	0	0	0	0	1	1

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ENSG00000243836	ENSG00000243836	WDR86-AS1	7:151038784-151110440	NOTEST	0	0	0	0	1	1
ENSG00000243838	ENSG00000243838	PSMC1P7	3:161046711-161048026	NOTEST	0	0	0	0	1	1
ENSG00000243844	ENSG00000243844	RPL17P33	8:29489606-29490160	NOTEST	0	0	0	0	1	1
ENSG00000243845	ENSG00000243845	RN7SL30P	9:128199671-128469513	NOTEST	0.214266	0	#NAME?	0	1	1
ENSG00000243847	ENSG00000243847	RN7SL610P	2:24150154-24227779	NOTEST	0.123179	0	#NAME?	0	1	1
ENSG00000243849	ENSG00000243849	WDR52-AS1	3:112929849-113160457	NOTEST	0	0	0	0	1	1
ENSG00000243853	ENSG00000243853	ALDH7A1P3	7:150238841-150239186	NOTEST	0	0	0	0	1	1
ENSG00000243855	ENSG00000243855	RP11-114O13.1	14:31091317-31291908	NOTEST	0	0	0	0	1	1
ENSG00000243856	ENSG00000243856	RN7SL551P	18:71878625-71907790	NOTEST	0	0	0	0	1	1
ENSG00000243859	ENSG00000243859	RPL5P17	5:84760251-84761128	NOTEST	0	0	0	0	1	1
ENSG00000243861	ENSG00000243861	RP11-656A15.1	3:154229323-154257098	NOTEST	0	0	0	0	1	1
ENSG00000243864	ENSG00000243864	RPS3AP50	19:33831591-33832890	NOTEST	0	0	0	0	1	1
ENSG00000243869	ENSG00000243869	RN7SL56P	11:9595227-9615004	NOTEST	0	0.431011	inf	0	1	1
ENSG00000243870	ENSG00000243870	RN7SL236P	17:76356533-76369992	NOTEST	0.256678	0	#NAME?	0	1	1
ENSG00000243871	ENSG00000243871	RN7SL487P	15:43650369-43699293	NOTEST	0	0.0935925	inf	0	1	1
ENSG00000243872	ENSG00000243872	RN7SL464P	1:220701567-220837803	NOTEST	0	0	0	0	1	1
ENSG00000243873	ENSG00000243873	HMGB1P36	3:70803004-70803724	NOTEST	0	0	0	0	1	1
ENSG00000243877	ENSG00000243877	HMGB1P38	3:80006715-80007292	NOTEST	0	0	0	0	1	1
ENSG00000243883	ENSG00000243883	RN7SL419P	4:154265800-154336270	NOTEST	0	0	0	0	1	1
ENSG00000243885	ENSG00000243885	RP11-278L15.2	3:149086808-149104370	NOTEST	0	0	0	0	1	1
ENSG00000243886	ENSG00000243886	RP11-575C1.1	3:137254413-137254984	NOTEST	0	0	0	0	1	1
ENSG00000243888	ENSG00000243888	RP11-548B3.3	9:72042445-72287222	NOTEST	0	0.0589181	inf	0	1	1
ENSG00000243889	ENSG00000243889	TRBV8-1	7:142273055-142273334	NOTEST	0	0	0	0	1	1
ENSG00000243894	ENSG00000243894	RP11-489M13.1	4:4078437-4079218	NOTEST	0.0243503	0	#NAME?	0	1	1
ENSG00000243896	ENSG00000243896	OR2A7	7:143883175-144077725	NOTEST	0.180203	0.243645	0.435154	0	1	1
ENSG00000243897	ENSG00000243897	EGFL8	HSCHR6_MHC_MANN:32155582-32185300	NOTEST	0	0	0	0	1	1
ENSG00000243899	ENSG00000243899	BMS1P7	10:49256240-49268060	NOTEST	0.187158	0.167638	-0.158909	0	1	1
ENSG00000243900	ENSG00000243900	RN7SL320P	13:51909908-52126500	NOTEST	0	0	0	0	1	1
ENSG00000243902	ENSG00000243902	RP1-63G5.5	22:37735623-37823505	NOTEST	0	0	0	0	1	1
ENSG00000243903	ENSG00000243903	RP11-285B24.1	3:59365749-59374430	NOTEST	0	0	0	0	1	1
ENSG00000243904	ENSG00000243904	RP11-600F24.1	14:103840369-103841253	NOTEST	0.038103	0.0146921	-1.37486	0	1	1
ENSG00000243905	ENSG00000243905	RN7SL679P	1:26919736-26920037	NOTEST	0	0	0	0	1	1
ENSG00000243910	ENSG00000243910	TUBA4B	2:220094478-220142892	NOTEST	0	0	0	0	1	1
ENSG00000243911	ENSG00000243911	RN7SL430P	9:114980714-115095947	NOTEST	0	0.163481	inf	0	1	1
ENSG00000243914	ENSG00000243914	RPL5P14	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000243915	ENSG00000243915	PRKRIRP2	3:85008131-86123579	NOTEST	0	0	0	0	1	1
ENSG00000243916	ENSG00000243916	RP11-6K23.1	12:15260716-15750333	NOTEST	0	0	0	0	1	1
ENSG00000243918	ENSG00000243918	EIF4BP8	3:122379459-122381285	NOTEST	0	0	0	0	1	1
ENSG00000243920	ENSG00000243920	RPS26P24	4:58219164-58219495	NOTEST	0	0	0	0	1	1
ENSG00000243925	ENSG00000243925	RPS24P18	18:23678802-23679190	NOTEST	0	0	0	0	1	1
ENSG00000243928	ENSG00000243928	RN7SL628P	15:30896328-30906764	NOTEST	0	0	0	0	1	1
ENSG00000243929	ENSG00000243929	RP11-61F5.1	4:52844244-52844538	NOTEST	0	0	0	0	1	1

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ENSG00000243935	ENSG00000243935	RP11-100J16.5	9:41500678-41514094	NOTEST	0	0	0	0	1	1
ENSG00000243939	ENSG00000243939	RP11-200A13.1	8:105602960-107072752	NOTEST	0.0605681	0.13533	1.15985	0	1	1
ENSG00000243944	ENSG00000243944	RP11-167H9.4	3:149478891-149942977	NOTEST	0.0787048	0.426806	2.43906	0	1	1
ENSG00000243945	ENSG00000243945	RP11-696F10.1	3:109696386-109696614	NOTEST	0	0	0	0	1	1
ENSG00000243951	ENSG00000243951	RN7SL308P	8:81540685-81787016	NOTEST	0	0	0	0	1	1
ENSG00000243953	ENSG00000243953	RP11-439C8.2	3:154687071-154688012	NOTEST	0	0	0	0	1	1
ENSG00000243954	ENSG00000243954	RN7SL743P	16:8768421-8962866	NOTEST	0	0	0	0	1	1
ENSG00000243957	ENSG00000243957	RN7SL647P	3:78164308-78164606	NOTEST	0	0	0	0	1	1
ENSG00000243958	ENSG00000243958	PSMB9	HSCHR6_MHC_SSTO:32898408-32937507	NOTEST	0	0	0	0	1	1
ENSG00000243959	ENSG00000243959	RN7SL684P	5:175969511-176037134	NOTEST	0	0	0	0	1	1
ENSG00000243961	ENSG00000243961	RP5-839B4.8	20:9966735-10349424	NOTEST	0	0	0	0	1	1
ENSG00000243967	ENSG00000243967	NBPF5P	1:108803817-109013624	NOTEST	0	0.0306237	inf	0	1	1
ENSG00000243968	ENSG00000243968	RN7SL402P	19:36372791-36373053	NOTEST	0	0	0	0	1	1
ENSG00000243969	ENSG00000243969	RP11-439C8.1	3:154544804-154578806	NOTEST	0	0	0	0	1	1
ENSG00000243970	ENSG00000243970	PPIEL	1:39957317-40024379	NOTEST	0.13494	0.23249	0.784858	0	1	1
ENSG00000243974	ENSG00000243974	VTI1BP1	3:99944217-99944917	NOTEST	0	0	0	0	1	1
ENSG00000243976	ENSG00000243976	RN7SL523P	14:100785407-100785707	NOTEST	0	0	0	0	1	1
ENSG00000243977	ENSG00000243977	RP11-473P24.2	3:179367281-179367988	NOTEST	0.027713	0	#NAME?	0	1	1
ENSG00000243978	ENSG00000243978	RGAG1	X:109437413-109699562	NOTEST	0.166127	0.073734	-1.17188	0	1	1
ENSG00000243979	ENSG00000243979	RP11-347C18.1	8:95825538-96128683	NOTEST	0	0	0	0	1	1
ENSG00000243980	ENSG00000243980	RN7SL702P	Y:14394176-14394465	NOTEST	0	0	0	0	1	1
ENSG00000243981	ENSG00000243981	RP11-368M16.3	7:57688184-57704895	NOTEST	0	0	0	0	1	1
ENSG00000243986	ENSG00000243986	ENO1P3	3:124480794-124620265	NOTEST	0	0.00993283	inf	0	1	1
ENSG00000243988	ENSG00000243988	RPS24P17	16:56899118-56949762	NOTEST	0	0	0	0	1	1
ENSG00000243991	ENSG00000243991	RN7SL447P	3:193458261-193458510	NOTEST	0	0	0	0	1	1
ENSG00000243993	ENSG00000243993	RP11-14D22.2	3:64053639-64440508	NOTEST	0	0	0	0	1	1
ENSG00000243995	ENSG00000243995	RP1-300I2.2	20:43859508-43861972	NOTEST	0	0	0	0	1	1
ENSG00000244000	ENSG00000244000	AC006366.3	Y:25163209-25163968	NOTEST	0	0	0	0	1	1
ENSG00000244002	ENSG00000244002	RP11-162K6.1	4:81082282-81083165	NOTEST	0	0	0	0	1	1
ENSG00000244003	ENSG00000244003	RN7SL143P	16:58741034-59142878	NOTEST	0	0	0	0	1	1
ENSG00000244004	ENSG00000244004	RP11-1396O13.2	4:9564790-9565570	NOTEST	0.0894686	0	#NAME?	0	1	1
ENSG00000244006	ENSG00000244006	RN7SL799P	X:63430569-63430866	NOTEST	0	0	0	0	1	1
ENSG00000244009	ENSG00000244009	RP11-227J5.3	3:159943422-160203561	NOTEST	0	0	0	0	1	1
ENSG00000244018	ENSG00000244018	RPL35P6	8:18384810-18942240	NOTEST	0	0.178444	inf	0	1	1
ENSG00000244019	ENSG00000244019	RPS2P24	5:76506273-76916436	NOTEST	0	0	0	0	1	1
ENSG00000244020	ENSG00000244020	MT1HL1	1:237167402-237167718	NOTEST	0	0	0	0	1	1
ENSG00000244021	ENSG00000244021	RP11-50D9.1	4:128702975-128765195	NOTEST	0.417973	0.617454	0.562923	0	1	1
ENSG00000244024	ENSG00000244024	RP11-622L21.1	3:145241324-145242202	NOTEST	0	0	0	0	1	1
ENSG00000244025	ENSG00000244025	KRTAP19-3	21:31863781-31864275	NOTEST	0	0	0	0	1	1
ENSG00000244030	ENSG00000244030	AC090939.1	3:11313994-11766453	NOTEST	0	0	0	0	1	1
ENSG00000244031	ENSG00000244031	RPS3AP17	4:29964265-29965380	NOTEST	0	0	0	0	1	1
ENSG00000244033	ENSG00000244033	RN7SL228P	8:117962511-118188953	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000244034	ENSG00000244034	RN7SL424P	4:55919226-55991756	NOTEST	0	0	0	0	1	1
ENSG00000244036	ENSG00000244036	RP11-306G20.1	7:129593073-129691291	NOTEST	0.0725198	0.0304479	-1.25203	0	1	1
ENSG00000244039	ENSG00000244039	RP11-379K17.2	3:169629359-169656963	NOTEST	0	0	0	0	1	1
ENSG00000244040	ENSG00000244040	IL12A-AS1	3:159631188-159943086	NOTEST	0	0	0	0	1	1
ENSG00000244043	ENSG00000244043	RPS27P27	16:58741034-59142878	NOTEST	0	0.13165	inf	0	1	1
ENSG00000244044	ENSG00000244044	RN7SL735P	17:64298753-64806861	NOTEST	0	0	0	0	1	1
ENSG00000244048	ENSG00000244048	RPS18P6	3:94890763-94891221	NOTEST	0	0	0	0	1	1
ENSG00000244050	ENSG00000244050	RP11-266K4.1	12:8276227-8371507	NOTEST	0.199175	0	#NAME?	0	1	1
ENSG00000244052	ENSG00000244052	RPL5P24	8:103838584-103990104	NOTEST	0	0	0	0	1	1
ENSG00000244053	ENSG00000244053	RPL13AP2	14:47308825-48144157	NOTEST	0.0827547	0.0322326	-1.36032	0	1	1
ENSG00000244055	ENSG00000244055	AC007566.10	7:92076766-92157845	NOTEST	0	0.282811	inf	0	1	1
ENSG00000244056	ENSG00000244056	RN7SL417P	15:84944426-84950601	NOTEST	0.390456	0.404267	0.0501493	0	1	1
ENSG00000244057	ENSG00000244057	LCE3C	1:152573137-152573562	NOTEST	0	0	0	0	1	1
ENSG00000244060	ENSG00000244060	RPS2P41	12:112277570-112334343	NOTEST	0	0	0	0	1	1
ENSG00000244061	ENSG00000244061	RP11-389C8.1	5:71677620-71678220	NOTEST	0	0	0	0	1	1
ENSG00000244062	ENSG00000244062	RP11-404G16.2	3:133380841-133497850	NOTEST	0	0	0	0	1	1
ENSG00000244063	ENSG00000244063	AC024704.2	2:114586966-114600933	NOTEST	0	0	0	0	1	1
ENSG00000244065	ENSG00000244065	RP11-221E20.5	3:128562406-128563247	NOTEST	0	0	0	0	1	1
ENSG00000244066	ENSG00000244066	RN7SL148P	1:244267233-244267510	NOTEST	0	0	0	0	1	1
ENSG00000244067	ENSG00000244067	GSTA2	6:52614896-52628367	NOTEST	0.0500959	0.0667543	0.414166	0	1	1
ENSG00000244071	ENSG00000244071	RPL9P33	19:52114780-52150151	NOTEST	0	0	0	0	1	1
ENSG00000244073	ENSG00000244073	RPS4XP6	5:37085157-37085954	NOTEST	0.0237277	0.035207	0.56929	0	1	1
ENSG00000244076	ENSG00000244076	CTC-512J14.1	5:79611489-79611645	NOTEST	0	0	0	0	1	1
ENSG00000244078	ENSG00000244078	RP11-431I8.1	3:159943422-160203561	NOTEST	0	0	0	0	1	1
ENSG00000244080	ENSG00000244080	RN7SL833P	19:11562140-11639989	NOTEST	0	0.376569	inf	0	1	1
ENSG00000244081	ENSG00000244081	RP11-350D23.4	9:66930568-66930965	NOTEST	0	0	0	0	1	1
ENSG00000244083	ENSG00000244083	RP11-170N16.1	4:123736925-123737272	NOTEST	0	0	0	0	1	1
ENSG00000244086	ENSG00000244086	RPS20P35	17:37011566-37011923	NOTEST	0.0795279	0	#NAME?	0	1	1
ENSG00000244088	ENSG00000244088	RP11-510I6.1	5:120911542-120912015	NOTEST	0	0	0	0	1	1
ENSG00000244089	ENSG00000244089	HMGB1P30	3:148508888-148677899	NOTEST	0	0	0	0	1	1
ENSG00000244091	ENSG00000244091	RN7SL483P	12:94909251-94909536	NOTEST	0	0	0	0	1	1
ENSG00000244094	ENSG00000244094	SPRR2F	1:153042699-153113927	NOTEST	0	0	0	0	1	1
ENSG00000244097	ENSG00000244097	RPS4XP17	17:406410-624957	NOTEST	0.101913	0.211399	1.05263	0	1	1
ENSG00000244099	ENSG00000244099	RPS23P3	4:67296809-67297239	NOTEST	0	0	0	0	1	1
ENSG00000244101	ENSG00000244101	HMGN1P10	3:135969147-136471220	NOTEST	0	0	0	0	1	1
ENSG00000244104	ENSG00000244104	RN7SL659P	9:110573899-110574195	NOTEST	0	0	0	0	1	1
ENSG00000244107	ENSG00000244107	RN7SL250P	8:55333027-55333338	NOTEST	0	0	0	0	1	1
ENSG00000244112	ENSG00000244112	RN7SL508P	12:119419299-119600856	NOTEST	0	0	0	0	1	1
ENSG00000244113	ENSG00000244113	RP11-468H14.1	8:17007809-17008397	NOTEST	0	0	0	0	1	1
ENSG00000244116	ENSG00000244116	IGKV2-28	2:89521178-89521942	NOTEST	0	0	0	0	1	1
ENSG00000244122	ENSG00000244122	UGT1A7	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000244124	ENSG00000244124	ATP1B3-AS1	3:141594965-141645356	NOTEST	0	0.324652	inf	0	1	1
ENSG00000244125	ENSG00000244125	AC078882.1	2:140988991-142895399	NOTEST	0	0	0	0	1	1

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ENSG00000244130	ENSG00000244130	UBE2Q2P9	3:72055924-72056126	NOTEST	0	0	0	0	1	1
ENSG00000244131	ENSG00000244131	RPSAP51	12:8834195-9039597	NOTEST	0	0	0	0	1	1
ENSG00000244134	ENSG00000244134	RPS12P20	11:72396113-72504726	NOTEST	0	0	0	0	1	1
ENSG00000244137	ENSG00000244137	RP11-99J16__A.2	1:230838268-230937749	NOTEST	0	0	0	0	1	1
ENSG00000244139	ENSG00000244139	RN7SL397P	3:119813741-119855630	NOTEST	0	0	0	0	1	1
ENSG00000244142	ENSG00000244142	ATP6V0CP2	3:111011565-111384597	NOTEST	0	0	0	0	1	1
ENSG00000244144	ENSG00000244144	RP11-757F18.3	3:111859733-112013105	NOTEST	0.0794051	0	#NAME?	0	1	1
ENSG00000244146	ENSG00000244146	RP11-366M4.2	4:165841769-165842215	NOTEST	0	0	0	0	1	1
ENSG00000244152	ENSG00000244152	RN7SL59P	11:67309205-67309475	NOTEST	0	0	0	0	1	1
ENSG00000244153	ENSG00000244153	WWP1P1	3:98376645-98379414	NOTEST	0.010335	0	#NAME?	0	1	1
ENSG00000244155	ENSG00000244155	CYP4F34P	13:19315869-19316858	NOTEST	0	0	0	0	1	1
ENSG00000244157	ENSG00000244157	RP11-190P13.1	3:114970042-115004194	NOTEST	0	0	0	0	1	1
ENSG00000244158	ENSG00000244158	RP1-93H18.6	6:116781901-116784934	NOTEST	0	0	0	0	1	1
ENSG00000244161	ENSG00000244161	FLNB-AS1	3:57994126-58157982	NOTEST	0.383885	0.371081	-0.0489399	0	1	1
ENSG00000244169	ENSG00000244169	RN7SL120P	3:1107265-1107559	NOTEST	0	0	0	0	1	1
ENSG00000244176	ENSG00000244176	RP11-810P12.1	11:61779222-61780074	NOTEST	0.079848	0.0634951	-0.330612	0	1	1
ENSG00000244180	ENSG00000244180	AL592188.2	GL000220.1:107447-107561	NOTEST	0	0	0	0	1	1
ENSG00000244183	ENSG00000244183	RP11-641C17.1	3:59735035-61237133	NOTEST	0	0	0	0	1	1
ENSG00000244184	ENSG00000244184	RP11-314A20.2	17:4574678-4608824	NOTEST	0.0986881	0	#NAME?	0	1	1
ENSG00000244192	ENSG00000244192	RP11-114H7.1	5:130325589-130326121	NOTEST	0	0	0	0	1	1
ENSG00000244193	ENSG00000244193	RP11-379K17.5	3:169657140-169716161	NOTEST	0	0	0	0	1	1
ENSG00000244194	ENSG00000244194	RN7SL218P	4:74877294-74877595	NOTEST	0	0	0	0	1	1
ENSG00000244196	ENSG00000244196	PPIAP15	3:109128524-109214014	NOTEST	0	0	0	0	1	1
ENSG00000244197	ENSG00000244197	RN7SL766P	13:22364675-22364982	NOTEST	0	0	0	0	1	1
ENSG00000244199	ENSG00000244199	RP11-139K4.4	3:182164757-182204152	NOTEST	0	0	0	0	1	1
ENSG00000244203	ENSG00000244203	FOXP1-AS1	3:71003843-71633140	NOTEST	0	0	0	0	1	1
ENSG00000244207	ENSG00000244207	C4A	HSCHR6_MHC_DBB:31919772-31953483	NOTEST	0	0	0	0	1	1
ENSG00000244211	ENSG00000244211	PDZK1P2	1:147466093-147484460	NOTEST	0	0.019583	inf	0	1	1
ENSG00000244213	ENSG00000244213	ZFAND6P1	9:35406751-35483026	NOTEST	0.000440176	0.0242349	5.78286	0	1	1
ENSG00000244214	ENSG00000244214	RP11-298O21.7	3:167582560-167601170	NOTEST	0	0	0	0	1	1
ENSG00000244215	ENSG00000244215	RP11-88I21.2	3:127041149-127109513	NOTEST	0	0	0	0	1	1
ENSG00000244217	ENSG00000244217	RPS4XP10	8:95365150-95365881	NOTEST	0	0	0	0	1	1
ENSG00000244219	ENSG00000244219	GS1-259H13.2	7:99143930-99208439	NOTEST	0.564993	0.159731	-1.82259	0	1	1
ENSG00000244222	ENSG00000244222	OR7E121P	3:75647802-75648824	NOTEST	0	0	0	0	1	1
ENSG00000244226	ENSG00000244226	ILF2P1	3:65339199-66024509	NOTEST	0	0	0	0	1	1
ENSG00000244227	ENSG00000244227	RP11-298O21.5	3:167613735-167641799	NOTEST	0	0	0	0	1	1
ENSG00000244229	ENSG00000244229	RPL26P35	18:74534562-74682683	NOTEST	0	0	0	0	1	1
ENSG00000244230	ENSG00000244230	RN7SL151P	9:21699312-21699569	NOTEST	0	0	0	0	1	1
ENSG00000244231	ENSG00000244231	CSPG4P2Y	Y:26325462-26338017	NOTEST	0	0	0	0	1	1
ENSG00000244232	ENSG00000244232	RN7SL698P	3:128444964-128533639	NOTEST	0	0	0	0	1	1
ENSG00000244234	ENSG00000244234	GMCL1P1	5:177612719-177614300	NOTEST	0.010533	0.0507934	2.26972	0	1	1

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ENSG00000244236	ENSG00000244236	RN7SL604P	2:69685128-70053596	NOTEST	0	0	0	0	1	1
ENSG00000244237	ENSG00000244237	RP11-1046B16.1	14:70027735-70028187	NOTEST	0	0	0	0	1	1
ENSG00000244239	ENSG00000244239	AC007009.1	7:8152813-8384146	NOTEST	0	0.228984	inf	0	1	1
ENSG00000244242	ENSG00000244242	IFITM10	11:1753639-1785255	NOTEST	0.358308	0.363986	0.0226824	0	1	1
ENSG00000244244	ENSG00000244244	RPS3AP42	11:92085261-92629618	NOTEST	0	0	0	0	1	1
ENSG00000244245	ENSG00000244245	RP11-120B7.1	5:107929309-107929668	NOTEST	0	0	0	0	1	1
ENSG00000244246	ENSG00000244246	ZNF736P8Y	Y:7781462-7782131	NOTEST	0	0	0	0	1	1
ENSG00000244247	ENSG00000244247	RP11-139K4.2	3:182216051-182224912	NOTEST	0	0	0	0	1	1
ENSG00000244249	ENSG00000244249	RP11-441M10.1	3:158680023-159615155	NOTEST	0	0	0	0	1	1
ENSG00000244251	ENSG00000244251	RP11-64K12.1	15:40772950-40773514	NOTEST	0	0	0	0	1	1
ENSG00000244252	ENSG00000244252	RP11-495P10.7	1:147762995-147769663	NOTEST	0	0	0	0	1	1
ENSG00000244253	ENSG00000244253	RPS29P24	19:40079594-40079765	NOTEST	0	0	0	0	1	1
ENSG00000244255	ENSG00000244255	CFB	6:31865561-31919861	NOTEST	0	0	0	0	1	1
ENSG00000244257	ENSG00000244257	PKD1P1	16:16404197-16444447	NOTEST	0.212474	0.242865	0.192866	0	1	1
ENSG00000244259	ENSG00000244259	AP000797.1	11:115820913-115821519	NOTEST	0	0.0241786	inf	0	1	1
ENSG00000244260	ENSG00000244260	RP11-521D12.2	2:9814151-9848542	NOTEST	0	0	0	0	1	1
ENSG00000244264	ENSG00000244264	RN7SL597P	13:41696011-41696305	NOTEST	0	0	0	0	1	1
ENSG00000244265	ENSG00000244265	SIAH2-AS1	3:150458913-150481264	NOTEST	0	0	0	0	1	1
ENSG00000244266	ENSG00000244266	RP11-112N23.1	12:50720012-50873787	NOTEST	0	0	0	0	1	1
ENSG00000244267	ENSG00000244267	RPL34P22	11:44650906-44651224	NOTEST	0	0	0	0	1	1
ENSG00000244268	ENSG00000244268	RP11-529G21.2	3:152874299-152879564	NOTEST	0.0968141	0	#NAME?	0	1	1
ENSG00000244273	ENSG00000244273	PGBD4P1	7:142430181-142430588	NOTEST	0	0	0	0	1	1
ENSG00000244278	ENSG00000244278	AP000235.3	21:26212863-26442219	NOTEST	0	0	0	0	1	1
ENSG00000244280	ENSG00000244280	ECEL1P2	2:233250459-233252167	NOTEST	0	0	0	0	1	1
ENSG00000244281	ENSG00000244281	RP11-564P9.1	3:81416140-81417172	NOTEST	0	0	0	0	1	1
ENSG00000244283	ENSG00000244283	RPL23AP73	17:6653003-6653507	NOTEST	0	0	0	0	1	1
ENSG00000244286	ENSG00000244286	ITGB5-AS1	3:124480794-124620265	NOTEST	0	0	0	0	1	1
ENSG00000244289	ENSG00000244289	RPS3AP35	8:12485984-12486765	NOTEST	0.0243503	0.0537526	1.1424	0	1	1
ENSG00000244292	ENSG00000244292	OR9N1P	7:141607612-141806547	NOTEST	0	0	0	0	1	1
ENSG00000244294	ENSG00000244294	RN7SL740P	21:34876237-35349992	NOTEST	0	0	0	0	1	1
ENSG00000244295	ENSG00000244295	RPS20P21	8:74884671-74895018	NOTEST	0	0	0	0	1	1
ENSG00000244296	ENSG00000244296	RN7SL168P	22:19318220-19466738	NOTEST	0	0	0	0	1	1
ENSG00000244297	ENSG00000244297	RN7SL465P	6:38683116-38998301	NOTEST	0	0	0	0	1	1
ENSG00000244301	ENSG00000244301	AOX3P	2:201542955-201688569	NOTEST	0	0	0	0	1	1
ENSG00000244302	ENSG00000244302	PEX5L-AS2	3:179512745-179754841	NOTEST	0	0	0	0	1	1
ENSG00000244307	ENSG00000244307	RN7SL395P	8:145998498-146012730	NOTEST	0	0	0	0	1	1
ENSG00000244308	ENSG00000244308	RN7SL762P	3:119813741-119855630	NOTEST	0	0	0	0	1	1
ENSG00000244310	ENSG00000244310	RP11-734K21.3	2:9255325-9257013	NOTEST	0.218361	0.0587219	-1.89475	0	1	1
ENSG00000244314	ENSG00000244314	RN7SL36P	3:194789007-194991896	NOTEST	0	0.446895	inf	0	1	1
ENSG00000244318	ENSG00000244318	RN7SL252P	7:96569381-96569676	NOTEST	0	0	0	0	1	1
ENSG00000244321	ENSG00000244321	RP11-450H5.1	3:166287480-166288551	NOTEST	0	0	0	0	1	1
ENSG00000244326	ENSG00000244326	RN7SL814P	5:73613810-73614107	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000244328	ENSG00000244328	RN7SL845P	7:152454746-152455034	NOTEST	0.124161	0.300161	1.27352	0	1	1
ENSG00000244329	ENSG00000244329	UBA52P9	18:24916342-25175128	NOTEST	0	0	0	0	1	1
ENSG00000244331	ENSG00000244331	CTB-47B8.1	5:157358265-157358571	NOTEST	0	0	0	0	1	1
ENSG00000244332	ENSG00000244332	RP11-119K6.6	10:96305546-96373662	NOTEST	0	0	0	0	1	1
ENSG00000244335	ENSG00000244335	RN7SL687P	X:152931680-152931970	NOTEST	0	0	0	0	1	1
ENSG00000244337	ENSG00000244337	AJ239322.3	2:132715849-132737446	NOTEST	0	0	0	0	1	1
ENSG00000244345	ENSG00000244345	RP11-654C22.2	3:72553956-72599703	NOTEST	0	0	0	0	1	1
ENSG00000244346	ENSG00000244346	RP11-531F16.3	3:182655861-182703741	NOTEST	0	0.0886398	inf	0	1	1
ENSG00000244349	ENSG00000244349	HCG16	6:28953979-28956313	NOTEST	0.100646	0.451844	2.16654	0	1	1
ENSG00000244355	ENSG00000244355	LY6G6D	6:31654725-31685695	NOTEST	0	0	0	0	1	1
ENSG00000244356	ENSG00000244356	RN7SL398P	10:33466419-33625190	NOTEST	0	0	0	0	1	1
ENSG00000244358	ENSG00000244358	RP11-88H10.2	3:145657698-145679323	NOTEST	0	0	0	0	1	1
ENSG00000244361	ENSG00000244361	RPL30P7	5:10488931-10489254	NOTEST	0	0	0	0	1	1
ENSG00000244362	ENSG00000244362	KRTAP19-7	21:31933193-31933633	NOTEST	0	0	0	0	1	1
ENSG00000244371	ENSG00000244371	PFN1P8	1:146373545-146467744	NOTEST	0.26805	0.0933089	-1.52242	0	1	1
ENSG00000244372	ENSG00000244372	RN7SL423P	2:161734057-161734359	NOTEST	0	0	0	0	1	1
ENSG00000244376	ENSG00000244376	RN7SL636P	20:49045728-49046020	NOTEST	0	0	0	0	1	1
ENSG00000244378	ENSG00000244378	RPS2P45	16:68877506-69119083	NOTEST	0	0	0	0	1	1
ENSG00000244380	ENSG00000244380	RP11-24C3.2	3:48473573-48488060	NOTEST	0.0392812	0.030218	-0.378432	0	1	1
ENSG00000244381	ENSG00000244381	RP11-3K16.1	3:169427082-169427553	NOTEST	0	0	0	0	1	1
ENSG00000244382	ENSG00000244382	RP11-373I8.1	3:150570270-150798513	NOTEST	0	0	0	0	1	1
ENSG00000244383	ENSG00000244383	RP11-475O23.3	3:58549843-58652575	NOTEST	0	0	0	0	1	1
ENSG00000244384	ENSG00000244384	RN7SL359P	2:233412778-233547491	NOTEST	0	0	0	0	1	1
ENSG00000244389	ENSG00000244389	RN7SL242P	1:70034080-70671303	NOTEST	0.117586	0	#NAME?	0	1	1
ENSG00000244390	ENSG00000244390	RPS6P22	12:59314419-59458019	NOTEST	0	0	0	0	1	1
ENSG00000244391	ENSG00000244391	RN7SL330P	12:94542498-94853764	NOTEST	0	0	0	0	1	1
ENSG00000244392	ENSG00000244392	RN7SL869P	7:79875241-79875538	NOTEST	0	0	0	0	1	1
ENSG00000244395	ENSG00000244395	RBMY1D	Y:24026222-24064214	NOTEST	0	0	0	0	1	1
ENSG00000244399	ENSG00000244399	RN7SL251P	2:85669617-85669912	NOTEST	0	0	0	0	1	1
ENSG00000244400	ENSG00000244400	RPS4XP12	11:121120978-121121687	NOTEST	0	0	0	0	1	1
ENSG00000244402	ENSG00000244402	RN7SL314P	10:37414784-37673039	NOTEST	0	0	0	0	1	1
ENSG00000244404	ENSG00000244404	RN7SL216P	3:24729409-25215796	NOTEST	0	0	0	0	1	1
ENSG00000244411	ENSG00000244411	KRTAP5-7	11:71238312-71239210	NOTEST	0.0204306	0	#NAME?	0	1	1
ENSG00000244413	ENSG00000244413	RP11-1057B8.1	8:135991069-135991522	NOTEST	0	0	0	0	1	1
ENSG00000244414	ENSG00000244414	CFHR1	1:196788886-196928356	NOTEST	0.0961991	0.0116367	-3.04734	0	1	1
ENSG00000244422	ENSG00000244422	RPL38P3	4:55842325-55842538	NOTEST	0	0.680655	inf	0	1	1
ENSG00000244424	ENSG00000244424	RN7SL829P	15:28764756-28778160	NOTEST	0	0	0	0	1	1
ENSG00000244427	ENSG00000244427	RP11-52B19.1	8:7953467-7954248	NOTEST	0	0	0	0	1	1
ENSG00000244429	ENSG00000244429	RP11-12N13.1	3:166011543-166012141	NOTEST	0	0	0	0	1	1
ENSG00000244432	ENSG00000244432	RPL39P28	12:68383224-68628466	NOTEST	0	0	0	0	1	1
ENSG00000244433	ENSG00000244433	PGBD4P7	1:95104016-95285837	NOTEST	0	0	0	0	1	1
ENSG00000244436	ENSG00000244436	RP11-428G5.1	12:32050753-32051057	NOTEST	0	0	0	0	1	1
ENSG00000244437	ENSG00000244437	IGKV3-15	2:89384672-89385283	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000244438	ENSG00000244438	RN7SL327P	15:75575175-75586816	NOTEST	0	0	0	0	1	1
ENSG00000244441	ENSG00000244441	RP11-359H3.1	3:120231696-120232035	NOTEST	0	0	0	0	1	1
ENSG00000244444	ENSG00000244444	EGFL8	HSCHR6_MHC_QBL:32073754-32103496	NOTEST	0	0	0	0	1	1
ENSG00000244451	ENSG00000244451	RPL34P21	11:129936835-130014699	NOTEST	0	0	0	0	1	1
ENSG00000244456	ENSG00000244456	AC090774.2	17:20717932-20947073	NOTEST	0	0	0	0	1	1
ENSG00000244457	ENSG00000244457	ENO1P1	1:236511561-236648214	NOTEST	0.339287	0.371962	0.132649	0	1	1
ENSG00000244459	ENSG00000244459	RP11-1398P2.1	4:1575788-1581980	NOTEST	0.0674033	0.168661	1.32324	0	1	1
ENSG00000244461	ENSG00000244461	RP11-354H21.1	3:78087855-78095945	NOTEST	0	0	0	0	1	1
ENSG00000244464	ENSG00000244464	RP11-201E8.1	3:99316907-99342664	NOTEST	0	0	0	0	1	1
ENSG00000244468	ENSG00000244468	RP11-206M11.7	3:148947142-149052201	NOTEST	0	0.0581646	inf	0	1	1
ENSG00000244470	ENSG00000244470	RP11-395M19.1	4:105389468-106041157	NOTEST	0	0	0	0	1	1
ENSG00000244471	ENSG00000244471	RP11-78J21.4	13:53063127-53161222	NOTEST	0	0	0	0	1	1
ENSG00000244474	ENSG00000244474	UGT1A4	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000244476	ENSG00000244476	ERVFRD-1	6:11094265-11138964	NOTEST	0.162948	0.162016	-0.00827133	0	1	1
ENSG00000244482	ENSG00000244482	LILRA6	19:54704609-54752862	NOTEST	0	0.0613749	inf	0	1	1
ENSG00000244485	ENSG00000244485	RPL18P13	16:76262282-76296263	NOTEST	0	0	0	0	1	1
ENSG00000244490	ENSG00000244490	RWDD4P1	7:104653871-105039755	NOTEST	0.537867	0.605855	0.171723	0	1	1
ENSG00000244491	ENSG00000244491	RP3-508I15.18	22:39101727-39190203	NOTEST	0	0	0	0	1	1
ENSG00000244493	ENSG00000244493	SLC9A9-AS2	3:142984063-143567373	NOTEST	0	0	0	0	1	1
ENSG00000244501	ENSG00000244501	RN7SL623P	5:170288873-170727019	NOTEST	0	0	0	0	1	1
ENSG00000244502	ENSG00000244502	HDAC11-AS1	3:13518481-13547916	NOTEST	0	0	0	0	1	1
ENSG00000244503	ENSG00000244503	RP11-278L15.6	3:149191760-149221068	NOTEST	0.0231733	0.0307439	0.407836	0	1	1
ENSG00000244510	ENSG00000244510	GS1-124K5.7	7:65670185-65955095	NOTEST	0	0	0	0	1	1
ENSG00000244512	ENSG00000244512	RN7SL28P	4:185200088-185200384	NOTEST	0	0	0	0	1	1
ENSG00000244514	ENSG00000244514	RN7SL125P	17:46839596-46894576	NOTEST	0	0	0	0	1	1
ENSG00000244515	ENSG00000244515	KRT18P34	3:156880451-156886922	NOTEST	0.121627	0.0505368	-1.26706	0	1	1
ENSG00000244521	ENSG00000244521	RN7SL700P	13:48033077-48033369	NOTEST	0	0	0	0	1	1
ENSG00000244522	ENSG00000244522	AC092669.1	2:66653866-66801001	NOTEST	0	0	0	0	1	1
ENSG00000244527	ENSG00000244527	RP11-254G11.1	18:18699142-18699622	NOTEST	0	0	0	0	1	1
ENSG00000244528	ENSG00000244528	AC134873.1	2:243030783-243102304	NOTEST	0	0	0	0	1	1
ENSG00000244532	ENSG00000244532	RN7SL380P	12:6893019-6893327	NOTEST	0	0	0	0	1	1
ENSG00000244534	ENSG00000244534	RN7SL211P	2:65133998-65134272	NOTEST	0	0	0	0	1	1
ENSG00000244535	ENSG00000244535	RP1-181J22.1	11:32605343-32816204	NOTEST	0	0	0	0	1	1
ENSG00000244537	ENSG00000244537	KRTAP4-2	17:39333697-39334460	NOTEST	0	0	0	0	1	1
ENSG00000244538	ENSG00000244538	RP11-10G12.1	4:22595818-22596073	NOTEST	0	0.13165	inf	0	1	1
ENSG00000244540	ENSG00000244540	RP11-416A17.1	12:51487445-51566926	NOTEST	0	0	0	0	1	1
ENSG00000244541	ENSG00000244541	RP11-167H9.6	3:149956305-149957996	NOTEST	0	0	0	0	1	1
ENSG00000244544	ENSG00000244544	RN7SL446P	4:153185300-153185597	NOTEST	0	0	0	0	1	1
ENSG00000244545	ENSG00000244545	RP11-788A4.1	3:152365934-152368236	NOTEST	0	0	0	0	1	1
ENSG00000244550	ENSG00000244550	RP5-905H7.3	7:62693412-62708699	NOTEST	0	0	0	0	1	1
ENSG00000244551	ENSG00000244551	RPL34P29	16:49968938-49969263	NOTEST	0	0	0	0	1	1
ENSG00000244556	ENSG00000244556	ODCP	7:128594947-128695198	NOTEST	0.14612	0.251321	0.782373	0	1	1
ENSG00000244558	ENSG00000244558	RP11-445H22.4	20:43285091-43379675	NOTEST	0.505916	0.622696	0.299629	0	1	1

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ENSG00000244561	ENSG00000244561	RP11-702L6.1	3:109115462-109116717	NOTEST	0	0	0	0	1	1
ENSG00000244564	ENSG00000244564	RP11-14D22.1	3:64053639-64440508	NOTEST	0	0	0	0	1	1
ENSG00000244565	ENSG00000244565	RP11-222O23.1	7:115143420-115144135	NOTEST	0	0	0	0	1	1
ENSG00000244568	ENSG00000244568	RN7SL654P	1:184304791-184305081	NOTEST	0	0	0	0	1	1
ENSG00000244571	ENSG00000244571	RP11-535I24.2	3:162744183-163079351	NOTEST	0	0	0	0	1	1
ENSG00000244573	ENSG00000244573	RPL30P11	12:14509775-14518437	NOTEST	0	0	0	0	1	1
ENSG00000244575	ENSG00000244575	IGKV1-27	2:89512907-89513413	NOTEST	0	0	0	0	1	1
ENSG00000244578	ENSG00000244578	RP11-548O1.3	3:138654030-138662862	NOTEST	0	0	0	0	1	1
ENSG00000244582	ENSG00000244582	RPL21P120	17:21407883-21408385	NOTEST	0.385484	0.46473	0.269721	0	1	1
ENSG00000244585	ENSG00000244585	RPL12P33	12:121354547-121355039	NOTEST	0	0	0	0	1	1
ENSG00000244586	ENSG00000244586	WNT5A-AS1	3:55499742-55523973	NOTEST	0.556169	0.0703607	-2.98268	0	1	1
ENSG00000244588	ENSG00000244588	RAD21L1	20:1206699-1289972	NOTEST	0.0825125	0	#NAME?	0	1	1
ENSG00000244593	ENSG00000244593	RP11-685B14.1	8:18240783-18241427	NOTEST	0	0	0	0	1	1
ENSG00000244604	ENSG00000244604	RP11-713H12.1	17:8316448-8534079	NOTEST	0	0	0	0	1	1
ENSG00000244607	ENSG00000244607	CCDC13	3:42734154-42846023	NOTEST	0.181403	0.277393	0.612736	0	1	1
ENSG00000244609	ENSG00000244609	RN7SL532P	1:24063099-24063380	NOTEST	0.258977	0.103148	-1.32811	0	1	1
ENSG00000244610	ENSG00000244610	RN7SL756P	17:65373574-65693372	NOTEST	0	0	0	0	1	1
ENSG00000244612	ENSG00000244612	RN7SL429P	15:74362197-74374891	NOTEST	0	0	0	0	1	1
ENSG00000244615	ENSG00000244615	PSPC1P2	13:24982294-25171814	NOTEST	0.281872	0	#NAME?	0	1	1
ENSG00000244617	ENSG00000244617	ASPRV1	2:70187225-70316332	NOTEST	0.220258	0.179508	-0.295148	0	1	1
ENSG00000244618	ENSG00000244618	RN7SL334P	6:24797548-25057301	NOTEST	0	0	0	0	1	1
ENSG00000244619	ENSG00000244619	RP11-315I20.3	1:145524890-145543868	NOTEST	0	0.0446868	inf	0	1	1
ENSG00000244620	ENSG00000244620	AL122127.25	14:106355941-106362435	NOTEST	0	0	0	0	1	1
ENSG00000244621	ENSG00000244621	RPS17P11	5:51578400-51578693	NOTEST	0	0	0	0	1	1
ENSG00000244623	ENSG00000244623	OR2AE1	7:99473609-99517223	NOTEST	0	0	0	0	1	1
ENSG00000244624	ENSG00000244624	KRTAP20-1	21:31988749-31989003	NOTEST	0	0	0	0	1	1
ENSG00000244630	ENSG00000244630	RP11-241J12.1	5:79922046-80172279	NOTEST	0	0	0	0	1	1
ENSG00000244632	ENSG00000244632	RN7SL863P	3:62384021-62861054	NOTEST	0	0	0	0	1	1
ENSG00000244640	ENSG00000244640	RP11-436J20.1	3:68682856-68683507	NOTEST	0	0	0	0	1	1
ENSG00000244641	ENSG00000244641	RPS26P43	11:122920494-122921061	NOTEST	0	0	0	0	1	1
ENSG00000244642	ENSG00000244642	RN7SL396P	8:120874901-120875181	NOTEST	0	0	0	0	1	1
ENSG00000244646	ENSG00000244646	AC024183.3	Y:20290495-20298913	NOTEST	0	0	0	0	1	1
ENSG00000244649	ENSG00000244649	CTD-2377D24.6	17:46782359-46784708	NOTEST	0.0575299	0.137031	1.25212	0	1	1
ENSG00000244650	ENSG00000244650	RP11-501O2.3	3:147878697-147997885	NOTEST	0	0	0	0	1	1
ENSG00000244652	ENSG00000244652	RP11-93B21.1	3:106044583-106045140	NOTEST	0	0	0	0	1	1
ENSG00000244653	ENSG00000244653	UBFD1P1	3:97952494-98176742	NOTEST	0	0	0	0	1	1
ENSG00000244656	ENSG00000244656	CU463998.3	GL000240.1:3771-3853	NOTEST	0	0	0	0	1	1
ENSG00000244657	ENSG00000244657	GS1-124K5.8	7:65670185-65955095	NOTEST	0	0	0	0	1	1
ENSG00000244661	ENSG00000244661	TRBV12-1	7:142216289-142216732	NOTEST	0	0	0	0	1	1
ENSG00000244662	ENSG00000244662	RP11-615I16.1	12:24795620-24796100	NOTEST	0	0	0	0	1	1
ENSG00000244666	ENSG00000244666	RN7SL853P	15:72947078-72958735	NOTEST	0	0	0	0	1	1
ENSG00000244668	ENSG00000244668	RP11-103G8.1	3:150377671-150438623	NOTEST	0	0	0	0	1	1

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ENSG00000244669	ENSG00000244669	RP11-158O16.1	4:65632847-65633615	NOTEST	0	0	0	0	1	1
ENSG00000244671	ENSG00000244671	RN7SL280P	22:22006558-22090123	NOTEST	0	0	0	0	1	1
ENSG00000244672	ENSG00000244672	LY6G5B	HSCHR6_MHC_DBB:31611187-31653368	NOTEST	0	0	0	0	1	1
ENSG00000244674	ENSG00000244674	RPS3AP15	3:75589199-75629150	NOTEST	0	0	0	0	1	1
ENSG00000244675	ENSG00000244675	AC108676.1	3:194123400-194239008	NOTEST	0.042736	0.0388821	-0.136347	0	1	1
ENSG00000244677	ENSG00000244677	RN7SL706P	14:68286495-69196935	NOTEST	0	0	0	0	1	1
ENSG00000244681	ENSG00000244681	MTHFD2P1	3:95373266-95402037	NOTEST	0.0212188	0.0318411	0.585543	0	1	1
ENSG00000244682	ENSG00000244682	FCGR2C	1:161475219-161648444	NOTEST	0.171283	0.109367	-0.6472	0	1	1
ENSG00000244691	ENSG00000244691	RP11-600F24.2	14:103851728-103970168	NOTEST	0	0.0696323	inf	0	1	1
ENSG00000244692	ENSG00000244692	RN7SL724P	3:139108656-139396859	NOTEST	0	0.336192	inf	0	1	1
ENSG00000244693	ENSG00000244693	CTAGE8	7:143883175-144077725	NOTEST	0.034514	0.0238984	-0.530269	0	1	1
ENSG00000244695	ENSG00000244695	HCG17	HSCHR6_MHC_QBL:30191333-30304165	NOTEST	0	0	0	0	1	1
ENSG00000244699	ENSG00000244699	RP11-803B1.2	3:75433209-75440961	NOTEST	0	0	0	0	1	1
ENSG00000244701	ENSG00000244701	RP5-894A10.2	7:141229002-141401953	NOTEST	0.616069	0.581946	-0.0822045	0	1	1
ENSG00000244703	ENSG00000244703	CD46P1	1:207818457-207911761	NOTEST	0	0	0	0	1	1
ENSG00000244705	ENSG00000244705	RP11-133K1.1	15:40604552-40608835	NOTEST	0	0	0	0	1	1
ENSG00000244706	ENSG00000244706	RP11-298O21.3	3:167582560-167601170	NOTEST	0	0	0	0	1	1
ENSG00000244708	ENSG00000244708	RPL23P10	8:36394908-36636682	NOTEST	0	0	0	0	1	1
ENSG00000244710	ENSG00000244710	RN7SL47P	6:106632350-106773666	NOTEST	0	0	0	0	1	1
ENSG00000244712	ENSG00000244712	RP11-874G11.1	12:28286181-28732883	NOTEST	0.145549	0.0395219	-1.88078	0	1	1
ENSG00000244717	ENSG00000244717	RPS27P14	5:68765709-68765963	NOTEST	0	0	0	0	1	1
ENSG00000244720	ENSG00000244720	RP11-402J7.2	3:111011565-111384597	NOTEST	0	0	0	0	1	1
ENSG00000244721	ENSG00000244721	HLA-L	HSCHR6_MHC_QBL:30191333-30304165	NOTEST	0	0	0	0	1	1
ENSG00000244722	ENSG00000244722	RP11-179A18.1	3:110401132-110402001	NOTEST	0.0212796	0.209873	3.30197	0	1	1
ENSG00000244723	ENSG00000244723	ASLP1	22:23950638-24059543	NOTEST	0	0	0	0	1	1
ENSG00000244730	ENSG00000244730	RP13-1056D16.2	3:49761726-49823975	NOTEST	0	0	0	0	1	1
ENSG00000244731	ENSG00000244731	C4A	6:31937586-31971298	NOTEST	0.222356	0.114117	-0.962359	0	1	1
ENSG00000244732	ENSG00000244732	RN7SL870P	3:47601720-47602014	NOTEST	0	0	0	0	1	1
ENSG00000244734	ENSG00000244734	HBB	11:5246693-5250625	NOTEST	0	0	0	0	1	1
ENSG00000244736	ENSG00000244736	RN7SL495P	15:23255241-23268823	NOTEST	0	0	0	0	1	1
ENSG00000244738	ENSG00000244738	RP11-373E16.3	3:170136652-170578169	NOTEST	0	0	0	0	1	1
ENSG00000244740	ENSG00000244740	RP11-463H24.1	3:135924381-135924757	NOTEST	0	0	0	0	1	1
ENSG00000244743	ENSG00000244743	RP11-8P13.1	12:32943678-33049774	NOTEST	0	0	0	0	1	1
ENSG00000244748	ENSG00000244748	RN7SL153P	5:71515235-71656052	NOTEST	0.361786	0	#NAME?	0	1	1
ENSG00000244752	ENSG00000244752	CRYBB2	22:25615488-25627836	NOTEST	0.0207736	0.0146508	-0.503774	0	1	1
ENSG00000244753	ENSG00000244753	RPL15P21	17:10752857-10784212	NOTEST	0	0	0	0	1	1
ENSG00000244756	ENSG00000244756	RP11-1042B17.1	14:61038741-61039029	NOTEST	0	0	0	0	1	1
ENSG00000244757	ENSG00000244757	RP11-45A16.4	9:118916082-119164601	NOTEST	0	0	0	0	1	1
ENSG00000244791	ENSG00000244791	RP11-65D17.1	8:127337739-127341780	NOTEST	0	0	0	0	1	1
ENSG00000244921	ENSG00000244921	CTB-36O1.7	5:134240595-134347392	NOTEST	0	0.0569531	inf	0	1	1
ENSG00000244926	ENSG00000244926	ALKBH3-AS1	11:43902360-43942494	NOTEST	0.323107	0.4083	0.337616	0	1	1
ENSG00000244932	ENSG00000244932	RP11-529F4.1	3:129100140-129118498	NOTEST	0.159758	0.0334486	-2.25587	0	1	1

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ENSG00000244945	ENSG00000244945	RP11-1379J22.2	5:178977558-179037027	NOTEST	0.0563587	0.042746	-0.398849	0	1	1
ENSG00000244952	ENSG00000244952	RP11-1000B6.5	15:32898618-32932150	NOTEST	0	0.0804602	inf	0	1	1
ENSG00000244953	ENSG00000244953	RP11-613D13.8	11:43942608-44022707	NOTEST	0.0302426	0.0849472	1.48998	0	1	1
ENSG00000244968	ENSG00000244968	LIFR-AS1	5:38475064-38671318	NOTEST	0.00817762	0.00286973	-1.51077	0	1	1
ENSG00000244998	ENSG00000244998	CTD-3064M3.4	8:142400038-142441620	NOTEST	0	0.039172	inf	0	1	1
ENSG00000245008	ENSG00000245008	RP11-744N12.3	11:128499547-128683162	NOTEST	0	0	0	0	1	1
ENSG00000245017	ENSG00000245017	RP11-181C3.1	12:98879321-98897633	NOTEST	0.0252536	0	#NAME?	0	1	1
ENSG00000245025	ENSG00000245025	RP11-875O11.1	8:22545171-22941132	NOTEST	0.181139	0.262873	0.53727	0	1	1
ENSG00000245059	ENSG00000245059	RP11-303E16.7	16:81087101-81130008	NOTEST	0.0161967	0	#NAME?	0	1	1
ENSG00000245067	ENSG00000245067	IGFBP7-AS1	4:57829535-58071676	NOTEST	0.119261	0.0875801	-0.445445	0	1	1
ENSG00000245080	ENSG00000245080	MIR3150A	8:95825538-96128683	NOTEST	0.119675	0.0852279	-0.489719	0	1	1
ENSG00000245105	ENSG00000245105	A2M-AS1	12:9217772-9268825	NOTEST	0.116994	0.070326	-0.7343	0	1	1
ENSG00000245112	ENSG00000245112	SMARCA5-AS1	4:144434615-144478639	NOTEST	0	0.0313768	inf	0	1	1
ENSG00000245148	ENSG00000245148	ARAP1-AS2	11:72396113-72504726	NOTEST	0.068834	0.13256	0.945453	0	1	1
ENSG00000245156	ENSG00000245156	RP11-867G23.3	11:66036003-66056641	NOTEST	0.149963	0.131784	-0.186429	0	1	1
ENSG00000245164	ENSG00000245164	LINC00861	8:126934551-126963493	NOTEST	0	0.00693624	inf	0	1	1
ENSG00000245205	ENSG00000245205	EEF1A1P4	12:19556978-19873735	NOTEST	0.113738	0.195919	0.784541	0	1	1
ENSG00000245261	ENSG00000245261	RP3-330M21.5	6:43149912-43192325	NOTEST	0.112642	0.0981185	-0.19915	0	1	1
ENSG00000245293	ENSG00000245293	RP11-286E11.1	4:108745718-108899955	NOTEST	0.184588	0.0991064	-0.897256	0	1	1
ENSG00000245311	ENSG00000245311	RP11-165P7.1	12:27485786-27599558	NOTEST	0.0234653	0	#NAME?	0	1	1
ENSG00000245317	ENSG00000245317	CTC-241N9.1	5:179224596-179334859	NOTEST	0.441696	0.391617	-0.173608	0	1	1
ENSG00000245322	ENSG00000245322	RP11-15B17.1	4:100869242-101136662	NOTEST	0	0	0	0	1	1
ENSG00000245330	ENSG00000245330	KB-1471A8.1	8:120879658-121063152	NOTEST	0.0168764	0.0375306	1.15306	0	1	1
ENSG00000245384	ENSG00000245384	AC004053.1	4:105389468-106041157	NOTEST	0	0	0	0	1	1
ENSG00000245385	ENSG00000245385	RP11-334E6.10	11:119205236-119208023	NOTEST	0	0	0	0	1	1
ENSG00000245466	ENSG00000245466	CTD-2540L5.6	14:71047973-71108015	NOTEST	0	0	0	0	1	1
ENSG00000245468	ENSG00000245468	RP11-367J11.3	4:7096297-7105112	NOTEST	0	0.0479476	inf	0	1	1
ENSG00000245479	ENSG00000245479	RP11-387D10.3	15:91073156-91260372	NOTEST	0	0	0	0	1	1
ENSG00000245482	ENSG00000245482	RP11-847H18.2	12:34175215-34209675	NOTEST	0	0	0	0	1	1
ENSG00000245498	ENSG00000245498	RP11-677M14.7	11:124636393-124704383	NOTEST	0.0599293	0.0377797	-0.665653	0	1	1
ENSG00000245522	ENSG00000245522	RP11-540A21.2	11:9776316-10315754	NOTEST	0.225227	0.366771	0.703504	0	1	1
ENSG00000245526	ENSG00000245526	LINC00461	5:87803362-88762215	NOTEST	0.185897	0.222029	0.256249	0	1	1
ENSG00000245552	ENSG00000245552	RP11-712B9.2	11:94883702-94967268	NOTEST	0.578739	0.484182	-0.257364	0	1	1
ENSG00000245573	ENSG00000245573	BDNF-AS	11:27528384-27899195	NOTEST	0.297475	0.344083	0.209985	0	1	1
ENSG00000245598	ENSG00000245598	DACT3-AS1	19:47150868-47220384	NOTEST	0.263615	0.412238	0.645048	0	1	1
ENSG00000245648	ENSG00000245648	RP11-277P12.20	12:10516367-10562745	NOTEST	0.167772	0.135391	-0.309371	0	1	1
ENSG00000245651	ENSG00000245651	RP11-620J15.2	12:58263617-58290265	NOTEST	0	0	0	0	1	1
ENSG00000245662	ENSG00000245662	RP11-184E9.1	5:25190790-25306281	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000245667	ENSG00000245667	RP5-940J5.8	12:6647540-6665239	NOTEST	0.185355	0.22457	0.276875	0	1	1
ENSG00000245685	ENSG00000245685	AF146191.4	4:190701489-190861426	NOTEST	0.163553	0.254493	0.637867	0	1	1
ENSG00000245688	ENSG00000245688	CTB-26E19.1	5:177664618-178017556	NOTEST	0	0	0	0	1	1
ENSG00000245711	ENSG00000245711	NADK2-AS1	5:36192693-36242381	NOTEST	0.465089	0.306839	-0.600023	0	1	1
ENSG00000245719	ENSG00000245719	RP11-34F13.2	15:68112041-68166204	NOTEST	0	0	0	0	1	1
ENSG00000245729	ENSG00000245729	RP11-480D4.1	5:8333595-8463208	NOTEST	0.0820786	0.140351	0.773961	0	1	1
ENSG00000245748	ENSG00000245748	RP11-367J11.2	4:6910968-7059679	NOTEST	0.0608791	0.0987759	0.698214	0	1	1
ENSG00000245750	ENSG00000245750	RP11-279F6.1	15:69755364-69863775	NOTEST	0.0857382	0.0767038	-0.160641	0	1	1
ENSG00000245768	ENSG00000245768	RP11-410D17.2	16:58741034-59142878	NOTEST	0	0	0	0	1	1
ENSG00000245812	ENSG00000245812	RP11-175K6.1	5:158527490-158544486	NOTEST	0	0	0	0	1	1
ENSG00000245832	ENSG00000245832	RP11-179A16.1	11:81590892-82429124	NOTEST	0	0	0	0	1	1
ENSG00000245848	ENSG00000245848	CEBPA	19:33790839-33793470	NOTEST	2.54E-06	3.90E-06	0.61695	0	1	1
ENSG00000245857	ENSG00000245857	GS1-24F4.2	8:6666037-6742798	NOTEST	0	0	0	0	1	1
ENSG00000245864	ENSG00000245864	CTC-467M3.1	5:87803362-88762215	NOTEST	0	0	0	0	1	1
ENSG00000245869	ENSG00000245869	RP11-158I9.5	11:118754474-118829269	NOTEST	0	0	0	0	1	1
ENSG00000245870	ENSG00000245870	LINC00682	4:41878497-41884628	NOTEST	0	0.00861367	inf	0	1	1
ENSG00000245888	ENSG00000245888	CTD-3203P2.2	16:27236311-27301813	NOTEST	0.0690855	0.00476189	-3.85878	0	1	1
ENSG00000245904	ENSG00000245904	RP11-796E2.4	12:92378755-92583436	NOTEST	0.0258388	0.0219899	-0.232695	0	1	1
ENSG00000245928	ENSG00000245928	RP11-630D6.5	4:76831808-76928641	NOTEST	0	0	0	0	1	1
ENSG00000245954	ENSG00000245954	RP11-18H21.1	4:153021905-153025872	NOTEST	0	0	0	0	1	1
ENSG00000245975	ENSG00000245975	RP11-30K9.6	15:59060270-59063173	NOTEST	0.080427	0.0273758	-1.55478	0	1	1
ENSG00000246016	ENSG00000246016	RP11-1C1.7	5:10479482-10482421	NOTEST	0.0476031	0.108042	1.18247	0	1	1
ENSG00000246022	ENSG00000246022	ALDH1L1-AS2	3:125822411-125929012	NOTEST	0	0	0	0	1	1
ENSG00000246082	ENSG00000246082	NUDT16P1	3:130569438-131100319	NOTEST	0	0.00512166	inf	0	1	1
ENSG00000246084	ENSG00000246084	CTD-2506J14.1	14:97925152-98047938	NOTEST	0	0	0	0	1	1
ENSG00000246090	ENSG00000246090	RP11-696N14.1	4:100010007-100222513	NOTEST	0.104333	0.131039	0.328805	0	1	1
ENSG00000246095	ENSG00000246095	LINC01096	4:13547698-13549425	NOTEST	0.0519403	0.0973563	0.906419	0	1	1
ENSG00000246100	ENSG00000246100	LINC00900	11:115530375-115713864	NOTEST	0.331779	0.568797	0.777694	0	1	1
ENSG00000246115	ENSG00000246115	RP11-561P12.2	12:8662070-8674962	NOTEST	0	0	0	0	1	1
ENSG00000246130	ENSG00000246130	RP11-875O11.2	8:22545171-22941132	NOTEST	0.121903	0.0389767	-1.64505	0	1	1
ENSG00000246145	ENSG00000246145	RP11-346I3.4	8:67331823-67341212	NOTEST	0.0163196	0	#NAME?	0	1	1
ENSG00000246203	ENSG00000246203	RP11-29H23.5	1:155579566-155829191	NOTEST	0.0239477	0.0641167	1.42082	0	1	1
ENSG00000246211	ENSG00000246211	RP11-632K5.3	11:73723762-74035750	NOTEST	0	0	0	0	1	1
ENSG00000246214	ENSG00000246214	RP11-260E18.1	5:16473146-16630078	NOTEST	0.0866022	0.276893	1.67685	0	1	1
ENSG00000246223	ENSG00000246223	C14orf64	14:98391946-98444461	NOTEST	0	0	0	0	1	1
ENSG00000246225	ENSG00000246225	RP11-17A1.3	11:22835344-22966939	NOTEST	0.37933	0.167556	-1.17881	0	1	1
ENSG00000246228	ENSG00000246228	CASC8	8:128302061-128494384	NOTEST	0	0.0356626	inf	0	1	1
ENSG00000246250	ENSG00000246250	RP11-613D13.5	11:43577985-43902276	NOTEST	0.24577	0.157977	-0.637591	0	1	1
ENSG00000246283	ENSG00000246283	CTD-2036P10.3	15:43030931-43213007	NOTEST	0.128093	0.344999	1.4294	0	1	1
ENSG00000246308	ENSG00000246308	RP11-685M7.3	11:10830843-10928349	NOTEST	0.165364	0.108195	-0.612014	0	1	1
ENSG00000246316	ENSG00000246316	RP11-492A10.1	5:113696641-114004107	NOTEST	0	0	0	0	1	1
ENSG00000246323	ENSG00000246323	RP11-325L7.1	5:137150021-137387650	NOTEST	0.0499398	0.0310014	-0.687855	0	1	1
ENSG00000246331	ENSG00000246331	RP11-77I22.2	12:30908007-30933673	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000246339	ENSG00000246339	EXTL3-AS1	8:28457985-28613116	NOTEST	0.259244	0.295104	0.186913	0	1	1
ENSG00000246350	ENSG00000246350	RP5-1186N24.3	6:28539406-28583989	NOTEST	0	0	0	0	1	1
ENSG00000246363	ENSG00000246363	RP11-13A1.1	12:89404457-89413456	NOTEST	0.0515489	0.0385833	-0.417963	0	1	1
ENSG00000246366	ENSG00000246366	RP11-382J12.1	8:71520811-71581409	NOTEST	0.0596883	0.0668456	0.163384	0	1	1
ENSG00000246375	ENSG00000246375	RP11-10L7.1	4:89206093-89252573	NOTEST	0	0	0	0	1	1
ENSG00000246379	ENSG00000246379	RP11-461O7.1	16:56126898-56225006	NOTEST	0.095252	0.142984	0.586034	0	1	1
ENSG00000246394	ENSG00000246394	RP11-386I8.6	12:133606974-133613808	NOTEST	0	0	0	0	1	1
ENSG00000246422	ENSG00000246422	CTD-2024I7.13	5:140894582-141016437	NOTEST	0	0	0	0	1	1
ENSG00000246430	ENSG00000246430	LINC00968	8:57349232-57472382	NOTEST	0	0	0	0	1	1
ENSG00000246448	ENSG00000246448	RP13-578N3.3	4:144480624-144786225	NOTEST	0.209059	0.117533	-0.830837	0	1	1
ENSG00000246465	ENSG00000246465	RP11-57A19.2	16:28296205-28303385	NOTEST	0	0	0	0	1	1
ENSG00000246477	ENSG00000246477	AF131216.6	8:11141924-11185646	NOTEST	0.0545473	0.0991227	0.861707	0	1	1
ENSG00000246523	ENSG00000246523	RP11-736K20.6	11:86666660-86712001	NOTEST	0.250587	0.0427834	-2.55019	0	1	1
ENSG00000246526	ENSG00000246526	RP11-539L10.2	4:6689174-6692246	NOTEST	0.0090008	0	#NAME?	0	1	1
ENSG00000246541	ENSG00000246541	RP11-363G15.2	4:95038942-95128707	NOTEST	0	0	0	0	1	1
ENSG00000246548	ENSG00000246548	RP11-7F17.5	14:77507406-77552789	NOTEST	0	0.00419077	inf	0	1	1
ENSG00000246575	ENSG00000246575	AC093162.5	2:85542163-85543652	NOTEST	0.0791216	0	#NAME?	0	1	1
ENSG00000246627	ENSG00000246627	CACNA1C-AS1	12:2055219-2802108	NOTEST	0	0	0	0	1	1
ENSG00000246640	ENSG00000246640	RP11-1094H24.4	17:48127712-48133103	NOTEST	0.0529801	0.0980871	0.888613	0	1	1
ENSG00000246662	ENSG00000246662	LINC00535	8:94225530-94753245	NOTEST	0.017041	0	#NAME?	0	1	1
ENSG00000246740	ENSG00000246740	CTD-2382E5.1	15:42264960-42343388	NOTEST	0	0	0	0	1	1
ENSG00000246774	ENSG00000246774	AC004051.2	4:110224190-110237291	NOTEST	0.00834338	0.011726	0.491004	0	1	1
ENSG00000246777	ENSG00000246777	RP11-61A14.4	16:66754795-66788643	NOTEST	0.00545567	0.0118968	1.12475	0	1	1
ENSG00000246790	ENSG00000246790	RP11-730K11.1	11:121318039-121504402	NOTEST	0	0	0	0	1	1
ENSG00000246792	ENSG00000246792	RP11-68L18.1	8:91634222-91997485	NOTEST	0.0279355	0.0699503	1.32423	0	1	1
ENSG00000246820	ENSG00000246820	RP11-379P15.1	11:8190713-8200450	NOTEST	0	0	0	0	1	1
ENSG00000246851	ENSG00000246851	RP11-544A12.8	9:134000947-134110057	NOTEST	0.0439235	0.0423495	-0.0526486	0	1	1
ENSG00000246859	ENSG00000246859	STARD4-AS1	5:110831730-111353006	NOTEST	0.057597	0.0419644	-0.456827	0	1	1
ENSG00000246863	ENSG00000246863	RP11-325N19.3	15:40213242-40218081	NOTEST	0	0	0	0	1	1
ENSG00000246876	ENSG00000246876	RP11-519M16.1	4:130645325-130692636	NOTEST	0	0.0744324	inf	0	1	1
ENSG00000246889	ENSG00000246889	AP000487.5	11:70116805-70282690	NOTEST	0.54576	0.335488	-0.702005	0	1	1
ENSG00000246982	ENSG00000246982	RP1-179N16.6	6:36114474-36200567	NOTEST	0.330838	0.271651	-0.284373	0	1	1
ENSG00000247011	ENSG00000247011	RP11-700H6.1	17:49012349-49026111	NOTEST	0.0221702	0.0183849	-0.270101	0	1	1
ENSG00000247033	ENSG00000247033	RP11-252E2.1	16:74907467-75144892	NOTEST	0	0.00821942	inf	0	1	1
ENSG00000247049	ENSG00000247049	CTC-338M12.7	5:180649498-180662809	NOTEST	0	0.0204778	inf	0	1	1
ENSG00000247121	ENSG00000247121	CTD-2260A17.2	5:96149730-96373219	NOTEST	0.184483	0.170604	-0.112832	0	1	1
ENSG00000247130	ENSG00000247130	RP11-366H4.3	4:189060572-189068897	NOTEST	0	0	0	0	1	1
ENSG00000247131	ENSG00000247131	RP11-588G21.2	12:70107412-70132348	NOTEST	0	0	0	0	1	1
ENSG00000247151	ENSG00000247151	CSTF3-AS1	11:33060962-33213144	NOTEST	0.0598635	0	#NAME?	0	1	1
ENSG00000247157	ENSG00000247157	RP11-434C1.1	12:11694328-11743303	NOTEST	0.261309	0.405	0.632168	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000247193	ENSG00000247193	RP11-431M7.3	4:35949842-36275842	NOTEST	0	0	0	0	1	1
ENSG00000247199	ENSG00000247199	RP11-373N22.3	5:147647742-147763346	NOTEST	0.0448425	0.0287231	-0.642657	0	1	1
ENSG00000247213	ENSG00000247213	RP11-13G14.4	12:108827906-108886362	NOTEST	0	0	0	0	1	1
ENSG00000247270	ENSG00000247270	AC132186.1	16:66461199-66586447	NOTEST	0	0.00021477	inf	0	1	1
ENSG00000247287	ENSG00000247287	RP11-902B17.1	14:61654276-62125414	NOTEST	0	0	0	0	1	1
ENSG00000247311	ENSG00000247311	CTC-441N14.2	5:121464456-121518353	NOTEST	0	0	0	0	1	1
ENSG00000247324	ENSG00000247324	RP11-510M2.2	16:71481499-71598992	NOTEST	0.0113292	0.00397701	-1.51029	0	1	1
ENSG00000247345	ENSG00000247345	RP11-266N13.2	5:58264864-59843484	NOTEST	0	0.0588065	inf	0	1	1
ENSG00000247363	ENSG00000247363	RP11-637A17.2	12:69068150-69136785	NOTEST	0.317755	0.110521	-1.52359	0	1	1
ENSG00000247372	ENSG00000247372	CTD-2235C13.2	5:74615979-74657929	NOTEST	0	0	0	0	1	1
ENSG00000247373	ENSG00000247373	RP11-486O12.2	12:124066766-124083116	NOTEST	0.340142	0.302315	-0.170086	0	1	1
ENSG00000247381	ENSG00000247381	PDX1-AS1	13:28407580-28500368	NOTEST	0	0	0	0	1	1
ENSG00000247402	ENSG00000247402	CTD-2340E1.2	5:101917071-102007263	NOTEST	0	0	0	0	1	1
ENSG00000247416	ENSG00000247416	RP11-629G13.1	11:112830001-113149158	NOTEST	0.187405	0.241003	0.362891	0	1	1
ENSG00000247473	ENSG00000247473	CARS-AS1	11:3022151-3078843	NOTEST	0.022793	0.0309725	0.442396	0	1	1
ENSG00000247570	ENSG00000247570	SDCBPP2	8:70855182-70856883	NOTEST	0.0760975	0.111902	0.556319	0	1	1
ENSG00000247595	ENSG00000247595	SPTY2D1-AS1	11:18621333-18656338	NOTEST	0.318355	0.37161	0.223153	0	1	1
ENSG00000247624	ENSG00000247624	CPEB2-AS1	4:14911584-15003669	NOTEST	0	0.0218988	inf	0	1	1
ENSG00000247627	ENSG00000247627	MTND4P12	5:134240595-134347392	NOTEST	0.0940163	0.093177	-0.0129369	0	1	1
ENSG00000247675	ENSG00000247675	LRP4-AS1	11:46867962-46940193	NOTEST	0.306738	0.126684	-1.27578	0	1	1
ENSG00000247699	ENSG00000247699	CTB-127C13.1	5:159614373-159665742	NOTEST	0	0	0	0	1	1
ENSG00000247700	ENSG00000247700	HLA-H	HSCHR6_MHC_MCF:29846326-29992167	NOTEST	0	0	0	0	1	1
ENSG00000247732	ENSG00000247732	RP11-404K5.1	5:7290935-7296458	NOTEST	0	0	0	0	1	1
ENSG00000247735	ENSG00000247735	CTD-2574D22.2	16:29911695-29940254	NOTEST	0.386285	0.270507	-0.514002	0	1	1
ENSG00000247763	ENSG00000247763	RP11-447H19.1	5:43192172-43280952	NOTEST	0.0351326	0.0184661	-0.927931	0	1	1
ENSG00000247765	ENSG00000247765	RP11-32B5.7	15:21941146-21968151	NOTEST	0.0284365	0.029031	0.0298496	0	1	1
ENSG00000247774	ENSG00000247774	PCED1B-AS1	12:47469489-47630443	NOTEST	0	0.00496823	inf	0	1	1
ENSG00000247775	ENSG00000247775	RP11-67M1.1	4:90472506-90763129	NOTEST	0.187319	0.168939	-0.148999	0	1	1
ENSG00000247810	ENSG00000247810	RP11-103J17.1	4:37080198-37127046	NOTEST	0	0	0	0	1	1
ENSG00000247844	ENSG00000247844	CCAT1	8:128220110-128231333	NOTEST	0	0	0	0	1	1
ENSG00000247853	ENSG00000247853	RP5-940J5.6	12:6679248-6716642	NOTEST	0.22598	0.167998	-0.427753	0	1	1
ENSG00000247867	ENSG00000247867	CTD-2530H12.1	11:75469499-75514460	NOTEST	0	0	0	0	1	1
ENSG00000247872	ENSG00000247872	SPCS2P3	5:710470-919472	NOTEST	0	0	0	0	1	1
ENSG00000247877	ENSG00000247877	CTD-2001C12.1	5:99785457-99870966	NOTEST	0.0874412	0.0415544	-1.07331	0	1	1
ENSG00000247911	ENSG00000247911	HMGN1P12	5:70751441-70863649	NOTEST	0	0	0	0	1	1
ENSG00000247925	ENSG00000247925	RP3-510L9.1	6:11173684-11382581	NOTEST	0	0	0	0	1	1
ENSG00000247934	ENSG00000247934	RP11-967K21.1	12:28286181-28732883	NOTEST	0.174513	0.124182	-0.490877	0	1	1
ENSG00000247950	ENSG00000247950	SEC24B-AS1	4:110268630-110462052	NOTEST	0.163508	0.244889	0.582768	0	1	1
ENSG00000247970	ENSG00000247970	RP11-543C4.1	14:100070892-100092077	NOTEST	0	0.0361649	inf	0	1	1
ENSG00000247982	ENSG00000247982	LINC00926	15:57592562-57599959	NOTEST	0.0734713	0.0403441	-0.864822	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248015	ENSG00000248015	AC005329.7	19:1383525-1396466	NOTEST	0.0177721	0.0382738	1.10674	0	1	1
ENSG00000248019	ENSG00000248019	FAM13A-AS1	4:89630939-90032549	NOTEST	0.461941	0.572703	0.31008	0	1	1
ENSG00000248027	ENSG00000248027	CTD-2383M3.1	11:100554892-100862668	NOTEST	0.00892025	0.0129755	0.540629	0	1	1
ENSG00000248029	ENSG00000248029	CTD-2313F11.3	5:54359006-54362058	NOTEST	0	0	0	0	1	1
ENSG00000248050	ENSG00000248050	RP11-422N16.3	8:110586206-110704020	NOTEST	0	0	0	0	1	1
ENSG00000248079	ENSG00000248079	DPH6-AS1	15:35838395-36151202	NOTEST	0.194876	0.107611	-0.856735	0	1	1
ENSG00000248099	ENSG00000248099	INSL3	19:17927320-17932383	NOTEST	0	0	0	0	1	1
ENSG00000248100	ENSG00000248100	RP11-709A23.1	12:27676363-27848497	NOTEST	0	0.00422565	inf	0	1	1
ENSG00000248101	ENSG00000248101	AC002116.8	19:36494208-36505141	NOTEST	0.497846	0.401799	-0.309226	0	1	1
ENSG00000248103	ENSG00000248103	CTC-338M12.9	5:180708375-180710653	NOTEST	0	0.0278667	inf	0	1	1
ENSG00000248104	ENSG00000248104	TARS2P1	4:136486271-136488312	NOTEST	0	0	0	0	1	1
ENSG00000248105	ENSG00000248105	CTD-2218K11.3	5:82120702-82121003	NOTEST	0	0	0	0	1	1
ENSG00000248106	ENSG00000248106	AC005609.2	5:140143694-140144406	NOTEST	0	0	0	0	1	1
ENSG00000248107	ENSG00000248107	CTC-339D2.1	5:125412492-125615493	NOTEST	0	0	0	0	1	1
ENSG00000248109	ENSG00000248109	CTC-295J13.3	5:147618132-147622157	NOTEST	0	0	0	0	1	1
ENSG00000248112	ENSG00000248112	RP11-78C3.1	5:82215194-82216938	NOTEST	0	0	0	0	1	1
ENSG00000248113	ENSG00000248113	RP11-791G16.4	4:83501269-83502537	NOTEST	0	0.101342	inf	0	1	1
ENSG00000248114	ENSG00000248114	AC114812.9	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000248115	ENSG00000248115	RP11-752D24.2	4:53739148-54232242	NOTEST	0.00633087	0.0222289	1.81196	0	1	1
ENSG00000248117	ENSG00000248117	MINOS1P4	4:78978723-79465423	NOTEST	0	0	0	0	1	1
ENSG00000248118	ENSG00000248118	LINC01019	5:3417265-3536208	NOTEST	0	0	0	0	1	1
ENSG00000248120	ENSG00000248120	RP11-301A5.2	5:40909353-40983041	NOTEST	0	0	0	0	1	1
ENSG00000248121	ENSG00000248121	SMURF2P1	17:28900488-28999807	NOTEST	0	0.160699	inf	0	1	1
ENSG00000248122	ENSG00000248122	APOOP4	4:69170060-69170657	NOTEST	0	0	0	0	1	1
ENSG00000248124	ENSG00000248124	RRN3P1	16:21807950-21831731	NOTEST	0.0171149	0.0106057	-0.690406	0	1	1
ENSG00000248125	ENSG00000248125	CTB-73N10.1	5:144809430-144830662	NOTEST	0	0	0	0	1	1
ENSG00000248126	ENSG00000248126	CTD-2012J19.2	5:1594740-1634120	NOTEST	0	0	0	0	1	1
ENSG00000248127	ENSG00000248127	CTC-235G5.3	5:75377770-75649764	NOTEST	0	0	0	0	1	1
ENSG00000248128	ENSG00000248128	RP11-777B9.4	4:78924296-78924593	NOTEST	0	0	0	0	1	1
ENSG00000248132	ENSG00000248132	CTD-2037L6.2	5:57403908-57418168	NOTEST	0	0	0	0	1	1
ENSG00000248133	ENSG00000248133	RP11-302F12.7	4:25721376-25721652	NOTEST	0	0	0	0	1	1
ENSG00000248134	ENSG00000248134	AC079395.1	2:97541619-97684341	NOTEST	0	0	0	0	1	1
ENSG00000248136	ENSG00000248136	MTND6P8	2:131037871-131040179	NOTEST	0	0	0	0	1	1
ENSG00000248137	ENSG00000248137	RP11-468D11.1	5:2831134-2835253	NOTEST	0	0	0	0	1	1
ENSG00000248138	ENSG00000248138	RP11-446J8.1	4:16402052-16900432	NOTEST	0	0	0	0	1	1
ENSG00000248139	ENSG00000248139	CUL4AP1	4:117347138-117352048	NOTEST	0	0	0	0	1	1
ENSG00000248143	ENSG00000248143	RP11-324J13.2	4:43459543-43494560	NOTEST	0	0	0	0	1	1
ENSG00000248144	ENSG00000248144	ADH1C	4:100257648-100274184	NOTEST	0.0362308	0	#NAME?	0	1	1
ENSG00000248145	ENSG00000248145	CTC-305H11.1	5:13175957-13179684	NOTEST	0	0	0	0	1	1
ENSG00000248147	ENSG00000248147	RP11-395P13.1	5:124704260-124705035	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248148	ENSG00000248148	RP11-357F12.1	5:45035300-45098749	NOTEST	0	0	0	0	1	1
ENSG00000248150	ENSG00000248150	RP1-167G20.1	5:16373469-16440190	NOTEST	0	0	0	0	1	1
ENSG00000248152	ENSG00000248152	RP11-650J17.1	4:113739264-114304896	NOTEST	0	0	0	0	1	1
ENSG00000248155	ENSG00000248155	WI2-89927D4.1	4:2420700-2734292	NOTEST	0.272073	0	#NAME?	0	1	1
ENSG00000248156	ENSG00000248156	RP11-12P19.1	5:24786950-24787133	NOTEST	0	0	0	0	1	1
ENSG00000248159	ENSG00000248159	HSPA8P11	8:30094897-30098513	NOTEST	0	0	0	0	1	1
ENSG00000248160	ENSG00000248160	RP11-432M8.14	5:17647820-17648053	NOTEST	0	0	0	0	1	1
ENSG00000248162	ENSG00000248162	RP11-294O2.1	4:165646461-165647858	NOTEST	0	0	0	0	1	1
ENSG00000248165	ENSG00000248165	RP11-44F21.2	4:75858304-75975325	NOTEST	0	0	0	0	1	1
ENSG00000248166	ENSG00000248166	AC008984.2	19:54818352-54850421	NOTEST	0	0	0	0	1	1
ENSG00000248167	ENSG00000248167	TRIM39-RPP21	6:30201815-30314661	NOTEST	0	0.0443809	inf	0	1	1
ENSG00000248170	ENSG00000248170	RP11-1072N2.4	5:84533498-84533892	NOTEST	0	0	0	0	1	1
ENSG00000248172	ENSG00000248172	RP11-1094H24.3	17:48074252-48094208	NOTEST	0	0	0	0	1	1
ENSG00000248173	ENSG00000248173	RP11-659O3.1	4:116843170-117218316	NOTEST	0	0	0	0	1	1
ENSG00000248174	ENSG00000248174	RP11-148L24.1	4:175015810-175141549	NOTEST	0	0	0	0	1	1
ENSG00000248175	ENSG00000248175	CTC-428G20.3	5:114539712-114541943	NOTEST	0.544882	0.462189	-0.237463	0	1	1
ENSG00000248176	ENSG00000248176	RP11-472K22.1	4:29119929-29204392	NOTEST	0	0	0	0	1	1
ENSG00000248180	ENSG00000248180	GAPDHP60	4:88081254-88161466	NOTEST	0	0	0	0	1	1
ENSG00000248182	ENSG00000248182	OR12D1	HSCHR6_MHC_MANN:29323056-29424418	NOTEST	0	0	0	0	1	1
ENSG00000248184	ENSG00000248184	RP11-231C18.1	4:55199058-55222121	NOTEST	0	0	0	0	1	1
ENSG00000248185	ENSG00000248185	CTD-2049O17.1	5:62597349-62597883	NOTEST	0	0	0	0	1	1
ENSG00000248187	ENSG00000248187	RP11-184M15.1	4:129489126-129491686	NOTEST	0	0.00719149	inf	0	1	1
ENSG00000248188	ENSG00000248188	RP11-442P12.2	4:15744818-15745205	NOTEST	0	0	0	0	1	1
ENSG00000248191	ENSG00000248191	PES1P1	4:135176327-135249953	NOTEST	0	0	0	0	1	1
ENSG00000248192	ENSG00000248192	ATG10-AS1	5:81267843-81574396	NOTEST	0.031142	0	#NAME?	0	1	1
ENSG00000248195	ENSG00000248195	CTC-261N6.3	5:85630841-85631626	NOTEST	0	0	0	0	1	1
ENSG00000248196	ENSG00000248196	RP11-476C8.2	4:88081254-88161466	NOTEST	0	0	0	0	1	1
ENSG00000248197	ENSG00000248197	LINC00290	4:181985241-182080302	NOTEST	0	0	0	0	1	1
ENSG00000248199	ENSG00000248199	CTD-2244C20.2	5:61173935-61181956	NOTEST	0	0	0	0	1	1
ENSG00000248200	ENSG00000248200	RP11-115A14.1	4:110967001-111120355	NOTEST	0	0	0	0	1	1
ENSG00000248202	ENSG00000248202	RP11-455B3.1	5:97217123-97258399	NOTEST	0.0511545	0.0811317	0.665404	0	1	1
ENSG00000248203	ENSG00000248203	CTC-503K11.2	5:102581748-102589220	NOTEST	0	0	0	0	1	1
ENSG00000248205	ENSG00000248205	RP11-321E2.11	5:17502151-17502472	NOTEST	0	0	0	0	1	1
ENSG00000248206	ENSG00000248206	RP11-739P1.2	4:184774583-184944679	NOTEST	0.0608124	0	#NAME?	0	1	1
ENSG00000248208	ENSG00000248208	RP11-153M7.1	4:154561319-154602332	NOTEST	0	0	0	0	1	1
ENSG00000248209	ENSG00000248209	RP11-18O11.1	4:128414659-128414983	NOTEST	0	0	0	0	1	1
ENSG00000248210	ENSG00000248210	RP11-24I21.1	4:150075446-150199275	NOTEST	0	0	0	0	1	1
ENSG00000248211	ENSG00000248211	TRPC7-AS1	5:135548998-135701225	NOTEST	0.102765	0.0766264	-0.42344	0	1	1
ENSG00000248213	ENSG00000248213	CICP16	4:119557055-119559937	NOTEST	0.170962	0.34614	1.01768	0	1	1
ENSG00000248215	ENSG00000248215	RP11-722M1.1	4:36498158-36643522	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248216	ENSG00000248216	RP11-648M2.2	5:37379313-37753537	NOTEST	0	0	0	0	1	1
ENSG00000248221	ENSG00000248221	STX18-IT1	4:4349866-4712665	NOTEST	0	0	0	0	1	1
ENSG00000248222	ENSG00000248222	CTB-174D11.1	5:168081517-168728133	NOTEST	0	0	0	0	1	1
ENSG00000248223	ENSG00000248223	CTD-2139B15.2	5:17353803-17355008	NOTEST	0	0	0	0	1	1
ENSG00000248227	ENSG00000248227	RP11-83C7.1	4:38368534-38387380	NOTEST	0	0	0	0	1	1
ENSG00000248228	ENSG00000248228	SLIT2-IT1	4:20254882-20622184	NOTEST	0.0345464	0	#NAME?	0	1	1
ENSG00000248229	ENSG00000248229	RP11-366M4.12	4:165908416-165908939	NOTEST	0	0	0	0	1	1
ENSG00000248230	ENSG00000248230	MICE	HSCHR6_MHC_DBB:29688036-29714307	NOTEST	0	0	0	0	1	1
ENSG00000248231	ENSG00000248231	KRT8P4	8:90424849-90427300	NOTEST	0.0210229	0.0162841	-0.368492	0	1	1
ENSG00000248234	ENSG00000248234	CTD-2108O9.4	5:38258510-38468441	NOTEST	0	0	0	0	1	1
ENSG00000248236	ENSG00000248236	CTD-2151A2.2	5:98930032-98930444	NOTEST	0	0	0	0	1	1
ENSG00000248237	ENSG00000248237	RP11-593F5.1	4:61616303-61655717	NOTEST	0	0	0	0	1	1
ENSG00000248238	ENSG00000248238	RP11-3J1.1	4:19173957-19911315	NOTEST	0	0	0	0	1	1
ENSG00000248240	ENSG00000248240	RP11-159F24.5	5:43484060-43525412	NOTEST	0	0.0309274	inf	0	1	1
ENSG00000248242	ENSG00000248242	RP11-556I14.2	4:105389468-106041157	NOTEST	0	0	0	0	1	1
ENSG00000248243	ENSG00000248243	RP11-93K22.13	3:129800673-129839422	NOTEST	0.0274061	0.0605577	1.14381	0	1	1
ENSG00000248245	ENSG00000248245	CTB-49A3.2	5:132496129-132948255	NOTEST	0	0	0	0	1	1
ENSG00000248249	ENSG00000248249	RP11-598O12.1	4:176554084-176923815	NOTEST	0	0	0	0	1	1
ENSG00000248254	ENSG00000248254	AC092597.3	4:47487304-47595503	NOTEST	0.190936	0.134037	-0.510457	0	1	1
ENSG00000248256	ENSG00000248256	OCIAD1-AS1	4:48807228-48863834	NOTEST	0	0	0	0	1	1
ENSG00000248257	ENSG00000248257	PSG10P	19:43256837-43359870	NOTEST	0	0	0	0	1	1
ENSG00000248259	ENSG00000248259	RP11-63H19.5	4:65476333-65476627	NOTEST	0	0	0	0	1	1
ENSG00000248261	ENSG00000248261	CTD-2333K2.1	5:101479780-101482276	NOTEST	0	0	0	0	1	1
ENSG00000248262	ENSG00000248262	RP11-1J7.1	4:11916290-11921312	NOTEST	0	0	0	0	1	1
ENSG00000248265	ENSG00000248265	RP11-834C11.3	12:54452037-54519776	NOTEST	0.116012	0.107951	-0.10389	0	1	1
ENSG00000248266	ENSG00000248266	RP11-402C9.1	4:182795590-183724177	NOTEST	0	0	0	0	1	1
ENSG00000248268	ENSG00000248268	CTC-499J9.1	5:110559350-110830584	NOTEST	0	0	0	0	1	1
ENSG00000248271	ENSG00000248271	PGAM1P1	5:57457023-57457579	NOTEST	0	0	0	0	1	1
ENSG00000248279	ENSG00000248279	CTD-2218G20.2	5:32925744-33298016	NOTEST	0	0	0	0	1	1
ENSG00000248280	ENSG00000248280	RP11-33B1.2	4:120361715-120371312	NOTEST	0	0	0	0	1	1
ENSG00000248281	ENSG00000248281	RP11-174E22.2	4:30008572-30009938	NOTEST	0	0	0	0	1	1
ENSG00000248282	ENSG00000248282	RP11-112L18.1	4:82347546-82965397	NOTEST	0	0	0	0	1	1
ENSG00000248283	ENSG00000248283	RP11-473D24.1	4:42410389-42659122	NOTEST	0	0	0	0	1	1
ENSG00000248285	ENSG00000248285	RP11-158J3.2	5:63253719-63276870	NOTEST	0	0	0	0	1	1
ENSG00000248286	ENSG00000248286	RP11-811J10.1	5:21196828-21196969	NOTEST	0	0	0	0	1	1
ENSG00000248287	ENSG00000248287	SCGB1D5P	4:166438406-166438653	NOTEST	0	0	0	0	1	1
ENSG00000248288	ENSG00000248288	CTD-2194F4.2	5:64444562-64777747	NOTEST	0	0	0	0	1	1
ENSG00000248290	ENSG00000248290	TNXA	6:31976390-31980249	NOTEST	0	0	0	0	1	1
ENSG00000248293	ENSG00000248293	CTC-281M20.3	5:174346084-174422516	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248294	ENSG00000248294	CTD-2023N9.2	5:56869853-56910168	NOTEST	0.0623366	0	#NAME?	0	1	1
ENSG00000248295	ENSG00000248295	CTC-555I19.1	5:115298150-115395815	NOTEST	0	0	0	0	1	1
ENSG00000248296	ENSG00000248296	CTD-2308B18.3	5:123828467-123872041	NOTEST	0	0	0	0	1	1
ENSG00000248300	ENSG00000248300	RP11-74M11.2	4:11627337-11815582	NOTEST	0	0	0	0	1	1
ENSG00000248302	ENSG00000248302	Z95704.4	4:48990-50018	NOTEST	0	0.0263172	inf	0	1	1
ENSG00000248305	ENSG00000248305	RP11-310A13.2	4:139402408-139403250	NOTEST	0	0	0	0	1	1
ENSG00000248307	ENSG00000248307	LINC00616	4:138948575-139163503	NOTEST	0	0	0	0	1	1
ENSG00000248308	ENSG00000248308	RP11-697E23.1	5:20611948-20937800	NOTEST	0	0	0	0	1	1
ENSG00000248311	ENSG00000248311	CTD-2161F6.2	5:4452042-4866334	NOTEST	0	0	0	0	1	1
ENSG00000248313	ENSG00000248313	CYP4F27P	2:130748028-130808704	NOTEST	0	0	0	0	1	1
ENSG00000248315	ENSG00000248315	RP11-3N2.11	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000248317	ENSG00000248317	RP11-463H12.2	4:55809795-55822985	NOTEST	0	0	0	0	1	1
ENSG00000248318	ENSG00000248318	RP11-713M15.1	8:121392999-121825599	NOTEST	0	0	0	0	1	1
ENSG00000248319	ENSG00000248319	RP11-205M3.3	4:170838911-170897053	NOTEST	0	0	0	0	1	1
ENSG00000248320	ENSG00000248320	PRKRIRP9	4:45325269-45328045	NOTEST	0	0	0	0	1	1
ENSG00000248322	ENSG00000248322	RP4-559A3.6	1:226124110-226129189	NOTEST	0	0	0	0	1	1
ENSG00000248323	ENSG00000248323	LUCAT1	5:90598845-90610219	NOTEST	0.187707	0.19961	0.0887016	0	1	1
ENSG00000248327	ENSG00000248327	RP11-443J23.1	4:166468683-166472212	NOTEST	0	0	0	0	1	1
ENSG00000248328	ENSG00000248328	RP11-63H19.6	4:65477091-65477606	NOTEST	0	0	0	0	1	1
ENSG00000248329	ENSG00000248329	RP11-366M4.3	4:165798155-165820117	NOTEST	0	0	0	0	1	1
ENSG00000248330	ENSG00000248330	LINC00613	4:136788137-136834835	NOTEST	0	0	0	0	1	1
ENSG00000248332	ENSG00000248332	RP11-236J17.5	11:8040790-8190602	NOTEST	0	0	0	0	1	1
ENSG00000248335	ENSG00000248335	RP11-102N12.2	4:141541918-141677274	NOTEST	0	0	0	0	1	1
ENSG00000248336	ENSG00000248336	HMGN1P11	4:63376186-63376489	NOTEST	0	0	0	0	1	1
ENSG00000248337	ENSG00000248337	RP11-432M8.18	5:17654481-17654752	NOTEST	0	0	0	0	1	1
ENSG00000248338	ENSG00000248338	RP11-472K22.2	4:29216019-29222784	NOTEST	0	0	0	0	1	1
ENSG00000248339	ENSG00000248339	RP11-717H13.1	4:172210625-172219418	NOTEST	0	0	0	0	1	1
ENSG00000248340	ENSG00000248340	RP11-293A21.2	4:26859299-27027003	NOTEST	0	0	0	0	1	1
ENSG00000248341	ENSG00000248341	AC115115.2	2:113033170-113097640	NOTEST	0.135504	0.34722	1.35751	0	1	1
ENSG00000248343	ENSG00000248343	RP11-556G22.2	4:20697904-21950422	NOTEST	0	0	0	0	1	1
ENSG00000248345	ENSG00000248345	RP11-262D11.1	X:71130937-71363424	NOTEST	0	0	0	0	1	1
ENSG00000248346	ENSG00000248346	RP11-292D4.1	4:147878589-147896609	NOTEST	0	0	0	0	1	1
ENSG00000248347	ENSG00000248347	RP11-1134I14.2	8:48001194-48110484	NOTEST	0.215369	0.192523	-0.161778	0	1	1
ENSG00000248349	ENSG00000248349	RP11-79C6.1	5:35896289-35896392	NOTEST	0	0	0	0	1	1
ENSG00000248350	ENSG00000248350	CTC-470E21.1	5:111478137-111755013	NOTEST	0	0	0	0	1	1
ENSG00000248351	ENSG00000248351	HSPD1P18	5:135712035-135732730	NOTEST	0	0	0	0	1	1
ENSG00000248352	ENSG00000248352	TNXA	HSCHR6_MHC_DBB:31958576-31962435	NOTEST	0	0	0	0	1	1
ENSG00000248355	ENSG00000248355	ARL2BPP6	5:174717733-174718255	NOTEST	0	0	0	0	1	1
ENSG00000248356	ENSG00000248356	RP11-557J10.4	4:146539414-146581187	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248358	ENSG00000248358	AE000658.31	14:22183017-22184486	NOTEST	0	0	0	0	1	1
ENSG00000248359	ENSG00000248359	CTC-537E7.2	5:67827516-67829357	NOTEST	0	0	0	0	1	1
ENSG00000248360	ENSG00000248360	LINC00504	4:14472088-14889793	NOTEST	0.6059	0.441423	-0.456919	0	1	1
ENSG00000248362	ENSG00000248362	CTC-327F10.5	5:147250244-147286101	NOTEST	0	0	0	0	1	1
ENSG00000248363	ENSG00000248363	CTC-261N6.1	5:85649620-85664672	NOTEST	0	0	0	0	1	1
ENSG00000248364	ENSG00000248364	OR7E86P	4:9460980-9461970	NOTEST	0	0	0	0	1	1
ENSG00000248365	ENSG00000248365	POU5F1P7	3:97818751-97866978	NOTEST	0	0	0	0	1	1
ENSG00000248366	ENSG00000248366	TRAJ51	14:22956170-22956233	NOTEST	0	0	0	0	1	1
ENSG00000248367	ENSG00000248367	CTB-129O4.1	5:179720244-179722253	NOTEST	0.0667909	0.104292	0.6429	0	1	1
ENSG00000248369	ENSG00000248369	RP11-62N21.1	4:133356956-133368390	NOTEST	0	0	0	0	1	1
ENSG00000248370	ENSG00000248370	RP11-366H4.1	4:189081218-189082293	NOTEST	0	0	0	0	1	1
ENSG00000248371	ENSG00000248371	CTC-347C20.2	5:71869946-71956496	NOTEST	0	0	0	0	1	1
ENSG00000248373	ENSG00000248373	RP11-556I14.1	4:105389468-106041157	NOTEST	0	0	0	0	1	1
ENSG00000248374	ENSG00000248374	RP11-501M7.1	3:142984063-143567373	NOTEST	0	0	0	0	1	1
ENSG00000248375	ENSG00000248375	RP11-177B4.1	4:53578596-53586998	NOTEST	0.143563	0.257939	0.845344	0	1	1
ENSG00000248376	ENSG00000248376	RP11-692E14.1	4:184340042-184340958	NOTEST	0	0	0	0	1	1
ENSG00000248377	ENSG00000248377	HMGN1P9	3:134104038-134104336	NOTEST	0	0	0	0	1	1
ENSG00000248378	ENSG00000248378	RP11-5N11.5	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000248383	ENSG00000248383	PCDHAC1	5:140165875-140391936	NOTEST	0.0162429	0	#NAME?	0	1	1
ENSG00000248385	ENSG00000248385	TARM1	19:54573148-54584634	NOTEST	0	0	0	0	1	1
ENSG00000248387	ENSG00000248387	RP11-781M16.1	4:159236462-159574524	NOTEST	0	0	0	0	1	1
ENSG00000248388	ENSG00000248388	RP11-313E19.2	4:177590771-177713881	NOTEST	0	0	0	0	1	1
ENSG00000248391	ENSG00000248391	CTD-2010I22.2	5:29380402-29396088	NOTEST	0	0	0	0	1	1
ENSG00000248393	ENSG00000248393	CTD-2015A6.1	5:81841680-81842129	NOTEST	0	0	0	0	1	1
ENSG00000248394	ENSG00000248394	FOSL1P1	4:128982422-129144086	NOTEST	0	0	0	0	1	1
ENSG00000248396	ENSG00000248396	TOMM22P4	4:163442833-163443193	NOTEST	0	0	0	0	1	1
ENSG00000248397	ENSG00000248397	LINC00498	4:139220009-139345498	NOTEST	0	0	0	0	1	1
ENSG00000248399	ENSG00000248399	RP11-503N18.4	4:2420700-2734292	NOTEST	0	0	0	0	1	1
ENSG00000248400	ENSG00000248400	ST13P12	5:82264706-82272972	NOTEST	0	0	0	0	1	1
ENSG00000248401	ENSG00000248401	RP11-576N17.3	4:84154664-84169359	NOTEST	0	0.0122105	inf	0	1	1
ENSG00000248403	ENSG00000248403	NACAP6	5:16192196-16192818	NOTEST	0	0	0	0	1	1
ENSG00000248405	ENSG00000248405	PRR5-ARHGAP8	22:45064592-45258665	NOTEST	0	0.0106352	inf	0	1	1
ENSG00000248406	ENSG00000248406	CTD-3105H18.4	19:12490002-12750912	NOTEST	0.016235	0.0285555	0.814657	0	1	1
ENSG00000248408	ENSG00000248408	RP11-452C8.1	4:80584914-80617991	NOTEST	0	0	0	0	1	1
ENSG00000248409	ENSG00000248409	KB-1269D1.8	22:23732792-23744913	NOTEST	0.0973023	0.122279	0.329631	0	1	1
ENSG00000248415	ENSG00000248415	GAPDHP61	15:64752940-64978264	NOTEST	0	0.0126005	inf	0	1	1
ENSG00000248416	ENSG00000248416	RP11-1191J2.4	4:699536-775637	NOTEST	0	0.0290684	inf	0	1	1
ENSG00000248417	ENSG00000248417	RP11-802H3.2	4:33435131-33439499	NOTEST	0	0	0	0	1	1
ENSG00000248418	ENSG00000248418	UBL5P1	5:29600782-29600975	NOTEST	0	0	0	0	1	1
ENSG00000248419	ENSG00000248419	RP11-136I13.2	4:10480147-10480547	NOTEST	0	0	0	0	1	1
ENSG00000248420	ENSG00000248420	MTATP6P9	4:156379112-156379792	NOTEST	0	0	0	0	1	1
ENSG00000248422	ENSG00000248422	RP11-432M8.7	5:17598540-17598668	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248423	ENSG00000248423	RP11-235P11.1	8:15274723-15624158	NOTEST	0	0	0	0	1	1
ENSG00000248424	ENSG00000248424	OR51K1P	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000248425	ENSG00000248425	AC006296.2	4:14384746-14410702	NOTEST	0	0	0	0	1	1
ENSG00000248426	ENSG00000248426	CTD-2533K21.2	5:26669454-26670098	NOTEST	0	0	0	0	1	1
ENSG00000248428	ENSG00000248428	CTC-551A13.1	5:110306649-110344598	NOTEST	0	0	0	0	1	1
ENSG00000248430	ENSG00000248430	HMGB3P16	5:111788399-111788686	NOTEST	0	0	0	0	1	1
ENSG00000248431	ENSG00000248431	AC005150.1	4:163661819-163663200	NOTEST	0	0	0	0	1	1
ENSG00000248432	ENSG00000248432	RP11-269F21.2	4:112723956-112993854	NOTEST	0	0.25926	inf	0	1	1
ENSG00000248434	ENSG00000248434	RP11-553P9.2	4:135988387-136018813	NOTEST	0	0	0	0	1	1
ENSG00000248439	ENSG00000248439	RP11-402J6.2	4:113434671-113578748	NOTEST	0	0	0	0	1	1
ENSG00000248440	ENSG00000248440	RP11-231G15.1	5:108833577-108834809	NOTEST	0	0	0	0	1	1
ENSG00000248441	ENSG00000248441	CTD-2536I1.1	15:95819689-95870358	NOTEST	0	0	0	0	1	1
ENSG00000248442	ENSG00000248442	OR10J7P	1:159315955-159453166	NOTEST	0	0	0	0	1	1
ENSG00000248443	ENSG00000248443	RP11-284A20.3	5:124165164-124165983	NOTEST	0	0	0	0	1	1
ENSG00000248444	ENSG00000248444	HNRNPA1P65	4:24773088-24774042	NOTEST	0	0	0	0	1	1
ENSG00000248447	ENSG00000248447	RP11-633G11.1	4:65900351-65901735	NOTEST	0	0	0	0	1	1
ENSG00000248448	ENSG00000248448	COX5BP1	4:82347546-82965397	NOTEST	0	0	0	0	1	1
ENSG00000248449	ENSG00000248449	PCDHGB8P	5:140710251-140892546	NOTEST	0.0325255	0.078463	1.27044	0	1	1
ENSG00000248452	ENSG00000248452	RP11-324H7.1	4:26113486-26115461	NOTEST	0	0	0	0	1	1
ENSG00000248455	ENSG00000248455	RP11-321E2.3	5:17404127-17441803	NOTEST	0	0	0	0	1	1
ENSG00000248456	ENSG00000248456	RP11-553P9.3	4:136034059-136044934	NOTEST	0	0	0	0	1	1
ENSG00000248457	ENSG00000248457	RP11-419C19.2	5:12914179-13032998	NOTEST	0	0	0	0	1	1
ENSG00000248458	ENSG00000248458	AL139147.1	1:66999065-67213982	NOTEST	0	0	0	0	1	1
ENSG00000248459	ENSG00000248459	RP11-93K22.1	3:129717373-129717779	NOTEST	0	0.0450708	inf	0	1	1
ENSG00000248462	ENSG00000248462	CTD-2042D5.1	5:13553762-13554075	NOTEST	0	0	0	0	1	1
ENSG00000248464	ENSG00000248464	FGF10-AS1	5:44303645-44414091	NOTEST	0	0	0	0	1	1
ENSG00000248466	ENSG00000248466	RP11-640B6.1	4:35949842-36275842	NOTEST	0	0	0	0	1	1
ENSG00000248467	ENSG00000248467	CTD-2161F6.1	5:4452042-4866334	NOTEST	0	0	0	0	1	1
ENSG00000248468	ENSG00000248468	RP11-517B11.4	3:131236674-131239724	NOTEST	0.0367698	0.0260541	-0.497007	0	1	1
ENSG00000248469	ENSG00000248469	RP11-826N14.2	5:175476680-175559261	NOTEST	0	0	0	0	1	1
ENSG00000248471	ENSG00000248471	RP11-432M8.15	5:17643070-17643337	NOTEST	0	0	0	0	1	1
ENSG00000248472	ENSG00000248472	DDX11L9	15:102500050-102519298	NOTEST	0	0.0335517	inf	0	1	1
ENSG00000248473	ENSG00000248473	CTC-338M12.2	5:180618045-180618852	NOTEST	0	0	0	0	1	1
ENSG00000248474	ENSG00000248474	CTD-2292M14.1	5:73379892-73399041	NOTEST	0	0	0	0	1	1
ENSG00000248475	ENSG00000248475	RP11-479O16.1	5:57878047-58159241	NOTEST	0.121521	0	#NAME?	0	1	1
ENSG00000248476	ENSG00000248476	BACH1-IT1	21:30565800-31312351	NOTEST	0.0457029	0.0161337	-1.50221	0	1	1
ENSG00000248477	ENSG00000248477	RP11-848G14.2	5:68773298-69006341	NOTEST	0	0	0	0	1	1
ENSG00000248478	ENSG00000248478	RP11-3G20.2	8:122684012-122719871	NOTEST	0	0	0	0	1	1
ENSG00000248479	ENSG00000248479	RP11-807H7.2	4:66567919-66571271	NOTEST	0.470636	0.488528	0.0538317	0	1	1
ENSG00000248480	ENSG00000248480	RP11-313E19.1	4:177552542-177554382	NOTEST	0	0	0	0	1	1

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ENSG00000248482	ENSG00000248482	CTC-276P9.3	5:134363424-134736986	NOTEST	0	0	0	0	1	1
ENSG00000248483	ENSG00000248483	POU5F2	5:92953774-93447404	NOTEST	0.0473907	0	#NAME?	0	1	1
ENSG00000248484	ENSG00000248484	RP11-375B1.1	5:176134356-176153244	NOTEST	0	0	0	0	1	1
ENSG00000248485	ENSG00000248485	PCP4L1	1:161228516-161255240	NOTEST	0	0	0	0	1	1
ENSG00000248486	ENSG00000248486	RP1-137K24.1	5:15192247-15266650	NOTEST	0	0	0	0	1	1
ENSG00000248488	ENSG00000248488	PGAM4P2	4:116685254-116685975	NOTEST	0	0	0	0	1	1
ENSG00000248489	ENSG00000248489	CTD-2007H13.3	5:98264874-98330717	NOTEST	0	0.154708	inf	0	1	1
ENSG00000248490	ENSG00000248490	CTD-3007L5.1	5:27412719-27436518	NOTEST	0	0	0	0	1	1
ENSG00000248491	ENSG00000248491	RP11-125O18.1	4:128018045-128391724	NOTEST	0	0	0	0	1	1
ENSG00000248492	ENSG00000248492	ZFAT-AS1	8:135490030-135725292	NOTEST	0	0	0	0	1	1
ENSG00000248493	ENSG00000248493	AC005351.1	5:145316141-145461354	NOTEST	0	0	0	0	1	1
ENSG00000248494	ENSG00000248494	LNX1-AS2	4:54243809-55164414	NOTEST	0	0	0	0	1	1
ENSG00000248496	ENSG00000248496	SCAND3	HSCHR6_MHC_COX:28539407-28555112	NOTEST	0	0	0	0	1	1
ENSG00000248498	ENSG00000248498	ASNSP1	8:47490834-47526145	NOTEST	0	0.00638045	inf	0	1	1
ENSG00000248505	ENSG00000248505	RP11-319E12.1	4:58292037-58332152	NOTEST	0	0	0	0	1	1
ENSG00000248506	ENSG00000248506	RP11-93I21.2	4:125356904-125358275	NOTEST	0	0	0	0	1	1
ENSG00000248507	ENSG00000248507	OR5H4P	3:97940887-97941810	NOTEST	0	0	0	0	1	1
ENSG00000248510	ENSG00000248510	RP11-145G20.1	4:97231851-97740015	NOTEST	0	0	0	0	1	1
ENSG00000248511	ENSG00000248511	RP11-9B6.1	4:93218401-93225329	NOTEST	0	0	0	0	1	1
ENSG00000248514	ENSG00000248514	CTC-338M12.1	5:180632360-180633120	NOTEST	0	0.116073	inf	0	1	1
ENSG00000248515	ENSG00000248515	RP11-608O21.1	4:19173957-19911315	NOTEST	0	0	0	0	1	1
ENSG00000248516	ENSG00000248516	RP11-265O12.1	4:4323688-4335909	NOTEST	0	0	0	0	1	1
ENSG00000248517	ENSG00000248517	RP11-386B13.4	4:185910150-185926340	NOTEST	0.0200716	0	#NAME?	0	1	1
ENSG00000248518	ENSG00000248518	RP11-231C18.2	4:55242168-55242919	NOTEST	0	0	0	0	1	1
ENSG00000248521	ENSG00000248521	RP11-174F8.1	4:151185593-151936879	NOTEST	0	0	0	0	1	1
ENSG00000248522	ENSG00000248522	SBF1P1	8:56014948-56454613	NOTEST	0.00271984	0	#NAME?	0	1	1
ENSG00000248525	ENSG00000248525	CTD-2001E22.1	5:9621488-9903938	NOTEST	0	0	0	0	1	1
ENSG00000248528	ENSG00000248528	CTC-458G6.2	5:92242886-92275298	NOTEST	0	0	0	0	1	1
ENSG00000248529	ENSG00000248529	RP11-2O17.2	5:60933534-61047590	NOTEST	0	0	0	0	1	1
ENSG00000248530	ENSG00000248530	RP11-517B11.2	3:131245290-131246023	NOTEST	0	0	0	0	1	1
ENSG00000248531	ENSG00000248531	NDUFA5P12	8:48001194-48110484	NOTEST	0	0	0	0	1	1
ENSG00000248532	ENSG00000248532	RP11-241F15.5	4:49525664-49525874	NOTEST	0	0	0	0	1	1
ENSG00000248533	ENSG00000248533	CTD-2130F23.1	5:37953503-37967066	NOTEST	0.0877275	0	#NAME?	0	1	1
ENSG00000248537	ENSG00000248537	CTD-2201E9.4	5:9001885-9546187	NOTEST	0	0	0	0	1	1
ENSG00000248538	ENSG00000248538	RP11-10A14.5	8:9046520-9060364	NOTEST	0.397386	0.309827	-0.359078	0	1	1
ENSG00000248539	ENSG00000248539	CTD-2194L12.2	5:37899464-37920971	NOTEST	0	0	0	0	1	1
ENSG00000248540	ENSG00000248540	RP11-247C2.2	15:74392651-74430881	NOTEST	0	0	0	0	1	1
ENSG00000248542	ENSG00000248542	RP11-432M8.16	5:17649154-17649752	NOTEST	0	0	0	0	1	1
ENSG00000248543	ENSG00000248543	NPM1P41	4:82347546-82965397	NOTEST	0	0	0	0	1	1
ENSG00000248544	ENSG00000248544	CTB-47B11.3	5:156687131-157002783	NOTEST	0.0152792	0.0435973	1.51267	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248545	ENSG00000248545	RP11-302F12.3	4:25610332-25621087	NOTEST	0	0	0	0	1	1
ENSG00000248546	ENSG00000248546	ANP32C	4:164445449-165305202	NOTEST	0	0	0	0	1	1
ENSG00000248547	ENSG00000248547	RP11-468N14.6	4:69749602-69750158	NOTEST	0	0	0	0	1	1
ENSG00000248548	ENSG00000248548	MTND4P8	4:156376201-156377563	NOTEST	0	0	0	0	1	1
ENSG00000248550	ENSG00000248550	OTX2-AS1	14:57279900-57618895	NOTEST	0	0	0	0	1	1
ENSG00000248551	ENSG00000248551	RP11-287F9.2	4:176267508-176324261	NOTEST	0	0	0	0	1	1
ENSG00000248552	ENSG00000248552	RP11-138A23.1	4:160296250-160296474	NOTEST	0	0	0	0	1	1
ENSG00000248553	ENSG00000248553	OR52H2P	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000248554	ENSG00000248554	RP11-159F24.6	5:43484060-43525412	NOTEST	0.0686271	0.142018	1.04923	0	1	1
ENSG00000248555	ENSG00000248555	RP11-61G23.1	5:89454155-89585888	NOTEST	0	0	0	0	1	1
ENSG00000248557	ENSG00000248557	RP11-390G14.1	3:126290621-126373998	NOTEST	0.160589	0.259309	0.691304	0	1	1
ENSG00000248559	ENSG00000248559	RP11-215P8.3	5:133735185-133737612	NOTEST	0	0.063369	inf	0	1	1
ENSG00000248560	ENSG00000248560	CTB-14A14.2	5:180541105-180542674	NOTEST	0	0	0	0	1	1
ENSG00000248563	ENSG00000248563	RPSAP2	HSCHR6_MHC_SSTO:28699793-28700681	NOTEST	0	0	0	0	1	1
ENSG00000248564	ENSG00000248564	RP11-478C6.2	4:331602-378653	NOTEST	0.0940031	0.0366319	-1.35961	0	1	1
ENSG00000248565	ENSG00000248565	TECRP2	4:125384017-125384945	NOTEST	0	0	0	0	1	1
ENSG00000248567	ENSG00000248567	RP11-545L5.1	4:72687021-72689697	NOTEST	0	0	0	0	1	1
ENSG00000248568	ENSG00000248568	KRT8P48	5:145942788-146464347	NOTEST	0	0	0	0	1	1
ENSG00000248571	ENSG00000248571	RP11-768B22.2	4:153539783-153601317	NOTEST	0	0	0	0	1	1
ENSG00000248572	ENSG00000248572	EGFLAM-AS2	5:38258510-38468441	NOTEST	0	0	0	0	1	1
ENSG00000248573	ENSG00000248573	PRYP6	Y:20835918-20991373	NOTEST	0	0	0	0	1	1
ENSG00000248574	ENSG00000248574	ADAM20P2	4:176496018-176497291	NOTEST	0	0	0	0	1	1
ENSG00000248576	ENSG00000248576	RP11-834C11.8	12:54555848-54582778	NOTEST	0	0	0	0	1	1
ENSG00000248577	ENSG00000248577	RP11-122C5.2	5:38736156-38845931	NOTEST	0	0	0	0	1	1
ENSG00000248578	ENSG00000248578	NPM1P21	8:57013757-57014826	NOTEST	0	0	0	0	1	1
ENSG00000248585	ENSG00000248585	RP11-90P5.1	8:37962759-38070819	NOTEST	0	0	0	0	1	1
ENSG00000248586	ENSG00000248586	CTD-2516K3.3	5:56613815-56615847	NOTEST	0.0239406	0.0224288	-0.0941104	0	1	1
ENSG00000248588	ENSG00000248588	CTC-458G6.4	5:92161961-92179711	NOTEST	0	0	0	0	1	1
ENSG00000248590	ENSG00000248590	GLDCP1	4:57396774-57469673	NOTEST	0	0	0	0	1	1
ENSG00000248591	ENSG00000248591	CTD-2351A8.1	5:23456576-23456959	NOTEST	0	0	0	0	1	1
ENSG00000248596	ENSG00000248596	RP11-844P9.2	5:175564159-175626298	NOTEST	0.0263368	0.00301167	-3.12844	0	1	1
ENSG00000248597	ENSG00000248597	RP11-259O2.2	5:1963722-1967268	NOTEST	0	0	0	0	1	1
ENSG00000248599	ENSG00000248599	RP11-302J23.1	8:102064281-102088479	NOTEST	0	0	0	0	1	1
ENSG00000248600	ENSG00000248600	CTD-2308B18.4	5:123791065-123796242	NOTEST	0	0	0	0	1	1
ENSG00000248601	ENSG00000248601	RP11-310I9.1	4:168867824-169108841	NOTEST	0	0	0	0	1	1
ENSG00000248605	ENSG00000248605	CTD-2306M5.1	5:25404841-25446034	NOTEST	0	0	0	0	1	1
ENSG00000248607	ENSG00000248607	RP11-158I23.1	3:125725197-125820404	NOTEST	0	0	0	0	1	1
ENSG00000248608	ENSG00000248608	RP11-206P5.2	4:25506618-25508297	NOTEST	0.00984844	0	#NAME?	0	1	1
ENSG00000248610	ENSG00000248610	HSPA8P4	5:128795251-129522327	NOTEST	0.0578411	0.0436632	-0.405679	0	1	1
ENSG00000248611	ENSG00000248611	RP11-158C21.3	4:155476359-155477137	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000248616	ENSG00000248616	CTB-1I21.2	5:136193316-136194031	NOTEST	0	0	0	0	1	1
ENSG00000248618	ENSG00000248618	ENPP7P3	3:129886632-129886873	NOTEST	0	0	0	0	1	1
ENSG00000248621	ENSG00000248621	RP11-5K16.3	4:141521554-141521729	NOTEST	0	0	0	0	1	1
ENSG00000248624	ENSG00000248624	RP11-5N11.2	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000248625	ENSG00000248625	RP11-205M3.1	4:170753803-170754514	NOTEST	0	0	0	0	1	1
ENSG00000248626	ENSG00000248626	GAPDHP40	5:159343789-159399551	NOTEST	0.381066	0.129516	-1.55691	0	1	1
ENSG00000248627	ENSG00000248627	RP11-428L21.1	4:93225549-94695707	NOTEST	0	0	0	0	1	1
ENSG00000248629	ENSG00000248629	RP11-154F14.2	4:157681605-157892546	NOTEST	0	0	0	0	1	1
ENSG00000248631	ENSG00000248631	RP11-425E13.1	5:124537580-124538223	NOTEST	0	0	0	0	1	1
ENSG00000248632	ENSG00000248632	RP11-366M4.11	4:165869230-165899980	NOTEST	0	0	0	0	1	1
ENSG00000248633	ENSG00000248633	WRBP1	4:113614202-113627966	NOTEST	0	0	0	0	1	1
ENSG00000248634	ENSG00000248634	CTC-573M9.1	5:127593600-128369335	NOTEST	0	0	0	0	1	1
ENSG00000248635	ENSG00000248635	RP11-1267H10.4	4:69570317-69578216	NOTEST	0	0	0	0	1	1
ENSG00000248636	ENSG00000248636	RP11-768F21.1	12:119772516-120119435	NOTEST	0	0	0	0	1	1
ENSG00000248637	ENSG00000248637	RP11-485C11.1	4:172733404-173962710	NOTEST	0	0	0	0	1	1
ENSG00000248639	ENSG00000248639	RP11-642E20.2	4:69158844-69160082	NOTEST	0	0	0	0	1	1
ENSG00000248640	ENSG00000248640	HNRNPA1P56	4:78909013-78909967	NOTEST	0	0	0	0	1	1
ENSG00000248642	ENSG00000248642	OR10J2P	1:159248830-159249791	NOTEST	0	0	0	0	1	1
ENSG00000248645	ENSG00000248645	RP11-366M4.6	4:165859473-165861142	NOTEST	0	0	0	0	1	1
ENSG00000248646	ENSG00000248646	RP11-567N4.2	4:76194277-76359659	NOTEST	0	0	0	0	1	1
ENSG00000248647	ENSG00000248647	RP11-331K21.1	5:148521045-148721365	NOTEST	0	0	0	0	1	1
ENSG00000248648	ENSG00000248648	RP11-485M7.1	5:132332676-132362296	NOTEST	0.18253	0	#NAME?	0	1	1
ENSG00000248651	ENSG00000248651	GCSHP1	5:39888677-39889161	NOTEST	0	0	0	0	1	1
ENSG00000248652	ENSG00000248652	RP11-101B14.4	5:56377571-56377778	NOTEST	0	0	0	0	1	1
ENSG00000248654	ENSG00000248654	RP11-302F12.5	4:25722137-25722678	NOTEST	0	0	0	0	1	1
ENSG00000248655	ENSG00000248655	NOL5BP	HSCHR6_MHC_SSTO:28751411-28751783	NOTEST	0	0	0	0	1	1
ENSG00000248656	ENSG00000248656	RP11-255I10.2	4:112561650-112569964	NOTEST	0	0	0	0	1	1
ENSG00000248659	ENSG00000248659	RP11-263I1.1	3:129350861-129351335	NOTEST	0	0	0	0	1	1
ENSG00000248660	ENSG00000248660	SRIP1	4:58969312-58969600	NOTEST	0	0	0	0	1	1
ENSG00000248663	ENSG00000248663	LINC00992	5:116751204-116881993	NOTEST	0.0700512	0.0535829	-0.386637	0	1	1
ENSG00000248664	ENSG00000248664	CTC-498J12.3	5:68389472-68432221	NOTEST	0.115011	0.0435059	-1.4025	0	1	1
ENSG00000248667	ENSG00000248667	CTD-2331D11.2	5:84715845-84716269	NOTEST	0	0	0	0	1	1
ENSG00000248669	ENSG00000248669	RP11-489M13.2	4:4119651-4120011	NOTEST	0	0	0	0	1	1
ENSG00000248671	ENSG00000248671	CTD-2313N18.5	11:71498555-71532594	NOTEST	0.0458679	0.126615	1.46489	0	1	1
ENSG00000248672	ENSG00000248672	LY75-CD302	2:160568999-160761260	NOTEST	0.00219053	0.00226635	0.0490964	0	1	1
ENSG00000248673	ENSG00000248673	CTC-419K13.1	5:73665200-73832801	NOTEST	0	0	0	0	1	1
ENSG00000248674	ENSG00000248674	RBBP4P6	5:84486446-84486648	NOTEST	0	0	0	0	1	1
ENSG00000248676	ENSG00000248676	RP11-766F14.1	4:100467865-100547070	NOTEST	0	0	0	0	1	1
ENSG00000248677	ENSG00000248677	CTD-2044J15.1	5:6686437-6707824	NOTEST	0.0261064	0.0202853	-0.363966	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248682	ENSG00000248682	ARHGAP22-IT1	10:49654076-49864310	NOTEST	0	0	0	0	1	1
ENSG00000248684	ENSG00000248684	BIN2P2	5:75206107-75207692	NOTEST	0	0	0	0	1	1
ENSG00000248685	ENSG00000248685	RP11-548L20.1	4:34122515-34271369	NOTEST	0	0	0	0	1	1
ENSG00000248686	ENSG00000248686	RP11-557J10.5	4:146520260-146521704	NOTEST	0	0	0	0	1	1
ENSG00000248687	ENSG00000248687	RP11-42L13.2	5:29104986-29105545	NOTEST	0	0	0	0	1	1
ENSG00000248692	ENSG00000248692	RP11-84A1.3	4:62066975-63031272	NOTEST	0	0	0	0	1	1
ENSG00000248693	ENSG00000248693	CTD-2023M8.1	5:18704541-18746282	NOTEST	0.411433	0	#NAME?	0	1	1
ENSG00000248694	ENSG00000248694	RP11-18D7.2	4:182795590-183724177	NOTEST	0	0	0	0	1	1
ENSG00000248696	ENSG00000248696	AC011406.2	5:149340299-149432386	NOTEST	0	0	0	0	1	1
ENSG00000248697	ENSG00000248697	TOX4P1	4:113377079-113378941	NOTEST	0	0	0	0	1	1
ENSG00000248698	ENSG00000248698	LINC01085	4:14113591-14145216	NOTEST	0.0312346	0	#NAME?	0	1	1
ENSG00000248699	ENSG00000248699	CTD-2313D3.1	5:15450809-15451920	NOTEST	0	0	0	0	1	1
ENSG00000248701	ENSG00000248701	CTC-493L21.2	5:86093501-86096097	NOTEST	0	0	0	0	1	1
ENSG00000248702	ENSG00000248702	RP11-294J22.5	17:48874726-48875012	NOTEST	0	0	0	0	1	1
ENSG00000248703	ENSG00000248703	RP11-495K9.3	12:131780066-131782763	NOTEST	0	0	0	0	1	1
ENSG00000248704	ENSG00000248704	MTND4P2	7:63560682-63611099	NOTEST	0	0	0	0	1	1
ENSG00000248705	ENSG00000248705	AC114812.10	2:234526290-234681956	NOTEST	0	0	0	0	1	1
ENSG00000248708	ENSG00000248708	CTD-2316B1.2	5:87008951-87029086	NOTEST	0	0	0	0	1	1
ENSG00000248709	ENSG00000248709	CTC-505O3.2	5:115091340-115091983	NOTEST	0	0	0	0	1	1
ENSG00000248710	ENSG00000248710	RP11-432B6.3	3:159943422-160203561	NOTEST	0.0708994	0	#NAME?	0	1	1
ENSG00000248711	ENSG00000248711	AC006023.8	7:40174574-40900362	NOTEST	0	0	0	0	1	1
ENSG00000248712	ENSG00000248712	CCDC153	11:119056165-119067479	NOTEST	0.513646	0.380386	-0.433309	0	1	1
ENSG00000248713	ENSG00000248713	RP11-766F14.2	4:100557685-100575805	NOTEST	0.196617	0.280685	0.513566	0	1	1
ENSG00000248715	ENSG00000248715	RP11-758B24.1	4:132301167-132462552	NOTEST	0	0	0	0	1	1
ENSG00000248716	ENSG00000248716	RP11-362M19.1	4:115025093-115025381	NOTEST	0	0	0	0	1	1
ENSG00000248717	ENSG00000248717	RP11-451H23.3	5:180111765-180113546	NOTEST	0	0	0	0	1	1
ENSG00000248719	ENSG00000248719	RP11-377G16.2	4:81104433-81125483	NOTEST	0	0	0	0	1	1
ENSG00000248720	ENSG00000248720	RFPL4AP5	8:127186429-127187258	NOTEST	0	0	0	0	1	1
ENSG00000248722	ENSG00000248722	AK3P4	5:114738076-114738659	NOTEST	0	0	0	0	1	1
ENSG00000248724	ENSG00000248724	NPHP3-AS1	3:132276981-132593067	NOTEST	0	0.00894209	inf	0	1	1
ENSG00000248725	ENSG00000248725	RP11-218C23.1	4:86167309-86168065	NOTEST	0	0	0	0	1	1
ENSG00000248727	ENSG00000248727	CTC-236F12.4	5:55753621-55777773	NOTEST	0.167614	0.17325	0.0477114	0	1	1
ENSG00000248729	ENSG00000248729	RP11-531A21.3	5:5395490-5396070	NOTEST	0.0363203	0.0257322	-0.497199	0	1	1
ENSG00000248730	ENSG00000248730	EGFLAM-AS4	5:38258510-38468441	NOTEST	0	0	0	0	1	1
ENSG00000248731	ENSG00000248731	AC090103.1	8:25699245-25902913	NOTEST	0	0	0	0	1	1
ENSG00000248733	ENSG00000248733	CTD-2176I21.2	5:57878047-58159241	NOTEST	0.0994615	0	#NAME?	0	1	1
ENSG00000248734	ENSG00000248734	CTD-2260A17.1	5:95220801-96143803	NOTEST	0.0946846	0.111327	0.233599	0	1	1
ENSG00000248735	ENSG00000248735	R3HDM2P1	4:133996465-134070271	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248736	ENSG00000248736	RP11-35O7.1	5:2965119-2967742	NOTEST	0	0	0	0	1	1
ENSG00000248738	ENSG00000248738	RP11-87E22.2	8:22545171-22941132	NOTEST	0	0	0	0	1	1
ENSG00000248739	ENSG00000248739	RP11-654F3.1	4:171062442-171063683	NOTEST	0	0	0	0	1	1
ENSG00000248740	ENSG00000248740	RP11-328K4.1	4:104177315-104374815	NOTEST	0	0	0	0	1	1
ENSG00000248744	ENSG00000248744	RP11-362I1.1	4:45011556-45053669	NOTEST	0	0	0	0	1	1
ENSG00000248745	ENSG00000248745	NMNAT1P4	4:146377156-146377996	NOTEST	0	0	0	0	1	1
ENSG00000248746	ENSG00000248746	ACTN3	11:66313865-66330800	NOTEST	0.0107282	0.0117708	0.133798	0	1	1
ENSG00000248747	ENSG00000248747	RP11-586L23.1	4:142161892-142199943	NOTEST	0	0	0	0	1	1
ENSG00000248748	ENSG00000248748	MTND5P9	4:156374200-156375955	NOTEST	0	0	0	0	1	1
ENSG00000248749	ENSG00000248749	RP11-42A4.1	4:85292545-85301342	NOTEST	0	0	0	0	1	1
ENSG00000248750	ENSG00000248750	RP11-131K17.1	4:93225549-94695707	NOTEST	0	0	0	0	1	1
ENSG00000248751	ENSG00000248751	RP1-130H16.18	22:30681105-30723035	NOTEST	0.545203	0.495903	-0.136735	0	1	1
ENSG00000248752	ENSG00000248752	RP11-114J13.1	5:125412492-125615493	NOTEST	0	0	0	0	1	1
ENSG00000248753	ENSG00000248753	CTC-276P9.2	5:134363424-134736986	NOTEST	0	0	0	0	1	1
ENSG00000248755	ENSG00000248755	RP11-384D10.1	4:172090359-172091093	NOTEST	0	0	0	0	1	1
ENSG00000248757	ENSG00000248757	CTD-2193G5.1	5:102865376-102877686	NOTEST	0	0	0	0	1	1
ENSG00000248758	ENSG00000248758	CTD-2215E18.2	5:96424778-96772921	NOTEST	0	0	0	0	1	1
ENSG00000248760	ENSG00000248760	RP11-727M10.2	4:75418300-75514664	NOTEST	0	0	0	0	1	1
ENSG00000248761	ENSG00000248761	CTD-2593A12.2	5:180394188-180397762	NOTEST	0	0	0	0	1	1
ENSG00000248762	ENSG00000248762	RP11-31K23.2	8:96998335-97005331	NOTEST	0	0	0	0	1	1
ENSG00000248763	ENSG00000248763	RP13-644M16.5	4:69917080-69978705	NOTEST	0	0	0	0	1	1
ENSG00000248764	ENSG00000248764	RP11-292D4.2	4:147627789-147867034	NOTEST	0	0	0	0	1	1
ENSG00000248765	ENSG00000248765	RP11-417J1.3	5:8619289-8620422	NOTEST	0	0.0108716	inf	0	1	1
ENSG00000248766	ENSG00000248766	RP11-61K20.1	5:19473059-20575982	NOTEST	0	0	0	0	1	1
ENSG00000248767	ENSG00000248767	WI2-2373I1.2	7:331309-334388	NOTEST	0	0	0	0	1	1
ENSG00000248769	ENSG00000248769	RP11-974F13.5	5:68773298-69006341	NOTEST	0	0	0	0	1	1
ENSG00000248770	ENSG00000248770	RP11-665C14.1	4:182158510-182158717	NOTEST	0	0	0	0	1	1
ENSG00000248771	ENSG00000248771	RP11-294O2.2	4:165675215-165724947	NOTEST	0	0.0599462	inf	0	1	1
ENSG00000248772	ENSG00000248772	RP11-639F1.1	3:155093368-155462856	NOTEST	0	0	0	0	1	1
ENSG00000248773	ENSG00000248773	RP11-231L11.3	3:140660671-140698775	NOTEST	0.193323	0.299134	0.629781	0	1	1
ENSG00000248774	ENSG00000248774	RP11-798M19.3	4:174053078-174250845	NOTEST	0	0	0	0	1	1
ENSG00000248775	ENSG00000248775	RP11-404K5.3	5:7288036-7288590	NOTEST	0	0	0	0	1	1
ENSG00000248777	ENSG00000248777	AC006499.6	4:10201446-10202296	NOTEST	0	0	0	0	1	1
ENSG00000248778	ENSG00000248778	RP11-311D14.1	4:106473776-106943635	NOTEST	0	0.0132133	inf	0	1	1
ENSG00000248779	ENSG00000248779	RP11-53O19.2	5:44745001-44808879	NOTEST	0	0	0	0	1	1
ENSG00000248780	ENSG00000248780	RP11-632F7.1	4:40751913-40812002	NOTEST	0	0	0	0	1	1
ENSG00000248781	ENSG00000248781	PSMC1P4	5:55571130-55572457	NOTEST	0	0	0	0	1	1
ENSG00000248783	ENSG00000248783	RP11-308B16.2	5:12554001-12574749	NOTEST	0.147369	0.0575626	-1.35623	0	1	1
ENSG00000248785	ENSG00000248785	HIGD1AP14	4:110481360-110624739	NOTEST	0	0	0	0	1	1
ENSG00000248787	ENSG00000248787	RP11-666A20.4	3:125546080-125629115	NOTEST	0.231917	0.261229	0.171708	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000248790	ENSG00000248790	RP11-319G6.3	3:139108656-139396859	NOTEST	0	0	0	0	1	1
ENSG00000248791	ENSG00000248791	CTD-2165H16.3	5:14620128-14621422	NOTEST	0	0	0	0	1	1
ENSG00000248792	ENSG00000248792	LINC00266-2P	Y:26424483-26437493	NOTEST	0	0	0	0	1	1
ENSG00000248794	ENSG00000248794	CTD-2248H3.1	5:80243515-80597379	NOTEST	0.434305	0.769467	0.825153	0	1	1
ENSG00000248795	ENSG00000248795	RP11-173E2.1	4:139481857-139483095	NOTEST	0	0.0108205	inf	0	1	1
ENSG00000248796	ENSG00000248796	MED15P8	2:131862419-132111282	NOTEST	0	0	0	0	1	1
ENSG00000248799	ENSG00000248799	CTC-548H10.2	5:126984735-126999721	NOTEST	0	0	0	0	1	1
ENSG00000248801	ENSG00000248801	RP11-664D7.4	8:69215702-69731257	NOTEST	0	0	0	0	1	1
ENSG00000248802	ENSG00000248802	RP11-184M15.2	4:129504153-129522562	NOTEST	0	0	0	0	1	1
ENSG00000248803	ENSG00000248803	RP11-287J9.1	5:65892175-66465423	NOTEST	0	0	0	0	1	1
ENSG00000248807	ENSG00000248807	KRTAP9-12P	17:39368957-39369489	NOTEST	0	0	0	0	1	1
ENSG00000248809	ENSG00000248809	LINC01095	4:147030606-147043065	NOTEST	0	0	0	0	1	1
ENSG00000248810	ENSG00000248810	RP11-362F19.1	4:142240603-142253772	NOTEST	0	0	0	0	1	1
ENSG00000248813	ENSG00000248813	RP11-5N11.4	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000248816	ENSG00000248816	RP11-18D7.3	4:182795590-183724177	NOTEST	0	0	0	0	1	1
ENSG00000248817	ENSG00000248817	RP11-562F9.1	4:93103627-93105203	NOTEST	0	0.00743282	inf	0	1	1
ENSG00000248820	ENSG00000248820	RP11-15B17.3	4:100869242-101136662	NOTEST	0	0	0	0	1	1
ENSG00000248821	ENSG00000248821	AC009238.6	2:96068468-96082364	NOTEST	0	0	0	0	1	1
ENSG00000248822	ENSG00000248822	APOBEC3AP1	4:171020968-171021255	NOTEST	0	0	0	0	1	1
ENSG00000248824	ENSG00000248824	RP11-790I12.6	4:70272648-70273373	NOTEST	0	0	0	0	1	1
ENSG00000248826	ENSG00000248826	PCBP2P3	5:91139503-91140346	NOTEST	0	0	0	0	1	1
ENSG00000248827	ENSG00000248827	RP11-252I13.1	5:107060661-107062818	NOTEST	0	0	0	0	1	1
ENSG00000248828	ENSG00000248828	RP11-673E1.4	4:144833483-145061904	NOTEST	0	0	0	0	1	1
ENSG00000248830	ENSG00000248830	ZNF807	19:35033366-35036300	NOTEST	0	0	0	0	1	1
ENSG00000248831	ENSG00000248831	CTB-179I1.2	4:78078303-78415440	NOTEST	0	0	0	0	1	1
ENSG00000248834	ENSG00000248834	MARK2P5	5:15384328-15384962	NOTEST	0	0	0	0	1	1
ENSG00000248837	ENSG00000248837	RP11-412P11.1	4:22999173-23058485	NOTEST	0	0	0	0	1	1
ENSG00000248838	ENSG00000248838	PGAM1P13	8:108659506-108660260	NOTEST	0	0	0	0	1	1
ENSG00000248839	ENSG00000248839	RP11-227H4.5	3:98216447-98312567	NOTEST	0	0.0489249	inf	0	1	1
ENSG00000248840	ENSG00000248840	RP11-357G3.2	4:3294754-3441640	NOTEST	0	0.308332	inf	0	1	1
ENSG00000248842	ENSG00000248842	CTB-1H10.1	5:145780543-145786922	NOTEST	0.104069	0	#NAME?	0	1	1
ENSG00000248843	ENSG00000248843	RP11-357G3.1	4:3294754-3441640	NOTEST	0	0	0	0	1	1
ENSG00000248844	ENSG00000248844	RP11-626H12.3	11:69902335-69911477	NOTEST	0	0	0	0	1	1
ENSG00000248846	ENSG00000248846	CTD-2016O11.1	5:65502039-65505275	NOTEST	0	0	0	0	1	1
ENSG00000248847	ENSG00000248847	RP11-26C10.1	4:63355212-63355936	NOTEST	0	0	0	0	1	1
ENSG00000248848	ENSG00000248848	PPBPP2	4:74919754-74921116	NOTEST	0	0	0	0	1	1
ENSG00000248850	ENSG00000248850	RP11-605F14.2	3:126390948-126392066	NOTEST	0	0	0	0	1	1
ENSG00000248851	ENSG00000248851	AC006427.2	4:16162127-16321763	NOTEST	0	0	0	0	1	1
ENSG00000248853	ENSG00000248853	CTD-2613O8.1	5:120394938-120396648	NOTEST	0	0	0	0	1	1
ENSG00000248854	ENSG00000248854	HNRNPH1P3	5:55134628-55135853	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248858	ENSG00000248858	RP11-100L22.2	8:93711969-93889865	NOTEST	0	0	0	0	1	1
ENSG00000248859	ENSG00000248859	RP11-375B1.3	5:176170205-176170872	NOTEST	0	0	0	0	1	1
ENSG00000248861	ENSG00000248861	RP11-321E2.2	5:17518474-17519069	NOTEST	0	0	0	0	1	1
ENSG00000248863	ENSG00000248863	RP11-83A24.1	4:140187316-140397763	NOTEST	0	0	0	0	1	1
ENSG00000248864	ENSG00000248864	RP11-348J24.1	5:91378413-92023961	NOTEST	0	0	0	0	1	1
ENSG00000248867	ENSG00000248867	CTD-2128F4.1	5:108784049-108784764	NOTEST	0	0	0	0	1	1
ENSG00000248869	ENSG00000248869	RP11-138I17.1	4:137717876-138133953	NOTEST	0	0.00697466	inf	0	1	1
ENSG00000248870	ENSG00000248870	CTD-2015A6.2	5:81882594-81883230	NOTEST	0	0	0	0	1	1
ENSG00000248871	ENSG00000248871	TNFSF12-TNFSF13	17:7452207-7464925	NOTEST	0	0.173013	inf	0	1	1
ENSG00000248872	ENSG00000248872	RP11-344G13.1	4:171961752-171980314	NOTEST	0	0	0	0	1	1
ENSG00000248874	ENSG00000248874	C5orf17	5:23951456-24178372	NOTEST	0	0.00636508	inf	0	1	1
ENSG00000248876	ENSG00000248876	RP11-231G15.3	5:108806543-108807287	NOTEST	0	0	0	0	1	1
ENSG00000248877	ENSG00000248877	PGBD4P4	4:131415827-131416440	NOTEST	0	0	0	0	1	1
ENSG00000248878	ENSG00000248878	RP11-5N11.1	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000248880	ENSG00000248880	NARG2P1	4:189308624-189310820	NOTEST	0	0	0	0	1	1
ENSG00000248881	ENSG00000248881	CTC-366B18.2	5:74664310-74896969	NOTEST	0.0354374	0.115217	1.70101	0	1	1
ENSG00000248883	ENSG00000248883	CTD-2244F11.2	17:47162872-47164064	NOTEST	0	0	0	0	1	1
ENSG00000248884	ENSG00000248884	CTC-537E7.3	5:67726253-67730308	NOTEST	0.0620776	0.0443093	-0.486464	0	1	1
ENSG00000248885	ENSG00000248885	RP11-950K24.2	5:118342041-118584833	NOTEST	0	0	0	0	1	1
ENSG00000248886	ENSG00000248886	UGT2A3P7	4:70345882-70391732	NOTEST	0	0	0	0	1	1
ENSG00000248890	ENSG00000248890	HHIP-AS1	4:145564073-145666423	NOTEST	0.0374084	0.142508	1.92961	0	1	1
ENSG00000248891	ENSG00000248891	CTD-2335O3.2	5:50723829-50724261	NOTEST	0	0	0	0	1	1
ENSG00000248893	ENSG00000248893	FAM138E	15:102495087-102496615	NOTEST	0	0.0956385	inf	0	1	1
ENSG00000248895	ENSG00000248895	RP11-463M16.5	17:46952221-47006418	NOTEST	0	0	0	0	1	1
ENSG00000248896	ENSG00000248896	CTD-2135J3.3	8:10581277-10697394	NOTEST	0	0.0874157	inf	0	1	1
ENSG00000248898	ENSG00000248898	CTD-2288O8.1	5:51971026-52390609	NOTEST	0	0	0	0	1	1
ENSG00000248901	ENSG00000248901	AC008834.1	5:97421963-97496897	NOTEST	0	0	0	0	1	1
ENSG00000248903	ENSG00000248903	AP000867.14	11:71276608-71279980	NOTEST	0	0	0	0	1	1
ENSG00000248907	ENSG00000248907	MTND2P33	4:156382784-156383815	NOTEST	0	0	0	0	1	1
ENSG00000248908	ENSG00000248908	RP11-730N24.1	5:24835388-24840692	NOTEST	0	0	0	0	1	1
ENSG00000248909	ENSG00000248909	HMGB1P21	5:77781037-78065844	NOTEST	0.0724634	0.110389	0.607277	0	1	1
ENSG00000248911	ENSG00000248911	RP11-182E14.1	8:53887670-53888676	NOTEST	0	0	0	0	1	1
ENSG00000248912	ENSG00000248912	RP11-171N4.4	4:157607815-157613788	NOTEST	0	0	0	0	1	1
ENSG00000248913	ENSG00000248913	PHBP14	4:168569580-168569947	NOTEST	0	0	0	0	1	1
ENSG00000248915	ENSG00000248915	ACTR6P1	4:107757654-107758758	NOTEST	0	0	0	0	1	1
ENSG00000248916	ENSG00000248916	NUP210P3	3:129033614-129045068	NOTEST	0	0	0	0	1	1
ENSG00000248918	ENSG00000248918	CTD-2089N3.3	5:50265050-50266021	NOTEST	0	0	0	0	1	1
ENSG00000248920	ENSG00000248920	USP17L19	4:9255103-9256696	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248921	ENSG00000248921	RP11-774G5.1	4:180778005-180778734	NOTEST	0	0	0	0	1	1
ENSG00000248923	ENSG00000248923	MTND5P11	5:134240595-134347392	NOTEST	0.0181007	0	#NAME?	0	1	1
ENSG00000248924	ENSG00000248924	RP11-481K16.2	4:144434615-144478639	NOTEST	0	0	0	0	1	1
ENSG00000248925	ENSG00000248925	CTD-2083E4.6	5:269972-271631	NOTEST	0.532353	0.44428	-0.260914	0	1	1
ENSG00000248926	ENSG00000248926	RP11-777B9.1	4:78879153-78879934	NOTEST	0	0	0	0	1	1
ENSG00000248927	ENSG00000248927	CTD-2334D19.1	5:120116912-120126473	NOTEST	0.162033	0	#NAME?	0	1	1
ENSG00000248928	ENSG00000248928	CTD-2151A2.3	5:98930583-98931001	NOTEST	0	0	0	0	1	1
ENSG00000248929	ENSG00000248929	HIGD1AP3	5:174059934-174060212	NOTEST	0	0	0	0	1	1
ENSG00000248930	ENSG00000248930	CTC-250P20.1	5:72251807-72386349	NOTEST	0	0	0	0	1	1
ENSG00000248931	ENSG00000248931	RP11-72K17.2	5:97013250-97014385	NOTEST	0	0	0	0	1	1
ENSG00000248933	ENSG00000248933	USP17L22	4:9269344-9270937	NOTEST	0	0	0	0	1	1
ENSG00000248935	ENSG00000248935	CTD-2254N19.1	5:58264864-59843484	NOTEST	0	0	0	0	1	1
ENSG00000248936	ENSG00000248936	RP11-36B15.1	4:37455562-37687998	NOTEST	0.233921	0.0318764	-2.87546	0	1	1
ENSG00000248939	ENSG00000248939	RP11-395F4.1	4:43135883-43236973	NOTEST	0	0	0	0	1	1
ENSG00000248942	ENSG00000248942	CTD-2275D24.4	5:73602234-73604150	NOTEST	0	0	0	0	1	1
ENSG00000248943	ENSG00000248943	RP11-1026M7.3	5:177228204-177230345	NOTEST	0	0	0	0	1	1
ENSG00000248944	ENSG00000248944	FAM90A6P	8:7406574-7409584	NOTEST	0	0	0	0	1	1
ENSG00000248946	ENSG00000248946	RP11-1281K21.7	4:49248617-49248932	NOTEST	0	0	0	0	1	1
ENSG00000248949	ENSG00000248949	RP11-661C8.2	5:946429-956635	NOTEST	0	0	0	0	1	1
ENSG00000248950	ENSG00000248950	LDHBP3	5:92161961-92179711	NOTEST	0	0	0	0	1	1
ENSG00000248951	ENSG00000248951	RP11-325I22.1	5:1363696-1380182	NOTEST	0	0	0	0	1	1
ENSG00000248954	ENSG00000248954	RP11-304F15.4	17:47964960-47978257	NOTEST	0	0	0	0	1	1
ENSG00000248955	ENSG00000248955	RP11-114H7.3	5:130344275-130344435	NOTEST	0	0	0	0	1	1
ENSG00000248956	ENSG00000248956	HMGB1P44	4:78885093-78885665	NOTEST	0	0	0	0	1	1
ENSG00000248958	ENSG00000248958	ZSWIM5P3	4:130057080-130060895	NOTEST	0	0	0	0	1	1
ENSG00000248962	ENSG00000248962	CTD-2287N17.1	5:4012821-4013763	NOTEST	0	0	0	0	1	1
ENSG00000248965	ENSG00000248965	CTB-174D11.2	5:168081517-168728133	NOTEST	0	0	0	0	1	1
ENSG00000248966	ENSG00000248966	CTD-2089O24.1	5:110283727-110286479	NOTEST	0	0	0	0	1	1
ENSG00000248967	ENSG00000248967	RP11-241J12.3	5:79922046-80172279	NOTEST	0	0	0	0	1	1
ENSG00000248968	ENSG00000248968	CTD-2256P15.1	5:10226441-10250027	NOTEST	0.196533	0.0629825	-1.64175	0	1	1
ENSG00000248969	ENSG00000248969	CTD-2113L7.1	5:35617945-35827120	NOTEST	0	0	0	0	1	1
ENSG00000248971	ENSG00000248971	KRT8P46	4:103552659-103682151	NOTEST	0.235507	0.164798	-0.51507	0	1	1
ENSG00000248973	ENSG00000248973	RP11-445O3.2	5:4452042-4866334	NOTEST	0	0	0	0	1	1
ENSG00000248975	ENSG00000248975	CTD-2251F13.1	14:30045686-30766249	NOTEST	0	0	0	0	1	1
ENSG00000248977	ENSG00000248977	RP11-395I6.1	4:40044536-40159872	NOTEST	0	0	0	0	1	1
ENSG00000248978	ENSG00000248978	RP11-98H4.1	8:85095021-85834079	NOTEST	0	0	0	0	1	1
ENSG00000248979	ENSG00000248979	LAMTOR3P2	5:118342041-118584833	NOTEST	0	0	0	0	1	1
ENSG00000248980	ENSG00000248980	RP11-87F15.2	4:177229418-177253396	NOTEST	0	0	0	0	1	1
ENSG00000248984	ENSG00000248984	AC004054.1	4:91048685-92523064	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000248986	ENSG00000248986	RP11-774O3.1	4:8321902-8325692	NOTEST	0	0	0	0	1	1
ENSG00000248987	ENSG00000248987	PRDX4P1	4:44946031-44946978	NOTEST	0	0	0	0	1	1
ENSG00000248988	ENSG00000248988	RP11-815N9.2	4:159690289-159959912	NOTEST	0.0500062	0.0656858	0.393475	0	1	1
ENSG00000248989	ENSG00000248989	STK19P	HSCHR6_MHC_SSTO:31965199-32027628	NOTEST	0	0	0	0	1	1
ENSG00000248990	ENSG00000248990	RP11-960D24.1	11:28700729-28705016	NOTEST	0	0	0	0	1	1
ENSG00000248991	ENSG00000248991	RP11-73G16.2	4:152826083-152865085	NOTEST	0	0	0	0	1	1
ENSG00000248993	ENSG00000248993	XXbac-BPG181M17.5	6:32902405-32949282	NOTEST	0	0	0	0	1	1
ENSG00000248994	ENSG00000248994	RP11-259O2.1	5:1933976-1959290	NOTEST	0	0	0	0	1	1
ENSG00000248995	ENSG00000248995	RP11-766N7.4	12:65277173-65376304	NOTEST	0	0	0	0	1	1
ENSG00000248996	ENSG00000248996	RP11-1334A24.6	5:176910394-176938275	NOTEST	0	0.0440265	inf	0	1	1
ENSG00000248998	ENSG00000248998	EFTUD1P2	4:66008420-66011481	NOTEST	0	0	0	0	1	1
ENSG00000248999	ENSG00000248999	WI2-2373I1.1	7:330616-330787	NOTEST	0	0	0	0	1	1
ENSG00000249000	ENSG00000249000	CTD-2012I17.1	4:135680553-135738444	NOTEST	0	0	0	0	1	1
ENSG00000249001	ENSG00000249001	RP11-742B18.1	4:88489186-88655108	NOTEST	0	0	0	0	1	1
ENSG00000249002	ENSG00000249002	RP11-358D17.1	4:119809995-119982402	NOTEST	0	0	0	0	1	1
ENSG00000249003	ENSG00000249003	CLUHP4	4:190979056-190984160	NOTEST	0	0	0	0	1	1
ENSG00000249004	ENSG00000249004	RP11-752L20.1	4:148379875-148380473	NOTEST	0	0	0	0	1	1
ENSG00000249005	ENSG00000249005	FAM90A4P	8:7122047-7132680	NOTEST	0	0	0	0	1	1
ENSG00000249006	ENSG00000249006	RP11-317B7.2	4:2073644-2243891	NOTEST	0	0.00603726	inf	0	1	1
ENSG00000249007	ENSG00000249007	RP11-510N19.5	1:201951499-201986316	NOTEST	0	0.0222613	inf	0	1	1
ENSG00000249008	ENSG00000249008	RP11-487E13.1	4:178163692-178169927	NOTEST	0	0	0	0	1	1
ENSG00000249012	ENSG00000249012	RP11-731D1.1	4:152020724-152246784	NOTEST	0	0	0	0	1	1
ENSG00000249013	ENSG00000249013	FTH1P21	4:156927629-156928140	NOTEST	0	0	0	0	1	1
ENSG00000249014	ENSG00000249014	HMGN2P4	5:75377770-75649764	NOTEST	0	0	0	0	1	1
ENSG00000249016	ENSG00000249016	RP11-45H22.3	5:54252062-54253674	NOTEST	0	0	0	0	1	1
ENSG00000249017	ENSG00000249017	RP11-58B2.1	5:101836244-101841374	NOTEST	0	0	0	0	1	1
ENSG00000249018	ENSG00000249018	GAPDHP56	4:131424511-131425499	NOTEST	0	0	0	0	1	1
ENSG00000249019	ENSG00000249019	RP11-539G18.1	4:39699663-39784412	NOTEST	0	0	0	0	1	1
ENSG00000249020	ENSG00000249020	SNORA58	3:131181055-131221827	NOTEST	0	0	0	0	1	1
ENSG00000249021	ENSG00000249021	CTC-505O3.3	5:115027158-115027864	NOTEST	0	0	0	0	1	1
ENSG00000249022	ENSG00000249022	RP11-285C1.2	4:153955362-154012317	NOTEST	0	0	0	0	1	1
ENSG00000249023	ENSG00000249023	CTD-2331D11.3	5:84725519-84726002	NOTEST	0	0	0	0	1	1
ENSG00000249025	ENSG00000249025	RP11-2H3.2	4:387322-387447	NOTEST	0	0	0	0	1	1
ENSG00000249026	ENSG00000249026	CTNNAP1	5:114725339-114728067	NOTEST	0.0500424	0.026667	-0.908094	0	1	1
ENSG00000249028	ENSG00000249028	RP5-951N9.1	12:1021242-1605099	NOTEST	0	0.00544314	inf	0	1	1
ENSG00000249030	ENSG00000249030	OR12D1	HSCHR6_MHC_COX:29319721-29421426	NOTEST	0	0	0	0	1	1
ENSG00000249031	ENSG00000249031	SUMO2P6	5:173988778-173989066	NOTEST	0	0	0	0	1	1
ENSG00000249032	ENSG00000249032	LINC00533	HSCHR6_MHC_COX:28616025-28622258	NOTEST	0	0	0	0	1	1
ENSG00000249034	ENSG00000249034	AC005609.1	5:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000249035	ENSG00000249035	CTB-113P19.1	5:151040656-151104343	NOTEST	0.11072	0.0751091	-0.559858	0	1	1
ENSG00000249036	ENSG00000249036	RP11-625I7.1	4:78078303-78415440	NOTEST	0	0	0	0	1	1
ENSG00000249038	ENSG00000249038	RP11-149A7.1	4:133512243-133599658	NOTEST	0	0	0	0	1	1
ENSG00000249041	ENSG00000249041	RP11-21G20.3	4:155675907-155749965	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000249045	ENSG00000249045	RP11-63H19.8	4:65476697-65477026	NOTEST	0	0	0	0	1	1
ENSG00000249047	ENSG00000249047	COX6B1P5	4:2073644-2243891	NOTEST	0.359205	0.129879	-1.46764	0	1	1
ENSG00000249048	ENSG00000249048	TRAV31	14:22645169-22645761	NOTEST	0	0	0	0	1	1
ENSG00000249049	ENSG00000249049	RP11-763F8.1	4:91048685-92523064	NOTEST	0	0	0	0	1	1
ENSG00000249050	ENSG00000249050	RP11-375N15.1	8:9311207-9314928	NOTEST	0	0	0	0	1	1
ENSG00000249051	ENSG00000249051	RP11-447E20.1	4:74643352-74643777	NOTEST	0	0	0	0	1	1
ENSG00000249052	ENSG00000249052	RP11-354O24.1	4:92809036-92825486	NOTEST	0	0	0	0	1	1
ENSG00000249053	ENSG00000249053	RP11-419C19.1	5:12574968-12804475	NOTEST	0	0	0	0	1	1
ENSG00000249054	ENSG00000249054	RP11-598F7.1	12:67606-69138	NOTEST	0	0	0	0	1	1
ENSG00000249055	ENSG00000249055	TBCAP3	4:99792834-99916145	NOTEST	0	0	0	0	1	1
ENSG00000249056	ENSG00000249056	RP11-326I11.1	4:185480328-185480937	NOTEST	0	0	0	0	1	1
ENSG00000249057	ENSG00000249057	MAST4-IT1	5:65892175-66465423	NOTEST	0	0	0	0	1	1
ENSG00000249061	ENSG00000249061	RP11-72L22.1	5:86263137-86433529	NOTEST	0	0	0	0	1	1
ENSG00000249064	ENSG00000249064	KRT18P25	4:40021859-40023137	NOTEST	0	0	0	0	1	1
ENSG00000249065	ENSG00000249065	PCNAP1	4:100010007-100222513	NOTEST	0	0	0	0	1	1
ENSG00000249066	ENSG00000249066	RP11-593F5.2	4:61616303-61655717	NOTEST	0	0	0	0	1	1
ENSG00000249068	ENSG00000249068	CTC-287O8.1	5:109025066-109205326	NOTEST	0	0.0267227	inf	0	1	1
ENSG00000249069	ENSG00000249069	LINC01033	5:53616773-53710955	NOTEST	0	0	0	0	1	1
ENSG00000249071	ENSG00000249071	EGFLAM-AS3	5:38258510-38468441	NOTEST	0	0	0	0	1	1
ENSG00000249072	ENSG00000249072	RP11-777B9.5	4:78929665-78929842	NOTEST	0	0	0	0	1	1
ENSG00000249073	ENSG00000249073	CTD-2131I18.1	5:133249367-133252960	NOTEST	0	0	0	0	1	1
ENSG00000249074	ENSG00000249074	RP11-21G20.1	4:155548096-155674270	NOTEST	0	0	0	0	1	1
ENSG00000249077	ENSG00000249077	RP11-478C1.8	4:2271308-2420390	NOTEST	0	0	0	0	1	1
ENSG00000249079	ENSG00000249079	RP11-1281K21.3	4:49214267-49214641	NOTEST	0	0	0	0	1	1
ENSG00000249081	ENSG00000249081	OR5M14P	4:41724554-41725529	NOTEST	0	0	0	0	1	1
ENSG00000249082	ENSG00000249082	CTC-276P9.1	5:134363424-134736986	NOTEST	0	0	0	0	1	1
ENSG00000249084	ENSG00000249084	RP11-376O6.2	4:178230989-178284097	NOTEST	0.0468511	0	#NAME?	0	1	1
ENSG00000249085	ENSG00000249085	CTD-2631K10.1	5:72090231-72212560	NOTEST	0	0	0	0	1	1
ENSG00000249086	ENSG00000249086	AC051649.12	11:1874199-1913497	NOTEST	0	0	0	0	1	1
ENSG00000249089	ENSG00000249089	AIG1P1	5:38845959-39074510	NOTEST	0	0	0	0	1	1
ENSG00000249091	ENSG00000249091	RP11-733C7.1	4:139198268-139202938	NOTEST	0	0.0452652	inf	0	1	1
ENSG00000249092	ENSG00000249092	CTD-2325A15.3	5:42892420-42892919	NOTEST	0	0	0	0	1	1
ENSG00000249094	ENSG00000249094	RP1-7G5.6	12:110318480-110326272	NOTEST	0	0	0	0	1	1
ENSG00000249096	ENSG00000249096	RP11-290F5.1	4:185286335-185303460	NOTEST	0.0143523	0.078672	2.45457	0	1	1
ENSG00000249098	ENSG00000249098	RP11-39E3.4	3:130569438-131100319	NOTEST	0	0	0	0	1	1
ENSG00000249099	ENSG00000249099	RP11-351N6.1	5:26382627-26399928	NOTEST	0	0	0	0	1	1
ENSG00000249100	ENSG00000249100	CTD-2218K11.2	5:82061222-82062152	NOTEST	0	0	0	0	1	1
ENSG00000249101	ENSG00000249101	AC008834.2	5:97361668-97361843	NOTEST	0	0	0	0	1	1
ENSG00000249102	ENSG00000249102	CTD-2066L21.1	5:32925744-33298016	NOTEST	0	0	0	0	1	1
ENSG00000249103	ENSG00000249103	OR12D1	HSCHR6_MHC_DBB:29341258-29424782	NOTEST	0	0	0	0	1	1
ENSG00000249104	ENSG00000249104	USP17L17	4:9245604-9247197	NOTEST	0	0	0	0	1	1
ENSG00000249105	ENSG00000249105	RP11-25L5.2	4:58983923-58984236	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000249106	ENSG00000249106	RP11-806K15.1	4:176554084-176923815	NOTEST	0	0	0	0	1	1
ENSG00000249109	ENSG00000249109	RP11-1026M7.2	5:177109294-177221397	NOTEST	0	0	0	0	1	1
ENSG00000249111	ENSG00000249111	RP11-622J8.1	4:60018551-60041864	NOTEST	0	0	0	0	1	1
ENSG00000249112	ENSG00000249112	RP11-43D2.2	5:123972607-124084500	NOTEST	0	0	0	0	1	1
ENSG00000249114	ENSG00000249114	RP11-5N11.3	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000249116	ENSG00000249116	CTD-2194D22.3	5:1877540-1887350	NOTEST	0	0	0	0	1	1
ENSG00000249119	ENSG00000249119	MTND6P4	5:134240595-134347392	NOTEST	0.0423217	0.030036	-0.494704	0	1	1
ENSG00000249122	ENSG00000249122	RP11-227F19.2	4:41746098-41826136	NOTEST	0	0	0	0	1	1
ENSG00000249123	ENSG00000249123	MICE	HSCHR6_MHC_SSTO:29687513-29713718	NOTEST	0	0	0	0	1	1
ENSG00000249125	ENSG00000249125	RP11-381N20.2	4:124411422-124448680	NOTEST	0	0	0	0	1	1
ENSG00000249127	ENSG00000249127	MTND3P3	4:156377789-156378133	NOTEST	0	0	0	0	1	1
ENSG00000249128	ENSG00000249128	RP11-2N5.1	5:117931882-117963787	NOTEST	0	0	0	0	1	1
ENSG00000249131	ENSG00000249131	CTB-35F21.2	5:139064229-139125808	NOTEST	0	0	0	0	1	1
ENSG00000249135	ENSG00000249135	RP11-274E7.1	5:97538762-97540897	NOTEST	0	0	0	0	1	1
ENSG00000249138	ENSG00000249138	RP11-701P16.1	4:185676748-185747972	NOTEST	0.0470378	0	#NAME?	0	1	1
ENSG00000249139	ENSG00000249139	EPPIN-WFDC6	20:44162834-44176391	NOTEST	0	0	0	0	1	1
ENSG00000249140	ENSG00000249140	PRDX2P3	5:178977558-179037027	NOTEST	0.0358059	0.0793095	1.1473	0	1	1
ENSG00000249141	ENSG00000249141	RP11-514O12.4	6:166822851-167370679	NOTEST	0.130447	0.227088	0.79979	0	1	1
ENSG00000249142	ENSG00000249142	CTD-2290P7.1	5:32522863-32523971	NOTEST	0.108137	0.0358104	-1.5944	0	1	1
ENSG00000249145	ENSG00000249145	RP11-774O3.2	4:8321902-8325692	NOTEST	0	0	0	0	1	1
ENSG00000249148	ENSG00000249148	AC006445.7	4:13633443-13634223	NOTEST	0	0	0	0	1	1
ENSG00000249149	ENSG00000249149	RP11-79P5.3	5:72678210-72706336	NOTEST	0	0	0	0	1	1
ENSG00000249150	ENSG00000249150	CTC-472C24.1	5:116156688-116165883	NOTEST	0	0	0	0	1	1
ENSG00000249152	ENSG00000249152	RP11-562F9.2	4:93189917-93198226	NOTEST	0	0	0	0	1	1
ENSG00000249153	ENSG00000249153	CTD-2036A18.2	5:85144319-85145017	NOTEST	0	0	0	0	1	1
ENSG00000249156	ENSG00000249156	RP11-432M8.9	5:17611098-17611692	NOTEST	0	0	0	0	1	1
ENSG00000249157	ENSG00000249157	RP11-229C3.4	5:74213550-74319753	NOTEST	0	0	0	0	1	1
ENSG00000249158	ENSG00000249158	PCDHA11	5:140165875-140391936	NOTEST	0.0286363	0.0431669	0.59208	0	1	1
ENSG00000249159	ENSG00000249159	RP11-480D4.2	5:8333595-8463208	NOTEST	0.452287	0.00354698	-6.99451	0	1	1
ENSG00000249160	ENSG00000249160	RP11-1C1.5	5:10505107-10522196	NOTEST	0	0	0	0	1	1
ENSG00000249162	ENSG00000249162	ADAM20P3	4:188667247-188669353	NOTEST	0	0	0	0	1	1
ENSG00000249163	ENSG00000249163	CTD-3028N15.1	14:45552247-45553180	NOTEST	0	0	0	0	1	1
ENSG00000249166	ENSG00000249166	RP11-1C1.6	5:10493402-10502840	NOTEST	0	0	0	0	1	1
ENSG00000249167	ENSG00000249167	CTB-118N6.2	5:115779311-115927094	NOTEST	0	0	0	0	1	1
ENSG00000249169	ENSG00000249169	CTC-529L17.1	5:91378413-92023961	NOTEST	0	0	0	0	1	1
ENSG00000249170	ENSG00000249170	RP11-1J11.1	4:72053002-72437804	NOTEST	0	0	0	0	1	1
ENSG00000249171	ENSG00000249171	RP11-767N15.1	4:84589662-84652908	NOTEST	0	0	0	0	1	1
ENSG00000249173	ENSG00000249173	LINC01093	4:185815024-185820608	NOTEST	0	0	0	0	1	1
ENSG00000249174	ENSG00000249174	RP11-124N3.3	5:18965969-19142455	NOTEST	0	0	0	0	1	1
ENSG00000249175	ENSG00000249175	CTC-484P3.3	5:93488670-94620279	NOTEST	0	0.00589954	inf	0	1	1
ENSG00000249176	ENSG00000249176	RP11-304F15.5	17:48016485-48017183	NOTEST	0	0	0	0	1	1

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ENSG00000249177	ENSG00000249177	MTND4P29	2:202352147-202483901	NOTEST	0	0.00961194	inf	0	1	1
ENSG00000249180	ENSG00000249180	CTC-506B8.1	5:95220801-96143803	NOTEST	0.0699375	0.0881286	0.333544	0	1	1
ENSG00000249183	ENSG00000249183	SUMO2P4	5:68364751-68365027	NOTEST	0	0	0	0	1	1
ENSG00000249184	ENSG00000249184	RP11-424M21.1	4:152720651-152722500	NOTEST	0	0	0	0	1	1
ENSG00000249186	ENSG00000249186	RP11-423H2.5	5:177236407-177410055	NOTEST	0	0	0	0	1	1
ENSG00000249188	ENSG00000249188	ENPP7P1	8:8011829-8084136	NOTEST	0	0.0395165	inf	0	1	1
ENSG00000249189	ENSG00000249189	AC010492.4	19:54704609-54752862	NOTEST	0	0	0	0	1	1
ENSG00000249191	ENSG00000249191	UBE2V1P12	5:18886730-18887204	NOTEST	0	0	0	0	1	1
ENSG00000249192	ENSG00000249192	CTB-36O1.3	5:134240595-134347392	NOTEST	0	0	0	0	1	1
ENSG00000249193	ENSG00000249193	HSPD1P5	4:145766776-145768496	NOTEST	0	0	0	0	1	1
ENSG00000249196	ENSG00000249196	RP11-669N7.2	12:129556269-130388211	NOTEST	0.0412624	0.125099	1.60016	0	1	1
ENSG00000249197	ENSG00000249197	OR10J9P	1:159315955-159453166	NOTEST	0	0	0	0	1	1
ENSG00000249198	ENSG00000249198	RP11-772C9.1	5:57047018-57047544	NOTEST	0	0.0622904	inf	0	1	1
ENSG00000249199	ENSG00000249199	CTD-2139B15.5	5:17369333-17375686	NOTEST	0	0	0	0	1	1
ENSG00000249200	ENSG00000249200	RP11-290O12.1	4:155153398-155412930	NOTEST	0	0	0	0	1	1
ENSG00000249201	ENSG00000249201	CTD-3080P12.3	5:1173255-1178720	NOTEST	0	0	0	0	1	1
ENSG00000249203	ENSG00000249203	RP11-473L15.3	5:44495719-44510384	NOTEST	0	0	0	0	1	1
ENSG00000249206	ENSG00000249206	GCNT1P2	5:21616370-22853731	NOTEST	0	0	0	0	1	1
ENSG00000249207	ENSG00000249207	RP11-360F5.1	4:39046658-39128477	NOTEST	0	0	0	0	1	1
ENSG00000249209	ENSG00000249209	AP000304.12	21:34876237-35349992	NOTEST	0	0	0	0	1	1
ENSG00000249210	ENSG00000249210	GAPDHP38	19:46984052-47114050	NOTEST	0	0	0	0	1	1
ENSG00000249212	ENSG00000249212	ATP1B1P1	4:41992488-42092474	NOTEST	0.0199637	0.0296033	0.568379	0	1	1
ENSG00000249213	ENSG00000249213	RP11-98P2.1	8:26112398-26114144	NOTEST	0	0	0	0	1	1
ENSG00000249214	ENSG00000249214	AC022558.1	15:83509837-83772195	NOTEST	0	0	0	0	1	1
ENSG00000249215	ENSG00000249215	AC138517.4	5:138873840-138875701	NOTEST	0	0	0	0	1	1
ENSG00000249216	ENSG00000249216	RP11-227F19.5	4:41361623-41702061	NOTEST	0.0562366	0	#NAME?	0	1	1
ENSG00000249219	ENSG00000249219	RP13-560N11.1	4:9772776-10056560	NOTEST	0	0	0	0	1	1
ENSG00000249222	ENSG00000249222	ATP5L2	22:43013845-43045574	NOTEST	0	0.0166949	inf	0	1	1
ENSG00000249225	ENSG00000249225	RP11-343D2.11	3:97818751-97866978	NOTEST	0	0	0	0	1	1
ENSG00000249226	ENSG00000249226	SUCLG2P4	5:29001866-29003464	NOTEST	0	0	0	0	1	1
ENSG00000249228	ENSG00000249228	RP11-769N22.1	4:29048212-29050387	NOTEST	0	0	0	0	1	1
ENSG00000249229	ENSG00000249229	CTC-342P15.1	5:144381415-144385352	NOTEST	0	0	0	0	1	1
ENSG00000249230	ENSG00000249230	CDH12P2	5:69281030-69281328	NOTEST	0.114958	0	#NAME?	0	1	1
ENSG00000249231	ENSG00000249231	CASC16	16:52586001-52686017	NOTEST	0	0	0	0	1	1
ENSG00000249234	ENSG00000249234	RP11-452J21.2	4:16162127-16321763	NOTEST	0	0.184112	inf	0	1	1
ENSG00000249235	ENSG00000249235	RP11-468N14.4	4:69727049-69727328	NOTEST	0	0	0	0	1	1
ENSG00000249236	ENSG00000249236	CTD-2227I18.1	5:55354876-55363199	NOTEST	0	0.0497648	inf	0	1	1
ENSG00000249237	ENSG00000249237	RP11-376N17.4	1:84764048-84863514	NOTEST	0	0.0230543	inf	0	1	1
ENSG00000249238	ENSG00000249238	RP11-83M16.2	5:66675205-67198428	NOTEST	0	0	0	0	1	1
ENSG00000249239	ENSG00000249239	RP11-428L21.2	4:93225549-94695707	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000249240	ENSG00000249240	AC069368.3	15:65134081-65251042	NOTEST	0	0.310253	inf	0	1	1
ENSG00000249241	ENSG00000249241	AC195454.1	4:40318501-40332436	NOTEST	0	0	0	0	1	1
ENSG00000249244	ENSG00000249244	RP11-548H18.2	4:120312985-120316490	NOTEST	0.0455454	0.0239081	-0.929805	0	1	1
ENSG00000249245	ENSG00000249245	RP11-557J10.3	4:146539414-146581187	NOTEST	0	0	0	0	1	1
ENSG00000249247	ENSG00000249247	RP11-627H22.9	4:156372768-156373557	NOTEST	0	0	0	0	1	1
ENSG00000249249	ENSG00000249249	AC010226.4	5:114914338-114968689	NOTEST	0.22014	0.0975715	-1.17389	0	1	1
ENSG00000249251	ENSG00000249251	PGAM1P8	11:64941587-64943941	NOTEST	0.000161233	0.0358301	7.79588	0	1	1
ENSG00000249252	ENSG00000249252	RP11-665G4.1	4:15004297-15447790	NOTEST	0	0	0	0	1	1
ENSG00000249253	ENSG00000249253	RP11-77P16.1	3:130012179-130012603	NOTEST	0	0	0	0	1	1
ENSG00000249255	ENSG00000249255	PGAM1P9	11:92085261-92629618	NOTEST	0	0	0	0	1	1
ENSG00000249256	ENSG00000249256	ATP5LP3	4:24659694-24659998	NOTEST	0	0	0	0	1	1
ENSG00000249257	ENSG00000249257	RP11-75N20.2	4:109694768-109695176	NOTEST	0	0	0	0	1	1
ENSG00000249258	ENSG00000249258	RP11-468H14.2	8:16988689-17007298	NOTEST	0.0140038	0.0469099	1.74408	0	1	1
ENSG00000249259	ENSG00000249259	RP11-166J5.1	4:116843170-117218316	NOTEST	0	0	0	0	1	1
ENSG00000249261	ENSG00000249261	RP11-284A20.2	5:124204664-124205607	NOTEST	0	0	0	0	1	1
ENSG00000249262	ENSG00000249262	RP11-710E1.1	4:88331795-88332540	NOTEST	0	0	0	0	1	1
ENSG00000249263	ENSG00000249263	PARP4P3	22:17082776-17185367	NOTEST	0	0	0	0	1	1
ENSG00000249264	ENSG00000249264	EEF1A1P9	4:106405854-106407237	NOTEST	0.144806	0.318968	1.13929	0	1	1
ENSG00000249265	ENSG00000249265	AC113167.2	5:89240726-89243390	NOTEST	0	0	0	0	1	1
ENSG00000249266	ENSG00000249266	MTHFD2P6	5:41967240-41968468	NOTEST	0	0	0	0	1	1
ENSG00000249267	ENSG00000249267	LINC00939	12:126443233-126467920	NOTEST	0	0	0	0	1	1
ENSG00000249269	ENSG00000249269	RP11-756P10.4	4:189678832-189717787	NOTEST	0	0	0	0	1	1
ENSG00000249270	ENSG00000249270	KATNBL1P4	5:51226641-51227870	NOTEST	0	0	0	0	1	1
ENSG00000249271	ENSG00000249271	HNRNPA1P44	15:65903703-66184329	NOTEST	0	0	0	0	1	1
ENSG00000249272	ENSG00000249272	UNC93B8	4:8961353-8965707	NOTEST	0.0278168	0.0614732	1.144	0	1	1
ENSG00000249275	ENSG00000249275	RP11-364P22.2	4:158558838-158588196	NOTEST	0	0	0	0	1	1
ENSG00000249276	ENSG00000249276	RP11-8L21.1	5:43874468-43886730	NOTEST	0	0	0	0	1	1
ENSG00000249277	ENSG00000249277	RP11-302F12.4	4:25687823-25688080	NOTEST	0	0	0	0	1	1
ENSG00000249278	ENSG00000249278	RP11-688H10.1	4:77356252-77723117	NOTEST	0	0	0	0	1	1
ENSG00000249279	ENSG00000249279	CTC-436P18.3	5:60453535-60560756	NOTEST	0	0	0	0	1	1
ENSG00000249282	ENSG00000249282	RP11-432M8.6	5:17601990-17602243	NOTEST	0	0	0	0	1	1
ENSG00000249283	ENSG00000249283	ACTR3BP4	4:103790134-103940896	NOTEST	0	0	0	0	1	1
ENSG00000249284	ENSG00000249284	RP11-287F9.1	4:176207755-176211918	NOTEST	0	0	0	0	1	1
ENSG00000249285	ENSG00000249285	RP11-81B23.1	5:18908974-18909652	NOTEST	0	0	0	0	1	1
ENSG00000249287	ENSG00000249287	CTD-2593A12.3	5:180394188-180397762	NOTEST	0	0	0	0	1	1
ENSG00000249288	ENSG00000249288	SLC25A15P5	22:17082776-17185367	NOTEST	0	0	0	0	1	1
ENSG00000249289	ENSG00000249289	CTD-2272G21.1	5:23329535-23330001	NOTEST	0	0	0	0	1	1
ENSG00000249290	ENSG00000249290	RP11-68L1.2	3:139654026-140296239	NOTEST	0	0	0	0	1	1
ENSG00000249293	ENSG00000249293	CTC-575I10.1	5:72921982-73237818	NOTEST	0	0	0	0	1	1
ENSG00000249295	ENSG00000249295	RP11-241G9.3	5:68773298-69006341	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000249297	ENSG00000249297	RP11-97E7.2	4:172523833-172559914	NOTEST	0	0	0	0	1	1
ENSG00000249301	ENSG00000249301	RP11-524L6.3	5:75206107-75207692	NOTEST	0	0	0	0	1	1
ENSG00000249302	ENSG00000249302	FTH1P24	4:140417094-140527853	NOTEST	0	0	0	0	1	1
ENSG00000249304	ENSG00000249304	RP11-26P13.2	4:114821439-114900883	NOTEST	0	0	0	0	1	1
ENSG00000249305	ENSG00000249305	RP11-13L2.1	3:140338535-140338679	NOTEST	0	0	0	0	1	1
ENSG00000249306	ENSG00000249306	RP11-267A15.1	5:173763297-173959460	NOTEST	0	0	0	0	1	1
ENSG00000249307	ENSG00000249307	LINC01088	4:79892901-80247204	NOTEST	0.133333	0.0358643	-1.89441	0	1	1
ENSG00000249309	ENSG00000249309	RP11-153M7.5	4:154631276-154681387	NOTEST	0	0	0	0	1	1
ENSG00000249310	ENSG00000249310	APOBEC3B-AS1	22:39378351-39394214	NOTEST	0	0	0	0	1	1
ENSG00000249311	ENSG00000249311	TERF1P3	4:137039829-137316626	NOTEST	0	0	0	0	1	1
ENSG00000249312	ENSG00000249312	ARL2BPP4	5:129865111-129865582	NOTEST	0	0	0	0	1	1
ENSG00000249316	ENSG00000249316	CTC-493P15.2	8:11138872-11140010	NOTEST	0	0	0	0	1	1
ENSG00000249317	ENSG00000249317	CTB-191D16.1	4:149862092-149863530	NOTEST	0	0	0	0	1	1
ENSG00000249318	ENSG00000249318	AC010468.2	5:110559350-110830584	NOTEST	0	0	0	0	1	1
ENSG00000249320	ENSG00000249320	RP11-206P5.1	4:25474138-25475437	NOTEST	0	0	0	0	1	1
ENSG00000249321	ENSG00000249321	OR5H5P	3:97916054-97916982	NOTEST	0	0	0	0	1	1
ENSG00000249326	ENSG00000249326	CTD-2194D22.4	5:1887445-1900607	NOTEST	0	0	0	0	1	1
ENSG00000249328	ENSG00000249328	RP11-26J3.1	8:80680376-80783994	NOTEST	0.0379823	0.0996647	1.39175	0	1	1
ENSG00000249329	ENSG00000249329	RP11-432M8.5	5:17597340-17597937	NOTEST	0	0	0	0	1	1
ENSG00000249330	ENSG00000249330	RP11-436F23.1	4:46250443-46477247	NOTEST	0	0	0	0	1	1
ENSG00000249332	ENSG00000249332	RP1-251I12.1	5:15112485-15117116	NOTEST	0	0	0	0	1	1
ENSG00000249333	ENSG00000249333	LL22NC03-23C6.12	22:22345495-22398340	NOTEST	0	0	0	0	1	1
ENSG00000249334	ENSG00000249334	RP11-61G19.1	4:10686626-10699285	NOTEST	0	0	0	0	1	1
ENSG00000249335	ENSG00000249335	CTC-340D7.1	5:68128411-68257985	NOTEST	0	0	0	0	1	1
ENSG00000249337	ENSG00000249337	SNX18P25	4:49590788-49591546	NOTEST	0	0	0	0	1	1
ENSG00000249338	ENSG00000249338	HMGB1P47	5:50705450-50706039	NOTEST	0	0	0	0	1	1
ENSG00000249339	ENSG00000249339	RP11-321E2.7	5:17521909-17522504	NOTEST	0	0	0	0	1	1
ENSG00000249343	ENSG00000249343	CTD-2275D24.2	5:73617455-73635977	NOTEST	0	0	0	0	1	1
ENSG00000249345	ENSG00000249345	RP11-575F12.1	12:127399765-127544946	NOTEST	0.197821	0.350283	0.824327	0	1	1
ENSG00000249346	ENSG00000249346	LINC01016	6:33835282-33895408	NOTEST	0	0	0	0	1	1
ENSG00000249347	ENSG00000249347	RP11-747H12.4	4:8992180-8992532	NOTEST	0	0	0	0	1	1
ENSG00000249348	ENSG00000249348	UGDH-AS1	4:39500374-39640710	NOTEST	0.0340615	0.0291777	-0.223275	0	1	1
ENSG00000249349	ENSG00000249349	CTC-384G19.1	5:84408159-84408574	NOTEST	0	0	0	0	1	1
ENSG00000249351	ENSG00000249351	RP11-498E11.2	4:66082333-66083151	NOTEST	0	0	0	0	1	1
ENSG00000249352	ENSG00000249352	7SK	5:68266265-68325992	NOTEST	0.0425959	0	#NAME?	0	1	1
ENSG00000249356	ENSG00000249356	RP11-21I10.2	4:119990478-119991452	NOTEST	0	0	0	0	1	1
ENSG00000249357	ENSG00000249357	RP11-432M8.8	5:17604865-17605486	NOTEST	0	0	0	0	1	1
ENSG00000249359	ENSG00000249359	RP11-374A4.1	5:21323981-21341484	NOTEST	0.00562194	0	#NAME?	0	1	1
ENSG00000249360	ENSG00000249360	CTD-2233C11.3	5:33502176-33503240	NOTEST	0	0	0	0	1	1
ENSG00000249362	ENSG00000249362	CTD-2316B1.1	5:86957858-86974964	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000249363	ENSG00000249363	CTB-78O21.1	5:144851361-145214932	NOTEST	0.136699	0.233118	0.77006	0	1	1
ENSG00000249364	ENSG00000249364	RP11-434D9.1	5:66675205-67198428	NOTEST	0.195216	0	#NAME?	0	1	1
ENSG00000249365	ENSG00000249365	RP11-508M8.1	5:124443896-124485622	NOTEST	0	0	0	0	1	1
ENSG00000249367	ENSG00000249367	FABP5P12	4:159690289-159959912	NOTEST	0	0	0	0	1	1
ENSG00000249368	ENSG00000249368	RP11-782K4.1	8:15182804-15183078	NOTEST	0	0	0	0	1	1
ENSG00000249372	ENSG00000249372	ATP6V1G1P6	5:77296348-77590579	NOTEST	0	0	0	0	1	1
ENSG00000249373	ENSG00000249373	RP11-650J17.2	4:113739264-114304896	NOTEST	0	0	0	0	1	1
ENSG00000249375	ENSG00000249375	CASC11	8:128698587-128746213	NOTEST	0.0423771	0	#NAME?	0	1	1
ENSG00000249378	ENSG00000249378	LINC01060	4:189321889-189602205	NOTEST	0	0.0355686	inf	0	1	1
ENSG00000249379	ENSG00000249379	RP1-27K12.4	6:53362138-53481969	NOTEST	0	0.115666	inf	0	1	1
ENSG00000249380	ENSG00000249380	RP11-1325J9.1	5:34373132-34373955	NOTEST	0	0	0	0	1	1
ENSG00000249381	ENSG00000249381	LINC00500	4:139346676-139358023	NOTEST	0	0.031442	inf	0	1	1
ENSG00000249382	ENSG00000249382	RP11-340A13.1	4:59849999-59912677	NOTEST	0	0	0	0	1	1
ENSG00000249383	ENSG00000249383	RP11-1018N14.1	17:49389969-49412526	NOTEST	0	0	0	0	1	1
ENSG00000249386	ENSG00000249386	RP11-627H22.6	4:156380021-156380715	NOTEST	0	0	0	0	1	1
ENSG00000249387	ENSG00000249387	KRTAP5-14P	11:71290773-71290894	NOTEST	0	0	0	0	1	1
ENSG00000249388	ENSG00000249388	RP11-834C11.6	12:54452037-54519776	NOTEST	0	0	0	0	1	1
ENSG00000249392	ENSG00000249392	RP11-725D20.1	4:60416859-60496042	NOTEST	0	0	0	0	1	1
ENSG00000249395	ENSG00000249395	CASC9	8:76135638-76236976	NOTEST	0	0	0	0	1	1
ENSG00000249396	ENSG00000249396	RP11-1C1.4	5:10493402-10502840	NOTEST	0	0	0	0	1	1
ENSG00000249400	ENSG00000249400	HMGB3P17	5:122804474-122805123	NOTEST	0	0	0	0	1	1
ENSG00000249403	ENSG00000249403	CTC-281M20.4	5:174346084-174422516	NOTEST	0	0	0	0	1	1
ENSG00000249404	ENSG00000249404	CTD-2234B20.1	5:23013156-23014636	NOTEST	0	0	0	0	1	1
ENSG00000249405	ENSG00000249405	RP11-317O24.1	5:50154593-50155854	NOTEST	0	0	0	0	1	1
ENSG00000249406	ENSG00000249406	RP11-893F2.5	17:48286332-48292781	NOTEST	0	0	0	0	1	1
ENSG00000249407	ENSG00000249407	IL20RB-AS1	3:136581049-136729927	NOTEST	0	0	0	0	1	1
ENSG00000249409	ENSG00000249409	RP11-501E14.1	4:121560244-121571951	NOTEST	0	0.0293448	inf	0	1	1
ENSG00000249410	ENSG00000249410	AK4P2	5:54847712-54848382	NOTEST	0	0	0	0	1	1
ENSG00000249411	ENSG00000249411	RP11-391J13.1	4:175938166-175940365	NOTEST	0	0	0	0	1	1
ENSG00000249412	ENSG00000249412	CTC-563A5.2	5:179338650-179499118	NOTEST	0.037324	0.111804	1.58279	0	1	1
ENSG00000249413	ENSG00000249413	RP11-25H12.1	4:66864563-67015730	NOTEST	0	0	0	0	1	1
ENSG00000249415	ENSG00000249415	OR2U2P	HSCHR6_MHC_MANN:29236258-29237218	NOTEST	0	0	0	0	1	1
ENSG00000249416	ENSG00000249416	RP11-614F17.1	4:132689294-132689733	NOTEST	0	0	0	0	1	1
ENSG00000249417	ENSG00000249417	RP11-438D8.2	3:140947567-141168634	NOTEST	0.177414	0.0843393	-1.07284	0	1	1
ENSG00000249418	ENSG00000249418	AC005741.2	5:129934040-129934472	NOTEST	0	0	0	0	1	1
ENSG00000249419	ENSG00000249419	RP11-497K21.1	4:162300104-163085187	NOTEST	0	0	0	0	1	1
ENSG00000249421	ENSG00000249421	ADAMTS19-AS1	5:128795251-129522327	NOTEST	0	0	0	0	1	1
ENSG00000249423	ENSG00000249423	RP11-284A20.1	5:124255639-124257291	NOTEST	0	0	0	0	1	1
ENSG00000249425	ENSG00000249425	RP11-502M1.2	4:161460405-161507969	NOTEST	0	0	0	0	1	1
ENSG00000249426	ENSG00000249426	CTC-448D22.1	5:118096168-118121154	NOTEST	0.0849462	0.0323679	-1.39199	0	1	1

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ENSG00000249428	ENSG00000249428	RP11-503N18.3	4:2420700-2734292	NOTEST	0	0	0	0	1	1
ENSG00000249429	ENSG00000249429	CTD-2050E21.1	5:142869419-142910915	NOTEST	0	0	0	0	1	1
ENSG00000249430	ENSG00000249430	CTD-2231H16.1	5:92265-139978	NOTEST	0	0	0	0	1	1
ENSG00000249433	ENSG00000249433	CTB-161J7.2	5:114829253-114829518	NOTEST	0	0	0	0	1	1
ENSG00000249434	ENSG00000249434	TRIM26BP	HSCHR6_MHC_APD:30138606-30146877	NOTEST	0	0	0	0	1	1
ENSG00000249435	ENSG00000249435	CTD-2224J9.7	19:53868945-53930574	NOTEST	0.302604	0.0847804	-1.83563	0	1	1
ENSG00000249436	ENSG00000249436	CTD-2023N9.3	5:56910215-56913258	NOTEST	0.129629	0.033954	-1.93273	0	1	1
ENSG00000249437	ENSG00000249437	NAIP	5:70264309-70320941	NOTEST	0.190822	0.152872	-0.319909	0	1	1
ENSG00000249438	ENSG00000249438	KRT18P45	5:79584267-79585600	NOTEST	0	0	0	0	1	1
ENSG00000249439	ENSG00000249439	HMGN1P14	5:110831730-111353006	NOTEST	0	0	0	0	1	1
ENSG00000249441	ENSG00000249441	RP11-94H6.1	4:19173957-19911315	NOTEST	0	0	0	0	1	1
ENSG00000249443	ENSG00000249443	RP11-1396O13.22	4:9523554-9523921	NOTEST	0	0	0	0	1	1
ENSG00000249444	ENSG00000249444	RP11-93O17.1	5:98825262-98835071	NOTEST	0	0	0	0	1	1
ENSG00000249446	ENSG00000249446	TRAJ60	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000249448	ENSG00000249448	RP11-474J18.1	5:97745938-97747496	NOTEST	0	0	0	0	1	1
ENSG00000249449	ENSG00000249449	MRP63P6	5:162439270-162864332	NOTEST	0	0	0	0	1	1
ENSG00000249451	ENSG00000249451	RP11-94C24.6	17:48580772-48585689	NOTEST	0	0	0	0	1	1
ENSG00000249452	ENSG00000249452	RP11-638O6.1	4:33239860-33240292	NOTEST	0	0	0	0	1	1
ENSG00000249453	ENSG00000249453	RP13-497K6.1	4:23562545-23905712	NOTEST	0	0	0	0	1	1
ENSG00000249454	ENSG00000249454	GZMAP1	5:54368842-54392381	NOTEST	0	0	0	0	1	1
ENSG00000249458	ENSG00000249458	RP11-624A4.1	4:177787767-177796611	NOTEST	0	0	0	0	1	1
ENSG00000249460	ENSG00000249460	RP11-665C14.2	4:182182313-182186182	NOTEST	0	0	0	0	1	1
ENSG00000249462	ENSG00000249462	MLLT10P2	4:190894753-190895002	NOTEST	0	0	0	0	1	1
ENSG00000249463	ENSG00000249463	RP11-1E22.1	4:132925964-133045186	NOTEST	0.244856	0	#NAME?	0	1	1
ENSG00000249464	ENSG00000249464	LINC01091	4:124571421-124851561	NOTEST	0.00526269	0.029648	2.49406	0	1	1
ENSG00000249465	ENSG00000249465	RBMXP4	4:110267481-110268615	NOTEST	0.0308459	0.0228508	-0.432835	0	1	1
ENSG00000249467	ENSG00000249467	RP11-492O8.1	X:36737990-36738294	NOTEST	0	0	0	0	1	1
ENSG00000249472	ENSG00000249472	RP11-1267H10.2	4:69480136-69480731	NOTEST	0	0	0	0	1	1
ENSG00000249474	ENSG00000249474	RP11-49I4.3	3:101498045-101579866	NOTEST	0.0953641	0	#NAME?	0	1	1
ENSG00000249476	ENSG00000249476	CTD-2587M2.1	5:108572820-108662070	NOTEST	0.035327	0.0226886	-0.638803	0	1	1
ENSG00000249478	ENSG00000249478	CTB-49A3.5	5:132496129-132948255	NOTEST	0	0.0288708	inf	0	1	1
ENSG00000249479	ENSG00000249479	RP11-171N4.3	4:157563731-157564721	NOTEST	0	0	0	0	1	1
ENSG00000249480	ENSG00000249480	STK19P	HSCHR6_MHC_DBB:31963232-31963750	NOTEST	0	0	0	0	1	1
ENSG00000249482	ENSG00000249482	USP17L14P	4:9231366-9232959	NOTEST	0	0	0	0	1	1
ENSG00000249483	ENSG00000249483	CTD-2249K22.1	5:81147419-81148020	NOTEST	0	0	0	0	1	1
ENSG00000249484	ENSG00000249484	AC091969.1	5:151998524-152603103	NOTEST	0	0	0	0	1	1
ENSG00000249486	ENSG00000249486	RP11-215I16.1	5:8157653-8157901	NOTEST	0	0	0	0	1	1
ENSG00000249487	ENSG00000249487	RP11-97O12.2	15:89128801-89148341	NOTEST	0	0	0	0	1	1
ENSG00000249488	ENSG00000249488	NACAP5	4:17553739-17554375	NOTEST	0	0	0	0	1	1

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ENSG00000249489	ENSG00000249489	GAPDHP70	11:88141346-88142391	NOTEST	0.0309911	0	#NAME?	0	1	1
ENSG00000249490	ENSG00000249490	CTD-2333M24.1	5:20611948-20937800	NOTEST	0	0	0	0	1	1
ENSG00000249491	ENSG00000249491	EGFLAM-AS1	5:38258510-38468441	NOTEST	0	0	0	0	1	1
ENSG00000249492	ENSG00000249492	RP11-159F24.3	5:43484060-43525412	NOTEST	0.42666	0.2864	-0.575053	0	1	1
ENSG00000249493	ENSG00000249493	ANKRD20A18P	21:15399741-15583166	NOTEST	0.0462714	0.135755	1.55281	0	1	1
ENSG00000249494	ENSG00000249494	CTB-161M19.4	5:118342041-118584833	NOTEST	0	0	0	0	1	1
ENSG00000249495	ENSG00000249495	RP11-1152B5.1	5:101311999-101312502	NOTEST	0	0	0	0	1	1
ENSG00000249497	ENSG00000249497	RP11-1079K10.5	17:47448101-47554350	NOTEST	0	0	0	0	1	1
ENSG00000249500	ENSG00000249500	RP11-340B18.1	4:166605790-166683930	NOTEST	0	0	0	0	1	1
ENSG00000249501	ENSG00000249501	USP9YP2	Y:20835918-20991373	NOTEST	0	0	0	0	1	1
ENSG00000249502	ENSG00000249502	AC006160.5	4:17578814-17616194	NOTEST	0.124065	0	#NAME?	0	1	1
ENSG00000249503	ENSG00000249503	HMGN1P16	5:147600922-147601205	NOTEST	0	0	0	0	1	1
ENSG00000249504	ENSG00000249504	PCDHA14	5:140165875-140391936	NOTEST	0.0886003	0.0157205	-2.49466	0	1	1
ENSG00000249505	ENSG00000249505	RP11-434H6.2	3:128764605-128765764	NOTEST	0	0	0	0	1	1
ENSG00000249506	ENSG00000249506	ZEB2P1	4:16362308-16398946	NOTEST	0.0371499	0	#NAME?	0	1	1
ENSG00000249510	ENSG00000249510	KB-1247B1.1	8:95139398-95229531	NOTEST	0	0	0	0	1	1
ENSG00000249513	ENSG00000249513	RP11-404I7.1	4:133906664-133909832	NOTEST	0	0	0	0	1	1
ENSG00000249514	ENSG00000249514	CTD-2266L18.1	5:89811427-90460038	NOTEST	0	0	0	0	1	1
ENSG00000249515	ENSG00000249515	CTD-2151A2.1	5:98885135-98913661	NOTEST	0	0	0	0	1	1
ENSG00000249516	ENSG00000249516	CTD-2201E18.2	5:42917515-42918086	NOTEST	0	0	0	0	1	1
ENSG00000249518	ENSG00000249518	CTC-327F10.1	5:147231206-147232222	NOTEST	0	0	0	0	1	1
ENSG00000249519	ENSG00000249519	RP11-777N19.1	4:111715558-111718500	NOTEST	0	0	0	0	1	1
ENSG00000249520	ENSG00000249520	RP11-386B13.1	4:185973049-186028402	NOTEST	0	0	0	0	1	1
ENSG00000249521	ENSG00000249521	CTD-2161F6.3	5:4452042-4866334	NOTEST	0	0	0	0	1	1
ENSG00000249522	ENSG00000249522	RP11-718M20.5	4:3912009-3912331	NOTEST	0	0	0	0	1	1
ENSG00000249525	ENSG00000249525	RP11-344G13.2	4:172034939-172035732	NOTEST	0	0	0	0	1	1
ENSG00000249526	ENSG00000249526	CTB-35F21.1	5:139064229-139125808	NOTEST	0	0	0	0	1	1
ENSG00000249531	ENSG00000249531	RP11-642E20.3	4:69166042-69168177	NOTEST	0	0	0	0	1	1
ENSG00000249532	ENSG00000249532	MIR302B	4:113434671-113578748	NOTEST	0.171155	0.048159	-1.82942	0	1	1
ENSG00000249534	ENSG00000249534	RP11-83C7.2	4:38422282-38524801	NOTEST	0.00786607	0	#NAME?	0	1	1
ENSG00000249539	ENSG00000249539	MRPS36P2	4:187821693-187821992	NOTEST	0	0	0	0	1	1
ENSG00000249540	ENSG00000249540	RP11-789L4.1	3:140947567-141168634	NOTEST	0.0974835	0	#NAME?	0	1	1
ENSG00000249541	ENSG00000249541	RP11-692C23.1	5:2787564-2788663	NOTEST	0	0	0	0	1	1
ENSG00000249542	ENSG00000249542	EEF1A1P21	4:29750378-29751722	NOTEST	0	0	0	0	1	1
ENSG00000249545	ENSG00000249545	CTC-558O19.1	5:93488670-94620279	NOTEST	0	0	0	0	1	1
ENSG00000249547	ENSG00000249547	RP11-453O5.1	4:23236247-23287196	NOTEST	0	0	0	0	1	1
ENSG00000249550	ENSG00000249550	RP11-438N16.1	12:114117263-114211488	NOTEST	0.145914	0.228439	0.646693	0	1	1
ENSG00000249551	ENSG00000249551	RP11-2N5.2	5:117911269-117917019	NOTEST	0	0	0	0	1	1
ENSG00000249553	ENSG00000249553	PPP2R2B-IT1	5:145942788-146464347	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000249555	ENSG00000249555	TMEM248P1	4:126597872-126673948	NOTEST	0	0	0	0	1	1
ENSG00000249557	ENSG00000249557	HSPD1P15	5:19233474-19234596	NOTEST	0	0	0	0	1	1
ENSG00000249558	ENSG00000249558	RCC2P4	3:126423062-126679249	NOTEST	0	0	0	0	1	1
ENSG00000249562	ENSG00000249562	RP11-116O11.2	5:24487208-24645087	NOTEST	0	0	0	0	1	1
ENSG00000249563	ENSG00000249563	RP11-751L19.1	4:9734993-9743985	NOTEST	0	0	0	0	1	1
ENSG00000249564	ENSG00000249564	RP11-390C19.1	4:29909280-29909413	NOTEST	0	0	0	0	1	1
ENSG00000249568	ENSG00000249568	RP11-234O6.2	4:162300104-163085187	NOTEST	0	0.00947882	inf	0	1	1
ENSG00000249571	ENSG00000249571	OR12D1	HSCHR6_MHC_MCF:29323243-29424633	NOTEST	0	0	0	0	1	1
ENSG00000249574	ENSG00000249574	AC226118.1	7:419324-422678	NOTEST	0	0	0	0	1	1
ENSG00000249577	ENSG00000249577	CTD-2195M15.1	5:126801513-126801810	NOTEST	0.231639	0.167233	-0.47002	0	1	1
ENSG00000249579	ENSG00000249579	RP11-586E1.1	5:62318745-62319316	NOTEST	0	0	0	0	1	1
ENSG00000249580	ENSG00000249580	RP11-52L11.6	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000249581	ENSG00000249581	CLRN2	4:17516787-17528727	NOTEST	0	0	0	0	1	1
ENSG00000249582	ENSG00000249582	RPL7L1P4	5:117114520-117115227	NOTEST	0	0	0	0	1	1
ENSG00000249584	ENSG00000249584	RP11-478P10.1	5:57186153-57194989	NOTEST	0	0	0	0	1	1
ENSG00000249588	ENSG00000249588	CTC-537E7.1	5:67819704-67825834	NOTEST	0	0	0	0	1	1
ENSG00000249593	ENSG00000249593	CTB-46B19.2	5:138282408-138667360	NOTEST	0	0	0	0	1	1
ENSG00000249595	ENSG00000249595	AC004878.7	7:74807498-74867509	NOTEST	0	0	0	0	1	1
ENSG00000249599	ENSG00000249599	RP11-168E14.1	4:95664950-95678684	NOTEST	0	0	0	0	1	1
ENSG00000249600	ENSG00000249600	RP11-510I6.3	5:121007067-121007567	NOTEST	0.0841457	0	#NAME?	0	1	1
ENSG00000249601	ENSG00000249601	CTB-27N1.1	5:169618582-169626145	NOTEST	0	0	0	0	1	1
ENSG00000249602	ENSG00000249602	RP11-98D18.3	1:151728016-151766878	NOTEST	0	0.170052	inf	0	1	1
ENSG00000249604	ENSG00000249604	RP11-286E11.2	4:108745718-108899955	NOTEST	0.0520044	0.0391924	-0.408059	0	1	1
ENSG00000249605	ENSG00000249605	CTC-218H9.1	5:143550395-143865249	NOTEST	0	0	0	0	1	1
ENSG00000249606	ENSG00000249606	TRAPPC2P7	Y:20817405-20818076	NOTEST	0	0	0	0	1	1
ENSG00000249607	ENSG00000249607	RP11-197O8.1	5:23689035-23689495	NOTEST	0	0	0	0	1	1
ENSG00000249609	ENSG00000249609	RP11-635L1.3	4:169277885-169931426	NOTEST	0	0	0	0	1	1
ENSG00000249610	ENSG00000249610	CTC-441N14.1	5:121464456-121518353	NOTEST	0	0	0	0	1	1
ENSG00000249613	ENSG00000249613	RP13-612N21.1	4:107354780-107374605	NOTEST	0	0	0	0	1	1
ENSG00000249614	ENSG00000249614	RP11-703G6.1	4:104882772-104958080	NOTEST	0	0	0	0	1	1
ENSG00000249616	ENSG00000249616	CTD-2194F12.1	5:26711659-26750106	NOTEST	0	0	0	0	1	1
ENSG00000249617	ENSG00000249617	RP11-366M4.17	4:165967120-165967432	NOTEST	0	0.0814945	inf	0	1	1
ENSG00000249618	ENSG00000249618	RP11-422J15.1	4:130692813-130876523	NOTEST	0	0	0	0	1	1
ENSG00000249619	ENSG00000249619	HMGN1P13	5:110831730-111353006	NOTEST	0	0	0	0	1	1
ENSG00000249620	ENSG00000249620	RP11-321E2.10	5:17511941-17512347	NOTEST	0	0	0	0	1	1
ENSG00000249621	ENSG00000249621	CTD-2544H17.1	5:121646991-121814782	NOTEST	0	0	0	0	1	1
ENSG00000249623	ENSG00000249623	RP11-610J23.1	4:169277885-169931426	NOTEST	0	0	0	0	1	1
ENSG00000249624	ENSG00000249624	AP000295.9	21:34602205-34669539	NOTEST	0.264865	0.132143	-1.00315	0	1	1
ENSG00000249626	ENSG00000249626	RP11-496H1.1	3:197361185-197362682	NOTEST	0.0966721	0.126823	0.391643	0	1	1
ENSG00000249627	ENSG00000249627	RP11-312A15.1	4:158736161-158736632	NOTEST	0	0	0	0	1	1
ENSG00000249628	ENSG00000249628	LINC00942	12:1609690-1616484	NOTEST	0.00661218	0.0849337	3.68314	0	1	1
ENSG00000249631	ENSG00000249631	RP11-281P23.2	4:11627337-11815582	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000249633	ENSG00000249633	OR52V1P	11:5274419-5667019	NOTEST	0	0	0	0	1	1
ENSG00000249634	ENSG00000249634	USP9YP5	Y:20652800-20790963	NOTEST	0	0	0	0	1	1
ENSG00000249635	ENSG00000249635	RP11-710F7.3	4:106473776-106943635	NOTEST	0.0079951	0	#NAME?	0	1	1
ENSG00000249637	ENSG00000249637	CTC-329D1.2	5:139739786-139780952	NOTEST	0.263727	0.214668	-0.296938	0	1	1
ENSG00000249638	ENSG00000249638	CTD-2296D1.3	5:7363091-7364644	NOTEST	0	0	0	0	1	1
ENSG00000249639	ENSG00000249639	CTB-138E5.1	5:134779904-134794387	NOTEST	0	0	0	0	1	1
ENSG00000249641	ENSG00000249641	HOXC13-AS	12:54329111-54340328	NOTEST	0.179889	0.0936864	-0.941197	0	1	1
ENSG00000249642	ENSG00000249642	RP11-565A3.1	4:188454031-188593795	NOTEST	0	0	0	0	1	1
ENSG00000249643	ENSG00000249643	RP11-436H11.6	5:123972607-124084500	NOTEST	0	0	0	0	1	1
ENSG00000249645	ENSG00000249645	RP11-552M14.1	4:23107124-23125110	NOTEST	0	0	0	0	1	1
ENSG00000249646	ENSG00000249646	OR7E94P	4:80508455-80509284	NOTEST	0	0	0	0	1	1
ENSG00000249647	ENSG00000249647	CTC-349C3.2	5:134363424-134736986	NOTEST	0	0	0	0	1	1
ENSG00000249649	ENSG00000249649	MRPS33P2	4:37892707-38140796	NOTEST	0	0	0	0	1	1
ENSG00000249650	ENSG00000249650	RP11-310P5.1	5:602734-612325	NOTEST	0.035369	0.0250512	-0.497604	0	1	1
ENSG00000249654	ENSG00000249654	VN1R104P	19:54818352-54850421	NOTEST	0	0	0	0	1	1
ENSG00000249655	ENSG00000249655	CTC-325J23.2	5:79922046-80172279	NOTEST	0.117901	0.210024	0.832979	0	1	1
ENSG00000249658	ENSG00000249658	RP11-1018N14.4	17:49412621-49413601	NOTEST	0	0	0	0	1	1
ENSG00000249661	ENSG00000249661	TNRC18P1	4:141541918-141677274	NOTEST	0.0205168	0.0279798	0.447583	0	1	1
ENSG00000249662	ENSG00000249662	RP11-321E2.4	5:17444118-17484055	NOTEST	0	0	0	0	1	1
ENSG00000249663	ENSG00000249663	HCG4P11	HSCHR6_MHC_MCF:29687667-29690477	NOTEST	0	0	0	0	1	1
ENSG00000249664	ENSG00000249664	CTD-2227C6.2	5:82308103-82308928	NOTEST	0.128626	0	#NAME?	0	1	1
ENSG00000249666	ENSG00000249666	RP11-432M8.12	5:17632196-17632792	NOTEST	0	0	0	0	1	1
ENSG00000249667	ENSG00000249667	RP11-213G21.1	4:38422282-38524801	NOTEST	0	0	0	0	1	1
ENSG00000249668	ENSG00000249668	KRT18P56	5:40066752-40067302	NOTEST	0	0	0	0	1	1
ENSG00000249669	ENSG00000249669	MIR143HG	5:148786251-148808241	NOTEST	0	0	0	0	1	1
ENSG00000249675	ENSG00000249675	RP11-217C7.1	4:167309852-167447271	NOTEST	0	0	0	0	1	1
ENSG00000249677	ENSG00000249677	RP11-395P13.3	5:124705857-124706617	NOTEST	0	0	0	0	1	1
ENSG00000249678	ENSG00000249678	RP11-619J20.1	4:30722036-31148422	NOTEST	0	0	0	0	1	1
ENSG00000249679	ENSG00000249679	RP11-279O9.4	4:186347393-186393417	NOTEST	0.577256	0.252711	-1.19172	0	1	1
ENSG00000249680	ENSG00000249680	TUBA3GP	22:21419748-21424386	NOTEST	0	0	0	0	1	1
ENSG00000249681	ENSG00000249681	KRT19P3	4:110800225-110801053	NOTEST	0	0	0	0	1	1
ENSG00000249684	ENSG00000249684	RP11-423H2.3	5:177236407-177410055	NOTEST	0	0	0	0	1	1
ENSG00000249685	ENSG00000249685	RP11-360F5.3	4:39135532-39137228	NOTEST	0.4508	0.589863	0.387892	0	1	1
ENSG00000249686	ENSG00000249686	RP11-790I12.4	4:70315731-70317331	NOTEST	0	0	0	0	1	1
ENSG00000249688	ENSG00000249688	RP11-5N11.7	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000249689	ENSG00000249689	AC138517.5	5:138872122-138872690	NOTEST	0	0	0	0	1	1
ENSG00000249690	ENSG00000249690	RP11-1336O20.2	4:151185593-151936879	NOTEST	0.00728707	0	#NAME?	0	1	1
ENSG00000249691	ENSG00000249691	RP11-445J14.1	3:134196547-134293859	NOTEST	0	0	0	0	1	1
ENSG00000249692	ENSG00000249692	RP11-21G20.4	4:155675907-155749965	NOTEST	0	0	0	0	1	1
ENSG00000249693	ENSG00000249693	THEGL	4:57396774-57469673	NOTEST	0.0401663	0.0359794	-0.158812	0	1	1
ENSG00000249694	ENSG00000249694	RP11-378A12.1	8:2447075-2480453	NOTEST	0	0	0	0	1	1

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ENSG00000249697	ENSG00000249697	RP11-155L15.1	5:55609731-55617224	NOTEST	0	0	0	0	1	1
ENSG00000249698	ENSG00000249698	RP11-627H22.8	4:156378331-156379112	NOTEST	0	0	0	0	1	1
ENSG00000249699	ENSG00000249699	RP11-415C15.2	4:27209126-27283847	NOTEST	0	0	0	0	1	1
ENSG00000249700	ENSG00000249700	SRD5A3-AS1	4:56212275-56262014	NOTEST	0.165686	0.0964768	-0.780194	0	1	1
ENSG00000249706	ENSG00000249706	RP11-89B16.1	4:54243809-55164414	NOTEST	0	0	0	0	1	1
ENSG00000249708	ENSG00000249708	RP11-503L23.1	4:152808694-152812415	NOTEST	0	0	0	0	1	1
ENSG00000249710	ENSG00000249710	RP11-588P8.1	4:100869242-101136662	NOTEST	0	0	0	0	1	1
ENSG00000249713	ENSG00000249713	CTD-2236F14.1	5:75699073-76031606	NOTEST	0	0	0	0	1	1
ENSG00000249715	ENSG00000249715	FER1L5	2:97258906-97370624	NOTEST	0.0156798	0.0279434	0.833603	0	1	1
ENSG00000249717	ENSG00000249717	RP11-44F21.3	4:75858304-75975325	NOTEST	0	0	0	0	1	1
ENSG00000249721	ENSG00000249721	RP11-83M16.4	5:66675205-67198428	NOTEST	0	0	0	0	1	1
ENSG00000249722	ENSG00000249722	CTC-430J12.2	5:173756614-173757506	NOTEST	0	0	0	0	1	1
ENSG00000249725	ENSG00000249725	RP11-469L4.1	3:132733847-132755896	NOTEST	0	0	0	0	1	1
ENSG00000249726	ENSG00000249726	TUBB1P1	Y:20548859-20551037	NOTEST	0	0	0	0	1	1
ENSG00000249727	ENSG00000249727	RP11-273B19.2	4:55702326-55711568	NOTEST	0	0	0	0	1	1
ENSG00000249729	ENSG00000249729	RP11-55C6.1	4:44842396-44843419	NOTEST	0	0	0	0	1	1
ENSG00000249730	ENSG00000249730	OR10J4	1:159315955-159453166	NOTEST	0	0	0	0	1	1
ENSG00000249731	ENSG00000249731	RP11-259O2.3	5:1968207-1969127	NOTEST	0	0	0	0	1	1
ENSG00000249734	ENSG00000249734	RP11-332J15.1	5:6795992-6826841	NOTEST	0	0	0	0	1	1
ENSG00000249735	ENSG00000249735	RP11-468N14.12	4:69850726-69854251	NOTEST	0	0	0	0	1	1
ENSG00000249736	ENSG00000249736	RP11-83M16.5	5:66675205-67198428	NOTEST	0	0	0	0	1	1
ENSG00000249737	ENSG00000249737	RP1-167G20.2	5:16373469-16440190	NOTEST	0	0	0	0	1	1
ENSG00000249738	ENSG00000249738	AC008697.1	5:158737940-158789842	NOTEST	0.104789	0.131967	0.332684	0	1	1
ENSG00000249740	ENSG00000249740	CTD-2127H9.1	5:38736156-38845931	NOTEST	0	0	0	0	1	1
ENSG00000249741	ENSG00000249741	RP11-673E1.3	4:144832666-144833206	NOTEST	0	0.120682	inf	0	1	1
ENSG00000249742	ENSG00000249742	RP11-217E13.1	4:187900643-187943127	NOTEST	0	0	0	0	1	1
ENSG00000249743	ENSG00000249743	RP11-60A8.1	5:72509773-72590761	NOTEST	0	0	0	0	1	1
ENSG00000249744	ENSG00000249744	CTD-2057J6.2	5:29848790-29849325	NOTEST	0	0	0	0	1	1
ENSG00000249745	ENSG00000249745	HMGB1P28	4:41844170-41845967	NOTEST	0	0	0	0	1	1
ENSG00000249746	ENSG00000249746	RP11-254I22.3	5:95220801-96143803	NOTEST	0	0	0	0	1	1
ENSG00000249747	ENSG00000249747	RP11-308K2.1	4:188123139-188130500	NOTEST	0	0	0	0	1	1
ENSG00000249748	ENSG00000249748	RP11-79C6.3	5:35938923-35940095	NOTEST	0	0	0	0	1	1
ENSG00000249751	ENSG00000249751	ECSCR	5:138837129-138842328	NOTEST	0	0.0414993	inf	0	1	1
ENSG00000249752	ENSG00000249752	RP11-563M4.1	4:149948596-149983674	NOTEST	0	0	0	0	1	1
ENSG00000249753	ENSG00000249753	RP11-415I12.3	12:63952692-64217675	NOTEST	0	0	0	0	1	1
ENSG00000249754	ENSG00000249754	RP11-425I13.2	4:141178439-141306880	NOTEST	0	0	0	0	1	1
ENSG00000249755	ENSG00000249755	RP11-466G12.2	4:89442135-89629693	NOTEST	0.06113	0	#NAME?	0	1	1
ENSG00000249761	ENSG00000249761	CTD-2278B20.1	5:96424778-96772921	NOTEST	0	0	0	0	1	1
ENSG00000249763	ENSG00000249763	RP11-618I10.1	4:70108345-70116533	NOTEST	0	0	0	0	1	1

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ENSG00000249766	ENSG00000249766	RP11-802H3.1	4:33402159-33402301	NOTEST	0	0	0	0	1	1
ENSG00000249767	ENSG00000249767	ENPP7P10	4:9080748-9143334	NOTEST	0	0	0	0	1	1
ENSG00000249768	ENSG00000249768	HSPE1P10	5:126073129-126073687	NOTEST	0	0	0	0	1	1
ENSG00000249770	ENSG00000249770	MTND6P17	4:156373677-156374196	NOTEST	0	0	0	0	1	1
ENSG00000249771	ENSG00000249771	RP11-457P14.5	4:41885076-41896596	NOTEST	0	0	0	0	1	1
ENSG00000249772	ENSG00000249772	CTD-2193P3.2	5:80243515-80597379	NOTEST	0	0	0	0	1	1
ENSG00000249774	ENSG00000249774	CTD-2206G10.2	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000249776	ENSG00000249776	RP11-133F8.2	5:91378413-92023961	NOTEST	0.153128	0.464241	1.60013	0	1	1
ENSG00000249777	ENSG00000249777	CTC-235G5.1	5:75371355-75371745	NOTEST	0	0	0	0	1	1
ENSG00000249778	ENSG00000249778	TRMT112P2	5:79287133-79379477	NOTEST	0	0	0	0	1	1
ENSG00000249779	ENSG00000249779	RP11-447H19.3	5:43192172-43280952	NOTEST	0.015936	0.0348363	1.1283	0	1	1
ENSG00000249780	ENSG00000249780	RP11-352E6.2	4:12640709-12642633	NOTEST	0	0	0	0	1	1
ENSG00000249781	ENSG00000249781	CTD-2143L24.1	5:9621488-9903938	NOTEST	0	0	0	0	1	1
ENSG00000249782	ENSG00000249782	RP11-417J1.1	5:8525290-8528791	NOTEST	0.173039	0	#NAME?	0	1	1
ENSG00000249784	ENSG00000249784	SCARNA22	4:1873150-1983934	NOTEST	0	0	0	0	1	1
ENSG00000249785	ENSG00000249785	CTD-2061E9.1	5:28286495-28287772	NOTEST	0	0	0	0	1	1
ENSG00000249786	ENSG00000249786	EAF1-AS1	3:15422781-15563258	NOTEST	0.0999927	0.0555209	-0.848792	0	1	1
ENSG00000249787	ENSG00000249787	RP11-346J10.1	5:99737144-99744603	NOTEST	0	0	0	0	1	1
ENSG00000249790	ENSG00000249790	RP11-20D14.6	12:8834195-9039597	NOTEST	0.0494519	0.0649701	0.393751	0	1	1
ENSG00000249791	ENSG00000249791	CTC-428G20.2	5:114524259-114524629	NOTEST	0	0.0532839	inf	0	1	1
ENSG00000249792	ENSG00000249792	RP11-1072N2.3	5:84508775-84509432	NOTEST	0	0	0	0	1	1
ENSG00000249795	ENSG00000249795	RP11-18O11.2	4:128419481-128419962	NOTEST	0	0	0	0	1	1
ENSG00000249797	ENSG00000249797	CTD-3179P9.1	5:117260702-117601730	NOTEST	0	0	0	0	1	1
ENSG00000249798	ENSG00000249798	HSD3BP3	1:120081131-120088536	NOTEST	0.0870796	0.0267511	-1.70274	0	1	1
ENSG00000249799	ENSG00000249799	RP11-264E23.1	4:9585565-9585755	NOTEST	0	0	0	0	1	1
ENSG00000249803	ENSG00000249803	RP11-114H21.2	5:135802365-135855987	NOTEST	0	0	0	0	1	1
ENSG00000249806	ENSG00000249806	RP11-223C24.1	4:142944312-143768585	NOTEST	0.33049	0.288409	-0.196492	0	1	1
ENSG00000249807	ENSG00000249807	CTD-2199O4.1	5:10137249-10138477	NOTEST	0.0192395	0	#NAME?	0	1	1
ENSG00000249808	ENSG00000249808	CTD-2029E14.1	5:3178208-3181346	NOTEST	0	0	0	0	1	1
ENSG00000249811	ENSG00000249811	USP17L21	4:9264597-9266190	NOTEST	0	0	0	0	1	1
ENSG00000249814	ENSG00000249814	RPSAP2	HSCHR6_MHC_COX:28700591-28701479	NOTEST	0	0	0	0	1	1
ENSG00000249816	ENSG00000249816	LINC00964	8:125847125-125966570	NOTEST	0.0545733	0	#NAME?	0	1	1
ENSG00000249818	ENSG00000249818	RP11-73G16.3	4:152826083-152865085	NOTEST	0	0	0	0	1	1
ENSG00000249819	ENSG00000249819	RP11-392C20.1	4:158125333-158287227	NOTEST	0	0	0	0	1	1
ENSG00000249820	ENSG00000249820	RP11-503I22.2	3:133118838-133194066	NOTEST	0	0	0	0	1	1
ENSG00000249825	ENSG00000249825	CTD-2201I18.1	5:79287133-79379477	NOTEST	0.298489	0.187811	-0.668396	0	1	1
ENSG00000249828	ENSG00000249828	RP11-1281K21.2	4:49205187-49205743	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000249830	ENSG00000249830	RP11-121L11.3	5:3417265-3536208	NOTEST	0	0	0	0	1	1
ENSG00000249831	ENSG00000249831	RP11-4O3.2	4:58586200-58590821	NOTEST	0	0	0	0	1	1
ENSG00000249833	ENSG00000249833	RP11-71E19.5	3:126111874-126113694	NOTEST	0	0	0	0	1	1
ENSG00000249834	ENSG00000249834	PGBD4P3	5:147647742-147763346	NOTEST	0	0	0	0	1	1
ENSG00000249835	ENSG00000249835	VCAN-AS1	5:82767283-82878122	NOTEST	0	0	0	0	1	1
ENSG00000249837	ENSG00000249837	CTD-2325B11.1	4:125070531-125173199	NOTEST	0	0	0	0	1	1
ENSG00000249838	ENSG00000249838	SUMO2P7	17:48313205-48313490	NOTEST	0	0	0	0	1	1
ENSG00000249839	ENSG00000249839	AC011330.5	15:43885251-44010458	NOTEST	0.111427	0.0716428	-0.6372	0	1	1
ENSG00000249840	ENSG00000249840	AC020947.2	19:11670188-11729950	NOTEST	0.0184627	0.0143505	-0.363521	0	1	1
ENSG00000249842	ENSG00000249842	CTD-2331D11.4	5:84742791-84743576	NOTEST	0	0	0	0	1	1
ENSG00000249843	ENSG00000249843	RP11-45H22.2	5:54174065-54174416	NOTEST	0	0	0	0	1	1
ENSG00000249844	ENSG00000249844	OR7E43P	4:4176045-4176965	NOTEST	0	0	0	0	1	1
ENSG00000249846	ENSG00000249846	RP11-77P16.4	3:129800673-129839422	NOTEST	0.226899	0.139073	-0.70621	0	1	1
ENSG00000249847	ENSG00000249847	RP11-192C21.2	4:135854043-135855286	NOTEST	0	0	0	0	1	1
ENSG00000249848	ENSG00000249848	RP11-212F11.1	8:9911777-10286401	NOTEST	0	0	0	0	1	1
ENSG00000249849	ENSG00000249849	RP11-1101H11.	5:177109294-177221397	NOTEST	0	0	0	0	1	1
ENSG00000249850	ENSG00000249850	KRT18P31	5:36876860-37066515	NOTEST	0.0506081	0.0196269	-1.36654	0	1	1
ENSG00000249851	ENSG00000249851	RP11-166J22.1	5:137588067-137610360	NOTEST	0	0	0	0	1	1
ENSG00000249852	ENSG00000249852	AC145676.2	7:182934-300711	NOTEST	0.0146753	0	#NAME?	0	1	1
ENSG00000249853	ENSG00000249853	HS3ST5	6:114254191-114792869	NOTEST	0.0263274	0.0294356	0.160998	0	1	1
ENSG00000249854	ENSG00000249854	RP11-420O16.1	5:19473059-20575982	NOTEST	0	0	0	0	1	1
ENSG00000249856	ENSG00000249856	CTD-2503O16.4	5:74213550-74319753	NOTEST	0	0	0	0	1	1
ENSG00000249857	ENSG00000249857	CTD-2227C6.3	5:82236276-82236802	NOTEST	0	0	0	0	1	1
ENSG00000249858	ENSG00000249858	SNX5P1	4:77234153-77343021	NOTEST	0	0.041185	inf	0	1	1
ENSG00000249860	ENSG00000249860	MTRNR2L5	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000249861	ENSG00000249861	LGALS16	19:40146533-40151287	NOTEST	0	0	0	0	1	1
ENSG00000249865	ENSG00000249865	CTD-2296D1.4	5:7368041-7373187	NOTEST	0	0	0	0	1	1
ENSG00000249866	ENSG00000249866	OR7E83P	4:9514553-9515523	NOTEST	0	0	0	0	1	1
ENSG00000249867	ENSG00000249867	RP11-115J23.1	11:28724161-29085368	NOTEST	0	0	0	0	1	1
ENSG00000249868	ENSG00000249868	RP11-63E5.6	8:255305-281026	NOTEST	0.0209494	0	#NAME?	0	1	1
ENSG00000249869	ENSG00000249869	RP11-93K22.7	3:129732024-129732384	NOTEST	0	0	0	0	1	1
ENSG00000249870	ENSG00000249870	RP11-481C4.1	17:49039534-49198226	NOTEST	0	0	0	0	1	1
ENSG00000249873	ENSG00000249873	RP11-983C2.2	12:127354035-127359236	NOTEST	0	0	0	0	1	1
ENSG00000249875	ENSG00000249875	RP11-51M24.1	4:175276004-175297596	NOTEST	0	0	0	0	1	1
ENSG00000249876	ENSG00000249876	CTC-563A5.4	5:179338650-179499118	NOTEST	0	0	0	0	1	1
ENSG00000249877	ENSG00000249877	RP11-706F1.2	4:190209830-190212490	NOTEST	0	0	0	0	1	1
ENSG00000249878	ENSG00000249878	CTD-2244C20.1	5:61127773-61128851	NOTEST	0	0	0	0	1	1
ENSG00000249881	ENSG00000249881	CTB-57H20.1	5:142985192-143208337	NOTEST	0	0	0	0	1	1
ENSG00000249882	ENSG00000249882	RP11-665I14.1	4:31508287-31560443	NOTEST	0	0	0	0	1	1
ENSG00000249883	ENSG00000249883	RP11-460H9.1	4:181652316-181680191	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000249885	ENSG00000249885	ARHGEF38-IT1	4:106473776-106943635	NOTEST	0	0	0	0	1	1
ENSG00000249887	ENSG00000249887	RP11-457P14.6	4:41926196-41926397	NOTEST	0	0	0	0	1	1
ENSG00000249888	ENSG00000249888	RP11-447H19.2	5:43192172-43280952	NOTEST	0	0	0	0	1	1
ENSG00000249889	ENSG00000249889	ALG1L11P	8:12036205-12051642	NOTEST	0	0	0	0	1	1
ENSG00000249890	ENSG00000249890	RP11-813N20.2	4:69887373-69888058	NOTEST	0	0	0	0	1	1
ENSG00000249891	ENSG00000249891	KRT19P6	4:92806196-92806405	NOTEST	0	0	0	0	1	1
ENSG00000249892	ENSG00000249892	RP11-525J21.1	4:60633533-60657832	NOTEST	0	0	0	0	1	1
ENSG00000249893	ENSG00000249893	MTND6P16	4:65474622-65475142	NOTEST	0	0	0	0	1	1
ENSG00000249894	ENSG00000249894	RP11-434D9.2	5:66675205-67198428	NOTEST	0	0	0	0	1	1
ENSG00000249896	ENSG00000249896	RP11-586D19.1	4:6202459-6240044	NOTEST	0	0	0	0	1	1
ENSG00000249898	ENSG00000249898	CTD-2541M15.1	8:6261071-6565730	NOTEST	0.281597	0.182998	-0.621808	0	1	1
ENSG00000249899	ENSG00000249899	CTD-2175A23.1	5:51971026-52390609	NOTEST	0	0	0	0	1	1
ENSG00000249901	ENSG00000249901	RP11-781M16.2	4:159236462-159574524	NOTEST	0	0	0	0	1	1
ENSG00000249904	ENSG00000249904	CTC-394G3.2	5:125221977-125222446	NOTEST	0	0	0	0	1	1
ENSG00000249906	ENSG00000249906	RP5-1029K10.2	17:47572654-47661189	NOTEST	0	0.0101959	inf	0	1	1
ENSG00000249909	ENSG00000249909	CYCTP	2:178487979-178973066	NOTEST	0	0	0	0	1	1
ENSG00000249911	ENSG00000249911	RP11-122C5.1	5:38710468-38720375	NOTEST	0	0	0	0	1	1
ENSG00000249912	ENSG00000249912	TRBV26	7:142403510-142403995	NOTEST	0	0	0	0	1	1
ENSG00000249916	ENSG00000249916	CTD-2280E9.1	5:121646991-121814782	NOTEST	0.037896	0	#NAME?	0	1	1
ENSG00000249917	ENSG00000249917	LINC00536	8:116962735-117337297	NOTEST	0	0	0	0	1	1
ENSG00000249919	ENSG00000249919	FABP5P6	5:118788137-118972894	NOTEST	0	0	0	0	1	1
ENSG00000249920	ENSG00000249920	HNRNPA1P55	4:74804320-74805275	NOTEST	0	0	0	0	1	1
ENSG00000249921	ENSG00000249921	CTC-329H14.1	5:108083522-108532542	NOTEST	0	0	0	0	1	1
ENSG00000249923	ENSG00000249923	XXbac-B444P24.8	22:20186251-20192441	NOTEST	0	0	0	0	1	1
ENSG00000249924	ENSG00000249924	RP11-27G13.1	4:156197840-156302498	NOTEST	0	0	0	0	1	1
ENSG00000249926	ENSG00000249926	RP11-495K9.6	12:132147140-132149249	NOTEST	0	0.0234831	inf	0	1	1
ENSG00000249927	ENSG00000249927	CTD-2151L9.2	5:18894010-18894277	NOTEST	0	0	0	0	1	1
ENSG00000249928	ENSG00000249928	UQCRBP3	5:14874508-14874820	NOTEST	0	0	0	0	1	1
ENSG00000249930	ENSG00000249930	AC007016.3	4:15471488-15603180	NOTEST	0	0	0	0	1	1
ENSG00000249931	ENSG00000249931	GOLGA8K	15:32684982-32727434	NOTEST	0.0156185	0.0377444	1.27301	0	1	1
ENSG00000249932	ENSG00000249932	RP11-395P13.2	5:124704260-124705035	NOTEST	0	0	0	0	1	1
ENSG00000249934	ENSG00000249934	RP11-466G12.3	4:89429741-89431554	NOTEST	0	0	0	0	1	1
ENSG00000249937	ENSG00000249937	RP11-454P21.1	5:17684692-17955966	NOTEST	0	0	0	0	1	1
ENSG00000249941	ENSG00000249941	CTD-2046I8.1	5:4866633-4874872	NOTEST	0	0	0	0	1	1
ENSG00000249942	ENSG00000249942	AC142293.3	4:75418300-75514664	NOTEST	0	0	0	0	1	1
ENSG00000249943	ENSG00000249943	RP11-213L8.1	4:171735489-171735699	NOTEST	0	0	0	0	1	1
ENSG00000249944	ENSG00000249944	CTB-161J7.1	5:114825330-114825628	NOTEST	0	0	0	0	1	1
ENSG00000249945	ENSG00000249945	RP11-598D14.1	4:176379439-176387848	NOTEST	0	0	0	0	1	1
ENSG00000249947	ENSG00000249947	XBP1P1	5:112043194-112258236	NOTEST	0.0617657	0	#NAME?	0	1	1

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ENSG00000249950	ENSG00000249950	CTC-394G3.1	5:125198438-125198886	NOTEST	0	0	0	0	1	1
ENSG00000249951	ENSG00000249951	RP11-554D13.1	4:95596395-95623721	NOTEST	0	0	0	0	1	1
ENSG00000249955	ENSG00000249955	RP11-6E9.4	4:170902897-170954182	NOTEST	0.155081	0	#NAME?	0	1	1
ENSG00000249956	ENSG00000249956	RP11-790I12.2	4:70274553-70288882	NOTEST	0	0	0	0	1	1
ENSG00000249958	ENSG00000249958	CCT7P2	5:92225093-92226547	NOTEST	0	0	0	0	1	1
ENSG00000249959	ENSG00000249959	RP11-252I13.2	5:107035535-107052542	NOTEST	0	0	0	0	1	1
ENSG00000249960	ENSG00000249960	RP11-791G16.5	4:83492289-83492967	NOTEST	0	0	0	0	1	1
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ENSG00000249963	ENSG00000249963	EEF1A1P20	5:99332250-99333636	NOTEST	0	0	0	0	1	1
ENSG00000249965	ENSG00000249965	CDC42P4	4:110476325-110476888	NOTEST	0.0378952	0	#NAME?	0	1	1
ENSG00000249966	ENSG00000249966	CTD-2194D22.1	5:1851063-1851611	NOTEST	0	0	0	0	1	1
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ENSG00000249971	ENSG00000249971	RP11-256P1.1	5:137620953-137685416	NOTEST	0	0.310742	inf	0	1	1
ENSG00000249973	ENSG00000249973	CHCHD2P7	4:88707071-88707523	NOTEST	0	0	0	0	1	1
ENSG00000249975	ENSG00000249975	OR5H3P	3:97926266-97927185	NOTEST	0	0	0	0	1	1
ENSG00000249976	ENSG00000249976	RP11-580P21.1	4:74202949-74203488	NOTEST	0	0	0	0	1	1
ENSG00000249977	ENSG00000249977	RP11-155G15.3	5:96785061-96785445	NOTEST	0	0	0	0	1	1
ENSG00000249978	ENSG00000249978	TRGV7	7:38374641-38375115	NOTEST	0	0.0635068	inf	0	1	1
ENSG00000249981	ENSG00000249981	RP11-136K7.1	5:70647681-70742396	NOTEST	0	0	0	0	1	1
ENSG00000249982	ENSG00000249982	RP11-1018N14.3	17:49389969-49412526	NOTEST	0	0	0	0	1	1
ENSG00000249984	ENSG00000249984	CTC-529L17.2	5:91378413-92023961	NOTEST	0.053145	0	#NAME?	0	1	1
ENSG00000249985	ENSG00000249985	RP11-468N14.8	4:69773635-69773752	NOTEST	0	0	0	0	1	1
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ENSG00000249987	ENSG00000249987	RPS4XP20	19:34513560-34514332	NOTEST	0	0	0	0	1	1
ENSG00000249988	ENSG00000249988	RP11-669M16.1	4:14166078-14244437	NOTEST	0	0	0	0	1	1
ENSG00000249990	ENSG00000249990	RP11-474J18.2	5:97745378-97745804	NOTEST	0	0	0	0	1	1
ENSG00000249993	ENSG00000249993	BFSP2-AS1	3:133118838-133194066	NOTEST	0	0.0144876	inf	0	1	1
ENSG00000249994	ENSG00000249994	CTD-2383I20.1	5:4033825-4041877	NOTEST	0	0	0	0	1	1
ENSG00000249995	ENSG00000249995	RP11-352E6.1	4:12640709-12642633	NOTEST	0	0	0	0	1	1
ENSG00000249996	ENSG00000249996	RP11-359P5.1	5:122179133-122390362	NOTEST	0.0706059	0	#NAME?	0	1	1
ENSG00000249997	ENSG00000249997	AC068137.8	2:131034079-131035530	NOTEST	0	0	0	0	1	1
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ENSG00000250001	ENSG00000250001	CTD-2201E9.2	5:9001885-9546187	NOTEST	0	0	0	0	1	1
ENSG00000250003	ENSG00000250003	CTD-2116N24.1	5:38025798-38184034	NOTEST	0	0	0	0	1	1
ENSG00000250006	ENSG00000250006	CTB-179I1.1	4:78078303-78415440	NOTEST	0	0	0	0	1	1
ENSG00000250007	ENSG00000250007	RP11-814P5.1	15:35047284-35105124	NOTEST	0	0.0140038	inf	0	1	1
ENSG00000250011	ENSG00000250011	HMGB1P3	2:231280656-231444721	NOTEST	0.0150898	0	#NAME?	0	1	1
ENSG00000250012	ENSG00000250012	RP11-124N2.1	3:125725197-125820404	NOTEST	0.283313	0	#NAME?	0	1	1
ENSG00000250013	ENSG00000250013	RP11-456A14.1	5:83170984-83171640	NOTEST	0	0	0	0	1	1
ENSG00000250015	ENSG00000250015	CTC-339F2.2	5:115419503-115748459	NOTEST	0.322161	0	#NAME?	0	1	1
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ENSG00000250020	ENSG00000250020	RP11-811I15.1	5:58312-59030	NOTEST	0	0	0	0	1	1
ENSG00000250024	ENSG00000250024	RP11-818C3.1	4:189911868-189923229	NOTEST	0	0	0	0	1	1
ENSG00000250025	ENSG00000250025	CTC-359M8.1	5:145583112-145756526	NOTEST	0	0	0	0	1	1
ENSG00000250026	ENSG00000250026	RP11-646E20.6	4:69048009-69111438	NOTEST	0	0	0	0	1	1
ENSG00000250027	ENSG00000250027	RP11-563E2.2	4:164029936-164088073	NOTEST	0.218993	0.0568028	-1.94685	0	1	1
ENSG00000250030	ENSG00000250030	RP11-584P21.4	4:68283022-68333969	NOTEST	0	0	0	0	1	1
ENSG00000250031	ENSG00000250031	RP11-114M5.1	8:59323822-59364060	NOTEST	0.0594663	0.0274671	-1.11437	0	1	1
ENSG00000250032	ENSG00000250032	CTD-2194L12.3	5:37939466-37948057	NOTEST	0	0	0	0	1	1
ENSG00000250033	ENSG00000250033	SLC7A11-AS1	4:138948575-139163503	NOTEST	0.652264	0.186715	-1.80462	0	1	1
ENSG00000250034	ENSG00000250034	RP11-793B23.1	4:138728859-138737556	NOTEST	0	0	0	0	1	1
ENSG00000250036	ENSG00000250036	IGKV1D-37	2:89923549-89924026	NOTEST	0	0	0	0	1	1
ENSG00000250038	ENSG00000250038	RP11-180C1.1	4:28363900-28404486	NOTEST	0	0	0	0	1	1
ENSG00000250039	ENSG00000250039	RP11-17E2.2	4:21950637-22331953	NOTEST	0	0.00612877	inf	0	1	1
ENSG00000250040	ENSG00000250040	AC006499.8	4:10256549-10258245	NOTEST	0	0	0	0	1	1
ENSG00000250041	ENSG00000250041	CTD-2003C8.2	11:10830843-10928349	NOTEST	0.0713592	0	#NAME?	0	1	1
ENSG00000250042	ENSG00000250042	RP11-91J3.2	4:188291801-188293075	NOTEST	0	0	0	0	1	1
ENSG00000250043	ENSG00000250043	RP11-161D15.2	4:174798621-174912012	NOTEST	0	0	0	0	1	1
ENSG00000250045	ENSG00000250045	CBX3P3	5:112043194-112258236	NOTEST	0	0	0	0	1	1
ENSG00000250046	ENSG00000250046	RP11-148B6.2	4:113614202-113627966	NOTEST	0	0	0	0	1	1
ENSG00000250048	ENSG00000250048	LINC00603	5:40052392-40053426	NOTEST	0	0	0	0	1	1
ENSG00000250049	ENSG00000250049	RP11-348J24.2	5:91378413-92023961	NOTEST	0.0053305	0	#NAME?	0	1	1
ENSG00000250050	ENSG00000250050	MTND4P9	4:25719703-25721367	NOTEST	0	0	0	0	1	1
ENSG00000250053	ENSG00000250053	RARRES2P4	4:190959070-190959554	NOTEST	0	0	0	0	1	1
ENSG00000250055	ENSG00000250055	RP11-321E2.8	5:17525343-17525938	NOTEST	0	0	0	0	1	1
ENSG00000250056	ENSG00000250056	LINC01018	5:6582248-6588612	NOTEST	0	0	0	0	1	1
ENSG00000250057	ENSG00000250057	RP11-576N17.5	4:84154664-84169359	NOTEST	0	0	0	0	1	1
ENSG00000250060	ENSG00000250060	RP11-332J15.2	5:6868671-6886900	NOTEST	0	0	0	0	1	1
ENSG00000250061	ENSG00000250061	RP11-541P9.3	5:162439270-162864332	NOTEST	0.0925415	0.0417955	-1.14675	0	1	1
ENSG00000250062	ENSG00000250062	RP11-778J15.1	4:86936275-87515284	NOTEST	0	0	0	0	1	1
ENSG00000250064	ENSG00000250064	RP11-123O22.1	4:28437070-28601897	NOTEST	0.0504784	0	#NAME?	0	1	1
ENSG00000250066	ENSG00000250066	RP11-141O11.1	5:68259072-68263672	NOTEST	0	0	0	0	1	1
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ENSG00000250069	ENSG00000250069	CTB-131B5.2	5:139554226-139682706	NOTEST	0.010407	0.0040424	-1.36427	0	1	1
ENSG00000250071	ENSG00000250071	CTD-2060C23.1	5:74073398-74163679	NOTEST	0	0	0	0	1	1
ENSG00000250073	ENSG00000250073	RP11-677M14.3	11:124617367-124635832	NOTEST	0.0203973	0.0472426	1.21171	0	1	1
ENSG00000250074	ENSG00000250074	AC006499.4	4:10269518-10269855	NOTEST	0	0	0	0	1	1
ENSG00000250075	ENSG00000250075	RP11-584P21.2	4:68283022-68333969	NOTEST	0.00815999	0	#NAME?	0	1	1
ENSG00000250076	ENSG00000250076	RP11-141P6.1	4:33012569-33013368	NOTEST	0	0	0	0	1	1
ENSG00000250078	ENSG00000250078	RP11-577G20.2	4:59428329-59431287	NOTEST	0	0	0	0	1	1

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ENSG00000250080	ENSG00000250080	CTB-88F18.2	5:126506226-126507958	NOTEST	0	0	0	0	1	1
ENSG00000250081	ENSG00000250081	CTD-2116N20.1	5:64782270-64782875	NOTEST	0.457819	0.163984	-1.48123	0	1	1
ENSG00000250082	ENSG00000250082	RP11-796L2.1	4:171402845-171403346	NOTEST	0	0	0	0	1	1
ENSG00000250084	ENSG00000250084	RP11-485B17.5	X:52164595-52202209	NOTEST	0	0	0	0	1	1
ENSG00000250088	ENSG00000250088	RP11-432M8.1	5:17587398-17587632	NOTEST	0	0	0	0	1	1
ENSG00000250090	ENSG00000250090	RP13-401N8.3	20:25744101-25848861	NOTEST	0	0	0	0	1	1
ENSG00000250091	ENSG00000250091	DNAH10OS	12:124247041-124800570	NOTEST	0.0967596	0.048996	-0.981741	0	1	1
ENSG00000250092	ENSG00000250092	RP11-556G22.3	4:20697904-21950422	NOTEST	0	0	0	0	1	1
ENSG00000250095	ENSG00000250095	NREP-AS1	5:110831730-111353006	NOTEST	0	0	0	0	1	1
ENSG00000250098	ENSG00000250098	RP11-22A3.1	4:12949197-12950294	NOTEST	0	0	0	0	1	1
ENSG00000250099	ENSG00000250099	RP11-12P19.2	5:24749482-24749881	NOTEST	0	0	0	0	1	1
ENSG00000250100	ENSG00000250100	RP13-644M16.3	4:69997068-70000532	NOTEST	0	0	0	0	1	1
ENSG00000250101	ENSG00000250101	RP11-1252I4.2	5:177236407-177410055	NOTEST	0	0	0	0	1	1
ENSG00000250102	ENSG00000250102	RP11-314N14.1	4:132301167-132462552	NOTEST	0	0	0	0	1	1
ENSG00000250103	ENSG00000250103	RP11-380D23.2	4:111516670-111536614	NOTEST	0.140027	0	#NAME?	0	1	1
ENSG00000250105	ENSG00000250105	CTD-3074O7.2	11:66313865-66330800	NOTEST	0	0	0	0	1	1
ENSG00000250106	ENSG00000250106	ANKRD33B-AS1	5:10564441-10650308	NOTEST	0	0	0	0	1	1
ENSG00000250107	ENSG00000250107	CACNA1G-AS1	17:48633567-48709301	NOTEST	0.021376	0	#NAME?	0	1	1
ENSG00000250111	ENSG00000250111	AC107982.4	17:18739019-18834581	NOTEST	0.0765443	0.0194839	-1.97401	0	1	1
ENSG00000250113	ENSG00000250113	RP13-221M14.6	1:13123245-13126086	NOTEST	0	0	0	0	1	1
ENSG00000250114	ENSG00000250114	CTB-95B16.1	5:162439270-162864332	NOTEST	0	0	0	0	1	1
ENSG00000250115	ENSG00000250115	AK3P2	8:144120625-144141359	NOTEST	0	0	0	0	1	1
ENSG00000250118	ENSG00000250118	RP11-136H13.2	5:30365511-30365791	NOTEST	0	0	0	0	1	1
ENSG00000250120	ENSG00000250120	PCDHA10	5:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000250122	ENSG00000250122	CTD-2013M15.1	5:45890317-45896072	NOTEST	0.0378952	0	#NAME?	0	1	1
ENSG00000250124	ENSG00000250124	CTC-261N6.2	5:85676477-85677244	NOTEST	0	0	0	0	1	1
ENSG00000250125	ENSG00000250125	RP11-707A18.1	4:65779998-65870218	NOTEST	0.0106605	0	#NAME?	0	1	1
ENSG00000250126	ENSG00000250126	RP13-884E18.2	4:138566418-138576328	NOTEST	0	0	0	0	1	1
ENSG00000250127	ENSG00000250127	CTD-2117L12.1	5:57837393-57854070	NOTEST	0	0	0	0	1	1
ENSG00000250129	ENSG00000250129	RP11-265F19.1	3:130569438-131100319	NOTEST	0	0.116424	inf	0	1	1
ENSG00000250130	ENSG00000250130	RP11-616K22.1	15:44580926-44719342	NOTEST	0	0.043133	inf	0	1	1
ENSG00000250131	ENSG00000250131	RP11-130F10.1	4:178366132-178598280	NOTEST	0.0135108	0	#NAME?	0	1	1
ENSG00000250133	ENSG00000250133	HOXC-AS2	12:54375292-54449814	NOTEST	0.296385	0.238511	-0.313418	0	1	1
ENSG00000250135	ENSG00000250135	RP4-622L5.2	1:32573638-32642169	NOTEST	0	0	0	0	1	1
ENSG00000250137	ENSG00000250137	RP11-380P13.1	4:23562545-23905712	NOTEST	0	0	0	0	1	1
ENSG00000250138	ENSG00000250138	RP11-848G14.5	5:68773298-69006341	NOTEST	0.0254265	0.0186658	-0.445933	0	1	1
ENSG00000250140	ENSG00000250140	CTD-2517O10.5	5:34837653-34899561	NOTEST	0.0584386	0.130465	1.15867	0	1	1
ENSG00000250141	ENSG00000250141	RP11-208N20.1	4:142491083-142497230	NOTEST	0	0	0	0	1	1
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ENSG00000250147	ENSG00000250147	MORF4L2P1	4:54243809-55164414	NOTEST	0	0.0476848	inf	0	1	1
ENSG00000250148	ENSG00000250148	KRT8P31	5:60039389-60040797	NOTEST	0	0	0	0	1	1
ENSG00000250149	ENSG00000250149	RP11-399F2.2	4:126597872-126673948	NOTEST	0	0	0	0	1	1
ENSG00000250150	ENSG00000250150	RP11-436A7.1	4:168228060-168229940	NOTEST	0	0	0	0	1	1
ENSG00000250154	ENSG00000250154	MICE	HSCHR6_MHC_MANN:29687659-29713937	NOTEST	0	0	0	0	1	1
ENSG00000250155	ENSG00000250155	CTD-2353F22.1	5:36606456-36725297	NOTEST	0.220953	0	#NAME?	0	1	1
ENSG00000250156	ENSG00000250156	CTC-498M16.2	5:87485449-87794514	NOTEST	0	0	0	0	1	1
ENSG00000250158	ENSG00000250158	RP11-254I22.2	5:95220801-96143803	NOTEST	0	0	0	0	1	1
ENSG00000250161	ENSG00000250161	TRMT112P5	3:139556061-139578736	NOTEST	0	0	0	0	1	1
ENSG00000250162	ENSG00000250162	CSNK1A1P3	5:98169085-98169415	NOTEST	0	0	0	0	1	1
ENSG00000250164	ENSG00000250164	RP11-5N11.6	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000250166	ENSG00000250166	RP11-268P4.5	12:22754358-22777949	NOTEST	0	0	0	0	1	1
ENSG00000250167	ENSG00000250167	CTC-321K16.1	5:134895266-134970564	NOTEST	0	0	0	0	1	1
ENSG00000250169	ENSG00000250169	MTND5P13	4:65475171-65476250	NOTEST	0	0	0	0	1	1
ENSG00000250170	ENSG00000250170	RASA2-IT1	3:141205888-141334184	NOTEST	0	0	0	0	1	1
ENSG00000250173	ENSG00000250173	RP11-661C8.3	5:979479-981415	NOTEST	0	0	0	0	1	1
ENSG00000250174	ENSG00000250174	MYLK-AS2	3:123304388-123603178	NOTEST	0	0	0	0	1	1
ENSG00000250180	ENSG00000250180	RP11-138A23.2	4:160319684-160322398	NOTEST	0	0	0	0	1	1
ENSG00000250183	ENSG00000250183	RP11-96A1.4	4:120858711-120885448	NOTEST	0	0	0	0	1	1
ENSG00000250185	ENSG00000250185	RCC2P8	4:109709900-109710935	NOTEST	0.0313546	0	#NAME?	0	1	1
ENSG00000250186	ENSG00000250186	RP11-1079K10.4	17:47448101-47554350	NOTEST	0	0.147997	inf	0	1	1
ENSG00000250189	ENSG00000250189	RP11-362F19.2	4:142326325-142328740	NOTEST	0	0	0	0	1	1
ENSG00000250190	ENSG00000250190	RP11-292B1.2	4:28998145-29016216	NOTEST	0	0	0	0	1	1
ENSG00000250191	ENSG00000250191	RP11-285A15.1	4:134495720-134496363	NOTEST	0	0	0	0	1	1
ENSG00000250192	ENSG00000250192	RP11-300M6.1	4:57829535-58071676	NOTEST	0	0	0	0	1	1
ENSG00000250193	ENSG00000250193	RP11-419L4.1	4:130220329-130226177	NOTEST	0	0	0	0	1	1
ENSG00000250194	ENSG00000250194	RP11-257I8.1	5:124410357-124410673	NOTEST	0	0	0	0	1	1
ENSG00000250195	ENSG00000250195	RP11-371F15.3	4:139741107-139933800	NOTEST	0	0	0	0	1	1
ENSG00000250197	ENSG00000250197	HMGN1P15	5:114602884-114632528	NOTEST	0	0	0	0	1	1
ENSG00000250200	ENSG00000250200	RP13-577H12.3	4:175750818-175900532	NOTEST	0	0	0	0	1	1
ENSG00000250202	ENSG00000250202	RP11-397E7.2	4:87797357-88062206	NOTEST	0	0	0	0	1	1
ENSG00000250204	ENSG00000250204	AC006335.6	Y:6109808-6113324	NOTEST	0	0	0	0	1	1
ENSG00000250205	ENSG00000250205	YWHAEP4	4:156197840-156302498	NOTEST	0	0	0	0	1	1
ENSG00000250206	ENSG00000250206	RP11-436H11.2	5:123972607-124084500	NOTEST	0	0	0	0	1	1
ENSG00000250207	ENSG00000250207	AC079776.6	2:130748028-130808704	NOTEST	0	0	0	0	1	1
ENSG00000250208	ENSG00000250208	FZD10-AS1	12:130634893-130646801	NOTEST	0	0	0	0	1	1
ENSG00000250210	ENSG00000250210	RP11-585F1.10	8:142090-150563	NOTEST	0	0	0	0	1	1
ENSG00000250213	ENSG00000250213	RP11-488I4.2	4:132033902-132034410	NOTEST	0	0	0	0	1	1
ENSG00000250214	ENSG00000250214	RP13-488H8.1	4:78783673-78873944	NOTEST	0	0	0	0	1	1
ENSG00000250215	ENSG00000250215	CIR1P2	4:115634734-115636076	NOTEST	0.168312	0.0554121	-1.60287	0	1	1
ENSG00000250218	ENSG00000250218	ALDH1L1-AS1	3:125822411-125929012	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000250219	ENSG00000250219	LTV1P1	4:120976762-121337921	NOTEST	0	0	0	0	1	1
ENSG00000250220	ENSG00000250220	RP11-692D12.1	4:74124925-74183670	NOTEST	0.299459	0.0879008	-1.76841	0	1	1
ENSG00000250221	ENSG00000250221	KRT8P32	5:97727773-97729234	NOTEST	0	0	0	0	1	1
ENSG00000250223	ENSG00000250223	EMCN-IT3	4:101316497-101801283	NOTEST	0	0	0	0	1	1
ENSG00000250227	ENSG00000250227	TRIM60P14	4:165836716-165838135	NOTEST	0	0	0	0	1	1
ENSG00000250229	ENSG00000250229	RP11-397D21.1	4:114761205-114761392	NOTEST	0	0	0	0	1	1
ENSG00000250230	ENSG00000250230	RP11-855O10.2	11:61355965-61375022	NOTEST	0	0	0	0	1	1
ENSG00000250231	ENSG00000250231	USP17L16P	4:9240855-9242448	NOTEST	0	0	0	0	1	1
ENSG00000250232	ENSG00000250232	AF196779.12	X:48928812-48958108	NOTEST	0	0	0	0	1	1
ENSG00000250234	ENSG00000250234	CTD-2024P10.1	5:34656341-34832732	NOTEST	0	0	0	0	1	1
ENSG00000250237	ENSG00000250237	CTC-498J12.1	5:68334344-68339648	NOTEST	0	0	0	0	1	1
ENSG00000250238	ENSG00000250238	Z95704.3	4:105844-107000	NOTEST	0	0	0	0	1	1
ENSG00000250240	ENSG00000250240	CTD-2154I11.2	5:95036952-95160087	NOTEST	0.261454	0.424081	0.697786	0	1	1
ENSG00000250241	ENSG00000250241	RP11-9G1.3	4:133996465-134070271	NOTEST	0.17919	0.0877404	-1.03018	0	1	1
ENSG00000250242	ENSG00000250242	RP11-438C19.1	5:114423588-114424172	NOTEST	0	0	0	0	1	1
ENSG00000250243	ENSG00000250243	RP11-120A1.1	4:20697904-21950422	NOTEST	0	0	0	0	1	1
ENSG00000250244	ENSG00000250244	CTB-49A3.4	5:132496129-132948255	NOTEST	0	0	0	0	1	1
ENSG00000250247	ENSG00000250247	SEPHS2P1	5:14960340-14961502	NOTEST	0	0	0	0	1	1
ENSG00000250249	ENSG00000250249	RP11-30P21.2	4:63157279-63158055	NOTEST	0	0	0	0	1	1
ENSG00000250250	ENSG00000250250	CTD-2350J17.1	5:15500304-15939900	NOTEST	0	0	0	0	1	1
ENSG00000250252	ENSG00000250252	RP11-342A1.1	4:150068953-150070932	NOTEST	0	0	0	0	1	1
ENSG00000250253	ENSG00000250253	RP11-1072N2.2	5:84505877-84506721	NOTEST	0	0	0	0	1	1
ENSG00000250254	ENSG00000250254	PTTG2	4:37892707-38140796	NOTEST	0	0	0	0	1	1
ENSG00000250256	ENSG00000250256	RP11-267A15.3	5:174045166-174052778	NOTEST	0	0	0	0	1	1
ENSG00000250257	ENSG00000250257	LDHAL6DP	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000250258	ENSG00000250258	CTC-431G16.2	5:78985699-79112013	NOTEST	0	0	0	0	1	1
ENSG00000250259	ENSG00000250259	RP11-460I19.2	4:1021465-1022760	NOTEST	0	0	0	0	1	1
ENSG00000250260	ENSG00000250260	RP11-325L7.2	5:137150021-137387650	NOTEST	0.0312831	0	#NAME?	0	1	1
ENSG00000250261	ENSG00000250261	AC007050.18	22:20850199-20946505	NOTEST	0.0596315	0.0121349	-2.29691	0	1	1
ENSG00000250263	ENSG00000250263	RP11-765K14.1	4:177796855-177801759	NOTEST	0	0	0	0	1	1
ENSG00000250266	ENSG00000250266	RP11-789C1.1	4:171195069-171204230	NOTEST	0	0	0	0	1	1
ENSG00000250267	ENSG00000250267	RP11-122A21.2	8:110253147-110358182	NOTEST	0	0	0	0	1	1
ENSG00000250268	ENSG00000250268	ALG1L14P	4:9168022-9171996	NOTEST	0	0	0	0	1	1
ENSG00000250269	ENSG00000250269	RP11-395P13.5	5:124718551-124719148	NOTEST	0	0	0	0	1	1
ENSG00000250271	ENSG00000250271	RP11-64D22.5	3:151451703-151645963	NOTEST	0	0	0	0	1	1
ENSG00000250272	ENSG00000250272	TRMT112P1	4:117300074-117300425	NOTEST	0	0	0	0	1	1
ENSG00000250273	ENSG00000250273	PSMC1P5	5:106530856-106531033	NOTEST	0	0	0	0	1	1
ENSG00000250274	ENSG00000250274	CTB-114C7.4	5:169735704-169739720	NOTEST	0.0147698	0	#NAME?	0	1	1
ENSG00000250277	ENSG00000250277	RP11-468N14.11	4:69862652-69863427	NOTEST	0	0	0	0	1	1
ENSG00000250280	ENSG00000250280	RP11-305O6.3	12:65672422-66036152	NOTEST	0.00816361	0	#NAME?	0	1	1

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ENSG00000250282	ENSG00000250282	RP5-875H18.4	17:48172100-48207246	NOTEST	0.165118	0.179552	0.120905	0	1	1
ENSG00000250284	ENSG00000250284	CTB-1I21.1	5:136070615-136090375	NOTEST	0	0	0	0	1	1
ENSG00000250286	ENSG00000250286	RP11-94C24.8	17:48609903-48633213	NOTEST	0.136027	0.098893	-0.459947	0	1	1
ENSG00000250289	ENSG00000250289	VWA8P1	5:68128411-68257985	NOTEST	0	0	0	0	1	1
ENSG00000250290	ENSG00000250290	CTC-820M8.1	8:121392999-121825599	NOTEST	0.0163849	0.00635322	-1.36681	0	1	1
ENSG00000250292	ENSG00000250292	RP11-451F20.1	4:184301497-184302858	NOTEST	0	0	0	0	1	1
ENSG00000250293	ENSG00000250293	CRYZP2	4:98105243-99064391	NOTEST	0	0	0	0	1	1
ENSG00000250294	ENSG00000250294	OR12D1	HSCHR6_MHC_SSTO:29323120-29424524	NOTEST	0	0	0	0	1	1
ENSG00000250295	ENSG00000250295	RP11-434I12.2	8:74202505-74268696	NOTEST	0.0500801	0.0186677	-1.4237	0	1	1
ENSG00000250296	ENSG00000250296	RP11-321E2.9	5:17528777-17529372	NOTEST	0	0	0	0	1	1
ENSG00000250298	ENSG00000250298	GIMD1	4:107279554-107288359	NOTEST	0	0	0	0	1	1
ENSG00000250299	ENSG00000250299	MRPS31P4	13:53191604-53217919	NOTEST	0.0578492	0	#NAME?	0	1	1
ENSG00000250300	ENSG00000250300	RP11-696N14.3	4:100390754-100419855	NOTEST	0	0	0	0	1	1
ENSG00000250302	ENSG00000250302	RP11-752D24.3	4:53656160-53681631	NOTEST	0	0	0	0	1	1
ENSG00000250304	ENSG00000250304	ZBED1P1	4:111212799-111214729	NOTEST	0	0	0	0	1	1
ENSG00000250306	ENSG00000250306	CTC-498M16.3	5:87485449-87794514	NOTEST	0	0	0	0	1	1
ENSG00000250307	ENSG00000250307	TUBB8P3	4:112998753-112999556	NOTEST	0	0	0	0	1	1
ENSG00000250308	ENSG00000250308	SALL4P1	5:56690886-56829251	NOTEST	0.024728	0	#NAME?	0	1	1
ENSG00000250309	ENSG00000250309	CTC-345K18.2	5:150040435-150058927	NOTEST	0	0	0	0	1	1
ENSG00000250310	ENSG00000250310	RP5-1029K10.4	17:47572654-47661189	NOTEST	0	0	0	0	1	1
ENSG00000250312	ENSG00000250312	ZNF718	4:123965-157779	NOTEST	0.421828	0.484254	0.199109	0	1	1
ENSG00000250313	ENSG00000250313	RP11-5P22.3	5:65803371-65807432	NOTEST	0	0	0	0	1	1
ENSG00000250315	ENSG00000250315	RP11-44F21.4	4:76026686-76027153	NOTEST	0	0	0	0	1	1
ENSG00000250316	ENSG00000250316	RP11-618M23.1	8:18942501-19116979	NOTEST	0	0	0	0	1	1
ENSG00000250319	ENSG00000250319	CTD-2272G21.3	5:23262267-23263294	NOTEST	0	0	0	0	1	1
ENSG00000250320	ENSG00000250320	CTD-2269F5.1	5:83236372-83786583	NOTEST	0	0.0303549	inf	0	1	1
ENSG00000250321	ENSG00000250321	RP11-478C6.4	4:331602-378653	NOTEST	0	1.70224	inf	0	1	1
ENSG00000250322	ENSG00000250322	CTB-51E13.1	4:123844228-124240605	NOTEST	0	0	0	0	1	1
ENSG00000250324	ENSG00000250324	MRPL22P1	4:57036360-57194791	NOTEST	0	0	0	0	1	1
ENSG00000250325	ENSG00000250325	IGBP1P4	4:83322730-83323609	NOTEST	0.0383765	0	#NAME?	0	1	1
ENSG00000250326	ENSG00000250326	RP11-284M14.1	4:143854347-144106014	NOTEST	0.361021	0.297244	-0.280436	0	1	1
ENSG00000250328	ENSG00000250328	CTC-210G5.1	5:121646991-121814782	NOTEST	0	0	0	0	1	1
ENSG00000250329	ENSG00000250329	KDELC1P1	5:127419457-127525380	NOTEST	0	0	0	0	1	1
ENSG00000250330	ENSG00000250330	CTC-422A18.2	5:78293437-78531861	NOTEST	0	0	0	0	1	1
ENSG00000250331	ENSG00000250331	RP11-1E3.1	5:96840399-97006750	NOTEST	0	0	0	0	1	1
ENSG00000250332	ENSG00000250332	CTD-2272G21.2	5:23303673-23305252	NOTEST	0	0	0	0	1	1
ENSG00000250333	ENSG00000250333	RP11-4O3.1	4:58462105-58524966	NOTEST	0	0	0	0	1	1
ENSG00000250334	ENSG00000250334	LINC00989	4:80413569-80497614	NOTEST	0	0	0	0	1	1
ENSG00000250337	ENSG00000250337	LINC01021	5:27472398-27496508	NOTEST	0.085223	0.0363516	-1.22922	0	1	1
ENSG00000250338	ENSG00000250338	RP11-395I6.2	4:40267091-40268077	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000250340	ENSG00000250340	RP11-577G20.1	4:59390679-59402493	NOTEST	0	0	0	0	1	1
ENSG00000250341	ENSG00000250341	RP11-785F11.1	4:137717876-138133953	NOTEST	0	0	0	0	1	1
ENSG00000250342	ENSG00000250342	RP11-747H12.6	4:9053567-9053777	NOTEST	0	0	0	0	1	1
ENSG00000250344	ENSG00000250344	RP11-647P12.1	4:121956767-122001631	NOTEST	0	0	0	0	1	1
ENSG00000250345	ENSG00000250345	RP11-780M14.1	4:144480624-144786225	NOTEST	0	0	0	0	1	1
ENSG00000250346	ENSG00000250346	EEF1GP2	5:147301741-147302984	NOTEST	0	0	0	0	1	1
ENSG00000250347	ENSG00000250347	AC005740.4	5:141416271-141416690	NOTEST	0	0	0	0	1	1
ENSG00000250348	ENSG00000250348	RP11-466P24.6	5:75377770-75649764	NOTEST	0	0	0	0	1	1
ENSG00000250349	ENSG00000250349	TM4SF2	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000250350	ENSG00000250350	RP11-731D1.3	4:152020724-152246784	NOTEST	0	0	0	0	1	1
ENSG00000250351	ENSG00000250351	RP11-432M8.10	5:17620641-17621048	NOTEST	0	0	0	0	1	1
ENSG00000250354	ENSG00000250354	RP11-76G10.1	4:148999912-149365850	NOTEST	0	0	0	0	1	1
ENSG00000250355	ENSG00000250355	RP11-79L21.1	3:132276981-132593067	NOTEST	0	0	0	0	1	1
ENSG00000250356	ENSG00000250356	HSPE1P23	4:75843031-75843348	NOTEST	0	0	0	0	1	1
ENSG00000250357	ENSG00000250357	RP11-503L19.1	4:149614183-149615475	NOTEST	0	0	0	0	1	1
ENSG00000250358	ENSG00000250358	RP11-159K7.2	5:111964132-111967797	NOTEST	0	0	0	0	1	1
ENSG00000250359	ENSG00000250359	PTP4A1P4	5:85383343-85383665	NOTEST	0	0	0	0	1	1
ENSG00000250360	ENSG00000250360	CTD-2089N3.1	5:50261520-50262842	NOTEST	0	0	0	0	1	1
ENSG00000250361	ENSG00000250361	GYPB	4:144833483-145061904	NOTEST	0	0.104864	inf	0	1	1
ENSG00000250362	ENSG00000250362	AC008592.5	5:95197489-95210223	NOTEST	0.0264306	0	#NAME?	0	1	1
ENSG00000250363	ENSG00000250363	KRT18P21	4:116841862-116843134	NOTEST	0	0	0	0	1	1
ENSG00000250364	ENSG00000250364	OR12D3	HSCHR6_MHC_SSTO:29323120-29424524	NOTEST	0	0	0	0	1	1
ENSG00000250366	ENSG00000250366	LINC00617	14:96342728-96391908	NOTEST	0	0	0	0	1	1
ENSG00000250371	ENSG00000250371	RP11-22A3.2	4:12860724-12866585	NOTEST	0	0.00413334	inf	0	1	1
ENSG00000250372	ENSG00000250372	MARK2P4	4:176933188-176935568	NOTEST	0	0	0	0	1	1
ENSG00000250374	ENSG00000250374	RP11-219C20.1	4:165980299-165981706	NOTEST	0	0.0264206	inf	0	1	1
ENSG00000250375	ENSG00000250375	RP11-340A13.3	4:59912737-59940974	NOTEST	0	0	0	0	1	1
ENSG00000250376	ENSG00000250376	CTD-2005D20.1	4:69650335-69653192	NOTEST	0	0	0	0	1	1
ENSG00000250377	ENSG00000250377	CTC-467M3.3	5:87803362-88762215	NOTEST	0	0	0	0	1	1
ENSG00000250378	ENSG00000250378	RP11-119J18.1	5:135148355-135162271	NOTEST	0	0.0514656	inf	0	1	1
ENSG00000250379	ENSG00000250379	RP11-23P13.4	15:42066631-42120134	NOTEST	0	0	0	0	1	1
ENSG00000250381	ENSG00000250381	UNC93B4	4:4145184-4152148	NOTEST	0	0	0	0	1	1
ENSG00000250383	ENSG00000250383	CTD-2197I11.1	5:108083522-108532542	NOTEST	0	0	0	0	1	1
ENSG00000250384	ENSG00000250384	UBE2CP3	4:57829535-58071676	NOTEST	0	0	0	0	1	1
ENSG00000250385	ENSG00000250385	RP11-310P5.2	5:524819-526709	NOTEST	0	0	0	0	1	1
ENSG00000250386	ENSG00000250386	RP11-432M8.11	5:17625659-17626068	NOTEST	0	0	0	0	1	1
ENSG00000250387	ENSG00000250387	RP11-136K7.2	5:70647681-70742396	NOTEST	0.010343	0	#NAME?	0	1	1
ENSG00000250389	ENSG00000250389	MTND6P2	5:8618692-8619216	NOTEST	0	0	0	0	1	1
ENSG00000250390	ENSG00000250390	RP11-338H14.1	11:95215569-95230717	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000250392	ENSG00000250392	RP11-700N1.1	4:120858711-120885448	NOTEST	0	0	0	0	1	1
ENSG00000250393	ENSG00000250393	RP11-480G3.1	4:10144990-10145279	NOTEST	0	0	0	0	1	1
ENSG00000250398	ENSG00000250398	RP11-27G13.4	4:156304258-156305254	NOTEST	0	0	0	0	1	1
ENSG00000250400	ENSG00000250400	LINC00977	8:130228712-130253496	NOTEST	0.0967571	0.0933084	-0.0523606	0	1	1
ENSG00000250402	ENSG00000250402	RP11-395P13.4	5:124712526-124713132	NOTEST	0	0	0	0	1	1
ENSG00000250403	ENSG00000250403	RP11-15B17.2	4:100869242-101136662	NOTEST	0	0	0	0	1	1
ENSG00000250404	ENSG00000250404	AC090587.2	11:3686816-3847601	NOTEST	0.446501	0.48713	0.125643	0	1	1
ENSG00000250405	ENSG00000250405	RP11-114H7.2	5:130329945-130331857	NOTEST	0	0	0	0	1	1
ENSG00000250406	ENSG00000250406	RP13-539F13.3	4:145772723-145795939	NOTEST	0	0	0	0	1	1
ENSG00000250407	ENSG00000250407	CTB-99A3.1	5:145942788-146464347	NOTEST	0	0	0	0	1	1
ENSG00000250409	ENSG00000250409	CTB-3M24.3	5:132496129-132948255	NOTEST	0	0	0	0	1	1
ENSG00000250410	ENSG00000250410	RP11-714G18.1	4:186080818-186317053	NOTEST	0.0661027	0	#NAME?	0	1	1
ENSG00000250411	ENSG00000250411	RP11-257I8.2	5:124372523-124377932	NOTEST	0	0	0	0	1	1
ENSG00000250412	ENSG00000250412	KLHL2P1	4:120255483-120299388	NOTEST	0.0424406	0.124363	1.55104	0	1	1
ENSG00000250413	ENSG00000250413	RP11-448G15.1	4:9772776-10056560	NOTEST	0	0	0	0	1	1
ENSG00000250415	ENSG00000250415	CTC-461F20.1	5:16473146-16630078	NOTEST	0	0	0	0	1	1
ENSG00000250416	ENSG00000250416	SEC63P2	4:35489433-35491372	NOTEST	0	0	0	0	1	1
ENSG00000250417	ENSG00000250417	CTD-2194D22.2	5:1856083-1856682	NOTEST	0	0	0	0	1	1
ENSG00000250418	ENSG00000250418	RP11-503D12.1	5:44698532-44700910	NOTEST	0	0	0	0	1	1
ENSG00000250420	ENSG00000250420	AACSP1	5:178191861-178245436	NOTEST	0	0.079161	inf	0	1	1
ENSG00000250421	ENSG00000250421	RP11-83M16.6	5:66675205-67198428	NOTEST	0	0	0	0	1	1
ENSG00000250422	ENSG00000250422	RP11-484L7.1	5:45259348-45696253	NOTEST	0	0	0	0	1	1
ENSG00000250423	ENSG00000250423	KIAA1210	X:118212597-118284542	NOTEST	0.00194045	0.0252224	3.70025	0	1	1
ENSG00000250425	ENSG00000250425	OR7E35P	4:9756521-9757402	NOTEST	0	0	0	0	1	1
ENSG00000250426	ENSG00000250426	FTLP10	4:69048009-69111438	NOTEST	0	0	0	0	1	1
ENSG00000250427	ENSG00000250427	CTD-3179P9.2	5:117618269-117620477	NOTEST	0	0	0	0	1	1
ENSG00000250428	ENSG00000250428	RP11-1082L8.1	8:125847125-125966570	NOTEST	0	0	0	0	1	1
ENSG00000250430	ENSG00000250430	RP11-366M4.15	4:165947412-165948096	NOTEST	0	0	0	0	1	1
ENSG00000250431	ENSG00000250431	RP13-577H12.2	4:175750818-175900532	NOTEST	0	0	0	0	1	1
ENSG00000250432	ENSG00000250432	RP11-834C11.5	12:54452037-54519776	NOTEST	0.213975	0.114593	-0.900917	0	1	1
ENSG00000250433	ENSG00000250433	CLSTN2-AS1	3:139654026-140296239	NOTEST	0	0	0	0	1	1
ENSG00000250436	ENSG00000250436	RP11-622A1.2	4:74374519-74399845	NOTEST	0	0	0	0	1	1
ENSG00000250437	ENSG00000250437	RP11-116A1.1	5:88877025-88973518	NOTEST	0	0	0	0	1	1
ENSG00000250438	ENSG00000250438	CTD-2308B18.2	5:123805283-123805594	NOTEST	0	0	0	0	1	1
ENSG00000250439	ENSG00000250439	FGD5P1	3:13974552-14124311	NOTEST	0	0.0237583	inf	0	1	1
ENSG00000250441	ENSG00000250441	RP11-47F1.1	5:108083522-108532542	NOTEST	0	0	0	0	1	1
ENSG00000250442	ENSG00000250442	EIF3KP3	4:116843170-117218316	NOTEST	0	0	0	0	1	1
ENSG00000250443	ENSG00000250443	AC128709.1	3:197232132-197233857	NOTEST	0.04046	0.0172726	-1.22801	0	1	1
ENSG00000250444	ENSG00000250444	CCT5P1	5:114847773-114849391	NOTEST	0.0391485	0.0144328	-1.4396	0	1	1
ENSG00000250446	ENSG00000250446	CTD-2275D24.3	5:73617455-73635977	NOTEST	0	0	0	0	1	1

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ENSG00000250447	ENSG00000250447	CTD-2081C10.1	5:53072473-53115516	NOTEST	0	0	0	0	1	1
ENSG00000250448	ENSG00000250448	RP11-19O2.2	5:16067247-16185694	NOTEST	0	0	0	0	1	1
ENSG00000250453	ENSG00000250453	CTD-2134P3.1	5:28782784-28809362	NOTEST	0	0	0	0	1	1
ENSG00000250455	ENSG00000250455	RP11-648M2.1	5:37377150-37378073	NOTEST	0	0.0757722	inf	0	1	1
ENSG00000250456	ENSG00000250456	AC006552.1	4:55469377-55473298	NOTEST	0.0539605	0.0714219	0.404463	0	1	1
ENSG00000250458	ENSG00000250458	RP11-107E21.1	4:124571421-124851561	NOTEST	0	0	0	0	1	1
ENSG00000250464	ENSG00000250464	RP11-148K14.1	4:56179177-56180091	NOTEST	0	0	0	0	1	1
ENSG00000250467	ENSG00000250467	RP11-227F19.1	4:41746098-41826136	NOTEST	0	0	0	0	1	1
ENSG00000250470	ENSG00000250470	AP000351.3	22:24309088-24326106	NOTEST	0	0	0	0	1	1
ENSG00000250472	ENSG00000250472	TRIM36-IT1	5:114460458-114516243	NOTEST	0	0	0	0	1	1
ENSG00000250473	ENSG00000250473	DUTP7	4:52709165-52783003	NOTEST	0	0	0	0	1	1
ENSG00000250475	ENSG00000250475	RP11-312A15.3	4:158889563-158890767	NOTEST	0	0	0	0	1	1
ENSG00000250476	ENSG00000250476	ENPP7P9	4:3968760-3969387	NOTEST	0	0	0	0	1	1
ENSG00000250480	ENSG00000250480	RP11-101B14.1	5:56416622-56418451	NOTEST	0	0	0	0	1	1
ENSG00000250481	ENSG00000250481	CTD-2247C11.1	5:4974802-5034380	NOTEST	0	0	0	0	1	1
ENSG00000250482	ENSG00000250482	RP11-152K4.1	5:31094083-31329253	NOTEST	0	0	0	0	1	1
ENSG00000250483	ENSG00000250483	PPM1AP1	8:15663657-15664792	NOTEST	0.0154069	0.0371633	1.2703	0	1	1
ENSG00000250484	ENSG00000250484	RP11-728C8.1	4:124983616-124984145	NOTEST	0	0	0	0	1	1
ENSG00000250485	ENSG00000250485	EXOC7P1	4:109338860-109340919	NOTEST	0	0	0	0	1	1
ENSG00000250486	ENSG00000250486	FAM218A	4:165869230-165899980	NOTEST	0	0.0236336	inf	0	1	1
ENSG00000250488	ENSG00000250488	RP11-6C14.1	4:160587654-160698936	NOTEST	0	0	0	0	1	1
ENSG00000250490	ENSG00000250490	CTD-2324F15.2	5:6310553-6339997	NOTEST	0	0	0	0	1	1
ENSG00000250492	ENSG00000250492	INTS6P1	5:39719085-39721615	NOTEST	0.132481	0.186845	0.496057	0	1	1
ENSG00000250493	ENSG00000250493	RP11-640N11.2	11:120382467-120859613	NOTEST	0	0	0	0	1	1
ENSG00000250494	ENSG00000250494	RP11-162D9.1	8:54074898-54075547	NOTEST	0	0	0	0	1	1
ENSG00000250496	ENSG00000250496	ABT1P1	4:99916770-99983964	NOTEST	0	0	0	0	1	1
ENSG00000250497	ENSG00000250497	AC007126.1	4:13656802-13978699	NOTEST	0	0.00776252	inf	0	1	1
ENSG00000250500	ENSG00000250500	RP11-119H12.3	4:113718205-113719847	NOTEST	0	0	0	0	1	1
ENSG00000250501	ENSG00000250501	RP11-98O2.1	4:139694703-139722793	NOTEST	0	0	0	0	1	1
ENSG00000250503	ENSG00000250503	RP11-401I19.1	4:131802181-131806796	NOTEST	0	0	0	0	1	1
ENSG00000250504	ENSG00000250504	KRT18P51	4:145493389-145494135	NOTEST	0	0	0	0	1	1
ENSG00000250505	ENSG00000250505	AC006499.3	4:10286584-10287332	NOTEST	0	0	0	0	1	1
ENSG00000250507	ENSG00000250507	AC008984.6	19:54818352-54850421	NOTEST	0	0	0	0	1	1
ENSG00000250508	ENSG00000250508	RP11-757G1.6	11:68638131-68642010	NOTEST	0	0	0	0	1	1
ENSG00000250509	ENSG00000250509	CTC-573N18.1	5:179868558-179870238	NOTEST	0	0	0	0	1	1
ENSG00000250510	ENSG00000250510	GPR162	12:6930710-6949018	NOTEST	0.0804629	0.229233	1.51042	0	1	1
ENSG00000250511	ENSG00000250511	RP11-380D23.1	4:111286888-111486441	NOTEST	0.0793356	0.0996463	0.328847	0	1	1
ENSG00000250514	ENSG00000250514	RP11-96P7.1	16:76311175-76692375	NOTEST	0	0	0	0	1	1
ENSG00000250515	ENSG00000250515	RP11-515C16.7	5:140111874-140112448	NOTEST	0	0	0	0	1	1
ENSG00000250516	ENSG00000250516	RP11-380I10.2	8:28083445-28085079	NOTEST	0	0	0	0	1	1
ENSG00000250517	ENSG00000250517	LDHAL6CP	12:63397332-63400682	NOTEST	0	0	0	0	1	1
ENSG00000250519	ENSG00000250519	RP11-680H20.2	11:93971315-94012372	NOTEST	0.0396017	0.0263842	-0.585887	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000250522	ENSG00000250522	AC004066.3	4:106461346-106473512	NOTEST	0	0.0262512	inf	0	1	1
ENSG00000250523	ENSG00000250523	RP11-756P10.1	4:189321889-189602205	NOTEST	0	0	0	0	1	1
ENSG00000250524	ENSG00000250524	RP11-730N24.2	5:24882051-24885570	NOTEST	0	0	0	0	1	1
ENSG00000250526	ENSG00000250526	CCT6P2	5:14639534-14641127	NOTEST	0	0.0228042	inf	0	1	1
ENSG00000250529	ENSG00000250529	CTD-2247C11.5	5:5034471-5078424	NOTEST	0	0	0	0	1	1
ENSG00000250530	ENSG00000250530	RP11-436H11.3	5:123972607-124084500	NOTEST	0	0	0	0	1	1
ENSG00000250532	ENSG00000250532	RP11-727M10.1	4:75284633-75306174	NOTEST	0	0	0	0	1	1
ENSG00000250535	ENSG00000250535	STK19P	6:31981046-31981564	NOTEST	0	0	0	0	1	1
ENSG00000250536	ENSG00000250536	ABHD17AP3	1:214776537-214837931	NOTEST	0.235017	0.200497	-0.229185	0	1	1
ENSG00000250537	ENSG00000250537	DUX4L8	4:190988795-190990406	NOTEST	0	0	0	0	1	1
ENSG00000250538	ENSG00000250538	RP11-92A5.2	4:156127680-156138230	NOTEST	0	0	0	0	1	1
ENSG00000250539	ENSG00000250539	KRT8P33	5:122680578-122759286	NOTEST	0.0334119	0.0166888	-1.00148	0	1	1
ENSG00000250540	ENSG00000250540	RP11-58H15.3	4:144418564-144419279	NOTEST	0	0	0	0	1	1
ENSG00000250541	ENSG00000250541	RP11-302F12.10	4:25749054-25931435	NOTEST	0	0	0	0	1	1
ENSG00000250543	ENSG00000250543	RP11-442N1.1	3:139407244-139408184	NOTEST	0	0	0	0	1	1
ENSG00000250544	ENSG00000250544	CTC-493L21.1	5:86042634-86045589	NOTEST	0	0	0	0	1	1
ENSG00000250546	ENSG00000250546	RP11-8L2.1	4:84717588-85214565	NOTEST	0.0599023	0.0400492	-0.580838	0	1	1
ENSG00000250547	ENSG00000250547	RP11-719L21.1	4:164186726-164187735	NOTEST	0	0	0	0	1	1
ENSG00000250548	ENSG00000250548	RP11-47I22.2	14:61654276-62125414	NOTEST	0	0.0387188	inf	0	1	1
ENSG00000250550	ENSG00000250550	PPBPP1	4:74702213-74714781	NOTEST	0	0	0	0	1	1
ENSG00000250551	ENSG00000250551	RP11-254I22.1	5:95220801-96143803	NOTEST	0	0	0	0	1	1
ENSG00000250555	ENSG00000250555	CTC-467M3.2	5:87803362-88762215	NOTEST	0	0	0	0	1	1
ENSG00000250556	ENSG00000250556	CCDC34P1	4:112723956-112993854	NOTEST	0	0	0	0	1	1
ENSG00000250558	ENSG00000250558	RP11-432M8.3	5:17590472-17591069	NOTEST	0	0	0	0	1	1
ENSG00000250560	ENSG00000250560	RP11-598G2.1	4:76120076-76120289	NOTEST	0	0	0	0	1	1
ENSG00000250561	ENSG00000250561	OR7E59P	7:6919257-6920257	NOTEST	0	0	0	0	1	1
ENSG00000250562	ENSG00000250562	RPL38P4	3:98216447-98312567	NOTEST	0	0	0	0	1	1
ENSG00000250563	ENSG00000250563	KNOP1P5	8:127084830-127086475	NOTEST	0	0	0	0	1	1
ENSG00000250564	ENSG00000250564	RP11-215P8.4	5:133764741-133828210	NOTEST	0	0	0	0	1	1
ENSG00000250566	ENSG00000250566	UGT2B29P	4:69375158-69383365	NOTEST	0	0	0	0	1	1
ENSG00000250567	ENSG00000250567	CTD-2154H6.1	5:102744641-102748212	NOTEST	0.154738	0	#NAME?	0	1	1
ENSG00000250569	ENSG00000250569	NTAN1P2	8:87345502-87777251	NOTEST	0.276431	0.158857	-0.799189	0	1	1
ENSG00000250572	ENSG00000250572	RP11-529H2.1	4:88183082-88187974	NOTEST	0	0	0	0	1	1
ENSG00000250573	ENSG00000250573	AC006499.5	4:10261068-10261762	NOTEST	0	0	0	0	1	1
ENSG00000250574	ENSG00000250574	CTD-2275D10.2	5:75699073-76031606	NOTEST	0	0	0	0	1	1
ENSG00000250575	ENSG00000250575	RP4-669L17.8	1:317719-461954	NOTEST	0	0	0	0	1	1
ENSG00000250576	ENSG00000250576	CTD-2154B17.1	5:10775169-10777174	NOTEST	0	0	0	0	1	1
ENSG00000250577	ENSG00000250577	RP11-577B7.1	4:139741107-139933800	NOTEST	0	0	0	0	1	1
ENSG00000250579	ENSG00000250579	CTD-2297D10.2	5:5132892-5140167	NOTEST	0	0	0	0	1	1
ENSG00000250580	ENSG00000250580	RP11-93K22.14	3:129918550-129918761	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000250582	ENSG00000250582	SMAD1-AS2	4:146402345-146479231	NOTEST	0	0	0	0	1	1
ENSG00000250583	ENSG00000250583	CTD-2233C11.2	5:33519720-33522335	NOTEST	0	0	0	0	1	1
ENSG00000250584	ENSG00000250584	RP11-325I22.2	5:1363696-1380182	NOTEST	0	0	0	0	1	1
ENSG00000250585	ENSG00000250585	LINC00604	5:40260758-40267759	NOTEST	0	0	0	0	1	1
ENSG00000250587	ENSG00000250587	RP11-136H13.1	5:30248456-30249000	NOTEST	0	0	0	0	1	1
ENSG00000250590	ENSG00000250590	RP11-565A3.2	4:188454031-188593795	NOTEST	0	0	0	0	1	1
ENSG00000250591	ENSG00000250591	PRSS3P1	7:142468263-142471794	NOTEST	0	0	0	0	1	1
ENSG00000250592	ENSG00000250592	RP11-39E3.3	3:130569438-131100319	NOTEST	0	0	0	0	1	1
ENSG00000250594	ENSG00000250594	RP11-433B3.1	4:111186020-111186173	NOTEST	0	0	0	0	1	1
ENSG00000250596	ENSG00000250596	RP11-440I14.2	4:175444851-175461935	NOTEST	0.0146244	0.0486074	1.7328	0	1	1
ENSG00000250597	ENSG00000250597	RP11-725M22.1	4:34659227-34671054	NOTEST	0	0	0	0	1	1
ENSG00000250599	ENSG00000250599	AC064853.3	2:228474805-228513322	NOTEST	0	0	0	0	1	1
ENSG00000250600	ENSG00000250600	ROPN1L-AS1	5:10441401-10472141	NOTEST	0	1.10045	inf	0	1	1
ENSG00000250602	ENSG00000250602	RP11-517I3.1	5:125695823-125832186	NOTEST	0	0	0	0	1	1
ENSG00000250603	ENSG00000250603	CTC-228N24.2	5:127039081-127418864	NOTEST	0	0	0	0	1	1
ENSG00000250604	ENSG00000250604	RP11-597D13.8	4:159045625-159176563	NOTEST	0.201808	0.392743	0.960605	0	1	1
ENSG00000250606	ENSG00000250606	PRSS3P2	7:142478063-142482416	NOTEST	0	0	0	0	1	1
ENSG00000250608	ENSG00000250608	RP11-933H2.4	3:130569438-131100319	NOTEST	0	0	0	0	1	1
ENSG00000250609	ENSG00000250609	RP11-158C21.2	4:155444638-155445959	NOTEST	0	0	0	0	1	1
ENSG00000250611	ENSG00000250611	RP11-339D20.1	4:20039182-20039595	NOTEST	0	0	0	0	1	1
ENSG00000250612	ENSG00000250612	RP11-618I10.2	4:70212326-70223895	NOTEST	0	0	0	0	1	1
ENSG00000250613	ENSG00000250613	RP11-136I13.1	4:10412619-10413268	NOTEST	0	0	0	0	1	1
ENSG00000250614	ENSG00000250614	AC007078.4	7:76090992-76135312	NOTEST	0	0	0	0	1	1
ENSG00000250616	ENSG00000250616	RP11-455F5.3	16:30103634-30115437	NOTEST	0.0301251	0.00705987	-2.09325	0	1	1
ENSG00000250618	ENSG00000250618	RP11-548K12.9	7:57877306-57877903	NOTEST	0	0	0	0	1	1
ENSG00000250619	ENSG00000250619	CTD-2215L10.1	5:9001885-9546187	NOTEST	0	0	0	0	1	1
ENSG00000250620	ENSG00000250620	RP11-91J3.3	4:188334717-188336851	NOTEST	0	0	0	0	1	1
ENSG00000250622	ENSG00000250622	RP11-612J15.3	4:157893782-157894108	NOTEST	0	0	0	0	1	1
ENSG00000250623	ENSG00000250623	RP11-317B7.3	4:2073644-2243891	NOTEST	0	0	0	0	1	1
ENSG00000250624	ENSG00000250624	RP11-93M12.1	4:30722036-31148422	NOTEST	0.0261053	0	#NAME?	0	1	1
ENSG00000250625	ENSG00000250625	RP1-142F18.2	X:141282137-141283276	NOTEST	0	0	0	0	1	1
ENSG00000250626	ENSG00000250626	RP11-756P10.2	4:189678832-189717787	NOTEST	0	0	0	0	1	1
ENSG00000250627	ENSG00000250627	TTC39CP1	4:116843170-117218316	NOTEST	0	0	0	0	1	1
ENSG00000250629	ENSG00000250629	RP11-122C5.3	5:38736156-38845931	NOTEST	0	0	0	0	1	1
ENSG00000250630	ENSG00000250630	RP11-52L11.4	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000250632	ENSG00000250632	RP3-513G18.2	4:3675319-3679582	NOTEST	0	0	0	0	1	1
ENSG00000250634	ENSG00000250634	RP11-341G5.1	4:13656802-13978699	NOTEST	0.0130683	0	#NAME?	0	1	1
ENSG00000250635	ENSG00000250635	CTD-3224K15.2	5:139026883-139063467	NOTEST	0	0	0	0	1	1
ENSG00000250636	ENSG00000250636	RP11-335L23.2	4:183949753-183950873	NOTEST	0	0	0	0	1	1
ENSG00000250637	ENSG00000250637	RP11-359P18.1	8:43298044-43308055	NOTEST	0	0	0	0	1	1
ENSG00000250640	ENSG00000250640	RP11-7O20.4	11:14926542-15103888	NOTEST	0	0	0	0	1	1

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ENSG00000250642	ENSG00000250642	RP11-642E20.5	4:69148178-69151677	NOTEST	0	0	0	0	1	1
ENSG00000250643	ENSG00000250643	RP11-93K22.6	3:129672947-129688137	NOTEST	0	0	0	0	1	1
ENSG00000250646	ENSG00000250646	RP11-530I17.1	4:55919226-55991756	NOTEST	0	0	0	0	1	1
ENSG00000250650	ENSG00000250650	RP11-492L8.1	5:116355243-116355375	NOTEST	0	0	0	0	1	1
ENSG00000250651	ENSG00000250651	PABPC1P7	4:103790134-103940896	NOTEST	0	0	0	0	1	1
ENSG00000250654	ENSG00000250654	RP11-834C11.7	12:54452037-54519776	NOTEST	0	0	0	0	1	1
ENSG00000250655	ENSG00000250655	RP11-61G24.1	4:97133429-97134251	NOTEST	0	0	0	0	1	1
ENSG00000250656	ENSG00000250656	ST3GAL1P1	4:68566997-68995598	NOTEST	0.134768	0.038529	-1.80646	0	1	1
ENSG00000250657	ENSG00000250657	RP11-1E6.1	4:43342891-43347617	NOTEST	0	0	0	0	1	1
ENSG00000250658	ENSG00000250658	RP11-138B4.1	4:188225236-188230836	NOTEST	0	0.00537	inf	0	1	1
ENSG00000250659	ENSG00000250659	RP11-864I4.3	11:62201015-62323707	NOTEST	0.153152	0	#NAME?	0	1	1
ENSG00000250662	ENSG00000250662	HNRNPKP5	5:14877775-14878028	NOTEST	0	0	0	0	1	1
ENSG00000250665	ENSG00000250665	RP11-775H9.1	4:137039829-137316626	NOTEST	0	0	0	0	1	1
ENSG00000250666	ENSG00000250666	RP11-463J17.1	4:190701489-190861426	NOTEST	0	0	0	0	1	1
ENSG00000250667	ENSG00000250667	RP11-321E2.12	5:17495766-17495935	NOTEST	0	0	0	0	1	1
ENSG00000250668	ENSG00000250668	CTD-2296D1.2	5:7347098-7348090	NOTEST	0	0	0	0	1	1
ENSG00000250669	ENSG00000250669	RP11-83M16.3	5:66675205-67198428	NOTEST	0	0	0	0	1	1
ENSG00000250670	ENSG00000250670	AC004063.1	4:105389468-106041157	NOTEST	0	0	0	0	1	1
ENSG00000250672	ENSG00000250672	CTD-2017D15.1	5:32925744-33298016	NOTEST	0	0	0	0	1	1
ENSG00000250673	ENSG00000250673	RP11-6L6.2	4:147145708-147150208	NOTEST	0	0	0	0	1	1
ENSG00000250674	ENSG00000250674	RP11-798K23.1	5:178882415-178883096	NOTEST	0	0	0	0	1	1
ENSG00000250677	ENSG00000250677	RP11-576N17.2	4:84154664-84169359	NOTEST	0	0	0	0	1	1
ENSG00000250678	ENSG00000250678	CTB-161M19.1	5:118342041-118584833	NOTEST	0	0	0	0	1	1
ENSG00000250681	ENSG00000250681	RP3-368B9.2	4:3634755-3635702	NOTEST	0	0	0	0	1	1
ENSG00000250682	ENSG00000250682	LINC00491	5:101917071-102007263	NOTEST	0	0.0786334	inf	0	1	1
ENSG00000250684	ENSG00000250684	KB-1042C11.1	8:103700544-103701134	NOTEST	0	0	0	0	1	1
ENSG00000250685	ENSG00000250685	RP11-486L19.2	16:84224743-84230774	NOTEST	0	0	0	0	1	1
ENSG00000250686	ENSG00000250686	RP1-240B8.3	6:62340137-62996132	NOTEST	0	0.0209228	inf	0	1	1
ENSG00000250687	ENSG00000250687	RP11-497H16.7	5:69758070-69775042	NOTEST	0	0	0	0	1	1
ENSG00000250688	ENSG00000250688	TRAJ55	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000250692	ENSG00000250692	CTB-35F21.4	5:139226363-139422884	NOTEST	0	0	0	0	1	1
ENSG00000250693	ENSG00000250693	RPF2P2	4:116549967-116550863	NOTEST	0	0	0	0	1	1
ENSG00000250694	ENSG00000250694	CTD-2074D8.1	5:24352417-24353552	NOTEST	0	0	0	0	1	1
ENSG00000250696	ENSG00000250696	RP11-704M14.1	4:70047377-70082484	NOTEST	0	0	0	0	1	1
ENSG00000250697	ENSG00000250697	CTD-2066L21.3	5:32925744-33298016	NOTEST	0	0	0	0	1	1
ENSG00000250698	ENSG00000250698	RP11-392B6.1	4:140586921-141075338	NOTEST	0	0	0	0	1	1
ENSG00000250699	ENSG00000250699	AP000892.4	11:117103340-117283984	NOTEST	0	0	0	0	1	1
ENSG00000250703	ENSG00000250703	CTD-2533K21.1	5:26670442-26670590	NOTEST	0	0	0	0	1	1
ENSG00000250704	ENSG00000250704	RP11-423J7.1	4:150877359-150879724	NOTEST	0	0	0	0	1	1

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ENSG00000250706	ENSG00000250706	RP11-18H21.2	4:153067536-153099725	NOTEST	0	0	0	0	1	1
ENSG00000250708	ENSG00000250708	RP11-161D15.1	4:174798621-174912012	NOTEST	0	0	0	0	1	1
ENSG00000250709	ENSG00000250709	CCDC169-SOHLH2	13:36742344-36871979	NOTEST	0.125638	0	#NAME?	0	1	1
ENSG00000250710	ENSG00000250710	OR7E99P	4:4158248-4159170	NOTEST	0	0	0	0	1	1
ENSG00000250711	ENSG00000250711	CTD-2201E18.1	5:42972725-42973194	NOTEST	0	0	0	0	1	1
ENSG00000250712	ENSG00000250712	RP11-366M4.14	4:165931610-165933003	NOTEST	0	0	0	0	1	1
ENSG00000250714	ENSG00000250714	RP11-1149O23.4	8:23046791-23088439	NOTEST	0.0361774	0.0143857	-1.33046	0	1	1
ENSG00000250715	ENSG00000250715	RP11-432M8.19	5:17670276-17670680	NOTEST	0	0	0	0	1	1
ENSG00000250716	ENSG00000250716	RP11-121L11.2	5:3417265-3536208	NOTEST	0	0	0	0	1	1
ENSG00000250719	ENSG00000250719	RP11-322N21.2	1:46505811-46651630	NOTEST	0	0	0	0	1	1
ENSG00000250721	ENSG00000250721	HMGB1P22	5:124601220-124601344	NOTEST	0	0	0	0	1	1
ENSG00000250723	ENSG00000250723	RP11-79E3.2	4:33777968-34041515	NOTEST	0	0	0	0	1	1
ENSG00000250725	ENSG00000250725	RP11-511B7.1	4:166585501-166586823	NOTEST	0	0	0	0	1	1
ENSG00000250726	ENSG00000250726	RP11-616K6.1	4:184993555-184994192	NOTEST	0	0	0	0	1	1
ENSG00000250727	ENSG00000250727	RP11-959I15.1	8:124864226-125183763	NOTEST	0	0	0	0	1	1
ENSG00000250728	ENSG00000250728	AC010468.3	5:110490941-110491850	NOTEST	0	0	0	0	1	1
ENSG00000250730	ENSG00000250730	HMGB3P3	5:6289969-6290737	NOTEST	0	0	0	0	1	1
ENSG00000250731	ENSG00000250731	TPM3P6	19:53970988-54015941	NOTEST	0.0737861	0.117927	0.676473	0	1	1
ENSG00000250732	ENSG00000250732	RPEP1	5:64444562-64777747	NOTEST	0	0	0	0	1	1
ENSG00000250733	ENSG00000250733	C8orf17	8:140742585-141468678	NOTEST	0	0	0	0	1	1
ENSG00000250734	ENSG00000250734	RP11-404E16.1	1:151584513-151671567	NOTEST	0.269094	0.56936	1.08123	0	1	1
ENSG00000250735	ENSG00000250735	RP11-567N4.3	4:76194277-76359659	NOTEST	0	0	0	0	1	1
ENSG00000250739	ENSG00000250739	RP11-462G22.1	4:190580758-190582640	NOTEST	0	0	0	0	1	1
ENSG00000250740	ENSG00000250740	RP11-710F7.2	4:106473776-106943635	NOTEST	0	0	0	0	1	1
ENSG00000250741	ENSG00000250741	NT5C1B-RDH14	2:18735988-18770838	NOTEST	0	0	0	0	1	1
ENSG00000250745	ENSG00000250745	USP17L20	4:9259849-9261442	NOTEST	0	0	0	0	1	1
ENSG00000250746	ENSG00000250746	RP11-39C10.1	4:164445449-165305202	NOTEST	0	0	0	0	1	1
ENSG00000250747	ENSG00000250747	RP11-232L2.1	5:72448242-72448765	NOTEST	0	0	0	0	1	1
ENSG00000250748	ENSG00000250748	RP11-230G5.2	12:65672422-66036152	NOTEST	0.149944	0.337015	1.16839	0	1	1
ENSG00000250749	ENSG00000250749	RP11-451H23.1	5:179921411-180005405	NOTEST	0	0.0366938	inf	0	1	1
ENSG00000250750	ENSG00000250750	OR5BM1P	3:97772217-97772583	NOTEST	0	0	0	0	1	1
ENSG00000250751	ENSG00000250751	RP11-613C6.2	17:47778304-47906458	NOTEST	0	0	0	0	1	1
ENSG00000250752	ENSG00000250752	GS1-24F4.1	8:6756399-6756990	NOTEST	0	0	0	0	1	1
ENSG00000250753	ENSG00000250753	RP11-241F15.10	4:49581849-49582206	NOTEST	0.455928	0.285073	-0.677473	0	1	1
ENSG00000250754	ENSG00000250754	RP11-386B13.3	4:185973049-186028402	NOTEST	0	0	0	0	1	1
ENSG00000250756	ENSG00000250756	RP11-225B17.1	7:32535037-33102409	NOTEST	0	0	0	0	1	1
ENSG00000250760	ENSG00000250760	RP11-440I14.4	4:175444851-175461935	NOTEST	0	0	0	0	1	1
ENSG00000250761	ENSG00000250761	RP11-711G10.1	5:7396320-7830194	NOTEST	0	0	0	0	1	1
ENSG00000250762	ENSG00000250762	RP1-313L4.4	1:167778624-167883453	NOTEST	0	0	0	0	1	1

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ENSG00000250765	ENSG00000250765	AC138035.1	5:180756241-180769214	NOTEST	0	0	0	0	1	1
ENSG00000250767	ENSG00000250767	RP11-1084J3.3	5:33986282-34124633	NOTEST	0.139449	0.350874	1.33122	0	1	1
ENSG00000250768	ENSG00000250768	RP11-204H9.2	4:65296626-65298933	NOTEST	0	0	0	0	1	1
ENSG00000250769	ENSG00000250769	RP11-241F15.3	4:49509780-49510823	NOTEST	0	0.0175093	inf	0	1	1
ENSG00000250770	ENSG00000250770	RP5-1063M23.1	12:3405367-3409390	NOTEST	0	0	0	0	1	1
ENSG00000250771	ENSG00000250771	RP11-153M7.3	4:154561319-154602332	NOTEST	0	0	0	0	1	1
ENSG00000250772	ENSG00000250772	RP11-236P13.1	4:120720243-120725670	NOTEST	0	0	0	0	1	1
ENSG00000250775	ENSG00000250775	RP11-12K22.1	4:64334418-64359996	NOTEST	0	0	0	0	1	1
ENSG00000250777	ENSG00000250777	RP13-884E18.4	4:138611630-138656131	NOTEST	0	0	0	0	1	1
ENSG00000250778	ENSG00000250778	AC004980.8	7:76139744-77045717	NOTEST	0	0	0	0	1	1
ENSG00000250781	ENSG00000250781	RP11-63A11.1	4:42283846-42393285	NOTEST	0	0	0	0	1	1
ENSG00000250782	ENSG00000250782	RP11-432M8.13	5:17634568-17635162	NOTEST	0	0	0	0	1	1
ENSG00000250787	ENSG00000250787	HMGN1P17	5:55677607-55677902	NOTEST	0	0.0921612	inf	0	1	1
ENSG00000250788	ENSG00000250788	TUBB8P4	12:34317707-34319889	NOTEST	0	0	0	0	1	1
ENSG00000250790	ENSG00000250790	RP11-46H11.3	12:133345494-133532892	NOTEST	0.028573	0.0345373	0.273507	0	1	1
ENSG00000250791	ENSG00000250791	RP11-55L3.1	4:117410519-117436302	NOTEST	0	0	0	0	1	1
ENSG00000250794	ENSG00000250794	ALG1L12P	8:12278540-12282509	NOTEST	0.162549	0	#NAME?	0	1	1
ENSG00000250796	ENSG00000250796	RP11-723O4.3	3:128580155-128590383	NOTEST	0.0932542	0	#NAME?	0	1	1
ENSG00000250799	ENSG00000250799	PRODH2	19:36290889-36304201	NOTEST	0	0	0	0	1	1
ENSG00000250801	ENSG00000250801	RP11-91H12.3	5:175333941-175461683	NOTEST	0	0	0	0	1	1
ENSG00000250803	ENSG00000250803	CTC-441N14.4	5:121464456-121518353	NOTEST	0.0559915	0	#NAME?	0	1	1
ENSG00000250804	ENSG00000250804	RP11-747H12.3	4:8983161-8984086	NOTEST	0	0	0	0	1	1
ENSG00000250806	ENSG00000250806	CTC-293G12.1	5:99989815-99993674	NOTEST	0	0	0	0	1	1
ENSG00000250807	ENSG00000250807	RP11-432M8.2	5:17585270-17585876	NOTEST	0	0	0	0	1	1
ENSG00000250808	ENSG00000250808	RP11-531A21.4	5:5396084-5396448	NOTEST	0	0	0	0	1	1
ENSG00000250812	ENSG00000250812	RP11-530I17.2	4:56085510-56086140	NOTEST	0	0	0	0	1	1
ENSG00000250813	ENSG00000250813	SERF1AP1	4:138222154-138222341	NOTEST	0	0	0	0	1	1
ENSG00000250814	ENSG00000250814	RP11-447B18.1	5:9621488-9903938	NOTEST	0	0	0	0	1	1
ENSG00000250815	ENSG00000250815	RP11-89B16.2	4:54243809-55164414	NOTEST	0	0	0	0	1	1
ENSG00000250816	ENSG00000250816	DCAF13P2	5:17065706-17276943	NOTEST	0	0	0	0	1	1
ENSG00000250819	ENSG00000250819	RP11-576E20.1	4:17173379-17187682	NOTEST	0	0	0	0	1	1
ENSG00000250820	ENSG00000250820	RP11-91H12.4	5:175333941-175461683	NOTEST	0	0	0	0	1	1
ENSG00000250821	ENSG00000250821	RP11-345F18.1	4:56686168-56703548	NOTEST	0	0	0	0	1	1
ENSG00000250822	ENSG00000250822	CTD-2139B15.4	5:17379014-17387419	NOTEST	0	0	0	0	1	1
ENSG00000250825	ENSG00000250825	PGAM1P12	15:96981799-96987496	NOTEST	0	0	0	0	1	1
ENSG00000250826	ENSG00000250826	HNRNPA3P13	4:83049687-83050809	NOTEST	0	0	0	0	1	1
ENSG00000250827	ENSG00000250827	CTD-2141G3.1	5:51875388-51876940	NOTEST	0	0	0	0	1	1
ENSG00000250828	ENSG00000250828	RP11-790I12.3	4:70303074-70306768	NOTEST	0	0	0	0	1	1
ENSG00000250829	ENSG00000250829	RP11-11N5.1	4:187812122-187813520	NOTEST	0	0	0	0	1	1
ENSG00000250830	ENSG00000250830	MRPS35P2	5:97738245-97738436	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000250833	ENSG00000250833	DNM1P17	10:30598729-30663377	NOTEST	0	0	0	0	1	1
ENSG00000250834	ENSG00000250834	KRT18P54	4:136292331-136293079	NOTEST	0	0	0	0	1	1
ENSG00000250835	ENSG00000250835	LSM3P4	4:142944312-143768585	NOTEST	0	0	0	0	1	1
ENSG00000250838	ENSG00000250838	RP11-501C14.5	17:47072627-47133012	NOTEST	0	0	0	0	1	1
ENSG00000250839	ENSG00000250839	RP11-296L20.1	4:179990590-179990748	NOTEST	0	0	0	0	1	1
ENSG00000250842	ENSG00000250842	CTC-806A22.1	5:144717494-144761233	NOTEST	0	0	0	0	1	1
ENSG00000250844	ENSG00000250844	USP17L18	4:9250355-9251948	NOTEST	0	0	0	0	1	1
ENSG00000250847	ENSG00000250847	CTD-2020P22.1	5:120531674-120531905	NOTEST	0	0	0	0	1	1
ENSG00000250848	ENSG00000250848	CTD-2083E4.5	5:271735-438406	NOTEST	0.558986	0.480744	-0.217543	0	1	1
ENSG00000250850	ENSG00000250850	RP11-297B17.3	9:36833271-37034103	NOTEST	0	0	0	0	1	1
ENSG00000250852	ENSG00000250852	AC131180.1	2:131862419-132111282	NOTEST	0.00542018	0	#NAME?	0	1	1
ENSG00000250853	ENSG00000250853	RNF138P1	5:54603587-54830878	NOTEST	0	0	0	0	1	1
ENSG00000250855	ENSG00000250855	RP11-269F21.1	4:112723956-112993854	NOTEST	0	0	0	0	1	1
ENSG00000250857	ENSG00000250857	TRIM60P15	8:47703686-47704686	NOTEST	0	0	0	0	1	1
ENSG00000250858	ENSG00000250858	IGBP1P5	4:27586766-27587766	NOTEST	0	0	0	0	1	1
ENSG00000250859	ENSG00000250859	HNRNPKP1	5:126847155-126848534	NOTEST	0	0	0	0	1	1
ENSG00000250860	ENSG00000250860	CTD-2265D6.2	5:42423878-42721979	NOTEST	0.0120063	0	#NAME?	0	1	1
ENSG00000250862	ENSG00000250862	HMGB1P29	5:123556271-123556770	NOTEST	0	0	0	0	1	1
ENSG00000250863	ENSG00000250863	RP11-663P9.1	4:43982022-43983637	NOTEST	0	0	0	0	1	1
ENSG00000250865	ENSG00000250865	RP11-780O17.1	4:136713538-136727059	NOTEST	0	0	0	0	1	1
ENSG00000250866	ENSG00000250866	CTD-2297D10.1	5:5140442-5320417	NOTEST	0	0	0	0	1	1
ENSG00000250867	ENSG00000250867	RP11-1415C14.2	5:69515744-69580686	NOTEST	0	0	0	0	1	1
ENSG00000250868	ENSG00000250868	AC007742.7	Y:19880861-19889280	NOTEST	0	0	0	0	1	1
ENSG00000250869	ENSG00000250869	RP11-453N18.1	8:67876333-68255912	NOTEST	0.013591	0.0163746	0.268811	0	1	1
ENSG00000250874	ENSG00000250874	CTC-480C2.1	5:84959049-84960502	NOTEST	0	0	0	0	1	1
ENSG00000250877	ENSG00000250877	RP11-373J21.1	4:73146685-73434516	NOTEST	0	0	0	0	1	1
ENSG00000250878	ENSG00000250878	METTL21EP	13:103532448-103548383	NOTEST	0	0.0247553	inf	0	1	1
ENSG00000250882	ENSG00000250882	CTC-459M5.1	5:111478137-111755013	NOTEST	0	0	0	0	1	1
ENSG00000250884	ENSG00000250884	OR7E85P	4:9485364-9486349	NOTEST	0	0	0	0	1	1
ENSG00000250885	ENSG00000250885	CTD-2004A9.1	5:32646669-32652082	NOTEST	0	0	0	0	1	1
ENSG00000250886	ENSG00000250886	CTD-2046J7.1	5:35048860-35230794	NOTEST	0	0	0	0	1	1
ENSG00000250887	ENSG00000250887	RP11-366M4.13	4:165928237-165929111	NOTEST	0	0	0	0	1	1
ENSG00000250888	ENSG00000250888	RP11-168A11.1	5:79232401-79263449	NOTEST	0	0	0	0	1	1
ENSG00000250889	ENSG00000250889	RP11-229C3.2	5:74343543-74348668	NOTEST	0.0760223	0	#NAME?	0	1	1
ENSG00000250890	ENSG00000250890	RP5-837O21.8	1:94390961-94391744	NOTEST	0	0	0	0	1	1
ENSG00000250891	ENSG00000250891	CTD-2281M20.1	5:117803850-117897812	NOTEST	0	0.0211303	inf	0	1	1
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ENSG00000250894	ENSG00000250894	RP11-450I1.4	1:12998180-13117751	NOTEST	0	0	0	0	1	1
ENSG00000250895	ENSG00000250895	CTD-2158P22.4	5:118988217-118988695	NOTEST	0	0	0	0	1	1
ENSG00000250897	ENSG00000250897	HMGB3P15	4:95038942-95128707	NOTEST	0	0	0	0	1	1
ENSG00000250900	ENSG00000250900	CTC-338M12.6	5:180618923-180632293	NOTEST	0	0	0	0	1	1
ENSG00000250902	ENSG00000250902	SMAD1-AS1	4:146402345-146479231	NOTEST	0	0	0	0	1	1
ENSG00000250905	ENSG00000250905	RP11-707F2.1	4:150273168-150817385	NOTEST	0	0	0	0	1	1
ENSG00000250906	ENSG00000250906	RP11-632F7.3	4:40812043-41218731	NOTEST	0	0	0	0	1	1
ENSG00000250908	ENSG00000250908	RP11-703C10.1	4:93225549-94695707	NOTEST	0	0	0	0	1	1
ENSG00000250909	ENSG00000250909	RP11-843P14.2	5:175773063-175788971	NOTEST	0.0892104	0.0347565	-1.35993	0	1	1
ENSG00000250910	ENSG00000250910	AC097467.2	4:156197840-156302498	NOTEST	0	0	0	0	1	1
ENSG00000250913	ENSG00000250913	USP17L23	4:9274089-9274640	NOTEST	0	0	0	0	1	1
ENSG00000250915	ENSG00000250915	RP11-1338A24.1	4:8747122-8747759	NOTEST	0	0	0	0	1	1
ENSG00000250917	ENSG00000250917	RP4-785G19.5	20:32782374-32899608	NOTEST	0	0	0	0	1	1
ENSG00000250918	ENSG00000250918	RP11-497H16.4	5:69812213-69851093	NOTEST	0	0	0	0	1	1
ENSG00000250919	ENSG00000250919	RP11-813N20.3	4:69893548-69910296	NOTEST	0	0	0	0	1	1
ENSG00000250920	ENSG00000250920	RP11-297P16.4	4:104469901-104640973	NOTEST	0	0	0	0	1	1
ENSG00000250921	ENSG00000250921	CTD-2008N3.1	5:4135794-4143761	NOTEST	0	0	0	0	1	1
ENSG00000250922	ENSG00000250922	ATP5EP1	4:106453631-106453787	NOTEST	0	0	0	0	1	1
ENSG00000250923	ENSG00000250923	RP11-548K12.8	7:57832289-57833087	NOTEST	0	0	0	0	1	1
ENSG00000250927	ENSG00000250927	MESTP3	4:28824865-28825833	NOTEST	0	0	0	0	1	1
ENSG00000250928	ENSG00000250928	CTB-161M19.2	5:118342041-118584833	NOTEST	0	0	0	0	1	1
ENSG00000250929	ENSG00000250929	KB-1639H6.4	8:104133259-104345094	NOTEST	0.110134	0	#NAME?	0	1	1
ENSG00000250930	ENSG00000250930	LNX1-AS1	4:54243809-55164414	NOTEST	0	0	0	0	1	1
ENSG00000250933	ENSG00000250933	GAPDHP66	18:3496029-4455335	NOTEST	0.0373186	0.0290263	-0.362535	0	1	1
ENSG00000250934	ENSG00000250934	RP11-71E19.1	3:125985638-126012867	NOTEST	0	0.0319709	inf	0	1	1
ENSG00000250938	ENSG00000250938	RP11-679C8.2	4:120976762-121337921	NOTEST	0.0369527	0	#NAME?	0	1	1
ENSG00000250939	ENSG00000250939	AC034198.7	3:12837970-12913415	NOTEST	0	0	0	0	1	1
ENSG00000250940	ENSG00000250940	RP11-489M13.3	4:4088364-4088541	NOTEST	0	0	0	0	1	1
ENSG00000250942	ENSG00000250942	ENPP7P11	4:9678931-9679558	NOTEST	0	0	0	0	1	1
ENSG00000250945	ENSG00000250945	RP11-810P8.1	4:127964584-127998917	NOTEST	0	0	0	0	1	1
ENSG00000250946	ENSG00000250946	RP11-358N4.6	11:89553249-89560090	NOTEST	0	0	0	0	1	1
ENSG00000250947	ENSG00000250947	TRPC7-AS2	5:135548998-135701225	NOTEST	0	0	0	0	1	1
ENSG00000250948	ENSG00000250948	RP11-1079K10.2	17:47448101-47554350	NOTEST	0	0	0	0	1	1
ENSG00000250949	ENSG00000250949	RP11-492L8.2	5:116366895-116374265	NOTEST	0	0.042512	inf	0	1	1
ENSG00000250950	ENSG00000250950	RP11-33B1.3	4:120375945-120550146	NOTEST	0	0.0811522	inf	0	1	1
ENSG00000250951	ENSG00000250951	USP9YP1	Y:20652800-20790963	NOTEST	0	0	0	0	1	1
ENSG00000250954	ENSG00000250954	RP11-79E3.3	4:33777968-34041515	NOTEST	0	0	0	0	1	1
ENSG00000250955	ENSG00000250955	AC008592.7	5:95220801-96143803	NOTEST	0	0	0	0	1	1

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ENSG00000250957	ENSG00000250957	RP11-248N22.1	4:175015810-175141549	NOTEST	0	0	0	0	1	1
ENSG00000250958	ENSG00000250958	LINC00492	5:101917071-102007263	NOTEST	0.100308	0.0249313	-2.0084	0	1	1
ENSG00000250962	ENSG00000250962	RP11-69I13.1	8:89044236-89749363	NOTEST	0	0.0152976	inf	0	1	1
ENSG00000250966	ENSG00000250966	RP11-402J6.3	4:113434671-113578748	NOTEST	0.0618216	0.136492	1.14263	0	1	1
ENSG00000250968	ENSG00000250968	RP11-322J23.1	4:171663619-171664869	NOTEST	0	0	0	0	1	1
ENSG00000250969	ENSG00000250969	RP11-364L4.3	4:144207445-144251011	NOTEST	0	0	0	0	1	1
ENSG00000250971	ENSG00000250971	RP11-696F12.1	4:187981252-187982084	NOTEST	0	0	0	0	1	1
ENSG00000250972	ENSG00000250972	CKS1BP5	5:143550395-143865249	NOTEST	0	0	0	0	1	1
ENSG00000250973	ENSG00000250973	KRTAP13-6P	21:31728832-31729203	NOTEST	0	0	0	0	1	1
ENSG00000250974	ENSG00000250974	RP11-122F24.1	5:6933782-7190925	NOTEST	0	0	0	0	1	1
ENSG00000250976	ENSG00000250976	RP11-94C24.11	17:48633567-48709301	NOTEST	0	0	0	0	1	1
ENSG00000250977	ENSG00000250977	RP11-173E2.2	4:139585878-139586723	NOTEST	0	0	0	0	1	1
ENSG00000250978	ENSG00000250978	RP11-357D18.1	5:66675205-67198428	NOTEST	0	0	0	0	1	1
ENSG00000250979	ENSG00000250979	RP11-656G20.1	8:73114985-73163800	NOTEST	0.00516188	0	#NAME?	0	1	1
ENSG00000250980	ENSG00000250980	RP11-529H22.1	4:153701088-153839615	NOTEST	0	0	0	0	1	1
ENSG00000250981	ENSG00000250981	RP11-19O2.1	5:16067247-16185694	NOTEST	0	0	0	0	1	1
ENSG00000250982	ENSG00000250982	RP11-159J3.1	16:28251013-28251989	NOTEST	0.0890376	0.0950575	0.0943867	0	1	1
ENSG00000250984	ENSG00000250984	CTD-2011G17.1	5:29796044-29796375	NOTEST	0	0	0	0	1	1
ENSG00000250986	ENSG00000250986	AC141928.1	4:3760474-3765117	NOTEST	0	0	0	0	1	1
ENSG00000250989	ENSG00000250989	RP11-392E22.5	9:38540563-38624987	NOTEST	0.336484	0.712152	1.08165	0	1	1
ENSG00000250990	ENSG00000250990	AC073635.5	7:76139744-77045717	NOTEST	0	0.0263909	inf	0	1	1
ENSG00000250992	ENSG00000250992	RP11-826N14.1	5:175467746-175469881	NOTEST	0	0	0	0	1	1
ENSG00000250993	ENSG00000250993	RP11-404J23.1	4:180310287-180386459	NOTEST	0	0	0	0	1	1
ENSG00000250994	ENSG00000250994	AC005355.1	5:133764741-133828210	NOTEST	0	0	0	0	1	1
ENSG00000250995	ENSG00000250995	RP13-128O4.3	X:117861534-117928502	NOTEST	0	0	0	0	1	1
ENSG00000250997	ENSG00000250997	RP11-502M1.1	4:161442980-161443463	NOTEST	0	0	0	0	1	1
ENSG00000251000	ENSG00000251000	AC008592.3	5:95170127-95170750	NOTEST	0	0	0	0	1	1
ENSG00000251001	ENSG00000251001	CTD-2193P3.1	5:80243515-80597379	NOTEST	0	0	0	0	1	1
ENSG00000251002	ENSG00000251002	AE000661.37	14:22849082-22951948	NOTEST	0.0536887	0	#NAME?	0	1	1
ENSG00000251005	ENSG00000251005	RP11-318I4.2	4:127027293-127028078	NOTEST	0	0	0	0	1	1
ENSG00000251007	ENSG00000251007	RP11-1415C14.1	5:69510768-69511950	NOTEST	0	0	0	0	1	1
ENSG00000251008	ENSG00000251008	ORAOV1P1	4:187025572-187093821	NOTEST	0	0	0	0	1	1
ENSG00000251009	ENSG00000251009	RP13-494C23.1	4:25749054-25931435	NOTEST	0	0	0	0	1	1
ENSG00000251010	ENSG00000251010	RP11-6L6.7	4:147162957-147164821	NOTEST	0	0	0	0	1	1
ENSG00000251011	ENSG00000251011	RP11-402L6.1	3:132757234-133116636	NOTEST	0	0.0537662	inf	0	1	1
ENSG00000251012	ENSG00000251012	RP11-484M3.5	3:118864996-118924000	NOTEST	0	0	0	0	1	1
ENSG00000251013	ENSG00000251013	GAPDHP62	8:101521979-101572012	NOTEST	0.113177	0.371403	1.71441	0	1	1
ENSG00000251014	ENSG00000251014	RP11-159K7.1	5:111882669-111883202	NOTEST	0	0	0	0	1	1

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ENSG00000251015	ENSG00000251015	SLC25A30-AS1	13:45967450-45994506	NOTEST	0.0560537	0.0619531	0.144367	0	1	1
ENSG00000251017	ENSG00000251017	RP11-629B11.4	4:74951711-74952389	NOTEST	0.0292986	0	#NAME?	0	1	1
ENSG00000251018	ENSG00000251018	RP11-80G7.1	5:162887208-162921064	NOTEST	0	0	0	0	1	1
ENSG00000251019	ENSG00000251019	HIGD1AP13	4:79567056-79603853	NOTEST	0	0	0	0	1	1
ENSG00000251023	ENSG00000251023	RP11-549J18.1	5:92953774-93447404	NOTEST	0.114574	0.144987	0.339643	0	1	1
ENSG00000251024	ENSG00000251024	RP11-203B7.1	4:146998997-147029309	NOTEST	0	0	0	0	1	1
ENSG00000251025	ENSG00000251025	RP11-751A18.1	4:181494616-181495180	NOTEST	0	0	0	0	1	1
ENSG00000251026	ENSG00000251026	RP11-138J23.1	5:103415611-103441104	NOTEST	0	0	0	0	1	1
ENSG00000251027	ENSG00000251027	CTC-254B4.1	5:106150897-106346715	NOTEST	0	0	0	0	1	1
ENSG00000251031	ENSG00000251031	CTC-367F4.1	5:144602172-144609617	NOTEST	0.0860374	0	#NAME?	0	1	1
ENSG00000251032	ENSG00000251032	RP11-483H11.1	5:127039081-127418864	NOTEST	0	0	0	0	1	1
ENSG00000251033	ENSG00000251033	CTD-2533K21.4	5:26711659-26750106	NOTEST	0	0	0	0	1	1
ENSG00000251034	ENSG00000251034	RP11-582J16.4	8:22298331-22433301	NOTEST	0.165324	0.20894	0.337791	0	1	1
ENSG00000251035	ENSG00000251035	WBP1LP4	5:180805695-180806039	NOTEST	0	0	0	0	1	1
ENSG00000251038	ENSG00000251038	AC090958.5	3:11948000-11953787	NOTEST	0	0	0	0	1	1
ENSG00000251039	ENSG00000251039	IGKV2D-40	2:89890600-89891307	NOTEST	0	0	0	0	1	1
ENSG00000251040	ENSG00000251040	RP11-535C7.1	4:52910970-52913120	NOTEST	0.0622276	0	#NAME?	0	1	1
ENSG00000251041	ENSG00000251041	CTD-2275D24.1	5:73617455-73635977	NOTEST	0	0	0	0	1	1
ENSG00000251044	ENSG00000251044	CTD-2582M21.1	5:67670592-67670955	NOTEST	0	0	0	0	1	1
ENSG00000251045	ENSG00000251045	CTC-321K16.4	5:134984272-134989624	NOTEST	0	0	0	0	1	1
ENSG00000251046	ENSG00000251046	ZNF969P	4:111286888-111486441	NOTEST	0	0	0	0	1	1
ENSG00000251048	ENSG00000251048	RP11-608B3.1	4:18489684-18491131	NOTEST	0	0	0	0	1	1
ENSG00000251049	ENSG00000251049	RP11-685F15.1	4:58462105-58524966	NOTEST	0	0	0	0	1	1
ENSG00000251050	ENSG00000251050	RP11-168A11.4	5:79287133-79379477	NOTEST	0.104069	0.0749839	-0.472888	0	1	1
ENSG00000251051	ENSG00000251051	ELL2P2	4:133288940-133289634	NOTEST	0	0	0	0	1	1
ENSG00000251054	ENSG00000251054	CTD-2215E18.3	5:96424778-96772921	NOTEST	0	0	0	0	1	1
ENSG00000251055	ENSG00000251055	RP11-257A22.1	4:63994028-64009599	NOTEST	0	0	0	0	1	1
ENSG00000251058	ENSG00000251058	RP11-68L1.1	3:139654026-140296239	NOTEST	0	0	0	0	1	1
ENSG00000251059	ENSG00000251059	RP11-100N20.1	4:82009836-82136218	NOTEST	0	0	0	0	1	1
ENSG00000251061	ENSG00000251061	RP11-789C1.2	4:171264239-171293462	NOTEST	0	0	0	0	1	1
ENSG00000251062	ENSG00000251062	CTD-2218G20.1	5:32888095-32888251	NOTEST	0	0	0	0	1	1
ENSG00000251066	ENSG00000251066	CTC-534B23.1	5:84845226-84845770	NOTEST	0	0	0	0	1	1
ENSG00000251070	ENSG00000251070	BMS1P6	10:48187415-48237508	NOTEST	0	0	0	0	1	1
ENSG00000251072	ENSG00000251072	RP11-434D11.4	5:126087654-126112178	NOTEST	0.0199906	0	#NAME?	0	1	1
ENSG00000251073	ENSG00000251073	NUDT19P5	4:159045625-159176563	NOTEST	0.0691752	0.0827415	0.258356	0	1	1
ENSG00000251074	ENSG00000251074	RP11-1267H10.3	4:69492564-69494617	NOTEST	0	0	0	0	1	1
ENSG00000251075	ENSG00000251075	HTT-AS	4:3065197-3076241	NOTEST	0	0	0	0	1	1
ENSG00000251076	ENSG00000251076	RP11-526F3.1	5:111478137-111755013	NOTEST	0	0	0	0	1	1
ENSG00000251078	ENSG00000251078	SLC25A5P9	5:75048394-75049304	NOTEST	0	0	0	0	1	1
ENSG00000251079	ENSG00000251079	BMS1P2	10:47186202-47243502	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000251080	ENSG00000251080	RP11-415C15.1	4:27135617-27141673	NOTEST	0	0	0	0	1	1
ENSG00000251081	ENSG00000251081	RP11-713M6.2	4:107842958-108223027	NOTEST	0	0	0	0	1	1
ENSG00000251085	ENSG00000251085	RP11-893F2.6	17:48286332-48292781	NOTEST	0	0	0	0	1	1
ENSG00000251087	ENSG00000251087	ALG1L3P	4:9705373-9712436	NOTEST	0	0	0	0	1	1
ENSG00000251088	ENSG00000251088	RP11-325B23.2	3:97952494-98176742	NOTEST	0	0	0	0	1	1
ENSG00000251090	ENSG00000251090	OR5AC4P	3:97818751-97866978	NOTEST	0	0	0	0	1	1
ENSG00000251093	ENSG00000251093	RP11-414H23.3	5:90522291-90522888	NOTEST	0	0	0	0	1	1
ENSG00000251095	ENSG00000251095	RP11-115D19.1	4:90472506-90763129	NOTEST	0.054511	0.0678805	0.316449	0	1	1
ENSG00000251099	ENSG00000251099	CTD-2367A17.1	5:110831730-111353006	NOTEST	0	0	0	0	1	1
ENSG00000251101	ENSG00000251101	RP11-1267H10.1	4:69481110-69481855	NOTEST	0	0	0	0	1	1
ENSG00000251102	ENSG00000251102	CTBP2P4	5:97912044-97912964	NOTEST	0.0560737	0.0882116	0.653645	0	1	1
ENSG00000251105	ENSG00000251105	RP11-571I18.2	4:54243809-55164414	NOTEST	0.500799	0	#NAME?	0	1	1
ENSG00000251106	ENSG00000251106	FAM206BP	13:46786082-46851501	NOTEST	0	0	0	0	1	1
ENSG00000251107	ENSG00000251107	RP11-466P24.4	5:75377770-75649764	NOTEST	0	0	0	0	1	1
ENSG00000251108	ENSG00000251108	YBX1P5	5:71713315-71714162	NOTEST	0	0	0	0	1	1
ENSG00000251111	ENSG00000251111	FCF1P8	4:56212275-56262014	NOTEST	0.0348708	0.0842468	1.2726	0	1	1
ENSG00000251112	ENSG00000251112	RP11-419C19.3	5:12574968-12804475	NOTEST	0	0	0	0	1	1
ENSG00000251113	ENSG00000251113	RP11-68D16.2	4:29467322-29469472	NOTEST	0	0	0	0	1	1
ENSG00000251118	ENSG00000251118	CTC-505O3.1	5:115106282-115106686	NOTEST	0	0	0	0	1	1
ENSG00000251122	ENSG00000251122	NIFKP2	5:174346084-174422516	NOTEST	0	0	0	0	1	1
ENSG00000251123	ENSG00000251123	RP11-580J4.1	4:163905946-163906568	NOTEST	0	0	0	0	1	1
ENSG00000251125	ENSG00000251125	CTD-2335O3.3	5:50746991-50757923	NOTEST	0	0	0	0	1	1
ENSG00000251126	ENSG00000251126	RP11-119H12.6	4:113739264-114304896	NOTEST	0	0	0	0	1	1
ENSG00000251127	ENSG00000251127	RP11-280G9.1	8:62671652-62678528	NOTEST	0	0	0	0	1	1
ENSG00000251128	ENSG00000251128	WWC2-AS1	4:184020445-184241930	NOTEST	0	0	0	0	1	1
ENSG00000251129	ENSG00000251129	RP11-734I18.1	4:31999018-32157028	NOTEST	0	0	0	0	1	1
ENSG00000251131	ENSG00000251131	CTD-2035E11.3	5:43014515-43192123	NOTEST	0.12542	0	#NAME?	0	1	1
ENSG00000251132	ENSG00000251132	RP11-438C19.2	5:114366969-114367591	NOTEST	0	0	0	0	1	1
ENSG00000251135	ENSG00000251135	AC008565.1	5:120375784-120379727	NOTEST	0	0	0	0	1	1
ENSG00000251137	ENSG00000251137	RPL7L1P7	3:138722803-139108574	NOTEST	0	0	0	0	1	1
ENSG00000251138	ENSG00000251138	RP11-81H3.2	12:74526945-74796315	NOTEST	0.47363	0.521978	0.140228	0	1	1
ENSG00000251139	ENSG00000251139	RP11-701P16.2	4:185676748-185747972	NOTEST	0	0	0	0	1	1
ENSG00000251142	ENSG00000251142	RP11-513O17.1	8:58055247-58153100	NOTEST	0	0	0	0	1	1
ENSG00000251143	ENSG00000251143	RP11-849H4.4	11:71709586-71823826	NOTEST	0.388267	0.388497	0.000852929	0	1	1
ENSG00000251144	ENSG00000251144	CTD-2532K18.2	5:174178306-174277728	NOTEST	0	0	0	0	1	1
ENSG00000251147	ENSG00000251147	RP11-701P16.3	4:185832042-185832506	NOTEST	0	0	0	0	1	1
ENSG00000251148	ENSG00000251148	RP11-478C1.7	4:2271308-2420390	NOTEST	0	0	0	0	1	1
ENSG00000251149	ENSG00000251149	MTND5P5	4:102332442-102995969	NOTEST	0	0	0	0	1	1
ENSG00000251151	ENSG00000251151	HOXC-AS3	12:54375292-54449814	NOTEST	0.164625	0.541833	1.71866	0	1	1
ENSG00000251152	ENSG00000251152	RP11-281P23.1	4:11470873-11479820	NOTEST	0	0	0	0	1	1

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ENSG00000251155	ENSG00000251155	RP11-384K6.4	4:119561827-119562013	NOTEST	0	0	0	0	1	1
ENSG00000251158	ENSG00000251158	RP11-98J23.1	5:69171097-69274436	NOTEST	0	0.00277227	inf	0	1	1
ENSG00000251159	ENSG00000251159	RP11-500G9.1	4:44535631-44535897	NOTEST	0	0	0	0	1	1
ENSG00000251161	ENSG00000251161	RP11-540O11.1	15:41199008-41201540	NOTEST	0.142153	0.0858639	-0.727321	0	1	1
ENSG00000251162	ENSG00000251162	RP11-75A5.1	4:165518870-165519128	NOTEST	0	0	0	0	1	1
ENSG00000251163	ENSG00000251163	CTD-2325A15.2	5:42897363-42897934	NOTEST	0	0	0	0	1	1
ENSG00000251165	ENSG00000251165	F11-AS1	4:187187098-187476721	NOTEST	0	0	0	0	1	1
ENSG00000251166	ENSG00000251166	OR7E163P	4:3891082-3891976	NOTEST	0	0	0	0	1	1
ENSG00000251168	ENSG00000251168	CTD-2072I24.1	5:7924404-7925511	NOTEST	0	0	0	0	1	1
ENSG00000251169	ENSG00000251169	AC005355.2	5:133842242-133844920	NOTEST	0	0	0	0	1	1
ENSG00000251170	ENSG00000251170	RP11-729M20.1	4:105151536-105332192	NOTEST	0	0	0	0	1	1
ENSG00000251171	ENSG00000251171	RP11-327O17.2	4:170015406-170192256	NOTEST	0	0	0	0	1	1
ENSG00000251172	ENSG00000251172	RP11-529P9.1	3:96533424-97471304	NOTEST	0	0	0	0	1	1
ENSG00000251173	ENSG00000251173	UCHL1-AS1	4:41222090-41270472	NOTEST	0	0	0	0	1	1
ENSG00000251174	ENSG00000251174	TSEN2P1	4:176415764-176417151	NOTEST	0	0	0	0	1	1
ENSG00000251175	ENSG00000251175	RP11-45L9.1	4:106473776-106943635	NOTEST	0	0	0	0	1	1
ENSG00000251176	ENSG00000251176	RP11-97E7.1	4:172474150-172485418	NOTEST	0	0	0	0	1	1
ENSG00000251177	ENSG00000251177	RP11-401E5.2	4:70438108-70451245	NOTEST	0	0	0	0	1	1
ENSG00000251178	ENSG00000251178	OR7E21P	3:129753395-129754382	NOTEST	0	0	0	0	1	1
ENSG00000251179	ENSG00000251179	RP11-893F2.9	17:48358937-48365216	NOTEST	0	0.01996	inf	0	1	1
ENSG00000251180	ENSG00000251180	CU459201.1	GL000242.1:12835-34543	NOTEST	0	0	0	0	1	1
ENSG00000251182	ENSG00000251182	RP11-617I14.1	4:31172765-31213297	NOTEST	0	0	0	0	1	1
ENSG00000251183	ENSG00000251183	AC091962.3	5:153266987-153278547	NOTEST	0	0	0	0	1	1
ENSG00000251184	ENSG00000251184	RP11-101E3.5	9:131683173-131790582	NOTEST	0	0	0	0	1	1
ENSG00000251185	ENSG00000251185	RP11-542G1.1	4:76194277-76359659	NOTEST	0	0	0	0	1	1
ENSG00000251186	ENSG00000251186	RP11-689P11.3	4:8368008-8514337	NOTEST	0	0	0	0	1	1
ENSG00000251187	ENSG00000251187	CTC-459M5.2	5:111478137-111755013	NOTEST	0	0	0	0	1	1
ENSG00000251188	ENSG00000251188	RP11-478C6.6	4:262770-263320	NOTEST	0.0391948	0.150311	1.93922	0	1	1
ENSG00000251189	ENSG00000251189	CTD-2196P11.2	5:38682171-38685228	NOTEST	0	0	0	0	1	1
ENSG00000251193	ENSG00000251193	RP11-72K17.1	5:97073597-97074617	NOTEST	0	0	0	0	1	1
ENSG00000251194	ENSG00000251194	RP1-68D18.2	11:35160416-35253949	NOTEST	0.479379	0.49014	0.0320267	0	1	1
ENSG00000251195	ENSG00000251195	RP11-378N18.1	4:130098540-130100249	NOTEST	0	0	0	0	1	1
ENSG00000251197	ENSG00000251197	MICE	HSCHR6_MHC_QBL:29688013-29714292	NOTEST	0	0	0	0	1	1
ENSG00000251199	ENSG00000251199	RP11-400D2.2	4:135176327-135249953	NOTEST	0	0	0	0	1	1
ENSG00000251200	ENSG00000251200	RP11-6E9.5	4:170838911-170897053	NOTEST	0	0	0	0	1	1
ENSG00000251203	ENSG00000251203	RP11-14I17.1	8:26236774-26371608	NOTEST	0	0.0210991	inf	0	1	1
ENSG00000251204	ENSG00000251204	CTC-278L1.1	5:105751276-105752942	NOTEST	0	0	0	0	1	1
ENSG00000251205	ENSG00000251205	CTD-2050E21.2	5:142938783-142942113	NOTEST	0	0	0	0	1	1
ENSG00000251206	ENSG00000251206	CTD-2187J20.1	5:66563849-66566010	NOTEST	0	0	0	0	1	1
ENSG00000251209	ENSG00000251209	LINC00923	15:98285447-98417780	NOTEST	0.0115214	0	#NAME?	0	1	1
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ENSG00000251212	ENSG00000251212	MTND5P4	4:16974897-17075526	NOTEST	0	0	0	0	1	1
ENSG00000251213	ENSG00000251213	RP11-248N22.2	4:175015810-175141549	NOTEST	0	0	0	0	1	1
ENSG00000251214	ENSG00000251214	CTD-2308B18.1	5:123791065-123796242	NOTEST	0	0	0	0	1	1
ENSG00000251215	ENSG00000251215	GOLGA5P1	5:39105337-39274630	NOTEST	0	0	0	0	1	1
ENSG00000251216	ENSG00000251216	RP11-161D15.3	4:174798621-174912012	NOTEST	0	0	0	0	1	1
ENSG00000251218	ENSG00000251218	RP11-1057B8.2	8:135862177-135894142	NOTEST	0	0	0	0	1	1
ENSG00000251219	ENSG00000251219	EMCN-IT2	4:101316497-101801283	NOTEST	0	0	0	0	1	1
ENSG00000251220	ENSG00000251220	RFPL4AP3	4:23516562-23516907	NOTEST	0	0	0	0	1	1
ENSG00000251221	ENSG00000251221	CTC-325J23.3	5:79904441-79918343	NOTEST	0	0.0393173	inf	0	1	1
ENSG00000251223	ENSG00000251223	RP11-627H22.5	4:156380855-156382389	NOTEST	0	0	0	0	1	1
ENSG00000251224	ENSG00000251224	CNOT10-AS1	3:32726636-32815367	NOTEST	0	0	0	0	1	1
ENSG00000251226	ENSG00000251226	RP11-469N6.1	11:134605489-134633704	NOTEST	0	0.00328382	inf	0	1	1
ENSG00000251228	ENSG00000251228	RP11-192C21.3	4:135865429-135865678	NOTEST	0	0	0	0	1	1
ENSG00000251229	ENSG00000251229	RP11-503N18.5	4:2420700-2734292	NOTEST	0	0	0	0	1	1
ENSG00000251230	ENSG00000251230	RP11-701P16.5	4:185765738-185776905	NOTEST	0	0	0	0	1	1
ENSG00000251234	ENSG00000251234	PSMA2P2	8:94951591-94955105	NOTEST	0	0	0	0	1	1
ENSG00000251235	ENSG00000251235	RP11-156N15.1	5:75672499-75672974	NOTEST	0	0	0	0	1	1
ENSG00000251236	ENSG00000251236	RP11-468N14.1	4:69679712-69680445	NOTEST	0	0	0	0	1	1
ENSG00000251237	ENSG00000251237	CTD-2207L17.2	5:51971026-52390609	NOTEST	0	0	0	0	1	1
ENSG00000251239	ENSG00000251239	CTB-22K21.2	17:48633567-48709301	NOTEST	0	0	0	0	1	1
ENSG00000251243	ENSG00000251243	AC005178.1	5:133056185-133056625	NOTEST	0	0	0	0	1	1
ENSG00000251244	ENSG00000251244	RP13-487K5.1	4:156436878-156438611	NOTEST	0	0	0	0	1	1
ENSG00000251246	ENSG00000251246	EFNA3	1:155036206-155060014	NOTEST	0	0.00439759	inf	0	1	1
ENSG00000251248	ENSG00000251248	RP11-223C24.2	4:142944312-143768585	NOTEST	0	0	0	0	1	1
ENSG00000251249	ENSG00000251249	RP11-73G16.1	4:152877142-152890533	NOTEST	0	0	0	0	1	1
ENSG00000251250	ENSG00000251250	RP11-404K5.4	5:7326176-7326722	NOTEST	0	0	0	0	1	1
ENSG00000251252	ENSG00000251252	MTND2P31	4:14472088-14889793	NOTEST	0	0	0	0	1	1
ENSG00000251253	ENSG00000251253	MTHFD2P4	4:163243339-163245059	NOTEST	0	0	0	0	1	1
ENSG00000251254	ENSG00000251254	GTF2F2P1	4:148402068-148466106	NOTEST	0	0	0	0	1	1
ENSG00000251256	ENSG00000251256	RP11-273B19.1	4:55711733-55725407	NOTEST	0	0	0	0	1	1
ENSG00000251257	ENSG00000251257	CTD-2263F21.1	5:38258510-38468441	NOTEST	0	0	0	0	1	1
ENSG00000251258	ENSG00000251258	RFPL4B	6:112429962-112672498	NOTEST	0	0	0	0	1	1
ENSG00000251259	ENSG00000251259	AC004069.2	4:106058436-106061776	NOTEST	0.14583	0.0863412	-0.756167	0	1	1
ENSG00000251260	ENSG00000251260	WDFY3-AS1	4:85590703-85932430	NOTEST	0	0	0	0	1	1
ENSG00000251261	ENSG00000251261	OR7H2P	5:101152178-101152484	NOTEST	0	0	0	0	1	1
ENSG00000251264	ENSG00000251264	RP11-545H22.1	4:55306668-55312890	NOTEST	0	0	0	0	1	1
ENSG00000251266	ENSG00000251266	RP11-340A13.2	4:59849999-59912677	NOTEST	0	0	0	0	1	1
ENSG00000251270	ENSG00000251270	RP11-231L11.1	3:140770243-140867453	NOTEST	0	0	0	0	1	1

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ENSG00000251273	ENSG00000251273	RP11-549K20.1	5:25126413-25190765	NOTEST	0.0409216	0.0637527	0.639624	0	1	1
ENSG00000251274	ENSG00000251274	RP11-436H11.4	5:123972607-124084500	NOTEST	0	0	0	0	1	1
ENSG00000251275	ENSG00000251275	AC006335.2	Y:6109808-6113324	NOTEST	0	0	0	0	1	1
ENSG00000251276	ENSG00000251276	MAGI2-AS1	7:77646392-79100524	NOTEST	0	0	0	0	1	1
ENSG00000251278	ENSG00000251278	AC006499.2	4:10293818-10294332	NOTEST	0	0	0	0	1	1
ENSG00000251279	ENSG00000251279	CTC-436P18.1	5:60453535-60560756	NOTEST	0.0306419	0.109243	1.83396	0	1	1
ENSG00000251281	ENSG00000251281	CTD-2066L21.2	5:32925744-33298016	NOTEST	0	0	0	0	1	1
ENSG00000251283	ENSG00000251283	RP11-171N4.2	4:157555645-157563606	NOTEST	0	0	0	0	1	1
ENSG00000251284	ENSG00000251284	RP13-644M16.1	4:69990991-69992169	NOTEST	0	0	0	0	1	1
ENSG00000251285	ENSG00000251285	RP11-147K6.2	4:89011415-89152474	NOTEST	0	0	0	0	1	1
ENSG00000251286	ENSG00000251286	RP11-588F10.1	4:53306659-53307701	NOTEST	0	0	0	0	1	1
ENSG00000251287	ENSG00000251287	ALG1L2	3:129800673-129839422	NOTEST	0.023062	0.230954	3.32401	0	1	1
ENSG00000251288	ENSG00000251288	RP11-10L12.2	4:103552659-103682151	NOTEST	0.0252797	0.0431623	0.771791	0	1	1
ENSG00000251291	ENSG00000251291	RP11-400D2.3	4:135345021-135379007	NOTEST	0	0	0	0	1	1
ENSG00000251292	ENSG00000251292	RP11-380P13.2	4:23562545-23905712	NOTEST	0	0.101376	inf	0	1	1
ENSG00000251293	ENSG00000251293	CTC-552D5.1	5:119581142-119669197	NOTEST	0	0	0	0	1	1
ENSG00000251294	ENSG00000251294	RP11-116O11.1	5:24487208-24645087	NOTEST	0	0	0	0	1	1
ENSG00000251296	ENSG00000251296	AC006499.7	4:10168782-10169389	NOTEST	0	0	0	0	1	1
ENSG00000251297	ENSG00000251297	TUBB7P	4:190903677-190906026	NOTEST	0.176215	0.146346	-0.267959	0	1	1
ENSG00000251298	ENSG00000251298	RP11-425A23.1	4:148530702-148538396	NOTEST	0	0	0	0	1	1
ENSG00000251299	ENSG00000251299	SLC25A15P3	13:25498814-25542625	NOTEST	0	0	0	0	1	1
ENSG00000251300	ENSG00000251300	RP11-54P19.1	4:143854347-144106014	NOTEST	0	0	0	0	1	1
ENSG00000251301	ENSG00000251301	RP11-81H14.2	12:68726667-68845443	NOTEST	0	0	0	0	1	1
ENSG00000251303	ENSG00000251303	CTD-2003D5.1	5:59892738-59996017	NOTEST	0.154148	0.151017	-0.0296075	0	1	1
ENSG00000251304	ENSG00000251304	RP11-321E2.5	5:17486335-17486938	NOTEST	0	0	0	0	1	1
ENSG00000251306	ENSG00000251306	NDUFB4P2	5:58264864-59843484	NOTEST	0	0	0	0	1	1
ENSG00000251307	ENSG00000251307	RP11-506H20.1	5:54529761-54603550	NOTEST	0.235677	0.0543398	-2.11673	0	1	1
ENSG00000251308	ENSG00000251308	MRPS33P3	4:116064137-116064459	NOTEST	0	0	0	0	1	1
ENSG00000251309	ENSG00000251309	RP11-498M5.2	4:102332442-102995969	NOTEST	0	0	0	0	1	1
ENSG00000251310	ENSG00000251310	RP11-706F1.1	4:190114253-190126031	NOTEST	0	0	0	0	1	1
ENSG00000251311	ENSG00000251311	RP11-249M12.2	5:116078686-116097905	NOTEST	0	0	0	0	1	1
ENSG00000251312	ENSG00000251312	AC004062.2	4:111984738-111985383	NOTEST	0	0	0	0	1	1
ENSG00000251313	ENSG00000251313	RP11-747H12.5	4:9032011-9032792	NOTEST	0	0	0	0	1	1
ENSG00000251314	ENSG00000251314	CTD-2337A12.1	5:95220801-96143803	NOTEST	0.0854079	0	#NAME?	0	1	1
ENSG00000251317	ENSG00000251317	KLF17P2	4:14113591-14145216	NOTEST	0	0	0	0	1	1
ENSG00000251320	ENSG00000251320	CTC-327F10.4	5:147250244-147286101	NOTEST	0	0	0	0	1	1
ENSG00000251321	ENSG00000251321	PCAT4	4:80748624-80798924	NOTEST	0	0	0	0	1	1
ENSG00000251323	ENSG00000251323	RP11-452H21.4	11:77926342-78285919	NOTEST	0.237386	0.176174	-0.430233	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000251325	ENSG00000251325	RP11-415C15.3	4:27209126-27283847	NOTEST	0	0	0	0	1	1
ENSG00000251326	ENSG00000251326	RP11-521E5.1	4:131297383-131307526	NOTEST	0	0	0	0	1	1
ENSG00000251329	ENSG00000251329	RP11-240A16.1	4:32352659-32354842	NOTEST	0	0	0	0	1	1
ENSG00000251330	ENSG00000251330	CTD-2283N19.1	5:147763497-147822399	NOTEST	0.043306	0	#NAME?	0	1	1
ENSG00000251331	ENSG00000251331	RP11-689K5.3	4:82347546-82965397	NOTEST	0	0	0	0	1	1
ENSG00000251332	ENSG00000251332	RP11-177C12.4	4:37892707-38140796	NOTEST	0.0275587	0.0194746	-0.500916	0	1	1
ENSG00000251333	ENSG00000251333	RTN3P1	4:146296694-146297405	NOTEST	0.0275077	0.0388765	0.499063	0	1	1
ENSG00000251334	ENSG00000251334	RP11-317G22.2	4:48938598-48938897	NOTEST	0	0	0	0	1	1
ENSG00000251336	ENSG00000251336	RP11-540E16.2	4:182741171-182751126	NOTEST	0	0	0	0	1	1
ENSG00000251338	ENSG00000251338	AC006499.1	4:10296086-10297203	NOTEST	0	0	0	0	1	1
ENSG00000251339	ENSG00000251339	RP11-506N2.1	4:59646790-59849870	NOTEST	0	0	0	0	1	1
ENSG00000251340	ENSG00000251340	RP11-461G12.2	5:93488670-94620279	NOTEST	0	0	0	0	1	1
ENSG00000251342	ENSG00000251342	CTC-235G5.2	5:75374490-75375588	NOTEST	0	0	0	0	1	1
ENSG00000251345	ENSG00000251345	RP11-392L5.2	4:130054260-130055253	NOTEST	0	0	0	0	1	1
ENSG00000251347	ENSG00000251347	IRF5P1	8:93895211-94029901	NOTEST	0	0	0	0	1	1
ENSG00000251348	ENSG00000251348	HSPD1P11	5:95036952-95160087	NOTEST	0.337212	0.291947	-0.207949	0	1	1
ENSG00000251350	ENSG00000251350	RP11-328N19.1	4:44018877-44024080	NOTEST	0.472711	0.38941	-0.279668	0	1	1
ENSG00000251352	ENSG00000251352	RP11-451H23.2	5:180098891-180099598	NOTEST	0	0	0	0	1	1
ENSG00000251353	ENSG00000251353	MTND3P5	4:25721720-25722053	NOTEST	0	0	0	0	1	1
ENSG00000251354	ENSG00000251354	RP11-697N18.1	8:48173166-48648868	NOTEST	0	0	0	0	1	1
ENSG00000251356	ENSG00000251356	RAB5CP2	5:90772198-90772835	NOTEST	0.0318772	0	#NAME?	0	1	1
ENSG00000251357	ENSG00000251357	AP000350.10	22:24198613-24241117	NOTEST	0	0.261876	inf	0	1	1
ENSG00000251359	ENSG00000251359	WWC2-AS2	4:184018169-184020352	NOTEST	0	0.0289394	inf	0	1	1
ENSG00000251360	ENSG00000251360	KHDC1P1	6:73918805-74020088	NOTEST	0	0	0	0	1	1
ENSG00000251361	ENSG00000251361	CTD-2091N23.1	5:92355368-92404375	NOTEST	0	0	0	0	1	1
ENSG00000251363	ENSG00000251363	RP11-129M6.1	14:41424102-41445082	NOTEST	0	0	0	0	1	1
ENSG00000251364	ENSG00000251364	CTD-2516F10.2	11:7490917-7533746	NOTEST	0.50799	0.253058	-1.00533	0	1	1
ENSG00000251365	ENSG00000251365	RP11-332J15.3	5:6766003-6772066	NOTEST	0	0.284233	inf	0	1	1
ENSG00000251366	ENSG00000251366	DBIP2	5:79899201-79899463	NOTEST	0	0	0	0	1	1
ENSG00000251367	ENSG00000251367	RP11-231G15.2	5:108803053-108803653	NOTEST	0	0	0	0	1	1
ENSG00000251368	ENSG00000251368	RP11-175M2.1	5:54921672-55112985	NOTEST	0	0	0	0	1	1
ENSG00000251370	ENSG00000251370	CTD-2201E9.1	5:9001885-9546187	NOTEST	0.0652698	0.0292933	-1.15584	0	1	1
ENSG00000251371	ENSG00000251371	CTD-2318H23.1	5:4452042-4866334	NOTEST	0	0	0	0	1	1
ENSG00000251372	ENSG00000251372	LINC00499	4:139220009-139345498	NOTEST	0.217752	0.0848209	-1.36019	0	1	1
ENSG00000251373	ENSG00000251373	RP11-68D16.1	4:29408721-29409634	NOTEST	0	0	0	0	1	1
ENSG00000251374	ENSG00000251374	RPS23P5	5:81267843-81574396	NOTEST	0	0	0	0	1	1
ENSG00000251376	ENSG00000251376	CTD-2313F11.2	5:54350255-54350968	NOTEST	0	0	0	0	1	1
ENSG00000251377	ENSG00000251377	RP11-18H21.3	4:153128572-153147022	NOTEST	0	0	0	0	1	1
ENSG00000251378	ENSG00000251378	AC096582.9	7:45855814-45860663	NOTEST	0.0541381	0.0285884	-0.921214	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000251380	ENSG00000251380	C5orf20	5:134779904-134794387	NOTEST	0	0	0	0	1	1
ENSG00000251381	ENSG00000251381	LINC00958	11:12984056-13011095	NOTEST	0.0633619	0.133994	1.08048	0	1	1
ENSG00000251383	ENSG00000251383	RP11-542G1.3	4:76194277-76359659	NOTEST	0	0	0	0	1	1
ENSG00000251385	ENSG00000251385	RP11-63H19.2	4:65473420-65474549	NOTEST	0	0	0	0	1	1
ENSG00000251387	ENSG00000251387	CTB-35F21.3	5:139152112-139155057	NOTEST	0	0	0	0	1	1
ENSG00000251388	ENSG00000251388	RP11-427M20.1	4:134792400-134931845	NOTEST	0	0	0	0	1	1
ENSG00000251389	ENSG00000251389	YTHDF1P1	5:96424778-96772921	NOTEST	0	0	0	0	1	1
ENSG00000251391	ENSG00000251391	RP11-305P14.1	5:65594295-65618772	NOTEST	0.101691	0	#NAME?	0	1	1
ENSG00000251393	ENSG00000251393	RP1-240K6.3	14:73741814-73943880	NOTEST	0	0	0	0	1	1
ENSG00000251394	ENSG00000251394	OR12D3	HSCHR6_MHC_COX:29319721-29421426	NOTEST	0	0	0	0	1	1
ENSG00000251395	ENSG00000251395	FTH1P9	5:82722494-82722849	NOTEST	0	0	0	0	1	1
ENSG00000251398	ENSG00000251398	RP11-149A7.2	4:133512243-133599658	NOTEST	0	0	0	0	1	1
ENSG00000251399	ENSG00000251399	RP11-234K19.1	4:80517695-80518327	NOTEST	0	0	0	0	1	1
ENSG00000251401	ENSG00000251401	RP11-11N6.1	4:91048685-92523064	NOTEST	0	0	0	0	1	1
ENSG00000251402	ENSG00000251402	FAM90A25P	8:12272588-12275599	NOTEST	0	0	0	0	1	1
ENSG00000251405	ENSG00000251405	CTB-109A12.1	5:156687131-157002783	NOTEST	0	0	0	0	1	1
ENSG00000251407	ENSG00000251407	MTND1P22	4:156384024-156384975	NOTEST	0	0	0	0	1	1
ENSG00000251408	ENSG00000251408	RP11-586D19.2	4:6202459-6240044	NOTEST	0	0	0	0	1	1
ENSG00000251409	ENSG00000251409	AC008592.4	5:95171646-95195837	NOTEST	0	0	0	0	1	1
ENSG00000251410	ENSG00000251410	AC007106.1	4:27969344-27986685	NOTEST	0	0	0	0	1	1
ENSG00000251411	ENSG00000251411	RP11-397E7.4	4:87797357-88062206	NOTEST	0	0.0604422	inf	0	1	1
ENSG00000251412	ENSG00000251412	AC006296.1	4:14384746-14410702	NOTEST	0	0	0	0	1	1
ENSG00000251413	ENSG00000251413	RP11-534L6.5	10:49654076-49864310	NOTEST	0	0	0	0	1	1
ENSG00000251414	ENSG00000251414	RP11-843P14.1	5:175773063-175788971	NOTEST	0.208045	0.476909	1.19682	0	1	1
ENSG00000251416	ENSG00000251416	RP11-140M13.1	4:178607826-178612222	NOTEST	0	0	0	0	1	1
ENSG00000251417	ENSG00000251417	RP11-1348G14.4	16:28814096-28829149	NOTEST	0.0643654	0.0882447	0.455223	0	1	1
ENSG00000251418	ENSG00000251418	RP11-655B23.1	4:149447644-149448291	NOTEST	0	0	0	0	1	1
ENSG00000251419	ENSG00000251419	RP11-524L6.4	5:75127079-75128589	NOTEST	0	0	0	0	1	1
ENSG00000251421	ENSG00000251421	CTC-369A16.2	5:123641922-123740772	NOTEST	0	0	0	0	1	1
ENSG00000251423	ENSG00000251423	CTB-51A17.1	5:13690439-13944652	NOTEST	0	0	0	0	1	1
ENSG00000251424	ENSG00000251424	RP11-468N14.3	4:69699930-69700086	NOTEST	0	0	0	0	1	1
ENSG00000251426	ENSG00000251426	CTD-2247C11.4	5:5034471-5078424	NOTEST	0	0	0	0	1	1
ENSG00000251427	ENSG00000251427	RP13-644M16.2	4:70010451-70013389	NOTEST	0	0	0	0	1	1
ENSG00000251430	ENSG00000251430	RP11-63H19.1	4:65472135-65472331	NOTEST	0	0	0	0	1	1
ENSG00000251431	ENSG00000251431	AC008984.5	19:54799853-54809952	NOTEST	0	0	0	0	1	1
ENSG00000251433	ENSG00000251433	RP11-540E16.1	4:182795590-183724177	NOTEST	0	0	0	0	1	1
ENSG00000251434	ENSG00000251434	RP11-315A17.1	4:31351905-31353347	NOTEST	0	0	0	0	1	1
ENSG00000251435	ENSG00000251435	RP11-365H8.2	5:55395506-55529186	NOTEST	0	0	0	0	1	1
ENSG00000251436	ENSG00000251436	NUPL1P1	4:126597872-126673948	NOTEST	0	0.0228499	inf	0	1	1
ENSG00000251437	ENSG00000251437	NDUFS5P4	4:99792834-99916145	NOTEST	0	0	0	0	1	1

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ENSG00000251439	ENSG00000251439	AC006070.12	17:39343195-39343388	NOTEST	0	0	0	0	1	1
ENSG00000251440	ENSG00000251440	STMN1P2	4:138346579-138347018	NOTEST	0	0	0	0	1	1
ENSG00000251441	ENSG00000251441	RTEL1P1	4:113195697-113363776	NOTEST	0	0	0	0	1	1
ENSG00000251442	ENSG00000251442	LINC01094	4:79567056-79603853	NOTEST	0.155198	0.135225	-0.198747	0	1	1
ENSG00000251443	ENSG00000251443	RP11-113I22.1	5:32925744-33298016	NOTEST	0.257585	0.167709	-0.619092	0	1	1
ENSG00000251445	ENSG00000251445	RP11-483A20.3	4:169931580-169932090	NOTEST	0	0	0	0	1	1
ENSG00000251446	ENSG00000251446	RP11-375B1.2	5:176153942-176166459	NOTEST	0	0	0	0	1	1
ENSG00000251447	ENSG00000251447	RP11-517B11.6	3:131252398-132004254	NOTEST	0	0	0	0	1	1
ENSG00000251448	ENSG00000251448	RP11-71E19.2	3:125985638-126012867	NOTEST	0	0	0	0	1	1
ENSG00000251449	ENSG00000251449	MTND1P19	4:93225549-94695707	NOTEST	0	0	0	0	1	1
ENSG00000251450	ENSG00000251450	CTC-459I6.1	5:80243515-80597379	NOTEST	0	0	0	0	1	1
ENSG00000251451	ENSG00000251451	GS1-124K5.6	7:65670185-65955095	NOTEST	0.331703	0.243409	-0.446512	0	1	1
ENSG00000251452	ENSG00000251452	RP13-539F13.2	4:145841864-145842316	NOTEST	0	0.245586	inf	0	1	1
ENSG00000251453	ENSG00000251453	HAUS1P1	5:139781398-139973337	NOTEST	0	0	0	0	1	1
ENSG00000251454	ENSG00000251454	RP11-542G1.2	4:76194277-76359659	NOTEST	0	0	0	0	1	1
ENSG00000251455	ENSG00000251455	RP11-164P12.3	4:152591655-152682175	NOTEST	0.127878	0.0708059	-0.852827	0	1	1
ENSG00000251456	ENSG00000251456	RP11-436H11.5	5:123972607-124084500	NOTEST	0	0	0	0	1	1
ENSG00000251458	ENSG00000251458	RP11-844P9.1	5:175476680-175559261	NOTEST	0	0	0	0	1	1
ENSG00000251459	ENSG00000251459	RP11-319E12.2	4:58357555-58361399	NOTEST	0.0242707	0	#NAME?	0	1	1
ENSG00000251460	ENSG00000251460	RP11-1258F18.1	4:7967038-8160559	NOTEST	0	0	0	0	1	1
ENSG00000251461	ENSG00000251461	RP11-501C14.6	17:47072627-47133012	NOTEST	0	0	0	0	1	1
ENSG00000251463	ENSG00000251463	FKBP4P1	4:118954772-119179803	NOTEST	0	0	0	0	1	1
ENSG00000251464	ENSG00000251464	RPL7L1P13	4:111286888-111486441	NOTEST	0.0261513	0	#NAME?	0	1	1
ENSG00000251467	ENSG00000251467	CTC-250P20.2	5:72251807-72386349	NOTEST	0	0.0594508	inf	0	1	1
ENSG00000251468	ENSG00000251468	RP11-369K16.1	8:12803150-12889012	NOTEST	0.0670908	0.017635	-1.92767	0	1	1
ENSG00000251470	ENSG00000251470	ASNSP4	8:47609251-47610310	NOTEST	0	0	0	0	1	1
ENSG00000251471	ENSG00000251471	RP11-166D18.1	3:139556061-139578736	NOTEST	0	0	0	0	1	1
ENSG00000251473	ENSG00000251473	AC004069.1	4:105389468-106041157	NOTEST	0	0	0	0	1	1
ENSG00000251476	ENSG00000251476	RP11-531A21.2	5:5396589-5397081	NOTEST	0	0.0328782	inf	0	1	1
ENSG00000251477	ENSG00000251477	RP11-74D3.2	5:117054934-117057792	NOTEST	0	0	0	0	1	1
ENSG00000251478	ENSG00000251478	CTD-2122P11.1	5:41585983-41587889	NOTEST	0	0	0	0	1	1
ENSG00000251482	ENSG00000251482	RP11-707F2.2	4:150273168-150817385	NOTEST	0	0	0	0	1	1
ENSG00000251483	ENSG00000251483	LYPLA1P2	4:111866264-111866955	NOTEST	0	0	0	0	1	1
ENSG00000251484	ENSG00000251484	RP5-1065J22.4	1:109646156-109647388	NOTEST	0	0	0	0	1	1
ENSG00000251487	ENSG00000251487	RP11-124N3.2	5:18965969-19142455	NOTEST	0	0	0	0	1	1
ENSG00000251488	ENSG00000251488	RP11-404I7.2	4:133757926-133902832	NOTEST	0	0	0	0	1	1
ENSG00000251489	ENSG00000251489	RP11-736K12.1	4:70754594-70755124	NOTEST	0	0	0	0	1	1
ENSG00000251490	ENSG00000251490	RP11-237D3.1	4:188437306-188438362	NOTEST	0	0	0	0	1	1
ENSG00000251491	ENSG00000251491	OR7E28P	2:159651828-159719797	NOTEST	0	0	0	0	1	1
ENSG00000251492	ENSG00000251492	RP11-782E2.2	4:136925663-136926057	NOTEST	0	0	0	0	1	1
ENSG00000251493	ENSG00000251493	FOXD1	5:72740653-72744352	NOTEST	0.18938	0.521765	1.46212	0	1	1

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ENSG00000251497	ENSG00000251497	RP11-197N18.7	12:123468026-123634562	NOTEST	0	0.00516485	inf	0	1	1
ENSG00000251498	ENSG00000251498	RP11-468N14.10	4:69838716-69841711	NOTEST	0	0	0	0	1	1
ENSG00000251501	ENSG00000251501	RP11-466J24.1	4:43588344-43590114	NOTEST	0	0	0	0	1	1
ENSG00000251503	ENSG00000251503	APITD1-CORT	1:10489937-10512210	NOTEST	0.549454	0.484362	-0.181913	0	1	1
ENSG00000251504	ENSG00000251504	LINC01099	4:178649910-178911904	NOTEST	0	0	0	0	1	1
ENSG00000251506	ENSG00000251506	CTD-2247C11.2	5:4967876-4970538	NOTEST	0	0	0	0	1	1
ENSG00000251508	ENSG00000251508	RP5-862P8.3	1:233086350-233431473	NOTEST	0	0	0	0	1	1
ENSG00000251510	ENSG00000251510	AC022486.1	Y:20652800-20790963	NOTEST	0	0	0	0	1	1
ENSG00000251511	ENSG00000251511	RP11-171N4.1	4:157507130-157511191	NOTEST	0	0	0	0	1	1
ENSG00000251513	ENSG00000251513	RP11-155G15.2	5:96424778-96772921	NOTEST	0	0	0	0	1	1
ENSG00000251515	ENSG00000251515	CCDC11P1	5:39571579-39572741	NOTEST	0	0	0	0	1	1
ENSG00000251516	ENSG00000251516	RP11-10G12.2	4:22609123-22612686	NOTEST	0	0	0	0	1	1
ENSG00000251517	ENSG00000251517	RP11-109E24.1	4:42708123-42709352	NOTEST	0	0	0	0	1	1
ENSG00000251518	ENSG00000251518	CTD-2130F23.2	5:37948592-37951157	NOTEST	0.113129	0.140461	0.312202	0	1	1
ENSG00000251520	ENSG00000251520	RP11-46A10.6	1:180882289-180992047	NOTEST	0	0	0	0	1	1
ENSG00000251521	ENSG00000251521	IMPA1P	8:82517803-82543369	NOTEST	0	0.0534243	inf	0	1	1
ENSG00000251523	ENSG00000251523	RP11-724M22.1	4:99391517-99579780	NOTEST	0	0	0	0	1	1
ENSG00000251525	ENSG00000251525	TCP11X3P	X:101428071-101439994	NOTEST	0	0	0	0	1	1
ENSG00000251526	ENSG00000251526	RP11-381N20.1	4:124411422-124448680	NOTEST	0	0.0280067	inf	0	1	1
ENSG00000251527	ENSG00000251527	RP11-51P8.1	4:66724478-66725922	NOTEST	0	0	0	0	1	1
ENSG00000251529	ENSG00000251529	RP11-468N14.5	4:69743343-69745849	NOTEST	0	0	0	0	1	1
ENSG00000251532	ENSG00000251532	CTD-2245E15.3	5:1544221-1551825	NOTEST	0.214401	0.0688461	-1.63886	0	1	1
ENSG00000251533	ENSG00000251533	LINC00605	14:103653557-103655365	NOTEST	0.0107077	0	#NAME?	0	1	1
ENSG00000251535	ENSG00000251535	RP11-478C6.1	4:330046-330575	NOTEST	0	0	0	0	1	1
ENSG00000251536	ENSG00000251536	RP11-572C21.1	12:129556269-130388211	NOTEST	0	0	0	0	1	1
ENSG00000251537	ENSG00000251537	RP11-385D13.1	17:15468796-15587625	NOTEST	0	0	0	0	1	1
ENSG00000251538	ENSG00000251538	RP11-166A12.1	5:121964646-122066380	NOTEST	0	0.0208809	inf	0	1	1
ENSG00000251539	ENSG00000251539	SNX18P24	4:49563495-49564166	NOTEST	0	0	0	0	1	1
ENSG00000251542	ENSG00000251542	CTC-313D10.1	5:113696641-114004107	NOTEST	0	0	0	0	1	1
ENSG00000251543	ENSG00000251543	RP11-60A8.2	5:72633732-72634360	NOTEST	0	0	0	0	1	1
ENSG00000251544	ENSG00000251544	MTND5P12	5:93488670-94620279	NOTEST	0	0	0	0	1	1
ENSG00000251545	ENSG00000251545	RP11-798K23.3	5:178949457-178952075	NOTEST	0	0	0	0	1	1
ENSG00000251546	ENSG00000251546	IGKV1D-39	2:89901291-89901791	NOTEST	0	0	0	0	1	1
ENSG00000251547	ENSG00000251547	OR12D1	HSCHR6_MHC_QBL:29384950-29424735	NOTEST	0	0	0	0	1	1
ENSG00000251548	ENSG00000251548	RP11-215G15.4	5:10664606-10665225	NOTEST	0.260179	0.623828	1.26164	0	1	1
ENSG00000251549	ENSG00000251549	RP11-480D4.5	5:8333595-8463208	NOTEST	0	0	0	0	1	1
ENSG00000251550	ENSG00000251550	RP11-501C14.7	17:47072627-47133012	NOTEST	0	0.0771155	inf	0	1	1
ENSG00000251552	ENSG00000251552	COQ10BP2	5:82348664-82649606	NOTEST	0	0	0	0	1	1
ENSG00000251553	ENSG00000251553	CTC-463N11.1	5:98015105-98017071	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000251555	ENSG00000251555	RP11-745L13.2	4:132851185-132897107	NOTEST	0	0	0	0	1	1
ENSG00000251556	ENSG00000251556	RP11-118M9.3	5:145463948-145562223	NOTEST	0	0	0	0	1	1
ENSG00000251557	ENSG00000251557	HNRNPKP3	11:43142311-43290943	NOTEST	0	0	0	0	1	1
ENSG00000251563	ENSG00000251563	AF121898.1	8:87878669-88767946	NOTEST	0	0	0	0	1	1
ENSG00000251564	ENSG00000251564	AC012441.1	7:51452462-51452868	NOTEST	0.0631265	0.305604	2.27535	0	1	1
ENSG00000251566	ENSG00000251566	HMGB1P35	5:76367896-76462734	NOTEST	0	0	0	0	1	1
ENSG00000251567	ENSG00000251567	RP11-775H9.2	4:137039829-137316626	NOTEST	0	0	0	0	1	1
ENSG00000251568	ENSG00000251568	ALG3P1	5:5375835-5376949	NOTEST	0	0.0346724	inf	0	1	1
ENSG00000251571	ENSG00000251571	DDX3YP3	4:104469901-104640973	NOTEST	0	0	0	0	1	1
ENSG00000251572	ENSG00000251572	AF213884.1	4:103382406-103383309	NOTEST	0	0	0	0	1	1
ENSG00000251573	ENSG00000251573	CTD-2089N3.2	5:50265050-50266021	NOTEST	0	0	0	0	1	1
ENSG00000251574	ENSG00000251574	RP11-6N13.1	5:103718998-104728671	NOTEST	0.412041	0.652043	0.662177	0	1	1
ENSG00000251575	ENSG00000251575	CTD-2170G1.2	5:60933534-61047590	NOTEST	0	0	0	0	1	1
ENSG00000251576	ENSG00000251576	RP11-536I6.1	3:14389950-14394068	NOTEST	0	0	0	0	1	1
ENSG00000251577	ENSG00000251577	RP11-297P16.3	4:104469901-104640973	NOTEST	0	0	0	0	1	1
ENSG00000251578	ENSG00000251578	TRBV21-1	7:142344426-142344887	NOTEST	0	0	0	0	1	1
ENSG00000251579	ENSG00000251579	RP11-39E3.5	3:130569438-131100319	NOTEST	0	0	0	0	1	1
ENSG00000251581	ENSG00000251581	MICE	HSCHR6_MHC_COX:29684536-29710797	NOTEST	0	0	0	0	1	1
ENSG00000251583	ENSG00000251583	AC008427.2	5:149237518-149324356	NOTEST	0	0	0	0	1	1
ENSG00000251584	ENSG00000251584	RP11-440I14.3	4:175444851-175461935	NOTEST	0.203317	0.110528	-0.87932	0	1	1
ENSG00000251585	ENSG00000251585	CTD-2299E8.1	5:85698282-85698778	NOTEST	0	0	0	0	1	1
ENSG00000251586	ENSG00000251586	TET2-AS1	4:106067031-106200973	NOTEST	0	0	0	0	1	1
ENSG00000251587	ENSG00000251587	LDHAP1	4:4895908-4896900	NOTEST	0	0	0	0	1	1
ENSG00000251588	ENSG00000251588	RP11-698E18.1	4:36498158-36643522	NOTEST	0	0	0	0	1	1
ENSG00000251590	ENSG00000251590	NIFKP7	3:31699381-32119072	NOTEST	0	0	0	0	1	1
ENSG00000251591	ENSG00000251591	CTD-2197M16.1	5:36071892-36072181	NOTEST	0	0	0	0	1	1
ENSG00000251593	ENSG00000251593	MSNP1	5:25909611-25911343	NOTEST	0	0.0133758	inf	0	1	1
ENSG00000251596	ENSG00000251596	HADHAP1	4:166282345-166419472	NOTEST	0	0	0	0	1	1
ENSG00000251597	ENSG00000251597	RPL37P25	5:53616773-53710955	NOTEST	0	0	0	0	1	1
ENSG00000251598	ENSG00000251598	RP11-789C2.1	4:132925964-133045186	NOTEST	0	0	0	0	1	1
ENSG00000251599	ENSG00000251599	RP11-232L2.2	5:72427834-72446419	NOTEST	0	0	0	0	1	1
ENSG00000251600	ENSG00000251600	RP11-673E1.1	4:144833483-145061904	NOTEST	0.0620776	0.0678767	0.128844	0	1	1
ENSG00000251601	ENSG00000251601	RP11-317O24.2	5:50225317-50230355	NOTEST	0	0	0	0	1	1
ENSG00000251602	ENSG00000251602	RP11-521B24.3	14:105864915-105937066	NOTEST	0.435376	0.4328	-0.00855959	0	1	1
ENSG00000251603	ENSG00000251603	RP11-164P12.4	4:152588375-152591654	NOTEST	0	0.158731	inf	0	1	1
ENSG00000251604	ENSG00000251604	RP11-79P5.7	5:72747322-72749220	NOTEST	0.0935148	0	#NAME?	0	1	1
ENSG00000251605	ENSG00000251605	CTD-2037K23.1	5:77603326-77603738	NOTEST	0	0	0	0	1	1
ENSG00000251606	ENSG00000251606	CTD-2215E18.1	5:96424778-96772921	NOTEST	0	0.0281948	inf	0	1	1
ENSG00000251608	ENSG00000251608	OR12D1	6:29323006-29424848	NOTEST	0	0	0	0	1	1
ENSG00000251609	ENSG00000251609	SETP12	4:121606073-121844025	NOTEST	0.042938	0.107661	1.32617	0	1	1

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ENSG00000251611	ENSG00000251611	RP11-610P16.1	4:152328702-152329987	NOTEST	0	0	0	0	1	1
ENSG00000251613	ENSG00000251613	CTC-347C20.1	5:71982938-72058554	NOTEST	0	0	0	0	1	1
ENSG00000251614	ENSG00000251614	HSPA8P19	3:132276981-132593067	NOTEST	0	0	0	0	1	1
ENSG00000251615	ENSG00000251615	RP11-774O3.3	4:8356816-8360065	NOTEST	0.088874	0.0977792	0.137766	0	1	1
ENSG00000251616	ENSG00000251616	RP11-485M7.3	5:132446746-132450167	NOTEST	0	0	0	0	1	1
ENSG00000251617	ENSG00000251617	RP11-382F24.1	X:55306271-55315218	NOTEST	0	0	0	0	1	1
ENSG00000251618	ENSG00000251618	AC007322.3	Y:24026222-24064214	NOTEST	0	0	0	0	1	1
ENSG00000251619	ENSG00000251619	RP11-756P10.5	4:189678832-189717787	NOTEST	0	0	0	0	1	1
ENSG00000251620	ENSG00000251620	STPG2-AS1	4:98105243-99064391	NOTEST	0	0	0	0	1	1
ENSG00000251621	ENSG00000251621	AC009487.5	2:162272604-162841792	NOTEST	0	0	0	0	1	1
ENSG00000251623	ENSG00000251623	RP11-826N14.4	5:175564159-175626298	NOTEST	0	0	0	0	1	1
ENSG00000251624	ENSG00000251624	UNC93B7	4:9495379-9499710	NOTEST	0.18128	0	#NAME?	0	1	1
ENSG00000251627	ENSG00000251627	CTD-2089O24.2	5:110306649-110344598	NOTEST	0	0.0142888	inf	0	1	1
ENSG00000251628	ENSG00000251628	RP11-371M22.1	5:113391702-113392871	NOTEST	0.0689675	0.0527684	-0.386243	0	1	1
ENSG00000251629	ENSG00000251629	RP11-774D14.1	5:20611948-20937800	NOTEST	0	0.00761309	inf	0	1	1
ENSG00000251630	ENSG00000251630	RP11-241F15.9	4:49563301-49563487	NOTEST	0	0	0	0	1	1
ENSG00000251632	ENSG00000251632	RP11-714L20.1	4:138466884-138524584	NOTEST	0	0	0	0	1	1
ENSG00000251633	ENSG00000251633	GYG1P1	8:74817591-74827245	NOTEST	0	0	0	0	1	1
ENSG00000251634	ENSG00000251634	RP11-1280N14.3	5:70398724-70424580	NOTEST	0.0854656	0.0160499	-2.41278	0	1	1
ENSG00000251635	ENSG00000251635	RP11-213G21.2	4:38565623-38572292	NOTEST	0	0	0	0	1	1
ENSG00000251636	ENSG00000251636	EMCN-IT1	4:101316497-101801283	NOTEST	0	0	0	0	1	1
ENSG00000251637	ENSG00000251637	RP11-119D9.1	11:67653947-67673821	NOTEST	0	0	0	0	1	1
ENSG00000251638	ENSG00000251638	AC006390.4	4:24769670-24769953	NOTEST	0	0	0	0	1	1
ENSG00000251639	ENSG00000251639	RP11-20I20.1	4:1050037-1107350	NOTEST	0	0	0	0	1	1
ENSG00000251642	ENSG00000251642	RP11-600L4.1	4:38288614-38289112	NOTEST	0	0	0	0	1	1
ENSG00000251643	ENSG00000251643	RP11-91J3.1	4:188362830-188365452	NOTEST	0	0	0	0	1	1
ENSG00000251644	ENSG00000251644	RP11-442P12.1	4:15866560-15867563	NOTEST	0	0	0	0	1	1
ENSG00000251647	ENSG00000251647	RP11-576N17.4	4:84298515-84299229	NOTEST	0	0	0	0	1	1
ENSG00000251648	ENSG00000251648	CTD-2353N24.1	5:64885506-65167553	NOTEST	0	0	0	0	1	1
ENSG00000251649	ENSG00000251649	RP11-318I4.1	4:126991862-126993159	NOTEST	0	0	0	0	1	1
ENSG00000251652	ENSG00000251652	RP11-20I20.2	4:1107426-1147514	NOTEST	0	0	0	0	1	1
ENSG00000251654	ENSG00000251654	RP11-192H6.2	5:25190790-25306281	NOTEST	0	0	0	0	1	1
ENSG00000251655	ENSG00000251655	PRB1	12:11504756-11653975	NOTEST	0	0	0	0	1	1
ENSG00000251656	ENSG00000251656	CTD-2201E18.4	5:42908309-42908769	NOTEST	0	0	0	0	1	1
ENSG00000251660	ENSG00000251660	AC007036.5	7:30174425-30202378	NOTEST	0	0	0	0	1	1
ENSG00000251661	ENSG00000251661	RP11-326C3.11	11:318639-330122	NOTEST	0.0151642	0.0451431	1.57384	0	1	1
ENSG00000251662	ENSG00000251662	CTC-369A16.3	5:123641922-123740772	NOTEST	0	0	0	0	1	1
ENSG00000251663	ENSG00000251663	SUMO2P5	5:74364099-74532703	NOTEST	0	0	0	0	1	1
ENSG00000251664	ENSG00000251664	PCDHA12	5:140165875-140391936	NOTEST	0.016672	0.00367547	-2.18143	0	1	1

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ENSG00000251667	ENSG00000251667	RP11-844P9.3	5:175665364-175772994	NOTEST	0.275723	0.342826	0.314255	0	1	1
ENSG00000251668	ENSG00000251668	RP11-466P24.5	5:75377770-75649764	NOTEST	0	0	0	0	1	1
ENSG00000251670	ENSG00000251670	CTD-2532K18.1	5:174178306-174277728	NOTEST	0	0	0	0	1	1
ENSG00000251676	ENSG00000251676	RP11-614F17.2	4:132694456-132712637	NOTEST	0	0	0	0	1	1
ENSG00000251678	ENSG00000251678	CTD-2296D1.1	5:7344691-7346034	NOTEST	0	0	0	0	1	1
ENSG00000251679	ENSG00000251679	RP11-669M16.2	4:14113591-14145216	NOTEST	0	0	0	0	1	1
ENSG00000251680	ENSG00000251680	CTC-575N7.1	5:128795251-129522327	NOTEST	0	0	0	0	1	1
ENSG00000251682	ENSG00000251682	RP11-631M6.3	5:60628099-60841997	NOTEST	0	0	0	0	1	1
ENSG00000251685	ENSG00000251685	RP11-813N20.1	4:69870573-69886132	NOTEST	0	0	0	0	1	1
ENSG00000251686	ENSG00000251686	OR10J8P	1:159315955-159453166	NOTEST	0	0	0	0	1	1
ENSG00000251687	ENSG00000251687	RP11-181K12.2	4:146601355-146859787	NOTEST	0	0.0168299	inf	0	1	1
ENSG00000251688	ENSG00000251688	RP11-752L20.5	4:148488757-148515739	NOTEST	0	0	0	0	1	1
ENSG00000251689	ENSG00000251689	RP11-478C6.5	4:263654-263964	NOTEST	0	0	0	0	1	1
ENSG00000251691	ENSG00000251691	RP11-618I10.4	4:70172186-70172891	NOTEST	0	0	0	0	1	1
ENSG00000251692	ENSG00000251692	PTX4	16:1535886-1538982	NOTEST	0.0286026	0.0110558	-1.37134	0	1	1
ENSG00000251694	ENSG00000251694	USP17L9P	4:9360108-9361701	NOTEST	0	0	0	0	1	1
ENSG00000251695	ENSG00000251695	AC124890.1	12:69139885-69187743	NOTEST	0.0102566	0.00721142	-0.508204	0	1	1
ENSG00000251696	ENSG00000251696	AL583832.1	1:205012324-205047627	NOTEST	0	0	0	0	1	1
ENSG00000251697	ENSG00000251697	RN7SKP24	9:34398181-34520982	NOTEST	0	0	0	0	1	1
ENSG00000251698	ENSG00000251698	RNA5SP445	17:64298753-64806861	NOTEST	0	0	0	0	1	1
ENSG00000251699	ENSG00000251699	SNORD27	9:8314245-10612723	NOTEST	0	0	0	0	1	1
ENSG00000251700	ENSG00000251700	SNORD112	16:70841280-71264625	NOTEST	0	0	0	0	1	1
ENSG00000251702	ENSG00000251702	RNU6-857P	18:28564071-28564181	NOTEST	0	0	0	0	1	1
ENSG00000251703	ENSG00000251703	RNU6-998P	4:57829535-58071676	NOTEST	0	0	0	0	1	1
ENSG00000251704	ENSG00000251704	SNORA40	2:16380470-16380563	NOTEST	0	0	0	0	1	1
ENSG00000251705	ENSG00000251705	RNA5-8SP6	Y:10037763-10037915	NOTEST	0	0	0	0	1	1
ENSG00000251706	ENSG00000251706	RNU7-61P	16:30483978-30534506	NOTEST	0	0	0	0	1	1
ENSG00000251707	ENSG00000251707	RNU7-37P	X:53122891-53196196	NOTEST	0	0	0	0	1	1
ENSG00000251708	ENSG00000251708	RNU7-198P	3:135969147-136471220	NOTEST	0	0	0	0	1	1
ENSG00000251709	ENSG00000251709	snoU13	19:39540544-39540607	NOTEST	0	0	0	0	1	1
ENSG00000251710	ENSG00000251710	AC010295.1	5:153369687-153825410	NOTEST	0	0	0	0	1	1
ENSG00000251711	ENSG00000251711	RNU6-632P	10:26108291-26108355	NOTEST	0	0	0	0	1	1
ENSG00000251712	ENSG00000251712	RNU7-20P	7:148504474-148581413	NOTEST	0	0	0	0	1	1
ENSG00000251713	ENSG00000251713	AL050321.1	20:18118516-18169031	NOTEST	0	0	0	0	1	1
ENSG00000251714	ENSG00000251714	RN7SKP67	4:182795590-183724177	NOTEST	0	0	0	0	1	1
ENSG00000251715	ENSG00000251715	SNORA68	13:73034656-73034739	NOTEST	0	0	0	0	1	1
ENSG00000251716	ENSG00000251716	Y_RNA	4:88333379-88333498	NOTEST	0	0	0	0	1	1
ENSG00000251717	ENSG00000251717	RNA5SP419	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000251718	ENSG00000251718	RNU2-13P	2:11674241-11782914	NOTEST	0	0	0	0	1	1
ENSG00000251719	ENSG00000251719	RNU6-408P	18:26628583-26628683	NOTEST	0	0	0	0	1	1
ENSG00000251720	ENSG00000251720	RNU7-123P	1:63906440-64125916	NOTEST	0	0	0	0	1	1
ENSG00000251721	ENSG00000251721	snoZ5	2:159313475-159610287	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000251723	ENSG00000251723	RNU6-357P	9:135600964-135765588	NOTEST	0	0	0	0	1	1
ENSG00000251724	ENSG00000251724	RNU7-175P	5:74664310-74896969	NOTEST	0	0	0	0	1	1
ENSG00000251725	ENSG00000251725	MIR2277	5:92953774-93447404	NOTEST	0	0	0	0	1	1
ENSG00000251726	ENSG00000251726	RNU7-41P	14:35221936-35345665	NOTEST	0	0	0	0	1	1
ENSG00000251727	ENSG00000251727	RNU6-488P	3:93562607-93562706	NOTEST	0	0	0	0	1	1
ENSG00000251728	ENSG00000251728	Y_RNA	7:139784545-139876835	NOTEST	0	0	0	0	1	1
ENSG00000251729	ENSG00000251729	RNA5SP401	15:98015355-98015482	NOTEST	0	0	0	0	1	1
ENSG00000251730	ENSG00000251730	SNORA4	3:183165395-183173801	NOTEST	0	0	0	0	1	1
ENSG00000251731	ENSG00000251731	AL512359.1	14:48963135-48963267	NOTEST	0	0	0	0	1	1
ENSG00000251732	ENSG00000251732	RN7SKP122	5:107146329-107146625	NOTEST	0	0	0	0	1	1
ENSG00000251733	ENSG00000251733	SCARNA8	9:19053140-19103117	NOTEST	0	0	0	0	1	1
ENSG00000251735	ENSG00000251735	SNORA25	14:47308825-48144157	NOTEST	0	0	0	0	1	1
ENSG00000251737	ENSG00000251737	snoU13	22:18111620-18213388	NOTEST	0	0	0	0	1	1
ENSG00000251738	ENSG00000251738	AC073215.1	2:58134785-58468821	NOTEST	0	0	0	0	1	1
ENSG00000251739	ENSG00000251739	RNU6-1053P	4:184580419-184634745	NOTEST	0	0	0	0	1	1
ENSG00000251740	ENSG00000251740	U8	10:5077545-5149878	NOTEST	0	0	0	0	1	1
ENSG00000251741	ENSG00000251741	RNU4ATAC13P	5:112829531-112829657	NOTEST	0	0	0	0	1	1
ENSG00000251742	ENSG00000251742	RN7SKP13	4:182756017-182756261	NOTEST	0	0	0	0	1	1
ENSG00000251744	ENSG00000251744	SNORA25	8:140120672-140120777	NOTEST	0	0	0	0	1	1
ENSG00000251745	ENSG00000251745	RNU7-124P	9:37510888-38069210	NOTEST	0	0	0	0	1	1
ENSG00000251746	ENSG00000251746	RNA5SP112	2:177855235-178088686	NOTEST	0	0	0	0	1	1
ENSG00000251747	ENSG00000251747	RNU7-60P	12:11694328-11743303	NOTEST	0	0	0	0	1	1
ENSG00000251748	ENSG00000251748	RNU4ATAC11P	9:33750514-33920402	NOTEST	0	0	0	0	1	1
ENSG00000251749	ENSG00000251749	U3	10:21774566-21774666	NOTEST	0	0	0	0	1	1
ENSG00000251750	ENSG00000251750	RNU5F-8P	1:240816666-240816777	NOTEST	0	0	0	0	1	1
ENSG00000251751	ENSG00000251751	RN7SKP46	3:157648280-157648514	NOTEST	0	0	0	0	1	1
ENSG00000251752	ENSG00000251752	RNU4-29P	9:85857904-86153461	NOTEST	0	0	0	0	1	1
ENSG00000251753	ENSG00000251753	RNU6-75P	13:91434019-91434123	NOTEST	0	0	0	0	1	1
ENSG00000251754	ENSG00000251754	RNU6-999P	1:245132651-245290466	NOTEST	0	0	0	0	1	1
ENSG00000251755	ENSG00000251755	RNU7-131P	4:33777968-34041515	NOTEST	0	0	0	0	1	1
ENSG00000251756	ENSG00000251756	RNA5SP385	14:51921229-52197445	NOTEST	0	0	0	0	1	1
ENSG00000251757	ENSG00000251757	RNU6-848P	2:131369053-131415664	NOTEST	0	0	0	0	1	1
ENSG00000251758	ENSG00000251758	RNU6-350P	4:15961865-16086001	NOTEST	0	0	0	0	1	1
ENSG00000251759	ENSG00000251759	RN7SKP298	3:166387816-166387910	NOTEST	0	0	0	0	1	1
ENSG00000251760	ENSG00000251760	RNA5SP418	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000251761	ENSG00000251761	RNU6-138P	3:18996434-18996541	NOTEST	0	0	0	0	1	1
ENSG00000251762	ENSG00000251762	snoU13	6:7040692-7040779	NOTEST	0	0	0	0	1	1
ENSG00000251763	ENSG00000251763	RNU6-470P	17:41489794-41489898	NOTEST	0	0	0	0	1	1
ENSG00000251764	ENSG00000251764	RNA5SP446	17:64891607-64891689	NOTEST	0	0	0	0	1	1
ENSG00000251766	ENSG00000251766	RNA5SP518	Y:9928018-9928137	NOTEST	0	0	0	0	1	1
ENSG00000251767	ENSG00000251767	RNU7-8P	1:77747735-78025651	NOTEST	0	0	0	0	1	1
ENSG00000251768	ENSG00000251768	RNA5SP217	6:127609854-127664754	NOTEST	0	0	0	0	1	1
ENSG00000251769	ENSG00000251769	SNORD112	14:101361106-101402336	NOTEST	0	0	0	0	1	1
ENSG00000251770	ENSG00000251770	RNA5SP486	20:46501934-46502017	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000251771	ENSG00000251771	RNU6-1033P	14:51921229-52197445	NOTEST	0	0	0	0	1	1
ENSG00000251772	ENSG00000251772	AL117380.2	20:55575142-55575213	NOTEST	0	0	0	0	1	1
ENSG00000251773	ENSG00000251773	RNU6-1129P	3:86284470-86284574	NOTEST	0	0	0	0	1	1
ENSG00000251774	ENSG00000251774	RNU6-377P	3:12525930-12705725	NOTEST	0	0	0	0	1	1
ENSG00000251775	ENSG00000251775	ACA59	2:64068073-64118696	NOTEST	0	0	0	0	1	1
ENSG00000251776	ENSG00000251776	RN7SKP242	9:85815854-85816143	NOTEST	0	0	0	0	1	1
ENSG00000251777	ENSG00000251777	RNU6-404P	3:12525930-12705725	NOTEST	0	0	0	0	1	1
ENSG00000251778	ENSG00000251778	SNORA3	21:43302313-43302409	NOTEST	0	0	0	0	1	1
ENSG00000251779	ENSG00000251779	Y_RNA	17:74305566-74383941	NOTEST	0	0	0	0	1	1
ENSG00000251780	ENSG00000251780	RNU7-150P	1:155115746-155115808	NOTEST	0	0	0	0	1	1
ENSG00000251781	ENSG00000251781	RNA5SP356	12:30459363-30459457	NOTEST	0	0	0	0	1	1
ENSG00000251783	ENSG00000251783	RNU6-1170P	10:43069632-43134016	NOTEST	0	0	0	0	1	1
ENSG00000251784	ENSG00000251784	U4atac	GL000223.1:93510-119608	NOTEST	0	0	0	0	1	1
ENSG00000251785	ENSG00000251785	RNA5SP20	1:78028100-78149104	NOTEST	0	0	0	0	1	1
ENSG00000251787	ENSG00000251787	RNU7-47P	3:142442915-142526730	NOTEST	0	0	0	0	1	1
ENSG00000251788	ENSG00000251788	RNU5A-7P	12:64616116-64790845	NOTEST	0	0	0	0	1	1
ENSG00000251789	ENSG00000251789	RNU4-57P	1:223547163-223547266	NOTEST	0	0	0	0	1	1
ENSG00000251791	ENSG00000251791	SCARNA6	2:234118696-234204320	NOTEST	0	0.110029	inf	0	1	1
ENSG00000251792	ENSG00000251792	Y_RNA	14:50448429-50559361	NOTEST	0	0	0	0	1	1
ENSG00000251793	ENSG00000251793	U3	6:16148517-16148676	NOTEST	0	0	0	0	1	1
ENSG00000251794	ENSG00000251794	RNU6-237P	16:74485855-74641012	NOTEST	0	0	0	0	1	1
ENSG00000251795	ENSG00000251795	SNORA66	1:93297581-93307481	NOTEST	0	0	0	0	1	1
ENSG00000251796	ENSG00000251796	SNORA70	Y:28393530-28393668	NOTEST	0	0	0	0	1	1
ENSG00000251797	ENSG00000251797	RNU7-98P	X:148412431-148412492	NOTEST	0	0	0	0	1	1
ENSG00000251798	ENSG00000251798	RNU6-863P	7:75716761-75716865	NOTEST	0	0	0	0	1	1
ENSG00000251799	ENSG00000251799	Y_RNA	4:57676025-57687908	NOTEST	0	0	0	0	1	1
ENSG00000251800	ENSG00000251800	U3	3:146627471-147088443	NOTEST	0	0	0	0	1	1
ENSG00000251801	ENSG00000251801	SNORD112	2:229347976-229476111	NOTEST	0	0	0	0	1	1
ENSG00000251802	ENSG00000251802	SNORA31	7:34932028-34932161	NOTEST	0	0	0	0	1	1
ENSG00000251803	ENSG00000251803	Y_RNA	10:17360381-17496329	NOTEST	0	0	0	0	1	1
ENSG00000251804	ENSG00000251804	RNU6-1294P	3:142025448-142166904	NOTEST	0	0	0	0	1	1
ENSG00000251805	ENSG00000251805	SCARNA21	2:24425732-24583583	NOTEST	0	0	0	0	1	1
ENSG00000251806	ENSG00000251806	SNORD119	20:2442279-2505348	NOTEST	0	0	0	0	1	1
ENSG00000251807	ENSG00000251807	RNU6-202P	X:41374186-41782716	NOTEST	0	0	0	0	1	1
ENSG00000251808	ENSG00000251808	AC024198.1	4:111774531-111774626	NOTEST	0	0	0	0	1	1
ENSG00000251809	ENSG00000251809	RN7SKP14	17:52848309-52848638	NOTEST	0	0	0	0	1	1
ENSG00000251810	ENSG00000251810	RN7SKP132	10:28064114-28287977	NOTEST	0	0	0	0	1	1
ENSG00000251811	ENSG00000251811	Y_RNA	3:43328003-43775863	NOTEST	0	0	0	0	1	1
ENSG00000251812	ENSG00000251812	Y_RNA	17:4046461-4167274	NOTEST	0	0	0	0	1	1
ENSG00000251813	ENSG00000251813	RNU6-983P	1:194457232-194457335	NOTEST	0	0	0	0	1	1
ENSG00000251814	ENSG00000251814	RN7SKP18	6:117609462-117923691	NOTEST	0	0	0	0	1	1
ENSG00000251815	ENSG00000251815	SNORD116-26	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000251816	ENSG00000251816	RNA5SP157	4:19173957-19911315	NOTEST	0	0	0	0	1	1
ENSG00000251817	ENSG00000251817	snoU13	1:173250215-173250309	NOTEST	0	0	0	0	1	1
ENSG00000251818	ENSG00000251818	SCARNA20	17:26345795-26345933	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000251819	ENSG00000251819	RNU6-322P	15:101092024-101092127	NOTEST	0	0	0	0	1	1
ENSG00000251821	ENSG00000251821	RNU6-583P	4:128802015-128820350	NOTEST	0	0	0	0	1	1
ENSG00000251822	ENSG00000251822	SNORA19	12:60757602-60757716	NOTEST	0	0	0	0	1	1
ENSG00000251823	ENSG00000251823	RNA5SP162	4:57197342-57197383	NOTEST	0	0	0	0	1	1
ENSG00000251824	ENSG00000251824	SNORD112	14:49410649-49410717	NOTEST	0	0	0	0	1	1
ENSG00000251825	ENSG00000251825	RN7SKP19	1:73657286-73657538	NOTEST	0	0	0	0	1	1
ENSG00000251827	ENSG00000251827	RN7SKP215	4:47596014-47840123	NOTEST	0	0	0	0	1	1
ENSG00000251828	ENSG00000251828	SNORA31	5:79602053-79602187	NOTEST	0	0	0	0	1	1
ENSG00000251829	ENSG00000251829	RNA5SP436	17:15685654-15685769	NOTEST	0	0	0	0	1	1
ENSG00000251830	ENSG00000251830	SNORD46	6:24166500-24166602	NOTEST	0	0	0	0	1	1
ENSG00000251831	ENSG00000251831	RNU6-1114P	6:16205244-16205351	NOTEST	0	0	0	0	1	1
ENSG00000251833	ENSG00000251833	snoR26	20:6841660-6841755	NOTEST	0	0	0	0	1	1
ENSG00000251834	ENSG00000251834	RNU6-319P	9:15422701-15511017	NOTEST	0	0	0	0	1	1
ENSG00000251835	ENSG00000251835	RNU6ATAC32P	8:55065366-55065442	NOTEST	0	0	0	0	1	1
ENSG00000251836	ENSG00000251836	U3	10:120545263-120545475	NOTEST	0	0	0	0	1	1
ENSG00000251837	ENSG00000251837	Y_RNA	1:93492966-93493063	NOTEST	0	0	0	0	1	1
ENSG00000251838	ENSG00000251838	SNORA31	11:37723674-37723770	NOTEST	0	0	0	0	1	1
ENSG00000251839	ENSG00000251839	RNU7-12P	10:27484145-27531059	NOTEST	0	0	0	0	1	1
ENSG00000251840	ENSG00000251840	RN7SKP155	8:124600998-124601286	NOTEST	0	0	0	0	1	1
ENSG00000251841	ENSG00000251841	RNU6-1334P	Y:2652789-2652894	NOTEST	0	0	0	0	1	1
ENSG00000251842	ENSG00000251842	RNU6-732P	5:148303201-148442726	NOTEST	0	0	0	0	1	1
ENSG00000251843	ENSG00000251843	RNU6-803P	19:54222317-54222419	NOTEST	0	0	0	0	1	1
ENSG00000251844	ENSG00000251844	snoMe28S-Am2634	12:97825430-97958813	NOTEST	0	0	0	0	1	1
ENSG00000251846	ENSG00000251846	SNORD36	X:153121157-153121222	NOTEST	0	0	0	0	1	1
ENSG00000251847	ENSG00000251847	snoZ13_snr52	9:120493652-120493749	NOTEST	0	0	0	0	1	1
ENSG00000251848	ENSG00000251848	snoU13	X:2670090-2734539	NOTEST	0	0	0	0	1	1
ENSG00000251849	ENSG00000251849	AC010887.1	2:218041220-218041305	NOTEST	0	0	0	0	1	1
ENSG00000251850	ENSG00000251850	RNA5SP96	2:69240309-69476459	NOTEST	0	0	0	0	1	1
ENSG00000251851	ENSG00000251851	RNU6-772P	21:21728059-21728164	NOTEST	0	0	0	0	1	1
ENSG00000251852	ENSG00000251852	Y_RNA	7:102937868-103629963	NOTEST	0	0	0	0	1	1
ENSG00000251854	ENSG00000251854	RNU6-507P	3:149478891-149942977	NOTEST	0	0	0	0	1	1
ENSG00000251856	ENSG00000251856	MIR449C	5:54408798-54469005	NOTEST	0	0	0	0	1	1
ENSG00000251857	ENSG00000251857	RNA5SP362	12:66460000-66460118	NOTEST	0	0	0	0	1	1
ENSG00000251858	ENSG00000251858	SNORA31	14:42057063-42074059	NOTEST	0	0	0	0	1	1
ENSG00000251859	ENSG00000251859	RNU6-1288P	2:13850655-14541087	NOTEST	0	0	0	0	1	1
ENSG00000251860	ENSG00000251860	snoU13	17:7465191-7536700	NOTEST	0	0	0	0	1	1
ENSG00000251861	ENSG00000251861	SCARNA20	1:204697118-204697234	NOTEST	0	0	0	0	1	1
ENSG00000251862	ENSG00000251862	MIR1343	11:34874640-35042138	NOTEST	0	0	0	0	1	1
ENSG00000251863	ENSG00000251863	SNORD112	12:33515517-33515590	NOTEST	0	0	0	0	1	1
ENSG00000251864	ENSG00000251864	Y_RNA	6:36640614-36640721	NOTEST	0	0	0	0	1	1
ENSG00000251865	ENSG00000251865	RNU6-518P	17:56833229-57058983	NOTEST	0	0	0	0	1	1
ENSG00000251866	ENSG00000251866	SCARNA21	1:15853307-15930121	NOTEST	0	0	0	0	1	1
ENSG00000251867	ENSG00000251867	Y_RNA	8:81396795-81438500	NOTEST	0.272517	0.388114	0.510137	0	1	1
ENSG00000251868	ENSG00000251868	RNU7-71P	16:72699068-73093597	NOTEST	0	0	0	0	1	1
ENSG00000251869	ENSG00000251869	SCARNA23	X:24712035-25015103	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000251870	ENSG00000251870	RNU2-69P	18:56529831-56653712	NOTEST	0	0	0	0	1	1
ENSG00000251871	ENSG00000251871	AC016113.1	8:53950188-53950309	NOTEST	0	0	0	0	1	1
ENSG00000251872	ENSG00000251872	RNU6-688P	2:47922668-48134949	NOTEST	0	0	0	0	1	1
ENSG00000251873	ENSG00000251873	RNA5SP182	5:51182521-51182603	NOTEST	0	0	0	0	1	1
ENSG00000251874	ENSG00000251874	RNU6-615P	4:83739813-83934079	NOTEST	0	0	0	0	1	1
ENSG00000251875	ENSG00000251875	RNU5F-2P	1:179545402-179545484	NOTEST	0	0	0	0	1	1
ENSG00000251876	ENSG00000251876	AL035106.1	20:47240789-47444420	NOTEST	0	0	0	0	1	1
ENSG00000251877	ENSG00000251877	RNU2-45P	6:28378046-28378233	NOTEST	0	0	0	0	1	1
ENSG00000251878	ENSG00000251878	SNORD79	4:185308866-185395734	NOTEST	0	0	0	0	1	1
ENSG00000251879	ENSG00000251879	AC010874.1	Y:5742286-5742379	NOTEST	0	0	0	0	1	1
ENSG00000251880	ENSG00000251880	RNU7-75P	5:37288238-37371283	NOTEST	0	0	0	0	1	1
ENSG00000251881	ENSG00000251881	SNORD112	15:80434399-80434469	NOTEST	0	0	0	0	1	1
ENSG00000251882	ENSG00000251882	RNU6-475P	6:115188036-115188140	NOTEST	0	0	0	0	1	1
ENSG00000251883	ENSG00000251883	RNU6ATAC17P	20:25591788-25591859	NOTEST	0	0	0	0	1	1
ENSG00000251884	ENSG00000251884	RNA5SP288	9:97861335-98079991	NOTEST	0	0	0	0	1	1
ENSG00000251885	ENSG00000251885	RNA5SP381	14:20614275-20614314	NOTEST	0	0	0	0	1	1
ENSG00000251886	ENSG00000251886	RNU6-120P	18:18700364-18700467	NOTEST	0	0	0	0	1	1
ENSG00000251887	ENSG00000251887	RNU6-760P	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000251888	ENSG00000251888	RN7SKP190	16:82226109-82226395	NOTEST	0	0	0	0	1	1
ENSG00000251889	ENSG00000251889	RNU4-49P	2:48541775-48606433	NOTEST	0	0	0	0	1	1
ENSG00000251890	ENSG00000251890	RNA5SP497	22:32908538-33454358	NOTEST	0	0	0	0	1	1
ENSG00000251891	ENSG00000251891	RNU7-79P	15:85923801-86293512	NOTEST	0	0	0	0	1	1
ENSG00000251892	ENSG00000251892	RNU7-84P	8:107282371-107764922	NOTEST	0	0	0	0	1	1
ENSG00000251893	ENSG00000251893	SNORA70	12:75956981-76377795	NOTEST	0	0	0	0	1	1
ENSG00000251894	ENSG00000251894	RNU6-872P	21:30115529-30115613	NOTEST	0	0	0	0	1	1
ENSG00000251895	ENSG00000251895	RNU6-976P	14:85206285-85206396	NOTEST	0	0	0	0	1	1
ENSG00000251896	ENSG00000251896	SNORD116-27	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000251897	ENSG00000251897	RNU6-916P	18:6936910-6937019	NOTEST	0	0	0	0	1	1
ENSG00000251898	ENSG00000251898	SCARNA11	12:6679248-6716642	NOTEST	0	0	0	0	1	1
ENSG00000251899	ENSG00000251899	AC104169.1	1:85258750-85258882	NOTEST	0	0	0	0	1	1
ENSG00000251900	ENSG00000251900	VTRNA2-2P	2:65663844-66311773	NOTEST	0	0	0	0	1	1
ENSG00000251901	ENSG00000251901	snR65	13:96329392-96447243	NOTEST	0	0	0	0	1	1
ENSG00000251902	ENSG00000251902	RNU6-51P	13:21547170-21635686	NOTEST	0	0	0	0	1	1
ENSG00000251904	ENSG00000251904	RNA5SP272	8:89044236-89749363	NOTEST	0	0	0	0	1	1
ENSG00000251905	ENSG00000251905	RNU7-2P	2:146902723-146902785	NOTEST	0	0	0	0	1	1
ENSG00000251906	ENSG00000251906	RNU6-351P	4:105389468-106041157	NOTEST	0	0	0	0	1	1
ENSG00000251907	ENSG00000251907	RNU6-240P	14:74111577-74170435	NOTEST	0	0	0	0	1	1
ENSG00000251908	ENSG00000251908	RNU6-491P	12:14403165-14403275	NOTEST	0	0	0	0	1	1
ENSG00000251909	ENSG00000251909	U8	10:5202774-5260912	NOTEST	0	0	0	0	1	1
ENSG00000251911	ENSG00000251911	SNORD112	7:104581509-104653491	NOTEST	0	0	0	0	1	1
ENSG00000251912	ENSG00000251912	AL954742.1	22:48885271-49246724	NOTEST	0	0	0	0	1	1
ENSG00000251913	ENSG00000251913	RNU6-513P	22:42949622-42978044	NOTEST	0	0	0	0	1	1
ENSG00000251914	ENSG00000251914	RNU7-200P	1:21132962-21503377	NOTEST	0	0	0	0	1	1
ENSG00000251915	ENSG00000251915	RNA5SP406	16:34968763-34968875	NOTEST	0	0	0	0	1	1
ENSG00000251916	ENSG00000251916	RNU1-61P	6:32517716-32517867	NOTEST	0	0	0	0	1	1

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ENSG00000251917	ENSG00000251917	RNU1-86P	Y:26092073-26098440	NOTEST	0	0	0	0	1	1
ENSG00000251918	ENSG00000251918	SNORD112	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000251919	ENSG00000251919	RNU7-105P	11:72287184-72385635	NOTEST	0	0	0	0	1	1
ENSG00000251920	ENSG00000251920	RNA5SP216	6:126277926-126301387	NOTEST	0	0	0	0	1	1
ENSG00000251922	ENSG00000251922	SNORA14	10:6052651-6104288	NOTEST	0	0	0	0	1	1
ENSG00000251923	ENSG00000251923	RNU6-276P	4:56664801-56664897	NOTEST	0	0	0	0	1	1
ENSG00000251924	ENSG00000251924	RNA5SP408	16:34969742-34969842	NOTEST	0	0	0	0	1	1
ENSG00000251925	ENSG00000251925	SNORA70	Y:25569245-25569383	NOTEST	0	0	0	0	1	1
ENSG00000251926	ENSG00000251926	snoU13	10:70472714-70472835	NOTEST	0	0	0	0	1	1
ENSG00000251927	ENSG00000251927	AC099539.1	3:45596885-45786916	NOTEST	0	0	0	0	1	1
ENSG00000251928	ENSG00000251928	RNU6-585P	11:16799841-17074583	NOTEST	0	0	0	0	1	1
ENSG00000251929	ENSG00000251929	RNU6-189P	14:50368567-50368668	NOTEST	0	0	0	0	1	1
ENSG00000251930	ENSG00000251930	U3	6:52991761-53013627	NOTEST	0	0	0	0	1	1
ENSG00000251931	ENSG00000251931	RNU6-871P	12:59844453-59844553	NOTEST	0	0	0	0	1	1
ENSG00000251933	ENSG00000251933	AL596330.1	1:224572844-224928251	NOTEST	0	0	0	0	1	1
ENSG00000251934	ENSG00000251934	RNU6-1143P	11:3686816-3847601	NOTEST	0	0	0	0	1	1
ENSG00000251935	ENSG00000251935	RN7SKP179	2:191399580-191432828	NOTEST	0	0	0	0	1	1
ENSG00000251936	ENSG00000251936	RNA5SP249	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000251937	ENSG00000251937	RNU7-129P	18:12400410-12400472	NOTEST	0	0	0	0	1	1
ENSG00000251938	ENSG00000251938	snoU13	3:47057918-47205457	NOTEST	0	0	0	0	1	1
ENSG00000251939	ENSG00000251939	RNU6-1278P	18:43664109-43708299	NOTEST	0	0	0	0	1	1
ENSG00000251940	ENSG00000251940	SNORA15	22:19166985-19279239	NOTEST	0	0	0	0	1	1
ENSG00000251941	ENSG00000251941	RNA5SP116	2:208918884-208918982	NOTEST	0	0	0	0	1	1
ENSG00000251942	ENSG00000251942	SCARNA16	2:53697584-53697767	NOTEST	0	0	0	0	1	1
ENSG00000251943	ENSG00000251943	RNU6-693P	1:172582567-172582674	NOTEST	0	0	0	0	1	1
ENSG00000251944	ENSG00000251944	U3	8:20472339-20472437	NOTEST	0	0	0	0	1	1
ENSG00000251946	ENSG00000251946	RNU6-1023P	6:54651184-54651290	NOTEST	0	0	0	0	1	1
ENSG00000251947	ENSG00000251947	RN7SKP164	2:76822538-76822804	NOTEST	0	0	0	0	1	1
ENSG00000251949	ENSG00000251949	SNORD112	14:101361106-101402336	NOTEST	0	0	0	0	1	1
ENSG00000251950	ENSG00000251950	RMRPP4	10:52065359-52401211	NOTEST	0	0	0	0	1	1
ENSG00000251951	ENSG00000251951	RN7SKP34	5:86263137-86433529	NOTEST	0	0	0	0	1	1
ENSG00000251952	ENSG00000251952	RNU6-1219P	22:29587684-29587796	NOTEST	0	0	0	0	1	1
ENSG00000251953	ENSG00000251953	RNA5SP522	Y:20488138-20515096	NOTEST	0	0	0	0	1	1
ENSG00000251954	ENSG00000251954	RNU6-496P	X:110664737-110664836	NOTEST	0	0	0	0	1	1
ENSG00000251955	ENSG00000251955	RNU6-27P	20:17168154-17168261	NOTEST	0	0	0	0	1	1
ENSG00000251956	ENSG00000251956	RNU6-617P	2:132349324-132384839	NOTEST	0	0	0	0	1	1
ENSG00000251957	ENSG00000251957	RNU6-1095P	10:11962020-12085169	NOTEST	0	0	0	0	1	1
ENSG00000251958	ENSG00000251958	RNU6-1102P	1:78444858-78604133	NOTEST	0	0	0	0	1	1
ENSG00000251959	ENSG00000251959	snoR442	10:17686123-17757913	NOTEST	0	0	0	0	1	1
ENSG00000251960	ENSG00000251960	RNU6-559P	9:14987299-15146399	NOTEST	0	0	0	0	1	1
ENSG00000251961	ENSG00000251961	RNU6ATAC13P	4:171812617-171812748	NOTEST	0	0	0	0	1	1
ENSG00000251962	ENSG00000251962	AL591668.1	X:133507282-133562820	NOTEST	0	0	0	0	1	1
ENSG00000251963	ENSG00000251963	AC090420.1	8:18384810-18942240	NOTEST	0	0	0	0	1	1
ENSG00000251964	ENSG00000251964	RNU7-135P	17:47366567-47447360	NOTEST	0	0	0	0	1	1
ENSG00000251965	ENSG00000251965	RNA5SP208	6:68177123-68177201	NOTEST	0	0	0	0	1	1

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ENSG00000251966	ENSG00000251966	AC010970.1	Y:10033980-10034093	NOTEST	0	0	0	0	1	1
ENSG00000251967	ENSG00000251967	SNORD77	3:46691999-46692080	NOTEST	0	0	0	0	1	1
ENSG00000251968	ENSG00000251968	AL133376.1	11:30851915-31391357	NOTEST	0	0	0	0	1	1
ENSG00000251969	ENSG00000251969	AL356776.1	6:79577188-79787953	NOTEST	0	0	0	0	1	1
ENSG00000251970	ENSG00000251970	RNU1-41P	Y:20994887-21001199	NOTEST	0	0	0	0	1	1
ENSG00000251971	ENSG00000251971	RNU6-1333P	2:238875468-239008054	NOTEST	0	0	0	0	1	1
ENSG00000251972	ENSG00000251972	RNU6-123P	21:27252860-27589700	NOTEST	0	0	0	0	1	1
ENSG00000251973	ENSG00000251973	RNU6-473P	2:131217027-131267239	NOTEST	0	0	0	0	1	1
ENSG00000251974	ENSG00000251974	SNORA19	2:86591258-86591388	NOTEST	0	0	0	0	1	1
ENSG00000251975	ENSG00000251975	RNU6-718P	5:119673243-119673348	NOTEST	0	0	0	0	1	1
ENSG00000251976	ENSG00000251976	RN7SKP141	2:137147901-137148239	NOTEST	0	0	0	0	1	1
ENSG00000251977	ENSG00000251977	RNU6-991P	1:8352216-8352323	NOTEST	0	0	0	0	1	1
ENSG00000251978	ENSG00000251978	RNA5SP236	7:106415456-106436010	NOTEST	0	0	0	0	1	1
ENSG00000251979	ENSG00000251979	U3	4:160428046-160428180	NOTEST	0	0	0	0	1	1
ENSG00000251980	ENSG00000251980	RNU6-436P	2:158733213-158992666	NOTEST	0	0	0	0	1	1
ENSG00000251981	ENSG00000251981	RNU7-52P	17:60447578-60493837	NOTEST	0	0	0	0	1	1
ENSG00000251982	ENSG00000251982	RN7SKP43	2:218116278-218116598	NOTEST	0	0	0	0	1	1
ENSG00000251983	ENSG00000251983	RN7SKP157	5:61442491-61442773	NOTEST	0	0	0	0	1	1
ENSG00000251985	ENSG00000251985	RNU6-1161P	22:46020410-46020512	NOTEST	0	0	0	0	1	1
ENSG00000251986	ENSG00000251986	Y_RNA	3:41236327-42003922	NOTEST	0	0	0	0	1	1
ENSG00000251987	ENSG00000251987	SNORD63	3:53528682-53880417	NOTEST	0	0	0	0	1	1
ENSG00000251988	ENSG00000251988	RNU4ATAC18P	6:160090088-160210781	NOTEST	0	0	0	0	1	1
ENSG00000251989	ENSG00000251989	AL160011.1	10:104005288-104142656	NOTEST	0	0	0	0	1	1
ENSG00000251990	ENSG00000251990	RNA5SP180	5:17065706-17276943	NOTEST	0	0	0	0	1	1
ENSG00000251991	ENSG00000251991	RNU7-49P	11:14464985-14665181	NOTEST	0	0	0	0	1	1
ENSG00000251992	ENSG00000251992	SCARNA17	18:47309868-47721463	NOTEST	0	4.2151	inf	0	1	1
ENSG00000251993	ENSG00000251993	RNA5SP227	7:22157855-22396763	NOTEST	0	0	0	0	1	1
ENSG00000251994	ENSG00000251994	RNU2-27P	18:9475006-9538114	NOTEST	0	0	0	0	1	1
ENSG00000251995	ENSG00000251995	Y_RNA	11:57252006-57283259	NOTEST	0	0	0	0	1	1
ENSG00000251996	ENSG00000251996	Y_RNA	Y:7142012-7249589	NOTEST	0	0	0	0	1	1
ENSG00000251997	ENSG00000251997	RNA5SP458	18:47845371-47845490	NOTEST	0	0	0	0	1	1
ENSG00000251998	ENSG00000251998	RNU6-168P	5:163223070-163223171	NOTEST	0	0	0	0	1	1
ENSG00000251999	ENSG00000251999	SNORA31	7:32535037-33102409	NOTEST	0	0	0	0	1	1
ENSG00000252000	ENSG00000252000	ACA59	2:179385909-179914813	NOTEST	0	0	0	0	1	1
ENSG00000252001	ENSG00000252001	RNA5SP303	10:19492778-20079330	NOTEST	0	0	0	0	1	1
ENSG00000252002	ENSG00000252002	RNA5SP154	4:9772776-10056560	NOTEST	0	0	0	0	1	1
ENSG00000252003	ENSG00000252003	RNU7-154P	7:121715700-121784334	NOTEST	0	0	0	0	1	1
ENSG00000252004	ENSG00000252004	AC068718.1	2:188577542-189152418	NOTEST	0	0	0	0	1	1
ENSG00000252005	ENSG00000252005	RNU4ATAC8P	1:74349395-74349505	NOTEST	0	0	0	0	1	1
ENSG00000252008	ENSG00000252008	RNU6-927P	12:125386057-125386157	NOTEST	0	0	0	0	1	1
ENSG00000252009	ENSG00000252009	SNORD112	14:101463989-101464061	NOTEST	0	0	0	0	1	1
ENSG00000252010	ENSG00000252010	SCARNA5	2:234118696-234204320	NOTEST	0.137223	0	#NAME?	0	1	1
ENSG00000252011	ENSG00000252011	SNORA25	1:246996749-246996831	NOTEST	0	0	0	0	1	1
ENSG00000252012	ENSG00000252012	RNA5SP521	Y:19664679-19691634	NOTEST	0	0	0	0	1	1
ENSG00000252013	ENSG00000252013	RNU4ATAC14P	14:75668783-75668872	NOTEST	0	0	0	0	1	1

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ENSG00000252014	ENSG00000252014	SNORA70	4:132689294-132689733	NOTEST	0	0	0	0	1	1
ENSG00000252015	ENSG00000252015	RNU6-904P	2:140988991-142895399	NOTEST	0	0	0	0	1	1
ENSG00000252016	ENSG00000252016	ACA64	X:87403792-87403919	NOTEST	0	0	0	0	1	1
ENSG00000252017	ENSG00000252017	RNU6-1194P	3:237440-451090	NOTEST	0	0	0	0	1	1
ENSG00000252018	ENSG00000252018	RNU2-30P	1:53192125-53293014	NOTEST	0	0	0	0	1	1
ENSG00000252019	ENSG00000252019	RNU6ATAC9P	14:55308725-55369570	NOTEST	0	0	0	0	1	1
ENSG00000252020	ENSG00000252020	SCARNA17	22:21744084-21744227	NOTEST	0	0	0	0	1	1
ENSG00000252021	ENSG00000252021	Y_RNA	20:43595114-43708600	NOTEST	0	0	0	0	1	1
ENSG00000252022	ENSG00000252022	SNORD33	16:76311175-76692375	NOTEST	0	0	0	0	1	1
ENSG00000252023	ENSG00000252023	RNU6-581P	7:119913721-120392568	NOTEST	0	0	0	0	1	1
ENSG00000252024	ENSG00000252024	SCARNA18	22:20455449-20455532	NOTEST	0	0	0	0	1	1
ENSG00000252025	ENSG00000252025	RNU6-982P	19:54248257-54248359	NOTEST	0	0	0	0	1	1
ENSG00000252026	ENSG00000252026	RNU6-1262P	16:68298432-68344849	NOTEST	0	0	0	0	1	1
ENSG00000252027	ENSG00000252027	RNU6ATAC14P	2:177529403-177529494	NOTEST	0	0	0	0	1	1
ENSG00000252028	ENSG00000252028	RN7SKP52	3:177159708-177470093	NOTEST	0	0	0	0	1	1
ENSG00000252029	ENSG00000252029	RNA5SP253	8:11944904-11944954	NOTEST	0	0	0	0	1	1
ENSG00000252030	ENSG00000252030	RNU6-1196P	4:154073493-154260472	NOTEST	0	0	0	0	1	1
ENSG00000252031	ENSG00000252031	RNU6-561P	2:79384131-80875905	NOTEST	0	0	0	0	1	1
ENSG00000252032	ENSG00000252032	RNU6-1281P	1:51819934-52027301	NOTEST	0	0	0	0	1	1
ENSG00000252033	ENSG00000252033	RNU6-311P	11:78290299-78290401	NOTEST	0	0	0	0	1	1
ENSG00000252034	ENSG00000252034	Y_RNA	18:43656969-43657065	NOTEST	0	0	0	0	1	1
ENSG00000252035	ENSG00000252035	RNU6-397P	8:13947372-15095848	NOTEST	0	0	0	0	1	1
ENSG00000252036	ENSG00000252036	RN7SKP288	10:112404154-112599227	NOTEST	0	0	0	0	1	1
ENSG00000252037	ENSG00000252037	RNU6-162P	7:143271838-143271941	NOTEST	0	0	0	0	1	1
ENSG00000252038	ENSG00000252038	AC068704.1	Y:19733138-19737712	NOTEST	0	0	0	0	1	1
ENSG00000252039	ENSG00000252039	RNU6-287P	17:41026686-41050751	NOTEST	0	0	0	0	1	1
ENSG00000252040	ENSG00000252040	snoU109	16:68664125-68664257	NOTEST	0	0	0	0	1	1
ENSG00000252041	ENSG00000252041	RNA5SP228	7:24172323-24172456	NOTEST	0	0	0	0	1	1
ENSG00000252042	ENSG00000252042	Y_RNA	17:73131342-73179078	NOTEST	0	0	0	0	1	1
ENSG00000252045	ENSG00000252045	SNORA33	21:33910608-33910744	NOTEST	0	0	0	0	1	1
ENSG00000252046	ENSG00000252046	RNU6-150P	6:20534687-21232635	NOTEST	0	0	0	0	1	1
ENSG00000252047	ENSG00000252047	Y_RNA	7:102937868-103629963	NOTEST	0	0	0	0	1	1
ENSG00000252048	ENSG00000252048	U3	4:184020445-184241930	NOTEST	0	0	0	0	1	1
ENSG00000252049	ENSG00000252049	SNORA40	10:23455913-23456030	NOTEST	0	0	0	0	1	1
ENSG00000252050	ENSG00000252050	SNORA31	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000252051	ENSG00000252051	RN7SKP276	1:229546246-229546514	NOTEST	0	0	0	0	1	1
ENSG00000252053	ENSG00000252053	RNU6-1101P	3:194254231-194254312	NOTEST	0	0	0	0	1	1
ENSG00000252054	ENSG00000252054	SNORA73	7:54933510-54933717	NOTEST	0	0	0	0	1	1
ENSG00000252055	ENSG00000252055	RNU6-69P	13:45694649-45858237	NOTEST	0	0	0	0	1	1
ENSG00000252056	ENSG00000252056	RNU5E-2P	1:235824340-236046940	NOTEST	0	0	0	0	1	1
ENSG00000252057	ENSG00000252057	RNU7-174P	8:58405442-58504118	NOTEST	0	0	0	0	1	1
ENSG00000252058	ENSG00000252058	snoU13	20:4833001-4990939	NOTEST	0	0	0	0	1	1
ENSG00000252059	ENSG00000252059	AC012667.1	Y:4868266-5610265	NOTEST	0	0	0	0	1	1
ENSG00000252060	ENSG00000252060	RNA5SP464	19:12098431-12167127	NOTEST	0	0	0	0	1	1
ENSG00000252061	ENSG00000252061	RNU6-415P	15:79191181-79191278	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000252062	ENSG00000252062	RNU6-469P	4:85590703-85932430	NOTEST	0	0	0	0	1	1
ENSG00000252063	ENSG00000252063	RNU6-1041P	19:54263340-54263442	NOTEST	0	0	0	0	1	1
ENSG00000252064	ENSG00000252064	Y_RNA	20:55886909-55887014	NOTEST	0	0	0	0	1	1
ENSG00000252065	ENSG00000252065	RNU6-864P	14:29299449-29497969	NOTEST	0	0	0	0	1	1
ENSG00000252066	ENSG00000252066	RNU2-53P	15:53805937-54055075	NOTEST	0	0	0	0	1	1
ENSG00000252067	ENSG00000252067	RNU4-71P	8:23457538-23457651	NOTEST	0	0	0	0	1	1
ENSG00000252068	ENSG00000252068	RNU6-390P	5:157006504-157006607	NOTEST	0	0	0	0	1	1
ENSG00000252069	ENSG00000252069	Y_RNA	X:108987871-108987978	NOTEST	0	0	0	0	1	1
ENSG00000252070	ENSG00000252070	RNA5SP341	11:57217655-57217772	NOTEST	0	0	0	0	1	1
ENSG00000252071	ENSG00000252071	snoU13	19:47421932-47508334	NOTEST	0	0	0	0	1	1
ENSG00000252072	ENSG00000252072	RNA5SP320	10:75404638-75490272	NOTEST	0	0	0	0	1	1
ENSG00000252073	ENSG00000252073	RNU6-947P	1:245118159-245118265	NOTEST	0	0	0	0	1	1
ENSG00000252074	ENSG00000252074	RNU6-416P	16:30686620-30686723	NOTEST	0	0	0	0	1	1
ENSG00000252075	ENSG00000252075	RNU7-109P	8:144718182-144735900	NOTEST	0	0	0	0	1	1
ENSG00000252076	ENSG00000252076	RN7SKP196	10:60628943-60629288	NOTEST	0	0	0	0	1	1
ENSG00000252077	ENSG00000252077	SNORD112	16:50532071-50532141	NOTEST	0	0	0	0	1	1
ENSG00000252078	ENSG00000252078	SNORD112	18:33877676-34812135	NOTEST	0	0	0	0	1	1
ENSG00000252079	ENSG00000252079	RNU6-327P	12:133345494-133532892	NOTEST	0	0	0	0	1	1
ENSG00000252080	ENSG00000252080	RNU7-99P	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000252081	ENSG00000252081	RNU6-277P	11:105480720-105852819	NOTEST	0	0	0	0	1	1
ENSG00000252082	ENSG00000252082	RNU6-547P	3:172348038-172429008	NOTEST	0	0	0	0	1	1
ENSG00000252083	ENSG00000252083	SNORA40	5:23951456-24178372	NOTEST	0	0	0	0	1	1
ENSG00000252084	ENSG00000252084	RN7SKP12	1:242246287-242687998	NOTEST	0	0	0	0	1	1
ENSG00000252085	ENSG00000252085	Y_RNA	3:15247658-15294425	NOTEST	0	0	0	0	1	1
ENSG00000252086	ENSG00000252086	RNA5SP76	1:219858768-220131989	NOTEST	0	0	0	0	1	1
ENSG00000252087	ENSG00000252087	RN7SKP248	4:91048685-92523064	NOTEST	0	0	0	0	1	1
ENSG00000252088	ENSG00000252088	snoU13	17:45277811-45301045	NOTEST	0	0	0	0	1	1
ENSG00000252089	ENSG00000252089	RNU4ATAC7P	20:53476226-53476351	NOTEST	0	0	0	0	1	1
ENSG00000252091	ENSG00000252091	RNU6-1146P	20:55242485-55242587	NOTEST	0	0	0	0	1	1
ENSG00000252092	ENSG00000252092	AC098830.1	4:13656802-13978699	NOTEST	0	0	0	0	1	1
ENSG00000252093	ENSG00000252093	AC011626.1	8:121925304-122131994	NOTEST	0	0	0	0	1	1
ENSG00000252094	ENSG00000252094	RNA5SP410	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000252096	ENSG00000252096	SNORA31	20:4833001-4990939	NOTEST	0	2.74529	inf	0	1	1
ENSG00000252097	ENSG00000252097	RNU6-346P	18:74506687-74534251	NOTEST	0	0	0	0	1	1
ENSG00000252098	ENSG00000252098	Y_RNA	1:27561006-27635110	NOTEST	0	0	0	0	1	1
ENSG00000252100	ENSG00000252100	AC002539.2	17:67945001-67945088	NOTEST	0	0	0	0	1	1
ENSG00000252101	ENSG00000252101	RNU6-758P	16:75320609-75320696	NOTEST	0	0	0	0	1	1
ENSG00000252102	ENSG00000252102	SNORA63	7:64791631-64791729	NOTEST	0	0	0	0	1	1
ENSG00000252103	ENSG00000252103	RNU6-917P	20:1497404-1600707	NOTEST	0	0	0	0	1	1
ENSG00000252104	ENSG00000252104	RNU6-191P	4:65140974-65275186	NOTEST	0	0	0	0	1	1
ENSG00000252105	ENSG00000252105	RNU1-143P	1:149284644-149286975	NOTEST	0	0	0	0	1	1
ENSG00000252106	ENSG00000252106	Y_RNA	6:52842750-52860176	NOTEST	0	0	0	0	1	1
ENSG00000252107	ENSG00000252107	RNA5SP220	6:140479727-140479831	NOTEST	0	0	0	0	1	1
ENSG00000252108	ENSG00000252108	RNU6-1232P	5:67454888-67454974	NOTEST	0	0	0	0	1	1
ENSG00000252109	ENSG00000252109	snoZ178	17:50303617-50303707	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000252110	ENSG00000252110	snoU13	9:6532463-6645650	NOTEST	0	0	0	0	1	1
ENSG00000252111	ENSG00000252111	AC002981.1	X:12156584-12742642	NOTEST	0	0	0	0	1	1
ENSG00000252112	ENSG00000252112	SNORD63	17:28565758-28619074	NOTEST	0	0	0	0	1	1
ENSG00000252113	ENSG00000252113	RNU6-523P	X:44732756-44971847	NOTEST	0	0	0	0	1	1
ENSG00000252114	ENSG00000252114	SNORA73	14:23485751-23504439	NOTEST	0	0	0	0	1	1
ENSG00000252115	ENSG00000252115	Y_RNA	7:116451123-116562103	NOTEST	0	0	0	0	1	1
ENSG00000252116	ENSG00000252116	RNU4ATAC4P	1:67733283-67733409	NOTEST	0	0	0	0	1	1
ENSG00000252117	ENSG00000252117	RNU6-1108P	15:45206999-45222820	NOTEST	0	0	0	0	1	1
ENSG00000252118	ENSG00000252118	RNU6ATAC39P	10:12391480-12877545	NOTEST	0	0	0	0	1	1
ENSG00000252119	ENSG00000252119	ACA64	11:119194002-119194119	NOTEST	0	0	0	0	1	1
ENSG00000252120	ENSG00000252120	AL136137.1	X:44436599-44436684	NOTEST	0	0	0	0	1	1
ENSG00000252121	ENSG00000252121	RNU6-970P	1:93435160-93435267	NOTEST	0	0	0	0	1	1
ENSG00000252122	ENSG00000252122	SNORA76	16:75327595-75499395	NOTEST	0	0	0	0	1	1
ENSG00000252123	ENSG00000252123	RNU7-72P	20:48429249-48508779	NOTEST	0	0	0	0	1	1
ENSG00000252124	ENSG00000252124	AL031594.1	22:40742506-41032706	NOTEST	0	0	0	0	1	1
ENSG00000252125	ENSG00000252125	RNU6-1299P	6:107454274-107454374	NOTEST	0	0	0	0	1	1
ENSG00000252126	ENSG00000252126	RNU6-313P	7:65670185-65955095	NOTEST	0	0	0	0	1	1
ENSG00000252127	ENSG00000252127	SNORA70	GL000193.1:175229-175324	NOTEST	0	0	0	0	1	1
ENSG00000252128	ENSG00000252128	SNORD27	13:21714024-21714096	NOTEST	0	0	0	0	1	1
ENSG00000252129	ENSG00000252129	SNORA74	17:15468796-15587625	NOTEST	0	0	0	0	1	1
ENSG00000252130	ENSG00000252130	RNU6-1045P	2:192093890-192290115	NOTEST	0	0	0	0	1	1
ENSG00000252131	ENSG00000252131	AL844165.1	1:231114726-231136341	NOTEST	0	0	0	0	1	1
ENSG00000252132	ENSG00000252132	RNU6-795P	10:38299577-38354016	NOTEST	0	0	0	0	1	1
ENSG00000252133	ENSG00000252133	SNORA70	9:46669491-46669586	NOTEST	0	0	0	0	1	1
ENSG00000252134	ENSG00000252134	Y_RNA	1:171783651-171783766	NOTEST	0	0	0	0	1	1
ENSG00000252135	ENSG00000252135	RNVU1-2	1:143647637-143745417	NOTEST	0	0	0	0	1	1
ENSG00000252136	ENSG00000252136	SNORA31	4:105389468-106041157	NOTEST	0	0	0	0	1	1
ENSG00000252137	ENSG00000252137	RNU6-1338P	6:76302770-76302861	NOTEST	0	0	0	0	1	1
ENSG00000252138	ENSG00000252138	SNORA40	16:7776842-7776953	NOTEST	0	0	0	0	1	1
ENSG00000252139	ENSG00000252139	SCARNA18	18:47309868-47721463	NOTEST	0	0	0	0	1	1
ENSG00000252141	ENSG00000252141	RNU6-65P	13:52139547-52139645	NOTEST	0	0	0	0	1	1
ENSG00000252142	ENSG00000252142	AL022314.1	22:37521877-37595425	NOTEST	0	0	0	0	1	1
ENSG00000252143	ENSG00000252143	SCARNA17	22:21899185-21899328	NOTEST	0	0	0	0	1	1
ENSG00000252144	ENSG00000252144	SNORD112	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000252145	ENSG00000252145	RNU6-1225P	X:67262185-67653755	NOTEST	0	0	0	0	1	1
ENSG00000252146	ENSG00000252146	AL390776.1	1:44686741-44820932	NOTEST	0	0	0	0	1	1
ENSG00000252147	ENSG00000252147	Y_RNA	X:118590520-118590621	NOTEST	0	0	0	0	1	1
ENSG00000252148	ENSG00000252148	RNU6-1206P	2:201773695-201950473	NOTEST	0	0	0	0	1	1
ENSG00000252149	ENSG00000252149	RNA5SP315	10:49248475-49248591	NOTEST	0	0	0	0	1	1
ENSG00000252150	ENSG00000252150	AC092574.2	4:419223-492945	NOTEST	0	0	0	0	1	1
ENSG00000252151	ENSG00000252151	RNU6-1265P	1:14450727-14450830	NOTEST	0	0	0	0	1	1
ENSG00000252153	ENSG00000252153	MIR2278	9:97488982-97849441	NOTEST	0	0	0	0	1	1
ENSG00000252154	ENSG00000252154	SNORD112	13:97593534-97636426	NOTEST	0	0	0	0	1	1
ENSG00000252155	ENSG00000252155	RNU6-941P	Y:7142012-7249589	NOTEST	0	0	0	0	1	1
ENSG00000252156	ENSG00000252156	RNU6-155P	6:76458908-76629254	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000252157	ENSG00000252157	RNU6-479P	4:184560787-184580378	NOTEST	0	0	0	0	1	1
ENSG00000252158	ENSG00000252158	SNORA72	8:132445022-132445116	NOTEST	0	0	0	0	1	1
ENSG00000252159	ENSG00000252159	RNY4P1	9:77337410-77503010	NOTEST	0	0	0	0	1	1
ENSG00000252161	ENSG00000252161	RNA5SP318	10:55217956-55218048	NOTEST	0	0	0	0	1	1
ENSG00000252162	ENSG00000252162	RNU6-830P	1:55864186-55864293	NOTEST	0	0	0	0	1	1
ENSG00000252163	ENSG00000252163	RN7SKP31	X:137479509-137479787	NOTEST	0	0	0	0	1	1
ENSG00000252164	ENSG00000252164	RNA5SP282	9:34179002-34329198	NOTEST	0	0	0	0	1	1
ENSG00000252166	ENSG00000252166	RNU1-95P	Y:20278412-20279581	NOTEST	0	0	0	0	1	1
ENSG00000252167	ENSG00000252167	RNA5SP287	9:84500410-84500513	NOTEST	0	0	0	0	1	1
ENSG00000252169	ENSG00000252169	RNA5SP200	5:172719519-172719622	NOTEST	0	0	0	0	1	1
ENSG00000252170	ENSG00000252170	SNORD112	3:121902529-122005342	NOTEST	0	0	0	0	1	1
ENSG00000252171	ENSG00000252171	Y_RNA	15:45315301-45369383	NOTEST	0	0	0	0	1	1
ENSG00000252172	ENSG00000252172	RNU6-720P	3:149478891-149942977	NOTEST	0	0	0	0	1	1
ENSG00000252173	ENSG00000252173	RNU6-109P	Y:18360814-18360921	NOTEST	0	0	0	0	1	1
ENSG00000252174	ENSG00000252174	RNU7-18P	3:195754053-195809060	NOTEST	0	0	0	0	1	1
ENSG00000252175	ENSG00000252175	U3	X:54091277-54091399	NOTEST	0	0	0	0	1	1
ENSG00000252176	ENSG00000252176	AC123767.1	8:39418455-39418546	NOTEST	0	0	0	0	1	1
ENSG00000252177	ENSG00000252177	AC005513.1	19:13317255-13734804	NOTEST	0	0	0	0	1	1
ENSG00000252178	ENSG00000252178	RNU7-69P	X:122905927-122905989	NOTEST	0	0	0	0	1	1
ENSG00000252179	ENSG00000252179	RNA5SP255	8:13393537-13393644	NOTEST	0	0	0	0	1	1
ENSG00000252180	ENSG00000252180	Y_RNA	1:17484691-17484779	NOTEST	0	0	0	0	1	1
ENSG00000252181	ENSG00000252181	AC020703.1	4:154794518-154794603	NOTEST	0	0	0	0	1	1
ENSG00000252182	ENSG00000252182	RNA5SP413	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000252183	ENSG00000252183	RNU6-948P	4:122052562-122148621	NOTEST	0	0	0	0	1	1
ENSG00000252184	ENSG00000252184	RNU2-10P	3:61547242-62355005	NOTEST	0	0	0	0	1	1
ENSG00000252185	ENSG00000252185	RNU6-752P	5:126087654-126112178	NOTEST	0	0	0	0	1	1
ENSG00000252186	ENSG00000252186	RNU6-781P	12:6818617-6818718	NOTEST	0	0	0	0	1	1
ENSG00000252187	ENSG00000252187	AC051649.1	11:1940791-1959936	NOTEST	0	0	0	0	1	1
ENSG00000252188	ENSG00000252188	SNORA40	7:138279029-138386097	NOTEST	0	0	0	0	1	1
ENSG00000252189	ENSG00000252189	U3	10:88505596-88505706	NOTEST	0	0	0	0	1	1
ENSG00000252190	ENSG00000252190	SCARNA17	1:26332496-26332621	NOTEST	0	0	0	0	1	1
ENSG00000252191	ENSG00000252191	RNU6-751P	19:54253104-54253205	NOTEST	0	0	0	0	1	1
ENSG00000252192	ENSG00000252192	SNORA9	12:122957416-122985518	NOTEST	0	0	0	0	1	1
ENSG00000252193	ENSG00000252193	SCARNA15	20:41933194-41933319	NOTEST	0	0	0	0	1	1
ENSG00000252196	ENSG00000252196	AL590482.1	6:165740775-166401536	NOTEST	0	0	0	0	1	1
ENSG00000252198	ENSG00000252198	Y_RNA	14:58862633-59015216	NOTEST	0	0	0	0	1	1
ENSG00000252199	ENSG00000252199	SNORA70	21:10385952-10386047	NOTEST	0	0	0	0	1	1
ENSG00000252200	ENSG00000252200	snoZ6	19:45229247-45229322	NOTEST	0	0	0	0	1	1
ENSG00000252201	ENSG00000252201	RNU6-1058P	1:44115828-44396831	NOTEST	0	0	0	0	1	1
ENSG00000252202	ENSG00000252202	Y_RNA	5:179224596-179334859	NOTEST	0	0	0	0	1	1
ENSG00000252203	ENSG00000252203	snoR442	10:67672275-69455927	NOTEST	0	0	0	0	1	1
ENSG00000252204	ENSG00000252204	SNORA25	12:31964021-31964124	NOTEST	0	0	0	0	1	1
ENSG00000252205	ENSG00000252205	RNU6-764P	X:151307354-151619830	NOTEST	0	0	0	0	1	1
ENSG00000252206	ENSG00000252206	RNU7-40P	12:56735380-56753939	NOTEST	0	0	0	0	1	1
ENSG00000252207	ENSG00000252207	RNA5SP365	12:90120712-90120819	NOTEST	0	0	0	0	1	1

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ENSG00000252209	ENSG00000252209	RNU1-48P	Y:20642972-20649286	NOTEST	0	0	0	0	1	1
ENSG00000252210	ENSG00000252210	Y_RNA	8:68864352-69149265	NOTEST	0	0	0	0	1	1
ENSG00000252211	ENSG00000252211	RNA5SP473	19:58856543-58877958	NOTEST	0	0	0	0	1	1
ENSG00000252212	ENSG00000252212	RNU2-58P	17:57059998-57232630	NOTEST	0	0	0	0	1	1
ENSG00000252213	ENSG00000252213	SNORA74	5:138282408-138667360	NOTEST	0	0	0	0	1	1
ENSG00000252214	ENSG00000252214	RNU6-542P	2:74425688-74621009	NOTEST	0	0	0	0	1	1
ENSG00000252215	ENSG00000252215	AL357514.1	6:112853383-112853487	NOTEST	0	0	0	0	1	1
ENSG00000252216	ENSG00000252216	AC007041.1	2:20553402-20553477	NOTEST	0	0	0	0	1	1
ENSG00000252217	ENSG00000252217	Y_RNA	15:65734800-65810042	NOTEST	0	0	0	0	1	1
ENSG00000252218	ENSG00000252218	SCARNA15	6:43474706-43543812	NOTEST	0	0	0	0	1	1
ENSG00000252219	ENSG00000252219	hsa-mir-892c	X:145074270-145074343	NOTEST	0	0	0	0	1	1
ENSG00000252220	ENSG00000252220	RNU6-977P	12:83080658-83528649	NOTEST	0	0	0	0	1	1
ENSG00000252222	ENSG00000252222	RNU7-13P	1:184759857-184943682	NOTEST	0	0	0	0	1	1
ENSG00000252223	ENSG00000252223	RNU6-1049P	2:130831107-130886795	NOTEST	0	0	0	0	1	1
ENSG00000252224	ENSG00000252224	RNU4ATAC15P	9:33104079-33179981	NOTEST	0	0	0	0	1	1
ENSG00000252225	ENSG00000252225	Y_RNA	22:36836924-36837015	NOTEST	0	0	0	0	1	1
ENSG00000252226	ENSG00000252226	AL451051.1	1:100295020-100295093	NOTEST	0	0	0	0	1	1
ENSG00000252227	ENSG00000252227	SNORD36	20:46764685-46764766	NOTEST	0	0	0	0	1	1
ENSG00000252228	ENSG00000252228	SNORA48	6:30100581-30100743	NOTEST	0	0	0	0	1	1
ENSG00000252230	ENSG00000252230	SNORD111	19:35084233-35166604	NOTEST	0	0	0	0	1	1
ENSG00000252231	ENSG00000252231	RNA5SP67	1:173890207-173890338	NOTEST	0	0	0	0	1	1
ENSG00000252233	ENSG00000252233	RN7SKP253	4:140586921-141075338	NOTEST	0	0	0	0	1	1
ENSG00000252234	ENSG00000252234	AC006557.1	18:14057455-14132489	NOTEST	0	0	0	0	1	1
ENSG00000252235	ENSG00000252235	RNU6-962P	4:13052965-13053035	NOTEST	0	0	0	0	1	1
ENSG00000252236	ENSG00000252236	SNORA26	1:156161853-156161994	NOTEST	0	0	0	0	1	1
ENSG00000252237	ENSG00000252237	RNU4-54P	12:28286181-28732883	NOTEST	0	0	0	0	1	1
ENSG00000252238	ENSG00000252238	SNORA31	2:4874590-4874674	NOTEST	0	0	0	0	1	1
ENSG00000252239	ENSG00000252239	RNU6-1185P	2:39476406-39945103	NOTEST	0	0	0	0	1	1
ENSG00000252240	ENSG00000252240	AC096643.1	1:219836718-219836809	NOTEST	0	0	0	0	1	1
ENSG00000252241	ENSG00000252241	U3	1:193700987-193701074	NOTEST	0	0	0	0	1	1
ENSG00000252242	ENSG00000252242	RNU7-115P	17:62745780-62833272	NOTEST	0	0	0	0	1	1
ENSG00000252243	ENSG00000252243	RNU6-412P	4:46533253-46533359	NOTEST	0	0	0	0	1	1
ENSG00000252244	ENSG00000252244	RNU7-3P	6:149825868-149867174	NOTEST	0	0	0	0	1	1
ENSG00000252245	ENSG00000252245	RNU6-736P	3:138722803-139108574	NOTEST	0	0	0	0	1	1
ENSG00000252246	ENSG00000252246	RNA5SP92	2:33172038-33624576	NOTEST	0	0	0	0	1	1
ENSG00000252247	ENSG00000252247	RNU6-70P	13:27917784-27917883	NOTEST	0	0	0	0	1	1
ENSG00000252249	ENSG00000252249	SNORA18	6:94588823-94588947	NOTEST	0	0	0	0	1	1
ENSG00000252250	ENSG00000252250	Y_RNA	2:69546904-69614382	NOTEST	0	0	0	0	1	1
ENSG00000252251	ENSG00000252251	RNA5SP348	11:104123306-104123343	NOTEST	0	0	0	0	1	1
ENSG00000252252	ENSG00000252252	RNU6-687P	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000252254	ENSG00000252254	Y_RNA	1:8377885-8404227	NOTEST	0	0	0	0	1	1
ENSG00000252255	ENSG00000252255	RNU2-35P	11:125439111-125551018	NOTEST	0	0	0	0	1	1
ENSG00000252256	ENSG00000252256	SNORD112	9:85857904-86153461	NOTEST	0	0	0	0	1	1
ENSG00000252257	ENSG00000252257	RN7SKP265	3:181670130-181728466	NOTEST	0	0	0	0	1	1
ENSG00000252258	ENSG00000252258	SNORA70	18:3025431-3025564	NOTEST	0	0	0	0	1	1

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ENSG00000252259	ENSG00000252259	RNA5SP49	1:63652006-63652121	NOTEST	0	0	0	0	1	1
ENSG00000252260	ENSG00000252260	RNA5SP461	18:75575419-75575523	NOTEST	0	0	0	0	1	1
ENSG00000252261	ENSG00000252261	RNA5SP262	8:31496901-32622548	NOTEST	0	0	0	0	1	1
ENSG00000252262	ENSG00000252262	RNA5SP61	1:162039563-162356600	NOTEST	0	0	0	0	1	1
ENSG00000252263	ENSG00000252263	RNU6-659P	14:70892528-71014181	NOTEST	0	0	0	0	1	1
ENSG00000252264	ENSG00000252264	RNU7-153P	8:13947372-15095848	NOTEST	0	0	0	0	1	1
ENSG00000252265	ENSG00000252265	snoU13	7:65670185-65955095	NOTEST	0	0	0	0	1	1
ENSG00000252266	ENSG00000252266	Y_RNA	4:5053168-5502725	NOTEST	0	0	0	0	1	1
ENSG00000252267	ENSG00000252267	RNA5SP495	22:26786632-26786742	NOTEST	0	0	0	0	1	1
ENSG00000252268	ENSG00000252268	RNA5SP417	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000252269	ENSG00000252269	RNU4ATAC12P	12:133562950-133589154	NOTEST	0	0	0	0	1	1
ENSG00000252270	ENSG00000252270	AC034205.1	5:150745993-150810913	NOTEST	0	0	0	0	1	1
ENSG00000252271	ENSG00000252271	RNU6-1110P	16:58328983-58440048	NOTEST	0	0	0	0	1	1
ENSG00000252272	ENSG00000252272	RNA5SP470	19:29492576-29492682	NOTEST	0	0	0	0	1	1
ENSG00000252273	ENSG00000252273	RNU6-426P	21:17407732-17407829	NOTEST	0	0	0	0	1	1
ENSG00000252274	ENSG00000252274	SCARNA24	17:70642087-71088851	NOTEST	0	0	0	0	1	1
ENSG00000252275	ENSG00000252275	RNU7-192P	4:189637818-189637879	NOTEST	0	0	0	0	1	1
ENSG00000252277	ENSG00000252277	SNORD116-30	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000252278	ENSG00000252278	RNU6-866P	17:36908988-36920484	NOTEST	0	0	0	0	1	1
ENSG00000252279	ENSG00000252279	RNU6-406P	17:41522074-41528568	NOTEST	0	0	0	0	1	1
ENSG00000252280	ENSG00000252280	RNU7-16P	7:128864863-129070052	NOTEST	0	0	0	0	1	1
ENSG00000252281	ENSG00000252281	snoZ247	2:41961516-41961596	NOTEST	0	0	0	0	1	1
ENSG00000252282	ENSG00000252282	RNU6-1089P	1:245132651-245290466	NOTEST	0	0	0	0	1	1
ENSG00000252283	ENSG00000252283	Vault	17:26368762-26523407	NOTEST	0	0	0	0	1	1
ENSG00000252284	ENSG00000252284	SNORD28	18:56148478-56296189	NOTEST	0	0	0	0	1	1
ENSG00000252285	ENSG00000252285	RNU7-5P	15:45722726-45878488	NOTEST	0	0	0	0	1	1
ENSG00000252287	ENSG00000252287	RNA5SP24	13:19662626-19662721	NOTEST	0	0	0	0	1	1
ENSG00000252288	ENSG00000252288	RNU6-966P	15:45248899-45271427	NOTEST	0	0	0	0	1	1
ENSG00000252289	ENSG00000252289	RNA5SP519	Y:9930483-9930602	NOTEST	0	0	0	0	1	1
ENSG00000252290	ENSG00000252290	SNORA25	1:237205504-237997288	NOTEST	0	0	0	0	1	1
ENSG00000252291	ENSG00000252291	SNORA31	X:5758677-6146904	NOTEST	0	0	0	0	1	1
ENSG00000252292	ENSG00000252292	RN7SKP238	10:87359311-88126250	NOTEST	0	0	0	0	1	1
ENSG00000252293	ENSG00000252293	RNU7-64P	2:85669038-85669100	NOTEST	0	0	0	0	1	1
ENSG00000252294	ENSG00000252294	RNU6-589P	X:101854095-101973607	NOTEST	0	0	0	0	1	1
ENSG00000252295	ENSG00000252295	snoU13	5:122110690-122165803	NOTEST	0	0	0	0	1	1
ENSG00000252296	ENSG00000252296	SNORA25	X:99355081-99355219	NOTEST	0	0	0	0	1	1
ENSG00000252297	ENSG00000252297	RNU6-875P	8:124332089-124428590	NOTEST	0	0	0	0	1	1
ENSG00000252298	ENSG00000252298	SNORD112	2:84085946-84086023	NOTEST	0	0	0	0	1	1
ENSG00000252299	ENSG00000252299	U3	9:90989183-90989274	NOTEST	0	0	0	0	1	1
ENSG00000252300	ENSG00000252300	SNORD112	4:141178439-141306880	NOTEST	0	0	0	0	1	1
ENSG00000252301	ENSG00000252301	RNA5SP134	3:63213990-63602597	NOTEST	0	0	0	0	1	1
ENSG00000252302	ENSG00000252302	RNA5SP147	3:176361728-176585626	NOTEST	0	0	0	0	1	1
ENSG00000252303	ENSG00000252303	RNU6-1221P	4:29512256-29512359	NOTEST	0	0	0	0	1	1
ENSG00000252305	ENSG00000252305	SNORA74	17:13972812-14111994	NOTEST	0	0	0	0	1	1
ENSG00000252306	ENSG00000252306	AC104183.1	3:21430024-21430109	NOTEST	0	0	0	0	1	1

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ENSG00000252307	ENSG00000252307	RNA5SP153	4:9412903-9412979	NOTEST	0	0	0	0	1	1
ENSG00000252308	ENSG00000252308	AC011738.1	7:43618486-43618571	NOTEST	0	0	0	0	1	1
ENSG00000252309	ENSG00000252309	AL391416.1	6:83920107-84140797	NOTEST	0	0	0	0	1	1
ENSG00000252310	ENSG00000252310	RNY5	7:148638579-148638658	NOTEST	0	0	0	0	1	1
ENSG00000252311	ENSG00000252311	RNU1-103P	16:85805363-85840650	NOTEST	0	0	0	0	1	1
ENSG00000252312	ENSG00000252312	RN7SKP21	14:36683812-36704814	NOTEST	0	0	0	0	1	1
ENSG00000252313	ENSG00000252313	RNA5SP281	9:32293555-32293690	NOTEST	0	0	0	0	1	1
ENSG00000252314	ENSG00000252314	SCARNA18	22:21743916-21743999	NOTEST	0	0	0	0	1	1
ENSG00000252315	ENSG00000252315	RNA5SP520	Y:19664679-19691634	NOTEST	0	0	0	0	1	1
ENSG00000252316	ENSG00000252316	RNY4	7:148660406-148660502	NOTEST	0	0	0	0	1	1
ENSG00000252317	ENSG00000252317	Y_RNA	1:240177647-240643504	NOTEST	0	0	0	0	1	1
ENSG00000252319	ENSG00000252319	Y_RNA	18:8695853-8832776	NOTEST	0	0	0	0	1	1
ENSG00000252320	ENSG00000252320	RNU6-320P	X:135665398-135665504	NOTEST	0	0	0	0	1	1
ENSG00000252321	ENSG00000252321	RN7SKP83	2:86042252-86052514	NOTEST	0	0	0	0	1	1
ENSG00000252322	ENSG00000252322	RN7SKP244	4:89442135-89629693	NOTEST	0	0	0	0	1	1
ENSG00000252323	ENSG00000252323	RNU6-184P	Y:18448162-18448269	NOTEST	0	0	0	0	1	1
ENSG00000252324	ENSG00000252324	AL163193.1	9:20341662-20622542	NOTEST	0	0	0	0	1	1
ENSG00000252325	ENSG00000252325	RNU6-1038P	18:19451406-19473957	NOTEST	0	0	0	0	1	1
ENSG00000252326	ENSG00000252326	SNORD116-25	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000252327	ENSG00000252327	RNU6-1302P	11:47459307-47470730	NOTEST	0	0	0	0	1	1
ENSG00000252328	ENSG00000252328	Vault	17:33332106-33448541	NOTEST	0	0	0	0	1	1
ENSG00000252329	ENSG00000252329	SCARNA16	11:12695968-12966298	NOTEST	0	0	0	0	1	1
ENSG00000252330	ENSG00000252330	AC105105.1	18:56133494-56133559	NOTEST	0	0	0	0	1	1
ENSG00000252332	ENSG00000252332	RNU6-911P	7:139133485-139133589	NOTEST	0	0	0	0	1	1
ENSG00000252333	ENSG00000252333	RNU6-964P	2:230628553-230877825	NOTEST	0	0	0	0	1	1
ENSG00000252334	ENSG00000252334	RNU6-1337P	19:58985383-59023780	NOTEST	0	0	0	0	1	1
ENSG00000252335	ENSG00000252335	RNU6-62P	13:95671488-95671590	NOTEST	0	0	0	0	1	1
ENSG00000252336	ENSG00000252336	RNA5SP148	3:177919837-178578193	NOTEST	0	0	0	0	1	1
ENSG00000252337	ENSG00000252337	SNORA31	5:105882365-105882504	NOTEST	0	0	0	0	1	1
ENSG00000252338	ENSG00000252338	RNU6-503P	1:75667815-76076801	NOTEST	0	0	0	0	1	1
ENSG00000252339	ENSG00000252339	RNU6-1061P	16:71481499-71598992	NOTEST	0	0	0	0	1	1
ENSG00000252341	ENSG00000252341	Y_RNA	5:10275986-10308138	NOTEST	0	0	0	0	1	1
ENSG00000252342	ENSG00000252342	RNA5SP164	4:94741321-94741431	NOTEST	0	0	0	0	1	1
ENSG00000252343	ENSG00000252343	RNU2-34P	4:182795590-183724177	NOTEST	0	0	0	0	1	1
ENSG00000252346	ENSG00000252346	RNA5SP121	2:228627767-228627868	NOTEST	0	0	0	0	1	1
ENSG00000252347	ENSG00000252347	RNU6-1046P	14:23654524-23795394	NOTEST	0	0	0	0	1	1
ENSG00000252348	ENSG00000252348	RNU6-1256P	3:101334669-101334772	NOTEST	0	0	0	0	1	1
ENSG00000252349	ENSG00000252349	SNORA31	17:19551448-19580911	NOTEST	0	0	0	0	1	1
ENSG00000252350	ENSG00000252350	RPPH1-3P	4:157907523-157907845	NOTEST	0	0	0	0	1	1
ENSG00000252351	ENSG00000252351	RNU6ATAC12P	11:131240372-132206716	NOTEST	0	0	0	0	1	1
ENSG00000252352	ENSG00000252352	SNORA40	17:67351273-67351359	NOTEST	0	0	0	0	1	1
ENSG00000252353	ENSG00000252353	RNU7-25P	18:3066804-3247275	NOTEST	0	0	0	0	1	1
ENSG00000252354	ENSG00000252354	SNORD112	1:171810620-172437971	NOTEST	0	0	0	0	1	1
ENSG00000252355	ENSG00000252355	RN7SKP287	11:43333512-43516483	NOTEST	0.298769	0.108973	-1.45506	0	1	1
ENSG00000252356	ENSG00000252356	SNORD112	19:42590262-42700737	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000252357	ENSG00000252357	Y_RNA	1:173768687-173827684	NOTEST	0	0	0	0	1	1
ENSG00000252358	ENSG00000252358	RN7SKP135	8:64521911-64522158	NOTEST	0	0	0	0	1	1
ENSG00000252359	ENSG00000252359	SNORD112	1:165041709-165041781	NOTEST	0	0	0	0	1	1
ENSG00000252361	ENSG00000252361	RNU6-118P	11:62574368-62599560	NOTEST	0	0	0	0	1	1
ENSG00000252362	ENSG00000252362	RNU6-506P	4:140152179-140152273	NOTEST	0	0	0	0	1	1
ENSG00000252363	ENSG00000252363	RNU7-43P	17:8316448-8534079	NOTEST	0	0	0	0	1	1
ENSG00000252364	ENSG00000252364	RNA5SP360	12:42052477-42052595	NOTEST	0	0	0	0	1	1
ENSG00000252365	ENSG00000252365	SNORD22	13:93879094-95059655	NOTEST	0	0	0	0	1	1
ENSG00000252366	ENSG00000252366	RNA5SP367	12:101866116-101866234	NOTEST	0	0	0	0	1	1
ENSG00000252367	ENSG00000252367	Y_RNA	20:5094638-5094729	NOTEST	0	0	0	0	1	1
ENSG00000252368	ENSG00000252368	RNA5SP43	1:37728339-37790701	NOTEST	0	0	0	0	1	1
ENSG00000252369	ENSG00000252369	RNU7-51P	14:83514922-83514984	NOTEST	0	0	0	0	1	1
ENSG00000252370	ENSG00000252370	RNA5SP438	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000252371	ENSG00000252371	RNU6-725P	1:238488986-238489088	NOTEST	0	0	0	0	1	1
ENSG00000252372	ENSG00000252372	SNORD112	15:76109432-76109504	NOTEST	0	0	0	0	1	1
ENSG00000252373	ENSG00000252373	RNU6-358P	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000252374	ENSG00000252374	Y_RNA	7:14050293-14050388	NOTEST	0	0	0	0	1	1
ENSG00000252375	ENSG00000252375	AC099339.1	4:153701088-153839615	NOTEST	0	0	0	0	1	1
ENSG00000252376	ENSG00000252376	RNA5SP395	15:50716576-50838905	NOTEST	0	0	0	0	1	1
ENSG00000252377	ENSG00000252377	RNU6-504P	X:51546102-51645453	NOTEST	0	0	0	0	1	1
ENSG00000252378	ENSG00000252378	AC004851.1	7:73868119-74016931	NOTEST	0	0	0	0	1	1
ENSG00000252379	ENSG00000252379	RNU6-1002P	18:29202209-29266786	NOTEST	0	0	0	0	1	1
ENSG00000252380	ENSG00000252380	SNORD112	14:61654276-62125414	NOTEST	0	0	0	0	1	1
ENSG00000252382	ENSG00000252382	AC108865.1	4:187778528-187778610	NOTEST	0	0	0	0	1	1
ENSG00000252383	ENSG00000252383	RNU6-314P	17:15879873-16256970	NOTEST	0	0	0	0	1	1
ENSG00000252385	ENSG00000252385	RNU6-68P	13:46916138-47012325	NOTEST	0	0	0	0	1	1
ENSG00000252386	ENSG00000252386	RNU6-1018P	20:40313624-40313730	NOTEST	0	0	0	0	1	1
ENSG00000252387	ENSG00000252387	snoU13	5:170288873-170727019	NOTEST	0	0	0	0	1	1
ENSG00000252388	ENSG00000252388	snoU13	4:178649910-178911904	NOTEST	0	0	0	0	1	1
ENSG00000252390	ENSG00000252390	RNU5F-4P	12:31535156-31768600	NOTEST	0	0	0	0	1	1
ENSG00000252391	ENSG00000252391	RNU6-638P	17:76670129-76778379	NOTEST	0	0	0	0	1	1
ENSG00000252392	ENSG00000252392	SNORD112	GL000192.1:107277-107339	NOTEST	0	0	0	0	1	1
ENSG00000252393	ENSG00000252393	RNU6-1004P	12:122042806-122042917	NOTEST	0	0	0	0	1	1
ENSG00000252394	ENSG00000252394	RNU6-691P	1:247670359-247910364	NOTEST	0	0	0	0	1	1
ENSG00000252395	ENSG00000252395	RNU6-1007P	2:88714416-88714523	NOTEST	0	0	0	0	1	1
ENSG00000252396	ENSG00000252396	RN7SKP195	1:237205504-237997288	NOTEST	0	0	0	0	1	1
ENSG00000252397	ENSG00000252397	RNU5A-4P	13:34392185-34540695	NOTEST	0	0	0	0	1	1
ENSG00000252398	ENSG00000252398	Y_RNA	3:31699381-32119072	NOTEST	0	0	0	0	1	1
ENSG00000252399	ENSG00000252399	RNU6-1259P	6:26353198-26353264	NOTEST	0	0	0	0	1	1
ENSG00000252400	ENSG00000252400	RNU6-1291P	14:51921229-52197445	NOTEST	0	0	0	0	1	1
ENSG00000252401	ENSG00000252401	RNU4ATAC6P	10:28941558-28941684	NOTEST	0	0	0	0	1	1
ENSG00000252402	ENSG00000252402	snoU13	22:21765338-21765415	NOTEST	0	0	0	0	1	1
ENSG00000252403	ENSG00000252403	RNY4P11	20:18303195-18339944	NOTEST	0	0	0	0	1	1
ENSG00000252404	ENSG00000252404	SCARNA16	1:9095165-9148537	NOTEST	0	0	0	0	1	1
ENSG00000252405	ENSG00000252405	snoMe28SAm2634	16:5289802-7763340	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000252406	ENSG00000252406	RNU7-36P	9:33921690-34048947	NOTEST	0	0	0	0	1	1
ENSG00000252407	ENSG00000252407	RNU7-183P	1:185403375-185403437	NOTEST	0	0	0	0	1	1
ENSG00000252408	ENSG00000252408	SNORD38	19:3506270-3579086	NOTEST	0	0	0	0	1	1
ENSG00000252409	ENSG00000252409	SCARNA21	3:41236327-42003922	NOTEST	0	0.612338	inf	0	1	1
ENSG00000252410	ENSG00000252410	RNU5B-3P	3:44956748-45077563	NOTEST	0	0	0	0	1	1
ENSG00000252411	ENSG00000252411	RNU6-1087P	X:35612289-35612390	NOTEST	0	0	0	0	1	1
ENSG00000252412	ENSG00000252412	Y_RNA	22:37406899-37425863	NOTEST	0	0	0	0	1	1
ENSG00000252413	ENSG00000252413	RNU7-121P	1:40157853-40254533	NOTEST	0	0	0	0	1	1
ENSG00000252414	ENSG00000252414	RNU6-100P	2:64751464-64820139	NOTEST	0	0	0	0	1	1
ENSG00000252415	ENSG00000252415	RNU6-1012P	12:74072967-74073076	NOTEST	0	0	0	0	1	1
ENSG00000252416	ENSG00000252416	RNU6-885P	10:43278248-43330385	NOTEST	0	0	0	0	1	1
ENSG00000252417	ENSG00000252417	RNU7-179P	1:15934572-15934640	NOTEST	0	0	0	0	1	1
ENSG00000252418	ENSG00000252418	RNU6-779P	11:59266464-59266539	NOTEST	0	0	0	0	1	1
ENSG00000252420	ENSG00000252420	Y_RNA	3:61547242-62355005	NOTEST	0	0	0	0	1	1
ENSG00000252421	ENSG00000252421	RNU6-1069P	12:31955891-31956024	NOTEST	0	0	0	0	1	1
ENSG00000252422	ENSG00000252422	RNA5SP476	20:18364010-18465287	NOTEST	0	0	0	0	1	1
ENSG00000252423	ENSG00000252423	RNU6-229P	7:68689682-68895909	NOTEST	0	0	0	0	1	1
ENSG00000252424	ENSG00000252424	RNA5SP384	14:50019350-50019466	NOTEST	0	0	0	0	1	1
ENSG00000252425	ENSG00000252425	SNORA18	15:34889658-34889759	NOTEST	0	0	0	0	1	1
ENSG00000252426	ENSG00000252426	RNU1-107P	Y:27869162-27870333	NOTEST	0	0	0	0	1	1
ENSG00000252427	ENSG00000252427	SNORD67	11:46764597-46867847	NOTEST	0	0	0	0	1	1
ENSG00000252428	ENSG00000252428	RNA5SP285	9:74914635-74914754	NOTEST	0	0	0	0	1	1
ENSG00000252429	ENSG00000252429	RNU7-29P	1:28470666-28470728	NOTEST	0	0	0	0	1	1
ENSG00000252430	ENSG00000252430	AL109750.1	X:98640192-98640274	NOTEST	0	0	0	0	1	1
ENSG00000252431	ENSG00000252431	RNU6-1247P	6:151561133-151679692	NOTEST	0	0	0	0	1	1
ENSG00000252432	ENSG00000252432	AP001032.1	18:5661943-5662049	NOTEST	0	0	0	0	1	1
ENSG00000252433	ENSG00000252433	SNORA31	1:67557847-67725662	NOTEST	0	0	0	0	1	1
ENSG00000252434	ENSG00000252434	SNORD112	20:39045514-39045586	NOTEST	0	0	0	0	1	1
ENSG00000252435	ENSG00000252435	snoU13	3:128792138-128792241	NOTEST	0	0	0	0	1	1
ENSG00000252436	ENSG00000252436	Y_RNA	2:62900985-63275775	NOTEST	0	0	0	0	1	1
ENSG00000252437	ENSG00000252437	RNA5SP459	18:52813776-52813876	NOTEST	0	0	0	0	1	1
ENSG00000252438	ENSG00000252438	SNORD45	10:12391480-12877545	NOTEST	0	0	0	0	1	1
ENSG00000252439	ENSG00000252439	AC007241.1	Y:20442063-20446647	NOTEST	0	0	0	0	1	1
ENSG00000252440	ENSG00000252440	U3	9:139496966-139497062	NOTEST	0	0	0	0	1	1
ENSG00000252441	ENSG00000252441	SNORA64	X:114752489-114885181	NOTEST	0	0	0	0	1	1
ENSG00000252442	ENSG00000252442	RNY4P22	3:20234273-20234366	NOTEST	0	0	0	0	1	1
ENSG00000252443	ENSG00000252443	SNORA62	16:69796208-69975644	NOTEST	0	0	0	0	1	1
ENSG00000252444	ENSG00000252444	RNU6-344P	6:106632350-106773666	NOTEST	0	0	0	0	1	1
ENSG00000252445	ENSG00000252445	AC007535.1	12:13679787-14133053	NOTEST	0	0	0	0	1	1
ENSG00000252446	ENSG00000252446	RNU6-405P	17:16592850-16719854	NOTEST	0	0	0	0	1	1
ENSG00000252447	ENSG00000252447	snoU13	11:47738071-47788995	NOTEST	0	0	0	0	1	1
ENSG00000252448	ENSG00000252448	SNORA63	1:38326368-38412729	NOTEST	0	0	0	0	1	1
ENSG00000252449	ENSG00000252449	RNU6-139P	3:62384021-62861054	NOTEST	0	0	0	0	1	1
ENSG00000252450	ENSG00000252450	Y_RNA	1:32752052-32752162	NOTEST	0	0	0	0	1	1
ENSG00000252451	ENSG00000252451	RNA5SP168	4:151185593-151936879	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000252452	ENSG00000252452	RNU6-107P	2:233562008-233880595	NOTEST	0	0	0	0	1	1
ENSG00000252453	ENSG00000252453	AC015971.1	2:86730553-87005164	NOTEST	0	0	0	0	1	1
ENSG00000252454	ENSG00000252454	MIR2114	X:149396238-149396318	NOTEST	0	0	0	0	1	1
ENSG00000252455	ENSG00000252455	AC007179.2	2:59444842-60327335	NOTEST	0	0	0	0	1	1
ENSG00000252456	ENSG00000252456	RNA5SP434	17:3907738-4046314	NOTEST	0	0	0	0	1	1
ENSG00000252457	ENSG00000252457	RNU7-65P	6:49312459-49312521	NOTEST	0	0	0	0	1	1
ENSG00000252458	ENSG00000252458	SNORA68	5:158584416-158675804	NOTEST	0	0	0	0	1	1
ENSG00000252459	ENSG00000252459	SNORA27	12:115151615-115205762	NOTEST	0	0	0	0	1	1
ENSG00000252460	ENSG00000252460	RNU6-635P	4:104845696-104845798	NOTEST	0	0	0	0	1	1
ENSG00000252461	ENSG00000252461	SNORA43	16:28889725-28950667	NOTEST	0	0	0	0	1	1
ENSG00000252462	ENSG00000252462	RNU6-113P	21:18803864-18803965	NOTEST	0	0	0	0	1	1
ENSG00000252463	ENSG00000252463	RNU6-852P	14:63838074-64010092	NOTEST	0	0	0	0	1	1
ENSG00000252465	ENSG00000252465	RMRPP3	2:161128661-161350305	NOTEST	0	0	0	0	1	1
ENSG00000252466	ENSG00000252466	MIR2115	3:48348335-48369831	NOTEST	0	0	0	0	1	1
ENSG00000252467	ENSG00000252467	RNU6-347P	20:50518829-50518934	NOTEST	0	0	0	0	1	1
ENSG00000252468	ENSG00000252468	RNU2-57P	Y:4868266-5610265	NOTEST	0	0	0	0	1	1
ENSG00000252469	ENSG00000252469	RNU7-160P	14:104016681-104016743	NOTEST	0	0	0	0	1	1
ENSG00000252470	ENSG00000252470	RNU6-551P	4:108356274-108356377	NOTEST	0	0	0	0	1	1
ENSG00000252471	ENSG00000252471	AC006328.1	Y:27600707-27606719	NOTEST	0	0	0	0	1	1
ENSG00000252472	ENSG00000252472	RNU6-521P	Y:7291094-7291199	NOTEST	0	0	0	0	1	1
ENSG00000252473	ENSG00000252473	SNORA67	2:39476406-39945103	NOTEST	0	0	0	0	1	1
ENSG00000252474	ENSG00000252474	RNU6-539P	14:50249996-50319921	NOTEST	0	0	0	0	1	1
ENSG00000252475	ENSG00000252475	RNU6-1332P	15:45248899-45271427	NOTEST	0	0	0	0	1	1
ENSG00000252476	ENSG00000252476	SNORD112	6:137861536-137861608	NOTEST	0	0	0	0	1	1
ENSG00000252477	ENSG00000252477	RNU6-134P	15:98569270-98569368	NOTEST	0	0	0	0	1	1
ENSG00000252478	ENSG00000252478	RNU7-162P	2:85569210-85618875	NOTEST	0	0	0	0	1	1
ENSG00000252479	ENSG00000252479	RNA5SP309	10:31476811-31818742	NOTEST	0	0	0	0	1	1
ENSG00000252480	ENSG00000252480	RNU6-719P	7:39773230-39832691	NOTEST	0	0	0	0	1	1
ENSG00000252482	ENSG00000252482	RNU7-22P	10:32462611-32462672	NOTEST	0	0	0	0	1	1
ENSG00000252483	ENSG00000252483	RNU6-1178P	17:20717932-20947073	NOTEST	0	0	0	0	1	1
ENSG00000252484	ENSG00000252484	RN7SKP49	1:224294983-224295243	NOTEST	0	0	0	0	1	1
ENSG00000252485	ENSG00000252485	Vault	2:206854308-206951288	NOTEST	0	0	0	0	1	1
ENSG00000252486	ENSG00000252486	Y_RNA	X:27061023-27417114	NOTEST	0	0	0	0	1	1
ENSG00000252487	ENSG00000252487	RNY4P20	6:151561133-151679692	NOTEST	0	0	0	0	1	1
ENSG00000252489	ENSG00000252489	RNU6-197P	4:57036360-57194791	NOTEST	0	0	0	0	1	1
ENSG00000252490	ENSG00000252490	RN7SKP66	2:43999258-43999489	NOTEST	0	0	0	0	1	1
ENSG00000252491	ENSG00000252491	RNU1-142P	X:26808258-26808403	NOTEST	0	0	0	0	1	1
ENSG00000252494	ENSG00000252494	RNU6-126P	11:77811981-77850706	NOTEST	0	0	0	0	1	1
ENSG00000252495	ENSG00000252495	SNORD112	1:246935138-246993361	NOTEST	0	0	0	0	1	1
ENSG00000252496	ENSG00000252496	RNA5SP33	13:79885961-79998463	NOTEST	0	0	0	0	1	1
ENSG00000252497	ENSG00000252497	RPPH1-2P	14:65376205-65376498	NOTEST	0	0	0	0	1	1
ENSG00000252498	ENSG00000252498	RNU6-1016P	6:76311224-76427997	NOTEST	0	0	0	0	1	1
ENSG00000252499	ENSG00000252499	RNU6-63P	13:28062274-28062369	NOTEST	0	0	0	0	1	1
ENSG00000252500	ENSG00000252500	AC087433.1	15:47249730-47249815	NOTEST	0	0	0	0	1	1
ENSG00000252501	ENSG00000252501	RNU4-77P	1:233584371-233584527	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000252502	ENSG00000252502	SNORD112	2:33172038-33624576	NOTEST	0	0	0	0	1	1
ENSG00000252503	ENSG00000252503	RNU6-531P	4:139936942-140098372	NOTEST	0	0	0	0	1	1
ENSG00000252504	ENSG00000252504	AC097015.1	3:53243968-53244062	NOTEST	0	0	0	0	1	1
ENSG00000252505	ENSG00000252505	SNORA70	8:33397557-33397655	NOTEST	0	0	0	0	1	1
ENSG00000252506	ENSG00000252506	RNU6-180P	1:229518874-229518935	NOTEST	0	0	0	0	1	1
ENSG00000252507	ENSG00000252507	RNU7-81P	2:54950635-55199157	NOTEST	0	0	0	0	1	1
ENSG00000252508	ENSG00000252508	RNU4ATAC3P	13:92050928-93519490	NOTEST	0	0	0	0	1	1
ENSG00000252509	ENSG00000252509	RNA5SP271	8:73269962-73270050	NOTEST	0	0	0	0	1	1
ENSG00000252510	ENSG00000252510	RNA5SP55	1:117452678-117532980	NOTEST	0	0	0	0	1	1
ENSG00000252511	ENSG00000252511	AC019330.2	2:199164086-199637080	NOTEST	0	0	0	0	1	1
ENSG00000252512	ENSG00000252512	RNA5SP206	6:32006041-32096030	NOTEST	0	0	0	0	1	1
ENSG00000252513	ENSG00000252513	RNU1-128P	Y:19900194-19901364	NOTEST	0	0	0	0	1	1
ENSG00000252514	ENSG00000252514	RNU7-53P	5:129722313-129722373	NOTEST	0	0	0	0	1	1
ENSG00000252515	ENSG00000252515	RNU6-1171P	1:25568727-25756683	NOTEST	0	0	0	0	1	1
ENSG00000252516	ENSG00000252516	RNA5SP82	1:247353152-247405125	NOTEST	0	0	0	0	1	1
ENSG00000252517	ENSG00000252517	SNORD59	2:195528830-195528898	NOTEST	0	0	0	0	1	1
ENSG00000252518	ENSG00000252518	RNU6-846P	2:37070782-37193615	NOTEST	0	0	0	0	1	1
ENSG00000252519	ENSG00000252519	RNU6-783P	11:23871323-23871428	NOTEST	0	0	0	0	1	1
ENSG00000252521	ENSG00000252521	RNU5D-2P	9:135285429-135448704	NOTEST	0	0	0	0	1	1
ENSG00000252522	ENSG00000252522	Y_RNA	14:89591214-90421121	NOTEST	0	0	0	0	1	1
ENSG00000252523	ENSG00000252523	RNU6-267P	7:143318042-143534026	NOTEST	0	0	0	0	1	1
ENSG00000252524	ENSG00000252524	Y_RNA	4:157985708-157985815	NOTEST	0	0	0	0	1	1
ENSG00000252525	ENSG00000252525	snoU13	X:70586113-70752224	NOTEST	0	0	0	0	1	1
ENSG00000252526	ENSG00000252526	SNORA70	16:50185552-50185642	NOTEST	0	0	0	0	1	1
ENSG00000252529	ENSG00000252529	RNU3P3	14:85738275-85738405	NOTEST	0	0	0	0	1	1
ENSG00000252530	ENSG00000252530	RNU6-965P	1:102189297-102195170	NOTEST	0	0	0	0	1	1
ENSG00000252532	ENSG00000252532	RNU7-193P	10:43932281-43991517	NOTEST	0	0	0	0	1	1
ENSG00000252533	ENSG00000252533	RNU6-572P	5:138282408-138667360	NOTEST	0	0	0	0	1	1
ENSG00000252534	ENSG00000252534	Y_RNA	17:58754813-59488916	NOTEST	0	0	0	0	1	1
ENSG00000252535	ENSG00000252535	RNA5SP254	8:12191152-12191202	NOTEST	0	0	0	0	1	1
ENSG00000252536	ENSG00000252536	U3	20:55182732-55182849	NOTEST	0	0	0	0	1	1
ENSG00000252537	ENSG00000252537	SNORA31	10:16047806-16047922	NOTEST	0	0	0	0	1	1
ENSG00000252538	ENSG00000252538	RNU6-1070P	7:73672855-73672946	NOTEST	0	0	0	0	1	1
ENSG00000252539	ENSG00000252539	RNA5SP462	19:416582-460996	NOTEST	0	0	0	0	1	1
ENSG00000252540	ENSG00000252540	RNU6-919P	20:48411347-48411451	NOTEST	0	0	0	0	1	1
ENSG00000252541	ENSG00000252541	AC092905.1	3:109216491-109216576	NOTEST	0	0	0	0	1	1
ENSG00000252542	ENSG00000252542	SNORD36C	9:136215068-136218281	NOTEST	0	0	0	0	1	1
ENSG00000252543	ENSG00000252543	U3	8:8859656-8974256	NOTEST	0	0	0	0	1	1
ENSG00000252544	ENSG00000252544	RNU6-1282P	4:152020724-152246784	NOTEST	0	0	0	0	1	1
ENSG00000252545	ENSG00000252545	RNU6-362P	17:73027191-73027281	NOTEST	0	0	0	0	1	1
ENSG00000252546	ENSG00000252546	RNA5SP466	19:12175513-12192380	NOTEST	0	0	0	0	1	1
ENSG00000252547	ENSG00000252547	AC139931.1	12:69511347-69511432	NOTEST	0	0	0	0	1	1
ENSG00000252548	ENSG00000252548	RNU7-149P	4:99792834-99916145	NOTEST	0	0	0	0	1	1
ENSG00000252549	ENSG00000252549	RNU6-759P	20:34213952-34288906	NOTEST	0	0	0	0	1	1
ENSG00000252550	ENSG00000252550	SNORA25	13:106549871-106549992	NOTEST	0	0	0	0	1	1

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ENSG00000252553	ENSG00000252553	RNA5SP73	1:189635278-189635386	NOTEST	0	0	0	0	1	1
ENSG00000252554	ENSG00000252554	RNU6-861P	6:129204341-129837714	NOTEST	0	0	0	0	1	1
ENSG00000252555	ENSG00000252555	RNU6-567P	18:57685856-57685963	NOTEST	0	0	0	0	1	1
ENSG00000252556	ENSG00000252556	RNU6-256P	11:121875062-121875159	NOTEST	0	0	0	0	1	1
ENSG00000252557	ENSG00000252557	SNORD112	7:148959261-148994403	NOTEST	0	0	0	0	1	1
ENSG00000252558	ENSG00000252558	RNU6-914P	8:99202060-99306621	NOTEST	62.203	0	#NAME?	0	1	1
ENSG00000252559	ENSG00000252559	SNORD112	8:110586206-110704020	NOTEST	0	0	0	0	1	1
ENSG00000252560	ENSG00000252560	RNU4-18P	6:131949581-132068553	NOTEST	0	0	0	0	1	1
ENSG00000252561	ENSG00000252561	RNU1-125P	16:3115297-3137101	NOTEST	0	0	0	0	1	1
ENSG00000252562	ENSG00000252562	RNU6-922P	3:23655151-23655250	NOTEST	0	0	0	0	1	1
ENSG00000252563	ENSG00000252563	RNA5SP45	1:41932607-41932699	NOTEST	0	0	0	0	1	1
ENSG00000252565	ENSG00000252565	SNORD112	8:10581277-10697394	NOTEST	0	0	0	0	1	1
ENSG00000252566	ENSG00000252566	SNORD112	4:107842958-108223027	NOTEST	0	0	0	0	1	1
ENSG00000252568	ENSG00000252568	RNU7-28P	11:9776316-10315754	NOTEST	0	0	0	0	1	1
ENSG00000252569	ENSG00000252569	RNU6-1153P	16:53467888-53538323	NOTEST	0	0	0	0	1	1
ENSG00000252571	ENSG00000252571	SCARNA17	22:20455221-20455364	NOTEST	0	0	0	0	1	1
ENSG00000252572	ENSG00000252572	SNORD112	18:5392382-5630699	NOTEST	0	0	0	0	1	1
ENSG00000252574	ENSG00000252574	RNU5B-6P	10:110944650-110944765	NOTEST	0	0	0	0	1	1
ENSG00000252575	ENSG00000252575	BX470187.1	22:36834868-36834971	NOTEST	0	0	0	0	1	1
ENSG00000252576	ENSG00000252576	snR65	18:5392382-5630699	NOTEST	0	0	0	0	1	1
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ENSG00000252578	ENSG00000252578	RNU6-135P	1:23345940-23504301	NOTEST	0	0	0	0	1	1
ENSG00000252579	ENSG00000252579	RNU7-117P	16:89557324-89624176	NOTEST	0	0	0	0	1	1
ENSG00000252580	ENSG00000252580	SNORA31	9:26796170-26796302	NOTEST	0	0	0	0	1	1
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ENSG00000252582	ENSG00000252582	SNORA31	9:133884468-133969860	NOTEST	0	0	0	0	1	1
ENSG00000252583	ENSG00000252583	MIR514B	X:146331668-146331748	NOTEST	0	0	0	0	1	1
ENSG00000252584	ENSG00000252584	AC023050.1	12:32068569-32068641	NOTEST	0	0	0	0	1	1
ENSG00000252585	ENSG00000252585	Y_RNA	12:27863705-27909228	NOTEST	0	0	0	0	1	1
ENSG00000252586	ENSG00000252586	AC002992.1	Y:14474826-14532255	NOTEST	0	0	0	0	1	1
ENSG00000252587	ENSG00000252587	RNA5SP422	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000252590	ENSG00000252590	RNU7-143P	7:23338357-23510086	NOTEST	0	0	0	0	1	1
ENSG00000252591	ENSG00000252591	RNA5SP468	19:18062101-18110889	NOTEST	0	0	0	0	1	1
ENSG00000252592	ENSG00000252592	SNORD112	11:81590892-82429124	NOTEST	0	0	0	0	1	1
ENSG00000252593	ENSG00000252593	RNU6-1224P	8:103540967-103550896	NOTEST	0	0	0	0	1	1
ENSG00000252594	ENSG00000252594	RNU6-656P	8:47733858-47765929	NOTEST	0	0	0	0	1	1
ENSG00000252595	ENSG00000252595	RN7SKP82	4:42894412-42894635	NOTEST	0	0	0	0	1	1
ENSG00000252596	ENSG00000252596	U6	GL000211.1:113981-114087	NOTEST	0	0	0	0	1	1
ENSG00000252597	ENSG00000252597	RNU7-137P	20:18076214-18076276	NOTEST	0	0	0	0	1	1
ENSG00000252598	ENSG00000252598	RNA5SP460	18:70409548-70535381	NOTEST	0	0	0	0	1	1
ENSG00000252599	ENSG00000252599	RNU6-566P	2:44381927-44382034	NOTEST	0	0	0	0	1	1
ENSG00000252601	ENSG00000252601	SNORA18	5:29070602-29070717	NOTEST	0	0	0	0	1	1
ENSG00000252602	ENSG00000252602	U8	15:30909160-31065196	NOTEST	0	0	0	0	1	1
ENSG00000252603	ENSG00000252603	RNU6ATAC22P	22:42095502-42195460	NOTEST	0	0	0	0	1	1

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ENSG00000252605	ENSG00000252605	SCARNA18	22:21899413-21899496	NOTEST	0	0	0	0	1	1
ENSG00000252606	ENSG00000252606	RNU6-1150P	21:45416202-45416301	NOTEST	0	0	0	0	1	1
ENSG00000252607	ENSG00000252607	Y_RNA	12:60735604-60735722	NOTEST	0	0	0	0	1	1
ENSG00000252608	ENSG00000252608	RNU6-1191P	16:81134479-81253975	NOTEST	0	0	0	0	1	1
ENSG00000252609	ENSG00000252609	snoU13	6:157710417-157744633	NOTEST	0	0	0	0	1	1
ENSG00000252611	ENSG00000252611	RNU6-1121P	10:116697951-116737430	NOTEST	0	0	0	0	1	1
ENSG00000252612	ENSG00000252612	Y_RNA	1:185126211-185260897	NOTEST	0	0	0	0	1	1
ENSG00000252613	ENSG00000252613	RNU7-168P	21:18824998-18825052	NOTEST	0	0	0	0	1	1
ENSG00000252614	ENSG00000252614	RNU6-807P	15:102161846-102192594	NOTEST	0	0	0	0	1	1
ENSG00000252615	ENSG00000252615	Y_RNA	6:151685251-151712683	NOTEST	0	0	0	0	1	1
ENSG00000252616	ENSG00000252616	AC079140.1	4:206398-249774	NOTEST	0	0	0	0	1	1
ENSG00000252617	ENSG00000252617	SNORA70	9:46042780-46042875	NOTEST	0	0	0	0	1	1
ENSG00000252618	ENSG00000252618	RNA5SP441	17:38530340-38530428	NOTEST	0	0	0	0	1	1
ENSG00000252619	ENSG00000252619	RNU6-1149P	21:43824007-43867791	NOTEST	0	0	0	0	1	1
ENSG00000252620	ENSG00000252620	RNU6ATAC24P	3:195241220-195270209	NOTEST	0	0	0	0	1	1
ENSG00000252621	ENSG00000252621	Y_RNA	10:37414784-37673039	NOTEST	0	0	0	0	1	1
ENSG00000252622	ENSG00000252622	RNU6-881P	9:134000947-134110057	NOTEST	0	0	0	0	1	1
ENSG00000252623	ENSG00000252623	RNA5SP481	20:30596153-30596275	NOTEST	0	0	0	0	1	1
ENSG00000252624	ENSG00000252624	RNA5SP409	16:34969995-34970104	NOTEST	0	0	0	0	1	1
ENSG00000252625	ENSG00000252625	RNU1-40P	Y:28069534-28075973	NOTEST	0	0	0	0	1	1
ENSG00000252626	ENSG00000252626	RNU6-1308P	3:106555657-106959488	NOTEST	0	0	0	0	1	1
ENSG00000252627	ENSG00000252627	RNU6-122P	X:122993573-123047829	NOTEST	0	0	0	0	1	1
ENSG00000252628	ENSG00000252628	RNU6-453P	17:42376941-42396039	NOTEST	0	0	0	0	1	1
ENSG00000252629	ENSG00000252629	AL050316.1	20:51588945-52120853	NOTEST	0	0	0	0	1	1
ENSG00000252633	ENSG00000252633	RN7SKP282	Y:7142012-7249589	NOTEST	0	0	0	0	1	1
ENSG00000252634	ENSG00000252634	RN7SKP219	10:22045465-22292698	NOTEST	0	0	0	0	1	1
ENSG00000252635	ENSG00000252635	RNU2-56P	20:18246333-18246523	NOTEST	0	0	0	0	1	1
ENSG00000252636	ENSG00000252636	RNU6-826P	17:47072627-47133012	NOTEST	0	0	0	0	1	1
ENSG00000252637	ENSG00000252637	RNA5SP268	8:67876333-68255912	NOTEST	0	0	0	0	1	1
ENSG00000252638	ENSG00000252638	snoU13	1:236464279-236464351	NOTEST	0	0	0	0	1	1
ENSG00000252639	ENSG00000252639	RNU2-24P	10:27482286-27482429	NOTEST	0	0	0	0	1	1
ENSG00000252640	ENSG00000252640	snoU109	16:68664753-68864871	NOTEST	0	0	0	0	1	1
ENSG00000252641	ENSG00000252641	RNU6-678P	3:133380841-133497850	NOTEST	0	0	0	0	1	1
ENSG00000252642	ENSG00000252642	RNA5SP137	3:124777147-124777282	NOTEST	0	0	0	0	1	1
ENSG00000252643	ENSG00000252643	RNU6-1136P	7:102453307-102715286	NOTEST	0	0	0	0	1	1
ENSG00000252644	ENSG00000252644	RNU7-30P	14:91336798-91691976	NOTEST	0	0	0	0	1	1
ENSG00000252645	ENSG00000252645	RNU7-111P	15:90373830-90456188	NOTEST	0	0	0	0	1	1
ENSG00000252646	ENSG00000252646	SNORD112	1:54991058-54991126	NOTEST	0	0	0	0	1	1
ENSG00000252647	ENSG00000252647	RNA5SP416	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000252648	ENSG00000252648	AC078993.1	X:16316512-16316597	NOTEST	0	0	0	0	1	1
ENSG00000252649	ENSG00000252649	RNA5SP480	20:29944672-29944781	NOTEST	0	0	0	0	1	1
ENSG00000252650	ENSG00000252650	RNA5SP75	1:204676447-204676558	NOTEST	0	0	0	0	1	1
ENSG00000252651	ENSG00000252651	RNU6-557P	3:73141298-73141408	NOTEST	0	0	0	0	1	1
ENSG00000252652	ENSG00000252652	Y_RNA	11:43333512-43516483	NOTEST	0	0	0	0	1	1

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ENSG00000252654	ENSG00000252654	RNU7-6P	20:50521507-50521569	NOTEST	0	0	0	0	1	1
ENSG00000252655	ENSG00000252655	Y_RNA	14:89591214-90421121	NOTEST	0	0	0	0	1	1
ENSG00000252656	ENSG00000252656	RN7SKP88	1:144836156-145076186	NOTEST	0	0	0	0	1	1
ENSG00000252657	ENSG00000252657	SNORA70	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000252658	ENSG00000252658	RNU6-786P	6:158244295-158366109	NOTEST	0	0	0	0	1	1
ENSG00000252659	ENSG00000252659	RNU6-1088P	12:120740118-120751144	NOTEST	0	0	0	0	1	1
ENSG00000252660	ENSG00000252660	Y_RNA	12:63329480-63329582	NOTEST	0	0	0	0	1	1
ENSG00000252661	ENSG00000252661	RNU6-782P	19:15256025-15256129	NOTEST	0	0	0	0	1	1
ENSG00000252662	ENSG00000252662	AC099545.1	3:63213990-63602597	NOTEST	0	0	0	0	1	1
ENSG00000252663	ENSG00000252663	RN7SKP201	8:36124002-36124282	NOTEST	0	0	0	0	1	1
ENSG00000252664	ENSG00000252664	AC017020.1	Y:18174645-18174709	NOTEST	0	0	0	0	1	1
ENSG00000252667	ENSG00000252667	RNA5SP523	Y:20488138-20515096	NOTEST	0	0	0	0	1	1
ENSG00000252668	ENSG00000252668	snoU13	6:4021500-4157619	NOTEST	0	0	0	0	1	1
ENSG00000252669	ENSG00000252669	U3	1:153965160-154127592	NOTEST	0	0	0	0	1	1
ENSG00000252670	ENSG00000252670	Y_RNA	16:69796208-69975644	NOTEST	0	0	0	0	1	1
ENSG00000252671	ENSG00000252671	Y_RNA	5:10337388-10337498	NOTEST	0	0	0	0	1	1
ENSG00000252672	ENSG00000252672	snoZ185	7:115850546-116148595	NOTEST	0	0	0	0	1	1
ENSG00000252673	ENSG00000252673	RNA5SP421	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000252674	ENSG00000252674	RNA5SP102	2:125690491-125690597	NOTEST	0	0	0	0	1	1
ENSG00000252675	ENSG00000252675	RNU6-52P	13:19717121-19717217	NOTEST	0	0	0	0	1	1
ENSG00000252676	ENSG00000252676	AL391559.1	6:91156490-91156565	NOTEST	0	0	0	0	1	1
ENSG00000252677	ENSG00000252677	SNORA81	18:19284917-19450918	NOTEST	0	0	0	0	1	1
ENSG00000252679	ENSG00000252679	snoU13	11:101918173-101955291	NOTEST	0	0	0	0	1	1
ENSG00000252680	ENSG00000252680	RNA5SP449	18:9708161-9862548	NOTEST	0	0	0	0	1	1
ENSG00000252681	ENSG00000252681	RNU1-97P	Y:25886404-25892840	NOTEST	0	0	0	0	1	1
ENSG00000252682	ENSG00000252682	SNORD59	1:154260935-154261003	NOTEST	0	0	0	0	1	1
ENSG00000252683	ENSG00000252683	U3	19:57645417-57656570	NOTEST	0	0	0	0	1	1
ENSG00000252684	ENSG00000252684	RNU6ATAC36P	5:76244615-76244695	NOTEST	0	0	0	0	1	1
ENSG00000252685	ENSG00000252685	RNU6-928P	17:64298753-64806861	NOTEST	0	0	0	0	1	1
ENSG00000252686	ENSG00000252686	RNU6-1234P	14:30045686-30766249	NOTEST	0	0	0	0	1	1
ENSG00000252687	ENSG00000252687	SNORD112	6:37151372-37151444	NOTEST	0	0	0	0	1	1
ENSG00000252688	ENSG00000252688	RNU6-579P	2:133429373-134326034	NOTEST	0	0	0	0	1	1
ENSG00000252689	ENSG00000252689	SNORA20	Y:18250127-18250259	NOTEST	0	0	0	0	1	1
ENSG00000252691	ENSG00000252691	SCARNA18	1:26332706-26332790	NOTEST	0	0	0	0	1	1
ENSG00000252692	ENSG00000252692	SNORD60	1:206238871-206306131	NOTEST	0	0	0	0	1	1
ENSG00000252693	ENSG00000252693	SNORA40	X:123093082-124097666	NOTEST	0	0	0	0	1	1
ENSG00000252694	ENSG00000252694	AC006371.1	Y:15779839-15779936	NOTEST	0	0	0	0	1	1
ENSG00000252695	ENSG00000252695	MIR2276	13:24553838-24896673	NOTEST	0	0	0	0	1	1
ENSG00000252696	ENSG00000252696	RNA5SP34	13:90787965-90788095	NOTEST	0	0	0	0	1	1
ENSG00000252697	ENSG00000252697	RN7SKP209	6:87792950-87793254	NOTEST	0	0	0	0	1	1
ENSG00000252698	ENSG00000252698	RNU7-101P	17:44107281-44302733	NOTEST	0	0	0	0	1	1
ENSG00000252699	ENSG00000252699	SNORA21	17:37004117-37010096	NOTEST	0	0	0	0	1	1
ENSG00000252700	ENSG00000252700	RNU7-110P	3:33318516-33482863	NOTEST	0	0	0	0	1	1
ENSG00000252702	ENSG00000252702	RNU7-158P	4:184020445-184241930	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000252703	ENSG00000252703	RNU6-1182P	11:132284870-133402414	NOTEST	0	0	0	0	1	1
ENSG00000252704	ENSG00000252704	RN7SKP277	7:121376496-121376779	NOTEST	0	0	0	0	1	1
ENSG00000252705	ENSG00000252705	RNU6-175P	2:133164324-133164431	NOTEST	0	0	0	0	1	1
ENSG00000252706	ENSG00000252706	snoU13	7:33155177-33155242	NOTEST	0	0	0	0	1	1
ENSG00000252707	ENSG00000252707	RNU11-2P	17:11901669-12047147	NOTEST	0	0	0	0	1	1
ENSG00000252709	ENSG00000252709	U3	11:66762949-66763096	NOTEST	0	0	0	0	1	1
ENSG00000252710	ENSG00000252710	RNU6-295P	8:49220486-49220590	NOTEST	0	0	0	0	1	1
ENSG00000252711	ENSG00000252711	RN7SKP116	6:47624171-47689757	NOTEST	0	0	0	0	1	1
ENSG00000252712	ENSG00000252712	SCARNA14	15:66628543-66679084	NOTEST	0	0	0	0	1	1
ENSG00000252713	ENSG00000252713	RNU6-1198P	7:72854727-72936608	NOTEST	0	0	0	0	1	1
ENSG00000252714	ENSG00000252714	RNA5SP392	15:40623652-40633168	NOTEST	0	0	0	0	1	1
ENSG00000252715	ENSG00000252715	RNU6-265P	15:65903703-66184329	NOTEST	0	0	0	0	1	1
ENSG00000252716	ENSG00000252716	RN7SKP260	2:207124789-207124938	NOTEST	0	0	0	0	1	1
ENSG00000252717	ENSG00000252717	RNU6-352P	1:102268129-102462586	NOTEST	0	0	0	0	1	1
ENSG00000252718	ENSG00000252718	RNU6-612P	2:60946774-60946876	NOTEST	0	0	0	0	1	1
ENSG00000252719	ENSG00000252719	SNORA18	X:138808504-139027435	NOTEST	0	0	0	0	1	1
ENSG00000252720	ENSG00000252720	RNU6-1258P	14:93799564-94174222	NOTEST	0	0	0	0	1	1
ENSG00000252721	ENSG00000252721	RNU6-798P	9:99918851-100140806	NOTEST	0	0	0	0	1	1
ENSG00000252722	ENSG00000252722	SCARNA20	15:75413876-75414007	NOTEST	0	0	0	0	1	1
ENSG00000252723	ENSG00000252723	RNU6-677P	9:97007970-97008041	NOTEST	0	0	0	0	1	1
ENSG00000252724	ENSG00000252724	SNORA70	9:42037463-42037558	NOTEST	0	0	0	0	1	1
ENSG00000252725	ENSG00000252725	RNU6-765P	9:38680002-38680101	NOTEST	0	0	0	0	1	1
ENSG00000252726	ENSG00000252726	RNA5SP94	2:59444842-60327335	NOTEST	0	0	0	0	1	1
ENSG00000252727	ENSG00000252727	SCARNA11	12:8750104-8750236	NOTEST	0	0	0	0	1	1
ENSG00000252728	ENSG00000252728	SNORD112	1:35409356-35409425	NOTEST	0	0	0	0	1	1
ENSG00000252729	ENSG00000252729	RNU6-971P	17:41550952-41551058	NOTEST	0	0	0	0	1	1
ENSG00000252730	ENSG00000252730	RN7SKP84	10:87318480-87318829	NOTEST	0	0	0	0	1	1
ENSG00000252731	ENSG00000252731	AL161793.1	1:204586297-204654861	NOTEST	0	0	0	0	1	1
ENSG00000252732	ENSG00000252732	Y_RNA	11:73375559-73375642	NOTEST	0	0	0	0	1	1
ENSG00000252733	ENSG00000252733	AC067718.1	3:189674516-189862635	NOTEST	0	0	0	0	1	1
ENSG00000252734	ENSG00000252734	RNU6-980P	19:54236234-54236337	NOTEST	0	0	0	0	1	1
ENSG00000252735	ENSG00000252735	RNU6-528P	8:33196384-33196484	NOTEST	0	0	0	0	1	1
ENSG00000252736	ENSG00000252736	Y_RNA	8:101975162-101975271	NOTEST	0	0	0	0	1	1
ENSG00000252738	ENSG00000252738	RNU6-515P	6:44777053-45632086	NOTEST	0	0	0	0	1	1
ENSG00000252739	ENSG00000252739	RNU7-151P	4:103715539-103790053	NOTEST	0	0	0	0	1	1
ENSG00000252740	ENSG00000252740	SNORD112	1:163355654-163355726	NOTEST	0	0	0	0	1	1
ENSG00000252742	ENSG00000252742	Y_RNA	2:129108402-129108501	NOTEST	0	0	0	0	1	1
ENSG00000252743	ENSG00000252743	RNU6-850P	6:31707724-31733365	NOTEST	0	0	0	0	1	1
ENSG00000252744	ENSG00000252744	Y_RNA	1:147801123-147816764	NOTEST	0	0	0	0	1	1
ENSG00000252745	ENSG00000252745	RNA5SP143	3:142310518-142310633	NOTEST	0	0	0	0	1	1
ENSG00000252746	ENSG00000252746	RNU6-273P	14:37656423-37656519	NOTEST	0	0	0	0	1	1
ENSG00000252747	ENSG00000252747	RNA5SP364	12:88373815-88535993	NOTEST	0	0	0	0	1	1
ENSG00000252748	ENSG00000252748	AL096869.1	14:91006931-91282823	NOTEST	0	0	0	0	1	1
ENSG00000252749	ENSG00000252749	RNU7-116P	14:64203161-64203223	NOTEST	0	0	0	0	1	1
ENSG00000252750	ENSG00000252750	RNU7-70P	1:113009162-113214241	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000252751	ENSG00000252751	RNU6-143P	3:123798869-124445172	NOTEST	0	0	0	0	1	1
ENSG00000252752	ENSG00000252752	RNU6-210P	1:93475813-93475908	NOTEST	0	0	0	0	1	1
ENSG00000252753	ENSG00000252753	RNU6-1202P	8:61297146-61429354	NOTEST	0	0	0	0	1	1
ENSG00000252754	ENSG00000252754	RNA5SP313	10:48187415-48237508	NOTEST	0	0	0	0	1	1
ENSG00000252755	ENSG00000252755	RNU6-703P	8:99061083-99061190	NOTEST	0	0	0	0	1	1
ENSG00000252756	ENSG00000252756	RNU6-577P	2:37070782-37193615	NOTEST	0	0	0	0	1	1
ENSG00000252757	ENSG00000252757	RN7SKP96	4:86936275-87515284	NOTEST	0	0	0	0	1	1
ENSG00000252758	ENSG00000252758	RNU6-445P	9:77337410-77503010	NOTEST	0	0	0	0	1	1
ENSG00000252759	ENSG00000252759	Y_RNA	2:201717731-201729422	NOTEST	0	0	0	0	1	1
ENSG00000252760	ENSG00000252760	RNA5SP54	1:111584455-111584547	NOTEST	0	0	0	0	1	1
ENSG00000252761	ENSG00000252761	Y_RNA	6:30900394-30900486	NOTEST	0	0	0	0	1	1
ENSG00000252762	ENSG00000252762	SNORA31	4:82347546-82965397	NOTEST	0	0	0	0	1	1
ENSG00000252763	ENSG00000252763	RNU2-31P	3:158680023-159615155	NOTEST	0	0	0	0	1	1
ENSG00000252764	ENSG00000252764	RNU6-1092P	8:101695715-101695802	NOTEST	0	0	0	0	1	1
ENSG00000252765	ENSG00000252765	SCARNA16	1:101598708-101598895	NOTEST	0	0	0	0	1	1
ENSG00000252766	ENSG00000252766	RNU6-255P	Y:21034386-21239302	NOTEST	0	0	0	0	1	1
ENSG00000252767	ENSG00000252767	RNU6-250P	6:40359324-40555204	NOTEST	0	0	0	0	1	1
ENSG00000252768	ENSG00000252768	RNU6-856P	3:52529353-52742182	NOTEST	0	0	0	0	1	1
ENSG00000252769	ENSG00000252769	RNU6-943P	11:7710668-7927502	NOTEST	0	0	0	0	1	1
ENSG00000252770	ENSG00000252770	RNU7-4P	12:69201955-69365350	NOTEST	0	0	0	0	1	1
ENSG00000252771	ENSG00000252771	snoU13	21:43024745-43024843	NOTEST	0	0	0	0	1	1
ENSG00000252772	ENSG00000252772	RNU6-714P	9:95571669-95661890	NOTEST	0	0	0	0	1	1
ENSG00000252774	ENSG00000252774	SNORA48	15:64457715-64679886	NOTEST	0	0.715903	inf	0	1	1
ENSG00000252776	ENSG00000252776	RNU4ATAC10P	11:122319917-122320039	NOTEST	0	0	0	0	1	1
ENSG00000252777	ENSG00000252777	SCARNA24	1:28995243-29045865	NOTEST	0	0	0	0	1	1
ENSG00000252778	ENSG00000252778	SCARNA20	11:8413417-8615836	NOTEST	0	0	0	0	1	1
ENSG00000252779	ENSG00000252779	RNU6-182P	2:172640879-172947158	NOTEST	0	0	0	0	1	1
ENSG00000252780	ENSG00000252780	RNA5SP471	19:32146261-32146367	NOTEST	0	0	0	0	1	1
ENSG00000252782	ENSG00000252782	RNU6-341P	14:58466452-58764857	NOTEST	0	0	0	0	1	1
ENSG00000252783	ENSG00000252783	RNU6-835P	14:88462688-88462792	NOTEST	0	0	0	0	1	1
ENSG00000252784	ENSG00000252784	Y_RNA	1:63803933-63804043	NOTEST	0	0	0	0	1	1
ENSG00000252785	ENSG00000252785	AC103809.1	17:72270385-72311023	NOTEST	0	0	0	0	1	1
ENSG00000252786	ENSG00000252786	RNU6-1142P	3:129366634-129612419	NOTEST	0	0	0	0	1	1
ENSG00000252787	ENSG00000252787	SNORD19B	3:52529353-52742182	NOTEST	0	0	0	0	1	1
ENSG00000252789	ENSG00000252789	AC006487.1	17:47572654-47661189	NOTEST	0	0	0	0	1	1
ENSG00000252790	ENSG00000252790	SNORD112	1:184647067-184647141	NOTEST	0	0	0	0	1	1
ENSG00000252791	ENSG00000252791	Y_RNA	20:36661947-36720768	NOTEST	0	0	0	0	1	1
ENSG00000252792	ENSG00000252792	U3	14:68168602-68283307	NOTEST	0	0	0	0	1	1
ENSG00000252793	ENSG00000252793	RNA5SP196	5:145942788-146464347	NOTEST	0	0	0	0	1	1
ENSG00000252794	ENSG00000252794	RN7SKP60	5:164776035-165205694	NOTEST	0	0	0	0	1	1
ENSG00000252795	ENSG00000252795	RNU6-56P	13:39261265-39460074	NOTEST	0	0	0	0	1	1
ENSG00000252796	ENSG00000252796	RNU7-11P	4:39500374-39640710	NOTEST	0	0	0	0	1	1
ENSG00000252797	ENSG00000252797	RN7SKP272	1:90453271-90453503	NOTEST	0	0	0	0	1	1
ENSG00000252798	ENSG00000252798	SCARNA6	16:21598947-21599185	NOTEST	0	0	0	0	1	1
ENSG00000252799	ENSG00000252799	snoU13	22:21878046-21878123	NOTEST	0	0	0	0	1	1

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ENSG00000252800	ENSG00000252800	SCARNA20	14:63838074-64010092	NOTEST	0	0	0	0	1	1
ENSG00000252801	ENSG00000252801	AC067735.1	12:39307041-39307128	NOTEST	0	0	0	0	1	1
ENSG00000252802	ENSG00000252802	Y_RNA	1:26920430-26920532	NOTEST	0	0	0	0	1	1
ENSG00000252803	ENSG00000252803	RNU6-870P	1:43489219-43489308	NOTEST	0	0	0	0	1	1
ENSG00000252804	ENSG00000252804	RNU6-958P	2:43393799-43823185	NOTEST	0	0	0	0	1	1
ENSG00000252805	ENSG00000252805	U3	2:219472487-219501907	NOTEST	0	0	0	0	1	1
ENSG00000252806	ENSG00000252806	RNA5SP420	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000252807	ENSG00000252807	RNU6-1006P	2:170976505-170976608	NOTEST	0	0	0	0	1	1
ENSG00000252808	ENSG00000252808	SCARNA4	1:155882833-155904191	NOTEST	0	0	0	0	1	1
ENSG00000252809	ENSG00000252809	AC135050.1	16:31117427-31124110	NOTEST	0	0	0	0	1	1
ENSG00000252810	ENSG00000252810	RNU6-345P	X:101137261-101187004	NOTEST	0	0	0	0	1	1
ENSG00000252811	ENSG00000252811	AC008085.1	7:131537438-131537533	NOTEST	0	0	0	0	1	1
ENSG00000252812	ENSG00000252812	RN7SKP2	13:40981258-40981577	NOTEST	0	0	0	0	1	1
ENSG00000252813	ENSG00000252813	AC108861.1	15:71389290-72075722	NOTEST	0	0	0	0	1	1
ENSG00000252814	ENSG00000252814	RN7SKP233	16:76311175-76692375	NOTEST	0	0	0	0	1	1
ENSG00000252815	ENSG00000252815	RNU6-410P	4:55898131-55898238	NOTEST	0	0	0	0	1	1
ENSG00000252816	ENSG00000252816	RNA5SP337	11:20691116-21597227	NOTEST	0	0	0	0	1	1
ENSG00000252817	ENSG00000252817	AL590431.1	1:154179181-154243986	NOTEST	0	0	0	0	1	1
ENSG00000252818	ENSG00000252818	RNU7-146P	18:62216689-62216742	NOTEST	0	0	0	0	1	1
ENSG00000252819	ENSG00000252819	AL121898.1	20:9047480-9047555	NOTEST	0	0	0	0	1	1
ENSG00000252820	ENSG00000252820	Y_RNA	7:137859790-137859882	NOTEST	0	0	0	0	1	1
ENSG00000252821	ENSG00000252821	RNU6-388P	7:32535037-33102409	NOTEST	0	0	0	0	1	1
ENSG00000252822	ENSG00000252822	Y_RNA	1:236139129-236228462	NOTEST	0	0	0	0	1	1
ENSG00000252823	ENSG00000252823	RNU6-148P	12:90147835-90147929	NOTEST	0	0	0	0	1	1
ENSG00000252824	ENSG00000252824	SNORA48	7:101458958-101927249	NOTEST	0	0	0	0	1	1
ENSG00000252825	ENSG00000252825	RNU6-1253P	1:50905149-51425935	NOTEST	0	0	0	0	1	1
ENSG00000252826	ENSG00000252826	RNU1-92P	1:149215165-149215300	NOTEST	0	0	0	0	1	1
ENSG00000252827	ENSG00000252827	RN7SKP11	12:96816103-96879220	NOTEST	0	0	0	0	1	1
ENSG00000252828	ENSG00000252828	RNA5SP135	3:68780916-68981761	NOTEST	0	0	0	0	1	1
ENSG00000252829	ENSG00000252829	SCARNA4	2:131588550-131804836	NOTEST	0	0	0	0	1	1
ENSG00000252830	ENSG00000252830	RNA5SP59	HG1287_PATCH:144126019-144126129	NOTEST	0	0	0	0	1	1
ENSG00000252831	ENSG00000252831	AC005215.1	5:141689991-142077617	NOTEST	0	0	0	0	1	1
ENSG00000252832	ENSG00000252832	RNU6-1212P	10:20081926-20082030	NOTEST	0	0	0	0	1	1
ENSG00000252833	ENSG00000252833	RNA5SP186	5:75377770-75649764	NOTEST	0	0	0	0	1	1
ENSG00000252834	ENSG00000252834	snoR442	4:83739813-83934079	NOTEST	0	0	0	0	1	1
ENSG00000252835	ENSG00000252835	SCARNA21	17:7760002-7816078	NOTEST	0	0	0	0	1	1
ENSG00000252837	ENSG00000252837	RN7SKP99	14:58030639-58448912	NOTEST	0	0	0	0	1	1
ENSG00000252838	ENSG00000252838	RN7SKP23	16:23399813-23468927	NOTEST	0.467379	0.280779	-0.735158	0	1	1
ENSG00000252839	ENSG00000252839	RNU6-419P	14:73704204-73741348	NOTEST	0	0	0	0	1	1
ENSG00000252840	ENSG00000252840	SNORA44	1:151482985-151511168	NOTEST	0	0	0	0	1	1
ENSG00000252841	ENSG00000252841	Z98044.1	1:9338449-9338592	NOTEST	0	0	0	0	1	1
ENSG00000252842	ENSG00000252842	RNU1-135P	1:147835126-147931933	NOTEST	0	0	0	0	1	1
ENSG00000252844	ENSG00000252844	SNORD112	10:102986732-103029905	NOTEST	0	0	0	0	1	1
ENSG00000252845	ENSG00000252845	RNA5SP101	2:97541619-97684341	NOTEST	0	0	0	0	1	1
ENSG00000252846	ENSG00000252846	AC090206.1	18:24034873-24770662	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000252847	ENSG00000252847	RNU2-46P	9:98521512-98776842	NOTEST	0	0	0	0	1	1
ENSG00000252848	ENSG00000252848	RNA5SP230	7:44165350-44165472	NOTEST	0	0	0	0	1	1
ENSG00000252849	ENSG00000252849	snosnR60_Z15	7:131582399-131633712	NOTEST	0	0	0	0	1	1
ENSG00000252850	ENSG00000252850	RNU1-117P	12:88975415-88975573	NOTEST	0	0	0	0	1	1
ENSG00000252852	ENSG00000252852	SNORA31	8:118325766-118325900	NOTEST	0	0	0	0	1	1
ENSG00000252853	ENSG00000252853	SNORD112	1:206807993-206857764	NOTEST	0	0	0	0	1	1
ENSG00000252854	ENSG00000252854	RN7SKP5	13:46786082-46851501	NOTEST	0.142168	0	#NAME?	0	1	1
ENSG00000252855	ENSG00000252855	AC134878.1	Y:13340550-13340633	NOTEST	0	0	0	0	1	1
ENSG00000252856	ENSG00000252856	RNA5SP503	X:48065692-48065809	NOTEST	0	0	0	0	1	1
ENSG00000252857	ENSG00000252857	RNU6-389P	7:55748766-55780945	NOTEST	0	0	0	0	1	1
ENSG00000252858	ENSG00000252858	RNU6-1271P	12:76533346-76533451	NOTEST	0	0	0	0	1	1
ENSG00000252859	ENSG00000252859	RNU6-375P	22:41487789-41593460	NOTEST	0	0	0	0	1	1
ENSG00000252860	ENSG00000252860	RNU6-570P	1:199996729-200146552	NOTEST	0	0	0	0	1	1
ENSG00000252861	ENSG00000252861	RNU6-448P	5:83236372-83786583	NOTEST	0	0	0	0	1	1
ENSG00000252863	ENSG00000252863	RNU6-1183P	12:102265519-102265579	NOTEST	0	0	0	0	1	1
ENSG00000252864	ENSG00000252864	RNA5SP278	8:141667998-142012315	NOTEST	0	0	0	0	1	1
ENSG00000252865	ENSG00000252865	RNU6-594P	12:57853917-57914300	NOTEST	0	0	0	0	1	1
ENSG00000252866	ENSG00000252866	RNA5SP243	7:128337763-128337798	NOTEST	0	0	0	0	1	1
ENSG00000252867	ENSG00000252867	RNU6-909P	5:28624763-28624870	NOTEST	0	0	0	0	1	1
ENSG00000252868	ENSG00000252868	snoZ278	15:29412456-29862927	NOTEST	0	0	0	0	1	1
ENSG00000252869	ENSG00000252869	AL159140.1	14:59866740-59866869	NOTEST	0	0	0	0	1	1
ENSG00000252870	ENSG00000252870	ACA59	11:114998937-114999093	NOTEST	0	0	0	0	1	1
ENSG00000252872	ENSG00000252872	RNU7-188P	7:96007168-96007232	NOTEST	0	0	0	0	1	1
ENSG00000252873	ENSG00000252873	SNORD112	14:101361106-101402336	NOTEST	0	0	0	0	1	1
ENSG00000252874	ENSG00000252874	Y_RNA	11:47799638-47870107	NOTEST	0	0	0	0	1	1
ENSG00000252876	ENSG00000252876	RNU7-199P	16:31271310-31344213	NOTEST	0	0	0	0	1	1
ENSG00000252877	ENSG00000252877	RNA5SP312	10:47186202-47243502	NOTEST	0	0	0	0	1	1
ENSG00000252878	ENSG00000252878	SNORA70	9:67864532-67864627	NOTEST	0	0	0	0	1	1
ENSG00000252879	ENSG00000252879	RN7SKP98	1:212208918-212280742	NOTEST	0	0	0	0	1	1
ENSG00000252880	ENSG00000252880	RNU6-459P	4:71713852-71713935	NOTEST	0	0	0	0	1	1
ENSG00000252881	ENSG00000252881	RNU6-334P	5:103718998-104728671	NOTEST	0	0	0	0	1	1
ENSG00000252882	ENSG00000252882	RNU6-1137P	17:41473360-41473459	NOTEST	0	0	0	0	1	1
ENSG00000252883	ENSG00000252883	SNORD112	12:62102039-62811211	NOTEST	0	0	0	0	1	1
ENSG00000252884	ENSG00000252884	RNU6-1213P	8:81317750-81317844	NOTEST	0	0	0	0	1	1
ENSG00000252886	ENSG00000252886	RN7SKP197	12:119772516-120119435	NOTEST	0	0	0	0	1	1
ENSG00000252887	ENSG00000252887	RNU6-430P	16:89334037-89556969	NOTEST	0	0	0	0	1	1
ENSG00000252888	ENSG00000252888	SNORA31	10:78595134-78595260	NOTEST	0	0	0	0	1	1
ENSG00000252889	ENSG00000252889	RNU6-1236P	3:108943975-108944074	NOTEST	0	0	0	0	1	1
ENSG00000252890	ENSG00000252890	RNU6-699P	4:67762979-67763089	NOTEST	0	0	0	0	1	1
ENSG00000252891	ENSG00000252891	Y_RNA	6:90608001-90608111	NOTEST	0	0	0	0	1	1
ENSG00000252892	ENSG00000252892	RNU6-548P	2:65215610-65250999	NOTEST	0	0	0	0	1	1
ENSG00000252893	ENSG00000252893	RNU7-58P	11:59326272-59326334	NOTEST	0	0	0	0	1	1
ENSG00000252894	ENSG00000252894	Y_RNA	3:130569438-131100319	NOTEST	0	0	0	0	1	1
ENSG00000252895	ENSG00000252895	RNY4P26	10:95753745-96122716	NOTEST	0	0	0	0	1	1
ENSG00000252896	ENSG00000252896	AC067957.1	2:45009184-45009269	NOTEST	0	0	0	0	1	1

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ENSG00000252897	ENSG00000252897	RNU6-685P	2:82495550-82497051	NOTEST	0	0	0	0	1	1
ENSG00000252898	ENSG00000252898	RNU6-1096P	4:174367753-174367855	NOTEST	0	0	0	0	1	1
ENSG00000252900	ENSG00000252900	RNU6-303P	Y:4043025-4043131	NOTEST	0	0	0	0	1	1
ENSG00000252901	ENSG00000252901	AL669914.1	6:30056597-30056730	NOTEST	0	0	0	0	1	1
ENSG00000252902	ENSG00000252902	RNA5SP342	11:71556241-71556291	NOTEST	0	0	0	0	1	1
ENSG00000252903	ENSG00000252903	RNU6-894P	X:31115793-33357558	NOTEST	0	0	0	0	1	1
ENSG00000252904	ENSG00000252904	SNORA76	5:65222302-65378377	NOTEST	0	0	0	0	1	1
ENSG00000252905	ENSG00000252905	RNA5SP330	11:8703957-8932498	NOTEST	0	0	0	0	1	1
ENSG00000252906	ENSG00000252906	SCARNA3	1:175913966-176176629	NOTEST	0	0	0	0	1	1
ENSG00000252908	ENSG00000252908	RNU6-1003P	5:17065706-17276943	NOTEST	0	0	0	0	1	1
ENSG00000252909	ENSG00000252909	RNU6-201P	22:32149943-32303012	NOTEST	0	0	0	0	1	1
ENSG00000252910	ENSG00000252910	RNU7-177P	8:98786205-98786261	NOTEST	0	0	0	0	1	1
ENSG00000252912	ENSG00000252912	RNA5SP439	17:34842472-34899284	NOTEST	0	0	0	0	1	1
ENSG00000252913	ENSG00000252913	RNU6-158P	4:48934771-48934871	NOTEST	0	0	0	0	1	1
ENSG00000252914	ENSG00000252914	RNU6-789P	3:135969147-136471220	NOTEST	0	0	0	0	1	1
ENSG00000252915	ENSG00000252915	Y_RNA	21:40714240-40721573	NOTEST	0	0	0	0	1	1
ENSG00000252916	ENSG00000252916	RNU6-762P	2:201754049-201768655	NOTEST	0	0	0	0	1	1
ENSG00000252917	ENSG00000252917	SNORA74	12:42632248-42984157	NOTEST	0	0	0	0	1	1
ENSG00000252918	ENSG00000252918	AL359709.2	6:105644727-105644811	NOTEST	0	0	0	0	1	1
ENSG00000252919	ENSG00000252919	Y_RNA	14:50043389-50081390	NOTEST	0	0	0	0	1	1
ENSG00000252920	ENSG00000252920	SNORA31	1:152984957-152985090	NOTEST	0	0	0	0	1	1
ENSG00000252921	ENSG00000252921	U3	18:23805899-23971649	NOTEST	0	0	0	0	1	1
ENSG00000252922	ENSG00000252922	RNU6-365P	11:40135752-41481323	NOTEST	0	0	0	0	1	1
ENSG00000252923	ENSG00000252923	SCARNA16	2:197504277-197664449	NOTEST	0	0	0	0	1	1
ENSG00000252925	ENSG00000252925	RNU1-68P	1:149646784-149719362	NOTEST	0	0	0	0	1	1
ENSG00000252927	ENSG00000252927	RNA5SP404	16:9693953-9694085	NOTEST	0	0	0	0	1	1
ENSG00000252928	ENSG00000252928	RNU6-64P	13:30776766-30881621	NOTEST	0	0	0	0	1	1
ENSG00000252929	ENSG00000252929	RNU6-218P	7:6048875-6098861	NOTEST	0	0	0	0	1	1
ENSG00000252930	ENSG00000252930	RNU6-1015P	X:112162359-112162458	NOTEST	0	0	0	0	1	1
ENSG00000252931	ENSG00000252931	RNU6-231P	15:86365085-86365188	NOTEST	0	0	0	0	1	1
ENSG00000252932	ENSG00000252932	SNORD112	6:78646917-78646988	NOTEST	0	0	0	0	1	1
ENSG00000252933	ENSG00000252933	RNU6-1223P	19:1609290-1652604	NOTEST	0	0	0	0	1	1
ENSG00000252934	ENSG00000252934	RNU7-172P	2:54091203-54532437	NOTEST	0	0	0	0	1	1
ENSG00000252935	ENSG00000252935	RNU6-1220P	8:79310749-79310857	NOTEST	0	0	0	0	1	1
ENSG00000252936	ENSG00000252936	RNA5SP423	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000252937	ENSG00000252937	RNU6-1270P	3:73290939-73291047	NOTEST	0	0	0	0	1	1
ENSG00000252940	ENSG00000252940	AL357936.1	9:124302154-124302241	NOTEST	0	0	0	0	1	1
ENSG00000252941	ENSG00000252941	RNA5SP340	11:47799638-47870107	NOTEST	0	0	0	0	1	1
ENSG00000252942	ENSG00000252942	RNA5SP290	9:101866319-101916474	NOTEST	0	0	0	0	1	1
ENSG00000252943	ENSG00000252943	RNU6-264P	9:19053140-19103117	NOTEST	0	0	0	0	1	1
ENSG00000252944	ENSG00000252944	RNU6-897P	6:105175967-105307794	NOTEST	0	0	0	0	1	1
ENSG00000252945	ENSG00000252945	snoU83B	14:51311342-51311430	NOTEST	0	0	0	0	1	1
ENSG00000252946	ENSG00000252946	SNORD112	1:204797778-204991950	NOTEST	0	0	0	0	1	1
ENSG00000252947	ENSG00000252947	SCARNA1	1:28157288-28178187	NOTEST	0	0	0	0	1	1
ENSG00000252948	ENSG00000252948	RNU6-1314P	Y:28507135-28507239	NOTEST	0	0	0	0	1	1

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ENSG00000252949	ENSG00000252949	AL136303.1	6:20402397-20493941	NOTEST	0	0	0	0	1	1
ENSG00000252950	ENSG00000252950	RNA5SP490	21:33935384-33935520	NOTEST	0	0	0	0	1	1
ENSG00000252951	ENSG00000252951	RNA5SP165	4:148653213-148993931	NOTEST	0	0	0	0	1	1
ENSG00000252952	ENSG00000252952	RNU6-58P	13:23755090-23899304	NOTEST	0	0	0	0	1	1
ENSG00000252953	ENSG00000252953	RNU6-232P	3:125107777-125107841	NOTEST	0	0	0	0	1	1
ENSG00000252955	ENSG00000252955	RNU4ATAC9P	4:73830894-73831020	NOTEST	0	0	0	0	1	1
ENSG00000252956	ENSG00000252956	RNA5SP40	1:9497727-9497837	NOTEST	0	0	0	0	1	1
ENSG00000252957	ENSG00000252957	RNA5SP402	15:100510419-100882210	NOTEST	0	0	0	0	1	1
ENSG00000252958	ENSG00000252958	AC009065.3	16:2254248-2261951	NOTEST	0	0	0	0	1	1
ENSG00000252959	ENSG00000252959	RNA5SP170	4:166794409-167025047	NOTEST	0	0	0	0	1	1
ENSG00000252960	ENSG00000252960	RN7SKP258	9:18473891-18910948	NOTEST	0	0	0	0	1	1
ENSG00000252961	ENSG00000252961	SNORD112	X:55930019-55930089	NOTEST	0	0	0	0	1	1
ENSG00000252962	ENSG00000252962	RNU6-993P	19:2503044-2503139	NOTEST	0	0	0	0	1	1
ENSG00000252963	ENSG00000252963	RN7SKP147	21:21728964-21729208	NOTEST	0	0	0	0	1	1
ENSG00000252964	ENSG00000252964	RNA5SP400	15:86681499-86681610	NOTEST	0	0	0	0	1	1
ENSG00000252965	ENSG00000252965	Y_RNA	3:125247087-125247193	NOTEST	0	0	0	0	1	1
ENSG00000252966	ENSG00000252966	RNU7-91P	6:13615558-13711796	NOTEST	0	0	0	0	1	1
ENSG00000252968	ENSG00000252968	AC005370.1	5:141689991-142077617	NOTEST	0	0	0	0	1	1
ENSG00000252969	ENSG00000252969	SNORA70	1:12281204-12281328	NOTEST	0	0	0	0	1	1
ENSG00000252970	ENSG00000252970	RNA5SP159	4:39824482-39979576	NOTEST	0	0	0	0	1	1
ENSG00000252971	ENSG00000252971	RNU6-1057P	17:19912656-20306870	NOTEST	0	0	0	0	1	1
ENSG00000252972	ENSG00000252972	RNA5SP398	15:69591285-69740764	NOTEST	0	0	0	0	1	1
ENSG00000252973	ENSG00000252973	RNU6-1028P	19:19322781-19363042	NOTEST	0	0	0	0	1	1
ENSG00000252974	ENSG00000252974	AC121334.1	12:39687029-39837192	NOTEST	0	0	0	0	1	1
ENSG00000252975	ENSG00000252975	Y_RNA	4:39699663-39784412	NOTEST	0	0	0	0	1	1
ENSG00000252976	ENSG00000252976	AC090644.1	3:17177141-17177214	NOTEST	0	0	0	0	1	1
ENSG00000252977	ENSG00000252977	RNA5SP70	1:181382237-181777219	NOTEST	0	0	0	0	1	1
ENSG00000252978	ENSG00000252978	RN7SKP183	X:20470225-20470549	NOTEST	0	0	0	0	1	1
ENSG00000252979	ENSG00000252979	RNU6-165P	19:54269787-54269886	NOTEST	0	0	0	0	1	1
ENSG00000252980	ENSG00000252980	RNU6-367P	3:44112578-44112678	NOTEST	0	0	0	0	1	1
ENSG00000252981	ENSG00000252981	U3	2:170648442-170681441	NOTEST	0	0	0	0	1	1
ENSG00000252982	ENSG00000252982	RN7SKP234	3:173114073-174004434	NOTEST	0	0	0	0	1	1
ENSG00000252983	ENSG00000252983	RNU7-35P	7:43152197-43605600	NOTEST	0	0	0	0	1	1
ENSG00000252984	ENSG00000252984	RNU6-844P	15:57668164-57842925	NOTEST	0	0	0	0	1	1
ENSG00000252985	ENSG00000252985	SNORD116	9:129089127-129269320	NOTEST	0	0	0	0	1	1
ENSG00000252986	ENSG00000252986	AC147651.2	7:588833-829190	NOTEST	0	0	0	0	1	1
ENSG00000252987	ENSG00000252987	RNA5SP66	1:168873142-169056243	NOTEST	0	0	0	0	1	1
ENSG00000252988	ENSG00000252988	RNU6-111P	2:73525810-73525915	NOTEST	0	0	0	0	1	1
ENSG00000252989	ENSG00000252989	SNORA31	3:100328432-100414323	NOTEST	0	0	0	0	1	1
ENSG00000252990	ENSG00000252990	RNU1-54P	6:39297765-39693181	NOTEST	0	0	0	0	1	1
ENSG00000252991	ENSG00000252991	RNU6-1073P	9:1001857-1001963	NOTEST	0	0	0	0	1	1
ENSG00000252992	ENSG00000252992	SCARNA11	11:117103340-117283984	NOTEST	0	0	0	0	1	1
ENSG00000252993	ENSG00000252993	SNORA25	10:93806448-94050844	NOTEST	0	0	0	0	1	1
ENSG00000252994	ENSG00000252994	RNU6-1231P	10:104503726-104576021	NOTEST	0	0	0	0	1	1
ENSG00000252995	ENSG00000252995	RNU6-667P	15:80109690-80109792	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000252997	ENSG00000252997	AC068533.1	7:65521220-65521305	NOTEST	0	0	0	0	1	1
ENSG00000252998	ENSG00000252998	RNU6-889P	10:2140360-2140463	NOTEST	0	0	0	0	1	1
ENSG00000252999	ENSG00000252999	RNA5SP380	14:20558288-20558386	NOTEST	0	0	0	0	1	1
ENSG00000253000	ENSG00000253000	RNU1-45P	4:179037874-179038015	NOTEST	0	0	0	0	1	1
ENSG00000253001	ENSG00000253001	RN7SKP105	4:164445449-165305202	NOTEST	0	0	0	0	1	1
ENSG00000253002	ENSG00000253002	AC005725.1	17:11144579-11467380	NOTEST	0	0	0	0	1	1
ENSG00000253003	ENSG00000253003	RNU6-1261P	14:35145096-35145200	NOTEST	0	0	0	0	1	1
ENSG00000253004	ENSG00000253004	U8	3:135518535-135518622	NOTEST	0	0	0	0	1	1
ENSG00000253005	ENSG00000253005	RNU6-176P	1:28469247-28469352	NOTEST	0	0	0	0	1	1
ENSG00000253006	ENSG00000253006	RN7SKP283	2:229715241-230136001	NOTEST	0	0	0	0	1	1
ENSG00000253007	ENSG00000253007	SNORA76	22:33558211-34318829	NOTEST	0	0	0	0	1	1
ENSG00000253008	ENSG00000253008	MIR2355	2:207938860-208031991	NOTEST	0	0	0	0	1	1
ENSG00000253009	ENSG00000253009	U3	X:150070593-150070709	NOTEST	0	0	0	0	1	1
ENSG00000253010	ENSG00000253010	RN7SKP256	6:53280091-53280405	NOTEST	0	0	0	0	1	1
ENSG00000253011	ENSG00000253011	AC010928.1	18:58222375-58222457	NOTEST	0	0	0	0	1	1
ENSG00000253012	ENSG00000253012	AC022538.1	10:67330095-67526299	NOTEST	0	0	0	0	1	1
ENSG00000253013	ENSG00000253013	SNORA31	4:187025572-187093821	NOTEST	0	0	0	0	1	1
ENSG00000253014	ENSG00000253014	U3	14:61073784-61073883	NOTEST	0	0	0	0	1	1
ENSG00000253015	ENSG00000253015	RN7SKP64	5:138668726-138669054	NOTEST	0	0	0	0	1	1
ENSG00000253016	ENSG00000253016	Y_RNA	12:38668249-38668351	NOTEST	0	0	0	0	1	1
ENSG00000253017	ENSG00000253017	AL160037.1	6:25279305-25620758	NOTEST	0	0	0	0	1	1
ENSG00000253018	ENSG00000253018	RNY4P31	13:61390830-61390923	NOTEST	0	0	0	0	1	1
ENSG00000253019	ENSG00000253019	RN7SKP35	4:152330367-152584784	NOTEST	0	0	0	0	1	1
ENSG00000253020	ENSG00000253020	RN7SKP40	3:174156362-175523428	NOTEST	0	0	0	0	1	1
ENSG00000253021	ENSG00000253021	RNU6-902P	19:44529493-44593766	NOTEST	0	0	0	0	1	1
ENSG00000253022	ENSG00000253022	RNU6-731P	1:6581406-6614595	NOTEST	0	0	0	0	1	1
ENSG00000253023	ENSG00000253023	RNU7-156P	5:142922078-142922152	NOTEST	0	0	0	0	1	1
ENSG00000253024	ENSG00000253024	RNU6-1238P	11:67159175-67193078	NOTEST	0	0	0	0	1	1
ENSG00000253025	ENSG00000253025	RNU2-12P	1:176212997-176213165	NOTEST	0	0	0	0	1	1
ENSG00000253026	ENSG00000253026	RNU6-464P	6:53018592-53018696	NOTEST	0	0	0	0	1	1
ENSG00000253027	ENSG00000253027	SNORA70	19:45268206-45268357	NOTEST	0	0	0	0	1	1
ENSG00000253028	ENSG00000253028	SNORA31	7:52337132-52337265	NOTEST	0	0	0	0	1	1
ENSG00000253029	ENSG00000253029	RNU6-568P	2:88667311-88667381	NOTEST	0	0	0	0	1	1
ENSG00000253030	ENSG00000253030	MIR2116	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000253031	ENSG00000253031	RNA5SP291	9:106451754-106451859	NOTEST	0	0	0	0	1	1
ENSG00000253032	ENSG00000253032	RNU6-299P	5:55395506-55529186	NOTEST	0	0	0	0	1	1
ENSG00000253033	ENSG00000253033	RNU7-191P	18:45553043-45937123	NOTEST	0	0	0	0	1	1
ENSG00000253035	ENSG00000253035	RNU4ATAC5P	11:122322181-122322307	NOTEST	0	0	0	0	1	1
ENSG00000253036	ENSG00000253036	snR65	2:146092637-146092740	NOTEST	0	0	0	0	1	1
ENSG00000253037	ENSG00000253037	AL109947.2	6:109809108-110012420	NOTEST	0	0	0	0	1	1
ENSG00000253038	ENSG00000253038	RNU6-706P	18:36613970-36614074	NOTEST	0	0	0	0	1	1
ENSG00000253039	ENSG00000253039	RNA5SP47	1:45316449-45452282	NOTEST	0	0	0	0	1	1
ENSG00000253040	ENSG00000253040	RNA5SP454	18:39739246-40271387	NOTEST	0	0	0	0	1	1
ENSG00000253041	ENSG00000253041	SNORA31	9:103790990-104087417	NOTEST	0	0	0	0	1	1

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ENSG00000253042	ENSG00000253042	SNORA70	1:202317826-202679545	NOTEST	0	0	0	0	1	1
ENSG00000253043	ENSG00000253043	RNU7-181P	8:130844546-131029375	NOTEST	0	0	0	0	1	1
ENSG00000253044	ENSG00000253044	AL691452.1	1:207669491-207813992	NOTEST	0	0	0	0	1	1
ENSG00000253045	ENSG00000253045	RMRPP1	10:75531934-75540009	NOTEST	0	0.223169	inf	0	1	1
ENSG00000253046	ENSG00000253046	AC092841.1	2:162272604-162841792	NOTEST	0	0	0	0	1	1
ENSG00000253047	ENSG00000253047	SNORA40	1:150573014-150573135	NOTEST	0	0	0	0	1	1
ENSG00000253048	ENSG00000253048	RNU4-60P	19:42901279-43156507	NOTEST	0	0	0	0	1	1
ENSG00000253049	ENSG00000253049	SNORA43	3:3111232-3168297	NOTEST	0	0	0	0	1	1
ENSG00000253050	ENSG00000253050	RNU6-868P	4:48068409-48136273	NOTEST	0	0	0	0	1	1
ENSG00000253051	ENSG00000253051	SNORA31	13:45910448-45910582	NOTEST	0	0	0	0	1	1
ENSG00000253052	ENSG00000253052	U3	12:30052835-30052940	NOTEST	0	0	0	0	1	1
ENSG00000253053	ENSG00000253053	RN7SKP289	12:54209968-54210263	NOTEST	0	0	0	0	1	1
ENSG00000253054	ENSG00000253054	RNU7-77P	10:35386933-35501886	NOTEST	0	0	0	0	1	1
ENSG00000253055	ENSG00000253055	RNA5SP415	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000253056	ENSG00000253056	RNU7-128P	3:48198635-48229892	NOTEST	0	0	0	0	1	1
ENSG00000253057	ENSG00000253057	RN7SKP57	5:110831730-111353006	NOTEST	0	0	0	0	1	1
ENSG00000253058	ENSG00000253058	RNA5SP437	17:30264036-30328064	NOTEST	0	0	0	0	1	1
ENSG00000253059	ENSG00000253059	SNORA31	14:36007557-36278510	NOTEST	0	0	0	0	1	1
ENSG00000253060	ENSG00000253060	SCARNA20	1:171737209-171737315	NOTEST	0	0	0	0	1	1
ENSG00000253062	ENSG00000253062	RNU7-108P	3:93698982-93847389	NOTEST	0	0	0	0	1	1
ENSG00000253063	ENSG00000253063	RNU6-494P	12:32552462-32798984	NOTEST	0	0	0	0	1	1
ENSG00000253064	ENSG00000253064	RNU6-711P	17:27679086-27878922	NOTEST	0	0	0	0	1	1
ENSG00000253065	ENSG00000253065	SNORA40	5:166711803-167691162	NOTEST	0	0	0	0	1	1
ENSG00000253066	ENSG00000253066	RNU6-709P	10:115871172-115871276	NOTEST	0	0	0	0	1	1
ENSG00000253067	ENSG00000253067	snoZ6	5:131415758-131415826	NOTEST	0	0	0	0	1	1
ENSG00000253068	ENSG00000253068	SNORD112	10:103862018-103862089	NOTEST	0	0	0	0	1	1
ENSG00000253069	ENSG00000253069	AC021205.1	4:123747862-123844123	NOTEST	0	0	0	0	1	1
ENSG00000253070	ENSG00000253070	RNU6-794P	10:35520258-35520322	NOTEST	0	0	0	0	1	1
ENSG00000253071	ENSG00000253071	RNU7-31P	17:5402746-5522744	NOTEST	0	0	0	0	1	1
ENSG00000253072	ENSG00000253072	snoMBII-202	11:15503353-15503439	NOTEST	0	0	0	0	1	1
ENSG00000253073	ENSG00000253073	RN7SKP295	5:82933623-83017432	NOTEST	0	0	0	0	1	1
ENSG00000253074	ENSG00000253074	RNU6-586P	1:67557847-67725662	NOTEST	0	0	0	0	1	1
ENSG00000253075	ENSG00000253075	RN7SKP92	14:100800124-100996640	NOTEST	0	0	0	0	1	1
ENSG00000253076	ENSG00000253076	SNORD112	3:112709293-112902148	NOTEST	0	0	0	0	1	1
ENSG00000253077	ENSG00000253077	RNA5SP169	4:152892648-152892765	NOTEST	0	0	0	0	1	1
ENSG00000253078	ENSG00000253078	RNU6-1116P	2:37662652-37662751	NOTEST	0	0	0	0	1	1
ENSG00000253079	ENSG00000253079	NRON	9:129089127-129269320	NOTEST	0	0	0	0	1	1
ENSG00000253080	ENSG00000253080	RNA5SP373	12:111471827-111788358	NOTEST	0	0	0	0	1	1
ENSG00000253081	ENSG00000253081	RNU4ATAC17P	3:7994491-8653610	NOTEST	0	0	0	0	1	1
ENSG00000253082	ENSG00000253082	AC007365.2	2:65003237-65003321	NOTEST	0	0	0	0	1	1
ENSG00000253083	ENSG00000253083	RNA5SP106	2:148471023-148471123	NOTEST	0	0	0	0	1	1
ENSG00000253084	ENSG00000253084	RNU6-840P	17:33332106-33448541	NOTEST	0	0	0	0	1	1
ENSG00000253085	ENSG00000253085	SCARNA11	1:14022564-14022694	NOTEST	0	0	0	0	1	1
ENSG00000253086	ENSG00000253086	RNU6-537P	1:11166591-11322564	NOTEST	0	0	0	0	1	1
ENSG00000253087	ENSG00000253087	RNU6-1174P	3:134316642-134979309	NOTEST	0	0	0	0	1	1

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ENSG00000253088	ENSG00000253088	Y_RNA	7:151832009-152133090	NOTEST	0	0	0	0	1	1
ENSG00000253089	ENSG00000253089	RNU1-104P	12:127805899-127806074	NOTEST	0	0	0	0	1	1
ENSG00000253090	ENSG00000253090	SNORA73	6:108306292-108306983	NOTEST	0	0	0	0	1	1
ENSG00000253091	ENSG00000253091	U3	6:114102517-114102667	NOTEST	0	0	0	0	1	1
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ENSG00000253093	ENSG00000253093	RNA5SP179	5:16665394-16936372	NOTEST	0	0	0	0	1	1
ENSG00000253094	ENSG00000253094	SNORD36	13:23377283-23377363	NOTEST	0	0	0	0	1	1
ENSG00000253095	ENSG00000253095	RNU6-676P	12:10977558-11324212	NOTEST	0	0	0	0	1	1
ENSG00000253096	ENSG00000253096	Y_RNA	14:104182066-104200005	NOTEST	0	0	0	0	1	1
ENSG00000253097	ENSG00000253097	RNU2-19P	1:205535843-205535927	NOTEST	0	0	0	0	1	1
ENSG00000253098	ENSG00000253098	RNU7-161P	5:40909353-40983041	NOTEST	0	0	0	0	1	1
ENSG00000253099	ENSG00000253099	RNU2-60P	11:111222976-111328876	NOTEST	0	0	0	0	1	1
ENSG00000253100	ENSG00000253100	RP11-219J21.1	8:25543313-25545040	NOTEST	0	0	0	0	1	1
ENSG00000253102	ENSG00000253102	RP1-117B12.4	17:48450580-48475249	NOTEST	0.037019	0	#NAME?	0	1	1
ENSG00000253103	ENSG00000253103	RP11-946L20.4	8:112111189-112248432	NOTEST	0	0	0	0	1	1
ENSG00000253104	ENSG00000253104	RP11-855C21.1	5:21616370-22853731	NOTEST	0	0	0	0	1	1
ENSG00000253105	ENSG00000253105	KB-1448A5.1	8:97384092-97399666	NOTEST	0	0	0	0	1	1
ENSG00000253106	ENSG00000253106	RP11-158K1.3	8:125500725-125740730	NOTEST	0.486698	0.464713	-0.0666885	0	1	1
ENSG00000253107	ENSG00000253107	CTD-2544L4.1	8:111567636-111568747	NOTEST	0	0	0	0	1	1
ENSG00000253108	ENSG00000253108	RP1-84O15.2	8:34085956-34204249	NOTEST	0	0	0	0	1	1
ENSG00000253109	ENSG00000253109	RP11-619L12.1	5:173466753-173467243	NOTEST	0	0	0	0	1	1
ENSG00000253110	ENSG00000253110	CTB-78H18.1	5:171200655-171201743	NOTEST	0	0	0	0	1	1
ENSG00000253111	ENSG00000253111	RP11-136O12.2	8:126479180-126553615	NOTEST	0	0	0	0	1	1
ENSG00000253112	ENSG00000253112	CTD-2373N4.5	8:30435834-30515768	NOTEST	0	0.0449142	inf	0	1	1
ENSG00000253114	ENSG00000253114	RP11-550I15.1	8:55561552-55782463	NOTEST	0	0	0	0	1	1
ENSG00000253115	ENSG00000253115	RP11-6I2.4	8:75015750-75018979	NOTEST	0	0	0	0	1	1
ENSG00000253116	ENSG00000253116	RP11-648L3.2	8:58907067-59116838	NOTEST	0	0	0	0	1	1
ENSG00000253118	ENSG00000253118	RP11-700E23.3	8:93364139-93364376	NOTEST	0	0	0	0	1	1
ENSG00000253119	ENSG00000253119	HNRNPA3P7	5:153369687-153825410	NOTEST	0	0	0	0	1	1
ENSG00000253120	ENSG00000253120	IGLV2-34	22:22922477-22922760	NOTEST	0	0	0	0	1	1
ENSG00000253121	ENSG00000253121	RP11-659E9.4	8:63927637-63951730	NOTEST	0	0	0	0	1	1
ENSG00000253122	ENSG00000253122	RP11-238I10.1	8:111621469-111644623	NOTEST	0	0	0	0	1	1
ENSG00000253123	ENSG00000253123	RP11-527N22.1	8:37188189-37189502	NOTEST	0	0	0	0	1	1
ENSG00000253124	ENSG00000253124	TRAPPC2P2	8:72315674-72504260	NOTEST	0	0	0	0	1	1
ENSG00000253125	ENSG00000253125	RP11-459E5.1	8:22545171-22941132	NOTEST	0.0655814	0.141867	1.11318	0	1	1
ENSG00000253126	ENSG00000253126	IGLVI-56	22:22552959-22553411	NOTEST	0	0	0	0	1	1
ENSG00000253127	ENSG00000253127	IGKV2D-36	2:89925831-89926057	NOTEST	0	0	0	0	1	1
ENSG00000253128	ENSG00000253128	IGHV4-80	14:107280999-107281252	NOTEST	0	0	0	0	1	1
ENSG00000253130	ENSG00000253130	CTD-3023L14.2	8:8413247-8427198	NOTEST	0	0	0	0	1	1
ENSG00000253131	ENSG00000253131	IGHV7-56	14:107065771-107066206	NOTEST	0	0	0	0	1	1
ENSG00000253132	ENSG00000253132	IGHV3-62	14:107099144-107099588	NOTEST	0	0	0	0	1	1
ENSG00000253133	ENSG00000253133	RP11-360L9.4	8:41386724-41482520	NOTEST	0	0.112047	inf	0	1	1

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ENSG00000253135	ENSG00000253135	RP11-589C21.2	8:41986291-41986767	NOTEST	0	0	0	0	1	1
ENSG00000253137	ENSG00000253137	RP11-509P12.1	8:85095021-85834079	NOTEST	0	0	0	0	1	1
ENSG00000253138	ENSG00000253138	LINC00967	8:67104327-67109550	NOTEST	0	0	0	0	1	1
ENSG00000253139	ENSG00000253139	RP11-17A4.3	8:57349232-57472382	NOTEST	0	0	0	0	1	1
ENSG00000253140	ENSG00000253140	RP11-567J20.3	8:49428411-49429649	NOTEST	0	0	0	0	1	1
ENSG00000253141	ENSG00000253141	CTB-164N12.1	5:172890502-172911587	NOTEST	0	0	0	0	1	1
ENSG00000253142	ENSG00000253142	RP11-87E22.1	8:22545171-22941132	NOTEST	0	0	0	0	1	1
ENSG00000253143	ENSG00000253143	Metazoa_SRP	8:71383346-71397922	NOTEST	0	0	0	0	1	1
ENSG00000253146	ENSG00000253146	CIR1P1	5:153938867-153940000	NOTEST	0	0	0	0	1	1
ENSG00000253147	ENSG00000253147	RP11-369E15.4	8:20810155-20852630	NOTEST	0	0	0	0	1	1
ENSG00000253148	ENSG00000253148	RGS21	1:192286121-192336415	NOTEST	0	0	0	0	1	1
ENSG00000253149	ENSG00000253149	IGHVII-31-1	14:106810596-106810633	NOTEST	0	0	0	0	1	1
ENSG00000253152	ENSG00000253152	IGLV3-17	22:23081431-23081675	NOTEST	0	0	0	0	1	1
ENSG00000253153	ENSG00000253153	KB-1562D12.3	8:102473404-102681954	NOTEST	0	0	0	0	1	1
ENSG00000253154	ENSG00000253154	CTA-392E5.1	8:86851933-86963312	NOTEST	0	0	0	0	1	1
ENSG00000253155	ENSG00000253155	CTB-47B11.1	5:156687131-157002783	NOTEST	0	0	0	0	1	1
ENSG00000253156	ENSG00000253156	RP11-58O3.1	8:112633686-112634026	NOTEST	0	0	0	0	1	1
ENSG00000253158	ENSG00000253158	IGKV3-31	2:89551696-89552222	NOTEST	0	0	0	0	1	1
ENSG00000253160	ENSG00000253160	RP11-1113C11.	8:39167427-39167962	NOTEST	0	0	0	0	1	1
ENSG00000253161	ENSG00000253161	RP11-150O12.1	8:37278858-37411701	NOTEST	0.365571	0.0186712	-4.29126	0	1	1
ENSG00000253162	ENSG00000253162	RP11-279L11.1	8:2792874-4852494	NOTEST	0	0	0	0	1	1
ENSG00000253163	ENSG00000253163	RP11-443C10.1	5:178804505-178805866	NOTEST	0	0	0	0	1	1
ENSG00000253164	ENSG00000253164	RP11-563N12.2	8:20207720-20230280	NOTEST	0	0	0	0	1	1
ENSG00000253165	ENSG00000253165	CTD-2309H9.3	8:134783651-134826780	NOTEST	0	0	0	0	1	1
ENSG00000253166	ENSG00000253166	RP11-585F1.6	8:152659-152897	NOTEST	0	0	0	0	1	1
ENSG00000253167	ENSG00000253167	KIAA0196-AS1	8:126036501-126379362	NOTEST	0.27613	0.37655	0.447494	0	1	1
ENSG00000253168	ENSG00000253168	RP11-326L2.1	8:17433941-17658426	NOTEST	0.0484028	0	#NAME?	0	1	1
ENSG00000253169	ENSG00000253169	IGHVII-65-1	14:107127812-107128060	NOTEST	0	0	0	0	1	1
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ENSG00000253171	ENSG00000253171	CTB-118P15.2	8:88986392-89031341	NOTEST	0	0	0	0	1	1
ENSG00000253172	ENSG00000253172	CTC-209H22.3	5:172571164-172591390	NOTEST	0	0	0	0	1	1
ENSG00000253173	ENSG00000253173	RP11-152C15.1	8:71016027-71016414	NOTEST	0	0.054794	inf	0	1	1
ENSG00000253175	ENSG00000253175	RP11-267M23.6	8:95565949-95581973	NOTEST	0	0.162947	inf	0	1	1
ENSG00000253176	ENSG00000253176	RP11-1149M3.2	8:27695993-27697899	NOTEST	0	0	0	0	1	1
ENSG00000253177	ENSG00000253177	RP11-100L22.1	8:93681063-93691822	NOTEST	0	0	0	0	1	1
ENSG00000253178	ENSG00000253178	RP11-404E12.1	8:20408711-20408916	NOTEST	0	0	0	0	1	1
ENSG00000253179	ENSG00000253179	CALCP	11:14926542-15103888	NOTEST	0	0	0	0	1	1
ENSG00000253180	ENSG00000253180	RP11-410L14.1	8:100008990-100025272	NOTEST	0	0.124969	inf	0	1	1

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ENSG00000253182	ENSG00000253182	RP11-486M23.2	8:29405687-29421858	NOTEST	0	0	0	0	1	1
ENSG00000253183	ENSG00000253183	RP4-701O16.5	7:139187198-139188558	NOTEST	0	0	0	0	1	1
ENSG00000253184	ENSG00000253184	RP11-13N12.2	8:16461763-16522388	NOTEST	0	0	0	0	1	1
ENSG00000253186	ENSG00000253186	RP11-726G23.3	8:43108874-43109232	NOTEST	0	0	0	0	1	1
ENSG00000253187	ENSG00000253187	HOXA10-AS	7:27202053-27219880	NOTEST	0.172612	0.0857684	-1.00901	0	1	1
ENSG00000253188	ENSG00000253188	TRBV6-7	7:142143651-142144084	NOTEST	0	0	0	0	1	1
ENSG00000253189	ENSG00000253189	RP11-158A14.1	8:5893954-5894496	NOTEST	0	0	0	0	1	1
ENSG00000253190	ENSG00000253190	AC084082.3	8:67024901-67027440	NOTEST	0	0.0295028	inf	0	1	1
ENSG00000253191	ENSG00000253191	IGKV1D-32	2:89967231-89967677	NOTEST	0	0	0	0	1	1
ENSG00000253193	ENSG00000253193	FCGR1C	1:149369293-149429348	NOTEST	0	0	0	0	1	1
ENSG00000253194	ENSG00000253194	RP11-351A11.1	6:119134604-119470552	NOTEST	0	0	0	0	1	1
ENSG00000253195	ENSG00000253195	RP11-359P18.6	8:43397218-43399200	NOTEST	0	0	0	0	1	1
ENSG00000253196	ENSG00000253196	RP11-706C16.7	8:143844533-143859640	NOTEST	0	0	0	0	1	1
ENSG00000253197	ENSG00000253197	CTD-3239E11.2	8:93895211-94029901	NOTEST	0	0	0	0	1	1
ENSG00000253198	ENSG00000253198	RP11-643N23.1	8:43529412-43529734	NOTEST	0	0	0	0	1	1
ENSG00000253199	ENSG00000253199	RP11-421P23.1	8:20810155-20852630	NOTEST	0	0	0	0	1	1
ENSG00000253202	ENSG00000253202	IGKV3-25	2:89491987-89492240	NOTEST	0	0	0	0	1	1
ENSG00000253205	ENSG00000253205	CTD-3046C4.1	8:64297396-64388040	NOTEST	0	0.022505	inf	0	1	1
ENSG00000253206	ENSG00000253206	RP11-738G5.2	8:50448944-50466973	NOTEST	0	0	0	0	1	1
ENSG00000253207	ENSG00000253207	RP11-67H2.1	8:114612538-114629187	NOTEST	0	0	0	0	1	1
ENSG00000253208	ENSG00000253208	RP11-1G11.2	8:26371790-26515694	NOTEST	0	0	0	0	1	1
ENSG00000253209	ENSG00000253209	IGHV3-65	14:107122107-107122548	NOTEST	0	0	0	0	1	1
ENSG00000253213	ENSG00000253213	RP11-546B8.3	5:170288873-170727019	NOTEST	0.0157014	0	#NAME?	0	1	1
ENSG00000253214	ENSG00000253214	RP11-1149M10.2	8:82066513-82076834	NOTEST	0.290304	0.393666	0.43941	0	1	1
ENSG00000253215	ENSG00000253215	RP11-156K13.2	8:17721888-17767874	NOTEST	0	0	0	0	1	1
ENSG00000253216	ENSG00000253216	RP11-744J10.2	8:70337269-70360479	NOTEST	0	0	0	0	1	1
ENSG00000253217	ENSG00000253217	KB-1991G8.1	8:101349822-101362935	NOTEST	0	0	0	0	1	1
ENSG00000253218	ENSG00000253218	KLF3P1	5:171636643-171711075	NOTEST	0	0.0122971	inf	0	1	1
ENSG00000253219	ENSG00000253219	KRT18P41	5:169567667-169568944	NOTEST	0	0	0	0	1	1
ENSG00000253220	ENSG00000253220	RP11-103H7.2	8:127510393-127512548	NOTEST	0	0	0	0	1	1
ENSG00000253222	ENSG00000253222	NRG1-IT2	8:31496901-32622548	NOTEST	0	0	0	0	1	1
ENSG00000253223	ENSG00000253223	RP11-409C19.2	8:67876333-68255912	NOTEST	0.0157937	0.0173291	0.133845	0	1	1
ENSG00000253224	ENSG00000253224	PGAM5P1	5:109218882-109221124	NOTEST	0	0	0	0	1	1
ENSG00000253225	ENSG00000253225	RP11-1057N3.2	8:130263212-130263384	NOTEST	0	0	0	0	1	1
ENSG00000253226	ENSG00000253226	HAUS1P3	8:73449625-73850584	NOTEST	0	0	0	0	1	1
ENSG00000253227	ENSG00000253227	RP11-383J24.1	8:125283923-125289825	NOTEST	0.116661	0.0275716	-2.08107	0	1	1
ENSG00000253228	ENSG00000253228	NRBF2P4	8:108911543-109095913	NOTEST	0	0	0	0	1	1
ENSG00000253229	ENSG00000253229	HIGD1AP6	8:76135638-76236976	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000253230	ENSG00000253230	LINC00599	8:9757573-9762876	NOTEST	0	0	0	0	1	1
ENSG00000253231	ENSG00000253231	COX6CP8	8:64599736-65281115	NOTEST	0	0	0	0	1	1
ENSG00000253232	ENSG00000253232	RP11-359B20.5	8:33380671-33380809	NOTEST	0	0	0	0	1	1
ENSG00000253233	ENSG00000253233	KB-1582A10.2	8:39724954-39725331	NOTEST	0	0	0	0	1	1
ENSG00000253234	ENSG00000253234	IGLV2-5	22:23198936-23199213	NOTEST	0	0	0	0	1	1
ENSG00000253235	ENSG00000253235	RP11-434I12.4	8:74281004-74281530	NOTEST	0	0	0	0	1	1
ENSG00000253236	ENSG00000253236	CTD-2313P7.1	5:163723701-164598649	NOTEST	0	0	0	0	1	1
ENSG00000253237	ENSG00000253237	RP11-775E10.1	8:81263366-81263651	NOTEST	0	0	0	0	1	1
ENSG00000253238	ENSG00000253238	RP11-941H19.3	8:81177762-81252075	NOTEST	0	0	0	0	1	1
ENSG00000253239	ENSG00000253239	IGLVI-70	22:22345495-22398340	NOTEST	0	0	0	0	1	1
ENSG00000253240	ENSG00000253240	IGHV3-36	14:106848684-106849142	NOTEST	0	0	0	0	1	1
ENSG00000253241	ENSG00000253241	IGHV3-50	14:107022104-107022543	NOTEST	0	0	0	0	1	1
ENSG00000253242	ENSG00000253242	IGLVIV-64	22:22429776-22430077	NOTEST	0	0	0	0	1	1
ENSG00000253244	ENSG00000253244	RP11-619L12.3	5:173472606-173670504	NOTEST	0	0	0	0	1	1
ENSG00000253245	ENSG00000253245	MTND1P36	11:102980159-103350591	NOTEST	0	0	0	0	1	1
ENSG00000253247	ENSG00000253247	IGHV3-76	14:107236096-107236391	NOTEST	0	0	0	0	1	1
ENSG00000253248	ENSG00000253248	RP11-149P24.1	8:137059263-137178365	NOTEST	0	0	0	0	1	1
ENSG00000253252	ENSG00000253252	RP11-10A14.6	8:9037760-9040029	NOTEST	0	0	0	0	1	1
ENSG00000253256	ENSG00000253256	CTB-11I22.1	5:158584416-158675804	NOTEST	0	0	0	0	1	1
ENSG00000253257	ENSG00000253257	MTND4P7	8:12940869-13373167	NOTEST	0	0	0	0	1	1
ENSG00000253258	ENSG00000253258	RP11-539E17.5	8:124191199-124222314	NOTEST	0	0	0	0	1	1
ENSG00000253259	ENSG00000253259	RP11-737F9.2	8:131792546-132054672	NOTEST	0	0	0	0	1	1
ENSG00000253260	ENSG00000253260	RP11-379I19.1	8:60473885-60506260	NOTEST	0	0	0	0	1	1
ENSG00000253261	ENSG00000253261	CTC-280C13.1	5:154373157-154374005	NOTEST	0	0	0	0	1	1
ENSG00000253262	ENSG00000253262	RP11-221H10.1	8:4930166-4930391	NOTEST	0	0	0	0	1	1
ENSG00000253263	ENSG00000253263	KB-1507C5.3	8:103838584-103990104	NOTEST	0.117283	0	#NAME?	0	1	1
ENSG00000253264	ENSG00000253264	PCAT2	8:128084938-128094466	NOTEST	0.0367698	0	#NAME?	0	1	1
ENSG00000253265	ENSG00000253265	IGKV2-14	2:89377505-89378280	NOTEST	0	0	0	0	1	1
ENSG00000253266	ENSG00000253266	RP11-128L5.1	8:142065388-142070695	NOTEST	0	0.105455	inf	0	1	1
ENSG00000253267	ENSG00000253267	RP11-666I19.2	8:1449531-1656642	NOTEST	0	0	0	0	1	1
ENSG00000253269	ENSG00000253269	CTB-37A13.1	5:169064250-169510386	NOTEST	0	0	0	0	1	1
ENSG00000253270	ENSG00000253270	RP11-1105O14.1	8:19261671-19615540	NOTEST	0	0	0	0	1	1
ENSG00000253271	ENSG00000253271	RP11-1059L18.1	8:117962511-118188953	NOTEST	0	0	0	0	1	1
ENSG00000253273	ENSG00000253273	RP11-99A14.1	8:74332238-74791145	NOTEST	0	0	0	0	1	1
ENSG00000253274	ENSG00000253274	IGHV1-67	14:107136619-107137059	NOTEST	0	0	0	0	1	1
ENSG00000253275	ENSG00000253275	RP11-566H8.1	8:31354938-31356128	NOTEST	0	0	0	0	1	1
ENSG00000253278	ENSG00000253278	IGKV2-10	2:89319488-89320183	NOTEST	0	0	0	0	1	1
ENSG00000253279	ENSG00000253279	FAM183CP	8:29779028-29811240	NOTEST	0	0	0	0	1	1
ENSG00000253280	ENSG00000253280	RP11-618M23.4	8:18942501-19116979	NOTEST	0	0	0	0	1	1
ENSG00000253281	ENSG00000253281	RP11-716D16.1	8:59168329-59184678	NOTEST	0	0	0	0	1	1
ENSG00000253282	ENSG00000253282	KB-1410C5.3	8:102299672-102306011	NOTEST	0	0	0	0	1	1
ENSG00000253283	ENSG00000253283	RP11-146E23.2	8:85998849-85999421	NOTEST	0	0	0	0	1	1

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ENSG00000253286	ENSG00000253286	CTD-2552K11.2	8:124626464-124670810	NOTEST	0.0696862	0.0825954	0.245188	0	1	1
ENSG00000253287	ENSG00000253287	RP11-281N10.1	8:72691839-72705110	NOTEST	0	0	0	0	1	1
ENSG00000253288	ENSG00000253288	RP11-238K6.1	8:138821686-139095813	NOTEST	0	0	0	0	1	1
ENSG00000253290	ENSG00000253290	RP11-597M17.3	8:27727398-27850244	NOTEST	0	0	0	0	1	1
ENSG00000253291	ENSG00000253291	TRBV7-7	7:142119819-142120321	NOTEST	0	0	0	0	1	1
ENSG00000253292	ENSG00000253292	RP11-298P6.5	8:87345502-87777251	NOTEST	0	0	0	0	1	1
ENSG00000253294	ENSG00000253294	IGHVII-40-1	14:106896860-106896918	NOTEST	0	0	0	0	1	1
ENSG00000253295	ENSG00000253295	RP11-779O18.1	5:172185228-172204777	NOTEST	0	0	0	0	1	1
ENSG00000253297	ENSG00000253297	HTR4-IT1	5:147830594-148056798	NOTEST	0	0	0	0	1	1
ENSG00000253298	ENSG00000253298	AC008703.1	5:158875563-158893284	NOTEST	0	0	0	0	1	1
ENSG00000253299	ENSG00000253299	RP11-316J7.4	8:101170133-101348446	NOTEST	0	0.134581	inf	0	1	1
ENSG00000253300	ENSG00000253300	RP11-108E14.1	8:20513201-20557645	NOTEST	0	0	0	0	1	1
ENSG00000253302	ENSG00000253302	STAU2-AS1	8:74332238-74791145	NOTEST	0.0400396	0	#NAME?	0	1	1
ENSG00000253303	ENSG00000253303	IGHVIII-82	14:107287769-107288019	NOTEST	0	0	0	0	1	1
ENSG00000253304	ENSG00000253304	TMEM200B	1:29213602-29450447	NOTEST	0.0206229	0.0413582	1.00392	0	1	1
ENSG00000253305	ENSG00000253305	PCDHGB6	5:140710251-140892546	NOTEST	0.0640944	0.113953	0.830167	0	1	1
ENSG00000253307	ENSG00000253307	RP11-10J21.4	8:142217264-142318404	NOTEST	0	0.261343	inf	0	1	1
ENSG00000253308	ENSG00000253308	RP1-170O19.17	7:27278861-27280847	NOTEST	0	0	0	0	1	1
ENSG00000253309	ENSG00000253309	SERPINE3	13:51909908-52126500	NOTEST	0.527251	0.438527	-0.265826	0	1	1
ENSG00000253310	ENSG00000253310	IGHVIII-76-1	14:107239993-107240279	NOTEST	0	0	0	0	1	1
ENSG00000253311	ENSG00000253311	AC011343.1	5:159203778-159298391	NOTEST	0	0	0	0	1	1
ENSG00000253312	ENSG00000253312	RP11-359P18.2	8:43106853-43107001	NOTEST	0	0	0	0	1	1
ENSG00000253313	ENSG00000253313	C1orf210	1:43747553-43751288	NOTEST	0.0324341	0	#NAME?	0	1	1
ENSG00000253314	ENSG00000253314	LINC00293	8:47733858-47765929	NOTEST	0	0	0	0	1	1
ENSG00000253315	ENSG00000253315	CTB-11I22.2	5:158584416-158675804	NOTEST	0	0	0	0	1	1
ENSG00000253317	ENSG00000253317	RP11-142A23.1	8:73108568-73114504	NOTEST	0.0868524	0.0167217	-2.37684	0	1	1
ENSG00000253318	ENSG00000253318	TMCC1P1	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000253319	ENSG00000253319	RP11-359P18.8	8:43366962-43367176	NOTEST	0	0	0	0	1	1
ENSG00000253321	ENSG00000253321	RP11-61G23.2	5:89648853-89652426	NOTEST	0	0	0	0	1	1
ENSG00000253322	ENSG00000253322	RP11-388G22.1	8:58506724-58717588	NOTEST	0	0	0	0	1	1
ENSG00000253325	ENSG00000253325	IGHV7-34-1	14:106833230-106833664	NOTEST	0	0	0	0	1	1
ENSG00000253326	ENSG00000253326	RP11-261C10.7	1:243218162-243219696	NOTEST	0.314983	0.236178	-0.415396	0	1	1
ENSG00000253327	ENSG00000253327	RAD21-AS1	8:117654368-117889107	NOTEST	0.0162148	0	#NAME?	0	1	1
ENSG00000253328	ENSG00000253328	SUMO2P19	8:103251621-103425069	NOTEST	0	0	0	0	1	1
ENSG00000253329	ENSG00000253329	IGLV3-30	22:22961041-22961633	NOTEST	0	0	0	0	1	1
ENSG00000253330	ENSG00000253330	RP11-697N18.3	8:48173166-48648868	NOTEST	0.494881	0.116526	-2.08643	0	1	1
ENSG00000253331	ENSG00000253331	CTC-207P7.1	5:163546103-163661103	NOTEST	0	0	0	0	1	1
ENSG00000253332	ENSG00000253332	KB-1582A10.1	8:39717737-39718044	NOTEST	0	0	0	0	1	1
ENSG00000253333	ENSG00000253333	RP11-497H16.8	5:69790926-69796730	NOTEST	0.222143	0.216898	-0.0344753	0	1	1

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ENSG00000253335	ENSG00000253335	RP11-420B22.1	8:18384810-18942240	NOTEST	0.0397186	0	#NAME?	0	1	1
ENSG00000253336	ENSG00000253336	RP11-468O2.1	8:124300594-124302743	NOTEST	0.0135933	0	#NAME?	0	1	1
ENSG00000253338	ENSG00000253338	IGLV3-29	22:23003768-23004012	NOTEST	0	0	0	0	1	1
ENSG00000253339	ENSG00000253339	RP11-434I12.3	8:74271147-74275023	NOTEST	0	0	0	0	1	1
ENSG00000253340	ENSG00000253340	RP11-139G7.1	8:51772089-51772622	NOTEST	0	0	0	0	1	1
ENSG00000253342	ENSG00000253342	RP11-219J21.2	8:25634194-25634972	NOTEST	0	0	0	0	1	1
ENSG00000253343	ENSG00000253343	CTD-3023L14.3	8:8413247-8427198	NOTEST	0	0	0	0	1	1
ENSG00000253344	ENSG00000253344	RP11-346L1.2	8:37483532-37531905	NOTEST	0.0446717	0.0539073	0.271118	0	1	1
ENSG00000253345	ENSG00000253345	IGHVII-22-1	14:106719954-106720219	NOTEST	0	0	0	0	1	1
ENSG00000253346	ENSG00000253346	CTD-3107M8.1	8:30189476-30189793	NOTEST	0	0	0	0	1	1
ENSG00000253347	ENSG00000253347	CTD-2026D20.2	17:45331211-45518678	NOTEST	0.0808787	0	#NAME?	0	1	1
ENSG00000253348	ENSG00000253348	MIR4454	5:170174050-170241051	NOTEST	0	0	0	0	1	1
ENSG00000253349	ENSG00000253349	COX6B1P6	8:90835775-90836030	NOTEST	0	0	0	0	1	1
ENSG00000253350	ENSG00000253350	RP11-127H5.1	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000253351	ENSG00000253351	KB-1047C11.1	8:96216683-96822364	NOTEST	0	0	0	0	1	1
ENSG00000253354	ENSG00000253354	CTA-392C11.2	8:40227546-40259367	NOTEST	0	0	0	0	1	1
ENSG00000253355	ENSG00000253355	KB-1460A1.2	8:102141214-102145714	NOTEST	0	0	0	0	1	1
ENSG00000253356	ENSG00000253356	RP11-90P5.2	8:37962759-38070819	NOTEST	0	0.143035	inf	0	1	1
ENSG00000253357	ENSG00000253357	CTB-78F1.2	5:166711803-167691162	NOTEST	0	0	0	0	1	1
ENSG00000253358	ENSG00000253358	GS1-251I9.3	8:92006023-92053292	NOTEST	0	0	0	0	1	1
ENSG00000253359	ENSG00000253359	IGHV3-37	14:106852587-106853026	NOTEST	0	0	0	0	1	1
ENSG00000253361	ENSG00000253361	RP11-675F6.3	8:38401169-38416538	NOTEST	0	0	0	0	1	1
ENSG00000253362	ENSG00000253362	RP11-120I21.3	8:85075683-85076799	NOTEST	0	0	0	0	1	1
ENSG00000253363	ENSG00000253363	RP11-962G15.1	8:36394908-36636682	NOTEST	0	0	0	0	1	1
ENSG00000253364	ENSG00000253364	RP11-731F5.2	14:106109388-106115394	NOTEST	0	0	0	0	1	1
ENSG00000253365	ENSG00000253365	IGKV1D-22	2:90049550-90049994	NOTEST	0	0	0	0	1	1
ENSG00000253367	ENSG00000253367	IGHVIII-25-1	14:106750161-106750402	NOTEST	0	0	0	0	1	1
ENSG00000253369	ENSG00000253369	RP11-1081M5.1	8:54307770-54308506	NOTEST	0	0	0	0	1	1
ENSG00000253370	ENSG00000253370	CTB-56J15.1	5:155297353-156194799	NOTEST	0	0	0	0	1	1
ENSG00000253371	ENSG00000253371	RP11-587H10.1	8:93512810-93522044	NOTEST	0	0	0	0	1	1
ENSG00000253372	ENSG00000253372	RP11-44N11.1	8:123793632-123986750	NOTEST	0	0	0	0	1	1
ENSG00000253373	ENSG00000253373	RP11-21C17.1	8:70087813-70090424	NOTEST	0	0	0	0	1	1
ENSG00000253374	ENSG00000253374	RP11-257P3.3	8:82351670-82445510	NOTEST	0	0.0853426	inf	0	1	1
ENSG00000253376	ENSG00000253376	RP11-44D19.1	8:58802134-58803368	NOTEST	0.0447343	0	#NAME?	0	1	1
ENSG00000253377	ENSG00000253377	RP11-566H8.3	8:31133111-31241795	NOTEST	0	0	0	0	1	1
ENSG00000253380	ENSG00000253380	RP11-738G5.1	8:50409321-50424739	NOTEST	0	0	0	0	1	1
ENSG00000253381	ENSG00000253381	RP11-359E19.1	8:39961687-39965454	NOTEST	0	0	0	0	1	1
ENSG00000253382	ENSG00000253382	POU5F1P2	8:103633736-103634559	NOTEST	0	0	0	0	1	1
ENSG00000253383	ENSG00000253383	RP11-116B19.2	8:74332238-74791145	NOTEST	0	0	0	0	1	1
ENSG00000253384	ENSG00000253384	CTD-2547L16.3	8:17913933-17953903	NOTEST	0.104086	0.0452792	-1.20086	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000253386	ENSG00000253386	IGHVII-49-1	14:107020362-107020586	NOTEST	0	0	0	0	1	1
ENSG00000253387	ENSG00000253387	IGHVIII-5-1	14:106495897-106495996	NOTEST	0	0	0	0	1	1
ENSG00000253388	ENSG00000253388	RP11-150O12.2	8:37278858-37411701	NOTEST	0	0	0	0	1	1
ENSG00000253389	ENSG00000253389	RP11-930P14.1	8:41510738-41754280	NOTEST	0	0	0	0	1	1
ENSG00000253390	ENSG00000253390	CTC-756D1.2	8:23316113-23342484	NOTEST	0.179177	0.189056	0.0774245	0	1	1
ENSG00000253391	ENSG00000253391	RP11-758H6.1	8:80432379-80432884	NOTEST	0	0	0	0	1	1
ENSG00000253392	ENSG00000253392	AC006277.2	19:2900895-2926805	NOTEST	0.0941388	0	#NAME?	0	1	1
ENSG00000253393	ENSG00000253393	RANP9	8:32853695-32902373	NOTEST	0	0	0	0	1	1
ENSG00000253394	ENSG00000253394	LINC00534	8:91233715-91632298	NOTEST	0	0	0	0	1	1
ENSG00000253395	ENSG00000253395	KB-1460A1.1	8:102134372-102138386	NOTEST	0.609974	0.208119	-1.55134	0	1	1
ENSG00000253396	ENSG00000253396	RP11-15G16.1	8:41292816-41297938	NOTEST	0	0	0	0	1	1
ENSG00000253397	ENSG00000253397	RP11-597M17.1	8:27727398-27850244	NOTEST	0	0	0	0	1	1
ENSG00000253398	ENSG00000253398	RP11-775B15.2	8:120428545-120474590	NOTEST	0	0	0	0	1	1
ENSG00000253399	ENSG00000253399	AC078852.2	4:1341053-1381837	NOTEST	0.103275	0.175927	0.768486	0	1	1
ENSG00000253400	ENSG00000253400	RP11-337A23.6	9:26801730-26805860	NOTEST	0.215025	0.163881	-0.391856	0	1	1
ENSG00000253401	ENSG00000253401	AF121898.2	8:87878669-88767946	NOTEST	0	0	0	0	1	1
ENSG00000253403	ENSG00000253403	RP11-348M17.2	5:160715435-161129599	NOTEST	0	0	0	0	1	1
ENSG00000253404	ENSG00000253404	AC034243.1	5:137946655-138270723	NOTEST	0.0661592	0.111608	0.754427	0	1	1
ENSG00000253405	ENSG00000253405	EVX1-AS	7:27281047-27290112	NOTEST	0	0	0	0	1	1
ENSG00000253406	ENSG00000253406	AC012613.2	5:148521045-148721365	NOTEST	0.0293174	0.0206452	-0.505953	0	1	1
ENSG00000253407	ENSG00000253407	RP11-381I15.1	8:132142634-132157128	NOTEST	0	0	0	0	1	1
ENSG00000253408	ENSG00000253408	RP11-231D20.2	8:42091192-42128715	NOTEST	0.0354169	0.0275973	-0.359909	0	1	1
ENSG00000253409	ENSG00000253409	TRBV7-4	7:142176328-142176790	NOTEST	0	0	0	0	1	1
ENSG00000253410	ENSG00000253410	RP11-539E17.3	8:124191199-124222314	NOTEST	0	0	0	0	1	1
ENSG00000253412	ENSG00000253412	IGHVIII-13-1	14:106598994-106599285	NOTEST	0	0	0	0	1	1
ENSG00000253413	ENSG00000253413	RP11-960H2.2	8:60672605-60672822	NOTEST	0	0	0	0	1	1
ENSG00000253414	ENSG00000253414	RP11-150O12.6	8:37278858-37411701	NOTEST	0.213032	0.202299	-0.0745857	0	1	1
ENSG00000253415	ENSG00000253415	RP11-44N12.4	8:99413630-99955055	NOTEST	0	0	0	0	1	1
ENSG00000253416	ENSG00000253416	RP11-48D4.2	8:77816826-77825635	NOTEST	0	0	0	0	1	1
ENSG00000253417	ENSG00000253417	RP11-109J4.1	5:160358784-160365633	NOTEST	0	0	0	0	1	1
ENSG00000253418	ENSG00000253418	SNX18P27	8:43368785-43369564	NOTEST	0	0	0	0	1	1
ENSG00000253420	ENSG00000253420	RP11-642D21.2	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000253421	ENSG00000253421	ZNHIT1P1	8:143915553-143999259	NOTEST	0	0	0	0	1	1
ENSG00000253422	ENSG00000253422	CTB-47B8.4	5:157505106-157505772	NOTEST	0	0	0	0	1	1
ENSG00000253423	ENSG00000253423	RP11-813B8.1	8:84113186-84114666	NOTEST	0	0	0	0	1	1
ENSG00000253424	ENSG00000253424	CTC-436K13.3	5:157683144-157685444	NOTEST	0	0	0	0	1	1
ENSG00000253425	ENSG00000253425	HSPA8P13	8:47460710-47462424	NOTEST	0	0	0	0	1	1
ENSG00000253427	ENSG00000253427	RP11-103H7.1	8:127486433-127504841	NOTEST	0	0	0	0	1	1
ENSG00000253428	ENSG00000253428	CTB-43E15.2	5:173116461-173132852	NOTEST	0	0	0	0	1	1
ENSG00000253429	ENSG00000253429	KB-1090H4.2	8:95721179-95721472	NOTEST	0	0	0	0	1	1
ENSG00000253430	ENSG00000253430	RP11-14I17.2	8:26236774-26371608	NOTEST	0	0	0	0	1	1

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ENSG00000253432	ENSG00000253432	RP11-324F11.1	8:140108547-140115073	NOTEST	0	0	0	0	1	1
ENSG00000253433	ENSG00000253433	AC083843.3	8:135850311-135854880	NOTEST	0.0794051	0	#NAME?	0	1	1
ENSG00000253434	ENSG00000253434	RP11-1101K5.1	8:112388867-112555202	NOTEST	0	0	0	0	1	1
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ENSG00000253437	ENSG00000253437	RP11-90P5.4	8:37962759-38070819	NOTEST	0	0	0	0	1	1
ENSG00000253438	ENSG00000253438	PCAT1	8:127859299-128033259	NOTEST	0.140939	0.0923509	-0.609878	0	1	1
ENSG00000253439	ENSG00000253439	CDC42P5	5:172483354-172566291	NOTEST	0	0	0	0	1	1
ENSG00000253440	ENSG00000253440	IGHV3-33-2	14:106825037-106825477	NOTEST	0	0	0	0	1	1
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ENSG00000253444	ENSG00000253444	AC133633.2	8:2350991-2369693	NOTEST	0	0	0	0	1	1
ENSG00000253445	ENSG00000253445	CTB-79E8.2	5:172068268-172124723	NOTEST	4.09E-05	0.0923628	11.1399	0	1	1
ENSG00000253447	ENSG00000253447	RP11-619L12.4	5:173472606-173670504	NOTEST	0	0	0	0	1	1
ENSG00000253448	ENSG00000253448	IGLV3-6	22:23192549-23192799	NOTEST	0	0	0	0	1	1
ENSG00000253449	ENSG00000253449	CTC-436K13.6	5:157652359-157661384	NOTEST	0	0	0	0	1	1
ENSG00000253451	ENSG00000253451	IGLV2-28	22:23006897-23007377	NOTEST	0	0	0	0	1	1
ENSG00000253452	ENSG00000253452	RP11-473J6.1	8:35719640-35828183	NOTEST	0	0	0	0	1	1
ENSG00000253454	ENSG00000253454	NDUFA5P2	8:105501458-105601252	NOTEST	0	0	0	0	1	1
ENSG00000253455	ENSG00000253455	RP11-770E5.3	8:49464126-49611069	NOTEST	0	0	0	0	1	1
ENSG00000253456	ENSG00000253456	CTD-2363C16.2	5:158122927-158526769	NOTEST	0	0	0	0	1	1
ENSG00000253457	ENSG00000253457	SMIM18	8:30435834-30515768	NOTEST	0	0.0588949	inf	0	1	1
ENSG00000253458	ENSG00000253458	IGHVII-15-1	14:106620269-106620489	NOTEST	0	0	0	0	1	1
ENSG00000253459	ENSG00000253459	AL139099.1	14:50043389-50081390	NOTEST	0.168675	0.0340267	-2.3095	0	1	1
ENSG00000253460	ENSG00000253460	IGKV2OR22-3	22:17402332-17403063	NOTEST	0	0	0	0	1	1
ENSG00000253461	ENSG00000253461	IGKV1-35	2:89586445-89586730	NOTEST	0	0	0	0	1	1
ENSG00000253462	ENSG00000253462	IGHVIII-26-1	14:106765677-106765927	NOTEST	0	0	0	0	1	1
ENSG00000253463	ENSG00000253463	HMGB1P19	8:124014799-124164393	NOTEST	0	0	0	0	1	1
ENSG00000253464	ENSG00000253464	IGHV3-29	14:106787367-106787804	NOTEST	0	0	0	0	1	1
ENSG00000253465	ENSG00000253465	IGHVIV-44-1	14:106938444-106977000	NOTEST	0	0	0	0	1	1
ENSG00000253467	ENSG00000253467	IGHV7-40	14:106881269-106881468	NOTEST	0	0	0	0	1	1
ENSG00000253468	ENSG00000253468	KB-1517D11.	8:99413630-99955055	NOTEST	0	0	0	0	1	1
ENSG00000253469	ENSG00000253469	CTC-264O10.1	5:166591938-166595406	NOTEST	0	0	0	0	1	1
ENSG00000253470	ENSG00000253470	RP11-697B24.1	8:126761298-126762485	NOTEST	0	0	0	0	1	1
ENSG00000253471	ENSG00000253471	RP11-175E9.1	8:23564653-23647000	NOTEST	0	0	0	0	1	1
ENSG00000253472	ENSG00000253472	CTB-23I7.2	5:150745993-150810913	NOTEST	0	0	0	0	1	1
ENSG00000253474	ENSG00000253474	RP11-10H3.1	8:50081097-50141484	NOTEST	0	0	0	0	1	1
ENSG00000253475	ENSG00000253475	RP11-110G21.2	8:52730139-52811735	NOTEST	0	0	0	0	1	1
ENSG00000253476	ENSG00000253476	RP11-395I14.2	8:25283036-25284096	NOTEST	0.517406	0.183832	-1.49291	0	1	1
ENSG00000253477	ENSG00000253477	RP11-1C8.4	8:104495625-105268322	NOTEST	0.148629	0.0590714	-1.33119	0	1	1
ENSG00000253479	ENSG00000253479	RP11-744J10.3	8:70337269-70360479	NOTEST	0	0	0	0	1	1
ENSG00000253480	ENSG00000253480	RP11-39H3.1	5:179512716-179514038	NOTEST	0	0	0	0	1	1
ENSG00000253481	ENSG00000253481	IGKV1OR22-1	22:17414410-17414893	NOTEST	0	0	0	0	1	1
ENSG00000253482	ENSG00000253482	IGHVII-26-2	14:106770913-106771238	NOTEST	0	0	0	0	1	1

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ENSG00000253485	ENSG00000253485	PCDHGA5	5:140710251-140892546	NOTEST	0.0618539	0.117933	0.931028	0	1	1
ENSG00000253486	ENSG00000253486	RP11-726G23.7	8:43129924-43130434	NOTEST	0	0	0	0	1	1
ENSG00000253487	ENSG00000253487	IGKV2-36	2:89594989-89595212	NOTEST	0	0	0	0	1	1
ENSG00000253488	ENSG00000253488	RP11-583M2.2	8:23492388-23493020	NOTEST	0	0	0	0	1	1
ENSG00000253489	ENSG00000253489	RP11-114O8.1	8:112111189-112248432	NOTEST	0	0	0	0	1	1
ENSG00000253491	ENSG00000253491	IGHVII-30-1	14:106798645-106798877	NOTEST	0	0	0	0	1	1
ENSG00000253492	ENSG00000253492	CDH12P3	5:69428505-69428800	NOTEST	0	0	0	0	1	1
ENSG00000253493	ENSG00000253493	RP11-89A16.1	8:65885722-65886083	NOTEST	0	0	0	0	1	1
ENSG00000253495	ENSG00000253495	RP11-99I9.2	8:120569325-120685693	NOTEST	0	0	0	0	1	1
ENSG00000253496	ENSG00000253496	RP11-13N12.1	8:16534413-16772553	NOTEST	0	0	0	0	1	1
ENSG00000253497	ENSG00000253497	IGKV1-13	2:89345491-89345963	NOTEST	0	0	0	0	1	1
ENSG00000253499	ENSG00000253499	RP11-393K19.1	8:115330628-115331140	NOTEST	0	0	0	0	1	1
ENSG00000253500	ENSG00000253500	AF121898.3	8:87878669-88767946	NOTEST	0	0	0	0	1	1
ENSG00000253501	ENSG00000253501	IGKV3D-34	2:89945566-89946056	NOTEST	0	0	0	0	1	1
ENSG00000253502	ENSG00000253502	ATP6V1G1P2	8:48001194-48110484	NOTEST	0	0	0	0	1	1
ENSG00000253503	ENSG00000253503	RP11-653B10.1	8:83426802-83589388	NOTEST	0	0	0	0	1	1
ENSG00000253504	ENSG00000253504	RP11-593P24.2	8:36135280-36136404	NOTEST	0	0	0	0	1	1
ENSG00000253505	ENSG00000253505	CTA-398F10.1	8:8272199-8282142	NOTEST	0	0	0	0	1	1
ENSG00000253506	ENSG00000253506	NACA2	17:59667793-59668563	NOTEST	0	1.14E-05	inf	0	1	1
ENSG00000253507	ENSG00000253507	CTD-2501M5.1	8:132320791-132329879	NOTEST	0	0	0	0	1	1
ENSG00000253508	ENSG00000253508	RP1-170O19.14	7:27221128-27233067	NOTEST	0.0385841	0	#NAME?	0	1	1
ENSG00000253509	ENSG00000253509	CTD-3080F16.3	8:41119480-41167016	NOTEST	0	0	0	0	1	1
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ENSG00000253512	ENSG00000253512	CTC-535M15.1	5:165209809-165210139	NOTEST	0	0	0	0	1	1
ENSG00000253513	ENSG00000253513	RP11-6D1.3	8:126009226-126010440	NOTEST	0.116176	0	#NAME?	0	1	1
ENSG00000253515	ENSG00000253515	RP11-417F21.2	2:46717888-46852881	NOTEST	0.0650532	0	#NAME?	0	1	1
ENSG00000253516	ENSG00000253516	HMGB1P41	8:81540685-81787016	NOTEST	0.0551959	0.172865	1.64701	0	1	1
ENSG00000253517	ENSG00000253517	XRCC6P4	8:63161149-63912211	NOTEST	0	0	0	0	1	1
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ENSG00000253520	ENSG00000253520	RP11-798K23.5	5:178954224-178954514	NOTEST	0	0	0	0	1	1
ENSG00000253521	ENSG00000253521	HPYR1	8:133572744-133573726	NOTEST	0	0	0	0	1	1
ENSG00000253523	ENSG00000253523	RP11-1112C15.2	8:58907067-59116838	NOTEST	0	0	0	0	1	1
ENSG00000253524	ENSG00000253524	RP11-89M20.2	8:35861833-35952564	NOTEST	0	0	0	0	1	1
ENSG00000253525	ENSG00000253525	CTD-2114J12.1	8:92114059-92410378	NOTEST	0	0	0	0	1	1
ENSG00000253526	ENSG00000253526	RP11-152P17.3	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000253527	ENSG00000253527	CTB-105L4.2	5:166711803-167691162	NOTEST	0	0	0	0	1	1
ENSG00000253528	ENSG00000253528	RP11-347C18.4	8:95825538-96128683	NOTEST	0	0	0	0	1	1
ENSG00000253530	ENSG00000253530	RP11-103H7.3	8:127530942-127534596	NOTEST	0	0	0	0	1	1

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ENSG00000253534	ENSG00000253534	TRBV6-8	7:142124136-142124565	NOTEST	0	0	0	0	1	1
ENSG00000253535	ENSG00000253535	RP11-624C23.1	8:24151552-24769586	NOTEST	0	0	0	0	1	1
ENSG00000253536	ENSG00000253536	RP11-1174L13.2	5:70751441-70863649	NOTEST	0	0	0	0	1	1
ENSG00000253537	ENSG00000253537	PCDHGA7	5:140710251-140892546	NOTEST	0.0639018	0.157551	1.30189	0	1	1
ENSG00000253538	ENSG00000253538	CTB-32P11.1	5:163546103-163661103	NOTEST	0	0	0	0	1	1
ENSG00000253539	ENSG00000253539	RP11-402L5.1	8:100025493-100906290	NOTEST	0	0	0	0	1	1
ENSG00000253541	ENSG00000253541	SEPT10P1	8:57349232-57472382	NOTEST	0	0.0329847	inf	0	1	1
ENSG00000253542	ENSG00000253542	SDR16C6P	8:57285622-57307924	NOTEST	0	0	0	0	1	1
ENSG00000253543	ENSG00000253543	RP11-89K10.2	8:127564686-127725660	NOTEST	0	0	0	0	1	1
ENSG00000253544	ENSG00000253544	RP11-705O24.4	8:62697605-62856739	NOTEST	0	0	0	0	1	1
ENSG00000253545	ENSG00000253545	IGHV3-52	14:107042359-107042810	NOTEST	0	0	0	0	1	1
ENSG00000253546	ENSG00000253546	IGLVVI-22-1	22:23043244-23043455	NOTEST	0	0	0	0	1	1
ENSG00000253547	ENSG00000253547	RP11-959F10.5	11:62814256-62815598	NOTEST	0	0.00985845	inf	0	1	1
ENSG00000253548	ENSG00000253548	PYDC2	3:191178951-191179245	NOTEST	0	0	0	0	1	1
ENSG00000253549	ENSG00000253549	RP11-317J10.2	8:86239836-86393722	NOTEST	0	0.0271405	inf	0	1	1
ENSG00000253550	ENSG00000253550	RP11-115C21.4	8:6261071-6565730	NOTEST	0	0.121263	inf	0	1	1
ENSG00000253551	ENSG00000253551	RP11-26M5.2	8:53023398-53373519	NOTEST	0	0	0	0	1	1
ENSG00000253553	ENSG00000253553	RP11-586K2.1	8:89044236-89749363	NOTEST	0.108306	0.0412641	-1.39216	0	1	1
ENSG00000253554	ENSG00000253554	RP11-32K4.1	8:64599736-65281115	NOTEST	0	0	0	0	1	1
ENSG00000253555	ENSG00000253555	RP11-16E18.1	8:64048781-64050643	NOTEST	0	0	0	0	1	1
ENSG00000253556	ENSG00000253556	KB-1639H6.7	8:104101023-104102899	NOTEST	0	0	0	0	1	1
ENSG00000253557	ENSG00000253557	RP11-1080G15.1	8:18942501-19116979	NOTEST	0	0	0	0	1	1
ENSG00000253558	ENSG00000253558	CTD-2179L22.1	5:77296348-77590579	NOTEST	0	0	0	0	1	1
ENSG00000253559	ENSG00000253559	OSGEPL1-AS1	2:190539015-190630282	NOTEST	0.389878	0.093058	-2.06682	0	1	1
ENSG00000253560	ENSG00000253560	RP11-16P20.2	8:27554733-27555043	NOTEST	0	0	0	0	1	1
ENSG00000253561	ENSG00000253561	CTD-2588J1.1	8:134783651-134826780	NOTEST	0	0	0	0	1	1
ENSG00000253562	ENSG00000253562	CTD-2340D6.2	8:100025493-100906290	NOTEST	0	0.0327749	inf	0	1	1
ENSG00000253563	ENSG00000253563	NKX2-1-AS1	14:36942411-36992221	NOTEST	0	0.00650707	inf	0	1	1
ENSG00000253564	ENSG00000253564	RP11-956J14.2	8:74128163-74128862	NOTEST	0	0	0	0	1	1
ENSG00000253567	ENSG00000253567	RP11-181B11.2	8:28203101-28347835	NOTEST	0.484803	0.199467	-1.28125	0	1	1
ENSG00000253568	ENSG00000253568	RP11-386D6.3	8:87778162-87830786	NOTEST	0	0	0	0	1	1
ENSG00000253569	ENSG00000253569	VENTXP5	8:33462373-33896526	NOTEST	0	0	0	0	1	1
ENSG00000253570	ENSG00000253570	RNF5P1	8:38458178-38458718	NOTEST	0.12077	0.0285542	-2.08048	0	1	1
ENSG00000253571	ENSG00000253571	RP11-728L1.1	8:5706218-5707214	NOTEST	0	0	0	0	1	1
ENSG00000253572	ENSG00000253572	RP11-107N7.1	5:77238580-77242262	NOTEST	0	0	0	0	1	1
ENSG00000253573	ENSG00000253573	RP11-351C8.1	8:127779120-127802882	NOTEST	0	0	0	0	1	1
ENSG00000253574	ENSG00000253574	RP11-284H18.1	8:140742585-141468678	NOTEST	0	0	0	0	1	1
ENSG00000253576	ENSG00000253576	GS1-5L10.1	8:92967202-93115514	NOTEST	0	0	0	0	1	1
ENSG00000253577	ENSG00000253577	RP11-100L22.3	8:93711969-93889865	NOTEST	0	0	0	0	1	1
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ENSG00000253581	ENSG00000253581	CTD-2272D18.2	8:83891645-83892121	NOTEST	0	0	0	0	1	1
ENSG00000253582	ENSG00000253582	RP11-649G15.2	8:107282371-107764922	NOTEST	0.0831069	0	#NAME?	0	1	1
ENSG00000253583	ENSG00000253583	RP11-573J24.1	8:64498557-64501966	NOTEST	0	0.0206757	inf	0	1	1
ENSG00000253584	ENSG00000253584	CTD-2374C24.1	5:103718998-104728671	NOTEST	0.050683	0	#NAME?	0	1	1
ENSG00000253585	ENSG00000253585	KB-1184D12.1	8:95109991-95116550	NOTEST	0	0.066095	inf	0	1	1
ENSG00000253586	ENSG00000253586	RP11-723D22.2	8:38585703-38710546	NOTEST	0	0.0624899	inf	0	1	1
ENSG00000253587	ENSG00000253587	IGHV3-30-2	14:106800318-106800757	NOTEST	0	0	0	0	1	1
ENSG00000253588	ENSG00000253588	IGHVIII-44	14:106934225-106934399	NOTEST	0	0	0	0	1	1
ENSG00000253590	ENSG00000253590	IGLV3-13	22:23104786-23105009	NOTEST	0	0	0	0	1	1
ENSG00000253591	ENSG00000253591	CTC-265N9.1	5:169780490-170163636	NOTEST	0	0	0	0	1	1
ENSG00000253592	ENSG00000253592	IGKV2-38	2:89609654-89609901	NOTEST	0	0	0	0	1	1
ENSG00000253593	ENSG00000253593	RP11-157E21.1	8:134898738-134914650	NOTEST	0	0	0	0	1	1
ENSG00000253595	ENSG00000253595	CTD-3064M3.1	8:142350647-142354720	NOTEST	0	0	0	0	1	1
ENSG00000253596	ENSG00000253596	CTD-2320G14.2	8:75146934-75401107	NOTEST	0.0354535	0	#NAME?	0	1	1
ENSG00000253597	ENSG00000253597	IGHVII-43-1	14:106928716-106928888	NOTEST	0	0	0	0	1	1
ENSG00000253598	ENSG00000253598	SLC10A5	8:82605841-82608409	NOTEST	0.0819967	0.0940484	0.197836	0	1	1
ENSG00000253600	ENSG00000253600	CTC-340A15.1	5:163723701-164598649	NOTEST	0	0	0	0	1	1
ENSG00000253602	ENSG00000253602	CTD-3135A9.3	8:143293440-143484601	NOTEST	0	0	0	0	1	1
ENSG00000253603	ENSG00000253603	CTA-397H3.3	8:56987150-56987833	NOTEST	0	0	0	0	1	1
ENSG00000253604	ENSG00000253604	RP11-489E7.1	8:29763250-29766472	NOTEST	0	0	0	0	1	1
ENSG00000253605	ENSG00000253605	HNRNPA1P38	8:142443928-142517330	NOTEST	0	0	0	0	1	1
ENSG00000253606	ENSG00000253606	AFG3L2P1	8:43125340-43127105	NOTEST	0	0	0	0	1	1
ENSG00000253607	ENSG00000253607	RP11-557C18.3	8:124014799-124164393	NOTEST	0.0606682	0.0255822	-1.2458	0	1	1
ENSG00000253608	ENSG00000253608	RP11-770E5.1	8:49464126-49611069	NOTEST	0	0	0	0	1	1
ENSG00000253610	ENSG00000253610	RP11-139F9.1	8:36165762-36165882	NOTEST	0	0	0	0	1	1
ENSG00000253611	ENSG00000253611	VN1R46P	8:43075102-43075952	NOTEST	0	0	0	0	1	1
ENSG00000253612	ENSG00000253612	WBP1LP3	8:105273-105481	NOTEST	0	0	0	0	1	1
ENSG00000253613	ENSG00000253613	CTC-551A13.2	5:110405759-110466200	NOTEST	0	0	0	0	1	1
ENSG00000253614	ENSG00000253614	RP11-513O17.3	8:58173784-58179172	NOTEST	0	0	0	0	1	1
ENSG00000253615	ENSG00000253615	RP11-597M17.2	8:27727398-27850244	NOTEST	0	0	0	0	1	1
ENSG00000253616	ENSG00000253616	RP11-875O11.3	8:22545171-22941132	NOTEST	0.147263	0	#NAME?	0	1	1
ENSG00000253617	ENSG00000253617	RP11-443C10.3	5:178812819-178812993	NOTEST	0	0	0	0	1	1
ENSG00000253618	ENSG00000253618	GRPEL2-AS1	5:148724992-148737205	NOTEST	0.385953	0.194661	-0.987461	0	1	1
ENSG00000253619	ENSG00000253619	RP11-369K17.1	8:121925304-122131994	NOTEST	0.0245516	0.0191004	-0.362209	0	1	1
ENSG00000253620	ENSG00000253620	AC144568.4	8:14090-14320	NOTEST	0	0	0	0	1	1
ENSG00000253621	ENSG00000253621	RP11-255L13.1	8:90255629-90256022	NOTEST	0	0	0	0	1	1
ENSG00000253622	ENSG00000253622	RP11-654G14.1	8:117962511-118188953	NOTEST	0	0	0	0	1	1
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test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000253628	ENSG00000253628	RP11-536N17.1	5:172243623-172246961	NOTEST	0	0	0	0	1	1
ENSG00000253629	ENSG00000253629	KB-1107E3.1	8:102698770-103137135	NOTEST	0	0.0438454	inf	0	1	1
ENSG00000253630	ENSG00000253630	CTC-370J7.1	5:157170702-157187717	NOTEST	0	0	0	0	1	1
ENSG00000253631	ENSG00000253631	IGLV7-35	22:22804539-22804990	NOTEST	0	0	0	0	1	1
ENSG00000253632	ENSG00000253632	RP11-486M23.1	8:29384828-29387840	NOTEST	0.184321	0.145957	-0.336674	0	1	1
ENSG00000253633	ENSG00000253633	KB-1980E6.3	8:103540967-103550896	NOTEST	0.49214	0.215531	-1.19117	0	1	1
ENSG00000253634	ENSG00000253634	RP11-587H10.2	8:93577670-93667722	NOTEST	0	0	0	0	1	1
ENSG00000253635	ENSG00000253635	IGHVIII-67-3	14:107148673-107148905	NOTEST	0	0	0	0	1	1
ENSG00000253636	ENSG00000253636	RP11-531A24.5	8:73964412-73975296	NOTEST	0.10125	0.148249	0.550097	0	1	1
ENSG00000253637	ENSG00000253637	IGLVV-58	22:22536971-22537275	NOTEST	0	0	0	0	1	1
ENSG00000253638	ENSG00000253638	CTC-369M3.1	8:134404453-134404933	NOTEST	0	0	0	0	1	1
ENSG00000253639	ENSG00000253639	SUMO2P18	8:98870276-98871175	NOTEST	0	0	0	0	1	1
ENSG00000253640	ENSG00000253640	CTD-2281E23.1	8:1244291-1250829	NOTEST	0	0	0	0	1	1
ENSG00000253641	ENSG00000253641	RP11-981G7.2	8:10332074-10339484	NOTEST	0.0420802	0.0859235	1.02991	0	1	1
ENSG00000253642	ENSG00000253642	RP11-317N12.1	8:33462373-33896526	NOTEST	0	0	0	0	1	1
ENSG00000253643	ENSG00000253643	RP11-561E1.1	8:24151552-24769586	NOTEST	0	0	0	0	1	1
ENSG00000253644	ENSG00000253644	KB-1930G5.3	8:102399526-102405414	NOTEST	0	0	0	0	1	1
ENSG00000253645	ENSG00000253645	CTD-2544N14.3	8:38758752-38831428	NOTEST	0.103391	0.491902	2.25026	0	1	1
ENSG00000253646	ENSG00000253646	CTD-2311A18.1	5:154490743-154491884	NOTEST	0	0	0	0	1	1
ENSG00000253647	ENSG00000253647	CTD-2270F17.1	5:169780490-170163636	NOTEST	0	0	0	0	1	1
ENSG00000253648	ENSG00000253648	RP11-77B22.2	8:15830823-15857833	NOTEST	0	0	0	0	1	1
ENSG00000253649	ENSG00000253649	PRSS51	8:10340387-10411676	NOTEST	0	0.0376324	inf	0	1	1
ENSG00000253650	ENSG00000253650	SMARCE1P4	8:36952667-36952908	NOTEST	0	0	0	0	1	1
ENSG00000253651	ENSG00000253651	SOD1P3	8:126964104-126964558	NOTEST	0	0	0	0	1	1
ENSG00000253652	ENSG00000253652	RP11-798K23.4	5:178930322-178942580	NOTEST	0	0	0	0	1	1
ENSG00000253653	ENSG00000253653	CTC-248O19.1	5:156687131-157002783	NOTEST	0	0	0	0	1	1
ENSG00000253654	ENSG00000253654	CTD-2210A23.1	8:49206585-49207254	NOTEST	0	0	0	0	1	1
ENSG00000253655	ENSG00000253655	IGJP1	8:85892307-85892782	NOTEST	0	0	0	0	1	1
ENSG00000253656	ENSG00000253656	KB-1568E2.1	8:131607544-131667958	NOTEST	0	0	0	0	1	1
ENSG00000253657	ENSG00000253657	RP11-25P11.2	8:109584871-109585403	NOTEST	0	0	0	0	1	1
ENSG00000253658	ENSG00000253658	RP11-600K15.1	8:69824037-70016425	NOTEST	0	0	0	0	1	1
ENSG00000253659	ENSG00000253659	RP11-1114I9.1	8:80209951-80226706	NOTEST	0	0.0250285	inf	0	1	1
ENSG00000253660	ENSG00000253660	CTC-353G13.1	5:166711803-167691162	NOTEST	0	0	0	0	1	1
ENSG00000253661	ENSG00000253661	ZFHX4-AS1	8:77316232-77779521	NOTEST	0.0354931	0	#NAME?	0	1	1
ENSG00000253663	ENSG00000253663	NPM1P52	8:104028971-104029817	NOTEST	0	0	0	0	1	1
ENSG00000253664	ENSG00000253664	RP11-401H2.1	8:52170247-52722005	NOTEST	0	0	0	0	1	1
ENSG00000253665	ENSG00000253665	RP11-359E19.2	8:39972169-39984987	NOTEST	0	0	0	0	1	1

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ENSG00000253667	ENSG00000253667	RP11-30L15.4	8:54879111-54935089	NOTEST	0.0980364	0.212848	1.11843	0	1	1
ENSG00000253668	ENSG00000253668	RP11-463C14.1	8:54625256-54625456	NOTEST	0	0	0	0	1	1
ENSG00000253669	ENSG00000253669	KB-1732A1.1	8:103817744-103822199	NOTEST	0.136703	0.274508	1.0058	0	1	1
ENSG00000253670	ENSG00000253670	RP11-429O2.1	8:24998908-24999483	NOTEST	0	0	0	0	1	1
ENSG00000253671	ENSG00000253671	RP11-806O11.1	8:17658853-17718578	NOTEST	0.279911	0.153635	-0.865459	0	1	1
ENSG00000253672	ENSG00000253672	RP11-536K17.1	8:117414780-117415995	NOTEST	0	0	0	0	1	1
ENSG00000253673	ENSG00000253673	CTC-436K13.1	5:157600608-157627024	NOTEST	0	0	0	0	1	1
ENSG00000253674	ENSG00000253674	IGHVII-78-1	14:107273841-107274110	NOTEST	0	0	0	0	1	1
ENSG00000253675	ENSG00000253675	CTD-3118D11.2	8:86999551-87166457	NOTEST	0.112711	0.0550953	-1.03262	0	1	1
ENSG00000253677	ENSG00000253677	UBE2HP1	8:82167104-82167464	NOTEST	0	0	0	0	1	1
ENSG00000253678	ENSG00000253678	RP11-981G7.3	8:10332074-10339484	NOTEST	0	0	0	0	1	1
ENSG00000253679	ENSG00000253679	KB-1410C5.2	8:102273768-102275131	NOTEST	0	0	0	0	1	1
ENSG00000253680	ENSG00000253680	RP11-59O2.1	8:86529572-86529741	NOTEST	0.753706	0	#NAME?	0	1	1
ENSG00000253681	ENSG00000253681	RP11-115I9.1	8:77316232-77779521	NOTEST	0	0	0	0	1	1
ENSG00000253682	ENSG00000253682	RP11-700E23.2	8:93415772-93425873	NOTEST	0	0	0	0	1	1
ENSG00000253684	ENSG00000253684	RP11-10D7.2	8:33462373-33896526	NOTEST	0	0	0	0	1	1
ENSG00000253685	ENSG00000253685	RP11-593P24.3	8:36137008-36137214	NOTEST	0	0	0	0	1	1
ENSG00000253686	ENSG00000253686	CTB-43E15.3	5:173134616-173173214	NOTEST	0	0	0	0	1	1
ENSG00000253687	ENSG00000253687	CTC-348L5.1	5:159990126-160279221	NOTEST	0.026525	0	#NAME?	0	1	1
ENSG00000253688	ENSG00000253688	RP11-567J20.2	8:49464126-49611069	NOTEST	0	0	0	0	1	1
ENSG00000253689	ENSG00000253689	IGHV3-54	14:107057357-107057795	NOTEST	0	0	0	0	1	1
ENSG00000253690	ENSG00000253690	RP11-380I10.4	8:28107579-28200872	NOTEST	0	3.01E-07	inf	0	1	1
ENSG00000253691	ENSG00000253691	IGKV2OR22-4	22:17395124-17395871	NOTEST	0	0	0	0	1	1
ENSG00000253692	ENSG00000253692	IGHEP1	14:106185954-106188864	NOTEST	0	0	0	0	1	1
ENSG00000253693	ENSG00000253693	CTC-535M15.2	5:164776035-165205694	NOTEST	0	0	0	0	1	1
ENSG00000253695	ENSG00000253695	RP11-177H2.2	8:10698085-10704011	NOTEST	0	0	0	0	1	1
ENSG00000253696	ENSG00000253696	KBTBD11-OT1	8:1919562-1955102	NOTEST	0.107583	0.129279	0.265044	0	1	1
ENSG00000253697	ENSG00000253697	RP11-1081K18.1	8:9412655-9639856	NOTEST	0	0	0	0	1	1
ENSG00000253698	ENSG00000253698	RP11-1259L22.1	5:177664618-178017556	NOTEST	0	0.0212214	inf	0	1	1
ENSG00000253699	ENSG00000253699	CTD-3118D11.3	8:87192646-87224465	NOTEST	0	0	0	0	1	1
ENSG00000253701	ENSG00000253701	AL928768.3	14:106170300-106170939	NOTEST	0	0	0	0	1	1
ENSG00000253702	ENSG00000253702	RP11-567J20.1	8:49464126-49611069	NOTEST	0	0	0	0	1	1
ENSG00000253703	ENSG00000253703	IGHV1-68	14:107159868-107160163	NOTEST	0	0	0	0	1	1
ENSG00000253704	ENSG00000253704	RP11-267M23.4	8:95565949-95581973	NOTEST	0.00917883	0.0499791	2.44494	0	1	1
ENSG00000253705	ENSG00000253705	IGHV3-41	14:106899043-106899493	NOTEST	0.244856	0	#NAME?	0	1	1
ENSG00000253707	ENSG00000253707	RP11-726G23.8	8:43139768-43139949	NOTEST	0	0	0	0	1	1
ENSG00000253708	ENSG00000253708	RP11-51J9.4	8:29952913-30041156	NOTEST	0	0	0	0	1	1
ENSG00000253709	ENSG00000253709	IGHV1-14	14:106602579-106602820	NOTEST	0	0	0	0	1	1
ENSG00000253711	ENSG00000253711	RP11-787D18.1	8:61969716-62627155	NOTEST	0	0	0	0	1	1

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ENSG00000253713	ENSG00000253713	CTC-264O10.2	5:166543322-166546590	NOTEST	0	0	0	0	1	1
ENSG00000253714	ENSG00000253714	IGHVII-53-1	14:107055681-107055936	NOTEST	0	0	0	0	1	1
ENSG00000253715	ENSG00000253715	RP11-706C16.8	8:143866295-143893536	NOTEST	0	0	0	0	1	1
ENSG00000253717	ENSG00000253717	KB-1299A7.2	8:111779091-111784988	NOTEST	0	0	0	0	1	1
ENSG00000253720	ENSG00000253720	RP11-473O4.3	8:130844546-131029375	NOTEST	0	0	0	0	1	1
ENSG00000253721	ENSG00000253721	SUMO2P20	8:70899649-70899932	NOTEST	0	0	0	0	1	1
ENSG00000253722	ENSG00000253722	RP11-10N23.4	8:94225530-94753245	NOTEST	0	0.0600521	inf	0	1	1
ENSG00000253723	ENSG00000253723	RP11-960H2.1	8:60733682-60733992	NOTEST	0	0	0	0	1	1
ENSG00000253725	ENSG00000253725	RP11-21I4.2	5:178267097-178268135	NOTEST	0	0	0	0	1	1
ENSG00000253726	ENSG00000253726	RP11-313C15.1	8:73449625-73850584	NOTEST	0	0	0	0	1	1
ENSG00000253728	ENSG00000253728	RP11-706C16.5	8:143915553-143999259	NOTEST	0	0	0	0	1	1
ENSG00000253731	ENSG00000253731	PCDHGA6	5:140710251-140892546	NOTEST	0.0920647	0.212737	1.20835	0	1	1
ENSG00000253732	ENSG00000253732	IGKV2-19	2:89434457-89434740	NOTEST	0	0	0	0	1	1
ENSG00000253733	ENSG00000253733	LZTS1-AS1	8:20103675-20161474	NOTEST	0	0	0	0	1	1
ENSG00000253734	ENSG00000253734	RP11-579E24.1	8:64599736-65281115	NOTEST	0	0	0	0	1	1
ENSG00000253735	ENSG00000253735	RP11-115J16.3	8:9106926-9293715	NOTEST	0	0	0	0	1	1
ENSG00000253736	ENSG00000253736	RP11-779O18.3	5:172185228-172204777	NOTEST	0	0	0	0	1	1
ENSG00000253737	ENSG00000253737	KB-1460A1.3	8:102151892-102153157	NOTEST	0.282231	0.143251	-0.978331	0	1	1
ENSG00000253739	ENSG00000253739	RP11-90P5.7	8:37962759-38070819	NOTEST	0	0	0	0	1	1
ENSG00000253740	ENSG00000253740	KB-1083B1.1	8:101585115-101675643	NOTEST	0	0	0	0	1	1
ENSG00000253741	ENSG00000253741	CTD-2292P10.4	8:143781528-143808391	NOTEST	0.0311528	0.0268604	-0.213882	0	1	1
ENSG00000253742	ENSG00000253742	IGHV3-60	14:107087201-107087658	NOTEST	0	0	0	0	1	1
ENSG00000253743	ENSG00000253743	MARK2P11	5:157411665-157416998	NOTEST	0	0	0	0	1	1
ENSG00000253744	ENSG00000253744	AC025442.3	5:65435798-65479443	NOTEST	0	0	0	0	1	1
ENSG00000253745	ENSG00000253745	RP11-350F16.1	8:47834182-47840454	NOTEST	0	0	0	0	1	1
ENSG00000253746	ENSG00000253746	RP11-527N22.2	8:37262956-37264242	NOTEST	0	0.0568416	inf	0	1	1
ENSG00000253747	ENSG00000253747	IGHVII-62-1	14:107106554-107106789	NOTEST	0	0	0	0	1	1
ENSG00000253748	ENSG00000253748	CYP4F44P	8:43395115-43396070	NOTEST	0	0	0	0	1	1
ENSG00000253749	ENSG00000253749	RP11-700E23.1	8:93433077-93434026	NOTEST	0	0	0	0	1	1
ENSG00000253750	ENSG00000253750	RP11-21C4.4	8:65466792-65467032	NOTEST	0	0	0	0	1	1
ENSG00000253752	ENSG00000253752	IGLVI-63	22:22434179-22434673	NOTEST	0	0	0	0	1	1
ENSG00000253753	ENSG00000253753	AC145123.2	8:143719948-143722027	NOTEST	0	0	0	0	1	1
ENSG00000253754	ENSG00000253754	RP11-35G22.1	8:109213444-109447562	NOTEST	0	0.0383519	inf	0	1	1
ENSG00000253755	ENSG00000253755	IGHGP	14:106130969-106136180	NOTEST	0	0	0	0	1	1
ENSG00000253756	ENSG00000253756	RP11-192P9.1	8:115803881-115804158	NOTEST	0	0	0	0	1	1
ENSG00000253759	ENSG00000253759	IGHV3-57	14:107074906-107075186	NOTEST	0	0	0	0	1	1
ENSG00000253760	ENSG00000253760	RP11-48B3.2	8:81480284-81480741	NOTEST	0	0	0	0	1	1
ENSG00000253762	ENSG00000253762	RP11-579E24.2	8:64599736-65281115	NOTEST	0	0	0	0	1	1
ENSG00000253763	ENSG00000253763	IGHV3-6	14:106511781-106512231	NOTEST	0	0	0	0	1	1

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ENSG00000253765	ENSG00000253765	IGKV2D-19	2:90085627-90085889	NOTEST	0	0	0	0	1	1
ENSG00000253766	ENSG00000253766	RP11-804N13.1	5:21616370-22853731	NOTEST	0.0436219	0	#NAME?	0	1	1
ENSG00000253767	ENSG00000253767	PCDHGA8	5:140710251-140892546	NOTEST	0.0508903	0.111416	1.1305	0	1	1
ENSG00000253768	ENSG00000253768	CTB-33O18.1	5:172989480-173000202	NOTEST	0	0	0	0	1	1
ENSG00000253770	ENSG00000253770	HMGB1P23	8:28924795-29120641	NOTEST	0	0	0	0	1	1
ENSG00000253772	ENSG00000253772	RP11-34P1.1	5:159674523-159675224	NOTEST	0	0	0	0	1	1
ENSG00000253773	ENSG00000253773	KB-1047C11.2	8:96216683-96822364	NOTEST	0	0.02693	inf	0	1	1
ENSG00000253774	ENSG00000253774	CTD-3023L14.1	8:8413247-8427198	NOTEST	0	0	0	0	1	1
ENSG00000253775	ENSG00000253775	AC100802.3	8:19936815-19975953	NOTEST	0	0	0	0	1	1
ENSG00000253776	ENSG00000253776	RP11-6N13.4	5:103718998-104728671	NOTEST	0	0	0	0	1	1
ENSG00000253777	ENSG00000253777	RP11-758M4.3	8:75512009-75779174	NOTEST	0	0	0	0	1	1
ENSG00000253778	ENSG00000253778	RP11-386D6.2	8:87778162-87830786	NOTEST	0	0	0	0	1	1
ENSG00000253779	ENSG00000253779	IGLVVI-25-1	22:23021569-23021818	NOTEST	0	0	0	0	1	1
ENSG00000253780	ENSG00000253780	IGHVIII-2-1	14:106467676-106467967	NOTEST	0	0	0	0	1	1
ENSG00000253781	ENSG00000253781	ZNF317P1	8:94225530-94753245	NOTEST	0	0	0	0	1	1
ENSG00000253782	ENSG00000253782	RP11-350F16.2	8:47842461-47846068	NOTEST	0	0	0	0	1	1
ENSG00000253783	ENSG00000253783	CTD-2534J5.1	8:140126435-140140196	NOTEST	0	0	0	0	1	1
ENSG00000253784	ENSG00000253784	RP11-1145L24.1	8:73449625-73850584	NOTEST	0	0	0	0	1	1
ENSG00000253786	ENSG00000253786	IGLV3-15	22:23098042-23098286	NOTEST	0	0	0	0	1	1
ENSG00000253787	ENSG00000253787	RP11-404L6.2	5:67485703-67494235	NOTEST	0	0	0	0	1	1
ENSG00000253789	ENSG00000253789	CTD-2571E19.1	8:63023082-63032457	NOTEST	0	0	0	0	1	1
ENSG00000253790	ENSG00000253790	RP11-44K6.5	8:39759793-39873910	NOTEST	0	0	0	0	1	1
ENSG00000253792	ENSG00000253792	CTC-436K13.5	5:157600608-157627024	NOTEST	0	0	0	0	1	1
ENSG00000253793	ENSG00000253793	RP11-293D9.2	8:30840974-30841837	NOTEST	0	0	0	0	1	1
ENSG00000253794	ENSG00000253794	IGLV10-67	22:22345495-22398340	NOTEST	0	0	0	0	1	1
ENSG00000253795	ENSG00000253795	MTND1P5	8:104097878-104098818	NOTEST	0	0	0	0	1	1
ENSG00000253796	ENSG00000253796	RP11-1084E5.1	8:109907257-110075646	NOTEST	0	0	0	0	1	1
ENSG00000253798	ENSG00000253798	AC008694.3	5:157109992-157117274	NOTEST	0	0	0	0	1	1
ENSG00000253799	ENSG00000253799	LINC01030	8:91233715-91632298	NOTEST	0	0	0	0	1	1
ENSG00000253800	ENSG00000253800	RP11-21C4.5	8:65483469-65483889	NOTEST	0	0	0	0	1	1
ENSG00000253801	ENSG00000253801	CTD-2060F24.1	5:67382988-67383322	NOTEST	0	0	0	0	1	1
ENSG00000253802	ENSG00000253802	CTA-392C11.1	8:40156259-40200921	NOTEST	0	0	0	0	1	1
ENSG00000253803	ENSG00000253803	RP11-101E19.7	8:47782523-47783667	NOTEST	0	0	0	0	1	1
ENSG00000253805	ENSG00000253805	RP11-1049H7.2	8:1981649-1983729	NOTEST	0	0	0	0	1	1
ENSG00000253806	ENSG00000253806	CTD-2292P10.2	8:143808620-143818345	NOTEST	0	0	0	0	1	1
ENSG00000253807	ENSG00000253807	LINC01170	5:123641922-123740772	NOTEST	0	0	0	0	1	1
ENSG00000253808	ENSG00000253808	IGHVII-46-1	14:106938444-106977000	NOTEST	0	0	0	0	1	1
ENSG00000253809	ENSG00000253809	RP1-149L1.1	6:70924763-71012786	NOTEST	0	0	0	0	1	1
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ENSG00000253813	ENSG00000253813	COX6B1P4	8:26605666-26724790	NOTEST	0	0	0	0	1	1
ENSG00000253814	ENSG00000253814	MRPS36P3	8:122966878-123139423	NOTEST	0	0	0	0	1	1
ENSG00000253817	ENSG00000253817	RP11-1134I14.6	8:48001194-48110484	NOTEST	0	0	0	0	1	1
ENSG00000253818	ENSG00000253818	IGLV1-41	22:22758538-22759053	NOTEST	0	0	0	0	1	1
ENSG00000253819	ENSG00000253819	LINC01151	8:123682623-123706345	NOTEST	0	0	0	0	1	1
ENSG00000253820	ENSG00000253820	IGHVII-67-1	14:107142533-107142579	NOTEST	0	0	0	0	1	1
ENSG00000253821	ENSG00000253821	RP11-246K15.1	8:58405442-58504118	NOTEST	0	0	0	0	1	1
ENSG00000253822	ENSG00000253822	IGLV3-24	22:23036923-23037437	NOTEST	0	0	0	0	1	1
ENSG00000253823	ENSG00000253823	IGLV1-62	22:22440971-22441521	NOTEST	0	0	0	0	1	1
ENSG00000253824	ENSG00000253824	KB-173C10.2	8:101393487-101426687	NOTEST	0	0	0	0	1	1
ENSG00000253825	ENSG00000253825	RP11-96A1.5	4:120956187-120961770	NOTEST	0	0	0	0	1	1
ENSG00000253826	ENSG00000253826	RP11-304M2.1	11:75779-76143	NOTEST	0	0	0	0	1	1
ENSG00000253828	ENSG00000253828	MTND1P7	8:47733858-47765929	NOTEST	0	0	0	0	1	1
ENSG00000253829	ENSG00000253829	RP11-723D22.3	8:38585703-38710546	NOTEST	0	0	0	0	1	1
ENSG00000253831	ENSG00000253831	ETV3L	1:157061835-157069600	NOTEST	0	0.00639331	inf	0	1	1
ENSG00000253832	ENSG00000253832	CTD-2168K21.1	8:24849515-24867292	NOTEST	0.0343865	0.0486965	0.501977	0	1	1
ENSG00000253833	ENSG00000253833	RP11-367E12.4	8:74896727-74897118	NOTEST	0.134784	0.0481706	-1.48443	0	1	1
ENSG00000253834	ENSG00000253834	RP11-705O24.3	8:62697605-62856739	NOTEST	0	0	0	0	1	1
ENSG00000253836	ENSG00000253836	RP11-731N10.1	8:83775013-83874161	NOTEST	0	0	0	0	1	1
ENSG00000253837	ENSG00000253837	RP11-177H13.2	8:23154701-23315208	NOTEST	0.026323	0.0266083	0.0155526	0	1	1
ENSG00000253838	ENSG00000253838	RP11-44K6.2	8:39759793-39873910	NOTEST	0	0	0	0	1	1
ENSG00000253839	ENSG00000253839	RP11-431D12.1	8:137501690-137542119	NOTEST	0	0	0	0	1	1
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ENSG00000253841	ENSG00000253841	RP11-622O11.5	8:127084830-127086475	NOTEST	0	0	0	0	1	1
ENSG00000253842	ENSG00000253842	KB-173C10.1	8:101441061-101443225	NOTEST	0	0	0	0	1	1
ENSG00000253843	ENSG00000253843	RP11-769N21.2	8:49106409-49107187	NOTEST	0	0	0	0	1	1
ENSG00000253844	ENSG00000253844	RP11-546K22.1	8:52874017-52935534	NOTEST	0	0	0	0	1	1
ENSG00000253845	ENSG00000253845	RP11-643N23.2	8:43527965-43528218	NOTEST	0	0	0	0	1	1
ENSG00000253846	ENSG00000253846	PCDHGA10	5:140710251-140892546	NOTEST	0.0722093	0.141503	0.970575	0	1	1
ENSG00000253848	ENSG00000253848	RP11-10N23.5	8:94753420-94756762	NOTEST	0.159651	0	#NAME?	0	1	1
ENSG00000253849	ENSG00000253849	RP11-759A9.1	8:50822348-51706678	NOTEST	0	0	0	0	1	1
ENSG00000253851	ENSG00000253851	RP11-318M2.3	8:104133259-104345094	NOTEST	0	0	0	0	1	1
ENSG00000253852	ENSG00000253852	CTB-140J7.2	5:149980641-150038782	NOTEST	0	0	0	0	1	1
ENSG00000253853	ENSG00000253853	GS1-57L11.1	8:2523590-2680004	NOTEST	0	0	0	0	1	1
ENSG00000253854	ENSG00000253854	RP11-10N23.2	8:94225530-94753245	NOTEST	0.482767	0.418789	-0.205103	0	1	1
ENSG00000253855	ENSG00000253855	AC133633.1	8:2376123-2379308	NOTEST	0	0	0	0	1	1
ENSG00000253857	ENSG00000253857	RP11-386G21.2	8:56014948-56454613	NOTEST	0	0	0	0	1	1
ENSG00000253858	ENSG00000253858	CTB-147C13.1	5:169780490-170163636	NOTEST	0	0	0	0	1	1
ENSG00000253859	ENSG00000253859	RP11-157I4.4	8:82351670-82445510	NOTEST	0	0	0	0	1	1
ENSG00000253860	ENSG00000253860	IGKV3-34	2:89575055-89575545	NOTEST	0	0	0	0	1	1

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ENSG00000253864	ENSG00000253864	AC131025.8	5:148786251-148808241	NOTEST	0	0.00656433	inf	0	1	1
ENSG00000253865	ENSG00000253865	RP11-394O4.3	5:148750886-148783765	NOTEST	0	0	0	0	1	1
ENSG00000253866	ENSG00000253866	TMEM97P2	8:20791945-20792348	NOTEST	0	0	0	0	1	1
ENSG00000253868	ENSG00000253868	FER1L6-AS2	8:124864226-125183763	NOTEST	0.0100347	0	#NAME?	0	1	1
ENSG00000253869	ENSG00000253869	PIGFP1	5:178322894-178360213	NOTEST	0	0	0	0	1	1
ENSG00000253870	ENSG00000253870	IGKV1-32	2:89553056-89553501	NOTEST	0	0	0	0	1	1
ENSG00000253871	ENSG00000253871	RP11-756K15.2	8:58256345-58277416	NOTEST	0	0	0	0	1	1
ENSG00000253872	ENSG00000253872	RP11-90D11.1	8:96216683-96822364	NOTEST	0	0	0	0	1	1
ENSG00000253874	ENSG00000253874	IGLVIV-66-1	22:22412844-22413304	NOTEST	0	0	0	0	1	1
ENSG00000253875	ENSG00000253875	RP11-16P20.3	8:27590834-27695612	NOTEST	0	0	0	0	1	1
ENSG00000253877	ENSG00000253877	RP11-946L20.2	8:111949918-112039662	NOTEST	0.147845	0.0269998	-2.45306	0	1	1
ENSG00000253878	ENSG00000253878	RP11-347C18.3	8:95825538-96128683	NOTEST	0.209407	0.325038	0.634296	0	1	1
ENSG00000253879	ENSG00000253879	RP11-379I19.3	8:60513936-60526334	NOTEST	0	0	0	0	1	1
ENSG00000253880	ENSG00000253880	RP11-124B13.1	8:5901874-6115058	NOTEST	0	0	0	0	1	1
ENSG00000253881	ENSG00000253881	RP11-52B19.8	8:7906440-7906789	NOTEST	0	0	0	0	1	1
ENSG00000253882	ENSG00000253882	RP11-61L23.2	7:143318042-143534026	NOTEST	0.491401	0.0443531	-3.46979	0	1	1
ENSG00000253883	ENSG00000253883	IGHV3-19	14:106653370-106653661	NOTEST	0	0	0	0	1	1
ENSG00000253884	ENSG00000253884	RP11-726G23.2	8:43101897-43102078	NOTEST	0	0	0	0	1	1
ENSG00000253885	ENSG00000253885	ARF1P3	8:124864226-125183763	NOTEST	0	0	0	0	1	1
ENSG00000253886	ENSG00000253886	CTB-158E9.2	5:153873135-153874303	NOTEST	0	0	0	0	1	1
ENSG00000253887	ENSG00000253887	RP11-10A14.7	8:9106926-9293715	NOTEST	0	0	0	0	1	1
ENSG00000253888	ENSG00000253888	RP11-521M14.1	8:27041837-27068011	NOTEST	0	0	0	0	1	1
ENSG00000253889	ENSG00000253889	IGLVI-38	22:22780157-22780651	NOTEST	0	0	0	0	1	1
ENSG00000253891	ENSG00000253891	RP11-203E8.1	8:24027469-24034593	NOTEST	0	0	0	0	1	1
ENSG00000253892	ENSG00000253892	RP11-770E5.2	8:49464126-49611069	NOTEST	0	0	0	0	1	1
ENSG00000253893	ENSG00000253893	FAM85B	8:8011829-8084136	NOTEST	0.0916913	0.0168845	-2.44109	0	1	1
ENSG00000253894	ENSG00000253894	RP11-45K10.2	8:64297396-64388040	NOTEST	0.00486748	0.0192933	1.98686	0	1	1
ENSG00000253896	ENSG00000253896	AC144568.2	8:22600-29775	NOTEST	0	0	0	0	1	1
ENSG00000253897	ENSG00000253897	CTB-23I7.1	5:150745993-150810913	NOTEST	0	0	0	0	1	1
ENSG00000253898	ENSG00000253898	RP11-51M18.1	8:84315992-84321135	NOTEST	0.0110012	0	#NAME?	0	1	1
ENSG00000253899	ENSG00000253899	RP11-613H2.2	8:26921512-26922795	NOTEST	0	0	0	0	1	1
ENSG00000253900	ENSG00000253900	CDH12P4	5:70428819-70429114	NOTEST	0.352739	0.269233	-0.389745	0	1	1
ENSG00000253901	ENSG00000253901	RP11-122C21.1	8:92555151-92919847	NOTEST	0	0	0	0	1	1
ENSG00000253903	ENSG00000253903	RP11-521M14.2	8:26943693-26944766	NOTEST	0	0	0	0	1	1
ENSG00000253906	ENSG00000253906	IGKV2D-10	2:90218729-90219428	NOTEST	0	0	0	0	1	1
ENSG00000253907	ENSG00000253907	RP11-380I10.3	8:28095946-28096422	NOTEST	0	0	0	0	1	1
ENSG00000253908	ENSG00000253908	RP11-252I14.2	5:179660142-179719099	NOTEST	0.298281	0.310363	0.0572819	0	1	1
ENSG00000253910	ENSG00000253910	PCDHGB2	5:140710251-140892546	NOTEST	0.27331	0.265423	-0.0422425	0	1	1
ENSG00000253911	ENSG00000253911	KB-1205A7.2	8:99413630-99955055	NOTEST	0	0	0	0	1	1
ENSG00000253912	ENSG00000253912	RP11-402L5.2	8:100025493-100906290	NOTEST	0	0	0	0	1	1
ENSG00000253913	ENSG00000253913	IGLV3-26	22:23015621-23016072	NOTEST	0	0	0	0	1	1
ENSG00000253915	ENSG00000253915	MAPRE1P1	8:136469699-136668965	NOTEST	0	0	0	0	1	1

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ENSG00000253917	ENSG00000253917	AC226119.5	4:3916909-3957148	NOTEST	0.0631295	0.0428994	-0.557355	0	1	1
ENSG00000253920	ENSG00000253920	IGLV3-31	22:22946914-22947635	NOTEST	0	0	0	0	1	1
ENSG00000253921	ENSG00000253921	CTB-113P19.3	5:151121876-151192346	NOTEST	0.0372305	0.0263896	-0.496514	0	1	1
ENSG00000253923	ENSG00000253923	KB-1980E6.2	8:103430206-103431181	NOTEST	0	0	0	0	1	1
ENSG00000253924	ENSG00000253924	RP11-1023P17.2	8:53023398-53373519	NOTEST	0	0	0	0	1	1
ENSG00000253925	ENSG00000253925	CTB-178M22.1	5:166711803-167691162	NOTEST	0	0	0	0	1	1
ENSG00000253926	ENSG00000253926	RP11-26E5.1	8:130363936-130695925	NOTEST	0	0	0	0	1	1
ENSG00000253927	ENSG00000253927	GS1-39E22.1	5:135236041-135253850	NOTEST	0	0	0	0	1	1
ENSG00000253929	ENSG00000253929	RP11-382A18.2	8:128302061-128494384	NOTEST	0.122211	0.383802	1.65099	0	1	1
ENSG00000253930	ENSG00000253930	RP11-1149O23.2	8:23046791-23088439	NOTEST	0.0637543	0.0997739	0.646139	0	1	1
ENSG00000253931	ENSG00000253931	RP11-909N17.2	8:144494918-144499224	NOTEST	0.18767	0	#NAME?	0	1	1
ENSG00000253932	ENSG00000253932	RP11-10C8.2	8:12940869-13373167	NOTEST	0	0	0	0	1	1
ENSG00000253934	ENSG00000253934	MRPL49P2	8:15965386-16424999	NOTEST	0	0	0	0	1	1
ENSG00000253935	ENSG00000253935	IGLVIV-53	22:22574038-22574525	NOTEST	0	0	0	0	1	1
ENSG00000253936	ENSG00000253936	IGHV3-63	14:107108251-107108696	NOTEST	0	0	0	0	1	1
ENSG00000253937	ENSG00000253937	NATP	8:18228115-18228993	NOTEST	0	0	0	0	1	1
ENSG00000253939	ENSG00000253939	RP11-44K6.3	8:39759793-39873910	NOTEST	0	0	0	0	1	1
ENSG00000253940	ENSG00000253940	CTD-2127O16.2	5:31066076-31066239	NOTEST	0	0	0	0	1	1
ENSG00000253941	ENSG00000253941	IGHVII-51-2	14:107040701-107040960	NOTEST	0	0	0	0	1	1
ENSG00000253942	ENSG00000253942	KB-1410C5.1	8:102236168-102236801	NOTEST	0	0	0	0	1	1
ENSG00000253943	ENSG00000253943	KRT18P37	8:41368758-41370040	NOTEST	0	0	0	0	1	1
ENSG00000253944	ENSG00000253944	RP11-156K13.1	8:17658853-17718578	NOTEST	0.13145	0.133531	0.0226657	0	1	1
ENSG00000253945	ENSG00000253945	RP11-328L11.1	8:96216683-96822364	NOTEST	0	0	0	0	1	1
ENSG00000253946	ENSG00000253946	CTC-425K20.1	5:165332130-165332613	NOTEST	0	0	0	0	1	1
ENSG00000253947	ENSG00000253947	CTB-77H17.1	5:166711803-167691162	NOTEST	0	0	0	0	1	1
ENSG00000253948	ENSG00000253948	RP11-410L14.2	8:100008990-100025272	NOTEST	0.474965	0.489662	0.043967	0	1	1
ENSG00000253949	ENSG00000253949	RP11-790J24.1	8:109593290-109799844	NOTEST	0	0	0	0	1	1
ENSG00000253951	ENSG00000253951	RP11-447G11.1	8:15965386-16424999	NOTEST	0	0	0	0	1	1
ENSG00000253952	ENSG00000253952	HIGD1AP18	8:77925986-77926264	NOTEST	0	0	0	0	1	1
ENSG00000253954	ENSG00000253954	HMGN1P38	15:93146139-93353114	NOTEST	0.221671	0.0977479	-1.18128	0	1	1
ENSG00000253955	ENSG00000253955	CTB-33O18.3	5:173006645-173012071	NOTEST	0	0.0143722	inf	0	1	1
ENSG00000253956	ENSG00000253956	RP11-211F2.1	8:111346971-111361836	NOTEST	0	0	0	0	1	1
ENSG00000253957	ENSG00000253957	IGHV3-22	14:106714359-106714821	NOTEST	0	0	0	0	1	1
ENSG00000253958	ENSG00000253958	CLDN23	8:8559447-8561616	NOTEST	0.508156	0.563303	0.148641	0	1	1
ENSG00000253959	ENSG00000253959	CTB-43E15.1	5:173069521-173085197	NOTEST	0	0	0	0	1	1
ENSG00000253960	ENSG00000253960	RP11-388K12.1	8:94225530-94753245	NOTEST	0	0	0	0	1	1
ENSG00000253961	ENSG00000253961	RP11-363L24.3	8:30891316-31034683	NOTEST	0	0	0	0	1	1
ENSG00000253963	ENSG00000253963	IGLV3-2	22:23215390-23215619	NOTEST	0	0	0	0	1	1
ENSG00000253964	ENSG00000253964	RPL31P40	8:69205680-69206053	NOTEST	0	0	0	0	1	1

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ENSG00000253966	ENSG00000253966	CTC-455F18.3	5:170288873-170727019	NOTEST	0.0741041	0.167799	1.17911	0	1	1
ENSG00000253967	ENSG00000253967	RP11-333A23.4	8:71383346-71397922	NOTEST	0	0	0	0	1	1
ENSG00000253968	ENSG00000253968	CTB-32H22.1	5:172841037-172878168	NOTEST	0	0.0286327	inf	0	1	1
ENSG00000253970	ENSG00000253970	MTND2P7	8:134767053-134767693	NOTEST	0	0	0	0	1	1
ENSG00000253971	ENSG00000253971	CDC42P3	8:144063154-144105249	NOTEST	0	0.102692	inf	0	1	1
ENSG00000253972	ENSG00000253972	RP11-4K16.2	8:120177272-120259088	NOTEST	0	0	0	0	1	1
ENSG00000253973	ENSG00000253973	RP11-467K18.2	11:9025708-9159661	NOTEST	0	0.110291	inf	0	1	1
ENSG00000253974	ENSG00000253974	NRG1-IT1	8:31496901-32622548	NOTEST	0	0	0	0	1	1
ENSG00000253975	ENSG00000253975	RP11-577N1.2	8:63161149-63912211	NOTEST	0	0	0	0	1	1
ENSG00000253976	ENSG00000253976	RP11-386G21.1	8:56014948-56454613	NOTEST	0	0	0	0	1	1
ENSG00000253977	ENSG00000253977	KB-1639H6.8	8:104103490-104103737	NOTEST	0	0	0	0	1	1
ENSG00000253979	ENSG00000253979	RP11-443C10.2	5:178804505-178805866	NOTEST	0	0	0	0	1	1
ENSG00000253980	ENSG00000253980	CTB-4E7.1	5:156512842-156682201	NOTEST	0	0	0	0	1	1
ENSG00000253981	ENSG00000253981	ALG1L13P	8:8086116-8102387	NOTEST	0	0.145747	inf	0	1	1
ENSG00000253983	ENSG00000253983	RP1-16A9.1	8:75111630-75120676	NOTEST	0	0	0	0	1	1
ENSG00000253985	ENSG00000253985	RP11-136K7.3	5:70647681-70742396	NOTEST	0	0	0	0	1	1
ENSG00000253986	ENSG00000253986	CTC-756D1.3	8:23350521-23351711	NOTEST	0.050194	0	#NAME?	0	1	1
ENSG00000253988	ENSG00000253988	RP11-489O18.1	8:138821686-139095813	NOTEST	0	0	0	0	1	1
ENSG00000253989	ENSG00000253989	IGHVIII-38-1	14:106873941-106873995	NOTEST	0	0	0	0	1	1
ENSG00000253991	ENSG00000253991	KB-1562D12.2	8:102473404-102681954	NOTEST	0	0	0	0	1	1
ENSG00000253992	ENSG00000253992	RP11-737F9.1	8:131792546-132054672	NOTEST	0	0	0	0	1	1
ENSG00000253993	ENSG00000253993	RP11-451O18.1	8:33084365-33084665	NOTEST	0	0	0	0	1	1
ENSG00000253994	ENSG00000253994	KB-1299A7.1	8:111821622-111822123	NOTEST	0	0	0	0	1	1
ENSG00000253995	ENSG00000253995	RP11-10D7.5	8:33397702-33398011	NOTEST	0	0	0	0	1	1
ENSG00000253996	ENSG00000253996	IGHVII-20-1	14:106669467-106669951	NOTEST	0	0	0	0	1	1
ENSG00000253997	ENSG00000253997	RP11-200A13.3	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000253998	ENSG00000253998	IGKV2-29	2:89533654-89534393	NOTEST	0	0	0	0	1	1
ENSG00000253999	ENSG00000253999	IGKV3D-31	2:89968510-89969012	NOTEST	0	0	0	0	1	1
ENSG00000254000	ENSG00000254000	RP11-245A18.1	8:124864226-125183763	NOTEST	0	0	0	0	1	1
ENSG00000254001	ENSG00000254001	RP11-91P17.1	8:79060335-79066148	NOTEST	0	0	0	0	1	1
ENSG00000254002	ENSG00000254002	RP11-213G6.2	8:23564653-23647000	NOTEST	0	0	0	0	1	1
ENSG00000254003	ENSG00000254003	CTB-167B5.1	7:87834432-87936206	NOTEST	0.036679	0.107296	1.54857	0	1	1
ENSG00000254006	ENSG00000254006	RP11-1D12.2	8:65713792-65730130	NOTEST	0	0	0	0	1	1
ENSG00000254007	ENSG00000254007	RP11-281H11.1	8:5517200-5527599	NOTEST	0	0	0	0	1	1
ENSG00000254008	ENSG00000254008	LINC00051	8:143279716-143290364	NOTEST	0	0	0	0	1	1
ENSG00000254009	ENSG00000254009	IGKV2D-38	2:89911272-89911512	NOTEST	0	0	0	0	1	1
ENSG00000254010	ENSG00000254010	RP11-103H7.5	8:127564686-127725660	NOTEST	0.160289	0.260441	0.700283	0	1	1
ENSG00000254011	ENSG00000254011	CTC-229L21.1	5:173472606-173670504	NOTEST	0	0	0	0	1	1
ENSG00000254012	ENSG00000254012	RP11-546B8.5	5:170792598-170794697	NOTEST	0	0.0744683	inf	0	1	1
ENSG00000254013	ENSG00000254013	MAP2K1P1	8:29885228-29886416	NOTEST	0.0146039	0	#NAME?	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000254014	ENSG00000254014	RP11-363E6.1	8:82156390-82156573	NOTEST	0	0	0	0	1	1
ENSG00000254015	ENSG00000254015	CTD-2547L16.2	8:18027985-18081198	NOTEST	0	0	0	0	1	1
ENSG00000254016	ENSG00000254016	ALG1L10P	12:8380329-8384360	NOTEST	0	0	0	0	1	1
ENSG00000254017	ENSG00000254017	IGHEP2	9:4985032-5128183	NOTEST	0	0	0	0	1	1
ENSG00000254018	ENSG00000254018	RP11-785H20.1	8:122896962-122916512	NOTEST	0	0	0	0	1	1
ENSG00000254019	ENSG00000254019	RP11-10J21.3	8:142217264-142318404	NOTEST	0	0	0	0	1	1
ENSG00000254020	ENSG00000254020	RP11-100L22.4	8:93711969-93889865	NOTEST	0	0	0	0	1	1
ENSG00000254021	ENSG00000254021	RP11-778D12.2	8:107277662-107280969	NOTEST	0	0	0	0	1	1
ENSG00000254023	ENSG00000254023	PKMP4	8:76288943-76289249	NOTEST	0	0	0	0	1	1
ENSG00000254024	ENSG00000254024	KB-1562D12.1	8:102473404-102681954	NOTEST	0	0	0	0	1	1
ENSG00000254025	ENSG00000254025	RP11-119N19.1	8:52170247-52722005	NOTEST	0	0	0	0	1	1
ENSG00000254026	ENSG00000254026	RP11-369E15.2	8:20810155-20852630	NOTEST	0	0	0	0	1	1
ENSG00000254028	ENSG00000254028	AC083843.2	8:135844989-135846725	NOTEST	0	0	0	0	1	1
ENSG00000254029	ENSG00000254029	IGLC4	22:23252997-23253245	NOTEST	0	0	0	0	1	1
ENSG00000254030	ENSG00000254030	IGLC5	22:23257804-23258097	NOTEST	0	0	0	0	1	1
ENSG00000254031	ENSG00000254031	RP11-326E22.1	8:72067691-72274467	NOTEST	0	0	0	0	1	1
ENSG00000254033	ENSG00000254033	RP11-431M3.2	8:34085956-34204249	NOTEST	0	0	0	0	1	1
ENSG00000254034	ENSG00000254034	RP11-662B19.2	8:28625177-28747759	NOTEST	0.185639	0.0306926	-2.59654	0	1	1
ENSG00000254035	ENSG00000254035	RP11-281O15.4	5:178396390-178423207	NOTEST	0	0	0	0	1	1
ENSG00000254036	ENSG00000254036	IGHVIII-67-2	14:107143129-107143217	NOTEST	0	0	0	0	1	1
ENSG00000254037	ENSG00000254037	RP11-775B15.3	8:120492518-120493015	NOTEST	0	0	0	0	1	1
ENSG00000254038	ENSG00000254038	RP11-419C23.1	8:36924958-36926936	NOTEST	0	0.139855	inf	0	1	1
ENSG00000254039	ENSG00000254039	RP11-304F15.6	17:47991766-48010282	NOTEST	0	0	0	0	1	1
ENSG00000254040	ENSG00000254040	RP11-421P23.2	8:20880806-20886569	NOTEST	0	0	0	0	1	1
ENSG00000254041	ENSG00000254041	RP11-574O7.1	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000254042	ENSG00000254042	CTC-558O2.1	5:168081517-168728133	NOTEST	0.00811155	0.00348845	-1.21739	0	1	1
ENSG00000254043	ENSG00000254043	RP11-3N13.2	8:75803385-75808537	NOTEST	0	0	0	0	1	1
ENSG00000254044	ENSG00000254044	RP11-681L8.1	4:98105243-99064391	NOTEST	0	0	0	0	1	1
ENSG00000254045	ENSG00000254045	IGHVIII-22-2	14:106721280-106721308	NOTEST	0	0	0	0	1	1
ENSG00000254046	ENSG00000254046	IGHV1-17	14:106631030-106631449	NOTEST	0	0	0	0	1	1
ENSG00000254047	ENSG00000254047	CTC-436K13.4	5:157600608-157627024	NOTEST	0	0	0	0	1	1
ENSG00000254048	ENSG00000254048	RP11-328K2.1	8:59717976-60033905	NOTEST	0	0	0	0	1	1
ENSG00000254049	ENSG00000254049	NRG1-IT3	8:31496901-32622548	NOTEST	0	0	0	0	1	1
ENSG00000254050	ENSG00000254050	RP11-577N1.1	8:63161149-63912211	NOTEST	0	0	0	0	1	1
ENSG00000254051	ENSG00000254051	RP11-403D15.1	8:68864352-69149265	NOTEST	0	0	0	0	1	1
ENSG00000254052	ENSG00000254052	IGHVIII-67-4	14:107151118-107151414	NOTEST	0	0	0	0	1	1
ENSG00000254053	ENSG00000254053	IGHVIII-5-2	14:106501830-106502091	NOTEST	0	0	0	0	1	1
ENSG00000254054	ENSG00000254054	RP11-156K13.3	8:17721888-17767874	NOTEST	0	0.0774957	inf	0	1	1
ENSG00000254055	ENSG00000254055	RP11-17A4.4	8:57552459-57569024	NOTEST	0	0	0	0	1	1
ENSG00000254056	ENSG00000254056	IGHV3-71	14:107183395-107183857	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000254057	ENSG00000254057	RP3-388N13.3	8:94846681-94858971	NOTEST	0.041609	0.0295253	-0.494941	0	1	1
ENSG00000254060	ENSG00000254060	RP11-172E10.1	8:81880044-82024303	NOTEST	0	0	0	0	1	1
ENSG00000254061	ENSG00000254061	RP11-359B20.1	8:33228341-33371119	NOTEST	0	0	0	0	1	1
ENSG00000254063	ENSG00000254063	DUXAP2	8:102374021-102384935	NOTEST	0	0	0	0	1	1
ENSG00000254065	ENSG00000254065	RP11-697N18.2	8:48173166-48648868	NOTEST	0	0	0	0	1	1
ENSG00000254066	ENSG00000254066	CTB-181F24.1	5:164647582-164668758	NOTEST	0	0	0	0	1	1
ENSG00000254067	ENSG00000254067	RP11-122L4.1	8:39413664-39416052	NOTEST	0	0	0	0	1	1
ENSG00000254069	ENSG00000254069	RP11-359P18.7	8:43349079-43349905	NOTEST	0	0	0	0	1	1
ENSG00000254070	ENSG00000254070	RP11-790L1.3	8:47583460-47583548	NOTEST	0	0	0	0	1	1
ENSG00000254073	ENSG00000254073	IGLVVII-41-1	22:22753183-22753334	NOTEST	0	0	0	0	1	1
ENSG00000254075	ENSG00000254075	IGLVV-66	22:22415488-22415950	NOTEST	0	0	0	0	1	1
ENSG00000254076	ENSG00000254076	CTD-3145H4.1	8:138708966-138710710	NOTEST	0	0	0	0	1	1
ENSG00000254077	ENSG00000254077	IGLV3-7	22:23180778-23181049	NOTEST	0	0	0	0	1	1
ENSG00000254079	ENSG00000254079	RP11-31K23.1	8:96960008-96960461	NOTEST	0	0	0	0	1	1
ENSG00000254080	ENSG00000254080	RP11-730G20.1	8:75512009-75779174	NOTEST	0.0293566	0.10642	1.85801	0	1	1
ENSG00000254081	ENSG00000254081	CTD-3025N20.2	8:66439242-66475015	NOTEST	0	0	0	0	1	1
ENSG00000254082	ENSG00000254082	CTD-2024D23.1	8:39424223-39437653	NOTEST	0	0	0	0	1	1
ENSG00000254083	ENSG00000254083	RP11-452N4.1	8:136246373-136311962	NOTEST	0	0	0	0	1	1
ENSG00000254084	ENSG00000254084	KB-1930G5.4	8:102424100-102464680	NOTEST	0	0	0	0	1	1
ENSG00000254086	ENSG00000254086	RP11-94H18.2	8:29722159-29729177	NOTEST	0	0	0	0	1	1
ENSG00000254088	ENSG00000254088	SLC2A3P4	8:87345502-87777251	NOTEST	0.0114738	0	#NAME?	0	1	1
ENSG00000254089	ENSG00000254089	RP11-388K12.2	8:94225530-94753245	NOTEST	0	0	0	0	1	1
ENSG00000254090	ENSG00000254090	MTND2P32	8:32853695-32902373	NOTEST	0	0	0	0	1	1
ENSG00000254091	ENSG00000254091	RP11-10A14.8	8:9090522-9090959	NOTEST	0	0	0	0	1	1
ENSG00000254092	ENSG00000254092	RP11-369E15.3	8:20810155-20852630	NOTEST	0	0	0	0	1	1
ENSG00000254094	ENSG00000254094	AC078852.1	4:1341053-1381837	NOTEST	0.0775803	0.0917235	0.2416	0	1	1
ENSG00000254095	ENSG00000254095	RP11-566H8.2	8:31133111-31241795	NOTEST	0	0	0	0	1	1
ENSG00000254097	ENSG00000254097	IGKV3D-25	2:90028796-90029031	NOTEST	0	0	0	0	1	1
ENSG00000254098	ENSG00000254098	IGKV2-26	2:89495583-89496317	NOTEST	0	0	0	0	1	1
ENSG00000254099	ENSG00000254099	AC005740.5	5:141323149-141369856	NOTEST	0	0	0	0	1	1
ENSG00000254100	ENSG00000254100	RP11-675F6.4	8:38401169-38416538	NOTEST	0	0	0	0	1	1
ENSG00000254101	ENSG00000254101	RP11-30J20.1	8:137543040-137997178	NOTEST	0	0	0	0	1	1
ENSG00000254102	ENSG00000254102	RP11-21C4.1	8:65486862-65496181	NOTEST	0.112271	0.0604054	-0.894235	0	1	1
ENSG00000254103	ENSG00000254103	RP11-114M5.3	8:59416146-59416627	NOTEST	0	0	0	0	1	1
ENSG00000254104	ENSG00000254104	RP11-63E5.1	8:214314-214672	NOTEST	0	0	0	0	1	1
ENSG00000254105	ENSG00000254105	VENTXP6	8:74332238-74791145	NOTEST	0	0	0	0	1	1
ENSG00000254106	ENSG00000254106	AC011366.3	5:109218882-109221124	NOTEST	0	0	0	0	1	1
ENSG00000254111	ENSG00000254111	RP11-150O12.5	8:37417883-37422884	NOTEST	0	0	0	0	1	1
ENSG00000254112	ENSG00000254112	KB-1205A7.1	8:99413630-99955055	NOTEST	0	0	0	0	1	1
ENSG00000254113	ENSG00000254113	RP11-174I12.2	8:124575309-124581002	NOTEST	0	0	0	0	1	1
ENSG00000254114	ENSG00000254114	HMGN1P28	17:58754813-59488916	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000254115	ENSG00000254115	RP11-386D6.1	8:87345502-87777251	NOTEST	0	0	0	0	1	1
ENSG00000254117	ENSG00000254117	IGHV2-10	14:106559545-106559975	NOTEST	0	0	0	0	1	1
ENSG00000254118	ENSG00000254118	RP11-101E19.4	8:47733858-47765929	NOTEST	0	0	0	0	1	1
ENSG00000254119	ENSG00000254119	RP11-705O24.1	8:62697605-62856739	NOTEST	0	0	0	0	1	1
ENSG00000254120	ENSG00000254120	RP11-705O24.2	8:62697605-62856739	NOTEST	0	0	0	0	1	1
ENSG00000254123	ENSG00000254123	RP11-99H20.1	8:83010685-83072812	NOTEST	0	0	0	0	1	1
ENSG00000254124	ENSG00000254124	EEF1A1P37	8:112111189-112248432	NOTEST	0	0	0	0	1	1
ENSG00000254126	ENSG00000254126	CD8BP	2:107099727-107123396	NOTEST	0	0	0	0	1	1
ENSG00000254127	ENSG00000254127	IGLCOR22-1	22:32586421-32600718	NOTEST	0.392568	0.0793202	-2.30718	0	1	1
ENSG00000254129	ENSG00000254129	CTD-2647L4.1	8:28924795-29120641	NOTEST	0.0490719	0.0402028	-0.287601	0	1	1
ENSG00000254130	ENSG00000254130	CTB-7E3.1	5:166332226-166353375	NOTEST	0	0	0	0	1	1
ENSG00000254131	ENSG00000254131	RP11-1007J8.1	8:42273992-42409603	NOTEST	0	0.144243	inf	0	1	1
ENSG00000254132	ENSG00000254132	MTND6P3	5:93488670-94620279	NOTEST	0	0	0	0	1	1
ENSG00000254133	ENSG00000254133	RP11-1198D22.3	5:70435715-70585611	NOTEST	0	0	0	0	1	1
ENSG00000254134	ENSG00000254134	IGHVII-74-1	14:107229404-107229645	NOTEST	0	0	0	0	1	1
ENSG00000254135	ENSG00000254135	RP11-32D16.1	5:157912197-157961446	NOTEST	0	0	0	0	1	1
ENSG00000254136	ENSG00000254136	RP11-546K22.2	8:52874017-52935534	NOTEST	0	0	0	0	1	1
ENSG00000254138	ENSG00000254138	RP11-152K4.2	5:31094083-31329253	NOTEST	0	0	0	0	1	1
ENSG00000254139	ENSG00000254139	CTD-2339F6.1	8:58506724-58717588	NOTEST	0	0	0	0	1	1
ENSG00000254140	ENSG00000254140	RP11-731F5.1	14:106064027-106071694	NOTEST	0	0	0	0	1	1
ENSG00000254141	ENSG00000254141	RP11-642D21.1	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000254142	ENSG00000254142	RP11-53M11.3	8:55466920-55474487	NOTEST	0	0	0	0	1	1
ENSG00000254143	ENSG00000254143	RP11-470M17.2	8:40018976-40030131	NOTEST	0	0	0	0	1	1
ENSG00000254144	ENSG00000254144	7SK	8:144624142-144631899	NOTEST	0.241484	0.088924	-1.44128	0	1	1
ENSG00000254145	ENSG00000254145	RP11-359P18.5	8:43394279-43394615	NOTEST	0	0	0	0	1	1
ENSG00000254146	ENSG00000254146	HMGB1P46	8:108185427-108186037	NOTEST	0	0	0	0	1	1
ENSG00000254148	ENSG00000254148	RP11-84E24.2	17:70017991-70216859	NOTEST	0.0158161	0.0284209	0.845556	0	1	1
ENSG00000254150	ENSG00000254150	RP11-379I19.2	8:60470086-60470414	NOTEST	0	0	0	0	1	1
ENSG00000254151	ENSG00000254151	NIPA2P4	8:82517803-82543369	NOTEST	0	0	0	0	1	1
ENSG00000254152	ENSG00000254152	CTD-3107M8.2	8:30207381-30207863	NOTEST	0	0	0	0	1	1
ENSG00000254153	ENSG00000254153	CTA-398F10.2	8:8314418-8318847	NOTEST	0	0	0	0	1	1
ENSG00000254154	ENSG00000254154	RP4-798P15.3	1:177893090-178007142	NOTEST	0.293747	0.276546	-0.0870516	0	1	1
ENSG00000254156	ENSG00000254156	MTND6P20	8:47733858-47765929	NOTEST	0	0	0	0	1	1
ENSG00000254157	ENSG00000254157	IGKV2-18	2:89428206-89428966	NOTEST	0	0	0	0	1	1
ENSG00000254158	ENSG00000254158	RP11-281O15.5	5:178424969-178425816	NOTEST	0	0.0155016	inf	0	1	1
ENSG00000254160	ENSG00000254160	CTD-2281E23.3	8:564745-1212580	NOTEST	0	0	0	0	1	1
ENSG00000254161	ENSG00000254161	IGLVIV-65	22:22424635-22425118	NOTEST	0	0	0	0	1	1
ENSG00000254162	ENSG00000254162	RP11-48B3.3	8:81447240-81451370	NOTEST	0.0306407	0.0460375	0.587358	0	1	1
ENSG00000254163	ENSG00000254163	CTC-340I23.2	5:155297353-156194799	NOTEST	0	0	0	0	1	1
ENSG00000254164	ENSG00000254164	CTB-33O18.2	5:173001940-173003278	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000254165	ENSG00000254165	RP11-503E24.2	8:42273992-42409603	NOTEST	0.456894	0.143281	-1.67301	0	1	1
ENSG00000254166	ENSG00000254166	CASC19	8:128197879-128215467	NOTEST	0	0	0	0	1	1
ENSG00000254167	ENSG00000254167	IGHVIII-51-1	14:107039492-107039794	NOTEST	0	0	0	0	1	1
ENSG00000254170	ENSG00000254170	CTD-2073O6.1	5:77781037-78065844	NOTEST	0	0.0186928	inf	0	1	1
ENSG00000254171	ENSG00000254171	RP11-67M9.1	5:165555502-165582444	NOTEST	0	0	0	0	1	1
ENSG00000254172	ENSG00000254172	RNU5A-3P	8:30435834-30515768	NOTEST	0	0	0	0	1	1
ENSG00000254173	ENSG00000254173	RP11-96G10.1	5:161851383-161854351	NOTEST	0	0	0	0	1	1
ENSG00000254174	ENSG00000254174	IGHV1-12	14:106579013-106579303	NOTEST	0	0	0	0	1	1
ENSG00000254175	ENSG00000254175	IGLVI-42	22:22751368-22751861	NOTEST	0	0	0	0	1	1
ENSG00000254176	ENSG00000254176	IGHV3-75	14:107231916-107232377	NOTEST	0	0	0	0	1	1
ENSG00000254177	ENSG00000254177	RP11-1149M10.1	8:81880044-82024303	NOTEST	0.0570913	0.0407002	-0.488235	0	1	1
ENSG00000254178	ENSG00000254178	RP11-299D14.2	8:25691644-25697651	NOTEST	0	0	0	0	1	1
ENSG00000254180	ENSG00000254180	AB015752.3	8:91233715-91632298	NOTEST	0.0675736	0.230664	1.77126	0	1	1
ENSG00000254181	ENSG00000254181	SLC25A51P3	8:81507049-81507938	NOTEST	0	0	0	0	1	1
ENSG00000254182	ENSG00000254182	RP11-68L18.2	8:91634222-91997485	NOTEST	0	0	0	0	1	1
ENSG00000254183	ENSG00000254183	RP11-953B20.2	8:143049451-143050202	NOTEST	0	0	0	0	1	1
ENSG00000254185	ENSG00000254185	RP11-419L20.2	8:110374705-110542559	NOTEST	0	0	0	0	1	1
ENSG00000254186	ENSG00000254186	RP11-167P20.1	5:161985690-162050467	NOTEST	0	0	0	0	1	1
ENSG00000254187	ENSG00000254187	CTB-78F1.1	5:166711803-167691162	NOTEST	0	0	0	0	1	1
ENSG00000254189	ENSG00000254189	RP11-296C13.1	8:84012210-84013081	NOTEST	0	0	0	0	1	1
ENSG00000254190	ENSG00000254190	RP11-267M23.5	8:95602342-95602487	NOTEST	0	0	0	0	1	1
ENSG00000254192	ENSG00000254192	CTC-558O2.2	5:168081517-168728133	NOTEST	0	0.00574234	inf	0	1	1
ENSG00000254193	ENSG00000254193	RP11-585F1.8	8:100583-100728	NOTEST	0	0	0	0	1	1
ENSG00000254194	ENSG00000254194	RP1-273G13.3	8:33462373-33896526	NOTEST	0	0	0	0	1	1
ENSG00000254195	ENSG00000254195	TPM3P3	8:85074352-85074706	NOTEST	0	0	0	0	1	1
ENSG00000254197	ENSG00000254197	RP11-10J21.5	8:142217264-142318404	NOTEST	0	0	0	0	1	1
ENSG00000254199	ENSG00000254199	AC008691.1	5:159175239-159188068	NOTEST	0	0	0	0	1	1
ENSG00000254200	ENSG00000254200	RPL7AP33	5:172652838-172653426	NOTEST	0	0.0252334	inf	0	1	1
ENSG00000254201	ENSG00000254201	RP11-618M23.2	8:18942501-19116979	NOTEST	0	0	0	0	1	1
ENSG00000254202	ENSG00000254202	RP11-120I21.2	8:84824947-85052518	NOTEST	0.0584207	0	#NAME?	0	1	1
ENSG00000254203	ENSG00000254203	IGHVII-33-1	14:106823314-106823594	NOTEST	0	0	0	0	1	1
ENSG00000254204	ENSG00000254204	RP11-400K9.3	8:54427729-54436491	NOTEST	0.158543	0.056891	-1.4786	0	1	1
ENSG00000254205	ENSG00000254205	RP11-92K15.1	8:80830951-81143467	NOTEST	0	0	0	0	1	1
ENSG00000254206	ENSG00000254206	NPIPB11	16:29262828-29519817	NOTEST	0.327259	0.254845	-0.360812	0	1	1
ENSG00000254207	ENSG00000254207	RP11-43A14.1	8:564745-1212580	NOTEST	0.101313	0.308994	1.60875	0	1	1
ENSG00000254208	ENSG00000254208	RP11-219B4.3	8:86089459-86132650	NOTEST	0.102174	0.28087	1.45887	0	1	1
ENSG00000254209	ENSG00000254209	RP11-3G20.1	8:122684012-122719871	NOTEST	0	0	0	0	1	1
ENSG00000254210	ENSG00000254210	IGHVIII-16-1	14:106627588-106627721	NOTEST	0	0	0	0	1	1
ENSG00000254211	ENSG00000254211	CTB-43E15.4	5:173213792-173236042	NOTEST	0	0	0	0	1	1
ENSG00000254212	ENSG00000254212	RP11-98H4.4	8:85095021-85834079	NOTEST	0	0	0	0	1	1

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ENSG00000254214	ENSG00000254214	IGHVII-28-1	14:106785675-106785916	NOTEST	0	0	0	0	1	1
ENSG00000254215	ENSG00000254215	IGHVIII-11-1	14:106576802-106577069	NOTEST	0	0	0	0	1	1
ENSG00000254216	ENSG00000254216	RP11-140I16.2	8:57165518-57165931	NOTEST	0	0	0	0	1	1
ENSG00000254219	ENSG00000254219	GS1-251I9.2	8:92054917-92056990	NOTEST	0	0	0	0	1	1
ENSG00000254220	ENSG00000254220	IGKV2D-18	2:90091426-90092218	NOTEST	0	0	0	0	1	1
ENSG00000254222	ENSG00000254222	RP11-787D18.2	8:61969716-62627155	NOTEST	0	0	0	0	1	1
ENSG00000254223	ENSG00000254223	RP11-419K12.1	8:130363936-130695925	NOTEST	0.407648	0.496908	0.285653	0	1	1
ENSG00000254224	ENSG00000254224	KB-1043D8.6	8:97238147-97250262	NOTEST	0	0	0	0	1	1
ENSG00000254225	ENSG00000254225	RP11-11C20.1	8:52170247-52722005	NOTEST	0	0	0	0	1	1
ENSG00000254226	ENSG00000254226	CTB-12O2.1	5:151329131-151650009	NOTEST	0.123129	0.0230368	-2.41816	0	1	1
ENSG00000254227	ENSG00000254227	RP11-622O11.4	8:127011237-127013245	NOTEST	0	0	0	0	1	1
ENSG00000254228	ENSG00000254228	IGHV3-42	14:106919182-106919483	NOTEST	0	0	0	0	1	1
ENSG00000254229	ENSG00000254229	FAM90A12P	8:7876950-7889827	NOTEST	0	0	0	0	1	1
ENSG00000254230	ENSG00000254230	RP11-582J16.3	8:22298331-22433301	NOTEST	0	0.000995993	inf	0	1	1
ENSG00000254231	ENSG00000254231	CTD-2284J15.1	8:87345502-87777251	NOTEST	0.0318497	0.0272333	-0.225908	0	1	1
ENSG00000254233	ENSG00000254233	RP11-242J7.1	4:185505246-185546184	NOTEST	0	0	0	0	1	1
ENSG00000254235	ENSG00000254235	RP11-115J16.1	8:9106926-9293715	NOTEST	0.0392787	0.103134	1.3927	0	1	1
ENSG00000254236	ENSG00000254236	KB-1639H6.2	8:104032414-104085279	NOTEST	0	0.0435759	inf	0	1	1
ENSG00000254237	ENSG00000254237	RP11-115J16.2	8:9106926-9293715	NOTEST	0	0	0	0	1	1
ENSG00000254238	ENSG00000254238	RP11-300E4.2	8:75896749-75946793	NOTEST	0	0	0	0	1	1
ENSG00000254239	ENSG00000254239	GS1-39E22.2	5:135233325-135235939	NOTEST	0	0	0	0	1	1
ENSG00000254240	ENSG00000254240	IGLVI-20	22:23057774-23057904	NOTEST	0	0	0	0	1	1
ENSG00000254241	ENSG00000254241	RP11-946L20.1	8:111945491-111946762	NOTEST	0	0	0	0	1	1
ENSG00000254242	ENSG00000254242	RP11-1080G15.2	8:18942501-19116979	NOTEST	0	0	0	0	1	1
ENSG00000254244	ENSG00000254244	PAICSP4	8:2792874-4852494	NOTEST	0.0137265	0.059984	2.12761	0	1	1
ENSG00000254245	ENSG00000254245	PCDHGA3	5:140710251-140892546	NOTEST	0.208996	0.240996	0.205535	0	1	1
ENSG00000254246	ENSG00000254246	CTB-120L21.1	5:156512842-156682201	NOTEST	0	0	0	0	1	1
ENSG00000254247	ENSG00000254247	RP11-278I4.1	8:119994817-119995114	NOTEST	0	0	0	0	1	1
ENSG00000254248	ENSG00000254248	RP11-320N21.2	8:95825538-96128683	NOTEST	0	0.0168299	inf	0	1	1
ENSG00000254249	ENSG00000254249	RP11-959I15.4	8:124864226-125183763	NOTEST	0	0	0	0	1	1
ENSG00000254251	ENSG00000254251	RP11-662G23.1	8:91634222-91997485	NOTEST	0.022446	0	#NAME?	0	1	1
ENSG00000254252	ENSG00000254252	RPL7P20	5:165455571-165456316	NOTEST	0	0	0	0	1	1
ENSG00000254253	ENSG00000254253	RP11-343B22.2	8:68334359-68658620	NOTEST	0	0	0	0	1	1
ENSG00000254254	ENSG00000254254	RP11-17A4.2	8:57349232-57472382	NOTEST	0	0.0144799	inf	0	1	1
ENSG00000254255	ENSG00000254255	CTD-2008O4.1	8:132724758-132725227	NOTEST	0	0	0	0	1	1
ENSG00000254256	ENSG00000254256	RP11-117L6.1	5:170792598-170794697	NOTEST	0.0211886	0	#NAME?	0	1	1
ENSG00000254258	ENSG00000254258	RP11-398H6.1	8:140472304-140475259	NOTEST	0.0171508	0	#NAME?	0	1	1
ENSG00000254260	ENSG00000254260	RP11-369E15.1	8:20798938-20807686	NOTEST	0	0	0	0	1	1
ENSG00000254261	ENSG00000254261	RP11-18A15.1	9:26746950-26786872	NOTEST	0	0	0	0	1	1

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ENSG00000254263	ENSG00000254263	RP11-473O4.4	8:130844546-131029375	NOTEST	0	0	0	0	1	1
ENSG00000254264	ENSG00000254264	IGKV3OR22-2	22:17406841-17407334	NOTEST	0	0	0	0	1	1
ENSG00000254265	ENSG00000254265	CTD-2336O2.2	8:1678371-1679618	NOTEST	0	0	0	0	1	1
ENSG00000254266	ENSG00000254266	RP11-594N15.2	8:79338337-79517502	NOTEST	0.0357768	0.158311	2.14567	0	1	1
ENSG00000254267	ENSG00000254267	KB-1458E12.1	8:99383582-99400475	NOTEST	0.105689	0.0438596	-1.26886	0	1	1
ENSG00000254268	ENSG00000254268	RFPL4AP7	8:50265188-50265403	NOTEST	0	0	0	0	1	1
ENSG00000254269	ENSG00000254269	CTD-2281E23.2	8:564745-1212580	NOTEST	0	0	0	0	1	1
ENSG00000254270	ENSG00000254270	ERHP1	7:139208601-139229730	NOTEST	0	0	0	0	1	1
ENSG00000254271	ENSG00000254271	RP11-131N11.4	10:62494099-62501586	NOTEST	0	0.136581	inf	0	1	1
ENSG00000254272	ENSG00000254272	RP11-382J24.2	8:22298331-22433301	NOTEST	0	0	0	0	1	1
ENSG00000254273	ENSG00000254273	RP11-181D18.4	8:74332238-74791145	NOTEST	0	0	0	0	1	1
ENSG00000254274	ENSG00000254274	TDGF1P5	8:54958937-55014577	NOTEST	0.052671	0	#NAME?	0	1	1
ENSG00000254275	ENSG00000254275	RP11-89M16.1	8:129417514-129576925	NOTEST	0	0.018225	inf	0	1	1
ENSG00000254276	ENSG00000254276	RP11-1198D22.2	5:70435715-70585611	NOTEST	0	0	0	0	1	1
ENSG00000254277	ENSG00000254277	RP11-1144P22.1	8:72587534-72615021	NOTEST	0	0	0	0	1	1
ENSG00000254278	ENSG00000254278	RP11-278I4.2	8:120007690-120118821	NOTEST	0	0	0	0	1	1
ENSG00000254279	ENSG00000254279	IGHVII-1-1	14:106411065-106411245	NOTEST	0	0	0	0	1	1
ENSG00000254281	ENSG00000254281	KB-1507C5.4	8:103991012-104012412	NOTEST	0	0	0	0	1	1
ENSG00000254283	ENSG00000254283	RP11-267M23.7	8:95606638-95606829	NOTEST	0	0	0	0	1	1
ENSG00000254284	ENSG00000254284	IGHV3-79	14:107275872-107276304	NOTEST	0	0	0	0	1	1
ENSG00000254285	ENSG00000254285	KRT8P3	8:61969716-62627155	NOTEST	0.0582035	0.0112474	-2.37151	0	1	1
ENSG00000254286	ENSG00000254286	RP11-89K10.1	8:127564686-127725660	NOTEST	0	0.172403	inf	0	1	1
ENSG00000254287	ENSG00000254287	RP11-44K6.4	8:39759793-39873910	NOTEST	0	0	0	0	1	1
ENSG00000254288	ENSG00000254288	RP11-6I2.3	8:74964574-75012088	NOTEST	0	0	0	0	1	1
ENSG00000254289	ENSG00000254289	IGHV3-32	14:106812090-106812517	NOTEST	0	0	0	0	1	1
ENSG00000254290	ENSG00000254290	RP11-150O12.3	8:37454997-37457376	NOTEST	0.181449	0.077573	-1.22594	0	1	1
ENSG00000254291	ENSG00000254291	RP11-10J21.6	8:142336228-142337236	NOTEST	0	0	0	0	1	1
ENSG00000254292	ENSG00000254292	IGKV2D-14	2:90160637-90161416	NOTEST	0	0	0	0	1	1
ENSG00000254293	ENSG00000254293	CTB-158E9.1	5:153863476-153865710	NOTEST	0	0	0	0	1	1
ENSG00000254294	ENSG00000254294	IMPDH1P6	8:124332089-124428590	NOTEST	0.0110585	0.00778307	-0.506751	0	1	1
ENSG00000254295	ENSG00000254295	CTC-308K20.2	5:172381788-172396774	NOTEST	0	0	0	0	1	1
ENSG00000254297	ENSG00000254297	CTC-286N12.1	5:166711803-167691162	NOTEST	0	0	0	0	1	1
ENSG00000254298	ENSG00000254298	CTB-17P3.4	5:150537666-150538023	NOTEST	0	0	0	0	1	1
ENSG00000254299	ENSG00000254299	CTB-54I1.1	5:171984394-171986017	NOTEST	0	0	0	0	1	1
ENSG00000254300	ENSG00000254300	LINC01111	8:77316232-77779521	NOTEST	0	0	0	0	1	1
ENSG00000254302	ENSG00000254302	RP11-431M3.1	8:34032403-34042413	NOTEST	0	0	0	0	1	1
ENSG00000254303	ENSG00000254303	RP11-398G24.2	8:122966878-123139423	NOTEST	0	0	0	0	1	1
ENSG00000254305	ENSG00000254305	MRPL9P1	8:77316232-77779521	NOTEST	0	0	0	0	1	1
ENSG00000254306	ENSG00000254306	RP11-150O12.4	8:37458054-37483391	NOTEST	0	0	0	0	1	1

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ENSG00000254308	ENSG00000254308	IGLVIV-59	22:22533617-22533867	NOTEST	0	0	0	0	1	1
ENSG00000254309	ENSG00000254309	RP11-89M20.1	8:35978915-35979201	NOTEST	0	0	0	0	1	1
ENSG00000254310	ENSG00000254310	CTD-2045M21.1	5:77781037-78065844	NOTEST	0	0	0	0	1	1
ENSG00000254311	ENSG00000254311	RP11-52B19.7	8:7974266-7974471	NOTEST	0	0	0	0	1	1
ENSG00000254312	ENSG00000254312	MRP63P7	8:99413630-99955055	NOTEST	0	0	0	0	1	1
ENSG00000254313	ENSG00000254313	CTD-2309H9.4	8:134783651-134826780	NOTEST	0	0	0	0	1	1
ENSG00000254314	ENSG00000254314	RP11-26M5.3	8:53023398-53373519	NOTEST	0	0	0	0	1	1
ENSG00000254315	ENSG00000254315	RP11-267M23.3	8:95499920-95565757	NOTEST	0	0	0	0	1	1
ENSG00000254316	ENSG00000254316	CTD-2345M20.2	8:30107017-30107608	NOTEST	0	0	0	0	1	1
ENSG00000254317	ENSG00000254317	RP11-473O4.5	8:130844546-131029375	NOTEST	0.078873	0.145924	0.88761	0	1	1
ENSG00000254318	ENSG00000254318	C8orf87	8:94146323-94179079	NOTEST	0	0	0	0	1	1
ENSG00000254319	ENSG00000254319	RP11-134O21.1	8:2523590-2680004	NOTEST	0	0	0	0	1	1
ENSG00000254320	ENSG00000254320	RP11-593P24.4	8:36178556-36178922	NOTEST	0	0	0	0	1	1
ENSG00000254321	ENSG00000254321	RP11-495O10.1	8:38558143-38562373	NOTEST	0	0	0	0	1	1
ENSG00000254324	ENSG00000254324	MIR151A	8:141667998-142012315	NOTEST	0	0	0	0	1	1
ENSG00000254325	ENSG00000254325	RP11-318K15.2	8:56792371-56923940	NOTEST	0	0	0	0	1	1
ENSG00000254326	ENSG00000254326	IGHV7-27	14:106774085-106774499	NOTEST	0	0	0	0	1	1
ENSG00000254328	ENSG00000254328	CTC-308K20.4	5:172410759-172462448	NOTEST	0	0	0	0	1	1
ENSG00000254329	ENSG00000254329	IGHVII-60-1	14:107093722-107093978	NOTEST	0	0	0	0	1	1
ENSG00000254330	ENSG00000254330	RP11-1D12.1	8:65500319-65711318	NOTEST	0	0.0548401	inf	0	1	1
ENSG00000254331	ENSG00000254331	CKS1BP7	8:81540685-81787016	NOTEST	0	0.165528	inf	0	1	1
ENSG00000254333	ENSG00000254333	CTC-367J11.1	5:149855093-149937773	NOTEST	0.0751951	0.0538368	-0.482046	0	1	1
ENSG00000254334	ENSG00000254334	RP11-24P4.1	8:21155716-21166960	NOTEST	0	0	0	0	1	1
ENSG00000254335	ENSG00000254335	CDH12P1	5:70156111-70156406	NOTEST	0	0	0	0	1	1
ENSG00000254336	ENSG00000254336	AC008694.2	5:157031714-157032645	NOTEST	0	0	0	0	1	1
ENSG00000254337	ENSG00000254337	RP11-865I6.2	8:69760976-69764998	NOTEST	0	0.0336421	inf	0	1	1
ENSG00000254338	ENSG00000254338	RP11-909N17.3	8:144499848-144501320	NOTEST	0	0.0430359	inf	0	1	1
ENSG00000254339	ENSG00000254339	RP11-267L5.1	8:115294295-115308068	NOTEST	0	0	0	0	1	1
ENSG00000254340	ENSG00000254340	RP11-10A14.3	8:8993764-9009084	NOTEST	0.133849	0.144774	0.113198	0	1	1
ENSG00000254341	ENSG00000254341	SNORD87	8:67782983-67838633	NOTEST	0	0	0	0	1	1
ENSG00000254342	ENSG00000254342	RP11-726G23.6	8:43227701-43227820	NOTEST	0	0	0	0	1	1
ENSG00000254343	ENSG00000254343	RP11-760H22.2	8:121064418-121068440	NOTEST	0.421616	0.29609	-0.509896	0	1	1
ENSG00000254344	ENSG00000254344	RP11-258J10.1	8:34641569-34722316	NOTEST	0	0	0	0	1	1
ENSG00000254345	ENSG00000254345	IGKV2D-23	2:90048211-90048737	NOTEST	0	0	0	0	1	1
ENSG00000254346	ENSG00000254346	MTND1P6	8:32853695-32902373	NOTEST	0	0	0	0	1	1
ENSG00000254347	ENSG00000254347	RP11-351E7.1	8:73374545-73383207	NOTEST	0	0	0	0	1	1
ENSG00000254348	ENSG00000254348	RP11-1134I14.4	8:48001194-48110484	NOTEST	0	0	0	0	1	1
ENSG00000254349	ENSG00000254349	RP11-758M4.1	8:75512009-75779174	NOTEST	0	0.0871558	inf	0	1	1
ENSG00000254350	ENSG00000254350	RP11-542A14.1	5:157851592-157879766	NOTEST	0.0555296	0.153701	1.4688	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000254352	ENSG00000254352	RP11-578O24.2	8:79578281-79717758	NOTEST	0	0	0	0	1	1
ENSG00000254355	ENSG00000254355	IGLVI-68	22:22345495-22398340	NOTEST	0	0	0	0	1	1
ENSG00000254357	ENSG00000254357	RP11-628E19.2	8:56014948-56454613	NOTEST	0	0	0	0	1	1
ENSG00000254358	ENSG00000254358	CYCSP22	8:50822348-51706678	NOTEST	0	0	0	0	1	1
ENSG00000254361	ENSG00000254361	RP11-238K6.2	8:138821686-139095813	NOTEST	0	0	0	0	1	1
ENSG00000254362	ENSG00000254362	RP11-14I17.3	8:26236774-26371608	NOTEST	0.0749704	0	#NAME?	0	1	1
ENSG00000254363	ENSG00000254363	CTB-131B5.5	5:139536903-139552636	NOTEST	0.016976	0.0146444	-0.213149	0	1	1
ENSG00000254364	ENSG00000254364	KB-1615E4.3	8:101487902-101513376	NOTEST	0	0	0	0	1	1
ENSG00000254365	ENSG00000254365	CTB-180C19.1	5:166711803-167691162	NOTEST	0	0	0	0	1	1
ENSG00000254366	ENSG00000254366	RP11-38H17.1	8:78311307-78449526	NOTEST	0	0	0	0	1	1
ENSG00000254367	ENSG00000254367	RP11-211C9.1	8:8581202-8639989	NOTEST	0	0	0	0	1	1
ENSG00000254369	ENSG00000254369	HOXA-AS3	7:27145802-27197555	NOTEST	0.359544	0.472662	0.394638	0	1	1
ENSG00000254370	ENSG00000254370	RP11-181B11.1	8:28203101-28347835	NOTEST	0.0436979	0.0310201	-0.494362	0	1	1
ENSG00000254372	ENSG00000254372	RP11-343P9.1	8:136468107-136469195	NOTEST	0	0	0	0	1	1
ENSG00000254373	ENSG00000254373	RP11-34P1.2	5:159678658-159772403	NOTEST	0.623525	0.738264	0.243688	0	1	1
ENSG00000254374	ENSG00000254374	GOLGA6L21P	15:83188578-83195251	NOTEST	0.244016	0.237986	-0.0361015	0	1	1
ENSG00000254376	ENSG00000254376	SOX5P	8:88800789-88801916	NOTEST	0	0	0	0	1	1
ENSG00000254377	ENSG00000254377	LINC00966	8:65285884-65296344	NOTEST	0	0	0	0	1	1
ENSG00000254380	ENSG00000254380	RP11-317J10.4	8:86436127-86452740	NOTEST	0	0	0	0	1	1
ENSG00000254381	ENSG00000254381	TUBB8P5	12:38595367-38597594	NOTEST	0	0	0	0	1	1
ENSG00000254383	ENSG00000254383	RP11-465K16.1	8:40757534-40759373	NOTEST	0	0	0	0	1	1
ENSG00000254384	ENSG00000254384	MTND6P19	8:36136477-36137001	NOTEST	0	0	0	0	1	1
ENSG00000254387	ENSG00000254387	RP3-388N13.2	8:94861788-94862303	NOTEST	0	0	0	0	1	1
ENSG00000254388	ENSG00000254388	DUTP2	8:124332089-124428590	NOTEST	0	0.0723979	inf	0	1	1
ENSG00000254391	ENSG00000254391	CTC-529G1.1	5:159990126-160279221	NOTEST	0.0517397	0.115255	1.15548	0	1	1
ENSG00000254392	ENSG00000254392	RP11-759A9.2	8:50822348-51706678	NOTEST	0	0	0	0	1	1
ENSG00000254394	ENSG00000254394	CTD-2272D18.1	8:83775013-83874161	NOTEST	0	0	0	0	1	1
ENSG00000254395	ENSG00000254395	IGHV4-55	14:107062110-107062561	NOTEST	0	0	0	0	1	1
ENSG00000254396	ENSG00000254396	RP11-56F10.3	9:27102627-27104726	NOTEST	0	0	0	0	1	1
ENSG00000254397	ENSG00000254397	CTD-2371O3.2	11:9406168-9469673	NOTEST	0	0.0246966	inf	0	1	1
ENSG00000254398	ENSG00000254398	RP11-578F21.2	15:28834637-28930410	NOTEST	0.0735177	0	#NAME?	0	1	1
ENSG00000254399	ENSG00000254399	GLYATL1P4	11:58672870-58826132	NOTEST	0	0	0	0	1	1
ENSG00000254401	ENSG00000254401	RP11-179A10.1	11:11139400-11205158	NOTEST	0	0	0	0	1	1
ENSG00000254402	ENSG00000254402	LRRC24	8:145743375-145754516	NOTEST	0.24541	0.372847	0.60339	0	1	1
ENSG00000254403	ENSG00000254403	OR10Y1P	11:59480295-59573354	NOTEST	0	0	0	0	1	1
ENSG00000254404	ENSG00000254404	RP11-703H8.9	11:61976139-62028021	NOTEST	0	0	0	0	1	1
ENSG00000254405	ENSG00000254405	MSH5-SAPCD1	HSCHR6_MHC_COX:31695129-31720748	NOTEST	0	0	0	0	1	1
ENSG00000254406	ENSG00000254406	RP11-215D10.1	11:119692012-119692838	NOTEST	0	0	0	0	1	1
ENSG00000254407	ENSG00000254407	RP11-109E10.2	11:123210881-123211422	NOTEST	0	0	0	0	1	1
ENSG00000254408	ENSG00000254408	OR4A1P	11:49919818-49920738	NOTEST	0	0	0	0	1	1
ENSG00000254409	ENSG00000254409	RP11-613D13.4	11:43942608-44022707	NOTEST	0.0388877	0.027572	-0.49611	0	1	1

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ENSG00000254412	ENSG00000254412	RP11-107P7.6	11:49119714-49122720	NOTEST	0	0	0	0	1	1
ENSG00000254413	ENSG00000254413	CHKB-CPT1B	22:51007289-51052409	NOTEST	0.480835	0.290805	-0.72549	0	1	1
ENSG00000254414	ENSG00000254414	RP11-182J1.1	15:85174681-85185695	NOTEST	0.224146	0.163784	-0.452646	0	1	1
ENSG00000254415	ENSG00000254415	SIGLEC14	19:52114780-52150151	NOTEST	0	0	0	0	1	1
ENSG00000254417	ENSG00000254417	ANO1-AS2	11:69918539-69921575	NOTEST	0	0	0	0	1	1
ENSG00000254418	ENSG00000254418	RP11-21L19.1	11:13983913-14295237	NOTEST	0	0	0	0	1	1
ENSG00000254419	ENSG00000254419	RP11-261P9.4	20:57226327-57294294	NOTEST	0	0.271793	inf	0	1	1
ENSG00000254420	ENSG00000254420	RP11-452H21.1	11:77926342-78285919	NOTEST	0	0.0436422	inf	0	1	1
ENSG00000254422	ENSG00000254422	RP11-864G5.3	11:101981191-102104154	NOTEST	0	0	0	0	1	1
ENSG00000254423	ENSG00000254423	RP11-351I21.7	8:12219526-12268510	NOTEST	0	0.0114319	inf	0	1	1
ENSG00000254424	ENSG00000254424	RP11-810P12.6	11:61840353-61840524	NOTEST	0	0	0	0	1	1
ENSG00000254425	ENSG00000254425	RP11-480O10.2	8:13766739-13767289	NOTEST	0	0	0	0	1	1
ENSG00000254427	ENSG00000254427	RP11-430H10.1	11:45376921-45387672	NOTEST	0	0	0	0	1	1
ENSG00000254428	ENSG00000254428	RP11-110I1.11	11:118868851-118901616	NOTEST	0.45237	0.501564	0.14893	0	1	1
ENSG00000254430	ENSG00000254430	OR6M3P	11:123732529-123733229	NOTEST	0	0	0	0	1	1
ENSG00000254431	ENSG00000254431	RP11-550A5.2	8:126036501-126379362	NOTEST	0	0	0	0	1	1
ENSG00000254432	ENSG00000254432	RP11-33I11.2	8:61591336-61779465	NOTEST	0	0	0	0	1	1
ENSG00000254433	ENSG00000254433	RP11-677I18.3	11:105921824-105972702	NOTEST	0.0680309	0.050032	-0.44334	0	1	1
ENSG00000254434	ENSG00000254434	CTD-2555I5.1	11:80032663-80038955	NOTEST	0	0	0	0	1	1
ENSG00000254436	ENSG00000254436	AP000648.6	11:89831588-89831985	NOTEST	0	0	0	0	1	1
ENSG00000254437	ENSG00000254437	RP11-170L9.1	11:80668359-80668677	NOTEST	0	0	0	0	1	1
ENSG00000254438	ENSG00000254438	RP11-231N3.1	11:13942996-13946410	NOTEST	0	0	0	0	1	1
ENSG00000254440	ENSG00000254440	PBOV1	6:138483057-138665800	NOTEST	0	0	0	0	1	1
ENSG00000254441	ENSG00000254441	RP11-718B12.5	11:82534543-82782965	NOTEST	0	0	0	0	1	1
ENSG00000254442	ENSG00000254442	AP000859.4	11:134144138-134189458	NOTEST	0	0	0	0	1	1
ENSG00000254443	ENSG00000254443	RP11-304C12.3	11:6384028-6386497	NOTEST	0	0	0	0	1	1
ENSG00000254444	ENSG00000254444	RP11-290F24.3	11:6128913-6206806	NOTEST	0	0	0	0	1	1
ENSG00000254445	ENSG00000254445	HSPB2-C11orf52	11:111779288-111797596	NOTEST	0	0	0	0	1	1
ENSG00000254447	ENSG00000254447	OR7E11P	11:67503078-67504030	NOTEST	0	0	0	0	1	1
ENSG00000254449	ENSG00000254449	SF3A3P2	11:123396343-123498482	NOTEST	0	0.0575223	inf	0	1	1
ENSG00000254450	ENSG00000254450	ALG9-IT1	11:111652918-111756699	NOTEST	0	0	0	0	1	1
ENSG00000254451	ENSG00000254451	RP11-560G2.1	12:75628519-75784708	NOTEST	0	0.0421702	inf	0	1	1
ENSG00000254452	ENSG00000254452	RP11-867G23.4	11:66036003-66056641	NOTEST	0.0221698	0.253367	3.51456	0	1	1
ENSG00000254453	ENSG00000254453	NAV2-AS2	11:19372270-20143144	NOTEST	0	0.0255776	inf	0	1	1
ENSG00000254454	ENSG00000254454	RCC2P6	11:62104382-62160882	NOTEST	0.0603264	0.0559897	-0.107628	0	1	1
ENSG00000254455	ENSG00000254455	HIGD1AP10	11:64913161-64913443	NOTEST	0	0	0	0	1	1
ENSG00000254456	ENSG00000254456	RP11-405K6.1	11:25756316-25803305	NOTEST	0	0	0	0	1	1
ENSG00000254457	ENSG00000254457	OR5D2P	11:55482471-55483108	NOTEST	0	0	0	0	1	1
ENSG00000254458	ENSG00000254458	RP11-867G23.13	11:66080323-66086708	NOTEST	0	0	0	0	1	1
ENSG00000254459	ENSG00000254459	RP11-91P24.7	11:77532154-77705724	NOTEST	0.0717633	0	#NAME?	0	1	1
ENSG00000254460	ENSG00000254460	RP11-939C17.4	11:75145684-75236948	NOTEST	0	0	0	0	1	1

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ENSG00000254462	ENSG00000254462	TMX2-CTNND1	11:57480071-57587018	NOTEST	0	0.0835058	inf	0	1	1
ENSG00000254463	ENSG00000254463	RP11-484D2.3	11:43333512-43516483	NOTEST	0.0898242	0	#NAME?	0	1	1
ENSG00000254464	ENSG00000254464	OR4A3P	11:51455829-51456700	NOTEST	0	0	0	0	1	1
ENSG00000254465	ENSG00000254465	PRKRIRP4	11:23499613-23501976	NOTEST	0	0	0	0	1	1
ENSG00000254466	ENSG00000254466	OR4D10	11:59244845-59245869	NOTEST	0	0	0	0	1	1
ENSG00000254467	ENSG00000254467	RP11-634B22.4	11:123539206-123542345	NOTEST	0	0	0	0	1	1
ENSG00000254468	ENSG00000254468	RP11-304M2.6	11:121278-126123	NOTEST	0	0	0	0	1	1
ENSG00000254471	ENSG00000254471	RP11-885L14.1	11:79698555-79700673	NOTEST	0	0	0	0	1	1
ENSG00000254472	ENSG00000254472	OR4A49P	11:49936564-49937196	NOTEST	0	0	0	0	1	1
ENSG00000254475	ENSG00000254475	OR2AT1P	11:74810216-74917594	NOTEST	0	0	0	0	1	1
ENSG00000254478	ENSG00000254478	RP11-158I9.1	11:118692603-118692793	NOTEST	0	0	0	0	1	1
ENSG00000254479	ENSG00000254479	SLC25A1P1	11:85645779-85646706	NOTEST	0.0196467	0	#NAME?	0	1	1
ENSG00000254480	ENSG00000254480	RP11-23F23.2	11:4208369-4223885	NOTEST	0	0.113644	inf	0	1	1
ENSG00000254481	ENSG00000254481	PTP4A2P2	11:133938819-134117686	NOTEST	0	0	0	0	1	1
ENSG00000254482	ENSG00000254482	RP11-386B1.1	11:109508193-109508854	NOTEST	0	0	0	0	1	1
ENSG00000254483	ENSG00000254483	RP11-23J9.6	9:99918851-100140806	NOTEST	0	0	0	0	1	1
ENSG00000254484	ENSG00000254484	CTA-797E19.1	11:70116805-70282690	NOTEST	0	0	0	0	1	1
ENSG00000254485	ENSG00000254485	RP11-380O24.1	3:9022274-9520924	NOTEST	0.258667	0.480729	0.894126	0	1	1
ENSG00000254486	ENSG00000254486	RP13-631K18.2	11:12052421-12083332	NOTEST	0.00946807	0	#NAME?	0	1	1
ENSG00000254487	ENSG00000254487	RP11-707M1.7	11:49839329-49848276	NOTEST	0	0	0	0	1	1
ENSG00000254488	ENSG00000254488	RP11-65G9.1	Y:23200174-23206610	NOTEST	0	0	0	0	1	1
ENSG00000254489	ENSG00000254489	RP5-1024C24.1	11:30406039-30652055	NOTEST	0.104108	0	#NAME?	0	1	1
ENSG00000254490	ENSG00000254490	OR5M7P	11:56267775-56268747	NOTEST	0	0	0	0	1	1
ENSG00000254491	ENSG00000254491	RP11-145O15.2	8:13415165-13462119	NOTEST	0	0.0756923	inf	0	1	1
ENSG00000254492	ENSG00000254492	KB-1073A2.1	8:103166777-103166953	NOTEST	0	0	0	0	1	1
ENSG00000254495	ENSG00000254495	AP000487.4	11:70116805-70282690	NOTEST	0	0	0	0	1	1
ENSG00000254496	ENSG00000254496	CBX3P8	11:49426526-49437299	NOTEST	0	0	0	0	1	1
ENSG00000254497	ENSG00000254497	CTD-2560E9.5	11:45261851-45307870	NOTEST	0	0	0	0	1	1
ENSG00000254498	ENSG00000254498	CTD-2119L1.1	11:36717866-36719417	NOTEST	0	0	0	0	1	1
ENSG00000254499	ENSG00000254499	AC002056.5	22:51176623-51183762	NOTEST	0	0	0	0	1	1
ENSG00000254500	ENSG00000254500	RANP3	11:74202756-74380162	NOTEST	0	0	0	0	1	1
ENSG00000254502	ENSG00000254502	FNTAL1	11:85906173-85907308	NOTEST	0.028063	0.0479124	0.771727	0	1	1
ENSG00000254503	ENSG00000254503	CTD-2521M24.4	19:17516502-17544533	NOTEST	0	0	0	0	1	1
ENSG00000254506	ENSG00000254506	RP11-748H22.1	11:101322294-101743293	NOTEST	0	0	0	0	1	1
ENSG00000254507	ENSG00000254507	RP11-481A20.10	8:11860908-11861591	NOTEST	0.454955	0.411433	-0.145067	0	1	1
ENSG00000254508	ENSG00000254508	RP11-646J21.5	11:33796244-33797216	NOTEST	0	0	0	0	1	1
ENSG00000254509	ENSG00000254509	RP11-677M14.6	11:124636393-124704383	NOTEST	0.163194	0.177482	0.12108	0	1	1
ENSG00000254510	ENSG00000254510	RP11-867G23.10	11:66176628-66184608	NOTEST	0.0501703	0	#NAME?	0	1	1
ENSG00000254511	ENSG00000254511	RP11-876F14.1	11:81590892-82429124	NOTEST	0	0	0	0	1	1

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ENSG00000254514	ENSG00000254514	RP11-958J22.3	11:45604074-45605024	NOTEST	0	0	0	0	1	1
ENSG00000254515	ENSG00000254515	RP11-775A1.2	11:121109012-121109397	NOTEST	0	0	0	0	1	1
ENSG00000254516	ENSG00000254516	RP11-159D8.1	11:37960150-37976213	NOTEST	0	0	0	0	1	1
ENSG00000254517	ENSG00000254517	RP11-56P9.8	11:48981479-48983362	NOTEST	0	0	0	0	1	1
ENSG00000254518	ENSG00000254518	RP11-347H15.4	11:50257749-50263827	NOTEST	0	0	0	0	1	1
ENSG00000254519	ENSG00000254519	CTD-2210P24.1	11:45743857-45765801	NOTEST	0	0	0	0	1	1
ENSG00000254521	ENSG00000254521	SIGLEC12	19:51994610-52005043	NOTEST	0	0	0	0	1	1
ENSG00000254522	ENSG00000254522	RP11-113K21.1	11:82534543-82782965	NOTEST	0	0	0	0	1	1
ENSG00000254524	ENSG00000254524	OR8I4P	11:55864719-55864860	NOTEST	0	0	0	0	1	1
ENSG00000254526	ENSG00000254526	RP11-466I1.1	11:29181502-29288281	NOTEST	0	0	0	0	1	1
ENSG00000254527	ENSG00000254527	ENPP7P12	8:12063267-12063898	NOTEST	0.427135	0.409275	-0.0616205	0	1	1
ENSG00000254528	ENSG00000254528	RP11-728F11.4	11:117298488-117748201	NOTEST	0	0	0	0	1	1
ENSG00000254529	ENSG00000254529	RP11-583F24.7	11:18885104-18886056	NOTEST	0	0	0	0	1	1
ENSG00000254530	ENSG00000254530	RP11-460B17.3	11:29357424-29615842	NOTEST	0	0	0	0	1	1
ENSG00000254532	ENSG00000254532	RP11-624D11.2	11:30065604-30105890	NOTEST	0.0575318	0	#NAME?	0	1	1
ENSG00000254533	ENSG00000254533	AF186192.1	8:145923998-145924570	NOTEST	0	0	0	0	1	1
ENSG00000254534	ENSG00000254534	RP11-748H22.2	11:101322294-101743293	NOTEST	0	0	0	0	1	1
ENSG00000254535	ENSG00000254535	PABPC4L	4:135117487-135122903	NOTEST	0.209343	0.190516	-0.135959	0	1	1
ENSG00000254536	ENSG00000254536	RP11-108K14.8	10:135192694-135382916	NOTEST	0.0815888	0.0699811	-0.221406	0	1	1
ENSG00000254537	ENSG00000254537	RP1-130L23.1	11:33424761-33425151	NOTEST	0	0	0	0	1	1
ENSG00000254538	ENSG00000254538	RP11-463D19.1	8:74332238-74791145	NOTEST	0	0	0	0	1	1
ENSG00000254539	ENSG00000254539	RP4-791M13.3	1:144833167-144835867	NOTEST	0.294291	0.362856	0.302153	0	1	1
ENSG00000254540	ENSG00000254540	CTD-2140G10.4	11:22305275-22401049	NOTEST	0	0	0	0	1	1
ENSG00000254541	ENSG00000254541	RP11-583F24.6	11:18908479-18909467	NOTEST	0	0	0	0	1	1
ENSG00000254542	ENSG00000254542	NAV2-AS3	11:19372270-20143144	NOTEST	0	0	0	0	1	1
ENSG00000254543	ENSG00000254543	HSPD1P2	8:7748524-7750077	NOTEST	0	0	0	0	1	1
ENSG00000254544	ENSG00000254544	PCNAP4	11:19203577-19302973	NOTEST	0	0	0	0	1	1
ENSG00000254545	ENSG00000254545	RP11-84A19.3	1:32254730-32281652	NOTEST	0	0	0	0	1	1
ENSG00000254546	ENSG00000254546	RP11-113D6.9	11:18218203-18218884	NOTEST	0	0	0	0	1	1
ENSG00000254547	ENSG00000254547	RP11-738O11.13	11:55631407-55648719	NOTEST	0.215184	0.378475	0.814627	0	1	1
ENSG00000254548	ENSG00000254548	RP11-429J17.5	8:144798428-144804628	NOTEST	0	0	0	0	1	1
ENSG00000254550	ENSG00000254550	OMP	11:76777978-76837201	NOTEST	0.0462705	0.24765	2.42014	0	1	1
ENSG00000254551	ENSG00000254551	RP11-727A23.7	11:82868029-83134559	NOTEST	0	0.0194226	inf	0	1	1
ENSG00000254552	ENSG00000254552	XIRP2-AS1	2:167744996-168116263	NOTEST	0	0	0	0	1	1
ENSG00000254553	ENSG00000254553	RP1-27O5.3	1:32930657-33116504	NOTEST	0.310826	0.494151	0.668846	0	1	1
ENSG00000254554	ENSG00000254554	RP11-351I24.1	11:10324203-10325251	NOTEST	0.160588	0.0867382	-0.888628	0	1	1
ENSG00000254555	ENSG00000254555	RP11-379J13.1	11:97749780-97813762	NOTEST	0	0	0	0	1	1
ENSG00000254556	ENSG00000254556	AF131215.4	8:10753554-11058875	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000254558	ENSG00000254558	RP11-81M19.3	11:89597015-89598718	NOTEST	0	0	0	0	1	1
ENSG00000254559	ENSG00000254559	RP11-304M2.5	11:127114-207428	NOTEST	0	0	0	0	1	1
ENSG00000254560	ENSG00000254560	RP11-1L12.3	11:27062271-27241660	NOTEST	0	0	0	0	1	1
ENSG00000254561	ENSG00000254561	RP11-196E1.3	11:119479134-119599794	NOTEST	0	0	0	0	1	1
ENSG00000254562	ENSG00000254562	RP11-64I17.1	11:38668025-38695791	NOTEST	0	0	0	0	1	1
ENSG00000254563	ENSG00000254563	RP11-673F18.1	11:78363875-79151992	NOTEST	0	0	0	0	1	1
ENSG00000254564	ENSG00000254564	RP11-787P24.2	11:23453222-23453345	NOTEST	0	0	0	0	1	1
ENSG00000254565	ENSG00000254565	MTND2P26	11:102980159-103350591	NOTEST	0	0	0	0	1	1
ENSG00000254566	ENSG00000254566	RP11-514F3.4	11:36317837-36486754	NOTEST	0	0	0	0	1	1
ENSG00000254567	ENSG00000254567	RP11-107P7.4	11:49155204-49156352	NOTEST	0	0	0	0	1	1
ENSG00000254568	ENSG00000254568	RP11-664I21.5	11:124753586-124768396	NOTEST	0	0	0	0	1	1
ENSG00000254569	ENSG00000254569	RP11-693N9.1	11:104743990-104744144	NOTEST	0	0	0	0	1	1
ENSG00000254571	ENSG00000254571	RP11-60I3.4	9:102668914-102732618	NOTEST	0	0	0	0	1	1
ENSG00000254572	ENSG00000254572	GLULP3	11:122484151-122485194	NOTEST	0	0	0	0	1	1
ENSG00000254573	ENSG00000254573	AP004550.1	11:134433289-134442950	NOTEST	0	0	0	0	1	1
ENSG00000254574	ENSG00000254574	RP11-429J17.4	8:144766621-144796068	NOTEST	0	0	0	0	1	1
ENSG00000254575	ENSG00000254575	RP11-3G21.1	8:13947372-15095848	NOTEST	0	0	0	0	1	1
ENSG00000254576	ENSG00000254576	OR4C1P	11:55277216-55278147	NOTEST	0	0.0471567	inf	0	1	1
ENSG00000254577	ENSG00000254577	RP11-484D2.4	11:43333512-43516483	NOTEST	0	0	0	0	1	1
ENSG00000254578	ENSG00000254578	CTD-2517M22.16	8:145674964-145691060	NOTEST	0	0	0	0	1	1
ENSG00000254579	ENSG00000254579	RP11-407P18.1	11:40135752-41481323	NOTEST	0	0	0	0	1	1
ENSG00000254580	ENSG00000254580	RP11-677I18.4	11:105983185-106002843	NOTEST	0	0	0	0	1	1
ENSG00000254581	ENSG00000254581	RP11-303G3.10	8:12533543-12533898	NOTEST	0	0	0	0	1	1
ENSG00000254582	ENSG00000254582	PSMA2P1	11:87040448-87041094	NOTEST	0	0	0	0	1	1
ENSG00000254583	ENSG00000254583	RP11-15D14.1	11:13499879-13500584	NOTEST	0	0	0	0	1	1
ENSG00000254584	ENSG00000254584	RP1-17K7.2	11:31806339-32127301	NOTEST	0	0	0	0	1	1
ENSG00000254585	ENSG00000254585	MAGEL2	15:23888690-23891175	NOTEST	0	6.49E-06	inf	0	1	1
ENSG00000254586	ENSG00000254586	RP11-358H18.3	11:17716568-17719018	NOTEST	0	0	0	0	1	1
ENSG00000254587	ENSG00000254587	RP11-360K13.1	11:96461316-96584822	NOTEST	0	0	0	0	1	1
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ENSG00000254590	ENSG00000254590	RP11-334E6.2	11:119252487-119397374	NOTEST	0	0	0	0	1	1
ENSG00000254591	ENSG00000254591	RP11-822P1.1	11:127527462-127527772	NOTEST	0	0	0	0	1	1
ENSG00000254592	ENSG00000254592	RP5-1173A5.1	11:3357950-3400448	NOTEST	0	0	0	0	1	1
ENSG00000254593	ENSG00000254593	OR7E126P	11:71576554-71639700	NOTEST	0.107854	0.0749998	-0.524127	0	1	1
ENSG00000254594	ENSG00000254594	RP11-2F20.1	11:24257022-24283764	NOTEST	0	0	0	0	1	1
ENSG00000254596	ENSG00000254596	CTD-3074O7.7	11:66202545-66234209	NOTEST	0	0	0	0	1	1
ENSG00000254597	ENSG00000254597	FAM90A10P	8:7626498-7629510	NOTEST	0	0	0	0	1	1
ENSG00000254599	ENSG00000254599	RP11-115E19.1	11:98547120-98554465	NOTEST	0	0	0	0	1	1
ENSG00000254601	ENSG00000254601	CYCSP26	11:57772857-57773177	NOTEST	0	0	0	0	1	1
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ENSG00000254605	ENSG00000254605	RP11-626H12.2	11:69831981-69867165	NOTEST	0	0	0	0	1	1
ENSG00000254606	ENSG00000254606	RP11-22P4.2	11:28373653-28548588	NOTEST	0	0.0200642	inf	0	1	1
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ENSG00000254608	ENSG00000254608	RP11-56A10.1	8:55561552-55782463	NOTEST	0	0	0	0	1	1
ENSG00000254609	ENSG00000254609	RP11-719K4.3	16:14821138-14827204	NOTEST	0	0	0	0	1	1
ENSG00000254610	ENSG00000254610	RP5-903G2.2	11:67702033-67707245	NOTEST	0	0	0	0	1	1
ENSG00000254613	ENSG00000254613	OR6M2P	11:123711713-123712584	NOTEST	0	0	0	0	1	1
ENSG00000254616	ENSG00000254616	RP11-700F16.2	11:133938819-134117686	NOTEST	0	0	0	0	1	1
ENSG00000254617	ENSG00000254617	AP000648.3	11:89620533-89623159	NOTEST	0	0	0	0	1	1
ENSG00000254618	ENSG00000254618	TMED10P1	8:146198974-146231432	NOTEST	0.101608	0.141952	0.482391	0	1	1
ENSG00000254619	ENSG00000254619	RP11-646J21.4	11:33831690-33832724	NOTEST	0	0	0	0	1	1
ENSG00000254620	ENSG00000254620	RP5-907D15.3	20:57090434-57194944	NOTEST	0.0442074	0	#NAME?	0	1	1
ENSG00000254621	ENSG00000254621	SETP16	11:118704554-118705265	NOTEST	0	0	0	0	1	1
ENSG00000254622	ENSG00000254622	NAV2-AS4	11:19372270-20143144	NOTEST	0	0	0	0	1	1
ENSG00000254623	ENSG00000254623	DEFB108P4	8:12198934-12203285	NOTEST	0	0	0	0	1	1
ENSG00000254624	ENSG00000254624	OR4R3P	11:49944600-49945438	NOTEST	0	0	0	0	1	1
ENSG00000254625	ENSG00000254625	GS1-24F4.3	8:6786129-6787995	NOTEST	0	0	0	0	1	1
ENSG00000254626	ENSG00000254626	RP11-27G22.1	11:112658026-112666577	NOTEST	0.0224711	0.0971418	2.11202	0	1	1
ENSG00000254627	ENSG00000254627	RP1-17K7.1	11:31806339-32127301	NOTEST	0	0	0	0	1	1
ENSG00000254629	ENSG00000254629	RP11-160H12.3	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000254630	ENSG00000254630	CTD-2530H12.7	11:75294240-75380165	NOTEST	0	0	0	0	1	1
ENSG00000254631	ENSG00000254631	RP11-702H23.4	11:74041362-74197096	NOTEST	0	0	0	0	1	1
ENSG00000254632	ENSG00000254632	RP11-21L23.4	11:76470959-76479267	NOTEST	0	0	0	0	1	1
ENSG00000254633	ENSG00000254633	RP11-23J9.7	9:99918851-100140806	NOTEST	0	0	0	0	1	1
ENSG00000254634	ENSG00000254634	RP11-231C14.3	16:29262828-29519817	NOTEST	0.308424	0.113172	-1.4464	0	1	1
ENSG00000254636	ENSG00000254636	ARMS2	10:124214168-124216868	NOTEST	0	0.0162013	inf	0	1	1
ENSG00000254637	ENSG00000254637	OR4A18P	11:49938942-49940030	NOTEST	0	0	0	0	1	1
ENSG00000254638	ENSG00000254638	RP11-356J5.4	11:111895537-112095422	NOTEST	0	0	0	0	1	1
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ENSG00000254640	ENSG00000254640	RP11-384C21.9	11:59235716-59236130	NOTEST	0	0	0	0	1	1
ENSG00000254641	ENSG00000254641	RP11-732A19.2	11:6624871-6633898	NOTEST	0	0	0	0	1	1
ENSG00000254642	ENSG00000254642	COX6CP5	11:7991797-8023409	NOTEST	0	0	0	0	1	1
ENSG00000254644	ENSG00000254644	RP11-5A11.2	8:104495625-105268322	NOTEST	0	0	0	0	1	1
ENSG00000254646	ENSG00000254646	OR8B10P	11:124386206-124387138	NOTEST	0	0	0	0	1	1
ENSG00000254647	ENSG00000254647	INS	11:2150341-2182571	NOTEST	0	0	0	0	1	1
ENSG00000254648	ENSG00000254648	RP11-713P17.4	11:133902166-133916744	NOTEST	0	0	0	0	1	1
ENSG00000254649	ENSG00000254649	RP11-452H21.2	11:77926342-78285919	NOTEST	0	0	0	0	1	1
ENSG00000254650	ENSG00000254650	RP11-665E10.5	11:87525926-87527049	NOTEST	0	0	0	0	1	1

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ENSG00000254653	ENSG00000254653	RP11-702F3.1	11:45950870-46142985	NOTEST	0	0	0	0	1	1
ENSG00000254654	ENSG00000254654	AC068858.1	11:44995452-44999579	NOTEST	0	0	0	0	1	1
ENSG00000254655	ENSG00000254655	RP11-529A4.5	11:89693589-89693792	NOTEST	0	0	0	0	1	1
ENSG00000254656	ENSG00000254656	RTL1	14:101346991-101351184	NOTEST	0	0	0	0	1	1
ENSG00000254658	ENSG00000254658	OR8J2	11:55978333-55979298	NOTEST	0	0	0	0	1	1
ENSG00000254659	ENSG00000254659	RP11-262A12.1	11:109622167-109694573	NOTEST	0	0	0	0	1	1
ENSG00000254660	ENSG00000254660	CTD-3051L14.14	11:56277048-56277671	NOTEST	0	0	0	0	1	1
ENSG00000254661	ENSG00000254661	RP11-222N13.1	11:15932502-15948989	NOTEST	0	0	0	0	1	1
ENSG00000254662	ENSG00000254662	RP11-872D17.4	11:57093076-57103351	NOTEST	0.111704	0	#NAME?	0	1	1
ENSG00000254663	ENSG00000254663	OR4A11P	11:55086035-55086941	NOTEST	0	0	0	0	1	1
ENSG00000254664	ENSG00000254664	CTD-2560E9.3	11:45115563-45256843	NOTEST	0	0.0265863	inf	0	1	1
ENSG00000254665	ENSG00000254665	RP11-152H18.3	11:8703957-8932498	NOTEST	0	0	0	0	1	1
ENSG00000254668	ENSG00000254668	RP11-375D13.1	11:41736117-41857992	NOTEST	0	0	0	0	1	1
ENSG00000254669	ENSG00000254669	RP5-945I17.2	11:35600977-35606858	NOTEST	0	0	0	0	1	1
ENSG00000254670	ENSG00000254670	CTC-497E21.3	11:13022636-13032647	NOTEST	0	0	0	0	1	1
ENSG00000254671	ENSG00000254671	STT3A-AS1	11:125439111-125551018	NOTEST	0	0.0959632	inf	0	1	1
ENSG00000254672	ENSG00000254672	RP5-916O11.3	11:35965530-36253686	NOTEST	0	0.0436283	inf	0	1	1
ENSG00000254674	ENSG00000254674	OR4A42P	11:48631614-48632552	NOTEST	0	0	0	0	1	1
ENSG00000254675	ENSG00000254675	RP11-7I15.4	11:77726760-77791265	NOTEST	0	0	0	0	1	1
ENSG00000254676	ENSG00000254676	RP11-727A23.4	11:82868029-83134559	NOTEST	0.0774827	0.0157382	-2.29961	0	1	1
ENSG00000254677	ENSG00000254677	OSBPL9P2	11:90847891-90849119	NOTEST	0	0	0	0	1	1
ENSG00000254678	ENSG00000254678	RP11-109L13.5	11:117014606-117014907	NOTEST	0	0	0	0	1	1
ENSG00000254680	ENSG00000254680	RP11-265D17.2	11:12115542-12285334	NOTEST	0.44049	0.313828	-0.489137	0	1	1
ENSG00000254683	ENSG00000254683	AF228730.12	8:7001153-7001363	NOTEST	0	0	0	0	1	1
ENSG00000254684	ENSG00000254684	RP11-882I15.1	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000254686	ENSG00000254686	RP1-276E15.1	11:35678241-35682887	NOTEST	0	0	0	0	1	1
ENSG00000254687	ENSG00000254687	RP11-162D9.3	8:54090130-54164257	NOTEST	0	0	0	0	1	1
ENSG00000254688	ENSG00000254688	RP11-47J17.3	11:12695968-12966298	NOTEST	0	0	0	0	1	1
ENSG00000254689	ENSG00000254689	RP11-354A14.1	8:82797611-82835428	NOTEST	0	0	0	0	1	1
ENSG00000254691	ENSG00000254691	RP11-91P24.5	11:77532154-77705724	NOTEST	0.0390916	0	#NAME?	0	1	1
ENSG00000254693	ENSG00000254693	RP11-58K22.5	11:44585976-44641913	NOTEST	0	0	0	0	1	1
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ENSG00000254695	ENSG00000254695	RP11-396O20.1	11:15665430-15780444	NOTEST	0	0	0	0	1	1
ENSG00000254696	ENSG00000254696	RP11-72M10.7	11:55046922-55052999	NOTEST	0	0.0346245	inf	0	1	1
ENSG00000254697	ENSG00000254697	COPS8P3	11:78292719-78293201	NOTEST	0	0	0	0	1	1
ENSG00000254698	ENSG00000254698	RP11-659G9.3	11:82534543-82782965	NOTEST	0	0	0	0	1	1
ENSG00000254699	ENSG00000254699	RP11-12D16.2	11:85903828-85904524	NOTEST	0	0	0	0	1	1
ENSG00000254700	ENSG00000254700	RP11-1236K1.11	8:11901014-11901179	NOTEST	0	0	0	0	1	1

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ENSG00000254704	ENSG00000254704	RP11-1036E20.7	11:59054811-59056959	NOTEST	0	0	0	0	1	1
ENSG00000254705	ENSG00000254705	RP11-675M1.2	11:92085261-92629618	NOTEST	0	0	0	0	1	1
ENSG00000254707	ENSG00000254707	RP11-35J10.4	11:7710668-7927502	NOTEST	0	0	0	0	1	1
ENSG00000254708	ENSG00000254708	RP1-145M24.1	11:34172534-34379555	NOTEST	0	0	0	0	1	1
ENSG00000254709	ENSG00000254709	IGLL5	22:23229959-23238287	NOTEST	0	0	0	0	1	1
ENSG00000254710	ENSG00000254710	CTD-2216M2.1	11:122943034-123098985	NOTEST	0	0	0	0	1	1
ENSG00000254712	ENSG00000254712	RP11-560B16.5	11:6864894-6865897	NOTEST	0	0	0	0	1	1
ENSG00000254713	ENSG00000254713	HNRNPA1P72	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000254714	ENSG00000254714	RP11-163O19.1	11:49872180-49884080	NOTEST	0	0	0	0	1	1
ENSG00000254715	ENSG00000254715	OR7E154P	8:7562703-7564413	NOTEST	0	0	0	0	1	1
ENSG00000254717	ENSG00000254717	GLYATL1P2	11:58601541-58671688	NOTEST	0	0	0	0	1	1
ENSG00000254718	ENSG00000254718	CTD-2184C24.2	14:60706838-60765805	NOTEST	0	0.012123	inf	0	1	1
ENSG00000254720	ENSG00000254720	RP11-583F24.3	11:18993292-18994250	NOTEST	0	0	0	0	1	1
ENSG00000254722	ENSG00000254722	FAM8A2P	11:56098822-56099964	NOTEST	0	0.0455592	inf	0	1	1
ENSG00000254723	ENSG00000254723	OR4A12P	11:55093231-55094149	NOTEST	0	0	0	0	1	1
ENSG00000254724	ENSG00000254724	OR7E10P	8:12560574-12561565	NOTEST	0	0.0127645	inf	0	1	1
ENSG00000254725	ENSG00000254725	RP11-111A24.1	11:43085186-43087626	NOTEST	0	0	0	0	1	1
ENSG00000254727	ENSG00000254727	PTP4A1P6	11:86142631-86383678	NOTEST	0	0	0	0	1	1
ENSG00000254728	ENSG00000254728	RP11-56P9.10	11:48901662-48923733	NOTEST	0	0	0	0	1	1
ENSG00000254730	ENSG00000254730	RP11-801G16.2	11:108535751-108811657	NOTEST	0	0	0	0	1	1
ENSG00000254731	ENSG00000254731	CTD-2005H7.1	11:86414140-86425134	NOTEST	0	0	0	0	1	1
ENSG00000254732	ENSG00000254732	RP11-691N7.6	11:57480071-57587018	NOTEST	0	0	0	0	1	1
ENSG00000254733	ENSG00000254733	RP11-317J19.1	11:86142631-86383678	NOTEST	0	0	0	0	1	1
ENSG00000254734	ENSG00000254734	CTD-3138F19.1	11:29735455-29903261	NOTEST	0	0	0	0	1	1
ENSG00000254735	ENSG00000254735	HMGB1P42	11:120382467-120859613	NOTEST	0	0	0	0	1	1
ENSG00000254736	ENSG00000254736	RP11-867G23.9	11:66157079-66157639	NOTEST	0	0	0	0	1	1
ENSG00000254737	ENSG00000254737	OR10G4	11:123886281-123887217	NOTEST	0	0	0	0	1	1
ENSG00000254738	ENSG00000254738	RP11-583F24.4	11:18977601-18978562	NOTEST	0	0	0	0	1	1
ENSG00000254739	ENSG00000254739	RP13-46H24.1	11:528906-529659	NOTEST	0	0.0954842	inf	0	1	1
ENSG00000254740	ENSG00000254740	RP11-334E6.3	11:119225924-119252436	NOTEST	0	0.00456182	inf	0	1	1
ENSG00000254741	ENSG00000254741	RP11-661A12.7	8:144661805-144682485	NOTEST	0	0	0	0	1	1
ENSG00000254743	ENSG00000254743	OR10V3P	11:59480295-59573354	NOTEST	0	0	0	0	1	1
ENSG00000254744	ENSG00000254744	CTD-3076O17.1	15:100510419-100882210	NOTEST	0.218339	0.0382304	-2.51378	0	1	1
ENSG00000254746	ENSG00000254746	RP11-958J22.1	11:45392947-45564024	NOTEST	0	0	0	0	1	1
ENSG00000254747	ENSG00000254747	RP11-664H7.1	11:81263267-81263558	NOTEST	0	0	0	0	1	1
ENSG00000254748	ENSG00000254748	HNRNPCP8	11:86735624-86736819	NOTEST	0	0	0	0	1	1
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test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000254751	ENSG00000254751	TRIM64DP	11:89510148-89515545	NOTEST	0	0	0	0	1	1
ENSG00000254752	ENSG00000254752	OR5M2P	11:56246967-56247903	NOTEST	0	0	0	0	1	1
ENSG00000254753	ENSG00000254753	RP11-480O10.1	8:13701609-13706618	NOTEST	0	0	0	0	1	1
ENSG00000254754	ENSG00000254754	RP11-20J1.1	11:25945734-25948355	NOTEST	0	0	0	0	1	1
ENSG00000254755	ENSG00000254755	RP11-672A2.7	11:76302066-76302255	NOTEST	0	0	0	0	1	1
ENSG00000254756	ENSG00000254756	RP11-867G23.12	11:66097712-66112596	NOTEST	0	0	0	0	1	1
ENSG00000254757	ENSG00000254757	RP13-726E6.1	11:3490548-3602441	NOTEST	0	0	0	0	1	1
ENSG00000254758	ENSG00000254758	AP000889.1	11:107461816-107537505	NOTEST	0	0	0	0	1	1
ENSG00000254759	ENSG00000254759	NAP1L1P1	11:125937433-125938496	NOTEST	0.0303576	0.011729	-1.37198	0	1	1
ENSG00000254760	ENSG00000254760	CTD-2616J11.3	19:51913274-51921057	NOTEST	0	0	0	0	1	1
ENSG00000254761	ENSG00000254761	RP11-672A2.1	11:76423439-76430652	NOTEST	0	0	0	0	1	1
ENSG00000254762	ENSG00000254762	RP11-867G23.2	11:66024764-66035600	NOTEST	0	0	0	0	1	1
ENSG00000254764	ENSG00000254764	TRIM53CP	11:49007422-49013433	NOTEST	0	0	0	0	1	1
ENSG00000254765	ENSG00000254765	RP11-1H15.1	11:9776316-10315754	NOTEST	0.0247543	0	#NAME?	0	1	1
ENSG00000254767	ENSG00000254767	OR2AL1P	11:105028653-105402424	NOTEST	0	0	0	0	1	1
ENSG00000254768	ENSG00000254768	CTD-2140G10.2	11:22305275-22401049	NOTEST	0.0419548	0.0297744	-0.494762	0	1	1
ENSG00000254769	ENSG00000254769	OR4A4P	11:51458684-51459614	NOTEST	0	0	0	0	1	1
ENSG00000254770	ENSG00000254770	OR4D7P	11:59299226-59300168	NOTEST	0	0	0	0	1	1
ENSG00000254771	ENSG00000254771	RP11-50B3.1	11:126049391-126049593	NOTEST	0	0	0	0	1	1
ENSG00000254774	ENSG00000254774	RP11-148O21.3	8:11351509-11422113	NOTEST	0.0562302	0.0801412	0.511198	0	1	1
ENSG00000254775	ENSG00000254775	RP11-27P7.1	8:60962145-60987274	NOTEST	0	0	0	0	1	1
ENSG00000254776	ENSG00000254776	AC084121.17	8:7651237-7653392	NOTEST	0	0	0	0	1	1
ENSG00000254777	ENSG00000254777	AC022182.1	8:61822611-61880334	NOTEST	0	0	0	0	1	1
ENSG00000254778	ENSG00000254778	XXbac-BCX105D18.9	HSCHR6_MHC_COX:32064597-32094350	NOTEST	0	0	0	0	1	1
ENSG00000254779	ENSG00000254779	EGLN1P1	15:85174681-85185695	NOTEST	0.104204	0.370372	1.82956	0	1	1
ENSG00000254780	ENSG00000254780	RP11-793I11.1	11:47926874-47927159	NOTEST	0	0	0	0	1	1
ENSG00000254781	ENSG00000254781	GVINP2	11:6769361-6771555	NOTEST	0	0	0	0	1	1
ENSG00000254782	ENSG00000254782	RP11-155D18.12	3:51989329-52023213	NOTEST	0	0	0	0	1	1
ENSG00000254783	ENSG00000254783	RP11-320L11.2	11:85994968-85995710	NOTEST	0.125814	0.154676	0.297961	0	1	1
ENSG00000254784	ENSG00000254784	RP11-436H16.1	11:38232938-38234349	NOTEST	0	0	0	0	1	1
ENSG00000254785	ENSG00000254785	RP11-81M19.1	11:89628966-89633617	NOTEST	0	0	0	0	1	1
ENSG00000254786	ENSG00000254786	RP11-142C4.5	11:58672870-58826132	NOTEST	0	0	0	0	1	1
ENSG00000254787	ENSG00000254787	CTD-2537O9.1	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000254788	ENSG00000254788	CKLF-CMTM1	16:66586465-66613040	NOTEST	0.511486	0.546717	0.0961017	0	1	1
ENSG00000254789	ENSG00000254789	RP11-531H8.2	11:15574400-15643937	NOTEST	0	0	0	0	1	1
ENSG00000254790	ENSG00000254790	RP11-680F20.4	11:125809106-125813597	NOTEST	0	0	0	0	1	1
ENSG00000254791	ENSG00000254791	FAR1-IT1	11:13690216-13753893	NOTEST	0	0.0587283	inf	0	1	1
ENSG00000254792	ENSG00000254792	RP11-119D9.4	11:67608412-67608520	NOTEST	0	0	0	0	1	1
ENSG00000254793	ENSG00000254793	FDPSP4	15:43231507-43232556	NOTEST	0	0.013153	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000254794	ENSG00000254794	RP11-665E10.3	11:87628839-87628891	NOTEST	0	0	0	0	1	1
ENSG00000254795	ENSG00000254795	OR5AP1P	11:56400639-56401579	NOTEST	0	0	0	0	1	1
ENSG00000254796	ENSG00000254796	RP11-1118M6.2	8:7458525-7458789	NOTEST	0	0	0	0	1	1
ENSG00000254798	ENSG00000254798	TFAMP2	11:109777729-109778467	NOTEST	0	0	0	0	1	1
ENSG00000254799	ENSG00000254799	SLC25A47P1	11:59030861-59031275	NOTEST	0	0	0	0	1	1
ENSG00000254800	ENSG00000254800	RP11-163O19.3	11:49904550-49905645	NOTEST	0	0	0	0	1	1
ENSG00000254801	ENSG00000254801	CTD-2132H18.3	11:49092303-49092552	NOTEST	0	0	0	0	1	1
ENSG00000254802	ENSG00000254802	AC022182.3	8:61822611-61880334	NOTEST	0	0	0	0	1	1
ENSG00000254803	ENSG00000254803	RP11-529A4.9	11:89764273-89806558	NOTEST	0	0	0	0	1	1
ENSG00000254804	ENSG00000254804	RP11-674C21.9	11:55450714-55453636	NOTEST	0	0	0	0	1	1
ENSG00000254805	ENSG00000254805	RP11-167J8.4	11:71401498-71401703	NOTEST	0	0	0	0	1	1
ENSG00000254807	ENSG00000254807	OR10AK1P	11:55724691-55725106	NOTEST	0	0	0	0	1	1
ENSG00000254810	ENSG00000254810	RP11-672A2.4	11:76365212-76367756	NOTEST	0	0	0	0	1	1
ENSG00000254811	ENSG00000254811	RP11-680E19.1	11:106120745-106135632	NOTEST	0	0	0	0	1	1
ENSG00000254812	ENSG00000254812	RP11-661A12.12	8:144714240-144715926	NOTEST	0.0280268	0.188524	2.74987	0	1	1
ENSG00000254814	ENSG00000254814	RP11-535A19.1	11:75469499-75514460	NOTEST	0	0	0	0	1	1
ENSG00000254815	ENSG00000254815	RP11-496I9.1	11:537526-564021	NOTEST	0.102801	0.157823	0.618454	0	1	1
ENSG00000254816	ENSG00000254816	RP11-670N15.2	11:20691116-21597227	NOTEST	0	0	0	0	1	1
ENSG00000254817	ENSG00000254817	OR7E160P	8:11891154-11892121	NOTEST	0	0	0	0	1	1
ENSG00000254818	ENSG00000254818	RP11-529A4.4	11:89677202-89682570	NOTEST	0	0	0	0	1	1
ENSG00000254819	ENSG00000254819	RP11-430L3.1	11:26210669-26684835	NOTEST	0	0	0	0	1	1
ENSG00000254820	ENSG00000254820	CTD-2019O4.1	11:22134993-22138547	NOTEST	0	0	0	0	1	1
ENSG00000254821	ENSG00000254821	RP3-400B16.4	6:4021500-4157619	NOTEST	0	0	0	0	1	1
ENSG00000254822	ENSG00000254822	RP11-375D13.3	11:41898183-41898628	NOTEST	0	0	0	0	1	1
ENSG00000254823	ENSG00000254823	RP11-109E10.1	11:123184381-123185478	NOTEST	0	0	0	0	1	1
ENSG00000254824	ENSG00000254824	RP11-37O16.8	11:102980159-103350591	NOTEST	0	0	0	0	1	1
ENSG00000254825	ENSG00000254825	OR9G2P	11:56518498-56519378	NOTEST	0	0	0	0	1	1
ENSG00000254826	ENSG00000254826	CTD-2530H12.2	11:75469499-75514460	NOTEST	0	0	0	0	1	1
ENSG00000254828	ENSG00000254828	RP11-72M10.5	11:55069765-55072536	NOTEST	0	0	0	0	1	1
ENSG00000254829	ENSG00000254829	RP11-7I15.3	11:77726760-77791265	NOTEST	0.0865318	0.0203914	-2.08527	0	1	1
ENSG00000254830	ENSG00000254830	RP11-99C10.1	11:98809641-98815809	NOTEST	0	0	0	0	1	1
ENSG00000254831	ENSG00000254831	KRT18P58	11:6015105-6016225	NOTEST	0	0	0	0	1	1
ENSG00000254832	ENSG00000254832	OR4A40P	11:48533824-48534772	NOTEST	0	0	0	0	1	1
ENSG00000254833	ENSG00000254833	RP11-50B3.2	11:126030608-126045930	NOTEST	0	0	0	0	1	1
ENSG00000254834	ENSG00000254834	OR5M10	11:56344211-56345263	NOTEST	0	0	0	0	1	1
ENSG00000254836	ENSG00000254836	RP1-17K7.3	11:31806339-32127301	NOTEST	0	0	0	0	1	1
ENSG00000254838	ENSG00000254838	GVINP1	11:6734766-6767670	NOTEST	0.0137324	0.00944074	-0.540616	0	1	1
ENSG00000254839	ENSG00000254839	AF131215.6	8:10753554-11058875	NOTEST	0	0	0	0	1	1
ENSG00000254840	ENSG00000254840	RP11-574M7.1	11:50266851-50320877	NOTEST	0	0	0	0	1	1
ENSG00000254841	ENSG00000254841	OR4V1P	11:55441011-55442151	NOTEST	0	0	0	0	1	1

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ENSG00000254843	ENSG00000254843	RP11-648O15.1	11:86748885-87035401	NOTEST	0	0.00686565	inf	0	1	1
ENSG00000254844	ENSG00000254844	RP11-728F11.3	11:117298488-117748201	NOTEST	0	0	0	0	1	1
ENSG00000254845	ENSG00000254845	OR8G7P	11:124109120-124110228	NOTEST	0	0	0	0	1	1
ENSG00000254846	ENSG00000254846	RP11-203M5.2	14:20811206-20826064	NOTEST	0	0	0	0	1	1
ENSG00000254847	ENSG00000254847	RP11-51B23.3	11:12559629-12562514	NOTEST	0	0	0	0	1	1
ENSG00000254848	ENSG00000254848	OR5BN1P	11:55900141-55900970	NOTEST	0	0	0	0	1	1
ENSG00000254849	ENSG00000254849	hsa-mir-939	HG243_PATCH:145428003-145464191	NOTEST	0	0	0	0	1	1
ENSG00000254850	ENSG00000254850	RP5-901A4.4	11:67702033-67707245	NOTEST	0	0	0	0	1	1
ENSG00000254851	ENSG00000254851	RP11-109L13.1	11:117006243-117009298	NOTEST	0	0	0	0	1	1
ENSG00000254853	ENSG00000254853	RP11-659P15.2	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000254854	ENSG00000254854	CTD-2523D13.2	11:119600292-119610333	NOTEST	0.162873	0.189398	0.217669	0	1	1
ENSG00000254855	ENSG00000254855	RP11-867G23.1	11:66024764-66035600	NOTEST	0	0.03759	inf	0	1	1
ENSG00000254856	ENSG00000254856	NDUFA3P2	11:68228185-68384179	NOTEST	0	0	0	0	1	1
ENSG00000254857	ENSG00000254857	RP11-113D6.3	11:18161732-18211168	NOTEST	0	0	0	0	1	1
ENSG00000254859	ENSG00000254859	RP11-661A12.5	8:144624142-144631899	NOTEST	0	0	0	0	1	1
ENSG00000254861	ENSG00000254861	RP11-945A11.2	11:23752133-23826144	NOTEST	0	0	0	0	1	1
ENSG00000254862	ENSG00000254862	RP11-159H22.2	11:27387507-27503980	NOTEST	0.012597	0.00979148	-0.363481	0	1	1
ENSG00000254863	ENSG00000254863	RP11-831A10.2	11:119858662-119865746	NOTEST	0	0	0	0	1	1
ENSG00000254864	ENSG00000254864	CTD-2516F10.4	11:7534528-7678358	NOTEST	0	0	0	0	1	1
ENSG00000254865	ENSG00000254865	RP11-748C4.1	11:9776316-10315754	NOTEST	0	0	0	0	1	1
ENSG00000254866	ENSG00000254866	DEFB109P3	8:11973290-12008698	NOTEST	0	0	0	0	1	1
ENSG00000254867	ENSG00000254867	RP11-1167A19.6	11:65751149-65751802	NOTEST	0	0	0	0	1	1
ENSG00000254869	ENSG00000254869	RP11-91I20.2	8:61565060-61566120	NOTEST	0	0	0	0	1	1
ENSG00000254871	ENSG00000254871	RP11-702F3.2	11:46164266-46165145	NOTEST	0	0	0	0	1	1
ENSG00000254872	ENSG00000254872	RP13-870H17.3	11:1049879-1055284	NOTEST	0	0	0	0	1	1
ENSG00000254873	ENSG00000254873	RP11-770J1.5	11:118230299-118302211	NOTEST	0.386317	0.267418	-0.530691	0	1	1
ENSG00000254874	ENSG00000254874	RP11-676F20.1	11:92698962-92699769	NOTEST	0	0	0	0	1	1
ENSG00000254875	ENSG00000254875	EGFL8	HSCHR6_MHC_QBL:32073754-32103496	NOTEST	0	0	0	0	1	1
ENSG00000254877	ENSG00000254877	RP11-142C4.4	11:58672870-58826132	NOTEST	0	0	0	0	1	1
ENSG00000254878	ENSG00000254878	CTD-3096P4.1	11:15987994-16778428	NOTEST	0	0	0	0	1	1
ENSG00000254879	ENSG00000254879	AC103828.1	11:48002112-48189670	NOTEST	0	0	0	0	1	1
ENSG00000254880	ENSG00000254880	RP11-687M24.5	11:125028356-125034505	NOTEST	0	0	0	0	1	1
ENSG00000254883	ENSG00000254883	RP11-655M14.14	11:67511792-67512116	NOTEST	0	0	0	0	1	1
ENSG00000254884	ENSG00000254884	RP11-682B13.2	11:9302200-9336327	NOTEST	0	0	0	0	1	1
ENSG00000254885	ENSG00000254885	RP11-802F5.1	11:78363875-79151992	NOTEST	0	0	0	0	1	1
ENSG00000254886	ENSG00000254886	OR4A10P	11:55199432-55199843	NOTEST	0	0	0	0	1	1
ENSG00000254887	ENSG00000254887	CTC-378H22.1	19:42590262-42700737	NOTEST	0	0.0927817	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000254888	ENSG00000254888	RP11-716D19.1	11:89808006-89808264	NOTEST	0	0	0	0	1	1
ENSG00000254889	ENSG00000254889	AC084121.14	8:7554351-7554615	NOTEST	0	0	0	0	1	1
ENSG00000254890	ENSG00000254890	RP11-10A7.1	11:109225811-109454633	NOTEST	0	0	0	0	1	1
ENSG00000254891	ENSG00000254891	OR4A9P	11:55156004-55156948	NOTEST	0	0	0	0	1	1
ENSG00000254892	ENSG00000254892	RP11-334E6.4	11:119252487-119397374	NOTEST	0	0	0	0	1	1
ENSG00000254894	ENSG00000254894	NAV2-AS1	11:19372270-20143144	NOTEST	0	0	0	0	1	1
ENSG00000254895	ENSG00000254895	RP11-37O16.7	11:102980159-103350591	NOTEST	0	0	0	0	1	1
ENSG00000254896	ENSG00000254896	OPCML-IT1	11:132284870-133402414	NOTEST	0	0	0	0	1	1
ENSG00000254897	ENSG00000254897	RP11-482L11.1	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000254898	ENSG00000254898	RP11-513D5.2	8:38082735-38239790	NOTEST	0	0	0	0	1	1
ENSG00000254899	ENSG00000254899	DASS-161H22.6	HSCHR6_MHC_SSTO:31486440-31504572	NOTEST	0	0	0	0	1	1
ENSG00000254900	ENSG00000254900	RP11-152H18.4	11:8700635-8702460	NOTEST	0	0.028791	inf	0	1	1
ENSG00000254902	ENSG00000254902	ANO1-AS1	11:69924407-70035634	NOTEST	0.0235702	0	#NAME?	0	1	1
ENSG00000254903	ENSG00000254903	OR8L1P	11:56149110-56150065	NOTEST	0	0	0	0	1	1
ENSG00000254905	ENSG00000254905	RP11-712L6.7	11:126152959-126215644	NOTEST	0.0357617	0.000297093	-6.91136	0	1	1
ENSG00000254906	ENSG00000254906	RP11-701I24.3	11:20691116-21597227	NOTEST	0	0	0	0	1	1
ENSG00000254907	ENSG00000254907	RP11-484D2.2	11:43333512-43516483	NOTEST	0.0690805	0.180771	1.38781	0	1	1
ENSG00000254910	ENSG00000254910	RP11-326C3.7	11:307630-315272	NOTEST	0.39547	0.56044	0.50299	0	1	1
ENSG00000254911	ENSG00000254911	SCARNA9	11:93394804-93547861	NOTEST	0.155433	0.18004	0.21203	0	1	1
ENSG00000254912	ENSG00000254912	RP11-632K20.2	15:32786203-32792547	NOTEST	0	0	0	0	1	1
ENSG00000254913	ENSG00000254913	RP4-791M13.5	1:144836156-145076186	NOTEST	0	0	0	0	1	1
ENSG00000254914	ENSG00000254914	CTD-2537L20.1	11:42961324-42961548	NOTEST	0	0	0	0	1	1
ENSG00000254915	ENSG00000254915	RP11-263C24.3	11:75514475-75854239	NOTEST	0	0	0	0	1	1
ENSG00000254916	ENSG00000254916	RP11-529A4.12	11:89764273-89806558	NOTEST	0	0	0	0	1	1
ENSG00000254917	ENSG00000254917	OR7E15P	8:12553815-12554782	NOTEST	0	0	0	0	1	1
ENSG00000254919	ENSG00000254919	RP11-698N11.2	11:35936600-35940289	NOTEST	0	0	0	0	1	1
ENSG00000254920	ENSG00000254920	RP11-56P9.6	11:48901662-48923733	NOTEST	0	0	0	0	1	1
ENSG00000254921	ENSG00000254921	RP11-236J17.6	11:8040790-8190602	NOTEST	0	0	0	0	1	1
ENSG00000254923	ENSG00000254923	RP11-1236K1.8	8:11973290-12008698	NOTEST	0	0	0	0	1	1
ENSG00000254924	ENSG00000254924	RP11-684B2.3	11:71164154-71235153	NOTEST	0	0	0	0	1	1
ENSG00000254925	ENSG00000254925	OR4C9P	11:48485604-48486529	NOTEST	0	0	0	0	1	1
ENSG00000254926	ENSG00000254926	AP000445.2	11:58516471-58528526	NOTEST	0	0	0	0	1	1
ENSG00000254927	ENSG00000254927	RP11-98J9.2	11:13806936-13901046	NOTEST	0	0	0	0	1	1
ENSG00000254928	ENSG00000254928	RP11-702H23.6	11:74041362-74197096	NOTEST	0	0	0	0	1	1
ENSG00000254929	ENSG00000254929	RP11-144G6.12	10:47186202-47243502	NOTEST	0.407652	0.449477	0.140907	0	1	1
ENSG00000254930	ENSG00000254930	RP11-98J9.3	11:13806936-13901046	NOTEST	0	0	0	0	1	1
ENSG00000254931	ENSG00000254931	RP11-37O16.6	11:102980159-103350591	NOTEST	0	0	0	0	1	1
ENSG00000254932	ENSG00000254932	RP11-687M24.8	11:125034582-125303285	NOTEST	0	0.0221723	inf	0	1	1
ENSG00000254933	ENSG00000254933	RP11-619A14.2	11:75897368-75921780	NOTEST	0	0	0	0	1	1
ENSG00000254934	ENSG00000254934	LINC00678	11:27528384-27899195	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000254935	ENSG00000254935	RP11-266E8.2	11:122489558-122489982	NOTEST	0	0	0	0	1	1
ENSG00000254936	ENSG00000254936	AF131215.3	8:10753554-11058875	NOTEST	0	0	0	0	1	1
ENSG00000254937	ENSG00000254937	RP11-728D14.6	11:124408395-124409230	NOTEST	0	0	0	0	1	1
ENSG00000254938	ENSG00000254938	RP11-688I9.4	11:126225534-126875953	NOTEST	0	0	0	0	1	1
ENSG00000254939	ENSG00000254939	CTD-2342I9.1	11:98435803-98437557	NOTEST	0	0	0	0	1	1
ENSG00000254940	ENSG00000254940	OR4A19P	11:49941863-49942966	NOTEST	0	0	0	0	1	1
ENSG00000254941	ENSG00000254941	RP11-677M14.5	11:124636393-124704383	NOTEST	0.254711	0.129683	-0.973875	0	1	1
ENSG00000254942	ENSG00000254942	RP5-1160K1.8	1:110082493-110091028	NOTEST	0	0.0209818	inf	0	1	1
ENSG00000254943	ENSG00000254943	RP11-664I21.6	11:124753586-124768396	NOTEST	0	0	0	0	1	1
ENSG00000254944	ENSG00000254944	ATP5F1P5	11:122831034-122831794	NOTEST	0	0.055238	inf	0	1	1
ENSG00000254946	ENSG00000254946	RP11-531H8.1	11:15574400-15643937	NOTEST	0	0	0	0	1	1
ENSG00000254947	ENSG00000254947	OR8K4P	11:55909991-55910863	NOTEST	0	0	0	0	1	1
ENSG00000254948	ENSG00000254948	OR7E158P	8:11777408-11778318	NOTEST	0.0200988	0.0468935	1.22228	0	1	1
ENSG00000254949	ENSG00000254949	GNG5P3	11:111652918-111756699	NOTEST	0	0	0	0	1	1
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ENSG00000254952	ENSG00000254952	AP001257.1	11:59927159-59928295	NOTEST	0	0	0	0	1	1
ENSG00000254953	ENSG00000254953	RP11-100N3.2	11:56503791-56503938	NOTEST	0	0	0	0	1	1
ENSG00000254954	ENSG00000254954	SLC2A13P1	8:61054379-61054701	NOTEST	0	0.235874	inf	0	1	1
ENSG00000254957	ENSG00000254957	RP11-179A10.2	11:11139400-11205158	NOTEST	0	0	0	0	1	1
ENSG00000254959	ENSG00000254959	INMT-FAM188B	7:30692199-30965131	NOTEST	3.60E-05	0.000167983	2.22303	0	1	1
ENSG00000254960	ENSG00000254960	KIRREL3-AS2	11:126225534-126875953	NOTEST	0	0	0	0	1	1
ENSG00000254961	ENSG00000254961	TUBB4BP4	11:91682896-91683200	NOTEST	0	0	0	0	1	1
ENSG00000254962	ENSG00000254962	OR4A14P	11:55245026-55245985	NOTEST	0	0	0	0	1	1
ENSG00000254963	ENSG00000254963	CTD-2562J17.9	11:74975225-75062873	NOTEST	0	0	0	0	1	1
ENSG00000254964	ENSG00000254964	RP11-831H9.3	11:62369689-62382592	NOTEST	0	0	0	0	1	1
ENSG00000254965	ENSG00000254965	RP11-113K21.2	11:82822101-82822484	NOTEST	0	0	0	0	1	1
ENSG00000254966	ENSG00000254966	RP11-1081L13.4	11:18714668-18814268	NOTEST	0.0211283	0.194655	3.20368	0	1	1
ENSG00000254967	ENSG00000254967	RP11-680F20.6	11:125820010-125933230	NOTEST	0	0	0	0	1	1
ENSG00000254968	ENSG00000254968	RP11-65M17.3	11:112263840-112492452	NOTEST	0	0	0	0	1	1
ENSG00000254971	ENSG00000254971	RP11-313I2.11	11:89487149-89488121	NOTEST	0	0	0	0	1	1
ENSG00000254972	ENSG00000254972	RP11-167J8.3	11:71412313-71416450	NOTEST	0	0	0	0	1	1
ENSG00000254973	ENSG00000254973	RP11-429J17.7	8:144840322-144853992	NOTEST	0.00906674	0	#NAME?	0	1	1
ENSG00000254974	ENSG00000254974	RP11-702H23.2	11:74041362-74197096	NOTEST	0.0922557	0	#NAME?	0	1	1
ENSG00000254975	ENSG00000254975	RP11-672A2.3	11:76386122-76418685	NOTEST	0	0	0	0	1	1
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ENSG00000254977	ENSG00000254977	AC004878.8	7:74807498-74867509	NOTEST	0	0	0	0	1	1
ENSG00000254978	ENSG00000254978	ALG1L9P	11:71498555-71532594	NOTEST	0	0.0334136	inf	0	1	1
ENSG00000254979	ENSG00000254979	RP11-872D17.8	11:57154266-57195053	NOTEST	0	0.0626884	inf	0	1	1
ENSG00000254980	ENSG00000254980	RP11-794P6.6	11:111384767-111407756	NOTEST	0	0	0	0	1	1
ENSG00000254981	ENSG00000254981	RP11-350N15.3	8:38243724-38267045	NOTEST	0	0	0	0	1	1

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ENSG00000254983	ENSG00000254983	RP11-573E11.2	11:12297626-12380691	NOTEST	0	0	0	0	1	1
ENSG00000254984	ENSG00000254984	FTLP6	11:66511921-66614017	NOTEST	0	0	0	0	1	1
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ENSG00000254987	ENSG00000254987	RP11-563P16.1	11:103546721-103765999	NOTEST	0	0.0918109	inf	0	1	1
ENSG00000254988	ENSG00000254988	CTD-2547H18.1	11:76571910-76737841	NOTEST	0	0	0	0	1	1
ENSG00000254989	ENSG00000254989	RP11-469N6.3	11:134541319-134541918	NOTEST	0	0	0	0	1	1
ENSG00000254990	ENSG00000254990	RP11-108O10.2	11:111639391-111649074	NOTEST	0	0.026833	inf	0	1	1
ENSG00000254991	ENSG00000254991	RP13-631K18.3	11:12088475-12094561	NOTEST	0	0.0143875	inf	0	1	1
ENSG00000254992	ENSG00000254992	RP11-215H18.5	11:118193503-118193798	NOTEST	0	0	0	0	1	1
ENSG00000254993	ENSG00000254993	RP11-107P7.5	11:49138570-49146122	NOTEST	0	0	0	0	1	1
ENSG00000254995	ENSG00000254995	STX16-NPEPL1	20:57226327-57294294	NOTEST	0.227445	0.219006	-0.0545435	0	1	1
ENSG00000254997	ENSG00000254997	KRTAP5-9	11:71259465-71260653	NOTEST	0	0	0	0	1	1
ENSG00000254998	ENSG00000254998	RP11-94P11.4	11:105028653-105402424	NOTEST	0	0	0	0	1	1
ENSG00000255000	ENSG00000255000	AC139103.1	8:146273245-146274275	NOTEST	0.0172905	0.0134444	-0.362982	0	1	1
ENSG00000255001	ENSG00000255001	RP11-347H15.3	11:50246831-50254505	NOTEST	0	0	0	0	1	1
ENSG00000255002	ENSG00000255002	CTD-2509G16.2	14:65679610-65689065	NOTEST	0	0	0	0	1	1
ENSG00000255003	ENSG00000255003	CYCSP28	11:82868029-83134559	NOTEST	0	0	0	0	1	1
ENSG00000255004	ENSG00000255004	RP1-68D18.3	11:35272752-35442549	NOTEST	0	0	0	0	1	1
ENSG00000255005	ENSG00000255005	RP11-90K17.2	11:85566143-85634725	NOTEST	0	0	0	0	1	1
ENSG00000255006	ENSG00000255006	TCEB1P22	11:120382467-120859613	NOTEST	0	0	0	0	1	1
ENSG00000255007	ENSG00000255007	CTD-2589M5.4	11:46277905-46296098	NOTEST	0	0	0	0	1	1
ENSG00000255008	ENSG00000255008	AP000442.4	11:59328618-59333547	NOTEST	0.024839	0	#NAME?	0	1	1
ENSG00000255009	ENSG00000255009	UBTFL1	11:89819080-89820299	NOTEST	0	0	0	0	1	1
ENSG00000255010	ENSG00000255010	RP11-113K21.3	11:82783107-82818003	NOTEST	0.140471	0.170052	0.275703	0	1	1
ENSG00000255011	ENSG00000255011	RP11-529A4.10	11:89764273-89806558	NOTEST	0	0	0	0	1	1
ENSG00000255012	ENSG00000255012	OR5M1	11:56380030-56380978	NOTEST	0	0	0	0	1	1
ENSG00000255014	ENSG00000255014	ARL6IP1P3	11:80364472-80365032	NOTEST	0	0	0	0	1	1
ENSG00000255015	ENSG00000255015	RP11-716H6.1	11:122026129-122293579	NOTEST	0	0	0	0	1	1
ENSG00000255016	ENSG00000255016	RP11-481A20.8	8:11882752-11883107	NOTEST	0	0	0	0	1	1
ENSG00000255018	ENSG00000255018	RP11-413N13.1	11:13173746-13173895	NOTEST	0	0	0	0	1	1
ENSG00000255019	ENSG00000255019	OR5D15P	11:55554439-55555381	NOTEST	0	0	0	0	1	1
ENSG00000255020	ENSG00000255020	AF131216.5	8:11197145-11332224	NOTEST	0	0.0352358	inf	0	1	1
ENSG00000255021	ENSG00000255021	RP11-536I6.2	3:14313872-14345345	NOTEST	0	0	0	0	1	1
ENSG00000255022	ENSG00000255022	RP11-665E10.1	11:87527115-87527416	NOTEST	0	0	0	0	1	1
ENSG00000255025	ENSG00000255025	AF228730.13	8:7095807-7096153	NOTEST	0	0	0	0	1	1
ENSG00000255026	ENSG00000255026	RP11-326C3.2	11:287304-288987	NOTEST	0.0333055	0.016354	-1.02612	0	1	1
ENSG00000255027	ENSG00000255027	RP11-680F20.9	11:125773141-125808811	NOTEST	0	0	0	0	1	1
ENSG00000255028	ENSG00000255028	RP11-708B6.2	11:109225811-109454633	NOTEST	0.12077	0.313875	1.37793	0	1	1
ENSG00000255029	ENSG00000255029	CTD-3012A18.1	11:29357424-29615842	NOTEST	0	0.0295115	inf	0	1	1
ENSG00000255030	ENSG00000255030	OR8B5P	11:124227455-124228365	NOTEST	0	0	0	0	1	1

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ENSG00000255032	ENSG00000255032	RP11-45A12.2	11:44740941-44972840	NOTEST	0	0	0	0	1	1
ENSG00000255033	ENSG00000255033	RP11-1101K5.2	8:112388867-112555202	NOTEST	0	0	0	0	1	1
ENSG00000255035	ENSG00000255035	SDHCP4	11:17414431-17498449	NOTEST	0	0	0	0	1	1
ENSG00000255036	ENSG00000255036	RP11-23J9.4	9:99918851-100140806	NOTEST	0.291713	0.137404	-1.08613	0	1	1
ENSG00000255037	ENSG00000255037	RP11-680G24.1	16:14860258-14863932	NOTEST	0	0	0	0	1	1
ENSG00000255038	ENSG00000255038	RP11-1167A19.2	11:65818199-65837090	NOTEST	0	0.00930707	inf	0	1	1
ENSG00000255039	ENSG00000255039	RP11-882G5.1	11:97093643-97130987	NOTEST	0	0	0	0	1	1
ENSG00000255040	ENSG00000255040	RP11-677N16.1	11:14665268-14892350	NOTEST	0	0	0	0	1	1
ENSG00000255041	ENSG00000255041	RP11-430H10.4	11:45392947-45564024	NOTEST	0	0	0	0	1	1
ENSG00000255042	ENSG00000255042	RP11-347H15.5	11:50246831-50254505	NOTEST	0	0	0	0	1	1
ENSG00000255043	ENSG00000255043	NAV2-AS5	11:19372270-20143144	NOTEST	0	0	0	0	1	1
ENSG00000255045	ENSG00000255045	RP11-677M14.2	11:124609741-124617106	NOTEST	0	0	0	0	1	1
ENSG00000255046	ENSG00000255046	RP11-297N6.4	8:11653081-11696818	NOTEST	0.502257	0.142998	-1.81243	0	1	1
ENSG00000255047	ENSG00000255047	HNRNPRP2	11:29690432-29691175	NOTEST	0	0	0	0	1	1
ENSG00000255048	ENSG00000255048	OR8X1P	11:124274129-124274998	NOTEST	0	0	0	0	1	1
ENSG00000255050	ENSG00000255050	RP11-661A12.9	8:144655659-144660819	NOTEST	0	0.0350246	inf	0	1	1
ENSG00000255051	ENSG00000255051	BCAS2P1	11:82843097-82845779	NOTEST	0	0	0	0	1	1
ENSG00000255052	ENSG00000255052	FAM66D	8:11973290-12008698	NOTEST	0.0165027	0.0594737	1.84955	0	1	1
ENSG00000255053	ENSG00000255053	OR4A44P	11:48649097-48650045	NOTEST	0	0	0	0	1	1
ENSG00000255054	ENSG00000255054	RP1-317E23.6	1:26126666-26185903	NOTEST	0	0	0	0	1	1
ENSG00000255055	ENSG00000255055	MTND1P35	11:89641707-89642215	NOTEST	0	0	0	0	1	1
ENSG00000255057	ENSG00000255057	RP11-567M21.3	11:129878480-129879660	NOTEST	0	0	0	0	1	1
ENSG00000255058	ENSG00000255058	AP003068.17	11:64927664-64927853	NOTEST	0	0	0	0	1	1
ENSG00000255059	ENSG00000255059	AP000620.1	11:100537189-100537693	NOTEST	0	0	0	0	1	1
ENSG00000255060	ENSG00000255060	RP11-219O3.2	11:36317837-36486754	NOTEST	0	0	0	0	1	1
ENSG00000255062	ENSG00000255062	RP11-712L6.5	11:126152959-126215644	NOTEST	0.283491	0.0902674	-1.65102	0	1	1
ENSG00000255063	ENSG00000255063	RP11-718B12.1	11:82502703-82528188	NOTEST	0	0	0	0	1	1
ENSG00000255065	ENSG00000255065	RP11-680E19.2	11:106180771-106182518	NOTEST	0	0	0	0	1	1
ENSG00000255067	ENSG00000255067	RP11-47J17.1	11:12695968-12966298	NOTEST	0	0	0	0	1	1
ENSG00000255069	ENSG00000255069	RP11-145O15.3	8:13415165-13462119	NOTEST	0.00908338	0.00638437	-0.508685	0	1	1
ENSG00000255070	ENSG00000255070	OSBPL9P3	11:90849128-90849723	NOTEST	0	0	0	0	1	1
ENSG00000255071	ENSG00000255071	SAA2-SAA4	11:18252895-18270190	NOTEST	0.13091	1.56E-06	-16.3561	0	1	1
ENSG00000255073	ENSG00000255073	ZFP91-CNTF	11:58346583-58393198	NOTEST	0.0987118	0.315156	1.67477	0	1	1
ENSG00000255074	ENSG00000255074	RP11-140L24.3	11:14462332-14463223	NOTEST	0.0435598	0	#NAME?	0	1	1
ENSG00000255075	ENSG00000255075	RP11-23B7.3	11:13777573-13779107	NOTEST	0	0	0	0	1	1
ENSG00000255076	ENSG00000255076	CTD-2023J5.1	8:13947372-15095848	NOTEST	0	0	0	0	1	1
ENSG00000255077	ENSG00000255077	OR4X7P	11:55179001-55179193	NOTEST	0	0	0	0	1	1
ENSG00000255078	ENSG00000255078	OR4A6P	11:51393463-51394433	NOTEST	0	0	0	0	1	1
ENSG00000255079	ENSG00000255079	RP11-45A12.1	11:44716412-44717851	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000255081	ENSG00000255081	RP11-263C24.1	11:75514475-75854239	NOTEST	0	0	0	0	1	1
ENSG00000255082	ENSG00000255082	GRM5-AS1	11:88237743-88799113	NOTEST	0.00319345	0.0114383	1.84068	0	1	1
ENSG00000255083	ENSG00000255083	OR5AK1P	11:56785574-56786361	NOTEST	0	0	0	0	1	1
ENSG00000255084	ENSG00000255084	RP11-843A23.1	11:77926342-78285919	NOTEST	0	0	0	0	1	1
ENSG00000255085	ENSG00000255085	AF186192.5	8:145925737-145933902	NOTEST	0.0705349	0	#NAME?	0	1	1
ENSG00000255086	ENSG00000255086	RP11-336F14.1	11:26067533-26069145	NOTEST	0	0	0	0	1	1
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ENSG00000255088	ENSG00000255088	RP11-23B7.4	11:13779657-13779892	NOTEST	0	0	0	0	1	1
ENSG00000255089	ENSG00000255089	RP11-326C3.10	11:318639-330122	NOTEST	0	0	0	0	1	1
ENSG00000255090	ENSG00000255090	RP11-820L6.1	11:122026129-122293579	NOTEST	0.246266	0	#NAME?	0	1	1
ENSG00000255091	ENSG00000255091	RP11-495O11.1	11:45670426-45687172	NOTEST	0	0	0	0	1	1
ENSG00000255092	ENSG00000255092	RP11-58K22.4	11:44585976-44641913	NOTEST	0	0.0265863	inf	0	1	1
ENSG00000255093	ENSG00000255093	RP11-794P6.2	11:111222976-111328876	NOTEST	0	0	0	0	1	1
ENSG00000255094	ENSG00000255094	RP11-406D1.2	11:28000215-28041122	NOTEST	0	0	0	0	1	1
ENSG00000255095	ENSG00000255095	OR1D4	17:3143969-3144908	NOTEST	0	0	0	0	1	1
ENSG00000255096	ENSG00000255096	OR5B10P	11:58116461-58117103	NOTEST	0	0	0	0	1	1
ENSG00000255097	ENSG00000255097	RP11-5L12.1	11:9160371-9286937	NOTEST	0	0	0	0	1	1
ENSG00000255099	ENSG00000255099	RP11-25D10.2	8:110790140-110794517	NOTEST	0	0	0	0	1	1
ENSG00000255100	ENSG00000255100	RP11-21L23.3	11:76493294-76509198	NOTEST	0.522755	0.586607	0.166259	0	1	1
ENSG00000255101	ENSG00000255101	RP11-412B14.1	8:42552518-42592550	NOTEST	0	0	0	0	1	1
ENSG00000255102	ENSG00000255102	RP11-164N3.2	11:87783273-87831315	NOTEST	0	0	0	0	1	1
ENSG00000255104	ENSG00000255104	ZNF286A	17:15602890-15652629	NOTEST	0.0244944	0.118734	2.2772	0	1	1
ENSG00000255105	ENSG00000255105	RP11-5A11.1	8:104495625-105268322	NOTEST	0	0	0	0	1	1
ENSG00000255106	ENSG00000255106	RP11-58K22.2	11:44561327-44562243	NOTEST	0	0	0	0	1	1
ENSG00000255107	ENSG00000255107	RP11-159H10.1	8:70771498-70772775	NOTEST	0	0	0	0	1	1
ENSG00000255108	ENSG00000255108	AP006621.8	11:818901-842545	NOTEST	0.0551618	0.0740024	0.423902	0	1	1
ENSG00000255109	ENSG00000255109	CTD-2572N17.1	11:42204841-42275262	NOTEST	0	0	0	0	1	1
ENSG00000255110	ENSG00000255110	RP11-72M10.8	11:55046922-55052999	NOTEST	0	0	0	0	1	1
ENSG00000255111	ENSG00000255111	RP11-163O19.8	11:49913813-49915329	NOTEST	0	0	0	0	1	1
ENSG00000255113	ENSG00000255113	OR4A48P	11:48513577-48513968	NOTEST	0	0	0	0	1	1
ENSG00000255114	ENSG00000255114	RP11-110I1.6	11:118914898-118927913	NOTEST	0	0	0	0	1	1
ENSG00000255115	ENSG00000255115	RP11-91P24.3	11:77532154-77705724	NOTEST	0	0	0	0	1	1
ENSG00000255116	ENSG00000255116	SLC5A4P1	11:124143865-124144477	NOTEST	0	0	0	0	1	1
ENSG00000255117	ENSG00000255117	RP5-1027O15.1	11:29616464-29652211	NOTEST	0	0	0	0	1	1
ENSG00000255118	ENSG00000255118	RP11-703H8.7	11:62104382-62160882	NOTEST	0	0	0	0	1	1
ENSG00000255119	ENSG00000255119	RP11-655M14.12	11:67370350-67374177	NOTEST	0.220853	0.140646	-0.651022	0	1	1
ENSG00000255120	ENSG00000255120	OVOL1-AS1	11:65554492-65564690	NOTEST	0	0	0	0	1	1
ENSG00000255121	ENSG00000255121	RP11-110I1.12	11:118865533-118868714	NOTEST	0.161633	0.137574	-0.232515	0	1	1
ENSG00000255122	ENSG00000255122	RP11-303G3.6	8:12437795-12438572	NOTEST	0	0	0	0	1	1
ENSG00000255123	ENSG00000255123	MTND5P21	11:11261305-11261827	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000255124	ENSG00000255124	RP11-680F20.5	11:125809106-125813597	NOTEST	0	0	0	0	1	1
ENSG00000255125	ENSG00000255125	RP11-685M7.5	11:10804859-10830657	NOTEST	0	0	0	0	1	1
ENSG00000255126	ENSG00000255126	CTD-2531D15.5	11:62104382-62160882	NOTEST	0	0.000942558	inf	0	1	1
ENSG00000255127	ENSG00000255127	RP11-676F20.2	11:92647767-92649757	NOTEST	0	0	0	0	1	1
ENSG00000255128	ENSG00000255128	HSPD1P3	8:7276512-7278068	NOTEST	0	0	0	0	1	1
ENSG00000255129	ENSG00000255129	RP11-839D17.3	11:113149158-113185159	NOTEST	0.265361	0.578364	1.12402	0	1	1
ENSG00000255130	ENSG00000255130	RP11-396J6.1	8:68334359-68658620	NOTEST	0	0	0	0	1	1
ENSG00000255131	ENSG00000255131	OR9L1P	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000255132	ENSG00000255132	RP11-63C8.1	11:40135752-41481323	NOTEST	0	0	0	0	1	1
ENSG00000255133	ENSG00000255133	RP11-646J21.2	11:33836422-33843641	NOTEST	0.106973	0.342656	1.67952	0	1	1
ENSG00000255134	ENSG00000255134	OR8K2P	11:56102617-56103544	NOTEST	0.0196467	0.0571559	1.54061	0	1	1
ENSG00000255136	ENSG00000255136	CTD-2562J17.4	11:74919098-74954742	NOTEST	0	0	0	0	1	1
ENSG00000255138	ENSG00000255138	GLTPP1	11:18161732-18211168	NOTEST	0.000793317	0	#NAME?	0	1	1
ENSG00000255140	ENSG00000255140	OR5BN2P	11:55884114-55884732	NOTEST	0	0	0	0	1	1
ENSG00000255141	ENSG00000255141	HNRNPA1P76	11:3875547-4114439	NOTEST	0	0	0	0	1	1
ENSG00000255142	ENSG00000255142	AP006621.6	11:777577-784297	NOTEST	0	0.293401	inf	0	1	1
ENSG00000255143	ENSG00000255143	RP11-805J14.3	11:69924407-70035634	NOTEST	0	0	0	0	1	1
ENSG00000255144	ENSG00000255144	RP11-589N15.1	8:11753358-11754379	NOTEST	0	0	0	0	1	1
ENSG00000255146	ENSG00000255146	RP11-659P15.1	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000255147	ENSG00000255147	RP11-655M14.4	11:67516513-67524439	NOTEST	0	0	0	0	1	1
ENSG00000255148	ENSG00000255148	RP4-791M13.4	1:144836156-145076186	NOTEST	0.116357	0.0550068	-1.08087	0	1	1
ENSG00000255149	ENSG00000255149	RP11-97I14.1	11:110747717-110747901	NOTEST	0	0	0	0	1	1
ENSG00000255150	ENSG00000255150	EID3	12:104609556-104744061	NOTEST	0.158863	0.256881	0.693312	0	1	1
ENSG00000255151	ENSG00000255151	GLYATL1P3	11:58853779-58862259	NOTEST	0	0	0	0	1	1
ENSG00000255153	ENSG00000255153	TOLLIP-AS1	11:1330998-1331937	NOTEST	0.588754	0.250332	-1.23382	0	1	1
ENSG00000255155	ENSG00000255155	RP11-535N6.2	11:130414537-130414751	NOTEST	0	0	0	0	1	1
ENSG00000255156	ENSG00000255156	KLHL22-IT1	22:20778873-20850170	NOTEST	0	0	0	0	1	1
ENSG00000255157	ENSG00000255157	CTD-2313N18.8	11:71567322-71574704	NOTEST	0	0	0	0	1	1
ENSG00000255158	ENSG00000255158	RP11-754B17.1	11:644232-727727	NOTEST	0.0566873	0.0753652	0.410872	0	1	1
ENSG00000255159	ENSG00000255159	RP11-318C2.1	11:8703957-8932498	NOTEST	0	0	0	0	1	1
ENSG00000255160	ENSG00000255160	RP11-428C19.5	11:19321429-19329905	NOTEST	0	0.156287	inf	0	1	1
ENSG00000255161	ENSG00000255161	RP11-646J21.7	11:33808599-33809341	NOTEST	0	0	0	0	1	1
ENSG00000255162	ENSG00000255162	RP11-358N4.3	11:89519112-89521006	NOTEST	0	0	0	0	1	1
ENSG00000255163	ENSG00000255163	HSPE1P18	11:118064454-118095809	NOTEST	0	0	0	0	1	1
ENSG00000255164	ENSG00000255164	RP5-1047A19.4	8:146198974-146231432	NOTEST	0.193771	0.109143	-0.828125	0	1	1
ENSG00000255165	ENSG00000255165	CTD-2609K8.3	11:44087474-44105772	NOTEST	0.0948656	0.111633	0.234813	0	1	1
ENSG00000255166	ENSG00000255166	RP11-726G23.11	8:43102333-43102553	NOTEST	0	0	0	0	1	1
ENSG00000255167	ENSG00000255167	RP11-670N15.1	11:20691116-21597227	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000255169	ENSG00000255169	RP11-646J21.3	11:33826313-33827187	NOTEST	0	0	0	0	1	1
ENSG00000255170	ENSG00000255170	RP11-313I2.6	11:89498051-89498306	NOTEST	0	0	0	0	1	1
ENSG00000255171	ENSG00000255171	RP11-375D13.2	11:41736117-41857992	NOTEST	0	0	0	0	1	1
ENSG00000255172	ENSG00000255172	OR5AM1P	11:56387254-56388286	NOTEST	0	0	0	0	1	1
ENSG00000255173	ENSG00000255173	AP003068.12	11:64883874-64885170	NOTEST	0	0	0	0	1	1
ENSG00000255174	ENSG00000255174	RP11-481A20.4	8:11856595-11856977	NOTEST	0	0.100479	inf	0	1	1
ENSG00000255175	ENSG00000255175	RP11-277K23.1	11:38639813-38667906	NOTEST	0	0	0	0	1	1
ENSG00000255176	ENSG00000255176	AP002954.3	11:118477154-118550399	NOTEST	0.083204	0.178368	1.10013	0	1	1
ENSG00000255177	ENSG00000255177	RP11-532E4.2	11:1244295-1283406	NOTEST	0	0	0	0	1	1
ENSG00000255178	ENSG00000255178	RP11-686G23.2	11:80462242-80473869	NOTEST	0	0	0	0	1	1
ENSG00000255179	ENSG00000255179	RP11-324J3.1	11:7244163-7252094	NOTEST	0	0	0	0	1	1
ENSG00000255181	ENSG00000255181	CCDC166	8:144766621-144796068	NOTEST	0	0.0265252	inf	0	1	1
ENSG00000255182	ENSG00000255182	CTD-2517M22.14	8:145703351-145732557	NOTEST	0.256066	0.306331	0.258575	0	1	1
ENSG00000255183	ENSG00000255183	RP11-720D4.3	11:87429245-87430303	NOTEST	0	0	0	0	1	1
ENSG00000255184	ENSG00000255184	RP11-313I2.7	11:89750778-89757679	NOTEST	0	0	0	0	1	1
ENSG00000255186	ENSG00000255186	RP11-514F3.5	11:36317837-36486754	NOTEST	0	0	0	0	1	1
ENSG00000255187	ENSG00000255187	RP11-699F16.2	11:90891250-90900462	NOTEST	0	0	0	0	1	1
ENSG00000255188	ENSG00000255188	RP11-507F16.1	11:129657958-129658085	NOTEST	0	0	0	0	1	1
ENSG00000255189	ENSG00000255189	GLYATL1P1	11:58672870-58826132	NOTEST	0	0	0	0	1	1
ENSG00000255190	ENSG00000255190	TRIM51DP	11:49896496-49898190	NOTEST	0	0	0	0	1	1
ENSG00000255191	ENSG00000255191	RP11-626H12.1	11:69831981-69867165	NOTEST	0	0	0	0	1	1
ENSG00000255192	ENSG00000255192	NANOGP8	15:35376393-35377311	NOTEST	0	0	0	0	1	1
ENSG00000255193	ENSG00000255193	RP11-945A11.1	11:23752133-23826144	NOTEST	0	0	0	0	1	1
ENSG00000255194	ENSG00000255194	SSU72P2	11:4263285-4263871	NOTEST	0	0	0	0	1	1
ENSG00000255196	ENSG00000255196	OR4A17P	11:55211910-55212814	NOTEST	0	0	0	0	1	1
ENSG00000255197	ENSG00000255197	RP11-750H9.5	11:47404698-47438047	NOTEST	0.0785088	0.0759284	-0.0482162	0	1	1
ENSG00000255199	ENSG00000255199	RP11-227P3.1	11:50060062-50062069	NOTEST	0	0	0	0	1	1
ENSG00000255200	ENSG00000255200	AP003068.18	11:64941587-64943941	NOTEST	0.0943343	0.142964	0.599801	0	1	1
ENSG00000255201	ENSG00000255201	RP11-350N15.4	8:38268655-38326352	NOTEST	0	0	0	0	1	1
ENSG00000255202	ENSG00000255202	RP4-541C22.5	11:33563617-33718247	NOTEST	0.0885588	0.066704	-0.408864	0	1	1
ENSG00000255203	ENSG00000255203	OR7E2P	11:86502100-86666433	NOTEST	0	0	0	0	1	1
ENSG00000255204	ENSG00000255204	RP11-738O11.9	11:55631407-55648719	NOTEST	0	0	0	0	1	1
ENSG00000255205	ENSG00000255205	MED28P5	11:96871273-96871711	NOTEST	0	0	0	0	1	1
ENSG00000255206	ENSG00000255206	RP11-403D15.2	8:68864352-69149265	NOTEST	0	0	0	0	1	1
ENSG00000255207	ENSG00000255207	RP1-305G21.1	11:33472191-33472489	NOTEST	0	0	0	0	1	1
ENSG00000255208	ENSG00000255208	RP11-794P6.3	11:111222976-111328876	NOTEST	0	0	0	0	1	1
ENSG00000255209	ENSG00000255209	RP11-258O13.1	11:79316010-79323344	NOTEST	0	0	0	0	1	1
ENSG00000255210	ENSG00000255210	RP11-344L21.1	11:109920252-109920885	NOTEST	0	0	0	0	1	1
ENSG00000255211	ENSG00000255211	RP11-1195F20.7	8:7812535-7866277	NOTEST	0	0	0	0	1	1
ENSG00000255213	ENSG00000255213	NPM1P35	11:62098417-62099285	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000255214	ENSG00000255214	RP11-163O19.10	11:49893377-49895619	NOTEST	0	0	0	0	1	1
ENSG00000255215	ENSG00000255215	OR4R1P	11:48507914-48508377	NOTEST	0	0	0	0	1	1
ENSG00000255216	ENSG00000255216	RP11-831A10.1	11:119879312-119882867	NOTEST	0	0	0	0	1	1
ENSG00000255217	ENSG00000255217	OR5J7P	11:55932975-55933397	NOTEST	0	0	0	0	1	1
ENSG00000255218	ENSG00000255218	OR5BC1P	11:58085108-58085847	NOTEST	0	0	0	0	1	1
ENSG00000255219	ENSG00000255219	RP11-716H6.2	11:122026129-122293579	NOTEST	0	0	0	0	1	1
ENSG00000255220	ENSG00000255220	DDX18P5	11:130096571-130184581	NOTEST	0	0	0	0	1	1
ENSG00000255221	ENSG00000255221	CARD17	11:104896169-104972158	NOTEST	0	0	0	0	1	1
ENSG00000255222	ENSG00000255222	SETP17	11:86005801-86006618	NOTEST	0	0	0	0	1	1
ENSG00000255223	ENSG00000255223	OR5M11	11:56309745-56310757	NOTEST	0	0	0	0	1	1
ENSG00000255225	ENSG00000255225	OR8B6P	11:124208678-124209558	NOTEST	0	0	0	0	1	1
ENSG00000255226	ENSG00000255226	CTD-2210P24.3	11:45772373-45773422	NOTEST	0	0	0	0	1	1
ENSG00000255227	ENSG00000255227	RP11-460B17.2	11:29357424-29615842	NOTEST	0	0	0	0	1	1
ENSG00000255229	ENSG00000255229	RP11-304M2.3	11:127114-207428	NOTEST	0	0	0	0	1	1
ENSG00000255230	ENSG00000255230	RP5-901A4.5	11:67733343-67733698	NOTEST	0	0	0	0	1	1
ENSG00000255231	ENSG00000255231	MRPS36P4	11:111895537-112095422	NOTEST	0	0	0	0	1	1
ENSG00000255232	ENSG00000255232	RP11-438N5.4	11:3875547-4114439	NOTEST	0	0	0	0	1	1
ENSG00000255233	ENSG00000255233	RP11-755E23.3	11:92973298-92974334	NOTEST	0	0	0	0	1	1
ENSG00000255234	ENSG00000255234	RP11-727A23.10	11:82868029-83134559	NOTEST	0	0	0	0	1	1
ENSG00000255235	ENSG00000255235	RP11-313I2.8	11:89617094-89619381	NOTEST	0	0	0	0	1	1
ENSG00000255236	ENSG00000255236	CTD-2655K5.1	11:67889519-67897985	NOTEST	0.267978	0.268971	0.0053381	0	1	1
ENSG00000255237	ENSG00000255237	RP13-317D12.3	11:448267-491393	NOTEST	0.0903927	0.17961	0.99059	0	1	1
ENSG00000255238	ENSG00000255238	RFPL4AP1	19:56288918-56290266	NOTEST	0	0	0	0	1	1
ENSG00000255239	ENSG00000255239	AP002954.6	11:118558747-118561309	NOTEST	0	0	0	0	1	1
ENSG00000255240	ENSG00000255240	RP11-142C4.6	11:58672870-58826132	NOTEST	0	0	0	0	1	1
ENSG00000255241	ENSG00000255241	RP11-164N3.3	11:87831758-87908635	NOTEST	0	0	0	0	1	1
ENSG00000255243	ENSG00000255243	CTD-2507G9.1	11:26210669-26684835	NOTEST	0	0	0	0	1	1
ENSG00000255244	ENSG00000255244	RP11-583F24.8	11:18955359-18961268	NOTEST	0	0	0	0	1	1
ENSG00000255245	ENSG00000255245	FXYD6-FXYD2	11:117298488-117748201	NOTEST	0	0	0	0	1	1
ENSG00000255246	ENSG00000255246	RP11-179A16.2	11:81590892-82429124	NOTEST	0	0	0	0	1	1
ENSG00000255247	ENSG00000255247	CTD-2523D13.1	11:119479134-119599794	NOTEST	0	0	0	0	1	1
ENSG00000255248	ENSG00000255248	RP11-166D19.1	11:121899062-121987031	NOTEST	0.533266	0.273059	-0.965642	0	1	1
ENSG00000255250	ENSG00000255250	CTD-2005H7.2	11:86438396-86476307	NOTEST	0	0	0	0	1	1
ENSG00000255251	ENSG00000255251	PRR23D1	8:7397149-7399972	NOTEST	0	0	0	0	1	1
ENSG00000255252	ENSG00000255252	RP1-65P5.3	11:31806339-32127301	NOTEST	0	0	0	0	1	1
ENSG00000255253	ENSG00000255253	RP11-303G3.9	8:12495936-12496111	NOTEST	0	0	0	0	1	1
ENSG00000255254	ENSG00000255254	HIGD1AP5	11:18128129-18128388	NOTEST	0	0	0	0	1	1
ENSG00000255255	ENSG00000255255	PPP1R1AP1	11:75514475-75854239	NOTEST	0	0	0	0	1	1
ENSG00000255256	ENSG00000255256	RP5-916O11.2	11:35965530-36253686	NOTEST	0	0	0	0	1	1
ENSG00000255257	ENSG00000255257	AC025016.1	11:5959980-5966214	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000255258	ENSG00000255258	RP11-448P19.1	11:133653565-133680271	NOTEST	0	0	0	0	1	1
ENSG00000255259	ENSG00000255259	ZNF123P	11:129165180-129166376	NOTEST	0	0	0	0	1	1
ENSG00000255260	ENSG00000255260	CTD-3224I3.3	11:11264734-11265262	NOTEST	0	0	0	0	1	1
ENSG00000255261	ENSG00000255261	OR7E4P	11:71331065-71332078	NOTEST	0	0	0	0	1	1
ENSG00000255262	ENSG00000255262	TCEB2P2	11:129902758-129903115	NOTEST	0	0	0	0	1	1
ENSG00000255265	ENSG00000255265	TMA16P1	11:58563709-58564327	NOTEST	0	0	0	0	1	1
ENSG00000255266	ENSG00000255266	RP11-734C14.2	11:57637793-57638043	NOTEST	0.355043	0	#NAME?	0	1	1
ENSG00000255267	ENSG00000255267	RP11-430H10.2	11:45392947-45564024	NOTEST	0	0	0	0	1	1
ENSG00000255268	ENSG00000255268	RP11-707M1.9	11:49839329-49848276	NOTEST	0	0	0	0	1	1
ENSG00000255269	ENSG00000255269	RP11-702F3.4	11:46235371-46237409	NOTEST	0	0	0	0	1	1
ENSG00000255270	ENSG00000255270	NAV2-IT1	11:19372270-20143144	NOTEST	0	0	0	0	1	1
ENSG00000255271	ENSG00000255271	RP4-594L9.2	11:34554560-34579471	NOTEST	0	0	0	0	1	1
ENSG00000255272	ENSG00000255272	RP11-646J21.6	11:33797733-33801041	NOTEST	0	0	0	0	1	1
ENSG00000255273	ENSG00000255273	AF238378.7	8:6940492-6940850	NOTEST	0	0	0	0	1	1
ENSG00000255274	ENSG00000255274	TMPRSS4-AS1	11:117886486-117992605	NOTEST	0	0	0	0	1	1
ENSG00000255275	ENSG00000255275	RP13-279N23.2	1:19166092-19283180	NOTEST	0.00693415	0	#NAME?	0	1	1
ENSG00000255276	ENSG00000255276	RRM1-AS1	11:4115936-4160106	NOTEST	0	0	0	0	1	1
ENSG00000255277	ENSG00000255277	ABCC6P2	16:14914648-14918563	NOTEST	0.0354514	0.106078	1.58121	0	1	1
ENSG00000255279	ENSG00000255279	RP11-375D13.4	11:41877469-41897547	NOTEST	0	0	0	0	1	1
ENSG00000255280	ENSG00000255280	CTD-2530H12.5	11:75294240-75380165	NOTEST	0	0	0	0	1	1
ENSG00000255281	ENSG00000255281	RP11-460B17.1	11:29357424-29615842	NOTEST	0	0	0	0	1	1
ENSG00000255282	ENSG00000255282	WTAPP1	11:102617698-102714534	NOTEST	0	0	0	0	1	1
ENSG00000255283	ENSG00000255283	RP11-72M10.4	11:55046922-55052999	NOTEST	0	0	0	0	1	1
ENSG00000255285	ENSG00000255285	RP11-358N4.5	11:89522579-89522901	NOTEST	0	0	0	0	1	1
ENSG00000255286	ENSG00000255286	RP11-708L7.7	11:111797867-111893308	NOTEST	0	0	0	0	1	1
ENSG00000255287	ENSG00000255287	SNRPGP16	11:92670606-92670832	NOTEST	0	0	0	0	1	1
ENSG00000255288	ENSG00000255288	RP4-562D20.2	11:30188709-30188853	NOTEST	0	0	0	0	1	1
ENSG00000255289	ENSG00000255289	RP11-91I20.1	8:61573378-61577089	NOTEST	0	0	0	0	1	1
ENSG00000255291	ENSG00000255291	RP11-701I24.1	11:20595731-20596496	NOTEST	0	0	0	0	1	1
ENSG00000255292	ENSG00000255292	SDHD	11:111895537-112095422	NOTEST	0	0	0	0	1	1
ENSG00000255293	ENSG00000255293	RP11-787P24.1	11:23425350-23427649	NOTEST	0	0	0	0	1	1
ENSG00000255294	ENSG00000255294	OR4A50P	11:55243418-55243904	NOTEST	0	0	0	0	1	1
ENSG00000255295	ENSG00000255295	RP11-745I13.1	11:89057523-89322779	NOTEST	0	0	0	0	1	1
ENSG00000255296	ENSG00000255296	RP11-757C15.4	11:71639746-71708643	NOTEST	0.0381874	0	#NAME?	0	1	1
ENSG00000255297	ENSG00000255297	OR4A41P	11:48611311-48612239	NOTEST	0	0	0	0	1	1
ENSG00000255298	ENSG00000255298	OR8G5	11:124120422-124135763	NOTEST	0	0	0	0	1	1
ENSG00000255299	ENSG00000255299	RP11-655C2.3	11:58265360-58273231	NOTEST	0.0717634	0.0323177	-1.15092	0	1	1
ENSG00000255300	ENSG00000255300	RP11-148I19.1	11:42014934-42185401	NOTEST	0	0	0	0	1	1
ENSG00000255301	ENSG00000255301	RP11-624G17.3	11:57228021-57245007	NOTEST	0.123054	0.05878	-1.0659	0	1	1
ENSG00000255303	ENSG00000255303	OR5BA1P	11:57633769-57634751	NOTEST	0.051747	0.0403499	-0.358912	0	1	1
ENSG00000255304	ENSG00000255304	OR4A46P	11:48517899-48518832	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000255305	ENSG00000255305	RP11-529A4.7	11:89711707-89713829	NOTEST	0	0	0	0	1	1
ENSG00000255306	ENSG00000255306	RP5-901A4.1	11:67776047-67797928	NOTEST	0.0784539	0.122303	0.640549	0	1	1
ENSG00000255307	ENSG00000255307	OR52B2	11:6128913-6206806	NOTEST	0	0	0	0	1	1
ENSG00000255308	ENSG00000255308	RP11-428C19.4	11:19203577-19302973	NOTEST	0	0	0	0	1	1
ENSG00000255309	ENSG00000255309	RP11-756D7.1	11:11780647-11780980	NOTEST	0	0	0	0	1	1
ENSG00000255310	ENSG00000255310	AF131215.2	8:10753554-11058875	NOTEST	0.0236184	0	#NAME?	0	1	1
ENSG00000255311	ENSG00000255311	RP11-160H12.2	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000255312	ENSG00000255312	OR4C7P	11:51483324-51484243	NOTEST	0	0	0	0	1	1
ENSG00000255313	ENSG00000255313	RP11-1082L8.2	8:125847125-125966570	NOTEST	0	0	0	0	1	1
ENSG00000255314	ENSG00000255314	RP11-702F3.3	11:46193497-46198656	NOTEST	0.0192895	0.13234	2.77837	0	1	1
ENSG00000255315	ENSG00000255315	OR8A3P	11:124401520-124401806	NOTEST	0	0	0	0	1	1
ENSG00000255316	ENSG00000255316	RP11-664H7.2	11:81266951-81267467	NOTEST	0	0	0	0	1	1
ENSG00000255317	ENSG00000255317	RP11-688I9.2	11:126225534-126875953	NOTEST	0	0	0	0	1	1
ENSG00000255318	ENSG00000255318	RP11-655M14.13	11:67385749-67394775	NOTEST	0.146155	0.0701965	-1.05803	0	1	1
ENSG00000255319	ENSG00000255319	ENPP7P8	11:71422785-71492229	NOTEST	0	0.0376549	inf	0	1	1
ENSG00000255321	ENSG00000255321	RP11-91I20.4	8:61429415-61536186	NOTEST	0	0	0	0	1	1
ENSG00000255322	ENSG00000255322	RP11-22P4.1	11:28373653-28548588	NOTEST	0.0287875	0.149144	2.37319	0	1	1
ENSG00000255323	ENSG00000255323	CTD-2140G10.1	11:22467233-22513565	NOTEST	0	0	0	0	1	1
ENSG00000255325	ENSG00000255325	RP11-96B2.1	8:123497753-123502054	NOTEST	0	0	0	0	1	1
ENSG00000255326	ENSG00000255326	CTD-2530H12.4	11:75294240-75380165	NOTEST	0.0879966	0.0459782	-0.936497	0	1	1
ENSG00000255327	ENSG00000255327	RP11-555G19.1	11:134820601-134821462	NOTEST	0.0251333	0	#NAME?	0	1	1
ENSG00000255328	ENSG00000255328	RP11-326C3.12	11:318639-330122	NOTEST	0	0	0	0	1	1
ENSG00000255329	ENSG00000255329	H2AFZP4	11:70116805-70282690	NOTEST	0	0.0516326	inf	0	1	1
ENSG00000255330	ENSG00000255330	SOGA3	6:127759550-127840500	NOTEST	0.494337	0.36889	-0.422303	0	1	1
ENSG00000255331	ENSG00000255331	RP11-736I10.2	11:59844822-59845874	NOTEST	0	0	0	0	1	1
ENSG00000255332	ENSG00000255332	RP11-201M22.1	11:91527527-91545460	NOTEST	0	0	0	0	1	1
ENSG00000255333	ENSG00000255333	AP000435.3	11:58121476-58121972	NOTEST	0	0	0	0	1	1
ENSG00000255334	ENSG00000255334	RP11-708L7.6	11:111797867-111893308	NOTEST	0	0	0	0	1	1
ENSG00000255335	ENSG00000255335	RP11-358H18.2	11:17716568-17719018	NOTEST	0	0	0	0	1	1
ENSG00000255336	ENSG00000255336	RP11-94P11.3	11:105028653-105402424	NOTEST	0	0	0	0	1	1
ENSG00000255337	ENSG00000255337	RP11-315O6.1	11:102267062-102369532	NOTEST	0.0525588	0.13134	1.3213	0	1	1
ENSG00000255338	ENSG00000255338	RP11-107P7.2	11:49132307-49132772	NOTEST	0	0	0	0	1	1
ENSG00000255340	ENSG00000255340	RP11-484D2.5	11:43333512-43516483	NOTEST	0	0	0	0	1	1
ENSG00000255341	ENSG00000255341	OR8Q1P	11:124471479-124472134	NOTEST	0	0	0	0	1	1
ENSG00000255342	ENSG00000255342	RP11-762B21.5	11:122943034-123098985	NOTEST	0	0	0	0	1	1
ENSG00000255343	ENSG00000255343	RP11-299M14.2	8:144915439-144924200	NOTEST	0	0.0729613	inf	0	1	1
ENSG00000255344	ENSG00000255344	RP11-469N6.2	11:134584435-134585816	NOTEST	0	0	0	0	1	1
ENSG00000255345	ENSG00000255345	CTD-2337I7.1	11:78363875-79151992	NOTEST	0	0	0	0	1	1
ENSG00000255346	ENSG00000255346	NOX5	15:69070873-69355083	NOTEST	0.215781	0.202245	-0.093464	0	1	1
ENSG00000255347	ENSG00000255347	RP11-40H19.1	11:40105259-40106067	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000255348	ENSG00000255348	RP11-700F16.3	11:133938819-134117686	NOTEST	0	0	0	0	1	1
ENSG00000255349	ENSG00000255349	OR4A7P	11:51425920-51426830	NOTEST	0	0	0	0	1	1
ENSG00000255350	ENSG00000255350	RP11-37O16.3	11:102980159-103350591	NOTEST	0	0	0	0	1	1
ENSG00000255352	ENSG00000255352	PPP1R10P1	11:130659125-130660920	NOTEST	0	0	0	0	1	1
ENSG00000255353	ENSG00000255353	RP11-382M14.1	11:107047011-107048256	NOTEST	0	0	0	0	1	1
ENSG00000255354	ENSG00000255354	RP11-148O21.2	8:11351509-11422113	NOTEST	0.064948	0.0777923	0.260342	0	1	1
ENSG00000255355	ENSG00000255355	AP000640.2	11:59436784-59443514	NOTEST	0.145601	0	#NAME?	0	1	1
ENSG00000255356	ENSG00000255356	RP11-277E18.2	12:8045171-8052736	NOTEST	0	0	0	0	1	1
ENSG00000255357	ENSG00000255357	RP11-34N19.1	11:22513657-22524392	NOTEST	0	0	0	0	1	1
ENSG00000255358	ENSG00000255358	RP11-567O18.1	11:130096571-130184581	NOTEST	0	0	0	0	1	1
ENSG00000255359	ENSG00000255359	CCDC179	11:22835344-22966939	NOTEST	0	0	0	0	1	1
ENSG00000255360	ENSG00000255360	RP11-529A4.15	11:89688313-89690333	NOTEST	0	0	0	0	1	1
ENSG00000255361	ENSG00000255361	RP11-412B14.2	8:42552518-42592550	NOTEST	0	0	0	0	1	1
ENSG00000255362	ENSG00000255362	RP11-619A14.3	11:75921999-75927069	NOTEST	0	0.316417	inf	0	1	1
ENSG00000255363	ENSG00000255363	RP11-672A2.5	11:76339139-76341407	NOTEST	0	0	0	0	1	1
ENSG00000255364	ENSG00000255364	RP11-94A24.1	8:123426570-123440790	NOTEST	0	0	0	0	1	1
ENSG00000255365	ENSG00000255365	RP11-776K3.1	8:13947372-15095848	NOTEST	0	0	0	0	1	1
ENSG00000255366	ENSG00000255366	RP11-1134I14.8	8:48001194-48110484	NOTEST	0.0115795	0.0235188	1.02224	0	1	1
ENSG00000255367	ENSG00000255367	RP13-726E6.2	11:3490548-3602441	NOTEST	0	0	0	0	1	1
ENSG00000255368	ENSG00000255368	RP11-54J7.2	11:25162078-25162569	NOTEST	0	0	0	0	1	1
ENSG00000255369	ENSG00000255369	RP11-740D6.3	11:128750219-128750563	NOTEST	0	0	0	0	1	1
ENSG00000255370	ENSG00000255370	CYCSP25	11:30851915-31391357	NOTEST	0	0	0	0	1	1
ENSG00000255371	ENSG00000255371	OPCML-IT2	11:132284870-133402414	NOTEST	0	0	0	0	1	1
ENSG00000255372	ENSG00000255372	CTD-3064C13.1	11:22214721-22304903	NOTEST	0	0	0	0	1	1
ENSG00000255374	ENSG00000255374	TAS2R43	12:10977558-11324212	NOTEST	0.0663539	0.0122257	-2.44026	0	1	1
ENSG00000255375	ENSG00000255375	RP1-65P5.5	11:32133594-32364955	NOTEST	0.444688	0.391805	-0.182657	0	1	1
ENSG00000255376	ENSG00000255376	RP11-360K13.2	11:96461316-96584822	NOTEST	0	0	0	0	1	1
ENSG00000255377	ENSG00000255377	DUXAP5	11:119252487-119397374	NOTEST	0	0	0	0	1	1
ENSG00000255378	ENSG00000255378	PRR23D2	8:7636112-7638935	NOTEST	0	0	0	0	1	1
ENSG00000255379	ENSG00000255379	CYCSP29	11:108535751-108811657	NOTEST	0	0	0	0	1	1
ENSG00000255380	ENSG00000255380	RP11-684B20.1	11:98000966-98001926	NOTEST	0	0	0	0	1	1
ENSG00000255381	ENSG00000255381	AP001258.5	11:58897605-58922512	NOTEST	0	0	0	0	1	1
ENSG00000255382	ENSG00000255382	RP11-718B12.2	11:82502703-82528188	NOTEST	0	0	0	0	1	1
ENSG00000255384	ENSG00000255384	RP11-770J1.4	11:118303835-118305921	NOTEST	0	0	0	0	1	1
ENSG00000255385	ENSG00000255385	RP11-313I2.2	11:89433931-89434493	NOTEST	0	0	0	0	1	1
ENSG00000255386	ENSG00000255386	OR5BR1P	11:59100229-59101559	NOTEST	0	0	0	0	1	1
ENSG00000255387	ENSG00000255387	RP11-23F23.3	11:4231583-4233321	NOTEST	0	0	0	0	1	1
ENSG00000255388	ENSG00000255388	RP11-124G5.3	11:41540444-41735998	NOTEST	0	0	0	0	1	1
ENSG00000255389	ENSG00000255389	C6orf3	6:111620233-111927481	NOTEST	0.210563	0.111037	-0.923207	0	1	1
ENSG00000255390	ENSG00000255390	RP11-732A19.5	11:6642555-6677085	NOTEST	0.121826	0.0743464	-0.71249	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000255393	ENSG00000255393	RP11-736I10.1	11:59792380-59798550	NOTEST	0	0	0	0	1	1
ENSG00000255394	ENSG00000255394	C8orf49	8:11618895-11620309	NOTEST	0.180218	0.184184	0.0314007	0	1	1
ENSG00000255395	ENSG00000255395	CTD-2562J17.2	11:74810216-74917594	NOTEST	0.0381874	0.0922847	1.27299	0	1	1
ENSG00000255396	ENSG00000255396	AP000857.2	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000255397	ENSG00000255397	AC022182.2	8:61822611-61880334	NOTEST	0	0	0	0	1	1
ENSG00000255398	ENSG00000255398	HCAR3	12:123011792-123215390	NOTEST	0	0	0	0	1	1
ENSG00000255399	ENSG00000255399	TBX5-AS1	12:114791735-114850636	NOTEST	0	0	0	0	1	1
ENSG00000255400	ENSG00000255400	RP13-631K18.5	11:12108437-12110988	NOTEST	0	0	0	0	1	1
ENSG00000255401	ENSG00000255401	RP11-15D14.2	11:13510158-13510937	NOTEST	0	0	0	0	1	1
ENSG00000255402	ENSG00000255402	RP11-696P8.2	8:110975873-110988076	NOTEST	0	0.0934644	inf	0	1	1
ENSG00000255403	ENSG00000255403	AP000641.1	11:105480720-105852819	NOTEST	0	0	0	0	1	1
ENSG00000255404	ENSG00000255404	RP11-770G2.5	11:65554492-65564690	NOTEST	0.00235527	3.69E-06	-9.31819	0	1	1
ENSG00000255406	ENSG00000255406	RP11-713P17.5	11:133896881-133898013	NOTEST	0	0	0	0	1	1
ENSG00000255408	ENSG00000255408	PCDHA3	5:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000255409	ENSG00000255409	RSF1-IT1	11:77371040-77532063	NOTEST	0.123906	0	#NAME?	0	1	1
ENSG00000255410	ENSG00000255410	RP11-732A19.6	11:6642555-6677085	NOTEST	0	0	0	0	1	1
ENSG00000255411	ENSG00000255411	RP11-98J9.1	11:13806936-13901046	NOTEST	0	0	0	0	1	1
ENSG00000255413	ENSG00000255413	RP11-436P7.2	8:13599317-13600290	NOTEST	0	0	0	0	1	1
ENSG00000255415	ENSG00000255415	RP11-684B2.5	11:71340090-71340467	NOTEST	0	0	0	0	1	1
ENSG00000255416	ENSG00000255416	OR10AF1P	11:55715595-55716400	NOTEST	0	0	0	0	1	1
ENSG00000255417	ENSG00000255417	RP11-37O16.4	11:102980159-103350591	NOTEST	0	0	0	0	1	1
ENSG00000255418	ENSG00000255418	RP11-266A24.1	11:23186445-23224707	NOTEST	0	0	0	0	1	1
ENSG00000255419	ENSG00000255419	MSH5-SAPCD1	HSCHR6_MHC_SSTO:31714323-31722583	NOTEST	0	0	0	0	1	1
ENSG00000255420	ENSG00000255420	RP11-236J17.3	11:8032824-8038036	NOTEST	0	0	0	0	1	1
ENSG00000255421	ENSG00000255421	CTD-2011F17.2	11:75514475-75854239	NOTEST	0	0	0	0	1	1
ENSG00000255422	ENSG00000255422	AP002954.4	11:118575315-118661858	NOTEST	0	0	0	0	1	1
ENSG00000255424	ENSG00000255424	RP11-589F4.2	11:19051243-19051985	NOTEST	0	0	0	0	1	1
ENSG00000255425	ENSG00000255425	OR8G3P	11:124085345-124086394	NOTEST	0	0	0	0	1	1
ENSG00000255426	ENSG00000255426	CTD-2210P24.2	11:45743857-45765801	NOTEST	0	0	0	0	1	1
ENSG00000255427	ENSG00000255427	RP11-350D17.2	11:34592422-34595529	NOTEST	0	0	0	0	1	1
ENSG00000255428	ENSG00000255428	RP11-794P6.1	11:111222976-111328876	NOTEST	0	0	0	0	1	1
ENSG00000255429	ENSG00000255429	RP11-643G5.6	11:89057523-89322779	NOTEST	0	0	0	0	1	1
ENSG00000255430	ENSG00000255430	CASP1P1	11:104993387-104994066	NOTEST	0	0	0	0	1	1
ENSG00000255431	ENSG00000255431	OR5B19P	11:58111209-58112137	NOTEST	0	0	0	0	1	1
ENSG00000255432	ENSG00000255432	RP11-831H9.11	11:62414319-62441159	NOTEST	0	0	0	0	1	1
ENSG00000255433	ENSG00000255433	AP000479.1	11:56615953-56645554	NOTEST	0.0847498	0.14788	0.803141	0	1	1
ENSG00000255434	ENSG00000255434	CTD-2530H12.8	11:75294240-75380165	NOTEST	0	0	0	0	1	1
ENSG00000255435	ENSG00000255435	RP11-770J1.3	11:118307204-118473748	NOTEST	0.121009	0.0515921	-1.22989	0	1	1
ENSG00000255436	ENSG00000255436	Z95704.2	4:53178-88099	NOTEST	0.202111	0.222738	0.140194	0	1	1
ENSG00000255437	ENSG00000255437	RP11-510I21.1	8:13880195-13880931	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000255439	ENSG00000255439	RP11-196G11.1	16:31085742-31107301	NOTEST	0.45399	0.399197	-0.185558	0	1	1
ENSG00000255440	ENSG00000255440	RP11-632K5.2	11:74041362-74197096	NOTEST	0	0	0	0	1	1
ENSG00000255441	ENSG00000255441	CTD-2616J11.2	19:51913274-51921057	NOTEST	0	0.0994016	inf	0	1	1
ENSG00000255442	ENSG00000255442	RP11-347H15.1	11:50129326-50149612	NOTEST	0	0	0	0	1	1
ENSG00000255443	ENSG00000255443	RP1-68D18.4	11:35160416-35253949	NOTEST	0.550168	0.375366	-0.551575	0	1	1
ENSG00000255444	ENSG00000255444	CYCSP27	11:74041362-74197096	NOTEST	0	0	0	0	1	1
ENSG00000255445	ENSG00000255445	RP11-573M3.3	11:92877340-92931130	NOTEST	0.0541601	0	#NAME?	0	1	1
ENSG00000255446	ENSG00000255446	CTD-2531D15.4	11:62172574-62194196	NOTEST	0.13145	0.0311121	-2.07896	0	1	1
ENSG00000255447	ENSG00000255447	CTD-2210P24.6	11:45834769-45846809	NOTEST	0	0	0	0	1	1
ENSG00000255448	ENSG00000255448	RP1-59M18.2	11:17809594-18063973	NOTEST	0.000949809	0	#NAME?	0	1	1
ENSG00000255449	ENSG00000255449	RP11-91P24.6	11:77532154-77705724	NOTEST	0.0274568	0.145867	2.40942	0	1	1
ENSG00000255450	ENSG00000255450	CTD-2063L20.1	11:29297201-29298112	NOTEST	0	0	0	0	1	1
ENSG00000255451	ENSG00000255451	RP11-58K22.1	11:44490013-44491979	NOTEST	0	0	0	0	1	1
ENSG00000255452	ENSG00000255452	RP11-107P7.1	11:49113955-49114319	NOTEST	0	0	0	0	1	1
ENSG00000255454	ENSG00000255454	RP11-46P12.1	11:25652265-25652587	NOTEST	0	0	0	0	1	1
ENSG00000255456	ENSG00000255456	CTD-2517M22.9	8:145754562-145911194	NOTEST	0	0	0	0	1	1
ENSG00000255457	ENSG00000255457	RP11-436P7.1	8:13553082-13563015	NOTEST	0	0	0	0	1	1
ENSG00000255459	ENSG00000255459	RP11-52B19.10	8:7943543-7944287	NOTEST	0	0	0	0	1	1
ENSG00000255460	ENSG00000255460	ZDHHC20P3	11:74919098-74954742	NOTEST	0	0	0	0	1	1
ENSG00000255461	ENSG00000255461	OR8I1P	11:56064016-56064947	NOTEST	0	0	0	0	1	1
ENSG00000255462	ENSG00000255462	RP11-483L5.1	11:11292422-11643552	NOTEST	0	0	0	0	1	1
ENSG00000255463	ENSG00000255463	RP11-16F15.4	11:9652554-9652906	NOTEST	0	0	0	0	1	1
ENSG00000255464	ENSG00000255464	RP11-585F1.2	8:142090-150563	NOTEST	0	0	0	0	1	1
ENSG00000255465	ENSG00000255465	RP11-264E20.1	11:128485761-128491701	NOTEST	0	0	0	0	1	1
ENSG00000255466	ENSG00000255466	OR5AL2P	11:56161204-56162124	NOTEST	0	0	0	0	1	1
ENSG00000255467	ENSG00000255467	RP11-144G7.2	11:107879458-108018503	NOTEST	0	0	0	0	1	1
ENSG00000255469	ENSG00000255469	RP11-725K16.2	11:102751221-102751576	NOTEST	0	0	0	0	1	1
ENSG00000255470	ENSG00000255470	RP11-113D6.6	11:18161732-18211168	NOTEST	0	0	0	0	1	1
ENSG00000255471	ENSG00000255471	RP11-736K20.5	11:86502100-86666433	NOTEST	0.0549184	0.0331867	-0.726686	0	1	1
ENSG00000255472	ENSG00000255472	RP11-998D10.1	14:21484921-21572881	NOTEST	0	0	0	0	1	1
ENSG00000255474	ENSG00000255474	RP11-234B24.2	12:4671369-4960277	NOTEST	0	0	0	0	1	1
ENSG00000255475	ENSG00000255475	RP11-687M24.4	11:125002742-125009483	NOTEST	0	0	0	0	1	1
ENSG00000255476	ENSG00000255476	RP11-1H15.2	11:9776316-10315754	NOTEST	0	0	0	0	1	1
ENSG00000255477	ENSG00000255477	RP11-63D14.1	11:38520544-38521736	NOTEST	0	0	0	0	1	1
ENSG00000255478	ENSG00000255478	RP11-867O8.5	11:65134908-65151172	NOTEST	0	0	0	0	1	1
ENSG00000255479	ENSG00000255479	RP11-672A2.6	11:76336505-76337878	NOTEST	0	0	0	0	1	1
ENSG00000255480	ENSG00000255480	RP4-710M3.2	11:30406039-30652055	NOTEST	0.0763123	0.114288	0.582689	0	1	1
ENSG00000255481	ENSG00000255481	OR56A7P	11:6067036-6067977	NOTEST	0	0	0	0	1	1
ENSG00000255482	ENSG00000255482	RP11-315O6.2	11:102267062-102369532	NOTEST	0	0	0	0	1	1

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ENSG00000255485	ENSG00000255485	OR5G4P	11:56557681-56558441	NOTEST	0	0	0	0	1	1
ENSG00000255486	ENSG00000255486	RP11-313I2.13	11:89456649-89460421	NOTEST	0	0	0	0	1	1
ENSG00000255487	ENSG00000255487	RP11-513D5.5	8:38082735-38239790	NOTEST	0	0	0	0	1	1
ENSG00000255489	ENSG00000255489	CTC-830E23.1	11:24518515-25104150	NOTEST	0	0	0	0	1	1
ENSG00000255490	ENSG00000255490	EIF4A2P5	11:31806339-32127301	NOTEST	0	0	0	0	1	1
ENSG00000255491	ENSG00000255491	RP11-1082L8.4	8:125823859-125827924	NOTEST	0	0	0	0	1	1
ENSG00000255492	ENSG00000255492	CTD-2381F24.1	11:11862969-11980870	NOTEST	0	0	0	0	1	1
ENSG00000255493	ENSG00000255493	RP11-131J4.12	11:55197962-55198470	NOTEST	0	0	0	0	1	1
ENSG00000255496	ENSG00000255496	RP11-587D21.4	11:27528384-27899195	NOTEST	0	0	0	0	1	1
ENSG00000255497	ENSG00000255497	RP11-726G23.12	8:43147625-43218661	NOTEST	0	0	0	0	1	1
ENSG00000255499	ENSG00000255499	RP11-738O11.12	11:55631407-55648719	NOTEST	0	0	0	0	1	1
ENSG00000255500	ENSG00000255500	RP11-347H15.2	11:50227331-50228444	NOTEST	0.0287265	0	#NAME?	0	1	1
ENSG00000255501	ENSG00000255501	CARD18	11:105008447-105010453	NOTEST	0	0	0	0	1	1
ENSG00000255502	ENSG00000255502	RP11-379J13.2	11:97749780-97813762	NOTEST	0	0	0	0	1	1
ENSG00000255503	ENSG00000255503	RP11-113K21.4	11:82783107-82818003	NOTEST	4.70E-05	0	#NAME?	0	1	1
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ENSG00000255506	ENSG00000255506	RP11-203F8.1	11:92085261-92629618	NOTEST	0	0	0	0	1	1
ENSG00000255507	ENSG00000255507	RP11-535A19.2	11:75514475-75854239	NOTEST	0.489872	0.440343	-0.153777	0	1	1
ENSG00000255508	ENSG00000255508	MIR3654	11:62327072-62359649	NOTEST	0.485431	0.549966	0.180076	0	1	1
ENSG00000255509	ENSG00000255509	RP11-445F12.1	17:35218934-35293960	NOTEST	0	0	0	0	1	1
ENSG00000255510	ENSG00000255510	OR8A2P	11:124330429-124331381	NOTEST	0	0	0	0	1	1
ENSG00000255511	ENSG00000255511	RP11-1081L13.3	11:18892535-18895009	NOTEST	0	0	0	0	1	1
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ENSG00000255513	ENSG00000255513	AC005363.9	16:2012052-2014861	NOTEST	0.584035	0.508837	-0.19885	0	1	1
ENSG00000255514	ENSG00000255514	OR4B2P	11:48248980-48249862	NOTEST	0	0	0	0	1	1
ENSG00000255515	ENSG00000255515	RP11-178H8.3	11:93342925-93343499	NOTEST	0	0	0	0	1	1
ENSG00000255516	ENSG00000255516	RP11-164N3.1	11:87783273-87831315	NOTEST	0	0	0	0	1	1
ENSG00000255518	ENSG00000255518	RP11-148O21.4	8:11351509-11422113	NOTEST	0.039825	0	#NAME?	0	1	1
ENSG00000255519	ENSG00000255519	RP11-958J22.2	11:45392947-45564024	NOTEST	0	0	0	0	1	1
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ENSG00000255522	ENSG00000255522	RP13-726E6.3	11:3490548-3602441	NOTEST	0	0	0	0	1	1
ENSG00000255523	ENSG00000255523	RP11-780O24.2	11:58672870-58826132	NOTEST	0	0	0	0	1	1
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ENSG00000255525	ENSG00000255525	RP1-296L11.1	11:30851915-31391357	NOTEST	0	0	0	0	1	1
ENSG00000255526	ENSG00000255526	NEDD8-MDP1	14:24641061-24708448	NOTEST	0.131011	0.261766	0.998591	0	1	1
ENSG00000255527	ENSG00000255527	RP11-56P9.4	11:48928654-48930498	NOTEST	0	0	0	0	1	1
ENSG00000255528	ENSG00000255528	RP11-25I9.2	11:108873191-108908694	NOTEST	0	0	0	0	1	1

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ENSG00000255531	ENSG00000255531	NDUFS5P6	8:68761278-68761573	NOTEST	0	0	0	0	1	1
ENSG00000255532	ENSG00000255532	CTD-2026G22.1	11:49327265-49401221	NOTEST	0.0675736	0.0284208	-1.24951	0	1	1
ENSG00000255533	ENSG00000255533	RP11-326C3.4	11:303855-304144	NOTEST	0	0	0	0	1	1
ENSG00000255534	ENSG00000255534	OR4A43P	11:48547615-48548523	NOTEST	0	0	0	0	1	1
ENSG00000255535	ENSG00000255535	RP11-679I18.4	11:129910259-129910966	NOTEST	0	0	0	0	1	1
ENSG00000255536	ENSG00000255536	RP11-583F24.5	11:18931982-18932943	NOTEST	0	0	0	0	1	1
ENSG00000255537	ENSG00000255537	AP000708.1	11:125315645-125369424	NOTEST	0	0	0	0	1	1
ENSG00000255538	ENSG00000255538	OR10V2P	11:59480295-59573354	NOTEST	0.0962932	0.0194878	-2.30486	0	1	1
ENSG00000255539	ENSG00000255539	CTA-797E19.2	11:70116805-70282690	NOTEST	0.0770464	0	#NAME?	0	1	1
ENSG00000255540	ENSG00000255540	RP11-313I2.5	11:89464184-89467950	NOTEST	0	0	0	0	1	1
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ENSG00000255542	ENSG00000255542	RP4-683L5.1	11:35272752-35442549	NOTEST	0	0	0	0	1	1
ENSG00000255543	ENSG00000255543	RP11-72M10.2	11:55029657-55038595	NOTEST	0	0	0	0	1	1
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ENSG00000255545	ENSG00000255545	RP11-627G23.1	11:134306366-134375555	NOTEST	0	0	0	0	1	1
ENSG00000255546	ENSG00000255546	RP11-168K9.1	11:126891648-126923448	NOTEST	0	0	0	0	1	1
ENSG00000255547	ENSG00000255547	RPA2P3	11:98891682-100229616	NOTEST	0	0	0	0	1	1
ENSG00000255548	ENSG00000255548	RP11-617B3.2	11:103777913-104035107	NOTEST	0	0.0307711	inf	0	1	1
ENSG00000255549	ENSG00000255549	ENPP7P6	8:12305521-12368787	NOTEST	0.0391898	0	#NAME?	0	1	1
ENSG00000255550	ENSG00000255550	RP11-163O19.11	11:49872180-49884080	NOTEST	0	0	0	0	1	1
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ENSG00000255552	ENSG00000255552	LY6G6E	6:31654725-31685695	NOTEST	0	0.0191042	inf	0	1	1
ENSG00000255553	ENSG00000255553	RP11-810P12.5	11:61844748-61849656	NOTEST	0	0	0	0	1	1
ENSG00000255554	ENSG00000255554	OR7E1P	11:67741756-67742714	NOTEST	0	0	0	0	1	1
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ENSG00000255556	ENSG00000255556	RP11-351I21.6	8:12219526-12268510	NOTEST	0.0104884	0.0483394	2.20441	0	1	1
ENSG00000255557	ENSG00000255557	RP11-770G2.2	11:65513199-65539056	NOTEST	0	0.0360601	inf	0	1	1
ENSG00000255558	ENSG00000255558	CTC-497E21.5	11:13076161-13156386	NOTEST	0	0	0	0	1	1
ENSG00000255559	ENSG00000255559	ZNF252P-AS1	8:146198974-146231432	NOTEST	0.137328	0.165024	0.265056	0	1	1
ENSG00000255560	ENSG00000255560	OR4R2P	11:51461563-51462160	NOTEST	0	0	0	0	1	1
ENSG00000255562	ENSG00000255562	UNC93B6	11:71292900-71319086	NOTEST	0.0305602	0.0800301	1.38889	0	1	1
ENSG00000255563	ENSG00000255563	RP11-124G5.2	11:41540444-41735998	NOTEST	0	0	0	0	1	1
ENSG00000255565	ENSG00000255565	RP11-6B19.1	12:15773091-16035263	NOTEST	0	0	0	0	1	1
ENSG00000255566	ENSG00000255566	RP11-114F3.5	12:64798129-64844907	NOTEST	0	0.0316794	inf	0	1	1
ENSG00000255568	ENSG00000255568	BRWD1-IT2	21:40556101-40695144	NOTEST	0.205589	0.0734209	-1.4855	0	1	1
ENSG00000255569	ENSG00000255569	TRAV1-1	14:22089990-22090720	NOTEST	0	0	0	0	1	1
ENSG00000255571	ENSG00000255571	LINC00925	15:89904809-89939471	NOTEST	0.0610324	0.051604	-0.242092	0	1	1
ENSG00000255572	ENSG00000255572	RP11-273B20.3	12:7319269-7371170	NOTEST	0	0	0	0	1	1
ENSG00000255575	ENSG00000255575	RP1-267D11.1	12:120427672-120532298	NOTEST	0	0	0	0	1	1
ENSG00000255580	ENSG00000255580	AP000462.2	11:115039937-115375675	NOTEST	0	0	0	0	1	1
ENSG00000255581	ENSG00000255581	RP11-69M1.4	12:8169796-8170456	NOTEST	0	0	0	0	1	1

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ENSG00000255583	ENSG00000255583	RP11-415I12.2	12:63952692-64217675	NOTEST	0	0	0	0	1	1
ENSG00000255585	ENSG00000255585	RP11-188C12.2	9:140513443-141019076	NOTEST	0.0666675	0.064236	-0.0536007	0	1	1
ENSG00000255587	ENSG00000255587	RAB44	6:36683255-36699870	NOTEST	0	0	0	0	1	1
ENSG00000255594	ENSG00000255594	Z82188.1	22:37621300-37640488	NOTEST	0.160635	0.127756	-0.330389	0	1	1
ENSG00000255595	ENSG00000255595	RP4-809F18.1	12:126843847-126845611	NOTEST	0.0130394	0	#NAME?	0	1	1
ENSG00000255599	ENSG00000255599	AP000997.1	11:115498782-115500461	NOTEST	0	0	0	0	1	1
ENSG00000255605	ENSG00000255605	RP11-644L4.1	11:95431249-95433787	NOTEST	0	0.107203	inf	0	1	1
ENSG00000255606	ENSG00000255606	AP000439.2	11:69253132-69259511	NOTEST	0	0	0	0	1	1
ENSG00000255608	ENSG00000255608	RP3-377H17.2	12:4671369-4960277	NOTEST	0	0	0	0	1	1
ENSG00000255618	ENSG00000255618	RP11-357K6.1	12:119210836-119212942	NOTEST	0	0	0	0	1	1
ENSG00000255619	ENSG00000255619	CT476828.3	GL000228.1:112298-113921	NOTEST	0	0	0	0	1	1
ENSG00000255621	ENSG00000255621	RP11-377D9.3	12:13080659-13193613	NOTEST	0	0.0212075	inf	0	1	1
ENSG00000255622	ENSG00000255622	PCDHB17	5:140535576-140538639	NOTEST	0.0493709	0.0275648	-0.840834	0	1	1
ENSG00000255627	ENSG00000255627	RP11-547L9.1	12:22161281-22161814	NOTEST	0	0	0	0	1	1
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ENSG00000255629	ENSG00000255629	RP11-196H14.3	12:64238072-64541637	NOTEST	0.435682	0	#NAME?	0	1	1
ENSG00000255633	ENSG00000255633	MTRNR2L9	6:62284007-62284534	NOTEST	0	0	0	0	1	1
ENSG00000255637	ENSG00000255637	AC109992.1	3:142025448-142166904	NOTEST	0	0	0	0	1	1
ENSG00000255638	ENSG00000255638	CT476828.4	GL000228.1:85850-87473	NOTEST	0	0	0	0	1	1
ENSG00000255639	ENSG00000255639	RP11-234B24.6	12:4671369-4960277	NOTEST	0.0713483	0	#NAME?	0	1	1
ENSG00000255641	ENSG00000255641	NKG2-E	12:10564910-10607284	NOTEST	0.0634565	0.000583423	-6.76508	0	1	1
ENSG00000255642	ENSG00000255642	PABPC1P4	12:63952692-64217675	NOTEST	0	0	0	0	1	1
ENSG00000255644	ENSG00000255644	RP11-59N23.1	12:21788275-21928515	NOTEST	0	0	0	0	1	1
ENSG00000255647	ENSG00000255647	AC093510.1	5:89705816-89706485	NOTEST	0.0555095	0	#NAME?	0	1	1
ENSG00000255648	ENSG00000255648	RP11-361I14.2	12:18836102-18890991	NOTEST	0	0	0	0	1	1
ENSG00000255649	ENSG00000255649	RP11-502N13.2	12:14656594-14910897	NOTEST	0	0	0	0	1	1
ENSG00000255651	ENSG00000255651	RP11-466C23.4	11:63527363-63536113	NOTEST	0.149571	0	#NAME?	0	1	1
ENSG00000255652	ENSG00000255652	RP11-313F23.4	12:34343971-34371788	NOTEST	0	0.0202048	inf	0	1	1
ENSG00000255653	ENSG00000255653	RP11-60C6.3	11:94745021-94745696	NOTEST	0	0	0	0	1	1
ENSG00000255655	ENSG00000255655	RP11-256L11.3	12:109785707-109974507	NOTEST	0.034425	0.0243489	-0.4996	0	1	1
ENSG00000255660	ENSG00000255660	RERG-AS1	12:15260716-15750333	NOTEST	0	0	0	0	1	1
ENSG00000255663	ENSG00000255663	RP11-212D19.4	11:114262164-114321001	NOTEST	0.126076	0.402135	1.67338	0	1	1
ENSG00000255664	ENSG00000255664	ARL6IP1P1	14:22117943-22118553	NOTEST	0	0	0	0	1	1
ENSG00000255666	ENSG00000255666	RP11-867G2.6	11:94277005-94658686	NOTEST	0	0	0	0	1	1
ENSG00000255669	ENSG00000255669	RP11-885B4.2	12:2851791-2881074	NOTEST	0	0	0	0	1	1
ENSG00000255670	ENSG00000255670	RP11-253I19.3	12:12628828-12715317	NOTEST	0	0.043938	inf	0	1	1
ENSG00000255671	ENSG00000255671	RP11-283I3.1	12:299242-323736	NOTEST	0	0	0	0	1	1
ENSG00000255672	ENSG00000255672	RP11-45F15.2	11:72003468-72145692	NOTEST	0	0	0	0	1	1
ENSG00000255679	ENSG00000255679	JRKL-AS1	11:96123152-96240738	NOTEST	0	0	0	0	1	1
ENSG00000255680	ENSG00000255680	RP11-732A19.9	11:6633999-6640995	NOTEST	0.050683	0	#NAME?	0	1	1

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ENSG00000255686	ENSG00000255686	RP11-227B21.2	12:117890816-118406788	NOTEST	0	0	0	0	1	1
ENSG00000255689	ENSG00000255689	RP11-136I14.5	11:115453014-115471057	NOTEST	0	0	0	0	1	1
ENSG00000255690	ENSG00000255690	AC005013.1	7:28992973-28998961	NOTEST	0.000371482	0.000370024	-0.00567236	0	1	1
ENSG00000255692	ENSG00000255692	RP1-127H14.3	12:120123594-120315095	NOTEST	0.106058	0	#NAME?	0	1	1
ENSG00000255693	ENSG00000255693	RP11-766N7.3	12:65277173-65376304	NOTEST	0	0.0106042	inf	0	1	1
ENSG00000255700	ENSG00000255700	APOOP3	12:65528467-65529053	NOTEST	0	0	0	0	1	1
ENSG00000255701	ENSG00000255701	AC090953.1	3:16216155-16273499	NOTEST	0.0101612	0.344336	5.08268	0	1	1
ENSG00000255703	ENSG00000255703	RP11-46H11.2	12:133345494-133532892	NOTEST	0	0	0	0	1	1
ENSG00000255704	ENSG00000255704	RP11-292I17.1	12:132081401-132081660	NOTEST	0	0	0	0	1	1
ENSG00000255707	ENSG00000255707	CT476828.5	GL000228.1:102380-104003	NOTEST	0	0	0	0	1	1
ENSG00000255710	ENSG00000255710	RP11-667M19.9	11:113668595-113746292	NOTEST	0.111909	0.0121835	-3.19933	0	1	1
ENSG00000255713	ENSG00000255713	OR4D2	17:56247016-56247940	NOTEST	0	0	0	0	1	1
ENSG00000255714	ENSG00000255714	RP11-121J20.1	12:119083119-119086529	NOTEST	0	0	0	0	1	1
ENSG00000255723	ENSG00000255723	RP11-529H2.2	4:88224940-88312538	NOTEST	0.0830886	0	#NAME?	0	1	1
ENSG00000255726	ENSG00000255726	XXbac-BPG299F13.15	6:31190689-31190870	NOTEST	0	0	0	0	1	1
ENSG00000255727	ENSG00000255727	RP11-508P1.2	12:15154766-15159617	NOTEST	0	0	0	0	1	1
ENSG00000255729	ENSG00000255729	AC005618.1	5:140698056-140700339	NOTEST	0.544758	0.0769467	-2.82368	0	1	1
ENSG00000255730	ENSG00000255730	CTC-435M10.3	19:41768400-41930910	NOTEST	0.267695	0.109511	-1.28951	0	1	1
ENSG00000255733	ENSG00000255733	IFNG-AS1	12:68383224-68628466	NOTEST	0	0	0	0	1	1
ENSG00000255734	ENSG00000255734	HNRNPABP1	12:10264336-10265070	NOTEST	0	0	0	0	1	1
ENSG00000255735	ENSG00000255735	AC110619.1	2:241375087-241407493	NOTEST	0.00993526	0.0287738	1.53413	0	1	1
ENSG00000255740	ENSG00000255740	RP11-239A17.1	12:16939695-16940779	NOTEST	0	0	0	0	1	1
ENSG00000255741	ENSG00000255741	RP11-757G1.5	11:68708970-68710320	NOTEST	0.111972	0.0819678	-0.45001	0	1	1
ENSG00000255743	ENSG00000255743	AL360078.1	20:172863-172940	NOTEST	0	0	0	0	1	1
ENSG00000255745	ENSG00000255745	RP11-625L16.1	12:24857498-24927147	NOTEST	0	0	0	0	1	1
ENSG00000255746	ENSG00000255746	RP11-283I3.4	12:329788-372039	NOTEST	0	0	0	0	1	1
ENSG00000255748	ENSG00000255748	AC226150.4	12:133787245-133787772	NOTEST	0.471274	0.608278	0.368164	0	1	1
ENSG00000255749	ENSG00000255749	GNAI2P1	12:14407845-14408160	NOTEST	0	0	0	0	1	1
ENSG00000255750	ENSG00000255750	RP11-283G6.5	12:26272958-26986131	NOTEST	0	0	0	0	1	1
ENSG00000255752	ENSG00000255752	AL451105.1	X:75119638-75119715	NOTEST	0	0	0	0	1	1
ENSG00000255753	ENSG00000255753	RP11-22B23.2	12:9466997-9468769	NOTEST	0.402765	0.325479	-0.307373	0	1	1
ENSG00000255757	ENSG00000255757	RP11-749H20.3	12:128361543-128362061	NOTEST	0	0	0	0	1	1
ENSG00000255760	ENSG00000255760	RP11-428G5.5	12:32030012-32040137	NOTEST	0	0	0	0	1	1
ENSG00000255763	ENSG00000255763	MRPS18CP4	12:14390024-14390255	NOTEST	0	0	0	0	1	1
ENSG00000255767	ENSG00000255767	RP13-512J5.1	2:3579402-3609324	NOTEST	0	0.516141	inf	0	1	1
ENSG00000255772	ENSG00000255772	GS1-410F4.4	12:68323014-68363797	NOTEST	0.09833	0.0342409	-1.52191	0	1	1
ENSG00000255774	ENSG00000255774	AP000439.3	11:69291900-69294708	NOTEST	0	0	0	0	1	1
ENSG00000255775	ENSG00000255775	RP3-454B23.1	12:6264200-6269885	NOTEST	0.056807	0	#NAME?	0	1	1
ENSG00000255776	ENSG00000255776	RP11-436I9.3	12:9188939-9189840	NOTEST	0	0	0	0	1	1
ENSG00000255778	ENSG00000255778	RP4-765H13.1	12:126675923-126709860	NOTEST	0	0	0	0	1	1
ENSG00000255780	ENSG00000255780	RP11-1029F8.1	12:64238072-64541637	NOTEST	0	0	0	0	1	1

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ENSG00000255782	ENSG00000255782	Z83840.1	22:42069933-42094140	NOTEST	0.448512	0.421247	-0.0904828	0	1	1
ENSG00000255783	ENSG00000255783	AC018692.3	GL000193.1:95247-95324	NOTEST	0	0	0	0	1	1
ENSG00000255786	ENSG00000255786	RP11-809N8.6	11:73111531-73309234	NOTEST	0	0	0	0	1	1
ENSG00000255790	ENSG00000255790	RP11-711K1.7	12:11504756-11653975	NOTEST	0	0	0	0	1	1
ENSG00000255794	ENSG00000255794	RMST	12:97825430-97958813	NOTEST	0	0	0	0	1	1
ENSG00000255798	ENSG00000255798	RP11-817J15.3	11:102552040-102554644	NOTEST	0	0	0	0	1	1
ENSG00000255800	ENSG00000255800	OR13C5	9:107360649-107361788	NOTEST	0	0	0	0	1	1
ENSG00000255801	ENSG00000255801	RP11-561P12.5	12:8700956-8720209	NOTEST	0	0	0	0	1	1
ENSG00000255804	ENSG00000255804	OR6J1	14:23102672-23103716	NOTEST	0	0	0	0	1	1
ENSG00000255807	ENSG00000255807	PTP4A1P2	12:133606974-133613808	NOTEST	0	0	0	0	1	1
ENSG00000255808	ENSG00000255808	RP11-31L22.3	11:72287184-72385635	NOTEST	0	0	0	0	1	1
ENSG00000255811	ENSG00000255811	RP1-34M23.5	1:35178337-35325417	NOTEST	0	0	0	0	1	1
ENSG00000255814	ENSG00000255814	RP11-357K6.2	12:119256608-119271341	NOTEST	0	0	0	0	1	1
ENSG00000255815	ENSG00000255815	KRT8P11	9:102067393-102068893	NOTEST	0	0.0340657	inf	0	1	1
ENSG00000255817	ENSG00000255817	RP11-196H14.4	12:64238072-64541637	NOTEST	0	0.0530735	inf	0	1	1
ENSG00000255819	ENSG00000255819	KLRC4-KLRK1	12:10516367-10562745	NOTEST	0.0543947	0.0728683	0.421824	0	1	1
ENSG00000255823	ENSG00000255823	MTRNR2L8	11:10529433-10530723	NOTEST	0.0506808	0.0902018	0.831716	0	1	1
ENSG00000255824	ENSG00000255824	AL590369.1	9:132500609-132515326	NOTEST	6.03E-05	0.067862	10.1368	0	1	1
ENSG00000255825	ENSG00000255825	RP5-1154L15.1	12:673461-772945	NOTEST	0	0	0	0	1	1
ENSG00000255829	ENSG00000255829	RP11-20D14.3	12:8816606-8821607	NOTEST	0	0	0	0	1	1
ENSG00000255830	ENSG00000255830	RP11-385N17.3	12:114986658-114987657	NOTEST	0	0	0	0	1	1
ENSG00000255833	ENSG00000255833	TIFAB	5:134779904-134794387	NOTEST	0	0	0	0	1	1
ENSG00000255835	ENSG00000255835	RP4-559A3.7	1:226073981-226111978	NOTEST	0.147972	0.128761	-0.200629	0	1	1
ENSG00000255836	ENSG00000255836	RP11-157G21.2	12:7499280-7656489	NOTEST	0.0259895	0.0100527	-1.37035	0	1	1
ENSG00000255837	ENSG00000255837	TAS2R20	12:10977558-11324212	NOTEST	0.0736454	0.202428	1.45874	0	1	1
ENSG00000255838	ENSG00000255838	RP11-753B7.2	12:129337971-129469509	NOTEST	0	0	0	0	1	1
ENSG00000255839	ENSG00000255839	RP11-338K17.8	12:124155659-124192948	NOTEST	0	0	0	0	1	1
ENSG00000255840	ENSG00000255840	AC022555.1	8:61297146-61429354	NOTEST	0	0	0	0	1	1
ENSG00000255843	ENSG00000255843	AP000593.7	11:72003468-72145692	NOTEST	0.337868	0.600075	0.828684	0	1	1
ENSG00000255845	ENSG00000255845	RP11-804A23.1	11:60581404-60589212	NOTEST	0	0	0	0	1	1
ENSG00000255847	ENSG00000255847	RP11-167N4.2	11:73661363-73681411	NOTEST	0	0	0	0	1	1
ENSG00000255850	ENSG00000255850	TMEM5-AS1	12:63952692-64217675	NOTEST	0	0	0	0	1	1
ENSG00000255851	ENSG00000255851	AC061975.9	17:26525464-26525619	NOTEST	0	0	0	0	1	1
ENSG00000255853	ENSG00000255853	RP11-407A16.1	12:126995455-126996257	NOTEST	0	0	0	0	1	1
ENSG00000255854	ENSG00000255854	PPIAL4B	1:144275917-144521970	NOTEST	0	0	0	0	1	1
ENSG00000255855	ENSG00000255855	RP11-735A19.2	11:94782585-94784109	NOTEST	0	0	0	0	1	1
ENSG00000255856	ENSG00000255856	RP11-87C12.5	12:122445339-122499948	NOTEST	0	0	0	0	1	1
ENSG00000255858	ENSG00000255858	RP11-612B6.1	12:26272958-26986131	NOTEST	0	0	0	0	1	1
ENSG00000255860	ENSG00000255860	RP11-807H22.6	11:71874365-71920285	NOTEST	0	0	0	0	1	1
ENSG00000255863	ENSG00000255863	AC073610.5	12:49297200-49351334	NOTEST	0	0	0	0	1	1
ENSG00000255866	ENSG00000255866	RP11-221N13.2	12:65672422-66036152	NOTEST	0	0	0	0	1	1
ENSG00000255867	ENSG00000255867	DENND5B-AS1	12:31535156-31768600	NOTEST	0.0377988	0.083804	1.14868	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000255870	ENSG00000255870	RP11-667M19.5	11:113659952-113662088	NOTEST	0.0241522	0.0170496	-0.502418	0	1	1
ENSG00000255871	ENSG00000255871	RP11-69C13.1	12:16846733-16848911	NOTEST	0	0	0	0	1	1
ENSG00000255872	ENSG00000255872	RP11-613M10.9	9:37510888-38069210	NOTEST	0	0.0126039	inf	0	1	1
ENSG00000255874	ENSG00000255874	LINC00346	13:111521577-111522162	NOTEST	0.0717633	0.242454	1.75639	0	1	1
ENSG00000255875	ENSG00000255875	CTD-2102P23.1	19:53300661-53360902	NOTEST	0.0208027	0	#NAME?	0	1	1
ENSG00000255882	ENSG00000255882	RP11-290C10.1	12:10005582-10022735	NOTEST	0	0	0	0	1	1
ENSG00000255885	ENSG00000255885	RP11-815D16.1	12:7965107-8043744	NOTEST	0	0	0	0	1	1
ENSG00000255886	ENSG00000255886	RP11-196H14.2	12:64238072-64541637	NOTEST	0	0	0	0	1	1
ENSG00000255892	ENSG00000255892	RP11-459D22.2	12:18233802-18801348	NOTEST	0	0	0	0	1	1
ENSG00000255893	ENSG00000255893	RP11-685N10.1	11:94152894-94232749	NOTEST	0.175776	0.107775	-0.705716	0	1	1
ENSG00000255899	ENSG00000255899	XXbac-BPG299F13.16	6:31192118-31192835	NOTEST	0	0	0	0	1	1
ENSG00000255900	ENSG00000255900	RP11-407A16.8	12:127094579-127174868	NOTEST	0	0	0	0	1	1
ENSG00000255902	ENSG00000255902	AP001062.1	21:45748826-45760353	NOTEST	0	0	0	0	1	1
ENSG00000255903	ENSG00000255903	RP11-136I14.4	11:115448766-115448961	NOTEST	0	0	0	0	1	1
ENSG00000255905	ENSG00000255905	AL391319.1	6:168841830-169073984	NOTEST	0	0	0	0	1	1
ENSG00000255909	ENSG00000255909	RP11-841C19.3	12:19556978-19873735	NOTEST	0	0	0	0	1	1
ENSG00000255910	ENSG00000255910	RP11-405A12.2	12:19928384-20162871	NOTEST	0	0	0	0	1	1
ENSG00000255913	ENSG00000255913	AL805909.1	HSCHR6_MHC_QBL:31021148-31025764	NOTEST	0	0	0	0	1	1
ENSG00000255915	ENSG00000255915	AC113134.1	8:47172181-47172472	NOTEST	0	0	0	0	1	1
ENSG00000255916	ENSG00000255916	RP13-895J2.7	12:132906435-132908161	NOTEST	0	0	0	0	1	1
ENSG00000255919	ENSG00000255919	AC226150.3	12:133793795-133794261	NOTEST	0	0	0	0	1	1
ENSG00000255920	ENSG00000255920	CCND2-AS2	12:4357930-4414516	NOTEST	0	0	0	0	1	1
ENSG00000255921	ENSG00000255921	RP11-662I13.2	12:24964294-25113092	NOTEST	0	0	0	0	1	1
ENSG00000255923	ENSG00000255923	RP11-983C2.1	12:127349010-127349968	NOTEST	0	0	0	0	1	1
ENSG00000255928	ENSG00000255928	RP11-456I15.2	11:73386682-73472182	NOTEST	0	0	0	0	1	1
ENSG00000255929	ENSG00000255929	RP11-867G2.8	11:94277005-94658686	NOTEST	0.167046	0	#NAME?	0	1	1
ENSG00000255931	ENSG00000255931	RP11-286N22.10	11:61263911-61267548	NOTEST	0	0	0	0	1	1
ENSG00000255933	ENSG00000255933	RP11-495K9.5	12:132195625-132284282	NOTEST	0.491232	0.298632	-0.718035	0	1	1
ENSG00000255940	ENSG00000255940	REXO1L10P	8:86756717-86758745	NOTEST	0	0	0	0	1	1
ENSG00000255944	ENSG00000255944	RP11-407A16.4	12:127094579-127174868	NOTEST	0	0	0	0	1	1
ENSG00000255945	ENSG00000255945	RP11-351O2.1	12:128082712-128084260	NOTEST	0	0	0	0	1	1
ENSG00000255946	ENSG00000255946	RP11-173P15.7	12:121178272-121199395	NOTEST	0	0	0	0	1	1
ENSG00000255947	ENSG00000255947	RP11-855O10.3	11:61422136-61423174	NOTEST	0	0	0	0	1	1
ENSG00000255949	ENSG00000255949	AP003419.16	11:67195930-67202872	NOTEST	0	0	0	0	1	1
ENSG00000255951	ENSG00000255951	RP11-967K21.2	12:28286181-28732883	NOTEST	0	0	0	0	1	1
ENSG00000255958	ENSG00000255958	RP11-656E20.5	12:10365056-10375727	NOTEST	0	0	0	0	1	1
ENSG00000255959	ENSG00000255959	RP11-804A23.2	11:60603468-60623444	NOTEST	0.230591	0.0491688	-2.22952	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000255963	ENSG00000255963	PPIAL4A	1:147954634-147955419	NOTEST	0	0	0	0	1	1
ENSG00000255964	ENSG00000255964	RP11-69M1.3	12:8167619-8169002	NOTEST	0	0	0	0	1	1
ENSG00000255965	ENSG00000255965	RP11-408I18.9	12:124808960-125052135	NOTEST	0	0	0	0	1	1
ENSG00000255966	ENSG00000255966	RP5-940J5.3	12:6641455-6642664	NOTEST	0.145604	0.0345099	-2.07697	0	1	1
ENSG00000255967	ENSG00000255967	RP11-438L7.3	12:8786962-8815484	NOTEST	0.0521922	0.00545826	-3.25732	0	1	1
ENSG00000255968	ENSG00000255968	RP11-513G19.1	12:26272958-26986131	NOTEST	0.118895	0.0191357	-2.63535	0	1	1
ENSG00000255970	ENSG00000255970	RP11-43N5.1	12:68102826-68123255	NOTEST	0.0572237	0.0406311	-0.49403	0	1	1
ENSG00000255972	ENSG00000255972	RP11-324E6.8	12:123011792-123215390	NOTEST	0	0	0	0	1	1
ENSG00000255973	ENSG00000255973	RP11-592H6.3	12:5641034-6055398	NOTEST	0	0	0	0	1	1
ENSG00000255974	ENSG00000255974	CYP2A6	19:41277552-41406413	NOTEST	0.0357565	0	#NAME?	0	1	1
ENSG00000255976	ENSG00000255976	RAB11AP2	12:67525346-67525985	NOTEST	0	0	0	0	1	1
ENSG00000255977	ENSG00000255977	RP11-444J21.2	12:7759429-7759927	NOTEST	0	0	0	0	1	1
ENSG00000255980	ENSG00000255980	AP000439.1	11:69240457-69244389	NOTEST	0	0.0362514	inf	0	1	1
ENSG00000255982	ENSG00000255982	NXPE2P1	11:114383427-114384153	NOTEST	0	0	0	0	1	1
ENSG00000255983	ENSG00000255983	RP11-1038A11.1	12:5497754-5515817	NOTEST	0.101703	0.109126	0.101634	0	1	1
ENSG00000255986	ENSG00000255986	MT1JP	16:56669650-56670998	NOTEST	0	0	0	0	1	1
ENSG00000255987	ENSG00000255987	RP11-1094M14.4	17:33791267-33864880	NOTEST	0	0	0	0	1	1
ENSG00000255988	ENSG00000255988	TUBB4BP1	12:25562226-25801513	NOTEST	0	0	0	0	1	1
ENSG00000255989	ENSG00000255989	RP11-711M9.1	2:74213652-74220867	NOTEST	0.160905	0.10746	-0.582401	0	1	1
ENSG00000255991	ENSG00000255991	RP11-242C24.2	12:39860243-39861147	NOTEST	0	0	0	0	1	1
ENSG00000255992	ENSG00000255992	RP11-417L19.4	12:132409280-132428406	NOTEST	0	0.0869092	inf	0	1	1
ENSG00000255993	ENSG00000255993	PSMC1P9	12:18836102-18890991	NOTEST	0	0	0	0	1	1
ENSG00000255994	ENSG00000255994	CCDC177	14:70037482-70038032	NOTEST	0	0	0	0	1	1
ENSG00000255995	ENSG00000255995	HPRTP4	11:93724511-93724595	NOTEST	0	0	0	0	1	1
ENSG00000255996	ENSG00000255996	RP11-429A20.2	12:5141553-5142107	NOTEST	0	0	0	0	1	1
ENSG00000255998	ENSG00000255998	RP11-407A16.7	12:127175024-127180378	NOTEST	0	0	0	0	1	1
ENSG00000256004	ENSG00000256004	RP11-20D14.4	12:8831368-8832266	NOTEST	0	0	0	0	1	1
ENSG00000256006	ENSG00000256006	AC084117.3	11:18415934-18429972	NOTEST	0.574549	0.104964	-2.45253	0	1	1
ENSG00000256007	ENSG00000256007	ARAP1-AS1	11:72396113-72504726	NOTEST	0	0	0	0	1	1
ENSG00000256008	ENSG00000256008	RP11-728G15.1	12:121067907-121105127	NOTEST	0	0	0	0	1	1
ENSG00000256011	ENSG00000256011	RP11-392P7.7	12:13080659-13193613	NOTEST	0	0	0	0	1	1
ENSG00000256013	ENSG00000256013	RP11-27M24.1	16:10622278-10674555	NOTEST	0.00112374	0.000836135	-0.426503	0	1	1
ENSG00000256014	ENSG00000256014	AL031390.1	6:144438985-144439062	NOTEST	0	0	0	0	1	1
ENSG00000256018	ENSG00000256018	HIST1H3G	6:26271145-26271612	NOTEST	0	0	0	0	1	1
ENSG00000256019	ENSG00000256019	TAS2R63P	12:10977558-11324212	NOTEST	0.0359993	0	#NAME?	0	1	1
ENSG00000256020	ENSG00000256020	RP5-1154L15.2	12:673461-772945	NOTEST	0	0	0	0	1	1
ENSG00000256021	ENSG00000256021	TCEB1P31	12:21590548-21654603	NOTEST	0	0	0	0	1	1
ENSG00000256022	ENSG00000256022	RP11-526P6.1	12:128115792-128121012	NOTEST	0	0	0	0	1	1
ENSG00000256024	ENSG00000256024	CT476828.6	GL000228.1:92462-94085	NOTEST	0	0	0	0	1	1
ENSG00000256025	ENSG00000256025	CACNA1CAS4	12:2055219-2802108	NOTEST	0	0	0	0	1	1
ENSG00000256029	ENSG00000256029	RP11-190A12.7	1:159796539-159869953	NOTEST	0.0570927	0.127409	1.15809	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000256031	ENSG00000256031	RP11-364C11.3	12:119419299-119600856	NOTEST	0	0	0	0	1	1
ENSG00000256034	ENSG00000256034	RP11-707G14.1	11:73386682-73472182	NOTEST	0	0	0	0	1	1
ENSG00000256035	ENSG00000256035	AP000619.6	11:102617698-102714534	NOTEST	0	0	0	0	1	1
ENSG00000256037	ENSG00000256037	MRPL40P1	12:67745215-67745819	NOTEST	0.126816	0	#NAME?	0	1	1
ENSG00000256039	ENSG00000256039	RP11-291B21.2	12:10705961-10710648	NOTEST	0	0	0	0	1	1
ENSG00000256040	ENSG00000256040	PAPPA-AS1	9:118916082-119164601	NOTEST	0.021942	0.0261602	0.253674	0	1	1
ENSG00000256041	ENSG00000256041	RP11-959F10.4	11:62799974-62800575	NOTEST	0	0	0	0	1	1
ENSG00000256044	ENSG00000256044	RP11-324E6.4	12:123234027-123234133	NOTEST	0	0	0	0	1	1
ENSG00000256045	ENSG00000256045	MTRNR2L10	X:55207823-55208944	NOTEST	0	0	0	0	1	1
ENSG00000256049	ENSG00000256049	PADI6	1:17698690-17728195	NOTEST	0	0.0321623	inf	0	1	1
ENSG00000256050	ENSG00000256050	RP11-982M15.6	14:105147482-105151269	NOTEST	0.0392217	0.303538	2.95216	0	1	1
ENSG00000256056	ENSG00000256056	RP11-709A23.2	12:27676363-27848497	NOTEST	0.0196208	0	#NAME?	0	1	1
ENSG00000256062	ENSG00000256062	ABO	HG79_PATCH:136125798-136150736	NOTEST	0	0	0	0	1	1
ENSG00000256064	ENSG00000256064	RP11-117L5.4	12:130880681-131200826	NOTEST	0	0	0	0	1	1
ENSG00000256066	ENSG00000256066	AC013269.1	2:131217027-131267239	NOTEST	0	0	0	0	1	1
ENSG00000256069	ENSG00000256069	A2MP1	12:9381128-9428413	NOTEST	0.00375108	0	#NAME?	0	1	1
ENSG00000256070	ENSG00000256070	RP11-56H16.1	12:33607279-33608387	NOTEST	0	0	0	0	1	1
ENSG00000256071	ENSG00000256071	RP11-465L8.1	12:117890816-118406788	NOTEST	0	0	0	0	1	1
ENSG00000256072	ENSG00000256072	RP11-335I12.2	12:66582658-66651214	NOTEST	0	0	0	0	1	1
ENSG00000256075	ENSG00000256075	RP11-81H14.3	12:68867520-68868682	NOTEST	0	0	0	0	1	1
ENSG00000256077	ENSG00000256077	RP11-335O4.1	12:67964976-67983767	NOTEST	0	0	0	0	1	1
ENSG00000256079	ENSG00000256079	RP11-318G8.2	12:25562226-25801513	NOTEST	0	0	0	0	1	1
ENSG00000256081	ENSG00000256081	AE000658.25	14:22053413-22054404	NOTEST	0.0330608	0	#NAME?	0	1	1
ENSG00000256083	ENSG00000256083	RP11-366L20.3	12:66151799-66360075	NOTEST	0.196699	0	#NAME?	0	1	1
ENSG00000256084	ENSG00000256084	RP11-134N1.2	12:14369523-14374231	NOTEST	0	0.0448183	inf	0	1	1
ENSG00000256085	ENSG00000256085	RP11-337L12.1	12:129556269-130388211	NOTEST	0	0	0	0	1	1
ENSG00000256091	ENSG00000256091	RP11-627G1.1	11:113582441-113583120	NOTEST	0	0	0	0	1	1
ENSG00000256092	ENSG00000256092	hsa-mir-8072	12:123773655-123850660	NOTEST	0.270589	0.254008	-0.0912291	0	1	1
ENSG00000256093	ENSG00000256093	RP11-158L12.2	12:125540904-125541127	NOTEST	0	0	0	0	1	1
ENSG00000256097	ENSG00000256097	LINC00696	3:52097075-52097567	NOTEST	0	0	0	0	1	1
ENSG00000256098	ENSG00000256098	RP11-691F15.1	11:73723762-74035750	NOTEST	0	0	0	0	1	1
ENSG00000256100	ENSG00000256100	AP000721.4	11:63742078-63933578	NOTEST	0	0.101631	inf	0	1	1
ENSG00000256101	ENSG00000256101	RP11-90D4.3	12:8407122-8549399	NOTEST	0	0	0	0	1	1
ENSG00000256103	ENSG00000256103	RP1-96H9.5	12:6379324-6379591	NOTEST	0	0	0	0	1	1
ENSG00000256108	ENSG00000256108	RP13-672B3.5	12:133302253-133338474	NOTEST	0.0682635	0	#NAME?	0	1	1
ENSG00000256115	ENSG00000256115	RP11-319E16.1	12:5343162-5352317	NOTEST	0	0.0198227	inf	0	1	1
ENSG00000256116	ENSG00000256116	RP11-783K16.14	11:63974149-64001824	NOTEST	0.203302	0.361548	0.830565	0	1	1
ENSG00000256120	ENSG00000256120	RP11-778H2.1	12:24366189-24715524	NOTEST	0	0	0	0	1	1
ENSG00000256122	ENSG00000256122	AC093334.1	15:67263383-67263457	NOTEST	0	0	0	0	1	1
ENSG00000256125	ENSG00000256125	RP5-944M2.4	12:126927026-126957336	NOTEST	0	0	0	0	1	1

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ENSG00000256134	ENSG00000256134	RP11-674J14.3	12:16064105-16190220	NOTEST	0.0270566	0.125148	2.20958	0	1	1
ENSG00000256136	ENSG00000256136	RP11-113C12.8	12:8559428-8559791	NOTEST	0	0	0	0	1	1
ENSG00000256137	ENSG00000256137	RP11-174M13.2	12:129556269-130388211	NOTEST	0	0	0	0	1	1
ENSG00000256138	ENSG00000256138	RP11-127B1.1	12:18233802-18801348	NOTEST	0	0	0	0	1	1
ENSG00000256142	ENSG00000256142	AL513327.1	1:33722145-33766320	NOTEST	0	0	0	0	1	1
ENSG00000256143	ENSG00000256143	Z95704.5	4:123965-157779	NOTEST	0.0621068	0.0229551	-1.43593	0	1	1
ENSG00000256146	ENSG00000256146	RP11-319E16.2	12:5399645-5492819	NOTEST	0	0.0222573	inf	0	1	1
ENSG00000256148	ENSG00000256148	RP11-809N8.5	11:73111531-73309234	NOTEST	0	0	0	0	1	1
ENSG00000256149	ENSG00000256149	RP11-357K6.3	12:119287158-119346735	NOTEST	0	0	0	0	1	1
ENSG00000256150	ENSG00000256150	RP11-885B4.1	12:2851791-2881074	NOTEST	0	0	0	0	1	1
ENSG00000256151	ENSG00000256151	RP11-76C10.5	12:131438451-131626014	NOTEST	0.0134286	0.0323861	1.27007	0	1	1
ENSG00000256152	ENSG00000256152	RP11-463O12.3	12:123349881-123380991	NOTEST	0.00387691	0	#NAME?	0	1	1
ENSG00000256155	ENSG00000256155	RP11-277P12.9	12:10511062-10513644	NOTEST	0	0	0	0	1	1
ENSG00000256157	ENSG00000256157	RP11-80N2.2	12:20963635-21392180	NOTEST	0	0	0	0	1	1
ENSG00000256159	ENSG00000256159	RP11-820K3.4	12:31535156-31768600	NOTEST	0	0.034027	inf	0	1	1
ENSG00000256162	ENSG00000256162	SMLR1	6:131148545-131158275	NOTEST	0	0.00445529	inf	0	1	1
ENSG00000256164	ENSG00000256164	CCND2-AS1	12:4357930-4414516	NOTEST	0	0	0	0	1	1
ENSG00000256166	ENSG00000256166	XXbac-BPG248L24.13	6:31261684-31269419	NOTEST	0	0	0	0	1	1
ENSG00000256167	ENSG00000256167	ATF4P4	11:113659952-113662088	NOTEST	0	0.0357509	inf	0	1	1
ENSG00000256171	ENSG00000256171	GCSHP4	12:8276227-8371507	NOTEST	0	0	0	0	1	1
ENSG00000256172	ENSG00000256172	RP11-473M14.3	12:67834777-67836339	NOTEST	0	0	0	0	1	1
ENSG00000256176	ENSG00000256176	RP11-627K11.3	12:31433517-31479992	NOTEST	0	0	0	0	1	1
ENSG00000256178	ENSG00000256178	AC004889.1	7:143880547-143883173	NOTEST	0.00092001	0.000817421	-0.17057	0	1	1
ENSG00000256181	ENSG00000256181	AP000438.4	11:62847411-63137190	NOTEST	0	0	0	0	1	1
ENSG00000256182	ENSG00000256182	AL590325.1	X:134193714-134257880	NOTEST	0	0	0	0	1	1
ENSG00000256185	ENSG00000256185	RP11-612B6.2	12:26272958-26986131	NOTEST	0.689043	0	#NAME?	0	1	1
ENSG00000256186	ENSG00000256186	AL732372.1	1:317719-461954	NOTEST	0	0	0	0	1	1
ENSG00000256188	ENSG00000256188	TAS2R30	12:10977558-11324212	NOTEST	0	0	0	0	1	1
ENSG00000256189	ENSG00000256189	RP11-167N4.5	11:73702327-73703225	NOTEST	0	0	0	0	1	1
ENSG00000256192	ENSG00000256192	RP11-290I21.2	12:64616116-64790845	NOTEST	0	0	0	0	1	1
ENSG00000256193	ENSG00000256193	LINC00507	12:128399916-128436097	NOTEST	0	0	0	0	1	1
ENSG00000256195	ENSG00000256195	RP11-64D24.4	11:114231356-114250767	NOTEST	0	0	0	0	1	1
ENSG00000256196	ENSG00000256196	RP11-881M11.4	11:60680637-60720002	NOTEST	0.0770357	0.0166733	-2.20799	0	1	1
ENSG00000256197	ENSG00000256197	TSPAN9-IT1	12:3186520-3395730	NOTEST	0	0	0	0	1	1
ENSG00000256199	ENSG00000256199	RP11-439H13.2	12:64900945-64927418	NOTEST	0	0	0	0	1	1
ENSG00000256204	ENSG00000256204	RP11-243M5.1	12:131438451-131626014	NOTEST	0	0	0	0	1	1
ENSG00000256209	ENSG00000256209	RP11-897M7.1	12:131953855-131977496	NOTEST	0	0	0	0	1	1
ENSG00000256211	ENSG00000256211	RP11-1018J11.1	12:17142059-17142870	NOTEST	0	0.109496	inf	0	1	1
ENSG00000256212	ENSG00000256212	AL773602.1	21:45917774-46131495	NOTEST	0	0	0	0	1	1
ENSG00000256218	ENSG00000256218	RP11-1038A11.2	12:5399645-5492819	NOTEST	0	0.0276794	inf	0	1	1

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ENSG00000256221	ENSG00000256221	AE000661.36	14:22801351-22803115	NOTEST	0	0	0	0	1	1
ENSG00000256222	ENSG00000256222	MTRNR2L3	20:55926065-55954267	NOTEST	0	0.0172416	inf	0	1	1
ENSG00000256225	ENSG00000256225	AL590710.1	9:136627015-136857726	NOTEST	0	0.00421082	inf	0	1	1
ENSG00000256226	ENSG00000256226	RP11-582E3.2	12:27258083-27314326	NOTEST	0	0	0	0	1	1
ENSG00000256229	ENSG00000256229	ZNF486	19:20188802-20432114	NOTEST	0.019471	0.0214868	0.14212	0	1	1
ENSG00000256232	ENSG00000256232	RP11-771K4.1	12:31516414-31522235	NOTEST	0	0	0	0	1	1
ENSG00000256234	ENSG00000256234	RP11-283G6.4	12:26272958-26986131	NOTEST	0	0	0	0	1	1
ENSG00000256235	ENSG00000256235	SMIM3	5:150157507-150176297	NOTEST	0	0	0	0	1	1
ENSG00000256237	ENSG00000256237	RP11-434C1.2	12:11694328-11743303	NOTEST	0	0	0	0	1	1
ENSG00000256238	ENSG00000256238	RP11-473N11.2	12:16500075-16763528	NOTEST	0.333375	0.247324	-0.430744	0	1	1
ENSG00000256240	ENSG00000256240	AC010620.1	19:21264964-21308073	NOTEST	0	0.679826	inf	0	1	1
ENSG00000256243	ENSG00000256243	RPL7AP3	14:35514112-35786699	NOTEST	0	0	0	0	1	1
ENSG00000256248	ENSG00000256248	RP11-123O10.4	12:67285655-67490186	NOTEST	0.4205	0.641864	0.610162	0	1	1
ENSG00000256249	ENSG00000256249	RP11-324E6.6	12:123011792-123215390	NOTEST	0	0	0	0	1	1
ENSG00000256250	ENSG00000256250	RP11-989F5.1	12:131274144-131323811	NOTEST	0.335703	0.106921	-1.65064	0	1	1
ENSG00000256252	ENSG00000256252	CT476828.7	GL000228.1:89156-90779	NOTEST	0	0	0	0	1	1
ENSG00000256254	ENSG00000256254	AP000647.3	11:102617698-102714534	NOTEST	0	0	0	0	1	1
ENSG00000256256	ENSG00000256256	RP11-443N24.4	12:26035887-26038788	NOTEST	0	0	0	0	1	1
ENSG00000256257	ENSG00000256257	CACNA1CIT2	12:2055219-2802108	NOTEST	0	0	0	0	1	1
ENSG00000256258	ENSG00000256258	RP11-495K9.9	12:132106435-132107748	NOTEST	0	0	0	0	1	1
ENSG00000256259	ENSG00000256259	RP11-366L20.4	12:66421504-66424846	NOTEST	0	0	0	0	1	1
ENSG00000256261	ENSG00000256261	AC104698.1	2:30454396-30546596	NOTEST	0.332593	0.437647	0.396012	0	1	1
ENSG00000256262	ENSG00000256262	USP30-AS1	12:109460893-109525831	NOTEST	0.0870848	0.0240798	-1.8546	0	1	1
ENSG00000256263	ENSG00000256263	DDX11L8	12:92238-93430	NOTEST	0	0	0	0	1	1
ENSG00000256271	ENSG00000256271	CACNA1CAS2	12:2055219-2802108	NOTEST	0	0	0	0	1	1
ENSG00000256273	ENSG00000256273	RP11-71J4.2	12:68726667-68845443	NOTEST	0	0	0	0	1	1
ENSG00000256274	ENSG00000256274	TAS2R64P	12:10977558-11324212	NOTEST	0	0.014605	inf	0	1	1
ENSG00000256276	ENSG00000256276	RP5-916L7.2	12:126468247-126470780	NOTEST	0	0	0	0	1	1
ENSG00000256278	ENSG00000256278	RP11-182J1.5	15:85144216-85171027	NOTEST	0.0495292	0.0633382	0.354798	0	1	1
ENSG00000256280	ENSG00000256280	RP11-466C23.5	11:63602138-63602415	NOTEST	0	0	0	0	1	1
ENSG00000256281	ENSG00000256281	RP11-136I14.2	11:115403039-115403671	NOTEST	0	0	0	0	1	1
ENSG00000256282	ENSG00000256282	RP11-504G3.4	11:18617005-18621230	NOTEST	0.218023	0.253682	0.218542	0	1	1
ENSG00000256283	ENSG00000256283	RP11-365O10.1	12:15260716-15750333	NOTEST	0	0	0	0	1	1
ENSG00000256285	ENSG00000256285	OSBPL9P5	12:66741210-67197966	NOTEST	0	0	0	0	1	1
ENSG00000256286	ENSG00000256286	RP11-983C2.3	12:127359366-127360778	NOTEST	0	0	0	0	1	1
ENSG00000256287	ENSG00000256287	RP11-664H17.1	12:20167713-20251802	NOTEST	0	0	0	0	1	1
ENSG00000256288	ENSG00000256288	RP11-277P12.10	12:10485459-10490891	NOTEST	0	0	0	0	1	1
ENSG00000256292	ENSG00000256292	RP11-955H22.1	12:127759011-127768828	NOTEST	0	0	0	0	1	1
ENSG00000256293	ENSG00000256293	RP11-114F3.2	12:64616116-64790845	NOTEST	0	0.149855	inf	0	1	1
ENSG00000256295	ENSG00000256295	AC005086.2	7:101458958-101927249	NOTEST	0	0	0	0	1	1
ENSG00000256298	ENSG00000256298	RP11-474D1.1	12:130531676-130532921	NOTEST	0	0	0	0	1	1

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ENSG00000256301	ENSG00000256301	AC138031.2	5:180878877-180878968	NOTEST	0	0	0	0	1	1
ENSG00000256304	ENSG00000256304	RP11-512M8.3	12:122755978-122907179	NOTEST	0.0930743	0.0533153	-0.803835	0	1	1
ENSG00000256305	ENSG00000256305	AL359757.1	13:25715793-25716046	NOTEST	0	0	0	0	1	1
ENSG00000256306	ENSG00000256306	RP11-4N23.1	12:13679787-14133053	NOTEST	0.0299972	0	#NAME?	0	1	1
ENSG00000256309	ENSG00000256309	AC009469.1	2:218664511-218867718	NOTEST	0.0995007	0.27062	1.44349	0	1	1
ENSG00000256310	ENSG00000256310	NDUFA5P6	12:127008793-127009172	NOTEST	0	0	0	0	1	1
ENSG00000256311	ENSG00000256311	RP11-64B16.5	12:119663638-119696822	NOTEST	0	0	0	0	1	1
ENSG00000256312	ENSG00000256312	RP13-977J11.8	12:132674757-132675542	NOTEST	0	0	0	0	1	1
ENSG00000256314	ENSG00000256314	RP11-338E21.3	12:65004292-65091347	NOTEST	0	0	0	0	1	1
ENSG00000256315	ENSG00000256315	AP000462.1	11:115039937-115375675	NOTEST	0	0	0	0	1	1
ENSG00000256316	ENSG00000256316	HIST1H3F	6:26250369-26250835	NOTEST	0.578159	0.157579	-1.8754	0	1	1
ENSG00000256321	ENSG00000256321	RP11-153K16.1	12:22852792-23404433	NOTEST	0.0878896	0.0691838	-0.345258	0	1	1
ENSG00000256323	ENSG00000256323	AL049542.1	16:475618-573011	NOTEST	0.345669	1.05386	1.60823	0	1	1
ENSG00000256325	ENSG00000256325	RP11-611O2.1	12:69201955-69365350	NOTEST	0.139035	0	#NAME?	0	1	1
ENSG00000256331	ENSG00000256331	NIFKP3	12:7756945-7757810	NOTEST	0.0214023	0	#NAME?	0	1	1
ENSG00000256339	ENSG00000256339	RP11-233G1.4	12:14956505-15059520	NOTEST	0	0	0	0	1	1
ENSG00000256340	ENSG00000256340	ABCC6P1	16:18581769-18609650	NOTEST	0	0	0	0	1	1
ENSG00000256341	ENSG00000256341	RP11-21A7A.3	11:63742078-63933578	NOTEST	0	0.350943	inf	0	1	1
ENSG00000256342	ENSG00000256342	RP3-446N13.1	12:126580537-126588481	NOTEST	0	0	0	0	1	1
ENSG00000256343	ENSG00000256343	RP11-662M24.1	12:130880681-131200826	NOTEST	0	0	0	0	1	1
ENSG00000256344	ENSG00000256344	CT476828.8	GL000228.1:79238-80861	NOTEST	0	0	0	0	1	1
ENSG00000256346	ENSG00000256346	RP11-72J9.1	12:14322679-14322811	NOTEST	0	0	0	0	1	1
ENSG00000256347	ENSG00000256347	OR8R1P	11:72959823-72960912	NOTEST	0	0	0	0	1	1
ENSG00000256349	ENSG00000256349	CTD-3074O7.11	11:66234215-66313709	NOTEST	0	0	0	0	1	1
ENSG00000256350	ENSG00000256350	AE000658.30	14:22167175-22167373	NOTEST	0	0	0	0	1	1
ENSG00000256351	ENSG00000256351	RP1-7G5.5	12:110288747-110318293	NOTEST	0	0	0	0	1	1
ENSG00000256352	ENSG00000256352	AL109922.2	6:64345724-66417118	NOTEST	0	0	0	0	1	1
ENSG00000256353	ENSG00000256353	RP11-686N4.1	12:22852792-23404433	NOTEST	0	0	0	0	1	1
ENSG00000256354	ENSG00000256354	AC104304.1	3:46556912-46668033	NOTEST	0	0	0	0	1	1
ENSG00000256355	ENSG00000256355	NTAN1P3	12:67818051-67818766	NOTEST	0	0	0	0	1	1
ENSG00000256356	ENSG00000256356	HSPA8P5	12:4206616-4208685	NOTEST	0.0219943	0.0176573	-0.316866	0	1	1
ENSG00000256357	ENSG00000256357	RP11-349I1.2	14:94896969-94946026	NOTEST	0	0	0	0	1	1
ENSG00000256358	ENSG00000256358	RPL31P57	17:62385675-62386050	NOTEST	0	0	0	0	1	1
ENSG00000256360	ENSG00000256360	RP11-707G14.7	11:73639577-73641417	NOTEST	0.209724	0	#NAME?	0	1	1
ENSG00000256361	ENSG00000256361	RP11-613F22.6	11:18477370-18548779	NOTEST	0.056661	0.214907	1.92329	0	1	1
ENSG00000256362	ENSG00000256362	RP11-955H22.3	12:127808699-127824617	NOTEST	0	0	0	0	1	1
ENSG00000256364	ENSG00000256364	RP11-173P15.3	12:121124671-121139667	NOTEST	0.14591	0.109732	-0.411105	0	1	1
ENSG00000256371	ENSG00000256371	RP11-359J14.3	12:22726358-22728039	NOTEST	0	0	0	0	1	1
ENSG00000256372	ENSG00000256372	RP11-428G5.4	12:32005954-32006341	NOTEST	0	0	0	0	1	1
ENSG00000256373	ENSG00000256373	RP11-711K1.8	12:11365125-11404303	NOTEST	0	0	0	0	1	1
ENSG00000256374	ENSG00000256374	PPIAL4D	1:148201751-148202536	NOTEST	0	0	0	0	1	1

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ENSG00000256377	ENSG00000256377	RP11-1060J15.4	12:27849320-27863703	NOTEST	0.0765617	0.0776166	0.0197419	0	1	1
ENSG00000256378	ENSG00000256378	RP11-993B23.1	12:28088455-28088682	NOTEST	0	0	0	0	1	1
ENSG00000256379	ENSG00000256379	TRAV8-5	14:22371256-22371778	NOTEST	0	0	0	0	1	1
ENSG00000256381	ENSG00000256381	RP11-500M8.4	12:4671369-4960277	NOTEST	0	0.0262701	inf	0	1	1
ENSG00000256383	ENSG00000256383	AC020910.2	19:35166997-35168486	NOTEST	0	0	0	0	1	1
ENSG00000256385	ENSG00000256385	AE000658.27	14:22080077-22080535	NOTEST	0	0	0	0	1	1
ENSG00000256386	ENSG00000256386	AP000244.1	21:32201356-32202078	NOTEST	0	0.273218	inf	0	1	1
ENSG00000256389	ENSG00000256389	RP11-606D9.1	12:17662286-17768397	NOTEST	0	0	0	0	1	1
ENSG00000256391	ENSG00000256391	SDIM1	6:165740775-166401536	NOTEST	0.0587986	0.0453012	-0.376231	0	1	1
ENSG00000256393	ENSG00000256393	AC138123.2	12:93392993-93609455	NOTEST	0	0	0	0	1	1
ENSG00000256394	ENSG00000256394	ASIC5	4:156750880-156841558	NOTEST	0	0	0	0	1	1
ENSG00000256399	ENSG00000256399	RP11-274J7.3	12:64238072-64541637	NOTEST	0.0257641	0	#NAME?	0	1	1
ENSG00000256400	ENSG00000256400	RP11-673D15.7	12:10977558-11324212	NOTEST	0	0	0	0	1	1
ENSG00000256403	ENSG00000256403	RP11-7N14.1	11:72003468-72145692	NOTEST	0	0	0	0	1	1
ENSG00000256404	ENSG00000256404	AC109133.1	5:59892738-59996017	NOTEST	0	0	0	0	1	1
ENSG00000256407	ENSG00000256407	RP11-446E24.4	1:54598746-54879152	NOTEST	0.0104326	0	#NAME?	0	1	1
ENSG00000256420	ENSG00000256420	OSBPL9P4	12:66741210-67197966	NOTEST	0.00911684	0	#NAME?	0	1	1
ENSG00000256424	ENSG00000256424	RP11-495K9.7	12:132131657-132132666	NOTEST	0	0	0	0	1	1
ENSG00000256425	ENSG00000256425	AC092989.1	3:135656149-135656226	NOTEST	0	0	0	0	1	1
ENSG00000256427	ENSG00000256427	RP11-118B22.4	12:9381128-9428413	NOTEST	0	0	0	0	1	1
ENSG00000256433	ENSG00000256433	RP1-102E24.8	12:6503070-6504235	NOTEST	0.452272	0.172721	-1.38875	0	1	1
ENSG00000256436	ENSG00000256436	TAS2R31	12:10977558-11324212	NOTEST	0.0812298	0.14603	0.84618	0	1	1
ENSG00000256439	ENSG00000256439	AC008731.1	16:24930705-25026987	NOTEST	0.164562	0.0355918	-2.20902	0	1	1
ENSG00000256440	ENSG00000256440	RP11-443N24.3	12:25984349-25987116	NOTEST	0	0	0	0	1	1
ENSG00000256441	ENSG00000256441	RP11-300I6.5	11:69552065-69552785	NOTEST	0	0	0	0	1	1
ENSG00000256442	ENSG00000256442	RP11-705C15.4	12:9787187-9811008	NOTEST	0	0.0291946	inf	0	1	1
ENSG00000256443	ENSG00000256443	RP11-794G24.1	11:61282784-61348620	NOTEST	0	0.0410502	inf	0	1	1
ENSG00000256448	ENSG00000256448	RP11-809N8.4	11:73111531-73309234	NOTEST	0	0	0	0	1	1
ENSG00000256450	ENSG00000256450	RP11-424M22.1	12:16500075-16763528	NOTEST	0	0	0	0	1	1
ENSG00000256452	ENSG00000256452	RP11-667M19.10	11:113668595-113746292	NOTEST	0	0	0	0	1	1
ENSG00000256453	ENSG00000256453	DND1	5:140044260-140086248	NOTEST	0	0.0941211	inf	0	1	1
ENSG00000256456	ENSG00000256456	CT476828.9	GL000228.1:108992-110615	NOTEST	0	0	0	0	1	1
ENSG00000256458	ENSG00000256458	RP11-363J17.1	2:204192941-204400133	NOTEST	0	0	0	0	1	1
ENSG00000256462	ENSG00000256462	RP11-116G8.5	10:5556206-5568225	NOTEST	0	0	0	0	1	1
ENSG00000256463	ENSG00000256463	SALL3	18:76740274-76762677	NOTEST	0	0.00279095	inf	0	1	1
ENSG00000256464	ENSG00000256464	RP11-613F22.5	11:18477370-18548779	NOTEST	0.0822201	0.188264	1.19519	0	1	1
ENSG00000256465	ENSG00000256465	RP11-428G5.6	12:32046303-32046636	NOTEST	0	0	0	0	1	1
ENSG00000256466	ENSG00000256466	AP003026.1	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000256469	ENSG00000256469	RP11-856F16.2	11:94277005-94658686	NOTEST	0	0	0	0	1	1

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ENSG00000256474	ENSG00000256474	TRAV11	14:22297691-22298223	NOTEST	0	0	0	0	1	1
ENSG00000256480	ENSG00000256480	RP11-185H22.1	12:7390027-7393582	NOTEST	0	0	0	0	1	1
ENSG00000256481	ENSG00000256481	RP11-21A7A.4	11:63742078-63933578	NOTEST	0.0264777	0	#NAME?	0	1	1
ENSG00000256482	ENSG00000256482	RP11-625L16.3	12:24964294-25113092	NOTEST	0	0	0	0	1	1
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ENSG00000256490	ENSG00000256490	CT476828.10	GL000228.1:72626-74249	NOTEST	0	0	0	0	1	1
ENSG00000256492	ENSG00000256492	AL118508.1	20:23059985-23066977	NOTEST	0	0	0	0	1	1
ENSG00000256494	ENSG00000256494	RP5-944M2.1	12:126885337-126890074	NOTEST	0	0	0	0	1	1
ENSG00000256496	ENSG00000256496	RP11-955H22.4	12:127802253-127804531	NOTEST	0	0.0155889	inf	0	1	1
ENSG00000256498	ENSG00000256498	AL928654.1	14:105675622-105864484	NOTEST	0.071515	0.229896	1.68466	0	1	1
ENSG00000256499	ENSG00000256499	CTC-465D4.1	12:20273913-20282747	NOTEST	0	0	0	0	1	1
ENSG00000256502	ENSG00000256502	RP11-955H22.2	12:127828802-127828947	NOTEST	0	0	0	0	1	1
ENSG00000256504	ENSG00000256504	RP11-1060J15.7	12:27849320-27863703	NOTEST	0	0	0	0	1	1
ENSG00000256508	ENSG00000256508	RP11-554A11.6	11:68771861-68785915	NOTEST	0	0	0	0	1	1
ENSG00000256512	ENSG00000256512	RP11-860B13.3	12:27932753-27955973	NOTEST	0	0	0	0	1	1
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ENSG00000256518	ENSG00000256518	RP11-807H22.5	11:71869865-71870905	NOTEST	0	0	0	0	1	1
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ENSG00000256527	ENSG00000256527	AP002833.1	11:126225534-126875953	NOTEST	0	0	0	0	1	1
ENSG00000256528	ENSG00000256528	AP006285.1	11:1686826-1689086	NOTEST	0	0	0	0	1	1
ENSG00000256530	ENSG00000256530	AC019294.1	15:76016317-76055662	NOTEST	0.380918	0.453415	0.251351	0	1	1
ENSG00000256533	ENSG00000256533	RP11-212D19.5	11:114323785-114324845	NOTEST	0	0	0	0	1	1
ENSG00000256538	ENSG00000256538	RP11-847H18.3	12:34175215-34209675	NOTEST	0.0238433	0	#NAME?	0	1	1
ENSG00000256540	ENSG00000256540	RP11-598F7.6	12:175930-291565	NOTEST	0	0	0	0	1	1
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ENSG00000256551	ENSG00000256551	RP13-653N12.1	12:128571529-128602677	NOTEST	0	0	0	0	1	1
ENSG00000256552	ENSG00000256552	RP11-113C12.4	12:8407122-8549399	NOTEST	0	0	0	0	1	1
ENSG00000256553	ENSG00000256553	TRAV1-2	14:22111108-22111798	NOTEST	0	0	0	0	1	1
ENSG00000256557	ENSG00000256557	RP11-1060J15.3	12:27676363-27848497	NOTEST	0	0	0	0	1	1
ENSG00000256560	ENSG00000256560	RP11-256L11.1	12:109785707-109974507	NOTEST	0.0773857	0	#NAME?	0	1	1
ENSG00000256563	ENSG00000256563	NANOGNBP2	12:133548923-133549476	NOTEST	0	0	0	0	1	1
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ENSG00000256566	ENSG00000256566	RP4-734P14.4	20:2442279-2505348	NOTEST	0.353431	0	#NAME?	0	1	1
ENSG00000256568	ENSG00000256568	RP11-800A3.3	11:72887738-72892741	NOTEST	0	0	0	0	1	1
ENSG00000256571	ENSG00000256571	RP11-274J7.2	12:64238072-64541637	NOTEST	0	0.0306545	inf	0	1	1
ENSG00000256574	ENSG00000256574	OR13A1	10:45798101-45811056	NOTEST	0	0	0	0	1	1
ENSG00000256576	ENSG00000256576	RP13-977J11.2	12:132671286-132674240	NOTEST	0.205594	0.162541	-0.338989	0	1	1
ENSG00000256577	ENSG00000256577	RP11-283I3.2	12:299242-323736	NOTEST	0	0	0	0	1	1
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ENSG00000256582	ENSG00000256582	RP11-75L1.1	12:9856672-9861946	NOTEST	0	0.02707	inf	0	1	1
ENSG00000256588	ENSG00000256588	RP11-613F22.8	11:18477370-18548779	NOTEST	0.0920911	0.050385	-0.870068	0	1	1
ENSG00000256589	ENSG00000256589	ENPP7P5	12:8407122-8549399	NOTEST	0	0	0	0	1	1
ENSG00000256590	ENSG00000256590	TRDV3	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000256596	ENSG00000256596	RP11-522N14.2	12:124247041-124800570	NOTEST	0	0.00553422	inf	0	1	1
ENSG00000256597	ENSG00000256597	RP11-749H20.4	12:128366161-128367536	NOTEST	0	0	0	0	1	1
ENSG00000256599	ENSG00000256599	AC020663.1	16:4853203-4932361	NOTEST	0	0.0185054	inf	0	1	1
ENSG00000256603	ENSG00000256603	RP11-667M19.2	11:113603908-113644533	NOTEST	0.0357952	0	#NAME?	0	1	1
ENSG00000256604	ENSG00000256604	AC093668.2	7:102120178-102121095	NOTEST	0	0.0140383	inf	0	1	1
ENSG00000256609	ENSG00000256609	RP11-64B16.4	12:119616446-119658936	NOTEST	0	0	0	0	1	1
ENSG00000256612	ENSG00000256612	CYP2B7P	19:41430123-41456565	NOTEST	0	0	0	0	1	1
ENSG00000256614	ENSG00000256614	RP13-7D7.1	12:34402415-34402893	NOTEST	0	0	0	0	1	1
ENSG00000256615	ENSG00000256615	RP11-59N23.3	12:21788275-21928515	NOTEST	0	0	0	0	1	1
ENSG00000256618	ENSG00000256618	MTRNR2L1	17:22022436-22025022	NOTEST	0	0	0	0	1	1
ENSG00000256619	ENSG00000256619	CT476828.12	GL000228.1:99074-100697	NOTEST	0	0	0	0	1	1
ENSG00000256625	ENSG00000256625	RP11-582E3.4	12:27258083-27314326	NOTEST	0.298189	0.459821	0.624846	0	1	1
ENSG00000256626	ENSG00000256626	RP11-133L14.2	12:10183275-10218565	NOTEST	0	0	0	0	1	1
ENSG00000256627	ENSG00000256627	RP11-6B19.3	12:15773091-16035263	NOTEST	0	0	0	0	1	1
ENSG00000256629	ENSG00000256629	TAS2R67P	12:11332271-11333061	NOTEST	0	0.0338788	inf	0	1	1
ENSG00000256630	ENSG00000256630	RP11-428I12.1	12:128751947-129192460	NOTEST	0	0	0	0	1	1
ENSG00000256631	ENSG00000256631	CT476828.13	GL000228.1:75932-77555	NOTEST	0	0	0	0	1	1
ENSG00000256632	ENSG00000256632	RP13-672B3.2	12:133264191-133299228	NOTEST	0	0	0	0	1	1
ENSG00000256633	ENSG00000256633	RP11-169D4.2	11:72287184-72385635	NOTEST	0	0.178033	inf	0	1	1
ENSG00000256637	ENSG00000256637	RP11-76I14.1	2:104473427-104694236	NOTEST	0	0	0	0	1	1
ENSG00000256640	ENSG00000256640	RP11-666F17.2	12:26272958-26986131	NOTEST	0	0	0	0	1	1
ENSG00000256642	ENSG00000256642	LINC00273	16:33961051-33962503	NOTEST	0	0	0	0	1	1
ENSG00000256643	ENSG00000256643	RP11-349K16.1	12:128508332-128511711	NOTEST	0	0	0	0	1	1
ENSG00000256650	ENSG00000256650	RERG-IT1	12:15260716-15750333	NOTEST	0	0	0	0	1	1
ENSG00000256651	ENSG00000256651	RP11-144O23.8	12:10977558-11324212	NOTEST	0.0351473	0.0271265	-0.373711	0	1	1
ENSG00000256654	ENSG00000256654	RP11-429A20.4	12:5132847-5134758	NOTEST	0	0	0	0	1	1
ENSG00000256655	ENSG00000256655	TMEM75	8:128806778-129113499	NOTEST	0.0114723	0.132209	3.52659	0	1	1
ENSG00000256657	ENSG00000256657	RP11-144O23.20	12:11348986-11349908	NOTEST	0	0	0	0	1	1
ENSG00000256658	ENSG00000256658	RP11-180M15.4	12:12876230-12876945	NOTEST	0	0	0	0	1	1
ENSG00000256659	ENSG00000256659	RP13-653N12.2	12:128602761-128606497	NOTEST	0	0	0	0	1	1
ENSG00000256660	ENSG00000256660	CLEC12B	12:10100735-10183205	NOTEST	0.0251291	0.0433628	0.787101	0	1	1
ENSG00000256661	ENSG00000256661	A2ML1-AS1	12:8834195-9039597	NOTEST	0	0	0	0	1	1
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ENSG00000256671	ENSG00000256671	LIMS3L	2:111143953-111230652	NOTEST	0	0	0	0	1	1
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ENSG00000256678	ENSG00000256678	RP11-611O2.2	12:69198790-69199259	NOTEST	0	0	0	0	1	1
ENSG00000256681	ENSG00000256681	CCDC58P5	11:73498360-73576178	NOTEST	0	0	0	0	1	1
ENSG00000256682	ENSG00000256682	TAS2R12	12:10977558-11324212	NOTEST	0.0898875	0	#NAME?	0	1	1
ENSG00000256684	ENSG00000256684	RP11-49K4.2	11:96241588-96247912	NOTEST	0	0	0	0	1	1
ENSG00000256686	ENSG00000256686	RP11-443N24.2	12:25935639-25967105	NOTEST	0	0	0	0	1	1
ENSG00000256690	ENSG00000256690	RP11-727F15.9	11:62599705-62609281	NOTEST	0.150315	0.184709	0.29726	0	1	1
ENSG00000256691	ENSG00000256691	RP11-476M19.3	12:3490514-3703139	NOTEST	0	0	0	0	1	1
ENSG00000256692	ENSG00000256692	AC139099.1	17:81159764-81188573	NOTEST	0	0	0	0	1	1
ENSG00000256694	ENSG00000256694	RP11-598F7.5	12:175930-291565	NOTEST	0	0	0	0	1	1
ENSG00000256695	ENSG00000256695	RP1-166H1.2	12:120827348-120833797	NOTEST	0	0	0	0	1	1
ENSG00000256699	ENSG00000256699	RP11-669N7.3	12:129556269-130388211	NOTEST	0	0	0	0	1	1
ENSG00000256704	ENSG00000256704	SDCCAG3P1	18:57677223-57681490	NOTEST	0.0165543	0	#NAME?	0	1	1
ENSG00000256705	ENSG00000256705	CTD-2017C7.1	14:102228134-102394326	NOTEST	0	0	0	0	1	1
ENSG00000256706	ENSG00000256706	RP5-1096D14.3	12:1901122-2032033	NOTEST	0	0	0	0	1	1
ENSG00000256708	ENSG00000256708	RP11-444B24.2	12:68383224-68628466	NOTEST	0	0	0	0	1	1
ENSG00000256709	ENSG00000256709	AL139812.1	X:105570886-105571051	NOTEST	0	0	0	0	1	1
ENSG00000256712	ENSG00000256712	RP11-785H5.2	12:10977558-11324212	NOTEST	0	0	0	0	1	1
ENSG00000256713	ENSG00000256713	PGA5	11:60989687-61018929	NOTEST	0	0	0	0	1	1
ENSG00000256714	ENSG00000256714	RP11-73M14.1	12:22199107-22589975	NOTEST	0	0	0	0	1	1
ENSG00000256715	ENSG00000256715	AL050302.1	21:14741930-14745386	NOTEST	0	0	0	0	1	1
ENSG00000256717	ENSG00000256717	AP000797.3	11:115530375-115713864	NOTEST	0	0	0	0	1	1
ENSG00000256720	ENSG00000256720	RP11-436I9.6	12:9287679-9288187	NOTEST	0	0	0	0	1	1
ENSG00000256721	ENSG00000256721	CACNA1CIT3	12:2055219-2802108	NOTEST	0	0	0	0	1	1
ENSG00000256723	ENSG00000256723	RP11-167N4.4	11:73706016-73707196	NOTEST	0	0	0	0	1	1
ENSG00000256725	ENSG00000256725	RP11-662M24.2	12:130880681-131200826	NOTEST	0	0	0	0	1	1
ENSG00000256731	ENSG00000256731	AL591069.1	6:160769299-160932156	NOTEST	0	0	0	0	1	1
ENSG00000256732	ENSG00000256732	RP11-407A16.3	12:127094579-127174868	NOTEST	0	0	0	0	1	1
ENSG00000256733	ENSG00000256733	RP11-881M11.8	11:60823208-60835007	NOTEST	0	0	0	0	1	1
ENSG00000256734	ENSG00000256734	RP11-613F22.7	11:18433853-18473605	NOTEST	0	0	0	0	1	1
ENSG00000256737	ENSG00000256737	RBBP4P5	14:22031949-22033215	NOTEST	0	0	0	0	1	1
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ENSG00000256747	ENSG00000256747	RP11-860B13.1	12:27932753-27955973	NOTEST	0	0	0	0	1	1
ENSG00000256748	ENSG00000256748	RP11-234B24.5	12:4671369-4960277	NOTEST	0	0	0	0	1	1
ENSG00000256750	ENSG00000256750	RP11-3L23.2	12:119196558-119199484	NOTEST	0	0	0	0	1	1
ENSG00000256751	ENSG00000256751	RP11-695J4.2	12:14656594-14910897	NOTEST	0	0	0	0	1	1
ENSG00000256752	ENSG00000256752	HPRTP3	11:93731808-93732384	NOTEST	0	0	0	0	1	1
ENSG00000256756	ENSG00000256756	RP11-871F6.2	12:17553332-17553848	NOTEST	0	0	0	0	1	1
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ENSG00000256762	ENSG00000256762	STH	17:43921016-44105700	NOTEST	0	0.0422575	inf	0	1	1
ENSG00000256763	ENSG00000256763	RP1-116K23.1	12:126652780-126656212	NOTEST	0	0	0	0	1	1
ENSG00000256769	ENSG00000256769	CACNA1CAS3	12:2055219-2802108	NOTEST	0	0	0	0	1	1
ENSG00000256774	ENSG00000256774	RP11-268P4.2	12:22749161-22749485	NOTEST	0	0	0	0	1	1
ENSG00000256777	ENSG00000256777	PDCL3P7	12:66669719-66670431	NOTEST	0	0	0	0	1	1
ENSG00000256779	ENSG00000256779	RP11-60C6.5	11:94770645-94771620	NOTEST	0	0	0	0	1	1
ENSG00000256783	ENSG00000256783	RP11-503G7.1	12:133033745-133036610	NOTEST	0	0	0	0	1	1
ENSG00000256789	ENSG00000256789	RP11-697H9.2	11:63391558-63439393	NOTEST	0	0	0	0	1	1
ENSG00000256790	ENSG00000256790	RP11-429A20.3	12:5127630-5130879	NOTEST	0	0	0	0	1	1
ENSG00000256797	ENSG00000256797	KLRF2	12:10034087-10048432	NOTEST	0	0	0	0	1	1
ENSG00000256799	ENSG00000256799	RP11-500M8.6	12:4671369-4960277	NOTEST	0	0	0	0	1	1
ENSG00000256802	ENSG00000256802	RP11-680F8.1	15:29967193-29973161	NOTEST	0	0	0	0	1	1
ENSG00000256803	ENSG00000256803	RP11-133L14.5	12:10100735-10183205	NOTEST	0	0	0	0	1	1
ENSG00000256804	ENSG00000256804	RP13-977J11.5	12:132568827-132613029	NOTEST	0.560639	0.188667	-1.57123	0	1	1
ENSG00000256806	ENSG00000256806	AC004706.1	17:6554970-6558328	NOTEST	0.365439	0.571402	0.644877	0	1	1
ENSG00000256810	ENSG00000256810	RP11-76C10.2	12:131438451-131626014	NOTEST	0	0	0	0	1	1
ENSG00000256811	ENSG00000256811	RP11-7M8.2	12:122277432-122301502	NOTEST	0	0	0	0	1	1
ENSG00000256812	ENSG00000256812	CAPNS2	16:55542909-55620582	NOTEST	0.0175832	0	#NAME?	0	1	1
ENSG00000256813	ENSG00000256813	RP11-804A23.4	11:60603468-60623444	NOTEST	0	0	0	0	1	1
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ENSG00000256815	ENSG00000256815	AL590325.2	X:134193714-134257880	NOTEST	0	0	0	0	1	1
ENSG00000256817	ENSG00000256817	TPT1P12	12:9301435-9360966	NOTEST	0	0	0	0	1	1
ENSG00000256818	ENSG00000256818	AP001069.1	21:31964758-31965394	NOTEST	0	0	0	0	1	1
ENSG00000256822	ENSG00000256822	AC084125.2	8:145754562-145911194	NOTEST	0	0	0	0	1	1
ENSG00000256824	ENSG00000256824	RP11-21A7A.2	11:63742078-63933578	NOTEST	0	0.0451032	inf	0	1	1
ENSG00000256826	ENSG00000256826	AC138744.2	17:62473901-62493154	NOTEST	0	0	0	0	1	1
ENSG00000256827	ENSG00000256827	RP11-214K3.5	12:124247041-124800570	NOTEST	0.153684	0.0576375	-1.41489	0	1	1
ENSG00000256835	ENSG00000256835	GS1-410F4.5	12:68371886-68372167	NOTEST	0	0	0	0	1	1
ENSG00000256837	ENSG00000256837	CACNA1CIT1	12:2055219-2802108	NOTEST	0.0288083	0	#NAME?	0	1	1
ENSG00000256840	ENSG00000256840	CT476828.14	GL000228.1:105686-107309	NOTEST	0	0	0	0	1	1
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ENSG00000256844	ENSG00000256844	RP11-282K24.2	12:19260787-19261117	NOTEST	0	0	0	0	1	1
ENSG00000256845	ENSG00000256845	AC007401.1	2:36583068-36873230	NOTEST	0.0085254	0	#NAME?	0	1	1
ENSG00000256847	ENSG00000256847	CCND2P1	11:62847411-63137190	NOTEST	0	0	0	0	1	1
ENSG00000256849	ENSG00000256849	RP11-405A12.1	12:19928384-20162871	NOTEST	0	0	0	0	1	1
ENSG00000256851	ENSG00000256851	XXbac-BPG16N22.5	6:31483755-31483988	NOTEST	0	0	0	0	1	1
ENSG00000256852	ENSG00000256852	KNOP1P1	12:24719897-24737483	NOTEST	0	0	0	0	1	1
ENSG00000256862	ENSG00000256862	RP11-664D1.1	12:3900212-4019504	NOTEST	0	0	0	0	1	1
ENSG00000256863	ENSG00000256863	RP11-959F10.6	11:62847411-63137190	NOTEST	0	0	0	0	1	1
ENSG00000256868	ENSG00000256868	CT476828.15	GL000228.1:95768-97391	NOTEST	0	0	0	0	1	1
ENSG00000256870	ENSG00000256870	SLC5A8	12:101549270-101604185	NOTEST	0.00741228	0.0396625	2.41979	0	1	1

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ENSG00000256874	ENSG00000256874	AL080274.1	20:11781110-11851363	NOTEST	0	0	0	0	1	1
ENSG00000256875	ENSG00000256875	RP11-503G7.2	12:133038827-133039442	NOTEST	0	0	0	0	1	1
ENSG00000256878	ENSG00000256878	AC087897.1	12:38866645-38866722	NOTEST	0	0	0	0	1	1
ENSG00000256879	ENSG00000256879	RP11-284H19.1	12:20514665-20837315	NOTEST	0	0.00711371	inf	0	1	1
ENSG00000256882	ENSG00000256882	AC091320.1	7:119209293-119209370	NOTEST	0	0	0	0	1	1
ENSG00000256884	ENSG00000256884	RP11-64B16.3	12:119611869-119614289	NOTEST	0	0	0	0	1	1
ENSG00000256885	ENSG00000256885	AP001877.1	11:95502105-95565857	NOTEST	0.343492	0.597915	0.799665	0	1	1
ENSG00000256888	ENSG00000256888	RP13-81N3.2	12:10902832-10930043	NOTEST	0	0	0	0	1	1
ENSG00000256889	ENSG00000256889	AC093847.1	4:92949928-92950119	NOTEST	0	0	0	0	1	1
ENSG00000256892	ENSG00000256892	MTRNR2L7	10:37890365-37891859	NOTEST	0	0	0	0	1	1
ENSG00000256896	ENSG00000256896	PSMC1P8	12:17536285-17537581	NOTEST	0	0	0	0	1	1
ENSG00000256897	ENSG00000256897	RP11-17G12.2	11:47236492-47260767	NOTEST	0.385454	0.64943	0.752616	0	1	1
ENSG00000256898	ENSG00000256898	RP11-707G14.8	11:73583711-73638790	NOTEST	0	0.032083	inf	0	1	1
ENSG00000256902	ENSG00000256902	RP11-986G18.1	12:2851791-2881074	NOTEST	0	0	0	0	1	1
ENSG00000256904	ENSG00000256904	A2ML1-AS2	12:8834195-9039597	NOTEST	0	0	0	0	1	1
ENSG00000256905	ENSG00000256905	AC090571.1	8:41786996-41909508	NOTEST	0	0	0	0	1	1
ENSG00000256906	ENSG00000256906	RP11-474D1.2	12:130554869-130557230	NOTEST	0	0	0	0	1	1
ENSG00000256912	ENSG00000256912	RP11-75L1.6	12:9969945-9970621	NOTEST	0	0	0	0	1	1
ENSG00000256913	ENSG00000256913	RP1-102E24.6	12:6586879-6589373	NOTEST	0	0	0	0	1	1
ENSG00000256915	ENSG00000256915	RP11-221N13.4	12:66038113-66057079	NOTEST	0.0733146	0	#NAME?	0	1	1
ENSG00000256916	ENSG00000256916	RP11-817J15.2	11:102447565-102498801	NOTEST	0.0259684	0.0183422	-0.501586	0	1	1
ENSG00000256917	ENSG00000256917	RP11-81H14.4	12:68881466-68881643	NOTEST	0	0	0	0	1	1
ENSG00000256920	ENSG00000256920	CR753846.1	HSCHR6_MHC_DBB:32663185-32663364	NOTEST	0	0	0	0	1	1
ENSG00000256922	ENSG00000256922	RP11-749H20.1	12:128278071-128305728	NOTEST	0	0	0	0	1	1
ENSG00000256925	ENSG00000256925	GPR123-AS1	10:134884432-134945179	NOTEST	0	0	0	0	1	1
ENSG00000256927	ENSG00000256927	RP5-944M2.2	12:126910535-126918554	NOTEST	0	0	0	0	1	1
ENSG00000256928	ENSG00000256928	RP11-809N8.2	11:73087308-73108519	NOTEST	0	0	0	0	1	1
ENSG00000256937	ENSG00000256937	RP11-436I9.5	12:9280378-9281241	NOTEST	0	0	0	0	1	1
ENSG00000256943	ENSG00000256943	RP13-895J2.2	12:132680923-132905935	NOTEST	0	0	0	0	1	1
ENSG00000256944	ENSG00000256944	RP11-881M11.1	11:60680637-60720002	NOTEST	0.119785	0.141788	0.243289	0	1	1
ENSG00000256947	ENSG00000256947	RP11-64D24.2	11:113930314-114227293	NOTEST	0	0	0	0	1	1
ENSG00000256948	ENSG00000256948	RP11-598F7.3	12:175930-291565	NOTEST	0	0	0	0	1	1
ENSG00000256950	ENSG00000256950	RP11-87C12.2	12:122326636-122441833	NOTEST	0.108996	0.131734	0.273342	0	1	1
ENSG00000256951	ENSG00000256951	AC055876.1	15:29033388-29101361	NOTEST	0	0	0	0	1	1
ENSG00000256953	ENSG00000256953	RP11-6B19.2	12:15773091-16035263	NOTEST	0	0	0	0	1	1
ENSG00000256955	ENSG00000256955	RP11-417L19.2	12:132341964-132348596	NOTEST	0	0	0	0	1	1
ENSG00000256963	ENSG00000256963	RP11-216P16.4	12:121517644-121517927	NOTEST	0	0	0	0	1	1
ENSG00000256966	ENSG00000256966	RP11-613M10.8	9:37510888-38069210	NOTEST	0.110762	0.418856	1.919	0	1	1
ENSG00000256967	ENSG00000256967	RP11-273B20.1	12:7281674-7311541	NOTEST	0.278887	0.0591118	-2.23816	0	1	1
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ENSG00000256971	ENSG00000256971	LINC00508	12:128399916-128436097	NOTEST	0	0	0	0	1	1
ENSG00000256972	ENSG00000256972	AP000462.3	11:115039937-115375675	NOTEST	0	0	0	0	1	1
ENSG00000256973	ENSG00000256973	RP11-359J14.2	12:22601516-22697480	NOTEST	0.402044	0.511428	0.347177	0	1	1
ENSG00000256974	ENSG00000256974	AC018692.4	GL000193.1:96644-96721	NOTEST	0	0	0	0	1	1
ENSG00000256975	ENSG00000256975	RP11-525E9.1	12:9620147-9728864	NOTEST	0.00793755	0.042142	2.40849	0	1	1
ENSG00000256977	ENSG00000256977	LIMS3	2:110656004-110677180	NOTEST	0	0	0	0	1	1
ENSG00000256980	ENSG00000256980	KHDC1L	6:73918805-74020088	NOTEST	0	0	0	0	1	1
ENSG00000256981	ENSG00000256981	TAS2R18	12:10977558-11324212	NOTEST	0.0568402	0.0156314	-1.86246	0	1	1
ENSG00000256982	ENSG00000256982	CTD-2555A7.2	16:89112579-89119373	NOTEST	0.0074892	0.0116381	0.635976	0	1	1
ENSG00000256984	ENSG00000256984	RP11-551L14.6	12:31165436-31168601	NOTEST	0	0	0	0	1	1
ENSG00000256986	ENSG00000256986	RP11-313F23.2	12:34315396-34315903	NOTEST	0	0	0	0	1	1
ENSG00000256987	ENSG00000256987	RP11-428G5.7	12:32106822-32108202	NOTEST	0	0	0	0	1	1
ENSG00000256988	ENSG00000256988	RP11-234B24.4	12:4671369-4960277	NOTEST	0	0	0	0	1	1
ENSG00000256989	ENSG00000256989	AC010335.1	19:18552228-18632937	NOTEST	0	0	0	0	1	1
ENSG00000256994	ENSG00000256994	RP11-871F6.3	12:17662286-17768397	NOTEST	0	0	0	0	1	1
ENSG00000256995	ENSG00000256995	RP11-114G22.1	12:22852792-23404433	NOTEST	0.416011	0.219827	-0.920253	0	1	1
ENSG00000257000	ENSG00000257000	RP13-820C6.2	12:132434507-132565005	NOTEST	0	0	0	0	1	1
ENSG00000257002	ENSG00000257002	AP000438.2	11:62676150-62689279	NOTEST	0.0256987	0.0199946	-0.362087	0	1	1
ENSG00000257004	ENSG00000257004	RP11-180M15.3	12:12813824-12849141	NOTEST	0	0	0	0	1	1
ENSG00000257005	ENSG00000257005	RP11-972L6.2	12:63952692-64217675	NOTEST	0	0	0	0	1	1
ENSG00000257008	ENSG00000257008	GPR142	17:72363545-72368761	NOTEST	0	0	0	0	1	1
ENSG00000257009	ENSG00000257009	RP11-685B13.2	12:25562226-25801513	NOTEST	0	0	0	0	1	1
ENSG00000257010	ENSG00000257010	AC140481.1	2:131369053-131415664	NOTEST	0	0	0	0	1	1
ENSG00000257012	ENSG00000257012	RP11-60C6.6	11:94773574-94774735	NOTEST	0	0	0	0	1	1
ENSG00000257016	ENSG00000257016	SLC25A39P2	12:10703864-10704134	NOTEST	0	0	0	0	1	1
ENSG00000257017	ENSG00000257017	HP	16:72078187-72210777	NOTEST	0	0	0	0	1	1
ENSG00000257019	ENSG00000257019	OR13C2	9:107366923-107367951	NOTEST	0	0	0	0	1	1
ENSG00000257021	ENSG00000257021	HSPE1P20	12:127396579-127396868	NOTEST	0	0	0	0	1	1
ENSG00000257022	ENSG00000257022	RP11-729I10.2	12:21950334-22094336	NOTEST	0	0	0	0	1	1
ENSG00000257023	ENSG00000257023	RP11-268P4.4	12:22754358-22777949	NOTEST	0.0214953	0	#NAME?	0	1	1
ENSG00000257025	ENSG00000257025	RP11-553N19.1	12:128751947-129192460	NOTEST	0	0	0	0	1	1
ENSG00000257034	ENSG00000257034	AL021707.2	22:39101727-39190203	NOTEST	0	0	0	0	1	1
ENSG00000257035	ENSG00000257035	RP11-351O2.2	12:128108697-128110812	NOTEST	0	0	0	0	1	1
ENSG00000257037	ENSG00000257037	RP13-200J3.2	12:27619742-27655118	NOTEST	0	0	0	0	1	1
ENSG00000257038	ENSG00000257038	RP11-800A3.7	11:73018279-73080136	NOTEST	0.170407	0.139458	-0.289153	0	1	1
ENSG00000257040	ENSG00000257040	AC005477.1	14:72399155-73061833	NOTEST	0	0	0	0	1	1
ENSG00000257042	ENSG00000257042	RP11-993B23.3	12:28111016-28125638	NOTEST	0.0677725	0	#NAME?	0	1	1
ENSG00000257043	ENSG00000257043	RP11-137N23.1	11:18686596-18687095	NOTEST	0	0	0	0	1	1
ENSG00000257045	ENSG00000257045	RP11-486F17.1	2:200134222-200341658	NOTEST	0	0.0175057	inf	0	1	1
ENSG00000257046	ENSG00000257046	LST3	12:20963635-21392180	NOTEST	0	0	0	0	1	1
ENSG00000257048	ENSG00000257048	RP11-476M19.2	12:3476998-3480512	NOTEST	0	0	0	0	1	1

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ENSG00000257053	ENSG00000257053	Z98941.1	12:121570621-121623876	NOTEST	0	0	0	0	1	1
ENSG00000257056	ENSG00000257056	RP11-966I7.2	14:29241909-29299410	NOTEST	0	0	0	0	1	1
ENSG00000257057	ENSG00000257057	LINC01171	11:94245746-94265289	NOTEST	0	0	0	0	1	1
ENSG00000257058	ENSG00000257058	RP11-864I4.4	11:62201015-62323707	NOTEST	0	0.150998	inf	0	1	1
ENSG00000257060	ENSG00000257060	RP11-266O8.1	15:93855785-94112712	NOTEST	0	0	0	0	1	1
ENSG00000257061	ENSG00000257061	RP4-809F18.2	12:126842579-126843442	NOTEST	0	0	0	0	1	1
ENSG00000257062	ENSG00000257062	RP11-125O5.2	12:20963635-21392180	NOTEST	0	0	0	0	1	1
ENSG00000257065	ENSG00000257065	RP3-468K18.5	6:143857981-144184949	NOTEST	0	0.0249131	inf	0	1	1
ENSG00000257067	ENSG00000257067	AP000797.4	11:115803491-115813713	NOTEST	0	0	0	0	1	1
ENSG00000257069	ENSG00000257069	RP11-783K16.10	11:64058773-64072242	NOTEST	0	0	0	0	1	1
ENSG00000257070	ENSG00000257070	RP11-667M19.4	11:113603908-113644533	NOTEST	0	0	0	0	1	1
ENSG00000257074	ENSG00000257074	RPL29P33	19:34745441-34850317	NOTEST	0.101625	0.152329	0.583946	0	1	1
ENSG00000257075	ENSG00000257075	RPEP6	11:71825914-71850936	NOTEST	0	0	0	0	1	1
ENSG00000257078	ENSG00000257078	RP3-461F17.2	12:7072407-7178336	NOTEST	0	0	0	0	1	1
ENSG00000257083	ENSG00000257083	RP11-123O10.3	12:67285655-67490186	NOTEST	0	0	0	0	1	1
ENSG00000257084	ENSG00000257084	U47924.27	12:7072407-7178336	NOTEST	0	0	0	0	1	1
ENSG00000257087	ENSG00000257087	RP11-136I14.3	11:115409586-115410102	NOTEST	0	0	0	0	1	1
ENSG00000257088	ENSG00000257088	PNMA6D	X:152240818-152340864	NOTEST	0	0	0	0	1	1
ENSG00000257094	ENSG00000257094	RP11-50I19.1	12:32160060-32160369	NOTEST	0	0	0	0	1	1
ENSG00000257095	ENSG00000257095	RP11-364C11.2	12:119419299-119600856	NOTEST	0	0	0	0	1	1
ENSG00000257096	ENSG00000257096	AE000658.22	14:21989231-22005350	NOTEST	0	0	0	0	1	1
ENSG00000257097	ENSG00000257097	RP11-450K4.1	12:122755978-122907179	NOTEST	0.0200898	0.046447	1.20912	0	1	1
ENSG00000257101	ENSG00000257101	LRRC37A13P	11:113662187-113662474	NOTEST	0	0	0	0	1	1
ENSG00000257105	ENSG00000257105	RP11-259O18.4	12:9102639-9163356	NOTEST	0	0	0	0	1	1
ENSG00000257108	ENSG00000257108	NHLRC4	16:616994-634136	NOTEST	0.176739	0.18091	0.0336446	0	1	1
ENSG00000257109	ENSG00000257109	OR4F28P	15:102416166-102417104	NOTEST	0	0	0	0	1	1
ENSG00000257110	ENSG00000257110	AL354808.1	13:20207787-20247599	NOTEST	0	0	0	0	1	1
ENSG00000257113	ENSG00000257113	RP11-274M17.2	12:74526945-74796315	NOTEST	0	0	0	0	1	1
ENSG00000257114	ENSG00000257114	RP11-25I15.3	12:43086017-43110653	NOTEST	0.0747141	0	#NAME?	0	1	1
ENSG00000257115	ENSG00000257115	OR11H12	14:19377521-19378606	NOTEST	0	0	0	0	1	1
ENSG00000257119	ENSG00000257119	EEF1B2P4	12:107295060-107295762	NOTEST	0	0	0	0	1	1
ENSG00000257120	ENSG00000257120	CTD-2503I6.1	14:30045686-30766249	NOTEST	0	0	0	0	1	1
ENSG00000257121	ENSG00000257121	RP11-129B9.2	12:95470524-95611258	NOTEST	0	0	0	0	1	1
ENSG00000257123	ENSG00000257123	BX927168.1	HSCHR6_MHC_MANN:32778164-32778539	NOTEST	0	0	0	0	1	1
ENSG00000257124	ENSG00000257124	RP11-384P14.1	12:84054787-84055498	NOTEST	0	0	0	0	1	1
ENSG00000257125	ENSG00000257125	KRT127P	12:53145761-53147605	NOTEST	0	0	0	0	1	1
ENSG00000257126	ENSG00000257126	RP11-966I7.1	14:29198288-29234483	NOTEST	0	0	0	0	1	1
ENSG00000257127	ENSG00000257127	CLLU1	12:92813869-92885867	NOTEST	0	0	0	0	1	1
ENSG00000257128	ENSG00000257128	RP11-2A1.1	12:42223699-42326394	NOTEST	0	0	0	0	1	1
ENSG00000257129	ENSG00000257129	RP11-554D14.1	12:108304179-108306397	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000257135	ENSG00000257135	RP11-320M2.1	2:10588819-10591453	NOTEST	0.0676087	0.0203882	-1.72947	0	1	1
ENSG00000257137	ENSG00000257137	C12orf80	12:52599367-52604639	NOTEST	0	0	0	0	1	1
ENSG00000257138	ENSG00000257138	TAS2R38	7:141607612-141806547	NOTEST	0	0	0	0	1	1
ENSG00000257139	ENSG00000257139	RP11-320P7.2	12:70132460-70748773	NOTEST	0	0	0	0	1	1
ENSG00000257141	ENSG00000257141	RP11-554D14.7	12:108226634-108228807	NOTEST	0	0	0	0	1	1
ENSG00000257142	ENSG00000257142	RP11-536C10.19	14:20168637-20168809	NOTEST	0	0	0	0	1	1
ENSG00000257146	ENSG00000257146	RP11-813P10.1	12:59989847-60176395	NOTEST	0	0	0	0	1	1
ENSG00000257147	ENSG00000257147	AL663093.1	HSCHR6_MHC_COX:31028108-31031915	NOTEST	0	0	0	0	1	1
ENSG00000257148	ENSG00000257148	CR753819.1	HSCHR6_MHC_DBB:31103948-31119721	NOTEST	0	0	0	0	1	1
ENSG00000257149	ENSG00000257149	AC127032.1	HSCHR17_1:44001605-44145324	NOTEST	0	0	0	0	1	1
ENSG00000257150	ENSG00000257150	PGAM1P5	12:96043030-96184930	NOTEST	0	0	0	0	1	1
ENSG00000257151	ENSG00000257151	PWAR6	15:25068793-25492435	NOTEST	0.00333948	0.00259395	-0.364473	0	1	1
ENSG00000257153	ENSG00000257153	BX088523.1	HSCHR6_MHC_SSTO:28730510-28730618	NOTEST	0	0	0	0	1	1
ENSG00000257154	ENSG00000257154	AL662822.1	HSCHR6_MHC_COX:30446361-30446488	NOTEST	0	0	0	0	1	1
ENSG00000257155	ENSG00000257155	CTD-2213F21.3	14:31959161-32330430	NOTEST	0	0	0	0	1	1
ENSG00000257156	ENSG00000257156	RP11-13A1.3	12:89441963-89703330	NOTEST	0	0	0	0	1	1
ENSG00000257157	ENSG00000257157	RP11-528M18.3	12:98073656-98073825	NOTEST	0	0	0	0	1	1
ENSG00000257158	ENSG00000257158	BX284927.1	HSCHR6_MHC_SSTO:32221187-32221358	NOTEST	0	0	0	0	1	1
ENSG00000257159	ENSG00000257159	RP11-58A17.3	12:58360840-58362182	NOTEST	0	0	0	0	1	1
ENSG00000257160	ENSG00000257160	AL662822.2	HSCHR6_MHC_COX:30490515-30490640	NOTEST	0	0	0	0	1	1
ENSG00000257162	ENSG00000257162	MED15P6	14:20071067-20074896	NOTEST	0	0	0	0	1	1
ENSG00000257164	ENSG00000257164	RP11-25I15.2	12:43040384-43080503	NOTEST	0	0	0	0	1	1
ENSG00000257165	ENSG00000257165	RP11-171L9.1	12:78720459-78934455	NOTEST	0	0	0	0	1	1
ENSG00000257168	ENSG00000257168	BX927214.1	HSCHR6_MHC_MANN:30368690-30368778	NOTEST	0	0	0	0	1	1
ENSG00000257169	ENSG00000257169	RP11-117N2.2	12:96672038-96794338	NOTEST	0	0.0514656	inf	0	1	1
ENSG00000257170	ENSG00000257170	CR382280.1	HSCHR6_MHC_MANN:30522149-30522222	NOTEST	0	0	0	0	1	1
ENSG00000257171	ENSG00000257171	RP11-754I20.3	14:19172102-19188741	NOTEST	0	0	0	0	1	1
ENSG00000257172	ENSG00000257172	AL662822.3	HSCHR6_MHC_COX:30469051-30469136	NOTEST	0	0	0	0	1	1
ENSG00000257173	ENSG00000257173	RP11-297L6.2	12:38472330-38472801	NOTEST	0	0	0	0	1	1
ENSG00000257175	ENSG00000257175	RP11-536C10.12	14:19406794-19427443	NOTEST	0	0	0	0	1	1
ENSG00000257176	ENSG00000257176	RP11-996F15.2	12:29302035-29534122	NOTEST	0.221224	0.111986	-0.982194	0	1	1
ENSG00000257177	ENSG00000257177	BX936369.1	HSCHR6_MHC_SSTO:30447933-30448060	NOTEST	0	0	0	0	1	1
ENSG00000257178	ENSG00000257178	MIR10A	17:46618255-46683776	NOTEST	0	0	0	0	1	1
ENSG00000257179	ENSG00000257179	HMGN2P6	14:25736269-25736542	NOTEST	0	0	0	0	1	1
ENSG00000257180	ENSG00000257180	RP11-509E10.1	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000257182	ENSG00000257182	BX927220.1	HSCHR6_MHC_MANN:30545346-30545471	NOTEST	0	0	0	0	1	1
ENSG00000257183	ENSG00000257183	RP11-274M17.3	12:74526945-74796315	NOTEST	0	0.0323228	inf	0	1	1
ENSG00000257184	ENSG00000257184	RP1-170O19.20	7:27202053-27219880	NOTEST	0	0	0	0	1	1
ENSG00000257185	ENSG00000257185	RP11-626P14.2	14:27067617-27305664	NOTEST	0.036861	0.138409	1.90877	0	1	1
ENSG00000257187	ENSG00000257187	BX248519.1	HSCHR6_MHC_SSTO:31543844-31550705	NOTEST	0	0	0	0	1	1
ENSG00000257188	ENSG00000257188	BX005432.1	HSCHR6_MHC_SSTO:29267110-29267650	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000257189	ENSG00000257189	AC139677.1	HSCHR17_1:44736660-44752551	NOTEST	0	0	0	0	1	1
ENSG00000257190	ENSG00000257190	BX927220.2	HSCHR6_MHC_MANN:30553828-30576175	NOTEST	0	0	0	0	1	1
ENSG00000257191	ENSG00000257191	RP11-390N6.1	12:79257772-79897176	NOTEST	0	0	0	0	1	1
ENSG00000257192	ENSG00000257192	AL662866.1	HSCHR6_MHC_COX:31376217-31376551	NOTEST	0	0	0	0	1	1
ENSG00000257193	ENSG00000257193	RP11-818F20.4	12:104564172-104571437	NOTEST	0	0	0	0	1	1
ENSG00000257194	ENSG00000257194	RP11-567C2.1	12:90501515-90506556	NOTEST	0	0	0	0	1	1
ENSG00000257195	ENSG00000257195	HNRNPA1P50	12:93115280-93323107	NOTEST	0.0358594	0.0585139	0.706428	0	1	1
ENSG00000257198	ENSG00000257198	FAM205B	9:34832291-34838583	NOTEST	0	0	0	0	1	1
ENSG00000257199	ENSG00000257199	RP11-669B18.1	12:77377858-77378449	NOTEST	0	0	0	0	1	1
ENSG00000257202	ENSG00000257202	RP11-512N21.3	12:102271128-102405908	NOTEST	0	0	0	0	1	1
ENSG00000257206	ENSG00000257206	CR762481.1	HSCHR6_MHC_DBB:30456385-30456976	NOTEST	0	0	0	0	1	1
ENSG00000257207	ENSG00000257207	LIMS3	2:111143953-111230652	NOTEST	0	0	0	0	1	1
ENSG00000257210	ENSG00000257210	NACAP3	12:93392993-93609455	NOTEST	0	0	0	0	1	1
ENSG00000257211	ENSG00000257211	AC138688.1	HSCHR17_1:43776445-43865069	NOTEST	0	0	0	0	1	1
ENSG00000257212	ENSG00000257212	BX248419.1	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000257213	ENSG00000257213	AL773543.1	HSCHR6_MHC_QBL:32624039-32628148	NOTEST	0	0	0	0	1	1
ENSG00000257215	ENSG00000257215	CR847794.1	HSCHR6_MHC_MANN:31171309-31199405	NOTEST	0	0	0	0	1	1
ENSG00000257216	ENSG00000257216	AL845450.1	HSCHR6_MHC_COX:30141446-30141664	NOTEST	0	0	0	0	1	1
ENSG00000257217	ENSG00000257217	CR759904.1	HSCHR6_MHC_APD:33015767-33038372	NOTEST	0	0	0	0	1	1
ENSG00000257219	ENSG00000257219	RP11-54A9.1	12:76653618-76698911	NOTEST	0	0.18116	inf	0	1	1
ENSG00000257220	ENSG00000257220	RP11-136F16.2	12:78224684-78606790	NOTEST	0	0	0	0	1	1
ENSG00000257221	ENSG00000257221	RP11-689B22.2	12:109015685-109035094	NOTEST	0	0	0	0	1	1
ENSG00000257222	ENSG00000257222	RP11-554E23.4	12:102457132-102513902	NOTEST	0	0.176748	inf	0	1	1
ENSG00000257223	ENSG00000257223	CR753309.1	HSCHR6_MHC_DBB:32574290-32596644	NOTEST	0	0	0	0	1	1
ENSG00000257224	ENSG00000257224	RP11-536C10.9	14:19478757-19478940	NOTEST	0	0	0	0	1	1
ENSG00000257225	ENSG00000257225	RP11-328C8.4	12:42632248-42984157	NOTEST	0.0424537	0.0360693	-0.23512	0	1	1
ENSG00000257226	ENSG00000257226	CTD-2252P21.1	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000257227	ENSG00000257227	DUXAP10	14:19650017-19718563	NOTEST	0	0	0	0	1	1
ENSG00000257228	ENSG00000257228	RP11-413B19.2	12:41582249-41968392	NOTEST	0	0	0	0	1	1
ENSG00000257230	ENSG00000257230	RP11-272B17.2	12:59917058-59917965	NOTEST	0	0	0	0	1	1
ENSG00000257231	ENSG00000257231	RP11-438N16.2	12:114227346-114227612	NOTEST	0	0	0	0	1	1
ENSG00000257232	ENSG00000257232	DPCR1	HSCHR6_MHC_MCF:30987292-30997453	NOTEST	0	0	0	0	1	1
ENSG00000257233	ENSG00000257233	CR936921.1	HSCHR6_MHC_APD:32679934-32684035	NOTEST	0	0	0	0	1	1
ENSG00000257235	ENSG00000257235	RP11-848D3.5	12:63397332-63400682	NOTEST	0	0	0	0	1	1
ENSG00000257236	ENSG00000257236	AL773541.1	HSCHR6_MHC_QBL:30955253-30955549	NOTEST	0	0	0	0	1	1
ENSG00000257237	ENSG00000257237	RP11-554L12.2	12:39451829-39453735	NOTEST	0	0	0	0	1	1
ENSG00000257238	ENSG00000257238	BX511262.1	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000257239	ENSG00000257239	RP11-630C16.2	12:42223699-42326394	NOTEST	0	0	0	0	1	1
ENSG00000257240	ENSG00000257240	CR753309.2	HSCHR6_MHC_DBB:32552036-32552223	NOTEST	0	0	0	0	1	1
ENSG00000257241	ENSG00000257241	RP11-611E13.3	12:70132460-70748773	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000257242	ENSG00000257242	C12orf79	12:92378755-92583436	NOTEST	0.286358	0.443764	0.631973	0	1	1
ENSG00000257243	ENSG00000257243	RP11-133N21.7	12:49962000-50158717	NOTEST	0.154836	0.520318	1.74866	0	1	1
ENSG00000257245	ENSG00000257245	CR388229.1	HSCHR6_MHC_DBB:31223319-31223661	NOTEST	0	0	0	0	1	1
ENSG00000257246	ENSG00000257246	RP11-416A17.6	12:51487445-51566926	NOTEST	0	0.0813324	inf	0	1	1
ENSG00000257247	ENSG00000257247	BX294158.1	HSCHR6_MHC_SSTO:30377449-30377537	NOTEST	0	0	0	0	1	1
ENSG00000257248	ENSG00000257248	BX294158.2	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000257249	ENSG00000257249	CR759890.1	HSCHR6_MHC_APD:30340492-30340616	NOTEST	0	0	0	0	1	1
ENSG00000257251	ENSG00000257251	AL844213.1	HSCHR6_MHC_QBL:30490177-30490302	NOTEST	0	0	0	0	1	1
ENSG00000257253	ENSG00000257253	RP11-70F11.7	12:50254989-50259528	NOTEST	0	0	0	0	1	1
ENSG00000257254	ENSG00000257254	RP11-210L7.1	12:102907028-102907433	NOTEST	0	0	0	0	1	1
ENSG00000257255	ENSG00000257255	CR759772.1	HSCHR6_MHC_MCF:31044058-31044360	NOTEST	0	0	0	0	1	1
ENSG00000257256	ENSG00000257256	RP3-405J10.4	12:50569570-50677329	NOTEST	0	0	0	0	1	1
ENSG00000257258	ENSG00000257258	RP11-946L16.1	12:29296128-29301608	NOTEST	0	0	0	0	1	1
ENSG00000257259	ENSG00000257259	RP11-767I20.1	12:58937906-59206842	NOTEST	0	0	0	0	1	1
ENSG00000257260	ENSG00000257260	CR847794.2	HSCHR6_MHC_MANN:31155176-31170971	NOTEST	0	0	0	0	1	1
ENSG00000257262	ENSG00000257262	RP11-776A13.1	12:30353915-30370849	NOTEST	0	0	0	0	1	1
ENSG00000257263	ENSG00000257263	CR938714.1	HSCHR6_MHC_MCF:31161054-31186363	NOTEST	0	0	0	0	1	1
ENSG00000257264	ENSG00000257264	MIR3179-1	16:14995355-14996031	NOTEST	0	0.0918307	inf	0	1	1
ENSG00000257265	ENSG00000257265	CTD-2021H9.1	12:71401552-71425863	NOTEST	0	0	0	0	1	1
ENSG00000257266	ENSG00000257266	BX248408.1	HSCHR6_MHC_SSTO:33344435-33344689	NOTEST	0	0	0	0	1	1
ENSG00000257268	ENSG00000257268	RP1-74B13.2	12:111269582-111283767	NOTEST	0	0	0	0	1	1
ENSG00000257271	ENSG00000257271	KIRREL3-AS1	11:126225534-126875953	NOTEST	0.0358941	0	#NAME?	0	1	1
ENSG00000257272	ENSG00000257272	RP11-317N8.3	14:36288429-36536396	NOTEST	0	0.0244627	inf	0	1	1
ENSG00000257273	ENSG00000257273	CR382280.2	HSCHR6_MHC_MANN:30501182-30501309	NOTEST	0	0	0	0	1	1
ENSG00000257275	ENSG00000257275	RP11-164H13.1	14:96176303-96223993	NOTEST	0	0	0	0	1	1
ENSG00000257276	ENSG00000257276	CR759737.1	HSCHR6_MHC_DBB:32236324-32315209	NOTEST	0	0	0	0	1	1
ENSG00000257277	ENSG00000257277	RP11-434H14.1	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000257278	ENSG00000257278	AC139677.2	HSCHR17_1:44771953-44775602	NOTEST	0	0	0	0	1	1
ENSG00000257279	ENSG00000257279	RP11-231I16.1	12:117348760-117468953	NOTEST	0.0453462	0.0362414	-0.323342	0	1	1
ENSG00000257281	ENSG00000257281	RP11-1K3.1	12:108674879-108676012	NOTEST	0	0	0	0	1	1
ENSG00000257283	ENSG00000257283	RP11-1060G2.1	12:94288740-94337379	NOTEST	0.0805131	0	#NAME?	0	1	1
ENSG00000257284	ENSG00000257284	RP11-190J23.1	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000257285	ENSG00000257285	RP11-298I3.1	14:23398817-23451851	NOTEST	0.313835	0.329391	0.0697964	0	1	1
ENSG00000257286	ENSG00000257286	RP11-545P7.4	12:113623330-113630173	NOTEST	0	0	0	0	1	1
ENSG00000257287	ENSG00000257287	RP11-98E6.1	12:72332625-73059422	NOTEST	0	0	0	0	1	1
ENSG00000257288	ENSG00000257288	RP11-557F20.2	12:59314419-59458019	NOTEST	0	0	0	0	1	1
ENSG00000257289	ENSG00000257289	RP11-611O2.6	12:69201955-69365350	NOTEST	0	0	0	0	1	1
ENSG00000257292	ENSG00000257292	RP11-266O15.4	12:38599187-38599814	NOTEST	0	0	0	0	1	1
ENSG00000257294	ENSG00000257294	RP11-316A16.1	12:60486644-60489632	NOTEST	0	0	0	0	1	1
ENSG00000257295	ENSG00000257295	BX927214.2	HSCHR6_MHC_MANN:30376934-30377058	NOTEST	0	0	0	0	1	1
ENSG00000257296	ENSG00000257296	RP11-701B6.1	12:85065376-85065805	NOTEST	0	0	0	0	1	1
ENSG00000257298	ENSG00000257298	RP3-405J10.3	12:50569570-50677329	NOTEST	0.0556587	0.0883949	0.667357	0	1	1
ENSG00000257299	ENSG00000257299	AL773535.1	HSCHR6_MHC_QBL:30325458-30325567	NOTEST	0	0	0	0	1	1
ENSG00000257300	ENSG00000257300	HAUS8P1	12:114518185-114551294	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000257301	ENSG00000257301	CR762481.2	HSCHR6_MHC_DBB:30461232-30465132	NOTEST	0	0	0	0	1	1
ENSG00000257302	ENSG00000257302	FAHD2P1	12:71031852-71314623	NOTEST	0.0193397	0	#NAME?	0	1	1
ENSG00000257305	ENSG00000257305	AC225613.1	HSCHR17_1:44560985-44561298	NOTEST	0	0	0	0	1	1
ENSG00000257307	ENSG00000257307	RP11-317N8.4	14:36288429-36536396	NOTEST	0.0828301	0.131132	0.662797	0	1	1
ENSG00000257308	ENSG00000257308	RP11-471N19.1	12:61624939-61626718	NOTEST	0	0	0	0	1	1
ENSG00000257310	ENSG00000257310	RP11-496I2.2	14:19740032-19742744	NOTEST	0	0	0	0	1	1
ENSG00000257311	ENSG00000257311	AC225613.2	HSCHR17_1:44544029-44544362	NOTEST	0	0	0	0	1	1
ENSG00000257313	ENSG00000257313	CR753846.2	HSCHR6_MHC_DBB:32574290-32596644	NOTEST	0	0	0	0	1	1
ENSG00000257314	ENSG00000257314	CR753835.1	HSCHR6_MHC_MANN:3272646 9-32726656	NOTEST	0	0	0	0	1	1
ENSG00000257316	ENSG00000257316	RP11-267D19.2	12:33138771-33140004	NOTEST	0	0	0	0	1	1
ENSG00000257318	ENSG00000257318	AC138688.2	HSCHR17_1:43752300-43767276	NOTEST	0	0	0	0	1	1
ENSG00000257319	ENSG00000257319	RP11-478B9.1	12:45408454-45496890	NOTEST	0	0	0	0	1	1
ENSG00000257320	ENSG00000257320	AL662834.1	HSCHR6_MHC_COX:31853113-31907413	NOTEST	0	0	0	0	1	1
ENSG00000257321	ENSG00000257321	AL662822.4	HSCHR6_MHC_COX:30447103-30451842	NOTEST	0	0	0	0	1	1
ENSG00000257322	ENSG00000257322	RP11-511B23.2	12:93392993-93609455	NOTEST	0.572585	0.252273	-1.18251	0	1	1
ENSG00000257323	ENSG00000257323	RP11-361A23.1	12:75050340-75050640	NOTEST	0	0	0	0	1	1
ENSG00000257324	ENSG00000257324	AL844213.2	HSCHR6_MHC_QBL:30487772-30488859	NOTEST	0	0	0	0	1	1
ENSG00000257325	ENSG00000257325	RP11-263E1.1	12:101111303-101522419	NOTEST	0	0	0	0	1	1
ENSG00000257326	ENSG00000257326	CR936880.1	HSCHR6_MHC_MCF:31161054-31186363	NOTEST	0	0	0	0	1	1
ENSG00000257327	ENSG00000257327	RP11-650K20.3	12:104235228-104359486	NOTEST	0.486839	0.464695	-0.0671584	0	1	1
ENSG00000257328	ENSG00000257328	AL049543.1	HSCHR6_MHC_COX:28478549-28503695	NOTEST	0	0	0	0	1	1
ENSG00000257329	ENSG00000257329	RP11-290L1.5	12:75956981-76377795	NOTEST	0	0	0	0	1	1
ENSG00000257331	ENSG00000257331	RP11-478B9.3	12:45408454-45496890	NOTEST	0	0	0	0	1	1
ENSG00000257332	ENSG00000257332	HNRNPA1P69	12:63665183-63666116	NOTEST	0	0	0	0	1	1
ENSG00000257333	ENSG00000257333	BX248518.1	HSCHR6_MHC_SSTO:30500572-30522918	NOTEST	0	0	0	0	1	1
ENSG00000257334	ENSG00000257334	CR759281.1	HSCHR6_MHC_DBB:30314267-30314355	NOTEST	0	0	0	0	1	1
ENSG00000257335	ENSG00000257335	MGAM	7:141607612-141806547	NOTEST	0.018824	0.0260592	0.469217	0	1	1
ENSG00000257336	ENSG00000257336	PRELID2P1	12:69201955-69365350	NOTEST	0	0	0	0	1	1
ENSG00000257338	ENSG00000257338	BX936369.2	HSCHR6_MHC_SSTO:30463126-30463248	NOTEST	0	0	0	0	1	1
ENSG00000257339	ENSG00000257339	PLEKHM1	HSCHR17_1:43513191-43568077	NOTEST	0	0	0	0	1	1
ENSG00000257340	ENSG00000257340	CR762481.3	HSCHR6_MHC_DBB:30415018-30415142	NOTEST	0	0	0	0	1	1
ENSG00000257341	ENSG00000257341	CRIP1	14:105952653-105965912	NOTEST	0	0.0442957	inf	0	1	1
ENSG00000257342	ENSG00000257342	RP11-571M6.7	12:58087737-58115340	NOTEST	0	0	0	0	1	1
ENSG00000257343	ENSG00000257343	RP11-641A6.8	12:53140379-53142092	NOTEST	0	0	0	0	1	1
ENSG00000257345	ENSG00000257345	RP11-511B23.1	12:93392993-93609455	NOTEST	0	0	0	0	1	1
ENSG00000257346	ENSG00000257346	RP11-386G11.8	12:49483203-49488602	NOTEST	0.276857	0.100261	-1.46538	0	1	1
ENSG00000257348	ENSG00000257348	AC217779.1	HSCHR17_1:44150124-44280402	NOTEST	0	0	0	0	1	1
ENSG00000257350	ENSG00000257350	RP11-616L12.4	12:55516451-55517904	NOTEST	0	0	0	0	1	1
ENSG00000257351	ENSG00000257351	AL773544.1	HSCHR6_MHC_QBL:31074947-31100262	NOTEST	0	0	0	0	1	1
ENSG00000257354	ENSG00000257354	RP11-631N16.2	12:62995530-63007855	NOTEST	0.309476	0.0274264	-3.49619	0	1	1
ENSG00000257355	ENSG00000257355	CTD-2006C1.10	19:12098431-12167127	NOTEST	0	0.0283985	inf	0	1	1
ENSG00000257356	ENSG00000257356	RP11-754I20.2	14:19195251-19195750	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000257357	ENSG00000257357	RP11-244H18.3	14:20078032-20152898	NOTEST	0	0	0	0	1	1
ENSG00000257359	ENSG00000257359	RP11-780K2.1	12:114254542-114404176	NOTEST	0	0	0	0	1	1
ENSG00000257360	ENSG00000257360	RP11-74K11.1	12:94533852-94535113	NOTEST	0.0272514	0.00958966	-1.50678	0	1	1
ENSG00000257361	ENSG00000257361	CR753835.2	HSCHR6_MHC_MANN:32748723-32777985	NOTEST	0	0	0	0	1	1
ENSG00000257362	ENSG00000257362	BX927220.3	HSCHR6_MHC_MANN:30551129-30551350	NOTEST	0	0	0	0	1	1
ENSG00000257363	ENSG00000257363	AL662831.1	HSCHR6_MHC_COX:30313815-30313903	NOTEST	0	0	0	0	1	1
ENSG00000257364	ENSG00000257364	RP11-81H3.1	12:74526945-74796315	NOTEST	0.0905285	0	#NAME?	0	1	1
ENSG00000257366	ENSG00000257366	MIR3180-2	16:16402398-16403857	NOTEST	0	0	0	0	1	1
ENSG00000257368	ENSG00000257368	RP11-438E8.2	12:45838548-45839221	NOTEST	0	0	0	0	1	1
ENSG00000257369	ENSG00000257369	CR812479.1	HSCHR6_MHC_DBB:30350524-30350612	NOTEST	0	0	0	0	1	1
ENSG00000257373	ENSG00000257373	RP11-547C5.2	12:43373056-43390289	NOTEST	0	0	0	0	1	1
ENSG00000257374	ENSG00000257374	AC217778.1	HSCHR17_1:43580584-43647125	NOTEST	0	0	0	0	1	1
ENSG00000257376	ENSG00000257376	RP11-328C8.2	12:42632248-42984157	NOTEST	0.0246013	0	#NAME?	0	1	1
ENSG00000257377	ENSG00000257377	AC217775.1	HSCHR17_1:44907917-44922890	NOTEST	0	0	0	0	1	1
ENSG00000257378	ENSG00000257378	RP11-469H8.8	12:50344523-50359464	NOTEST	0	0.0846764	inf	0	1	1
ENSG00000257381	ENSG00000257381	MIR3179-2	16:16394006-16394683	NOTEST	0.112764	0.0228467	-2.30325	0	1	1
ENSG00000257382	ENSG00000257382	AC217772.1	HSCHR17_1:44001605-44145324	NOTEST	0	0	0	0	1	1
ENSG00000257383	ENSG00000257383	CR759784.1	HSCHR6_MHC_MCF:31897465-31898542	NOTEST	0	0	0	0	1	1
ENSG00000257389	ENSG00000257389	RP11-153F5.3	12:53231186-53231523	NOTEST	0	0	0	0	1	1
ENSG00000257391	ENSG00000257391	MIR3180-4	16:15248706-15250877	NOTEST	0.116265	0.0641368	-0.858198	0	1	1
ENSG00000257392	ENSG00000257392	RP11-554D14.5	12:108281506-108283663	NOTEST	0	0	0	0	1	1
ENSG00000257393	ENSG00000257393	AL662822.5	HSCHR6_MHC_COX:30496296-30496517	NOTEST	0	0	0	0	1	1
ENSG00000257394	ENSG00000257394	CR759281.2	HSCHR6_MHC_DBB:30322511-30322635	NOTEST	0	0	0	0	1	1
ENSG00000257395	ENSG00000257395	RP11-597A11.2	14:20078032-20152898	NOTEST	0	0	0	0	1	1
ENSG00000257396	ENSG00000257396	CR759815.1	HSCHR6_MHC_MCF:31188754-31204550	NOTEST	0	0	0	0	1	1
ENSG00000257398	ENSG00000257398	RP11-554D14.6	12:108233067-108258339	NOTEST	0	0	0	0	1	1
ENSG00000257399	ENSG00000257399	CR388372.1	HSCHR6_MHC_DBB:30490905-30491030	NOTEST	0	0	0	0	1	1
ENSG00000257400	ENSG00000257400	RP11-778J16.3	12:94885321-94890218	NOTEST	0	0	0	0	1	1
ENSG00000257402	ENSG00000257402	KRT126P	12:53109350-53112824	NOTEST	0	0	0	0	1	1
ENSG00000257403	ENSG00000257403	CTD-2547E10.3	16:21358459-21363459	NOTEST	0.167491	0	#NAME?	0	1	1
ENSG00000257404	ENSG00000257404	RP11-153F5.2	12:53176433-53176623	NOTEST	0	0	0	0	1	1
ENSG00000257405	ENSG00000257405	RP11-609L23.2	12:43009304-43040300	NOTEST	0	0	0	0	1	1
ENSG00000257407	ENSG00000257407	RP11-1028N23.4	12:116019865-116077539	NOTEST	0	0	0	0	1	1
ENSG00000257408	ENSG00000257408	RP11-645C24.4	16:21950185-21956451	NOTEST	0	0.0179975	inf	0	1	1
ENSG00000257410	ENSG00000257410	RP11-2H8.2	12:72187634-72193407	NOTEST	0.0685585	0.428253	2.64306	0	1	1
ENSG00000257412	ENSG00000257412	BX927178.1	HSCHR6_MHC_MANN:31274581-31274949	NOTEST	0	0	0	0	1	1
ENSG00000257413	ENSG00000257413	YTHDC1	HSCHR4_1:69176102-69215822	NOTEST	0	0	0	0	1	1
ENSG00000257414	ENSG00000257414	OR6C73P	12:55790123-55790481	NOTEST	0	0	0	0	1	1
ENSG00000257415	ENSG00000257415	RP11-626I20.1	12:103897158-103898714	NOTEST	0	0	0	0	1	1
ENSG00000257416	ENSG00000257416	CR759912.1	HSCHR6_MHC_APD:30506511-30507598	NOTEST	0	0	0	0	1	1
ENSG00000257418	ENSG00000257418	CR759787.1	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000257420	ENSG00000257420	AL845557.1	HSCHR6_MHC_COX:32209048-32287940	NOTEST	0	0	0	0	1	1

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ENSG00000257421	ENSG00000257421	CR354443.1	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000257423	ENSG00000257423	AL844213.3	HSCHR6_MHC_QBL:30446761-30451500	NOTEST	0	0	0	0	1	1
ENSG00000257425	ENSG00000257425	AL844213.4	HSCHR6_MHC_QBL:30414328-30414452	NOTEST	0	0	0	0	1	1
ENSG00000257426	ENSG00000257426	RP11-554D14.3	12:108293414-108293592	NOTEST	0	0	0	0	1	1
ENSG00000257427	ENSG00000257427	AL731683.1	HSCHR6_MHC_COX:32542404-32557884	NOTEST	0	0	0	0	1	1
ENSG00000257428	ENSG00000257428	BX248096.1	HSCHR6_MHC_SSTO:30470621-30470706	NOTEST	0	0	0	0	1	1
ENSG00000257429	ENSG00000257429	RP11-272K23.3	12:80799773-81072802	NOTEST	0	0	0	0	1	1
ENSG00000257431	ENSG00000257431	RP11-263K4.3	12:82906455-82909596	NOTEST	0	0	0	0	1	1
ENSG00000257432	ENSG00000257432	RP11-244H18.4	14:20078032-20152898	NOTEST	0	0	0	0	1	1
ENSG00000257433	ENSG00000257433	RP1-197B17.3	12:48099867-48231681	NOTEST	0.190046	0.258499	0.443809	0	1	1
ENSG00000257434	ENSG00000257434	RP11-81K13.1	12:75414748-75603648	NOTEST	0	0	0	0	1	1
ENSG00000257435	ENSG00000257435	RP11-267D19.1	12:33141696-33146688	NOTEST	0	0	0	0	1	1
ENSG00000257436	ENSG00000257436	AC217778.2	HSCHR17_1:43578254-43578590	NOTEST	0	0	0	0	1	1
ENSG00000257437	ENSG00000257437	AC217779.2	HSCHR17_1:44150124-44280402	NOTEST	0	0	0	0	1	1
ENSG00000257438	ENSG00000257438	RP11-114F10.3	12:106457117-106533811	NOTEST	0	0	0	0	1	1
ENSG00000257440	ENSG00000257440	AL662822.6	HSCHR6_MHC_COX:30467329-30467402	NOTEST	0	0	0	0	1	1
ENSG00000257443	ENSG00000257443	RP11-150C16.1	12:59314419-59458019	NOTEST	0	0.113219	inf	0	1	1
ENSG00000257444	ENSG00000257444	SETP7	12:107665170-107665623	NOTEST	0	0	0	0	1	1
ENSG00000257446	ENSG00000257446	ZNF878	19:12098431-12167127	NOTEST	0.0362001	0.0644688	0.832606	0	1	1
ENSG00000257449	ENSG00000257449	RP11-603J24.4	12:56401442-56435590	NOTEST	0	0	0	0	1	1
ENSG00000257451	ENSG00000257451	CR388372.2	HSCHR6_MHC_DBB:30496686-30496907	NOTEST	0	0	0	0	1	1
ENSG00000257452	ENSG00000257452	RP1-71H24.1	12:113344581-113455556	NOTEST	0	0	0	0	1	1
ENSG00000257454	ENSG00000257454	CTD-2021H9.2	12:71427901-71512027	NOTEST	0	0	0	0	1	1
ENSG00000257456	ENSG00000257456	RP11-310I24.1	12:29653772-29937692	NOTEST	0	0	0	0	1	1
ENSG00000257457	ENSG00000257457	BX936369.3	HSCHR6_MHC_SSTO:30457571-30458162	NOTEST	0	0	0	0	1	1
ENSG00000257458	ENSG00000257458	RP11-473C19.1	12:99038918-100378432	NOTEST	0	0	0	0	1	1
ENSG00000257461	ENSG00000257461	AL844203.1	HSCHR6_MHC_QBL:30350285-30350373	NOTEST	0	0	0	0	1	1
ENSG00000257464	ENSG00000257464	RP11-161H23.8	12:49760366-49921205	NOTEST	0	0	0	0	1	1
ENSG00000257465	ENSG00000257465	TCEB1P32	12:117645946-117889975	NOTEST	0	0	0	0	1	1
ENSG00000257467	ENSG00000257467	RP11-121G22.3	12:81652044-82153332	NOTEST	0	0	0	0	1	1
ENSG00000257468	ENSG00000257468	AC225613.3	HSCHR17_1:44588765-44589837	NOTEST	0	0	0	0	1	1
ENSG00000257469	ENSG00000257469	BX936375.1	HSCHR6_MHC_SSTO:30413825-30413949	NOTEST	0	0	0	0	1	1
ENSG00000257470	ENSG00000257470	RP11-397H6.1	12:97379433-97579387	NOTEST	0	0	0	0	1	1
ENSG00000257472	ENSG00000257472	RP11-159D23.2	14:32395006-32399352	NOTEST	0	0	0	0	1	1
ENSG00000257473	ENSG00000257473	DQ-A1	HSCHR6_MHC_COX:32533366-32539589	NOTEST	0	0	0	0	1	1
ENSG00000257474	ENSG00000257474	RP11-359M6.1	12:79933982-79944315	NOTEST	0	0	0	0	1	1
ENSG00000257475	ENSG00000257475	RP11-983P16.2	12:53399941-53458156	NOTEST	0.0814575	0.031741	-1.3597	0	1	1
ENSG00000257476	ENSG00000257476	RP11-139B1.1	12:114676774-114679575	NOTEST	0	0	0	0	1	1
ENSG00000257477	ENSG00000257477	LINC01154	12:54747444-54891472	NOTEST	0	0	0	0	1	1
ENSG00000257478	ENSG00000257478	AL773535.2	HSCHR6_MHC_QBL:30321756-30321880	NOTEST	0	0	0	0	1	1
ENSG00000257480	ENSG00000257480	MRPL2P1	12:90146689-90147608	NOTEST	0	0	0	0	1	1

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ENSG00000257482	ENSG00000257482	ZNF727	7:63505820-63545179	NOTEST	0	0	0	0	1	1
ENSG00000257485	ENSG00000257485	CR812479.2	HSCHR6_MHC_DBB:30351039-30351127	NOTEST	0	0	0	0	1	1
ENSG00000257488	ENSG00000257488	RP5-1057I20.2	12:48099867-48231681	NOTEST	0	0	0	0	1	1
ENSG00000257489	ENSG00000257489	RP11-175P13.3	12:100550134-100660857	NOTEST	0.266553	0.473467	0.828838	0	1	1
ENSG00000257493	ENSG00000257493	RP11-536C10.20	14:20078032-20152898	NOTEST	0	0	0	0	1	1
ENSG00000257494	ENSG00000257494	RP3-521E19.2	12:112597991-112819896	NOTEST	0	0	0	0	1	1
ENSG00000257495	ENSG00000257495	RP11-641A6.2	12:52979372-53012343	NOTEST	0	0	0	0	1	1
ENSG00000257496	ENSG00000257496	RP11-474P2.4	12:46777461-46850051	NOTEST	0.0379921	0	#NAME?	0	1	1
ENSG00000257497	ENSG00000257497	RP11-585P4.5	12:75874459-75905416	NOTEST	0.111979	0.279367	1.31893	0	1	1
ENSG00000257499	ENSG00000257499	RP11-571M6.8	12:58117543-58154190	NOTEST	0	0	0	0	1	1
ENSG00000257500	ENSG00000257500	RP11-1020M18.10	12:52801363-52828309	NOTEST	0	0	0	0	1	1
ENSG00000257501	ENSG00000257501	RP11-1016B18.1	12:98107189-98155637	NOTEST	0	0	0	0	1	1
ENSG00000257502	ENSG00000257502	BX248406.1	HSCHR6_MHC_SSTO:32795637-32805799	NOTEST	0	0	0	0	1	1
ENSG00000257503	ENSG00000257503	CYB5AP5	14:26677241-26677630	NOTEST	0	0	0	0	1	1
ENSG00000257504	ENSG00000257504	RP11-536C10.7	14:19406794-19427443	NOTEST	0	0	0	0	1	1
ENSG00000257506	ENSG00000257506	RP11-231C14.5	16:29262828-29519817	NOTEST	0	0	0	0	1	1
ENSG00000257507	ENSG00000257507	RP11-956E11.1	12:69843249-69854504	NOTEST	0	0	0	0	1	1
ENSG00000257509	ENSG00000257509	RP11-762I7.4	12:56137063-56236750	NOTEST	0.11861	0.280286	1.24067	0	1	1
ENSG00000257510	ENSG00000257510	RP11-609L23.1	12:43009304-43040300	NOTEST	0	0	0	0	1	1
ENSG00000257512	ENSG00000257512	RP11-486A14.1	12:93708584-93709717	NOTEST	0.0281221	0.0480121	0.771695	0	1	1
ENSG00000257513	ENSG00000257513	NPIPB1P	18:11619507-11639698	NOTEST	0	0	0	0	1	1
ENSG00000257514	ENSG00000257514	RP11-755O11.2	12:101962130-102079796	NOTEST	0	0	0	0	1	1
ENSG00000257515	ENSG00000257515	RP11-498M15.1	12:72102950-72104154	NOTEST	0	0	0	0	1	1
ENSG00000257516	ENSG00000257516	CR354443.2	HSCHR6_MHC_MANN:31665566-31668042	NOTEST	0	0	0	0	1	1
ENSG00000257517	ENSG00000257517	RP4-601P9.1	12:115206478-115209656	NOTEST	0	0	0	0	1	1
ENSG00000257519	ENSG00000257519	RP11-116D17.2	12:115700974-115708401	NOTEST	0	0	0	0	1	1
ENSG00000257520	ENSG00000257520	RP11-896J10.3	14:36942411-36992221	NOTEST	0	0	0	0	1	1
ENSG00000257522	ENSG00000257522	RP11-562L8.1	14:29734030-29850501	NOTEST	0	0	0	0	1	1
ENSG00000257523	ENSG00000257523	CTD-2384A14.2	14:29299449-29497969	NOTEST	0	0	0	0	1	1
ENSG00000257526	ENSG00000257526	RP11-20E24.1	12:76956073-77009211	NOTEST	0	0	0	0	1	1
ENSG00000257527	ENSG00000257527	MIR3179-3	16:18505165-18505708	NOTEST	0	0	0	0	1	1
ENSG00000257528	ENSG00000257528	KRT8P19	12:62102039-62811211	NOTEST	0	0	0	0	1	1
ENSG00000257530	ENSG00000257530	RP11-843B15.2	12:32257050-32536567	NOTEST	0	0	0	0	1	1
ENSG00000257531	ENSG00000257531	RP3-405J10.2	12:50569570-50677329	NOTEST	0	0	0	0	1	1
ENSG00000257534	ENSG00000257534	RP11-834C11.10	12:54555848-54582778	NOTEST	0.144506	0.137606	-0.0705834	0	1	1
ENSG00000257535	ENSG00000257535	CR759890.2	HSCHR6_MHC_APD:30368501-30368589	NOTEST	0	0	0	0	1	1
ENSG00000257536	ENSG00000257536	AL845509.1	HSCHR6_MHC_QBL:32191852-32192020	NOTEST	0	0	0	0	1	1
ENSG00000257537	ENSG00000257537	AC139677.3	HSCHR17_1:44811785-44811978	NOTEST	0	0	0	0	1	1
ENSG00000257538	ENSG00000257538	AL935026.1	HSCHR6_MHC_QBL:32547664-32563145	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000257539	ENSG00000257539	HSPA8P14	12:111807085-111841114	NOTEST	0.00908894	0	#NAME?	0	1	1
ENSG00000257541	ENSG00000257541	RP11-58A17.4	12:58481674-58487145	NOTEST	0	0	0	0	1	1
ENSG00000257542	ENSG00000257542	OR7E47P	12:52463029-52502045	NOTEST	0	0	0	0	1	1
ENSG00000257543	ENSG00000257543	RP11-321F8.4	12:101802149-101802838	NOTEST	0.0712364	0.0509682	-0.483017	0	1	1
ENSG00000257544	ENSG00000257544	CR847849.1	HSCHR6_MHC_MANN:33186488-33209127	NOTEST	0	0	0	0	1	1
ENSG00000257545	ENSG00000257545	RP11-144F15.1	12:106751435-107283090	NOTEST	0.106198	0.0268273	-1.98498	0	1	1
ENSG00000257548	ENSG00000257548	RP11-797M17.1	12:107385141-107517092	NOTEST	0	0	0	0	1	1
ENSG00000257549	ENSG00000257549	AL662822.7	HSCHR6_MHC_COX:30445940-30446025	NOTEST	0	0	0	0	1	1
ENSG00000257550	ENSG00000257550	RP11-793H13.3	12:53900471-54020199	NOTEST	0.0272771	0	#NAME?	0	1	1
ENSG00000257554	ENSG00000257554	CR751550.1	HSCHR6_MHC_SSTO:30492088-30492213	NOTEST	0	0	0	0	1	1
ENSG00000257556	ENSG00000257556	RP11-44N21.1	14:105559945-105565341	NOTEST	0.415312	0.330726	-0.328559	0	1	1
ENSG00000257557	ENSG00000257557	RP11-84G21.1	12:79968758-80334448	NOTEST	0.156426	0.143787	-0.121554	0	1	1
ENSG00000257558	ENSG00000257558	RP11-536C10.15	14:19443725-19443847	NOTEST	0	0	0	0	1	1
ENSG00000257559	ENSG00000257559	CR382280.3	HSCHR6_MHC_MANN:30500761-30500846	NOTEST	0	0	0	0	1	1
ENSG00000257560	ENSG00000257560	BX247900.2	HSCHR6_MHC_SSTO:31051900-31052166	NOTEST	0	0	0	0	1	1
ENSG00000257561	ENSG00000257561	AC138688.3	HSCHR17_1:43735637-43740507	NOTEST	0	0	0	0	1	1
ENSG00000257562	ENSG00000257562	AL671859.1	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1
ENSG00000257563	ENSG00000257563	MIR3180-3	16:18496002-18497461	NOTEST	0	0	0	0	1	1
ENSG00000257564	ENSG00000257564	RP11-123M21.2	12:79187305-79187894	NOTEST	0.207899	0.0503447	-2.04597	0	1	1
ENSG00000257565	ENSG00000257565	AC217770.1	HSCHR17_1:44449946-44450193	NOTEST	0	0	0	0	1	1
ENSG00000257568	ENSG00000257568	RP11-863H1.1	12:62860596-62991363	NOTEST	0	0	0	0	1	1
ENSG00000257569	ENSG00000257569	GSTP1P1	12:56294083-56294402	NOTEST	0	0	0	0	1	1
ENSG00000257570	ENSG00000257570	RP11-133N21.12	12:49962000-50158717	NOTEST	0	0	0	0	1	1
ENSG00000257571	ENSG00000257571	CR933842.1	HSCHR6_MHC_MCF:29267208-29267748	NOTEST	0	0	0	0	1	1
ENSG00000257572	ENSG00000257572	RP11-478B9.2	12:45408454-45496890	NOTEST	0	0	0	0	1	1
ENSG00000257573	ENSG00000257573	RP11-496I2.5	14:19719544-19720589	NOTEST	0.29891	0.239289	-0.320958	0	1	1
ENSG00000257575	ENSG00000257575	AL805934.1	HSCHR6_MHC_QBL:31619245-31631569	NOTEST	0	0	0	0	1	1
ENSG00000257576	ENSG00000257576	RP11-153M3.1	12:56904785-56906487	NOTEST	0.0194009	0.0356713	0.878635	0	1	1
ENSG00000257578	ENSG00000257578	AC074378.1	HSCHR4_1:69242119-69242246	NOTEST	0	0	0	0	1	1
ENSG00000257579	ENSG00000257579	RP11-128P10.1	12:107712189-108053419	NOTEST	0.0442074	0	#NAME?	0	1	1
ENSG00000257580	ENSG00000257580	RP11-718L23.1	12:98711518-98712127	NOTEST	0	0	0	0	1	1
ENSG00000257582	ENSG00000257582	RP11-129J12.2	10:101286106-101290934	NOTEST	0	0	0	0	1	1
ENSG00000257583	ENSG00000257583	RP11-167N24.4	12:95782374-95799280	NOTEST	0	0	0	0	1	1
ENSG00000257585	ENSG00000257585	LINC00609	14:36539632-36645674	NOTEST	0	0	0	0	1	1
ENSG00000257586	ENSG00000257586	RP11-554L12.3	12:39388604-39390684	NOTEST	0	0	0	0	1	1
ENSG00000257587	ENSG00000257587	RP11-711C17.1	12:74300719-74313117	NOTEST	0	0	0	0	1	1
ENSG00000257588	ENSG00000257588	RP11-469H8.6	12:50344523-50359464	NOTEST	0	0.0630283	inf	0	1	1
ENSG00000257589	ENSG00000257589	AL805913.1	HSCHR6_MHC_QBL:32961399-32984034	NOTEST	0	0	0	0	1	1
ENSG00000257590	ENSG00000257590	CR759772.2	HSCHR6_MHC_MCF:31039434-31040043	NOTEST	0	0	0	0	1	1
ENSG00000257591	ENSG00000257591	ZNF625	19:12203077-12267546	NOTEST	0.0333394	0.181043	2.44103	0	1	1
ENSG00000257593	ENSG00000257593	CR759793.1	HSCHR6_MHC_MCF:33456680-33468861	NOTEST	0	0	0	0	1	1
ENSG00000257595	ENSG00000257595	RP3-473L9.4	12:111807085-111841114	NOTEST	0	0	0	0	1	1
ENSG00000257599	ENSG00000257599	OVCH1-AS1	12:29542226-29650619	NOTEST	0	0.0217803	inf	0	1	1

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ENSG00000257601	ENSG00000257601	CR759784.2	HSCHR6_MHC_MCF:31897465-31898542	NOTEST	0	0	0	0	1	1
ENSG00000257602	ENSG00000257602	BX927220.4	HSCHR6_MHC_MANN:30542941-30544028	NOTEST	0	0	0	0	1	1
ENSG00000257603	ENSG00000257603	RP11-100F15.1	12:114514937-114517707	NOTEST	0	0	0	0	1	1
ENSG00000257604	ENSG00000257604	RP11-359M6.2	12:79257772-79897176	NOTEST	0	0	0	0	1	1
ENSG00000257607	ENSG00000257607	RP11-449P15.1	7:1036621-1177896	NOTEST	0.382782	0.173664	-1.14023	0	1	1
ENSG00000257608	ENSG00000257608	GRAMD4P3	14:19611767-19643377	NOTEST	0	0	0	0	1	1
ENSG00000257609	ENSG00000257609	RP11-275O18.1	12:82262146-82262825	NOTEST	0	0	0	0	1	1
ENSG00000257611	ENSG00000257611	RP11-185N2.1	12:106563781-106566215	NOTEST	0	0	0	0	1	1
ENSG00000257612	ENSG00000257612	RP11-384J4.1	14:27305933-27629626	NOTEST	0	0	0	0	1	1
ENSG00000257613	ENSG00000257613	RP11-320P7.1	12:70132460-70748773	NOTEST	0	0	0	0	1	1
ENSG00000257614	ENSG00000257614	RP11-116N8.2	14:36288429-36536396	NOTEST	0	0	0	0	1	1
ENSG00000257615	ENSG00000257615	AC139677.4	HSCHR17_1:44705730-44708833	NOTEST	0	0	0	0	1	1
ENSG00000257616	ENSG00000257616	RP11-641A6.5	12:53124208-53126649	NOTEST	0	0	0	0	1	1
ENSG00000257618	ENSG00000257618	BX000357.1	HSCHR6_MHC_QBL:30495958-30496179	NOTEST	0	0	0	0	1	1
ENSG00000257622	ENSG00000257622	RP11-44N21.4	14:105607317-105647660	NOTEST	0	0.259218	inf	0	1	1
ENSG00000257624	ENSG00000257624	RP1-128M12.3	12:112369085-112450970	NOTEST	0	0	0	0	1	1
ENSG00000257626	ENSG00000257626	CR753819.2	HSCHR6_MHC_DBB:31076301-31101556	NOTEST	0	0	0	0	1	1
ENSG00000257629	ENSG00000257629	RP11-13A1.2	12:89421533-89422299	NOTEST	0	0	0	0	1	1
ENSG00000257630	ENSG00000257630	CR388372.3	HSCHR6_MHC_DBB:30467711-30467784	NOTEST	0	0	0	0	1	1
ENSG00000257632	ENSG00000257632	CR759828.1	HSCHR6_MHC_MCF:31381069-31381196	NOTEST	0	0	0	0	1	1
ENSG00000257634	ENSG00000257634	RP11-850F7.7	12:55076756-55081218	NOTEST	0	0	0	0	1	1
ENSG00000257635	ENSG00000257635	RP11-536C10.10	14:19475115-19476455	NOTEST	0	0	0	0	1	1
ENSG00000257636	ENSG00000257636	RP11-1103G16.1	14:30907197-31089269	NOTEST	0	0	0	0	1	1
ENSG00000257637	ENSG00000257637	CR759795.1	HSCHR6_MHC_MCF:33065821-33088426	NOTEST	0	0	0	0	1	1
ENSG00000257639	ENSG00000257639	CTB-31N19.2	16:21544265-21561694	NOTEST	0	0	0	0	1	1
ENSG00000257640	ENSG00000257640	RP11-570L15.2	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000257642	ENSG00000257642	RP11-474B16.1	12:105567073-105789875	NOTEST	0	0.0278817	inf	0	1	1
ENSG00000257643	ENSG00000257643	RP11-278C7.2	12:32832133-32908836	NOTEST	0	0	0	0	1	1
ENSG00000257644	ENSG00000257644	RP11-536C10.13	14:19406794-19427443	NOTEST	0	0	0	0	1	1
ENSG00000257645	ENSG00000257645	RP11-804F13.2	12:38926696-38926852	NOTEST	0	0	0	0	1	1
ENSG00000257646	ENSG00000257646	BX936369.4	HSCHR6_MHC_SSTO:30448675-30453414	NOTEST	0	0	0	0	1	1
ENSG00000257647	ENSG00000257647	RP11-701H24.3	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000257648	ENSG00000257648	CYCSP30	12:88143918-88144090	NOTEST	0	0	0	0	1	1
ENSG00000257649	ENSG00000257649	METTL7AP1	12:52622876-52623372	NOTEST	0	0	0	0	1	1
ENSG00000257651	ENSG00000257651	CR759890.3	HSCHR6_MHC_APD:30403282-30403496	NOTEST	0	0	0	0	1	1
ENSG00000257652	ENSG00000257652	AC019173.1	HSCHR4_1:69313164-69363317	NOTEST	0	0	0	0	1	1
ENSG00000257653	ENSG00000257653	RP11-579D7.2	12:49159974-49182820	NOTEST	0.203171	0	#NAME?	0	1	1
ENSG00000257654	ENSG00000257654	RP11-497G19.2	12:117136140-117140935	NOTEST	0	0	0	0	1	1
ENSG00000257656	ENSG00000257656	AL844213.5	HSCHR6_MHC_QBL:30445599-30445684	NOTEST	0	0	0	0	1	1
ENSG00000257657	ENSG00000257657	RP11-352M15.1	12:45875653-46004403	NOTEST	0.037418	0	#NAME?	0	1	1

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ENSG00000257658	ENSG00000257658	RP3-521E19.3	12:112597991-112819896	NOTEST	0	0	0	0	1	1
ENSG00000257659	ENSG00000257659	CR759912.2	HSCHR6_MHC_APD:30487451-30487536	NOTEST	0	0	0	0	1	1
ENSG00000257660	ENSG00000257660	RP11-579D7.4	12:49182929-49184318	NOTEST	0	0.0432018	inf	0	1	1
ENSG00000257661	ENSG00000257661	AL845509.2	HSCHR6_MHC_QBL:32171955-32172096	NOTEST	0	0	0	0	1	1
ENSG00000257662	ENSG00000257662	EIF4A1P12	14:29061428-29082829	NOTEST	0	1.80038	inf	0	1	1
ENSG00000257664	ENSG00000257664	RSL24D1P5	12:63449054-63449545	NOTEST	0	0	0	0	1	1
ENSG00000257665	ENSG00000257665	AL773535.3	HSCHR6_MHC_QBL:30349770-30349858	NOTEST	0	0	0	0	1	1
ENSG00000257666	ENSG00000257666	CBX3P5	12:95611521-95696566	NOTEST	0	0	0	0	1	1
ENSG00000257668	ENSG00000257668	RP11-58A17.2	12:58377577-58378544	NOTEST	0	0	0	0	1	1
ENSG00000257670	ENSG00000257670	BX511262.2	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000257671	ENSG00000257671	RP3-416H24.1	12:52626303-52702947	NOTEST	0	0	0	0	1	1
ENSG00000257672	ENSG00000257672	RP11-536C10.17	14:19390864-19391038	NOTEST	0	0	0	0	1	1
ENSG00000257674	ENSG00000257674	RP11-76E16.2	12:42632248-42984157	NOTEST	0.0383071	0.046136	0.268282	0	1	1
ENSG00000257675	ENSG00000257675	RP11-641A6.9	12:53142559-53143911	NOTEST	0.0228563	0.00884795	-1.36918	0	1	1
ENSG00000257677	ENSG00000257677	RP1-81P11.1	12:77613382-77622473	NOTEST	0	0	0	0	1	1
ENSG00000257679	ENSG00000257679	UGT2A3	HSCHR4_1:69676503-69699836	NOTEST	0	0	0	0	1	1
ENSG00000257680	ENSG00000257680	RP11-367O10.1	12:41086243-41466220	NOTEST	0	0	0	0	1	1
ENSG00000257682	ENSG00000257682	RP11-314D7.3	12:73552969-73602097	NOTEST	0	0	0	0	1	1
ENSG00000257683	ENSG00000257683	RP11-110L15.2	12:116248163-116323942	NOTEST	0	0	0	0	1	1
ENSG00000257686	ENSG00000257686	CR759912.3	HSCHR6_MHC_APD:30485726-30485799	NOTEST	0	0	0	0	1	1
ENSG00000257687	ENSG00000257687	RP11-609L23.3	12:43009304-43040300	NOTEST	0	0	0	0	1	1
ENSG00000257690	ENSG00000257690	CR759890.4	HSCHR6_MHC_APD:30344192-30344910	NOTEST	0	0	0	0	1	1
ENSG00000257691	ENSG00000257691	RP11-345J4.1	16:29262828-29519817	NOTEST	0	0	0	0	1	1
ENSG00000257693	ENSG00000257693	CR759912.4	HSCHR6_MHC_APD:30517399-30529581	NOTEST	0	0	0	0	1	1
ENSG00000257696	ENSG00000257696	RP11-175P13.2	12:100536835-100538449	NOTEST	0	0	0	0	1	1
ENSG00000257697	ENSG00000257697	BX927180.1	HSCHR6_MHC_MANN:3227 3521-32273689	NOTEST	0	0	0	0	1	1
ENSG00000257700	ENSG00000257700	RP11-641A6.3	12:53083409-53097247	NOTEST	0	0	0	0	1	1
ENSG00000257701	ENSG00000257701	BX247900.3	HSCHR6_MHC_SSTO:3105 9238-31062047	NOTEST	0	0	0	0	1	1
ENSG00000257702	ENSG00000257702	LBX2-AS1	2:74724643-74731805	NOTEST	0.373509	0.497325	0.413047	0	1	1
ENSG00000257703	ENSG00000257703	RP11-328J6.1	12:103474727-103572453	NOTEST	0.0659067	0	#NAME?	0	1	1
ENSG00000257705	ENSG00000257705	AL844853.1	HSCHR6_MHC_QBL:31811418-31812495	NOTEST	0	0	0	0	1	1
ENSG00000257707	ENSG00000257707	AL662890.2	HSCHR6_MHC_DBB:28706708-28709409	NOTEST	0	0	0	0	1	1
ENSG00000257709	ENSG00000257709	BX927139.1	HSCHR6_MHC_MANN:3112 7486-31152786	NOTEST	0	0	0	0	1	1
ENSG00000257711	ENSG00000257711	RP11-482D24.2	12:106751435-107283090	NOTEST	0.1393	0.0791766	-0.815053	0	1	1
ENSG00000257712	ENSG00000257712	BX936369.5	HSCHR6_MHC_SSTO:3044 7512-30447597	NOTEST	0	0	0	0	1	1
ENSG00000257713	ENSG00000257713	AL662822.8	HSCHR6_MHC_COX:30488110-30489197	NOTEST	0	0	0	0	1	1
ENSG00000257715	ENSG00000257715	RP11-256L6.2	12:96390298-96437298	NOTEST	0	0	0	0	1	1
ENSG00000257717	ENSG00000257717	AC225613.4	HSCHR17_1:44566754-44567102	NOTEST	0	0	0	0	1	1
ENSG00000257720	ENSG00000257720	ILF2P2	14:36288429-36536396	NOTEST	0	0.0110563	inf	0	1	1
ENSG00000257721	ENSG00000257721	RP11-536C10.2	14:19332153-19372787	NOTEST	0	0	0	0	1	1
ENSG00000257723	ENSG00000257723	CHCHD3P2	12:72332625-73059422	NOTEST	0	0	0	0	1	1
ENSG00000257725	ENSG00000257725	RP11-654D12.3	12:90276441-90383066	NOTEST	0	0	0	0	1	1
ENSG00000257726	ENSG00000257726	RP11-116D17.1	12:115800816-115802550	NOTEST	0	0	0	0	1	1

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ENSG00000257730	ENSG00000257730	LSM6P2	12:50164742-50164919	NOTEST	0	0	0	0	1	1
ENSG00000257731	ENSG00000257731	RP11-536C10.11	14:19406794-19427443	NOTEST	0	0	0	0	1	1
ENSG00000257732	ENSG00000257732	RP11-818F20.5	12:104609556-104744061	NOTEST	0	0	0	0	1	1
ENSG00000257733	ENSG00000257733	CR759782.1	HSCHR6_MHC_MCF:31942046-31996308	NOTEST	0	0	0	0	1	1
ENSG00000257735	ENSG00000257735	RP11-370I10.6	12:48733790-48836730	NOTEST	0	0	0	0	1	1
ENSG00000257736	ENSG00000257736	CR933877.1	HSCHR6_MHC_MANN:31860646-31861723	NOTEST	0	0	0	0	1	1
ENSG00000257737	ENSG00000257737	RP11-341G23.2	12:103981050-104162636	NOTEST	0	0	0	0	1	1
ENSG00000257738	ENSG00000257738	RP11-139E19.2	12:45566846-45834187	NOTEST	0	0.0582138	inf	0	1	1
ENSG00000257739	ENSG00000257739	CR753819.3	HSCHR6_MHC_DBB:31076301-31101556	NOTEST	0	0	0	0	1	1
ENSG00000257741	ENSG00000257741	RP11-540D4.3	12:81156932-81164496	NOTEST	0	0	0	0	1	1
ENSG00000257743	ENSG00000257743	RP11-1220K2.2	7:141811548-141922124	NOTEST	0	0	0	0	1	1
ENSG00000257744	ENSG00000257744	AL662833.1	HSCHR6_MHC_COX:31222159-31222501	NOTEST	0	0	0	0	1	1
ENSG00000257745	ENSG00000257745	UGT2B10	HSCHR4_1:69564039-69580068	NOTEST	0	0	0	0	1	1
ENSG00000257746	ENSG00000257746	RP11-202G11.2	12:93392993-93609455	NOTEST	0	0	0	0	1	1
ENSG00000257747	ENSG00000257747	RP11-362A1.1	12:82347497-82386912	NOTEST	0	0	0	0	1	1
ENSG00000257748	ENSG00000257748	RP11-966I7.3	14:29241909-29299410	NOTEST	0	0	0	0	1	1
ENSG00000257749	ENSG00000257749	CTD-2314B22.2	14:19812175-19925348	NOTEST	0	0.0622575	inf	0	1	1
ENSG00000257750	ENSG00000257750	RP11-295G12.1	12:74154468-74192507	NOTEST	0	0	0	0	1	1
ENSG00000257751	ENSG00000257751	RP11-536C10.21	14:20078032-20152898	NOTEST	0	0	0	0	1	1
ENSG00000257752	ENSG00000257752	RP11-474L23.3	12:88373815-88535993	NOTEST	0.0792725	0	#NAME?	0	1	1
ENSG00000257754	ENSG00000257754	RP11-650K20.2	12:104164230-104234975	NOTEST	0	0	0	0	1	1
ENSG00000257756	ENSG00000257756	RP11-776A13.3	12:30383711-30449640	NOTEST	0	0	0	0	1	1
ENSG00000257757	ENSG00000257757	OR6C7P	12:55736624-55737558	NOTEST	0	0	0	0	1	1
ENSG00000257758	ENSG00000257758	KRT18P20	12:105370526-105371805	NOTEST	0	0	0	0	1	1
ENSG00000257759	ENSG00000257759	RP11-486O13.4	14:70892528-71014181	NOTEST	0	0	0	0	1	1
ENSG00000257761	ENSG00000257761	RP11-186F10.2	12:71518864-71980090	NOTEST	0	0	0	0	1	1
ENSG00000257762	ENSG00000257762	RP11-626I20.3	12:103941571-103953593	NOTEST	0	0	0	0	1	1
ENSG00000257763	ENSG00000257763	OR5BK1P	12:48733790-48836730	NOTEST	0	0	0	0	1	1
ENSG00000257764	ENSG00000257764	RP11-1143G9.4	12:69742120-69748014	NOTEST	0.0347079	0.160725	2.21126	0	1	1
ENSG00000257766	ENSG00000257766	RP11-341G23.3	12:103981050-104162636	NOTEST	0	0	0	0	1	1
ENSG00000257767	ENSG00000257767	RP11-162P23.2	12:112123856-112247782	NOTEST	0.00379617	0.0748473	4.30133	0	1	1
ENSG00000257769	ENSG00000257769	CTB-193M12.1	16:15489610-15737023	NOTEST	0	0	0	0	1	1
ENSG00000257770	ENSG00000257770	GPX5	HSCHR6_MHC_COX:28478549-28503695	NOTEST	0	0	0	0	1	1
ENSG00000257771	ENSG00000257771	RP11-70F11.8	12:50305735-50324103	NOTEST	0	0	0	0	1	1
ENSG00000257773	ENSG00000257773	ST13P3	12:106409674-106410784	NOTEST	0.0158172	0.0715716	2.17789	0	1	1
ENSG00000257774	ENSG00000257774	AC139677.5	HSCHR17_1:44831765-44898747	NOTEST	0	0	0	0	1	1

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ENSG00000257775	ENSG00000257775	AC127032.2	HSCHR17_1:43956273-43956914	NOTEST	0	0	0	0	1	1
ENSG00000257777	ENSG00000257777	RP11-25J3.2	12:75956981-76377795	NOTEST	0	0	0	0	1	1
ENSG00000257778	ENSG00000257778	AL390196.1	HSCHR6_MHC_SSTO:28659680-28659895	NOTEST	0	0	0	0	1	1
ENSG00000257779	ENSG00000257779	RP11-848D3.4	12:63396248-63396575	NOTEST	0	0	0	0	1	1
ENSG00000257780	ENSG00000257780	GLYCAM1	12:55001970-55004246	NOTEST	0	0	0	0	1	1
ENSG00000257781	ENSG00000257781	RP11-110L15.1	12:116193066-116237741	NOTEST	0	0	0	0	1	1
ENSG00000257782	ENSG00000257782	CR354443.3	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000257783	ENSG00000257783	AL773544.2	HSCHR6_MHC_QBL:31074947-31100262	NOTEST	0	0	0	0	1	1
ENSG00000257784	ENSG00000257784	RP11-630C16.1	12:42157990-42159383	NOTEST	0	0	0	0	1	1
ENSG00000257786	ENSG00000257786	RP11-272K23.4	12:80799773-81072802	NOTEST	0	0	0	0	1	1
ENSG00000257787	ENSG00000257787	RP11-20L19.1	12:91203052-91204457	NOTEST	0	0	0	0	1	1
ENSG00000257790	ENSG00000257790	RP11-1136G11.6	12:53547055-53548268	NOTEST	0.0142535	0	#NAME?	0	1	1
ENSG00000257791	ENSG00000257791	BX294158.3	HSCHR6_MHC_SSTO:30349386-30349474	NOTEST	0	0	0	0	1	1
ENSG00000257792	ENSG00000257792	OR5BJ1P	12:48733790-48836730	NOTEST	0	0	0	0	1	1
ENSG00000257793	ENSG00000257793	CRHR1	HSCHR17_1:44339178-44390746	NOTEST	0	0	0	0	1	1
ENSG00000257794	ENSG00000257794	RP11-125N22.4	12:37935813-37936188	NOTEST	0	0	0	0	1	1
ENSG00000257796	ENSG00000257796	CR936918.1	HSCHR6_MHC_APD:29267100-29267640	NOTEST	0	0	0	0	1	1
ENSG00000257797	ENSG00000257797	CTD-2382E5.2	15:42264960-42343388	NOTEST	0	0	0	0	1	1
ENSG00000257798	ENSG00000257798	CR751550.2	HSCHR6_MHC_SSTO:30489683-30490770	NOTEST	0	0	0	0	1	1
ENSG00000257800	ENSG00000257800	FNBP1P1	2:74347806-74350345	NOTEST	0.235176	0.211607	-0.152351	0	1	1
ENSG00000257802	ENSG00000257802	MRS2P2	12:72233486-72320629	NOTEST	0	0.0112097	inf	0	1	1
ENSG00000257803	ENSG00000257803	RP11-575G13.2	12:100967460-101022064	NOTEST	0.463704	0.0883299	-2.39223	0	1	1
ENSG00000257805	ENSG00000257805	BX908738.1	HSCHR6_MHC_MANN:29267066-29267606	NOTEST	0	0	0	0	1	1
ENSG00000257806	ENSG00000257806	AC225613.5	HSCHR17_1:44575672-44578193	NOTEST	0	0	0	0	1	1
ENSG00000257807	ENSG00000257807	RP1-90J4.3	12:47878471-47879505	NOTEST	0	0	0	0	1	1
ENSG00000257808	ENSG00000257808	RP11-1136G11.8	12:53551446-53584596	NOTEST	0	0	0	0	1	1
ENSG00000257809	ENSG00000257809	RP11-603J24.14	12:56544579-56584068	NOTEST	0	0.0408147	inf	0	1	1
ENSG00000257811	ENSG00000257811	AL662867.1	HSCHR6_MHC_COX:31075026-31100333	NOTEST	0	0	0	0	1	1
ENSG00000257813	ENSG00000257813	RP11-73B8.2	12:43963571-43965841	NOTEST	0	0	0	0	1	1
ENSG00000257814	ENSG00000257814	ARL17	HSCHR17_1:43580584-43647125	NOTEST	0	0	0	0	1	1
ENSG00000257817	ENSG00000257817	RP4-601P9.2	12:115151615-115205762	NOTEST	0	0	0	0	1	1
ENSG00000257818	ENSG00000257818	RP11-1143G9.2	12:69678176-69679265	NOTEST	0.0161791	0.0113952	-0.505706	0	1	1
ENSG00000257819	ENSG00000257819	BX927214.3	HSCHR6_MHC_MANN:30394979-30395064	NOTEST	0	0	0	0	1	1
ENSG00000257820	ENSG00000257820	MRPS6P4	12:89713140-89713426	NOTEST	0	0	0	0	1	1
ENSG00000257822	ENSG00000257822	AC217770.2	HSCHR17_1:44410811-44414829	NOTEST	0	0	0	0	1	1
ENSG00000257823	ENSG00000257823	RP11-560G2.2	12:75628519-75784708	NOTEST	0	0.0142498	inf	0	1	1
ENSG00000257824	ENSG00000257824	RP11-1049A21.2	12:54891494-54937889	NOTEST	0	0	0	0	1	1
ENSG00000257825	ENSG00000257825	RP11-536C10.5	14:19332153-19372787	NOTEST	0	0	0	0	1	1
ENSG00000257826	ENSG00000257826	RP11-116N8.4	14:36288429-36536396	NOTEST	0	0	0	0	1	1
ENSG00000257829	ENSG00000257829	RP11-845M18.6	12:52626303-52702947	NOTEST	0	0.0255271	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000257830	ENSG00000257830	RP11-845M18.7	12:52626303-52702947	NOTEST	0	0	0	0	1	1
ENSG00000257831	ENSG00000257831	RP11-596D21.1	14:31717833-31926716	NOTEST	0.0396978	0.0155131	-1.35557	0	1	1
ENSG00000257832	ENSG00000257832	AL671879.1	HSCHR6_MHC_COX:28658640-28659004	NOTEST	0	0	0	0	1	1
ENSG00000257834	ENSG00000257834	AL662822.9	HSCHR6_MHC_COX:30350589-30350674	NOTEST	0	0	0	0	1	1
ENSG00000257835	ENSG00000257835	RP1-97G4.1	12:77718420-77966055	NOTEST	0.0348722	0	#NAME?	0	1	1
ENSG00000257837	ENSG00000257837	RP11-263K4.4	12:82898989-82899967	NOTEST	0	0	0	0	1	1
ENSG00000257838	ENSG00000257838	RP11-368J21.3	16:22557018-22588186	NOTEST	0.0400788	0.0390445	-0.037723	0	1	1
ENSG00000257839	ENSG00000257839	RP11-290L1.2	12:76419226-76427712	NOTEST	0.0550469	0.0430025	-0.35624	0	1	1
ENSG00000257841	ENSG00000257841	BX294158.4	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000257842	ENSG00000257842	NOVA1-AS1	14:27067617-27305664	NOTEST	0.260292	0.377954	0.538081	0	1	1
ENSG00000257843	ENSG00000257843	AL845450.2	HSCHR6_MHC_COX:30142136-30171100	NOTEST	0	0	0	0	1	1
ENSG00000257844	ENSG00000257844	KRT124P	12:52801363-52828309	NOTEST	0	0	0	0	1	1
ENSG00000257845	ENSG00000257845	RP11-626P14.1	14:27067617-27305664	NOTEST	0	0	0	0	1	1
ENSG00000257846	ENSG00000257846	RP11-597A11.3	14:20078032-20152898	NOTEST	0	0	0	0	1	1
ENSG00000257847	ENSG00000257847	LSM3P2	12:94960899-95044338	NOTEST	0	0	0	0	1	1
ENSG00000257848	ENSG00000257848	RP11-474C8.5	12:48541570-48574996	NOTEST	0	0	0	0	1	1
ENSG00000257849	ENSG00000257849	RP11-547C5.1	12:43359924-43361156	NOTEST	0	0	0	0	1	1
ENSG00000257850	ENSG00000257850	CR388372.4	HSCHR6_MHC_DBB:30469436-30469521	NOTEST	0	0	0	0	1	1
ENSG00000257852	ENSG00000257852	RP11-843B15.1	12:32225667-32225814	NOTEST	0	0	0	0	1	1
ENSG00000257853	ENSG00000257853	MED15P1	14:19498564-19502394	NOTEST	0	0	0	0	1	1
ENSG00000257854	ENSG00000257854	BX000357.2	HSCHR6_MHC_QBL:30498659-30521007	NOTEST	0	0	0	0	1	1
ENSG00000257855	ENSG00000257855	RP11-629O19.1	12:85961655-85962017	NOTEST	0	0	0	0	1	1
ENSG00000257856	ENSG00000257856	CR759792.1	HSCHR6_MHC_MCF:32082522-32172461	NOTEST	0	0	0	0	1	1
ENSG00000257858	ENSG00000257858	MTND1P24	12:42093192-42094053	NOTEST	0	0	0	0	1	1
ENSG00000257859	ENSG00000257859	CASC18	12:106097980-106137840	NOTEST	0	0	0	0	1	1
ENSG00000257860	ENSG00000257860	RP11-552I14.1	12:103474727-103572453	NOTEST	0	0	0	0	1	1
ENSG00000257862	ENSG00000257862	CR759281.3	HSCHR6_MHC_DBB:30326211-30326320	NOTEST	0	0	0	0	1	1
ENSG00000257863	ENSG00000257863	RP11-587P21.3	12:92295233-92299963	NOTEST	0	0.012459	inf	0	1	1
ENSG00000257864	ENSG00000257864	RP11-46I1.2	12:44229769-44783545	NOTEST	0	0.0524134	inf	0	1	1
ENSG00000257865	ENSG00000257865	RP11-154D9.1	12:60812763-60813074	NOTEST	0	0	0	0	1	1
ENSG00000257867	ENSG00000257867	CR753815.1	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000257868	ENSG00000257868	CTD-2311B13.8	14:19983558-20020272	NOTEST	0	0	0	0	1	1
ENSG00000257869	ENSG00000257869	CTD-2591A6.2	14:28787346-28887818	NOTEST	0.170235	0.0343428	-2.30945	0	1	1
ENSG00000257870	ENSG00000257870	RP11-616L12.1	12:55403529-55408031	NOTEST	0	0	0	0	1	1
ENSG00000257872	ENSG00000257872	RP11-453D16.2	12:76531204-76532390	NOTEST	0	0	0	0	1	1
ENSG00000257873	ENSG00000257873	AC127032.3	HSCHR17_1:43912819-43913891	NOTEST	0	0	0	0	1	1
ENSG00000257874	ENSG00000257874	BX927320.1	HSCHR6_MHC_MANN:31593387-31600249	NOTEST	0	0	0	0	1	1
ENSG00000257875	ENSG00000257875	RP11-263K4.1	12:82617459-82873015	NOTEST	0	0	0	0	1	1
ENSG00000257877	ENSG00000257877	RP3-462E2.3	12:112250596-112251224	NOTEST	0	0	0	0	1	1
ENSG00000257878	ENSG00000257878	RP11-256L6.3	12:96390298-96437298	NOTEST	0	0	0	0	1	1
ENSG00000257879	ENSG00000257879	RP11-90C1.1	12:78720459-78934455	NOTEST	0	0	0	0	1	1
ENSG00000257880	ENSG00000257880	RP11-769N19.2	12:62102039-62811211	NOTEST	0	0	0	0	1	1

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ENSG00000257882	ENSG00000257882	AC217770.3	HSCHR17_1:44327964-44330147	NOTEST	0	0	0	0	1	1
ENSG00000257883	ENSG00000257883	RP11-497G19.1	12:117099386-117135870	NOTEST	0	0	0	0	1	1
ENSG00000257884	ENSG00000257884	RP11-597A11.4	14:20078032-20152898	NOTEST	0	0	0	0	1	1
ENSG00000257885	ENSG00000257885	RP11-474C8.4	12:48541570-48574996	NOTEST	0	0	0	0	1	1
ENSG00000257886	ENSG00000257886	RP11-61E11.1	12:105380087-105478355	NOTEST	0	0	0	0	1	1
ENSG00000257887	ENSG00000257887	AC138688.4	HSCHR17_1:43886502-43890161	NOTEST	0	0	0	0	1	1
ENSG00000257888	ENSG00000257888	AC127032.4	HSCHR17_1:43977150-43980249	NOTEST	0	0	0	0	1	1
ENSG00000257889	ENSG00000257889	AC225613.6	HSCHR17_1:44499891-44500132	NOTEST	0	0	0	0	1	1
ENSG00000257890	ENSG00000257890	RP11-114F10.2	12:106444738-106452032	NOTEST	0	0	0	0	1	1
ENSG00000257891	ENSG00000257891	CTD-2311B13.1	14:19505870-19519837	NOTEST	0	0	0	0	1	1
ENSG00000257892	ENSG00000257892	AL844213.6	HSCHR6_MHC_QBL:30455662-30456253	NOTEST	0	0	0	0	1	1
ENSG00000257893	ENSG00000257893	RP11-587P21.2	12:92271166-92274431	NOTEST	0	0	0	0	1	1
ENSG00000257894	ENSG00000257894	RP1-78O14.1	12:79257772-79897176	NOTEST	0	0	0	0	1	1
ENSG00000257895	ENSG00000257895	BX511262.3	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000257896	ENSG00000257896	RP11-210N13.1	12:44122409-44152620	NOTEST	0.135947	0.117982	-0.204475	0	1	1
ENSG00000257897	ENSG00000257897	RP11-812D23.1	12:86372515-87232775	NOTEST	0	0	0	0	1	1
ENSG00000257899	ENSG00000257899	RP11-125N22.3	12:37938086-37938386	NOTEST	0	0	0	0	1	1
ENSG00000257900	ENSG00000257900	RP11-454K7.1	14:45846470-45858489	NOTEST	0	0	0	0	1	1
ENSG00000257901	ENSG00000257901	CR759890.5	HSCHR6_MHC_APD:30369016-30369104	NOTEST	0	0	0	0	1	1
ENSG00000257902	ENSG00000257902	BX936369.6	HSCHR6_MHC_SSTO:30462425-30462546	NOTEST	0	0	0	0	1	1
ENSG00000257904	ENSG00000257904	RP11-269C4.2	14:30045686-30766249	NOTEST	0.0228514	0	#NAME?	0	1	1
ENSG00000257905	ENSG00000257905	RP3-432I18.1	12:47986990-47987223	NOTEST	0	0	0	0	1	1
ENSG00000257906	ENSG00000257906	RP1-90J4.1	12:47808790-47813962	NOTEST	0	0	0	0	1	1
ENSG00000257907	ENSG00000257907	EEF1A1P17	12:44053629-44054904	NOTEST	0	0	0	0	1	1
ENSG00000257910	ENSG00000257910	RP11-461F16.3	12:77252494-77274132	NOTEST	0	0	0	0	1	1
ENSG00000257911	ENSG00000257911	CR382280.4	HSCHR6_MHC_MANN:30523871-30523956	NOTEST	0	0	0	0	1	1
ENSG00000257912	ENSG00000257912	RP11-248E9.5	12:88189509-88195805	NOTEST	0	0	0	0	1	1
ENSG00000257914	ENSG00000257914	AL662834.2	HSCHR6_MHC_COX:31808913-31809602	NOTEST	0	0	0	0	1	1
ENSG00000257915	ENSG00000257915	GLULP5	12:114518185-114551294	NOTEST	0	0	0	0	1	1
ENSG00000257916	ENSG00000257916	AL662822.10	HSCHR6_MHC_COX:30456002-30456593	NOTEST	0	0	0	0	1	1
ENSG00000257917	ENSG00000257917	AL901607.1	HSCHR6_MHC_COX:28731300-28731408	NOTEST	0	0	0	0	1	1
ENSG00000257918	ENSG00000257918	RP11-482D24.3	12:106751435-107283090	NOTEST	0.201734	0.140033	-0.526689	0	1	1
ENSG00000257920	ENSG00000257920	RP11-541G9.2	12:97666469-97669987	NOTEST	0	0	0	0	1	1
ENSG00000257924	ENSG00000257924	RP11-493L12.5	12:47747536-47763718	NOTEST	0	0	0	0	1	1
ENSG00000257925	ENSG00000257925	RP11-493L12.3	12:47631516-47672804	NOTEST	0	0	0	0	1	1
ENSG00000257927	ENSG00000257927	MRPS36P5	12:43447891-43448189	NOTEST	0	0	0	0	1	1
ENSG00000257931	ENSG00000257931	CTD-2311B13.7	14:19932011-19972292	NOTEST	0	0.104502	inf	0	1	1
ENSG00000257932	ENSG00000257932	RP11-155I9.1	12:30473766-30474550	NOTEST	0	0	0	0	1	1
ENSG00000257933	ENSG00000257933	RP11-125N22.1	12:37938408-37938600	NOTEST	0	0	0	0	1	1
ENSG00000257934	ENSG00000257934	BX927214.4	HSCHR6_MHC_MANN:30405461-30405549	NOTEST	0	0	0	0	1	1
ENSG00000257935	ENSG00000257935	RP11-82C23.2	12:113899838-113918429	NOTEST	0	0	0	0	1	1
ENSG00000257936	ENSG00000257936	AC139677.6	HSCHR17_1:44736660-44752551	NOTEST	0	0	0	0	1	1

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ENSG00000257937	ENSG00000257937	AL844213.7	HSCHR6_MHC_QBL:30469810-30469898	NOTEST	0	0	0	0	1	1
ENSG00000257939	ENSG00000257939	AC019319.1	HSCHR17_1:45030983-45041395	NOTEST	0	0	0	0	1	1
ENSG00000257940	ENSG00000257940	RP11-248E9.6	12:88210262-88211608	NOTEST	0	0	0	0	1	1
ENSG00000257941	ENSG00000257941	RP11-290L1.4	12:76438669-76478813	NOTEST	0.126273	0.297935	1.23845	0	1	1
ENSG00000257943	ENSG00000257943	RP11-167N24.3	12:95801710-95830604	NOTEST	0	0	0	0	1	1
ENSG00000257944	ENSG00000257944	AL844853.2	HSCHR6_MHC_QBL:31811418-31812495	NOTEST	0	0	0	0	1	1
ENSG00000257945	ENSG00000257945	CR759912.5	HSCHR6_MHC_APD:30514698-30514919	NOTEST	0	0	0	0	1	1
ENSG00000257947	ENSG00000257947	RP11-46I1.1	12:44229769-44783545	NOTEST	0	0	0	0	1	1
ENSG00000257948	ENSG00000257948	RP11-123M21.1	12:79198127-79202279	NOTEST	0	0	0	0	1	1
ENSG00000257950	ENSG00000257950	P2RX5-TAX1BP3	17:3566195-3599698	NOTEST	0.0728121	0.0637571	-0.191592	0	1	1
ENSG00000257951	ENSG00000257951	RP11-554D14.4	12:108275018-108277159	NOTEST	0	0	0	0	1	1
ENSG00000257953	ENSG00000257953	RP11-620J15.1	12:58213709-58240522	NOTEST	0	0.2936	inf	0	1	1
ENSG00000257954	ENSG00000257954	RP11-161H23.10	12:49760368-49921205	NOTEST	0.276002	0.248203	-0.153158	0	1	1
ENSG00000257955	ENSG00000257955	RP1-228P16.5	12:48405086-48419252	NOTEST	0.0187773	0	#NAME?	0	1	1
ENSG00000257956	ENSG00000257956	RP11-359M6.3	12:79952561-79952946	NOTEST	0.0692618	0	#NAME?	0	1	1
ENSG00000257957	ENSG00000257957	QRSL1P3	14:36007557-36278510	NOTEST	0.0129711	0.038613	1.57378	0	1	1
ENSG00000257958	ENSG00000257958	RP11-25E2.1	12:115515129-115517958	NOTEST	0	0	0	0	1	1
ENSG00000257959	ENSG00000257959	RP11-536C10.4	14:19332153-19372787	NOTEST	0	0	0	0	1	1
ENSG00000257961	ENSG00000257961	AC003070.1	HSCHR17_1:43471267-43510270	NOTEST	0	0	0	0	1	1
ENSG00000257962	ENSG00000257962	RP11-219B4.6	8:86132815-86196302	NOTEST	0	0	0	0	1	1
ENSG00000257964	ENSG00000257964	RP11-133N21.10	12:49962000-50158717	NOTEST	0.25512	0	#NAME?	0	1	1
ENSG00000257966	ENSG00000257966	OLA1P3	12:56263831-56266386	NOTEST	0	0	0	0	1	1
ENSG00000257967	ENSG00000257967	BX927178.2	HSCHR6_MHC_MANN:31347551-31347678	NOTEST	0	0	0	0	1	1
ENSG00000257972	ENSG00000257972	AL663093.2	HSCHR6_MHC_COX:30964484-30993378	NOTEST	0	0	0	0	1	1
ENSG00000257975	ENSG00000257975	CR547132.1	HSCHR6_MHC_MANN:32072021-32105429	NOTEST	0	0	0	0	1	1
ENSG00000257976	ENSG00000257976	RP11-388G3.1	14:25900398-25901440	NOTEST	0	0	0	0	1	1
ENSG00000257977	ENSG00000257977	RP11-496I2.6	14:19812175-19925348	NOTEST	0	0	0	0	1	1
ENSG00000257978	ENSG00000257978	BX927180.2	HSCHR6_MHC_MANN:32299913-32391764	NOTEST	0	0	0	0	1	1
ENSG00000257979	ENSG00000257979	SNRPGP18	12:116395710-116715143	NOTEST	0	0	0	0	1	1
ENSG00000257980	ENSG00000257980	AL844213.8	HSCHR6_MHC_QBL:30468710-30468795	NOTEST	0	0	0	0	1	1
ENSG00000257981	ENSG00000257981	CR547129.1	HSCHR6_MHC_MANN:33355727-33367637	NOTEST	0	0	0	0	1	1
ENSG00000257984	ENSG00000257984	BX927220.5	HSCHR6_MHC_MANN:30553828-30576175	NOTEST	0	0	0	0	1	1
ENSG00000257985	ENSG00000257985	RP1-228P16.4	12:48405086-48419252	NOTEST	0.00504954	0	#NAME?	0	1	1
ENSG00000257986	ENSG00000257986	RP11-314P15.2	14:26305063-26612511	NOTEST	0	0	0	0	1	1
ENSG00000257987	ENSG00000257987	LINC00935	12:49121217-49159569	NOTEST	0	0	0	0	1	1
ENSG00000257989	ENSG00000257989	RP1-288H2.2	12:52463029-52502045	NOTEST	0	0	0	0	1	1
ENSG00000257990	ENSG00000257990	NF1P4	14:19485969-19495426	NOTEST	0	0	0	0	1	1
ENSG00000257991	ENSG00000257991	RP11-2H8.3	12:72228813-72229176	NOTEST	0	0	0	0	1	1
ENSG00000257993	ENSG00000257993	AL662867.2	HSCHR6_MHC_COX:31075026-31100333	NOTEST	0	0	0	0	1	1
ENSG00000257994	ENSG00000257994	RP11-626I20.2	12:103899188-103899952	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000257995	ENSG00000257995	RP11-632B21.1	12:91011535-91016599	NOTEST	0	0	0	0	1	1
ENSG00000257997	ENSG00000257997	RP11-100F15.2	12:114518185-114551294	NOTEST	0	0	0	0	1	1
ENSG00000257998	ENSG00000257998	RP11-361A23.3	12:75121817-75122631	NOTEST	0	0	0	0	1	1
ENSG00000257999	ENSG00000257999	RP11-61E11.2	12:105496249-105500957	NOTEST	0	0.044722	inf	0	1	1
ENSG00000258001	ENSG00000258001	RP11-756H6.1	12:57824898-57827718	NOTEST	0	0	0	0	1	1
ENSG00000258002	ENSG00000258002	CR759815.2	HSCHR6_MHC_MCF:31204888-31232984	NOTEST	0	0	0	0	1	1
ENSG00000258003	ENSG00000258003	AC139677.7	HSCHR17_1:44831765-44898747	NOTEST	0	0	0	0	1	1
ENSG00000258004	ENSG00000258004	BX248096.2	HSCHR6_MHC_SSTO:30471721-30471809	NOTEST	0	0	0	0	1	1
ENSG00000258007	ENSG00000258007	RP11-350G24.1	12:101111303-101522419	NOTEST	0	0	0	0	1	1
ENSG00000258008	ENSG00000258008	AL845509.3	HSCHR6_MHC_QBL:32218296-32297155	NOTEST	0	0	0	0	1	1
ENSG00000258009	ENSG00000258009	AL662833.2	HSCHR6_MHC_COX:31265839-31266054	NOTEST	0	0	0	0	1	1
ENSG00000258010	ENSG00000258010	RP11-210M15.1	15:80696691-80890278	NOTEST	0.00922444	0.0273454	1.56776	0	1	1
ENSG00000258011	ENSG00000258011	HMGA1P3	12:110810704-110888227	NOTEST	0	0.217929	inf	0	1	1
ENSG00000258012	ENSG00000258012	RP11-603K19.1	12:93115280-93323107	NOTEST	0	0	0	0	1	1
ENSG00000258013	ENSG00000258013	RPL3P13	4:85465456-85465672	NOTEST	0	0	0	0	1	1
ENSG00000258014	ENSG00000258014	CR759747.1	HSCHR6_MHC_DBB:30956226-30956528	NOTEST	0	0	0	0	1	1
ENSG00000258015	ENSG00000258015	CR753846.3	HSCHR6_MHC_DBB:32674533-32678642	NOTEST	0	0	0	0	1	1
ENSG00000258016	ENSG00000258016	HIGD1AP1	12:53535836-53536111	NOTEST	0.412041	0.635508	0.625121	0	1	1
ENSG00000258018	ENSG00000258018	RP11-148B3.1	12:116955662-116956625	NOTEST	0	0	0	0	1	1
ENSG00000258020	ENSG00000258020	CR759814.1	HSCHR6_MHC_DBB:31266958-31267173	NOTEST	0	0	0	0	1	1
ENSG00000258021	ENSG00000258021	RP11-1100L3.4	12:52294348-52295120	NOTEST	0	0	0	0	1	1
ENSG00000258022	ENSG00000258022	AL662822.11	HSCHR6_MHC_COX:30460849-30464750	NOTEST	0	0	0	0	1	1
ENSG00000258023	ENSG00000258023	BX296568.1	HSCHR6_MHC_SSTO:32637567-32670792	NOTEST	0	0	0	0	1	1
ENSG00000258024	ENSG00000258024	OR5BT1P	12:48733790-48836730	NOTEST	0	0	0	0	1	1
ENSG00000258025	ENSG00000258025	CR759912.6	HSCHR6_MHC_APD:30488551-30488639	NOTEST	0	0	0	0	1	1
ENSG00000258026	ENSG00000258026	RP11-543H12.1	12:81186298-81650533	NOTEST	0	0	0	0	1	1
ENSG00000258027	ENSG00000258027	RP11-597A11.1	14:20078032-20152898	NOTEST	0	0	0	0	1	1
ENSG00000258028	ENSG00000258028	RP11-148E17.1	14:29299449-29497969	NOTEST	0	0	0	0	1	1
ENSG00000258030	ENSG00000258030	AL662825.1	HSCHR6_MHC_COX:30498997-30521345	NOTEST	0	0	0	0	1	1
ENSG00000258032	ENSG00000258032	BX927214.5	HSCHR6_MHC_MANN:30380634-30380743	NOTEST	0	0	0	0	1	1
ENSG00000258033	ENSG00000258033	RP11-350G24.2	12:101111303-101522419	NOTEST	0	0	0	0	1	1
ENSG00000258034	ENSG00000258034	RP11-493P1.2	12:116395710-116715143	NOTEST	0	0	0	0	1	1
ENSG00000258035	ENSG00000258035	RP11-74K11.2	12:94542498-94853764	NOTEST	0	0	0	0	1	1
ENSG00000258036	ENSG00000258036	KRT125P	12:53129049-53129926	NOTEST	0	0	0	0	1	1
ENSG00000258037	ENSG00000258037	AC127032.5	HSCHR17_1:44001605-44145324	NOTEST	0	0	0	0	1	1
ENSG00000258038	ENSG00000258038	CTD-2384A14.1	14:29299449-29497969	NOTEST	0	0.0203791	inf	0	1	1
ENSG00000258039	ENSG00000258039	RP11-406H4.1	12:99038918-100378432	NOTEST	0	0	0	0	1	1
ENSG00000258040	ENSG00000258040	AC005086.3	7:101458958-101927249	NOTEST	0	0	0	0	1	1
ENSG00000258044	ENSG00000258044	RP11-530C5.2	12:79968758-80334448	NOTEST	0.165498	0.0233085	-2.82789	0	1	1
ENSG00000258045	ENSG00000258045	CR382280.5	HSCHR6_MHC_MANN:30515666-30519569	NOTEST	0	0	0	0	1	1
ENSG00000258048	ENSG00000258048	RP11-530C5.1	12:79968758-80334448	NOTEST	0	0.273761	inf	0	1	1
ENSG00000258049	ENSG00000258049	AC217775.2	HSCHR17_1:44934643-44939509	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258050	ENSG00000258050	RP11-698F20.3	14:55663444-55665731	NOTEST	0	0	0	0	1	1
ENSG00000258051	ENSG00000258051	RP11-474C8.3	12:48541570-48574996	NOTEST	0	0	0	0	1	1
ENSG00000258052	ENSG00000258052	AC025263.3	12:70132460-70748773	NOTEST	0	0	0	0	1	1
ENSG00000258053	ENSG00000258053	CTD-2021H9.3	12:71427901-71512027	NOTEST	0	0	0	0	1	1
ENSG00000258054	ENSG00000258054	CR382280.6	HSCHR6_MHC_MANN:30515666-30519569	NOTEST	0	0	0	0	1	1
ENSG00000258058	ENSG00000258058	CR759828.2	HSCHR6_MHC_MCF:31308227-31308595	NOTEST	0	0	0	0	1	1
ENSG00000258059	ENSG00000258059	AL662857.1	HSCHR6_MHC_COX:29263740-29264280	NOTEST	0	0	0	0	1	1
ENSG00000258060	ENSG00000258060	AL662833.3	HSCHR6_MHC_COX:31102771-31118543	NOTEST	0	0	0	0	1	1
ENSG00000258062	ENSG00000258062	BX927168.2	HSCHR6_MHC_MANN:32748723-32777985	NOTEST	0	0	0	0	1	1
ENSG00000258065	ENSG00000258065	RP11-30H9.1	14:29299449-29497969	NOTEST	0	0	0	0	1	1
ENSG00000258066	ENSG00000258066	RP11-781A6.1	12:78169562-78177356	NOTEST	0.216797	0.0564473	-1.94137	0	1	1
ENSG00000258067	ENSG00000258067	AL773535.4	HSCHR6_MHC_QBL:30313512-30313600	NOTEST	0	0	0	0	1	1
ENSG00000258068	ENSG00000258068	RP11-328C8.5	12:42632248-42984157	NOTEST	0	0	0	0	1	1
ENSG00000258069	ENSG00000258069	CR753509.1	HSCHR6_MHC_DBB:29267068-29267608	NOTEST	0	0	0	0	1	1
ENSG00000258070	ENSG00000258070	CR774188.1	HSCHR6_MHC_APD:30432996-30433120	NOTEST	0	0	0	0	1	1
ENSG00000258071	ENSG00000258071	ARL2BPP2	12:53157188-53157677	NOTEST	0	0	0	0	1	1
ENSG00000258072	ENSG00000258072	RP11-554D14.2	12:108297046-108297725	NOTEST	0	0.0227565	inf	0	1	1
ENSG00000258073	ENSG00000258073	RP11-1079J22.1	12:85333302-85333447	NOTEST	0	0	0	0	1	1
ENSG00000258074	ENSG00000258074	VTI1BP3	12:53525133-53525769	NOTEST	0	0	0	0	1	1
ENSG00000258075	ENSG00000258075	CR762481.4	HSCHR6_MHC_DBB:30446323-30446408	NOTEST	0	0	0	0	1	1
ENSG00000258076	ENSG00000258076	RP11-536C10.14	14:19406794-19427443	NOTEST	0	0	0	0	1	1
ENSG00000258077	ENSG00000258077	RP11-114H23.1	12:75956981-76377795	NOTEST	0.309536	0.391756	0.339847	0	1	1
ENSG00000258080	ENSG00000258080	ARHGAP42P4	14:20156419-20159353	NOTEST	0	0	0	0	1	1
ENSG00000258081	ENSG00000258081	RP11-384J4.2	14:27305933-27629626	NOTEST	0	0	0	0	1	1
ENSG00000258082	ENSG00000258082	RP11-443B7.3	1:235115393-235116551	NOTEST	0	0.0155247	inf	0	1	1
ENSG00000258083	ENSG00000258083	OR9A4	7:141607612-141806547	NOTEST	0	0	0	0	1	1
ENSG00000258084	ENSG00000258084	RP11-754N21.1	12:78720459-78934455	NOTEST	0	0	0	0	1	1
ENSG00000258085	ENSG00000258085	UGT2B15	HSCHR4_1:69394990-69419037	NOTEST	0	0	0	0	1	1
ENSG00000258086	ENSG00000258086	RP11-753H16.5	12:54747444-54891472	NOTEST	0.0735161	0	#NAME?	0	1	1
ENSG00000258088	ENSG00000258088	RP11-114H23.2	12:75956981-76377795	NOTEST	0.151828	0.113979	-0.413667	0	1	1
ENSG00000258090	ENSG00000258090	RP11-734E19.1	12:77150970-77151694	NOTEST	0	0	0	0	1	1
ENSG00000258091	ENSG00000258091	RP11-290L1.6	12:75956981-76377795	NOTEST	0	0	0	0	1	1
ENSG00000258092	ENSG00000258092	RP4-816N1.7	12:2904118-3050306	NOTEST	0	0	0	0	1	1
ENSG00000258093	ENSG00000258093	AC005086.4	7:101458958-101927249	NOTEST	0	0	0	0	1	1
ENSG00000258094	ENSG00000258094	CR759912.7	HSCHR6_MHC_APD:30515141-30515229	NOTEST	0	0	0	0	1	1
ENSG00000258096	ENSG00000258096	RP11-474P2.2	12:46751971-46767561	NOTEST	0	0	0	0	1	1
ENSG00000258097	ENSG00000258097	AL670886.1	HSCHR6_MHC_COX:31616420-31658607	NOTEST	0	0	0	0	1	1
ENSG00000258098	ENSG00000258098	RP11-89K22.1	14:25593692-25596204	NOTEST	0	0.307442	inf	0	1	1
ENSG00000258099	ENSG00000258099	RP11-686G8.2	12:111890017-112038060	NOTEST	0.501479	0.435399	-0.203852	0	1	1
ENSG00000258100	ENSG00000258100	RP11-121E16.1	12:91755972-91762383	NOTEST	0	0	0	0	1	1
ENSG00000258101	ENSG00000258101	RP11-977B10.2	12:49578578-49667114	NOTEST	0.142984	0.153649	0.103786	0	1	1
ENSG00000258102	ENSG00000258102	RP11-809C9.2	12:116985910-116992186	NOTEST	0.0486414	0	#NAME?	0	1	1

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ENSG00000258104	ENSG00000258104	HIGD1AP9	12:49962000-50158717	NOTEST	0	0	0	0	1	1
ENSG00000258107	ENSG00000258107	RP11-260G13.1	14:29859551-29905618	NOTEST	0	0	0	0	1	1
ENSG00000258108	ENSG00000258108	RP11-1028N23.3	12:116007468-116019544	NOTEST	0	0	0	0	1	1
ENSG00000258110	ENSG00000258110	CR812479.3	HSCHR6_MHC_DBB:30340557-30340642	NOTEST	0	0	0	0	1	1
ENSG00000258111	ENSG00000258111	RP11-43D4.2	12:104849072-105155792	NOTEST	0	0	0	0	1	1
ENSG00000258112	ENSG00000258112	RP11-404O18.1	12:75628519-75784708	NOTEST	0	0	0	0	1	1
ENSG00000258113	ENSG00000258113	CR847852.1	HSCHR6_MHC_MANN:31428752-31429053	NOTEST	0	0	0	0	1	1
ENSG00000258114	ENSG00000258114	CTA-109P11.4	10:119184704-119309056	NOTEST	0	0	0	0	1	1
ENSG00000258115	ENSG00000258115	RP11-89M22.3	12:72332625-73059422	NOTEST	0	0	0	0	1	1
ENSG00000258116	ENSG00000258116	RP11-493L12.6	12:47735396-47735872	NOTEST	0	0	0	0	1	1
ENSG00000258117	ENSG00000258117	RP11-1022B3.1	12:63686408-63753817	NOTEST	0	0	0	0	1	1
ENSG00000258118	ENSG00000258118	RP11-77I22.4	12:31014854-31015113	NOTEST	0	0	0	0	1	1
ENSG00000258119	ENSG00000258119	RP11-804F13.1	12:38937978-38983614	NOTEST	0	0	0	0	1	1
ENSG00000258120	ENSG00000258120	KRT128P	12:53026649-53028240	NOTEST	0	0	0	0	1	1
ENSG00000258121	ENSG00000258121	RP11-722P11.4	12:48876285-48894744	NOTEST	0	0	0	0	1	1
ENSG00000258122	ENSG00000258122	RP11-61A14.1	16:66836777-66907159	NOTEST	0.0564461	0	#NAME?	0	1	1
ENSG00000258123	ENSG00000258123	RP11-314D7.2	12:73552969-73602097	NOTEST	0	0	0	0	1	1
ENSG00000258124	ENSG00000258124	BX927214.6	HSCHR6_MHC_MANN:30404946-30405034	NOTEST	0	0	0	0	1	1
ENSG00000258125	ENSG00000258125	RP11-1041F24.1	12:92073907-92074650	NOTEST	0	0	0	0	1	1
ENSG00000258126	ENSG00000258126	CR933877.2	HSCHR6_MHC_MANN:31860646-31861723	NOTEST	0	0	0	0	1	1
ENSG00000258128	ENSG00000258128	MKRN9P	12:88175939-88178345	NOTEST	0.0116029	0.0649757	2.48542	0	1	1
ENSG00000258130	ENSG00000258130	RP11-347C12.3	16:30215636-30220392	NOTEST	0.0691458	0.0235261	-1.55538	0	1	1
ENSG00000258131	ENSG00000258131	RP11-541G9.1	12:97379433-97579387	NOTEST	0	0	0	0	1	1
ENSG00000258133	ENSG00000258133	RP11-340M11.1	12:58788378-58788921	NOTEST	0	0	0	0	1	1
ENSG00000258134	ENSG00000258134	RP11-956A19.1	12:32257050-32536567	NOTEST	0	0	0	0	1	1
ENSG00000258135	ENSG00000258135	RP11-70F11.11	12:50302664-50305646	NOTEST	0	0	0	0	1	1
ENSG00000258136	ENSG00000258136	RP11-864J10.4	12:108126642-108155049	NOTEST	0.289054	0.216519	-0.416846	0	1	1
ENSG00000258137	ENSG00000258137	RP11-753H16.3	12:54747444-54891472	NOTEST	0	0	0	0	1	1
ENSG00000258138	ENSG00000258138	AL935156.1	HSCHR6_MHC_QBL:29143288-29163375	NOTEST	0	0	0	0	1	1
ENSG00000258140	ENSG00000258140	RP11-324P9.1	12:69605902-69618022	NOTEST	0	0	0	0	1	1
ENSG00000258141	ENSG00000258141	CR388372.5	HSCHR6_MHC_DBB:30470536-30470624	NOTEST	0	0	0	0	1	1
ENSG00000258142	ENSG00000258142	RP11-18O15.1	12:102623804-102624311	NOTEST	0	0	0	0	1	1
ENSG00000258143	ENSG00000258143	AC225613.7	HSCHR17_1:44624077-44624636	NOTEST	0	0	0	0	1	1
ENSG00000258144	ENSG00000258144	RP11-554L12.1	12:39481514-39486676	NOTEST	0	0	0	0	1	1
ENSG00000258145	ENSG00000258145	BX927168.3	HSCHR6_MHC_MANN:32748723-32777985	NOTEST	0	0	0	0	1	1
ENSG00000258146	ENSG00000258146	AL662822.12	HSCHR6_MHC_COX:30414651-30414775	NOTEST	0	0	0	0	1	1
ENSG00000258147	ENSG00000258147	CR762481.5	HSCHR6_MHC_DBB:30447486-30452225	NOTEST	0	0	0	0	1	1
ENSG00000258148	ENSG00000258148	AC007115.3	12:91587485-91587719	NOTEST	0	0	0	0	1	1
ENSG00000258149	ENSG00000258149	CR759890.6	HSCHR6_MHC_APD:30358534-30358619	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000258151	ENSG00000258151	CR759761.1	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000258153	ENSG00000258153	HSPE1P4	12:102267093-102267401	NOTEST	0	0	0	0	1	1
ENSG00000258154	ENSG00000258154	RP11-44N21.2	14:105579026-105579201	NOTEST	0	0	0	0	1	1
ENSG00000258155	ENSG00000258155	BX927220.6	HSCHR6_MHC_MANN:30528709-30531661	NOTEST	0	0	0	0	1	1
ENSG00000258158	ENSG00000258158	AL662822.13	HSCHR6_MHC_COX:30350071-30350159	NOTEST	0	0	0	0	1	1
ENSG00000258159	ENSG00000258159	RP1-71H24.4	12:113344581-113455556	NOTEST	0	0	0	0	1	1
ENSG00000258160	ENSG00000258160	AL713890.1	HSCHR6_MHC_COX:32618751-32622852	NOTEST	0	0	0	0	1	1
ENSG00000258162	ENSG00000258162	RP11-315E17.1	12:81652044-82153332	NOTEST	0	0	0	0	1	1
ENSG00000258164	ENSG00000258164	AL845454.1	HSCHR6_MHC_QBL:29958304-30022269	NOTEST	0	0	0	0	1	1
ENSG00000258165	ENSG00000258165	CR762481.6	HSCHR6_MHC_DBB:30446744-30446871	NOTEST	0	0	0	0	1	1
ENSG00000258166	ENSG00000258166	CR753842.1	HSCHR6_MHC_DBB:31611187-31653368	NOTEST	0	0	0	0	1	1
ENSG00000258167	ENSG00000258167	RP11-115F18.1	12:40787196-40964632	NOTEST	0	0	0	0	1	1
ENSG00000258168	ENSG00000258168	RP11-588H23.3	12:70861859-71031220	NOTEST	0.0727169	0.0884871	0.283176	0	1	1
ENSG00000258169	ENSG00000258169	LINC00485	12:103203057-103218177	NOTEST	0	0.0100784	inf	0	1	1
ENSG00000258170	ENSG00000258170	RP11-263K4.5	12:82874896-82891339	NOTEST	0	0	0	0	1	1
ENSG00000258172	ENSG00000258172	RP11-1105G2.4	12:94542498-94853764	NOTEST	0	0.0687386	inf	0	1	1
ENSG00000258173	ENSG00000258173	RP11-248E9.4	12:88147190-88147224	NOTEST	0	0	0	0	1	1
ENSG00000258175	ENSG00000258175	RP11-412H8.2	14:29061428-29082829	NOTEST	0	0.162523	inf	0	1	1
ENSG00000258177	ENSG00000258177	RP11-394J1.2	12:96588159-96663613	NOTEST	0	0	0	0	1	1
ENSG00000258178	ENSG00000258178	RP11-18J9.3	12:86352464-86354725	NOTEST	0	0	0	0	1	1
ENSG00000258179	ENSG00000258179	RP11-248E9.7	12:88214430-88214695	NOTEST	0	0	0	0	1	1
ENSG00000258181	ENSG00000258181	RP11-493L12.4	12:47631516-47672804	NOTEST	0	0	0	0	1	1
ENSG00000258182	ENSG00000258182	CR759848.1	HSCHR6_MHC_MCF:32729152-32733261	NOTEST	0	0	0	0	1	1
ENSG00000258183	ENSG00000258183	RP11-753N8.1	12:90674670-90694117	NOTEST	0	0	0	0	1	1
ENSG00000258184	ENSG00000258184	RP11-335M9.1	12:60609774-60610165	NOTEST	0	0	0	0	1	1
ENSG00000258185	ENSG00000258185	RP11-202H2.1	12:86372515-87232775	NOTEST	0	0	0	0	1	1
ENSG00000258188	ENSG00000258188	RP11-146E13.4	14:19812175-19925348	NOTEST	0.137829	0.107183	-0.362808	0	1	1
ENSG00000258191	ENSG00000258191	AL805909.2	HSCHR6_MHC_QBL:31028014-31031837	NOTEST	0	0	0	0	1	1
ENSG00000258192	ENSG00000258192	AL670886.2	HSCHR6_MHC_COX:31613488-31615961	NOTEST	0	0	0	0	1	1
ENSG00000258193	ENSG00000258193	RP11-362A1.2	12:82392410-82392741	NOTEST	0	0	0	0	1	1
ENSG00000258194	ENSG00000258194	BX294158.5	HSCHR6_MHC_SSTO:30179164-30328137	NOTEST	0	0	0	0	1	1
ENSG00000258195	ENSG00000258195	BX005439.1	HSCHR6_MHC_SSTO:31378661-31378995	NOTEST	0	0	0	0	1	1
ENSG00000258196	ENSG00000258196	CTD-2213F21.4	14:31959161-32330430	NOTEST	0	0	0	0	1	1
ENSG00000258197	ENSG00000258197	NKX2-2-AS1	20:21491647-21494664	NOTEST	0	0.0143822	inf	0	1	1
ENSG00000258198	ENSG00000258198	RP11-146E13.3	14:19812175-19925348	NOTEST	0	0	0	0	1	1
ENSG00000258199	ENSG00000258199	RP11-977G19.5	12:56544579-56584068	NOTEST	0.554636	0.304654	-0.864367	0	1	1
ENSG00000258200	ENSG00000258200	BX247900.4	HSCHR6_MHC_SSTO:31054556-31054985	NOTEST	0	0	0	0	1	1
ENSG00000258202	ENSG00000258202	RP11-776A13.2	12:30607851-30645235	NOTEST	0	0	0	0	1	1
ENSG00000258203	ENSG00000258203	RP1-228P16.3	12:48399059-48405010	NOTEST	0.0727169	0.0869388	0.25771	0	1	1
ENSG00000258204	ENSG00000258204	RP11-90E9.1	12:99038918-100378432	NOTEST	0	0	0	0	1	1
ENSG00000258205	ENSG00000258205	RP11-248E9.1	12:88140343-88140460	NOTEST	0	0	0	0	1	1
ENSG00000258206	ENSG00000258206	RP13-619I2.2	12:86175669-86176222	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258207	ENSG00000258207	AL662831.2	HSCHR6_MHC_COX:30340101-30340186	NOTEST	0	0	0	0	1	1
ENSG00000258208	ENSG00000258208	AL805909.3	HSCHR6_MHC_QBL:30964800-30993617	NOTEST	0	0	0	0	1	1
ENSG00000258209	ENSG00000258209	AL845450.3	HSCHR6_MHC_COX:30138279-30138496	NOTEST	0	0	0	0	1	1
ENSG00000258211	ENSG00000258211	BX294158.6	HSCHR6_MHC_SSTO:30339424-30339509	NOTEST	0	0	0	0	1	1
ENSG00000258212	ENSG00000258212	RP11-624G19.1	12:44229769-44783545	NOTEST	0.0199262	0	#NAME?	0	1	1
ENSG00000258213	ENSG00000258213	AL844527.1	HSCHR6_MHC_QBL:33130641-33142541	NOTEST	0	0	0	0	1	1
ENSG00000258214	ENSG00000258214	RP11-272B17.1	12:59759998-59804952	NOTEST	0	0	0	0	1	1
ENSG00000258215	ENSG00000258215	RP11-299A16.1	12:81186298-81650533	NOTEST	0	0	0	0	1	1
ENSG00000258216	ENSG00000258216	RP11-654D12.2	12:90276441-90383066	NOTEST	0	0	0	0	1	1
ENSG00000258218	ENSG00000258218	CR762481.7	HSCHR6_MHC_DBB:30461232-30465132	NOTEST	0	0	0	0	1	1
ENSG00000258219	ENSG00000258219	BX927143.1	HSCHR6_MHC_MANN:30469420-30469544	NOTEST	0	0	0	0	1	1
ENSG00000258220	ENSG00000258220	RP11-38F22.1	12:78720459-78934455	NOTEST	0	0	0	0	1	1
ENSG00000258221	ENSG00000258221	BX322539.1	HSCHR6_MHC_QBL:31220947-31221315	NOTEST	0	0	0	0	1	1
ENSG00000258223	ENSG00000258223	PRSS58	7:141951962-141957878	NOTEST	0	0	0	0	1	1
ENSG00000258224	ENSG00000258224	RP11-587P21.1	12:92264897-92265006	NOTEST	0	0	0	0	1	1
ENSG00000258225	ENSG00000258225	RP11-136F16.1	12:78224684-78606790	NOTEST	0	0	0	0	1	1
ENSG00000258226	ENSG00000258226	AL805934.2	HSCHR6_MHC_QBL:31616314-31618789	NOTEST	0	0	0	0	1	1
ENSG00000258227	ENSG00000258227	CLEC5A	7:141607612-141806547	NOTEST	0	0	0	0	1	1
ENSG00000258228	ENSG00000258228	AL844213.9	HSCHR6_MHC_QBL:30446020-30446144	NOTEST	0	0	0	0	1	1
ENSG00000258231	ENSG00000258231	RP11-362K2.2	12:58937906-59206842	NOTEST	0	0	0	0	1	1
ENSG00000258233	ENSG00000258233	ARHGAP42P5	14:19400328-19403264	NOTEST	0	0	0	0	1	1
ENSG00000258234	ENSG00000258234	RP11-370I10.2	12:48624880-48677993	NOTEST	0	0	0	0	1	1
ENSG00000258235	ENSG00000258235	RP11-12K6.2	12:73121702-73122624	NOTEST	0	0	0	0	1	1
ENSG00000258238	ENSG00000258238	AL662867.3	HSCHR6_MHC_COX:31059651-31059916	NOTEST	0	0	0	0	1	1
ENSG00000258239	ENSG00000258239	MTND2P17	12:42092296-42092984	NOTEST	0	0	0	0	1	1
ENSG00000258240	ENSG00000258240	RP1-46F2.3	12:111374388-111396012	NOTEST	0	0	0	0	1	1
ENSG00000258241	ENSG00000258241	BX571801.1	HSCHR6_MHC_SSTO:30793112-30793333	NOTEST	0	0	0	0	1	1
ENSG00000258243	ENSG00000258243	CR759912.8	HSCHR6_MHC_APD:30508917-30509042	NOTEST	0	0	0	0	1	1
ENSG00000258244	ENSG00000258244	OSTF1P1	12:115025998-115026607	NOTEST	0	0	0	0	1	1
ENSG00000258245	ENSG00000258245	RP11-114H23.3	12:75956981-76377795	NOTEST	0.443311	0.354977	-0.320596	0	1	1
ENSG00000258247	ENSG00000258247	RP11-167N24.6	12:95770983-95774672	NOTEST	0	0	0	0	1	1
ENSG00000258248	ENSG00000258248	AL773544.3	HSCHR6_MHC_QBL:31102652-31118444	NOTEST	0	0	0	0	1	1
ENSG00000258249	ENSG00000258249	RP11-497G19.3	12:117037074-117041390	NOTEST	0	0.0367478	inf	0	1	1
ENSG00000258251	ENSG00000258251	RP11-256L6.4	12:96453801-96454153	NOTEST	0	0	0	0	1	1
ENSG00000258252	ENSG00000258252	CTD-2311B13.5	14:19553364-19590078	NOTEST	0	0	0	0	1	1
ENSG00000258253	ENSG00000258253	RP3-416H24.4	12:52771595-52800139	NOTEST	0	0	0	0	1	1
ENSG00000258254	ENSG00000258254	RP11-162N7.1	12:115059565-115060727	NOTEST	0	0	0	0	1	1
ENSG00000258256	ENSG00000258256	RP11-219B4.5	8:86132815-86196302	NOTEST	0	0	0	0	1	1
ENSG00000258259	ENSG00000258259	CR759761.2	HSCHR6_MHC_MCF:31702357-31704832	NOTEST	0	0	0	0	1	1
ENSG00000258260	ENSG00000258260	RP11-977G19.14	12:56660641-56664750	NOTEST	0	0.116685	inf	0	1	1
ENSG00000258261	ENSG00000258261	CR753803.1	HSCHR6_MHC_DBB:31981893-32071805	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258262	ENSG00000258262	RP11-693J15.3	12:92924235-92925100	NOTEST	0	0	0	0	1	1
ENSG00000258263	ENSG00000258263	AL773535.5	HSCHR6_MHC_QBL:30339803-30339888	NOTEST	0	0	0	0	1	1
ENSG00000258264	ENSG00000258264	CR753651.1	HSCHR6_MHC_DBB:28730492-28730600	NOTEST	0	0	0	0	1	1
ENSG00000258265	ENSG00000258265	CTD-2311B13.2	14:19529957-19530898	NOTEST	0	0	0	0	1	1
ENSG00000258268	ENSG00000258268	RP11-570L15.1	2:143848930-144533642	NOTEST	0	0	0	0	1	1
ENSG00000258269	ENSG00000258269	BX248096.3	HSCHR6_MHC_SSTO:30468899-30468972	NOTEST	0	0	0	0	1	1
ENSG00000258270	ENSG00000258270	AC138688.5	HSCHR17_1:43904775-43906058	NOTEST	0	0	0	0	1	1
ENSG00000258271	ENSG00000258271	RP11-356O22.4	12:93923335-93923765	NOTEST	0	0	0	0	1	1
ENSG00000258272	ENSG00000258272	RP11-510I5.4	12:96816103-96879220	NOTEST	0	0	0	0	1	1
ENSG00000258273	ENSG00000258273	RP11-370I10.4	12:48727537-48727684	NOTEST	0	0	0	0	1	1
ENSG00000258274	ENSG00000258274	RP11-887P2.5	12:94071150-94288616	NOTEST	0	0	0	0	1	1
ENSG00000258275	ENSG00000258275	OR7K1P	14:25826969-25827895	NOTEST	0	0	0	0	1	1
ENSG00000258276	ENSG00000258276	RP11-244H18.1	14:19983558-20020272	NOTEST	0	0	0	0	1	1
ENSG00000258278	ENSG00000258278	RP11-297L6.1	12:38475847-38477884	NOTEST	0	0	0	0	1	1
ENSG00000258279	ENSG00000258279	LINC00592	12:52604713-52617588	NOTEST	0	0	0	0	1	1
ENSG00000258280	ENSG00000258280	RP11-1028N23.2	12:116007468-116019544	NOTEST	0	0	0	0	1	1
ENSG00000258281	ENSG00000258281	CR753819.4	HSCHR6_MHC_DBB:31076301-31101556	NOTEST	0	0	0	0	1	1
ENSG00000258282	ENSG00000258282	BTF3P2	14:29142446-29142933	NOTEST	0	0	0	0	1	1
ENSG00000258283	ENSG00000258283	RP11-386G11.3	12:49388931-49453557	NOTEST	0.0222963	0.0615064	1.46393	0	1	1
ENSG00000258284	ENSG00000258284	POLR2KP1	12:49962000-50158717	NOTEST	0	0	0	0	1	1
ENSG00000258285	ENSG00000258285	RP11-103B5.2	12:117537285-117579896	NOTEST	0	0	0	0	1	1
ENSG00000258286	ENSG00000258286	AL844213.10	HSCHR6_MHC_QBL:30460510-30464409	NOTEST	0	0	0	0	1	1
ENSG00000258287	ENSG00000258287	AC021146.1	HSCHR4_1:69752900-69753179	NOTEST	0	0	0	0	1	1
ENSG00000258288	ENSG00000258288	RP11-554E23.3	12:102271128-102405908	NOTEST	0	0	0	0	1	1
ENSG00000258290	ENSG00000258290	RP11-654D12.1	12:90276441-90383066	NOTEST	0	0	0	0	1	1
ENSG00000258291	ENSG00000258291	BX248321.1	HSCHR6_MHC_SSTO:30978725-30994957	NOTEST	0	0	0	0	1	1
ENSG00000258292	ENSG00000258292	RP11-536G4.1	12:96189122-96252617	NOTEST	0	0	0	0	1	1
ENSG00000258294	ENSG00000258294	RP11-314D7.1	12:73509736-73537638	NOTEST	0.230235	0.335962	0.54519	0	1	1
ENSG00000258296	ENSG00000258296	BX927168.4	HSCHR6_MHC_MANN:32849114-32853223	NOTEST	0	0	0	0	1	1
ENSG00000258298	ENSG00000258298	BX927139.2	HSCHR6_MHC_MANN:31127486-31152786	NOTEST	0	0	0	0	1	1
ENSG00000258299	ENSG00000258299	AL844213.11	HSCHR6_MHC_QBL:30460510-30464409	NOTEST	0	0	0	0	1	1
ENSG00000258300	ENSG00000258300	NUTF2P2	14:36288429-36536396	NOTEST	0	0	0	0	1	1
ENSG00000258302	ENSG00000258302	RP11-981P6.1	12:89954905-90106367	NOTEST	0.123104	0.110922	-0.150339	0	1	1
ENSG00000258303	ENSG00000258303	RP11-887P2.6	12:94071150-94288616	NOTEST	0.158861	0.147407	-0.107961	0	1	1
ENSG00000258304	ENSG00000258304	RP11-453D16.1	12:76509490-76509880	NOTEST	0	0	0	0	1	1
ENSG00000258308	ENSG00000258308	RP11-554E23.2	12:102271128-102405908	NOTEST	0	0.0133827	inf	0	1	1
ENSG00000258312	ENSG00000258312	RP11-690J15.1	12:98506791-98686223	NOTEST	0	0	0	0	1	1
ENSG00000258313	ENSG00000258313	RP11-167N24.5	12:95781665-95782334	NOTEST	0	0	0	0	1	1
ENSG00000258316	ENSG00000258316	KLF17P1	12:62102039-62811211	NOTEST	0	0	0	0	1	1
ENSG00000258317	ENSG00000258317	RP11-603J24.5	12:56511942-56538455	NOTEST	0.110178	0.195554	0.827738	0	1	1
ENSG00000258318	ENSG00000258318	BX294158.7	HSCHR6_MHC_SSTO:30349901-30349989	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258320	ENSG00000258320	RP11-274M17.1	12:74526945-74796315	NOTEST	0	0	0	0	1	1
ENSG00000258321	ENSG00000258321	AL662822.14	HSCHR6_MHC_COX:30470151-30470239	NOTEST	0	0	0	0	1	1
ENSG00000258322	ENSG00000258322	AC138688.6	HSCHR17_1:43774682-43774961	NOTEST	0	0	0	0	1	1
ENSG00000258323	ENSG00000258323	RP1-267L14.3	12:112464499-112546826	NOTEST	0	0.0247535	inf	0	1	1
ENSG00000258324	ENSG00000258324	RP11-536C10.22	14:20078032-20152898	NOTEST	0	0	0	0	1	1
ENSG00000258325	ENSG00000258325	RP4-816N1.6	12:2904118-3050306	NOTEST	0.385333	0.392226	0.025579	0	1	1
ENSG00000258326	ENSG00000258326	AL662831.3	HSCHR6_MHC_COX:30322072-30322196	NOTEST	0	0	0	0	1	1
ENSG00000258330	ENSG00000258330	CR753842.2	HSCHR6_MHC_DBB:31608256-31610731	NOTEST	0	0	0	0	1	1
ENSG00000258331	ENSG00000258331	RP11-118A3.1	12:43549117-43556913	NOTEST	0	0	0	0	1	1
ENSG00000258332	ENSG00000258332	RP11-711C17.2	12:74432865-74439608	NOTEST	0	0	0	0	1	1
ENSG00000258333	ENSG00000258333	AL662822.15	HSCHR6_MHC_COX:30460849-30464750	NOTEST	0	0	0	0	1	1
ENSG00000258334	ENSG00000258334	RP11-161H23.9	12:49686413-49725514	NOTEST	0.02423	0.0199325	-0.281667	0	1	1
ENSG00000258336	ENSG00000258336	RP11-410B16.1	12:61994230-61994624	NOTEST	0	0	0	0	1	1
ENSG00000258337	ENSG00000258337	RP11-115H15.2	12:116395710-116715143	NOTEST	0	0	0	0	1	1
ENSG00000258338	ENSG00000258338	RP11-87P13.2	12:83565368-83566519	NOTEST	0	0	0	0	1	1
ENSG00000258342	ENSG00000258342	RP11-116N8.1	14:36288429-36536396	NOTEST	0	0	0	0	1	1
ENSG00000258343	ENSG00000258343	RP11-536G4.2	12:96189122-96252617	NOTEST	0	0.15955	inf	0	1	1
ENSG00000258344	ENSG00000258344	RP11-968A15.8	12:54624723-54745633	NOTEST	0.294618	0.638267	1.11532	0	1	1
ENSG00000258345	ENSG00000258345	RP11-603J24.6	12:56511942-56538455	NOTEST	0	0.0400823	inf	0	1	1
ENSG00000258346	ENSG00000258346	RP11-148B3.2	12:116806568-116827276	NOTEST	0	0	0	0	1	1
ENSG00000258348	ENSG00000258348	AL662831.4	HSCHR6_MHC_COX:30325774-30325883	NOTEST	0	0	0	0	1	1
ENSG00000258349	ENSG00000258349	AL663093.3	HSCHR6_MHC_COX:30955217-30955519	NOTEST	0	0	0	0	1	1
ENSG00000258350	ENSG00000258350	SYF2P1	14:30907197-31089269	NOTEST	0	0	0	0	1	1
ENSG00000258352	ENSG00000258352	RP11-23J18.1	12:47469489-47630443	NOTEST	0	0	0	0	1	1
ENSG00000258353	ENSG00000258353	CR382280.7	HSCHR6_MHC_MANN:30501924-30506663	NOTEST	0	0	0	0	1	1
ENSG00000258354	ENSG00000258354	MIR3180-1	16:15003743-15005202	NOTEST	0	0.00896205	inf	0	1	1
ENSG00000258355	ENSG00000258355	RP11-651L5.2	12:106631654-106740793	NOTEST	0	0.0749841	inf	0	1	1
ENSG00000258356	ENSG00000258356	CR388372.6	HSCHR6_MHC_DBB:30488499-30489586	NOTEST	0	0	0	0	1	1
ENSG00000258357	ENSG00000258357	RP11-778J16.2	12:94914865-94915645	NOTEST	0	0	0	0	1	1
ENSG00000258358	ENSG00000258358	RP11-228G3.1	12:84842403-84843657	NOTEST	0	0	0	0	1	1
ENSG00000258360	ENSG00000258360	RP11-266O15.3	12:38600032-38600994	NOTEST	0	0	0	0	1	1
ENSG00000258361	ENSG00000258361	BX284927.2	HSCHR6_MHC_SSTO:32241008-32241176	NOTEST	0	0	0	0	1	1
ENSG00000258363	ENSG00000258363	GRAMD4P4	14:19932011-19972292	NOTEST	0	0	0	0	1	1
ENSG00000258364	ENSG00000258364	RP11-536C10.16	14:19406794-19427443	NOTEST	0	0	0	0	1	1
ENSG00000258365	ENSG00000258365	RP11-1105G2.3	12:94542498-94853764	NOTEST	0.33644	0.469104	0.479559	0	1	1
ENSG00000258367	ENSG00000258367	RP11-536C10.3	14:19332153-19372787	NOTEST	0	0	0	0	1	1
ENSG00000258368	ENSG00000258368	RP11-125N22.2	12:37969250-37970186	NOTEST	0	0	0	0	1	1
ENSG00000258369	ENSG00000258369	RP1-90J4.2	12:47856869-47857404	NOTEST	0	0	0	0	1	1
ENSG00000258370	ENSG00000258370	AL845443.1	HSCHR6_MHC_QBL:31375871-31376202	NOTEST	0	0	0	0	1	1
ENSG00000258372	ENSG00000258372	ARL17A	HSCHR17_1:43776445-43865069	NOTEST	0	0	0	0	1	1
ENSG00000258373	ENSG00000258373	SLC25A3P2	12:112369085-112450970	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258374	ENSG00000258374	CR759928.1	HSCHR6_MHC_APD:30332248-30332336	NOTEST	0	0	0	0	1	1
ENSG00000258375	ENSG00000258375	RP11-617J18.1	12:81652044-82153332	NOTEST	0	0	0	0	1	1
ENSG00000258377	ENSG00000258377	RP11-649E7.5	14:50087488-50090198	NOTEST	0.0650449	0.0662975	0.0275177	0	1	1
ENSG00000258378	ENSG00000258378	RP11-517O13.1	14:58862633-59015216	NOTEST	0	0	0	0	1	1
ENSG00000258379	ENSG00000258379	RP11-204N11.2	14:98252901-98255593	NOTEST	0	0	0	0	1	1
ENSG00000258380	ENSG00000258380	RP11-33N16.2	14:89591214-90421121	NOTEST	0	0	0	0	1	1
ENSG00000258381	ENSG00000258381	RP11-737F10.1	14:49288562-49288796	NOTEST	0	0	0	0	1	1
ENSG00000258383	ENSG00000258383	CTD-2200A16.1	14:99791135-99798352	NOTEST	0	0	0	0	1	1
ENSG00000258384	ENSG00000258384	AC068831.6	15:91473409-91506349	NOTEST	0.067255	0.0685032	0.026529	0	1	1
ENSG00000258385	ENSG00000258385	RP11-629F19.1	14:41765488-41767937	NOTEST	0	0	0	0	1	1
ENSG00000258386	ENSG00000258386	RP11-187E13.2	14:32476107-32487891	NOTEST	0	0	0	0	1	1
ENSG00000258387	ENSG00000258387	RP11-557C9.3	14:44061344-44061465	NOTEST	0	0	0	0	1	1
ENSG00000258389	ENSG00000258389	DUX4	4:191005266-191007077	NOTEST	0	0	0	0	1	1
ENSG00000258390	ENSG00000258390	RP11-1070N10.4	14:96039898-96048293	NOTEST	0	0	0	0	1	1
ENSG00000258392	ENSG00000258392	RPA2P1	14:47308825-48144157	NOTEST	0	0	0	0	1	1
ENSG00000258393	ENSG00000258393	RP11-907D1.2	14:97576752-97587838	NOTEST	0	0	0	0	1	1
ENSG00000258394	ENSG00000258394	CTD-2307P3.1	14:42832185-43172858	NOTEST	0	0	0	0	1	1
ENSG00000258395	ENSG00000258395	RP11-65I12.1	2:113969098-114036527	NOTEST	0	0.0281434	inf	0	1	1
ENSG00000258397	ENSG00000258397	RP11-173D3.2	15:20278951-20279587	NOTEST	0	0	0	0	1	1
ENSG00000258399	ENSG00000258399	MEG8	14:101361106-101402336	NOTEST	0	0	0	0	1	1
ENSG00000258400	ENSG00000258400	RP11-831F12.2	14:50159822-50219870	NOTEST	0	0	0	0	1	1
ENSG00000258401	ENSG00000258401	RP11-326E7.1	14:49840683-49841101	NOTEST	0	0	0	0	1	1
ENSG00000258402	ENSG00000258402	RP11-516J2.1	14:76747285-76776409	NOTEST	0	0	0	0	1	1
ENSG00000258403	ENSG00000258403	RP11-355I22.6	14:62570095-62596352	NOTEST	0	0	0	0	1	1
ENSG00000258404	ENSG00000258404	RP11-1029J19.5	14:102100790-102198859	NOTEST	0	0	0	0	1	1
ENSG00000258405	ENSG00000258405	ZNF578	19:52956828-53015595	NOTEST	0.180928	0.1243	-0.541587	0	1	1
ENSG00000258406	ENSG00000258406	RP11-88E18.1	14:43744026-43744900	NOTEST	0	0	0	0	1	1
ENSG00000258407	ENSG00000258407	RP11-300J18.2	14:88471467-88481955	NOTEST	0	0	0	0	1	1
ENSG00000258408	ENSG00000258408	NT5CP2	14:73945188-74025651	NOTEST	0	0	0	0	1	1
ENSG00000258410	ENSG00000258410	RP11-173D3.1	15:20333997-20353206	NOTEST	0	0	0	0	1	1
ENSG00000258411	ENSG00000258411	RP11-804M7.2	14:64228730-64228867	NOTEST	0	0	0	0	1	1
ENSG00000258412	ENSG00000258412	RP11-404P21.5	14:96671015-96735304	NOTEST	0	0	0	0	1	1
ENSG00000258413	ENSG00000258413	RP11-665C16.6	14:55729484-55828636	NOTEST	0.054584	0	#NAME?	0	1	1
ENSG00000258414	ENSG00000258414	RP11-356O9.1	14:38025362-38048330	NOTEST	0	0	0	0	1	1
ENSG00000258415	ENSG00000258415	RP11-32B5.4	15:21987457-21987995	NOTEST	0	0	0	0	1	1
ENSG00000258416	ENSG00000258416	RP11-526N18.1	14:80359422-80440512	NOTEST	0	0	0	0	1	1
ENSG00000258418	ENSG00000258418	RP11-662J14.1	14:40855455-40855998	NOTEST	0	0	0	0	1	1
ENSG00000258419	ENSG00000258419	RP11-588P7.1	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000258420	ENSG00000258420	RP11-403B2.3	15:20980792-20981327	NOTEST	0	0	0	0	1	1
ENSG00000258421	ENSG00000258421	FRDAP	14:78526284-78526621	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258422	ENSG00000258422	RP11-486O13.2	14:70510933-70696904	NOTEST	0	0	0	0	1	1
ENSG00000258423	ENSG00000258423	OR7E105P	14:52217277-52230794	NOTEST	0	0	0	0	1	1
ENSG00000258424	ENSG00000258424	RP11-471B22.2	14:90862845-90874605	NOTEST	0	0.259278	inf	0	1	1
ENSG00000258425	ENSG00000258425	CTD-2207P18.1	14:74964872-75079306	NOTEST	0	0	0	0	1	1
ENSG00000258426	ENSG00000258426	RP11-452D21.1	14:83484544-83505946	NOTEST	0	0	0	0	1	1
ENSG00000258428	ENSG00000258428	RP11-1085N6.2	14:56955071-57197253	NOTEST	0	0	0	0	1	1
ENSG00000258431	ENSG00000258431	RP1-292L20.2	14:71325560-71326146	NOTEST	0	0	0	0	1	1
ENSG00000258433	ENSG00000258433	RP11-255M2.1	15:95577612-95578966	NOTEST	0	0	0	0	1	1
ENSG00000258434	ENSG00000258434	DUX4L11	10:135483661-135488584	NOTEST	0	0	0	0	1	1
ENSG00000258435	ENSG00000258435	RP11-711D18.2	12:121746047-121837699	NOTEST	0.0723686	0.088377	0.288308	0	1	1
ENSG00000258436	ENSG00000258436	RNASE12	14:21051050-21078043	NOTEST	0	0	0	0	1	1
ENSG00000258437	ENSG00000258437	RP11-661G16.1	14:91006931-91282823	NOTEST	0	0	0	0	1	1
ENSG00000258438	ENSG00000258438	OR11K2P	14:20187173-20296531	NOTEST	0	0	0	0	1	1
ENSG00000258439	ENSG00000258439	RP11-173A8.2	14:75120139-75179818	NOTEST	0.263135	0.325307	0.305997	0	1	1
ENSG00000258440	ENSG00000258440	RP11-1033H12.3	14:52622457-52622897	NOTEST	0	0	0	0	1	1
ENSG00000258442	ENSG00000258442	RP11-474N8.5	12:57388229-57392225	NOTEST	0	0	0	0	1	1
ENSG00000258443	ENSG00000258443	RP3-414A15.11	14:73945188-74025651	NOTEST	0	0.028751	inf	0	1	1
ENSG00000258444	ENSG00000258444	CTD-2201G16.1	14:23881946-23904927	NOTEST	0	0	0	0	1	1
ENSG00000258445	ENSG00000258445	RP11-307P22.1	14:61201459-61550451	NOTEST	0	0	0	0	1	1
ENSG00000258446	ENSG00000258446	RP11-895M11.2	14:91884609-91887520	NOTEST	0	0	0	0	1	1
ENSG00000258448	ENSG00000258448	RP11-109N23.5	14:73525138-73588122	NOTEST	0.0436878	0	#NAME?	0	1	1
ENSG00000258449	ENSG00000258449	RP11-713N11.4	12:25173935-25261268	NOTEST	0	0	0	0	1	1
ENSG00000258450	ENSG00000258450	RP11-649E7.7	14:50091891-50101948	NOTEST	0.501849	0.0963971	-2.38019	0	1	1
ENSG00000258451	ENSG00000258451	RP11-903H12.3	14:21152258-21175279	NOTEST	0	0.0512737	inf	0	1	1
ENSG00000258452	ENSG00000258452	RP11-757H14.2	14:80943329-81636758	NOTEST	0	0	0	0	1	1
ENSG00000258453	ENSG00000258453	OR11H2	14:20181103-20182079	NOTEST	0	0	0	0	1	1
ENSG00000258454	ENSG00000258454	RP11-361H10.3	14:76618258-76729817	NOTEST	0.170249	0.0302102	-2.49454	0	1	1
ENSG00000258455	ENSG00000258455	RP11-665C16.5	14:55729484-55828636	NOTEST	0	0	0	0	1	1
ENSG00000258456	ENSG00000258456	PTCD2P1	14:20992445-20993581	NOTEST	0	0	0	0	1	1
ENSG00000258457	ENSG00000258457	RP11-298I3.4	14:23451906-23479375	NOTEST	0.270431	0.228853	-0.240838	0	1	1
ENSG00000258458	ENSG00000258458	CTD-2555K7.2	14:23171351-23241007	NOTEST	0.203656	0.227063	0.156956	0	1	1
ENSG00000258459	ENSG00000258459	CTD-2292M16.7	14:20724716-20774970	NOTEST	0	0	0	0	1	1
ENSG00000258460	ENSG00000258460	RP11-168L7.1	14:101798852-101800668	NOTEST	0	0	0	0	1	1
ENSG00000258461	ENSG00000258461	RP11-164J13.1	15:42500610-42704516	NOTEST	0.363259	0.299045	-0.280635	0	1	1
ENSG00000258462	ENSG00000258462	RP11-831F12.4	14:50110272-50155140	NOTEST	0	0	0	0	1	1
ENSG00000258463	ENSG00000258463	RP11-173D3.3	15:20104586-20104812	NOTEST	0	0	0	0	1	1
ENSG00000258464	ENSG00000258464	RP11-388E23.2	14:24198246-24198950	NOTEST	0	0	0	0	1	1
ENSG00000258466	ENSG00000258466	RP11-1012A1.4	14:68086514-68162531	NOTEST	0.0933797	0.0750799	-0.314682	0	1	1

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ENSG00000258467	ENSG00000258467	PHKBP2	14:37002710-37003743	NOTEST	0	0	0	0	1	1
ENSG00000258468	ENSG00000258468	OR11G1P	14:20647347-20648315	NOTEST	0	0	0	0	1	1
ENSG00000258469	ENSG00000258469	CHMP4BP1	14:55729484-55828636	NOTEST	0.0356241	0.0789247	1.14762	0	1	1
ENSG00000258471	ENSG00000258471	RP11-84C10.4	14:21457928-21467322	NOTEST	0.0745863	0.0822654	0.141375	0	1	1
ENSG00000258473	ENSG00000258473	RP11-7F17.4	14:77507406-77552789	NOTEST	0	0	0	0	1	1
ENSG00000258474	ENSG00000258474	RP11-187E13.1	14:32414058-32419588	NOTEST	0.0391948	0	#NAME?	0	1	1
ENSG00000258475	ENSG00000258475	U85056.3	4:190986387-190987069	NOTEST	0	0	0	0	1	1
ENSG00000258476	ENSG00000258476	RP11-76E17.3	15:94133095-94651167	NOTEST	0	0	0	0	1	1
ENSG00000258477	ENSG00000258477	PPIAP6	14:68286495-69196935	NOTEST	0.168822	0	#NAME?	0	1	1
ENSG00000258478	ENSG00000258478	RP11-232C2.1	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000258479	ENSG00000258479	LINC00640	14:51800110-51852321	NOTEST	0.249383	0.0195477	-3.67329	0	1	1
ENSG00000258480	ENSG00000258480	RP11-662J14.2	14:40856761-40858344	NOTEST	0	0	0	0	1	1
ENSG00000258481	ENSG00000258481	RP11-472N19.3	14:92719836-92730000	NOTEST	0	0	0	0	1	1
ENSG00000258482	ENSG00000258482	TRAV15	14:22418628-22418877	NOTEST	0	0	0	0	1	1
ENSG00000258483	ENSG00000258483	AC144835.1	15:98563823-98565007	NOTEST	0	0	0	0	1	1
ENSG00000258484	ENSG00000258484	SPESP1	15:69070873-69355083	NOTEST	0	0	0	0	1	1
ENSG00000258485	ENSG00000258485	SRMP2	14:61201459-61550451	NOTEST	0.0728818	0	#NAME?	0	1	1
ENSG00000258487	ENSG00000258487	RP11-99L13.1	14:44913949-44949821	NOTEST	0	0	0	0	1	1
ENSG00000258488	ENSG00000258488	RP11-467L19.8	15:20721491-20725870	NOTEST	0.0483773	0.0186045	-1.37868	0	1	1
ENSG00000258489	ENSG00000258489	RP11-398J10.2	15:95976323-96051076	NOTEST	0	0	0	0	1	1
ENSG00000258490	ENSG00000258490	RP11-862P13.1	14:66679527-67648520	NOTEST	0	0	0	0	1	1
ENSG00000258491	ENSG00000258491	ZFP64P1	14:51171060-51172229	NOTEST	0	0	0	0	1	1
ENSG00000258493	ENSG00000258493	RP11-73E17.3	14:35390063-35498773	NOTEST	0	0	0	0	1	1
ENSG00000258494	ENSG00000258494	OR11J5P	15:21145766-21198632	NOTEST	0	0	0	0	1	1
ENSG00000258496	ENSG00000258496	RP11-1141N12.	14:87717446-87718023	NOTEST	0	0	0	0	1	1
ENSG00000258497	ENSG00000258497	CTD-2561F5.1	14:101723668-101744655	NOTEST	0	0	0	0	1	1
ENSG00000258498	ENSG00000258498	DIO3OS	14:102018557-102026768	NOTEST	0	0	0	0	1	1
ENSG00000258499	ENSG00000258499	RP11-862G15.2	14:93372041-93373827	NOTEST	0.0444952	0	#NAME?	0	1	1
ENSG00000258500	ENSG00000258500	CTD-2062F14.2	14:100800124-100996640	NOTEST	0	0	0	0	1	1
ENSG00000258501	ENSG00000258501	EIF3LP1	14:82194123-82496693	NOTEST	0	0	0	0	1	1
ENSG00000258502	ENSG00000258502	RP11-783L4.1	14:66578298-66592565	NOTEST	0	0	0	0	1	1
ENSG00000258503	ENSG00000258503	RP11-368P15.1	14:53478688-53478985	NOTEST	0	0	0	0	1	1
ENSG00000258505	ENSG00000258505	RP11-90P16.1	14:42832185-43172858	NOTEST	0	0	0	0	1	1
ENSG00000258506	ENSG00000258506	RP11-688D15.1	14:85417617-85417717	NOTEST	0	0	0	0	1	1
ENSG00000258507	ENSG00000258507	RP13-582L3.4	4:8847801-8873543	NOTEST	0	0	0	0	1	1
ENSG00000258509	ENSG00000258509	RP11-857B24.3	14:45346076-45366280	NOTEST	0	0	0	0	1	1
ENSG00000258510	ENSG00000258510	RP11-493G17.4	14:77801363-77857840	NOTEST	0.085762	0.102231	0.253418	0	1	1
ENSG00000258511	ENSG00000258511	RP11-61O1.2	14:98534576-98671480	NOTEST	0	0	0	0	1	1
ENSG00000258512	ENSG00000258512	RP11-796G6.2	14:102100790-102198859	NOTEST	0	0.137606	inf	0	1	1
ENSG00000258513	ENSG00000258513	RP5-892G5.2	14:74551498-74667936	NOTEST	0	0	0	0	1	1
ENSG00000258514	ENSG00000258514	DUX4L14	10:135490271-135495193	NOTEST	0	0	0	0	1	1
ENSG00000258516	ENSG00000258516	RP11-185P18.2	14:96321884-96332801	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258517	ENSG00000258517	RP6-91H8.1	14:71679349-71684933	NOTEST	0	0	0	0	1	1
ENSG00000258519	ENSG00000258519	RP11-349A22.3	14:58466452-58764857	NOTEST	0	0	0	0	1	1
ENSG00000258520	ENSG00000258520	RP11-363J20.2	14:69649736-69821183	NOTEST	0	0	0	0	1	1
ENSG00000258521	ENSG00000258521	RP11-638I2.9	14:100800124-100996640	NOTEST	0.339605	0.17218	-0.979943	0	1	1
ENSG00000258524	ENSG00000258524	NT5CP1	14:74034323-74042357	NOTEST	0	0.0996871	inf	0	1	1
ENSG00000258525	ENSG00000258525	RP11-829H16.3	14:31343719-31562818	NOTEST	0.118572	0.0170536	-2.79762	0	1	1
ENSG00000258526	ENSG00000258526	RP11-111A21.1	14:39944043-39982984	NOTEST	0.170531	0.146607	-0.218076	0	1	1
ENSG00000258527	ENSG00000258527	ASB9P1	15:93146139-93353114	NOTEST	0.0238836	0	#NAME?	0	1	1
ENSG00000258529	ENSG00000258529	ALG9	11:111652918-111756699	NOTEST	0.188847	0.330561	0.807698	0	1	1
ENSG00000258531	ENSG00000258531	BANF1P1	14:69340859-69446157	NOTEST	0	0	0	0	1	1
ENSG00000258532	ENSG00000258532	RP11-353P15.1	14:84373215-84381394	NOTEST	0	0	0	0	1	1
ENSG00000258534	ENSG00000258534	CTD-2134A5.4	14:104314057-104346448	NOTEST	0	0	0	0	1	1
ENSG00000258535	ENSG00000258535	RP11-280K24.4	14:52231993-52292140	NOTEST	0	0	0	0	1	1
ENSG00000258536	ENSG00000258536	RP11-1053O12.1	14:42076772-42373752	NOTEST	0	0	0	0	1	1
ENSG00000258537	ENSG00000258537	FRMD6-AS2	14:51921229-52197445	NOTEST	0	0	0	0	1	1
ENSG00000258538	ENSG00000258538	RP11-753D20.3	14:88641734-88646542	NOTEST	0	0	0	0	1	1
ENSG00000258539	ENSG00000258539	RP11-12J10.3	10:126150402-126480439	NOTEST	0.237654	0.218744	-0.119618	0	1	1
ENSG00000258540	ENSG00000258540	RP11-692C24.3	15:92220000-92220290	NOTEST	0	0	0	0	1	1
ENSG00000258541	ENSG00000258541	OR4K4P	14:20374075-20374759	NOTEST	0	0	0	0	1	1
ENSG00000258542	ENSG00000258542	AC068831.11	15:91565848-91579841	NOTEST	0	0	0	0	1	1
ENSG00000258543	ENSG00000258543	CSNK2B-LY6G5B-1181	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000258544	ENSG00000258544	RP11-750I4.2	14:90528108-90652201	NOTEST	0	0	0	0	1	1
ENSG00000258545	ENSG00000258545	RP4-755D9.1	X:119170200-119379122	NOTEST	0	0.0328656	inf	0	1	1
ENSG00000258546	ENSG00000258546	RP11-713N11.3	12:25173935-25261268	NOTEST	0	0	0	0	1	1
ENSG00000258548	ENSG00000258548	LINC00645	14:27727922-28314492	NOTEST	0.0296188	0.059494	1.00623	0	1	1
ENSG00000258549	ENSG00000258549	RP11-22K10.1	14:84271839-84271984	NOTEST	0	0	0	0	1	1
ENSG00000258550	ENSG00000258550	OR7E106P	14:52217277-52230794	NOTEST	0	0	0	0	1	1
ENSG00000258551	ENSG00000258551	RP11-661P17.1	15:91951937-92148441	NOTEST	0	0	0	0	1	1
ENSG00000258552	ENSG00000258552	RP11-463C8.5	14:77564439-77725838	NOTEST	0	0	0	0	1	1
ENSG00000258553	ENSG00000258553	RP11-16B13.1	14:60386140-60558501	NOTEST	0	0	0	0	1	1
ENSG00000258554	ENSG00000258554	RP11-973D8.4	12:56347888-56367101	NOTEST	0	0	0	0	1	1
ENSG00000258555	ENSG00000258555	SPECC1L-ADORA2A	22:24666785-24924358	NOTEST	0.0996439	9.10E-05	-10.0959	0	1	1
ENSG00000258556	ENSG00000258556	CTD-2568P8.1	14:60789953-60790625	NOTEST	0.169843	0	#NAME?	0	1	1
ENSG00000258557	ENSG00000258557	AE000659.41	14:22431046-22431270	NOTEST	0	0	0	0	1	1
ENSG00000258558	ENSG00000258558	RP11-159L20.2	14:31091317-31291908	NOTEST	0	0	0	0	1	1
ENSG00000258560	ENSG00000258560	CTD-2376I20.1	14:100437785-100610573	NOTEST	0	0	0	0	1	1
ENSG00000258561	ENSG00000258561	RP11-72M17.1	14:66679527-67648520	NOTEST	0.126172	0.0912891	-0.466877	0	1	1
ENSG00000258562	ENSG00000258562	CTD-2313J17.3	15:93146139-93353114	NOTEST	0	0	0	0	1	1

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ENSG00000258564	ENSG00000258564	OR4N1P	14:20187173-20296531	NOTEST	0	0	0	0	1	1
ENSG00000258565	ENSG00000258565	BLZF2P	14:69334573-69336668	NOTEST	0	0.0373574	inf	0	1	1
ENSG00000258566	ENSG00000258566	RP11-99E15.3	14:76776956-77227731	NOTEST	0	0	0	0	1	1
ENSG00000258567	ENSG00000258567	DUX4L16	Y:13462593-13463857	NOTEST	0	0	0	0	1	1
ENSG00000258568	ENSG00000258568	RHOQP1	14:50043389-50081390	NOTEST	0.571802	0.537988	-0.0879414	0	1	1
ENSG00000258569	ENSG00000258569	RP11-99E15.2	14:76776956-77227731	NOTEST	0	0	0	0	1	1
ENSG00000258570	ENSG00000258570	RP11-452K20.1	15:94711577-94711980	NOTEST	0	0	0	0	1	1
ENSG00000258571	ENSG00000258571	PTTG4P	14:71374121-71582099	NOTEST	0	0	0	0	1	1
ENSG00000258572	ENSG00000258572	RP11-1070N10.3	14:95982472-95984248	NOTEST	0.0659584	0.0281009	-1.23094	0	1	1
ENSG00000258573	ENSG00000258573	RP11-14J7.6	14:21051050-21078043	NOTEST	0	0	0	0	1	1
ENSG00000258576	ENSG00000258576	CTD-2644I21.1	14:101054111-101055663	NOTEST	0	0	0	0	1	1
ENSG00000258577	ENSG00000258577	SNRPGP1	14:50885218-51135049	NOTEST	0	0	0	0	1	1
ENSG00000258578	ENSG00000258578	RP11-98L12.2	14:76041230-76550928	NOTEST	0	0	0	0	1	1
ENSG00000258581	ENSG00000258581	RP11-638I2.10	14:100800124-100996640	NOTEST	0	0.288721	inf	0	1	1
ENSG00000258582	ENSG00000258582	RP11-44L9.1	16:73517215-73521643	NOTEST	0	0	0	0	1	1
ENSG00000258583	ENSG00000258583	RP11-112J1.2	14:59294951-59484046	NOTEST	0	0	0	0	1	1
ENSG00000258584	ENSG00000258584	FAM181A-AS1	14:94371075-94395954	NOTEST	0	0	0	0	1	1
ENSG00000258585	ENSG00000258585	RP11-928F19.2	15:22117082-22118114	NOTEST	0	0	0	0	1	1
ENSG00000258586	ENSG00000258586	RP5-1021I20.2	14:74289261-74296838	NOTEST	0	0	0	0	1	1
ENSG00000258587	ENSG00000258587	RP11-316E14.2	14:75340386-75340957	NOTEST	0	0	0	0	1	1
ENSG00000258588	ENSG00000258588	TRIM6-TRIM34	11:5274419-5667019	NOTEST	0.119437	0.408961	1.77571	0	1	1
ENSG00000258589	ENSG00000258589	CSNK2B-LY6G5B-1181	HSCHR6_MHC_DBB:31611187-31653368	NOTEST	0	0	0	0	1	1
ENSG00000258590	ENSG00000258590	NBEAP1	15:20862966-20893737	NOTEST	0.0519409	0.106372	1.03417	0	1	1
ENSG00000258591	ENSG00000258591	RP11-545M17.3	14:39501122-39578850	NOTEST	0	0	0	0	1	1
ENSG00000258592	ENSG00000258592	RP11-108M12.3	14:57279900-57618895	NOTEST	0	0	0	0	1	1
ENSG00000258593	ENSG00000258593	CTD-3051D23.4	14:105324128-105325173	NOTEST	0.0509812	0.0901249	0.821959	0	1	1
ENSG00000258594	ENSG00000258594	RP11-30G8.2	15:27866679-27874435	NOTEST	0	0	0	0	1	1
ENSG00000258595	ENSG00000258595	RP11-371E8.2	14:93604410-93604810	NOTEST	0	0	0	0	1	1
ENSG00000258597	ENSG00000258597	SERPINA2P	14:94830052-94833039	NOTEST	0	0	0	0	1	1
ENSG00000258598	ENSG00000258598	RP11-260M19.1	14:104842866-104845288	NOTEST	0	0	0	0	1	1
ENSG00000258599	ENSG00000258599	RP11-84C10.1	14:21451313-21453225	NOTEST	0	0	0	0	1	1
ENSG00000258600	ENSG00000258600	RP11-452D21.2	14:83483449-83484488	NOTEST	0	0	0	0	1	1
ENSG00000258601	ENSG00000258601	RP11-81F13.2	14:37116287-37643016	NOTEST	0	0	0	0	1	1
ENSG00000258602	ENSG00000258602	RP11-7F17.7	14:77425980-77432145	NOTEST	0	0	0	0	1	1
ENSG00000258603	ENSG00000258603	RP3-414A15.10	14:74077648-74100644	NOTEST	0.458396	0.416268	-0.139083	0	1	1
ENSG00000258604	ENSG00000258604	AL161668.5	14:21484921-21572881	NOTEST	0	0	0	0	1	1
ENSG00000258605	ENSG00000258605	RP11-299L17.4	14:81726999-81902809	NOTEST	0	0	0	0	1	1
ENSG00000258609	ENSG00000258609	LINC-ROR	18:54721812-54739350	NOTEST	0.00616475	0	#NAME?	0	1	1

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ENSG00000258611	ENSG00000258611	RP11-368J22.2	15:93586635-93632433	NOTEST	0	0	0	0	1	1
ENSG00000258612	ENSG00000258612	RP11-671J11.6	14:35013704-35015183	NOTEST	0	0	0	0	1	1
ENSG00000258613	ENSG00000258613	RPL21P7	14:65703197-65785508	NOTEST	0	0	0	0	1	1
ENSG00000258615	ENSG00000258615	RP11-725G5.3	14:95648276-95786243	NOTEST	0	0	0	0	1	1
ENSG00000258616	ENSG00000258616	RP11-369C8.1	14:46175452-46185155	NOTEST	0.0206868	0.133942	2.69483	0	1	1
ENSG00000258617	ENSG00000258617	DUX4L13	10:135490271-135495193	NOTEST	0	0	0	0	1	1
ENSG00000258618	ENSG00000258618	RPL21P9	14:68168602-68283307	NOTEST	0	0	0	0	1	1
ENSG00000258619	ENSG00000258619	RP11-134E15.1	14:32710729-32712299	NOTEST	0	0	0	0	1	1
ENSG00000258620	ENSG00000258620	RP11-362L22.1	14:100800124-100996640	NOTEST	0	0	0	0	1	1
ENSG00000258622	ENSG00000258622	RP11-90P16.2	14:42832185-43172858	NOTEST	0	0	0	0	1	1
ENSG00000258623	ENSG00000258623	CTD-2325P2.3	14:68286495-69196935	NOTEST	0.0958824	0.228084	1.25023	0	1	1
ENSG00000258624	ENSG00000258624	AC145436.1	15:27216428-27787137	NOTEST	0	0	0	0	1	1
ENSG00000258625	ENSG00000258625	OR11H5P	14:20677398-20678369	NOTEST	0	0	0	0	1	1
ENSG00000258626	ENSG00000258626	COX7A2P1	14:68086514-68162531	NOTEST	0.102009	0.304739	1.57889	0	1	1
ENSG00000258627	ENSG00000258627	RP11-76E17.1	15:94133095-94651167	NOTEST	0	0	0	0	1	1
ENSG00000258628	ENSG00000258628	RP11-492D6.3	15:20433872-20482756	NOTEST	0	0.0228341	inf	0	1	1
ENSG00000258629	ENSG00000258629	CTD-2014B16.1	14:66346309-66347788	NOTEST	0	0	0	0	1	1
ENSG00000258630	ENSG00000258630	RP11-725G5.2	14:95795920-95801841	NOTEST	0	0	0	0	1	1
ENSG00000258631	ENSG00000258631	RP11-739G5.1	15:94133095-94651167	NOTEST	0	0	0	0	1	1
ENSG00000258632	ENSG00000258632	RP11-354B3.1	15:94774766-95023632	NOTEST	0	0	0	0	1	1
ENSG00000258633	ENSG00000258633	RP11-857B24.1	14:45346076-45366280	NOTEST	0	0	0	0	1	1
ENSG00000258635	ENSG00000258635	MEGT1	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000258636	ENSG00000258636	CTD-2298J14.2	14:42057063-42074059	NOTEST	0	0	0	0	1	1
ENSG00000258637	ENSG00000258637	RP11-242P2.1	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000258638	ENSG00000258638	RP11-395B20.2	14:62981589-62981841	NOTEST	0	0	0	0	1	1
ENSG00000258639	ENSG00000258639	RP11-10A2.1	14:48514683-48515419	NOTEST	0	0	0	0	1	1
ENSG00000258640	ENSG00000258640	RPL21P5	14:31569317-31677010	NOTEST	0	0	0	0	1	1
ENSG00000258641	ENSG00000258641	OR4T1P	14:20561511-20562422	NOTEST	0	0	0	0	1	1
ENSG00000258642	ENSG00000258642	RP11-219E7.2	14:21342463-21343927	NOTEST	0	0.117131	inf	0	1	1
ENSG00000258646	ENSG00000258646	RP11-950C14.3	14:75469613-75476292	NOTEST	0	0	0	0	1	1
ENSG00000258647	ENSG00000258647	LINC00930	15:93111047-93115272	NOTEST	0	0	0	0	1	1
ENSG00000258648	ENSG00000258648	UBE2CP1	14:31091317-31291908	NOTEST	0.14387	0.027523	-2.38605	0	1	1
ENSG00000258649	ENSG00000258649	CTD-2142D14.1	14:38059188-38672128	NOTEST	0	0	0	0	1	1
ENSG00000258650	ENSG00000258650	HSBP1P1	14:58862633-59015216	NOTEST	0	0	0	0	1	1
ENSG00000258651	ENSG00000258651	RP11-545M17.1	14:39501122-39578850	NOTEST	0.0451772	0	#NAME?	0	1	1
ENSG00000258652	ENSG00000258652	OR4Q1P	15:22278009-22413497	NOTEST	0	0	0	0	1	1
ENSG00000258653	ENSG00000258653	RP5-1021I20.4	14:74318546-74551196	NOTEST	0.177335	0.17467	-0.0218482	0	1	1
ENSG00000258654	ENSG00000258654	RP11-509A17.3	15:20549988-20564419	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000258658	ENSG00000258658	RP11-517O13.3	14:58765102-58862359	NOTEST	0	0.157529	inf	0	1	1
ENSG00000258659	ENSG00000258659	TRIM34	11:5274419-5667019	NOTEST	0.429051	0.149929	-1.51687	0	1	1
ENSG00000258660	ENSG00000258660	RP4-693M11.3	14:74111577-74170435	NOTEST	0	0.580653	inf	0	1	1
ENSG00000258661	ENSG00000258661	RP11-964E11.2	14:37116287-37643016	NOTEST	0	0	0	0	1	1
ENSG00000258662	ENSG00000258662	RP11-588P7.2	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000258663	ENSG00000258663	RP11-123M6.2	14:101245746-101327368	NOTEST	0	0	0	0	1	1
ENSG00000258665	ENSG00000258665	AC068831.12	15:91565848-91579841	NOTEST	0	0	0	0	1	1
ENSG00000258666	ENSG00000258666	RP11-638I2.8	14:100800124-100996640	NOTEST	0	0	0	0	1	1
ENSG00000258667	ENSG00000258667	HIF1A-AS2	14:62147758-62263146	NOTEST	0.0762484	0.0319716	-1.25392	0	1	1
ENSG00000258668	ENSG00000258668	COX6CP11	14:78119169-78119398	NOTEST	0	0	0	0	1	1
ENSG00000258670	ENSG00000258670	RP11-1042B17.3	14:60863186-61021634	NOTEST	0.564032	0.380708	-0.567092	0	1	1
ENSG00000258671	ENSG00000258671	RP11-407N17.2	14:39680984-39681459	NOTEST	0	0.108715	inf	0	1	1
ENSG00000258672	ENSG00000258672	RP11-543C4.3	14:100150640-100193638	NOTEST	0	0	0	0	1	1
ENSG00000258673	ENSG00000258673	RP4-773N10.6	1:110625309-110652341	NOTEST	0.0364093	0.0541469	0.572572	0	1	1
ENSG00000258674	ENSG00000258674	CTC-260F20.3	19:19623226-19648390	NOTEST	0.564352	0.286291	-0.979116	0	1	1
ENSG00000258675	ENSG00000258675	RP11-299L17.3	14:81908330-81916501	NOTEST	0	0	0	0	1	1
ENSG00000258676	ENSG00000258676	RP11-386M24.3	15:93124058-93143775	NOTEST	0	0	0	0	1	1
ENSG00000258678	ENSG00000258678	RP11-1078H9.1	14:90918406-90921461	NOTEST	0	0	0	0	1	1
ENSG00000258679	ENSG00000258679	RP11-74M13.4	12:57216768-57268052	NOTEST	0	0	0	0	1	1
ENSG00000258680	ENSG00000258680	RP11-506K19.1	14:39218544-39417477	NOTEST	0	0	0	0	1	1
ENSG00000258681	ENSG00000258681	RP11-8L8.1	14:101683708-101684578	NOTEST	0	0	0	0	1	1
ENSG00000258682	ENSG00000258682	CTD-2002H8.2	14:58466452-58764857	NOTEST	0.214645	0.422222	0.976051	0	1	1
ENSG00000258683	ENSG00000258683	RP11-11K13.1	14:83254821-83262565	NOTEST	0	0	0	0	1	1
ENSG00000258684	ENSG00000258684	BMS1P16	15:21365633-21372686	NOTEST	0.0277139	0.0118306	-1.22808	0	1	1
ENSG00000258685	ENSG00000258685	CTD-2315A10.2	14:59602205-59603139	NOTEST	0	0	0	0	1	1
ENSG00000258687	ENSG00000258687	RP11-218E20.2	14:51314839-51411454	NOTEST	0.651889	0	#NAME?	0	1	1
ENSG00000258689	ENSG00000258689	RP6-65G23.1	14:71165414-71178870	NOTEST	0	0	0	0	1	1
ENSG00000258690	ENSG00000258690	RP11-81F13.1	14:37116287-37643016	NOTEST	0	0	0	0	1	1
ENSG00000258691	ENSG00000258691	RP11-404P21.8	14:96671015-96735304	NOTEST	0	0	0	0	1	1
ENSG00000258692	ENSG00000258692	SALL4P7	14:60863186-61021634	NOTEST	0	0	0	0	1	1
ENSG00000258693	ENSG00000258693	RP11-436M15.3	14:100437785-100610573	NOTEST	0	0	0	0	1	1
ENSG00000258694	ENSG00000258694	RP11-1033H12.1	14:52577839-52596343	NOTEST	0	0	0	0	1	1
ENSG00000258695	ENSG00000258695	RP3-414A15.2	14:73945188-74025651	NOTEST	0	0.0332543	inf	0	1	1
ENSG00000258696	ENSG00000258696	CTD-2058B24.3	14:38059188-38672128	NOTEST	0	0	0	0	1	1
ENSG00000258697	ENSG00000258697	DUX4L6	4:190995379-190997190	NOTEST	0	0	0	0	1	1
ENSG00000258698	ENSG00000258698	RP11-589M4.3	14:53259592-53286752	NOTEST	0	0	0	0	1	1
ENSG00000258699	ENSG00000258699	RP11-356K23.2	14:89591214-90421121	NOTEST	0	0	0	0	1	1

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ENSG00000258701	ENSG00000258701	LINC00638	14:105287537-105290055	NOTEST	0.102731	0.203772	0.988081	0	1	1
ENSG00000258702	ENSG00000258702	RP11-433J8.1	14:97059069-97062099	NOTEST	0.00519438	0	#NAME?	0	1	1
ENSG00000258703	ENSG00000258703	RP11-1085N6.4	14:57226096-57232475	NOTEST	0	0	0	0	1	1
ENSG00000258705	ENSG00000258705	AE000660.4	14:22480148-22483203	NOTEST	0	0	0	0	1	1
ENSG00000258706	ENSG00000258706	SLC20A1P3	15:20172666-20173605	NOTEST	0	0	0	0	1	1
ENSG00000258707	ENSG00000258707	RP11-467L19.11	15:20832121-20832668	NOTEST	0	0	0	0	1	1
ENSG00000258708	ENSG00000258708	SLC25A21-AS1	14:37116287-37643016	NOTEST	0.146117	0.0909405	-0.684127	0	1	1
ENSG00000258710	ENSG00000258710	CT60	15:21145766-21198632	NOTEST	0	0	0	0	1	1
ENSG00000258711	ENSG00000258711	RP11-218E20.3	14:51422976-51428720	NOTEST	0.00916796	0.0117549	0.358587	0	1	1
ENSG00000258712	ENSG00000258712	CXADRP2	15:22015702-22016791	NOTEST	0	0	0	0	1	1
ENSG00000258713	ENSG00000258713	C20orf141	20:2795613-2800930	NOTEST	0	0	0	0	1	1
ENSG00000258714	ENSG00000258714	RP11-998D10.7	14:21484921-21572881	NOTEST	0	0	0	0	1	1
ENSG00000258716	ENSG00000258716	RP11-661G16.2	14:91006931-91282823	NOTEST	0	0	0	0	1	1
ENSG00000258717	ENSG00000258717	RP11-566J3.2	14:101123586-101146221	NOTEST	0	0	0	0	1	1
ENSG00000258718	ENSG00000258718	RP11-226P1.2	14:82194123-82496693	NOTEST	0	0	0	0	1	1
ENSG00000258719	ENSG00000258719	RP11-232C2.3	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000258721	ENSG00000258721	OR11H3P	15:22278009-22413497	NOTEST	0	0	0	0	1	1
ENSG00000258722	ENSG00000258722	RP11-998D10.5	14:21576201-21584862	NOTEST	0	0	0	0	1	1
ENSG00000258723	ENSG00000258723	RP11-332E19.2	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000258724	ENSG00000258724	SOX7	8:10581277-10697394	NOTEST	0.0799384	0.110285	0.464275	0	1	1
ENSG00000258725	ENSG00000258725	PRC1-AS1	15:91509269-91538859	NOTEST	0.318069	0.0844911	-1.91247	0	1	1
ENSG00000258726	ENSG00000258726	DUXAP6	15:92396924-92874267	NOTEST	0	0	0	0	1	1
ENSG00000258728	ENSG00000258728	GALT	9:34638129-34681295	NOTEST	0	0	0	0	1	1
ENSG00000258729	ENSG00000258729	DKFZP434O1614	14:96741382-96743060	NOTEST	0	0	0	0	1	1
ENSG00000258730	ENSG00000258730	ITPK1-AS1	14:93403258-93582665	NOTEST	0.00591874	0.00254639	-1.21684	0	1	1
ENSG00000258731	ENSG00000258731	RP11-547D23.1	14:53620071-53624246	NOTEST	0.0463275	0.0243198	-0.92974	0	1	1
ENSG00000258732	ENSG00000258732	RP11-603B24.1	15:22566921-22570823	NOTEST	0	0	0	0	1	1
ENSG00000258733	ENSG00000258733	CTD-2341M24.1	14:86401053-86596117	NOTEST	0.316723	0.404522	0.352997	0	1	1
ENSG00000258735	ENSG00000258735	LINC00637	14:104314057-104346448	NOTEST	0	0	0	0	1	1
ENSG00000258736	ENSG00000258736	RP11-982M15.7	14:105119884-105122124	NOTEST	0	0	0	0	1	1
ENSG00000258737	ENSG00000258737	SUB1P2	14:74769771-74826711	NOTEST	0	0	0	0	1	1
ENSG00000258738	ENSG00000258738	RP11-73E17.2	14:35221936-35345665	NOTEST	0.166398	0.255214	0.617074	0	1	1
ENSG00000258739	ENSG00000258739	ENO1P2	15:92937057-93011958	NOTEST	0.0522675	0	#NAME?	0	1	1
ENSG00000258740	ENSG00000258740	RP11-293M10.1	14:75705318-75738653	NOTEST	0.0292986	0.0228015	-0.361704	0	1	1
ENSG00000258742	ENSG00000258742	RP11-862G15.1	14:93352696-93359851	NOTEST	0	0	0	0	1	1
ENSG00000258743	ENSG00000258743	RP11-406A9.2	14:83108963-83173169	NOTEST	0	0	0	0	1	1
ENSG00000258744	ENSG00000258744	RP11-80A15.1	14:24970799-24977894	NOTEST	0.0800355	0	#NAME?	0	1	1
ENSG00000258745	ENSG00000258745	RP11-218E20.5	14:51314839-51411454	NOTEST	0.0759908	0.336046	2.14476	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258746	ENSG00000258746	RP11-454K7.2	14:45971944-45972343	NOTEST	0	0	0	0	1	1
ENSG00000258747	ENSG00000258747	RP11-163M18.1	14:44976609-45007716	NOTEST	0	0	0	0	1	1
ENSG00000258748	ENSG00000258748	CTD-2223O18.1	14:104603486-104604235	NOTEST	0	0	0	0	1	1
ENSG00000258749	ENSG00000258749	RP11-688G15.3	14:99947505-100070363	NOTEST	0	0.139878	inf	0	1	1
ENSG00000258750	ENSG00000258750	RP11-2G1.2	14:48865710-48960970	NOTEST	0	0	0	0	1	1
ENSG00000258751	ENSG00000258751	RP11-2G1.1	14:48865710-48960970	NOTEST	0	0	0	0	1	1
ENSG00000258752	ENSG00000258752	RP11-356K23.1	14:89591214-90421121	NOTEST	0	0	0	0	1	1
ENSG00000258753	ENSG00000258753	RP11-794A8.1	14:54937426-54937936	NOTEST	0	0	0	0	1	1
ENSG00000258754	ENSG00000258754	CTD-3049M7.1	15:94133095-94651167	NOTEST	0	0	0	0	1	1
ENSG00000258755	ENSG00000258755	DUX4L7	4:190992086-190993897	NOTEST	0	0	0	0	1	1
ENSG00000258757	ENSG00000258757	RP11-841O20.2	14:53106633-53162618	NOTEST	0	0.00083175	inf	0	1	1
ENSG00000258758	ENSG00000258758	RP11-613G13.1	14:57279900-57618895	NOTEST	0	0	0	0	1	1
ENSG00000258759	ENSG00000258759	RP11-1012A1.7	14:68168602-68283307	NOTEST	0	0.0825528	inf	0	1	1
ENSG00000258760	ENSG00000258760	CTD-2509G16.5	14:65703197-65785508	NOTEST	0	0	0	0	1	1
ENSG00000258761	ENSG00000258761	RP11-24J19.1	15:92396924-92874267	NOTEST	0	0.0702489	inf	0	1	1
ENSG00000258762	ENSG00000258762	CTD-2320B12.3	14:84639184-84639950	NOTEST	0	0	0	0	1	1
ENSG00000258763	ENSG00000258763	RP11-110A12.2	12:55828520-55979255	NOTEST	0.0849277	0.11016	0.375298	0	1	1
ENSG00000258764	ENSG00000258764	RP11-1042B17.4	14:60863186-61021634	NOTEST	0	0	0	0	1	1
ENSG00000258765	ENSG00000258765	RP11-692C24.2	15:92186246-92192344	NOTEST	0	0	0	0	1	1
ENSG00000258766	ENSG00000258766	DIO2-AS1	14:80663872-80921812	NOTEST	0	0	0	0	1	1
ENSG00000258767	ENSG00000258767	RP11-32B5.5	15:22025292-22025752	NOTEST	0	0	0	0	1	1
ENSG00000258768	ENSG00000258768	CTD-2292M16.8	14:20724716-20774970	NOTEST	0.284511	0.346484	0.284303	0	1	1
ENSG00000258769	ENSG00000258769	RAP1AP	14:74942894-74963809	NOTEST	0.457423	0.536598	0.230312	0	1	1
ENSG00000258770	ENSG00000258770	CTD-2007A10.1	14:88100722-88121638	NOTEST	0	0	0	0	1	1
ENSG00000258771	ENSG00000258771	RP11-854K16.2	15:21286140-21286776	NOTEST	0	0	0	0	1	1
ENSG00000258772	ENSG00000258772	RP11-84C10.3	14:21366143-21404414	NOTEST	0	0	0	0	1	1
ENSG00000258773	ENSG00000258773	RP11-255M2.2	15:95623323-95676088	NOTEST	0	0	0	0	1	1
ENSG00000258774	ENSG00000258774	NANOGP7	14:92047039-92333880	NOTEST	0	0	0	0	1	1
ENSG00000258776	ENSG00000258776	RP11-1085N6.5	14:57279900-57618895	NOTEST	0	0	0	0	1	1
ENSG00000258777	ENSG00000258777	HIF1A-AS1	14:62147758-62263146	NOTEST	0.0570745	0.0218899	-1.38258	0	1	1
ENSG00000258778	ENSG00000258778	RP11-804M7.1	14:64201414-64202641	NOTEST	0	0	0	0	1	1
ENSG00000258779	ENSG00000258779	RP11-140I24.1	16:73420703-73455292	NOTEST	0	0	0	0	1	1
ENSG00000258780	ENSG00000258780	BMS1P15	15:20359028-20366079	NOTEST	0.0765581	0.0334669	-1.19382	0	1	1
ENSG00000258781	ENSG00000258781	RP11-496I2.4	14:19742774-19758782	NOTEST	0	0	0	0	1	1
ENSG00000258782	ENSG00000258782	RP11-701B16.2	14:59895739-60043549	NOTEST	0	0	0	0	1	1
ENSG00000258783	ENSG00000258783	KRT18P6	14:35981030-35982295	NOTEST	0	0	0	0	1	1
ENSG00000258784	ENSG00000258784	RP11-813I20.2	14:56214925-56239921	NOTEST	0	0	0	0	1	1
ENSG00000258785	ENSG00000258785	CTD-2643K12.2	15:94133095-94651167	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258786	ENSG00000258786	RP11-928F19.3	15:22185844-22186733	NOTEST	0	0	0	0	1	1
ENSG00000258787	ENSG00000258787	RP11-164C12.1	15:93855785-94112712	NOTEST	0	0	0	0	1	1
ENSG00000258788	ENSG00000258788	RP11-404P21.9	14:96671015-96735304	NOTEST	0	0	0	0	1	1
ENSG00000258789	ENSG00000258789	RP11-507K2.3	14:88851267-89021077	NOTEST	0.308275	0.117561	-1.3908	0	1	1
ENSG00000258792	ENSG00000258792	RP11-944C7.1	14:89591214-90421121	NOTEST	0	0	0	0	1	1
ENSG00000258793	ENSG00000258793	RP11-404P21.3	14:96671015-96735304	NOTEST	0	0	0	0	1	1
ENSG00000258794	ENSG00000258794	RP11-313F23.5	12:34343971-34371788	NOTEST	0.0136257	0.039565	1.5379	0	1	1
ENSG00000258795	ENSG00000258795	RP11-1082A3.1	14:98963468-98981135	NOTEST	0	0	0	0	1	1
ENSG00000258796	ENSG00000258796	CTD-2560C21.1	14:66679527-67648520	NOTEST	0	0	0	0	1	1
ENSG00000258797	ENSG00000258797	RP11-467L19.6	15:20750882-20754751	NOTEST	0	0	0	0	1	1
ENSG00000258798	ENSG00000258798	RP11-895M11.3	14:91884609-91887520	NOTEST	0	0.159895	inf	0	1	1
ENSG00000258799	ENSG00000258799	RP11-810K23.5	15:21106769-21106938	NOTEST	0	0	0	0	1	1
ENSG00000258800	ENSG00000258800	CTD-2302E22.2	14:64063756-64108579	NOTEST	0	0	0	0	1	1
ENSG00000258802	ENSG00000258802	RP11-589M4.2	14:53259592-53286752	NOTEST	0	0	0	0	1	1
ENSG00000258803	ENSG00000258803	RP11-624J12.1	14:56955071-57197253	NOTEST	0	0	0	0	1	1
ENSG00000258804	ENSG00000258804	RP11-322L20.1	14:87372121-87389099	NOTEST	0	0	0	0	1	1
ENSG00000258805	ENSG00000258805	ADIPOR1P2	14:95100041-95100861	NOTEST	0	0	0	0	1	1
ENSG00000258806	ENSG00000258806	OR11H7	14:20697560-20698500	NOTEST	0	0	0	0	1	1
ENSG00000258807	ENSG00000258807	RP11-1152H15.	14:88176762-88460009	NOTEST	0.0226872	0.0532834	1.23181	0	1	1
ENSG00000258808	ENSG00000258808	RP11-255G12.3	14:51858845-51863853	NOTEST	0	0	0	0	1	1
ENSG00000258809	ENSG00000258809	CTD-2555O16.1	14:64812888-64846036	NOTEST	0	0	0	0	1	1
ENSG00000258810	ENSG00000258810	RP11-219E7.1	14:21252046-21252452	NOTEST	0	0	0	0	1	1
ENSG00000258811	ENSG00000258811	CTD-3051D23.1	14:105308999-105312253	NOTEST	0.0192678	0.00374201	-2.36431	0	1	1
ENSG00000258812	ENSG00000258812	TRAV33	14:22658051-22658607	NOTEST	0	0	0	0	1	1
ENSG00000258813	ENSG00000258813	RP11-109N23.4	14:73525138-73588122	NOTEST	0.138566	0.0728585	-0.9274	0	1	1
ENSG00000258814	ENSG00000258814	CTD-2128A3.3	14:85828800-85983278	NOTEST	0	0	0	0	1	1
ENSG00000258815	ENSG00000258815	RP11-408B11.2	12:85711837-85736690	NOTEST	0	0	0	0	1	1
ENSG00000258816	ENSG00000258816	RP11-74M13.3	12:57216768-57268052	NOTEST	0	0	0	0	1	1
ENSG00000258817	ENSG00000258817	OR4C13	11:49973942-49974971	NOTEST	0	0	0	0	1	1
ENSG00000258819	ENSG00000258819	RP11-7F17.3	14:77507406-77552789	NOTEST	0	0.0435047	inf	0	1	1
ENSG00000258820	ENSG00000258820	RP11-293M10.2	14:75705318-75738653	NOTEST	0	0	0	0	1	1
ENSG00000258821	ENSG00000258821	AC005041.17	2:74724643-74731805	NOTEST	0.177742	0.0919823	-0.95036	0	1	1
ENSG00000258822	ENSG00000258822	OR4K16P	14:20424758-20425727	NOTEST	0	0	0	0	1	1
ENSG00000258823	ENSG00000258823	CTD-2555K7.3	14:23171351-23241007	NOTEST	0	0	0	0	1	1
ENSG00000258826	ENSG00000258826	RP11-300J18.1	14:88484948-88563276	NOTEST	0	0	0	0	1	1
ENSG00000258827	ENSG00000258827	RP11-537P22.2	14:37116287-37643016	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258828	ENSG00000258828	KRT8P2	14:44010085-44011029	NOTEST	0	0	0	0	1	1
ENSG00000258829	ENSG00000258829	CTD-2243E23.1	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000258831	ENSG00000258831	RP11-76E17.4	15:94133095-94651167	NOTEST	0	0	0	0	1	1
ENSG00000258834	ENSG00000258834	DUX4L4	4:191001978-191003777	NOTEST	0	0	0	0	1	1
ENSG00000258835	ENSG00000258835	TRAV28	14:22623011-22623571	NOTEST	0	0	0	0	1	1
ENSG00000258836	ENSG00000258836	RP11-349A22.2	14:58466452-58764857	NOTEST	0	0.0856754	inf	0	1	1
ENSG00000258837	ENSG00000258837	CTD-2566J3.1	14:68286495-69196935	NOTEST	0	0	0	0	1	1
ENSG00000258838	ENSG00000258838	ERCC6-PGBD3	10:50627322-50747584	NOTEST	7.14E-05	0.000119159	0.737986	0	1	1
ENSG00000258841	ENSG00000258841	RP11-226P1.3	14:82127771-82129218	NOTEST	0	0	0	0	1	1
ENSG00000258842	ENSG00000258842	RP11-355I22.5	14:62453802-62568431	NOTEST	0	0	0	0	1	1
ENSG00000258843	ENSG00000258843	RP11-286O18.1	14:51186480-51297839	NOTEST	0	0	0	0	1	1
ENSG00000258844	ENSG00000258844	RP11-259K15.2	14:36683812-36704814	NOTEST	0	0	0	0	1	1
ENSG00000258845	ENSG00000258845	RP11-945F5.1	14:46037197-46038272	NOTEST	0	0	0	0	1	1
ENSG00000258846	ENSG00000258846	EEF1A1P33	12:97294474-97296476	NOTEST	0	0	0	0	1	1
ENSG00000258847	ENSG00000258847	CTD-2014B16.3	14:66424014-66471241	NOTEST	0	0	0	0	1	1
ENSG00000258848	ENSG00000258848	GRAMD4P6	15:22026730-22026974	NOTEST	0	0	0	0	1	1
ENSG00000258849	ENSG00000258849	OR7E159P	14:52231993-52292140	NOTEST	0	0	0	0	1	1
ENSG00000258850	ENSG00000258850	RP11-214N1.1	14:42832185-43172858	NOTEST	0	0	0	0	1	1
ENSG00000258851	ENSG00000258851	RP11-894P9.2	14:104019757-104181841	NOTEST	0.111057	0	#NAME?	0	1	1
ENSG00000258853	ENSG00000258853	RP11-30G8.1	15:27929643-27930914	NOTEST	0	0	0	0	1	1
ENSG00000258854	ENSG00000258854	RP11-463J10.4	14:52449237-52453937	NOTEST	0	0	0	0	1	1
ENSG00000258855	ENSG00000258855	OR11J2P	15:21145766-21198632	NOTEST	0	0	0	0	1	1
ENSG00000258856	ENSG00000258856	CTD-2325K12.1	14:58030639-58448912	NOTEST	0	0	0	0	1	1
ENSG00000258857	ENSG00000258857	RP11-247L20.3	14:50704280-50883179	NOTEST	0.128892	0.0840745	-0.616428	0	1	1
ENSG00000258858	ENSG00000258858	RP11-982M15.5	14:105155942-105185942	NOTEST	0.131867	0	#NAME?	0	1	1
ENSG00000258859	ENSG00000258859	RP11-594C13.1	14:87819413-88039366	NOTEST	0	0	0	0	1	1
ENSG00000258860	ENSG00000258860	RP11-561B11.3	14:35831437-35832834	NOTEST	0.0327922	0.097471	1.57162	0	1	1
ENSG00000258861	ENSG00000258861	MIR381HG	14:101511493-101518132	NOTEST	0	0	0	0	1	1
ENSG00000258863	ENSG00000258863	SETP1	14:20996273-20997118	NOTEST	0	0	0	0	1	1
ENSG00000258864	ENSG00000258864	CTC-554D6.1	5:112043194-112258236	NOTEST	0	0.240718	inf	0	1	1
ENSG00000258866	ENSG00000258866	RP11-991C1.2	14:95514556-95517290	NOTEST	0	0	0	0	1	1
ENSG00000258867	ENSG00000258867	LINC01146	14:88484948-88563276	NOTEST	0	0	0	0	1	1
ENSG00000258868	ENSG00000258868	RP11-816J8.1	14:49524430-49544223	NOTEST	0	0	0	0	1	1
ENSG00000258869	ENSG00000258869	RP11-204N11.1	14:98215600-98230326	NOTEST	0	0	0	0	1	1
ENSG00000258870	ENSG00000258870	EIF4EBP1P1	14:21853352-21924285	NOTEST	0	0.210293	inf	0	1	1
ENSG00000258871	ENSG00000258871	RP3-514A23.2	14:72399155-73061833	NOTEST	0	0	0	0	1	1
ENSG00000258872	ENSG00000258872	FDPSP3	14:55308725-55369570	NOTEST	0	0	0	0	1	1
ENSG00000258873	ENSG00000258873	DUXA	19:57665388-57678811	NOTEST	0	0	0	0	1	1
ENSG00000258874	ENSG00000258874	RP11-232C2.2	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000258875	ENSG00000258875	CTD-2547L24.3	14:91698875-91720269	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258876	ENSG00000258876	RP11-270M14.5	14:76041230-76550928	NOTEST	0	0	0	0	1	1
ENSG00000258877	ENSG00000258877	RP11-395B20.1	14:63070830-63072435	NOTEST	0	0	0	0	1	1
ENSG00000258878	ENSG00000258878	CTD-2509G16.3	14:65701232-65701819	NOTEST	0	0	0	0	1	1
ENSG00000258879	ENSG00000258879	RP11-713N11.5	12:25164348-25173827	NOTEST	0	0	0	0	1	1
ENSG00000258880	ENSG00000258880	DASS-312M4.10	HSCHR6_MHC_SSTO:31664594-31675654	NOTEST	0	0	0	0	1	1
ENSG00000258881	ENSG00000258881	AC007040.11	2:71163011-71306935	NOTEST	0.509826	0.39189	-0.379554	0	1	1
ENSG00000258882	ENSG00000258882	CTD-2277K2.1	14:62278691-62437037	NOTEST	0	0	0	0	1	1
ENSG00000258883	ENSG00000258883	RP11-32B5.2	15:21893089-21903057	NOTEST	0	0	0	0	1	1
ENSG00000258885	ENSG00000258885	RP11-344B23.2	9:36833271-37034103	NOTEST	0	0	0	0	1	1
ENSG00000258886	ENSG00000258886	HIGD1AP17	14:31343719-31562818	NOTEST	0	0	0	0	1	1
ENSG00000258887	ENSG00000258887	RP11-388E23.3	14:24294844-24296605	NOTEST	0	0	0	0	1	1
ENSG00000258888	ENSG00000258888	RP11-326A13.1	15:93800426-93803704	NOTEST	0	0	0	0	1	1
ENSG00000258891	ENSG00000258891	RP5-1021I20.5	14:74318546-74551196	NOTEST	0.00848103	0.0225253	1.40923	0	1	1
ENSG00000258892	ENSG00000258892	RP11-193F5.1	14:61201459-61550451	NOTEST	0	0.349488	inf	0	1	1
ENSG00000258893	ENSG00000258893	SETP2	14:51902755-51903681	NOTEST	0	0	0	0	1	1
ENSG00000258894	ENSG00000258894	RP11-557C9.1	14:44064338-44065886	NOTEST	0	0	0	0	1	1
ENSG00000258895	ENSG00000258895	CTD-2643K12.1	15:94133095-94651167	NOTEST	0.0425621	0.219237	2.36485	0	1	1
ENSG00000258896	ENSG00000258896	SCOCP1	14:60558628-60636574	NOTEST	0	0	0	0	1	1
ENSG00000258897	ENSG00000258897	EGLN3-AS1	14:34393436-34931980	NOTEST	0	0	0	0	1	1
ENSG00000258899	ENSG00000258899	OR4U1P	14:20512074-20512986	NOTEST	0	0	0	0	1	1
ENSG00000258901	ENSG00000258901	CTD-2298J14.1	14:42024864-42025258	NOTEST	0	0	0	0	1	1
ENSG00000258902	ENSG00000258902	CTD-2128A3.2	14:85828800-85983278	NOTEST	0	0	0	0	1	1
ENSG00000258903	ENSG00000258903	RP11-355I22.2	14:62570095-62596352	NOTEST	0	0	0	0	1	1
ENSG00000258904	ENSG00000258904	RP11-638I2.2	14:100673743-100772884	NOTEST	0.117549	0.155005	0.39905	0	1	1
ENSG00000258905	ENSG00000258905	TRAV32	14:22653457-22653953	NOTEST	0	0	0	0	1	1
ENSG00000258906	ENSG00000258906	CTD-2552B11.3	14:21652499-21653118	NOTEST	0	0	0	0	1	1
ENSG00000258907	ENSG00000258907	RP11-644F5.15	12:56032695-56053579	NOTEST	0	0	0	0	1	1
ENSG00000258908	ENSG00000258908	RP11-203M5.8	14:20937112-20945253	NOTEST	0	0.084677	inf	0	1	1
ENSG00000258909	ENSG00000258909	RP11-164C12.2	15:93855785-94112712	NOTEST	0	0	0	0	1	1
ENSG00000258910	ENSG00000258910	RP11-19E11.1	2:119591275-119592686	NOTEST	0	0	0	0	1	1
ENSG00000258911	ENSG00000258911	DUX4L10	10:135480653-135481921	NOTEST	0	0	0	0	1	1
ENSG00000258912	ENSG00000258912	RP11-1079H9.1	14:86401053-86596117	NOTEST	0	0.0600616	inf	0	1	1
ENSG00000258913	ENSG00000258913	RP11-260M19.2	14:104689920-104754406	NOTEST	0	0	0	0	1	1
ENSG00000258914	ENSG00000258914	CTD-2134A5.3	14:104314057-104346448	NOTEST	0	0	0	0	1	1
ENSG00000258915	ENSG00000258915	RP11-114N19.2	14:80943329-81636758	NOTEST	0	0	0	0	1	1
ENSG00000258916	ENSG00000258916	SPATA31E2P	15:20798817-20804500	NOTEST	0	0	0	0	1	1
ENSG00000258917	ENSG00000258917	ZMYND19P1	14:78138746-78174363	NOTEST	0.048226	0.109272	1.18005	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258918	ENSG00000258918	RP11-219E7.4	14:21366143-21404414	NOTEST	0	0.0589128	inf	0	1	1
ENSG00000258919	ENSG00000258919	RP11-1029J19.4	14:102095320-102098867	NOTEST	0	0	0	0	1	1
ENSG00000258921	ENSG00000258921	RP11-644F5.16	12:56032695-56053579	NOTEST	0	0	0	0	1	1
ENSG00000258922	ENSG00000258922	CTD-2313J17.1	15:93146139-93353114	NOTEST	0	0	0	0	1	1
ENSG00000258923	ENSG00000258923	CTD-2320B12.1	14:84640134-84641854	NOTEST	0	0	0	0	1	1
ENSG00000258924	ENSG00000258924	CTB-96E2.3	17:26684603-26734215	NOTEST	0.0811733	0.482621	2.57181	0	1	1
ENSG00000258925	ENSG00000258925	NPM1P5	15:92396924-92874267	NOTEST	0.0222689	0.0537465	1.27114	0	1	1
ENSG00000258926	ENSG00000258926	RP11-47I22.1	14:61654276-62125414	NOTEST	0.0651303	0.105388	0.694303	0	1	1
ENSG00000258927	ENSG00000258927	RP11-1070N10.5	14:96087250-96109622	NOTEST	0.175691	0.363748	1.04989	0	1	1
ENSG00000258928	ENSG00000258928	RP11-463J10.2	14:52292912-52446060	NOTEST	0	0	0	0	1	1
ENSG00000258930	ENSG00000258930	RP5-1163L11.2	14:71374121-71582099	NOTEST	0	0	0	0	1	1
ENSG00000258931	ENSG00000258931	RP11-1084I9.2	15:26147506-26298267	NOTEST	0	0	0	0	1	1
ENSG00000258932	ENSG00000258932	CTD-3006G17.2	14:27727922-28314492	NOTEST	0.106466	0.175381	0.720105	0	1	1
ENSG00000258933	ENSG00000258933	RP11-991C1.1	14:95426613-95429313	NOTEST	0	0	0	0	1	1
ENSG00000258934	ENSG00000258934	RP11-97N10.1	14:43276580-43277315	NOTEST	0	0	0	0	1	1
ENSG00000258935	ENSG00000258935	RP11-1078H9.2	14:91006931-91282823	NOTEST	0	0	0	0	1	1
ENSG00000258938	ENSG00000258938	RP11-317N8.5	14:36288429-36536396	NOTEST	0.0336191	0.0506165	0.590326	0	1	1
ENSG00000258940	ENSG00000258940	RP11-407N17.5	14:39699434-39856306	NOTEST	0.226845	0.0128039	-4.14705	0	1	1
ENSG00000258941	ENSG00000258941	RP11-407N17.3	14:39699434-39856306	NOTEST	0	0	0	0	1	1
ENSG00000258942	ENSG00000258942	RP11-255G12.2	14:51800110-51852321	NOTEST	0.0462725	0.0163283	-1.50278	0	1	1
ENSG00000258943	ENSG00000258943	RP11-696D21.2	14:63764843-63766265	NOTEST	0	0.0505554	inf	0	1	1
ENSG00000258944	ENSG00000258944	RP4-647C14.3	14:73704204-73741348	NOTEST	0.104379	0.0754968	-0.467346	0	1	1
ENSG00000258945	ENSG00000258945	RP11-497E19.2	14:85991476-85996332	NOTEST	0	0	0	0	1	1
ENSG00000258946	ENSG00000258946	RP11-58E21.4	14:50394288-50428678	NOTEST	0	0.0142405	inf	0	1	1
ENSG00000258948	ENSG00000258948	KRT8P1	14:39196478-39197685	NOTEST	0	0	0	0	1	1
ENSG00000258949	ENSG00000258949	RP11-857B24.5	14:45366497-45381066	NOTEST	0.0782895	0	#NAME?	0	1	1
ENSG00000258951	ENSG00000258951	KRT18P7	14:71047973-71108015	NOTEST	0.0941025	0.171805	0.868464	0	1	1
ENSG00000258952	ENSG00000258952	RP11-1042B17.5	14:61107447-61109307	NOTEST	0	0	0	0	1	1
ENSG00000258954	ENSG00000258954	RP11-692C24.1	15:91951937-92148441	NOTEST	0	0	0	0	1	1
ENSG00000258955	ENSG00000258955	LINC00519	14:51771133-51795104	NOTEST	0	0	0	0	1	1
ENSG00000258956	ENSG00000258956	COX4I1P1	14:62278691-62437037	NOTEST	0	0	0	0	1	1
ENSG00000258957	ENSG00000258957	RP11-363J20.1	14:69649736-69821183	NOTEST	0	0	0	0	1	1
ENSG00000258958	ENSG00000258958	RP11-594C13.2	14:87790096-87798734	NOTEST	0	0	0	0	1	1
ENSG00000258959	ENSG00000258959	RP11-1017G21.4	14:102430864-102532565	NOTEST	0.130084	0.347285	1.41667	0	1	1
ENSG00000258960	ENSG00000258960	CTD-2014B16.2	14:66367649-66368169	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000258962	ENSG00000258962	RP11-747H7.1	14:92047039-92333880	NOTEST	0	0	0	0	1	1
ENSG00000258963	ENSG00000258963	RP11-903H12.4	14:21202736-21203170	NOTEST	0	0	0	0	1	1
ENSG00000258965	ENSG00000258965	RP11-446P9.1	15:26147506-26298267	NOTEST	0	0	0	0	1	1
ENSG00000258966	ENSG00000258966	RP5-1163L11.3	14:71374121-71582099	NOTEST	0	0	0	0	1	1
ENSG00000258968	ENSG00000258968	RP11-829H16.5	14:31343719-31562818	NOTEST	0	0	0	0	1	1
ENSG00000258969	ENSG00000258969	RP11-305B6.3	14:44464983-44853748	NOTEST	0	0	0	0	1	1
ENSG00000258970	ENSG00000258970	RP11-100M12.1	15:27216428-27787137	NOTEST	0	0	0	0	1	1
ENSG00000258971	ENSG00000258971	RP11-326A13.3	15:93844644-93844876	NOTEST	0	0	0	0	1	1
ENSG00000258972	ENSG00000258972	NDUFB8P1	14:74077648-74100644	NOTEST	0	0	0	0	1	1
ENSG00000258973	ENSG00000258973	RP11-934B9.3	14:24787554-24809251	NOTEST	0	0	0	0	1	1
ENSG00000258975	ENSG00000258975	RP11-753D20.1	14:88603076-88626935	NOTEST	0	0	0	0	1	1
ENSG00000258976	ENSG00000258976	CTD-2207P18.2	14:75081395-75083350	NOTEST	0	0	0	0	1	1
ENSG00000258977	ENSG00000258977	RP11-799P8.1	14:82071690-82089405	NOTEST	0	0.0321692	inf	0	1	1
ENSG00000258978	ENSG00000258978	HIF1AP1	14:75548821-75643334	NOTEST	0	0	0	0	1	1
ENSG00000258979	ENSG00000258979	RP11-433J8.2	14:97207527-97256950	NOTEST	0	0	0	0	1	1
ENSG00000258980	ENSG00000258980	EIF1AXP2	14:65877309-66210839	NOTEST	0	0	0	0	1	1
ENSG00000258981	ENSG00000258981	COX5AP2	14:52577839-52596343	NOTEST	0	0	0	0	1	1
ENSG00000258982	ENSG00000258982	RP11-638I2.4	14:100673743-100772884	NOTEST	0.184472	0.518218	1.49016	0	1	1
ENSG00000258983	ENSG00000258983	RP11-507K2.2	14:88851267-89021077	NOTEST	0.0462705	0	#NAME?	0	1	1
ENSG00000258984	ENSG00000258984	UBE2F-SCLY	2:238875468-239008054	NOTEST	0.223504	0.176668	-0.33926	0	1	1
ENSG00000258986	ENSG00000258986	TMEM179	14:104941014-105071984	NOTEST	0.0422592	0.104158	1.30144	0	1	1
ENSG00000258987	ENSG00000258987	RP11-131H24.4	14:94400498-94443137	NOTEST	0.1888	0.121554	-0.635257	0	1	1
ENSG00000258988	ENSG00000258988	RP11-125H8.1	14:67656109-67695267	NOTEST	0.0392329	6.17E-07	-15.9554	0	1	1
ENSG00000258989	ENSG00000258989	RP11-47I22.4	14:61654276-62125414	NOTEST	0	0.0326049	inf	0	1	1
ENSG00000258990	ENSG00000258990	MPPE1P1	14:89576491-89577567	NOTEST	0	0	0	0	1	1
ENSG00000258991	ENSG00000258991	DUX4L19	Y:13488004-13489271	NOTEST	0	0	0	0	1	1
ENSG00000258992	ENSG00000258992	TSPY1	Y:9236029-9344176	NOTEST	0	0	0	0	1	1
ENSG00000258993	ENSG00000258993	RP11-368P15.2	14:53489772-53490315	NOTEST	0	0	0	0	1	1
ENSG00000258994	ENSG00000258994	RP11-26L16.1	14:86798719-86867629	NOTEST	0	0	0	0	1	1
ENSG00000258995	ENSG00000258995	RP11-1112J20.1	14:63589724-63594932	NOTEST	0	0	0	0	1	1
ENSG00000258996	ENSG00000258996	CTD-2315A10.1	14:59648310-59648658	NOTEST	0	0	0	0	1	1
ENSG00000258997	ENSG00000258997	NF1P2	15:22133180-22152165	NOTEST	0	0	0	0	1	1
ENSG00000258998	ENSG00000258998	RP11-398E10.1	14:45232359-45252032	NOTEST	0.348595	0.340928	-0.0320845	0	1	1
ENSG00000258999	ENSG00000258999	RP11-114N19.3	14:80943329-81636758	NOTEST	0.289996	0.338512	0.223176	0	1	1
ENSG00000259000	ENSG00000259000	CTD-2373J19.1	14:45329518-45335450	NOTEST	0	0	0	0	1	1
ENSG00000259002	ENSG00000259002	RP11-671J11.7	14:35011022-35011650	NOTEST	0	0	0	0	1	1
ENSG00000259003	ENSG00000259003	AE000662.92	14:23025204-23027939	NOTEST	0	0	0	0	1	1
ENSG00000259004	ENSG00000259004	RP11-8L8.2	14:101587192-101589879	NOTEST	0	0	0	0	1	1
ENSG00000259005	ENSG00000259005	RP3-449M8.6	14:74940709-74941567	NOTEST	0.101285	0.189417	0.903148	0	1	1
ENSG00000259007	ENSG00000259007	RP11-463J10.3	14:52292912-52446060	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000259009	ENSG00000259009	TPRX2P	19:48322702-48364769	NOTEST	0	0	0	0	1	1
ENSG00000259010	ENSG00000259010	RP11-973N13.2	14:65066960-65068362	NOTEST	0	0	0	0	1	1
ENSG00000259011	ENSG00000259011	RP11-2C7.1	15:26110441-26122358	NOTEST	0	0	0	0	1	1
ENSG00000259012	ENSG00000259012	CTD-2320B12.2	14:84642762-84643432	NOTEST	0	0	0	0	1	1
ENSG00000259013	ENSG00000259013	RP11-1017G21.3	14:102430864-102532565	NOTEST	0	0	0	0	1	1
ENSG00000259015	ENSG00000259015	RP11-109N23.6	14:73427302-73428701	NOTEST	0	0.26709	inf	0	1	1
ENSG00000259016	ENSG00000259016	CTD-2335L22.6	14:20376254-20376808	NOTEST	0	0	0	0	1	1
ENSG00000259017	ENSG00000259017	RP11-561B11.6	14:35916208-35916831	NOTEST	0	0.139527	inf	0	1	1
ENSG00000259018	ENSG00000259018	RP11-124D2.3	14:23825610-23834961	NOTEST	0	0	0	0	1	1
ENSG00000259019	ENSG00000259019	RP11-305B6.2	14:44464983-44853748	NOTEST	0	0	0	0	1	1
ENSG00000259020	ENSG00000259020	RP11-529H20.3	14:92432334-92507240	NOTEST	0	0.197219	inf	0	1	1
ENSG00000259021	ENSG00000259021	TPRX1P1	10:81259421-81259740	NOTEST	0	0	0	0	1	1
ENSG00000259022	ENSG00000259022	DNAJC8P1	14:35899465-35899837	NOTEST	0	0	0	0	1	1
ENSG00000259023	ENSG00000259023	LINC00524	14:101872323-101874259	NOTEST	0	0	0	0	1	1
ENSG00000259025	ENSG00000259025	RP11-810K23.6	15:21258332-21260031	NOTEST	0	0	0	0	1	1
ENSG00000259026	ENSG00000259026	RP11-907D1.1	14:97576752-97587838	NOTEST	0	0	0	0	1	1
ENSG00000259028	ENSG00000259028	RP11-325D8.1	14:87819413-88039366	NOTEST	0	0	0	0	1	1
ENSG00000259029	ENSG00000259029	DUX4L18	Y:13477232-13478499	NOTEST	0	0	0	0	1	1
ENSG00000259031	ENSG00000259031	CTD-2062F14.3	14:101003485-101053750	NOTEST	0.170299	0.504142	1.56576	0	1	1
ENSG00000259033	ENSG00000259033	RP11-718G2.5	14:70742012-70758576	NOTEST	0	0	0	0	1	1
ENSG00000259034	ENSG00000259034	DUX4L3	4:191008559-191010370	NOTEST	0	0	0	0	1	1
ENSG00000259035	ENSG00000259035	RP11-666E17.1	14:82194123-82496693	NOTEST	0	0	0	0	1	1
ENSG00000259036	ENSG00000259036	RP11-404P21.1	14:96671015-96735304	NOTEST	0	0	0	0	1	1
ENSG00000259037	ENSG00000259037	RP11-614O9.1	14:104941014-105071984	NOTEST	0	0	0	0	1	1
ENSG00000259038	ENSG00000259038	CTD-2325P2.4	14:68286495-69196935	NOTEST	0.531134	0.306479	-0.793286	0	1	1
ENSG00000259039	ENSG00000259039	RP11-409I10.2	14:58030639-58448912	NOTEST	0	0	0	0	1	1
ENSG00000259041	ENSG00000259041	RP11-167B3.1	15:98589895-98836406	NOTEST	0	0.0495308	inf	0	1	1
ENSG00000259042	ENSG00000259042	AE000661.50	14:22849082-22951948	NOTEST	0	0	0	0	1	1
ENSG00000259043	ENSG00000259043	BRD7P1	14:24218444-24220359	NOTEST	0	0	0	0	1	1
ENSG00000259044	ENSG00000259044	RP11-789A21.1	14:85669192-85705818	NOTEST	0	0	0	0	1	1
ENSG00000259045	ENSG00000259045	RP11-320M16.1	14:32798478-33300567	NOTEST	0	0	0	0	1	1
ENSG00000259046	ENSG00000259046	RP11-857B24.2	14:45346076-45366280	NOTEST	0	0	0	0	1	1
ENSG00000259047	ENSG00000259047	RP11-16O13.1	14:43458403-43458686	NOTEST	0	0	0	0	1	1
ENSG00000259048	ENSG00000259048	CTD-2058B24.2	14:38059188-38672128	NOTEST	0	0	0	0	1	1
ENSG00000259049	ENSG00000259049	RP11-589M4.1	14:53241911-53258386	NOTEST	0	0.136353	inf	0	1	1
ENSG00000259050	ENSG00000259050	CHORDC2P	14:89591214-90421121	NOTEST	0	0	0	0	1	1
ENSG00000259051	ENSG00000259051	HNRNPUP1	14:43769465-43769798	NOTEST	0	0.0654168	inf	0	1	1
ENSG00000259052	ENSG00000259052	AL157871.2	14:100673743-100772884	NOTEST	0.335753	0	#NAME?	0	1	1

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ENSG00000259054	ENSG00000259054	AE000662.93	14:23025204-23027939	NOTEST	0.130791	0	#NAME?	0	1	1
ENSG00000259055	ENSG00000259055	RP11-1140I5.1	14:51441979-51562779	NOTEST	0	0.0108943	inf	0	1	1
ENSG00000259056	ENSG00000259056	DUXAP1	2:84743578-85046713	NOTEST	0	0	0	0	1	1
ENSG00000259057	ENSG00000259057	CTD-2343P13.1	15:92286070-92287185	NOTEST	0	0	0	0	1	1
ENSG00000259058	ENSG00000259058	RP11-488C13.4	14:77388182-77390992	NOTEST	0	0	0	0	1	1
ENSG00000259059	ENSG00000259059	PEBP1P1	14:96858447-96955764	NOTEST	0	0	0	0	1	1
ENSG00000259060	ENSG00000259060	RNASE11	14:21051050-21078043	NOTEST	0	0	0	0	1	1
ENSG00000259061	ENSG00000259061	RP11-736P16.1	14:87402983-87455469	NOTEST	0	0	0	0	1	1
ENSG00000259062	ENSG00000259062	ACTN1-AS1	14:69446398-69454180	NOTEST	0	0	0	0	1	1
ENSG00000259063	ENSG00000259063	DUX4L5	4:190998672-191000532	NOTEST	0	0	0	0	1	1
ENSG00000259064	ENSG00000259064	RP11-386M24.5	15:93146139-93353114	NOTEST	0	0	0	0	1	1
ENSG00000259066	ENSG00000259066	RP11-371E8.4	14:93651295-93695561	NOTEST	0	0.0890838	inf	0	1	1
ENSG00000259067	ENSG00000259067	CTD-3051D23.3	14:105370678-105371541	NOTEST	0	0	0	0	1	1
ENSG00000259068	ENSG00000259068	TRAV37	14:22733631-22734147	NOTEST	0	0	0	0	1	1
ENSG00000259069	ENSG00000259069	RP11-597A11.6	14:20078032-20152898	NOTEST	0	0	0	0	1	1
ENSG00000259070	ENSG00000259070	LINC00639	14:39218544-39417477	NOTEST	0	0	0	0	1	1
ENSG00000259072	ENSG00000259072	RP11-96D24.1	14:38760156-38781134	NOTEST	0	0	0	0	1	1
ENSG00000259073	ENSG00000259073	FOXN3-AS2	14:89591214-90421121	NOTEST	0	0	0	0	1	1
ENSG00000259074	ENSG00000259074	PSMB7P1	14:20617390-20617904	NOTEST	0	0	0	0	1	1
ENSG00000259075	ENSG00000259075	POC1B-GALNT4	12:89813494-89934079	NOTEST	0.516135	0.31944	-0.692204	0	1	1
ENSG00000259076	ENSG00000259076	RP11-973N13.3	14:65016619-65063254	NOTEST	0	0	0	0	1	1
ENSG00000259077	ENSG00000259077	RP11-804L24.2	14:88176762-88460009	NOTEST	0	0	0	0	1	1
ENSG00000259078	ENSG00000259078	PTBP1P	14:65703197-65785508	NOTEST	0	0.00730247	inf	0	1	1
ENSG00000259079	ENSG00000259079	RP1-261D10.1	14:71759441-72207946	NOTEST	0	0	0	0	1	1
ENSG00000259080	ENSG00000259080	RP11-158I13.2	2:27805896-27917840	NOTEST	0.148346	0.305993	1.04453	0	1	1
ENSG00000259081	ENSG00000259081	RP11-488C13.6	14:77228531-77253067	NOTEST	0.0256987	0.149808	2.54335	0	1	1
ENSG00000259082	ENSG00000259082	RP11-168L7.3	14:101908412-101910652	NOTEST	0	0	0	0	1	1
ENSG00000259083	ENSG00000259083	RP11-407N17.4	14:39644088-39652422	NOTEST	0.124135	0.0293615	-2.07991	0	1	1
ENSG00000259084	ENSG00000259084	RP11-1070N10.6	14:96116834-96158980	NOTEST	0	0	0	0	1	1
ENSG00000259087	ENSG00000259087	RP11-356O9.2	14:38025362-38048330	NOTEST	0	0	0	0	1	1
ENSG00000259088	ENSG00000259088	CTD-2017C7.2	14:102228134-102394326	NOTEST	0	0	0	0	1	1
ENSG00000259089	ENSG00000259089	GRAMD4P5	15:21018627-21020287	NOTEST	0	0	0	0	1	1
ENSG00000259090	ENSG00000259090	RP11-173D9.5	14:35514112-35786699	NOTEST	0	0	0	0	1	1
ENSG00000259091	ENSG00000259091	LINC00517	14:38059188-38672128	NOTEST	0	0	0	0	1	1
ENSG00000259092	ENSG00000259092	TRAV30	14:22636324-22636884	NOTEST	0	0	0	0	1	1
ENSG00000259093	ENSG00000259093	RP11-1112J20.2	14:63589724-63594932	NOTEST	0	0.0557556	inf	0	1	1
ENSG00000259094	ENSG00000259094	RP11-77A13.1	2:119699741-119752236	NOTEST	0	0	0	0	1	1
ENSG00000259095	ENSG00000259095	RP11-98N22.6	14:20641790-20641972	NOTEST	0	0	0	0	1	1
ENSG00000259096	ENSG00000259096	FAM35CP	14:88176762-88460009	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000259097	ENSG00000259097	RP11-61O1.1	14:98534576-98671480	NOTEST	0	0	0	0	1	1
ENSG00000259098	ENSG00000259098	RP11-603B24.2	15:22546088-22546799	NOTEST	0.183671	0.312481	0.766649	0	1	1
ENSG00000259099	ENSG00000259099	RP11-348M3.2	12:56774144-56776495	NOTEST	0	0	0	0	1	1
ENSG00000259100	ENSG00000259100	RP11-1074O12.1	14:39699434-39856306	NOTEST	0.00971952	0	#NAME?	0	1	1
ENSG00000259101	ENSG00000259101	MEGT1	HSCHR6_MHC_DBB:31656814-31667868	NOTEST	0	0	0	0	1	1
ENSG00000259102	ENSG00000259102	CTD-2552B11.2	14:21630671-21631902	NOTEST	0	0	0	0	1	1
ENSG00000259103	ENSG00000259103	RP11-270M14.4	14:76041230-76550928	NOTEST	0	0	0	0	1	1
ENSG00000259104	ENSG00000259104	PTCSC3	14:36539632-36645674	NOTEST	0	0	0	0	1	1
ENSG00000259105	ENSG00000259105	RPS3AP4	14:35937477-35938536	NOTEST	0	0	0	0	1	1
ENSG00000259106	ENSG00000259106	RP11-242P2.2	14:78708733-80330762	NOTEST	0	0	0	0	1	1
ENSG00000259107	ENSG00000259107	LINC00911	14:85828800-85983278	NOTEST	0	0	0	0	1	1
ENSG00000259108	ENSG00000259108	CTD-3098H1.2	19:48366739-48368598	NOTEST	0	0	0	0	1	1
ENSG00000259109	ENSG00000259109	RP4-687K1.2	14:73603125-73690399	NOTEST	0	0	0	0	1	1
ENSG00000259110	ENSG00000259110	RP11-359N5.1	14:97621193-97625073	NOTEST	0	0	0	0	1	1
ENSG00000259111	ENSG00000259111	RP11-280K24.1	14:52217277-52230794	NOTEST	0	0	0	0	1	1
ENSG00000259112	ENSG00000259112	NDUFC2-KCTD14	11:77726760-77791265	NOTEST	0.135255	0	#NAME?	0	1	1
ENSG00000259113	ENSG00000259113	RP11-406H23.2	14:50885218-51135049	NOTEST	0	0.066861	inf	0	1	1
ENSG00000259114	ENSG00000259114	AC005484.5	14:74318546-74551196	NOTEST	0.0419191	0.00642913	-2.70491	0	1	1
ENSG00000259115	ENSG00000259115	CTD-2540L5.5	14:71047973-71108015	NOTEST	0	0	0	0	1	1
ENSG00000259116	ENSG00000259116	RP11-973N13.4	14:64854748-65009955	NOTEST	0.301478	0.0597903	-2.33407	0	1	1
ENSG00000259117	ENSG00000259117	RP11-476J6.1	14:48271128-48271404	NOTEST	0	0	0	0	1	1
ENSG00000259118	ENSG00000259118	RP11-840I19.3	14:65381078-65569413	NOTEST	0.0819132	0.134597	0.716477	0	1	1
ENSG00000259119	ENSG00000259119	RP11-1127D7.1	14:99391473-99394142	NOTEST	0	0	0	0	1	1
ENSG00000259120	ENSG00000259120	SMIM6	17:73584138-73704142	NOTEST	0.0345238	0.029945	-0.205276	0	1	1
ENSG00000259121	ENSG00000259121	RP11-545M17.2	14:39501122-39578850	NOTEST	0	0	0	0	1	1
ENSG00000259122	ENSG00000259122	TVP23BP1	15:27210063-27215532	NOTEST	0	0	0	0	1	1
ENSG00000259123	ENSG00000259123	RP11-76E17.2	15:94133095-94651167	NOTEST	0	0	0	0	1	1
ENSG00000259124	ENSG00000259124	RP11-187O7.3	14:76776956-77227731	NOTEST	0	0	0	0	1	1
ENSG00000259125	ENSG00000259125	RP11-545N8.3	12:57482676-57607134	NOTEST	0.0957553	0.0748191	-0.355945	0	1	1
ENSG00000259126	ENSG00000259126	RP11-99L13.2	14:44861733-44862919	NOTEST	0.543851	0.121451	-2.16284	0	1	1
ENSG00000259128	ENSG00000259128	DUX4L2	4:191011859-191013719	NOTEST	0	0	0	0	1	1
ENSG00000259129	ENSG00000259129	LINC00648	14:48234156-48264295	NOTEST	0.0164157	0.0966414	2.55756	0	1	1
ENSG00000259130	ENSG00000259130	RP11-219E7.3	14:21338436-21341751	NOTEST	0	0	0	0	1	1
ENSG00000259133	ENSG00000259133	RP11-1085N6.3	14:56955071-57197253	NOTEST	0	0	0	0	1	1
ENSG00000259134	ENSG00000259134	LINC00924	15:95976323-96051076	NOTEST	0	0	0	0	1	1
ENSG00000259135	ENSG00000259135	RP11-671J11.4	14:35025979-35099389	NOTEST	0	0	0	0	1	1
ENSG00000259136	ENSG00000259136	RP11-108M12.2	14:57279900-57618895	NOTEST	0	0	0	0	1	1
ENSG00000259137	ENSG00000259137	RP11-305B6.1	14:44464983-44853748	NOTEST	0	0	0	0	1	1

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ENSG00000259138	ENSG00000259138	RP11-950C14.7	14:75548821-75643334	NOTEST	0	0	0	0	1	1
ENSG00000259139	ENSG00000259139	DUX4L12	10:135483661-135488584	NOTEST	0	0	0	0	1	1
ENSG00000259140	ENSG00000259140	RP11-986E7.2	14:95141213-95142166	NOTEST	0	0	0	0	1	1
ENSG00000259142	ENSG00000259142	LINC00644	14:62600866-62606691	NOTEST	0	0	0	0	1	1
ENSG00000259143	ENSG00000259143	CTD-2240H23.2	14:95648276-95786243	NOTEST	0	0.0170286	inf	0	1	1
ENSG00000259144	ENSG00000259144	RANBP20P	14:21188900-21191286	NOTEST	0	0.0215914	inf	0	1	1
ENSG00000259145	ENSG00000259145	RP11-566K19.9	15:23572031-23579274	NOTEST	0	0	0	0	1	1
ENSG00000259146	ENSG00000259146	RP1-261D10.2	14:71759441-72207946	NOTEST	0	0	0	0	1	1
ENSG00000259148	ENSG00000259148	RP11-322L17.1	14:44464983-44853748	NOTEST	0	0	0	0	1	1
ENSG00000259149	ENSG00000259149	RP11-313C4.1	14:42728933-42737789	NOTEST	0	0	0	0	1	1
ENSG00000259150	ENSG00000259150	LINC00929	15:26360959-26378184	NOTEST	0	0	0	0	1	1
ENSG00000259151	ENSG00000259151	CAP2P1	14:89591214-90421121	NOTEST	0	0.0180439	inf	0	1	1
ENSG00000259152	ENSG00000259152	RP11-100M12.2	15:27216428-27787137	NOTEST	0	0	0	0	1	1
ENSG00000259154	ENSG00000259154	DUX4L17	Y:13470596-13471863	NOTEST	0	0	0	0	1	1
ENSG00000259155	ENSG00000259155	RP11-831F12.3	14:50110272-50155140	NOTEST	0.23405	0.0297785	-2.97447	0	1	1
ENSG00000259156	ENSG00000259156	CHEK2P2	15:20487996-20496839	NOTEST	0	0	0	0	1	1
ENSG00000259157	ENSG00000259157	RP11-280K24.6	14:52231993-52292140	NOTEST	0	0	0	0	1	1
ENSG00000259158	ENSG00000259158	ADAM20P1	14:70892528-71014181	NOTEST	0.0137761	0.0181731	0.399637	0	1	1
ENSG00000259159	ENSG00000259159	MFRP	11:119209651-119217383	NOTEST	0.00344418	0.0174157	2.33815	0	1	1
ENSG00000259160	ENSG00000259160	RP11-973N13.5	14:64854748-65009955	NOTEST	0	0	0	0	1	1
ENSG00000259161	ENSG00000259161	CTD-2017C7.3	14:102228134-102394326	NOTEST	0	0	0	0	1	1
ENSG00000259162	ENSG00000259162	RP11-203M5.6	14:20906140-20909427	NOTEST	0	0	0	0	1	1
ENSG00000259163	ENSG00000259163	RP11-1078H9.5	14:91006931-91282823	NOTEST	0.0883201	0.0336028	-1.39416	0	1	1
ENSG00000259164	ENSG00000259164	RP11-463C8.4	14:77564439-77725838	NOTEST	0	0.0259401	inf	0	1	1
ENSG00000259165	ENSG00000259165	DDX18P1	14:69517597-69619867	NOTEST	0.0310978	0.0299779	-0.0529138	0	1	1
ENSG00000259166	ENSG00000259166	RP11-1029J19.2	14:101913978-101923454	NOTEST	0	0	0	0	1	1
ENSG00000259167	ENSG00000259167	NMNAT1P1	14:80943329-81636758	NOTEST	0	0	0	0	1	1
ENSG00000259168	ENSG00000259168	RP11-100M12.3	15:27216428-27787137	NOTEST	0	0.0351979	inf	0	1	1
ENSG00000259169	ENSG00000259169	GNRHR2P1	14:60863186-61021634	NOTEST	0	0	0	0	1	1
ENSG00000259170	ENSG00000259170	RP11-763K15.1	15:93013462-93014776	NOTEST	0	0	0	0	1	1
ENSG00000259173	ENSG00000259173	RP11-30K9.7	15:59047823-59048446	NOTEST	0	0	0	0	1	1
ENSG00000259174	ENSG00000259174	RP11-1180F24.1	15:23181937-23182642	NOTEST	0	0.0216459	inf	0	1	1
ENSG00000259175	ENSG00000259175	RP11-379K22.2	15:80696691-80890278	NOTEST	0.0126444	0	#NAME?	0	1	1
ENSG00000259176	ENSG00000259176	RP11-69H14.6	15:22278009-22413497	NOTEST	0	0	0	0	1	1
ENSG00000259177	ENSG00000259177	RP11-154B12.3	15:90931449-91045475	NOTEST	0	0	0	0	1	1
ENSG00000259178	ENSG00000259178	CTD-2184D3.3	15:52121824-52392720	NOTEST	0	0	0	0	1	1
ENSG00000259179	ENSG00000259179	UBE2CP4	15:31619057-31727868	NOTEST	0	0	0	0	1	1
ENSG00000259180	ENSG00000259180	RP11-420M1.2	15:55903743-56035288	NOTEST	0	0	0	0	1	1

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ENSG00000259182	ENSG00000259182	RP11-424I19.2	15:101708734-101711026	NOTEST	0.031339	0.196853	2.65109	0	1	1
ENSG00000259183	ENSG00000259183	MED28P6	15:88418229-88814297	NOTEST	0	0	0	0	1	1
ENSG00000259184	ENSG00000259184	RP11-566K19.4	15:22747312-22789974	NOTEST	0	0	0	0	1	1
ENSG00000259185	ENSG00000259185	RP11-56B16.4	15:52121824-52392720	NOTEST	0	0	0	0	1	1
ENSG00000259186	ENSG00000259186	MRPS15P1	15:73735498-73926475	NOTEST	0.0472725	0	#NAME?	0	1	1
ENSG00000259187	ENSG00000259187	CTD-2008A1.1	15:45118568-45176978	NOTEST	0	0	0	0	1	1
ENSG00000259188	ENSG00000259188	CTD-2647E9.3	15:50150434-50528592	NOTEST	0	0	0	0	1	1
ENSG00000259191	ENSG00000259191	RP11-253M7.3	15:69591285-69740764	NOTEST	0.1697	0.0980135	-0.791933	0	1	1
ENSG00000259192	ENSG00000259192	AC109631.1	15:38746327-38779911	NOTEST	0	0	0	0	1	1
ENSG00000259194	ENSG00000259194	RP11-108K3.4	15:51633825-51700210	NOTEST	0	0	0	0	1	1
ENSG00000259195	ENSG00000259195	RP11-158M2.6	15:86302553-86338261	NOTEST	0	0	0	0	1	1
ENSG00000259196	ENSG00000259196	HMBOX1-IT1	8:28747910-28922281	NOTEST	0	0	0	0	1	1
ENSG00000259198	ENSG00000259198	RP11-133K1.6	15:40604552-40608835	NOTEST	0	0	0	0	1	1
ENSG00000259199	ENSG00000259199	CTD-2544M6.1	15:98589895-98836406	NOTEST	0	0	0	0	1	1
ENSG00000259200	ENSG00000259200	RP11-718O11.1	15:45997275-46223267	NOTEST	0	0	0	0	1	1
ENSG00000259201	ENSG00000259201	RP11-56B16.5	15:52121824-52392720	NOTEST	0	0	0	0	1	1
ENSG00000259202	ENSG00000259202	RP11-342M21.2	15:67356100-67487533	NOTEST	0	0	0	0	1	1
ENSG00000259203	ENSG00000259203	RP11-209K10.2	15:53093810-53097139	NOTEST	0	0	0	0	1	1
ENSG00000259204	ENSG00000259204	RP11-394B5.2	15:51329684-51630807	NOTEST	0	0	0	0	1	1
ENSG00000259205	ENSG00000259205	PRKXP1	15:101093733-101191910	NOTEST	0.494209	0.540748	0.129835	0	1	1
ENSG00000259206	ENSG00000259206	RP13-608F4.8	15:82647359-82748784	NOTEST	0	0.00987633	inf	0	1	1
ENSG00000259208	ENSG00000259208	RP11-621H8.1	15:79960683-79961158	NOTEST	0	0	0	0	1	1
ENSG00000259209	ENSG00000259209	RP5-991G20.2	16:72699068-73093597	NOTEST	0	0.0322677	inf	0	1	1
ENSG00000259211	ENSG00000259211	RP11-64K12.8	15:40731919-40760441	NOTEST	0	0.0222063	inf	0	1	1
ENSG00000259213	ENSG00000259213	CTD-2071N1.1	15:77905368-78113242	NOTEST	0	0	0	0	1	1
ENSG00000259214	ENSG00000259214	RP11-810K23.7	15:21031782-21031969	NOTEST	0	0	0	0	1	1
ENSG00000259215	ENSG00000259215	RP11-253M7.4	15:69750860-69754145	NOTEST	0	0.105236	inf	0	1	1
ENSG00000259216	ENSG00000259216	RP11-227D13.2	15:49005124-49103785	NOTEST	0.0465602	0.103531	1.15289	0	1	1
ENSG00000259217	ENSG00000259217	RP11-702M1.2	15:35838395-36151202	NOTEST	0	0	0	0	1	1
ENSG00000259218	ENSG00000259218	LINC00928	15:90048507-90198682	NOTEST	0	0	0	0	1	1
ENSG00000259219	ENSG00000259219	CTD-3076O17.2	15:100510419-100882210	NOTEST	0.140668	0.0959187	-0.552411	0	1	1
ENSG00000259221	ENSG00000259221	CTD-2050N2.1	15:47476297-48066420	NOTEST	0.014749	0.0257552	0.80424	0	1	1
ENSG00000259222	ENSG00000259222	RP11-809H16.5	15:69365265-69392275	NOTEST	0.19981	0.0151189	-3.72421	0	1	1
ENSG00000259223	ENSG00000259223	RP11-82L7.4	15:60365866-60410519	NOTEST	0	0.0244968	inf	0	1	1
ENSG00000259224	ENSG00000259224	SLC35G6	17:7362684-7387582	NOTEST	0.0580162	0.0102104	-2.50641	0	1	1
ENSG00000259225	ENSG00000259225	RP11-1008C21.1	15:38276966-38354541	NOTEST	0	0	0	0	1	1
ENSG00000259227	ENSG00000259227	RP11-64K10.1	15:70894462-70894855	NOTEST	0	0	0	0	1	1

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ENSG00000259229	ENSG00000259229	RP11-38G5.3	15:80050890-80051104	NOTEST	0	0	0	0	1	1
ENSG00000259230	ENSG00000259230	CTD-2555C10.3	14:103011590-103022163	NOTEST	0	0	0	0	1	1
ENSG00000259231	ENSG00000259231	CTD-2014N11.2	15:45206999-45222820	NOTEST	0	0	0	0	1	1
ENSG00000259232	ENSG00000259232	RP11-349G13.1	15:65734800-65810042	NOTEST	0.226291	0.181542	-0.317878	0	1	1
ENSG00000259233	ENSG00000259233	RP11-467N20.6	15:23417957-23421818	NOTEST	0	0	0	0	1	1
ENSG00000259234	ENSG00000259234	RP11-17L5.4	15:79484048-79590580	NOTEST	0	0	0	0	1	1
ENSG00000259235	ENSG00000259235	RP11-605F22.2	15:48481233-48596275	NOTEST	0.0370448	0	#NAME?	0	1	1
ENSG00000259236	ENSG00000259236	CTD-2611K5.5	15:102291234-102334505	NOTEST	0	0.0220145	inf	0	1	1
ENSG00000259237	ENSG00000259237	RP11-209E8.1	15:53408561-53421895	NOTEST	0	0	0	0	1	1
ENSG00000259238	ENSG00000259238	RP11-361D15.2	15:59887073-59981733	NOTEST	0	0	0	0	1	1
ENSG00000259239	ENSG00000259239	RP11-521C20.1	15:40425968-40427415	NOTEST	0	0	0	0	1	1
ENSG00000259240	ENSG00000259240	RP11-108K3.1	15:51329684-51630807	NOTEST	0	0	0	0	1	1
ENSG00000259241	ENSG00000259241	RP11-313P18.2	15:51973549-52013223	NOTEST	0	0	0	0	1	1
ENSG00000259242	ENSG00000259242	AC002306.1	19:19672521-19729725	NOTEST	0	0.0136696	inf	0	1	1
ENSG00000259243	ENSG00000259243	GOLGA6L19	15:83011378-83018198	NOTEST	0.0258181	0.0207172	-0.317551	0	1	1
ENSG00000259245	ENSG00000259245	RP11-684B21.1	15:36231367-36544458	NOTEST	0.032223	0	#NAME?	0	1	1
ENSG00000259246	ENSG00000259246	HMGN2P47	15:67278698-67351591	NOTEST	0	0	0	0	1	1
ENSG00000259247	ENSG00000259247	TTTY25P	Y:24454969-24564028	NOTEST	0	0	0	0	1	1
ENSG00000259251	ENSG00000259251	RP11-643M14.1	15:62352701-62354633	NOTEST	0.0621577	0.171902	1.46758	0	1	1
ENSG00000259252	ENSG00000259252	AC011648.1	15:70487976-70490848	NOTEST	0	0	0	0	1	1
ENSG00000259254	ENSG00000259254	CTD-2339L15.3	15:40886217-40956540	NOTEST	0.1232	0.0335445	-1.87685	0	1	1
ENSG00000259255	ENSG00000259255	RP11-627D16.1	15:46985485-47097042	NOTEST	0	0	0	0	1	1
ENSG00000259256	ENSG00000259256	RP11-838N2.3	18:3347773-3350557	NOTEST	0	0	0	0	1	1
ENSG00000259257	ENSG00000259257	RP11-616M17.1	15:99791566-99930934	NOTEST	0.0327231	0	#NAME?	0	1	1
ENSG00000259258	ENSG00000259258	RP11-325L12.3	15:65385337-65407535	NOTEST	0	0	0	0	1	1
ENSG00000259259	ENSG00000259259	NPM1P42	15:73191739-73192601	NOTEST	0	0	0	0	1	1
ENSG00000259261	ENSG00000259261	IGHV4OR15-8	15:22472917-22473353	NOTEST	0	0	0	0	1	1
ENSG00000259262	ENSG00000259262	NDUFA3P4	15:90929045-90929295	NOTEST	0	0.820206	inf	0	1	1
ENSG00000259264	ENSG00000259264	RP11-60L3.1	15:74471806-74628813	NOTEST	0	0	0	0	1	1
ENSG00000259265	ENSG00000259265	RP11-809H16.4	15:69070873-69355083	NOTEST	0	0	0	0	1	1
ENSG00000259266	ENSG00000259266	RP11-183E24.1	15:98589895-98836406	NOTEST	0	0	0	0	1	1
ENSG00000259267	ENSG00000259267	RP11-432J9.6	10:72698809-72715398	NOTEST	0	0	0	0	1	1
ENSG00000259268	ENSG00000259268	AC007950.1	15:63748492-63761550	NOTEST	0	0	0	0	1	1
ENSG00000259269	ENSG00000259269	RP11-624L4.2	15:39764903-39773407	NOTEST	0	0	0	0	1	1
ENSG00000259270	ENSG00000259270	RP11-561C5.1	15:85721858-85722037	NOTEST	0	0	0	0	1	1
ENSG00000259271	ENSG00000259271	ANKRD62P1	22:17082776-17185367	NOTEST	5.17E-05	1.24E-05	-2.06443	0	1	1
ENSG00000259273	ENSG00000259273	RP11-493E3.2	15:90479723-90480237	NOTEST	0	0	0	0	1	1
ENSG00000259274	ENSG00000259274	CTD-2501E16.2	15:60771376-61521518	NOTEST	0	0	0	0	1	1
ENSG00000259275	ENSG00000259275	RP11-522B15.3	15:96897465-96948419	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000259277	ENSG00000259277	RP13-126C7.1	15:29129628-29410518	NOTEST	0.0256102	0.0542618	1.08322	0	1	1
ENSG00000259278	ENSG00000259278	RP11-62C7.2	15:39157522-39719396	NOTEST	0	0	0	0	1	1
ENSG00000259279	ENSG00000259279	CTD-2033D15.1	15:39873279-39891667	NOTEST	0	0	0	0	1	1
ENSG00000259280	ENSG00000259280	RP11-122D10.1	15:37168579-37179236	NOTEST	0	0	0	0	1	1
ENSG00000259281	ENSG00000259281	CTD-2632K10.1	15:77905368-78113242	NOTEST	0	0	0	0	1	1
ENSG00000259282	ENSG00000259282	SPATA8-AS1	15:97315234-97326542	NOTEST	0	0	0	0	1	1
ENSG00000259283	ENSG00000259283	RP11-26L20.3	16:55293880-55367500	NOTEST	0	0	0	0	1	1
ENSG00000259284	ENSG00000259284	RP11-162I7.1	15:62022048-62023588	NOTEST	0	0	0	0	1	1
ENSG00000259285	ENSG00000259285	CTD-2330J20.2	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000259286	ENSG00000259286	RP11-696L21.2	15:69070873-69355083	NOTEST	0	0	0	0	1	1
ENSG00000259287	ENSG00000259287	RP11-3D4.2	15:33603162-34158303	NOTEST	0.161385	0.160519	-0.00776134	0	1	1
ENSG00000259288	ENSG00000259288	RP11-133K1.2	15:40453223-40569688	NOTEST	0	0	0	0	1	1
ENSG00000259289	ENSG00000259289	RP11-798K3.3	15:67212148-67248856	NOTEST	0	0	0	0	1	1
ENSG00000259290	ENSG00000259290	RP11-687M24.7	11:125034582-125303285	NOTEST	0	0	0	0	1	1
ENSG00000259291	ENSG00000259291	RP11-617F23.1	15:90544623-90625439	NOTEST	0.444828	0.30109	-0.563052	0	1	1
ENSG00000259293	ENSG00000259293	RP11-355N15.1	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000259294	ENSG00000259294	CTA-339C12.1	7:101458958-101927249	NOTEST	0.0608124	0	#NAME?	0	1	1
ENSG00000259295	ENSG00000259295	CSPG4P12	15:85734668-85778026	NOTEST	0.030413	0.209254	2.78249	0	1	1
ENSG00000259296	ENSG00000259296	RP11-313P18.1	15:51973549-52013223	NOTEST	0	0	0	0	1	1
ENSG00000259298	ENSG00000259298	RP11-562A8.4	15:50716576-50838905	NOTEST	0.0776859	0.110939	0.514036	0	1	1
ENSG00000259299	ENSG00000259299	RP11-37J13.1	15:29412456-29862927	NOTEST	0	0.0252319	inf	0	1	1
ENSG00000259300	ENSG00000259300	TUBBP8	15:29904773-29906478	NOTEST	0	0	0	0	1	1
ENSG00000259301	ENSG00000259301	RP11-643A5.1	15:54129467-54129757	NOTEST	0	0	0	0	1	1
ENSG00000259302	ENSG00000259302	RP11-182J1.11	15:85048693-85048726	NOTEST	0	0	0	0	1	1
ENSG00000259303	ENSG00000259303	IGHV2OR16-5	16:32859033-32859477	NOTEST	0.230246	0	#NAME?	0	1	1
ENSG00000259304	ENSG00000259304	CTD-2014N11.3	15:45248899-45271427	NOTEST	0	0	0	0	1	1
ENSG00000259306	ENSG00000259306	RP11-108K3.2	15:51329684-51630807	NOTEST	0	0	0	0	1	1
ENSG00000259307	ENSG00000259307	PLCB2-AS1	15:40570376-40600136	NOTEST	0	0	0	0	1	1
ENSG00000259308	ENSG00000259308	RP11-382A20.1	15:83509837-83772195	NOTEST	0	0	0	0	1	1
ENSG00000259309	ENSG00000259309	RP11-19J5.2	15:70113094-70115195	NOTEST	0	0	0	0	1	1
ENSG00000259310	ENSG00000259310	RP11-152F13.8	15:83023846-83125316	NOTEST	0	0.0188206	inf	0	1	1
ENSG00000259312	ENSG00000259312	RP11-522B15.5	15:96981799-96987496	NOTEST	0	0	0	0	1	1
ENSG00000259314	ENSG00000259314	CTD-3065B20.3	15:91073156-91260372	NOTEST	0.08951	0.0697077	-0.360731	0	1	1
ENSG00000259315	ENSG00000259315	RP11-752G15.9	15:83394624-83407656	NOTEST	0.115966	0.105199	-0.14058	0	1	1
ENSG00000259317	ENSG00000259317	RP11-561C5.7	15:85798599-85873565	NOTEST	0	0	0	0	1	1
ENSG00000259319	ENSG00000259319	RP11-293M10.6	14:75890385-75940814	NOTEST	0.0431733	0.0957262	1.14878	0	1	1
ENSG00000259320	ENSG00000259320	RP11-183E24.2	15:98589895-98836406	NOTEST	0	0	0	0	1	1
ENSG00000259321	ENSG00000259321	RP11-468E2.5	14:24605366-24610797	NOTEST	0.454082	0.194557	-1.22276	0	1	1
ENSG00000259322	ENSG00000259322	RP11-762H8.1	15:78542843-78592136	NOTEST	0.423303	0.528971	0.321498	0	1	1

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ENSG00000259324	ENSG00000259324	OR11K1P	15:22278009-22413497	NOTEST	0	0	0	0	1	1
ENSG00000259325	ENSG00000259325	SPATA31E3P	15:23466151-23471888	NOTEST	0	0	0	0	1	1
ENSG00000259326	ENSG00000259326	RP11-102L12.2	15:38780303-38857776	NOTEST	0.0364875	0	#NAME?	0	1	1
ENSG00000259327	ENSG00000259327	CTD-2184D3.6	15:52408770-52587995	NOTEST	0	0.116636	inf	0	1	1
ENSG00000259331	ENSG00000259331	RP11-57P19.1	15:95143242-95144050	NOTEST	0	0	0	0	1	1
ENSG00000259333	ENSG00000259333	RP11-630H24.4	17:61978002-61978239	NOTEST	0	0	0	0	1	1
ENSG00000259334	ENSG00000259334	LINC00596	14:24391455-24403777	NOTEST	0	0	0	0	1	1
ENSG00000259335	ENSG00000259335	HNRNPMP1	15:44719431-44829121	NOTEST	0	0	0	0	1	1
ENSG00000259336	ENSG00000259336	RP11-323I15.5	15:35391222-35461899	NOTEST	0.0126831	0	#NAME?	0	1	1
ENSG00000259337	ENSG00000259337	IGHV1OR15-2	15:20178034-20178471	NOTEST	0	0	0	0	1	1
ENSG00000259338	ENSG00000259338	CTD-2651B20.2	15:45507744-45508141	NOTEST	0	0	0	0	1	1
ENSG00000259339	ENSG00000259339	TGIF1P1	19:46604379-46706340	NOTEST	0	0	0	0	1	1
ENSG00000259340	ENSG00000259340	CTD-2027G2.1	15:97094610-97094747	NOTEST	0	0	0	0	1	1
ENSG00000259341	ENSG00000259341	RP11-20G13.1	15:99967213-99971233	NOTEST	0	0.0516819	inf	0	1	1
ENSG00000259342	ENSG00000259342	RP11-519G16.5	15:45722726-45878488	NOTEST	0	0	0	0	1	1
ENSG00000259344	ENSG00000259344	RP11-566K19.6	15:23043276-23115256	NOTEST	0.0679892	0	#NAME?	0	1	1
ENSG00000259345	ENSG00000259345	RP11-624L4.1	15:39157522-39719396	NOTEST	0.111893	0.00956411	-3.54834	0	1	1
ENSG00000259346	ENSG00000259346	RP11-349G13.2	15:65594259-65594649	NOTEST	0	0.0528573	inf	0	1	1
ENSG00000259347	ENSG00000259347	RP11-798K3.2	15:67278698-67351591	NOTEST	0	0	0	0	1	1
ENSG00000259348	ENSG00000259348	RP11-4G2.1	15:96571317-96590159	NOTEST	0	0	0	0	1	1
ENSG00000259349	ENSG00000259349	RP11-15E18.1	17:58603653-58628159	NOTEST	0.110696	0.0302259	-1.87274	0	1	1
ENSG00000259350	ENSG00000259350	RP11-63A23.2	15:89495913-89496691	NOTEST	0	0	0	0	1	1
ENSG00000259351	ENSG00000259351	RP11-111E14.1	15:64199234-64364232	NOTEST	0	0	0	0	1	1
ENSG00000259352	ENSG00000259352	RP11-109D20.2	15:45315301-45369383	NOTEST	0	0.123395	inf	0	1	1
ENSG00000259353	ENSG00000259353	RP11-30K9.5	15:59063390-59389618	NOTEST	0	0	0	0	1	1
ENSG00000259354	ENSG00000259354	RP11-519G16.3	15:45722726-45878488	NOTEST	0.0279749	0.00517887	-2.43342	0	1	1
ENSG00000259356	ENSG00000259356	RP11-90E5.1	15:100510419-100882210	NOTEST	0	0	0	0	1	1
ENSG00000259358	ENSG00000259358	RP11-456J20.1	15:31775328-32162992	NOTEST	0.032454	0.0608888	0.907783	0	1	1
ENSG00000259359	ENSG00000259359	RP11-327J17.2	15:96670597-96883492	NOTEST	0	0	0	0	1	1
ENSG00000259360	ENSG00000259360	RP11-142J21.1	15:47476297-48066420	NOTEST	0.103297	0.0256713	-2.00858	0	1	1
ENSG00000259361	ENSG00000259361	LINC00927	15:80555409-80634147	NOTEST	0	0	0	0	1	1
ENSG00000259362	ENSG00000259362	RP11-307C19.1	15:77817881-77826452	NOTEST	0.0195904	0.00633319	-1.62915	0	1	1
ENSG00000259364	ENSG00000259364	RP11-64K12.9	15:40731919-40760441	NOTEST	0	0	0	0	1	1
ENSG00000259365	ENSG00000259365	RP11-424I19.1	15:101656807-101657751	NOTEST	0	0	0	0	1	1
ENSG00000259367	ENSG00000259367	RP11-815J21.4	15:85923801-86293512	NOTEST	0	0.073364	inf	0	1	1
ENSG00000259368	ENSG00000259368	RP11-64K12.4	15:40650435-40663257	NOTEST	0.00224691	0	#NAME?	0	1	1
ENSG00000259369	ENSG00000259369	RP11-291H24.1	15:56038836-56038965	NOTEST	0	0	0	0	1	1
ENSG00000259370	ENSG00000259370	RP11-1069G10.1	15:62682724-63176233	NOTEST	0.0254342	0.0235427	-0.111488	0	1	1
ENSG00000259371	ENSG00000259371	RP11-468E2.6	14:24549315-24602058	NOTEST	0.0475221	0	#NAME?	0	1	1
ENSG00000259374	ENSG00000259374	RP11-736N17.4	14:103606011-103608296	NOTEST	0	0	0	0	1	1

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ENSG00000259376	ENSG00000259376	RP11-505E24.3	15:101389765-101626271	NOTEST	0	0.0723923	inf	0	1	1
ENSG00000259377	ENSG00000259377	CTD-2308G16.1	15:52015207-52108565	NOTEST	0	0	0	0	1	1
ENSG00000259378	ENSG00000259378	DCAF13P3	15:51200868-51298097	NOTEST	0.0127703	0.028086	1.13705	0	1	1
ENSG00000259379	ENSG00000259379	RP11-925D8.5	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000259380	ENSG00000259380	RP11-346D14.1	15:38431795-38519088	NOTEST	0.0452158	0.0175858	-1.36242	0	1	1
ENSG00000259381	ENSG00000259381	RP11-192M23.1	15:101093733-101191910	NOTEST	0.161944	0.340124	1.07056	0	1	1
ENSG00000259383	ENSG00000259383	RP11-403B2.6	15:20964639-20980200	NOTEST	0	0	0	0	1	1
ENSG00000259384	ENSG00000259384	GH1	17:61986956-61996198	NOTEST	0	0	0	0	1	1
ENSG00000259385	ENSG00000259385	RP11-605F22.1	15:48481233-48596275	NOTEST	0	0.0119115	inf	0	1	1
ENSG00000259387	ENSG00000259387	ADAMTS7P2	15:82888223-82924290	NOTEST	0	0	0	0	1	1
ENSG00000259388	ENSG00000259388	CTD-2647E9.1	15:50086442-50088294	NOTEST	0	0.0318245	inf	0	1	1
ENSG00000259389	ENSG00000259389	H3F3AP1	15:40226346-40327797	NOTEST	0	0	0	0	1	1
ENSG00000259390	ENSG00000259390	RP11-27M9.1	15:39804606-39812055	NOTEST	0	0	0	0	1	1
ENSG00000259393	ENSG00000259393	RP11-313H3.1	15:59063390-59389618	NOTEST	0	0	0	0	1	1
ENSG00000259394	ENSG00000259394	RP11-244F12.1	15:63245371-63246323	NOTEST	0	0	0	0	1	1
ENSG00000259395	ENSG00000259395	RP11-475A13.2	15:36633939-36636367	NOTEST	0	0	0	0	1	1
ENSG00000259396	ENSG00000259396	RP11-16O9.2	15:41624891-41673248	NOTEST	0.0910083	0	#NAME?	0	1	1
ENSG00000259397	ENSG00000259397	RP11-323I15.2	15:35384681-35385413	NOTEST	0.0265253	0	#NAME?	0	1	1
ENSG00000259398	ENSG00000259398	RP11-430B1.1	15:52121824-52392720	NOTEST	0	0.0505112	inf	0	1	1
ENSG00000259400	ENSG00000259400	ELMO2P1	15:22747312-22789974	NOTEST	0	0	0	0	1	1
ENSG00000259401	ENSG00000259401	RP11-566K19.8	15:23499525-23501360	NOTEST	0.0429513	0.109247	1.34682	0	1	1
ENSG00000259402	ENSG00000259402	RP11-30K9.4	15:59063390-59389618	NOTEST	0	0	0	0	1	1
ENSG00000259403	ENSG00000259403	RP11-315L6.1	15:97815406-97975324	NOTEST	0	0	0	0	1	1
ENSG00000259404	ENSG00000259404	EFTUD1P1	15:84748919-84795356	NOTEST	0	0.422423	inf	0	1	1
ENSG00000259405	ENSG00000259405	ISCA1P4	15:41240933-41241067	NOTEST	0	0	0	0	1	1
ENSG00000259407	ENSG00000259407	RP11-158M2.3	15:85923801-86293512	NOTEST	0.0433261	0.040719	-0.0895328	0	1	1
ENSG00000259408	ENSG00000259408	RP11-3D4.3	15:33603162-34158303	NOTEST	0.114059	0.124835	0.130243	0	1	1
ENSG00000259409	ENSG00000259409	RP11-521C20.3	15:40380090-40401093	NOTEST	0	0	0	0	1	1
ENSG00000259410	ENSG00000259410	RP11-34F13.3	15:68112041-68166204	NOTEST	0	0	0	0	1	1
ENSG00000259411	ENSG00000259411	HNRNPA1P45	15:35473999-35838394	NOTEST	0.0163757	0	#NAME?	0	1	1
ENSG00000259413	ENSG00000259413	RP11-5O23.1	15:78674914-78675497	NOTEST	0	0	0	0	1	1
ENSG00000259414	ENSG00000259414	HERC2P7	15:23388288-23392657	NOTEST	0.107056	0.0586423	-0.868353	0	1	1
ENSG00000259415	ENSG00000259415	RP11-7M10.2	15:85291865-85349659	NOTEST	0	0	0	0	1	1
ENSG00000259416	ENSG00000259416	RP11-158M2.5	15:86298171-86299468	NOTEST	0.0397459	0.095791	1.26908	0	1	1
ENSG00000259418	ENSG00000259418	RP11-109D20.1	15:45315301-45369383	NOTEST	0	0	0	0	1	1
ENSG00000259419	ENSG00000259419	HNRNPCP3	15:79484048-79590580	NOTEST	0	0	0	0	1	1
ENSG00000259420	ENSG00000259420	RP11-307C19.2	15:77861311-77901023	NOTEST	0	0	0	0	1	1
ENSG00000259421	ENSG00000259421	CTA-150C2.20	22:39436608-39483748	NOTEST	0	0	0	0	1	1

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ENSG00000259423	ENSG00000259423	RP11-265N7.2	15:39157522-39719396	NOTEST	0	0	0	0	1	1
ENSG00000259424	ENSG00000259424	RP11-35O15.1	15:99190179-99190600	NOTEST	0	0.0650194	inf	0	1	1
ENSG00000259425	ENSG00000259425	RP11-566K19.5	15:23043276-23115256	NOTEST	0	0	0	0	1	1
ENSG00000259427	ENSG00000259427	DPPA5P2	15:45722726-45878488	NOTEST	0	0	0	0	1	1
ENSG00000259428	ENSG00000259428	HMGB3P26	14:103830575-103831157	NOTEST	0	0	0	0	1	1
ENSG00000259429	ENSG00000259429	UBE2Q2P3	15:83023846-83125316	NOTEST	0	0	0	0	1	1
ENSG00000259430	ENSG00000259430	RP11-168G16.2	15:100913143-101085200	NOTEST	0	0	0	0	1	1
ENSG00000259432	ENSG00000259432	RP11-37C7.2	15:39892231-40213093	NOTEST	0	0	0	0	1	1
ENSG00000259433	ENSG00000259433	CTD-2651B20.4	15:45622406-45624832	NOTEST	0	0	0	0	1	1
ENSG00000259434	ENSG00000259434	RP11-720L8.1	15:37657227-37783304	NOTEST	0	0	0	0	1	1
ENSG00000259435	ENSG00000259435	OR4N3P	15:22413568-22414386	NOTEST	0	0	0	0	1	1
ENSG00000259436	ENSG00000259436	CTC-378H22.2	19:42590262-42700737	NOTEST	0	0.00646864	inf	0	1	1
ENSG00000259437	ENSG00000259437	RP11-798K3.4	15:67212148-67248856	NOTEST	0	0	0	0	1	1
ENSG00000259438	ENSG00000259438	CTD-2650P22.1	15:52121824-52392720	NOTEST	0	0	0	0	1	1
ENSG00000259439	ENSG00000259439	RP11-89K21.1	2:45147331-45166338	NOTEST	0	0.0279415	inf	0	1	1
ENSG00000259440	ENSG00000259440	NPM1P43	15:73344050-73597547	NOTEST	0	0	0	0	1	1
ENSG00000259441	ENSG00000259441	MRPL15P1	15:90295526-90296724	NOTEST	0	0	0	0	1	1
ENSG00000259442	ENSG00000259442	RP11-752G15.8	15:83412974-83419041	NOTEST	0.045566	0.0364738	-0.321097	0	1	1
ENSG00000259443	ENSG00000259443	RP11-403B2.5	15:20964639-20980200	NOTEST	0	0.0115854	inf	0	1	1
ENSG00000259444	ENSG00000259444	RP11-736N17.8	14:103561059-103565222	NOTEST	0	0	0	0	1	1
ENSG00000259445	ENSG00000259445	RP11-276M12.1	15:82245643-82288007	NOTEST	0	0	0	0	1	1
ENSG00000259446	ENSG00000259446	RP11-489D6.2	15:33595857-33602860	NOTEST	0	0	0	0	1	1
ENSG00000259447	ENSG00000259447	RP11-462P6.1	15:39157522-39719396	NOTEST	0	0	0	0	1	1
ENSG00000259448	ENSG00000259448	RP11-16E12.1	15:31508222-31523041	NOTEST	0	0.00816762	inf	0	1	1
ENSG00000259449	ENSG00000259449	NIFKP8	15:85724440-85725314	NOTEST	0	0	0	0	1	1
ENSG00000259450	ENSG00000259450	RP11-265N7.1	15:39157522-39719396	NOTEST	0.0150301	0	#NAME?	0	1	1
ENSG00000259452	ENSG00000259452	RP11-138H8.4	15:71083351-71083825	NOTEST	0	0	0	0	1	1
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ENSG00000259454	ENSG00000259454	WBP1LP5	15:102427556-102427970	NOTEST	0	0	0	0	1	1
ENSG00000259455	ENSG00000259455	RP11-467N20.5	15:23405068-23414193	NOTEST	0	0	0	0	1	1
ENSG00000259457	ENSG00000259457	RP11-279F6.2	15:69755364-69863775	NOTEST	0	0	0	0	1	1
ENSG00000259458	ENSG00000259458	RP11-625H11.1	15:62682724-63176233	NOTEST	0	0	0	0	1	1
ENSG00000259459	ENSG00000259459	RP11-321G12.1	15:63682334-63729347	NOTEST	0	0	0	0	1	1
ENSG00000259460	ENSG00000259460	RP11-128A17.1	15:37181405-37393504	NOTEST	0	0.324223	inf	0	1	1
ENSG00000259461	ENSG00000259461	ANP32BP3	15:81299373-81441516	NOTEST	0	0	0	0	1	1
ENSG00000259462	ENSG00000259462	RP11-752G15.3	15:83205503-83378666	NOTEST	0.160735	0.181261	0.173385	0	1	1
ENSG00000259463	ENSG00000259463	RP11-540O11.7	15:41271077-41408552	NOTEST	0	0	0	0	1	1
ENSG00000259464	ENSG00000259464	RP11-14C10.1	15:102102738-102103177	NOTEST	0	0	0	0	1	1
ENSG00000259465	ENSG00000259465	AHCYP7	15:50709581-50710889	NOTEST	0	0	0	0	1	1
ENSG00000259466	ENSG00000259466	NPM1P47	15:62374648-62375504	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000259468	ENSG00000259468	RP11-1084A12.2	15:34525459-34630261	NOTEST	0	0	0	0	1	1
ENSG00000259469	ENSG00000259469	RP11-227D13.4	15:49005124-49103785	NOTEST	0.189786	0.0313566	-2.59753	0	1	1
ENSG00000259470	ENSG00000259470	KRT8P9	15:71123862-71342414	NOTEST	0	0	0	0	1	1
ENSG00000259471	ENSG00000259471	RP11-321F6.1	15:66874527-66978132	NOTEST	0	0.0174527	inf	0	1	1
ENSG00000259472	ENSG00000259472	RP13-996F3.3	15:83128127-83182928	NOTEST	0.46336	0.592326	0.354258	0	1	1
ENSG00000259473	ENSG00000259473	RP11-96C21.1	15:70796245-70798267	NOTEST	0	0	0	0	1	1
ENSG00000259474	ENSG00000259474	RP11-650L12.1	15:78729772-78793798	NOTEST	0	0	0	0	1	1
ENSG00000259475	ENSG00000259475	RP11-654A16.3	15:99192199-99675798	NOTEST	0	0.0252993	inf	0	1	1
ENSG00000259476	ENSG00000259476	RP11-50C13.2	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000259477	ENSG00000259477	RP11-86K22.1	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000259478	ENSG00000259478	RP11-753A21.1	15:98525738-98534372	NOTEST	0	0	0	0	1	1
ENSG00000259481	ENSG00000259481	RP11-39M21.1	15:60771376-61521518	NOTEST	0	0	0	0	1	1
ENSG00000259482	ENSG00000259482	RP11-219B17.2	15:60771376-61521518	NOTEST	0	0	0	0	1	1
ENSG00000259483	ENSG00000259483	RP11-930O11.2	14:56770207-56777479	NOTEST	0	0	0	0	1	1
ENSG00000259485	ENSG00000259485	CTD-2147F2.1	15:97815406-97975324	NOTEST	0	0	0	0	1	1
ENSG00000259488	ENSG00000259488	RP11-154J22.1	15:48604549-48635570	NOTEST	0.0657675	0.0779696	0.245538	0	1	1
ENSG00000259489	ENSG00000259489	KRT18P47	15:89503300-89504277	NOTEST	0	0	0	0	1	1
ENSG00000259490	ENSG00000259490	IGHV3OR15-7	15:20192908-20193370	NOTEST	0	0	0	0	1	1
ENSG00000259493	ENSG00000259493	RP11-621H8.2	15:79851597-79852646	NOTEST	0	0.011917	inf	0	1	1
ENSG00000259496	ENSG00000259496	RP11-19J5.1	15:70095654-70096385	NOTEST	0	0	0	0	1	1
ENSG00000259498	ENSG00000259498	RP11-244F12.3	15:63334830-63364114	NOTEST	0.101191	0.118784	0.231269	0	1	1
ENSG00000259499	ENSG00000259499	RP11-616K22.2	15:44580926-44719342	NOTEST	0	0	0	0	1	1
ENSG00000259500	ENSG00000259500	KRT8P24	15:49263999-49265558	NOTEST	0.0320999	0	#NAME?	0	1	1
ENSG00000259501	ENSG00000259501	RP11-467N20.1	15:22646602-22647417	NOTEST	0	0	0	0	1	1
ENSG00000259502	ENSG00000259502	RP11-643G16.3	14:68077702-68080581	NOTEST	0	0	0	0	1	1
ENSG00000259503	ENSG00000259503	RP11-543G18.1	15:70613914-70619081	NOTEST	0	0	0	0	1	1
ENSG00000259504	ENSG00000259504	RP11-352D13.5	15:69570666-69591097	NOTEST	0	0	0	0	1	1
ENSG00000259505	ENSG00000259505	RP11-74D7.1	15:34158427-34357291	NOTEST	0	0	0	0	1	1
ENSG00000259507	ENSG00000259507	RP11-719C20.1	15:98980390-99057611	NOTEST	0	0	0	0	1	1
ENSG00000259508	ENSG00000259508	RP11-661D19.3	14:103236376-103241128	NOTEST	0	0.0265863	inf	0	1	1
ENSG00000259509	ENSG00000259509	RP11-627D16.2	15:47119723-47120156	NOTEST	0	0	0	0	1	1
ENSG00000259512	ENSG00000259512	HNRNPA1P5	15:67835046-68099461	NOTEST	0.0186876	0	#NAME?	0	1	1
ENSG00000259513	ENSG00000259513	CYCSP38	15:60771376-61521518	NOTEST	0	0	0	0	1	1
ENSG00000259514	ENSG00000259514	RP11-685G9.2	15:76629064-76634817	NOTEST	0	0.115992	inf	0	1	1
ENSG00000259515	ENSG00000259515	RP11-365N19.2	14:103388992-103523799	NOTEST	0.299303	0.226039	-0.405034	0	1	1
ENSG00000259517	ENSG00000259517	RP11-324D17.1	16:54279455-54304658	NOTEST	0	0	0	0	1	1
ENSG00000259518	ENSG00000259518	RP11-597K23.2	15:82380934-82390035	NOTEST	0	0.00435101	inf	0	1	1
ENSG00000259519	ENSG00000259519	RP11-519G16.2	15:45384847-45493373	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000259520	ENSG00000259520	CTD-2651B20.3	15:45543883-45571449	NOTEST	0.153155	0.133918	-0.193647	0	1	1
ENSG00000259521	ENSG00000259521	RP11-540O11.4	15:41271077-41408552	NOTEST	0	0	0	0	1	1
ENSG00000259522	ENSG00000259522	RP11-468E2.2	14:24641061-24708448	NOTEST	0.0814959	0	#NAME?	0	1	1
ENSG00000259523	ENSG00000259523	RP11-680F8.3	15:29991570-30261068	NOTEST	0	0	0	0	1	1
ENSG00000259524	ENSG00000259524	RP11-461F11.1	15:98058516-98065041	NOTEST	0	0	0	0	1	1
ENSG00000259525	ENSG00000259525	GCSHP2	14:103650540-103651376	NOTEST	0	0	0	0	1	1
ENSG00000259527	ENSG00000259527	LINC00052	15:87975288-88247083	NOTEST	0.044258	0.163929	1.88906	0	1	1
ENSG00000259528	ENSG00000259528	RP11-272D12.2	15:73344050-73597547	NOTEST	0	0	0	0	1	1
ENSG00000259529	ENSG00000259529	RP11-468E2.4	14:24612573-24636611	NOTEST	0.291795	0.272777	-0.0972366	0	1	1
ENSG00000259530	ENSG00000259530	RP11-259A24.1	15:61592524-61927648	NOTEST	0	0	0	0	1	1
ENSG00000259531	ENSG00000259531	RP11-295H24.3	15:49398267-49913128	NOTEST	0.0300547	0.0300315	-0.0011132	0	1	1
ENSG00000259532	ENSG00000259532	RP11-138H8.2	15:70946892-71055932	NOTEST	0	0	0	0	1	1
ENSG00000259533	ENSG00000259533	RP11-630H24.3	17:61963210-61963411	NOTEST	0	0	0	0	1	1
ENSG00000259534	ENSG00000259534	RP11-522B15.7	15:96992071-96992979	NOTEST	0	0	0	0	1	1
ENSG00000259535	ENSG00000259535	RPL21P12	14:103614933-103615745	NOTEST	0	0	0	0	1	1
ENSG00000259536	ENSG00000259536	RP11-111A22.1	15:40780239-40857256	NOTEST	0.14523	0.103752	-0.4852	0	1	1
ENSG00000259538	ENSG00000259538	UBE2Q2P11	15:84967470-84976535	NOTEST	0.327567	0	#NAME?	0	1	1
ENSG00000259539	ENSG00000259539	CTD-2651B20.1	15:45384847-45493373	NOTEST	0	0.0134087	inf	0	1	1
ENSG00000259540	ENSG00000259540	RP11-526I2.1	15:101093733-101191910	NOTEST	0.0644741	0.186981	1.5361	0	1	1
ENSG00000259541	ENSG00000259541	RP11-778O17.4	11:120107348-120190653	NOTEST	0	0	0	0	1	1
ENSG00000259542	ENSG00000259542	RP11-522B15.4	15:96897465-96948419	NOTEST	0	0	0	0	1	1
ENSG00000259543	ENSG00000259543	CTD-2034I4.1	15:81719788-82163466	NOTEST	0	0	0	0	1	1
ENSG00000259544	ENSG00000259544	RP11-158M2.2	15:85923801-86293512	NOTEST	0	0.0879463	inf	0	1	1
ENSG00000259545	ENSG00000259545	RP11-325E5.4	15:49398267-49913128	NOTEST	0	0	0	0	1	1
ENSG00000259546	ENSG00000259546	RP11-351M8.2	15:81071683-81282219	NOTEST	0.109649	0.0451811	-1.2791	0	1	1
ENSG00000259547	ENSG00000259547	CYCSP2	15:41271077-41408552	NOTEST	0	0	0	0	1	1
ENSG00000259548	ENSG00000259548	RP11-38G5.2	15:80124807-80125896	NOTEST	0.0807318	0.255206	1.66046	0	1	1
ENSG00000259549	ENSG00000259549	RP11-115K3.1	17:36046434-36108563	NOTEST	0	0	0	0	1	1
ENSG00000259550	ENSG00000259550	HNRNPA1P74	15:54305100-54920806	NOTEST	0	0	0	0	1	1
ENSG00000259551	ENSG00000259551	RP11-182J1.10	15:85034710-85045612	NOTEST	0	0.0308534	inf	0	1	1
ENSG00000259553	ENSG00000259553	MIR1302-11	15:102500050-102519298	NOTEST	0	0.0420005	inf	0	1	1
ENSG00000259554	ENSG00000259554	RP11-408J6.1	15:47476297-48066420	NOTEST	0	0	0	0	1	1
ENSG00000259555	ENSG00000259555	RP11-335K5.2	15:78916460-79027837	NOTEST	0	0	0	0	1	1
ENSG00000259556	ENSG00000259556	RP11-56B16.2	15:52121824-52392720	NOTEST	0	0	0	0	1	1
ENSG00000259557	ENSG00000259557	HMGN1P26	15:62654227-62654530	NOTEST	0	0	0	0	1	1
ENSG00000259558	ENSG00000259558	MESTP2	15:60296420-60353929	NOTEST	0	0	0	0	1	1
ENSG00000259560	ENSG00000259560	RP11-648K4.2	15:87975288-88247083	NOTEST	0	0	0	0	1	1
ENSG00000259561	ENSG00000259561	RP11-300G22.2	15:90234027-90286869	NOTEST	0	0	0	0	1	1
ENSG00000259562	ENSG00000259562	RP11-762H8.2	15:78542843-78592136	NOTEST	0.463782	0.524488	0.177462	0	1	1
ENSG00000259563	ENSG00000259563	CTD-2329K10.1	15:44719431-44829121	NOTEST	0	0	0	0	1	1
ENSG00000259564	ENSG00000259564	RP11-16B9.1	15:62126950-62144351	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000259567	ENSG00000259567	DNM1P38	15:82816059-82818549	NOTEST	0	0	0	0	1	1
ENSG00000259569	ENSG00000259569	RP11-97O12.3	15:89111517-89111793	NOTEST	0	0	0	0	1	1
ENSG00000259570	ENSG00000259570	RP11-671M22.4	15:84944426-84950601	NOTEST	0.257847	0.0530988	-2.27976	0	1	1
ENSG00000259571	ENSG00000259571	BLID	11:121899062-121987031	NOTEST	0	0	0	0	1	1
ENSG00000259572	ENSG00000259572	RP11-198M11.2	15:48095580-48138433	NOTEST	0	0	0	0	1	1
ENSG00000259573	ENSG00000259573	NMNAT1P5	15:60257140-60258283	NOTEST	0	0	0	0	1	1
ENSG00000259575	ENSG00000259575	RP11-39M21.2	15:60771376-61521518	NOTEST	0	0	0	0	1	1
ENSG00000259577	ENSG00000259577	RP11-430B1.2	15:52408770-52587995	NOTEST	0.0668808	0.0362151	-0.885001	0	1	1
ENSG00000259579	ENSG00000259579	RP11-66B24.5	15:101256453-101368702	NOTEST	0	0	0	0	1	1
ENSG00000259580	ENSG00000259580	RP11-37C7.1	15:39892231-40213093	NOTEST	0	0.0568891	inf	0	1	1
ENSG00000259581	ENSG00000259581	TYRO3P	15:76352177-76603813	NOTEST	0	0.0127841	inf	0	1	1
ENSG00000259582	ENSG00000259582	RP11-461F11.3	15:98096513-98103932	NOTEST	0	0	0	0	1	1
ENSG00000259584	ENSG00000259584	RP11-521C20.2	15:40367404-40370905	NOTEST	0.0606543	0.0500118	-0.278341	0	1	1
ENSG00000259585	ENSG00000259585	RP11-150L8.4	15:35473999-35838394	NOTEST	0	0	0	0	1	1
ENSG00000259586	ENSG00000259586	RP11-66B24.3	15:101386808-101386972	NOTEST	0	0	0	0	1	1
ENSG00000259587	ENSG00000259587	RP11-463I20.2	15:35300669-35303392	NOTEST	0	0	0	0	1	1
ENSG00000259588	ENSG00000259588	RP11-552E10.1	15:47476297-48066420	NOTEST	0	0	0	0	1	1
ENSG00000259589	ENSG00000259589	RP11-317G6.1	15:63900816-64126141	NOTEST	0	0	0	0	1	1
ENSG00000259590	ENSG00000259590	RP11-20G13.3	15:99935383-99936798	NOTEST	0	0.0696621	inf	0	1	1
ENSG00000259591	ENSG00000259591	RP11-554D20.1	15:60771376-61521518	NOTEST	0	0	0	0	1	1
ENSG00000259592	ENSG00000259592	PRELID1P4	15:35391222-35461899	NOTEST	0	0.0967613	inf	0	1	1
ENSG00000259593	ENSG00000259593	RP11-640I2.1	15:46633551-46633797	NOTEST	0	0	0	0	1	1
ENSG00000259594	ENSG00000259594	CTD-2034I4.2	15:81719788-82163466	NOTEST	0.244146	0.0430044	-2.50518	0	1	1
ENSG00000259595	ENSG00000259595	RP11-516C1.1	15:44580926-44719342	NOTEST	0	0	0	0	1	1
ENSG00000259596	ENSG00000259596	RP11-566K19.3	15:22747312-22789974	NOTEST	0	0	0	0	1	1
ENSG00000259598	ENSG00000259598	RP11-275I4.1	15:38780303-38857776	NOTEST	0	0	0	0	1	1
ENSG00000259600	ENSG00000259600	RP11-925D8.3	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000259601	ENSG00000259601	RP11-568G20.2	15:60163709-60165694	NOTEST	0	0	0	0	1	1
ENSG00000259602	ENSG00000259602	RP11-138E16.1	15:49115931-49255641	NOTEST	0.0300904	0.0663647	1.14111	0	1	1
ENSG00000259603	ENSG00000259603	CTD-2012M11.3	5:3596167-3601517	NOTEST	0	0	0	0	1	1
ENSG00000259606	ENSG00000259606	RP11-316E14.6	14:75230068-75330537	NOTEST	0.498872	0.174572	-1.51485	0	1	1
ENSG00000259607	ENSG00000259607	CTD-2647L4.5	8:28924795-29120641	NOTEST	0	0	0	0	1	1
ENSG00000259608	ENSG00000259608	RP11-23A22.1	15:86501947-86502202	NOTEST	0	0	0	0	1	1
ENSG00000259609	ENSG00000259609	RP11-342A23.1	15:84721864-84748849	NOTEST	0	0	0	0	1	1
ENSG00000259610	ENSG00000259610	RP11-499F3.1	15:81719788-82163466	NOTEST	0	0	0	0	1	1
ENSG00000259611	ENSG00000259611	CTD-2544M6.2	15:98589895-98836406	NOTEST	0.10898	0.149094	0.452158	0	1	1
ENSG00000259612	ENSG00000259612	EEF1A1P22	15:53229335-53230715	NOTEST	0.0346063	0.0259268	-0.416589	0	1	1
ENSG00000259613	ENSG00000259613	RP13-608F4.6	15:82829004-82829110	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000259615	ENSG00000259615	RP11-429B14.3	15:90048507-90198682	NOTEST	0	0	0	0	1	1
ENSG00000259616	ENSG00000259616	RP11-507B12.2	15:61592524-61927648	NOTEST	0	0	0	0	1	1
ENSG00000259617	ENSG00000259617	RP11-540O11.6	15:41271077-41408552	NOTEST	0	0.0351802	inf	0	1	1
ENSG00000259618	ENSG00000259618	RP11-562A8.5	15:50716576-50838905	NOTEST	0	0	0	0	1	1
ENSG00000259619	ENSG00000259619	RP11-390M11.1	15:54305100-54920806	NOTEST	0	0	0	0	1	1
ENSG00000259620	ENSG00000259620	RP11-133L19.1	15:86685226-87572283	NOTEST	0	0	0	0	1	1
ENSG00000259621	ENSG00000259621	RP11-654A16.1	15:99192199-99675798	NOTEST	0	0	0	0	1	1
ENSG00000259622	ENSG00000259622	RP11-597K23.1	15:82302552-82302948	NOTEST	0	0	0	0	1	1
ENSG00000259624	ENSG00000259624	RP11-138H8.3	15:71060349-71071207	NOTEST	0	0	0	0	1	1
ENSG00000259626	ENSG00000259626	RP11-925D8.2	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000259628	ENSG00000259628	RP11-467H10.2	7:76139744-77045717	NOTEST	0	0.122399	inf	0	1	1
ENSG00000259630	ENSG00000259630	CTD-2262B20.1	15:85923801-86293512	NOTEST	0	0	0	0	1	1
ENSG00000259631	ENSG00000259631	RP11-557C18.4	8:123989265-123997869	NOTEST	0	0	0	0	1	1
ENSG00000259632	ENSG00000259632	RP11-56B16.1	15:52121824-52392720	NOTEST	0	0	0	0	1	1
ENSG00000259633	ENSG00000259633	UBE2Q2P8	15:84924664-84924766	NOTEST	0	0	0	0	1	1
ENSG00000259634	ENSG00000259634	RP11-529H20.5	14:92524895-92572965	NOTEST	0.235257	0.00271593	-6.43665	0	1	1
ENSG00000259635	ENSG00000259635	AC100830.3	15:64979771-65011801	NOTEST	0	0	0	0	1	1
ENSG00000259636	ENSG00000259636	RP11-133L19.2	15:86685226-87572283	NOTEST	0	0	0	0	1	1
ENSG00000259637	ENSG00000259637	DNM1P42	15:83200403-83202890	NOTEST	0	0	0	0	1	1
ENSG00000259639	ENSG00000259639	RP11-184D12.1	15:36231367-36544458	NOTEST	0	0	0	0	1	1
ENSG00000259640	ENSG00000259640	RP6-33F8.1	X:83572881-83757487	NOTEST	0.475747	0.378614	-0.329466	0	1	1
ENSG00000259641	ENSG00000259641	RP11-279F6.3	15:69884467-69988089	NOTEST	0	0	0	0	1	1
ENSG00000259644	ENSG00000259644	RP11-680F8.4	15:29991570-30261068	NOTEST	0.0229742	0.0277979	0.274965	0	1	1
ENSG00000259645	ENSG00000259645	RP11-253M7.6	15:69591285-69740764	NOTEST	0	0	0	0	1	1
ENSG00000259646	ENSG00000259646	AC140725.7	15:102443356-102443407	NOTEST	0	0	0	0	1	1
ENSG00000259647	ENSG00000259647	RP11-143J24.1	15:30297407-30338051	NOTEST	0	0	0	0	1	1
ENSG00000259648	ENSG00000259648	RP11-643G16.4	14:68081645-68083343	NOTEST	0.0339612	0.0492481	0.536178	0	1	1
ENSG00000259649	ENSG00000259649	RP11-351M8.1	15:81071683-81282219	NOTEST	0.122532	0.0289537	-2.08134	0	1	1
ENSG00000259650	ENSG00000259650	RP11-272D12.1	15:73612199-73661605	NOTEST	0	0	0	0	1	1
ENSG00000259651	ENSG00000259651	CTD-2330J20.1	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000259652	ENSG00000259652	RP11-797A18.3	15:77336021-77376326	NOTEST	0.305144	0	#NAME?	0	1	1
ENSG00000259654	ENSG00000259654	RP11-245C17.2	15:85212774-85259947	NOTEST	0	0	0	0	1	1
ENSG00000259655	ENSG00000259655	CTD-2054N24.1	15:100330360-100347132	NOTEST	0	0	0	0	1	1
ENSG00000259656	ENSG00000259656	RP11-325E5.1	15:49393987-49395461	NOTEST	0	0.0959012	inf	0	1	1
ENSG00000259657	ENSG00000259657	PIGHP1	15:59887073-59981733	NOTEST	0.107599	0.142328	0.403556	0	1	1
ENSG00000259659	ENSG00000259659	RP11-151N17.1	15:44829254-44955876	NOTEST	0.175294	0.218638	0.318768	0	1	1
ENSG00000259660	ENSG00000259660	DNM1P47	15:102291234-102334505	NOTEST	0.0119163	0.0145354	0.286628	0	1	1
ENSG00000259661	ENSG00000259661	AC068831.15	15:91445447-91465814	NOTEST	0.00295296	0.0133	2.17119	0	1	1

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ENSG00000259664	ENSG00000259664	CTD-2147F2.2	15:97815406-97975324	NOTEST	0	0	0	0	1	1
ENSG00000259665	ENSG00000259665	RP11-323I15.3	15:35373344-35373714	NOTEST	0	0	0	0	1	1
ENSG00000259666	ENSG00000259666	RP11-307C19.3	15:77905368-78113242	NOTEST	0	0	0	0	1	1
ENSG00000259668	ENSG00000259668	RP11-707P17.2	15:51706293-51915030	NOTEST	0.318955	0.108603	-1.55429	0	1	1
ENSG00000259669	ENSG00000259669	RP11-643A5.2	15:54239820-54269105	NOTEST	0	0	0	0	1	1
ENSG00000259670	ENSG00000259670	RP11-485O10.2	15:49005124-49103785	NOTEST	0	0.0521715	inf	0	1	1
ENSG00000259671	ENSG00000259671	RP11-925D8.6	15:58245621-58861151	NOTEST	0	0	0	0	1	1
ENSG00000259672	ENSG00000259672	RP11-69G7.1	15:63391068-63402602	NOTEST	0	0	0	0	1	1
ENSG00000259673	ENSG00000259673	IQCH-AS1	15:67493370-67819628	NOTEST	0.385167	0.471664	0.292274	0	1	1
ENSG00000259674	ENSG00000259674	RP11-356M20.1	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000259675	ENSG00000259675	RP11-507B12.1	15:61931547-62007370	NOTEST	0	0	0	0	1	1
ENSG00000259676	ENSG00000259676	RP11-343B18.2	15:89340643-89341965	NOTEST	0	0.0289196	inf	0	1	1
ENSG00000259677	ENSG00000259677	RP11-493E3.1	15:90373830-90456188	NOTEST	0.0775006	0.155234	1.00217	0	1	1
ENSG00000259678	ENSG00000259678	RP11-707P17.1	15:51706293-51915030	NOTEST	0	0	0	0	1	1
ENSG00000259680	ENSG00000259680	RP11-812E19.9	16:33647043-33647696	NOTEST	0	0	0	0	1	1
ENSG00000259681	ENSG00000259681	RP11-96O20.2	15:45722726-45878488	NOTEST	0	0	0	0	1	1
ENSG00000259682	ENSG00000259682	RP11-702L15.4	15:64752940-64978264	NOTEST	0	0	0	0	1	1
ENSG00000259683	ENSG00000259683	RP11-182J1.14	15:84944426-84950601	NOTEST	0.139005	0.149836	0.108239	0	1	1
ENSG00000259684	ENSG00000259684	RP11-120K9.2	15:50844669-50979012	NOTEST	0.133861	0.0251895	-2.40985	0	1	1
ENSG00000259685	ENSG00000259685	CTD-2315E11.	15:90645880-90676674	NOTEST	0	0	0	0	1	1
ENSG00000259686	ENSG00000259686	HNRNPA1P71	15:33057746-33486897	NOTEST	0	0.0148273	inf	0	1	1
ENSG00000259687	ENSG00000259687	RP11-293M10.5	14:75761106-75763341	NOTEST	0.332886	0.121624	-1.4526	0	1	1
ENSG00000259688	ENSG00000259688	RP11-139F4.2	15:35473999-35838394	NOTEST	0	0	0	0	1	1
ENSG00000259689	ENSG00000259689	ABCB10P1	15:22691015-22693200	NOTEST	0.0133489	0	#NAME?	0	1	1
ENSG00000259690	ENSG00000259690	CTD-3118D7.1	15:29412456-29862927	NOTEST	0	0	0	0	1	1
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ENSG00000259692	ENSG00000259692	RP11-499F3.2	15:81719788-82163466	NOTEST	0	0.0292868	inf	0	1	1
ENSG00000259694	ENSG00000259694	RP13-262C2.3	15:84839929-84850986	NOTEST	0	0	0	0	1	1
ENSG00000259695	ENSG00000259695	RP11-14C10.2	15:102121095-102121759	NOTEST	0	0	0	0	1	1
ENSG00000259696	ENSG00000259696	RP11-126F18.2	15:31745403-31746342	NOTEST	0	0	0	0	1	1
ENSG00000259697	ENSG00000259697	RP11-299H22.1	15:62488343-62495517	NOTEST	0	0	0	0	1	1
ENSG00000259698	ENSG00000259698	KIAA0125P2	15:21224716-21226180	NOTEST	0	0	0	0	1	1
ENSG00000259700	ENSG00000259700	RP11-485O10.3	15:49005124-49103785	NOTEST	0	0	0	0	1	1
ENSG00000259701	ENSG00000259701	RP11-108K3.3	15:51329684-51630807	NOTEST	0	0	0	0	1	1
ENSG00000259702	ENSG00000259702	RP11-236L14.1	15:96592503-96607655	NOTEST	0	0	0	0	1	1
ENSG00000259703	ENSG00000259703	LINC00593	15:70127572-70135459	NOTEST	0	0	0	0	1	1
ENSG00000259704	ENSG00000259704	CTD-3094K11.1	15:91382953-91384608	NOTEST	0	0	0	0	1	1
ENSG00000259705	ENSG00000259705	RP11-227D13.1	15:48938147-48944213	NOTEST	0	0.00651246	inf	0	1	1
ENSG00000259706	ENSG00000259706	HSP90B2P	15:99791566-99930934	NOTEST	0.0121428	0.0293723	1.27436	0	1	1

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ENSG00000259708	ENSG00000259708	RP11-762H8.3	15:78542843-78592136	NOTEST	0	0.0545943	inf	0	1	1
ENSG00000259709	ENSG00000259709	CTD-2184D3.7	15:52408770-52587995	NOTEST	0.103593	0.0839423	-0.303454	0	1	1
ENSG00000259710	ENSG00000259710	RP11-150L8.3	15:35473999-35838394	NOTEST	0	0	0	0	1	1
ENSG00000259711	ENSG00000259711	CTD-3032H12.2	16:54968824-54988577	NOTEST	0	0	0	0	1	1
ENSG00000259712	ENSG00000259712	CTD-2184D3.5	15:52121824-52392720	NOTEST	0.0640557	0.0935154	0.545877	0	1	1
ENSG00000259713	ENSG00000259713	RP11-429B14.1	15:90048507-90198682	NOTEST	0	0	0	0	1	1
ENSG00000259714	ENSG00000259714	LINC00594	15:40664025-40664677	NOTEST	0	0	0	0	1	1
ENSG00000259715	ENSG00000259715	CTD-3110H11.	15:50569388-50659636	NOTEST	0.196966	0.232261	0.2378	0	1	1
ENSG00000259716	ENSG00000259716	RP5-977B1.11	20:34894257-35274619	NOTEST	0	0	0	0	1	1
ENSG00000259717	ENSG00000259717	LINC00677	14:103587183-103589344	NOTEST	0	0	0	0	1	1
ENSG00000259719	ENSG00000259719	RP11-930O11.1	14:56777597-56811719	NOTEST	0	0	0	0	1	1
ENSG00000259720	ENSG00000259720	RP11-348B17.1	15:31293263-31453476	NOTEST	0.154742	0	#NAME?	0	1	1
ENSG00000259721	ENSG00000259721	RP11-758N13.1	15:33009470-33026870	NOTEST	0	0	0	0	1	1
ENSG00000259722	ENSG00000259722	RP11-94P14.1	15:77400470-77712486	NOTEST	0	0	0	0	1	1
ENSG00000259723	ENSG00000259723	RP5-823G15.5	20:51588945-52120853	NOTEST	0	0	0	0	1	1
ENSG00000259724	ENSG00000259724	CTD-2643K12.3	15:94133095-94651167	NOTEST	0	0	0	0	1	1
ENSG00000259725	ENSG00000259725	CTD-3032H12.1	16:54968824-54988577	NOTEST	0	0	0	0	1	1
ENSG00000259726	ENSG00000259726	CSPG4P11	15:84855503-84866136	NOTEST	0.392126	0.466798	0.251482	0	1	1
ENSG00000259727	ENSG00000259727	RP11-1069G10.2	15:63188010-63191742	NOTEST	0	0.0099186	inf	0	1	1
ENSG00000259728	ENSG00000259728	LINC00933	15:85051115-85123406	NOTEST	0.115037	0.0904808	-0.346413	0	1	1
ENSG00000259730	ENSG00000259730	CTD-2007H18.1	15:48176506-48341309	NOTEST	0	0	0	0	1	1
ENSG00000259731	ENSG00000259731	RP11-326N17.1	15:39048754-39051614	NOTEST	0	0	0	0	1	1
ENSG00000259732	ENSG00000259732	RP11-59H7.3	15:59397276-59425449	NOTEST	0	0.0750937	inf	0	1	1
ENSG00000259734	ENSG00000259734	RP11-182L7.1	15:86685226-87572283	NOTEST	0	0	0	0	1	1
ENSG00000259735	ENSG00000259735	RP11-356M20.3	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000259736	ENSG00000259736	RP11-387D10.2	15:91073156-91260372	NOTEST	0.128496	0	#NAME?	0	1	1
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ENSG00000259738	ENSG00000259738	ZNF444P1	15:59063390-59389618	NOTEST	0	0	0	0	1	1
ENSG00000259740	ENSG00000259740	RP11-142J21.2	15:47476297-48066420	NOTEST	0	0	0	0	1	1
ENSG00000259742	ENSG00000259742	CTD-2014N11.1	15:45206999-45222820	NOTEST	0	0	0	0	1	1
ENSG00000259743	ENSG00000259743	RP11-315O8.1	15:46391390-46392590	NOTEST	0	0	0	0	1	1
ENSG00000259744	ENSG00000259744	RP11-138H8.6	15:71123862-71342414	NOTEST	0.118837	0.137364	0.209016	0	1	1
ENSG00000259745	ENSG00000259745	RP11-809H16.3	15:69070873-69355083	NOTEST	0	0	0	0	1	1
ENSG00000259747	ENSG00000259747	RP11-275I4.2	15:38964047-38981392	NOTEST	0	0	0	0	1	1
ENSG00000259749	ENSG00000259749	CTD-2022H16.2	15:30297407-30338051	NOTEST	0	0	0	0	1	1
ENSG00000259750	ENSG00000259750	RP11-356M20.2	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000259751	ENSG00000259751	RP11-83J16.3	15:35141337-35142596	NOTEST	0.0384815	0.0600615	0.642275	0	1	1

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ENSG00000259754	ENSG00000259754	RP11-208K4.1	15:48176506-48341309	NOTEST	0	0	0	0	1	1
ENSG00000259755	ENSG00000259755	RP11-505E24.2	15:101389765-101626271	NOTEST	0	0	0	0	1	1
ENSG00000259756	ENSG00000259756	RP11-625H11.2	15:62682724-63176233	NOTEST	0	0	0	0	1	1
ENSG00000259757	ENSG00000259757	RP11-129I19.2	5:2736775-2737873	NOTEST	0	0	0	0	1	1
ENSG00000259759	ENSG00000259759	RP11-324D17.2	16:54273604-54274566	NOTEST	0	0	0	0	1	1
ENSG00000259760	ENSG00000259760	RP11-20G13.2	15:99936817-99941520	NOTEST	0	0	0	0	1	1
ENSG00000259761	ENSG00000259761	RP11-138H10.2	15:87585284-87590392	NOTEST	0	0	0	0	1	1
ENSG00000259762	ENSG00000259762	RP11-158M2.4	15:86293566-86296132	NOTEST	0	0	0	0	1	1
ENSG00000259763	ENSG00000259763	RP11-327J17.1	15:96670597-96883492	NOTEST	0	0	0	0	1	1
ENSG00000259764	ENSG00000259764	RP11-299G20.3	15:101835623-102065405	NOTEST	0	0.0224575	inf	0	1	1
ENSG00000259767	ENSG00000259767	RP11-90B9.2	15:83509837-83772195	NOTEST	0.0524697	0.0409141	-0.358887	0	1	1
ENSG00000259768	ENSG00000259768	RP5-991G20.1	16:72699068-73093597	NOTEST	0.102061	0.402549	1.97973	0	1	1
ENSG00000259769	ENSG00000259769	RP11-1360M22.2	15:20251548-20253247	NOTEST	0	0	0	0	1	1
ENSG00000259770	ENSG00000259770	RP11-81A1.3	15:80236839-80237920	NOTEST	0	0	0	0	1	1
ENSG00000259771	ENSG00000259771	RP11-429D19.1	15:59427112-59815748	NOTEST	0	0.0418243	inf	0	1	1
ENSG00000259772	ENSG00000259772	RP11-16E12.2	15:31508222-31523041	NOTEST	0	0	0	0	1	1
ENSG00000259773	ENSG00000259773	RP11-507J18.2	15:50999505-51058005	NOTEST	0	0	0	0	1	1
ENSG00000259774	ENSG00000259774	RP11-182J1.13	15:84977315-84980581	NOTEST	0.267353	0.333642	0.319558	0	1	1
ENSG00000259775	ENSG00000259775	RP11-45P15.4	14:103798010-103798704	NOTEST	0.109059	0.129085	0.24322	0	1	1
ENSG00000259776	ENSG00000259776	RP11-544D21.2	1:239411107-239414118	NOTEST	0	0	0	0	1	1
ENSG00000259777	ENSG00000259777	SLC39A12	HG544_PATCH:17993890-18085286	NOTEST	0	0	0	0	1	1
ENSG00000259779	ENSG00000259779	RP11-231E4.2	18:72076649-72080444	NOTEST	0	0.0068104	inf	0	1	1
ENSG00000259780	ENSG00000259780	RP11-304L19.12	16:2273566-2288712	NOTEST	0.0282427	0.0109541	-1.36641	0	1	1
ENSG00000259782	ENSG00000259782	CTD-2270L9.2	16:23399813-23468927	NOTEST	0	0.017348	inf	0	1	1
ENSG00000259783	ENSG00000259783	RP11-1006G14.2	15:72897523-72929260	NOTEST	0	0	0	0	1	1
ENSG00000259784	ENSG00000259784	ATP6C	16:2525146-2581423	NOTEST	0.0860808	0	#NAME?	0	1	1
ENSG00000259785	ENSG00000259785	ADAMTS7P1	15:82590890-82626963	NOTEST	0	0	0	0	1	1
ENSG00000259786	ENSG00000259786	CTD-2118P12.1	5:29143609-29172465	NOTEST	0	0	0	0	1	1
ENSG00000259788	ENSG00000259788	RP11-359K18.3	1:162530016-162531098	NOTEST	0	0	0	0	1	1
ENSG00000259789	ENSG00000259789	RP11-1078H9.6	14:90955355-90957981	NOTEST	0	0	0	0	1	1
ENSG00000259790	ENSG00000259790	ANP32BP1	15:75613737-75615034	NOTEST	0	0.0370762	inf	0	1	1
ENSG00000259791	ENSG00000259791	RP11-14K3.7	16:34872993-34879551	NOTEST	0	0	0	0	1	1
ENSG00000259792	ENSG00000259792	RP11-114H24.6	15:78268383-78370066	NOTEST	0	0	0	0	1	1
ENSG00000259793	ENSG00000259793	RP11-400N9.1	2:234259777-234262062	NOTEST	0	0.0308441	inf	0	1	1
ENSG00000259795	ENSG00000259795	TBC1D3	HG75_PATCH:34581014-34591935	NOTEST	0	0	0	0	1	1
ENSG00000259796	ENSG00000259796	RP11-355I22.7	14:62570095-62596352	NOTEST	0	0	0	0	1	1
ENSG00000259797	ENSG00000259797	RP11-96D1.3	16:68344876-68482591	NOTEST	0.224187	0.399967	0.835178	0	1	1
ENSG00000259798	ENSG00000259798	RP11-23E19.2	16:70841280-71264625	NOTEST	0	0	0	0	1	1

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ENSG00000259800	ENSG00000259800	RP11-19N8.6	16:33140636-33145820	NOTEST	0	0	0	0	1	1
ENSG00000259801	ENSG00000259801	AC126327.5	HG75_PATCH:34704906-34715799	NOTEST	0	0	0	0	1	1
ENSG00000259803	ENSG00000259803	SLC22A31	16:89262405-89268072	NOTEST	0	0	0	0	1	1
ENSG00000259804	ENSG00000259804	CTD-2012K14.7	16:67583116-67673086	NOTEST	0.0577396	0.044659	-0.370611	0	1	1
ENSG00000259805	ENSG00000259805	RP11-382A20.5	15:83509837-83772195	NOTEST	0	0	0	0	1	1
ENSG00000259807	ENSG00000259807	RP11-426C22.4	16:29065052-29231352	NOTEST	0.0384522	0.142062	1.88538	0	1	1
ENSG00000259808	ENSG00000259808	FRG2	HG1032_PATCH:190945505-190948412	NOTEST	0	0	0	0	1	1
ENSG00000259809	ENSG00000259809	RP11-163O19.8	HG281_PATCH:49913813-49915329	NOTEST	0	0	0	0	1	1
ENSG00000259810	ENSG00000259810	AC002519.8	16:31724549-31806190	NOTEST	0	0.00397853	inf	0	1	1
ENSG00000259813	ENSG00000259813	RP5-1142A6.5	16:88762902-88772829	NOTEST	0	0	0	0	1	1
ENSG00000259814	ENSG00000259814	RP11-300A12.2	15:29901879-29903416	NOTEST	0	0	0	0	1	1
ENSG00000259815	ENSG00000259815	RP11-565N2.2	1:208800085-208801430	NOTEST	0	0	0	0	1	1
ENSG00000259817	ENSG00000259817	RP11-53L24.1	16:73846519-73849953	NOTEST	0	0	0	0	1	1
ENSG00000259818	ENSG00000259818	RP5-1024G6.7	1:53686334-53689925	NOTEST	0	0	0	0	1	1
ENSG00000259819	ENSG00000259819	RP11-568A19.1	16:8419865-8426278	NOTEST	0	0	0	0	1	1
ENSG00000259821	ENSG00000259821	RP11-169E6.4	16:47038423-47069296	NOTEST	0	0	0	0	1	1
ENSG00000259822	ENSG00000259822	RP11-1292F20.1	16:32290186-32290436	NOTEST	0	0	0	0	1	1
ENSG00000259823	ENSG00000259823	XX-CR54.3	HG999_1_PATCH:248881949-248914431	NOTEST	0	0	0	0	1	1
ENSG00000259824	ENSG00000259824	TRBV12-4	HG7_PATCH:142305348-142305854	NOTEST	0	0	0	0	1	1
ENSG00000259825	ENSG00000259825	TRBV4-3	HG7_PATCH:142062480-142062934	NOTEST	0	0	0	0	1	1
ENSG00000259826	ENSG00000259826	RP11-467D6.1	7:39987120-39989354	NOTEST	0.075084	0.0871747	0.215404	0	1	1
ENSG00000259827	ENSG00000259827	RP11-343H19.2	16:56716335-56721964	NOTEST	0	0	0	0	1	1
ENSG00000259828	ENSG00000259828	RP11-63E9.1	6:141768147-141772143	NOTEST	0.216122	0.1318	-0.713495	0	1	1
ENSG00000259829	ENSG00000259829	TRBV4-2	HG7_PATCH:142045251-142045816	NOTEST	0	0	0	0	1	1
ENSG00000259831	ENSG00000259831	LINC00567	13:111462022-111465431	NOTEST	0	0	0	0	1	1
ENSG00000259832	ENSG00000259832	CYP4A26P	1:47427035-47516423	NOTEST	0	0	0	0	1	1
ENSG00000259833	ENSG00000259833	RP11-23E19.1	16:70841280-71264625	NOTEST	0	0	0	0	1	1
ENSG00000259834	ENSG00000259834	RP11-284N8.3	1:111196181-111199662	NOTEST	0	0	0	0	1	1
ENSG00000259836	ENSG00000259836	RP11-80F22.5	16:34723607-34724583	NOTEST	0.0336857	0.0406524	0.271206	0	1	1
ENSG00000259837	ENSG00000259837	RP11-672L10.1	18:926083-927994	NOTEST	0	0	0	0	1	1
ENSG00000259838	ENSG00000259838	TCEB1P2	15:41849224-41849633	NOTEST	0	0	0	0	1	1
ENSG00000259839	ENSG00000259839	RP11-491F9.6	16:49370593-49372904	NOTEST	0	0	0	0	1	1
ENSG00000259840	ENSG00000259840	LA16c-380A1.1	16:760745-761277	NOTEST	0	0	0	0	1	1
ENSG00000259841	ENSG00000259841	RP11-488I20.3	16:34597782-34624955	NOTEST	0	0	0	0	1	1
ENSG00000259842	ENSG00000259842	IGHV3OR16-16	16:33752442-33752887	NOTEST	0	0	0	0	1	1
ENSG00000259843	ENSG00000259843	RP11-429P3.3	16:50080339-50155854	NOTEST	0	0	0	0	1	1
ENSG00000259844	ENSG00000259844	GNPATP	16:60688138-60690553	NOTEST	0	0	0	0	1	1
ENSG00000259846	ENSG00000259846	RP11-467L24.1	16:64398683-64634150	NOTEST	0	0	0	0	1	1
ENSG00000259847	ENSG00000259847	RP11-95H3.1	16:65175658-65210616	NOTEST	0	0	0	0	1	1
ENSG00000259848	ENSG00000259848	AC097374.2	2:95533230-95613086	NOTEST	0.0047025	0	#NAME?	0	1	1

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ENSG00000259851	ENSG00000259851	TRBV28	HG7_PATCH:142461161-142461662	NOTEST	0	0	0	0	1	1
ENSG00000259852	ENSG00000259852	IGHV1OR16-2	16:32963313-33039358	NOTEST	0	0	0	0	1	1
ENSG00000259853	ENSG00000259853	OR4A19P	HG281_PATCH:49941863-49942966	NOTEST	0	0	0	0	1	1
ENSG00000259854	ENSG00000259854	RP11-211G23.1	11:69229074-69231600	NOTEST	0	0	0	0	1	1
ENSG00000259855	ENSG00000259855	RP11-574O16.1	2:217860628-217861213	NOTEST	0	0	0	0	1	1
ENSG00000259857	ENSG00000259857	C17orf51	HG987_PATCH:21428101-21477829	NOTEST	0	0	0	0	1	1
ENSG00000259858	ENSG00000259858	MGAM	HG7_PATCH:141607612-141806547	NOTEST	0	0	0	0	1	1
ENSG00000259859	ENSG00000259859	RP11-439I14.2	16:64769827-64771183	NOTEST	0	0	0	0	1	1
ENSG00000259861	ENSG00000259861	CTC-471C19.2	5:6030147-6030954	NOTEST	0	0	0	0	1	1
ENSG00000259862	ENSG00000259862	RP11-143E21.6	12:130734223-130751270	NOTEST	0	0	0	0	1	1
ENSG00000259863	ENSG00000259863	SH3RF3-AS1	2:109743782-109745386	NOTEST	0	0.00728714	inf	0	1	1
ENSG00000259864	ENSG00000259864	RP11-370P15.1	16:63737386-63737569	NOTEST	0	0	0	0	1	1
ENSG00000259866	ENSG00000259866	RP11-177N22.2	16:47178233-47735434	NOTEST	0	0	0	0	1	1
ENSG00000259867	ENSG00000259867	RP11-525K10.3	16:80099732-80597032	NOTEST	0	0	0	0	1	1
ENSG00000259868	ENSG00000259868	RP11-1012E15.	14:56382444-56383044	NOTEST	0	0	0	0	1	1
ENSG00000259869	ENSG00000259869	AL022344.7	10:43246625-43247593	NOTEST	0	0	0	0	1	1
ENSG00000259870	ENSG00000259870	RP11-753A21.2	15:98419518-98421616	NOTEST	0	0	0	0	1	1
ENSG00000259871	ENSG00000259871	CTA-363E6.1	16:19297060-19333467	NOTEST	0	0	0	0	1	1
ENSG00000259872	ENSG00000259872	RP11-514P8.2	HG115_PATCH:102070097-102078060	NOTEST	0	0	0	0	1	1
ENSG00000259873	ENSG00000259873	RP11-481E4.1	16:82468432-82468986	NOTEST	0	0	0	0	1	1
ENSG00000259874	ENSG00000259874	RP11-170L3.2	16:31882207-31882445	NOTEST	0	0	0	0	1	1
ENSG00000259875	ENSG00000259875	CTA-313A17.5	HG115_PATCH:101991667-101998642	NOTEST	0	0	0	0	1	1
ENSG00000259876	ENSG00000259876	CTD-3037G24.4	16:12070593-12704901	NOTEST	0	0.0268606	inf	0	1	1
ENSG00000259877	ENSG00000259877	RP11-46C24.7	16:89281637-89284061	NOTEST	0.199614	0.0549249	-1.86168	0	1	1
ENSG00000259878	ENSG00000259878	RP11-1O10.1	15:62520094-62545434	NOTEST	0	0	0	0	1	1
ENSG00000259879	ENSG00000259879	RP11-244N20.7	HG79_PATCH:136214524-136215000	NOTEST	0	0	0	0	1	1
ENSG00000259880	ENSG00000259880	MANF	HG186_PATCH:51422477-51426828	NOTEST	0	0	0	0	1	1
ENSG00000259881	ENSG00000259881	RP11-830F9.5	16:88941265-89043612	NOTEST	0	0	0	0	1	1
ENSG00000259882	ENSG00000259882	RP11-293B20.2	16:33390405-33425011	NOTEST	0	0.00922738	inf	0	1	1
ENSG00000259883	ENSG00000259883	CTD-2382E5.4	15:42190949-42264776	NOTEST	0	0.0597606	inf	0	1	1
ENSG00000259884	ENSG00000259884	RP11-1100L3.8	12:52416615-52453291	NOTEST	0.111874	0.326164	1.54372	0	1	1
ENSG00000259885	ENSG00000259885	SH2B2	HG115_PATCH:101928440-101964991	NOTEST	0	0	0	0	1	1
ENSG00000259887	ENSG00000259887	RP11-923I11.5	12:52242006-52246513	NOTEST	0	0	0	0	1	1
ENSG00000259888	ENSG00000259888	CTD-2540M10.1	16:24621586-24652278	NOTEST	0	0	0	0	1	1
ENSG00000259889	ENSG00000259889	RP11-315F22.1	2:240656649-240657232	NOTEST	0	0	0	0	1	1
ENSG00000259890	ENSG00000259890	DNM1P50	15:30860024-30863292	NOTEST	0	0	0	0	1	1
ENSG00000259891	ENSG00000259891	CTA-204B4.2	8:141515911-141518142	NOTEST	0.359818	0.373716	0.0546728	0	1	1
ENSG00000259892	ENSG00000259892	RP11-1H8.4	15:34671268-34880704	NOTEST	0	0	0	0	1	1
ENSG00000259893	ENSG00000259893	AC073464.6	HG686_PATCH:95514328-95515040	NOTEST	0	0	0	0	1	1
ENSG00000259894	ENSG00000259894	RP11-697E2.4	15:90788644-90789043	NOTEST	0.188108	0.097245	-0.951866	0	1	1
ENSG00000259895	ENSG00000259895	RP11-715J22.2	16:2510080-2518214	NOTEST	0.046158	0.105084	1.18689	0	1	1

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ENSG00000259898	ENSG00000259898	CYP4F33P	9:38540563-38624987	NOTEST	0.279862	0	#NAME?	0	1	1
ENSG00000259899	ENSG00000259899	CTD-3037G24.3	16:12070593-12704901	NOTEST	0.0281864	0.0418786	0.571214	0	1	1
ENSG00000259900	ENSG00000259900	RP11-343C2.7	16:69139466-69442474	NOTEST	0	0.0737669	inf	0	1	1
ENSG00000259902	ENSG00000259902	CTD-3065J16.6	HG104_HG975_PATCH:145131298-145146004	NOTEST	0	0	0	0	1	1
ENSG00000259903	ENSG00000259903	TRBV7-5	HG7_PATCH:142195613-142196085	NOTEST	0	0	0	0	1	1
ENSG00000259904	ENSG00000259904	RP11-602M11.3	15:34665741-34666804	NOTEST	0	0	0	0	1	1
ENSG00000259905	ENSG00000259905	PWRN1	15:24738283-24897277	NOTEST	0	0	0	0	1	1
ENSG00000259906	ENSG00000259906	RP11-932O9.4	15:30462765-30472146	NOTEST	0	0	0	0	1	1
ENSG00000259907	ENSG00000259907	RP6-91H8.2	14:71648172-71648823	NOTEST	0	0	0	0	1	1
ENSG00000259908	ENSG00000259908	RP11-429J17.7	HG104_HG975_PATCH:144840322-144853992	NOTEST	0	0	0	0	1	1
ENSG00000259909	ENSG00000259909	RP11-1006G14.3	15:72931161-72932466	NOTEST	0	0	0	0	1	1
ENSG00000259910	ENSG00000259910	RP11-616M22.2	16:1203240-1275257	NOTEST	0	0	0	0	1	1
ENSG00000259912	ENSG00000259912	CTC-527H23.2	16:48654229-48655944	NOTEST	0	0	0	0	1	1
ENSG00000259913	ENSG00000259913	TRBV7-4	HG7_PATCH:142176672-142177134	NOTEST	0	0	0	0	1	1
ENSG00000259914	ENSG00000259914	RP11-298D21.2	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000259915	ENSG00000259915	RP11-410E4.1	2:187219298-187221500	NOTEST	0.0337853	0.0217353	-0.636356	0	1	1
ENSG00000259916	ENSG00000259916	RP11-407P15.2	HG686_PATCH:95352268-95368320	NOTEST	0	0	0	0	1	1
ENSG00000259919	ENSG00000259919	GALNT9	HG996_PATCH:132680923-132910380	NOTEST	0	0	0	0	1	1
ENSG00000259920	ENSG00000259920	RP11-2E11.5	7:130121331-130124233	NOTEST	0	0	0	0	1	1
ENSG00000259921	ENSG00000259921	AC022819.3	15:99676527-99791428	NOTEST	0.0406013	0.0142354	-1.51205	0	1	1
ENSG00000259922	ENSG00000259922	RP11-322D14.1	16:57023396-57117443	NOTEST	0	0	0	0	1	1
ENSG00000259923	ENSG00000259923	RP11-249C24.11	16:56682159-56687116	NOTEST	0	0	0	0	1	1
ENSG00000259924	ENSG00000259924	RP11-16E23.4	15:65903703-66184329	NOTEST	0.0716683	0	#NAME?	0	1	1
ENSG00000259925	ENSG00000259925	CTA-363E6.2	16:19354968-19413015	NOTEST	0	0	0	0	1	1
ENSG00000259926	ENSG00000259926	RP11-44F14.5	16:53467888-53538323	NOTEST	0	0	0	0	1	1
ENSG00000259927	ENSG00000259927	RPL7P3	HG506_HG507_HG1000_PATCH:61147726-61148440	NOTEST	0	0	0	0	1	1
ENSG00000259928	ENSG00000259928	RP11-218M11.1	17:28891074-28892594	NOTEST	0	0	0	0	1	1
ENSG00000259929	ENSG00000259929	CTA-481E9.4	16:18026576-18266920	NOTEST	0	0	0	0	1	1
ENSG00000259930	ENSG00000259930	HLA-P	HSCHR6_MHC_MCF:29765074-29767083	NOTEST	0	0	0	0	1	1
ENSG00000259931	ENSG00000259931	CTD-2323K18.2	15:75759461-75918810	NOTEST	0	0	0	0	1	1
ENSG00000259932	ENSG00000259932	CTD-2651B20.7	15:45384847-45493373	NOTEST	0	0.0232603	inf	0	1	1
ENSG00000259933	ENSG00000259933	RP11-304L19.1	16:2089815-2185899	NOTEST	0.276718	0.176075	-0.652223	0	1	1
ENSG00000259934	ENSG00000259934	RP11-989E6.1	16:32857284-32857501	NOTEST	0	0	0	0	1	1
ENSG00000259935	ENSG00000259935	RP11-519C12.1	15:52870038-53002014	NOTEST	0	0	0	0	1	1
ENSG00000259937	ENSG00000259937	RP11-438D14.2	12:33527172-33592754	NOTEST	0	0	0	0	1	1
ENSG00000259938	ENSG00000259938	CUX1	HG115_PATCH:101459218-101927238	NOTEST	0	0	0	0	1	1
ENSG00000259939	ENSG00000259939	RP11-77H9.5	16:8768421-8962866	NOTEST	0	0	0	0	1	1

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ENSG00000259941	ENSG00000259941	RP11-48G14.2	15:56536206-56757335	NOTEST	4.27E-05	0	#NAME?	0	1	1
ENSG00000259942	ENSG00000259942	RP11-292F22.7	10:47656083-47657233	NOTEST	0.0427988	0	#NAME?	0	1	1
ENSG00000259944	ENSG00000259944	CDRT7	17:14918121-14955593	NOTEST	0	0	0	0	1	1
ENSG00000259945	ENSG00000259945	CTD-2012K14.3	16:67552320-67580691	NOTEST	0	0	0	0	1	1
ENSG00000259946	ENSG00000259946	RP11-490G2.2	1:98432560-98434370	NOTEST	0	0	0	0	1	1
ENSG00000259947	ENSG00000259947	XX-DJ76P10_A.2	16:1939114-1940435	NOTEST	0	0	0	0	1	1
ENSG00000259950	ENSG00000259950	RP11-170L3.4	16:31885078-31928668	NOTEST	0	0	0	0	1	1
ENSG00000259951	ENSG00000259951	TRBV5-2	HG7_PATCH:142094140-142094414	NOTEST	0	0	0	0	1	1
ENSG00000259953	ENSG00000259953	RP11-4O1.2	9:114794834-114800010	NOTEST	0.101221	0.0621862	-0.702848	0	1	1
ENSG00000259954	ENSG00000259954	IL21R-AS1	16:27413482-27464714	NOTEST	0	0.0146459	inf	0	1	1
ENSG00000259955	ENSG00000259955	CTD-2547G23.2	16:25247321-25269252	NOTEST	0	0.0158615	inf	0	1	1
ENSG00000259956	ENSG00000259956	RBM15B	HG186_PATCH:51428698-51537425	NOTEST	0	0	0	0	1	1
ENSG00000259957	ENSG00000259957	RP11-491F9.8	16:49328796-49330647	NOTEST	0	0	0	0	1	1
ENSG00000259958	ENSG00000259958	KAT2A	HG185_PATCH:40269359-40277610	NOTEST	0	0	0	0	1	1
ENSG00000259959	ENSG00000259959	RP11-121C2.2	4:47842138-47846356	NOTEST	0.208637	0.145786	-0.517147	0	1	1
ENSG00000259960	ENSG00000259960	TRBJ2-2P	HG7_PATCH:142557589-142557635	NOTEST	0	0	0	0	1	1
ENSG00000259961	ENSG00000259961	RP4-597A16.2	1:13801444-13842765	NOTEST	0	0	0	0	1	1
ENSG00000259962	ENSG00000259962	RP11-44F14.4	16:53395930-53397590	NOTEST	0	0	0	0	1	1
ENSG00000259963	ENSG00000259963	RP11-185J20.2	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000259964	ENSG00000259964	RP11-673C5.2	15:71389290-72075722	NOTEST	0	0	0	0	1	1
ENSG00000259965	ENSG00000259965	CTA-313A17.3	HG115_PATCH:101980595-101982395	NOTEST	0	0	0	0	1	1
ENSG00000259966	ENSG00000259966	RP11-652G5.1	16:32611619-32626960	NOTEST	0	0	0	0	1	1
ENSG00000259967	ENSG00000259967	RP11-2E17.2	15:80444831-80479288	NOTEST	0.0715501	0.123296	0.785096	0	1	1
ENSG00000259968	ENSG00000259968	RP11-428C6.2	5:73248764-73249839	NOTEST	0	0	0	0	1	1
ENSG00000259970	ENSG00000259970	AC099668.5	3:49711434-49761384	NOTEST	0.455686	0.177141	-1.36314	0	1	1
ENSG00000259971	ENSG00000259971	RP11-44L9.3	16:73545074-73545553	NOTEST	0	0	0	0	1	1
ENSG00000259972	ENSG00000259972	AC009120.6	16:74330672-74403724	NOTEST	0.294141	0.304844	0.0515658	0	1	1
ENSG00000259973	ENSG00000259973	IL9RP2	HG905_PATCH:130393-136265	NOTEST	0	0	0	0	1	1
ENSG00000259974	ENSG00000259974	LINC00261	20:22528308-22559280	NOTEST	0	0	0	0	1	1
ENSG00000259977	ENSG00000259977	AL121578.2	X:37208527-38548169	NOTEST	0	0	0	0	1	1
ENSG00000259978	ENSG00000259978	MRPS21P8	16:49521434-49891830	NOTEST	0	0	0	0	1	1
ENSG00000259979	ENSG00000259979	VN1R68P	16:34352608-34353327	NOTEST	0.027106	0	#NAME?	0	1	1
ENSG00000259980	ENSG00000259980	MRPL45	HG745_PATCH:36452988-36479101	NOTEST	0	0	0	0	1	1
ENSG00000259981	ENSG00000259981	AF096876.1	21:31462034-31470154	NOTEST	0	0	0	0	1	1
ENSG00000259982	ENSG00000259982	CDC37P1	16:28671016-28752102	NOTEST	0.0533167	0.0265716	-1.0047	0	1	1
ENSG00000259983	ENSG00000259983	RP11-169E6.3	16:47038423-47069296	NOTEST	0	0	0	0	1	1
ENSG00000259984	ENSG00000259984	RP11-335G20.7	1:25568727-25756683	NOTEST	0.418825	0.257344	-0.702646	0	1	1
ENSG00000259986	ENSG00000259986	RP11-382A20.4	15:83776158-84108197	NOTEST	0	0	0	0	1	1
ENSG00000259987	ENSG00000259987	CTD-2522B17.4	16:33943722-33944473	NOTEST	0	0	0	0	1	1

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ENSG00000259989	ENSG00000259989	CTD-2555A7.1	16:89050439-89061777	NOTEST	0	0	0	0	1	1
ENSG00000259990	ENSG00000259990	RP11-598D12.1	16:33815860-33816297	NOTEST	0	0	0	0	1	1
ENSG00000259991	ENSG00000259991	OR4C13	HG281_PATCH:49973942-49974971	NOTEST	0	0	0	0	1	1
ENSG00000259992	ENSG00000259992	RP11-77K12.8	16:75562429-75657198	NOTEST	0	0	0	0	1	1
ENSG00000259993	ENSG00000259993	RP11-261B23.1	15:30515219-30517767	NOTEST	0.0113005	0.0278079	1.29911	0	1	1
ENSG00000259994	ENSG00000259994	RP11-305E6.4	10:30591754-30594995	NOTEST	0.227848	0.149259	-0.61026	0	1	1
ENSG00000259995	ENSG00000259995	CTD-2336H13.2	16:76770238-76962066	NOTEST	0	0	0	0	1	1
ENSG00000259996	ENSG00000259996	RARRES2P8	16:34777649-34778016	NOTEST	0	0	0	0	1	1
ENSG00000259997	ENSG00000259997	IGHV1OR16-4	16:32963313-33039358	NOTEST	0	0	0	0	1	1
ENSG00000259998	ENSG00000259998	RP11-753D20.4	14:88603076-88626935	NOTEST	0	0	0	0	1	1
ENSG00000259999	ENSG00000259999	RP11-252K23.1	16:75327595-75499395	NOTEST	0	0	0	0	1	1
ENSG00000260000	ENSG00000260000	RP3-467N11.1	6:101329346-101330863	NOTEST	0.110339	0.122985	0.156543	0	1	1
ENSG00000260001	ENSG00000260001	TGFBR3L	19:7981029-7984042	NOTEST	0.471744	0.569797	0.272444	0	1	1
ENSG00000260002	ENSG00000260002	RP11-1049H7.2	HG19_PATCH:1981649-1983729	NOTEST	0	0	0	0	1	1
ENSG00000260003	ENSG00000260003	RP11-279O17.2	16:8326264-8345702	NOTEST	0	0	0	0	1	1
ENSG00000260004	ENSG00000260004	RP11-351A20.2	16:65614570-65680850	NOTEST	0	0	0	0	1	1
ENSG00000260005	ENSG00000260005	AC027601.1	17:79202076-79212891	NOTEST	0.250878	0.287028	0.194203	0	1	1
ENSG00000260006	ENSG00000260006	RP11-469M7.1	2:201689395-201692061	NOTEST	0.160065	0.26059	0.703119	0	1	1
ENSG00000260007	ENSG00000260007	RP11-315D16.2	15:68346516-68549549	NOTEST	0	0.279285	inf	0	1	1
ENSG00000260008	ENSG00000260008	RP11-732A21.2	11:101978616-101980573	NOTEST	0	0.0200459	inf	0	1	1
ENSG00000260009	ENSG00000260009	RP11-65J21.1	16:14456965-14464123	NOTEST	0	0	0	0	1	1
ENSG00000260010	ENSG00000260010	ZNF720P1	16:31612913-31614852	NOTEST	0	0	0	0	1	1
ENSG00000260011	ENSG00000260011	RP13-20L14.1	17:80338985-80340566	NOTEST	0	0	0	0	1	1
ENSG00000260012	ENSG00000260012	RP11-329J18.4	16:47178233-47735434	NOTEST	0	0	0	0	1	1
ENSG00000260013	ENSG00000260013	APOOP5	16:59743896-59788930	NOTEST	0	0	0	0	1	1
ENSG00000260014	ENSG00000260014	LSM3P5	16:78133309-79246564	NOTEST	0	0	0	0	1	1
ENSG00000260015	ENSG00000260015	RP11-510M2.5	16:71481499-71598992	NOTEST	0	0	0	0	1	1
ENSG00000260016	ENSG00000260016	LINC01054	HG531_PATCH:115095033-115099423	NOTEST	0	0	0	0	1	1
ENSG00000260017	ENSG00000260017	RP11-1035H13.2	16:18814404-18937776	NOTEST	0	0.175097	inf	0	1	1
ENSG00000260019	ENSG00000260019	RP11-218F4.1	17:26256573-26301249	NOTEST	0.0127048	0.0286898	1.17517	0	1	1
ENSG00000260020	ENSG00000260020	U85056.3	HG1032_PATCH:190986385-190987070	NOTEST	0	0	0	0	1	1
ENSG00000260021	ENSG00000260021	RP11-480I12.10	1:202779365-202779957	NOTEST	0	0.0524641	inf	0	1	1
ENSG00000260022	ENSG00000260022	LA16c-306A4.1	16:903633-1031663	NOTEST	0.0413773	0.0322349	-0.360218	0	1	1
ENSG00000260023	ENSG00000260023	RP11-49C24.1	16:70610203-70611571	NOTEST	0.506314	0.245268	-1.04567	0	1	1
ENSG00000260024	ENSG00000260024	MRPS21P7	16:49521434-49891830	NOTEST	0	0	0	0	1	1
ENSG00000260025	ENSG00000260025	RP11-490M8.1	2:36581891-36582257	NOTEST	0.075918	0.0543802	-0.481359	0	1	1
ENSG00000260026	ENSG00000260026	CTD-2015G9.1	16:86754293-86755560	NOTEST	0	0	0	0	1	1
ENSG00000260027	ENSG00000260027	HOXB7	17:46684593-46712294	NOTEST	0.0124596	0.145337	3.54407	0	1	1

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ENSG00000260030	ENSG00000260030	RP11-686F15.2	12:54148141-54155888	NOTEST	0	0	0	0	1	1
ENSG00000260031	ENSG00000260031	RPL10P14	16:50185190-50185488	NOTEST	0	0	0	0	1	1
ENSG00000260033	ENSG00000260033	CTC-527H23.1	16:48572636-48654059	NOTEST	0	0	0	0	1	1
ENSG00000260034	ENSG00000260034	RP11-266L9.2	16:25123049-25189552	NOTEST	0.090847	0.165517	0.865465	0	1	1
ENSG00000260035	ENSG00000260035	CTD-2651B20.6	15:45384847-45493373	NOTEST	0	0	0	0	1	1
ENSG00000260036	ENSG00000260036	RP11-178D12.2	15:55495163-55800432	NOTEST	0	0	0	0	1	1
ENSG00000260037	ENSG00000260037	CTD-2524L6.3	15:72110736-72447800	NOTEST	0.212379	0.078173	-1.4419	0	1	1
ENSG00000260038	ENSG00000260038	RP11-407G23.4	16:57279009-57287516	NOTEST	0	0	0	0	1	1
ENSG00000260039	ENSG00000260039	TNRC18P3	HG736_PATCH:57059580-57076842	NOTEST	0	0	0	0	1	1
ENSG00000260040	ENSG00000260040	KEL	HG7_PATCH:142701709-142723277	NOTEST	0	0	0	0	1	1
ENSG00000260041	ENSG00000260041	RP11-355E10.1	16:56126898-56225006	NOTEST	0	0	0	0	1	1
ENSG00000260042	ENSG00000260042	CTD-2034I21.1	16:50890524-50913189	NOTEST	0	0	0	0	1	1
ENSG00000260045	ENSG00000260045	STAM	HG544_PATCH:17686123-17757913	NOTEST	0	0	0	0	1	1
ENSG00000260046	ENSG00000260046	RP11-454K7.3	14:45838417-45840042	NOTEST	0	0	0	0	1	1
ENSG00000260047	ENSG00000260047	RP11-989E6.2	16:32881305-32883370	NOTEST	0.302271	0.0618295	-2.28948	0	1	1
ENSG00000260048	ENSG00000260048	IGHV1OR16-3	16:32019758-32096106	NOTEST	0	0	0	0	1	1
ENSG00000260049	ENSG00000260049	RP3-404K8.2	6:22260652-22318027	NOTEST	0	0	0	0	1	1
ENSG00000260050	ENSG00000260050	TRBV20-1	HG7_PATCH:142368230-142368981	NOTEST	0	0	0	0	1	1
ENSG00000260052	ENSG00000260052	CTC-527H23.3	16:48657346-48778553	NOTEST	0.386336	0.16045	-1.26774	0	1	1
ENSG00000260053	ENSG00000260053	ABCB10P4	15:28751770-28753954	NOTEST	0	0	0	0	1	1
ENSG00000260055	ENSG00000260055	HLA-P	HSCHR6_MHC_COX:29761889-29763899	NOTEST	0	0	0	0	1	1
ENSG00000260056	ENSG00000260056	RP11-429J17.5	HG104_HG975_PATCH:144798428-144804628	NOTEST	0	0	0	0	1	1
ENSG00000260057	ENSG00000260057	RP11-7O14.1	16:51796429-51807084	NOTEST	0	0	0	0	1	1
ENSG00000260058	ENSG00000260058	RP11-279O17.3	16:8359963-8407862	NOTEST	0	0	0	0	1	1
ENSG00000260059	ENSG00000260059	RP11-231E19.1	2:139357232-139359996	NOTEST	0	0.00444948	inf	0	1	1
ENSG00000260060	ENSG00000260060	RP11-388M20.1	16:31207451-31208284	NOTEST	0.127054	0.0699838	-0.860351	0	1	1
ENSG00000260061	ENSG00000260061	RP11-163O19.3	HG281_PATCH:49904550-49904926	NOTEST	0	0	0	0	1	1
ENSG00000260062	ENSG00000260062	RP11-299H22.5	15:62545928-62562879	NOTEST	0	0.0159198	inf	0	1	1
ENSG00000260063	ENSG00000260063	RP5-968P14.2	1:27018622-27020622	NOTEST	0.100962	0.117352	0.217036	0	1	1
ENSG00000260064	ENSG00000260064	RP11-18F14.4	16:80631802-80838226	NOTEST	0	0	0	0	1	1
ENSG00000260065	ENSG00000260065	CTA-445C9.15	22:26917948-26921002	NOTEST	0.165022	0.244321	0.566118	0	1	1
ENSG00000260066	ENSG00000260066	CTD-2587M23.1	5:1725263-1728287	NOTEST	0	0	0	0	1	1
ENSG00000260067	ENSG00000260067	RP11-98C8.1	16:49100477-49100640	NOTEST	0	0	0	0	1	1
ENSG00000260068	ENSG00000260068	RP11-439I14.3	16:64772225-64772467	NOTEST	0	0	0	0	1	1
ENSG00000260069	ENSG00000260069	TBC1D3B	HG75_PATCH:34443569-34504870	NOTEST	0	0	0	0	1	1
ENSG00000260070	ENSG00000260070	RP11-182J23.1	7:36359383-36360088	NOTEST	0	0	0	0	1	1
ENSG00000260071	ENSG00000260071	RP11-418I22.2	16:9560511-9611421	NOTEST	0	0	0	0	1	1

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ENSG00000260073	ENSG00000260073	RP11-488I20.9	16:34427060-34430032	NOTEST	0	0	0	0	1	1
ENSG00000260074	ENSG00000260074	TRBV6-9	HG7_PATCH:142248909-142249342	NOTEST	0	0	0	0	1	1
ENSG00000260076	ENSG00000260076	TRBV23-1	HG7_PATCH:142387532-142388029	NOTEST	0	0	0	0	1	1
ENSG00000260078	ENSG00000260078	RP11-44F14.1	16:53398893-53406995	NOTEST	0	0	0	0	1	1
ENSG00000260079	ENSG00000260079	OR4C48P	HG281_PATCH:50040321-50041219	NOTEST	0	0	0	0	1	1
ENSG00000260080	ENSG00000260080	TRBV7-3	HG7_PATCH:142105844-142106351	NOTEST	0	0	0	0	1	1
ENSG00000260082	ENSG00000260082	RP11-2C24.5	16:30832388-30833431	NOTEST	0	0	0	0	1	1
ENSG00000260083	ENSG00000260083	MIR4519	16:30844946-30906541	NOTEST	0.383783	0.169563	-1.17847	0	1	1
ENSG00000260084	ENSG00000260084	RP11-615I2.1	16:68563992-68623415	NOTEST	0.0733146	0	#NAME?	0	1	1
ENSG00000260087	ENSG00000260087	PCMTD1P2	16:33941655-33942010	NOTEST	0	0	0	0	1	1
ENSG00000260088	ENSG00000260088	RP11-92G12.3	1:200593023-200663378	NOTEST	0	0.0204557	inf	0	1	1
ENSG00000260089	ENSG00000260089	ADAM3B	16:49521434-49891830	NOTEST	0	0	0	0	1	1
ENSG00000260090	ENSG00000260090	RP11-292D4.3	4:147926643-147930297	NOTEST	0	0	0	0	1	1
ENSG00000260091	ENSG00000260091	RP11-33B1.4	4:120330487-120331388	NOTEST	0.443531	0.254735	-0.800038	0	1	1
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ENSG00000260093	ENSG00000260093	RP11-1E4.1	8:9907994-9911764	NOTEST	0.0041263	0.0298318	2.85393	0	1	1
ENSG00000260094	ENSG00000260094	LINC00564	13:81799999-81801118	NOTEST	0	0	0	0	1	1
ENSG00000260095	ENSG00000260095	RP11-715J22.3	16:2479394-2509980	NOTEST	0.517907	0.102452	-2.33775	0	1	1
ENSG00000260096	ENSG00000260096	DNM1P33	15:74355120-74356126	NOTEST	0	0	0	0	1	1
ENSG00000260097	ENSG00000260097	SPDYE6	HG115_PATCH:101991667-101998642	NOTEST	0	0	0	0	1	1
ENSG00000260099	ENSG00000260099	ADAMTS13	HG79_PATCH:136251901-136334921	NOTEST	0	0	0	0	1	1
ENSG00000260100	ENSG00000260100	RP11-220I1.5	9:37078809-37079773	NOTEST	0	0.0412714	inf	0	1	1
ENSG00000260101	ENSG00000260101	RP11-568N6.1	2:64749320-64751227	NOTEST	0.0171097	0.0386596	1.17601	0	1	1
ENSG00000260102	ENSG00000260102	LINC01070	13:112851663-112855314	NOTEST	0	0	0	0	1	1
ENSG00000260103	ENSG00000260103	RP11-10O17.1	15:74753605-74809300	NOTEST	0.234126	0.116277	-1.00972	0	1	1
ENSG00000260104	ENSG00000260104	RP11-817O13.1	15:75541572-75541748	NOTEST	0	0	0	0	1	1
ENSG00000260105	ENSG00000260105	AOC4P	17:41017938-41026386	NOTEST	0	0	0	0	1	1
ENSG00000260106	ENSG00000260106	TRBV5-6	HG7_PATCH:142221544-142222051	NOTEST	0	0	0	0	1	1
ENSG00000260107	ENSG00000260107	AC005606.15	16:2047654-2059824	NOTEST	0.0712866	0	#NAME?	0	1	1
ENSG00000260108	ENSG00000260108	RP11-140H17.1	16:69458427-69500169	NOTEST	0	0	0	0	1	1
ENSG00000260109	ENSG00000260109	RP11-883G10.1	15:68277396-68278626	NOTEST	0	0	0	0	1	1
ENSG00000260111	ENSG00000260111	RP11-529K1.4	16:70413337-70473140	NOTEST	0	0	0	0	1	1
ENSG00000260112	ENSG00000260112	CTC-543D15.1	19:9628825-9630017	NOTEST	0	0	0	0	1	1
ENSG00000260113	ENSG00000260113	RP11-146F11.2	16:30638296-30638499	NOTEST	0	0	0	0	1	1
ENSG00000260115	ENSG00000260115	CTC-420A11.2	16:61681145-62070939	NOTEST	0	0	0	0	1	1
ENSG00000260116	ENSG00000260116	TRBV6-6	HG7_PATCH:142191055-142191532	NOTEST	0	0	0	0	1	1
ENSG00000260117	ENSG00000260117	CHAMP1	HG531_PATCH:115079987-115092796	NOTEST	0	0	0	0	1	1
ENSG00000260118	ENSG00000260118	RP6-201G10.2	X:67233311-67234743	NOTEST	0.0235555	0.0183083	-0.363568	0	1	1
ENSG00000260119	ENSG00000260119	TRPV6	HG7_PATCH:142632168-142653708	NOTEST	0	0	0	0	1	1
ENSG00000260120	ENSG00000260120	RP11-177B4.2	4:53546775-53558816	NOTEST	0	0	0	0	1	1
ENSG00000260121	ENSG00000260121	RP5-1142A6.9	16:88772870-88851619	NOTEST	0.429561	0.288965	-0.57197	0	1	1

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ENSG00000260123	ENSG00000260123	RP11-326A19.4	15:89584453-89626050	NOTEST	0	0.0246948	inf	0	1	1
ENSG00000260125	ENSG00000260125	AGBL1-AS1	15:86685226-87572283	NOTEST	0	0	0	0	1	1
ENSG00000260126	ENSG00000260126	RP11-14N9.2	16:16752083-16757992	NOTEST	0	0	0	0	1	1
ENSG00000260128	ENSG00000260128	ULK4P2	15:30864940-30892918	NOTEST	0.0246739	0.136862	2.47166	0	1	1
ENSG00000260129	ENSG00000260129	DUX4L3	HG1032_PATCH:191008859-191010142	NOTEST	0	0	0	0	1	1
ENSG00000260130	ENSG00000260130	MYOM2	HG19_PATCH:1993154-2142890	NOTEST	0	0	0	0	1	1
ENSG00000260131	ENSG00000260131	LINC00556	13:20755669-20756081	NOTEST	0	0	0	0	1	1
ENSG00000260132	ENSG00000260132	LA16c-312E8.2	16:1401923-1464752	NOTEST	0.341957	0.215412	-0.666712	0	1	1
ENSG00000260133	ENSG00000260133	CA5AP1	16:29630105-29647649	NOTEST	0	0	0	0	1	1
ENSG00000260134	ENSG00000260134	RP11-14K3.2	16:34809204-34809865	NOTEST	0	0	0	0	1	1
ENSG00000260135	ENSG00000260135	RP11-212I21.2	16:55423611-55540603	NOTEST	0	0	0	0	1	1
ENSG00000260137	ENSG00000260137	RP11-258F22.2	10:38080507-38080865	NOTEST	0	0	0	0	1	1
ENSG00000260138	ENSG00000260138	AC073464.7	HG686_PATCH:95524520-95524863	NOTEST	0	0	0	0	1	1
ENSG00000260139	ENSG00000260139	CSPG4P13	15:78187025-78197016	NOTEST	0.31484	0.572375	0.862343	0	1	1
ENSG00000260142	ENSG00000260142	RP11-764E7.1	2:194763090-194764118	NOTEST	0.0173309	0	#NAME?	0	1	1
ENSG00000260143	ENSG00000260143	TRBV13	HG7_PATCH:142277447-142277943	NOTEST	0	0	0	0	1	1
ENSG00000260144	ENSG00000260144	RP11-361M10.3	15:72897523-72929260	NOTEST	0.0264263	0	#NAME?	0	1	1
ENSG00000260145	ENSG00000260145	RP11-322D14.2	16:57023396-57117443	NOTEST	0	0	0	0	1	1
ENSG00000260146	ENSG00000260146	CTD-2258A20.3	16:66461199-66586447	NOTEST	0	0.0579642	inf	0	1	1
ENSG00000260147	ENSG00000260147	CTD-3032H12.3	16:55041893-55042218	NOTEST	0	0	0	0	1	1
ENSG00000260148	ENSG00000260148	RP11-407G23.1	16:57125124-57126215	NOTEST	0	0	0	0	1	1
ENSG00000260150	ENSG00000260150	ZMYND11	HG905_PATCH:184464-304637	NOTEST	0	0	0	0	1	1
ENSG00000260151	ENSG00000260151	RP11-748L13.6	10:27632364-27633846	NOTEST	0	0	0	0	1	1
ENSG00000260152	ENSG00000260152	RP11-69H7.4	15:75315895-75409803	NOTEST	0	0	0	0	1	1
ENSG00000260153	ENSG00000260153	RP11-80F22.7	16:34720136-34720596	NOTEST	0.0513826	0	#NAME?	0	1	1
ENSG00000260155	ENSG00000260155	DUX4L7	HG1032_PATCH:190992386-190993946	NOTEST	0	0	0	0	1	1
ENSG00000260156	ENSG00000260156	RP11-394B2.6	16:70721341-70835064	NOTEST	0	0.0304463	inf	0	1	1
ENSG00000260157	ENSG00000260157	NCOR1P2	HG987_PATCH:21536036-21544675	NOTEST	0	0	0	0	1	1
ENSG00000260159	ENSG00000260159	RP11-483E23.4	15:28699805-28702929	NOTEST	0	0.0196204	inf	0	1	1
ENSG00000260160	ENSG00000260160	CTC-471J1.2	19:52534631-52599018	NOTEST	0.196963	0.15063	-0.386912	0	1	1
ENSG00000260161	ENSG00000260161	CTD-2588J6.1	16:82068608-82173236	NOTEST	0.015455	0	#NAME?	0	1	1
ENSG00000260162	ENSG00000260162	RP11-863P13.1	16:88210894-88219696	NOTEST	0	0	0	0	1	1
ENSG00000260163	ENSG00000260163	RP11-521O16.2	2:127781827-127787262	NOTEST	0	0	0	0	1	1
ENSG00000260164	ENSG00000260164	MYO19	HG75_PATCH:34814004-34869611	NOTEST	0	0	0	0	1	1
ENSG00000260165	ENSG00000260165	CTD-2323K18.3	15:75759461-75918810	NOTEST	0	0	0	0	1	1
ENSG00000260166	ENSG00000260166	RP11-863P13.6	16:88120992-88121538	NOTEST	0	0	0	0	1	1
ENSG00000260167	ENSG00000260167	RP11-146F11.5	16:30597227-30635333	NOTEST	0	0.033949	inf	0	1	1
ENSG00000260168	ENSG00000260168	TRBV1	HG7_PATCH:141999016-141999300	NOTEST	0	0	0	0	1	1
ENSG00000260169	ENSG00000260169	RP11-163O19.11	HG281_PATCH:49872180-49884080	NOTEST	0	0	0	0	1	1

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ENSG00000260171	ENSG00000260171	RP11-95H11.1	2:207685913-207687018	NOTEST	0	0	0	0	1	1
ENSG00000260172	ENSG00000260172	RP11-358M11.3	15:57611335-57616106	NOTEST	0	0	0	0	1	1
ENSG00000260173	ENSG00000260173	RP11-2I17.4	15:72110736-72447800	NOTEST	0	0	0	0	1	1
ENSG00000260174	ENSG00000260174	CTD-2022H16.3	15:30297407-30338051	NOTEST	0	0	0	0	1	1
ENSG00000260176	ENSG00000260176	CTD-3126B10.4	16:2694084-2695215	NOTEST	0	0	0	0	1	1
ENSG00000260177	ENSG00000260177	RP4-536B24.3	16:87813739-87840082	NOTEST	0	0	0	0	1	1
ENSG00000260178	ENSG00000260178	DHX58	HG185_PATCH:40257655-40268985	NOTEST	0	0	0	0	1	1
ENSG00000260179	ENSG00000260179	RP5-902P8.12	1:1185156-1186714	NOTEST	0.0602823	0.0901691	0.580899	0	1	1
ENSG00000260181	ENSG00000260181	SURF4	HG79_PATCH:136236983-136251634	NOTEST	0	0	0	0	1	1
ENSG00000260182	ENSG00000260182	RP11-616M22.5	16:1306059-1308532	NOTEST	0	0	0	0	1	1
ENSG00000260183	ENSG00000260183	RP11-109P11.1	16:80099732-80597032	NOTEST	0	0	0	0	1	1
ENSG00000260184	ENSG00000260184	RP11-42I10.3	16:48883829-48883926	NOTEST	0	0	0	0	1	1
ENSG00000260185	ENSG00000260185	RP11-432I5.6	16:71657610-71758604	NOTEST	0	0.0566318	inf	0	1	1
ENSG00000260186	ENSG00000260186	RP11-481J2.2	16:58455229-58496374	NOTEST	0	0	0	0	1	1
ENSG00000260187	ENSG00000260187	RP11-439I14.1	16:64769827-64771183	NOTEST	0	0	0	0	1	1
ENSG00000260188	ENSG00000260188	CTA-331P3.1	6:110799109-110800639	NOTEST	0	0	0	0	1	1
ENSG00000260189	ENSG00000260189	EXOSC4	HG104_HG975_PATCH:145160173-145162819	NOTEST	0	0	0	0	1	1
ENSG00000260190	ENSG00000260190	RP11-229P13.25	9:139831620-139832440	NOTEST	0.0686599	0.0875411	0.350491	0	1	1
ENSG00000260191	ENSG00000260191	AL672296.1	HG999_2_PATCH:249074512-249076670	NOTEST	0	0	0	0	1	1
ENSG00000260192	ENSG00000260192	RP11-756H20.1	5:124828953-124937920	NOTEST	0	0	0	0	1	1
ENSG00000260193	ENSG00000260193	RP11-83N9.5	9:138999653-139001270	NOTEST	0.46877	0.233833	-1.00341	0	1	1
ENSG00000260194	ENSG00000260194	RP11-357N13.2	16:53737874-54155853	NOTEST	0	0	0	0	1	1
ENSG00000260195	ENSG00000260195	EPHB6	HG7_PATCH:142615935-142632056	NOTEST	0	0	0	0	1	1
ENSG00000260196	ENSG00000260196	RP1-239B22.5	11:17402195-17405078	NOTEST	0.35446	0.528676	0.576759	0	1	1
ENSG00000260197	ENSG00000260197	RP11-424G14.1	Y:21853826-21856492	NOTEST	0	0	0	0	1	1
ENSG00000260198	ENSG00000260198	RP11-441F2.2	16:56225301-56391356	NOTEST	0.0520262	0.042483	-0.292354	0	1	1
ENSG00000260199	ENSG00000260199	CCL3L3	HG75_PATCH:34522244-34524134	NOTEST	0	0	0	0	1	1
ENSG00000260201	ENSG00000260201	RP11-143N13.2	16:20592209-20618429	NOTEST	0	0	0	0	1	1
ENSG00000260202	ENSG00000260202	RP3-333B15.4	20:23497520-23498706	NOTEST	0	0	0	0	1	1
ENSG00000260204	ENSG00000260204	TRBV18	HG7_PATCH:142357298-142357998	NOTEST	0	0	0	0	1	1
ENSG00000260205	ENSG00000260205	RP11-108B14.5	10:22507002-22510097	NOTEST	0	0	0	0	1	1
ENSG00000260206	ENSG00000260206	CTD-2026K11.2	15:75928479-75954642	NOTEST	0	0	0	0	1	1
ENSG00000260207	ENSG00000260207	CTD-2522B17.6	16:33944922-33945316	NOTEST	0	0	0	0	1	1
ENSG00000260209	ENSG00000260209	RP11-680F20.10	11:125742925-125744423	NOTEST	0.410709	0.216043	-0.926797	0	1	1
ENSG00000260211	ENSG00000260211	RP13-395E19.2	15:32605326-32607855	NOTEST	0	0	0	0	1	1
ENSG00000260212	ENSG00000260212	RP11-325O24.5	6:127980568-127981724	NOTEST	0	0	0	0	1	1

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ENSG00000260215	ENSG00000260215	TRBV12-1	HG7_PATCH:142136730-142137173	NOTEST	0	0	0	0	1	1
ENSG00000260216	ENSG00000260216	TRBV7-6	HG7_PATCH:142213647-142214185	NOTEST	0	0	0	0	1	1
ENSG00000260217	ENSG00000260217	RP11-809F4.3	3:175656716-175658825	NOTEST	0	0	0	0	1	1
ENSG00000260218	ENSG00000260218	RP11-170L3.6	16:31973383-31985682	NOTEST	0	0	0	0	1	1
ENSG00000260219	ENSG00000260219	RP11-347C12.10	16:30366761-30367848	NOTEST	0.236321	0.368213	0.639794	0	1	1
ENSG00000260220	ENSG00000260220	WI2-2610K16.1	HG998_1_PATCH:139173225-139198747	NOTEST	0	0	0	0	1	1
ENSG00000260221	ENSG00000260221	HLA-P	HSCHR6_MHC_SSTO:29764889-29766920	NOTEST	0	0	0	0	1	1
ENSG00000260222	ENSG00000260222	TRBV3-1	HG7_PATCH:142008364-142008871	NOTEST	0	0	0	0	1	1
ENSG00000260223	ENSG00000260223	RP11-293N14.1	16:76141180-76181704	NOTEST	0	0	0	0	1	1
ENSG00000260224	ENSG00000260224	UBL5P4	16:12021229-12070500	NOTEST	0	0	0	0	1	1
ENSG00000260225	ENSG00000260225	PCDHB2	HG1082_HG167_PATCH:140474227-140476963	NOTEST	0	0	0	0	1	1
ENSG00000260226	ENSG00000260226	GPAA1	HG104_HG975_PATCH:145164761-145168388	NOTEST	0	0	0	0	1	1
ENSG00000260227	ENSG00000260227	TRBV5-1	HG7_PATCH:142020495-142021363	NOTEST	0	0	0	0	1	1
ENSG00000260228	ENSG00000260228	RP11-483P21.2	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000260229	ENSG00000260229	RP11-391L3.5	16:81478774-81745367	NOTEST	0	0	0	0	1	1
ENSG00000260230	ENSG00000260230	FRRS1L	9:111892572-111929571	NOTEST	0.021473	0.0518825	1.27272	0	1	1
ENSG00000260231	ENSG00000260231	JHDM1D-AS1	7:139877060-139879440	NOTEST	0.578785	0.500281	-0.210288	0	1	1
ENSG00000260232	ENSG00000260232	PWRN4	15:24220318-24248582	NOTEST	0	0	0	0	1	1
ENSG00000260234	ENSG00000260234	RP11-166N6.3	3:150570270-150798513	NOTEST	0	0	0	0	1	1
ENSG00000260235	ENSG00000260235	CTD-2026K11.3	15:75759461-75918810	NOTEST	0	0	0	0	1	1
ENSG00000260236	ENSG00000260236	RP11-708J19.1	3:47420578-47422489	NOTEST	0.326958	0.305612	-0.0974063	0	1	1
ENSG00000260237	ENSG00000260237	RP11-148M9.1	16:80074558-80079642	NOTEST	0	0	0	0	1	1
ENSG00000260239	ENSG00000260239	RP11-274H24.1	6:4492040-4496003	NOTEST	0	0	0	0	1	1
ENSG00000260240	ENSG00000260240	RP11-105C20.2	16:59743896-59788930	NOTEST	0	0	0	0	1	1
ENSG00000260241	ENSG00000260241	TRBV11-2	HG7_PATCH:142155393-142155893	NOTEST	0	0	0	0	1	1
ENSG00000260242	ENSG00000260242	CTA-481E9.3	16:18026576-18266920	NOTEST	0	0	0	0	1	1
ENSG00000260244	ENSG00000260244	RP11-588K22.2	4:156655599-156658214	NOTEST	0.0402079	0	#NAME?	0	1	1
ENSG00000260245	ENSG00000260245	ACLY	HG185_PATCH:40023159-40075239	NOTEST	0	0	0	0	1	1
ENSG00000260246	ENSG00000260246	AC000032.2	1:110210643-110252171	NOTEST	0	0	0	0	1	1
ENSG00000260247	ENSG00000260247	SUB1P4	16:23533334-23585710	NOTEST	0	0	0	0	1	1
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ENSG00000260249	ENSG00000260249	RP11-401P9.5	16:50700121-50715264	NOTEST	0	0	0	0	1	1
ENSG00000260250	ENSG00000260250	U66061.39	HG7_PATCH:142511505-142515082	NOTEST	0	0	0	0	1	1
ENSG00000260251	ENSG00000260251	RP11-46D6.4	16:46607674-46609006	NOTEST	0	0	0	0	1	1
ENSG00000260252	ENSG00000260252	RP11-384M15.3	16:72078187-72210777	NOTEST	0	0	0	0	1	1
ENSG00000260253	ENSG00000260253	RP4-676L2.1	8:29209936-29210687	NOTEST	0.192268	0.428422	1.15592	0	1	1
ENSG00000260254	ENSG00000260254	AP000997.2	11:115509280-115517680	NOTEST	0	0	0	0	1	1
ENSG00000260255	ENSG00000260255	RP11-185O21.1	16:25703346-26149009	NOTEST	0	0	0	0	1	1
ENSG00000260256	ENSG00000260256	AP001063.1	21:45767649-45768178	NOTEST	0	0	0	0	1	1

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ENSG00000260259	ENSG00000260259	RP11-368I7.4	16:89747144-89768113	NOTEST	0.0540151	0.210609	1.96313	0	1	1
ENSG00000260262	ENSG00000260262	RP11-440L14.3	4:830299-831012	NOTEST	0	0	0	0	1	1
ENSG00000260264	ENSG00000260264	AC004125.3	16:24247424-24264184	NOTEST	0	0	0	0	1	1
ENSG00000260265	ENSG00000260265	RP11-44F21.5	4:76006911-76009927	NOTEST	0	0	0	0	1	1
ENSG00000260266	ENSG00000260266	CTD-2311M21.2	15:74630099-74660081	NOTEST	0	0	0	0	1	1
ENSG00000260268	ENSG00000260268	LINC00919	16:52116976-52119021	NOTEST	0	0.00759421	inf	0	1	1
ENSG00000260271	ENSG00000260271	RP1-45N11.1	6:91054937-91072351	NOTEST	0	0	0	0	1	1
ENSG00000260272	ENSG00000260272	RP11-20I23.1	16:2525146-2581423	NOTEST	0.00134788	0	#NAME?	0	1	1
ENSG00000260273	ENSG00000260273	RP11-425D10.10	6:109703997-109704869	NOTEST	0.119909	0.0840935	-0.511877	0	1	1
ENSG00000260274	ENSG00000260274	RP11-817O13.8	15:75648132-75748183	NOTEST	0.449614	0.215972	-1.05784	0	1	1
ENSG00000260275	ENSG00000260275	RP11-326A19.2	15:89581207-89581517	NOTEST	0	0	0	0	1	1
ENSG00000260277	ENSG00000260277	RP11-101E7.2	16:22018958-22103552	NOTEST	0.466601	0.294076	-0.666001	0	1	1
ENSG00000260278	ENSG00000260278	RP11-109G23.3	4:79694807-79697127	NOTEST	0.0263272	0.0166577	-0.660363	0	1	1
ENSG00000260279	ENSG00000260279	AC137932.5	16:89334037-89556969	NOTEST	0.535931	0.196311	-1.44891	0	1	1
ENSG00000260280	ENSG00000260280	SLX1B-SULT1A4	16:29262828-29519817	NOTEST	0	0	0	0	1	1
ENSG00000260281	ENSG00000260281	RP11-329J18.2	16:47178233-47735434	NOTEST	0	0.0364946	inf	0	1	1
ENSG00000260282	ENSG00000260282	EIF4EBP2P2	15:42867856-43013179	NOTEST	0	0	0	0	1	1
ENSG00000260283	ENSG00000260283	CNP	HG185_PATCH:40122992-40131428	NOTEST	0	0	0	0	1	1
ENSG00000260284	ENSG00000260284	TPSP2	16:1336351-1338838	NOTEST	0	0	0	0	1	1
ENSG00000260285	ENSG00000260285	RP11-600F24.7	14:103991346-103995409	NOTEST	0.35473	0.232115	-0.611881	0	1	1
ENSG00000260286	ENSG00000260286	C6orf229	6:24797548-25057301	NOTEST	0	0	0	0	1	1
ENSG00000260287	ENSG00000260287	TBC1D3G	HG75_PATCH:34601601-34662129	NOTEST	0	0	0	0	1	1
ENSG00000260288	ENSG00000260288	RP11-24M17.4	15:76016317-76055662	NOTEST	0.103835	0.0275716	-1.91304	0	1	1
ENSG00000260289	ENSG00000260289	CTD-2535I10.1	16:7938490-7944397	NOTEST	0	0	0	0	1	1
ENSG00000260291	ENSG00000260291	RP11-488I20.2	16:34597782-34624955	NOTEST	0	0	0	0	1	1
ENSG00000260293	ENSG00000260293	RP11-715J22.6	16:2525146-2581423	NOTEST	0.0892104	0.275504	1.62679	0	1	1
ENSG00000260294	ENSG00000260294	CTA-305I2.2	HG115_PATCH:101459218-101927238	NOTEST	0	0	0	0	1	1
ENSG00000260295	ENSG00000260295	RP11-163O19.1	HG281_PATCH:49872180-49884080	NOTEST	0	0	0	0	1	1
ENSG00000260296	ENSG00000260296	RP11-395I6.3	4:40168294-40169451	NOTEST	0.0849853	0.106693	0.328175	0	1	1
ENSG00000260297	ENSG00000260297	AC005086.5	HG115_PATCH:101459218-101927238	NOTEST	0	0	0	0	1	1
ENSG00000260298	ENSG00000260298	RP11-429P3.4	16:50080339-50155854	NOTEST	0	0	0	0	1	1
ENSG00000260299	ENSG00000260299	RP13-100B2.4	HG79_PATCH:136335501-136346383	NOTEST	0	0	0	0	1	1
ENSG00000260300	ENSG00000260300	RP11-505K9.4	16:83932730-83999937	NOTEST	0.117279	0.174491	0.573208	0	1	1
ENSG00000260301	ENSG00000260301	RP11-429J17.4	HG104_HG975_PATCH:144766621-144796068	NOTEST	0	0	0	0	1	1
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ENSG00000260304	ENSG00000260304	RP11-388M20.6	16:31191430-31203127	NOTEST	0	0	0	0	1	1
ENSG00000260305	ENSG00000260305	NTRK3-AS1	15:88418229-88814297	NOTEST	0	0	0	0	1	1
ENSG00000260306	ENSG00000260306	RP11-645C24.5	16:21805415-21807080	NOTEST	0	0	0	0	1	1

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ENSG00000260308	ENSG00000260308	RP11-104C4.4	16:33573501-33573715	NOTEST	0	0	0	0	1	1
ENSG00000260309	ENSG00000260309	TRBV2	HG7_PATCH:142000746-142001255	NOTEST	0	0	0	0	1	1
ENSG00000260310	ENSG00000260310	RP11-27M24.2	16:10622278-10674555	NOTEST	0	0.0400718	inf	0	1	1
ENSG00000260311	ENSG00000260311	RP11-586K12.10	16:32660513-32677854	NOTEST	0	0	0	0	1	1
ENSG00000260312	ENSG00000260312	RP11-812E19.7	16:33660401-33661331	NOTEST	0	0	0	0	1	1
ENSG00000260313	ENSG00000260313	VPS28	HG243_PATCH:145478519-145483451	NOTEST	0	0	0	0	1	1
ENSG00000260314	ENSG00000260314	MRC1	HG544_PATCH:17851342-17953161	NOTEST	0	0	0	0	1	1
ENSG00000260315	ENSG00000260315	VN1R28P	HG14_PATCH:57490536-57491432	NOTEST	0	0	0	0	1	1
ENSG00000260316	ENSG00000260316	LA16c-306A4.2	16:903633-1031663	NOTEST	0.00494364	0.00384074	-0.36419	0	1	1
ENSG00000260317	ENSG00000260317	RP11-48B3.4	8:81453534-81455339	NOTEST	0.0528309	0.252711	2.25803	0	1	1
ENSG00000260318	ENSG00000260318	COX6CP1	16:11945505-12009939	NOTEST	0.277751	0.219108	-0.342154	0	1	1
ENSG00000260319	ENSG00000260319	SPATC1	HG104_HG975_PATCH:145059322-145129202	NOTEST	0	0	0	0	1	1
ENSG00000260320	ENSG00000260320	ZNF385C	HG185_PATCH:40132690-40219330	NOTEST	0	0	0	0	1	1
ENSG00000260321	ENSG00000260321	RP11-598F7.6	HG858_PATCH:116764-232399	NOTEST	0	0	0	0	1	1
ENSG00000260322	ENSG00000260322	RP11-339A11.2	1:80580627-80582603	NOTEST	0	0	0	0	1	1
ENSG00000260323	ENSG00000260323	RP11-378A12.1	HG19_PATCH:2522435-2555813	NOTEST	0	0	0	0	1	1
ENSG00000260324	ENSG00000260324	TMEM236	HG544_PATCH:17794250-17842867	NOTEST	0	0	0	0	1	1
ENSG00000260325	ENSG00000260325	HSPB9	HG185_PATCH:40277682-40279604	NOTEST	0	0	0	0	1	1
ENSG00000260326	ENSG00000260326	RP11-467J12.1	16:52968724-52969547	NOTEST	0.0417314	0	#NAME?	0	1	1
ENSG00000260327	ENSG00000260327	ACTR3BP3	16:32390391-32391370	NOTEST	0	0	0	0	1	1
ENSG00000260328	ENSG00000260328	RP11-416I2.1	17:16915227-16918304	NOTEST	0	0	0	0	1	1
ENSG00000260329	ENSG00000260329	RP11-412D9.4	12:107347806-107349275	NOTEST	0.356523	0.491317	0.462657	0	1	1
ENSG00000260331	ENSG00000260331	RP11-111J6.2	2:18728651-18729470	NOTEST	0.0419936	0.149681	1.83365	0	1	1
ENSG00000260332	ENSG00000260332	RP11-50O21.1	16:62842125-62842610	NOTEST	0	0	0	0	1	1
ENSG00000260333	ENSG00000260333	FAM83H-AS1	HG104_HG975_PATCH:144816309-144828507	NOTEST	0	0	0	0	1	1
ENSG00000260334	ENSG00000260334	GAST	HG185_PATCH:39868577-39872221	NOTEST	0	0	0	0	1	1
ENSG00000260335	ENSG00000260335	RP11-345J4.6	16:29262828-29519817	NOTEST	0	0	0	0	1	1
ENSG00000260337	ENSG00000260337	RP11-386M24.6	15:93124058-93143775	NOTEST	0	0	0	0	1	1
ENSG00000260338	ENSG00000260338	RP11-124K4.1	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000260339	ENSG00000260339	HEXA-AS1	15:72533521-72671129	NOTEST	0.218641	0.152382	-0.520873	0	1	1
ENSG00000260340	ENSG00000260340	RP11-254F19.3	16:84961958-84973209	NOTEST	0	0	0	0	1	1
ENSG00000260341	ENSG00000260341	RP11-80F22.6	16:34725544-34727817	NOTEST	0	0	0	0	1	1
ENSG00000260343	ENSG00000260343	LINC01043	13:112967780-112976072	NOTEST	0	0	0	0	1	1
ENSG00000260344	ENSG00000260344	RP11-56L13.6	16:32224700-32224824	NOTEST	0	0	0	0	1	1
ENSG00000260345	ENSG00000260345	AC009052.12	16:57462080-57521239	NOTEST	0	0	0	0	1	1
ENSG00000260346	ENSG00000260346	TRBV26	HG7_PATCH:142436168-142436653	NOTEST	0	0	0	0	1	1
ENSG00000260347	ENSG00000260347	MOCS1P1	16:48530900-48532512	NOTEST	0	0	0	0	1	1
ENSG00000260348	ENSG00000260348	RP11-643C9.1	HG536_PATCH:69723951-69725762	NOTEST	0	0	0	0	1	1
ENSG00000260350	ENSG00000260350	RP11-152P23.2	16:8768421-8962866	NOTEST	0	0	0	0	1	1
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ENSG00000260355	ENSG00000260355	ZNF716	HG14_PATCH:57517883-57541253	NOTEST	0	0	0	0	1	1
ENSG00000260357	ENSG00000260357	DNM1P34	15:75592293-75595306	NOTEST	0.0127687	0.0170061	0.413443	0	1	1
ENSG00000260359	ENSG00000260359	RP11-4F5.2	15:95024039-95027181	NOTEST	0.00499855	0.0307145	2.61934	0	1	1
ENSG00000260360	ENSG00000260360	RP11-533E19.5	1:179922318-179923575	NOTEST	0.0683795	0.0426083	-0.68243	0	1	1
ENSG00000260361	ENSG00000260361	CTD-2313J17.5	15:93146139-93353114	NOTEST	0	0.00667119	inf	0	1	1
ENSG00000260362	ENSG00000260362	RP11-297M9.1	16:9760741-9770700	NOTEST	0	0	0	0	1	1
ENSG00000260363	ENSG00000260363	OR9A1P	HG7_PATCH:141586947-141587892	NOTEST	0	0	0	0	1	1
ENSG00000260364	ENSG00000260364	RP11-256I9.3	16:65224875-65610203	NOTEST	0	0	0	0	1	1
ENSG00000260366	ENSG00000260366	CTD-2639E6.4	19:49429427-49429701	NOTEST	0	0.21923	inf	0	1	1
ENSG00000260368	ENSG00000260368	RP11-521I2.3	8:101925474-101926616	NOTEST	0.05845	0.267311	2.19325	0	1	1
ENSG00000260369	ENSG00000260369	CTD-2526A2.2	17:78427534-78428529	NOTEST	0	0.0127022	inf	0	1	1
ENSG00000260370	ENSG00000260370	RP11-631M21.1	HG905_PATCH:64060-66544	NOTEST	0	0	0	0	1	1
ENSG00000260372	ENSG00000260372	AQP4-AS1	18:24034873-24770662	NOTEST	0.255647	0.133513	-0.937171	0	1	1
ENSG00000260373	ENSG00000260373	TRBJ2-5	HG7_PATCH:142558011-142558059	NOTEST	0	0	0	0	1	1
ENSG00000260374	ENSG00000260374	ARHGAP23	HG745_PATCH:36584662-36668629	NOTEST	0	0	0	0	1	1
ENSG00000260375	ENSG00000260375	RP11-299H22.4	15:62545928-62562879	NOTEST	0	0	0	0	1	1
ENSG00000260376	ENSG00000260376	DUX4L5	HG1032_PATCH:190998972-191000255	NOTEST	0	0	0	0	1	1
ENSG00000260377	ENSG00000260377	RP11-646E18.4	3:182457456-182458636	NOTEST	0	0	0	0	1	1
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ENSG00000260379	ENSG00000260379	RP11-483K5.2	16:8558070-8558587	NOTEST	0	0	0	0	1	1
ENSG00000260380	ENSG00000260380	FRG1	HG1032_PATCH:190861942-190884359	NOTEST	0	0	0	0	1	1
ENSG00000260381	ENSG00000260381	RP11-429P3.5	16:50080339-50155854	NOTEST	0	0	0	0	1	1
ENSG00000260382	ENSG00000260382	RP11-540B6.2	15:31174469-31175434	NOTEST	0.255381	0.462542	0.856932	0	1	1
ENSG00000260383	ENSG00000260383	MROH1	HG243_PATCH:145202918-145316830	NOTEST	0	0	0	0	1	1
ENSG00000260384	ENSG00000260384	SERINC2	HG989_PATCH:31882411-31907525	NOTEST	0	0	0	0	1	1
ENSG00000260385	ENSG00000260385	RP11-450H6.3	13:112737862-112739785	NOTEST	0	0	0	0	1	1
ENSG00000260386	ENSG00000260386	RP11-439L8.3	HG989_PATCH:31972931-32013732	NOTEST	0	0	0	0	1	1
ENSG00000260387	ENSG00000260387	RP11-463O9.6	16:86669933-86670751	NOTEST	0	0	0	0	1	1
ENSG00000260388	ENSG00000260388	LINC00562	13:48504289-48506757	NOTEST	0.0258614	0.182448	2.81861	0	1	1
ENSG00000260389	ENSG00000260389	WBP11P1	18:30091625-30094597	NOTEST	0	0	0	0	1	1
ENSG00000260390	ENSG00000260390	RP11-575I8.1	9:27829273-27844479	NOTEST	0.0218212	0.0187142	-0.221599	0	1	1
ENSG00000260391	ENSG00000260391	RP11-71H17.7	3:123798869-124445172	NOTEST	0.0113485	0	#NAME?	0	1	1
ENSG00000260392	ENSG00000260392	RP11-1129I3.1	15:56835149-56921790	NOTEST	0	0	0	0	1	1
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ENSG00000260394	ENSG00000260394	LA16c-313D11.9	16:728503-729777	NOTEST	0.136546	0.0110064	-3.63298	0	1	1
ENSG00000260395	ENSG00000260395	CTD-2649C14.1	16:21995185-22012433	NOTEST	0	0.0137238	inf	0	1	1
ENSG00000260396	ENSG00000260396	AC012065.7	2:20877568-20879005	NOTEST	0.0204319	0.0257922	0.33611	0	1	1

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ENSG00000260399	ENSG00000260399	RP11-529J17.5	15:23583131-23586995	NOTEST	0	0	0	0	1	1
ENSG00000260400	ENSG00000260400	RP11-119F7.5	10:70458256-70460551	NOTEST	0.308672	0.172454	-0.839863	0	1	1
ENSG00000260401	ENSG00000260401	RP11-800A3.4	11:72950019-72953380	NOTEST	0.00465538	0	#NAME?	0	1	1
ENSG00000260402	ENSG00000260402	RP11-56L13.1	16:32274147-32276835	NOTEST	0	0	0	0	1	1
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ENSG00000260405	ENSG00000260405	CTD-2576D5.2	16:17190058-17190278	NOTEST	0	0	0	0	1	1
ENSG00000260406	ENSG00000260406	RP11-402F9.3	15:43568477-43594970	NOTEST	0	0	0	0	1	1
ENSG00000260407	ENSG00000260407	TRBV7-1	HG7_PATCH:142032005-142032527	NOTEST	0	0	0	0	1	1
ENSG00000260409	ENSG00000260409	RP11-403B2.7	15:20935075-20961512	NOTEST	0.129142	0.0866234	-0.576133	0	1	1
ENSG00000260410	ENSG00000260410	RP11-505K9.3	16:84152897-84154758	NOTEST	0.0497057	0.0424558	-0.22745	0	1	1
ENSG00000260411	ENSG00000260411	RP11-420N3.2	16:5289802-7763340	NOTEST	0.150409	0.134125	-0.165314	0	1	1
ENSG00000260412	ENSG00000260412	RP11-438B23.2	9:27937614-27944495	NOTEST	0.372999	0.346936	-0.104502	0	1	1
ENSG00000260413	ENSG00000260413	RP11-231C14.6	16:29262828-29519817	NOTEST	0.00116346	0	#NAME?	0	1	1
ENSG00000260414	ENSG00000260414	RP11-1437A8.2	16:33165672-33165796	NOTEST	0	0	0	0	1	1
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ENSG00000260416	ENSG00000260416	RP5-963E22.5	20:61758846-61760811	NOTEST	0	0	0	0	1	1
ENSG00000260417	ENSG00000260417	CTD-2542L18.1	16:85625871-85629326	NOTEST	0	0	0	0	1	1
ENSG00000260418	ENSG00000260418	RP3-406A7.7	6:136656851-136657225	NOTEST	0	0	0	0	1	1
ENSG00000260419	ENSG00000260419	RP11-1437A8.3	16:33202881-33264727	NOTEST	0.311144	0.483013	0.63448	0	1	1
ENSG00000260420	ENSG00000260420	LA16c-444G7.2	16:88227919-88228823	NOTEST	0	0	0	0	1	1
ENSG00000260424	ENSG00000260424	TRBV19	HG7_PATCH:142360431-142361115	NOTEST	0	0	0	0	1	1
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ENSG00000260427	ENSG00000260427	RP11-488I20.5	16:34581755-34582668	NOTEST	0	0	0	0	1	1
ENSG00000260428	ENSG00000260428	SCXA	HG243_PATCH:145317004-145346273	NOTEST	0	0	0	0	1	1
ENSG00000260429	ENSG00000260429	TRBV6-7	HG7_PATCH:142209378-142209811	NOTEST	0	0	0	0	1	1
ENSG00000260430	ENSG00000260430	RP11-626G11.4	16:19098177-19109432	NOTEST	0	0	0	0	1	1
ENSG00000260431	ENSG00000260431	RP11-382N13.6	16:5257088-5257440	NOTEST	0	0	0	0	1	1
ENSG00000260432	ENSG00000260432	RP11-297M9.2	16:9847271-9851895	NOTEST	0.00333493	0.0129668	1.95909	0	1	1
ENSG00000260433	ENSG00000260433	RP11-202D1.2	18:51094816-51124221	NOTEST	0	0	0	0	1	1
ENSG00000260435	ENSG00000260435	TRIM51DP	HG281_PATCH:49895724-49898365	NOTEST	0	0	0	0	1	1
ENSG00000260436	ENSG00000260436	RP11-20I23.7	16:2587964-2653189	NOTEST	0	0	0	0	1	1
ENSG00000260437	ENSG00000260437	TRBV11-1	HG7_PATCH:142129178-142129643	NOTEST	0	0	0	0	1	1
ENSG00000260438	ENSG00000260438	RP11-405F3.2	16:57702098-57765717	NOTEST	0	0	0	0	1	1
ENSG00000260439	ENSG00000260439	LA16c-366D3.1	16:903633-1031663	NOTEST	0.0665285	0.0742047	0.157539	0	1	1
ENSG00000260440	ENSG00000260440	RP11-1096D5.1	18:59252978-59421928	NOTEST	0	0	0	0	1	1
ENSG00000260441	ENSG00000260441	RP11-96D1.7	16:68279206-68294961	NOTEST	0	0.0973623	inf	0	1	1
ENSG00000260443	ENSG00000260443	CTD-3057O21.1	16:87978663-87978808	NOTEST	0	0	0	0	1	1

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ENSG00000260445	ENSG00000260445	CTD-3244O18.5	7:99467463-99467517	NOTEST	0	0	0	0	1	1
ENSG00000260446	ENSG00000260446	MOXD2P	HG7_PATCH:141940558-141946886	NOTEST	0	0	0	0	1	1
ENSG00000260447	ENSG00000260447	RP11-304L19.2	16:2089815-2185899	NOTEST	0.0325845	0.0230543	-0.499148	0	1	1
ENSG00000260448	ENSG00000260448	RP11-449H11.1	16:25096912-25122876	NOTEST	0.339775	0.226464	-0.585296	0	1	1
ENSG00000260449	ENSG00000260449	RP11-244B22.14	16:34375268-34375779	NOTEST	0	0	0	0	1	1
ENSG00000260450	ENSG00000260450	RP11-523L20.1	16:47999582-48005598	NOTEST	0	0	0	0	1	1
ENSG00000260451	ENSG00000260451	GEMIN8P2	16:58741034-59142878	NOTEST	0	0	0	0	1	1
ENSG00000260452	ENSG00000260452	TPRKBP2	16:28109299-28223241	NOTEST	0.0488533	0.0381218	-0.357839	0	1	1
ENSG00000260454	ENSG00000260454	RP11-367F23.2	9:93759335-93764153	NOTEST	0	0	0	0	1	1
ENSG00000260455	ENSG00000260455	CASC14	6:21665002-22214734	NOTEST	0.0503796	0.0269709	-0.901433	0	1	1
ENSG00000260457	ENSG00000260457	RP11-723G8.1	18:69504274-69538024	NOTEST	0	0	0	0	1	1
ENSG00000260458	ENSG00000260458	KCNJ12	HG987_PATCH:21606052-21607836	NOTEST	0	0	0	0	1	1
ENSG00000260459	ENSG00000260459	FTLP14	16:68771127-68869451	NOTEST	0	0.0369832	inf	0	1	1
ENSG00000260460	ENSG00000260460	RP11-284F21.8	1:156479645-156481473	NOTEST	0	0.00696478	inf	0	1	1
ENSG00000260461	ENSG00000260461	RP11-541N10.3	10:105637131-105639519	NOTEST	0.256453	0.190058	-0.432254	0	1	1
ENSG00000260463	ENSG00000260463	MAPK15	HG104_HG975_PATCH:144798428-144804628	NOTEST	0	0	0	0	1	1
ENSG00000260464	ENSG00000260464	RP4-561L24.3	1:94312729-94314495	NOTEST	0.0744896	0.0507006	-0.555037	0	1	1
ENSG00000260465	ENSG00000260465	RP11-63M22.2	16:66754795-66788643	NOTEST	0	0	0	0	1	1
ENSG00000260466	ENSG00000260466	RP4-536B24.2	16:87863628-87903094	NOTEST	0.0787048	0.0416099	-0.919525	0	1	1
ENSG00000260467	ENSG00000260467	RP11-405F3.4	16:57702098-57765717	NOTEST	0	0	0	0	1	1
ENSG00000260468	ENSG00000260468	RP11-27M24.3	16:10608698-10622059	NOTEST	0	0	0	0	1	1
ENSG00000260469	ENSG00000260469	RP11-8P11.3	15:74060554-74061978	NOTEST	0	0	0	0	1	1
ENSG00000260470	ENSG00000260470	RP11-834C11.11	12:54538852-54541009	NOTEST	0.0990201	0.0602179	-0.717529	0	1	1
ENSG00000260471	ENSG00000260471	AC009120.8	16:74088049-74330660	NOTEST	0	0	0	0	1	1
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ENSG00000260473	ENSG00000260473	RP11-923I11.4	12:52217286-52229280	NOTEST	0.0173512	0.0122249	-0.505214	0	1	1
ENSG00000260474	ENSG00000260474	PRSS3P3	HG7_PATCH:141985578-141991423	NOTEST	0	0	0	0	1	1
ENSG00000260475	ENSG00000260475	RP11-85A1.3	10:101380811-101381675	NOTEST	0.0606543	0.126328	1.05849	0	1	1
ENSG00000260476	ENSG00000260476	RP11-254F7.1	2:10161704-10162952	NOTEST	0	0	0	0	1	1
ENSG00000260477	ENSG00000260477	RP11-553E24.2	15:86626575-86659948	NOTEST	0	0	0	0	1	1
ENSG00000260478	ENSG00000260478	RP11-142G1.1	16:52271993-52314211	NOTEST	0	0	0	0	1	1
ENSG00000260479	ENSG00000260479	RP11-556H2.3	16:78133309-79246564	NOTEST	0	0	0	0	1	1
ENSG00000260480	ENSG00000260480	RP11-488I20.4	16:34586852-34587393	NOTEST	0	0	0	0	1	1
ENSG00000260481	ENSG00000260481	TRBV12-5	HG7_PATCH:142322554-142323065	NOTEST	0	0	0	0	1	1
ENSG00000260483	ENSG00000260483	RP11-151H2.1	15:75315320-75315597	NOTEST	0	0	0	0	1	1
ENSG00000260484	ENSG00000260484	RP11-1081M5.2	8:54301260-54303432	NOTEST	0	0	0	0	1	1
ENSG00000260485	ENSG00000260485	PUF60	HG104_HG975_PATCH:144898513-144912029	NOTEST	0	0	0	0	1	1

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ENSG00000260488	ENSG00000260488	RP11-166B2.7	16:12070593-12704901	NOTEST	0	0	0	0	1	1
ENSG00000260489	ENSG00000260489	C9orf96	HG79_PATCH:136251901-136334921	NOTEST	0	0	0	0	1	1
ENSG00000260490	ENSG00000260490	RP11-265N6.3	15:42864124-42864631	NOTEST	0.126542	0.0313932	-2.0111	0	1	1
ENSG00000260491	ENSG00000260491	U66059.29	HG7_PATCH:141965649-141972054	NOTEST	0	0	0	0	1	1
ENSG00000260492	ENSG00000260492	RP11-686F15.3	12:54144230-54145619	NOTEST	0	0	0	0	1	1
ENSG00000260493	ENSG00000260493	RP11-219B4.7	8:86084311-86089297	NOTEST	0.047001	0.0191265	-1.29712	0	1	1
ENSG00000260494	ENSG00000260494	AC002310.10	16:30535324-30569819	NOTEST	0.0494635	0	#NAME?	0	1	1
ENSG00000260495	ENSG00000260495	RP11-55K13.1	16:81344335-81347028	NOTEST	0.0672746	0.081992	0.285422	0	1	1
ENSG00000260496	ENSG00000260496	RP11-161M6.3	16:1041147-1050926	NOTEST	0	0	0	0	1	1
ENSG00000260497	ENSG00000260497	CTB-55P19.1	16:47758478-47942342	NOTEST	0	0	0	0	1	1
ENSG00000260498	ENSG00000260498	RP4-536B24.4	16:87807093-87812980	NOTEST	0	0	0	0	1	1
ENSG00000260500	ENSG00000260500	CTD-3193O13.1	19:7981029-7984042	NOTEST	0.121423	0.122106	0.00809552	0	1	1
ENSG00000260501	ENSG00000260501	RPL7A	HG79_PATCH:136223748-136226961	NOTEST	0	0	0	0	1	1
ENSG00000260502	ENSG00000260502	CACFD1	HG79_PATCH:136335501-136346383	NOTEST	0	0	0	0	1	1
ENSG00000260504	ENSG00000260504	RP11-558A11.3	16:84376069-84377013	NOTEST	0	0	0	0	1	1
ENSG00000260505	ENSG00000260505	RP11-410C4.5	1:220574463-220577375	NOTEST	0	0	0	0	1	1
ENSG00000260506	ENSG00000260506	RP11-648F7.1	2:239928721-239931139	NOTEST	0	0	0	0	1	1
ENSG00000260507	ENSG00000260507	RP11-356C4.3	16:90168678-90244752	NOTEST	0	0	0	0	1	1
ENSG00000260508	ENSG00000260508	GGNBP2	HG75_PATCH:34872291-34917807	NOTEST	0	0	0	0	1	1
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ENSG00000260510	ENSG00000260510	AC004381.7	16:20621564-20936328	NOTEST	0	0	0	0	1	1
ENSG00000260511	ENSG00000260511	RP11-556H2.2	16:78133309-79246564	NOTEST	0	0	0	0	1	1
ENSG00000260513	ENSG00000260513	ZNF479	HG736_PATCH:57187306-57207557	NOTEST	0	0	0	0	1	1
ENSG00000260514	ENSG00000260514	RP11-368N21.1	16:29630105-29647649	NOTEST	0	0	0	0	1	1
ENSG00000260515	ENSG00000260515	CTD-2199O4.3	5:10195232-10197740	NOTEST	0.000262969	0	#NAME?	0	1	1
ENSG00000260516	ENSG00000260516	RP11-17M15.4	16:32368301-32375016	NOTEST	0	0	0	0	1	1
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ENSG00000260518	ENSG00000260518	BMS1P8	16:33489491-33500971	NOTEST	0.0619393	0.293621	2.24503	0	1	1
ENSG00000260519	ENSG00000260519	RP11-109E24.2	4:42659512-42659945	NOTEST	0	0	0	0	1	1
ENSG00000260520	ENSG00000260520	RP11-510M2.6	16:71481499-71598992	NOTEST	0	0	0	0	1	1
ENSG00000260521	ENSG00000260521	CTD-2576F9.1	15:95398702-95400240	NOTEST	0	0.00822571	inf	0	1	1
ENSG00000260522	ENSG00000260522	RP11-352B15.5	16:34956638-34956900	NOTEST	0	0	0	0	1	1
ENSG00000260523	ENSG00000260523	RP11-483P21.3	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000260524	ENSG00000260524	CYP3A52P	7:99469790-99469881	NOTEST	0	0	0	0	1	1
ENSG00000260525	ENSG00000260525	RP11-812E19.10	16:33677505-33677935	NOTEST	0	0	0	0	1	1
ENSG00000260526	ENSG00000260526	RP11-73K9.2	4:113150716-113152752	NOTEST	0.287997	0.346859	0.268295	0	1	1
ENSG00000260528	ENSG00000260528	FAM157C	16:90168678-90244752	NOTEST	0.461245	0.215591	-1.09724	0	1	1
ENSG00000260529	ENSG00000260529	RP11-439L8.4	HG989_PATCH:31972931-32013732	NOTEST	0	0	0	0	1	1

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ENSG00000260532	ENSG00000260532	LA16c-381G6.1	16:1161626-1163399	NOTEST	0	0	0	0	1	1
ENSG00000260533	ENSG00000260533	NRBP2	HG104_HG975_PATCH:144915439-144923144	NOTEST	0	0	0	0	1	1
ENSG00000260535	ENSG00000260535	TRBJ2-3	HG7_PATCH:142557739-142557788	NOTEST	0	0	0	0	1	1
ENSG00000260536	ENSG00000260536	RP5-1085F17.4	20:31407698-31442063	NOTEST	0	0	0	0	1	1
ENSG00000260538	ENSG00000260538	HLA-P	HSCHR6_MHC_APD:29768234-29770242	NOTEST	0	0	0	0	1	1
ENSG00000260540	ENSG00000260540	FAM108A9P	16:32211222-32214143	NOTEST	0.0682635	0	#NAME?	0	1	1
ENSG00000260541	ENSG00000260541	LA16c-429E7.1	16:1845620-1934295	NOTEST	0	0	0	0	1	1
ENSG00000260542	ENSG00000260542	RP13-379O24.2	20:61088964-61091152	NOTEST	0	0	0	0	1	1
ENSG00000260545	ENSG00000260545	CTB-134F13.1	16:58147495-58163354	NOTEST	0	0	0	0	1	1
ENSG00000260546	ENSG00000260546	TRBV10-2	HG7_PATCH:142146451-142146952	NOTEST	0	0	0	0	1	1
ENSG00000260548	ENSG00000260548	RP6-24A23.6	X:107963178-107982133	NOTEST	0.170079	0.0298808	-2.50892	0	1	1
ENSG00000260549	ENSG00000260549	MT1L	16:56651387-56652730	NOTEST	0	0	0	0	1	1
ENSG00000260550	ENSG00000260550	RP11-457I16.2	16:18581769-18609650	NOTEST	0	0	0	0	1	1
ENSG00000260551	ENSG00000260551	PWRN2	15:24407900-24415095	NOTEST	0	0	0	0	1	1
ENSG00000260554	ENSG00000260554	TRBV8-2	HG7_PATCH:142107886-142108157	NOTEST	0	0	0	0	1	1
ENSG00000260555	ENSG00000260555	RP11-728K20.2	7:149697840-149702213	NOTEST	0	0	0	0	1	1
ENSG00000260557	ENSG00000260557	C7orf34	HG7_PATCH:142699948-142701464	NOTEST	0	0	0	0	1	1
ENSG00000260558	ENSG00000260558	RP11-63M22.1	16:66754795-66788643	NOTEST	0	0.161806	inf	0	1	1
ENSG00000260559	ENSG00000260559	OR4A49P	HG281_PATCH:49936564-49937196	NOTEST	0	0	0	0	1	1
ENSG00000260562	ENSG00000260562	RP11-227P3.1	HG281_PATCH:50124154-50124436	NOTEST	0	0	0	0	1	1
ENSG00000260564	ENSG00000260564	RP11-403N16.3	9:82503915-82506922	NOTEST	0	0	0	0	1	1
ENSG00000260566	ENSG00000260566	RP11-20G6.3	16:23072726-23160591	NOTEST	0	0	0	0	1	1
ENSG00000260568	ENSG00000260568	CTD-2358C21.3	16:31710996-31711786	NOTEST	0	0	0	0	1	1
ENSG00000260569	ENSG00000260569	RP11-669I1.1	18:71878625-71907790	NOTEST	0	0	0	0	1	1
ENSG00000260570	ENSG00000260570	RP11-24N18.1	16:28834355-28848558	NOTEST	0	0.0073445	inf	0	1	1
ENSG00000260571	ENSG00000260571	RP11-546B15.2	15:42500610-42704516	NOTEST	0.0714063	0.268591	1.91129	0	1	1
ENSG00000260572	ENSG00000260572	RP11-16N11.2	3:160471215-160472930	NOTEST	0.119659	0.0419968	-1.51058	0	1	1
ENSG00000260573	ENSG00000260573	RP11-21B23.3	16:50441611-50442424	NOTEST	0	0	0	0	1	1
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ENSG00000260576	ENSG00000260576	RP11-390D11.2	15:72110736-72447800	NOTEST	0	0.0365653	inf	0	1	1
ENSG00000260577	ENSG00000260577	RP11-615I2.2	16:68670091-68756519	NOTEST	0.151112	0.0583192	-1.37357	0	1	1
ENSG00000260578	ENSG00000260578	CTD-2541J13.1	18:65149027-65152203	NOTEST	0	0	0	0	1	1
ENSG00000260579	ENSG00000260579	RP11-382A20.2	15:83776158-84108197	NOTEST	0.197735	0	#NAME?	0	1	1
ENSG00000260580	ENSG00000260580	RP11-142A12.1	16:26733194-26740447	NOTEST	0	0	0	0	1	1
ENSG00000260581	ENSG00000260581	CTB-113P19.4	5:151031835-151035010	NOTEST	0	0.0391308	inf	0	1	1
ENSG00000260582	ENSG00000260582	TPST2P1	15:36871811-37110660	NOTEST	0	0	0	0	1	1
ENSG00000260583	ENSG00000260583	LINC00515	21:26955081-26955638	NOTEST	0	0.0930036	inf	0	1	1
ENSG00000260584	ENSG00000260584	RP11-1166P10.7	16:32114565-32199434	NOTEST	0	0	0	0	1	1

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ENSG00000260586	ENSG00000260586	RP11-592N21.2	15:71389290-72075722	NOTEST	0	0	0	0	1	1
ENSG00000260587	ENSG00000260587	DOCK3	HG186_PATCH:50712671-51421329	NOTEST	0	0	0	0	1	1
ENSG00000260588	ENSG00000260588	RP11-930P14.2	8:41510738-41754280	NOTEST	0.132369	0.185588	0.487541	0	1	1
ENSG00000260589	ENSG00000260589	RP11-390B4.5	10:17683282-17685877	NOTEST	0.262796	0.201157	-0.385621	0	1	1
ENSG00000260590	ENSG00000260590	RP11-244B22.7	16:34427060-34430032	NOTEST	0	0	0	0	1	1
ENSG00000260591	ENSG00000260591	RP11-817O13.6	15:75639295-75648087	NOTEST	0.0858605	0.193584	1.17289	0	1	1
ENSG00000260592	ENSG00000260592	CTA-363E6.6	16:19421817-19510435	NOTEST	0	0	0	0	1	1
ENSG00000260593	ENSG00000260593	RP11-432I5.2	16:71657610-71758604	NOTEST	0	0	0	0	1	1
ENSG00000260594	ENSG00000260594	CTD-2055G21.1	16:80631802-80838226	NOTEST	0	0	0	0	1	1
ENSG00000260595	ENSG00000260595	OR4C49P	HG281_PATCH:50074947-50075847	NOTEST	0	0	0	0	1	1
ENSG00000260596	ENSG00000260596	DUX4	HG1032_PATCH:191094928-191107097	NOTEST	0	0	0	0	1	1
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ENSG00000260598	ENSG00000260598	RP11-80F22.13	16:34640117-34641720	NOTEST	0	0	0	0	1	1
ENSG00000260599	ENSG00000260599	CTC-457E21.1	19:22573820-22715287	NOTEST	0	0	0	0	1	1
ENSG00000260600	ENSG00000260600	RP11-109D24.1	16:61681145-62070939	NOTEST	0	0	0	0	1	1
ENSG00000260601	ENSG00000260601	RP11-552C15.1	16:12070593-12704901	NOTEST	0	0	0	0	1	1
ENSG00000260602	ENSG00000260602	HMGN2P40	15:68346516-68549549	NOTEST	0	0	0	0	1	1
ENSG00000260603	ENSG00000260603	GS1-21A4.1	16:87921624-87970135	NOTEST	0	0	0	0	1	1
ENSG00000260604	ENSG00000260604	RP1-140K8.5	6:3905143-3912213	NOTEST	0.0181012	0.0808964	2.15999	0	1	1
ENSG00000260605	ENSG00000260605	RP11-883G14.3	16:51051668-51072675	NOTEST	0	0	0	0	1	1
ENSG00000260606	ENSG00000260606	ANO1-AS2	HG536_PATCH:69887201-69890237	NOTEST	0	0	0	0	1	1
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ENSG00000260610	ENSG00000260610	RP11-989E6.11	16:32943088-32943890	NOTEST	0	0	0	0	1	1
ENSG00000260611	ENSG00000260611	RP11-352B15.2	16:35019939-35021258	NOTEST	0	0.0182066	inf	0	1	1
ENSG00000260612	ENSG00000260612	RP11-432I5.4	16:71760877-71761895	NOTEST	0	0	0	0	1	1
ENSG00000260613	ENSG00000260613	RP3-522J7.6	22:50226263-50231434	NOTEST	0	0	0	0	1	1
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ENSG00000260616	ENSG00000260616	RP11-327F22.4	16:50774820-50837249	NOTEST	0.151136	0	#NAME?	0	1	1
ENSG00000260617	ENSG00000260617	RP5-1142A6.7	16:88772870-88851619	NOTEST	0	0	0	0	1	1
ENSG00000260618	ENSG00000260618	RP11-23N2.4	15:52870038-53002014	NOTEST	0.18217	0.0738729	-1.30217	0	1	1
ENSG00000260620	ENSG00000260620	RP11-883G14.4	16:51088638-51090310	NOTEST	0	0	0	0	1	1
ENSG00000260621	ENSG00000260621	RP11-413H22.2	16:56395363-56459450	NOTEST	0	0	0	0	1	1
ENSG00000260622	ENSG00000260622	RP11-690I21.3	2:232674555-232677062	NOTEST	0.131932	0.264267	1.0022	0	1	1
ENSG00000260623	ENSG00000260623	VPRBP	HG186_PATCH:51428698-51537425	NOTEST	0	0	0	0	1	1
ENSG00000260624	ENSG00000260624	RP11-24D15.1	15:74163290-74165707	NOTEST	0	0	0	0	1	1

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ENSG00000260626	ENSG00000260626	RP11-23E10.3	16:33336282-33337443	NOTEST	0	0	0	0	1	1
ENSG00000260628	ENSG00000260628	RP11-1166P10.1	16:31987123-32015049	NOTEST	0	0.0256333	inf	0	1	1
ENSG00000260629	ENSG00000260629	CTD-2643I7.1	11:5265783-5266777	NOTEST	0	0	0	0	1	1
ENSG00000260631	ENSG00000260631	RBM22P12	16:31692167-31693422	NOTEST	0	0	0	0	1	1
ENSG00000260632	ENSG00000260632	OR6W1P	HG7_PATCH:142822935-142824191	NOTEST	0	0	0	0	1	1
ENSG00000260633	ENSG00000260633	RP11-375I20.6	3:134066129-134068075	NOTEST	0.0167338	0.0610062	1.86619	0	1	1
ENSG00000260634	ENSG00000260634	RP11-521O16.1	2:127781827-127787262	NOTEST	0	0.00802903	inf	0	1	1
ENSG00000260635	ENSG00000260635	RP11-21M24.3	16:22357256-22547842	NOTEST	0	0	0	0	1	1
ENSG00000260636	ENSG00000260636	RP11-439L8.5	HG989_PATCH:31972931-32013732	NOTEST	0	0	0	0	1	1
ENSG00000260637	ENSG00000260637	RP11-46C24.5	16:89323586-89333938	NOTEST	0	0	0	0	1	1
ENSG00000260638	ENSG00000260638	HLA-P	HSCHR6_MHC_QBL:29765388-29767393	NOTEST	0	0	0	0	1	1
ENSG00000260639	ENSG00000260639	RP11-602M11.4	15:34671268-34880704	NOTEST	0	0	0	0	1	1
ENSG00000260640	ENSG00000260640	KB-1000E4.2	8:98253969-98254432	NOTEST	0	0	0	0	1	1
ENSG00000260641	ENSG00000260641	RP11-1299A16.3	4:99580054-99585701	NOTEST	0.0027119	0.00784779	1.53298	0	1	1
ENSG00000260642	ENSG00000260642	RP11-717I24.1	15:32651738-32659985	NOTEST	0	0	0	0	1	1
ENSG00000260643	ENSG00000260643	RP11-303E16.8	16:81087101-81130008	NOTEST	0.0512371	0.110438	1.10798	0	1	1
ENSG00000260645	ENSG00000260645	RP11-250B2.5	6:81176674-81178797	NOTEST	0.187726	0.158716	-0.242179	0	1	1
ENSG00000260646	ENSG00000260646	LA16c-385E7.1	16:1543344-1662111	NOTEST	0.0581509	0.0928205	0.674642	0	1	1
ENSG00000260647	ENSG00000260647	RP1-178F10.1	17:18171393-18172142	NOTEST	0.0513975	0.0599838	0.222875	0	1	1
ENSG00000260648	ENSG00000260648	RP11-133K1.7	15:40453223-40569688	NOTEST	0.014668	0	#NAME?	0	1	1
ENSG00000260649	ENSG00000260649	RP11-56L13.4	16:32199653-32204851	NOTEST	0	0	0	0	1	1
ENSG00000260650	ENSG00000260650	RP11-403P17.2	16:66613350-66622178	NOTEST	0	0	0	0	1	1
ENSG00000260651	ENSG00000260651	AF213884.2	4:103421997-103422476	NOTEST	0.276613	0.294639	0.0910806	0	1	1
ENSG00000260653	ENSG00000260653	RP11-114G11.3	HG14_PATCH:57472477-57483910	NOTEST	0	0	0	0	1	1
ENSG00000260655	ENSG00000260655	CTA-250D10.23	22:42318026-42319104	NOTEST	0.0327507	0.0395024	0.270413	0	1	1
ENSG00000260657	ENSG00000260657	RP11-315D16.4	15:68560129-68588203	NOTEST	0	0	0	0	1	1
ENSG00000260658	ENSG00000260658	RP11-368L12.1	16:63348167-63651950	NOTEST	0.190409	0.680649	1.8378	0	1	1
ENSG00000260659	ENSG00000260659	RP11-46C24.6	16:89284117-89295363	NOTEST	0	0	0	0	1	1
ENSG00000260660	ENSG00000260660	RP11-69H7.2	15:75519093-75526292	NOTEST	0	0	0	0	1	1
ENSG00000260661	ENSG00000260661	RP11-152L20.3	15:92396924-92874267	NOTEST	0	0	0	0	1	1
ENSG00000260662	ENSG00000260662	RP11-626K17.2	16:32471586-32471683	NOTEST	0	0	0	0	1	1
ENSG00000260664	ENSG00000260664	AC004158.3	16:72459383-72698908	NOTEST	4.24E-07	3.10E-07	-0.451109	0	1	1
ENSG00000260665	ENSG00000260665	DUX4L4	HG1032_PATCH:191002272-191003549	NOTEST	0	0	0	0	1	1
ENSG00000260666	ENSG00000260666	AC142293.3	HG706_PATCH:75418300-75455198	NOTEST	0	0	0	0	1	1
ENSG00000260667	ENSG00000260667	AC097374.4	HG686_PATCH:95632415-95711088	NOTEST	0	0	0	0	1	1
ENSG00000260668	ENSG00000260668	RP11-744D14.1	16:64276511-64377813	NOTEST	0.376583	0.50012	0.409306	0	1	1
ENSG00000260670	ENSG00000260670	RP11-447M4.1	3:72370201-72373178	NOTEST	0	0	0	0	1	1
ENSG00000260671	ENSG00000260671	RP11-278A23.2	16:87634131-87799598	NOTEST	0	0	0	0	1	1
ENSG00000260672	ENSG00000260672	RP11-1006G14.1	15:72897523-72929260	NOTEST	0	0.00508295	inf	0	1	1

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ENSG00000260675	ENSG00000260675	CTD-2576D5.3	16:17188207-17188784	NOTEST	0	0	0	0	1	1
ENSG00000260676	ENSG00000260676	RP11-510D19.1	18:69187197-69246192	NOTEST	0	0	0	0	1	1
ENSG00000260677	ENSG00000260677	RP11-546O6.4	9:100505489-100507217	NOTEST	0	0	0	0	1	1
ENSG00000260678	ENSG00000260678	RP11-146F11.4	16:30597227-30635333	NOTEST	0	0	0	0	1	1
ENSG00000260679	ENSG00000260679	RP11-643C9.2	HG536_PATCH:69736405-69741581	NOTEST	0	0	0	0	1	1
ENSG00000260680	ENSG00000260680	RP11-80F22.1	16:34654661-34655580	NOTEST	0	0	0	0	1	1
ENSG00000260681	ENSG00000260681	CTA-363E6.5	16:19421817-19510435	NOTEST	0	0	0	0	1	1
ENSG00000260682	ENSG00000260682	7SK	16:81993523-81996298	NOTEST	0.206481	0.0939939	-1.13537	0	1	1
ENSG00000260683	ENSG00000260683	CTD-2076M15.1	X:126794611-126796511	NOTEST	0	0	0	0	1	1
ENSG00000260685	ENSG00000260685	RP11-326L17.1	15:76228309-76352136	NOTEST	0.0536169	0	#NAME?	0	1	1
ENSG00000260686	ENSG00000260686	CTB-36H16.2	5:122168050-122170228	NOTEST	0.127579	0.208421	0.708107	0	1	1
ENSG00000260687	ENSG00000260687	RP11-44L9.2	16:73533207-73533662	NOTEST	0	0	0	0	1	1
ENSG00000260688	ENSG00000260688	RP11-44I10.5	16:48504863-48505044	NOTEST	0	0	0	0	1	1
ENSG00000260689	ENSG00000260689	HNRNPA3P11	15:57210820-57591479	NOTEST	0.0355684	0.0151478	-1.23149	0	1	1
ENSG00000260690	ENSG00000260690	CYCSP39	16:25465659-25465968	NOTEST	0	0	0	0	1	1
ENSG00000260691	ENSG00000260691	AC073464.10	HG686_PATCH:95578782-95620920	NOTEST	0	0	0	0	1	1
ENSG00000260692	ENSG00000260692	SURF1	HG79_PATCH:136227289-136236704	NOTEST	0	0	0	0	1	1
ENSG00000260693	ENSG00000260693	AC026150.8	15:30832295-30838172	NOTEST	0.234223	0.105045	-1.15687	0	1	1
ENSG00000260694	ENSG00000260694	RP11-556H2.4	16:78133309-79246564	NOTEST	0	0	0	0	1	1
ENSG00000260695	ENSG00000260695	RP11-513N24.1	16:65895014-65897687	NOTEST	0	0	0	0	1	1
ENSG00000260696	ENSG00000260696	TAS2R38	HG7_PATCH:141607612-141806547	NOTEST	0	0	0	0	1	1
ENSG00000260698	ENSG00000260698	RP11-439E19.9	1:246845409-246848377	NOTEST	0.0849524	0.0854201	0.00792075	0	1	1
ENSG00000260701	ENSG00000260701	RP11-449J10.1	16:77224731-77478233	NOTEST	0	0	0	0	1	1
ENSG00000260702	ENSG00000260702	LA16c-349E11.1	16:1153279-1155461	NOTEST	0	0	0	0	1	1
ENSG00000260703	ENSG00000260703	TTC25	HG185_PATCH:40086886-40121903	NOTEST	0	0	0	0	1	1
ENSG00000260704	ENSG00000260704	LINC00543	13:28527662-28529507	NOTEST	0.00887174	0	#NAME?	0	1	1
ENSG00000260705	ENSG00000260705	TRBV11-3	HG7_PATCH:142296464-142296947	NOTEST	0	0	0	0	1	1
ENSG00000260706	ENSG00000260706	RP11-525K10.1	16:80099732-80597032	NOTEST	0	0	0	0	1	1
ENSG00000260707	ENSG00000260707	AC108004.3	HG990_PATCH:254331-264367	NOTEST	0	0	0	0	1	1
ENSG00000260709	ENSG00000260709	RARRES2P4	HG1032_PATCH:190959070-190959554	NOTEST	0	0	0	0	1	1
ENSG00000260710	ENSG00000260710	RP11-616M22.7	16:1344551-1349167	NOTEST	0	0	0	0	1	1
ENSG00000260711	ENSG00000260711	RP11-747H7.3	14:92047039-92333880	NOTEST	0	0	0	0	1	1
ENSG00000260712	ENSG00000260712	TRBJ2-6	HG7_PATCH:142558131-142558184	NOTEST	0	0	0	0	1	1
ENSG00000260713	ENSG00000260713	AC073464.11	HG686_PATCH:95559554-95570199	NOTEST	0	0	0	0	1	1
ENSG00000260714	ENSG00000260714	RP11-266L9.1	16:25027298-25032344	NOTEST	0	0	0	0	1	1
ENSG00000260715	ENSG00000260715	RP11-744D14.2	16:64189072-64190478	NOTEST	0	0	0	0	1	1
ENSG00000260716	ENSG00000260716	TONSL	HG243_PATCH:145483684-145499347	NOTEST	0	0	0	0	1	1
ENSG00000260717	ENSG00000260717	CCL4L1	HG75_PATCH:34538283-34540254	NOTEST	0	0	0	0	1	1
ENSG00000260719	ENSG00000260719	AC009133.17	16:29753783-29759620	NOTEST	0	0	0	0	1	1
ENSG00000260720	ENSG00000260720	RP11-271O3.1	9:31371608-31381488	NOTEST	0	0	0	0	1	1
ENSG00000260721	ENSG00000260721	AF067845.1	8:1316807-1317999	NOTEST	0	0	0	0	1	1

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ENSG00000260722	ENSG00000260722	VN1R67P	16:31812905-31813818	NOTEST	0	0	0	0	1	1
ENSG00000260723	ENSG00000260723	RP11-165M1.2	16:12070593-12704901	NOTEST	0	0	0	0	1	1
ENSG00000260724	ENSG00000260724	VN1R69P	16:34368884-34369446	NOTEST	0	0	0	0	1	1
ENSG00000260725	ENSG00000260725	AC005307.1	19:28909389-28920397	NOTEST	0	0	0	0	1	1
ENSG00000260726	ENSG00000260726	KLF8P1	16:48657346-48778553	NOTEST	0	0	0	0	1	1
ENSG00000260729	ENSG00000260729	RP11-106M3.2	15:72533521-72671129	NOTEST	0.0729851	0.0437433	-0.73854	0	1	1
ENSG00000260730	ENSG00000260730	AF146191.4	HG1032_PATCH:190701489-190861426	NOTEST	0	0	0	0	1	1
ENSG00000260731	ENSG00000260731	KRT8P22	16:78048579-78100658	NOTEST	0	0	0	0	1	1
ENSG00000260732	ENSG00000260732	TRBV5-5	HG7_PATCH:142204063-142204535	NOTEST	0	0	0	0	1	1
ENSG00000260733	ENSG00000260733	RP11-264L1.4	16:78133309-79246564	NOTEST	0	0	0	0	1	1
ENSG00000260734	ENSG00000260734	RP11-510M2.4	16:71464164-71466185	NOTEST	0	0	0	0	1	1
ENSG00000260735	ENSG00000260735	RP11-721I8.1	16:15068447-15248421	NOTEST	0.0477807	0.0190458	-1.32695	0	1	1
ENSG00000260736	ENSG00000260736	PRSS58	HG7_PATCH:141951962-141957878	NOTEST	0	0	0	0	1	1
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ENSG00000260738	ENSG00000260738	LINC00554	13:100647152-100650163	NOTEST	0	0	0	0	1	1
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ENSG00000260740	ENSG00000260740	AC026471.6	16:31494322-31520630	NOTEST	0	0	0	0	1	1
ENSG00000260741	ENSG00000260741	CTC-391G2.1	16:23194035-23228204	NOTEST	0	0	0	0	1	1
ENSG00000260742	ENSG00000260742	RP11-366L5.1	2:182752577-182756390	NOTEST	0.0587875	0.0390559	-0.589967	0	1	1
ENSG00000260743	ENSG00000260743	RP11-255C15.3	3:179058109-179059675	NOTEST	0.0299674	0.0555549	0.890523	0	1	1
ENSG00000260744	ENSG00000260744	RP11-329J18.3	16:47178233-47735434	NOTEST	0	0	0	0	1	1
ENSG00000260745	ENSG00000260745	TRBV4-1	HG7_PATCH:142013006-142013489	NOTEST	0	0	0	0	1	1
ENSG00000260746	ENSG00000260746	RP11-14K3.1	16:34872993-34879551	NOTEST	0	0	0	0	1	1
ENSG00000260748	ENSG00000260748	RP11-429J17.2	HG104_HG975_PATCH:144766621-144796068	NOTEST	0	0	0	0	1	1
ENSG00000260749	ENSG00000260749	RP11-114G11.2	HG14_PATCH:57492209-57493383	NOTEST	0	0	0	0	1	1
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ENSG00000260755	ENSG00000260755	RP11-403P17.3	16:66461199-66586447	NOTEST	0	0	0	0	1	1
ENSG00000260756	ENSG00000260756	RP11-609N14.1	16:10420290-10577495	NOTEST	0	0	0	0	1	1
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ENSG00000260758	ENSG00000260758	RP11-553E24.3	15:86621973-86623023	NOTEST	0	0	0	0	1	1
ENSG00000260759	ENSG00000260759	RP11-677O4.2	18:11666454-11670164	NOTEST	0	0.00325968	inf	0	1	1
ENSG00000260760	ENSG00000260760	PWRN3	15:24686273-24693114	NOTEST	0	0	0	0	1	1
ENSG00000260761	ENSG00000260761	RP11-184E9.2	5:25319942-25321455	NOTEST	0	0.0266849	inf	0	1	1
ENSG00000260762	ENSG00000260762	RP11-143N13.1	16:20592209-20618429	NOTEST	0	0	0	0	1	1
ENSG00000260763	ENSG00000260763	RP11-445O3.3	5:4436962-4440372	NOTEST	0	0	0	0	1	1
ENSG00000260764	ENSG00000260764	RNU7-63P	16:8768421-8962866	NOTEST	0	0	0	0	1	1
ENSG00000260765	ENSG00000260765	CES1P2	16:55762026-55784023	NOTEST	0	0	0	0	1	1
ENSG00000260767	ENSG00000260767	TRBV24-1	HG7_PATCH:142396837-142397350	NOTEST	0	0	0	0	1	1
ENSG00000260768	ENSG00000260768	TRBV21-1	HG7_PATCH:142378491-142378952	NOTEST	0	0	0	0	1	1
ENSG00000260769	ENSG00000260769	RP11-491F9.5	16:49370593-49372904	NOTEST	0	0	0	0	1	1
ENSG00000260770	ENSG00000260770	NKIRAS2	HG185_PATCH:40132690-40219330	NOTEST	0	0	0	0	1	1

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ENSG00000260773	ENSG00000260773	RP11-352G18.2	15:66570835-66626236	NOTEST	0.219626	0.137619	-0.674375	0	1	1
ENSG00000260775	ENSG00000260775	RP13-30A9.2	HG506_HG507_HG1000_PATCH:61208736-61210918	NOTEST	0	0	0	0	1	1
ENSG00000260776	ENSG00000260776	RP11-114H24.2	15:78206558-78219188	NOTEST	0	0	0	0	1	1
ENSG00000260777	ENSG00000260777	CTD-2008P7.1	17:26583400-26593395	NOTEST	0	0.00899615	inf	0	1	1
ENSG00000260779	ENSG00000260779	RP11-856M7.1	18:10661929-11148587	NOTEST	0	0	0	0	1	1
ENSG00000260780	ENSG00000260780	RP11-580I1.1	15:24451930-24471001	NOTEST	0	0	0	0	1	1
ENSG00000260781	ENSG00000260781	ARHGAP23P1	16:33709885-33739634	NOTEST	0	0.0124442	inf	0	1	1
ENSG00000260782	ENSG00000260782	RP11-480G7.2	16:46740890-46825952	NOTEST	0	0	0	0	1	1
ENSG00000260783	ENSG00000260783	TRBJ2-7	HG7_PATCH:142558348-142558395	NOTEST	0	0	0	0	1	1
ENSG00000260784	ENSG00000260784	AC026150.6	15:30808281-30810070	NOTEST	0	0	0	0	1	1
ENSG00000260785	ENSG00000260785	CASC17	17:69093915-69198318	NOTEST	0	0	0	0	1	1
ENSG00000260786	ENSG00000260786	RP11-112L7.1	5:42188367-42191625	NOTEST	0	0	0	0	1	1
ENSG00000260787	ENSG00000260787	RP11-797A18.4	15:77334177-77335533	NOTEST	0.168601	0.141768	-0.250081	0	1	1
ENSG00000260788	ENSG00000260788	RP11-298D21.1	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000260789	ENSG00000260789	GPSM1	HG998_2_PATCH:139235597-139267507	NOTEST	0	0	0	0	1	1
ENSG00000260790	ENSG00000260790	RP11-21M24.2	16:22357256-22547842	NOTEST	0.033629	0.0550405	0.710787	0	1	1
ENSG00000260791	ENSG00000260791	OR9A3P	HG7_PATCH:141562659-141563537	NOTEST	0	0	0	0	1	1
ENSG00000260792	ENSG00000260792	RP11-982M15.8	14:105127456-105131895	NOTEST	0.0261452	0.0155373	-0.750812	0	1	1
ENSG00000260793	ENSG00000260793	RP5-882C2.2	17:42269172-42301078	NOTEST	0.220916	0.304113	0.461113	0	1	1
ENSG00000260794	ENSG00000260794	TRBVA	HG7_PATCH:142421875-142422330	NOTEST	0	0	0	0	1	1
ENSG00000260795	ENSG00000260795	RP11-107C10.1	16:86939780-86940078	NOTEST	0	0	0	0	1	1
ENSG00000260796	ENSG00000260796	RP11-1348G14.5	16:28831890-28833354	NOTEST	0	0	0	0	1	1
ENSG00000260797	ENSG00000260797	CTD-2336H13.1	16:76770238-76962066	NOTEST	0	0	0	0	1	1
ENSG00000260798	ENSG00000260798	RP11-354M1.2	16:68771127-68869451	NOTEST	0	0	0	0	1	1
ENSG00000260799	ENSG00000260799	KRT8P50	15:43030931-43213007	NOTEST	0	0	0	0	1	1
ENSG00000260801	ENSG00000260801	OR4R3P	HG281_PATCH:49944600-49945438	NOTEST	0	0	0	0	1	1
ENSG00000260802	ENSG00000260802	LINC00890	X:110754889-110765627	NOTEST	0	0.00808898	inf	0	1	1
ENSG00000260803	ENSG00000260803	Z84812.4	16:61552-88321	NOTEST	0.0699397	0.0905718	0.372951	0	1	1
ENSG00000260805	ENSG00000260805	RP11-61J19.4	1:212731174-212733073	NOTEST	0.27069	0.37768	0.480522	0	1	1
ENSG00000260806	ENSG00000260806	RP11-872J21.3	14:96967146-97033448	NOTEST	0.329016	0.221419	-0.571382	0	1	1
ENSG00000260810	ENSG00000260810	CTD-2547L24.4	14:91724642-91725347	NOTEST	0	0	0	0	1	1
ENSG00000260811	ENSG00000260811	OR4C45	HG281_PATCH:50054411-50055332	NOTEST	0	0	0	0	1	1
ENSG00000260812	ENSG00000260812	RARRES2P7	16:34648649-34649118	NOTEST	0	0	0	0	1	1
ENSG00000260813	ENSG00000260813	AC073464.4	HG686_PATCH:95498402-95499591	NOTEST	0	0	0	0	1	1
ENSG00000260814	ENSG00000260814	RP11-107F6.3	15:42062953-42064930	NOTEST	0.101313	0	#NAME?	0	1	1
ENSG00000260815	ENSG00000260815	RP11-24M17.3	15:76016317-76055662	NOTEST	0	0	0	0	1	1
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ENSG00000260817	ENSG00000260817	RP11-382N13.4	16:5289802-7763340	NOTEST	0	0	0	0	1	1
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ENSG00000260823	ENSG00000260823	RP11-249C24.10	16:56643412-56645287	NOTEST	0	0	0	0	1	1
ENSG00000260824	ENSG00000260824	CTD-2235H24.2	15:75192327-75199462	NOTEST	0	0	0	0	1	1
ENSG00000260825	ENSG00000260825	GPR179	HG745_PATCH:36481412-36499730	NOTEST	0	0	0	0	1	1
ENSG00000260827	ENSG00000260827	RP11-1437A8.4	16:33202881-33264727	NOTEST	0	0	0	0	1	1
ENSG00000260828	ENSG00000260828	HMGB3P32	16:57637048-57637609	NOTEST	0	0	0	0	1	1
ENSG00000260829	ENSG00000260829	OR9P1P	HG7_PATCH:142807822-142808190	NOTEST	0	0	0	0	1	1
ENSG00000260830	ENSG00000260830	RP11-524O1.4	14:21852450-21853079	NOTEST	0	0.0459052	inf	0	1	1
ENSG00000260831	ENSG00000260831	GHc-362H12.3	X:103172004-103229570	NOTEST	0.00688661	0.00267457	-1.36449	0	1	1
ENSG00000260832	ENSG00000260832	CTD-3253I12.1	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000260833	ENSG00000260833	AC124789.1	17:36584661-36668628	NOTEST	0	0	0	0	1	1
ENSG00000260834	ENSG00000260834	RP11-256I9.2	16:65224875-65610203	NOTEST	0	0	0	0	1	1
ENSG00000260835	ENSG00000260835	RP11-468I15.1	16:5289802-7763340	NOTEST	0	0	0	0	1	1
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ENSG00000260838	ENSG00000260838	RP11-531A24.3	8:73859384-73862680	NOTEST	0	0	0	0	1	1
ENSG00000260839	ENSG00000260839	AC144838.3	HG987_PATCH:21559154-21560945	NOTEST	0	0	0	0	1	1
ENSG00000260840	ENSG00000260840	RP11-60H5.1	2:85291230-85294470	NOTEST	0	0.00388968	inf	0	1	1
ENSG00000260841	ENSG00000260841	CTC-205M6.5	5:180211781-180214869	NOTEST	0.228481	0.30613	0.42207	0	1	1
ENSG00000260842	ENSG00000260842	TEKT4	HG686_PATCH:95632415-95711088	NOTEST	0	0	0	0	1	1
ENSG00000260843	ENSG00000260843	TRBV5-4	HG7_PATCH:142184417-142185083	NOTEST	0	0	0	0	1	1
ENSG00000260844	ENSG00000260844	RP11-578F21.9	15:29008585-29009297	NOTEST	0.0274568	0	#NAME?	0	1	1
ENSG00000260845	ENSG00000260845	RP11-586K12.4	16:32747229-32752415	NOTEST	0	0	0	0	1	1
ENSG00000260846	ENSG00000260846	RP11-488I20.7	16:34569647-34571260	NOTEST	0.0411532	0	#NAME?	0	1	1
ENSG00000260847	ENSG00000260847	RP11-17M15.1	16:32199653-32204851	NOTEST	0	0	0	0	1	1
ENSG00000260848	ENSG00000260848	CTD-2009A10.1	16:73577839-73592421	NOTEST	0	0	0	0	1	1
ENSG00000260849	ENSG00000260849	TRBV3-2	HG7_PATCH:142059021-142059481	NOTEST	0	0	0	0	1	1
ENSG00000260850	ENSG00000260850	RP11-437L7.1	16:51388366-51390443	NOTEST	0	0	0	0	1	1
ENSG00000260851	ENSG00000260851	RP11-403P17.5	16:66461199-66586447	NOTEST	0	0	0	0	1	1
ENSG00000260852	ENSG00000260852	FBXL19-AS1	16:30930639-30967832	NOTEST	0.47505	0.332746	-0.513659	0	1	1
ENSG00000260854	ENSG00000260854	CTD-2144E22.8	16:34213114-34214215	NOTEST	0.0389891	0.0276448	-0.496061	0	1	1
ENSG00000260855	ENSG00000260855	RP11-439E19.10	1:246935138-246993361	NOTEST	0.113484	0.127926	0.172814	0	1	1
ENSG00000260856	ENSG00000260856	RP11-309M23.1	HG480_HG481_PATCH:950955-955100	NOTEST	0	0	0	0	1	1
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ENSG00000260858	ENSG00000260858	RP11-558A11.1	16:84288875-84294655	NOTEST	0	0	0	0	1	1
ENSG00000260859	ENSG00000260859	RP11-254F19.2	16:84853589-84954374	NOTEST	0	0	0	0	1	1
ENSG00000260860	ENSG00000260860	RP11-615I2.3	16:68670091-68756519	NOTEST	0	0	0	0	1	1
ENSG00000260861	ENSG00000260861	RP4-576H24.4	20:1497404-1600707	NOTEST	0	0	0	0	1	1
ENSG00000260862	ENSG00000260862	RP11-22H5.2	16:82660407-83841439	NOTEST	0	0	0	0	1	1

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ENSG00000260865	ENSG00000260865	CTA-331F8.1	16:58549382-58663790	NOTEST	0	0	0	0	1	1
ENSG00000260866	ENSG00000260866	RP11-626K17.5	16:32399455-32447521	NOTEST	0	0	0	0	1	1
ENSG00000260867	ENSG00000260867	RP11-459F6.1	16:58163432-58251709	NOTEST	0	0	0	0	1	1
ENSG00000260868	ENSG00000260868	RP11-394I13.1	2:174890007-174891891	NOTEST	0	0	0	0	1	1
ENSG00000260869	ENSG00000260869	AC002310.13	16:30535324-30569819	NOTEST	0	0.597251	inf	0	1	1
ENSG00000260870	ENSG00000260870	RP11-358M11.4	15:57617669-57618645	NOTEST	0	0	0	0	1	1
ENSG00000260871	ENSG00000260871	CTD-2373J6.1	5:89684284-89685180	NOTEST	0.040974	0.0144474	-1.50389	0	1	1
ENSG00000260872	ENSG00000260872	RP11-680G24.5	16:15068447-15248421	NOTEST	0.366198	0.399093	0.124104	0	1	1
ENSG00000260873	ENSG00000260873	SNTB2	HSCHR16_2_CTG3_1:69221024-69348087	NOTEST	0	0	0	0	1	1
ENSG00000260875	ENSG00000260875	RPS24P6	HG686_PATCH:95632415-95711088	NOTEST	0	0	0	0	1	1
ENSG00000260876	ENSG00000260876	RP11-345M22.1	16:79710004-79861047	NOTEST	0	0	0	0	1	1
ENSG00000260877	ENSG00000260877	RP11-211G23.2	11:69186230-69187279	NOTEST	0	0.179297	inf	0	1	1
ENSG00000260878	ENSG00000260878	RP11-320H14.1	4:46245564-46246232	NOTEST	0.0550523	0.066095	0.263738	0	1	1
ENSG00000260879	ENSG00000260879	RP11-483I13.5	1:108676657-108744113	NOTEST	0.106613	0.102934	-0.050655	0	1	1
ENSG00000260881	ENSG00000260881	TRBC2	HG7_PATCH:142561933-142563641	NOTEST	0	0	0	0	1	1
ENSG00000260882	ENSG00000260882	RP11-10K17.3	16:4932507-5147809	NOTEST	0.0556112	0.0433692	-0.358706	0	1	1
ENSG00000260883	ENSG00000260883	VN1R65P	16:31565425-31566233	NOTEST	0	0	0	0	1	1
ENSG00000260884	ENSG00000260884	AC009120.5	16:74330672-74403724	NOTEST	0.422301	0.401029	-0.0745659	0	1	1
ENSG00000260885	ENSG00000260885	TRBV6-2	HG7_PATCH:142049014-142049495	NOTEST	0	0	0	0	1	1
ENSG00000260886	ENSG00000260886	RP11-432I5.1	16:71599562-71612090	NOTEST	0	0.0149238	inf	0	1	1
ENSG00000260887	ENSG00000260887	RP11-142G1.2	16:52271993-52314211	NOTEST	0	0	0	0	1	1
ENSG00000260888	ENSG00000260888	RP13-30A9.1	HG506_HG507_HG1000_PATCH:61208736-61210918	NOTEST	0	0	0	0	1	1
ENSG00000260889	ENSG00000260889	CKBP1	16:46876543-46878530	NOTEST	0	0	0	0	1	1
ENSG00000260890	ENSG00000260890	TRBV7-9	HG7_PATCH:142270878-142271415	NOTEST	0	0	0	0	1	1
ENSG00000260891	ENSG00000260891	RP11-96D1.5	16:68021296-68272005	NOTEST	0	0	0	0	1	1
ENSG00000260892	ENSG00000260892	CTD-2026K11.1	15:75966662-76005189	NOTEST	0	0	0	0	1	1
ENSG00000260893	ENSG00000260893	AC133633.2	HG19_PATCH:2426351-2445053	NOTEST	0	0	0	0	1	1
ENSG00000260894	ENSG00000260894	CTD-2012K14.4	16:67552320-67580691	NOTEST	0	0	0	0	1	1
ENSG00000260896	ENSG00000260896	RP11-314O13.1	16:80862631-80926492	NOTEST	0.00725503	0.093066	3.6812	0	1	1
ENSG00000260897	ENSG00000260897	DNM1P30	15:30443074-30445612	NOTEST	0	0	0	0	1	1
ENSG00000260898	ENSG00000260898	ADPGK-AS1	15:73043709-73090540	NOTEST	0.130193	0.0727696	-0.839239	0	1	1
ENSG00000260899	ENSG00000260899	RP11-2C24.4	16:30709029-30787628	NOTEST	0.0976122	0.185675	0.92765	0	1	1
ENSG00000260900	ENSG00000260900	RP11-19N8.3	16:33054929-33140411	NOTEST	0	0	0	0	1	1
ENSG00000260901	ENSG00000260901	RP13-895J2.3	HG996_PATCH:132680923-132910380	NOTEST	0	0	0	0	1	1
ENSG00000260902	ENSG00000260902	RP11-95M5.1	3:14840837-14852921	NOTEST	0	0	0	0	1	1
ENSG00000260903	ENSG00000260903	XKR7	20:30555804-30591190	NOTEST	0	0	0	0	1	1
ENSG00000260904	ENSG00000260904	TRBV12-3	HG7_PATCH:142302037-142302543	NOTEST	0	0	0	0	1	1
ENSG00000260905	ENSG00000260905	RP11-105C19.1	16:22623863-22624804	NOTEST	0	0.0567221	inf	0	1	1
ENSG00000260907	ENSG00000260907	AC008088.4	17:20433354-20434194	NOTEST	0.0222023	0.0485996	1.13024	0	1	1

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ENSG00000260910	ENSG00000260910	LINC00565	13:114629486-114631817	NOTEST	0.0661364	0.024147	-1.4536	0	1	1
ENSG00000260911	ENSG00000260911	RP11-196G11.2	16:31054470-31061201	NOTEST	0.147088	0.0399227	-1.8814	0	1	1
ENSG00000260913	ENSG00000260913	RP11-243E13.1	18:10405129-10414512	NOTEST	0	0	0	0	1	1
ENSG00000260915	ENSG00000260915	TRBV14	HG7_PATCH:142329503-142329995	NOTEST	0	0	0	0	1	1
ENSG00000260918	ENSG00000260918	RP11-731J8.2	4:47433976-47440976	NOTEST	0.00392107	0.0101339	1.36987	0	1	1
ENSG00000260919	ENSG00000260919	CTD-3154N5.1	15:74890840-74988633	NOTEST	0.05692	0	#NAME?	0	1	1
ENSG00000260920	ENSG00000260920	RP1-228H13.5	1:40929990-40932436	NOTEST	0.392566	0.223602	-0.811999	0	1	1
ENSG00000260921	ENSG00000260921	RP11-989E6.8	16:32963313-33039358	NOTEST	0	0	0	0	1	1
ENSG00000260922	ENSG00000260922	RP11-538I12.3	16:77224731-77478233	NOTEST	0	0	0	0	1	1
ENSG00000260925	ENSG00000260925	TRBV8-1	HG7_PATCH:142080130-142080409	NOTEST	0	0	0	0	1	1
ENSG00000260926	ENSG00000260926	RP11-380D11.2	15:41901663-41904925	NOTEST	0	0	0	0	1	1
ENSG00000260927	ENSG00000260927	RP11-459F6.3	16:58163432-58251709	NOTEST	0	0.0810944	inf	0	1	1
ENSG00000260928	ENSG00000260928	SPCS2P1	15:43398422-43513481	NOTEST	0	0	0	0	1	1
ENSG00000260929	ENSG00000260929	RP11-327F22.1	16:50774820-50837249	NOTEST	0	0	0	0	1	1
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ENSG00000260931	ENSG00000260931	RP11-65L3.1	2:179265560-179267618	NOTEST	0.0157405	0.0189722	0.269408	0	1	1
ENSG00000260932	ENSG00000260932	RP11-483P21.6	16:83932730-83999937	NOTEST	0.0683191	0	#NAME?	0	1	1
ENSG00000260933	ENSG00000260933	RP11-164A6.1	16:18026576-18266920	NOTEST	0	0	0	0	1	1
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ENSG00000260936	ENSG00000260936	FTO-IT1	16:53737874-54155853	NOTEST	0.014118	0.0439108	1.63704	0	1	1
ENSG00000260937	ENSG00000260937	RP11-548M13.1	15:55348944-55384371	NOTEST	0	0	0	0	1	1
ENSG00000260938	ENSG00000260938	RP4-593C16.3	1:178449741-178450341	NOTEST	0.2613	0.20661	-0.338793	0	1	1
ENSG00000260939	ENSG00000260939	RP11-467J12.3	16:53044306-53045198	NOTEST	0	0	0	0	1	1
ENSG00000260940	ENSG00000260940	RP4-575N6.5	1:101708713-101709305	NOTEST	0	0	0	0	1	1
ENSG00000260943	ENSG00000260943	RP11-476D10.1	12:40534727-40536678	NOTEST	0	0	0	0	1	1
ENSG00000260944	ENSG00000260944	RP11-463O9.5	16:86598750-86602539	NOTEST	0	0	0	0	1	1
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ENSG00000260949	ENSG00000260949	KB-1836B5.1	8:37920398-37921309	NOTEST	0	0.0625864	inf	0	1	1
ENSG00000260950	ENSG00000260950	C17orf97	HG990_PATCH:254331-264367	NOTEST	0	0	0	0	1	1
ENSG00000260951	ENSG00000260951	RP5-978I12.1	7:25397858-25399527	NOTEST	0	0	0	0	1	1
ENSG00000260952	ENSG00000260952	ZNHIT3	HG75_PATCH:34814004-34869611	NOTEST	0	0	0	0	1	1
ENSG00000260953	ENSG00000260953	RP11-426C22.6	16:29262828-29519817	NOTEST	0	0	0	0	1	1
ENSG00000260954	ENSG00000260954	LA16c-425C2.1	16:1543344-1662111	NOTEST	0.127356	0.049691	-1.35781	0	1	1
ENSG00000260957	ENSG00000260957	RP11-299H22.7	15:62576388-62577205	NOTEST	0	0	0	0	1	1
ENSG00000260959	ENSG00000260959	RP11-350A1.2	15:24480224-24521976	NOTEST	0	0	0	0	1	1
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ENSG00000260963	ENSG00000260963	RP11-297L17.2	16:52586001-52686017	NOTEST	0	0	0	0	1	1
ENSG00000260965	ENSG00000260965	CTC-661I16.1	16:57355263-57356029	NOTEST	0	0	0	0	1	1
ENSG00000260966	ENSG00000260966	RP11-690D19.3	11:102921415-102926528	NOTEST	0.110723	0.192642	0.798971	0	1	1
ENSG00000260967	ENSG00000260967	RARRES2P5	16:34442273-34518517	NOTEST	0.33942	0.282777	-0.263409	0	1	1
ENSG00000260968	ENSG00000260968	SCRIB	HG104_HG975_PATCH:144873089-144897549	NOTEST	0	0	0	0	1	1
ENSG00000260969	ENSG00000260969	RP11-190D6.2	16:78133309-79246564	NOTEST	0	0	0	0	1	1
ENSG00000260970	ENSG00000260970	RP11-295D22.1	9:122257652-122286403	NOTEST	0	0	0	0	1	1
ENSG00000260971	ENSG00000260971	RP11-504A18.1	1:56713965-56724243	NOTEST	0	0	0	0	1	1
ENSG00000260972	ENSG00000260972	RP1-58B11.1	1:5553037-5554734	NOTEST	0	0	0	0	1	1
ENSG00000260973	ENSG00000260973	RP11-105C19.2	16:22621851-22623517	NOTEST	0	0	0	0	1	1
ENSG00000260974	ENSG00000260974	RP11-586K12.8	16:32684851-32690152	NOTEST	0	0	0	0	1	1
ENSG00000260975	ENSG00000260975	RP11-142G1.3	16:52231923-52261868	NOTEST	0.114858	0	#NAME?	0	1	1
ENSG00000260976	ENSG00000260976	GS1-120K12.4	1:184970658-184977815	NOTEST	0	0	0	0	1	1
ENSG00000260977	ENSG00000260977	RP11-333I13.1	2:47004921-47007384	NOTEST	0.0610829	0.0646271	0.0813699	0	1	1
ENSG00000260978	ENSG00000260978	RP11-73C9.1	15:23810453-23873064	NOTEST	0	0	0	0	1	1
ENSG00000260979	ENSG00000260979	RP11-77H9.8	16:8985950-9060847	NOTEST	0	0	0	0	1	1
ENSG00000260980	ENSG00000260980	RP11-626H12.3	HG536_PATCH:69870997-69880139	NOTEST	0	0	0	0	1	1
ENSG00000260981	ENSG00000260981	RP11-315A16.1	5:8785153-8785580	NOTEST	0.057979	0.226877	1.96831	0	1	1
ENSG00000260982	ENSG00000260982	RP5-1077H22.2	6:905461-909594	NOTEST	0	0	0	0	1	1
ENSG00000260983	ENSG00000260983	RP11-150D5.2	16:76262282-76296263	NOTEST	0	0	0	0	1	1
ENSG00000260984	ENSG00000260984	FGFR3P5	16:34442273-34518517	NOTEST	0.100315	0.12489	0.316116	0	1	1
ENSG00000260985	ENSG00000260985	RP11-457D2.3	HG544_PATCH:17851342-17953161	NOTEST	0	0	0	0	1	1
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ENSG00000260987	ENSG00000260987	RP11-423G4.7	12:109301516-109303778	NOTEST	0	0	0	0	1	1
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ENSG00000260989	ENSG00000260989	LA16c-395F10.2	16:1543344-1662111	NOTEST	0.0946209	0.188119	0.991414	0	1	1
ENSG00000260990	ENSG00000260990	RP3-518E13.2	1:175276353-175712906	NOTEST	0	0	0	0	1	1
ENSG00000260991	ENSG00000260991	RP11-616M22.9	16:1330161-1330545	NOTEST	0	0	0	0	1	1
ENSG00000260992	ENSG00000260992	DOCK9-AS2	13:99740072-99740879	NOTEST	0.112864	0.0893375	-0.33725	0	1	1
ENSG00000260993	ENSG00000260993	RP11-163E9.1	HG115_PATCH:102007151-102069956	NOTEST	0	0	0	0	1	1
ENSG00000260994	ENSG00000260994	RP11-14K3.3	16:34782287-34783200	NOTEST	0	0	0	0	1	1
ENSG00000260995	ENSG00000260995	RP11-165H23.1	9:81750336-81760589	NOTEST	0	0	0	0	1	1
ENSG00000260996	ENSG00000260996	RP13-122B23.8	9:140188319-140190173	NOTEST	0	0.0062018	inf	0	1	1
ENSG00000260997	ENSG00000260997	RP4-647J21.1	7:44998597-45000508	NOTEST	0	0	0	0	1	1
ENSG00000260998	ENSG00000260998	CNN2P8	HG686_PATCH:95501083-95501996	NOTEST	0	0	0	0	1	1
ENSG00000260999	ENSG00000260999	RP11-521L9.1	16:68877506-69119083	NOTEST	0	0	0	0	1	1
ENSG00000261000	ENSG00000261000	RP11-534L20.5	1:206677280-206677789	NOTEST	0.043946	0.0342409	-0.360011	0	1	1
ENSG00000261001	ENSG00000261001	RP11-598F7.1	HG858_PATCH:86601-88133	NOTEST	0	0	0	0	1	1
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ENSG00000261006	ENSG00000261006	RP11-439L8.2	HG989_PATCH:31960437-31961608	NOTEST	0	0	0	0	1	1
ENSG00000261007	ENSG00000261007	RP11-382N13.3	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000261008	ENSG00000261008	AC004158.2	16:72459383-72698908	NOTEST	0.0789291	0.0701459	-0.170198	0	1	1
ENSG00000261009	ENSG00000261009	RP11-1437A8.5	16:33271713-33274156	NOTEST	0	0	0	0	1	1
ENSG00000261011	ENSG00000261011	RP11-96C23.11	10:88695296-88784489	NOTEST	0.121478	0.102343	-0.24729	0	1	1
ENSG00000261012	ENSG00000261012	RP11-116D2.1	2:21222184-21223789	NOTEST	0	0	0	0	1	1
ENSG00000261013	ENSG00000261013	CTD-2050B12.1	16:56126898-56225006	NOTEST	0.0238038	0	#NAME?	0	1	1
ENSG00000261014	ENSG00000261014	RP11-370P15.2	16:63764180-63788661	NOTEST	0	0	0	0	1	1
ENSG00000261015	ENSG00000261015	RP1-90J20.11	6:3025024-3027659	NOTEST	0.216076	0.288302	0.416039	0	1	1
ENSG00000261016	ENSG00000261016	LCN1P2	HG79_PATCH:136193328-136194004	NOTEST	0	0	0	0	1	1
ENSG00000261017	ENSG00000261017	RP11-3M1.3	16:48093581-48093906	NOTEST	0	0	0	0	1	1
ENSG00000261018	ENSG00000261018	LL09NC01-254D11.1	9:136476919-136498221	NOTEST	0	0	0	0	1	1
ENSG00000261019	ENSG00000261019	RP11-111K18.2	7:42940870-42942238	NOTEST	0.0124075	0.00964409	-0.363501	0	1	1
ENSG00000261020	ENSG00000261020	RP11-744K17.1	17:21919350-21924060	NOTEST	0.0183521	0.0104253	-0.815855	0	1	1
ENSG00000261021	ENSG00000261021	PRPF38AP2	HG544_PATCH:17619360-17620211	NOTEST	0	0	0	0	1	1
ENSG00000261022	ENSG00000261022	TRBV7-7	HG7_PATCH:142233141-142233643	NOTEST	0	0	0	0	1	1
ENSG00000261023	ENSG00000261023	TRRAP	HG946_PATCH:98507244-98642555	NOTEST	0	0	0	0	1	1
ENSG00000261024	ENSG00000261024	GS1-279B7.1	1:185290288-185304171	NOTEST	0.0626512	0	#NAME?	0	1	1
ENSG00000261025	ENSG00000261025	RP11-84D1.2	1:25294913-25297356	NOTEST	0.0485492	0.00966934	-2.32796	0	1	1
ENSG00000261026	ENSG00000261026	CTD-3247F14.2	8:22536525-22541522	NOTEST	0.00307717	0.00890583	1.53315	0	1	1
ENSG00000261027	ENSG00000261027	TUBB7P	HG1032_PATCH:190903677-190906026	NOTEST	0	0	0	0	1	1
ENSG00000261028	ENSG00000261028	AC012322.1	16:64276511-64377813	NOTEST	0	0	0	0	1	1
ENSG00000261029	ENSG00000261029	CTD-2588J6.2	16:82203900-82209408	NOTEST	0	0	0	0	1	1
ENSG00000261030	ENSG00000261030	RP11-791M20.1	X:13111778-13112692	NOTEST	0	0	0	0	1	1
ENSG00000261031	ENSG00000261031	TRBV9	HG7_PATCH:142113401-142113923	NOTEST	0	0	0	0	1	1
ENSG00000261032	ENSG00000261032	CH17-235K9.4	HG75_PATCH:34569074-34569182	NOTEST	0	0	0	0	1	1
ENSG00000261033	ENSG00000261033	RP11-209D14.2	17:19911363-19912547	NOTEST	0.109393	0.0995766	-0.135648	0	1	1
ENSG00000261034	ENSG00000261034	CTD-3065J16.9	HG104_HG975_PATCH:145160173-145162819	NOTEST	0	0	0	0	1	1
ENSG00000261035	ENSG00000261035	RP11-151E14.1	20:59387059-59389267	NOTEST	0	0	0	0	1	1
ENSG00000261037	ENSG00000261037	CTC-471C19.1	5:6019141-6022396	NOTEST	0	0	0	0	1	1
ENSG00000261038	ENSG00000261038	RP1-149C7.1	6:93097558-93098545	NOTEST	0	0	0	0	1	1
ENSG00000261039	ENSG00000261039	RP11-417E7.2	6:169575400-169582835	NOTEST	0	0	0	0	1	1
ENSG00000261040	ENSG00000261040	CTD-2319I12.1	17:58156669-58169246	NOTEST	0.0375043	0.173917	2.21327	0	1	1
ENSG00000261041	ENSG00000261041	RP11-536P16.4	15:28791057-28794923	NOTEST	0	0	0	0	1	1
ENSG00000261042	ENSG00000261042	SLC52A2	HG243_PATCH:145407121-145416175	NOTEST	0	0	0	0	1	1
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ENSG00000261044	ENSG00000261044	AP006547.3	8:143701733-143702425	NOTEST	0	0.0630216	inf	0	1	1

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ENSG00000261046	ENSG00000261046	RP11-14K3.4	16:34787279-34788372	NOTEST	0.0293574	0.0354663	0.272723	0	1	1
ENSG00000261047	ENSG00000261047	AC137527.2	16:51277964-51278034	NOTEST	0	0	0	0	1	1
ENSG00000261048	ENSG00000261048	RP11-810K23.9	15:21095534-21095935	NOTEST	0	0	0	0	1	1
ENSG00000261049	ENSG00000261049	RP11-357N13.1	16:53737874-54155853	NOTEST	0	0	0	0	1	1
ENSG00000261051	ENSG00000261051	RP11-274H2.5	3:145777371-145779466	NOTEST	0.107019	0.158818	0.569509	0	1	1
ENSG00000261053	ENSG00000261053	CTD-2144E22.2	16:34320266-34320490	NOTEST	0	0	0	0	1	1
ENSG00000261055	ENSG00000261055	RP11-195M16.3	1:110438594-110440483	NOTEST	0.0156642	0	#NAME?	0	1	1
ENSG00000261056	ENSG00000261056	RP11-454F8.2	16:53088944-53363062	NOTEST	0.0192812	0.0736537	1.93356	0	1	1
ENSG00000261057	ENSG00000261057	LINC00555	13:103241721-103242163	NOTEST	0	0	0	0	1	1
ENSG00000261058	ENSG00000261058	RP11-252E2.2	16:75153455-75178098	NOTEST	0	0	0	0	1	1
ENSG00000261059	ENSG00000261059	OBP2B	HG79_PATCH:136080663-136084628	NOTEST	0	0	0	0	1	1
ENSG00000261060	ENSG00000261060	RP11-545A16.4	1:179559506-179560440	NOTEST	0	0	0	0	1	1
ENSG00000261063	ENSG00000261063	RP11-538I12.2	16:77224731-77478233	NOTEST	0.0397691	0	#NAME?	0	1	1
ENSG00000261065	ENSG00000261065	RP11-74C13.4	1:204100189-204121307	NOTEST	0	0	0	0	1	1
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ENSG00000261067	ENSG00000261067	RP11-264B17.3	16:28985541-29002104	NOTEST	0.281771	0.263606	-0.0961396	0	1	1
ENSG00000261068	ENSG00000261068	RP11-7K24.3	6:42059975-42061997	NOTEST	0	0	0	0	1	1
ENSG00000261069	ENSG00000261069	SNORD116-20	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000261070	ENSG00000261070	RP11-554A11.8	11:68914695-68939032	NOTEST	0.0331017	0.0268822	-0.300258	0	1	1
ENSG00000261071	ENSG00000261071	RP1-223E5.4	6:13574815-13615387	NOTEST	0.341007	0.146918	-1.21479	0	1	1
ENSG00000261072	ENSG00000261072	RP11-5N19.3	15:56379477-56535483	NOTEST	0	0	0	0	1	1
ENSG00000261073	ENSG00000261073	RP11-163E9.2	HG115_PATCH:102007151-102069956	NOTEST	0	0	0	0	1	1
ENSG00000261074	ENSG00000261074	QSOX2	HG998_1_PATCH:139098178-139137687	NOTEST	0	0	0	0	1	1
ENSG00000261075	ENSG00000261075	RP11-243A14.3	16:9539866-9549362	NOTEST	0	0	0	0	1	1
ENSG00000261076	ENSG00000261076	RP11-179B15.6	10:60085373-60086790	NOTEST	0.0433059	0	#NAME?	0	1	1
ENSG00000261077	ENSG00000261077	RP11-553E24.1	15:86683068-86683471	NOTEST	0	0	0	0	1	1
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ENSG00000261079	ENSG00000261079	RP11-252A24.3	16:74330672-74403724	NOTEST	0.00804337	0.0106862	0.40987	0	1	1
ENSG00000261080	ENSG00000261080	RP1-166H4.2	6:44777053-45632086	NOTEST	0	0	0	0	1	1
ENSG00000261081	ENSG00000261081	RP11-1H8.1	15:34671268-34880704	NOTEST	0	0	0	0	1	1
ENSG00000261082	ENSG00000261082	RP11-345M22.3	16:79710004-79861047	NOTEST	0	0	0	0	1	1
ENSG00000261083	ENSG00000261083	RP11-93I21.3	4:125421096-125479589	NOTEST	0.0168278	0.00721309	-1.22215	0	1	1
ENSG00000261084	ENSG00000261084	PPP1R1AP2	16:35146490-35146887	NOTEST	0	0	0	0	1	1
ENSG00000261085	ENSG00000261085	RP11-1049H7.1	HG19_PATCH:1993154-2142690	NOTEST	0	0	0	0	1	1
ENSG00000261086	ENSG00000261086	RP11-379H8.1	15:83205503-83378666	NOTEST	0	0	0	0	1	1
ENSG00000261089	ENSG00000261089	RP11-435I10.3	16:28425023-28426339	NOTEST	0	0	0	0	1	1
ENSG00000261090	ENSG00000261090	RP11-20G6.2	16:23031657-23034932	NOTEST	0	0	0	0	1	1
ENSG00000261091	ENSG00000261091	RP13-895J2.2	HG996_PATCH:132680923-132910380	NOTEST	0	0	0	0	1	1
ENSG00000261092	ENSG00000261092	RP11-21B23.2	16:50424826-50429044	NOTEST	0	0	0	0	1	1
ENSG00000261095	ENSG00000261095	RP11-899L11.1	16:87117167-87438385	NOTEST	0	0	0	0	1	1

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ENSG00000261096	ENSG00000261096	RP11-690I21.2	2:232674555-232677062	NOTEST	0.100249	0.145428	0.536708	0	1	1
ENSG00000261097	ENSG00000261097	LINC00563	13:46870579-46871979	NOTEST	0.0362533	0	#NAME?	0	1	1
ENSG00000261098	ENSG00000261098	RP11-819C21.1	11:107182857-107186997	NOTEST	0.0989371	0.0568226	-0.800045	0	1	1
ENSG00000261099	ENSG00000261099	CH17-260O16.3	HG75_PATCH:34601601-34662129	NOTEST	0	0	0	0	1	1
ENSG00000261102	ENSG00000261102	ATP5J2P6	15:66679154-66790151	NOTEST	0	0	0	0	1	1
ENSG00000261103	ENSG00000261103	RP11-298D21.3	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000261104	ENSG00000261104	RP11-734K21.5	2:9246721-9249994	NOTEST	0	0	0	0	1	1
ENSG00000261105	ENSG00000261105	RP11-173B14.5	13:76123618-76434004	NOTEST	0	0	0	0	1	1
ENSG00000261106	ENSG00000261106	U66061.31	HG7_PATCH:142445731-142458950	NOTEST	0	0	0	0	1	1
ENSG00000261107	ENSG00000261107	PHKG1P4	HG736_PATCH:57128282-57128994	NOTEST	0	0	0	0	1	1
ENSG00000261108	ENSG00000261108	RP11-586K12.5	16:32747229-32752415	NOTEST	0	0	0	0	1	1
ENSG00000261109	ENSG00000261109	PLEC	HG104_HG975_PATCH:144997316-145058904	NOTEST	0	0	0	0	1	1
ENSG00000261110	ENSG00000261110	TRBV27	HG7_PATCH:142445731-142458950	NOTEST	0	0	0	0	1	1
ENSG00000261111	ENSG00000261111	RP11-96K14.1	16:32646993-32647366	NOTEST	0	0	0	0	1	1
ENSG00000261112	ENSG00000261112	TRBV17	HG7_PATCH:142343261-142343994	NOTEST	0	0	0	0	1	1
ENSG00000261114	ENSG00000261114	RP11-325K4.2	16:56965959-56977798	NOTEST	0.610951	0.444592	-0.458576	0	1	1
ENSG00000261115	ENSG00000261115	TMEM178B	7:140774031-141180180	NOTEST	0.160598	0.214299	0.416169	0	1	1
ENSG00000261116	ENSG00000261116	RP3-523K23.2	6:54807964-54809897	NOTEST	0.0236991	0.00654944	-1.85539	0	1	1
ENSG00000261117	ENSG00000261117	RP11-333O1.1	2:12855540-12856353	NOTEST	0.223604	0.155699	-0.522182	0	1	1
ENSG00000261118	ENSG00000261118	RP11-104N10.1	16:89557324-89624176	NOTEST	0.162224	0.254338	0.648754	0	1	1
ENSG00000261119	ENSG00000261119	TRBJ2-4	HG7_PATCH:142557890-142557940	NOTEST	0	0	0	0	1	1
ENSG00000261120	ENSG00000261120	RP11-62H20.1	14:60386140-60558501	NOTEST	0	0	0	0	1	1
ENSG00000261121	ENSG00000261121	RP11-496D24.2	4:24661478-24673191	NOTEST	0	0	0	0	1	1
ENSG00000261122	ENSG00000261122	5S_rRNA	16:34977638-34990886	NOTEST	0	0	0	0	1	1
ENSG00000261123	ENSG00000261123	RP11-304L19.3	16:2089815-2185899	NOTEST	0.427541	0.406399	-0.0731676	0	1	1
ENSG00000261124	ENSG00000261124	AC135050.5	16:31072163-31085641	NOTEST	0.133817	0.0664424	-1.01008	0	1	1
ENSG00000261125	ENSG00000261125	HAP1	HG185_PATCH:39873993-39890896	NOTEST	0	0	0	0	1	1
ENSG00000261126	ENSG00000261126	RBFADN	18:77794345-77854968	NOTEST	0.213763	0.334356	0.645369	0	1	1
ENSG00000261127	ENSG00000261127	RP11-17M15.2	16:32300867-32321876	NOTEST	0	0.00474029	inf	0	1	1
ENSG00000261129	ENSG00000261129	RP11-361D14.2	4:145427051-145430153	NOTEST	0	0	0	0	1	1
ENSG00000261130	ENSG00000261130	RP11-1021N1.1	16:15489610-15737023	NOTEST	0	0	0	0	1	1
ENSG00000261131	ENSG00000261131	RP11-93O14.2	16:46690053-46723430	NOTEST	0	0	0	0	1	1
ENSG00000261132	ENSG00000261132	HSF1	HG243_PATCH:145346493-145370041	NOTEST	0	0	0	0	1	1
ENSG00000261134	ENSG00000261134	HLA-P	HSCHR6_MHC_MANN:29765136-29767145	NOTEST	0	0	0	0	1	1
ENSG00000261135	ENSG00000261135	RP4-798A10.7	1:16841139-16842249	NOTEST	0.548641	0.437311	-0.327203	0	1	1
ENSG00000261136	ENSG00000261136	RP11-37C7.3	15:39892231-40213093	NOTEST	0.131458	0.0943943	-0.477834	0	1	1
ENSG00000261137	ENSG00000261137	RP11-220H4.2	HG736_PATCH:57008033-57012046	NOTEST	0	0	0	0	1	1
ENSG00000261138	ENSG00000261138	AC016489.1	HG183_PATCH:62385675-62386050	NOTEST	0	0	0	0	1	1
ENSG00000261139	ENSG00000261139	CTD-2517M14.5	8:145703351-145732557	NOTEST	0.416446	0.211864	-0.974991	0	1	1
ENSG00000261140	ENSG00000261140	RP11-20I23.6	16:2587964-2653189	NOTEST	0	0	0	0	1	1
ENSG00000261141	ENSG00000261141	RP11-303E16.5	16:81087101-81130008	NOTEST	0	0	0	0	1	1

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ENSG00000261144	ENSG00000261144	RP11-102D18.1	16:59200854-59201056	NOTEST	0	0	0	0	1	1
ENSG00000261145	ENSG00000261145	RP11-296I10.5	16:70236256-70236362	NOTEST	0	0	0	0	1	1
ENSG00000261146	ENSG00000261146	RP11-2A4.4	3:137510814-137515520	NOTEST	0	0	0	0	1	1
ENSG00000261147	ENSG00000261147	RP11-697E2.6	15:90792761-90816463	NOTEST	0.0219612	0.0125734	-0.804585	0	1	1
ENSG00000261148	ENSG00000261148	RP13-895J2.7	HG996_PATCH:132910880-132912606	NOTEST	0	0	0	0	1	1
ENSG00000261149	ENSG00000261149	TMEM130	HG946_PATCH:98475799-98500083	NOTEST	0	0	0	0	1	1
ENSG00000261150	ENSG00000261150	EPPK1	HG104_HG975_PATCH:144940156-144955423	NOTEST	0	0	0	0	1	1
ENSG00000261151	ENSG00000261151	RP11-332G1.1	16:58125956-58126851	NOTEST	0	0	0	0	1	1
ENSG00000261152	ENSG00000261152	CTB-91J4.1	HG75_PATCH:34777515-34784896	NOTEST	0	0	0	0	1	1
ENSG00000261153	ENSG00000261153	RP11-104C4.2	16:33611244-33613234	NOTEST	0	0	0	0	1	1
ENSG00000261154	ENSG00000261154	RP11-571O6.1	16:77624702-77644578	NOTEST	0	0	0	0	1	1
ENSG00000261155	ENSG00000261155	FGF3	HG536_PATCH:69624991-69633792	NOTEST	0	0	0	0	1	1
ENSG00000261156	ENSG00000261156	RP11-215E13.1	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000261157	ENSG00000261157	AF146191.7	HG1032_PATCH:190942561-190943820	NOTEST	0	0	0	0	1	1
ENSG00000261158	ENSG00000261158	CTD-2583P5.3	16:12756918-12897874	NOTEST	0	0	0	0	1	1
ENSG00000261159	ENSG00000261159	RP11-723O4.9	3:128578558-128579369	NOTEST	0.17789	0.23339	0.391751	0	1	1
ENSG00000261160	ENSG00000261160	OR4A1P	HG281_PATCH:49919818-49920738	NOTEST	0	0	0	0	1	1
ENSG00000261161	ENSG00000261161	RP11-58A18.1	16:86679906-86702529	NOTEST	0	0	0	0	1	1
ENSG00000261162	ENSG00000261162	U85056.1	HG1032_PATCH:190962496-190964569	NOTEST	0	0	0	0	1	1
ENSG00000261163	ENSG00000261163	LEPREL4	HG185_PATCH:39958198-39968855	NOTEST	0	0	0	0	1	1
ENSG00000261164	ENSG00000261164	RP11-429J17.8	HG104_HG975_PATCH:144871089-144872629	NOTEST	0	0	0	0	1	1
ENSG00000261165	ENSG00000261165	CYP4F32P	HG686_PATCH:95523005-95524026	NOTEST	0	0	0	0	1	1
ENSG00000261166	ENSG00000261166	RP11-775H9.3	4:137018951-137020395	NOTEST	0	0	0	0	1	1
ENSG00000261168	ENSG00000261168	RP11-68I18.10	1:151102550-151104086	NOTEST	0.0544015	0.0153027	-1.82986	0	1	1
ENSG00000261170	ENSG00000261170	RP11-252A24.5	16:74456017-74469152	NOTEST	0	0	0	0	1	1
ENSG00000261171	ENSG00000261171	RP11-1136G4.1	16:54881158-54882145	NOTEST	0	0	0	0	1	1
ENSG00000261172	ENSG00000261172	RP11-356C4.5	16:90168678-90244752	NOTEST	0	0	0	0	1	1
ENSG00000261173	ENSG00000261173	RP11-169E6.1	16:47007899-47012894	NOTEST	0	0	0	0	1	1
ENSG00000261174	ENSG00000261174	RP11-844G16.1	15:56536206-56757335	NOTEST	0	0	0	0	1	1
ENSG00000261175	ENSG00000261175	CTD-2015G9.2	16:86755696-86771432	NOTEST	0	0	0	0	1	1
ENSG00000261176	ENSG00000261176	RP11-2L4.1	16:82587653-82608815	NOTEST	0	0	0	0	1	1
ENSG00000261177	ENSG00000261177	RP11-805I24.1	16:86115014-86123132	NOTEST	0	0	0	0	1	1
ENSG00000261178	ENSG00000261178	RP11-90K18.1	16:60959636-60962445	NOTEST	0	0	0	0	1	1
ENSG00000261180	ENSG00000261180	CLEC5A	HG7_PATCH:141607612-141806547	NOTEST	0	0	0	0	1	1
ENSG00000261181	ENSG00000261181	RP11-467M13.2	16:16488768-16492451	NOTEST	0	0	0	0	1	1
ENSG00000261182	ENSG00000261182	RP11-201A3.1	1:188187530-188189807	NOTEST	0	0	0	0	1	1
ENSG00000261183	ENSG00000261183	RP11-532F12.5	15:41128005-41150405	NOTEST	0	0.256447	inf	0	1	1
ENSG00000261184	ENSG00000261184	RP11-196O2.1	7:36134881-36140263	NOTEST	0	0	0	0	1	1
ENSG00000261185	ENSG00000261185	RP11-317P15.5	1:182610950-182612442	NOTEST	0	0	0	0	1	1
ENSG00000261186	ENSG00000261186	RP11-341N2.1	2:243029504-243030608	NOTEST	0.124521	0.180278	0.533838	0	1	1

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ENSG00000261189	ENSG00000261189	RP3-512B11.3	6:7540683-7541571	NOTEST	0.037887	0.0161116	-1.2336	0	1	1
ENSG00000261190	ENSG00000261190	C16orf97	16:52039398-52112386	NOTEST	0	0	0	0	1	1
ENSG00000261191	ENSG00000261191	RP11-16L14.2	15:36871811-37110660	NOTEST	0	0	0	0	1	1
ENSG00000261192	ENSG00000261192	RNF126P1	17:55122838-55124158	NOTEST	0	0	0	0	1	1
ENSG00000261193	ENSG00000261193	RP11-863P13.5	16:88112766-88120989	NOTEST	0	0.0271405	inf	0	1	1
ENSG00000261194	ENSG00000261194	RP11-704C2.1	18:73408033-73424340	NOTEST	0	0	0	0	1	1
ENSG00000261196	ENSG00000261196	CYP4A43P	1:47427035-47516423	NOTEST	0	0	0	0	1	1
ENSG00000261197	ENSG00000261197	RP11-598D12.2	16:33817728-33853828	NOTEST	0	0	0	0	1	1
ENSG00000261198	ENSG00000261198	RP11-26O3.1	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000261199	ENSG00000261199	UBE2FP2	16:63214513-63214975	NOTEST	0	0	0	0	1	1
ENSG00000261200	ENSG00000261200	RP11-989E6.10	16:33344308-33348279	NOTEST	0.0226881	0.0337211	0.571712	0	1	1
ENSG00000261201	ENSG00000261201	DUX4L2	HG1032_PATCH:191012159-191013719	NOTEST	0	0	0	0	1	1
ENSG00000261202	ENSG00000261202	RP3-496C20.1	22:40390952-40440534	NOTEST	0	0.00808516	inf	0	1	1
ENSG00000261203	ENSG00000261203	RP11-347C12.8	16:30229540-30233251	NOTEST	0	0	0	0	1	1
ENSG00000261204	ENSG00000261204	AC004449.6	19:637104-637537	NOTEST	0	0	0	0	1	1
ENSG00000261205	ENSG00000261205	NIFKP4	15:75544083-75545275	NOTEST	0	0	0	0	1	1
ENSG00000261206	ENSG00000261206	LINC00561	13:76506530-76509268	NOTEST	0	0	0	0	1	1
ENSG00000261207	ENSG00000261207	LA16c-361A3.3	16:1756183-1821731	NOTEST	0.468004	0.262009	-0.836905	0	1	1
ENSG00000261208	ENSG00000261208	RP11-452D12.1	14:52753514-52755986	NOTEST	0	0	0	0	1	1
ENSG00000261209	ENSG00000261209	RP11-443K8.1	2:108934180-108935067	NOTEST	0	0	0	0	1	1
ENSG00000261210	ENSG00000261210	CLEC19A	16:19297060-19333467	NOTEST	0	0	0	0	1	1
ENSG00000261211	ENSG00000261211	RP1-80N2.3	6:6680541-6683866	NOTEST	0.00470852	0	#NAME?	0	1	1
ENSG00000261212	ENSG00000261212	RP3-507I15.2	X:140267419-140267773	NOTEST	0	0	0	0	1	1
ENSG00000261213	ENSG00000261213	RP11-510C10.4	1:75588202-75589612	NOTEST	0	0	0	0	1	1
ENSG00000261214	ENSG00000261214	TRBV12-2	HG7_PATCH:142162382-142162825	NOTEST	0	0	0	0	1	1
ENSG00000261215	ENSG00000261215	RP11-195F19.30	9:34638129-34681295	NOTEST	0.0862981	0.0179449	-2.26576	0	1	1
ENSG00000261216	ENSG00000261216	RP11-166B2.5	16:11945505-12009939	NOTEST	0	0	0	0	1	1
ENSG00000261217	ENSG00000261217	RP11-598D12.3	16:33790872-33794018	NOTEST	0	0	0	0	1	1
ENSG00000261218	ENSG00000261218	RP11-960L18.1	16:81771852-81991899	NOTEST	0	0	0	0	1	1
ENSG00000261219	ENSG00000261219	RP11-344A16.2	15:57884105-58074960	NOTEST	0	0	0	0	1	1
ENSG00000261220	ENSG00000261220	RP11-629O1.2	8:134585425-134586104	NOTEST	0.473851	0.387797	-0.289131	0	1	1
ENSG00000261222	ENSG00000261222	CTD-2006K23.1	17:72595978-72603368	NOTEST	0.0170156	0.0318841	0.905981	0	1	1
ENSG00000261225	ENSG00000261225	PRSS3P1	HG7_PATCH:142500929-142504458	NOTEST	0	0	0	0	1	1
ENSG00000261226	ENSG00000261226	RP11-830F9.7	16:88941265-89043612	NOTEST	0.00993553	0	#NAME?	0	1	1
ENSG00000261227	ENSG00000261227	AC140912.1	16:73265953-73267869	NOTEST	0	0	0	0	1	1
ENSG00000261228	ENSG00000261228	AC078899.1	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000261229	ENSG00000261229	RP11-38G5.4	15:80125926-80217194	NOTEST	0.223585	0.313805	0.489046	0	1	1
ENSG00000261230	ENSG00000261230	CPSF1	HG243_PATCH:145428003-145464191	NOTEST	0	0	0	0	1	1
ENSG00000261231	ENSG00000261231	RP11-523L20.2	16:47758478-47942342	NOTEST	0	0	0	0	1	1

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ENSG00000261233	ENSG00000261233	ABCD1P3	16:32486371-32489571	NOTEST	0	0	0	0	1	1
ENSG00000261234	ENSG00000261234	RP11-356O24.1	16:65972091-65972356	NOTEST	0	0	0	0	1	1
ENSG00000261235	ENSG00000261235	RP11-510J16.5	16:82068608-82173236	NOTEST	0	0	0	0	1	1
ENSG00000261236	ENSG00000261236	BOP1	HG243_PATCH:145317004-145346273	NOTEST	0	0	0	0	1	1
ENSG00000261237	ENSG00000261237	TRBV5-3	HG7_PATCH:142110712-142111179	NOTEST	0	0	0	0	1	1
ENSG00000261238	ENSG00000261238	AC009166.5	16:51169885-51185278	NOTEST	0	0	0	0	1	1
ENSG00000261239	ENSG00000261239	ANKRD26P1	16:46503252-46603009	NOTEST	0	0.0280619	inf	0	1	1
ENSG00000261240	ENSG00000261240	RP11-304L19.4	16:2089815-2185899	NOTEST	0	0	0	0	1	1
ENSG00000261241	ENSG00000261241	RP11-883G14.1	16:50918119-50934962	NOTEST	0	0	0	0	1	1
ENSG00000261242	ENSG00000261242	CTD-2302E22.4	14:64010286-64011382	NOTEST	0.0745787	0.0829353	0.153224	0	1	1
ENSG00000261243	ENSG00000261243	RP11-517C16.4	16:84511680-84587639	NOTEST	0	0.166087	inf	0	1	1
ENSG00000261244	ENSG00000261244	RP11-114H24.7	15:78206558-78219188	NOTEST	0	0	0	0	1	1
ENSG00000261245	ENSG00000261245	RP11-120K18.3	16:31366454-31394318	NOTEST	0	0	0	0	1	1
ENSG00000261246	ENSG00000261246	CCDC166	HG104_HG975_PATCH:144766621-144796068	NOTEST	0	0	0	0	1	1
ENSG00000261247	ENSG00000261247	GOLGA8T	15:30427351-30437770	NOTEST	0.0156002	0.0187908	0.268461	0	1	1
ENSG00000261248	ENSG00000261248	AC009120.10	16:74088049-74330660	NOTEST	0	0	0	0	1	1
ENSG00000261249	ENSG00000261249	RP11-19D2.2	20:7282702-7288079	NOTEST	0	0	0	0	1	1
ENSG00000261250	ENSG00000261250	RP11-545A16.1	1:179334854-179545087	NOTEST	0	0	0	0	1	1
ENSG00000261251	ENSG00000261251	RP3-388M5.9	22:44208335-44213274	NOTEST	0.108641	0.0849364	-0.355117	0	1	1
ENSG00000261252	ENSG00000261252	RP11-318L16.6	1:211608413-211608675	NOTEST	0.156119	0.349264	1.16167	0	1	1
ENSG00000261254	ENSG00000261254	RP4-714D9.5	1:100496121-100501188	NOTEST	0.0849941	0.0843382	-0.0111776	0	1	1
ENSG00000261256	ENSG00000261256	AC126327.6	HG75_PATCH:34756461-34765353	NOTEST	0	0	0	0	1	1
ENSG00000261257	ENSG00000261257	RP11-673E11.2	11:125970399-125972308	NOTEST	0	0	0	0	1	1
ENSG00000261258	ENSG00000261258	FKBP10	HG185_PATCH:39968961-39979465	NOTEST	0	0	0	0	1	1
ENSG00000261259	ENSG00000261259	RP11-19N8.2	16:32963313-33039358	NOTEST	0	0	0	0	1	1
ENSG00000261260	ENSG00000261260	CTD-2520I13.1	16:71335485-71336772	NOTEST	0	0	0	0	1	1
ENSG00000261261	ENSG00000261261	RP11-297L17.4	16:52586001-52686017	NOTEST	0	0	0	0	1	1
ENSG00000261262	ENSG00000261262	TRBV30	HG7_PATCH:142573478-142574292	NOTEST	0	0	0	0	1	1
ENSG00000261263	ENSG00000261263	RP11-586K12.13	16:32660513-32677854	NOTEST	0	0	0	0	1	1
ENSG00000261264	ENSG00000261264	TRPV5	HG7_PATCH:142668775-142694414	NOTEST	0	0	0	0	1	1
ENSG00000261265	ENSG00000261265	CTD-2515H24.4	15:57668164-57842925	NOTEST	0	0	0	0	1	1
ENSG00000261266	ENSG00000261266	CTD-2196E14.5	16:23688976-23724821	NOTEST	0.19033	0.144431	-0.398122	0	1	1
ENSG00000261267	ENSG00000261267	RP11-44I10.3	16:48572636-48654059	NOTEST	0	0	0	0	1	1
ENSG00000261268	ENSG00000261268	RP11-308D13.3	4:140539289-140544386	NOTEST	0	0	0	0	1	1
ENSG00000261269	ENSG00000261269	RP11-389C8.2	5:71735729-71738214	NOTEST	0.00641786	0	#NAME?	0	1	1
ENSG00000261270	ENSG00000261270	RP11-325K4.3	16:56965959-56977798	NOTEST	0.0639003	0.106023	0.730486	0	1	1
ENSG00000261272	ENSG00000261272	MUC22	6:30978250-31003179	NOTEST	0	0.00178145	inf	0	1	1
ENSG00000261273	ENSG00000261273	LA16c-444G7.1	16:88268390-88336117	NOTEST	0	0	0	0	1	1
ENSG00000261274	ENSG00000261274	RP11-244B22.5	16:34442273-34518517	NOTEST	0.529212	0.594441	0.167687	0	1	1

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ENSG00000261276	ENSG00000261276	RP11-554A11.5	11:68771861-68785915	NOTEST	0	0	0	0	1	1
ENSG00000261277	ENSG00000261277	OR4H6P	15:22278009-22413497	NOTEST	0	0	0	0	1	1
ENSG00000261278	ENSG00000261278	RP11-430C1.2	16:59889256-60087875	NOTEST	0	0	0	0	1	1
ENSG00000261279	ENSG00000261279	ULK4P1	15:32684982-32727434	NOTEST	0.0496331	0.0727451	0.551547	0	1	1
ENSG00000261280	ENSG00000261280	CTD-3105H18.13	19:12456762-12458752	NOTEST	0	0	0	0	1	1
ENSG00000261281	ENSG00000261281	RP11-361M10.4	15:72968123-72978490	NOTEST	0	0	0	0	1	1
ENSG00000261282	ENSG00000261282	SOD1P2	16:51141481-51141932	NOTEST	0	0	0	0	1	1
ENSG00000261283	ENSG00000261283	PRKRIP1	HG115_PATCH:102007151-102069956	NOTEST	0	0	0	0	1	1
ENSG00000261284	ENSG00000261284	RBM22P13	16:31874953-31876197	NOTEST	0	0	0	0	1	1
ENSG00000261285	ENSG00000261285	RP11-481E4.2	16:82529597-82544524	NOTEST	0	0	0	0	1	1
ENSG00000261286	ENSG00000261286	RP11-517C16.2	16:84402132-84500967	NOTEST	0.0157595	0.00737541	-1.09543	0	1	1
ENSG00000261287	ENSG00000261287	TRBV6-4	HG7_PATCH:142102302-142102758	NOTEST	0	0	0	0	1	1
ENSG00000261288	ENSG00000261288	RP11-20I23.11	16:2587964-2653189	NOTEST	0	0	0	0	1	1
ENSG00000261289	ENSG00000261289	RP11-170L3.5	16:31963480-31963794	NOTEST	0	0	0	0	1	1
ENSG00000261290	ENSG00000261290	CYP4A44P	1:47427035-47516423	NOTEST	0	0	0	0	1	1
ENSG00000261291	ENSG00000261291	RP11-295M3.2	16:53088944-53363062	NOTEST	0	0	0	0	1	1
ENSG00000261292	ENSG00000261292	RP11-389G6.3	3:97478366-97480374	NOTEST	0	0	0	0	1	1
ENSG00000261293	ENSG00000261293	RP11-276H1.2	16:12070593-12704901	NOTEST	0	0	0	0	1	1
ENSG00000261294	ENSG00000261294	RP11-616M22.3	16:1203240-1275257	NOTEST	0	0	0	0	1	1
ENSG00000261295	ENSG00000261295	RP11-524D16__A.3	X:99928326-99928978	NOTEST	0	0	0	0	1	1
ENSG00000261296	ENSG00000261296	RP11-299H22.6	15:62566361-62570564	NOTEST	0.0133389	0.0163278	0.291691	0	1	1
ENSG00000261297	ENSG00000261297	SLC39A4	HG243_PATCH:145464394-145471798	NOTEST	0	0	0	0	1	1
ENSG00000261298	ENSG00000261298	RP11-309M7.1	2:235131481-235133158	NOTEST	0	0	0	0	1	1
ENSG00000261299	ENSG00000261299	RP11-80F22.11	16:34659734-34660854	NOTEST	0	0	0	0	1	1
ENSG00000261300	ENSG00000261300	PIGW	HG75_PATCH:34814004-34869611	NOTEST	0	0	0	0	1	1
ENSG00000261301	ENSG00000261301	OR9A4	HG7_PATCH:141607612-141806547	NOTEST	0	0	0	0	1	1
ENSG00000261302	ENSG00000261302	RP11-343H19.1	16:56742683-56763880	NOTEST	0.0987499	0.115092	0.220937	0	1	1
ENSG00000261303	ENSG00000261303	RP11-160C18.2	15:78916460-79027837	NOTEST	0	0.00915418	inf	0	1	1
ENSG00000261304	ENSG00000261304	CTD-2125J1.1	15:34943335-34947965	NOTEST	0	0	0	0	1	1
ENSG00000261305	ENSG00000261305	RP4-584D14.7	7:150038859-150039696	NOTEST	0	0	0	0	1	1
ENSG00000261306	ENSG00000261306	SURF6	HG79_PATCH:136206250-136211933	NOTEST	0	0	0	0	1	1
ENSG00000261307	ENSG00000261307	RP11-157P23.2	18:44812095-45120914	NOTEST	0	0	0	0	1	1
ENSG00000261308	ENSG00000261308	RP11-923I11.7	12:52214242-52216199	NOTEST	0.0717047	0.0569598	-0.332125	0	1	1
ENSG00000261309	ENSG00000261309	KCNJ12	HG987_PATCH:21279508-21323179	NOTEST	0	0	0	0	1	1
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ENSG00000261312	ENSG00000261312	AC002550.5	16:19566561-19897489	NOTEST	0.0500273	0.0452085	-0.146121	0	1	1
ENSG00000261313	ENSG00000261313	RP11-2C15.1	16:75872527-75894765	NOTEST	0	0	0	0	1	1
ENSG00000261314	ENSG00000261314	RP11-359E8.5	1:211756356-211757067	NOTEST	0	0	0	0	1	1
ENSG00000261315	ENSG00000261315	LARP4P	15:36871811-37110660	NOTEST	0	0	0	0	1	1
ENSG00000261316	ENSG00000261316	CTC-400I9.1	19:31398105-31400062	NOTEST	0	0	0	0	1	1

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ENSG00000261318	ENSG00000261318	RP11-653J6.1	15:66570835-66626236	NOTEST	0	0	0	0	1	1
ENSG00000261319	ENSG00000261319	RP11-279O17.1	16:8348493-8349774	NOTEST	0	0	0	0	1	1
ENSG00000261320	ENSG00000261320	RP11-297D21.2	16:67464554-67471456	NOTEST	0	0.0380806	inf	0	1	1
ENSG00000261321	ENSG00000261321	FAM101B	HG990_PATCH:289768-295730	NOTEST	0	0	0	0	1	1
ENSG00000261322	ENSG00000261322	RP11-598F7.5	HG858_PATCH:116764-232399	NOTEST	0	0	0	0	1	1
ENSG00000261323	ENSG00000261323	OR6V1	HG7_PATCH:142812925-142813953	NOTEST	0	0	0	0	1	1
ENSG00000261324	ENSG00000261324	RP11-174G6.5	12:14915437-14920865	NOTEST	0.500628	0.541258	0.112578	0	1	1
ENSG00000261325	ENSG00000261325	AC140542.2	16:47758478-47942342	NOTEST	0	0	0	0	1	1
ENSG00000261326	ENSG00000261326	RP5-1057J7.6	1:23607801-23613245	NOTEST	0.518213	0.418352	-0.308828	0	1	1
ENSG00000261327	ENSG00000261327	RP11-863P13.3	16:88210894-88219696	NOTEST	0.0253911	0	#NAME?	0	1	1
ENSG00000261328	ENSG00000261328	AC097374.3	HG686_PATCH:95632415-95711088	NOTEST	0	0	0	0	1	1
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ENSG00000261331	ENSG00000261331	CTD-2144E22.7	16:34213114-34214215	NOTEST	0	0	0	0	1	1
ENSG00000261332	ENSG00000261332	RP11-297C4.1	16:30483978-30534506	NOTEST	0	0	0	0	1	1
ENSG00000261333	ENSG00000261333	CD24P2	15:56363618-56363837	NOTEST	0	0	0	0	1	1
ENSG00000261334	ENSG00000261334	RP11-65J3.14	9:132242883-132244817	NOTEST	0.0610472	0	#NAME?	0	1	1
ENSG00000261335	ENSG00000261335	RP11-318A15.2	17:74668023-74707098	NOTEST	0.269639	0.0683488	-1.98004	0	1	1
ENSG00000261336	ENSG00000261336	EIF4BP5	16:47178233-47735434	NOTEST	0	0.0220473	inf	0	1	1
ENSG00000261337	ENSG00000261337	RP11-498D10.5	16:71879893-71962913	NOTEST	0.0251333	0.0177481	-0.501937	0	1	1
ENSG00000261338	ENSG00000261338	RP11-378A13.1	2:219120041-219122087	NOTEST	0.330547	0.195012	-0.761291	0	1	1
ENSG00000261339	ENSG00000261339	TRBJ2-2	HG7_PATCH:142557452-142557503	NOTEST	0	0	0	0	1	1
ENSG00000261340	ENSG00000261340	RP11-215H22.1	11:30001659-30003939	NOTEST	0	0	0	0	1	1
ENSG00000261341	ENSG00000261341	CTD-2568A17.1	19:51279397-51289467	NOTEST	0.0458427	0	#NAME?	0	1	1
ENSG00000261342	ENSG00000261342	AC006538.1	19:2714564-2740150	NOTEST	0.355948	0.515691	0.534841	0	1	1
ENSG00000261345	ENSG00000261345	GATA5	HG506_HG507_HG1000_PATCH:61038552-61051026	NOTEST	0	0	0	0	1	1
ENSG00000261346	ENSG00000261346	RP11-297C4.2	16:30483978-30534506	NOTEST	0	0	0	0	1	1
ENSG00000261347	ENSG00000261347	AP000439.5	11:69282365-69284473	NOTEST	0	0	0	0	1	1
ENSG00000261348	ENSG00000261348	RP11-510M2.1	16:71444342-71460367	NOTEST	0	0	0	0	1	1
ENSG00000261349	ENSG00000261349	RP3-465N24.5	1:25568727-25756683	NOTEST	0.0515606	0.080414	0.641179	0	1	1
ENSG00000261350	ENSG00000261350	RP11-80F22.14	16:34725544-34727817	NOTEST	0	0	0	0	1	1
ENSG00000261352	ENSG00000261352	ZNF90	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000261353	ENSG00000261353	CTA-14H9.5	6:26527290-26527632	NOTEST	0	0	0	0	1	1
ENSG00000261354	ENSG00000261354	OR4A18P	HG281_PATCH:49938942-49940030	NOTEST	0	0	0	0	1	1
ENSG00000261355	ENSG00000261355	RP11-698N11.4	11:35835881-35839557	NOTEST	0.294501	0.409063	0.47405	0	1	1
ENSG00000261356	ENSG00000261356	RP11-46D6.5	16:46605448-46606048	NOTEST	0	0	0	0	1	1
ENSG00000261357	ENSG00000261357	RP11-626G11.1	16:18995255-19091417	NOTEST	0	0	0	0	1	1
ENSG00000261358	ENSG00000261358	RP11-598F7.4	HG858_PATCH:116764-232399	NOTEST	0	0	0	0	1	1
ENSG00000261359	ENSG00000261359	C16orf98	16:31212805-31214773	NOTEST	0.222322	0.0345188	-2.6872	0	1	1
ENSG00000261360	ENSG00000261360	CTD-2165H16.4	5:14661916-14664713	NOTEST	0.402124	0.215958	-0.896892	0	1	1

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ENSG00000261362	ENSG00000261362	RP11-467M13.3	16:16635073-16635704	NOTEST	0	0	0	0	1	1
ENSG00000261363	ENSG00000261363	RP11-134D3.2	16:87100310-87103354	NOTEST	0	0	0	0	1	1
ENSG00000261364	ENSG00000261364	RP11-59E19.4	3:108895284-108896212	NOTEST	0.133958	0.205533	0.617585	0	1	1
ENSG00000261365	ENSG00000261365	RP11-483E23.5	15:28718467-28718594	NOTEST	0	0	0	0	1	1
ENSG00000261366	ENSG00000261366	MANEA-AS1	6:96023058-96025326	NOTEST	0.134909	0.0943088	-0.516518	0	1	1
ENSG00000261367	ENSG00000261367	RP11-455F5.4	16:30116130-30125177	NOTEST	0	0	0	0	1	1
ENSG00000261368	ENSG00000261368	RP11-96B5.4	10:52724029-52724980	NOTEST	0	0	0	0	1	1
ENSG00000261369	ENSG00000261369	RP11-474B12.1	16:47178233-47735434	NOTEST	0	0	0	0	1	1
ENSG00000261370	ENSG00000261370	RPL14P5	HG480_HG481_PATCH:969237-970836	NOTEST	0	0	0	0	1	1
ENSG00000261371	ENSG00000261371	PECAM1	HG183_PATCH:62399862-62491136	NOTEST	0	0	0	0	1	1
ENSG00000261372	ENSG00000261372	RP11-529H20.6	14:92511118-92516990	NOTEST	0.204891	0.0231215	-3.14754	0	1	1
ENSG00000261374	ENSG00000261374	RP11-64K12.10	15:40666598-40668192	NOTEST	0	0	0	0	1	1
ENSG00000261375	ENSG00000261375	RP11-632K20.6	15:32781467-32783787	NOTEST	0	0	0	0	1	1
ENSG00000261376	ENSG00000261376	RP11-525K10.2	16:80099732-80597032	NOTEST	0	0	0	0	1	1
ENSG00000261378	ENSG00000261378	RAB5C	HG185_PATCH:40281227-40311269	NOTEST	0	0	0	0	1	1
ENSG00000261379	ENSG00000261379	RP11-395N3.1	2:227664861-227675745	NOTEST	0.0347429	0.0257466	-0.432337	0	1	1
ENSG00000261380	ENSG00000261380	FAM83H	HG104_HG975_PATCH:144806102-144815971	NOTEST	0	0	0	0	1	1
ENSG00000261381	ENSG00000261381	CNN2P11	HG686_PATCH:95489420-95489682	NOTEST	0	0	0	0	1	1
ENSG00000261382	ENSG00000261382	RP11-461L18.1	5:153281018-153282783	NOTEST	0	0	0	0	1	1
ENSG00000261383	ENSG00000261383	OR4C12	HG281_PATCH:50003005-50004068	NOTEST	0	0	0	0	1	1
ENSG00000261384	ENSG00000261384	RP11-60L3.2	15:74471806-74628813	NOTEST	0	0	0	0	1	1
ENSG00000261385	ENSG00000261385	RP11-388M20.2	16:31142753-31147083	NOTEST	0	0	0	0	1	1
ENSG00000261386	ENSG00000261386	CTD-2012K14.6	16:67583116-67673086	NOTEST	0	0.109514	inf	0	1	1
ENSG00000261387	ENSG00000261387	AC138744.2	HG183_PATCH:62555144-62574426	NOTEST	0	0	0	0	1	1
ENSG00000261390	ENSG00000261390	RP11-345M22.2	16:79710004-79861047	NOTEST	0	0	0	0	1	1
ENSG00000261391	ENSG00000261391	RP11-586K12.7	16:32727251-32727377	NOTEST	0	0	0	0	1	1
ENSG00000261392	ENSG00000261392	RP11-473I1.6	16:9162410-9166269	NOTEST	0	0	0	0	1	1
ENSG00000261393	ENSG00000261393	RP11-21B23.1	16:50280047-50405391	NOTEST	0	0	0	0	1	1
ENSG00000261394	ENSG00000261394	RP11-165M1.3	16:12070593-12704901	NOTEST	0	0	0	0	1	1
ENSG00000261395	ENSG00000261395	HSPE1P5	16:68670091-68756519	NOTEST	0	0	0	0	1	1
ENSG00000261396	ENSG00000261396	CTD-2012K14.2	16:67552320-67580691	NOTEST	0	0	0	0	1	1
ENSG00000261397	ENSG00000261397	RP11-243A14.2	16:9535150-9538842	NOTEST	0	0	0	0	1	1
ENSG00000261398	ENSG00000261398	RP11-244B22.6	16:34430149-34431915	NOTEST	0.0168809	0	#NAME?	0	1	1
ENSG00000261399	ENSG00000261399	LA16c-329F2.1	16:1756183-1821731	NOTEST	0.0500053	0	#NAME?	0	1	1
ENSG00000261400	ENSG00000261400	AC011525.2	19:32078945-32086626	NOTEST	0	0	0	0	1	1
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ENSG00000261402	ENSG00000261402	RP11-378I6.1	9:19926091-19929935	NOTEST	0.00404317	0	#NAME?	0	1	1
ENSG00000261403	ENSG00000261403	RP11-114H24.3	15:78246416-78255996	NOTEST	0	0	0	0	1	1
ENSG00000261404	ENSG00000261404	AC009120.4	16:74088049-74330660	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000261407	ENSG00000261407	RP11-326A19.3	15:89630308-89745591	NOTEST	0	0	0	0	1	1
ENSG00000261409	ENSG00000261409	RP6-24A23.7	X:107963178-107982133	NOTEST	0.055898	0.0975034	0.802655	0	1	1
ENSG00000261410	ENSG00000261410	RP11-543N12.1	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000261411	ENSG00000261411	RP11-268G13.1	20:11665791-11667971	NOTEST	0	0	0	0	1	1
ENSG00000261412	ENSG00000261412	TRBV6-5	HG7_PATCH:142172446-142172948	NOTEST	0	0	0	0	1	1
ENSG00000261413	ENSG00000261413	SOCS7	HG745_PATCH:36508110-36556020	NOTEST	0	0	0	0	1	1
ENSG00000261414	ENSG00000261414	TRBV15	HG7_PATCH:142334563-142335109	NOTEST	0	0	0	0	1	1
ENSG00000261416	ENSG00000261416	RP11-455F5.5	16:30194147-30200397	NOTEST	0	0	0	0	1	1
ENSG00000261418	ENSG00000261418	RP11-529J17.3	15:23675985-23680359	NOTEST	0	0	0	0	1	1
ENSG00000261419	ENSG00000261419	RP11-57A19.4	16:28671016-28752102	NOTEST	0	0	0	0	1	1
ENSG00000261420	ENSG00000261420	RP1-168L15.5	6:166796676-166798312	NOTEST	0.0773314	0.0459119	-0.752186	0	1	1
ENSG00000261421	ENSG00000261421	RP11-22D3.1	16:49193418-49195934	NOTEST	0	0	0	0	1	1
ENSG00000261423	ENSG00000261423	RP11-1007O24.3	15:72690613-72879692	NOTEST	0.0263942	0.143965	2.44743	0	1	1
ENSG00000261424	ENSG00000261424	ATP5F1P7	16:75661621-75795770	NOTEST	0	0	0	0	1	1
ENSG00000261425	ENSG00000261425	RP11-709B3.2	15:68591127-68593343	NOTEST	0.00726213	0.0318873	2.13452	0	1	1
ENSG00000261426	ENSG00000261426	AC144833.1	15:27216428-27787137	NOTEST	0.00379033	0	#NAME?	0	1	1
ENSG00000261427	ENSG00000261427	CTD-2349B8.1	16:19125253-19279652	NOTEST	0	0	0	0	1	1
ENSG00000261428	ENSG00000261428	RP11-16P6.1	2:223431623-223434438	NOTEST	0.15857	0.292465	0.883141	0	1	1
ENSG00000261429	ENSG00000261429	DPPA2P4	16:56716335-56721964	NOTEST	0	0	0	0	1	1
ENSG00000261430	ENSG00000261430	LA16c-390E6.3	16:1494934-1525581	NOTEST	0.107723	0	#NAME?	0	1	1
ENSG00000261432	ENSG00000261432	RP11-360A18.2	9:122697330-122700110	NOTEST	0	0	0	0	1	1
ENSG00000261433	ENSG00000261433	CTC-297N7.1	17:10561858-10562399	NOTEST	0.344063	0.0597477	-2.52572	0	1	1
ENSG00000261434	ENSG00000261434	CTD-2083E4.7	5:195892-196456	NOTEST	0	0.0294362	inf	0	1	1
ENSG00000261435	ENSG00000261435	MIR1587	X:39696789-39707612	NOTEST	0	0	0	0	1	1
ENSG00000261436	ENSG00000261436	RP11-354I13.2	16:60393745-60476149	NOTEST	0	0	0	0	1	1
ENSG00000261437	ENSG00000261437	RP11-22C11.2	8:95649512-95651695	NOTEST	0	0	0	0	1	1
ENSG00000261438	ENSG00000261438	RP11-399O19.9	10:90775592-90776816	NOTEST	0.147518	0.292062	0.985381	0	1	1
ENSG00000261439	ENSG00000261439	CTD-2050B12.2	16:56225301-56391356	NOTEST	0.00856473	0	#NAME?	0	1	1
ENSG00000261440	ENSG00000261440	CTD-2522B17.5	16:33938202-33939259	NOTEST	0	0	0	0	1	1
ENSG00000261441	ENSG00000261441	RP11-217B1.2	15:89878283-89879392	NOTEST	0.0679315	0.0600032	-0.179041	0	1	1
ENSG00000261442	ENSG00000261442	RP11-709D24.6	16:4666493-4740975	NOTEST	0.0412973	0.0550417	0.414478	0	1	1
ENSG00000261443	ENSG00000261443	RAD54L2	HG186_PATCH:51579010-51701025	NOTEST	0	0	0	0	1	1
ENSG00000261444	ENSG00000261444	RP11-347C12.9	16:30225729-30226020	NOTEST	0	0	0	0	1	1
ENSG00000261445	ENSG00000261445	RP11-80F22.4	16:34728124-34730828	NOTEST	0	0	0	0	1	1
ENSG00000261446	ENSG00000261446	LINC00559	13:90712505-90771973	NOTEST	0	0	0	0	1	1
ENSG00000261447	ENSG00000261447	RP11-109D9.4	9:72287664-72288629	NOTEST	0.0374126	0.0544039	0.540188	0	1	1
ENSG00000261448	ENSG00000261448	CTD-2576D5.4	16:17195625-17564738	NOTEST	0	0	0	0	1	1
ENSG00000261449	ENSG00000261449	RP11-589C21.5	8:42009289-42010281	NOTEST	0	0	0	0	1	1

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ENSG00000261451	ENSG00000261451	RP11-981G7.1	8:10291181-10295822	NOTEST	0.013289	0.00749233	-0.826745	0	1	1
ENSG00000261453	ENSG00000261453	RP11-565N2.1	1:208780444-208785537	NOTEST	0	0	0	0	1	1
ENSG00000261456	ENSG00000261456	TUBB8	HG905_PATCH:96891-100113	NOTEST	0	0	0	0	1	1
ENSG00000261457	ENSG00000261457	AC002519.6	16:31814267-31820165	NOTEST	0	0	0	0	1	1
ENSG00000261458	ENSG00000261458	RP11-787D11.1	16:74876484-74877781	NOTEST	0	0	0	0	1	1
ENSG00000261460	ENSG00000261460	RP11-106M3.3	15:72533521-72671129	NOTEST	0.614921	0.603667	-0.0266473	0	1	1
ENSG00000261462	ENSG00000261462	CTA-254O6.1	7:86738854-86740598	NOTEST	0	0	0	0	1	1
ENSG00000261463	ENSG00000261463	TRBV6-8	HG7_PATCH:142228897-142229326	NOTEST	0	0	0	0	1	1
ENSG00000261465	ENSG00000261465	RP11-626G11.5	16:18995255-19091417	NOTEST	0.123184	0.237213	0.945365	0	1	1
ENSG00000261466	ENSG00000261466	RP11-23E10.2	16:33350763-33356875	NOTEST	0	0	0	0	1	1
ENSG00000261467	ENSG00000261467	RP11-731K22.1	7:73400321-73403097	NOTEST	0	0	0	0	1	1
ENSG00000261468	ENSG00000261468	RP11-1024P17.1	3:30739152-30741068	NOTEST	0.00851074	0.0739024	3.11827	0	1	1
ENSG00000261469	ENSG00000261469	RP11-96D1.6	16:68021296-68272005	NOTEST	0	0	0	0	1	1
ENSG00000261470	ENSG00000261470	RP11-152O14.4	16:52112533-52114401	NOTEST	0	0	0	0	1	1
ENSG00000261471	ENSG00000261471	RP11-61F12.1	16:84599199-84651683	NOTEST	0	0.0144155	inf	0	1	1
ENSG00000261472	ENSG00000261472	RP11-467I17.1	16:79539499-79550190	NOTEST	0	0	0	0	1	1
ENSG00000261473	ENSG00000261473	PRSS1	HG7_PATCH:142489984-142493589	NOTEST	0	0	0	0	1	1
ENSG00000261474	ENSG00000261474	RP11-452L6.1	16:31460855-31464814	NOTEST	0.106819	0.285634	1.41901	0	1	1
ENSG00000261475	ENSG00000261475	CTD-2014E2.6	16:31560463-31564888	NOTEST	0	0	0	0	1	1
ENSG00000261476	ENSG00000261476	RP11-77K12.3	16:75327595-75499395	NOTEST	0.0399294	0.0816689	1.03234	0	1	1
ENSG00000261478	ENSG00000261478	RP11-429B14.4	15:90048507-90198682	NOTEST	0	0	0	0	1	1
ENSG00000261479	ENSG00000261479	OPLAH	HG104_HG975_PATCH:145131298-145146004	NOTEST	0	0	0	0	1	1
ENSG00000261480	ENSG00000261480	RP11-578F21.6	15:28947099-29002537	NOTEST	0	0	0	0	1	1
ENSG00000261481	ENSG00000261481	RP11-77H9.6	16:8963107-8963889	NOTEST	0.0454227	0.145227	1.67683	0	1	1
ENSG00000261482	ENSG00000261482	RP11-673P17.2	16:27078027-27080486	NOTEST	0	0	0	0	1	1
ENSG00000261484	ENSG00000261484	TRBV5-7	HG7_PATCH:142241603-142242070	NOTEST	0	0	0	0	1	1
ENSG00000261485	ENSG00000261485	PAN3-AS1	13:28710979-28712330	NOTEST	0.219663	0.282495	0.362929	0	1	1
ENSG00000261486	ENSG00000261486	RARRES2P9	16:34578461-34578930	NOTEST	0	0	0	0	1	1
ENSG00000261488	ENSG00000261488	RP11-757F18.5	3:111852269-111854206	NOTEST	0.411962	0.343864	-0.260672	0	1	1
ENSG00000261489	ENSG00000261489	CTD-2515H24.3	15:57668164-57842925	NOTEST	0	0	0	0	1	1
ENSG00000261490	ENSG00000261490	RP11-448G15.3	4:10069712-10074643	NOTEST	0.0783338	0.191529	1.28985	0	1	1
ENSG00000261491	ENSG00000261491	DNM1P31	15:32677137-32679685	NOTEST	0	0	0	0	1	1
ENSG00000261492	ENSG00000261492	MLLT10P2	HG1032_PATCH:190894753-190895002	NOTEST	0	0	0	0	1	1
ENSG00000261493	ENSG00000261493	REXO4	HG79_PATCH:136251901-136334921	NOTEST	0	0	0	0	1	1
ENSG00000261495	ENSG00000261495	AHCYP8	HG999_1_PATCH:248881949-248914431	NOTEST	0	0	0	0	1	1
ENSG00000261496	ENSG00000261496	RP13-514E23.1	4:86933448-86935027	NOTEST	0.010548	0.0500255	2.2457	0	1	1
ENSG00000261497	ENSG00000261497	RP11-483E23.3	15:28607941-28610877	NOTEST	0	0	0	0	1	1
ENSG00000261498	ENSG00000261498	LINC00566	13:24905587-24911259	NOTEST	0	0	0	0	1	1
ENSG00000261499	ENSG00000261499	CH17-260O16.2	HG75_PATCH:34601601-34662129	NOTEST	0	0	0	0	1	1
ENSG00000261500	ENSG00000261500	RP11-390B4.3	HG544_PATCH:17686123-17757913	NOTEST	0	0	0	0	1	1
ENSG00000261501	ENSG00000261501	RP11-63B13.1	4:122791737-122794003	NOTEST	0	0	0	0	1	1

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ENSG00000261503	ENSG00000261503	CTC-260E6.2	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000261504	ENSG00000261504	RP11-317P15.4	1:182584388-182585764	NOTEST	0.047047	0.0748954	0.670773	0	1	1
ENSG00000261506	ENSG00000261506	TRBV6-1	HG7_PATCH:142028120-142028610	NOTEST	0	0	0	0	1	1
ENSG00000261507	ENSG00000261507	RP11-1437A8.6	16:33202881-33264727	NOTEST	0	0	0	0	1	1
ENSG00000261508	ENSG00000261508	DHRS11	HG75_PATCH:34919857-34928764	NOTEST	0	0	0	0	1	1
ENSG00000261509	ENSG00000261509	TP53TG3B	16:33202881-33264727	NOTEST	0	0	0	0	1	1
ENSG00000261510	ENSG00000261510	RP11-244B22.13	16:34383827-34384161	NOTEST	0	0	0	0	1	1
ENSG00000261511	ENSG00000261511	CTD-3244O18.7	7:99417640-99417709	NOTEST	0	0	0	0	1	1
ENSG00000261513	ENSG00000261513	RP11-432I5.8	16:71657610-71758604	NOTEST	0	0	0	0	1	1
ENSG00000261514	ENSG00000261514	RP11-527L4.2	17:42015730-42016327	NOTEST	0.0564431	0.341506	2.59704	0	1	1
ENSG00000261515	ENSG00000261515	VN1R70P	16:35071256-35072103	NOTEST	0	0	0	0	1	1
ENSG00000261516	ENSG00000261516	ZNF707	HG104_HG975_PATCH:144766621-144796068	NOTEST	0	0	0	0	1	1
ENSG00000261517	ENSG00000261517	LINC00558	13:54389553-54450254	NOTEST	0	0	0	0	1	1
ENSG00000261518	ENSG00000261518	CTA-313A17.2	HG115_PATCH:101970535-101972810	NOTEST	0	0	0	0	1	1
ENSG00000261519	ENSG00000261519	Y_RNA	16:66461199-66586447	NOTEST	0.0206255	0.0268173	0.378732	0	1	1
ENSG00000261520	ENSG00000261520	DLGAP1-AS5	18:3496029-4455335	NOTEST	0	0	0	0	1	1
ENSG00000261521	ENSG00000261521	RP11-408H20.1	18:28638805-28639359	NOTEST	0	0	0	0	1	1
ENSG00000261522	ENSG00000261522	RP11-407P15.1	HG686_PATCH:95339722-95350930	NOTEST	0	0	0	0	1	1
ENSG00000261523	ENSG00000261523	RP11-82O18.2	16:14789423-14800912	NOTEST	0	0	0	0	1	1
ENSG00000261524	ENSG00000261524	ABCB10P3	15:28648013-28650179	NOTEST	0.0134768	0	#NAME?	0	1	1
ENSG00000261527	ENSG00000261527	RP11-343C2.10	16:69458427-69500169	NOTEST	0	0.0629297	inf	0	1	1
ENSG00000261528	ENSG00000261528	AC002400.1	16:23474862-23533316	NOTEST	0.151899	0.398275	1.39066	0	1	1
ENSG00000261529	ENSG00000261529	RP13-487P22.1	15:25497371-25684128	NOTEST	0.0188179	0.0307046	0.706353	0	1	1
ENSG00000261530	ENSG00000261530	BTC	HG706_PATCH:75610475-75660403	NOTEST	0	0	0	0	1	1
ENSG00000261531	ENSG00000261531	SNX18P14	HG686_PATCH:95550434-95551008	NOTEST	0	0	0	0	1	1
ENSG00000261532	ENSG00000261532	RP11-304L19.8	16:2261997-2264808	NOTEST	0	0	0	0	1	1
ENSG00000261533	ENSG00000261533	RP11-15N24.4	3:99898410-99900574	NOTEST	0.0791421	0.0999553	0.336838	0	1	1
ENSG00000261534	ENSG00000261534	RP11-244O19.1	9:124577952-124581731	NOTEST	0.26698	0.105153	-1.34425	0	1	1
ENSG00000261535	ENSG00000261535	CTA-305I2.1	HG115_PATCH:101459218-101927238	NOTEST	0	0	0	0	1	1
ENSG00000261536	ENSG00000261536	FAM108A10P	16:33152170-33155118	NOTEST	0	0	0	0	1	1
ENSG00000261537	ENSG00000261537	RP11-319G9.5	16:78133309-79246564	NOTEST	0	0	0	0	1	1
ENSG00000261538	ENSG00000261538	RP11-3M1.1	16:48198862-48482313	NOTEST	0	0	0	0	1	1
ENSG00000261539	ENSG00000261539	FBXL6	HG243_PATCH:145407121-145416175	NOTEST	0	0	0	0	1	1
ENSG00000261540	ENSG00000261540	RP11-281J9.2	16:78048579-78100658	NOTEST	0	0	0	0	1	1
ENSG00000261541	ENSG00000261541	RP11-626K17.3	16:32465932-32470079	NOTEST	0	0	0	0	1	1
ENSG00000261542	ENSG00000261542	RP11-16E18.3	8:64128538-64130592	NOTEST	0.105945	0.0623454	-0.764967	0	1	1
ENSG00000261543	ENSG00000261543	RP11-665J16.1	15:74445140-74471567	NOTEST	0	0	0	0	1	1
ENSG00000261544	ENSG00000261544	RP11-16E23.3	15:65903703-66184329	NOTEST	0	0	0	0	1	1
ENSG00000261545	ENSG00000261545	CH17-260O16.1	HG75_PATCH:34561824-34561930	NOTEST	0	0	0	0	1	1

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ENSG00000261546	ENSG00000261546	CTD-2555A7.3	16:89154782-89222254	NOTEST	0.0449489	0.0114156	-1.97728	0	1	1
ENSG00000261547	ENSG00000261547	RP11-626H12.2	HG536_PATCH:69800643-69835827	NOTEST	0	0	0	0	1	1
ENSG00000261548	ENSG00000261548	HLA-P	6:29768191-29770202	NOTEST	0.047349	0.0182139	-1.3783	0	1	1
ENSG00000261549	ENSG00000261549	RP11-320A16.1	15:89532749-89533476	NOTEST	0	0	0	0	1	1
ENSG00000261550	ENSG00000261550	RP11-467J12.4	16:53069601-53086785	NOTEST	0	0	0	0	1	1
ENSG00000261552	ENSG00000261552	RP11-264B17.5	16:28985541-29002104	NOTEST	0	0.0287465	inf	0	1	1
ENSG00000261553	ENSG00000261553	RP11-29G8.3	13:76123618-76434004	NOTEST	0.382704	0.392009	0.0346565	0	1	1
ENSG00000261554	ENSG00000261554	RP11-810K23.10	15:21098711-21099309	NOTEST	0	0	0	0	1	1
ENSG00000261555	ENSG00000261555	CTD-3229J4.1	16:17919108-17920763	NOTEST	0	0	0	0	1	1
ENSG00000261557	ENSG00000261557	EEF1A1P38	16:27144803-27146500	NOTEST	0	0.00857818	inf	0	1	1
ENSG00000261558	ENSG00000261558	CTD-2291D10.2	19:23197876-23206499	NOTEST	0	0	0	0	1	1
ENSG00000261559	ENSG00000261559	RP11-1H8.3	15:34671268-34880704	NOTEST	0	0	0	0	1	1
ENSG00000261560	ENSG00000261560	RP11-166B2.3	16:11945505-12009939	NOTEST	0.240585	0.151415	-0.668039	0	1	1
ENSG00000261561	ENSG00000261561	RP11-536P16.2	15:28591635-28591793	NOTEST	0	0	0	0	1	1
ENSG00000261562	ENSG00000261562	GS1-393G12.12	HG243_PATCH:145346493-145370041	NOTEST	0	0	0	0	1	1
ENSG00000261563	ENSG00000261563	TRBV5-8	HG7_PATCH:142261248-142262208	NOTEST	0	0	0	0	1	1
ENSG00000261564	ENSG00000261564	RP11-616M22.10	16:1323751-1326523	NOTEST	0	0	0	0	1	1
ENSG00000261565	ENSG00000261565	RP11-299M14.2	HG104_HG975_PATCH:144915439-144923144	NOTEST	0	0	0	0	1	1
ENSG00000261566	ENSG00000261566	CTD-2144E22.6	16:34256506-34258621	NOTEST	0	0	0	0	1	1
ENSG00000261567	ENSG00000261567	RP11-680G10.1	16:85391068-85393055	NOTEST	0	0.377921	inf	0	1	1
ENSG00000261568	ENSG00000261568	RP11-524C21.2	6:22221009-22222624	NOTEST	0	0	0	0	1	1
ENSG00000261569	ENSG00000261569	RP11-586K12.11	16:32660513-32677854	NOTEST	0	0	0	0	1	1
ENSG00000261570	ENSG00000261570	RP11-744I24.2	7:141229002-141401953	NOTEST	0	0	0	0	1	1
ENSG00000261571	ENSG00000261571	TRBV7-8	HG7_PATCH:142253485-142254008	NOTEST	0	0	0	0	1	1
ENSG00000261572	ENSG00000261572	RP11-384L8.1	3:32278179-32280070	NOTEST	0.0242803	0.00670949	-1.85551	0	1	1
ENSG00000261573	ENSG00000261573	RP11-553K8.5	1:198607800-198726545	NOTEST	0	0	0	0	1	1
ENSG00000261574	ENSG00000261574	RP1-168P16.2	16:89334037-89556969	NOTEST	0	0.042512	inf	0	1	1
ENSG00000261575	ENSG00000261575	RP11-259G18.1	17:44344402-44346060	NOTEST	0.355565	0.319817	-0.152867	0	1	1
ENSG00000261577	ENSG00000261577	JUP	HG185_PATCH:39910855-39943183	NOTEST	0	0	0	0	1	1
ENSG00000261578	ENSG00000261578	RP11-21L23.2	11:76511407-76515599	NOTEST	0.173871	0.0975041	-0.834483	0	1	1
ENSG00000261579	ENSG00000261579	MED22	HG79_PATCH:136216439-136223666	NOTEST	0	0	0	0	1	1
ENSG00000261580	ENSG00000261580	ENPP7P13	16:33571887-33572146	NOTEST	0	0	0	0	1	1
ENSG00000261581	ENSG00000261581	RP11-665A22.1	15:28820164-28824546	NOTEST	0	0	0	0	1	1
ENSG00000261582	ENSG00000261582	RP4-614O4.11	20:33703166-33872788	NOTEST	0.156452	0	#NAME?	0	1	1
ENSG00000261583	ENSG00000261583	CTD-2385L22.1	16:23688976-23724821	NOTEST	0	0	0	0	1	1
ENSG00000261584	ENSG00000261584	RP11-457M11.5	6:26686468-26688192	NOTEST	0.380225	0.412129	0.116245	0	1	1
ENSG00000261585	ENSG00000261585	LCN1P1	HG79_PATCH:136100291-136103978	NOTEST	0	0	0	0	1	1

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ENSG00000261587	ENSG00000261587	TMEM249	HG243_PATCH:145407121-145416175	NOTEST	0	0	0	0	1	1
ENSG00000261588	ENSG00000261588	AC002310.17	16:30597227-30635333	NOTEST	0.160817	0	#NAME?	0	1	1
ENSG00000261589	ENSG00000261589	CTC-462L7.1	17:53246183-53250993	NOTEST	0.36405	0.170473	-1.09459	0	1	1
ENSG00000261590	ENSG00000261590	RP11-457D20.1	16:60391117-60391378	NOTEST	0	0	0	0	1	1
ENSG00000261591	ENSG00000261591	U85056.2	HG1032_PATCH:190979056-190984160	NOTEST	0	0	0	0	1	1
ENSG00000261592	ENSG00000261592	RP11-178L8.3	16:87117167-87438385	NOTEST	0	0	0	0	1	1
ENSG00000261593	ENSG00000261593	CYP4A27P	1:47427035-47516423	NOTEST	0	0	0	0	1	1
ENSG00000261595	ENSG00000261595	RP11-426L16.9	1:113258293-113260418	NOTEST	0	0	0	0	1	1
ENSG00000261597	ENSG00000261597	RP11-353B9.1	15:49944335-49948429	NOTEST	0.0553088	0.0611923	0.145842	0	1	1
ENSG00000261598	ENSG00000261598	RP11-107D24.2	15:24544895-24545785	NOTEST	0	0	0	0	1	1
ENSG00000261600	ENSG00000261600	RP11-575H3.1	2:91768392-91768920	NOTEST	0.166436	0.40829	1.29463	0	1	1
ENSG00000261601	ENSG00000261601	TRBV10-3	HG7_PATCH:142285818-142286316	NOTEST	0	0	0	0	1	1
ENSG00000261602	ENSG00000261602	CTD-2033A16.1	16:69740898-69760854	NOTEST	0	0.157231	inf	0	1	1
ENSG00000261603	ENSG00000261603	PRSS46	3:46753604-46854064	NOTEST	0	0	0	0	1	1
ENSG00000261604	ENSG00000261604	CTD-2636A23.2	5:43287702-43313614	NOTEST	0.283929	0.298995	0.0745947	0	1	1
ENSG00000261605	ENSG00000261605	ABC7-42389800N19.1	HG858_PATCH:64521-82015	NOTEST	0	0	0	0	1	1
ENSG00000261606	ENSG00000261606	RP11-414J4.2	15:75105056-75124141	NOTEST	0	0.0131313	inf	0	1	1
ENSG00000261607	ENSG00000261607	RP11-812E19.5	16:33750744-33751015	NOTEST	0	0	0	0	1	1
ENSG00000261608	ENSG00000261608	SLC25A1P4	16:34407686-34408464	NOTEST	0	0	0	0	1	1
ENSG00000261610	ENSG00000261610	AP000265.1	21:33632114-33633896	NOTEST	0.00921871	0.0071638	-0.36384	0	1	1
ENSG00000261611	ENSG00000261611	AC010547.9	16:71481499-71598992	NOTEST	0.129542	0.0986681	-0.392767	0	1	1
ENSG00000261612	ENSG00000261612	SUB1P3	16:4606490-4650715	NOTEST	0	0	0	0	1	1
ENSG00000261613	ENSG00000261613	RP11-20I23.13	16:2587964-2653189	NOTEST	0.092791	0.0647592	-0.5189	0	1	1
ENSG00000261614	ENSG00000261614	YBX3P1	16:31579706-31580796	NOTEST	0.0161615	0.0365136	1.17587	0	1	1
ENSG00000261615	ENSG00000261615	CTD-2291D10.1	19:23229759-23244554	NOTEST	0	0	0	0	1	1
ENSG00000261617	ENSG00000261617	RP11-243A14.1	16:9449444-9501950	NOTEST	0	0	0	0	1	1
ENSG00000261618	ENSG00000261618	RP11-79H23.3	8:79749763-79752757	NOTEST	0.0347977	0	#NAME?	0	1	1
ENSG00000261619	ENSG00000261619	TRBV22-1	HG7_PATCH:142383313-142383764	NOTEST	0	0	0	0	1	1
ENSG00000261620	ENSG00000261620	HMGN2P41	16:35037239-35037651	NOTEST	0	0	0	0	1	1
ENSG00000261621	ENSG00000261621	RP11-580I1.2	15:24480224-24521976	NOTEST	0	0	0	0	1	1
ENSG00000261622	ENSG00000261622	RP11-484P15.1	15:24157555-24186863	NOTEST	0	0	0	0	1	1
ENSG00000261623	ENSG00000261623	RP11-189E14.4	16:49500016-49503786	NOTEST	0	0	0	0	1	1
ENSG00000261624	ENSG00000261624	RP5-914M6.1	7:140774031-141180180	NOTEST	0	0	0	0	1	1
ENSG00000261625	ENSG00000261625	RP11-554A11.4	11:68768232-68769516	NOTEST	0	0	0	0	1	1
ENSG00000261626	ENSG00000261626	TRBV6-3	HG7_PATCH:142070667-142071148	NOTEST	0	0	0	0	1	1
ENSG00000261627	ENSG00000261627	RP11-91I8.1	18:6641969-6642477	NOTEST	0	0	0	0	1	1
ENSG00000261629	ENSG00000261629	RP5-842K16.2	7:140774031-141180180	NOTEST	0	0	0	0	1	1
ENSG00000261630	ENSG00000261630	RP11-357N13.3	16:53737874-54155853	NOTEST	0	0	0	0	1	1
ENSG00000261631	ENSG00000261631	KLHL10	HG185_PATCH:39981432-40004636	NOTEST	0	0	0	0	1	1

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ENSG00000261633	ENSG00000261633	RP11-405F3.5	16:57644563-57698944	NOTEST	0.148963	0.21658	0.539941	0	1	1
ENSG00000261634	ENSG00000261634	RP11-352D13.6	15:69570666-69591097	NOTEST	0	0	0	0	1	1
ENSG00000261635	ENSG00000261635	RP11-618N24.1	15:36871811-37110660	NOTEST	0	0.0647406	inf	0	1	1
ENSG00000261636	ENSG00000261636	CTA-249B10.1	16:25431134-25435490	NOTEST	0	0	0	0	1	1
ENSG00000261637	ENSG00000261637	RP11-883G14.2	16:51051668-51072675	NOTEST	0	0	0	0	1	1
ENSG00000261638	ENSG00000261638	RP11-700H13.1	16:58741034-59142878	NOTEST	0	0	0	0	1	1
ENSG00000261640	ENSG00000261640	U66059.58	HG7_PATCH:141985578-141991423	NOTEST	0	0	0	0	1	1
ENSG00000261641	ENSG00000261641	LA16c-390E6.5	16:1494934-1525581	NOTEST	0.326682	0.056102	-2.54176	0	1	1
ENSG00000261642	ENSG00000261642	RP11-309H21.3	1:191120639-191123764	NOTEST	0	0	0	0	1	1
ENSG00000261643	ENSG00000261643	RP11-529E10.6	4:3505323-3506184	NOTEST	0.204289	0.416639	1.02819	0	1	1
ENSG00000261644	ENSG00000261644	RP11-327F22.2	16:50769623-50774627	NOTEST	0	0	0	0	1	1
ENSG00000261645	ENSG00000261645	DISC1FP1	11:89984399-90648220	NOTEST	0.179132	0.245159	0.4527	0	1	1
ENSG00000261646	ENSG00000261646	RP11-489G11.3	4:174388983-174391192	NOTEST	0	0	0	0	1	1
ENSG00000261647	ENSG00000261647	IMPDH1P11	16:9852375-10276611	NOTEST	0	0	0	0	1	1
ENSG00000261648	ENSG00000261648	CTD-2014E2.2	16:31558018-31559058	NOTEST	0	0	0	0	1	1
ENSG00000261649	ENSG00000261649	GOLGA6L7P	15:29033388-29101361	NOTEST	0	0.0115132	inf	0	1	1
ENSG00000261650	ENSG00000261650	RP11-474D1.4	12:130509037-130529602	NOTEST	0	0	0	0	1	1
ENSG00000261651	ENSG00000261651	RP11-899L11.3	16:87117167-87438385	NOTEST	0	0	0	0	1	1
ENSG00000261652	ENSG00000261652	C15orf65	15:55495163-55800432	NOTEST	0.515027	0.200285	-1.36259	0	1	1
ENSG00000261653	ENSG00000261653	RP11-21L1.1	16:63969681-63970810	NOTEST	0	0	0	0	1	1
ENSG00000261654	ENSG00000261654	RP11-96K19.4	1:111478990-111484975	NOTEST	0.0194309	0.00739118	-1.39447	0	1	1
ENSG00000261655	ENSG00000261655	CTD-3064M3.3	8:142363502-142365465	NOTEST	0	0.0182008	inf	0	1	1
ENSG00000261656	ENSG00000261656	CTD-2258A20.5	16:66461199-66586447	NOTEST	0.0483806	0	#NAME?	0	1	1
ENSG00000261657	ENSG00000261657	SLC25A26	HG991_PATCH:66119284-66465398	NOTEST	0	0	0	0	1	1
ENSG00000261659	ENSG00000261659	LA16c-313D11.12	16:734621-755829	NOTEST	0.181836	0.304362	0.74315	0	1	1
ENSG00000261660	ENSG00000261660	PARP10	HG104_HG975_PATCH:145059322-145129202	NOTEST	0	0	0	0	1	1
ENSG00000261662	ENSG00000261662	RP5-1042I8.7	1:120451877-120453236	NOTEST	0.145453	0.275371	0.920821	0	1	1
ENSG00000261663	ENSG00000261663	RP11-304L19.11	16:2289395-2302301	NOTEST	0.369169	0.450184	0.286236	0	1	1
ENSG00000261664	ENSG00000261664	RP11-275F13.1	1:51752929-51810788	NOTEST	0	0	0	0	1	1
ENSG00000261665	ENSG00000261665	TUBA8P2	15:84322837-84708594	NOTEST	0	0	0	0	1	1
ENSG00000261666	ENSG00000261666	LINC00560	13:89279106-89282651	NOTEST	0	0	0	0	1	1
ENSG00000261667	ENSG00000261667	RP11-520P18.5	8:144161873-144164418	NOTEST	0	0	0	0	1	1
ENSG00000261668	ENSG00000261668	RP11-50D9.3	4:128702975-128765195	NOTEST	0.0295815	0.0388985	0.395022	0	1	1
ENSG00000261669	ENSG00000261669	CTD-2515A14.1	16:24741015-24838953	NOTEST	0.176631	0.11095	-0.670837	0	1	1
ENSG00000261670	ENSG00000261670	RP11-1C8.5	8:104476616-104481213	NOTEST	0.00605544	0	#NAME?	0	1	1
ENSG00000261671	ENSG00000261671	RP11-573G6.6	10:22546714-22547477	NOTEST	0	0	0	0	1	1
ENSG00000261672	ENSG00000261672	RP11-475B2.1	4:174514822-174515707	NOTEST	0	0	0	0	1	1

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ENSG00000261674	ENSG00000261674	RP11-1407O15.2	HG745_PATCH:36337716-36421858	NOTEST	0	0	0	0	1	1
ENSG00000261675	ENSG00000261675	RP5-1119A7.1	22:36956916-36958962	NOTEST	0	0	0	0	1	1
ENSG00000261676	ENSG00000261676	RP13-580B18.1	HG736_PATCH:56943077-56949839	NOTEST	0	0	0	0	1	1
ENSG00000261677	ENSG00000261677	PTPLA	HG544_PATCH:17631957-17659376	NOTEST	0	0	0	0	1	1
ENSG00000261678	ENSG00000261678	SCRT1	HG243_PATCH:145387964-145391184	NOTEST	0	0	0	0	1	1
ENSG00000261679	ENSG00000261679	ATP5HP1	15:43560101-43560586	NOTEST	0	0	0	0	1	1
ENSG00000261680	ENSG00000261680	RP11-146F11.3	16:30635605-30636035	NOTEST	0	0	0	0	1	1
ENSG00000261682	ENSG00000261682	RP11-19N8.7	16:33140636-33145820	NOTEST	0	0	0	0	1	1
ENSG00000261683	ENSG00000261683	LINC00838	10:34048640-34061586	NOTEST	0	0	0	0	1	1
ENSG00000261684	ENSG00000261684	RP11-265N6.1	15:42783430-42841000	NOTEST	0	0	0	0	1	1
ENSG00000261685	ENSG00000261685	RP11-401P9.4	16:50679719-50683160	NOTEST	0.180045	0.110257	-0.707495	0	1	1
ENSG00000261686	ENSG00000261686	OR9A2	HG7_PATCH:142786753-142787791	NOTEST	0	0	0	0	1	1
ENSG00000261687	ENSG00000261687	RP11-473C18.3	15:43398422-43513481	NOTEST	0	0	0	0	1	1
ENSG00000261688	ENSG00000261688	CTB-75G16.1	HG75_PATCH:34872291-34917807	NOTEST	0	0	0	0	1	1
ENSG00000261689	ENSG00000261689	AGGF1P4	16:34597782-34624955	NOTEST	0	0	0	0	1	1
ENSG00000261691	ENSG00000261691	LA16c-366D1.3	16:577716-604636	NOTEST	0	0	0	0	1	1
ENSG00000261692	ENSG00000261692	RP1-168P16.1	16:89334037-89556969	NOTEST	0	0	0	0	1	1
ENSG00000261693	ENSG00000261693	RP13-467H17.1	8:143485012-143488389	NOTEST	0.00463214	0.0245761	2.4075	0	1	1
ENSG00000261694	ENSG00000261694	ADCK5	HG243_PATCH:145428003-145464191	NOTEST	0	0	0	0	1	1
ENSG00000261695	ENSG00000261695	RP11-719K4.6	16:14828541-14840034	NOTEST	0	0	0	0	1	1
ENSG00000261696	ENSG00000261696	RP11-354P17.15	9:21394886-21396345	NOTEST	0	0	0	0	1	1
ENSG00000261697	ENSG00000261697	RP11-178L8.5	16:87117167-87438385	NOTEST	0	0	0	0	1	1
ENSG00000261698	ENSG00000261698	DGAT1	HG243_PATCH:145371193-145381813	NOTEST	0	0	0	0	1	1
ENSG00000261700	ENSG00000261700	TRBV10-1	HG7_PATCH:142121372-142121890	NOTEST	0	0	0	0	1	1
ENSG00000261701	ENSG00000261701	HPR	16:72078187-72210777	NOTEST	0	0	0	0	1	1
ENSG00000261702	ENSG00000261702	RP11-282M16.1	15:68266728-68266963	NOTEST	0	0	0	0	1	1
ENSG00000261703	ENSG00000261703	RP11-327F22.5	16:50840578-50841540	NOTEST	0	0	0	0	1	1
ENSG00000261704	ENSG00000261704	IGHV1OR16-1	16:32019758-32096106	NOTEST	0	0	0	0	1	1
ENSG00000261706	ENSG00000261706	AP001505.9	21:46414276-46415100	NOTEST	0	0	0	0	1	1
ENSG00000261707	ENSG00000261707	RP11-264M12.2	16:77756410-77776897	NOTEST	1.70E-05	1.42E-05	-0.26296	0	1	1
ENSG00000261708	ENSG00000261708	DNM1P32	15:32728703-32731968	NOTEST	0	0	0	0	1	1
ENSG00000261709	ENSG00000261709	SNORA11	15:45506645-45507242	NOTEST	0	0	0	0	1	1
ENSG00000261710	ENSG00000261710	RP11-953B20.1	8:143171187-143172980	NOTEST	0	0	0	0	1	1
ENSG00000261712	ENSG00000261712	RP11-358L4.1	15:79705699-79706228	NOTEST	0.444685	0.500778	0.171388	0	1	1
ENSG00000261713	ENSG00000261713	SSTR5-AS1	16:1114092-1131454	NOTEST	0	0	0	0	1	1
ENSG00000261714	ENSG00000261714	CTD-2562G15.2	15:75648132-75748183	NOTEST	0	0	0	0	1	1
ENSG00000261715	ENSG00000261715	RP11-653G8.2	18:37646249-37679197	NOTEST	0	0	0	0	1	1
ENSG00000261717	ENSG00000261717	RP11-77K12.1	16:75327595-75499395	NOTEST	0	0	0	0	1	1
ENSG00000261718	ENSG00000261718	RP11-598F7.3	HG858_PATCH:116764-232399	NOTEST	0	0	0	0	1	1
ENSG00000261719	ENSG00000261719	RP11-67H24.1	16:32820876-32835966	NOTEST	0.246614	0	#NAME?	0	1	1

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ENSG00000261721	ENSG00000261721	GRINA	HG104_HG975_PATCH:145059322-145129202	NOTEST	0	0	0	0	1	1
ENSG00000261722	ENSG00000261722	RP11-679B19.2	16:79246607-79263350	NOTEST	0	0	0	0	1	1
ENSG00000261723	ENSG00000261723	CTD-2196E14.3	16:23614487-23652631	NOTEST	0	0.0786888	inf	0	1	1
ENSG00000261725	ENSG00000261725	RP11-480G7.3	16:46884910-46885166	NOTEST	0	0	0	0	1	1
ENSG00000261727	ENSG00000261727	RP11-1166P10.6	16:32019758-32096106	NOTEST	0	0	0	0	1	1
ENSG00000261728	ENSG00000261728	RP11-307O13.1	13:35499970-35502213	NOTEST	0.0215025	0.0172771	-0.315638	0	1	1
ENSG00000261729	ENSG00000261729	GS1-204I12.4	1:185624133-185626300	NOTEST	0.267394	0.138475	-0.949339	0	1	1
ENSG00000261731	ENSG00000261731	CTD-2358C21.4	16:31711910-31723305	NOTEST	0.240047	0	#NAME?	0	1	1
ENSG00000261732	ENSG00000261732	LA16c-431H6.6	16:1662325-1752281	NOTEST	0.0183964	0.0851426	2.21045	0	1	1
ENSG00000261733	ENSG00000261733	RP11-80F22.8	16:34763492-34763688	NOTEST	0	0	0	0	1	1
ENSG00000261734	ENSG00000261734	RP11-669C19.1	3:20429740-20432054	NOTEST	0	0	0	0	1	1
ENSG00000261735	ENSG00000261735	TRBVB	HG7_PATCH:142445731-142458950	NOTEST	0	0	0	0	1	1
ENSG00000261736	ENSG00000261736	AC002551.1	16:27561453-27791690	NOTEST	0	0	0	0	1	1
ENSG00000261737	ENSG00000261737	RP4-612B15.3	1:87169184-87170145	NOTEST	0.159407	0.123983	-0.362578	0	1	1
ENSG00000261738	ENSG00000261738	RP11-945C19.1	18:5748817-5876327	NOTEST	0	0	0	0	1	1
ENSG00000261739	ENSG00000261739	GOLGA8S	15:23599894-23612378	NOTEST	0.0199406	0.00774954	-1.36353	0	1	1
ENSG00000261741	ENSG00000261741	CTD-2014E2.5	16:31574402-31579037	NOTEST	0	0	0	0	1	1
ENSG00000261742	ENSG00000261742	LINC00922	16:65224875-65610203	NOTEST	0	0	0	0	1	1
ENSG00000261743	ENSG00000261743	RP11-2K6.2	16:63348167-63651950	NOTEST	0	0	0	0	1	1
ENSG00000261744	ENSG00000261744	RP11-21B21.4	16:88519724-88603424	NOTEST	0.101415	0	#NAME?	0	1	1
ENSG00000261745	ENSG00000261745	RP11-506E9.3	6:52990444-52990944	NOTEST	0	0	0	0	1	1
ENSG00000261747	ENSG00000261747	RP11-932O9.3	15:30446112-30446313	NOTEST	0	0	0	0	1	1
ENSG00000261748	ENSG00000261748	RP11-419L9.1	16:17046358-17047325	NOTEST	0	0	0	0	1	1
ENSG00000261749	ENSG00000261749	RP11-152O14.1	16:52119191-52132979	NOTEST	0	0	0	0	1	1
ENSG00000261751	ENSG00000261751	RP11-305A4.3	16:49954640-49958065	NOTEST	0	0	0	0	1	1
ENSG00000261753	ENSG00000261753	RP11-631M21.6	HG905_PATCH:94711-96884	NOTEST	0	0	0	0	1	1
ENSG00000261754	ENSG00000261754	CTC-523E23.1	19:35279485-35323773	NOTEST	0	0	0	0	1	1
ENSG00000261755	ENSG00000261755	DUX4L6	HG1032_PATCH:190995679-190997180	NOTEST	0	0	0	0	1	1
ENSG00000261756	ENSG00000261756	SLC29A4P1	HG736_PATCH:57081977-57087966	NOTEST	0	0	0	0	1	1
ENSG00000261757	ENSG00000261757	AC005592.3	5:142083346-142084986	NOTEST	0.132141	0.178567	0.434388	0	1	1
ENSG00000261758	ENSG00000261758	RP11-102M11.2	3:136471471-136474622	NOTEST	0.0139885	0	#NAME?	0	1	1
ENSG00000261760	ENSG00000261760	RP11-1223D19.1	2:110969105-111043433	NOTEST	0	0	0	0	1	1
ENSG00000261761	ENSG00000261761	RP11-103J17.2	4:37003437-37022330	NOTEST	0	0	0	0	1	1
ENSG00000261763	ENSG00000261763	RP11-442N1.2	3:139397461-139401406	NOTEST	0	0	0	0	1	1
ENSG00000261764	ENSG00000261764	KRT18P18	16:72699068-73093597	NOTEST	0	0	0	0	1	1
ENSG00000261765	ENSG00000261765	RP11-498D10.3	16:71879893-71962913	NOTEST	0	0	0	0	1	1
ENSG00000261766	ENSG00000261766	RP11-22P6.2	16:28857920-28885526	NOTEST	0.0796557	0.0847594	0.0895969	0	1	1
ENSG00000261768	ENSG00000261768	SLC2A6	HG79_PATCH:136346629-136354672	NOTEST	0	0	0	0	1	1
ENSG00000261770	ENSG00000261770	CTC-459F4.1	19:28175487-28475892	NOTEST	0.341959	0.454342	0.409957	0	1	1

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ENSG00000261772	ENSG00000261772	IQSEC3	HG858_PATCH:116764-232399	NOTEST	0	0	0	0	1	1
ENSG00000261773	ENSG00000261773	WI2-89031B12.1	X:153746163-153746955	NOTEST	0.0438537	0.0168845	-1.377	0	1	1
ENSG00000261774	ENSG00000261774	RP11-328J14.2	16:72312166-72312467	NOTEST	0	0	0	0	1	1
ENSG00000261775	ENSG00000261775	RP11-10O17.3	15:74753605-74809300	NOTEST	0.0778832	0	#NAME?	0	1	1
ENSG00000261776	ENSG00000261776	RP11-358L22.2	16:78048579-78100658	NOTEST	0	0	0	0	1	1
ENSG00000261777	ENSG00000261777	RP11-529K1.2	16:70323565-70407286	NOTEST	0.107965	0.0587375	-0.87821	0	1	1
ENSG00000261778	ENSG00000261778	RP5-1173P7.1	7:140774031-141180180	NOTEST	0	0	0	0	1	1
ENSG00000261779	ENSG00000261779	RP11-69H7.3	15:75487983-75504510	NOTEST	0	0	0	0	1	1
ENSG00000261780	ENSG00000261780	CTD-2354A18.1	18:70992175-71017113	NOTEST	0	0	0	0	1	1
ENSG00000261781	ENSG00000261781	RP11-174G17.2	1:18392150-18400906	NOTEST	0	0	0	0	1	1
ENSG00000261782	ENSG00000261782	RP11-43P5.1	16:35113406-35113869	NOTEST	0	0	0	0	1	1
ENSG00000261783	ENSG00000261783	RP11-252K23.2	16:75327595-75499395	NOTEST	0.562412	0.10923	-2.36426	0	1	1
ENSG00000261784	ENSG00000261784	DUX4L7	HG1032_PATCH:191005566-191007067	NOTEST	0	0	0	0	1	1
ENSG00000261785	ENSG00000261785	TRBV7-2	HG7_PATCH:142074310-142074850	NOTEST	0	0	0	0	1	1
ENSG00000261787	ENSG00000261787	TCF24	8:67858735-67874825	NOTEST	0	0	0	0	1	1
ENSG00000261788	ENSG00000261788	RP11-480G7.1	16:46737280-46737937	NOTEST	0.06113	0.145186	1.24795	0	1	1
ENSG00000261789	ENSG00000261789	RP11-709D24.5	16:4606490-4650715	NOTEST	0	0	0	0	1	1
ENSG00000261791	ENSG00000261791	RP11-1220K2.2	HG7_PATCH:141811548-141921088	NOTEST	0	0	0	0	1	1
ENSG00000261792	ENSG00000261792	DNM1P28	15:30391028-30394296	NOTEST	0	0	0	0	1	1
ENSG00000261793	ENSG00000261793	RP11-350O14.18	9:140063209-140066861	NOTEST	0	0	0	0	1	1
ENSG00000261794	ENSG00000261794	GOLGA8H	15:30896328-30906764	NOTEST	0.0966698	0.0273977	-1.81901	0	1	1
ENSG00000261795	ENSG00000261795	RP11-90P13.1	7:161764-164972	NOTEST	0.0225607	0.00343276	-2.71638	0	1	1
ENSG00000261797	ENSG00000261797	RP11-744I24.3	7:141212497-141212983	NOTEST	0	0	0	0	1	1
ENSG00000261798	ENSG00000261798	RP1-118J21.25	1:40254647-40255843	NOTEST	0.0698438	0.109764	0.652196	0	1	1
ENSG00000261800	ENSG00000261800	RP11-244B22.11	16:34378092-34379252	NOTEST	0	0	0	0	1	1
ENSG00000261801	ENSG00000261801	LOXL1-AS1	15:74200423-74244478	NOTEST	0.411533	0.401859	-0.0343166	0	1	1
ENSG00000261802	ENSG00000261802	RP11-44I10.6	16:48198862-48482313	NOTEST	0	0	0	0	1	1
ENSG00000261803	ENSG00000261803	RP11-434E6.2	16:54399918-54404611	NOTEST	0	0	0	0	1	1
ENSG00000261804	ENSG00000261804	RP11-44F14.2	16:53407404-53418657	NOTEST	0	0	0	0	1	1
ENSG00000261805	ENSG00000261805	RP11-114L10.2	HG7_PATCH:142632168-142653708	NOTEST	0	0	0	0	1	1
ENSG00000261806	ENSG00000261806	hsa-mir-8078	HG1032_PATCH:190989170-190990605	NOTEST	0	0	0	0	1	1
ENSG00000261807	ENSG00000261807	RP11-430C1.1	16:59889256-60087875	NOTEST	0	0	0	0	1	1
ENSG00000261808	ENSG00000261808	WBP1LP1	HG7_PATCH:142539535-142540431	NOTEST	0	0	0	0	1	1
ENSG00000261809	ENSG00000261809	CYP3A54P	7:4551589-4551664	NOTEST	0	0	0	0	1	1
ENSG00000261810	ENSG00000261810	RP11-895K13.2	16:9852375-10276611	NOTEST	0	0	0	0	1	1
ENSG00000261811	ENSG00000261811	RP11-382N13.2	16:5265394-5270595	NOTEST	0	0	0	0	1	1
ENSG00000261813	ENSG00000261813	RP11-151H2.3	15:75246756-75313837	NOTEST	0	0	0	0	1	1
ENSG00000261814	ENSG00000261814	HLA-P	HSCHR6_MHC_DBB:29765417-29767426	NOTEST	0	0	0	0	1	1
ENSG00000261815	ENSG00000261815	RP11-22D3.2	16:49204462-49205697	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000261816	ENSG00000261816	RP11-863P13.2	16:88225091-88227273	NOTEST	0	0	0	0	1	1
ENSG00000261817	ENSG00000261817	RP11-502H18.2	1:180086274-180093025	NOTEST	0	0	0	0	1	1
ENSG00000261818	ENSG00000261818	RP11-351A20.1	16:65614570-65680850	NOTEST	0	0	0	0	1	1
ENSG00000261819	ENSG00000261819	RP11-680G24.4	16:15068447-15248421	NOTEST	0.0514775	0.111114	1.11003	0	1	1
ENSG00000261820	ENSG00000261820	DNM1P49	15:76083810-76085024	NOTEST	0	0	0	0	1	1
ENSG00000261821	ENSG00000261821	CTD-2311M21.3	15:74630099-74660081	NOTEST	0	0	0	0	1	1
ENSG00000261822	ENSG00000261822	RP11-265N6.2	15:42841007-42862192	NOTEST	0	0.110645	inf	0	1	1
ENSG00000261823	ENSG00000261823	RP11-48G14.1	15:56536206-56757335	NOTEST	0	0.0156885	inf	0	1	1
ENSG00000261826	ENSG00000261826	RP11-691G17.1	3:140583916-140586625	NOTEST	0	0	0	0	1	1
ENSG00000261829	ENSG00000261829	RP11-223I10.1	2:231916754-231917352	NOTEST	0	0	0	0	1	1
ENSG00000261830	ENSG00000261830	TRBJ2-1	HG7_PATCH:142557257-142557307	NOTEST	0	0	0	0	1	1
ENSG00000261831	ENSG00000261831	RP11-533E19.2	1:179895775-179910931	NOTEST	0	0	0	0	1	1
ENSG00000261832	ENSG00000261832	CLN3	16:28467692-28510291	NOTEST	0.00554082	0.00153845	-1.84862	0	1	1
ENSG00000261833	ENSG00000261833	RP11-58C22.1	16:76311175-76692375	NOTEST	0	0	0	0	1	1
ENSG00000261834	ENSG00000261834	IGHV3OR16-15	16:32914762-32915215	NOTEST	0	0	0	0	1	1
ENSG00000261835	ENSG00000261835	RP11-429P3.2	16:50080339-50155854	NOTEST	0	0	0	0	1	1
ENSG00000261836	ENSG00000261836	RP11-244B22.12	16:34378092-34379252	NOTEST	0	0	0	0	1	1
ENSG00000261837	ENSG00000261837	RP11-264L1.3	16:78133309-79246564	NOTEST	0	0	0	0	1	1
ENSG00000261838	ENSG00000261838	RP11-303E16.6	16:81087101-81130008	NOTEST	0	0	0	0	1	1
ENSG00000261839	ENSG00000261839	RP1-265C24.8	6:28089572-28107456	NOTEST	0.016352	0.00392171	-2.05991	0	1	1
ENSG00000261840	ENSG00000261840	RP11-146F11.1	16:30709029-30787628	NOTEST	0.163022	0.22881	0.489078	0	1	1
ENSG00000261841	ENSG00000261841	RP11-928F19.5	15:22195621-22199970	NOTEST	0	0	0	0	1	1
ENSG00000261842	ENSG00000261842	RP11-143I21.1	7:149119765-149121981	NOTEST	0	0.00564254	inf	0	1	1
ENSG00000261843	ENSG00000261843	9-Sep	HSCHR17_3_CTG4:75265440-75508300	NOTEST	0	0	0	0	1	1
ENSG00000261844	ENSG00000261844	ST13P11	HG348_PATCH:94607216-94658686	NOTEST	0	0	0	0	1	1
ENSG00000261845	ENSG00000261845	RP13-638C3.4	17:80477588-80606429	NOTEST	0	0	0	0	1	1
ENSG00000261846	ENSG00000261846	AADACL2	HSCHR3_1_CTG2_1:151462241-151656501	NOTEST	0	0	0	0	1	1
ENSG00000261847	ENSG00000261847	AP000705.6	HSCHR21_2_CTG1_1:23526269-23526619	NOTEST	0	0	0	0	1	1
ENSG00000261848	ENSG00000261848	CTD-2309O5.3	17:3038262-3080325	NOTEST	0	0	0	0	1	1
ENSG00000261849	ENSG00000261849	KIR3DP1	HSCHR19LRC_COX2_CTG1:54933098-54937062	NOTEST	0	0	0	0	1	1
ENSG00000261850	ENSG00000261850	MIR1-1	HG506_HG507_HG1000_PATCH:61119398-61145820	NOTEST	0	0	0	0	1	1
ENSG00000261851	ENSG00000261851	AC005077.8	HG1257_PATCH:75577982-75578357	NOTEST	0	0	0	0	1	1
ENSG00000261852	ENSG00000261852	KRTAP2-1	HSCHR17_4_CTG4:39202917-39203693	NOTEST	0	0	0	0	1	1
ENSG00000261853	ENSG00000261853	TAS2R18	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000261855	ENSG00000261855	HYAL3	HG325_PATCH:50316458-50336900	NOTEST	0	0	0	0	1	1
ENSG00000261856	ENSG00000261856	CTD-2135D7.4	16:14112736-14114934	NOTEST	0	0	0	0	1	1
ENSG00000261858	ENSG00000261858	RP11-110I1.5	HG299_PATCH:118868851-118901597	NOTEST	0	0	0	0	1	1
ENSG00000261859	ENSG00000261859	AC134873.1	HG1007_PATCH:243064437-243064620	NOTEST	0	0	0	0	1	1
ENSG00000261860	ENSG00000261860	KIR3DL1	HSCHR19LRC_PGF1_CTG1:55157744-55300469	NOTEST	0	0	0	0	1	1

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ENSG00000261862	ENSG00000261862	KRTAP1-5	HSCHR17_4_CTG4:39182404-39183581	NOTEST	0	0	0	0	1	1
ENSG00000261863	ENSG00000261863	RP11-141J13.5	17:4513743-4520945	NOTEST	0	0	0	0	1	1
ENSG00000261864	ENSG00000261864	RP11-67A1.2	16:68021296-68272005	NOTEST	0	0.131872	inf	0	1	1
ENSG00000261865	ENSG00000261865	U6	HSCHR19LRC_LRC_S_CTG1:55379764-55379871	NOTEST	0	0	0	0	1	1
ENSG00000261866	ENSG00000261866	AC092566.1	19:8786678-8786903	NOTEST	0	0	0	0	1	1
ENSG00000261867	ENSG00000261867	U6	HSCHR12_3_CTG2_1:101555446-101610166	NOTEST	0	0	0	0	1	1
ENSG00000261868	ENSG00000261868	RP11-104O19.2	17:4172553-4269923	NOTEST	0.0233565	0	#NAME?	0	1	1
ENSG00000261869	ENSG00000261869	LSMEM2	HG325_PATCH:50316458-50336900	NOTEST	0	0	0	0	1	1
ENSG00000261870	ENSG00000261870	KIR2DS5	HSCHR19LRC_COX2_CTG1:54991290-55006271	NOTEST	0	0	0	0	1	1
ENSG00000261871	ENSG00000261871	NAT6	HG325_PATCH:50316458-50336900	NOTEST	0	0	0	0	1	1
ENSG00000261872	ENSG00000261872	RP5-867C24.5	17:45195068-45266788	NOTEST	0	0	0	0	1	1
ENSG00000261873	ENSG00000261873	RP11-515E23.1	17:53545426-53588299	NOTEST	0	0	0	0	1	1
ENSG00000261874	ENSG00000261874	RP11-735A19.2	HG348_PATCH:94782586-94784110	NOTEST	0	0	0	0	1	1
ENSG00000261875	ENSG00000261875	AC006014.8	HG1257_PATCH:74856911-74881744	NOTEST	0	0	0	0	1	1
ENSG00000261876	ENSG00000261876	PMS2P3	HG1257_PATCH:74959037-74993105	NOTEST	0	0	0	0	1	1
ENSG00000261878	ENSG00000261878	ANKRD30BP3	HSCHR10_1_CTG5:45652222-45676875	NOTEST	0	0	0	0	1	1
ENSG00000261880	ENSG00000261880	NCR1	HSCHR19LRC_PGF2_CTG1:55147186-55157187	NOTEST	0	0	0	0	1	1
ENSG00000261882	ENSG00000261882	RP11-502F1.2	17:54188318-54589020	NOTEST	0	0	0	0	1	1
ENSG00000261883	ENSG00000261883	HMBS	HG299_PATCH:118955574-118964258	NOTEST	0	0	0	0	1	1
ENSG00000261885	ENSG00000261885	TAS2R18	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000261886	ENSG00000261886	RP11-63A1.1	17:44994135-45000400	NOTEST	0.125341	0	#NAME?	0	1	1
ENSG00000261887	ENSG00000261887	C5orf30	HG1063_PATCH:102594405-102614364	NOTEST	0	0	0	0	1	1
ENSG00000261888	ENSG00000261888	AC144831.1	17:81061204-81063860	NOTEST	0.0108071	0.0139289	0.366097	0	1	1
ENSG00000261889	ENSG00000261889	RP11-473M20.16	16:3206736-3207484	NOTEST	0.150238	0.317414	1.07911	0	1	1
ENSG00000261890	ENSG00000261890	AC010492.5	HSCHR19LRC_COX1_CTG1:54771629-54772673	NOTEST	0	0	0	0	1	1
ENSG00000261891	ENSG00000261891	SEMA3B-AS1	HG325_PATCH:50304072-50304803	NOTEST	0	0	0	0	1	1
ENSG00000261893	ENSG00000261893	CLK2	HSCHR1_2_CTG31:155248062-155286629	NOTEST	0	0	0	0	1	1
ENSG00000261894	ENSG00000261894	SPDYE7P	HG1257_PATCH:72327713-72335467	NOTEST	0	0	0	0	1	1
ENSG00000261895	ENSG00000261895	U6	HSCHR5_1_CTG1:68773019-68852251	NOTEST	0	0	0	0	1	1
ENSG00000261896	ENSG00000261896	RP11-498B4.4	HG311_PATCH:118509417-118510778	NOTEST	0	0	0	0	1	1
ENSG00000261897	ENSG00000261897	OR5T3	HG142_HG150_NOVEL_TEST:56019675-56020698	NOTEST	0	0	0	0	1	1
ENSG00000261898	ENSG00000261898	RP11-314A20.5	17:4634722-4643217	NOTEST	0	0.000496211	inf	0	1	1
ENSG00000261899	ENSG00000261899	CRIM1	HSCHR2_1_CTG1:36589101-36784311	NOTEST	0	0	0	0	1	1
ENSG00000261900	ENSG00000261900	ZNF518A	HG339_PATCH:97889471-98031303	NOTEST	0	0	0	0	1	1
ENSG00000261904	ENSG00000261904	RP11-109M19.3	16:10813689-10815321	NOTEST	0	0	0	0	1	1
ENSG00000261905	ENSG00000261905	ABC13-48559800H2.1	HSCHR1_2_CTG31:155195548-155198898	NOTEST	0	0	0	0	1	1
ENSG00000261906	ENSG00000261906	LENG9	HSCHR19LRC_PGF1_CTG1:54878386-54897289	NOTEST	0	0	0	0	1	1
ENSG00000261908	ENSG00000261908	LINC00035	HG1257_PATCH:73199994-73201011	NOTEST	0	0	0	0	1	1
ENSG00000261910	ENSG00000261910	MYO7A	HG414_PATCH:76839306-76926281	NOTEST	0	0	0	0	1	1
ENSG00000261911	ENSG00000261911	RFC2	HG1257_PATCH:73696455-73719401	NOTEST	0	0	0	0	1	1
ENSG00000261912	ENSG00000261912	KIR2DL3	HSCHR19LRC_COX1_CTG1:55173046-55218870	NOTEST	0	0	0	0	1	1
ENSG00000261913	ENSG00000261913	MTRNR2L6	HG7_PATCH:142406771-142408166	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000261914	ENSG00000261914	ABC7-42391500H16.2	HG1032_PATCH:191116881-191117345	NOTEST	0	0	0	0	1	1
ENSG00000261915	ENSG00000261915	RP11-542C16.2	17:7210317-7232712	NOTEST	0	0.0812209	inf	0	1	1
ENSG00000261916	ENSG00000261916	RP11-235E17.4	17:3468737-3539616	NOTEST	0.0871301	0	#NAME?	0	1	1
ENSG00000261917	ENSG00000261917	MBOAT7	HSCHR19LRC_COX1_CTG1:54677071-54693566	NOTEST	0	0	0	0	1	1
ENSG00000261918	ENSG00000261918	RNA5SP233	HG1257_PATCH:73918746-74067561	NOTEST	0	0	0	0	1	1
ENSG00000261919	ENSG00000261919	NCF1	HG1257_PATCH:74238918-74254272	NOTEST	0	0	0	0	1	1
ENSG00000261920	ENSG00000261920	GTF2IRD1	HG1257_PATCH:73918746-74067561	NOTEST	0	0	0	0	1	1
ENSG00000261921	ENSG00000261921	HYAL2	HG325_PATCH:50355221-50365683	NOTEST	0	0	0	0	1	1
ENSG00000261923	ENSG00000261923	PDE3B	HG873_PATCH:14665268-14892350	NOTEST	0	0	0	0	1	1
ENSG00000261924	ENSG00000261924	CTD-2561B21.5	17:78518618-78945013	NOTEST	0.0872394	0.151116	0.792608	0	1	1
ENSG00000261925	ENSG00000261925	RP11-388M20.9	16:31237280-31238481	NOTEST	0	0	0	0	1	1
ENSG00000261926	ENSG00000261926	RP11-470P21.2	HSCHR9_1_CTG35:72095577-72117625	NOTEST	0	0	0	0	1	1
ENSG00000261927	ENSG00000261927	CTD-2542C24.4	HSCHR19_1_CTG3:20857728-20879339	NOTEST	0	0	0	0	1	1
ENSG00000261928	ENSG00000261928	RP11-641C17.4	HG1091_PATCH:59735035-61237194	NOTEST	0	0	0	0	1	1
ENSG00000261929	ENSG00000261929	LILRA4	HSCHR19LRC_PGF2_CTG1:54843569-54849537	NOTEST	0	0	0	0	1	1
ENSG00000261930	ENSG00000261930	KIR3DL2	HSCHR19LRC_LRC_T_CTG1:55297896-55314683	NOTEST	0	0	0	0	1	1
ENSG00000261931	ENSG00000261931	CDC42EP5	HSCHR19LRC_PGF1_CTG1:54898604-54906806	NOTEST	0	0	0	0	1	1
ENSG00000261932	ENSG00000261932	BDP1	HSCHR5_1_CTG1:69966744-70078950	NOTEST	0	0	0	0	1	1
ENSG00000261934	ENSG00000261934	PCDHGA9	5:140710251-140892546	NOTEST	0.114792	0.16283	0.504352	0	1	1
ENSG00000261935	ENSG00000261935	LILRA3	HSCHR19LRC_COX1_CTG1:54799625-54809724	NOTEST	0	0	0	0	1	1
ENSG00000261936	ENSG00000261936	RP11-673D15.8	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000261937	ENSG00000261937	LILRA3	HSCHR19LRC_COX2_CTG1:54799505-54809605	NOTEST	0	0	0	0	1	1
ENSG00000261938	ENSG00000261938	RP11-461A8.1	16:3631181-3661599	NOTEST	0	0	0	0	1	1
ENSG00000261939	ENSG00000261939	CTC-496I23.1	16:19566561-19897489	NOTEST	0	0	0	0	1	1
ENSG00000261940	ENSG00000261940	DNAJC30	HG1257_PATCH:73145925-73184629	NOTEST	0	0	0	0	1	1
ENSG00000261941	ENSG00000261941	OMP	HG414_PATCH:76777975-76835592	NOTEST	0	0	0	0	1	1
ENSG00000261946	ENSG00000261946	KDM4D	HG348_PATCH:94706845-94732679	NOTEST	0	0	0	0	1	1
ENSG00000261948	ENSG00000261948	RP11-396K3.1	HG1257_PATCH:72619901-72670574	NOTEST	0	0	0	0	1	1
ENSG00000261949	ENSG00000261949	GFY	19:49927005-49932075	NOTEST	0.0489898	0.0122431	-2.00051	0	1	1
ENSG00000261950	ENSG00000261950	AC010492.2	HSCHR19LRC_PGF1_CTG1:54704600-54752858	NOTEST	0	0	0	0	1	1
ENSG00000261951	ENSG00000261951	RP11-536P16.3	HSCHR15_1_CTG4:28594195-28603160	NOTEST	0	0	0	0	1	1
ENSG00000261952	ENSG00000261952	POM121B	HG1257_PATCH:72758453-72767456	NOTEST	0	0	0	0	1	1
ENSG00000261953	ENSG00000261953	RNU6-863P	HG1257_PATCH:75552400-75552504	NOTEST	0	0	0	0	1	1
ENSG00000261954	ENSG00000261954	5S_rRNA	HG388_HG400_PATCH:111797866-111893307	NOTEST	0	0	0	0	1	1
ENSG00000261955	ENSG00000261955	SNORA18	HSCHR5_3_CTG1:29079490-29079605	NOTEST	0	0	0	0	1	1
ENSG00000261956	ENSG00000261956	U6	HSCHR10_1_CTG5:45682909-45693771	NOTEST	0	0	0	0	1	1
ENSG00000261957	ENSG00000261957	RP11-578F21.4	HSCHR15_1_CTG4:28810337-28818145	NOTEST	0	0	0	0	1	1
ENSG00000261958	ENSG00000261958	OR9G1	HG151_NOVEL_TEST:56467861-56468779	NOTEST	0	0	0	0	1	1
ENSG00000261960	ENSG00000261960	RP11-66N11.8	HG1497_PATCH:152767811-152772825	NOTEST	0	0	0	0	1	1
ENSG00000261961	ENSG00000261961	GP6	HSCHR19LRC_LRC_I_CTG1:55515064-55580163	NOTEST	0	0	0	0	1	1
ENSG00000261962	ENSG00000261962	AC009133.20	16:29817426-29859355	NOTEST	0	0.160855	inf	0	1	1

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ENSG00000261963	ENSG00000261963	RP11-74E22.4	17:2627713-2652714	NOTEST	0	0	0	0	1	1
ENSG00000261964	ENSG00000261964	ADAMTS10	HG729_PATCH:8645125-8675619	NOTEST	0	0	0	0	1	1
ENSG00000261965	ENSG00000261965	ISCA1P3	17:52555156-52555529	NOTEST	0	0	0	0	1	1
ENSG00000261967	ENSG00000261967	GOLGA8F	HSCHR15_1_CTG4:28623775-28637136	NOTEST	0	0	0	0	1	1
ENSG00000261968	ENSG00000261968	AC037482.3	HSCHR17_4_CTG4:39254168-39254756	NOTEST	0	0	0	0	1	1
ENSG00000261970	ENSG00000261970	RP11-342L8.2	6:80262510-80262877	NOTEST	0.0755366	0.16968	1.16757	0	1	1
ENSG00000261972	ENSG00000261972	CES5A	HSCHR16_1_CTG3_1:55892483-56002378	NOTEST	0	0	0	0	1	1
ENSG00000261974	ENSG00000261974	CWC15	HG348_PATCH:94695786-94706777	NOTEST	0	0	0	0	1	1
ENSG00000261975	ENSG00000261975	RDH13	HSCHR19LRC_COX1_CTG1:55438477-55503576	NOTEST	0	0	0	0	1	1
ENSG00000261976	ENSG00000261976	RP11-506D12.5	17:48912010-48919709	NOTEST	0	0	0	0	1	1
ENSG00000261978	ENSG00000261978	CTD-2529O21.2	17:77906141-78009647	NOTEST	0	0	0	0	1	1
ENSG00000261979	ENSG00000261979	AC010492.4	HSCHR19LRC_COX1_CTG1:54704427-54752625	NOTEST	0	0	0	0	1	1
ENSG00000261981	ENSG00000261981	ENPP7	HG748_PATCH:77727000-77738304	NOTEST	0	0	0	0	1	1
ENSG00000261982	ENSG00000261982	RP11-748L13.6	HSCHR10_1_CTG2:27679664-27681146	NOTEST	0	0	0	0	1	1
ENSG00000261984	ENSG00000261984	TAS2R14	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000261986	ENSG00000261986	KRT33A	HSCHR17_1_CTG4:39502343-39507064	NOTEST	0	0	0	0	1	1
ENSG00000261987	ENSG00000261987	KYNUP1	17:19067521-19077749	NOTEST	0	0	0	0	1	1
ENSG00000261988	ENSG00000261988	AC008984.6	HSCHR19LRC_COX2_CTG1:54838503-54841666	NOTEST	0	0	0	0	1	1
ENSG00000261989	ENSG00000261989	RP11-136K7.1	HSCHR5_1_CTG1:69863006-69957699	NOTEST	0	0	0	0	1	1
ENSG00000261990	ENSG00000261990	snoU13	HG946_PATCH:98507244-98642555	NOTEST	0	0	0	0	1	1
ENSG00000261991	ENSG00000261991	RP11-100N3.2	HG151_NOVEL_TEST:56514865-56515012	NOTEST	0	0	0	0	1	1
ENSG00000261992	ENSG00000261992	GATAD2B	HSCHR1_1_CTG31:153794431-153912682	NOTEST	0	0	0	0	1	1
ENSG00000261994	ENSG00000261994	WEE2-AS1	HSCHR7_1_CTG6:141410145-141493730	NOTEST	0	0	0	0	1	1
ENSG00000261996	ENSG00000261996	CTC-281F24.1	17:6554970-6558328	NOTEST	0.041958	0.11605	1.46773	0	1	1
ENSG00000261997	ENSG00000261997	RP11-212I21.4	16:55542909-55620582	NOTEST	0.0530146	0.045688	-0.214575	0	1	1
ENSG00000261998	ENSG00000261998	AC011515.2	HSCHR19LRC_PGF2_CTG1:54926620-54927981	NOTEST	0	0	0	0	1	1
ENSG00000261999	ENSG00000261999	RP11-629G13.1	HG306_PATCH:112830001-113149158	NOTEST	0	0	0	0	1	1
ENSG00000262000	ENSG00000262000	CTD-2526A2.5	17:78489014-78489189	NOTEST	0	0	0	0	1	1
ENSG00000262003	ENSG00000262003	RP11-676J12.7	17:702552-883010	NOTEST	0.0228867	0	#NAME?	0	1	1
ENSG00000262004	ENSG00000262004	LILRA2	HSCHR19LRC_COX1_CTG1:55008196-55074165	NOTEST	0	0	0	0	1	1
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ENSG00000262006	ENSG00000262006	RP11-700H6.4	17:48939583-48987593	NOTEST	0	0	0	0	1	1
ENSG00000262007	ENSG00000262007	KIR3DL2	HSCHR19LRC_LRC_S_CTG1:55361246-55378033	NOTEST	0	0	0	0	1	1
ENSG00000262008	ENSG00000262008	RP11-510M2.8	16:71476957-71477759	NOTEST	0	0	0	0	1	1
ENSG00000262009	ENSG00000262009	NLRP7	HSCHR19LRC_PGF2_CTG1:55164555-55242189	NOTEST	0	0	0	0	1	1
ENSG00000262011	ENSG00000262011	AC003009.1	16:13340172-13656775	NOTEST	0	0	0	0	1	1
ENSG00000262013	ENSG00000262013	Y_RNA	HG1257_PATCH:72868744-72868846	NOTEST	0	0	0	0	1	1
ENSG00000262015	ENSG00000262015	SEMA3B	HG325_PATCH:50304989-50314978	NOTEST	0	0	0	0	1	1
ENSG00000262016	ENSG00000262016	RP11-598F7.5	HSCHR12_1_CTG1:120779-236414	NOTEST	0	0	0	0	1	1
ENSG00000262017	ENSG00000262017	5S_rRNA	HG75_PATCH:34814004-34869611	NOTEST	0	0	0	0	1	1
ENSG00000262018	ENSG00000262018	VPS37D	HG1257_PATCH:73132781-73137069	NOTEST	0	0	0	0	1	1
ENSG00000262020	ENSG00000262020	RP11-66H6.3	16:11038344-11276046	NOTEST	0	0.026352	inf	0	1	1
ENSG00000262022	ENSG00000262022	ZNF100	HSCHR19_2_CTG3:21915046-21959807	NOTEST	0	0	0	0	1	1

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ENSG00000262023	ENSG00000262023	JH8	HG418_PATCH:143738820-143751344	NOTEST	0	0	0	0	1	1
ENSG00000262024	ENSG00000262024	TCF20	HSCHR22_1_CTG1:42543862-42727524	NOTEST	0	0	0	0	1	1
ENSG00000262025	ENSG00000262025	RP11-216N14.7	HSCHR1_1_CTG31:153794431-153912682	NOTEST	0	0	0	0	1	1
ENSG00000262027	ENSG00000262027	CUBNP2	HSCHR10_1_CTG5:45727473-45742809	NOTEST	0	0	0	0	1	1
ENSG00000262028	ENSG00000262028	FDXACB1	HG388_HG400_PATCH:111652918-111756698	NOTEST	0	0	0	0	1	1
ENSG00000262029	ENSG00000262029	CCL26	HG1257_PATCH:75234489-75254853	NOTEST	0	0	0	0	1	1
ENSG00000262030	ENSG00000262030	WBSCR22	HG1257_PATCH:73145925-73184629	NOTEST	0	0	0	0	1	1
ENSG00000262031	ENSG00000262031	RP11-63A1.2	17:44987107-44988878	NOTEST	0	0	0	0	1	1
ENSG00000262032	ENSG00000262032	CT49	HSCHR5_2_CTG1:12574968-12824618	NOTEST	0	0	0	0	1	1
ENSG00000262033	ENSG00000262033	NCAM1-AS1	HG306_PATCH:112830001-113149158	NOTEST	0	0	0	0	1	1
ENSG00000262034	ENSG00000262034	RP11-124L9.4	HSCHR5_1_CTG1:691518806-69194073	NOTEST	0	0	0	0	1	1
ENSG00000262035	ENSG00000262035	AC098789.1	HSCHR19LRC_PGF2_CTG1:54771883-54772927	NOTEST	0	0	0	0	1	1
ENSG00000262036	ENSG00000262036	RP11-557F20.2	HSCHR12_2_CTG2_1:59314419-59465068	NOTEST	0	0	0	0	1	1
ENSG00000262037	ENSG00000262037	CTD-2626G11.1	HSCHR19_1_CTG3:20959109-20990226	NOTEST	0	0	0	0	1	1
ENSG00000262038	ENSG00000262038	RP11-177N22.3	16:47178233-47735434	NOTEST	0	0	0	0	1	1
ENSG00000262039	ENSG00000262039	RP11-81K2.1	17:47448101-47554350	NOTEST	0.133364	0	#NAME?	0	1	1
ENSG00000262040	ENSG00000262040	AC003958.1	HSCHR17_1_CTG4:39565992-39588626	NOTEST	0	0	0	0	1	1
ENSG00000262041	ENSG00000262041	RP11-974F13.1	HSCHR5_1_CTG1:690509063-69144625	NOTEST	0	0	0	0	1	1
ENSG00000262042	ENSG00000262042	U6	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000262044	ENSG00000262044	LILRB3	HSCHR19LRC_COX1_CTG1:54704427-54752625	NOTEST	0	0	0	0	1	1
ENSG00000262045	ENSG00000262045	RP1-18F17.1	HSCHR17_1_CTG4:39533916-39538652	NOTEST	0	0	0	0	1	1
ENSG00000262046	ENSG00000262046	TMEM97	HG883_PATCH:26646120-26662515	NOTEST	0	0	0	0	1	1
ENSG00000262047	ENSG00000262047	RNU6-1070P	HG1257_PATCH:73723482-73723573	NOTEST	0	0	0	0	1	1
ENSG00000262048	ENSG00000262048	RP1-232L24.4	6:80115956-80116491	NOTEST	0	0	0	0	1	1
ENSG00000262052	ENSG00000262052	RP11-763E3.1	17:53828339-53950300	NOTEST	0	0	0	0	1	1
ENSG00000262053	ENSG00000262053	MBOAT7	HSCHR19LRC_PGF1_CTG1:54677077-54693733	NOTEST	0	0	0	0	1	1
ENSG00000262055	ENSG00000262055	CYP2D8P	HSCHR22_1_CTG1:42533737-42538854	NOTEST	0	0	0	0	1	1
ENSG00000262057	ENSG00000262057	MCCC2	HSCHR5_1_CTG1:70098417-70169834	NOTEST	0	0	0	0	1	1
ENSG00000262058	ENSG00000262058	CTB-51J22.1	HG1257_PATCH:73492745-73534864	NOTEST	0	0	0	0	1	1
ENSG00000262059	ENSG00000262059	KRT18P40	HSCHR19_1_CTG3:21150278-21154362	NOTEST	0	0	0	0	1	1
ENSG00000262060	ENSG00000262060	RP11-313P13.4	HG1257_PATCH:72434652-72606602	NOTEST	0	0	0	0	1	1
ENSG00000262061	ENSG00000262061	RP11-1260E13.4	17:62292-236045	NOTEST	0.0129168	0	#NAME?	0	1	1
ENSG00000262062	ENSG00000262062	VTN	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000262063	ENSG00000262063	LIMK1	HG1257_PATCH:73547889-73587482	NOTEST	0	0	0	0	1	1
ENSG00000262064	ENSG00000262064	snoU13	HG1257_PATCH:75577754-75577853	NOTEST	0	0	0	0	1	1
ENSG00000262065	ENSG00000262065	AC010492.5	HSCHR19LRC_PGF2_CTG1:54771883-54772927	NOTEST	0	0	0	0	1	1
ENSG00000262067	ENSG00000262067	CTD-2545G14.2	17:6962252-6962523	NOTEST	0	0	0	0	1	1
ENSG00000262068	ENSG00000262068	KRTAP3-1	HSCHR17_4_CTG4:39164899-39175703	NOTEST	0	0	0	0	1	1
ENSG00000262069	ENSG00000262069	GP6	HSCHR19LRC_COX2_CTG1:55180280-55245379	NOTEST	0	0	0	0	1	1
ENSG00000262072	ENSG00000262072	OR6D1P	HSCHR10_1_CTG5:45753632-45754571	NOTEST	0	0	0	0	1	1
ENSG00000262073	ENSG00000262073	CLDN3	HG1257_PATCH:73233954-73235227	NOTEST	0	0	0	0	1	1
ENSG00000262074	ENSG00000262074	SNORD3B-2	17:18966761-18967449	NOTEST	0.0528746	0.0203105	-1.38035	0	1	1

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ENSG00000262075	ENSG00000262075	WI2-2942J8.1	HG998_2_PATCH:139230204-139235225	NOTEST	0	0	0	0	1	1
ENSG00000262076	ENSG00000262076	RP11-66N11.6	HG1497_PATCH:152774988-152775360	NOTEST	0	0	0	0	1	1
ENSG00000262077	ENSG00000262077	MLXIPL	HG1257_PATCH:73058150-73089500	NOTEST	0	0	0	0	1	1
ENSG00000262079	ENSG00000262079	RP11-515O17.3	17:53403117-53405152	NOTEST	0	0	0	0	1	1
ENSG00000262080	ENSG00000262080	RP11-578F21.1	HSCHR15_1_CTG4:28846257-28942030	NOTEST	0	0	0	0	1	1
ENSG00000262081	ENSG00000262081	IL9RP4	18:80139-88570	NOTEST	0	0	0	0	1	1
ENSG00000262082	ENSG00000262082	RP11-58A17.2	HSCHR12_1_CTG2_1:58377577-58378544	NOTEST	0	0	0	0	1	1
ENSG00000262083	ENSG00000262083	RP11-108O10.2	HG388_HG400_PATCH:111639391-111649074	NOTEST	0	0	0	0	1	1
ENSG00000262085	ENSG00000262085	OR1P1	17:3038262-3080325	NOTEST	0	0	0	0	1	1
ENSG00000262087	ENSG00000262087	LILRB3	HSCHR19LRC_PGF1_CTG1:54704600-54752858	NOTEST	0	0	0	0	1	1
ENSG00000262088	ENSG00000262088	RPS25	HG299_PATCH:118868851-118901597	NOTEST	0	0	0	0	1	1
ENSG00000262090	ENSG00000262090	RP11-23E10.5	16:33298409-33298560	NOTEST	0	0	0	0	1	1
ENSG00000262091	ENSG00000262091	CTB-96E2.3	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000262092	ENSG00000262092	EPS8L1	HSCHR19LRC_COX2_CTG1:55246107-55262011	NOTEST	0	0	0	0	1	1
ENSG00000262093	ENSG00000262093	AL512324.1	HSCHR10_1_CTG5:45682909-45693771	NOTEST	0	0	0	0	1	1
ENSG00000262094	ENSG00000262094	AC139099.5	17:81159764-81188573	NOTEST	0.23373	0.21617	-0.112674	0	1	1
ENSG00000262095	ENSG00000262095	RP3-433F14.4	6:92436527-92436788	NOTEST	0	0	0	0	1	1
ENSG00000262096	ENSG00000262096	PCDHB19P	5:140619517-140621864	NOTEST	0.0068249	0.0212447	1.63822	0	1	1
ENSG00000262097	ENSG00000262097	CTD-2135D7.5	16:14103136-14109873	NOTEST	0	0	0	0	1	1
ENSG00000262098	ENSG00000262098	CTD-2561B21.10	17:78997344-78999303	NOTEST	0	0	0	0	1	1
ENSG00000262099	ENSG00000262099	CTC-524C5.5	17:5372411-5373680	NOTEST	0	0	0	0	1	1
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ENSG00000262102	ENSG00000262102	DSEL	HSCHR18_2_CTG2:65243267-65636305	NOTEST	0	0	0	0	1	1
ENSG00000262103	ENSG00000262103	TAS2R14	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000262104	ENSG00000262104	Y_RNA	HSCHR18_1_CTG2_1:76304095-76304188	NOTEST	0	0	0	0	1	1
ENSG00000262105	ENSG00000262105	AC008746.10	HSCHR19LRC_PGF1_CTG1:54813027-54813499	NOTEST	0	0	0	0	1	1
ENSG00000262106	ENSG00000262106	OR1D3P	17:3168904-3169835	NOTEST	0	0	0	0	1	1
ENSG00000262107	ENSG00000262107	RP11-109M19.5	16:10813689-10815321	NOTEST	0	0	0	0	1	1
ENSG00000262110	ENSG00000262110	RDH13	HSCHR19LRC_LRC_J_CTG1:55542601-55607700	NOTEST	0	0	0	0	1	1
ENSG00000262111	ENSG00000262111	TAS2R30	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000262112	ENSG00000262112	RP11-670E13.5	17:54965269-54991399	NOTEST	0	0	0	0	1	1
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ENSG00000262115	ENSG00000262115	RP11-455O6.2	17:79163392-79196799	NOTEST	0	0.0929989	inf	0	1	1
ENSG00000262116	ENSG00000262116	AC009134.1	16:12995476-13334272	NOTEST	0	0	0	0	1	1
ENSG00000262117	ENSG00000262117	BCAR4	16:11913685-11922702	NOTEST	0	0	0	0	1	1
ENSG00000262118	ENSG00000262118	RP11-433P17.3	16:3415098-3627401	NOTEST	0.0855439	0.0872536	0.0285494	0	1	1
ENSG00000262119	ENSG00000262119	RP11-483C6.1	14:26912298-27066960	NOTEST	0.0185642	0	#NAME?	0	1	1
ENSG00000262120	ENSG00000262120	RP11-510M2.7	16:71444342-71460367	NOTEST	0	0	0	0	1	1
ENSG00000262121	ENSG00000262121	KRTAP4-9	HSCHR17_4_CTG4:39262002-39263159	NOTEST	0	0	0	0	1	1
ENSG00000262122	ENSG00000262122	POM121	HG1257_PATCH:72344321-72419747	NOTEST	0	0	0	0	1	1
ENSG00000262123	ENSG00000262123	RNU6-1198P	HG1257_PATCH:72905354-72987235	NOTEST	0	0	0	0	1	1
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test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000262127	ENSG00000262127	Metazoa_SRP	HSCHR15_1_CTG4:28776380-28789737	NOTEST	0	0	0	0	1	1
ENSG00000262128	ENSG00000262128	LAT2	HG1257_PATCH:73664608-73694788	NOTEST	0	0	0	0	1	1
ENSG00000262129	ENSG00000262129	RP11-708L7.7	HG388_HG400_PATCH:111797866-111893307	NOTEST	0	0	0	0	1	1
ENSG00000262131	ENSG00000262131	GP6	HSCHR19LRC_LRC_S_CTG1:55517150-55582249	NOTEST	0	0	0	0	1	1
ENSG00000262132	ENSG00000262132	5S_rRNA	HSCHR18_1_CTG1_1:47845371-47845490	NOTEST	0	0	0	0	1	1
ENSG00000262133	ENSG00000262133	RP11-676J12.6	17:702552-883010	NOTEST	0	0	0	0	1	1
ENSG00000262134	ENSG00000262134	TRBC1	HG7_PATCH:142552586-142554261	NOTEST	0	0	0	0	1	1
ENSG00000262135	ENSG00000262135	CTD-2033D24.1	17:53604324-53638938	NOTEST	0	0	0	0	1	1
ENSG00000262136	ENSG00000262136	CTD-2033A16.3	16:69760915-69788843	NOTEST	0	0	0	0	1	1
ENSG00000262138	ENSG00000262138	AC012314.1	HSCHR19LRC_COX1_CTG1:54641435-54663619	NOTEST	0	0	0	0	1	1
ENSG00000262139	ENSG00000262139	ANO4	HSCHR12_3_CTG2_1:101505376-101522419	NOTEST	0	0	0	0	1	1
ENSG00000262140	ENSG00000262140	RP11-417N10.3	16:71867689-71869835	NOTEST	0	0	0	0	1	1
ENSG00000262141	ENSG00000262141	CTC-479C5.11	16:67840667-67906470	NOTEST	0	0	0	0	1	1
ENSG00000262143	ENSG00000262143	AC009892.10	HSCHR19LRC_PGF1_CTG1:55006690-55072658	NOTEST	0	0	0	0	1	1
ENSG00000262145	ENSG00000262145	XRCC6BP1	HSCHR12_1_CTG2_1:58335323-58351052	NOTEST	0	0	0	0	1	1
ENSG00000262146	ENSG00000262146	RP11-241G9.3	HSCHR5_1_CTG1:68773019-68852251	NOTEST	0	0	0	0	1	1
ENSG00000262148	ENSG00000262148	RPS5P3	HSCHR21_4_CTG1_1:34863443-34864059	NOTEST	0	0	0	0	1	1
ENSG00000262149	ENSG00000262149	MYO1F	HG729_PATCH:8585995-8642307	NOTEST	0	0	0	0	1	1
ENSG00000262150	ENSG00000262150	PSCA	HG418_PATCH:143751668-143764085	NOTEST	0	0	0	0	1	1
ENSG00000262151	ENSG00000262151	RP11-876N24.2	16:10958770-11036878	NOTEST	0	0	0	0	1	1
ENSG00000262152	ENSG00000262152	LINC00514	16:3038961-3044510	NOTEST	0.0129677	0	#NAME?	0	1	1
ENSG00000262153	ENSG00000262153	CTC-550B14.1	HSCHR19LRC_PGF2_CTG1:55164555-55242189	NOTEST	0	0	0	0	1	1
ENSG00000262154	ENSG00000262154	LA16c-352F10.1	16:2867163-2876305	NOTEST	0.173039	0	#NAME?	0	1	1
ENSG00000262155	ENSG00000262155	RP11-266L9.5	16:25078257-25080264	NOTEST	0.0261466	0.059825	1.19412	0	1	1
ENSG00000262156	ENSG00000262156	APOBEC3A	HSCHR22_1_CTG2:39353527-39364275	NOTEST	0	0	0	0	1	1
ENSG00000262158	ENSG00000262158	CTD-2318B16.2	16:10817692-10818474	NOTEST	0	0	0	0	1	1
ENSG00000262159	ENSG00000262159	RPS6P22	HSCHR12_2_CTG2_1:59314419-59465068	NOTEST	0	0	0	0	1	1
ENSG00000262160	ENSG00000262160	RP11-96D1.11	16:68021296-68272005	NOTEST	0	0.0612951	inf	0	1	1
ENSG00000262161	ENSG00000262161	KIR2DS4	HSCHR19LRC_LRC_I_CTG1:55341440-55357334	NOTEST	0	0	0	0	1	1
ENSG00000262162	ENSG00000262162	FAM8A2P	HG142_HG150_NOVEL_TEST:56098822-56099964	NOTEST	0	0	0	0	1	1
ENSG00000262163	ENSG00000262163	RDH13	HSCHR19LRC_LRC_S_CTG1:55517150-55582249	NOTEST	0	0	0	0	1	1
ENSG00000262164	ENSG00000262164	KRT39	HSCHR17_4_CTG4:39077681-39132305	NOTEST	0	0	0	0	1	1
ENSG00000262165	ENSG00000262165	RP11-81A22.5	17:4704453-4710308	NOTEST	0.146404	0	#NAME?	0	1	1
ENSG00000262168	ENSG00000262168	LENG1	HSCHR19LRC_PGF1_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000262169	ENSG00000262169	GTF2H2	HSCHR5_1_CTG1:68855800-68888468	NOTEST	0	0	0	0	1	1
ENSG00000262170	ENSG00000262170	SMN2	HSCHR5_1_CTG1:68969493-68998376	NOTEST	0	0	0	0	1	1
ENSG00000262171	ENSG00000262171	CTA-972D3.2	16:15959576-15982482	NOTEST	0.273294	0.424691	0.635962	0	1	1
ENSG00000262172	ENSG00000262172	CTD-2529O21.1	17:77906141-78009647	NOTEST	0.15705	0.170947	0.122324	0	1	1
ENSG00000262174	ENSG00000262174	LENG1	HSCHR19LRC_COX1_CTG1:54641435-54663619	NOTEST	0	0	0	0	1	1
ENSG00000262175	ENSG00000262175	NLRP2	HSCHR19LRC_LRC_J_CTG1:55459917-55537551	NOTEST	0	0	0	0	1	1
ENSG00000262176	ENSG00000262176	C11orf1	HG388_HG400_PATCH:111652918-111756698	NOTEST	0	0	0	0	1	1

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ENSG00000262178	ENSG00000262178	AC008984.6	HSCHR19LRC_PGF2_CTG1:54838657-54841820	NOTEST	0	0	0	0	1	1
ENSG00000262179	ENSG00000262179	RP1-302G2.5	6:44184675-44185973	NOTEST	0	0	0	0	1	1
ENSG00000262181	ENSG00000262181	RP11-683L23.2	18:45003-45556	NOTEST	0	0	0	0	1	1
ENSG00000262182	ENSG00000262182	NCR1	HSCHR19LRC_COX2_CTG1:55080218-55090214	NOTEST	0	0	0	0	1	1
ENSG00000262184	ENSG00000262184	ELN	HG1257_PATCH:73492745-73534864	NOTEST	0	0	0	0	1	1
ENSG00000262185	ENSG00000262185	RP11-462G12.1	16:3997609-4000445	NOTEST	0.163342	0.0368595	-2.14778	0	1	1
ENSG00000262186	ENSG00000262186	SLC46A1	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000262187	ENSG00000262187	RP11-652G5.2	16:32630053-32630173	NOTEST	0	0	0	0	1	1
ENSG00000262188	ENSG00000262188	RP11-353N14.4	17:77889050-77900524	NOTEST	0.339373	0.423472	0.319395	0	1	1
ENSG00000262189	ENSG00000262189	RP11-641C17.2	HG1091_PATCH:59735035-61237194	NOTEST	0	0	0	0	1	1
ENSG00000262191	ENSG00000262191	OR9G9	HG151_NOVEL_TEST:56478941-56479859	NOTEST	0	0	0	0	1	1
ENSG00000262192	ENSG00000262192	AC008984.5	HSCHR19LRC_COX1_CTG1:54799625-54809724	NOTEST	0	0	0	0	1	1
ENSG00000262193	ENSG00000262193	RP11-598F7.6	HSCHR12_1_CTG1:120779-236414	NOTEST	0	0	0	0	1	1
ENSG00000262196	ENSG00000262196	CALCP	HG873_PATCH:14929063-14929532	NOTEST	0	0	0	0	1	1
ENSG00000262197	ENSG00000262197	RP11-1305N21.2	HSCHR5_1_CTG1:69433885-69439126	NOTEST	0	0	0	0	1	1
ENSG00000262198	ENSG00000262198	RP11-124N19.3	13:23492729-23498741	NOTEST	0	0	0	0	1	1
ENSG00000262199	ENSG00000262199	SRCIN1	HG745_PATCH:36686251-36762184	NOTEST	0	0	0	0	1	1
ENSG00000262201	ENSG00000262201	RP11-58A17.4	HSCHR12_1_CTG2_1:58490833-58496304	NOTEST	0	0	0	0	1	1
ENSG00000262202	ENSG00000262202	SNORD3D	17:19015312-19015949	NOTEST	0.117612	0.0225548	-2.38253	0	1	1
ENSG00000262205	ENSG00000262205	snoU13	HSCHR5_1_CTG1:68773019-68852251	NOTEST	0	0	0	0	1	1
ENSG00000262206	ENSG00000262206	LINC00674	HG747_PATCH:66098023-66111634	NOTEST	0	0	0	0	1	1
ENSG00000262207	ENSG00000262207	RDH13	HSCHR19LRC_LRC_T_CTG1:55453443-55518542	NOTEST	0	0	0	0	1	1
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ENSG00000262209	ENSG00000262209	PCDHGB3	5:140710251-140892546	NOTEST	0.110143	0.197013	0.838913	0	1	1
ENSG00000262210	ENSG00000262210	PEBP1P3	HSCHR1_3_CTG31:198619287-198737899	NOTEST	0	0	0	0	1	1
ENSG00000262211	ENSG00000262211	CTD-2031P19.5	5:55230922-55290821	NOTEST	0	0	0	0	1	1
ENSG00000262212	ENSG00000262212	RP11-67C2.2	HSCHR10_1_CTG5:45885737-45964632	NOTEST	0	0	0	0	1	1
ENSG00000262213	ENSG00000262213	AC144836.1	17:1145232-1157294	NOTEST	0.0873472	0	#NAME?	0	1	1
ENSG00000262214	ENSG00000262214	KRTAP9-12P	HSCHR17_6_CTG4:39368961-39369493	NOTEST	0	0	0	0	1	1
ENSG00000262216	ENSG00000262216	LAIR2	HSCHR19LRC_PGF1_CTG1:54931485-54944292	NOTEST	0	0	0	0	1	1
ENSG00000262217	ENSG00000262217	SLC5A8	HSCHR12_3_CTG2_1:101555446-101610166	NOTEST	0	0	0	0	1	1
ENSG00000262218	ENSG00000262218	KRTAP29-1	HSCHR17_5_CTG4:39447755-39448781	NOTEST	0	0	0	0	1	1
ENSG00000262219	ENSG00000262219	AC010492.5	HSCHR19LRC_PGF1_CTG1:54771872-54772916	NOTEST	0	0	0	0	1	1
ENSG00000262220	ENSG00000262220	VN1R105P	HSCHR19LRC_PGF1_CTG1:55077654-55083366	NOTEST	0	0	0	0	1	1
ENSG00000262221	ENSG00000262221	KRTAP9-7	HSCHR17_6_CTG4:39420540-39421579	NOTEST	0	0	0	0	1	1
ENSG00000262225	ENSG00000262225	EPS8L1	HSCHR19LRC_LRC_T_CTG1:55519270-55535174	NOTEST	0	0	0	0	1	1
ENSG00000262226	ENSG00000262226	RP11-598F7.3	HSCHR12_1_CTG1:120779-236414	NOTEST	0	0	0	0	1	1
ENSG00000262228	ENSG00000262228	RP11-676J12.4	17:660336-695749	NOTEST	0.0451267	0.034347	-0.393798	0	1	1
ENSG00000262230	ENSG00000262230	AC069067.2	HSCHR3_1_CTG2_1:151352137-151352251	NOTEST	0	0	0	0	1	1
ENSG00000262231	ENSG00000262231	RP11-960B9.2	17:6092680-6093861	NOTEST	0	0	0	0	1	1
ENSG00000262232	ENSG00000262232	CTD-2292P10.2	HG418_PATCH:143808563-143818288	NOTEST	0	0	0	0	1	1
ENSG00000262233	ENSG00000262233	CH17-93H22.2	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000262235	ENSG00000262235	AC003009.2	16:13340172-13656775	NOTEST	0	0	0	0	1	1
ENSG00000262236	ENSG00000262236	TTYH1	HSCHR19LRC_PGF1_CTG1:54848799-54870475	NOTEST	0	0	0	0	1	1
ENSG00000262237	ENSG00000262237	RP11-553K8.5	HSCHR1_3_CTG31:198619287-198737899	NOTEST	0	0	0	0	1	1
ENSG00000262238	ENSG00000262238	VN1R105P	HSCHR19LRC_COX1_CTG1:55079161-55084871	NOTEST	0	0	0	0	1	1
ENSG00000262239	ENSG00000262239	GP6	HSCHR19LRC_COX1_CTG1:55438477-55503576	NOTEST	0	0	0	0	1	1
ENSG00000262240	ENSG00000262240	snoU13	HG748_PATCH:77709812-77709908	NOTEST	0	0	0	0	1	1
ENSG00000262241	ENSG00000262241	RP11-748L13.2	HSCHR10_1_CTG2:27667585-27677481	NOTEST	0	0	0	0	1	1
ENSG00000262243	ENSG00000262243	CES1	HSCHR16_1_CTG3_1:55849156-55879488	NOTEST	0	0	0	0	1	1
ENSG00000262244	ENSG00000262244	RDH13	HSCHR19LRC_PGF2_CTG1:55247239-55312338	NOTEST	0	0	0	0	1	1
ENSG00000262245	ENSG00000262245	FOXR1	HG299_PATCH:118842416-118852001	NOTEST	0	0	0	0	1	1
ENSG00000262247	ENSG00000262247	U6	HSCHR19LRC_PGF1_CTG1:54767819-54767928	NOTEST	0	0	0	0	1	1
ENSG00000262248	ENSG00000262248	RP11-235E17.5	17:3468737-3539616	NOTEST	0.249367	0.133521	-0.901205	0	1	1
ENSG00000262249	ENSG00000262249	ZNF626	HG730_PATCH:20646633-20772405	NOTEST	0	0	0	0	1	1
ENSG00000262250	ENSG00000262250	ABCB10P4	HSCHR15_1_CTG4:28763389-28765572	NOTEST	0	0	0	0	1	1
ENSG00000262255	ENSG00000262255	FAM210CP	HSCHR10_1_CTG2:27685945-27686519	NOTEST	0	0	0	0	1	1
ENSG00000262257	ENSG00000262257	RP11-110I1.11	HG299_PATCH:118868851-118901597	NOTEST	0	0	0	0	1	1
ENSG00000262258	ENSG00000262258	KDM4E	HG348_PATCH:94758422-94760761	NOTEST	0	0	0	0	1	1
ENSG00000262259	ENSG00000262259	CTD-2318B16.4	16:10815554-10817212	NOTEST	0	0	0	0	1	1
ENSG00000262260	ENSG00000262260	NLRP2	HSCHR19LRC_PGF2_CTG1:55164555-55242189	NOTEST	0	0	0	0	1	1
ENSG00000262261	ENSG00000262261	GTF2H2D	HSCHR5_1_CTG1:69477954-69510579	NOTEST	0	0	0	0	1	1
ENSG00000262262	ENSG00000262262	RP11-815I9.3	17:18538318-18585575	NOTEST	0	0	0	0	1	1
ENSG00000262263	ENSG00000262263	STYXL1	HG1257_PATCH:75461294-75512961	NOTEST	0	0	0	0	1	1
ENSG00000262264	ENSG00000262264	B3GNT6	HG414_PATCH:76745441-76753017	NOTEST	0	0	0	0	1	1
ENSG00000262265	ENSG00000262265	RP5-867C24.4	17:45195068-45266788	NOTEST	0	0	0	0	1	1
ENSG00000262266	ENSG00000262266	AC010518.3	HSCHR19LRC_COX2_CTG1:54797553-54797871	NOTEST	0	0	0	0	1	1
ENSG00000262267	ENSG00000262267	U95743.1	16:13823993-13873617	NOTEST	0	0	0	0	1	1
ENSG00000262268	ENSG00000262268	OR9G3P	HG151_NOVEL_TEST:56518728-56519646	NOTEST	0	0	0	0	1	1
ENSG00000262269	ENSG00000262269	MIR1270-1	HG730_PATCH:20510080-20510163	NOTEST	0	0	0	0	1	1
ENSG00000262270	ENSG00000262270	AC005077.9	HG1257_PATCH:75555387-75573736	NOTEST	0	0	0	0	1	1
ENSG00000262271	ENSG00000262271	CTD-2535P7.1	17:51511491-51513190	NOTEST	0	0	0	0	1	1
ENSG00000262273	ENSG00000262273	PNLIPRP1	HG311_PATCH:118349896-118368687	NOTEST	0	0	0	0	1	1
ENSG00000262274	ENSG00000262274	HMGN1P12	HSCHR5_1_CTG1:69966744-70078950	NOTEST	0	0	0	0	1	1
ENSG00000262275	ENSG00000262275	SLC16A6	HG747_PATCH:66255297-66418847	NOTEST	0	0	0	0	1	1
ENSG00000262276	ENSG00000262276	U7	HG305_PATCH:102774622-102774684	NOTEST	0	0	0	0	1	1
ENSG00000262277	ENSG00000262277	DIXDC1	HG388_HG400_PATCH:111797866-111893307	NOTEST	0	0	0	0	1	1
ENSG00000262278	ENSG00000262278	U2	HSCHR9_2_CTG35:72659113-72847028	NOTEST	0	0	0	0	1	1
ENSG00000262279	ENSG00000262279	NCAM1	HG306_PATCH:112830001-113149158	NOTEST	0	0	0	0	1	1
ENSG00000262280	ENSG00000262280	RP11-849I19.1	HSCHR18_2_CTG2_1:76736554-76739074	NOTEST	0	0	0	0	1	1
ENSG00000262281	ENSG00000262281	RP11-641C17.1	HG1091_PATCH:59735035-61237194	NOTEST	0	0	0	0	1	1
ENSG00000262282	ENSG00000262282	AC003958.6	HSCHR17_1_CTG4:39490883-39491985	NOTEST	0	0	0	0	1	1
ENSG00000262284	ENSG00000262284	LILRA4	HSCHR19LRC_COX2_CTG1:54843415-54849383	NOTEST	0	0	0	0	1	1
ENSG00000262285	ENSG00000262285	RPL5P29	HG142_HG150_NOVEL_TEST:56124803-56125697	NOTEST	0	0	0	0	1	1
ENSG00000262286	ENSG00000262286	RP1-232L24.4	HSCHR6_1_CTG5:80094500-80095390	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000262287	ENSG00000262287	EPS8L1	HSCHR19LRC_LRC_I_CTG1:55580891-55596795	NOTEST	0	0	0	0	1	1
ENSG00000262288	ENSG00000262288	AC078899.6	HG730_PATCH:20473326-20473432	NOTEST	0	0	0	0	1	1
ENSG00000262289	ENSG00000262289	KIR3DL3	HSCHR19LRC_LRC_T_CTG1:55236242-55248260	NOTEST	0	0	0	0	1	1
ENSG00000262292	ENSG00000262292	RP11-160E2.11	17:19064101-19065587	NOTEST	0	0	0	0	1	1
ENSG00000262293	ENSG00000262293	RP11-673D15.7	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000262294	ENSG00000262294	RP11-1260E13.2	17:62292-236045	NOTEST	0	0	0	0	1	1
ENSG00000262295	ENSG00000262295	SBDSP1	HG1257_PATCH:72294381-72302287	NOTEST	0	0	0	0	1	1
ENSG00000262296	ENSG00000262296	RP11-55L4.1	17:9479943-9633008	NOTEST	0	0	0	0	1	1
ENSG00000262297	ENSG00000262297	AC010518.3	HSCHR19LRC_PGF2_CTG1:54797928-54798246	NOTEST	0	0	0	0	1	1
ENSG00000262298	ENSG00000262298	RP5-1107A17.3	17:55015547-55038415	NOTEST	0	0	0	0	1	1
ENSG00000262299	ENSG00000262299	RP11-216N14.5	HSCHR1_1_CTG31:153784879-153791798	NOTEST	0	0	0	0	1	1
ENSG00000262300	ENSG00000262300	VN1R104P	HSCHR19LRC_COX2_CTG1:54830435-54831444	NOTEST	0	0	0	0	1	1
ENSG00000262301	ENSG00000262301	CTD-2557P19.1	HG729_PATCH:8793618-8794088	NOTEST	0	0	0	0	1	1
ENSG00000262302	ENSG00000262302	RP1-4G17.5	17:7143332-7167302	NOTEST	0.104346	0	#NAME?	0	1	1
ENSG00000262303	ENSG00000262303	RP4-669P10.16	HSCHR22_1_CTG1:42520284-42523779	NOTEST	0	0	0	0	1	1
ENSG00000262304	ENSG00000262304	SHPK	17:3468737-3539616	NOTEST	0.434252	0.489664	0.173259	0	1	1
ENSG00000262305	ENSG00000262305	SERF1B	HSCHR5_1_CTG1:69004900-69022788	NOTEST	0	0	0	0	1	1
ENSG00000262306	ENSG00000262306	CCL24	HG1257_PATCH:75276621-75288313	NOTEST	0	0	0	0	1	1
ENSG00000262307	ENSG00000262307	5S_rRNA	HG256_PATCH:13984235-14295238	NOTEST	0	0	0	0	1	1
ENSG00000262309	ENSG00000262309	TMEM120A	HG1257_PATCH:75364156-75459616	NOTEST	0	0	0	0	1	1
ENSG00000262312	ENSG00000262312	LA16c-390H2.4	16:3415098-3627401	NOTEST	0	0	0	0	1	1
ENSG00000262313	ENSG00000262313	CTD-2561B21.4	17:78518618-78945013	NOTEST	0	0	0	0	1	1
ENSG00000262315	ENSG00000262315	OR8U9	HG142_HG150_NOVEL_TEST:56143100-56152270	NOTEST	0	0	0	0	1	1
ENSG00000262316	ENSG00000262316	RP11-433P17.1	16:3373191-3373925	NOTEST	0	0	0	0	1	1
ENSG00000262317	ENSG00000262317	LAIR2	HSCHR19LRC_COX1_CTG1:54932959-54945775	NOTEST	0	0	0	0	1	1
ENSG00000262318	ENSG00000262318	CTB-96E2.2	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000262319	ENSG00000262319	CTC-457L16.2	17:19030781-19062489	NOTEST	0	0.00416809	inf	0	1	1
ENSG00000262320	ENSG00000262320	LILRA6	HSCHR19LRC_PGF1_CTG1:54704600-54752858	NOTEST	0	0	0	0	1	1
ENSG00000262321	ENSG00000262321	SRRM3	HG1257_PATCH:75666854-75752244	NOTEST	0	0	0	0	1	1
ENSG00000262322	ENSG00000262322	RP11-109M19.2	16:10815554-10817212	NOTEST	0	0	0	0	1	1
ENSG00000262324	ENSG00000262324	CH17-93H22.3	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000262325	ENSG00000262325	MMP13	HG305_PATCH:102813724-102826464	NOTEST	0	0	0	0	1	1
ENSG00000262326	ENSG00000262326	AC013759.1	HSCHR18_1_CTG1_1:47927310-47927418	NOTEST	0	0	0	0	1	1
ENSG00000262327	ENSG00000262327	AGK	HSCHR7_1_CTG6:141250988-141401956	NOTEST	0	0	0	0	1	1
ENSG00000262329	ENSG00000262329	NLRP2	HSCHR19LRC_LRC_I_CTG1:55432380-55510014	NOTEST	0	0	0	0	1	1
ENSG00000262330	ENSG00000262330	AC012616.1	HG729_PATCH:8836095-8838684	NOTEST	0	0	0	0	1	1
ENSG00000262331	ENSG00000262331	RP11-1151M9.3	HSCHR5_1_CTG1:69359869-69430017	NOTEST	0	0	0	0	1	1
ENSG00000262332	ENSG00000262332	RP11-517A5.7	16:16242784-16318118	NOTEST	0	0	0	0	1	1
ENSG00000262333	ENSG00000262333	HNRNPA1P16	17:1963132-2284352	NOTEST	0.476157	0.223337	-1.09221	0	1	1
ENSG00000262334	ENSG00000262334	RPH3AL	HSCHR17_1_CTG1:62292-253878	NOTEST	0	0	0	0	1	1
ENSG00000262335	ENSG00000262335	KIR3DL3	HSCHR19LRC_COX1_CTG1:55159053-55171068	NOTEST	0	0	0	0	1	1
ENSG00000262336	ENSG00000262336	RP11-1260E13.2	HSCHR17_1_CTG1:62292-253878	NOTEST	0	0	0	0	1	1

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ENSG00000262339	ENSG00000262339	RP11-1197K16.2	17:80709939-81009686	NOTEST	0	0	0	0	1	1
ENSG00000262340	ENSG00000262340	RP11-856F16.2	HG348_PATCH:94607216-94658686	NOTEST	0	0	0	0	1	1
ENSG00000262341	ENSG00000262341	U73169.2	HG325_PATCH:50263723-50296787	NOTEST	0	0	0	0	1	1
ENSG00000262342	ENSG00000262342	VPS11	HG299_PATCH:118938083-118952681	NOTEST	0	0	0	0	1	1
ENSG00000262343	ENSG00000262343	RP11-353N14.3	17:77821856-77823909	NOTEST	0	0	0	0	1	1
ENSG00000262344	ENSG00000262344	RP11-21L19.1	HG256_PATCH:13984235-14295238	NOTEST	0	0	0	0	1	1
ENSG00000262347	ENSG00000262347	KRTAP1-3	HSCHR17_4_CTG4:39190262-39191234	NOTEST	0	0	0	0	1	1
ENSG00000262348	ENSG00000262348	RDH13	HSCHR19LRC_LRC_I_CTG1:55515064-55580163	NOTEST	0	0	0	0	1	1
ENSG00000262349	ENSG00000262349	RP11-620J15.3	HSCHR12_1_CTG2_1:58325310-58329958	NOTEST	0	0	0	0	1	1
ENSG00000262351	ENSG00000262351	OR13A1	HSCHR10_1_CTG5:45798101-45811056	NOTEST	0	0	0	0	1	1
ENSG00000262352	ENSG00000262352	AP005530.1	18:11102-16898	NOTEST	0	0	0	0	1	1
ENSG00000262353	ENSG00000262353	RP11-147B8.1	HSCHR15_1_CTG4:28711608-28714548	NOTEST	0	0	0	0	1	1
ENSG00000262354	ENSG00000262354	Y_RNA	HSCHR16_2_CTG3_1:69221024-69348087	NOTEST	0	0	0	0	1	1
ENSG00000262358	ENSG00000262358	CTD-3195I5.4	17:3617921-3704537	NOTEST	0	0.158157	inf	0	1	1
ENSG00000262360	ENSG00000262360	RP11-1275J23.2	HSCHR5_1_CTG1:69475595-69477340	NOTEST	0	0	0	0	1	1
ENSG00000262361	ENSG00000262361	U6	HSCHR10_1_CTG2:27667585-27677481	NOTEST	0	0	0	0	1	1
ENSG00000262362	ENSG00000262362	LA16c-380H5.2	16:3053431-3055102	NOTEST	0	0	0	0	1	1
ENSG00000262363	ENSG00000262363	CTC-550B14.1	HSCHR19LRC_COX1_CTG1:55355793-55433427	NOTEST	0	0	0	0	1	1
ENSG00000262364	ENSG00000262364	RP11-665A22.1	HSCHR15_1_CTG4:28831784-28836166	NOTEST	0	0	0	0	1	1
ENSG00000262366	ENSG00000262366	NDUFA3P6	16:31185893-31186143	NOTEST	0	0	0	0	1	1
ENSG00000262369	ENSG00000262369	CNOT3	HSCHR19LRC_PGF1_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000262370	ENSG00000262370	RP11-473M20.9	16:3115297-3137101	NOTEST	0	0	0	0	1	1
ENSG00000262373	ENSG00000262373	RP11-444K7.8	HG142_HG150_NOVEL_TEST:55972600-55973101	NOTEST	0	0	0	0	1	1
ENSG00000262374	ENSG00000262374	RP11-483G21.3	HG1257_PATCH:72777495-72793039	NOTEST	0	0	0	0	1	1
ENSG00000262375	ENSG00000262375	RP11-553K8.2	HSCHR1_3_CTG31:198578340-198579485	NOTEST	0	0	0	0	1	1
ENSG00000262376	ENSG00000262376	KRTAP2-5P	HSCHR17_4_CTG4:39228429-39228825	NOTEST	0	0	0	0	1	1
ENSG00000262377	ENSG00000262377	TTC12	HG306_PATCH:113185250-113254266	NOTEST	0	0	0	0	1	1
ENSG00000262378	ENSG00000262378	LY6K	HG418_PATCH:143781471-143808334	NOTEST	0	0	0	0	1	1
ENSG00000262379	ENSG00000262379	TAS2R31	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000262380	ENSG00000262380	CTB-193M12.3	16:15737123-15950890	NOTEST	0.0833652	0.0348615	-1.25781	0	1	1
ENSG00000262381	ENSG00000262381	CTD-2318B16.1	16:10818476-10819153	NOTEST	0	0	0	0	1	1
ENSG00000262382	ENSG00000262382	CTC-550B14.1	HSCHR19LRC_LRC_S_CTG1:55434466-55512100	NOTEST	0	0	0	0	1	1
ENSG00000262383	ENSG00000262383	LILRA3	HSCHR19LRC_PGF2_CTG1:54799880-54809979	NOTEST	0	0	0	0	1	1
ENSG00000262384	ENSG00000262384	RP11-312B18.1	17:51758990-51759472	NOTEST	0	0	0	0	1	1
ENSG00000262385	ENSG00000262385	RP5-944M2.1	HSCHR12_1_CTG5:126891379-126896116	NOTEST	0	0	0	0	1	1
ENSG00000262386	ENSG00000262386	CTC-550B14.1	HSCHR19LRC_LRC_T_CTG1:55370759-55448393	NOTEST	0	0	0	0	1	1
ENSG00000262387	ENSG00000262387	RN7SL265P	HG1257_PATCH:73197527-73197828	NOTEST	0	0	0	0	1	1
ENSG00000262388	ENSG00000262388	AC138783.13	HG1257_PATCH:74429910-74430016	NOTEST	0	0	0	0	1	1
ENSG00000262390	ENSG00000262390	AC098784.1	HSCHR19LRC_PGF2_CTG1:54959179-54959463	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000262391	ENSG00000262391	RP11-846E15.4	HSCHR5_1_CTG1:69050903-69144625	NOTEST	0	0	0	0	1	1
ENSG00000262393	ENSG00000262393	TAS2R19	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000262395	ENSG00000262395	RP11-515E23.2	17:53531406-53535811	NOTEST	0	0	0	0	1	1
ENSG00000262396	ENSG00000262396	RP11-785H5.1	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000262397	ENSG00000262397	LILRB4	HSCHR19LRC_PGF2_CTG1:54917503-54925749	NOTEST	0	0	0	0	1	1
ENSG00000262398	ENSG00000262398	AC005086.6	HG115_PATCH:101459218-101927238	NOTEST	0	0	0	0	1	1
ENSG00000262399	ENSG00000262399	RP11-42L13.2	HSCHR5_3_CTG1:29113865-29114424	NOTEST	0	0	0	0	1	1
ENSG00000262400	ENSG00000262400	RP11-191A15.1	6:25081547-25166793	NOTEST	0	0	0	0	1	1
ENSG00000262401	ENSG00000262401	XAGE1B	HG1433_PATCH:52255076-52263803	NOTEST	0	0	0	0	1	1
ENSG00000262402	ENSG00000262402	RP11-667K14.8	17:1963132-2284352	NOTEST	0	0	0	0	1	1
ENSG00000262403	ENSG00000262403	AL713999.2	HSCHR1_2_CTG31:155219646-155229865	NOTEST	0	0	0	0	1	1
ENSG00000262406	ENSG00000262406	MMP12	HG305_PATCH:102733466-102745765	NOTEST	0	0	0	0	1	1
ENSG00000262407	ENSG00000262407	CCDC125	HSCHR5_1_CTG1:685771664-68628568	NOTEST	0	0	0	0	1	1
ENSG00000262408	ENSG00000262408	RP11-670E13.3	17:54961999-54962180	NOTEST	0	0	0	0	1	1
ENSG00000262411	ENSG00000262411	RP11-454C18.1	HSCHR3_1_CTG2_1:15135496 1-151375744	NOTEST	0	0	0	0	1	1
ENSG00000262412	ENSG00000262412	RP11-85G18.6	10:27532058-27577753	NOTEST	0.0171536	0.00362773	-2.24138	0	1	1
ENSG00000262413	ENSG00000262413	RP11-498C9.3	17:79825596-79829282	NOTEST	0	0.343387	inf	0	1	1
ENSG00000262414	ENSG00000262414	AC010492.4	HSCHR19LRC_PGF2_CTG1:54749977-54751212	NOTEST	0	0	0	0	1	1
ENSG00000262416	ENSG00000262416	CTC-550B14.1	HSCHR19LRC_LRC_I_CTG1:55432380-55510014	NOTEST	0	0	0	0	1	1
ENSG00000262417	ENSG00000262417	RP11-136K7.2	HSCHR5_1_CTG1:698630066-69957699	NOTEST	0	0	0	0	1	1
ENSG00000262418	ENSG00000262418	PTPRC	HSCHR1_3_CTG31:198619287-198737899	NOTEST	0	0	0	0	1	1
ENSG00000262420	ENSG00000262420	RP11-490O6.2	16:11762269-11838362	NOTEST	0.0117131	0.0481326	2.03889	0	1	1
ENSG00000262421	ENSG00000262421	TRIM74	HG1257_PATCH:72424441-72434423	NOTEST	0	0	0	0	1	1
ENSG00000262422	ENSG00000262422	AC009892.2	HSCHR19LRC_COX1_CTG1:54987050-54987337	NOTEST	0	0	0	0	1	1
ENSG00000262423	ENSG00000262423	AC008746.10	HSCHR19LRC_COX2_CTG1:54889778-54890250	NOTEST	0	0	0	0	1	1
ENSG00000262424	ENSG00000262424	KRT18P48	HG1497_PATCH:152772968-152773820	NOTEST	0	0	0	0	1	1
ENSG00000262426	ENSG00000262426	AC012314.19	HSCHR19LRC_COX1_CTG1:54704427-54752625	NOTEST	0	0	0	0	1	1
ENSG00000262429	ENSG00000262429	RP5-1050D4.3	17:4871286-4890972	NOTEST	0	0	0	0	1	1
ENSG00000262430	ENSG00000262430	EPS8L1	HSCHR19LRC_PGF2_CTG1:55313066-55328970	NOTEST	0	0	0	0	1	1
ENSG00000262431	ENSG00000262431	TAS2R63P	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000262432	ENSG00000262432	SNORA14A	HG1257_PATCH:75364156-75459616	NOTEST	0	0	0	0	1	1
ENSG00000262434	ENSG00000262434	RP11-676J12.8	17:660336-695749	NOTEST	0	0.0335262	inf	0	1	1
ENSG00000262435	ENSG00000262435	ABC7-42389800N19.1	HSCHR12_1_CTG1:64521-82015	NOTEST	0	0	0	0	1	1
ENSG00000262436	ENSG00000262436	CTC-550B14.1	HSCHR19LRC_LRC_J_CTG1:55459917-55537551	NOTEST	0	0	0	0	1	1
ENSG00000262437	ENSG00000262437	AC098784.1	HSCHR19LRC_PGF1_CTG1:55137464-55137748	NOTEST	0	0	0	0	1	1
ENSG00000262438	ENSG00000262438	OR5G1P	HG151_NOVEL_TEST:56553810-56554756	NOTEST	0	0	0	0	1	1
ENSG00000262439	ENSG00000262439	KIR3DL3	HSCHR19LRC_LRC_J_CTG1:55342149-55354167	NOTEST	0	0	0	0	1	1
ENSG00000262444	ENSG00000262444	RP11-653J6.1	HSCHR15_1_CTG8:66582972-66597832	NOTEST	0	0	0	0	1	1
ENSG00000262445	ENSG00000262445	CTD-2545H1.2	17:1837970-1928639	NOTEST	0.0388788	0	#NAME?	0	1	1
ENSG00000262446	ENSG00000262446	GBA	HSCHR1_2_CTG31:155219646-155229865	NOTEST	0	0	0	0	1	1
ENSG00000262447	ENSG00000262447	TNFAIP1	HG883_PATCH:26662627-26674035	NOTEST	0	0	0	0	1	1
ENSG00000262448	ENSG00000262448	8-Mar	HSCHR10_1_CTG5:45966097-46046882	NOTEST	0	0	0	0	1	1
ENSG00000262451	ENSG00000262451	LENG8-AS1	HSCHR19LRC_PGF1_CTG1:54878386-54897289	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000262452	ENSG00000262452	SPC25	HSCHR2_1_CTG12:169643048-169786870	NOTEST	0	0	0	0	1	1
ENSG00000262453	ENSG00000262453	CTA-150C2.13	HSCHR22_1_CTG2:39317231-39320713	NOTEST	0	0	0	0	1	1
ENSG00000262454	ENSG00000262454	RP11-65J21.3	16:14396144-14420210	NOTEST	0.658832	0.436821	-0.592868	0	1	1
ENSG00000262455	ENSG00000262455	RP1-232L24.4	HSCHR6_1_CTG5:80143788-80144323	NOTEST	0	0	0	0	1	1
ENSG00000262456	ENSG00000262456	RP1-59D14.1	17:2287353-2304412	NOTEST	0.000277962	0.234236	9.71886	0	1	1
ENSG00000262457	ENSG00000262457	NLRP7	HSCHR19LRC_LRC_S_CTG1:55434466-55512100	NOTEST	0	0	0	0	1	1
ENSG00000262459	ENSG00000262459	WBSCR28	HG1257_PATCH:73326115-73330850	NOTEST	0	0	0	0	1	1
ENSG00000262460	ENSG00000262460	AC008746.9	HSCHR19LRC_COX1_CTG1:54956783-54957092	NOTEST	0	0	0	0	1	1
ENSG00000262461	ENSG00000262461	SPDYE8P	HG1257_PATCH:72434652-72606602	NOTEST	0	0	0	0	1	1
ENSG00000262462	ENSG00000262462	LILRA1	HSCHR19LRC_PGF1_CTG1:55006690-55072658	NOTEST	0	0	0	0	1	1
ENSG00000262463	ENSG00000262463	KIR2DP1	HSCHR19LRC_LRC_T_CTG1:55266744-55279093	NOTEST	0	0	0	0	1	1
ENSG00000262464	ENSG00000262464	POLDIP2	HG883_PATCH:26674232-26684545	NOTEST	0	0	0	0	1	1
ENSG00000262466	ENSG00000262466	RP11-454C18.2	HSCHR3_1_CTG2_1:151462241-151656501	NOTEST	0	0	0	0	1	1
ENSG00000262467	ENSG00000262467	EPS8L1	HSCHR19LRC_LRC_S_CTG1:55582977-55598881	NOTEST	0	0	0	0	1	1
ENSG00000262468	ENSG00000262468	RP11-95P2.1	16:4295825-4303790	NOTEST	0.283268	0.50234	0.826494	0	1	1
ENSG00000262469	ENSG00000262469	Y_RNA	HSCHR1_1_CTG31:153715958-153716060	NOTEST	0	0	0	0	1	1
ENSG00000262470	ENSG00000262470	TVP23CP2	16:14165177-14360630	NOTEST	0	0	0	0	1	1
ENSG00000262471	ENSG00000262471	RP11-95P2.4	16:4180555-4180821	NOTEST	0	0	0	0	1	1
ENSG00000262472	ENSG00000262472	KPNA2	HG747_PATCH:66031634-66042958	NOTEST	0	0	0	0	1	1
ENSG00000262473	ENSG00000262473	GART	HSCHR21_4_CTG1_1:34880497-34925355	NOTEST	0	0	0	0	1	1
ENSG00000262474	ENSG00000262474	RP11-1275J23.3	HSCHR5_1_CTG1:69517116-69536103	NOTEST	0	0	0	0	1	1
ENSG00000262476	ENSG00000262476	AP000705.7	HSCHR21_2_CTG1_1:23582257-23799841	NOTEST	0	0	0	0	1	1
ENSG00000262478	ENSG00000262478	Metazoa_SRP	HG299_PATCH:118865043-118865343	NOTEST	0	0	0	0	1	1
ENSG00000262480	ENSG00000262480	SAMD11P1	17:2496503-2588909	NOTEST	0	0.0214399	inf	0	1	1
ENSG00000262481	ENSG00000262481	C17orf61-PLSCR3	17:7283852-7307456	NOTEST	0	0.127759	inf	0	1	1
ENSG00000262482	ENSG00000262482	LA16c-321D4.2	16:2961937-3004277	NOTEST	0.414045	0.565175	0.448912	0	1	1
ENSG00000262484	ENSG00000262484	CCER2	19:39399619-39402798	NOTEST	0.0335271	0	#NAME?	0	1	1
ENSG00000262485	ENSG00000262485	TUSC2	HG325_PATCH:50355221-50365683	NOTEST	0	0	0	0	1	1
ENSG00000262486	ENSG00000262486	LILRP2	HSCHR19LRC_PGF2_CTG1:54963143-54968401	NOTEST	0	0	0	0	1	1
ENSG00000262487	ENSG00000262487	AC004231.2	HSCHR17_4_CTG4:39077681-39132305	NOTEST	0	0	0	0	1	1
ENSG00000262488	ENSG00000262488	RP11-876N24.1	16:10934240-10935401	NOTEST	0	0	0	0	1	1
ENSG00000262489	ENSG00000262489	RRAS2	HG256_PATCH:14299510-14386053	NOTEST	0	0	0	0	1	1
ENSG00000262491	ENSG00000262491	RP11-846E15.2	HSCHR5_1_CTG1:69050903-69144625	NOTEST	0	0	0	0	1	1
ENSG00000262492	ENSG00000262492	RP11-1099M24.8	17:7858185-7858940	NOTEST	0	0	0	0	1	1
ENSG00000262494	ENSG00000262494	CU467816.1	HSCHR19LRC_PGF2_CTG1:55026195-55031822	NOTEST	0	0	0	0	1	1
ENSG00000262495	ENSG00000262495	RP11-46I8.1	17:4963650-4965418	NOTEST	0	0	0	0	1	1
ENSG00000262497	ENSG00000262497	FAM187B2P	19:35723193-35723906	NOTEST	0	0	0	0	1	1
ENSG00000262499	ENSG00000262499	WBSCR27	HG1257_PATCH:73299546-73307492	NOTEST	0	0	0	0	1	1
ENSG00000262501	ENSG00000262501	PPIHP1	HG388_HG400_PATCH:111895536-111955873	NOTEST	0	0	0	0	1	1
ENSG00000262502	ENSG00000262502	RP11-641C17.3	HG1091_PATCH:59735035-61237194	NOTEST	0	0	0	0	1	1
ENSG00000262503	ENSG00000262503	RP11-530N7.2	17:6757179-6922978	NOTEST	0	0	0	0	1	1
ENSG00000262504	ENSG00000262504	RP11-536P16.2	HSCHR15_1_CTG4:28591634-28591792	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000262505	ENSG00000262505	ASIC5	HSCHR4_1_CTG12:156750880-156841558	NOTEST	0	0	0	0	1	1
ENSG00000262506	ENSG00000262506	C11orf57	HG388_HG400_PATCH:111895536-111955873	NOTEST	0	0	0	0	1	1
ENSG00000262508	ENSG00000262508	RP1-232L24.2	HSCHR6_1_CTG5:80064159-80064430	NOTEST	0	0	0	0	1	1
ENSG00000262509	ENSG00000262509	BLNK	HG339_PATCH:97889471-98031303	NOTEST	0	0	0	0	1	1
ENSG00000262510	ENSG00000262510	LINC00308	HSCHR21_2_CTG1_1:23470935-23488847	NOTEST	0	0	0	0	1	1
ENSG00000262511	ENSG00000262511	RAD17	HSCHR5_1_CTG1:68646821-68710869	NOTEST	0	0	0	0	1	1
ENSG00000262512	ENSG00000262512	KRTAP9-4	HSCHR17_5_CTG4:39405870-39406837	NOTEST	0	0	0	0	1	1
ENSG00000262513	ENSG00000262513	RP11-96G10.1	HSCHR5_1_CTG5:161851383-161854351	NOTEST	0	0	0	0	1	1
ENSG00000262514	ENSG00000262514	RP11-96D1.9	16:68021296-68272005	NOTEST	0.0146225	0.0330245	1.17535	0	1	1
ENSG00000262515	ENSG00000262515	LPHN3	HSCHR4_2_CTG9:62066975-62959961	NOTEST	0	0	0	0	1	1
ENSG00000262516	ENSG00000262516	RP11-95J11.1	16:3775054-3930727	NOTEST	0	0	0	0	1	1
ENSG00000262517	ENSG00000262517	RP5-905G11.5	HSCHR20_1_CTG1:17795252-17795683	NOTEST	0	0	0	0	1	1
ENSG00000262518	ENSG00000262518	CTD-2535P7.2	17:51515916-51517082	NOTEST	0	0	0	0	1	1
ENSG00000262519	ENSG00000262519	TXNP4	17:4475500-4475810	NOTEST	0	0	0	0	1	1
ENSG00000262520	ENSG00000262520	KRTAP4-16P	HSCHR17_4_CTG4:39258172-39258880	NOTEST	0	0	0	0	1	1
ENSG00000262521	ENSG00000262521	AJ003147.8	16:3231232-3234018	NOTEST	0	0	0	0	1	1
ENSG00000262522	ENSG00000262522	snoR442	HG544_PATCH:17686123-17757913	NOTEST	0	0	0	0	1	1
ENSG00000262523	ENSG00000262523	ENDOD1	HG348_PATCH:94822975-94865811	NOTEST	0	0	0	0	1	1
ENSG00000262525	ENSG00000262525	TAS2R46	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000262526	ENSG00000262526	CTD-2545G14.7	17:7143332-7167302	NOTEST	0	0	0	0	1	1
ENSG00000262528	ENSG00000262528	LA16c-349E10.1	16:699310-717833	NOTEST	0.269224	0.397061	0.560551	0	1	1
ENSG00000262529	ENSG00000262529	CTA-276F8.2	16:14165177-14360630	NOTEST	0	0	0	0	1	1
ENSG00000262530	ENSG00000262530	AC008746.3	HSCHR19LRC_COX1_CTG1:54850623-54872311	NOTEST	0	0	0	0	1	1
ENSG00000262531	ENSG00000262531	RP11-785H5.2	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000262532	ENSG00000262532	FKBP6	HG1257_PATCH:72793120-72823582	NOTEST	0	0	0	0	1	1
ENSG00000262533	ENSG00000262533	RP11-667K14.4	17:1933403-1946724	NOTEST	0	0	0	0	1	1
ENSG00000262535	ENSG00000262535	OR5G5P	HG151_NOVEL_TEST:56580405-56599054	NOTEST	0	0	0	0	1	1
ENSG00000262536	ENSG00000262536	WI2-1043J20.1	HSCHR22_1_CTG2:39345117-39345132	NOTEST	0	0	0	0	1	1
ENSG00000262537	ENSG00000262537	Y_RNA	HG745_PATCH:36337716-36421858	NOTEST	0	0	0	0	1	1
ENSG00000262538	ENSG00000262538	U6	HG536_PATCH:69887201-69890237	NOTEST	0	0	0	0	1	1
ENSG00000262540	ENSG00000262540	RP11-725K16.5	HG305_PATCH:102751224-102751577	NOTEST	0	0	0	0	1	1
ENSG00000262542	ENSG00000262542	KRTAP29-1	HSCHR17_6_CTG4:39446707-39447733	NOTEST	0	0	0	0	1	1
ENSG00000262543	ENSG00000262543	RP3-422G23.4	6:138699041-138704212	NOTEST	0	0	0	0	1	1
ENSG00000262544	ENSG00000262544	OR8I1P	HG142_HG150_NOVEL_TEST:56064016-56064947	NOTEST	0	0	0	0	1	1
ENSG00000262546	ENSG00000262546	Y_RNA	HG79_PATCH:136213262-136213359	NOTEST	0	0	0	0	1	1
ENSG00000262548	ENSG00000262548	LILRP2	HSCHR19LRC_COX1_CTG1:55142796-55148024	NOTEST	0	0	0	0	1	1
ENSG00000262550	ENSG00000262550	OR8L1P	HG142_HG150_NOVEL_TEST:56156716-56157671	NOTEST	0	0	0	0	1	1
ENSG00000262552	ENSG00000262552	ALOX5	HSCHR10_1_CTG5:45885737-45964632	NOTEST	0	0	0	0	1	1
ENSG00000262554	ENSG00000262554	LA16c-360H6.2	16:3313742-3368852	NOTEST	0.508184	0.162161	-1.64792	0	1	1
ENSG00000262555	ENSG00000262555	AC011515.2	HSCHR19LRC_COX1_CTG1:55106520-55107881	NOTEST	0	0	0	0	1	1
ENSG00000262556	ENSG00000262556	KIR2DL1	HSCHR19LRC_PGF1_CTG1:55157744-55300469	NOTEST	0	0	0	0	1	1
ENSG00000262558	ENSG00000262558	RP11-1260E13.3	17:62292-236045	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000262560	ENSG00000262560	RP11-296A16.1	15:44019115-44095241	NOTEST	0	0.0104911	inf	0	1	1
ENSG00000262561	ENSG00000262561	CTD-2522B17.8	16:33922936-33923144	NOTEST	0	0	0	0	1	1
ENSG00000262562	ENSG00000262562	ZNF85	HSCHR19_1_CTG3:21112509-21139919	NOTEST	0	0	0	0	1	1
ENSG00000262563	ENSG00000262563	G6PC2	HSCHR2_1_CTG12:169643048-169786870	NOTEST	0	0	0	0	1	1
ENSG00000262564	ENSG00000262564	C10orf82	HG311_PATCH:118423207-118502086	NOTEST	0	0	0	0	1	1
ENSG00000262565	ENSG00000262565	PCDHB11	HG1082_HG167_PATCH:140579194-140582630	NOTEST	0	0	0	0	1	1
ENSG00000262566	ENSG00000262566	RP11-448N11.3	6:63321057-63321232	NOTEST	0	0	0	0	1	1
ENSG00000262569	ENSG00000262569	POR	HG1257_PATCH:75364156-75459616	NOTEST	0	0	0	0	1	1
ENSG00000262571	ENSG00000262571	RP11-110I1.12	HG299_PATCH:118865533-118868714	NOTEST	0	0	0	0	1	1
ENSG00000262572	ENSG00000262572	CBX8	HG748_PATCH:77788213-77797765	NOTEST	0	0	0	0	1	1
ENSG00000262573	ENSG00000262573	KRTAP9-2	HSCHR17_6_CTG4:39382878-39383883	NOTEST	0	0	0	0	1	1
ENSG00000262574	ENSG00000262574	Y_RNA	HG1257_PATCH:72434652-72606602	NOTEST	0	0	0	0	1	1
ENSG00000262575	ENSG00000262575	AC009892.5	HSCHR19LRC_COX1_CTG1:55008196-55074165	NOTEST	0	0	0	0	1	1
ENSG00000262576	ENSG00000262576	PCDHGA4	5:140710251-140892546	NOTEST	0.156201	0.249699	0.676786	0	1	1
ENSG00000262577	ENSG00000262577	ALG9	HG388_HG400_PATCH:111652918-111756698	NOTEST	0	0	0	0	1	1
ENSG00000262578	ENSG00000262578	ZNF737	HG730_PATCH:20646633-20772405	NOTEST	0	0	0	0	1	1
ENSG00000262579	ENSG00000262579	U6	HSCHR16_2_CTG3_1:69209564-69209671	NOTEST	0	0	0	0	1	1
ENSG00000262581	ENSG00000262581	RP11-536P16.2	HSCHR15_1_CTG4:28577375-28581745	NOTEST	0	0	0	0	1	1
ENSG00000262582	ENSG00000262582	CU234142.1	HSCHR19LRC_COX1_CTG1:54967786-54979072	NOTEST	0	0	0	0	1	1
ENSG00000262583	ENSG00000262583	RP11-77K12.5	16:75533685-75550178	NOTEST	0.188399	0	#NAME?	0	1	1
ENSG00000262585	ENSG00000262585	RP11-353N14.5	17:77889050-77900524	NOTEST	0.120076	0.179995	0.584008	0	1	1
ENSG00000262586	ENSG00000262586	AC009892.2	HSCHR19LRC_PGF1_CTG1:54985566-54985853	NOTEST	0	0	0	0	1	1
ENSG00000262587	ENSG00000262587	RP11-266L9.4	16:25043201-25069430	NOTEST	0.173388	0.199473	0.202187	0	1	1
ENSG00000262589	ENSG00000262589	NSUN5	HG1257_PATCH:72767473-72773824	NOTEST	0	0	0	0	1	1
ENSG00000262591	ENSG00000262591	TBC1D3P7	HSCHR17_1_CTG4:39479678-39485797	NOTEST	0	0	0	0	1	1
ENSG00000262592	ENSG00000262592	RP11-150C16.1	HSCHR12_2_CTG2_1:59314419-59465068	NOTEST	0	0	0	0	1	1
ENSG00000262594	ENSG00000262594	KRTAP9-9	HSCHR17_6_CTG4:39400265-39401246	NOTEST	0	0	0	0	1	1
ENSG00000262595	ENSG00000262595	MRM1	HG75_PATCH:34929529-34936936	NOTEST	0	0	0	0	1	1
ENSG00000262596	ENSG00000262596	KIR2DS1	HSCHR19LRC_PGF2_CTG1:54979402-55007752	NOTEST	0	0	0	0	1	1
ENSG00000262599	ENSG00000262599	KIAA1147	HSCHR7_1_CTG6:141250988-141401956	NOTEST	0	0	0	0	1	1
ENSG00000262600	ENSG00000262600	C11orf52	HG388_HG400_PATCH:111779287-111797595	NOTEST	0	0	0	0	1	1
ENSG00000262601	ENSG00000262601	CTC-786C10.1	16:85204881-85218969	NOTEST	0.04496	0.205526	2.19261	0	1	1
ENSG00000262602	ENSG00000262602	LENG8	HSCHR19LRC_PGF1_CTG1:54878386-54897289	NOTEST	0	0	0	0	1	1
ENSG00000262603	ENSG00000262603	AC003958.2	HSCHR17_1_CTG4:39565992-39588626	NOTEST	0	0	0	0	1	1
ENSG00000262604	ENSG00000262604	LILRP1	HSCHR19LRC_PGF2_CTG1:54951831-54956133	NOTEST	0	0	0	0	1	1
ENSG00000262605	ENSG00000262605	MRPS36	HSCHR5_1_CTG1:68513586-68525954	NOTEST	0	0	0	0	1	1
ENSG00000262607	ENSG00000262607	IQSEC3	HSCHR12_1_CTG1:120779-236414	NOTEST	0	0	0	0	1	1
ENSG00000262608	ENSG00000262608	U6	HG946_PATCH:98424029-98424136	NOTEST	0	0	0	0	1	1
ENSG00000262609	ENSG00000262609	BTF3P14	17:6225732-6226548	NOTEST	0	0	0	0	1	1
ENSG00000262610	ENSG00000262610	LILRA5	HG1079_PATCH:54810570-54816336	NOTEST	0	0	0	0	1	1
ENSG00000262611	ENSG00000262611	OR8H1	HG142_HG150_NOVEL_TEST:56057528-56058566	NOTEST	0	0	0	0	1	1
ENSG00000262612	ENSG00000262612	TAS2R43	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000262614	ENSG00000262614	AC008746.3	HSCHR19LRC_PGF1_CTG1:54848799-54870475	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000262615	ENSG00000262615	NLRP2	HSCHR19LRC_COX2_CTG1:55097597-55175230	NOTEST	0	0	0	0	1	1
ENSG00000262616	ENSG00000262616	KRTAP3-4P	HSCHR17_4_CTG4:39160859-39161139	NOTEST	0	0	0	0	1	1
ENSG00000262617	ENSG00000262617	AC020766.1	HSCHR16_1_CTG3_1:55822854-55840290	NOTEST	0	0	0	0	1	1
ENSG00000262618	ENSG00000262618	RP11-420K14.1	HSCHR19_2_CTG3:21837955-21839341	NOTEST	0	0	0	0	1	1
ENSG00000262619	ENSG00000262619	LINC00621	13:23468794-23490662	NOTEST	0	0	0	0	1	1
ENSG00000262620	ENSG00000262620	U3	HG1091_PATCH:59735035-61237194	NOTEST	0	0	0	0	1	1
ENSG00000262623	ENSG00000262623	RP5-1107A17.2	17:55015547-55038415	NOTEST	0.0620776	0	#NAME?	0	1	1
ENSG00000262624	ENSG00000262624	RP11-104H15.9	17:7323421-7361026	NOTEST	0	0	0	0	1	1
ENSG00000262625	ENSG00000262625	KIR3DP1	HSCHR19LRC_COX1_CTG1:55220900-55224864	NOTEST	0	0	0	0	1	1
ENSG00000262627	ENSG00000262627	RP11-536P16.5	HSCHR15_1_CTG4:28647911-28650069	NOTEST	0	0	0	0	1	1
ENSG00000262628	ENSG00000262628	OR1D5	17:2965962-2966901	NOTEST	0	0	0	0	1	1
ENSG00000262630	ENSG00000262630	AC012314.2	HSCHR19LRC_PGF2_CTG1:54720146-54746736	NOTEST	0	0	0	0	1	1
ENSG00000262631	ENSG00000262631	VN1R104P	HSCHR19LRC_COX1_CTG1:54830507-54831516	NOTEST	0	0	0	0	1	1
ENSG00000262633	ENSG00000262633	RP11-156P1.2	17:45000482-45177689	NOTEST	0	0.0291534	inf	0	1	1
ENSG00000262634	ENSG00000262634	SKA1	HSCHR18_1_CTG1_1:47901364-47920543	NOTEST	0	0	0	0	1	1
ENSG00000262635	ENSG00000262635	TDO2	HSCHR4_1_CTG12:156750880-156841558	NOTEST	0	0	0	0	1	1
ENSG00000262636	ENSG00000262636	CTD-3088G3.4	16:11453701-11617444	NOTEST	0.317765	0	#NAME?	0	1	1
ENSG00000262638	ENSG00000262638	CTB-61M7.1	HSCHR19LRC_PGF1_CTG1:55157744-55300469	NOTEST	0	0	0	0	1	1
ENSG00000262639	ENSG00000262639	5S_rRNA	HG905_PATCH:184464-304637	NOTEST	0	0	0	0	1	1
ENSG00000262640	ENSG00000262640	RP5-905G11.4	HSCHR20_1_CTG1:17853224-17858989	NOTEST	0	0	0	0	1	1
ENSG00000262641	ENSG00000262641	RP11-124L9.6	HSCHR5_1_CTG1:69640520-69650987	NOTEST	0	0	0	0	1	1
ENSG00000262642	ENSG00000262642	LILRA6	HSCHR19LRC_COX1_CTG1:54704427-54752625	NOTEST	0	0	0	0	1	1
ENSG00000262645	ENSG00000262645	AC009892.9	HSCHR19LRC_PGF2_CTG1:54907455-54907601	NOTEST	0	0	0	0	1	1
ENSG00000262646	ENSG00000262646	AC010492.2	HSCHR19LRC_COX1_CTG1:54704427-54752625	NOTEST	0	0	0	0	1	1
ENSG00000262647	ENSG00000262647	OR9G4	HG151_NOVEL_TEST:56521376-56522361	NOTEST	0	0	0	0	1	1
ENSG00000262648	ENSG00000262648	PHBP15	HG1257_PATCH:74668897-74669562	NOTEST	0	0	0	0	1	1
ENSG00000262650	ENSG00000262650	RPL7L1P3	HG1257_PATCH:75364156-75459616	NOTEST	0	0	0	0	1	1
ENSG00000262651	ENSG00000262651	RP11-164N20.2	6:64322665-64322808	NOTEST	0	0	0	0	1	1
ENSG00000262652	ENSG00000262652	RP13-638C3.2	17:80477588-80606429	NOTEST	0.165034	0.179062	0.117699	0	1	1
ENSG00000262653	ENSG00000262653	RP4-809F18.1	HSCHR12_1_CTG5:126849889-126851653	NOTEST	0	0	0	0	1	1
ENSG00000262654	ENSG00000262654	SLC13A2	HG883_PATCH:26782770-26941216	NOTEST	0	0	0	0	1	1
ENSG00000262655	ENSG00000262655	SPON1	HG256_PATCH:13984235-14295238	NOTEST	0	0	0	0	1	1
ENSG00000262656	ENSG00000262656	U1	HSCHR7_1_CTG6:141410145-141493730	NOTEST	0	0	0	0	1	1
ENSG00000262658	ENSG00000262658	AC092566.1	HG729_PATCH:8741727-8741952	NOTEST	0	0	0	0	1	1
ENSG00000262659	ENSG00000262659	RP11-839D17.3	HG306_PATCH:113149158-113185159	NOTEST	0	0	0	0	1	1
ENSG00000262660	ENSG00000262660	SLC25A10	17:79670386-79688042	NOTEST	0.0811741	0.054442	-0.576298	0	1	1
ENSG00000262661	ENSG00000262661	NCR1	HSCHR19LRC_LRC_S_CTG1:55417097-55427098	NOTEST	0	0	0	0	1	1
ENSG00000262662	ENSG00000262662	CTD-2561B21.3	17:78518618-78945013	NOTEST	0	0	0	0	1	1
ENSG00000262666	ENSG00000262666	FAM189B	HSCHR1_2_CTG31:155232399-155240678	NOTEST	0	0	0	0	1	1
ENSG00000262667	ENSG00000262667	OCLN	HSCHR5_1_CTG1:68773019-68852251	NOTEST	0	0	0	0	1	1
ENSG00000262668	ENSG00000262668	AJ003147.9	16:3238211-3286221	NOTEST	0.244447	0.220745	-0.147142	0	1	1
ENSG00000262670	ENSG00000262670	RP11-64J4.2	17:3181192-3290132	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000262671	ENSG00000262671	RP5-894A10.2	HSCHR7_1_CTG6:141250988-141401956	NOTEST	0	0	0	0	1	1
ENSG00000262672	ENSG00000262672	PTCHD3	HSCHR10_1_CTG2:27734415-27750597	NOTEST	0	0	0	0	1	1
ENSG00000262673	ENSG00000262673	MAPK4	HSCHR18_1_CTG1_1:48093679-48265426	NOTEST	0	0	0	0	1	1
ENSG00000262675	ENSG00000262675	OR9G2P	HG151_NOVEL_TEST:56529572-56530452	NOTEST	0	0	0	0	1	1
ENSG00000262676	ENSG00000262676	SLC37A4	HG299_PATCH:118868851-118901597	NOTEST	0	0	0	0	1	1
ENSG00000262678	ENSG00000262678	RP5-1050D4.4	17:4871286-4890972	NOTEST	0.074333	0.341011	2.19774	0	1	1
ENSG00000262679	ENSG00000262679	APOBEC3B-AS1	HSCHR22_1_CTG2:39353527-39364275	NOTEST	0	0	0	0	1	1
ENSG00000262680	ENSG00000262680	NCR1	HSCHR19LRC_LRC_I_CTG1:55415011-55425012	NOTEST	0	0	0	0	1	1
ENSG00000262681	ENSG00000262681	RP11-311F12.1	17:19622371-19625741	NOTEST	0	0	0	0	1	1
ENSG00000262683	ENSG00000262683	FHIT	HG1091_PATCH:59735035-61237194	NOTEST	0	0	0	0	1	1
ENSG00000262684	ENSG00000262684	DNAJC7	HG185_PATCH:40132690-40219330	NOTEST	0	0	0	0	1	1
ENSG00000262685	ENSG00000262685	RP11-390B4.5	HG544_PATCH:17683282-17685877	NOTEST	0	0	0	0	1	1
ENSG00000262686	ENSG00000262686	AC005356.1	16:4364761-4475706	NOTEST	0	0	0	0	1	1
ENSG00000262688	ENSG00000262688	Metazoa_SRP	HG185_PATCH:39873993-39890896	NOTEST	0	0	0	0	1	1
ENSG00000262689	ENSG00000262689	AC097374.2	HG686_PATCH:95632415-95711088	NOTEST	0	0	0	0	1	1
ENSG00000262690	ENSG00000262690	NLRP7	HSCHR19LRC_LRC_I_CTG1:55432380-55510014	NOTEST	0	0	0	0	1	1
ENSG00000262691	ENSG00000262691	CTC-277H1.7	16:67263289-67306093	NOTEST	0.127212	0.193812	0.607423	0	1	1
ENSG00000262692	ENSG00000262692	CTD-3195I5.3	17:3617921-3704537	NOTEST	0.475157	0.665033	0.485021	0	1	1
ENSG00000262693	ENSG00000262693	RP11-461I8.3	17:4978972-4981408	NOTEST	0	0	0	0	1	1
ENSG00000262694	ENSG00000262694	BAZ1B	HG1257_PATCH:72905354-72987235	NOTEST	0	0	0	0	1	1
ENSG00000262696	ENSG00000262696	NSUN5P2	HG1257_PATCH:72344321-72419747	NOTEST	0	0	0	0	1	1
ENSG00000262698	ENSG00000262698	snoU13	HSCHR1_1_CTG31:153717773-153763786	NOTEST	0	0	0	0	1	1
ENSG00000262700	ENSG00000262700	RP11-266L9.3	16:25096912-25122876	NOTEST	0.00874634	0	#NAME?	0	1	1
ENSG00000262703	ENSG00000262703	RP11-485G7.6	16:11343475-11445619	NOTEST	0.397941	0.350299	-0.183964	0	1	1
ENSG00000262704	ENSG00000262704	U4	HSCHR21_2_CTG1_1:23577510-23577651	NOTEST	0	0	0	0	1	1
ENSG00000262705	ENSG00000262705	CR392000.1	HG998_1_PATCH:139141816-139143051	NOTEST	0	0	0	0	1	1
ENSG00000262706	ENSG00000262706	CTC-550B14.1	HSCHR19LRC_COX2_CTG1:55097597-55175230	NOTEST	0	0	0	0	1	1
ENSG00000262708	ENSG00000262708	RP11-411G7.2	17:406410-624957	NOTEST	0	0.027343	inf	0	1	1
ENSG00000262709	ENSG00000262709	Y_RNA	HG1257_PATCH:72434652-72606602	NOTEST	0	0	0	0	1	1
ENSG00000262710	ENSG00000262710	Y_RNA	HSCHR1_1_CTG31:153775426-153775528	NOTEST	0	0	0	0	1	1
ENSG00000262711	ENSG00000262711	AC005077.7	HG1257_PATCH:75582681-75597144	NOTEST	0	0	0	0	1	1
ENSG00000262713	ENSG00000262713	RP11-1305N21.3	HSCHR5_1_CTG1:69446750-69463695	NOTEST	0	0	0	0	1	1
ENSG00000262714	ENSG00000262714	RP11-44F14.8	16:53420855-53422997	NOTEST	0	0	0	0	1	1
ENSG00000262715	ENSG00000262715	AC008984.7	HSCHR19LRC_PGF2_CTG1:54812329-54816445	NOTEST	0	0	0	0	1	1
ENSG00000262716	ENSG00000262716	TSEN34	HSCHR19LRC_COX1_CTG1:54693621-54697413	NOTEST	0	0	0	0	1	1
ENSG00000262717	ENSG00000262717	NCR1	HSCHR19LRC_PGF1_CTG1:55339393-55349377	NOTEST	0	0	0	0	1	1
ENSG00000262719	ENSG00000262719	U6	HSCHR19LRC_PGF2_CTG1:54767830-54767939	NOTEST	0	0	0	0	1	1
ENSG00000262721	ENSG00000262721	AC106782.20	16:30844946-30906541	NOTEST	0.0417792	0	#NAME?	0	1	1
ENSG00000262722	ENSG00000262722	GPRIN2	HG1211_PATCH:47039421-47050978	NOTEST	0	0	0	0	1	1
ENSG00000262724	ENSG00000262724	AC008984.5	HSCHR19LRC_PGF2_CTG1:54799880-54809979	NOTEST	0	0	0	0	1	1
ENSG00000262726	ENSG00000262726	RP11-1174L13.2	HSCHR5_1_CTG1:69966744-70078950	NOTEST	0	0	0	0	1	1
ENSG00000262727	ENSG00000262727	LILRB1	HSCHR19LRC_COX1_CTG1:55008196-55074165	NOTEST	0	0	0	0	1	1
ENSG00000262728	ENSG00000262728	AC123768.4	15:32898618-32932150	NOTEST	0.304607	0.243495	-0.323059	0	1	1

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ENSG00000262729	ENSG00000262729	GP6	HSCHR19LRC_PGF2_CTG1:55247239-55312338	NOTEST	0	0	0	0	1	1
ENSG00000262730	ENSG00000262730	RP11-1099M24.7	17:7825176-7853236	NOTEST	0	0	0	0	1	1
ENSG00000262731	ENSG00000262731	KRTAP2-1	HSCHR17_4_CTG4:39210878-39211741	NOTEST	0	0	0	0	1	1
ENSG00000262732	ENSG00000262732	CTD-2135D7.2	16:14014013-14046202	NOTEST	0.0925563	0.00925877	-3.32144	0	1	1
ENSG00000262733	ENSG00000262733	RP11-147B8.2	HSCHR15_1_CTG4:28730091-28730212	NOTEST	0	0	0	0	1	1
ENSG00000262734	ENSG00000262734	ABC13-48559800H2.2	HSCHR1_2_CTG31:155180969-155183462	NOTEST	0	0	0	0	1	1
ENSG00000262736	ENSG00000262736	NLRP7	HSCHR19LRC_COX1_CTG1:55355793-55433427	NOTEST	0	0	0	0	1	1
ENSG00000262737	ENSG00000262737	RP11-1260E13.1	HSCHR17_1_CTG1:62292-253878	NOTEST	0	0	0	0	1	1
ENSG00000262739	ENSG00000262739	PRSS2	HG7_PATCH:142531858-142535452	NOTEST	0	0	0	0	1	1
ENSG00000262740	ENSG00000262740	PIH1D2	HG388_HG400_PATCH:111895536-111955873	NOTEST	0	0	0	0	1	1
ENSG00000262741	ENSG00000262741	LENG8-AS1	HSCHR19LRC_COX1_CTG1:54880209-54897417	NOTEST	0	0	0	0	1	1
ENSG00000262742	ENSG00000262742	MCTP1	HSCHR5_1_CTG2:940394455-94636885	NOTEST	0	0	0	0	1	1
ENSG00000262743	ENSG00000262743	CICP10	HG1007_PATCH:2430620006-243062204	NOTEST	0	0	0	0	1	1
ENSG00000262744	ENSG00000262744	RHBDD2	HG1257_PATCH:75307558-75353883	NOTEST	0	0	0	0	1	1
ENSG00000262745	ENSG00000262745	CTD-2377D24.8	17:46760728-46781844	NOTEST	0.0332324	0.0994404	1.58124	0	1	1
ENSG00000262747	ENSG00000262747	AMZ2	HG747_PATCH:66242744-66253272	NOTEST	0	0	0	0	1	1
ENSG00000262748	ENSG00000262748	AC004231.7	HSCHR17_1_CTG4:39541223-39545959	NOTEST	0	0	0	0	1	1
ENSG00000262749	ENSG00000262749	KRTAP9-3	HSCHR17_5_CTG4:39388713-39389705	NOTEST	0	0	0	0	1	1
ENSG00000262750	ENSG00000262750	AC009892.9	HSCHR19LRC_COX1_CTG1:55087356-55087502	NOTEST	0	0	0	0	1	1
ENSG00000262751	ENSG00000262751	AC005077.5	HG1257_PATCH:75638689-75642162	NOTEST	0	0	0	0	1	1
ENSG00000262752	ENSG00000262752	AP000705.8	HSCHR21_2_CTG1_1:23507017-23508403	NOTEST	0	0	0	0	1	1
ENSG00000262754	ENSG00000262754	LILRA2	HSCHR19LRC_PGF1_CTG1:55006690-55072658	NOTEST	0	0	0	0	1	1
ENSG00000262755	ENSG00000262755	OR8K3	HG142_HG150_NOVEL_TEST:56085782-56086721	NOTEST	0	0	0	0	1	1
ENSG00000262756	ENSG00000262756	AC009133.21	16:29793245-29794294	NOTEST	0	0	0	0	1	1
ENSG00000262759	ENSG00000262759	MRPS21P9	17:48503518-48552206	NOTEST	0	0	0	0	1	1
ENSG00000262760	ENSG00000262760	AC006014.7	HG1257_PATCH:74939663-74951065	NOTEST	0	0	0	0	1	1
ENSG00000262762	ENSG00000262762	CBX2	HG748_PATCH:77774213-77784065	NOTEST	0	0	0	0	1	1
ENSG00000262763	ENSG00000262763	KIR3DL3	HSCHR19LRC_PGF1_CTG1:55157744-55300469	NOTEST	0	0	0	0	1	1
ENSG00000262764	ENSG00000262764	PPP2R1B	HG388_HG400_PATCH:111597631-111637151	NOTEST	0	0	0	0	1	1
ENSG00000262767	ENSG00000262767	RP11-216N14.1	HSCHR1_1_CTG31:153686308-153687353	NOTEST	0	0	0	0	1	1
ENSG00000262768	ENSG00000262768	RP11-353N14.1	17:77765930-77776326	NOTEST	0	0.0266578	inf	0	1	1
ENSG00000262769	ENSG00000262769	RP11-1113L8.1	17:19398697-19501235	NOTEST	0	0	0	0	1	1
ENSG00000262771	ENSG00000262771	SSBP1	HSCHR7_1_CTG6:141410145-141493730	NOTEST	0	0	0	0	1	1
ENSG00000262772	ENSG00000262772	RP11-353N14.2	17:77797250-77801503	NOTEST	0.254315	0.222661	-0.191765	0	1	1
ENSG00000262773	ENSG00000262773	NOSTRIN	HSCHR2_1_CTG12:169643048-169786870	NOTEST	0	0	0	0	1	1
ENSG00000262774	ENSG00000262774	ZNF92P2	HSCHR19_3_CTG3:22311549-22313125	NOTEST	0	0	0	0	1	1
ENSG00000262776	ENSG00000262776	7SK	HSCHR12_1_CTG2_1:58371747-58372060	NOTEST	0	0	0	0	1	1
ENSG00000262777	ENSG00000262777	RP11-818O24.3	17:1323982-1366456	NOTEST	0.244158	0.181658	-0.426587	0	1	1
ENSG00000262778	ENSG00000262778	SNORA48	HG115_PATCH:101459218-101927238	NOTEST	0	0	0	0	1	1
ENSG00000262779	ENSG00000262779	Y_RNA	HG1257_PATCH:74846594-74846695	NOTEST	0	0	0	0	1	1
ENSG00000262780	ENSG00000262780	RP13-379O24.2	HG506_HG507_HG1000_PATCH:61088964-61091152	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000262783	ENSG00000262783	MAMDC2	HSCHR9_2_CTG35:72659113-72847028	NOTEST	0	0	0	0	1	1
ENSG00000262784	ENSG00000262784	OR5T1	HG142_HG150_NOVEL_TEST:56043028-56044146	NOTEST	0	0	0	0	1	1
ENSG00000262785	ENSG00000262785	PKLR	HSCHR1_2_CTG31:155248062-155286629	NOTEST	0	0	0	0	1	1
ENSG00000262786	ENSG00000262786	RP11-214O1.1	17:14198828-14200917	NOTEST	0	0	0	0	1	1
ENSG00000262788	ENSG00000262788	CIRH1A	HSCHR16_2_CTG3_1:69166417-69202911	NOTEST	0	0	0	0	1	1
ENSG00000262789	ENSG00000262789	CTC-503K11.2	HG1063_PATCH:10258175-102589223	NOTEST	0	0	0	0	1	1
ENSG00000262791	ENSG00000262791	RP11-961A15.1	17:1614804-1641893	NOTEST	0	0	0	0	1	1
ENSG00000262795	ENSG00000262795	IFNGR2	HSCHR21_4_CTG1_1:34757298-34861875	NOTEST	0	0	0	0	1	1
ENSG00000262796	ENSG00000262796	OR8J1	HG142_HG150_NOVEL_TEST:56127690-56128764	NOTEST	0	0	0	0	1	1
ENSG00000262797	ENSG00000262797	GP6	HSCHR19LRC_PGF1_CTG1:55437861-55502960	NOTEST	0	0	0	0	1	1
ENSG00000262798	ENSG00000262798	AC012314.20	HSCHR19LRC_COX1_CTG1:54703139-54703657	NOTEST	0	0	0	0	1	1
ENSG00000262799	ENSG00000262799	RP11-735A19.3	HG348_PATCH:94770646-94771621	NOTEST	0	0	0	0	1	1
ENSG00000262800	ENSG00000262800	LILRA5	HSCHR19LRC_COX1_CTG1:54817384-54823441	NOTEST	0	0	0	0	1	1
ENSG00000262801	ENSG00000262801	U91319.1	16:13340172-13656775	NOTEST	0	0	0	0	1	1
ENSG00000262802	ENSG00000262802	RP5-905G11.3	HSCHR20_1_CTG1:17874022-17874820	NOTEST	0	0	0	0	1	1
ENSG00000262803	ENSG00000262803	RP11-160A9.3	6:71377478-71666741	NOTEST	0	0	0	0	1	1
ENSG00000262805	ENSG00000262805	U6	HG388_HG400_PATCH:111895536-111955873	NOTEST	0	0	0	0	1	1
ENSG00000262806	ENSG00000262806	FCAR	HSCHR19LRC_COX2_CTG1:55048401-55064587	NOTEST	0	0	0	0	1	1
ENSG00000262808	ENSG00000262808	KRTAP1-1	HSCHR17_4_CTG4:39196935-39197838	NOTEST	0	0	0	0	1	1
ENSG00000262809	ENSG00000262809	WTAPP1	HG305_PATCH:102617698-102714534	NOTEST	0	0	0	0	1	1
ENSG00000262810	ENSG00000262810	RP11-667K14.5	17:1963132-2284352	NOTEST	0.0416773	0	#NAME?	0	1	1
ENSG00000262811	ENSG00000262811	NLRP2	HSCHR19LRC_LRC_S_CTG1:55434466-55512100	NOTEST	0	0	0	0	1	1
ENSG00000262812	ENSG00000262812	HYOU1	HG299_PATCH:118914897-118927912	NOTEST	0	0	0	0	1	1
ENSG00000262815	ENSG00000262815	RP11-565F19.4	17:9153787-9479908	NOTEST	0	0	0	0	1	1
ENSG00000262817	ENSG00000262817	MAMDC2-AS1	HSCHR9_2_CTG35:72659113-72847028	NOTEST	0	0	0	0	1	1
ENSG00000262818	ENSG00000262818	RP11-636N17.1	17:6297012-6338519	NOTEST	0	0	0	0	1	1
ENSG00000262819	ENSG00000262819	RP11-58A17.3	HSCHR12_1_CTG2_1:58360840-58362182	NOTEST	0	0	0	0	1	1
ENSG00000262821	ENSG00000262821	RP11-536P16.4	HSCHR15_1_CTG4:28802677-28806543	NOTEST	0	0	0	0	1	1
ENSG00000262823	ENSG00000262823	RP13-580F15.2	17:4336982-4391503	NOTEST	0	0	0	0	1	1
ENSG00000262824	ENSG00000262824	RP11-483E23.7	HSCHR15_1_CTG4:28821751-28821918	NOTEST	0	0	0	0	1	1
ENSG00000262826	ENSG00000262826	INTS3	HSCHR1_1_CTG31:153717773-153763786	NOTEST	0	0	0	0	1	1
ENSG00000262827	ENSG00000262827	FCAR	HSCHR19LRC_PGF1_CTG1:55307509-55323724	NOTEST	0	0	0	0	1	1
ENSG00000262828	ENSG00000262828	RP11-325M4.2	6:57793931-57794280	NOTEST	0	0	0	0	1	1
ENSG00000262829	ENSG00000262829	RP11-673D15.9	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000262830	ENSG00000262830	AC098784.1	HSCHR19LRC_COX1_CTG1:55138832-55139116	NOTEST	0	0	0	0	1	1
ENSG00000262831	ENSG00000262831	RP11-498C9.2	17:79801034-79818570	NOTEST	0	0.104662	inf	0	1	1
ENSG00000262832	ENSG00000262832	NCR1	HSCHR19LRC_LRC_T_CTG1:55353390-55363391	NOTEST	0	0	0	0	1	1
ENSG00000262833	ENSG00000262833	RP11-28G8.1	17:78518618-78945013	NOTEST	0.00489637	0.0290908	2.57078	0	1	1
ENSG00000262834	ENSG00000262834	AC018720.10	HG1257_PATCH:74959037-74993105	NOTEST	0	0	0	0	1	1
ENSG00000262835	ENSG00000262835	EPS8L1	HSCHR19LRC_LRC_J_CTG1:55608428-55624332	NOTEST	0	0	0	0	1	1
ENSG00000262837	ENSG00000262837	RP11-304F15.7	17:47911600-47913816	NOTEST	0	0.146591	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000262840	ENSG00000262840	DNAH12	HG280_PATCH:57327726-57578372	NOTEST	0	0	0	0	1	1
ENSG00000262841	ENSG00000262841	CDK7	HSCHR5_1_CTG1:68530665-68573234	NOTEST	0	0	0	0	1	1
ENSG00000262843	ENSG00000262843	LILRA5	HSCHR19LRC_PGF2_CTG1:54817735-54823469	NOTEST	0	0	0	0	1	1
ENSG00000262844	ENSG00000262844	RP11-7O20.4	HG873_PATCH:15009216-15010240	NOTEST	0	0	0	0	1	1
ENSG00000262845	ENSG00000262845	KRT40	HSCHR17_4_CTG4:39134094-39143514	NOTEST	0	0	0	0	1	1
ENSG00000262847	ENSG00000262847	MDH2	HG1257_PATCH:75513007-75532465	NOTEST	0	0	0	0	1	1
ENSG00000262848	ENSG00000262848	RP11-517A5.5	16:16326351-16388668	NOTEST	0	0	0	0	1	1
ENSG00000262849	ENSG00000262849	AC098789.1	HSCHR19LRC_PGF1_CTG1:54771872-54772916	NOTEST	0	0	0	0	1	1
ENSG00000262850	ENSG00000262850	RP4-809F18.2	HSCHR12_1_CTG5:126848621-126849484	NOTEST	0	0	0	0	1	1
ENSG00000262851	ENSG00000262851	OR5T2	HG142_HG150_NOVEL_TEST:55999489-56000737	NOTEST	0	0	0	0	1	1
ENSG00000262852	ENSG00000262852	HSPB2	HG388_HG400_PATCH:111779287-111797595	NOTEST	0	0	0	0	1	1
ENSG00000262853	ENSG00000262853	RP11-445N18.5	HSCHR10_1_CTG5:45652222-45676875	NOTEST	0	0	0	0	1	1
ENSG00000262854	ENSG00000262854	AC011515.2	HSCHR19LRC_PGF1_CTG1:55104999-55106360	NOTEST	0	0	0	0	1	1
ENSG00000262855	ENSG00000262855	RP11-461I8.4	17:5008835-5078329	NOTEST	0	0	0	0	1	1
ENSG00000262856	ENSG00000262856	PCGF7P	HSCHR19_3_CTG3:22320732-22321783	NOTEST	0	0	0	0	1	1
ENSG00000262858	ENSG00000262858	BPTF	HG747_PATCH:65821639-65980494	NOTEST	0	0	0	0	1	1
ENSG00000262860	ENSG00000262860	LSM14A	HSCHR19_1_CTG3_1:34663351-34720227	NOTEST	0	0	0	0	1	1
ENSG00000262862	ENSG00000262862	KRTAP2-3	HSCHR17_4_CTG4:39215721-39216596	NOTEST	0	0	0	0	1	1
ENSG00000262863	ENSG00000262863	AC005488.11	HG1257_PATCH:72434652-72606602	NOTEST	0	0	0	0	1	1
ENSG00000262864	ENSG00000262864	RPS27P14	HSCHR5_1_CTG1:68765414-68765668	NOTEST	0	0	0	0	1	1
ENSG00000262866	ENSG00000262866	IFT20	HG883_PATCH:26646120-26662515	NOTEST	0	0	0	0	1	1
ENSG00000262867	ENSG00000262867	GP6	HSCHR19LRC_LRC_J_CTG1:55542601-55607700	NOTEST	0	0	0	0	1	1
ENSG00000262868	ENSG00000262868	TSEN34	HSCHR19LRC_PGF1_CTG1:54693788-54697580	NOTEST	0	0	0	0	1	1
ENSG00000262869	ENSG00000262869	CTD-2545H1.1	17:1837970-1928639	NOTEST	0	0.0922843	inf	0	1	1
ENSG00000262870	ENSG00000262870	CYCSP40	17:75082797-75213179	NOTEST	0	0	0	0	1	1
ENSG00000262872	ENSG00000262872	GOLGA8G	HSCHR15_1_CTG4:28776380-28789737	NOTEST	0	0	0	0	1	1
ENSG00000262873	ENSG00000262873	CTD-2561B21.11	17:78991768-78993811	NOTEST	0.559971	0.420843	-0.412071	0	1	1
ENSG00000262874	ENSG00000262874	C19orf84	19:51891542-51893828	NOTEST	0.0470813	0.018728	-1.32996	0	1	1
ENSG00000262875	ENSG00000262875	CAPN5	HG414_PATCH:76777975-76835592	NOTEST	0	0	0	0	1	1
ENSG00000262876	ENSG00000262876	AC005077.12	HG1257_PATCH:75555387-75573736	NOTEST	0	0	0	0	1	1
ENSG00000262878	ENSG00000262878	EPS8L1	HSCHR19LRC_PGF1_CTG1:55503688-55519592	NOTEST	0	0	0	0	1	1
ENSG00000262880	ENSG00000262880	RP11-104H15.7	17:7323421-7361026	NOTEST	0.0827792	0.085238	0.0422272	0	1	1
ENSG00000262881	ENSG00000262881	RP11-669E14.4	17:43921016-44105700	NOTEST	0.0716252	0.0356786	-1.00541	0	1	1
ENSG00000262884	ENSG00000262884	CTD-3060P21.1	17:2680349-2941033	NOTEST	0	0	0	0	1	1
ENSG00000262885	ENSG00000262885	CTD-2144E22.11	16:34256506-34258621	NOTEST	0	0	0	0	1	1
ENSG00000262886	ENSG00000262886	NLRP2	HSCHR19LRC_COX1_CTG1:55355793-55433427	NOTEST	0	0	0	0	1	1
ENSG00000262887	ENSG00000262887	CU467002.1	HSCHR19LRC_COX1_CTG1:54897490-54898993	NOTEST	0	0	0	0	1	1
ENSG00000262888	ENSG00000262888	RP11-462G12.2	16:3981217-3996306	NOTEST	0.024633	0.0960188	1.96272	0	1	1
ENSG00000262889	ENSG00000262889	TAS2R46	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000262890	ENSG00000262890	RP11-424M24.5	16:70835985-70836743	NOTEST	0	0	0	0	1	1
ENSG00000262892	ENSG00000262892	RP11-429H5.1	HSCHR18_1_CTG1_1:47991471-47992380	NOTEST	0	0	0	0	1	1

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ENSG00000262896	ENSG00000262896	KRTAP9-4	HSCHR17_6_CTG4:39394568-39395535	NOTEST	0	0	0	0	1	1
ENSG00000262897	ENSG00000262897	KIR3DL2	HSCHR19LRC_COX2_CTG1:55024580-55041367	NOTEST	0	0	0	0	1	1
ENSG00000262898	ENSG00000262898	AC139099.4	17:81091899-81125376	NOTEST	0	0	0	0	1	1
ENSG00000262899	ENSG00000262899	LA16c-360H6.3	16:3313742-3368852	NOTEST	0	0	0	0	1	1
ENSG00000262900	ENSG00000262900	LILRA1	HSCHR19LRC_COX1_CTG1:55008196-55074165	NOTEST	0	0	0	0	1	1
ENSG00000262901	ENSG00000262901	RNU6-1080P	HG1257_PATCH:72793120-72823582	NOTEST	0	0	0	0	1	1
ENSG00000262902	ENSG00000262902	RP11-750B16.1	17:51183094-51183719	NOTEST	0	0	0	0	1	1
ENSG00000262903	ENSG00000262903	RP11-235E17.6	17:3539761-3564836	NOTEST	0.404556	0.269356	-0.586826	0	1	1
ENSG00000262904	ENSG00000262904	RP11-144N1.1	16:74701403-74702604	NOTEST	0.0550838	0.0652309	0.243929	0	1	1
ENSG00000262906	ENSG00000262906	RP11-536P16.4	HSCHR15_1_CTG4:28606967-28610830	NOTEST	0	0	0	0	1	1
ENSG00000262907	ENSG00000262907	KIF5C	HSCHR2_2_CTG12:149632818-149889353	NOTEST	0	0	0	0	1	1
ENSG00000262908	ENSG00000262908	TAS2R30	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000262909	ENSG00000262909	SMURF2	HG183_PATCH:62619654-62739428	NOTEST	0	0	0	0	1	1
ENSG00000262911	ENSG00000262911	DNAJC28	HSCHR21_4_CTG1_1:34870053-34873585	NOTEST	0	0	0	0	1	1
ENSG00000262912	ENSG00000262912	AC238894.1	HSCHR12_1_CTG1:82417-82555	NOTEST	0	0	0	0	1	1
ENSG00000262913	ENSG00000262913	AC098789.1	HSCHR19LRC_COX1_CTG1:54771629-54772673	NOTEST	0	0	0	0	1	1
ENSG00000262915	ENSG00000262915	RP11-1280N14.3	HSCHR5_1_CTG1:69545806-69571649	NOTEST	0	0	0	0	1	1
ENSG00000262916	ENSG00000262916	CTD-2292P10.4	HG418_PATCH:143781471-143808334	NOTEST	0	0	0	0	1	1
ENSG00000262917	ENSG00000262917	POLG2	HG183_PATCH:62555144-62574426	NOTEST	0	0	0	0	1	1
ENSG00000262918	ENSG00000262918	ZNF729	HSCHR19_3_CTG3:22477416-22508185	NOTEST	0	0	0	0	1	1
ENSG00000262919	ENSG00000262919	FAM58A	HG1497_PATCH:152756398-152767649	NOTEST	0	0	0	0	1	1
ENSG00000262920	ENSG00000262920	RP11-1260E13.1	17:62292-236045	NOTEST	0	0	0	0	1	1
ENSG00000262921	ENSG00000262921	RP11-141J13.3	17:4469046-4475055	NOTEST	0.0811727	0.090067	0.150003	0	1	1
ENSG00000262922	ENSG00000262922	U6	HSCHR5_1_CTG5:161904896-161904999	NOTEST	0	0	0	0	1	1
ENSG00000262923	ENSG00000262923	NCR1	HSCHR19LRC_LRC_J_CTG1:55442548-55452549	NOTEST	0	0	0	0	1	1
ENSG00000262924	ENSG00000262924	KIAA0355	HSCHR19_1_CTG3_1:34752614-34853664	NOTEST	0	0	0	0	1	1
ENSG00000262925	ENSG00000262925	RP11-689N19.6	HG414_PATCH:76835713-76837198	NOTEST	0	0	0	0	1	1
ENSG00000262927	ENSG00000262927	FAM138D	HSCHR12_1_CTG1:86666-88073	NOTEST	0	0	0	0	1	1
ENSG00000262928	ENSG00000262928	ZNF43	HSCHR19_2_CTG3:21997230-22044406	NOTEST	0	0	0	0	1	1
ENSG00000262929	ENSG00000262929	NLRP2	HSCHR19LRC_LRC_T_CTG1:55370759-55448393	NOTEST	0	0	0	0	1	1
ENSG00000262931	ENSG00000262931	U6	HSCHR19LRC_COX2_CTG1:55043098-55043205	NOTEST	0	0	0	0	1	1
ENSG00000262932	ENSG00000262932	RP11-124L9.3	HSCHR5_1_CTG1:69145315-69148817	NOTEST	0	0	0	0	1	1
ENSG00000262933	ENSG00000262933	CALCA	HG873_PATCH:14988216-14993851	NOTEST	0	0	0	0	1	1
ENSG00000262935	ENSG00000262935	AC005086.7	HG115_PATCH:101459218-101927238	NOTEST	0	0	0	0	1	1
ENSG00000262936	ENSG00000262936	LAIR1	HSCHR19LRC_COX2_CTG1:54864044-54880850	NOTEST	0	0	0	0	1	1
ENSG00000262937	ENSG00000262937	Y_RNA	HG79_PATCH:136178004-136178098	NOTEST	0	0	0	0	1	1
ENSG00000262938	ENSG00000262938	C21orf62	HSCHR21_3_CTG1_1:34144410-34271837	NOTEST	0	0	0	0	1	1
ENSG00000262939	ENSG00000262939	OR5G4P	HG151_NOVEL_TEST:56568755-56569515	NOTEST	0	0	0	0	1	1
ENSG00000262941	ENSG00000262941	AC010518.3	HSCHR19LRC_COX1_CTG1:54797674-54797992	NOTEST	0	0	0	0	1	1
ENSG00000262942	ENSG00000262942	ZNF676	HSCHR19_3_CTG3:22362751-22379435	NOTEST	0	0	0	0	1	1
ENSG00000262943	ENSG00000262943	ALOX12P2	17:6757179-6922978	NOTEST	0	0	0	0	1	1
ENSG00000262946	ENSG00000262946	KRTAP9-11P	HSCHR17_6_CTG4:39416192-39416717	NOTEST	0	0	0	0	1	1

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ENSG00000262948	ENSG00000262948	RPL23AP64	HG299_PATCH:118868851-118901597	NOTEST	0	0	0	0	1	1
ENSG00000262949	ENSG00000262949	RP11-490M8.1	HSCHR2_1_CTG1:36587924-36588290	NOTEST	0	0	0	0	1	1
ENSG00000262950	ENSG00000262950	RP11-189E14.5	16:49476820-49487989	NOTEST	0	0	0	0	1	1
ENSG00000262951	ENSG00000262951	RP11-670E13.2	17:54946307-54946925	NOTEST	0	0	0	0	1	1
ENSG00000262952	ENSG00000262952	AC139099.6	17:81159764-81188573	NOTEST	0	0	0	0	1	1
ENSG00000262953	ENSG00000262953	EIF4A1P9	17:2489623-2491160	NOTEST	0	0	0	0	1	1
ENSG00000262957	ENSG00000262957	RP11-124L9.5	HSCHR5_1_CTG1:69050903-69144625	NOTEST	0	0	0	0	1	1
ENSG00000262958	ENSG00000262958	RPL37AP8	HG388_HG400_PATCH:111759921-111760194	NOTEST	0	0	0	0	1	1
ENSG00000262959	ENSG00000262959	LA16c-321D4.1	16:2961937-3004277	NOTEST	0.114762	0.18293	0.672649	0	1	1
ENSG00000262960	ENSG00000262960	NCF1C	HG1257_PATCH:74621595-74637001	NOTEST	0	0	0	0	1	1
ENSG00000262961	ENSG00000262961	CTB-162E12.1	17:5633608-5634405	NOTEST	0	0	0	0	1	1
ENSG00000262962	ENSG00000262962	KARSP3	16:68021296-68272005	NOTEST	0	0	0	0	1	1
ENSG00000262964	ENSG00000262964	TRIM50	HG1257_PATCH:72777495-72793039	NOTEST	0	0	0	0	1	1
ENSG00000262966	ENSG00000262966	RP11-85B7.2	17:8924858-9147317	NOTEST	0.00486963	0.00209681	-1.21561	0	1	1
ENSG00000262967	ENSG00000262967	RP11-294J22.6	17:48770550-48785285	NOTEST	0	0	0	0	1	1
ENSG00000262968	ENSG00000262968	CYP2R1	HG873_PATCH:14899552-14913798	NOTEST	0	0	0	0	1	1
ENSG00000262970	ENSG00000262970	ACER3	HG414_PATCH:76571910-76737841	NOTEST	0	0	0	0	1	1
ENSG00000262971	ENSG00000262971	U6	HG686_PATCH:95578782-95620920	NOTEST	0	0	0	0	1	1
ENSG00000262973	ENSG00000262973	RP11-708H21.4	17:47249256-47250608	NOTEST	0	0	0	0	1	1
ENSG00000262974	ENSG00000262974	RP11-457I16.4	16:18511181-18573533	NOTEST	0	0	0	0	1	1
ENSG00000262975	ENSG00000262975	CTD-2542C24.1	HSCHR19_1_CTG3:20998049-21005050	NOTEST	0	0	0	0	1	1
ENSG00000262977	ENSG00000262977	RP11-1151M9.1	HSCHR5_1_CTG1:68889082-68890825	NOTEST	0	0	0	0	1	1
ENSG00000262978	ENSG00000262978	HSPB2-C11orf52	HG388_HG400_PATCH:111779287-111797595	NOTEST	0	0	0	0	1	1
ENSG00000262979	ENSG00000262979	CTD-2047H16.2	17:78234664-78411886	NOTEST	0.144433	0	#NAME?	0	1	1
ENSG00000262980	ENSG00000262980	OR52L2P	11:6078545-6079505	NOTEST	0	0	0	0	1	1
ENSG00000262981	ENSG00000262981	RP11-731K22.1	HG1257_PATCH:73450948-73453724	NOTEST	0	0	0	0	1	1
ENSG00000262982	ENSG00000262982	RDH13	HSCHR19LRC_COX2_CTG1:55180280-55245379	NOTEST	0	0	0	0	1	1
ENSG00000262983	ENSG00000262983	AF001550.7	16:21206167-21225831	NOTEST	0	0	0	0	1	1
ENSG00000262984	ENSG00000262984	NCF1B	HG1257_PATCH:72685532-72700902	NOTEST	0	0	0	0	1	1
ENSG00000262985	ENSG00000262985	LILRB1	HSCHR19LRC_PGF1_CTG1:55006690-55072658	NOTEST	0	0	0	0	1	1
ENSG00000262986	ENSG00000262986	RP11-785H5.1	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000262987	ENSG00000262987	RP11-520H11.1	HG7_PATCH:142521597-142525182	NOTEST	0	0	0	0	1	1
ENSG00000262988	ENSG00000262988	CLDN4	HG1257_PATCH:73264498-73297641	NOTEST	0	0	0	0	1	1
ENSG00000262989	ENSG00000262989	RP11-846E15.3	HSCHR5_1_CTG1:69050903-69144625	NOTEST	0	0	0	0	1	1
ENSG00000262990	ENSG00000262990	CTC-281F24.2	17:6653003-6653507	NOTEST	0	0	0	0	1	1
ENSG00000262991	ENSG00000262991	CU457734.1	HSCHR19LRC_COX1_CTG1:54754030-54760926	NOTEST	0	0	0	0	1	1
ENSG00000262993	ENSG00000262993	KRT31	HSCHR17_1_CTG4:39557275-39561144	NOTEST	0	0	0	0	1	1
ENSG00000262994	ENSG00000262994	RP11-216N14.10	HSCHR1_1_CTG31:153706998-153708022	NOTEST	0	0	0	0	1	1
ENSG00000262995	ENSG00000262995	CTD-2194A8.2	16:20420855-20458322	NOTEST	0	0	0	0	1	1
ENSG00000262996	ENSG00000262996	RP11-110I1.14	HG299_PATCH:118914897-118927912	NOTEST	0	0	0	0	1	1

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ENSG00000263000	ENSG00000263000	ACTL9	HG729_PATCH:8762286-8763706	NOTEST	0	0	0	0	1	1
ENSG00000263001	ENSG00000263001	GTF2I	HG1257_PATCH:74122660-74225649	NOTEST	0	0	0	0	1	1
ENSG00000263003	ENSG00000263003	AC008746.5	HSCHR19LRC_PGF1_CTG1:54878386-54897289	NOTEST	0	0	0	0	1	1
ENSG00000263005	ENSG00000263005	RASSF1	HG325_PATCH:50367219-50378412	NOTEST	0	0	0	0	1	1
ENSG00000263007	ENSG00000263007	CRYAB	HG388_HG400_PATCH:111779287-111797595	NOTEST	0	0	0	0	1	1
ENSG00000263008	ENSG00000263008	WBSCR16	HG1257_PATCH:74507133-74538820	NOTEST	0	0	0	0	1	1
ENSG00000263010	ENSG00000263010	RP11-708L7.6	HG388_HG400_PATCH:111797866-111893307	NOTEST	0	0	0	0	1	1
ENSG00000263011	ENSG00000263011	RP11-473M20.11	16:3156764-3159577	NOTEST	0	0	0	0	1	1
ENSG00000263012	ENSG00000263012	KRT33B	HSCHR17_1_CTG4:39519745-39526052	NOTEST	0	0	0	0	1	1
ENSG00000263014	ENSG00000263014	ATP6V1G3	HSCHR1_3_CTG31:198503839-198521562	NOTEST	0	0	0	0	1	1
ENSG00000263015	ENSG00000263015	RP5-1029F21.3	17:406410-624957	NOTEST	0	0	0	0	1	1
ENSG00000263017	ENSG00000263017	RP11-356I18.1	17:702552-883010	NOTEST	0	0	0	0	1	1
ENSG00000263019	ENSG00000263019	RP11-785H5.2	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000263021	ENSG00000263021	LILRB5	HSCHR19LRC_PGF2_CTG1:54754288-54761190	NOTEST	0	0	0	0	1	1
ENSG00000263022	ENSG00000263022	KRT37	HSCHR17_1_CTG4:39565992-39588626	NOTEST	0	0	0	0	1	1
ENSG00000263024	ENSG00000263024	STX1A	HG1257_PATCH:73145925-73184629	NOTEST	0	0	0	0	1	1
ENSG00000263025	ENSG00000263025	AC009892.9	HSCHR19LRC_PGF1_CTG1:55085851-55085997	NOTEST	0	0	0	0	1	1
ENSG00000263026	ENSG00000263026	NLRP7	HSCHR19LRC_COX2_CTG1:55097597-55175230	NOTEST	0	0	0	0	1	1
ENSG00000263027	ENSG00000263027	KIR2DL3	HSCHR19LRC_PGF1_CTG1:55157744-55300469	NOTEST	0	0	0	0	1	1
ENSG00000263028	ENSG00000263028	TAS2R19	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000263029	ENSG00000263029	RP11-517A5.6	16:16326351-16388668	NOTEST	0	0	0	0	1	1
ENSG00000263030	ENSG00000263030	CDC42EP5	HSCHR19LRC_COX1_CTG1:54900425-54908565	NOTEST	0	0	0	0	1	1
ENSG00000263031	ENSG00000263031	GIN1	HG1063_PATCH:102421703-102538940	NOTEST	0	0	0	0	1	1
ENSG00000263032	ENSG00000263032	DLAT	HG388_HG400_PATCH:111895536-111955873	NOTEST	0	0	0	0	1	1
ENSG00000263033	ENSG00000263033	RP11-396B14.2	16:11290033-11318373	NOTEST	0.0344663	0	#NAME?	0	1	1
ENSG00000263035	ENSG00000263035	RP11-124L9.1	HSCHR5_1_CTG1:69151880-69194073	NOTEST	0	0	0	0	1	1
ENSG00000263037	ENSG00000263037	MTX1P1	HSCHR1_2_CTG31:155216169-155219520	NOTEST	0	0	0	0	1	1
ENSG00000263040	ENSG00000263040	PRR4	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000263041	ENSG00000263041	RP11-355F22.1	10:119585413-119590029	NOTEST	0	0	0	0	1	1
ENSG00000263042	ENSG00000263042	WEE2	HSCHR7_1_CTG6:141410145-141493730	NOTEST	0	0	0	0	1	1
ENSG00000263043	ENSG00000263043	MARVELD2	HSCHR5_1_CTG1:68711179-68739968	NOTEST	0	0	0	0	1	1
ENSG00000263044	ENSG00000263044	NSUN5P1	HG1257_PATCH:74856911-74881744	NOTEST	0	0	0	0	1	1
ENSG00000263045	ENSG00000263045	RP11-28B23.1	17:18853657-18950950	NOTEST	0	0	0	0	1	1
ENSG00000263046	ENSG00000263046	CEP95	HG183_PATCH:62576979-62615309	NOTEST	0	0	0	0	1	1
ENSG00000263049	ENSG00000263049	TBL2	HG1257_PATCH:73033888-73043748	NOTEST	0	0	0	0	1	1
ENSG00000263050	ENSG00000263050	RP11-667K14.3	17:1946768-1948262	NOTEST	0.102467	0.0777572	-0.39811	0	1	1
ENSG00000263051	ENSG00000263051	RP11-565F19.3	17:9153787-9479908	NOTEST	0	0	0	0	1	1
ENSG00000263052	ENSG00000263052	HSPA12A	HG311_PATCH:118423207-118502086	NOTEST	0	0	0	0	1	1
ENSG00000263054	ENSG00000263054	CU467002.2	HSCHR19LRC_COX1_CTG1:54880209-54897417	NOTEST	0	0	0	0	1	1
ENSG00000263055	ENSG00000263055	TRIAP1P1	HSCHR10_1_CTG2:27714366-27714591	NOTEST	0	0	0	0	1	1
ENSG00000263057	ENSG00000263057	KRT20	HSCHR17_4_CTG4:39032192-39041479	NOTEST	0	0	0	0	1	1
ENSG00000263059	ENSG00000263059	AP000479.1	HG151_NOVEL_TEST:56627027-56656628	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263060	ENSG00000263060	RP1-232L24.3	HSCHR6_1_CTG5:80157845-80158854	NOTEST	0	0	0	0	1	1
ENSG00000263061	ENSG00000263061	LILRB4	HSCHR19LRC_PGF1_CTG1:55095895-55104128	NOTEST	0	0	0	0	1	1
ENSG00000263062	ENSG00000263062	NAIP	HSCHR5_1_CTG1:68898376-68954986	NOTEST	0	0	0	0	1	1
ENSG00000263063	ENSG00000263063	RP11-388C12.1	17:80671783-80674131	NOTEST	0	0.0594509	inf	0	1	1
ENSG00000263064	ENSG00000263064	AC118758.1	HG736_PATCH:56870560-56872546	NOTEST	0	0	0	0	1	1
ENSG00000263065	ENSG00000263065	AF001548.6	16:15737123-15950890	NOTEST	0	0	0	0	1	1
ENSG00000263066	ENSG00000263066	LILRP2	HSCHR19LRC_PGF1_CTG1:55141427-55146730	NOTEST	0	0	0	0	1	1
ENSG00000263067	ENSG00000263067	STAG3L3	HG1257_PATCH:72434652-72606602	NOTEST	0	0	0	0	1	1
ENSG00000263068	ENSG00000263068	NLRP7	HSCHR19LRC_LRC_T_CTG1:55370759-55448393	NOTEST	0	0	0	0	1	1
ENSG00000263069	ENSG00000263069	CTD-2047H16.4	17:78234664-78411886	NOTEST	0.182774	0.413957	1.17942	0	1	1
ENSG00000263070	ENSG00000263070	RP11-382B18.3	15:30653442-30686052	NOTEST	0	0	0	0	1	1
ENSG00000263071	ENSG00000263071	CFL1P5	HSCHR5_1_CTG1:68577164-68628568	NOTEST	0	0	0	0	1	1
ENSG00000263074	ENSG00000263074	ARSG	HG747_PATCH:66255297-66418847	NOTEST	0	0	0	0	1	1
ENSG00000263076	ENSG00000263076	RPS9	HSCHR19LRC_COX1_CTG1:54704427-54752625	NOTEST	0	0	0	0	1	1
ENSG00000263077	ENSG00000263077	DDX5	HG183_PATCH:62576979-62615309	NOTEST	0	0	0	0	1	1
ENSG00000263080	ENSG00000263080	RP11-485G7.5	16:11343475-11445619	NOTEST	0	0.202774	inf	0	1	1
ENSG00000263081	ENSG00000263081	AC004878.8	HG1257_PATCH:74697884-74698881	NOTEST	0	0	0	0	1	1
ENSG00000263082	ENSG00000263082	CTD-2034I21.2	16:50914119-50918012	NOTEST	0	0	0	0	1	1
ENSG00000263083	ENSG00000263083	TAS2R64P	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000263085	ENSG00000263085	C17orf58	HG747_PATCH:65987216-65989765	NOTEST	0	0	0	0	1	1
ENSG00000263086	ENSG00000263086	5S_rRNA	HG1032_PATCH:190936292-190936410	NOTEST	0	0	0	0	1	1
ENSG00000263087	ENSG00000263087	AC215219.2	HG858_PATCH:82417-82555	NOTEST	0	0	0	0	1	1
ENSG00000263089	ENSG00000263089	RP11-166P13.4	17:55162452-55198710	NOTEST	0.0209754	0.0344135	0.714277	0	1	1
ENSG00000263090	ENSG00000263090	KRTAP9-2	HSCHR17_5_CTG4:39382899-39383904	NOTEST	0	0	0	0	1	1
ENSG00000263091	ENSG00000263091	KRTAP2-4	HSCHR17_4_CTG4:39221597-39222361	NOTEST	0	0	0	0	1	1
ENSG00000263092	ENSG00000263092	VN1R105P	HSCHR19LRC_PGF2_CTG1:54899258-54904970	NOTEST	0	0	0	0	1	1
ENSG00000263093	ENSG00000263093	IFRD2	HG325_PATCH:50316458-50336900	NOTEST	0	0	0	0	1	1
ENSG00000263094	ENSG00000263094	hsa-mir-661	HG104_HG975_PATCH:144997316-145058904	NOTEST	0	0	0	0	1	1
ENSG00000263095	ENSG00000263095	RP11-136K7.3	HSCHR5_1_CTG1:69863006-69957699	NOTEST	0	0	0	0	1	1
ENSG00000263096	ENSG00000263096	RP11-515O17.2	17:53342372-53402426	NOTEST	0	0.0348059	inf	0	1	1
ENSG00000263097	ENSG00000263097	TAS2R31	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000263098	ENSG00000263098	RP11-567O16.1	17:80709939-81009686	NOTEST	0.115709	0	#NAME?	0	1	1
ENSG00000263100	ENSG00000263100	NCR1	HSCHR19LRC_COX1_CTG1:55338424-55348425	NOTEST	0	0	0	0	1	1
ENSG00000263101	ENSG00000263101	KRTAP3-3	HSCHR17_4_CTG4:39149808-39150512	NOTEST	0	0	0	0	1	1
ENSG00000263102	ENSG00000263102	CTC-352P4.1	HSCHR19_1_CTG3:21027634-21036574	NOTEST	0	0	0	0	1	1
ENSG00000263103	ENSG00000263103	KRTAP9-10P	HSCHR17_5_CTG4:39426533-39426740	NOTEST	0	0	0	0	1	1
ENSG00000263104	ENSG00000263104	AC005102.1	HG1257_PATCH:75300619-75301098	NOTEST	0	0	0	0	1	1
ENSG00000263105	ENSG00000263105	RP11-95P2.3	16:4230117-4233516	NOTEST	0	0.531396	inf	0	1	1
ENSG00000263106	ENSG00000263106	U6	HSCHR19LRC_LRC_T_CTG1:55316414-55316521	NOTEST	0	0	0	0	1	1
ENSG00000263107	ENSG00000263107	RP11-1113L8.2	17:19398697-19501235	NOTEST	0	0	0	0	1	1
ENSG00000263108	ENSG00000263108	LILRB4	HSCHR19LRC_COX1_CTG1:55097404-55105649	NOTEST	0	0	0	0	1	1
ENSG00000263109	ENSG00000263109	TTYH1	HSCHR19LRC_COX1_CTG1:54850623-54872311	NOTEST	0	0	0	0	1	1
ENSG00000263110	ENSG00000263110	RP11-189E14.3	16:49488139-49491180	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263112	ENSG00000263112	AC008984.7	HSCHR19LRC_COX2_CTG1:54811987-54816264	NOTEST	0	0	0	0	1	1
ENSG00000263113	ENSG00000263113	RP11-124L9.2	HSCHR5_1_CTG1:69050903-69144625	NOTEST	0	0	0	0	1	1
ENSG00000263114	ENSG00000263114	RP11-399D15.1	HSCHR12_3_CTG2_1:101628095-101628831	NOTEST	0	0	0	0	1	1
ENSG00000263115	ENSG00000263115	KRTAP9-10P	HSCHR17_6_CTG4:39425485-39425692	NOTEST	0	0	0	0	1	1
ENSG00000263118	ENSG00000263118	RP1-232L24.1	HSCHR6_1_CTG5:80174456-80174716	NOTEST	0	0	0	0	1	1
ENSG00000263120	ENSG00000263120	RP5-1107A17.4	17:55055465-55084129	NOTEST	0	0.0398945	inf	0	1	1
ENSG00000263122	ENSG00000263122	RP11-66N11.7	HG1497_PATCH:152779165-152781397	NOTEST	0	0	0	0	1	1
ENSG00000263125	ENSG00000263125	ARL2BPP8	17:52831525-52832010	NOTEST	0	0	0	0	1	1
ENSG00000263126	ENSG00000263126	CTC-479C5.10	16:67906925-67922758	NOTEST	0.0889076	0.107633	0.275746	0	1	1
ENSG00000263127	ENSG00000263127	RPL4P5	HSCHR9_1_CTG1:7491856-7493132	NOTEST	0	0	0	0	1	1
ENSG00000263128	ENSG00000263128	U6	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000263129	ENSG00000263129	OR5G3	HG151_NOVEL_TEST:56580405-56599054	NOTEST	0	0	0	0	1	1
ENSG00000263130	ENSG00000263130	RP11-216N14.8	HSCHR1_1_CTG31:153717773-153763786	NOTEST	0	0	0	0	1	1
ENSG00000263132	ENSG00000263132	U6	HG339_PATCH:97872503-97872608	NOTEST	0	0	0	0	1	1
ENSG00000263134	ENSG00000263134	CTD-2118P12.1	HSCHR5_3_CTG1:29152547-29181345	NOTEST	0	0	0	0	1	1
ENSG00000263137	ENSG00000263137	RP11-598F7.4	HSCHR12_1_CTG1:120779-236414	NOTEST	0	0	0	0	1	1
ENSG00000263138	ENSG00000263138	MEGF11	HSCHR15_1_CTG8:66187416-66558222	NOTEST	0	0	0	0	1	1
ENSG00000263140	ENSG00000263140	C21orf49	HSCHR21_3_CTG1_1:34144410-34271837	NOTEST	0	0	0	0	1	1
ENSG00000263141	ENSG00000263141	PAXBP1	HSCHR21_3_CTG1_1:34106209-34144169	NOTEST	0	0	0	0	1	1
ENSG00000263144	ENSG00000263144	U6	HSCHR19LRC_COX1_CTG1:54767576-54767685	NOTEST	0	0	0	0	1	1
ENSG00000263145	ENSG00000263145	KIR2DP1	HSCHR19LRC_COX1_CTG1:55173046-55218870	NOTEST	0	0	0	0	1	1
ENSG00000263146	ENSG00000263146	RP11-849I19.1	18:76736554-76739074	NOTEST	0	0	0	0	1	1
ENSG00000263147	ENSG00000263147	U6	HG989_PATCH:31970423-31970530	NOTEST	0	0	0	0	1	1
ENSG00000263148	ENSG00000263148	ATP2B3	HG1497_PATCH:152686147-152751411	NOTEST	0	0	0	0	1	1
ENSG00000263149	ENSG00000263149	AC009892.5	HSCHR19LRC_PGF1_CTG1:55006690-55072658	NOTEST	0	0	0	0	1	1
ENSG00000263150	ENSG00000263150	OR8J2	HG142_HG150_NOVEL_TEST:55978333-55979298	NOTEST	0	0	0	0	1	1
ENSG00000263151	ENSG00000263151	BCL7B	HG1257_PATCH:73001312-73022959	NOTEST	0	0	0	0	1	1
ENSG00000263152	ENSG00000263152	Y_RNA	HG115_PATCH:101980148-101980250	NOTEST	0	0	0	0	1	1
ENSG00000263153	ENSG00000263153	AC008984.7	HSCHR19LRC_COX1_CTG1:54812074-54816341	NOTEST	0	0	0	0	1	1
ENSG00000263154	ENSG00000263154	RP11-1055B8.2	17:79336071-79348014	NOTEST	0.300699	0.132433	-1.18306	0	1	1
ENSG00000263155	ENSG00000263155	MYZAP	15:57884105-58074960	NOTEST	0	0.0318926	inf	0	1	1
ENSG00000263156	ENSG00000263156	GNAI2	HG325_PATCH:50263723-50296787	NOTEST	0	0	0	0	1	1
ENSG00000263157	ENSG00000263157	AC008746.5	HSCHR19LRC_COX1_CTG1:54880209-54897417	NOTEST	0	0	0	0	1	1
ENSG00000263158	ENSG00000263158	TAS2R63P	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000263159	ENSG00000263159	RP11-462G12.4	16:4003387-4166186	NOTEST	0	0	0	0	1	1
ENSG00000263160	ENSG00000263160	TMEM50B	HSCHR21_4_CTG1_1:34757298-34861875	NOTEST	0	0	0	0	1	1
ENSG00000263162	ENSG00000263162	HERC2	HSCHR15_1_CTG4:28356185-28567298	NOTEST	0	0	0	0	1	1
ENSG00000263163	ENSG00000263163	SLC27A3	HSCHR1_1_CTG31:153764060-153769864	NOTEST	0	0	0	0	1	1
ENSG00000263164	ENSG00000263164	RP11-333E1.2	17:5095378-5151364	NOTEST	0	0.0999314	inf	0	1	1
ENSG00000263166	ENSG00000263166	CU457734.2	HSCHR19LRC_COX1_CTG1:54663834-54676909	NOTEST	0	0	0	0	1	1
ENSG00000263167	ENSG00000263167	RP11-149I9.2	17:79008947-79156964	NOTEST	0	0	0	0	1	1
ENSG00000263168	ENSG00000263168	NLRP7	HSCHR19LRC_LRC_J_CTG1:55459917-55537551	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263169	ENSG00000263169	RP11-1E11.1	HSCHR9_3_CTG35:90795583-90796324	NOTEST	0	0	0	0	1	1
ENSG00000263171	ENSG00000263171	RP11-542C16.1	17:7255207-7258263	NOTEST	0	0	0	0	1	1
ENSG00000263172	ENSG00000263172	5S_rRNA	HG185_PATCH:39873993-39890896	NOTEST	0	0	0	0	1	1
ENSG00000263173	ENSG00000263173	CTC-550B14.1	HSCHR19LRC_PGF1_CTG1:55405458-55406059	NOTEST	0	0	0	0	1	1
ENSG00000263174	ENSG00000263174	AC012314.20	HSCHR19LRC_PGF1_CTG1:54703311-54703829	NOTEST	0	0	0	0	1	1
ENSG00000263175	ENSG00000263175	KIR2DL2	HSCHR19LRC_PGF2_CTG1:55009654-55024167	NOTEST	0	0	0	0	1	1
ENSG00000263176	ENSG00000263176	RP11-893F2.15	17:48286332-48292781	NOTEST	0	0	0	0	1	1
ENSG00000263177	ENSG00000263177	RP11-433P17.2	16:3415098-3627401	NOTEST	0.234658	0.0417129	-2.49199	0	1	1
ENSG00000263179	ENSG00000263179	HNRNPCP4	16:11336509-11337409	NOTEST	0.0372534	0	#NAME?	0	1	1
ENSG00000263180	ENSG00000263180	VN1R104P	HSCHR19LRC_PGF2_CTG1:54830589-54831598	NOTEST	0	0	0	0	1	1
ENSG00000263181	ENSG00000263181	CYP2D7P	HSCHR22_1_CTG1:42524054-42528427	NOTEST	0	0	0	0	1	1
ENSG00000263182	ENSG00000263182	RP11-504P24.6	1:224183596-224198314	NOTEST	0.0441399	0.341838	2.95316	0	1	1
ENSG00000263183	ENSG00000263183	ARMC4P1	HSCHR10_1_CTG2:27547690-27577753	NOTEST	0	0	0	0	1	1
ENSG00000263184	ENSG00000263184	KIR3DL2	HSCHR19LRC_PGF1_CTG1:55157744-55300469	NOTEST	0	0	0	0	1	1
ENSG00000263185	ENSG00000263185	TEX2	HG183_PATCH:62224586-62340661	NOTEST	0	0	0	0	1	1
ENSG00000263186	ENSG00000263186	KRTAP16-1	HSCHR17_1_CTG4:39463951-39465505	NOTEST	0	0	0	0	1	1
ENSG00000263188	ENSG00000263188	CDH12P4	HSCHR5_1_CTG1:69575888-69576183	NOTEST	0	0	0	0	1	1
ENSG00000263189	ENSG00000263189	RP11-618P13.1	17:52030296-52032685	NOTEST	0	0	0	0	1	1
ENSG00000263190	ENSG00000263190	MIR590	HG1257_PATCH:73639201-73662058	NOTEST	0	0	0	0	1	1
ENSG00000263191	ENSG00000263191	RN7SL625P	HG1257_PATCH:72306395-72306684	NOTEST	0	0	0	0	1	1
ENSG00000263192	ENSG00000263192	CCDC84	HG299_PATCH:118868851-118901597	NOTEST	0	0	0	0	1	1
ENSG00000263194	ENSG00000263194	THEM6	HG418_PATCH:143808563-143818288	NOTEST	0	0	0	0	1	1
ENSG00000263196	ENSG00000263196	CTD-2318B16.3	16:10817280-10817623	NOTEST	0	0	0	0	1	1
ENSG00000263197	ENSG00000263197	CHCHD2P2	HSCHR5_1_CTG1:68629687-68630008	NOTEST	0	0	0	0	1	1
ENSG00000263198	ENSG00000263198	RP11-517A5.4	16:16326351-16388668	NOTEST	0	0	0	0	1	1
ENSG00000263199	ENSG00000263199	RP11-372K20.1	17:52780296-52780791	NOTEST	0	0	0	0	1	1
ENSG00000263201	ENSG00000263201	CTC-479C5.6	16:68021296-68272005	NOTEST	0	0	0	0	1	1
ENSG00000263202	ENSG00000263202	AC012314.19	HSCHR19LRC_PGF1_CTG1:54704600-54752858	NOTEST	0	0	0	0	1	1
ENSG00000263204	ENSG00000263204	RP11-1437A8.7	16:33287357-33287592	NOTEST	0	0	0	0	1	1
ENSG00000263206	ENSG00000263206	KYNUP3	17:19107137-19117358	NOTEST	0	0	0	0	1	1
ENSG00000263207	ENSG00000263207	RP11-26L20.4	16:55293880-55367500	NOTEST	0.0336084	0	#NAME?	0	1	1
ENSG00000263208	ENSG00000263208	KIR2DL1	HSCHR19LRC_COX1_CTG1:55173046-55218870	NOTEST	0	0	0	0	1	1
ENSG00000263209	ENSG00000263209	OR8K2P	HG142_HG150_NOVEL_TEST:56102617-56103544	NOTEST	0	0	0	0	1	1
ENSG00000263211	ENSG00000263211	OR2Z1	HG729_PATCH:8795837-8796893	NOTEST	0	0	0	0	1	1
ENSG00000263212	ENSG00000263212	LA16c-306E5.3	16:3415098-3627401	NOTEST	0	0.309976	inf	0	1	1
ENSG00000263213	ENSG00000263213	PHBP5	HG1257_PATCH:72619901-72670574	NOTEST	0	0	0	0	1	1
ENSG00000263214	ENSG00000263214	ZNF205-AS1	16:3160460-3192806	NOTEST	0.158306	0.0222704	-2.82951	0	1	1
ENSG00000263216	ENSG00000263216	AC009892.10	HSCHR19LRC_COX1_CTG1:55008196-55074165	NOTEST	0	0	0	0	1	1
ENSG00000263218	ENSG00000263218	CTD-2561B21.7	17:78965397-78983317	NOTEST	0	0	0	0	1	1
ENSG00000263219	ENSG00000263219	RYKP1	17:4046461-4167274	NOTEST	0.00947759	0.0207068	1.12751	0	1	1
ENSG00000263220	ENSG00000263220	RP11-420A6.2	17:5185557-5372380	NOTEST	0.0436067	0.0618549	0.504338	0	1	1
ENSG00000263221	ENSG00000263221	LILRP1	HSCHR19LRC_PGF1_CTG1:55130119-55134419	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263222	ENSG00000263222	CU457734.3	HSCHR19LRC_COX1_CTG1:54777977-54784721	NOTEST	0	0	0	0	1	1
ENSG00000263224	ENSG00000263224	AC010492.4	HSCHR19LRC_PGF1_CTG1:54704600-54752858	NOTEST	0	0	0	0	1	1
ENSG00000263225	ENSG00000263225	SEBOX	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000263226	ENSG00000263226	CLIP2	HG1257_PATCH:73754431-73870900	NOTEST	0	0	0	0	1	1
ENSG00000263227	ENSG00000263227	AC005077.14	HG1257_PATCH:75536425-75539920	NOTEST	0	0	0	0	1	1
ENSG00000263228	ENSG00000263228	RP11-44D15.6	HG339_PATCH:97889471-98031303	NOTEST	0	0	0	0	1	1
ENSG00000263229	ENSG00000263229	KRTAP4-11	HSCHR17_4_CTG4:39273914-39275094	NOTEST	0	0	0	0	1	1
ENSG00000263231	ENSG00000263231	RP11-263K19.8	HSCHR1_2_CTG31:155199567-155204076	NOTEST	0	0	0	0	1	1
ENSG00000263232	ENSG00000263232	ATP5A1P3	16:72038935-72040442	NOTEST	0	0	0	0	1	1
ENSG00000263233	ENSG00000263233	KIR2DS2	HSCHR19LRC_LRC_I_CTG1:55250099-55264425	NOTEST	0	0	0	0	1	1
ENSG00000263234	ENSG00000263234	CTD-2135D7.3	16:14047011-14048682	NOTEST	0	0	0	0	1	1
ENSG00000263235	ENSG00000263235	RP11-461A8.4	16:3661728-3767598	NOTEST	0.33441	0.318233	-0.0715355	0	1	1
ENSG00000263236	ENSG00000263236	KRTAP4-12	HSCHR17_4_CTG4:39279810-39280887	NOTEST	0	0	0	0	1	1
ENSG00000263237	ENSG00000263237	RP11-429K17.1	16:20370491-20416059	NOTEST	0	0	0	0	1	1
ENSG00000263238	ENSG00000263238	CTSO	HSCHR4_1_CTG12:156845269-156875063	NOTEST	0	0	0	0	1	1
ENSG00000263239	ENSG00000263239	GP6	HSCHR19LRC_LRC_T_CTG1:55453443-55518542	NOTEST	0	0	0	0	1	1
ENSG00000263240	ENSG00000263240	AC009414.1	HSCHR2_1_CTG1:36526530-36526973	NOTEST	0	0	0	0	1	1
ENSG00000263241	ENSG00000263241	RP11-109M19.4	16:10812489-10813619	NOTEST	0	0	0	0	1	1
ENSG00000263242	ENSG00000263242	KRTAP1-4	HSCHR17_4_CTG4:39186075-39186483	NOTEST	0	0	0	0	1	1
ENSG00000263243	ENSG00000263243	KRT12	HSCHR17_4_CTG4:39007051-39023462	NOTEST	0	0	0	0	1	1
ENSG00000263247	ENSG00000263247	PRR4	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000263249	ENSG00000263249	ZNF430	HSCHR19_1_CTG3:21209841-21223406	NOTEST	0	0	0	0	1	1
ENSG00000263251	ENSG00000263251	LILRP1	HSCHR19LRC_COX1_CTG1:55131486-55135787	NOTEST	0	0	0	0	1	1
ENSG00000263252	ENSG00000263252	RP11-146P2.1	17:51430787-51431495	NOTEST	0	0	0	0	1	1
ENSG00000263253	ENSG00000263253	RP11-204E4.3	16:20220246-20220847	NOTEST	0	0	0	0	1	1
ENSG00000263254	ENSG00000263254	FZD9	HG1257_PATCH:72898735-72901077	NOTEST	0	0	0	0	1	1
ENSG00000263255	ENSG00000263255	ZNF486	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000263257	ENSG00000263257	RP11-65J21.4	16:14501895-14512729	NOTEST	0.0363203	0.0257322	-0.497199	0	1	1
ENSG00000263258	ENSG00000263258	RDH13	HSCHR19LRC_PGF1_CTG1:55437861-55502960	NOTEST	0	0	0	0	1	1
ENSG00000263259	ENSG00000263259	AL035045.2	HSCHR20_1_CTG1:17823226-17823372	NOTEST	0	0	0	0	1	1
ENSG00000263260	ENSG00000263260	KIR2DP1	HSCHR19LRC_PGF1_CTG1:55157744-55300469	NOTEST	0	0	0	0	1	1
ENSG00000263261	ENSG00000263261	ALG9-IT1	HG388_HG400_PATCH:111652918-111756698	NOTEST	0	0	0	0	1	1
ENSG00000263262	ENSG00000263262	AC008746.9	HSCHR19LRC_PGF1_CTG1:54955334-54955643	NOTEST	0	0	0	0	1	1
ENSG00000263263	ENSG00000263263	KRTAP9-6	HSCHR17_6_CTG4:39410220-39411523	NOTEST	0	0	0	0	1	1
ENSG00000263264	ENSG00000263264	CTB-133G6.1	19:7413847-7537363	NOTEST	0.0408599	0.00752959	-2.44004	0	1	1
ENSG00000263266	ENSG00000263266	RPS7P1	HG883_PATCH:26782770-26941216	NOTEST	0	0	0	0	1	1
ENSG00000263267	ENSG00000263267	RP11-1260E13.4	HSCHR17_1_CTG1:62292-253878	NOTEST	0	0	0	0	1	1
ENSG00000263270	ENSG00000263270	RP11-725M22.1	HSCHR4_1_CTG6:34659227-34671054	NOTEST	0	0	0	0	1	1
ENSG00000263271	ENSG00000263271	RP11-1055B8.8	17:79369274-79433357	NOTEST	0	0	0	0	1	1
ENSG00000263273	ENSG00000263273	WI2-87327B8.1	HG506_HG507_HG1000_PATCH:61150645-61152563	NOTEST	0	0	0	0	1	1
ENSG00000263274	ENSG00000263274	GNG5P3	HG388_HG400_PATCH:111652918-111756698	NOTEST	0	0	0	0	1	1

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ENSG00000263276	ENSG00000263276	RP11-96D1.10	16:68021296-68272005	NOTEST	0.0278351	0.0792045	1.50868	0	1	1
ENSG00000263277	ENSG00000263277	RP11-293B20.3	16:33379961-33380091	NOTEST	0	0	0	0	1	1
ENSG00000263278	ENSG00000263278	CH17-351M24.1	HG748_PATCH:77594113-77600003	NOTEST	0	0	0	0	1	1
ENSG00000263279	ENSG00000263279	RP11-109M19.1	16:10721357-10788802	NOTEST	0	0	0	0	1	1
ENSG00000263280	ENSG00000263280	LA16c-325D7.2	16:2916348-2917619	NOTEST	0.14028	0.116812	-0.26412	0	1	1
ENSG00000263282	ENSG00000263282	AC005086.8	HG115_PATCH:101459218-101927238	NOTEST	0	0	0	0	1	1
ENSG00000263283	ENSG00000263283	RP11-1E11.2	HSCHR9_3_CTG35:90802649-90805117	NOTEST	0	0	0	0	1	1
ENSG00000263285	ENSG00000263285	U7	HG306_PATCH:112830001-113149158	NOTEST	0	0	0	0	1	1
ENSG00000263290	ENSG00000263290	SCAMP3	HSCHR1_2_CTG31:155241173-155247625	NOTEST	0	0	0	0	1	1
ENSG00000263291	ENSG00000263291	RP11-735A19.5	HG348_PATCH:94773580-94774736	NOTEST	0	0	0	0	1	1
ENSG00000263293	ENSG00000263293	RP11-290H9.4	17:45331211-45518678	NOTEST	0.0816185	0.295923	1.85825	0	1	1
ENSG00000263294	ENSG00000263294	AC004851.2	HG1257_PATCH:73918746-74067561	NOTEST	0	0	0	0	1	1
ENSG00000263295	ENSG00000263295	EPS8L1	HSCHR19LRC_COX1_CTG1:55504304-55520208	NOTEST	0	0	0	0	1	1
ENSG00000263296	ENSG00000263296	KRTAP3-2	HSCHR17_4_CTG4:39155571-39156273	NOTEST	0	0	0	0	1	1
ENSG00000263297	ENSG00000263297	RP11-195E11.3	HSCHR9_2_CTG35:72659113-72847028	NOTEST	0	0	0	0	1	1
ENSG00000263298	ENSG00000263298	ABCB11	HSCHR2_1_CTG12:169796436-169904821	NOTEST	0	0	0	0	1	1
ENSG00000263299	ENSG00000263299	RP11-548B3.3	HSCHR9_1_CTG35:72051358-72051832	NOTEST	0	0	0	0	1	1
ENSG00000263300	ENSG00000263300	RP5-1029F21.4	17:406410-624957	NOTEST	0	0	0	0	1	1
ENSG00000263301	ENSG00000263301	RP11-104H15.8	17:7323421-7361026	NOTEST	0.0923152	0.321639	1.8008	0	1	1
ENSG00000263302	ENSG00000263302	TAF9	HSCHR5_1_CTG1:68646821-68710869	NOTEST	0	0	0	0	1	1
ENSG00000263303	ENSG00000263303	LAIR1	HSCHR19LRC_PGF2_CTG1:54864473-54875961	NOTEST	0	0	0	0	1	1
ENSG00000263304	ENSG00000263304	MILR1	HG183_PATCH:62526396-62546003	NOTEST	0	0	0	0	1	1
ENSG00000263305	ENSG00000263305	AP005530.2	18:11102-16898	NOTEST	0	0	0	0	1	1
ENSG00000263307	ENSG00000263307	RP11-166B2.8	16:11945505-12009939	NOTEST	0.0380003	0.0861072	1.18012	0	1	1
ENSG00000263308	ENSG00000263308	5S_rRNA	HG1032_PATCH:190938850-190938969	NOTEST	0	0	0	0	1	1
ENSG00000263309	ENSG00000263309	KRT23	HSCHR17_4_CTG4:39077681-39132305	NOTEST	0	0	0	0	1	1
ENSG00000263310	ENSG00000263310	SALL3	HSCHR18_2_CTG2_1:76740274-76762678	NOTEST	0	0	0	0	1	1
ENSG00000263311	ENSG00000263311	RP11-498D10.8	16:72038137-72038702	NOTEST	0	0	0	0	1	1
ENSG00000263312	ENSG00000263312	RP11-459C13.1	17:3880396-3885193	NOTEST	0	0	0	0	1	1
ENSG00000263313	ENSG00000263313	MMP3	HG305_PATCH:102617698-102714534	NOTEST	0	0	0	0	1	1
ENSG00000263314	ENSG00000263314	AP000302.58	HSCHR21_4_CTG1_1:34864362-34866122	NOTEST	0	0	0	0	1	1
ENSG00000263315	ENSG00000263315	U6	HG75_PATCH:34732196-34732303	NOTEST	0	0	0	0	1	1
ENSG00000263316	ENSG00000263316	RP11-530N7.3	17:6757179-6922978	NOTEST	0	0	0	0	1	1
ENSG00000263317	ENSG00000263317	RP11-429O1.1	17:50467874-50613061	NOTEST	0	0.0837858	inf	0	1	1
ENSG00000263321	ENSG00000263321	RP11-388C12.5	17:80674558-80692019	NOTEST	0	0.291662	inf	0	1	1
ENSG00000263322	ENSG00000263322	CTD-2541J13.1	HSCHR18_2_CTG2:65218479-65221652	NOTEST	0	0	0	0	1	1
ENSG00000263323	ENSG00000263323	U73166.2	HG325_PATCH:50297734-50300790	NOTEST	0	0	0	0	1	1
ENSG00000263324	ENSG00000263324	HCN3	HSCHR1_2_CTG31:155248062-155286629	NOTEST	0	0	0	0	1	1
ENSG00000263325	ENSG00000263325	LA16c-325D7.1	16:2902727-2909727	NOTEST	0	0	0	0	1	1
ENSG00000263326	ENSG00000263326	RP11-266L9.6	16:25082810-25084048	NOTEST	0.0294147	0.0436895	0.570748	0	1	1

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ENSG00000263327	ENSG00000263327	TAPT1-AS1	4:16162127-16321763	NOTEST	0.434055	0.312346	-0.474733	0	1	1
ENSG00000263328	ENSG00000263328	OR8K1	HG142_HG150_NOVEL_TEST:56113420-56114507	NOTEST	0	0	0	0	1	1
ENSG00000263329	ENSG00000263329	hsa-mir-548o	HG115_PATCH:102007151-102069956	NOTEST	0	0	0	0	1	1
ENSG00000263330	ENSG00000263330	RP11-1264N5.1	HSCHR5_1_CTG1:69359869-69430017	NOTEST	0	0	0	0	1	1
ENSG00000263331	ENSG00000263331	CTC-508F8.1	16:20944432-21191937	NOTEST	0	0	0	0	1	1
ENSG00000263332	ENSG00000263332	RPS9	HSCHR19LRC_PGF1_CTG1:54704600-54752858	NOTEST	0	0	0	0	1	1
ENSG00000263334	ENSG00000263334	HIP1	HG1257_PATCH:74998256-75203919	NOTEST	0	0	0	0	1	1
ENSG00000263335	ENSG00000263335	AF001548.5	16:15737123-15950890	NOTEST	0.330362	0.480306	0.539907	0	1	1
ENSG00000263336	ENSG00000263336	RP11-846E15.1	HSCHR5_1_CTG1:69050903-69144625	NOTEST	0	0	0	0	1	1
ENSG00000263337	ENSG00000263337	RP11-1277H1.3	16:33202881-33264727	NOTEST	0	0	0	0	1	1
ENSG00000263338	ENSG00000263338	RP11-235E17.3	17:3468737-3539616	NOTEST	0.0381966	0	#NAME?	0	1	1
ENSG00000263340	ENSG00000263340	RPL41P2	HSCHR15_1_CTG4:28356185-28567298	NOTEST	0	0	0	0	1	1
ENSG00000263341	ENSG00000263341	KRTAP17-1	HSCHR17_1_CTG4:39471168-39471947	NOTEST	0	0	0	0	1	1
ENSG00000263342	ENSG00000263342	RP1-4G17.2	17:7184985-7197934	NOTEST	0	0	0	0	1	1
ENSG00000263343	ENSG00000263343	RP11-388M20.7	16:31176968-31177248	NOTEST	0	0	0	0	1	1
ENSG00000263344	ENSG00000263344	EIF4H	HG1257_PATCH:73639201-73662058	NOTEST	0	0	0	0	1	1
ENSG00000263346	ENSG00000263346	RP11-60C6.9	HG348_PATCH:94745022-94745697	NOTEST	0	0	0	0	1	1
ENSG00000263347	ENSG00000263347	RP11-498B4.6	HG311_PATCH:118423207-118502086	NOTEST	0	0	0	0	1	1
ENSG00000263349	ENSG00000263349	AC145141.1	HSCHR5_1_CTG1:69863006-69957699	NOTEST	0	0	0	0	1	1
ENSG00000263350	ENSG00000263350	RP11-13N13.2	18:19192227-19213485	NOTEST	0.522921	0.395199	-0.404014	0	1	1
ENSG00000263351	ENSG00000263351	MIR4329	X:112017730-112084043	NOTEST	0	0	0	0	1	1
ENSG00000263353	ENSG00000263353	PPIAL4A	HG1292_PATCH:121432368-121433153	NOTEST	0	0	0	0	1	1
ENSG00000263354	ENSG00000263354	MIR5011	18:64748820-64748923	NOTEST	0	0	0	0	1	1
ENSG00000263355	ENSG00000263355	AKR1B10P2	18:66123187-66124114	NOTEST	0	0	0	0	1	1
ENSG00000263357	ENSG00000263357	AL133167.1	14:96317817-96317927	NOTEST	0	0	0	0	1	1
ENSG00000263358	ENSG00000263358	SNORD83	HSCHR6_MHC_SSTO:31486440-31504572	NOTEST	0	0	0	0	1	1
ENSG00000263359	ENSG00000263359	SNORD83	HSCHR6_MHC_COX:31483951-31502076	NOTEST	0	0	0	0	1	1
ENSG00000263360	ENSG00000263360	RN7SL134P	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000263361	ENSG00000263361	MIR378H	5:154198050-154256353	NOTEST	0	0	0	0	1	1
ENSG00000263362	ENSG00000263362	SNORD52	HSCHR6_MHC_COX:31789756-31794910	NOTEST	0	0	0	0	1	1
ENSG00000263363	ENSG00000263363	MIR5702	2:227523425-227523509	NOTEST	0	0	0	0	1	1
ENSG00000263364	ENSG00000263364	AC021052.1	12:96816103-96879220	NOTEST	0	0	0	0	1	1
ENSG00000263365	ENSG00000263365	AC123788.1	11:3357950-3400448	NOTEST	0	0	0	0	1	1
ENSG00000263366	ENSG00000263366	ABHD17AP1	HG1287_PATCH:148788460-148838605	NOTEST	0	0	0	0	1	1
ENSG00000263367	ENSG00000263367	U6	HSCHR6_MHC_MANN:31095735-31095835	NOTEST	0	0	0	0	1	1
ENSG00000263368	ENSG00000263368	RP11-720N19.1	17:25783669-25976586	NOTEST	0	0	0	0	1	1
ENSG00000263369	ENSG00000263369	RP11-640N20.9	17:30433348-30441144	NOTEST	0	0	0	0	1	1
ENSG00000263370	ENSG00000263370	RP11-68I3.5	17:27887564-28513493	NOTEST	0	0.104938	inf	0	1	1
ENSG00000263371	ENSG00000263371	AP000673.1	11:105480720-105852819	NOTEST	0	0	0	0	1	1
ENSG00000263372	ENSG00000263372	MIR548AO	8:41119480-41167016	NOTEST	0	0	0	0	1	1
ENSG00000263374	ENSG00000263374	RNVU1-11	HG1287_PATCH:149074904-149075066	NOTEST	0	0	0	0	1	1
ENSG00000263375	ENSG00000263375	RP11-822E23.5	17:21496059-21497446	NOTEST	0	0	0	0	1	1
ENSG00000263376	ENSG00000263376	HIST2H2BF	HG1287_PATCH:150469085-150498788	NOTEST	0	0	0	0	1	1
ENSG00000263377	ENSG00000263377	AL121875.1	X:139486263-139486355	NOTEST	0	0	0	0	1	1

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ENSG00000263378	ENSG00000263378	AC019205.1	6:73918805-74020088	NOTEST	0	0	0	0	1	1
ENSG00000263379	ENSG00000263379	RNU1-143P	HG1287_PATCH:144476424-144478755	NOTEST	0	0	0	0	1	1
ENSG00000263380	ENSG00000263380	AC096534.1	1:61330930-61928465	NOTEST	0	0	0	0	1	1
ENSG00000263381	ENSG00000263381	MIR5584	1:44870865-45140227	NOTEST	0	0	0	0	1	1
ENSG00000263382	ENSG00000263382	RP11-552O4.1	18:24034873-24770662	NOTEST	0	0	0	0	1	1
ENSG00000263383	ENSG00000263383	AC005549.1	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000263384	ENSG00000263384	AL354732.1	1:170338363-170339508	NOTEST	0	0	0	0	1	1
ENSG00000263385	ENSG00000263385	AC092798.1	3:25760434-25836025	NOTEST	0	0	0	0	1	1
ENSG00000263386	ENSG00000263386	RN7SL358P	4:585358-585697	NOTEST	0	0	0	0	1	1
ENSG00000263387	ENSG00000263387	RP4-704D21.2	HG1287_PATCH:147688345-147690033	NOTEST	0	0	0	0	1	1
ENSG00000263388	ENSG00000263388	CTC-297N7.10	17:10583653-10718481	NOTEST	0	0	0	0	1	1
ENSG00000263389	ENSG00000263389	MIR3973	11:35965530-36253686	NOTEST	0	0	0	0	1	1
ENSG00000263390	ENSG00000263390	MIR3119-1	1:170115141-170136931	NOTEST	0	0	0	0	1	1
ENSG00000263391	ENSG00000263391	AL512428.1	6:24797548-25057301	NOTEST	0	0	0	0	1	1
ENSG00000263392	ENSG00000263392	AC084262.2	8:29171272-29171365	NOTEST	0	0	0	0	1	1
ENSG00000263393	ENSG00000263393	RP11-53I6.4	18:29598334-30050447	NOTEST	0.0721323	0	#NAME?	0	1	1
ENSG00000263394	ENSG00000263394	RP11-160E2.19	17:18994381-18995138	NOTEST	0	0	0	0	1	1
ENSG00000263395	ENSG00000263395	AC093844.1	4:184305705-184305773	NOTEST	0	0	0	0	1	1
ENSG00000263396	ENSG00000263396	RP11-288C17.3	18:1254383-1408345	NOTEST	0	0	0	0	1	1
ENSG00000263397	ENSG00000263397	MIR5196	19:35810163-35838258	NOTEST	0	0	0	0	1	1
ENSG00000263398	ENSG00000263398	RP11-666A1.5	HG1287_PATCH:145104537-145105671	NOTEST	0	0	0	0	1	1
ENSG00000263399	ENSG00000263399	MIR3170	13:98794815-99102027	NOTEST	0	0	0	0	1	1
ENSG00000263400	ENSG00000263400	CTC-297N7.5	17:10583653-10718481	NOTEST	0	0.0299739	inf	0	1	1
ENSG00000263401	ENSG00000263401	AC008674.1	5:173134616-173173214	NOTEST	0	0	0	0	1	1
ENSG00000263402	ENSG00000263402	Metazoa_SRP	HSCHR6_MHC_MANN:30919336-30919595	NOTEST	0	0	0	0	1	1
ENSG00000263403	ENSG00000263403	MIR4673	9:139388895-139440314	NOTEST	0	0	0	0	1	1
ENSG00000263404	ENSG00000263404	AL158154.1	9:84420910-84420996	NOTEST	0	0	0	0	1	1
ENSG00000263405	ENSG00000263405	PA2G4P3	18:24916342-25175128	NOTEST	0	0	0	0	1	1
ENSG00000263406	ENSG00000263406	RN7SL821P	3:53317446-53381654	NOTEST	0	0.123001	inf	0	1	1
ENSG00000263407	ENSG00000263407	MIR4660	8:8859656-8974256	NOTEST	0	0	0	0	1	1
ENSG00000263409	ENSG00000263409	MIR4747	19:4903091-4962165	NOTEST	0	0	0	0	1	1
ENSG00000263410	ENSG00000263410	RN7SL460P	X:77081860-77151090	NOTEST	0	0	0	0	1	1
ENSG00000263411	ENSG00000263411	MIR4723	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000263412	ENSG00000263412	RP5-890E16.2	17:46122502-46125435	NOTEST	0.535522	0.621431	0.21465	0	1	1
ENSG00000263413	ENSG00000263413	AL928742.1	14:106056272-106056350	NOTEST	0	0	0	0	1	1
ENSG00000263414	ENSG00000263414	MIR3187	19:812517-821967	NOTEST	0	0	0	0	1	1
ENSG00000263415	ENSG00000263415	AC021760.1	8:13947372-15095848	NOTEST	0	0	0	0	1	1
ENSG00000263416	ENSG00000263416	AC006145.1	7:81549518-81549586	NOTEST	0	0	0	0	1	1
ENSG00000263417	ENSG00000263417	GTSCR1	18:68297754-68317980	NOTEST	0	0	0	0	1	1
ENSG00000263418	ENSG00000263418	5S_rRNA	HSCHR6_MHC_MANN:32072021-32105429	NOTEST	0	0	0	0	1	1
ENSG00000263419	ENSG00000263419	RN7SL257P	HSCHR6_MHC_COX:28941850-28942146	NOTEST	0	0	0	0	1	1
ENSG00000263421	ENSG00000263421	MIR4687	11:3875547-4114439	NOTEST	0	0	0	0	1	1
ENSG00000263422	ENSG00000263422	AC005702.1	17:58119721-58119803	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263423	ENSG00000263423	CR936913.1	HSCHR6_MHC_APD:32885992-32904491	NOTEST	0	0	0	0	1	1
ENSG00000263424	ENSG00000263424	CTD-2541J13.2	18:65173818-65566856	NOTEST	0.0659979	0.0671056	0.024014	0	1	1
ENSG00000263425	ENSG00000263425	AC131011.1	X:23720369-23784592	NOTEST	0	0	0	0	1	1
ENSG00000263426	ENSG00000263426	RN7SL471P	6:28945251-28945547	NOTEST	0	0.265942	inf	0	1	1
ENSG00000263427	ENSG00000263427	RP11-599B13.3	17:7959542-7960939	NOTEST	0	0	0	0	1	1
ENSG00000263428	ENSG00000263428	AKR1C5P	HG871_PATCH:5164278-5177418	NOTEST	0	0	0	0	1	1
ENSG00000263429	ENSG00000263429	LINC00675	17:10583653-10718481	NOTEST	0	0	0	0	1	1
ENSG00000263430	ENSG00000263430	Metazoa_SRP	HSCHR6_MHC_SSTO:28894770-28895052	NOTEST	0	0	0	0	1	1
ENSG00000263431	ENSG00000263431	CH17-76K2.4	HG1293_PATCH:206567508-206568017	NOTEST	0	0	0	0	1	1
ENSG00000263432	ENSG00000263432	RN7SL689P	5:122179133-122390362	NOTEST	0.11761	0.369283	1.65071	0	1	1
ENSG00000263433	ENSG00000263433	RP11-260A9.1	17:25308719-25309116	NOTEST	0	0	0	0	1	1
ENSG00000263435	ENSG00000263435	RP11-17M24.2	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000263436	ENSG00000263436	MIR3158-2	10:103330316-103369425	NOTEST	0	0	0	0	1	1
ENSG00000263437	ENSG00000263437	AC020892.1	15:51706293-51915030	NOTEST	0	0	0	0	1	1
ENSG00000263438	ENSG00000263438	RP11-202D1.3	18:51094816-51124221	NOTEST	0	0	0	0	1	1
ENSG00000263439	ENSG00000263439	MIR4753	1:235294497-235507847	NOTEST	0	0	0	0	1	1
ENSG00000263440	ENSG00000263440	TUBAL3	HG871_PATCH:5435289-5447022	NOTEST	0	0	0	0	1	1
ENSG00000263441	ENSG00000263441	AC012181.1	16:56991176-56991273	NOTEST	0	0	0	0	1	1
ENSG00000263442	ENSG00000263442	SNORD83	HSCHR6_MHC_SSTO:31486440-31504572	NOTEST	0	0	0	0	1	1
ENSG00000263443	ENSG00000263443	RP11-973F15.2	8:123712507-123715662	NOTEST	0	0	0	0	1	1
ENSG00000263445	ENSG00000263445	MIR4450	4:77356252-77723117	NOTEST	0	0	0	0	1	1
ENSG00000263446	ENSG00000263446	RP11-403I13.4	HG1287_PATCH:144431294-144457279	NOTEST	0	0	0	0	1	1
ENSG00000263447	ENSG00000263447	AC079117.3	2:76974844-77820445	NOTEST	0	0	0	0	1	1
ENSG00000263448	ENSG00000263448	AL133410.1	9:35792150-35812269	NOTEST	0	0	0	0	1	1
ENSG00000263449	ENSG00000263449	AC021887.1	12:86041030-86041098	NOTEST	0	0	0	0	1	1
ENSG00000263450	ENSG00000263450	RP11-680N20.1	18:30413416-31021065	NOTEST	0	0	0	0	1	1
ENSG00000263451	ENSG00000263451	RNVU1-8	HG1287_PATCH:147705750-147810940	NOTEST	0	0	0	0	1	1
ENSG00000263452	ENSG00000263452	AL121899.1	20:2082256-2157684	NOTEST	0	0	0	0	1	1
ENSG00000263453	ENSG00000263453	MIR4532	20:56470449-56470500	NOTEST	0	0	0	0	1	1
ENSG00000263455	ENSG00000263455	AC011841.8	GL000205.1:168184-168260	NOTEST	0	0	0	0	1	1
ENSG00000263456	ENSG00000263456	MIR5189	16:88519724-88603424	NOTEST	0	0	0	0	1	1
ENSG00000263457	ENSG00000263457	AC079804.2	7:6918175-6918263	NOTEST	0	0	0	0	1	1
ENSG00000263458	ENSG00000263458	MIR4455	4:185859536-185859594	NOTEST	0	0	0	0	1	1
ENSG00000263459	ENSG00000263459	AL359552.1	9:110195820-110195890	NOTEST	0	0	0	0	1	1
ENSG00000263460	ENSG00000263460	RP11-838N2.8	18:3411605-3458409	NOTEST	0	0	0	0	1	1
ENSG00000263461	ENSG00000263461	PIAS3	HG1287_PATCH:146532043-146546251	NOTEST	0	0	0	0	1	1
ENSG00000263462	ENSG00000263462	MIR4750	19:50372294-50392005	NOTEST	0	0	0	0	1	1
ENSG00000263463	ENSG00000263463	MIR378I	22:42319225-42319301	NOTEST	0	0	0	0	1	1
ENSG00000263464	ENSG00000263464	PPIAL4G	HG1287_PATCH:149169082-149169742	NOTEST	0	0	0	0	1	1
ENSG00000263465	ENSG00000263465	RP11-735A19.4	HG348_PATCH:94800156-94801323	NOTEST	0	0	0	0	1	1
ENSG00000263466	ENSG00000263466	RP1-56K13.2	17:37026111-37078023	NOTEST	0.104865	0.0435296	-1.26846	0	1	1
ENSG00000263467	ENSG00000263467	U6	HSCHR6_MHC_DBB:31044568-31044668	NOTEST	0	0	0	0	1	1
ENSG00000263468	ENSG00000263468	MIR3130-1	2:207602486-207657233	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263469	ENSG00000263469	RP11-495P10.9	HG1287_PATCH:14897441-148975366	NOTEST	0	0	0	0	1	1
ENSG00000263471	ENSG00000263471	AHCYP1	HG1211_PATCH:46718590-46719863	NOTEST	0	0	0	0	1	1
ENSG00000263472	ENSG00000263472	RN7SL576P	17:26029937-26030241	NOTEST	0	0	0	0	1	1
ENSG00000263473	ENSG00000263473	MIR548O2	20:37101458-37207504	NOTEST	0	0	0	0	1	1
ENSG00000263474	ENSG00000263474	U6	HSCHR6_MHC_MCF:31129314-31129414	NOTEST	0	0	0	0	1	1
ENSG00000263475	ENSG00000263475	AL353805.1	9:103157933-103158007	NOTEST	0	0	0	0	1	1
ENSG00000263476	ENSG00000263476	MIR3156-1	10:45493145-45676875	NOTEST	0	0	0	0	1	1
ENSG00000263477	ENSG00000263477	RP11-338L22.2	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000263478	ENSG00000263478	RN7SL439P	5:154083076-154083344	NOTEST	0	0	0	0	1	1
ENSG00000263479	ENSG00000263479	RN7SL509P	6:97362576-97362871	NOTEST	0	0	0	0	1	1
ENSG00000263480	ENSG00000263480	SYT15	HG1211_PATCH:47073664-47147473	NOTEST	0	0	0	0	1	1
ENSG00000263481	ENSG00000263481	AL603766.1	6:149497842-149497930	NOTEST	0	0	0	0	1	1
ENSG00000263482	ENSG00000263482	ANTXRLP1	HG1211_PATCH:46729422-46769005	NOTEST	0	0	0	0	1	1
ENSG00000263483	ENSG00000263483	MTATP6P3	17:22029259-22029935	NOTEST	0	0	0	0	1	1
ENSG00000263484	ENSG00000263484	RNA5SP315	HG1211_PATCH:48454690-48454806	NOTEST	0	0	0	0	1	1
ENSG00000263485	ENSG00000263485	CTC-304I17.4	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000263486	ENSG00000263486	snoU13	HG1287_PATCH:150944188-150951476	NOTEST	0	0	0	0	1	1
ENSG00000263487	ENSG00000263487	MIR335	HG1308_PATCH:130126045-130351086	NOTEST	0	0	0	0	1	1
ENSG00000263488	ENSG00000263488	RN7SL301P	17:34437542-34437838	NOTEST	0	0	0	0	1	1
ENSG00000263489	ENSG00000263489	CTC-264K15.6	17:62050279-62066782	NOTEST	0	0	0	0	1	1
ENSG00000263490	ENSG00000263490	RN7SL155P	19:18742458-18742718	NOTEST	0	0	0	0	1	1
ENSG00000263491	ENSG00000263491	Metazoa_SRP	HSCHR6_MHC_DBB:28945265-28945561	NOTEST	0	0	0	0	1	1
ENSG00000263493	ENSG00000263493	RN7SL94P	19:9920942-9938492	NOTEST	0	0	0	0	1	1
ENSG00000263494	ENSG00000263494	AC004702.2	17:19912656-20306870	NOTEST	0	0	0	0	1	1
ENSG00000263495	ENSG00000263495	U8	HG871_PATCH:5077545-5149878	NOTEST	0	0	0	0	1	1
ENSG00000263496	ENSG00000263496	RP11-638L3.1	HSCHR18_2_CTG2:65243267-65636305	NOTEST	0	0	0	0	1	1
ENSG00000263497	ENSG00000263497	AL109844.1	1:143876890-143876982	NOTEST	0	0	0	0	1	1
ENSG00000263498	ENSG00000263498	RP11-38J22.2	HG1293_PATCH:206224447-206224837	NOTEST	0	0	0	0	1	1
ENSG00000263499	ENSG00000263499	RP11-118E18.4	17:55333211-55762046	NOTEST	0	0.0279167	inf	0	1	1
ENSG00000263501	ENSG00000263501	RP11-269G24.2	17:61086916-61509572	NOTEST	0	0.0918119	inf	0	1	1
ENSG00000263502	ENSG00000263502	AC134878.2	Y:13340358-13340440	NOTEST	0	0	0	0	1	1
ENSG00000263503	ENSG00000263503	RP11-707O23.5	17:43678234-43679706	NOTEST	0.194972	0.233436	0.259759	0	1	1
ENSG00000263504	ENSG00000263504	AC092104.1	7:7106997-7107080	NOTEST	0	0	0	0	1	1
ENSG00000263505	ENSG00000263505	RP11-78F17.3	18:962592-1174824	NOTEST	0	0	0	0	1	1
ENSG00000263506	ENSG00000263506	MIR5193	3:49842639-49851379	NOTEST	0	0	0	0	1	1
ENSG00000263507	ENSG00000263507	AL603650.1	9:137741836-137741914	NOTEST	0	0	0	0	1	1
ENSG00000263508	ENSG00000263508	RP11-963H4.3	17:10752857-10784212	NOTEST	0	0	0	0	1	1
ENSG00000263509	ENSG00000263509	AC078988.1	X:28395079-28395178	NOTEST	0	0	0	0	1	1
ENSG00000263510	ENSG00000263510	MIR4497	12:110220889-110271241	NOTEST	0	0	0	0	1	1
ENSG00000263511	ENSG00000263511	MIR5699	10:320129-735683	NOTEST	0	0	0	0	1	1
ENSG00000263512	ENSG00000263512	MIR4311	15:66187416-66546085	NOTEST	0	0	0	0	1	1
ENSG00000263513	ENSG00000263513	FAM72C	HG1287_PATCH:144641705-144658404	NOTEST	0	0	0	0	1	1
ENSG00000263514	ENSG00000263514	MIR3668	6:140526388-140526463	NOTEST	0	0	0	0	1	1

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ENSG00000263515	ENSG00000263515	MIR548AN	X:105855159-105922672	NOTEST	0	0	0	0	1	1
ENSG00000263516	ENSG00000263516	AC009994.1	HG183_PATCH:62576979-62615309	NOTEST	0	0	0	0	1	1
ENSG00000263517	ENSG00000263517	SNORA48	HSCHR6_MHC_MCF:30179081-30179244	NOTEST	0	0	0	0	1	1
ENSG00000263518	ENSG00000263518	AL009050.1	20:38731859-38731998	NOTEST	0	0	0	0	1	1
ENSG00000263519	ENSG00000263519	AL157871.1	14:100789164-100789270	NOTEST	0	0	0	0	1	1
ENSG00000263520	ENSG00000263520	CTD-2535L24.3	17:63453658-63454526	NOTEST	0	0	0	0	1	1
ENSG00000263521	ENSG00000263521	HIST2H2AC	HG1287_PATCH:150573389-150573826	NOTEST	0	0	0	0	1	1
ENSG00000263522	ENSG00000263522	Z97054.1	X:53513658-53513758	NOTEST	0	0	0	0	1	1
ENSG00000263524	ENSG00000263524	AC016697.3	2:209098167-209098229	NOTEST	0	0	0	0	1	1
ENSG00000263525	ENSG00000263525	AC022909.1	8:122555136-122555235	NOTEST	0	0	0	0	1	1
ENSG00000263526	ENSG00000263526	MIR378G	1:95104016-95285837	NOTEST	0	0	0	0	1	1
ENSG00000263527	ENSG00000263527	MIR4526	18:13217496-13652754	NOTEST	0	0	0	0	1	1
ENSG00000263528	ENSG00000263528	IKBKE	HG1293_PATCH:206534036-206561289	NOTEST	0	0	0	0	1	1
ENSG00000263529	ENSG00000263529	RN7SL122P	1:32923435-32923733	NOTEST	0	0	0	0	1	1
ENSG00000263530	ENSG00000263530	AC006994.3	2:210867288-211036115	NOTEST	0	0	0	0	1	1
ENSG00000263531	ENSG00000263531	RP13-753N3.1	17:29158987-29222887	NOTEST	0.0637427	0.0333861	-0.933011	0	1	1
ENSG00000263532	ENSG00000263532	AL901607.2	HSCHR6_MHC_COX:28744521-28744629	NOTEST	0	0	0	0	1	1
ENSG00000263533	ENSG00000263533	MIR4463	6:75994729-76203454	NOTEST	0	0	0	0	1	1
ENSG00000263534	ENSG00000263534	RP11-744H18.1	HG1287_PATCH:144228182-144259249	NOTEST	0	0	0	0	1	1
ENSG00000263536	ENSG00000263536	RP11-534L20.4	HG1293_PATCH:206571090-206676024	NOTEST	0	0	0	0	1	1
ENSG00000263537	ENSG00000263537	RN7SL387P	12:111051831-111142755	NOTEST	0	0	0	0	1	1
ENSG00000263538	ENSG00000263538	AC097103.1	3:139108656-139396859	NOTEST	0	0	0	0	1	1
ENSG00000263539	ENSG00000263539	AC024475.1	11:45950870-46142985	NOTEST	0	0	0	0	1	1
ENSG00000263540	ENSG00000263540	MIR5582	11:46764597-46867847	NOTEST	0	0	0	0	1	1
ENSG00000263542	ENSG00000263542	AL157407.1	1:68167148-68698803	NOTEST	0	0	0	0	1	1
ENSG00000263545	ENSG00000263545	AC005195.1	5:132961535-132961639	NOTEST	0	0	0	0	1	1
ENSG00000263546	ENSG00000263546	AP002517.1	11:56405462-56405549	NOTEST	0	0	0	0	1	1
ENSG00000263547	ENSG00000263547	RP11-1O2.1	18:73834952-73857210	NOTEST	0	0	0	0	1	1
ENSG00000263548	ENSG00000263548	MIR5187	1:161195792-161208092	NOTEST	0	0	0	0	1	1
ENSG00000263549	ENSG00000263549	RP11-433J22.3	HG1287_PATCH:148464004-148475368	NOTEST	0	0	0	0	1	1
ENSG00000263550	ENSG00000263550	CR753328.1	HSCHR6_MHC_DBB:30605055-30631079	NOTEST	0	0	0	0	1	1
ENSG00000263551	ENSG00000263551	RP11-78F17.1	18:962592-1174824	NOTEST	0	0.0406239	inf	0	1	1
ENSG00000263552	ENSG00000263552	hsa-mir-219a-1	HSCHR6_MHC_QBL:33104441-33104551	NOTEST	0	0	0	0	1	1
ENSG00000263553	ENSG00000263553	RP11-449D8.2	18:22253126-22254312	NOTEST	0	0	0	0	1	1
ENSG00000263554	ENSG00000263554	MIR4788	3:134156446-134157053	NOTEST	0	0	0	0	1	1
ENSG00000263555	ENSG00000263555	RN7SL533P	19:47567443-47713886	NOTEST	0	0	0	0	1	1
ENSG00000263556	ENSG00000263556	RN7SL383P	5:44716291-44716587	NOTEST	0	0	0	0	1	1
ENSG00000263557	ENSG00000263557	AC073320.1	7:129593073-129691291	NOTEST	0	0	0	0	1	1
ENSG00000263558	ENSG00000263558	RN7SL716P	17:57059998-57232630	NOTEST	0	0	0	0	1	1
ENSG00000263559	ENSG00000263559	MIR4640	HSCHR6_MHC_MCF:30927311-30938427	NOTEST	0	0	0	0	1	1
ENSG00000263560	ENSG00000263560	AC241377.1	HG1292_PATCH:121455773-121456861	NOTEST	0	0	0	0	1	1
ENSG00000263561	ENSG00000263561	MIR4704	13:66792381-66792456	NOTEST	0	0	0	0	1	1
ENSG00000263565	ENSG00000263565	MIR4738	17:73772514-73821886	NOTEST	0	0	0	0	1	1
ENSG00000263566	ENSG00000263566	AC096753.1	2:79384131-80875905	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263567	ENSG00000263567	RP11-805L22.3	17:30089458-30096067	NOTEST	0	0	0	0	1	1
ENSG00000263568	ENSG00000263568	MIR3916	1:247353152-247405125	NOTEST	0	0	0	0	1	1
ENSG00000263569	ENSG00000263569	RN7SL212P	7:75918107-75918371	NOTEST	0	0	0	0	1	1
ENSG00000263570	ENSG00000263570	AC074264.1	2:2898819-3129798	NOTEST	0	0	0	0	1	1
ENSG00000263571	ENSG00000263571	CTC-304I17.5	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000263572	ENSG00000263572	MIR5683	6:6144317-6321246	NOTEST	0	0	0	0	1	1
ENSG00000263573	ENSG00000263573	MIR4270	3:15422781-15563258	NOTEST	0	0	0	0	1	1
ENSG00000263574	ENSG00000263574	CTD-2532D12.4	17:71733992-71824659	NOTEST	0	0	0	0	1	1
ENSG00000263575	ENSG00000263575	MIR4665	9:5881595-6007904	NOTEST	0	0	0	0	1	1
ENSG00000263576	ENSG00000263576	AL121748.1	10:33385184-33405600	NOTEST	0	0	0	0	1	1
ENSG00000263577	ENSG00000263577	AL160291.1	10:27484145-27531059	NOTEST	0	0	0	0	1	1
ENSG00000263578	ENSG00000263578	AL359546.1	10:31354879-31354976	NOTEST	0	0	0	0	1	1
ENSG00000263579	ENSG00000263579	AC138747.1	HSCHR15_1_CTG4:28623775-28637136	NOTEST	0	0	0	0	1	1
ENSG00000263581	ENSG00000263581	MIR548X2	13:66540461-66540561	NOTEST	0	0	0	0	1	1
ENSG00000263582	ENSG00000263582	RN7SL768P	1:22328148-22339032	NOTEST	0	0	0	0	1	1
ENSG00000263583	ENSG00000263583	MIR4522	17:25620935-25621022	NOTEST	0	0	0	0	1	1
ENSG00000263584	ENSG00000263584	MIR4480	10:12391480-12877545	NOTEST	0	0	0	0	1	1
ENSG00000263585	ENSG00000263585	RP11-498C9.13	17:79890259-79905477	NOTEST	0	0.424491	inf	0	1	1
ENSG00000263586	ENSG00000263586	RP11-309N17.4	17:72946837-72971823	NOTEST	0	0	0	0	1	1
ENSG00000263587	ENSG00000263587	RN7SL296P	3:33144499-33144796	NOTEST	0	0	0	0	1	1
ENSG00000263588	ENSG00000263588	RP11-595B24.2	18:19668020-19678741	NOTEST	0	0	0	0	1	1
ENSG00000263589	ENSG00000263589	SNORA48	HSCHR6_MHC_MANN:30145744-30145906	NOTEST	0	0	0	0	1	1
ENSG00000263590	ENSG00000263590	RP11-403I13.8	HG1287_PATCH:144479230-144483523	NOTEST	0	0	0	0	1	1
ENSG00000263591	ENSG00000263591	RN7SL136P	1:35729822-35730083	NOTEST	0	0	0	0	1	1
ENSG00000263592	ENSG00000263592	AL035457.1	20:49794041-49794136	NOTEST	0	0	0	0	1	1
ENSG00000263593	ENSG00000263593	MIR4804	5:72090231-72212560	NOTEST	0	0	0	0	1	1
ENSG00000263594	ENSG00000263594	RP11-28O3.2	18:65173818-65566856	NOTEST	0	0	0	0	1	1
ENSG00000263595	ENSG00000263595	RN7SL823P	19:17003757-17137625	NOTEST	0	0	0	0	1	1
ENSG00000263596	ENSG00000263596	AC013477.1	4:154265800-154336270	NOTEST	0	0	0	0	1	1
ENSG00000263597	ENSG00000263597	MIR3936	5:131520568-131731306	NOTEST	0	0	0	0	1	1
ENSG00000263598	ENSG00000263598	U6	HSCHR6_MHC_MCF:28883587-28883687	NOTEST	0	0	0	0	1	1
ENSG00000263599	ENSG00000263599	RN7SL171P	17:4736682-4806369	NOTEST	0	0	0	0	1	1
ENSG00000263600	ENSG00000263600	MIR3915	X:31115793-33357558	NOTEST	0	0	0	0	1	1
ENSG00000263602	ENSG00000263602	MIR3185	17:46800529-46806540	NOTEST	0	0	0	0	1	1
ENSG00000263603	ENSG00000263603	CTD-2349P21.5	17:29036316-29151794	NOTEST	0.289448	0	#NAME?	0	1	1
ENSG00000263604	ENSG00000263604	RP11-19P22.3	17:26010971-26011170	NOTEST	0	0	0	0	1	1
ENSG00000263605	ENSG00000263605	BMS1P6	HG1211_PATCH:47997301-48047394	NOTEST	0	0	0	0	1	1
ENSG00000263606	ENSG00000263606	RP11-737O24.3	18:2916991-3013313	NOTEST	0.209399	0.0954564	-1.13334	0	1	1
ENSG00000263607	ENSG00000263607	RN7SL80P	13:21714652-21723221	NOTEST	0.1133	0	#NAME?	0	1	1
ENSG00000263608	ENSG00000263608	RN7SL353P	6:30718814-30719062	NOTEST	0	0	0	0	1	1
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ENSG00000263611	ENSG00000263611	RP11-612A1.1	18:24916342-25175128	NOTEST	0	0	0	0	1	1
ENSG00000263612	ENSG00000263612	AF186192.6	8:145939283-145940230	NOTEST	0	0.0148847	inf	0	1	1
ENSG00000263613	ENSG00000263613	RP11-321A17.5	17:27232267-27384234	NOTEST	0	0	0	0	1	1
ENSG00000263614	ENSG00000263614	CR786580.1	9:68513104-68513187	NOTEST	0	0	0	0	1	1
ENSG00000263615	ENSG00000263615	MIR4306	13:100258918-100549387	NOTEST	0	0	0	0	1	1
ENSG00000263616	ENSG00000263616	RN7SL178P	8:8439863-8440165	NOTEST	0	0	0	0	1	1
ENSG00000263619	ENSG00000263619	AC016831.7	HG1308_PATCH:130517373-130592303	NOTEST	0	0	0	0	1	1
ENSG00000263621	ENSG00000263621	RN7SL650P	14:21853352-21924285	NOTEST	0.115819	0	#NAME?	0	1	1
ENSG00000263622	ENSG00000263622	RP11-389J22.3	18:63585017-63588178	NOTEST	0	0	0	0	1	1
ENSG00000263623	ENSG00000263623	AC005701.1	17:11501747-11900827	NOTEST	0	0	0	0	1	1
ENSG00000263624	ENSG00000263624	RP11-45M22.3	17:16945858-17140502	NOTEST	0.163079	0.352173	1.11072	0	1	1
ENSG00000263625	ENSG00000263625	SNORD83	HSCHR6_MHC_MCF:31572847-31602942	NOTEST	0	0	0	0	1	1
ENSG00000263626	ENSG00000263626	AL392111.1	10:76944715-76944816	NOTEST	0	0	0	0	1	1
ENSG00000263627	ENSG00000263627	RP11-692N5.1	18:9615261-9619361	NOTEST	0	0	0	0	1	1
ENSG00000263628	ENSG00000263628	MIR3155A	10:6186880-6277495	NOTEST	0	0	0	0	1	1
ENSG00000263629	ENSG00000263629	MIR5586	14:60062693-60337684	NOTEST	0	0	0	0	1	1
ENSG00000263630	ENSG00000263630	AP005271.1	18:10005096-10005194	NOTEST	0	0	0	0	1	1
ENSG00000263631	ENSG00000263631	MIR378D1	4:5925001-5925055	NOTEST	0	0	0	0	1	1
ENSG00000263632	ENSG00000263632	AC126177.1	12:108193411-108193497	NOTEST	0	0	0	0	1	1
ENSG00000263633	ENSG00000263633	RN7SL374P	1:179333447-179333743	NOTEST	0	0	0	0	1	1
ENSG00000263634	ENSG00000263634	MIR3919	3:158680023-159615155	NOTEST	0	0	0	0	1	1
ENSG00000263635	ENSG00000263635	RP11-805F19.2	18:15075443-15122766	NOTEST	0	0.121354	inf	0	1	1
ENSG00000263636	ENSG00000263636	AC138304.1	16:82068608-82173236	NOTEST	0	0	0	0	1	1
ENSG00000263637	ENSG00000263637	RP11-106E15.1	18:66340924-66722426	NOTEST	0	0	0	0	1	1
ENSG00000263638	ENSG00000263638	U6	HSCHR6_MHC_SSTO:31714323-31722583	NOTEST	0	0	0	0	1	1
ENSG00000263639	ENSG00000263639	MSMB	HG1211_PATCH:46528752-46541772	NOTEST	0	0	0	0	1	1
ENSG00000263640	ENSG00000263640	AF235103.1	8:146052848-146127553	NOTEST	0	0	0	0	1	1
ENSG00000263641	ENSG00000263641	MIR4777	2:232063259-232239548	NOTEST	0	0	0	0	1	1
ENSG00000263642	ENSG00000263642	MIR4802	4:40425271-40632892	NOTEST	0	0	0	0	1	1
ENSG00000263643	ENSG00000263643	MIR4515	15:83509837-83772195	NOTEST	0	0	0	0	1	1
ENSG00000263644	ENSG00000263644	RP11-269G24.3	17:61086916-61509572	NOTEST	0	0	0	0	1	1
ENSG00000263645	ENSG00000263645	AL079339.1	20:49993771-49993858	NOTEST	0	0	0	0	1	1
ENSG00000263646	ENSG00000263646	CU234142.2	HSCHR19LRC_COX1_CTG1:55008196-55074165	NOTEST	0	0	0	0	1	1
ENSG00000263647	ENSG00000263647	RP11-927P21.5	17:62745780-62833272	NOTEST	0.402915	0.580943	0.527922	0	1	1
ENSG00000263648	ENSG00000263648	RP11-471L13.3	17:11901669-12047147	NOTEST	0	0	0	0	1	1
ENSG00000263649	ENSG00000263649	MIR3135B	6:32717688-32717756	NOTEST	0	0	0	0	1	1
ENSG00000263650	ENSG00000263650	RN7SL270P	17:45000482-45177689	NOTEST	0	0	0	0	1	1
ENSG00000263651	ENSG00000263651	AC139451.1	3:49856386-49856486	NOTEST	0	0	0	0	1	1
ENSG00000263652	ENSG00000263652	MIR548AX	X:11129420-11683821	NOTEST	0	0	0	0	1	1
ENSG00000263653	ENSG00000263653	AC007025.1	X:113818550-114144624	NOTEST	0	0	0	0	1	1
ENSG00000263654	ENSG00000263654	RN7SL711P	5:122406476-122406773	NOTEST	0	0	0	0	1	1
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ENSG00000263657	ENSG00000263657	RP11-82O19.1	17:27887564-28513493	NOTEST	0	0.0285615	inf	0	1	1
ENSG00000263658	ENSG00000263658	AL356865.1	10:120390434-120390554	NOTEST	0	0	0	0	1	1
ENSG00000263659	ENSG00000263659	RN7SL603P	20:50557082-50557372	NOTEST	0	0	0	0	1	1
ENSG00000263660	ENSG00000263660	AC087793.1	8:144386553-144442149	NOTEST	0	0	0	0	1	1
ENSG00000263661	ENSG00000263661	AC009132.1	16:74746852-74808729	NOTEST	0	0	0	0	1	1
ENSG00000263662	ENSG00000263662	AL591856.4	GL000224.1:38210-38291	NOTEST	0	0	0	0	1	1
ENSG00000263663	ENSG00000263663	AL161891.1	13:34392185-34540695	NOTEST	0	0	0	0	1	1
ENSG00000263665	ENSG00000263665	CCT8P1	HG1287_PATCH:14785918-147982177	NOTEST	0	0	0	0	1	1
ENSG00000263666	ENSG00000263666	SNORA70D	16:71657610-71758604	NOTEST	0	0	0	0	1	1
ENSG00000263667	ENSG00000263667	RP3-416J7.4	6:181465-206392	NOTEST	0	0	0	0	1	1
ENSG00000263668	ENSG00000263668	RPL7AP7	HG1322_PATCH:29770728-29771525	NOTEST	0	0	0	0	1	1
ENSG00000263669	ENSG00000263669	RN7SL470P	2:70187225-70316332	NOTEST	0	0	0	0	1	1
ENSG00000263670	ENSG00000263670	MIR4457	5:1309424-1309492	NOTEST	0	0	0	0	1	1
ENSG00000263671	ENSG00000263671	Metazoa_SRP	HSCHR6_MHC_MANN:30763501-30763749	NOTEST	0	0	0	0	1	1
ENSG00000263672	ENSG00000263672	RN7SL750P	7:100400186-100464631	NOTEST	0	0	0	0	1	1
ENSG00000263673	ENSG00000263673	RP11-292F22.7	HG1211_PATCH:46780295-46781445	NOTEST	0	0	0	0	1	1
ENSG00000263674	ENSG00000263674	RP11-443G13.2	17:30593194-30708905	NOTEST	0	0	0	0	1	1
ENSG00000263675	ENSG00000263675	MIR5581	1:37958175-37980375	NOTEST	0	0	0	0	1	1
ENSG00000263676	ENSG00000263676	MIR4632	1:12227059-12269285	NOTEST	0	0	0	0	1	1
ENSG00000263677	ENSG00000263677	RP11-17A19.2	18:24034873-24770662	NOTEST	0	0	0	0	1	1
ENSG00000263678	ENSG00000263678	AC072031.1	3:121612935-121662949	NOTEST	0	0	0	0	1	1
ENSG00000263679	ENSG00000263679	Y_RNA	HSCHR6_MHC_MCF:31540832-31540934	NOTEST	0	0	0	0	1	1
ENSG00000263680	ENSG00000263680	RP11-57A1.1	17:70319263-70636611	NOTEST	0	0.195744	inf	0	1	1
ENSG00000263681	ENSG00000263681	MIR3197	21:42539483-42539556	NOTEST	0	0	0	0	1	1
ENSG00000263682	ENSG00000263682	RP11-93H10.1	18:11326268-11328831	NOTEST	0	0	0	0	1	1
ENSG00000263683	ENSG00000263683	RP4-777O23.1	7:30536236-30673649	NOTEST	0	0	0	0	1	1
ENSG00000263684	ENSG00000263684	RP11-628O18.1	17:11501747-11900827	NOTEST	0	0	0	0	1	1
ENSG00000263685	ENSG00000263685	AC010884.2	2:105552868-105719402	NOTEST	0	0	0	0	1	1
ENSG00000263686	ENSG00000263686	AL391375.1	X:125866418-125866503	NOTEST	0	0	0	0	1	1
ENSG00000263687	ENSG00000263687	FAM72A	HG1293_PATCH:206249816-206265981	NOTEST	0	0	0	0	1	1
ENSG00000263688	ENSG00000263688	RP11-386P4.1	18:30161490-30162791	NOTEST	0	0	0	0	1	1
ENSG00000263689	ENSG00000263689	AC128653.1	3:74583933-74584022	NOTEST	0	0	0	0	1	1
ENSG00000263690	ENSG00000263690	AC011591.1	17:66762613-66762700	NOTEST	0	0	0	0	1	1
ENSG00000263691	ENSG00000263691	AL355885.1	14:35221936-35345665	NOTEST	0	0	0	0	1	1
ENSG00000263692	ENSG00000263692	AC091320.2	7:119124378-119124463	NOTEST	0	0	0	0	1	1
ENSG00000263693	ENSG00000263693	MIR3161	11:48002112-48189670	NOTEST	0	0	0	0	1	1
ENSG00000263694	ENSG00000263694	RN7SL224P	14:69312518-69312772	NOTEST	0	0	0	0	1	1
ENSG00000263695	ENSG00000263695	SNORD112	HG1293_PATCH:206698209-206747980	NOTEST	0	0	0	0	1	1
ENSG00000263697	ENSG00000263697	MIR3621	9:140063209-140066861	NOTEST	0	0	0	0	1	1
ENSG00000263698	ENSG00000263698	RP11-408H20.3	18:28645939-28742819	NOTEST	0	0	0	0	1	1
ENSG00000263699	ENSG00000263699	LAMA4	HG1304_PATCH:112430062-112671296	NOTEST	0	0	0	0	1	1
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ENSG00000263702	ENSG00000263702	CU104682.1	HSCHR19LRC_PGF2_CTG1:54785988-54786060	NOTEST	0	0	0	0	1	1
ENSG00000263703	ENSG00000263703	RP11-463P17.1	HG1211_PATCH:47902612-47910022	NOTEST	0	0	0	0	1	1
ENSG00000263705	ENSG00000263705	MIR5689	6:10429487-10457014	NOTEST	0	0	0	0	1	1
ENSG00000263706	ENSG00000263706	RN7SL450P	10:111756125-111895323	NOTEST	0	0	0	0	1	1
ENSG00000263707	ENSG00000263707	RP11-597M12.1	17:12569206-12894960	NOTEST	0	0	0	0	1	1
ENSG00000263708	ENSG00000263708	RP11-85B7.4	17:9153787-9479908	NOTEST	0	0	0	0	1	1
ENSG00000263709	ENSG00000263709	RP11-321A17.4	17:27400527-27507430	NOTEST	0	0	0	0	1	1
ENSG00000263710	ENSG00000263710	AC025175.1	5:53072473-53115516	NOTEST	0	0	0	0	1	1
ENSG00000263711	ENSG00000263711	RP11-169F17.1	18:70818475-70931715	NOTEST	0.0043208	0.0728916	4.07638	0	1	1
ENSG00000263712	ENSG00000263712	MIR4639	6:16129355-16148479	NOTEST	0	0	0	0	1	1
ENSG00000263713	ENSG00000263713	AC109994.1	X:149529688-149682448	NOTEST	0	0	0	0	1	1
ENSG00000263714	ENSG00000263714	RN7SL755P	15:90645880-90676674	NOTEST	0	0	0	0	1	1
ENSG00000263715	ENSG00000263715	RP11-105N13.4	17:43697693-43913194	NOTEST	0	0	0	0	1	1
ENSG00000263716	ENSG00000263716	SLC25A51P2	18:7134929-7135818	NOTEST	0	0	0	0	1	1
ENSG00000263717	ENSG00000263717	RP11-466A19.6	17:30819539-31205655	NOTEST	0.345332	0.368207	0.0925326	0	1	1
ENSG00000263718	ENSG00000263718	RP11-285E9.6	17:75253818-75496678	NOTEST	0	0	0	0	1	1
ENSG00000263719	ENSG00000263719	MIR4523	17:27679086-27878922	NOTEST	0	0	0	0	1	1
ENSG00000263720	ENSG00000263720	RP11-389J22.1	18:63417487-63548638	NOTEST	0.0478377	0.0372146	-0.362277	0	1	1
ENSG00000263721	ENSG00000263721	MIR4444-2	2:177855235-178088686	NOTEST	0	0	0	0	1	1
ENSG00000263723	ENSG00000263723	SNORD39	2:238767535-238820756	NOTEST	0	0	0	0	1	1
ENSG00000263724	ENSG00000263724	DLGAP1-AS3	18:3496029-4455335	NOTEST	0	0	0	0	1	1
ENSG00000263725	ENSG00000263725	FTLP13	17:21747826-21748211	NOTEST	0	0	0	0	1	1
ENSG00000263726	ENSG00000263726	CTB-187M2.3	17:19374431-19396273	NOTEST	0	0	0	0	1	1
ENSG00000263727	ENSG00000263727	RP11-806L2.5	18:596987-712676	NOTEST	0	0	0	0	1	1
ENSG00000263728	ENSG00000263728	RN7SL579P	HSCHR6_MHC_COX:30708645-30708893	NOTEST	0	0	0	0	1	1
ENSG00000263729	ENSG00000263729	RP11-746M1.8	17:20717932-20947073	NOTEST	0	0	0	0	1	1
ENSG00000263730	ENSG00000263730	MIR3937	X:39520469-39520575	NOTEST	0	0	0	0	1	1
ENSG00000263731	ENSG00000263731	RP11-498C9.15	17:79836300-79838982	NOTEST	0.47483	0.413956	-0.197935	0	1	1
ENSG00000263732	ENSG00000263732	AC012564.1	8:105602960-107072752	NOTEST	0	0	0	0	1	1
ENSG00000263733	ENSG00000263733	RP11-47G4.1	18:68883939-68904338	NOTEST	0	0	0	0	1	1
ENSG00000263734	ENSG00000263734	MIR4643	6:92231377-92231455	NOTEST	0	0	0	0	1	1
ENSG00000263735	ENSG00000263735	MIR4662A	8:125834219-125834300	NOTEST	0	0	0	0	1	1
ENSG00000263736	ENSG00000263736	RP11-196G18.22	HG1287_PATCH:150530912-150535439	NOTEST	0	0	0	0	1	1
ENSG00000263737	ENSG00000263737	RN7SL476P	5:68751401-68751659	NOTEST	0	0	0	0	1	1
ENSG00000263738	ENSG00000263738	AC079233.1	4:158125333-158287227	NOTEST	0	0	0	0	1	1
ENSG00000263739	ENSG00000263739	AC091390.1	HG115_PATCH:101928440-101964991	NOTEST	0	0	0	0	1	1
ENSG00000263741	ENSG00000263741	MIR548AS	13:92050928-93519490	NOTEST	0	0	0	0	1	1
ENSG00000263742	ENSG00000263742	MIR3165	11:71709586-71823826	NOTEST	0	0	0	0	1	1
ENSG00000263743	ENSG00000263743	AC017028.2	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000263744	ENSG00000263744	MIR3664	11:70313960-70963623	NOTEST	0	0	0	0	1	1
ENSG00000263745	ENSG00000263745	RP11-161I6.2	18:1883524-2240847	NOTEST	0	0	0	0	1	1
ENSG00000263746	ENSG00000263746	MIR4277	5:1708899-1708983	NOTEST	0	0	0	0	1	1

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ENSG00000263748	ENSG00000263748	EXOGP1	18:18762463-18763460	NOTEST	0	0	0	0	1	1
ENSG00000263749	ENSG00000263749	OOSP1P2	17:30593194-30708905	NOTEST	0	0	0	0	1	1
ENSG00000263750	ENSG00000263750	MIR548AV	18:70409548-70535381	NOTEST	0	0	0	0	1	1
ENSG00000263751	ENSG00000263751	AL122127.1	14:106324503-106324581	NOTEST	0	0	0	0	1	1
ENSG00000263752	ENSG00000263752	MIR3133	2:242295657-242449145	NOTEST	0	0	0	0	1	1
ENSG00000263754	ENSG00000263754	CR786580.2	9:68512345-68512422	NOTEST	0	0	0	0	1	1
ENSG00000263755	ENSG00000263755	RN7SL498P	20:5982378-5982674	NOTEST	0	0	0	0	1	1
ENSG00000263756	ENSG00000263756	XXbac-BPG181M17.6	6:32902405-32949282	NOTEST	0	0	0	0	1	1
ENSG00000263757	ENSG00000263757	AC027288.1	12:79257772-79897176	NOTEST	0	0	0	0	1	1
ENSG00000263758	ENSG00000263758	AKR1C7P	HG871_PATCH:5317364-5330662	NOTEST	0	0	0	0	1	1
ENSG00000263759	ENSG00000263759	AC122714.1	5:180009444-180009530	NOTEST	0	0	0	0	1	1
ENSG00000263760	ENSG00000263760	CU463998.4	GL000240.1:3915-3999	NOTEST	0	0	0	0	1	1
ENSG00000263761	ENSG00000263761	GDF2	HG1211_PATCH:47817956-47821718	NOTEST	0	0	0	0	1	1
ENSG00000263762	ENSG00000263762	MIR4286	8:10463858-10569697	NOTEST	0	0	0	0	1	1
ENSG00000263763	ENSG00000263763	MIR3686	8:130363936-130695925	NOTEST	0	0	0	0	1	1
ENSG00000263764	ENSG00000263764	SNORD43	22:39708886-39716394	NOTEST	0	0	0	0	1	1
ENSG00000263765	ENSG00000263765	RP11-746B8.1	18:30413416-31021065	NOTEST	0	0	0	0	1	1
ENSG00000263767	ENSG00000263767	AC083906.1	3:129752300-129752388	NOTEST	0	0	0	0	1	1
ENSG00000263768	ENSG00000263768	AC060226.1	12:116395710-116715143	NOTEST	0	0	0	0	1	1
ENSG00000263769	ENSG00000263769	RN7SL367P	16:1944685-1944937	NOTEST	0	0	0	0	1	1
ENSG00000263770	ENSG00000263770	AL031666.1	20:45837858-45985567	NOTEST	0	0	0	0	1	1
ENSG00000263771	ENSG00000263771	NKAIN1P1	HG1287_PATCH:144999834-145000416	NOTEST	0	0	0	0	1	1
ENSG00000263772	ENSG00000263772	RP11-549B18.3	18:29304160-29306919	NOTEST	0.0105023	0.0642225	2.61237	0	1	1
ENSG00000263773	ENSG00000263773	ANKRD35	HG1287_PATCH:146552974-146572260	NOTEST	0	0	0	0	1	1
ENSG00000263774	ENSG00000263774	AC017104.1	2:232354914-232355000	NOTEST	0	0	0	0	1	1
ENSG00000263775	ENSG00000263775	AC080008.1	3:123798869-124445172	NOTEST	0	0	0	0	1	1
ENSG00000263776	ENSG00000263776	SNORA4	3:186499568-186524847	NOTEST	0	0	0	0	1	1
ENSG00000263777	ENSG00000263777	AC145343.2	HG747_PATCH:66092161-66097590	NOTEST	0	0	0	0	1	1
ENSG00000263778	ENSG00000263778	AL671879.2	HSCHR6_MHC_COX:28615936-28616005	NOTEST	0	0	0	0	1	1
ENSG00000263779	ENSG00000263779	RN7SL467P	1:230838268-230937749	NOTEST	0	0	0	0	1	1
ENSG00000263780	ENSG00000263780	AC005621.1	19:32991761-32991847	NOTEST	0	0	0	0	1	1
ENSG00000263781	ENSG00000263781	RP11-321A17.3	17:27232267-27384234	NOTEST	0	0	0	0	1	1
ENSG00000263782	ENSG00000263782	AC117481.1	3:75395289-75395366	NOTEST	0	0	0	0	1	1
ENSG00000263783	ENSG00000263783	MIR5590	2:135493033-135716912	NOTEST	0	0	0	0	1	1
ENSG00000263784	ENSG00000263784	AL136418.1	14:31717833-31926716	NOTEST	0	0	0	0	1	1
ENSG00000263785	ENSG00000263785	MIR3182	16:82660407-83841439	NOTEST	0	0	0	0	1	1
ENSG00000263786	ENSG00000263786	RP11-649A18.4	17:73131342-73179078	NOTEST	0.386058	0.428291	0.149774	0	1	1
ENSG00000263787	ENSG00000263787	RP11-456D7.1	17:46210801-46507637	NOTEST	0	0	0	0	1	1
ENSG00000263788	ENSG00000263788	CTD-2008P7.7	17:26583400-26593395	NOTEST	0	0	0	0	1	1
ENSG00000263790	ENSG00000263790	MIR4473	9:20341662-20622542	NOTEST	0	0	0	0	1	1
ENSG00000263791	ENSG00000263791	MIR4727	17:36982090-36982145	NOTEST	0	0	0	0	1	1
ENSG00000263793	ENSG00000263793	MIR3115	1:23345940-23504301	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263794	ENSG00000263794	RN7SL457P	8:33462373-33896526	NOTEST	0	0	0	0	1	1
ENSG00000263795	ENSG00000263795	MIR5100	10:43493010-43493129	NOTEST	0	0	0	0	1	1
ENSG00000263796	ENSG00000263796	RN7SL609P	21:24052991-24053286	NOTEST	0	0	0	0	1	1
ENSG00000263797	ENSG00000263797	RP11-146G7.2	18:6728819-6915715	NOTEST	0	0	0	0	1	1
ENSG00000263798	ENSG00000263798	RP11-6N17.9	17:46018871-46073562	NOTEST	0	0	0	0	1	1
ENSG00000263799	ENSG00000263799	RP11-728E14.3	HG987_PATCH:21359824-21363527	NOTEST	0	0	0	0	1	1
ENSG00000263800	ENSG00000263800	MIR5684	19:12873816-12985765	NOTEST	0	0	0	0	1	1
ENSG00000263801	ENSG00000263801	AL591684.2	HG1211_PATCH:47955609-47987141	NOTEST	0	0	0	0	1	1
ENSG00000263802	ENSG00000263802	AL121655.1	2:32288679-32382706	NOTEST	0	0	0	0	1	1
ENSG00000263803	ENSG00000263803	RN7SL816P	7:57032954-57033214	NOTEST	0	0	0	0	1	1
ENSG00000263804	ENSG00000263804	RN7SL409P	17:62745780-62833272	NOTEST	0	0	0	0	1	1
ENSG00000263805	ENSG00000263805	AL450244.1	1:199584315-199584408	NOTEST	0	0	0	0	1	1
ENSG00000263806	ENSG00000263806	AL592188.3	GL000220.1:100713-100791	NOTEST	0	0	0	0	1	1
ENSG00000263808	ENSG00000263808	AC093376.1	7:5313999-5465045	NOTEST	0	0	0	0	1	1
ENSG00000263809	ENSG00000263809	RP11-849F2.7	17:8268880-8286531	NOTEST	0.0909072	0.0722564	-0.33127	0	1	1
ENSG00000263810	ENSG00000263810	AC055723.1	3:99357318-99518070	NOTEST	0	0	0	0	1	1
ENSG00000263811	ENSG00000263811	MIR3675	1:17066767-17299474	NOTEST	0	0	0	0	1	1
ENSG00000263812	ENSG00000263812	LINC00908	18:74240611-74322925	NOTEST	0	0	0	0	1	1
ENSG00000263813	ENSG00000263813	MIR3679	2:134877553-135212192	NOTEST	0	0	0	0	1	1
ENSG00000263814	ENSG00000263814	AC093786.1	4:34388375-34388459	NOTEST	0	0	0	0	1	1
ENSG00000263815	ENSG00000263815	RN7SL426P	17:21100592-21133348	NOTEST	0.119391	0	#NAME?	0	1	1
ENSG00000263816	ENSG00000263816	MIR548AW	9:135820931-135867083	NOTEST	0	0	0	0	1	1
ENSG00000263817	ENSG00000263817	RN7SL157P	9:15348165-15348453	NOTEST	0	0	0	0	1	1
ENSG00000263818	ENSG00000263818	CTD-2206N4.4	17:37213271-37310647	NOTEST	0.138034	0.068248	-1.01616	0	1	1
ENSG00000263819	ENSG00000263819	RN7SL478P	7:97627636-97627932	NOTEST	0	0	0	0	1	1
ENSG00000263820	ENSG00000263820	AC005702.2	17:58120165-58120243	NOTEST	0	0	0	0	1	1
ENSG00000263823	ENSG00000263823	RP11-326K13.4	18:29409135-29533099	NOTEST	0.438936	0.377932	-0.215884	0	1	1
ENSG00000263824	ENSG00000263824	AC022882.1	HG142_HG150_NOVEL_TEST:56063543-56063651	NOTEST	0	0	0	0	1	1
ENSG00000263825	ENSG00000263825	AL358813.2	1:149646784-149719362	NOTEST	0	0	0	0	1	1
ENSG00000263827	ENSG00000263827	AP005118.1	18:7566779-8406951	NOTEST	0	0	0	0	1	1
ENSG00000263828	ENSG00000263828	MIR4439	2:225629806-225907162	NOTEST	0	0	0	0	1	1
ENSG00000263829	ENSG00000263829	FAM60BP	18:23805899-23971649	NOTEST	0	0.0215776	inf	0	1	1
ENSG00000263830	ENSG00000263830	RN7SL871P	17:39981334-40004636	NOTEST	0	0	0	0	1	1
ENSG00000263831	ENSG00000263831	MIR378E	5:169064250-169510386	NOTEST	0	0	0	0	1	1
ENSG00000263832	ENSG00000263832	AC023237.1	12:57482676-57607134	NOTEST	0	0	0	0	1	1
ENSG00000263833	Y_RNA	HSCHR6_MHC_DBB:31446484-31446586		NOTEST	0	0	0	0	1	1
ENSG00000263834	ENSG00000263834	MIR4635	5:1050498-1112150	NOTEST	0	0	0	0	1	1
ENSG00000263835	ENSG00000263835	BX649553.1	X:1387692-1429274	NOTEST	0	0	0	0	1	1
ENSG00000263836	ENSG00000263836	RP11-822E23.2	HG987_PATCH:21428101-21477829	NOTEST	0	0	0	0	1	1
ENSG00000263837	ENSG00000263837	RP11-285E9.5	HSCHR17_3_CTG4:75265440-75508300	NOTEST	0	0	0	0	1	1
ENSG00000263838	ENSG00000263838	MIR4698	12:47469489-47630443	NOTEST	0	0	0	0	1	1
ENSG00000263839	ENSG00000263839	CR381653.1	21:10199942-10200025	NOTEST	0	0	0	0	1	1
ENSG00000263840	ENSG00000263840	AC011431.2	5:135136917-135137003	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263841	ENSG00000263841	RN7SL44P	1:153472942-153473240	NOTEST	0	0	0	0	1	1
ENSG00000263842	ENSG00000263842	AC104986.1	8:100008990-100025272	NOTEST	0	0	0	0	1	1
ENSG00000263843	ENSG00000263843	RP11-649A18.12	17:73267449-73285591	NOTEST	0.499246	0.376682	-0.406402	0	1	1
ENSG00000263844	ENSG00000263844	RNU1-135P	HG1287_PATCH:14907224-149072378	NOTEST	0	0	0	0	1	1
ENSG00000263845	ENSG00000263845	AL390879.1	X:135991553-136103789	NOTEST	0	0	0	0	1	1
ENSG00000263846	ENSG00000263846	CIAPIN1P	18:24034873-24770662	NOTEST	0	0	0	0	1	1
ENSG00000263847	ENSG00000263847	RP11-143J12.3	18:9102627-9285983	NOTEST	0.386828	0.217565	-0.830244	0	1	1
ENSG00000263848	ENSG00000263848	AC108057.1	2:157871683-157871769	NOTEST	0	0	0	0	1	1
ENSG00000263849	ENSG00000263849	MIR4744	18:46550072-46987717	NOTEST	0	0	0	0	1	1
ENSG00000263850	ENSG00000263850	FCGR1B	HG1292_PATCH:121629974-121659880	NOTEST	0	0	0	0	1	1
ENSG00000263853	ENSG00000263853	AC139530.1	17:79643030-79643116	NOTEST	0	0	0	0	1	1
ENSG00000263854	ENSG00000263854	AL591856.5	GL000224.1:47210-47293	NOTEST	0	0	0	0	1	1
ENSG00000263855	ENSG00000263855	AC105081.1	8:94986081-94986151	NOTEST	0	0	0	0	1	1
ENSG00000263856	ENSG00000263856	AL121756.1	20:31643229-31661434	NOTEST	0	0	0	0	1	1
ENSG00000263857	ENSG00000263857	MIR4729	17:57409049-57480664	NOTEST	0	0	0	0	1	1
ENSG00000263858	ENSG00000263858	MIR4769	X:47420515-47479252	NOTEST	0	0	0	0	1	1
ENSG00000263859	ENSG00000263859	RP11-498C9.16	17:79836300-79838982	NOTEST	0.00175693	0.0538565	4.93799	0	1	1
ENSG00000263860	ENSG00000263860	RP11-218M11.3	17:28877510-28878207	NOTEST	0	0	0	0	1	1
ENSG00000263861	ENSG00000263861	MIR3927	9:112273754-112273825	NOTEST	0	0	0	0	1	1
ENSG00000263862	ENSG00000263862	RP11-107K17.1	18:24002958-24006065	NOTEST	0	0	0	0	1	1
ENSG00000263863	ENSG00000263863	AC007948.1	18:62773108-62792946	NOTEST	0	0	0	0	1	1
ENSG00000263864	ENSG00000263864	SNORD48	HSCHR6_MHC_APD:31813741-31818898	NOTEST	0	0	0	0	1	1
ENSG00000263865	ENSG00000263865	RP13-766D20.1	HG271_PATCH:79483770-79501576	NOTEST	0	0	0	0	1	1
ENSG00000263866	ENSG00000263866	hsa-mir-877	HSCHR6_MHC_DBB:30529390-30555197	NOTEST	0	0	0	0	1	1
ENSG00000263867	ENSG00000263867	RP11-822E23.3	HG987_PATCH:21428101-21477829	NOTEST	0	0	0	0	1	1
ENSG00000263868	ENSG00000263868	AL139319.1	13:79239972-79240065	NOTEST	0	0	0	0	1	1
ENSG00000263869	ENSG00000263869	RNU6-825P	HSCHR6_MHC_COX:32209048-32287940	NOTEST	0	0	0	0	1	1
ENSG00000263870	ENSG00000263870	CTD-2350C19.5	17:26771080-26772581	NOTEST	0	0	0	0	1	1
ENSG00000263871	ENSG00000263871	U1	HSCHR6_MHC_MANN:32688632-32688781	NOTEST	0	0	0	0	1	1
ENSG00000263872	ENSG00000263872	hsa-mir-4528	18:49866541-51094653	NOTEST	0	0	0	0	1	1
ENSG00000263873	ENSG00000263873	RP11-334E6.12	11:119252487-119397374	NOTEST	0.031311	0.081945	1.38799	0	1	1
ENSG00000263874	ENSG00000263874	LINC00672	17:37081420-37084310	NOTEST	0.0338445	0.0780354	1.20521	0	1	1
ENSG00000263875	ENSG00000263875	AL353629.1	9:96208775-96328397	NOTEST	0	0	0	0	1	1
ENSG00000263876	ENSG00000263876	Y_RNA	HSCHR6_MHC_COX:29712117-29712219	NOTEST	0	0	0	0	1	1
ENSG00000263877	ENSG00000263877	RN7SL276P	1:222841354-222908538	NOTEST	0	0	0	0	1	1
ENSG00000263878	ENSG00000263878	DLGAP1-AS4	18:3496029-4455335	NOTEST	0	0	0	0	1	1
ENSG00000263879	ENSG00000263879	SNORA38	HSCHR6_MHC_COX:31575862-31592960	NOTEST	0	0	0	0	1	1
ENSG00000263880	ENSG00000263880	RN7SL747P	14:76776956-77227731	NOTEST	0	0	0	0	1	1
ENSG00000263881	ENSG00000263881	MIR4436B1	2:110969105-111043433	NOTEST	0	0	0	0	1	1
ENSG00000263882	ENSG00000263882	RN7SL774P	17:4172553-4269923	NOTEST	0	0	0	0	1	1
ENSG00000263883	ENSG00000263883	RP11-51F16.5	17:61699774-61778532	NOTEST	0.0809388	0	#NAME?	0	1	1
ENSG00000263884	ENSG00000263884	RP11-705O1.8	18:268147-270278	NOTEST	0.079042	0.102411	0.373674	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263885	ENSG00000263885	MIR3920	11:101322294-101743293	NOTEST	0	0	0	0	1	1
ENSG00000263886	ENSG00000263886	AL953885.1	X:124421624-124421692	NOTEST	0	0	0	0	1	1
ENSG00000263887	ENSG00000263887	RP11-51L5.5	17:60342065-60374387	NOTEST	0	0	0	0	1	1
ENSG00000263888	ENSG00000263888	RN7SL777P	8:92114059-92410378	NOTEST	0	0	0	0	1	1
ENSG00000263889	ENSG00000263889	RN7SL86P	11:118230299-118302211	NOTEST	0	0	0	0	1	1
ENSG00000263890	ENSG00000263890	MIR4303	12:98389160-98389226	NOTEST	0	0	0	0	1	1
ENSG00000263891	ENSG00000263891	AC092634.1	7:63361200-63378372	NOTEST	0	0	0	0	1	1
ENSG00000263892	ENSG00000263892	MIR4667	9:35605366-35647096	NOTEST	0	0	0	0	1	1
ENSG00000263893	ENSG00000263893	CTD-3010D24.3	17:70638869-70640629	NOTEST	0	0	0	0	1	1
ENSG00000263894	ENSG00000263894	MIR3925	6:36590212-36590289	NOTEST	0	0	0	0	1	1
ENSG00000263895	ENSG00000263895	RP11-110H1.9	18:46550072-46987717	NOTEST	0	0	0	0	1	1
ENSG00000263896	ENSG00000263896	U6	HSCHR6_MHC_DBB:31689901-31715550	NOTEST	0	0	0	0	1	1
ENSG00000263897	ENSG00000263897	MIR4669	9:137208943-137332431	NOTEST	0	0	0	0	1	1
ENSG00000263898	ENSG00000263898	MIR4793	3:48673901-48700348	NOTEST	0	0	0	0	1	1
ENSG00000263900	ENSG00000263900	AC006483.1	7:5566781-5603415	NOTEST	0	0	0	0	1	1
ENSG00000263901	ENSG00000263901	RN7SL544P	9:46674881-46675163	NOTEST	0	0	0	0	1	1
ENSG00000263902	ENSG00000263902	RN7SL437P	17:55333211-55762046	NOTEST	0	0	0	0	1	1
ENSG00000263903	ENSG00000263903	AL035250.1	20:57921433-57921535	NOTEST	0	0	0	0	1	1
ENSG00000263904	ENSG00000263904	RP11-344B2.3	18:29598334-30050447	NOTEST	0	0	0	0	1	1
ENSG00000263905	ENSG00000263905	RN7SL555P	20:3074860-3075153	NOTEST	0	0	0	0	1	1
ENSG00000263906	ENSG00000263906	RP11-680F20.11	11:125773141-125808811	NOTEST	0	0.00676614	inf	0	1	1
ENSG00000263907	ENSG00000263907	AL354833.1	13:42019426-42019503	NOTEST	0	0	0	0	1	1
ENSG00000263908	ENSG00000263908	MIR3116-2	1:62208148-62629592	NOTEST	0	0	0	0	1	1
ENSG00000263909	ENSG00000263909	MIR5000	2:75273589-75426826	NOTEST	0	0	0	0	1	1
ENSG00000263910	ENSG00000263910	AC133749.1	12:69201955-69365350	NOTEST	0	0	0	0	1	1
ENSG00000263911	ENSG00000263911	RN7SL31P	20:43509478-43509775	NOTEST	0	0	0	0	1	1
ENSG00000263912	ENSG00000263912	Metazoa_SRP	HSCHR6_MHC_SSTO:30710245-30710493	NOTEST	0	0	0	0	1	1
ENSG00000263913	ENSG00000263913	AC004812.1	12:120565006-120632513	NOTEST	0	0	0	0	1	1
ENSG00000263914	ENSG00000263914	RP11-846F4.5	17:22025224-22026263	NOTEST	0	0	0	0	1	1
ENSG00000263915	ENSG00000263915	RP11-325P15.2	HG1287_PATCH:14770575-147810940	NOTEST	0	0	0	0	1	1
ENSG00000263916	ENSG00000263916	RP11-110H1.4	18:47008027-47018906	NOTEST	0	0	0	0	1	1
ENSG00000263918	ENSG00000263918	MIR3670-1	16:15001573-15001638	NOTEST	0	0	0	0	1	1
ENSG00000263919	ENSG00000263919	RN7SL686P	10:112393588-112393883	NOTEST	0	0	0	0	1	1
ENSG00000263920	ENSG00000263920	AC067751.1	10:64133950-64431771	NOTEST	0	0	0	0	1	1
ENSG00000263921	ENSG00000263921	AC013737.1	10:55562530-57387702	NOTEST	0	0	0	0	1	1
ENSG00000263922	ENSG00000263922	AC138827.1	HSCHR5_1_CTG1:69515270-69515340	NOTEST	0	0	0	0	1	1
ENSG00000263923	ENSG00000263923	RP11-571L19.7	4:99792834-99916145	NOTEST	0	0	0	0	1	1
ENSG00000263924	ENSG00000263924	RP11-210K20.2	18:29409135-29533099	NOTEST	0	0	0	0	1	1
ENSG00000263925	ENSG00000263925	AC092364.1	HSCHR19_2_CTG3:21889687-21889796	NOTEST	0	0	0	0	1	1
ENSG00000263926	ENSG00000263926	MIR4462	6:37523140-37523198	NOTEST	0	0	0	0	1	1
ENSG00000263927	ENSG00000263927	AC099759.1	7:22419622-22419720	NOTEST	0	0	0	0	1	1
ENSG00000263928	ENSG00000263928	AL354833.2	13:42020192-42020261	NOTEST	0	0	0	0	1	1
ENSG00000263929	ENSG00000263929	RN7SL186P	1:22328148-22339032	NOTEST	0	0	0	0	1	1
ENSG00000263930	ENSG00000263930	MIR4509-1	15:22675147-22675241	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263931	ENSG00000263931	RP11-180P8.1	17:61012762-61044171	NOTEST	0.351046	0.106188	-1.72504	0	1	1
ENSG00000263932	ENSG00000263932	MIR4448	3:183547172-183606237	NOTEST	0	0	0	0	1	1
ENSG00000263933	ENSG00000263933	AL365502.1	9:140354403-140444986	NOTEST	0	0	0	0	1	1
ENSG00000263935	ENSG00000263935	RP11-674N23.2	18:8688019-8688408	NOTEST	0	0	0	0	1	1
ENSG00000263936	ENSG00000263936	AL592183.7	GL000219.1:47190-47266	NOTEST	0	0	0	0	1	1
ENSG00000263937	ENSG00000263937	RNU6-1173P	HSCHR6_MHC_COX:28871598-28892590	NOTEST	0	0	0	0	1	1
ENSG00000263938	ENSG00000263938	RP11-579O24.3	17:56833229-57058983	NOTEST	0.0245516	0.0173343	-0.502183	0	1	1
ENSG00000263939	ENSG00000263939	RP11-38L15.3	HG1211_PATCH:47073664-47147473	NOTEST	0	0	0	0	1	1
ENSG00000263940	ENSG00000263940	RN7SL275P	4:110967001-111120355	NOTEST	0	0	0	0	1	1
ENSG00000263941	ENSG00000263941	RN7SL32P	2:233924676-234116549	NOTEST	0	0	0	0	1	1
ENSG00000263942	ENSG00000263942	SNORA48	HSCHR6_MHC_SSTO:30090183-30090346	NOTEST	0	0	0	0	1	1
ENSG00000263943	ENSG00000263943	RN7SL680P	20:37977738-37978035	NOTEST	0	0	0	0	1	1
ENSG00000263944	ENSG00000263944	RN7SL435P	11:59058525-59058806	NOTEST	0	0	0	0	1	1
ENSG00000263945	ENSG00000263945	MIR548Y	14:48230197-48230307	NOTEST	0	0	0	0	1	1
ENSG00000263946	ENSG00000263946	RP11-434D2.11	17:20458283-20462723	NOTEST	0	0	0	0	1	1
ENSG00000263947	ENSG00000263947	RN7SL694P	2:201773695-201950473	NOTEST	0	0	0	0	1	1
ENSG00000263948	ENSG00000263948	MIR4785	2:161128661-161350305	NOTEST	0	0	0	0	1	1
ENSG00000263950	ENSG00000263950	Y_RNA	HSCHR6_MHC_DBB:30685746-30700772	NOTEST	0	0	0	0	1	1
ENSG00000263952	ENSG00000263952	RP11-513M1.1	18:10661929-11148587	NOTEST	0	0	0	0	1	1
ENSG00000263953	ENSG00000263953	CU459202.3	GL000243.1:5754-5838	NOTEST	0	0	0	0	1	1
ENSG00000263954	ENSG00000263954	AC004769.1	5:129613317-129613386	NOTEST	0	0	0	0	1	1
ENSG00000263955	ENSG00000263955	RN7SL850P	16:4666493-4740975	NOTEST	0	0	0	0	1	1
ENSG00000263956	ENSG00000263956	NBPF11	HG1287_PATCH:148788460-148838605	NOTEST	0	0	0	0	1	1
ENSG00000263957	ENSG00000263957	AC105398.1	2:29304135-29304217	NOTEST	0	0	0	0	1	1
ENSG00000263958	ENSG00000263958	RP11-676J15.1	18:70535622-70548634	NOTEST	0	0	0	0	1	1
ENSG00000263959	ENSG00000263959	AC092988.1	3:139654026-140296239	NOTEST	0	0	0	0	1	1
ENSG00000263960	ENSG00000263960	AC007773.1	19:32836499-32878573	NOTEST	0	0	0	0	1	1
ENSG00000263961	ENSG00000263961	C1orf186	HG1293_PATCH:206098791-206166009	NOTEST	0	0	0	0	1	1
ENSG00000263962	ENSG00000263962	AC245100.1	HG1287_PATCH:149145228-149146286	NOTEST	0	0	0	0	1	1
ENSG00000263963	ENSG00000263963	MIR4461	5:134240595-134347392	NOTEST	0	0	0	0	1	1
ENSG00000263964	ENSG00000263964	MIR4509-2	15:28735897-28735991	NOTEST	0	0	0	0	1	1
ENSG00000263965	ENSG00000263965	HIST2H2AB	HG1287_PATCH:150573883-150587213	NOTEST	0	0	0	0	1	1
ENSG00000263966	ENSG00000263966	AP000765.1	11:94149875-94149927	NOTEST	0	0	0	0	1	1
ENSG00000263967	ENSG00000263967	MIR4290	9:92782935-92803781	NOTEST	0	0	0	0	1	1
ENSG00000263968	ENSG00000263968	RN7SL381P	16:85645014-85723679	NOTEST	0.116693	0.282343	1.27473	0	1	1
ENSG00000263969	ENSG00000263969	RN7SL678P	21:38580803-38640785	NOTEST	0	0	0	0	1	1
ENSG00000263970	ENSG00000263970	RP11-789C17.5	18:7566779-8406951	NOTEST	0.411843	0.962871	1.22525	0	1	1
ENSG00000263971	ENSG00000263971	U1	HSCHR6_MHC_MCF:32576145-32576297	NOTEST	0	0	0	0	1	1
ENSG00000263972	ENSG00000263972	MIR1587	X:39696789-39707612	NOTEST	0	0	0	0	1	1
ENSG00000263973	ENSG00000263973	MIR4760	21:41382925-42219065	NOTEST	0	0	0	0	1	1
ENSG00000263974	ENSG00000263974	RN7SL121P	19:4542599-4559820	NOTEST	0	0	0	0	1	1
ENSG00000263975	ENSG00000263975	CTB-58E17.9	17:36858704-36886056	NOTEST	0	0	0	0	1	1
ENSG00000263976	ENSG00000263976	YWHAEP3	17:20394635-20394756	NOTEST	0	0	0	0	1	1
ENSG00000263977	ENSG00000263977	SF3B4	HG1287_PATCH:150609731-150614759	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000263978	ENSG00000263978	MIR4499	13:20977805-21099996	NOTEST	0	0	0	0	1	1
ENSG00000263979	ENSG00000263979	MIR4672	9:130628758-130667687	NOTEST	0	0	0	0	1	1
ENSG00000263980	ENSG00000263980	BX649553.2	X:1387692-1429274	NOTEST	0	0	0	0	1	1
ENSG00000263981	ENSG00000263981	MIR5705	4:88221646-88221735	NOTEST	0	0	0	0	1	1
ENSG00000263982	ENSG00000263982	RP11-504I13.3	18:74069643-74207146	NOTEST	0.065333	0.294927	2.17447	0	1	1
ENSG00000263984	ENSG00000263984	AC092380.1	16:12995476-13334272	NOTEST	0	0	0	0	1	1
ENSG00000263985	ENSG00000263985	AC116407.1	17:30462747-30462833	NOTEST	0	0	0	0	1	1
ENSG00000263986	ENSG00000263986	RP11-746M1.1	17:20717932-20947073	NOTEST	0	0	0	0	1	1
ENSG00000263987	ENSG00000263987	MIR5698	1:153965160-154127592	NOTEST	0	0	0	0	1	1
ENSG00000263988	ENSG00000263988	RN7SL147P	3:11994263-11994559	NOTEST	0	0	0	0	1	1
ENSG00000263989	ENSG00000263989	RN7SL615P	20:39657457-39946312	NOTEST	0	0	0	0	1	1
ENSG00000263990	ENSG00000263990	CTC-542B22.2	17:30187922-30228784	NOTEST	0	0.14076	inf	0	1	1
ENSG00000263991	ENSG00000263991	RN7SL386P	1:22303513-22325135	NOTEST	0	0	0	0	1	1
ENSG00000263992	ENSG00000263992	HLA-W	HG1322_PATCH:29916220-29918195	NOTEST	0	0	0	0	1	1
ENSG00000263993	ENSG00000263993	RN7SL786P	11:75453173-75453469	NOTEST	0	0	0	0	1	1
ENSG00000263994	ENSG00000263994	SNORA38	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000263995	ENSG00000263995	AC011499.1	19:5822935-5823035	NOTEST	0	0	0	0	1	1
ENSG00000263996	ENSG00000263996	Metazoa_SRP	HSCHR5_1_CTG1:68751159-68751417	NOTEST	0	0	0	0	1	1
ENSG00000263997	ENSG00000263997	AC006130.1	19:2867332-2878515	NOTEST	0	0	0	0	1	1
ENSG00000263998	ENSG00000263998	BX119957.1	HSCHR6_MHC_SSTO:30606237-30632260	NOTEST	0	0	0	0	1	1
ENSG00000263999	ENSG00000263999	RN7SL42P	11:58981879-58982172	NOTEST	0	0	0	0	1	1
ENSG00000264000	ENSG00000264000	RP11-286N3.2	18:5392382-5630699	NOTEST	0	0	0	0	1	1
ENSG00000264001	ENSG00000264001	CT867976.3	GL000230.1:19096-19180	NOTEST	0	0	0	0	1	1
ENSG00000264002	ENSG00000264002	RN7SL52P	21:10380379-10380661	NOTEST	0	0	0	0	1	1
ENSG00000264003	ENSG00000264003	CR759763.1	HSCHR6_MHC_MCF:30135098-30135231	NOTEST	0	0	0	0	1	1
ENSG00000264004	ENSG00000264004	MIR4717	16:2324620-2324692	NOTEST	0	0	0	0	1	1
ENSG00000264005	ENSG00000264005	MIR4314	17:7991373-7991465	NOTEST	0	0	0	0	1	1
ENSG00000264006	ENSG00000264006	AKR1CL1	HG871_PATCH:5196334-5227379	NOTEST	0	0	0	0	1	1
ENSG00000264007	ENSG00000264007	RP11-68I3.10	17:27887564-28513493	NOTEST	0.0318089	0	#NAME?	0	1	1
ENSG00000264008	ENSG00000264008	MIR4640	HSCHR6_MHC_COX:30838645-30857829	NOTEST	0	0	0	0	1	1
ENSG00000264009	ENSG00000264009	AP001631.1	21:44547629-44547729	NOTEST	0	0	0	0	1	1
ENSG00000264010	ENSG00000264010	MIR4429	2:11674241-11782914	NOTEST	0	0	0	0	1	1
ENSG00000264011	ENSG00000264011	RP11-314N2.2	HG1287_PATCH:148527376-148528774	NOTEST	0	0	0	0	1	1
ENSG00000264012	ENSG00000264012	RP11-627G18.2	18:19749403-19785192	NOTEST	0	0	0	0	1	1
ENSG00000264013	ENSG00000264013	MIR3938	3:55542335-56502391	NOTEST	0	0	0	0	1	1
ENSG00000264014	ENSG00000264014	MIR4253	1:23037331-23241818	NOTEST	0	0	0	0	1	1
ENSG00000264015	ENSG00000264015	RP11-176N18.2	18:75133574-75272719	NOTEST	0	0	0	0	1	1
ENSG00000264016	ENSG00000264016	CTC-297N7.9	17:10583653-10718481	NOTEST	0	0	0	0	1	1
ENSG00000264017	ENSG00000264017	RN7SL336P	6:89800664-89800959	NOTEST	0	0	0	0	1	1
ENSG00000264018	ENSG00000264018	RN7SL207P	7:145793179-145793471	NOTEST	0	0	0	0	1	1
ENSG00000264020	ENSG00000264020	AC027806.1	11:39752358-39752453	NOTEST	0	0	0	0	1	1
ENSG00000264021	ENSG00000264021	MIR3917	1:26210671-26233482	NOTEST	0	0	0	0	1	1
ENSG00000264022	ENSG00000264022	AL732363.1	1:149036311-149036377	NOTEST	0	0	0	0	1	1
ENSG00000264023	ENSG00000264023	RP11-728E14.2	17:21359824-21363527	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264024	ENSG00000264024	AL901608.1	14:106178259-106178329	NOTEST	0	0	0	0	1	1
ENSG00000264025	ENSG00000264025	U6	HSCHR6_MHC_APD:28870782-28891771	NOTEST	0	0	0	0	1	1
ENSG00000264026	ENSG00000264026	RP11-1124B17.1	17:70319263-70636611	NOTEST	0	0	0	0	1	1
ENSG00000264027	ENSG00000264027	Metazoa_SRP	HG747_PATCH:65821639-65980494	NOTEST	0	0	0	0	1	1
ENSG00000264028	ENSG00000264028	RN7SL744P	12:54624723-54745633	NOTEST	0	0	0	0	1	1
ENSG00000264029	ENSG00000264029	CTD-2008P7.5	17:26601682-26602742	NOTEST	0	0	0	0	1	1
ENSG00000264030	ENSG00000264030	RN7SL66P	2:10420756-10421017	NOTEST	0	0	0	0	1	1
ENSG00000264031	ENSG00000264031	RP11-68I3.2	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000264032	ENSG00000264032	MIR4491	11:111218481-111218549	NOTEST	0	0	0	0	1	1
ENSG00000264033	ENSG00000264033	PFN1P7	HG1287_PATCH:145107800-145148089	NOTEST	0	0	0	0	1	1
ENSG00000264034	ENSG00000264034	AC010139.1	3:16628298-16711813	NOTEST	0	0	0	0	1	1
ENSG00000264035	ENSG00000264035	RNA5SP246	HG1308_PATCH:130126045-130351086	NOTEST	0	0	0	0	1	1
ENSG00000264036	ENSG00000264036	RN7SL198P	10:12370134-12370388	NOTEST	0	0	0	0	1	1
ENSG00000264037	ENSG00000264037	MIR4472-2	12:116866056-116866123	NOTEST	0	0	0	0	1	1
ENSG00000264038	ENSG00000264038	AC091132.2	17:43471274-43511787	NOTEST	0	0	0	0	1	1
ENSG00000264039	ENSG00000264039	AC114296.1	5:135140193-135140282	NOTEST	0	0	0	0	1	1
ENSG00000264040	ENSG00000264040	RP11-29O13.1	18:65173818-65566856	NOTEST	0	0	0	0	1	1
ENSG00000264041	ENSG00000264041	RN7SL670P	2:204103662-204163009	NOTEST	0	0	0	0	1	1
ENSG00000264042	ENSG00000264042	AL354833.3	13:42024147-42024235	NOTEST	0	0	0	0	1	1
ENSG00000264043	ENSG00000264043	SNORA40	12:109171919-109174194	NOTEST	0.588921	0.566352	-0.0563744	0	1	1
ENSG00000264044	ENSG00000264044	RP11-192H23.7	17:26782769-26972472	NOTEST	0.170959	0.287495	0.749882	0	1	1
ENSG00000264045	ENSG00000264045	AC073127.1	7:102453307-102715286	NOTEST	0	0	0	0	1	1
ENSG00000264046	ENSG00000264046	RN7SL312P	12:57853917-57914300	NOTEST	0	0	0	0	1	1
ENSG00000264047	ENSG00000264047	RN7SL455P	2:165848493-166060577	NOTEST	0	0	0	0	1	1
ENSG00000264048	ENSG00000264048	AL121992.1	1:16010826-16076391	NOTEST	0	0	0	0	1	1
ENSG00000264049	ENSG00000264049	MIR4737	17:58120385-58120466	NOTEST	0	0	0	0	1	1
ENSG00000264050	ENSG00000264050	RP11-22N12.2	17:27524088-27524803	NOTEST	0	0	0	0	1	1
ENSG00000264051	ENSG00000264051	AC007881.1	2:71336813-71357369	NOTEST	0	0	0	0	1	1
ENSG00000264052	ENSG00000264052	MIR3655	5:140018324-140042064	NOTEST	0	0	0	0	1	1
ENSG00000264053	ENSG00000264053	AC078899.7	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000264054	ENSG00000264054	RPL31P9	18:64804847-64804988	NOTEST	0	0	0	0	1	1
ENSG00000264055	ENSG00000264055	AP000261.1	21:33452628-33570125	NOTEST	0	0	0	0	1	1
ENSG00000264056	ENSG00000264056	MIR5685	6:53132195-53213947	NOTEST	0	0	0	0	1	1
ENSG00000264057	ENSG00000264057	RP11-583F2.1	17:62923751-62930321	NOTEST	0.204011	0.124909	-0.707766	0	1	1
ENSG00000264058	ENSG00000264058	KRT222	17:38781213-38821433	NOTEST	0.40752	0.449678	0.142024	0	1	1
ENSG00000264059	ENSG00000264059	AC013558.1	18:68029358-68029459	NOTEST	0	0	0	0	1	1
ENSG00000264060	ENSG00000264060	MIR4316	17:75253818-75496678	NOTEST	0	0	0	0	1	1
ENSG00000264061	ENSG00000264061	FGF7P1	18:14888707-14890085	NOTEST	0	0	0	0	1	1
ENSG00000264062	ENSG00000264062	AC131012.1	12:75956981-76377795	NOTEST	0	0	0	0	1	1
ENSG00000264063	ENSG00000264063	MIR3687	21:9826202-9826263	NOTEST	0	0	0	0	1	1
ENSG00000264064	ENSG00000264064	RP11-758G22.1	HSCHR3_1_CTG1:119011466-11934974	NOTEST	0	0	0	0	1	1
ENSG00000264065	ENSG00000264065	RN7SL139P	X:48863968-48864276	NOTEST	0	0	0	0	1	1
ENSG00000264066	ENSG00000264066	MIR451B	17:27188089-27188984	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264067	ENSG00000264067	RP11-401O9.3	17:10195136-10276447	NOTEST	0.189635	0.373043	0.976119	0	1	1
ENSG00000264068	ENSG00000264068	Metazoa_SRP	HSCHR17_1:43513191-43568077	NOTEST	0	0	0	0	1	1
ENSG00000264069	ENSG00000264069	MIR3943	7:43152197-43605600	NOTEST	0	0	0	0	1	1
ENSG00000264071	ENSG00000264071	RN7SL531P	2:4077270-4077549	NOTEST	0	0	0	0	1	1
ENSG00000264072	ENSG00000264072	RP11-856M7.4	18:10627642-10628843	NOTEST	0	0	0	0	1	1
ENSG00000264073	ENSG00000264073	MIR3199-2	22:28247656-29075853	NOTEST	0	0	0	0	1	1
ENSG00000264074	ENSG00000264074	AC110086.1	2:165280034-165280116	NOTEST	0	0	0	0	1	1
ENSG00000264075	ENSG00000264075	MIR4783	2:128176002-128186822	NOTEST	0	0	0	0	1	1
ENSG00000264076	ENSG00000264076	AL158040.1	10:93806448-94050844	NOTEST	0	0	0	0	1	1
ENSG00000264077	ENSG00000264077	AC010196.1	12:86372515-87232775	NOTEST	0	0	0	0	1	1
ENSG00000264078	ENSG00000264078	RP11-73M7.9	1:32083286-32169920	NOTEST	0	0	0	0	1	1
ENSG00000264079	ENSG00000264079	AC079412.1	16:54583214-54583308	NOTEST	0	0	0	0	1	1
ENSG00000264080	ENSG00000264080	CTD-2015H3.1	18:1780329-1782065	NOTEST	0	0	0	0	1	1
ENSG00000264081	ENSG00000264081	AL136985.1	1:59230520-59230607	NOTEST	0	0	0	0	1	1
ENSG00000264082	ENSG00000264082	VPS45	HG1287_PATCH:150753699-150831742	NOTEST	0	0	0	0	1	1
ENSG00000264083	ENSG00000264083	RP11-227G15.9	17:30757985-30759860	NOTEST	0	0	0	0	1	1
ENSG00000264084	ENSG00000264084	MIR5688	3:85008131-86123579	NOTEST	0	0	0	0	1	1
ENSG00000264085	ENSG00000264085	MIR5004	6:33387846-33421466	NOTEST	0	0	0	0	1	1
ENSG00000264086	ENSG00000264086	SNORD48	HSCHR6_MHC_DBB:31784574-31789730	NOTEST	0	0	0	0	1	1
ENSG00000264088	ENSG00000264088	RP5-998N21.4	HG1287_PATCH:144561207-144621191	NOTEST	0	0	0	0	1	1
ENSG00000264089	ENSG00000264089	MIR3681	2:11988747-12718474	NOTEST	0	0	0	0	1	1
ENSG00000264090	ENSG00000264090	MIR4666B	X:28605515-29974840	NOTEST	0	0	0	0	1	1
ENSG00000264091	ENSG00000264091	AP002495.1	11:71498555-71532594	NOTEST	0	0	0	0	1	1
ENSG00000264092	ENSG00000264092	RN7SL474P	8:16534413-16772553	NOTEST	0	0	0	0	1	1
ENSG00000264093	ENSG00000264093	RP11-401F2.2	17:65272233-65272467	NOTEST	0	0	0	0	1	1
ENSG00000264094	ENSG00000264094	AC022616.1	8:43221855-43221930	NOTEST	0	0	0	0	1	1
ENSG00000264095	ENSG00000264095	AP000560.1	11:74459912-74660245	NOTEST	0	0	0	0	1	1
ENSG00000264096	ENSG00000264096	PDLIM1P2	HG987_PATCH:21348144-21348751	NOTEST	0	0	0	0	1	1
ENSG00000264097	ENSG00000264097	AC034187.1	3:8661085-9005457	NOTEST	0	0	0	0	1	1
ENSG00000264098	ENSG00000264098	CTD-2350C19.1	17:26684603-26734215	NOTEST	0.518818	0.210532	-1.30119	0	1	1
ENSG00000264099	ENSG00000264099	MIR4803	5:71403060-71505395	NOTEST	0	0	0	0	1	1
ENSG00000264100	ENSG00000264100	HLA-T	HG1322_PATCH:29858198-29859330	NOTEST	0	0	0	0	1	1
ENSG00000264101	ENSG00000264101	MIR4689	1:5922731-5922801	NOTEST	0	0	0	0	1	1
ENSG00000264102	ENSG00000264102	MIR4688	11:46354454-46402104	NOTEST	0	0	0	0	1	1
ENSG00000264103	ENSG00000264103	AC017028.3	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000264104	ENSG00000264104	RP11-638L3.4	18:65173818-65566856	NOTEST	0	0	0	0	1	1
ENSG00000264105	ENSG00000264105	MIR3688-1	4:160025329-160281321	NOTEST	0	0	0	0	1	1
ENSG00000264106	ENSG00000264106	AC116562.2	4:4038810-4038914	NOTEST	0	0	0	0	1	1
ENSG00000264107	ENSG00000264107	RP11-848P1.5	17:29335514-29709134	NOTEST	0.0951685	0.112863	0.246022	0	1	1
ENSG00000264108	ENSG00000264108	RP11-357H3.1	18:73720072-73727816	NOTEST	0	0	0	0	1	1
ENSG00000264109	ENSG00000264109	MIR4712	15:50569388-50659636	NOTEST	0	0	0	0	1	1
ENSG00000264110	ENSG00000264110	MIR4300	11:81590892-82429124	NOTEST	0	0	0	0	1	1
ENSG00000264111	ENSG00000264111	WI2-925H4.1	HG1287_PATCH:146288360-146294273	NOTEST	0	0	0	0	1	1
ENSG00000264113	ENSG00000264113	RN7SL784P	17:4736682-4806369	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264114	ENSG00000264114	AC063932.1	3:187868993-188608460	NOTEST	0	0	0	0	1	1
ENSG00000264115	ENSG00000264115	hsa-mir-3180-4	16:15248706-15250877	NOTEST	0	0	0	0	1	1
ENSG00000264116	ENSG00000264116	RP11-321M21.3	18:73118966-73139658	NOTEST	0	0	0	0	1	1
ENSG00000264117	ENSG00000264117	RP11-337C18.7	HG1287_PATCH:14785918-147982177	NOTEST	0	0	0	0	1	1
ENSG00000264118	ENSG00000264118	RN7SL572P	5:23201553-23201836	NOTEST	0	0	0	0	1	1
ENSG00000264119	ENSG00000264119	MIR4795	3:87275338-87275427	NOTEST	0	0	0	0	1	1
ENSG00000264120	ENSG00000264120	AF274855.1	X:151121595-151143152	NOTEST	0	0	0	0	1	1
ENSG00000264121	ENSG00000264121	AL157775.1	6:6046675-6046777	NOTEST	0	0	0	0	1	1
ENSG00000264122	ENSG00000264122	RN7SL697P	HG1497_PATCH:153664284-153664581	NOTEST	0	0	0	0	1	1
ENSG00000264123	ENSG00000264123	RN7SL599P	15:93399732-93400024	NOTEST	0	0	0	0	1	1
ENSG00000264124	ENSG00000264124	AC104687.1	4:77775116-77775213	NOTEST	0	0	0	0	1	1
ENSG00000264125	ENSG00000264125	RP11-354P11.4	17:28521336-28563020	NOTEST	0	0	0	0	1	1
ENSG00000264126	ENSG00000264126	RN7SL158P	9:19106478-19106788	NOTEST	0	0	0	0	1	1
ENSG00000264127	ENSG00000264127	SCML2P1	18:6919494-6929965	NOTEST	0	0.0703953	inf	0	1	1
ENSG00000264128	ENSG00000264128	RN7SL713P	1:59031300-59031604	NOTEST	0	0	0	0	1	1
ENSG00000264129	ENSG00000264129	AC020900.2	5:95220801-96143803	NOTEST	0	0	0	0	1	1
ENSG00000264130	ENSG00000264130	AC110794.1	4:176959233-176959339	NOTEST	0	0	0	0	1	1
ENSG00000264131	ENSG00000264131	AC007631.1	18:62853394-62854254	NOTEST	0	0	0	0	1	1
ENSG00000264133	ENSG00000264133	AC006953.1	19:44150246-44174699	NOTEST	0	0	0	0	1	1
ENSG00000264134	ENSG00000264134	AL121893.1	20:18488136-18542059	NOTEST	0	0	0	0	1	1
ENSG00000264135	ENSG00000264135	AC104306.2	3:32557217-32557312	NOTEST	0	0	0	0	1	1
ENSG00000264136	ENSG00000264136	MIR3689D2	9:137742122-137742202	NOTEST	0	0	0	0	1	1
ENSG00000264137	ENSG00000264137	AC079298.1	4:155140060-155140145	NOTEST	0	0	0	0	1	1
ENSG00000264138	ENSG00000264138	RP11-20B24.3	17:27082995-27188085	NOTEST	0	0	0	0	1	1
ENSG00000264139	ENSG00000264139	MIR3667	22:49808175-50051190	NOTEST	0	0	0	0	1	1
ENSG00000264140	ENSG00000264140	RP5-998N21.7	HG1287_PATCH:144561207-144621191	NOTEST	0	0	0	0	1	1
ENSG00000264141	ENSG00000264141	MIR3928	22:31556047-31556105	NOTEST	0	0	0	0	1	1
ENSG00000264142	ENSG00000264142	AC114969.1	5:81267843-81574396	NOTEST	0	0	0	0	1	1
ENSG00000264143	ENSG00000264143	MIR4664	HG104_HG975_PATCH:144806102-144815971	NOTEST	0	0	0	0	1	1
ENSG00000264144	ENSG00000264144	AC105049.1	8:144926239-144926325	NOTEST	0	0	0	0	1	1
ENSG00000264145	ENSG00000264145	DRD5P2	HG1287_PATCH:144135690-144138791	NOTEST	0	0	0	0	1	1
ENSG00000264146	ENSG00000264146	AC021654.1	3:158680023-159615155	NOTEST	0	0	0	0	1	1
ENSG00000264147	ENSG00000264147	MIR4763	22:46445357-46509808	NOTEST	0	0	0	0	1	1
ENSG00000264148	ENSG00000264148	RP11-848P1.7	17:29335171-29335337	NOTEST	0	0	0	0	1	1
ENSG00000264149	ENSG00000264149	RP11-268I9.3	18:19451406-19473957	NOTEST	0	0	0	0	1	1
ENSG00000264150	ENSG00000264150	RP11-715F3.1	18:2537523-2571508	NOTEST	0	0	0	0	1	1
ENSG00000264151	ENSG00000264151	RP11-739N10.1	18:24916342-25175128	NOTEST	0	0	0	0	1	1
ENSG00000264153	ENSG00000264153	SNORA38	HSCHR6_MHC_QBL:31578693-31595788	NOTEST	0	0	0	0	1	1
ENSG00000264154	ENSG00000264154	OR13Z1P	HG1287_PATCH:148105464-148106298	NOTEST	0	0	0	0	1	1
ENSG00000264155	ENSG00000264155	AC090015.1	12:74411554-74411636	NOTEST	0	0	0	0	1	1
ENSG00000264157	ENSG00000264157	MIR3127	2:97426638-97477628	NOTEST	0	0	0	0	1	1
ENSG00000264158	ENSG00000264158	MIR4670	9:95059639-95432547	NOTEST	0	0	0	0	1	1
ENSG00000264159	ENSG00000264159	RN7SL866P	19:3501315-3501587	NOTEST	0	0	0	0	1	1
ENSG00000264160	ENSG00000264160	MIR4762	22:46067677-46241187	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264162	ENSG00000264162	ITGA10	HG1287_PATCH:146577622-146596604	NOTEST	0	0	0	0	1	1
ENSG00000264163	ENSG00000264163	MIR3689B	9:137741970-137742118	NOTEST	0	0	0	0	1	1
ENSG00000264164	ENSG00000264164	RP11-640N20.6	17:30410197-30424084	NOTEST	0	0	0	0	1	1
ENSG00000264165	ENSG00000264165	AL845439.1	HSCHR6_MHC_QBL:30046173-30046306	NOTEST	0	0	0	0	1	1
ENSG00000264166	ENSG00000264166	RN7SL115P	19:7953389-7968427	NOTEST	0	0	0	0	1	1
ENSG00000264167	ENSG00000264167	RP1-253P7.1	17:17584786-17740325	NOTEST	0	0	0	0	1	1
ENSG00000264168	ENSG00000264168	MTND1P15	17:22022436-22025022	NOTEST	0	0	0	0	1	1
ENSG00000264169	ENSG00000264169	RN7SL665P	9:133259835-133309510	NOTEST	0	0	0	0	1	1
ENSG00000264171	ENSG00000264171	MIR4305	13:40229763-40365802	NOTEST	0	0	0	0	1	1
ENSG00000264172	ENSG00000264172	PDLIM1P3	17:25329686-25330285	NOTEST	0	0	0	0	1	1
ENSG00000264173	ENSG00000264173	MIR3175	15:93425936-93571237	NOTEST	0	0	0	0	1	1
ENSG00000264174	ENSG00000264174	RP11-212E8.1	17:33052527-33053189	NOTEST	0	0	0	0	1	1
ENSG00000264175	ENSG00000264175	MIR3189	19:18485540-18499986	NOTEST	0	0	0	0	1	1
ENSG00000264176	ENSG00000264176	MAGOH2	17:10583653-10718481	NOTEST	0.0574579	0.128417	1.16026	0	1	1
ENSG00000264177	ENSG00000264177	RP1-37N7.1	17:18280975-18292961	NOTEST	0	0	0	0	1	1
ENSG00000264178	ENSG00000264178	AC137674.1	3:30179738-30179806	NOTEST	0	0	0	0	1	1
ENSG00000264179	ENSG00000264179	RP11-672L10.5	18:856526-857046	NOTEST	0	0	0	0	1	1
ENSG00000264180	ENSG00000264180	MIR3135B	HSCHR6_MHC_APD:32702570-32702638	NOTEST	0	0	0	0	1	1
ENSG00000264181	ENSG00000264181	AL713997.1	1:11058232-11058320	NOTEST	0	0	0	0	1	1
ENSG00000264182	ENSG00000264182	AC126763.1	16:15252313-15252378	NOTEST	0	0	0	0	1	1
ENSG00000264183	ENSG00000264183	AC091038.1	18:19284917-19450918	NOTEST	0	0	0	0	1	1
ENSG00000264184	ENSG00000264184	AC096509.1	X:24304661-24304794	NOTEST	0	0	0	0	1	1
ENSG00000264185	ENSG00000264185	RNU6-683P	HSCHR6_MHC_COX:31328371-31328478	NOTEST	0	0	0	0	1	1
ENSG00000264186	ENSG00000264186	RP11-737O24.4	18:2916991-3013313	NOTEST	0	0	0	0	1	1
ENSG00000264187	ENSG00000264187	RP11-45M22.4	17:16945858-17140502	NOTEST	0.520636	0.494612	-0.0739762	0	1	1
ENSG00000264188	ENSG00000264188	RP11-13N13.5	18:19230857-19284766	NOTEST	0	0.0699404	inf	0	1	1
ENSG00000264189	ENSG00000264189	CTD-2533G20.1	18:1883524-2240847	NOTEST	0	0	0	0	1	1
ENSG00000264190	ENSG00000264190	MIR5006	13:42140972-42535256	NOTEST	0	0	0	0	1	1
ENSG00000264192	ENSG00000264192	RN7SL117P	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000264193	ENSG00000264193	RP11-737G21.1	18:23533179-23533432	NOTEST	0	0	0	0	1	1
ENSG00000264194	ENSG00000264194	AC000003.2	17:9813925-10101868	NOTEST	0	0	0	0	1	1
ENSG00000264196	ENSG00000264196	RP11-171G2.1	17:70642087-71088851	NOTEST	0.0327922	0	#NAME?	0	1	1
ENSG00000264197	ENSG00000264197	AP001781.1	HG388_HG400_PATCH:111597631-111637151	NOTEST	0	0	0	0	1	1
ENSG00000264198	ENSG00000264198	RP11-94L15.2	17:37913973-37920089	NOTEST	0.0769905	0.0642329	-0.261369	0	1	1
ENSG00000264199	ENSG00000264199	FAM25C	HG1211_PATCH:48405840-48414013	NOTEST	0	0	0	0	1	1
ENSG00000264200	ENSG00000264200	MIR4693	11:103546721-103765999	NOTEST	0	0	0	0	1	1
ENSG00000264201	ENSG00000264201	MIR4701	12:49159974-49182820	NOTEST	0	0	0	0	1	1
ENSG00000264202	ENSG00000264202	SNORD48	HSCHR6_MHC_COX:31789756-31794910	NOTEST	0	0	0	0	1	1
ENSG00000264203	ENSG00000264203	AC092377.1	16:85475028-85475098	NOTEST	0	0	0	0	1	1
ENSG00000264204	ENSG00000264204	AGAP7	HG1211_PATCH:46604942-46627108	NOTEST	0	0	0	0	1	1
ENSG00000264205	ENSG00000264205	RN7SL71P	5:178893833-178894126	NOTEST	0	0	0	0	1	1
ENSG00000264206	ENSG00000264206	AL590391.1	6:51464520-51952423	NOTEST	0	0	0	0	1	1
ENSG00000264207	ENSG00000264207	RP11-196G18.23	1:149802875-149804109	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264208	ENSG00000264208	MIR4781	1:54519259-54578192	NOTEST	0	0	0	0	1	1
ENSG00000264209	ENSG00000264209	AC104448.1	3:48509196-48542259	NOTEST	0	0	0	0	1	1
ENSG00000264210	ENSG00000264210	MIR4716	15:49398267-49913128	NOTEST	0	0	0	0	1	1
ENSG00000264211	ENSG00000264211	MIR4492	11:118754474-118829269	NOTEST	0	0	0	0	1	1
ENSG00000264212	ENSG00000264212	RP11-94B19.3	18:73968845-73970292	NOTEST	0	0	0	0	1	1
ENSG00000264213	ENSG00000264213	RN7SL324P	19:50887460-50934570	NOTEST	0	0	0	0	1	1
ENSG00000264214	ENSG00000264214	RP11-344P13.4	HG1292_PATCH:122037001-122053006	NOTEST	0	0	0	0	1	1
ENSG00000264215	ENSG00000264215	RP11-283C24.1	17:20691383-20692908	NOTEST	0	0	0	0	1	1
ENSG00000264216	ENSG00000264216	NOS2P1	17:25978359-25992738	NOTEST	0	0	0	0	1	1
ENSG00000264217	ENSG00000264217	RP11-592B15.6	HG1211_PATCH:46435969-46436302	NOTEST	0	0	0	0	1	1
ENSG00000264218	ENSG00000264218	Y_RNA	HSCHR6_MHC_DBB:29715627-29715729	NOTEST	0	0	0	0	1	1
ENSG00000264219	ENSG00000264219	MIR4442	3:25639474-25706430	NOTEST	0	0	0	0	1	1
ENSG00000264221	ENSG00000264221	RP11-292F22.5	HG1211_PATCH:46694724-46698084	NOTEST	0	0	0	0	1	1
ENSG00000264222	ENSG00000264222	RP11-757O6.1	18:14179095-14252139	NOTEST	0	0	0	0	1	1
ENSG00000264223	ENSG00000264223	RP13-766D20.2	HG271_PATCH:79483770-79501576	NOTEST	0	0	0	0	1	1
ENSG00000264224	ENSG00000264224	AC004655.1	X:24712035-25015103	NOTEST	0	0	0	0	1	1
ENSG00000264225	ENSG00000264225	RN7SL730P	17:43513265-43568115	NOTEST	0	0	0	0	1	1
ENSG00000264226	ENSG00000264226	MIR3168	13:41675154-41675236	NOTEST	0	0	0	0	1	1
ENSG00000264227	ENSG00000264227	RN7SL227P	9:124999902-125085743	NOTEST	0	0	0	0	1	1
ENSG00000264228	ENSG00000264228	CR753651.2	HSCHR6_MHC_DBB:28763750-28763814	NOTEST	0	0	0	0	1	1
ENSG00000264229	ENSG00000264229	RNU4ATAC	2:122095351-122407163	NOTEST	0	0	0	0	1	1
ENSG00000264230	ENSG00000264230	AC244230.1	HG1211_PATCH:46871074-46887229	NOTEST	0	0	0	0	1	1
ENSG00000264231	ENSG00000264231	AC026241.1	8:47996974-47997049	NOTEST	0	0	0	0	1	1
ENSG00000264232	ENSG00000264232	RP11-453M23.1	18:63091248-63114748	NOTEST	0	0	0	0	1	1
ENSG00000264233	ENSG00000264233	MIR4456	5:535954-535997	NOTEST	0	0	0	0	1	1
ENSG00000264234	ENSG00000264234	AL161751.1	14:38716911-38716980	NOTEST	0	0	0	0	1	1
ENSG00000264235	ENSG00000264235	RP13-270P17.1	18:3247478-3261848	NOTEST	0.332352	0.258758	-0.361112	0	1	1
ENSG00000264236	ENSG00000264236	RP11-861L17.2	18:66340924-66722426	NOTEST	0	0	0	0	1	1
ENSG00000264237	ENSG00000264237	AL137846.1	9:127019884-127115586	NOTEST	0	0	0	0	1	1
ENSG00000264238	ENSG00000264238	AL590084.1	6:25203480-25203568	NOTEST	0	0	0	0	1	1
ENSG00000264239	ENSG00000264239	AL360297.1	1:71547006-72748417	NOTEST	0	0	0	0	1	1
ENSG00000264240	ENSG00000264240	RP11-19P22.6	17:26004830-26005113	NOTEST	0	0	0	0	1	1
ENSG00000264241	ENSG00000264241	AL138721.1	6:35085847-35116387	NOTEST	0	0	0	0	1	1
ENSG00000264242	ENSG00000264242	RP11-271K11.1	17:28880714-28890511	NOTEST	0	0	0	0	1	1
ENSG00000264243	ENSG00000264243	RP11-6N17.1	17:45940707-45942556	NOTEST	0	0	0	0	1	1
ENSG00000264244	ENSG00000264244	CR753846.4	HSCHR6_MHC_DBB:32696849-32696917	NOTEST	0	0	0	0	1	1
ENSG00000264245	ENSG00000264245	RP11-822E23.4	17:21428050-21477781	NOTEST	0	0	0	0	1	1
ENSG00000264246	ENSG00000264246	RP11-138C24.2	18:3496029-4455335	NOTEST	0	0	0	0	1	1
ENSG00000264248	ENSG00000264248	AL603831.1	10:320129-735683	NOTEST	0	0	0	0	1	1
ENSG00000264249	ENSG00000264249	MIR3912	5:170813659-170813764	NOTEST	0	0	0	0	1	1
ENSG00000264250	ENSG00000264250	RN7SL835P	19:17003757-17137625	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264251	ENSG00000264251	RN7SL819P	17:42785975-42829632	NOTEST	0	0	0	0	1	1
ENSG00000264252	ENSG00000264252	RNVU1-12	HG1287_PATCH:14908912-149089290	NOTEST	0	0	0	0	1	1
ENSG00000264253	ENSG00000264253	FOXN1	HG883_PATCH:26782770-26941216	NOTEST	0	0	0	0	1	1
ENSG00000264254	ENSG00000264254	CTD-3096M3.1	18:5310394-5317663	NOTEST	0	0	0	0	1	1
ENSG00000264255	ENSG00000264255	RN7SL463P	9:37438110-37465396	NOTEST	0	0	0	0	1	1
ENSG00000264256	ENSG00000264256	AC025166.1	15:41167510-41167608	NOTEST	0	0	0	0	1	1
ENSG00000264257	ENSG00000264257	KIR3DP1	19:55235968-55378662	NOTEST	0	0	0	0	1	1
ENSG00000264258	ENSG00000264258	hsa-mir-1236	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000264259	ENSG00000264259	RNU1-116P	HSCHR6_MHC_COX:32473483-32473630	NOTEST	0	0	0	0	1	1
ENSG00000264260	ENSG00000264260	RP11-94B19.1	18:73921464-73927657	NOTEST	0	0	0	0	1	1
ENSG00000264261	ENSG00000264261	AC024908.1	10:2495328-2495418	NOTEST	0	0	0	0	1	1
ENSG00000264262	ENSG00000264262	RP11-285M22.3	17:22176021-22191945	NOTEST	0	0	0	0	1	1
ENSG00000264263	ENSG00000264263	RP11-671P2.1	18:49866541-51094653	NOTEST	0	0	0	0	1	1
ENSG00000264264	ENSG00000264264	Metazoa_SRP	HSCHR6_MHC_DBB:30865365-30865629	NOTEST	0	0	0	0	1	1
ENSG00000264265	ENSG00000264265	RP11-14P20.1	18:508567-515294	NOTEST	0	0	0	0	1	1
ENSG00000264266	ENSG00000264266	MIR4322	19:10244020-10341962	NOTEST	0	0	0	0	1	1
ENSG00000264267	ENSG00000264267	AC069303.1	2:33931952-34522820	NOTEST	0	0	0	0	1	1
ENSG00000264268	ENSG00000264268	MIR4767	X:6966960-7066231	NOTEST	0	0	0	0	1	1
ENSG00000264269	ENSG00000264269	RP11-15F12.1	18:46550072-46987717	NOTEST	0	0	0	0	1	1
ENSG00000264270	ENSG00000264270	RP11-474I11.7	17:73584138-73704142	NOTEST	0.111631	0	#NAME?	0	1	1
ENSG00000264271	ENSG00000264271	RN7SL488P	1:63906440-64125916	NOTEST	0	0	0	0	1	1
ENSG00000264272	ENSG00000264272	CTD-2514K5.4	17:72209652-72258159	NOTEST	0	0.513704	inf	0	1	1
ENSG00000264273	ENSG00000264273	CTD-2145A24.4	17:18739019-18834581	NOTEST	0.0508562	0.123023	1.27443	0	1	1
ENSG00000264274	ENSG00000264274	MIR4799	4:148653213-148993931	NOTEST	0	0	0	0	1	1
ENSG00000264275	ENSG00000264275	RN7SL753P	2:203198161-203198451	NOTEST	0	0	0	0	1	1
ENSG00000264276	ENSG00000264276	RN7SL287P	19:36673187-36737159	NOTEST	0	0	0	0	1	1
ENSG00000264277	ENSG00000264277	AC011073.1	17:54132147-54132247	NOTEST	0	0	0	0	1	1
ENSG00000264278	ENSG00000264278	RP11-162A12.2	18:74506687-74534251	NOTEST	0.142949	0.111198	-0.362362	0	1	1
ENSG00000264279	ENSG00000264279	MIR4786	2:240831866-240964819	NOTEST	0	0	0	0	1	1
ENSG00000264280	ENSG00000264280	RN7SL322P	19:48084279-48084576	NOTEST	0	0	0	0	1	1
ENSG00000264282	ENSG00000264282	FAM25E	HG1211_PATCH:46310875-46313036	NOTEST	0	0	0	0	1	1
ENSG00000264283	ENSG00000264283	AC025300.1	11:12297626-12380691	NOTEST	0	0	0	0	1	1
ENSG00000264284	ENSG00000264284	AL391380.1	X:134654007-134716435	NOTEST	0	0	0	0	1	1
ENSG00000264286	ENSG00000264286	AL138930.2	1:160506862-160549306	NOTEST	0	0	0	0	1	1
ENSG00000264288	ENSG00000264288	AL138999.1	13:33677271-33924767	NOTEST	0	0	0	0	1	1
ENSG00000264289	ENSG00000264289	RP11-268I9.4	18:19494329-19494621	NOTEST	0	0	0	0	1	1
ENSG00000264290	ENSG00000264290	RP11-68I3.4	17:27887564-28513493	NOTEST	0.101022	0.227178	1.16915	0	1	1
ENSG00000264291	ENSG00000264291	RNA5SP310	HG1211_PATCH:46349540-46411619	NOTEST	0	0	0	0	1	1
ENSG00000264292	ENSG00000264292	MIR2467	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000264294	ENSG00000264294	SNORD55	1:45205489-45244451	NOTEST	0	0	0	0	1	1
ENSG00000264295	ENSG00000264295	MIR3922	12:104849072-105155792	NOTEST	0	0	0	0	1	1
ENSG00000264296	ENSG00000264296	RP11-116K4.1	18:51668502-51668947	NOTEST	0	0.0385915	inf	0	1	1
ENSG00000264297	ENSG00000264297	MIR4433	2:64565200-64568781	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264298	ENSG00000264298	AL353803.1	9:132240834-132240931	NOTEST	0	0	0	0	1	1
ENSG00000264299	ENSG00000264299	RP11-680F20.12	11:125820010-125933230	NOTEST	0.000103301	0.258224	11.2876	0	1	1
ENSG00000264300	ENSG00000264300	RP11-640N20.1	17:30330128-30333707	NOTEST	0	0	0	0	1	1
ENSG00000264302	ENSG00000264302	MIR4723	17:26684603-26734215	NOTEST	0	0	0	0	1	1
ENSG00000264303	ENSG00000264303	AC011410.1	5:171197533-171197724	NOTEST	0	0	0	0	1	1
ENSG00000264304	ENSG00000264304	RP11-20B24.7	17:27206352-27224697	NOTEST	0.113976	0.328967	1.52921	0	1	1
ENSG00000264305	ENSG00000264305	RN7SL99P	16:10420290-10577495	NOTEST	0	0	0	0	1	1
ENSG00000264306	ENSG00000264306	AC104304.2	3:46556912-46668033	NOTEST	0	0	0	0	1	1
ENSG00000264307	ENSG00000264307	AC016831.6	HG1308_PATCH:130503857-130507379	NOTEST	0	0	0	0	1	1
ENSG00000264308	ENSG00000264308	AL121897.1	20:30865466-30922814	NOTEST	0	0	0	0	1	1
ENSG00000264309	ENSG00000264309	MIR4694	11:19372270-20143144	NOTEST	0	0	0	0	1	1
ENSG00000264310	ENSG00000264310	AL157883.1	9:78338660-78338746	NOTEST	0	0	0	0	1	1
ENSG00000264311	ENSG00000264311	CCDC58P1	18:10612300-10626350	NOTEST	0	0	0	0	1	1
ENSG00000264312	ENSG00000264312	RN7SL642P	7:75162620-75368280	NOTEST	0	0	0	0	1	1
ENSG00000264313	ENSG00000264313	RN7SL644P	10:94418800-94419055	NOTEST	0	0	0	0	1	1
ENSG00000264314	ENSG00000264314	MIR548AT	17:40610861-40674629	NOTEST	0	0	0	0	1	1
ENSG00000264315	ENSG00000264315	HNRNPA1P11	18:70203914-70305756	NOTEST	0	0	0	0	1	1
ENSG00000264316	ENSG00000264316	RP11-846F4.9	17:22029937-22030718	NOTEST	0	0	0	0	1	1
ENSG00000264317	ENSG00000264317	RN7SL154P	19:34850384-34919178	NOTEST	0	0	0	0	1	1
ENSG00000264318	ENSG00000264318	RN7SL802P	5:100917533-100917830	NOTEST	0	0	0	0	1	1
ENSG00000264319	ENSG00000264319	MIR4801	4:37243531-37243613	NOTEST	0	0	0	0	1	1
ENSG00000264321	ENSG00000264321	AL358134.1	6:153552454-153668623	NOTEST	0	0	0	0	1	1
ENSG00000264322	ENSG00000264322	RN7SL448P	17:58754813-59488916	NOTEST	0	0	0	0	1	1
ENSG00000264323	ENSG00000264323	AC093887.1	4:147560044-147563626	NOTEST	0	0	0	0	1	1
ENSG00000264324	ENSG00000264324	RP11-287D1.3	2:74425688-74621009	NOTEST	0	0.0032818	inf	0	1	1
ENSG00000264325	ENSG00000264325	CR925767.1	HG1322_PATCH:29759096-29769948	NOTEST	0	0	0	0	1	1
ENSG00000264326	ENSG00000264326	MIR4657	7:44915895-44925992	NOTEST	0	0	0	0	1	1
ENSG00000264327	ENSG00000264327	AC024149.1	3:53528682-53880417	NOTEST	0	0	0	0	1	1
ENSG00000264328	ENSG00000264328	RN7SL781P	8:28924795-29120641	NOTEST	0	0	0	0	1	1
ENSG00000264329	ENSG00000264329	MIR3911	9:130374543-130497604	NOTEST	0	0	0	0	1	1
ENSG00000264330	ENSG00000264330	MIR5186	3:151283663-151283783	NOTEST	0	0	0	0	1	1
ENSG00000264331	ENSG00000264331	AC003035.1	X:14093909-14094010	NOTEST	0	0	0	0	1	1
ENSG00000264332	ENSG00000264332	AC111194.1	4:55876999-55877099	NOTEST	0	0	0	0	1	1
ENSG00000264333	ENSG00000264333	AC020915.1	19:58739959-58827023	NOTEST	0	0	0	0	1	1
ENSG00000264334	ENSG00000264334	RP11-671C19.2	18:75683249-75705678	NOTEST	0	0	0	0	1	1
ENSG00000264335	ENSG00000264335	RP11-439A17.5	HG1292_PATCH:121660748-121689449	NOTEST	0	0	0	0	1	1
ENSG00000264336	ENSG00000264336	AC140479.1	2:111058888-111058970	NOTEST	0	0	0	0	1	1
ENSG00000264337	ENSG00000264337	GPR89A	HG1287_PATCH:146294374-146357063	NOTEST	0	0	0	0	1	1
ENSG00000264338	ENSG00000264338	AL359973.1	X:125606710-125606867	NOTEST	0	0	0	0	1	1
ENSG00000264339	ENSG00000264339	RP11-769O8.2	18:721587-812547	NOTEST	0	0.136409	inf	0	1	1
ENSG00000264340	ENSG00000264340	RP11-231E4.3	18:72201674-72254448	NOTEST	0	0.274393	inf	0	1	1
ENSG00000264341	ENSG00000264341	MIR4417	1:5624130-5624203	NOTEST	0	0	0	0	1	1
ENSG00000264342	ENSG00000264342	MIR3660	5:89312437-89312537	NOTEST	0	0	0	0	1	1
ENSG00000264343	ENSG00000264343	NOTCH2NL	HG1287_PATCH:146838680-146915449	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264344	ENSG00000264344	AP000936.2	11:116706466-116969153	NOTEST	0	0	0	0	1	1
ENSG00000264345	ENSG00000264345	RP11-958F21.1	18:22513450-22567646	NOTEST	0	0	0	0	1	1
ENSG00000264346	ENSG00000264346	SNORA77	22:20067754-20114878	NOTEST	0	0	0	0	1	1
ENSG00000264347	ENSG00000264347	RN7SL24P	1:24197015-24285549	NOTEST	0	0	0	0	1	1
ENSG00000264349	ENSG00000264349	MIR4258	1:154947128-154951725	NOTEST	0	0	0	0	1	1
ENSG00000264350	ENSG00000264350	SNRPGP2	18:51933258-51933484	NOTEST	0	0	0	0	1	1
ENSG00000264351	ENSG00000264351	snoU13	HSCHR5_1_CTG1:69517116-69536103	NOTEST	0	0	0	0	1	1
ENSG00000264352	ENSG00000264352	RN7SL602P	2:35024916-35410755	NOTEST	0	0	0	0	1	1
ENSG00000264353	ENSG00000264353	Y_RNA	HSCHR6_MHC_DBB:31611187-31653368	NOTEST	0	0	0	0	1	1
ENSG00000264354	ENSG00000264354	MIR3134	3:15708742-15901278	NOTEST	0	0	0	0	1	1
ENSG00000264355	ENSG00000264355	AC008738.2	19:33667977-33668061	NOTEST	0	0	0	0	1	1
ENSG00000264356	ENSG00000264356	RN7SL763P	9:42031880-42032162	NOTEST	0	0	0	0	1	1
ENSG00000264357	ENSG00000264357	MIR4648	7:2552162-2568811	NOTEST	0	0	0	0	1	1
ENSG00000264358	ENSG00000264358	MIR3122	1:212208918-212280742	NOTEST	0	0	0	0	1	1
ENSG00000264359	ENSG00000264359	NEK4P2	17:16569420-16570432	NOTEST	0	0	0	0	1	1
ENSG00000264360	ENSG00000264360	RP11-495P10.8	HG1287_PATCH:14897730-148983971	NOTEST	0	0	0	0	1	1
ENSG00000264361	ENSG00000264361	RN7SL607P	20:20719077-20719374	NOTEST	0	0	0	0	1	1
ENSG00000264362	ENSG00000264362	AC093875.1	4:137628332-137628416	NOTEST	0	0	0	0	1	1
ENSG00000264363	ENSG00000264363	HIST2H2BB	HG1287_PATCH:144561207-144621191	NOTEST	0	0	0	0	1	1
ENSG00000264365	ENSG00000264365	RP11-621L6.2	18:21718941-21977844	NOTEST	0.11255	0.0531931	-1.08125	0	1	1
ENSG00000264366	ENSG00000264366	Z95400.1	X:86740881-86740963	NOTEST	0	0	0	0	1	1
ENSG00000264369	ENSG00000264369	TAMM41	HSCHR3_1_CTG1:11831915-11888393	NOTEST	0	0	0	0	1	1
ENSG00000264370	ENSG00000264370	MIR3125	2:12857014-12882860	NOTEST	0	0	0	0	1	1
ENSG00000264371	ENSG00000264371	MIR4425	1:25349993-25350077	NOTEST	0	0	0	0	1	1
ENSG00000264372	ENSG00000264372	AC108519.1	4:9168022-9171996	NOTEST	0	0	0	0	1	1
ENSG00000264373	ENSG00000264373	RP11-227G15.6	17:30761957-30762047	NOTEST	0	0	0	0	1	1
ENSG00000264374	ENSG00000264374	AL357115.1	X:80457441-80554046	NOTEST	0	0	0	0	1	1
ENSG00000264375	ENSG00000264375	RP11-343H5.6	HG1293_PATCH:206698209-206747980	NOTEST	0	0	0	0	1	1
ENSG00000264376	ENSG00000264376	RN7SL613P	15:62144587-62352672	NOTEST	0	0	0	0	1	1
ENSG00000264377	ENSG00000264377	MIR4671	1:234040678-234460262	NOTEST	0	0	0	0	1	1
ENSG00000264378	ENSG00000264378	AC116533.2	11:17076458-17076554	NOTEST	0	0	0	0	1	1
ENSG00000264379	ENSG00000264379	SNORD39	9:21455482-21559668	NOTEST	0	0	0	0	1	1
ENSG00000264380	ENSG00000264380	AL590113.1	1:85731930-86043933	NOTEST	0	0	0	0	1	1
ENSG00000264382	ENSG00000264382	AC007881.2	2:71163011-71306935	NOTEST	0	0	0	0	1	1
ENSG00000264383	ENSG00000264383	AC068014.1	17:80709939-81009686	NOTEST	0	0	0	0	1	1
ENSG00000264384	ENSG00000264384	RN7SL431P	1:154127783-154167124	NOTEST	0	0.0799475	inf	0	1	1
ENSG00000264385	ENSG00000264385	RN7SL421P	1:22303513-22325135	NOTEST	0	0	0	0	1	1
ENSG00000264386	ENSG00000264386	MIR4513	15:75074397-75095539	NOTEST	0	0	0	0	1	1
ENSG00000264387	ENSG00000264387	MIR5007	13:55748588-55748683	NOTEST	0	0	0	0	1	1
ENSG00000264388	ENSG00000264388	RP11-752P2.1	18:69255772-69256120	NOTEST	0	0	0	0	1	1
ENSG00000264389	ENSG00000264389	U1	HSCHR6_MHC_QBL:32452833-32452980	NOTEST	0	0	0	0	1	1
ENSG00000264390	ENSG00000264390	MIR4465	6:141004950-141005020	NOTEST	0	0	0	0	1	1
ENSG00000264391	ENSG00000264391	RN7SL208P	5:76132726-76133020	NOTEST	0	0	0	0	1	1
ENSG00000264392	ENSG00000264392	AC002477.1	X:119058423-119058513	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264393	ENSG00000264393	Y_RNA	HSCHR6_MHC_APD:31756647-31775083	NOTEST	0	0	0	0	1	1
ENSG00000264395	ENSG00000264395	MIR3193	20:30194988-30195043	NOTEST	0	0	0	0	1	1
ENSG00000264396	ENSG00000264396	RN7SL264P	X:71401202-71527037	NOTEST	0	0	0	0	1	1
ENSG00000264397	ENSG00000264397	MIR3180-5	16:2185977-2186130	NOTEST	0	0	0	0	1	1
ENSG00000264398	ENSG00000264398	AL031601.1	10:42730350-42730423	NOTEST	0	0	0	0	1	1
ENSG00000264399	ENSG00000264399	MIR4736	17:56378591-56494956	NOTEST	0	0	0	0	1	1
ENSG00000264400	ENSG00000264400	RN7SL491P	19:35890412-35910287	NOTEST	0.301677	0.468755	0.635828	0	1	1
ENSG00000264401	ENSG00000264401	AL935042.1	HSCHR6_MHC_QBL:32831135-32878022	NOTEST	0	0	0	0	1	1
ENSG00000264402	ENSG00000264402	MIR548AL	11:74041362-74197096	NOTEST	0	0	0	0	1	1
ENSG00000264404	ENSG00000264404	RP11-508M1.7	HG1211_PATCH:47236043-47246689	NOTEST	0	0	0	0	1	1
ENSG00000264405	ENSG00000264405	MIR3913-1	12:69978501-69978603	NOTEST	0	0	0	0	1	1
ENSG00000264406	ENSG00000264406	MIR548AP	15:86368865-86368961	NOTEST	0	0	0	0	1	1
ENSG00000264407	ENSG00000264407	RN7SL528P	19:4457958-4471490	NOTEST	0	0	0	0	1	1
ENSG00000264408	ENSG00000264408	MIR4470	8:62627346-62627418	NOTEST	0	0	0	0	1	1
ENSG00000264409	ENSG00000264409	AC113195.1	18:64710603-64710681	NOTEST	0	0	0	0	1	1
ENSG00000264410	ENSG00000264410	AL121931.1	6:63436739-63436829	NOTEST	0	0	0	0	1	1
ENSG00000264411	ENSG00000264411	BX470194.1	HSCHR6_MHC_SSTO:28763740-28763804	NOTEST	0	0	0	0	1	1
ENSG00000264412	ENSG00000264412	MIR3135B	HSCHR6_MHC_COX:32641387-32641455	NOTEST	0	0	0	0	1	1
ENSG00000264413	ENSG00000264413	AC011495.1	19:50179042-50193832	NOTEST	0	0	0	0	1	1
ENSG00000264415	ENSG00000264415	7SK	HSCHR6_MHC_QBL:30821624-30821927	NOTEST	0	0	0	0	1	1
ENSG00000264416	ENSG00000264416	FAM72D	HG1287_PATCH:145782414-145799107	NOTEST	0	0	0	0	1	1
ENSG00000264417	ENSG00000264417	Metazoa_SRP	HSCHR6_MHC_DBB:30709196-30709444	NOTEST	0	0	0	0	1	1
ENSG00000264419	ENSG00000264419	MIR548AC	1:117057156-117113661	NOTEST	0	0	0	0	1	1
ENSG00000264420	ENSG00000264420	AL158111.1	14:46285345-46285432	NOTEST	0	0	0	0	1	1
ENSG00000264421	ENSG00000264421	RP11-401F2.4	17:65066553-65242105	NOTEST	0	0	0	0	1	1
ENSG00000264422	ENSG00000264422	RP11-434D2.12	17:20479979-20482061	NOTEST	0	0	0	0	1	1
ENSG00000264423	ENSG00000264423	RN7SL718P	19:41696851-41697134	NOTEST	0	0	0	0	1	1
ENSG00000264424	ENSG00000264424	MYH4	17:10286448-10527203	NOTEST	0	0	0	0	1	1
ENSG00000264425	ENSG00000264425	MIR4653	7:100797677-100804877	NOTEST	0	0	0	0	1	1
ENSG00000264426	ENSG00000264426	MIR4283-2	7:57023491-57023571	NOTEST	0	0	0	0	1	1
ENSG00000264427	ENSG00000264427	MIR4650-2	HG1257_PATCH:72039492-72293191	NOTEST	0	0	0	0	1	1
ENSG00000264428	ENSG00000264428	AL691523.1	1:3773844-3801993	NOTEST	0	0	0	0	1	1
ENSG00000264429	ENSG00000264429	MIR3183	17:900356-1132315	NOTEST	0	0	0	0	1	1
ENSG00000264430	ENSG00000264430	RP11-495P10.5	HG1287_PATCH:148977304-148983971	NOTEST	0	0	0	0	1	1
ENSG00000264431	ENSG00000264431	RP11-285M22.2	17:22192160-22194158	NOTEST	0	0	0	0	1	1
ENSG00000264433	ENSG00000264433	RP11-720L2.3	18:316736-319165	NOTEST	0	0	0	0	1	1
ENSG00000264434	ENSG00000264434	CTD-2006O16.2	18:22641889-22932154	NOTEST	0	0	0	0	1	1
ENSG00000264435	ENSG00000264435	RP11-338L22.3	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000264436	ENSG00000264436	DUSP8P2	HG1211_PATCH:48058999-48065145	NOTEST	0	0	0	0	1	1
ENSG00000264437	ENSG00000264437	AC091517.1	12:60420551-60420638	NOTEST	0	0	0	0	1	1
ENSG00000264438	ENSG00000264438	RN7SL560P	9:131464801-131486406	NOTEST	0	0	0	0	1	1
ENSG00000264439	ENSG00000264439	AL136001.1	14:104394798-104519004	NOTEST	0	0	0	0	1	1
ENSG00000264440	ENSG00000264440	FAM229B	HG1304_PATCH:112408801-112423993	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264441	ENSG00000264441	AC006539.1	19:20107866-20150315	NOTEST	0	0	0	0	1	1
ENSG00000264442	ENSG00000264442	RN7SL119P	11:62574368-62599560	NOTEST	0	0	0	0	1	1
ENSG00000264443	ENSG00000264443	RP4-594I10.3	1:24829386-24882515	NOTEST	0	0	0	0	1	1
ENSG00000264444	ENSG00000264444	SDHCP1	18:66340924-66722426	NOTEST	0	0	0	0	1	1
ENSG00000264445	ENSG00000264445	AC087269.2	8:8490973-8491058	NOTEST	0	0	0	0	1	1
ENSG00000264446	ENSG00000264446	AC046130.1	12:34175215-34209675	NOTEST	0	0	0	0	1	1
ENSG00000264447	ENSG00000264447	AL445256.1	6:72596405-73112845	NOTEST	0	0	0	0	1	1
ENSG00000264448	ENSG00000264448	MIR378D2	8:94870034-94938294	NOTEST	0.200072	0.248503	0.312743	0	1	1
ENSG00000264449	ENSG00000264449	RP11-945C19.4	18:5882070-5909121	NOTEST	0	0	0	0	1	1
ENSG00000264450	ENSG00000264450	RP5-1110E20.1	HSCHR17_4_CTG4:39007051-39023462	NOTEST	0	0	0	0	1	1
ENSG00000264451	ENSG00000264451	RP11-433M22.2	17:46537731-46543402	NOTEST	0	0	0	0	1	1
ENSG00000264452	ENSG00000264452	snoZ6	21:45770045-45862964	NOTEST	0	0	0	0	1	1
ENSG00000264453	ENSG00000264453	AC003006.1	19:58193336-58269527	NOTEST	0	0	0	0	1	1
ENSG00000264454	ENSG00000264454	AL049745.1	1:54231132-54304533	NOTEST	0	0	0	0	1	1
ENSG00000264455	ENSG00000264455	MIR4721	16:28853731-28857729	NOTEST	0	0	0	0	1	1
ENSG00000264456	ENSG00000264456	RP11-848P1.2	17:29295802-29326929	NOTEST	0.18196	0.0816576	-1.15597	0	1	1
ENSG00000264457	ENSG00000264457	MIR4509-3	HSCHR15_1_CTG4:28747517-28747611	NOTEST	0	0	0	0	1	1
ENSG00000264458	ENSG00000264458	RP11-220C2.1	17:30819539-31205655	NOTEST	0	0	0	0	1	1
ENSG00000264461	ENSG00000264461	RN7SL179P	12:98906750-98944157	NOTEST	0.256678	0	#NAME?	0	1	1
ENSG00000264463	ENSG00000264463	AC090133.1	8:12763346-12763430	NOTEST	0	0	0	0	1	1
ENSG00000264464	ENSG00000264464	RP11-110H1.8	18:47025759-47028230	NOTEST	0	0	0	0	1	1
ENSG00000264465	ENSG00000264465	AC008938.1	16:24450308-24450408	NOTEST	0	0	0	0	1	1
ENSG00000264466	ENSG00000264466	U8	HG871_PATCH:5029586-5060223	NOTEST	0	0	0	0	1	1
ENSG00000264467	ENSG00000264467	RN7SL29P	X:122734411-122866906	NOTEST	0	0	0	0	1	1
ENSG00000264468	ENSG00000264468	MIR4520A	17:6558758-6558828	NOTEST	0	0	0	0	1	1
ENSG00000264470	ENSG00000264470	MIR4794	1:64936427-65158741	NOTEST	0	0	0	0	1	1
ENSG00000264471	ENSG00000264471	MIR4467	7:102105375-102119354	NOTEST	0	0	0	0	1	1
ENSG00000264472	ENSG00000264472	RP11-861L17.3	18:66340924-66722426	NOTEST	0	0	0	0	1	1
ENSG00000264473	ENSG00000264473	hsa-mir-4538	14:106324333-106324411	NOTEST	0	0	0	0	1	1
ENSG00000264474	ENSG00000264474	MIR4656	7:4815252-4833943	NOTEST	0	0	0	0	1	1
ENSG00000264475	ENSG00000264475	RP11-76K13.3	18:6941742-7117813	NOTEST	0	0	0	0	1	1
ENSG00000264477	ENSG00000264477	MIR5682	3:120626918-121143608	NOTEST	0	0	0	0	1	1
ENSG00000264478	ENSG00000264478	AC100767.1	11:23493189-23493259	NOTEST	0	0	0	0	1	1
ENSG00000264479	ENSG00000264479	AC023824.1	16:34442273-34518517	NOTEST	0	0	0	0	1	1
ENSG00000264480	ENSG00000264480	MIR4714	15:99192199-99675798	NOTEST	0	0	0	0	1	1
ENSG00000264481	ENSG00000264481	RP11-337C18.4	HG1287_PATCH:14800552-148006639	NOTEST	0	0	0	0	1	1
ENSG00000264482	ENSG00000264482	MIR4705	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000264483	ENSG00000264483	MIR5008	1:228106356-228135599	NOTEST	0	0	0	0	1	1
ENSG00000264484	ENSG00000264484	RN7SL697P	X:153724166-153724463	NOTEST	0	0	0	0	1	1
ENSG00000264485	ENSG00000264485	RN7SL627P	17:18739019-18834581	NOTEST	0	0	0	0	1	1
ENSG00000264486	ENSG00000264486	CTD-2008P7.3	17:26583400-26593395	NOTEST	0	0.0173343	inf	0	1	1
ENSG00000264487	ENSG00000264487	HLA-U	HG1322_PATCH:29893935-29894121	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264488	ENSG00000264488	RP11-605F20.1	17:38959995-38965548	NOTEST	0	0	0	0	1	1
ENSG00000264489	ENSG00000264489	AC120120.1	5:91378413-92023961	NOTEST	0	0	0	0	1	1
ENSG00000264490	ENSG00000264490	WI2-87327B8.1	20:61172796-61174714	NOTEST	0	0	0	0	1	1
ENSG00000264491	ENSG00000264491	RP11-349A8.3	17:64961025-65029514	NOTEST	0	0	0	0	1	1
ENSG00000264492	ENSG00000264492	RP11-822E23.7	HG987_PATCH:21422825-21424581	NOTEST	0	0	0	0	1	1
ENSG00000264493	ENSG00000264493	MIR4298	11:1874199-1913497	NOTEST	0	0	0	0	1	1
ENSG00000264494	ENSG00000264494	MIR4650-2	7:72023728-72298777	NOTEST	0	0	0	0	1	1
ENSG00000264495	ENSG00000264495	Y_RNA	HSCHR6_MHC_MANN:29715257-29715359	NOTEST	0	0	0	0	1	1
ENSG00000264496	ENSG00000264496	AC108218.1	4:25314406-25372005	NOTEST	0	0	0	0	1	1
ENSG00000264497	ENSG00000264497	RP11-640N20.5	17:30334890-30380523	NOTEST	0	0	0	0	1	1
ENSG00000264498	ENSG00000264498	AC139463.1	HSCHR5_1_CTG1:69863006-69957699	NOTEST	0	0	0	0	1	1
ENSG00000264499	ENSG00000264499	GJA8	HG1287_PATCH:148589234-148595681	NOTEST	0	0	0	0	1	1
ENSG00000264500	ENSG00000264500	MIR3124	1:249104647-249120832	NOTEST	0	0	0	0	1	1
ENSG00000264502	ENSG00000264502	AC024590.1	16:82381111-82381184	NOTEST	0	0	0	0	1	1
ENSG00000264503	ENSG00000264503	RP11-856M7.7	18:10612300-10626350	NOTEST	0	0	0	0	1	1
ENSG00000264504	ENSG00000264504	RP11-1055B8.3	HG271_PATCH:79349800-79359160	NOTEST	0	0	0	0	1	1
ENSG00000264505	ENSG00000264505	MIR4534	22:38339527-38437922	NOTEST	0	0	0	0	1	1
ENSG00000264506	ENSG00000264506	RP11-147L13.2	HG747_PATCH:66242744-66253272	NOTEST	0	0	0	0	1	1
ENSG00000264507	ENSG00000264507	U6	HSCHR10_1_CTG2:27604048-27604155	NOTEST	0	0	0	0	1	1
ENSG00000264508	ENSG00000264508	RN7SL473P	1:150539039-150539336	NOTEST	0	0.544017	inf	0	1	1
ENSG00000264509	ENSG00000264509	CPA1	HG1308_PATCH:130020179-130027955	NOTEST	0	0	0	0	1	1
ENSG00000264510	ENSG00000264510	BX649553.3	X:1387692-1429274	NOTEST	0	0	0	0	1	1
ENSG00000264511	ENSG00000264511	MIR3678	17:73402149-73402243	NOTEST	0	0	0	0	1	1
ENSG00000264512	ENSG00000264512	MIR5692A1	8:12576635-12576704	NOTEST	0	0	0	0	1	1
ENSG00000264513	ENSG00000264513	RP11-556O9.2	17:61086916-61509572	NOTEST	0	0	0	0	1	1
ENSG00000264514	ENSG00000264514	RP11-720L2.4	18:316736-319165	NOTEST	0	0	0	0	1	1
ENSG00000264516	ENSG00000264516	AC233702.1	HG987_PATCH:21481129-21481217	NOTEST	0	0	0	0	1	1
ENSG00000264517	ENSG00000264517	AC003001.1	X:84498996-84528368	NOTEST	0	0	0	0	1	1
ENSG00000264518	ENSG00000264518	AC017028.4	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000264519	ENSG00000264519	RN7SL596P	11:63565259-63565543	NOTEST	0	0	0	0	1	1
ENSG00000264520	ENSG00000264520	RP4-777O23.2	7:30536236-30673649	NOTEST	0.0751593	0	#NAME?	0	1	1
ENSG00000264522	ENSG00000264522	OTUD7B	HG1287_PATCH:150626746-150697152	NOTEST	0	0	0	0	1	1
ENSG00000264523	ENSG00000264523	RP11-158I9.7	11:118754474-118829269	NOTEST	0	0.00913399	inf	0	1	1
ENSG00000264524	ENSG00000264524	MTMR11	HG1287_PATCH:150615065-150623313	NOTEST	0	0	0	0	1	1
ENSG00000264525	ENSG00000264525	MIR4778	2:66585380-66585460	NOTEST	0	0	0	0	1	1
ENSG00000264526	ENSG00000264526	AL136123.1	13:50526669-50526750	NOTEST	0	0	0	0	1	1
ENSG00000264527	ENSG00000264527	WI2-1959D15.1	9:139141823-139143051	NOTEST	0	0	0	0	1	1
ENSG00000264528	ENSG00000264528	TUBE1	HG1304_PATCH:112375274-112408732	NOTEST	0	0	0	0	1	1
ENSG00000264529	ENSG00000264529	RP11-556O9.3	17:61086916-61509572	NOTEST	0	0	0	0	1	1
ENSG00000264530	ENSG00000264530	RN7SL25P	9:6532463-6645650	NOTEST	0	0	0	0	1	1
ENSG00000264531	ENSG00000264531	RN7SL641P	X:73641084-73753752	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264532	ENSG00000264532	RP4-791M13.3	HG1287_PATCH:14973499 0-149737688	NOTEST	0	0	0	0	1	1
ENSG00000264533	ENSG00000264533	RP11-343H5.4	HG1293_PATCH:20674850 4-206797844	NOTEST	0	0	0	0	1	1
ENSG00000264534	ENSG00000264534	MIR378B	3:10365706-10749716	NOTEST	0	0	0	0	1	1
ENSG00000264535	ENSG00000264535	AC093788.1	4:164444443-164444538	NOTEST	0	0	0	0	1	1
ENSG00000264536	ENSG00000264536	MIR5706	5:118342041-118584833	NOTEST	0	0	0	0	1	1
ENSG00000264537	ENSG00000264537	AC118758.2	HG736_PATCH:56933772-56933842	NOTEST	0	0	0	0	1	1
ENSG00000264539	ENSG00000264539	MIR548AR	13:115000361-115038198	NOTEST	0	0	0	0	1	1
ENSG00000264540	ENSG00000264540	RN7SL405P	17:42923720-42994305	NOTEST	0	0	0	0	1	1
ENSG00000264541	ENSG00000264541	AL162381.1	6:5102826-5261172	NOTEST	0	0	0	0	1	1
ENSG00000264542	ENSG00000264542	AP001282.1	11:106544737-106889250	NOTEST	0	0	0	0	1	1
ENSG00000264543	ENSG00000264543	RP11-744K17.7	17:21934504-21938362	NOTEST	0	0	0	0	1	1
ENSG00000264544	ENSG00000264544	AL355512.2	10:112188597-112255962	NOTEST	0	0	0	0	1	1
ENSG00000264545	ENSG00000264545	RP11-145E5.5	9:21802541-22121096	NOTEST	0	0	0	0	1	1
ENSG00000264546	ENSG00000264546	RP11-464D20.6	17:60536018-60692842	NOTEST	0	0.00679706	inf	0	1	1
ENSG00000264547	ENSG00000264547	RP11-192H23.4	HG883_PATCH:26782770-26941216	NOTEST	0	0	0	0	1	1
ENSG00000264548	ENSG00000264548	RP13-516M14.2	17:80172102-80175228	NOTEST	0.0447414	0.0396761	-0.173338	0	1	1
ENSG00000264549	ENSG00000264549	SNORD95	5:180663908-180699308	NOTEST	0	0	0	0	1	1
ENSG00000264551	ENSG00000264551	AC099791.1	1:62094702-62094793	NOTEST	0	0	0	0	1	1
ENSG00000264552	ENSG00000264552	AC105030.1	17:47072627-47133012	NOTEST	0	0	0	0	1	1
ENSG00000264553	ENSG00000264553	MIR4257	1:150521039-150533413	NOTEST	0	0	0	0	1	1
ENSG00000264554	ENSG00000264554	RN7SL793P	12:102611097-102611391	NOTEST	0.231789	0	#NAME?	0	1	1
ENSG00000264555	ENSG00000264555	hsa-mir-1236	HSCHR6_MHC_SSTO:3191 1715-31929380	NOTEST	0	0	0	0	1	1
ENSG00000264556	ENSG00000264556	U6	HSCHR6_MHC_QBL:31698 008-31719779	NOTEST	0	0	0	0	1	1
ENSG00000264557	ENSG00000264557	U6	HSCHR6_MHC_MCF:32360 674-32415872	NOTEST	0	0	0	0	1	1
ENSG00000264558	ENSG00000264558	RP11-138C9.1	17:45726841-45762871	NOTEST	0	0.393571	inf	0	1	1
ENSG00000264559	ENSG00000264559	MIR3162	11:59341870-59383617	NOTEST	0	0	0	0	1	1
ENSG00000264560	ENSG00000264560	AC073973.1	2:195422897-195422998	NOTEST	0	0	0	0	1	1
ENSG00000264561	ENSG00000264561	AGAP9	HG1211_PATCH:47997301-48047394	NOTEST	0	0	0	0	1	1
ENSG00000264562	ENSG00000264562	RP11-1109M24.12	17:21832276-21832619	NOTEST	0	0	0	0	1	1
ENSG00000264563	ENSG00000264563	MIR4633	5:128430443-128449721	NOTEST	0	0	0	0	1	1
ENSG00000264564	ENSG00000264564	RP11-61D1.2	18:52051803-52051933	NOTEST	0	0	0	0	1	1
ENSG00000264566	ENSG00000264566	MIR23C	X:20024830-20135035	NOTEST	0	0	0	0	1	1
ENSG00000264567	ENSG00000264567	AL391803.1	X:117480035-117583924	NOTEST	0	0	0	0	1	1
ENSG00000264569	ENSG00000264569	RP13-650J16.1	17:79995780-79997256	NOTEST	0.152298	0.374488	1.29802	0	1	1
ENSG00000264570	ENSG00000264570	SNX19P3	18:14629830-14632805	NOTEST	0	0	0	0	1	1
ENSG00000264571	ENSG00000264571	MIR4529	18:52889561-53332018	NOTEST	0	0	0	0	1	1
ENSG00000264572	ENSG00000264572	MIR4296	10:126605711-126849739	NOTEST	0	0	0	0	1	1
ENSG00000264573	ENSG00000264573	RN7SL15P	X:41192650-41223725	NOTEST	0.11758	0.284372	1.27414	0	1	1
ENSG00000264574	ENSG00000264574	MIR1254-2	10:23682333-23682396	NOTEST	0	0	0	0	1	1
ENSG00000264576	ENSG00000264576	AC104012.1	8:72740401-73030628	NOTEST	0	0	0	0	1	1
ENSG00000264579	ENSG00000264579	hsa-mir-877	HSCHR6_MHC_SSTO:3053 0572-30556377	NOTEST	0	0	0	0	1	1
ENSG00000264580	ENSG00000264580	MIR5692B	21:44371037-44371124	NOTEST	0	0	0	0	1	1
ENSG00000264582	ENSG00000264582	RN7SL326P	1:41249683-41306124	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264583	ENSG00000264583	MIR4487	11:47404698-47438047	NOTEST	0	0	0	0	1	1
ENSG00000264584	ENSG00000264584	RN7SL600P	1:150541448-150541745	NOTEST	0.115819	0	#NAME?	0	1	1
ENSG00000264585	ENSG00000264585	MIR4449	4:53578596-53586998	NOTEST	0	0	0	0	1	1
ENSG00000264586	ENSG00000264586	RP11-109G10.2	HG1211_PATCH:46558697-46559168	NOTEST	0	0	0	0	1	1
ENSG00000264587	ENSG00000264587	RP11-784B15.1	18:27098223-27128206	NOTEST	0	0	0	0	1	1
ENSG00000264588	ENSG00000264588	RN7SL872P	8:2792874-4852494	NOTEST	0	0	0	0	1	1
ENSG00000264589	ENSG00000264589	MAPT-AS1	17:43921016-44105700	NOTEST	0	0.0341326	inf	0	1	1
ENSG00000264590	ENSG00000264590	RN7SL512P	1:212738675-212794119	NOTEST	0	0	0	0	1	1
ENSG00000264591	ENSG00000264591	SNORD83	HSCHR6_MHC_DBB:31478677-31496802	NOTEST	0	0	0	0	1	1
ENSG00000264592	ENSG00000264592	RN7SL131P	1:36657515-36657769	NOTEST	0	0	0	0	1	1
ENSG00000264593	ENSG00000264593	Metazoa_SRP	HSCHR17_1:43776445-43865069	NOTEST	0	0	0	0	1	1
ENSG00000264594	ENSG00000264594	MIR4640	6:30844197-30867933	NOTEST	0	0	0	0	1	1
ENSG00000264595	ENSG00000264595	RP11-94B19.5	18:73939944-73945342	NOTEST	0	0	0	0	1	1
ENSG00000264596	ENSG00000264596	RP11-678G15.1	18:7566779-8406951	NOTEST	0	0	0	0	1	1
ENSG00000264597	ENSG00000264597	Metazoa_SRP	HSCHR6_MHC_MCF:28894880-28895162	NOTEST	0	0	0	0	1	1
ENSG00000264598	ENSG00000264598	RP1-29G21.1	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000264599	ENSG00000264599	AL109754.1	20:9966735-10349424	NOTEST	0	0	0	0	1	1
ENSG00000264600	ENSG00000264600	RN7SL595P	15:64679946-64747502	NOTEST	0	0	0	0	1	1
ENSG00000264601	ENSG00000264601	RP4-791M13.5	HG1287_PATCH:14957587-149719430	NOTEST	0	0	0	0	1	1
ENSG00000264602	ENSG00000264602	Y_RNA	HSCHR6_MHC_QBL:30889969-30890061	NOTEST	0	0	0	0	1	1
ENSG00000264603	ENSG00000264603	MIR3159	11:18409333-18409407	NOTEST	0	0	0	0	1	1
ENSG00000264604	ENSG00000264604	AL158069.1	X:68724547-68724666	NOTEST	0	0	0	0	1	1
ENSG00000264605	ENSG00000264605	AC004895.1	7:6120733-6132716	NOTEST	0	0	0	0	1	1
ENSG00000264606	ENSG00000264606	CTSE	HG1293_PATCH:206072824-206087470	NOTEST	0	0	0	0	1	1
ENSG00000264607	ENSG00000264607	MIR3173	14:95552564-95646263	NOTEST	0	0	0	0	1	1
ENSG00000264609	ENSG00000264609	AL603910.1	6:74171300-74218959	NOTEST	0	0	0	0	1	1
ENSG00000264610	ENSG00000264610	MIR4685	10:100175954-100206684	NOTEST	0	0	0	0	1	1
ENSG00000264611	ENSG00000264611	SRGAP2-AS1	HG1293_PATCH:206266905-206527996	NOTEST	0	0	0	0	1	1
ENSG00000264612	ENSG00000264612	AP000539.1	22:16575147-16575230	NOTEST	0	0	0	0	1	1
ENSG00000264613	ENSG00000264613	RN7SL290P	1:52461411-52461709	NOTEST	0	0	0	0	1	1
ENSG00000264614	ENSG00000264614	MIR5588	3:184880658-184999778	NOTEST	0	0	0	0	1	1
ENSG00000264615	ENSG00000264615	RN7SL592P	9:2228962-2229241	NOTEST	0	0	0	0	1	1
ENSG00000264616	ENSG00000264616	MIR4755	20:32570857-32700138	NOTEST	0	0	0	0	1	1
ENSG00000264617	ENSG00000264617	AC144838.3	17:21560547-21562330	NOTEST	0	0	0	0	1	1
ENSG00000264618	ENSG00000264618	RN7SL732P	X:39645779-39646077	NOTEST	0	0	0	0	1	1
ENSG00000264619	ENSG00000264619	MSH5-SAPCD1	HSCHR6_MHC_APD:31735722-31744719	NOTEST	0	0	0	0	1	1
ENSG00000264620	ENSG00000264620	AL139022.1	14:65381078-65569413	NOTEST	0	0	0	0	1	1
ENSG00000264621	ENSG00000264621	MIR5591	4:39408472-39453156	NOTEST	0	0	0	0	1	1
ENSG00000264622	ENSG00000264622	RP11-642M2.1	17:33164889-33186065	NOTEST	0	0	0	0	1	1
ENSG00000264623	ENSG00000264623	MIR4796	3:114056940-114866118	NOTEST	0	0	0	0	1	1
ENSG00000264624	ENSG00000264624	MIR3615	17:72666716-72765492	NOTEST	0	0	0	0	1	1
ENSG00000264625	ENSG00000264625	RN7SL859P	3:27414213-27525911	NOTEST	0	0	0	0	1	1
ENSG00000264626	ENSG00000264626	RN7SL769P	12:110798254-110798551	NOTEST	0	0	0	0	1	1
ENSG00000264627	ENSG00000264627	RN7SL820P	2:197059093-197458416	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264628	ENSG00000264628	RN7SL565P	9:45661986-45662268	NOTEST	0	0	0	0	1	1
ENSG00000264629	ENSG00000264629	D87007.1	22:23077062-23077584	NOTEST	0	0	0	0	1	1
ENSG00000264630	ENSG00000264630	RP11-4F22.2	17:64298753-64806861	NOTEST	0	0	0	0	1	1
ENSG00000264631	ENSG00000264631	RN7SL742P	X:153724533-153724819	NOTEST	0	0	0	0	1	1
ENSG00000264632	ENSG00000264632	Metazoa_SRP	HSCHR1_1_CTG31:153673134-153673430	NOTEST	0	0	0	0	1	1
ENSG00000264633	ENSG00000264633	MIR4271	3:49306034-49378145	NOTEST	0	0	0	0	1	1
ENSG00000264634	ENSG00000264634	RP11-659F24.1	18:65608185-65623663	NOTEST	0	0	0	0	1	1
ENSG00000264635	ENSG00000264635	RP11-769O8.3	18:721587-812547	NOTEST	0.176822	0.182707	0.0472357	0	1	1
ENSG00000264637	ENSG00000264637	AC110283.1	11:51264008-51264094	NOTEST	0	0	0	0	1	1
ENSG00000264638	ENSG00000264638	MIR3152	9:18473891-18910948	NOTEST	0	0	0	0	1	1
ENSG00000264639	ENSG00000264639	NBPF13P	HG1287_PATCH:147705750-147810940	NOTEST	0	0	0	0	1	1
ENSG00000264640	ENSG00000264640	U1	HSCHR6_MHC_MANN:32579306-32579454	NOTEST	0	0	0	0	1	1
ENSG00000264641	ENSG00000264641	AL354928.1	9:127640645-127905785	NOTEST	0	0	0	0	1	1
ENSG00000264642	ENSG00000264642	AC005088.1	7:101458958-101927249	NOTEST	0	0	0	0	1	1
ENSG00000264643	ENSG00000264643	RP11-118G23.2	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000264644	ENSG00000264644	KRT18P8	18:9678244-9679490	NOTEST	0	0	0	0	1	1
ENSG00000264645	ENSG00000264645	AC010528.1	16:76311175-76692375	NOTEST	0	0	0	0	1	1
ENSG00000264646	ENSG00000264646	Y_RNA	HSCHR6_MHC_MCF:29715284-29715386	NOTEST	0	0	0	0	1	1
ENSG00000264647	ENSG00000264647	RP11-68I3.7	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000264649	ENSG00000264649	RP11-38J22.3	HG1293_PATCH:206181343-206190366	NOTEST	0	0	0	0	1	1
ENSG00000264650	ENSG00000264650	AL359473.1	1:45482070-45771881	NOTEST	0	0	0	0	1	1
ENSG00000264651	ENSG00000264651	FAM35BP	HG1211_PATCH:47073664-47147473	NOTEST	0	0	0	0	1	1
ENSG00000264652	ENSG00000264652	MIR4649	7:44143959-44154161	NOTEST	0	0	0	0	1	1
ENSG00000264653	ENSG00000264653	MIR5194	8:130844546-131029375	NOTEST	0	0	0	0	1	1
ENSG00000264654	ENSG00000264654	CA14	HG1287_PATCH:150944188-150951476	NOTEST	0	0	0	0	1	1
ENSG00000264655	ENSG00000264655	CTD-2267D19.4	17:38524203-38524690	NOTEST	0	0	0	0	1	1
ENSG00000264656	ENSG00000264656	RNU6-465P	HG1292_PATCH:120669596-120669697	NOTEST	0	0	0	0	1	1
ENSG00000264657	ENSG00000264657	hsa-mir-3171	14:27727922-28314492	NOTEST	0	0	0	0	1	1
ENSG00000264658	ENSG00000264658	MIR4798	4:7194264-7744554	NOTEST	0	0	0	0	1	1
ENSG00000264659	ENSG00000264659	CTD-2006K23.2	17:72666716-72765492	NOTEST	0	0	0	0	1	1
ENSG00000264660	ENSG00000264660	RP11-381P6.1	17:20717932-20947073	NOTEST	0.0330108	0	#NAME?	0	1	1
ENSG00000264661	ENSG00000264661	MIR3200	22:31089768-31303811	NOTEST	0	0	0	0	1	1
ENSG00000264662	ENSG00000264662	RP11-283C24.2	17:20691383-20692908	NOTEST	0	0	0	0	1	1
ENSG00000264663	ENSG00000264663	KRT8P34	17:37921197-38020441	NOTEST	0	0	0	0	1	1
ENSG00000264664	ENSG00000264664	RNA5SP314	HG1211_PATCH:47283837-47333708	NOTEST	0	0	0	0	1	1
ENSG00000264665	ENSG00000264665	RP11-315I20.1	HG1287_PATCH:146607982-146645521	NOTEST	0	0	0	0	1	1
ENSG00000264666	ENSG00000264666	RP11-524F11.2	17:17408876-17513799	NOTEST	0	0	0	0	1	1
ENSG00000264667	ENSG00000264667	AL137224.1	11:34500339-34535352	NOTEST	0	0	0	0	1	1
ENSG00000264668	ENSG00000264668	ZFP41	8:144328990-144359101	NOTEST	0.618555	0.522079	-0.244634	0	1	1
ENSG00000264669	ENSG00000264669	AL136090.1	20:19106428-19106551	NOTEST	0	0	0	0	1	1
ENSG00000264671	ENSG00000264671	AP006477.1	11:924893-1012239	NOTEST	0	0	0	0	1	1
ENSG00000264672	ENSG00000264672	RP11-112H10.4	17:56597197-56769416	NOTEST	0.0179315	0.207265	3.53091	0	1	1
ENSG00000264673	ENSG00000264673	RP11-92B11.3	17:16592850-16719854	NOTEST	0	0	0	0	1	1

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ENSG00000264675	ENSG00000264675	MIR4285	7:101928404-101962178	NOTEST	0	0	0	0	1	1
ENSG00000264676	ENSG00000264676	RN7SL204P	2:236402732-237040444	NOTEST	0	0	0	0	1	1
ENSG00000264677	ENSG00000264677	AL355490.2	10:99218080-99258551	NOTEST	0	0	0	0	1	1
ENSG00000264678	ENSG00000264678	MIR3140	4:153242409-153457253	NOTEST	0	0	0	0	1	1
ENSG00000264679	ENSG00000264679	AC092104.2	7:7106241-7106323	NOTEST	0	0	0	0	1	1
ENSG00000264680	ENSG00000264680	hsa-mir-3669	8:130363936-130695925	NOTEST	0	0	0	0	1	1
ENSG00000264681	ENSG00000264681	AL445665.2	9:69587377-69587444	NOTEST	0	0	0	0	1	1
ENSG00000264682	ENSG00000264682	AC008463.1	HSCHR19_1_CTG3:20959109-20990226	NOTEST	0	0	0	0	1	1
ENSG00000264683	ENSG00000264683	DDX39BP1	HG1322_PATCH:29868163-29868530	NOTEST	0	0	0	0	1	1
ENSG00000264684	ENSG00000264684	MIR4773-2	2:152214105-152236560	NOTEST	0	0	0	0	1	1
ENSG00000264685	ENSG00000264685	PRPF19P1	18:63735985-63736883	NOTEST	0	0	0	0	1	1
ENSG00000264686	ENSG00000264686	AC104458.1	1:77183824-77183926	NOTEST	0	0	0	0	1	1
ENSG00000264687	ENSG00000264687	AL050335.1	6:15149929-15150030	NOTEST	0	0	0	0	1	1
ENSG00000264688	ENSG00000264688	Metazoa_SRP	HSCHR6_MHC_QBL:30708328-30708576	NOTEST	0	0	0	0	1	1
ENSG00000264689	ENSG00000264689	RP11-19P22.2	17:26009501-26009763	NOTEST	0	0	0	0	1	1
ENSG00000264690	ENSG00000264690	RN7SL534P	12:129556269-130388211	NOTEST	0	0	0	0	1	1
ENSG00000264691	ENSG00000264691	AP001427.1	21:39323727-39493454	NOTEST	0	0	0	0	1	1
ENSG00000264692	ENSG00000264692	Y_RNA	HSCHR6_MHC_COX:31358052-31374512	NOTEST	0	0	0	0	1	1
ENSG00000264693	ENSG00000264693	RP11-63N3.1	18:75334507-75336471	NOTEST	0	0	0	0	1	1
ENSG00000264694	ENSG00000264694	AC092122.1	16:9407691-9407761	NOTEST	0	0	0	0	1	1
ENSG00000264695	ENSG00000264695	RP11-178F10.2	18:22069338-22071044	NOTEST	0.0965723	0	#NAME?	0	1	1
ENSG00000264696	ENSG00000264696	AC108078.1	4:70345048-70345152	NOTEST	0	0	0	0	1	1
ENSG00000264697	ENSG00000264697	RP11-585K6.2	18:66195206-66195360	NOTEST	0	0	0	0	1	1
ENSG00000264698	ENSG00000264698	MIR4255	1:37627163-37627235	NOTEST	0	0	0	0	1	1
ENSG00000264699	ENSG00000264699	RP11-421N8.2	18:65925575-65932064	NOTEST	0	0	0	0	1	1
ENSG00000264700	ENSG00000264700	RN7SL588P	14:53241911-53258386	NOTEST	0	0	0	0	1	1
ENSG00000264701	ENSG00000264701	RP11-6N17.10	17:46018871-46073562	NOTEST	0	0	0	0	1	1
ENSG00000264702	ENSG00000264702	AC231656.1	X:148393762-148393845	NOTEST	0	0	0	0	1	1
ENSG00000264703	ENSG00000264703	MIR4752	19:54785963-54786035	NOTEST	0	0	0	0	1	1
ENSG00000264704	ENSG00000264704	U1	HSCHR6_MHC_SSTO:32485001-32485149	NOTEST	0	0	0	0	1	1
ENSG00000264705	ENSG00000264705	RP11-674P19.2	18:66879513-66881587	NOTEST	0	0	0	0	1	1
ENSG00000264706	ENSG00000264706	RN7SL217P	3:49895420-49907655	NOTEST	0	0	0	0	1	1
ENSG00000264708	ENSG00000264708	PDE4DIP	HG1287_PATCH:149575877-149719430	NOTEST	0	0	0	0	1	1
ENSG00000264709	ENSG00000264709	Y_RNA	HSCHR17_1:43958569-43958671	NOTEST	0	0	0	0	1	1
ENSG00000264710	ENSG00000264710	RN7SL453P	10:47379726-47420712	NOTEST	0	0	0	0	1	1
ENSG00000264711	ENSG00000264711	AC007919.1	3:172348038-172429008	NOTEST	0	0	0	0	1	1
ENSG00000264712	ENSG00000264712	MIR4504	14:50704280-50883179	NOTEST	0	0	0	0	1	1
ENSG00000264713	ENSG00000264713	AC106878.1	4:170706344-170706431	NOTEST	0	0	0	0	1	1
ENSG00000264714	ENSG00000264714	RP11-21G15.1	18:10661929-11148587	NOTEST	0.0795325	0.0634984	-0.324824	0	1	1
ENSG00000264715	ENSG00000264715	AC104996.1	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000264716	ENSG00000264716	AC106827.2	3:65339199-66024509	NOTEST	0	0	0	0	1	1
ENSG00000264717	ENSG00000264717	NPY4R	HG1211_PATCH:48332967-48337753	NOTEST	0	0	0	0	1	1
ENSG00000264718	ENSG00000264718	AC007050.1	22:21011321-21011403	NOTEST	0	0	0	0	1	1
ENSG00000264719	ENSG00000264719	HIST2H2BE	HG1287_PATCH:150570874-150573097	NOTEST	0	0	0	0	1	1

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ENSG00000264720	ENSG00000264720	MIR3117	1:66999065-67213982	NOTEST	0	0	0	0	1	1
ENSG00000264721	ENSG00000264721	AC104592.1	8:145202918-145316843	NOTEST	0	0	0	0	1	1
ENSG00000264722	ENSG00000264722	MIR3670-2	16:16400226-16400291	NOTEST	0	0	0	0	1	1
ENSG00000264723	ENSG00000264723	Metazoa_SRP	GL000193.1:169659-169941	NOTEST	0	0	0	0	1	1
ENSG00000264724	ENSG00000264724	AC099332.1	3:39458970-39459056	NOTEST	0	0	0	0	1	1
ENSG00000264725	ENSG00000264725	MIR3129	2:189896621-190044605	NOTEST	0	0	0	0	1	1
ENSG00000264726	ENSG00000264726	AL162711.1	13:113344642-113541482	NOTEST	0	0	0	0	1	1
ENSG00000264727	ENSG00000264727	RP11-680C21.1	17:11144579-11467380	NOTEST	0	0	0	0	1	1
ENSG00000264728	ENSG00000264728	CU442762.3	GL000247.1:10270-10353	NOTEST	0	0	0	0	1	1
ENSG00000264729	ENSG00000264729	RP11-219A15.2	17:16592850-16719854	NOTEST	0	0	0	0	1	1
ENSG00000264730	ENSG00000264730	AC017028.5	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000264731	ENSG00000264731	RN7SL175P	6:30874654-30874913	NOTEST	0	0	0	0	1	1
ENSG00000264732	ENSG00000264732	MIR4638	5:180649498-180662809	NOTEST	0	0	0	0	1	1
ENSG00000264733	ENSG00000264733	MIR4718	16:12756918-12897874	NOTEST	0	0	0	0	1	1
ENSG00000264734	ENSG00000264734	RP11-260A9.6	17:25316214-25326967	NOTEST	0	0	0	0	1	1
ENSG00000264735	ENSG00000264735	RP11-498C9.17	17:79923507-79924465	NOTEST	0.0344675	0	#NAME?	0	1	1
ENSG00000264736	ENSG00000264736	BDP1P	18:75133574-75272719	NOTEST	0	0	0	0	1	1
ENSG00000264737	ENSG00000264737	MIR4511	15:65903703-66184329	NOTEST	0	0	0	0	1	1
ENSG00000264738	ENSG00000264738	RP11-458I7.1	HG1287_PATCH:15074027-150741449	NOTEST	0	0	0	0	1	1
ENSG00000264739	ENSG00000264739	RP11-138I1.2	17:16317837-16340317	NOTEST	0.0218073	0.0120169	-0.85975	0	1	1
ENSG00000264740	ENSG00000264740	AC008064.1	2:53759809-54087297	NOTEST	0	0	0	0	1	1
ENSG00000264741	ENSG00000264741	MIR4505	14:74181824-74269973	NOTEST	0	0	0	0	1	1
ENSG00000264742	ENSG00000264742	AL021920.1	1:17007749-17007823	NOTEST	0	0	0	0	1	1
ENSG00000264743	ENSG00000264743	DPRXP4	17:29295802-29326929	NOTEST	0	0	0	0	1	1
ENSG00000264744	ENSG00000264744	MIR3689C	9:137741143-137741215	NOTEST	0	0	0	0	1	1
ENSG00000264745	ENSG00000264745	RP11-403A21.2	18:21572736-21715574	NOTEST	0	0	0	0	1	1
ENSG00000264746	ENSG00000264746	AC004552.1	X:24366925-24367023	NOTEST	0	0	0	0	1	1
ENSG00000264747	ENSG00000264747	MIR3924	10:59064238-59064319	NOTEST	0	0	0	0	1	1
ENSG00000264748	ENSG00000264748	AC025470.1	5:56690886-56829251	NOTEST	0	0	0	0	1	1
ENSG00000264749	ENSG00000264749	AC011313.1	12:105567073-105789875	NOTEST	0	0	0	0	1	1
ENSG00000264750	ENSG00000264750	RP11-277J6.2	17:71330522-71640228	NOTEST	0	0	0	0	1	1
ENSG00000264751	ENSG00000264751	HLA-G	HG1322_PATCH:29794490-29798554	NOTEST	0	0	0	0	1	1
ENSG00000264752	ENSG00000264752	RN7SL90P	16:16731111-16731387	NOTEST	0	0	0	0	1	1
ENSG00000264753	ENSG00000264753	AL390036.1	1:108561274-108561393	NOTEST	0	0	0	0	1	1
ENSG00000264754	ENSG00000264754	CTD-2653B5.1	17:65373574-65693372	NOTEST	0	0.0238482	inf	0	1	1
ENSG00000264755	ENSG00000264755	MIR3131	2:219919141-219925189	NOTEST	0	0	0	0	1	1
ENSG00000264756	ENSG00000264756	RN7SL805P	17:61909443-61920425	NOTEST	0.111631	0.336002	1.58973	0	1	1
ENSG00000264757	ENSG00000264757	MIR3198-1	22:18216905-18257536	NOTEST	0	0	0	0	1	1
ENSG00000264758	ENSG00000264758	RN7SL161P	7:100054237-100076902	NOTEST	0	0	0	0	1	1
ENSG00000264759	ENSG00000264759	AC005000.2	X:114937130-114938440	NOTEST	0	0	0	0	1	1
ENSG00000264760	ENSG00000264760	MIR3141	5:153975571-153975632	NOTEST	0	0	0	0	1	1
ENSG00000264761	ENSG00000264761	RN7SL43P	7:66445106-66445395	NOTEST	0	0	0	0	1	1
ENSG00000264763	ENSG00000264763	MIR4295	10:114206755-114578503	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000264765	ENSG00000264765	RP11-92B11.4	17:16557217-16558101	NOTEST	0	0	0	0	1	1
ENSG00000264766	ENSG00000264766	AC079756.1	7:9634246-9634353	NOTEST	0	0	0	0	1	1
ENSG00000264767	ENSG00000264767	RN7SL237P	20:36726797-36727102	NOTEST	0	0	0	0	1	1
ENSG00000264768	ENSG00000264768	AL450304.1	1:182928208-182929540	NOTEST	0	0	0	0	1	1
ENSG00000264769	ENSG00000264769	RP11-498C9.12	17:79869814-79885590	NOTEST	0.30863	0.115412	-1.41908	0	1	1
ENSG00000264770	ENSG00000264770	MIR3135B	HSCHR6_MHC_SSTO:32808497-32808565	NOTEST	0	0	0	0	1	1
ENSG00000264771	ENSG00000264771	AC022819.1	15:99791566-99930934	NOTEST	0	0	0	0	1	1
ENSG00000264773	ENSG00000264773	MIR4420	1:31205315-31230667	NOTEST	0	0	0	0	1	1
ENSG00000264774	ENSG00000264774	AC099669.1	3:44556707-44556793	NOTEST	0	0	0	0	1	1
ENSG00000264775	ENSG00000264775	PPIAP14	18:4775052-5004536	NOTEST	0.35324	0.207395	-0.768271	0	1	1
ENSG00000264776	ENSG00000264776	GPR89B	HG1287_PATCH:148614807-148679936	NOTEST	0	0	0	0	1	1
ENSG00000264777	ENSG00000264777	U6	HSCHR6_MHC_MANN:28882557-28891771	NOTEST	0	0	0	0	1	1
ENSG00000264778	ENSG00000264778	Y_RNA	HSCHR6_MHC_SSTO:31735248-31822599	NOTEST	0	0	0	0	1	1
ENSG00000264779	ENSG00000264779	AC107871.1	15:68346516-68549549	NOTEST	0	0	0	0	1	1
ENSG00000264780	ENSG00000264780	MIR4683	10:35927176-35930362	NOTEST	0	0	0	0	1	1
ENSG00000264781	ENSG00000264781	hsa-mir-4537	14:106325652-106325722	NOTEST	0	0	0	0	1	1
ENSG00000264783	ENSG00000264783	BX664739.1	X:153722475-153722545	NOTEST	0	0	0	0	1	1
ENSG00000264785	ENSG00000264785	RP11-311F12.2	17:19640994-19652256	NOTEST	0	0	0	0	1	1
ENSG00000264786	ENSG00000264786	CU041368.1	HSCHR19LRC_PGF1_CTG1:55139743-55139813	NOTEST	0	0	0	0	1	1
ENSG00000264787	ENSG00000264787	AL591856.6	GL000224.1:165116-165199	NOTEST	0	0	0	0	1	1
ENSG00000264788	ENSG00000264788	MIR3148	8:29814787-29814864	NOTEST	0	0	0	0	1	1
ENSG00000264789	ENSG00000264789	CR759798.1	HSCHR6_MHC_MCF:32935859-32980443	NOTEST	0	0	0	0	1	1
ENSG00000264790	ENSG00000264790	RP11-26N15.2	18:24916342-25175128	NOTEST	0	0	0	0	1	1
ENSG00000264791	ENSG00000264791	CTC-304I17.2	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000264792	ENSG00000264792	MIR4637	5:14704909-14871887	NOTEST	0	0	0	0	1	1
ENSG00000264793	ENSG00000264793	MIR4771-1	2:87352512-87423770	NOTEST	0	0	0	0	1	1
ENSG00000264794	ENSG00000264794	AC024996.1	8:113235156-114449328	NOTEST	0	0	0	0	1	1
ENSG00000264795	ENSG00000264795	AC144838.2	HG987_PATCH:21752642-21752811	NOTEST	0	0	0	0	1	1
ENSG00000264796	ENSG00000264796	MIR5009	15:90373830-90456188	NOTEST	0	0	0	0	1	1
ENSG00000264797	ENSG00000264797	AL356756.1	14:30045686-30766249	NOTEST	0	0	0	0	1	1
ENSG00000264798	ENSG00000264798	AC105381.1	2:201170603-201346986	NOTEST	0	0	0	0	1	1
ENSG00000264799	ENSG00000264799	AC009892.1	19:55084386-55150343	NOTEST	0	0	0	0	1	1
ENSG00000264800	ENSG00000264800	MIR4294	10:49892920-50323554	NOTEST	0	0	0	0	1	1
ENSG00000264801	ENSG00000264801	RP11-149I2.5	9:21802541-22121096	NOTEST	0.0905502	0.0247641	-1.87047	0	1	1
ENSG00000264802	ENSG00000264802	MIR5191	1:201592012-201853422	NOTEST	0	0	0	0	1	1
ENSG00000264803	ENSG00000264803	MIR378C	10:132760850-132760931	NOTEST	0	0	0	0	1	1
ENSG00000264804	ENSG00000264804	AC098848.1	18:52668526-52668629	NOTEST	0	0	0	0	1	1
ENSG00000264805	ENSG00000264805	RP11-666A1.4	HG1287_PATCH:145158949-145161205	NOTEST	0	0	0	0	1	1
ENSG00000264806	ENSG00000264806	POLR3C	HG1287_PATCH:146510502-146528920	NOTEST	0	0	0	0	1	1
ENSG00000264807	ENSG00000264807	AL845353.1	HSCHR6_MHC_QBL:30604325-30630349	NOTEST	0	0	0	0	1	1
ENSG00000264808	ENSG00000264808	MIR4523	17:27679086-27878922	NOTEST	0.0724039	0.0757287	0.0647734	0	1	1
ENSG00000264809	ENSG00000264809	AL513344.1	1:182726053-182726153	NOTEST	0	0	0	0	1	1
ENSG00000264810	ENSG00000264810	MIR4441	2:239969863-240324058	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264811	ENSG00000264811	RP11-1109M24.14	17:21825296-21826499	NOTEST	0	0	0	0	1	1
ENSG00000264812	ENSG00000264812	RP13-20L14.4	17:80347098-80408705	NOTEST	0	0.0454234	inf	0	1	1
ENSG00000264813	ENSG00000264813	ACE	17:61554421-61599209	NOTEST	0	0	0	0	1	1
ENSG00000264814	ENSG00000264814	MIR1273C	6:155054458-155635627	NOTEST	0	0	0	0	1	1
ENSG00000264815	ENSG00000264815	AF130343.1	8:116962735-117337297	NOTEST	0	0	0	0	1	1
ENSG00000264816	ENSG00000264816	Metazoa_SRP	HG736_PATCH:57032940-57033200	NOTEST	0	0	0	0	1	1
ENSG00000264817	ENSG00000264817	MIR4741	18:20279443-20606451	NOTEST	0	0	0	0	1	1
ENSG00000264818	ENSG00000264818	MIR3714	3:16844158-17132086	NOTEST	0	0	0	0	1	1
ENSG00000264819	ENSG00000264819	BX649553.4	X:1387692-1429274	NOTEST	0	0	0	0	1	1
ENSG00000264820	ENSG00000264820	FAM72B	HG1292_PATCH:121710268-121730136	NOTEST	0	0	0	0	1	1
ENSG00000264821	ENSG00000264821	AC091738.1	HG1257_PATCH:72039492-72293191	NOTEST	0	0	0	0	1	1
ENSG00000264822	ENSG00000264822	CR753328.2	HSCHR6_MHC_DBB:30558417-30584413	NOTEST	0	0	0	0	1	1
ENSG00000264823	ENSG00000264823	MIR3154	9:130928342-131017527	NOTEST	0	0	0	0	1	1
ENSG00000264824	ENSG00000264824	hsa-mir-5571	22:23228446-23228559	NOTEST	0	0	0	0	1	1
ENSG00000264825	ENSG00000264825	RP11-627G18.4	18:19793740-19807992	NOTEST	0	0	0	0	1	1
ENSG00000264827	ENSG00000264827	AL592188.4	GL000220.1:107908-108088	NOTEST	0	0	0	0	1	1
ENSG00000264829	ENSG00000264829	RP11-474I11.8	17:73584138-73704142	NOTEST	0	0	0	0	1	1
ENSG00000264830	ENSG00000264830	BX088556.1	HSCHR6_MHC_SSTO:32992301-33089202	NOTEST	0	0	0	0	1	1
ENSG00000264831	ENSG00000264831	MIR4260	1:209788214-209825811	NOTEST	0	0	0	0	1	1
ENSG00000264832	ENSG00000264832	PTPN20B	HG1211_PATCH:47406843-47497936	NOTEST	0	0	0	0	1	1
ENSG00000264833	ENSG00000264833	RN7SL468P	2:119927397-119927691	NOTEST	0	0	0	0	1	1
ENSG00000264834	ENSG00000264834	MIR1273F	1:53392900-53517375	NOTEST	0	0	0	0	1	1
ENSG00000264835	ENSG00000264835	RN7SL345P	19:49187291-49187563	NOTEST	0	0	0	0	1	1
ENSG00000264836	ENSG00000264836	hsa-mir-219a-1	HSCHR6_MHC_DBB:33153521-33153631	NOTEST	0	0	0	0	1	1
ENSG00000264837	ENSG00000264837	VN1R71P	17:25384424-25385247	NOTEST	0	0	0	0	1	1
ENSG00000264838	ENSG00000264838	AP003305.1	11:83166054-85338966	NOTEST	0	0	0	0	1	1
ENSG00000264839	ENSG00000264839	AC113407.1	5:99384691-99386354	NOTEST	0	0	0	0	1	1
ENSG00000264840	ENSG00000264840	RN7SL404P	17:62850429-62915598	NOTEST	0	0	0	0	1	1
ENSG00000264841	ENSG00000264841	AC134729.1	3:77975855-77975937	NOTEST	0	0	0	0	1	1
ENSG00000264842	ENSG00000264842	AGAP4	HG1211_PATCH:46321041-46349323	NOTEST	0	0	0	0	1	1
ENSG00000264843	ENSG00000264843	RP11-856M7.2	18:10661929-11148587	NOTEST	0.0897907	0.153465	0.773268	0	1	1
ENSG00000264844	ENSG00000264844	AC018767.1	16:8359540-8359659	NOTEST	0	0	0	0	1	1
ENSG00000264845	ENSG00000264845	RP11-465I4.3	18:67068290-67629039	NOTEST	0	0	0	0	1	1
ENSG00000264846	ENSG00000264846	Y_RNA	HSCHR6_MHC_COX:31451932-31452034	NOTEST	0	0	0	0	1	1
ENSG00000264847	ENSG00000264847	Y_RNA	HSCHR6_MHC_MCF:30978937-30979029	NOTEST	0	0	0	0	1	1
ENSG00000264849	ENSG00000264849	AC019198.1	2:55699879-55699977	NOTEST	0	0	0	0	1	1
ENSG00000264850	ENSG00000264850	MIR4310	15:42120282-42190773	NOTEST	0	0	0	0	1	1
ENSG00000264852	ENSG00000264852	RP11-481A12.2	HG1211_PATCH:46555795-46556144	NOTEST	0	0	0	0	1	1
ENSG00000264853	ENSG00000264853	RP11-16C1.2	17:73314156-73401790	NOTEST	0	0.00398551	inf	0	1	1
ENSG00000264855	ENSG00000264855	AL590763.1	X:70845602-70845705	NOTEST	0	0	0	0	1	1
ENSG00000264856	ENSG00000264856	RN7SL206P	2:128848773-128953251	NOTEST	0	0	0	0	1	1
ENSG00000264857	ENSG00000264857	MIR5696	2:101925911-101925996	NOTEST	0	0	0	0	1	1
ENSG00000264858	ENSG00000264858	AL358134.2	6:153740155-153740225	NOTEST	0	0	0	0	1	1
ENSG00000264859	ENSG00000264859	RP11-75N4.2	18:29078005-29136874	NOTEST	0.0425959	0.0224149	-0.926254	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264860	ENSG00000264860	RP11-143K11.5	17:71161115-71258491	NOTEST	0	0	0	0	1	1
ENSG00000264861	ENSG00000264861	AC108683.1	X:4501462-4501541	NOTEST	0	0	0	0	1	1
ENSG00000264862	ENSG00000264862	RN7SL45P	17:29718641-29865236	NOTEST	0	0.0914618	inf	0	1	1
ENSG00000264863	ENSG00000264863	AC241585.1	HG1287_PATCH:14590126-145902353	NOTEST	0	0	0	0	1	1
ENSG00000264864	ENSG00000264864	MIR3613	13:50570023-50595058	NOTEST	0	0	0	0	1	1
ENSG00000264866	ENSG00000264866	Metazoa_SRP	HSCHR6_MHC_QBL:28945252-28945548	NOTEST	0	0	0	0	1	1
ENSG00000264867	ENSG00000264867	BX248408.2	HSCHR6_MHC_SSTO:33321903-33321964	NOTEST	0	0	0	0	1	1
ENSG00000264868	ENSG00000264868	CTB-167B5.2	7:87834432-87936206	NOTEST	0	0	0	0	1	1
ENSG00000264869	ENSG00000264869	RP11-526H11.1	18:65769352-65781614	NOTEST	0	0	0	0	1	1
ENSG00000264871	ENSG00000264871	AC104331.1	3:65218574-65218658	NOTEST	0	0	0	0	1	1
ENSG00000264872	ENSG00000264872	MEST	HG1308_PATCH:130126045-130351086	NOTEST	0	0	0	0	1	1
ENSG00000264873	ENSG00000264873	MIR4646	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000264874	ENSG00000264874	AC087499.8	17:20613737-20613846	NOTEST	0	0	0	0	1	1
ENSG00000264875	ENSG00000264875	MIR3610	8:117654368-117889107	NOTEST	0	0	0	0	1	1
ENSG00000264876	ENSG00000264876	RP11-138E9.2	18:10323128-10372377	NOTEST	0	0	0	0	1	1
ENSG00000264877	ENSG00000264877	AL603650.2	9:137740818-137740966	NOTEST	0	0	0	0	1	1
ENSG00000264878	ENSG00000264878	Z85986.1	6:36461668-36515247	NOTEST	0	0	0	0	1	1
ENSG00000264879	ENSG00000264879	RN7SL690P	20:20015011-20341346	NOTEST	0	0	0	0	1	1
ENSG00000264880	ENSG00000264880	RP11-805F19.1	18:15159722-15164466	NOTEST	0	0	0	0	1	1
ENSG00000264881	ENSG00000264881	MIR1273D	1:10270862-10441661	NOTEST	0	0	0	0	1	1
ENSG00000264882	ENSG00000264882	MIR376A1	14:101507103-101507206	NOTEST	0	0	0	0	1	1
ENSG00000264883	ENSG00000264883	FAM25G	HG1211_PATCH:47955609-47987141	NOTEST	0	0	0	0	1	1
ENSG00000264884	ENSG00000264884	AL590684.1	6:74779166-75443995	NOTEST	0	0	0	0	1	1
ENSG00000264885	ENSG00000264885	RP11-815I9.4	17:18538318-18585575	NOTEST	0.314985	0.424697	0.43115	0	1	1
ENSG00000264887	ENSG00000264887	Y_RNA	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000264888	ENSG00000264888	AL121753.1	20:33703166-33872788	NOTEST	0	0	0	0	1	1
ENSG00000264889	ENSG00000264889	RP11-175I17.2	HG1211_PATCH:46349540-46411619	NOTEST	0	0	0	0	1	1
ENSG00000264890	ENSG00000264890	AC011379.1	5:139554226-139682706	NOTEST	0	0	0	0	1	1
ENSG00000264891	ENSG00000264891	AL359091.1	9:131217464-131263571	NOTEST	0	0	0	0	1	1
ENSG00000264892	ENSG00000264892	RP11-219A15.3	17:16592850-16719854	NOTEST	0	0	0	0	1	1
ENSG00000264893	ENSG00000264893	U1	HSCHR6_MHC_MCF:32554351-32554499	NOTEST	0	0	0	0	1	1
ENSG00000264894	ENSG00000264894	AL590282.1	X:134335661-134349163	NOTEST	0	0	0	0	1	1
ENSG00000264895	ENSG00000264895	RP11-421E14.2	17:49254785-49337524	NOTEST	0	0.011545	inf	0	1	1
ENSG00000264896	ENSG00000264896	AL451006.1	1:41972035-42501596	NOTEST	0	0	0	0	1	1
ENSG00000264897	ENSG00000264897	MIR3921	3:99536677-99897447	NOTEST	0	0	0	0	1	1
ENSG00000264898	ENSG00000264898	AL353626.2	9:66861460-66861543	NOTEST	0	0	0	0	1	1
ENSG00000264899	ENSG00000264899	AC027319.2	19:4876723-4876810	NOTEST	0	0	0	0	1	1
ENSG00000264900	ENSG00000264900	MIR4775	2:208576263-208626563	NOTEST	0	0	0	0	1	1
ENSG00000264901	ENSG00000264901	MIR3616	20:45523262-45817492	NOTEST	0	0	0	0	1	1
ENSG00000264902	ENSG00000264902	MIR5701-2	15:22156765-22156847	NOTEST	0	0	0	0	1	1
ENSG00000264903	ENSG00000264903	AC122720.1	5:165586437-165586525	NOTEST	0	0	0	0	1	1
ENSG00000264904	ENSG00000264904	AL139300.1	14:104019757-104181841	NOTEST	0	0	0	0	1	1
ENSG00000264905	ENSG00000264905	Y_RNA	HSCHR6_MHC_SSTO:29715037-29715139	NOTEST	0	0	0	0	1	1
ENSG00000264906	ENSG00000264906	MIR4494	12:47747536-47763718	NOTEST	0	0	0	0	1	1
ENSG00000264907	ENSG00000264907	SLMO2P3	17:60918461-60919006	NOTEST	0	0	0	0	1	1

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ENSG00000264908	ENSG00000264908	AC000403.1	13:77454311-77460540	NOTEST	0	0	0	0	1	1
ENSG00000264909	ENSG00000264909	U1	HSCHR6_MHC_COX:32447523-32447670	NOTEST	0	0	0	0	1	1
ENSG00000264910	ENSG00000264910	RN7SL525P	19:59054669-59054945	NOTEST	0	0	0	0	1	1
ENSG00000264911	ENSG00000264911	RP11-107K17.2	18:23805899-23971649	NOTEST	0	0	0	0	1	1
ENSG00000264912	ENSG00000264912	RN7SL640P	9:39072763-39288312	NOTEST	0	0	0	0	1	1
ENSG00000264913	ENSG00000264913	AL590233.1	9:91975701-92113045	NOTEST	0	0	0	0	1	1
ENSG00000264914	ENSG00000264914	RP11-343K8.3	17:55938603-56032684	NOTEST	0	0	0	0	1	1
ENSG00000264915	ENSG00000264915	Y_RNA	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000264916	ENSG00000264916	RN7SL230P	1:179850741-179894135	NOTEST	0	0	0	0	1	1
ENSG00000264917	ENSG00000264917	LOC732538	HG747_PATCH:66091183-66091873	NOTEST	0	0	0	0	1	1
ENSG00000264918	ENSG00000264918	AC005229.1	7:148393558-148498128	NOTEST	0	0	0	0	1	1
ENSG00000264919	ENSG00000264919	MIR4697	11:133768398-133768476	NOTEST	0	0	0	0	1	1
ENSG00000264921	ENSG00000264921	AC106771.1	5:12574968-12804475	NOTEST	0	0	0	0	1	1
ENSG00000264922	ENSG00000264922	MIR4540	9:36833271-37034103	NOTEST	0	0	0	0	1	1
ENSG00000264923	ENSG00000264923	RN7SL511P	20:32046604-32046854	NOTEST	0	0	0	0	1	1
ENSG00000264924	ENSG00000264924	RP11-799B12.2	18:21572736-21715574	NOTEST	0.214991	0.405672	0.916033	0	1	1
ENSG00000264925	ENSG00000264925	Z98949.1	22:26138110-26427007	NOTEST	0	0	0	0	1	1
ENSG00000264926	ENSG00000264926	MIR378F	1:24197015-24285549	NOTEST	0	0	0	0	1	1
ENSG00000264927	ENSG00000264927	AC093816.1	4:122323741-122323826	NOTEST	0	0	0	0	1	1
ENSG00000264928	ENSG00000264928	AC118463.1	5:19473059-20575982	NOTEST	0	0	0	0	1	1
ENSG00000264929	ENSG00000264929	RN7SL348P	15:65134081-65251042	NOTEST	0	0	0	0	1	1
ENSG00000264930	ENSG00000264930	RP11-846F4.10	17:22105714-22106030	NOTEST	0	0	0	0	1	1
ENSG00000264931	ENSG00000264931	MIR3138	4:10075962-10118573	NOTEST	0	0	0	0	1	1
ENSG00000264932	ENSG00000264932	Y_RNA	17:19551448-19580911	NOTEST	0.0378966	0	#NAME?	0	1	1
ENSG00000264933	ENSG00000264933	RN7SL190P	X:152163779-152164039	NOTEST	0	0	0	0	1	1
ENSG00000264934	ENSG00000264934	MIR4265	2:109745803-110262207	NOTEST	0	0	0	0	1	1
ENSG00000264935	ENSG00000264935	AC009035.1	16:26747549-26747638	NOTEST	0	0	0	0	1	1
ENSG00000264937	ENSG00000264937	AC100830.5	15:64979771-65011801	NOTEST	0.593499	0.443885	-0.41906	0	1	1
ENSG00000264938	ENSG00000264938	RP11-344P13.3	HG1292_PATCH:122037001-122053006	NOTEST	0	0	0	0	1	1
ENSG00000264939	ENSG00000264939	RP11-1109M24.9	17:21906416-21913070	NOTEST	0.035285	0.027473	-0.361041	0	1	1
ENSG00000264940	ENSG00000264940	SNORD3C	17:19092977-19093558	NOTEST	0	0	0	0	1	1
ENSG00000264941	ENSG00000264941	MIR4474	9:20341662-20622542	NOTEST	0	0	0	0	1	1
ENSG00000264942	ENSG00000264942	RN7SL642P	HG1257_PATCH:74998256-75203919	NOTEST	0	0	0	0	1	1
ENSG00000264943	ENSG00000264943	SH3GL1P2	17:28900488-28999807	NOTEST	0.157254	0.162879	0.0507078	0	1	1
ENSG00000264944	ENSG00000264944	MIR3620	1:228270360-228286912	NOTEST	0	0	0	0	1	1
ENSG00000264945	ENSG00000264945	KIR3DP1	HSCHR19LRC_PGF1_CTG1:55157744-55300469	NOTEST	0	0	0	0	1	1
ENSG00000264946	ENSG00000264946	RN7SL197P	20:48338485-48338782	NOTEST	0	0	0	0	1	1
ENSG00000264947	ENSG00000264947	hsa-mir-3181	16:50774820-50837249	NOTEST	0	0	0	0	1	1
ENSG00000264948	ENSG00000264948	RN7SL639P	17:18414534-18528930	NOTEST	0	0	0	0	1	1
ENSG00000264949	ENSG00000264949	RN7SL412P	9:213107-746105	NOTEST	0	0	0	0	1	1
ENSG00000264950	ENSG00000264950	AC113208.1	15:75518211-75518312	NOTEST	0	0	0	0	1	1
ENSG00000264951	ENSG00000264951	U6	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000264952	ENSG00000264952	AC004000.1	X:118533022-118588441	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000264953	ENSG00000264953	AC093602.1	4:139936942-140098372	NOTEST	0	0	0	0	1	1
ENSG00000264954	ENSG00000264954	RP11-214C8.2	17:62073430-62097994	NOTEST	0	0	0	0	1	1
ENSG00000264955	ENSG00000264955	Y_RNA	HSCHR6_MHC_COX:31732661-31751095	NOTEST	0	0	0	0	1	1
ENSG00000264957	ENSG00000264957	AL109805.1	20:3451686-3631769	NOTEST	0	0	0	0	1	1
ENSG00000264958	ENSG00000264958	ALOX12P1	17:28856705-28869434	NOTEST	0	0	0	0	1	1
ENSG00000264960	ENSG00000264960	U1	HSCHR6_MHC_SSTO:32546222-32546370	NOTEST	0	0	0	0	1	1
ENSG00000264961	ENSG00000264961	MIR4730	17:78234664-78411886	NOTEST	0	0	0	0	1	1
ENSG00000264962	ENSG00000264962	CR752645.1	HSCHR6_MHC_DBB:32880345-32898843	NOTEST	0	0	0	0	1	1
ENSG00000264963	ENSG00000264963	RN7SL440P	1:94614543-94740624	NOTEST	0.100646	0	#NAME?	0	1	1
ENSG00000264964	ENSG00000264964	RP11-888D10.3	18:9315191-9334439	NOTEST	0.591121	0.494832	-0.256516	0	1	1
ENSG00000264965	ENSG00000264965	AC144573.1	8:37807253-37807349	NOTEST	0	0	0	0	1	1
ENSG00000264966	ENSG00000264966	MIR5094	15:90373830-90456188	NOTEST	0	0	0	0	1	1
ENSG00000264967	ENSG00000264967	RN7SL722P	9:46048171-46048453	NOTEST	0	0	0	0	1	1
ENSG00000264968	ENSG00000264968	RP11-387H17.4	17:38083994-38095854	NOTEST	0.319032	0.324763	0.0256875	0	1	1
ENSG00000264969	ENSG00000264969	AC009941.1	8:80009597-80009688	NOTEST	0	0	0	0	1	1
ENSG00000264970	ENSG00000264970	RP11-846F4.11	17:22203741-22205012	NOTEST	0	0	0	0	1	1
ENSG00000264971	ENSG00000264971	RP11-110H1.1	18:46996172-46996593	NOTEST	0	0	0	0	1	1
ENSG00000264972	ENSG00000264972	AL445675.1	1:243061171-243061255	NOTEST	0	0	0	0	1	1
ENSG00000264973	ENSG00000264973	RN7SL701P	2:132632203-132632480	NOTEST	0	0	0	0	1	1
ENSG00000264974	ENSG00000264974	MIR4789	3:174156362-175523428	NOTEST	0	0	0	0	1	1
ENSG00000264975	ENSG00000264975	MIR4431	2:52929659-52929753	NOTEST	0	0	0	0	1	1
ENSG00000264976	ENSG00000264976	AC009478.2	2:181436438-181557181	NOTEST	0	0	0	0	1	1
ENSG00000264977	ENSG00000264977	RN7SL248P	10:46897591-46971400	NOTEST	0	0	0	0	1	1
ENSG00000264978	ENSG00000264978	RN7SL630P	12:94071150-94288616	NOTEST	0	0	0	0	1	1
ENSG00000264979	ENSG00000264979	MIR4436B2	2:110841446-110874143	NOTEST	0	0	0	0	1	1
ENSG00000264980	ENSG00000264980	CHD1L	HG1287_PATCH:147859185-147982177	NOTEST	0	0	0	0	1	1
ENSG00000264981	ENSG00000264981	RP11-434D2.10	17:20446286-20454276	NOTEST	0	0	0	0	1	1
ENSG00000264982	ENSG00000264982	RP11-344B2.2	18:29598334-30050447	NOTEST	0.534485	0.531221	-0.00883872	0	1	1
ENSG00000264983	ENSG00000264983	NOTCH2NL	HG1287_PATCH:150092790-150154445	NOTEST	0	0	0	0	1	1
ENSG00000264984	ENSG00000264984	MIR5691	11:9025708-9159661	NOTEST	0	0	0	0	1	1
ENSG00000264985	ENSG00000264985	RP11-449L23.2	17:71330522-71640228	NOTEST	0.00705511	0.00495585	-0.509536	0	1	1
ENSG00000264986	ENSG00000264986	MIR5092	3:124801479-125094198	NOTEST	0	0	0	0	1	1
ENSG00000264987	ENSG00000264987	AC110280.1	8:145456007-145456099	NOTEST	0	0	0	0	1	1
ENSG00000264988	ENSG00000264988	RP11-855A2.3	HG747_PATCH:65821639-65980494	NOTEST	0	0	0	0	1	1
ENSG00000264989	ENSG00000264989	AL136302.1	13:112563078-112563148	NOTEST	0	0	0	0	1	1
ENSG00000264990	ENSG00000264990	RP11-215E13.2	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000264991	ENSG00000264991	AP001205.1	8:101698043-101735037	NOTEST	0	0	0	0	1	1
ENSG00000264992	ENSG00000264992	AC239802.1	HG1287_PATCH:149575877-149719430	NOTEST	0	0	0	0	1	1
ENSG00000264994	ENSG00000264994	SNORD92	2:29117508-29171088	NOTEST	0	0	0	0	1	1
ENSG00000264995	ENSG00000264995	RN7SL540P	14:63838074-64010092	NOTEST	0	0	0	0	1	1
ENSG00000264996	ENSG00000264996	RP11-561O23.7	HG962_PATCH:70921452-71114201	NOTEST	0	0	0	0	1	1
ENSG00000264997	ENSG00000264997	SNORD39	11:109134220-109134291	NOTEST	0	0	0	0	1	1
ENSG00000264998	ENSG00000264998	U1	HSCHR6_MHC_APD:32468459-32468608	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000265000	ENSG00000265000	RP11-453A12.1	17:60885860-60913732	NOTEST	0	0	0	0	1	1
ENSG00000265001	ENSG00000265001	AC092846.2	4:24431454-24431523	NOTEST	0	0	0	0	1	1
ENSG00000265002	ENSG00000265002	AC026495.1	15:20549988-20564419	NOTEST	0	0	0	0	1	1
ENSG00000265003	ENSG00000265003	MIR4780	2:88367298-88412906	NOTEST	0	0	0	0	1	1
ENSG00000265004	ENSG00000265004	RN7SL458P	HG745_PATCH:36566042-36566303	NOTEST	0	0	0	0	1	1
ENSG00000265005	ENSG00000265005	MIR548W	16:25703346-26149009	NOTEST	0	0	0	0	1	1
ENSG00000265006	ENSG00000265006	AC138747.2	HSCHR15_1_CTG4:28682936-28683030	NOTEST	0	0	0	0	1	1
ENSG00000265007	ENSG00000265007	MIR4327	21:31747611-31747696	NOTEST	0	0	0	0	1	1
ENSG00000265008	ENSG00000265008	RP11-53I6.3	18:29598334-30050447	NOTEST	0	0	0	0	1	1
ENSG00000265009	ENSG00000265009	AC078864.1	12:52504417-52504488	NOTEST	0	0	0	0	1	1
ENSG00000265010	ENSG00000265010	RP11-661C3.2	17:71161115-71258491	NOTEST	0	0	0	0	1	1
ENSG00000265011	ENSG00000265011	RN7SL315P	4:17578814-17616194	NOTEST	0	0	0	0	1	1
ENSG00000265012	ENSG00000265012	AC024896.1	12:27124518-27167367	NOTEST	0	0	0	0	1	1
ENSG00000265013	ENSG00000265013	SNORD33	HSCHR6_MHC_MCF:29523203-29600766	NOTEST	0	0	0	0	1	1
ENSG00000265014	ENSG00000265014	MIR3160-1	11:46417963-46615675	NOTEST	0	0	0	0	1	1
ENSG00000265015	ENSG00000265015	RP11-454P7.3	18:15196997-15197774	NOTEST	0	0.671222	inf	0	1	1
ENSG00000265017	ENSG00000265017	AC092634.2	7:63387213-63387279	NOTEST	0	0	0	0	1	1
ENSG00000265018	ENSG00000265018	CTGLF12P	HG1211_PATCH:48424101-48445940	NOTEST	0	0	0	0	1	1
ENSG00000265019	ENSG00000265019	NCOR1P2	17:21536013-21544603	NOTEST	0	0	0	0	1	1
ENSG00000265020	ENSG00000265020	MIR4651	7:75528517-75623977	NOTEST	0	0	0	0	1	1
ENSG00000265021	ENSG00000265021	RNU1-92P	HG1287_PATCH:144406924-144407059	NOTEST	0	0	0	0	1	1
ENSG00000265022	ENSG00000265022	MIR133A2	HG506_HG507_HG1000_PATCH:61119398-61145820	NOTEST	0	0	0	0	1	1
ENSG00000265023	ENSG00000265023	AC011450.1	19:49769739-49769825	NOTEST	0	0	0	0	1	1
ENSG00000265024	ENSG00000265024	AC073089.1	7:66452663-66704501	NOTEST	0	0	0	0	1	1
ENSG00000265025	ENSG00000265025	AC127032.6	HSCHR17_1:43918343-43918413	NOTEST	0	0	0	0	1	1
ENSG00000265027	ENSG00000265027	AVPR1B	HG1293_PATCH:206173252-206181260	NOTEST	0	0	0	0	1	1
ENSG00000265028	ENSG00000265028	MIR4792	3:24562852-24562926	NOTEST	0	0	0	0	1	1
ENSG00000265029	ENSG00000265029	AC023158.1	12:33527172-33592754	NOTEST	0	0	0	0	1	1
ENSG00000265030	ENSG00000265030	RP11-763B22.6	HG1287_PATCH:144185601-144186927	NOTEST	0	0	0	0	1	1
ENSG00000265031	ENSG00000265031	hsa-mir-1273e	HG183_PATCH:62502428-62502530	NOTEST	0	0	0	0	1	1
ENSG00000265032	ENSG00000265032	AL132709.2	14:101505679-101505774	NOTEST	0	0	0	0	1	1
ENSG00000265033	ENSG00000265033	RN7SL262P	X:49008985-49009277	NOTEST	0.120317	0	#NAME?	0	1	1
ENSG00000265034	ENSG00000265034	MIR4739	HG748_PATCH:77703257-77703331	NOTEST	0	0	0	0	1	1
ENSG00000265035	ENSG00000265035	AC079772.1	4:33538365-33538464	NOTEST	0	0	0	0	1	1
ENSG00000265036	ENSG00000265036	AC217778.3	HSCHR17_1:43471267-43510270	NOTEST	0	0	0	0	1	1
ENSG00000265037	ENSG00000265037	MIR4707	14:23398817-23451851	NOTEST	0	0	0	0	1	1
ENSG00000265038	ENSG00000265038	PMM2P1	18:10636666-10637396	NOTEST	0	0	0	0	1	1
ENSG00000265039	ENSG00000265039	AC107016.2	12:53290976-53346686	NOTEST	0	0	0	0	1	1
ENSG00000265040	ENSG00000265040	RN7SL556P	7:5911385-5911681	NOTEST	0	0	0	0	1	1
ENSG00000265041	ENSG00000265041	RP11-19P22.7	17:25993774-25999829	NOTEST	0	0	0	0	1	1
ENSG00000265042	ENSG00000265042	AL137800.1	1:183441350-183567381	NOTEST	0	0	0	0	1	1
ENSG00000265043	ENSG00000265043	RP11-728E14.3	17:21359824-21363527	NOTEST	0	0	0	0	1	1
ENSG00000265044	ENSG00000265044	RNVU1-15	HG1287_PATCH:145098990-145099155	NOTEST	0	0	0	0	1	1

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ENSG00000265045	ENSG00000265045	RN7SL486P	3:189674516-189862635	NOTEST	0	0	0	0	1	1
ENSG00000265046	ENSG00000265046	CTC-542B22.1	17:30157749-30158769	NOTEST	0	0	0	0	1	1
ENSG00000265047	ENSG00000265047	AC026992.1	15:69452922-69564556	NOTEST	0	0	0	0	1	1
ENSG00000265048	ENSG00000265048	U6	HSCHR6_MHC_SSTO:32267411-32346296	NOTEST	0	0	0	0	1	1
ENSG00000265049	ENSG00000265049	AC009480.1	2:148602085-149275805	NOTEST	0	0	0	0	1	1
ENSG00000265050	ENSG00000265050	AC092022.1	7:84295239-84295324	NOTEST	0	0	0	0	1	1
ENSG00000265052	ENSG00000265052	RN7SL622P	17:65821639-65980494	NOTEST	0	0	0	0	1	1
ENSG00000265053	ENSG00000265053	RN7SL321P	3:48413708-48442666	NOTEST	0	0	0	0	1	1
ENSG00000265054	ENSG00000265054	AC090051.1	12:105196330-105352522	NOTEST	0	0	0	0	1	1
ENSG00000265055	ENSG00000265055	AC145343.2	17:66092186-66097615	NOTEST	0.441391	0.296714	-0.572986	0	1	1
ENSG00000265056	ENSG00000265056	MIR548S	2:11817720-11967535	NOTEST	0	0	0	0	1	1
ENSG00000265057	ENSG00000265057	MIR4765	2:32853098-33046118	NOTEST	0	0	0	0	1	1
ENSG00000265058	ENSG00000265058	RN7SL245P	16:22647775-22648065	NOTEST	0	0	0	0	1	1
ENSG00000265059	ENSG00000265059	U1	HSCHR6_MHC_MANN:32517758-32517906	NOTEST	0	0	0	0	1	1
ENSG00000265060	ENSG00000265060	PPY2	17:26573479-26575315	NOTEST	0	0	0	0	1	1
ENSG00000265061	ENSG00000265061	MIR4419B	12:128729050-128729118	NOTEST	0	0	0	0	1	1
ENSG00000265062	ENSG00000265062	AL133228.1	20:49411430-49493714	NOTEST	0	0	0	0	1	1
ENSG00000265063	ENSG00000265063	AC009831.1	18:29598334-30050447	NOTEST	0	0	0	0	1	1
ENSG00000265064	ENSG00000265064	MIR4692	11:72396113-72504726	NOTEST	0	0	0	0	1	1
ENSG00000265066	ENSG00000265066	RP5-998N21.3	HG1287_PATCH:14453251-144532919	NOTEST	0	0	0	0	1	1
ENSG00000265067	ENSG00000265067	RN7SL707P	15:64679946-64747502	NOTEST	0	0.090091	inf	0	1	1
ENSG00000265068	ENSG00000265068	AL591377.1	9:104296132-104325622	NOTEST	0	0	0	0	1	1
ENSG00000265069	ENSG00000265069	RP11-781P6.1	18:6941742-7117813	NOTEST	0.0164659	0.0368934	1.16388	0	1	1
ENSG00000265070	ENSG00000265070	AC006115.1	19:57202053-57352097	NOTEST	0	0	0	0	1	1
ENSG00000265071	ENSG00000265071	Y_RNA	HSCHR6_MHC_QBL:33090189-33101042	NOTEST	0	0	0	0	1	1
ENSG00000265072	ENSG00000265072	MIR3652	12:104235228-104359486	NOTEST	0	0	0	0	1	1
ENSG00000265073	ENSG00000265073	AC010761.6	17:27046410-27070473	NOTEST	0.0379083	0.101729	1.42415	0	1	1
ENSG00000265074	ENSG00000265074	U1	HSCHR6_MHC_MANN:32640267-32640431	NOTEST	0	0	0	0	1	1
ENSG00000265075	ENSG00000265075	MIR3622B	8:27559189-27559284	NOTEST	0	0	0	0	1	1
ENSG00000265076	ENSG00000265076	AC016970.1	3:103773551-103773640	NOTEST	0	0	0	0	1	1
ENSG00000265077	ENSG00000265077	RN7SL54P	16:48198862-48482313	NOTEST	0	0	0	0	1	1
ENSG00000265078	ENSG00000265078	RN7SL664P	3:48136292-48136595	NOTEST	0	0	0	0	1	1
ENSG00000265080	ENSG00000265080	MIR4800	4:2249158-2264021	NOTEST	0	0	0	0	1	1
ENSG00000265081	ENSG00000265081	RN7SL102P	17:36777452-36777733	NOTEST	0	0	0	0	1	1
ENSG00000265082	ENSG00000265082	AL356213.1	X:122318005-122624766	NOTEST	0	0	0	0	1	1
ENSG00000265083	ENSG00000265083	MIR3691	6:5102826-5261172	NOTEST	0	0	0	0	1	1
ENSG00000265084	ENSG00000265084	AC092364.2	19:21905567-21950430	NOTEST	0	0	0	0	1	1
ENSG00000265085	ENSG00000265085	AC110810.1	4:63461094-63461180	NOTEST	0	0	0	0	1	1
ENSG00000265086	ENSG00000265086	AC006534.2	17:65821639-65980494	NOTEST	0	0	0	0	1	1
ENSG00000265087	ENSG00000265087	MIR4761	22:19863039-20004331	NOTEST	0	0	0	0	1	1
ENSG00000265088	ENSG00000265088	HCG4P5	HG1322_PATCH:29901733-29909270	NOTEST	0	0	0	0	1	1
ENSG00000265089	ENSG00000265089	MIR4655	7:1855428-2272878	NOTEST	0	0	0	0	1	1
ENSG00000265090	ENSG00000265090	AC104637.1	3:163234189-163234275	NOTEST	0	0	0	0	1	1
ENSG00000265091	ENSG00000265091	RP11-835E18.5	18:5232874-5246507	NOTEST	0	0.0189477	inf	0	1	1

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ENSG00000265093	ENSG00000265093	RN7SL246P	12:46123447-46301823	NOTEST	0	0	0	0	1	1
ENSG00000265094	ENSG00000265094	RP11-178F10.1	18:22006579-22033499	NOTEST	0	0.0951639	inf	0	1	1
ENSG00000265095	ENSG00000265095	FTLP12	17:16294747-16295196	NOTEST	0.100175	0	#NAME?	0	1	1
ENSG00000265096	ENSG00000265096	C1QTNF1-AS1	17:77015290-77045870	NOTEST	0.0361195	0.140748	1.96226	0	1	1
ENSG00000265097	ENSG00000265097	RBM22P1	18:24916342-25175128	NOTEST	0	0	0	0	1	1
ENSG00000265098	ENSG00000265098	MIR4510	15:36219056-36219124	NOTEST	0	0	0	0	1	1
ENSG00000265099	ENSG00000265099	RP11-344E13.1	17:20717932-20947073	NOTEST	0	0	0	0	1	1
ENSG00000265100	ENSG00000265100	RP11-147L13.2	17:66242769-66253297	NOTEST	0.235998	0.102683	-1.20058	0	1	1
ENSG00000265101	ENSG00000265101	CTD-2382H12.1	18:76685063-76687441	NOTEST	0	0	0	0	1	1
ENSG00000265102	ENSG00000265102	MIR3942	15:35473999-35838394	NOTEST	0	0	0	0	1	1
ENSG00000265104	ENSG00000265104	AC011416.1	5:126596627-126596690	NOTEST	0	0	0	0	1	1
ENSG00000265105	ENSG00000265105	Y_RNA	HSCHR6_MHC_QBL:29715612-29715714	NOTEST	0	0	0	0	1	1
ENSG00000265106	ENSG00000265106	Z93241.1	22:42948193-42948279	NOTEST	0	0	0	0	1	1
ENSG00000265107	ENSG00000265107	GJA5	HG1287_PATCH:148443602-148445686	NOTEST	0	0	0	0	1	1
ENSG00000265108	ENSG00000265108	AL357932.1	1:195095810-195095906	NOTEST	0	0	0	0	1	1
ENSG00000265109	ENSG00000265109	AC055811.1	17:17145323-17146200	NOTEST	0	0	0	0	1	1
ENSG00000265110	ENSG00000265110	MIR4731	17:15133094-15169024	NOTEST	0	0	0	0	1	1
ENSG00000265111	ENSG00000265111	PDZK1	HG1287_PATCH:146357399-146394563	NOTEST	0	0	0	0	1	1
ENSG00000265112	ENSG00000265112	MIR3153	9:91926112-91931618	NOTEST	0	0	0	0	1	1
ENSG00000265113	ENSG00000265113	RP11-70O5.2	16:69139466-69442474	NOTEST	0	0	0	0	1	1
ENSG00000265114	ENSG00000265114	RP11-285M22.1	17:22192160-22194158	NOTEST	0	0	0	0	1	1
ENSG00000265115	ENSG00000265115	RP11-31I22.2	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000265116	ENSG00000265116	SNORD83	HSCHR6_MHC_MANN:31536012-31554120	NOTEST	0	0	0	0	1	1
ENSG00000265117	ENSG00000265117	CU013544.3	GL000233.1:35451-35534	NOTEST	0	0	0	0	1	1
ENSG00000265118	ENSG00000265118	CTD-2370N5.3	17:29335514-29709134	NOTEST	0	0.0655744	inf	0	1	1
ENSG00000265119	ENSG00000265119	RN7SL676P	12:14464276-14464549	NOTEST	0	0	0	0	1	1
ENSG00000265120	ENSG00000265120	RP11-285E9.6	HSCHR17_3_CTG4:75265440-75508300	NOTEST	0	0	0	0	1	1
ENSG00000265121	ENSG00000265121	RP11-285E9.5	17:75253818-75496678	NOTEST	0	0	0	0	1	1
ENSG00000265122	ENSG00000265122	AC010247.1	19:42590262-42700737	NOTEST	0	0	0	0	1	1
ENSG00000265123	ENSG00000265123	RN7SL200P	6:34555064-34665247	NOTEST	0	0	0	0	1	1
ENSG00000265124	ENSG00000265124	BMS1P5	HG1211_PATCH:47283837-47333708	NOTEST	0	0	0	0	1	1
ENSG00000265125	ENSG00000265125	RP11-31I22.3	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000265126	ENSG00000265126	CTB-187M2.2	17:19314437-19320589	NOTEST	0	0	0	0	1	1
ENSG00000265127	ENSG00000265127	AC009080.1	16:60803882-60803987	NOTEST	0	0	0	0	1	1
ENSG00000265128	ENSG00000265128	RP11-15F12.3	18:46550072-46987717	NOTEST	0	0	0	0	1	1
ENSG00000265129	ENSG00000265129	AC064837.1	2:182818967-182996125	NOTEST	0	0	0	0	1	1
ENSG00000265130	ENSG00000265130	CTB-58E17.2	17:36686250-36762183	NOTEST	0	0	0	0	1	1
ENSG00000265132	ENSG00000265132	AC145141.2	5:70647681-70742396	NOTEST	0	0	0	0	1	1
ENSG00000265133	ENSG00000265133	HIST2H3D	HG1287_PATCH:150499685-150500096	NOTEST	0	0	0	0	1	1
ENSG00000265134	ENSG00000265134	MIR3191	19:47724080-47736023	NOTEST	0	0	0	0	1	1
ENSG00000265135	ENSG00000265135	MIR5687	5:54603587-54830878	NOTEST	0	0	0	0	1	1
ENSG00000265136	ENSG00000265136	RP13-638C3.6	17:80477588-80606429	NOTEST	0	0.0406411	inf	0	1	1
ENSG00000265137	ENSG00000265137	MIR3192	20:18364010-18465287	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000265138	ENSG00000265138	SNORA48	HSCHR6_MHC_DBB:30090905-30091067	NOTEST	0	0	0	0	1	1
ENSG00000265139	ENSG00000265139	RP11-227G15.2	17:30593194-30708905	NOTEST	0	0	0	0	1	1
ENSG00000265140	ENSG00000265140	MIR4301	11:113276042-113346413	NOTEST	0	0	0	0	1	1
ENSG00000265141	ENSG00000265141	RN7SL451P	1:9039636-9039933	NOTEST	0	0	0	0	1	1
ENSG00000265142	ENSG00000265142	MIR1-2	18:19284917-19450918	NOTEST	0.00366227	0.00257002	-0.510957	0	1	1
ENSG00000265143	ENSG00000265143	RN7SL490P	1:26648349-26680621	NOTEST	0	0	0	0	1	1
ENSG00000265144	ENSG00000265144	MIR548AM	X:16606125-16731059	NOTEST	0	0	0	0	1	1
ENSG00000265145	ENSG00000265145	SNORD53	2:29117508-29171088	NOTEST	0	0	0	0	1	1
ENSG00000265146	ENSG00000265146	MIR4752	HSCHR19LRC_COX2_CTG1:54785612-54785684	NOTEST	0	0	0	0	1	1
ENSG00000265148	ENSG00000265148	BZRAP1-AS1	17:56378591-56494956	NOTEST	0.0860097	0	#NAME?	0	1	1
ENSG00000265149	ENSG00000265149	RN7SL669P	19:11562140-11639989	NOTEST	0	0	0	0	1	1
ENSG00000265151	ENSG00000265151	AL158175.1	20:22713439-22714727	NOTEST	0	0	0	0	1	1
ENSG00000265152	ENSG00000265152	AF222686.1	X:49687224-49863892	NOTEST	0	0	0	0	1	1
ENSG00000265153	ENSG00000265153	RP11-822E23.5	HG987_PATCH:21496105-21497492	NOTEST	0	0	0	0	1	1
ENSG00000265154	ENSG00000265154	MIR151B	14:100437785-100610573	NOTEST	0	0	0	0	1	1
ENSG00000265155	ENSG00000265155	AC092104.3	7:7107674-7107757	NOTEST	0	0	0	0	1	1
ENSG00000265156	ENSG00000265156	SNORD52	HSCHR6_MHC_QBL:31792646-31797799	NOTEST	0	0	0	0	1	1
ENSG00000265157	ENSG00000265157	AF070718.1	8:91233715-91632298	NOTEST	0	0	0	0	1	1
ENSG00000265158	ENSG00000265158	LRRC37A7P	18:29304160-29306919	NOTEST	0.185888	0.184645	-0.00968071	0	1	1
ENSG00000265159	ENSG00000265159	Y_RNA	HSCHR6_MHC_MANN:33315283-33326135	NOTEST	0	0	0	0	1	1
ENSG00000265160	ENSG00000265160	MIR5003	5:172068268-172124723	NOTEST	0	0	0	0	1	1
ENSG00000265161	ENSG00000265161	AC011293.1	Y:13947442-13947512	NOTEST	0	0	0	0	1	1
ENSG00000265163	ENSG00000265163	CDRT8	17:15008553-15009504	NOTEST	0	0.111697	inf	0	1	1
ENSG00000265164	ENSG00000265164	MIR2681	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000265165	ENSG00000265165	MIR4307	14:27305933-27629626	NOTEST	0	0	0	0	1	1
ENSG00000265166	ENSG00000265166	AF186996.1	3:125455058-125455146	NOTEST	0	0	0	0	1	1
ENSG00000265167	ENSG00000265167	AC009081.1	16:60393745-60476149	NOTEST	0	0	0	0	1	1
ENSG00000265168	ENSG00000265168	RP11-192H23.5	17:26782769-26972472	NOTEST	0	0	0	0	1	1
ENSG00000265169	ENSG00000265169	AC034187.3	3:8661085-9005457	NOTEST	0	0	0	0	1	1
ENSG00000265170	ENSG00000265170	RN7SL667P	X:152669305-152669599	NOTEST	0	0	0	0	1	1
ENSG00000265171	ENSG00000265171	RN7SL699P	17:49672866-49673118	NOTEST	0	0	0	0	1	1
ENSG00000265172	ENSG00000265172	MIR4262	2:11977058-11977112	NOTEST	0	0	0	0	1	1
ENSG00000265174	ENSG00000265174	CTD-2124B20.3	18:6511414-6590652	NOTEST	0	0	0	0	1	1
ENSG00000265175	ENSG00000265175	AC092685.1	7:64728308-64728404	NOTEST	0	0	0	0	1	1
ENSG00000265176	ENSG00000265176	MIR3202-1	X:153237777-153248646	NOTEST	0	0	0	0	1	1
ENSG00000265177	ENSG00000265177	LINC-PINT	HG1308_PATCH:13060541-130773830	NOTEST	0	0	0	0	1	1
ENSG00000265178	ENSG00000265178	MIR4728	17:37827374-37887040	NOTEST	0	0	0	0	1	1
ENSG00000265179	ENSG00000265179	RP11-672L10.2	18:894435-912173	NOTEST	0	0	0	0	1	1
ENSG00000265180	ENSG00000265180	MIR4790	3:5291861-5291940	NOTEST	0	0	0	0	1	1
ENSG00000265181	ENSG00000265181	MIR4674	9:139440624-139444345	NOTEST	0	0	0	0	1	1
ENSG00000265182	ENSG00000265182	SRP72P1	18:47021516-47023266	NOTEST	0	0	0	0	1	1
ENSG00000265183	ENSG00000265183	SNORD60	HG1293_PATCH:206098791-206166009	NOTEST	0	0	0	0	1	1
ENSG00000265184	ENSG00000265184	DYRK3	HG1293_PATCH:206698209-206747980	NOTEST	0	0	0	0	1	1

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ENSG00000265185	ENSG00000265185	SNORD3B-1	17:18965224-18965807	NOTEST	0.0667306	0	#NAME?	0	1	1
ENSG00000265186	ENSG00000265186	AC068706.2	2:177246959-177247060	NOTEST	0	0	0	0	1	1
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ENSG00000265189	ENSG00000265189	AC006080.1	17:63416700-63416778	NOTEST	0	0	0	0	1	1
ENSG00000265190	ENSG00000265190	ANXA8	HG1211_PATCH:47955609-47987141	NOTEST	0	0	0	0	1	1
ENSG00000265191	ENSG00000265191	RN7SL347P	15:44719431-44829121	NOTEST	0	0	0	0	1	1
ENSG00000265192	ENSG00000265192	RN7SL85P	1:19638819-19655794	NOTEST	0	0	0	0	1	1
ENSG00000265193	ENSG00000265193	MIR3923	3:78646389-79816965	NOTEST	0	0	0	0	1	1
ENSG00000265194	ENSG00000265194	RP11-70L8.4	9:21802541-22121096	NOTEST	0.559446	0.360668	-0.633328	0	1	1
ENSG00000265195	ENSG00000265195	MIR4312	15:69070873-69355083	NOTEST	0	0	0	0	1	1
ENSG00000265196	ENSG00000265196	PDIA3P1	HG1287_PATCH:147859185-147982177	NOTEST	0	0	0	0	1	1
ENSG00000265197	ENSG00000265197	AC053516.1	Y:18398126-18398238	NOTEST	0	0	0	0	1	1
ENSG00000265199	ENSG00000265199	AL359218.1	14:20501819-20501923	NOTEST	0	0	0	0	1	1
ENSG00000265200	ENSG00000265200	AC090324.1	18:55684015-55684116	NOTEST	0	0	0	0	1	1
ENSG00000265201	ENSG00000265201	MIR4677	1:243419319-244014381	NOTEST	0	0	0	0	1	1
ENSG00000265203	ENSG00000265203	RBP3	HG1211_PATCH:47843818-47853323	NOTEST	0	0	0	0	1	1
ENSG00000265204	ENSG00000265204	RP11-403A21.3	18:21572736-21715574	NOTEST	0	0	0	0	1	1
ENSG00000265205	ENSG00000265205	AC010761.13	17:26975373-27029697	NOTEST	0.395284	0.364236	-0.118013	0	1	1
ENSG00000265206	ENSG00000265206	MIR142	17:56378591-56494956	NOTEST	0	0.0079382	inf	0	1	1
ENSG00000265207	ENSG00000265207	BX927160.1	HSCHR6_MHC_MANN:32871476-32871544	NOTEST	0	0	0	0	1	1
ENSG00000265208	ENSG00000265208	AC015600.1	11:100554892-100862668	NOTEST	0	0	0	0	1	1
ENSG00000265209	ENSG00000265209	AC010543.1	16:57908287-57908434	NOTEST	0	0	0	0	1	1
ENSG00000265210	ENSG00000265210	MIR4486	11:19372270-20143144	NOTEST	0	0	0	0	1	1
ENSG00000265211	ENSG00000265211	AL121865.1	X:50334646-50557302	NOTEST	0	0	0	0	1	1
ENSG00000265212	ENSG00000265212	AC007009.2	7:8152813-8384146	NOTEST	0	0	0	0	1	1
ENSG00000265213	ENSG00000265213	MIR3684	4:99916770-99983964	NOTEST	0	0	0	0	1	1
ENSG00000265214	ENSG00000265214	MIR4283-1	7:63081467-63081547	NOTEST	0	0	0	0	1	1
ENSG00000265215	ENSG00000265215	MIR4269	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000265216	ENSG00000265216	AL592310.1	1:227751243-227865144	NOTEST	0	0	0	0	1	1
ENSG00000265217	ENSG00000265217	RP11-775G23.1	18:63273325-63319289	NOTEST	0	0	0	0	1	1
ENSG00000265218	ENSG00000265218	RP11-927P21.1	17:62850429-62915598	NOTEST	0.0645861	0.193377	1.58212	0	1	1
ENSG00000265219	ENSG00000265219	AC011652.1	8:130363936-130695925	NOTEST	0	0	0	0	1	1
ENSG00000265220	ENSG00000265220	RP11-88I18.2	HG962_PATCH:70921452-71114201	NOTEST	0	0	0	0	1	1
ENSG00000265223	ENSG00000265223	RNU1-79P	HSCHR6_MHC_COX:32409333-32409482	NOTEST	0	0	0	0	1	1
ENSG00000265224	ENSG00000265224	AC012353.1	2:140988991-142895399	NOTEST	0	0	0	0	1	1
ENSG00000265225	ENSG00000265225	AL118525.1	20:48203217-48203311	NOTEST	0	0	0	0	1	1
ENSG00000265226	ENSG00000265226	MIR548AI	6:99572484-99572572	NOTEST	0	0	0	0	1	1
ENSG00000265227	ENSG00000265227	MIR4699	12:81186298-81650533	NOTEST	0	0	0	0	1	1
ENSG00000265228	ENSG00000265228	PRPF3	HG1287_PATCH:151007890-151039610	NOTEST	0	0	0	0	1	1
ENSG00000265229	ENSG00000265229	RN7SL112P	18:56470252-56470561	NOTEST	0	0	0	0	1	1
ENSG00000265230	ENSG00000265230	RN7SL407P	16:70286197-70323446	NOTEST	0	0	0	0	1	1
ENSG00000265231	ENSG00000265231	AKR1C2	HG871_PATCH:5029586-5060223	NOTEST	0	0	0	0	1	1
ENSG00000265232	ENSG00000265232	HIST2H3PS2	HG1287_PATCH:144561207-144621191	NOTEST	0	0	0	0	1	1
ENSG00000265233	ENSG00000265233	AC144838.2	17:21549810-21549979	NOTEST	0	0	0	0	1	1
ENSG00000265234	ENSG00000265234	RN7SL212P	HG1257_PATCH:75753746-75754010	NOTEST	0	0	0	0	1	1

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ENSG00000265235	ENSG00000265235	AC083908.1	3:130569438-131100319	NOTEST	0	0	0	0	1	1
ENSG00000265236	ENSG00000265236	SNORD84	6:31496493-31526606	NOTEST	0	0	0	0	1	1
ENSG00000265237	ENSG00000265237	MIR3142	5:159895274-159914433	NOTEST	0	0	0	0	1	1
ENSG00000265238	ENSG00000265238	MIR3614	17:54965269-54991399	NOTEST	0	0	0	0	1	1
ENSG00000265239	ENSG00000265239	AC073587.1	10:122216465-122349367	NOTEST	0	0	0	0	1	1
ENSG00000265240	ENSG00000265240	RP11-638L3.2	18:65173818-65566856	NOTEST	0	0	0	0	1	1
ENSG00000265241	ENSG00000265241	RBM8A	HG1287_PATCH:146607982-146645521	NOTEST	0	0	0	0	1	1
ENSG00000265242	ENSG00000265242	RP11-649A18.7	17:73131342-73179078	NOTEST	0.429116	0.515248	0.2639	0	1	1
ENSG00000265243	ENSG00000265243	IGLJCOR18	18:3394886-3395310	NOTEST	0	0	0	0	1	1
ENSG00000265244	ENSG00000265244	AL358340.1	14:34393436-34931980	NOTEST	0	0	0	0	1	1
ENSG00000265245	ENSG00000265245	AC073343.2	7:6703604-6748532	NOTEST	0	0	0	0	1	1
ENSG00000265246	ENSG00000265246	RP11-663N22.1	17:25564884-25568687	NOTEST	0	0	0	0	1	1
ENSG00000265247	ENSG00000265247	MIR4472-1	8:143257699-143257779	NOTEST	0	0	0	0	1	1
ENSG00000265248	ENSG00000265248	U1	HSCHR6_MHC_SSTO:32586785-32586949	NOTEST	0	0	0	0	1	1
ENSG00000265249	ENSG00000265249	AC025280.1	16:84853589-84954374	NOTEST	0	0	0	0	1	1
ENSG00000265250	ENSG00000265250	AL132709.3	14:101518339-101518436	NOTEST	0	0	0	0	1	1
ENSG00000265251	ENSG00000265251	MIR4288	8:28351728-28431775	NOTEST	0	0	0	0	1	1
ENSG00000265252	ENSG00000265252	MIR3132	2:220403668-220415317	NOTEST	0	0	0	0	1	1
ENSG00000265253	ENSG00000265253	MIR4446	3:113251142-113348425	NOTEST	0	0	0	0	1	1
ENSG00000265254	ENSG00000265254	CTD-2350C19.2	17:26684603-26734215	NOTEST	0	0	0	0	1	1
ENSG00000265255	ENSG00000265255	7SK	HSCHR6_MHC_DBB:30822710-30823013	NOTEST	0	0	0	0	1	1
ENSG00000265257	ENSG00000265257	RP11-21J18.1	18:9102627-9285983	NOTEST	0	0	0	0	1	1
ENSG00000265258	ENSG00000265258	MIR4686	11:2194292-2194368	NOTEST	0	0	0	0	1	1
ENSG00000265259	ENSG00000265259	RN7SL247P	18:21718941-21977844	NOTEST	0	0	0	0	1	1
ENSG00000265260	ENSG00000265260	RN7SL74P	X:95939661-96897588	NOTEST	0	0	0	0	1	1
ENSG00000265261	ENSG00000265261	RP11-162A12.3	18:74534562-74682683	NOTEST	0.00576507	0	#NAME?	0	1	1
ENSG00000265262	ENSG00000265262	RP11-180P8.2	17:61012762-61044171	NOTEST	0	0	0	0	1	1
ENSG00000265263	ENSG00000265263	RP11-135L13.4	17:19118927-19240028	NOTEST	0	5.95E-05	inf	0	1	1
ENSG00000265264	ENSG00000265264	TIMM10B	11:6502676-6614988	NOTEST	0.108146	0.177555	0.715278	0	1	1
ENSG00000265265	ENSG00000265265	RP11-822E23.7	17:21422774-21424530	NOTEST	0	0	0	0	1	1
ENSG00000265266	ENSG00000265266	AC022681.1	8:136246373-136311962	NOTEST	0	0	0	0	1	1
ENSG00000265267	ENSG00000265267	AL121652.3	2:32047659-32048886	NOTEST	0	0	0	0	1	1
ENSG00000265268	ENSG00000265268	AL356140.1	10:85196789-85196885	NOTEST	0	0	0	0	1	1
ENSG00000265269	ENSG00000265269	MIR4311	HSCHR15_1_CTG8:66187416-66558222	NOTEST	0	0	0	0	1	1
ENSG00000265270	ENSG00000265270	AP000539.2	22:16576108-16576191	NOTEST	0	0	0	0	1	1
ENSG00000265272	ENSG00000265272	RN7SL693P	19:58985383-59023780	NOTEST	0	0	0	0	1	1
ENSG00000265273	ENSG00000265273	PGDP1	18:29542140-29543581	NOTEST	0	0	0	0	1	1
ENSG00000265274	ENSG00000265274	Metazoa_SRP	HSCHR17_1:44831765-44898747	NOTEST	0	0	0	0	1	1
ENSG00000265275	ENSG00000265275	AF104455.1	7:152753821-152753904	NOTEST	0	0	0	0	1	1
ENSG00000265277	ENSG00000265277	ACP6	HG1287_PATCH:148333780-148356927	NOTEST	0	0	0	0	1	1
ENSG00000265278	ENSG00000265278	Y_RNA	HSCHR6_MHC_QBL:31619245-31631569	NOTEST	0	0	0	0	1	1
ENSG00000265279	ENSG00000265279	RP11-53I6.5	18:29598334-30050447	NOTEST	0	0	0	0	1	1
ENSG00000265280	ENSG00000265280	AC018804.1	2:130908980-130948302	NOTEST	0	0	0	0	1	1

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ENSG00000265282	ENSG00000265282	RP11-269G24.4	17:61086916-61509572	NOTEST	0	0.0303661	inf	0	1	1
ENSG00000265283	ENSG00000265283	MIR3118-5	GL000213.1:104741-104817	NOTEST	0	0	0	0	1	1
ENSG00000265284	ENSG00000265284	MIR4770	X:6301946-6302004	NOTEST	0	0	0	0	1	1
ENSG00000265285	ENSG00000265285	AL591379.1	9:67094932-67094999	NOTEST	0	0	0	0	1	1
ENSG00000265286	ENSG00000265286	AL603650.3	9:137741020-137741098	NOTEST	0	0	0	0	1	1
ENSG00000265287	ENSG00000265287	RP11-192H23.6	17:26782769-26972472	NOTEST	0.333872	0.17428	-0.937888	0	1	1
ENSG00000265289	ENSG00000265289	AC104984.4	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000265290	ENSG00000265290	CR759778.1	HSCHR6_MHC_MCF:30693276-30719302	NOTEST	0	0	0	0	1	1
ENSG00000265291	ENSG00000265291	MIR4710	14:105144030-105144086	NOTEST	0	0	0	0	1	1
ENSG00000265292	ENSG00000265292	RN7SL195P	11:93394804-93547861	NOTEST	0	0	0	0	1	1
ENSG00000265293	ENSG00000265293	ARGFXP2	17:30468244-30580393	NOTEST	0.203382	0.102672	-0.986154	0	1	1
ENSG00000265294	ENSG00000265294	AL671883.1	6:31342094-31342180	NOTEST	0	0	0	0	1	1
ENSG00000265295	ENSG00000265295	AC084125.3	8:145754562-145911194	NOTEST	0	0	0	0	1	1
ENSG00000265296	ENSG00000265296	FEM1AP2	18:14391911-14393908	NOTEST	0	0	0	0	1	1
ENSG00000265297	ENSG00000265297	RNU1-120P	HG1287_PATCH:148949890-148950047	NOTEST	0	0	0	0	1	1
ENSG00000265299	ENSG00000265299	CR753651.3	HSCHR6_MHC_DBB:28743703-28743811	NOTEST	0	0	0	0	1	1
ENSG00000265300	ENSG00000265300	AC007731.1	22:20778873-20850170	NOTEST	0	0	0	0	1	1
ENSG00000265301	ENSG00000265301	MIR548AD	2:35696470-35696552	NOTEST	0	0	0	0	1	1
ENSG00000265303	ENSG00000265303	CTD-2510F5.6	17:57232859-57292608	NOTEST	0	0	0	0	1	1
ENSG00000265304	ENSG00000265304	MIR3650	5:38475064-38671318	NOTEST	0	0	0	0	1	1
ENSG00000265305	ENSG00000265305	EMBP1	HG1292_PATCH:122061967-122111416	NOTEST	0	0	0	0	1	1
ENSG00000265306	ENSG00000265306	hsa-mir-3195	20:60528524-60640866	NOTEST	0	0	0	0	1	1
ENSG00000265307	ENSG00000265307	SV2A	HG1287_PATCH:150589732-150604297	NOTEST	0	0	0	0	1	1
ENSG00000265310	ENSG00000265310	RP11-728E14.2	HG987_PATCH:21359824-21363527	NOTEST	0	0	0	0	1	1
ENSG00000265311	ENSG00000265311	AL020993.1	22:38670344-38670430	NOTEST	0	0	0	0	1	1
ENSG00000265313	ENSG00000265313	RP11-567L7.6	17:57508229-57604307	NOTEST	0	0	0	0	1	1
ENSG00000265314	ENSG00000265314	MIR548AH	4:77356252-77723117	NOTEST	0	0	0	0	1	1
ENSG00000265315	ENSG00000265315	RN7SL199P	17:44588876-44657088	NOTEST	0	0	0	0	1	1
ENSG00000265316	ENSG00000265316	RP11-286N3.1	18:5392382-5630699	NOTEST	0	0	0	0	1	1
ENSG00000265317	ENSG00000265317	AC103740.1	15:62682724-63176233	NOTEST	0	0	0	0	1	1
ENSG00000265318	ENSG00000265318	RP11-89F3.2	HG1287_PATCH:145973024-145974170	NOTEST	0	0	0	0	1	1
ENSG00000265319	ENSG00000265319	RN7SL847P	10:33189246-33371030	NOTEST	0	0	0	0	1	1
ENSG00000265320	ENSG00000265320	AL391650.1	1:26398068-26398168	NOTEST	0	0	0	0	1	1
ENSG00000265321	ENSG00000265321	MIR4263	2:27994583-28561768	NOTEST	0	0	0	0	1	1
ENSG00000265322	ENSG00000265322	MIR3118-6	15:21038123-21038198	NOTEST	0	0	0	0	1	1
ENSG00000265323	ENSG00000265323	Y_RNA	HSCHR6_MHC_MANN:30945078-30945170	NOTEST	0	0	0	0	1	1
ENSG00000265324	ENSG00000265324	AC005020.1	7:99143930-99208439	NOTEST	0	0	0	0	1	1
ENSG00000265325	ENSG00000265325	SNORD83	HSCHR6_MHC_MANN:31536012-31554120	NOTEST	0	0	0	0	1	1
ENSG00000265326	ENSG00000265326	Metazoa_SRP	HSCHR6_MHC_MANN:28945257-28945553	NOTEST	0	0	0	0	1	1
ENSG00000265327	ENSG00000265327	RN7SL411P	3:39850404-40301812	NOTEST	0	0	0	0	1	1
ENSG00000265328	ENSG00000265328	MIR548AB	3:103242876-103242960	NOTEST	0	0	0	0	1	1
ENSG00000265329	ENSG00000265329	MIR4758	20:60877148-60942368	NOTEST	0	0	0	0	1	1
ENSG00000265330	ENSG00000265330	AC034187.4	3:8661085-9005457	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000265332	ENSG00000265332	AC017028.6	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000265333	ENSG00000265333	MIR3137	3:194789007-194991896	NOTEST	0	0	0	0	1	1
ENSG00000265334	ENSG00000265334	CTD-2349P21.11	17:29158987-29222887	NOTEST	0.0664142	0	#NAME?	0	1	1
ENSG00000265335	ENSG00000265335	snoMe28SAm2634	17:19322347-19327670	NOTEST	0	0	0	0	1	1
ENSG00000265336	ENSG00000265336	MIR4640	HSCHR6_MHC_QBL:30838341-30857525	NOTEST	0	0	0	0	1	1
ENSG00000265337	ENSG00000265337	RP11-466A19.5	17:30819539-31205655	NOTEST	0	0.108865	inf	0	1	1
ENSG00000265339	ENSG00000265339	AC011477.1	19:19976694-20006656	NOTEST	0	0	0	0	1	1
ENSG00000265340	ENSG00000265340	OR4K7P	18:14570842-14571787	NOTEST	0	0	0	0	1	1
ENSG00000265341	ENSG00000265341	AC092332.1	16:80631802-80838226	NOTEST	0	0	0	0	1	1
ENSG00000265342	ENSG00000265342	RP11-16C1.1	17:73314156-73401790	NOTEST	0	0	0	0	1	1
ENSG00000265343	ENSG00000265343	Metazoa_SRP	GL000222.1:40455-40754	NOTEST	0	0	0	0	1	1
ENSG00000265344	ENSG00000265344	AP001992.1	11:74459912-74660245	NOTEST	0	0	0	0	1	1
ENSG00000265345	ENSG00000265345	MIR5188	12:125396149-125401914	NOTEST	0	0	0	0	1	1
ENSG00000265346	ENSG00000265346	ANP32E	HG1287_PATCH:150906789-150922509	NOTEST	0	0	0	0	1	1
ENSG00000265347	ENSG00000265347	MIR4291	9:96581638-96581703	NOTEST	0	0	0	0	1	1
ENSG00000265348	ENSG00000265348	HYDIN2	HG1287_PATCH:147561735-147600709	NOTEST	0	0	0	0	1	1
ENSG00000265349	ENSG00000265349	RP11-55L4.2	17:9479943-9633008	NOTEST	0	0	0	0	1	1
ENSG00000265350	ENSG00000265350	RN7SL355P	X:1437738-1438052	NOTEST	0	0	0	0	1	1
ENSG00000265351	ENSG00000265351	U6	HSCHR6_MHC_DBB:32236324-32315209	NOTEST	0	0	0	0	1	1
ENSG00000265352	ENSG00000265352	RP11-723G8.2	18:69399850-69455364	NOTEST	0	0	0	0	1	1
ENSG00000265353	ENSG00000265353	AC020895.1	19:6887576-6940470	NOTEST	0	0	0	0	1	1
ENSG00000265354	ENSG00000265354	TIMM23B	HG1211_PATCH:46467921-46484300	NOTEST	0	0	0	0	1	1
ENSG00000265355	ENSG00000265355	MIR3136	3:69024364-69129559	NOTEST	0	0	0	0	1	1
ENSG00000265356	ENSG00000265356	RP11-17M24.1	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000265357	ENSG00000265357	MIR4493	11:123252147-123252220	NOTEST	0	0	0	0	1	1
ENSG00000265359	ENSG00000265359	RP5-1110E20.1	17:39007051-39023462	NOTEST	0	0	0	0	1	1
ENSG00000265360	ENSG00000265360	RP11-337C18.8	HG1287_PATCH:147859185-147982177	NOTEST	0	0	0	0	1	1
ENSG00000265361	ENSG00000265361	RN7SL867P	5:137946655-138270723	NOTEST	0	0	0	0	1	1
ENSG00000265362	ENSG00000265362	AL358133.1	6:70331264-70331364	NOTEST	0	0	0	0	1	1
ENSG00000265364	ENSG00000265364	AC010323.1	19:8410893-8410980	NOTEST	0	0	0	0	1	1
ENSG00000265366	ENSG00000265366	GLUD1P2	HG1211_PATCH:47253536-47282319	NOTEST	0	0	0	0	1	1
ENSG00000265367	ENSG00000265367	AL160269.1	9:98997587-99064434	NOTEST	0	0	0	0	1	1
ENSG00000265368	ENSG00000265368	MIR4476	9:36833271-37034103	NOTEST	0	0	0	0	1	1
ENSG00000265369	ENSG00000265369	U3	18:24034873-24770662	NOTEST	0	0	0	0	1	1
ENSG00000265370	ENSG00000265370	MIR4682	10:121718024-121718104	NOTEST	0	0	0	0	1	1
ENSG00000265371	ENSG00000265371	MIR3198-2	12:54624723-54745633	NOTEST	0	0	0	0	1	1
ENSG00000265372	ENSG00000265372	MIR4675	10:20840898-20840975	NOTEST	0	0	0	0	1	1
ENSG00000265373	ENSG00000265373	hsa-mir-3180-3	16:16402398-16403857	NOTEST	0	0	0	0	1	1
ENSG00000265374	ENSG00000265374	RP11-57J16.1	18:24805705-24827152	NOTEST	0	0	0	0	1	1
ENSG00000265375	ENSG00000265375	MIR4679-2	10:90823091-90823168	NOTEST	0	0	0	0	1	1
ENSG00000265376	ENSG00000265376	hsa-mir-466	3:31203195-31203279	NOTEST	0	0	0	0	1	1
ENSG00000265377	ENSG00000265377	AL773543.2	HSCHR6_MHC_QBL:32646401-32646469	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000265378	ENSG00000265378	RP11-123I22.1	18:76265164-76266410	NOTEST	0	0	0	0	1	1
ENSG00000265379	ENSG00000265379	AC008752.2	19:9862668-9903856	NOTEST	0	0	0	0	1	1
ENSG00000265380	ENSG00000265380	RP11-126K15.1	18:71378563-71382725	NOTEST	0	0	0	0	1	1
ENSG00000265381	ENSG00000265381	AL121987.1	1:160171988-160185166	NOTEST	0	0	0	0	1	1
ENSG00000265382	ENSG00000265382	RN7SL365P	7:27773013-28283536	NOTEST	0	0	0	0	1	1
ENSG00000265383	ENSG00000265383	AL731561.1	HG1211_PATCH:47843818-47853323	NOTEST	0	0	0	0	1	1
ENSG00000265384	ENSG00000265384	CU024913.1	HSCHR19LRC_PGF1_CTG1:55006690-55072658	NOTEST	0	0	0	0	1	1
ENSG00000265385	ENSG00000265385	AL353608.2	HG962_PATCH:70856396-70914929	NOTEST	0	0	0	0	1	1
ENSG00000265386	ENSG00000265386	RN7SL219P	16:2059926-2070756	NOTEST	0	0	0	0	1	1
ENSG00000265387	ENSG00000265387	MIR3064	HG183_PATCH:62576979-62615309	NOTEST	0	0	0	0	1	1
ENSG00000265388	ENSG00000265388	RN7SL391P	12:6453719-6453999	NOTEST	0	0	0	0	1	1
ENSG00000265389	ENSG00000265389	RP11-439A17.7	HG1292_PATCH:121710268-121730136	NOTEST	0	0	0	0	1	1
ENSG00000265390	ENSG00000265390	MIR4999	19:8428172-8469318	NOTEST	0	0	0	0	1	1
ENSG00000265391	ENSG00000265391	AC112504.1	3:141496989-141537332	NOTEST	0	0	0	0	1	1
ENSG00000265392	ENSG00000265392	MIR4252	1:6484847-6580121	NOTEST	0	0	0	0	1	1
ENSG00000265394	ENSG00000265394	RP11-1148O4.2	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000265395	ENSG00000265395	MIR3944	10:135175983-135187193	NOTEST	0	0	0	0	1	1
ENSG00000265396	ENSG00000265396	MIR3128	2:178092322-178408564	NOTEST	0	0	0	0	1	1
ENSG00000265397	ENSG00000265397	FRMPD2P1	HG1211_PATCH:47366305-47390774	NOTEST	0	0	0	0	1	1
ENSG00000265398	ENSG00000265398	AL139239.1	10:99609995-99790585	NOTEST	0	0	0	0	1	1
ENSG00000265399	ENSG00000265399	RP13-270P17.2	18:3066804-3247275	NOTEST	0.198542	0.398528	1.00524	0	1	1
ENSG00000265400	ENSG00000265400	RP11-471L13.2	17:12104916-12118584	NOTEST	0	0	0	0	1	1
ENSG00000265401	ENSG00000265401	RP11-138I1.4	17:16284111-16286059	NOTEST	0	0	0	0	1	1
ENSG00000265402	ENSG00000265402	RSL24D1P9	18:49139008-49139480	NOTEST	0	0	0	0	1	1
ENSG00000265403	ENSG00000265403	AC015884.1	17:885275-885361	NOTEST	0	0	0	0	1	1
ENSG00000265404	ENSG00000265404	AC099796.1	1:54970340-54970443	NOTEST	0	0	0	0	1	1
ENSG00000265406	ENSG00000265406	AP000539.3	22:16569923-16570006	NOTEST	0	0	0	0	1	1
ENSG00000265407	ENSG00000265407	MIR4324	19:49792894-49828482	NOTEST	0	0	0	0	1	1
ENSG00000265408	ENSG00000265408	RP11-361L15.4	16:66968346-67009051	NOTEST	0	0	0	0	1	1
ENSG00000265409	ENSG00000265409	RNU6-1030P	HSCHR6_MHC_COX:31695129-31720748	NOTEST	0	0	0	0	1	1
ENSG00000265410	ENSG00000265410	MIR29B1	HG1308_PATCH:130517373-130592303	NOTEST	0	0	0	0	1	1
ENSG00000265411	ENSG00000265411	RN7SL656P	17:44352149-44439130	NOTEST	0	0	0	0	1	1
ENSG00000265412	ENSG00000265412	MIR4646	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000265413	ENSG00000265413	RP11-789C17.1	18:7566779-8406951	NOTEST	0.587481	0.574773	-0.0315505	0	1	1
ENSG00000265414	ENSG00000265414	RN7SL729P	1:8335183-8335438	NOTEST	0	0	0	0	1	1
ENSG00000265416	ENSG00000265416	AC017028.7	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000265417	ENSG00000265417	RP11-288C17.1	18:1254383-1408345	NOTEST	0.0159019	0.0123633	-0.36313	0	1	1
ENSG00000265418	ENSG00000265418	MIR4261	2:10281508-10351851	NOTEST	0	0	0	0	1	1
ENSG00000265419	ENSG00000265419	AL359987.1	6:93354458-93354526	NOTEST	0	0	0	0	1	1
ENSG00000265420	ENSG00000265420	MIR4779	2:86371054-86423172	NOTEST	0	0	0	0	1	1
ENSG00000265421	ENSG00000265421	MIR4459	5:53179774-53606412	NOTEST	0	0	0	0	1	1
ENSG00000265422	ENSG00000265422	MIR4684	1:23037331-23241818	NOTEST	0	0	0	0	1	1
ENSG00000265423	ENSG00000265423	MIR4652	7:93220884-93540577	NOTEST	0	0	0	0	1	1
ENSG00000265424	ENSG00000265424	DUSP8P1	HG1211_PATCH:47253536-47282319	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000265425	ENSG00000265425	RP11-128D14.1	18:66094266-66104155	NOTEST	0	0	0	0	1	1
ENSG00000265426	ENSG00000265426	MIR4740	HG271_PATCH:79369274-79440126	NOTEST	0	0	0	0	1	1
ENSG00000265428	ENSG00000265428	RP1-56K13.6	17:37152575-37152877	NOTEST	0	0	0	0	1	1
ENSG00000265429	ENSG00000265429	MIR4782	2:114462587-114514400	NOTEST	0	0	0	0	1	1
ENSG00000265430	ENSG00000265430	AC108721.1	12:59921957-59922049	NOTEST	0	0	0	0	1	1
ENSG00000265431	ENSG00000265431	U8	HG871_PATCH:5237653-5261139	NOTEST	0	0	0	0	1	1
ENSG00000265432	ENSG00000265432	MIR4308	14:55308725-55369570	NOTEST	0	0	0	0	1	1
ENSG00000265433	ENSG00000265433	MIR4447	3:115521234-117716439	NOTEST	0	0	0	0	1	1
ENSG00000265434	ENSG00000265434	HLA-ABC	HG1322_PATCH:29901733-29909270	NOTEST	0	0	0	0	1	1
ENSG00000265435	ENSG00000265435	MIR3121	1:180199420-180472089	NOTEST	0	0	0	0	1	1
ENSG00000265436	ENSG00000265436	BX088647.1	HSCHR6_MHC_SSTO:30046178-30046311	NOTEST	0	0	0	0	1	1
ENSG00000265437	ENSG00000265437	RP11-757O6.4	18:14361432-14361942	NOTEST	0	0	0	0	1	1
ENSG00000265438	ENSG00000265438	MIR4751	19:50392910-50464429	NOTEST	0	0	0	0	1	1
ENSG00000265439	ENSG00000265439	RN7SL811P	7:152435526-152435815	NOTEST	0	0	0	0	1	1
ENSG00000265441	ENSG00000265441	AL132768.1	20:35280168-35374533	NOTEST	0	0	0	0	1	1
ENSG00000265442	ENSG00000265442	MIR3941	10:124134211-124191867	NOTEST	0	0	0	0	1	1
ENSG00000265443	ENSG00000265443	CTD-2349P21.6	17:29036316-29151794	NOTEST	0	0	0	0	1	1
ENSG00000265444	ENSG00000265444	MIR4733	17:29335514-29709134	NOTEST	0	0	0	0	1	1
ENSG00000265445	ENSG00000265445	RP11-849N15.1	17:15133094-15169024	NOTEST	0.0733248	0.0524895	-0.482273	0	1	1
ENSG00000265446	ENSG00000265446	CR759778.2	HSCHR6_MHC_MCF:30646634-30672631	NOTEST	0	0	0	0	1	1
ENSG00000265447	ENSG00000265447	CTD-2350C19.5	HG883_PATCH:26771081-26772582	NOTEST	0	0	0	0	1	1
ENSG00000265448	ENSG00000265448	RP11-421E17.4	HG1293_PATCH:206266905-206527996	NOTEST	0	0	0	0	1	1
ENSG00000265449	ENSG00000265449	RP11-301M17.2	HG1287_PATCH:148920715-148920750	NOTEST	0	0	0	0	1	1
ENSG00000265450	ENSG00000265450	MIR4502	13:115039302-115039383	NOTEST	0	0	0	0	1	1
ENSG00000265451	ENSG00000265451	RP11-204L24.2	2:122095351-122407163	NOTEST	0.0323011	0.0483755	0.582692	0	1	1
ENSG00000265452	ENSG00000265452	MIR3682	2:53759809-54087297	NOTEST	0	0	0	0	1	1
ENSG00000265453	ENSG00000265453	RP11-173M1.3	17:25608119-25608441	NOTEST	0	0	0	0	1	1
ENSG00000265454	ENSG00000265454	AC012362.1	2:209224437-209719227	NOTEST	0	0	0	0	1	1
ENSG00000265455	ENSG00000265455	MIR4700	12:121148237-121161443	NOTEST	0	0	0	0	1	1
ENSG00000265456	ENSG00000265456	MIR3672	X:120504825-120504907	NOTEST	0	0	0	0	1	1
ENSG00000265457	ENSG00000265457	AC093611.2	3:13692195-13788132	NOTEST	0	0	0	0	1	1
ENSG00000265458	ENSG00000265458	RP13-20L14.6	17:80412148-80448413	NOTEST	0	0.0622338	inf	0	1	1
ENSG00000265459	ENSG00000265459	hsa-mir-219a-1	HSCHR6_MHC_MCF:33345975-33346085	NOTEST	0	0	0	0	1	1
ENSG00000265460	ENSG00000265460	RP11-690G19.4	17:37394718-37407071	NOTEST	0	0	0	0	1	1
ENSG00000265461	ENSG00000265461	AC068014.2	17:80709939-81009686	NOTEST	0	0	0	0	1	1
ENSG00000265462	ENSG00000265462	MIR3680-1	16:21413557-21531765	NOTEST	0	0	0	0	1	1
ENSG00000265463	ENSG00000265463	AC012391.1	10:124975617-124975704	NOTEST	0	0	0	0	1	1
ENSG00000265464	ENSG00000265464	RP11-495P10.10	HG1287_PATCH:149121519-149123341	NOTEST	0	0	0	0	1	1
ENSG00000265465	ENSG00000265465	MIR4768	X:17393542-17754114	NOTEST	0	0	0	0	1	1
ENSG00000265466	ENSG00000265466	AL583842.2	1:142618768-142729975	NOTEST	0	0	0	0	1	1
ENSG00000265467	ENSG00000265467	AC090559.1	11:47487495-47606114	NOTEST	0	0	0	0	1	1
ENSG00000265468	ENSG00000265468	RP11-495P10.6	HG1287_PATCH:148958298-148967164	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000265470	ENSG00000265470	MIR548AQ	3:185361526-185542844	NOTEST	0	0	0	0	1	1
ENSG00000265471	ENSG00000265471	AL034400.1	X:132425320-132425399	NOTEST	0	0	0	0	1	1
ENSG00000265472	ENSG00000265472	RP11-28O3.1	18:65173818-65566856	NOTEST	0	0	0	0	1	1
ENSG00000265473	ENSG00000265473	BX908728.1	HSCHR6_MHC_MANN:30612851-30638847	NOTEST	0	0	0	0	1	1
ENSG00000265475	ENSG00000265475	RP11-403I13.6	HG1287_PATCH:144431294-144457279	NOTEST	0	0	0	0	1	1
ENSG00000265476	ENSG00000265476	C1orf147	HG1293_PATCH:206534036-206561289	NOTEST	0	0	0	0	1	1
ENSG00000265477	ENSG00000265477	RP11-720L2.2	18:319360-500722	NOTEST	0	0	0	0	1	1
ENSG00000265478	ENSG00000265478	CTD-2145A24.3	17:18713268-18714253	NOTEST	0.106294	0.143472	0.432701	0	1	1
ENSG00000265479	ENSG00000265479	DTX2P1-UPK3BP1-PMS2P11	7:76139744-77045717	NOTEST	0	0.220497	inf	0	1	1
ENSG00000265480	ENSG00000265480	KRT18P55	17:26603011-26644809	NOTEST	0.055741	0	#NAME?	0	1	1
ENSG00000265481	ENSG00000265481	AP006564.1	18:14728270-14852737	NOTEST	0	0	0	0	1	1
ENSG00000265483	ENSG00000265483	MIR4443	3:48238053-48238106	NOTEST	0	0	0	0	1	1
ENSG00000265484	ENSG00000265484	RP11-47G4.2	18:68883939-68904338	NOTEST	0	0	0	0	1	1
ENSG00000265485	ENSG00000265485	RP11-449D8.1	18:22208145-22242162	NOTEST	0.00690744	0	#NAME?	0	1	1
ENSG00000265486	ENSG00000265486	RN7SL518P	10:77360997-78320752	NOTEST	0	0	0	0	1	1
ENSG00000265487	ENSG00000265487	RP11-793A3.1	18:5954704-6415236	NOTEST	0	0	0	0	1	1
ENSG00000265488	ENSG00000265488	AL359314.1	9:79226291-79521003	NOTEST	0	0	0	0	1	1
ENSG00000265489	ENSG00000265489	RP11-1090M7.1	17:12569206-12894960	NOTEST	0	0	0	0	1	1
ENSG00000265490	ENSG00000265490	RP11-806L2.6	18:596987-712676	NOTEST	0.289589	0.0919815	-1.65459	0	1	1
ENSG00000265491	ENSG00000265491	RNF115	HG1287_PATCH:146432833-146510487	NOTEST	0	0	0	0	1	1
ENSG00000265492	ENSG00000265492	MIR5047	HG183_PATCH:62576979-62615309	NOTEST	0	0	0	0	1	1
ENSG00000265493	ENSG00000265493	AC105914.1	4:175750818-175900532	NOTEST	0	0	0	0	1	1
ENSG00000265494	ENSG00000265494	RP11-131K5.2	17:13659794-13972812	NOTEST	0	0.0301438	inf	0	1	1
ENSG00000265495	ENSG00000265495	SNORA48	HSCHR6_MHC_COX:30090512-30090672	NOTEST	0	0	0	0	1	1
ENSG00000265496	ENSG00000265496	MIR1539	18:47008027-47018906	NOTEST	0	0	0	0	1	1
ENSG00000265497	ENSG00000265497	RP11-439A17.9	HG1292_PATCH:121629974-121659880	NOTEST	0	0	0	0	1	1
ENSG00000265498	ENSG00000265498	AL158051.1	6:69345258-70099403	NOTEST	0	0	0	0	1	1
ENSG00000265499	ENSG00000265499	MIR3156-2	18:14728270-14852737	NOTEST	0	0	0	0	1	1
ENSG00000265500	ENSG00000265500	SENP3-EIF4A1	17:7465191-7536700	NOTEST	0.184302	0.0260276	-2.82395	0	1	1
ENSG00000265501	ENSG00000265501	AC005549.2	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000265502	ENSG00000265502	RN7SL746P	X:70304338-70304637	NOTEST	0	0	0	0	1	1
ENSG00000265503	ENSG00000265503	MIR1269B	17:12569206-12894960	NOTEST	0	0	0	0	1	1
ENSG00000265504	ENSG00000265504	AC130689.1	17:1682778-1803376	NOTEST	0	0	0	0	1	1
ENSG00000265505	ENSG00000265505	MIR4640	HSCHR6_MHC_DBB:30839457-30858654	NOTEST	0	0	0	0	1	1
ENSG00000265506	ENSG00000265506	AC004656.1	X:24483337-24557954	NOTEST	0	0	0	0	1	1
ENSG00000265507	ENSG00000265507	MIR4435-1	2:87929273-87929353	NOTEST	0	0	0	0	1	1
ENSG00000265509	ENSG00000265509	Y_RNA	HSCHR6_MHC_SSTO:31454423-31454525	NOTEST	0	0	0	0	1	1
ENSG00000265510	ENSG00000265510	MIR4436A	2:89109983-89165653	NOTEST	0	0	0	0	1	1
ENSG00000265512	ENSG00000265512	RP11-1055B8.4	HG271_PATCH:79361929-79364056	NOTEST	0	0	0	0	1	1
ENSG00000265513	ENSG00000265513	hsa-mir-3673	8:130363936-130695925	NOTEST	0	0	0	0	1	1
ENSG00000265514	ENSG00000265514	RP11-92G19.2	18:5081180-5095814	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000265515	ENSG00000265515	AC092287.1	16:18938184-18948365	NOTEST	0	0	0	0	1	1
ENSG00000265516	ENSG00000265516	Z84488.1	6:116778485-116779832	NOTEST	0	0	0	0	1	1
ENSG00000265517	ENSG00000265517	AL122127.2	14:106323911-106323971	NOTEST	0	0	0	0	1	1
ENSG00000265518	ENSG00000265518	AL109615.1	6:43963459-44045689	NOTEST	0	0	0	0	1	1
ENSG00000265520	ENSG00000265520	MIR548V	8:17433941-17658426	NOTEST	0	0	0	0	1	1
ENSG00000265521	ENSG00000265521	MIR5697	1:9982172-10045559	NOTEST	0	0	0	0	1	1
ENSG00000265522	ENSG00000265522	AC097473.1	4:109709900-109710935	NOTEST	0	0	0	0	1	1
ENSG00000265523	ENSG00000265523	AC073647.1	7:141559617-141559669	NOTEST	0	0	0	0	1	1
ENSG00000265524	ENSG00000265524	AC134300.1	16:19901822-19901919	NOTEST	0	0	0	0	1	1
ENSG00000265525	ENSG00000265525	AL592188.5	GL000220.1:152251-152312	NOTEST	0	0	0	0	1	1
ENSG00000265526	ENSG00000265526	MIR4304	12:123468026-123634562	NOTEST	0	0	0	0	1	1
ENSG00000265527	ENSG00000265527	MIR5690	6:35541361-35696360	NOTEST	0	0	0	0	1	1
ENSG00000265528	ENSG00000265528	AC092316.2	19:8585673-8642461	NOTEST	0	0	0	0	1	1
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ENSG00000265530	ENSG00000265530	AL121594.1	14:35514112-35786699	NOTEST	0	0	0	0	1	1
ENSG00000265531	ENSG00000265531	FCGR1C	HG1287_PATCH:144561207-144621191	NOTEST	0	0	0	0	1	1
ENSG00000265532	ENSG00000265532	RN7SL243P	20:45837858-45985567	NOTEST	0	0	0	0	1	1
ENSG00000265533	ENSG00000265533	RP11-638L3.1	18:65173818-65566856	NOTEST	0	0	0	0	1	1
ENSG00000265534	ENSG00000265534	AL512638.1	1:116028271-116028364	NOTEST	0	0	0	0	1	1
ENSG00000265535	ENSG00000265535	RN7SL475P	1:60440430-60440726	NOTEST	0	0	0	0	1	1
ENSG00000265536	ENSG00000265536	AL591042.1	1:108113781-108537229	NOTEST	0	0	0	0	1	1
ENSG00000265537	ENSG00000265537	hsa-mir-3180-3	16:15003743-15005202	NOTEST	0	0	0	0	1	1
ENSG00000265538	ENSG00000265538	MIR4421	1:51525508-51525577	NOTEST	0	0	0	0	1	1
ENSG00000265539	ENSG00000265539	MIR3164	11:68816364-68858072	NOTEST	0	0	0	0	1	1
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ENSG00000265541	ENSG00000265541	H3F3BP2	17:26743939-26744510	NOTEST	0	0	0	0	1	1
ENSG00000265542	ENSG00000265542	RP11-60A24.3	17:55849306-55912110	NOTEST	0	0	0	0	1	1
ENSG00000265543	ENSG00000265543	AL451010.1	1:92683496-92711370	NOTEST	0	0	0	0	1	1
ENSG00000265544	ENSG00000265544	RP11-31I22.1	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000265545	ENSG00000265545	RP11-183C12.1	18:4459229-4459458	NOTEST	0.22712	0	#NAME?	0	1	1
ENSG00000265546	ENSG00000265546	RN7SL289P	13:25946208-26599989	NOTEST	0	0	0	0	1	1
ENSG00000265547	ENSG00000265547	RP11-293E1.2	17:43697693-43913194	NOTEST	0	0	0	0	1	1
ENSG00000265548	ENSG00000265548	AL662825.2	HSCHR6_MHC_COX:30558025-30584021	NOTEST	0	0	0	0	1	1
ENSG00000265549	ENSG00000265549	AL935156.2	HSCHR6_MHC_QBL:29169590-29169657	NOTEST	0	0	0	0	1	1
ENSG00000265550	ENSG00000265550	AC097382.1	4:6910968-7059679	NOTEST	0	0	0	0	1	1
ENSG00000265551	ENSG00000265551	FAM21C	HG1211_PATCH:46222647-46288409	NOTEST	0	0	0	0	1	1
ENSG00000265552	ENSG00000265552	RP11-958F21.3	18:22635563-22636724	NOTEST	0	0	0	0	1	1
ENSG00000265553	ENSG00000265553	AC013275.1	2:120302007-120419827	NOTEST	0	0	0	0	1	1
ENSG00000265554	ENSG00000265554	RP11-419J16.1	18:10125336-10144403	NOTEST	0.116176	0	#NAME?	0	1	1
ENSG00000265555	ENSG00000265555	RP11-638L3.3	18:65173818-65566856	NOTEST	0	0	0	0	1	1
ENSG00000265556	ENSG00000265556	RP11-434D2.2	17:20336518-20337598	NOTEST	0	0	0	0	1	1
ENSG00000265557	ENSG00000265557	CT867977.1	GL000231.1:21877-21950	NOTEST	0	0	0	0	1	1
ENSG00000265558	ENSG00000265558	MIR3918	6:159071045-159185908	NOTEST	0	0	0	0	1	1
ENSG00000265559	ENSG00000265559	RN7SL652P	11:47487495-47606114	NOTEST	0	0.0901731	inf	0	1	1
ENSG00000265560	ENSG00000265560	AC098612.1	8:34827723-34827817	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000265561	ENSG00000265561	AC025458.1	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000265562	ENSG00000265562	AC104037.1	8:33053354-33053455	NOTEST	0	0	0	0	1	1
ENSG00000265563	ENSG00000265563	hsa-mir-937	HG104_HG975_PATCH:144873089-144897549	NOTEST	0	0	0	0	1	1
ENSG00000265564	ENSG00000265564	PIGPP4	18:9880576-9880883	NOTEST	0	0	0	0	1	1
ENSG00000265565	ENSG00000265565	MIR3143	6:27115404-27115467	NOTEST	0	0	0	0	1	1
ENSG00000265566	ENSG00000265566	RN7SL605P	17:2657125-2657430	NOTEST	0	0	0	0	1	1
ENSG00000265567	ENSG00000265567	RP11-1109M24.13	17:21827938-21828263	NOTEST	0	0	0	0	1	1
ENSG00000265568	ENSG00000265568	AC091043.1	18:19561081-19631120	NOTEST	0	0	0	0	1	1
ENSG00000265569	ENSG00000265569	AC011453.1	19:54261122-54261223	NOTEST	0	0	0	0	1	1
ENSG00000265570	ENSG00000265570	BOLA1	HG1287_PATCH:150573883-150587213	NOTEST	0	0	0	0	1	1
ENSG00000265571	ENSG00000265571	AC016831.3	HG1308_PATCH:130486521-130487165	NOTEST	0	0	0	0	1	1
ENSG00000265572	ENSG00000265572	AL391117.1	9:22953017-22953102	NOTEST	0	0	0	0	1	1
ENSG00000265573	ENSG00000265573	AC004943.1	16:72699068-73093597	NOTEST	0	0	0	0	1	1
ENSG00000265574	ENSG00000265574	CTD-2095E4.1	17:30433348-30441144	NOTEST	0	0.0121962	inf	0	1	1
ENSG00000265575	ENSG00000265575	MIR4784	2:132222472-132250316	NOTEST	0	0	0	0	1	1
ENSG00000265577	ENSG00000265577	RN7SL9P	5:69345349-69374349	NOTEST	0	0	0	0	1	1
ENSG00000265578	ENSG00000265578	FAM35DP	HG1211_PATCH:48185154-48226140	NOTEST	0	0	0	0	1	1
ENSG00000265579	ENSG00000265579	RP11-713C5.1	18:70409548-70535381	NOTEST	0	0	0	0	1	1
ENSG00000265580	ENSG00000265580	AC091042.1	18:64963518-64963619	NOTEST	0	0	0	0	1	1
ENSG00000265581	ENSG00000265581	PFN1P12	HG1287_PATCH:144281630-144322056	NOTEST	0	0	0	0	1	1
ENSG00000265582	ENSG00000265582	AL034553.1	20:49505584-49575092	NOTEST	0	0	0	0	1	1
ENSG00000265583	ENSG00000265583	AC011994.1	2:11674241-11782914	NOTEST	0	0	0	0	1	1
ENSG00000265584	ENSG00000265584	MIR3978	X:109245858-109425962	NOTEST	0	0	0	0	1	1
ENSG00000265585	ENSG00000265585	AL161421.1	13:49504255-49504348	NOTEST	0	0	0	0	1	1
ENSG00000265586	ENSG00000265586	RP11-561O23.9	HG962_PATCH:70921452-71114201	NOTEST	0	0	0	0	1	1
ENSG00000265587	ENSG00000265587	AC068580.1	11:1753639-1785255	NOTEST	0	0	0	0	1	1
ENSG00000265588	ENSG00000265588	MIR5708	8:81153623-81153708	NOTEST	0	0	0	0	1	1
ENSG00000265589	ENSG00000265589	AL359753.1	1:159029038-159029116	NOTEST	0	0	0	0	1	1
ENSG00000265591	ENSG00000265591	AC119751.5	4:49585041-49585116	NOTEST	0	0	0	0	1	1
ENSG00000265592	ENSG00000265592	RN7SL92P	3:75758793-75834734	NOTEST	0	0	0	0	1	1
ENSG00000265593	ENSG00000265593	NPM1P45	17:9725522-9795419	NOTEST	0	0	0	0	1	1
ENSG00000265594	ENSG00000265594	CEP41	HG1308_PATCH:130036374-130082274	NOTEST	0	0	0	0	1	1
ENSG00000265595	ENSG00000265595	MIR4756	20:52553315-52687304	NOTEST	0	0	0	0	1	1
ENSG00000265596	ENSG00000265596	MIR3659	1:38512985-38584697	NOTEST	0	0	0	0	1	1
ENSG00000265597	ENSG00000265597	AL590764.1	X:70338405-70362303	NOTEST	0	0	0	0	1	1
ENSG00000265598	ENSG00000265598	MIR5707	7:158384307-158384388	NOTEST	0	0	0	0	1	1
ENSG00000265599	ENSG00000265599	MIR4471	8:101393487-101426687	NOTEST	0	0	0	0	1	1
ENSG00000265600	ENSG00000265600	AC006480.1	7:66821666-66821766	NOTEST	0	0	0	0	1	1
ENSG00000265601	ENSG00000265601	AL845321.1	9:67225385-67225452	NOTEST	0	0	0	0	1	1
ENSG00000265602	ENSG00000265602	SNORA48	HSCHR6_MHC_QBL:30090142-30090303	NOTEST	0	0	0	0	1	1
ENSG00000265603	ENSG00000265603	RN7SL133P	12:123468026-123634562	NOTEST	0	0	0	0	1	1
ENSG00000265604	ENSG00000265604	CT867976.4	GL000230.1:37002-37085	NOTEST	0	0	0	0	1	1
ENSG00000265605	ENSG00000265605	RN7SL422P	9:40491621-40633282	NOTEST	0	0	0	0	1	1
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ENSG00000265608	ENSG00000265608	UCN3	HG871_PATCH:5407200-5416884	NOTEST	0	0	0	0	1	1
ENSG00000265609	ENSG00000265609	PDZK1P2	HG1287_PATCH:148680276-148698643	NOTEST	0	0	0	0	1	1
ENSG00000265610	ENSG00000265610	CR536603.1	22:46316241-46373009	NOTEST	0	0	0	0	1	1
ENSG00000265611	ENSG00000265611	MIR5010	17:40610861-40674629	NOTEST	0	0	0	0	1	1
ENSG00000265612	ENSG00000265612	hsa-mir-4539	14:106323681-106323741	NOTEST	0	0	0	0	1	1
ENSG00000265613	ENSG00000265613	AC143336.1	5:70883114-70954531	NOTEST	0	0	0	0	1	1
ENSG00000265614	ENSG00000265614	RP11-521P1.1	17:32658880-32659247	NOTEST	0	0	0	0	1	1
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ENSG00000265617	ENSG00000265617	MIR548AG2	20:59139619-59139683	NOTEST	0	0	0	0	1	1
ENSG00000265618	ENSG00000265618	CTB-96E2.7	17:26684603-26734215	NOTEST	0	0	0	0	1	1
ENSG00000265619	ENSG00000265619	AC093824.1	4:186043475-186043576	NOTEST	0	0	0	0	1	1
ENSG00000265620	ENSG00000265620	RP11-822E23.4	HG987_PATCH:21428101-21477829	NOTEST	0	0	0	0	1	1
ENSG00000265621	ENSG00000265621	AC013476.1	2:223725651-223809357	NOTEST	0	0	0	0	1	1
ENSG00000265622	ENSG00000265622	RP11-445P17.8	HG871_PATCH:5308224-5313428	NOTEST	0	0	0	0	1	1
ENSG00000265623	ENSG00000265623	MIR3139	4:144256417-144395721	NOTEST	0	0	0	0	1	1
ENSG00000265624	ENSG00000265624	RN7SL166P	13:20248763-20357142	NOTEST	0	0	0	0	1	1
ENSG00000265625	ENSG00000265625	RP11-68I3.11	17:27887564-28513493	NOTEST	0.125945	0.24328	0.949827	0	1	1
ENSG00000265626	ENSG00000265626	AC139085.2	18:74471640-74471822	NOTEST	0	0	0	0	1	1
ENSG00000265627	ENSG00000265627	AC093807.1	4:26578058-26756973	NOTEST	0	0	0	0	1	1
ENSG00000265628	ENSG00000265628	RN7SL723P	18:6437062-6437337	NOTEST	0	0	0	0	1	1
ENSG00000265629	ENSG00000265629	AC011897.1	2:14772809-14790933	NOTEST	0.00791217	0.0347488	2.13482	0	1	1
ENSG00000265630	ENSG00000265630	GLUD1P6	HG1211_PATCH:48058999-48065145	NOTEST	0	0	0	0	1	1
ENSG00000265631	ENSG00000265631	BNIP3P3	18:15247427-15247996	NOTEST	0	0	0	0	1	1
ENSG00000265632	ENSG00000265632	AC069240.1	12:114988566-114988654	NOTEST	0	0	0	0	1	1
ENSG00000265633	ENSG00000265633	7SK	HSCHR6_MHC_MCF:30910595-30910898	NOTEST	0	0	0	0	1	1
ENSG00000265634	ENSG00000265634	SNORD33	HSCHR6_MHC_APD:29523503-29601074	NOTEST	0	0	0	0	1	1
ENSG00000265635	ENSG00000265635	MIR3612	12:128751947-129192460	NOTEST	0	0	0	0	1	1
ENSG00000265636	ENSG00000265636	AC100787.1	17:73437239-73496171	NOTEST	0	0	0	0	1	1
ENSG00000265637	ENSG00000265637	AC010235.1	5:125412492-125615493	NOTEST	0	0	0	0	1	1
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ENSG00000265640	ENSG00000265640	RP11-38J22.1	HG1293_PATCH:206238620-206240807	NOTEST	0	0	0	0	1	1
ENSG00000265641	ENSG00000265641	MIR3929	18:33514050-33514105	NOTEST	0	0	0	0	1	1
ENSG00000265642	ENSG00000265642	AL034375.1	6:16299342-16762883	NOTEST	0	0	0	0	1	1
ENSG00000265643	ENSG00000265643	RP11-465I4.2	18:67068290-67629039	NOTEST	0	0	0	0	1	1
ENSG00000265644	ENSG00000265644	RP11-451L19.1	18:76240548-76244867	NOTEST	0	0	0	0	1	1
ENSG00000265645	ENSG00000265645	AC092038.2	3:23244510-23633284	NOTEST	0	0	0	0	1	1
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ENSG00000265647	ENSG00000265647	AL358815.1	9:111934254-112083244	NOTEST	0	0	0	0	1	1
ENSG00000265648	ENSG00000265648	RN7SL279P	16:70286197-70323446	NOTEST	0	0	0	0	1	1
ENSG00000265649	ENSG00000265649	MIR4709	14:74942894-74963809	NOTEST	0	0	0	0	1	1
ENSG00000265650	ENSG00000265650	AC012627.1	19:21203425-21242856	NOTEST	0	0	0	0	1	1
ENSG00000265651	ENSG00000265651	SNORD36	HG79_PATCH:136223748-136226961	NOTEST	0	0	0	0	1	1

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ENSG00000265654	ENSG00000265654	AL513547.1	6:169857306-170102159	NOTEST	0	0	0	0	1	1
ENSG00000265655	ENSG00000265655	AC069280.1	7:68655127-68655211	NOTEST	0	0	0	0	1	1
ENSG00000265656	ENSG00000265656	RP11-13N13.6	18:19230857-19284766	NOTEST	0	0.119915	inf	0	1	1
ENSG00000265657	ENSG00000265657	MIR3151	8:104133259-104345094	NOTEST	0	0	0	0	1	1
ENSG00000265658	ENSG00000265658	MIR3690	X:1387692-1429274	NOTEST	0	0	0	0	1	1
ENSG00000265660	ENSG00000265660	MIR4664	8:144806102-144815971	NOTEST	0	0	0	0	1	1
ENSG00000265661	ENSG00000265661	MIR3118-2	1:143118703-143240439	NOTEST	0	0	0	0	1	1
ENSG00000265662	ENSG00000265662	AL354981.1	9:119187503-120177348	NOTEST	0	0	0	0	1	1
ENSG00000265663	ENSG00000265663	SNORD33	HSCHR6_MHC_MANN:29522993-29600557	NOTEST	0	0	0	0	1	1
ENSG00000265664	ENSG00000265664	RP11-74H8.1	17:64961025-65029514	NOTEST	0	0	0	0	1	1
ENSG00000265665	ENSG00000265665	AC008391.1	5:55752864-55752965	NOTEST	0	0	0	0	1	1
ENSG00000265666	ENSG00000265666	CTD-2267D19.2	17:38465443-38513094	NOTEST	0.233886	0.486091	1.05542	0	1	1
ENSG00000265667	ENSG00000265667	AP003550.1	8:104104851-104104949	NOTEST	0	0	0	0	1	1
ENSG00000265669	ENSG00000265669	MIR548AJ1	6:132436331-132436403	NOTEST	0	0	0	0	1	1
ENSG00000265670	ENSG00000265670	RP11-25I11.1	18:28534785-28560883	NOTEST	0	0	0	0	1	1
ENSG00000265671	ENSG00000265671	RP11-672L10.3	18:894435-912173	NOTEST	0	0	0	0	1	1
ENSG00000265672	ENSG00000265672	MIR4722	16:88772870-88851619	NOTEST	0	0	0	0	1	1
ENSG00000265673	ENSG00000265673	MIR4508	15:23807208-23807278	NOTEST	0	0	0	0	1	1
ENSG00000265674	ENSG00000265674	SNORA48	HSCHR6_MHC_APD:30037416-30037578	NOTEST	0	0	0	0	1	1
ENSG00000265675	ENSG00000265675	RN7SL708P	19:49584588-49584885	NOTEST	0	0	0	0	1	1
ENSG00000265676	ENSG00000265676	RN7SL64P	7:55954969-56067874	NOTEST	0	0	0	0	1	1
ENSG00000265677	ENSG00000265677	AL137229.1	14:102783713-102829253	NOTEST	0	0	0	0	1	1
ENSG00000265679	ENSG00000265679	AL139328.1	13:42614175-42830714	NOTEST	0	0	0	0	1	1
ENSG00000265680	ENSG00000265680	RN7SL620P	17:16592850-16719854	NOTEST	0	0	0	0	1	1
ENSG00000265682	ENSG00000265682	MIR4267	2:110827537-110827619	NOTEST	0	0	0	0	1	1
ENSG00000265683	ENSG00000265683	RP11-173M1.5	17:25678883-25679610	NOTEST	0.280843	0.413084	0.556672	0	1	1
ENSG00000265684	ENSG00000265684	RN7SL378P	5:81267843-81574396	NOTEST	0	0	0	0	1	1
ENSG00000265685	ENSG00000265685	AKR1C3	HG871_PATCH:5077545-5149878	NOTEST	0	0	0	0	1	1
ENSG00000265686	ENSG00000265686	AL109749.1	X:131130872-131130961	NOTEST	0	0	0	0	1	1
ENSG00000265687	ENSG00000265687	AC016178.1	8:130363936-130695925	NOTEST	0	0	0	0	1	1
ENSG00000265689	ENSG00000265689	RP11-118G23.1	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000265691	ENSG00000265691	MIR4460	5:128732754-128732840	NOTEST	0	0	0	0	1	1
ENSG00000265692	ENSG00000265692	RP13-516M14.4	17:80247921-80250690	NOTEST	0.0509715	0.00704133	-2.85577	0	1	1
ENSG00000265693	ENSG00000265693	RP11-815I9.5	17:18601310-18639431	NOTEST	0	0	0	0	1	1
ENSG00000265694	ENSG00000265694	MIR4774	2:169312371-169769881	NOTEST	0	0	0	0	1	1
ENSG00000265695	ENSG00000265695	MIR3064	17:62495733-62658186	NOTEST	0	0	0	0	1	1
ENSG00000265696	ENSG00000265696	AP003064.2	11:62104382-62160882	NOTEST	0	0	0	0	1	1
ENSG00000265697	ENSG00000265697	RP11-31I22.4	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000265698	ENSG00000265698	RP11-41O4.3	18:68079290-68079627	NOTEST	0	0	0	0	1	1
ENSG00000265699	ENSG00000265699	MIR548AE2	5:57825869-57825936	NOTEST	0	0	0	0	1	1
ENSG00000265700	ENSG00000265700	MIR4647	6:44221832-44225291	NOTEST	0	0	0	0	1	1
ENSG00000265702	ENSG00000265702	RP11-156L14.1	17:60776604-60885705	NOTEST	0	0.00350558	inf	0	1	1
ENSG00000265703	ENSG00000265703	AC011841.9	GL000205.1:144570-144653	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000265704	ENSG00000265704	AC010595.1	5:84930229-84930291	NOTEST	0	0	0	0	1	1
ENSG00000265705	ENSG00000265705	RP11-744K17.8	17:21934504-21938362	NOTEST	0	0	0	0	1	1
ENSG00000265706	ENSG00000265706	SNORD53_SNORD92	2:29117508-29171088	NOTEST	0	0	0	0	1	1
ENSG00000265707	ENSG00000265707	SNORD52	HSCHR6_MHC_DBB:31784574-31789730	NOTEST	0	0	0	0	1	1
ENSG00000265708	ENSG00000265708	AC027348.1	16:49521434-49891830	NOTEST	0	0	0	0	1	1
ENSG00000265709	ENSG00000265709	AC019046.1	2:173926459-173926540	NOTEST	0	0	0	0	1	1
ENSG00000265710	ENSG00000265710	AL161772.1	13:21276265-21297237	NOTEST	0	0	0	0	1	1
ENSG00000265711	ENSG00000265711	AL049871.1	14:63670831-63759937	NOTEST	0	0	0	0	1	1
ENSG00000265712	ENSG00000265712	RP11-440L16.1	18:49213894-49214579	NOTEST	0	0	0	0	1	1
ENSG00000265713	ENSG00000265713	RP11-82O19.2	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000265714	ENSG00000265714	AL122127.3	14:106325957-106326024	NOTEST	0	0	0	0	1	1
ENSG00000265715	ENSG00000265715	MIR3118-1	1:142618768-142729975	NOTEST	0	0	0	0	1	1
ENSG00000265717	ENSG00000265717	RP11-94B19.7	18:73966246-73967169	NOTEST	0	0	0	0	1	1
ENSG00000265719	ENSG00000265719	MIR4681	10:120967100-121215131	NOTEST	0	0	0	0	1	1
ENSG00000265720	ENSG00000265720	AC097470.1	4:75192602-75192680	NOTEST	0	0	0	0	1	1
ENSG00000265721	ENSG00000265721	U8	HG871_PATCH:5077545-5149878	NOTEST	0	0	0	0	1	1
ENSG00000265722	ENSG00000265722	AC099326.1	3:69788585-70017488	NOTEST	0	0	0	0	1	1
ENSG00000265723	ENSG00000265723	HIST2H3DP1	HG1292_PATCH:121660748-121689449	NOTEST	0	0	0	0	1	1
ENSG00000265724	ENSG00000265724	MIR4284	7:73095298-73134002	NOTEST	0	0	0	0	1	1
ENSG00000265725	ENSG00000265725	MIR3144	6:120336324-120336403	NOTEST	0	0	0	0	1	1
ENSG00000265726	ENSG00000265726	MIR4651	HG1257_PATCH:75364156-75459616	NOTEST	0	0	0	0	1	1
ENSG00000265727	ENSG00000265727	RN7SL648P	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000265728	ENSG00000265728	RP11-883A18.3	18:10594586-10604795	NOTEST	0	0	0	0	1	1
ENSG00000265729	ENSG00000265729	RP11-1055B8.8	HG271_PATCH:79369274-79440126	NOTEST	0	0	0	0	1	1
ENSG00000265730	ENSG00000265730	AC090349.1	18:26675538-26675643	NOTEST	0	0	0	0	1	1
ENSG00000265731	ENSG00000265731	RN7SL522P	16:11453701-11617444	NOTEST	0	0	0	0	1	1
ENSG00000265732	ENSG00000265732	SNORD48	HSCHR6_MHC_QBL:31792646-31797799	NOTEST	0	0	0	0	1	1
ENSG00000265733	ENSG00000265733	SNORA74	HG1211_PATCH:46467921-46484300	NOTEST	0	0	0	0	1	1
ENSG00000265734	ENSG00000265734	MIR4438	2:214149112-215548970	NOTEST	0	0	0	0	1	1
ENSG00000265735	ENSG00000265735	RN7SL5P	9:8314245-10612723	NOTEST	0	0.0897782	inf	0	1	1
ENSG00000265736	ENSG00000265736	AL049539.1	20:30697308-30755061	NOTEST	0	0	0	0	1	1
ENSG00000265737	ENSG00000265737	RP11-1157N2__B.2	18:14728270-14852737	NOTEST	0.0834715	0.0253656	-1.71841	0	1	1
ENSG00000265738	ENSG00000265738	Y_RNA	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000265739	ENSG00000265739	RP11-354P11.3	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000265740	ENSG00000265740	RN7SL339P	5:170786120-170786414	NOTEST	0	0	0	0	1	1
ENSG00000265741	ENSG00000265741	RN7SL406P	X:41374186-41782716	NOTEST	0	0	0	0	1	1
ENSG00000265742	ENSG00000265742	CTD-2541J13.2	HSCHR18_2_CTG2:65243267-65636305	NOTEST	0	0	0	0	1	1
ENSG00000265743	ENSG00000265743	RP11-848P1.3	17:29291952-29292518	NOTEST	0	0	0	0	1	1
ENSG00000265744	ENSG00000265744	MIR4427	1:233749749-233808258	NOTEST	0	0	0	0	1	1
ENSG00000265745	ENSG00000265745	RN7SL375P	13:60239716-60738121	NOTEST	0	0	0	0	1	1
ENSG00000265746	ENSG00000265746	KYNUP2	17:18981087-18991191	NOTEST	0	0	0	0	1	1
ENSG00000265747	ENSG00000265747	RN7SL298P	19:11309970-11373157	NOTEST	0	0	0	0	1	1
ENSG00000265748	ENSG00000265748	AC125387.1	19:7309262-7309362	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000265749	ENSG00000265749	RP11-849F2.5	17:8268880-8286531	NOTEST	0.44909	0.201734	-1.15455	0	1	1
ENSG00000265750	ENSG00000265750	RP11-799B12.4	18:21718941-21977844	NOTEST	0.618005	0.488516	-0.339215	0	1	1
ENSG00000265751	ENSG00000265751	RP11-296E23.1	18:18822202-19105378	NOTEST	0	0	0	0	1	1
ENSG00000265752	ENSG00000265752	RP11-403A21.1	18:21537717-21562520	NOTEST	0	0	0	0	1	1
ENSG00000265753	ENSG00000265753	RN7SL444P	1:151252499-151300191	NOTEST	0.573777	0.43241	-0.408089	0	1	1
ENSG00000265754	ENSG00000265754	SNORA38	HSCHR6_MHC_MCF:31664742-31681839	NOTEST	0	0	0	0	1	1
ENSG00000265756	ENSG00000265756	CTB-96E2.7	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000265758	ENSG00000265758	RP11-595B24.1	18:19561081-19631120	NOTEST	0	0	0	0	1	1
ENSG00000265759	ENSG00000265759	AC020934.1	19:12873816-12985765	NOTEST	0	0	0	0	1	1
ENSG00000265761	ENSG00000265761	RP11-445P17.6	HG871_PATCH:5237653-5261139	NOTEST	0	0	0	0	1	1
ENSG00000265762	ENSG00000265762	AL671859.2	HSCHR6_MHC_COX:29958300-30072425	NOTEST	0	0	0	0	1	1
ENSG00000265763	ENSG00000265763	ZNF488	HG1211_PATCH:47860943-47879786	NOTEST	0	0	0	0	1	1
ENSG00000265764	ENSG00000265764	AL662890.3	6:28763748-28763812	NOTEST	0	0	0	0	1	1
ENSG00000265765	ENSG00000265765	RP11-495P10.3	HG1287_PATCH:149015413-149031051	NOTEST	0	0	0	0	1	1
ENSG00000265766	ENSG00000265766	CXADRP3	18:14477953-14499277	NOTEST	0	0	0	0	1	1
ENSG00000265767	ENSG00000265767	MIR4745	19:797074-812327	NOTEST	0	0	0	0	1	1
ENSG00000265768	ENSG00000265768	MIR4506	14:94400498-94443137	NOTEST	0	0	0	0	1	1
ENSG00000265769	ENSG00000265769	AL589663.1	1:52366591-52366643	NOTEST	0	0	0	0	1	1
ENSG00000265770	ENSG00000265770	RN7SL660P	14:32798478-33300567	NOTEST	0	0	0	0	1	1
ENSG00000265771	ENSG00000265771	AL592205.2	1:97401100-97401219	NOTEST	0	0	0	0	1	1
ENSG00000265773	ENSG00000265773	NUP210P2	HSCHR3_1_CTG1:119434055-11944640	NOTEST	0	0	0	0	1	1
ENSG00000265774	ENSG00000265774	AC098870.1	4:86396266-86923823	NOTEST	0	0	0	0	1	1
ENSG00000265775	ENSG00000265775	CTC-304I17.3	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000265776	ENSG00000265776	hsa-mir-3670-2	16:18499554-18499619	NOTEST	0	0	0	0	1	1
ENSG00000265777	ENSG00000265777	RN7SL624P	17:1963132-2284352	NOTEST	0	0	0	0	1	1
ENSG00000265780	ENSG00000265780	RP11-449L23.3	17:71330522-71640228	NOTEST	0	0	0	0	1	1
ENSG00000265781	ENSG00000265781	RP11-384E22.1	18:68667712-68678726	NOTEST	0	0	0	0	1	1
ENSG00000265783	ENSG00000265783	AP000445.3	11:58407898-58499447	NOTEST	0	0	0	0	1	1
ENSG00000265784	ENSG00000265784	RP1-56K13.3	17:37026111-37078023	NOTEST	0	0	0	0	1	1
ENSG00000265786	ENSG00000265786	RP11-527H14.6	18:14877609-14884051	NOTEST	0	0	0	0	1	1
ENSG00000265787	ENSG00000265787	CYP4F35P	18:14337421-14342524	NOTEST	0.112498	0.190991	0.763606	0	1	1
ENSG00000265788	ENSG00000265788	RP11-19P22.5	17:25978359-25992738	NOTEST	0	0	0	0	1	1
ENSG00000265789	ENSG00000265789	MIR4330	X:150336693-150336798	NOTEST	0	0	0	0	1	1
ENSG00000265790	ENSG00000265790	RNASEH1P1	17:20717932-20947073	NOTEST	0	0	0	0	1	1
ENSG00000265791	ENSG00000265791	CTD-2349P21.10	17:29036316-29151794	NOTEST	0.106973	0.0771155	-0.472148	0	1	1
ENSG00000265792	ENSG00000265792	AL592494.5	HG1292_PATCH:121902778-122005752	NOTEST	0	0	0	0	1	1
ENSG00000265793	ENSG00000265793	MIR3118-4	15:22049273-22049348	NOTEST	0	0	0	0	1	1
ENSG00000265794	ENSG00000265794	RP11-227G15.3	17:30593194-30708905	NOTEST	0	0	0	0	1	1
ENSG00000265795	ENSG00000265795	U6	HSCHR6_MHC_QBL:28870782-28891770	NOTEST	0	0	0	0	1	1
ENSG00000265796	ENSG00000265796	AC084357.1	12:64224533-64224603	NOTEST	0	0	0	0	1	1
ENSG00000265797	ENSG00000265797	SRGAP2B	HG1287_PATCH:145601106-145781943	NOTEST	0	0	0	0	1	1

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ENSG00000265798	ENSG00000265798	RP11-271K11.5	17:29335514-29709134	NOTEST	0	0.0181602	inf	0	1	1
ENSG00000265799	ENSG00000265799	RP11-387H17.6	17:38168478-38170958	NOTEST	0.0242311	0	#NAME?	0	1	1
ENSG00000265800	ENSG00000265800	RP11-649A18.5	17:73131342-73179078	NOTEST	0.30977	0.432978	0.483096	0	1	1
ENSG00000265801	ENSG00000265801	RP11-720N19.2	17:25783669-25976586	NOTEST	0	0	0	0	1	1
ENSG00000265802	ENSG00000265802	RN7SL49P	13:45513383-45657260	NOTEST	0	0	0	0	1	1
ENSG00000265803	ENSG00000265803	AL590703.1	6:158589383-158620376	NOTEST	0	0	0	0	1	1
ENSG00000265804	ENSG00000265804	AC078864.2	12:52507708-52507796	NOTEST	0	0	0	0	1	1
ENSG00000265806	ENSG00000265806	MIR4292	9:139685806-139735639	NOTEST	0	0	0	0	1	1
ENSG00000265807	ENSG00000265807	AL592188.6	GL000220.1:151880-152060	NOTEST	0	0	0	0	1	1
ENSG00000265808	ENSG00000265808	SEC22B	HG1292_PATCH:120698574-120719144	NOTEST	0	0	0	0	1	1
ENSG00000265809	ENSG00000265809	AC007114.1	17:55055465-55084129	NOTEST	0	0	0	0	1	1
ENSG00000265810	ENSG00000265810	MIR3907	7:151124768-151137899	NOTEST	0	0	0	0	1	1
ENSG00000265812	ENSG00000265812	AC007040.1	2:71163011-71306935	NOTEST	0	0	0	0	1	1
ENSG00000265813	ENSG00000265813	RN7SL300P	3:152917490-152917806	NOTEST	0.303939	0.324555	0.0946781	0	1	1
ENSG00000265814	ENSG00000265814	RN7SL376P	15:40886217-40956540	NOTEST	0	0	0	0	1	1
ENSG00000265815	ENSG00000265815	MIR1273G	1:53392900-53517375	NOTEST	0	0	0	0	1	1
ENSG00000265816	ENSG00000265816	5S_rRNA	HSCHR6_MHC_COX:31954521-32044486	NOTEST	0	0	0	0	1	1
ENSG00000265818	ENSG00000265818	EEF1E1-BLOC1S5	6:7727029-8102811	NOTEST	0	0	0	0	1	1
ENSG00000265819	ENSG00000265819	AC092832.1	X:22277913-23311263	NOTEST	0	0	0	0	1	1
ENSG00000265820	ENSG00000265820	MIR3177	16:1756183-1821731	NOTEST	0	0	0	0	1	1
ENSG00000265821	ENSG00000265821	RN7SL739P	17:43578684-43640596	NOTEST	0	0	0	0	1	1
ENSG00000265822	ENSG00000265822	MIR4422	1:55683533-55699850	NOTEST	0	0	0	0	1	1
ENSG00000265823	ENSG00000265823	EIF2D	HG1293_PATCH:206571090-206676024	NOTEST	0	0	0	0	1	1
ENSG00000265824	ENSG00000265824	RN7SL232P	10:12303669-12303926	NOTEST	0	0	0	0	1	1
ENSG00000265826	ENSG00000265826	AC087203.1	8:12278540-12282509	NOTEST	0	0	0	0	1	1
ENSG00000265827	ENSG00000265827	MIR4680	10:112629500-112679032	NOTEST	0	0	0	0	1	1
ENSG00000265828	ENSG00000265828	MIR3939	6:167383113-167412553	NOTEST	0	0	0	0	1	1
ENSG00000265829	ENSG00000265829	MIR548AG1	4:61788336-61788402	NOTEST	0	0	0	0	1	1
ENSG00000265830	ENSG00000265830	AL592188.7	GL000220.1:158122-158214	NOTEST	0	0	0	0	1	1
ENSG00000265831	ENSG00000265831	MIR3123	1:240928856-241520530	NOTEST	0	0	0	0	1	1
ENSG00000265832	ENSG00000265832	PEX11B	HG1287_PATCH:146597764-146605252	NOTEST	0	0	0	0	1	1
ENSG00000265833	ENSG00000265833	RP1-66C13.1	17:26034203-26034276	NOTEST	0	0	0	0	1	1
ENSG00000265834	ENSG00000265834	RP11-439A17.10	HG1292_PATCH:121629974-121659880	NOTEST	0	0	0	0	1	1
ENSG00000265835	ENSG00000265835	AC009800.1	8:53907921-53907993	NOTEST	0	0	0	0	1	1
ENSG00000265836	ENSG00000265836	AC139085.1	18:74463260-74463797	NOTEST	0	0	0	0	1	1
ENSG00000265837	ENSG00000265837	AC015820.1	11:25558823-25558917	NOTEST	0	0	0	0	1	1
ENSG00000265838	ENSG00000265838	U1	HSCHR6_MHC_SSTO:32506794-32506946	NOTEST	0	0	0	0	1	1
ENSG00000265839	ENSG00000265839	RN7SL360P	2:101217327-101217618	NOTEST	0	0	0	0	1	1
ENSG00000265840	ENSG00000265840	AC010761.10	17:27071001-27077974	NOTEST	0	0	0	0	1	1
ENSG00000265841	ENSG00000265841	MIR548X	21:19933582-20132321	NOTEST	0	0	0	0	1	1
ENSG00000265842	ENSG00000265842	RN7SL53P	19:44596256-44596551	NOTEST	0	0	0	0	1	1
ENSG00000265843	ENSG00000265843	LINC01029	18:75683249-75705678	NOTEST	0	0	0	0	1	1
ENSG00000265844	ENSG00000265844	RP11-751H17.1	18:74892061-74947386	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000265845	ENSG00000265845	RP11-20B24.5	17:27232267-27384234	NOTEST	0	0.0165811	inf	0	1	1
ENSG00000265846	ENSG00000265846	MIR4276	4:175344945-175345015	NOTEST	0	0	0	0	1	1
ENSG00000265847	ENSG00000265847	MIR4287	8:27727398-27850244	NOTEST	0	0	0	0	1	1
ENSG00000265848	ENSG00000265848	MIR3689D1	9:137741454-137741528	NOTEST	0	0	0	0	1	1
ENSG00000265849	ENSG00000265849	SNORD83	HSCHR6_MHC_APD:31507784-31518252	NOTEST	0	0	0	0	1	1
ENSG00000265850	ENSG00000265850	MIR4797	3:196769430-197030618	NOTEST	0	0	0	0	1	1
ENSG00000265852	ENSG00000265852	Y_RNA	HSCHR6_MHC_QBL:31454787-31454889	NOTEST	0	0	0	0	1	1
ENSG00000265853	ENSG00000265853	RP1-48J14.1	17:16796511-16796743	NOTEST	0	0	0	0	1	1
ENSG00000265854	ENSG00000265854	CTSLP3	HG1211_PATCH:47253536-47282319	NOTEST	0	0	0	0	1	1
ENSG00000265855	ENSG00000265855	MIR4514	15:81289757-81289814	NOTEST	0	0	0	0	1	1
ENSG00000265856	ENSG00000265856	AL133153.1	14:91737666-91884188	NOTEST	0	0	0	0	1	1
ENSG00000265858	ENSG00000265858	AL031176.1	X:111502720-111502802	NOTEST	0	0	0	0	1	1
ENSG00000265859	ENSG00000265859	MIR5704	3:131252398-132004254	NOTEST	0	0	0	0	1	1
ENSG00000265860	ENSG00000265860	RN7SL548P	2:101436613-101886778	NOTEST	0	0	0	0	1	1
ENSG00000265861	ENSG00000265861	MIR4495	12:98332833-98332899	NOTEST	0	0	0	0	1	1
ENSG00000265862	ENSG00000265862	RN7SKP88	HG1287_PATCH:149525897-149526147	NOTEST	0	0	0	0	1	1
ENSG00000265863	ENSG00000265863	RP11-805L22.2	17:30086813-30088404	NOTEST	0	0	0	0	1	1
ENSG00000265864	ENSG00000265864	AC092117.2	16:2787076-2827298	NOTEST	0	0	0	0	1	1
ENSG00000265865	ENSG00000265865	AC069285.1	7:62528464-62528529	NOTEST	0	0	0	0	1	1
ENSG00000265866	ENSG00000265866	AC067805.1	15:89515631-89515683	NOTEST	0	0	0	0	1	1
ENSG00000265867	ENSG00000265867	MIR4516	16:2089815-2185899	NOTEST	0	0	0	0	1	1
ENSG00000265868	ENSG00000265868	RN7SL436P	X:22050558-22269427	NOTEST	0	0	0	0	1	1
ENSG00000265869	ENSG00000265869	RP11-76K13.2	18:6941742-7117813	NOTEST	0	0	0	0	1	1
ENSG00000265870	ENSG00000265870	AC026166.1	3:12045875-12232900	NOTEST	0	0	0	0	1	1
ENSG00000265871	ENSG00000265871	MIR3174	15:90544623-90625439	NOTEST	0	0	0	0	1	1
ENSG00000265872	ENSG00000265872	MIR3689A	9:137741332-137741410	NOTEST	0	0	0	0	1	1
ENSG00000265873	ENSG00000265873	MIR4289	9:91360750-91360820	NOTEST	0	0	0	0	1	1
ENSG00000265874	ENSG00000265874	MIR4489	11:65405567-65418401	NOTEST	0	0	0	0	1	1
ENSG00000265875	ENSG00000265875	AC011357.1	5:145942788-146464347	NOTEST	0	0	0	0	1	1
ENSG00000265876	ENSG00000265876	AC080080.1	7:18033057-18033123	NOTEST	0	0	0	0	1	1
ENSG00000265878	ENSG00000265878	MIR3914-1	7:70597154-71178585	NOTEST	0	0	0	0	1	1
ENSG00000265879	ENSG00000265879	MIR4748	19:10828754-10946994	NOTEST	0	0	0	0	1	1
ENSG00000265880	ENSG00000265880	CBWD3	HG962_PATCH:70856396-70914929	NOTEST	0	0	0	0	1	1
ENSG00000265881	ENSG00000265881	PDLIM1P2	17:21348144-21348751	NOTEST	0	0.0265252	inf	0	1	1
ENSG00000265882	ENSG00000265882	RN7SL73P	21:37529079-37666572	NOTEST	0	0	0	0	1	1
ENSG00000265883	ENSG00000265883	RP11-169I9.2	17:63133548-63223821	NOTEST	0	0	0	0	1	1
ENSG00000265885	ENSG00000265885	RN7SL783P	13:110750199-110750498	NOTEST	0	0	0	0	1	1
ENSG00000265886	ENSG00000265886	RP11-289H16.1	HG1287_PATCH:145601106-145781943	NOTEST	0	0	0	0	1	1
ENSG00000265887	ENSG00000265887	AC073136.1	7:56337475-56337544	NOTEST	0	0	0	0	1	1
ENSG00000265888	ENSG00000265888	RP11-408H20.2	18:28645939-28742819	NOTEST	0	0	0	0	1	1
ENSG00000265889	ENSG00000265889	Y_RNA	HG75_PATCH:34601601-34662129	NOTEST	0	0	0	0	1	1
ENSG00000265890	ENSG00000265890	RN7SL537P	18:6941742-7117813	NOTEST	0	0	0	0	1	1
ENSG00000265891	ENSG00000265891	AC017028.8	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000265892	ENSG00000265892	RN7SL311P	4:140106594-140106897	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000265893	ENSG00000265893	AL132772.1	20:42984339-43061485	NOTEST	0	0	0	0	1	1
ENSG00000265894	ENSG00000265894	RN7SL357P	4:57671999-57672295	NOTEST	0	0	0	0	1	1
ENSG00000265895	ENSG00000265895	hsa-mir-1236	HSCHR6_MHC_DBB:31902054-31919714	NOTEST	0	0	0	0	1	1
ENSG00000265896	ENSG00000265896	Y_RNA	HSCHR6_MHC_QBL:31357609-31374165	NOTEST	0	0	0	0	1	1
ENSG00000265897	ENSG00000265897	RP11-763B22.7	HG1287_PATCH:14501068-145011001	NOTEST	0	0	0	0	1	1
ENSG00000265898	ENSG00000265898	AP003354.1	8:103838584-103990104	NOTEST	0	0	0	0	1	1
ENSG00000265899	ENSG00000265899	AC007389.4	2:65663844-66311773	NOTEST	0	0	0	0	1	1
ENSG00000265900	ENSG00000265900	RN7SL226P	19:1985446-2034880	NOTEST	0	0	0	0	1	1
ENSG00000265901	ENSG00000265901	AC097493.1	4:9601951-9602051	NOTEST	0	0	0	0	1	1
ENSG00000265902	ENSG00000265902	MIR4696	11:74407473-74442430	NOTEST	0	0	0	0	1	1
ENSG00000265903	ENSG00000265903	RN7SKP138	HSCHR6_MHC_COX:30821899-30822202	NOTEST	0	0	0	0	1	1
ENSG00000265904	ENSG00000265904	AC005288.1	17:37415383-37607539	NOTEST	0	0	0	0	1	1
ENSG00000265905	ENSG00000265905	RN7SL96P	2:39103102-39202590	NOTEST	0	0	0	0	1	1
ENSG00000265906	ENSG00000265906	RP11-163O19.15	HG281_PATCH:49895724-49898365	NOTEST	0	0	0	0	1	1
ENSG00000265907	ENSG00000265907	RP11-737O24.2	18:2916991-3013313	NOTEST	0	0	0	0	1	1
ENSG00000265908	ENSG00000265908	RP11-20B24.6	17:27232267-27384234	NOTEST	0.0694158	0.0245782	-1.49789	0	1	1
ENSG00000265910	ENSG00000265910	AC090559.2	11:47404698-47438047	NOTEST	0	0	0	0	1	1
ENSG00000265911	ENSG00000265911	AC117422.1	3:125725197-125820404	NOTEST	0	0	0	0	1	1
ENSG00000265912	ENSG00000265912	RP11-583F2.2	17:62936699-62952664	NOTEST	0.183603	0.173619	-0.0806627	0	1	1
ENSG00000265913	ENSG00000265913	RP11-445P17.3	HG871_PATCH:5276549-5305600	NOTEST	0	0	0	0	1	1
ENSG00000265914	ENSG00000265914	Y_RNA	HG1287_PATCH:14810661-148106715	NOTEST	0	0	0	0	1	1
ENSG00000265915	ENSG00000265915	RP11-499O7.7	HG871_PATCH:5029586-5060223	NOTEST	0	0	0	0	1	1
ENSG00000265916	ENSG00000265916	RP11-434D2.9	17:20435560-20436194	NOTEST	0	0.0774957	inf	0	1	1
ENSG00000265917	ENSG00000265917	MIR3685	12:95703698-95703760	NOTEST	0	0	0	0	1	1
ENSG00000265918	ENSG00000265918	RN7SL543P	16:67053421-67053718	NOTEST	0	0	0	0	1	1
ENSG00000265919	ENSG00000265919	MIR4280	5:86263137-86433529	NOTEST	0	0	0	0	1	1
ENSG00000265920	ENSG00000265920	U6	HSCHR6_MHC_QBL:32218296-32297155	NOTEST	0	0	0	0	1	1
ENSG00000265921	ENSG00000265921	RNU6-186P	HSCHR6_MHC_COX:31043286-31043386	NOTEST	0	0	0	0	1	1
ENSG00000265922	ENSG00000265922	RP11-196G18.21	HG1287_PATCH:15046908-150498788	NOTEST	0	0	0	0	1	1
ENSG00000265923	ENSG00000265923	PGM5-AS1	HG962_PATCH:70921452-71114201	NOTEST	0	0	0	0	1	1
ENSG00000265924	ENSG00000265924	MIR5692C1	5:135138673-135138764	NOTEST	0	0	0	0	1	1
ENSG00000265925	ENSG00000265925	RP11-495P10.7	HG1287_PATCH:14897730-148983971	NOTEST	0	0	0	0	1	1
ENSG00000265926	ENSG00000265926	SNORD33	HSCHR6_MHC_DBB:29523342-29600923	NOTEST	0	0	0	0	1	1
ENSG00000265927	ENSG00000265927	CTD-2532D12.5	17:71827710-71832158	NOTEST	0	0	0	0	1	1
ENSG00000265929	ENSG00000265929	hsa-mir-5195	14:107259099-107259214	NOTEST	0	0	0	0	1	1
ENSG00000265930	ENSG00000265930	MIR4734	17:36858514-36858584	NOTEST	0	0	0	0	1	1
ENSG00000265931	ENSG00000265931	AC112719.1	4:76932336-77033955	NOTEST	0	0	0	0	1	1
ENSG00000265932	ENSG00000265932	MIR3146	7:19735084-19748710	NOTEST	0	0	0	0	1	1
ENSG00000265933	ENSG00000265933	LINC00668	18:6919494-6929965	NOTEST	0.33724	0.595885	0.821257	0	1	1
ENSG00000265934	ENSG00000265934	ARL2BPP1	18:74415399-74416210	NOTEST	0	0	0	0	1	1
ENSG00000265935	ENSG00000265935	RP11-277J6.3	17:71658706-71659987	NOTEST	0	0	0	0	1	1
ENSG00000265936	ENSG00000265936	RP11-563H6.1	18:65042369-65042542	NOTEST	0	0	0	0	1	1
ENSG00000265937	ENSG00000265937	RP11-289I10.2	HG1287_PATCH:14591924-145919953	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000265939	ENSG00000265939	UBE2CP2	18:20279443-20606451	NOTEST	0.131452	0.0341433	-1.94486	0	1	1
ENSG00000265940	ENSG00000265940	AC103974.1	11:18825954-18826033	NOTEST	0	0	0	0	1	1
ENSG00000265941	ENSG00000265941	SNORD36	HG79_PATCH:136223748-136226961	NOTEST	0	0	0	0	1	1
ENSG00000265942	ENSG00000265942	RN7SL577P	15:49280672-49338760	NOTEST	0	0	0	0	1	1
ENSG00000265943	ENSG00000265943	RP11-739L10.1	18:20279443-20606451	NOTEST	0.0744632	0.0289954	-1.3607	0	1	1
ENSG00000265944	ENSG00000265944	C18orf64	18:6511414-6590652	NOTEST	0	0	0	0	1	1
ENSG00000265945	ENSG00000265945	RN7SL721P	1:10450058-10450353	NOTEST	0	0.0921612	inf	0	1	1
ENSG00000265946	ENSG00000265946	RP11-752P2.2	18:69332383-69332761	NOTEST	0	0	0	0	1	1
ENSG00000265947	ENSG00000265947	CR759834.1	HSCHR6_MHC_MCF:29169702-29169769	NOTEST	0	0	0	0	1	1
ENSG00000265948	ENSG00000265948	RP11-296E23.2	18:18822202-19105378	NOTEST	0	0	0	0	1	1
ENSG00000265950	ENSG00000265950	AL901607.3	HSCHR6_MHC_COX:28764544-28764608	NOTEST	0	0	0	0	1	1
ENSG00000265951	ENSG00000265951	CU459007.1	HSCHR19LRC_COX1_CTG1:55141111-55141181	NOTEST	0	0	0	0	1	1
ENSG00000265952	ENSG00000265952	RP11-344P13.1	HG1292_PATCH:122116568-122123147	NOTEST	0	0	0	0	1	1
ENSG00000265953	ENSG00000265953	AC092463.1	4:6910968-7059679	NOTEST	0	0	0	0	1	1
ENSG00000265954	ENSG00000265954	MIR4749	19:50321538-50364001	NOTEST	0	0	0	0	1	1
ENSG00000265955	ENSG00000265955	Y_RNA	HSCHR6_MHC_QBL:30685020-30700042	NOTEST	0	0	0	0	1	1
ENSG00000265956	ENSG00000265956	MIR4445	3:109321674-109321744	NOTEST	0	0	0	0	1	1
ENSG00000265957	ENSG00000265957	MIR4319	18:42260137-42648475	NOTEST	0	0	0	0	1	1
ENSG00000265958	ENSG00000265958	Metazoa_SRP	HSCHR17_1:43580584-43647125	NOTEST	0	0	0	0	1	1
ENSG00000265959	ENSG00000265959	AL354720.1	13:73698848-73698947	NOTEST	0	0	0	0	1	1
ENSG00000265960	ENSG00000265960	AL365181.1	1:156557647-156557747	NOTEST	0	0	0	0	1	1
ENSG00000265961	ENSG00000265961	Y_RNA	HG989_PATCH:31972931-32013732	NOTEST	0	0	0	0	1	1
ENSG00000265962	ENSG00000265962	RP11-674N23.1	18:8695853-8832776	NOTEST	0	0	0	0	1	1
ENSG00000265963	ENSG00000265963	RP11-403I13.5	HG1287_PATCH:144422480-144424319	NOTEST	0	0	0	0	1	1
ENSG00000265964	ENSG00000265964	RP11-293E1.1	17:43697693-43913194	NOTEST	0	0.02707	inf	0	1	1
ENSG00000265965	ENSG00000265965	MIR4266	2:109745803-110262207	NOTEST	0	0	0	0	1	1
ENSG00000265967	ENSG00000265967	AC100830.4	15:64979771-65011801	NOTEST	0.169831	0.204771	0.269908	0	1	1
ENSG00000265968	ENSG00000265968	RN7SL103P	5:68455862-68456123	NOTEST	0	0	0	0	1	1
ENSG00000265970	ENSG00000265970	HFE2	HG1287_PATCH:146703882-146708333	NOTEST	0	0	0	0	1	1
ENSG00000265971	ENSG00000265971	RP11-269G24.6	17:61532353-61533178	NOTEST	0	0	0	0	1	1
ENSG00000265972	ENSG00000265972	TXNIP	HG1287_PATCH:146678959-146682902	NOTEST	0	0	0	0	1	1
ENSG00000265973	ENSG00000265973	RP11-163O19.16	HG281_PATCH:49865039-49868085	NOTEST	0	0	0	0	1	1
ENSG00000265974	ENSG00000265974	MIR3147	HG14_PATCH:57472477-57483910	NOTEST	0	0	0	0	1	1
ENSG00000265975	ENSG00000265975	CTB-41I6.2	17:8870839-8880312	NOTEST	0	0	0	0	1	1
ENSG00000265976	ENSG00000265976	MIR4725	17:29898160-29902678	NOTEST	0	0	0	0	1	1
ENSG00000265977	ENSG00000265977	AL450307.2	10:133489514-133489584	NOTEST	0	0	0	0	1	1
ENSG00000265978	ENSG00000265978	AL008721.1	22:25928686-25928776	NOTEST	0	0	0	0	1	1
ENSG00000265979	ENSG00000265979	AC017028.9	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000265980	ENSG00000265980	CTD-2515C13.2	18:26858473-26941928	NOTEST	0	0	0	0	1	1
ENSG00000265981	ENSG00000265981	MIR544B	3:124449212-124464040	NOTEST	0	0	0	0	1	1
ENSG00000265982	ENSG00000265982	RP11-927P21.4	17:62745780-62833272	NOTEST	0	0	0	0	1	1
ENSG00000265983	ENSG00000265983	U1	HSCHR6_MHC_DBB:32514189-32514338	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000265985	ENSG00000265985	AC005686.1	7:34352561-34352657	NOTEST	0	0	0	0	1	1
ENSG00000265986	ENSG00000265986	MIR4735	1:196194908-196578355	NOTEST	0	0	0	0	1	1
ENSG00000265987	ENSG00000265987	RP11-16C1.3	17:73314156-73401790	NOTEST	0	0	0	0	1	1
ENSG00000265988	ENSG00000265988	CR753815.2	HSCHR6_MHC_DBB:29958736-30072822	NOTEST	0	0	0	0	1	1
ENSG00000265989	ENSG00000265989	MIR4646	HSCHR6_MHC_DBB:31611187-31653368	NOTEST	0	0	0	0	1	1
ENSG00000265990	ENSG00000265990	AL356154.1	10:82904407-82904487	NOTEST	0	0	0	0	1	1
ENSG00000265991	ENSG00000265991	MIR4519	16:30844946-30906541	NOTEST	0	0	0	0	1	1
ENSG00000265992	ENSG00000265992	ESRG	3:54156573-55108584	NOTEST	0	0	0	0	1	1
ENSG00000265993	ENSG00000265993	MIR5694	14:67908571-67908647	NOTEST	0	0	0	0	1	1
ENSG00000265994	ENSG00000265994	RP11-510D21.1	18:26365031-26369224	NOTEST	0	0	0	0	1	1
ENSG00000265995	ENSG00000265995	RP11-736G13.1	18:69557644-69611813	NOTEST	0	0	0	0	1	1
ENSG00000265996	ENSG00000265996	MIR3671	1:65523437-65523525	NOTEST	0	0	0	0	1	1
ENSG00000265997	ENSG00000265997	RN7SL852P	12:1021242-1605099	NOTEST	0	0	0	0	1	1
ENSG00000265998	ENSG00000265998	AC092364.3	HSCHR19_2_CTG3:21915046-21959807	NOTEST	0	0	0	0	1	1
ENSG00000265999	ENSG00000265999	AL499628.1	16:1845620-1934295	NOTEST	0	0	0	0	1	1
ENSG00000266000	ENSG00000266000	AL731561.2	10:48381486-48390991	NOTEST	0	0	0	0	1	1
ENSG00000266001	ENSG00000266001	AC018506.1	3:9022274-9520924	NOTEST	0	0	0	0	1	1
ENSG00000266002	ENSG00000266002	RP11-567L7.5	17:57409049-57480664	NOTEST	0	0	0	0	1	1
ENSG00000266003	ENSG00000266003	RP11-267C16.2	18:48872618-49088939	NOTEST	0	0	0	0	1	1
ENSG00000266004	ENSG00000266004	SNORA38	HSCHR6_MHC_DBB:31570624-31587723	NOTEST	0	0	0	0	1	1
ENSG00000266005	ENSG00000266005	RN7SL611P	2:101172511-101172782	NOTEST	0	0	0	0	1	1
ENSG00000266006	ENSG00000266006	MIR4488	11:61276067-61276129	NOTEST	0	0	0	0	1	1
ENSG00000266007	ENSG00000266007	AP000318.1	21:35445523-35732332	NOTEST	0	0	0	0	1	1
ENSG00000266008	ENSG00000266008	AC092364.4	19:21880208-21880317	NOTEST	0	0	0	0	1	1
ENSG00000266009	ENSG00000266009	RP11-746M1.2	17:20717932-20947073	NOTEST	0	0	0	0	1	1
ENSG00000266010	ENSG00000266010	GATA6-AS1	18:19746858-19748929	NOTEST	0	0	0	0	1	1
ENSG00000266011	ENSG00000266011	Y_RNA	HG1287_PATCH:14901541-149031051	NOTEST	0	0	0	0	1	1
ENSG00000266012	ENSG00000266012	MIR4764	22:33558211-34318829	NOTEST	0	0	0	0	1	1
ENSG00000266013	ENSG00000266013	CTD-2206N4.2	17:37182967-37183363	NOTEST	0	0	0	0	1	1
ENSG00000266014	ENSG00000266014	RP11-94B19.2	18:73959679-73963343	NOTEST	0	0	0	0	1	1
ENSG00000266015	ENSG00000266015	MIR4309	14:103005980-103006063	NOTEST	0	0	0	0	1	1
ENSG00000266016	ENSG00000266016	AC009779.1	12:55828520-55979255	NOTEST	0	0	0	0	1	1
ENSG00000266017	ENSG00000266017	MIR4477A	9:68415307-68415388	NOTEST	0	0	0	0	1	1
ENSG00000266018	ENSG00000266018	AP000781.1	11:57105847-57138073	NOTEST	0	0	0	0	1	1
ENSG00000266019	ENSG00000266019	MIR3609	7:98475555-98741723	NOTEST	0	0	0	0	1	1
ENSG00000266020	ENSG00000266020	AC010092.1	2:171772718-171772804	NOTEST	0	0	0	0	1	1
ENSG00000266021	ENSG00000266021	AL353763.2	9:68997408-68997484	NOTEST	0	0	0	0	1	1
ENSG00000266022	ENSG00000266022	MIR3609	HG946_PATCH:98507244-98642555	NOTEST	0	0	0	0	1	1
ENSG00000266023	ENSG00000266023	RN7SL770P	12:56588930-56589180	NOTEST	0	0	0	0	1	1
ENSG00000266024	ENSG00000266024	AF250324.1	4:190701489-190861426	NOTEST	0	0	0	0	1	1
ENSG00000266025	ENSG00000266025	AC132660.1	3:84954829-84954896	NOTEST	0	0	0	0	1	1
ENSG00000266026	ENSG00000266026	AC092111.1	12:8380329-8384360	NOTEST	0	0	0	0	1	1
ENSG00000266027	ENSG00000266027	MSH5-SAPCD1	HSCHR6_MHC_DBB:31689901-31715550	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000266028	ENSG00000266028	SRGAP2	HG1293_PATCH:206268905-206527996	NOTEST	0	0	0	0	1	1
ENSG00000266029	ENSG00000266029	AC007040.2	2:71163011-71306935	NOTEST	0	0	0	0	1	1
ENSG00000266030	ENSG00000266030	AC078828.1	3:99085644-99085733	NOTEST	0	0	0	0	1	1
ENSG00000266032	ENSG00000266032	AL357515.1	6:111290975-111291075	NOTEST	0	0	0	0	1	1
ENSG00000266033	ENSG00000266033	AL606519.1	1:80795063-80795173	NOTEST	0	0	0	0	1	1
ENSG00000266034	ENSG00000266034	RHEBP2	HG1211_PATCH:48185154-48226140	NOTEST	0	0	0	0	1	1
ENSG00000266035	ENSG00000266035	5S_rRNA	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000266038	ENSG00000266038	MIR4659B	8:6565877-6617184	NOTEST	0	0	0	0	1	1
ENSG00000266039	ENSG00000266039	MIR4509-3	15:28671636-28671730	NOTEST	0	0	0	0	1	1
ENSG00000266040	ENSG00000266040	CTB-58E17.3	17:36858704-36886056	NOTEST	0.0471505	0	#NAME?	0	1	1
ENSG00000266041	ENSG00000266041	MIR4690	11:65383243-65404910	NOTEST	0	0	0	0	1	1
ENSG00000266042	ENSG00000266042	AC015818.6	17:20422624-20432000	NOTEST	0	0	0	0	1	1
ENSG00000266043	ENSG00000266043	MIR3649	12:1769480-1769546	NOTEST	0	0	0	0	1	1
ENSG00000266044	ENSG00000266044	MIR4469	8:42704779-42940931	NOTEST	0	0	0	0	1	1
ENSG00000266045	ENSG00000266045	RP11-466P24.7	5:75377770-75649764	NOTEST	0.0214166	0.0219809	0.0375255	0	1	1
ENSG00000266046	ENSG00000266046	AC084209.1	4:109459345-109541616	NOTEST	0	0	0	0	1	1
ENSG00000266047	ENSG00000266047	AL139377.1	13:36875774-36944317	NOTEST	0	0	0	0	1	1
ENSG00000266048	ENSG00000266048	CTD-2206N4.1	17:37183529-37209458	NOTEST	0	0	0	0	1	1
ENSG00000266049	ENSG00000266049	RP11-703M24.5	18:2655736-2833063	NOTEST	0	0	0	0	1	1
ENSG00000266050	ENSG00000266050	RP11-822E23.6	17:21428050-21477781	NOTEST	0	0	0	0	1	1
ENSG00000266051	ENSG00000266051	AC023992.1	17:56497527-56565745	NOTEST	0	0	0	0	1	1
ENSG00000266052	ENSG00000266052	MIR4500	13:88079454-88323514	NOTEST	0	0	0	0	1	1
ENSG00000266054	ENSG00000266054	NUDT17	HG1287_PATCH:146532043-146546251	NOTEST	0	0	0	0	1	1
ENSG00000266055	ENSG00000266055	AC004079.1	7:27062155-27062295	NOTEST	0	0	0	0	1	1
ENSG00000266056	ENSG00000266056	RP11-343N15.2	HG1292_PATCH:121902778-122005752	NOTEST	0	0	0	0	1	1
ENSG00000266057	ENSG00000266057	AL607076.1	10:132793568-132793650	NOTEST	0	0	0	0	1	1
ENSG00000266058	ENSG00000266058	AC084010.1	4:42410389-42659122	NOTEST	0	0	0	0	1	1
ENSG00000266059	ENSG00000266059	RN7SL140P	2:20375106-20375397	NOTEST	0	0	0	0	1	1
ENSG00000266060	ENSG00000266060	AL603650.4	9:137741658-137741806	NOTEST	0	0	0	0	1	1
ENSG00000266061	ENSG00000266061	AL355531.1	10:131265447-131566271	NOTEST	0	0	0	0	1	1
ENSG00000266062	ENSG00000266062	CTD-2350C19.1	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000266063	ENSG00000266063	MIR4771-2	2:112523847-112642267	NOTEST	0	0	0	0	1	1
ENSG00000266064	ENSG00000266064	RP11-1055B8.2	HG271_PATCH:79336071-79348014	NOTEST	0	0	0	0	1	1
ENSG00000266065	ENSG00000266065	CTD-2124B20.2	18:6493418-6495667	NOTEST	0	0	0	0	1	1
ENSG00000266066	ENSG00000266066	POLRMTP1	17:60214332-60218000	NOTEST	0.01274	0.0198124	0.63704	0	1	1
ENSG00000266069	ENSG00000266069	AL139821.1	10:25380384-25380483	NOTEST	0	0	0	0	1	1
ENSG00000266070	ENSG00000266070	MIR3960	9:130547957-130553066	NOTEST	0	0	0	0	1	1
ENSG00000266071	ENSG00000266071	MIR3617	20:44313291-44337456	NOTEST	0	0	0	0	1	1
ENSG00000266072	ENSG00000266072	MIR5693	13:51909908-52126500	NOTEST	0	0	0	0	1	1
ENSG00000266073	ENSG00000266073	AL590874.1	6:67859401-67859492	NOTEST	0	0	0	0	1	1
ENSG00000266074	ENSG00000266074	BAHCC1	HG271_PATCH:79369274-79440126	NOTEST	0	0	0	0	1	1

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ENSG00000266076	ENSG00000266076	CTD-2535L24.2	17:63524680-64188202	NOTEST	0.0863916	0	#NAME?	0	1	1
ENSG00000266077	ENSG00000266077	AC139149.1	17:79476996-79494802	NOTEST	0	0	0	0	1	1
ENSG00000266078	ENSG00000266078	MIR4432	2:60586350-60618510	NOTEST	0	0	0	0	1	1
ENSG00000266079	ENSG00000266079	SNORA59B	17:19398697-19501235	NOTEST	0.0280278	0	#NAME?	0	1	1
ENSG00000266080	ENSG00000266080	H3F3BP2	HG883_PATCH:26743940-26744511	NOTEST	0	0	0	0	1	1
ENSG00000266081	ENSG00000266081	U1	HSCHR6_MHC_MANN:32539879-32540023	NOTEST	0	0	0	0	1	1
ENSG00000266082	ENSG00000266082	AL138925.1	10:71561643-71724031	NOTEST	0	0	0	0	1	1
ENSG00000266083	ENSG00000266083	AC138965.1	5:175333941-175461683	NOTEST	0	0	0	0	1	1
ENSG00000266084	ENSG00000266084	RP6-74O6.2	HG1287_PATCH:148680276-148698643	NOTEST	0	0	0	0	1	1
ENSG00000266085	ENSG00000266085	AL109658.1	20:1422806-1472233	NOTEST	0	0	0	0	1	1
ENSG00000266087	ENSG00000266087	RN7SL462P	9:39720398-39720657	NOTEST	0	0	0	0	1	1
ENSG00000266088	ENSG00000266088	RP5-1028K7.2	17:38673277-38683254	NOTEST	0.0829232	0.0372432	-1.1548	0	1	1
ENSG00000266089	ENSG00000266089	RN7SL562P	5:176758562-176778853	NOTEST	0	0	0	0	1	1
ENSG00000266090	ENSG00000266090	AC012603.1	5:109021280-109021393	NOTEST	0	0	0	0	1	1
ENSG00000266094	ENSG00000266094	RASSF5	HG1293_PATCH:206571090-206676024	NOTEST	0	0	0	0	1	1
ENSG00000266095	ENSG00000266095	BCL9	HG1287_PATCH:148227826-148312631	NOTEST	0	0	0	0	1	1
ENSG00000266096	ENSG00000266096	AC011652.2	8:130363936-130695925	NOTEST	0	0	0	0	1	1
ENSG00000266097	ENSG00000266097	MIR5192	2:62423247-62451866	NOTEST	0	0	0	0	1	1
ENSG00000266098	ENSG00000266098	AL137127.1	1:19398603-19536770	NOTEST	0	0	0	0	1	1
ENSG00000266099	ENSG00000266099	MIR5700	12:94955564-94955635	NOTEST	0	0	0	0	1	1
ENSG00000266100	ENSG00000266100	RP11-118E18.2	17:55333211-55762046	NOTEST	0.0379961	0.0295472	-0.362829	0	1	1
ENSG00000266101	ENSG00000266101	RP5-906A24.2	17:37329542-37353956	NOTEST	0	0.0728052	inf	0	1	1
ENSG00000266102	ENSG00000266102	RP11-243E13.2	18:10375099-10378111	NOTEST	0	0	0	0	1	1
ENSG00000266103	ENSG00000266103	RN7SL458P	17:36566041-36566302	NOTEST	0	0	0	0	1	1
ENSG00000266104	ENSG00000266104	MIR4326	20:61904136-61921142	NOTEST	0	0	0	0	1	1
ENSG00000266105	ENSG00000266105	RP11-326K13.2	18:29546922-29547508	NOTEST	0	0	0	0	1	1
ENSG00000266106	ENSG00000266106	RP11-647F2.2	17:72270385-72311023	NOTEST	0	0	0	0	1	1
ENSG00000266107	ENSG00000266107	MIR4525	17:80612848-80656604	NOTEST	0	0	0	0	1	1
ENSG00000266108	ENSG00000266108	AC152005.1	X:152468713-152468765	NOTEST	0	0	0	0	1	1
ENSG00000266109	ENSG00000266109	MIR4440	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000266110	ENSG00000266110	MIR4423	1:85599476-85599556	NOTEST	0	0	0	0	1	1
ENSG00000266111	ENSG00000266111	RP11-296K13.4	17:27679086-27878922	NOTEST	0.0610625	0.0436133	-0.48552	0	1	1
ENSG00000266112	ENSG00000266112	AC007567.1	7:107788067-108097161	NOTEST	0	0	0	0	1	1
ENSG00000266113	ENSG00000266113	Y_RNA	HSCHR6_MHC_DBB:31727479-31745915	NOTEST	0	0	0	0	1	1
ENSG00000266114	ENSG00000266114	RP11-963H4.5	17:10583653-10718481	NOTEST	0	0	0	0	1	1
ENSG00000266115	ENSG00000266115	AC005375.1	17:13399005-13505244	NOTEST	0	0	0	0	1	1
ENSG00000266116	ENSG00000266116	RP11-439A17.4	HG1292_PATCH:121660748-121689449	NOTEST	0	0	0	0	1	1
ENSG00000266117	ENSG00000266117	LOC732538	17:66091208-66091898	NOTEST	0	0	0	0	1	1
ENSG00000266118	ENSG00000266118	RP11-507M3.1	2:24299395-24424567	NOTEST	0	0	0	0	1	1
ENSG00000266119	ENSG00000266119	Y_RNA	HSCHR6_MHC_COX:30685347-30700375	NOTEST	0	0	0	0	1	1
ENSG00000266120	ENSG00000266120	RP11-354P11.2	17:28565758-28619074	NOTEST	0	0	0	0	1	1

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ENSG00000266121	ENSG00000266121	AC092104.4	7:7108453-7108535	NOTEST	0	0	0	0	1	1
ENSG00000266122	ENSG00000266122	RN7SL373P	10:70715883-70744829	NOTEST	0	0	0	0	1	1
ENSG00000266123	ENSG00000266123	RN7SL114P	11:64808372-64826021	NOTEST	0	0	0	0	1	1
ENSG00000266124	ENSG00000266124	MIR5587	16:577716-604636	NOTEST	0	0	0	0	1	1
ENSG00000266125	ENSG00000266125	AL022400.1	1:174084437-174964445	NOTEST	0	0	0	0	1	1
ENSG00000266126	ENSG00000266126	RP11-209D14.4	17:19807614-19881656	NOTEST	0.0759296	0.0543858	-0.481433	0	1	1
ENSG00000266127	ENSG00000266127	RP11-474N24.2	18:9708161-9862548	NOTEST	0	0	0	0	1	1
ENSG00000266128	ENSG00000266128	RN7SL366P	6:164261592-164261882	NOTEST	0	0	0	0	1	1
ENSG00000266129	ENSG00000266129	SRP68P1	17:16592850-16719854	NOTEST	0	0	0	0	1	1
ENSG00000266130	ENSG00000266130	hsa-mir-219a-1	HSCHR6_MHC_COX:33097237-33097347	NOTEST	0	0	0	0	1	1
ENSG00000266131	ENSG00000266131	RP11-196G18.23	HG1287_PATCH:150547685-150548919	NOTEST	0	0	0	0	1	1
ENSG00000266132	ENSG00000266132	SNORD33	HSCHR6_MHC_QBL:29523309-29600897	NOTEST	0	0	0	0	1	1
ENSG00000266133	ENSG00000266133	MIR4759	21:28261694-28338832	NOTEST	0	0	0	0	1	1
ENSG00000266134	ENSG00000266134	WISP3	HG1304_PATCH:112375274-112408732	NOTEST	0	0	0	0	1	1
ENSG00000266135	ENSG00000266135	RN7SL625P	7:72312016-72312305	NOTEST	0	0	0	0	1	1
ENSG00000266136	ENSG00000266136	AL031055.1	20:45439476-45439561	NOTEST	0	0	0	0	1	1
ENSG00000266138	ENSG00000266138	RN7SL501P	1:27022523-27108595	NOTEST	0	0	0	0	1	1
ENSG00000266139	ENSG00000266139	MIR4435-2	2:111953539-112268567	NOTEST	0	0	0	0	1	1
ENSG00000266140	ENSG00000266140	MIR4533	20:58662894-59102516	NOTEST	0	0	0	0	1	1
ENSG00000266141	ENSG00000266141	MIR2909	17:35306174-35414171	NOTEST	0	0	0	0	1	1
ENSG00000266142	ENSG00000266142	CT009552.1	HSCHR6_MHC_MANN:30051789-30051922	NOTEST	0	0	0	0	1	1
ENSG00000266143	ENSG00000266143	AC066612.1	15:48413168-48470714	NOTEST	0	0	0	0	1	1
ENSG00000266144	ENSG00000266144	MIR4654	1:162039563-162356600	NOTEST	0	0	0	0	1	1
ENSG00000266145	ENSG00000266145	RHOT1P1	18:14179095-14252139	NOTEST	0.378218	0.225876	-0.743689	0	1	1
ENSG00000266146	ENSG00000266146	MIR5190	18:13217496-13652754	NOTEST	0	0	0	0	1	1
ENSG00000266147	ENSG00000266147	RN7SL377P	HG1257_PATCH:72039492-72293191	NOTEST	0	0	0	0	1	1
ENSG00000266148	ENSG00000266148	MIR5583-1	18:36786887-37380282	NOTEST	0	0	0	0	1	1
ENSG00000266149	ENSG00000266149	RP11-789C17.3	18:7566779-8406951	NOTEST	0	0.0236299	inf	0	1	1
ENSG00000266150	ENSG00000266150	MIR4711	1:59762309-60254854	NOTEST	0	0	0	0	1	1
ENSG00000266151	ENSG00000266151	MIR3646	20:42984339-43061485	NOTEST	0	0	0	0	1	1
ENSG00000266152	ENSG00000266152	RN7SL550P	17:12569206-12894960	NOTEST	0	0	0	0	1	1
ENSG00000266153	ENSG00000266153	RP11-190I17.2	18:5145283-5197502	NOTEST	0	0	0	0	1	1
ENSG00000266154	ENSG00000266154	MIR4658	7:99746529-99756338	NOTEST	0	0	0	0	1	1
ENSG00000266155	ENSG00000266155	RP11-927P21.6	17:62932602-62936347	NOTEST	0.164089	0	#NAME?	0	1	1
ENSG00000266156	ENSG00000266156	AC010329.1	19:20959109-20991922	NOTEST	0	0	0	0	1	1
ENSG00000266157	ENSG00000266157	FOXD4L3	HG962_PATCH:70917782-70920000	NOTEST	0	0	0	0	1	1
ENSG00000266158	ENSG00000266158	RN7SL785P	X:47140213-47140462	NOTEST	0	0	0	0	1	1
ENSG00000266159	ENSG00000266159	TSGA13	HG1308_PATCH:130126045-130351086	NOTEST	0	0	0	0	1	1
ENSG00000266160	ENSG00000266160	RN7SL612P	1:156904631-157015162	NOTEST	0	0	0	0	1	1
ENSG00000266161	ENSG00000266161	HLA-K	HG1322_PATCH:29887571-29890825	NOTEST	0	0	0	0	1	1
ENSG00000266162	ENSG00000266162	YWHAEP2	17:18319041-18328411	NOTEST	0	0	0	0	1	1
ENSG00000266163	ENSG00000266163	AC007216.1	16:11945505-12009939	NOTEST	0	0	0	0	1	1
ENSG00000266164	ENSG00000266164	RN7SL758P	19:41098788-41135725	NOTEST	0	0	0	0	1	1

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ENSG00000266166	ENSG00000266166	RN7SL557P	16:25196527-25196808	NOTEST	0	0	0	0	1	1
ENSG00000266167	ENSG00000266167	CU467612.1	HSCHR19LRC_PGF2_CTG1:54961458-54961528	NOTEST	0	0	0	0	1	1
ENSG00000266168	ENSG00000266168	MIR3147	7:57472730-57472796	NOTEST	0	0	0	0	1	1
ENSG00000266169	ENSG00000266169	RP11-445P17.5	HG871_PATCH:5346622-5347057	NOTEST	0	0	0	0	1	1
ENSG00000266170	ENSG00000266170	AC244230.2	HG1211_PATCH:46956546-46961329	NOTEST	0	0	0	0	1	1
ENSG00000266171	ENSG00000266171	RP11-769O8.1	18:721587-812547	NOTEST	0.17434	0.155566	-0.164375	0	1	1
ENSG00000266172	ENSG00000266172	RP11-1109M24.11	17:21904123-21904694	NOTEST	0.105928	0.0289196	-1.87296	0	1	1
ENSG00000266174	ENSG00000266174	MIR4666A	1:228649774-228649853	NOTEST	0	0	0	0	1	1
ENSG00000266175	ENSG00000266175	AL080243.1	22:41456635-41456705	NOTEST	0	0	0	0	1	1
ENSG00000266176	ENSG00000266176	RP11-855A2.5	17:65989995-65992547	NOTEST	0.0610625	0.417383	2.77301	0	1	1
ENSG00000266177	ENSG00000266177	C1orf54	HG1287_PATCH:150951818-150967331	NOTEST	0	0	0	0	1	1
ENSG00000266178	ENSG00000266178	Y_RNA	HSCHR6_MHC_COX:30890114-30890203	NOTEST	0	0	0	0	1	1
ENSG00000266179	ENSG00000266179	RP11-1113L8.6	17:19504172-19504658	NOTEST	0	0	0	0	1	1
ENSG00000266180	ENSG00000266180	MIR4282	6:73331519-73908574	NOTEST	0	0	0	0	1	1
ENSG00000266181	ENSG00000266181	RP11-178F10.4	18:22102236-22102883	NOTEST	0	0	0	0	1	1
ENSG00000266182	ENSG00000266182	BX088523.2	HSCHR6_MHC_SSTO:28743731-28743839	NOTEST	0	0	0	0	1	1
ENSG00000266183	ENSG00000266183	AL662800.2	6:30614815-30640814	NOTEST	0	0	0	0	1	1
ENSG00000266184	ENSG00000266184	RP11-552O4.2	18:24034873-24770662	NOTEST	0	0	0	0	1	1
ENSG00000266185	ENSG00000266185	RN7SL804P	12:69794682-69794978	NOTEST	0	0	0	0	1	1
ENSG00000266186	ENSG00000266186	AC007040.3	2:71163011-71306935	NOTEST	0	0	0	0	1	1
ENSG00000266187	ENSG00000266187	RN7SL480P	1:150183929-150184221	NOTEST	0	0	0	0	1	1
ENSG00000266188	ENSG00000266188	MIR5095	1:53392900-53517375	NOTEST	0	0	0	0	1	1
ENSG00000266189	ENSG00000266189	MIR3186	17:79369274-79433357	NOTEST	0	0	0	0	1	1
ENSG00000266190	ENSG00000266190	RP11-218F4.2	17:26348693-26349291	NOTEST	0	0	0	0	1	1
ENSG00000266191	ENSG00000266191	Metazoa_SRP	HSCHR6_MHC_SSTO:28945365-28945661	NOTEST	0	0	0	0	1	1
ENSG00000266192	ENSG00000266192	MIR1260B	11:95709761-96076344	NOTEST	0	0	0	0	1	1
ENSG00000266193	ENSG00000266193	MIR4468	7:137806947-137809341	NOTEST	0	0	0	0	1	1
ENSG00000266194	ENSG00000266194	MIR4661	8:92114059-92410378	NOTEST	0	0	0	0	1	1
ENSG00000266195	ENSG00000266195	RN7SL163P	21:18878770-18879044	NOTEST	0	0	0	0	1	1
ENSG00000266196	ENSG00000266196	RP11-675P14.1	18:28293240-28294252	NOTEST	0	0	0	0	1	1
ENSG00000266197	ENSG00000266197	RN7SL527P	10:49087397-49094515	NOTEST	0	0	0	0	1	1
ENSG00000266198	ENSG00000266198	PRKAB2	HG1287_PATCH:147841520-147858965	NOTEST	0	0	0	0	1	1
ENSG00000266199	ENSG00000266199	RN7SL514P	20:5006364-5006628	NOTEST	0	0	0	0	1	1
ENSG00000266200	ENSG00000266200	PNLIPRP2	HG311_PATCH:118380351-118404649	NOTEST	0	0	0	0	1	1
ENSG00000266201	ENSG00000266201	SS18L2P2	18:48872618-49088939	NOTEST	0	0	0	0	1	1
ENSG00000266202	ENSG00000266202	RP1-66C13.4	17:26083791-26221778	NOTEST	0	0	0	0	1	1
ENSG00000266203	ENSG00000266203	MIR5585	1:32479429-32568467	NOTEST	0	0	0	0	1	1
ENSG00000266204	ENSG00000266204	MIR5589	19:10148478-10184811	NOTEST	0	0	0	0	1	1
ENSG00000266205	ENSG00000266205	AC025678.1	15:34665741-34666804	NOTEST	0	0	0	0	1	1
ENSG00000266206	ENSG00000266206	MIR3926-2	8:12579402-12613582	NOTEST	0	0	0	0	1	1
ENSG00000266207	ENSG00000266207	AL583784.1	13:100105649-100105723	NOTEST	0	0	0	0	1	1
ENSG00000266208	ENSG00000266208	CTD-2267D19.3	17:38516906-38520945	NOTEST	0.211592	0.374599	0.824061	0	1	1
ENSG00000266209	ENSG00000266209	AC005783.1	19:4726302-4726391	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000266211	ENSG00000266211	MIR3156-3	21:14756569-14800094	NOTEST	0	0	0	0	1	1
ENSG00000266212	ENSG00000266212	RP11-2E11.5	HG1308_PATCH:13012133-130124233	NOTEST	0	0	0	0	1	1
ENSG00000266213	ENSG00000266213	RP11-100K18.1	18:75897222-75900887	NOTEST	0	0	0	0	1	1
ENSG00000266214	ENSG00000266214	AC073647.2	HG7_PATCH:141559617-141559669	NOTEST	0	0	0	0	1	1
ENSG00000266215	ENSG00000266215	MIR3167	11:126225534-126875953	NOTEST	0	0	0	0	1	1
ENSG00000266216	ENSG00000266216	AL359538.2	13:24982294-25171814	NOTEST	0	0	0	0	1	1
ENSG00000266217	ENSG00000266217	CTSLP2	HG1211_PATCH:48076661-48077769	NOTEST	0	0	0	0	1	1
ENSG00000266218	ENSG00000266218	AC092865.2	12:8579195-8579283	NOTEST	0	0	0	0	1	1
ENSG00000266219	ENSG00000266219	AL592188.8	GL000220.1:108279-108340	NOTEST	0	0	0	0	1	1
ENSG00000266220	ENSG00000266220	AC010723.2	Y:16364064-16364171	NOTEST	0	0	0	0	1	1
ENSG00000266222	ENSG00000266222	RP11-433M22.1	17:46210801-46507637	NOTEST	0	0	0	0	1	1
ENSG00000266223	ENSG00000266223	RN7SL84P	19:4183350-4224811	NOTEST	0	0	0	0	1	1
ENSG00000266224	ENSG00000266224	AL158077.1	9:19829750-19829845	NOTEST	0	0	0	0	1	1
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ENSG00000266226	ENSG00000266226	MIR4323	19:42590262-42700737	NOTEST	0	0	0	0	1	1
ENSG00000266227	ENSG00000266227	NPM1P2	18:23784832-23785868	NOTEST	0	0	0	0	1	1
ENSG00000266228	ENSG00000266228	MIR3611	10:35297478-35379570	NOTEST	0	0	0	0	1	1
ENSG00000266229	ENSG00000266229	AC020606.1	7:113726381-114333827	NOTEST	0	0	0	0	1	1
ENSG00000266230	ENSG00000266230	AL591925.1	13:20504943-20505031	NOTEST	0	0	0	0	1	1
ENSG00000266231	ENSG00000266231	U6	HSCHR6_MHC_APD:31735722-31744719	NOTEST	0	0	0	0	1	1
ENSG00000266232	ENSG00000266232	MIR3178	16:2581922-2582006	NOTEST	0	0	0	0	1	1
ENSG00000266233	ENSG00000266233	AC021660.1	3:98342792-98342888	NOTEST	0	0	0	0	1	1
ENSG00000266234	ENSG00000266234	CTD-2350C19.2	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000266235	ENSG00000266235	MIR3176	16:577716-604636	NOTEST	0	0	0	0	1	1
ENSG00000266236	ENSG00000266236	NARF-IT1	17:80412148-80448413	NOTEST	0.584054	0.432654	-0.432888	0	1	1
ENSG00000266237	ENSG00000266237	RP11-25D3.1	18:23805899-23971649	NOTEST	0	0	0	0	1	1
ENSG00000266239	ENSG00000266239	MIR3605	1:33772366-33896653	NOTEST	0	0	0	0	1	1
ENSG00000266240	ENSG00000266240	MIR5091	4:13629488-13629581	NOTEST	0	0	0	0	1	1
ENSG00000266241	ENSG00000266241	MIR5047	17:62495733-62658186	NOTEST	0	0	0	0	1	1
ENSG00000266242	ENSG00000266242	GRAMD4P7	18:14477953-14499277	NOTEST	0	0.00985288	inf	0	1	1
ENSG00000266243	ENSG00000266243	MIR4279	5:31639516-32122047	NOTEST	0	0	0	0	1	1
ENSG00000266244	ENSG00000266244	AC079340.1	4:153149619-153149686	NOTEST	0	0	0	0	1	1
ENSG00000266245	ENSG00000266245	MIR4644	6:170599790-170716153	NOTEST	0	0	0	0	1	1
ENSG00000266246	ENSG00000266246	AC116655.1	4:9472696-9472784	NOTEST	0	0	0	0	1	1
ENSG00000266247	ENSG00000266247	AC008752.3	19:9962103-9962192	NOTEST	0	0	0	0	1	1
ENSG00000266249	ENSG00000266249	CD160	HG1287_PATCH:146414639-146425703	NOTEST	0	0	0	0	1	1
ENSG00000266250	ENSG00000266250	Y_RNA	HSCHR6_MHC_SSTO:31360500-31376956	NOTEST	0	0	0	0	1	1
ENSG00000266251	ENSG00000266251	COX6CP3	18:1176790-1177013	NOTEST	0	0	0	0	1	1
ENSG00000266252	ENSG00000266252	AL031768.1	6:2245981-2482256	NOTEST	0	0	0	0	1	1
ENSG00000266253	ENSG00000266253	RP11-38L15.2	HG1211_PATCH:47073664-47147473	NOTEST	0	0	0	0	1	1
ENSG00000266254	ENSG00000266254	AC093874.1	4:167148916-167148984	NOTEST	0	0	0	0	1	1
ENSG00000266255	ENSG00000266255	MIR4475	9:36823535-36823596	NOTEST	0	0	0	0	1	1
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ENSG00000266261	ENSG00000266261	RP11-640I15.1	17:15468796-15587625	NOTEST	0.226567	0.0574865	-1.97864	0	1	1
ENSG00000266262	ENSG00000266262	MIR4428	1:237205504-237997288	NOTEST	0	0	0	0	1	1
ENSG00000266263	ENSG00000266263	7SK	HSCHR6_MHC_MANN:30876717-30877020	NOTEST	0	0	0	0	1	1
ENSG00000266264	ENSG00000266264	AL162311.1	14:36007557-36278510	NOTEST	0	0	0	0	1	1
ENSG00000266265	ENSG00000266265	KLF14	HG1308_PATCH:130394888-130397715	NOTEST	0	0	0	0	1	1
ENSG00000266268	ENSG00000266268	RP11-172F10.1	18:4775052-5004536	NOTEST	0	0	0	0	1	1
ENSG00000266269	ENSG00000266269	AC002395.1	12:111890017-112038060	NOTEST	0	0	0	0	1	1
ENSG00000266270	ENSG00000266270	MIR5096	4:79697495-79860592	NOTEST	0	0	0	0	1	1
ENSG00000266271	ENSG00000266271	MIR4646	HSCHR6_MHC_QBL:31644971-31661447	NOTEST	0	0	0	0	1	1
ENSG00000266272	ENSG00000266272	Z97632.1	X:135569450-135569551	NOTEST	0	0	0	0	1	1
ENSG00000266273	ENSG00000266273	RP11-715C4.1	18:76555611-76556672	NOTEST	0	0	0	0	1	1
ENSG00000266274	ENSG00000266274	RN7SL138P	17:29286582-29286867	NOTEST	0	0	0	0	1	1
ENSG00000266275	ENSG00000266275	AC034187.5	3:8661085-9005457	NOTEST	0	0	0	0	1	1
ENSG00000266276	ENSG00000266276	MIR4743	18:46065416-46389588	NOTEST	0	0	0	0	1	1
ENSG00000266277	ENSG00000266277	AC096763.1	4:134964621-134964708	NOTEST	0	0	0	0	1	1
ENSG00000266278	ENSG00000266278	RP11-41O4.2	18:68047375-68051827	NOTEST	0.0180667	0	#NAME?	0	1	1
ENSG00000266279	ENSG00000266279	RP11-849F2.4	17:8241014-8242076	NOTEST	0	0	0	0	1	1
ENSG00000266280	ENSG00000266280	MIR4284	HG1257_PATCH:73145925-73184629	NOTEST	0	0	0	0	1	1
ENSG00000266281	ENSG00000266281	AL356865.2	10:120305605-120305676	NOTEST	0	0	0	0	1	1
ENSG00000266282	ENSG00000266282	UBL5P2	17:30468244-30580393	NOTEST	0	0	0	0	1	1
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ENSG00000266284	ENSG00000266284	SNORD36	HG79_PATCH:136223748-136226961	NOTEST	0	0	0	0	1	1
ENSG00000266285	ENSG00000266285	RN7SL682P	5:137614782-137615041	NOTEST	0	0	0	0	1	1
ENSG00000266286	ENSG00000266286	AC037482.2	HSCHR17_4_CTG4:39240637-39241794	NOTEST	0	0	0	0	1	1
ENSG00000266287	ENSG00000266287	MIR3683	7:7106594-7106676	NOTEST	0	0	0	0	1	1
ENSG00000266288	ENSG00000266288	CTD-3096M3.2	18:5381639-5385329	NOTEST	0	0	0	0	1	1
ENSG00000266289	ENSG00000266289	RP11-1C8.6	8:104395305-104396082	NOTEST	0.396377	0.227458	-0.801273	0	1	1
ENSG00000266290	ENSG00000266290	RP11-159D12.10	17:56154251-56160565	NOTEST	0.00249921	0	#NAME?	0	1	1
ENSG00000266291	ENSG00000266291	hsa-mir-3180-3	16:18496002-18497461	NOTEST	0	0	0	0	1	1
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ENSG00000266293	ENSG00000266293	AC069276.1	3:7994491-8653610	NOTEST	0	0	0	0	1	1
ENSG00000266294	ENSG00000266294	AL136380.1	1:45316449-45452282	NOTEST	0	0	0	0	1	1
ENSG00000266295	ENSG00000266295	SNORD83	HSCHR6_MHC_QBL:31486777-31504899	NOTEST	0	0	0	0	1	1
ENSG00000266296	ENSG00000266296	ARIH2P1	18:26231695-26233172	NOTEST	0	0	0	0	1	1
ENSG00000266297	ENSG00000266297	MIR744	17:11901669-12047147	NOTEST	0	0	0	0	1	1
ENSG00000266298	ENSG00000266298	RP11-463P17.3	HG1211_PATCH:47860943-47879786	NOTEST	0	0	0	0	1	1
ENSG00000266299	ENSG00000266299	MIR3118-5	21:15017095-15017171	NOTEST	0	0	0	0	1	1
ENSG00000266300	ENSG00000266300	SNORD52	HSCHR6_MHC_APD:31813741-31818898	NOTEST	0	0	0	0	1	1
ENSG00000266301	ENSG00000266301	CTGLF8P	HG1211_PATCH:46832671-46848689	NOTEST	0	0	0	0	1	1
ENSG00000266302	ENSG00000266302	RP11-219A15.1	17:16592850-16719854	NOTEST	0.0145435	0.00285348	-2.34958	0	1	1
ENSG00000266303	ENSG00000266303	MIR3186	HG271_PATCH:79369274-79440126	NOTEST	0	0	0	0	1	1

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ENSG00000266305	ENSG00000266305	MIR4518	16:30483978-30534506	NOTEST	0	0	0	0	1	1
ENSG00000266306	ENSG00000266306	CTD-2008P7.6	17:26596228-26599391	NOTEST	0	0.0173149	inf	0	1	1
ENSG00000266307	ENSG00000266307	MIR5093	16:85339831-85339931	NOTEST	0	0	0	0	1	1
ENSG00000266308	ENSG00000266308	RN7SL510P	15:76135621-76193419	NOTEST	0	0	0	0	1	1
ENSG00000266309	ENSG00000266309	AC012671.4	2:88673657-88673758	NOTEST	0	0	0	0	1	1
ENSG00000266310	ENSG00000266310	AC106899.1	2:29415639-30144432	NOTEST	0	0	0	0	1	1
ENSG00000266311	ENSG00000266311	AC007952.4	17:19067521-19077749	NOTEST	0	0	0	0	1	1
ENSG00000266312	ENSG00000266312	RP11-111H3.3	18:74327168-74350968	NOTEST	0	0.100671	inf	0	1	1
ENSG00000266313	ENSG00000266313	RP11-173M1.4	17:25660281-25675517	NOTEST	0	0	0	0	1	1
ENSG00000266315	ENSG00000266315	MIR4668	9:114659045-114697649	NOTEST	0	0	0	0	1	1
ENSG00000266316	ENSG00000266316	AC145060.1	GL000196.1:24522-24637	NOTEST	0	0	0	0	1	1
ENSG00000266317	ENSG00000266317	RN7SL703P	3:180701496-181554668	NOTEST	0	0	0	0	1	1
ENSG00000266318	ENSG00000266318	MIR5692A2	7:97592969-97593038	NOTEST	0	0	0	0	1	1
ENSG00000266319	ENSG00000266319	AL080272.1	X:141694645-141694731	NOTEST	0	0	0	0	1	1
ENSG00000266320	ENSG00000266320	MIR3909	22:35694830-35743985	NOTEST	0	0	0	0	1	1
ENSG00000266321	ENSG00000266321	MIR4293	10:13628926-14504141	NOTEST	0	0	0	0	1	1
ENSG00000266322	ENSG00000266322	RNU1-114P	HG1287_PATCH:144338464-144338630	NOTEST	0	0	0	0	1	1
ENSG00000266323	ENSG00000266323	RN7SL733P	10:88810242-88951225	NOTEST	0	0	0	0	1	1
ENSG00000266324	ENSG00000266324	MIR4663	8:124228027-124228103	NOTEST	0	0	0	0	1	1
ENSG00000266325	ENSG00000266325	MIR3665	13:78272022-78338377	NOTEST	0	0	0	0	1	1
ENSG00000266327	ENSG00000266327	MIR4503	14:37116287-37643016	NOTEST	0	0	0	0	1	1
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ENSG00000266329	ENSG00000266329	MIR4281	5:176047084-176057530	NOTEST	0	0	0	0	1	1
ENSG00000266330	ENSG00000266330	AL355353.1	6:47430586-47430652	NOTEST	0	0	0	0	1	1
ENSG00000266331	ENSG00000266331	AL662845.1	HSCHR6_MHC_COX:32824725-32871622	NOTEST	0	0	0	0	1	1
ENSG00000266332	ENSG00000266332	FCGR1A	HG1287_PATCH:150469085-150498788	NOTEST	0	0	0	0	1	1
ENSG00000266333	ENSG00000266333	AC117372.1	12:38710379-38717784	NOTEST	0	0	0	0	1	1
ENSG00000266334	ENSG00000266334	APH1A	HG1287_PATCH:150951818-150967331	NOTEST	0	0	0	0	1	1
ENSG00000266335	ENSG00000266335	RP11-25O3.1	18:49862730-49865395	NOTEST	0	0	0	0	1	1
ENSG00000266336	ENSG00000266336	AL356019.1	14:20685312-20685398	NOTEST	0	0	0	0	1	1
ENSG00000266337	ENSG00000266337	AC118282.4	4:49211390-49211465	NOTEST	0	0	0	0	1	1
ENSG00000266338	ENSG00000266338	NBPF15	HG1287_PATCH:145107800-145148089	NOTEST	0	0	0	0	1	1
ENSG00000266339	ENSG00000266339	RN7SL17P	17:19912656-20306870	NOTEST	0	0	0	0	1	1
ENSG00000266340	ENSG00000266340	RP11-848P1.4	17:29295802-29326929	NOTEST	0.0298883	0	#NAME?	0	1	1
ENSG00000266341	ENSG00000266341	RP5-890E16.4	17:46125690-46138849	NOTEST	0	0	0	0	1	1
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ENSG00000266343	ENSG00000266343	RN7SL506P	14:91336798-91691976	NOTEST	0	0	0	0	1	1
ENSG00000266344	ENSG00000266344	AL353731.1	10:75183338-75193319	NOTEST	0	0	0	0	1	1
ENSG00000266345	ENSG00000266345	RN7SL349P	22:36677326-36784063	NOTEST	0	0	0	0	1	1
ENSG00000266346	ENSG00000266346	AC019205.2	6:74078277-74161999	NOTEST	0	0	0	0	1	1
ENSG00000266347	ENSG00000266347	AC068641.1	12:89954905-90106367	NOTEST	0	0	0	0	1	1
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ENSG00000266353	ENSG00000266353	AL591471.1	9:42579906-42579973	NOTEST	0	0	0	0	1	1
ENSG00000266354	ENSG00000266354	MIR4776-2	2:213446080-214017151	NOTEST	0	0	0	0	1	1
ENSG00000266355	ENSG00000266355	AL117334.1	20:3229950-3388272	NOTEST	0	0	0	0	1	1
ENSG00000266356	ENSG00000266356	RP11-578C11.2	17:25738463-25739832	NOTEST	0	0	0	0	1	1
ENSG00000266357	ENSG00000266357	RP11-101O21.1	17:72039590-72150351	NOTEST	0	0	0	0	1	1
ENSG00000266358	ENSG00000266358	AL359771.1	1:13950396-13950497	NOTEST	0	0	0	0	1	1
ENSG00000266359	ENSG00000266359	AKR1C4	HG871_PATCH:5237653-5261139	NOTEST	0	0	0	0	1	1
ENSG00000266360	ENSG00000266360	AC017028.10	2:239969863-240324058	NOTEST	0	0	0	0	1	1
ENSG00000266361	ENSG00000266361	BX248507.1	HSCHR6_MHC_QBL:30557687-30583682	NOTEST	0	0	0	0	1	1
ENSG00000266362	ENSG00000266362	hsa-mir-877	HSCHR6_MHC_COX:30528999-30554805	NOTEST	0	0	0	0	1	1
ENSG00000266363	ENSG00000266363	AC069243.1	3:167921296-167921388	NOTEST	0	0	0	0	1	1
ENSG00000266364	ENSG00000266364	RP11-218E15.1	17:20515979-20536572	NOTEST	0	0	0	0	1	1
ENSG00000266365	ENSG00000266365	RP11-51L5.3	17:60308830-60324514	NOTEST	0	0.0155945	inf	0	1	1
ENSG00000266366	ENSG00000266366	RN7SL389P	22:21309448-21309714	NOTEST	0	0	0	0	1	1
ENSG00000266367	ENSG00000266367	AC207981.1	HSCHR21_4_CTG1_1:34757298-34861875	NOTEST	0	0	0	0	1	1
ENSG00000266368	ENSG00000266368	RP11-1096G20.5	17:11501747-11900827	NOTEST	0.0508562	0	#NAME?	0	1	1
ENSG00000266369	ENSG00000266369	RP11-344E13.4	17:20717932-20947073	NOTEST	0	0	0	0	1	1
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ENSG00000266371	ENSG00000266371	RP11-142O6.1	17:29335514-29709134	NOTEST	0	0.00799371	inf	0	1	1
ENSG00000266372	ENSG00000266372	AC092849.1	7:100081380-100081466	NOTEST	0	0	0	0	1	1
ENSG00000266373	ENSG00000266373	RP11-710M11.1	18:3496029-4455335	NOTEST	0.245211	0.025362	-3.27328	0	1	1
ENSG00000266374	ENSG00000266374	AC026512.1	15:69452922-69564556	NOTEST	0	0	0	0	1	1
ENSG00000266375	ENSG00000266375	U6	HSCHR6_MHC_QBL:31043215-31043315	NOTEST	0	0	0	0	1	1
ENSG00000266376	ENSG00000266376	AC093165.1	2:55199324-55339757	NOTEST	0	0	0	0	1	1
ENSG00000266377	ENSG00000266377	AC095064.1	4:160025329-160281321	NOTEST	0	0	0	0	1	1
ENSG00000266378	ENSG00000266378	RP11-214O1.3	17:14204399-14252721	NOTEST	0	0	0	0	1	1
ENSG00000266379	ENSG00000266379	RP11-640N20.8	17:30410197-30424084	NOTEST	0	0	0	0	1	1
ENSG00000266380	ENSG00000266380	Metazoa_SRP	HSCHR1_1_CTG31:153693803-153694099	NOTEST	0	0	0	0	1	1
ENSG00000266381	ENSG00000266381	RN7SL147P	HSCHR3_1_CTG1:119961844-11996480	NOTEST	0	0	0	0	1	1
ENSG00000266382	ENSG00000266382	MIR5703	2:228336847-228425930	NOTEST	0	0	0	0	1	1
ENSG00000266383	ENSG00000266383	MIR5002	3:123798869-124445172	NOTEST	0	0	0	0	1	1
ENSG00000266384	ENSG00000266384	MIR4646	HSCHR6_MHC_COX:31616420-31658607	NOTEST	0	0	0	0	1	1
ENSG00000266385	ENSG00000266385	RP11-227G15.8	17:30738235-30739439	NOTEST	0	0	0	0	1	1
ENSG00000266386	ENSG00000266386	RP11-196G18.3	HG1287_PATCH:150469085-150498788	NOTEST	0	0	0	0	1	1
ENSG00000266387	ENSG00000266387	AC016178.2	8:130363936-130695925	NOTEST	0	0	0	0	1	1
ENSG00000266388	ENSG00000266388	AC093430.1	1:79600817-79600911	NOTEST	0	0	0	0	1	1
ENSG00000266389	ENSG00000266389	CTB-41I6.1	17:8869212-8870387	NOTEST	0	0	0	0	1	1
ENSG00000266390	ENSG00000266390	AC027288.2	12:79257772-79897176	NOTEST	0	0	0	0	1	1
ENSG00000266391	ENSG00000266391	AC074389.1	7:1820329-1820427	NOTEST	0	0	0	0	1	1
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ENSG00000266393	ENSG00000266393	AL122019.1	1:177362422-177566844	NOTEST	0	0	0	0	1	1
ENSG00000266394	ENSG00000266394	RP11-196G18.1	HG1287_PATCH:15044071-150441125	NOTEST	0	0	0	0	1	1
ENSG00000266396	ENSG00000266396	MIR4273	3:75758793-75834734	NOTEST	0	0	0	0	1	1
ENSG00000266397	ENSG00000266397	RP11-737O24.1	18:2916991-3013313	NOTEST	0	0	0	0	1	1
ENSG00000266398	ENSG00000266398	MIR3656	11:118868851-118901616	NOTEST	0	0	0	0	1	1
ENSG00000266399	ENSG00000266399	AC027307.2	19:1553979-1554031	NOTEST	0	0	0	0	1	1
ENSG00000266400	ENSG00000266400	AC113171.1	3:67705120-67998137	NOTEST	0	0	0	0	1	1
ENSG00000266401	ENSG00000266401	RP11-874J12.4	18:3496029-4455335	NOTEST	0.0535795	0.105621	0.979149	0	1	1
ENSG00000266403	ENSG00000266403	AL161731.1	9:129480521-129480612	NOTEST	0	0	0	0	1	1
ENSG00000266404	ENSG00000266404	U85056.5	HG1032_PATCH:190979056-190984160	NOTEST	0	0	0	0	1	1
ENSG00000266405	ENSG00000266405	CBX3P2	18:2652168-2655394	NOTEST	0.0450562	0.101781	1.17567	0	1	1
ENSG00000266406	ENSG00000266406	hsa-mir-1236	HSCHR6_MHC_COX:31907415-31925080	NOTEST	0	0	0	0	1	1
ENSG00000266407	ENSG00000266407	MIR3157	10:97471535-97849995	NOTEST	0	0	0	0	1	1
ENSG00000266408	ENSG00000266408	AL122127.4	14:106324722-106324792	NOTEST	0	0	0	0	1	1
ENSG00000266409	ENSG00000266409	AC092104.5	7:7107817-7107900	NOTEST	0	0	0	0	1	1
ENSG00000266410	ENSG00000266410	Y_RNA	HSCHR6_MHC_DBB:33139274-33150126	NOTEST	0	0	0	0	1	1
ENSG00000266411	ENSG00000266411	RP11-180P8.3	17:61044177-61045910	NOTEST	0	0	0	0	1	1
ENSG00000266412	ENSG00000266412	NCOA4	HG1211_PATCH:46500535-46526162	NOTEST	0	0	0	0	1	1
ENSG00000266413	ENSG00000266413	RP11-88L24.4	2:179385909-179914813	NOTEST	0	0	0	0	1	1
ENSG00000266414	ENSG00000266414	U7	HSCHR17_1:44001605-44145324	NOTEST	0	0	0	0	1	1
ENSG00000266415	ENSG00000266415	MIR4636	5:9001885-9546187	NOTEST	0	0	0	0	1	1
ENSG00000266416	ENSG00000266416	RP1-66C13.2	17:26035136-26035164	NOTEST	0	0	0	0	1	1
ENSG00000266417	ENSG00000266417	MIR4424	1:178646883-178646969	NOTEST	0	0	0	0	1	1
ENSG00000266418	ENSG00000266418	MIR4646	HSCHR6_MHC_MANN:31668498-31859776	NOTEST	0	0	0	0	1	1
ENSG00000266419	ENSG00000266419	SNORD83	HSCHR6_MHC_DBB:31478677-31496802	NOTEST	0	0	0	0	1	1
ENSG00000266420	ENSG00000266420	RN7SL118P	X:118533022-118588441	NOTEST	0.113271	0.0887583	-0.351829	0	1	1
ENSG00000266421	ENSG00000266421	MIR4451	4:86396266-86923823	NOTEST	0	0	0	0	1	1
ENSG00000266423	ENSG00000266423	MIR3163	11:66615703-66725847	NOTEST	0	0	0	0	1	1
ENSG00000266424	ENSG00000266424	RP11-123I22.1	HSCHR18_1_CTG2_1:76265164-76266410	NOTEST	0	0	0	0	1	1
ENSG00000266425	ENSG00000266425	RN7SL343P	9:43684901-43924049	NOTEST	0	0	0	0	1	1
ENSG00000266426	ENSG00000266426	MIR4719	16:76770238-76962066	NOTEST	0	0	0	0	1	1
ENSG00000266427	ENSG00000266427	AC098784.2	19:55218007-55218077	NOTEST	0	0	0	0	1	1
ENSG00000266428	ENSG00000266428	RN7SL663P	19:38397867-38699012	NOTEST	0	0	0	0	1	1
ENSG00000266429	ENSG00000266429	AL442639.1	9:26614037-26614123	NOTEST	0	0	0	0	1	1
ENSG00000266430	ENSG00000266430	AC004520.1	7:26099958-26100058	NOTEST	0	0	0	0	1	1
ENSG00000266431	ENSG00000266431	MIR5580	14:54415144-54415202	NOTEST	0	0	0	0	1	1
ENSG00000266432	ENSG00000266432	AC008703.2	5:158952945-158953018	NOTEST	0	0	0	0	1	1
ENSG00000266433	ENSG00000266433	TBC1D3P5	17:25744715-25758649	NOTEST	0	0	0	0	1	1
ENSG00000266434	ENSG00000266434	RP5-998N21.8	HG1287_PATCH:144561207-144621191	NOTEST	0	0	0	0	1	1
ENSG00000266435	ENSG00000266435	U6	HSCHR6_MHC_APD:32295496-32350672	NOTEST	0	0	0	0	1	1
ENSG00000266436	ENSG00000266436	MIR4264	2:79384131-80875905	NOTEST	0	0	0	0	1	1
ENSG00000266437	ENSG00000266437	MIR4746	19:4402658-4457819	NOTEST	0	0	0	0	1	1
ENSG00000266439	ENSG00000266439	RN7SL493P	16:10315633-10315930	NOTEST	0	0	0	0	1	1
ENSG00000266440	ENSG00000266440	AL359542.1	X:128937263-128977885	NOTEST	0	0	0	0	1	1

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ENSG00000266442	ENSG00000266442	MSH5-SAPCD1	HSCHR6_MHC_MCF:31705288-31896594	NOTEST	0	0	0	0	1	1
ENSG00000266443	ENSG00000266443	AC099778.1	3:47581503-47581590	NOTEST	0	0	0	0	1	1
ENSG00000266444	ENSG00000266444	RN7SL480P	HG1287_PATCH:150898046-150898338	NOTEST	0	0	0	0	1	1
ENSG00000266445	ENSG00000266445	RP13-991F5.2	17:80412148-80448413	NOTEST	0.229933	0.296864	0.368589	0	1	1
ENSG00000266446	ENSG00000266446	RP11-149I2.4	9:21802541-22121096	NOTEST	0.105751	0.131585	0.315323	0	1	1
ENSG00000266447	ENSG00000266447	AC046143.2	3:194304739-194393206	NOTEST	0	0	0	0	1	1
ENSG00000266448	ENSG00000266448	RP11-805L22.1	17:30036586-30036878	NOTEST	0	0	0	0	1	1
ENSG00000266449	ENSG00000266449	MIR3713	15:76640525-77197785	NOTEST	0	0	0	0	1	1
ENSG00000266450	ENSG00000266450	CTD-2015H3.2	18:1655177-1779956	NOTEST	0	0	0	0	1	1
ENSG00000266451	ENSG00000266451	AP003385.1	11:67501991-67502079	NOTEST	0	0	0	0	1	1
ENSG00000266452	ENSG00000266452	RN7SL590P	8:126456806-126457060	NOTEST	0	0	0	0	1	1
ENSG00000266453	ENSG00000266453	RN7SL142P	7:157098486-157098765	NOTEST	0	0	0	0	1	1
ENSG00000266454	ENSG00000266454	MIR3179-3	16:18505750-18505834	NOTEST	0	0	0	0	1	1
ENSG00000266455	ENSG00000266455	RN7SL765P	19:36155397-36155724	NOTEST	0	0	0	0	1	1
ENSG00000266456	ENSG00000266456	RP11-806L2.2	18:596987-712676	NOTEST	0.0676221	0.181919	1.42773	0	1	1
ENSG00000266457	ENSG00000266457	AC026318.1	3:47626761-47823596	NOTEST	0	0	0	0	1	1
ENSG00000266458	ENSG00000266458	hsa-mir-4259	1:159796539-159869953	NOTEST	0	0	0	0	1	1
ENSG00000266459	ENSG00000266459	MIR4724	17:29718641-29865236	NOTEST	0	0	0	0	1	1
ENSG00000266460	ENSG00000266460	RP11-173L6.1	18:73556879-73580207	NOTEST	0	0	0	0	1	1
ENSG00000266461	ENSG00000266461	MIR2392	14:101245746-101327368	NOTEST	0	0	0	0	1	1
ENSG00000266462	ENSG00000266462	AC010327.1	19:55738006-55770363	NOTEST	0	0	0	0	1	1
ENSG00000266463	ENSG00000266463	MIR3196	20:61867234-61871859	NOTEST	0	0	0	0	1	1
ENSG00000266464	ENSG00000266464	Y_RNA	HSCHR6_MHC_MCF:33331731-33342580	NOTEST	0	0	0	0	1	1
ENSG00000266465	ENSG00000266465	AC025165.1	12:58156116-58212487	NOTEST	0	0	0	0	1	1
ENSG00000266466	ENSG00000266466	RP11-822E23.2	17:21428050-21477781	NOTEST	0	0.0131848	inf	0	1	1
ENSG00000266467	ENSG00000266467	RN7SL220P	10:69681664-69835105	NOTEST	0	0	0	0	1	1
ENSG00000266468	ENSG00000266468	AL031284.1	1:25568727-25756683	NOTEST	0	0	0	0	1	1
ENSG00000266470	ENSG00000266470	RP11-856M7.8	18:10632234-10632393	NOTEST	0	0	0	0	1	1
ENSG00000266472	ENSG00000266472	AC242988.1	HG1287_PATCH:150980263-150994799	NOTEST	0	0	0	0	1	1
ENSG00000266473	ENSG00000266473	RP11-401F2.3	17:65066553-65242105	NOTEST	0.138953	0.0857677	-0.696085	0	1	1
ENSG00000266474	ENSG00000266474	RP11-315I20.3	HG1287_PATCH:146577622-146596604	NOTEST	0	0	0	0	1	1
ENSG00000266475	ENSG00000266475	AC106753.1	5:137150021-137387650	NOTEST	0	0	0	0	1	1
ENSG00000266476	ENSG00000266476	AC084262.3	8:29180780-29180873	NOTEST	0	0	0	0	1	1
ENSG00000266477	ENSG00000266477	RN7SL616P	5:68773298-69006341	NOTEST	0	0	0	0	1	1
ENSG00000266478	ENSG00000266478	MIR5197	5:142985192-143208337	NOTEST	0	0	0	0	1	1
ENSG00000266479	ENSG00000266479	CTD-2515C13.1	18:26836781-26837025	NOTEST	0	0	0	0	1	1
ENSG00000266480	ENSG00000266480	LINC00869	HG1287_PATCH:144476424-144478755	NOTEST	0	0	0	0	1	1
ENSG00000266481	ENSG00000266481	AC092174.1	7:39017597-39532694	NOTEST	0	0	0	0	1	1
ENSG00000266482	ENSG00000266482	AC023157.1	12:31800093-31882108	NOTEST	0	0	0	0	1	1
ENSG00000266483	ENSG00000266483	AC010311.1	19:7112265-7294045	NOTEST	0	0	0	0	1	1
ENSG00000266484	ENSG00000266484	AC005088.2	HG115_PATCH:101459218-101927238	NOTEST	0	0	0	0	1	1
ENSG00000266485	ENSG00000266485	AL365214.1	6:112682638-112684039	NOTEST	0	0	0	0	1	1
ENSG00000266486	ENSG00000266486	FAM106CP	17:16592850-16719854	NOTEST	0	0	0	0	1	1
ENSG00000266487	ENSG00000266487	RN7SL855P	7:63071822-63072082	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000266488	ENSG00000266488	RP11-758G22.2	HSCHR3_1_CTG1:119011466-11934974	NOTEST	0	0	0	0	1	1
ENSG00000266489	ENSG00000266489	RP11-178F10.3	18:22096846-22097970	NOTEST	0	0	0	0	1	1
ENSG00000266491	ENSG00000266491	AC109335.1	8:67876333-68255912	NOTEST	0	0	0	0	1	1
ENSG00000266492	ENSG00000266492	AC092122.2	16:9407763-9407831	NOTEST	0	0	0	0	1	1
ENSG00000266493	ENSG00000266493	AC116533.3	11:16799841-17074583	NOTEST	0	0	0	0	1	1
ENSG00000266494	ENSG00000266494	MIR4641	6:41462590-41570122	NOTEST	0	0	0	0	1	1
ENSG00000266495	ENSG00000266495	RP11-17J14.2	18:20714527-21017925	NOTEST	0.168959	0.267752	0.664222	0	1	1
ENSG00000266496	ENSG00000266496	AC131951.1	4:44175925-44450824	NOTEST	0	0	0	0	1	1
ENSG00000266497	ENSG00000266497	RP11-995C19.2	17:44581311-44586705	NOTEST	0	0	0	0	1	1
ENSG00000266498	ENSG00000266498	RP11-45M22.5	17:16945858-17140502	NOTEST	0.110771	0.0224592	-2.30221	0	1	1
ENSG00000266499	ENSG00000266499	AC008536.1	5:112043194-112258236	NOTEST	0	0	0	0	1	1
ENSG00000266500	ENSG00000266500	AL138498.1	14:42421678-42421763	NOTEST	0	0	0	0	1	1
ENSG00000266502	ENSG00000266502	MIR5681A	8:75460777-75460852	NOTEST	0	0	0	0	1	1
ENSG00000266503	ENSG00000266503	RN7SL162P	22:28247656-29075853	NOTEST	0	0	0	0	1	1
ENSG00000266504	ENSG00000266504	RP11-798G7.4	17:43578684-43640596	NOTEST	0	0	0	0	1	1
ENSG00000266505	ENSG00000266505	RP11-629E24.2	13:30596157-30597937	NOTEST	0.00923017	0	#NAME?	0	1	1
ENSG00000266507	ENSG00000266507	MIR4479	9:139776363-139821059	NOTEST	0	0	0	0	1	1
ENSG00000266508	ENSG00000266508	MIR3201	22:48670175-48670227	NOTEST	0	0	0	0	1	1
ENSG00000266509	ENSG00000266509	MIR3934	6:33588141-33679504	NOTEST	0	0	0	0	1	1
ENSG00000266510	ENSG00000266510	AC007435.1	2:175899244-175899318	NOTEST	0	0	0	0	1	1
ENSG00000266511	ENSG00000266511	AL590683.2	1:24606256-24606345	NOTEST	0	0	0	0	1	1
ENSG00000266512	ENSG00000266512	AC008166.1	2:154728425-155313950	NOTEST	0	0	0	0	1	1
ENSG00000266513	ENSG00000266513	RP11-874J12.3	18:3496029-4455335	NOTEST	0	0	0	0	1	1
ENSG00000266514	ENSG00000266514	MIR3689F	9:137742587-137742653	NOTEST	0	0	0	0	1	1
ENSG00000266515	ENSG00000266515	MIR4452	4:86936275-87515284	NOTEST	0	0	0	0	1	1
ENSG00000266516	ENSG00000266516	RP11-303K3.1	HG1308_PATCH:130126045-130351086	NOTEST	0	0	0	0	1	1
ENSG00000266517	ENSG00000266517	MIR4715	15:25922419-26110317	NOTEST	0	0	0	0	1	1
ENSG00000266518	ENSG00000266518	MIR4268	2:220771222-220771286	NOTEST	0	0	0	0	1	1
ENSG00000266519	ENSG00000266519	MCCD1P1	HG1322_PATCH:29869402-29870265	NOTEST	0	0	0	0	1	1
ENSG00000266520	ENSG00000266520	RAC1P1	18:22265735-22266315	NOTEST	0	0	0	0	1	1
ENSG00000266521	ENSG00000266521	RP11-650P15.1	18:29076607-29077158	NOTEST	0	0	0	0	1	1
ENSG00000266522	ENSG00000266522	RP11-805F19.4	18:15003973-15006351	NOTEST	0	0	0	0	1	1
ENSG00000266523	ENSG00000266523	Y_RNA	HSCHR6_MHC_MCF:30773971-30787802	NOTEST	0	0	0	0	1	1
ENSG00000266524	ENSG00000266524	GDF10	HG1211_PATCH:47795833-47808995	NOTEST	0	0	0	0	1	1
ENSG00000266525	ENSG00000266525	MIR4650-1	7:66452663-66704501	NOTEST	0	0	0	0	1	1
ENSG00000266526	ENSG00000266526	AC090720.1	11:40135752-41481323	NOTEST	0	0	0	0	1	1
ENSG00000266527	ENSG00000266527	RP11-138P22.1	17:26083791-26221778	NOTEST	0	0	0	0	1	1
ENSG00000266528	ENSG00000266528	Metazoa_SRP	HSCHR5_1_CTG1:68773019-68852251	NOTEST	0	0	0	0	1	1
ENSG00000266529	ENSG00000266529	RP11-846F4.1	17:22018942-22020035	NOTEST	0	0	0	0	1	1
ENSG00000266530	ENSG00000266530	MIR4318	18:35237097-35237178	NOTEST	0	0	0	0	1	1
ENSG00000266531	ENSG00000266531	MIR4706	14:65381078-65569413	NOTEST	0	0	0	0	1	1
ENSG00000266532	ENSG00000266532	RN7SL235P	1:92404825-92405131	NOTEST	0	0	0	0	1	1
ENSG00000266533	ENSG00000266533	MIR3619	22:46445357-46509808	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000266534	ENSG00000266534	AL162571.1	13:75783113-75783173	NOTEST	0	0	0	0	1	1
ENSG00000266535	ENSG00000266535	RP11-40A13.1	17:31340104-32522956	NOTEST	0	0	0	0	1	1
ENSG00000266536	ENSG00000266536	RN7SL126P	2:85788684-85809154	NOTEST	0	0	0	0	1	1
ENSG00000266537	ENSG00000266537	CTD-2510F5.2	17:57232859-57292608	NOTEST	0	0.018435	inf	0	1	1
ENSG00000266538	ENSG00000266538	RP11-385D13.3	17:15339331-15466909	NOTEST	0.389828	0.0724732	-2.42732	0	1	1
ENSG00000266539	ENSG00000266539	AC078889.1	12:66582658-66651214	NOTEST	0	0	0	0	1	1
ENSG00000266540	ENSG00000266540	RN7SL772P	11:47227395-47227672	NOTEST	0	0	0	0	1	1
ENSG00000266541	ENSG00000266541	RP11-881L2.1	18:9546788-9615238	NOTEST	0	0	0	0	1	1
ENSG00000266542	ENSG00000266542	MIR5572	15:80696691-80890278	NOTEST	0	0	0	0	1	1
ENSG00000266543	ENSG00000266543	AC027811.1	15:79603403-79704334	NOTEST	0	0	0	0	1	1
ENSG00000266544	ENSG00000266544	RN7SL662P	18:15075443-15122766	NOTEST	0	0	0	0	1	1
ENSG00000266545	ENSG00000266545	MIR5701-1	15:21145580-21145662	NOTEST	0	0	0	0	1	1
ENSG00000266546	ENSG00000266546	AC137674.2	3:30180450-30180524	NOTEST	0	0	0	0	1	1
ENSG00000266547	ENSG00000266547	AL161645.1	10:135192694-135382916	NOTEST	0	0	0	0	1	1
ENSG00000266548	ENSG00000266548	Y_RNA	HSCHR6_MHC_APD:31475775-31475877	NOTEST	0	0	0	0	1	1
ENSG00000266549	ENSG00000266549	RP11-526I8.2	18:24034873-24770662	NOTEST	0	0	0	0	1	1
ENSG00000266550	ENSG00000266550	AP002958.1	11:78363875-79151992	NOTEST	0	0	0	0	1	1
ENSG00000266551	ENSG00000266551	RN7SL857P	1:24829386-24882515	NOTEST	0	0	0	0	1	1
ENSG00000266552	ENSG00000266552	AL356020.1	14:53510685-53620000	NOTEST	0	0	0	0	1	1
ENSG00000266553	ENSG00000266553	RN7SL356P	14:77433862-77434108	NOTEST	0	0	0	0	1	1
ENSG00000266555	ENSG00000266555	MIR3145	6:138723721-139018425	NOTEST	0	0	0	0	1	1
ENSG00000266556	ENSG00000266556	AL137251.1	6:130686878-130764208	NOTEST	0	0	0	0	1	1
ENSG00000266557	ENSG00000266557	CR759960.1	HSCHR6_MHC_APD:29993431-29993564	NOTEST	0	0	0	0	1	1
ENSG00000266558	ENSG00000266558	CT867976.5	GL000230.1:33747-33830	NOTEST	0	0	0	0	1	1
ENSG00000266559	ENSG00000266559	MIR4530	19:39900262-39900318	NOTEST	0	0	0	0	1	1
ENSG00000266560	ENSG00000266560	RP11-1007I13.4	X:151282525-151307033	NOTEST	0	0	0	0	1	1
ENSG00000266561	ENSG00000266561	CTD-2200P10.3	17:56597197-56769416	NOTEST	0	0	0	0	1	1
ENSG00000266562	ENSG00000266562	RPRD2	HG1287_PATCH:151049505-151162981	NOTEST	0	0	0	0	1	1
ENSG00000266563	ENSG00000266563	RP11-64J19.1	17:21163279-21163813	NOTEST	0	0	0	0	1	1
ENSG00000266564	ENSG00000266564	MIR4418	1:22592731-22592793	NOTEST	0	0	0	0	1	1
ENSG00000266566	ENSG00000266566	AC009994.2	17:62495733-62658186	NOTEST	0	0	0	0	1	1
ENSG00000266567	ENSG00000266567	MIR3618	22:20067754-20114878	NOTEST	0	0	0	0	1	1
ENSG00000266568	ENSG00000266568	AL049610.1	X:102862378-102885881	NOTEST	0	0	0	0	1	1
ENSG00000266569	ENSG00000266569	RN7SL377P	7:72023728-72298777	NOTEST	0	0	0	0	1	1
ENSG00000266570	ENSG00000266570	MIR5579	11:78363875-79151992	NOTEST	0	0	0	0	1	1
ENSG00000266571	ENSG00000266571	Metazoa_SRP	HG185_PATCH:39981432-40004636	NOTEST	0	0	0	0	1	1
ENSG00000266572	ENSG00000266572	AC016831.5	HG1308_PATCH:130486521-130487165	NOTEST	0	0	0	0	1	1
ENSG00000266573	ENSG00000266573	RP11-449D8.5	18:22305744-22509040	NOTEST	0	0	0	0	1	1
ENSG00000266574	ENSG00000266574	hsa-mir-219a-1	HSCHR6_MHC_MANN:33329534-33329644	NOTEST	0	0	0	0	1	1
ENSG00000266575	ENSG00000266575	RP11-672L10.4	18:832238-832470	NOTEST	0	0	0	0	1	1
ENSG00000266576	ENSG00000266576	MARK2P14	HSCHR3_1_CTG1:119499211-11955708	NOTEST	0	0	0	0	1	1
ENSG00000266577	ENSG00000266577	RN7SL830P	2:85759466-85759749	NOTEST	0	0	0	0	1	1
ENSG00000266579	ENSG00000266579	RP1-71H19.2	6:57179602-57513375	NOTEST	0	0	0	0	1	1
ENSG00000266580	ENSG00000266580	MIR4254	1:32192717-32230494	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000266581	ENSG00000266581	MIR3166	11:87909669-87909761	NOTEST	0	0	0	0	1	1
ENSG00000266582	ENSG00000266582	MIR4527	18:44812095-45120914	NOTEST	0	0	0	0	1	1
ENSG00000266583	ENSG00000266583	MIR4478	9:124882360-124882446	NOTEST	0	0	0	0	1	1
ENSG00000266584	ENSG00000266584	AL355149.1	1:16875145-16879026	NOTEST	0	0	0	0	1	1
ENSG00000266585	ENSG00000266585	RN7SL248P	HG1211_PATCH:47073664-47147473	NOTEST	0	0	0	0	1	1
ENSG00000266586	ENSG00000266586	CTD-2382H12.2	18:76668628-76678993	NOTEST	0	0	0	0	1	1
ENSG00000266587	ENSG00000266587	AC027320.1	5:118593034-118593132	NOTEST	0	0	0	0	1	1
ENSG00000266588	ENSG00000266588	RP1-56K13.5	17:37159500-37169285	NOTEST	0	0	0	0	1	1
ENSG00000266589	ENSG00000266589	MIR4512	15:66679154-66790151	NOTEST	0	0	0	0	1	1
ENSG00000266590	ENSG00000266590	AC090692.1	11:35881798-35883048	NOTEST	0	0	0	0	1	1
ENSG00000266591	ENSG00000266591	AC022537.1	10:52750944-54073888	NOTEST	0	0	0	0	1	1
ENSG00000266592	ENSG00000266592	AKR1C1	HG871_PATCH:4934795-5025475	NOTEST	0	0	0	0	1	1
ENSG00000266593	ENSG00000266593	MIR4713	15:51329684-51630807	NOTEST	0	0	0	0	1	1
ENSG00000266594	ENSG00000266594	MIR4766	22:41165633-41215403	NOTEST	0	0	0	0	1	1
ENSG00000266595	ENSG00000266595	AL133269.1	6:153177800-153177879	NOTEST	0	0	0	0	1	1
ENSG00000266596	ENSG00000266596	AC011841.10	GL000205.1:139015-139098	NOTEST	0	0	0	0	1	1
ENSG00000266597	ENSG00000266597	AL928742.2	14:106057406-106057466	NOTEST	0	0	0	0	1	1
ENSG00000266598	ENSG00000266598	RP11-583F2.5	17:63006832-63052957	NOTEST	0	0	0	0	1	1
ENSG00000266599	ENSG00000266599	RP11-466A19.3	17:30819539-31205655	NOTEST	0	0	0	0	1	1
ENSG00000266600	ENSG00000266600	BX927138.1	HSCHR6_MHC_MANN:33056219-33103106	NOTEST	0	0	0	0	1	1
ENSG00000266601	ENSG00000266601	RP11-6N17.3	17:45973515-46018776	NOTEST	0	0.0646294	inf	0	1	1
ENSG00000266602	ENSG00000266602	RP11-476K15.1	18:1509183-1647098	NOTEST	0	0	0	0	1	1
ENSG00000266603	ENSG00000266603	AL591856.7	GL000224.1:126780-126862	NOTEST	0	0	0	0	1	1
ENSG00000266604	ENSG00000266604	RP11-856M7.6	18:10612300-10626350	NOTEST	0	0	0	0	1	1
ENSG00000266605	ENSG00000266605	LONRF2P1	18:14450214-14450882	NOTEST	0	0	0	0	1	1
ENSG00000266606	ENSG00000266606	AP001010.1	18:13663345-13764557	NOTEST	0	0	0	0	1	1
ENSG00000266607	ENSG00000266607	PGM5	HG962_PATCH:70921452-71114201	NOTEST	0	0	0	0	1	1
ENSG00000266608	ENSG00000266608	AL445531.1	9:100461203-100463016	NOTEST	0	0	0	0	1	1
ENSG00000266609	ENSG00000266609	AC078899.8	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000266610	ENSG00000266610	RN7SL176P	12:100550134-100660857	NOTEST	0	0	0	0	1	1
ENSG00000266611	ENSG00000266611	MIR4703	13:52126724-52126803	NOTEST	0	0	0	0	1	1
ENSG00000266612	ENSG00000266612	hsa-mir-1236	HSCHR6_MHC_MCF:31996310-32013975	NOTEST	0	0	0	0	1	1
ENSG00000266613	ENSG00000266613	RFWD2P1	18:8412126-8414302	NOTEST	0	0.0115104	inf	0	1	1
ENSG00000266614	ENSG00000266614	RP11-94B19.4	18:73971120-73972069	NOTEST	0	0	0	0	1	1
ENSG00000266615	ENSG00000266615	5S_rRNA	HSCHR6_MHC_DBB:31981893-32071805	NOTEST	0	0	0	0	1	1
ENSG00000266616	ENSG00000266616	AP003558.1	11:98891682-100229616	NOTEST	0	0	0	0	1	1
ENSG00000266617	ENSG00000266617	MIR3692	6:157802164-158099178	NOTEST	0	0	0	0	1	1
ENSG00000266618	ENSG00000266618	MIR4742	1:224572844-224928251	NOTEST	0	0	0	0	1	1
ENSG00000266619	ENSG00000266619	MIR4642	6:44355261-44418163	NOTEST	0	0	0	0	1	1
ENSG00000266620	ENSG00000266620	MIR5001	2:233412778-233547491	NOTEST	0	0	0	0	1	1
ENSG00000266621	ENSG00000266621	AC104841.1	2:242166678-242293442	NOTEST	0	0	0	0	1	1
ENSG00000266622	ENSG00000266622	RP11-561O23.8	HG962_PATCH:70843566-70844228	NOTEST	0	0	0	0	1	1
ENSG00000266624	ENSG00000266624	AC233992.1	HG243_PATCH:145428003-145464191	NOTEST	0	0	0	0	1	1
ENSG00000266625	ENSG00000266625	AC084859.1	11:12984056-13011095	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000266626	ENSG00000266626	U6	HSCHR6_MHC_SSTO:31044939-31045039	NOTEST	0	0	0	0	1	1
ENSG00000266627	ENSG00000266627	RN7SL202P	19:3879861-3928077	NOTEST	0	0	0	0	1	1
ENSG00000266628	ENSG00000266628	RN7SL137P	14:77801363-77857840	NOTEST	0	0	0	0	1	1
ENSG00000266629	ENSG00000266629	MIR3656	HG299_PATCH:118868851-118901597	NOTEST	0	0	0	0	1	1
ENSG00000266630	ENSG00000266630	AC022716.1	8:21407508-21407595	NOTEST	0	0	0	0	1	1
ENSG00000266631	ENSG00000266631	AC006116.1	19:56905024-56947404	NOTEST	0	0	0	0	1	1
ENSG00000266632	ENSG00000266632	MIR4726	17:36858704-36886056	NOTEST	0	0	0	0	1	1
ENSG00000266633	ENSG00000266633	AC006432.1	12:9620147-9728864	NOTEST	0	0	0	0	1	1
ENSG00000266634	ENSG00000266634	MIR3972	1:17575592-17610728	NOTEST	0	0	0	0	1	1
ENSG00000266635	ENSG00000266635	AC096887.1	3:52937587-53164478	NOTEST	0	0	0	0	1	1
ENSG00000266636	ENSG00000266636	AC090340.1	18:55102916-55158529	NOTEST	0	0	0	0	1	1
ENSG00000266637	ENSG00000266637	AC145124.1	8:12036205-12051642	NOTEST	0	0	0	0	1	1
ENSG00000266638	ENSG00000266638	AC129492.1	17:8090492-8090577	NOTEST	0	0	0	0	1	1
ENSG00000266639	ENSG00000266639	RP11-666A1.3	HG1287_PATCH:145104537-145105671	NOTEST	0	0	0	0	1	1
ENSG00000266640	ENSG00000266640	MIR4754	19:58897766-58906173	NOTEST	0	0	0	0	1	1
ENSG00000266641	ENSG00000266641	MAPKAPK2	HG1293_PATCH:206748504-206797844	NOTEST	0	0	0	0	1	1
ENSG00000266643	ENSG00000266643	MIR3677	16:2303116-2323419	NOTEST	0	0	0	0	1	1
ENSG00000266644	ENSG00000266644	RP11-927P21.2	17:62850429-62915598	NOTEST	0	0	0	0	1	1
ENSG00000266645	ENSG00000266645	MIR4299	11:11678197-11678269	NOTEST	0	0	0	0	1	1
ENSG00000266646	ENSG00000266646	SNORD83	HSCHR6_MHC_QBL:31486777-31504899	NOTEST	0	0	0	0	1	1
ENSG00000266647	ENSG00000266647	RP11-51L5.4	17:60337994-60339297	NOTEST	0	0	0	0	1	1
ENSG00000266648	ENSG00000266648	RP11-112H10.6	17:56497527-56565745	NOTEST	0	0	0	0	1	1
ENSG00000266649	ENSG00000266649	MIR3126	2:69240309-69476459	NOTEST	0	0	0	0	1	1
ENSG00000266650	ENSG00000266650	AL357519.2	6:113924116-113924227	NOTEST	0	0	0	0	1	1
ENSG00000266651	ENSG00000266651	RP11-138I1.3	17:16342135-16395467	NOTEST	0.220071	0.51158	1.21699	0	1	1
ENSG00000266652	ENSG00000266652	AC107025.1	3:84545726-84545814	NOTEST	0	0	0	0	1	1
ENSG00000266653	ENSG00000266653	5S_rRNA	HSCHR6_MHC_APD:32052786-32065237	NOTEST	0	0	0	0	1	1
ENSG00000266654	ENSG00000266654	RP11-1376P16.1	17:80059335-80170706	NOTEST	0	0	0	0	1	1
ENSG00000266655	ENSG00000266655	MIR3908	12:124020955-124021081	NOTEST	0	0	0	0	1	1
ENSG00000266656	ENSG00000266656	AC104066.1	4:53588784-53617807	NOTEST	0	0	0	0	1	1
ENSG00000266657	ENSG00000266657	AL583842.3	1:142618768-142729975	NOTEST	0	0	0	0	1	1
ENSG00000266659	ENSG00000266659	SRGAP2C	HG1292_PATCH:121902778-122005752	NOTEST	0	0	0	0	1	1
ENSG00000266660	ENSG00000266660	U6	HSCHR6_MHC_MANN:32299913-32391764	NOTEST	0	0	0	0	1	1
ENSG00000266662	ENSG00000266662	FSCN2	HG271_PATCH:79502195-79510930	NOTEST	0	0	0	0	1	1
ENSG00000266663	ENSG00000266663	MIR3169	13:61773931-61774014	NOTEST	0	0	0	0	1	1
ENSG00000266664	ENSG00000266664	RP11-160E2.21	17:19030781-19062489	NOTEST	0	0	0	0	1	1
ENSG00000266665	ENSG00000266665	MIR4739	17:77680984-77681058	NOTEST	0	0	0	0	1	1
ENSG00000266666	ENSG00000266666	MIR4325	20:55896557-55896647	NOTEST	0	0	0	0	1	1
ENSG00000266667	ENSG00000266667	RP11-849N15.4	17:15283180-15321195	NOTEST	0	0	0	0	1	1
ENSG00000266668	ENSG00000266668	MIR5692C2	7:97593716-97593793	NOTEST	0	0	0	0	1	1
ENSG00000266669	ENSG00000266669	AC097452.1	4:12014970-12015065	NOTEST	0	0	0	0	1	1
ENSG00000266670	ENSG00000266670	RN7SL637P	3:185699824-185700083	NOTEST	0	0	0	0	1	1
ENSG00000266671	ENSG00000266671	AC113342.1	5:171469076-171615390	NOTEST	0	0	0	0	1	1
ENSG00000266672	ENSG00000266672	SNORD33	HSCHR6_MHC_COX:29519994-29597568	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000266673	ENSG00000266673	RP11-822E23.3	17:21428050-21477781	NOTEST	0	0	0	0	1	1
ENSG00000266675	ENSG00000266675	AL606923.1	6:69203330-69203418	NOTEST	0	0	0	0	1	1
ENSG00000266676	ENSG00000266676	MIR4297	10:131633546-131762105	NOTEST	0	0	0	0	1	1
ENSG00000266677	ENSG00000266677	RP11-258F1.1	17:18012019-18113268	NOTEST	0.0148665	0.0194788	0.389841	0	1	1
ENSG00000266678	ENSG00000266678	AL139151.1	1:29758992-29759074	NOTEST	0	0	0	0	1	1
ENSG00000266681	ENSG00000266681	RP11-301M17.1	HG1287_PATCH:14893258-148933100	NOTEST	0	0	0	0	1	1
ENSG00000266682	ENSG00000266682	AL590558.1	6:63692988-63693075	NOTEST	0	0	0	0	1	1
ENSG00000266683	ENSG00000266683	AL358354.1	1:180514967-180515067	NOTEST	0	0	0	0	1	1
ENSG00000266684	ENSG00000266684	AL117337.1	10:38238499-38265561	NOTEST	0	0	0	0	1	1
ENSG00000266685	ENSG00000266685	AC139453.1	3:75418409-75418497	NOTEST	0	0	0	0	1	1
ENSG00000266686	ENSG00000266686	RNU1-122P	HG1287_PATCH:149015413-149031051	NOTEST	0	0	0	0	1	1
ENSG00000266687	ENSG00000266687	AL356261.1	1:5922870-6161253	NOTEST	0	0	0	0	1	1
ENSG00000266688	ENSG00000266688	AC079398.1	7:70597154-71178585	NOTEST	0	0	0	0	1	1
ENSG00000266689	ENSG00000266689	U1	HSCHR6_MHC_QBL:32478739-32478886	NOTEST	0	0	0	0	1	1
ENSG00000266690	ENSG00000266690	MIR4274	4:7194264-7744554	NOTEST	0	0	0	0	1	1
ENSG00000266691	ENSG00000266691	RP11-1109M24.15	17:21793030-21814739	NOTEST	0.0118624	0.08312	2.8088	0	1	1
ENSG00000266692	ENSG00000266692	snoZ6	21:45770045-45862964	NOTEST	0	0	0	0	1	1
ENSG00000266693	ENSG00000266693	OR4K8P	18:14613135-14614183	NOTEST	0	0	0	0	1	1
ENSG00000266694	ENSG00000266694	RN7SL626P	19:5409468-5409766	NOTEST	0	0	0	0	1	1
ENSG00000266695	ENSG00000266695	AC090958.5	HSCHR3_1_CTG1:11949921-11955708	NOTEST	0	0	0	0	1	1
ENSG00000266696	ENSG00000266696	RP11-30L3.2	18:46550072-46987717	NOTEST	0	0	0	0	1	1
ENSG00000266697	ENSG00000266697	AC105339.2	15:83394624-83407656	NOTEST	0	0	0	0	1	1
ENSG00000266698	ENSG00000266698	MIR3945	4:185765738-185776905	NOTEST	0	0	0	0	1	1
ENSG00000266699	ENSG00000266699	AL512655.1	13:55380001-55380092	NOTEST	0	0	0	0	1	1
ENSG00000266700	ENSG00000266700	AL139396.1	X:53122891-53196196	NOTEST	0	0	0	0	1	1
ENSG00000266701	ENSG00000266701	AC005702.4	17:58119906-58119988	NOTEST	0	0	0	0	1	1
ENSG00000266702	ENSG00000266702	AL732442.1	HSCHR6_MHC_COX:30604662-30630683	NOTEST	0	0	0	0	1	1
ENSG00000266703	ENSG00000266703	MIR4490	11:89984399-90648220	NOTEST	0	0	0	0	1	1
ENSG00000266704	ENSG00000266704	MIR4498	12:120565006-120632513	NOTEST	0	0	0	0	1	1
ENSG00000266705	ENSG00000266705	MIR4437	2:181831974-182264286	NOTEST	0	0	0	0	1	1
ENSG00000266706	ENSG00000266706	AL122127.5	14:106323741-106323801	NOTEST	0	0	0	0	1	1
ENSG00000266707	ENSG00000266707	PSMD7P1	17:64193810-64194356	NOTEST	0	0	0	0	1	1
ENSG00000266708	ENSG00000266708	RP11-661O13.1	18:8609442-8639379	NOTEST	0	0.107256	inf	0	1	1
ENSG00000266709	ENSG00000266709	RP11-214O1.2	17:14204399-14252721	NOTEST	0	0	0	0	1	1
ENSG00000266710	ENSG00000266710	RN7SL48P	X:18908413-19002716	NOTEST	0	0	0	0	1	1
ENSG00000266711	ENSG00000266711	RP11-398J5.1	17:77085426-77613550	NOTEST	0	0	0	0	1	1
ENSG00000266712	ENSG00000266712	hsa-mir-3149	8:77879003-77879086	NOTEST	0	0	0	0	1	1
ENSG00000266713	ENSG00000266713	AC009695.1	8:21351538-21351627	NOTEST	0	0	0	0	1	1
ENSG00000266715	ENSG00000266715	MIR5090	7:102105375-102119354	NOTEST	0	0	0	0	1	1
ENSG00000266716	ENSG00000266716	Y_RNA	HSCHR6_MHC_SSTO:31551175-31661153	NOTEST	0	0	0	0	1	1
ENSG00000266717	ENSG00000266717	RP11-855A2.3	17:65821639-65980494	NOTEST	0.0507944	0.224084	2.1413	0	1	1
ENSG00000266718	ENSG00000266718	RP11-466A19.1	17:30819539-31205655	NOTEST	0.0491572	0.143368	1.54425	0	1	1
ENSG00000266719	ENSG00000266719	MIR4676	10:74451888-74647452	NOTEST	0	0	0	0	1	1
ENSG00000266720	ENSG00000266720	RN7SL14P	20:18239199-18239495	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000266721	ENSG00000266721	MIR5695	19:13031133-13031218	NOTEST	0	0	0	0	1	1
ENSG00000266722	ENSG00000266722	MIR3940	19:6413358-6424805	NOTEST	0	0	0	0	1	1
ENSG00000266723	ENSG00000266723	RP11-533N14.3	HG1287_PATCH:14838420-148385750	NOTEST	0	0	0	0	1	1
ENSG00000266724	ENSG00000266724	AC108721.2	12:59921839-59921922	NOTEST	0	0	0	0	1	1
ENSG00000266726	ENSG00000266726	5S_rRNA	HSCHR6_MHC_MCF:32082522-32172461	NOTEST	0	0	0	0	1	1
ENSG00000266727	ENSG00000266727	AC004824.1	1:17733255-17766220	NOTEST	0	0	0	0	1	1
ENSG00000266728	ENSG00000266728	AC015688.3	17:25783669-25976586	NOTEST	0.0610233	0.0702409	0.202951	0	1	1
ENSG00000266729	ENSG00000266729	RP11-534N16.1	18:28898051-29006951	NOTEST	0.210616	0.0749679	-1.49027	0	1	1
ENSG00000266730	ENSG00000266730	RN7SL773P	3:195647714-195648000	NOTEST	0	0	0	0	1	1
ENSG00000266731	ENSG00000266731	AL732314.1	X:425315-425416	NOTEST	0	0	0	0	1	1
ENSG00000266732	ENSG00000266732	AL359922.1	9:21802541-22121096	NOTEST	0	0	0	0	1	1
ENSG00000266733	ENSG00000266733	TBC1D29	17:28880714-28890511	NOTEST	0	0.00919061	inf	0	1	1
ENSG00000266734	ENSG00000266734	AP003471.3	8:105342551-105479281	NOTEST	0	0	0	0	1	1
ENSG00000266735	ENSG00000266735	RNU6-1226P	HG1304_PATCH:11243006-112671296	NOTEST	0	0	0	0	1	1
ENSG00000266736	ENSG00000266736	RP11-260A9.4	17:25346552-25374960	NOTEST	0	0	0	0	1	1
ENSG00000266737	ENSG00000266737	MIR4691	11:67798083-67804111	NOTEST	0	0	0	0	1	1
ENSG00000266738	ENSG00000266738	MIR4757	2:19548189-19548266	NOTEST	0	0	0	0	1	1
ENSG00000266739	ENSG00000266739	AL138796.1	1:144836156-145076186	NOTEST	0	0	0	0	1	1
ENSG00000266740	ENSG00000266740	MIR4708	14:65801834-65801901	NOTEST	0	0	0	0	1	1
ENSG00000266741	ENSG00000266741	POLR3GL	HG1287_PATCH:146651117-146665263	NOTEST	0	0	0	0	1	1
ENSG00000266743	ENSG00000266743	RP11-94B19.6	18:73885258-73889693	NOTEST	0	0	0	0	1	1
ENSG00000266744	ENSG00000266744	RP11-131K5.1	17:13659794-13972812	NOTEST	0	0.0310195	inf	0	1	1
ENSG00000266745	ENSG00000266745	MIR3135A	3:20081514-20195896	NOTEST	0	0	0	0	1	1
ENSG00000266746	ENSG00000266746	RP11-1109M24.7	17:21906416-21913070	NOTEST	0	0.195516	inf	0	1	1
ENSG00000266747	ENSG00000266747	Y_RNA	HSCHR6_MHC_MANN:31410599-31427049	NOTEST	0	0	0	0	1	1
ENSG00000266748	ENSG00000266748	FMO5	HG1287_PATCH:147859185-147982177	NOTEST	0	0	0	0	1	1
ENSG00000266749	ENSG00000266749	RN7SL46P	12:14366027-14366299	NOTEST	0	0	0	0	1	1
ENSG00000266750	ENSG00000266750	MIR4645	6:2854264-2854341	NOTEST	0	0	0	0	1	1
ENSG00000266751	ENSG00000266751	MIR3661	5:133450401-133706738	NOTEST	0	0	0	0	1	1
ENSG00000266754	ENSG00000266754	RN7SL524P	10:105726958-105788991	NOTEST	0	0	0	0	1	1
ENSG00000266755	ENSG00000266755	SNORD83	HSCHR6_MHC_MCF:31572847-31602942	NOTEST	0	0	0	0	1	1
ENSG00000266756	ENSG00000266756	MIR5680	8:103137659-103137743	NOTEST	0	0	0	0	1	1
ENSG00000266757	ENSG00000266757	AC092962.1	3:163373091-163373169	NOTEST	0	0	0	0	1	1
ENSG00000266758	ENSG00000266758	MIR3680-2	16:29610499-29610586	NOTEST	0	0	0	0	1	1
ENSG00000266759	ENSG00000266759	Y_RNA	HSCHR6_MHC_COX:31616420-31658607	NOTEST	0	0	0	0	1	1
ENSG00000266760	ENSG00000266760	MIR4464	6:91022460-91022552	NOTEST	0	0	0	0	1	1
ENSG00000266761	ENSG00000266761	MIR3194	20:50003493-50179370	NOTEST	0	0	0	0	1	1
ENSG00000266763	ENSG00000266763	AL033528.1	1:26238239-26238313	NOTEST	0	0	0	0	1	1
ENSG00000266764	ENSG00000266764	C1orf51	HG1287_PATCH:150968957-150973508	NOTEST	0	0	0	0	1	1
ENSG00000266765	ENSG00000266765	CTD-2582D11.1	17:71890887-71908017	NOTEST	0	0	0	0	1	1
ENSG00000266766	ENSG00000266766	AL512503.1	HG1292_PATCH:120477736-120612326	NOTEST	0	0	0	0	1	1
ENSG00000266767	ENSG00000266767	RP11-678G15.2	18:7566779-8406951	NOTEST	0	0	0	0	1	1
ENSG00000266768	ENSG00000266768	AC016727.1	2:61782494-61782593	NOTEST	0	0	0	0	1	1

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ENSG00000266770	ENSG00000266770	RN7SL619P	19:13906273-13943044	NOTEST	0	0	0	0	1	1
ENSG00000266771	ENSG00000266771	RP11-19P22.10	17:26002919-26003023	NOTEST	0	0	0	0	1	1
ENSG00000266772	ENSG00000266772	AC091738.2	7:72023728-72298777	NOTEST	0	0	0	0	1	1
ENSG00000266773	ENSG00000266773	RP11-495P10.1	HG1287_PATCH:149101611-149115776	NOTEST	0	0	0	0	1	1
ENSG00000266774	ENSG00000266774	RP11-321M21.1	18:73144657-73148912	NOTEST	0	0	0	0	1	1
ENSG00000266775	ENSG00000266775	RP11-218M11.6	17:28880714-28890511	NOTEST	0	0	0	0	1	1
ENSG00000266776	ENSG00000266776	MIR4646	6:31654725-31685695	NOTEST	0	0	0	0	1	1
ENSG00000266777	ENSG00000266777	SH3GL1P1	17:30334890-30380523	NOTEST	0.336838	0.469972	0.480522	0	1	1
ENSG00000266778	ENSG00000266778	hsa-mir-548ba	3:8661085-9005457	NOTEST	0	0	0	0	1	1
ENSG00000266779	ENSG00000266779	COPG2	HG1308_PATCH:130126045-130351086	NOTEST	0	0	0	0	1	1
ENSG00000266780	ENSG00000266780	MIR4444-1	3:75263626-75263700	NOTEST	0	0	0	0	1	1
ENSG00000266781	ENSG00000266781	Y_RNA	HSCHR6_MHC_COX:33082996-33093846	NOTEST	0	0	0	0	1	1
ENSG00000266782	ENSG00000266782	MIR3663	10:118918166-118928570	NOTEST	0	0	0	0	1	1
ENSG00000266784	ENSG00000266784	U6	HSCHR6_MHC_SSTO:31330790-31330897	NOTEST	0	0	0	0	1	1
ENSG00000266785	ENSG00000266785	hsa-mir-877	HSCHR6_MHC_MANN:30583827-30609632	NOTEST	0	0	0	0	1	1
ENSG00000266786	ENSG00000266786	RP1-66C13.3	17:26073157-26081980	NOTEST	0	0	0	0	1	1
ENSG00000266787	ENSG00000266787	RNA5SP313	HG1211_PATCH:47997301-48047394	NOTEST	0	0	0	0	1	1
ENSG00000266788	ENSG00000266788	MIR4283-1	HG736_PATCH:57023477-57023557	NOTEST	0	0	0	0	1	1
ENSG00000266790	ENSG00000266790	RNU6-1071P	HG1287_PATCH:146975010-146975111	NOTEST	0	0	0	0	1	1
ENSG00000266791	ENSG00000266791	5S_rRNA	HSCHR17_1:43404730-43404862	NOTEST	0	0	0	0	1	1
ENSG00000266792	ENSG00000266792	RN7SL839P	20:3229950-3388272	NOTEST	0	0	0	0	1	1
ENSG00000266793	ENSG00000266793	AL137008.1	6:56296747-56298011	NOTEST	0	0	0	0	1	1
ENSG00000266794	ENSG00000266794	RN7SL7P	7:92600317-92600613	NOTEST	0	0	0	0	1	1
ENSG00000266795	ENSG00000266795	RP11-744K17.9	17:21906416-21913070	NOTEST	0.164032	0.0603112	-1.44348	0	1	1
ENSG00000266796	ENSG00000266796	CT009496.1	HG1322_PATCH:29849262-29852708	NOTEST	0	0	0	0	1	1
ENSG00000266797	ENSG00000266797	NBPF23	HG1287_PATCH:144281630-144322056	NOTEST	0	0	0	0	1	1
ENSG00000266798	ENSG00000266798	AC078816.1	3:150803483-151176497	NOTEST	0	0	0	0	1	1
ENSG00000266799	ENSG00000266799	AP003356.1	8:103745862-103745947	NOTEST	0	0	0	0	1	1
ENSG00000266800	ENSG00000266800	AL135791.1	10:38091750-38148038	NOTEST	0	0	0	0	1	1
ENSG00000266801	ENSG00000266801	RP11-521L9.2	16:68877506-69119083	NOTEST	0	0.199646	inf	0	1	1
ENSG00000266802	ENSG00000266802	MIR4419A	1:23345940-23504301	NOTEST	0	0	0	0	1	1
ENSG00000266803	ENSG00000266803	RP1-77H15.1	17:16454700-16472520	NOTEST	0.0286872	0	#NAME?	0	1	1
ENSG00000266804	ENSG00000266804	AC234063.1	HG183_PATCH:62526396-62546003	NOTEST	0	0	0	0	1	1
ENSG00000266805	ENSG00000266805	RP11-61L19.1	18:9475006-9538114	NOTEST	0	0	0	0	1	1
ENSG00000266806	ENSG00000266806	RP11-744K17.3	17:21858202-21859016	NOTEST	0	0	0	0	1	1
ENSG00000266807	ENSG00000266807	MIR548H5	6:132113311-132113371	NOTEST	0	0	0	0	1	1
ENSG00000266808	ENSG00000266808	MIR548AE1	2:185243701-185243771	NOTEST	0	0	0	0	1	1
ENSG00000266809	ENSG00000266809	RP11-449D8.3	18:22269877-22270125	NOTEST	0	0	0	0	1	1
ENSG00000266810	ENSG00000266810	MICG	HG1322_PATCH:29780096-29780228	NOTEST	0	0	0	0	1	1
ENSG00000266811	ENSG00000266811	MIR3118-3	1:143347957-143467632	NOTEST	0	0	0	0	1	1
ENSG00000266812	ENSG00000266812	RP11-855A2.5	HG747_PATCH:65989995-65992547	NOTEST	0	0	0	0	1	1
ENSG00000266813	ENSG00000266813	AF196779.1	X:49059701-49059788	NOTEST	0	0	0	0	1	1
ENSG00000266814	ENSG00000266814	AP000868.1	11:123579380-123579478	NOTEST	0	0	0	0	1	1

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ENSG00000266816	ENSG00000266816	AL356750.1	13:30776766-30881621	NOTEST	0	0	0	0	1	1
ENSG00000266817	ENSG00000266817	AC118063.1	2:190175988-190176693	NOTEST	0	0	0	0	1	1
ENSG00000266818	ENSG00000266818	RP11-454P7.1	18:15254416-15271743	NOTEST	0	0	0	0	1	1
ENSG00000266819	ENSG00000266819	Metazoa_SRP	HSCHR6_MHC_QBL:30864237-30864501	NOTEST	0	0	0	0	1	1
ENSG00000266821	ENSG00000266821	RP11-6N17.2	17:45956837-45959764	NOTEST	0	0	0	0	1	1
ENSG00000266822	ENSG00000266822	AL928874.1	X:21392535-21672813	NOTEST	0	0	0	0	1	1
ENSG00000266823	ENSG00000266823	RP1-142L7.5	HG1304_PATCH:112430062-112671296	NOTEST	0	0	0	0	1	1
ENSG00000266824	ENSG00000266824	RP11-599B13.7	17:8080129-8086130	NOTEST	0	0	0	0	1	1
ENSG00000266825	ENSG00000266825	AL590085.1	1:180601139-180859387	NOTEST	0	0	0	0	1	1
ENSG00000266826	ENSG00000266826	CTD-2200P10.1	17:56597197-56769416	NOTEST	0.0319161	0	#NAME?	0	1	1
ENSG00000266827	ENSG00000266827	MIR3689E	9:137742415-137742487	NOTEST	0	0	0	0	1	1
ENSG00000266828	ENSG00000266828	RN7SL712P	X:115108800-115109100	NOTEST	0	0	0	0	1	1
ENSG00000266829	ENSG00000266829	RN7SL661P	X:110859124-110859401	NOTEST	0	0	0	0	1	1
ENSG00000266830	ENSG00000266830	CTD-2008P7.8	17:26573479-26575315	NOTEST	0	0.0501725	inf	0	1	1
ENSG00000266831	ENSG00000266831	MIR4273	GL000222.1:15193-15277	NOTEST	0	0	0	0	1	1
ENSG00000266832	ENSG00000266832	AL445464.1	1:76262566-76378923	NOTEST	0	0	0	0	1	1
ENSG00000266833	ENSG00000266833	RP11-343N15.1	HG1292_PATCH:121902778-122005752	NOTEST	0	0	0	0	1	1
ENSG00000266834	ENSG00000266834	SNORD24	HG79_PATCH:136223748-136226961	NOTEST	0	0	0	0	1	1
ENSG00000266836	ENSG00000266836	RP11-1109M24.8	17:21906416-21913070	NOTEST	0	0	0	0	1	1
ENSG00000266837	ENSG00000266837	Z97055.1	22:44300475-44300561	NOTEST	0	0	0	0	1	1
ENSG00000266838	ENSG00000266838	AP001634.1	21:15357767-15357840	NOTEST	0	0	0	0	1	1
ENSG00000266839	ENSG00000266839	U6	17:19912656-20306870	NOTEST	0	0	0	0	1	1
ENSG00000266840	ENSG00000266840	RP11-543H23.2	18:67068290-67629039	NOTEST	0	0	0	0	1	1
ENSG00000266841	ENSG00000266841	Y_RNA	HSCHR6_MHC_DBB:30891108-30891200	NOTEST	0	0	0	0	1	1
ENSG00000266842	ENSG00000266842	RP11-495P10.4	HG1287_PATCH:149004097-149004428	NOTEST	0	0	0	0	1	1
ENSG00000266843	ENSG00000266843	AL360007.1	6:142583779-142583871	NOTEST	0	0	0	0	1	1
ENSG00000266844	ENSG00000266844	RP11-862L9.3	18:74686645-74845639	NOTEST	0	0.0829494	inf	0	1	1
ENSG00000266845	ENSG00000266845	RP11-325P15.1	HG1287_PATCH:147705750-147810940	NOTEST	0	0	0	0	1	1
ENSG00000266846	ENSG00000266846	RP11-793A3.2	18:5954704-6415236	NOTEST	0	0.0310254	inf	0	1	1
ENSG00000266847	ENSG00000266847	SNORA38	HSCHR6_MHC_MANN:31627936-31645035	NOTEST	0	0	0	0	1	1
ENSG00000266849	ENSG00000266849	AC083906.2	3:129800673-129839422	NOTEST	0	0	0	0	1	1
ENSG00000266850	ENSG00000266850	RP11-370A5.1	18:20279443-20606451	NOTEST	0.0705701	0.158233	1.16492	0	1	1
ENSG00000266851	ENSG00000266851	CR759848.2	HSCHR6_MHC_MCF:32751468-32751536	NOTEST	0	0	0	0	1	1
ENSG00000266852	ENSG00000266852	MIR4482-1	10:106028079-106028177	NOTEST	0	0	0	0	1	1
ENSG00000266853	ENSG00000266853	ITM2BP1	17:25783669-25976586	NOTEST	0	0.0213083	inf	0	1	1
ENSG00000266854	ENSG00000266854	AP003096.1	11:68386966-68387063	NOTEST	0	0	0	0	1	1
ENSG00000266855	ENSG00000266855	MIR3910-2	9:94325372-94712444	NOTEST	0	0	0	0	1	1
ENSG00000266856	ENSG00000266856	MIR5004	HSCHR6_MHC_SSTO:33527234-33560852	NOTEST	0	0	0	0	1	1
ENSG00000266857	ENSG00000266857	AF186996.2	3:125409099-125409187	NOTEST	0	0	0	0	1	1
ENSG00000266858	ENSG00000266858	RP11-557B23.3	17:65770706-65773440	NOTEST	0	0	0	0	1	1
ENSG00000266859	ENSG00000266859	AP000719.1	11:71576554-71639700	NOTEST	0	0	0	0	1	1

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ENSG00000266861	ENSG00000266861	AC097506.1	2:33931952-34522820	NOTEST	0	0	0	0	1	1
ENSG00000266862	ENSG00000266862	AC004595.1	7:21461886-21461986	NOTEST	0	0	0	0	1	1
ENSG00000266863	ENSG00000266863	RN7SL123P	9:6645955-6670635	NOTEST	0	0	0	0	1	1
ENSG00000266864	ENSG00000266864	AC116606.1	5:57168765-57168873	NOTEST	0	0	0	0	1	1
ENSG00000266865	ENSG00000266865	RP11-848P1.9	17:29335514-29709134	NOTEST	0	0	0	0	1	1
ENSG00000266866	ENSG00000266866	AP002761.1	11:73018279-73080136	NOTEST	0	0	0	0	1	1
ENSG00000266867	ENSG00000266867	AL031005.1	1:21132962-21503377	NOTEST	0	0	0	0	1	1
ENSG00000266868	ENSG00000266868	MIR4517	16:28962127-28978418	NOTEST	0	0	0	0	1	1
ENSG00000266869	ENSG00000266869	RP6-114E22.1	14:72315322-72375147	NOTEST	0	0	0	0	1	1
ENSG00000266870	ENSG00000266870	U6	HSCHR6_MHC_SSTO:28870843-28891821	NOTEST	0	0	0	0	1	1
ENSG00000266871	ENSG00000266871	hsa-mir-877	HSCHR6_MHC_MCF:30617609-30643414	NOTEST	0	0	0	0	1	1
ENSG00000266872	ENSG00000266872	RP11-19P22.8	17:25783669-25976586	NOTEST	0.450823	0.600007	0.412419	0	1	1
ENSG00000266874	ENSG00000266874	RP4-791M13.4	HG1287_PATCH:14957587-149719430	NOTEST	0	0	0	0	1	1
ENSG00000266875	ENSG00000266875	RN7SL408P	6:134454710-134455004	NOTEST	0	0	0	0	1	1
ENSG00000266876	ENSG00000266876	RP11-1148O4.1	17:27887564-28513493	NOTEST	0.0179164	0.0139316	-0.362915	0	1	1
ENSG00000266877	ENSG00000266877	RP1-41C23.1	17:29910180-29964562	NOTEST	0	0.0265186	inf	0	1	1
ENSG00000266879	ENSG00000266879	MIR4752	HSCHR19LRC_COX1_CTG1:54785734-54785806	NOTEST	0	0	0	0	1	1
ENSG00000266880	ENSG00000266880	RHEBP1	HG1211_PATCH:47073664-47147473	NOTEST	0	0	0	0	1	1
ENSG00000266881	ENSG00000266881	AL353662.4	9:34179002-34329198	NOTEST	0	0	0	0	1	1
ENSG00000266882	ENSG00000266882	AC138749.2	HSCHR15_1_CTG4:28776380-28789737	NOTEST	0	0	0	0	1	1
ENSG00000266883	ENSG00000266883	RNU2-17P	HG1287_PATCH:150923381-150923571	NOTEST	0	0	0	0	1	1
ENSG00000266884	ENSG00000266884	U1	HSCHR6_MHC_QBL:32414983-32415132	NOTEST	0	0	0	0	1	1
ENSG00000266885	ENSG00000266885	RP11-744K17.2	17:21934504-21938362	NOTEST	0.00772256	0.00332165	-1.21718	0	1	1
ENSG00000266886	ENSG00000266886	U6	HSCHR6_MHC_QBL:31328025-31328132	NOTEST	0	0	0	0	1	1
ENSG00000266887	ENSG00000266887	MIR4535	22:48885271-49246724	NOTEST	0	0	0	0	1	1
ENSG00000266888	ENSG00000266888	RP11-506B6.6	HG1304_PATCH:112430062-112671296	NOTEST	0	0	0	0	1	1
ENSG00000266889	ENSG00000266889	RN7SL88P	12:96495730-96496027	NOTEST	0	0	0	0	1	1
ENSG00000266890	ENSG00000266890	MIR4634	5:174178306-174277728	NOTEST	0	0	0	0	1	1
ENSG00000266891	ENSG00000266891	RP11-692N5.2	18:9708161-9862548	NOTEST	0	0	0	0	1	1
ENSG00000266892	ENSG00000266892	AP000301.1	21:34775201-34852318	NOTEST	0	0	0	0	1	1
ENSG00000266893	ENSG00000266893	AC005616.1	19:28926294-29218684	NOTEST	0	0	0	0	1	1
ENSG00000266895	ENSG00000266895	CTC-268N12.2	17:35306174-35414171	NOTEST	0	0	0	0	1	1
ENSG00000266896	ENSG00000266896	RP1-266L20.9	6:170151717-170181680	NOTEST	0.0738675	0.135899	0.879523	0	1	1
ENSG00000266897	ENSG00000266897	AC005546.2	19:13228916-13251961	NOTEST	0.262492	0.247298	-0.0860233	0	1	1
ENSG00000266899	ENSG00000266899	AKR1B1P7	19:33851405-33852354	NOTEST	0	0	0	0	1	1
ENSG00000266900	ENSG00000266900	RP11-173A16.2	18:59854490-59974355	NOTEST	0.0188179	0	#NAME?	0	1	1
ENSG00000266901	ENSG00000266901	RP11-567M16.5	18:77439800-77514510	NOTEST	0	0	0	0	1	1
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ENSG00000266904	ENSG00000266904	LINC00663	19:19868174-19945736	NOTEST	0.608897	0.322027	-0.919015	0	1	1
ENSG00000266905	ENSG00000266905	RP11-1058N17.1	18:46489320-46490311	NOTEST	0	0	0	0	1	1
ENSG00000266906	ENSG00000266906	AC005357.1	19:28175487-28475892	NOTEST	0	0	0	0	1	1
ENSG00000266907	ENSG00000266907	AC006116.22	19:56732680-56904914	NOTEST	0.00742557	0.00576963	-0.364022	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000266908	ENSG00000266908	RP5-1022P6.7	20:5476712-5485259	NOTEST	0	0	0	0	1	1
ENSG00000266909	ENSG00000266909	SLC25A6P4	18:77794345-77854968	NOTEST	0	0	0	0	1	1
ENSG00000266910	ENSG00000266910	CTC-448F2.6	19:30528329-30529063	NOTEST	0.202464	0.123392	-0.714415	0	1	1
ENSG00000266911	ENSG00000266911	RP1-161P9.5	17:34083267-34122711	NOTEST	0	0	0	0	1	1
ENSG00000266912	ENSG00000266912	CTC-325H20.2	19:9434447-9493293	NOTEST	0.0314722	0.125824	1.99925	0	1	1
ENSG00000266913	ENSG00000266913	CTC-548K16.2	19:14416269-14481008	NOTEST	0	0	0	0	1	1
ENSG00000266915	ENSG00000266915	MRPS5P4	18:58187073-58187398	NOTEST	0	0	0	0	1	1
ENSG00000266916	ENSG00000266916	CTD-3064H18.1	19:37988062-38210691	NOTEST	0.0536014	0.0381686	-0.489883	0	1	1
ENSG00000266918	ENSG00000266918	RP11-798G7.8	17:43578684-43640596	NOTEST	0.0470163	0.00997821	-2.23631	0	1	1
ENSG00000266920	ENSG00000266920	ACTBP9	18:60109260-60110359	NOTEST	0	0	0	0	1	1
ENSG00000266921	ENSG00000266921	RP11-15A1.7	19:44472013-44506988	NOTEST	0.16027	0.157069	-0.0291027	0	1	1
ENSG00000266922	ENSG00000266922	CTC-499B15.6	19:11832079-11849824	NOTEST	0	0	0	0	1	1
ENSG00000266923	ENSG00000266923	RP11-693J15.4	12:92813869-92885867	NOTEST	0.0149712	0.01815	0.27778	0	1	1
ENSG00000266924	ENSG00000266924	RP11-154H12.2	18:77547120-77551432	NOTEST	0	0	0	0	1	1
ENSG00000266925	ENSG00000266925	RP11-434D2.7	17:20404825-20415670	NOTEST	0	0	0	0	1	1
ENSG00000266926	ENSG00000266926	AC005943.4	19:1576638-1605480	NOTEST	0.274809	0.087095	-1.65777	0	1	1
ENSG00000266927	ENSG00000266927	AC006273.7	19:786649-787037	NOTEST	0	0	0	0	1	1
ENSG00000266928	ENSG00000266928	CTB-70G10.1	19:28784999-28804407	NOTEST	0	0	0	0	1	1
ENSG00000266929	ENSG00000266929	RP11-400F19.8	17:40688189-40718295	NOTEST	0	0.0365735	inf	0	1	1
ENSG00000266931	ENSG00000266931	RP11-1252D15.1	2:87257799-87303536	NOTEST	0	0	0	0	1	1
ENSG00000266932	ENSG00000266932	AC006116.13	19:56732680-56904914	NOTEST	0	0	0	0	1	1
ENSG00000266933	ENSG00000266933	AC005775.2	19:489175-519654	NOTEST	0.149804	0.117591	-0.349298	0	1	1
ENSG00000266935	ENSG00000266935	CTD-3234P18.2	19:37119694-37121092	NOTEST	0.0727169	0.0583192	-0.31832	0	1	1
ENSG00000266936	ENSG00000266936	CTC-215O4.4	19:11071597-11176071	NOTEST	0.586091	0.338639	-0.791377	0	1	1
ENSG00000266938	ENSG00000266938	AC119403.1	19:2896622-2897220	NOTEST	0.0643231	0	#NAME?	0	1	1
ENSG00000266939	ENSG00000266939	AC005559.2	19:589892-617159	NOTEST	0	0	0	0	1	1
ENSG00000266941	ENSG00000266941	AC104532.3	19:5865836-5904017	NOTEST	0	0.0623642	inf	0	1	1
ENSG00000266942	ENSG00000266942	RP11-378E13.3	17:35441922-35766909	NOTEST	0	0	0	0	1	1
ENSG00000266943	ENSG00000266943	RP11-15E18.2	17:58641907-58663984	NOTEST	0	0	0	0	1	1
ENSG00000266944	ENSG00000266944	AC005262.4	19:3130714-3131396	NOTEST	0	0	0	0	1	1
ENSG00000266945	ENSG00000266945	OR4G3P	19:94061-96511	NOTEST	0	0	0	0	1	1
ENSG00000266946	ENSG00000266946	MRPL37P1	18:56337711-56421709	NOTEST	0	0	0	0	1	1
ENSG00000266947	ENSG00000266947	RP11-799D4.4	17:33558468-33569982	NOTEST	0.0838489	0.0763775	-0.134643	0	1	1
ENSG00000266949	ENSG00000266949	LYPD8	1:248902715-248903150	NOTEST	0	0	0	0	1	1
ENSG00000266950	ENSG00000266950	CTD-2623N2.5	19:9904296-9912977	NOTEST	0	0.0446868	inf	0	1	1
ENSG00000266951	ENSG00000266951	AD000091.2	19:15724057-15725364	NOTEST	0	0	0	0	1	1
ENSG00000266952	ENSG00000266952	RP11-909B2.1	18:61747242-62090836	NOTEST	0	0	0	0	1	1
ENSG00000266953	ENSG00000266953	RP11-618P17.4	19:34850384-34919178	NOTEST	0	0	0	0	1	1
ENSG00000266954	ENSG00000266954	RP11-701H16.4	18:13217496-13652754	NOTEST	0	0	0	0	1	1
ENSG00000266955	ENSG00000266955	RP11-820I16.3	18:11981023-12030876	NOTEST	0	0.0324171	inf	0	1	1

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ENSG00000266956	ENSG00000266956	CTB-186H2.3	17:34310326-34338658	NOTEST	0	0	0	0	1	1
ENSG00000266957	ENSG00000266957	RP11-49K24.4	18:44388352-44627658	NOTEST	0	0	0	0	1	1
ENSG00000266958	ENSG00000266958	AC006126.3	19:45574757-45808541	NOTEST	0	0	0	0	1	1
ENSG00000266959	ENSG00000266959	AC005786.3	19:3506270-3579086	NOTEST	0	0.954121	inf	0	1	1
ENSG00000266960	ENSG00000266960	FAM106DP	17:58250682-58251183	NOTEST	0	0	0	0	1	1
ENSG00000266961	ENSG00000266961	RP11-973H7.5	18:12738963-12750067	NOTEST	0	0	0	0	1	1
ENSG00000266963	ENSG00000266963	AC005625.1	19:38826414-38861589	NOTEST	0	0	0	0	1	1
ENSG00000266965	ENSG00000266965	RP11-712P20.2	18:33161080-33291798	NOTEST	0	0	0	0	1	1
ENSG00000266968	ENSG00000266968	RP11-116O18.1	18:42792959-43332485	NOTEST	0.0167539	0	#NAME?	0	1	1
ENSG00000266969	ENSG00000266969	RP11-773H22.4	18:12947131-12991172	NOTEST	0.103792	0	#NAME?	0	1	1
ENSG00000266970	ENSG00000266970	RP11-806H10.4	17:76356533-76369992	NOTEST	0.405811	0.619727	0.610826	0	1	1
ENSG00000266971	ENSG00000266971	OR4F8P	19:156278-157215	NOTEST	0	0	0	0	1	1
ENSG00000266972	ENSG00000266972	LRRC37A9P	17:34239638-34245014	NOTEST	0.0702674	0.0495895	-0.50282	0	1	1
ENSG00000266973	ENSG00000266973	CTD-3162L10.3	19:36827161-36870101	NOTEST	0	0	0	0	1	1
ENSG00000266975	ENSG00000266975	CTC-425F1.2	19:13033292-13044851	NOTEST	0	0	0	0	1	1
ENSG00000266976	ENSG00000266976	AC079466.1	19:28926294-29218684	NOTEST	0	0	0	0	1	1
ENSG00000266978	ENSG00000266978	CTD-2369P2.5	19:10362576-10399695	NOTEST	0.121392	0.0304772	-1.99387	0	1	1
ENSG00000266979	ENSG00000266979	RP11-1072C15.2	17:42723731-42727717	NOTEST	0	0	0	0	1	1
ENSG00000266980	ENSG00000266980	RP11-552F3.4	17:73772514-73821886	NOTEST	0.138991	0.129318	-0.104069	0	1	1
ENSG00000266981	ENSG00000266981	RP11-799D4.2	17:33474835-33518721	NOTEST	0	0	0	0	1	1
ENSG00000266982	ENSG00000266982	CTC-550B14.8	HSCHR19LRC_PGF1_CTG1:55356751-55397872	NOTEST	0	0	0	0	1	1
ENSG00000266983	ENSG00000266983	CTC-232P5.1	19:5978413-6199583	NOTEST	0	0	0	0	1	1
ENSG00000266984	ENSG00000266984	RP11-23B5.1	18:46004931-46005599	NOTEST	0	0	0	0	1	1
ENSG00000266985	ENSG00000266985	CTD-2329C7.2	19:34046473-34048376	NOTEST	0	0	0	0	1	1
ENSG00000266986	ENSG00000266986	RP11-428O23.1	HG75_PATCH:34443569-34504870	NOTEST	0	0	0	0	1	1
ENSG00000266987	ENSG00000266987	RP11-354P11.8	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000266988	ENSG00000266988	RP11-749H17.1	18:42792959-43332485	NOTEST	0	0	0	0	1	1
ENSG00000266989	ENSG00000266989	FTLP5	19:3870988-3872105	NOTEST	0	0	0	0	1	1
ENSG00000266990	ENSG00000266990	AC004528.4	19:999600-1021117	NOTEST	0	0	0	0	1	1
ENSG00000266992	ENSG00000266992	DHX40P1	17:57970446-58096413	NOTEST	0	0	0	0	1	1
ENSG00000266994	ENSG00000266994	RP11-127I20.7	16:4746512-4817625	NOTEST	0.0715557	0	#NAME?	0	1	1
ENSG00000266995	ENSG00000266995	RP11-703I16.3	18:12040099-12040299	NOTEST	0.358722	0	#NAME?	0	1	1
ENSG00000266996	ENSG00000266996	TCEB3CL2	18:44388352-44627658	NOTEST	0	0	0	0	1	1
ENSG00000266997	ENSG00000266997	RP11-886H22.1	18:47309868-47721463	NOTEST	0	0	0	0	1	1
ENSG00000266998	ENSG00000266998	RP11-936I5.1	17:75253818-75496678	NOTEST	0.0211343	0.00321432	-2.717	0	1	1
ENSG00000266999	ENSG00000266999	AC015849.16	17:34220710-34238027	NOTEST	0.0779321	0.0454178	-0.77896	0	1	1
ENSG00000267000	ENSG00000267000	RP11-27G24.3	18:57098171-57364644	NOTEST	0	0	0	0	1	1
ENSG00000267003	ENSG00000267003	CTC-507E2.1	17:33901813-34053436	NOTEST	0.0132106	0.0451832	1.77409	0	1	1
ENSG00000267004	ENSG00000267004	CTD-2659N19.4	19:12836330-12836700	NOTEST	0	0	0	0	1	1
ENSG00000267005	ENSG00000267005	AC002984.2	19:36664307-36664755	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267006	ENSG00000267006	CTC-448F2.4	19:30519647-30520823	NOTEST	0.0147783	0.0208087	0.493705	0	1	1
ENSG00000267007	ENSG00000267007	CTB-31O20.3	19:1815247-1848452	NOTEST	0	0.00041062	inf	0	1	1
ENSG00000267011	ENSG00000267011	CTB-50L17.16	19:4457958-4471490	NOTEST	0.229001	0.190564	-0.265083	0	1	1
ENSG00000267012	ENSG00000267012	CTC-360P9.1	19:32377609-32399190	NOTEST	0	0	0	0	1	1
ENSG00000267013	ENSG00000267013	CTD-2171N6.1	18:52773134-52791537	NOTEST	0	0	0	0	1	1
ENSG00000267014	ENSG00000267014	CTD-2081K17.2	19:29493461-29504862	NOTEST	0	0	0	0	1	1
ENSG00000267015	ENSG00000267015	RP11-800A18.4	18:76829284-77138283	NOTEST	0	0	0	0	1	1
ENSG00000267016	ENSG00000267016	RP11-75C10.9	17:75253818-75496678	NOTEST	0.333359	0.158368	-1.0738	0	1	1
ENSG00000267017	ENSG00000267017	CTC-260E6.6	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000267018	ENSG00000267018	AC010525.7	19:56186591-56249768	NOTEST	0.0573653	0.0719144	0.326104	0	1	1
ENSG00000267019	ENSG00000267019	NTF6A	19:49526125-49552400	NOTEST	0	0	0	0	1	1
ENSG00000267021	ENSG00000267021	MIR4321	19:2249307-2252072	NOTEST	0	0	0	0	1	1
ENSG00000267024	ENSG00000267024	CTD-2588C8.8	19:34850384-34919178	NOTEST	0	0.0854662	inf	0	1	1
ENSG00000267025	ENSG00000267025	AC015849.19	17:34136458-34195895	NOTEST	0.356031	0.430726	0.274768	0	1	1
ENSG00000267026	ENSG00000267026	RP11-92C4.3	9:101569980-101634697	NOTEST	0.155442	0.304449	0.969829	0	1	1
ENSG00000267027	ENSG00000267027	AC011524.2	19:29374336-29444152	NOTEST	0	0	0	0	1	1
ENSG00000267028	ENSG00000267028	RP11-619L19.1	18:52889561-53332018	NOTEST	0	0	0	0	1	1
ENSG00000267029	ENSG00000267029	AC092299.7	19:197074-205074	NOTEST	0	0	0	0	1	1
ENSG00000267030	ENSG00000267030	CTB-50L17.7	19:4402658-4457819	NOTEST	0	0.146693	inf	0	1	1
ENSG00000267032	ENSG00000267032	RP11-807E13.2	18:13151635-13152688	NOTEST	0	0.0406238	inf	0	1	1
ENSG00000267033	ENSG00000267033	CTD-2562J15.4	19:16296190-16302857	NOTEST	0	0.0808875	inf	0	1	1
ENSG00000267035	ENSG00000267035	RP11-1094M14.10	17:33867057-33867816	NOTEST	0	0.159554	inf	0	1	1
ENSG00000267036	ENSG00000267036	AC005559.3	19:589892-617159	NOTEST	0	0	0	0	1	1
ENSG00000267037	ENSG00000267037	AC005757.7	19:45574757-45808541	NOTEST	0	0.00368282	inf	0	1	1
ENSG00000267038	ENSG00000267038	RP11-1096D5.2	18:59252978-59421928	NOTEST	0	0	0	0	1	1
ENSG00000267039	ENSG00000267039	RP11-58G13.1	18:33877676-34812135	NOTEST	0	0	0	0	1	1
ENSG00000267042	ENSG00000267042	CTD-3193K9.4	17:40830906-40851832	NOTEST	0.0984943	0.120582	0.291901	0	1	1
ENSG00000267043	ENSG00000267043	CTB-91J4.3	17:34580901-34808104	NOTEST	0	0	0	0	1	1
ENSG00000267044	ENSG00000267044	AC005757.6	19:45574757-45808541	NOTEST	0	0	0	0	1	1
ENSG00000267045	ENSG00000267045	AC006126.4	19:45574757-45808541	NOTEST	0	0.248646	inf	0	1	1
ENSG00000267046	ENSG00000267046	RP11-1094M14.9	17:33791267-33864880	NOTEST	0	0	0	0	1	1
ENSG00000267047	ENSG00000267047	RP11-589P10.7	17:6757179-6922978	NOTEST	0.17613	0.191314	0.119299	0	1	1
ENSG00000267048	ENSG00000267048	RP11-566K11.7	16:89939999-90005169	NOTEST	0.12836	0	#NAME?	0	1	1
ENSG00000267049	ENSG00000267049	AC002398.13	19:36249043-36261930	NOTEST	0.374636	0	#NAME?	0	1	1
ENSG00000267050	ENSG00000267050	CTC-550B14.8	HSCHR19LRC_LRC_J_CTG1:55459917-55537551	NOTEST	0	0	0	0	1	1
ENSG00000267051	ENSG00000267051	RP11-128P17.2	18:11366911-11378408	NOTEST	0.197522	0.0905931	-1.12454	0	1	1
ENSG00000267052	ENSG00000267052	CTB-30L5.1	7:106012696-106410653	NOTEST	0.0727335	0.0278606	-1.3844	0	1	1
ENSG00000267053	ENSG00000267053	CTD-3162L10.1	19:36795481-36803570	NOTEST	0.0596215	0.12941	1.11805	0	1	1
ENSG00000267054	ENSG00000267054	CTD-2540B15.10	19:33668508-33698694	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000267056	ENSG00000267056	AC005336.4	19:16021391-16022634	NOTEST	0	0	0	0	1	1
ENSG00000267057	ENSG00000267057	RP11-456O19.2	18:53548918-53858493	NOTEST	0	0	0	0	1	1
ENSG00000267061	ENSG00000267061	RP11-760L24.1	18:57098171-57364644	NOTEST	0	0	0	0	1	1
ENSG00000267062	ENSG00000267062	CTD-2659N19.10	19:12873816-12985765	NOTEST	0	0	0	0	1	1
ENSG00000267063	ENSG00000267063	AC006130.3	19:2841432-2860482	NOTEST	0	0.0513901	inf	0	1	1
ENSG00000267064	ENSG00000267064	UXT-AS1	X:47511196-47519776	NOTEST	0.480205	0.371874	-0.368839	0	1	1
ENSG00000267065	ENSG00000267065	CTD-2246P4.1	17:74795125-74802035	NOTEST	0	0	0	0	1	1
ENSG00000267066	ENSG00000267066	RP11-866E20.1	18:57596457-57597562	NOTEST	0	0	0	0	1	1
ENSG00000267067	ENSG00000267067	CTB-75G16.3	17:34990526-34991156	NOTEST	0.0323634	0	#NAME?	0	1	1
ENSG00000267069	ENSG00000267069	RP11-64C12.8	18:12288306-12291487	NOTEST	0	0	0	0	1	1
ENSG00000267070	ENSG00000267070	RP11-10K17.6	16:5148739-5192596	NOTEST	0	0	0	0	1	1
ENSG00000267071	ENSG00000267071	RP11-147L13.7	HG747_PATCH:66148891-66155159	NOTEST	0	0	0	0	1	1
ENSG00000267072	ENSG00000267072	RP11-165E7.1	16:4932507-5147809	NOTEST	0	0.0389001	inf	0	1	1
ENSG00000267073	ENSG00000267073	AC005256.1	19:1748054-1748744	NOTEST	0	0	0	0	1	1
ENSG00000267074	ENSG00000267074	RP11-1094M14.5	17:33791267-33864880	NOTEST	0	0	0	0	1	1
ENSG00000267075	ENSG00000267075	RP11-434D2.3	17:20446286-20454276	NOTEST	0	0	0	0	1	1
ENSG00000267076	ENSG00000267076	CCDC58P3	18:12201980-12223538	NOTEST	0	0	0	0	1	1
ENSG00000267077	ENSG00000267077	RP11-127I20.5	16:4827669-4846533	NOTEST	0	0	0	0	1	1
ENSG00000267079	ENSG00000267079	RP11-820I16.1	18:11910632-11914343	NOTEST	0	0	0	0	1	1
ENSG00000267081	ENSG00000267081	CTC-400I9.2	19:31341881-31363414	NOTEST	0	0	0	0	1	1
ENSG00000267083	ENSG00000267083	KRT18P61	17:58754813-59488916	NOTEST	0	0.0289942	inf	0	1	1
ENSG00000267084	ENSG00000267084	RP11-666A8.11	17:74591665-74591854	NOTEST	0	0	0	0	1	1
ENSG00000267085	ENSG00000267085	RP11-15J10.9	9:70113592-70124467	NOTEST	0	0	0	0	1	1
ENSG00000267086	ENSG00000267086	YWHAEP6	17:34569146-34569252	NOTEST	0	0	0	0	1	1
ENSG00000267087	ENSG00000267087	RP11-147L13.8	HG747_PATCH:66185999-66188918	NOTEST	0	0	0	0	1	1
ENSG00000267088	ENSG00000267088	RP11-115N12.1	18:39669275-39669716	NOTEST	0.47472	0.334003	-0.507214	0	1	1
ENSG00000267089	ENSG00000267089	CTC-499B15.8	19:11952055-11953254	NOTEST	0	0	0	0	1	1
ENSG00000267090	ENSG00000267090	AC005789.9	19:38874904-38878722	NOTEST	0.0318701	0	#NAME?	0	1	1
ENSG00000267091	ENSG00000267091	CTBP2P7	19:36987817-36989061	NOTEST	0	0	0	0	1	1
ENSG00000267092	ENSG00000267092	CTB-25B13.9	19:1505016-1513603	NOTEST	0	0	0	0	1	1
ENSG00000267093	ENSG00000267093	CTD-2105E13.13	19:55896712-55919145	NOTEST	0.172162	0.0625172	-1.46145	0	1	1
ENSG00000267094	ENSG00000267094	CTC-360P9.5	19:32413789-32436304	NOTEST	0	0	0	0	1	1
ENSG00000267095	ENSG00000267095	CTD-2319I12.5	17:58213122-58217442	NOTEST	0	0	0	0	1	1
ENSG00000267096	ENSG00000267096	CTD-2537I9.13	19:56165511-56186081	NOTEST	0.113766	0.163296	0.521424	0	1	1
ENSG00000267097	ENSG00000267097	RP11-309E23.2	18:42792959-43332485	NOTEST	0	0	0	0	1	1
ENSG00000267098	ENSG00000267098	RP11-325K19.1	18:58279005-58569959	NOTEST	0	0	0	0	1	1
ENSG00000267099	ENSG00000267099	NTF6G	19:49526125-49552400	NOTEST	0	0	0	0	1	1
ENSG00000267101	ENSG00000267101	RP11-846C15.2	18:42710529-42761312	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267104	ENSG00000267104	TBC1D3P1-DHX40P1	17:57970446-58096413	NOTEST	0	0	0	0	1	1
ENSG00000267105	ENSG00000267105	CTD-2369P2.4	19:10362576-10399695	NOTEST	0	0.436992	inf	0	1	1
ENSG00000267107	ENSG00000267107	AC011526.1	19:41960073-42006559	NOTEST	0	0	0	0	1	1
ENSG00000267108	ENSG00000267108	RP11-861E21.1	18:12432895-12437634	NOTEST	0	0	0	0	1	1
ENSG00000267109	ENSG00000267109	CTD-2378E21.1	17:68308971-68365057	NOTEST	0	0	0	0	1	1
ENSG00000267110	ENSG00000267110	CTD-2587H24.4	19:55663136-55691809	NOTEST	0	0	0	0	1	1
ENSG00000267112	ENSG00000267112	RP11-839G9.1	18:52385090-52565314	NOTEST	0	0	0	0	1	1
ENSG00000267113	ENSG00000267113	AF038458.4	19:36438016-36450094	NOTEST	0	0	0	0	1	1
ENSG00000267114	ENSG00000267114	CTB-129P6.11	19:45453300-45457264	NOTEST	0	0	0	0	1	1
ENSG00000267115	ENSG00000267115	CTD-3064H18.2	19:37988062-38210691	NOTEST	0	0	0	0	1	1
ENSG00000267116	ENSG00000267116	RP11-64C12.7	18:12192201-12192933	NOTEST	0	0	0	0	1	1
ENSG00000267117	ENSG00000267117	AC010525.4	19:56186591-56249768	NOTEST	0	0	0	0	1	1
ENSG00000267118	ENSG00000267118	CTB-91J4.1	17:34443569-34504870	NOTEST	0	0	0	0	1	1
ENSG00000267119	ENSG00000267119	RPL10P15	19:9920942-9938492	NOTEST	0	0	0	0	1	1
ENSG00000267120	ENSG00000267120	AD000671.6	19:36230057-36245420	NOTEST	0.2202	0.0465772	-2.24112	0	1	1
ENSG00000267121	ENSG00000267121	CTD-2020K17.1	17:43268297-43394414	NOTEST	0.0143697	0.0837702	2.54341	0	1	1
ENSG00000267122	ENSG00000267122	AC004490.1	19:2100987-2248678	NOTEST	0.0166885	0.00407043	-2.0356	0	1	1
ENSG00000267123	ENSG00000267123	CTD-2357A8.3	17:76613470-76628139	NOTEST	0	0.0350729	inf	0	1	1
ENSG00000267124	ENSG00000267124	CTD-3113P16.5	19:305572-344798	NOTEST	0.335006	0.0981422	-1.77124	0	1	1
ENSG00000267126	ENSG00000267126	CTC-550B14.8	HSCHR19LRC_LRC_S_CTG1:55434466-55512100	NOTEST	0	0	0	0	1	1
ENSG00000267127	ENSG00000267127	RP11-795F19.5	18:77794345-77854968	NOTEST	0.0543839	0.0700822	0.365868	0	1	1
ENSG00000267128	ENSG00000267128	RNF157-AS1	17:74132413-74236454	NOTEST	0.213538	0.312162	0.5478	0	1	1
ENSG00000267129	ENSG00000267129	OR1AC1P	17:3181192-3290132	NOTEST	0	0	0	0	1	1
ENSG00000267130	ENSG00000267130	CTD-2540B15.9	19:33793762-33800293	NOTEST	0	0	0	0	1	1
ENSG00000267131	ENSG00000267131	RP11-332H18.5	17:58754813-59488916	NOTEST	0.149021	0.151486	0.02367	0	1	1
ENSG00000267132	ENSG00000267132	HMGB3P27	17:40800195-40800756	NOTEST	0	0	0	0	1	1
ENSG00000267133	ENSG00000267133	AC011518.2	19:32592993-32597443	NOTEST	0	0	0	0	1	1
ENSG00000267134	ENSG00000267134	RP11-146N18.1	18:61747242-62090836	NOTEST	0	0	0	0	1	1
ENSG00000267135	ENSG00000267135	AD000091.3	19:15722433-15722934	NOTEST	0.245729	7.31E-05	-11.7156	0	1	1
ENSG00000267136	ENSG00000267136	RP11-53B2.3	18:13217496-13652754	NOTEST	0.00974079	0.0149018	0.613374	0	1	1
ENSG00000267137	ENSG00000267137	RP11-15K2.2	17:59529764-59562471	NOTEST	0	0	0	0	1	1
ENSG00000267138	ENSG00000267138	AC005954.3	19:3750816-3761697	NOTEST	0.280146	0.0695238	-2.0106	0	1	1
ENSG00000267139	ENSG00000267139	AC005262.3	19:3094407-3124002	NOTEST	0	0	0	0	1	1
ENSG00000267140	ENSG00000267140	RP11-322E11.6	18:33023832-33077955	NOTEST	0.0866463	0	#NAME?	0	1	1
ENSG00000267141	ENSG00000267141	CTB-31O20.8	19:1852397-1863567	NOTEST	0	0.0241598	inf	0	1	1
ENSG00000267142	ENSG00000267142	CTD-3162L10.5	19:36912437-36913436	NOTEST	0	0	0	0	1	1
ENSG00000267143	ENSG00000267143	RP11-677O4.6	18:11619507-11639698	NOTEST	0	0	0	0	1	1
ENSG00000267144	ENSG00000267144	AC067968.3	19:44527755-44529414	NOTEST	0	0	0	0	1	1
ENSG00000267145	ENSG00000267145	AC006116.14	19:56732680-56904914	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267146	ENSG00000267146	RP11-383D22.1	18:54264438-54706076	NOTEST	0	0	0	0	1	1
ENSG00000267147	ENSG00000267147	CTC-548K16.1	19:14416269-14481008	NOTEST	0	0	0	0	1	1
ENSG00000267148	ENSG00000267148	AC005777.3	19:3775993-3776180	NOTEST	0	0	0	0	1	1
ENSG00000267149	ENSG00000267149	CTC-550B14.6	19:55517560-55582659	NOTEST	0	0	0	0	1	1
ENSG00000267150	ENSG00000267150	RP11-411B10.2	18:14057455-14132489	NOTEST	0.0946173	0.0506449	-0.901687	0	1	1
ENSG00000267151	ENSG00000267151	MIR2117	17:41522074-41528568	NOTEST	0	0	0	0	1	1
ENSG00000267152	ENSG00000267152	CTD-2528L19.6	19:38219486-38221544	NOTEST	0.228206	0.343527	0.590092	0	1	1
ENSG00000267153	ENSG00000267153	CTBP2P3	18:58279005-58569959	NOTEST	0	0	0	0	1	1
ENSG00000267154	ENSG00000267154	OR1M4P	19:9193787-9194074	NOTEST	0	0	0	0	1	1
ENSG00000267156	ENSG00000267156	TPMTP1	18:45156482-45157219	NOTEST	0	0	0	0	1	1
ENSG00000267157	ENSG00000267157	CTB-54O9.9	19:5782970-5791249	NOTEST	0.256219	0.110443	-1.21407	0	1	1
ENSG00000267159	ENSG00000267159	AC005391.2	19:925780-975939	NOTEST	0	0	0	0	1	1
ENSG00000267160	ENSG00000267160	RP11-1072C15.4	17:42733761-42767676	NOTEST	0.269704	0.454347	0.752418	0	1	1
ENSG00000267161	ENSG00000267161	AC005943.5	19:1573594-1575474	NOTEST	0.235157	0.157234	-0.580715	0	1	1
ENSG00000267162	ENSG00000267162	RP11-815J4.4	18:12093851-12129748	NOTEST	0	0	0	0	1	1
ENSG00000267163	ENSG00000267163	AC084219.3	19:44598491-44637027	NOTEST	0.51783	0.356779	-0.537446	0	1	1
ENSG00000267166	ENSG00000267166	RP11-527L4.5	17:41991800-42000369	NOTEST	0	0	0	0	1	1
ENSG00000267167	ENSG00000267167	RP11-687F6.1	18:44383186-44383857	NOTEST	0.114132	0.0693646	-0.718434	0	1	1
ENSG00000267168	ENSG00000267168	RP11-318A15.7	17:74722911-74777531	NOTEST	0	0	0	0	1	1
ENSG00000267170	ENSG00000267170	CALM2P1	17:68237464-68237902	NOTEST	0	0	0	0	1	1
ENSG00000267172	ENSG00000267172	RP11-397A16.3	18:53484397-53486990	NOTEST	0	0.0134569	inf	0	1	1
ENSG00000267173	ENSG00000267173	CTC-512J12.6	19:44830707-44952766	NOTEST	0	0	0	0	1	1
ENSG00000267174	ENSG00000267174	CTC-510F12.4	19:11406823-11465620	NOTEST	0	0	0	0	1	1
ENSG00000267175	ENSG00000267175	RP11-879F14.1	18:59252978-59421928	NOTEST	0.0421902	0	#NAME?	0	1	1
ENSG00000267177	ENSG00000267177	RP11-756J15.3	18:13217496-13652754	NOTEST	0	0	0	0	1	1
ENSG00000267178	ENSG00000267178	PHF5CP	19:19672521-19729725	NOTEST	0.0955986	0	#NAME?	0	1	1
ENSG00000267179	ENSG00000267179	ZNF763	19:12035882-12091196	NOTEST	0	0.0694295	inf	0	1	1
ENSG00000267180	ENSG00000267180	AC007136.1	19:1985446-2034880	NOTEST	0.776423	0	#NAME?	0	1	1
ENSG00000267181	ENSG00000267181	RP11-428O23.1	17:34443569-34504870	NOTEST	0	0	0	0	1	1
ENSG00000267182	ENSG00000267182	RP11-382N13.5	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000267183	ENSG00000267183	AC010525.6	19:56186591-56249768	NOTEST	0.1624	0.118863	-0.450258	0	1	1
ENSG00000267184	ENSG00000267184	RP1-200G19.1	17:67573391-67899141	NOTEST	0	0	0	0	1	1
ENSG00000267185	ENSG00000267185	PTP4A2P1	17:40685549-40686027	NOTEST	0.0967538	0.0343962	-1.49207	0	1	1
ENSG00000267186	ENSG00000267186	CTC-550B14.8	HSCHR19LRC_COX1_CTG1:55355793-55433427	NOTEST	0	0	0	0	1	1
ENSG00000267187	ENSG00000267187	RP11-767C4.1	18:45229545-45230116	NOTEST	0	0	0	0	1	1
ENSG00000267188	ENSG00000267188	CTC-512J12.4	19:44830707-44952766	NOTEST	0	0	0	0	1	1
ENSG00000267189	ENSG00000267189	ATP5LP7	17:40799851-40800161	NOTEST	0	0	0	0	1	1
ENSG00000267190	ENSG00000267190	AC002314.4	19:36174679-36175103	NOTEST	0	0	0	0	1	1
ENSG00000267191	ENSG00000267191	RP11-15A1.2	19:44406152-44439430	NOTEST	0.0429308	0	#NAME?	0	1	1
ENSG00000267192	ENSG00000267192	AC006116.12	19:56732680-56904914	NOTEST	0.0990712	0	#NAME?	0	1	1
ENSG00000267193	ENSG00000267193	RP11-116O18.3	18:42792959-43332485	NOTEST	0	0	0	0	1	1

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ENSG00000267195	ENSG00000267195	MIR212	17:1953564-1953674	NOTEST	0	0	0	0	1	1
ENSG00000267196	ENSG00000267196	RP11-813F20.4	18:47309868-47721463	NOTEST	0	0	0	0	1	1
ENSG00000267197	ENSG00000267197	CTC-429L19.3	19:10596795-10614417	NOTEST	0.0795279	0.0570147	-0.480127	0	1	1
ENSG00000267198	ENSG00000267198	RP11-798G7.6	17:43578684-43640596	NOTEST	0.10898	0.0297398	-1.8736	0	1	1
ENSG00000267199	ENSG00000267199	RP11-861E21.2	18:12438888-12725739	NOTEST	0.110482	0.18032	0.706741	0	1	1
ENSG00000267200	ENSG00000267200	MIR132	17:1953201-1953302	NOTEST	0	0	0	0	1	1
ENSG00000267202	ENSG00000267202	RP11-797E24.3	18:34823009-35146000	NOTEST	0	0	0	0	1	1
ENSG00000267204	ENSG00000267204	AC011518.1	19:32592993-32597443	NOTEST	0	0	0	0	1	1
ENSG00000267205	ENSG00000267205	AC005954.4	19:3750816-3761697	NOTEST	0.0645565	0.183846	1.50987	0	1	1
ENSG00000267206	ENSG00000267206	LCN6	9:139632618-139642980	NOTEST	0	0	0	0	1	1
ENSG00000267207	ENSG00000267207	RP11-264B14.1	17:58754813-59488916	NOTEST	0	0	0	0	1	1
ENSG00000267208	ENSG00000267208	ABC9-43961700F1.1	HSCHR17_5_CTG4:39394252-39394717	NOTEST	0	0	0	0	1	1
ENSG00000267209	ENSG00000267209	RP11-693L9.2	18:55628462-55631666	NOTEST	0	0	0	0	1	1
ENSG00000267211	ENSG00000267211	RP5-1067M6.3	17:42405980-42408830	NOTEST	0	0	0	0	1	1
ENSG00000267212	ENSG00000267212	CTD-2659N19.9	19:12873816-12985765	NOTEST	0	0	0	0	1	1
ENSG00000267214	ENSG00000267214	CTC-265F19.3	19:2511216-2702707	NOTEST	0	0	0	0	1	1
ENSG00000267215	ENSG00000267215	RP11-685A21.1	18:56749155-56752213	NOTEST	0	0	0	0	1	1
ENSG00000267218	ENSG00000267218	AC005336.5	19:16013109-16014048	NOTEST	0.0353331	0	#NAME?	0	1	1
ENSG00000267219	ENSG00000267219	AC010504.2	19:34745441-34850317	NOTEST	0.138277	0.40364	1.54551	0	1	1
ENSG00000267220	ENSG00000267220	CTC-260E6.9	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000267221	ENSG00000267221	CTD-2132N18.2	17:40118758-40217383	NOTEST	0.310712	0.319643	0.0408842	0	1	1
ENSG00000267222	ENSG00000267222	RP11-194N12.2	17:40610861-40674629	NOTEST	0	0.0225345	inf	0	1	1
ENSG00000267223	ENSG00000267223	AC005597.1	19:30710572-31204445	NOTEST	0	0.133155	inf	0	1	1
ENSG00000267224	ENSG00000267224	AC005498.4	19:57046667-57047132	NOTEST	0	0	0	0	1	1
ENSG00000267225	ENSG00000267225	WDR7-OT1	18:54264438-54706076	NOTEST	0.0786414	0	#NAME?	0	1	1
ENSG00000267226	ENSG00000267226	RP11-126O1.5	18:56337711-56421709	NOTEST	0.0786411	0.0243426	-1.6918	0	1	1
ENSG00000267227	ENSG00000267227	RP11-640I15.2	17:15602890-15652629	NOTEST	0	0	0	0	1	1
ENSG00000267228	ENSG00000267228	IER3IP1	18:44632316-44702745	NOTEST	0	0	0	0	1	1
ENSG00000267229	ENSG00000267229	ALG9	HG388_HG400_PATCH:111652918-111756698	NOTEST	0	0	0	0	1	1
ENSG00000267230	ENSG00000267230	RP11-376M2.2	17:41102542-41132545	NOTEST	0.0104884	0	#NAME?	0	1	1
ENSG00000267231	ENSG00000267231	AC005786.5	19:3506270-3579086	NOTEST	0	0.293754	inf	0	1	1
ENSG00000267232	ENSG00000267232	CTB-31O20.9	19:1874880-1876168	NOTEST	0	0	0	0	1	1
ENSG00000267233	ENSG00000267233	HNRNPA3P16	18:48324573-48351772	NOTEST	0	0	0	0	1	1
ENSG00000267234	ENSG00000267234	CTB-184G21.3	19:19496634-19619740	NOTEST	0	0	0	0	1	1
ENSG00000267235	ENSG00000267235	ZNF861P	19:15932605-15934607	NOTEST	0	0	0	0	1	1
ENSG00000267237	ENSG00000267237	AC092299.6	19:182672-196756	NOTEST	0	0	0	0	1	1
ENSG00000267238	ENSG00000267238	AC093074.1	19:28885757-28887335	NOTEST	0	0	0	0	1	1
ENSG00000267239	ENSG00000267239	RP11-794M8.1	18:13203772-13216366	NOTEST	0	0	0	0	1	1
ENSG00000267240	ENSG00000267240	AC011524.3	19:29451412-29455850	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267241	ENSG00000267241	CYP4F10P	19:15774915-15780636	NOTEST	0	0	0	0	1	1
ENSG00000267242	ENSG00000267242	AC069278.4	19:44978644-44979403	NOTEST	0.416968	0.453042	0.11971	0	1	1
ENSG00000267243	ENSG00000267243	AC005307.3	19:28926294-29218684	NOTEST	0.331971	0.124565	-1.41416	0	1	1
ENSG00000267245	ENSG00000267245	CTD-2085J24.5	19:33210658-33320483	NOTEST	0	0	0	0	1	1
ENSG00000267246	ENSG00000267246	RP11-798G7.7	17:43578684-43640596	NOTEST	0	0	0	0	1	1
ENSG00000267247	ENSG00000267247	RP11-64C12.6	18:12230409-12231572	NOTEST	0	0	0	0	1	1
ENSG00000267249	ENSG00000267249	RP11-973H7.3	18:12438888-12725739	NOTEST	0.392742	0.492465	0.326441	0	1	1
ENSG00000267250	ENSG00000267250	RP11-118B18.2	17:66789689-66793963	NOTEST	0	0	0	0	1	1
ENSG00000267251	ENSG00000267251	AC139100.3	18:77905806-78005429	NOTEST	0.154077	0.360383	1.22588	0	1	1
ENSG00000267252	ENSG00000267252	RP11-712C7.1	18:11447754-11506982	NOTEST	0	0	0	0	1	1
ENSG00000267253	ENSG00000267253	RP11-209M4.1	17:41795681-41797804	NOTEST	0	0	0	0	1	1
ENSG00000267255	ENSG00000267255	CTB-50L17.5	19:4402658-4457819	NOTEST	0	0.0290654	inf	0	1	1
ENSG00000267256	ENSG00000267256	CTC-260E6.8	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000267257	ENSG00000267257	RP11-1151B14.4	18:56148478-56296189	NOTEST	0	0	0	0	1	1
ENSG00000267258	ENSG00000267258	CTC-448F2.3	19:30412088-30412560	NOTEST	0	0	0	0	1	1
ENSG00000267259	ENSG00000267259	CTD-2008P7.9	17:26559615-26562307	NOTEST	0	0	0	0	1	1
ENSG00000267260	ENSG00000267260	CTD-2162K18.4	19:37264054-37267980	NOTEST	0.186955	0.217191	0.216276	0	1	1
ENSG00000267261	ENSG00000267261	CTD-2132N18.3	17:40265125-40307990	NOTEST	0	0.325821	inf	0	1	1
ENSG00000267262	ENSG00000267262	CTC-232P5.3	19:5978413-6199583	NOTEST	0	0	0	0	1	1
ENSG00000267263	ENSG00000267263	RP11-75C10.7	17:75253818-75496678	NOTEST	0.104325	0.252395	1.27459	0	1	1
ENSG00000267264	ENSG00000267264	CTC-459F4.6	19:28175487-28475892	NOTEST	0.367957	0.496596	0.432536	0	1	1
ENSG00000267267	ENSG00000267267	CTD-3199J23.4	17:41177257-41184057	NOTEST	0.0422566	0.0217226	-0.959981	0	1	1
ENSG00000267268	ENSG00000267268	AC007204.2	19:20011721-20074273	NOTEST	0	0	0	0	1	1
ENSG00000267269	ENSG00000267269	RP11-2N1.1	18:57098171-57364644	NOTEST	0	0	0	0	1	1
ENSG00000267271	ENSG00000267271	RP11-686D22.2	17:33671249-33671583	NOTEST	0	0	0	0	1	1
ENSG00000267272	ENSG00000267272	LINC01140	1:87380330-87634884	NOTEST	0.0367041	0.0486912	0.407719	0	1	1
ENSG00000267273	ENSG00000267273	CTC-543D15.3	19:9609353-9620755	NOTEST	0	0	0	0	1	1
ENSG00000267274	ENSG00000267274	CTD-2006C1.12	19:12035882-12091196	NOTEST	0.0500021	0	#NAME?	0	1	1
ENSG00000267275	ENSG00000267275	CTD-2562J15.6	19:16394169-16435325	NOTEST	0	0	0	0	1	1
ENSG00000267277	ENSG00000267277	CTD-2342J14.6	19:11478798-11487627	NOTEST	0.0731025	0.211806	1.53475	0	1	1
ENSG00000267281	ENSG00000267281	RP11-793H13.10	12:53900471-54020199	NOTEST	0.569299	0.224237	-1.34417	0	1	1
ENSG00000267282	ENSG00000267282	CTB-129P6.4	19:45349431-45406946	NOTEST	0.0597737	0	#NAME?	0	1	1
ENSG00000267284	ENSG00000267284	RP11-397A16.1	18:53388293-53455992	NOTEST	0	0	0	0	1	1
ENSG00000267285	ENSG00000267285	RP5-951N9.2	12:1021242-1605099	NOTEST	0	0	0	0	1	1
ENSG00000267286	ENSG00000267286	RP11-794M8.2	18:13183400-13185616	NOTEST	0	0	0	0	1	1
ENSG00000267287	ENSG00000267287	RP11-567M16.1	18:77336459-77349010	NOTEST	0	0	0	0	1	1
ENSG00000267288	ENSG00000267288	RP13-890H12.2	17:43224683-43248951	NOTEST	0.183645	0.241626	0.395855	0	1	1

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ENSG00000267289	ENSG00000267289	CTD-2623N2.1 1	19:9944754-9945689	NOTEST	0.0984074	0.0818932	-0.265024	0	1	1
ENSG00000267290	ENSG00000267290	AC092192 .1	19:176906-177913	NOTEST	0	0	0	0	1	1
ENSG00000267291	ENSG00000267291	CTB-186G2.1	19:39078280-39109522	NOTEST	0	0	0	0	1	1
ENSG00000267292	ENSG00000267292	RP11-703I16.2	18:12050307-12050671	NOTEST	0	0	0	0	1	1
ENSG00000267293	ENSG00000267293	RP11-8H2.1	18:43563501-43652238	NOTEST	0	0.02397	inf	0	1	1
ENSG00000267294	ENSG00000267294	SH3GL1P3	HG747_PATCH:66121892-66148584	NOTEST	0	0	0	0	1	1
ENSG00000267295	ENSG00000267295	CTD-2319I12.3	17:58191153-58198048	NOTEST	0	0	0	0	1	1
ENSG00000267296	ENSG00000267296	CEBPA-AS1	19:33793762-33800293	NOTEST	1.49E-06	6.33E-07	-1.23443	0	1	1
ENSG00000267297	ENSG00000267297	LRRC37A16P	HG747_PATCH:66121892-66148584	NOTEST	0	0	0	0	1	1
ENSG00000267298	ENSG00000267298	AC006116 .19	19:56732680-56904914	NOTEST	0.038286	0	#NAME?	0	1	1
ENSG00000267299	ENSG00000267299	CTB-66B24.1	19:5978413-6199583	NOTEST	0	0	0	0	1	1
ENSG00000267301	ENSG00000267301	RPL23AP77	18:21269406-21535030	NOTEST	0	0.0361851	inf	0	1	1
ENSG00000267302	ENSG00000267302	RP11-178C3.2	17:57970446-58096413	NOTEST	0.510977	0.4004	-0.351816	0	1	1
ENSG00000267303	ENSG00000267303	CTD-2369P2.1 2	19:10415478-10444316	NOTEST	0.427371	0.606595	0.505245	0	1	1
ENSG00000267304	ENSG00000267304	AC004637 .1	19:3630180-3700477	NOTEST	0	0.071182	inf	0	1	1
ENSG00000267305	ENSG00000267305	CTD-3113P16. 7	19:239144-239247	NOTEST	0	0	0	0	1	1
ENSG00000267306	ENSG00000267306	RP11-333J10.2	17:35306174-35414171	NOTEST	0.165846	0	#NAME?	0	1	1
ENSG00000267308	ENSG00000267308	AC004510 .3	19:15937854-15947130	NOTEST	0	0	0	0	1	1
ENSG00000267309	ENSG00000267309	CTD-2630F21.1	19:36936020-36981942	NOTEST	0.395396	0.367202	-0.106724	0	1	1
ENSG00000267310	ENSG00000267310	OR4G1P	19:104534-105471	NOTEST	0	0	0	0	1	1
ENSG00000267311	ENSG00000267311	RP11-99A1.2	18:52385090-52565314	NOTEST	0	0	0	0	1	1
ENSG00000267312	ENSG00000267312	RP11-1094M14. 7	17:33786499-33787569	NOTEST	0	0	0	0	1	1
ENSG00000267313	ENSG00000267313	RP11-142I20.1	18:39047394-39212149	NOTEST	0	0	0	0	1	1
ENSG00000267314	ENSG00000267314	AC104532 .2	19:5904851-5915888	NOTEST	0.110054	0	#NAME?	0	1	1
ENSG00000267315	ENSG00000267315	RP11-686D22.6	17:33704434-33704697	NOTEST	0	0	0	0	1	1
ENSG00000267316	ENSG00000267316	RP11-879F14.3	18:59238574-59246689	NOTEST	0	0	0	0	1	1
ENSG00000267318	ENSG00000267318	RP11-178C3.1	17:57970446-58096413	NOTEST	0.01404	0.143293	3.35136	0	1	1
ENSG00000267319	ENSG00000267319	CTD-2528L19.3	19:37988062-38210691	NOTEST	0	0.0919902	inf	0	1	1
ENSG00000267320	ENSG00000267320	AC005780 .1	19:28807611-28877111	NOTEST	0	0	0	0	1	1
ENSG00000267322	ENSG00000267322	SCARNA17	18:47309868-47721463	NOTEST	0.037322	0.00799302	-2.22321	0	1	1
ENSG00000267324	ENSG00000267324	RP11-411B10.5	18:14143594-14151138	NOTEST	0	0	0	0	1	1
ENSG00000267325	ENSG00000267325	RP11-397A16.2	18:53388293-53455992	NOTEST	0	0	0	0	1	1
ENSG00000267326	ENSG00000267326	AC015849 .14	17:34136458-34195895	NOTEST	0	0	0	0	1	1
ENSG00000267327	ENSG00000267327	CTD-2008L17.1	18:53548918-53858493	NOTEST	0	0	0	0	1	1
ENSG00000267328	ENSG00000267328	AC002398 .12	19:36245466-36248980	NOTEST	0.00984098	0.0599124	2.60598	0	1	1
ENSG00000267329	ENSG00000267329	CTC-550B14.6	HSCHR19LRC_COX1_CTG1:55438477-55503576	NOTEST	0	0	0	0	1	1
ENSG00000267330	ENSG00000267330	AC131056 .5	17:34552689-34554250	NOTEST	0	0	0	0	1	1
ENSG00000267332	ENSG00000267332	CTD-2596O15. 1	19:9130019-9130660	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267333	ENSG00000267333	RP11-677O4.7	18:11688954-11909222	NOTEST	0	0	0	0	1	1
ENSG00000267334	ENSG00000267334	CTD-2534I21.8	17:43025279-43026307	NOTEST	0	0	0	0	1	1
ENSG00000267335	ENSG00000267335	CTB-60B18.6	19:49526125-49552400	NOTEST	0	0	0	0	1	1
ENSG00000267336	ENSG00000267336	RP11-773H22.2	18:12785476-12929642	NOTEST	0	0	0	0	1	1
ENSG00000267337	ENSG00000267337	CTC-782O7.1	18:41903400-42111662	NOTEST	0	0	0	0	1	1
ENSG00000267338	ENSG00000267338	KB-7G2.9	22:17082776-17185367	NOTEST	0	0	0	0	1	1
ENSG00000267339	ENSG00000267339	LINC00906	19:29456037-29461781	NOTEST	0.0303322	0	#NAME?	0	1	1
ENSG00000267341	ENSG00000267341	RP11-640A1.3	18:59992519-60058516	NOTEST	0	0	0	0	1	1
ENSG00000267342	ENSG00000267342	RP11-552F3.10	17:73893140-73937221	NOTEST	0.33955	0.330774	-0.0377779	0	1	1
ENSG00000267343	ENSG00000267343	CTC-499B15.4	19:11750590-11797382	NOTEST	0.000696904	0.00260487	1.90218	0	1	1
ENSG00000267344	ENSG00000267344	CTB-39G8.3	17:43471274-43511787	NOTEST	0	0.0369548	inf	0	1	1
ENSG00000267345	ENSG00000267345	CTD-2293H3.2	19:37498758-37734828	NOTEST	0.33376	0.116235	-1.52176	0	1	1
ENSG00000267346	ENSG00000267346	EIF5AP3	19:45574757-45808541	NOTEST	0.0510326	0.233011	2.19091	0	1	1
ENSG00000267347	ENSG00000267347	AC015849.13	17:34136458-34195895	NOTEST	0.111837	0.0463161	-1.27182	0	1	1
ENSG00000267349	ENSG00000267349	RP11-686D22.9	17:33791267-33864880	NOTEST	0	0	0	0	1	1
ENSG00000267351	ENSG00000267351	CTC-550B14.8	HSCHR19LRC_LRC_T_CTG1:55370759-55448393	NOTEST	0	0	0	0	1	1
ENSG00000267353	ENSG00000267353	CTD-2162K18.3	19:37264054-37267980	NOTEST	0.0283799	0.00569549	-2.31698	0	1	1
ENSG00000267354	ENSG00000267354	RP11-749H17.2	18:42792959-43332485	NOTEST	0	0	0	0	1	1
ENSG00000267355	ENSG00000267355	RPL9P29	17:76842034-76842950	NOTEST	0.0352014	0.157017	2.15722	0	1	1
ENSG00000267356	ENSG00000267356	RP11-411B10.3	18:14057455-14132489	NOTEST	0.204749	0	#NAME?	0	1	1
ENSG00000267357	ENSG00000267357	CTC-550B14.6	HSCHR19LRC_LRC_T_CTG1:55453443-55518542	NOTEST	0	0	0	0	1	1
ENSG00000267359	ENSG00000267359	RP11-1094M14.12	17:33875143-33885117	NOTEST	0	0	0	0	1	1
ENSG00000267360	ENSG00000267360	CTC-454I21.3	19:37498758-37734828	NOTEST	0	0	0	0	1	1
ENSG00000267361	ENSG00000267361	LOC100421166	17:67074842-67138029	NOTEST	0	0	0	0	1	1
ENSG00000267362	ENSG00000267362	CTC-550B14.6	HSCHR19LRC_LRC_S_CTG1:55517150-55582249	NOTEST	0	0	0	0	1	1
ENSG00000267363	ENSG00000267363	CTD-3162L10.4	19:36870252-36871814	NOTEST	0	0	0	0	1	1
ENSG00000267364	ENSG00000267364	RP11-47L3.1	17:33640520-33651919	NOTEST	0	0	0	0	1	1
ENSG00000267365	ENSG00000267365	KCNJ2-AS1	17:68163101-68176189	NOTEST	0.339424	0.548384	0.692098	0	1	1
ENSG00000267366	ENSG00000267366	RP11-53B2.5	18:13217496-13652754	NOTEST	0	0.0700363	inf	0	1	1
ENSG00000267367	ENSG00000267367	CTC-550B14.7	HSCHR19LRC_LRC_T_CTG1:55453443-55518542	NOTEST	0	0	0	0	1	1
ENSG00000267369	ENSG00000267369	RP11-1094M14.8	17:33791267-33864880	NOTEST	0	0	0	0	1	1
ENSG00000267370	ENSG00000267370	CTD-2623N2.3	19:9862668-9903856	NOTEST	0.265698	0.0601698	-2.14267	0	1	1
ENSG00000267371	ENSG00000267371	RP11-712C7.2	18:11552364-11552846	NOTEST	0	0	0	0	1	1
ENSG00000267372	ENSG00000267372	AC005330.2	19:1285889-1378430	NOTEST	0	0.0202748	inf	0	1	1
ENSG00000267373	ENSG00000267373	CTD-2231E14.5	19:16214570-16215064	NOTEST	0	0	0	0	1	1
ENSG00000267374	ENSG00000267374	LINC00669	18:36786887-37380282	NOTEST	0	0	0	0	1	1
ENSG00000267375	ENSG00000267375	CTB-186G2.4	19:39138288-39260544	NOTEST	0	0	0	0	1	1
ENSG00000267376	ENSG00000267376	ATP5LP6	17:74132413-74236454	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000267378	ENSG00000267378	CTC-400I9.3	19:31437487-31448098	NOTEST	0	0	0	0	1	1
ENSG00000267379	ENSG00000267379	CTC-548K16.5	19:14491312-14519537	NOTEST	0	0	0	0	1	1
ENSG00000267380	ENSG00000267380	RP11-697E22.3	17:35969786-36044255	NOTEST	0	0	0	0	1	1
ENSG00000267381	ENSG00000267381	CTD-2086O20.3	19:37978900-37979554	NOTEST	0.574697	0.480117	-0.259415	0	1	1
ENSG00000267382	ENSG00000267382	RP11-325K19.2	18:58279005-58569959	NOTEST	0	0	0	0	1	1
ENSG00000267383	ENSG00000267383	CTC-260E6.6	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000267384	ENSG00000267384	RP11-1072C15.3	17:42722778-42722958	NOTEST	0	0	0	0	1	1
ENSG00000267385	ENSG00000267385	CTB-50L17.14	19:4522542-4540486	NOTEST	0.0164955	0	#NAME?	0	1	1
ENSG00000267386	ENSG00000267386	CTD-2378E21.1	HSCHR17_2_CTG4:68308971-68371110	NOTEST	0	0	0	0	1	1
ENSG00000267387	ENSG00000267387	CTD-2240E14.4	19:10196797-10213472	NOTEST	0.489705	0.34878	-0.489595	0	1	1
ENSG00000267388	ENSG00000267388	AF038458.5	19:36451413-36454965	NOTEST	0	0	0	0	1	1
ENSG00000267389	ENSG00000267389	CTC-459F4.7	19:28175487-28475892	NOTEST	0	0	0	0	1	1
ENSG00000267390	ENSG00000267390	RP11-635N19.1	18:60994958-61048862	NOTEST	0.348109	0.524773	0.592153	0	1	1
ENSG00000267391	ENSG00000267391	RP11-1151B14.3	18:56113506-56116856	NOTEST	0	0	0	0	1	1
ENSG00000267392	ENSG00000267392	CYP4F9P	19:16090644-16109830	NOTEST	0	0	0	0	1	1
ENSG00000267393	ENSG00000267393	RP11-691H4.3	18:13217496-13652754	NOTEST	0	0	0	0	1	1
ENSG00000267394	ENSG00000267394	CTB-175E5.7	17:42269172-42301078	NOTEST	0	0	0	0	1	1
ENSG00000267395	ENSG00000267395	AC074212.6	19:46268042-46296060	NOTEST	0.15637	0.249449	0.673783	0	1	1
ENSG00000267396	ENSG00000267396	RP11-845C23.3	18:55711598-56068772	NOTEST	0	0.131662	inf	0	1	1
ENSG00000267397	ENSG00000267397	RP11-873E20.1	18:33296333-33297942	NOTEST	0.0807061	0.0145234	-2.47429	0	1	1
ENSG00000267398	ENSG00000267398	AC006130.4	19:2867332-2878515	NOTEST	0	0	0	0	1	1
ENSG00000267399	ENSG00000267399	RP11-456O19.5	18:53548918-53858493	NOTEST	0	0	0	0	1	1
ENSG00000267400	ENSG00000267400	RP11-325K19.3	18:58163100-58163569	NOTEST	0	0	0	0	1	1
ENSG00000267401	ENSG00000267401	RP11-396N11.1	18:57961383-57968351	NOTEST	0	0	0	0	1	1
ENSG00000267402	ENSG00000267402	RP11-619L19.2	18:52889561-53332018	NOTEST	0	0	0	0	1	1
ENSG00000267404	ENSG00000267404	RP11-49I11.2	18:33853536-33854562	NOTEST	0.0173715	0	#NAME?	0	1	1
ENSG00000267405	ENSG00000267405	CTC-296K1.4	17:42872114-42875151	NOTEST	0.274979	0.294377	0.0983458	0	1	1
ENSG00000267406	ENSG00000267406	CTD-2189E23.2	19:14365000-14404017	NOTEST	0	0	0	0	1	1
ENSG00000267407	ENSG00000267407	CTD-2050I18.1	19:32032944-32045703	NOTEST	0	0	0	0	1	1
ENSG00000267408	ENSG00000267408	CTB-50L17.2	19:4621205-4622319	NOTEST	0	0	0	0	1	1
ENSG00000267409	ENSG00000267409	RP11-567M16.2	18:77370746-77372303	NOTEST	0	0	0	0	1	1
ENSG00000267412	ENSG00000267412	CTC-265F19.2	19:2511216-2702707	NOTEST	0.044708	0.015018	-1.57384	0	1	1
ENSG00000267413	ENSG00000267413	RP11-636O21.1	18:37421137-37504804	NOTEST	0	0	0	0	1	1
ENSG00000267414	ENSG00000267414	RP11-456K23.1	18:42256891-42259682	NOTEST	0.0156823	0.0282366	0.848428	0	1	1
ENSG00000267415	ENSG00000267415	CTC-503J8.2	19:5978413-6199583	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267416	ENSG00000267416	CTD-2319I12.2	17:58156669-58169246	NOTEST	0.103504	0.111718	0.110184	0	1	1
ENSG00000267417	ENSG00000267417	CTC-239J10.1	19:13106421-13209610	NOTEST	0	0.0300336	inf	0	1	1
ENSG00000267418	ENSG00000267418	TCEB1P29	19:9293044-9293724	NOTEST	0	0	0	0	1	1
ENSG00000267420	ENSG00000267420	RP11-527L4.6	17:42004930-42009990	NOTEST	0	0	0	0	1	1
ENSG00000267421	ENSG00000267421	AC005498.3	19:57047524-57049944	NOTEST	0.373652	0.191384	-0.965227	0	1	1
ENSG00000267422	ENSG00000267422	CTD-2554C21.1	19:38226733-38307940	NOTEST	0.200616	0.403041	1.00649	0	1	1
ENSG00000267423	ENSG00000267423	AC005616.2	19:28926294-29218684	NOTEST	0	0	0	0	1	1
ENSG00000267424	ENSG00000267424	CTD-2265O21.3	19:12873816-12985765	NOTEST	0.112615	0	#NAME?	0	1	1
ENSG00000267425	ENSG00000267425	RP11-128P17.1	18:11447754-11506982	NOTEST	0	0	0	0	1	1
ENSG00000267426	ENSG00000267426	RP11-552F3.12	17:73893140-73937221	NOTEST	0.0717629	0.0256298	-1.48542	0	1	1
ENSG00000267428	ENSG00000267428	RP11-289E15.1	18:52234227-52234534	NOTEST	0	0	0	0	1	1
ENSG00000267429	ENSG00000267429	AC006116.15	19:56732680-56904914	NOTEST	0.0159361	0.0224464	0.494186	0	1	1
ENSG00000267430	ENSG00000267430	RP11-635N19.2	18:61056422-61089716	NOTEST	0.015129	0	#NAME?	0	1	1
ENSG00000267431	ENSG00000267431	RP11-104J23.2	17:34339543-34339931	NOTEST	0	0	0	0	1	1
ENSG00000267432	ENSG00000267432	RP11-559N14.5	17:76374720-76573476	NOTEST	0.0356655	0.0694967	0.962416	0	1	1
ENSG00000267433	ENSG00000267433	CTD-2057D4.2	19:30392602-30392776	NOTEST	0.650778	0	#NAME?	0	1	1
ENSG00000267434	ENSG00000267434	CTC-550B14.7	HSCHR19LRC_COX2_CTG1:55180280-55245379	NOTEST	0	0	0	0	1	1
ENSG00000267437	ENSG00000267437	CTC-454I21.4	19:37498758-37734828	NOTEST	0	0	0	0	1	1
ENSG00000267438	ENSG00000267438	CTC-550B14.8	HSCHR19LRC_PGF2_CTG1:55164555-55242189	NOTEST	0	0	0	0	1	1
ENSG00000267439	ENSG00000267439	AC002398.11	19:36230057-36245420	NOTEST	0.507431	0.470197	-0.109946	0	1	1
ENSG00000267440	ENSG00000267440	CTC-501O10.1	17:41757640-41783252	NOTEST	0	0	0	0	1	1
ENSG00000267441	ENSG00000267441	RP1-37N7.5	17:18280975-18292961	NOTEST	0	0	0	0	1	1
ENSG00000267443	ENSG00000267443	AC010641.1	19:397588-398941	NOTEST	0	0	0	0	1	1
ENSG00000267444	ENSG00000267444	SMUG1P1	18:47176719-47177530	NOTEST	0	0	0	0	1	1
ENSG00000267445	ENSG00000267445	CTC-550B14.7	HSCHR19LRC_COX1_CTG1:55438477-55503576	NOTEST	0	0	0	0	1	1
ENSG00000267446	ENSG00000267446	CTB-39G8.2	17:43448767-43449423	NOTEST	0	0.154504	inf	0	1	1
ENSG00000267447	ENSG00000267447	VN2R11P	19:279494-280170	NOTEST	0	0	0	0	1	1
ENSG00000267448	ENSG00000267448	AC010649.1	19:3224700-3303001	NOTEST	0	0	0	0	1	1
ENSG00000267449	ENSG00000267449	RP11-264B14.2	17:58754813-59488916	NOTEST	0	0	0	0	1	1
ENSG00000267450	ENSG00000267450	OR1AB1P	19:16162738-16163499	NOTEST	0	0	0	0	1	1
ENSG00000267451	ENSG00000267451	LOC440461	HG747_PATCH:66195036-66195712	NOTEST	0	0	0	0	1	1
ENSG00000267452	ENSG00000267452	RP11-1018N14.5	17:49512787-49523163	NOTEST	0	0.028951	inf	0	1	1
ENSG00000267453	ENSG00000267453	AC004791.2	19:15962802-15975714	NOTEST	0	0	0	0	1	1
ENSG00000267454	ENSG00000267454	ZNF582-AS1	19:56905024-56947404	NOTEST	0.320831	0.453235	0.498448	0	1	1
ENSG00000267455	ENSG00000267455	RP11-78A19.2	18:11688954-11909222	NOTEST	0	0	0	0	1	1
ENSG00000267456	ENSG00000267456	RP11-49I11.3	18:33858697-33859082	NOTEST	0	0	0	0	1	1
ENSG00000267457	ENSG00000267457	RP5-837J1.4	17:33332106-33448541	NOTEST	0	0	0	0	1	1
ENSG00000267458	ENSG00000267458	CTC-425F1.4	19:13049391-13055303	NOTEST	0	0	0	0	1	1
ENSG00000267460	ENSG00000267460	CTB-186H2.1	17:34282480-34282601	NOTEST	0	0	0	0	1	1
ENSG00000267461	ENSG00000267461	RP11-120M18.5	17:66255322-66760023	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267462	ENSG00000267462	RP11-866E20.3	18:57677223-57681490	NOTEST	0	0	0	0	1	1
ENSG00000267463	ENSG00000267463	UBE2V2P2	17:76000248-76139049	NOTEST	0	0	0	0	1	1
ENSG00000267464	ENSG00000267464	CTC-260E6.7	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000267465	ENSG00000267465	AC011525.4	19:32078945-32086626	NOTEST	0	0	0	0	1	1
ENSG00000267466	ENSG00000267466	RP11-13K12.5	17:75559449-75564777	NOTEST	0	0	0	0	1	1
ENSG00000267467	ENSG00000267467	APOC4	19:45445494-45452822	NOTEST	0.113095	0.126169	0.157831	0	1	1
ENSG00000267468	ENSG00000267468	CTC-550B14.7	HSCHR19LRC_LRC_S_CTG1:55517150-55582249	NOTEST	0	0	0	0	1	1
ENSG00000267469	ENSG00000267469	AC005944.2	19:3052907-3063105	NOTEST	0	0	0	0	1	1
ENSG00000267471	ENSG00000267471	RP11-1058G23.1	17:68625057-68625406	NOTEST	0	0	0	0	1	1
ENSG00000267472	ENSG00000267472	LOC440461	17:66195061-66195737	NOTEST	0	0	0	0	1	1
ENSG00000267473	ENSG00000267473	AC005789.11	19:38888820-38890521	NOTEST	0.198413	0.16116	-0.300007	0	1	1
ENSG00000267474	ENSG00000267474	CTC-548K16.6	19:14543864-14582679	NOTEST	0.0756667	0.0499205	-0.600028	0	1	1
ENSG00000267476	ENSG00000267476	RP11-126O1.4	18:56337711-56421709	NOTEST	0	0	0	0	1	1
ENSG00000267477	ENSG00000267477	CTC-398G3.6	19:11562140-11639989	NOTEST	0	0	0	0	1	1
ENSG00000267478	ENSG00000267478	RP11-815J4.5	18:12091672-12093140	NOTEST	0	0	0	0	1	1
ENSG00000267479	ENSG00000267479	CTC-268N12.3	17:35306174-35414171	NOTEST	0	0	0	0	1	1
ENSG00000267480	ENSG00000267480	RP11-703I16.1	18:12031176-12032180	NOTEST	0.0834516	0.12224	0.550703	0	1	1
ENSG00000267481	ENSG00000267481	CTC-559E9.5	19:19868174-19945736	NOTEST	0.286819	0.253808	-0.176403	0	1	1
ENSG00000267482	ENSG00000267482	RNY4P13	17:27887564-28513493	NOTEST	0	0	0	0	1	1
ENSG00000267483	ENSG00000267483	RBFOX3	HG748_PATCH:77085426-77512230	NOTEST	0	0	0	0	1	1
ENSG00000267484	ENSG00000267484	CTC-518P12.6	19:4838343-4867780	NOTEST	0	0	0	0	1	1
ENSG00000267485	ENSG00000267485	CTC-550B14.6	HSCHR19LRC_COX2_CTG1:55180280-55245379	NOTEST	0	0	0	0	1	1
ENSG00000267486	ENSG00000267486	GLUD1P4	18:57445803-57446221	NOTEST	0	0	0	0	1	1
ENSG00000267487	ENSG00000267487	RP11-640A1.4	18:60085550-60085809	NOTEST	0	0	0	0	1	1
ENSG00000267488	ENSG00000267488	AC131056.3	17:34510614-34524157	NOTEST	0	0	0	0	1	1
ENSG00000267489	ENSG00000267489	CTC-360P9.4	19:32458004-32516697	NOTEST	0	0	0	0	1	1
ENSG00000267490	ENSG00000267490	CTD-3116E22.6	19:9834683-9835762	NOTEST	0	0	0	0	1	1
ENSG00000267491	ENSG00000267491	CTD-2373H9.5	17:76849058-76921469	NOTEST	0.370497	0.531874	0.521621	0	1	1
ENSG00000267492	ENSG00000267492	RP1-37N7.6	17:18353557-18379234	NOTEST	0	0	0	0	1	1
ENSG00000267494	ENSG00000267494	CTC-550B14.6	HSCHR19LRC_PGF2_CTG1:55247239-55312338	NOTEST	0	0	0	0	1	1
ENSG00000267496	ENSG00000267496	FAM215A	17:41991800-42000369	NOTEST	0	0	0	0	1	1
ENSG00000267497	ENSG00000267497	NFE2L3P1	18:57636669-57638628	NOTEST	0.015047	0	#NAME?	0	1	1
ENSG00000267498	ENSG00000267498	CTB-32O4.2	19:29698172-29706722	NOTEST	0.295737	0.0861762	-1.77895	0	1	1
ENSG00000267499	ENSG00000267499	CTD-3194G12.1	17:35041202-35041578	NOTEST	0	0	0	0	1	1
ENSG00000267500	ENSG00000267500	CTD-2006C1.6	19:11750590-11797382	NOTEST	0.591448	0.49111	-0.268207	0	1	1
ENSG00000267501	ENSG00000267501	RP11-108P20.2	18:56422090-56425074	NOTEST	0.0261053	0	#NAME?	0	1	1
ENSG00000267502	ENSG00000267502	CTC-550B14.8	19:55434876-55512510	NOTEST	0	0	0	0	1	1
ENSG00000267503	ENSG00000267503	RP11-53B2.4	18:13217496-13652754	NOTEST	0	0	0	0	1	1
ENSG00000267504	ENSG00000267504	RP11-845C23.2	18:55711598-56068772	NOTEST	0.365192	0.405201	0.149984	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267505	ENSG00000267505	CTC-296K1.3	17:42870566-42871842	NOTEST	0.515197	0.528006	0.0354285	0	1	1
ENSG00000267506	ENSG00000267506	RP11-13K12.1	17:75543021-75559325	NOTEST	0	0	0	0	1	1
ENSG00000267507	ENSG00000267507	CTD-2587H24.1	19:55630617-55631751	NOTEST	0	0	0	0	1	1
ENSG00000267508	ENSG00000267508	ZNF285	19:44830707-44952766	NOTEST	0.380219	0.564865	0.571076	0	1	1
ENSG00000267509	ENSG00000267509	CTD-2043I16.1	19:28556173-28616337	NOTEST	0	0	0	0	1	1
ENSG00000267510	ENSG00000267510	CTC-325H20.4	19:9402190-9420514	NOTEST	0.503285	0.148437	-1.76152	0	1	1
ENSG00000267511	ENSG00000267511	ADAD1P2	18:47309868-47721463	NOTEST	0	0	0	0	1	1
ENSG00000267513	ENSG00000267513	RP11-622J9.1	18:58279005-58569959	NOTEST	0	0	0	0	1	1
ENSG00000267514	ENSG00000267514	CTC-550B14.7	HSCHR19LRC_LRC_J_CTG1:55542601-55607700	NOTEST	0	0	0	0	1	1
ENSG00000267515	ENSG00000267515	RP11-861E21.3	18:12438888-12725739	NOTEST	0.193907	0.0247647	-2.96901	0	1	1
ENSG00000267516	ENSG00000267516	CTC-550B14.8	HSCHR19LRC_COX2_CTG1:55097597-55175230	NOTEST	0	0	0	0	1	1
ENSG00000267517	ENSG00000267517	CTD-2231E14.4	19:16176546-16177122	NOTEST	0	0	0	0	1	1
ENSG00000267518	ENSG00000267518	RP11-794C22.2	17:74305566-74383941	NOTEST	0	0	0	0	1	1
ENSG00000267520	ENSG00000267520	RP11-373L24.1	2:61108655-61158745	NOTEST	6.32E-05	0.0356019	9.13741	0	1	1
ENSG00000267521	ENSG00000267521	RP11-87G24.6	17:74864537-74965238	NOTEST	0	0	0	0	1	1
ENSG00000267522	ENSG00000267522	CTD-2621I17.6	19:56578049-56590167	NOTEST	0	0	0	0	1	1
ENSG00000267524	ENSG00000267524	RPSAP57	18:52385090-52565314	NOTEST	0	0	0	0	1	1
ENSG00000267525	ENSG00000267525	CTC-550B14.7	HSCHR19LRC_PGF1_CTG1:55437861-55502960	NOTEST	0	0	0	0	1	1
ENSG00000267526	ENSG00000267526	RP11-178C3.6	17:58120554-58156292	NOTEST	0	0	0	0	1	1
ENSG00000267529	ENSG00000267529	RP11-53B2.1	18:13217496-13652754	NOTEST	0	0	0	0	1	1
ENSG00000267530	ENSG00000267530	AC006273.5	19:782754-785080	NOTEST	0	0	0	0	1	1
ENSG00000267532	ENSG00000267532	MIR497HG	17:6757179-6922978	NOTEST	0.0315177	0.153817	2.28698	0	1	1
ENSG00000267533	ENSG00000267533	RP11-815J4.7	18:12067171-12068416	NOTEST	0	0	0	0	1	1
ENSG00000267535	ENSG00000267535	LINC00868	17:74846257-74857918	NOTEST	0	0.0153643	inf	0	1	1
ENSG00000267536	ENSG00000267536	AC131056.5	HG75_PATCH:34552621-34554183	NOTEST	0	0	0	0	1	1
ENSG00000267537	ENSG00000267537	AC005394.1	19:28926294-29218684	NOTEST	0	0	0	0	1	1
ENSG00000267539	ENSG00000267539	RP11-138H8.7	15:71121468-71123745	NOTEST	0	0	0	0	1	1
ENSG00000267540	ENSG00000267540	CTC-550B14.6	HSCHR19LRC_PGF1_CTG1:55437861-55502960	NOTEST	0	0	0	0	1	1
ENSG00000267541	ENSG00000267541	RP11-380M21.2	18:45357921-45457515	NOTEST	0.493107	0.175265	-1.49236	0	1	1
ENSG00000267542	ENSG00000267542	RP11-697E22.1	17:35969786-36044255	NOTEST	0	0.156349	inf	0	1	1
ENSG00000267543	ENSG00000267543	RP11-666A8.7	17:74523437-74553765	NOTEST	0.180659	0.166904	-0.114247	0	1	1
ENSG00000267544	ENSG00000267544	AC007229.3	19:10947250-10980466	NOTEST	0.116176	0.043938	-1.40277	0	1	1
ENSG00000267545	ENSG00000267545	AC005779.2	19:45574757-45808541	NOTEST	0.072717	0	#NAME?	0	1	1
ENSG00000267547	ENSG00000267547	RP11-686D22.4	17:33730855-33731392	NOTEST	0.156553	0.256606	0.712908	0	1	1
ENSG00000267549	ENSG00000267549	AC006116.17	19:56732680-56904914	NOTEST	0.0789709	0.023517	-1.74761	0	1	1
ENSG00000267550	ENSG00000267550	CTC-482H14.5	19:5158505-5340814	NOTEST	0	0	0	0	1	1
ENSG00000267551	ENSG00000267551	AC005264.2	19:3136190-3163767	NOTEST	0	0	0	0	1	1
ENSG00000267552	ENSG00000267552	CTD-2528L19.4	19:37988062-38210691	NOTEST	0.00202518	0	#NAME?	0	1	1

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ENSG00000267554	ENSG00000267554	RP11-686D22.10	17:33791267-33864880	NOTEST	0	0	0	0	1	1
ENSG00000267555	ENSG00000267555	CTD-2085J24.3	19:33321414-33360672	NOTEST	0	0	0	0	1	1
ENSG00000267556	ENSG00000267556	SARM1	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000267557	ENSG00000267557	CTC-379B2.4	19:33087912-33169206	NOTEST	0	0	0	0	1	1
ENSG00000267558	ENSG00000267558	RP11-618K16.4	18:43368494-43368632	NOTEST	0	0	0	0	1	1
ENSG00000267559	ENSG00000267559	RP11-383M4.6	9:84542935-84592004	NOTEST	0	0	0	0	1	1
ENSG00000267560	ENSG00000267560	RP11-173A16.1	18:59854490-59974355	NOTEST	0.0906833	0.0995571	0.134687	0	1	1
ENSG00000267561	ENSG00000267561	RP5-1052I5.2	1:87380330-87634884	NOTEST	0.046892	0.047292	0.0122554	0	1	1
ENSG00000267562	ENSG00000267562	CTC-421K24.1	17:35766964-35839835	NOTEST	0.157051	0	#NAME?	0	1	1
ENSG00000267563	ENSG00000267563	CTC-503J8.4	19:6212965-6279959	NOTEST	0	0	0	0	1	1
ENSG00000267564	ENSG00000267564	RP11-128P17.3	18:11447754-11506982	NOTEST	0	0	0	0	1	1
ENSG00000267565	ENSG00000267565	CTC-559E9.8	19:19976694-20006656	NOTEST	0.127873	0	#NAME?	0	1	1
ENSG00000267566	ENSG00000267566	RP11-104J23.1	17:34310326-34338658	NOTEST	0	0	0	0	1	1
ENSG00000267567	ENSG00000267567	CTD-2538C1.3	19:33209203-33210501	NOTEST	0	0	0	0	1	1
ENSG00000267568	ENSG00000267568	RP11-87G24.3	17:74864537-74965238	NOTEST	0	0.100724	inf	0	1	1
ENSG00000267570	ENSG00000267570	RP11-773H22.1	18:12785476-12929642	NOTEST	0	0	0	0	1	1
ENSG00000267571	ENSG00000267571	AC104532.4	19:5904851-5915888	NOTEST	0	0	0	0	1	1
ENSG00000267572	ENSG00000267572	CTC-550B14.8	HSCHR19LRC_LRC_I_CTG1:55432380-55510014	NOTEST	0	0	0	0	1	1
ENSG00000267573	ENSG00000267573	KRT8P5	18:41900764-41902222	NOTEST	0	0	0	0	1	1
ENSG00000267574	ENSG00000267574	CTC-525D6.5	19:29777917-30055386	NOTEST	0	0	0	0	1	1
ENSG00000267576	ENSG00000267576	CTC-510F12.6	19:11406823-11465620	NOTEST	0.0120451	0.330375	4.77758	0	1	1
ENSG00000267577	ENSG00000267577	CTD-2587H24.5	19:55663136-55691809	NOTEST	0	0	0	0	1	1
ENSG00000267578	ENSG00000267578	AC015849.12	17:34135492-34135901	NOTEST	0	0	0	0	1	1
ENSG00000267579	ENSG00000267579	RP11-126O1.2	18:56148478-56296189	NOTEST	0	0	0	0	1	1
ENSG00000267580	ENSG00000267580	CTD-2540B15.11	19:33790839-33793470	NOTEST	0	0.0100567	inf	0	1	1
ENSG00000267581	ENSG00000267581	CTC-559E9.4	19:19868174-19945736	NOTEST	0	0	0	0	1	1
ENSG00000267582	ENSG00000267582	CTD-3252C9.2	19:13906273-13943044	NOTEST	0	0	0	0	1	1
ENSG00000267583	ENSG00000267583	RP11-322E11.5	18:33023832-33077955	NOTEST	0	0	0	0	1	1
ENSG00000267584	ENSG00000267584	CTC-260E6.9	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000267585	ENSG00000267585	RP11-115P21.1	18:32073253-32471808	NOTEST	0	0	0	0	1	1
ENSG00000267586	ENSG00000267586	LINC00907	18:39739246-40271387	NOTEST	0.19528	0.0508441	-1.94139	0	1	1
ENSG00000267587	ENSG00000267587	RP11-687F6.4	18:44388352-44627658	NOTEST	0	0	0	0	1	1
ENSG00000267588	ENSG00000267588	MIR1302-2	19:60104-72719	NOTEST	0	0	0	0	1	1
ENSG00000267589	ENSG00000267589	CTC-232P5.4	19:5978413-6199583	NOTEST	0	0	0	0	1	1
ENSG00000267590	ENSG00000267590	NDUFA3P1	19:44711699-44809199	NOTEST	0	0.416057	inf	0	1	1
ENSG00000267591	ENSG00000267591	RP11-689E3.2	18:47309868-47721463	NOTEST	0	0	0	0	1	1
ENSG00000267592	ENSG00000267592	CTC-507E2.2	17:33901813-34053436	NOTEST	0.986207	0	#NAME?	0	1	1
ENSG00000267593	ENSG00000267593	RP11-108P20.4	18:56481111-56501596	NOTEST	0	0	0	0	1	1
ENSG00000267594	ENSG00000267594	CYP4F24P	19:15871050-15890719	NOTEST	0	0	0	0	1	1
ENSG00000267595	ENSG00000267595	RP11-242D8.2	17:41316199-41322420	NOTEST	0	0	0	0	1	1
ENSG00000267596	ENSG00000267596	CCL15	17:34310326-34338658	NOTEST	0	0.0211288	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267597	ENSG00000267597	RPIAP1	18:59624505-59625247	NOTEST	0	0	0	0	1	1
ENSG00000267598	ENSG00000267598	CTC-250I14.6	19:13261228-13265722	NOTEST	0.000735306	0	#NAME?	0	1	1
ENSG00000267599	ENSG00000267599	CTD-2050I18.2	19:31956558-31957337	NOTEST	0	0	0	0	1	1
ENSG00000267600	ENSG00000267600	AC098474.1	19:229639-230165	NOTEST	0	0	0	0	1	1
ENSG00000267601	ENSG00000267601	RP11-323N12.5	17:76849058-76921469	NOTEST	0	0	0	0	1	1
ENSG00000267602	ENSG00000267602	CTB-75G16.3	HG75_PATCH:34962055-34962685	NOTEST	0	0	0	0	1	1
ENSG00000267603	ENSG00000267603	LINC01028	17:68013464-68131749	NOTEST	0	0	0	0	1	1
ENSG00000267604	ENSG00000267604	RP5-905N1.2	17:41857802-41864980	NOTEST	0	0.0358354	inf	0	1	1
ENSG00000267605	ENSG00000267605	CTD-3220F14.1	19:37756840-37762420	NOTEST	0	0	0	0	1	1
ENSG00000267606	ENSG00000267606	AC006116.21	19:56732680-56904914	NOTEST	0	0.0907325	inf	0	1	1
ENSG00000267607	ENSG00000267607	CTD-2369P2.8	19:10362576-10399695	NOTEST	0.044985	0.0460507	0.0337766	0	1	1
ENSG00000267608	ENSG00000267608	CTC-550B14.6	HSCHR19LRC_LRC_J_CTG1:55542601-55607700	NOTEST	0	0	0	0	1	1
ENSG00000267609	ENSG00000267609	SNX33P1	19:16142116-16152926	NOTEST	0	0	0	0	1	1
ENSG00000267610	ENSG00000267610	AC007787.2	19:13106421-13209610	NOTEST	0	0.00743771	inf	0	1	1
ENSG00000267611	ENSG00000267611	CTC-461H2.2	19:33469498-33555794	NOTEST	0	0	0	0	1	1
ENSG00000267612	ENSG00000267612	CTD-3116E22.7	19:9841528-9842619	NOTEST	0	0	0	0	1	1
ENSG00000267613	ENSG00000267613	RP11-378E13.4	17:35766964-35839835	NOTEST	0.119393	0	#NAME?	0	1	1
ENSG00000267614	ENSG00000267614	AC138472.6	19:45040250-45040599	NOTEST	0	0	0	0	1	1
ENSG00000267615	ENSG00000267615	RP11-552F3.13	17:73937587-74023533	NOTEST	0	0	0	0	1	1
ENSG00000267616	ENSG00000267616	AC016626.2	19:159360-174665	NOTEST	0	0	0	0	1	1
ENSG00000267617	ENSG00000267617	AC007795.1	19:29360702-29370077	NOTEST	0	0	0	0	1	1
ENSG00000267618	ENSG00000267618	RAD51L3-RFFL	17:33332106-33448541	NOTEST	0	0.296702	inf	0	1	1
ENSG00000267619	ENSG00000267619	TRAPPC4	HG299_PATCH:118868851-118901597	NOTEST	0	0	0	0	1	1
ENSG00000267620	ENSG00000267620	RP11-795H16.2	18:57863787-57865405	NOTEST	0	0	0	0	1	1
ENSG00000267622	ENSG00000267622	CTC-550B14.7	HSCHR19LRC_LRC_I_CTG1:55515064-55580163	NOTEST	0	0	0	0	1	1
ENSG00000267623	ENSG00000267623	AC022153.1	19:28175487-28475892	NOTEST	0.176622	0.114387	-0.62674	0	1	1
ENSG00000267624	ENSG00000267624	RP11-219G17.6	17:76207698-76207989	NOTEST	0	0	0	0	1	1
ENSG00000267625	ENSG00000267625	RP11-1094M14.14	17:33888557-33889096	NOTEST	0	0	0	0	1	1
ENSG00000267626	ENSG00000267626	AC002115.9	19:36099186-36103568	NOTEST	0	0	0	0	1	1
ENSG00000267627	ENSG00000267627	RP11-905K4.1	18:33531765-33546081	NOTEST	0	0	0	0	1	1
ENSG00000267628	ENSG00000267628	RP11-1136J12.1	18:76829284-77138283	NOTEST	0	0	0	0	1	1
ENSG00000267629	ENSG00000267629	AC138430.4	19:19366449-19384200	NOTEST	0	6.17E-06	inf	0	1	1
ENSG00000267630	ENSG00000267630	AC005758.1	19:28175487-28475892	NOTEST	0	0	0	0	1	1
ENSG00000267631	ENSG00000267631	CGB1	19:49526125-49552400	NOTEST	0	0	0	0	1	1
ENSG00000267632	ENSG00000267632	RP11-400F19.18	17:40610861-40674629	NOTEST	0.569491	0.571118	0.00411635	0	1	1
ENSG00000267634	ENSG00000267634	RPL7L1P5	17:42442381-42443119	NOTEST	0	0	0	0	1	1
ENSG00000267635	ENSG00000267635	RP11-206C20.1	HSCHR17_5_CTG4:39421609-39422134	NOTEST	0	0	0	0	1	1
ENSG00000267636	ENSG00000267636	AC008992.1	19:31912902-31918208	NOTEST	0	0	0	0	1	1
ENSG00000267637	ENSG00000267637	RP11-619I22.1	17:57697218-57919616	NOTEST	0	0.588999	inf	0	1	1
ENSG00000267638	ENSG00000267638	RP11-546M21.6	17:42154113-42201070	NOTEST	0	0	0	0	1	1

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ENSG00000267639	ENSG00000267639	CICP19	19:182672-196756	NOTEST	0	0	0	0	1	1
ENSG00000267640	ENSG00000267640	CTD-2554C21.2	19:38307998-38345855	NOTEST	0	0	0	0	1	1
ENSG00000267641	ENSG00000267641	CTC-260E6.8	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000267642	ENSG00000267642	RP11-258B16.1	18:31132086-31158151	NOTEST	0	0	0	0	1	1
ENSG00000267643	ENSG00000267643	RP11-64C12.4	18:12200777-12201978	NOTEST	0	0	0	0	1	1
ENSG00000267644	ENSG00000267644	CTD-2008P7.10	17:26546310-26547031	NOTEST	0	0	0	0	1	1
ENSG00000267645	ENSG00000267645	POLR2J2	7:102122891-102312088	NOTEST	0.0324205	0.0156654	-1.04932	0	1	1
ENSG00000267646	ENSG00000267646	CTC-499B15.7	19:11906898-11920437	NOTEST	0.00633571	0.0394103	2.63699	0	1	1
ENSG00000267647	ENSG00000267647	MAP1LC3P	18:52568739-52626739	NOTEST	0	0	0	0	1	1
ENSG00000267648	ENSG00000267648	RP11-686D22.3	17:33733702-33737247	NOTEST	0.216651	0.465451	1.10325	0	1	1
ENSG00000267649	ENSG00000267649	CTD-2587H24.10	19:55728027-55732984	NOTEST	0.276474	0.114528	-1.27145	0	1	1
ENSG00000267650	ENSG00000267650	CTD-2553C6.1	19:10070236-10121147	NOTEST	0.027151	0	#NAME?	0	1	1
ENSG00000267651	ENSG00000267651	RP11-95O2.1	18:34814081-34816205	NOTEST	0.0565134	0.0634376	0.166746	0	1	1
ENSG00000267652	ENSG00000267652	RP11-188I24.1	18:39369126-39369360	NOTEST	0	0	0	0	1	1
ENSG00000267653	ENSG00000267653	RP1-193H18.3	17:67410838-67539472	NOTEST	0	0	0	0	1	1
ENSG00000267654	ENSG00000267654	RP11-973H7.4	18:12738963-12750067	NOTEST	0	0	0	0	1	1
ENSG00000267655	ENSG00000267655	CTD-2286N8.2	18:76829284-77138283	NOTEST	0.479134	0.296755	-0.691154	0	1	1
ENSG00000267656	ENSG00000267656	RP11-807E13.3	18:13139778-13140488	NOTEST	0	0	0	0	1	1
ENSG00000267657	ENSG00000267657	CTB-186H2.2	17:34290505-34292480	NOTEST	0	0	0	0	1	1
ENSG00000267658	ENSG00000267658	RP11-358B23.1	17:40265125-40307990	NOTEST	0	0	0	0	1	1
ENSG00000267659	ENSG00000267659	RP11-118B18.1	17:66255322-66760023	NOTEST	0	0	0	0	1	1
ENSG00000267660	ENSG00000267660	CTC-479C5.17	16:67973652-68003504	NOTEST	0.407354	0.242927	-0.745758	0	1	1
ENSG00000267661	ENSG00000267661	RP11-820I16.2	18:11928836-11929475	NOTEST	0	0	0	0	1	1
ENSG00000267662	ENSG00000267662	AC007796.1	19:31765850-31908700	NOTEST	0	0	0	0	1	1
ENSG00000267663	ENSG00000267663	RP11-64C12.9	18:12246587-12247054	NOTEST	0	0	0	0	1	1
ENSG00000267664	ENSG00000267664	RPL17P45	18:37723889-37724468	NOTEST	0	0	0	0	1	1
ENSG00000267665	ENSG00000267665	RP11-13K12.2	17:75523079-75532674	NOTEST	0	0	0	0	1	1
ENSG00000267666	ENSG00000267666	AC004156.3	19:663481-668063	NOTEST	0.0173597	0.00610004	-1.50885	0	1	1
ENSG00000267667	ENSG00000267667	RP11-136H19.1	17:58754813-59488916	NOTEST	0	0	0	0	1	1
ENSG00000267668	ENSG00000267668	RP11-697E22.2	17:35969786-36044255	NOTEST	0	0	0	0	1	1
ENSG00000267669	ENSG00000267669	RP11-824M15.3	18:57488271-57492493	NOTEST	0	0	0	0	1	1
ENSG00000267670	ENSG00000267670	CTB-55O6.4	19:14138959-14142369	NOTEST	0	0	0	0	1	1
ENSG00000267671	ENSG00000267671	YWHAEP7	17:36187924-36244363	NOTEST	0	0.00505177	inf	0	1	1
ENSG00000267672	ENSG00000267672	CTD-2293H3.1	19:37498758-37734828	NOTEST	0	0.0409646	inf	0	1	1
ENSG00000267674	ENSG00000267674	RP11-813F20.2	18:47266192-47268433	NOTEST	0	0	0	0	1	1
ENSG00000267675	ENSG00000267675	RP11-1151B14.2	18:56083996-56084860	NOTEST	0	0	0	0	1	1
ENSG00000267676	ENSG00000267676	THA1P	17:76244573-76250497	NOTEST	0.0152487	0	#NAME?	0	1	1
ENSG00000267677	ENSG00000267677	RP11-27G24.1	18:57027931-57053981	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267678	ENSG00000267678	RP11-15E18.3	17:58639370-58639522	NOTEST	0	0	0	0	1	1
ENSG00000267679	ENSG00000267679	EIF5AP2	17:76142433-76162258	NOTEST	0	0	0	0	1	1
ENSG00000267682	ENSG00000267682	CTD-3220F14.2	19:37803738-37860267	NOTEST	0.559571	0.387556	-0.529916	0	1	1
ENSG00000267684	ENSG00000267684	CTC-360P9.2	19:32456547-32457875	NOTEST	0	0	0	0	1	1
ENSG00000267685	ENSG00000267685	NTF6B	19:49526125-49552400	NOTEST	0	0	0	0	1	1
ENSG00000267686	ENSG00000267686	RP11-795H16.3	18:57792264-57828428	NOTEST	0	0	0	0	1	1
ENSG00000267687	ENSG00000267687	RP11-325K19.6	18:58192848-58193389	NOTEST	0	0	0	0	1	1
ENSG00000267688	ENSG00000267688	AC005262.2	19:3094407-3124002	NOTEST	0	0	0	0	1	1
ENSG00000267689	ENSG00000267689	AC010525.5	19:56186591-56249768	NOTEST	0	0	0	0	1	1
ENSG00000267690	ENSG00000267690	LDLRAD4-AS1	18:13217496-13652754	NOTEST	0	0	0	0	1	1
ENSG00000267691	ENSG00000267691	SHC1P2	17:42306127-42307596	NOTEST	0	0	0	0	1	1
ENSG00000267692	ENSG00000267692	TAF9P3	19:30528191-30528318	NOTEST	0	0	0	0	1	1
ENSG00000267693	ENSG00000267693	CTC-559E9.2	19:19868174-19945736	NOTEST	0	0	0	0	1	1
ENSG00000267694	ENSG00000267694	RP11-691H4.4	18:13217496-13652754	NOTEST	0	0	0	0	1	1
ENSG00000267695	ENSG00000267695	RP11-1030E3.1	18:47828559-47839965	NOTEST	0	0	0	0	1	1
ENSG00000267696	ENSG00000267696	CTB-151G24.1	19:28129390-28137391	NOTEST	0	0	0	0	1	1
ENSG00000267697	ENSG00000267697	LUZP6	7:135611202-135662101	NOTEST	0	0	0	0	1	1
ENSG00000267699	ENSG00000267699	RP11-729L2.2	18:48494360-48611415	NOTEST	0	0	0	0	1	1
ENSG00000267700	ENSG00000267700	CTC-550B14.7	HSCHR19LRC_PGF2_CTG1:55247239-55312338	NOTEST	0	0	0	0	1	1
ENSG00000267702	ENSG00000267702	RP11-53B2.2	18:13217496-13652754	NOTEST	0.0499812	0.040371	-0.308065	0	1	1
ENSG00000267703	ENSG00000267703	CTD-2013N17.4	19:16466049-16582896	NOTEST	0	0	0	0	1	1
ENSG00000267704	ENSG00000267704	RP11-411B10.6	18:14137708-14139271	NOTEST	0	0	0	0	1	1
ENSG00000267705	ENSG00000267705	RP11-108P20.3	18:56337711-56421709	NOTEST	0.0767252	0.0393085	-0.964861	0	1	1
ENSG00000267706	ENSG00000267706	CTD-2105E13.6	19:55860673-55874628	NOTEST	0	0	0	0	1	1
ENSG00000267707	ENSG00000267707	RP11-95O2.5	18:34823009-35146000	NOTEST	0.680028	0.27298	-1.3168	0	1	1
ENSG00000267708	ENSG00000267708	RP11-147L13.7	17:66148916-66155184	NOTEST	0	0	0	0	1	1
ENSG00000267709	ENSG00000267709	AC024592.9	19:5842898-5858250	NOTEST	0	0	0	0	1	1
ENSG00000267710	ENSG00000267710	AC006116.20	19:56732680-56904914	NOTEST	0	0.0881316	inf	0	1	1
ENSG00000267711	ENSG00000267711	RP11-686D22.5	17:33727896-33730025	NOTEST	0	0	0	0	1	1
ENSG00000267712	ENSG00000267712	RP11-456O19.4	18:53548918-53858493	NOTEST	0	0	0	0	1	1
ENSG00000267713	ENSG00000267713	RP11-10I6.2	18:48086447-48258194	NOTEST	0.0369586	0.2439	2.7223	0	1	1
ENSG00000267714	ENSG00000267714	CTD-2540B15.6	19:33699569-33716756	NOTEST	0	0	0	0	1	1
ENSG00000267715	ENSG00000267715	CTB-25B13.6	19:1481426-1490751	NOTEST	0.11618	0	#NAME?	0	1	1
ENSG00000267716	ENSG00000267716	AC083760.1	18:41619435-41620105	NOTEST	0	0	0	0	1	1
ENSG00000267717	ENSG00000267717	SRSF10P1	18:48684651-48685753	NOTEST	0	0.0604677	inf	0	1	1
ENSG00000267718	ENSG00000267718	CTD-2132N18.2	HG185_PATCH:40132690-40219330	NOTEST	0	0	0	0	1	1
ENSG00000267719	ENSG00000267719	CTD-2116F7.1	HG748_PATCH:77703347-77708399	NOTEST	0	0	0	0	1	1
ENSG00000267721	ENSG00000267721	TMEM199	HG883_PATCH:26684603-26734216	NOTEST	0	0	0	0	1	1
ENSG00000267722	ENSG00000267722	RP11-815J4.1	18:12081538-12085266	NOTEST	0	0	0	0	1	1
ENSG00000267723	ENSG00000267723	CTD-2189E23.1	19:14365000-14404017	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267724	ENSG00000267724	RP11-49K24.8	18:44632316-44702745	NOTEST	0.178401	0.0960858	-0.892726	0	1	1
ENSG00000267725	ENSG00000267725	CTC-461H2.3	19:33558080-33558339	NOTEST	0	0	0	0	1	1
ENSG00000267726	ENSG00000267726	CTD-2526M8.2	18:54836845-54838425	NOTEST	0	0	0	0	1	1
ENSG00000267727	ENSG00000267727	CTD-2540B15.7	19:33790839-33793470	NOTEST	0	0.144558	inf	0	1	1
ENSG00000267728	ENSG00000267728	RP11-206C20.2	HSCHR17_5_CTG4:39411572-39412558	NOTEST	0	0	0	0	1	1
ENSG00000267729	ENSG00000267729	AC010761.14	17:27046410-27070473	NOTEST	0	0	0	0	1	1
ENSG00000267730	ENSG00000267730	CTD-2537I9.5	19:56088135-56088780	NOTEST	0.062678	0.240067	1.9374	0	1	1
ENSG00000267731	ENSG00000267731	RP11-147L13.8	17:66186024-66188943	NOTEST	0.0108084	0.0214217	0.986917	0	1	1
ENSG00000267732	ENSG00000267732	RP11-456O19.3	18:53548918-53858493	NOTEST	0	0	0	0	1	1
ENSG00000267733	ENSG00000267733	RP11-64C12.3	18:12201980-12223538	NOTEST	0	0	0	0	1	1
ENSG00000267734	ENSG00000267734	RP4-604K5.3	1:87380330-87634884	NOTEST	0	0	0	0	1	1
ENSG00000267735	ENSG00000267735	CTD-2265O21.7	19:12986024-12994902	NOTEST	0	0	0	0	1	1
ENSG00000267736	ENSG00000267736	HMGB2P1	19:1189405-1238026	NOTEST	0	0	0	0	1	1
ENSG00000267737	ENSG00000267737	AC061992.2	17:76311809-76343879	NOTEST	0	0.0222644	inf	0	1	1
ENSG00000267738	ENSG00000267738	RP11-1030E3.1	HSCHR18_1_CTG1_1:47828559-47839965	NOTEST	0	0	0	0	1	1
ENSG00000267739	ENSG00000267739	CTC-550B14.6	HSCHR19LRC_LRC_I_CTG1:55515064-55580163	NOTEST	0	0	0	0	1	1
ENSG00000267741	ENSG00000267741	UBE2L4	19:9862668-9903856	NOTEST	0	0	0	0	1	1
ENSG00000267742	ENSG00000267742	FAM60CP	18:57684009-57684673	NOTEST	0.0301309	0	#NAME?	0	1	1
ENSG00000267743	ENSG00000267743	RP11-718I15.1	18:55711598-56068772	NOTEST	0	0	0	0	1	1
ENSG00000267744	ENSG00000267744	RP11-799D4.1	17:33474835-33518721	NOTEST	0	0	0	0	1	1
ENSG00000267745	ENSG00000267745	RP11-686D22.8	17:33733702-33737247	NOTEST	0.13196	0.373816	1.50222	0	1	1
ENSG00000267746	ENSG00000267746	RP11-379L18.1	18:31431063-31804916	NOTEST	0	0	0	0	1	1
ENSG00000267747	ENSG00000267747	RP11-392O1.4	17:41561232-41687706	NOTEST	0	0	0	0	1	1
ENSG00000267748	ENSG00000267748	CTB-102L5.4	19:38734674-38795649	NOTEST	0	0	0	0	1	1
ENSG00000267749	ENSG00000267749	CTC-265F19.1	19:2511216-2702707	NOTEST	0.0306781	0.00625461	-2.29422	0	1	1
ENSG00000267750	ENSG00000267750	AC003102.3	17:42376941-42396039	NOTEST	0.0714734	0.111595	0.642798	0	1	1
ENSG00000267751	ENSG00000267751	AC009005.2	19:567211-583493	NOTEST	0.501169	0.245245	-1.03108	0	1	1
ENSG00000267752	ENSG00000267752	RPS10P27	18:21252216-21252712	NOTEST	0	0	0	0	1	1
ENSG00000267755	ENSG00000267755	AC004623.2	19:1285889-1378430	NOTEST	0.156615	0.317099	1.01771	0	1	1
ENSG00000267758	ENSG00000267758	RP11-358B23.5	17:40351185-40428725	NOTEST	0	0.110509	inf	0	1	1
ENSG00000267759	ENSG00000267759	CTB-25B13.13	19:1407567-1435719	NOTEST	0	0.340171	inf	0	1	1
ENSG00000267760	ENSG00000267760	CTC-565M22.1	19:30710572-31204445	NOTEST	0	0.0577209	inf	0	1	1
ENSG00000267761	ENSG00000267761	CTD-2130O13.1	18:44812095-45120914	NOTEST	0	0.0670538	inf	0	1	1
ENSG00000267762	ENSG00000267762	RP11-426J5.2	18:46065416-46389588	NOTEST	0	0	0	0	1	1
ENSG00000267764	ENSG00000267764	RP11-484L8.1	18:46065416-46389588	NOTEST	0.038487	0.0834974	1.11736	0	1	1
ENSG00000267765	ENSG00000267765	CTD-3193K9.3	17:40830906-40851832	NOTEST	0.166922	0.113456	-0.557047	0	1	1
ENSG00000267766	ENSG00000267766	RP11-299P2.1	18:60790578-60987361	NOTEST	0	0	0	0	1	1
ENSG00000267767	ENSG00000267767	CTC-523E23.4	19:35279485-35323773	NOTEST	0	0	0	0	1	1
ENSG00000267768	ENSG00000267768	CTC-459F4.8	19:28175487-28475892	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000267770	ENSG00000267770	RP11-559N14.6	17:76374720-76573476	NOTEST	0	0	0	0	1	1
ENSG00000267771	ENSG00000267771	CTC-260E6.7	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000267772	ENSG00000267772	RP11-15E18.4	17:58641907-58663984	NOTEST	0	0	0	0	1	1
ENSG00000267773	ENSG00000267773	RP11-677O4.4	18:11644334-11644823	NOTEST	0	0	0	0	1	1
ENSG00000267774	ENSG00000267774	RP11-2N1.2	18:57098171-57364644	NOTEST	0	0	0	0	1	1
ENSG00000267775	ENSG00000267775	OR7E16P	19:9301961-9302846	NOTEST	0	0	0	0	1	1
ENSG00000267777	ENSG00000267777	CTC-439O9.3	19:31658421-31698569	NOTEST	0	0	0	0	1	1
ENSG00000267778	ENSG00000267778	AC004221.2	19:1238177-1239521	NOTEST	0.268245	0.067072	-1.99977	0	1	1
ENSG00000267779	ENSG00000267779	CTC-360P9.3	19:32516767-32547771	NOTEST	0	0	0	0	1	1
ENSG00000267780	ENSG00000267780	RP11-154H12.3	18:77552725-77576365	NOTEST	0	0	0	0	1	1
ENSG00000267781	ENSG00000267781	SLC25A36P1	19:56732680-56904914	NOTEST	0.189067	0	#NAME?	0	1	1
ENSG00000267782	ENSG00000267782	RP11-799D4.3	17:33474835-33518721	NOTEST	0	0	0	0	1	1
ENSG00000267783	ENSG00000267783	CTB-55O6.10	19:14229917-14247768	NOTEST	0	0.304738	inf	0	1	1
ENSG00000267784	ENSG00000267784	RP11-171I2.1	2:179385909-179914813	NOTEST	0	0	0	0	1	1
ENSG00000267785	ENSG00000267785	CTD-3194G12.2	17:35078893-35082651	NOTEST	0	0	0	0	1	1
ENSG00000267786	ENSG00000267786	AF038458.3	19:36438016-36450094	NOTEST	0	0	0	0	1	1
ENSG00000267788	ENSG00000267788	CTD-2534I21.9	17:43059881-43060140	NOTEST	0	0	0	0	1	1
ENSG00000267789	ENSG00000267789	CTD-2526M8.3	18:54803552-54814229	NOTEST	0	0	0	0	1	1
ENSG00000267790	ENSG00000267790	RP11-316M20.1	17:75718953-75724641	NOTEST	0	0	0	0	1	1
ENSG00000267791	ENSG00000267791	CTD-2659N19.2	19:12798866-12807457	NOTEST	0	0.0862231	inf	0	1	1
ENSG00000267792	ENSG00000267792	AC016626.1	19:145484-145812	NOTEST	0	0	0	0	1	1
ENSG00000267793	ENSG00000267793	RP11-576C2.1	Y:21729198-21768160	NOTEST	0	0	0	0	1	1
ENSG00000267794	ENSG00000267794	RP11-677O4.5	18:11618206-11618314	NOTEST	0	0	0	0	1	1
ENSG00000267795	ENSG00000267795	SMIM22	16:4827669-4846533	NOTEST	0.114872	0.241398	1.07139	0	1	1
ENSG00000267797	ENSG00000267797	NRBF2P1	18:33421722-33422581	NOTEST	0	0	0	0	1	1
ENSG00000267798	ENSG00000267798	RP11-333J10.3	17:35306174-35414171	NOTEST	0	0.105493	inf	0	1	1
ENSG00000267799	ENSG00000267799	CTC-478M6.1	19:29281718-29283778	NOTEST	0	0	0	0	1	1
ENSG00000267800	ENSG00000267800	RP11-49K24.5	18:44632316-44702745	NOTEST	0	0	0	0	1	1
ENSG00000267801	ENSG00000267801	RP11-552F3.9	17:73870241-73875627	NOTEST	0.131923	0.122537	-0.10648	0	1	1
ENSG00000267803	ENSG00000267803	AC244161.1	HG1146_PATCH:43846594-43847666	NOTEST	0	0	0	0	1	1
ENSG00000267804	ENSG00000267804	RP11-665N17.4	11:64658157-64658547	NOTEST	0	0	0	0	1	1
ENSG00000267805	ENSG00000267805	AC108004.2	HG417_PATCH:123821-131585	NOTEST	0	0	0	0	1	1
ENSG00000267806	ENSG00000267806	AL360004.2	HG1502_PATCH:132902888-132906498	NOTEST	0	0	0	0	1	1
ENSG00000267807	ENSG00000267807	ACTG1	HG271_PATCH:79483770-79501576	NOTEST	0	0	0	0	1	1
ENSG00000267808	ENSG00000267808	AC018755.17	19:52097813-52109403	NOTEST	0	0.0217629	inf	0	1	1
ENSG00000267811	ENSG00000267811	RP11-727F15.11	11:62538591-62559493	NOTEST	0.228732	0.227325	-0.00890227	0	1	1
ENSG00000267812	ENSG00000267812	FKSG68	21:36160097-37376965	NOTEST	0	0	0	0	1	1
ENSG00000267814	ENSG00000267814	RP11-457M11.5	HG27_PATCH:26686468-26688192	NOTEST	0	0	0	0	1	1
ENSG00000267815	ENSG00000267815	CTB-191K22.5	19:50691442-50813802	NOTEST	0	0	0	0	1	1
ENSG00000267816	ENSG00000267816	IDS	HG1459_PATCH:148558711-148615657	NOTEST	0	0	0	0	1	1
ENSG00000267817	ENSG00000267817	RP1-164F3.8	HG1439_PATCH:100673274-100788446	NOTEST	0	0	0	0	1	1

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ENSG00000267819	ENSG00000267819	AC092850.1	12:131780066-131782763	NOTEST	0	0	0	0	1	1
ENSG00000267820	ENSG00000267820	LL0XNC01-240C2.1	HG1441_PATCH:10323075-103231249	NOTEST	0	0	0	0	1	1
ENSG00000267821	ENSG00000267821	RPL19P21	HG1459_PATCH:15007522-150075813	NOTEST	0	0	0	0	1	1
ENSG00000267822	ENSG00000267822	VN1R85P	HSCHR19_3_CTG3:22357567-22357993	NOTEST	0	0	0	0	1	1
ENSG00000267823	ENSG00000267823	TIMM17B	HG1436_HG1432_PATCH:48752845-48762542	NOTEST	0	0	0	0	1	1
ENSG00000267824	ENSG00000267824	AC137056.1	16:20499023-20500981	NOTEST	0	0	0	0	1	1
ENSG00000267825	ENSG00000267825	ZNF185	HG1497_PATCH:152082913-152141952	NOTEST	0	0	0	0	1	1
ENSG00000267826	ENSG00000267826	RNU7-98P	HG1459_PATCH:14841262-148412683	NOTEST	0	0	0	0	1	1
ENSG00000267828	ENSG00000267828	Y_RNA	HG1257_PATCH:74762946-74763048	NOTEST	0	0	0	0	1	1
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ENSG00000267832	ENSG00000267832	NANOGNBP3	HG1439_PATCH:100592712-100593277	NOTEST	0	0	0	0	1	1
ENSG00000267833	ENSG00000267833	SSX8	HG1433_PATCH:52365934-52376948	NOTEST	0	0	0	0	1	1
ENSG00000267834	ENSG00000267834	RP11-167N5.5	9:131683173-131790582	NOTEST	0.215476	0.249058	0.208953	0	1	1
ENSG00000267836	ENSG00000267836	RP11-104D21.1	HG1433_PATCH:50773421-50774357	NOTEST	0	0	0	0	1	1
ENSG00000267838	ENSG00000267838	AC008746.12	19:54949846-54950362	NOTEST	0.0430552	0.198761	2.20678	0	1	1
ENSG00000267839	ENSG00000267839	AC020956.3	19:42337739-42340005	NOTEST	0	0	0	0	1	1
ENSG00000267840	ENSG00000267840	BX005439.2	HSCHR6_MHC_SSTO:31474451-31474925	NOTEST	0	0	0	0	1	1
ENSG00000267841	ENSG00000267841	GATA1	HG1436_HG1432_PATCH:48645952-48653708	NOTEST	0	0	0	0	1	1
ENSG00000267843	ENSG00000267843	WDR13	HG1436_HG1432_PATCH:48449440-48464592	NOTEST	0	0	0	0	1	1
ENSG00000267845	ENSG00000267845	DKFZP434A062	9:139219088-139219640	NOTEST	0	0	0	0	1	1
ENSG00000267846	ENSG00000267846	AC239803.1	HG1287_PATCH:148846102-148846564	NOTEST	0	0	0	0	1	1
ENSG00000267848	ENSG00000267848	AL118506.1	20:62571185-62587769	NOTEST	0.653906	0.315369	-1.05204	0	1	1
ENSG00000267849	ENSG00000267849	AL133262.1	6:44355261-44418163	NOTEST	0	0	0	0	1	1
ENSG00000267851	ENSG00000267851	AC239395.1	HG1458_PATCH:142372762-142605261	NOTEST	0	0	0	0	1	1
ENSG00000267852	ENSG00000267852	CTB-133G6.2	19:7413847-7537363	NOTEST	0.147089	0	#NAME?	0	1	1
ENSG00000267853	ENSG00000267853	RP4-545K15.5	HG1439_PATCH:100882854-100883505	NOTEST	0	0	0	0	1	1
ENSG00000267854	ENSG00000267854	KIR2DL4	HSCHR19LRC_PGF1_CTG1:55157744-55300469	NOTEST	0	0	0	0	1	1
ENSG00000267856	ENSG00000267856	RP3-507I15.1	HG1453_PATCH:140220642-140221339	NOTEST	0	0	0	0	1	1
ENSG00000267857	ENSG00000267857	PRED58	21:46491647-46646478	NOTEST	0	0	0	0	1	1
ENSG00000267860	ENSG00000267860	EEF1A1P31	HG1497_PATCH:154004255-154228771	NOTEST	0	0	0	0	1	1
ENSG00000267862	ENSG00000267862	RP1-279N11.1	HG1425_PATCH:75875332-75876394	NOTEST	0	0	0	0	1	1
ENSG00000267864	ENSG00000267864	SSX2	HG1433_PATCH:52439895-52450189	NOTEST	0	0	0	0	1	1
ENSG00000267865	ENSG00000267865	CTD-2611O12.8	19:56186591-56249768	NOTEST	0	0	0	0	1	1
ENSG00000267866	ENSG00000267866	RP3-481A17.1	HG1425_PATCH:75249729-75250165	NOTEST	0	0	0	0	1	1
ENSG00000267867	ENSG00000267867	PHLDB1	HG122_PATCH:118477212-118528753	NOTEST	0	0	0	0	1	1
ENSG00000267868	ENSG00000267868	RP11-120K24.3	13:113548691-113754053	NOTEST	0	0	0	0	1	1
ENSG00000267871	ENSG00000267871	CTC-444N24.6	19:57778587-57804937	NOTEST	0.0431802	0.0979388	1.18151	0	1	1
ENSG00000267872	ENSG00000267872	RP11-157B13.7	19:22426055-22428149	NOTEST	0	0	0	0	1	1
ENSG00000267873	ENSG00000267873	AC121757.1	12:52708084-52715182	NOTEST	0	0	0	0	1	1
ENSG00000267874	ENSG00000267874	CTD-2527I21.9	19:35521587-35531352	NOTEST	0	0	0	0	1	1
ENSG00000267876	ENSG00000267876	GSC2	HG329_PATCH:19136088-19137796	NOTEST	0	0	0	0	1	1
ENSG00000267877	ENSG00000267877	RPL13P5	HG344_PATCH:6976282-7032861	NOTEST	0	0	0	0	1	1

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ENSG00000267879	ENSG00000267879	CTB-147C22.9	19:51446558-51515385	NOTEST	0	0	0	0	1	1
ENSG00000267880	ENSG00000267880	AC037199.1	19:51364823-51383823	NOTEST	0	0	0	0	1	1
ENSG00000267881	ENSG00000267881	CEA	19:42212503-42290801	NOTEST	0	0	0	0	1	1
ENSG00000267882	ENSG00000267882	AL031666.2	20:45837858-45985567	NOTEST	0.0203476	0.0159034	-0.355527	0	1	1
ENSG00000267883	ENSG00000267883	PRED60	21:47063607-47362368	NOTEST	0	0	0	0	1	1
ENSG00000267884	ENSG00000267884	AL626787.1	1:166026673-166136206	NOTEST	0.140222	0.242322	0.789207	0	1	1
ENSG00000267885	ENSG00000267885	FKSG48	1:33439267-33439642	NOTEST	0	0	0	0	1	1
ENSG00000267886	ENSG00000267886	CTD-2291D10.4	19:23258002-23330021	NOTEST	0.0378952	0	#NAME?	0	1	1
ENSG00000267887	ENSG00000267887	AF196972.4	HG1436_HG1432_PATCH:48306291-48308278	NOTEST	0	0	0	0	1	1
ENSG00000267888	ENSG00000267888	CTB-83J4.1	HSCHR19LRC_COX1_CTG1:54704427-54752625	NOTEST	0	0	0	0	1	1
ENSG00000267889	ENSG00000267889	AC079354.2	2:203104291-203104435	NOTEST	0	0	0	0	1	1
ENSG00000267890	ENSG00000267890	CTD-2126E3.4	19:50578379-50579159	NOTEST	0	0.0260541	inf	0	1	1
ENSG00000267891	ENSG00000267891	PABPC1L2B	HG1438_PATCH:72223362-72225562	NOTEST	0	0	0	0	1	1
ENSG00000267892	ENSG00000267892	CTD-2540F13.2	19:39138288-39260544	NOTEST	0.0210834	0.00741166	-1.50824	0	1	1
ENSG00000267893	ENSG00000267893	AC007461.1	17:70017991-70216859	NOTEST	0.129144	0	#NAME?	0	1	1
ENSG00000267894	ENSG00000267894	ZNF322	HG27_PATCH:26634610-26659980	NOTEST	0	0	0	0	1	1
ENSG00000267895	ENSG00000267895	SIGLEC19P	19:51645555-51685222	NOTEST	0	0	0	0	1	1
ENSG00000267897	ENSG00000267897	RNA5SP505	HG1433_PATCH:53652053-53652161	NOTEST	0	0	0	0	1	1
ENSG00000267898	ENSG00000267898	CTD-2639E6.9	19:49467231-49468415	NOTEST	0.0454886	0.135897	1.57894	0	1	1
ENSG00000267899	ENSG00000267899	CROCCP1	HG1443_HG1444_PATCH:134566988-134572663	NOTEST	0	0	0	0	1	1
ENSG00000267900	ENSG00000267900	LUZP4	HG1462_PATCH:114526196-114544026	NOTEST	0	0	0	0	1	1
ENSG00000267901	ENSG00000267901	AC004817.1	14:71679349-71684933	NOTEST	0	0	0	0	1	1
ENSG00000267902	ENSG00000267902	FTH1P19	HG1424_PATCH:37209336-38547737	NOTEST	0	0	0	0	1	1
ENSG00000267905	ENSG00000267905	CTD-2616J11.16	19:51834789-51847371	NOTEST	0	0	0	0	1	1
ENSG00000267906	ENSG00000267906	AC073333.1	7:16828865-16829246	NOTEST	0	0	0	0	1	1
ENSG00000267908	ENSG00000267908	ZSCAN5D	19:56732680-56904914	NOTEST	0	0.00791307	inf	0	1	1
ENSG00000267909	ENSG00000267909	CCDC177	14:70038215-70040339	NOTEST	0	0	0	0	1	1
ENSG00000267910	ENSG00000267910	KMT2A	HG122_PATCH:118307204-118473748	NOTEST	0	0	0	0	1	1
ENSG00000267912	ENSG00000267912	WAS	HG1436_HG1432_PATCH:48535994-48550826	NOTEST	0	0	0	0	1	1
ENSG00000267913	ENSG00000267913	AP001055.1	21:45587817-45593580	NOTEST	0	0.0256977	inf	0	1	1
ENSG00000267915	ENSG00000267915	PDZD4	HG1497_PATCH:152970637-152999037	NOTEST	0	0	0	0	1	1
ENSG00000267917	ENSG00000267917	RP11-1260E13.1	HG417_PATCH:152499-326252	NOTEST	0	0	0	0	1	1
ENSG00000267918	ENSG00000267918	AL117190.2	14:101245746-101327368	NOTEST	0	0	0	0	1	1
ENSG00000267919	ENSG00000267919	RP11-256I23.3	2:220509811-220510353	NOTEST	0	0.0283985	inf	0	1	1
ENSG00000267920	ENSG00000267920	SNX6P1	19:23258002-23330021	NOTEST	0	0	0	0	1	1
ENSG00000267921	ENSG00000267921	RRM2P4	HG1458_PATCH:143396917-143397479	NOTEST	0	0	0	0	1	1
ENSG00000267922	ENSG00000267922	AC007193.6	19:46604379-46706340	NOTEST	0	0	0	0	1	1
ENSG00000267923	ENSG00000267923	LAIR1	HSCHR19LRC_PGF1_CTG1:54787289-54804060	NOTEST	0	0	0	0	1	1
ENSG00000267924	ENSG00000267924	RP11-255H23.4	19:23945745-24057503	NOTEST	0	0	0	0	1	1
ENSG00000267925	ENSG00000267925	CTB-61M7.2	HSCHR19LRC_PGF1_CTG1:55323924-55324672	NOTEST	0	0	0	0	1	1

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ENSG00000267928	ENSG00000267928	HMGB1P16	HG1423_PATCH:36229212-36229752	NOTEST	0	0	0	0	1	1
ENSG00000267929	ENSG00000267929	SLC35A2	HG1436_HG1432_PATCH:48762580-48771357	NOTEST	0	0	0	0	1	1
ENSG00000267930	ENSG00000267930	RPS26P8	HG1146_PATCH:43759013-43759454	NOTEST	0	0	0	0	1	1
ENSG00000267932	ENSG00000267932	Y_RNA	HG1257_PATCH:74959037-74993105	NOTEST	0	0	0	0	1	1
ENSG00000267933	ENSG00000267933	snoU13	HG1436_HG1432_PATCH:47941165-47941269	NOTEST	0	0	0	0	1	1
ENSG00000267934	ENSG00000267934	CTB-176F20.3	19:23487792-23578362	NOTEST	0	0.00209966	inf	0	1	1
ENSG00000267935	ENSG00000267935	AC016752.1	Y:25847478-25850592	NOTEST	0	0	0	0	1	1
ENSG00000267936	ENSG00000267936	MIR514B	HG1459_PATCH:146331865-146331945	NOTEST	0	0	0	0	1	1
ENSG00000267937	ENSG00000267937	AP001421.1	21:38737778-38889753	NOTEST	0	0.368334	inf	0	1	1
ENSG00000267938	ENSG00000267938	AC007292.1	19:4343523-4360083	NOTEST	0	0	0	0	1	1
ENSG00000267939	ENSG00000267939	CTD-2325M2.1	19:8073612-8080909	NOTEST	0.111837	0.322568	1.5282	0	1	1
ENSG00000267940	ENSG00000267940	RP11-290F24.6	11:6223130-6224483	NOTEST	0.231856	0.203085	-0.19114	0	1	1
ENSG00000267941	ENSG00000267941	AC008267.1	7:65670185-65955095	NOTEST	0.0271511	0	#NAME?	0	1	1
ENSG00000267942	ENSG00000267942	AC090673.2	12:66151799-66360075	NOTEST	0	0	0	0	1	1
ENSG00000267943	ENSG00000267943	CTD-2620I22.3	19:53430387-53541151	NOTEST	0	0	0	0	1	1
ENSG00000267944	ENSG00000267944	RP11-258C19.4	HG1433_PATCH:52836709-52910014	NOTEST	0	0	0	0	1	1
ENSG00000267945	ENSG00000267945	AC139677.8	HG1146_PATCH:44054524-44055596	NOTEST	0	0	0	0	1	1
ENSG00000267946	ENSG00000267946	TMLHE	HG1497_PATCH:154634437-154838412	NOTEST	0	0	0	0	1	1
ENSG00000267947	ENSG00000267947	AC078899.3	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
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ENSG00000267950	ENSG00000267950	AC136297.1	11:1295600-1330884	NOTEST	0.121598	0	#NAME?	0	1	1
ENSG00000267951	ENSG00000267951	L1CAM	HG1497_PATCH:153029985-153103693	NOTEST	0	0	0	0	1	1
ENSG00000267952	ENSG00000267952	CTD-2207O23.12	19:7541760-7585912	NOTEST	0.159356	0.339766	1.09229	0	1	1
ENSG00000267953	ENSG00000267953	MIR891B	HG1459_PATCH:145082767-145082846	NOTEST	0	0	0	0	1	1
ENSG00000267954	ENSG00000267954	AP000349.1	22:24105207-24126503	NOTEST	0.0450817	0.0777348	0.786019	0	1	1
ENSG00000267955	ENSG00000267955	RP11-770J1.4	HG122_PATCH:118303835-118305921	NOTEST	0	0	0	0	1	1
ENSG00000267956	ENSG00000267956	VN1R78P	HG730_PATCH:20646633-20772405	NOTEST	0	0	0	0	1	1
ENSG00000267958	ENSG00000267958	CATX-2	2:74418516-74418627	NOTEST	0	0	0	0	1	1
ENSG00000267959	ENSG00000267959	MIR3188	19:18392886-18392971	NOTEST	0	0	0	0	1	1
ENSG00000267960	ENSG00000267960	RHOXF2B	HG1442_PATCH:119170198-119280817	NOTEST	0	0	0	0	1	1
ENSG00000267961	ENSG00000267961	OR10B1P	19:15251942-15252849	NOTEST	0	0	0	0	1	1
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ENSG00000267963	ENSG00000267963	AC013469.1	2:241053906-241064304	NOTEST	0	0	0	0	1	1
ENSG00000267964	ENSG00000267964	AC022400.2	10:75531934-75540009	NOTEST	0.106085	0.185143	0.803424	0	1	1
ENSG00000267966	ENSG00000267966	RPL23AP82	HG497_PATCH:51195375-51239737	NOTEST	0	0	0	0	1	1
ENSG00000267967	ENSG00000267967	MTND1P33	HG1458_PATCH:142372762-142605261	NOTEST	0	0	0	0	1	1
ENSG00000267968	ENSG00000267968	AC011523.2	19:51328544-51354345	NOTEST	0	0	0	0	1	1
ENSG00000267970	ENSG00000267970	AC004899.1	7:48886021-48892494	NOTEST	0	0	0	0	1	1
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ENSG00000267972	ENSG00000267972	DGKK	HG1433_PATCH:50111879-50213722	NOTEST	0	0	0	0	1	1
ENSG00000267974	ENSG00000267974	HCFC1-AS1	HG1497_PATCH:153116020-153140275	NOTEST	0	0	0	0	1	1

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ENSG00000267976	ENSG00000267976	AP000695.1	21:37802657-37948867	NOTEST	0	0	0	0	1	1
ENSG00000267977	ENSG00000267977	BCAP31	HG1497_PATCH:152868963-152893169	NOTEST	0	0	0	0	1	1
ENSG00000267978	ENSG00000267978	MAGEA9	HG1459_PATCH:148663376-148669190	NOTEST	0	0	0	0	1	1
ENSG00000267979	ENSG00000267979	AC092964.2	3:171757417-172119455	NOTEST	0	0	0	0	1	1
ENSG00000267980	ENSG00000267980	AC007292.6	19:4360366-4400544	NOTEST	0.353643	0.478646	0.436664	0	1	1
ENSG00000267981	ENSG00000267981	AP003041.2	11:129936835-130014699	NOTEST	0	0	0	0	1	1
ENSG00000267983	ENSG00000267983	OTUD5	HG1436_HG1432_PATCH:48781426-48817785	NOTEST	0	0	0	0	1	1
ENSG00000267984	ENSG00000267984	CTD-2616J11.9	19:51848422-51872257	NOTEST	0	0	0	0	1	1
ENSG00000267985	ENSG00000267985	AC005488.1	7:72440226-72555749	NOTEST	0	0	0	0	1	1
ENSG00000267986	ENSG00000267986	AC130469.2	19:8645125-8675620	NOTEST	0	0	0	0	1	1
ENSG00000267987	ENSG00000267987	AL161784.1	9:124101354-124132531	NOTEST	0	0	0	0	1	1
ENSG00000267988	ENSG00000267988	AC096582.1	7:45902683-45906045	NOTEST	0	0	0	0	1	1
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ENSG00000267990	ENSG00000267990	CTD-3187F8.15	19:51641226-51641891	NOTEST	0	0	0	0	1	1
ENSG00000267992	ENSG00000267992	CTB-189B5.3	19:39481353-39523425	NOTEST	0	0	0	0	1	1
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ENSG00000267995	ENSG00000267995	SSX7	HG1433_PATCH:52387089-52397900	NOTEST	0	0	0	0	1	1
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ENSG00000268011	ENSG00000268011	RP11-104D21.2	HG1433_PATCH:50825817-50834228	NOTEST	0	0	0	0	1	1
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ENSG00000268014	ENSG00000268014	RPL36P18	HG1462_PATCH:114347091-114470542	NOTEST	0	0	0	0	1	1
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ENSG00000268019	ENSG00000268019	LDHBP2	HG1425_PATCH:75554675-75555680	NOTEST	0	0	0	0	1	1
ENSG00000268020	ENSG00000268020	OR4G4P	1:52472-54936	NOTEST	0	0	0	0	1	1
ENSG00000268021	ENSG00000268021	TREH	HG122_PATCH:118528946-118550387	NOTEST	0	0	0	0	1	1
ENSG00000268022	ENSG00000268022	RP11-344N17.6	HG1436_HG1432_PATCH:48166167-48168454	NOTEST	0	0	0	0	1	1
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ENSG00000268032	ENSG00000268032	CTB-52I2.4	19:18133211-18142909	NOTEST	0	0.00854946	inf	0	1	1
ENSG00000268033	ENSG00000268033	RNU6-722P	HG1436_HG1432_PATCH:48818577-48818681	NOTEST	0	0	0	0	1	1
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ENSG00000268037	ENSG00000268037	CU151838.1	HSCHR19LRC_PGF1_CTG1:54754263-54761159	NOTEST	0	0	0	0	1	1
ENSG00000268038	ENSG00000268038	AC011516.2	19:22798358-22806773	NOTEST	0	0	0	0	1	1
ENSG00000268040	ENSG00000268040	PRED62	21:47063607-47362368	NOTEST	0	0	0	0	1	1
ENSG00000268041	ENSG00000268041	CTD-2575K13.6	19:42387227-42434302	NOTEST	0	0	0	0	1	1
ENSG00000268042	ENSG00000268042	RP11-357C3.3	HG1437_PATCH:62562696-62780541	NOTEST	0	0	0	0	1	1
ENSG00000268043	ENSG00000268043	AC244394.1	HG1287_PATCH:147646385-147682613	NOTEST	0	0	0	0	1	1
ENSG00000268045	ENSG00000268045	RP6-204F4.2	HG1462_PATCH:114300405-114301264	NOTEST	0	0	0	0	1	1
ENSG00000268046	ENSG00000268046	AP001094.1	18:7566779-8406951	NOTEST	0	0	0	0	1	1
ENSG00000268047	ENSG00000268047	AC018766.6	19:50321538-50364001	NOTEST	0.230986	0.114757	-1.00922	0	1	1
ENSG00000268048	ENSG00000268048	RP3-461F17.1	HG344_PATCH:7085347-7180195	NOTEST	0	0	0	0	1	1
ENSG00000268049	ENSG00000268049	CTD-2619J13.9	19:58856543-58877958	NOTEST	0.276261	0.430625	0.640402	0	1	1
ENSG00000268050	ENSG00000268050	RP11-247A12.8	9:131937834-131972827	NOTEST	0	0	0	0	1	1
ENSG00000268051	ENSG00000268051	CTC-244M17.1	19:38397867-38699012	NOTEST	0	0	0	0	1	1
ENSG00000268053	ENSG00000268053	CTC-344H19.6	19:46604379-46706340	NOTEST	0	0	0	0	1	1
ENSG00000268054	ENSG00000268054	RP13-34L8.7	HG1433_PATCH:52288150-52290695	NOTEST	0	0	0	0	1	1
ENSG00000268055	ENSG00000268055	AC067969.2	19:38924338-39078204	NOTEST	0	0	0	0	1	1
ENSG00000268056	ENSG00000268056	CTD-3032J10.2	19:17186590-17325346	NOTEST	0	0	0	0	1	1
ENSG00000268057	ENSG00000268057	MIR532	HG1436_HG1432_PATCH:49732013-49908634	NOTEST	0	0	0	0	1	1
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ENSG00000268060	ENSG00000268060	PCDHB10	HG1082_HG167_PATCH:140571953-140575227	NOTEST	0	0	0	0	1	1
ENSG00000268062	ENSG00000268062	TOP1P1	1:171314227-171314459	NOTEST	0	0.268133	inf	0	1	1
ENSG00000268063	ENSG00000268063	U3	HG1459_PATCH:149983842-149983958	NOTEST	0	0	0	0	1	1
ENSG00000268064	ENSG00000268064	KIR3DX1	HSCHR19LRC_PGF1_CTG1:54966402-54977336	NOTEST	0	0	0	0	1	1
ENSG00000268065	ENSG00000268065	RNVU1-14	HG1287_PATCH:145967530-145967694	NOTEST	0	0	0	0	1	1
ENSG00000268066	ENSG00000268066	FMR1-AS1	X:146990948-146993335	NOTEST	0.106278	0.0129398	-3.03794	0	1	1
ENSG00000268067	ENSG00000268067	OR5AH1P	19:57202053-57352097	NOTEST	0	0	0	0	1	1
ENSG00000268069	ENSG00000268069	AC004466.1	12:48099867-48231681	NOTEST	0.512048	0.543065	0.084845	0	1	1
ENSG00000268070	ENSG00000268070	AC006539.3	19:20107866-20150315	NOTEST	0	0	0	0	1	1
ENSG00000268071	ENSG00000268071	RBM22P6	HG1433_PATCH:52269973-52270838	NOTEST	0	0	0	0	1	1
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ENSG00000268078	ENSG00000268078	RP11-805I24.4	16:86191811-86192404	NOTEST	0	0	0	0	1	1
ENSG00000268079	ENSG00000268079	RP11-157B13.6	19:22385929-22386805	NOTEST	0	0	0	0	1	1
ENSG00000268080	ENSG00000268080	AC016885.1	8:94225530-94753245	NOTEST	0	0	0	0	1	1
ENSG00000268081	ENSG00000268081	RP11-678G14.2	19:21579920-21752039	NOTEST	0	0	0	0	1	1
ENSG00000268082	ENSG00000268082	RP11-38O23.3	HG1436_HG1432_PATCH:47995056-47995558	NOTEST	0	0	0	0	1	1
ENSG00000268083	ENSG00000268083	AC104534.3	19:39306061-39342987	NOTEST	0	0	0	0	1	1
ENSG00000268084	ENSG00000268084	SMIM9	HG1497_PATCH:153991815-154003130	NOTEST	0	0	0	0	1	1
ENSG00000268085	ENSG00000268085	AC051642.1	8:23386317-23432976	NOTEST	0	0	0	0	1	1
ENSG00000268086	ENSG00000268086	RP1-172N19.3	HG1438_PATCH:71798663-71934169	NOTEST	0	0	0	0	1	1
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ENSG00000268089	ENSG00000268089	AC244102.1	HG1497_PATCH:151806654-151821834	NOTEST	0	0	0	0	1	1
ENSG00000268090	ENSG00000268090	PAGE4	HG1436_HG1432_PATCH:49638658-49643372	NOTEST	0	0	0	0	1	1
ENSG00000268091	ENSG00000268091	AC078925.1	12:131438451-131626014	NOTEST	0	0	0	0	1	1
ENSG00000268092	ENSG00000268092	RP11-38O23.7	HG1436_HG1432_PATCH:48037129-48037422	NOTEST	0	0	0	0	1	1
ENSG00000268093	ENSG00000268093	AC022154.7	19:49118584-49140695	NOTEST	0.233217	0.215725	-0.112479	0	1	1
ENSG00000268094	ENSG00000268094	PFN1P8	HG1287_PATCH:147643531-147644074	NOTEST	0	0	0	0	1	1
ENSG00000268095	ENSG00000268095	CTC-429C10.2	19:52359054-52408293	NOTEST	0	0.0806864	inf	0	1	1
ENSG00000268096	ENSG00000268096	MAGEA7P	HG1459_PATCH:148889935-148890877	NOTEST	0	0	0	0	1	1
ENSG00000268097	ENSG00000268097	MIR513C	HG1459_PATCH:146271418-146271502	NOTEST	0	0	0	0	1	1
ENSG00000268098	ENSG00000268098	AP000688.1	21:37402367-37498938	NOTEST	0	0	0	0	1	1
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ENSG00000268102	ENSG00000268102	MIR507	HG1459_PATCH:146312698-146312792	NOTEST	0	0	0	0	1	1
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ENSG00000268104	ENSG00000268104	SLC6A14	HG1463_PATCH:115552911-115575288	NOTEST	0	0	0	0	1	1
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ENSG00000268108	ENSG00000268108	CTB-60B18.12	19:49557530-49568333	NOTEST	0.0851242	0.0302102	-1.49454	0	1	1
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ENSG00000268110	ENSG00000268110	UBE4A	HG122_PATCH:118230299-118302211	NOTEST	0	0	0	0	1	1
ENSG00000268111	ENSG00000268111	AL031663.1	20:44095909-44110172	NOTEST	0	0	0	0	1	1
ENSG00000268112	ENSG00000268112	CTD-3149D2.4	19:17830050-17845325	NOTEST	0	0	0	0	1	1
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ENSG00000268116	ENSG00000268116	RP11-157B13.1	19:22311428-22314736	NOTEST	0	0	0	0	1	1
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ENSG00000268119	ENSG00000268119	CTD-2561J22.5	19:21579920-21752039	NOTEST	0	0	0	0	1	1
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ENSG00000268122	ENSG00000268122	HSFX1	HG1459_PATCH:148855789-148858589	NOTEST	0	0	0	0	1	1
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ENSG00000268127	ENSG00000268127	RN7SL712P	HG1463_PATCH:115108800-115109100	NOTEST	0	0	0	0	1	1
ENSG00000268128	ENSG00000268128	MIR508	HG1459_PATCH:146318627-146318742	NOTEST	0	0	0	0	1	1
ENSG00000268130	ENSG00000268130	AL137002.1	13:113755562-113756608	NOTEST	0	0	0	0	1	1
ENSG00000268131	ENSG00000268131	RNU6-648P	HG1462_PATCH:114268896-114269003	NOTEST	0	0	0	0	1	1
ENSG00000268132	ENSG00000268132	CSAG4	HG1497_PATCH:151902250-151909457	NOTEST	0	0	0	0	1	1
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ENSG00000268134	ENSG00000268134	FAM156A	HG1433_PATCH:52640399-52651556	NOTEST	0	0	0	0	1	1
ENSG00000268135	ENSG00000268135	LRRC23	HG344_PATCH:6976282-7032861	NOTEST	0	0	0	0	1	1
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ENSG00000268138	ENSG00000268138	PORCN	HG1436_HG1432_PATCH:48368360-48380213	NOTEST	0	0	0	0	1	1
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ENSG00000268140	ENSG00000268140	PCGF7P	19:22320732-22321783	NOTEST	0	0.0407162	inf	0	1	1
ENSG00000268141	ENSG00000268141	AL606500.1	1:154554537-154600475	NOTEST	0	0	0	0	1	1
ENSG00000268142	ENSG00000268142	PQBP1	HG1436_HG1432_PATCH:48752845-48762542	NOTEST	0	0	0	0	1	1
ENSG00000268143	ENSG00000268143	RP11-69A21.2	HG1438_PATCH:71996858-72068652	NOTEST	0	0	0	0	1	1
ENSG00000268144	ENSG00000268144	NIFKP6	19:51897741-51906904	NOTEST	0	0	0	0	1	1
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ENSG00000268162	ENSG00000268162	HBCBP	12:57388229-57392225	NOTEST	0	0.0783544	inf	0	1	1
ENSG00000268163	ENSG00000268163	AC004076.9	19:57874844-57988938	NOTEST	0.088329	0	#NAME?	0	1	1
ENSG00000268164	ENSG00000268164	CTD-2337J16.1	19:54753288-54753907	NOTEST	0	0	0	0	1	1

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ENSG00000268168	ENSG00000268168	RP5-937E21.8	HG1459_PATCH:14862207-148632232	NOTEST	0	0	0	0	1	1
ENSG00000268169	ENSG00000268169	RP11-357K9.2	HG1424_PATCH:37209336-38547737	NOTEST	0	0	0	0	1	1
ENSG00000268170	ENSG00000268170	AC073342.1	7:142919129-142920162	NOTEST	0	0	0	0	1	1
ENSG00000268171	ENSG00000268171	AC068620.1	4:57259527-57301781	NOTEST	0	0	0	0	1	1
ENSG00000268172	ENSG00000268172	AL590452.1	1:144836156-145076186	NOTEST	0.00787441	0.0607919	2.94864	0	1	1
ENSG00000268173	ENSG00000268173	PIK3R2	19:18263927-18288927	NOTEST	0	3.01E-05	inf	0	1	1
ENSG00000268174	ENSG00000268174	CTC-513N18.5	19:20451077-20607775	NOTEST	0	0	0	0	1	1
ENSG00000268176	ENSG00000268176	ZCCHC18	HG1441_PATCH:103354143-103411956	NOTEST	0	0	0	0	1	1
ENSG00000268179	ENSG00000268179	AL645608.1	1:860259-894689	NOTEST	0	0	0	0	1	1
ENSG00000268180	ENSG00000268180	Y_RNA	HG1462_PATCH:114347091-114470542	NOTEST	0	0	0	0	1	1
ENSG00000268181	ENSG00000268181	AC073188.1	7:62854126-62882424	NOTEST	0	0	0	0	1	1
ENSG00000268182	ENSG00000268182	SMIM17	19:57154512-57167134	NOTEST	0.0328231	0.176459	2.42655	0	1	1
ENSG00000268183	ENSG00000268183	ABCD1P4	HG1488_PATCH:16904969-16908163	NOTEST	0	0	0	0	1	1
ENSG00000268184	ENSG00000268184	RP11-420K14.8	19:21951573-21976662	NOTEST	0	0	0	0	1	1
ENSG00000268185	ENSG00000268185	SALL1P1	HG1436_HG1432_PATCH:49474242-49478079	NOTEST	0	0	0	0	1	1
ENSG00000268186	ENSG00000268186	CTC-241F20.4	19:48673948-48790865	NOTEST	0	0	0	0	1	1
ENSG00000268187	ENSG00000268187	AC118758.4	HG736_PATCH:56890420-56894804	NOTEST	0	0	0	0	1	1
ENSG00000268188	ENSG00000268188	HSD17B10	HG1433_PATCH:53174257-53177373	NOTEST	0	0	0	0	1	1
ENSG00000268189	ENSG00000268189	AC005785.2	19:15464195-15529952	NOTEST	0.129107	0.12248	-0.0760204	0	1	1
ENSG00000268190	ENSG00000268190	SPSB2	HG344_PATCH:6976282-7032861	NOTEST	0	0	0	0	1	1
ENSG00000268191	ENSG00000268191	CTD-2396E7.10	19:6494329-6502859	NOTEST	0	0	0	0	1	1
ENSG00000268192	ENSG00000268192	AP002956.1	11:119019721-119033360	NOTEST	0	0	0	0	1	1
ENSG00000268193	ENSG00000268193	AC002985.3	19:19010322-19057640	NOTEST	0	0	0	0	1	1
ENSG00000268194	ENSG00000268194	LINC01101	2:121221910-121223697	NOTEST	0	0	0	0	1	1
ENSG00000268195	ENSG00000268195	GNB3	HG344_PATCH:6949117-6961230	NOTEST	0	0	0	0	1	1
ENSG00000268196	ENSG00000268196	MAGEA3	HG1497_PATCH:151867223-151870818	NOTEST	0	0	0	0	1	1
ENSG00000268197	ENSG00000268197	AF196972.3	HG1436_HG1432_PATCH:48292599-48301018	NOTEST	0	0	0	0	1	1
ENSG00000268198	ENSG00000268198	GHc-602D8.2	HG1439_PATCH:100938766-100939436	NOTEST	0	0	0	0	1	1
ENSG00000268199	ENSG00000268199	CTD-3137H5.1	19:18552228-18632937	NOTEST	0	0.044739	inf	0	1	1
ENSG00000268200	ENSG00000268200	RP11-420K14.3	HSCHR19_2_CTG3:21901802-21902472	NOTEST	0	0	0	0	1	1
ENSG00000268203	ENSG00000268203	CTD-2396E7.9	19:6494329-6502859	NOTEST	0	0	0	0	1	1
ENSG00000268204	ENSG00000268204	CTD-3214H19.6	19:7694622-7712759	NOTEST	0.268651	0.338183	0.332071	0	1	1
ENSG00000268206	ENSG00000268206	AC061975.10	17:26603011-26644809	NOTEST	0	0	0	0	1	1
ENSG00000268208	ENSG00000268208	AC008372.1	14:78174413-78236085	NOTEST	0	0	0	0	1	1
ENSG00000268209	ENSG00000268209	RP11-618I10.3	4:70253297-70254025	NOTEST	0	0	0	0	1	1
ENSG00000268210	ENSG00000268210	TMEM257	HG1459_PATCH:144909124-144911565	NOTEST	0	0	0	0	1	1
ENSG00000268211	ENSG00000268211	AL359091.2	9:131062366-131064212	NOTEST	0	0	0	0	1	1
ENSG00000268212	ENSG00000268212	CXorf30	HG1423_PATCH:36246734-36458409	NOTEST	0	0	0	0	1	1
ENSG00000268213	ENSG00000268213	ARMCX6	HG1439_PATCH:100870106-100872988	NOTEST	0	0	0	0	1	1
ENSG00000268214	ENSG00000268214	KIR2DL4	HSCHR19LRC_COX2_CTG1:54950191-54961268	NOTEST	0	0	0	0	1	1
ENSG00000268217	ENSG00000268217	AC008387.1	5:72894202-72896845	NOTEST	0	0	0	0	1	1

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ENSG00000268218	ENSG00000268218	AC137932.1	16:89334037-89556969	NOTEST	0.15124	0.122788	-0.300664	0	1	1
ENSG00000268221	ENSG00000268221	OPN1MW	HG1497_PATCH:153351085-153364610	NOTEST	0	0	0	0	1	1
ENSG00000268222	ENSG00000268222	EEF1A1P7	19:35873073-35874954	NOTEST	0	0	0	0	1	1
ENSG00000268223	ENSG00000268223	ARL14EPL	5:115298150-115395815	NOTEST	0	0	0	0	1	1
ENSG00000268224	ENSG00000268224	MIR514A1	HG1459_PATCH:146360961-146361059	NOTEST	0	0	0	0	1	1
ENSG00000268225	ENSG00000268225	CTD-2331H12.5	19:53365059-53366119	NOTEST	0	0	0	0	1	1
ENSG00000268226	ENSG00000268226	DKC1	HG1497_PATCH:153931223-153946157	NOTEST	0	0	0	0	1	1
ENSG00000268227	ENSG00000268227	RN7SL190P	HG1497_PATCH:152163707-152163967	NOTEST	0	0	0	0	1	1
ENSG00000268229	ENSG00000268229	ARHGEF9	HG1437_PATCH:62854436-63005016	NOTEST	0	0	0	0	1	1
ENSG00000268230	ENSG00000268230	CTD-2619J13.8	19:58856543-58877958	NOTEST	0.46049	0.403988	-0.188859	0	1	1
ENSG00000268231	ENSG00000268231	CTD-2560K21.6	19:51020148-51071302	NOTEST	0	0.0539924	inf	0	1	1
ENSG00000268233	ENSG00000268233	RP13-36C9.5	HG1443_HG1444_PATCH:134885147-134886612	NOTEST	0	0	0	0	1	1
ENSG00000268234	ENSG00000268234	AL162415.2	9:44584982-44586314	NOTEST	0	0	0	0	1	1
ENSG00000268235	ENSG00000268235	AC234791.1	HG1440_PATCH:101470272-101481763	NOTEST	0	0	0	0	1	1
ENSG00000268236	ENSG00000268236	AC078899.4	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000268237	ENSG00000268237	SNORA70	HG1497_PATCH:153558422-153590188	NOTEST	0	0	0	0	1	1
ENSG00000268238	ENSG00000268238	IGFL1P2	19:46763676-46764115	NOTEST	0	0	0	0	1	1
ENSG00000268239	ENSG00000268239	SPANXA2	HG1453_PATCH:140671599-140672937	NOTEST	0	0	0	0	1	1
ENSG00000268240	ENSG00000268240	RP11-678G14.4	19:21770233-21777430	NOTEST	0	0	0	0	1	1
ENSG00000268241	ENSG00000268241	AC018470.1	2:175199673-175203220	NOTEST	0	0.00836404	inf	0	1	1
ENSG00000268242	ENSG00000268242	AC131935.1	11:11747059-11747257	NOTEST	0	0	0	0	1	1
ENSG00000268243	ENSG00000268243	AC005176.3	19:40135141-40135252	NOTEST	0	0	0	0	1	1
ENSG00000268244	ENSG00000268244	VTRNA3-1P	HG1433_PATCH:53205208-53205310	NOTEST	0	0	0	0	1	1
ENSG00000268245	ENSG00000268245	RBMX2P2	HG1453_PATCH:140343283-140346378	NOTEST	0	0	0	0	1	1
ENSG00000268246	ENSG00000268246	RP13-228J13.6	HG1497_PATCH:154444678-154503125	NOTEST	0	0	0	0	1	1
ENSG00000268247	ENSG00000268247	RP13-77O11.11	HG1433_PATCH:52567266-52572267	NOTEST	0	0	0	0	1	1
ENSG00000268248	ENSG00000268248	AC118758.5	HG736_PATCH:56881182-56883671	NOTEST	0	0	0	0	1	1
ENSG00000268249	ENSG00000268249	TIMM8A	HG1439_PATCH:100600648-100604184	NOTEST	0	0	0	0	1	1
ENSG00000268250	ENSG00000268250	Y_RNA	HG1257_PATCH:74790915-74791017	NOTEST	0	0	0	0	1	1
ENSG00000268251	ENSG00000268251	MIRLET7F2	HG1433_PATCH:53275143-53429752	NOTEST	0	0	0	0	1	1
ENSG00000268253	ENSG00000268253	AC232271.1	HG1436_HG1432_PATCH:49062640-49062727	NOTEST	0	0	0	0	1	1
ENSG00000268254	ENSG00000268254	RN7SL86P	HG122_PATCH:118230299-118302211	NOTEST	0	0	0	0	1	1
ENSG00000268256	ENSG00000268256	SSX5	HG1436_HG1432_PATCH:48045618-48056162	NOTEST	0	0	0	0	1	1
ENSG00000268257	ENSG00000268257	AIRN	6:160390130-160534539	NOTEST	0	0	0	0	1	1
ENSG00000268258	ENSG00000268258	RP11-492O8.1	HG1423_PATCH:36738034-36738338	NOTEST	0	0	0	0	1	1
ENSG00000268259	ENSG00000268259	ESX1	HG1441_PATCH:103504966-103509862	NOTEST	0	0	0	0	1	1
ENSG00000268260	ENSG00000268260	SPACA5	HG1436_HG1432_PATCH:47696300-47931057	NOTEST	0	0	0	0	1	1
ENSG00000268261	ENSG00000268261	SNORA36A	HG1497_PATCH:153931223-153946157	NOTEST	0	0	0	0	1	1
ENSG00000268263	ENSG00000268263	RNU6-707P	HG1436_HG1432_PATCH:48013266-48015340	NOTEST	0	0	0	0	1	1
ENSG00000268264	ENSG00000268264	CCNB3	HG1436_HG1432_PATCH:50012111-50159099	NOTEST	0	0	0	0	1	1
ENSG00000268265	ENSG00000268265	AP000304.1	21:34876237-35349992	NOTEST	0	0	0	0	1	1
ENSG00000268266	ENSG00000268266	AC003005.2	19:57989016-57994364	NOTEST	0	0.0616634	inf	0	1	1
ENSG00000268267	ENSG00000268267	SIGLEC29P	19:52067049-52068163	NOTEST	0	0	0	0	1	1

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ENSG00000268270	ENSG00000268270	RP11-161N3.3	HG1433_PATCH:53811323-53926281	NOTEST	0	0	0	0	1	1
ENSG00000268272	ENSG00000268272	VN1R78P	19:20718630-20844402	NOTEST	0	0	0	0	1	1
ENSG00000268273	ENSG00000268273	GSPT2	HG1433_PATCH:51486384-51489228	NOTEST	0	0	0	0	1	1
ENSG00000268274	ENSG00000268274	U82695.9	HG1497_PATCH:152613191-152678026	NOTEST	0	0	0	0	1	1
ENSG00000268275	ENSG00000268275	AL035588.1	6:41651715-41703997	NOTEST	0	0	0	0	1	1
ENSG00000268276	ENSG00000268276	AL590523.1	GL000221.1:62570-62753	NOTEST	0	0	0	0	1	1
ENSG00000268278	ENSG00000268278	RP11-420K14.1	19:21820775-21839102	NOTEST	0	0	0	0	1	1
ENSG00000268279	ENSG00000268279	RP11-434D12.1	3:14166439-14242619	NOTEST	0.0744658	0.0302457	-1.29985	0	1	1
ENSG00000268280	ENSG00000268280	AC008914.1	5:55224467-55224569	NOTEST	0	0	0	0	1	1
ENSG00000268281	ENSG00000268281	NAA10	HG1497_PATCH:153029985-153103693	NOTEST	0	0	0	0	1	1
ENSG00000268282	ENSG00000268282	CTD-2620I22.2	19:53430387-53541151	NOTEST	0	0	0	0	1	1
ENSG00000268283	ENSG00000268283	MIR509-3	HG1459_PATCH:146341366-146341441	NOTEST	0	0	0	0	1	1
ENSG00000268284	ENSG00000268284	RP11-707O23.5	HG1146_PATCH:43765667-43767139	NOTEST	0	0	0	0	1	1
ENSG00000268287	ENSG00000268287	CTB-60B18.18	19:49557530-49568333	NOTEST	0	0.0361076	inf	0	1	1
ENSG00000268288	ENSG00000268288	RP11-98D18.16	1:151728016-151766878	NOTEST	0	0.104391	inf	0	1	1
ENSG00000268289	ENSG00000268289	CTD-2528A14.3	19:17160538-17186435	NOTEST	0	0	0	0	1	1
ENSG00000268290	ENSG00000268290	AP001271.3	HG865_PATCH:70313960-71048647	NOTEST	0	0	0	0	1	1
ENSG00000268291	ENSG00000268291	RP11-420K14.7	HSCHR19_2_CTG3:21992760-21993547	NOTEST	0	0	0	0	1	1
ENSG00000268292	ENSG00000268292	AC006547.15	22:20004536-20058066	NOTEST	0	0	0	0	1	1
ENSG00000268293	ENSG00000268293	CTD-2623H2.7	19:58637618-58666477	NOTEST	0	0	0	0	1	1
ENSG00000268294	ENSG00000268294	RP11-353J17.3	HG1440_PATCH:101615367-101694980	NOTEST	0	0	0	0	1	1
ENSG00000268295	ENSG00000268295	RP11-248B24.4	14:92047039-92333880	NOTEST	0	0	0	0	1	1
ENSG00000268296	ENSG00000268296	CTD-2579N5.3	19:23089887-23097091	NOTEST	0	0	0	0	1	1
ENSG00000268297	ENSG00000268297	CLEC4GP1	19:7852434-7855507	NOTEST	0	0	0	0	1	1
ENSG00000268299	ENSG00000268299	CTD-2587H19.1	HSCHR19LRC_PGF2_CTG1:54862229-54864133	NOTEST	0	0	0	0	1	1
ENSG00000268300	ENSG00000268300	CTD-2183H9.3	HG1497_PATCH:154004255-154228771	NOTEST	0	0	0	0	1	1
ENSG00000268301	ENSG00000268301	AC018630.1	12:10977558-11324212	NOTEST	0	0	0	0	1	1
ENSG00000268304	ENSG00000268304	RNU2-68P	HG1438_PATCH:71549365-71792953	NOTEST	0	0	0	0	1	1
ENSG00000268305	ENSG00000268305	U3	HG1434_PATCH:113187413-113187626	NOTEST	0	0	0	0	1	1
ENSG00000268306	ENSG00000268306	RP11-1260E13.2	HG417_PATCH:152499-326252	NOTEST	0	0	0	0	1	1
ENSG00000268307	ENSG00000268307	CTD-2619J13.13	19:58911587-58912046	NOTEST	0.0515605	0	#NAME?	0	1	1
ENSG00000268309	ENSG00000268309	CTD-3222D19.11	19:16589867-16771253	NOTEST	0	0	0	0	1	1
ENSG00000268310	ENSG00000268310	AC087645.1	17:76210266-76221717	NOTEST	0	0	0	0	1	1
ENSG00000268312	ENSG00000268312	PHF8	HG1433_PATCH:53679675-53791958	NOTEST	0	0	0	0	1	1
ENSG00000268313	ENSG00000268313	AC119673.1	1:205681946-205719404	NOTEST	0	0.204612	inf	0	1	1
ENSG00000268314	ENSG00000268314	CXorf40A	HG1459_PATCH:148622076-148632232	NOTEST	0	0	0	0	1	1
ENSG00000268315	ENSG00000268315	RP11-157B13.8	HSCHR19_3_CTG3:22450701-22452344	NOTEST	0	0	0	0	1	1

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ENSG00000268317	ENSG00000268317	AC026461.1	16:56662970-56667898	NOTEST	0	0	0	0	1	1
ENSG00000268318	ENSG00000268318	CTD-3187F8.11	19:51774519-51786276	NOTEST	0	0	0	0	1	1
ENSG00000268319	ENSG00000268319	RP11-272G22.2	HG1433_PATCH:53511985-53512219	NOTEST	0	0	0	0	1	1
ENSG00000268320	ENSG00000268320	AC240565.1	HG417_PATCH:77570-79067	NOTEST	0	0	0	0	1	1
ENSG00000268322	ENSG00000268322	CTD-3030D20.2	19:21473961-21512227	NOTEST	0.0709805	0.0542811	-0.386974	0	1	1
ENSG00000268323	ENSG00000268323	FMR1-IT1	HG1459_PATCH:146993665-147032842	NOTEST	0	0	0	0	1	1
ENSG00000268324	ENSG00000268324	LUZPP1	3:46556912-46668033	NOTEST	0	0	0	0	1	1
ENSG00000268325	ENSG00000268325	AC002368.4	HG1459_PATCH:147579829-147582332	NOTEST	0	0	0	0	1	1
ENSG00000268326	ENSG00000268326	CTD-2542C24.8	19:21155067-21166016	NOTEST	0	0	0	0	1	1
ENSG00000268327	ENSG00000268327	C15ORF31	15:59427112-59815748	NOTEST	0	0	0	0	1	1
ENSG00000268328	ENSG00000268328	AC019206.1	2:70120691-70170077	NOTEST	0	0	0	0	1	1
ENSG00000268329	ENSG00000268329	KATNB1	HG1208_PATCH:57769641-57791162	NOTEST	0	0	0	0	1	1
ENSG00000268330	ENSG00000268330	AC211486.1	HG1257_PATCH:74835588-74841107	NOTEST	0	0	0	0	1	1
ENSG00000268331	ENSG00000268331	AP002954.4	HG122_PATCH:118575321-118661864	NOTEST	0	0	0	0	1	1
ENSG00000268332	ENSG00000268332	AL035406.1	1:5922870-6161253	NOTEST	0	0	0	0	1	1
ENSG00000268333	ENSG00000268333	RP4-806M20.3	20:57393973-57486247	NOTEST	0.0151288	0	#NAME?	0	1	1
ENSG00000268335	ENSG00000268335	CTC-513N18.3	19:20615357-20711421	NOTEST	0	0	0	0	1	1
ENSG00000268336	ENSG00000268336	SIGLEC20P	19:51688160-51694065	NOTEST	0	0	0	0	1	1
ENSG00000268337	ENSG00000268337	MAGEA9B	HG1459_PATCH:148863651-148869459	NOTEST	0	0	0	0	1	1
ENSG00000268340	ENSG00000268340	RP3-477O4.16	20:34106681-34107108	NOTEST	0.173937	0.127905	-0.443492	0	1	1
ENSG00000268341	ENSG00000268341	L47234.1	19:45836691-45874176	NOTEST	0	0	0	0	1	1
ENSG00000268342	ENSG00000268342	CTD-2340F8.1	9:41054826-41056158	NOTEST	0	0	0	0	1	1
ENSG00000268343	ENSG00000268343	AC012414.1	15:21004686-21005367	NOTEST	0	0	0	0	1	1
ENSG00000268344	ENSG00000268344	AL138815.2	13:25946208-26599989	NOTEST	0	0	0	0	1	1
ENSG00000268345	ENSG00000268345	RP11-432N13.2	HG1443_HG1444_PATCH:134717679-134719189	NOTEST	0	0	0	0	1	1
ENSG00000268346	ENSG00000268346	RP11-1260E13.3	HG417_PATCH:152499-326252	NOTEST	0	0	0	0	1	1
ENSG00000268347	ENSG00000268347	CTD-2267G17.2	HG1433_PATCH:52125052-52128614	NOTEST	0	0	0	0	1	1
ENSG00000268349	ENSG00000268349	RHOXF1	HG1442_PATCH:119170198-119280817	NOTEST	0	0	0	0	1	1
ENSG00000268350	ENSG00000268350	FAM156A	HG1433_PATCH:52690257-52701414	NOTEST	0	0	0	0	1	1
ENSG00000268351	ENSG00000268351	AP001888.1	11:69587253-69587718	NOTEST	0	0	0	0	1	1
ENSG00000268352	ENSG00000268352	AC007228.5	19:57183635-57196021	NOTEST	0	0	0	0	1	1
ENSG00000268353	ENSG00000268353	SYP	HG1436_HG1432_PATCH:49047214-49061853	NOTEST	0	0	0	0	1	1
ENSG00000268356	ENSG00000268356	RP1-172N19.4	HG1438_PATCH:71947826-71948671	NOTEST	0	0	0	0	1	1
ENSG00000268358	ENSG00000268358	EPB41L4A-AS2	5:111755279-111756310	NOTEST	0.0315024	0	#NAME?	0	1	1
ENSG00000268359	ENSG00000268359	RAB39B	HG1497_PATCH:154426708-154433057	NOTEST	0	0	0	0	1	1
ENSG00000268361	ENSG00000268361	L34079.2	19:44047191-44100287	NOTEST	0	0	0	0	1	1
ENSG00000268363	ENSG00000268363	RP11-232D9.2	HG1490_PATCH:115803777-115814271	NOTEST	0	0	0	0	1	1
ENSG00000268364	ENSG00000268364	SMC5-AS1	9:72658496-72873782	NOTEST	0.0777744	0	#NAME?	0	1	1
ENSG00000268365	ENSG00000268365	AL646016.1	1:240177647-240643504	NOTEST	0	0	0	0	1	1

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ENSG00000268366	ENSG00000268366	CTC-492K19.4	19:40946750-40950612	NOTEST	0.238996	0.299147	0.323866	0	1	1
ENSG00000268367	ENSG00000268367	AC126614.1	12:57637235-57824788	NOTEST	0.168803	0	#NAME?	0	1	1
ENSG00000268368	ENSG00000268368	TMSB15A	HG1440_PATCH:101768647-101771756	NOTEST	0	0	0	0	1	1
ENSG00000268369	ENSG00000268369	SNORA11E	HG1433_PATCH:51804826-51812272	NOTEST	0	0	0	0	1	1
ENSG00000268370	ENSG00000268370	RP11-45J1.1	HG1442_PATCH:119392612-119445519	NOTEST	0	0	0	0	1	1
ENSG00000268372	ENSG00000268372	IQSEC2	HG1433_PATCH:52975875-53064324	NOTEST	0	0	0	0	1	1
ENSG00000268374	ENSG00000268374	VN1R84P	HSCHR19_2_CTG3:21912081-21912316	NOTEST	0	0	0	0	1	1
ENSG00000268375	ENSG00000268375	CTD-2568A17.8	19:51293671-51298481	NOTEST	0	0	0	0	1	1
ENSG00000268376	ENSG00000268376	CTD-2586B10.1	HG729_PATCH:8695554-8703533	NOTEST	0	0	0	0	1	1
ENSG00000268377	ENSG00000268377	TCEAL6	HG1440_PATCH:101395447-101397942	NOTEST	0	0	0	0	1	1
ENSG00000268378	ENSG00000268378	AP002954.3	HG122_PATCH:118477212-118528753	NOTEST	0	0	0	0	1	1
ENSG00000268379	ENSG00000268379	CTC-360J11.4	19:57686600-57689289	NOTEST	0	0	0	0	1	1
ENSG00000268381	ENSG00000268381	H2BFWT	HG1441_PATCH:10326607-103268616	NOTEST	0	0	0	0	1	1
ENSG00000268382	ENSG00000268382	SYP-AS1	HG1436_HG1432_PATCH:49047214-49061853	NOTEST	0	0	0	0	1	1
ENSG00000268384	ENSG00000268384	TMEM187	HG1497_PATCH:153140794-153151663	NOTEST	0	0	0	0	1	1
ENSG00000268385	ENSG00000268385	RNU6-854P	HG1426_PATCH:77087317-77156547	NOTEST	0	0	0	0	1	1
ENSG00000268386	ENSG00000268386	VN1R79P	HSCHR19_1_CTG3:20941245-20941758	NOTEST	0	0	0	0	1	1
ENSG00000268387	ENSG00000268387	AL590714.1	1:161185023-161193421	NOTEST	0	0	0	0	1	1
ENSG00000268388	ENSG00000268388	FENDRR	16:86508134-86542705	NOTEST	0	0	0	0	1	1
ENSG00000268389	ENSG00000268389	API5P1	HG1463_PATCH:115223253-115224763	NOTEST	0	0	0	0	1	1
ENSG00000268390	ENSG00000268390	CTC-518B2.10	19:51547062-51555334	NOTEST	0	0	0	0	1	1
ENSG00000268391	ENSG00000268391	RP11-241F15.6	4:49550934-49551452	NOTEST	0	0.0637368	inf	0	1	1
ENSG00000268392	ENSG00000268392	AC003682.16	19:58136399-58138318	NOTEST	0	0	0	0	1	1
ENSG00000268393	ENSG00000268393	SPACA5B	HG1436_HG1432_PATCH:47990055-47992012	NOTEST	0	0	0	0	1	1
ENSG00000268394	ENSG00000268394	EBP	HG1436_HG1432_PATCH:48380556-48388115	NOTEST	0	0	0	0	1	1
ENSG00000268396	ENSG00000268396	AC012485.1	2:239140324-239198743	NOTEST	0	0	0	0	1	1
ENSG00000268398	ENSG00000268398	CTD-2587H19.2	HSCHR19LRC_COX1_CTG1:54850623-54872311	NOTEST	0	0	0	0	1	1
ENSG00000268399	ENSG00000268399	CTC-513N18.5	HG730_PATCH:20527322-20527878	NOTEST	0	0	0	0	1	1
ENSG00000268400	ENSG00000268400	CTD-3214H19.4	19:7694622-7712759	NOTEST	0.201528	0.232103	0.203779	0	1	1
ENSG00000268401	ENSG00000268401	CTC-344H19.4	19:46530911-46533419	NOTEST	0	0.192509	inf	0	1	1
ENSG00000268402	ENSG00000268402	AL031320.1	6:143743968-143771810	NOTEST	0	0	0	0	1	1
ENSG00000268405	ENSG00000268405	RNU6-504P	HG1433_PATCH:51546006-51645357	NOTEST	0	0	0	0	1	1
ENSG00000268406	ENSG00000268406	LINC01155	HG1433_PATCH:52836709-52910014	NOTEST	0	0	0	0	1	1
ENSG00000268407	ENSG00000268407	AC006115.6	19:57202053-57352097	NOTEST	0	0	0	0	1	1
ENSG00000268409	ENSG00000268409	RN7SL667P	HG1497_PATCH:152572319-152572613	NOTEST	0	0	0	0	1	1
ENSG00000268412	ENSG00000268412	AC013449.1	2:26251073-26251481	NOTEST	0	0	0	0	1	1
ENSG00000268413	ENSG00000268413	AC003043.1	17:42325752-42355825	NOTEST	0	0	0	0	1	1
ENSG00000268415	ENSG00000268415	AL035422.2	HG1439_PATCH:100673274-100788446	NOTEST	0	0	0	0	1	1
ENSG00000268416	ENSG00000268416	CTD-2626G11.2	19:20929728-20938056	NOTEST	0	0	0	0	1	1
ENSG00000268417	ENSG00000268417	LRCH2	HG1462_PATCH:114347091-114470542	NOTEST	0	0	0	0	1	1
ENSG00000268418	ENSG00000268418	AC233300.1	HG1436_HG1432_PATCH:48781426-48817785	NOTEST	0	0	0	0	1	1
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ENSG00000268421	ENSG00000268421	AL355531.2	10:131265447-131566271	NOTEST	0	0	0	0	1	1
ENSG00000268422	ENSG00000268422	MAGEA8	HG1459_PATCH:148962862-148967557	NOTEST	0	0	0	0	1	1
ENSG00000268423	ENSG00000268423	AC011551.3	19:46984052-47114050	NOTEST	0.229157	0.145589	-0.654432	0	1	1
ENSG00000268424	ENSG00000268424	AC008948.1	5:101569689-101632253	NOTEST	0	0	0	0	1	1
ENSG00000268425	ENSG00000268425	AF238380.8	HG1436_HG1432_PATCH:49721018-49721761	NOTEST	0	0	0	0	1	1
ENSG00000268426	ENSG00000268426	ERAS	HG1436_HG1432_PATCH:48688271-48689537	NOTEST	0	0	0	0	1	1
ENSG00000268427	ENSG00000268427	AL022328.1	22:50713407-50746056	NOTEST	0	0	0	0	1	1
ENSG00000268428	ENSG00000268428	AC235953.1	HG1459_PATCH:149443143-149595900	NOTEST	0	0	0	0	1	1
ENSG00000268429	ENSG00000268429	DOC2B	HG417_PATCH:96016-121634	NOTEST	0	0	0	0	1	1
ENSG00000268430	ENSG00000268430	SHANK2	HG865_PATCH:70313960-71048647	NOTEST	0	0	0	0	1	1
ENSG00000268431	ENSG00000268431	PRRG1	HG1424_PATCH:37209336-38547737	NOTEST	0	0	0	0	1	1
ENSG00000268432	ENSG00000268432	AC026407.1	5:157158204-157168456	NOTEST	0	0	0	0	1	1
ENSG00000268433	ENSG00000268433	RP11-420K14.2	19:21860351-21861023	NOTEST	0	0	0	0	1	1
ENSG00000268434	ENSG00000268434	AC011530.4	19:46268042-46296060	NOTEST	0	0	0	0	1	1
ENSG00000268435	ENSG00000268435	RP3-339A18.6	HG1433_PATCH:53174257-53177373	NOTEST	0	0	0	0	1	1
ENSG00000268437	ENSG00000268437	FAM47DP	HG1424_PATCH:37209336-38547737	NOTEST	0	0	0	0	1	1
ENSG00000268438	ENSG00000268438	CTD-2607J13.1	19:21987751-22034927	NOTEST	0	0	0	0	1	1
ENSG00000268439	ENSG00000268439	EMG1	HG344_PATCH:7074111-7085166	NOTEST	0	0	0	0	1	1
ENSG00000268440	ENSG00000268440	VBP1	HG1497_PATCH:154365474-154408285	NOTEST	0	0	0	0	1	1
ENSG00000268442	ENSG00000268442	HAVCR1P1	19:24345171-24346227	NOTEST	0	0.0523081	inf	0	1	1
ENSG00000268443	ENSG00000268443	ARHGEF9-IT1	HG1437_PATCH:62854436-63005016	NOTEST	0	0	0	0	1	1
ENSG00000268444	ENSG00000268444	SRPK3	HG1497_PATCH:152893339-152954204	NOTEST	0	0	0	0	1	1
ENSG00000268447	ENSG00000268447	SSX2	HG1433_PATCH:52494230-52504536	NOTEST	0	0	0	0	1	1
ENSG00000268448	ENSG00000268448	RP11-552J9.9	HG1433_PATCH:52398206-52400254	NOTEST	0	0	0	0	1	1
ENSG00000268449	ENSG00000268449	RP13-36C9.4	HG1443_HG1444_PATCH:134864761-134866226	NOTEST	0	0	0	0	1	1
ENSG00000268450	ENSG00000268450	MIR1912	HG1462_PATCH:113820547-114146531	NOTEST	0	0	0	0	1	1
ENSG00000268451	ENSG00000268451	FTH1P18	HG1423_PATCH:37061139-37061694	NOTEST	0	0	0	0	1	1
ENSG00000268454	ENSG00000268454	RNA5SP517	HG1459_PATCH:145509170-145509287	NOTEST	0	0	0	0	1	1
ENSG00000268455	ENSG00000268455	RP11-359H18.2	19:23708432-23870022	NOTEST	0	0	0	0	1	1
ENSG00000268456	ENSG00000268456	IL13RA2	HG1462_PATCH:114240444-114256447	NOTEST	0	0	0	0	1	1
ENSG00000268457	ENSG00000268457	AL160175.1	20:30252254-30311792	NOTEST	0	0	0	0	1	1
ENSG00000268458	ENSG00000268458	CTC-471J1.9	19:52616343-52680255	NOTEST	0	0	0	0	1	1
ENSG00000268459	ENSG00000268459	RP13-150K15.1	HG1459_PATCH:144711932-144714090	NOTEST	0	0	0	0	1	1
ENSG00000268460	ENSG00000268460	AC006262.6	19:46706682-46718094	NOTEST	0.367587	0.422119	0.199563	0	1	1
ENSG00000268461	ENSG00000268461	AC007204.1	19:20011721-20074273	NOTEST	0	0	0	0	1	1
ENSG00000268462	ENSG00000268462	USP5	HG344_PATCH:6961291-6975796	NOTEST	0	0	0	0	1	1
ENSG00000268465	ENSG00000268465	CTC-273B12.7	19:48949029-48985571	NOTEST	0	0	0	0	1	1
ENSG00000268466	ENSG00000268466	AL132989.1	14:58466452-58764857	NOTEST	0.151735	0.126733	-0.259762	0	1	1
ENSG00000268469	ENSG00000268469	RP11-15H20.3	19:23404400-23433192	NOTEST	0	0	0	0	1	1
ENSG00000268470	ENSG00000268470	DNAH17-AS1	17:76374720-76573476	NOTEST	0	0	0	0	1	1
ENSG00000268472	ENSG00000268472	AP002884.2	11:112097087-112140678	NOTEST	0.0309762	0.0109063	-1.506	0	1	1
ENSG00000268473	ENSG00000268473	RP11-158I3.1	16:86468435-86469490	NOTEST	0	0	0	0	1	1

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ENSG00000268476	ENSG00000268476	GPR173	HG1433_PATCH:52792090-52823615	NOTEST	0	0	0	0	1	1
ENSG00000268479	ENSG00000268479	CTD-2587H19.2	HSCHR19LRC_PGF1_CTG1:54848799-54870475	NOTEST	0	0	0	0	1	1
ENSG00000268480	ENSG00000268480	CTD-2586B10.1	19:8740120-8748103	NOTEST	0	0	0	0	1	1
ENSG00000268481	ENSG00000268481	PYY3	HG1436_HG1432_PATCH:49965557-49965770	NOTEST	0	0	0	0	1	1
ENSG00000268482	ENSG00000268482	AL160274.1	9:35161998-35405335	NOTEST	0	0	0	0	1	1
ENSG00000268483	ENSG00000268483	RPL7AP69	19:57576701-57577507	NOTEST	0	0	0	0	1	1
ENSG00000268484	ENSG00000268484	AC087477.1	15:96897465-96948419	NOTEST	0	0	0	0	1	1
ENSG00000268485	ENSG00000268485	AC104841.2	2:242166678-242293442	NOTEST	0	0	0	0	1	1
ENSG00000268486	ENSG00000268486	FP885535.1	HG1486_PATCH:16699847-16713306	NOTEST	0	0	0	0	1	1
ENSG00000268487	ENSG00000268487	VN1R110P	HG1436_HG1432_PATCH:48495563-48496534	NOTEST	0	0	0	0	1	1
ENSG00000268488	ENSG00000268488	AC018512.1	15:44019115-44095241	NOTEST	0	0	0	0	1	1
ENSG00000268489	ENSG00000268489	RBM3	HG1436_HG1432_PATCH:48432492-48438465	NOTEST	0	0	0	0	1	1
ENSG00000268490	ENSG00000268490	SPANXN3	HG1458_PATCH:142372762-142605261	NOTEST	0	0	0	0	1	1
ENSG00000268491	ENSG00000268491	5S_rRNA	HG1459_PATCH:147063045-147108384	NOTEST	0	0	0	0	1	1
ENSG00000268494	ENSG00000268494	RP13-77O11.8	HG1433_PATCH:52524451-52528786	NOTEST	0	0	0	0	1	1
ENSG00000268496	ENSG00000268496	CTD-2587H19.2	19:54926392-54948080	NOTEST	0	0	0	0	1	1
ENSG00000268497	ENSG00000268497	ARMCX3-AS1	HG1439_PATCH:100877783-100882830	NOTEST	0	0	0	0	1	1
ENSG00000268498	ENSG00000268498	HDAC8	HG1438_PATCH:71549365-71792953	NOTEST	0	0	0	0	1	1
ENSG00000268499	ENSG00000268499	CTB-102L5.8	19:38397867-38699012	NOTEST	0.107003	0.169804	0.666216	0	1	1
ENSG00000268500	ENSG00000268500	SIGLEC5	19:52114780-52150151	NOTEST	0	0.00692546	inf	0	1	1
ENSG00000268501	ENSG00000268501	CCDC22	HG1436_HG1432_PATCH:49094865-49124225	NOTEST	0	0	0	0	1	1
ENSG00000268502	ENSG00000268502	BX842568.4	HG1423_PATCH:37003639-37004210	NOTEST	0	0	0	0	1	1
ENSG00000268503	ENSG00000268503	AC007421.1	17:7465191-7536700	NOTEST	0	0	0	0	1	1
ENSG00000268504	ENSG00000268504	CTC-513N18.6	HG730_PATCH:20543360-20639424	NOTEST	0	0	0	0	1	1
ENSG00000268505	ENSG00000268505	RP11-805I24.3	16:86226398-86233326	NOTEST	0	0	0	0	1	1
ENSG00000268506	ENSG00000268506	CTB-83J4.2	HSCHR19LRC_PGF1_CTG1:55006690-55072658	NOTEST	0	0	0	0	1	1
ENSG00000268507	ENSG00000268507	AC078899.2	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000268509	ENSG00000268509	AC026202.1	3:5229226-5261642	NOTEST	0.0620094	0.224947	1.85903	0	1	1
ENSG00000268510	ENSG00000268510	IFNL3P1	19:39727072-39727933	NOTEST	0	0	0	0	1	1
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ENSG00000268512	ENSG00000268512	CETN2	HG1497_PATCH:151995444-151999249	NOTEST	0	0	0	0	1	1
ENSG00000268513	ENSG00000268513	SNORD77	HG1435_PATCH:45752156-45752224	NOTEST	0	0	0	0	1	1
ENSG00000268514	ENSG00000268514	RP11-85L21.5	HG1443_HG1444_PATCH:134269178-134269800	NOTEST	0	0	0	0	1	1
ENSG00000268515	ENSG00000268515	RP11-770J1.3	HG122_PATCH:118307204-118473748	NOTEST	0	0	0	0	1	1
ENSG00000268518	ENSG00000268518	CTD-2545M3.8	19:50990066-50990895	NOTEST	0.158208	0.289757	0.87302	0	1	1
ENSG00000268519	ENSG00000268519	AC073528.1	12:77718420-77966055	NOTEST	0	0	0	0	1	1
ENSG00000268520	ENSG00000268520	CTD-2616J11.10	19:51848422-51872257	NOTEST	0.14112	0.108314	-0.381711	0	1	1
ENSG00000268522	ENSG00000268522	MIR510	HG1459_PATCH:146354049-146354123	NOTEST	0	0	0	0	1	1
ENSG00000268523	ENSG00000268523	RP5-937E21.1	HG1459_PATCH:148730895-148731846	NOTEST	0	0	0	0	1	1
ENSG00000268524	ENSG00000268524	GAGE12B	HG1436_HG1432_PATCH:49339267-49339384	NOTEST	0	0	0	0	1	1
ENSG00000268526	ENSG00000268526	HNRNPH1P2	HG1458_PATCH:142764938-142766148	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000268530	ENSG00000268530	CTC-273B12.5	19:48949029-48985571	NOTEST	0.12584	0.025246	-2.31746	0	1	1
ENSG00000268531	ENSG00000268531	DKFZP547L112	15:22011369-22012050	NOTEST	0	0	0	0	1	1
ENSG00000268532	ENSG00000268532	RP11-514D23.1	16:86320032-86326995	NOTEST	0	0	0	0	1	1
ENSG00000268533	ENSG00000268533	AC004076.7	19:57874844-57988938	NOTEST	0	0	0	0	1	1
ENSG00000268534	ENSG00000268534	SSXP5	HG1433_PATCH:52415717-52420051	NOTEST	0	0	0	0	1	1
ENSG00000268535	ENSG00000268535	RP11-420K14.3	19:21892323-21892993	NOTEST	0	0	0	0	1	1
ENSG00000268536	ENSG00000268536	AC005523.3	19:4785131-4791219	NOTEST	0.0600797	0	#NAME?	0	1	1
ENSG00000268537	ENSG00000268537	AC109583.1	3:46899361-46945287	NOTEST	0	0	0	0	1	1
ENSG00000268538	ENSG00000268538	KIAA1658	22:30727976-30825045	NOTEST	0	0.127647	inf	0	1	1
ENSG00000268539	ENSG00000268539	RP11-322A17.1	HG1425_PATCH:75442471-75442932	NOTEST	0	0	0	0	1	1
ENSG00000268541	ENSG00000268541	VN1R88P	19:23044104-23044396	NOTEST	0	0	0	0	1	1
ENSG00000268542	ENSG00000268542	RP3-525N14.2	HG1442_PATCH:119336023-119336711	NOTEST	0	0	0	0	1	1
ENSG00000268544	ENSG00000268544	RP11-277L2.4	1:149575344-149637707	NOTEST	0	0	0	0	1	1
ENSG00000268545	ENSG00000268545	VN1R107P	19:57874844-57988938	NOTEST	0	0	0	0	1	1
ENSG00000268546	ENSG00000268546	SSX1	HG1436_HG1432_PATCH:48114715-48126843	NOTEST	0	0	0	0	1	1
ENSG00000268547	ENSG00000268547	RP11-183K14.1	HG1459_PATCH:145619249-145619763	NOTEST	0	0	0	0	1	1
ENSG00000268548	ENSG00000268548	TPI1	HG344_PATCH:6976282-7032861	NOTEST	0	0	0	0	1	1
ENSG00000268550	ENSG00000268550	AC090427.1	19:14729928-14889353	NOTEST	0	0	0	0	1	1
ENSG00000268551	ENSG00000268551	ATP5L	HG122_PATCH:118230299-118302211	NOTEST	0	0	0	0	1	1
ENSG00000268552	ENSG00000268552	AL109927.1	1:28157288-28178187	NOTEST	0	0	0	0	1	1
ENSG00000268553	ENSG00000268553	AC027309.1	5:172036244-172036436	NOTEST	0	0	0	0	1	1
ENSG00000268554	ENSG00000268554	RP11-353N4.7	1:149575344-149637707	NOTEST	0.0870231	0.229067	1.3963	0	1	1
ENSG00000268555	ENSG00000268555	RP11-678G14.3	19:21753623-21770124	NOTEST	0	0	0	0	1	1
ENSG00000268556	ENSG00000268556	AC012360.1	2:105867758-105869601	NOTEST	0	0	0	0	1	1
ENSG00000268557	ENSG00000268557	EMD	HG1497_PATCH:153547664-153549991	NOTEST	0	0	0	0	1	1
ENSG00000268558	ENSG00000268558	RP11-370B6.1	HG1441_PATCH:103159250-103159683	NOTEST	0	0	0	0	1	1
ENSG00000268559	ENSG00000268559	RP11-85L21.4	HG1443_HG1444_PATCH:134193714-134257982	NOTEST	0	0	0	0	1	1
ENSG00000268560	ENSG00000268560	CTD-2332E11.2	19:20718630-20844402	NOTEST	0	0	0	0	1	1
ENSG00000268561	ENSG00000268561	MIR509-1	HG1459_PATCH:146342246-146342340	NOTEST	0	0	0	0	1	1
ENSG00000268563	ENSG00000268563	MECP2	HG1497_PATCH:153190040-153266223	NOTEST	0	0	0	0	1	1
ENSG00000268564	ENSG00000268564	AC003956.1	19:15218213-15236985	NOTEST	0	0	0	0	1	1
ENSG00000268566	ENSG00000268566	RP11-687D19.1	18:36235172-36267962	NOTEST	0	0	0	0	1	1
ENSG00000268568	ENSG00000268568	AC007228.9	19:57183635-57196021	NOTEST	0.0490083	0	#NAME?	0	1	1
ENSG00000268569	ENSG00000268569	HIRA	HG329_PATCH:19318210-19435745	NOTEST	0	0	0	0	1	1
ENSG00000268570	ENSG00000268570	FAM199X	HG1441_PATCH:103421548-103450831	NOTEST	0	0	0	0	1	1
ENSG00000268571	ENSG00000268571	RP11-157B13.7	HSCHR19_3_CTG3:22434262-22436356	NOTEST	0	0	0	0	1	1
ENSG00000268572	ENSG00000268572	RP11-204I15.1	HG1433_PATCH:52191586-52194138	NOTEST	0	0	0	0	1	1
ENSG00000268574	ENSG00000268574	PABPC1L2A	HG1438_PATCH:72297125-72299362	NOTEST	0	0	0	0	1	1
ENSG00000268575	ENSG00000268575	RP1-283E3.8	1:1634168-1677431	NOTEST	0.401564	0.491041	0.290214	0	1	1
ENSG00000268576	ENSG00000268576	AC239811.1	HG1287_PATCH:149283883-149366178	NOTEST	0	0	0	0	1	1
ENSG00000268577	ENSG00000268577	CTD-2587H19.3	HSCHR19LRC_PGF1_CTG1:54871586-54871923	NOTEST	0	0	0	0	1	1

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ENSG00000268578	ENSG00000268578	AL354718.1	9:45441272-45441542	NOTEST	0	0.20987	inf	0	1	1
ENSG00000268579	ENSG00000268579	PHKA1	HG1438_PATCH:71798663-71934169	NOTEST	0	0	0	0	1	1
ENSG00000268580	ENSG00000268580	RP11-514A9.1	2:145425533-145940216	NOTEST	0	0	0	0	1	1
ENSG00000268581	ENSG00000268581	SIGLEC18P	19:51623243-51626222	NOTEST	0	0	0	0	1	1
ENSG00000268582	ENSG00000268582	AC005794.1	19:42156600-42156888	NOTEST	0	0	0	0	1	1
ENSG00000268583	ENSG00000268583	CTC-453G23.8	19:48673948-48790865	NOTEST	0.0904789	0.354524	1.97023	0	1	1
ENSG00000268584	ENSG00000268584	RP11-464F9.20	10:75385753-75386548	NOTEST	0.158689	0.136551	-0.216768	0	1	1
ENSG00000268585	ENSG00000268585	RP11-234P3.4	HG1433_PATCH:51666551-51666740	NOTEST	0	0	0	0	1	1
ENSG00000268586	ENSG00000268586	RP11-1260E13.4	HG417_PATCH:152499-326252	NOTEST	0	0	0	0	1	1
ENSG00000268587	ENSG00000268587	AC004463.6	HG329_PATCH:19158907-19160352	NOTEST	0	0	0	0	1	1
ENSG00000268589	ENSG00000268589	CTC-457E21.7	19:22798358-22806773	NOTEST	0	0	0	0	1	1
ENSG00000268590	ENSG00000268590	BAGE5	GL000237.1:898-2487	NOTEST	0	0	0	0	1	1
ENSG00000268591	ENSG00000268591	PLXNB3	HG1497_PATCH:152893339-152954204	NOTEST	0	0	0	0	1	1
ENSG00000268592	ENSG00000268592	RP11-244K5.8	6:150139933-150244257	NOTEST	0.499735	0.60595	0.278036	0	1	1
ENSG00000268593	ENSG00000268593	CTD-2611O12.6	19:56186591-56249768	NOTEST	0.234438	0.036317	-2.69049	0	1	1
ENSG00000268594	ENSG00000268594	MIR200C	HG344_PATCH:7072408-7073610	NOTEST	0	0	0	0	1	1
ENSG00000268595	ENSG00000268595	CTD-3187F8.2	19:51749602-51774433	NOTEST	0	0	0	0	1	1
ENSG00000268596	ENSG00000268596	MIR362	HG1436_HG1432_PATCH:49732013-49908634	NOTEST	0	0	0	0	1	1
ENSG00000268597	ENSG00000268597	RP11-157B13.8	19:22442494-22444137	NOTEST	0	0	0	0	1	1
ENSG00000268598	ENSG00000268598	VN1R80P	19:21246729-21247067	NOTEST	0	0	0	0	1	1
ENSG00000268599	ENSG00000268599	RNU6-1157P	HG122_PATCH:118307204-118473748	NOTEST	0	0	0	0	1	1
ENSG00000268600	ENSG00000268600	RP13-210D15.1	HG1443_HG1444_PATCH:134335760-134349262	NOTEST	0	0	0	0	1	1
ENSG00000268601	ENSG00000268601	AC115522.3	19:44298460-44299810	NOTEST	0	0	0	0	1	1
ENSG00000268602	ENSG00000268602	AP002353.1	11:107578103-107595135	NOTEST	0	0	0	0	1	1
ENSG00000268603	ENSG00000268603	RP11-316O14.1	2:220299567-220403494	NOTEST	0.063892	0.149432	1.22578	0	1	1
ENSG00000268604	ENSG00000268604	SLC10A3	HG1497_PATCH:153655773-153659145	NOTEST	0	0	0	0	1	1
ENSG00000268605	ENSG00000268605	CTB-50E14.4	19:42901279-43156507	NOTEST	0	0.0116803	inf	0	1	1
ENSG00000268606	ENSG00000268606	MAGEA2	HG1497_PATCH:151918356-151922350	NOTEST	0	0	0	0	1	1
ENSG00000268607	ENSG00000268607	HSPA8P7	HG1462_PATCH:113820547-114146531	NOTEST	0	0	0	0	1	1
ENSG00000268608	ENSG00000268608	IDSP1	HG1459_PATCH:148558711-148615657	NOTEST	0	0	0	0	1	1
ENSG00000268609	ENSG00000268609	AF277315.19	HG1497_PATCH:153774325-153774418	NOTEST	0	0	0	0	1	1
ENSG00000268610	ENSG00000268610	RNA5SP503	HG1436_HG1432_PATCH:48065656-48065773	NOTEST	0	0	0	0	1	1
ENSG00000268611	ENSG00000268611	AF196972.10	HG1436_HG1432_PATCH:48282740-48282867	NOTEST	0	0	0	0	1	1
ENSG00000268612	ENSG00000268612	ABT1	HG27_PATCH:26597179-26600278	NOTEST	0	0	0	0	1	1
ENSG00000268613	ENSG00000268613	CTD-2620I22.7	19:53611131-53662328	NOTEST	0	0	0	0	1	1
ENSG00000268614	ENSG00000268614	CTD-2207O23.10	19:7587511-7626650	NOTEST	0	0	0	0	1	1
ENSG00000268615	ENSG00000268615	RP11-65J3.15	9:132090539-132090680	NOTEST	0	0	0	0	1	1
ENSG00000268618	ENSG00000268618	AC092316.1	19:8585673-8642461	NOTEST	0	0	0	0	1	1
ENSG00000268619	ENSG00000268619	RP11-1148L6.5	HG1436_HG1432_PATCH:48439172-48440556	NOTEST	0	0	0	0	1	1
ENSG00000268620	ENSG00000268620	AC078899.4	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000268623	ENSG00000268623	CTB-52I2.3	19:18151164-18151893	NOTEST	0	0	0	0	1	1
ENSG00000268624	ENSG00000268624	AC243428.1	HG1497_PATCH:152225501-152227744	NOTEST	0	0	0	0	1	1

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ENSG00000268626	ENSG00000268626	AC103809.2	17:72322348-72351959	NOTEST	0	0	0	0	1	1
ENSG00000268628	ENSG00000268628	AL121761.2	20:19738295-19790319	NOTEST	0	0	0	0	1	1
ENSG00000268629	ENSG00000268629	TEX13A	HG375_PATCH:103810995-105011820	NOTEST	0	0	0	0	1	1
ENSG00000268630	ENSG00000268630	DDX26B	HG1443_HG1444_PATCH:134654111-134716539	NOTEST	0	0	0	0	1	1
ENSG00000268632	ENSG00000268632	AC073657.1	15:42066631-42120134	NOTEST	0	0	0	0	1	1
ENSG00000268633	ENSG00000268633	RP3-514P16.1	HG1439_PATCH:100792471-100794263	NOTEST	0	0	0	0	1	1
ENSG00000268634	ENSG00000268634	AC233299.1	HG1462_PATCH:113820547-114146531	NOTEST	0	0	0	0	1	1
ENSG00000268635	ENSG00000268635	DKFZP434E1119	11:77032751-77188074	NOTEST	0.0460267	0.0695913	0.596434	0	1	1
ENSG00000268636	ENSG00000268636	CTB-33G10.11	19:50094899-50129696	NOTEST	0	0	0	0	1	1
ENSG00000268637	ENSG00000268637	CR753820.1	HSCHR6_MHC_DBB:31441225-31443933	NOTEST	0	0	0	0	1	1
ENSG00000268638	ENSG00000268638	KRT18P62	HG329_PATCH:19166988-19279229	NOTEST	0	0	0	0	1	1
ENSG00000268640	ENSG00000268640	AC026369.1	12:147051-149350	NOTEST	0	0	0	0	1	1
ENSG00000268641	ENSG00000268641	RP11-157B13.3	HSCHR19_3_CTG3:22323333-22323919	NOTEST	0	0	0	0	1	1
ENSG00000268642	ENSG00000268642	HNRNPH2	HG1439_PATCH:100645811-100669121	NOTEST	0	0	0	0	1	1
ENSG00000268643	ENSG00000268643	AC006486.9	19:42734337-42759309	NOTEST	0	0	0	0	1	1
ENSG00000268644	ENSG00000268644	PNMA5	HG1497_PATCH:152157295-152162599	NOTEST	0	0	0	0	1	1
ENSG00000268645	ENSG00000268645	RP5-1014O16.10	HG1459_PATCH:148842500-148842596	NOTEST	0	0	0	0	1	1
ENSG00000268646	ENSG00000268646	PCSK1N	HG1436_HG1432_PATCH:48690492-48695033	NOTEST	0	0	0	0	1	1
ENSG00000268648	ENSG00000268648	RP13-228J13.9	HG1497_PATCH:154365474-154408285	NOTEST	0	0	0	0	1	1
ENSG00000268649	ENSG00000268649	MIR296	20:57392186-57392780	NOTEST	0	0	0	0	1	1
ENSG00000268650	ENSG00000268650	AC068499.10	19:18315539-18366229	NOTEST	0	0.583922	inf	0	1	1
ENSG00000268651	ENSG00000268651	CTAG1A	HG1497_PATCH:153753610-153755284	NOTEST	0	0	0	0	1	1
ENSG00000268652	ENSG00000268652	CTD-3187F8.7	19:51697373-51698796	NOTEST	0	0	0	0	1	1
ENSG00000268654	ENSG00000268654	MIMT1	19:57352269-57359924	NOTEST	0	0	0	0	1	1
ENSG00000268656	ENSG00000268656	AC110084.1	2:27994583-28561768	NOTEST	0	0	0	0	1	1
ENSG00000268657	ENSG00000268657	AL133373.1	14:92038787-92041383	NOTEST	0	0	0	0	1	1
ENSG00000268658	ENSG00000268658	LINC00664	19:21579920-21752039	NOTEST	0	0	0	0	1	1
ENSG00000268659	ENSG00000268659	RP11-310J24.3	10:77360997-78320752	NOTEST	0	0	0	0	1	1
ENSG00000268660	ENSG00000268660	LETM1P2	19:58545399-58565999	NOTEST	0	0	0	0	1	1
ENSG00000268661	ENSG00000268661	MIR448	HG1462_PATCH:113820547-114146531	NOTEST	0	0	0	0	1	1
ENSG00000268662	ENSG00000268662	AL596220.1	1:186344889-186390510	NOTEST	0	0	0	0	1	1
ENSG00000268663	ENSG00000268663	WBP1LP6	1:536815-660283	NOTEST	0	0	0	0	1	1
ENSG00000268664	ENSG00000268664	RNU6-376P	HG122_PATCH:118573056-118573162	NOTEST	0	0	0	0	1	1
ENSG00000268666	ENSG00000268666	MIR222	HG1435_PATCH:45604455-45629519	NOTEST	0	0	0	0	1	1
ENSG00000268667	ENSG00000268667	TMSB15B	HG1441_PATCH:103217579-103221224	NOTEST	0	0	0	0	1	1
ENSG00000268668	ENSG00000268668	SHROOM4	HG1433_PATCH:50334646-50557302	NOTEST	0	0	0	0	1	1
ENSG00000268669	ENSG00000268669	CTB-60B18.17	19:49526125-49552400	NOTEST	0	0	0	0	1	1
ENSG00000268671	ENSG00000268671	HAUS7	HG1497_PATCH:152613191-152678026	NOTEST	0	0	0	0	1	1
ENSG00000268673	ENSG00000268673	LLNLR-249E10.1	19:15871050-15890719	NOTEST	0	0	0	0	1	1
ENSG00000268674	ENSG00000268674	FAM231B	1:16865560-16866070	NOTEST	0	0	0	0	1	1
ENSG00000268675	ENSG00000268675	GPKOW	HG1436_HG1432_PATCH:48972794-48983200	NOTEST	0	0	0	0	1	1
ENSG00000268676	ENSG00000268676	MIR320D2	HG1453_PATCH:140008336-140008384	NOTEST	0	0	0	0	1	1
ENSG00000268677	ENSG00000268677	CTB-33G10.6	19:50179042-50193832	NOTEST	0	0.0500808	inf	0	1	1

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ENSG00000268679	ENSG00000268679	AC233294.1	HG1436_HG1432_PATCH:48836321-48861663	NOTEST	0	0	0	0	1	1
ENSG00000268681	ENSG00000268681	COX6CP7	19:50005688-50005896	NOTEST	0	0	0	0	1	1
ENSG00000268682	ENSG00000268682	MAGED4B	HG1433_PATCH:51804826-51812272	NOTEST	0	0	0	0	1	1
ENSG00000268683	ENSG00000268683	CTD-2553L13.4	19:35084233-35166604	NOTEST	0	0	0	0	1	1
ENSG00000268684	ENSG00000268684	CXorf51B	HG1459_PATCH:145891498-145892124	NOTEST	0	0	0	0	1	1
ENSG00000268685	ENSG00000268685	CTB-31C7.3	19:22545390-22545627	NOTEST	0	0	0	0	1	1
ENSG00000268686	ENSG00000268686	AC010524.2	19:49834873-49891338	NOTEST	0.0779371	0.0746082	-0.0629754	0	1	1
ENSG00000268688	ENSG00000268688	AC007382.1	2:37068326-37068530	NOTEST	0.666828	1.24183	0.897084	0	1	1
ENSG00000268690	ENSG00000268690	GDI1	HG1497_PATCH:153605387-153611935	NOTEST	0	0	0	0	1	1
ENSG00000268691	ENSG00000268691	LDOC1	HG1453_PATCH:140257913-140259290	NOTEST	0	0	0	0	1	1
ENSG00000268692	ENSG00000268692	RP11-272G22.3	HG1433_PATCH:53550775-53551623	NOTEST	0	0	0	0	1	1
ENSG00000268693	ENSG00000268693	RPH3AL	HG417_PATCH:152499-326252	NOTEST	0	0	0	0	1	1
ENSG00000268694	ENSG00000268694	DUTP4	HG1459_PATCH:148898891-148899366	NOTEST	0	0	0	0	1	1
ENSG00000268695	ENSG00000268695	CT55	HG1443_HG1444_PATCH:134290565-134305428	NOTEST	0	0	0	0	1	1
ENSG00000268696	ENSG00000268696	ZNF723	19:23015002-23042224	NOTEST	0	0	0	0	1	1
ENSG00000268699	ENSG00000268699	GAB3	HG1497_PATCH:153843719-153920051	NOTEST	0	0	0	0	1	1
ENSG00000268700	ENSG00000268700	MTCP1	HG1497_PATCH:154230089-154324971	NOTEST	0	0	0	0	1	1
ENSG00000268702	ENSG00000268702	AL049829.1	14:23654524-23795394	NOTEST	0	0	0	0	1	1
ENSG00000268703	ENSG00000268703	RP11-232D9.4	HG1490_PATCH:115822837-115824153	NOTEST	0	0	0	0	1	1
ENSG00000268705	ENSG00000268705	CTD-2561J22.6	19:21579920-21752039	NOTEST	0.0387855	0.0302071	-0.360632	0	1	1
ENSG00000268706	ENSG00000268706	AC009802.1	18:61538925-61609601	NOTEST	0	0	0	0	1	1
ENSG00000268707	ENSG00000268707	RP11-247A12.7	9:131932712-131933219	NOTEST	0	0	0	0	1	1
ENSG00000268708	ENSG00000268708	BX088651.2	9:44325915-44326077	NOTEST	0	0	0	0	1	1
ENSG00000268709	ENSG00000268709	MAGEA11	HG1459_PATCH:148769949-148798988	NOTEST	0	0	0	0	1	1
ENSG00000268711	ENSG00000268711	CTD-2616J11.15	19:51929600-51929922	NOTEST	0	0	0	0	1	1
ENSG00000268712	ENSG00000268712	GLOD5	HG1436_HG1432_PATCH:48621148-48633047	NOTEST	0	0	0	0	1	1
ENSG00000268714	ENSG00000268714	CTD-2287O16.3	5:115298150-115395815	NOTEST	0	0	0	0	1	1
ENSG00000268715	ENSG00000268715	YAP1P2	HG1462_PATCH:114305706-114306316	NOTEST	0	0	0	0	1	1
ENSG00000268716	ENSG00000268716	AC055736.1	12:52922914-52922980	NOTEST	0	0	0	0	1	1
ENSG00000268717	ENSG00000268717	AC025811.1	19:22573820-22715287	NOTEST	0	0	0	0	1	1
ENSG00000268718	ENSG00000268718	RP1-169P22.2	HG1458_PATCH:143396619-143396866	NOTEST	0	0	0	0	1	1
ENSG00000268719	ENSG00000268719	AL671561.1	HSCHR6_MHC_COX:29809935-29810766	NOTEST	0	0	0	0	1	1
ENSG00000268721	ENSG00000268721	RP11-588H23.5	12:70840239-70841365	NOTEST	0	0	0	0	1	1
ENSG00000268722	ENSG00000268722	ARMCX4	HG1439_PATCH:100673274-100788446	NOTEST	0	0	0	0	1	1
ENSG00000268723	ENSG00000268723	CTC-444N24.9	19:57828575-57828930	NOTEST	0	0	0	0	1	1
ENSG00000268726	ENSG00000268726	RP13-444K19.1	HG1433_PATCH:53568886-53569309	NOTEST	0	0	0	0	1	1
ENSG00000268727	ENSG00000268727	ASS1P5	HG1462_PATCH:114901364-114902603	NOTEST	0	0	0	0	1	1
ENSG00000268728	ENSG00000268728	BX001040.1	HSCHR6_MHC_QBL:31474802-31475278	NOTEST	0	0	0	0	1	1
ENSG00000268729	ENSG00000268729	CTD-2105E13.14	19:55793439-55823901	NOTEST	0	0	0	0	1	1

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ENSG00000268731	ENSG00000268731	CTD-2561J22.1	19:21564021-21564723	NOTEST	0	0	0	0	1	1
ENSG00000268733	ENSG00000268733	NCS1	HG1502_PATCH:132934856-132999583	NOTEST	0	0	0	0	1	1
ENSG00000268734	ENSG00000268734	CTB-61M7.2	19:55402038-55402786	NOTEST	0	0	0	0	1	1
ENSG00000268735	ENSG00000268735	AL139080.1	13:24304327-24476794	NOTEST	0	0	0	0	1	1
ENSG00000268736	ENSG00000268736	RP11-1281K21.6	4:49248037-49248555	NOTEST	0.0428072	0	#NAME?	0	1	1
ENSG00000268737	ENSG00000268737	SLITRK2	HG1459_PATCH:144899546-144907557	NOTEST	0	0	0	0	1	1
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ENSG00000268744	ENSG00000268744	CTD-3105H18.14	19:12490002-12750912	NOTEST	0.0126461	0	#NAME?	0	1	1
ENSG00000268745	ENSG00000268745	RP11-298J23.9	6:41737913-41863099	NOTEST	0	0	0	0	1	1
ENSG00000268746	ENSG00000268746	CTD-2571L23.8	19:48110780-48246391	NOTEST	0	0.192475	inf	0	1	1
ENSG00000268747	ENSG00000268747	CTD-3030D20.1	19:21458824-21459134	NOTEST	0	0	0	0	1	1
ENSG00000268748	ENSG00000268748	RP4-755D9.1	HG1442_PATCH:119170198-119280817	NOTEST	0	0	0	0	1	1
ENSG00000268749	ENSG00000268749	MIR513B	HG1459_PATCH:146280758-146280842	NOTEST	0	0	0	0	1	1
ENSG00000268751	ENSG00000268751	SCGB1B2P	19:35067637-35068606	NOTEST	0	0	0	0	1	1
ENSG00000268753	ENSG00000268753	LA16c-4G1.4	HG1487_PATCH:16109234-16109355	NOTEST	0	0	0	0	1	1
ENSG00000268754	ENSG00000268754	LINC01081	16:86259185-86309351	NOTEST	0	0	0	0	1	1
ENSG00000268755	ENSG00000268755	SPIN4-AS1	HG1437_PATCH:62562696-62780541	NOTEST	0	0	0	0	1	1
ENSG00000268756	ENSG00000268756	AC104534.2	19:39306061-39342987	NOTEST	0.112841	0.0293005	-1.9453	0	1	1
ENSG00000268757	ENSG00000268757	ABCD1	HG1497_PATCH:152893339-152954204	NOTEST	0	0	0	0	1	1
ENSG00000268758	ENSG00000268758	EMR4P	19:6952510-6990857	NOTEST	0	0	0	0	1	1
ENSG00000268759	ENSG00000268759	AC135983.2	15:32774821-32780287	NOTEST	0	0	0	0	1	1
ENSG00000268760	ENSG00000268760	TMEM255A	HG1442_PATCH:119392612-119445519	NOTEST	0	0	0	0	1	1
ENSG00000268762	ENSG00000268762	SPIN4	HG1437_PATCH:62562696-62780541	NOTEST	0	0	0	0	1	1
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ENSG00000268767	ENSG00000268767	PLS3	HG1462_PATCH:114754651-114887331	NOTEST	0	0	0	0	1	1
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ENSG00000268774	ENSG00000268774	CXorf51A	HG1459_PATCH:145895820-145896441	NOTEST	0	0	0	0	1	1
ENSG00000268775	ENSG00000268775	RP11-552J9.11	HG1433_PATCH:52430362-52430633	NOTEST	0	0	0	0	1	1
ENSG00000268776	ENSG00000268776	RP13-34L8.8	HG1433_PATCH:52304768-52305301	NOTEST	0	0	0	0	1	1
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ENSG00000268784	ENSG00000268784	MGC2752	19:59070495-59111168	NOTEST	0	0	0	0	1	1
ENSG00000268785	ENSG00000268785	RPL7P50	19:6583193-6604114	NOTEST	0	0	0	0	1	1
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ENSG00000268789	ENSG00000268789	VN1R87P	19:22925725-22926212	NOTEST	0	0	0	0	1	1
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ENSG00000268792	ENSG00000268792	SPANXN5	HG1433_PATCH:52539143-52541101	NOTEST	0	0	0	0	1	1
ENSG00000268793	ENSG00000268793	SSXP9	HG1436_HG1432_PATCH:48181747-48186082	NOTEST	0	0	0	0	1	1
ENSG00000268794	ENSG00000268794	VN1R90P	19:23471421-23472147	NOTEST	0	0	0	0	1	1
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ENSG00000268796	ENSG00000268796	SSU72P1	HG1462_PATCH:113627143-113627726	NOTEST	0	0	0	0	1	1
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ENSG00000268803	ENSG00000268803	RP11-704M14.2	4:70047377-70082484	NOTEST	0	0	0	0	1	1
ENSG00000268804	ENSG00000268804	RP11-542M13.3	16:85968886-85969829	NOTEST	0	0	0	0	1	1
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ENSG00000268808	ENSG00000268808	U52111.14	HG1497_PATCH:152893339-152954204	NOTEST	0	0	0	0	1	1
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ENSG00000268822	ENSG00000268822	AC011298.1	2:241624477-241624705	NOTEST	0	0	0	0	1	1
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ENSG00000268827	ENSG00000268827	FMR1NB	HG1459_PATCH:147063045-147108384	NOTEST	0	0	0	0	1	1
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ENSG00000268832	ENSG00000268832	OPN1LW	HG1497_PATCH:153312691-153327500	NOTEST	0	0	0	0	1	1
ENSG00000268833	ENSG00000268833	AC011513.4	19:42212503-42290801	NOTEST	0	0	0	0	1	1
ENSG00000268834	ENSG00000268834	OR7A1P	19:15002706-15003616	NOTEST	0	0	0	0	1	1
ENSG00000268836	ENSG00000268836	LA16c-OS12.2	16:235746-236293	NOTEST	0	0.0280166	inf	0	1	1
ENSG00000268837	ENSG00000268837	SHANK2-AS1	HG865_PATCH:70313960-71048647	NOTEST	0	0	0	0	1	1
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ENSG00000268839	ENSG00000268839	CTD-3073N11.7	19:52008312-52008616	NOTEST	0	0	0	0	1	1
ENSG00000268840	ENSG00000268840	RNU4-52P	HG1436_HG1432_PATCH:48931124-48960569	NOTEST	0	0	0	0	1	1
ENSG00000268842	ENSG00000268842	CTD-2245F17.2	19:53662465-53667152	NOTEST	0	0	0	0	1	1
ENSG00000268843	ENSG00000268843	AC118758.6	HG736_PATCH:56886600-56887395	NOTEST	0	0	0	0	1	1
ENSG00000268845	ENSG00000268845	RP11-1137G4.3	19:6952510-6990857	NOTEST	0	0	0	0	1	1
ENSG00000268846	ENSG00000268846	AC018867.2	2:187350882-187374090	NOTEST	0	0	0	0	1	1
ENSG00000268847	ENSG00000268847	SIGLEC31P	19:57100862-57101649	NOTEST	0	0	0	0	1	1
ENSG00000268848	ENSG00000268848	RP13-565O16.2	HG1443_HG1444_PATCH:134314284-134328709	NOTEST	0	0	0	0	1	1
ENSG00000268849	ENSG00000268849	SIGLEC22P	19:51714335-51715344	NOTEST	0	0	0	0	1	1
ENSG00000268850	ENSG00000268850	AF003626.1	HG1459_PATCH:149997534-150002660	NOTEST	0	0	0	0	1	1
ENSG00000268851	ENSG00000268851	AL162851.1	GL000215.1:23515-25354	NOTEST	0	0	0	0	1	1
ENSG00000268852	ENSG00000268852	AC132872.2	17:80186272-80231607	NOTEST	0.387057	0.569643	0.557512	0	1	1
ENSG00000268853	ENSG00000268853	FGF16	HG1426_PATCH:76715110-76718232	NOTEST	0	0	0	0	1	1
ENSG00000268855	ENSG00000268855	Y_RNA	HG1257_PATCH:74360772-74360874	NOTEST	0	0	0	0	1	1
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ENSG00000268861	ENSG00000268861	CTD-2207O23.3	19:7413847-7537363	NOTEST	0	4.01E-05	inf	0	1	1
ENSG00000268862	ENSG00000268862	PLXNA3	HG1497_PATCH:153626748-153642114	NOTEST	0	0	0	0	1	1
ENSG00000268863	ENSG00000268863	AC135048.1	16:30996518-31000473	NOTEST	0.525403	0.479937	-0.130579	0	1	1
ENSG00000268864	ENSG00000268864	CTB-167G5.5	19:54102881-54106751	NOTEST	0	0	0	0	1	1
ENSG00000268865	ENSG00000268865	AC026310.1	12:24964294-25113092	NOTEST	0	0.0296088	inf	0	1	1
ENSG00000268866	ENSG00000268866	AC020915.2	19:58735871-58736835	NOTEST	0	0	0	0	1	1
ENSG00000268867	ENSG00000268867	BX842568.2	HG1423_PATCH:36980312-36981542	NOTEST	0	0	0	0	1	1
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ENSG00000268869	ENSG00000268869	ESPNP	1:17013833-17046652	NOTEST	0.0833774	0	#NAME?	0	1	1
ENSG00000268870	ENSG00000268870	CTD-3105H18.16	19:12490002-12750912	NOTEST	0.116708	0.0272897	-2.09648	0	1	1
ENSG00000268871	ENSG00000268871	CXorf40B	HG1459_PATCH:149011248-149306302	NOTEST	0	0	0	0	1	1
ENSG00000268872	ENSG00000268872	ATN1	HG344_PATCH:7033625-7051484	NOTEST	0	0	0	0	1	1
ENSG00000268873	ENSG00000268873	RP11-138H11.1	18:32073253-32471808	NOTEST	0	0	0	0	1	1
ENSG00000268874	ENSG00000268874	SNORA56	HG1497_PATCH:153931223-153946157	NOTEST	0	0	0	0	1	1
ENSG00000268876	ENSG00000268876	ARHGAP4	HG1497_PATCH:153029985-153103693	NOTEST	0	0	0	0	1	1
ENSG00000268879	ENSG00000268879	IGFL1P1	19:46604379-46706340	NOTEST	0	0.0611829	inf	0	1	1
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ENSG00000268882	ENSG00000268882	AL360181.1	10:135192694-135382916	NOTEST	0	0	0	0	1	1
ENSG00000268883	ENSG00000268883	PNMA6B	HG1497_PATCH:152244084-152246021	NOTEST	0	0	0	0	1	1
ENSG00000268884	ENSG00000268884	CTD-2550O8.7	19:8411400-8412571	NOTEST	0	0	0	0	1	1
ENSG00000268885	ENSG00000268885	AC026740.1	5:612386-693510	NOTEST	0.207384	0.308524	0.573077	0	1	1
ENSG00000268886	ENSG00000268886	CTD-3099C6.7	19:53030904-53090427	NOTEST	0.0836376	0.153003	0.871338	0	1	1
ENSG00000268889	ENSG00000268889	CTD-2616J11.14	19:51897741-51906904	NOTEST	0	0.0596334	inf	0	1	1
ENSG00000268890	ENSG00000268890	SNORA15	HG329_PATCH:19166988-19279229	NOTEST	0	0	0	0	1	1
ENSG00000268891	ENSG00000268891	AC006014.1	7:74988447-75115548	NOTEST	0	0	0	0	1	1
ENSG00000268892	ENSG00000268892	CTD-3233P19.8	19:21404446-21405548	NOTEST	0	0	0	0	1	1
ENSG00000268893	ENSG00000268893	RP11-274K13.5	HG1443_HG1444_PATCH:135231863-135232377	NOTEST	0	0	0	0	1	1
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ENSG00000268897	ENSG00000268897	BTK	HG1439_PATCH:100604434-100641183	NOTEST	0	0	0	0	1	1
ENSG00000268898	ENSG00000268898	AC007377.1	2:40013592-40838193	NOTEST	0	0	0	0	1	1
ENSG00000268899	ENSG00000268899	CTD-2626G11.2	HSCHR19_1_CTG3:20929728-20938056	NOTEST	0	0	0	0	1	1
ENSG00000268902	ENSG00000268902	CSAG3	HG1497_PATCH:151876732-151883021	NOTEST	0	0	0	0	1	1
ENSG00000268903	ENSG00000268903	RP11-34P13.15	1:134900-139379	NOTEST	0	0	0	0	1	1
ENSG00000268904	ENSG00000268904	TAZ	HG1497_PATCH:153558422-153590188	NOTEST	0	0	0	0	1	1
ENSG00000268905	ENSG00000268905	RBM22P10	HG1433_PATCH:52228045-52228916	NOTEST	0	0	0	0	1	1
ENSG00000268906	ENSG00000268906	CTC-518B2.9	19:51532347-51538486	NOTEST	0	0	0	0	1	1
ENSG00000268908	ENSG00000268908	VN1R92P	19:23627063-23627991	NOTEST	0	0	0	0	1	1
ENSG00000268910	ENSG00000268910	RP11-22B10.3	HG1433_PATCH:51546006-51645357	NOTEST	0	0	0	0	1	1
ENSG00000268911	ENSG00000268911	SNORD30	HG1434_PATCH:113260259-113260329	NOTEST	0	0	0	0	1	1
ENSG00000268912	ENSG00000268912	CTD-2619J13.17	19:58939998-58942515	NOTEST	0.274253	0.385086	0.489671	0	1	1
ENSG00000268913	ENSG00000268913	AC026806.2	19:38822273-38822716	NOTEST	0	0.0425686	inf	0	1	1
ENSG00000268914	ENSG00000268914	HNRNPCP10	HG1459_PATCH:143922494-143923378	NOTEST	0	0	0	0	1	1
ENSG00000268915	ENSG00000268915	MIR506	HG1459_PATCH:146312434-146312558	NOTEST	0	0	0	0	1	1
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ENSG00000268917	ENSG00000268917	RP11-344N17.9	HG1436_HG1432_PATCH:48216523-48218894	NOTEST	0	0	0	0	1	1
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ENSG00000268921	ENSG00000268921	RP3-393P12.1	HG1436_HG1432_PATCH:47636225-47638096	NOTEST	0	0	0	0	1	1
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ENSG00000268923	ENSG00000268923	AL645922.1	6:31973412-31976228	NOTEST	0	0	0	0	1	1
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ENSG00000268925	ENSG00000268925	AL161645.2	10:135192694-135382916	NOTEST	0	0	0	0	1	1
ENSG00000268926	ENSG00000268926	DKFZP434H0512	9:98521512-98776842	NOTEST	0	0	0	0	1	1
ENSG00000268927	ENSG00000268927	FLJ00418	16:70695106-70719969	NOTEST	0.0676305	0.157507	1.21967	0	1	1
ENSG00000268928	ENSG00000268928	SLC25A1	HG329_PATCH:19163094-19166343	NOTEST	0	0	0	0	1	1

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ENSG00000268933	ENSG00000268933	U82671.8	HG1497_PATCH:152197256-152198918	NOTEST	0	0	0	0	1	1
ENSG00000268934	ENSG00000268934	RBM22P7	HG1433_PATCH:52252902-52253164	NOTEST	0	0	0	0	1	1
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ENSG00000268936	ENSG00000268936	AP003062.1	11:134855245-134856693	NOTEST	0	0	0	0	1	1
ENSG00000268937	ENSG00000268937	AC115617.2	HG1436_HG1432_PATCH:48635391-48636470	NOTEST	0	0	0	0	1	1
ENSG00000268938	ENSG00000268938	AC005387.3	19:18642422-18654887	NOTEST	0	0.320234	inf	0	1	1
ENSG00000268939	ENSG00000268939	RP11-348F1.3	HG1433_PATCH:51099943-51139462	NOTEST	0	0	0	0	1	1
ENSG00000268940	ENSG00000268940	CT45A1	HG1443_HG1444_PATCH:134847481-134857255	NOTEST	0	0	0	0	1	1
ENSG00000268941	ENSG00000268941	MGC4294	20:57209827-57210772	NOTEST	0	0	0	0	1	1
ENSG00000268943	ENSG00000268943	CLIC2	HG1497_PATCH:154444678-154503125	NOTEST	0	0	0	0	1	1
ENSG00000268944	ENSG00000268944	IRAK1	HG1497_PATCH:153178967-153188457	NOTEST	0	0	0	0	1	1
ENSG00000268945	ENSG00000268945	CTD-2192J16.26	19:12793506-12798093	NOTEST	0.0320146	0.0453059	0.500969	0	1	1
ENSG00000268946	ENSG00000268946	ATRX	HG1426_PATCH:76765831-77047170	NOTEST	0	0	0	0	1	1
ENSG00000268948	ENSG00000268948	AC004017.1	19:58193336-58269527	NOTEST	0.157655	0	#NAME?	0	1	1
ENSG00000268949	ENSG00000268949	MRPS17P1	1:45453905-45457506	NOTEST	0.00501883	0	#NAME?	0	1	1
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ENSG00000268951	ENSG00000268951	RP11-149F8.3	9:68315597-68316175	NOTEST	0	0	0	0	1	1
ENSG00000268952	ENSG00000268952	RP11-344N17.8	HG1436_HG1432_PATCH:48193073-48193838	NOTEST	0	0	0	0	1	1
ENSG00000268953	ENSG00000268953	AC020952.1	19:31640361-31640757	NOTEST	0	0	0	0	1	1
ENSG00000268954	ENSG00000268954	PTPN6	HG344_PATCH:7055630-7070479	NOTEST	0	0	0	0	1	1
ENSG00000268955	ENSG00000268955	LRLE1	8:8011829-8084136	NOTEST	0	0	0	0	1	1
ENSG00000268956	ENSG00000268956	RP11-313P13.3	HG1257_PATCH:72434652-72606602	NOTEST	0	0	0	0	1	1
ENSG00000268957	ENSG00000268957	SIGLEC26P	19:51971613-51971890	NOTEST	0	0	0	0	1	1
ENSG00000268958	ENSG00000268958	CTD-2542C24.8	HSCHR19_1_CTG3:21161483-21172432	NOTEST	0	0	0	0	1	1
ENSG00000268960	ENSG00000268960	AC091150.1	18:45553043-45937123	NOTEST	0	0	0	0	1	1
ENSG00000268961	ENSG00000268961	AFF2-IT1	HG1459_PATCH:147582335-148082384	NOTEST	0	0	0	0	1	1
ENSG00000268962	ENSG00000268962	RP11-552E4.4	HG1436_HG1432_PATCH:48088231-48088358	NOTEST	0	0	0	0	1	1
ENSG00000268963	ENSG00000268963	RPL10	HG1497_PATCH:153558422-153590188	NOTEST	0	0	0	0	1	1
ENSG00000268964	ENSG00000268964	ERVV-2	19:53547990-53554329	NOTEST	0	0	0	0	1	1
ENSG00000268965	ENSG00000268965	AC061992.1	17:76374720-76573476	NOTEST	0	0.303808	inf	0	1	1
ENSG00000268966	ENSG00000268966	RP11-348F1.2	HG1433_PATCH:51139510-51208661	NOTEST	0	0	0	0	1	1
ENSG00000268967	ENSG00000268967	RP11-1281K21.10	4:49550580-49550872	NOTEST	0	0	0	0	1	1
ENSG00000268969	ENSG00000268969	U82695.10	HG1497_PATCH:152592223-152594948	NOTEST	0	0	0	0	1	1
ENSG00000268970	ENSG00000268970	CTD-3099C6.11	19:53091757-53193749	NOTEST	0.0579178	0.140591	1.27943	0	1	1
ENSG00000268972	ENSG00000268972	RNU6ATAC	HG1500_PATCH:137029560-137029686	NOTEST	0	0	0	0	1	1
ENSG00000268975	ENSG00000268975	MIA-RAB4B	19:41277552-41406413	NOTEST	0.244553	0.20199	-0.275863	0	1	1
ENSG00000268977	ENSG00000268977	PIH1	16:78133309-79246564	NOTEST	0	0	0	0	1	1
ENSG00000268978	ENSG00000268978	Y_RNA	HG1257_PATCH:74818841-74818943	NOTEST	0	0	0	0	1	1
ENSG00000268980	ENSG00000268980	HUWE1	HG1433_PATCH:53275143-53429752	NOTEST	0	0	0	0	1	1
ENSG00000268981	ENSG00000268981	CTC-457E21.9	19:22817125-22899793	NOTEST	0	0.00216546	inf	0	1	1
ENSG00000268982	ENSG00000268982	SLC6A8	HG1497_PATCH:152838201-152865065	NOTEST	0	0	0	0	1	1

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ENSG00000268985	ENSG00000268985	CTD-2528A14.1	19:17003757-17137625	NOTEST	0	0	0	0	1	1
ENSG00000268986	ENSG00000268986	AC225613.8	HG1146_PATCH:43781089-43782161	NOTEST	0	0	0	0	1	1
ENSG00000268987	ENSG00000268987	CTC-435M10.10	19:41768400-41930910	NOTEST	0	0.0313566	inf	0	1	1
ENSG00000268988	ENSG00000268988	SPANXN2	HG1458_PATCH:142799740-142809209	NOTEST	0	0	0	0	1	1
ENSG00000268989	ENSG00000268989	CTB-83J4.1	HSCHR19LRC_PGF1_CTG1:54704600-54752858	NOTEST	0	0	0	0	1	1
ENSG00000268990	ENSG00000268990	U82670.9	HG1497_PATCH:152220621-152220885	NOTEST	0	0	0	0	1	1
ENSG00000268991	ENSG00000268991	FAM231C	1:17060446-17060956	NOTEST	0	0	0	0	1	1
ENSG00000268992	ENSG00000268992	CTB-175P5.2	19:23487792-23578362	NOTEST	0	0	0	0	1	1
ENSG00000268993	ENSG00000268993	RP11-439A17.5	1:120876494-120905159	NOTEST	0	0	0	0	1	1
ENSG00000268994	ENSG00000268994	RP1-172N19.1	HG1438_PATCH:71996858-72068652	NOTEST	0	0	0	0	1	1
ENSG00000268996	ENSG00000268996	AL807752.1	9:139980806-139981121	NOTEST	0.395345	0	#NAME?	0	1	1
ENSG00000268997	ENSG00000268997	DNAJC19P3	19:42144936-42145267	NOTEST	0	0	0	0	1	1
ENSG00000268998	ENSG00000268998	VN1R14P	HG27_PATCH:26630781-26632007	NOTEST	0	0	0	0	1	1
ENSG00000268999	ENSG00000268999	XRCC6P2	HG1459_PATCH:149312792-149314618	NOTEST	0	0	0	0	1	1
ENSG00000269000	ENSG00000269000	AC108868.1	2:107099727-107123396	NOTEST	0	0	0	0	1	1
ENSG00000269001	ENSG00000269001	ZNF818P	19:53716240-53716649	NOTEST	0.0623366	0.0931463	0.579419	0	1	1
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ENSG00000269003	ENSG00000269003	NUDT10	HG1433_PATCH:51075230-51080525	NOTEST	0	0	0	0	1	1
ENSG00000269004	ENSG00000269004	RP11-272G22.1	HG1433_PATCH:53502025-53502204	NOTEST	0	0	0	0	1	1
ENSG00000269007	ENSG00000269007	LAGE3	HG1497_PATCH:153645368-153647725	NOTEST	0	0	0	0	1	1
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ENSG00000269010	ENSG00000269010	CT83	HG1463_PATCH:115578014-115579336	NOTEST	0	0	0	0	1	1
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ENSG00000269014	ENSG00000269014	CTB-147N14.4	19:47330151-47331697	NOTEST	0	0	0	0	1	1
ENSG00000269016	ENSG00000269016	GAGE2A	HG1436_HG1432_PATCH:49398927-49406226	NOTEST	0	0	0	0	1	1
ENSG00000269017	ENSG00000269017	RP11-97N5.2	HG1443_HG1444_PATCH:135076506-135081168	NOTEST	0	0	0	0	1	1
ENSG00000269018	ENSG00000269018	AP001362.1	11:65343508-65360121	NOTEST	0	0.22771	inf	0	1	1
ENSG00000269019	ENSG00000269019	AC005932.1	19:19010322-19057640	NOTEST	0.0238258	0.0266398	0.161061	0	1	1
ENSG00000269020	ENSG00000269020	CR753864.1	HSCHR6_MHC_MCF:31560861-31561338	NOTEST	0	0	0	0	1	1
ENSG00000269021	ENSG00000269021	CTD-3187F8.12	19:51774519-51786276	NOTEST	0	0	0	0	1	1
ENSG00000269023	ENSG00000269023	SNORA35	HG1462_PATCH:114347091-114470542	NOTEST	0	0	0	0	1	1
ENSG00000269024	ENSG00000269024	RP6-29D12.3	HG1433_PATCH:53080782-53080973	NOTEST	0	0	0	0	1	1
ENSG00000269025	ENSG00000269025	CTC-457E21.5	19:22779058-22791303	NOTEST	0	0	0	0	1	1
ENSG00000269026	ENSG00000269026	AC003006.7	19:58193336-58269527	NOTEST	0	0.094811	inf	0	1	1
ENSG00000269027	ENSG00000269027	AC010368.2	5:35048860-35230794	NOTEST	0	0	0	0	1	1
ENSG00000269028	ENSG00000269028	MTRNR2L12	3:96335980-96337000	NOTEST	0	0	0	0	1	1
ENSG00000269029	ENSG00000269029	RP5-1158E12.2	HG1435_PATCH:45772362-45776285	NOTEST	0	0	0	0	1	1
ENSG00000269030	ENSG00000269030	GAGE10	HG1436_HG1432_PATCH:49163067-49179243	NOTEST	0	0	0	0	1	1
ENSG00000269031	ENSG00000269031	MTM1	HG1459_PATCH:149650340-149755044	NOTEST	0	0	0	0	1	1

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ENSG00000269034	ENSG00000269034	PLP2	HG1436_HG1432_PATCH:49031324-49034638	NOTEST	0	0	0	0	1	1
ENSG00000269035	ENSG00000269035	CTD-2521M24.10	19:17546317-17571763	NOTEST	0	0.0453783	inf	0	1	1
ENSG00000269036	ENSG00000269036	SLC9A6	HG1443_HG1444_PATCH:135119467-135181293	NOTEST	0	0	0	0	1	1
ENSG00000269037	ENSG00000269037	CTC-523E23.6	19:35396218-35399092	NOTEST	0	0	0	0	1	1
ENSG00000269038	ENSG00000269038	AP001462.6	11:64546425-64546877	NOTEST	0.0990664	0.120026	0.276878	0	1	1
ENSG00000269039	ENSG00000269039	Y_RNA	HG1436_HG1432_PATCH:49980595-49980696	NOTEST	0	0	0	0	1	1
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ENSG00000269041	ENSG00000269041	IDS	HG1459_PATCH:148558711-148615657	NOTEST	0	0	0	0	1	1
ENSG00000269042	ENSG00000269042	AP001925.1	11:108027941-108338258	NOTEST	0	0	0	0	1	1
ENSG00000269043	ENSG00000269043	CTC-513N18.6	19:20615357-20711421	NOTEST	0	0	0	0	1	1
ENSG00000269045	ENSG00000269045	RN7SKP189	HG1459_PATCH:144138824-144139154	NOTEST	0	0	0	0	1	1
ENSG00000269047	ENSG00000269047	AC009041.2	16:903633-1031663	NOTEST	0	0	0	0	1	1
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ENSG00000269049	ENSG00000269049	AC092291.2	16:14529557-14726585	NOTEST	0	0	0	0	1	1
ENSG00000269050	ENSG00000269050	CTC-360G5.6	19:39358469-39368919	NOTEST	0	0	0	0	1	1
ENSG00000269051	ENSG00000269051	CTD-2245F17.3	19:53700363-53714268	NOTEST	0.0737186	0.0281681	-1.38796	0	1	1
ENSG00000269052	ENSG00000269052	XAGE3	HG1433_PATCH:52605527-52611068	NOTEST	0	0	0	0	1	1
ENSG00000269053	ENSG00000269053	CTD-2521M24.8	19:17516502-17544533	NOTEST	0	0.0387188	inf	0	1	1
ENSG00000269054	ENSG00000269054	CTD-2619J13.3	19:58856543-58877958	NOTEST	0.0880018	0.0169394	-2.37715	0	1	1
ENSG00000269055	ENSG00000269055	AC078899.2	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000269056	ENSG00000269056	PBDC1	HG1425_PATCH:75392770-75398039	NOTEST	0	0	0	0	1	1
ENSG00000269057	ENSG00000269057	CACNA1F	HG1436_HG1432_PATCH:49064461-49092770	NOTEST	0	0	0	0	1	1
ENSG00000269058	ENSG00000269058	CALR3	19:16589867-16771253	NOTEST	0.0722833	0.135219	0.903566	0	1	1
ENSG00000269059	ENSG00000269059	CTD-2183H9.7	HG1497_PATCH:154004255-154228771	NOTEST	0	0	0	0	1	1
ENSG00000269060	ENSG00000269060	RP3-507I15.2	HG1453_PATCH:140255399-140255753	NOTEST	0	0	0	0	1	1
ENSG00000269062	ENSG00000269062	BX842568.1	HG1423_PATCH:36976029-36976256	NOTEST	0	0	0	0	1	1
ENSG00000269063	ENSG00000269063	SPANXA1	HG1453_PATCH:140665838-140667176	NOTEST	0	0	0	0	1	1
ENSG00000269064	ENSG00000269064	AL160286.1	1:179334854-179545087	NOTEST	0	0	0	0	1	1
ENSG00000269065	ENSG00000269065	LL0XNC01-116E7.4	HG1441_PATCH:10318302-103183946	NOTEST	0	0	0	0	1	1
ENSG00000269066	ENSG00000269066	CTD-2528A14.5	19:17186590-17325346	NOTEST	0	0.0263434	inf	0	1	1
ENSG00000269067	ENSG00000269067	ZNF728	19:23158269-23185978	NOTEST	0	0	0	0	1	1
ENSG00000269068	ENSG00000269068	RP11-256I23.2	2:220415450-220440435	NOTEST	0.0837816	0.465389	2.47373	0	1	1
ENSG00000269069	ENSG00000269069	CTC-471F3.5	19:40529290-40531409	NOTEST	0.103794	0.134405	0.372861	0	1	1
ENSG00000269070	ENSG00000269070	RP11-232D9.3	HG1490_PATCH:115826877-115828156	NOTEST	0	0	0	0	1	1
ENSG00000269071	ENSG00000269071	AC138517.1	5:138852107-138852506	NOTEST	0	0	0	0	1	1
ENSG00000269072	ENSG00000269072	CTD-3187F8.14	19:51645555-51685222	NOTEST	0	0	0	0	1	1
ENSG00000269074	ENSG00000269074	AC099344.1	2:11584500-11606297	NOTEST	0	0	0	0	1	1
ENSG00000269075	ENSG00000269075	HTR2C	HG1462_PATCH:113820547-114146531	NOTEST	0	0	0	0	1	1
ENSG00000269076	ENSG00000269076	XAGE2B	HG1433_PATCH:52112029-52118680	NOTEST	0	0	0	0	1	1

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ENSG00000269080	ENSG00000269080	RP11-232D9.1	HG1490_PATCH:11588249-7-115882845	NOTEST	0	0	0	0	1	1
ENSG00000269081	ENSG00000269081	MAGEA2	HG1497_PATCH:15188306-3-151887057	NOTEST	0	0	0	0	1	1
ENSG00000269082	ENSG00000269082	CTD-2620I22.1	19:53430387-53541151	NOTEST	0	0	0	0	1	1
ENSG00000269083	ENSG00000269083	COX7B	HG1426_PATCH:77160391-77168327	NOTEST	0	0	0	0	1	1
ENSG00000269084	ENSG00000269084	AC009977.1	Y:21729198-21768160	NOTEST	0	0	0	0	1	1
ENSG00000269085	ENSG00000269085	CTD-3222D19.10	19:16589867-16771253	NOTEST	0	0	0	0	1	1
ENSG00000269086	ENSG00000269086	CTC-523E23.5	19:35328792-35351480	NOTEST	0	0	0	0	1	1
ENSG00000269087	ENSG00000269087	G6PD	HG1497_PATCH:153699858-153733513	NOTEST	0	0	0	0	1	1
ENSG00000269088	ENSG00000269088	RP11-234P3.2	HG1433_PATCH:51646337-51646850	NOTEST	0	0	0	0	1	1
ENSG00000269089	ENSG00000269089	AP003733.1	11:61735452-61736755	NOTEST	0.361407	0.402932	0.156911	0	1	1
ENSG00000269090	ENSG00000269090	AF196972.9	HG1436_HG1432_PATCH:48365921-48368237	NOTEST	0	0	0	0	1	1
ENSG00000269091	ENSG00000269091	CTD-2126E3.3	19:50479723-50570050	NOTEST	0.0760066	0	#NAME?	0	1	1
ENSG00000269092	ENSG00000269092	CTD-2230M5.1	HG1462_PATCH:113625457-113626424	NOTEST	0	0	0	0	1	1
ENSG00000269095	ENSG00000269095	AC010646.3	19:17342691-17398455	NOTEST	0	0	0	0	1	1
ENSG00000269096	ENSG00000269096	CT45A3	HG1443_HG1444_PATCH:134893821-135019384	NOTEST	0	0	0	0	1	1
ENSG00000269097	ENSG00000269097	AC003682.17	19:58175647-58176407	NOTEST	0	0.055685	inf	0	1	1
ENSG00000269098	ENSG00000269098	RNU7-37P	HG1433_PATCH:52836709-52910014	NOTEST	0	0	0	0	1	1
ENSG00000269099	ENSG00000269099	LSP1	13:25591540-25591675	NOTEST	0	0	0	0	1	1
ENSG00000269100	ENSG00000269100	AC114494.2	HG989_PATCH:31882411-31907525	NOTEST	0	0	0	0	1	1
ENSG00000269101	ENSG00000269101	HDAC6	HG1436_HG1432_PATCH:48660775-48684381	NOTEST	0	0	0	0	1	1
ENSG00000269102	ENSG00000269102	CTD-2525I3.5	19:52772823-52871031	NOTEST	0.0537968	0	#NAME?	0	1	1
ENSG00000269103	ENSG00000269103	AC002472.1	22:21353392-21399306	NOTEST	0	0	0	0	1	1
ENSG00000269104	ENSG00000269104	AL035681.1	22:41685387-41685686	NOTEST	0	0	0	0	1	1
ENSG00000269105	ENSG00000269105	GS1-421I3.4	HG1442_PATCH:119170198-119280817	NOTEST	0	0	0	0	1	1
ENSG00000269106	ENSG00000269106	CTD-2619J13.23	19:58985383-59023780	NOTEST	0	0.103774	inf	0	1	1
ENSG00000269107	ENSG00000269107	RP11-15H20.7	19:23437854-23457053	NOTEST	0	0	0	0	1	1
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ENSG00000269109	ENSG00000269109	PNMA6C	HG1497_PATCH:152240907-152243488	NOTEST	0	0	0	0	1	1
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ENSG00000269113	ENSG00000269113	TRABD2B	1:48226199-48462567	NOTEST	0.00822925	0.00303562	-1.43877	0	1	1
ENSG00000269114	ENSG00000269114	MAGEA6	HG1497_PATCH:151934607-151938219	NOTEST	0	0	0	0	1	1
ENSG00000269115	ENSG00000269115	TTC36	HG122_PATCH:118307204-118473748	NOTEST	0	0	0	0	1	1
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ENSG00000269118	ENSG00000269118	FAM90A28P	19:53802303-53811897	NOTEST	0	0	0	0	1	1
ENSG00000269119	ENSG00000269119	HNRNPA1P52	19:42333745-42334992	NOTEST	0	0	0	0	1	1
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ENSG00000269121	ENSG00000269121	AC007216.2	16:12021229-12070500	NOTEST	0	0	0	0	1	1
ENSG00000269122	ENSG00000269122	SSX3	HG1436_HG1432_PATCH:48205826-48216106	NOTEST	0	0	0	0	1	1
ENSG00000269123	ENSG00000269123	RPL7P57	HG1436_HG1432_PATCH:47696300-47931057	NOTEST	0	0	0	0	1	1
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ENSG00000269126	ENSG00000269126	RP11-143H17.1	HG1497_PATCH:154230089-154324971	NOTEST	0	0	0	0	1	1
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ENSG00000269130	ENSG00000269130	SIGLEC28P	19:52063374-52063843	NOTEST	0	0	0	0	1	1
ENSG00000269132	ENSG00000269132	RP11-420K14.8	HSCHR19_2_CTG3:21961052-21986141	NOTEST	0	0	0	0	1	1
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ENSG00000269135	ENSG00000269135	PGAM4	HG1426_PATCH:77171650-77311349	NOTEST	0	0	0	0	1	1
ENSG00000269136	ENSG00000269136	RP11-420K14.7	19:21983281-21984068	NOTEST	0	0	0	0	1	1
ENSG00000269137	ENSG00000269137	Y_RNA	HG865_PATCH:70313960-71048647	NOTEST	0	0	0	0	1	1
ENSG00000269138	ENSG00000269138	ZNF209P	19:22573820-22715287	NOTEST	0	0	0	0	1	1
ENSG00000269139	ENSG00000269139	CTD-3193O13.8	19:7989371-8008805	NOTEST	0	0	0	0	1	1
ENSG00000269141	ENSG00000269141	RP11-56H2.2	HG1433_PATCH:51245089-51254005	NOTEST	0	0	0	0	1	1
ENSG00000269142	ENSG00000269142	RPL7L1P11	HG1459_PATCH:147546424-147547145	NOTEST	0	0	0	0	1	1
ENSG00000269143	ENSG00000269143	RNU6-434P	HG1433_PATCH:53935822-54101642	NOTEST	0	0	0	0	1	1
ENSG00000269144	ENSG00000269144	RP11-344N17.13	HG1436_HG1432_PATCH:48231303-48231494	NOTEST	0	0	0	0	1	1
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ENSG00000269149	ENSG00000269149	GAGE12J	HG1436_HG1432_PATCH:49181455-49188783	NOTEST	0	0	0	0	1	1
ENSG00000269151	ENSG00000269151	AC007193.8	19:46850250-46896238	NOTEST	0	0	0	0	1	1
ENSG00000269152	ENSG00000269152	RNU6-29P	HG1436_HG1432_PATCH:48635391-48636470	NOTEST	0	0	0	0	1	1
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ENSG00000269154	ENSG00000269154	AC006539.4	19:20173563-20174129	NOTEST	0	0	0	0	1	1
ENSG00000269155	ENSG00000269155	AL009178.1	6:168185216-168198927	NOTEST	0	0	0	0	1	1
ENSG00000269156	ENSG00000269156	AC234771.2	HG1443_HG1444_PATCH:134193714-134257982	NOTEST	0	0	0	0	1	1
ENSG00000269158	ENSG00000269158	SLITRK4	HG1458_PATCH:142715913-142722992	NOTEST	0	0	0	0	1	1
ENSG00000269159	ENSG00000269159	CU151838.2	HSCHR19LRC_PGF1_CTG1:54663835-54676915	NOTEST	0	0	0	0	1	1
ENSG00000269160	ENSG00000269160	U3	HG1433_PATCH:53807844-53807966	NOTEST	0	0	0	0	1	1
ENSG00000269161	ENSG00000269161	CTD-3131K8.3	19:17579577-17632097	NOTEST	0.199035	0.200946	0.0137827	0	1	1
ENSG00000269162	ENSG00000269162	ZNF75D	HG1443_HG1444_PATCH:134382949-134478116	NOTEST	0	0	0	0	1	1
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ENSG00000269164	ENSG00000269164	RP6-29D12.4	HG1433_PATCH:53065989-53066822	NOTEST	0	0	0	0	1	1
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ENSG00000269166	ENSG00000269166	RP11-218L14.4	HG1497_PATCH:154634437-154838412	NOTEST	0	0	0	0	1	1
ENSG00000269167	ENSG00000269167	CR753845.1	HSCHR6_MHC_DBB:31955598-31958414	NOTEST	0	0	0	0	1	1
ENSG00000269168	ENSG00000269168	BGN	HG1497_PATCH:152613191-152678026	NOTEST	0	0	0	0	1	1
ENSG00000269169	ENSG00000269169	AC004528.1	19:999600-1021117	NOTEST	0	0	0	0	1	1
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ENSG00000269173	ENSG00000269173	ARMCX3	HG1439_PATCH:100877783-100882830	NOTEST	0	0	0	0	1	1
ENSG00000269174	ENSG00000269174	RP11-6O2.4	HG971_PATCH:99497377-99678794	NOTEST	0	0	0	0	1	1
ENSG00000269175	ENSG00000269175	AC093157.1	1:101455178-101552821	NOTEST	0.133165	0.102913	-0.371788	0	1	1
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ENSG00000269181	ENSG00000269181	CTD-3073N11.5	19:51945632-51945904	NOTEST	0	0	0	0	1	1
ENSG00000269182	ENSG00000269182	AC010760.1	15:22456894-22460351	NOTEST	0	0	0	0	1	1
ENSG00000269183	ENSG00000269183	AKR1B1P8	HG1463_PATCH:115159815-115160751	NOTEST	0	0	0	0	1	1
ENSG00000269184	ENSG00000269184	AC234771.3	HG1443_HG1444_PATCH:134193714-134257982	NOTEST	0	0	0	0	1	1
ENSG00000269185	ENSG00000269185	FLJ00325	7:108540388-108540655	NOTEST	0	0	0	0	1	1
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ENSG00000269187	ENSG00000269187	CTAG1A	HG1497_PATCH:153786076-153787739	NOTEST	0	0	0	0	1	1
ENSG00000269188	ENSG00000269188	CTB-60E11.12	19:40074681-40077129	NOTEST	0	0	0	0	1	1
ENSG00000269189	ENSG00000269189	RP11-573N10.1	13:98794815-99102027	NOTEST	0	0	0	0	1	1
ENSG00000269191	ENSG00000269191	AC005387.2	19:18642422-18654887	NOTEST	0	0.133537	inf	0	1	1
ENSG00000269195	ENSG00000269195	MIR514A3	HG1459_PATCH:146366355-146366443	NOTEST	0	0	0	0	1	1
ENSG00000269197	ENSG00000269197	AC090574.1	8:70850402-70850635	NOTEST	0	0	0	0	1	1
ENSG00000269198	ENSG00000269198	RENBP	HG1497_PATCH:153103732-153113249	NOTEST	0	0	0	0	1	1
ENSG00000269199	ENSG00000269199	AC003973.5	19:22226301-22232807	NOTEST	0	0	0	0	1	1
ENSG00000269202	ENSG00000269202	RP4-614O4.12	20:33703166-33872788	NOTEST	0.0304948	0.0314335	0.0437379	0	1	1
ENSG00000269203	ENSG00000269203	NUDT11	HG1433_PATCH:51233010-51239596	NOTEST	0	0	0	0	1	1
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ENSG00000269205	ENSG00000269205	AC005606.1	16:2022037-2034193	NOTEST	0	0	0	0	1	1
ENSG00000269207	ENSG00000269207	MIR718	HG1497_PATCH:153178967-153188457	NOTEST	0	0	0	0	1	1
ENSG00000269210	ENSG00000269210	AC019171.1	2:39103102-39202590	NOTEST	0.0352976	0.0210547	-0.745427	0	1	1
ENSG00000269211	ENSG00000269211	SHANK2-AS3	HG865_PATCH:70313960-71048647	NOTEST	0	0	0	0	1	1
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ENSG00000269213	ENSG00000269213	MIR1911	HG1462_PATCH:113820547-114146531	NOTEST	0	0	0	0	1	1
ENSG00000269214	ENSG00000269214	RNU6-20P	HG1208_PATCH:57792128-57896965	NOTEST	0	0	0	0	1	1
ENSG00000269215	ENSG00000269215	AC008964.1	5:39105337-39274630	NOTEST	0.254938	0.124058	-1.03913	0	1	1
ENSG00000269216	ENSG00000269216	CLTCL1	HG329_PATCH:19166988-19279229	NOTEST	0	0	0	0	1	1
ENSG00000269218	ENSG00000269218	AC005000.3	HG1462_PATCH:114939280-114940590	NOTEST	0	0	0	0	1	1
ENSG00000269219	ENSG00000269219	RP11-316K19.3	HG1459_PATCH:149848058-149980538	NOTEST	0	0	0	0	1	1
ENSG00000269220	ENSG00000269220	LINC00528	22:18260087-18262247	NOTEST	0	0.0342912	inf	0	1	1
ENSG00000269223	ENSG00000269223	AL158091.1	20:62474778-62475273	NOTEST	0	0	0	0	1	1
ENSG00000269224	ENSG00000269224	MIR891A	HG1459_PATCH:145109508-145109587	NOTEST	0	0	0	0	1	1
ENSG00000269225	ENSG00000269225	RP11-15E1.3	9:43007104-43008297	NOTEST	0	0	0	0	1	1
ENSG00000269226	ENSG00000269226	TMSB15B	HG1441_PATCH:103327496-103331141	NOTEST	0	0	0	0	1	1
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ENSG00000269229	ENSG00000269229	RNU6-934P	HG1439_PATCH:100580391-100580498	NOTEST	0	0	0	0	1	1
ENSG00000269230	ENSG00000269230	FAM47C	HG1423_PATCH:37026475-37029783	NOTEST	0	0	0	0	1	1
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ENSG00000269233	ENSG00000269233	AC233728.1	HG1433_PATCH:53229671-53229771	NOTEST	0	0	0	0	1	1
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ENSG00000269235	ENSG00000269235	HCCAT3	19:52452386-52490109	NOTEST	0	0.0842423	inf	0	1	1
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ENSG00000269240	ENSG00000269240	CLCN5	HG1436_HG1432_PATCH:49732013-49908634	NOTEST	0	0	0	0	1	1
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ENSG00000269242	ENSG00000269242	CTD-2192J16.22	19:12754088-12792716	NOTEST	0.509342	0.58723	0.205291	0	1	1
ENSG00000269244	ENSG00000269244	RPL23AP78	19:8839096-8839566	NOTEST	0	0	0	0	1	1
ENSG00000269245	ENSG00000269245	RNU1-112P	HG1438_PATCH:71960555-71960719	NOTEST	0	0	0	0	1	1
ENSG00000269247	ENSG00000269247	GS1-256O22.5	HG1458_PATCH:142372762-142605261	NOTEST	0	0	0	0	1	1
ENSG00000269249	ENSG00000269249	XAGE5	HG1433_PATCH:52555203-52561301	NOTEST	0	0	0	0	1	1
ENSG00000269250	ENSG00000269250	MIR509-2	HG1459_PATCH:146340474-146340565	NOTEST	0	0	0	0	1	1
ENSG00000269251	ENSG00000269251	RP11-432N13.3	HG1443_HG1444_PATCH:134732955-134749460	NOTEST	0	0	0	0	1	1
ENSG00000269252	ENSG00000269252	RNA5SP504	HG1433_PATCH:52408230-52408347	NOTEST	0	0	0	0	1	1
ENSG00000269253	ENSG00000269253	SIGLEC21P	19:51702110-51704705	NOTEST	0	0	0	0	1	1
ENSG00000269254	ENSG00000269254	AF011889.2	HG1459_PATCH:148558711-148615657	NOTEST	0	0	0	0	1	1
ENSG00000269256	ENSG00000269256	RP11-325D15.2	10:77360997-78320752	NOTEST	0	0	0	0	1	1
ENSG00000269257	ENSG00000269257	TAF9B	HG1426_PATCH:77390701-77400660	NOTEST	0	0	0	0	1	1
ENSG00000269258	ENSG00000269258	RNU6-30P	HG1439_PATCH:100888992-100889099	NOTEST	0	0	0	0	1	1
ENSG00000269259	ENSG00000269259	HUG1	10:102849077-102899468	NOTEST	0	0	0	0	1	1
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ENSG00000269262	ENSG00000269262	RP11-145E17.2	HG1501_PATCH:137198747-137200214	NOTEST	0	0	0	0	1	1
ENSG00000269263	ENSG00000269263	LINC00633	HG1443_HG1444_PATCH:134193714-134257982	NOTEST	0	0	0	0	1	1
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ENSG00000269267	ENSG00000269267	AC008498.1	5:60240955-60448853	NOTEST	0	0	0	0	1	1
ENSG00000269268	ENSG00000269268	RP3-526F5.2	HG1458_PATCH:142845522-142915919	NOTEST	0	0	0	0	1	1
ENSG00000269269	ENSG00000269269	RNU7-1	HG344_PATCH:7052140-7055166	NOTEST	0	0	0	0	1	1
ENSG00000269271	ENSG00000269271	CTB-83J4.2	19:55084386-55150343	NOTEST	0	0	0	0	1	1
ENSG00000269274	ENSG00000269274	AC078899.3	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000269275	ENSG00000269275	CTD-2105E13.15	19:55888203-55889612	NOTEST	0	0	0	0	1	1
ENSG00000269277	ENSG00000269277	PPP2R2D	HG1479_PATCH:133787053-133812430	NOTEST	0	0	0	0	1	1
ENSG00000269278	ENSG00000269278	IFT46	HG122_PATCH:118307204-118473748	NOTEST	0	0	0	0	1	1
ENSG00000269279	ENSG00000269279	AL136376.1	1:116915289-116961244	NOTEST	0	0	0	0	1	1
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ENSG00000269281	ENSG00000269281	RP13-77O11.7	HG1433_PATCH:52513807-52514078	NOTEST	0	0	0	0	1	1
ENSG00000269282	ENSG00000269282	AC024257.1	12:48733790-48836730	NOTEST	0	0	0	0	1	1
ENSG00000269283	ENSG00000269283	AC036108.1	HG971_PATCH:99497377-99678794	NOTEST	0	0	0	0	1	1
ENSG00000269284	ENSG00000269284	CTC-513N18.3	HG730_PATCH:20543360-20639424	NOTEST	0	0	0	0	1	1
ENSG00000269285	ENSG00000269285	AKAP4	HG1436_HG1432_PATCH:50000161-50010412	NOTEST	0	0	0	0	1	1
ENSG00000269286	ENSG00000269286	GS1-421I3.2	HG1442_PATCH:119144680-119149507	NOTEST	0	0	0	0	1	1

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ENSG00000269288	ENSG00000269288	CTD-2245F17.6	19:53731576-53758151	NOTEST	0	0	0	0	1	1
ENSG00000269289	ENSG00000269289	CTB-92J24.3	19:24097677-24140732	NOTEST	0	0.0140005	inf	0	1	1
ENSG00000269290	ENSG00000269290	RP11-869B15.1	11:64552392-64553092	NOTEST	0.552575	0.52052	-0.0862168	0	1	1
ENSG00000269291	ENSG00000269291	AC010877.1	Y:15360258-15592553	NOTEST	0	0	0	0	1	1
ENSG00000269292	ENSG00000269292	CTB-12A17.3	19:46984052-47114050	NOTEST	0	0	0	0	1	1
ENSG00000269296	ENSG00000269296	AC005614.3	19:40534166-40600313	NOTEST	0.0162343	0.00630655	-1.36412	0	1	1
ENSG00000269297	ENSG00000269297	LL0XNC01-37G1.2	HG1497_PATCH:152502626-152528582	NOTEST	0	0	0	0	1	1
ENSG00000269299	ENSG00000269299	PGBD4P6	HG1458_PATCH:142372762-142605261	NOTEST	0	0	0	0	1	1
ENSG00000269300	ENSG00000269300	CTD-2529P6.3	19:8920379-8943004	NOTEST	0.113498	0	#NAME?	0	1	1
ENSG00000269301	ENSG00000269301	C22orf39	HG329_PATCH:19318210-19435745	NOTEST	0	0	0	0	1	1
ENSG00000269302	ENSG00000269302	AC110771.1	4:187111912-187112626	NOTEST	0.0776441	0.0599462	-0.373207	0	1	1
ENSG00000269303	ENSG00000269303	CTD-2527I21.7	19:35485687-35517375	NOTEST	0	0	0	0	1	1
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ENSG00000269307	ENSG00000269307	CTD-2278I10.6	19:17342691-17398455	NOTEST	0	0.0116015	inf	0	1	1
ENSG00000269308	ENSG00000269308	AL645608.2	1:818042-819983	NOTEST	0	0	0	0	1	1
ENSG00000269309	ENSG00000269309	SPANXC	HG1453_PATCH:140323627-140324661	NOTEST	0	0	0	0	1	1
ENSG00000269310	ENSG00000269310	MIR500B	HG1436_HG1432_PATCH:49732013-49908634	NOTEST	0	0	0	0	1	1
ENSG00000269312	ENSG00000269312	LINC00894	HG1459_PATCH:149011248-149306302	NOTEST	0	0	0	0	1	1
ENSG00000269313	ENSG00000269313	AC231657.1	HG1436_HG1432_PATCH:49022241-49026896	NOTEST	0	0	0	0	1	1
ENSG00000269314	ENSG00000269314	AC139677.9	HG1146_PATCH:43954673-43955041	NOTEST	0	0	0	0	1	1
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ENSG00000269316	ENSG00000269316	CTC-457E21.4	19:22792407-22793403	NOTEST	0	0	0	0	1	1
ENSG00000269317	ENSG00000269317	MIR221	HG1435_PATCH:45604455-45629519	NOTEST	0	0	0	0	1	1
ENSG00000269318	ENSG00000269318	AC007292.3	19:4343523-4360083	NOTEST	0.0968129	0.17649	0.866313	0	1	1
ENSG00000269319	ENSG00000269319	TMEM25	HG122_PATCH:118307204-118473748	NOTEST	0	0	0	0	1	1
ENSG00000269320	ENSG00000269320	VN1R93P	19:23708432-23870022	NOTEST	0	0	0	0	1	1
ENSG00000269321	ENSG00000269321	CTC-453G23.4	19:48618701-48673860	NOTEST	0	0.0564081	inf	0	1	1
ENSG00000269322	ENSG00000269322	RP3-461F17.2	HG344_PATCH:7085347-7180195	NOTEST	0	0	0	0	1	1
ENSG00000269324	ENSG00000269324	HMCN2	HG1502_PATCH:133290931-133340606	NOTEST	0	0	0	0	1	1
ENSG00000269325	ENSG00000269325	MIR3664	HG865_PATCH:70313960-71048647	NOTEST	0	0	0	0	1	1
ENSG00000269326	ENSG00000269326	MPP1	HG1497_PATCH:153947151-153989475	NOTEST	0	0	0	0	1	1
ENSG00000269327	ENSG00000269327	ZNF449	HG1443_HG1444_PATCH:134478824-134497181	NOTEST	0	0	0	0	1	1
ENSG00000269328	ENSG00000269328	RPL18AP16	HG1497_PATCH:152830627-152831164	NOTEST	0	0	0	0	1	1
ENSG00000269329	ENSG00000269329	FLNA	HG1497_PATCH:153516991-153543106	NOTEST	0	0	0	0	1	1
ENSG00000269332	ENSG00000269332	CTC-457E21.3	19:22779058-22791303	NOTEST	0	0	0	0	1	1
ENSG00000269333	ENSG00000269333	AL445258.2	HG1459_PATCH:145072581-145072652	NOTEST	0	0	0	0	1	1
ENSG00000269334	ENSG00000269334	ZNF182	HG1436_HG1432_PATCH:47696300-47931057	NOTEST	0	0	0	0	1	1
ENSG00000269335	ENSG00000269335	IKBKG	HG1497_PATCH:153699858-153733513	NOTEST	0	0	0	0	1	1
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ENSG00000269338	ENSG00000269338	WI2-89031B12.1	HG1497_PATCH:153686307-153687099	NOTEST	0	0	0	0	1	1
ENSG00000269339	ENSG00000269339	AC139768.1	12:51619859-51620085	NOTEST	0	0	0	0	1	1
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ENSG00000269342	ENSG00000269342	TREX2	HG1497_PATCH:152613191-152678026	NOTEST	0	0	0	0	1	1
ENSG00000269344	ENSG00000269344	RP3-433G13.1	HG1459_PATCH:146673326-146673624	NOTEST	0	0	0	0	1	1
ENSG00000269345	ENSG00000269345	VN1R85P	19:22357567-22357993	NOTEST	0	0	0	0	1	1
ENSG00000269346	ENSG00000269346	FNDC3CP	HG1426_PATCH:77426649-77433376	NOTEST	0	0	0	0	1	1
ENSG00000269348	ENSG00000269348	MOB1AP2	HG1424_PATCH:37151229-37152289	NOTEST	0	0	0	0	1	1
ENSG00000269349	ENSG00000269349	CTD-3099C6.5	19:52956828-53015595	NOTEST	0	0	0	0	1	1
ENSG00000269350	ENSG00000269350	CTD-2278I10.1	19:17462256-17488159	NOTEST	0	0	0	0	1	1
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ENSG00000269354	ENSG00000269354	AC005626.3	19:42146026-42146970	NOTEST	0	0	0	0	1	1
ENSG00000269356	ENSG00000269356	RP11-120K24.4	13:113548691-113754053	NOTEST	0	0	0	0	1	1
ENSG00000269358	ENSG00000269358	AC138393.1	1:224215759-224216371	NOTEST	0	0	0	0	1	1
ENSG00000269360	ENSG00000269360	AC112693.2	15:93749294-93751277	NOTEST	0	0	0	0	1	1
ENSG00000269361	ENSG00000269361	DSTNP2	HG344_PATCH:6976282-7032861	NOTEST	0	0	0	0	1	1
ENSG00000269362	ENSG00000269362	IPO7P1	HG1433_PATCH:51664863-51665499	NOTEST	0	0	0	0	1	1
ENSG00000269363	ENSG00000269363	MGC4771	2:232571516-232578251	NOTEST	0	0	0	0	1	1
ENSG00000269364	ENSG00000269364	CTC-457E21.2	19:22715427-22716296	NOTEST	0	0	0	0	1	1
ENSG00000269365	ENSG00000269365	RP11-380M21.4	18:45357921-45457515	NOTEST	0	0	0	0	1	1
ENSG00000269367	ENSG00000269367	AC020629.1	12:42550905-42632151	NOTEST	0	0	0	0	1	1
ENSG00000269368	ENSG00000269368	SNORA35	HG1462_PATCH:113820547-114146531	NOTEST	0	0	0	0	1	1
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ENSG00000269371	ENSG00000269371	CTD-2207O23.11	19:7541760-7585912	NOTEST	0	0	0	0	1	1
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ENSG00000269373	ENSG00000269373	CTD-2542C24.3	19:21021320-21030223	NOTEST	0	0	0	0	1	1
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ENSG00000269376	ENSG00000269376	RP11-120K24.5	13:113548691-113754053	NOTEST	0	0	0	0	1	1
ENSG00000269380	ENSG00000269380	XK	HG1424_PATCH:37209336-38547737	NOTEST	0	0	0	0	1	1
ENSG00000269381	ENSG00000269381	RP11-770J1.5	HG122_PATCH:118230299-118302211	NOTEST	0	0	0	0	1	1
ENSG00000269382	ENSG00000269382	ARCN1	HG122_PATCH:118307204-118473748	NOTEST	0	0	0	0	1	1
ENSG00000269383	ENSG00000269383	AC012493.2	2:100986704-100987007	NOTEST	0	0	0	0	1	1
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ENSG00000269385	ENSG00000269385	CTC-312O10.2	19:6887576-6940470	NOTEST	0	0	0	0	1	1
ENSG00000269386	ENSG00000269386	RAB11B-AS1	19:8428172-8469318	NOTEST	0.123958	0.258036	1.05771	0	1	1
ENSG00000269387	ENSG00000269387	RP11-298J23.8	6:41732029-41732198	NOTEST	0	0	0	0	1	1
ENSG00000269388	ENSG00000269388	AC018755.16	19:52097813-52109403	NOTEST	0.291805	0.0879443	-1.73034	0	1	1
ENSG00000269390	ENSG00000269390	RP1-241P17.4	HG1462_PATCH:114954799-114955835	NOTEST	0	0	0	0	1	1

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ENSG00000269393	ENSG00000269393	AC007965.1	Y:28111775-28114889	NOTEST	0	0	0	0	1	1
ENSG00000269394	ENSG00000269394	AC139677.10	HG1146_PATCH:44077976-44115835	NOTEST	0	0	0	0	1	1
ENSG00000269395	ENSG00000269395	ATP7A	HG1426_PATCH:77171650-77311349	NOTEST	0	0	0	0	1	1
ENSG00000269396	ENSG00000269396	AC187652.1	7:302917-304070	NOTEST	0	0	0	0	1	1
ENSG00000269397	ENSG00000269397	CTB-92J24.2	19:24097677-24140732	NOTEST	0.242598	0.229333	-0.0811211	0	1	1
ENSG00000269398	ENSG00000269398	RP5-1014O16.1	HG1459_PATCH:14883974-148840017	NOTEST	0	0	0	0	1	1
ENSG00000269400	ENSG00000269400	CTD-2529P6.4	19:8943073-8954016	NOTEST	0	0	0	0	1	1
ENSG00000269401	ENSG00000269401	RP11-493K23.1	HG1438_PATCH:72218237-72222706	NOTEST	0	0	0	0	1	1
ENSG00000269402	ENSG00000269402	AC116407.2	17:30468244-30580393	NOTEST	0.126543	0.236497	0.902199	0	1	1
ENSG00000269403	ENSG00000269403	CTD-2616J11.11	19:51848422-51872257	NOTEST	0.178366	0	#NAME?	0	1	1
ENSG00000269404	ENSG00000269404	SPIB	19:50887460-50934570	NOTEST	0.0822645	0.118865	0.530985	0	1	1
ENSG00000269405	ENSG00000269405	NXF2	HG1440_PATCH:10150207-101581691	NOTEST	0	0	0	0	1	1
ENSG00000269406	ENSG00000269406	AC211476.1	HG1257_PATCH:72434652-72606602	NOTEST	0	0	0	0	1	1
ENSG00000269407	ENSG00000269407	AL096677.1	20:23327577-23335414	NOTEST	0	0	0	0	1	1
ENSG00000269408	ENSG00000269408	AL390778.1	9:138150511-138151275	NOTEST	0	0	0	0	1	1
ENSG00000269410	ENSG00000269410	CTB-60E11.4	19:39903224-39919055	NOTEST	0	0.0788077	inf	0	1	1
ENSG00000269411	ENSG00000269411	HMGB3	HG1459_PATCH:150062230-150072497	NOTEST	0	0	0	0	1	1
ENSG00000269413	ENSG00000269413	RP11-104D21.3	HG1433_PATCH:50838843-50914400	NOTEST	0	0	0	0	1	1
ENSG00000269414	ENSG00000269414	AC231656.2	HG1459_PATCH:148393953-148394036	NOTEST	0	0	0	0	1	1
ENSG00000269415	ENSG00000269415	NPCDR1	3:59735035-61237133	NOTEST	0	0	0	0	1	1
ENSG00000269416	ENSG00000269416	CTB-175P5.4	19:23582034-23598877	NOTEST	0	0	0	0	1	1
ENSG00000269417	ENSG00000269417	AC022210.1	2:85048773-85134132	NOTEST	0	0	0	0	1	1
ENSG00000269419	ENSG00000269419	CTD-2538G9.3	19:16823127-16823245	NOTEST	0	0	0	0	1	1
ENSG00000269420	ENSG00000269420	CTD-2265M8.2	19:48551099-48614074	NOTEST	0.0540246	0.040915	-0.400989	0	1	1
ENSG00000269421	ENSG00000269421	ZNF92P3	19:24097677-24140732	NOTEST	0	0	0	0	1	1
ENSG00000269422	ENSG00000269422	AC092384.1	16:88880141-88933068	NOTEST	0	0	0	0	1	1
ENSG00000269423	ENSG00000269423	CTC-273B12.6	19:48949029-48985571	NOTEST	0.232992	0.221121	-0.0754433	0	1	1
ENSG00000269425	ENSG00000269425	AC007292.7	19:4324039-4343488	NOTEST	0.397421	0.30648	-0.374876	0	1	1
ENSG00000269426	ENSG00000269426	H3F3AP5	HG1433_PATCH:50648437-50648866	NOTEST	0	0	0	0	1	1
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ENSG00000269431	ENSG00000269431	CTB-175P5.1	19:23487792-23578362	NOTEST	0	0	0	0	1	1
ENSG00000269433	ENSG00000269433	OPN1MW	HG1497_PATCH:153426024-153439479	NOTEST	0	0	0	0	1	1
ENSG00000269436	ENSG00000269436	SPANXN1	HG1459_PATCH:144328544-144337829	NOTEST	0	0	0	0	1	1
ENSG00000269437	ENSG00000269437	NXF2	HG1440_PATCH:101615367-101694980	NOTEST	0	0	0	0	1	1
ENSG00000269438	ENSG00000269438	CCNB3	HG1433_PATCH:49967363-50094910	NOTEST	0	0	0	0	1	1
ENSG00000269441	ENSG00000269441	AC244090.1	HG1497_PATCH:153662597-153662667	NOTEST	0	0	0	0	1	1
ENSG00000269442	ENSG00000269442	RP13-210D15.4	HG1443_HG1444_PATCH:134382949-134478116	NOTEST	0	0	0	0	1	1
ENSG00000269444	ENSG00000269444	CTB-180A7.6	19:6379579-6412415	NOTEST	0.0537949	0.23983	2.15647	0	1	1
ENSG00000269445	ENSG00000269445	AC067969.1	19:38924338-39078204	NOTEST	0	0	0	0	1	1

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ENSG00000269447	ENSG00000269447	ELL2P4	HG1459_PATCH:145635442-145637480	NOTEST	0	0	0	0	1	1
ENSG00000269448	ENSG00000269448	CXorf67	HG1433_PATCH:51139510-51208661	NOTEST	0	0	0	0	1	1
ENSG00000269452	ENSG00000269452	MAGEA12	HG1497_PATCH:151902250-151909457	NOTEST	0	0	0	0	1	1
ENSG00000269453	ENSG00000269453	RPS15AP40	HG1423_PATCH:36246734-36458409	NOTEST	0	0	0	0	1	1
ENSG00000269454	ENSG00000269454	RNU6-1056P	HG1436_HG1432_PATCH:48554952-48596562	NOTEST	0	0	0	0	1	1
ENSG00000269455	ENSG00000269455	AF277315.13	HG1497_PATCH:153823013-153823793	NOTEST	0	0	0	0	1	1
ENSG00000269458	ENSG00000269458	CTD-2579N5.4	19:23108178-23108349	NOTEST	0	0	0	0	1	1
ENSG00000269459	ENSG00000269459	CU151839.1	HSCHR19LRC_PGF1_CTG1:55356751-55397872	NOTEST	0	0	0	0	1	1
ENSG00000269460	ENSG00000269460	AC093063.3	19:40170013-40186898	NOTEST	0	0	0	0	1	1
ENSG00000269461	ENSG00000269461	RPL36AP53	HG1462_PATCH:113820547-114146531	NOTEST	0	0	0	0	1	1
ENSG00000269462	ENSG00000269462	KDM5C-IT1	HG1433_PATCH:52934320-52968422	NOTEST	0	0	0	0	1	1
ENSG00000269463	ENSG00000269463	RP11-727F15.13	11:62574368-62599560	NOTEST	0.0702361	0.157473	1.16482	0	1	1
ENSG00000269464	ENSG00000269464	AC012067.1	Y:4868266-5610265	NOTEST	0	0	0	0	1	1
ENSG00000269466	ENSG00000269466	RP11-432M8.17	5:17655236-17655647	NOTEST	0	0	0	0	1	1
ENSG00000269468	ENSG00000269468	AC004824.2	1:17634689-17690499	NOTEST	0	0	0	0	1	1
ENSG00000269469	ENSG00000269469	CTD-3148I10.9	19:49949554-49995565	NOTEST	0	0	0	0	1	1
ENSG00000269470	ENSG00000269470	RN7SL262P	HG1436_HG1432_PATCH:49012049-49012341	NOTEST	0	0	0	0	1	1
ENSG00000269471	ENSG00000269471	RP11-15H20.2	19:23386811-23387358	NOTEST	0	0	0	0	1	1
ENSG00000269472	ENSG00000269472	hsa-mir-892c	HG1459_PATCH:145074467-145074540	NOTEST	0	0	0	0	1	1
ENSG00000269473	ENSG00000269473	CTD-2619J13.19	19:58951814-58957216	NOTEST	0.115954	0.155603	0.424317	0	1	1
ENSG00000269474	ENSG00000269474	BX649597.4	9:43425712-43427044	NOTEST	0	0	0	0	1	1
ENSG00000269475	ENSG00000269475	RP1-14D6.2	HG1497_PATCH:151851498-151852315	NOTEST	0	0	0	0	1	1
ENSG00000269476	ENSG00000269476	CTD-2583A14.9	19:58281022-58427978	NOTEST	0	0	0	0	1	1
ENSG00000269477	ENSG00000269477	RNU6-382P	HG1459_PATCH:146908993-146909099	NOTEST	0	0	0	0	1	1
ENSG00000269478	ENSG00000269478	CD99L2	HG1459_PATCH:149848058-149980538	NOTEST	0	0	0	0	1	1
ENSG00000269479	ENSG00000269479	BMP15	HG1433_PATCH:50653783-50659607	NOTEST	0	0	0	0	1	1
ENSG00000269480	ENSG00000269480	CTD-3032J10.3	19:17186590-17325346	NOTEST	0.0324341	0.0252476	-0.361363	0	1	1
ENSG00000269481	ENSG00000269481	CTD-2521M24.6	19:17516502-17544533	NOTEST	0.548474	0.282155	-0.958935	0	1	1
ENSG00000269482	ENSG00000269482	Z69720.2	16:127005-188859	NOTEST	0	0	0	0	1	1
ENSG00000269483	ENSG00000269483	AC006272.1	19:52343023-52346577	NOTEST	0	0	0	0	1	1
ENSG00000269485	ENSG00000269485	RP1-171K16.5	HG1453_PATCH:140708028-140708898	NOTEST	0	0	0	0	1	1
ENSG00000269486	ENSG00000269486	CTC-360G5.9	19:39405905-39466550	NOTEST	0.0275872	0.0211375	-0.384191	0	1	1
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ENSG00000269488	ENSG00000269488	HIST2H2BC	HG1287_PATCH:150536607-150537187	NOTEST	0	0	0	0	1	1
ENSG00000269489	ENSG00000269489	RP11-98D18.17	1:151770529-151771078	NOTEST	0	0.0306078	inf	0	1	1
ENSG00000269491	ENSG00000269491	RN7SL139P	HG1436_HG1432_PATCH:48868957-48867265	NOTEST	0	0	0	0	1	1
ENSG00000269492	ENSG00000269492	TMLHE-AS1	HG1497_PATCH:154634437-154838412	NOTEST	0	0	0	0	1	1
ENSG00000269493	ENSG00000269493	U40455.1	HG1459_PATCH:147279730-147280595	NOTEST	0	0	0	0	1	1
ENSG00000269494	ENSG00000269494	AL359693.1	6:82201155-82462491	NOTEST	0	0	0	0	1	1
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ENSG00000269498	ENSG00000269498	RP11-157B13.6	HSCHR19_3_CTG3:22385921-22386797	NOTEST	0	0	0	0	1	1
ENSG00000269499	ENSG00000269499	TBC1D25	HG1436_HG1432_PATCH:48398855-48422008	NOTEST	0	0	0	0	1	1
ENSG00000269500	ENSG00000269500	EEF1A1P30	HG1442_PATCH:119344423-119346643	NOTEST	0	0	0	0	1	1
ENSG00000269502	ENSG00000269502	DMRTC1	HG1438_PATCH:72091874-72097714	NOTEST	0	0	0	0	1	1
ENSG00000269503	ENSG00000269503	BEX5	HG1440_PATCH:101408679-101411029	NOTEST	0	0	0	0	1	1
ENSG00000269504	ENSG00000269504	AC003973.4	19:22200760-22219117	NOTEST	0	0	0	0	1	1
ENSG00000269505	ENSG00000269505	ZNF92P2	19:22311428-22314736	NOTEST	0	0	0	0	1	1
ENSG00000269506	ENSG00000269506	AC110792.1	4:54243809-55164414	NOTEST	0	0	0	0	1	1
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ENSG00000269509	ENSG00000269509	CTB-159G17.2	19:22939006-22966909	NOTEST	0	0	0	0	1	1
ENSG00000269510	ENSG00000269510	FLJ00273	9:35041091-35045988	NOTEST	0	0	0	0	1	1
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ENSG00000269512	ENSG00000269512	IL1RAPL2	HG375_PATCH:103810995-105011820	NOTEST	0	0	0	0	1	1
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ENSG00000269514	ENSG00000269514	DKFZP779L1853	12:48592169-48595814	NOTEST	0.0864535	0.0964957	0.158541	0	1	1
ENSG00000269515	ENSG00000269515	AL137026.1	10:44793037-44881941	NOTEST	0	0	0	0	1	1
ENSG00000269516	ENSG00000269516	CYP4F23P	19:15674884-15695520	NOTEST	0	0	0	0	1	1
ENSG00000269518	ENSG00000269518	AC234783.1	HG1441_PATCH:103331500-103331983	NOTEST	0	0	0	0	1	1
ENSG00000269519	ENSG00000269519	AC005176.1	19:40121939-40122086	NOTEST	0	0	0	0	1	1
ENSG00000269520	ENSG00000269520	SSR4	HG1497_PATCH:152954237-152966977	NOTEST	0	0	0	0	1	1
ENSG00000269523	ENSG00000269523	ZFP92	HG1497_PATCH:152586793-152590101	NOTEST	0	0	0	0	1	1
ENSG00000269524	ENSG00000269524	CTB-83J4.1	19:54704609-54752862	NOTEST	0	0	0	0	1	1
ENSG00000269525	ENSG00000269525	AC244163.1	HG1146_PATCH:43920022-43920169	NOTEST	0	0	0	0	1	1
ENSG00000269526	ENSG00000269526	ERVV-1	19:53430387-53541151	NOTEST	0	0	0	0	1	1
ENSG00000269527	ENSG00000269527	TPMTP3	HG1433_PATCH:51722222-51723012	NOTEST	0	0	0	0	1	1
ENSG00000269528	ENSG00000269528	ENO2	HG344_PATCH:6976282-7032861	NOTEST	0	0	0	0	1	1
ENSG00000269529	ENSG00000269529	AC140061.12	12:50690488-50691718	NOTEST	0	0	0	0	1	1
ENSG00000269530	ENSG00000269530	SSXP4	HG1433_PATCH:52341493-52346289	NOTEST	0	0	0	0	1	1
ENSG00000269531	ENSG00000269531	AC073569.1	12:79968758-80334448	NOTEST	0	0	0	0	1	1
ENSG00000269532	ENSG00000269532	MIR513A2	HG1459_PATCH:146307540-146307667	NOTEST	0	0	0	0	1	1
ENSG00000269533	ENSG00000269533	AC003002.6	19:57874844-57988938	NOTEST	0.358457	0.103202	-1.79633	0	1	1
ENSG00000269534	ENSG00000269534	CTC-453G23.5	19:48618701-48673860	NOTEST	0.0291263	0.0849857	1.5449	0	1	1
ENSG00000269535	ENSG00000269535	CTD-2525I3.6	19:52772823-52871031	NOTEST	0	0.0066569	inf	0	1	1
ENSG00000269536	ENSG00000269536	RP11-265D19.6	HG1443_HG1444_PATCH:134530457-134531793	NOTEST	0	0	0	0	1	1
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ENSG00000269545	ENSG00000269545	CTD-3138B18.4	19:58739959-58827023	NOTEST	0.0212448	0.00820993	-1.37167	0	1	1
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ENSG00000269549	ENSG00000269549	AL031663.2	20:44074070-44077220	NOTEST	0.337876	0.39566	0.227767	0	1	1
ENSG00000269550	ENSG00000269550	TM4SF2	HG1424_PATCH:37209336-38547737	NOTEST	0	0	0	0	1	1
ENSG00000269551	ENSG00000269551	RP11-434J24.2	HG1459_PATCH:146882719-146883017	NOTEST	0	0	0	0	1	1
ENSG00000269552	ENSG00000269552	AC005255.5	19:14962843-14963756	NOTEST	0	0	0	0	1	1
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ENSG00000269556	ENSG00000269556	FAM11A	HG1459_PATCH:148678278-148713446	NOTEST	0	0	0	0	1	1
ENSG00000269557	ENSG00000269557	RP11-49C9.2	HG1459_PATCH:149011248-149306302	NOTEST	0	0	0	0	1	1
ENSG00000269558	ENSG00000269558	AC104057.1	7:65112080-65180636	NOTEST	0	0	0	0	1	1
ENSG00000269559	ENSG00000269559	AC093677.1	4:74979890-75168816	NOTEST	0.0289505	0.024073	-0.266176	0	1	1
ENSG00000269560	ENSG00000269560	CTD-2192J16.21	19:12490002-12750912	NOTEST	0	0	0	0	1	1
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ENSG00000269562	ENSG00000269562	DLGAP4	HG144_PATCH:34894257-35116559	NOTEST	0	0	0	0	1	1
ENSG00000269563	ENSG00000269563	AC138655.1	2:47799600-47801998	NOTEST	0	0	0	0	1	1
ENSG00000269564	ENSG00000269564	AC008753.4	19:54292035-54292422	NOTEST	0	0	0	0	1	1
ENSG00000269565	ENSG00000269565	GPR32P1	19:51261638-51262449	NOTEST	0	0	0	0	1	1
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ENSG00000269567	ENSG00000269567	RP11-552E4.3	HG1436_HG1432_PATCH:48072189-48077409	NOTEST	0	0	0	0	1	1
ENSG00000269568	ENSG00000269568	MIR188	HG1436_HG1432_PATCH:49732013-49908634	NOTEST	0	0	0	0	1	1
ENSG00000269569	ENSG00000269569	RP11-29O6.2	HG1458_PATCH:142845522-142915919	NOTEST	0	0	0	0	1	1
ENSG00000269570	ENSG00000269570	AP001350.1	11:58346583-58393198	NOTEST	0	0	0	0	1	1
ENSG00000269571	ENSG00000269571	RXRA	HG1501_PATCH:137221914-137345402	NOTEST	0	0	0	0	1	1
ENSG00000269572	ENSG00000269572	RBMXL3	HG1462_PATCH:114347091-114470542	NOTEST	0	0	0	0	1	1
ENSG00000269574	ENSG00000269574	CTD-2611O12.7	19:56186591-56249768	NOTEST	0	0	0	0	1	1
ENSG00000269575	ENSG00000269575	RP11-157B13.3	19:22323333-22323919	NOTEST	0	0	0	0	1	1
ENSG00000269576	ENSG00000269576	HNRNPMP2	19:47312841-47313440	NOTEST	0	0	0	0	1	1
ENSG00000269578	ENSG00000269578	CTD-3222D19.5	19:16589867-16771253	NOTEST	0.0460821	0	#NAME?	0	1	1
ENSG00000269580	ENSG00000269580	SIGLEC27P	19:52011826-52012567	NOTEST	0	0	0	0	1	1
ENSG00000269581	ENSG00000269581	U82695.5	HG1497_PATCH:152565434-152567321	NOTEST	0	0	0	0	1	1
ENSG00000269582	ENSG00000269582	RNU6-154P	HG1463_PATCH:115517180-115517286	NOTEST	0	0	0	0	1	1
ENSG00000269583	ENSG00000269583	L34079.4	19:44047191-44100287	NOTEST	0	0	0	0	1	1
ENSG00000269584	ENSG00000269584	TDGF1P7	19:40025102-40025661	NOTEST	0.0382858	0	#NAME?	0	1	1
ENSG00000269586	ENSG00000269586	CT45A5	HG1443_HG1444_PATCH:134893821-135019384	NOTEST	0	0	0	0	1	1
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ENSG00000269588	ENSG00000269588	CTB-60E11.11	19:40043673-40045996	NOTEST	0	0	0	0	1	1
ENSG00000269590	ENSG00000269590	CTD-2192J16.24	19:12754088-12792716	NOTEST	0	0	0	0	1	1
ENSG00000269591	ENSG00000269591	AL354808.2	13:20248763-20357142	NOTEST	0	0	0	0	1	1
ENSG00000269592	ENSG00000269592	CTAG2	HG1497_PATCH:153820439-153822047	NOTEST	0	0	0	0	1	1
ENSG00000269593	ENSG00000269593	RNA5SP508	HG1425_PATCH:75874843-75874962	NOTEST	0	0	0	0	1	1
ENSG00000269594	ENSG00000269594	ZNF81	HG1436_HG1432_PATCH:47696300-47931057	NOTEST	0	0	0	0	1	1
ENSG00000269599	ENSG00000269599	RP11-261P24.2	13:98794815-99102027	NOTEST	0	0	0	0	1	1
ENSG00000269600	ENSG00000269600	AC016629.3	19:59070495-59111168	NOTEST	0.0840003	0.0455481	-0.883004	0	1	1

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ENSG00000269602	ENSG00000269602	AGTR2	HG1463_PATCH:115287054-115291305	NOTEST	0	0	0	0	1	1
ENSG00000269603	ENSG00000269603	ZBTB33	HG1442_PATCH:119384714-119392361	NOTEST	0	0	0	0	1	1
ENSG00000269605	ENSG00000269605	Z97053.1	20:43160425-43280874	NOTEST	0	0	0	0	1	1
ENSG00000269607	ENSG00000269607	CENPVP3	HG1433_PATCH:51361108-51361594	NOTEST	0	0	0	0	1	1
ENSG00000269608	ENSG00000269608	CTB-167G5.3	19:54120055-54120508	NOTEST	0	0	0	0	1	1
ENSG00000269611	ENSG00000269611	RN7SL687P	HG1497_PATCH:152834697-152834987	NOTEST	0	0	0	0	1	1
ENSG00000269612	ENSG00000269612	DDX6	HG122_PATCH:118575321-118661864	NOTEST	0	0	0	0	1	1
ENSG00000269614	ENSG00000269614	RP11-277L2.5	1:149575344-149637707	NOTEST	0	0	0	0	1	1
ENSG00000269615	ENSG00000269615	AC003973.1	19:22115759-22193751	NOTEST	0	0	0	0	1	1
ENSG00000269616	ENSG00000269616	RNA5SP509	HG1425_PATCH:76286543-76286662	NOTEST	0	0	0	0	1	1
ENSG00000269617	ENSG00000269617	RNU6-3P	HG1453_PATCH:140200194-140200301	NOTEST	0	0	0	0	1	1
ENSG00000269618	ENSG00000269618	CMC4	HG1497_PATCH:154230089-154324971	NOTEST	0	0	0	0	1	1
ENSG00000269619	ENSG00000269619	CTD-3023J11.2	19:47849964-47850584	NOTEST	0	0	0	0	1	1
ENSG00000269620	ENSG00000269620	AL590560.1	1:159879883-159880159	NOTEST	0	0	0	0	1	1
ENSG00000269621	ENSG00000269621	RP11-98D18.15	1:151728016-151766878	NOTEST	0	0.034252	inf	0	1	1
ENSG00000269622	ENSG00000269622	RP11-80F22.2	16:34740962-34741541	NOTEST	0	0	0	0	1	1
ENSG00000269623	ENSG00000269623	AVPR2	HG1497_PATCH:153029985-153103693	NOTEST	0	0	0	0	1	1
ENSG00000269624	ENSG00000269624	AL138847.1	1:62920398-63153969	NOTEST	0.0163943	0.0198684	0.277279	0	1	1
ENSG00000269625	ENSG00000269625	DPPA3P1	HG1441_PATCH:103216737-103217220	NOTEST	0	0	0	0	1	1
ENSG00000269626	ENSG00000269626	AF196970.3	HG1436_HG1432_PATCH:48554952-48596562	NOTEST	0	0	0	0	1	1
ENSG00000269627	ENSG00000269627	RPL5P30	HG122_PATCH:118307204-118473748	NOTEST	0	0	0	0	1	1
ENSG00000269628	ENSG00000269628	MIR513A1	HG1459_PATCH:146295177-146295306	NOTEST	0	0	0	0	1	1
ENSG00000269629	ENSG00000269629	SNORD36	HG1497_PATCH:153024174-153024239	NOTEST	0	0	0	0	1	1
ENSG00000269630	ENSG00000269630	AC015989.2	18:60382671-60647666	NOTEST	0	0	0	0	1	1
ENSG00000269631	ENSG00000269631	LINC00087	HG1443_HG1444_PATCH:134193714-134257982	NOTEST	0	0	0	0	1	1
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ENSG00000269634	ENSG00000269634	Y_RNA	HG1257_PATCH:72434652-72606602	NOTEST	0	0	0	0	1	1
ENSG00000269635	ENSG00000269635	AC004257.1	19:15331825-15333108	NOTEST	0	0	0	0	1	1
ENSG00000269637	ENSG00000269637	RPL12P41	19:46722679-46723177	NOTEST	0	0	0	0	1	1
ENSG00000269639	ENSG00000269639	MAGT1	HG1426_PATCH:77087317-77156547	NOTEST	0	0	0	0	1	1
ENSG00000269640	ENSG00000269640	CTD-2521M24.9	19:17516502-17544533	NOTEST	0.103354	0.284098	1.45879	0	1	1
ENSG00000269641	ENSG00000269641	CTB-167G5.6	19:54107655-54111705	NOTEST	0	0	0	0	1	1
ENSG00000269642	ENSG00000269642	KIR2DS4	HG1079_PATCH:55227717-55370462	NOTEST	0	0	0	0	1	1
ENSG00000269643	ENSG00000269643	AL139396.2	HG1433_PATCH:52836709-52910014	NOTEST	0	0	0	0	1	1
ENSG00000269644	ENSG00000269644	RP13-346H10.2	HG1433_PATCH:50838843-50914400	NOTEST	0	0	0	0	1	1
ENSG00000269645	ENSG00000269645	FAM50A	HG1497_PATCH:153612593-153619122	NOTEST	0	0	0	0	1	1
ENSG00000269646	ENSG00000269646	CTD-2331H12.7	19:53418448-53427328	NOTEST	0	0	0	0	1	1
ENSG00000269647	ENSG00000269647	BX842679.1	1:147574427-147634886	NOTEST	0	0	0	0	1	1
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ENSG00000269650	ENSG00000269650	AL121895.1	20:34679425-34820721	NOTEST	0	0	0	0	1	1
ENSG00000269651	ENSG00000269651	CTD-3020H12.3	19:8238155-8240451	NOTEST	0	0	0	0	1	1

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ENSG00000269654	ENSG00000269654	MAGEE1	HG1425_PATCH:75647487-75651186	NOTEST	0	0	0	0	1	1
ENSG00000269655	ENSG00000269655	LCA10	HG1497_PATCH:153029985-153103693	NOTEST	0	0	0	0	1	1
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ENSG00000269661	ENSG00000269661	MIR892A	HG1459_PATCH:145078383-145078458	NOTEST	0	0	0	0	1	1
ENSG00000269662	ENSG00000269662	RP11-255H23.3	19:23945745-24057503	NOTEST	0	0	0	0	1	1
ENSG00000269663	ENSG00000269663	GAGE1	HG1436_HG1432_PATCH:49408423-49417935	NOTEST	0	0	0	0	1	1
ENSG00000269664	ENSG00000269664	RP11-31H15.2	HG1423_PATCH:37095967-37096518	NOTEST	0	0	0	0	1	1
ENSG00000269666	ENSG00000269666	PGK1	HG1426_PATCH:77326141-77390250	NOTEST	0	0	0	0	1	1
ENSG00000269667	ENSG00000269667	RP11-542M13.2	16:86015355-86018329	NOTEST	0	0	0	0	1	1
ENSG00000269668	ENSG00000269668	ATP6AP1	HG1497_PATCH:153597099-153604984	NOTEST	0	0	0	0	1	1
ENSG00000269669	ENSG00000269669	HMGB1P15	HG1433_PATCH:50674113-50674548	NOTEST	0	0	0	0	1	1
ENSG00000269670	ENSG00000269670	LANCL3	HG1424_PATCH:37209336-38547737	NOTEST	0	0	0	0	1	1
ENSG00000269671	ENSG00000269671	RABL2B	HG497_PATCH:51195375-51239737	NOTEST	0	0	0	0	1	1
ENSG00000269672	ENSG00000269672	CYCSP45	HG1497_PATCH:153009722-153010037	NOTEST	0	0	0	0	1	1
ENSG00000269673	ENSG00000269673	SSX6	HG1436_HG1432_PATCH:47967380-47980085	NOTEST	0	0	0	0	1	1
ENSG00000269674	ENSG00000269674	RP5-964N17.1	HG1434_PATCH:112859526-113181445	NOTEST	0	0	0	0	1	1
ENSG00000269675	ENSG00000269675	RP5-1158E12.4	HG1435_PATCH:45772362-45776285	NOTEST	0	0	0	0	1	1
ENSG00000269676	ENSG00000269676	MUC8	12:133049333-133050726	NOTEST	0	0	0	0	1	1
ENSG00000269677	ENSG00000269677	MIR325	HG1425_PATCH:76225238-76225336	NOTEST	0	0	0	0	1	1
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ENSG00000269679	ENSG00000269679	AC018445.1	18:77155855-77289325	NOTEST	0	0	0	0	1	1
ENSG00000269680	ENSG00000269680	CTD-3128G10.6	19:6737935-6751537	NOTEST	0	0.0637628	inf	0	1	1
ENSG00000269681	ENSG00000269681	CTD-3187F8.6	19:51645555-51685222	NOTEST	0	0	0	0	1	1
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ENSG00000269685	ENSG00000269685	H2BFM	HG1441_PATCH:103268625-103297383	NOTEST	0	0	0	0	1	1
ENSG00000269686	ENSG00000269686	AC011755.1	2:133429373-134326034	NOTEST	0.00790796	0	#NAME?	0	1	1
ENSG00000269687	ENSG00000269687	RP11-995C19.2	HG1146_PATCH:44069222-44074616	NOTEST	0	0	0	0	1	1
ENSG00000269688	ENSG00000269688	AC008982.2	19:39306061-39342987	NOTEST	0.442716	0.140656	-1.65422	0	1	1
ENSG00000269689	ENSG00000269689	U3	HG1438_PATCH:71945972-71946187	NOTEST	0	0	0	0	1	1
ENSG00000269692	ENSG00000269692	RP11-45O22.1	9:41776063-41777434	NOTEST	0	0	0	0	1	1
ENSG00000269693	ENSG00000269693	CTD-2192J16.20	19:12490002-12750912	NOTEST	0.364997	0.201113	-0.859877	0	1	1
ENSG00000269694	ENSG00000269694	AC005197.2	19:18979360-19007536	NOTEST	0.135818	0.305568	1.16982	0	1	1
ENSG00000269696	ENSG00000269696	AC007228.11	19:57050316-57078780	NOTEST	0.0381274	0.190656	2.32207	0	1	1
ENSG00000269697	ENSG00000269697	MIR3202-2	HG1497_PATCH:153140794-153151663	NOTEST	0	0	0	0	1	1
ENSG00000269698	ENSG00000269698	WDR45	HG1436_HG1432_PATCH:48931124-48960569	NOTEST	0	0	0	0	1	1
ENSG00000269699	ENSG00000269699	ZIM2	19:57202053-57352097	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000269700	ENSG00000269700	AC069547.2	10:52065359-52401211	NOTEST	0	0	0	0	1	1
ENSG00000269701	ENSG00000269701	MAGEA8-AS1	HG1459_PATCH:148960557-148962792	NOTEST	0	0	0	0	1	1
ENSG00000269702	ENSG00000269702	RN7SL460P	HG1426_PATCH:77087317-77156547	NOTEST	0	0	0	0	1	1
ENSG00000269703	ENSG00000269703	AC244163.2	HG1146_PATCH:43907913-43908327	NOTEST	0	0	0	0	1	1
ENSG00000269704	ENSG00000269704	FTH1P27	HG1424_PATCH:37209336-38547737	NOTEST	0	0	0	0	1	1
ENSG00000269705	ENSG00000269705	L29074.3	HG1459_PATCH:146981892-146983174	NOTEST	0	0	0	0	1	1
ENSG00000269706	ENSG00000269706	CTB-60B18.15	19:49553473-49554103	NOTEST	0	0	0	0	1	1
ENSG00000269707	ENSG00000269707	RP11-13J10.1	2:105469742-105542510	NOTEST	0.593715	0.321167	-0.886445	0	1	1
ENSG00000269709	ENSG00000269709	AL109659.1	1:48561763-48648100	NOTEST	0	0	0	0	1	1
ENSG00000269710	ENSG00000269710	AC245177.1	HG1433_PATCH:51927822-51935266	NOTEST	0	0	0	0	1	1
ENSG00000269711	ENSG00000269711	CTD-3214H19.16	19:7741513-7747744	NOTEST	0	0	0	0	1	1
ENSG00000269712	ENSG00000269712	RNU6-935P	HG1433_PATCH:50334646-50557302	NOTEST	0	0	0	0	1	1
ENSG00000269713	ENSG00000269713	NBPF10	HG1287_PATCH:149740447-149768726	NOTEST	0	0	0	0	1	1
ENSG00000269714	ENSG00000269714	TTC23	HG971_PATCH:99679551-99794452	NOTEST	0	0	0	0	1	1
ENSG00000269715	ENSG00000269715	UBL4A	HG1497_PATCH:153652184-153655138	NOTEST	0	0	0	0	1	1
ENSG00000269718	ENSG00000269718	RN7SKP267	HG1459_PATCH:147582335-148082384	NOTEST	0	0	0	0	1	1
ENSG00000269719	ENSG00000269719	RPL36A-HNRNPH2	HG1439_PATCH:100645811-100669121	NOTEST	0	0	0	0	1	1
ENSG00000269720	ENSG00000269720	CTD-2521M24.5	19:17502237-17503093	NOTEST	0	0	0	0	1	1
ENSG00000269721	ENSG00000269721	RPL23AP51	7:7676148-8133902	NOTEST	0	0.120803	inf	0	1	1
ENSG00000269723	ENSG00000269723	AC244090.2	HG1497_PATCH:153596658-153596917	NOTEST	0	0	0	0	1	1
ENSG00000269724	ENSG00000269724	MIR1468	HG1437_PATCH:63005471-63005557	NOTEST	0	0	0	0	1	1
ENSG00000269725	ENSG00000269725	BX072566.2	GL000213.1:68441-70280	NOTEST	0	0	0	0	1	1
ENSG00000269726	ENSG00000269726	RP11-552J9.1	HG1433_PATCH:52326988-52329312	NOTEST	0	0	0	0	1	1
ENSG00000269729	ENSG00000269729	AC006262.4	19:46604379-46706340	NOTEST	0	0	0	0	1	1
ENSG00000269730	ENSG00000269730	AL662847.1	HSCHR6_MHC_COX:31471968-31472444	NOTEST	0	0	0	0	1	1
ENSG00000269731	ENSG00000269731	LA16c-13E4.3	HG1486_PATCH:16680766-16687245	NOTEST	0	0	0	0	1	1
ENSG00000269732	ENSG00000269732	WBP1LP7	1:317719-461954	NOTEST	0	0	0	0	1	1
ENSG00000269733	ENSG00000269733	PGPEP1L	HG971_PATCH:99497377-99678794	NOTEST	0	0	0	0	1	1
ENSG00000269734	ENSG00000269734	Y_RNA	HG1433_PATCH:53067561-53067674	NOTEST	0	0	0	0	1	1
ENSG00000269735	ENSG00000269735	AL121865.2	HG1433_PATCH:50334646-50557302	NOTEST	0	0	0	0	1	1
ENSG00000269736	ENSG00000269736	CTD-2521M24.11	19:17546317-17571763	NOTEST	0	0	0	0	1	1
ENSG00000269738	ENSG00000269738	AL162424.1	9:125132823-125157982	NOTEST	0	0	0	0	1	1
ENSG00000269740	ENSG00000269740	MIR764	HG1462_PATCH:113820547-114146531	NOTEST	0	0	0	0	1	1
ENSG00000269741	ENSG00000269741	KLK9	19:51446558-51515385	NOTEST	0	0	0	0	1	1
ENSG00000269742	ENSG00000269742	CTB-135N1.2	19:22235253-22274282	NOTEST	0	0	0	0	1	1
ENSG00000269743	ENSG00000269743	SLC25A53	HG1441_PATCH:103354143-103411956	NOTEST	0	0	0	0	1	1
ENSG00000269744	ENSG00000269744	FABP5P15	HG1426_PATCH:76765831-77047170	NOTEST	0	0	0	0	1	1
ENSG00000269745	ENSG00000269745	AC006262.10	19:46732220-46734500	NOTEST	0	0	0	0	1	1
ENSG00000269746	ENSG00000269746	AC009060.1	16:70239302-70239683	NOTEST	0	0	0	0	1	1
ENSG00000269747	ENSG00000269747	RNU6-383P	HG1459_PATCH:150037215-150037309	NOTEST	0	0	0	0	1	1
ENSG00000269748	ENSG00000269748	TFE3	HG1436_HG1432_PATCH:48888129-48902885	NOTEST	0	0	0	0	1	1
ENSG00000269749	ENSG00000269749	AC005614.5	19:40534166-40600313	NOTEST	0	0	0	0	1	1
ENSG00000269750	ENSG00000269750	CTD-2587H19.1	HSCHR19LRC_COX2_CTG1:54861673-54863577	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000269751	ENSG00000269751	CTC-273B12.8	19:48949029-48985571	NOTEST	0	0.105624	inf	0	1	1
ENSG00000269752	ENSG00000269752	CTD-3149D2.3	19:17712136-17799401	NOTEST	0	0	0	0	1	1
ENSG00000269753	ENSG00000269753	AL589739.1	1:2252691-2323146	NOTEST	0.153092	0.115882	-0.401736	0	1	1
ENSG00000269754	ENSG00000269754	AFF2	HG1459_PATCH:147582335-148082384	NOTEST	0	0	0	0	1	1
ENSG00000269755	ENSG00000269755	CTD-3105H18.18	19:12490002-12750912	NOTEST	0.0255501	0.17082	2.74107	0	1	1
ENSG00000269756	ENSG00000269756	RNU1-57P	HG1434_PATCH:113193143-113193309	NOTEST	0	0	0	0	1	1
ENSG00000269758	ENSG00000269758	CTD-2245F17.9	19:53771122-53774185	NOTEST	0	0	0	0	1	1
ENSG00000269759	ENSG00000269759	MTMR1	HG1459_PATCH:149774683-149846825	NOTEST	0	0	0	0	1	1
ENSG00000269761	ENSG00000269761	RP11-1137G4.4	19:7005022-7006085	NOTEST	0	0	0	0	1	1
ENSG00000269762	ENSG00000269762	RP11-236P24.3	HG1433_PATCH:52836709-52910014	NOTEST	0	0	0	0	1	1
ENSG00000269763	ENSG00000269763	EXOSC3P2	19:7878500-7879311	NOTEST	0	0	0	0	1	1
ENSG00000269764	ENSG00000269764	AC118758.7	HG736_PATCH:56884714-56885557	NOTEST	0	0	0	0	1	1
ENSG00000269765	ENSG00000269765	CTB-187L3.1	19:15619303-15663128	NOTEST	0	0	0	0	1	1
ENSG00000269766	ENSG00000269766	AL356215.1	11:35150090-35150215	NOTEST	0	0	0	0	1	1
ENSG00000269768	ENSG00000269768	AC008746.12	HSCHR19LRC_PGF1_CTG1:54872241-54872757	NOTEST	0	0	0	0	1	1
ENSG00000269769	ENSG00000269769	OR3B1P	HG1497_PATCH:153827257-153828150	NOTEST	0	0	0	0	1	1
ENSG00000269773	ENSG00000269773	PNCK	HG1497_PATCH:152838201-152865065	NOTEST	0	0	0	0	1	1
ENSG00000269774	ENSG00000269774	AC005399.1	22:17660193-17702879	NOTEST	0	0	0	0	1	1
ENSG00000269776	ENSG00000269776	DPPA5P1	19:52929115-52929455	NOTEST	0	0	0	0	1	1
ENSG00000269777	ENSG00000269777	FTH1P8	HG1459_PATCH:147133949-147134463	NOTEST	0	0	0	0	1	1
ENSG00000269778	ENSG00000269778	CTB-61M7.2	HSCHR19LRC_COX2_CTG1:55064787-55065535	NOTEST	0	0	0	0	1	1
ENSG00000269779	ENSG00000269779	CTD-2542C24.2	19:20874141-20880421	NOTEST	0	0	0	0	1	1
ENSG00000269780	ENSG00000269780	RP11-552J9.6	HG1433_PATCH:52355655-52356523	NOTEST	0	0	0	0	1	1
ENSG00000269781	ENSG00000269781	FLJ20306	7:6448756-6524873	NOTEST	0.123494	0.178514	0.531601	0	1	1
ENSG00000269782	ENSG00000269782	MIR1470	19:15532318-15560762	NOTEST	0	0	0	0	1	1
ENSG00000269783	ENSG00000269783	GOLGA7B	10:99609995-99790585	NOTEST	0.323127	0.302933	-0.0930996	0	1	1
ENSG00000269786	ENSG00000269786	CTC-258N23.3	19:57433385-57433581	NOTEST	0	0	0	0	1	1
ENSG00000269787	ENSG00000269787	OR7A3P	19:15014043-15014985	NOTEST	0	0	0	0	1	1
ENSG00000269788	ENSG00000269788	RP11-399F4.2	9:43009841-43010747	NOTEST	0	0	0	0	1	1
ENSG00000269790	ENSG00000269790	MAGEA1	HG1497_PATCH:152347755-152352350	NOTEST	0	0	0	0	1	1
ENSG00000269791	ENSG00000269791	SSX4	HG1436_HG1432_PATCH:48261480-48271309	NOTEST	0	0	0	0	1	1
ENSG00000269792	ENSG00000269792	CTB-60E11.9	19:40021629-40025062	NOTEST	0	0	0	0	1	1
ENSG00000269793	ENSG00000269793	AC006115.3	19:57202053-57352097	NOTEST	0	0	0	0	1	1
ENSG00000269794	ENSG00000269794	AC010642.2	19:58830642-58831855	NOTEST	0.137399	0.0776522	-0.823272	0	1	1
ENSG00000269795	ENSG00000269795	AC092782.1	1:243287729-243418650	NOTEST	0	0	0	0	1	1
ENSG00000269796	ENSG00000269796	AC011516.1	19:22573820-22715287	NOTEST	0	0	0	0	1	1
ENSG00000269797	ENSG00000269797	GPR107	HG1502_PATCH:132815704-132902448	NOTEST	0	0	0	0	1	1
ENSG00000269798	ENSG00000269798	DUSP9	HG1497_PATCH:152810962-152819798	NOTEST	0	0	0	0	1	1
ENSG00000269799	ENSG00000269799	CTD-2538G9.6	19:16830786-16928774	NOTEST	0	0	0	0	1	1
ENSG00000269800	ENSG00000269800	PLEKHA3P1	19:42027402-42028349	NOTEST	0.102718	0.0609307	-0.753454	0	1	1
ENSG00000269801	ENSG00000269801	ARMCX1	HG1439_PATCH:100805517-100809687	NOTEST	0	0	0	0	1	1

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ENSG00000269803	ENSG00000269803	RP5-1000K24.2	HG1426_PATCH:77171650-77311349	NOTEST	0	0	0	0	1	1
ENSG00000269804	ENSG00000269804	AL353354.2	1:28525966-28559536	NOTEST	0	0	0	0	1	1
ENSG00000269805	ENSG00000269805	XAGE1A	HG1433_PATCH:52238667-52243812	NOTEST	0	0	0	0	1	1
ENSG00000269806	ENSG00000269806	CTD-3001H11.1	19:48110780-48246391	NOTEST	0	0	0	0	1	1
ENSG00000269807	ENSG00000269807	AC007292.4	19:4343523-4360083	NOTEST	0	0	0	0	1	1
ENSG00000269810	ENSG00000269810	AC015660.1	15:100017369-100273766	NOTEST	0	0	0	0	1	1
ENSG00000269811	ENSG00000269811	SCGB2B3P	19:35084233-35166604	NOTEST	0	0	0	0	1	1
ENSG00000269813	ENSG00000269813	CTD-3193O13.14	19:8023462-8070543	NOTEST	0	0	0	0	1	1
ENSG00000269814	ENSG00000269814	CTC-273B12.10	19:49016463-49016917	NOTEST	0.347491	0.276991	-0.32714	0	1	1
ENSG00000269816	ENSG00000269816	KDM5C	HG1433_PATCH:52934320-52968422	NOTEST	0	0	0	0	1	1
ENSG00000269817	ENSG00000269817	TCP11X3P	HG1440_PATCH:101428071-101439993	NOTEST	0	0	0	0	1	1
ENSG00000269818	ENSG00000269818	CTD-2332E11.2	HG730_PATCH:20646633-20772405	NOTEST	0	0	0	0	1	1
ENSG00000269819	ENSG00000269819	EIF4A2P4	HG1433_PATCH:52575703-52576899	NOTEST	0	0	0	0	1	1
ENSG00000269820	ENSG00000269820	SAGE1	HG1443_HG1444_PATCH:135023244-135047090	NOTEST	0	0	0	0	1	1
ENSG00000269821	ENSG00000269821	KCNQ1OT1	11:2465913-2882798	NOTEST	0.0601547	0.0632146	0.0715805	0	1	1
ENSG00000269822	ENSG00000269822	LL0XNC01-116E7.1	HG1441_PATCH:103165233-103166281	NOTEST	0	0	0	0	1	1
ENSG00000269823	ENSG00000269823	AL513523.1	HSCHR1_1_CTG31:153717773-153763786	NOTEST	0	0	0	0	1	1
ENSG00000269824	ENSG00000269824	AL022578.1	HG1436_HG1432_PATCH:47695351-47696192	NOTEST	0	0	0	0	1	1
ENSG00000269825	ENSG00000269825	CTD-3099C6.9	19:53091757-53193749	NOTEST	0.374468	0.337872	-0.148366	0	1	1
ENSG00000269826	ENSG00000269826	RP11-158I3.3	16:86365449-86383289	NOTEST	0	0	0	0	1	1
ENSG00000269830	ENSG00000269830	GPR162	HG344_PATCH:6930710-6949018	NOTEST	0	0	0	0	1	1
ENSG00000269831	ENSG00000269831	AL669831.1	1:714149-755214	NOTEST	0	0	0	0	1	1
ENSG00000269832	ENSG00000269832	AL627171.2	14:50249996-50319921	NOTEST	0.038257	0.0499277	0.384115	0	1	1
ENSG00000269833	ENSG00000269833	RP13-210D15.6	HG1443_HG1444_PATCH:134370822-134371378	NOTEST	0	0	0	0	1	1
ENSG00000269834	ENSG00000269834	CTD-3018O17.3	19:52892094-52901019	NOTEST	0.0220826	0.0727462	1.71996	0	1	1
ENSG00000269836	ENSG00000269836	CTD-3032J10.4	19:17186590-17325346	NOTEST	0	0	0	0	1	1
ENSG00000269838	ENSG00000269838	SPANXD	HG1453_PATCH:140779575-140780904	NOTEST	0	0	0	0	1	1
ENSG00000269839	ENSG00000269839	CTD-3233P19.7	19:21407899-21428043	NOTEST	0	0	0	0	1	1
ENSG00000269840	ENSG00000269840	PAGE1	HG1436_HG1432_PATCH:49496848-49505392	NOTEST	0	0	0	0	1	1
ENSG00000269842	ENSG00000269842	MIR519A2	19:54265214-54267453	NOTEST	0	0.0228903	inf	0	1	1
ENSG00000269843	ENSG00000269843	CTC-490E21.10	19:41277552-41406413	NOTEST	0.232638	0.448361	0.94657	0	1	1
ENSG00000269844	ENSG00000269844	RP6-29D12.2	HG1433_PATCH:53083985-53084505	NOTEST	0	0	0	0	1	1
ENSG00000269845	ENSG00000269845	RP11-420K14.6	19:21905567-21950430	NOTEST	0.0283246	0.0270009	-0.06905	0	1	1
ENSG00000269846	ENSG00000269846	RBL1	20:35624751-35725581	NOTEST	0.0736023	0.0506285	-0.539801	0	1	1
ENSG00000269848	ENSG00000269848	RP11-1281K21.9	4:49526046-49526202	NOTEST	0	0	0	0	1	1
ENSG00000269849	ENSG00000269849	MAMLD1	HG1459_PATCH:149443143-149595900	NOTEST	0	0	0	0	1	1
ENSG00000269851	ENSG00000269851	U47924.27	HG344_PATCH:7072408-7073610	NOTEST	0	0	0	0	1	1
ENSG00000269853	ENSG00000269853	SPANXB1	HG1453_PATCH:140084755-140085871	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000269855	ENSG00000269855	AC012313.1	19:58907456-58908407	NOTEST	0	0	0	0	1	1
ENSG00000269856	ENSG00000269856	LA16c-4G1.3	HG1487_PATCH:16095339-16096419	NOTEST	0	0	0	0	1	1
ENSG00000269859	ENSG00000269859	CTD-2537I9.16	19:55987349-55995854	NOTEST	0.0451469	0.141231	1.64536	0	1	1
ENSG00000269860	ENSG00000269860	RP13-228J13.10	HG1497_PATCH:154444678-154503125	NOTEST	0	0	0	0	1	1
ENSG00000269861	ENSG00000269861	HIST2H2BD	HG1287_PATCH:150529455-150529948	NOTEST	0	0	0	0	1	1
ENSG00000269862	ENSG00000269862	RP11-654A16.3	HG971_PATCH:99497377-99678794	NOTEST	0	0	0	0	1	1
ENSG00000269863	ENSG00000269863	SHANK2-AS2	HG865_PATCH:70313960-71048647	NOTEST	0	0	0	0	1	1
ENSG00000269864	ENSG00000269864	RP5-1189K21.2	HG1458_PATCH:142372762-142605261	NOTEST	0	0	0	0	1	1
ENSG00000269865	ENSG00000269865	XX-FW83128A1.2	HG1497_PATCH:153502427-153503505	NOTEST	0	0	0	0	1	1
ENSG00000269866	ENSG00000269866	FKSG63	16:70253476-70279519	NOTEST	0	0	0	0	1	1
ENSG00000269868	ENSG00000269868	RP11-552J9.14	HG1433_PATCH:52465318-52465525	NOTEST	0	0	0	0	1	1
ENSG00000269870	ENSG00000269870	PPP1R3F	HG1436_HG1432_PATCH:49129241-49160849	NOTEST	0	0	0	0	1	1
ENSG00000269871	ENSG00000269871	AC040977.1	17:6757179-6922978	NOTEST	0	0	0	0	1	1
ENSG00000269873	ENSG00000269873	CTD-2587H19.3	19:54949191-54949528	NOTEST	0	0.200618	inf	0	1	1
ENSG00000269874	ENSG00000269874	snoU13	HG1497_PATCH:152502626-152528582	NOTEST	0	0	0	0	1	1
ENSG00000269875	ENSG00000269875	FTSJ1	HG1436_HG1432_PATCH:48335551-48345763	NOTEST	0	0	0	0	1	1
ENSG00000269876	ENSG00000269876	CYCSP44	HG1459_PATCH:144258298-144258611	NOTEST	0	0	0	0	1	1
ENSG00000269877	ENSG00000269877	MIR371B	19:54290850-54291423	NOTEST	0	0	0	0	1	1
ENSG00000269878	ENSG00000269878	PHKA1-AS1	HG1438_PATCH:71798663-71934169	NOTEST	0	0	0	0	1	1
ENSG00000269879	ENSG00000269879	AL353583.1	10:23983674-24836772	NOTEST	0	0	0	0	1	1
ENSG00000269880	ENSG00000269880	CTD-2557P19.4	HG729_PATCH:8843548-8843745	NOTEST	0	0	0	0	1	1
ENSG00000269881	ENSG00000269881	ITFG3	16:284544-333003	NOTEST	0	0	0	0	1	1
ENSG00000269882	ENSG00000269882	C1S	HG344_PATCH:7085347-7180195	NOTEST	0	0	0	0	1	1
ENSG00000269883	ENSG00000269883	AC007375.1	14:77564439-77725838	NOTEST	0	0	0	0	1	1
ENSG00000269884	ENSG00000269884	BRCC3	HG1497_PATCH:154230089-154324971	NOTEST	0	0	0	0	1	1
ENSG00000269885	ENSG00000269885	VN1R79P	19:20941245-20941758	NOTEST	0	0	0	0	1	1
ENSG00000269886	ENSG00000269886	RP11-266J6.2	3:9791627-9896822	NOTEST	0.0914004	0	#NAME?	0	1	1
ENSG00000269887	ENSG00000269887	RP11-477H21.2	1:164524820-164868533	NOTEST	0	0	0	0	1	1
ENSG00000269889	ENSG00000269889	RP11-816J6.3	3:169484708-169489831	NOTEST	0.0525046	0.0220695	-1.25039	0	1	1
ENSG00000269890	ENSG00000269890	RP5-1139B12.2	1:228391206-228566577	NOTEST	0.0235053	0.104925	2.1583	0	1	1
ENSG00000269892	ENSG00000269892	RP4-761J14.10	12:6852150-6852807	NOTEST	0.06113	0.119225	0.963739	0	1	1
ENSG00000269894	ENSG00000269894	RP11-1020A11.1	3:9975505-9987097	NOTEST	0.038887	0.414381	3.4136	0	1	1
ENSG00000269895	ENSG00000269895	AP000654.4	11:86502100-86666433	NOTEST	0	0.0102406	inf	0	1	1
ENSG00000269896	ENSG00000269896	RP4-740C4.6	1:2252691-2323146	NOTEST	0.547415	0.331465	-0.723781	0	1	1
ENSG00000269898	ENSG00000269898	RP11-568J23.4	16:85723689-85784735	NOTEST	0.0454227	0	#NAME?	0	1	1
ENSG00000269901	ENSG00000269901	RP11-178L8.9	16:87117167-87438385	NOTEST	0	0.0378929	inf	0	1	1
ENSG00000269902	ENSG00000269902	RP6-99M1.3	X:45604638-45629677	NOTEST	0.0773404	0	#NAME?	0	1	1
ENSG00000269903	ENSG00000269903	RP11-571M6.18	12:58156116-58212487	NOTEST	0	0.0441952	inf	0	1	1

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ENSG00000269905	ENSG00000269905	RP11-271K21.1	3:141663269-141868386	NOTEST	0.60626	0.447182	-0.439076	0	1	1
ENSG00000269907	ENSG00000269907	RP11-330M2.4	9:99660347-99775862	NOTEST	0.0926893	0.139157	0.586239	0	1	1
ENSG00000269908	ENSG00000269908	RP11-1406H17.1	4:6241167-6241664	NOTEST	0	0	0	0	1	1
ENSG00000269909	ENSG00000269909	RP11-489N22.3	9:129376721-129463312	NOTEST	0.110762	0.165685	0.580983	0	1	1
ENSG00000269911	ENSG00000269911	FAM226B	X:71996832-72068636	NOTEST	0	0	0	0	1	1
ENSG00000269913	ENSG00000269913	CTC-1337H24.1	11:67227338-67227784	NOTEST	0	0	0	0	1	1
ENSG00000269915	ENSG00000269915	AP006621.9	11:644232-727727	NOTEST	0	0	0	0	1	1
ENSG00000269916	ENSG00000269916	RP11-193M21.1	12:85657321-85658235	NOTEST	0.189584	0.131872	-0.5237	0	1	1
ENSG00000269918	ENSG00000269918	AF131215.9	8:10753554-11058875	NOTEST	0	0	0	0	1	1
ENSG00000269919	ENSG00000269919	RP1-134E15.3	6:106534194-106557814	NOTEST	0	0	0	0	1	1
ENSG00000269921	ENSG00000269921	RP11-646I6.5	4:57253790-57254319	NOTEST	0.237221	0.241297	0.0245808	0	1	1
ENSG00000269923	ENSG00000269923	RP11-214K3.24	12:124247041-124800570	NOTEST	0.078266	0.0425757	-0.878355	0	1	1
ENSG00000269924	ENSG00000269924	RP11-697N18.4	8:48173166-48648868	NOTEST	0.0469368	0.0180671	-1.37736	0	1	1
ENSG00000269925	ENSG00000269925	RP3-467L1.6	1:7831328-7841492	NOTEST	0.586982	0.598769	0.028685	0	1	1
ENSG00000269926	ENSG00000269926	RP11-442H21.2	10:74033677-74035794	NOTEST	0.00578599	0.275982	5.57587	0	1	1
ENSG00000269927	ENSG00000269927	RP6-91H8.3	14:71607841-71609970	NOTEST	0.00758483	0	#NAME?	0	1	1
ENSG00000269930	ENSG00000269930	RP11-932O9.9	15:30909160-31065196	NOTEST	0.415961	0.118568	-1.81074	0	1	1
ENSG00000269931	ENSG00000269931	RP5-1069C8.3	20:12845849-12933167	NOTEST	0	0	0	0	1	1
ENSG00000269933	ENSG00000269933	RP3-333A15.2	1:71318035-71513491	NOTEST	0	0.0241889	inf	0	1	1
ENSG00000269934	ENSG00000269934	RP5-1139B12.3	1:228391206-228566577	NOTEST	0	0.0468562	inf	0	1	1
ENSG00000269935	ENSG00000269935	RP11-482M8.3	16:87634131-87799598	NOTEST	0	0	0	0	1	1
ENSG00000269936	ENSG00000269936	MIR145	5:148809848-148812397	NOTEST	0	0	0	0	1	1
ENSG00000269937	ENSG00000269937	RP11-20I23.8	16:2587964-2653189	NOTEST	0.030088	0.0245726	-0.292139	0	1	1
ENSG00000269938	ENSG00000269938	RP11-214K3.20	12:124247041-124800570	NOTEST	0.373649	0.111821	-1.74049	0	1	1
ENSG00000269939	ENSG00000269939	RP11-727A23.11	11:82868029-83134559	NOTEST	0	0	0	0	1	1
ENSG00000269941	ENSG00000269941	RP5-1172N10.4	X:40944887-41095832	NOTEST	0	0	0	0	1	1
ENSG00000269942	ENSG00000269942	RP11-29B2.5	13:103331775-103332308	NOTEST	0.0410346	0.19223	2.22792	0	1	1
ENSG00000269944	ENSG00000269944	RP11-770J1.7	11:118230299-118302211	NOTEST	0	0	0	0	1	1
ENSG00000269945	ENSG00000269945	RP6-91H8.5	14:71685816-71689441	NOTEST	0	0.0103615	inf	0	1	1
ENSG00000269946	ENSG00000269946	RP11-2B6.3	9:96928570-96966850	NOTEST	0	0	0	0	1	1
ENSG00000269947	ENSG00000269947	RP11-849F2.9	17:8181080-8181754	NOTEST	0.138292	0.153027	0.146065	0	1	1
ENSG00000269948	ENSG00000269948	RP11-248J23.6	10:97471535-97849995	NOTEST	0.0501464	0.126732	1.33756	0	1	1
ENSG00000269949	ENSG00000269949	RP11-738E22.3	4:57827092-57827539	NOTEST	0.0537949	0	#NAME?	0	1	1
ENSG00000269950	ENSG00000269950	AP000962.2	21:17442841-17999716	NOTEST	0	0	0	0	1	1
ENSG00000269954	ENSG00000269954	RP11-148O21.6	8:11351509-11422113	NOTEST	0	0	0	0	1	1

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ENSG00000269957	ENSG00000269957	RP11-20A20.2	9:24545949-24591991	NOTEST	0	0	0	0	1	1
ENSG00000269959	ENSG00000269959	SPACA6P-AS	19:52188615-52215640	NOTEST	0.0337322	0.052866	0.648214	0	1	1
ENSG00000269961	ENSG00000269961	CTD-2033C11.1	5:65220456-65220963	NOTEST	0.214957	0.222804	0.0517287	0	1	1
ENSG00000269962	ENSG00000269962	RP13-238F13.5	10:126133807-126134344	NOTEST	0.0405864	0	#NAME?	0	1	1
ENSG00000269964	ENSG00000269964	MEI4	6:78400374-78636691	NOTEST	0.0334083	0.0142691	-1.22732	0	1	1
ENSG00000269966	ENSG00000269966	RP3-331H24.5	6:71931159-72130472	NOTEST	0	0	0	0	1	1
ENSG00000269967	ENSG00000269967	RP11-84A19.4	1:32307619-32410457	NOTEST	0.0660712	0.172557	1.38498	0	1	1
ENSG00000269970	ENSG00000269970	RP11-498E2.9	9:125132823-125157982	NOTEST	0	0	0	0	1	1
ENSG00000269971	ENSG00000269971	RP3-426I6.5	1:28099693-28150963	NOTEST	0	0	0	0	1	1
ENSG00000269972	ENSG00000269972	RP3-430N8.10	22:31366662-31375381	NOTEST	0	0	0	0	1	1
ENSG00000269976	ENSG00000269976	RP11-130L8.2	2:20760207-20850849	NOTEST	0.159673	0.163024	0.0299705	0	1	1
ENSG00000269978	ENSG00000269978	RP11-338N10.3	1:6845383-7829766	NOTEST	0	0	0	0	1	1
ENSG00000269980	ENSG00000269980	RP11-282O18.7	12:123636866-123756881	NOTEST	0.171721	0	#NAME?	0	1	1
ENSG00000269981	ENSG00000269981	RP11-34P13.16	1:134900-139379	NOTEST	0	0.0643821	inf	0	1	1
ENSG00000269983	ENSG00000269983	RP11-497H16.9	5:69745462-69746180	NOTEST	0	0	0	0	1	1
ENSG00000269984	ENSG00000269984	RP11-362K14.5	3:169490618-169507504	NOTEST	0.228082	0.296395	0.377968	0	1	1
ENSG00000269985	ENSG00000269985	RP1-232P20.1	6:5261276-5771813	NOTEST	0	0	0	0	1	1
ENSG00000269986	ENSG00000269986	RP11-96H17.3	16:63090689-63163558	NOTEST	0.0945314	0.0753145	-0.327865	0	1	1
ENSG00000269988	ENSG00000269988	RP11-395P17.11	9:130823511-130871604	NOTEST	0.111575	0.0638036	-0.806309	0	1	1
ENSG00000269989	ENSG00000269989	RP11-635N19.3	18:61143993-61172318	NOTEST	0	0	0	0	1	1
ENSG00000269993	ENSG00000269993	AF003625.3	X:150350857-150351327	NOTEST	0	0	0	0	1	1
ENSG00000269994	ENSG00000269994	RP11-276H19.2	9:89623369-89657041	NOTEST	0	0	0	0	1	1
ENSG00000269997	ENSG00000269997	RP11-214K3.21	12:124247041-124800570	NOTEST	0.555105	0.176702	-1.65144	0	1	1
ENSG00000269998	ENSG00000269998	RP11-272L13.3	1:98399029-98407302	NOTEST	0	0	0	0	1	1
ENSG00000269999	ENSG00000269999	CTD-3185P2.2	15:66679154-66790151	NOTEST	0.548344	0.567487	0.049506	0	1	1
ENSG00000270000	ENSG00000270000	RP3-449M8.9	14:74938632-74939063	NOTEST	0.221559	0.253332	0.193334	0	1	1
ENSG00000270001	ENSG00000270001	RP11-218C14.8	20:23608533-23619110	NOTEST	0	0	0	0	1	1
ENSG00000270002	ENSG00000270002	RP11-93H12.4	10:87359311-88126250	NOTEST	0	0	0	0	1	1
ENSG00000270004	ENSG00000270004	FAM226A	HG1438_PATCH:71996858-72068652	NOTEST	0	0	0	0	1	1
ENSG00000270005	ENSG00000270005	RP11-380L11.3	12:124247041-124800570	NOTEST	0.335917	0.199407	-0.752386	0	1	1
ENSG00000270006	ENSG00000270006	RP11-178L8.7	16:87117167-87438385	NOTEST	0.397212	0.148239	-1.42199	0	1	1
ENSG00000270008	ENSG00000270008	RP11-298P3.4	13:32974860-33112970	NOTEST	0.110765	0.109815	-0.0124253	0	1	1
ENSG00000270009	ENSG00000270009	RP1-127C7.6	1:183589980-183590626	NOTEST	0	0	0	0	1	1
ENSG00000270010	ENSG00000270010	CTD-2132N18.4	17:40118758-40217383	NOTEST	0.0447562	0.166101	1.8919	0	1	1
ENSG00000270012	ENSG00000270012	LL0XNC01-7P3.1	X:49126305-49157929	NOTEST	0.520738	0.535766	0.0410475	0	1	1
ENSG00000270016	ENSG00000270016	RP11-932O9.8	15:30896328-30906764	NOTEST	0.0844109	0	#NAME?	0	1	1

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ENSG00000270019	ENSG00000270019	RP11-141B14.1	2:114645779-114647327	NOTEST	0.095074	0.0571416	-0.73451	0	1	1
ENSG00000270020	ENSG00000270020	RP11-463O9.9	16:86553988-86557503	NOTEST	0.00444097	0	#NAME?	0	1	1
ENSG00000270021	ENSG00000270021	CTC-203F4.2	5:134363424-134736986	NOTEST	0.0306734	0.011307	-1.43977	0	1	1
ENSG00000270022	ENSG00000270022	RNU12	22:43011249-43011913	NOTEST	0.0555095	0	#NAME?	0	1	1
ENSG00000270024	ENSG00000270024	C8orf44-SGK3	8:67579830-67774257	NOTEST	0	0.340131	inf	0	1	1
ENSG00000270025	ENSG00000270025	BMS1P7	HG1211_PATCH:48462447-48474245	NOTEST	0	0	0	0	1	1
ENSG00000270026	ENSG00000270026	RP11-343N15.5	HG1292_PATCH:121902778-122005752	NOTEST	0	0	0	0	1	1
ENSG00000270027	ENSG00000270027	RP11-770J1.7	HG122_PATCH:118230299-118302211	NOTEST	0	0	0	0	1	1
ENSG00000270028	ENSG00000270028	RP11-380L11.4	12:124247041-124800570	NOTEST	0.1871	0	#NAME?	0	1	1
ENSG00000270030	ENSG00000270030	RP11-326C3.13	11:318639-330122	NOTEST	0.0652722	0	#NAME?	0	1	1
ENSG00000270031	ENSG00000270031	RP3-426I6.6	1:28099693-28150963	NOTEST	0.0787449	0.0615044	-0.356498	0	1	1
ENSG00000270033	ENSG00000270033	RP11-51L5.7	17:60342065-60374387	NOTEST	0	0	0	0	1	1
ENSG00000270035	ENSG00000270035	RP11-338N10.2	1:6845383-7829766	NOTEST	0	0	0	0	1	1
ENSG00000270036	ENSG00000270036	RP11-685G9.4	15:76635982-76636706	NOTEST	0.0268608	0.0593423	1.14356	0	1	1
ENSG00000270038	ENSG00000270038	RP11-1070N10.7	14:96110844-96111569	NOTEST	0.308681	0.205242	-0.588789	0	1	1
ENSG00000270039	ENSG00000270039	RP11-571M6.17	12:58156116-58212487	NOTEST	0.250082	0.213515	-0.228066	0	1	1
ENSG00000270040	ENSG00000270040	RP11-416A14.1	1:39546987-39952849	NOTEST	0	0	0	0	1	1
ENSG00000270042	ENSG00000270042	RP5-894A10.6	HSCHR7_1_CTG6:141250988-141401956	NOTEST	0	0	0	0	1	1
ENSG00000270043	ENSG00000270043	Metazoa_SRP	HSCHR15_1_CTG4:28623775-28637136	NOTEST	0	0	0	0	1	1
ENSG00000270046	ENSG00000270046	CTD-2132N18.4	HG185_PATCH:40132690-40219330	NOTEST	0	0	0	0	1	1
ENSG00000270048	ENSG00000270048	RP11-214K3.22	12:124247041-124800570	NOTEST	0.154715	0	#NAME?	0	1	1
ENSG00000270050	ENSG00000270050	RP4-769N13.7	X:101854095-101973607	NOTEST	0	0.128471	inf	0	1	1
ENSG00000270052	ENSG00000270052	WI2-80269A6.1	X:150666197-150666826	NOTEST	0	0	0	0	1	1
ENSG00000270058	ENSG00000270058	RP11-514D23.3	16:86255028-86256335	NOTEST	0	0	0	0	1	1
ENSG00000270059	ENSG00000270059	RP11-88H12.2	3:65339199-66024509	NOTEST	0	0	0	0	1	1
ENSG00000270060	ENSG00000270060	RP11-390K5.6	11:46958239-47198676	NOTEST	0.429854	0.314558	-0.450519	0	1	1
ENSG00000270061	ENSG00000270061	RP11-214K3.19	12:124247041-124800570	NOTEST	0.307368	0.120463	-1.35138	0	1	1
ENSG00000270063	ENSG00000270063	HCG4B	HG1322_PATCH:29887571-29890825	NOTEST	0	0	0	0	1	1
ENSG00000270066	ENSG00000270066	SCARNA2	1:109642814-109643241	NOTEST	0.112274	0.319791	1.5101	0	1	1
ENSG00000270067	ENSG00000270067	CTC-487M23.5	5:112043194-112258236	NOTEST	0.149142	0.128677	-0.212932	0	1	1
ENSG00000270068	ENSG00000270068	RP4-761J14.9	12:6832398-6832853	NOTEST	0.195964	0	#NAME?	0	1	1
ENSG00000270071	ENSG00000270071	AP001172.2	21:17442841-17999716	NOTEST	0	0	0	0	1	1
ENSG00000270072	ENSG00000270072	RP11-750H9.7	11:47487495-47606114	NOTEST	0	0	0	0	1	1
ENSG00000270073	ENSG00000270073	AC006156.2	Y:9345204-9347784	NOTEST	0	0	0	0	1	1
ENSG00000270074	ENSG00000270074	LINC00965	8:12270335-12271882	NOTEST	0	0	0	0	1	1
ENSG00000270075	ENSG00000270075	RP11-127L20.5	10:106071893-106098162	NOTEST	0	0	0	0	1	1
ENSG00000270076	ENSG00000270076	AF131215.8	8:11060473-11061180	NOTEST	0	0	0	0	1	1
ENSG00000270077	ENSG00000270077	KB-1958F4.1	8:97657454-98161882	NOTEST	0	0.0275675	inf	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000270082	ENSG00000270082	RP11-178L8.8	16:87117167-87438385	NOTEST	0	0	0	0	1	1
ENSG00000270084	ENSG00000270084	GAS5-AS1	1:173832385-173872687	NOTEST	0.355648	0.219529	-0.696035	0	1	1
ENSG00000270087	ENSG00000270087	RP11-399K21.11	10:77029576-77171600	NOTEST	0	0	0	0	1	1
ENSG00000270089	ENSG00000270089	RP6-99M1.3	HG1435_PATCH:45604455-45629519	NOTEST	0	0	0	0	1	1
ENSG00000270090	ENSG00000270090	RP11-529E10.7	4:3546281-3550523	NOTEST	0.0351182	0.0522145	0.572232	0	1	1
ENSG00000270091	ENSG00000270091	RP11-78O7.2	17:19799902-19800600	NOTEST	0.0488521	0.174554	1.83718	0	1	1
ENSG00000270092	ENSG00000270092	RP11-318K12.3	9:66836661-66836791	NOTEST	0	0	0	0	1	1
ENSG00000270093	ENSG00000270093	AP000473.8	21:18015847-18017384	NOTEST	0	0	0	0	1	1
ENSG00000270094	ENSG00000270094	RP11-245P10.8	1:228581373-228594541	NOTEST	0	0	0	0	1	1
ENSG00000270095	ENSG00000270095	RP11-214K3.18	12:124247041-124800570	NOTEST	0.487182	0.11798	-2.04592	0	1	1
ENSG00000270096	ENSG00000270096	RP11-362K14.6	3:169511215-169530774	NOTEST	0.264336	0.11245	-1.23308	0	1	1
ENSG00000270097	ENSG00000270097	LA16c-380H5.3	16:3049902-3050390	NOTEST	0	0	0	0	1	1
ENSG00000270098	ENSG00000270098	LDHAL6EP	4:72053002-72437804	NOTEST	0	0	0	0	1	1
ENSG00000270099	ENSG00000270099	RP11-248J23.7	10:97471535-97849995	NOTEST	0	0	0	0	1	1
ENSG00000270100	ENSG00000270100	RP11-130L8.1	2:20877568-20879005	NOTEST	0.00755387	0.0206733	1.45248	0	1	1
ENSG00000270103	ENSG00000270103	RNU11	1:28975111-28975245	NOTEST	0	0	0	0	1	1
ENSG00000270104	ENSG00000270104	RP11-245P10.6	1:228571814-228572717	NOTEST	0.105124	0	#NAME?	0	1	1
ENSG00000270105	ENSG00000270105	RP11-326C3.14	11:318639-330122	NOTEST	0	0	0	0	1	1
ENSG00000270106	ENSG00000270106	TSNAX-DISC1	1:231664398-232177018	NOTEST	0.123733	0.0662462	-0.901326	0	1	1
ENSG00000270107	ENSG00000270107	CTD-2306M10.1	5:66475440-66476415	NOTEST	0	0	0	0	1	1
ENSG00000270109	ENSG00000270109	RP11-393M11.2	4:57330323-57330745	NOTEST	0.288758	0.231399	-0.319482	0	1	1
ENSG00000270110	ENSG00000270110	RP5-1139B12.4	1:228391206-228566577	NOTEST	0.096062	0.10837	0.173922	0	1	1
ENSG00000270111	ENSG00000270111	RP11-271F18.4	10:10461500-10504312	NOTEST	0	0	0	0	1	1
ENSG00000270112	ENSG00000270112	RP11-742D12.2	18:44259080-44340307	NOTEST	0	0	0	0	1	1
ENSG00000270114	ENSG00000270114	RP5-1048B16.1	7:153584181-154685995	NOTEST	0	0	0	0	1	1
ENSG00000270115	ENSG00000270115	RP11-415J8.7	1:33722145-33766320	NOTEST	0.192893	0.305852	0.665035	0	1	1
ENSG00000270116	ENSG00000270116	AP001429.1	21:38445525-38575413	NOTEST	0.283783	0.0615915	-2.20398	0	1	1
ENSG00000270117	ENSG00000270117	AP000769.7	11:65265232-65273940	NOTEST	0	0	0	0	1	1
ENSG00000270118	ENSG00000270118	RP11-57A19.5	16:28465461-28465832	NOTEST	0	0	0	0	1	1
ENSG00000270119	ENSG00000270119	RP11-301J7.8	10:48247668-48279200	NOTEST	0	0	0	0	1	1
ENSG00000270120	ENSG00000270120	RP11-327F22.6	16:50727513-50766988	NOTEST	0	0	0	0	1	1
ENSG00000270124	ENSG00000270124	RP11-118F19.1	16:85613614-85617177	NOTEST	0.0345464	0	#NAME?	0	1	1
ENSG00000270129	ENSG00000270129	LL0XNC01-7P3.1	HG1436_HG1432_PATCH:49129241-49160849	NOTEST	0	0	0	0	1	1
ENSG00000270130	ENSG00000270130	RP11-214K3.23	12:124247041-124800570	NOTEST	0.279536	0.0914661	-1.61172	0	1	1
ENSG00000270131	ENSG00000270131	KB-1043D8.8	8:97152799-97153172	NOTEST	0	0	0	0	1	1
ENSG00000270132	ENSG00000270132	WISP1-OT1	8:134203281-134242587	NOTEST	0	0	0	0	1	1
ENSG00000270133	ENSG00000270133	CTC-303L1.2	5:93488670-94620279	NOTEST	0.0623368	0.0444973	-0.486367	0	1	1

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ENSG00000270135	ENSG00000270135	RP11-362K14.7	3:169511215-169530774	NOTEST	0	0.20698	inf	0	1	1
ENSG00000270137	ENSG00000270137	CTC-137K3.1	8:133787617-133861052	NOTEST	0.0268262	0	#NAME?	0	1	1
ENSG00000270139	ENSG00000270139	AP001172.3	21:17442841-17999716	NOTEST	0	0	0	0	1	1
ENSG00000270140	ENSG00000270140	RP5-1021I20.6	14:74318546-74551196	NOTEST	0	0	0	0	1	1
ENSG00000270141	ENSG00000270141	TERC	3:169482307-169482848	NOTEST	0.0401478	0	#NAME?	0	1	1
ENSG00000270145	ENSG00000270145	CTD-2267D19.6	17:38459456-38460909	NOTEST	0.571653	0.43859	-0.382268	0	1	1
ENSG00000270147	ENSG00000270147	RP11-646I6.6	4:57259527-57301781	NOTEST	0.115232	0.19398	0.751365	0	1	1
ENSG00000270154	ENSG00000270154	RP11-419I17.1	8:12305521-12368787	NOTEST	0.512264	0.374329	-0.45258	0	1	1
ENSG00000270156	ENSG00000270156	RP11-301J7.8	HG1211_PATCH:47955609-47987141	NOTEST	0	0	0	0	1	1
ENSG00000270159	ENSG00000270159	RP11-568J23.6	16:85805363-85840650	NOTEST	0	0.0447123	inf	0	1	1
ENSG00000270160	ENSG00000270160	RP11-264E20.2	11:128484234-128485131	NOTEST	0	0	0	0	1	1
ENSG00000270163	ENSG00000270163	RP11-1085N6.6	14:57266622-57267306	NOTEST	0	0	0	0	1	1
ENSG00000270165	ENSG00000270165	RP11-167P11.2	16:67757004-67840555	NOTEST	0.143977	0.140156	-0.0388053	0	1	1
ENSG00000270166	ENSG00000270166	RP11-158D2.1	9:86678357-86709492	NOTEST	0	0	0	0	1	1
ENSG00000270168	ENSG00000270168	LA16c-380H5.4	16:3051300-3052017	NOTEST	0.133008	0.242578	0.866929	0	1	1
ENSG00000270169	ENSG00000270169	CTC-1337H24.2	11:67229180-67229791	NOTEST	0	0	0	0	1	1
ENSG00000270171	ENSG00000270171	RP11-338N10.1	1:6845383-7829766	NOTEST	0	0	0	0	1	1
ENSG00000270173	ENSG00000270173	RP11-382B18.4	15:30649968-30650976	NOTEST	0	0.0390891	inf	0	1	1
ENSG00000270174	ENSG00000270174	RP1-256G22.2	6:5261276-5771813	NOTEST	0	0	0	0	1	1
ENSG00000270175	ENSG00000270175	RP11-793H13.11	12:53893945-53900215	NOTEST	0.467408	0.361813	-0.369437	0	1	1
ENSG00000270177	ENSG00000270177	CTD-2410N18.3	5:133450401-133706738	NOTEST	0.0909168	0.0784051	-0.213598	0	1	1
ENSG00000270178	ENSG00000270178	RP11-494H4.3	3:179512745-179754841	NOTEST	0.110036	0	#NAME?	0	1	1
ENSG00000270179	ENSG00000270179	RP11-159N11.4	11:113185250-113254266	NOTEST	0.338554	0.407459	0.267268	0	1	1
ENSG00000270182	ENSG00000270182	RP1-170O19.21	7:27197962-27198595	NOTEST	0	0.077664	inf	0	1	1
ENSG00000270184	ENSG00000270184	RP11-568J23.5	16:85805363-85840650	NOTEST	0.325838	0.38436	0.238306	0	1	1
ENSG00000270185	ENSG00000270185	IGHD1OR15-1B	15:21223128-21223145	NOTEST	0	0	0	0	1	1
ENSG00000270186	ENSG00000270186	KIR2DL1	HG1079_PATCH:55227717-55370462	NOTEST	0	0	0	0	1	1
ENSG00000270187	ENSG00000270187	IGKV1OR2-11	2:97987330-97987617	NOTEST	0	0	0	0	1	1
ENSG00000270188	ENSG00000270188	MTRNR2L11	1:238107023-238108575	NOTEST	0	0	0	0	1	1
ENSG00000270190	ENSG00000270190	RP11-803D5.4	2:111953539-112268567	NOTEST	0.126218	0.0241786	-2.38411	0	1	1
ENSG00000270191	ENSG00000270191	RP11-157B13.9	19:22469209-22499978	NOTEST	0	0	0	0	1	1
ENSG00000270192	ENSG00000270192	MRPS35P3	10:59742044-59742753	NOTEST	0	0	0	0	1	1
ENSG00000270193	ENSG00000270193	RP11-440D17.2	2:96272671-96282981	NOTEST	0	0	0	0	1	1
ENSG00000270194	ENSG00000270194	RP11-259K5.2	3:37283279-37408242	NOTEST	0.186779	0.028736	-2.7004	0	1	1
ENSG00000270195	ENSG00000270195	RP11-572O17.1	4:1714547-1715349	NOTEST	0.419781	0.300833	-0.480673	0	1	1
ENSG00000270196	ENSG00000270196	RP11-550A18.1	7:29019582-29603286	NOTEST	0	0	0	0	1	1
ENSG00000270197	ENSG00000270197	IGHVIII-44	HG1592_PATCH:106944556-106944730	NOTEST	0	0	0	0	1	1

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ENSG00000270201	ENSG00000270201	IGHVIII-67-3	HG1592_PATCH:107158993-107159225	NOTEST	0	0	0	0	1	1
ENSG00000270202	ENSG00000270202	RP11-89C3.2	11:110977783-110978474	NOTEST	0	0	0	0	1	1
ENSG00000270203	ENSG00000270203	AL928768.3	HG1592_PATCH:106170300-106170939	NOTEST	0	0	0	0	1	1
ENSG00000270204	ENSG00000270204	RP11-172C16.5	11:114388585-114389093	NOTEST	0	0	0	0	1	1
ENSG00000270206	ENSG00000270206	RP3-365I19.2	HG1287_PATCH:145601106-145781943	NOTEST	0	0	0	0	1	1
ENSG00000270207	ENSG00000270207	RP11-157E16.1	3:6532165-7783215	NOTEST	0.03238	0.105492	1.70395	0	1	1
ENSG00000270208	ENSG00000270208	IGHVIII-51-1	HG1592_PATCH:107049842-107050144	NOTEST	0	0	0	0	1	1
ENSG00000270209	ENSG00000270209	RP4-592A1.4	1:59018584-59019005	NOTEST	0	0	0	0	1	1
ENSG00000270210	ENSG00000270210	RP11-373D23.3	2:28648811-28649586	NOTEST	0	0	0	0	1	1
ENSG00000270212	ENSG00000270212	CTD-2540B15.12	19:33774883-33776645	NOTEST	0	0	0	0	1	1
ENSG00000270213	ENSG00000270213	RP11-452D24.1	6:58028200-58028363	NOTEST	0	0	0	0	1	1
ENSG00000270214	ENSG00000270214	IGHV3-16	HG1592_PATCH:106631541-106632067	NOTEST	0	0	0	0	1	1
ENSG00000270215	ENSG00000270215	IGHV3-75	HG1592_PATCH:107290023-107290484	NOTEST	0	0	0	0	1	1
ENSG00000270216	ENSG00000270216	LILRB3	HG1079_PATCH:54703995-54752257	NOTEST	0	0	0	0	1	1
ENSG00000270217	ENSG00000270217	AC009892.5	HG1079_PATCH:55076173-55142146	NOTEST	0	0	0	0	1	1
ENSG00000270218	ENSG00000270218	RP11-325L12.5	15:65294844-65321977	NOTEST	0	0	0	0	1	1
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ENSG00000270220	ENSG00000270220	KIR3DX1	HG1079_PATCH:55036044-55046986	NOTEST	0	0	0	0	1	1
ENSG00000270221	ENSG00000270221	AL901608.2	HG1592_PATCH:106178259-106178329	NOTEST	0	0	0	0	1	1
ENSG00000270222	ENSG00000270222	RP11-105C20.3	16:59689505-59690240	NOTEST	0	0	0	0	1	1
ENSG00000270223	ENSG00000270223	RP13-36G14.4	X:73164158-73513409	NOTEST	0.252641	0.305444	0.273817	0	1	1
ENSG00000270224	ENSG00000270224	AB019441.29	HG1592_PATCH:106444856-106445483	NOTEST	0	0	0	0	1	1
ENSG00000270225	ENSG00000270225	RP11-475J5.4	5:99388562-99389243	NOTEST	0	0	0	0	1	1
ENSG00000270226	ENSG00000270226	AC006548.26	22:17493293-17493822	NOTEST	0	0	0	0	1	1
ENSG00000270227	ENSG00000270227	IGHV3-36	HG1592_PATCH:106859110-106859568	NOTEST	0	0	0	0	1	1
ENSG00000270228	ENSG00000270228	RP11-453E17.3	4:68566997-68995598	NOTEST	0	0	0	0	1	1
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ENSG00000270234	ENSG00000270234	RP11-575N15.1	10:8765972-8766251	NOTEST	0	0	0	0	1	1
ENSG00000270235	ENSG00000270235	RP11-122K13.14	10:135093134-135166187	NOTEST	0	0	0	0	1	1
ENSG00000270236	ENSG00000270236	RP11-265B8.5	9:71722841-71723133	NOTEST	0	0	0	0	1	1
ENSG00000270237	ENSG00000270237	RP11-381K20.5	5:137081339-137081840	NOTEST	0.0450102	0.0350733	-0.35988	0	1	1
ENSG00000270238	ENSG00000270238	AC008746.5	HG1079_PATCH:54948066-54965270	NOTEST	0	0	0	0	1	1
ENSG00000270239	ENSG00000270239	RP11-763B22.10	1:148778319-148778606	NOTEST	0	0	0	0	1	1
ENSG00000270240	ENSG00000270240	AC015849.2	HG385_PATCH:34195985-34212882	NOTEST	0	0	0	0	1	1
ENSG00000270241	ENSG00000270241	RP4-657M3.2	1:34742459-34742893	NOTEST	0	0	0	0	1	1
ENSG00000270242	ENSG00000270242	RP11-295P22.1	Y:13551374-13552752	NOTEST	0	0	0	0	1	1
ENSG00000270243	ENSG00000270243	RP11-779O18.4	5:172212264-172212427	NOTEST	0	0	0	0	1	1

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ENSG00000270246	ENSG00000270246	SNORD109A	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000270247	ENSG00000270247	AC098784.1	HG1079_PATCH:55207205-55207489	NOTEST	0	0	0	0	1	1
ENSG00000270248	ENSG00000270248	CTC-471J1.10	19:52613570-52613979	NOTEST	0	0	0	0	1	1
ENSG00000270249	ENSG00000270249	RP11-514P8.7	7:102122891-102312088	NOTEST	0	0.137667	inf	0	1	1
ENSG00000270250	ENSG00000270250	IGHVIII-38-1	HG1592_PATCH:106884361-106884415	NOTEST	0	0	0	0	1	1
ENSG00000270251	ENSG00000270251	RP6-166C19.13	X:120120241-120120493	NOTEST	0	0	0	0	1	1
ENSG00000270252	ENSG00000270252	IGKV3OR2-5	2:98024519-98024800	NOTEST	0	0	0	0	1	1
ENSG00000270253	ENSG00000270253	RNU6-1189P	HG29_PATCH:46937810-46952748	NOTEST	0	0	0	0	1	1
ENSG00000270254	ENSG00000270254	IGHV5-78	HG1592_PATCH:107317459-107317754	NOTEST	0	0	0	0	1	1
ENSG00000270255	ENSG00000270255	RP11-420B22.2	8:18384810-18942240	NOTEST	0	0	0	0	1	1
ENSG00000270256	ENSG00000270256	RP11-175I17.6	HG1211_PATCH:46308095-46308392	NOTEST	0	0	0	0	1	1
ENSG00000270257	ENSG00000270257	RP11-17P16.2	4:68478369-68566897	NOTEST	0	0	0	0	1	1
ENSG00000270258	ENSG00000270258	DUXAP4	10:45493145-45676875	NOTEST	0	0	0	0	1	1
ENSG00000270259	ENSG00000270259	RP13-122B23.9	9:140180556-140180848	NOTEST	0	0	0	0	1	1
ENSG00000270262	ENSG00000270262	CNOT3	HG1079_PATCH:54640973-54663136	NOTEST	0	0	0	0	1	1
ENSG00000270263	ENSG00000270263	HIST2H3A	HG1287_PATCH:150539033-150540689	NOTEST	0	0	0	0	1	1
ENSG00000270264	ENSG00000270264	NDUFB8P2	17:57936850-57970304	NOTEST	0.346948	0.24183	-0.520727	0	1	1
ENSG00000270265	ENSG00000270265	RP11-731D1.4	4:152254926-152274376	NOTEST	0.0747483	0	#NAME?	0	1	1
ENSG00000270266	ENSG00000270266	RP11-521B24.3	HG1592_PATCH:105864915-105937066	NOTEST	0	0	0	0	1	1
ENSG00000270267	ENSG00000270267	AC012314.19	HG1079_PATCH:54703995-54752257	NOTEST	0	0	0	0	1	1
ENSG00000270268	ENSG00000270268	RP1-164L12.1	X:78624860-78625662	NOTEST	0	0	0	0	1	1
ENSG00000270269	ENSG00000270269	RP11-697H9.4	11:63391558-63439393	NOTEST	0	0.0332981	inf	0	1	1
ENSG00000270270	ENSG00000270270	CTC-559E9.10	19:19976694-20006656	NOTEST	0.0365887	0	#NAME?	0	1	1
ENSG00000270272	ENSG00000270272	NDUFB11	HG29_PATCH:47001650-47046248	NOTEST	0	0	0	0	1	1
ENSG00000270273	ENSG00000270273	RP11-242C24.3	12:39933382-39933653	NOTEST	0	0	0	0	1	1
ENSG00000270275	ENSG00000270275	RP11-53M11.4	8:55392156-55392523	NOTEST	0	0	0	0	1	1
ENSG00000270276	ENSG00000270276	HIST1H4A	HG1287_PATCH:150547178-150547574	NOTEST	0	0	0	0	1	1
ENSG00000270277	ENSG00000270277	RP11-65L3.2	2:179385909-179914813	NOTEST	0	0	0	0	1	1
ENSG00000270278	ENSG00000270278	RP1-290F12.3	HG1433_PATCH:52792090-52823615	NOTEST	0	0	0	0	1	1
ENSG00000270279	ENSG00000270279	RP4-806M20.5	20:57315587-57358877	NOTEST	0	0	0	0	1	1
ENSG00000270280	ENSG00000270280	RP11-265D20.1	X:42859422-42859645	NOTEST	0	0	0	0	1	1
ENSG00000270281	ENSG00000270281	CTC-523E23.10	19:35270315-35270925	NOTEST	0	0	0	0	1	1
ENSG00000270282	ENSG00000270282	RP5-1115A15.	1:8412456-8877702	NOTEST	0	0	0	0	1	1
ENSG00000270283	ENSG00000270283	RP11-731F5.1	HG1592_PATCH:106064027-106071694	NOTEST	0	0	0	0	1	1
ENSG00000270284	ENSG00000270284	IGHV3-62	HG1592_PATCH:107109478-107109922	NOTEST	0	0	0	0	1	1
ENSG00000270285	ENSG00000270285	RP11-1029M24.4	3:47892181-48130769	NOTEST	0	0	0	0	1	1
ENSG00000270287	ENSG00000270287	RP11-118H4.3	1:226599315-226599836	NOTEST	0	0	0	0	1	1
ENSG00000270288	ENSG00000270288	C14orf80	HG1592_PATCH:105952653-105965912	NOTEST	0	0	0	0	1	1

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ENSG00000270290	ENSG00000270290	GAGE12C	HG1436_HG1432_PATCH:49341609-49348937	NOTEST	0	0	0	0	1	1
ENSG00000270291	ENSG00000270291	IGHVII-65-1	HG1592_PATCH:107138133-107138381	NOTEST	0	0	0	0	1	1
ENSG00000270292	ENSG00000270292	RP11-453E17.4	4:68566997-68995598	NOTEST	0	0.0100333	inf	0	1	1
ENSG00000270293	ENSG00000270293	CTC-360J11.5	19:57661880-57662346	NOTEST	0	0	0	0	1	1
ENSG00000270294	ENSG00000270294	RP11-566F5.1	10:111440199-111440799	NOTEST	0	0	0	0	1	1
ENSG00000270295	ENSG00000270295	IGHV4-31	HG1592_PATCH:106815621-106816129	NOTEST	0	0	0	0	1	1
ENSG00000270296	ENSG00000270296	RP11-59H1.4	12:12878850-12982915	NOTEST	0	0	0	0	1	1
ENSG00000270298	ENSG00000270298	IGHV2-26	HG1592_PATCH:106767732-106768199	NOTEST	0	0	0	0	1	1
ENSG00000270299	ENSG00000270299	RP5-850E9.3	20:627258-656823	NOTEST	8.76E-05	1.88E-05	-2.2215	0	1	1
ENSG00000270301	ENSG00000270301	WI2-2334D6.1	15:29103027-29103544	NOTEST	0.0858617	0.0334471	-1.36013	0	1	1
ENSG00000270302	ENSG00000270302	RP11-461L13.4	4:153229434-153231135	NOTEST	0	0	0	0	1	1
ENSG00000270303	ENSG00000270303	RP11-1113N2.4	HSCHR5_1_CTG1:68645773-68646283	NOTEST	0	0	0	0	1	1
ENSG00000270304	ENSG00000270304	RP11-597G23.1	15:37546079-37547153	NOTEST	0	0	0	0	1	1
ENSG00000270305	ENSG00000270305	IGHV3-74	HG1592_PATCH:107276778-107277468	NOTEST	0	0	0	0	1	1
ENSG00000270306	ENSG00000270306	RP3-437C15.2	6:51250079-51250647	NOTEST	0	0	0	0	1	1
ENSG00000270307	ENSG00000270307	MTATP6P2	5:99387623-99388301	NOTEST	0	0	0	0	1	1
ENSG00000270308	ENSG00000270308	RP3-377O6.2	X:98716599-98976156	NOTEST	0	0	0	0	1	1
ENSG00000270309	ENSG00000270309	IGHVII-46-1	HG1592_PATCH:106982154-106982191	NOTEST	0	0	0	0	1	1
ENSG00000270310	ENSG00000270310	hsa-mir-4537	HG1592_PATCH:106325820-106325890	NOTEST	0	0	0	0	1	1
ENSG00000270311	ENSG00000270311	IGHD5-5	HG1592_PATCH:106378593-106378613	NOTEST	0	0	0	0	1	1
ENSG00000270313	ENSG00000270313	COX6CP16	16:85312425-85312641	NOTEST	0	0	0	0	1	1
ENSG00000270314	ENSG00000270314	GS1-165B14.2	7:7676148-8133902	NOTEST	0	0	0	0	1	1
ENSG00000270315	ENSG00000270315	IGHV3-43	HG1592_PATCH:106936600-106937137	NOTEST	0	0	0	0	1	1
ENSG00000270316	ENSG00000270316	C10orf32-ASMT	10:104613979-104661656	NOTEST	0	0.00103709	inf	0	1	1
ENSG00000270317	ENSG00000270317	AC004004.2	19:22573820-22715287	NOTEST	0	0	0	0	1	1
ENSG00000270318	ENSG00000270318	IGHV3OR16-11	16:33661362-33661819	NOTEST	0	0	0	0	1	1
ENSG00000270319	ENSG00000270319	LILRP1	HG1079_PATCH:55199857-55204159	NOTEST	0	0	0	0	1	1
ENSG00000270321	ENSG00000270321	RP11-2L8.2	3:177671853-177677586	NOTEST	0	0	0	0	1	1
ENSG00000270322	ENSG00000270322	RP11-697E2.10	15:90825079-90825263	NOTEST	0	1.24275	inf	0	1	1
ENSG00000270323	ENSG00000270323	AP000860.2	11:73351523-73352082	NOTEST	0	0	0	0	1	1
ENSG00000270324	ENSG00000270324	RP11-180P8.4	17:61055854-61056202	NOTEST	0	0	0	0	1	1
ENSG00000270325	ENSG00000270325	CTC-559E9.12	19:19967783-19968336	NOTEST	0	0	0	0	1	1
ENSG00000270326	ENSG00000270326	RP5-874C20.6	6:28287436-28287629	NOTEST	0	0	0	0	1	1
ENSG00000270328	ENSG00000270328	RP11-33E15.1	8:57688841-57689433	NOTEST	0	0	0	0	1	1
ENSG00000270330	ENSG00000270330	RP5-892F13.2	1:8002431-8002786	NOTEST	0	0	0	0	1	1
ENSG00000270332	ENSG00000270332	RP11-82L2.1	9:106842304-106855354	NOTEST	0.141023	0.315435	1.16141	0	1	1
ENSG00000270333	ENSG00000270333	RP11-566F5.2	10:111421571-111421808	NOTEST	0	0	0	0	1	1
ENSG00000270335	ENSG00000270335	RP11-642D6.1	2:62576082-62577874	NOTEST	0	0	0	0	1	1
ENSG00000270336	ENSG00000270336	RP11-521F1.1	4:168663029-168663438	NOTEST	0	0	0	0	1	1
ENSG00000270338	ENSG00000270338	VN1R104P	HG1079_PATCH:54823457-54824466	NOTEST	0	0	0	0	1	1
ENSG00000270339	ENSG00000270339	AC253578.1	HG1287_PATCH:145279282-145280067	NOTEST	0	0	0	0	1	1

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ENSG00000270341	ENSG00000270341	IGHV3-37	HG1592_PATCH:106863012-106863451	NOTEST	0	0	0	0	1	1
ENSG00000270342	ENSG00000270342	RP11-478L17.1	1:107086963-107087366	NOTEST	0	0	0	0	1	1
ENSG00000270343	ENSG00000270343	UNGP3	14:81725908-81726583	NOTEST	0	0.0208391	inf	0	1	1
ENSG00000270345	ENSG00000270345	IGHJ2P	HG1592_PATCH:106331129-106331189	NOTEST	0	0	0	0	1	1
ENSG00000270347	ENSG00000270347	CTC-339O9.2	19:54160653-54161716	NOTEST	0	0	0	0	1	1
ENSG00000270349	ENSG00000270349	RGN	HG29_PATCH:46937810-46952748	NOTEST	0	0	0	0	1	1
ENSG00000270350	ENSG00000270350	RP11-475J5.9	5:99384691-99386354	NOTEST	0	0	0	0	1	1
ENSG00000270352	ENSG00000270352	RP11-111N20.4	10:65417833-65418281	NOTEST	0	0	0	0	1	1
ENSG00000270353	ENSG00000270353	RP11-708L7.9	HG388_HG400_PATCH:111895536-111955873	NOTEST	0	0	0	0	1	1
ENSG00000270354	ENSG00000270354	RP11-547M24.1	2:64319785-64479993	NOTEST	0	0	0	0	1	1
ENSG00000270355	ENSG00000270355	IGHG3	HG1592_PATCH:106235438-106237742	NOTEST	0	0	0	0	1	1
ENSG00000270356	ENSG00000270356	IGHV1OR15-4	15:22482835-22483268	NOTEST	0	0	0	0	1	1
ENSG00000270357	ENSG00000270357	RPS20P33	HG1592_PATCH:105766899-105864484	NOTEST	0	0	0	0	1	1
ENSG00000270358	ENSG00000270358	IGHV4-61	HG1592_PATCH:107105457-107105994	NOTEST	0	0	0	0	1	1
ENSG00000270359	ENSG00000270359	RP11-2G1.3	14:48788270-48788597	NOTEST	0	0	0	0	1	1
ENSG00000270361	ENSG00000270361	RP11-307C12.13	1:154909845-154910535	NOTEST	0	0	0	0	1	1
ENSG00000270362	ENSG00000270362	HMGN3-AS1	6:79910961-79946514	NOTEST	0.284371	0.306717	0.109137	0	1	1
ENSG00000270363	ENSG00000270363	RP11-289I10.3	HG1287_PATCH:145956018-145956305	NOTEST	0	0	0	0	1	1
ENSG00000270365	ENSG00000270365	CDC42EP5	HG1079_PATCH:54968279-54976518	NOTEST	0	0	0	0	1	1
ENSG00000270366	ENSG00000270366	LILRA4	HG1079_PATCH:54836438-54842404	NOTEST	0	0	0	0	1	1
ENSG00000270367	ENSG00000270367	RP11-331G2.6	3:39327475-39329411	NOTEST	0	0	0	0	1	1
ENSG00000270369	ENSG00000270369	RP11-144G6.13	10:47174441-47174739	NOTEST	0	0	0	0	1	1
ENSG00000270370	ENSG00000270370	NLRP2	HG1079_PATCH:55426763-55504397	NOTEST	0	0	0	0	1	1
ENSG00000270371	ENSG00000270371	RP11-417P24.1	14:106251841-106252168	NOTEST	0	0	0	0	1	1
ENSG00000270372	ENSG00000270372	RP11-109M17.2	9:10948371-10948481	NOTEST	0	0	0	0	1	1
ENSG00000270373	ENSG00000270373	IGHV1-17	HG1592_PATCH:106640678-106641097	NOTEST	0	0	0	0	1	1
ENSG00000270375	ENSG00000270375	REXO1L2P	8:86839130-86840877	NOTEST	0	0	0	0	1	1
ENSG00000270376	ENSG00000270376	IGHV2-70	HG1592_PATCH:107189911-107190430	NOTEST	0	0	0	0	1	1
ENSG00000270377	ENSG00000270377	RP11-384L8.2	3:32280170-32411817	NOTEST	0	0	0	0	1	1
ENSG00000270378	ENSG00000270378	RP11-108K3.5	15:51633825-51700210	NOTEST	0	0	0	0	1	1
ENSG00000270379	ENSG00000270379	C17orf66	HG385_PATCH:34136473-34195910	NOTEST	0	0	0	0	1	1
ENSG00000270380	ENSG00000270380	RP11-470L19.5	1:110993821-110999976	NOTEST	0	0	0	0	1	1
ENSG00000270381	ENSG00000270381	RP11-290D2.5	13:45694649-45858237	NOTEST	0	0	0	0	1	1
ENSG00000270382	ENSG00000270382	RP1-152L7.9	6:52522170-52522449	NOTEST	0	0	0	0	1	1
ENSG00000270384	ENSG00000270384	RNU1-137P	HG1287_PATCH:145976420-146277520	NOTEST	0	0	0	0	1	1
ENSG00000270385	ENSG00000270385	GS1-21A4.2	16:87921624-87970135	NOTEST	0	0	0	0	1	1
ENSG00000270386	ENSG00000270386	UGT2A1	4:70454134-70518967	NOTEST	0	0	0	0	1	1
ENSG00000270387	ENSG00000270387	RP11-315D13.1	4:148653213-148993931	NOTEST	0	0.062944	inf	0	1	1
ENSG00000270388	ENSG00000270388	RP11-475J5.8	5:99386836-99387620	NOTEST	0	0	0	0	1	1
ENSG00000270390	ENSG00000270390	RP11-470B22.1	2:143635066-143799890	NOTEST	0	0	0	0	1	1
ENSG00000270392	ENSG00000270392	AC241952.1	HG1292_PATCH:120975012-120976326	NOTEST	0	0	0	0	1	1
ENSG00000270393	ENSG00000270393	AC000095.9	22:18958026-19018755	NOTEST	0	0	0	0	1	1

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ENSG00000270395	ENSG00000270395	RP11-627K11.4	12:31407294-31407379	NOTEST	0	0	0	0	1	1
ENSG00000270396	ENSG00000270396	IGHJ3	HG1592_PATCH:106330923-106330972	NOTEST	0	0	0	0	1	1
ENSG00000270397	ENSG00000270397	RP6-166C19.16	X:120086197-120086449	NOTEST	0	0	0	0	1	1
ENSG00000270398	ENSG00000270398	IGHV3-7	HG1592_PATCH:106528487-106529020	NOTEST	0	0	0	0	1	1
ENSG00000270399	ENSG00000270399	RP11-1407O15.3	17:36333638-36333776	NOTEST	0	0	0	0	1	1
ENSG00000270400	ENSG00000270400	RP11-464I4.1	13:83719674-83720038	NOTEST	0	0	0	0	1	1
ENSG00000270401	ENSG00000270401	RP11-812E19.14	16:33768121-33768558	NOTEST	0	0	0	0	1	1
ENSG00000270402	ENSG00000270402	CTC-412M14.5	19:19819773-19821274	NOTEST	0	0	0	0	1	1
ENSG00000270403	ENSG00000270403	RP11-35P15.1	11:117298488-117748201	NOTEST	0	0	0	0	1	1
ENSG00000270405	ENSG00000270405	RP11-208G20.3	7:151832009-152133090	NOTEST	0	0	0	0	1	1
ENSG00000270407	ENSG00000270407	CTC-260E6.10	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000270408	ENSG00000270408	JAG1	20:10618331-10975572	NOTEST	0	0	0	0	1	1
ENSG00000270409	ENSG00000270409	RP11-44D5.1	3:15708742-15901278	NOTEST	0	0.0175323	inf	0	1	1
ENSG00000270410	ENSG00000270410	MTA1	HG1592_PATCH:105864915-105937066	NOTEST	0	0	0	0	1	1
ENSG00000270411	ENSG00000270411	RP13-379L11.3	20:56672322-56672647	NOTEST	0	0	0	0	1	1
ENSG00000270412	ENSG00000270412	RP11-92C4.6	9:101705460-101833069	NOTEST	0.214843	0.303117	0.496588	0	1	1
ENSG00000270413	ENSG00000270413	RP11-810O3.2	X:113818550-114144624	NOTEST	0	0	0	0	1	1
ENSG00000270415	ENSG00000270415	DPPA3P3	13:81689000-81689430	NOTEST	0	0	0	0	1	1
ENSG00000270416	ENSG00000270416	REXO1L12P	8:86726453-86728113	NOTEST	0	0	0	0	1	1
ENSG00000270417	ENSG00000270417	IGHVIII-11-1	HG1592_PATCH:106586543-106586810	NOTEST	0	0	0	0	1	1
ENSG00000270418	ENSG00000270418	IGHD4-11	HG1592_PATCH:106369952-106369968	NOTEST	0	0	0	0	1	1
ENSG00000270419	ENSG00000270419	CAHM	6:163834096-163834992	NOTEST	0.255796	0.240942	-0.0863076	0	1	1
ENSG00000270420	ENSG00000270420	AC245884.1	HG1079_PATCH:54918684-54940126	NOTEST	0	0	0	0	1	1
ENSG00000270421	ENSG00000270421	RP11-351O1.4	10:64926980-65226323	NOTEST	0	0	0	0	1	1
ENSG00000270422	ENSG00000270422	AL133247.3	2:31876449-31876931	NOTEST	0	0	0	0	1	1
ENSG00000270423	ENSG00000270423	RP11-361A21.3	11:109855968-109856386	NOTEST	0	0	0	0	1	1
ENSG00000270424	ENSG00000270424	RP11-1348G14.6	16:28761279-28761916	NOTEST	0	0	0	0	1	1
ENSG00000270425	ENSG00000270425	CTA-369K23.1	7:108361051-108362045	NOTEST	0	0	0	0	1	1
ENSG00000270426	ENSG00000270426	RP11-326I11.5	4:185308866-185395734	NOTEST	0.0288561	0.0696511	1.27127	0	1	1
ENSG00000270427	ENSG00000270427	NRBF2P5	10:5807185-5884095	NOTEST	0.16055	0.124621	-0.365468	0	1	1
ENSG00000270428	ENSG00000270428	IGHVII-22-1	HG1592_PATCH:106729698-106729963	NOTEST	0	0	0	0	1	1
ENSG00000270429	ENSG00000270429	KNOP1P2	12:46123447-46301823	NOTEST	0	0.0285066	inf	0	1	1
ENSG00000270430	ENSG00000270430	RP11-42L13.3	5:29105674-29106968	NOTEST	0	0	0	0	1	1
ENSG00000270431	ENSG00000270431	RP1-241P17.7	X:114894032-114894342	NOTEST	0	0	0	0	1	1
ENSG00000270432	ENSG00000270432	OR7E108P	9:93513521-93514512	NOTEST	0	0	0	0	1	1
ENSG00000270433	ENSG00000270433	RP11-124D2.7	14:23654524-23795394	NOTEST	0.024511	0.0259169	0.0804667	0	1	1
ENSG00000270434	ENSG00000270434	RP11-175I17.6	10:46308095-46308392	NOTEST	0	0	0	0	1	1
ENSG00000270435	ENSG00000270435	RP11-304C12.4	11:6318418-6319836	NOTEST	0	0	0	0	1	1
ENSG00000270436	ENSG00000270436	IGHV3-63	HG1592_PATCH:107118573-107119018	NOTEST	0	0	0	0	1	1

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ENSG00000270439	ENSG00000270439	IGHV3-32	HG1592_PATCH:10682250-106822928	NOTEST	0	0	0	0	1	1
ENSG00000270440	ENSG00000270440	RP11-19H6.1	16:5289802-7763340	NOTEST	0	0	0	0	1	1
ENSG00000270441	ENSG00000270441	RP11-694I15.7	3:49177518-49198284	NOTEST	0	0.0264517	inf	0	1	1
ENSG00000270442	ENSG00000270442	CTB-95D12.1	5:154870895-154873158	NOTEST	0	0	0	0	1	1
ENSG00000270443	ENSG00000270443	RP1-223H12.5	1:182403027-182403596	NOTEST	0	0	0	0	1	1
ENSG00000270444	ENSG00000270444	AZU1P1	13:40430846-40431231	NOTEST	0	0	0	0	1	1
ENSG00000270445	ENSG00000270445	RP11-972P1.8	12:123926063-123926399	NOTEST	0	0	0	0	1	1
ENSG00000270446	ENSG00000270446	RP6-43L17.1	X:87061432-87061769	NOTEST	0	0	0	0	1	1
ENSG00000270447	ENSG00000270447	RP11-569H17.1	2:59444842-60327335	NOTEST	0	0	0	0	1	1
ENSG00000270449	ENSG00000270449	RP11-681H10.1	11:104553110-104553309	NOTEST	0	0	0	0	1	1
ENSG00000270450	ENSG00000270450	IGKV2OR2-7D	2:98037724-98038028	NOTEST	0	0	0	0	1	1
ENSG00000270451	ENSG00000270451	IGHD4OR15-4B	15:21216779-21216798	NOTEST	0	0	0	0	1	1
ENSG00000270452	ENSG00000270452	IGHV1-2	HG1592_PATCH:10645292-106453420	NOTEST	0	0	0	0	1	1
ENSG00000270453	ENSG00000270453	CTB-10G5.1	7:92071390-92071803	NOTEST	0	0	0	0	1	1
ENSG00000270454	ENSG00000270454	IGHD1-26	HG1592_PATCH:10634737-106347390	NOTEST	0	0	0	0	1	1
ENSG00000270455	ENSG00000270455	PABPC1P5	Y:13491302-13493369	NOTEST	0	0	0	0	1	1
ENSG00000270456	ENSG00000270456	RP6-166C19.14	X:120111459-120119642	NOTEST	0	0	0	0	1	1
ENSG00000270457	ENSG00000270457	RP11-467C18.1	1:59754974-59755312	NOTEST	0	0	0	0	1	1
ENSG00000270458	ENSG00000270458	RP11-644F5.17	12:56056120-56056285	NOTEST	0	0	0	0	1	1
ENSG00000270459	ENSG00000270459	CXorf31	HG29_PATCH:46746851-46759138	NOTEST	0	0	0	0	1	1
ENSG00000270460	ENSG00000270460	RP11-796E10.1	2:174675803-174676120	NOTEST	0	0	0	0	1	1
ENSG00000270461	ENSG00000270461	RP11-36B6.1	HG1308_PATCH:13045386-130455378	NOTEST	0	0	0	0	1	1
ENSG00000270462	ENSG00000270462	RP11-342K6.3	2:75873908-75938115	NOTEST	0	0.134795	inf	0	1	1
ENSG00000270463	ENSG00000270463	IGHVII-51-2	HG1592_PATCH:107051054-107051313	NOTEST	0	0	0	0	1	1
ENSG00000270464	ENSG00000270464	IGHA2	HG1592_PATCH:106053225-106054732	NOTEST	0	0	0	0	1	1
ENSG00000270465	ENSG00000270465	IGHVII-40-1	HG1592_PATCH:106907286-106907344	NOTEST	0	0	0	0	1	1
ENSG00000270466	ENSG00000270466	1-Sep	16:30389426-30411429	NOTEST	0	0.00414282	inf	0	1	1
ENSG00000270467	ENSG00000270467	IGHV3OR16-12	16:33605230-33605684	NOTEST	0	0	0	0	1	1
ENSG00000270468	ENSG00000270468	IGHVII-31-1	HG1592_PATCH:106821008-106821045	NOTEST	0	0	0	0	1	1
ENSG00000270469	ENSG00000270469	RP11-411B10.8	18:14053949-14054760	NOTEST	0.0425281	0.0163797	-1.37651	0	1	1
ENSG00000270470	ENSG00000270470	RP11-601H16.1	2:78664975-78666047	NOTEST	0	0	0	0	1	1
ENSG00000270471	ENSG00000270471	AC010492.4	HG1079_PATCH:54703995-54752257	NOTEST	0	0	0	0	1	1
ENSG00000270472	ENSG00000270472	IGHV3OR16-9	16:32019758-32096106	NOTEST	0	0	0	0	1	1
ENSG00000270473	ENSG00000270473	IGHD1-20	HG1592_PATCH:106356420-106362914	NOTEST	0	0	0	0	1	1
ENSG00000270474	ENSG00000270474	IGHV3-29	HG1592_PATCH:106797452-106797889	NOTEST	0	0	0	0	1	1
ENSG00000270475	ENSG00000270475	CTC-451A6.5	19:22817125-22899793	NOTEST	0	0	0	0	1	1
ENSG00000270476	ENSG00000270476	IGHVIII-47-1	HG1592_PATCH:106997477-106997808	NOTEST	0	0	0	0	1	1
ENSG00000270477	ENSG00000270477	RP1-72E17.2	6:3694156-3694309	NOTEST	0	0	0	0	1	1
ENSG00000270478	ENSG00000270478	AP2B1	HG385_PATCH:33905064-34053436	NOTEST	0	0	0	0	1	1
ENSG00000270479	ENSG00000270479	RP11-369G6.3	19:23258002-23330021	NOTEST	0	0	0	0	1	1
ENSG00000270480	ENSG00000270480	RP11-57B24.1	4:83550691-83720010	NOTEST	0.128077	0.0996955	-0.361406	0	1	1
ENSG00000270481	ENSG00000270481	KIR3DP1	HG1079_PATCH:55227717-55370462	NOTEST	0	0	0	0	1	1
ENSG00000270482	ENSG00000270482	RP11-131L12.2	12:118813154-118814080	NOTEST	0	0.0239011	inf	0	1	1

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ENSG00000270484	ENSG00000270484	RP3-399J4.4	6:95151747-95153527	NOTEST	0	0	0	0	1	1
ENSG00000270487	ENSG00000270487	RP11-230C9.3	6:157099062-157531913	NOTEST	0	0	0	0	1	1
ENSG00000270488	ENSG00000270488	RP11-245G13.1	2:11014416-11014693	NOTEST	0	0	0	0	1	1
ENSG00000270489	ENSG00000270489	IGHV3-65	HG1592_PATCH:107132428-107132869	NOTEST	0	0	0	0	1	1
ENSG00000270490	ENSG00000270490	RP11-622C24.1	15:67100741-67102898	NOTEST	0	0.00525347	inf	0	1	1
ENSG00000270491	ENSG00000270491	RP4-743O11.1	11:34764452-34764746	NOTEST	0	0	0	0	1	1
ENSG00000270492	ENSG00000270492	RP13-685P2.8	3:129053428-129053917	NOTEST	0	0	0	0	1	1
ENSG00000270493	ENSG00000270493	RP6-166C19.22	X:120071615-120071869	NOTEST	0	0	0	0	1	1
ENSG00000270494	ENSG00000270494	RP11-119F7.6	10:70477067-70477552	NOTEST	0	0	0	0	1	1
ENSG00000270495	ENSG00000270495	CTD-2134P3.2	5:28782784-28809362	NOTEST	0.0499129	0	#NAME?	0	1	1
ENSG00000270496	ENSG00000270496	BNIP3P7	13:19066043-19066559	NOTEST	0	0	0	0	1	1
ENSG00000270497	ENSG00000270497	RP1-290F12.3	X:53078272-53109797	NOTEST	0	0	0	0	1	1
ENSG00000270498	ENSG00000270498	IGHG4	HG1592_PATCH:106090686-106092403	NOTEST	0	0	0	0	1	1
ENSG00000270499	ENSG00000270499	MKI67P1	X:46420362-46422184	NOTEST	0	0	0	0	1	1
ENSG00000270500	ENSG00000270500	COX6CP4	15:36864185-36864413	NOTEST	0	0	0	0	1	1
ENSG00000270501	ENSG00000270501	LILRA2	HG1079_PATCH:55076173-55142146	NOTEST	0	0	0	0	1	1
ENSG00000270502	ENSG00000270502	TSEN34	HG1079_PATCH:54693191-54696984	NOTEST	0	0	0	0	1	1
ENSG00000270503	ENSG00000270503	RP11-407N17.6	14:39684268-39685539	NOTEST	0	0	0	0	1	1
ENSG00000270505	ENSG00000270505	IGHV1OR15-1	15:22448381-22448819	NOTEST	0	0	0	0	1	1
ENSG00000270506	ENSG00000270506	RP11-511B23.4	12:93392993-93609455	NOTEST	0	0	0	0	1	1
ENSG00000270507	ENSG00000270507	CTA-21C21.1	1:88778835-88778985	NOTEST	0	0	0	0	1	1
ENSG00000270509	ENSG00000270509	RP11-301G19.2	6:68643376-68644574	NOTEST	0	0	0	0	1	1
ENSG00000270510	ENSG00000270510	RP11-777F6.3	11:86748885-87035401	NOTEST	0.145047	0.164831	0.184474	0	1	1
ENSG00000270512	ENSG00000270512	RP5-1136G2.1	7:139982264-139982720	NOTEST	0	0	0	0	1	1
ENSG00000270513	ENSG00000270513	RP11-116B13.1	5:42729239-42729621	NOTEST	0	0.0548517	inf	0	1	1
ENSG00000270515	ENSG00000270515	RP11-2E11.8	HG1308_PATCH:130126045-130351086	NOTEST	0	0	0	0	1	1
ENSG00000270516	ENSG00000270516	RP11-500M10.1	7:118818230-118819203	NOTEST	0	0	0	0	1	1
ENSG00000270517	ENSG00000270517	RDM1	HG385_PATCH:34245084-34257792	NOTEST	0	0	0	0	1	1
ENSG00000270518	ENSG00000270518	RP11-210K20.3	18:29409135-29533099	NOTEST	0	0	0	0	1	1
ENSG00000270519	ENSG00000270519	AC241585.2	HG1287_PATCH:145818576-145818668	NOTEST	0	0	0	0	1	1
ENSG00000270521	ENSG00000270521	RP11-24C14.1	6:67420134-67420720	NOTEST	0	0	0	0	1	1
ENSG00000270522	ENSG00000270522	RP11-168P13.1	13:44361726-44361988	NOTEST	0	0	0	0	1	1
ENSG00000270523	ENSG00000270523	RP11-145P16.3	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000270524	ENSG00000270524	QTRT1P1	X:112859586-113181506	NOTEST	0	0	0	0	1	1
ENSG00000270526	ENSG00000270526	SNRPGP19	11:65281873-65282394	NOTEST	0	0	0	0	1	1
ENSG00000270528	ENSG00000270528	RP11-674I16.2	2:27994583-28561768	NOTEST	0.0510568	0	#NAME?	0	1	1
ENSG00000270529	ENSG00000270529	IGHV3-42	HG1592_PATCH:106929594-106929895	NOTEST	0	0	0	0	1	1
ENSG00000270530	ENSG00000270530	IGHV1-68	HG1592_PATCH:107170188-107170483	NOTEST	0	0	0	0	1	1
ENSG00000270531	ENSG00000270531	RP11-169K17.2	3:11313994-11766453	NOTEST	0	0	0	0	1	1
ENSG00000270532	ENSG00000270532	PEBP1P2	2:85568403-85568961	NOTEST	0.0767695	0.029894	-1.36068	0	1	1

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ENSG00000270534	ENSG00000270534	AC011515.2	HG1079_PATCH:55174484-55175845	NOTEST	0	0	0	0	1	1
ENSG00000270535	ENSG00000270535	TCEB1P34	Y:27809046-27809373	NOTEST	0	0	0	0	1	1
ENSG00000270536	ENSG00000270536	CTC-575C13.2	HG730_PATCH:20434800-20435377	NOTEST	0	0	0	0	1	1
ENSG00000270537	ENSG00000270537	AC242842.1	HG1287_PATCH:150270237-150271022	NOTEST	0	0	0	0	1	1
ENSG00000270538	ENSG00000270538	RP11-3B7.7	3:49235860-49295537	NOTEST	0	0	0	0	1	1
ENSG00000270540	ENSG00000270540	RP11-785G17.1	2:237232793-237416185	NOTEST	0	0	0	0	1	1
ENSG00000270541	ENSG00000270541	RP11-478B11.2	10:57506310-57506668	NOTEST	0	0	0	0	1	1
ENSG00000270542	ENSG00000270542	RP11-311H10.7	9:33449752-33449939	NOTEST	0	0	0	0	1	1
ENSG00000270544	ENSG00000270544	CTC-523E23.14	19:35393105-35395099	NOTEST	0	0	0	0	1	1
ENSG00000270545	ENSG00000270545	ATP5G1P1	HG1592_PATCH:106003197-106003576	NOTEST	0	0	0	0	1	1
ENSG00000270547	ENSG00000270547	RP11-536O18.2	9:13406378-13433052	NOTEST	0	0	0	0	1	1
ENSG00000270549	ENSG00000270549	RP11-293K19.1	1:62920398-63153969	NOTEST	0	0	0	0	1	1
ENSG00000270550	ENSG00000270550	IGHV3-30	HG1592_PATCH:106801418-106801950	NOTEST	0	0	0	0	1	1
ENSG00000270551	ENSG00000270551	IGHV3-76	HG1592_PATCH:107294205-107294500	NOTEST	0	0	0	0	1	1
ENSG00000270552	ENSG00000270552	DUXAP3	10:43242991-43244135	NOTEST	0	0	0	0	1	1
ENSG00000270553	ENSG00000270553	RP11-15E18.5	17:58520519-58603580	NOTEST	0	0.116683	inf	0	1	1
ENSG00000270554	ENSG00000270554	RP11-225N10.3	3:182511287-182639726	NOTEST	0	0	0	0	1	1
ENSG00000270555	ENSG00000270555	RP11-1394O16.1	7:72023728-72298777	NOTEST	0	0	0	0	1	1
ENSG00000270558	ENSG00000270558	CTD-2124B8.2	5:37286550-37287079	NOTEST	0.569163	0.53022	-0.102251	0	1	1
ENSG00000270559	ENSG00000270559	HOMER2P1	HG1592_PATCH:106926428-106927392	NOTEST	0	0	0	0	1	1
ENSG00000270560	ENSG00000270560	APOOP1	5:156346292-156390266	NOTEST	0	0	0	0	1	1
ENSG00000270561	ENSG00000270561	COPG2IT1	HG1308_PATCH:130126045-130351086	NOTEST	0	0	0	0	1	1
ENSG00000270562	ENSG00000270562	RP11-154H23.3	3:71634093-71636560	NOTEST	0.00646817	0.00454278	-0.509782	0	1	1
ENSG00000270564	ENSG00000270564	IGHJ4	HG1592_PATCH:106330551-106330597	NOTEST	0	0	0	0	1	1
ENSG00000270565	ENSG00000270565	IGHV3-33	HG1592_PATCH:106826129-106826661	NOTEST	0	0	0	0	1	1
ENSG00000270566	ENSG00000270566	IGHV3-19	HG1592_PATCH:106663036-106663327	NOTEST	0	0	0	0	1	1
ENSG00000270568	ENSG00000270568	RP11-592B15.8	10:51211724-51212022	NOTEST	0	0	0	0	1	1
ENSG00000270569	ENSG00000270569	RP11-127H13.1	2:57656682-57657828	NOTEST	0	0	0	0	1	1
ENSG00000270570	ENSG00000270570	RP1-85D24.1	Y:13263394-13263563	NOTEST	0	0	0	0	1	1
ENSG00000270571	ENSG00000270571	RP11-355F16.1	2:75273589-75426826	NOTEST	0.0873926	0.0924576	0.0812812	0	1	1
ENSG00000270572	ENSG00000270572	IGHV3-47	HG1592_PATCH:106984918-106985364	NOTEST	0	0	0	0	1	1
ENSG00000270574	ENSG00000270574	RP11-171I2.2	2:179385909-179914813	NOTEST	0.00521508	0	#NAME?	0	1	1
ENSG00000270575	ENSG00000270575	RP11-21M7.2	1:178060642-178448644	NOTEST	0	0	0	0	1	1
ENSG00000270576	ENSG00000270576	RP5-1021I20.7	14:74307222-74307312	NOTEST	0	0	0	0	1	1
ENSG00000270577	ENSG00000270577	RP5-1147A1.1	7:40155283-40155542	NOTEST	0	0	0	0	1	1
ENSG00000270578	ENSG00000270578	RP11-712B9.5	11:94878600-94879168	NOTEST	0.069325	0.201734	1.54101	0	1	1
ENSG00000270581	ENSG00000270581	RP11-811P12.3	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000270582	ENSG00000270582	RNU1-129P	HG1287_PATCH:148700831-148700998	NOTEST	0	0	0	0	1	1
ENSG00000270583	ENSG00000270583	RP11-471G13.5	X:94975241-94976143	NOTEST	0	0	0	0	1	1

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ENSG00000270585	ENSG00000270585	RP11-568G11.4	1:220321634-220445796	NOTEST	0.251679	0.273745	0.121249	0	1	1
ENSG00000270587	ENSG00000270587	RP11-51F16.9	17:61688131-61688544	NOTEST	0.299617	0.399561	0.415295	0	1	1
ENSG00000270588	ENSG00000270588	RP11-810F22.1	11:39895331-39895938	NOTEST	0	0	0	0	1	1
ENSG00000270589	ENSG00000270589	RP11-348N5.7	10:112629500-112679032	NOTEST	0.234387	0.102915	-1.18743	0	1	1
ENSG00000270591	ENSG00000270591	RP11-73M18.11	14:104200088-104313927	NOTEST	0	0	0	0	1	1
ENSG00000270592	ENSG00000270592	AC010492.2	HG1079_PATCH:54703995-54752257	NOTEST	0	0	0	0	1	1
ENSG00000270593	ENSG00000270593	RP11-455J15.1	7:16889580-16890349	NOTEST	0	0	0	0	1	1
ENSG00000270594	ENSG00000270594	CTC-550B14.7	HG1079_PATCH:55509447-55574546	NOTEST	0	0	0	0	1	1
ENSG00000270595	ENSG00000270595	CTD-2587H19.3	HG1079_PATCH:54941263-54941600	NOTEST	0	0	0	0	1	1
ENSG00000270596	ENSG00000270596	IGHV3-25	HG1592_PATCH:106755365-106755816	NOTEST	0	0	0	0	1	1
ENSG00000270597	ENSG00000270597	IGHV3-48	HG1592_PATCH:107004148-107004681	NOTEST	0	0	0	0	1	1
ENSG00000270598	ENSG00000270598	RP11-396C23.3	1:226314878-226315047	NOTEST	0	0	0	0	1	1
ENSG00000270599	ENSG00000270599	RP11-324O2.6	10:114133775-114188138	NOTEST	0	0	0	0	1	1
ENSG00000270600	ENSG00000270600	IGHVIII-5-1	HG1592_PATCH:106506002-106506101	NOTEST	0	0	0	0	1	1
ENSG00000270601	ENSG00000270601	PRAMEF23	1:12998180-13117751	NOTEST	0	0	0	0	1	1
ENSG00000270603	ENSG00000270603	RP11-344N17.15	HG1436_HG1432_PATCH:48196297-48196568	NOTEST	0	0	0	0	1	1
ENSG00000270604	ENSG00000270604	HCG17	6:30201815-30314661	NOTEST	0	0	0	0	1	1
ENSG00000270605	ENSG00000270605	RP5-1092A3.4	1:28562619-28573417	NOTEST	0.126062	0.111341	-0.179149	0	1	1
ENSG00000270606	ENSG00000270606	RP11-713H12.2	17:8316448-8534079	NOTEST	0	0	0	0	1	1
ENSG00000270608	ENSG00000270608	IGHD1-7	HG1592_PATCH:106376243-106376260	NOTEST	0	0	0	0	1	1
ENSG00000270609	ENSG00000270609	IGHV3-6	HG1592_PATCH:106521885-106522335	NOTEST	0	0	0	0	1	1
ENSG00000270610	ENSG00000270610	RP11-486O13.3	14:70701211-70701812	NOTEST	0	0	0	0	1	1
ENSG00000270611	ENSG00000270611	GS1-69O6.1	7:9890552-9891015	NOTEST	0	0	0	0	1	1
ENSG00000270612	ENSG00000270612	RP11-34P1.4	5:159678658-159772403	NOTEST	0	0	0	0	1	1
ENSG00000270613	ENSG00000270613	IGHVII-44-2	HG1592_PATCH:106955102-106961852	NOTEST	0	0	0	0	1	1
ENSG00000270614	ENSG00000270614	CTC-325H20.7	19:9434447-9493293	NOTEST	0.0643233	0	#NAME?	0	1	1
ENSG00000270615	ENSG00000270615	RP11-379C1.1	1:70034080-70671303	NOTEST	0	0	0	0	1	1
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ENSG00000270617	ENSG00000270617	URGCP-MRPS24	7:43906156-43966010	NOTEST	0.0894768	0	#NAME?	0	1	1
ENSG00000270618	ENSG00000270618	RP11-388E23.4	14:24236870-24238207	NOTEST	0	0	0	0	1	1
ENSG00000270619	ENSG00000270619	RP11-197B12.1	X:117412121-117417330	NOTEST	0	0	0	0	1	1
ENSG00000270620	ENSG00000270620	RP1-134O19.3	1:16160559-16266955	NOTEST	0	0	0	0	1	1
ENSG00000270622	ENSG00000270622	IGHD6-19	HG1592_PATCH:106356420-106362914	NOTEST	0	0	0	0	1	1
ENSG00000270623	ENSG00000270623	RP11-316M21.9	10:101902821-101903752	NOTEST	0	0	0	0	1	1
ENSG00000270624	ENSG00000270624	LOC401913	19:35357255-35357823	NOTEST	0	0	0	0	1	1
ENSG00000270625	ENSG00000270625	RP4-555N2.4	X:118356526-118357208	NOTEST	0	0	0	0	1	1
ENSG00000270626	ENSG00000270626	AC239798.1	HG1287_PATCH:144515181-144515273	NOTEST	0	0	0	0	1	1
ENSG00000270627	ENSG00000270627	RP11-216F5.1	9:81204073-81204455	NOTEST	0	0	0	0	1	1
ENSG00000270628	ENSG00000270628	RP11-26F2.2	15:23116382-23116940	NOTEST	0	0	0	0	1	1

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ENSG00000270630	ENSG00000270630	CTD-2587H19.2	HG1079_PATCH:54918684-54940126	NOTEST	0	0	0	0	1	1
ENSG00000270631	ENSG00000270631	RP11-710N8.3	1:116119849-116120407	NOTEST	0	0	0	0	1	1
ENSG00000270632	ENSG00000270632	RP11-340C20.3	13:100741268-101182686	NOTEST	0	0	0	0	1	1
ENSG00000270633	ENSG00000270633	CDK16	HG29_PATCH:47077294-47089432	NOTEST	0	0	0	0	1	1
ENSG00000270634	ENSG00000270634	RP4-777G9.1	7:145813452-148118090	NOTEST	0	0	0	0	1	1
ENSG00000270635	ENSG00000270635	IGHV3-35	HG1592_PATCH:106855728-106856195	NOTEST	0	0	0	0	1	1
ENSG00000270636	ENSG00000270636	IGHVIII-2-1	HG1592_PATCH:106467870-106468161	NOTEST	0	0	0	0	1	1
ENSG00000270638	ENSG00000270638	RP3-466P17.1	6:145822718-146058354	NOTEST	0.0182276	0.0226853	0.315629	0	1	1
ENSG00000270639	ENSG00000270639	RP11-307I14.4	9:4768616-4769895	NOTEST	0	0	0	0	1	1
ENSG00000270640	ENSG00000270640	RP11-373D23.2	2:28607275-28640179	NOTEST	0.116693	0.0914633	-0.351455	0	1	1
ENSG00000270641	ENSG00000270641	TSIX	X:73012039-73072588	NOTEST	0	7.62E-09	inf	0	1	1
ENSG00000270642	ENSG00000270642	IGHV3-21	HG1592_PATCH:106701400-106701931	NOTEST	0	0	0	0	1	1
ENSG00000270643	ENSG00000270643	IGHD4-17	HG1592_PATCH:106356420-106362914	NOTEST	0	0	0	0	1	1
ENSG00000270644	ENSG00000270644	IGHV1-45	HG1592_PATCH:106973334-106973828	NOTEST	0	0	0	0	1	1
ENSG00000270645	ENSG00000270645	KIR2DP1	HG1079_PATCH:55227717-55370462	NOTEST	0	0	0	0	1	1
ENSG00000270646	ENSG00000270646	RP6-166C19.15	X:120110521-120110773	NOTEST	0	0	0	0	1	1
ENSG00000270647	ENSG00000270647	TAF15	HG385_PATCH:34136473-34195910	NOTEST	0	0	0	0	1	1
ENSG00000270648	ENSG00000270648	CYP2C61P	10:66522639-66522929	NOTEST	0	0	0	0	1	1
ENSG00000270649	ENSG00000270649	IGHVIII-26-1	HG1592_PATCH:106775753-106776003	NOTEST	0	0	0	0	1	1
ENSG00000270650	ENSG00000270650	AC245389.1	HG1287_PATCH:149435201-149436370	NOTEST	0	0	0	0	1	1
ENSG00000270651	ENSG00000270651	RP11-731F5.2	HG1592_PATCH:106109388-106115394	NOTEST	0	0	0	0	1	1
ENSG00000270652	ENSG00000270652	DPRXP5	21:38123188-38362536	NOTEST	0	0	0	0	1	1
ENSG00000270654	ENSG00000270654	RP11-531P14.1	2:21444046-22753977	NOTEST	0	0	0	0	1	1
ENSG00000270655	ENSG00000270655	RP1-20N2.7	6:143707717-143708546	NOTEST	0	0	0	0	1	1
ENSG00000270656	ENSG00000270656	RP3-328E19.5	1:147983306-147983593	NOTEST	0	0	0	0	1	1
ENSG00000270659	ENSG00000270659	RP11-105N14.1	2:214017693-214018383	NOTEST	0.028621	0.0202316	-0.500468	0	1	1
ENSG00000270661	ENSG00000270661	RP1-142L7.9	6:112429962-112672498	NOTEST	0	0	0	0	1	1
ENSG00000270662	ENSG00000270662	IGHJ5	HG1592_PATCH:106330150-106330199	NOTEST	0	0	0	0	1	1
ENSG00000270663	ENSG00000270663	RP1-142L7.8	HG1304_PATCH:112430062-112671296	NOTEST	0	0	0	0	1	1
ENSG00000270664	ENSG00000270664	RP11-544H14.1	2:203739504-203879521	NOTEST	0	0	0	0	1	1
ENSG00000270665	ENSG00000270665	HNRNPA1P67	4:73672983-73673909	NOTEST	0	0	0	0	1	1
ENSG00000270666	ENSG00000270666	XXbac-BPGBPG34I8.1	6:27482817-27483053	NOTEST	0	0	0	0	1	1
ENSG00000270668	ENSG00000270668	IGHV4-59	HG1592_PATCH:107092128-107094162	NOTEST	0	0	0	0	1	1
ENSG00000270669	ENSG00000270669	CTB-179I1.3	4:78078303-78415440	NOTEST	0	0	0	0	1	1
ENSG00000270670	ENSG00000270670	RP11-248C1.3	10:91589266-91600618	NOTEST	0	0	0	0	1	1
ENSG00000270671	ENSG00000270671	AC245884.2	HG1079_PATCH:54856879-54868368	NOTEST	0	0	0	0	1	1
ENSG00000270672	ENSG00000270672	MTRNR2L6	7:142374103-142375550	NOTEST	0	0	0	0	1	1
ENSG00000270675	ENSG00000270675	AC092118.1	HG1208_PATCH:57792128-57896965	NOTEST	0	0	0	0	1	1
ENSG00000270676	ENSG00000270676	IGHV3-13	HG1592_PATCH:106595878-106596409	NOTEST	0	0	0	0	1	1
ENSG00000270677	ENSG00000270677	RP11-294L11.1	2:36883464-36884084	NOTEST	0	0	0	0	1	1
ENSG00000270678	ENSG00000270678	RP6-166C19.21	X:120066754-120067006	NOTEST	0	0	0	0	1	1

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ENSG00000270680	ENSG00000270680	RP11-351N4.4	13:29598747-30077892	NOTEST	0	0	0	0	1	1
ENSG00000270681	ENSG00000270681	RP11-372K14.2	4:152020724-152246784	NOTEST	0.133523	0.202194	0.598655	0	1	1
ENSG00000270682	ENSG00000270682	KB-1907C4.2	8:98787284-98865241	NOTEST	0	0	0	0	1	1
ENSG00000270683	ENSG00000270683	RP11-477G9.1	9:25937909-25938432	NOTEST	0	0	0	0	1	1
ENSG00000270684	ENSG00000270684	IGHV3-60	HG1592_PATCH:107097533-107097990	NOTEST	0	0	0	0	1	1
ENSG00000270685	ENSG00000270685	IGHV1OR15-6	15:20844767-20845194	NOTEST	0	0	0	0	1	1
ENSG00000270686	ENSG00000270686	IGHD1-14	HG1592_PATCH:106366974-106366991	NOTEST	0	0	0	0	1	1
ENSG00000270687	ENSG00000270687	AC009892.2	HG1079_PATCH:55055223-55055510	NOTEST	0	0	0	0	1	1
ENSG00000270688	ENSG00000270688	RP11-507D14.4	9:88835179-88874572	NOTEST	0	0	0	0	1	1
ENSG00000270689	ENSG00000270689	RP11-712B9.4	11:94876800-94878289	NOTEST	0.0225367	0.104392	2.21166	0	1	1
ENSG00000270690	ENSG00000270690	RP11-349G13.3	15:65734800-65810042	NOTEST	0	0	0	0	1	1
ENSG00000270691	ENSG00000270691	RP11-403N16.5	9:82465785-82466413	NOTEST	0	0	0	0	1	1
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ENSG00000270693	ENSG00000270693	IGHVIII-76-1	HG1592_PATCH:107298103-107298389	NOTEST	0	0	0	0	1	1
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ENSG00000270695	ENSG00000270695	RP1-21P18.1	6:4529955-4530242	NOTEST	0	0	0	0	1	1
ENSG00000270697	ENSG00000270697	RP11-381K20.4	5:137097234-137097625	NOTEST	0.127707	0	#NAME?	0	1	1
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ENSG00000270701	ENSG00000270701	RP11-876F14.2	11:81553476-81553711	NOTEST	0	0	0	0	1	1
ENSG00000270702	ENSG00000270702	RP11-107F6.4	15:41913421-42062141	NOTEST	0	0	0	0	1	1
ENSG00000270703	ENSG00000270703	IGHV6-1	HG1592_PATCH:106406092-106406590	NOTEST	0	0	0	0	1	1
ENSG00000270704	ENSG00000270704	SNORD64	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000270705	ENSG00000270705	RP11-736N17.9	14:103674084-103674126	NOTEST	0	0	0	0	1	1
ENSG00000270706	ENSG00000270706	CTD-2301A4.5	5:176560025-176727216	NOTEST	0.0177239	0.0653128	1.88167	0	1	1
ENSG00000270707	ENSG00000270707	ELK2BP	HG1592_PATCH:106012946-106016031	NOTEST	0	0	0	0	1	1
ENSG00000270708	ENSG00000270708	RP11-568G11.5	1:220321634-220445796	NOTEST	0	0	0	0	1	1
ENSG00000270709	ENSG00000270709	GS1-115M3.4	X:144849612-144849860	NOTEST	0	0	0	0	1	1
ENSG00000270710	ENSG00000270710	RP11-293G6__B.8	1:235710986-235814054	NOTEST	0.0508675	0	#NAME?	0	1	1
ENSG00000270711	ENSG00000270711	RP11-46A10.8	1:180882289-180992047	NOTEST	0.302142	0.0441229	-2.77563	0	1	1
ENSG00000270712	ENSG00000270712	RP11-378I6.2	9:19957391-19958145	NOTEST	0	0	0	0	1	1
ENSG00000270713	ENSG00000270713	RP11-506K19.2	14:39442602-39443289	NOTEST	0	0	0	0	1	1
ENSG00000270714	ENSG00000270714	MINOS1P2	17:62743381-62743610	NOTEST	0	0	0	0	1	1
ENSG00000270715	ENSG00000270715	IGHEP1	HG1592_PATCH:106185954-106188864	NOTEST	0	0	0	0	1	1
ENSG00000270716	ENSG00000270716	CTC-260E6.11	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000270717	ENSG00000270717	IGHVII-74-1	HG1592_PATCH:107287510-107287751	NOTEST	0	0	0	0	1	1
ENSG00000270718	ENSG00000270718	RP11-421H10.2	12:39564447-39564682	NOTEST	0	0	0	0	1	1
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ENSG00000270722	ENSG00000270722	RNVU1-7	HG1287_PATCH:145976420-146277520	NOTEST	0	0	0	0	1	1
ENSG00000270723	ENSG00000270723	RP11-401N16.1	2:70056773-70108528	NOTEST	0	0.121717	inf	0	1	1
ENSG00000270724	ENSG00000270724	IGHV3-73	HG1592_PATCH:107269030-107269570	NOTEST	0	0	0	0	1	1
ENSG00000270725	ENSG00000270725	RP11-383H17.4	13:98591609-98605793	NOTEST	0	0	0	0	1	1
ENSG00000270726	ENSG00000270726	AJ271736.10	X:155227245-155257848	NOTEST	0.357135	0	#NAME?	0	1	1
ENSG00000270727	ENSG00000270727	RP11-51E20.1	10:20836099-20836351	NOTEST	0	0	0	0	1	1
ENSG00000270729	ENSG00000270729	RP4-669B10.6	7:143651936-143694405	NOTEST	0	0	0	0	1	1
ENSG00000270733	ENSG00000270733	RP11-231P20.5	1:26560690-26605299	NOTEST	0	0.0618562	inf	0	1	1
ENSG00000270734	ENSG00000270734	RP11-719K4.7	16:14927537-14990017	NOTEST	0	0	0	0	1	1
ENSG00000270736	ENSG00000270736	RP6-166C19.19	X:120100801-120101053	NOTEST	0	0	0	0	1	1
ENSG00000270737	ENSG00000270737	ELK2AP	HG1592_PATCH:106138644-106139651	NOTEST	0	0	0	0	1	1
ENSG00000270738	ENSG00000270738	PFN1P4	HG1287_PATCH:148788460-148838605	NOTEST	0	0	0	0	1	1
ENSG00000270739	ENSG00000270739	RP11-608O8.2	3:16306705-16555533	NOTEST	0	0	0	0	1	1
ENSG00000270741	ENSG00000270741	RP11-565F4.1	5:119799972-120023027	NOTEST	0	0	0	0	1	1
ENSG00000270742	ENSG00000270742	RP4-802A10.1	1:61330930-61928465	NOTEST	0	0	0	0	1	1
ENSG00000270745	ENSG00000270745	RP13-324D24.1	X:88237215-88237354	NOTEST	0	0	0	0	1	1
ENSG00000270746	ENSG00000270746	RP4-725K1.1	HG1287_PATCH:149482211-149482740	NOTEST	0	0	0	0	1	1
ENSG00000270747	ENSG00000270747	RP11-344N17.15	X:48196333-48196604	NOTEST	0	0	0	0	1	1
ENSG00000270748	ENSG00000270748	IGKV2OR2-1	2:97712324-97712628	NOTEST	0	0	0	0	1	1
ENSG00000270749	ENSG00000270749	RP11-368M16.10	7:57688184-57704895	NOTEST	0	0	0	0	1	1
ENSG00000270750	ENSG00000270750	RP11-461L13.3	4:153241695-153242196	NOTEST	0.180041	0.102117	-0.818096	0	1	1
ENSG00000270751	ENSG00000270751	RP11-461L13.2	4:153242409-153457253	NOTEST	0	0	0	0	1	1
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ENSG00000270753	ENSG00000270753	RP11-693I21.1	11:96957159-96957682	NOTEST	0	0	0	0	1	1
ENSG00000270754	ENSG00000270754	NEK4P3	10:66814217-66814761	NOTEST	0	0	0	0	1	1
ENSG00000270755	ENSG00000270755	RP11-138E2.1	9:132806991-132807360	NOTEST	0	0	0	0	1	1
ENSG00000270756	ENSG00000270756	LILRB1	HG1079_PATCH:55076173-55142146	NOTEST	0	0	0	0	1	1
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ENSG00000270759	ENSG00000270759	CTD-2324A24.2	X:39650833-39651158	NOTEST	0	0	0	0	1	1
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ENSG00000270761	ENSG00000270761	RP11-385F7.1	6:47444978-47445308	NOTEST	0.456686	0.493669	0.112344	0	1	1
ENSG00000270762	ENSG00000270762	FXYD6P1	10:43050887-43051172	NOTEST	0	0	0	0	1	1
ENSG00000270763	ENSG00000270763	RP11-122G11.1	7:49298088-49299442	NOTEST	0	0	0	0	1	1
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ENSG00000270766	ENSG00000270766	RP11-627K11.5	12:31397373-31397619	NOTEST	0	0	0	0	1	1
ENSG00000270767	ENSG00000270767	RP11-733D4.2	10:44983782-44983893	NOTEST	0	0	0	0	1	1
ENSG00000270771	ENSG00000270771	RP6-166C19.12	X:120105661-120105913	NOTEST	0	0	0	0	1	1
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ENSG00000270776	ENSG00000270776	RP11-17G11.1	2:153191750-153506348	NOTEST	0	0	0	0	1	1
ENSG00000270777	ENSG00000270777	RP11-103J8.2	20:10981951-10982411	NOTEST	0	0	0	0	1	1
ENSG00000270778	ENSG00000270778	BUB1P1	10:129666144-129666751	NOTEST	0	0	0	0	1	1
ENSG00000270779	ENSG00000270779	CTD-2026D23.1	5:110243982-110244412	NOTEST	0	0	0	0	1	1
ENSG00000270780	ENSG00000270780	RP4-590F24.1	1:114544054-114544857	NOTEST	0	0	0	0	1	1
ENSG00000270781	ENSG00000270781	RP11-501C14.9	17:46952221-47006418	NOTEST	0	0	0	0	1	1
ENSG00000270782	ENSG00000270782	RP11-500K19.2	3:120626918-121143608	NOTEST	0	0	0	0	1	1
ENSG00000270783	ENSG00000270783	IGHD3OR15-3A	15:20211157-20211188	NOTEST	0	0	0	0	1	1
ENSG00000270784	ENSG00000270784	CRIP1	HG1592_PATCH:105952653-105965912	NOTEST	0	0	0	0	1	1
ENSG00000270785	ENSG00000270785	AC010518.3	HG1079_PATCH:54797302-54797620	NOTEST	0	0	0	0	1	1
ENSG00000270786	ENSG00000270786	IGHV3-49	HG1592_PATCH:107023274-107023814	NOTEST	0	0	0	0	1	1
ENSG00000270787	ENSG00000270787	KIR2DL3	HG1079_PATCH:55227717-55370462	NOTEST	0	0	0	0	1	1
ENSG00000270788	ENSG00000270788	PDLIM1P1	14:50448429-50559361	NOTEST	0	0	0	0	1	1
ENSG00000270789	ENSG00000270789	RP11-632K20.8	15:32753866-32754010	NOTEST	0	0	0	0	1	1
ENSG00000270790	ENSG00000270790	CTC-360J11.6	19:57662954-57663228	NOTEST	0	0	0	0	1	1
ENSG00000270791	ENSG00000270791	DPRXP6	X:40617735-40618303	NOTEST	0	0	0	0	1	1
ENSG00000270792	ENSG00000270792	RP11-103J8.1	20:10618331-10975572	NOTEST	0	0	0	0	1	1
ENSG00000270793	ENSG00000270793	RP11-23O13.1	20:20701829-20702522	NOTEST	0	0	0	0	1	1
ENSG00000270794	ENSG00000270794	GS1-383H3.6	X:30227539-30228326	NOTEST	0	0	0	0	1	1
ENSG00000270796	ENSG00000270796	IGHD3-16	HG1592_PATCH:106356420-106362914	NOTEST	0	0	0	0	1	1
ENSG00000270797	ENSG00000270797	RP5-1173I20.1	7:39773230-39832691	NOTEST	0	0	0	0	1	1
ENSG00000270798	ENSG00000270798	RP11-416H1.1	2:122494678-122525429	NOTEST	0	0	0	0	1	1
ENSG00000270799	ENSG00000270799	RP11-451F14.1	2:174937174-175113426	NOTEST	0	0	0	0	1	1
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ENSG00000270806	ENSG00000270806	C17orf50	HG385_PATCH:34087915-34092098	NOTEST	0	0	0	0	1	1
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ENSG00000270808	ENSG00000270808	RP11-574K11.27	10:75500295-75500581	NOTEST	0.757031	0.569877	-0.409702	0	1	1
ENSG00000270809	ENSG00000270809	CHCHD2P11	13:42614175-42830714	NOTEST	0	0	0	0	1	1
ENSG00000270810	ENSG00000270810	RP11-274B21.8	7:128327341-128327926	NOTEST	0.0358816	0.0812959	1.17994	0	1	1
ENSG00000270811	ENSG00000270811	RP11-393K12.4	10:7196081-7196198	NOTEST	0	0	0	0	1	1
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ENSG00000270813	ENSG00000270813	NANOGNBP3	X:100592712-100593277	NOTEST	0	0.0587226	inf	0	1	1
ENSG00000270814	ENSG00000270814	TMEM261P1	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000270815	ENSG00000270815	RP11-56O18.1	2:124782863-125672864	NOTEST	0	0	0	0	1	1
ENSG00000270816	ENSG00000270816	AC244452.1	HG1592_PATCH:106955102-106961852	NOTEST	0	0	0	0	1	1
ENSG00000270818	ENSG00000270818	RP11-498M14.1	1:243045367-243046777	NOTEST	0	0	0	0	1	1

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ENSG00000270822	ENSG00000270822	RP11-730B22.1	7:5013618-5112854	NOTEST	0	0.633339	inf	0	1	1
ENSG00000270823	ENSG00000270823	hsa-mir-335	7:130125882-130148500	NOTEST	0.00842333	0.0249581	1.56704	0	1	1
ENSG00000270824	ENSG00000270824	IGHD5OR15-5B	15:21215822-21215845	NOTEST	0	0	0	0	1	1
ENSG00000270825	ENSG00000270825	AC012314.3	HG1079_PATCH:54573200-54584619	NOTEST	0	0	0	0	1	1
ENSG00000270826	ENSG00000270826	RP1-60G11.1	X:93031909-93032383	NOTEST	0	0	0	0	1	1
ENSG00000270827	ENSG00000270827	HIST2H3C	HG1287_PATCH:150525952-150527608	NOTEST	0	0	0	0	1	1
ENSG00000270828	ENSG00000270828	RP3-466P17.2	6:145822718-146058354	NOTEST	0	0	0	0	1	1
ENSG00000270829	ENSG00000270829	AC015849.12	HG385_PATCH:34135507-34135916	NOTEST	0	0	0	0	1	1
ENSG00000270830	ENSG00000270830	RP11-317O24.3	5:50199441-50199577	NOTEST	0	0	0	0	1	1
ENSG00000270831	ENSG00000270831	NF1P1	15:21122014-21140987	NOTEST	0	0	0	0	1	1
ENSG00000270832	ENSG00000270832	RP1-168P16.3	16:89334037-89556969	NOTEST	0	0	0	0	1	1
ENSG00000270834	ENSG00000270834	RNVU1-10	HG1287_PATCH:149048784-149048948	NOTEST	0	0	0	0	1	1
ENSG00000270835	ENSG00000270835	AP001425.14	21:39493544-39679279	NOTEST	0	0	0	0	1	1
ENSG00000270836	ENSG00000270836	EPS8L1	HG1079_PATCH:55575274-55591178	NOTEST	0	0	0	0	1	1
ENSG00000270837	ENSG00000270837	HNRNPDLP4	19:58545399-58565999	NOTEST	0	0	0	0	1	1
ENSG00000270838	ENSG00000270838	RP5-1004I9.2	20:22324330-22324568	NOTEST	0	0	0	0	1	1
ENSG00000270839	ENSG00000270839	CTC-571O20.1	5:174904064-174956745	NOTEST	0	0.0246385	inf	0	1	1
ENSG00000270840	ENSG00000270840	RNVU1-6	HG1287_PATCH:146738495-146738659	NOTEST	0	0	0	0	1	1
ENSG00000270841	ENSG00000270841	IGHV3-57	HG1592_PATCH:107085230-107085510	NOTEST	0	0	0	0	1	1
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ENSG00000270844	ENSG00000270844	hsa-mir-4538	HG1592_PATCH:106324501-106324579	NOTEST	0	0	0	0	1	1
ENSG00000270846	ENSG00000270846	RP11-674I16.1	2:27994583-28561768	NOTEST	0	0	0	0	1	1
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ENSG00000270850	ENSG00000270850	RP11-395N6.4	1:32887579-32887920	NOTEST	0	0	0	0	1	1
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ENSG00000270856	ENSG00000270856	RP11-429G17.2	13:62501222-62501405	NOTEST	0	0	0	0	1	1
ENSG00000270857	ENSG00000270857	RP11-757G14.3	12:12202777-12419946	NOTEST	0	0	0	0	1	1
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ENSG00000270867	ENSG00000270867	AC243772.1	HG1287_PATCH:150423723-150423815	NOTEST	0	0	0	0	1	1
ENSG00000270868	ENSG00000270868	RP11-864G5.7	11:102176842-102177002	NOTEST	0	0	0	0	1	1
ENSG00000270869	ENSG00000270869	RP11-2E11.9	HG1308_PATCH:130126045-130351086	NOTEST	0	0	0	0	1	1
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ENSG00000270873	ENSG00000270873	IGHVIII-13-1	HG1592_PATCH:10660862-106608914	NOTEST	0	0	0	0	1	1
ENSG00000270874	ENSG00000270874	RP11-420K10.1	10:88516406-88692595	NOTEST	0	0	0	0	1	1
ENSG00000270876	ENSG00000270876	CTC-523E23.8	19:35414202-35417716	NOTEST	0	0.0254707	inf	0	1	1
ENSG00000270877	ENSG00000270877	IGHVIII-5-2	HG1592_PATCH:10651193-106512197	NOTEST	0	0	0	0	1	1
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ENSG00000270885	ENSG00000270885	RASL10B	HG385_PATCH:34058667-34070540	NOTEST	0	0	0	0	1	1
ENSG00000270886	ENSG00000270886	GP6	HG1079_PATCH:55509447-55574546	NOTEST	0	0	0	0	1	1
ENSG00000270888	ENSG00000270888	IGHD2-15	HG1592_PATCH:10636429-106364324	NOTEST	0	0	0	0	1	1
ENSG00000270889	ENSG00000270889	RP11-609L3.1	7:35985903-36013282	NOTEST	0	0	0	0	1	1
ENSG00000270890	ENSG00000270890	RP3-468K18.6	6:143857981-144184949	NOTEST	0.570053	0.583227	0.0329599	0	1	1
ENSG00000270891	ENSG00000270891	RP11-499P1.1	2:231701623-231702100	NOTEST	0	0	0	0	1	1
ENSG00000270892	ENSG00000270892	AC006077.4	5:134198780-134199123	NOTEST	0	0	0	0	1	1
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ENSG00000270894	ENSG00000270894	AC015849.13	HG385_PATCH:34136473-34195910	NOTEST	0	0	0	0	1	1
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ENSG00000270896	ENSG00000270896	XXbac-BPG170G13.31	6:29731034-29731169	NOTEST	0	0	0	0	1	1
ENSG00000270897	ENSG00000270897	RP11-179A10.3	11:11139400-11205158	NOTEST	0	0	0	0	1	1
ENSG00000270898	ENSG00000270898	ASB3	2:53759809-54087297	NOTEST	0	0.287766	inf	0	1	1
ENSG00000270899	ENSG00000270899	IGHD3-9	HG1592_PATCH:10637101-106371048	NOTEST	0	0	0	0	1	1
ENSG00000270900	ENSG00000270900	NUDT19P4	6:44777053-45632086	NOTEST	0	0	0	0	1	1
ENSG00000270901	ENSG00000270901	RP11-592P9.1	3:122135053-122233792	NOTEST	0	0	0	0	1	1
ENSG00000270902	ENSG00000270902	RP11-338O1.3	10:125082937-125083102	NOTEST	0	0	0	0	1	1
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ENSG00000270904	ENSG00000270904	CTC-224D3.1	5:150694538-150727151	NOTEST	0	0	0	0	1	1
ENSG00000270906	ENSG00000270906	RP11-475J5.6	5:99384691-99386354	NOTEST	0	0	0	0	1	1
ENSG00000270908	ENSG00000270908	AC098789.1	HG1079_PATCH:54771257-54772299	NOTEST	0	0	0	0	1	1
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ENSG00000270911	ENSG00000270911	RP11-272L13.4	1:97543298-98386605	NOTEST	0	0	0	0	1	1
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ENSG00000270914	ENSG00000270914	RP5-1077B9.5	1:12077272-12077365	NOTEST	0	0	0	0	1	1
ENSG00000270915	ENSG00000270915	RP11-27M5.1	2:203241658-203432474	NOTEST	0	0	0	0	1	1
ENSG00000270916	ENSG00000270916	RP4-741O10.1	X:150192079-150192195	NOTEST	0	0	0	0	1	1
ENSG00000270917	ENSG00000270917	RP11-27I1.6	9:123574752-123575123	NOTEST	0.215025	0.0530165	-2.01999	0	1	1

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ENSG00000270920	ENSG00000270920	CTA-277P6.1	1:185404970-185405179	NOTEST	0	0	0	0	1	1
ENSG00000270921	ENSG00000270921	CICP23	11:121278-126123	NOTEST	0	0	0	0	1	1
ENSG00000270923	ENSG00000270923	TAS2R6	7:141404137-141488440	NOTEST	0.196474	0.184988	-0.086907	0	1	1
ENSG00000270924	ENSG00000270924	RP11-812E19.13	16:33650942-33651111	NOTEST	0	0	0	0	1	1
ENSG00000270925	ENSG00000270925	IGHV3-22	HG1592_PATCH:106724098-106724560	NOTEST	0	0	0	0	1	1
ENSG00000270926	ENSG00000270926	RP11-551L14.7	12:31258038-31259764	NOTEST	0	0	0	0	1	1
ENSG00000270927	ENSG00000270927	RP11-179G8.1	1:30377711-30378204	NOTEST	0	0	0	0	1	1
ENSG00000270928	ENSG00000270928	GAGE12F	HG1436_HG1432_PATCH:49370274-49377604	NOTEST	0	0	0	0	1	1
ENSG00000270929	ENSG00000270929	SRD5A3P1	11:59665657-59666606	NOTEST	0	0	0	0	1	1
ENSG00000270930	ENSG00000270930	GRAMD4P8	2:132394597-132407188	NOTEST	0	0	0	0	1	1
ENSG00000270931	ENSG00000270931	CRIP2	HG1592_PATCH:105939298-105946499	NOTEST	0	0	0	0	1	1
ENSG00000270932	ENSG00000270932	RP11-138A9.1	HG1308_PATCH:130593862-130595860	NOTEST	0	0	0	0	1	1
ENSG00000270934	ENSG00000270934	RP11-346C16.6	6:110919295-110919908	NOTEST	0	0	0	0	1	1
ENSG00000270935	ENSG00000270935	XXbac-BPGBPG24O18.1	6:27235891-27237008	NOTEST	0	0	0	0	1	1
ENSG00000270936	ENSG00000270936	RP5-879K22.1	1:210501595-210849638	NOTEST	0.0299236	0	#NAME?	0	1	1
ENSG00000270937	ENSG00000270937	RP5-856G1.1	6:1026728-1027460	NOTEST	0.0529554	0	#NAME?	0	1	1
ENSG00000270938	ENSG00000270938	RAP2CP1	14:103745559-103746292	NOTEST	0	0	0	0	1	1
ENSG00000270939	ENSG00000270939	IGHV3-50	HG1592_PATCH:107032453-107032892	NOTEST	0	0	0	0	1	1
ENSG00000270940	ENSG00000270940	IGHJ1P	HG1592_PATCH:106331960-106332015	NOTEST	0	0	0	0	1	1
ENSG00000270941	ENSG00000270941	RP5-966M1.5	3:52744799-52804965	NOTEST	0.264049	0	#NAME?	0	1	1
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ENSG00000270946	ENSG00000270946	AC240441.1	HG1443_HG1444_PATCH:134893821-135019384	NOTEST	0	0	0	0	1	1
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ENSG00000270948	ENSG00000270948	RP11-460N20.7	7:64402520-64403304	NOTEST	0.0484621	0.0188506	-1.36224	0	1	1
ENSG00000270950	ENSG00000270950	XXbac-BPG170G13.31	HG1322_PATCH:29730997-29731132	NOTEST	0	0	0	0	1	1
ENSG00000270951	ENSG00000270951	RP1-309F20.4	20:57393973-57486247	NOTEST	0	0	0	0	1	1
ENSG00000270952	ENSG00000270952	AC246787.2	HG1592_PATCH:106324890-106324960	NOTEST	0	0	0	0	1	1
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ENSG00000270954	ENSG00000270954	RP11-174B4.2	9:77337410-77503010	NOTEST	0.219256	0	#NAME?	0	1	1
ENSG00000270955	ENSG00000270955	RP11-261B23.2	15:30574735-30580592	NOTEST	0	0	0	0	1	1
ENSG00000270956	ENSG00000270956	RP11-65L3.4	2:179385909-179914813	NOTEST	0	0	0	0	1	1
ENSG00000270957	ENSG00000270957	RP11-1324A7.2	7:57544871-57545601	NOTEST	0	0	0	0	1	1
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ENSG00000270965	ENSG00000270965	RP11-169K19.1	10:116853123-117708503	NOTEST	0	0	0	0	1	1
ENSG00000270966	ENSG00000270966	RP11-62H7.3	8:8791230-8791516	NOTEST	0	0	0	0	1	1
ENSG00000270967	ENSG00000270967	AL122127.25	HG1592_PATCH:106356420-106362914	NOTEST	0	0	0	0	1	1
ENSG00000270969	ENSG00000270969	CTD-2355J17.2	11:107456626-107457629	NOTEST	0	0	0	0	1	1
ENSG00000270971	ENSG00000270971	REXO1L8P	8:86554957-86556701	NOTEST	0	0	0	0	1	1
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ENSG00000270973	ENSG00000270973	RP11-324L3.5	10:102936079-102953904	NOTEST	0	0	0	0	1	1
ENSG00000270975	ENSG00000270975	RP11-723P16.3	14:69328478-69329242	NOTEST	0	0	0	0	1	1
ENSG00000270976	ENSG00000270976	RP11-110F24.1	1:107322844-107323057	NOTEST	0	0	0	0	1	1
ENSG00000270977	ENSG00000270977	AC015849.16	HG385_PATCH:34220725-34238042	NOTEST	0	0	0	0	1	1
ENSG00000270978	ENSG00000270978	RP11-54C4.2	5:151202073-151304403	NOTEST	0	0	0	0	1	1
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ENSG00000270980	ENSG00000270980	RP11-626A5.2	8:55104141-55104595	NOTEST	0	0	0	0	1	1
ENSG00000270981	ENSG00000270981	RP11-550I24.3	3:156893011-157251408	NOTEST	0	0	0	0	1	1
ENSG00000270982	ENSG00000270982	RP11-490D19.11	9:104212082-104212215	NOTEST	0	0	0	0	1	1
ENSG00000270983	ENSG00000270983	RP11-137J7.3	6:142379466-142410356	NOTEST	0	0	0	0	1	1
ENSG00000270984	ENSG00000270984	GS1-115M3.4	HG1459_PATCH:144849809-144850057	NOTEST	0	0	0	0	1	1
ENSG00000270985	ENSG00000270985	AC245884.3	HG1079_PATCH:54948066-54965270	NOTEST	0	0	0	0	1	1
ENSG00000270986	ENSG00000270986	RP11-123C21.2	15:58887402-59042177	NOTEST	0	0.0703857	inf	0	1	1
ENSG00000270987	ENSG00000270987	RP3-467N11.2	6:101337478-101338214	NOTEST	0	0	0	0	1	1
ENSG00000270988	ENSG00000270988	RP11-439C15.5	8:1919562-1955102	NOTEST	0	0.0355048	inf	0	1	1
ENSG00000270989	ENSG00000270989	RP11-844P9.4	5:175630316-175630713	NOTEST	0	0	0	0	1	1
ENSG00000270990	ENSG00000270990	RP11-632K21.6	7:150373920-150375006	NOTEST	0	0	0	0	1	1
ENSG00000270992	ENSG00000270992	RP11-190G13.4	7:129895741-129902610	NOTEST	0	0	0	0	1	1
ENSG00000270993	ENSG00000270993	RP11-1112G13.3	17:73028669-73061984	NOTEST	0	0	0	0	1	1
ENSG00000270994	ENSG00000270994	RP11-293B7.1	1:183605219-183897665	NOTEST	0	0	0	0	1	1
ENSG00000270995	ENSG00000270995	RP11-29B11.5	9:102861537-103063282	NOTEST	0	0.121771	inf	0	1	1
ENSG00000270996	ENSG00000270996	RP11-342K6.4	2:75946245-75947144	NOTEST	0.0204025	0.0158678	-0.362651	0	1	1
ENSG00000270997	ENSG00000270997	RP11-703P11.1	7:113055743-113056377	NOTEST	0	0	0	0	1	1
ENSG00000270998	ENSG00000270998	RDH13	HG1079_PATCH:55509447-55574546	NOTEST	0	0	0	0	1	1
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ENSG00000271000	ENSG00000271000	NCR1	HG1079_PATCH:55409404-55419395	NOTEST	0	0	0	0	1	1
ENSG00000271001	ENSG00000271001	AC243756.1	HG1287_PATCH:147030420-147031205	NOTEST	0	0	0	0	1	1
ENSG00000271002	ENSG00000271002	RP11-599B13.8	17:8102440-8102755	NOTEST	0	0	0	0	1	1
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ENSG00000271007	ENSG00000271007	CTC-550B14.8	HG1079_PATCH:55426763-55504397	NOTEST	0	0	0	0	1	1
ENSG00000271008	ENSG00000271008	IGHJ6	HG1592_PATCH:106329534-106329595	NOTEST	0	0	0	0	1	1
ENSG00000271009	ENSG00000271009	RP11-346C20.3	16:73094143-73096215	NOTEST	0	0	0	0	1	1
ENSG00000271010	ENSG00000271010	CTC-539A10.7	19:10708676-10709641	NOTEST	0	0	0	0	1	1
ENSG00000271011	ENSG00000271011	RP11-171I2.5	2:179385909-179914813	NOTEST	0	0	0	0	1	1
ENSG00000271012	ENSG00000271012	MIR4752	HG1079_PATCH:54785362-54785434	NOTEST	0	0	0	0	1	1
ENSG00000271013	ENSG00000271013	LRRC37A9P	HG385_PATCH:34239653-34245029	NOTEST	0	0	0	0	1	1
ENSG00000271014	ENSG00000271014	RP11-717A5.1	2:85569210-85618875	NOTEST	0	0	0	0	1	1
ENSG00000271015	ENSG00000271015	IGKV2OR2-7	2:98000863-98001167	NOTEST	0	0	0	0	1	1
ENSG00000271016	ENSG00000271016	NDUFA3	HG1079_PATCH:54605981-54634963	NOTEST	0	0	0	0	1	1
ENSG00000271018	ENSG00000271018	RP11-60E8.2	12:51150674-51151216	NOTEST	0	0	0	0	1	1
ENSG00000271019	ENSG00000271019	MBOAT7	HG1079_PATCH:54676666-54693136	NOTEST	0	0	0	0	1	1
ENSG00000271021	ENSG00000271021	RP5-878I13.2	X:114689493-114689955	NOTEST	0.146571	0.036311	-2.01313	0	1	1
ENSG00000271022	ENSG00000271022	RP11-142I2.1	11:121297353-121298125	NOTEST	0	0	0	0	1	1
ENSG00000271023	ENSG00000271023	IGHV4-34	HG1592_PATCH:106839999-106840482	NOTEST	0	0	0	0	1	1
ENSG00000271024	ENSG00000271024	HSPE1P19	3:90310563-90310858	NOTEST	0	0	0	0	1	1
ENSG00000271025	ENSG00000271025	RP11-708L7.9	11:111895537-112095422	NOTEST	0	0	0	0	1	1
ENSG00000271026	ENSG00000271026	KATNBL1P1	13:28577410-28674729	NOTEST	0	0	0	0	1	1
ENSG00000271027	ENSG00000271027	RP11-463M14.1	7:31370324-31370510	NOTEST	0	0	0	0	1	1
ENSG00000271028	ENSG00000271028	RP11-111A24.2	11:43085186-43087626	NOTEST	0	0	0	0	1	1
ENSG00000271029	ENSG00000271029	RP11-849F2.10	17:8199822-8200534	NOTEST	0	0	0	0	1	1
ENSG00000271030	ENSG00000271030	AC008746.9	HG1079_PATCH:55024976-55025285	NOTEST	0	0	0	0	1	1
ENSG00000271031	ENSG00000271031	IGHD3-3	HG1592_PATCH:106380695-106380726	NOTEST	0	0	0	0	1	1
ENSG00000271032	ENSG00000271032	CTD-2527I21.14	19:35485687-35517375	NOTEST	0.239311	0.0949087	-1.33427	0	1	1
ENSG00000271034	ENSG00000271034	RP11-963H1.1	3:70174220-70175760	NOTEST	0	0.00762892	inf	0	1	1
ENSG00000271035	ENSG00000271035	CTD-2269E23.3	5:28897891-28898381	NOTEST	0	0.0330869	inf	0	1	1
ENSG00000271036	ENSG00000271036	CLPTM1LP1	1:188874818-189006393	NOTEST	0	0	0	0	1	1
ENSG00000271037	ENSG00000271037	AC008746.10	HG1079_PATCH:54882742-54883214	NOTEST	0	0	0	0	1	1
ENSG00000271038	ENSG00000271038	AC012314.20	HG1079_PATCH:54702707-54703225	NOTEST	0	0	0	0	1	1
ENSG00000271039	ENSG00000271039	KIR3DL1	HG1079_PATCH:55227717-55370462	NOTEST	0	0	0	0	1	1
ENSG00000271040	ENSG00000271040	RP5-933K21.3	6:157744995-157745509	NOTEST	0.123906	0.0952304	-0.379757	0	1	1
ENSG00000271041	ENSG00000271041	RP6-166C19.18	X:120081336-120081589	NOTEST	0	0	0	0	1	1
ENSG00000271042	ENSG00000271042	RP3-364H10.1	6:99530324-99530637	NOTEST	0	0	0	0	1	1
ENSG00000271043	ENSG00000271043	MTRNR2L2	5:79922046-80172279	NOTEST	0.0484532	0.0120838	-2.00352	0	1	1
ENSG00000271044	ENSG00000271044	RP11-255M6.1	15:85427884-85518876	NOTEST	0	0	0	0	1	1
ENSG00000271045	ENSG00000271045	RP11-1113N2.4	5:68645762-68646272	NOTEST	0	0	0	0	1	1
ENSG00000271046	ENSG00000271046	RP11-138I18.2	10:11721673-11722513	NOTEST	0	0	0	0	1	1
ENSG00000271047	ENSG00000271047	RP11-760D2.12	7:56671102-56671246	NOTEST	0	0	0	0	1	1

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ENSG00000271048	ENSG00000271048	CTD-2342N23.2	8:135490030-135725292	NOTEST	0	0	0	0	1	1
ENSG00000271049	ENSG00000271049	CTD-2553L13.7	19:35084233-35166604	NOTEST	0	0	0	0	1	1
ENSG00000271050	ENSG00000271050	IGHV3-30-2	HG1592_PATCH:106810731-106811170	NOTEST	0	0	0	0	1	1
ENSG00000271052	ENSG00000271052	RP11-479I16.2	3:160801670-160971320	NOTEST	0	0	0	0	1	1
ENSG00000271053	ENSG00000271053	RP11-97F8.1	4:117779248-117780129	NOTEST	0	0	0	0	1	1
ENSG00000271055	ENSG00000271055	AL928742.3	HG1592_PATCH:106056272-106056350	NOTEST	0	0	0	0	1	1
ENSG00000271056	ENSG00000271056	RP6-43L17.2	X:87062548-87064883	NOTEST	0	0	0	0	1	1
ENSG00000271057	ENSG00000271057	RP11-747H12.7	4:9022582-9022887	NOTEST	0	0	0	0	1	1
ENSG00000271058	ENSG00000271058	IGHV3-15	HG1592_PATCH:106619960-106620500	NOTEST	0	0	0	0	1	1
ENSG00000271059	ENSG00000271059	RNU6-222P	HG1079_PATCH:55372193-55372300	NOTEST	0	0	0	0	1	1
ENSG00000271060	ENSG00000271060	IGHV3-71	HG1592_PATCH:107241493-107241955	NOTEST	0	0	0	0	1	1
ENSG00000271062	ENSG00000271062	IGHV2-5	HG1592_PATCH:106504239-106504702	NOTEST	0	0	0	0	1	1
ENSG00000271063	ENSG00000271063	SNRPGP17	17:57358490-57358704	NOTEST	0	0	0	0	1	1
ENSG00000271064	ENSG00000271064	RP11-792A8.3	7:66093867-66309813	NOTEST	0	0	0	0	1	1
ENSG00000271065	ENSG00000271065	RP11-607P23.1	12:51745030-51902980	NOTEST	0	0	0	0	1	1
ENSG00000271067	ENSG00000271067	CTB-61M7.2	HG1079_PATCH:55393927-55394675	NOTEST	0	0	0	0	1	1
ENSG00000271069	ENSG00000271069	RP5-878I13.2	HG1462_PATCH:114691202-114691664	NOTEST	0	0	0	0	1	1
ENSG00000271070	ENSG00000271070	RP11-465O11.2	2:108983571-108984394	NOTEST	0	0	0	0	1	1
ENSG00000271071	ENSG00000271071	RP11-457M11.6	6:26612130-26613337	NOTEST	0	0	0	0	1	1
ENSG00000271072	ENSG00000271072	RP11-1007O24.4	15:72690613-72879692	NOTEST	0	0.0162013	inf	0	1	1
ENSG00000271073	ENSG00000271073	RP11-258C19.7	HG1433_PATCH:52912096-52913914	NOTEST	0	0	0	0	1	1
ENSG00000271074	ENSG00000271074	RP11-212J19.1	2:211969657-211970456	NOTEST	0	0	0	0	1	1
ENSG00000271075	ENSG00000271075	RP11-589M4.4	14:53323985-53419153	NOTEST	0.0463397	0.0392519	-0.239486	0	1	1
ENSG00000271077	ENSG00000271077	AC096553.5	7:9673899-9675333	NOTEST	0	0	0	0	1	1
ENSG00000271078	ENSG00000271078	RP13-395E19.4	15:32542502-32548326	NOTEST	0	0	0	0	1	1
ENSG00000271079	ENSG00000271079	CTAGE15	7:143268818-143271480	NOTEST	0	0	0	0	1	1
ENSG00000271080	ENSG00000271080	IGHV1-58	HG1592_PATCH:107088695-107089192	NOTEST	0	0	0	0	1	1
ENSG00000271081	ENSG00000271081	RP11-465K4.4	8:30589763-30624522	NOTEST	0	0	0	0	1	1
ENSG00000271082	ENSG00000271082	IGHVII-67-1	HG1592_PATCH:107152853-107152899	NOTEST	0	0	0	0	1	1
ENSG00000271083	ENSG00000271083	IGHV4-39	HG1592_PATCH:106888047-106888555	NOTEST	0	0	0	0	1	1
ENSG00000271086	ENSG00000271086	NAMA	9:102117618-102139522	NOTEST	0.148648	0.113041	-0.395046	0	1	1
ENSG00000271087	ENSG00000271087	AC246787.3	HG1592_PATCH:106324079-106324139	NOTEST	0	0	0	0	1	1
ENSG00000271088	ENSG00000271088	RP11-497J7.4	X:35759716-35762699	NOTEST	0	0	0	0	1	1
ENSG00000271089	ENSG00000271089	IGHV3-53	HG1592_PATCH:107059014-107059684	NOTEST	0	0	0	0	1	1
ENSG00000271090	ENSG00000271090	AC012531.23	12:54348617-54352745	NOTEST	0.0238078	0.004621	-2.36516	0	1	1
ENSG00000271091	ENSG00000271091	RP2	HG29_PATCH:46696374-46741793	NOTEST	0	0	0	0	1	1
ENSG00000271092	ENSG00000271092	TMEM56-RWDD3	1:95582893-95729610	NOTEST	0.186336	0	#NAME?	0	1	1
ENSG00000271093	ENSG00000271093	IGLCOR22-2	22:32750871-32781618	NOTEST	0	0	0	0	1	1
ENSG00000271094	ENSG00000271094	RP3-380C13.2	X:94708367-94708580	NOTEST	0	0	0	0	1	1
ENSG00000271095	ENSG00000271095	AC003973.6	19:22115759-22193751	NOTEST	0	0	0	0	1	1

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ENSG00000271096	ENSG00000271096	SUMO2P14	7:24612886-24733812	NOTEST	0	0	0	0	1	1
ENSG00000271097	ENSG00000271097	RP11-223J6.1	2:87528780-87529374	NOTEST	0	0	0	0	1	1
ENSG00000271098	ENSG00000271098	RP5-1125K23.1	7:2291404-2420380	NOTEST	0	0	0	0	1	1
ENSG00000271099	ENSG00000271099	RP11-809N15.3	6:105308323-105309998	NOTEST	0	0	0	0	1	1
ENSG00000271100	ENSG00000271100	RP11-697H9.5	11:63448917-63527363	NOTEST	0	0	0	0	1	1
ENSG00000271101	ENSG00000271101	RP11-1003J3.1	17:69008137-69009728	NOTEST	0	0	0	0	1	1
ENSG00000271103	ENSG00000271103	AC008746.12	HG1079_PATCH:54941918-54942434	NOTEST	0	0	0	0	1	1
ENSG00000271104	ENSG00000271104	MIR500A	HG1436_HG1432_PATCH:49732013-49908634	NOTEST	0	0	0	0	1	1
ENSG00000271105	ENSG00000271105	SCML2P2	16:25080890-25081430	NOTEST	0	0.0571084	inf	0	1	1
ENSG00000271106	ENSG00000271106	AC247036.1	HG1592_PATCH:106672939-106674908	NOTEST	0	0	0	0	1	1
ENSG00000271107	ENSG00000271107	AC009892.10	HG1079_PATCH:55076173-55142146	NOTEST	0	0	0	0	1	1
ENSG00000271108	ENSG00000271108	KATNBL1P5	6:25245583-25261959	NOTEST	0	0	0	0	1	1
ENSG00000271109	ENSG00000271109	CTC-523E23.11	19:35328792-35351480	NOTEST	0	0	0	0	1	1
ENSG00000271111	ENSG00000271111	RP11-409K15.1	6:68166238-68167143	NOTEST	0	0	0	0	1	1
ENSG00000271112	ENSG00000271112	RP11-666A1.7	HG1287_PATCH:145087483-145087770	NOTEST	0	0	0	0	1	1
ENSG00000271113	ENSG00000271113	RP11-159H10.4	8:70579281-70767206	NOTEST	0	0.0209228	inf	0	1	1
ENSG00000271114	ENSG00000271114	RP11-453D21.1	6:88601141-88601587	NOTEST	0	0	0	0	1	1
ENSG00000271115	ENSG00000271115	RP11-443I9.1	2:57275484-57276471	NOTEST	0	0	0	0	1	1
ENSG00000271116	ENSG00000271116	LAIR2	HG1079_PATCH:55001132-55013941	NOTEST	0	0	0	0	1	1
ENSG00000271117	ENSG00000271117	RP11-377H23.1	7:36186450-36187633	NOTEST	0	0	0	0	1	1
ENSG00000271118	ENSG00000271118	RP11-175E9.2	8:23663445-23663667	NOTEST	0	0	0	0	1	1
ENSG00000271119	ENSG00000271119	CTD-2012J19.3	5:1594740-1634120	NOTEST	0.0859987	0.144388	0.747568	0	1	1
ENSG00000271121	ENSG00000271121	AC243756.2	HG1287_PATCH:146984418-146985587	NOTEST	0	0	0	0	1	1
ENSG00000271122	ENSG00000271122	RP11-379H18.1	7:35672268-35739023	NOTEST	0.430294	0.551013	0.356763	0	1	1
ENSG00000271123	ENSG00000271123	TCEB1P5	Y:23793568-23793901	NOTEST	0	0	0	0	1	1
ENSG00000271124	ENSG00000271124	KIR3DL3	HG1079_PATCH:55227717-55370462	NOTEST	0	0	0	0	1	1
ENSG00000271125	ENSG00000271125	CTB-83J4.1	HG1079_PATCH:54703995-54752257	NOTEST	0	0	0	0	1	1
ENSG00000271126	ENSG00000271126	AC008984.7	HG1079_PATCH:54805011-54809280	NOTEST	0	0	0	0	1	1
ENSG00000271127	ENSG00000271127	LL22NC03N64E9.1	22:16147978-16193004	NOTEST	0.0687548	0.00948545	-2.85767	0	1	1
ENSG00000271128	ENSG00000271128	CTB-113I20.1	5:133417604-133417731	NOTEST	0	0	0	0	1	1
ENSG00000271129	ENSG00000271129	RP11-123C5.5	16:68877506-69119083	NOTEST	0	0	0	0	1	1
ENSG00000271130	ENSG00000271130	IGHV3OR16-8	16:32963313-33039358	NOTEST	0	0	0	0	1	1
ENSG00000271131	ENSG00000271131	RP11-33A14.3	3:177919837-178578193	NOTEST	0	0	0	0	1	1
ENSG00000271132	ENSG00000271132	RP1-241P17.7	HG1462_PATCH:114896182-114896492	NOTEST	0	0	0	0	1	1
ENSG00000271134	ENSG00000271134	RP11-416L21.2	2:60910007-60910379	NOTEST	0	0	0	0	1	1
ENSG00000271135	ENSG00000271135	AC012314.8	HG1079_PATCH:54605981-54634963	NOTEST	0	0	0	0	1	1
ENSG00000271136	ENSG00000271136	RP11-320J16.1	X:34535036-34535475	NOTEST	0	0	0	0	1	1
ENSG00000271137	ENSG00000271137	RP5-966M1.4	3:52744799-52804965	NOTEST	0	0	0	0	1	1
ENSG00000271138	ENSG00000271138	IGLVIVOR22-1	22:25833272-25833790	NOTEST	0.313999	0.051226	-2.61581	0	1	1
ENSG00000271139	ENSG00000271139	CTB-61M7.1	HG1079_PATCH:55227717-55370462	NOTEST	0	0	0	0	1	1
ENSG00000271140	ENSG00000271140	PRR20FP	13:57747586-57747766	NOTEST	0	0	0	0	1	1
ENSG00000271141	ENSG00000271141	RP11-171I2.4	2:179385909-179914813	NOTEST	0	0	0	0	1	1
ENSG00000271142	ENSG00000271142	YWHAQP7	12:77013165-77013823	NOTEST	0	0	0	0	1	1

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ENSG00000271144	ENSG00000271144	IGHD2-8	HG1592_PATCH:106373547-106373578	NOTEST	0	0	0	0	1	1
ENSG00000271146	ENSG00000271146	RP11-479F13.1	2:61404552-61697904	NOTEST	0	0	0	0	1	1
ENSG00000271148	ENSG00000271148	RP11-401N18.1	8:50819422-50820006	NOTEST	0	0	0	0	1	1
ENSG00000271149	ENSG00000271149	CTC-457E21.10	19:22778280-22778965	NOTEST	0	0	0	0	1	1
ENSG00000271150	ENSG00000271150	CTD-2571L23.9	19:48297723-48298177	NOTEST	0	0	0	0	1	1
ENSG00000271151	ENSG00000271151	RP11-394I13.2	2:174833078-174834146	NOTEST	0.0467441	0.0399434	-0.226828	0	1	1
ENSG00000271153	ENSG00000271153	ABC7-43041300I9.1	2:243160371-243160825	NOTEST	0	0	0	0	1	1
ENSG00000271154	ENSG00000271154	RP6-166C19.23	X:120076476-120076729	NOTEST	0	0	0	0	1	1
ENSG00000271155	ENSG00000271155	RP11-435O5.5	9:98205261-98279339	NOTEST	0.0587465	0.0900671	0.616496	0	1	1
ENSG00000271156	ENSG00000271156	RP11-642C5.1	8:89820546-89821137	NOTEST	0.201587	0.0826158	-1.28692	0	1	1
ENSG00000271157	ENSG00000271157	RP1-249C1.1	X:88082554-88084859	NOTEST	0	0	0	0	1	1
ENSG00000271158	ENSG00000271158	RP11-265D19.7	X:134598253-134599409	NOTEST	0	0	0	0	1	1
ENSG00000271159	ENSG00000271159	GS1-200K5.1	7:94536513-94925727	NOTEST	0	0	0	0	1	1
ENSG00000271161	ENSG00000271161	RP11-708J19.2	3:47537129-47555251	NOTEST	0.0375148	0.265865	2.82516	0	1	1
ENSG00000271162	ENSG00000271162	RP1-57E3.1	6:48919706-48920418	NOTEST	0	0	0	0	1	1
ENSG00000271163	ENSG00000271163	RP4-607J2.1	7:2433481-2433766	NOTEST	0	0	0	0	1	1
ENSG00000271164	ENSG00000271164	RP4-789D17.4	1:36335408-36395211	NOTEST	0	0	0	0	1	1
ENSG00000271165	ENSG00000271165	RP11-42L13.3	HSCHR5_3_CTG1:29114553-29115847	NOTEST	0	0	0	0	1	1
ENSG00000271166	ENSG00000271166	RP11-409O11.3	9:74298281-74431606	NOTEST	0	0.0282445	inf	0	1	1
ENSG00000271167	ENSG00000271167	LINC01109	8:77316232-77779521	NOTEST	0	0	0	0	1	1
ENSG00000271169	ENSG00000271169	IGHJ2	HG1592_PATCH:106331535-106331587	NOTEST	0	0	0	0	1	1
ENSG00000271171	ENSG00000271171	CTC-523E23.15	19:35395295-35395961	NOTEST	0	0	0	0	1	1
ENSG00000271172	ENSG00000271172	RP11-660M5.1	4:25162262-25280714	NOTEST	0	0.0310195	inf	0	1	1
ENSG00000271173	ENSG00000271173	RP11-272J7.6	10:44223664-44224176	NOTEST	0	0	0	0	1	1
ENSG00000271174	ENSG00000271174	RP11-814M22.2	3:66673183-66673526	NOTEST	0	0	0	0	1	1
ENSG00000271175	ENSG00000271175	RP11-434J24.3	X:146894250-146894492	NOTEST	0	0	0	0	1	1
ENSG00000271176	ENSG00000271176	IGHV3-33-2	HG1592_PATCH:106835443-106835883	NOTEST	0	0	0	0	1	1
ENSG00000271177	ENSG00000271177	RP11-575G13.3	12:100867485-100958191	NOTEST	0	0	0	0	1	1
ENSG00000271178	ENSG00000271178	IGHV3OR16-13	16:33629680-33630128	NOTEST	0	0	0	0	1	1
ENSG00000271179	ENSG00000271179	RP11-629P16.1	2:132837862-132838328	NOTEST	0	0	0	0	1	1
ENSG00000271180	ENSG00000271180	RP11-665C16.8	14:55707339-55707798	NOTEST	0	0	0	0	1	1
ENSG00000271181	ENSG00000271181	CTA-221G9.10	22:25348696-25593415	NOTEST	0	0	0	0	1	1
ENSG00000271182	ENSG00000271182	RP11-678G14.5	19:21817634-21817977	NOTEST	0	0	0	0	1	1
ENSG00000271184	ENSG00000271184	RP4-800O15.3	12:126384966-126386029	NOTEST	0	0	0	0	1	1
ENSG00000271185	ENSG00000271185	RP5-855F16.1	7:10980049-10980362	NOTEST	0	0	0	0	1	1
ENSG00000271186	ENSG00000271186	IGHV3-38	HG1592_PATCH:106876829-106877358	NOTEST	0	0	0	0	1	1
ENSG00000271187	ENSG00000271187	RP11-309H21.4	1:191148650-191148869	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000271189	ENSG00000271189	IGHA1	HG1592_PATCH:106173456-106175002	NOTEST	0	0	0	0	1	1
ENSG00000271190	ENSG00000271190	RPP40P2	13:59836813-59837525	NOTEST	0	0	0	0	1	1
ENSG00000271191	ENSG00000271191	AB019440.50	HG1592_PATCH:106672939-106674908	NOTEST	0	0	0	0	1	1
ENSG00000271192	ENSG00000271192	RP4-555D20.3	3:44038387-44038935	NOTEST	0	0.0279415	inf	0	1	1
ENSG00000271193	ENSG00000271193	IGHVIII-25-1	HG1592_PATCH:106759904-106760145	NOTEST	0	0	0	0	1	1
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ENSG00000271195	ENSG00000271195	RP11-162I7.2	15:61931547-62007370	NOTEST	0	0	0	0	1	1
ENSG00000271196	ENSG00000271196	RP11-461O14.3	5:137790228-137790421	NOTEST	0	0	0	0	1	1
ENSG00000271197	ENSG00000271197	IGHD2OR15-2A	15:20213654-20213685	NOTEST	0	0	0	0	1	1
ENSG00000271198	ENSG00000271198	VDAC3P1	14:100430865-100431715	NOTEST	0	0	0	0	1	1
ENSG00000271199	ENSG00000271199	RP13-216E22.5	X:73164158-73513409	NOTEST	0	0	0	0	1	1
ENSG00000271200	ENSG00000271200	RP11-430G17.3	1:62207669-62208096	NOTEST	0.167097	0.0452308	-1.88531	0	1	1
ENSG00000271201	ENSG00000271201	AB019440.50	14:106663245-106665214	NOTEST	0	0	0	0	1	1
ENSG00000271202	ENSG00000271202	RP11-122C21.4	8:92921965-92922395	NOTEST	0	0	0	0	1	1
ENSG00000271203	ENSG00000271203	TFPT	HG1079_PATCH:54605981-54634963	NOTEST	0	0	0	0	1	1
ENSG00000271204	ENSG00000271204	RP11-138A9.1	7:130614967-130616965	NOTEST	0.0228525	0.0178512	-0.356336	0	1	1
ENSG00000271205	ENSG00000271205	RP1-138A5.2	X:86978088-86978238	NOTEST	0	0	0	0	1	1
ENSG00000271206	ENSG00000271206	CTC-550B14.6	HG1079_PATCH:55509447-55574546	NOTEST	0	0	0	0	1	1
ENSG00000271207	ENSG00000271207	RP11-475J5.5	5:99389389-99390749	NOTEST	0	0	0	0	1	1
ENSG00000271208	ENSG00000271208	RP1-142L7.8	6:112429962-112672498	NOTEST	0	0	0	0	1	1
ENSG00000271209	ENSG00000271209	RP13-40J16.1	X:95592234-95592911	NOTEST	0	0	0	0	1	1
ENSG00000271210	ENSG00000271210	FCAR	HG1079_PATCH:55377502-55393727	NOTEST	0	0	0	0	1	1
ENSG00000271211	ENSG00000271211	RP6-166C19.20	X:120092018-120100198	NOTEST	0	0	0	0	1	1
ENSG00000271212	ENSG00000271212	RP11-810O3.2	HG1462_PATCH:113820547-114146531	NOTEST	0	0	0	0	1	1
ENSG00000271214	ENSG00000271214	RP11-9M16.3	9:117164359-117267730	NOTEST	0	0	0	0	1	1
ENSG00000271215	ENSG00000271215	RP11-180M15.5	12:12764760-12798042	NOTEST	0	0	0	0	1	1
ENSG00000271216	ENSG00000271216	LINC01050	13:43384501-43386698	NOTEST	0.0925666	0.0748584	-0.306329	0	1	1
ENSG00000271217	ENSG00000271217	RP11-301J7.9	10:48247668-48279200	NOTEST	0	0	0	0	1	1
ENSG00000271218	ENSG00000271218	RP3-523E19.2	6:53659294-53788919	NOTEST	0.207512	0.0777568	-1.41615	0	1	1
ENSG00000271219	ENSG00000271219	RP11-369K17.2	8:121925304-122131994	NOTEST	0	0	0	0	1	1
ENSG00000271220	ENSG00000271220	RP11-478H13.4	10:29078116-29102387	NOTEST	0	0	0	0	1	1
ENSG00000271221	ENSG00000271221	IGHVII-26-2	HG1592_PATCH:106780987-106781312	NOTEST	0	0	0	0	1	1
ENSG00000271222	ENSG00000271222	RP11-1072C15.7	17:42673713-42674712	NOTEST	0	0	0	0	1	1
ENSG00000271223	ENSG00000271223	RP6-137J22.3	1:144275917-144521970	NOTEST	0	0	0	0	1	1
ENSG00000271224	ENSG00000271224	IGHV1-46	HG1592_PATCH:106977453-106978193	NOTEST	0	0	0	0	1	1
ENSG00000271225	ENSG00000271225	RP11-460N11.3	9:69823282-69823847	NOTEST	0.0377029	0.0854453	1.18033	0	1	1
ENSG00000271226	ENSG00000271226	IGKV2OR2-10	2:97996725-97997025	NOTEST	0	0	0	0	1	1
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ENSG00000271229	ENSG00000271229	AC008984.6	HG1079_PATCH:54831525-54834688	NOTEST	0	0	0	0	1	1
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ENSG00000271231	ENSG00000271231	KRT18P9	6:34157556-34158856	NOTEST	0	0	0	0	1	1
ENSG00000271232	ENSG00000271232	RP11-317N6.1	15:69041839-69043030	NOTEST	0	0	0	0	1	1
ENSG00000271233	ENSG00000271233	RP1-142L7.9	HG1304_PATCH:112430062-112671296	NOTEST	0	0	0	0	1	1
ENSG00000271234	ENSG00000271234	RP5-894D12.4	6:170599790-170716153	NOTEST	0	0	0	0	1	1
ENSG00000271235	ENSG00000271235	RP11-1037D22.1	3:22852880-22853538	NOTEST	0	0	0	0	1	1
ENSG00000271236	ENSG00000271236	SUMO2P15	15:41052794-41053072	NOTEST	0	0	0	0	1	1
ENSG00000271237	ENSG00000271237	RP11-140C5.3	10:50759353-50760698	NOTEST	0	0	0	0	1	1
ENSG00000271238	ENSG00000271238	RP11-510D21.2	18:26404615-26404790	NOTEST	0	0	0	0	1	1
ENSG00000271239	ENSG00000271239	RP11-238F2.1	17:68774744-68775371	NOTEST	0	0	0	0	1	1
ENSG00000271240	ENSG00000271240	RP11-157E21.2	8:134975234-134975502	NOTEST	0	0	0	0	1	1
ENSG00000271242	ENSG00000271242	SLMO2P2	13:51770016-51770217	NOTEST	0	0	0	0	1	1
ENSG00000271243	ENSG00000271243	RP11-355B11.1	2:61802908-61803529	NOTEST	0	0	0	0	1	1
ENSG00000271245	ENSG00000271245	RP4-761I2.5	6:11155161-11155383	NOTEST	0	0	0	0	1	1
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ENSG00000271247	ENSG00000271247	AC009892.9	HG1079_PATCH:55155338-55155484	NOTEST	0	0	0	0	1	1
ENSG00000271248	ENSG00000271248	RP11-745K9.2	8:5312739-5313187	NOTEST	0	0	0	0	1	1
ENSG00000271249	ENSG00000271249	RP11-424I3.1	3:109366953-109529708	NOTEST	0	0	0	0	1	1
ENSG00000271250	ENSG00000271250	RP11-101P17.1	13:21790693-21790799	NOTEST	0	0	0	0	1	1
ENSG00000271251	ENSG00000271251	RP11-543F8.3	10:8514681-8514915	NOTEST	0	0	0	0	1	1
ENSG00000271252	ENSG00000271252	RP11-286B14.2	1:95975671-96247898	NOTEST	0	0	0	0	1	1
ENSG00000271253	ENSG00000271253	CTD-2320J21.1	7:12725261-12725658	NOTEST	0	0	0	0	1	1
ENSG00000271254	ENSG00000271254	NBPF10	HG1287_PATCH:145976420-146277520	NOTEST	0	0	0	0	1	1
ENSG00000271255	ENSG00000271255	IGHD3OR15-3B	15:21217887-21217918	NOTEST	0	0	0	0	1	1
ENSG00000271257	ENSG00000271257	CTD-2117L12.3	5:57799121-57799527	NOTEST	0	0	0	0	1	1
ENSG00000271258	ENSG00000271258	IGHJ3P	HG1592_PATCH:106329752-106329802	NOTEST	0	0	0	0	1	1
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ENSG00000271261	ENSG00000271261	IGHV1-18	HG1592_PATCH:106651237-106651731	NOTEST	0	0	0	0	1	1
ENSG00000271263	ENSG00000271263	RP11-450H5.4	3:166325030-166325361	NOTEST	0	0	0	0	1	1
ENSG00000271264	ENSG00000271264	RP11-558F24.6	1:9711789-9884584	NOTEST	0	0	0	0	1	1
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ENSG00000271266	ENSG00000271266	RP11-728B21.3	3:72933384-72933830	NOTEST	0	0	0	0	1	1
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ENSG00000271269	ENSG00000271269	RP11-317P15.6	1:182702926-182703914	NOTEST	0	0	0	0	1	1
ENSG00000271271	ENSG00000271271	UGT2A2	4:70454134-70518967	NOTEST	0	0	0	0	1	1
ENSG00000271272	ENSG00000271272	RP11-510P12.1	12:43323650-43324382	NOTEST	0	0	0	0	1	1
ENSG00000271273	ENSG00000271273	RP11-157B13.9	HSCHR19_3_CTG3:22477416-22508185	NOTEST	0	0	0	0	1	1
ENSG00000271274	ENSG00000271274	IGHV1-14	HG1592_PATCH:106612227-106612468	NOTEST	0	0	0	0	1	1
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ENSG00000271277	ENSG00000271277	RP11-82O2.2	1:102268129-102462586	NOTEST	0	0	0	0	1	1
ENSG00000271278	ENSG00000271278	TCEB1P3	4:39824482-39979576	NOTEST	0	0	0	0	1	1
ENSG00000271279	ENSG00000271279	CTC-550B14.1	HG1079_PATCH:55426763-55504397	NOTEST	0	0	0	0	1	1
ENSG00000271281	ENSG00000271281	RP11-457M11.6	HG27_PATCH:26612130-26613337	NOTEST	0	0	0	0	1	1
ENSG00000271282	ENSG00000271282	RP11-417P24.1	HG1592_PATCH:106251841-106252168	NOTEST	0	0	0	0	1	1
ENSG00000271283	ENSG00000271283	CTC-412M14.6	19:19810011-19810218	NOTEST	0	0	0	0	1	1
ENSG00000271284	ENSG00000271284	RP11-465O11.1	2:109040067-109040341	NOTEST	0	0	0	0	1	1
ENSG00000271285	ENSG00000271285	CTD-2542C24.9	HSCHR19_1_CTG3:21209841-21223406	NOTEST	0	0	0	0	1	1
ENSG00000271286	ENSG00000271286	LL0XNC01-39B3.1	X:21957578-21958278	NOTEST	0.0280798	0	#NAME?	0	1	1
ENSG00000271287	ENSG00000271287	BCRP9	13:68364538-68364926	NOTEST	0	0	0	0	1	1
ENSG00000271288	ENSG00000271288	IGHV1OR15-3	15:22466057-22466493	NOTEST	0	0	0	0	1	1
ENSG00000271289	ENSG00000271289	IGHV1-67	HG1592_PATCH:107146939-107147379	NOTEST	0	0	0	0	1	1
ENSG00000271290	ENSG00000271290	RP11-345E19.2	X:85403461-86087607	NOTEST	0	0	0	0	1	1
ENSG00000271291	ENSG00000271291	RP11-289I10.3	1:148229951-148230238	NOTEST	0	0	0	0	1	1
ENSG00000271292	ENSG00000271292	IGHG1	HG1592_PATCH:106202679-106209408	NOTEST	0	0	0	0	1	1
ENSG00000271294	ENSG00000271294	IGHV7-56	HG1592_PATCH:107076098-107076533	NOTEST	0	0	0	0	1	1
ENSG00000271295	ENSG00000271295	IGHVIV-44-1	HG1592_PATCH:106955102-106961852	NOTEST	0	0	0	0	1	1
ENSG00000271296	ENSG00000271296	RP11-432M8.20	5:17614889-17615220	NOTEST	0	0	0	0	1	1
ENSG00000271298	ENSG00000271298	RP5-1012F16.2	20:11781110-11851363	NOTEST	0	0	0	0	1	1
ENSG00000271299	ENSG00000271299	CTD-2356P16.6	19:41579708-41580012	NOTEST	0	0	0	0	1	1
ENSG00000271300	ENSG00000271300	IGHVII-49-1	HG1592_PATCH:107030711-107030935	NOTEST	0	0	0	0	1	1
ENSG00000271302	ENSG00000271302	RP11-647P12.2	4:122039453-122039889	NOTEST	0	0	0	0	1	1
ENSG00000271304	ENSG00000271304	DPRXP2	6:35911290-35992645	NOTEST	0	0	0	0	1	1
ENSG00000271305	ENSG00000271305	IGHD2OR15-2B	15:21220376-21220407	NOTEST	0	0	0	0	1	1
ENSG00000271306	ENSG00000271306	RP11-678B3.3	7:53723201-53879624	NOTEST	0	0	0	0	1	1
ENSG00000271307	ENSG00000271307	AF146191.8	4:190901056-190901762	NOTEST	0	0	0	0	1	1
ENSG00000271308	ENSG00000271308	AP003900.6	21:11169719-11184046	NOTEST	0.233812	0.622659	1.41309	0	1	1
ENSG00000271309	ENSG00000271309	RP1-85D24.2	Y:13263064-13263272	NOTEST	0	0	0	0	1	1
ENSG00000271310	ENSG00000271310	UBA1	HG29_PATCH:47050295-47074563	NOTEST	0	0	0	0	1	1
ENSG00000271312	ENSG00000271312	IGHD3-10	HG1592_PATCH:106370833-106370864	NOTEST	0	0	0	0	1	1
ENSG00000271313	ENSG00000271313	RP11-736G13.2	18:69557644-69611813	NOTEST	0	0	0	0	1	1
ENSG00000271314	ENSG00000271314	RP11-435O5.6	9:98205261-98279339	NOTEST	0	0.0406243	inf	0	1	1
ENSG00000271315	ENSG00000271315	WI2-2221J1.1	2:16330518-16330662	NOTEST	0	0	0	0	1	1
ENSG00000271317	ENSG00000271317	IGHD4OR15-4A	15:20210049-20210068	NOTEST	0	0	0	0	1	1
ENSG00000271318	ENSG00000271318	AP000654.5	11:86502100-86666433	NOTEST	0	0.0253563	inf	0	1	1
ENSG00000271319	ENSG00000271319	hsa-mir-5195	HG1592_PATCH:107317221-107317336	NOTEST	0	0	0	0	1	1
ENSG00000271320	ENSG00000271320	RP11-1152H14.	2:158733213-158992666	NOTEST	0.0559744	0.047286	-0.243356	0	1	1
ENSG00000271321	ENSG00000271321	CTAGE6	7:143318042-143534026	NOTEST	0	0	0	0	1	1
ENSG00000271322	ENSG00000271322	RP11-390F10.3	X:97603448-97603746	NOTEST	0	0	0	0	1	1

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ENSG00000271324	ENSG00000271324	RP11-10C24.2	3:33835135-33835637	NOTEST	0.352867	0.0318731	-3.46871	0	1	1
ENSG00000271325	ENSG00000271325	CRIP1	HG1592_PATCH:105952653-105965912	NOTEST	0	0	0	0	1	1
ENSG00000271326	ENSG00000271326	LILRB4	HG1079_PATCH:55165381-55173613	NOTEST	0	0	0	0	1	1
ENSG00000271327	ENSG00000271327	RP11-1109F11.3	12:89761583-89763078	NOTEST	0.424746	0.272703	-0.639268	0	1	1
ENSG00000271328	ENSG00000271328	RP11-157D6.1	6:47336678-47336966	NOTEST	0	0	0	0	1	1
ENSG00000271329	ENSG00000271329	RP5-891H21.5	1:44653614-44654721	NOTEST	0.0237657	0	#NAME?	0	1	1
ENSG00000271330	ENSG00000271330	CTA-298G8.2	7:24612886-24733812	NOTEST	0	0	0	0	1	1
ENSG00000271331	ENSG00000271331	IGHVIII-67-2	HG1592_PATCH:107153449-107153537	NOTEST	0	0	0	0	1	1
ENSG00000271332	ENSG00000271332	RP11-797J4.1	11:28042166-28355054	NOTEST	0	0	0	0	1	1
ENSG00000271333	ENSG00000271333	RP11-382B18.5	15:30712485-30712632	NOTEST	0	0	0	0	1	1
ENSG00000271334	ENSG00000271334	CTD-2078B5.2	5:39520532-39524810	NOTEST	0.117578	0.170309	0.534534	0	1	1
ENSG00000271335	ENSG00000271335	RP11-324I22.4	10:35535952-35860852	NOTEST	0.228652	0.356729	0.641672	0	1	1
ENSG00000271336	ENSG00000271336	IGHD1OR15-1A	15:20216405-20216422	NOTEST	0	0	0	0	1	1
ENSG00000271337	ENSG00000271337	NDE1P2	13:37378334-37379439	NOTEST	0	0	0	0	1	1
ENSG00000271338	ENSG00000271338	RP11-96J19.4	6:53246316-53247001	NOTEST	0	0	0	0	1	1
ENSG00000271339	ENSG00000271339	RP11-1114A5.6	X:135870444-135870946	NOTEST	0	0	0	0	1	1
ENSG00000271340	ENSG00000271340	CTD-2526A2.6	17:78489456-78489612	NOTEST	0	0	0	0	1	1
ENSG00000271342	ENSG00000271342	SLC9A7	HG29_PATCH:46464752-46618490	NOTEST	0	0	0	0	1	1
ENSG00000271343	ENSG00000271343	RP11-435O11.5	10:120852651-120852853	NOTEST	0	0	0	0	1	1
ENSG00000271344	ENSG00000271344	RP11-274B21.9	7:128330504-128331771	NOTEST	0.108409	0.23783	1.13345	0	1	1
ENSG00000271345	ENSG00000271345	RNVU1-9	HG1287_PATCH:148725167-148725331	NOTEST	0	0	0	0	1	1
ENSG00000271346	ENSG00000271346	RP1-321E8.4	X:120010405-120010659	NOTEST	0	0	0	0	1	1
ENSG00000271347	ENSG00000271347	RP11-701H24.7	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000271349	ENSG00000271349	RP11-44N17.2	8:97139194-97140029	NOTEST	0	0	0	0	1	1
ENSG00000271350	ENSG00000271350	CTD-2384B9.1	11:46958239-47198676	NOTEST	0	0	0	0	1	1
ENSG00000271351	ENSG00000271351	IGKV1OR2-9	2:98051275-98051562	NOTEST	0	0	0	0	1	1
ENSG00000271352	ENSG00000271352	RBM10	HG29_PATCH:47001650-47046248	NOTEST	0	0	0	0	1	1
ENSG00000271353	ENSG00000271353	RP11-179H18.8	10:121321612-121322042	NOTEST	0	0	0	0	1	1
ENSG00000271354	ENSG00000271354	GAGE12H	HG1436_HG1432_PATCH:49389381-49396700	NOTEST	0	0	0	0	1	1
ENSG00000271355	ENSG00000271355	RP4-666O22.3	1:47949369-47949834	NOTEST	0	0	0	0	1	1
ENSG00000271356	ENSG00000271356	RP11-335E8.1	2:76487880-76488787	NOTEST	0	0	0	0	1	1
ENSG00000271357	ENSG00000271357	RP11-843B15.3	12:32253418-32253669	NOTEST	0	0	0	0	1	1
ENSG00000271358	ENSG00000271358	RP11-241N4.2	14:96485820-96486102	NOTEST	0	0	0	0	1	1
ENSG00000271360	ENSG00000271360	RP11-138I18.1	10:11495944-11654226	NOTEST	0	0	0	0	1	1
ENSG00000271362	ENSG00000271362	RP3-468B3.4	6:33835282-33895408	NOTEST	0	0	0	0	1	1
ENSG00000271363	ENSG00000271363	PHF16	HG29_PATCH:46771867-46920676	NOTEST	0	0	0	0	1	1
ENSG00000271364	ENSG00000271364	RP11-81A1.8	15:80276492-80278066	NOTEST	0.0191156	0	#NAME?	0	1	1
ENSG00000271365	ENSG00000271365	RP1-85D24.3	Y:13262740-13262939	NOTEST	0	0	0	0	1	1
ENSG00000271366	ENSG00000271366	AC002128.5	19:35739232-35758867	NOTEST	0	0	0	0	1	1

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ENSG00000271368	ENSG00000271368	RP11-10E6.1	7:109403630-109404414	NOTEST	0	0	0	0	1	1
ENSG00000271369	ENSG00000271369	RP11-350D17.3	11:34731146-34731708	NOTEST	0	0.02693	inf	0	1	1
ENSG00000271370	ENSG00000271370	RP11-253I19.4	12:12510012-12619840	NOTEST	0	0	0	0	1	1
ENSG00000271371	ENSG00000271371	IGHD6-6	HG1592_PATCH:106376746-106376764	NOTEST	0	0	0	0	1	1
ENSG00000271372	ENSG00000271372	PFN1P3	HG1287_PATCH:145976420-146277520	NOTEST	0	0	0	0	1	1
ENSG00000271373	ENSG00000271373	NANOGP3	6:53283249-53283535	NOTEST	0	0	0	0	1	1
ENSG00000271374	ENSG00000271374	PACS2	HG1592_PATCH:105766899-105864484	NOTEST	0	0	0	0	1	1
ENSG00000271375	ENSG00000271375	RP11-295P22.2	Y:13629402-13629913	NOTEST	0	0	0	0	1	1
ENSG00000271377	ENSG00000271377	RP11-33I11.3	8:61818617-61819011	NOTEST	0	0	0	0	1	1
ENSG00000271378	ENSG00000271378	CTD-2284O10.3	5:37106329-37249530	NOTEST	0	0	0	0	1	1
ENSG00000271379	ENSG00000271379	RP11-440G2.2	12:42463736-42464427	NOTEST	0	0	0	0	1	1
ENSG00000271380	ENSG00000271380	RP11-307C12.12	1:154929501-154946871	NOTEST	0.545162	0.60862	0.158858	0	1	1
ENSG00000271381	ENSG00000271381	REXO1L9P	8:86775086-86776836	NOTEST	0	0	0	0	1	1
ENSG00000271382	ENSG00000271382	RP11-1060G2.2	12:94338816-94341589	NOTEST	0.00570746	0	#NAME?	0	1	1
ENSG00000271383	ENSG00000271383	AC242842.2	HG1287_PATCH:150162302-150242670	NOTEST	0	0	0	0	1	1
ENSG00000271384	ENSG00000271384	RP11-435O5.7	9:98169271-98169944	NOTEST	0	0	0	0	1	1
ENSG00000271385	ENSG00000271385	RP11-108M11.3	10:93170095-93274586	NOTEST	0	0	0	0	1	1
ENSG00000271386	ENSG00000271386	SRGNP1	13:78469615-79233314	NOTEST	0	0.0413509	inf	0	1	1
ENSG00000271387	ENSG00000271387	RP11-382D12.2	1:184354886-184355838	NOTEST	0.253051	0.20165	-0.327578	0	1	1
ENSG00000271388	ENSG00000271388	hsa-mir-4539	HG1592_PATCH:106323849-106323909	NOTEST	0	0	0	0	1	1
ENSG00000271389	ENSG00000271389	OSBPL9P1	3:80212476-80213945	NOTEST	0	0	0	0	1	1
ENSG00000271390	ENSG00000271390	RP11-89C3.3	11:110960593-110961092	NOTEST	0.0452843	0.0321682	-0.493379	0	1	1
ENSG00000271391	ENSG00000271391	IGHD7-27	HG1592_PATCH:106331887-106331898	NOTEST	0	0	0	0	1	1
ENSG00000271392	ENSG00000271392	RP1-161P9.5	HG385_PATCH:34084217-34085344	NOTEST	0	0	0	0	1	1
ENSG00000271393	ENSG00000271393	IGHD3-22	HG1592_PATCH:106352367-106352398	NOTEST	0	0	0	0	1	1
ENSG00000271394	ENSG00000271394	RN7SKP274	HG385_PATCH:34216576-34216823	NOTEST	0	0	0	0	1	1
ENSG00000271395	ENSG00000271395	RP11-75N6.3	13:90200944-90206058	NOTEST	0	0	0	0	1	1
ENSG00000271396	ENSG00000271396	RP11-697E2.9	15:90827607-90828812	NOTEST	0	0.0655523	inf	0	1	1
ENSG00000271397	ENSG00000271397	RP5-1128N12.2	20:11589083-11589696	NOTEST	0	0	0	0	1	1
ENSG00000271398	ENSG00000271398	RP5-1092A3.5	1:28573654-28574079	NOTEST	0	0	0	0	1	1
ENSG00000271399	ENSG00000271399	RP4-799G3.2	1:228993756-228994303	NOTEST	0	0	0	0	1	1
ENSG00000271400	ENSG00000271400	RP13-266I11.1	X:111624619-111625448	NOTEST	0	0	0	0	1	1
ENSG00000271401	ENSG00000271401	RP11-171I2.3	2:179385909-179914813	NOTEST	0	0	0	0	1	1
ENSG00000271402	ENSG00000271402	IGKV2OR2-2	2:97716465-97716765	NOTEST	0	0	0	0	1	1
ENSG00000271403	ENSG00000271403	HOMER2P2	HG1592_PATCH:106753147-106753994	NOTEST	0	0	0	0	1	1
ENSG00000271404	ENSG00000271404	RP11-365F18.5	7:138912966-138913351	NOTEST	0	0	0	0	1	1
ENSG00000271408	ENSG00000271408	RP11-186O14.7	10:90459439-90460158	NOTEST	0	0	0	0	1	1
ENSG00000271409	ENSG00000271409	RP11-432J9.3	10:72689681-72691814	NOTEST	0	0	0	0	1	1
ENSG00000271410	ENSG00000271410	RP11-506H20.2	5:54603587-54830878	NOTEST	0	0	0	0	1	1

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ENSG00000271412	ENSG00000271412	AP000892.8	11:117103340-117283984	NOTEST	0	0	0	0	1	1
ENSG00000271413	ENSG00000271413	RP11-809F4.4	3:175786894-175787040	NOTEST	0	0	0	0	1	1
ENSG00000271414	ENSG00000271414	RP11-751K21.1	7:135335719-135336164	NOTEST	0	0	0	0	1	1
ENSG00000271415	ENSG00000271415	RP11-305E17.7	1:100652474-100715390	NOTEST	0	0	0	0	1	1
ENSG00000271416	ENSG00000271416	IGHVII-60-1	HG1592_PATCH:107104054-107104310	NOTEST	0	0	0	0	1	1
ENSG00000271417	ENSG00000271417	RP11-909M7.3	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000271418	ENSG00000271418	RP11-582E3.5	12:27246855-27247156	NOTEST	0	0	0	0	1	1
ENSG00000271419	ENSG00000271419	RP4-591B8.3	1:114896607-114897800	NOTEST	0	0	0	0	1	1
ENSG00000271420	ENSG00000271420	RP5-1057J7.7	1:23704872-23705522	NOTEST	0.0310118	0	#NAME?	0	1	1
ENSG00000271421	ENSG00000271421	RP1-269O5.3	X:111017542-111326004	NOTEST	0	0	0	0	1	1
ENSG00000271422	ENSG00000271422	SLC20A1P1	HG1592_PATCH:107149731-107150687	NOTEST	0	0	0	0	1	1
ENSG00000271423	ENSG00000271423	CYCSP1	14:76776956-77227731	NOTEST	0	0	0	0	1	1
ENSG00000271424	ENSG00000271424	RP11-647O20.1	14:39699434-39856306	NOTEST	0	0	0	0	1	1
ENSG00000271425	ENSG00000271425	AC239799.1	HG1287_PATCH:146752732-146831219	NOTEST	0	0	0	0	1	1
ENSG00000271426	ENSG00000271426	RP4-718P11.1	20:12989626-13147411	NOTEST	0	0	0	0	1	1
ENSG00000271427	ENSG00000271427	RP11-188D8.1	1:117907520-117908095	NOTEST	0.0367698	0	#NAME?	0	1	1
ENSG00000271428	ENSG00000271428	RP1-224A6.8	1:22379119-22419437	NOTEST	0	0	0	0	1	1
ENSG00000271429	ENSG00000271429	RPL17P51	13:40798761-40798999	NOTEST	0	0	0	0	1	1
ENSG00000271432	ENSG00000271432	IGHD1-1	HG1592_PATCH:106385838-106385855	NOTEST	0	0	0	0	1	1
ENSG00000271433	ENSG00000271433	PPATP2	X:77954880-77955388	NOTEST	0	0	0	0	1	1
ENSG00000271434	ENSG00000271434	RP13-238F13.3	10:126135591-126138753	NOTEST	0	0	0	0	1	1
ENSG00000271435	ENSG00000271435	RP11-803A13.1	2:131071506-131071984	NOTEST	0	0	0	0	1	1
ENSG00000271437	ENSG00000271437	RP11-295B17.6	13:99102454-99231084	NOTEST	0	0	0	0	1	1
ENSG00000271438	ENSG00000271438	IGHD	HG1592_PATCH:106303101-106312014	NOTEST	0	0	0	0	1	1
ENSG00000271439	ENSG00000271439	RP11-666A1.7	1:148616291-148616578	NOTEST	0	0	0	0	1	1
ENSG00000271440	ENSG00000271440	RP11-373N24.2	6:28601157-28601371	NOTEST	0	0	0	0	1	1
ENSG00000271442	ENSG00000271442	PRPF31	HG1079_PATCH:54605981-54634963	NOTEST	0	0	0	0	1	1
ENSG00000271443	ENSG00000271443	RP11-541E12.1	2:38762399-38763391	NOTEST	0.148433	0.352055	1.24599	0	1	1
ENSG00000271444	ENSG00000271444	IGHD2-21	HG1592_PATCH:106354887-106354915	NOTEST	0	0	0	0	1	1
ENSG00000271445	ENSG00000271445	CTC-575C13.1	HG730_PATCH:20462310-20462888	NOTEST	0	0	0	0	1	1
ENSG00000271446	ENSG00000271446	IGHVIII-22-2	HG1592_PATCH:106731024-106731052	NOTEST	0	0	0	0	1	1
ENSG00000271447	ENSG00000271447	MMP28	HG385_PATCH:34092875-34122655	NOTEST	0	0	0	0	1	1
ENSG00000271448	ENSG00000271448	IGHV3-52	HG1592_PATCH:107052712-107053163	NOTEST	0	0	0	0	1	1
ENSG00000271449	ENSG00000271449	AC240441.2	HG1443_HG1444_PATCH:134893821-135019384	NOTEST	0	0	0	0	1	1
ENSG00000271450	ENSG00000271450	IGHV3-64	HG1592_PATCH:107124061-107124595	NOTEST	0	0	0	0	1	1
ENSG00000271451	ENSG00000271451	RP11-521B24.5	HG1592_PATCH:105864915-105937066	NOTEST	0	0	0	0	1	1
ENSG00000271453	ENSG00000271453	ABC7-43041300I9.1	HG1007_PATCH:243117331-243117785	NOTEST	0	0	0	0	1	1
ENSG00000271454	ENSG00000271454	RP11-290L7.5	9:39072763-39288312	NOTEST	0.0137774	0.0193937	0.493285	0	1	1
ENSG00000271455	ENSG00000271455	RP11-269M20.2	5:49899062-49899345	NOTEST	0	0	0	0	1	1
ENSG00000271456	ENSG00000271456	CTC-661I16.2	16:57366290-57366511	NOTEST	0	0	0	0	1	1

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ENSG00000271459	ENSG00000271459	RP4-560B9.6	1:171724942-171725463	NOTEST	0	0	0	0	1	1
ENSG00000271461	ENSG00000271461	RP4-673D20.6	20:1737401-1739586	NOTEST	0	0	0	0	1	1
ENSG00000271462	ENSG00000271462	RP11-841C19.4	12:19556978-19873735	NOTEST	0	0	0	0	1	1
ENSG00000271464	ENSG00000271464	DPRXP7	X:111563179-111563645	NOTEST	0	0	0	0	1	1
ENSG00000271465	ENSG00000271465	SQSTM1P1	13:62980190-62981049	NOTEST	0	0	0	0	1	1
ENSG00000271466	ENSG00000271466	CICP24	7:63228634-63231425	NOTEST	0	0	0	0	1	1
ENSG00000271467	ENSG00000271467	GAGE12G	HG1436_HG1432_PATCH:49379832-49387153	NOTEST	0	0	0	0	1	1
ENSG00000271468	ENSG00000271468	RP11-14N4.1	14:39074458-39075302	NOTEST	0	0	0	0	1	1
ENSG00000271469	ENSG00000271469	IGHV1-69	HG1592_PATCH:107181020-107181518	NOTEST	0	0	0	0	1	1
ENSG00000271474	ENSG00000271474	RP11-710C12.1	4:96083654-96473608	NOTEST	0.0367115	0.0136169	-1.43084	0	1	1
ENSG00000271475	ENSG00000271475	RP4-799G3.1	1:228912058-228912612	NOTEST	0	0	0	0	1	1
ENSG00000271476	ENSG00000271476	RP11-265D19.7	HG1443_HG1444_PATCH:134598357-134599513	NOTEST	0	0	0	0	1	1
ENSG00000271477	ENSG00000271477	CTC-447K7.1	5:154776850-154777913	NOTEST	0	0	0	0	1	1
ENSG00000271479	ENSG00000271479	CTC-260E6.11	HG730_PATCH:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000271480	ENSG00000271480	RP11-475J5.10	5:99386422-99386767	NOTEST	0	0	0	0	1	1
ENSG00000271481	ENSG00000271481	LILRB2	HG1079_PATCH:54777074-54784438	NOTEST	0	0	0	0	1	1
ENSG00000271482	ENSG00000271482	CTB-152G17.4	7:104653871-105039755	NOTEST	0	0	0	0	1	1
ENSG00000271483	ENSG00000271483	RP11-384A12.1	3:194123400-194239008	NOTEST	0	0	0	0	1	1
ENSG00000271484	ENSG00000271484	RP11-132J14.3	14:55965995-56168244	NOTEST	0	0	0	0	1	1
ENSG00000271486	ENSG00000271486	AP000403.3	21:20993008-20993859	NOTEST	0	0	0	0	1	1
ENSG00000271487	ENSG00000271487	VN1R105P	HG1079_PATCH:55147142-55152854	NOTEST	0	0	0	0	1	1
ENSG00000271488	ENSG00000271488	RP1-55C23.8	6:133085798-133086597	NOTEST	0	0	0	0	1	1
ENSG00000271489	ENSG00000271489	AC008984.5	HG1079_PATCH:54801358-54802068	NOTEST	0	0	0	0	1	1
ENSG00000271490	ENSG00000271490	RP11-60E8.4	12:51157492-51214905	NOTEST	0	0	0	0	1	1
ENSG00000271491	ENSG00000271491	RP11-787P24.4	11:23391661-23399190	NOTEST	0	0	0	0	1	1
ENSG00000271492	ENSG00000271492	MEMO1P5	13:96046302-96046708	NOTEST	0	0	0	0	1	1
ENSG00000271493	ENSG00000271493	IGHV4-28	HG1592_PATCH:106790592-106791097	NOTEST	0	0	0	0	1	1
ENSG00000271494	ENSG00000271494	CTB-23I7.3	5:150745993-150810913	NOTEST	0	0	0	0	1	1
ENSG00000271495	ENSG00000271495	RP11-666O2.1	16:28559651-28559979	NOTEST	0	0	0	0	1	1
ENSG00000271496	ENSG00000271496	SNRPGP20	12:80382793-80382998	NOTEST	0	0	0	0	1	1
ENSG00000271497	ENSG00000271497	IGHVII-15-1	HG1592_PATCH:106629919-106630139	NOTEST	0	0	0	0	1	1
ENSG00000271498	ENSG00000271498	RP11-505K1.1	6:113147140-113147672	NOTEST	0	0	0	0	1	1
ENSG00000271499	ENSG00000271499	CTC-559E9.9	19:19861426-19863353	NOTEST	0	0	0	0	1	1
ENSG00000271500	ENSG00000271500	RP11-288K12.1	12:1797739-1897844	NOTEST	0.0164284	0.0295835	0.848603	0	1	1
ENSG00000271501	ENSG00000271501	RP1-73A14.2	HG1459_PATCH:146045890-146046200	NOTEST	0	0	0	0	1	1
ENSG00000271502	ENSG00000271502	RP6-166C19.17	X:120091080-120091333	NOTEST	0	0	0	0	1	1
ENSG00000271503	ENSG00000271503	CCL5	HG385_PATCH:34195985-34212882	NOTEST	0	0	0	0	1	1
ENSG00000271504	ENSG00000271504	IGHV4-55	HG1592_PATCH:107072437-107072888	NOTEST	0	0	0	0	1	1
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ENSG00000271507	ENSG00000271507	RP11-603B24.6	15:22490342-22490685	NOTEST	0	0	0	0	1	1
ENSG00000271508	ENSG00000271508	RP11-73B8.3	12:44026895-44027084	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000271510	ENSG00000271510	RPL17P42	HG385_PATCH:33905064-34053436	NOTEST	0	0	0	0	1	1
ENSG00000271511	ENSG00000271511	RP11-712C19.1	14:64812888-64846036	NOTEST	0	0	0	0	1	1
ENSG00000271512	ENSG00000271512	AL928742.4	HG1592_PATCH:106057406-106057466	NOTEST	0	0	0	0	1	1
ENSG00000271516	ENSG00000271516	LILRP2	HG1079_PATCH:55211169-55216707	NOTEST	0	0	0	0	1	1
ENSG00000271517	ENSG00000271517	RP11-434J24.3	HG1459_PATCH:146894447-146894689	NOTEST	0	0	0	0	1	1
ENSG00000271519	ENSG00000271519	RP11-307A17.2	X:35882974-35887748	NOTEST	0	0	0	0	1	1
ENSG00000271520	ENSG00000271520	IGHVII-33-1	HG1592_PATCH:106833721-106834001	NOTEST	0	0	0	0	1	1
ENSG00000271522	ENSG00000271522	RP11-36B6.1	7:130474966-130476483	NOTEST	0	0	0	0	1	1
ENSG00000271523	ENSG00000271523	RP4-576H24.5	20:1497404-1600707	NOTEST	0	0	0	0	1	1
ENSG00000271524	ENSG00000271524	CTC-260E6.10	19:20188802-20432114	NOTEST	0	0	0	0	1	1
ENSG00000271525	ENSG00000271525	RP11-349K21.1	9:136944025-136944566	NOTEST	0	0	0	0	1	1
ENSG00000271526	ENSG00000271526	RP4-668E10.2	7:9123651-9123805	NOTEST	0	0	0	0	1	1
ENSG00000271527	ENSG00000271527	RP11-7G12.2	1:165910471-165911006	NOTEST	0	0	0	0	1	1
ENSG00000271528	ENSG00000271528	AC246787.4	HG1592_PATCH:106323909-106323969	NOTEST	0	0	0	0	1	1
ENSG00000271530	ENSG00000271530	RP1-24O22.5	6:95123-95454	NOTEST	0	0	0	0	1	1
ENSG00000271531	ENSG00000271531	IGHV5-51	HG1592_PATCH:107045080-107045573	NOTEST	0	0	0	0	1	1
ENSG00000271532	ENSG00000271532	RP11-426K3.1	2:101436613-101886778	NOTEST	0.133723	0	#NAME?	0	1	1
ENSG00000271533	ENSG00000271533	RP3-368A4.6	X:73164158-73513409	NOTEST	0.514007	0.476777	-0.108474	0	1	1
ENSG00000271534	ENSG00000271534	IGHD5-18	HG1592_PATCH:106356420-106362914	NOTEST	0	0	0	0	1	1
ENSG00000271535	ENSG00000271535	IGHV1-3	HG1592_PATCH:106471433-106471911	NOTEST	0	0	0	0	1	1
ENSG00000271536	ENSG00000271536	RP11-51I5.1	2:74104692-74105989	NOTEST	0	0	0	0	1	1
ENSG00000271537	ENSG00000271537	RP11-365F18.6	7:138883302-138883888	NOTEST	0.250566	0.358738	0.517737	0	1	1
ENSG00000271538	ENSG00000271538	RP11-326I11.4	4:185427613-185458708	NOTEST	0	0	0	0	1	1
ENSG00000271539	ENSG00000271539	IGHVII-30-1	HG1592_PATCH:106809060-106809292	NOTEST	0	0	0	0	1	1
ENSG00000271541	ENSG00000271541	IGHM	HG1592_PATCH:106320580-106322555	NOTEST	0	0	0	0	1	1
ENSG00000271542	ENSG00000271542	LENG1	HG1079_PATCH:54640973-54663136	NOTEST	0	0	0	0	1	1
ENSG00000271543	ENSG00000271543	RP11-692M12.5	11:47799638-47870107	NOTEST	0	0	0	0	1	1
ENSG00000271544	ENSG00000271544	AC006499.9	4:10239836-10239859	NOTEST	0	0	0	0	1	1
ENSG00000271545	ENSG00000271545	RP11-301J7.9	HG1211_PATCH:47955609-47987141	NOTEST	0	0	0	0	1	1
ENSG00000271546	ENSG00000271546	RP4-725K1.1	1:145088038-145088567	NOTEST	0	0	0	0	1	1
ENSG00000271547	ENSG00000271547	RP11-579D7.8	12:49194358-49194869	NOTEST	0.0813348	0.034039	-1.25668	0	1	1
ENSG00000271548	ENSG00000271548	IGHVIII-67-4	HG1592_PATCH:107161438-107161734	NOTEST	0	0	0	0	1	1
ENSG00000271551	ENSG00000271551	RP11-230C9.2	6:157097493-157098211	NOTEST	0.0271556	0.0211303	-0.361932	0	1	1
ENSG00000271553	ENSG00000271553	RP11-274B21.10	7:128307096-128308210	NOTEST	0.170447	0.220458	0.371181	0	1	1
ENSG00000271554	ENSG00000271554	RP4-665N4.8	1:36396318-36538101	NOTEST	0	0	0	0	1	1
ENSG00000271555	ENSG00000271555	CTD-3214K23.1	8:53535015-53658403	NOTEST	0.606476	0.303418	-0.999144	0	1	1
ENSG00000271556	ENSG00000271556	CTD-2230M5.3	HG1462_PATCH:113625457-113626424	NOTEST	0	0	0	0	1	1
ENSG00000271557	ENSG00000271557	RP11-692M12.4	11:47799638-47870107	NOTEST	0.150304	0	#NAME?	0	1	1

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ENSG00000271558	ENSG00000271558	RP11-445P19.2	1:187475969-187476251	NOTEST	0	0	0	0	1	1
ENSG00000271559	ENSG00000271559	RP11-380N8.6	13:26803468-26803781	NOTEST	0	0	0	0	1	1
ENSG00000271560	ENSG00000271560	KB-1410C5.4	8:102349723-102349877	NOTEST	0	0	0	0	1	1
ENSG00000271561	ENSG00000271561	RNU6-1307P	HG1079_PATCH:54767204-54767313	NOTEST	0	0	0	0	1	1
ENSG00000271562	ENSG00000271562	IGHV3-23	HG1592_PATCH:106734944-106735477	NOTEST	0	0	0	0	1	1
ENSG00000271563	ENSG00000271563	HIRAP1	10:25980465-25981252	NOTEST	0	0	0	0	1	1
ENSG00000271564	ENSG00000271564	RP13-444H2.1	13:52908429-52916031	NOTEST	0	0	0	0	1	1
ENSG00000271565	ENSG00000271565	RP4-775C13.2	20:6199845-6200090	NOTEST	0	0	0	0	1	1
ENSG00000271567	ENSG00000271567	AC246785.1	HG1287_PATCH:145059289-145060074	NOTEST	0	0	0	0	1	1
ENSG00000271568	ENSG00000271568	RP11-632K21.7	7:150300648-150301732	NOTEST	0	0	0	0	1	1
ENSG00000271569	ENSG00000271569	IGKV1OR2-6	2:98018363-98018640	NOTEST	0	0	0	0	1	1
ENSG00000271571	ENSG00000271571	IGHD2-2	HG1592_PATCH:106383162-106383193	NOTEST	0	0	0	0	1	1
ENSG00000271572	ENSG00000271572	RPS9	HG1079_PATCH:54703995-54752257	NOTEST	0	0	0	0	1	1
ENSG00000271573	ENSG00000271573	RP11-96C23.12	10:88786940-88787234	NOTEST	0	0	0	0	1	1
ENSG00000271574	ENSG00000271574	IGHV1-12	HG1592_PATCH:106588756-106589046	NOTEST	0	0	0	0	1	1
ENSG00000271575	ENSG00000271575	IGHVII-62-1	HG1592_PATCH:107116887-107117122	NOTEST	0	0	0	0	1	1
ENSG00000271577	ENSG00000271577	IGHVII-1-1	HG1592_PATCH:106411546-106411726	NOTEST	0	0	0	0	1	1
ENSG00000271578	ENSG00000271578	RP5-1033H2.1	1:101656075-101656550	NOTEST	0	0	0	0	1	1
ENSG00000271579	ENSG00000271579	RP11-116D17.3	12:115737392-115738513	NOTEST	0	0	0	0	1	1
ENSG00000271580	ENSG00000271580	RP11-536L3.4	1:205055269-205091143	NOTEST	0.597805	0.403547	-0.56694	0	1	1
ENSG00000271581	ENSG00000271581	XXbac-BPG248L24.12	6:31321648-31325414	NOTEST	0	0	0	0	1	1
ENSG00000271582	ENSG00000271582	RP11-511P7.4	7:150181148-150182223	NOTEST	0	0	0	0	1	1
ENSG00000271583	ENSG00000271583	RP11-638D14.1	2:147591068-147591606	NOTEST	0	0	0	0	1	1
ENSG00000271584	ENSG00000271584	RP11-89C3.4	11:110962655-110968081	NOTEST	0.428623	0.300939	-0.510241	0	1	1
ENSG00000271585	ENSG00000271585	CTB-88F18.4	5:126512387-126512742	NOTEST	0	0	0	0	1	1
ENSG00000271586	ENSG00000271586	RP11-52M17.1	7:44640630-44641086	NOTEST	0	0	0	0	1	1
ENSG00000271587	ENSG00000271587	GS1-531I17.3	17:63524680-64188202	NOTEST	0	0	0	0	1	1
ENSG00000271588	ENSG00000271588	RP11-435P24.3	1:203369393-203369709	NOTEST	0	0	0	0	1	1
ENSG00000271589	ENSG00000271589	RP11-130N24.2	X:73952683-74145282	NOTEST	0	0	0	0	1	1
ENSG00000271590	ENSG00000271590	RP11-181E10.3	2:111953539-112268567	NOTEST	0.118352	0.19403	0.71319	0	1	1
ENSG00000271592	ENSG00000271592	IGHV7-40	HG1592_PATCH:106891701-106891900	NOTEST	0	0	0	0	1	1
ENSG00000271593	ENSG00000271593	RP11-335E6.4	1:63604920-63628824	NOTEST	0.0964827	0	#NAME?	0	1	1
ENSG00000271594	ENSG00000271594	RP11-277L2.6	1:149524786-149525073	NOTEST	0	0	0	0	1	1
ENSG00000271595	ENSG00000271595	TCEB1P35	Y:19576758-19577094	NOTEST	0	0	0	0	1	1
ENSG00000271596	ENSG00000271596	RP11-407N8.4	12:51342899-51343167	NOTEST	0	0	0	0	1	1
ENSG00000271597	ENSG00000271597	RP11-85D18.1	2:69478949-69479496	NOTEST	0	0	0	0	1	1
ENSG00000271598	ENSG00000271598	CTD-2542C24.9	19:21203425-21242856	NOTEST	0	0	0	0	1	1
ENSG00000271600	ENSG00000271600	RP11-864G5.8	11:102179287-102179528	NOTEST	0	0	0	0	1	1
ENSG00000271601	ENSG00000271601	AC243547.1	HG1287_PATCH:146607982-146645521	NOTEST	0	0	0	0	1	1
ENSG00000271602	ENSG00000271602	KRT8P49	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000271605	ENSG00000271605	MILR1	17:62461568-62464760	NOTEST	0.0357869	0.209332	2.54829	0	1	1

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ENSG00000271606	ENSG00000271606	RP11-27G13.5	4:156306503-156306644	NOTEST	0	0	0	0	1	1
ENSG00000271607	ENSG00000271607	RP3-418A9.3	6:111185062-111185654	NOTEST	0	0	0	0	1	1
ENSG00000271608	ENSG00000271608	RP11-697G4.4	6:108872220-108872410	NOTEST	0	0	0	0	1	1
ENSG00000271609	ENSG00000271609	CTB-31N19.4	16:21544265-21561694	NOTEST	0	0	0	0	1	1
ENSG00000271611	ENSG00000271611	RP4-813F11.3	7:140634666-140634810	NOTEST	0	0	0	0	1	1
ENSG00000271612	ENSG00000271612	HSPE1P14	8:103463990-103464711	NOTEST	0	0	0	0	1	1
ENSG00000271613	ENSG00000271613	KIR3DL2	HG1079_PATCH:55227717-55370462	NOTEST	0	0	0	0	1	1
ENSG00000271614	ENSG00000271614	LINC00936	12:89954905-90106367	NOTEST	0.128022	0.0879958	-0.540891	0	1	1
ENSG00000271615	ENSG00000271615	CTD-2026C7.1	2:57982562-57993187	NOTEST	0	0	0	0	1	1
ENSG00000271616	ENSG00000271616	RP11-578F21.13	15:29033388-29101361	NOTEST	0	0	0	0	1	1
ENSG00000271618	ENSG00000271618	RP11-175G14.2	1:71547006-72748417	NOTEST	0	0	0	0	1	1
ENSG00000271619	ENSG00000271619	AC243962.1	HG1079_PATCH:55209484-55209554	NOTEST	0	0	0	0	1	1
ENSG00000271620	ENSG00000271620	IGHV3OR16-7	16:33740803-33741266	NOTEST	0	0	0	0	1	1
ENSG00000271621	ENSG00000271621	RP11-60E8.3	12:51236702-51281667	NOTEST	0	0	0	0	1	1
ENSG00000271622	ENSG00000271622	IGHD5-24	HG1592_PATCH:10635023-106350259	NOTEST	0	0	0	0	1	1
ENSG00000271623	ENSG00000271623	RP11-435I10.5	16:28376020-28376654	NOTEST	0	0	0	0	1	1
ENSG00000271624	ENSG00000271624	RP11-651K21.1	11:131240372-132206716	NOTEST	0	0	0	0	1	1
ENSG00000271625	ENSG00000271625	PSMA6P4	13:98127995-98128713	NOTEST	0	0	0	0	1	1
ENSG00000271626	ENSG00000271626	RP11-3K24.2	17:58256454-58508782	NOTEST	0	0	0	0	1	1
ENSG00000271627	ENSG00000271627	RP11-165D20.1	2:91911048-91911631	NOTEST	0	0	0	0	1	1
ENSG00000271629	ENSG00000271629	RP11-79J24.1	2:21421389-21421768	NOTEST	0	0	0	0	1	1
ENSG00000271630	ENSG00000271630	IGKV2OR2-8	2:98041866-98042166	NOTEST	0	0	0	0	1	1
ENSG00000271631	ENSG00000271631	RP11-408O19.5	9:115513117-115653193	NOTEST	0.130198	0.122202	-0.0914386	0	1	1
ENSG00000271632	ENSG00000271632	RP11-496I2.7	14:19787426-19787943	NOTEST	0	0	0	0	1	1
ENSG00000271634	ENSG00000271634	IGHD6-13	HG1592_PATCH:106367478-106367499	NOTEST	0	0	0	0	1	1
ENSG00000271635	ENSG00000271635	RP11-68E19.1	2:112315989-112317514	NOTEST	0	0	0	0	1	1
ENSG00000271636	ENSG00000271636	AC239802.2	HG1287_PATCH:149575877-149719430	NOTEST	0	0	0	0	1	1
ENSG00000271637	ENSG00000271637	LENG8-AS1	HG1079_PATCH:54948066-54965270	NOTEST	0	0	0	0	1	1
ENSG00000271638	ENSG00000271638	CTC-575C13.2	19:20434800-20435377	NOTEST	0	0	0	0	1	1
ENSG00000271639	ENSG00000271639	RP11-289A15.1	2:234384165-234475428	NOTEST	0.0195329	0.023654	0.27618	0	1	1
ENSG00000271640	ENSG00000271640	AC245036.1	HG1079_PATCH:55076173-55142146	NOTEST	0	0	0	0	1	1
ENSG00000271641	ENSG00000271641	GAGE12D	HG1436_HG1432_PATCH:49351165-49358493	NOTEST	0	0	0	0	1	1
ENSG00000271642	ENSG00000271642	RP11-66E20.2	12:47075853-47076496	NOTEST	0	0	0	0	1	1
ENSG00000271644	ENSG00000271644	RP3-365I19.2	1:143913614-144094424	NOTEST	0	0	0	0	1	1
ENSG00000271646	ENSG00000271646	RP11-326I11.3	4:185395955-185398458	NOTEST	0.0254733	0.0332085	0.382569	0	1	1
ENSG00000271647	ENSG00000271647	KRT8P47	1:44501797-44570647	NOTEST	0.0107557	0.00862171	-0.319052	0	1	1
ENSG00000271648	ENSG00000271648	IGHV3-11	HG1592_PATCH:106582973-106583541	NOTEST	0	0	0	0	1	1
ENSG00000271649	ENSG00000271649	LINC00904	19:35382932-35389847	NOTEST	0	0	0	0	1	1
ENSG00000271650	ENSG00000271650	AL031601.4	10:42705437-42705831	NOTEST	0	0	0	0	1	1
ENSG00000271652	ENSG00000271652	RP11-168P6.2	13:54689923-54707001	NOTEST	0	0	0	0	1	1
ENSG00000271653	ENSG00000271653	RP11-259K5.1	3:37258269-37259479	NOTEST	0	0	0	0	1	1
ENSG00000271654	ENSG00000271654	RP11-685B14.3	8:18244617-18245287	NOTEST	0	0	0	0	1	1
ENSG00000271655	ENSG00000271655	CTD-2579N5.5	19:23015002-23042224	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
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ENSG00000271657	ENSG00000271657	RP11-270B14.1	2:62395996-62398298	NOTEST	0	0	0	0	1	1
ENSG00000271658	ENSG00000271658	OSCAR	HG1079_PATCH:54597921-54605946	NOTEST	0	0	0	0	1	1
ENSG00000271659	ENSG00000271659	RP11-435O5.4	9:98205261-98279339	NOTEST	0.370411	0.273492	-0.437629	0	1	1
ENSG00000271660	ENSG00000271660	RP1-73A14.2	X:146045693-146046003	NOTEST	0	0	0	0	1	1
ENSG00000271661	ENSG00000271661	CTB-87J17.2	19:23158269-23185978	NOTEST	0	0	0	0	1	1
ENSG00000271662	ENSG00000271662	RP11-141C7.3	3:195377016-195378343	NOTEST	0.0165211	0.076233	2.20611	0	1	1
ENSG00000271664	ENSG00000271664	RP4-800G7.3	7:148959261-148994403	NOTEST	0.0643024	0.153306	1.25347	0	1	1
ENSG00000271665	ENSG00000271665	RNU12-2P	HG29_PATCH:46992105-46992261	NOTEST	0	0	0	0	1	1
ENSG00000271666	ENSG00000271666	CTC-523E23.9	19:35279485-35323773	NOTEST	0	0	0	0	1	1
ENSG00000271667	ENSG00000271667	RP11-338I24.1	2:117444793-117444963	NOTEST	0	0	0	0	1	1
ENSG00000271668	ENSG00000271668	RP11-1324A7.2	HG14_PATCH:57552872-57553602	NOTEST	0	0	0	0	1	1
ENSG00000271669	ENSG00000271669	AC008746.3	HG1079_PATCH:54918684-54940126	NOTEST	0	0	0	0	1	1
ENSG00000271670	ENSG00000271670	RP11-95I16.4	10:122521323-122669036	NOTEST	0.222719	0.160484	-0.4728	0	1	1
ENSG00000271671	ENSG00000271671	RP11-598F17.2	3:95963575-95964179	NOTEST	0	0	0	0	1	1
ENSG00000271672	ENSG00000271672	DUXAP8	22:16147978-16193004	NOTEST	0	0	0	0	1	1
ENSG00000271674	ENSG00000271674	INE1	HG29_PATCH:47050295-47074563	NOTEST	0	0	0	0	1	1
ENSG00000271676	ENSG00000271676	RP11-1E1.2	4:78033647-78034611	NOTEST	0	0	0	0	1	1
ENSG00000271677	ENSG00000271677	RP1-274L7.3	X:129679559-129680448	NOTEST	0	0	0	0	1	1
ENSG00000271679	ENSG00000271679	CTB-107P3.1	5:163314511-163314833	NOTEST	0	0	0	0	1	1
ENSG00000271680	ENSG00000271680	RP11-564A8.8	1:207077730-207096592	NOTEST	0	0.107451	inf	0	1	1
ENSG00000271681	ENSG00000271681	RP11-1259L22.2	5:177664618-178017556	NOTEST	0	0	0	0	1	1
ENSG00000271682	ENSG00000271682	RP11-393B14.2	3:183180638-183180989	NOTEST	0	0	0	0	1	1
ENSG00000271684	ENSG00000271684	RNVU1-18	HG1287_PATCH:144415821-144415985	NOTEST	0	0	0	0	1	1
ENSG00000271686	ENSG00000271686	CTD-2230M5.3	X:113623440-113624407	NOTEST	0	0	0	0	1	1
ENSG00000271687	ENSG00000271687	MTND5P10	5:99382680-99384489	NOTEST	0	0	0	0	1	1
ENSG00000271688	ENSG00000271688	IGHD5-12	HG1592_PATCH:106368985-106369008	NOTEST	0	0	0	0	1	1
ENSG00000271689	ENSG00000271689	IGHV1-24	HG1592_PATCH:106742884-106743380	NOTEST	0	0	0	0	1	1
ENSG00000271691	ENSG00000271691	RP11-812E19.12	16:33654251-33654536	NOTEST	0	0	0	0	1	1
ENSG00000271692	ENSG00000271692	IGHVII-53-1	HG1592_PATCH:107066006-107066261	NOTEST	0	0	0	0	1	1
ENSG00000271693	ENSG00000271693	CTD-2194M22.1	X:87624343-87624460	NOTEST	0	0	0	0	1	1
ENSG00000271694	ENSG00000271694	TMEM121	HG1592_PATCH:105992939-105996539	NOTEST	0	0	0	0	1	1
ENSG00000271695	ENSG00000271695	IGHV3-72	HG1592_PATCH:107257030-107257570	NOTEST	0	0	0	0	1	1
ENSG00000271696	ENSG00000271696	RP11-548K12.13	7:57888036-57896752	NOTEST	0	0	0	0	1	1
ENSG00000271697	ENSG00000271697	RP11-1012A1.10	14:68168602-68283307	NOTEST	0	0	0	0	1	1
ENSG00000271698	ENSG00000271698	GS1-393G12.13	8:145575877-145584932	NOTEST	0.0105019	0.0186212	0.826303	0	1	1
ENSG00000271699	ENSG00000271699	SNX29P2	16:29262828-29519817	NOTEST	0.301582	0.151158	-0.99649	0	1	1
ENSG00000271701	ENSG00000271701	RP11-438F14.10	1:248764716-248765170	NOTEST	0	0	0	0	1	1
ENSG00000271702	ENSG00000271702	RP11-63N3.2	18:75344883-75345316	NOTEST	0	0	0	0	1	1
ENSG00000271703	ENSG00000271703	QTRT1P1	HG1434_PATCH:112859526-113181445	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000271704	ENSG00000271704	CTC-575C13.1	19:20451077-20607775	NOTEST	0	0	0	0	1	1
ENSG00000271705	ENSG00000271705	RPL17P3	14:80943329-81636758	NOTEST	0	0	0	0	1	1
ENSG00000271706	ENSG00000271706	hsa-mir-335	HG1308_PATCH:130126045-130351086	NOTEST	0	0	0	0	1	1
ENSG00000271707	ENSG00000271707	ATP1B3P1	2:60962029-60962850	NOTEST	0	0	0	0	1	1
ENSG00000271709	ENSG00000271709	RP11-297J22.1	2:121493198-121750229	NOTEST	0	0.0390955	inf	0	1	1
ENSG00000271710	ENSG00000271710	RP11-312P12.3	10:75910959-76469061	NOTEST	0	0	0	0	1	1
ENSG00000271711	ENSG00000271711	RP11-392O18.2	3:150259780-150348222	NOTEST	0	0	0	0	1	1
ENSG00000271712	ENSG00000271712	RP11-688D15.2	14:85464621-85465640	NOTEST	0	0	0	0	1	1
ENSG00000271713	ENSG00000271713	KIR2DL4	HG1079_PATCH:55227717-55370462	NOTEST	0	0	0	0	1	1
ENSG00000271714	ENSG00000271714	CTD-2377O17.1	5:74073398-74163679	NOTEST	0.0357391	0.0512767	0.520801	0	1	1
ENSG00000271715	ENSG00000271715	CTD-2256P15.5	5:10269600-10270030	NOTEST	0	0	0	0	1	1
ENSG00000271716	ENSG00000271716	RP11-169K17.4	3:11313994-11766453	NOTEST	0	0	0	0	1	1
ENSG00000271717	ENSG00000271717	CTD-3020H12.4	19:8271619-8327305	NOTEST	0	0	0	0	1	1
ENSG00000271718	ENSG00000271718	AC007040.8	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000271719	ENSG00000271719	OR13Z2P	HG1287_PATCH:148131993-148132548	NOTEST	0	0	0	0	1	1
ENSG00000271720	ENSG00000271720	RP13-941N14.1	HG1595_PATCH:121837843-122031307	NOTEST	0	0	0	0	1	1
ENSG00000271721	ENSG00000271721	RP11-337C18.9	1:146644349-146767443	NOTEST	0.516352	0.332602	-0.634559	0	1	1
ENSG00000271722	ENSG00000271722	RP11-446E9.2	8:56926045-56926727	NOTEST	0.0290692	0.0637248	1.13236	0	1	1
ENSG00000271723	ENSG00000271723	MROH7-TTC4	1:55107458-55208330	NOTEST	0	0.0122543	inf	0	1	1
ENSG00000271724	ENSG00000271724	CTC-359M8.3	5:145583112-145756526	NOTEST	0	0	0	0	1	1
ENSG00000271725	ENSG00000271725	RP11-761I4.4	15:81451915-81616524	NOTEST	0.0487006	0	#NAME?	0	1	1
ENSG00000271726	ENSG00000271726	CU442762.4	GL000247.1:12802-12884	NOTEST	0	0	0	0	1	1
ENSG00000271727	ENSG00000271727	RP11-532F6.4	6:711532-750729	NOTEST	0	0	0	0	1	1
ENSG00000271730	ENSG00000271730	RP11-787I22.3	6:109307639-109416022	NOTEST	0.0387577	0.157784	2.02539	0	1	1
ENSG00000271732	ENSG00000271732	RP5-1182A14.5	1:16943885-16944224	NOTEST	0	0	0	0	1	1
ENSG00000271735	ENSG00000271735	RP1-60O19.1	HG357_PATCH:107165326-107235416	NOTEST	0	0	0	0	1	1
ENSG00000271736	ENSG00000271736	RP11-85G21.3	1:157250505-157252858	NOTEST	0	0	0	0	1	1
ENSG00000271737	ENSG00000271737	CTB-113I20.2	5:133340837-133341253	NOTEST	0.591818	0.180948	-1.70958	0	1	1
ENSG00000271739	ENSG00000271739	U1	7:119646029-119646155	NOTEST	0	0	0	0	1	1
ENSG00000271743	ENSG00000271743	CTD-2541M15.3	8:6261071-6565730	NOTEST	0	0	0	0	1	1
ENSG00000271745	ENSG00000271745	AC093668.3	7:102120178-102121095	NOTEST	0	0	0	0	1	1
ENSG00000271746	ENSG00000271746	RP1-202O8.3	1:6324328-6454451	NOTEST	0	0	0	0	1	1
ENSG00000271748	ENSG00000271748	MIR92B	1:155164967-155165063	NOTEST	0	0	0	0	1	1
ENSG00000271749	ENSG00000271749	RP11-269G24.7	17:61086916-61509572	NOTEST	0	0	0	0	1	1
ENSG00000271751	ENSG00000271751	RP11-110I1.14	11:118935973-118936388	NOTEST	0.2902	0.0908466	-1.67554	0	1	1
ENSG00000271752	ENSG00000271752	RP11-269M20.3	5:49958692-49959100	NOTEST	0	0	0	0	1	1
ENSG00000271753	ENSG00000271753	BEND3	HG357_PATCH:107513056-107563144	NOTEST	0	0	0	0	1	1
ENSG00000271754	ENSG00000271754	RP3-337H4.9	6:43474706-43543812	NOTEST	0.399011	0.0960167	-2.05507	0	1	1
ENSG00000271755	ENSG00000271755	RP1-153G14.4	6:27371788-27374743	NOTEST	0.0824675	0.039516	-1.06139	0	1	1
ENSG00000271757	ENSG00000271757	RP11-111M22.5	11:76092356-76125663	NOTEST	0.10579	0.17033	0.687125	0	1	1

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ENSG00000271760	ENSG00000271760	ADD2	HG953_PATCH:70834749-70995357	NOTEST	0	0	0	0	1	1
ENSG00000271761	ENSG00000271761	XXbac-BPGBPG55C20.3	6:58228886-58229426	NOTEST	0	0.0285542	inf	0	1	1
ENSG00000271762	ENSG00000271762	RP11-213H15.4	5:90598845-90610219	NOTEST	4.35E-05	0.094738	11.0881	0	1	1
ENSG00000271763	ENSG00000271763	RP11-386M24.9	15:93146139-93353114	NOTEST	0	0	0	0	1	1
ENSG00000271764	ENSG00000271764	MIR587	HG357_PATCH:107165326-107235416	NOTEST	0	0	0	0	1	1
ENSG00000271765	ENSG00000271765	7SK	6:136663874-136873692	NOTEST	0	0	0	0	1	1
ENSG00000271766	ENSG00000271766	CTD-2195M15.3	5:126813986-126814429	NOTEST	0.102467	0.0388786	-1.39811	0	1	1
ENSG00000271767	ENSG00000271767	AP002789.1	11:77225980-77348850	NOTEST	0	0	0	0	1	1
ENSG00000271770	ENSG00000271770	Metazoa_SRP	17:47187123-47187413	NOTEST	0	0	0	0	1	1
ENSG00000271771	ENSG00000271771	RP11-1250I15.3	5:34158225-34158872	NOTEST	0	0	0	0	1	1
ENSG00000271772	ENSG00000271772	VAX2	HG953_PATCH:71127720-71160577	NOTEST	0	0	0	0	1	1
ENSG00000271774	ENSG00000271774	RP4-678D15.1	20:51588945-52120853	NOTEST	0	0	0	0	1	1
ENSG00000271776	ENSG00000271776	RP11-52L5.6	13:78469615-79233314	NOTEST	0.0058212	0.0326509	2.48774	0	1	1
ENSG00000271778	ENSG00000271778	RP11-379F4.8	3:158414680-158547508	NOTEST	0.140571	0.106747	-0.397104	0	1	1
ENSG00000271779	ENSG00000271779	RP11-87N3.6	17:62495733-62658186	NOTEST	0	0	0	0	1	1
ENSG00000271780	ENSG00000271780	RP11-1017G21.5	14:102414683-102415762	NOTEST	0.608947	0.452291	-0.429065	0	1	1
ENSG00000271782	ENSG00000271782	RP5-850O15.4	1:50902699-50902978	NOTEST	0	0.193585	inf	0	1	1
ENSG00000271784	ENSG00000271784	RP1-28H20.3	20:45313003-45318928	NOTEST	0.183771	0.363957	0.985859	0	1	1
ENSG00000271786	ENSG00000271786	RP11-139J15.7	10:18429605-18948214	NOTEST	0	0.0332107	inf	0	1	1
ENSG00000271787	ENSG00000271787	RP11-254F7.3	2:10182975-10194993	NOTEST	0	0	0	0	1	1
ENSG00000271788	ENSG00000271788	CTD-2201E18.5	5:43006834-43007645	NOTEST	0.0889452	0.0904511	0.0242206	0	1	1
ENSG00000271789	ENSG00000271789	RP5-1112D6.7	6:111618328-111619713	NOTEST	0.0344629	0.139707	2.01929	0	1	1
ENSG00000271790	ENSG00000271790	SNORA74	HG1074_PATCH:51162259-51162460	NOTEST	0	0	0	0	1	1
ENSG00000271792	ENSG00000271792	CTB-35F21.5	5:139152112-139155057	NOTEST	0	0	0	0	1	1
ENSG00000271794	ENSG00000271794	snoU13	1:11166591-11322564	NOTEST	0	0	0	0	1	1
ENSG00000271795	ENSG00000271795	CTC-251D13.1	5:150883653-150948505	NOTEST	0.0618062	0.0601652	-0.0388213	0	1	1
ENSG00000271796	ENSG00000271796	snoU13	22:20434076-20434153	NOTEST	0	0	0	0	1	1
ENSG00000271797	ENSG00000271797	CTC-428G20.6	5:114546526-114599145	NOTEST	0.0200897	0.0724486	1.8505	0	1	1
ENSG00000271798	ENSG00000271798	SNORA51	20:2632790-2639039	NOTEST	0	0	0	0	1	1
ENSG00000271799	ENSG00000271799	ANKRD53	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000271801	ENSG00000271801	MORN3	HG1595_PATCH:122088921-122110435	NOTEST	0	0	0	0	1	1
ENSG00000271803	ENSG00000271803	RP1-63M2.5	20:32262322-32263186	NOTEST	0.207305	0	#NAME?	0	1	1
ENSG00000271806	ENSG00000271806	RP5-892K4.1	1:1981908-2152177	NOTEST	0.0170114	0.0169204	-0.00773594	0	1	1
ENSG00000271809	ENSG00000271809	ATP6V1B1	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000271810	ENSG00000271810	RP11-426L16.10	1:113243727-113258099	NOTEST	0	0.0536746	inf	0	1	1
ENSG00000271811	ENSG00000271811	RP1-79C4.4	1:170631868-170708560	NOTEST	0	0	0	0	1	1
ENSG00000271812	ENSG00000271812	RP11-87N3.6	HG183_PATCH:62619654-62739428	NOTEST	0	0	0	0	1	1
ENSG00000271814	ENSG00000271814	7SK	X:12156584-12742642	NOTEST	0	0	0	0	1	1
ENSG00000271815	ENSG00000271815	CTD-2235C13.3	5:74659584-74660067	NOTEST	0.587265	0.291397	-1.01103	0	1	1

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ENSG00000271816	ENSG00000271816	RP11-574K11.2 8	10:75404638-75490272	NOTEST	0.475457	0.348576	-0.44784	0	1	1
ENSG00000271817	ENSG00000271817	U3	4:159587830-159644548	NOTEST	0	0	0	0	1	1
ENSG00000271818	ENSG00000271818	7SK	13:45694649-45858237	NOTEST	0	0	0	0	1	1
ENSG00000271819	ENSG00000271819	U6	15:50569388-50659636	NOTEST	0	0	0	0	1	1
ENSG00000271820	ENSG00000271820	RP5-894D12.5	6:170575756-170588975	NOTEST	0	0	0	0	1	1
ENSG00000271821	ENSG00000271821	XXbac-BPG299F 13.14	6:31162976-31171745	NOTEST	0	0.164725	inf	0	1	1
ENSG00000271824	ENSG00000271824	AC009014 .3	5:135527155-135528822	NOTEST	0	0.0239354	inf	0	1	1
ENSG00000271825	ENSG00000271825	RP11-337N6.2	2:178092322-178408564	NOTEST	0	0	0	0	1	1
ENSG00000271826	ENSG00000271826	RP1-93I3.1	X:114752489-114885181	NOTEST	0.277001	0.199842	-0.471034	0	1	1
ENSG00000271828	ENSG00000271828	CTD-2310F14.1	5:56195867-56267502	NOTEST	0.239863	0.101409	-1.24202	0	1	1
ENSG00000271829	ENSG00000271829	RNF34	HG1595_PATCH:12183784 3-122031307	NOTEST	0	0	0	0	1	1
ENSG00000271830	ENSG00000271830	RP11-1C8.7	8:104493493-104493847	NOTEST	0	0	0	0	1	1
ENSG00000271831	ENSG00000271831	AL022345 .9	10:43069632-43134016	NOTEST	0	0	0	0	1	1
ENSG00000271835	ENSG00000271835	RP11-129K12.4	3:37026533-37026975	NOTEST	0.109567	0.161185	0.556895	0	1	1
ENSG00000271840	ENSG00000271840	RP1-224A6.9	1:22427105-22427853	NOTEST	0.0730086	0.0200293	-1.86595	0	1	1
ENSG00000271841	ENSG00000271841	U7	3:17198653-18959184	NOTEST	0	0	0	0	1	1
ENSG00000271842	ENSG00000271842	snoU13	3:174156362-175523428	NOTEST	0	0	0	0	1	1
ENSG00000271845	ENSG00000271845	RP4-790G17.7	1:150227488-150237478	NOTEST	0.081916	0	#NAME?	0	1	1
ENSG00000271846	ENSG00000271846	CTD-3113P16. 9	19:259259-259346	NOTEST	0	0	0	0	1	1
ENSG00000271847	ENSG00000271847	RP4-740C4.8	1:2252691-2323146	NOTEST	0.129615	0.197983	0.611144	0	1	1
ENSG00000271848	ENSG00000271848	RP11-464F9.21	10:75404638-75490272	NOTEST	0	0	0	0	1	1
ENSG00000271849	ENSG00000271849	CTC-332L22.1	5:109023502-109024030	NOTEST	0	0	0	0	1	1
ENSG00000271850	ENSG00000271850	RP11-16D22.2	13:34922179-35245319	NOTEST	0	0	0	0	1	1
ENSG00000271851	ENSG00000271851	RP11-565F19.2	17:9153787-9479908	NOTEST	0.206727	0.240373	0.217547	0	1	1
ENSG00000271852	ENSG00000271852	SNORD11 B	2:203130438-203168389	NOTEST	0	0	0	0	1	1
ENSG00000271855	ENSG00000271855	RP11-214N9.1	2:9696027-9696904	NOTEST	0.553178	0.376807	-0.553916	0	1	1
ENSG00000271856	ENSG00000271856	RP11-861A13.4	3:107844667-107857457	NOTEST	0	0	0	0	1	1
ENSG00000271857	ENSG00000271857	RP1-244F24.1	6:44777053-45632086	NOTEST	0.111108	0.044414	-1.32288	0	1	1
ENSG00000271858	ENSG00000271858	XXcos-LUCA11.4	3:50384760-50541675	NOTEST	0.368713	0.508444	0.463592	0	1	1
ENSG00000271860	ENSG00000271860	RP11-436D23.1	6:98264584-98847748	NOTEST	0.0692868	0.0130488	-2.40866	0	1	1
ENSG00000271862	ENSG00000271862	RP11-343L5.2	5:82345194-82346783	NOTEST	0.219945	0.227999	0.0518828	0	1	1
ENSG00000271866	ENSG00000271866	RP11-711D18.2	HG1595_PATCH:12174604 7-121837699	NOTEST	0	0	0	0	1	1
ENSG00000271867	ENSG00000271867	C6orf203	HG357_PATCH:107476077-107499217	NOTEST	0	0	0	0	1	1
ENSG00000271868	ENSG00000271868	RP11-1293J14.1	2:3500726-3526968	NOTEST	0.233116	0.300525	0.366435	0	1	1
ENSG00000271871	ENSG00000271871	AC005740 .6	5:141323149-141369856	NOTEST	0.106844	0.0455941	-1.22859	0	1	1
ENSG00000271873	ENSG00000271873	AC017084 .2	HG953_PATCH:70674411-70781325	NOTEST	0	0	0	0	1	1
ENSG00000271874	ENSG00000271874	CTD-2024P10. 2	5:34651561-34651993	NOTEST	0	0	0	0	1	1
ENSG00000271875	ENSG00000271875	RP11-430N14.4	9:136125787-136150617	NOTEST	0	0	0	0	1	1

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ENSG00000271880	ENSG00000271880	RP11-96C23.5	10:88695296-88784489	NOTEST	0.0306248	0.0462932	0.596101	0	1	1
ENSG00000271882	ENSG00000271882	KB-1410C5.5	8:102220375-102220786	NOTEST	0.0618207	0.242	1.96885	0	1	1
ENSG00000271886	ENSG00000271886	MIR98	X:53559056-53713673	NOTEST	0	0	0	0	1	1
ENSG00000271888	ENSG00000271888	RP11-560J1.2	6:15244153-15245231	NOTEST	0.399645	0.31169	-0.358606	0	1	1
ENSG00000271889	ENSG00000271889	RP11-493E12.1	2:61293005-61391964	NOTEST	0.146277	0.0658188	-1.15213	0	1	1
ENSG00000271890	ENSG00000271890	OR10AE1P	1:159551409-159552438	NOTEST	0	0	0	0	1	1
ENSG00000271891	ENSG00000271891	MIR502	HG1436_HG1432_PATCH:49732013-49908634	NOTEST	0	0	0	0	1	1
ENSG00000271892	ENSG00000271892	CTD-2228A4.1	5:17065706-17276943	NOTEST	0	0.0447068	inf	0	1	1
ENSG00000271893	ENSG00000271893	RP11-762E8.1	2:196313255-196380423	NOTEST	0	0	0	0	1	1
ENSG00000271894	ENSG00000271894	RP11-482H16.1	2:56179292-56613308	NOTEST	0.14344	0.0112555	-3.67174	0	1	1
ENSG00000271897	ENSG00000271897	RP11-679B17.2	6:11607784-11608214	NOTEST	0	0	0	0	1	1
ENSG00000271898	ENSG00000271898	MIR4791	3:19189945-19577138	NOTEST	0	0	0	0	1	1
ENSG00000271899	ENSG00000271899	MIR4466	6:157099062-157531913	NOTEST	0	0	0	0	1	1
ENSG00000271900	ENSG00000271900	RP11-1113L8.7	17:19505152-19505569	NOTEST	0	0	0	0	1	1
ENSG00000271901	ENSG00000271901	RP11-266E6.3	13:34922179-35245319	NOTEST	0	0	0	0	1	1
ENSG00000271903	ENSG00000271903	RP4-669P10.16	HSCHR22_2_CTG1:42532423-42548066	NOTEST	0	0	0	0	1	1
ENSG00000271904	ENSG00000271904	CTC-498M16.4	5:87485449-87794514	NOTEST	0	0	0	0	1	1
ENSG00000271905	ENSG00000271905	AC137590.1	12:132434507-132565005	NOTEST	0	0	0	0	1	1
ENSG00000271907	ENSG00000271907	SNORA35	X:114345184-114468635	NOTEST	0	0	0	0	1	1
ENSG00000271910	ENSG00000271910	PARG	HG1074_PATCH:51026324-51130715	NOTEST	0	0	0	0	1	1
ENSG00000271911	ENSG00000271911	RP11-532F6.5	6:761674-780648	NOTEST	0.0221584	0.0228483	0.04423	0	1	1
ENSG00000271912	ENSG00000271912	RP11-661A12.14	8:144683415-144685394	NOTEST	0.370577	0.516983	0.480341	0	1	1
ENSG00000271913	ENSG00000271913	RP1-111C20.4	6:159393902-159486305	NOTEST	0.0179101	0	#NAME?	0	1	1
ENSG00000271914	ENSG00000271914	RP4-789D17.5	1:36395320-36395716	NOTEST	0.190671	0.0985448	-0.952237	0	1	1
ENSG00000271915	ENSG00000271915	EEF1GP5	HG1462_PATCH:114939280-114940590	NOTEST	0	0	0	0	1	1
ENSG00000271916	ENSG00000271916	RP11-884K10.6	3:53528682-53880417	NOTEST	0	0	0	0	1	1
ENSG00000271917	ENSG00000271917	RP11-506O24.2	1:164524820-164868533	NOTEST	0	0	0	0	1	1
ENSG00000271918	ENSG00000271918	CTD-2287O16.5	5:115419503-115748459	NOTEST	0.182691	0.158593	-0.204079	0	1	1
ENSG00000271919	ENSG00000271919	RP11-269G24.8	17:61086916-61509572	NOTEST	0	0	0	0	1	1
ENSG00000271921	ENSG00000271921	RP4-740C4.9	1:2252691-2323146	NOTEST	0.135031	0.0639418	-1.07846	0	1	1
ENSG00000271922	ENSG00000271922	snoU13	3:154047504-154047608	NOTEST	0	0	0	0	1	1
ENSG00000271923	ENSG00000271923	U6	9:90613143-90613250	NOTEST	0	0	0	0	1	1
ENSG00000271924	ENSG00000271924	5S_rRNA	2:162164548-162268228	NOTEST	0	0	0	0	1	1
ENSG00000271926	ENSG00000271926	CTD-2376I4.1	5:72249461-72250101	NOTEST	0.0633464	0.0694722	0.133172	0	1	1
ENSG00000271927	ENSG00000271927	CTD-2541M15.4	8:6261071-6565730	NOTEST	0.09123	0.119344	0.387548	0	1	1
ENSG00000271928	ENSG00000271928	OR13Z3P	HG1287_PATCH:148168652-148169043	NOTEST	0	0	0	0	1	1
ENSG00000271930	ENSG00000271930	RP11-44N12.5	8:99955822-99956326	NOTEST	0	0	0	0	1	1
ENSG00000271931	ENSG00000271931	RP11-63L7.5	6:89789882-89790386	NOTEST	0	0	0	0	1	1
ENSG00000271932	ENSG00000271932	U6	7:140218219-140624564	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000271933	ENSG00000271933	RP11-338I21.1	10:85898175-85913001	NOTEST	0.327398	0.338823	0.0494873	0	1	1
ENSG00000271934	ENSG00000271934	OR2AS2P	1:248661608-248661929	NOTEST	0	0	0	0	1	1
ENSG00000271937	ENSG00000271937	RP11-424N24.2	3:44379432-44450943	NOTEST	0.039386	0.0302056	-0.382869	0	1	1
ENSG00000271938	ENSG00000271938	RP11-589C21.6	8:41996978-41997270	NOTEST	0	0	0	0	1	1
ENSG00000271941	ENSG00000271941	RP11-188P20.3	3:43328003-43775863	NOTEST	0.259501	0.238186	-0.123655	0	1	1
ENSG00000271942	ENSG00000271942	OR7E91P	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
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ENSG00000271945	ENSG00000271945	RP11-354K4.2	6:77484699-77485577	NOTEST	0	0	0	0	1	1
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ENSG00000271947	ENSG00000271947	RP11-439M11.1	2:7045854-7046432	NOTEST	0.140571	0.106747	-0.397104	0	1	1
ENSG00000271948	ENSG00000271948	RP11-242F4.2	8:17082472-17082978	NOTEST	0.253856	0.540454	1.09016	0	1	1
ENSG00000271949	ENSG00000271949	RP11-302M6.4	1:89990394-90402170	NOTEST	0	0	0	0	1	1
ENSG00000271952	ENSG00000271952	RP11-245G13.2	2:11018394-11025244	NOTEST	0	0	0	0	1	1
ENSG00000271955	ENSG00000271955	RP11-444A22.1	2:59444842-60327335	NOTEST	0	0	0	0	1	1
ENSG00000271956	ENSG00000271956	DLX6-AS2	7:96584452-96643377	NOTEST	0	0	0	0	1	1
ENSG00000271958	ENSG00000271958	RP11-617D20.2	4:38614321-38702663	NOTEST	0	0	0	0	1	1
ENSG00000271959	ENSG00000271959	CTD-3064M3.7	8:142443928-142517330	NOTEST	0	0	0	0	1	1
ENSG00000271961	ENSG00000271961	AC007040.11	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000271962	ENSG00000271962	AGAP6	HG1074_PATCH:51196363-51218545	NOTEST	0	0	0	0	1	1
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ENSG00000271964	ENSG00000271964	RP11-415F23.2	3:16306705-16555533	NOTEST	0.493834	0.390926	-0.337132	0	1	1
ENSG00000271966	ENSG00000271966	RP11-7F18.2	8:68256209-68257322	NOTEST	0.177973	0.2923	0.715791	0	1	1
ENSG00000271967	ENSG00000271967	RP11-134K13.4	6:71306140-71306683	NOTEST	0.0741271	0	#NAME?	0	1	1
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ENSG00000271970	ENSG00000271970	RP3-337H4.10	6:43474706-43543812	NOTEST	0	0	0	0	1	1
ENSG00000271973	ENSG00000271973	RP11-572O6.1	3:48701208-48723797	NOTEST	0.133722	0.960864	2.84509	0	1	1
ENSG00000271974	ENSG00000271974	RP11-927P21.12	17:62850429-62915598	NOTEST	0	0	0	0	1	1
ENSG00000271977	ENSG00000271977	AC226119.4	4:3916909-3957148	NOTEST	0	0	0	0	1	1
ENSG00000271978	ENSG00000271978	RP11-428J1.4	6:5030205-5054657	NOTEST	0.149658	0.227259	0.602668	0	1	1
ENSG00000271980	ENSG00000271980	CTD-2256P15.4	5:10250032-10267258	NOTEST	0.0672846	0.00682957	-3.30041	0	1	1
ENSG00000271981	ENSG00000271981	RP11-573G6.8	10:22621332-22621916	NOTEST	5.11E-05	0	#NAME?	0	1	1
ENSG00000271982	ENSG00000271982	SNORD58B	18:47008027-47018906	NOTEST	0	0	0	0	1	1
ENSG00000271983	ENSG00000271983	RP11-28H5.2	15:80972024-81047962	NOTEST	0.086357	0.102894	0.252775	0	1	1
ENSG00000271984	ENSG00000271984	RP3-337O18.9	20:44517263-44540794	NOTEST	0	0	0	0	1	1
ENSG00000271985	ENSG00000271985	RP11-589B3.7	10:81286263-81286387	NOTEST	0	0	0	0	1	1
ENSG00000271986	ENSG00000271986	Metazoa_SRP	6:74171300-74218959	NOTEST	0	0.0989518	inf	0	1	1

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ENSG00000271992	ENSG00000271992	RP11-42O15.3	1:70910753-70911219	NOTEST	0.427138	0.157579	-1.43863	0	1	1
ENSG00000271993	ENSG00000271993	RP11-285J16.1	3:37034822-37225180	NOTEST	0.457508	0.408463	-0.163594	0	1	1
ENSG00000271995	ENSG00000271995	AC034154.1	4:98105243-99064391	NOTEST	0	0	0	0	1	1
ENSG00000271996	ENSG00000271996	RP11-337N6.1	2:178092322-178408564	NOTEST	0	0	0	0	1	1
ENSG00000271997	ENSG00000271997	RP11-97O12.6	15:89002706-89089906	NOTEST	0.422081	0.294544	-0.51904	0	1	1
ENSG00000271998	ENSG00000271998	CTD-2199O4.7	5:10195232-10197740	NOTEST	0.0378176	0	#NAME?	0	1	1
ENSG00000272000	ENSG00000272000	CYP2D6	HSCHR22_2_CTG1:42532423-42548066	NOTEST	0	0	0	0	1	1
ENSG00000272002	ENSG00000272002	RP11-557L19.1	2:7401001-7401635	NOTEST	0.150477	0.172849	0.199966	0	1	1
ENSG00000272004	ENSG00000272004	RP11-345P4.10	1:1590785-1624167	NOTEST	0	0	0	0	1	1
ENSG00000272006	ENSG00000272006	RP11-583F2.6	17:62936699-62952664	NOTEST	0	0	0	0	1	1
ENSG00000272008	ENSG00000272008	RP11-393I2.4	6:87860876-87973914	NOTEST	0.0706998	0.0328821	-1.1044	0	1	1
ENSG00000272009	ENSG00000272009	RP1-313I6.12	6:28046569-28057341	NOTEST	0.144217	0.0920967	-0.647019	0	1	1
ENSG00000272010	ENSG00000272010	CTD-3025N20.3	8:66504084-66504707	NOTEST	0.472751	0.213989	-1.14354	0	1	1
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ENSG00000272015	ENSG00000272015	SNORA62	21:40249214-40328392	NOTEST	0	0	0	0	1	1
ENSG00000272017	ENSG00000272017	RP1-199J3.7	6:99990255-100016972	NOTEST	0.0541107	0.103087	0.929881	0	1	1
ENSG00000272019	ENSG00000272019	Metazoa_SRP	22:23401592-23487208	NOTEST	0	0	0	0	1	1
ENSG00000272020	ENSG00000272020	U1	3:125822411-125929012	NOTEST	0	0	0	0	1	1
ENSG00000272021	ENSG00000272021	AC008592.8	5:95171646-95195837	NOTEST	0	0.0307711	inf	0	1	1
ENSG00000272023	ENSG00000272023	CTC-350I8.1	5:132299461-132299856	NOTEST	0.0662001	0	#NAME?	0	1	1
ENSG00000272024	ENSG00000272024	RP11-546K22.3	8:52862843-52863250	NOTEST	0	0	0	0	1	1
ENSG00000272025	ENSG00000272025	SNORA74	2:65385795-65385994	NOTEST	0	0	0	0	1	1
ENSG00000272026	ENSG00000272026	TGFA-IT1	HG953_PATCH:70674411-70781325	NOTEST	0	0	0	0	1	1
ENSG00000272027	ENSG00000272027	RP11-529E15.1	2:34902645-34963298	NOTEST	0	0	0	0	1	1
ENSG00000272028	ENSG00000272028	U6	12:51373183-51422349	NOTEST	0	0	0	0	1	1
ENSG00000272029	ENSG00000272029	RP3-511B24.6	20:39657457-39946312	NOTEST	0	0	0	0	1	1
ENSG00000272031	ENSG00000272031	ANKRD34A	HG1287_PATCH:146645855-146650997	NOTEST	0	0	0	0	1	1
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ENSG00000272033	ENSG00000272033	RP11-52A20.2	1:167190065-167396582	NOTEST	0	0.00670182	inf	0	1	1
ENSG00000272034	ENSG00000272034	SNORD14A	11:17095935-17229530	NOTEST	0	0	0	0	1	1
ENSG00000272036	ENSG00000272036	MIR139	11:72287184-72385635	NOTEST	0	0	0	0	1	1
ENSG00000272037	ENSG00000272037	KB-431C1.5	8:103251621-103425069	NOTEST	0.149023	0.258708	0.79579	0	1	1
ENSG00000272038	ENSG00000272038	RP5-1010E17.3	HG944_PATCH:54036873-54084752	NOTEST	0	0	0	0	1	1
ENSG00000272040	ENSG00000272040	CTC-366B18.4	5:74904641-74905808	NOTEST	0.191181	0.097771	-0.967464	0	1	1
ENSG00000272042	ENSG00000272042	Metazoa_SRP	Y:27600707-27606719	NOTEST	0	0	0	0	1	1
ENSG00000272043	ENSG00000272043	RP11-44N11.3	8:123792209-123793310	NOTEST	0	0	0	0	1	1
ENSG00000272044	ENSG00000272044	RNU6-1004P	HG1595_PATCH:122042704-122042815	NOTEST	0	0	0	0	1	1
ENSG00000272045	ENSG00000272045	MIR1914	20:62571185-62587769	NOTEST	0	0	0	0	1	1
ENSG00000272046	ENSG00000272046	RP11-471M2.3	13:88459888-88463487	NOTEST	0	0	0	0	1	1

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ENSG00000272050	ENSG00000272050	RP13-379O24.3	20:61052925-61053650	NOTEST	0	0	0	0	1	1
ENSG00000272051	ENSG00000272051	Y_RNA	1:55950543-55950645	NOTEST	0	0	0	0	1	1
ENSG00000272053	ENSG00000272053	RP11-367G6.3	6:24797548-25057301	NOTEST	0	0	0	0	1	1
ENSG00000272054	ENSG00000272054	RP11-423P10.2	2:37394962-37551951	NOTEST	0.204064	0.1177	-0.793905	0	1	1
ENSG00000272055	ENSG00000272055	RNU6-6P	10:13259268-13259375	NOTEST	0	0	0	0	1	1
ENSG00000272056	ENSG00000272056	RP11-503P10.1	2:27265231-27294641	NOTEST	0	0.0244854	inf	0	1	1
ENSG00000272057	ENSG00000272057	CTB-40H15.4	5:14872440-14872822	NOTEST	0	0	0	0	1	1
ENSG00000272058	ENSG00000272058	AC243772.2	HG1287_PATCH:150388742-150392131	NOTEST	0	0	0	0	1	1
ENSG00000272060	ENSG00000272060	RNA18S5	GL000220.1:109077-110946	NOTEST	0	0	0	0	1	1
ENSG00000272064	ENSG00000272064	FAM21A	HG1074_PATCH:51275933-51341555	NOTEST	0	0	0	0	1	1
ENSG00000272066	ENSG00000272066	RP3-326L13.2	X:82761030-82764775	NOTEST	0	0	0	0	1	1
ENSG00000272067	ENSG00000272067	CCDC120	HG1436_HG1432_PATCH:48912970-48927863	NOTEST	0	0	0	0	1	1
ENSG00000272068	ENSG00000272068	RP11-284F21.9	1:156607574-156610796	NOTEST	0.0379996	0.00341698	-3.47519	0	1	1
ENSG00000272070	ENSG00000272070	AC005618.6	5:140705776-140708924	NOTEST	0.00498848	0.00737735	0.564503	0	1	1
ENSG00000272071	ENSG00000272071	RP11-332J15.4	5:6779570-6780111	NOTEST	0.0401478	0.0882239	1.13585	0	1	1
ENSG00000272073	ENSG00000272073	RP5-1050E16.2	HG50_PATCH:92414609-92436668	NOTEST	0	0	0	0	1	1
ENSG00000272074	ENSG00000272074	RNA5SP317	HG1074_PATCH:51180808-51190099	NOTEST	0	0	0	0	1	1
ENSG00000272075	ENSG00000272075	Metazoa_SRP	11:117886486-117992605	NOTEST	0	0	0	0	1	1
ENSG00000272076	ENSG00000272076	RP11-11C20.3	8:52722669-52723241	NOTEST	0.105659	0.0262512	-2.00896	0	1	1
ENSG00000272077	ENSG00000272077	RP11-348P10.2	3:44596684-44727145	NOTEST	0.0567686	0.029282	-0.955077	0	1	1
ENSG00000272078	ENSG00000272078	RP4-734G22.3	1:10696660-10856707	NOTEST	0.0307703	0.0226912	-0.439406	0	1	1
ENSG00000272079	ENSG00000272079	LA16c-380H5.5	16:3056120-3057386	NOTEST	0.0382338	0.0625496	0.710152	0	1	1
ENSG00000272080	ENSG00000272080	MIR502	X:49687224-49863892	NOTEST	0	0	0	0	1	1
ENSG00000272081	ENSG00000272081	CTD-2376I4.2	5:72251032-72251526	NOTEST	0.131746	0.278769	1.08131	0	1	1
ENSG00000272082	ENSG00000272082	AC093628.1	4:105389468-106041157	NOTEST	0	0	0	0	1	1
ENSG00000272084	ENSG00000272084	RP5-1126H10.2	1:19398603-19536770	NOTEST	0.124585	0.136605	0.132882	0	1	1
ENSG00000272085	ENSG00000272085	RP11-542A14.2	5:157891472-157891686	NOTEST	0	0	0	0	1	1
ENSG00000272088	ENSG00000272088	RP11-168F9.2	1:3403809-3404191	NOTEST	0	0	0	0	1	1
ENSG00000272089	ENSG00000272089	AC244669.1	HG1292_PATCH:120823867-120825921	NOTEST	0	0	0	0	1	1
ENSG00000272091	ENSG00000272091	RP4-758J24.5	1:54492355-54494172	NOTEST	0.439863	0.459746	0.0637839	0	1	1
ENSG00000272092	ENSG00000272092	RP11-350N15.5	8:38239881-38240979	NOTEST	0.468213	0.313875	-0.576976	0	1	1
ENSG00000272094	ENSG00000272094	RP4-665J23.4	1:91326106-91328477	NOTEST	0	0	0	0	1	1
ENSG00000272095	ENSG00000272095	AC007395.4	HG953_PATCH:71035774-71047732	NOTEST	0	0	0	0	1	1
ENSG00000272096	ENSG00000272096	Metazoa_SRP	3:155093368-155462856	NOTEST	0	0	0	0	1	1
ENSG00000272098	ENSG00000272098	AC092299.8	19:197074-205074	NOTEST	0	0	0	0	1	1
ENSG00000272100	ENSG00000272100	RP11-155O18.6	1:52608045-52831865	NOTEST	0.456515	0.162557	-1.48972	0	1	1
ENSG00000272101	ENSG00000272101	FO393434.1	HG357_PATCH:107379651-107379921	NOTEST	0	0	0	0	1	1
ENSG00000272102	ENSG00000272102	RP3-355L5.5	6:105721094-105721635	NOTEST	0	0.097037	inf	0	1	1
ENSG00000272103	ENSG00000272103	CTD-2653M23.3	5:36861837-36862319	NOTEST	0	0.115493	inf	0	1	1

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ENSG00000272105	ENSG00000272105	AC007040.4	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000272106	ENSG00000272106	RP11-345P4.9	1:1549137-1565990	NOTEST	0.422055	0.558552	0.404259	0	1	1
ENSG00000272108	ENSG00000272108	AC005754.8	5:140498261-140500347	NOTEST	0.0498846	0.0355779	-0.487615	0	1	1
ENSG00000272109	ENSG00000272109	CTD-2260A17.3	5:95220801-96143803	NOTEST	0.159551	0	#NAME?	0	1	1
ENSG00000272110	ENSG00000272110	Y_RNA	3:47537129-47555251	NOTEST	0	0	0	0	1	1
ENSG00000272111	ENSG00000272111	TCEB1P21	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000272112	ENSG00000272112	CTB-113P19.5	5:151104391-151104917	NOTEST	0.0418432	0.0296936	-0.494841	0	1	1
ENSG00000272113	ENSG00000272113	Y_RNA	9:32820248-32820356	NOTEST	0	0	0	0	1	1
ENSG00000272115	ENSG00000272115	GS1-393G12.14	8:145634875-145642279	NOTEST	0.0946007	0.188118	0.991716	0	1	1
ENSG00000272120	ENSG00000272120	ZNF275	HG1497_PATCH:152502626-152528582	NOTEST	0	0	0	0	1	1
ENSG00000272121	ENSG00000272121	RP4-555D20.4	3:44039572-44040641	NOTEST	0.335622	0.498417	0.570517	0	1	1
ENSG00000272123	ENSG00000272123	CTD-2366F13.2	5:51971026-52390609	NOTEST	0.0527578	0	#NAME?	0	1	1
ENSG00000272125	ENSG00000272125	TEX261	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000272127	ENSG00000272127	RP11-129K12.3	3:37027356-37034795	NOTEST	0	0	0	0	1	1
ENSG00000272128	ENSG00000272128	KB-1836B5.4	8:37956988-37957449	NOTEST	0.0512059	0	#NAME?	0	1	1
ENSG00000272129	ENSG00000272129	RP11-250B2.6	6:81065140-81066576	NOTEST	0.41068	0.519644	0.339511	0	1	1
ENSG00000272130	ENSG00000272130	RP11-360I2.1	5:21341941-21589481	NOTEST	0.237578	0	#NAME?	0	1	1
ENSG00000272134	ENSG00000272134	RP11-927P21.8	17:62850429-62915598	NOTEST	0	0	0	0	1	1
ENSG00000272135	ENSG00000272135	RP11-107C16.2	10:124578331-124585965	NOTEST	0	0	0	0	1	1
ENSG00000272137	ENSG00000272137	RP11-177G23.2	6:80270848-80271319	NOTEST	0.234652	0.112387	-1.06204	0	1	1
ENSG00000272138	ENSG00000272138	RP11-27N21.3	8:80680376-80783994	NOTEST	0.540549	0.218605	-1.3061	0	1	1
ENSG00000272139	ENSG00000272139	CTD-2544H17.2	5:121646991-121814782	NOTEST	0	0	0	0	1	1
ENSG00000272141	ENSG00000272141	RP11-465B22.8	1:1104736-1105723	NOTEST	0	0	0	0	1	1
ENSG00000272143	ENSG00000272143	FGF14-AS2	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000272144	ENSG00000272144	CTD-2035E11.5	5:43014515-43192123	NOTEST	0.180524	0.144273	-0.323392	0	1	1
ENSG00000272145	ENSG00000272145	NFYC-AS1	1:41156051-41237275	NOTEST	0.462318	0.415238	-0.154948	0	1	1
ENSG00000272146	ENSG00000272146	RP11-755B10.4	3:57557089-57586654	NOTEST	0.3629	0.184237	-0.978005	0	1	1
ENSG00000272148	ENSG00000272148	RP11-195B17.1	2:27265231-27294641	NOTEST	0.27571	0.177439	-0.63583	0	1	1
ENSG00000272149	ENSG00000272149	RP11-627J17.1	3:33155470-33189265	NOTEST	0	0	0	0	1	1
ENSG00000272150	ENSG00000272150	AC239860.1	HG1287_PATCH:145976420-146277520	NOTEST	0	0	0	0	1	1
ENSG00000272151	ENSG00000272151	RP11-526K21.2	HG1074_PATCH:51026324-51130715	NOTEST	0	0	0	0	1	1
ENSG00000272154	ENSG00000272154	AC005754.7	5:140479828-140483406	NOTEST	0.284456	0.301263	0.0828219	0	1	1
ENSG00000272155	ENSG00000272155	RP11-707M3.3	8:66556968-66754557	NOTEST	0.623525	0.558024	-0.160122	0	1	1
ENSG00000272156	ENSG00000272156	RP11-477N3.1	2:54091203-54532437	NOTEST	0	0.0187048	inf	0	1	1
ENSG00000272157	ENSG00000272157	CTD-2168K21.2	8:24808467-24814624	NOTEST	0	0	0	0	1	1
ENSG00000272158	ENSG00000272158	RP11-840I19.5	14:65381078-65569413	NOTEST	0	0	0	0	1	1
ENSG00000272159	ENSG00000272159	RP11-350N15.6	8:38243724-38267045	NOTEST	0	0.0221684	inf	0	1	1

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ENSG00000272161	ENSG00000272161	RP4-713A8.1	1:2252691-2323146	NOTEST	0.270546	0.171275	-0.659555	0	1	1
ENSG00000272163	ENSG00000272163	GS1-72M22.1	8:24769677-24776607	NOTEST	0.224798	0.115517	-0.960529	0	1	1
ENSG00000272164	ENSG00000272164	RP11-180P8.5	17:61082032-61082513	NOTEST	0	0	0	0	1	1
ENSG00000272165	ENSG00000272165	AC010614.1	HSCHR19_1_CTG3_1:34752614-34853664	NOTEST	0	0	0	0	1	1
ENSG00000272166	ENSG00000272166	SNORD5	3:25215822-25639423	NOTEST	0	0	0	0	1	1
ENSG00000272167	ENSG00000272167	RP11-53A1.2	1:213991093-214214595	NOTEST	0	0	0	0	1	1
ENSG00000272169	ENSG00000272169	AC007395.3	HG953_PATCH:70834749-70995357	NOTEST	0	0	0	0	1	1
ENSG00000272170	ENSG00000272170	RP11-387M24.5	6:43005354-43042837	NOTEST	0	0.15093	inf	0	1	1
ENSG00000272171	ENSG00000272171	ORAI1	HG1595_PATCH:122064352-122080481	NOTEST	0	0	0	0	1	1
ENSG00000272173	ENSG00000272173	U47924.31	12:7052140-7055166	NOTEST	0.0942942	0.108145	0.19772	0	1	1
ENSG00000272174	ENSG00000272174	AC026703.2	5:32689175-32791819	NOTEST	0	0	0	0	1	1
ENSG00000272175	ENSG00000272175	RP4-657D16.6	1:52027537-52344477	NOTEST	0	0	0	0	1	1
ENSG00000272177	ENSG00000272177	RP11-340F16.1	2:65663844-66311773	NOTEST	0	0	0	0	1	1
ENSG00000272179	ENSG00000272179	snoU13	X:119658463-119709649	NOTEST	0	0	0	0	1	1
ENSG00000272180	ENSG00000272180	RP11-481J13.1	2:56179292-56613308	NOTEST	0	0	0	0	1	1
ENSG00000272181	ENSG00000272181	RP11-245J9.6	3:63989697-64009658	NOTEST	0	0	0	0	1	1
ENSG00000272183	ENSG00000272183	RP11-523H20.3	2:74724643-74731805	NOTEST	0.145665	0.207264	0.508819	0	1	1
ENSG00000272184	ENSG00000272184	RP1-93I3.1	HG1462_PATCH:114754651-114887331	NOTEST	0	0	0	0	1	1
ENSG00000272185	ENSG00000272185	AC233297.1	HG1424_PATCH:37209336-38547737	NOTEST	0	0	0	0	1	1
ENSG00000272187	ENSG00000272187	U47924.30	HG344_PATCH:7085347-7180195	NOTEST	0	0	0	0	1	1
ENSG00000272188	ENSG00000272188	MIR4640	HSCHR6_MHC_MANN:30893439-30912617	NOTEST	0	0	0	0	1	1
ENSG00000272189	ENSG00000272189	RP3-325F22.5	6:136663874-136873692	NOTEST	0.00861992	0	#NAME?	0	1	1
ENSG00000272191	ENSG00000272191	RP11-445F12.2	17:35294083-35301917	NOTEST	0	0.145512	inf	0	1	1
ENSG00000272192	ENSG00000272192	CTD-2532N20.1	8:66754986-66755566	NOTEST	0	0.0540136	inf	0	1	1
ENSG00000272195	ENSG00000272195	RP11-156E8.1	1:245132651-245290466	NOTEST	0.0988875	0.0643322	-0.620248	0	1	1
ENSG00000272196	ENSG00000272196	HIST2H2AA3	HG1287_PATCH:150528635-150529113	NOTEST	0	0	0	0	1	1
ENSG00000272197	ENSG00000272197	Metazoa_SRP	5:154092461-154197167	NOTEST	0	0	0	0	1	1
ENSG00000272202	ENSG00000272202	RP11-157F20.3	3:56761445-57114129	NOTEST	0.132637	0.125343	-0.0815975	0	1	1
ENSG00000272203	ENSG00000272203	AC004775.5	5:132152939-132153692	NOTEST	0	0	0	0	1	1
ENSG00000272204	ENSG00000272204	ANAPC5	HG1595_PATCH:121746047-121837699	NOTEST	0	0	0	0	1	1
ENSG00000272205	ENSG00000272205	RP11-277B15.3	1:167189067-167189749	NOTEST	0.408265	0.127992	-1.67346	0	1	1
ENSG00000272207	ENSG00000272207	PLEKHO1	HG1287_PATCH:150836332-150846010	NOTEST	0	0	0	0	1	1
ENSG00000272208	ENSG00000272208	RP11-110I1.13	HG299_PATCH:118938083-118952681	NOTEST	0	0	0	0	1	1
ENSG00000272209	ENSG00000272209	RP3-500L14.2	6:13825662-13826805	NOTEST	0.0736697	0.0974728	0.403929	0	1	1
ENSG00000272210	ENSG00000272210	CD207	HG953_PATCH:71057346-71062953	NOTEST	0	0	0	0	1	1
ENSG00000272211	ENSG00000272211	RP11-347P5.1	2:196998289-197041227	NOTEST	0.00784115	0.0665172	3.08459	0	1	1
ENSG00000272213	ENSG00000272213	MIR484	16:15737123-15950890	NOTEST	0	0	0	0	1	1
ENSG00000272214	ENSG00000272214	AC079602.1	12:121406415-121454305	NOTEST	0	0	0	0	1	1
ENSG00000272215	ENSG00000272215	U7	12:111890017-112038060	NOTEST	0	0	0	0	1	1
ENSG00000272216	ENSG00000272216	LL22NC03-2H8.5	22:22638311-22641586	NOTEST	0.231056	0.101903	-1.18105	0	1	1

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ENSG00000272218	ENSG00000272218	RP11-11N5.3	4:187813705-187814137	NOTEST	0	0	0	0	1	1
ENSG00000272219	ENSG00000272219	CTB-181H17.1	7:101458958-101927249	NOTEST	0	0	0	0	1	1
ENSG00000272220	ENSG00000272220	RP11-927P21.9	17:62850429-62915598	NOTEST	0	0	0	0	1	1
ENSG00000272221	ENSG00000272221	XXbac-BPG181B23.7	6:31362065-31363272	NOTEST	0.298476	0.26242	-0.185734	0	1	1
ENSG00000272222	ENSG00000272222	RP11-316P17.2	HG50_PATCH:92316565-92334585	NOTEST	0	0	0	0	1	1
ENSG00000272223	ENSG00000272223	RP1-20C7.6	6:42989382-43002143	NOTEST	0.0936771	0.0684819	-0.451974	0	1	1
ENSG00000272225	ENSG00000272225	RP11-592B15.9	10:51224680-51371338	NOTEST	0	0	0	0	1	1
ENSG00000272226	ENSG00000272226	RP11-63G10.3	1:59250822-59365384	NOTEST	0	0.0635771	inf	0	1	1
ENSG00000272228	ENSG00000272228	SLC9A3P3	HG1074_PATCH:51229227-51275849	NOTEST	0	0	0	0	1	1
ENSG00000272230	ENSG00000272230	MIR3666	7:113726381-114333827	NOTEST	0	0	0	0	1	1
ENSG00000272231	ENSG00000272231	AC136188.1	12:74293649-74293732	NOTEST	0	0	0	0	1	1
ENSG00000272232	ENSG00000272232	Metazoa_SRP	9:73143978-74061820	NOTEST	0	0	0	0	1	1
ENSG00000272233	ENSG00000272233	RP11-503E24.3	8:42409932-42410336	NOTEST	0	0	0	0	1	1
ENSG00000272234	ENSG00000272234	CTD-2325A15.5	5:42756902-42887494	NOTEST	0	0	0	0	1	1
ENSG00000272235	ENSG00000272235	RP11-22L13.1	1:2985731-3355185	NOTEST	0	0	0	0	1	1
ENSG00000272236	ENSG00000272236	XXbac-BPG170G13.32	6:29719741-29719984	NOTEST	0.38193	0.300491	-0.345988	0	1	1
ENSG00000272237	ENSG00000272237	SNORA25	2:228735769-228789060	NOTEST	0	0	0	0	1	1
ENSG00000272239	ENSG00000272239	CTB-108O6.2	5:146770373-146889619	NOTEST	0	0	0	0	1	1
ENSG00000272241	ENSG00000272241	AL160275.1	9:117373485-117408702	NOTEST	0	0	0	0	1	1
ENSG00000272242	ENSG00000272242	ACTG1P10	HG1433_PATCH:52836709-52910014	NOTEST	0	0	0	0	1	1
ENSG00000272243	ENSG00000272243	RP11-554D15.3	6:74779166-75443995	NOTEST	0	0	0	0	1	1
ENSG00000272244	ENSG00000272244	Metazoa_SRP	X:133348415-133348694	NOTEST	0	0	0	0	1	1
ENSG00000272245	ENSG00000272245	RP11-324H6.5	HG1074_PATCH:51229227-51275849	NOTEST	0	0	0	0	1	1
ENSG00000272246	ENSG00000272246	AC245177.2	HG1433_PATCH:51942839-51946226	NOTEST	0	0	0	0	1	1
ENSG00000272247	ENSG00000272247	RP11-379F4.9	3:158414680-158547508	NOTEST	0	0.157485	inf	0	1	1
ENSG00000272248	ENSG00000272248	RP3-406P24.4	6:4018946-4021449	NOTEST	0.0465602	0	#NAME?	0	1	1
ENSG00000272249	ENSG00000272249	KB-1958F4.2	8:97657454-98161882	NOTEST	0	0	0	0	1	1
ENSG00000272250	ENSG00000272250	RP11-346C20.4	16:73094143-73096215	NOTEST	0.0431802	0.095906	1.15125	0	1	1
ENSG00000272252	ENSG00000272252	AC242426.1	HG1287_PATCH:147859185-147982177	NOTEST	0	0	0	0	1	1
ENSG00000272253	ENSG00000272253	5S_rRNA	14:68086514-68162531	NOTEST	0	0	0	0	1	1
ENSG00000272254	ENSG00000272254	RP11-531A24.7	8:73921098-73960357	NOTEST	0	0	0	0	1	1
ENSG00000272255	ENSG00000272255	CTD-3224K15.3	5:139024044-139024587	NOTEST	0	0	0	0	1	1
ENSG00000272256	ENSG00000272256	RP11-489E7.4	8:29920527-29940983	NOTEST	0.0314725	0.0972458	1.62754	0	1	1
ENSG00000272257	ENSG00000272257	AC007040.5	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000272259	ENSG00000272259	RP11-305P22.9	20:61640734-61716423	NOTEST	0	0	0	0	1	1
ENSG00000272262	ENSG00000272262	U6	1:202317826-202679545	NOTEST	0	0	0	0	1	1
ENSG00000272263	ENSG00000272263	RP11-767C1.2	3:12837970-12913415	NOTEST	0.125429	0.0963677	-0.380246	0	1	1
ENSG00000272264	ENSG00000272264	RP11-92K15.3	8:80830951-81143467	NOTEST	0.172111	0.309029	0.844401	0	1	1

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ENSG00000272268	ENSG00000272268	DKFZP761K2322	2:6072818-6141407	NOTEST	0	0	0	0	1	1
ENSG00000272272	ENSG00000272272	snoU13	9:140201347-140317714	NOTEST	0	0	0	0	1	1
ENSG00000272274	ENSG00000272274	LINC00551	13:107270157-107283707	NOTEST	0.00992081	0	#NAME?	0	1	1
ENSG00000272275	ENSG00000272275	RP11-791G15.2	2:10861774-10978103	NOTEST	0.0668761	0.352711	2.39893	0	1	1
ENSG00000272278	ENSG00000272278	AL121932.1	6:28615973-28616042	NOTEST	0	0	0	0	1	1
ENSG00000272281	ENSG00000272281	TPTE2P2	13:52741843-52908412	NOTEST	0.0180009	0	#NAME?	0	1	1
ENSG00000272282	ENSG00000272282	RP11-222K16.2	3:27754400-27755496	NOTEST	0.251202	0.188344	-0.415478	0	1	1
ENSG00000272283	ENSG00000272283	Metazoa_SRP	21:47878811-47989926	NOTEST	0.229955	0.460806	1.00281	0	1	1
ENSG00000272284	ENSG00000272284	RP4-669P10.19	HSCHR22_2_CTG1:42528531-42528987	NOTEST	0	0	0	0	1	1
ENSG00000272286	ENSG00000272286	Z83307.3	11:31806339-32127301	NOTEST	0.0324963	0	#NAME?	0	1	1
ENSG00000272290	ENSG00000272290	RP5-1010E17.2	HG944_PATCH:54036873-54084752	NOTEST	0	0	0	0	1	1
ENSG00000272291	ENSG00000272291	MIR665	14:101341369-101341441	NOTEST	0	0	0	0	1	1
ENSG00000272292	ENSG00000272292	U6	1:180601139-180859387	NOTEST	0	0	0	0	1	1
ENSG00000272293	ENSG00000272293	RP11-91J19.3	8:356427-421225	NOTEST	0.189272	0.305898	0.692592	0	1	1
ENSG00000272294	ENSG00000272294	RP3-326L13.3	X:82766303-82767135	NOTEST	0	0	0	0	1	1
ENSG00000272295	ENSG00000272295	DAQB-331I12.15	HSCHR6_MHC_QBL:31815829-32011521	NOTEST	0	0	0	0	1	1
ENSG00000272296	ENSG00000272296	SNORD96A	5:180663908-180699308	NOTEST	0	0	0	0	1	1
ENSG00000272297	ENSG00000272297	RP11-215A19.2	4:187187098-187476721	NOTEST	0	0	0	0	1	1
ENSG00000272299	ENSG00000272299	RP11-394A14.4	13:64402972-64418258	NOTEST	0	0	0	0	1	1
ENSG00000272301	ENSG00000272301	RP11-111M22.4	11:76092356-76125663	NOTEST	0.508007	0.42192	-0.267879	0	1	1
ENSG00000272302	ENSG00000272302	BX004987.1	1:143347957-143467632	NOTEST	0	0	0	0	1	1
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ENSG00000272305	ENSG00000272305	RP11-894J14.5	3:52937587-53164478	NOTEST	0.0317384	0	#NAME?	0	1	1
ENSG00000272308	ENSG00000272308	RP11-231G3.1	5:60162283-60162762	NOTEST	0.366699	0.305107	-0.26528	0	1	1
ENSG00000272309	ENSG00000272309	PDSS2	HG357_PATCH:107600431-107907439	NOTEST	0	0	0	0	1	1
ENSG00000272310	ENSG00000272310	snoU13	16:11453701-11617444	NOTEST	0	0	0	0	1	1
ENSG00000272311	ENSG00000272311	IFNL4P1	19:39755021-39756457	NOTEST	0	0	0	0	1	1
ENSG00000272312	ENSG00000272312	RP11-239L20.6	6:26924770-26991703	NOTEST	0	0	0	0	1	1
ENSG00000272316	ENSG00000272316	XXbac-BPGBPG55C20.2	6:58234837-58240189	NOTEST	0.0476627	0.043091	-0.145476	0	1	1
ENSG00000272317	ENSG00000272317	AL162424.2	9:124999902-125085743	NOTEST	0	0	0	0	1	1
ENSG00000272318	ENSG00000272318	AC007040.6	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000272319	ENSG00000272319	AL022345.7	10:43069632-43134016	NOTEST	0	0	0	0	1	1
ENSG00000272320	ENSG00000272320	RP11-506K6.4	6:3224494-3457256	NOTEST	0.116372	0.0520808	-1.15992	0	1	1
ENSG00000272321	ENSG00000272321	KB-1517D11.1	8:99413630-99955055	NOTEST	0	0	0	0	1	1
ENSG00000272322	ENSG00000272322	U47924.31	HG344_PATCH:7052140-7055166	NOTEST	0	0	0	0	1	1
ENSG00000272324	ENSG00000272324	CTD-2154B17.4	5:10679341-10770406	NOTEST	0	0	0	0	1	1
ENSG00000272327	ENSG00000272327	RP11-1002K11.1	8:32623642-32625477	NOTEST	0	0	0	0	1	1

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ENSG00000272329	ENSG00000272329	RP11-65L19.4	13:97593534-97636426	NOTEST	0	0	0	0	1	1
ENSG00000272330	ENSG00000272330	AC002044.4	16:72699068-73093597	NOTEST	0	0	0	0	1	1
ENSG00000272331	ENSG00000272331	LINC00843	HG1074_PATCH:51180808-51190099	NOTEST	0	0	0	0	1	1
ENSG00000272334	ENSG00000272334	RP11-129K12.1	3:37014607-37015163	NOTEST	0	0.0300497	inf	0	1	1
ENSG00000272336	ENSG00000272336	RP11-110I1.14	HG299_PATCH:118935972-118936387	NOTEST	0	0	0	0	1	1
ENSG00000272337	ENSG00000272337	U6	15:52121824-52392720	NOTEST	0	0	0	0	1	1
ENSG00000272340	ENSG00000272340	RP11-38L15.8	HG1211_PATCH:47073664-47147473	NOTEST	0	0	0	0	1	1
ENSG00000272342	ENSG00000272342	RP13-539J13.1	2:739587-740164	NOTEST	0	0	0	0	1	1
ENSG00000272343	ENSG00000272343	RP11-140I16.3	8:57135246-57135732	NOTEST	0	0.184283	inf	0	1	1
ENSG00000272344	ENSG00000272344	SNORD114-21	14:101433988-101452987	NOTEST	0	0	0	0	1	1
ENSG00000272345	ENSG00000272345	RP1-30M3.5	6:24667262-24721064	NOTEST	0.185743	0.200858	0.112866	0	1	1
ENSG00000272346	ENSG00000272346	RP11-927P21.11	17:62936699-62952664	NOTEST	0.126253	0	#NAME?	0	1	1
ENSG00000272347	ENSG00000272347	RP11-43F13.4	5:1005153-1006738	NOTEST	0	0.0543291	inf	0	1	1
ENSG00000272348	ENSG00000272348	RN7SL160P	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000272349	ENSG00000272349	RP11-397O8.7	13:102104965-103054807	NOTEST	0	0	0	0	1	1
ENSG00000272351	ENSG00000272351	5S_rRNA	X:68835910-69259319	NOTEST	0	0	0	0	1	1
ENSG00000272352	ENSG00000272352	CLEC4F	HG953_PATCH:71035774-71047732	NOTEST	0	0	0	0	1	1
ENSG00000272353	ENSG00000272353	snoU13	HG953_PATCH:71127720-71160577	NOTEST	0	0	0	0	1	1
ENSG00000272354	ENSG00000272354	RP11-307L14.2	5:64316440-64316816	NOTEST	0	0.159883	inf	0	1	1
ENSG00000272356	ENSG00000272356	RP5-1112D6.8	6:111620233-111927481	NOTEST	0.121544	0.131974	0.118775	0	1	1
ENSG00000272357	ENSG00000272357	GS1-393G12.14	HG243_PATCH:145464394-145471798	NOTEST	0	0	0	0	1	1
ENSG00000272358	ENSG00000272358	KDM2B	HG1595_PATCH:121837843-122031307	NOTEST	0	0	0	0	1	1
ENSG00000272359	ENSG00000272359	U4	3:196466727-196559518	NOTEST	0	0	0	0	1	1
ENSG00000272360	ENSG00000272360	RP11-359I18.5	3:58476556-58477018	NOTEST	0	0.0760962	inf	0	1	1
ENSG00000272361	ENSG00000272361	GS1-166A23.2	7:16633252-16633849	NOTEST	0.139483	0.108942	-0.356539	0	1	1
ENSG00000272362	ENSG00000272362	RP4-781K5.9	1:234780411-234831900	NOTEST	0	0	0	0	1	1
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ENSG00000272365	ENSG00000272365	RP11-389C8.3	5:71663445-71664222	NOTEST	0.453523	0.417209	-0.120406	0	1	1
ENSG00000272366	ENSG00000272366	RP11-573G6.10	10:22629305-22629544	NOTEST	0	0.157546	inf	0	1	1
ENSG00000272367	ENSG00000272367	CTC-428H11.2	5:86563704-86708836	NOTEST	0.0989996	0.213469	1.10853	0	1	1
ENSG00000272368	ENSG00000272368	RP4-605O3.4	12:50505761-50561288	NOTEST	0.240819	0.406174	0.754147	0	1	1
ENSG00000272369	ENSG00000272369	RP11-446N19.1	12:46931284-47046333	NOTEST	0.254701	0.161275	-0.659282	0	1	1
ENSG00000272370	ENSG00000272370	RP11-307L14.1	5:64315864-64316378	NOTEST	0.501637	0.431557	-0.217091	0	1	1
ENSG00000272371	ENSG00000272371	RP11-25O10.2	1:53020489-53020945	NOTEST	0	0	0	0	1	1
ENSG00000272372	ENSG00000272372	RP11-441F2.5	16:56225301-56391356	NOTEST	0.162584	0.17078	0.0709505	0	1	1
ENSG00000272374	ENSG00000272374	RP3-329A5.8	6:35182189-35220856	NOTEST	0.274014	0.0693066	-1.98319	0	1	1
ENSG00000272375	ENSG00000272375	RP11-51J9.6	8:30054919-30055564	NOTEST	0.272274	0.142204	-0.937098	0	1	1
ENSG00000272377	ENSG00000272377	RP11-682N22.1	7:96110937-96339203	NOTEST	0.123926	0.136314	0.137465	0	1	1
ENSG00000272380	ENSG00000272380	MIR3976	18:5748817-5876327	NOTEST	0	0	0	0	1	1
ENSG00000272381	ENSG00000272381	RP11-192P3.4	10:31476811-31818742	NOTEST	0	0	0	0	1	1

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ENSG00000272383	ENSG00000272383	RP11-556O9.4	17:61086916-61509572	NOTEST	0.0171706	0	#NAME?	0	1	1
ENSG00000272384	ENSG00000272384	RP11-44N11.2	8:123792209-123793310	NOTEST	0	0	0	0	1	1
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ENSG00000272386	ENSG00000272386	RP11-666A8.12	17:74523437-74553765	NOTEST	0.499275	0.441633	-0.176988	0	1	1
ENSG00000272387	ENSG00000272387	AL022345.8	10:43069632-43134016	NOTEST	0	0	0	0	1	1
ENSG00000272389	ENSG00000272389	CTC-487M23.7	5:112043194-112258236	NOTEST	0.0830301	0	#NAME?	0	1	1
ENSG00000272391	ENSG00000272391	AC211429.1	HG1257_PATCH:74883569-74906074	NOTEST	0	0	0	0	1	1
ENSG00000272393	ENSG00000272393	U6	7:132767588-132767692	NOTEST	0	0	0	0	1	1
ENSG00000272395	ENSG00000272395	IFNL4	19:39737772-39739219	NOTEST	0	0	0	0	1	1
ENSG00000272396	ENSG00000272396	CTC-490G23.4	19:43857810-43873122	NOTEST	0	0	0	0	1	1
ENSG00000272397	ENSG00000272397	RP11-497D6.5	6:147163036-147706866	NOTEST	0	0	0	0	1	1
ENSG00000272398	ENSG00000272398	CD24	HG357_PATCH:107417707-107422630	NOTEST	0	0	0	0	1	1
ENSG00000272400	ENSG00000272400	RP11-927P21.7	17:62843503-62843846	NOTEST	0	0	0	0	1	1
ENSG00000272402	ENSG00000272402	RP1-30M3.6	6:24667262-24721064	NOTEST	0.183669	0.2325	0.340125	0	1	1
ENSG00000272403	ENSG00000272403	RP1-93H18.7	6:116765322-116766023	NOTEST	0.0795759	0.0198081	-2.00624	0	1	1
ENSG00000272405	ENSG00000272405	RP11-284F21.10	1:156611181-156631216	NOTEST	0.394306	0.151835	-1.37682	0	1	1
ENSG00000272406	ENSG00000272406	RP11-185E12.2	5:92953774-93447404	NOTEST	0	0	0	0	1	1
ENSG00000272407	ENSG00000272407	RP3-511B24.5	20:39657457-39946312	NOTEST	0	0.274543	inf	0	1	1
ENSG00000272411	ENSG00000272411	RP11-44B19.1	5:148303201-148442726	NOTEST	0	0	0	0	1	1
ENSG00000272412	ENSG00000272412	Metazoa_SRP	11:130096571-130184581	NOTEST	0	0	0	0	1	1
ENSG00000272416	ENSG00000272416	CTD-2081C10.7	5:53176122-53176881	NOTEST	0.214875	0.198767	-0.112423	0	1	1
ENSG00000272417	ENSG00000272417	CTD-2199O4.6	5:10203711-10204152	NOTEST	0.0549858	0.165504	1.58974	0	1	1
ENSG00000272418	ENSG00000272418	RP11-762H8.4	15:78542843-78592136	NOTEST	0	0	0	0	1	1
ENSG00000272419	ENSG00000272419	AC241585.3	HG1287_PATCH:145852606-145856510	NOTEST	0	0	0	0	1	1
ENSG00000272420	ENSG00000272420	RP4-740C4.7	1:2252691-2323146	NOTEST	0.314718	0.0795557	-1.98402	0	1	1
ENSG00000272421	ENSG00000272421	RP1-60O19.2	HG357_PATCH:107143409-107147869	NOTEST	0	0	0	0	1	1
ENSG00000272423	ENSG00000272423	AC007040.7	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000272425	ENSG00000272425	RP11-363E6.4	8:82187633-82189805	NOTEST	0.111327	0.150488	0.434841	0	1	1
ENSG00000272426	ENSG00000272426	RP11-108M9.6	1:17066767-17299474	NOTEST	0.0556151	0.246617	2.14872	0	1	1
ENSG00000272427	ENSG00000272427	AC241929.1	HG1287_PATCH:147429219-147460378	NOTEST	0	0	0	0	1	1
ENSG00000272428	ENSG00000272428	RP11-704J17.5	6:133561735-134216691	NOTEST	0.262492	0.312113	0.249797	0	1	1
ENSG00000272430	ENSG00000272430	RP11-38L15.8	10:46897591-46971400	NOTEST	0.150704	0.231579	0.619789	0	1	1
ENSG00000272431	ENSG00000272431	RP11-281O15.8	5:178365677-178366224	NOTEST	0	0	0	0	1	1
ENSG00000272432	ENSG00000272432	RP3-465N24.6	1:25568727-25756683	NOTEST	0.0946008	0.209374	1.14616	0	1	1
ENSG00000272433	ENSG00000272433	HMGN2P21	HG953_PATCH:71030288-71030558	NOTEST	0	0	0	0	1	1
ENSG00000272434	ENSG00000272434	RP13-131K19.6	3:49061757-49067139	NOTEST	0	0.0526393	inf	0	1	1
ENSG00000272435	ENSG00000272435	5S_rRNA	12:34343971-34371788	NOTEST	0	0	0	0	1	1
ENSG00000272436	ENSG00000272436	CUX2P1	10:10299131-10299429	NOTEST	0	0	0	0	1	1
ENSG00000272438	ENSG00000272438	RP11-54O7.16	1:840213-851356	NOTEST	0	0	0	0	1	1
ENSG00000272439	ENSG00000272439	U6	14:99864082-99947216	NOTEST	0	0	0	0	1	1

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ENSG00000272443	ENSG00000272443	OR13Z2P	1:146917311-146917866	NOTEST	0	0	0	0	1	1
ENSG00000272444	ENSG00000272444	RP11-1017G21.6	14:102418752-102419400	NOTEST	0.447661	0.490907	0.133042	0	1	1
ENSG00000272445	ENSG00000272445	U6	6:77232167-77303340	NOTEST	0	0	0	0	1	1
ENSG00000272446	ENSG00000272446	RP1-225E12.3	6:139456248-139613276	NOTEST	0	0	0	0	1	1
ENSG00000272448	ENSG00000272448	LLNLR-299G3.1	19:617222-633597	NOTEST	0.101376	0.0395724	-1.35715	0	1	1
ENSG00000272450	ENSG00000272450	BX119957.2	HSCHR6_MHC_SSTO:30559597-30585593	NOTEST	0	0	0	0	1	1
ENSG00000272452	ENSG00000272452	RP11-391M1.4	3:40507956-40510078	NOTEST	0.134538	0.107986	-0.317165	0	1	1
ENSG00000272453	ENSG00000272453	CTD-2612A24.1	HG79_PATCH:136125798-136150736	NOTEST	0	0	0	0	1	1
ENSG00000272456	ENSG00000272456	CTD-2342N23.3	8:135735189-135736192	NOTEST	0	0	0	0	1	1
ENSG00000272457	ENSG00000272457	RP11-1070A24.2	8:54764367-54871863	NOTEST	0.433058	0.467626	0.110795	0	1	1
ENSG00000272458	ENSG00000272458	MIR432	14:101346991-101351184	NOTEST	0	0	0	0	1	1
ENSG00000272459	ENSG00000272459	RP11-1277A3.3	5:176981824-176982365	NOTEST	0.07454	0.0882239	0.243154	0	1	1
ENSG00000272460	ENSG00000272460	SNORD115-40	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000272461	ENSG00000272461	RP11-689C9.1	18:962592-1174824	NOTEST	0	0	0	0	1	1
ENSG00000272462	ENSG00000272462	U91328.19	6:25963029-26002003	NOTEST	0.584502	0.420141	-0.476333	0	1	1
ENSG00000272463	ENSG00000272463	RP11-532F6.3	6:708591-711405	NOTEST	0.0101583	0.012256	0.270833	0	1	1
ENSG00000272464	ENSG00000272464	snoU13	12:120427672-120532298	NOTEST	0	0	0	0	1	1
ENSG00000272465	ENSG00000272465	RP1-136B1.1	6:2245981-2482256	NOTEST	0.187181	0.0218097	-3.10139	0	1	1
ENSG00000272468	ENSG00000272468	RP1-86C11.7	6:27090435-27091000	NOTEST	0.581096	0.597817	0.0409275	0	1	1
ENSG00000272469	ENSG00000272469	Metazoa_SRP	8:74332238-74791145	NOTEST	0	0	0	0	1	1
ENSG00000272470	ENSG00000272470	RP13-379O24.3	HG506_HG507_HG1000_PATCH:61052925-61053650	NOTEST	0	0	0	0	1	1
ENSG00000272472	ENSG00000272472	RP11-95G17.2	6:122793075-123047518	NOTEST	0	0	0	0	1	1
ENSG00000272473	ENSG00000272473	AC006273.4	19:781001-781862	NOTEST	0	0	0	0	1	1
ENSG00000272474	ENSG00000272474	SNORD113-5	14:101403737-101426536	NOTEST	0	0	0	0	1	1
ENSG00000272475	ENSG00000272475	RP11-342M3.2	10:81266125-81270678	NOTEST	0	0	0	0	1	1
ENSG00000272476	ENSG00000272476	RP1-191J18.66	6:108188959-108281190	NOTEST	0.0538533	0.0387822	-0.47364	0	1	1
ENSG00000272477	ENSG00000272477	RP11-158G18.1	3:17198653-18959184	NOTEST	0	0	0	0	1	1
ENSG00000272478	ENSG00000272478	RP1-317E23.7	1:26126666-26185903	NOTEST	0	0.228264	inf	0	1	1
ENSG00000272479	ENSG00000272479	RP11-301G7.1	8:40377083-40377677	NOTEST	0	0	0	0	1	1
ENSG00000272480	ENSG00000272480	OR13Z3P	1:146953987-146954378	NOTEST	0	0	0	0	1	1
ENSG00000272482	ENSG00000272482	RP11-474O21.5	1:12678905-12679250	NOTEST	0.332603	0.399278	0.263593	0	1	1
ENSG00000272483	ENSG00000272483	RP11-169K17.3	3:11313994-11766453	NOTEST	0	0	0	0	1	1
ENSG00000272485	ENSG00000272485	RP11-284J1.1	6:761674-780648	NOTEST	0.0131134	0	#NAME?	0	1	1
ENSG00000272486	ENSG00000272486	RP11-532M24.1	8:125500725-125740730	NOTEST	0.102165	0	#NAME?	0	1	1
ENSG00000272489	ENSG00000272489	RP11-182L21.5	10:81420646-81526085	NOTEST	0.0189247	0	#NAME?	0	1	1
ENSG00000272491	ENSG00000272491	RP5-1024N4.4	1:48688356-48714316	NOTEST	0.0128775	0.0746713	2.5357	0	1	1
ENSG00000272492	ENSG00000272492	AC007040.9	HG953_PATCH:71163012-71291874	NOTEST	0	0	0	0	1	1
ENSG00000272494	ENSG00000272494	OR1X1P	5:175333941-175461683	NOTEST	0	0	0	0	1	1

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ENSG00000272501	ENSG00000272501	XXbac-BPG299F13.17	6:31162976-31171745	NOTEST	0.053543	0.0861831	0.686708	0	1	1
ENSG00000272502	ENSG00000272502	RP11-713M15.2	8:121392999-121825599	NOTEST	0.087265	0.0323445	-1.43188	0	1	1
ENSG00000272503	ENSG00000272503	FIGLA	HG953_PATCH:71004441-71017775	NOTEST	0	0	0	0	1	1
ENSG00000272505	ENSG00000272505	RP11-981G7.6	8:10340387-10411676	NOTEST	0.0541661	0.0931203	0.781706	0	1	1
ENSG00000272506	ENSG00000272506	RP4-535B20.4	1:65469152-65469770	NOTEST	0.0613707	0	#NAME?	0	1	1
ENSG00000272507	ENSG00000272507	U6	10:12110970-12165224	NOTEST	0	0	0	0	1	1
ENSG00000272508	ENSG00000272508	RP11-96C23.14	10:88695296-88784489	NOTEST	0.0933904	0.0760625	-0.296088	0	1	1
ENSG00000272509	ENSG00000272509	RP11-347C18.5	8:95825538-96128683	NOTEST	0.204122	0.123442	-0.725594	0	1	1
ENSG00000272510	ENSG00000272510	RP4-680D5.8	1:15853307-15930121	NOTEST	0	0	0	0	1	1
ENSG00000272511	ENSG00000272511	RP11-180N14.1	3:21453713-21455436	NOTEST	0	0	0	0	1	1
ENSG00000272512	ENSG00000272512	RP11-54O7.17	1:931345-933431	NOTEST	0.0140431	0.0120517	-0.220634	0	1	1
ENSG00000272514	ENSG00000272514	C6ORF165	6:88117700-88222054	NOTEST	0	0	0	0	1	1
ENSG00000272515	ENSG00000272515	RP11-29P20.1	13:88079454-88323514	NOTEST	0	0	0	0	1	1
ENSG00000272516	ENSG00000272516	RP11-573G6.9	10:22621332-22621916	NOTEST	0.0719093	0	#NAME?	0	1	1
ENSG00000272517	ENSG00000272517	TGFA	HG953_PATCH:70674411-70781325	NOTEST	0	0	0	0	1	1
ENSG00000272519	ENSG00000272519	RP11-105N14.2	2:214131718-214140876	NOTEST	0	0	0	0	1	1
ENSG00000272522	ENSG00000272522	U47924.29	HG344_PATCH:7074111-7085166	NOTEST	0	0	0	0	1	1
ENSG00000272523	ENSG00000272523	LINC01023	5:108063525-108063961	NOTEST	0.497408	0.131082	-1.92396	0	1	1
ENSG00000272524	ENSG00000272524	RP11-254F7.4	2:10260860-10261192	NOTEST	0.359488	0.413741	0.202783	0	1	1
ENSG00000272525	ENSG00000272525	RP11-79P5.9	5:72793374-72794118	NOTEST	0.198896	0.277258	0.479212	0	1	1
ENSG00000272526	ENSG00000272526	LINC01143	HG953_PATCH:71115001-71117090	NOTEST	0	0	0	0	1	1
ENSG00000272528	ENSG00000272528	RNU6-117P	HG357_PATCH:107165326-107235416	NOTEST	0	0	0	0	1	1
ENSG00000272529	ENSG00000272529	RP11-415F23.4	3:16306705-16555533	NOTEST	0.407354	0.31937	-0.351057	0	1	1
ENSG00000272532	ENSG00000272532	CYP2D6	HSCHR22_2_CTG1:42522486-42526867	NOTEST	0	0	0	0	1	1
ENSG00000272533	ENSG00000272533	SNORA28	14:103799880-103811362	NOTEST	0	0	0	0	1	1
ENSG00000272535	ENSG00000272535	RP11-337C18.9	HG1287_PATCH:147859185-147982177	NOTEST	0	0	0	0	1	1
ENSG00000272536	ENSG00000272536	Metazoa_SRP	10:74127097-74385899	NOTEST	0	0	0	0	1	1
ENSG00000272537	ENSG00000272537	GS1-166A23.1	7:16501105-16621193	NOTEST	0	0	0	0	1	1
ENSG00000272541	ENSG00000272541	XXbac-BPGBPG55C20.1	6:58182168-58182746	NOTEST	0.0364988	0.02586	-0.497123	0	1	1
ENSG00000272542	ENSG00000272542	RP11-255P5.2	13:103532448-103548383	NOTEST	0	0	0	0	1	1
ENSG00000272543	ENSG00000272543	MIR4787	3:50712510-50712594	NOTEST	0	0	0	0	1	1
ENSG00000272544	ENSG00000272544	CTA-357J21.1	7:101458958-101927249	NOTEST	0	0	0	0	1	1
ENSG00000272545	ENSG00000272545	CTC-527H23.4	16:48657346-48778553	NOTEST	0	0.0257322	inf	0	1	1
ENSG00000272546	ENSG00000272546	OR3A5P	17:3181192-3290132	NOTEST	0	0	0	0	1	1
ENSG00000272547	ENSG00000272547	TMEM242	HG193_PATCH:157610519-157644735	NOTEST	0	0	0	0	1	1
ENSG00000272548	ENSG00000272548	PCDHAC2	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000272549	ENSG00000272549	RP11-351J23.2	6:168067519-168079950	NOTEST	0	0.0197154	inf	0	1	1
ENSG00000272550	ENSG00000272550	PCDHAC1	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000272551	ENSG00000272551	RP11-324L17.1	2:177476164-177476977	NOTEST	0	0.0690503	inf	0	1	1

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ENSG00000272553	ENSG00000272553	NDUFA3	HSCHR19LRC_COX2_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272554	ENSG00000272554	RP11-317L10.1	3:24158650-24541833	NOTEST	0	0	0	0	1	1
ENSG00000272555	ENSG00000272555	RP11-459I19.1	2:219683412-219683867	NOTEST	0.209138	0.278904	0.41531	0	1	1
ENSG00000272557	ENSG00000272557	RP11-478C6.6	HG174_HG254_PATCH:268981-269531	NOTEST	0	0	0	0	1	1
ENSG00000272558	ENSG00000272558	U91328.21	6:25963029-26002003	NOTEST	0	0	0	0	1	1
ENSG00000272559	ENSG00000272559	OR51F3P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000272560	ENSG00000272560	TFPT	HSCHR19LRC_COX1_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272561	ENSG00000272561	TSEN34	HSCHR19LRC_LRC_T_CTG1:54693788-54697585	NOTEST	0	0	0	0	1	1
ENSG00000272562	ENSG00000272562	RP11-396C23.4	1:226248412-226259702	NOTEST	0.0868743	0.0362859	-1.25952	0	1	1
ENSG00000272563	ENSG00000272563	RP11-480C16.1	2:114190176-114193619	NOTEST	0	0	0	0	1	1
ENSG00000272566	ENSG00000272566	RP11-462G22.2	4:190625034-190625644	NOTEST	0.0338381	0.197763	2.54705	0	1	1
ENSG00000272567	ENSG00000272567	RP11-73K9.3	4:113194123-113194472	NOTEST	0	0	0	0	1	1
ENSG00000272568	ENSG00000272568	CTB-113D17.1	7:29019582-29603286	NOTEST	0	0	0	0	1	1
ENSG00000272569	ENSG00000272569	OR5BL1P	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000272570	ENSG00000272570	RP11-2H3.2	HG174_HG254_PATCH:393533-393658	NOTEST	0	0	0	0	1	1
ENSG00000272571	ENSG00000272571	H2AFB3	HG1497_PATCH:154627886-154628403	NOTEST	0	0	0	0	1	1
ENSG00000272572	ENSG00000272572	RP11-179B2.2	10:102670859-102724893	NOTEST	0.0101306	0.0952425	3.23288	0	1	1
ENSG00000272573	ENSG00000272573	MUSTN1	3:52846990-52931612	NOTEST	0.199584	0.281818	0.497767	0	1	1
ENSG00000272574	ENSG00000272574	RP11-359K18.4	1:162531322-162569627	NOTEST	0.470892	0.439701	-0.098876	0	1	1
ENSG00000272575	ENSG00000272575	RP11-702B10.1	11:128078723-128111334	NOTEST	0	0	0	0	1	1
ENSG00000272576	ENSG00000272576	RP11-365H22.2	4:52784937-52785547	NOTEST	0.0963567	0.248732	1.36814	0	1	1
ENSG00000272577	ENSG00000272577	AC012314.19	HSCHR19LRC_LRC_S_CTG1:54712959-54713286	NOTEST	0	0	0	0	1	1
ENSG00000272580	ENSG00000272580	ZNF721	HG174_HG254_PATCH:425434-499156	NOTEST	0	0	0	0	1	1
ENSG00000272581	ENSG00000272581	AC012314.20	HSCHR19LRC_LRC_T_CTG1:54703320-54703838	NOTEST	0	0	0	0	1	1
ENSG00000272582	ENSG00000272582	RP5-1039K5.17	22:38339527-38437922	NOTEST	0.111802	0.104883	-0.0921688	0	1	1
ENSG00000272583	ENSG00000272583	RP11-344P13.6	1:121260163-121260627	NOTEST	0	0	0	0	1	1
ENSG00000272584	ENSG00000272584	ATP1A3	HG1350_HG959_PATCH:42472486-42503402	NOTEST	0	0	0	0	1	1
ENSG00000272585	ENSG00000272585	PCDHB3	HG1082_HG167_PATCH:140479829-140483407	NOTEST	0	0	0	0	1	1
ENSG00000272586	ENSG00000272586	KRTAP10-9	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272587	ENSG00000272587	PCDHB9	HG1082_HG167_PATCH:140566903-140571123	NOTEST	0	0	0	0	1	1
ENSG00000272588	ENSG00000272588	RP11-440L14.4	4:699536-775637	NOTEST	0.0769337	0.0977099	0.344889	0	1	1
ENSG00000272589	ENSG00000272589	ZSWIM8-AS1	10:75545339-75571589	NOTEST	0.119248	0.109278	-0.125959	0	1	1
ENSG00000272590	ENSG00000272590	TAS2R12	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000272591	ENSG00000272591	F8A2	HG1497_PATCH:154550567-154552268	NOTEST	0	0	0	0	1	1
ENSG00000272592	ENSG00000272592	RP11-63A2.2	10:63422718-63526524	NOTEST	0	0	0	0	1	1
ENSG00000272594	ENSG00000272594	KRTAP10-12	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272595	ENSG00000272595	OR10AH1P	7:5156799-5157718	NOTEST	0	0	0	0	1	1
ENSG00000272596	ENSG00000272596	AC012314.8	HSCHR19LRC_PGF2_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272597	ENSG00000272597	RP11-446H18.6	3:106959538-107101007	NOTEST	0	0	0	0	1	1
ENSG00000272598	ENSG00000272598	VSTM1	HSCHR19LRC_PGF1_CTG1:54544078-54567207	NOTEST	0	0	0	0	1	1

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ENSG00000272602	ENSG00000272602	ZNF595	HG174_HG254_PATCH:53332-162774	NOTEST	0	0	0	0	1	1
ENSG00000272603	ENSG00000272603	NOL5BP	HSCHR6_MHC_APD:28751413-28751785	NOTEST	0	0	0	0	1	1
ENSG00000272604	ENSG00000272604	RP11-251G23.5	7:105172531-105241322	NOTEST	0.186809	0.0961993	-0.957466	0	1	1
ENSG00000272605	ENSG00000272605	SNORA15	HG444_PATCH:65112079-65235723	NOTEST	0	0	0	0	1	1
ENSG00000272607	ENSG00000272607	PIGG	HG174_HG254_PATCH:499199-540196	NOTEST	0	0	0	0	1	1
ENSG00000272608	ENSG00000272608	AC012314.8	HSCHR19LRC_LRC_S_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272609	ENSG00000272609	RP11-461M2.2	3:137717576-137752494	NOTEST	0.0490142	0	#NAME?	0	1	1
ENSG00000272610	ENSG00000272610	MAGI1-IT1	3:65339199-66024509	NOTEST	0	0	0	0	1	1
ENSG00000272611	ENSG00000272611	CEACAM3	HG1350_HG959_PATCH:42302341-42317458	NOTEST	0	0	0	0	1	1
ENSG00000272612	ENSG00000272612	AL662890.4	HSCHR6_MHC_QBL:28743696-28743804	NOTEST	0	0	0	0	1	1
ENSG00000272613	ENSG00000272613	RPL13P	HSCHR6_MHC_APD:28827405-28831131	NOTEST	0	0	0	0	1	1
ENSG00000272614	ENSG00000272614	RPS9	HSCHR19LRC_PGF2_CTG1:54704725-54711511	NOTEST	0	0	0	0	1	1
ENSG00000272615	ENSG00000272615	PCDHA7	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000272616	ENSG00000272616	HNRNPA1P52	HG1350_HG959_PATCH:42335596-42336843	NOTEST	0	0	0	0	1	1
ENSG00000272618	ENSG00000272618	AC091738.3	HG1257_PATCH:72039492-72293191	NOTEST	0	0	0	0	1	1
ENSG00000272619	ENSG00000272619	RP11-563K23.1	7:143060991-143061322	NOTEST	0	0	0	0	1	1
ENSG00000272620	ENSG00000272620	AFAP1-AS1	4:7755816-7942022	NOTEST	0.0134513	0.0254437	0.91956	0	1	1
ENSG00000272621	ENSG00000272621	TMC4	HSCHR19LRC_LRC_S_CTG1:54663845-54676944	NOTEST	0	0	0	0	1	1
ENSG00000272622	ENSG00000272622	RP11-395N3.2	2:227664861-227675745	NOTEST	0.0359685	0.209626	2.54301	0	1	1
ENSG00000272623	ENSG00000272623	F8A1	HG1497_PATCH:154004255-154228771	NOTEST	0	0	0	0	1	1
ENSG00000272624	ENSG00000272624	AC091390.2	HG115_PATCH:101991667-101998642	NOTEST	0	0	0	0	1	1
ENSG00000272625	ENSG00000272625	RP11-737O24.5	18:2916991-3013313	NOTEST	0.0767861	0.0401712	-0.934685	0	1	1
ENSG00000272626	ENSG00000272626	RP11-468N14.13	4:69766725-69772701	NOTEST	0	0	0	0	1	1
ENSG00000272627	ENSG00000272627	RP11-354E23.5	10:74451888-74647452	NOTEST	0.138381	0.207225	0.582552	0	1	1
ENSG00000272628	ENSG00000272628	REXO1L3P	8:86566861-86568611	NOTEST	0	0	0	0	1	1
ENSG00000272629	ENSG00000272629	XXbac-BPG308K3.6	HSCHR6_MHC_QBL:28827405-28831131	NOTEST	0	0	0	0	1	1
ENSG00000272630	ENSG00000272630	RP11-344N10.5	10:74857801-74861055	NOTEST	0.0618729	0.0596141	-0.0536535	0	1	1
ENSG00000272631	ENSG00000272631	RP11-359E3.4	10:88509510-88516055	NOTEST	0.241083	0.235864	-0.0315745	0	1	1
ENSG00000272632	ENSG00000272632	RP11-362F19.3	4:142351984-142352438	NOTEST	0	0	0	0	1	1
ENSG00000272633	ENSG00000272633	PCDHB4	HG1082_HG167_PATCH:140501583-140505204	NOTEST	0	0	0	0	1	1
ENSG00000272634	ENSG00000272634	OR51F5P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000272635	ENSG00000272635	LLNLF-65H9.1	19:28175487-28475892	NOTEST	0	0.0203191	inf	0	1	1
ENSG00000272636	ENSG00000272636	DOC2B	17:5809-31427	NOTEST	0	0	0	0	1	1
ENSG00000272637	ENSG00000272637	RP11-478C6.4	HG174_HG254_PATCH:337813-384864	NOTEST	0	0	0	0	1	1
ENSG00000272639	ENSG00000272639	RP11-66B24.8	15:101389765-101626271	NOTEST	0	0.110674	inf	0	1	1
ENSG00000272640	ENSG00000272640	AC012314.4	HSCHR19LRC_LRC_J_CTG1:54530501-54530601	NOTEST	0	0	0	0	1	1
ENSG00000272641	ENSG00000272641	PCDHB15	HG1082_HG167_PATCH:140625163-140627816	NOTEST	0	0	0	0	1	1
ENSG00000272642	ENSG00000272642	CTD-2234N14.1	11:127060663-127093344	NOTEST	0	0	0	0	1	1
ENSG00000272643	ENSG00000272643	RPS9	HSCHR19LRC_LRC_T_CTG1:54704725-54711511	NOTEST	0	0	0	0	1	1
ENSG00000272646	ENSG00000272646	RP11-188P17.2	4:183802929-183803356	NOTEST	0.057979	0.0413371	-0.488092	0	1	1

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ENSG00000272648	ENSG00000272648	AC012314.8	HSCHR19LRC_LRC_J_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272649	ENSG00000272649	VSTM1	HSCHR19LRC_LRC_I_CTG1:54544078-54567207	NOTEST	0	0	0	0	1	1
ENSG00000272650	ENSG00000272650	RP11-571I18.4	4:54243809-55164414	NOTEST	0.114958	0	#NAME?	0	1	1
ENSG00000272651	ENSG00000272651	KRTAP10-8	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272652	ENSG00000272652	AL662890.5	HSCHR6_MHC_QBL:28730485-28730593	NOTEST	0	0	0	0	1	1
ENSG00000272653	ENSG00000272653	SLC25A2	HG1082_HG167_PATCH:140682213-140683630	NOTEST	0	0	0	0	1	1
ENSG00000272657	ENSG00000272657	AP000320.7	21:35445523-35732332	NOTEST	0	0	0	0	1	1
ENSG00000272659	ENSG00000272659	AP000295.10	21:34681795-34682486	NOTEST	0.028566	0.152064	2.41231	0	1	1
ENSG00000272660	ENSG00000272660	RP11-145M9.6	3:179280667-179322442	NOTEST	0	0	0	0	1	1
ENSG00000272662	ENSG00000272662	RP11-190C22.8	3:119216524-119217028	NOTEST	0.0446052	0.165554	1.89202	0	1	1
ENSG00000272663	ENSG00000272663	RP11-191L17.1	2:48667181-48667736	NOTEST	0.513448	0.265075	-0.953819	0	1	1
ENSG00000272664	ENSG00000272664	OR51C4P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000272665	ENSG00000272665	AC092574.3	HG174_HG254_PATCH:425434-499156	NOTEST	0	0	0	0	1	1
ENSG00000272666	ENSG00000272666	CTA-384D8.35	22:50980733-50981440	NOTEST	0	0.0244053	inf	0	1	1
ENSG00000272667	ENSG00000272667	RP11-395A13.2	2:128644129-128644759	NOTEST	0.0323634	0.0229021	-0.498883	0	1	1
ENSG00000272670	ENSG00000272670	DOC2B	HSCHR17_1_CTG1:5809-31427	NOTEST	0	0	0	0	1	1
ENSG00000272671	ENSG00000272671	MIR1184-2	HG1497_PATCH:154550567-154552268	NOTEST	0	0	0	0	1	1
ENSG00000272672	ENSG00000272672	RP11-302M6.5	1:90405159-90405706	NOTEST	0.0790147	0.0954842	0.27314	0	1	1
ENSG00000272673	ENSG00000272673	AC012314.19	HSCHR19LRC_PGF2_CTG1:54712959-54713286	NOTEST	0	0	0	0	1	1
ENSG00000272674	ENSG00000272674	AC244517.1	HG1082_HG167_PATCH:140560983-140565803	NOTEST	0	0	0	0	1	1
ENSG00000272675	ENSG00000272675	AC004019.18	22:17840836-18037850	NOTEST	0.00746778	0.0250938	1.74858	0	1	1
ENSG00000272676	ENSG00000272676	OR5AO1P	11:56812565-56812865	NOTEST	0	0	0	0	1	1
ENSG00000272678	ENSG00000272678	RP11-797D24.4	3:123001142-123168605	NOTEST	0.00231759	0.103978	5.4875	0	1	1
ENSG00000272679	ENSG00000272679	RP11-216L13.18	9:139685806-139735639	NOTEST	0.347379	0.312842	-0.151076	0	1	1
ENSG00000272680	ENSG00000272680	TFPT	HSCHR19LRC_LRC_S_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272681	ENSG00000272681	FAM223B	HG1497_PATCH:153800942-153801650	NOTEST	0	0	0	0	1	1
ENSG00000272682	ENSG00000272682	AC004471.10	22:19023794-19115962	NOTEST	0.0200809	0	#NAME?	0	1	1
ENSG00000272683	ENSG00000272683	CTD-3093M3.1	HSCHR19LRC_LRC_T_CTG1:54697730-54698394	NOTEST	0	0	0	0	1	1
ENSG00000272684	ENSG00000272684	CEACAM7	HG1350_HG959_PATCH:42179211-42212881	NOTEST	0	0	0	0	1	1
ENSG00000272685	ENSG00000272685	OR9I3P	11:57791352-57949088	NOTEST	0	0	0	0	1	1
ENSG00000272687	ENSG00000272687	TKT	HG957_PATCH:53258722-53290068	NOTEST	0	0	0	0	1	1
ENSG00000272689	ENSG00000272689	RP4-539M6.21	22:30727976-30825045	NOTEST	0.447256	0.289314	-0.628465	0	1	1
ENSG00000272690	ENSG00000272690	RP11-803B1.8	3:75484498-75540353	NOTEST	0.357818	0.36435	0.0261001	0	1	1
ENSG00000272691	ENSG00000272691	RP11-290M5.4	1:86044182-86044425	NOTEST	0	0	0	0	1	1
ENSG00000272692	ENSG00000272692	RP11-399K21.14	10:77029576-77171600	NOTEST	0.102404	0.0511881	-1.0004	0	1	1
ENSG00000272693	ENSG00000272693	AC104057.2	HG444_PATCH:64990541-65020372	NOTEST	0	0	0	0	1	1
ENSG00000272694	ENSG00000272694	RP1-63G5.8	22:37735623-37823505	NOTEST	0.000439574	0.0078415	4.15695	0	1	1
ENSG00000272695	ENSG00000272695	GAS6-AS2	13:114567140-114569806	NOTEST	0.0453197	0.0312725	-0.535241	0	1	1

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ENSG00000272697	ENSG00000272697	KRTAP10-13P	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272698	ENSG00000272698	AC012314.8	HSCHR19LRC_COX2_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272699	ENSG00000272699	RP11-145M9.5	3:179116989-179169378	NOTEST	0.0455618	0.0324214	-0.490878	0	1	1
ENSG00000272700	ENSG00000272700	RP11-245C23.3	3:178865901-178984790	NOTEST	0	0	0	0	1	1
ENSG00000272701	ENSG00000272701	RP11-2E11.10	7:130125882-130148500	NOTEST	0	0	0	0	1	1
ENSG00000272702	ENSG00000272702	RP11-44N22.3	2:73169164-73383849	NOTEST	0.189574	0.24229	0.353972	0	1	1
ENSG00000272703	ENSG00000272703	RP11-78A19.4	18:11688954-11909222	NOTEST	0	0.156784	inf	0	1	1
ENSG00000272704	ENSG00000272704	KRTAP10-10	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272705	ENSG00000272705	TSEN34	HSCHR19LRC_LRC_S_CTG1:54693788-54697585	NOTEST	0	0	0	0	1	1
ENSG00000272706	ENSG00000272706	GRIK5	HG1350_HG959_PATCH:42504225-42575403	NOTEST	0	0	0	0	1	1
ENSG00000272707	ENSG00000272707	RP11-534C12.1	3:194304739-194393206	NOTEST	0	0	0	0	1	1
ENSG00000272708	ENSG00000272708	CEACAM4	HG1350_HG959_PATCH:42124875-42132979	NOTEST	0	0	0	0	1	1
ENSG00000272709	ENSG00000272709	RP11-458D21.6	1:145200337-145200891	NOTEST	0	0.0274988	inf	0	1	1
ENSG00000272710	ENSG00000272710	CTD-2026G6.3	3:75589199-75629150	NOTEST	0	0.278221	inf	0	1	1
ENSG00000272712	ENSG00000272712	TAS2R8	HSCHR12_2_CTG2:10958649-10959892	NOTEST	0	0	0	0	1	1
ENSG00000272713	ENSG00000272713	AL662890.6	HSCHR6_MHC_MCF:28743696-28743804	NOTEST	0	0	0	0	1	1
ENSG00000272714	ENSG00000272714	RP1-276J11.3	6:121710469-121711503	NOTEST	0	0	0	0	1	1
ENSG00000272715	ENSG00000272715	RP4-753F5.1	1:117451770-117452153	NOTEST	0	0.223852	inf	0	1	1
ENSG00000272716	ENSG00000272716	RP11-563N4.1	2:32390114-32390826	NOTEST	0.311741	0.297922	-0.0654099	0	1	1
ENSG00000272717	ENSG00000272717	RP11-342I1.2	4:140417094-140527853	NOTEST	0	0.0703316	inf	0	1	1
ENSG00000272718	ENSG00000272718	RP11-144O23.8	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000272719	ENSG00000272719	CTB-161C1.1	7:5566781-5603415	NOTEST	0	0	0	0	1	1
ENSG00000272720	ENSG00000272720	CTA-228A9.3	22:38480895-38506677	NOTEST	0.0994329	0.00827804	-3.58636	0	1	1
ENSG00000272721	ENSG00000272721	RP11-778D9.12	3:183851806-184402546	NOTEST	0.0864885	0.067528	-0.357023	0	1	1
ENSG00000272722	ENSG00000272722	TFPT	HSCHR19LRC_PGF1_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272723	ENSG00000272723	TMC4	HSCHR19LRC_LRC_J_CTG1:54663845-54676944	NOTEST	0	0	0	0	1	1
ENSG00000272724	ENSG00000272724	RP1-288H2.4	12:52463029-52502045	NOTEST	0	0	0	0	1	1
ENSG00000272725	ENSG00000272725	RP11-667F9.1	HG444_PATCH:64990541-65020372	NOTEST	0	0	0	0	1	1
ENSG00000272726	ENSG00000272726	LENG1	HSCHR19LRC_LRC_S_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000272727	ENSG00000272727	RP11-142A22.4	4:146256414-146261573	NOTEST	0	0	0	0	1	1
ENSG00000272728	ENSG00000272728	TSPEAR	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272729	ENSG00000272729	RP11-387A1.5	2:176986338-177037830	NOTEST	0.181513	0.131524	-0.464745	0	1	1
ENSG00000272730	ENSG00000272730	AC079140.2	HG174_HG254_PATCH:212609-255985	NOTEST	0	0	0	0	1	1
ENSG00000272731	ENSG00000272731	PCDHB1	HG1082_HG167_PATCH:140430978-140433512	NOTEST	0	0	0	0	1	1
ENSG00000272732	ENSG00000272732	RP5-1159O4.2	7:7589734-7592071	NOTEST	0.094491	0.0218493	-2.11259	0	1	1
ENSG00000272733	ENSG00000272733	KB-208E9.1	22:23923066-23926046	NOTEST	0	0	0	0	1	1
ENSG00000272735	ENSG00000272735	RP11-467P9.1	2:71163011-71306935	NOTEST	0.0340823	0	#NAME?	0	1	1
ENSG00000272736	ENSG00000272736	RP11-799N11.1	17:10286448-10527203	NOTEST	0	0	0	0	1	1
ENSG00000272737	ENSG00000272737	AC005754.8	HG1082_HG167_PATCH:140498264-140500350	NOTEST	0	0	0	0	1	1
ENSG00000272738	ENSG00000272738	AC012314.19	HSCHR19LRC_LRC_I_CTG1:54712959-54713286	NOTEST	0	0	0	0	1	1
ENSG00000272739	ENSG00000272739	TSEN34	HSCHR19LRC_LRC_I_CTG1:54693788-54697585	NOTEST	0	0	0	0	1	1

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ENSG00000272741	ENSG00000272741	RP11-447L10.1	3:195938357-196065374	NOTEST	0	0	0	0	1	1
ENSG00000272743	ENSG00000272743	CEACAM5	HG1350_HG959_PATCH:42214489-42292798	NOTEST	0	0	0	0	1	1
ENSG00000272744	ENSG00000272744	RP11-367N14.3	4:184438046-184438680	NOTEST	0	0.0227023	inf	0	1	1
ENSG00000272745	ENSG00000272745	RP5-1007H16.1	7:7659502-7660174	NOTEST	0	0	0	0	1	1
ENSG00000272746	ENSG00000272746	RP11-53B2.6	18:13217496-13652754	NOTEST	0.197425	0.177163	-0.156224	0	1	1
ENSG00000272747	ENSG00000272747	RP11-2H3.6	HG174_HG254_PATCH:416117-416537	NOTEST	0	0	0	0	1	1
ENSG00000272748	ENSG00000272748	RP11-222G7.2	10:76581367-76581888	NOTEST	0	0	0	0	1	1
ENSG00000272749	ENSG00000272749	TARM1	HSCHR19LRC_PGF1_CTG1:54573148-54584634	NOTEST	0	0	0	0	1	1
ENSG00000272750	ENSG00000272750	RP11-378J18.8	1:222791427-222841354	NOTEST	0.273367	0.24279	-0.171132	0	1	1
ENSG00000272751	ENSG00000272751	TAS2R12	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000272753	ENSG00000272753	RP11-285M22.2	HG1591_PATCH:22192160-22194158	NOTEST	0	0	0	0	1	1
ENSG00000272754	ENSG00000272754	AL133245.2	2:32546706-32548071	NOTEST	0.022605	0	#NAME?	0	1	1
ENSG00000272755	ENSG00000272755	RP11-326G21.1	1:144836156-145076186	NOTEST	0.0754058	0.0267316	-1.49613	0	1	1
ENSG00000272756	ENSG00000272756	PCDHA4	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000272757	ENSG00000272757	TMC4	HSCHR19LRC_COX2_CTG1:54663845-54676944	NOTEST	0	0	0	0	1	1
ENSG00000272759	ENSG00000272759	VSTM1	HSCHR19LRC_COX1_CTG1:54544078-54567207	NOTEST	0	0	0	0	1	1
ENSG00000272761	ENSG00000272761	RP11-572C15.6	3:112315640-112320749	NOTEST	0.00601474	0.0216274	1.84628	0	1	1
ENSG00000272762	ENSG00000272762	RP11-155D18.14	3:51989329-52023213	NOTEST	0	0.220987	inf	0	1	1
ENSG00000272763	ENSG00000272763	RP11-357H14.17	17:46713284-46724385	NOTEST	0	0.010505	inf	0	1	1
ENSG00000272764	ENSG00000272764	RP11-318E3.9	10:5807185-5884095	NOTEST	0.137416	0.0993726	-0.467628	0	1	1
ENSG00000272765	ENSG00000272765	NDUFA6	HSCHR22_1_CTG1:42481528-42486959	NOTEST	0	0	0	0	1	1
ENSG00000272766	ENSG00000272766	KRTAP12-2	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272767	ENSG00000272767	JMJD1C-AS1	10:64926980-65226323	NOTEST	0.118884	0.118529	-0.00430367	0	1	1
ENSG00000272768	ENSG00000272768	RP4-673M15.1	7:44915895-44925992	NOTEST	0.11263	0.0628986	-0.840488	0	1	1
ENSG00000272769	ENSG00000272769	RP11-725P16.2	2:133103188-133104870	NOTEST	0.599748	0.427753	-0.487579	0	1	1
ENSG00000272770	ENSG00000272770	RP11-74E22.5	17:2496503-2588909	NOTEST	0	0	0	0	1	1
ENSG00000272771	ENSG00000272771	AC012314.8	HSCHR19LRC_PGF1_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272772	ENSG00000272772	CTD-2410N18.5	5:133450401-133706738	NOTEST	0.288306	0.211549	-0.446608	0	1	1
ENSG00000272773	ENSG00000272773	UBE2G2	HG237_PATCH:46188920-46221900	NOTEST	0	0	0	0	1	1
ENSG00000272774	ENSG00000272774	RP11-433A10.3	3:72084450-72291716	NOTEST	0	0	0	0	1	1
ENSG00000272775	ENSG00000272775	AC012314.20	HSCHR19LRC_COX2_CTG1:54703320-54703838	NOTEST	0	0	0	0	1	1
ENSG00000272776	ENSG00000272776	AL662890.7	HSCHR6_MHC_QBL:28763752-28763816	NOTEST	0	0	0	0	1	1
ENSG00000272778	ENSG00000272778	RP11-337C18.10	HG1287_PATCH:147859185-147982177	NOTEST	0	0	0	0	1	1
ENSG00000272781	ENSG00000272781	MDGA2	14:47308825-48144157	NOTEST	0.314634	0.0174322	-4.17385	0	1	1
ENSG00000272783	ENSG00000272783	RP13-1016M1.2	4:1552010-1552299	NOTEST	0	0	0	0	1	1
ENSG00000272784	ENSG00000272784	RP11-335L23.5	4:184015575-184016209	NOTEST	0	0	0	0	1	1
ENSG00000272785	ENSG00000272785	RP5-998N21.10	HG1287_PATCH:144561207-144621191	NOTEST	0	0	0	0	1	1

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ENSG00000272788	ENSG00000272788	RP11-674N23.4	18:8695853-8832776	NOTEST	0	0.0702126	inf	0	1	1
ENSG00000272789	ENSG00000272789	RP11-286H15.1	2:128293377-128395304	NOTEST	0	0	0	0	1	1
ENSG00000272790	ENSG00000272790	AP002884.3	11:111895537-112095422	NOTEST	0.0122442	0.0470463	1.94199	0	1	1
ENSG00000272791	ENSG00000272791	RP11-464F9.22	10:75390313-75391248	NOTEST	0.0744028	0.0288245	-1.36806	0	1	1
ENSG00000272793	ENSG00000272793	XXbac-BPG308K3.5	HSCHR6_MHC_APD:28805649-28806787	NOTEST	0	0	0	0	1	1
ENSG00000272794	ENSG00000272794	PCDHA9	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000272795	ENSG00000272795	RP11-602N24.3	4:110736202-110736566	NOTEST	0.376354	0	#NAME?	0	1	1
ENSG00000272796	ENSG00000272796	RP1-74M1.3	1:23243174-23247993	NOTEST	0	0	0	0	1	1
ENSG00000272797	ENSG00000272797	RP11-368I23.3	3:168645262-168645707	NOTEST	0	0	0	0	1	1
ENSG00000272798	ENSG00000272798	CTA-390C10.9	22:25832278-25832882	NOTEST	0.0343071	0	#NAME?	0	1	1
ENSG00000272799	ENSG00000272799	RP11-474N24.6	18:9912312-9912846	NOTEST	0	0	0	0	1	1
ENSG00000272800	ENSG00000272800	RP11-438L19.1	2:184079046-184080128	NOTEST	0.111234	0.16381	0.558435	0	1	1
ENSG00000272801	ENSG00000272801	RP1-170O19.23	7:27145802-27197555	NOTEST	0	0.0942421	inf	0	1	1
ENSG00000272802	ENSG00000272802	RP1-257I20.14	HSCHR22_1_CTG1:42481528-42486959	NOTEST	0	0	0	0	1	1
ENSG00000272803	ENSG00000272803	PRH2	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000272804	ENSG00000272804	AP001067.1	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272805	ENSG00000272805	TAS2R10	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000272806	ENSG00000272806	AC012314.8	HSCHR19LRC_COX1_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272808	ENSG00000272808	RP11-66B24.7	15:101389765-101626271	NOTEST	0.142198	0.16506	0.21509	0	1	1
ENSG00000272809	ENSG00000272809	MBOAT7	HSCHR19LRC_PGF2_CTG1:54677106-54693733	NOTEST	0	0	0	0	1	1
ENSG00000272810	ENSG00000272810	U91328.22	6:26013468-26013985	NOTEST	0.24562	0.0953441	-1.36521	0	1	1
ENSG00000272811	ENSG00000272811	ATRNL1	HG979_PATCH:116853123-117708745	NOTEST	0	0	0	0	1	1
ENSG00000272813	ENSG00000272813	OLA1P1	HSCHR22_1_CTG1:42503768-42504957	NOTEST	0	0	0	0	1	1
ENSG00000272814	ENSG00000272814	RP11-15I20.1	2:47126413-47403740	NOTEST	0	0.109625	inf	0	1	1
ENSG00000272815	ENSG00000272815	RP11-219A15.4	17:16592850-16719854	NOTEST	0	0	0	0	1	1
ENSG00000272816	ENSG00000272816	CEACAM P3	HG1350_HG959_PATCH:42105639-42111889	NOTEST	0	0	0	0	1	1
ENSG00000272817	ENSG00000272817	RP11-402D21.2	10:93666345-93669240	NOTEST	0.0742749	0	#NAME?	0	1	1
ENSG00000272818	ENSG00000272818	PCDHA3	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000272819	ENSG00000272819	RP5-933K21.3	HG193_PATCH:157645097-157645611	NOTEST	0	0	0	0	1	1
ENSG00000272820	ENSG00000272820	RP1-257I20.14	HSCHR22_2_CTG1:42481528-42486959	NOTEST	0	0	0	0	1	1
ENSG00000272822	ENSG00000272822	RP11-302B13.5	12:49297200-49351334	NOTEST	0	0.0901137	inf	0	1	1
ENSG00000272823	ENSG00000272823	RP11-295M18.6	1:221002017-221002553	NOTEST	0.616347	0.557779	-0.144048	0	1	1
ENSG00000272824	ENSG00000272824	RP6-74O6.6	1:147830373-147830815	NOTEST	0.102859	0.122161	0.248114	0	1	1
ENSG00000272825	ENSG00000272825	LL21NC02-1C16.2	21:46352728-46359828	NOTEST	0.0569279	0	#NAME?	0	1	1
ENSG00000272826	ENSG00000272826	AC253576.1	HG174_HG254_PATCH:53332-162774	NOTEST	0	0	0	0	1	1
ENSG00000272827	ENSG00000272827	RP11-445P19.3	1:187449424-187449746	NOTEST	0	0	0	0	1	1

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ENSG00000272828	ENSG00000272828	CTD-2555O16.3	14:64854748-65009955	NOTEST	0	0	0	0	1	1
ENSG00000272829	ENSG00000272829	XXbac-B135H6.18	22:21319395-21353327	NOTEST	0.250705	0.247227	-0.0201507	0	1	1
ENSG00000272830	ENSG00000272830	MIR1184-1	HG1497_PATCH:154004255-154228771	NOTEST	0	0	0	0	1	1
ENSG00000272832	ENSG00000272832	RP11-91K8.5	3:133261907-133262310	NOTEST	0	0	0	0	1	1
ENSG00000272833	ENSG00000272833	OSCAR	HSCHR19LRC_COX2_CTG1:54597932-54606000	NOTEST	0	0	0	0	1	1
ENSG00000272834	ENSG00000272834	RP5-1042K10.13	22:40742506-41032706	NOTEST	0.163771	0.426457	1.38072	0	1	1
ENSG00000272835	ENSG00000272835	SMDT1	HSCHR22_2_CTG1:42475694-42480288	NOTEST	0	0	0	0	1	1
ENSG00000272837	ENSG00000272837	OR10AE3P	12:56032695-56053579	NOTEST	0	0	0	0	1	1
ENSG00000272838	ENSG00000272838	TARM1	HSCHR19LRC_PGF2_CTG1:54573148-54584634	NOTEST	0	0	0	0	1	1
ENSG00000272839	ENSG00000272839	RP11-452C13.1	7:157331749-158380480	NOTEST	0	0	0	0	1	1
ENSG00000272840	ENSG00000272840	RP11-379B18.6	3:125493556-125516796	NOTEST	0	0	0	0	1	1
ENSG00000272841	ENSG00000272841	RP3-428L16.2	6:161411349-161538417	NOTEST	0.0242661	0.0243768	0.00656647	0	1	1
ENSG00000272843	ENSG00000272843	RP11-313P13.5	7:72349935-72425329	NOTEST	0.180254	0.497818	1.46558	0	1	1
ENSG00000272844	ENSG00000272844	RP11-484K9.4	3:112709293-112902148	NOTEST	0	0	0	0	1	1
ENSG00000272845	ENSG00000272845	PCDHB7	HG1082_HG167_PATCH:140552246-140555961	NOTEST	0	0	0	0	1	1
ENSG00000272846	ENSG00000272846	RP11-701H24.10	15:25068793-25492435	NOTEST	0	0	0	0	1	1
ENSG00000272847	ENSG00000272847	RP11-822E23.8	HG987_PATCH:21428101-21477829	NOTEST	0	0	0	0	1	1
ENSG00000272848	ENSG00000272848	RP1-137D17.2	6:169826514-169827164	NOTEST	0.0310118	0.0748999	1.27215	0	1	1
ENSG00000272850	ENSG00000272850	AC012314.20	HSCHR19LRC_LRC_I_CTG1:54703320-54703838	NOTEST	0	0	0	0	1	1
ENSG00000272852	ENSG00000272852	RPS19	HG1350_HG959_PATCH:42365822-42378831	NOTEST	0	0	0	0	1	1
ENSG00000272853	ENSG00000272853	RP11-398C13.6	10:14919686-14920685	NOTEST	0.462352	0.353019	-0.389248	0	1	1
ENSG00000272854	ENSG00000272854	RP4-593H12.1	7:107220001-107269943	NOTEST	0.476724	0.237275	-1.00659	0	1	1
ENSG00000272855	ENSG00000272855	RP5-1102E8.3	1:77102561-77103024	NOTEST	0.0952021	0.118946	0.321245	0	1	1
ENSG00000272856	ENSG00000272856	RP11-710E1.2	4:88381958-88383432	NOTEST	0	0.0329822	inf	0	1	1
ENSG00000272857	ENSG00000272857	XXbac-BPG308K3.6	HSCHR6_MHC_APD:28827405-28831131	NOTEST	0	0	0	0	1	1
ENSG00000272858	ENSG00000272858	CTA-292E10.8	22:29196670-29244547	NOTEST	0.0471819	0	#NAME?	0	1	1
ENSG00000272859	ENSG00000272859	RP11-352E8.2	4:73918078-73918634	NOTEST	0	0	0	0	1	1
ENSG00000272860	ENSG00000272860	AC108004.2	HSCHR17_1_CTG1:33614-41378	NOTEST	0	0	0	0	1	1
ENSG00000272862	ENSG00000272862	RP11-814H16.2	4:41990757-41991254	NOTEST	0.306578	0.100241	-1.61279	0	1	1
ENSG00000272863	ENSG00000272863	KRTAP12-1	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272864	ENSG00000272864	RP11-17E13.2	1:75164452-75165017	NOTEST	0.500153	0.106891	-2.22623	0	1	1
ENSG00000272865	ENSG00000272865	RP11-561I11.4	1:242246287-242687998	NOTEST	0	0	0	0	1	1
ENSG00000272866	ENSG00000272866	RP11-12D24.10	9:5351795-5352410	NOTEST	0	0	0	0	1	1
ENSG00000272867	ENSG00000272867	RP11-1365D11.1	HG174_HG254_PATCH:201408-205009	NOTEST	0	0	0	0	1	1
ENSG00000272868	ENSG00000272868	RP11-144O23.8	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000272871	ENSG00000272871	RP11-408A13.4	9:14588794-14590063	NOTEST	0.321006	0.110095	-1.54385	0	1	1
ENSG00000272873	ENSG00000272873	TAS2R20	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000272874	ENSG00000272874	RP5-1103G7.10	20:247826-249498	NOTEST	0	0	0	0	1	1

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ENSG00000272876	ENSG00000272876	AC243960.1	HG1350_HG959_PATCH:42082083-42092748	NOTEST	0	0	0	0	1	1
ENSG00000272877	ENSG00000272877	DDX11L8	HSCHR12_1_CTG1:62309-63501	NOTEST	0	0	0	0	1	1
ENSG00000272878	ENSG00000272878	AC005794.1	HG1350_HG959_PATCH:42158580-42158868	NOTEST	0	0	0	0	1	1
ENSG00000272879	ENSG00000272879	ARHGEF1	HG1350_HG959_PATCH:42389104-42413350	NOTEST	0	0	0	0	1	1
ENSG00000272880	ENSG00000272880	RP11-33M22.2	1:181781839-181782396	NOTEST	0	0	0	0	1	1
ENSG00000272881	ENSG00000272881	RABAC1	HG1350_HG959_PATCH:42462585-42465295	NOTEST	0	0	0	0	1	1
ENSG00000272882	ENSG00000272882	OR2BH1P	11:28724161-29085368	NOTEST	0	0	0	0	1	1
ENSG00000272883	ENSG00000272883	CNOT3	HSCHR19LRC_COX2_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000272884	ENSG00000272884	RP11-104H15.10	17:7323421-7361026	NOTEST	0.053679	0.018495	-1.53722	0	1	1
ENSG00000272885	ENSG00000272885	RP11-2H3.6	4:409906-410326	NOTEST	0	0	0	0	1	1
ENSG00000272886	ENSG00000272886	AC112218.1	HG957_PATCH:53317442-53381643	NOTEST	0	0	0	0	1	1
ENSG00000272887	ENSG00000272887	CSPG4P5	15:84953013-84966399	NOTEST	0.00508962	0.00611374	0.264497	0	1	1
ENSG00000272889	ENSG00000272889	ZNF732	HG174_HG254_PATCH:270674-305321	NOTEST	0	0	0	0	1	1
ENSG00000272890	ENSG00000272890	RP11-846F4.11	HG1591_PATCH:22203741-22205012	NOTEST	0	0	0	0	1	1
ENSG00000272891	ENSG00000272891	OSCAR	HSCHR19LRC_LRC_T_CTG1:54597932-54606000	NOTEST	0	0	0	0	1	1
ENSG00000272892	ENSG00000272892	RP11-57G10.8	10:69609282-69610504	NOTEST	0.0655604	0.112959	0.784906	0	1	1
ENSG00000272893	ENSG00000272893	CTD-3093M3.1	HSCHR19LRC_LRC_J_CTG1:54697730-54698394	NOTEST	0	0	0	0	1	1
ENSG00000272894	ENSG00000272894	RP5-1159O4.1	7:7592092-7648560	NOTEST	0.233883	0.708055	1.59807	0	1	1
ENSG00000272895	ENSG00000272895	RP11-98C1.2	2:118617002-118771709	NOTEST	0	0	0	0	1	1
ENSG00000272896	ENSG00000272896	RP11-216L13.17	9:139685806-139735639	NOTEST	0.345114	0.104591	-1.72232	0	1	1
ENSG00000272897	ENSG00000272897	RP1-309K20.6	20:34213952-34288906	NOTEST	0	0	0	0	1	1
ENSG00000272898	ENSG00000272898	VSTM1	HSCHR19LRC_LRC_T_CTG1:54544078-54567207	NOTEST	0	0	0	0	1	1
ENSG00000272899	ENSG00000272899	RP11-309L24.9	7:128470430-128550773	NOTEST	0.129347	0.108226	-0.257202	0	1	1
ENSG00000272900	ENSG00000272900	OR10Q2P	11:58059297-58060237	NOTEST	0	0	0	0	1	1
ENSG00000272901	ENSG00000272901	SMDT1	HSCHR22_1_CTG1:42475694-42480288	NOTEST	0	0	0	0	1	1
ENSG00000272902	ENSG00000272902	RP11-299H21.1	2:101436613-101886778	NOTEST	0.272418	0.22719	-0.261918	0	1	1
ENSG00000272903	ENSG00000272903	PCDHB12	HG1082_HG167_PATCH:140588281-140591709	NOTEST	0	0	0	0	1	1
ENSG00000272904	ENSG00000272904	RP11-392E22.11	9:38540563-38624987	NOTEST	0	0.0464507	inf	0	1	1
ENSG00000272905	ENSG00000272905	RP11-265E18.1	7:32535037-33102409	NOTEST	0.0896652	0.294764	1.71694	0	1	1
ENSG00000272906	ENSG00000272906	RP11-533E19.7	1:179850741-179894135	NOTEST	0.411494	0.343298	-0.26141	0	1	1
ENSG00000272907	ENSG00000272907	XXbac-BPG308K3.5	HSCHR6_MHC_QBL:28805649-28806787	NOTEST	0	0	0	0	1	1
ENSG00000272908	ENSG00000272908	RP11-121A8.1	7:38365670-38369244	NOTEST	0	0	0	0	1	1
ENSG00000272910	ENSG00000272910	RP11-15L13.4	3:179280667-179322442	NOTEST	0.302865	0.27594	-0.134321	0	1	1
ENSG00000272911	ENSG00000272911	RP11-74E22.6	17:2591766-2592254	NOTEST	0	0.166777	inf	0	1	1
ENSG00000272912	ENSG00000272912	RP11-724N1.1	10:104674341-104675161	NOTEST	0	0	0	0	1	1
ENSG00000272914	ENSG00000272914	RP11-330O11.3	10:31109135-31320866	NOTEST	0.0407903	0.0385378	-0.0819486	0	1	1
ENSG00000272915	ENSG00000272915	RP11-62J1.4	7:127904578-127904942	NOTEST	0	0.0599277	inf	0	1	1
ENSG00000272916	ENSG00000272916	RP11-574K11.31	10:75545339-75571589	NOTEST	0.291279	0.104478	-1.4792	0	1	1
ENSG00000272917	ENSG00000272917	RP11-705C15.5	12:9787187-9811008	NOTEST	0.187412	0	#NAME?	0	1	1

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ENSG00000272919	ENSG00000272919	OSCAR	HSCHR19LRC_COX1_CTG1:54597932-54606000	NOTEST	0	0	0	0	1	1
ENSG00000272922	ENSG00000272922	RP11-329B9.5	3:184460605-184461072	NOTEST	0	0	0	0	1	1
ENSG00000272923	ENSG00000272923	RP11-391L3.1	16:81348556-81424489	NOTEST	0.126756	0.0980727	-0.370132	0	1	1
ENSG00000272924	ENSG00000272924	CTC-513N18.7	HG730_PATCH:20646633-20772405	NOTEST	0	0	0	0	1	1
ENSG00000272925	ENSG00000272925	AC108004.4	HSCHR17_1_CTG1:4960-5048	NOTEST	0	0	0	0	1	1
ENSG00000272926	ENSG00000272926	AC012314.20	HSCHR19LRC_PGF2_CTG1:54703320-54703838	NOTEST	0	0	0	0	1	1
ENSG00000272927	ENSG00000272927	RP11-1191J2.5	4:619372-664571	NOTEST	0	0	0	0	1	1
ENSG00000272928	ENSG00000272928	AC012314.8	HSCHR19LRC_LRC_T_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272929	ENSG00000272929	C21orf90	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272930	ENSG00000272930	TAS2R9	HG1133_PATCH:10961735-10962767	NOTEST	0	0	0	0	1	1
ENSG00000272931	ENSG00000272931	RP5-943J3.2	1:89990394-90402170	NOTEST	0.363979	0.241409	-0.592376	0	1	1
ENSG00000272932	ENSG00000272932	PRPF31	HSCHR19LRC_LRC_J_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000272933	ENSG00000272933	RP11-47A8.5	10:104402548-104403897	NOTEST	0.383938	0.517935	0.431898	0	1	1
ENSG00000272934	ENSG00000272934	RP11-392E22.10	9:38540563-38624987	NOTEST	0	0.199396	inf	0	1	1
ENSG00000272935	ENSG00000272935	PCDHA10	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000272936	ENSG00000272936	RP11-700J17.2	4:44624085-44728612	NOTEST	0.019381	0.301587	3.95986	0	1	1
ENSG00000272937	ENSG00000272937	OR6U2P	12:56005406-56006338	NOTEST	0	0	0	0	1	1
ENSG00000272938	ENSG00000272938	AC006129.2	HG1350_HG959_PATCH:42051096-42061367	NOTEST	0	0	0	0	1	1
ENSG00000272939	ENSG00000272939	CEACAM6	HG1350_HG959_PATCH:42214489-42292798	NOTEST	0	0	0	0	1	1
ENSG00000272940	ENSG00000272940	CTA-384D8.33	22:51007289-51052409	NOTEST	0.0536014	0	#NAME?	0	1	1
ENSG00000272942	ENSG00000272942	CTA-246H3.12	22:25830290-25831037	NOTEST	0.0946981	0.0564919	-0.745291	0	1	1
ENSG00000272943	ENSG00000272943	RPS9	HSCHR19LRC_LRC_I_CTG1:54704725-54711511	NOTEST	0	0	0	0	1	1
ENSG00000272944	ENSG00000272944	CTD-2308L22.1	2:222282746-222439174	NOTEST	0.0599063	0.194583	1.69961	0	1	1
ENSG00000272945	ENSG00000272945	CTD-3216D2.5	20:32782374-32899608	NOTEST	0.286363	0.520571	0.862249	0	1	1
ENSG00000272946	ENSG00000272946	TMC4	HSCHR19LRC_LRC_T_CTG1:54663845-54676944	NOTEST	0	0	0	0	1	1
ENSG00000272948	ENSG00000272948	AP001412.1	21:38580803-38640785	NOTEST	0.176132	0.37039	1.07239	0	1	1
ENSG00000272949	ENSG00000272949	RP11-514P8.8	7:102122891-102312088	NOTEST	0.0341707	0	#NAME?	0	1	1
ENSG00000272950	ENSG00000272950	RP11-307C18.1	7:97881690-98030380	NOTEST	0	0.0542808	inf	0	1	1
ENSG00000272951	ENSG00000272951	KRTAP12-4	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272952	ENSG00000272952	TAS2R50	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000272953	ENSG00000272953	RP11-1275H24.2	7:5465400-5469303	NOTEST	0.436164	0.125718	-1.79468	0	1	1
ENSG00000272954	ENSG00000272954	KB-1440D3.13	22:22006558-22090123	NOTEST	0	0.0855598	inf	0	1	1
ENSG00000272955	ENSG00000272955	KB-226F1.1	22:24375561-24384680	NOTEST	0.269414	0.362933	0.429879	0	1	1
ENSG00000272956	ENSG00000272956	SNORA22	HG444_PATCH:65112079-65235723	NOTEST	0	0	0	0	1	1
ENSG00000272957	ENSG00000272957	ZNF141	HG174_HG254_PATCH:337813-384864	NOTEST	0	0	0	0	1	1
ENSG00000272958	ENSG00000272958	CMP21-97G8.2	21:35797805-35798315	NOTEST	0	0	0	0	1	1
ENSG00000272959	ENSG00000272959	RP13-157F18.2	HG444_PATCH:65081989-65084127	NOTEST	0	0	0	0	1	1
ENSG00000272961	ENSG00000272961	KRTAP10-6	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000272963	ENSG00000272963	OR7A19P	12:46931284-47046333	NOTEST	0	0	0	0	1	1
ENSG00000272964	ENSG00000272964	PRPF31	HSCHR19LRC_LRC_S_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1

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ENSG00000272966	ENSG00000272966	RP11-686O6.1	2:203201461-203201923	NOTEST	0.0510305	0.0397853	-0.359124	0	1	1
ENSG00000272967	ENSG00000272967	RP11-190C22.9	3:119298058-119308792	NOTEST	0.104059	0	#NAME?	0	1	1
ENSG00000272968	ENSG00000272968	RBAK-RBAKDN	7:5013618-5112854	NOTEST	0.405357	0.154305	-1.39341	0	1	1
ENSG00000272969	ENSG00000272969	RP11-528I4.2	4:56262123-56414056	NOTEST	0.0244708	0.0363167	0.569569	0	1	1
ENSG00000272970	ENSG00000272970	RP11-329B9.4	3:184451862-184456737	NOTEST	0.35534	0.190526	-0.899213	0	1	1
ENSG00000272971	ENSG00000272971	RP11-284F21.11	1:156584533-156585080	NOTEST	0	0	0	0	1	1
ENSG00000272972	ENSG00000272972	SPIDR	HG1699_PATCH:48173166-48648898	NOTEST	0	0	0	0	1	1
ENSG00000272973	ENSG00000272973	KB-1125A3.11	22:24198613-24241117	NOTEST	0.136953	0.0833272	-0.716822	0	1	1
ENSG00000272974	ENSG00000272974	PCDHA13	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000272975	ENSG00000272975	CTC-297N7.11	17:10286448-10527203	NOTEST	0	0.00548683	inf	0	1	1
ENSG00000272976	ENSG00000272976	FAM223B	HG1497_PATCH:153739715-153740423	NOTEST	0	0	0	0	1	1
ENSG00000272978	ENSG00000272978	RP11-478C6.2	HG174_HG254_PATCH:337813-384864	NOTEST	0	0	0	0	1	1
ENSG00000272979	ENSG00000272979	RP11-647K16.1	2:191273080-191399448	NOTEST	0.0573107	0.258202	2.17162	0	1	1
ENSG00000272980	ENSG00000272980	RP11-517H2.6	6:167412669-167553184	NOTEST	0.0780794	0.0841409	0.107865	0	1	1
ENSG00000272981	ENSG00000272981	CTD-2234N14.2	11:126989220-127009630	NOTEST	0	0	0	0	1	1
ENSG00000272982	ENSG00000272982	RP5-1180E21.4	1:111659954-111727724	NOTEST	0	0	0	0	1	1
ENSG00000272983	ENSG00000272983	RP11-508N22.12	10:38426264-38433327	NOTEST	0.0237353	0.0356759	0.587915	0	1	1
ENSG00000272984	ENSG00000272984	RP11-85E16.1	7:36773608-36774140	NOTEST	0	0	0	0	1	1
ENSG00000272985	ENSG00000272985	CD79A	HG1350_HG959_PATCH:42383024-42387277	NOTEST	0	0	0	0	1	1
ENSG00000272986	ENSG00000272986	RP11-46J23.1	4:71569463-71673032	NOTEST	0.0734038	0.0955682	0.380677	0	1	1
ENSG00000272987	ENSG00000272987	OR5AL1	11:56180171-56181156	NOTEST	0	0	0	0	1	1
ENSG00000272988	ENSG00000272988	RP11-150D20.5	10:73813051-73813795	NOTEST	0	0	0	0	1	1
ENSG00000272989	ENSG00000272989	RP13-616I3.1	3:197232132-197233857	NOTEST	0.0402518	0.0171829	-1.22807	0	1	1
ENSG00000272991	ENSG00000272991	AF129408.17	21:40556101-40695144	NOTEST	0	0.110328	inf	0	1	1
ENSG00000272992	ENSG00000272992	RP11-809C18.4	10:320129-735683	NOTEST	0.0909217	0.0781308	-0.218733	0	1	1
ENSG00000272995	ENSG00000272995	RP11-362J17.1	4:20697904-21950422	NOTEST	0.107571	0.273331	1.34536	0	1	1
ENSG00000272996	ENSG00000272996	LENG1	HSCHR19LRC_PGF2_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000272997	ENSG00000272997	ATP5SL	HG1350_HG959_PATCH:41937222-41946622	NOTEST	0	0	0	0	1	1
ENSG00000272998	ENSG00000272998	AL662890.9	HSCHR6_MHC_MCF:28730485-28730593	NOTEST	0	0	0	0	1	1
ENSG00000272999	ENSG00000272999	RP11-87M18.2	HG1423_PATCH:36246734-36458409	NOTEST	0	0	0	0	1	1
ENSG00000273001	ENSG00000273001	RP11-118K6.3	10:3107615-3108193	NOTEST	0.0675736	0	#NAME?	0	1	1
ENSG00000273002	ENSG00000273002	RP11-336K24.12	1:155916629-155976861	NOTEST	0.127515	0.212992	0.740135	0	1	1
ENSG00000273003	ENSG00000273003	RP11-399J13.3	11:64781584-64808044	NOTEST	0.126996	0	#NAME?	0	1	1
ENSG00000273004	ENSG00000273004	GS1-279B7.2	1:185286910-185287662	NOTEST	0.119433	0.501074	2.06883	0	1	1
ENSG00000273005	ENSG00000273005	RP11-2E11.10	HG1308_PATCH:130125882-130126024	NOTEST	0	0	0	0	1	1
ENSG00000273006	ENSG00000273006	RP11-314C9.2	2:38420489-38420771	NOTEST	0	0	0	0	1	1
ENSG00000273007	ENSG00000273007	RP11-170N16.3	4:123747862-123844123	NOTEST	0.0464816	0.0142925	-1.7014	0	1	1
ENSG00000273008	ENSG00000273008	RP11-351D16.3	10:43632271-43633782	NOTEST	0.260717	0.369254	0.502127	0	1	1

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ENSG00000273010	ENSG00000273010	RP11-96K19.5	1:111486088-111507271	NOTEST	0.0565893	0.185012	1.70901	0	1	1
ENSG00000273011	ENSG00000273011	RP11-728K20.3	7:149587827-149606793	NOTEST	0	0.0207147	inf	0	1	1
ENSG00000273012	ENSG00000273012	RP11-90B22.1	10:33630582-33630833	NOTEST	0	0	0	0	1	1
ENSG00000273013	ENSG00000273013	CTD-2002J20.1	3:196195653-196230639	NOTEST	0	0	0	0	1	1
ENSG00000273016	ENSG00000273016	AC012314.19	HSCHR19LRC_LRC_J_CTG1:54712959-54713286	NOTEST	0	0	0	0	1	1
ENSG00000273017	ENSG00000273017	AP000240.9	21:30565800-31312351	NOTEST	0.204748	0.0788484	-1.3767	0	1	1
ENSG00000273019	ENSG00000273019	RP11-508N22.13	10:38438895-38439221	NOTEST	0	0	0	0	1	1
ENSG00000273020	ENSG00000273020	CEA	HG1350_HG959_PATCH:42214489-42292798	NOTEST	0	0	0	0	1	1
ENSG00000273021	ENSG00000273021	snoU13	HG193_PATCH:157610519-157644735	NOTEST	0	0	0	0	1	1
ENSG00000273022	ENSG00000273022	ATF4P1	HG1497_PATCH:153790895-153791968	NOTEST	0	0	0	0	1	1
ENSG00000273023	ENSG00000273023	AL662890.10	HSCHR6_MHC_MCF:28763752-28763816	NOTEST	0	0	0	0	1	1
ENSG00000273024	ENSG00000273024	INTS4L2	HG444_PATCH:65112079-65235723	NOTEST	0	0	0	0	1	1
ENSG00000273025	ENSG00000273025	CELF6	15:72533521-72671129	NOTEST	0	0	0	0	1	1
ENSG00000273026	ENSG00000273026	RP11-422P24.10	1:153931574-153950164	NOTEST	0.297468	0.0908571	-1.71106	0	1	1
ENSG00000273027	ENSG00000273027	LL21NC02-1C16.1	21:46305867-46351904	NOTEST	0	0.0365654	inf	0	1	1
ENSG00000273028	ENSG00000273028	IFRD2	HG325_PATCH:50316458-50336900	NOTEST	0	0	0	0	1	1
ENSG00000273029	ENSG00000273029	AC005609.3	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000273030	ENSG00000273030	RP11-285F16.1	10:102172690-102173178	NOTEST	0.0468535	0	#NAME?	0	1	1
ENSG00000273031	ENSG00000273031	TFPT	HSCHR19LRC_COX2_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273032	ENSG00000273032	DGCR9	22:18958026-19018755	NOTEST	0.0119737	0.00514198	-1.21947	0	1	1
ENSG00000273034	ENSG00000273034	RNU6-912P	HG444_PATCH:65279584-65279688	NOTEST	0	0	0	0	1	1
ENSG00000273035	ENSG00000273035	RP11-449G16.1	2:39476406-39945103	NOTEST	0.278461	0.0378311	-2.87983	0	1	1
ENSG00000273036	ENSG00000273036	RP11-392E22.12	9:38540563-38624987	NOTEST	0.131856	0.388554	1.55915	0	1	1
ENSG00000273037	ENSG00000273037	TFPT	HSCHR19LRC_PGF2_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273038	ENSG00000273038	RP11-479G22.8	10:33176188-33178239	NOTEST	0.483177	0.479245	-0.0117902	0	1	1
ENSG00000273039	ENSG00000273039	PCDHB17	HG1082_HG167_PATCH:140535580-140538643	NOTEST	0	0	0	0	1	1
ENSG00000273040	ENSG00000273040	XXbac-BPG308K3.5	HSCHR6_MHC_MANN:28805649-28806787	NOTEST	0	0	0	0	1	1
ENSG00000273041	ENSG00000273041	ATF4P2	HG1497_PATCH:153749393-153750466	NOTEST	0	0	0	0	1	1
ENSG00000273042	ENSG00000273042	snoU13	HG957_PATCH:53317211-53317315	NOTEST	0	0	0	0	1	1
ENSG00000273043	ENSG00000273043	RP11-344P13.6	HG1292_PATCH:122060988-122061452	NOTEST	0	0	0	0	1	1
ENSG00000273044	ENSG00000273044	RP4-569D19.8	22:35922978-35923462	NOTEST	0	0	0	0	1	1
ENSG00000273045	ENSG00000273045	C2ORF15	2:99613723-100106497	NOTEST	0.355991	0.497406	0.482583	0	1	1
ENSG00000273048	ENSG00000273048	MIR4720	16:81348556-81424489	NOTEST	0	0	0	0	1	1
ENSG00000273050	ENSG00000273050	PRH2	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000273051	ENSG00000273051	OR51F4P	11:4726156-5013659	NOTEST	0	0	0	0	1	1
ENSG00000273052	ENSG00000273052	NDUFA3	HSCHR19LRC_LRC_I_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273053	ENSG00000273053	TSEN34	HSCHR19LRC_COX2_CTG1:54693788-54697585	NOTEST	0	0	0	0	1	1
ENSG00000273054	ENSG00000273054	KRTAP10-3	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000273056	ENSG00000273056	RP11-77E14.2	9:7786104-7786688	NOTEST	0	0	0	0	1	1

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ENSG00000273059	ENSG00000273059	XXyac-YX155B6.7	1:147466093-147484460	NOTEST	0	0	0	0	1	1
ENSG00000273060	ENSG00000273060	PRPF31	HSCHR19LRC_LRC_T_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273062	ENSG00000273062	RP11-428K3.1	1:178693440-178889238	NOTEST	0.0860697	0.0503304	-0.774076	0	1	1
ENSG00000273063	ENSG00000273063	RP11-334G22.1	2:58134785-58468821	NOTEST	0	0.0634895	inf	0	1	1
ENSG00000273064	ENSG00000273064	RP11-474G23.3	2:68350067-68488362	NOTEST	0.140671	0.107666	-0.385765	0	1	1
ENSG00000273065	ENSG00000273065	RP11-58E21.5	14:50448429-50559361	NOTEST	0.158353	0.259832	0.714439	0	1	1
ENSG00000273066	ENSG00000273066	RP11-216L13.19	9:139685806-139735639	NOTEST	0.452914	0.274196	-0.72403	0	1	1
ENSG00000273067	ENSG00000273067	PCDHB18	HG1082_HG167_PATCH:140613950-140617114	NOTEST	0	0	0	0	1	1
ENSG00000273068	ENSG00000273068	CTA-714B7.7	22:35515816-35627049	NOTEST	0	0	0	0	1	1
ENSG00000273069	ENSG00000273069	RP5-1186P10.2	7:74021238-74021625	NOTEST	0	0	0	0	1	1
ENSG00000273070	ENSG00000273070	AC012314.8	HSCHR19LRC_LRC_I_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273072	ENSG00000273072	RP11-313P13.5	HG1257_PATCH:72344321-72419747	NOTEST	0	0	0	0	1	1
ENSG00000273073	ENSG00000273073	RP11-109E12.1	2:132219393-132221188	NOTEST	0	0	0	0	1	1
ENSG00000273074	ENSG00000273074	OSCAR	HSCHR19LRC_PGF2_CTG1:54597932-54606000	NOTEST	0	0	0	0	1	1
ENSG00000273075	ENSG00000273075	RP11-122G18.8	1:161344551-161345130	NOTEST	0.316853	0.0799429	-1.98677	0	1	1
ENSG00000273076	ENSG00000273076	RP3-508I15.22	22:39101727-39190203	NOTEST	0.0606983	0.0472608	-0.361012	0	1	1
ENSG00000273077	ENSG00000273077	RP11-130C6.1	4:129473744-129474571	NOTEST	0	0	0	0	1	1
ENSG00000273078	ENSG00000273078	PCDHA1	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000273079	ENSG00000273079	GRIN2B	12:13679787-14133053	NOTEST	0.0653404	0.130184	0.994507	0	1	1
ENSG00000273080	ENSG00000273080	RP11-301O19.1	2:86371054-86423172	NOTEST	0.3532	0.350722	-0.0101573	0	1	1
ENSG00000273081	ENSG00000273081	RP4-813F11.4	7:140702409-140704649	NOTEST	0.129561	0.0491602	-1.39807	0	1	1
ENSG00000273082	ENSG00000273082	LL22NC03-32F9.1	22:33558211-34318829	NOTEST	0.162916	0.0663831	-1.29524	0	1	1
ENSG00000273083	ENSG00000273083	NOL5BP	HSCHR6_MHC_MANN:28751413-28751785	NOTEST	0	0	0	0	1	1
ENSG00000273084	ENSG00000273084	RP11-1275H24.3	7:5465400-5469303	NOTEST	0	0.0149814	inf	0	1	1
ENSG00000273085	ENSG00000273085	OR52E1	11:5090801-5091727	NOTEST	0	0	0	0	1	1
ENSG00000273086	ENSG00000273086	TAS2R9	HSCHR12_2_CTG2:10961735-10962767	NOTEST	0	0	0	0	1	1
ENSG00000273087	ENSG00000273087	RP11-566J3.4	14:101203921-101204561	NOTEST	0	0	0	0	1	1
ENSG00000273088	ENSG00000273088	RP11-201K10.3	1:155141883-155162707	NOTEST	0	0.39612	inf	0	1	1
ENSG00000273089	ENSG00000273089	AC240565.2	HG417_PATCH:867-3903	NOTEST	0	0	0	0	1	1
ENSG00000273090	ENSG00000273090	RP11-78I14.1	2:36583068-36873230	NOTEST	0	0	0	0	1	1
ENSG00000273091	ENSG00000273091	AP000255.6	21:33108044-33108720	NOTEST	0.0294147	0.0207974	-0.500133	0	1	1
ENSG00000273092	ENSG00000273092	TAS2R20	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000273093	ENSG00000273093	RP11-532L16.3	1:200284562-200285095	NOTEST	0	0	0	0	1	1
ENSG00000273094	ENSG00000273094	RP11-285M22.1	HG1591_PATCH:22192160-22194158	NOTEST	0	0	0	0	1	1
ENSG00000273095	ENSG00000273095	NDUFA3	HSCHR19LRC_LRC_S_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273096	ENSG00000273096	RP3-508I15.20	22:39101727-39190203	NOTEST	0	0.379345	inf	0	1	1
ENSG00000273097	ENSG00000273097	RP11-219C20.3	4:165991759-165992156	NOTEST	0.131239	0.299498	1.19035	0	1	1
ENSG00000273098	ENSG00000273098	RP11-488L1.1	17:12999224-13004245	NOTEST	0	0	0	0	1	1

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ENSG00000273099	ENSG00000273099	TMC4	HSCHR19LRC_PGF2_CTG1:54663845-54676944	NOTEST	0	0	0	0	1	1
ENSG00000273100	ENSG00000273100	RP11-302L19.3	6:170493904-170494884	NOTEST	0	0	0	0	1	1
ENSG00000273101	ENSG00000273101	AC005626.3	HG1350_HG959_PATCH:42145563-42146507	NOTEST	0	0	0	0	1	1
ENSG00000273102	ENSG00000273102	AP000569.9	21:34876237-35349992	NOTEST	0	0.181813	inf	0	1	1
ENSG00000273103	ENSG00000273103	TARM1	HSCHR19LRC_LRC_J_CTG1:54573148-54584634	NOTEST	0	0	0	0	1	1
ENSG00000273104	ENSG00000273104	CMP21-97G8.1	21:35784497-35784885	NOTEST	0	0	0	0	1	1
ENSG00000273105	ENSG00000273105	TAS2R13	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000273106	ENSG00000273106	RP11-559M23.1	2:44394763-44471523	NOTEST	0.0279218	0	#NAME?	0	1	1
ENSG00000273107	ENSG00000273107	RP11-165A20.3	10:25242169-25242442	NOTEST	0	0	0	0	1	1
ENSG00000273108	ENSG00000273108	RP11-416N2.4	10:105239359-105615301	NOTEST	0.132692	0.159969	0.269711	0	1	1
ENSG00000273109	ENSG00000273109	PRPF31	HSCHR19LRC_PGF1_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273110	ENSG00000273110	RP11-350G8.9	1:154442247-154474589	NOTEST	0.0553364	0	#NAME?	0	1	1
ENSG00000273111	ENSG00000273111	LYPD4	HG1350_HG959_PATCH:42342978-42350578	NOTEST	0	0	0	0	1	1
ENSG00000273112	ENSG00000273112	RP11-25K21.6	1:161475219-161648444	NOTEST	0.0898599	0.32841	1.86975	0	1	1
ENSG00000273113	ENSG00000273113	RP11-367H1.1	2:242521336-242522141	NOTEST	0	0.0165358	inf	0	1	1
ENSG00000273114	ENSG00000273114	KRTAP12-3	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000273115	ENSG00000273115	KB-1466C5.1	21:27750870-27945603	NOTEST	0	0	0	0	1	1
ENSG00000273116	ENSG00000273116	LLfos-48D6.1	19:2321515-2355099	NOTEST	0	0	0	0	1	1
ENSG00000273118	ENSG00000273118	AC079610.1	2:213446080-214017151	NOTEST	0	0	0	0	1	1
ENSG00000273119	ENSG00000273119	RP11-128P17.4	18:11390031-11390728	NOTEST	0	0.0219759	inf	0	1	1
ENSG00000273120	ENSG00000273120	AL662890.11	HSCHR6_MHC_MANN:28763752-28763816	NOTEST	0	0	0	0	1	1
ENSG00000273121	ENSG00000273121	FAM109B	HSCHR22_1_CTG1:42470254-42475445	NOTEST	0	0	0	0	1	1
ENSG00000273122	ENSG00000273122	RPL13P	HSCHR6_MHC_QBL:28827405-28831131	NOTEST	0	0	0	0	1	1
ENSG00000273123	ENSG00000273123	RP11-9N20.3	3:123304388-123603178	NOTEST	0	0.0871892	inf	0	1	1
ENSG00000273124	ENSG00000273124	RP11-236B18.5	10:92754376-92766147	NOTEST	0.425756	0	#NAME?	0	1	1
ENSG00000273125	ENSG00000273125	RP11-115H18.1	3:107149776-107182759	NOTEST	0	0	0	0	1	1
ENSG00000273126	ENSG00000273126	NDUFA3	HSCHR19LRC_PGF1_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273127	ENSG00000273127	DDX11L8	HG858_PATCH:62309-63501	NOTEST	0	0	0	0	1	1
ENSG00000273128	ENSG00000273128	LENG1	HSCHR19LRC_LRC_J_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000273129	ENSG00000273129	RP5-973M2.2	1:186649753-186650578	NOTEST	0	0.0160267	inf	0	1	1
ENSG00000273130	ENSG00000273130	MBOAT7	HSCHR19LRC_LRC_I_CTG1:54677106-54693733	NOTEST	0	0	0	0	1	1
ENSG00000273132	ENSG00000273132	RP11-350J20.12	6:150139933-150244257	NOTEST	0	0	0	0	1	1
ENSG00000273133	ENSG00000273133	RP11-799M12.2	4:15471488-15603180	NOTEST	0.187302	0.169517	-0.143939	0	1	1
ENSG00000273134	ENSG00000273134	RP11-326G21.1	HG1287_PATCH:149950666-149951231	NOTEST	0	0	0	0	1	1
ENSG00000273135	ENSG00000273135	RPS9	HSCHR19LRC_COX2_CTG1:54704725-54711511	NOTEST	0	0	0	0	1	1
ENSG00000273136	ENSG00000273136	AC253572.1	HG1292_PATCH:121356528-121384104	NOTEST	0	0	0	0	1	1
ENSG00000273137	ENSG00000273137	RP3-402G11.28	22:50639407-50656045	NOTEST	0.511796	0.422362	-0.277091	0	1	1
ENSG00000273139	ENSG00000273139	XXbac-B444P24.14	22:20308261-20308726	NOTEST	0.384616	0.366541	-0.0694439	0	1	1
ENSG00000273140	ENSG00000273140	CCT6P1	HG444_PATCH:65112079-65235723	NOTEST	0	0	0	0	1	1
ENSG00000273141	ENSG00000273141	RP11-820I16.4	18:11688954-11909222	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000273143	ENSG00000273143	RP11-525A16.4	10:112188597-112255962	NOTEST	0	0	0	0	1	1
ENSG00000273144	ENSG00000273144	TAS2R15	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000273145	ENSG00000273145	CITF22-92A6.1	22:46409485-46411378	NOTEST	0.337752	0.359346	0.0894081	0	1	1
ENSG00000273146	ENSG00000273146	PCDHA5	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000273147	ENSG00000273147	RP11-196G18.24	HG1287_PATCH:150530912-150535439	NOTEST	0	0	0	0	1	1
ENSG00000273148	ENSG00000273148	RP5-1068E13.7	20:18775172-18776711	NOTEST	0.0957006	0.159643	0.738245	0	1	1
ENSG00000273150	ENSG00000273150	AC245150.1	HG1257_PATCH:74557548-74611888	NOTEST	0	0	0	0	1	1
ENSG00000273152	ENSG00000273152	AC011526.1	HG1350_HG959_PATCH:41960073-42006554	NOTEST	0	0	0	0	1	1
ENSG00000273153	ENSG00000273153	RP11-406H21.2	10:17179334-17179584	NOTEST	0.355043	0.138859	-1.35437	0	1	1
ENSG00000273155	ENSG00000273155	MRPL30	2:99613723-100106497	NOTEST	0.34182	0.586536	0.778984	0	1	1
ENSG00000273156	ENSG00000273156	RP11-127B20.2	4:83266028-83266693	NOTEST	0.205744	0.32234	0.647731	0	1	1
ENSG00000273157	ENSG00000273157	KRTAP10-2	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000273158	ENSG00000273158	CTD-2575K13.6	HG1350_HG959_PATCH:42414423-42416002	NOTEST	0	0	0	0	1	1
ENSG00000273159	ENSG00000273159	CNOT3	HSCHR19LRC_LRC_T_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000273160	ENSG00000273160	RP11-104L21.3	1:167399876-167487847	NOTEST	0.110828	0.348095	1.65116	0	1	1
ENSG00000273161	ENSG00000273161	RP11-479O9.2	HG444_PATCH:65238532-65266980	NOTEST	0	0	0	0	1	1
ENSG00000273162	ENSG00000273162	RP11-108L7.15	10:102819785-102820762	NOTEST	0.616061	0.306711	-1.00619	0	1	1
ENSG00000273163	ENSG00000273163	AC012314.20	HSCHR19LRC_LRC_S_CTG1:54703320-54703838	NOTEST	0	0	0	0	1	1
ENSG00000273164	ENSG00000273164	DGCR10	22:18958026-19018755	NOTEST	0	0	0	0	1	1
ENSG00000273165	ENSG00000273165	RP11-1057B6.1	2:32078044-32078492	NOTEST	0	0.0417993	inf	0	1	1
ENSG00000273166	ENSG00000273166	DNAJC19P2	HG1350_HG959_PATCH:42105639-42111889	NOTEST	0	0	0	0	1	1
ENSG00000273167	ENSG00000273167	RP11-307N16.6	13:24553838-24896673	NOTEST	0.0401404	0.00924123	-2.1189	0	1	1
ENSG00000273168	ENSG00000273168	DNAJC19P3	HG1350_HG959_PATCH:42144473-42144804	NOTEST	0	0	0	0	1	1
ENSG00000273169	ENSG00000273169	IMMTP1	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000273170	ENSG00000273170	ANKRD18A	9:38540563-38624987	NOTEST	0.0243591	0.0853707	1.80928	0	1	1
ENSG00000273171	ENSG00000273171	CTB-96E2.2	17:26684603-26734215	NOTEST	0	0	0	0	1	1
ENSG00000273172	ENSG00000273172	AC108004.2	17:33614-41378	NOTEST	0	0	0	0	1	1
ENSG00000273173	ENSG00000273173	SNURF	15:25068793-25492435	NOTEST	0.213452	0.320775	0.587649	0	1	1
ENSG00000273174	ENSG00000273174	RP11-434H6.6	3:128806411-128880136	NOTEST	0.177519	0.0828509	-1.09938	0	1	1
ENSG00000273175	ENSG00000273175	RP11-11N7.4	1:245028039-245028574	NOTEST	0.0408092	0.057902	0.504717	0	1	1
ENSG00000273176	ENSG00000273176	RP3-510H16.3	22:35694830-35743985	NOTEST	0.0692734	0	#NAME?	0	1	1
ENSG00000273177	ENSG00000273177	RP11-368I23.4	3:168645956-168646386	NOTEST	0	0	0	0	1	1
ENSG00000273178	ENSG00000273178	NDUFA3	HSCHR19LRC_LRC_J_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273180	ENSG00000273180	RP11-335L23.4	4:183996632-183997186	NOTEST	0	0	0	0	1	1
ENSG00000273181	ENSG00000273181	RP11-778D9.13	3:183850729-183851349	NOTEST	0.0941746	0.103336	0.133938	0	1	1
ENSG00000273182	ENSG00000273182	LENG1	HSCHR19LRC_COX2_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000273183	ENSG00000273183	RP11-5C23.2	7:154720207-154794794	NOTEST	0.195389	0.114043	-0.77677	0	1	1
ENSG00000273184	ENSG00000273184	RP11-212P7.3	7:128095893-128146656	NOTEST	0	0	0	0	1	1
ENSG00000273185	ENSG00000273185	RP11-98C1.1	2:118617002-118771709	NOTEST	0	0	0	0	1	1
ENSG00000273187	ENSG00000273187	AC253576.2	HG174_HG254_PATCH:53332-162774	NOTEST	0	0	0	0	1	1

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ENSG00000273188	ENSG00000273188	RP3-402G11.25	22:50624343-50638976	NOTEST	0.175446	0.109617	-0.678558	0	1	1
ENSG00000273189	ENSG00000273189	CTD-3148I10.15	19:49949554-49995565	NOTEST	0	0	0	0	1	1
ENSG00000273190	ENSG00000273190	RP11-255C15.4	3:179055909-179056371	NOTEST	0.541775	0.512719	-0.0795261	0	1	1
ENSG00000273191	ENSG00000273191	TAS2R15	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000273193	ENSG00000273193	RP11-523G9.3	3:175527551-175528340	NOTEST	0.0921405	0.016967	-2.4411	0	1	1
ENSG00000273194	ENSG00000273194	OLA1P1	HSCHR22_2_CTG1:42503768-42504957	NOTEST	0	0	0	0	1	1
ENSG00000273195	ENSG00000273195	ABCA11P	HG174_HG254_PATCH:425434-499156	NOTEST	0	0	0	0	1	1
ENSG00000273196	ENSG00000273196	RP11-717A5.2	2:85569210-85618875	NOTEST	0	0	0	0	1	1
ENSG00000273197	ENSG00000273197	AL662890.12	HSCHR6_MHC_APD:28763752-28763816	NOTEST	0	0	0	0	1	1
ENSG00000273198	ENSG00000273198	GS1-304P7.3	1:186490904-186491436	NOTEST	0	0	0	0	1	1
ENSG00000273199	ENSG00000273199	AP000692.10	21:37692089-37791313	NOTEST	0.041958	0.147164	1.8104	0	1	1
ENSG00000273200	ENSG00000273200	XXbac-BPG308K3.6	HSCHR6_MHC_MANN:28827405-28831131	NOTEST	0	0	0	0	1	1
ENSG00000273201	ENSG00000273201	PCDHA2	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000273202	ENSG00000273202	CNOT3	HSCHR19LRC_LRC_I_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000273204	ENSG00000273204	RP4-549L20.3	1:101337942-101361554	NOTEST	0	0	0	0	1	1
ENSG00000273205	ENSG00000273205	C19orf69	HG1350_HG959_PATCH:41949062-41950670	NOTEST	0	0	0	0	1	1
ENSG00000273206	ENSG00000273206	RP5-933K21.2	HG193_PATCH:157687123-157688057	NOTEST	0	0	0	0	1	1
ENSG00000273207	ENSG00000273207	F8A3	HG1497_PATCH:154625382-154627083	NOTEST	0	0	0	0	1	1
ENSG00000273208	ENSG00000273208	H2AFB1	HG1497_PATCH:154004255-154228771	NOTEST	0	0	0	0	1	1
ENSG00000273209	ENSG00000273209	RP11-107N15.1	2:202897492-202898260	NOTEST	0.045651	0.0756391	0.728485	0	1	1
ENSG00000273210	ENSG00000273210	AP001437.1	21:38737778-38889753	NOTEST	0	0	0	0	1	1
ENSG00000273211	ENSG00000273211	RP13-131K19.7	3:48955220-49060928	NOTEST	0	0	0	0	1	1
ENSG00000273212	ENSG00000273212	AC000068.10	22:19318220-19466738	NOTEST	0	0	0	0	1	1
ENSG00000273213	ENSG00000273213	RP5-998N21.10	1:149369293-149429348	NOTEST	0.113367	0.141444	0.319222	0	1	1
ENSG00000273214	ENSG00000273214	RP5-1039K5.18	22:38439236-38439927	NOTEST	0.105125	0.176583	0.748235	0	1	1
ENSG00000273215	ENSG00000273215	TARM1	HSCHR19LRC_COX1_CTG1:54573148-54584634	NOTEST	0	0	0	0	1	1
ENSG00000273216	ENSG00000273216	AC002059.10	22:29708921-29715668	NOTEST	0	0	0	0	1	1
ENSG00000273217	ENSG00000273217	CTC-432M15.3	5:130759613-131132710	NOTEST	0.17514	0.0967706	-0.855865	0	1	1
ENSG00000273218	ENSG00000273218	LLNLR-246C6.1	19:15456878-15459228	NOTEST	0.115603	0.062981	-0.876191	0	1	1
ENSG00000273219	ENSG00000273219	RP11-644N4.1	7:135347243-135433594	NOTEST	0	0	0	0	1	1
ENSG00000273220	ENSG00000273220	PCDHA11	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000273221	ENSG00000273221	RP5-1180E21.5	1:111659954-111727724	NOTEST	0	0	0	0	1	1
ENSG00000273222	ENSG00000273222	OSCAR	HSCHR19LRC_LRC_J_CTG1:54597932-54606000	NOTEST	0	0	0	0	1	1
ENSG00000273223	ENSG00000273223	CNOT3	HSCHR19LRC_LRC_J_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000273224	ENSG00000273224	PRPF31	HSCHR19LRC_PGF2_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273225	ENSG00000273225	AC244230.3	HG1211_PATCH:46864534-46868997	NOTEST	0	0	0	0	1	1
ENSG00000273227	ENSG00000273227	PCDHB8	HG1082_HG167_PATCH:140557374-140560085	NOTEST	0	0	0	0	1	1
ENSG00000273228	ENSG00000273228	OR5BQ1P	11:56796882-56797197	NOTEST	0	0	0	0	1	1
ENSG00000273229	ENSG00000273229	KRTAP10-1	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000273231	ENSG00000273231	AC012314.19	HSCHR19LRC_COX2_CTG1:54712959-54713286	NOTEST	0	0	0	0	1	1
ENSG00000273232	ENSG00000273232	RP11-370A5.2	18:20279443-20606451	NOTEST	0	0	0	0	1	1

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ENSG00000273234	ENSG00000273234	OR2A13P	7:143839101-143840031	NOTEST	0.0195691	0.0137964	-0.504281	0	1	1
ENSG00000273235	ENSG00000273235	TSEN34	HSCHR19LRC_PGF2_CTG1:54693788-54697585	NOTEST	0	0	0	0	1	1
ENSG00000273236	ENSG00000273236	AC012314.5	HSCHR19LRC_LRC_T_CTG1:54530501-54530601	NOTEST	0	0	0	0	1	1
ENSG00000273238	ENSG00000273238	RP11-1263C18.1	4:567668-568201	NOTEST	0	0	0	0	1	1
ENSG00000273239	ENSG00000273239	OSCAR	HSCHR19LRC_LRC_I_CTG1:54597932-54606000	NOTEST	0	0	0	0	1	1
ENSG00000273240	ENSG00000273240	RP11-455J20.3	2:190539015-190630282	NOTEST	0.0695791	0	#NAME?	0	1	1
ENSG00000273241	ENSG00000273241	SNORD38	HG957_PATCH:53317442-53381643	NOTEST	0	0	0	0	1	1
ENSG00000273242	ENSG00000273242	VSTM1	HSCHR19LRC_COX2_CTG1:54544078-54567207	NOTEST	0	0	0	0	1	1
ENSG00000273244	ENSG00000273244	KB-7G2.8	22:17082776-17185367	NOTEST	0	0	0	0	1	1
ENSG00000273245	ENSG00000273245	RP11-434P11.2	2:73977382-73977913	NOTEST	0.241725	0	#NAME?	0	1	1
ENSG00000273246	ENSG00000273246	AC118758.8	HG736_PATCH:56897121-56900285	NOTEST	0	0	0	0	1	1
ENSG00000273247	ENSG00000273247	RP11-83A24.2	4:140187316-140397763	NOTEST	0.263243	0.248669	-0.0821682	0	1	1
ENSG00000273248	ENSG00000273248	RP11-399K21.13	10:77029576-77171600	NOTEST	0.459275	0.173868	-1.40136	0	1	1
ENSG00000273249	ENSG00000273249	LL09NC01251B2.3	9:136997363-137025093	NOTEST	0	0	0	0	1	1
ENSG00000273250	ENSG00000273250	AL662890.13	HSCHR6_MHC_APD:28743696-28743804	NOTEST	0	0	0	0	1	1
ENSG00000273251	ENSG00000273251	RP6-74O6.6	HG1287_PATCH:149044659-149045101	NOTEST	0	0	0	0	1	1
ENSG00000273252	ENSG00000273252	OR7E39P	7:6875050-6875425	NOTEST	0	0	0	0	1	1
ENSG00000273254	ENSG00000273254	RP1-100J12.1	21:30396575-30426809	NOTEST	0.0323189	0.0952507	1.55935	0	1	1
ENSG00000273255	ENSG00000273255	OR5BP1P	11:56823061-56823607	NOTEST	0	0	0	0	1	1
ENSG00000273256	ENSG00000273256	PCDHA6	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000273257	ENSG00000273257	RP11-177J6.1	4:56212275-56262014	NOTEST	0.0968141	0.145435	0.58709	0	1	1
ENSG00000273258	ENSG00000273258	RP11-394I13.3	2:174876583-174877703	NOTEST	0	0	0	0	1	1
ENSG00000273259	ENSG00000273259	RP11-986E7.7	14:95027427-95090983	NOTEST	0	0	0	0	1	1
ENSG00000273260	ENSG00000273260	Z95704.3	HG174_HG254_PATCH:53332-162774	NOTEST	0	0	0	0	1	1
ENSG00000273262	ENSG00000273262	RP11-18I14.11	10:104238985-104262482	NOTEST	0	0.316489	inf	0	1	1
ENSG00000273263	ENSG00000273263	PCDHA8	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000273264	ENSG00000273264	RP11-131L23.2	1:85731930-86043933	NOTEST	0	0	0	0	1	1
ENSG00000273265	ENSG00000273265	RP11-353K11.1	2:97477975-97479394	NOTEST	0.121628	0	#NAME?	0	1	1
ENSG00000273267	ENSG00000273267	RP11-338K13.1	4:7967038-8160559	NOTEST	0	0	0	0	1	1
ENSG00000273268	ENSG00000273268	OSCAR	HSCHR19LRC_LRC_S_CTG1:54597932-54606000	NOTEST	0	0	0	0	1	1
ENSG00000273269	ENSG00000273269	RP11-761B3.1	2:47126413-47403740	NOTEST	0	0	0	0	1	1
ENSG00000273270	ENSG00000273270	RP11-212P7.2	7:128164069-128171123	NOTEST	0.469794	0.352474	-0.41451	0	1	1
ENSG00000273272	ENSG00000273272	CTA-384D8.34	22:50980733-50981440	NOTEST	0	0	0	0	1	1
ENSG00000273273	ENSG00000273273	CNOT3	HSCHR19LRC_PGF2_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000273274	ENSG00000273274	ZBTB8B	1:32930657-33116504	NOTEST	0.106395	0.244185	1.19854	0	1	1
ENSG00000273276	ENSG00000273276	TARM1	HSCHR19LRC_LRC_I_CTG1:54573148-54584634	NOTEST	0	0	0	0	1	1
ENSG00000273277	ENSG00000273277	AC097015.2	HG957_PATCH:53243968-53244062	NOTEST	0	0	0	0	1	1
ENSG00000273278	ENSG00000273278	RP11-478C6.1	HG174_HG254_PATCH:336257-336786	NOTEST	0	0	0	0	1	1
ENSG00000273279	ENSG00000273279	TAS2R10	HG1133_PATCH:10977558-11320498	NOTEST	0	0	0	0	1	1
ENSG00000273280	ENSG00000273280	PLEKHA3P1	HG1350_HG959_PATCH:42026947-42027894	NOTEST	0	0	0	0	1	1
ENSG00000273282	ENSG00000273282	CTD-3093M3.1	HSCHR19LRC_LRC_S_CTG1:54697730-54698394	NOTEST	0	0	0	0	1	1

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ENSG00000273285	ENSG00000273285	AL662890.14	HSCHR6_MHC_MANN:28743696-28743804	NOTEST	0	0	0	0	1	1
ENSG00000273286	ENSG00000273286	RPL13P	HSCHR6_MHC_MANN:28827405-28831131	NOTEST	0	0	0	0	1	1
ENSG00000273287	ENSG00000273287	CTA-268H5.14	22:45658165-45659466	NOTEST	0.0262866	0.0696604	1.40601	0	1	1
ENSG00000273288	ENSG00000273288	AC108004.5	17:4960-5048	NOTEST	0	0	0	0	1	1
ENSG00000273289	ENSG00000273289	RP6-109B7.5	22:46445357-46509808	NOTEST	0.187086	0	#NAME?	0	1	1
ENSG00000273291	ENSG00000273291	KRBOX1	3:42846243-43101703	NOTEST	0	0	0	0	1	1
ENSG00000273292	ENSG00000273292	LENG1	HSCHR19LRC_LRC_I_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000273293	ENSG00000273293	RP11-445N20.3	7:149578447-149578669	NOTEST	0	0	0	0	1	1
ENSG00000273294	ENSG00000273294	RP11-1084J3.4	5:33986282-34124633	NOTEST	0.329388	0.254818	-0.370322	0	1	1
ENSG00000273295	ENSG00000273295	AP000350.5	22:24243618-24249255	NOTEST	0.127265	0.0719074	-0.823622	0	1	1
ENSG00000273296	ENSG00000273296	FP700107.1	HG1287_PATCH:145375926-145377287	NOTEST	0	0	0	0	1	1
ENSG00000273298	ENSG00000273298	LL09NC01139C3.1	HG1500_PATCH:137033890-137034462	NOTEST	0	0	0	0	1	1
ENSG00000273299	ENSG00000273299	CTB-13L3.1	7:89964536-90839905	NOTEST	0	0	0	0	1	1
ENSG00000273301	ENSG00000273301	RP11-314B1.2	2:226562969-226568370	NOTEST	0.0167582	0.00209644	-2.99885	0	1	1
ENSG00000273302	ENSG00000273302	RP11-493E12.2	2:61404552-61697904	NOTEST	0.29549	0.28502	-0.0520454	0	1	1
ENSG00000273303	ENSG00000273303	RP11-944L7.5	3:44596684-44727145	NOTEST	0	0	0	0	1	1
ENSG00000273304	ENSG00000273304	CTD-3093M3.1	HSCHR19LRC_LRC_I_CTG1:54697730-54698394	NOTEST	0	0	0	0	1	1
ENSG00000273305	ENSG00000273305	RP11-440D17.4	2:96203716-96204217	NOTEST	0.0450102	0.231018	2.35968	0	1	1
ENSG00000273307	ENSG00000273307	RP11-58E21.7	14:50448429-50559361	NOTEST	0.163686	0.000331304	-8.94856	0	1	1
ENSG00000273308	ENSG00000273308	RP11-496H1.2	3:197372539-197372888	NOTEST	0.0830301	0	#NAME?	0	1	1
ENSG00000273309	ENSG00000273309	AC004410.3	19:2321515-2355099	NOTEST	0	0	0	0	1	1
ENSG00000273310	ENSG00000273310	PCDHB14	HG1082_HG167_PATCH:140602943-140605871	NOTEST	0	0	0	0	1	1
ENSG00000273312	ENSG00000273312	RP11-425A6.5	10:35894337-35897863	NOTEST	0	0	0	0	1	1
ENSG00000273313	ENSG00000273313	RBAKDN	7:5013618-5112854	NOTEST	0.0705775	0.310229	2.13605	0	1	1
ENSG00000273315	ENSG00000273315	LENG1	HSCHR19LRC_LRC_T_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000273316	ENSG00000273316	MBOAT7	HSCHR19LRC_COX2_CTG1:54677106-54693733	NOTEST	0	0	0	0	1	1
ENSG00000273317	ENSG00000273317	PCDHA12	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000273318	ENSG00000273318	AC018755.2	19:52188615-52215640	NOTEST	0.491688	0.37213	-0.401938	0	1	1
ENSG00000273319	ENSG00000273319	RP11-138A9.2	7:130621222-130624420	NOTEST	0.0373537	0.0527327	0.497445	0	1	1
ENSG00000273321	ENSG00000273321	RP11-621L6.3	18:21982116-21982678	NOTEST	0.591181	0.455187	-0.377141	0	1	1
ENSG00000273322	ENSG00000273322	KRTAP10-5	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000273323	ENSG00000273323	NOL5BP	HSCHR6_MHC_QBL:28751413-28751785	NOTEST	0	0	0	0	1	1
ENSG00000273324	ENSG00000273324	AC253576.3	HG174_HG254_PATCH:53332-162774	NOTEST	0	0	0	0	1	1
ENSG00000273325	ENSG00000273325	RP1-90G24.11	22:32680669-32681118	NOTEST	0	0	0	0	1	1
ENSG00000273326	ENSG00000273326	TAS2R7	HSCHR12_2_CTG2:10954130-10955226	NOTEST	0	0	0	0	1	1
ENSG00000273327	ENSG00000273327	OR6L2P	10:135192694-135382916	NOTEST	0.0556981	0.0753096	0.435206	0	1	1
ENSG00000273328	ENSG00000273328	RP11-141M3.5	3:42846243-43101703	NOTEST	0.0301129	0.054391	0.852987	0	1	1
ENSG00000273329	ENSG00000273329	RP11-448A19.1	7:129244388-129251471	NOTEST	0.358182	0.382759	0.0957422	0	1	1
ENSG00000273330	ENSG00000273330	CYP4F36P	19:15982476-15982662	NOTEST	0	0	0	0	1	1

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ENSG00000273332	ENSG00000273332	PCDHA14	HG1082_HG167_PATCH:140165875-140391936	NOTEST	0	0	0	0	1	1
ENSG00000273333	ENSG00000273333	XXbac-BPG300A18.13	6:32152511-32157963	NOTEST	0	0	0	0	1	1
ENSG00000273334	ENSG00000273334	MIR571	HG174_HG254_PATCH:337813-384864	NOTEST	0	0	0	0	1	1
ENSG00000273335	ENSG00000273335	RP11-61L19.2	18:9473418-9474004	NOTEST	0	0.0253563	inf	0	1	1
ENSG00000273336	ENSG00000273336	OR7M1P	10:135192694-135382916	NOTEST	0	0	0	0	1	1
ENSG00000273337	ENSG00000273337	TSPEAR-AS1	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000273339	ENSG00000273339	AC138827.2	HSCHR5_1_CTG1:69433885-69439126	NOTEST	0	0	0	0	1	1
ENSG00000273341	ENSG00000273341	RP5-899E9.1	7:77045989-77054760	NOTEST	0	0	0	0	1	1
ENSG00000273342	ENSG00000273342	KB-1440D3.14	22:21995132-21995573	NOTEST	0.0549858	0	#NAME?	0	1	1
ENSG00000273345	ENSG00000273345	CTD-2410N18.4	5:133450401-133706738	NOTEST	0.0721398	0.0638078	-0.177063	0	1	1
ENSG00000273346	ENSG00000273346	RN7SL821P	HG957_PATCH:53317442-53381643	NOTEST	0	0	0	0	1	1
ENSG00000273347	ENSG00000273347	TMC4	HSCHR19LRC_LRC_I_CTG1:54663845-54676944	NOTEST	0	0	0	0	1	1
ENSG00000273348	ENSG00000273348	RP11-535A5.1	18:19927808-19928215	NOTEST	0	0	0	0	1	1
ENSG00000273349	ENSG00000273349	VSTM1	HSCHR19LRC_PGF2_CTG1:54544078-54567207	NOTEST	0	0	0	0	1	1
ENSG00000273350	ENSG00000273350	RP4-539M6.20	22:30727976-30825045	NOTEST	0	0.404357	inf	0	1	1
ENSG00000273351	ENSG00000273351	KRTAP10-4	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000273352	ENSG00000273352	RP11-61L19.3	18:9475006-9538114	NOTEST	0.542422	0.593453	0.129717	0	1	1
ENSG00000273354	ENSG00000273354	AC012314.19	HSCHR19LRC_LRC_T_CTG1:54712959-54713286	NOTEST	0	0	0	0	1	1
ENSG00000273355	ENSG00000273355	RP11-672L10.6	18:813274-813757	NOTEST	0.36188	0.576819	0.672608	0	1	1
ENSG00000273356	ENSG00000273356	RP11-804H8.6	3:50707419-50709479	NOTEST	0.054998	0.069931	0.346552	0	1	1
ENSG00000273357	ENSG00000273357	PCDHB13	HG1082_HG167_PATCH:140593521-140597006	NOTEST	0	0	0	0	1	1
ENSG00000273358	ENSG00000273358	TARM1	HSCHR19LRC_LRC_S_CTG1:54573148-54584634	NOTEST	0	0	0	0	1	1
ENSG00000273359	ENSG00000273359	TAS2R8	HG1133_PATCH:10958649-10959892	NOTEST	0	0	0	0	1	1
ENSG00000273360	ENSG00000273360	RP11-210G22.1	10:67672275-69455927	NOTEST	0	0	0	0	1	1
ENSG00000273361	ENSG00000273361	RP11-378A13.2	2:219262978-219270664	NOTEST	0.272124	0.117428	-1.21249	0	1	1
ENSG00000273362	ENSG00000273362	KB-67B5.17	22:17001948-17008127	NOTEST	0	0	0	0	1	1
ENSG00000273363	ENSG00000273363	RP11-285G1.14	10:45306471-45491339	NOTEST	0.114373	0.0907726	-0.333413	0	1	1
ENSG00000273364	ENSG00000273364	CTD-3093M3.1	HSCHR19LRC_COX2_CTG1:54697730-54698394	NOTEST	0	0	0	0	1	1
ENSG00000273365	ENSG00000273365	RP11-466F5.10	1:165631452-165679205	NOTEST	0.230938	0.0997552	-1.21104	0	1	1
ENSG00000273366	ENSG00000273366	CTA-989H11.1	22:42556018-42739622	NOTEST	0.0560919	0.0735147	0.390242	0	1	1
ENSG00000273367	ENSG00000273367	RP5-827C21.6	1:234507931-234519795	NOTEST	0	0	0	0	1	1
ENSG00000273368	ENSG00000273368	RP11-376P6.3	18:7566779-8406951	NOTEST	0.205137	0.320261	0.642661	0	1	1
ENSG00000273369	ENSG00000273369	RP11-700J17.1	4:44624085-44728612	NOTEST	0.536434	0.51602	-0.0559737	0	1	1
ENSG00000273370	ENSG00000273370	RP11-268E23.2	3:190377004-190377539	NOTEST	0	0	0	0	1	1
ENSG00000273371	ENSG00000273371	AC092574.4	HG174_HG254_PATCH:409808-409915	NOTEST	0	0	0	0	1	1
ENSG00000273372	ENSG00000273372	RP11-479O17.10	10:81664653-81742370	NOTEST	0.00307464	0.0067412	1.13259	0	1	1
ENSG00000273374	ENSG00000273374	RP11-383I23.2	3:99521542-99524902	NOTEST	0.0392088	0.0439505	0.164701	0	1	1
ENSG00000273375	ENSG00000273375	RP11-803P9.1	3:197516570-197517240	NOTEST	0.0297685	0.152145	2.35359	0	1	1

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ENSG00000273376	ENSG00000273376	PRPF31	HSCHR19LRC_LRC_I_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273377	ENSG00000273377	OR2Q1P	7:143651936-143694405	NOTEST	0	0	0	0	1	1
ENSG00000273378	ENSG00000273378	FAM109B	HSCHR22_2_CTG1:42470254-42475445	NOTEST	0	0	0	0	1	1
ENSG00000273379	ENSG00000273379	RP11-114O18.1	HG1292_PATCH:120619238-120619714	NOTEST	0	0	0	0	1	1
ENSG00000273380	ENSG00000273380	OSCAR	HSCHR19LRC_PGF1_CTG1:54597932-54606000	NOTEST	0	0	0	0	1	1
ENSG00000273381	ENSG00000273381	RP11-305L7.7	9:93968456-93972581	NOTEST	0.0180479	0.0145872	-0.30712	0	1	1
ENSG00000273382	ENSG00000273382	RP5-1065J22.8	1:109630592-109639556	NOTEST	0.0627361	0.0804849	0.359423	0	1	1
ENSG00000273383	ENSG00000273383	PCDHB5	HG1082_HG167_PATCH:140514802-140517706	NOTEST	0	0	0	0	1	1
ENSG00000273384	ENSG00000273384	RP5-1098D14.1	1:178620840-178621417	NOTEST	0.281844	0.132189	-1.0923	0	1	1
ENSG00000273385	ENSG00000273385	RPS9	HSCHR19LRC_LRC_J_CTG1:54704725-54711511	NOTEST	0	0	0	0	1	1
ENSG00000273386	ENSG00000273386	AC012314.20	HSCHR19LRC_LRC_J_CTG1:54703320-54703838	NOTEST	0	0	0	0	1	1
ENSG00000273387	ENSG00000273387	RP3-412A9.16	22:31460090-31500743	NOTEST	0.283763	0.215198	-0.399022	0	1	1
ENSG00000273389	ENSG00000273389	RP13-514E23.2	4:86396266-86923823	NOTEST	0.246515	0.110134	-1.16241	0	1	1
ENSG00000273390	ENSG00000273390	AC005754.7	HG1082_HG167_PATCH:140479829-140483407	NOTEST	0	0	0	0	1	1
ENSG00000273391	ENSG00000273391	RP11-634H22.1	7:139024202-139108198	NOTEST	0.204046	0.325892	0.675496	0	1	1
ENSG00000273392	ENSG00000273392	PCDHB6	HG1082_HG167_PATCH:140529686-140532872	NOTEST	0	0	0	0	1	1
ENSG00000273393	ENSG00000273393	AL773604.8	HG237_PATCH:46222457-46224598	NOTEST	0	0	0	0	1	1
ENSG00000273394	ENSG00000273394	RP11-255E6.6	3:113547028-113666417	NOTEST	0.0376075	0.181757	2.27292	0	1	1
ENSG00000273395	ENSG00000273395	FLJ00388	1:48226199-48462567	NOTEST	0	0	0	0	1	1
ENSG00000273396	ENSG00000273396	RP11-326I19.3	4:4846163-4852554	NOTEST	0	0	0	0	1	1
ENSG00000273397	ENSG00000273397	NDUFA6	HSCHR22_2_CTG1:42481528-42486959	NOTEST	0	0	0	0	1	1
ENSG00000273398	ENSG00000273398	RP11-474G23.1	2:68350067-68488362	NOTEST	0	0.387839	inf	0	1	1
ENSG00000273399	ENSG00000273399	RP11-408A13.3	9:14586766-14587324	NOTEST	0.0711694	0.0544229	-0.387042	0	1	1
ENSG00000273400	ENSG00000273400	AL662890.15	HSCHR6_MHC_MANN:28730485-28730593	NOTEST	0	0	0	0	1	1
ENSG00000273401	ENSG00000273401	RP5-1186P10.2	HG1257_PATCH:74071869-74072256	NOTEST	0	0	0	0	1	1
ENSG00000273402	ENSG00000273402	RP5-855D21.2	8:163185-197342	NOTEST	0.0327199	0.0509422	0.638691	0	1	1
ENSG00000273403	ENSG00000273403	RP11-329B9.3	3:184459724-184460250	NOTEST	0.0418432	0	#NAME?	0	1	1
ENSG00000273404	ENSG00000273404	TAS2R7	HG1133_PATCH:10954130-10955226	NOTEST	0	0	0	0	1	1
ENSG00000273405	ENSG00000273405	AC006129.1	HG1350_HG959_PATCH:42037110-42038079	NOTEST	0	0	0	0	1	1
ENSG00000273406	ENSG00000273406	RP11-114O18.1	1:120619222-120619698	NOTEST	0	0	0	0	1	1
ENSG00000273407	ENSG00000273407	RP11-757A13.1	7:99354603-99381888	NOTEST	0	0	0	0	1	1
ENSG00000273408	ENSG00000273408	OR5B15P	11:58155055-58155959	NOTEST	0	0	0	0	1	1
ENSG00000273409	ENSG00000273409	RP11-480C22.1	11:127140956-127206928	NOTEST	0	0	0	0	1	1
ENSG00000273410	ENSG00000273410	RP11-169K19.1	HG979_PATCH:116853123-117708745	NOTEST	0	0	0	0	1	1
ENSG00000273411	ENSG00000273411	CTD-3093M3.1	HSCHR19LRC_PGF2_CTG1:54697730-54698394	NOTEST	0	0	0	0	1	1
ENSG00000273412	ENSG00000273412	KRTAP10-11	HG237_PATCH:45917774-46131461	NOTEST	0	0	0	0	1	1
ENSG00000273413	ENSG00000273413	RP11-96C23.15	10:88695296-88784489	NOTEST	0	0	0	0	1	1
ENSG00000273414	ENSG00000273414	VSTM1	HSCHR19LRC_LRC_J_CTG1:54544078-54567207	NOTEST	0	0	0	0	1	1
ENSG00000273415	ENSG00000273415	RP11-702B10.2	11:128050321-128053449	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000273416	ENSG00000273416	RP4-597N16.4	1:235267494-235267924	NOTEST	0.0573107	0.168761	1.55811	0	1	1
ENSG00000273417	ENSG00000273417	TFPT	HSCHR19LRC_LRC_T_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273418	ENSG00000273418	TARM1	HSCHR19LRC_COX2_CTG1:54573148-54584634	NOTEST	0	0	0	0	1	1
ENSG00000273419	ENSG00000273419	RP4-751H13.7	7:149535455-149564568	NOTEST	0.0672796	0.0413059	-0.70382	0	1	1
ENSG00000273421	ENSG00000273421	VSTM1	HG1079_PATCH:54544078-54567207	NOTEST	0	0	0	0	1	1
ENSG00000273422	ENSG00000273422	ZNF876P	HG174_HG254_PATCH:212609-255985	NOTEST	0	0	0	0	1	1
ENSG00000273423	ENSG00000273423	OR13I1P	9:107392034-107393298	NOTEST	0	0	0	0	1	1
ENSG00000273424	ENSG00000273424	CTA-223H9.9	22:41826937-41827379	NOTEST	0	0	0	0	1	1
ENSG00000273425	ENSG00000273425	AC073107.1	HG444_PATCH:65112079-65235723	NOTEST	0	0	0	0	1	1
ENSG00000273426	ENSG00000273426	NDUFA3	HSCHR19LRC_PGF2_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273427	ENSG00000273427	NDUFA3	HSCHR19LRC_LRC_T_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273428	ENSG00000273428	RP4-539M6.22	22:30831530-30832234	NOTEST	0	0.0107604	inf	0	1	1
ENSG00000273429	ENSG00000273429	AC253572.2	HG1292_PATCH:121266730-121346462	NOTEST	0	0	0	0	1	1
ENSG00000273430	ENSG00000273430	TFPT	HSCHR19LRC_LRC_I_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273431	ENSG00000273431	TAS2R50	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000273432	ENSG00000273432	RP5-1165K10.2	7:43966036-44058774	NOTEST	0.288425	0.335296	0.217239	0	1	1
ENSG00000273433	ENSG00000273433	RP1-170O19.22	7:27145802-27197555	NOTEST	0	0	0	0	1	1
ENSG00000273434	ENSG00000273434	OR8S21P	12:48733790-48836730	NOTEST	0	0	0	0	1	1
ENSG00000273435	ENSG00000273435	AC006129.4	HG1350_HG959_PATCH:42041087-42042809	NOTEST	0	0	0	0	1	1
ENSG00000273436	ENSG00000273436	DMRTC2	HG1350_HG959_PATCH:42350647-42358238	NOTEST	0	0	0	0	1	1
ENSG00000273437	ENSG00000273437	RP11-434H6.7	3:128882448-128882783	NOTEST	0	0.396955	inf	0	1	1
ENSG00000273438	ENSG00000273438	MIR1184-2	HG1497_PATCH:154625382-154627083	NOTEST	0	0	0	0	1	1
ENSG00000273440	ENSG00000273440	H2AFB2	HG1497_PATCH:154549246-154549763	NOTEST	0	0	0	0	1	1
ENSG00000273441	ENSG00000273441	RP11-822E23.6	HG987_PATCH:21428101-21477829	NOTEST	0	0	0	0	1	1
ENSG00000273443	ENSG00000273443	RP11-54O7.18	1:995113-1004735	NOTEST	0.360933	0.615301	0.769563	0	1	1
ENSG00000273444	ENSG00000273444	RP5-1147A1.2	7:40146886-40147053	NOTEST	0.802454	0	#NAME?	0	1	1
ENSG00000273445	ENSG00000273445	RP11-1399P15.1	2:87754886-87906324	NOTEST	0	0	0	0	1	1
ENSG00000273446	ENSG00000273446	MBOAT7	HSCHR19LRC_LRC_S_CTG1:54677106-54693733	NOTEST	0	0	0	0	1	1
ENSG00000273447	ENSG00000273447	AC004067.5	4:110481360-110624739	NOTEST	0.163968	0.195415	0.253126	0	1	1
ENSG00000273448	ENSG00000273448	RP11-166O4.6	7:66798033-66799370	NOTEST	0.12041	0.0468764	-1.36102	0	1	1
ENSG00000273449	ENSG00000273449	RP11-218F10.3	4:164445449-165305202	NOTEST	0.189687	0.392558	1.04928	0	1	1
ENSG00000273450	ENSG00000273450	RP11-76P2.4	10:95753745-96122716	NOTEST	0.0593629	0	#NAME?	0	1	1
ENSG00000273451	ENSG00000273451	RP4-569M23.4	20:45837858-45985567	NOTEST	0.0711505	0.0692832	-0.0383676	0	1	1
ENSG00000273452	ENSG00000273452	AC005358.1	17:12569206-12894960	NOTEST	0	0	0	0	1	1
ENSG00000273453	ENSG00000273453	NDUFA3	HSCHR19LRC_COX1_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273454	ENSG00000273454	RP11-797D24.3	3:122996199-122996751	NOTEST	0.150302	0.140945	-0.0927271	0	1	1
ENSG00000273455	ENSG00000273455	RP11-305O4.3	3:135684514-135866733	NOTEST	0	0	0	0	1	1
ENSG00000273457	ENSG00000273457	TAS2R13	HSCHR12_2_CTG2:10977558-11356160	NOTEST	0	0	0	0	1	1
ENSG00000273458	ENSG00000273458	TFPT	HSCHR19LRC_LRC_J_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273459	ENSG00000273459	CNOT3	HSCHR19LRC_LRC_S_CTG1:54641443-54663620	NOTEST	0	0	0	0	1	1
ENSG00000273460	ENSG00000273460	VSTM1	HSCHR19LRC_LRC_S_CTG1:54544078-54567207	NOTEST	0	0	0	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000273461	ENSG00000273461	RP11-398A8.4	3:72084450-72291716	NOTEST	0	0	0	0	1	1
ENSG00000273462	ENSG00000273462	PRPF31	HSCHR19LRC_COX2_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273463	ENSG00000273463	AL138834.1	9:36002905-36003864	NOTEST	0	0	0	0	1	1
ENSG00000273464	ENSG00000273464	RP11-313P22.1	21:30565800-31312351	NOTEST	0	0	0	0	1	1
ENSG00000273465	ENSG00000273465	RP11-478C6.5	HG174_HG254_PATCH:269865-270175	NOTEST	0	0	0	0	1	1
ENSG00000273467	ENSG00000273467	RPS9	HSCHR19LRC_LRC_S_CTG1:54704725-54711511	NOTEST	0	0	0	0	1	1
ENSG00000273468	ENSG00000273468	PCDHB19P	HG1082_HG167_PATCH:140619534-140621881	NOTEST	0	0	0	0	1	1
ENSG00000273469	ENSG00000273469	PRPF31	HSCHR19LRC_COX1_CTG1:54606035-54635140	NOTEST	0	0	0	0	1	1
ENSG00000273470	ENSG00000273470	MBOAT7	HSCHR19LRC_LRC_T_CTG1:54677106-54693733	NOTEST	0	0	0	0	1	1
ENSG00000273471	ENSG00000273471	RP13-1039J1.4	2:111143953-111230652	NOTEST	4.17E-07	0	#NAME?	0	1	1
ENSG00000273472	ENSG00000273472	RP11-102N12.3	4:141677681-141679075	NOTEST	0.462317	0.267955	-0.786894	0	1	1
ENSG00000273473	ENSG00000273473	LL09NC01-139C3.1	9:137033890-137034462	NOTEST	0.0740897	0.108363	0.54853	0	1	1
ENSG00000273474	ENSG00000273474	RP11-295P9.12	10:13628926-14504141	NOTEST	0.247748	0.193723	-0.354876	0	1	1
ENSG00000273475	ENSG00000273475	LDHAL6FP	HG193_PATCH:157610519-157644735	NOTEST	0	0	0	0	1	1
ENSG00000273476	ENSG00000273476	RP11-108L7.14	10:102727444-102727892	NOTEST	0.0536014	0.119476	1.15637	0	1	1
ENSG00000273477	ENSG00000273477	RP11-196O16.1	7:16127151-16129275	NOTEST	0.152488	0.195761	0.360395	0	1	1
ENSG00000273479	ENSG00000273479	AC005795.1	HG1350_HG959_PATCH:42012056-42012803	NOTEST	0	0	0	0	1	1
ENSG00000273480	ENSG00000273480	SNORA26	HG957_PATCH:53421728-53421852	NOTEST	0	0	0	0	1	1
ENSG00000273481	ENSG00000273481	RP11-126K1.9	1:151300424-151300905	NOTEST	0.0958192	0	#NAME?	0	1	1
ENSG00000273482	ENSG00000273482	PRKCD	HG957_PATCH:53190024-53226733	NOTEST	0	0	0	0	1	1
ENSG00000273483	ENSG00000273483	RP4-671G15.2	1:113009162-113214241	NOTEST	0.0944158	0.0222654	-2.08422	0	1	1
ENSG00000273484	ENSG00000273484	OR6R2P	8:21547914-21669869	NOTEST	0	0	0	0	1	1
ENSG00000273486	ENSG00000273486	RP11-731C17.2	3:136537488-136580896	NOTEST	0.409951	0.380911	-0.105997	0	1	1
ENSG00000273487	ENSG00000273487	RP4-621B10.8	1:92654793-92656264	NOTEST	0	0	0	0	1	1
ENSG00000273488	ENSG00000273488	RP11-114I8.4	3:100080030-100080481	NOTEST	0.510416	0.203803	-1.3245	0	1	1
ENSG00000273489	ENSG00000273489	RP11-180C16.1	7:130626518-131182453	NOTEST	0.0343374	0.18994	2.46769	0	1	1
ENSG00000273490	ENSG00000273490	TSEN34	HSCHR19LRC_LRC_J_CTG1:54693788-54697585	NOTEST	0	0	0	0	1	1
ENSG00000273491	ENSG00000273491	RP11-138A9.2	HG1308_PATCH:13060011-130603315	NOTEST	0	0	0	0	1	1
ENSG00000273492	ENSG00000273492	AP000230.1	21:27252860-27589700	NOTEST	0.0148795	0.0115534	-0.365016	0	1	1
ENSG00000273493	ENSG00000273493	RP11-80H18.4	3:58315691-58315845	NOTEST	0	0	0	0	1	1

Table 6B. Differential expression of transcripts upon siRNA knockdown of *SLNCR* in WM1976

Table 6B lists the transcripts whose expression was significantly regulated by knockdown of *SLNCR* (p-value < 0.01). *SLNCR* (LINC00511 according to current annotation) is the last item listed.

Table 6B

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000128564	ENSG00000128564	VGF	7:100805789-100808874	OK	0.73792	10.7728	3.86778	5.79161	5.00E-05	0.0312848
ENSG00000170442	ENSG00000170442	KRT86	12:52626303-52702947	OK	0.093486	0.85226	3.18847	1.37006	0.003	0.362608
ENSG00000172247	ENSG00000172247	C1QTNF4	11:47611215-47616211	OK	0.193578	1.28168	2.72704	1.17078	0.00625	0.502479
ENSG00000135318	ENSG00000135318	NT5E	6:86159808-86205500	OK	0.401159	2.60483	2.69894	2.43235	0.0001	0.0513964
ENSG00000026751	ENSG00000026751	SLAMF7	1:160709036-160724611	OK	5.97929	38.2066	2.67578	4.41381	5.00E-05	0.0312848
ENSG00000179817	ENSG00000179817	MRGPRX4	11:18161732-18211168	OK	0.271425	1.63545	2.59106	2.50602	0.00245	0.339019
ENSG00000162892	ENSG00000162892	IL24	1:207070787-207077484	OK	3.22045	18.364	2.51155	3.6908	5.00E-05	0.0312848
ENSG00000167608	ENSG00000167608	TMC4	19:54663845-54676944	OK	0.165663	0.836146	2.3355	0.675342	0.0033	0.36531
ENSG00000184363	ENSG00000184363	PKP3	11:392613-404908	OK	0.135499	0.656222	2.27591	0.513756	0.005	0.452547
ENSG00000115956	ENSG00000115956	PLEK	2:68588345-68624585	OK	0.163438	0.751818	2.20164	1.59759	0.0072	0.525965
ENSG00000160588	ENSG00000160588	MPZL3	11:118097408-118123065	OK	0.166065	0.691753	2.05851	1.36449	0.00325	0.36531
ENSG00000064300	ENSG00000064300	NGFR	17:47572654-47661189	OK	1.67048	6.8959	2.04548	3.34679	5.00E-05	0.0312848
ENSG00000183668	ENSG00000183668	PSG9	19:43715942-43773682	OK	1.11182	4.3564	1.97022	2.06532	0.00305	0.362608
ENSG00000104783	ENSG00000104783	KCNN4	19:44270684-44285409	OK	0.348731	1.35945	1.96283	1.09381	0.00905	0.602956
ENSG00000136274	ENSG00000136274	NACAD	7:45120036-45128513	OK	0.281946	1.08894	1.94943	1.1403	0.0048	0.43998
ENSG00000131409	ENSG00000131409	LRRC4B	19:51020148-51071302	OK	0.715032	2.73315	1.93448	2.2952	0.00015	0.0654136
ENSG00000236719	ENSG00000236719	OVAAL	1:180528111-180535654	OK	0.464653	1.75045	1.9135	2.17005	0.0031	0.362608
ENSG00000166710	ENSG00000166710	B2M	15:45003674-45011075	OK	0.456503	1.68041	1.88012	0.978707	0.0072	0.525966
ENSG00000118640	ENSG00000118640	VAMP8	2:85788684-85809154	OK	0.464121	1.68446	1.85971	1.50169	0.00935	0.606107
ENSG00000139629	ENSG00000139629	GALNT6	12:51745030-51902980	OK	1.31767	4.66084	1.8226	1.24603	0.00015	0.0654136
ENSG00000186205	ENSG00000186205	1-Mar	1:220960100-220987735	OK	0.475762	1.67109	1.81248	1.25238	0.0016	0.26774
ENSG00000203837	ENSG00000203837	PNLIPRP3	10:118187378-118237469	OK	0.909978	3.17066	1.80088	2.63668	0.0001	0.0513964
ENSG00000221890	ENSG00000221890	NPTXR	22:39214456-39239987	OK	0.217667	0.758341	1.80073	2.44749	0.0006	0.156993
ENSG00000197540	ENSG00000197540	GZMM	19:544033-549919	OK	0.813084	2.82344	1.79598	2.03735	0.002	0.316286
ENSG00000237289	ENSG00000237289	CKMT1B	15:43885251-44010458	OK	0.310184	1.06677	1.78206	0.738184	0.0047	0.433575
ENSG00000161638	ENSG00000161638	ITGA5	12:54747444-54891472	OK	1.09852	3.7346	1.76539	1.3458	0.00135	0.249075
ENSG00000188725	ENSG00000188725	SMIM15	5:60453535-60560756	OK	14.5261	47.955	1.72303	2.43568	5.00E-05	0.0312848
ENSG00000178726	ENSG00000178726	THBD	20:23026269-23030378	OK	0.206776	0.680587	1.71871	2.01187	0.0046	0.43173
ENSG00000172183	ENSG00000172183	ISG20	15:89179383-89199714	OK	1.37799	4.51629	1.71257	1.48651	0.0083	0.568787
ENSG00000108924	ENSG00000108924	HLF	17:53342372-53402426	OK	0.287422	0.928197	1.69126	0.731493	0.00925	0.606107
ENSG00000121769	ENSG00000121769	FABP3	1:31838471-31849697	OK	6.3945	19.6954	1.62296	2.52296	0.00015	0.0654136
ENSG00000147434	ENSG00000147434	CHRNA6	8:42607762-42651535	OK	0.37526	1.15333	1.61985	1.07815	0.00935	0.606107
ENSG00000135218	ENSG00000135218	CD36	7:79959507-80308593	OK	1.65152	5.07246	1.61889	1.65931	5.00E-05	0.0312848
ENSG00000135046	ENSG00000135046	ANXA1	9:75766672-75785309	OK	25.4681	77.6662	1.6086	3.5394	5.00E-05	0.0312848
ENSG00000167693	ENSG00000167693	NXN	17:702552-883010	OK	0.811196	2.38063	1.55322	1.26365	0.00645	0.50635
ENSG00000107281	ENSG00000107281	NPDC1	9:139933921-139940655	OK	0.539845	1.57573	1.5454	1.12091	0.00845	0.576322
ENSG00000134594	ENSG00000134594	RAB33A	X:129305622-129318844	OK	1.32442	3.86526	1.5452	2.15278	0.00185	0.302538
ENSG00000142627	ENSG00000142627	EPHA2	1:16450831-16483824	OK	5.75231	16.7272	1.53998	3.01115	5.00E-05	0.0312848
ENSG00000138606	ENSG00000138606	SHF	15:45384847-45493373	OK	1.38259	3.94601	1.51302	1.64378	0.004	0.39975
ENSG00000176845	ENSG00000176845	METRNL	17:81037566-81052864	OK	2.55424	7.14771	1.48459	1.93361	0.00145	0.257617
ENSG00000127418	ENSG00000127418	FGFRL1	4:1003723-1020685	OK	1.00723	2.80924	1.47979	1.88378	0.0006	0.156993
ENSG00000166341	ENSG00000166341	DCHS1	11:6642555-6677085	OK	0.285433	0.767141	1.42634	2.1675	0.00085	0.20053
ENSG00000132170	ENSG00000132170	PPARG	3:12328866-12475855	OK	1.75238	4.59908	1.39203	1.94601	0.0006	0.156993
ENSG00000261087	ENSG00000261087	KB-1460A1.5	8:102179032-102181857	OK	0.388269	1.01224	1.38242	1.75909	0.0076	0.544137
ENSG00000072163	ENSG00000072163	LIMS2	2:128395955-128439360	OK	1.45637	3.70447	1.34689	1.78381	0.0013	0.242965
ENSG00000141934	ENSG00000141934	PPAP2C	19:281039-291393	OK	12.3733	31.2973	1.33881	2.66514	5.00E-05	0.0312848
ENSG00000143320	ENSG00000143320	CRABP2	1:156669397-156675608	OK	6.97026	17.5389	1.33127	2.28463	0.0004	0.125139
ENSG00000244486	ENSG00000244486	SCARF2	22:20778873-20850170	OK	8.94016	22.4294	1.32702	1.99562	0.00055	0.155197
ENSG00000112655	ENSG00000112655	PTK7	6:43044005-43129457	OK	3.15858	7.91906	1.32605	1.94636	5.00E-05	0.0312848
ENSG00000140044	ENSG00000140044	JDP2	14:75890385-75940814	OK	2.09781	5.19138	1.30723	1.70211	0.00445	0.424106
ENSG00000136999	ENSG00000136999	NOV	8:120428545-120474590	OK	25.789	62.1996	1.27015	2.45775	5.00E-05	0.0312848
ENSG00000169551	ENSG00000169551	CT55	X:134290460-134305322	OK	2.36382	5.62545	1.25085	2.00336	0.0021	0.324958
ENSG00000137752	ENSG00000137752	CASP1	11:104896169-104972158	OK	1.51173	3.5718	1.24045	1.09761	0.0065	0.50635
ENSG00000100522	ENSG00000100522	GNPNAT1	14:53241911-53258386	OK	8.64083	20.4092	1.23998	1.74834	0.00025	0.0856607
ENSG00000131196	ENSG00000131196	NFATC1	18:77155855-77289325	OK	1.75474	4.12983	1.23483	1.71553	0.0009	0.202373
ENSG00000076706	ENSG00000076706	MCAM	11:119179240-119192231	OK	100.539	234.556	1.22218	1.86587	5.00E-05	0.0312848
ENSG00000065809	ENSG00000065809	FAM107B	10:14560555-14816896	OK	1.10846	2.54432	1.19872	0.868112	0.00805	0.562367
ENSG00000166831	ENSG00000166831	RBPMS2	15:65032090-65067786	OK	1.40517	3.19285	1.18411	1.74456	0.0054	0.467076
ENSG00000203805	ENSG00000203805	PPAPDC1A	10:122216465-122349367	OK	5.33478	11.9924	1.16862	1.66146	0.007	0.525966
ENSG00000184584	ENSG00000184584	TMEM173	5:138855118-138862520	OK	7.01309	15.6661	1.15952	2.03032	0.00055	0.155197
ENSG00000130600	ENSG00000130600	H19	11:2016405-2022700	OK	7.79369	17.2386	1.14527	1.65485	0.0028	0.359775
ENSG00000158764	ENSG00000158764	ITLN2	1:160901528-160924589	OK	8.68181	19.0695	1.1352	1.83255	0.0037	0.385846
ENSG00000198682	ENSG00000198682	PAPSS2	10:89367741-89507462	OK	2.78637	6.08011	1.12571	1.47623	0.00425	0.413255
ENSG00000158050	ENSG00000158050	DUSP2	2:96808904-96811179	OK	2.29522	4.98394	1.11866	1.81251	0.00385	0.395752
ENSG00000118420	ENSG00000118420	UBE3D	6:83602116-83775560	OK	3.02825	6.54309	1.11149	1.93949	0.00615	0.500026
ENSG00000075618	ENSG00000075618	FSCN1	7:5632438-5646286	OK	1.59735	3.43963	1.10657	1.65237	0.00275	0.356534
ENSG00000080546	ENSG00000080546	SESN1	6:109307639-109416022	OK	7.60393	16.1685	1.08837	2.24271	0.0001	0.0513964
ENSG00000187135	ENSG00000187135	VSTM2B	19:29777917-30055386	OK	19.8708	42.1179	1.08379	2.39601	5.00E-05	0.0312848
ENSG00000184371	ENSG00000184371	CSF1	1:110452863-110473614	OK	2.64526	5.59344	1.08033	1.60331	0.00205	0.320669
ENSG00000160867	ENSG00000160867	FGFR4	5:176513886-176525145	OK	3.89227	8.17217	1.07011	1.50145	0.00115	0.223644
ENSG00000112237	ENSG00000112237	CCNC	6:99990255-100016972	OK	18.1063	37.9683	1.0683	1.93005	0.00035	0.114474
ENSG00000116741	ENSG00000116741	RGS2	1:192778168-192781403	OK	18.3603	38.3176	1.06142	2.24773	0.00015	0.0654136
ENSG00000142949	ENSG00000142949	PTPRF	1:43990857-44089343	OK	7.42886	15.4218	1.05376	2.3162	5.00E-05	0.0312848
ENSG00000110492	ENSG00000110492	MDK	11:46402305-46405375	OK	25.2382	52.2038	1.04855	2.20429	0.0006	0.156993
ENSG00000128283	ENSG00000128283	CDC42EP1	22:37956453-37965412	OK	4.01718	8.27091	1.04186	1.93046	0.0007	0.173684
ENSG00000116717	ENSG00000116717	GADD45A	1:68150743-68154021	OK	15.2303	31.2765	1.03814	2.22335	0.00035	0.114474
ENSG00000138798	ENSG00000138798	EGF	4:110834039-110933422	OK	1.73343	3.53428	1.02778	1.16683	0.0035	0.3731
ENSG00000104332	ENSG00000104332	SFRP1	8:41119480-41167016	OK	1.42489	2.87921	1.01482	1.74322	0.00665	0.50635
ENSG00000005884	ENSG00000005884	ITGA3	17:48133331-48167845	OK	49.5687	99.2248	1.00127	1.51567	0.0002	0.0777892
ENSG00000111057	ENSG00000111057	KRT18	12:53290976-53346686	OK	5.10018	10.1964	0.999441	1.73926	0.00415	0.409059

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000253276	ENSG00000253276	CCDC71L	7:106012696-106410653	OK	5.963	11.894	0.996121	2.21128	0.0004	0.125139
ENSG00000069424	ENSG00000069424	KCNAB2	1:5922870-6161253	OK	14.8258	29.5563	0.995352	1.49034	0.00585	0.485182
ENSG00000143479	ENSG00000143479	DYRK3	1:206807993-206857764	OK	13.5467	26.9437	0.992011	2.21373	0.00015	0.0654136
ENSG00000179627	ENSG00000179627	ZBTB42	14:105266932-105271049	OK	1.37187	2.72406	0.989613	1.62455	0.00865	0.581692
ENSG00000129946	ENSG00000129946	SHC2	19:416582-460996	OK	5.11101	10.1368	0.987918	1.65694	0.0066	0.50635
ENSG00000124762	ENSG00000124762	CDKN1A	6:36644304-36655116	OK	118.389	234.584	0.986566	2.20357	0.0002	0.0777892
ENSG00000204516	ENSG00000204516	MICB	6:31462657-31478901	OK	2.74406	5.42895	0.984358	1.56391	0.00715	0.525966
ENSG00000073670	ENSG00000073670	ADAM11	17:42836398-42859214	OK	4.03268	7.9687	0.982605	1.59961	0.0071	0.525966
ENSG00000102034	ENSG00000102034	ELF4	X:129198848-129244691	OK	1.69674	3.33841	0.976396	1.67715	0.00555	0.467076
ENSG00000151718	ENSG00000151718	WWC2	4:184020445-184241930	OK	3.3601	6.60421	0.974883	1.54712	0.00315	0.362608
ENSG00000114019	ENSG00000114019	AMOTL2	3:134070693-134094321	OK	8.38079	16.4089	0.969322	2.19786	0.0002	0.0777892
ENSG00000186654	ENSG00000186654	PRR5	22:45064592-45258665	OK	3.83389	7.50062	0.9682	1.59202	0.0083	0.568787
ENSG00000121579	ENSG00000121579	NAA50	3:113435306-113465147	OK	37.0055	71.9164	0.958582	1.64276	0.00705	0.525966
ENSG00000123643	ENSG00000123643	SLC36A1	5:150816606-150871942	OK	4.6104	8.95246	0.957393	1.41949	0.00265	0.353112
ENSG00000006327	ENSG00000006327	TNFRSF12A	16:3064712-3072384	OK	49.7551	96.5548	0.956506	1.66362	0.00025	0.0856607
ENSG00000121644	ENSG00000121644	DESI2	1:244816236-244872335	OK	12.0807	23.1934	0.941009	2.09924	5.00E-05	0.0312848
ENSG00000125355	ENSG00000125355	TMEM255A	X:119392504-119445411	OK	15.0477	28.5983	0.926389	1.34158	0.00245	0.339019
ENSG00000133816	ENSG00000133816	MICAL2	11:12115542-12285334	OK	5.11434	9.6951	0.922706	1.10154	0.00945	0.60712
ENSG00000147650	ENSG00000147650	LRP12	8:105501458-105601252	OK	32.5455	61.4048	0.915894	1.61471	0.0066	0.50635
ENSG00000110092	ENSG00000110092	CCND1	11:69455854-69490184	OK	192.129	360.135	0.906462	1.4578	0.00125	0.236694
ENSG00000180921	ENSG00000180921	FAM83H	8:144806102-144815971	OK	2.74058	5.12344	0.902631	1.85085	0.0031	0.362608
ENSG00000177606	ENSG00000177606	JUN	1:59246464-59249785	OK	10.4766	19.5204	0.897808	2.04886	0.00095	0.207143
ENSG00000170385	ENSG00000170385	SLC30A1	1:211744909-211752084	OK	8.72539	16.164	0.889494	2.11712	0.0005	0.153096
ENSG00000230836	ENSG00000230836	AC104135.4	2:75167384-75169797	OK	8.00754	14.7379	0.880096	1.68063	0.00675	0.511259
ENSG00000205213	ENSG00000205213	LGR4	11:27387507-27503980	OK	3.23452	5.88105	0.862522	1.5531	0.00305	0.362608
ENSG00000185909	ENSG00000185909	KLHDC8B	3:49209043-49213917	OK	16.2449	29.4712	0.859313	1.54404	0.0093	0.606107
ENSG00000114573	ENSG00000114573	ATP6V1A	3:113465718-113530903	OK	21.2949	38.5301	0.855479	2.10447	0.00055	0.155197
ENSG00000150093	ENSG00000150093	ITGB1	10:33189246-33371030	OK	52.4046	94.7021	0.853703	1.44068	0.00085	0.20053
ENSG00000070669	ENSG00000070669	ASNS	7:97481429-97501854	OK	10.5099	18.9779	0.852571	1.71265	0.0033	0.36531
ENSG00000073712	ENSG00000073712	FERMT2	14:53323985-53419153	OK	6.82605	12.2169	0.839753	1.70744	0.0023	0.334336
ENSG00000174705	ENSG00000174705	SH3PXD2B	5:171752184-171881527	OK	4.98931	8.89785	0.834616	1.24287	0.00275	0.356534
ENSG00000138119	ENSG00000138119	MYOF	10:95066185-95242074	OK	9.61062	17.1202	0.833	1.43307	0.0035	0.3731
ENSG00000184500	ENSG00000184500	PROS1	3:93591880-93692910	OK	41.7949	74.3832	0.831652	1.81377	0.0015	0.26325
ENSG00000135048	ENSG00000135048	TMEM2	9:74298281-74431606	OK	15.5166	27.5806	0.829844	1.33739	0.0073	0.530577
ENSG00000159840	ENSG00000159840	ZYX	7:143078172-143220542	OK	16.9019	29.9165	0.823754	1.77001	0.0024	0.338612
ENSG00000168461	ENSG00000168461	RAB31	18:9708161-9862548	OK	6.26355	11.0572	0.81993	1.17191	0.00635	0.50635
ENSG00000136048	ENSG00000136048	DRAM1	12:102271128-102405908	OK	4.98693	8.73904	0.809324	1.28224	0.0079	0.560044
ENSG00000135069	ENSG00000135069	PSAT1	9:80912058-80945009	OK	29.4253	51.3665	0.80377	1.84882	0.00285	0.362608
ENSG00000049449	ENSG00000049449	RCN1	11:31806339-32127301	OK	51.2029	89.2247	0.801218	1.56985	0.004	0.39975
ENSG00000170017	ENSG00000170017	ALCAM	3:105085752-105295744	OK	13.1829	22.8556	0.793874	1.60366	0.0054	0.467076
ENSG00000244694	ENSG00000244694	PTCHD4	6:47845763-48036425	OK	6.34424	10.9158	0.782898	1.62782	0.0076	0.544137
ENSG00000175602	ENSG00000175602	CCDC85B	11:65657874-65659105	OK	27.6634	47.5076	0.780179	1.70618	0.0059	0.485182
ENSG00000160075	ENSG00000160075	SSU72	1:1477052-1510249	OK	48.2648	82.4522	0.772586	1.84461	0.00235	0.338189
ENSG00000130513	ENSG00000130513	GDF15	19:18485540-18499986	OK	1046.11	1778.98	0.766015	1.60183	0.0091	0.603494
ENSG00000113758	ENSG00000113758	DBN1	5:176883608-176901402	OK	24.7406	41.949	0.761756	1.48535	0.00855	0.580392
ENSG00000135842	ENSG00000135842	FAM129A	1:184759857-184943682	OK	26.9178	45.3861	0.753693	1.69486	0.00225	0.330406
ENSG00000090621	ENSG00000090621	PABPC4	1:40026487-40042462	OK	49.7917	83.6748	0.748888	1.30039	0.008	0.5616
ENSG00000174307	ENSG00000174307	PHLDA3	1:201434619-201438365	OK	66.2584	110.097	0.732594	1.755	0.00385	0.395753
ENSG00000130203	ENSG00000130203	APOE	19:45409010-45412650	OK	251.199	414.985	0.72423	1.62993	0.0083	0.568787
ENSG00000011566	ENSG00000011566	MAP4K3	2:39476406-39945103	OK	11.8812	19.2447	0.695783	1.12394	0.0087	0.582333
ENSG00000101197	ENSG00000101197	BIRC7	20:61867234-61871859	OK	163.212	263.676	0.692021	1.54672	0.00935	0.606107
ENSG00000139645	ENSG00000139645	ANKRD52	12:56623832-56652175	OK	29.0711	17.9548	-0.695213	-1.40279	0.00545	0.467076
ENSG00000112773	ENSG00000112773	FAM46A	6:82201155-82462491	OK	13.8034	8.48817	-0.701499	-1.63757	0.0059	0.485182
ENSG00000165475	ENSG00000165475	CRYL1	13:20977805-21099996	OK	56.4969	34.0208	-0.731754	-1.68359	0.006	0.490602
ENSG00000198087	ENSG00000198087	CD2AP	6:47445524-47594999	OK	27.8033	16.6359	-0.740957	-1.67872	0.00275	0.356534
ENSG00000170961	ENSG00000170961	HAS2	8:122624355-122656933	OK	17.852	10.6641	-0.74332	-1.71857	0.0053	0.467076
ENSG00000118785	ENSG00000118785	SPP1	4:88896818-88904562	OK	74.2821	44.3676	-0.743508	-1.65602	0.005	0.452547
ENSG00000100417	ENSG00000100417	PMM1	22:41956766-41985894	OK	38.2446	22.7522	-0.749252	-1.64924	0.0065	0.50635
ENSG00000152291	ENSG00000152291	TGOLN2	2:85545146-85555548	OK	58.9807	34.646	-0.767556	-1.78771	0.0032	0.362608
ENSG00000144837	ENSG00000144837	PLA1A	3:119316688-119348658	OK	24.0294	14.0899	-0.770135	-1.67452	0.00585	0.485182
ENSG00000146670	ENSG00000146670	CDCA5	11:64833771-64851636	OK	28.692	16.7239	-0.778741	-1.65933	0.0035	0.3731
ENSG00000136816	ENSG00000136816	TOR1B	9:132565431-132573560	OK	15.6206	9.07792	-0.783017	-1.44047	0.00655	0.50635
ENSG00000184990	ENSG00000184990	SIVA1	14:105219436-105234831	OK	97.069	56.3659	-0.784188	-1.6355	0.00865	0.581692
ENSG00000106780	ENSG00000106780	MEGF9	9:123363090-123476748	OK	19.3849	11.2286	-0.787752	-1.91703	0.002	0.316286
ENSG00000116209	ENSG00000116209	TMEM59	1:54497346-54519177	OK	127.508	73.7472	-0.789927	-1.81063	0.00255	0.346199
ENSG00000056998	ENSG00000056998	GYG2	X:2746828-2800859	OK	60.914	35.0509	-0.797324	-1.54683	0.00555	0.467076
ENSG00000131374	ENSG00000131374	TBC1D5	3:17198653-18959184	OK	26.6305	15.2557	-0.803731	-0.875512	0.00815	0.566602
ENSG00000123240	ENSG00000123240	OPTN	10:12938626-13180291	OK	40.9391	23.2796	-0.814413	-1.41941	0.0032	0.362608
ENSG00000242265	ENSG00000242265	PEG10	7:94285636-94299007	OK	21.1897	12.0467	-0.814728	-1.92451	0.00105	0.212825
ENSG00000146072	ENSG00000146072	TNFRSF21	6:47199267-47277641	OK	50.0336	28.3262	-0.820761	-2.0503	0.00105	0.212825
ENSG00000231925	ENSG00000231925	TAPBP	6:33267470-33282164	OK	28.0034	15.7022	-0.834637	-1.73379	0.00455	0.430783
ENSG00000233461	ENSG00000233461	RP11-295G20.2	1:231658133-231664302	OK	241.367	135.24	-0.8357	-1.84518	0.0029	0.362608
ENSG00000172819	ENSG00000172819	RARG	12:53604353-53626764	OK	18.7399	10.4549	-0.841934	-1.50363	0.0052	0.464802
ENSG00000165304	ENSG00000165304	MELK	9:36572858-36677678	OK	20.7899	11.5941	-0.842489	-1.72809	0.0039	0.398049
ENSG00000100906	ENSG00000100906	NFKBIA	14:35870716-35873955	OK	55.9969	31.104	-0.848248	-1.8809	0.00105	0.212825
ENSG00000174371	ENSG00000174371	EXO1	1:242011268-242058450	OK	19.123	10.5998	-0.85128	-1.29699	0.0098	0.624035
ENSG00000143437	ENSG00000143437	ARNT	1:150782180-150849244	OK	26.4835	14.6511	-0.85408	-1.35707	0.0065	0.50635
ENSG00000112977	ENSG00000112977	DAP	5:10679341-10770406	OK	45.0937	24.9333	-0.854849	-1.89643	0.00155	0.26774
ENSG00000170915	ENSG00000170915	PAQR8	6:52226218-52272575	OK	7.05365	3.89604	-0.856361	-1.81448	0.00395	0.39975
ENSG00000115414	ENSG00000115414	FN1	2:216225162-216300895	OK	233.939	129.157	-0.857003	-1.4106	0.0037	0.385846
ENSG00000168610	ENSG00000168610	STAT3	17:40465341-40540586	OK	30.2507	16.4808	-0.876182	-1.70382	0.00145	0.257617

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value
ENSG00000139350	ENSG00000139350	NEDD1	12:97301000-97347129	OK	14.3328	7.72155	-0.892359	-1.55055	0.00255	0.346199
ENSG00000155111	ENSG00000155111	CDK19	6:110931180-111137161	OK	5.16057	2.77353	-0.895808	-1.10818	0.00665	0.50635
ENSG00000170264	ENSG00000170264	FAM161A	2:62051988-62081278	OK	15.1729	8.13648	-0.899016	-1.55989	0.00305	0.362608
ENSG00000066032	ENSG00000066032	CTNNA2	2:79384131-80875905	OK	21.563	11.5223	-0.904134	-1.40629	0.00115	0.223644
ENSG00000125148	ENSG00000125148	MT2A	16:56642110-56643409	OK	50.8286	27.0803	-0.908396	-1.80864	0.00465	0.43173
ENSG00000164172	ENSG00000164172	MOCS2	5:52391508-52410956	OK	56.145	29.8509	-0.911381	-2.00531	0.001	0.211632
ENSG00000115232	ENSG00000115232	ITGA4	2:182321928-182400914	OK	13.1927	6.96395	-0.921764	-1.90872	0.0011	0.219863
ENSG00000131016	ENSG00000131016	AKAP12	6:151561133-151679692	OK	27.5808	14.525	-0.925125	-2.2599	0.0002	0.0777892
ENSG00000044524	ENSG00000044524	EPHA3	3:89156673-89531284	OK	5.83338	3.05215	-0.934503	-1.87533	0.0024	0.338612
ENSG00000113657	ENSG00000113657	DPYSL3	5:146770373-146889619	OK	15.4293	8.06641	-0.935674	-1.79598	0.001	0.211632
ENSG00000165195	ENSG00000165195	PIGA	X:15337572-15353676	OK	22.0951	11.5056	-0.941392	-1.57152	0.0043	0.415311
ENSG00000012660	ENSG00000012660	ELOVL5	6:53132195-53213947	OK	81.5122	42.2344	-0.948598	-1.88364	0.0016	0.26774
ENSG00000031691	ENSG00000031691	CENPQ	6:49431090-49460820	OK	14.246	7.31419	-0.961787	-1.89876	0.00315	0.362608
ENSG00000151725	ENSG00000151725	CENPU	4:185570766-185655287	OK	25.8647	13.2643	-0.963431	-1.77309	0.00445	0.424106
ENSG00000117305	ENSG00000117305	HMGCL	1:24128374-24165110	OK	14.48	7.36592	-0.97512	-1.7663	0.00365	0.385846
ENSG00000163808	ENSG00000163808	KIF15	3:44803208-44914868	OK	10.1628	5.12214	-0.988477	-1.44087	0.00525	0.466375
ENSG00000118193	ENSG00000118193	KIF14	1:200520627-200589862	OK	9.48301	4.76494	-0.992889	-2.27274	0.00025	0.0856607
ENSG00000088451	ENSG00000088451	TGDS	13:95226307-95248511	OK	20.6139	10.2359	-1.00998	-2.11989	0.00055	0.155197
ENSG00000118513	ENSG00000118513	MYB	6:135502452-135540311	OK	3.20516	1.59044	-1.01097	-1.43408	0.00295	0.362608
ENSG00000130150	ENSG00000130150	MOSPD2	X:14891562-14940449	OK	13.5226	6.65653	-1.02253	-2.0274	0.0009	0.202373
ENSG00000164627	ENSG00000164627	KIF6	6:39297765-39693181	OK	8.20587	4.03378	-1.02453	-1.73798	0.00555	0.467076
ENSG00000146674	ENSG00000146674	IGFBP3	7:45951948-45961473	OK	131.778	64.7348	-1.02549	-2.3814	5.00E-05	0.0312848
ENSG00000122966	ENSG00000122966	CIT	12:120123594-120315095	OK	35.6414	17.4359	-1.03149	-1.06929	0.00225	0.330406
ENSG00000144355	ENSG00000144355	DLX1	2:172949467-172954405	OK	5.60562	2.73048	-1.03772	-1.56543	0.0078	0.555692
ENSG00000169499	ENSG00000169499	PLEKHA2	8:38758752-38831428	OK	22.9374	11.1184	-1.04475	-1.28826	0.00125	0.236694
ENSG00000188452	ENSG00000188452	CERKL	2:182401402-182545603	OK	3.54	1.71127	-1.04869	-1.6834	0.00145	0.257617
ENSG00000185875	ENSG00000185875	THNSL1	10:25305586-25315593	OK	1.7592	0.848754	-1.0515	-1.66905	0.00795	0.560826
ENSG00000168843	ENSG00000168843	FSTL5	4:162300104-163085187	OK	1.98116	0.951795	-1.05762	-1.40385	0.00945	0.60712
ENSG00000114739	ENSG00000114739	ACVR2B	3:38492517-38534633	OK	3.47377	1.64035	-1.0825	-1.68698	0.0022	0.330406
ENSG00000108387	ENSG00000108387	4-Sep	17:56597197-56769416	OK	94.4412	44.0601	-1.09994	-2.23588	0.00025	0.0856607
ENSG00000213390	ENSG00000213390	ARHGAP19	10:98757794-99052413	OK	6.99423	3.24805	-1.10659	-1.79453	0.0009	0.202373
ENSG00000159216	ENSG00000159216	RUNX1	21:36160097-37376965	OK	6.31318	2.92037	-1.11221	-1.39277	0.0022	0.330406
ENSG00000163430	ENSG00000163430	FSTL1	3:120111139-120170100	OK	42.0042	19.0439	-1.1412	-1.49289	0.00315	0.362608
ENSG00000151025	ENSG00000151025	GPR158	10:25401986-25891155	OK	17.3546	7.85686	-1.14329	-1.83734	0.0035	0.3731
ENSG00000139734	ENSG00000139734	DIAPH3	13:60239716-60738121	OK	11.8944	5.3762	-1.14562	-2.45815	0.0001	0.0513964
ENSG00000159167	ENSG00000159167	STC1	8:23699427-23712320	OK	11.5631	5.22023	-1.14735	-1.69133	0.0054	0.467076
ENSG00000166845	ENSG00000166845	C18orf54	18:51850727-51911588	OK	4.08815	1.83818	-1.15317	-1.52171	0.00225	0.330406
ENSG00000163735	ENSG00000163735	CXCL5	4:74861358-74864496	OK	1.6759	0.745335	-1.16897	-1.63257	0.00965	0.617214
ENSG00000172731	ENSG00000172731	LRRC20	10:72058728-72142382	OK	9.39818	4.15292	-1.17826	-1.84486	0.0026	0.349688
ENSG00000181315	ENSG00000181315	ZNF322	6:26634610-26659980	OK	5.2553	2.29499	-1.19528	-1.44822	0.00515	0.46321
ENSG00000158006	ENSG00000158006	PAFAH2	1:26286257-26324648	OK	5.65278	2.46761	-1.19584	-1.35907	0.00555	0.467076
ENSG00000146285	ENSG00000146285	SCML4	6:108025307-108145521	OK	9.4712	4.09559	-1.20948	-2.09148	0.00065	0.167038
ENSG00000105011	ENSG00000105011	ASF1B	19:14229917-14247768	OK	16.3743	7.03868	-1.21806	-2.0438	0.00185	0.302538
ENSG00000072571	ENSG00000072571	HMMR	5:162887208-162921064	OK	13.5653	5.79204	-1.22777	-1.83021	0.00085	0.20053
ENSG00000204291	ENSG00000204291	COL15A1	9:101705460-101833069	OK	6.55412	2.72614	-1.26554	-1.8544	0.00025	0.0856607
ENSG00000163739	ENSG00000163739	CXCL1	4:74735109-74736959	OK	193.549	79.2914	-1.28746	-3.10424	5.00E-05	0.0312848
ENSG00000156475	ENSG00000156475	PPP2R2B	5:145942788-146464347	OK	2.64995	1.05274	-1.33182	-1.14104	0.00405	0.401956
ENSG00000116199	ENSG00000116199	FAM20B	1:178994938-179045697	OK	29.2921	11.4249	-1.35833	-2.51375	5.00E-05	0.0312848
ENSG00000221869	ENSG00000221869	CEBPD	8:48649470-48651648	OK	18.1426	6.8175	-1.41207	-2.88943	5.00E-05	0.0312848
ENSG00000163734	ENSG00000163734	CXCL3	4:74902305-74904524	OK	2.06829	0.74806	-1.46721	-1.58927	0.00755	0.544137
ENSG00000106404	ENSG00000106404	CLDN15	7:100875372-100882101	OK	2.12577	0.756299	-1.49095	-1.63333	0.003	0.362608
ENSG00000106733	ENSG00000106733	NMRK1	9:77675488-77703133	OK	8.84129	3.04853	-1.53615	-2.27211	0.0007	0.173684
ENSG00000181458	ENSG00000181458	TMEM45A	3:100211462-100296288	OK	2.61078	0.895709	-1.54338	-1.59436	0.00425	0.413255
ENSG00000115461	ENSG00000115461	IGFBP5	2:217536827-217858802	OK	3.6735	1.24197	-1.56452	-1.32071	0.00625	0.502479
ENSG00000108691	ENSG00000108691	CCL2	17:32581899-32584222	OK	5.60181	1.72269	-1.70123	-2.04687	0.002	0.316286
ENSG00000250343	ENSG00000250343	CTC-255N20.1	5:146559766-146614422	OK	3.23806	0.993385	-1.7047	-1.9836	0.0035	0.3731
ENSG00000136244	ENSG00000136244	IL6	7:22765013-22771621	OK	5.02845	1.51731	-1.7286	-1.91983	0.00095	0.207143
ENSG00000133636	ENSG00000133636	NTS	12:86268072-86276770	OK	1.45476	0.434451	-1.74351	-1.66134	0.00715	0.525966
ENSG00000023445	ENSG00000023445	BIRC3	11:102188214-102210134	OK	4.13371	1.08253	-1.93303	-2.26856	5.00E-05	0.0312848
ENSG00000081041	ENSG00000081041	CXCL2	4:74962751-74965010	OK	14.0676	3.5472	-1.98762	-3.14041	5.00E-05	0.0312848
ENSG00000188783	ENSG00000188783	PRELP	1:203444955-203460480	OK	4.36771	1.01705	-2.10248	-3.80575	5.00E-05	0.0312848
ENSG00000227036	ENSG00000227036	LINC00511	17:70319263-70636611	OK	66.6256	14.7663	-2.17377	-3.78493	5.00E-05	0.0312848

Table 6C. Differential expression of transcripts upon siRNA knockdown of *SLNCR* in WM1976

Table 6C lists differentially regulated transcripts and includes Log2 (fold change) from previous RNA-seq experiments in which only *SLNCR1* was depleted. *SLNCR* is italicized. Genes in white boxes are also significantly dysregulated upon *SLNCR1* knockdown (p-value < 0.01), and genes in grey are not significantly dysregulated. Genes highlighted in bold font are significantly dysregulated upon knockdown of both *SLNCR* and *SLNCR1*, but in opposing directions.

gene	log2(fold_change) si-*SLNCR*	p_value	log2(fold_change) si-*SLNCR1*	p-value
LINC00511/SLNCR	*-2.17377*	*5.00E-05*	*-1.285961044*	*7.22542E-15*
ANKRD52	-0.695213	0.00545	-1.167074788	4.27813E-14
CDK19	-0.895808	0.00665	-1.50760447	1.53237E-11
DESI2	0.941009	5.00E-05	1.028630413	1.25232E-10
NOV	1.27015	5.00E-05	0.924282425	4.37855E-09
COL15A1	-1.26554	0.00025	-1.38020291	1.38048E-08
ACVR2B	-1.0825	0.0022	-0.95786338	1.79291E-08
SMIM15	1.72303	5.00E-05	0.872592076	3.69797E-07
DRAM1	0.809324	0.0079	0.967167703	3.75789E-07
JUN	0.897808	0.00095	0.812247613	1.38357E-06
TMEM2	0.829844	0.0073	0.70062641	3.60295E-06
PIGA	-0.941392	0.0043	-0.714024654	6.81504E-05
GADD45A	1.03814	0.00035	0.676346577	7.24128E-05
AKAP12	-0.925125	0.0002	-0.627994089	7.27494E-05
NAA50	0.958582	0.00705	0.610151367	8.15928E-05
RAB31	**0.81993**	**0.00635**	**-0.748412548**	**8.4259E-05**
ITGB1	**0.853703**	**0.00085**	**-0.616082372**	**0.000150832**
ANXA1	1.6086	5.00E-05	0.579131421	0.000531153
FERMT2	0.839753	0.0023	0.617463973	0.000607989
SESN1	1.08837	0.0001	0.662583976	0.000630562
CXCL1	**-1.28746**	**5.00E-05**	**0.572907828**	**0.000864034**
SSU72	0.772586	0.00235	0.527320347	0.000881997
FN1	**-0.857003**	**0.0037**	**0.472680187**	**0.001137893**
AMOTL2	0.969322	0.0002	0.515514275	0.001168983
PABPC4	0.748888	0.008	0.489621381	0.001378736
KCNAB2	0.995352	0.00585	0.492931013	0.002036119
FAM129A	0.753693	0.00225	0.457282085	0.002285646
KIF6	-1.02453	0.00555	-0.613100138	0.00287593
IL6	-1.7286	0.00095	-1.592393299	0.003290389
ITGA4	-0.921764	0.0011	-0.470147297	0.003930652

gene	log2(fold_change) si-*SLNCR*	p_value	log2(fold_change) si-*SLNCR1*	p-value
TMEM45A	**-1.54338**	**0.00425**	**0.832356565**	**0.004178168**
EGF	1.02778	0.0035	0.565121552	0.004438497
GDF15	0.766015	0.0091	0.417071189	0.004698661
GNPNAT1	**1.23998**	**0.00025**	**-0.535381278**	**0.00498145**
GPR158	-1.14329	0.0035	-0.448971795	0.005365547
ARNT	-0.85408	0.0065	-0.444021763	0.00570904
DUSP2	1.11866	0.00385	0.585791873	0.005764055
PPP2R2B	-1.33182	0.00405	-0.856619484	0.007448253
PHLDA3	0.732594	0.00385	0.39815139	0.009024771
CDKN1A	0.986566	0.0002	0.387287319	0.009123289
TNFRSF12A	0.956506	0.00025	0.434342522	0.009219318
MPZL3	2.05851	0.00325	1.178855055	0.00959217
PPAP2C	1.33881	5.00E-05	0.450881224	0.010118858
HMGCL	-0.97512	0.00365	-0.530459066	0.010451972
ATP6V1A	0.855479	0.00055	0.396109524	0.010879154
NMRK1	-1.53615	0.0007	-0.576847173	0.012050043
CCDC71L	0.996121	0.0004	0.448355712	0.012726161
PAFAH2	-1.19584	0.00555	-0.492924255	0.013111023
MYOF	0.833	0.0035	0.390467698	0.014627438
JDP2	1.30723	0.00445	0.530329237	0.016617277
CCND1	0.906462	0.00125	0.347076276	0.01672786
PTPRF	1.05376	5.00E-05	0.379680639	0.019419209
FSCN1	1.10657	0.00275	0.671248406	0.019580805
PRR5	0.9682	0.0083	0.517793373	0.020347763
FAM161A	-0.899016	0.00305	-0.385397876	0.021133885
MYB	-1.01097	0.00295	-0.555620362	0.021729996
CTNNA2	-0.904134	0.00115	-0.373611856	0.022402971
LRP12	0.915894	0.0066	0.359502382	0.024262057
MICB	0.984358	0.00715	0.481255484	0.025033227
RUNX1	-1.11221	0.0022	-0.371405061	0.026862062
CERKL	-1.04869	0.00145	-0.482093615	0.027101144
FSTL5	-1.05762	0.00945	-0.520124692	0.029337431
KRT86	3.18847	0.003	0.786445171	0.030276931
RAB33A	1.5452	0.00185	-0.904715914	0.031389647
STAT3	-0.876182	0.00145	-0.330575813	0.037525547
PSAT1	0.80377	0.00285	0.309117779	0.046666465
AC104135.4	0.880096	0.00675	0.395526072	0.04763791
BIRC7	0.692021	0.00935	0.295158719	0.047931248
CCNC	1.0683	0.00035	0.332778632	0.051321517
APOE	0.72423	0.0083	0.285558261	0.054817957
DAP	-0.854849	0.00155	0.295141452	0.057296664
TGOLN2	-0.767556	0.0032	0.277762545	0.059630119

gene	log2(fold_change) si-*SLNCR*	p_value	log2(fold_change) si-*SLNCR1*	p-value
NACAD	1.94943	0.0048	-0.813517878	0.061855404
ALCAM	0.793874	0.0054	0.295968254	0.069562282
MCAM	1.22218	5.00E-05	0.26674288	0.069669104
CD36	1.61889	5.00E-05	-0.63508838	0.080898303
MAP4K3	0.695783	0.0087	0.286890925	0.084646654
SFRP1	1.01482	0.00665	0.482509785	0.087622822
KIF15	-0.988477	0.00525	-0.298697476	0.093592021
CDCA5	-0.778741	0.0035	0.257772825	0.094780052
EPHA3	-0.934503	0.0024	-0.300434552	0.098744398
C18orf54	-1.15317	0.00225	-0.309775015	0.099709642
NT5E	2.69894	0.0001	0.607452421	0.102224517
PKP3	2.27591	0.005	-1.779219987	0.108433565
TOR1B	-0.783017	0.00655	-0.265289824	0.116857595
PPAPDC1A	1.16862	0.007	0.286368066	0.118675397
RARG	-0.841934	0.0052	-0.254612863	0.126017553
FAM46A	-0.701499	0.0059	-0.241918067	0.126543197
PROS1	0.831652	0.0015	0.236030423	0.127209612
CCDC85B	0.780179	0.0059	0.237017254	0.130404346
PRELP	-2.10248	5.00E-05	-0.276008312	0.135018084
GALNT6	1.8226	0.00015	0.404843655	0.13725057
SPP1	-0.743508	0.005	0.258503335	0.138263236
MOSPD2	-1.02253	0.0009	-0.244809103	0.147314624
FGFR4	1.07011	0.00115	0.253926678	0.15108101
ZYX	0.823754	0.0024	0.225448945	0.151889606
CDC42EP1	1.04186	0.0007	0.266122534	0.153095755
CHRNA6	1.61985	0.00935	-0.52111827	0.15650924
THBD	1.71871	0.0046	0.414949539	0.157314272
PEG10	-0.814728	0.00105	-0.222240317	0.158303758
DBN1	0.761756	0.00855	0.214056652	0.162631895
CT55	1.25085	0.0021	-0.358673099	0.16714216
CD2AP	-0.740957	0.00275	-0.221602387	0.171160328
PLEKHA2	-1.04475	0.00125	-0.219599644	0.173699319
ZBTB42	0.989613	0.00865	-0.331320946	0.176408587
SH3PXD2B	0.834616	0.00275	0.216777635	0.180640892
PLEK	2.20164	0.0072	1.267498759	0.182933106
CTC-255N20.1	-1.7047	0.0035	-0.383888406	0.183532611
FGFRL1	1.47979	0.0006	-0.320258242	0.185297803
ASNS	0.852571	0.0033	-0.232794969	0.188318273
KCNN4	1.96283	0.00905	-0.578701964	0.19662101
THNSL1	-1.0515	0.00795	-0.366132037	0.200152835
VGF	3.86778	5.00E-05	-0.262651175	0.201549568
CSF1	1.08033	0.00205	0.294887097	0.205788505

gene	log2(fold_change) si-*SLNCR*	p_value	log2(fold_change) si-*SLNCR1*	p-value
METRNL	1.48459	0.00145	-0.354065577	0.207678989
CASP1	1.24045	0.0065	0.516514507	0.20928774
NPDC1	1.5454	0.00845	-0.420987579	0.211094175
CLDN15	-1.49095	0.003	-0.308090806	0.213401906
NPTXR	1.80073	0.0006	0.470325452	0.218810758
LIMS2	1.34689	0.0013	0.294995524	0.220197726
CXCL5	-1.16897	0.00965	1.720620747	0.220840902
ADAM11	0.982605	0.0071	0.209412908	0.221608577
LGR4	0.862522	0.00305	-0.230361019	0.230530617
WWC2	0.974883	0.00315	-0.225666104	0.232422982
CCL2	-1.70123	0.002	2.597249175	0.238215361
DYRK3	0.992011	0.00015	0.201025102	0.238315987
ARHGAP19	-1.10659	0.0009	-0.216221554	0.245650216
SLAMF7	2.67578	5.00E-05	0.214628287	0.249041966
NXN	1.55322	0.00645	-0.340635633	0.249773127
MELK	-0.842489	0.0039	0.183840856	0.266333692
CEBPD	-1.41207	5.00E-05	0.188339719	0.270353854
PLA1A	-0.770135	0.00585	-0.185163304	0.279393631
CKMT1B	1.78206	0.0047	0.856472551	0.281028338
BIRC3	-1.93303	5.00E-05	-0.686225959	0.286914861
PTK7	1.32605	5.00E-05	0.207991924	0.294387119
ELF4	0.976396	0.00555	0.217878837	0.294655618
PAQR8	-0.856361	0.00395	-0.16831091	0.311071402
ELOVL5	-0.948598	0.0016	0.148418763	0.316150322
SCML4	-1.20948	0.00065	-0.205486305	0.317230296
NFATC1	1.23483	0.0009	-0.201222064	0.320040828
ISG20	1.71257	0.0083	0.324651023	0.33274382
MEGF9	-0.787752	0.002	-0.151748231	0.334620233
PSG9	1.97022	0.00305	0.48258437	0.337514995
CRYL1	-0.731754	0.006	-0.16336169	0.346418374
SLC36A1	0.957393	0.00265	0.160296911	0.35184282
FAM20B	-1.35833	5.00E-05	-0.143830431	0.359822035
HAS2	-0.74332	0.0053	-0.141949297	0.374959066
ZNF322	-1.19528	0.00515	-0.271908915	0.375514271
RGS2	1.06142	0.00015	0.181540524	0.376829991
KB-1460A1.5	1.38242	0.0076	-0.51052547	0.377466494
EPHA2	1.53998	5.00E-05	0.1488126	0.385772044
DCHS1	1.42634	0.00085	-0.321342877	0.392779844
MRGPRX4	2.59106	0.00245	0.372289432	0.393433449
SCARF2	1.32702	0.00055	0.135411437	0.395119606
TGDS	-1.00998	0.00055	-0.152231707	0.397073404
SHC2	0.987918	0.0066	-0.135444272	0.417496273

gene	log2(fold_change) si-*SLNCR*	p_value	log2(fold_change) si-*SLNCR1*	p-value
SEPT4	-1.09994	0.00025	-2.268467801	0.426337286
OVAAL	1.9135	0.0031	-0.48218541	0.43572954
DPYSL3	-0.935674	0.001	0.123831869	0.440689619
ITLN2	1.1352	0.0037	0.218442311	0.446165724
SIVA1	-0.784188	0.00865	0.119719871	0.447558795
LRRC20	-1.17826	0.0026	-0.129920579	0.456843898
RBPMS2	1.18411	0.0054	-0.214427576	0.461586519
GYG2	-0.797324	0.00555	-0.115365601	0.465345999
KLHDC8B	0.859313	0.0093	0.123830925	0.466530002
PAPSS2	1.12571	0.00425	-0.151115412	0.477985187
MICAL2	0.922706	0.00945	-0.129978541	0.478109315
RP11-295G20.2	-0.8357	0.0029	0.127126837	0.479906604
CXCL2	-1.98762	5.00E-05	0.545671862	0.487213263
NGFR	2.04548	5.00E-05	-0.11325294	0.496373519
VSTM2B	1.08379	5.00E-05	0.102675642	0.509732775
FAM83H	0.902631	0.0031	0.106632975	0.514773998
TNFRSF21	-0.820761	0.00105	0.09403426	0.514808091
MARC1	1.81248	0.0016	Inf	0.532980753
CENPU	-0.963431	0.00445	-0.104776418	0.537622778
NFKBIA	-0.848248	0.00105	-0.108988098	0.565980493
C1QTNF4	2.72704	0.00625	-0.612568153	0.581848469
ITGA5	1.76539	0.00135	-0.165976483	0.584873624
GZMM	1.79598	0.002	0.267429761	0.586451513
TAPBP	-0.834637	0.00455	0.082595915	0.588492373
PTCHD4	0.782898	0.0076	0.098372374	0.58939194
ITGA3	1.00127	0.0002	0.073164847	0.603581226
KIF14	-0.992889	0.00025	-0.085707824	0.603932536
PNLIPRP3	1.80088	0.0001	-0.194607225	0.609588422
NEDD1	-0.892359	0.00255	-0.083743828	0.62289139
HMMR	-1.22777	0.00085	-0.092410363	0.644345493
NTS	-1.74351	0.00715	-0.298071822	0.646312566
B2M	1.88012	0.0072	0.683799864	0.64683022
EXO1	-0.85128	0.0098	0.071720043	0.651739358
IGFBP3	-1.02549	5.00E-05	0.061586825	0.668525742
DLX1	-1.03772	0.0078	-0.070654407	0.67587728
FABP3	1.62296	0.00015	-0.150425979	0.6782384
MOCS2	-0.911381	0.001	0.063904032	0.681827104
MT2A	-0.908396	0.00465	0.076598901	0.69640878
SLC30A1	0.889494	0.0005	-0.060354902	0.704165113
IGFBP5	-1.56452	0.00625	0.073098249	0.707374293
CIT	-1.03149	0.00225	-0.055595046	0.727807666
CENPQ	-0.961787	0.00315	-0.068369313	0.742529149

gene	log2(fold_change) si-*SLNCR*	p_value	log2(fold_change) si-*SLNCR1*	p-value
DIAPH3	-1.14562	0.0001	-0.051080421	0.755551185
TMEM255A	0.926389	0.00245	0.054884051	0.761063047
TMC4	2.3355	0.0033	-0.241870723	0.762500657
VAMP8	1.85971	0.00935	0.308132465	0.769874713
CRABP2	1.33127	0.0004	0.099129194	0.774290433
TBC1D5	-0.803731	0.00815	-0.041029056	0.786724383
TMEM173	1.15952	0.00055	-0.036669132	0.799556083
FSTL1	-1.1412	0.00315	-0.031298105	0.817459043
CXCL3	-1.46721	0.00755	-0.206882296	0.83732663
FAM107B	1.19872	0.00805	0.102009774	0.840086966
UBE3D	1.11149	0.00615	0.075608242	0.85276652
RCN1	0.801218	0.004	-0.028594596	0.863138482
H19	1.14527	0.0028	0.03192378	0.883234477
OPTN	-0.814413	0.0032	-0.020699887	0.883995787
MDK	1.04855	0.0006	0.020890954	0.911598118
PPARG	1.39203	0.0006	-0.05156778	0.912344048
IL24	2.51155	5.00E-05	-0.030781859	0.940771945
HLF	1.69126	0.00925	-0.042030951	0.940775968
TMEM59	-0.789927	0.00255	-0.01942485	0.951856753
LRRC4B	1.93448	0.00015	-0.00926973	0.96332828
STC1	-1.14735	0.0054	0.003900326	0.989544813
PMM1	-0.749252	0.0065	-0.012315264	0.996502931
ASF1B	-1.21806	0.00185	0.005813463	0.999444169
KRT18	0.999441	0.00415	-0.004067504	1
SHF	1.51302	0.004	0.019547477	1

Table 6D. Correlation of *SLNCR*, *AR* and *EGR1* expression with *SLNCR* target genes

Table 6D lists spearman correlation coefficient, confidence intervals, and p-values for *SLNCR*, *AR* or *EGR1* gene expression with *SLNCR* target genes (identified via RNA-seq). Within *AR* gene correlations, genes that are bound by AR (as determined by ChIP-seq) are highlighted in bold font.

target gene	Spearman r (SLNCR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (AR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (EGR1)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)
ACVR2B	0.1071	0,01324 to 0,1991	0.0214	Yes	No	0.02104	-0,07311 to 0,1148	0.6523	No	No	0.1037	0,009796 to 0,1958	0.026	Yes	No

target gene	Spearman r (SLNCR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (AR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (EGR1)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)
ADAM11	-0.0805	-0,1732 to 0,01362	0.0843	No	No	-0.1338	-0,225 to -0,04028	0.004	Yes	No	-0.1074	-0,1994 to -0,01348	0.0211	Yes	No
AKAP12	0.2295	0,1385 to 0,3167	<0,0001	Yes	Yes	0.2566	0,1666 to 0,3423	<0,0001	Yes	Yes	0.2448	0,1543 to 0,3312	<0,0001	Yes	Yes
ALCAM	0.1564	0,06328 to 0,2467	0.0008	Yes	No	**0.2302**	**0,1392 to 0,3174**	**<0,0001**	**Yes**	**Yes**	0.2733	0,184 to 0,3581	<0,0001	Yes	Yes
AMOTL2	-0.0367	-0,1303 to 0,05751	0.4319	No	No	0.07034	-0,02383 to 0,1633	0.1316	No	No	0.1595	0,06646 to 0,2497	0.0006	Yes	No
ANKRD52	0.1246	0,03098 to 0,2161	0.0074	Yes	No	**0.1087**	**0,01482 to 0,2006**	**0.0196**	**Yes**	**No**	0.08062	-0,01349 to 0,1733	0.0838	No	No
ANXA1	0.1644	0,07153 to 0,2545	0.0004	Yes	No	0.2281	0,137 to 0,3154	<0,0001	Yes	Yes	0.2722	0,1829 to 0,3571	<0,0001	Yes	Yes
APOE	0.04614	-0,04808 to 0,1395	0.3229	No	No	-0.07016	-0,1631 to 0,02401	0.1326	No	No	-0.09974	-0,192 to -0,005785	0.0323	Yes	No
AR	0.06916	-0,02501 to 0,1621	0.1381	No	No	1	1 to 1	<0,0001	Yes	Yes	0.278	0,1889 to 0,3625	<0,0001	Yes	Yes
ARHGAP19	0.1368	0,04331 to 0,2279	0.0033	Yes	No	0.1685	0,07566 to 0,2584	0.0003	Yes	No	0.3353	0,2491 to 0,4162	<0,0001	Yes	Yes
ARNT	0.1504	0,05717 to 0,241	0.0012	Yes	No	**0.2647**	**0,175 to 0,35**	**<0,0001**	**Yes**	**Yes**	0.232	0,1411 to 0,3191	<0,0001	Yes	Yes
ASF1B	-0.02055	-0,1143 to 0,0736	0.6598	No	No	**-0.08693**	**-0,1795 to 0,007145**	**0.0622**	**No**	**No**	-0.05356	-0,1468 to 0,04065	0.2511	No	No
ASNS	-0.07971	-0,1724 to 0,01441	0.0873	No	No	0.161	0,06804 to 0,2512	0.0005	Yes	No	0.1721	0,07939 to 0,2619	0.0002	Yes	Yes
ATP6V1A	0.204	0,1122 to 0,2924	<0,0001	Yes	Yes	**0.2208**	**0,1295 to 0,3084**	**<0,0001**	**Yes**	**Yes**	0.08763	-0,006434 to 0,1802	0.0601	No	No
B2M	0.03778	-0,05643 to 0,1313	0.4184	No	No	**0.2318**	**0,1408 to 0,3188**	**<0,0001**	**Yes**	**Yes**	0.06242	-0,03177 to 0,1555	0.1809	No	No
BIRC3	0.01115	-0,08295 to 0,105	0.8114	No	No	**0.2129**	**0,1276 to 0,3067**	**<0,0001**	**Yes**	**Yes**	0.1543	0,06115 to 0,2447	0.0009	Yes	No
BIRC7	0.01016	-0,08393 to 0,1041	0.8278	No	No	-0.2101	-0,2981 to -0,1183	<0,0001	Yes	Yes	-0.2136	-0,3015 to -0,122	<0,0001	Yes	Yes
C18orf54	0.1289	0,0353 to 0,2202	0.0056	Yes	No	**0.1876**	**0,09529 to 0,2768**	**<0,0001**	**Yes**	**Yes**	0.1773	0,08469 to 0,2669	0.0001	Yes	Yes
C1QTNF4	0.1702	0,07747 to 0,2601	0.0002	Yes	Yes	0.1347	0,04119 to 0,2258	0.0038	Yes	No	0.06178	-0,03242 to 0,1549	0.1854	No	No
CASP1	-0.07049	-0,1634 to 0,02367	0.1307	No	No	0.2189	0,1275 to 0,3066	<0,0001	Yes	Yes	-0.001238	-0,09524 to 0,09278	0.9788	No	No
CCDC71L	0.07595	-0,01819 to 0,1688	0.1034	No	No	0.09642	0,002425 to 0,1887	0.0385	Yes	No	0.1107	0,01688 to 0,2026	0.0174	Yes	No
CCDC85B	-0.1639	-0,254 to -0,07098	0.0004	Yes	No	**-0.145**	**-0,2358 to -0,05172**	**0.0018**	**Yes**	**No**	-0.02664	-0,1203 to 0,06754	0.5684	No	No
CCL2	-0.1386	-0,2296 to -0,04519	0.0029	Yes	No	0.2571	0,1672 to 0,3429	<0,0001	Yes	Yes	0.2302	0,1392 to 0,3174	<0,0001	Yes	Yes
CCNC	0.1075	0,01367 to 0,1995	0.0209	Yes	No	0.2655	0,1759 to 0,3507	<0,0001	Yes	Yes	0.1447	0,05136 to 0,2355	0.0018	Yes	No
CCND1	0.04128	-0,05293 to 0,1348	0.3765	No	No	0.1151	0,0213 to 0,2069	0.0134	Yes	No	0.02008	-0,07408 to 0,1139	0.6673	No	No
CD2AP	0.16	0,06697 to 0,2502	0.0006	Yes	No	0.2112	0,1195 to 0,2992	<0,0001	Yes	Yes	0.1497	0,05645 to 0,2403	0.0013	Yes	No
CD36	0.04913	-0,04509 to 0,1425	0.2925	No	No	0.3611	0,2765 to 0,4402	<0,0001	Yes	Yes	0.2187	0,1273 to 0,3064	<0,0001	Yes	Yes
CDC42EP1	-0.06819	-0,1612 to 0,02599	0.1438	No	No	0.01549	-0,07863 to 0,1093	0.7401	No	No	0.1107	0,0169 to 0,2026	0.0174	Yes	No
CDCA5	0.01064	-0,08346 to 0,1045	0.8198	No	No	**0.0283**	**-0,122 to 0,06589**	**0.5444**	**No**	**No**	0.01305	-0,08107 to 0,1069	0.78	No	No
CDK19	0.2232	0,132 to 0,3107	<0,0001	Yes	Yes	**0.2709**	**0,1815 to 0,3559**	**<0,0001**	**Yes**	**Yes**	0.2208	0,1295 to 0,3084	<0,0001	Yes	Yes
CDKN1A	0.05994	-0,03427 to 0,1531	0.1989	No	No	**0.0709**	**-0,02323 to 0,1639**	**0.1283**	**No**	**No**	0.1135	0,01969 to 0,2053	0.0148	Yes	No
CEBPD	-0.1034	-0,1955 to -0,009494	0.0264	Yes	No	**0.0901**	**-0,003904 to 0,1826**	**0.0531**	**No**	**No**	0.1157	0,02192 to 0,2074	0.0129	Yes	No
CENPQ	0.1336	0,04006 to 0,2248	0.0041	Yes	No	0.1718	0,07921 to 0,2617	0.0002	Yes	Yes	0.1248	0,0312 to 0,2163	0.0073	Yes	No

target gene	Spearman r (SLNCR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (AR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (EGR1)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)
CENPU	0.1714	0,07862 to 0,2612	0.0002	Yes	Yes	-0.01943	-0,1132 to 0,07471	0.6773	No	No	0.00832	-0,08576 to 0,1023	0.8586	No	No
CERKL	0.05155	-0,04267 to 0,1449	0.2694	No	No	0.1913	0,09908 to 0,2803	<0,0001	Yes	Yes	0.1674	0,07454 to 0,2573	0.0003	Yes	No
CHRNA6	0.1447	0,05135 to 0,2355	0.0018	Yes	No	0.1845	0,09204 to 0,2737	<0,0001	Yes	Yes	0.09659	0,002605 to 0,1889	0.0382	Yes	No
CIT	0.04982	-0,0444 to 0,1432	0.2857	No	No	**0.00689**	**-0,1008 to 0,08718**	**0.8827**	**No**	**No**	-0.0332	-0,1268 to 0,061	0.477	No	No
CKMT1B	0.02869	-0,06549 to 0,1224	0.5388	No	No	-0.03361	-0,1272 to 0,06059	0.4716	No	No	-0.1035	-0,1956 to -0,00957	0.0263	Yes	No
CLDN15	0.08394	-0,01015 to 0,1766	0.0718	No	No	**0.1372**	**0,04374 to 0,2283**	**0.0032**	**Yes**	**No**	0.06238	-0,03182 to 0,1555	0.1812	No	No
COL15A1	0.1272	0,0336 to 0,2186	0.0062	Yes	No	0.3662	0,2819 to 0,4449	<0,0001	Yes	Yes	0.1589	0,06587 to 0,2492	0.0006	Yes	No
CRABP2	0.1335	0,04002 to 0,2247	0.0041	Yes	No	0.2329	0,142 to 0,3199	<0,0001	Yes	Yes	0.09991	0,005956 to 0,1921	0.032	Yes	No
CREB1	0.07	-0,02417 to 0,1629	0.1334	No	No	0.2661	0,1765 to 0,3513	<0,0001	Yes	Yes	0.2388	0,1481 to 0,3255	<0,0001	Yes	Yes
CRYL1	0.3455	0,26 to 0,4257	<0,0001	Yes	Yes	**0.04151**	**-0,0527 to 0,135**	**0.3738**	**No**	**No**	-0.003277	-0,09726 to 0,09076	0.9441	No	No
CSF1	-0.1599	-0,2502 to -0,06693	0.0006	Yes	No	0.1913	0,09906 to 0,2803	<0,0001	Yes	Yes	0.08397	-0,01013 to 0,1766	0.0717	No	No
CT55	0.03991	-0,0543 to 0,1334	0.3926	No	No	0.06629	-0,02789 to 0,1593	0.1553	No	No	-0.007392	-0,1013 to 0,08668	0.8742	No	No
CTNNA2	0.1705	0,07772 to 0,2603	0.0002	Yes	Yes	0.09992	0,005964 to 0,1921	0.032	Yes	No	0.04431	-0,04991 to 0,1378	0.3424	No	No
CXCL1	0.04151	-0,05271 to 0,135	0.3739	No	No	-0.05572	-0,149 to 0,03849	0.2325	No	No	0.01397	-0,08015 to 0,1078	0.7648	No	No
CXCL2	-0.02222	-0,116 to 0,07194	0.6342	No	No	**0.1267**	**0,03305 to 0,2181**	**0.0065**	**Yes**	**No**	0.2551	0,1651 to 0,3409	<0,0001	Yes	Yes
CXCL3	-0.001567	-0,09556 to 0,09246	0.9732	No	No	0.02662	-0,06756 to 0,1203	0.5686	No	No	0.1294	0,03579 to 0,2207	0.0054	Yes	No
CXCL5	0.00579	-0,08827 to 0,09975	0.9013	No	No	0.09287	-0,001157 to 0,1853	0.0463	Yes	No	0.09839	0,004414 to 0,1906	0.0347	Yes	No
DAP	0.06861	-0,02556 to 0,1616	0.1413	No	No	**0.205**	**0,1132 to 0,2934**	**<0,0001**	**Yes**	**Yes**	0.1118	0,01796 to 0,2037	0.0163	Yes	No
DBN1	-0.02508	-0,1188 to 0,06909	0.5911	No	No	**0.1972**	**0,1051 to 0,2859**	**<0,0001**	**Yes**	**Yes**	0.1881	0,09579 to 0,2772	<0,0001	Yes	Yes
DCHS1	0.09732	0,003335 to 0,1896	0.0367	Yes	No	0.3576	0,2727 to 0,4369	<0,0001	Yes	Yes	0.3114	0,224 to 0,3939	<0,0001	Yes	Yes
DESI2	0.2069	0,1152 to 0,2952	<0,0001	Yes	Yes	0.1903	0,09805 to 0,2793	<0,0001	Yes	Yes	0.2094	0,1177 to 0,2975	<0,0001	Yes	Yes
DIAPH3	0.1881	0,09574 to 0,2772	<0,0001	Yes	Yes	**0.1129**	**0,01913 to 0,2048**	**0.0153**	**Yes**	**No**	0.1706	0,07782 to 0,2604	0.0002	Yes	Yes
DLX1	0.1178	0,0241 to 0,2095	0.0113	Yes	No	**0.1213**	**0,02763 to 0,2129**	**0.0091**	**Yes**	**No**	0.1055	0,01164 to 0,1976	0.0234	Yes	No
DPYSL3	0.0936	-0,000412 6 to 0,186	0.0446	Yes	No	0.3855	0,3024 to 0,4627	<0,0001	Yes	Yes	0.216	0,1245 to 0,3038	<0,0001	Yes	Yes
DRAM1	0.001976	-0,09205 to 0,09597	0.9663	No	No	**0.2152**	**0,1237 to 0,3031**	**<0,0001**	**Yes**	**Yes**	0.1276	0,03399 to 0,219	0.0061	Yes	No
DUSP2	-0.1817	-0,2711 to -0,08924	<0,0001	Yes	Yes	0.02909	-0,0651 to 0,1228	0.5333	No	No	0.1879	0,09554 to 0,277	<0,0001	Yes	Yes
DYRK3	0.0009958	-0,08413 to 0,1039	0.8311	No	No	**0.1077**	**0,01386 to 0,1997**	**0.0207**	**Yes**	**No**	0.1209	0,02723 to 0,2125	0.0093	Yes	No
EGF	0.2182	0,1268 to 0,3059	<0,0001	Yes	Yes	0.05938	-0,03483 to 0,1525	0.2032	No	No	0.004361	-0,08969 to 0,09833	0.9256	No	No
EGR1	0.002511	-0,09152 to 0,0965	0.9571	No	No	0.278	0,1889 to 0,3625	<0,0001	Yes	Yes	1	1 to 1	<0,0001	Yes	Yes

target gene	Spearman r (SLNCR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (AR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (EGR1)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)
ELF4	-0.2202	-0,3079 to -0,1289	<0,0001	Yes	Yes	0.2202	0,1289 to 0,3079	<0,0001	Yes	Yes	0.02039	-0,07376 to 0,1142	0.6623	No	No
ELOVL5	0.07492	-0,01923 to 0,1678	0.1082	No	No	**0.23049**	**0,144 to 0,3218**	**<0,0001**	Yes	Yes	0.166	0,07316 to 0,256	0.0003	Yes	No
EPHA2	0.07716	-0,01698 to 0,1699	0.098	No	No	**0.02761**	**-0,06658 to 0,1213**	**0.5543**	No	No	0.123	0,02931 to 0,2145	0.0082	Yes	No
EPHA3	0.1468	0,05354 to 0,2375	0.0016	Yes	No	**0.3473**	**0,2619 to 0,4274**	**<0,0001**	Yes	Yes	0.2878	0,1992 to 0,3717	<0,0001	Yes	Yes
ESR1	0.1261	0,03251 to 0,2176	0.0067	Yes	No	0.3344	0,2482 to 0,4153	<0,0001	Yes	Yes	0.07263	-0,02153 to 0,1655	0.1194	No	No
EXO1	-0.1543	0,06113 to 0,2447	0.0009	Yes	No	**-0.02497**	**-0,1187 to 0,0692**	**0.5928**	No	No	-0.02248	-0,1162 to 0,07168	0.6302	No	No
FABP3	-0.208	-0,2962 to -0,1163	<0,0001	Yes	Yes	-0.05321	-0,1465 to 0,041	0.2542	No	No	-0.1013	-0,1935 to -0,007354	0.0297	Yes	No
FAM107B	-0.1898	-0,2789 to -0,09756	<0,0001	Yes	Yes	0.3341	0,2479 to 0,4151	<0,0001	Yes	Yes	0.2058	0,114 to 0,2942	<0,0001	Yes	Yes
FAM129A	0.07787	-0,01626 to 0,1706	0.0949	No	No	**0.1016**	**0,007645 to 0,1937**	**0.0292**	Yes	No	0.09425	0,0002392 to 0,1866	0.0431	Yes	No
FAM161A	0.2226	0,1313 to 0,3101	<0,0001	Yes	Yes	**0.06372**	**-0,03047 to 0,1568**	**0.172**	No	No	0.02712	-0,06707 to 0,1208	0.5614	No	No
FAM20B	0.3046	0,2168 to 0,3875	<0,0001	Yes	Yes	**0.2108**	**0,1191 to 0,2989**	**<0,0001**	Yes	Yes	0.1545	0,06134 to 0,2449	0.0009	Yes	No
FAM46A	0.2431	0,1526 to 0,3296	<0,0001	Yes	Yes	**0.3036**	**0,2157 to 0,3865**	**<0,0001**	Yes	Yes	0.2185	0,1271 to 0,3062	<0,0001	Yes	Yes
FAM83H	0.06807	-0,02611 to 0,161	0.1445	No	No	-0.0885	-0,181 to 0,005562	0.0576	No	No	-0.07474	-0,1676 to 0,01941	0.109	No	No
FERMT2	0.1019	0,007946 to 0,194	0.0287	Yes	No	**0.2335**	**0,1426 to 0,3204**	**<0,0001**	Yes	Yes	0.2533	0,1632 to 0,3393	<0,0001	Yes	Yes
FGFR4	0.09699	0,003002 to 0,1893	0.0374	Yes	No	-0.0979	-0,1862 to 0,000221	0.0441	Yes	No	0.01948	-0,07467 to 0,1133	0.6765	No	No
FGFRL1	0.1352	0,0417 to 0,2263	0.0036	Yes	No	0.2898	0,2013 to 0,3736	<0,0001	Yes	Yes	0.2258	0,1347 to 0,3132	<0,0001	Yes	Yes
FN1	0.02269	-0,07148 to 0,1165	0.6271	No	No	0.09015	-0,003894 to 0,1826	0.0531	No	No	0.1697	0,07691 to 0,2596	0.0003	Yes	No
FSCN1	0.02261	-0,07155 to 0,1164	0.6282	No	No	**0.07081**	**-0,02336 to 0,1637**	**0.129**	No	No	0.1659	0,07304 to 0,2559	0.0003	Yes	No
FSTL1	0.2064	0,1146 to 0,2947	<0,0001	Yes	Yes	**0.3611**	**0,2765 to 0,4402**	**<0,0001**	Yes	Yes	0.2075	0,1157 to 0,2957	<0,0001	Yes	Yes
FSTL5	0.1424	0,04906 to 0,2333	0.0022	Yes	No	-0.0389	-0,1324 to 0,05532	0.4047	No	No	0.04784	-0,04638 to 0,1412	0.3053	No	No
GADD45A	0.06476	-0,02943 to 0,1578	0.1651	No	No	0.1085	0,01464 to 0,2005	0.0198	Yes	No	0.1783	0,08569 to 0,2678	0.0001	Yes	Yes
GALNT6	-0.002185	-0,09618 to 0,09185	0.9627	No	No	0.1691	0,07635 to 0,259	0.0003	Yes	No	0.1166	0,02288 to 0,2084	0.0122	Yes	No
GDF15	-0.09001	-0,004041 to 0,1825	0.0535	No	No	**-0.1411**	**-0,2321 to -0,04774**	**0.0024**	Yes	No	-0.02745	-0,1211 to 0,06674	0.5567	No	No
GNPNAT1	0.1014	0,007469 to 0,1936	0.0295	Yes	No	0.1277	0,03409 to 0,2191	0.006	Yes	No	0.1628	0,06982 to 0,2529	0.0005	Yes	No
GPR158	0.2672	0,1777 to 0,3524	<0,0001	Yes	Yes	**0.1297**	**0,03609 to 0,221**	**0.0053**	Yes	No	-0.0000344	-0,09405 to 0,09398	0.9994	No	No
GYG2	0.3175	0,2303 to 0,3995	<0,0001	Yes	Yes	0.1265	-0,2179 to -0,03284	0.0066	Yes	No	-0.1549	-0,2453 to -0,06177	0.0008	Yes	No
GZMM	-0.1731	-0,2628 to -0,08038	0.0002	Yes	Yes	0.1067	0,01279 to 0,1987	0.022	Yes	No	0.07685	-0,01729 to 0,1696	0.0994	No	No
H19	-0.1036	-0,1957 to -0,009633	0.0262	Yes	No	0.07678	-0,01736 to 0,1696	0.0997	No	No	0.1247	0,0311 to 0,2162	0.0073	Yes	No
HAS2	0.2396	0,149 to 0,3263	<0,0001	Yes	Yes	0.0366	-0,05761 to 0,1302	0.453	No	No	0.01524	-0,07888 to 0,1091	0.7441	No	No
HLF	0.01439	-0,07973 to 0,1083	0.758	No	No	0.2361	0,1453 to 0,3229	<0,0001	Yes	Yes	0.1645	0,07155 to 0,2545	0.0004	Yes	No

target gene	Spearman r (SLNCR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (AR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (EGR1)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)
HMGCL	0.06018	-0,03402 to 0,1533	0.1971	No	No	-0.0408	-0,1343 to 0,05342	0.3821	No	No	-0.08013	-0,1728 to 0,01399	0.0857	No	No
HMMR	0.09265	-0,001375 to 0,185	0.0468	Yes	No	0.06633	-0,02785 to 0,1594	0.155	No	No	0.09939	0,00543 to 0,1916	0.0329	Yes	No
IGFBP3	0.1336	0,04011 to 0,2248	0.0041	Yes	No	0.1868	0,0944 to 0,2759	<0,0001	Yes	Yes	0.2254	0,1342 to 0,3128	<0,0001	Yes	Yes
IGFBP5	0.1476	0,05437 to 0,2383	0.0015	Yes	No	0.2927	0,2043 to 0,3763	<0,0001	Yes	Yes	0.2331	0,1422 to 0,3201	<0,0001	Yes	Yes
IL24	-0.198	-0,2866 to -0,1059	<0,0001	Yes	Yes	-0.04714	-0,04708 to 0,1405	0.3125	No	No	-0.01581	-0,1097 to 0,07832	0.735	No	No
IL6	-0.00374	-0,09772 to 0,0903	0.9362	No	No	0.1682	0,07543 to 0,2582	0.0003	Yes	No	0.2989	0,2108 to 0,3821	<0,0001	Yes	Yes
ISG20	-0.2124	-0,3004 to -0,1208	<0,0001	Yes	Yes	-0.02964	-0,1233 to 0,06455	0.5255	No	No	-0.02296	-0,1167 to 0,07121	0.623	No	No
ITGA3	0.07816	-0,01597 to 0,1709	0.0937	No	No	0.07278	-0,02137 to 0,1657	0.1186	No	No	0.1461	0,05282 to 0,2369	0.0017	Yes	No
ITGA4	0.05263	-0,04159 to 0,1459	0.2594	No	No	0.2147	0,1232 to 0,3026	<0,0001	Yes	Yes	0.1996	0,1076 to 0,2882	<0,0001	Yes	Yes
ITGA5	-0.1003	-0,1925 to -0,006348	0.0313	Yes	No	0.1922	0,09999 to 0,2811	<0,0001	Yes	Yes	0.1645	0,0716 to 0,2546	0.0004	Yes	No
ITGB1	0.1823	0,08981 to 0,2716	<0,0001	Yes	Yes	0.3114	0,224 to 0,3939	<0,0001	Yes	Yes	0.2959	0,2077 to 0,3794	<0,0001	Yes	Yes
ITLN2	0.083	-0,0111 to 0,1756	0.075	No	No	-0.05237	-0,1457 to 0,04185	0.2618	No	No	-0.05404	-0,1473 to 0,04018	0.2469	No	No
JDP2	-0.000168 7	-0,09418 to 0,09384	0.9971	No	No	0.3449	0,2593 to 0,4252	<0,0001	Yes	Yes	0.2344	0,1436 to 0,3214	<0,0001	Yes	Yes
JUN	-0.06711	-0,1601 to 0,02707	0.1502	No	No	0.2038	0,1119 to 0,2922	<0,0001	Yes	Yes	0.4616	0,3843 to 0,5325	<0,0001	Yes	Yes
KCNAB2	-0.2126	-0,3006 to -0,121	<0,0001	Yes	Yes	-0.2046	-0,293 to -0,1127	<0,0001	Yes	Yes	-0.2161	-0,304 to -0,1246	<0,0001	Yes	Yes
KCNN4	0.05118	-0,04304 to 0,1445	0.2728	No	No	0.08376	-0,01034 to 0,1764	0.0724	No	No	0.1035	0,009592 to 0,1956	0.0263	Yes	No
KIF14	0.1549	0,06174 to 0,2453	0.0008	Yes	No	0.06577	-0,02842 to 0,1588	0.1586	No	No	0.1124	0,01854 to 0,2042	0.0158	Yes	No
KIF15	0.1357	0,0422 to 0,2268	0.0035	Yes	No	0.06504	-0,02915 to 0,1581	0.1633	No	No	0.1294	0,03579 to 0,2207	0.0054	Yes	No
KIF6	0.1565	0,06343 to 0,2469	0.0007	Yes	No	-0.1151	-0,2069 to -0,02132	0.0134	Yes	No	-0.0002734	-0,09428 to 0,09374	0.9953	No	No
KLHDC8B	-0.01375	-0,1076 to 0,08037	0.7685	No	No	-0.01752	-0,1114 to 0,07661	0.7075	No	No	-0.05117	-0,1445 to 0,04304	0.2729	No	No
KRT18	-0.03747	-0,131 to 0,05675	0.4222	No	No	-0.04608	-0,1395 to 0,04814	0.3236	No	No	0.1216	0,02794 to 0,2132	0.0089	Yes	No
KRT86	-0.04236	-0,1358 to 0,05186	0.3642	No	No	0.1702	0,07738 to 0,26	0.0002	Yes	Yes	0.03722	-0,05699 to 0,1308	0.4253	No	No
LGR4	0.2687	0,1792 to 0,3538	<0,0001	Yes	Yes	0.2616	0,1719 to 0,3471	<0,0001	Yes	Yes	0.2299	0,1389 to 0,3171	<0,0001	Yes	Yes
LIMS2	-0.2059	-0,2942 to -0,114	<0,0001	Yes	Yes	-0.09456	-0,000548 1 to 0,1869	0.0424	Yes	No	-0.0316	-0,1252 to 0,0626	0.4985	No	No
LRP12	0.2013	0,1094 to 0,2898	<0,0001	Yes	Yes	0.254	0,1639 to 0,3399	<0,0001	Yes	Yes	0.2439	0,1534 to 0,3303	<0,0001	Yes	Yes
LRRC20	0.03021	-0,06399 to 0,1239	0.5176	No	No	0.1193	0,0256 to 0,211	0.0103	Yes	No	0.1297	0,03617 to 0,2211	0.0053	Yes	No
LRRC4B	-0.1416	-0,2325 to -0,04818	0.0023	Yes	No	0.05044	-0,04378 to 0,1438	0.2798	No	No	0.09476	0,0007502 to 0,1871	0.042	Yes	No
MAP4K3	0.1754	0,08272 to 0,265	0.0002	Yes	Yes	0.153	0,05989 to 0,2435	0.001	Yes	No	0.1656	0,0727 to 0,2556	0.0004	Yes	No
MARC1"	0.07806	-0,01607 to 0,1708	0.0941	No	No	0.07388	-0,02028 to 0,1667	0.1132	No	No	-0.003183	-0,09717 to 0,09086	0.9457	No	No

target gene	Spearman r (SLNCR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (AR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (EGR1)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)
MCAM	0.2765	0,1873 to 0,3611	<0,0001	Yes	Yes	-0.0257	-0,1194 to 0,06848	0.582	No	No	-0.01044	-0,1043 to 0,08366	0.8232	No	No
MDK	0.0744	-0,01975 to 0,1672	0.1106	No	No	0.04213	-0,05209 to 0,1356	0.3668	No	No	0.1133	0,01954 to 0,2052	0.0149	Yes	No
MEGF9	0.3485	0,2631 to 0,4285	<0,0001	Yes	Yes	0.2238	0,1326 to 0,3113	<0,0001	Yes	Yes	0.2301	0,1391 to 0,3172	<0,0001	Yes	Yes
MELK	0.01722	-0,07691 to 0,1111	0.7122	No	No	0.00087	-0,09315 to 0,09487	0.9851	No	No	0.01697	-0,07716 to 0,1108	0.7162	No	No
METRNL	0.005638	-0,08842 to 0,0996	0.9039	No	No	0.1756	0,08296 to 0,2652	0.0002	Yes	Yes	0.1229	0,02923 to 0,2144	0.0082	Yes	No
MICAL2	-0.2421	-0,3286 to -0,1515	<0,0001	Yes	Yes	0.2613	0,1715 to 0,3467	<0,0001	Yes	Yes	0.1018	0,007862 to 0,194	0.0289	Yes	No
MICB	-0.1461	-0,2369 to -0,05284	0.0017	Yes	No	0.04831	-0,04591 to 0,1417	0.3006	No	No	0.02142	-0,07274 to 0,1152	0.6464	No	No
MOCS2	0.3097	0,2222 to 0,3923	<0,0001	Yes	Yes	0.2739	0,1846 to 0,3587	<0,0001	Yes	Yes	0.133	0,03949 to 0,2242	0.0042	Yes	No
MOSPD2	0.2847	0,1959 to 0,3689	<0,0001	Yes	Yes	0.2081	0,1164 to 0,2963	<0,0001	Yes	Yes	0.2049	0,113 to 0,2932	<0,0001	Yes	Yes
MPZL3	0.07324	-0,02092 to 0,1661	0.1163	No	No	0.2472	0,1568 to 0,3334	<0,0001	Yes	Yes	0.1085	0,0146 to 0,2004	0.0198	Yes	No
MRGPRX4	0.1752	0,08252 to 0,2648	0.0002	Yes	Yes	0.08256	-0,1752 to 0,01154	0.0766	No	No	0.1171	0,02337 to 0,2088	0.0118	Yes	No
MT2A	0.001464	-0,09256 to 0,09546	0.975	No	No	0.03235	-0,06185 to 0,126	0.4884	No	No	0.1162	0,02248 to 0,208	0.0125	Yes	No
MYB	-0.02111	-0,1149 to 0,07304	0.6512	No	No	0.12081	0,03452 to 0,2195	0.0059	Yes	No	0.007868	-0,08621 to 0,1018	0.8662	No	No
MYOF	-0.07492	-0,1678 to 0,01922	0.1081	No	No	0.2911	0,2027 to 0,3749	<0,0001	Yes	Yes	0.164	0,07103 to 0,254	0.0004	Yes	No
NAA50	0.1086	0,01476 to 0,2006	0.0197	Yes	No	0.2721	0,1827 to 0,357	<0,0001	Yes	Yes	0.1778	0,08524 to 0,2674	0.0001	Yes	Yes
NACAD	0.2196	0,1282 to 0,3073	<0,0001	Yes	Yes	0.13	0,03804 to 0,2228	0.0047	Yes	No	0.08047	-0,01364 to 0,1732	0.0844	No	No
NEDD1	0.1279	0,0343 to 0,2193	0.006	Yes	No	0.2936	0,2052 to 0,3772	<0,0001	Yes	Yes	0.2098	0,1182 to 0,298	<0,0001	Yes	Yes
NFATC1	0.05647	-0,03774 to 0,1497	0.2262	No	No	0.12073	0,03369 to 0,2187	0.0062	Yes	No	0.1309	0,0373 to 0,2221	0.0049	Yes	No
NFKBIA	-0.05978	-0,1529 to 0,03442	0.2001	No	No	0.2117	0,1255 to 0,3048	<0,0001	Yes	Yes	0.1223	0,02866 to 0,2139	0.0085	Yes	No
NGFR	0.09839	0,004422 to 0,1906	0.0347	Yes	No	0.2214	0,1301 to 0,3089	<0,0001	Yes	Yes	0.2499	0,1596 to 0,336	<0,0001	Yes	Yes
NMRK1	0.05365	-0,04057 to 0,1469	0.2503	No	No	0.11091	0,02534 to 0,2107	0.0105	Yes	No	0.0471	-0,04712 to 0,1405	0.3129	No	No
NOV	0.04636	-0,04786 to 0,1398	0.3206	No	No	0.05155	-0,04267 to 0,1449	0.2693	No	No	-0.0651	-0,1581 to 0,02909	0.1629	No	No
NPDC1	-0.1959	-0,2847 to -0,1038	<0,0001	Yes	Yes	0.2881	0,191 to 0,3644	<0,0001	Yes	Yes	0.1966	0,1045 to 0,2853	<0,0001	Yes	Yes
NPTXR	0.009297	-0,08479 to 0,1032	0.8422	No	No	0.2854	0,1966 to 0,3695	<0,0001	Yes	Yes	0.1834	0,09094 to 0,2727	<0,0001	Yes	Yes
NT5E	-0.08421	-0,1768 to 0,009875	0.0708	No	No	0.1801	0,08761 to 0,2696	0.0001	Yes	Yes	0.2033	0,1115 to 0,2918	<0,0001	Yes	Yes
NTS	-0.0221	-0,1159 to 0,07207	0.6361	No	No	0.11059	0,02213 to 0,2076	0.0128	Yes	No	0.1928	0,1006 to 0,2817	<0,0001	Yes	Yes
NXN	0.0151	-0,07903 to 0,109	0.7465	No	No	0.1886	0,09624 to 0,2776	<0,0001	Yes	Yes	0.137	0,04354 to 0,2281	0.0032	Yes	No
OPTN	-0.02723	-0,1209 to 0,06696	0.5598	No	No	0.1247	0,03105 to 0,2162	0.0073	Yes	No	0.007554	-0,08652 to 0,1015	0.8715	No	No
PABPC4	-0.1371	-0,2281 to -0,04361	0.0032	Yes	No	-0.09943	-0,1917 to -0,005473	0.0328	Yes	No	-0.06612	-0,1591 to 0,02807	0.1564	No	No
PAFAH2	0.1443	0,05102 to 0,2352	0.0019	Yes	No	0.1908	0,09856 to 0,2798	<0,0001	Yes	Yes	0.1113	0,01743 to 0,2031	0.0169	Yes	No
PAPSS2	0.02342	-0,07074 to 0,1172	0.6159	No	No	0.2645	0,1748 to 0,3498	<0,0001	Yes	Yes	0.171	0,07821 to 0,2608	0.0002	Yes	Yes

target gene	Spearman r (SLNCR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (AR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (EGR1)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)
PAQR8	0.2664	0,1768 to 0,3516	<0,0001	Yes	Yes	0.1226	0,02893 to 0,2142	0.0084	Yes	No	-0.03315	-0,1268 to 0,06105	0.4776	No	No
PEG10	0.2069	0,1151 to 0,2952	<0,0001	Yes	Yes	0.097	-0,003069 to 0,1834	0.0509	No	No	0.02115	-0,07301 to 0,1149	0.6506	No	No
PHLDA3	0.2174	0,126 to 0,3052	<0,0001	Yes	Yes	-0.04628	-0,1397 to 0,04795	0.3215	No	No	0.03501	-0,0592 to 0,1286	0.4534	No	No
PIGA	0.2277	0,1366 to 0,3149	<0,0001	Yes	Yes	0.1138	0,01997 to 0,2056	0.0145	Yes	No	0.07922	-0,0149 to 0,172	0.0893	No	No
PKP3	0.05643	-0,03778 to 0,1496	0.2265	No	No	0.03095	-0,06325 to 0,1246	0.5075	No	No	0.03298	-0,06123 to 0,1266	0.48	No	No
PLA1A	0.1994	0,1074 to 0,288	<0,0001	Yes	Yes	-0.04559	-0,139 to 0,04863	0.3287	No	No	-0.05561	-0,1488 to 0,03861	0.2334	No	No
PLEK	-0.1784	-0,2679 to -0,08585	0.0001	Yes	Yes	0.2609	0,1711 to 0,3464	<0,0001	Yes	Yes	0.126	0,03241 to 0,2175	0.0067	Yes	No
PLEKHA2	0.13	0,03639 to 0,2213	0.0052	Yes	No	0.2007	0,1088 to 0,2893	<0,0001	Yes	Yes	0.03276	-0,06144 to 0,1264	0.4829	No	No
PLPP2/PPAP2	-0.01895	-0,1128 to 0,0752	0.6849	No	No	0.0819	-0,0122 to 0,1746	0.079	No	No	0.09864	0,004668 to 0,1909	0.0342	Yes	No
PLPP4/PAPDC1A	0.07007	-0,0241 to 0,163	0.133	No	No	0.02335	-0,1171 to 0,07082	0.6171	No	No	-0.07121	-0,1641 to 0,02295	0.1268	No	No
PMM1	0.09102	-0,003017 to 0,1835	0.0508	No	No	-0.1141	-0,2059 to -0,02032	0.0142	Yes	No	-0.08674	-0,1793 to 0,007333	0.0628	No	No
PNLIPRP3	0.07635	-0,01779 to 0,1691	0.1016	No	No	-0.04037	-0,1339 to 0,05385	0.3872	No	No	-0.07214	-0,165 to 0,02202	0.1219	No	No
PPARG	-0.05983	-0,153 to 0,03437	0.1997	No	No	**0.3197**	**0,2327 to 0,4017**	**<0,0001**	**Yes**	**Yes**	0.09993	0,005969 to 0,1921	0.032	Yes	No
PPP2R2B	0.3155	0,2283 to 0,3977	<0,0001	Yes	Yes	**0.2936**	**0,2052 to 0,3772**	**<0,0001**	**Yes**	**Yes**	0.1417	0,0483 to 0,2326	0.0023	Yes	No
PRELP	0.2035	0,1116 to 0,2919	<0,0001	Yes	Yes	**0.1744**	**0,08171 to 0,2641**	**0.0002**	**Yes**	**Yes**	-0.01463	-0,1085 to 0,07949	0.754	No	No
PROS1	0.2175	0,1261 to 0,3053	<0,0001	Yes	Yes	0.1336	0,04009 to 0,2248	0.0041	Yes	No	0.2328	0,1419 to 0,3198	<0,0001	Yes	Yes
PRR5	-0.141	-0,2319 to -0,04761	0.0024	Yes	No	-0.08701	-0,1796 to 0,007056	0.0619	No	No	-0.1338	-0,2249 to -0,04026	0.004	Yes	No
PSAT1	0.0712	-0,02297 to 0,1641	0.1269	No	No	**-0.0288**	**-0,1225 to 0,06539**	**0.5373**	**No**	**No**	-0.07768	-0,1704 to 0,01645	0.0957	No	No
PSG9	-0.09675	-0,189 to -0,002768	0.0378	Yes	No	-0.08206	-0,1747 to 0,01204	0.0784	No	No	0.0249	-0,06928 to 0,1186	0.5939	No	No
PTCHD4	0.3044	0,2165 to 0,3873	<0,0001	Yes	Yes	0.1441	0,0508 to 0,235	0.0019	Yes	No	0.09089	-0,003154 to 0,1833	0.0512	No	No
PTK7	0.07674	-0,01739 to 0,1695	0.0998	No	No	0.07338	-0,02078 to 0,1662	0.1156	No	No	0.14431	0,04972 to 0,2339	0.0021	Yes	No
PTPRF	-0.06738	-0,1604 to 0,02681	0.1486	No	No	**0.1609**	**0,06789 to 0,2511**	**0.0005**	**Yes**	**No**	0.1808	0,08833 to 0,2703	<0,0001	Yes	Yes
RAB31	-0.06962	-0,1626 to 0,02455	0.1355	No	No	0.3408	0,255 to 0,4213	<0,0001	Yes	Yes	0.2212	0,1299 to 0,3088	<0,0001	Yes	Yes
RAB33A	-0.1496	-0,2403 to -0,05642	0.0013	Yes	No	**0.04296**	**-0,05126 to 0,1364**	**0.3574**	**No**	**No**	-0.1074	-0,1994 to -0,01357	0.021	Yes	No
RARG	0.1895	0,09718 to 0,2785	<0,0001	Yes	Yes	**0.2089**	**0,1172 to 0,2971**	**<0,0001**	**Yes**	**Yes**	0.1746	0,08191 to 0,2643	0.0002	Yes	Yes
RBPMS2	0.08213	-0,01197 to 0,1748	0.0781	No	No	0.04922	-0,045 to 0,1426	0.2916	No	No	-0.006975	-0,1009 to 0,08709	0.8813	No	No
RCN1	0.1631	0,0702 to 0,2533	0.0004	Yes	No	**0.2123**	**0,1207 to 0,3003**	**<0,0001**	**Yes**	**Yes**	0.1828	0,09037 to 0,2722	<0,0001	Yes	Yes
RGS2	-0.06089	-0,154 to 0,03331	0.1919	No	No	**0.1207**	**0,02699 to 0,2123**	**0.0095**	**Yes**	**No**	0.2459	0,1554 to 0,3322	<0,0001	Yes	Yes
RUNX1	0.06495	-0,02924 to 0,158	0.1638	No	No	0.3688	0,2847 to 0,4473	<0,0001	Yes	Yes	0.312	0,2246 to 0,3945	<0,0001	Yes	Yes

target gene	Spearman r (SLNCR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (AR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (EGR1)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)
SCARF2	0.134	0,04054 to 0,2252	0.0039	Yes	No	0.03311	-0,06107 to 0,1268	0.4779	No	No	0.1632	0,07029 to 0,2533	0.0004	Yes	No
SCML4	-0.05795	-0,1511 to 0,03626	0.2143	No	No	-0.03423	-0,1278 to 0,05997	0.4634	No	No	-0.1152	-0,207 to -0,02143	0.0133	Yes	No
Sept4"	0.04939	-0,04483 to 0,1427	0.2899	No	No	-0.02618	-0,1199 to 0,068	0.575	No	No	-0.08144	-0,1741 to 0,01267	0.0807	No	No
SESN1	0.2247	0,1335 to 0,3121	<0,0001	Yes	Yes	0.2152	0,1236 to 0,303	<0,0001	Yes	Yes	0.03656	-0,05765 to 0,1301	0.4336	No	No
SFRP1	0.1321	0,03861 to 0,2234	0.0045	Yes	No	0.19	0,09776 to 0,279	<0,0001	Yes	Yes	0.2355	0,1447 to 0,3224	<0,0001	Yes	Yes
SH3PXD2B	-0.08025	-0,173 to 0,01387	0.0852	No	No	0.05316	-0,04106 to 0,1464	0.2547	No	No	0.04966	-0,04456 to 0,143	0.2873	No	No
SHC2	0.01182	-0,08229 to 0,1057	0.8003	No	No	**0.1476**	**0,0543 to 0,2383**	**0.0015**	**Yes**	**No**	0.09326	-0,0007637 to 0,1856	0.0454	Yes	No
SHF	0.1437	0,0504 to 0,2346	0.002	Yes	No	**0.114**	**0,02024 to 0,2058**	**0.0143**	**Yes**	**No**	0.1457	0,05241 to 0,2365	0.0017	Yes	No
SIVA1	0.0222	-0,07196 to 0,116	0.6345	No	No	-0.09338	-0,1858 to 0,0006423	0.0451	Yes	No	-0.07296	-0,1658 to 0,0212	0.1178	No	No
SLAMF7	-0.1893	-0,2784 to -0,09701	<0,0001	Yes	Yes	0.0227	-0,07146 to 0,1165	0.6269	No	No	-0.01567	-0,1095 to 0,07846	0.7372	No	No
SLC30A1	0.1825	0,09005 to 0,2719	<0,0001	Yes	Yes	**0.2512**	**0,161 to 0,3373**	**<0,0001**	**Yes**	**Yes**	0.2132	0,1217 to 0,3012	<0,0001	Yes	Yes
SLC36A1	-0.008233	-0,1022 to 0,08585	0.8601	No	No	**0.2837**	**0,1949 to 0,3679**	**<0,0001**	**Yes**	**Yes**	0.239	0,1483 to 0,3257	<0,0001	Yes	Yes
SLNCR	1	1 to 1	<0,0001	Yes	Yes	0.06916	-0,02501 to 0,1621	0.1381	No	No	0.002511	-0,09152 to 0,0965	0.9571	No	No
SMIM15	0.1645	0,07158 to 0,2546	0.0004	Yes	No	0.2489	0,1586 to 0,335	<0,0001	Yes	Yes	0.2753	0,1861 to 0,36	<0,0001	Yes	Yes
SPP1	0.1732	0,0805 to 0,2629	0.0002	Yes	Yes	0.05704	-0,03717 to 0,1502	0.2216	No	No	0.1539	0,0608 to 0,2444	0.0009	Yes	No
SSU72	-0.1782	-0,2677 to -0,08561	0.0001	Yes	Yes	**-0.1615**	**-0,2517 to -0,06856**	**0.0005**	**Yes**	**No**	-0.1156	-0,2074 to -0,02184	0.013	Yes	No
STAT3	0.2356	0,1448 to 0,3225	<0,0001	Yes	Yes	**0.3477**	**0,2622 to 0,4277**	**<0,0001**	**Yes**	**Yes**	0.2853	0,1965 to 0,3694	<0,0001	Yes	Yes
STC1	0.01186	-0,08225 to 0,1058	0.7996	No	No	0.13634	0,04282 to 0,2274	0.0034	Yes	No	0.2514	0,1612 to 0,3374	<0,0001	Yes	Yes
TAPBP	-0.01133	-0,1052 to 0,08277	0.8082	No	No	**0.1474**	**0,0541 to 0,2381**	**0.0015**	**Yes**	**No**	0.03414	-0,06006 to 0,1277	0.4646	No	No
TBC1D5	0.1508	0,05759 to 0,2414	0.0012	Yes	No	0.2903	0,2018 to 0,3741	<0,0001	Yes	Yes	0.2174	0,126 to 0,3052	<0,0001	Yes	Yes
TGDS	0.4447	0,366 to 0,5171	<0,0001	Yes	Yes	**0.1447**	**0,05135 to 0,2355**	**0.0018**	**Yes**	**No**	0.09785	0,003878 to 0,1901	0.0357	Yes	No
TGOLN2	0.1208	0,02705 to 0,2124	0.0095	Yes	No	**0.2896**	**0,2011 to 0,3735**	**<0,0001**	**Yes**	**Yes**	0.2986	0,2105 to 0,3819	<0,0001	Yes	Yes
THBD	-0.02192	-0,1157 to 0,07224	0.6388	No	No	0.2867	0,198 to 0,3707	<0,0001	Yes	Yes	0.1808	0,08827 to 0,2702	<0,0001	Yes	Yes
THNSL1	0.2219	0,1306 to 0,3095	<0,0001	Yes	Yes	0.1459	0,05257 to 0,2366	0.0017	Yes	No	-0.02416	-0,1179 to 0,07001	0.6048	No	No
TMC4	-0.09554	-0,1879 to -0,001544	0.0403	Yes	No	**0.02171**	**-0,07245 to 0,1155**	**0.642**	**No**	**No**	-0.003394	-0,09737 to 0,09065	0.9421	No	No
TMEM173	-0.05273	-0,146 to 0,04149	0.2586	No	No	0.2617	0,1719 to 0,3472	<0,0001	Yes	Yes	0.2029	0,111 to 0,2913	<0,0001	Yes	Yes
TMEM2	0.04252	-0,0517 to 0,136	0.3624	No	No	**0.1663**	**0,07349 to 0,2564**	**0.0003**	**Yes**	**No**	0.2006	0,1086 to 0,2891	<0,0001	Yes	Yes
TMEM255A	0.1599	0,06692 to 0,2502	0.0006	Yes	No	0.01015	-0,08394 to 0,1041	0.8279	No	No	-0.09941	-0,1916 to -0,005447	0.0329	Yes	No
TMEM45A	0.1792	0,08664 to 0,2687	0.0001	Yes	Yes	**0.1542**	**0,06106 to 0,2447**	**0.0009**	**Yes**	**No**	0.09195	-0,002085 to 0,1844	0.0485	Yes	No
TMEM59	0.3378	0,2517 to 0,4185	<0,0001	Yes	Yes	**0.2068**	**0,115 to 0,2951**	**<0,0001**	**Yes**	**Yes**	0.1047	0,01079 to 0,1968	0.0246	Yes	No

target gene	Spearman r (SLNCR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (AR)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)	Spearman r (EGR1)	95% CI	P (two-tailed)	Significant? (alpha = 0.05)	Significant with Bonferroni correction (p-value < 0.00023)
TNFRSF12A	-0.05555	-0,1488 to 0,03867	0.2339	No	No	**0.05398**	**0,04024 to 0,1472**	**0.2474**	**No**	**No**	0.1831	0,09062 to 0,2724	<0,0001	Yes	Yes
TNFRSF21	0.1687	0,07592 to 0,2586	0.0003	Yes	No	0.3149	0,2276 to 0,3971	<0,0001	Yes	Yes	0.1875	0,09519 to 0,2767	<0,0001	Yes	Yes
TOR1B	0.07421	-0,01994 to 0,1671	0.1116	No	No	**0.2241**	**0,1329 to 0,3116**	**<0,0001**	**Yes**	**Yes**	0.2704	0,181 to 0,3554	<0,0001	Yes	Yes
UBE3D	0.1296	0,036 to 0,2209	0.0053	Yes	No	0.1643	0,07142 to 0,2544	0.0004	Yes	No	0.05791	-0,0363 to 0,1511	0.2146	No	No
VAMP8	-0.03173	-0,1254 to 0,06247	0.4967	No	No	0.0378	-0,05642 to 0,1313	0.4182	No	No	0.02531	-0,06887 to 0,119	0.5878	No	No
VGF	-0.0853	-0,1779 to 0,00878	0.0673	No	No	**-0.1389**	**-0,2299 to -0,04544**	**0.0028**	**Yes**	**No**	-0.005902	-0,09986 to 0,08816	0.8994	No	No
VSTM2B	-0.04623	-0,1396 to 0,04799	0.322	No	No	0.07689	-0,01724 to 0,1697	0.0992	No	No	-0.02836	-0,122 to 0,06583	0.5436	No	No
WWC2	0.208	0,1162 to 0,2962	<0,0001	Yes	Yes	**0.159**	**0,06593 to 0,2492**	**0.0006**	**Yes**	**No**	0.2277	0,1366 to 0,315	<0,0001	Yes	Yes
ZBTB42	0.05779	-0,03642 to 0,151	0.2156	No	No	0.02635	-0,1201 to 0,06783	0.5725	No	No	0.02331	-0,07085 to 0,1171	0.6176	No	No
ZNF322	0.2889	0,2003 to 0,3728	<0,0001	Yes	Yes	0.2417	0,1511 to 0,3283	<0,0001	Yes	Yes	0.208	0,1163 to 0,2962	<0,0001	Yes	Yes
ZYX	-0.2452	-0,3316 to -0,1547	<0,0001	Yes	Yes	**0.1816**	**0,08911 to 0,271**	**<0,0001**	**Yes**	**Yes**	0.2491	0,1588 to 0,3353	<0,0001	Yes	Yes

Table 7. AR active regions as determined via AR ChIP-Seq

Table 7 lists the AR active regions as determined via AR ChIP-Seq. AR ChIP-seq was performed from hormone-deprived A375 cells transfected with either an empty or *SLNCR1*-expressing plasmid. Active regions for both the vector only control and cells ectopically-expressing *SLNCR1*.

1_A375_pNL7_minus_lncRNA_AR = vector control

2_A375_pNL97_plus_lncRNA_AR = SLNCR1-expressing vector

Table 7

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1	1	713,862	714,400	538	2	14.529	15.471	25	28	1	2	2	LOC100288069, LOC100287934	-63, -7189	upstream, upstream	ActReg chr1 #1	1	1
2	1	894,244	895,424	1,180	1	9.378	14.73	19	25	1	3	3	NOC2L, KLHL17, PLEKHN1	-155, -1133, -7043	upstream, upstream, upstream	ActReg chr1 #2	0	1
3	1	895,655	896,170	515	1	9.333	12.562	17	22	1	3	3	NOC2L, KLHL17, PLEKHN1	-1233, -55, -5965	upstream, upstream, upstream	ActReg chr1 #3	0	1
4	1	935,841	936,619	778	2	11.5	11.25	23	22	1	1	1	HES4	-678	upstream	ActReg chr1 #4	1	1
5	1	994,361	995,383	1,022	2	13.188	12.469	24	23	1	0	1	AGRN	39,369	downstream	ActReg chr1 #5	1	1
6	1	1,051,234	1,051,988	754	2	9	11.087	18	21	1	1	1	C1orf159	125	in gene	ActReg chr1 #6	1	1
7	1	1,093,223	1,094,185	962	1	8.8	11.233	14	16	1	0	2	MIR200B, MIR200A	-8780, -9539	upstream, upstream	ActReg chr1 #7	0	1
8	1	1,173,227	1,174,153	926	1	10.69	12.966	17	18	1	1	3	SDF4, B3GALT6, FAM132A	-6243, 6061, 8412	upstream, downstream, downstream	ActReg chr1 #8	0	1
9	1	1,234,197	1,234,895	698	2	11.546	13.682	23	30	0	0	3	SCNN1D, ACAP3, PUSL1	17057, 8723, -9448	downstream, in gene, upstream	ActReg chr1 #9	1	1
10	1	1,243,346	1,244,607	1,261	2	10.308	11.487	23	22	1	2	3	ACAP3, PUSL1, CPSF3L	-707, -18, 16070	upstream, upstream, downstream	ActReg chr1 #10	1	1
11	1	1,309,707	1,311,238	1,531	2	14.833	15.729	46	49	1	1	3	LOC100506404, AURKAIP1, CCNL2	6897, 346, 24246	in gene, in gene, downstream	ActReg chr1 #11	1	1
12	1	1,334,555	1,336,092	1,537	1	10.271	12.521	17	17	1	2	3	CCNL2, LOC148413, MRPL20	-605, 413, 7370	upstream, in gene, downstream	ActReg chr1 #12	0	1
13	1	1,342,139	1,343,495	1,356	1	7.558	14.326	11	30	1	2	3	CCNL2, LOC148413, MRPL20	-8099, 7907, -124	upstream, downstream, upstream	ActReg chr1 #13	0	1
14	1	1,406,700	1,407,293	593	1	11.167	13.5	15	24	1	1	2	ATAD3C, ATAD3B	21927, -168	downstream, upstream	ActReg chr1 #14	0	1
15	1	1,446,826	1,447,685	859	2	13.963	14.926	20	25	1	1	1	ATAD3A	-268	upstream	ActReg chr1 #15	1	1
16	1	1,510,002	1,510,689	687	2	11.546	12.773	22	27	1	1	1	SSU72	-83	upstream	ActReg chr1 #16	1	1
17	1	1,590,202	1,590,809	607	2	10.158	11.105	18	17	1	1	2	CDK11B, RP11-345P4.4	-32, 33738	upstream, downstream	ActReg chr1 #17	1	1
18	1	1,623,948	1,624,773	825	2	9.923	14.462	23	27	1	1	2	RP11-345P4.4, CDK11A	-117, 31431	upstream, downstream	ActReg chr1 #18	1	1
19	1	2,066,258	2,067,799	1,541	2	10.5	11.938	16	24	1	0	1	PRKCZ	85,119	in gene	ActReg chr1 #19	1	1
20	1	2,120,843	2,121,583	740	1	11.565	8.696	20	12	1	1	4	PRKCZ, LOC100506504, C1orf86, LOC100128003	139304, -5721, 17959, 3811	downstream, upstream, in gene, in gene	ActReg chr1 #20	1	0
21	1	2,162,283	2,162,864	581	1	11.611	10.222	18	13	0	1	1	SKI	2,439	in gene	ActReg chr1 #21	1	0
22	1	2,344,067	2,345,246	1,179	1	8.167	11	14	16	1	1	2	RER1, PEX10	21442, -646	downstream, upstream	ActReg chr1 #22	0	1
23	1	2,457,170	2,458,417	1,247	2	17.359	17.974	35	39	1	1	2	PANK4, HES5	242, 3891	in gene, downstream	ActReg chr1 #23	1	1
24	1	2,573,950	2,575,090	1,140	1	10.722	6.944	18	13	1	0	2	MMEL1, LOC100287898	-10039, 131710	upstream, in gene	ActReg chr1 #24	1	0
25	1	3,712,675	3,713,375	700	2	11.381	12.905	19	20	1	1	1	LRRC47	43	in gene	ActReg chr1 #25	1	1
26	1	3,773,500	3,774,058	558	1	12.889	9.722	18	13	1	2	2	KIAA0562, DFFB	18, -66	in gene, upstream	ActReg chr1 #26	1	0
27	1	3,817,294	3,818,114	820	1	8.346	12.885	12	20	1	2	2	C1orf174, LOC100133612	-847, 736	upstream, in gene	ActReg chr1 #27	0	1
28	1	4,028,784	4,029,366	582	1	9.167	12.944	15	24	0	0	0				ActReg chr1 #28	0	1
29	1	4,143,433	4,144,131	698	1	4.591	11.227	7	16	0	0	0				ActReg chr1 #29	0	1
30	1	4,696,297	4,697,491	1,194	1	5.892	14.865	9	25	0	0	0				ActReg chr1 #30	0	1
31	1	6,051,797	6,053,045	1,248	2	12.342	16.667	23	36	1	1	1	NPHP4	110	in gene	ActReg chr1 #31	1	1
32	1	6,076,000	6,076,687	687	1	7	11	11	16	0	0	1	KCNAB2	-10,037	upstream	ActReg chr1 #32	0	1
33	1	6,112,112	6,113,268	1,156	2	11.556	13.417	27	22	0	0	1	KCNAB2	26,310	in gene	ActReg chr1 #33	1	1
34	1	6,217,215	6,218,802	1,587	2	8.92	14.44	22	23	0	0	1	CHD5	22,186	in gene	ActReg chr1 #34	1	1
35	1	6,221,430	6,222,491	1,061	2	17.515	20.606	33	42	0	0	1	CHD5	18,234	in gene	ActReg chr1 #35	1	1
36	1	6,259,129	6,260,192	1,063	2	26.559	35.235	84	108	1	2	2	RPL22, RNF207	19, -6529	in gene, upstream	ActReg chr1 #36	1	1
37	1	6,269,147	6,269,834	687	1	10.864	15.364	19	27	1	0	2	RPL22, RNF207	-9811, 3301	upstream, in gene	ActReg chr1 #37	0	1
38	1	6,296,246	6,296,722	476	1	4.533	10.067	6	15	1	2	3	ICMT, C1orf211, HES3	-440, -1384, -7768	upstream, upstream, upstream	ActReg chr1 #38	0	1
39	1	6,305,133	6,305,870	737	2	15.13	14.609	36	27	1	1	4	ICMT, C1orf211, HES3, GPR153	-9457, 7633, 1249, 15534	upstream, downstream, in gene, downstream	ActReg chr1 #39	1	1
40	1	6,333,090	6,334,239	1,149	1	9.171	11.714	14	15	0	0	2	ACOT7, UNQ6193	120162, 7149	in gene, downstream	ActReg chr1 #40	0	1
41	1	6,506,951	6,507,730	779	1	8.125	14.417	14	25	1	0	1	ESPN	22,492	in gene	ActReg chr1 #41	0	1
42	1	6,613,807	6,615,100	1,293	2	27.75	30.825	93	110	1	2	2	NOL9, TAS1R1	205, -885	in gene, upstream	ActReg chr1 #42	1	1
43	1	6,662,196	6,663,581	1,385	1	12.698	9.698	24	20	1	1	1	KLHL21	41	in gene	ActReg chr1 #43	1	0
44	1	6,673,268	6,673,834	566	1	7.278	12.444	13	21	1	1	1	PHF13	-205	upstream	ActReg chr1 #44	0	1
45	1	6,760,807	6,762,473	1,666	2	38.423	42.346	169	181	1	1	1	DNAJC11	326	in gene	ActReg chr1 #45	1	1
46	1	7,106,253	7,106,865	612	1	8.684	11.579	15	23	0	0	2	CAMTA1, LOC100505910	261175, 5205	in gene, downstream	ActReg chr1 #46	0	1
47	1	7,135,189	7,136,179	990	2	14.806	15.452	39	30	0	0	1	CAMTA1	290,300	in gene	ActReg chr1 #47	1	1
48	1	7,325,799	7,326,684	885	2	12.111	10.518	21	18	0	0	1	CAMTA1	480,857	in gene	ActReg chr1 #48	1	1
49	1	7,373,017	7,373,752	735	1	5.261	9.565	13	12	0	0	1	CAMTA1	528,000	in gene	ActReg chr1 #49	0	1
50	1	7,676,182	7,677,489	1,307	2	11.585	15.39	30	34	0	0	1	CAMTA1	831,451	in gene	ActReg chr1 #50	1	1
51	1	8,014,046	8,014,659	613	1	12	9.15	19	12	1	1	1	PARK7	-7,362	upstream	ActReg chr1 #51	1	0
52	1	8,021,108	8,022,272	1,164	2	14.405	21.216	35	47	1	1	1	PARK7	-24	upstream	ActReg chr1 #52	1	1
53	1	8,086,067	8,087,530	1,463	2	11.587	14.696	25	27	1	1	1	ERRFI1	-405	upstream	ActReg chr1 #53	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
54	1	8,137,217	8,137,798	581	1	8.167	12	11	21	0	0	0				ActReg chr1 #54	0	1
55	1	8,181,224	8,181,902	678	1	11.857	9	19	13	0	0	0				ActReg chr1 #55	1	0
56	1	8,214,676	8,215,224	548	1	10.882	7.118	22	14	0	0	0				ActReg chr1 #56	1	0
57	1	8,229,126	8,229,876	750	1	8.348	11.783	16	18	0	0	0				ActReg chr1 #57	0	1
58	1	8,257,801	8,258,519	718	1	9.455	14.546	16	24	0	0	0				ActReg chr1 #58	0	1
59	1	8,377,831	8,378,549	718	1	7.182	13.591	13	19	1	1	1	SLC45A1	-6,200	upstream	ActReg chr1 #59	0	1
60	1	8,484,051	8,485,176	1,125	2	8.029	11.114	16	20	1	0	1	RERE	393,086	in gene	ActReg chr1 #60	1	1
61	1	8,763,319	8,763,896	577	1	10	12.944	15	23	1	0	1	RERE	114,092	in gene	ActReg chr1 #61	0	1
62	1	8,799,976	8,800,662	686	2	8.429	13.143	15	23	0	0	1	RERE	77,380	in gene	ActReg chr1 #62	1	1
63	1	8,937,767	8,938,367	600	1	12.611	10.056	21	17	1	2	2	ENO1, LOC100505975	713, -827	in gene, upstream	ActReg chr1 #63	1	0
64	1	8,938,490	8,939,489	999	2	10.531	12.219	16	20	1	2	2	ENO1, LOC100505975	-209, 95	upstream, in gene	ActReg chr1 #64	1	1
65	1	9,242,047	9,242,753	706	1	11.13	7.261	17	12	1	0	1	LOC727721	14,640	in gene	ActReg chr1 #65	1	0
66	1	9,488,754	9,489,369	615	1	11.632	13.158	21	23	1	1	1	LOC100506022	-6	upstream	ActReg chr1 #66	0	1
67	1	9,970,515	9,971,270	755	1	6.391	11.542	10	17	1	1	1	CTNNBIP1	-576	upstream	ActReg chr1 #67	0	1
68	1	10,002,889	10,003,833	944	2	13.724	9.586	25	22	1	2	2	LZIC, NMNAT1	-535, -125	upstream, upstream	ActReg chr1 #68	1	1
69	1	10,270,297	10,270,857	560	1	10	7.111	15	9	1	1	1	KIF1B	-187	upstream	ActReg chr1 #69	1	0
70	1	10,458,507	10,459,783	1,276	2	13.225	16.3	28	33	1	2	2	LOC100287506, PGD	-190, 60	upstream, in gene	ActReg chr1 #70	1	1
71	1	10,490,008	10,490,815	807	2	16.44	16.04	33	38	1	1	2	PGD, APITD1	31326, 252	downstream, in gene	ActReg chr1 #71	1	1
72	1	10,532,183	10,532,988	805	2	12.8	13.08	22	22	1	2	2	DFFA, PEX14	28, -2418	in gene, upstream	ActReg chr1 #72	1	1
73	1	10,534,575	10,535,374	799	2	13.72	14.52	29	34	1	2	2	DFFA, PEX14	-2361, -29	upstream, upstream	ActReg chr1 #73	1	1
74	1	10,856,437	10,857,148	711	2	14.591	15.773	33	32	1	1	1	CASZ1	-85	upstream	ActReg chr1 #74	1	1
75	1	11,039,305	11,039,967	662	1	13.05	5.45	19	10	0	1	1	C1orf127	2,458	in gene	ActReg chr1 #75	1	0
76	1	11,072,219	11,073,206	987	2	16.032	16.355	33	31	1	1	1	TARDBP	33	in gene	ActReg chr1 #76	1	1
77	1	11,159,358	11,160,085	727	1	7.957	12.391	14	18	1	1	2	EXOSC10, MTOR	217, 162887	in gene, downstream	ActReg chr1 #77	0	1
78	1	11,333,192	11,334,187	995	2	11.032	11	18	17	1	1	1	UBIAD1	434	in gene	ActReg chr1 #78	1	1
79	1	11,533,542	11,534,177	635	1	9.65	10.35	19	17	0	1	1	PTCHD2	-5,436	upstream	ActReg chr1 #79	1	0
80	1	11,538,702	11,539,827	1,125	2	10.971	11.429	19	22	1	1	1	PTCHD2	-31	upstream	ActReg chr1 #80	1	1
81	1	11,539,895	11,540,715	820	1	8.346	13.577	15	22	1	1	1	PTCHD2	1,010	in gene	ActReg chr1 #81	0	1
82	1	11,610,224	11,611,433	1,209	2	23.868	25.947	57	68	0	0	0				ActReg chr1 #82	1	1
83	1	11,695,942	11,696,547	605	2	13.474	10.895	22	16	0	0	0				ActReg chr1 #83	1	1
84	1	11,740,571	11,741,511	940	1	8.167	11.467	14	21	1	0	2	FBXO6, MAD2L2	16891, 10637	downstream, in gene	ActReg chr1 #84	0	1
85	1	11,865,596	11,866,464	868	1	12.929	8.679	25	14	1	2	2	MTHFR, CLCN6	130, -177	in gene, upstream	ActReg chr1 #85	1	0
86	1	11,919,116	11,919,999	883	2	12	15.259	27	27	1	1	1	NPPB	-565	upstream	ActReg chr1 #86	1	1
87	1	11,967,753	11,969,246	1,493	2	13.478	14.043	38	27	0	1	1	RNU5E	288	downstream	ActReg chr1 #87	1	1
88	1	11,969,588	11,970,431	843	2	12.423	10.577	24	24	0	1	2	RNU5E, KIAA2013	1798, 16471	downstream, downstream	ActReg chr1 #88	1	1
89	1	11,989,712	11,990,358	646	1	8.05	10.85	17	19	0	2	2	KIAA2013, PLOD1	-3555, -4711	upstream, upstream	ActReg chr1 #89	0	1
90	1	12,039,846	12,040,789	943	1	8.593	11.655	17	18	1	1	2	PLOD1, MFN2	45571, 79	downstream, in gene	ActReg chr1 #90	0	1
91	1	12,289,465	12,290,405	940	2	12.667	16.933	33	39	1	1	2	LOC390998, VPS13D	-8771, -178	upstream, upstream	ActReg chr1 #91	1	1
92	1	12,290,533	12,291,099	566	1	7.353	9.941	9	16	2	1	2	LOC390998, VPS13D	-9652, 703	upstream, in gene	ActReg chr1 #92	0	1
93	1	12,538,507	12,539,231	724	1	12.773	7.591	18	11	0	0	1	VPS13D	248,756	in gene	ActReg chr1 #93	1	0
94	1	12,609,004	12,609,988	984	1	7	11.161	17	17	0	0	0				ActReg chr1 #94	0	1
95	1	12,655,873	12,656,377	504	1	7	13.333	10	23	1	0	1	DHRS3	21,695	in gene	ActReg chr1 #95	0	1
96	1	12,676,793	12,677,412	619	1	6.2	10.15	9	19	1	1	1	DHRS3	718	in gene	ActReg chr1 #96	0	1
97	1	15,664,004	15,664,748	744	1	10.478	13.435	17	27	0	0	1	FHAD1	90,608	in gene	ActReg chr1 #97	0	1
98	1	15,678,716	15,679,370	654	1	12.619	10.809	21	15	0	0	1	FHAD1	105,275	in gene	ActReg chr1 #98	0	1
99	1	15,852,809	15,853,633	824	2	17.5	14.115	35	28	1	2	2	CASP9, DNAJC16	-2431, -131	upstream, upstream	ActReg chr1 #99	1	1
100	1	16,402,268	16,403,887	1,619	2	11.098	11.843	19	22	0	1	1	FAM131C	-2,950	upstream	ActReg chr1 #100	1	1
101	1	16,448,925	16,449,863	938	1	12.4	9.4	26	17	0	0	1	EPHA2	33,188	downstream	ActReg chr1 #101	1	0
102	1	16,482,028	16,482,788	760	1	11.167	10.125	16	16	1	2	2	EPHA2, LOC100506484	174, 678	in gene, in gene	ActReg chr1 #102	1	0
103	1	16,499,431	16,500,472	1,041	1	7.062	11.312	13	18	0	0	0				ActReg chr1 #103	0	1
104	1	16,678,343	16,679,533	1,190	2	13.703	10.46	24	15	1	1	1	FBXO42	10	in gene	ActReg chr1 #104	1	1
105	1	16,693,244	16,694,428	1,184	2	15.46	15.919	36	37	1	1	1	C1orf144	253	in gene	ActReg chr1 #105	1	1
106	1	16,766,615	16,767,825	1,210	2	12.5	16.421	36	39	1	2	2	SPATA21, NECAP2	-3301, 53	upstream, in gene	ActReg chr1 #106	1	1
107	1	16,938,892	16,940,781	1,889	1	20.339	23.881	53	59	1	1	1	NBPF1	146	in gene	ActReg chr1 #107	0	1
108	1	16,970,452	16,971,624	1,172	2	19	18.541	47	42	1	0	0				ActReg chr1 #108	1	1
109	1	17,026,863	17,028,818	1,955	2	16.738	17.754	48	51	1	0	0				ActReg chr1 #109	1	1
110	1	17,222,558	17,222,887	329	1	8.364	14.727	12	23	1	2	2	LOC100506687, RNU1-2	-6561, 247	upstream, downstream	ActReg chr1 #110	0	1
111	1	17,230,781	17,232,286	1,505	2	24.957	27.575	94	112	1	0	1	RNU1-2	9,058	downstream	ActReg chr1 #111	1	1
112	1	17,239,912	17,241,312	1,400	2	12.296	11.386	21	25	1	1	1	CROCC	-7,833	upstream	ActReg chr1 #112	1	1
113	1	17,620,161	17,621,008	847	1	7.654	10.577	12	16	0	0	1	PADI3	44,991	downstream	ActReg chr1 #113	0	1
114	1	17,765,396	17,766,271	875	1	8.407	11.074	15	18	1	1	1	RCC2	387	in gene	ActReg chr1 #114	0	1
115	1	17,871,844	17,872,519	675	1	11.191	6.524	20	11	0	0	1	ARHGEF10L	5,851	in gene	ActReg chr1 #115	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
116	1	18,157,817	18,158,756	939	2	12.6	15.833	28	32	0	0	1	ACTL8	8,809	downstream	ActReg chr1 #116	1	1
117	1	18,245,705	18,246,881	1,176	2	12.811	15.73	30	32	0	0	0				ActReg chr1 #117	1	1
118	1	19,228,989	19,229,471	482	1	12.133	11.4	21	14	1	2	3	ALDH4A1, MIR1290, IFFO2	63, -5588, 53596	in gene, upstream, downstream	ActReg chr1 #118	1	0
119	1	19,252,550	19,253,311	761	1	10.087	15.478	14	22	0	0	1	IFFO2	29,896	in gene	ActReg chr1 #119	0	1
120	1	19,258,669	19,259,660	991	2	10.065	9.677	19	16	0	0	1	IFFO2	23,662	in gene	ActReg chr1 #120	1	1
121	1	19,281,444	19,282,430	986	1	6.033	11.767	10	17	1	1	1	IFFO2	889	in gene	ActReg chr1 #121	0	1
122	1	19,536,388	19,537,307	919	2	13.714	11.929	28	19	1	1	2	UBR4, KIAA0090	-101, 41199	upstream, downstream	ActReg chr1 #122	1	1
123	1	19,577,657	19,578,671	1,014	2	14.281	17.094	36	36	1	2	2	KIAA0090, MRTO4	-118, 89	upstream, in gene	ActReg chr1 #123	1	1
124	1	20,002,155	20,003,587	1,432	2	15.556	18.022	39	50	0	0	2	HTR6, TMCO4	11091, 123539	in gene, downstream	ActReg chr1 #124	1	1
125	1	20,685,169	20,686,039	870	2	9.926	9.926	24	13	0	0	2	VWA5B1, LOC339505	68192, 69683	downstream, downstream	ActReg chr1 #125	1	1
126	1	20,697,690	20,698,942	1,252	2	12.128	18.692	32	42	0	0	1	LOC339505	56,971	in gene	ActReg chr1 #126	1	1
127	1	20,737,631	20,738,364	733	1	8.261	11.957	16	18	0	0	1	LOC339505	17,290	in gene	ActReg chr1 #127	0	1
128	1	20,820,850	20,821,860	1,010	1	8	11.844	16	18	0	0	2	CAMK2N1, MUL1	-8627, 13319	upstream, downstream	ActReg chr1 #128	0	1
129	1	20,834,206	20,835,152	946	2	12.2	11.767	22	19	1	1	1	MUL1	-5	upstream	ActReg chr1 #129	1	1
130	1	20,987,434	20,988,064	630	1	9.4	11	14	15	1	1	3	PINK1, DDOST, KIF17	27601, 288, 56568	downstream, in gene, downstream	ActReg chr1 #130	0	1
131	1	21,112,583	21,113,374	791	1	11.875	9.167	21	17	1	1	1	HP1BP3	203	in gene	ActReg chr1 #131	1	0
132	1	21,588,054	21,588,746	692	1	8.045	12.364	12	19	0	1	2	ECE1, LOC100506824	83634, -4175	in gene, upstream	ActReg chr1 #132	0	1
133	1	21,780,369	21,780,858	489	2	10.533	9.6	16	14	0	0	1	NBPF3	13,982	in gene	ActReg chr1 #133	1	1
134	1	21,974,111	21,975,008	897	2	16.517	14.621	34	30	0	0	1	RAP1GAP	21,297	in gene	ActReg chr1 #134	1	1
135	1	21,985,377	21,986,331	954	2	13.586	14.448	19	30	1	0	1	RAP1GAP	10,002	in gene	ActReg chr1 #135	1	1
136	1	22,032,920	22,033,464	544	1	11.588	6.333	23	10	0	0	1	USP48	76,496	in gene	ActReg chr1 #136	1	0
137	1	22,108,760	22,110,465	1,705	2	12.907	14.407	19	25	1	1	1	USP48	76	in gene	ActReg chr1 #137	1	1
138	1	22,263,895	22,264,502	607	1	11.368	11.947	18	19	0	0	0				ActReg chr1 #138	1	0
139	1	22,266,149	22,266,924	775	2	13.333	14.125	26	23	0	0	0				ActReg chr1 #139	1	1
140	1	22,351,100	22,352,190	1,090	1	10.294	11.647	18	17	1	1	1	HSPC157	-62	upstream	ActReg chr1 #140	0	1
141	1	22,778,096	22,779,149	1,053	1	7.697	10.848	12	16	1	1	1	ZBTB40	278	in gene	ActReg chr1 #141	0	1
142	1	22,937,354	22,938,821	1,467	2	24.304	26.413	72	79	0	0	1	EPHA8	48,083	downstream	ActReg chr1 #142	1	1
143	1	23,345,447	23,346,231	784	2	11.75	12.5	22	23	1	2	2	LOC729059, KDM1A	-3496, -102	upstream, upstream	ActReg chr1 #143	1	1
144	1	23,670,911	23,671,604	693	1	8.045	10.409	14	19	1	1	1	HNRNPR	-404	upstream	ActReg chr1 #144	0	1
145	1	23,694,556	23,695,867	1,311	1	12.22	10.683	20	18	1	2	2	ZNF436, C1orf213	1146, -253	in gene, upstream	ActReg chr1 #145	1	0
146	1	23,703,416	23,704,177	761	1	9.042	11.75	17	20	0	1	3	ZNF436, C1orf213, TCEA3	-7439, 8332, 47465	upstream, downstream, downstream	ActReg chr1 #146	0	1
147	1	23,857,297	23,858,292	995	1	8.903	11.355	15	20	1	1	1	E2F2	-81	upstream	ActReg chr1 #147	0	1
148	1	23,865,980	23,866,645	665	1	7.714	11.143	11	16	0	0	1	E2F2	-8,599	upstream	ActReg chr1 #148	0	1
149	1	23,999,481	24,000,565	1,084	2	16.412	17.529	32	36	0	1	1	LOC729856	2,755	downstream	ActReg chr1 #149	1	1
150	1	24,017,962	24,018,697	735	1	10	13.696	19	25	1	1	1	RPL11	35	in gene	ActReg chr1 #150	0	1
151	1	24,069,356	24,070,367	1,011	1	8.742	12.839	16	23	1	1	1	TCEB3	5	in gene	ActReg chr1 #151	0	1
152	1	24,125,765	24,127,698	1,933	2	11.083	13.483	20	32	1	1	3	LYPLA2, GALE, HMGCL	9085, 563, 25218	downstream, in gene, downstream	ActReg chr1 #152	1	1
153	1	24,306,432	24,307,204	772	2	12.04	13.36	23	28	1	1	1	SFRS13A	135	in gene	ActReg chr1 #153	1	1
154	1	24,377,967	24,378,391	424	1	12.308	9.846	16	15	0	0	1	MYOM3	60,486	downstream	ActReg chr1 #154	0	1
155	1	24,620,330	24,621,345	1,015	2	12.935	13.344	33	18	0	0	0				ActReg chr1 #155	1	1
156	1	24,691,639	24,692,517	878	2	9.679	12.571	22	19	0	0	2	GRHL3, C1orf201	46266, 35871	downstream, in gene	ActReg chr1 #156	1	1
157	1	24,741,750	24,742,874	1,124	2	11.229	10.943	20	28	1	1	1	NIPAL3	67	in gene	ActReg chr1 #157	1	1
158	1	25,275,780	25,276,340	560	1	12.647	9.941	20	15	0	0	1	RUNX3	15,441	in gene	ActReg chr1 #158	1	0
159	1	25,285,613	25,286,616	1,003	1	9.129	11.548	13	20	0	0	1	RUNX3	5,387	in gene	ActReg chr1 #159	0	1
160	1	25,343,890	25,344,728	838	1	8.269	10.385	13	16	0	0	0				ActReg chr1 #160	0	1
161	1	25,348,919	25,350,000	1,081	1	11.471	8.912	17	15	0	0	0				ActReg chr1 #161	1	0
162	1	25,493,889	25,494,566	677	1	9.429	12.333	14	21	0	0	0				ActReg chr1 #162	0	1
163	1	25,572,878	25,573,470	592	1	7.444	10.722	11	21	1	1	1	C1orf63	811	in gene	ActReg chr1 #163	0	1
164	1	25,573,541	25,574,361	820	1	9.4	12.4	16	16	1	1	1	C1orf63	34	in gene	ActReg chr1 #164	0	1
165	1	25,894,800	25,896,991	2,191	2	9.559	10.882	15	20	0	0	1	LDLRAP1	25,819	downstream	ActReg chr1 #165	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
166	1	26,146,168	26,147,276	1,108	1	11.571	9.314	17	18	1	1	3	SEPN1, FAM54B, LOC646471	20055, 325, 3375	downstream, in gene, in gene	ActReg chr1 #166	1	0
167	1	26,324,298	26,325,197	899	2	14.179	12.429	26	30	1	1	1	PAFAH2	-99	upstream	ActReg chr1 #167	1	1
168	1	26,354,660	26,355,779	1,119	2	10.686	13.086	18	26	0	0	2	EXTL1, SLC30A2	6948, 17385	in gene, downstream	ActReg chr1 #168	1	1
169	1	26,361,499	26,362,424	925	2	16.345	13.966	33	22	1	0	2	EXTL1, SLC30A2	13690, 10643	in gene, downstream	ActReg chr1 #169	1	1
170	1	26,437,186	26,438,913	1,727	2	12.796	13.87	25	26	1	1	1	PDIK1L	393	in gene	ActReg chr1 #170	1	1
171	1	26,495,996	26,496,758	762	2	11.542	12.583	25	26	1	3	4	CRRP1, LOC100128346, ZNF593, CNKSR1	10866, 1935, -11, -7604	downstream, in gene, upstream, upstream	ActReg chr1 #171	1	1
172	1	26,560,014	26,560,969	955	1	10.533	9.233	15	15	1	1	1	CCDC21	-202	upstream	ActReg chr1 #172	1	0
173	1	26,601,948	26,603,204	1,256	1	11.975	8.5	19	16	0	1	3	CCDC21, SH3BGRL3, UBXN11	41883, -3637, 42180	in gene, upstream, downstream	ActReg chr1 #173	1	0
174	1	26,606,101	26,607,029	928	1	7.69	12.931	14	19	1	1	3	CCDC21, SH3BGRL3, UBXN11	45872, 352, 38191	downstream, in gene, downstream	ActReg chr1 #174	0	1
175	1	26,734,602	26,735,795	1,193	2	18.135	26.405	50	71	0	1	1	LIN28	-2,071	upstream	ActReg chr1 #175	1	1
176	1	26,758,334	26,759,193	859	2	14.185	15.556	30	29	1	1	2	LIN28, DHDDS	21494, -39	downstream, upstream	ActReg chr1 #176	1	1
177	1	26,797,578	26,798,751	1,173	2	9.833	12.917	17	20	1	1	2	DHDDS, HMGN2	39362, -738	downstream, upstream	ActReg chr1 #177	1	1
178	1	26,826,581	26,827,601	1,020	2	10.469	11.844	19	18	1	0	0				ActReg chr1 #178	1	1
179	1	26,881,882	26,882,606	724	1	8.652	11.304	14	17	0	1	2	RPS6KA1, MIR1976	25995, 1211	in gene, downstream	ActReg chr1 #179	0	1
180	1	26,946,780	26,948,294	1,514	2	13.167	16.896	29	30	1	0	0				ActReg chr1 #180	1	1
181	1	27,018,495	27,020,112	1,617	2	17.235	20.706	39	58	0	1	1	ARID1A	-3,219	upstream	ActReg chr1 #181	1	1
182	1	27,021,700	27,022,445	745	2	15.522	20.913	31	45	1	1	1	ARID1A	-450	upstream	ActReg chr1 #182	1	1
183	1	27,191,092	27,192,084	992	1	10.032	13.097	16	18	1	1	2	ZDHHC18, SFN	38387, 1955	downstream, downstream	ActReg chr1 #183	0	1
184	1	27,215,955	27,216,924	969	2	11.8	12.667	23	19	1	1	2	GPN2, GPATCH3	430, 10523	in gene, downstream	ActReg chr1 #184	1	1
185	1	27,248,018	27,248,754	736	1	10.522	12.913	16	23	1	2	2	NR0B2, NUDC	-7819, 162	upstream, in gene	ActReg chr1 #185	0	1
186	1	27,328,178	27,328,963	785	1	10.36	12.96	18	26	0	0	2	TRNP1, FAM46B	8375, 10763	downstream, downstream	ActReg chr1 #186	0	1
187	1	27,335,609	27,336,446	837	1	6.692	10.462	13	14	0	0	2	TRNP1, FAM46B	15832, 3306	downstream, in gene	ActReg chr1 #187	0	1
188	1	27,560,743	27,561,388	645	1	12.1	7.5	21	12	1	1	1	WDTC1	58	in gene	ActReg chr1 #188	1	0
189	1	27,648,266	27,649,088	822	2	13.962	14.231	27	30	1	2	2	TMEM222, LOC644961	41, -1688	in gene, upstream	ActReg chr1 #189	1	1
190	1	27,675,520	27,676,643	1,123	1	8.278	12.139	15	17	1	0	2	SYTL1, MAP3K6	7598, 17256	in gene, downstream	ActReg chr1 #190	0	1
191	1	27,718,657	27,719,368	711	1	8.773	12.636	14	20	1	1	2	CD164L2, GPR3	-9207, -140	upstream, upstream	ActReg chr1 #191	0	1
192	1	27,816,247	27,817,374	1,127	2	11.629	12.171	15	23	1	1	1	WASF2	-141	upstream	ActReg chr1 #192	1	1
193	1	27,998,329	27,999,374	1,045	1	8.061	12.333	14	19	0	1	1	IFI6	-127	upstream	ActReg chr1 #193	0	1
194	1	28,470,910	28,471,645	735	2	11.304	15.522	20	35	0	0	1	PTAFR	49,170	downstream	ActReg chr1 #194	1	1
195	1	28,640,296	28,640,773	477	1	8.867	10.333	11	15	0	0	0				ActReg chr1 #195	0	1
196	1	28,672,525	28,673,196	671	1	9.952	2.286	17	3	0	0	0				ActReg chr1 #196	1	0
197	1	28,879,083	28,880,127	1,044	1	9.75	13.156	18	26	1	0	0				ActReg chr1 #197	0	1
198	1	28,908,112	28,908,787	675	1	13.667	13.381	20	22	1	5	6	SNHG12, SNORD99, SNORA61, SNORA44, SNORA16A, RAB42	-83, -3115, -2044, -1425, -884, -10263	upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr1 #198	0	1
199	1	28,974,483	28,975,784	1,301	2	13.317	13.268	28	23	0	2	2	TAF12, RNU11	-5529, 21	upstream, in gene	ActReg chr1 #199	1	1
200	1	28,994,805	28,995,345	540	1	12.765	10.353	21	18	0	1	1	GMEB1	-169	upstream	ActReg chr1 #200	1	0
201	1	29,062,788	29,063,946	1,158	2	20.861	17.306	54	35	1	1	1	YTHDF2	234	in gene	ActReg chr1 #201	1	1
202	1	29,213,261	29,213,933	672	1	9.571	12.571	13	20	1	1	1	EPB41	-6	upstream	ActReg chr1 #202	0	1
203	1	29,507,780	29,508,792	1,012	1	8.065	15.258	14	24	1	1	1	SFRS4	351	in gene	ActReg chr1 #203	0	1
204	1	29,557,143	29,557,756	613	1	8.947	11.79	12	18	1	2	2	MECR, PTPRU	5, -5579	in gene, upstream	ActReg chr1 #204	0	1
205	1	30,042,486	30,043,436	950	2	15.1	13.5	30	28	0	0	0				ActReg chr1 #205	1	1
206	1	30,112,255	30,113,136	881	1	6.643	10.393	13	15	0	0	0				ActReg chr1 #206	0	1
207	1	30,181,710	30,183,141	1,431	1	8.111	11.6	16	22	0	0	0				ActReg chr1 #207	0	1
208	1	30,208,823	30,210,063	1,240	2	12.769	12.615	26	32	0	0	0				ActReg chr1 #208	1	1
209	1	30,447,282	30,448,484	1,202	2	12.105	14.21	36	34	0	0	0				ActReg chr1 #209	1	1
210	1	31,084,565	31,085,264	699	1	8.591	11.954	14	19	0	0	0				ActReg chr1 #210	0	1
211	1	31,191,532	31,192,230	698	1	13.364	11.773	20	17	1	1	2	MATN1, LOC100129196	4551, 262	in gene, in gene	ActReg chr1 #211	1	0
212	1	31,205,244	31,206,090	846	1	8.556	12.704	13	20	0	0	3	MATN1, LOC100129196, LAPTM5	-9235, 14048, 25016	upstream, downstream, in gene	ActReg chr1 #212	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
213	1	31,229,317	31,230,145	828	2	14.885	14.615	32	27	0	1	1	LAPTM5	952	in gene	ActReg chr1 #213	1	1
214	1	31,270,675	31,271,320	645	1	7.75	10.85	11	14	0	0	0				ActReg chr1 #214	0	1
215	1	31,288,903	31,290,274	1,371	1	9.512	11.954	19	20	0	0	0				ActReg chr1 #215	0	1
216	1	31,296,592	31,297,486	894	2	11.429	13.143	22	19	0	0	0				ActReg chr1 #216	1	1
217	1	31,635,365	31,636,013	648	2	10.45	10.65	16	21	0	0	0				ActReg chr1 #217	1	1
218	1	31,654,365	31,655,839	1,474	2	14.152	12.87	27	26	1	0	1	NKAIN1	57,632	in gene	ActReg chr1 #218	1	1
219	1	31,769,128	31,769,776	648	1	6.75	13.8	9	25	1	2	2	SNRNP40, ZCCHC17	192, -390	in gene, upstream	ActReg chr1 #219	0	1
220	1	31,867,344	31,868,085	741	1	11.913	7.957	18	17	0	0	0				ActReg chr1 #220	1	0
221	1	31,906,771	31,908,254	1,483	2	11.152	10.826	21	25	0	0	1	SERINC2	21,549	in gene	ActReg chr1 #221	1	1
222	1	32,109,903	32,111,036	1,133	2	12.686	18.143	21	33	1	1	2	PEF1, COL16A1	369, 59299	in gene, downstream	ActReg chr1 #222	1	1
223	1	32,155,296	32,156,022	726	1	7.391	12.783	13	24	0	0	1	COL16A1	14,109	in gene	ActReg chr1 #223	0	1
224	1	32,180,884	32,181,670	786	1	10.12	10.04	15	15	0	0	0				ActReg chr1 #224	1	0
225	1	32,182,623	32,183,379	756	1	9.917	12.25	20	21	0	0	1	BAI2	46,647	downstream	ActReg chr1 #225	0	1
226	1	32,189,148	32,190,350	1,202	2	17.368	17.432	36	42	0	0	1	BAI2	39,899	downstream	ActReg chr1 #226	1	1
227	1	32,253,465	32,254,496	1,031	2	19.454	13.333	39	26	1	0	1	SPOCD1	27,600	downstream	ActReg chr1 #227	1	1
228	1	32,404,051	32,404,514	463	1	11.667	8.267	16	13	1	1	1	PTP4A2	-294	upstream	ActReg chr1 #228	1	0
229	1	32,537,923	32,538,928	1,005	2	13.387	14.097	22	21	1	1	1	TMEM39B	-78	upstream	ActReg chr1 #229	1	1
230	1	32,573,327	32,574,509	1,182	1	8.25	11.622	13	20	1	1	2	TMEM39B, KPNA6	35415, 274	downstream, in gene	ActReg chr1 #230	0	1
231	1	32,644,742	32,645,683	941	1	13.172	9.724	18	17	1	1	2	KPNA6, TXLNA	71568, -133	downstream, upstream	ActReg chr1 #231	1	0
232	1	32,670,811	32,671,829	1,018	1	10.375	10.625	15	15	1	2	6	TXLNA, CCDC28B, IQCC, DCDC2B, LOC100507457, C1orf91	25975, 5118, 84, -3375, 9738, 16606	downstream, downstream, in gene, upstream, downstream, downstream	ActReg chr1 #232	1	0
233	1	32,701,619	32,702,318	699	2	11.136	10.454	20	18	0	0	1	EIF3I	13,997	downstream	ActReg chr1 #233	1	1
234	1	32,757,629	32,758,621	992	1	7.935	11.645	17	20	1	1	2	LCK, HDAC1	41285, 417	downstream, in gene	ActReg chr1 #234	0	1
235	1	32,817,097	32,817,819	722	1	8.318	11.227	13	20	1	0	1	LOC100128071	10,386	downstream	ActReg chr1 #235	0	1
236	1	32,859,429	32,860,659	1,230	1	9.395	13.658	15	20	1	1	1	BSDC1	18	in gene	ActReg chr1 #236	0	1
237	1	33,282,504	33,283,792	1,288	2	18.95	24.45	68	86	1	2	2	YARS, S100PBP	485, -28	in gene, upstream	ActReg chr1 #237	1	1
238	1	33,438,279	33,438,889	610	1	5.579	9.211	9	17	1	0	1	RNF19B	-8,298	upstream	ActReg chr1 #238	0	1
239	1	33,564,979	33,565,686	707	1	6.136	11.682	12	17	0	0	1	ADC	18,618	in gene	ActReg chr1 #239	0	1
240	1	33,592,434	33,593,544	1,110	2	26.714	34.857	93	114	1	0	1	ADC	46,275	downstream	ActReg chr1 #240	1	1
241	1	33,626,629	33,627,555	926	1	9.069	10.448	14	15	0	0	1	TRIM62	20,579	in gene	ActReg chr1 #241	0	1
242	1	33,709,735	33,710,528	793	1	12.12	8.52	16	13	0	0	0				ActReg chr1 #242	1	0
243	1	33,713,696	33,714,219	523	1	12.588	10.294	25	19	0	0	1	ZNF362	-8,217	upstream	ActReg chr1 #243	1	0
244	1	33,896,448	33,897,059	611	1	10.05	7	22	15	1	0	0				ActReg chr1 #244	1	0
245	1	33,899,116	33,899,880	764	1	13.833	9.458	28	17	0	0	0				ActReg chr1 #245	1	0
246	1	33,908,777	33,909,765	988	1	10.677	7.161	16	11	0	0	0				ActReg chr1 #246	1	0
247	1	35,174,993	35,175,738	745	2	9.174	13.217	17	28	0	0	0				ActReg chr1 #247	1	1
248	1	35,246,801	35,247,479	678	1	5.952	12.429	10	22	1	1	1	GJB3	350	in gene	ActReg chr1 #248	0	1
249	1	35,324,571	35,325,999	1,428	2	34.178	31.6	133	136	1	1	2	C1orf212, DLGAP3	132, 45699	in gene, downstream	ActReg chr1 #249	1	1
250	1	35,389,867	35,391,142	1,275	2	13.5	16.125	31	43	0	0	0				ActReg chr1 #250	1	1
251	1	35,450,473	35,451,244	771	2	9.167	10.042	14	18	1	1	2	LOC100506144, ZMYM6	90, 46711	in gene, downstream	ActReg chr1 #251	1	1
252	1	35,497,027	35,497,833	806	2	11.4	11.68	17	20	1	1	1	ZMYM6	139	in gene	ActReg chr1 #252	1	1
253	1	35,658,098	35,659,045	947	2	10.133	11.667	15	19	1	1	1	SFPQ	172	in gene	ActReg chr1 #253	1	1
254	1	36,022,834	36,023,610	776	1	10.042	14.042	15	25	1	2	2	KIAA0319L, NCDN	-185, -171	upstream, upstream	ActReg chr1 #254	0	1
255	1	36,106,793	36,107,502	709	2	10.636	9.955	22	19	1	1	1	PSMB2	-4	upstream	ActReg chr1 #255	1	1
256	1	36,116,207	36,116,946	739	1	6.478	10.435	14	14	0	0	1	PSMB2	-9,433	upstream	ActReg chr1 #256	0	1
257	1	36,125,913	36,127,333	1,420	2	11.911	15.111	36	43	0	0	0				ActReg chr1 #257	1	1
258	1	36,184,078	36,184,958	880	1	8.852	11.63	14	14	1	1	1	C1orf216	272	in gene	ActReg chr1 #258	0	1
259	1	36,342,215	36,343,071	856	2	9.462	11.462	19	16	0	1	1	EIF2C1	-6,167	upstream	ActReg chr1 #259	1	1
260	1	36,396,508	36,397,233	725	1	6.217	12.913	9	22	1	1	2	EIF2C1, EIF2C3	48060, 98	downstream, in gene	ActReg chr1 #260	0	1
261	1	36,553,938	36,555,134	1,196	2	20.108	22.351	51	54	1	1	3	TEKT2, ADPRHL2, COL8A2	4860, 83, 11314	downstream, in gene, downstream	ActReg chr1 #261	1	1
262	1	36,616,117	36,616,839	722	1	7.565	11.652	12	16	0	2	2	TRAPPC3, MAP7D1	-1411, -5325	upstream, upstream	ActReg chr1 #262	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
263	1	36,689,402	36,690,576	1,174	2	11.27	13.892	25	24	1	1	1	THRAP3	-28	upstream	ActReg chr1 #263	1	1
264	1	36,765,530	36,766,116	586	1	10.79	7.579	15	11	0	1	2	THRAP3, C1orf113	75806, -6171	in gene, upstream	ActReg chr1 #264	1	0
265	1	36,817,501	36,818,797	1,296	1	8.878	11.78	15	18	0	0	1	STK40	33,336	in gene	ActReg chr1 #265	0	1
266	1	36,839,805	36,840,914	1,109	2	12.086	12.114	20	21	0	0	2	STK40, LOC100506594	11126, 7739	in gene, in gene	ActReg chr1 #266	1	1
267	1	36,851,857	36,852,735	878	2	11.778	13.963	19	25	1	1	3	STK40, LOC100506594, LSM10	-811, 19676, 11197	upstream, downstream, downstream	ActReg chr1 #267	1	1
268	1	36,863,023	36,863,775	752	2	12.652	11.609	23	19	1	1	1	LSM10	94	in gene	ActReg chr1 #268	1	1
269	1	36,929,460	36,930,414	954	2	17.667	21.267	47	55	1	1	2	MRPS15, CSF3R	103, 18978	in gene, downstream	ActReg chr1 #269	1	1
270	1	37,068,900	37,069,574	674	1	9.429	15	19	32	0	0	0				ActReg chr1 #270	0	1
271	1	37,389,541	37,390,389	848	1	9.731	15.269	17	31	0	0	1	GRIK3	109,879	in gene	ActReg chr1 #271	0	1
272	1	37,431,524	37,432,480	956	2	13.9	21.767	28	47	0	0	1	GRIK3	67,842	in gene	ActReg chr1 #272	1	1
273	1	37,486,139	37,486,719	580	2	9.778	9.125	18	17	0	0	1	GRIK3	13,415	in gene	ActReg chr1 #273	1	1
274	1	37,720,951	37,721,518	567	1	9.889	10.333	16	16	0	0	0				ActReg chr1 #274	0	1
275	1	37,875,753	37,876,845	1,092	1	7.5	12.706	12	29	0	0	0				ActReg chr1 #275	0	1
276	1	37,945,059	37,946,031	972	1	8.7	9.933	18	15	0	1	2	LOC728431, ZC3H12A	-5498, 5426	upstream, in gene	ActReg chr1 #276	0	1
277	1	38,157,047	38,158,512	1,465	2	10.674	11.587	18	21	1	2	2	C1orf109, CDCA8	-1587, -380	upstream, upstream	ActReg chr1 #277	1	1
278	1	38,229,522	38,231,062	1,540	2	11.75	14.167	25	36	1	1	1	EPHA10	532	in gene	ActReg chr1 #278	1	1
279	1	38,273,679	38,274,273	594	2	12.526	16.053	22	30	1	2	4	MANEAL, YRDC, C1orf122, MTF1	14202, -111, 503, 51316	downstream, upstream, in gene, downstream	ActReg chr1 #279	1	1
280	1	38,324,807	38,326,182	1,375	2	11.837	11.767	19	22	1	1	2	MTF1, INPP5B	-202, 87235	upstream, downstream	ActReg chr1 #280	1	1
281	1	38,455,077	38,456,298	1,221	2	43.763	48.947	172	183	1	1	2	SF3A3, FHL3	74, 15547	in gene, downstream	ActReg chr1 #281	1	1
282	1	38,477,875	38,478,979	1,104	2	10.2	13.2	17	23	1	2	2	FHL3, UTP11L	-7193, 43	upstream, in gene	ActReg chr1 #282	1	1
283	1	38,529,748	38,530,664	916	1	10.586	13.793	21	22	0	0	0				ActReg chr1 #283	0	1
284	1	38,541,485	38,542,355	870	2	12.63	13.333	28	28	0	0	0				ActReg chr1 #284	1	1
285	1	39,456,612	39,457,224	612	1	7.684	11.526	15	21	1	1	1	AKIRIN1	2	in gene	ActReg chr1 #285	0	1
286	1	40,042,471	40,043,250	779	2	11.208	11.917	18	20	1	1	3	PABPC4, LOC100506950, SNORA55	-339, 12091, -9678	upstream, downstream, upstream	ActReg chr1 #286	1	1
287	1	40,264,744	40,265,245	501	1	10	7.8	16	12	0	0	1	LOC100287437	10,340	downstream	ActReg chr1 #287	1	0
288	1	40,348,815	40,349,483	668	1	8.571	11	14	21	1	1	1	TRIT1	28	in gene	ActReg chr1 #288	0	1
289	1	40,420,615	40,421,445	830	1	7.692	10	13	14	1	1	1	MFSD2A	246	in gene	ActReg chr1 #289	0	1
290	1	40,626,658	40,627,856	1,198	2	11.46	11.514	22	26	1	1	1	RLF	216	in gene	ActReg chr1 #290	1	1
291	1	40,723,333	40,724,328	995	2	16.387	12.516	28	26	2	1	2	TMCO2, ZMPSTE24	10257, 97	downstream, in gene	ActReg chr1 #291	1	1
292	1	40,839,765	40,840,854	1,089	2	9.147	10.706	18	15	1	1	2	LOC100286988, SMAP2	32234, 581	in gene, in gene	ActReg chr1 #292	1	1
293	1	40,915,396	40,916,258	862	1	7.63	13.889	14	23	1	1	1	ZNF643	-510	upstream	ActReg chr1 #293	0	1
294	1	40,942,796	40,943,339	543	1	8.882	9.294	17	13	1	1	1	ZNF642	-235	upstream	ActReg chr1 #294	1	0
295	1	40,973,994	40,974,884	890	2	13.071	11.536	21	16	1	1	1	DEM1	6	in gene	ActReg chr1 #295	1	1
296	1	40,996,958	40,997,706	748	1	4.792	13.375	9	21	1	1	1	ZNF684	99	in gene	ActReg chr1 #296	0	1
297	1	41,091,415	41,092,244	829	1	7.385	12.269	17	19	0	0	1	RIMS3	39,495	in gene	ActReg chr1 #297	0	1
298	1	41,157,024	41,157,920	896	1	8.103	12.552	12	21	1	2	2	LOC100130557, NFYC	461, 230	in gene, in gene	ActReg chr1 #298	0	1
299	1	41,384,967	41,385,682	715	1	13.046	8.045	19	13	0	0	0				ActReg chr1 #299	1	0
300	1	41,444,553	41,445,435	882	1	8.815	11.185	16	16	1	1	1	CTPS	-13	upstream	ActReg chr1 #300	0	1
301	1	41,979,802	41,980,486	684	1	9.091	12.591	14	25	0	0	1	HIVEP3	404,352	in gene	ActReg chr1 #301	0	1
302	1	42,248,744	42,249,560	816	1	12.32	9.88	18	16	0	0	1	HIVEP3	135,344	in gene	ActReg chr1 #302	1	0
303	1	42,275,924	42,277,290	1,366	3	12.535	12.512	32	26	0	0	1	HIVEP3	107,889	in gene	ActReg chr1 #303	1	1
304	1	42,312,175	42,312,858	683	1	12.714	8.857	20	13	0	0	2	HIVEP3, LOC100507198	71980, 25374	in gene, downstream	ActReg chr1 #304	1	0
305	1	42,316,989	42,317,597	608	1	7.944	10.21	13	14	0	0	2	HIVEP3, LOC100507198	67203, 20597	in gene, in gene	ActReg chr1 #305	0	1
306	1	42,335,615	42,336,333	718	1	11.348	10.348	21	14	0	1	2	HIVEP3, LOC100507198	48522, 1916	in gene, in gene	ActReg chr1 #306	1	0
307	1	42,383,621	42,384,437	816	1	6.72	9.6	12	13	1	1	1	HIVEP3	467	in gene	ActReg chr1 #307	0	1
308	1	42,386,223	42,386,765	542	1	10.941	4.294	21	8	0	1	1	HIVEP3	-1,998	upstream	ActReg chr1 #308	1	0
309	1	42,401,577	42,402,356	779	2	12.773	10.667	29	18	0	0	0				ActReg chr1 #309	1	1
310	1	42,800,672	42,801,484	812	1	8.923	12.346	14	23	1	1	1	FOXJ3	-175	upstream	ActReg chr1 #310	0	1
311	1	42,845,405	42,846,088	683	2	12	12	18	19	1	1	1	RIMKLA	-722	upstream	ActReg chr1 #311	1	1
312	1	42,921,810	42,922,871	1,061	1	9.303	14.364	14	22	1	3	3	ZMYND12, PPCS, LOC100507214	-402, 167, -6617	upstream, in gene, upstream	ActReg chr1 #312	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
313	1	42,995,569	42,996,146	577	1	14.5	9.611	29	23	0	1	1	CCDC30	-4,703	upstream	ActReg chr1 #313	1	0
314	1	43,123,533	43,124,621	1,088	2	10.941	13.059	20	22	1	1	2	CCDC30, PPIH	123517, 29	downstream, in gene	ActReg chr1 #314	1	1
315	1	43,311,760	43,313,061	1,301	1	7.561	11.024	14	17	1	1	2	ERMAP, ZNF691	29634, 130	downstream, in gene	ActReg chr1 #315	0	1
316	1	43,365,418	43,366,100	682	1	4.524	11.905	7	17	0	0	0				ActReg chr1 #316	0	1
317	1	43,424,202	43,425,079	877	2	10.37	12.37	14	20	1	2	2	SLC2A1, FLJ32224	207, -80	in gene, upstream	ActReg chr1 #317	1	1
318	1	43,814,713	43,815,363	650	1	6	11.476	11	20	1	0	2	MPL, CDC20	11563, -9588	in gene, upstream	ActReg chr1 #318	0	1
319	1	43,855,060	43,855,982	922	2	11.552	11.724	17	24	1	2	2	MED8, C1orf84	-38, -35	upstream, upstream	ActReg chr1 #319	1	1
320	1	43,988,680	43,989,445	765	2	13.667	14.417	30	30	0	1	1	PTPRF	-7,485	upstream	ActReg chr1 #320	1	1
321	1	44,299,907	44,301,783	1,876	3	8.655	10.828	21	18	0	0	1	ST3GAL3	127,627	in gene	ActReg chr1 #321	1	1
322	1	44,395,080	44,395,774	694	1	11.762	11.619	24	22	0	1	2	ST3GAL3, ARTN	222209, -3565	in gene, upstream	ActReg chr1 #322	1	0
323	1	44,411,761	44,412,886	1,125	2	13.057	14.314	25	25	1	1	2	ARTN, IPO13	13331, -155	downstream, upstream	ActReg chr1 #323	1	1
324	1	44,433,895	44,434,603	708	1	12.954	10.954	24	17	0	2	3	IPO13, DPH2, ATP6V0B	21771, -1404, -6353	downstream, upstream, upstream	ActReg chr1 #324	1	0
325	1	44,496,049	44,496,676	627	1	7.8	11.45	12	18	1	1	1	SLC6A9	772	in gene	ActReg chr1 #325	0	1
326	1	44,678,818	44,679,363	545	1	15.059	12.235	30	25	1	1	2	DMAP1, ERI3	-35, 141849	upstream, downstream	ActReg chr1 #326	1	0
327	1	44,793,222	44,793,935	713	1	11.682	8.091	17	12	0	0	1	ERI3	27,361	in gene	ActReg chr1 #327	1	0
328	1	44,997,531	44,998,316	785	2	12.52	13.96	26	29	0	0	1	RNF220	126,963	in gene	ActReg chr1 #328	1	1
329	1	45,187,247	45,188,195	948	2	14.8	14.633	27	27	0	0	2	C1orf228, RNU5D	47327, 9119	in gene, downstream	ActReg chr1 #329	1	1
330	1	45,196,534	45,197,312	778	2	11.72	14.36	21	34	0	1	3	C1orf228, RNU5D, KIF2C	56529, -83, 8567	downstream, upstream, upstream	ActReg chr1 #330	1	1
331	1	45,240,634	45,241,542	908	2	11.448	10.862	23	24	1	5	7	KIF2C, RPS8, SNORD55, SNORD46, SNORD38A, SNORD38B, BEST4	35598, -158, -449, -1076, -2426, -2974, 12338	downstream, upstream, upstream, upstream, upstream, upstream, downstream	ActReg chr1 #331	1	1
332	1	45,285,114	45,286,589	1,475	2	11.717	13.761	31	35	0	0	2	BTBD19, PTCH2	11697, 22765	downstream, in gene	ActReg chr1 #332	1	1
333	1	45,451,807	45,452,717	910	2	17.379	22.69	47	57	1	1	1	EIF2B3	99	in gene	ActReg chr1 #333	1	1
334	1	45,476,288	45,478,190	1,902	2	13.233	17.45	46	43	1	2	3	HECTD3, UROD, ZSWIM5	-212, -566, 195011	upstream, upstream, downstream	ActReg chr1 #334	1	1
335	1	45,792,434	45,793,421	987	1	4.774	12.032	8	22	1	1	2	HPDL, MUTYH	382, 13215	in gene, downstream	ActReg chr1 #335	0	1
336	1	45,965,393	45,966,259	866	2	14.963	15.333	32	32	1	2	3	TESK2, CCDC163P, MMACHC	-8986, -75, 30	upstream, upstream, upstream	ActReg chr1 #336	1	1
337	1	45,986,853	45,988,003	1,150	1	8.694	13.111	17	25	1	1	1	PRDX1	181	in gene	ActReg chr1 #337	0	1
338	1	46,049,198	46,050,139	941	2	15.207	12.31	28	18	1	1	1	NASP	-49	upstream	ActReg chr1 #338	1	1
339	1	46,151,763	46,153,365	1,602	2	10.72	11.16	18	21	1	2	3	GPBP1L1, TMEM69, IPP	-262, -1283, 63921	upstream, upstream, downstream	ActReg chr1 #339	1	1
340	1	46,153,474	46,154,145	671	1	7.238	11.191	12	17	0	2	3	GPBP1L1, TMEM69, IPP	-1507, -38, 62676	upstream, upstream, downstream	ActReg chr1 #340	0	1
341	1	46,215,754	46,216,684	930	1	10.138	13.69	16	19	1	1	1	IPP	266	in gene	ActReg chr1 #341	0	1
342	1	46,597,993	46,598,875	882	2	15.148	19.926	36	42	1	1	1	PIK3R3	274	in gene	ActReg chr1 #342	1	1
343	1	46,600,351	46,600,935	584	1	8.789	10.316	14	16	0	1	1	PIK3R3	-1,935	upstream	ActReg chr1 #343	0	1
344	1	46,713,176	46,713,769	593	2	15.421	15.158	29	36	0	1	1	RAD54L	105	in gene	ActReg chr1 #344	1	1
345	1	46,767,286	46,768,893	1,607	2	11.12	13.74	19	21	1	2	2	LRRC41, UQCRH	949, -1291	in gene, upstream	ActReg chr1 #345	1	1
346	1	46,768,912	46,769,714	802	1	12.84	8.84	20	18	1	2	2	LRRC41, UQCRH	-275, -67	upstream, upstream	ActReg chr1 #346	1	0
347	1	47,184,250	47,185,300	1,050	2	19.394	17.424	45	41	1	1	1	KIAA0494	-39	upstream	ActReg chr1 #347	1	1
348	1	47,201,113	47,201,999	886	2	13.821	12.107	23	20	0	0	0				ActReg chr1 #348	1	1
349	1	47,644,778	47,645,375	597	1	4.5	12.944	7	20	0	0	1	PDZK1IP1	10,695	downstream	ActReg chr1 #349	0	1
350	1	47,779,422	47,780,018	596	2	11.632	10.421	20	18	1	1	1	STIL	99	in gene	ActReg chr1 #350	1	1
351	1	47,902,717	47,904,079	1,362	1	8.023	13.046	15	22	1	2	2	MGC12982, FOXD2	-3085, 1709	upstream, in gene	ActReg chr1 #351	0	1
352	1	48,043,088	48,044,397	1,309	2	9.756	10.78	17	16	0	0	0				ActReg chr1 #352	1	1
353	1	48,681,220	48,682,153	933	1	6.552	11.69	10	17	0	1	1	SLC5A9	-6,671	upstream	ActReg chr1 #353	0	1
354	1	48,937,241	48,937,839	598	1	10.21	7.789	16	11	1	1	1	SPATA6	336	in gene	ActReg chr1 #354	1	0
355	1	48,959,626	48,960,762	1,136	2	11	11.829	18	18	0	0	0				ActReg chr1 #355	1	1
356	1	48,996,252	48,997,388	1,136	2	15.833	15.028	36	37	0	0	1	AGBL4	1,492,806	downstream	ActReg chr1 #356	1	1
357	1	49,084,792	49,085,583	791	1	7.52	11.44	13	18	0	0	1	AGBL4	1,404,439	in gene	ActReg chr1 #357	0	1
358	1	49,318,448	49,319,254	806	2	12.36	12.84	23	22	0	0	1	AGBL4	1,170,775	in gene	ActReg chr1 #358	1	1
359	1	49,817,396	49,817,913	517	1	10.375	6.5	15	11	0	0	1	AGBL4	671,972	in gene	ActReg chr1 #359	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
360	1	50,733,590	50,734,269	679	2	12	10.524	26	19	0	0	0				ActReg chr1 #360	1	1
361	1	50,745,509	50,746,172	663	2	8.7	10.4	16	21	0	0	0				ActReg chr1 #361	1	1
362	1	50,774,327	50,775,043	716	2	12.13	14	24	29	0	0	0				ActReg chr1 #362	1	1
363	1	51,425,610	51,426,363	753	2	10.13	13.174	19	21	1	1	2	FAF1, CDKN2C	-50, -8381	upstream, upstream	ActReg chr1 #363	1	1
364	1	51,433,803	51,435,092	1,289	1	7.675	13.325	12	23	1	1	2	FAF1, CDKN2C	-8511, 80	upstream, in gene	ActReg chr1 #364	0	1
365	1	51,701,624	51,702,618	994	1	11.968	7.419	19	15	1	1	1	RNF11	176	in gene	ActReg chr1 #365	1	0
366	1	52,006,810	52,007,526	716	1	11.696	10.348	17	15	0	0	0				ActReg chr1 #366	1	0
367	1	52,035,069	52,036,118	1,049	1	11.546	10.061	16	16	0	0	0				ActReg chr1 #367	1	0
368	1	52,062,700	52,063,741	1,041	1	13.562	11.125	22	17	0	1	1	OSBPL9	673	in gene	ActReg chr1 #368	1	0
369	1	52,194,903	52,195,492	589	1	8.789	9.526	11	17	1	0	1	OSBPL9	112,650	in gene	ActReg chr1 #369	0	1
370	1	52,498,989	52,499,604	615	2	12.684	12.79	17	21	1	1	2	TXNDC12, KTI12	21751, 176	in gene, in gene	ActReg chr1 #370	1	1
371	1	52,520,590	52,521,397	807	1	9.64	13.28	14	21	1	2	2	TXNDC12, BTF3L4	54, -864	in gene, upstream	ActReg chr1 #371	0	1
372	1	52,521,644	52,522,610	966	2	12.233	11.533	17	20	1	2	2	TXNDC12, BTF3L4	-1080, 270	upstream, in gene	ActReg chr1 #372	1	1
373	1	52,869,271	52,870,569	1,298	2	10.439	12.439	18	17	1	2	2	ORC1L, PRPF38A	223, -299	in gene, upstream	ActReg chr1 #373	1	1
374	1	53,480,240	53,480,932	692	2	9.636	11.046	19	22	0	0	1	SCP2	87,685	in gene	ActReg chr1 #374	1	1
375	1	53,662,433	53,663,161	728	1	6.364	12.273	8	16	1	1	1	CPT2	696	in gene	ActReg chr1 #375	0	1
376	1	53,685,770	53,686,535	765	2	12.958	13.458	19	22	1	1	3	CPT2, C1orf123, MAGOH	24051, 137, 18055	downstream, in gene, downstream	ActReg chr1 #376	1	1
377	1	53,703,849	53,704,585	736	2	9.739	14.217	15	27	1	2	3	MAGOH, LOC100507564, LRP8	-10, -65, 89604	upstream, upstream, downstream	ActReg chr1 #377	1	1
378	1	53,791,032	53,793,088	2,056	1	8.344	12.846	18	21	1	1	1	LRP8	1,761	in gene	ActReg chr1 #378	0	1
379	1	54,303,337	54,304,612	1,275	2	19.975	27.025	50	78	1	1	1	TMEM48	251	in gene	ActReg chr1 #379	1	1
380	1	54,354,933	54,356,014	1,081	2	17.353	21.647	48	56	1	2	2	YIPF1, DIO1	-20, -4388	upstream, upstream	ActReg chr1 #380	1	1
381	1	54,518,504	54,519,866	1,362	2	9.143	12.643	22	20	1	2	2	TMEM59, C1orf83	-74, -89	upstream, upstream	ActReg chr1 #381	1	1
382	1	54,665,821	54,666,450	629	1	7.35	11.95	12	20	1	2	2	CYB5RL, MRPL37	-389, 295	upstream, in gene	ActReg chr1 #382	0	1
383	1	54,830,722	54,831,449	727	1	6.591	9.773	13	13	0	0	1	SSBP3	41,007	in gene	ActReg chr1 #383	0	1
384	1	55,181,064	55,181,844	780	1	9.083	13.625	14	25	1	1	2	C1orf175, TTC4	74027, -41	downstream, upstream	ActReg chr1 #384	0	1
385	1	55,269,354	55,269,986	632	1	7.7	10.9	15	15	0	2	2	TTC22, C1orf177	-2729, -2066	upstream, upstream	ActReg chr1 #385	0	1
386	1	55,680,861	55,681,596	735	1	9.174	12.826	14	21	1	2	2	USP24, LOC100507634	-189, 148	upstream, in gene	ActReg chr1 #386	0	1
387	1	55,894,612	55,895,530	918	2	10.828	11.966	16	20	0	0	0				ActReg chr1 #387	1	1
388	1	56,129,038	56,129,449	411	1	8	9.462	11	14	0	0	0				ActReg chr1 #388	0	1
389	1	57,142,245	57,142,838	593	1	9.667	11.389	15	22	0	0	1	PRKAA2	31,551	in gene	ActReg chr1 #389	0	1
390	1	59,012,174	59,012,830	656	1	10.15	13.95	19	23	1	1	1	OMA1	-56	upstream	ActReg chr1 #390	0	1
391	1	59,192,794	59,193,603	809	2	9.769	11.5	18	17	0	0	0				ActReg chr1 #391	1	1
392	1	59,197,522	59,198,074	552	2	9.706	10.059	15	17	0	0	0				ActReg chr1 #392	1	1
393	1	59,220,722	59,221,611	889	1	9.571	13.786	14	21	0	0	0				ActReg chr1 #393	0	1
394	1	59,247,401	59,248,223	822	1	11.24	9.12	16	15	1	2	2	JUN, LOC100131060	1973, -3011	in gene, upstream	ActReg chr1 #394	1	0
395	1	59,249,054	59,251,191	2,137	2	11.269	10.851	20	20	1	2	2	JUN, LOC100131060	-337, -701	upstream, upstream	ActReg chr1 #395	1	1
396	1	59,314,106	59,315,049	943	2	10.5	12.2	15	25	0	0	1	LOC100131060	63,754	in gene	ActReg chr1 #396	1	1
397	1	59,616,445	59,617,421	976	1	9.194	10.806	16	16	0	1	1	LOC729467	-4,454	upstream	ActReg chr1 #397	0	1
398	1	59,920,452	59,921,173	721	1	11.909	7.136	18	14	0	0	1	FGGY	158,187	in gene	ActReg chr1 #398	1	0
399	1	59,942,790	59,943,388	598	1	7.056	13.5	10	23	0	0	1	FGGY	180,464	in gene	ActReg chr1 #399	0	1
400	1	60,135,449	60,136,073	624	1	5.5	12.55	8	22	0	0	1	FGGY	373,136	in gene	ActReg chr1 #400	0	1
401	1	60,144,440	60,144,981	541	1	9.412	8.471	18	13	0	0	1	FGGY	382,085	in gene	ActReg chr1 #401	1	0
402	1	60,196,301	60,197,374	1,073	2	10.667	10.454	25	17	0	0	1	FGGY	434,212	in gene	ActReg chr1 #402	1	1
403	1	62,190,366	62,191,299	933	2	13.633	14.433	32	30	1	1	1	TM2D1	263	in gene	ActReg chr1 #403	1	1
404	1	62,458,852	62,459,515	663	1	4.1	13.35	8	23	0	0	1	INADL	251,034	in gene	ActReg chr1 #404	0	1
405	1	62,902,199	62,903,033	834	1	9.923	11.5	18	19	1	1	1	USP1	641	in gene	ActReg chr1 #405	0	1
406	1	63,154,123	63,154,659	536	1	5.176	9.882	9	16	1	1	1	DOCK7	-422	upstream	ActReg chr1 #406	0	1
407	1	63,833,135	63,833,772	637	1	6.8	13.15	11	22	1	1	1	ALG6	192	in gene	ActReg chr1 #407	0	1
408	1	63,988,602	63,989,646	1,044	2	15.424	14.727	39	42	0	2	2	ITGB3BP, EFCAB7	-289, 111	upstream, in gene	ActReg chr1 #408	1	1
409	1	64,058,705	64,059,772	1,067	2	10.121	13.788	16	22	1	1	1	PGM1	291	in gene	ActReg chr1 #409	1	1
410	1	64,127,668	64,129,099	1,431	1	12.222	7.889	19	14	0	0	1	PGM1	69,436	downstream	ActReg chr1 #410	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
411	1	64,434,846	64,435,526	680	2	10.182	12	17	21	0	0	1	ROR1	195,496	in gene	ActReg chr1 #411	1	1
412	1	64,509,494	64,510,134	640	1	10.2	6.3	17	13	0	0	1	ROR1	270,124	in gene	ActReg chr1 #412	1	0
413	1	64,542,884	64,543,579	695	1	8.842	12.286	16	17	0	0	1	ROR1	303,541	in gene	ActReg chr1 #413	0	1
414	1	64,598,672	64,599,608	936	1	8	12.414	16	19	0	0	1	ROR1	359,450	in gene	ActReg chr1 #414	0	1
415	1	64,935,465	64,936,028	563	1	9.059	11.059	12	14	1	1	1	CACHD1	-730	upstream	ActReg chr1 #415	0	1
416	1	65,210,917	65,211,340	423	1	10	5.385	15	9	1	1	1	RAVER2	350	in gene	ActReg chr1 #416	1	0
417	1	65,533,376	65,534,022	646	1	6.524	10.048	11	17	2	0	1	MIR101-1	-9,508	upstream	ActReg chr1 #417	0	1
418	1	65,640,031	65,640,633	602	1	7.158	10	9	20	0	0	1	AK3L1	27,100	in gene	ActReg chr1 #418	0	1
419	1	65,729,867	65,730,707	840	2	10.5	9.769	18	19	0	1	1	DNAJC6	-143	upstream	ActReg chr1 #419	1	1
420	1	65,775,319	65,775,895	576	2	16.667	13.444	30	24	1	0	2	DNAJC6, LOC100505510	45177, 11321	in gene, downstream	ActReg chr1 #420	1	1
421	1	65,924,590	65,925,440	850	2	7.37	10.63	17	17	0	0	1	LEPR	38,767	in gene	ActReg chr1 #421	1	1
422	1	66,488,495	66,489,183	688	2	11.286	11.381	23	22	0	0	1	PDE4B	230,646	in gene	ActReg chr1 #422	1	1
423	1	66,727,776	66,728,498	722	2	12.348	10.261	23	16	0	0	1	PDE4B	469,944	in gene	ActReg chr1 #423	1	1
424	1	66,736,715	66,737,265	550	1	11	7.412	16	12	0	0	1	PDE4B	478,797	in gene	ActReg chr1 #424	1	0
425	1	66,987,415	66,987,917	502	1	8.188	12.562	11	18	0	0	0				ActReg chr1 #425	0	1
426	1	67,390,452	67,391,599	1,147	1	9.167	14.472	15	22	1	2	2	WDR78, MIER1	-455, 447	upstream, in gene	ActReg chr1 #426	0	1
427	1	67,519,458	67,520,227	769	1	11.667	9.167	17	13	1	1	1	SLC35D1	238	in gene	ActReg chr1 #427	1	0
428	1	67,865,406	67,866,037	631	1	12.75	8.3	22	16	0	0	2	IL12RB2, SERBP1	92674, 30402	downstream, downstream	ActReg chr1 #428	1	0
429	1	67,895,759	67,896,734	975	2	14.533	9.233	27	15	1	1	1	SERBP1	-123	upstream	ActReg chr1 #429	1	1
430	1	68,298,318	68,299,211	893	1	6.929	10.857	12	16	1	2	2	GNG12, LOC100289178	391, 778	in gene, in gene	ActReg chr1 #430	0	1
431	1	68,299,214	68,299,698	484	1	5.8	10.133	12	16	1	2	2	GNG12, LOC100289178	-301, 1470	upstream, in gene	ActReg chr1 #431	0	1
432	1	68,353,832	68,354,603	771	2	14.375	12.375	32	26	0	0	1	LOC100289178	56,231	in gene	ActReg chr1 #432	1	1
433	1	68,578,005	68,579,165	1,160	1	10.806	7.417	20	19	0	0	2	LOC100289178, GPR177	280599, 119699	in gene, in gene	ActReg chr1 #433	1	0
434	1	68,796,270	68,797,163	893	2	12.821	11.25	23	21	0	0	0				ActReg chr1 #434	1	1
435	1	68,849,577	68,850,314	737	1	9.391	12.217	13	15	0	0	0				ActReg chr1 #435	0	1
436	1	68,962,277	68,963,127	850	1	8.769	12.808	14	23	1	1	1	DEPDC1	97	in gene	ActReg chr1 #436	0	1
437	1	70,137,212	70,137,707	495	1	9.188	9.562	13	16	0	0	0				ActReg chr1 #437	0	1
438	1	70,503,605	70,504,218	613	1	13.79	10.21	24	20	0	0	1	LRRC7	278,053	in gene	ActReg chr1 #438	1	0
439	1	70,670,949	70,671,823	874	1	11.185	12.963	20	22	1	2	2	LRRC40, SFRS11	-25, 21	upstream, in gene	ActReg chr1 #439	0	1
440	1	70,686,922	70,687,437	515	1	8.75	13.125	12	18	1	0	1	SFRS11	15,814	in gene	ActReg chr1 #440	0	1
441	1	70,819,834	70,821,024	1,190	2	8.842	11.316	19	17	1	2	2	ANKRD13C, HHLA3	-12, -64	upstream, upstream	ActReg chr1 #441	1	1
442	1	70,876,299	70,877,260	961	1	10.7	13	14	20	1	1	1	CTH	-122	upstream	ActReg chr1 #442	0	1
443	1	71,546,483	71,547,356	873	2	14.518	14.482	32	30	1	1	1	ZRANB2	53	in gene	ActReg chr1 #443	1	1
444	1	72,749,173	72,749,875	702	1	11.909	9.318	16	15	1	1	1	NEGR1	-1,247	upstream	ActReg chr1 #444	1	0
445	1	74,967,876	74,968,778	902	2	17.5	25.679	43	62	0	0	1	TNNI3K	304,380	in gene	ActReg chr1 #445	1	1
446	1	76,138,395	76,139,069	674	1	5.476	12.952	9	21	0	0	0				ActReg chr1 #446	0	1
447	1	76,190,093	76,190,649	556	1	8.941	11.941	15	17	1	1	1	ACADM	328	in gene	ActReg chr1 #447	0	1
448	1	76,251,543	76,252,233	690	1	4.476	11.182	9	16	0	4	4	RABGGTB, SNORD45C, SNORD45A, SNORD45B	2, -869, -1686, -3274	in gene, upstream, upstream, upstream	ActReg chr1 #448	0	1
449	1	77,333,881	77,334,537	656	1	8.238	10.619	14	15	1	1	1	ST6GALNAC5	1,023	in gene	ActReg chr1 #449	0	1
450	1	77,502,059	77,502,801	742	1	7.783	12.957	13	24	0	0	1	ST6GALNAC5	169,244	in gene	ActReg chr1 #450	0	1
451	1	77,505,296	77,506,034	738	1	12.522	9.957	29	15	0	0	1	ST6GALNAC5	172,479	in gene	ActReg chr1 #451	1	0
452	1	77,684,674	77,685,293	619	1	7.053	11.421	12	21	1	1	1	PIGK	149	in gene	ActReg chr1 #452	0	1
453	1	78,147,881	78,148,782	901	1	7.5	10.571	11	15	1	1	1	ZZZ3	12	in gene	ActReg chr1 #453	0	1
454	1	78,148,892	78,149,599	707	1	10.546	12.5	15	18	1	1	1	ZZZ3	-902	upstream	ActReg chr1 #454	0	1
455	1	78,262,223	78,262,712	489	1	11.333	6.8	13	9	0	0	1	FAM73A	17,158	in gene	ActReg chr1 #455	1	0
456	1	78,470,024	78,470,678	654	1	9.2	10.2	13	16	0	1	1	DNAJB4	-285	upstream	ActReg chr1 #456	0	1
457	1	81,640,525	81,641,066	541	1	5.118	10	7	15	0	0	0				ActReg chr1 #457	0	1
458	1	81,702,960	81,703,579	619	1	11.947	6.842	18	9	0	0	0				ActReg chr1 #458	1	0
459	1	81,879,972	81,880,537	565	1	4.812	8.353	8	16	0	0	0				ActReg chr1 #459	0	1
460	1	82,266,810	82,267,358	548	1	7.941	11.647	12	20	1	1	1	LPHN2	1,002	in gene	ActReg chr1 #460	0	1
461	1	82,385,964	82,386,390	426	1	7.769	10.462	11	14	0	0	1	LPHN2	120,095	in gene	ActReg chr1 #461	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
462	1	84,464,533	84,465,265	732	2	9	11.739	16	20	1	1	1	TTLL7	-66	upstream	ActReg chr1 #462	1	1
463	1	84,944,493	84,945,037	544	1	7.706	8.706	13	16	1	1	1	RPF1	-155	upstream	ActReg chr1 #463	0	1
464	1	85,985,946	85,987,770	1,824	2	12.123	13.018	22	28	0	0	1	DDAH1	57,188	in gene	ActReg chr1 #464	1	1
465	1	86,952,418	86,953,352	934	2	8	11.034	16	16	0	0	1	CLCA1	18,359	in gene	ActReg chr1 #465	1	1
466	1	87,379,546	87,380,022	476	1	6.429	9.133	9	13	1	2	2	SEP15, HS2ST1	323, -551	in gene, upstream	ActReg chr1 #466	0	1
467	1	87,900,932	87,901,570	638	1	5.4	9.7	11	18	0	0	0				ActReg chr1 #467	0	1
468	1	89,149,599	89,150,182	583	1	4.579	8.632	8	14	1	1	1	PKN2	-32	upstream	ActReg chr1 #468	0	1
469	1	89,356,975	89,357,624	649	1	8.312	11.15	16	22	1	1	1	GTF2B	2	in gene	ActReg chr1 #469	0	1
470	1	89,457,903	89,458,469	566	1	5.056	9.944	8	16	1	2	2	CCBL2, RBMXL1	457, 457	in gene, in gene	ActReg chr1 #470	0	1
471	1	90,460,375	90,461,096	721	2	10.348	10.87	18	15	1	1	1	ZNF326	57	in gene	ActReg chr1 #471	1	1
472	1	91,870,015	91,870,599	584	2	11	11.158	21	22	1	1	1	HFM1	119	in gene	ActReg chr1 #472	1	1
473	1	92,292,649	92,293,679	1,030	1	6.438	12.719	13	22	0	0	1	TGFBR3	58,623	in gene	ActReg chr1 #473	0	1
474	1	92,350,895	92,351,470	575	1	7.889	10.389	10	14	1	1	1	TGFBR3	605	in gene	ActReg chr1 #474	0	1
475	1	92,545,988	92,546,420	432	1	6.769	10.077	10	14	1	2	2	LOC646817, BTBD8	-5236, 342	upstream, in gene	ActReg chr1 #475	0	1
476	1	92,764,098	92,764,579	481	2	10.267	8.467	15	17	1	2	2	GLMN, RPAP2	228, -184	in gene, upstream	ActReg chr1 #476	1	1
477	1	93,297,097	93,298,189	1,092	2	44.765	44.941	156	158	1	2	4	RPL5, SNORD21, SNORA66, FAM69A	49, -5203, -8633, 129436	in gene, upstream, upstream, downstream	ActReg chr1 #477	1	1
478	1	93,544,388	93,545,115	727	1	9.136	12.818	13	23	1	1	1	MTF2	-41	upstream	ActReg chr1 #478	0	1
479	1	93,645,694	93,646,499	805	2	10.962	11.462	21	21	1	2	2	TMED5, CCDC18	150, 176	in gene, in gene	ActReg chr1 #479	1	1
480	1	94,071,306	94,071,857	551	1	10.882	7.706	18	14	0	0	2	BCAR3, LOC100129046	75804, 14056	in gene, downstream	ActReg chr1 #480	1	0
481	1	94,146,084	94,146,545	461	1	12	8.143	15	12	1	1	1	BCAR3	1,071	in gene	ActReg chr1 #481	1	0
482	1	94,790,840	94,791,591	751	2	8.625	10.5	17	14	0	0	1	LOC100505940	77,801	in gene	ActReg chr1 #482	1	1
483	1	95,045,155	95,045,722	567	1	7.882	9.941	15	15	0	0	0				ActReg chr1 #483	0	1
484	1	95,071,302	95,071,823	521	1	11.688	7.188	19	12	0	0	0				ActReg chr1 #484	1	0
485	1	95,538,128	95,538,933	805	1	10.68	14.16	20	21	1	1	1	ALG14	-23	upstream	ActReg chr1 #485	0	1
486	1	95,849,954	95,850,628	674	2	10.667	11.286	16	21	0	0	0				ActReg chr1 #486	1	1
487	1	96,541,965	96,542,518	553	1	10.412	6.706	19	11	0	0	0				ActReg chr1 #487	1	0
488	1	97,452,334	97,453,506	1,172	2	13.784	13.622	29	21	0	0	0				ActReg chr1 #488	1	1
489	1	98,385,910	98,387,079	1,169	2	12.46	12.595	22	20	1	1	1	DPYD	121	in gene	ActReg chr1 #489	1	1
490	1	98,510,730	98,511,298	568	1	8.333	10.778	11	14	1	2	2	FLJ35409, MIR137	0, 713	in gene, downstream	ActReg chr1 #490	0	1
491	1	98,511,461	98,512,255	794	1	6.417	11.667	12	20	1	2	2	FLJ35409, MIR137	-844, -131	upstream, upstream	ActReg chr1 #491	0	1
492	1	98,513,488	98,514,370	882	2	14	23.036	36	60	0	2	2	FLJ35409, MIR137	-2915, -2202	upstream, upstream	ActReg chr1 #492	1	1
493	1	98,789,131	98,789,906	775	1	9.333	10.667	14	14	0	0	0				ActReg chr1 #493	0	1
494	1	98,853,813	98,854,513	700	1	5.773	10.5	10	18	0	0	0				ActReg chr1 #494	0	1
495	1	100,147,924	100,148,428	504	1	6.5	10.188	11	14	0	0	1	PALMD	36,745	in gene	ActReg chr1 #495	0	1
496	1	100,315,143	100,316,025	882	2	11.407	14.037	15	22	1	1	1	AGL	-56	upstream	ActReg chr1 #496	1	1
497	1	100,435,189	100,435,990	801	1	13.56	17.12	23	33	1	2	2	LOC730081, SLC35A3	249, 49	in gene, in gene	ActReg chr1 #497	0	1
498	1	100,503,181	100,504,076	895	2	12.286	14.5	19	28	1	1	1	HIAT1	-161	upstream	ActReg chr1 #498	1	1
499	1	100,598,093	100,599,088	995	2	12.065	11	17	26	1	2	2	SASS6, CCDC76	-79, -116	upstream, upstream	ActReg chr1 #499	1	1
500	1	100,817,802	100,818,678	876	2	10.37	12.407	19	17	1	1	1	CDC14A	217	in gene	ActReg chr1 #500	1	1
501	1	101,250,880	101,251,685	805	2	15.769	12.538	37	30	0	0	0				ActReg chr1 #501	1	1
502	1	101,491,168	101,491,887	719	1	8.391	11.391	16	18	1	2	2	DPH5, LOC100506051	-165, 93	upstream, in gene	ActReg chr1 #502	0	1
503	1	101,972,907	101,973,572	665	1	9.857	6.571	15	11	0	0	0				ActReg chr1 #503	1	0
504	1	102,370,724	102,371,170	446	1	6.5	9.429	10	18	0	0	1	OLFM3	91,843	in gene	ActReg chr1 #504	0	1
505	1	102,462,106	102,462,984	878	2	17.357	19.5	37	52	0	1	1	OLFM3	245	in gene	ActReg chr1 #505	1	1
506	1	106,206,629	106,207,426	797	1	6.28	10.52	11	15	0	0	0				ActReg chr1 #506	0	1
507	1	106,220,999	106,221,444	445	1	10.286	7.357	15	10	0	0	0				ActReg chr1 #507	1	0
508	1	107,479,739	107,480,207	468	1	9.467	9.133	16	13	0	0	0				ActReg chr1 #508	1	0
509	1	107,596,924	107,600,385	1,461	2	10.957	13.022	16	25	1	1	1	PRMT6	387	in gene	ActReg chr1 #509	1	1
510	1	107,677,919	107,678,695	776	2	12	12.68	22	26	0	1	1	NTNG1	-4,322	upstream	ActReg chr1 #510	1	1
511	1	108,533,173	108,533,792	619	1	7.05	10.1	14	19	0	0	0				ActReg chr1 #511	0	1
512	1	108,591,940	108,592,477	537	1	9.875	11.875	14	21	0	0	0				ActReg chr1 #512	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
513	1	108,742,924	108,743,829	905	1	7.63	11.107	14	19	1	1	1	SLC25A24	-402	upstream	ActReg chr1 #513	0	1
514	1	109,419,200	109,420,027	827	2	9.846	10.192	18	15	1	1	1	GPSM2	10	in gene	ActReg chr1 #514	1	1
515	1	109,583,850	109,584,865	1,015	1	10.438	8.645	17	18	1	1	1	WDR47	493	in gene	ActReg chr1 #515	1	0
516	1	109,618,286	109,619,022	736	2	9.609	10.13	17	21	1	1	1	TAF13	-30	upstream	ActReg chr1 #516	1	1
517	1	109,632,887	109,633,829	942	2	22.833	23.933	66	64	1	1	2	TMEM167B, SCARNA2	-45, -9457	upstream, upstream	ActReg chr1 #517	1	1
518	1	109,642,298	109,643,520	1,222	2	14.256	17.769	39	45	1	1	3	TMEM167B, SCARNA2, C1orf194	9506, 94, 13570	downstream, in gene, downstream	ActReg chr1 #518	1	1
519	1	109,842,078	109,843,219	1,141	1	7.4	11.417	17	21	0	0	2	MYBPHL, SORT1	7015, 97915	in gene, downstream	ActReg chr1 #519	0	1
520	1	110,008,730	110,009,493	763	1	10.833	7.833	16	14	1	1	1	SYPL2	11	in gene	ActReg chr1 #520	1	0
521	1	110,025,720	110,027,514	1,794	3	20.286	22.071	69	84	1	1	3	SYPL2, ATXN7L2, CYB561D1	17517, 56, -10041	downstream, in gene, upstream	ActReg chr1 #521	1	1
522	1	110,035,971	110,037,264	1,293	2	22	22.15	68	75	1	1	2	ATXN7L2, CYB561D1	10056, -41	downstream, upstream	ActReg chr1 #522	1	1
523	1	110,394,864	110,395,548	684	2	11.762	11.762	24	22	0	0	0				ActReg chr1 #523	1	1
524	1	110,526,907	110,528,089	1,182	2	11.135	9.973	15	21	1	1	1	AHCYL1	190	in gene	ActReg chr1 #524	1	1
525	1	110,698,347	110,699,207	860	2	13.111	13.778	21	24	0	0	1	SLC6A17	5,645	in gene	ActReg chr1 #525	1	1
526	1	110,880,557	110,882,252	1,695	2	11.34	13.075	28	19	2	1	1	RBM15	-541	upstream	ActReg chr1 #526	1	1
527	1	110,883,553	110,884,217	664	1	7.35	11	11	15	0	1	1	RBM15	1,940	in gene	ActReg chr1 #527	0	1
528	1	110,949,698	110,950,675	977	1	8.467	17.267	14	28	1	1	1	HBXIP	360	in gene	ActReg chr1 #528	0	1
529	1	111,019,544	111,020,175	631	1	11.5	9.55	19	17	0	0	0				ActReg chr1 #529	1	0
530	1	111,085,203	111,086,125	922	2	15.103	16.035	33	39	0	0	0				ActReg chr1 #530	1	1
531	1	111,097,804	111,098,488	684	1	7.333	13.714	13	30	1	0	0				ActReg chr1 #531	0	1
532	1	111,289,020	111,289,986	966	2	15.387	20.71	37	52	0	0	0				ActReg chr1 #532	1	1
533	1	111,506,497	111,507,335	838	1	8.462	10.962	13	15	1	1	1	C1orf103	-350	upstream	ActReg chr1 #533	0	1
534	1	111,682,817	111,683,504	687	1	7.952	11.667	13	19	1	2	2	DRAM2, CEPT1	-322, 911	upstream, in gene	ActReg chr1 #534	0	1
535	1	112,297,753	112,298,721	968	2	13.419	13.613	25	23	1	2	3	C1orf183, LOC100506343, DDX20	182, 15774, 47	in gene, downstream, in gene	ActReg chr1 #535	1	1
536	1	112,375,780	112,376,594	814	2	15.2	14.84	28	32	0	0	1	KCND3	155,590	in gene	ActReg chr1 #536	1	1
537	1	112,407,102	112,407,956	854	1	7.185	12.741	18	23	0	0	1	KCND3	124,248	in gene	ActReg chr1 #537	0	1
538	1	112,714,676	112,715,450	774	2	13	17.25	30	36	0	0	0				ActReg chr1 #538	1	1
539	1	112,794,220	112,794,866	646	2	12.65	10.55	24	16	0	0	0				ActReg chr1 #539	1	1
540	1	113,161,463	113,162,867	1,404	2	11.386	10.75	20	18	1	2	2	ST7L, CAPZA1	-125, 90	upstream, in gene	ActReg chr1 #540	1	1
541	1	113,216,705	113,217,721	1,016	1	7.226	14.677	13	23	1	1	2	CAPZA1, MOV10	55138, 165	downstream, in gene	ActReg chr1 #541	0	1
542	1	113,247,110	113,248,223	1,113	2	9.324	11.529	19	18	0	1	3	MOV10, RHOC, PPM1J	30618, 2359, 10284	downstream, in gene, downstream	ActReg chr1 #542	1	1
543	1	113,497,873	113,499,223	1,350	2	11.167	14.976	21	30	2	2	2	SLC16A1, LOC100506392	427, -472	in gene, upstream	ActReg chr1 #543	1	1
544	1	113,615,114	113,616,415	1,301	2	13.55	19.7	25	40	1	1	1	LRIG2	-67	upstream	ActReg chr1 #544	1	1
545	1	113,999,421	113,999,929	508	1	7.062	9.875	12	14	0	0	1	MAGI3	66,200	in gene	ActReg chr1 #545	0	1
546	1	114,301,669	114,302,103	434	1	5.4	11.462	7	13	1	1	2	PHTF1, RSBN1	-109, 53184	upstream, downstream	ActReg chr1 #546	0	1
547	1	114,446,999	114,448,380	1,381	2	15.512	14.302	33	29	1	2	3	LOC100287722, AP4B1, DCLRE1B	48432, 52, -226	downstream, in gene, upstream	ActReg chr1 #547	1	1
548	1	114,471,606	114,472,527	921	2	15.483	12	30	21	1	1	1	HIPK1	70	in gene	ActReg chr1 #548	1	1
549	1	114,656,159	114,657,192	1,033	1	11.667	11.061	15	15	0	0	1	SYT6	39,797	in gene	ActReg chr1 #549	1	0
550	1	114,672,945	114,673,805	860	1	8.333	10.556	12	14	0	0	1	SYT6	23,097	in gene	ActReg chr1 #550	0	1
551	1	114,888,996	114,889,610	614	1	8.684	12.737	11	22	0	0	0				ActReg chr1 #551	0	1
552	1	115,299,957	115,300,832	875	1	10.786	12.571	14	19	0	1	1	CSDE1	277	in gene	ActReg chr1 #552	0	1
553	1	115,322,845	115,323,606	761	1	12.917	9.25	24	14	1	1	1	SIKE1	83	in gene	ActReg chr1 #553	1	0
554	1	115,721,708	115,722,570	862	2	12.482	10.482	23	22	0	0	0				ActReg chr1 #554	1	1
555	1	115,842,757	115,843,449	692	1	11.333	7.714	17	12	0	0	1	NGF	37,754	in gene	ActReg chr1 #555	1	0
556	1	115,973,257	115,973,887	630	1	10.526	12.737	18	23	0	0	0				ActReg chr1 #556	0	1
557	1	116,270,055	116,270,696	641	1	11.55	8.25	17	12	0	0	1	CASQ2	41,051	in gene	ActReg chr1 #557	1	0
558	1	116,270,704	116,271,097	393	1	12	5.417	19	11	0	0	1	CASQ2	40,526	in gene	ActReg chr1 #558	1	0
559	1	116,665,476	116,666,089	613	1	4	11.684	7	18	0	0	1	C1orf161	11,406	in gene	ActReg chr1 #559	0	1
560	1	116,694,581	116,695,089	508	1	9.812	13.062	13	21	1	0	0				ActReg chr1 #560	0	1
561	1	116,975,621	116,976,647	1,026	1	11.719	12.031	17	20	0	0	0				ActReg chr1 #561	0	1
562	1	117,046,919	117,047,603	684	1	10.571	8.905	16	17	0	1	2	LOC100506459, CD58	-5427, 66454	upstream, downstream	ActReg chr1 #562	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
563	1	117,051,331	117,052,117	786	1	7.75	10.708	14	14	0	0	2	LOC100506459, CD58	-9890, 61991	upstream, downstream	ActReg chr1 #563	0	1
564	1	117,113,179	117,113,856	677	1	9.773	11.5	13	20	1	1	2	CD58, IGSF3	198, 96797	in gene, downstream	ActReg chr1 #564	0	1
565	1	117,320,281	117,320,940	659	1	4.762	10.619	6	18	0	0	1	CD2	23,524	downstream	ActReg chr1 #565	0	1
566	1	117,416,488	117,417,117	629	1	10.474	7.737	17	11	0	0	0				ActReg chr1 #566	1	0
567	1	117,714,321	117,714,960	639	1	5.5	11.2	9	19	0	0	1	VTCN1	38,909	in gene	ActReg chr1 #567	0	1
568	1	117,833,404	117,834,009	605	1	9.895	6.789	16	13	0	0	0				ActReg chr1 #568	1	0
569	1	119,471,334	119,472,147	813	2	11.16	10.52	18	20	0	0	1	TBX15	60,439	in gene	ActReg chr1 #569	1	1
570	1	120,085,023	120,085,977	954	2	15.567	14.5	34	40	0	0	0				ActReg chr1 #570	1	1
571	1	120,146,012	120,146,654	642	1	5.25	9.95	8	15	0	1	1	LOC644242	-4,419	upstream	ActReg chr1 #571	0	1
572	1	120,190,412	120,191,303	891	1	6.643	10.786	12	16	1	1	1	ZNF697	-467	upstream	ActReg chr1 #572	0	1
573	1	120,611,907	120,612,288	381	1	8.75	11.667	15	18	1	1	1	NOTCH2	179	in gene	ActReg chr1 #573	0	1
574	1	142,618,430	142,619,257	827	2	14.577	12.577	29	28	1	0	0				ActReg chr1 #574	1	1
575	1	143,467,448	143,467,947	499	2	7.938	10.062	16	14	1	0	0				ActReg chr1 #575	1	1
576	1	144,532,889	144,534,647	1,758	1	30.454	30.8	62	84	1	0	0				ActReg chr1 #576	1	0
577	1	144,594,050	144,594,499	449	1	9.786	9.643	14	13	1	0	0				ActReg chr1 #577	1	0
578	1	144,890,733	144,892,793	2,060	1	13.594	15.141	27	31	0	0	1	PDE4DIP	184,316	in gene	ActReg chr1 #578	0	1
579	1	144,930,241	144,933,460	3,219	2	15.15	19.94	31	41	1	0	1	PDE4DIP	144,229	in gene	ActReg chr1 #579	1	1
580	1	145,007,670	145,012,854	5,184	1	15.037	13.086	32	28	0	1	2	PDE4DIP, LOC100505971	65817, -6211	in gene, upstream	ActReg chr1 #580	1	0
581	1	145,041,812	145,043,841	2,029	1	19.141	16.406	42	35	0	0	1	PDE4DIP	33,253	in gene	ActReg chr1 #581	1	0
582	1	145,091,349	145,092,989	1,640	1	12.902	16.628	29	38	0	1	1	SEC22B	-4,238	upstream	ActReg chr1 #582	0	1
583	1	145,382,170	145,383,344	1,174	2	13.649	15.973	30	35	1	1	1	LOC100505987	-359	upstream	ActReg chr1 #583	1	1
584	1	145,395,175	145,396,464	1,289	2	11.775	14.25	29	27	0	0	0				ActReg chr1 #584	1	1
585	1	145,396,619	145,398,264	1,645	2	13.745	10.804	24	17	0	0	0				ActReg chr1 #585	1	1
586	1	145,398,888	145,399,711	823	2	12.16	11.52	21	20	0	0	0				ActReg chr1 #586	1	1
587	1	145,470,192	145,471,049	857	1	9.593	12.593	19	23	1	3	3	POLR3GL, ANKRD34A, LIX1L	-233, 112, -6465	upstream, in gene, upstream	ActReg chr1 #587	0	1
588	1	145,507,235	145,508,221	986	2	11.667	11.733	22	17	1	1	3	LIX1L, RBM8A, PEX11B	30643, 90, -8437	downstream, in gene, upstream	ActReg chr1 #588	1	1
589	1	145,515,012	145,517,505	2,493	2	11.244	11.526	24	19	1	2	3	RBM8A, PEX11B, ITGA10	8620, 93, -8732	downstream, in gene, upstream	ActReg chr1 #589	1	1
590	1	145,575,356	145,576,284	928	1	10.207	14.207	18	23	1	1	2	ANKRD35, PIAS3	26611, -168	downstream, upstream	ActReg chr1 #590	0	1
591	1	145,588,525	145,589,759	1,234	1	12.237	10	18	19	1	1	3	PIAS3, NUDT17, POLR3C	13154, 293, 21742	downstream, in gene, downstream	ActReg chr1 #591	1	0
592	1	145,610,534	145,611,380	846	2	11.692	16	21	28	2	2	2	POLR3C, RNF115	-73, -79	upstream, upstream	ActReg chr1 #592	1	1
593	1	146,373,488	146,373,870	382	1	4.182	9.917	7	16	1	2	2	LOC100505723, LOC100505752	714, 124	in gene, in gene	ActReg chr1 #593	0	1
594	1	146,555,861	146,556,968	1,107	2	21.6	22.143	54	67	1	0	0				ActReg chr1 #594	1	1
595	1	146,642,971	146,644,828	1,857	2	12.19	14.448	27	29	1	2	2	PRKAB2, LOC100505794	230, -427	in gene, upstream	ActReg chr1 #595	1	1
596	1	146,696,706	146,697,475	769	1	5.625	10.75	10	14	0	1	1	FMO5	140	in gene	ActReg chr1 #596	0	1
597	1	146,713,837	146,715,089	1,252	2	10.282	13.59	21	24	1	1	1	CHD1L	172	in gene	ActReg chr1 #597	1	1
598	1	146,976,165	146,976,959	794	1	11.958	6.417	16	11	0	0	0				ActReg chr1 #598	1	0
599	1	147,006,071	147,006,709	638	1	8.95	12.8	14	23	0	1	1	BCL9	-6,792	upstream	ActReg chr1 #599	0	1
600	1	147,070,652	147,071,849	1,197	2	12.316	16.053	22	27	1	0	1	BCL9	58,068	in gene	ActReg chr1 #600	1	1
601	1	147,141,680	147,143,071	1,391	2	13.349	15.07	25	25	1	1	1	ACP6	259	in gene	ActReg chr1 #601	1	1
602	1	147,148,697	147,149,274	577	1	7.944	11	14	16	0	1	1	ACP6	-6,351	upstream	ActReg chr1 #602	0	1
603	1	147,222,216	147,223,414	1,198	2	16.216	16.486	39	41	0	0	1	GJA5	22,669	downstream	ActReg chr1 #603	1	1
604	1	147,735,294	147,736,374	1,080	2	14.588	13.618	40	32	1	0	0				ActReg chr1 #604	1	1
605	1	147,806,103	147,807,500	1,397	2	16.5	23.932	40	62	1	0	0				ActReg chr1 #605	1	1
606	1	148,000,426	148,001,011	585	2	10.353	12	20	24	1	0	1	NBPF14	25,130	downstream	ActReg chr1 #606	1	1
607	1	148,241,227	148,241,748	521	1	9.938	7.455	19	12	1	0	1	LOC100288142	119,694	downstream	ActReg chr1 #607	1	0
608	1	148,556,525	148,557,158	633	1	12.7	17.6	27	36	1	1	1	NBPF15	-1,347	upstream	ActReg chr1 #608	0	1
609	1	148,847,950	148,848,429	479	1	6.933	10.733	10	16	0	0	0				ActReg chr1 #609	0	1
610	1	148,849,969	148,850,383	394	1	6.25	10.25	10	15	0	0	0				ActReg chr1 #610	0	1
611	1	148,927,868	148,928,452	584	1	13.895	21.895	23	42	0	0	0				ActReg chr1 #611	0	1
612	1	149,222,280	149,225,467	3,187	2	21.798	19.818	49	42	1	1	1	RNU1-5	348	downstream	ActReg chr1 #612	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
613	1	149,857,940	149,860,136	2,196	3	14.536	13.246	24	28	1	3	3	HIST2H2BE, HIST2H2AC, HIST2H2AB	-806, 513, 428	upstream, downstream, in gene	ActReg chr1 #613	1	1
614	1	149,899,270	149,900,041	771	2	13.333	11.417	23	18	1	1	4	LOC100507640, SV2A, SF3B4, MTMR11	26119, -10221, -47, 9136	downstream, upstream, in gene, downstream	ActReg chr1 #614	1	1
615	1	149,910,857	149,911,620	763	1	9.875	12.375	15	18	0	1	2	MTMR11, OTUD7B	-2447, 71448	upstream, downstream	ActReg chr1 #615	0	1
616	1	149,978,609	149,979,443	834	1	15.115	11.923	28	25	0	0	1	OTUD7B	3,660	in gene	ActReg chr1 #616	1	0
617	1	149,982,021	149,983,054	1,033	1	11.906	10.75	23	16	1	1	1	OTUD7B	149	in gene	ActReg chr1 #617	1	0
618	1	150,039,079	150,040,191	1,112	1	11.441	15.529	17	27	1	1	1	VPS45	293	in gene	ActReg chr1 #618	0	1
619	1	150,206,583	150,207,824	1,241	1	8.692	12.718	19	19	1	1	1	ANP32E	1,301	in gene	ActReg chr1 #619	0	1
620	1	150,207,849	150,208,979	1,130	1	13.657	9.857	21	15	1	1	1	ANP32E	90	in gene	ActReg chr1 #620	1	0
621	1	150,240,464	150,241,843	1,379	1	9.465	12.046	17	19	1	2	3	CA14, APH1A, C1orf54	10935, 379, 4030	downstream, in gene, upstream	ActReg chr1 #621	0	1
622	1	150,335,001	150,336,751	1,750	2	9.345	10.927	19	17	1	1	2	PRPF3, RPRD2	41948, -1114	downstream, upstream	ActReg chr1 #622	1	1
623	1	150,459,448	150,460,280	832	2	10.615	15.538	20	29	0	1	1	TARS2	-56	upstream	ActReg chr1 #623	1	1
624	1	150,550,906	150,552,240	1,334	1	9.976	12.191	14	16	1	1	1	MCL1	563	in gene	ActReg chr1 #624	0	1
625	1	150,583,900	150,584,593	693	2	14.091	13.5	28	24	0	0	0				ActReg chr1 #625	1	1
626	1	150,849,226	150,849,834	608	1	10.737	9.789	17	16	1	1	1	ARNT	-344	upstream	ActReg chr1 #626	1	0
627	1	150,867,969	150,868,624	655	1	13	13.95	22	29	0	0	0				ActReg chr1 #627	0	1
628	1	150,898,363	150,899,114	751	2	11.75	11.5	18	21	1	1	1	SETDB1	-77	upstream	ActReg chr1 #628	1	1
629	1	150,949,593	150,950,311	718	1	14.067	16.217	29	35	0	2	2	LASS2, ANXA9	-2512, -4547	upstream, upstream	ActReg chr1 #629	0	1
630	1	150,980,558	150,981,396	838	1	13.192	8.923	19	15	1	2	2	FAM63A, PRUNE	-123, 4	upstream, in gene	ActReg chr1 #630	1	0
631	1	151,019,784	151,021,408	1,624	1	11.804	10.098	20	19	1	1	3	BNIPL, C1orf56, CDC42SE1	11567, 337, 11529	downstream, in gene, downstream	ActReg chr1 #631	1	0
632	1	151,042,659	151,043,800	1,141	2	12.886	13.829	29	25	1	1	2	MLLT11, GABPB2	11078, 149	downstream, in gene	ActReg chr1 #632	1	1
633	1	151,137,988	151,138,984	996	2	16.936	15	37	27	0	2	5	TNFAIP8L2, LYSMD1, SCNM1, TMOD4, VPS72	9381, -62, -31, 10061, 24154	downstream, upstream, upstream, downstream, downstream	ActReg chr1 #633	1	1
634	1	151,162,081	151,163,111	1,030	2	19.5	17.125	56	50	0	1	2	VPS72, PIP5K1A	44, -8425	in gene, upstream	ActReg chr1 #634	1	1
635	1	151,170,472	151,171,775	1,303	2	15.95	14.05	31	31	1	1	2	VPS72, PIP5K1A	-8483, 102	upstream, in gene	ActReg chr1 #635	1	1
636	1	151,226,731	151,227,523	792	1	11.52	14.4	18	27	0	1	2	PIP5K1A, PSMD4	56106, -70	downstream, upstream	ActReg chr1 #636	0	1
637	1	151,253,408	151,255,091	1,683	2	31.647	31.943	96	107	1	2	3	LOC100507670, ZNF687, PI4KB	516, -542, 44475	in gene, upstream, downstream	ActReg chr1 #637	1	1
638	1	151,371,631	151,372,702	1,071	2	15.242	13.636	30	21	1	2	3	PSMB4, LOC100505497, POGZ	125, 714, 59775	in gene, in gene, downstream	ActReg chr1 #638	1	1
639	1	151,373,196	151,374,189	993	1	8.161	11.065	14	15	0	2	3	PSMB4, LOC100505497, POGZ	1651, -812, 58249	in gene, upstream, downstream	ActReg chr1 #639	0	1
640	1	151,512,501	151,513,571	1,070	1	10.471	13.147	16	25	1	2	3	CGN, TUFT1, MIR554	29174, 255, 5236	downstream, in gene, upstream	ActReg chr1 #640	0	1
641	1	151,546,984	151,548,013	1,029	1	9.312	14.781	17	28	0	0	1	TUFT1	34,717	in gene	ActReg chr1 #641	0	1
642	1	151,551,027	151,552,573	1,546	1	9.792	11.458	20	17	0	0	1	TUFT1	39,019	in gene	ActReg chr1 #642	0	1
643	1	151,584,244	151,585,316	1,072	2	11	12.588	19	17	1	1	1	SNX27	118	in gene	ActReg chr1 #643	1	1
644	1	151,811,798	151,812,921	1,123	1	9.714	15.314	19	31	2	3	4	RORC, C2CD4D, LOC100132111, THEM5	-8011, 674, 1414, 13814	upstream, in gene, in gene, downstream	ActReg chr1 #644	0	1
645	1	151,813,486	151,814,155	669	1	11.191	9.619	16	16	0	1	4	RORC, C2CD4D, LOC100132111, THEM5	-9472, -787, 2875, 12353	upstream, upstream, in gene, downstream	ActReg chr1 #645	1	0
646	1	151,881,599	151,882,697	1,098	2	16.514	14.857	34	25	1	1	1	THEM4	-35	upstream	ActReg chr1 #646	1	1
647	1	151,918,105	151,919,735	1,630	2	10.294	12.392	21	26	0	0	0				ActReg chr1 #647	1	1
648	1	151,952,507	151,953,346	839	1	7.333	11.704	13	18	0	0	1	S100A10	13,788	downstream	ActReg chr1 #648	0	1
649	1	151,964,495	151,967,103	2,608	1	10.222	13.123	16	32	2	1	1	S100A10	915	in gene	ActReg chr1 #649	0	1
650	1	152,001,371	152,002,143	772	1	5.5	12.5	10	22	0	0	1	S100A11	7,754	downstream	ActReg chr1 #650	0	1
651	1	152,006,787	152,007,579	792	1	6.375	11.875	11	15	0	1	1	S100A11	2,328	in gene	ActReg chr1 #651	0	1
652	1	152,020,196	152,021,349	1,153	2	14.917	12.889	25	26	0	0	0				ActReg chr1 #652	1	1
653	1	152,160,993	152,162,118	1,125	1	10	14.057	16	22	1	0	0				ActReg chr1 #653	0	1
654	1	152,216,878	152,217,953	1,075	2	10.882	11.735	19	18	0	0	0				ActReg chr1 #654	1	1
655	1	153,072,689	153,073,096	407	1	11.231	8	19	13	0	1	1	SPRR2E	-5,891	upstream	ActReg chr1 #655	1	0
656	1	153,394,682	153,395,609	927	2	13.931	18.586	30	45	0	0	1	S100A7A	6,145	in gene	ActReg chr1 #656	1	1
657	1	153,424,691	153,425,444	753	2	13.708	13.667	30	27	0	0	1	S100A7	8,070	downstream	ActReg chr1 #657	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
658	1	153,462,462	153,463,542	1,080	1	10.353	11.647	16	16	0	0	0				ActReg chr1 #658	0	1
659	1	153,505,692	153,506,898	1,206	2	11.079	12.184	24	19	0	2	4	LOC100505623, S100A6, S100A5, S100A4	233, 2422, 7946, 11987	in gene, downstream, downstream, downstream	ActReg chr1 #659	1	1
660	1	153,507,469	153,509,633	2,164	2	13.853	13.323	25	29	1	2	4	LOC100505623, S100A6, S100A5, S100A4	2489, 166, 5690, 9731	downstream, in gene, downstream, downstream	ActReg chr1 #660	1	1
661	1	153,517,190	153,518,175	985	1	10.3	14.033	17	23	0	2	5	LOC100505623, S100A6, S100A5, S100A4, S100A3	11620, -8965, -3441, 600, 4052	downstream, upstream, upstream, in gene, downstream	ActReg chr1 #661	0	1
662	1	153,538,004	153,539,888	1,884	2	11.288	13.034	22	23	0	1	1	S100A2	-640	upstream	ActReg chr1 #662	1	1
663	1	153,540,021	153,541,549	1,528	2	11.167	12.625	23	18	0	1	1	S100A2	-2,479	upstream	ActReg chr1 #663	1	1
664	1	153,580,794	153,583,415	2,621	2	11.976	15.11	21	27	0	1	3	S100A16, S100A14, S100A13	3410, 6686, 24464	in gene, downstream, downstream	ActReg chr1 #664	1	1
665	1	153,599,308	153,600,221	913	1	12.786	10.714	17	16	0	2	3	S100A13, S100A1, C1orf77	6804, -1109, -6761	in gene, upstream, upstream	ActReg chr1 #665	1	0
666	1	153,605,958	153,607,020	1,062	1	7.485	12.697	14	21	1	2	3	S100A13, S100A1, C1orf77	79, 5616, -36	in gene, downstream, upstream	ActReg chr1 #666	0	1
667	1	153,699,795	153,700,535	740	2	10.478	9.909	19	21	1	1	1	INTS3	-402	upstream	ActReg chr1 #667	1	1
668	1	153,918,000	153,919,638	1,638	2	17.726	18.608	55	58	1	1	2	DENND4B, CRTC2	335, 12224	in gene, downstream	ActReg chr1 #668	1	1
669	1	153,930,070	153,931,529	1,459	2	14.391	11.609	27	20	1	1	3	CRTC2, SLC39A1, CREB3L4	244, 9389, -9598	in gene, downstream, upstream	ActReg chr1 #669	1	1
670	1	153,935,581	153,936,689	1,108	1	12.571	11.086	18	15	1	2	3	CRTC2, SLC39A1, CREB3L4	-5092, 4053, -4262	upstream, in gene, upstream	ActReg chr1 #670	0	1
671	1	153,949,338	153,950,678	1,340	2	13.309	12.214	22	19	1	1	4	SLC39A1, CREB3L4, JTB, RAB13	-9820, 9611, 443, 8798	upstream, downstream, in gene, downstream	ActReg chr1 #671	1	1
672	1	153,962,812	153,963,653	841	1	9.222	14	14	21	1	2	3	RAB13, RPS27, NUP210L	-4426, -7, 164360	upstream, upstream, downstream	ActReg chr1 #672	0	1
673	1	154,154,775	154,156,189	1,414	2	13.068	11.182	23	20	1	0	2	TPM3, MIR190B	9127, 10737	in gene, downstream	ActReg chr1 #673	1	1
674	1	154,192,495	154,193,605	1,110	1	9.8	12.771	19	20	1	2	2	C1orf43, UBAP2L	223, 395	in gene, in gene	ActReg chr1 #674	0	1
675	1	154,298,256	154,299,386	1,130	1	9.514	11.286	16	16	1	1	2	AQP10, ATP8B2	5229, 785	downstream, in gene	ActReg chr1 #675	0	1
676	1	154,378,048	154,379,038	990	1	9.194	11.645	14	17	1	1	1	IL6R	874	in gene	ActReg chr1 #676	0	1
677	1	154,531,130	154,532,421	1,291	2	13.244	12.293	21	22	1	1	2	UBE2Q1, CHRNB2	-655, -8482	upstream, upstream	ActReg chr1 #677	1	1
678	1	154,539,445	154,541,107	1,662	2	12.442	16.173	33	40	1	1	2	UBE2Q1, CHRNB2	-9156, 19	upstream, in gene	ActReg chr1 #678	1	1
679	1	154,580,019	154,580,975	956	1	9.967	12.933	15	19	1	0	1	ADAR	19,959	in gene	ActReg chr1 #679	0	1
680	1	154,599,730	154,600,712	982	1	9.387	12.29	18	18	1	1	1	ADAR	235	in gene	ActReg chr1 #680	0	1
681	1	154,908,704	154,910,382	1,678	2	17.868	19.038	40	41	1	1	2	PMVK, PBXIP1	-59, 19024	upstream, downstream	ActReg chr1 #681	1	1
682	1	154,933,753	154,935,125	1,372	2	13.814	15.395	27	38	1	2	3	PBXIP1, PYGO2, SHC1	-5872, -181, 12520	upstream, upstream, downstream	ActReg chr1 #682	1	1
683	1	154,942,921	154,944,121	1,200	1	11.703	13.919	20	24	0	2	4	PYGO2, SHC1, CKS1B, MIR4258	-9263, 3438, -3597, -4648	upstream, in gene, upstream, upstream	ActReg chr1 #683	0	1
684	1	154,955,308	154,956,043	735	1	12.043	17.826	20	36	0	1	4	SHC1, CKS1B, MIR4258, FLAD1	-8716, 8557, 7506, 95	upstream, downstream, downstream, upstream	ActReg chr1 #684	0	1
685	1	154,973,157	154,975,020	1,863	3	14.603	17.069	36	31	2	1	3	FLAD1, LENEP, ZBTB7B	18318, 8026, -1024	downstream, downstream, upstream	ActReg chr1 #685	1	1
686	1	154,975,676	154,976,955	1,279	1	12.325	10.975	20	19	1	1	2	LENEP, ZBTB7B	10253, 1203	downstream, in gene	ActReg chr1 #686	1	0
687	1	155,022,251	155,023,734	1,483	1	16.956	11.826	32	24	1	1	3	DCST1, LOC100505666, ADAM15	16692, 13427, -770	in gene, in gene, upstream	ActReg chr1 #687	1	0
688	1	155,035,292	155,036,667	1,375	1	9.907	13.698	16	26	1	2	3	LOC100505666, ADAM15, EFNA4	440, 12217, 234	in gene, downstream, upstream	ActReg chr1 #688	0	1
689	1	155,099,166	155,100,313	1,147	1	9.833	14.611	16	23	1	1	2	EFNA1, RAG1AP1	-610, -8549	upstream, upstream	ActReg chr1 #689	0	1
690	1	155,100,797	155,101,985	1,188	1	11	10.053	18	16	0	2	2	EFNA1, RAG1AP1	1042, -6897	in gene, upstream	ActReg chr1 #690	1	0
691	1	155,107,779	155,108,984	1,205	1	8.297	12.784	13	17	1	1	3	EFNA1, RAG1AP1, DPM3	8032, 93, 4615	downstream, in gene, downstream	ActReg chr1 #691	0	1
692	1	155,112,098	155,113,366	1,268	1	11.872	13.513	22	22	1	1	3	EFNA1, RAG1AP1, DPM3	12383, 4444, 264	downstream, downstream, in gene	ActReg chr1 #692	0	1
693	1	155,145,013	155,146,985	1,972	2	30.21	29.823	156	142	1	2	2	KRTCAP2, TRIM46	-195, -361	upstream, upstream	ActReg chr1 #693	1	1
694	1	155,163,121	155,165,003	1,882	2	10.983	13.136	20	21	2	3	5	TRIM46, MUC1, MIR92B, THBS3, LOC100129268	17702, -1362, -906, 13628, -6531	downstream, upstream, upstream, downstream, upstream	ActReg chr1 #694	1	1
695	1	155,196,396	155,198,112	1,716	1	10.111	13.185	16	21	1	0	1	GBA	17,399	downstream	ActReg chr1 #695	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
696	1	155,214,222	155,215,155	933	2	12.69	14.897	23	28	0	1	2	GBA, FAM189B	-35, 10586	upstream, downstream	ActReg chr1 #696	1	1
697	1	155,220,216	155,220,994	778	1	6.48	11.88	14	22	1	1	3	GBA, FAM189B, SCAMP3	-5952, 4669, 11590	upstream, in gene, downstream	ActReg chr1 #697	0	1
698	1	155,231,621	155,232,556	935	1	11.379	14.31	15	27	1	2	3	FAM189B, SCAMP3, CLK2	-6814, 107, 11193	upstream, in gene, downstream	ActReg chr1 #698	0	1
699	1	155,246,699	155,248,610	1,911	1	7.85	12.533	15	21	1	2	2	CLK2, HCN3	-4373, 280	upstream, in gene	ActReg chr1 #699	0	1
700	1	155,278,046	155,279,356	1,310	2	11.878	13.854	22	27	1	2	2	PKLR, FDPS	-7476, 162	upstream, in gene	ActReg chr1 #700	1	1
701	1	155,293,529	155,294,753	1,224	1	10.436	11.974	15	20	1	1	3	FDPS, C1orf104, RUSC1	15602, -203, 3501	downstream, upstream, in gene	ActReg chr1 #701	0	1
702	1	155,531,766	155,533,346	1,580	2	14.88	16.28	46	48	1	2	2	ASH1L, LOC645676	-232, 784	upstream, in gene	ActReg chr1 #702	1	1
703	1	155,657,876	155,659,182	1,306	2	17.537	24.585	53	70	1	2	2	YY1AP1, DAP3	262, -345	in gene, upstream	ActReg chr1 #703	1	1
704	1	155,714,828	155,715,658	830	1	9.269	14.423	17	25	1	1	3	DAP3, LOC100505728, GON4L	56369, 530, 111729	downstream, in gene, downstream	ActReg chr1 #704	0	1
705	1	155,826,490	155,827,535	1,045	2	19.212	22.909	46	66	0	2	2	GON4L, SYT11	-40, -2248	upstream, upstream	ActReg chr1 #705	1	1
706	1	155,829,813	155,830,676	863	1	8.741	13.037	17	22	1	2	2	GON4L, SYT11	-3272, 984	upstream, in gene	ActReg chr1 #706	0	1
707	1	155,903,735	155,904,681	946	2	13.6	16.8	27	28	1	2	3	KIAA0907, SCARNA4, RXFP4	-20, -8331, -7272	upstream, upstream, upstream	ActReg chr1 #707	1	1
708	1	155,940,174	155,941,039	865	1	11.148	7.741	19	17	0	0	1	ARHGEF2	7,730	in gene	ActReg chr1 #708	1	0
709	1	156,023,488	156,025,234	1,746	2	14.185	14.6	26	30	1	3	3	UBQLN4, ROBLD3, RAB25	-845, -156, -6605	upstream, upstream, upstream	ActReg chr1 #709	1	1
710	1	156,074,602	156,075,294	692	1	8.81	11.905	12	17	0	0	1	LMNA	-9,513	upstream	ActReg chr1 #710	0	1
711	1	156,083,705	156,086,002	2,297	2	11.194	13.764	22	26	1	1	1	LMNA	392	in gene	ActReg chr1 #711	1	1
712	1	156,092,209	156,093,040	831	1	9.615	11.654	15	17	0	0	1	LMNA	8,163	in gene	ActReg chr1 #712	0	1
713	1	156,095,807	156,097,296	1,489	2	14.702	11.915	24	19	0	0	1	LMNA	12,090	in gene	ActReg chr1 #713	1	1
714	1	156,163,245	156,164,373	1,128	1	7.152	12.686	12	20	1	1	1	SLC25A44	79	in gene	ActReg chr1 #714	0	1
715	1	156,230,329	156,231,168	839	1	9.037	14.37	16	23	0	0	1	SMG5	21,872	in gene	ActReg chr1 #715	0	1
716	1	156,308,017	156,308,843	826	1	11.192	12.115	18	20	1	3	3	CCT3, LOC100505747, C1orf182	-235, -1401, 1325	upstream, upstream, in gene	ActReg chr1 #716	0	1
717	1	156,383,635	156,384,769	1,134	1	10.694	14.222	20	28	0	1	3	C1orf61, LOC100505765, MIR9-1	14982, -1517, 6019	in gene, upstream, downstream	ActReg chr1 #717	0	1
718	1	156,390,973	156,391,946	973	2	14.677	11.032	27	19	1	1	3	C1orf61, LOC100505765, MIR9-1	7725, -8774, -1238	in gene, upstream, upstream	ActReg chr1 #718	1	1
719	1	156,425,795	156,427,206	1,411	2	12.5	12.523	19	24	1	0	1	MEF2D	44,029	downstream	ActReg chr1 #719	1	1
720	1	156,469,841	156,471,702	1,861	2	15.155	18.259	37	41	1	1	1	MEF2D	-242	upstream	ActReg chr1 #720	1	1
721	1	156,472,739	156,473,630	891	1	11.148	15.741	21	27	0	1	1	MEF2D	-2,655	upstream	ActReg chr1 #721	0	1
722	1	156,474,422	156,476,016	1,594	2	19.16	19.28	52	49	1	1	1	MEF2D	-4,690	upstream	ActReg chr1 #722	1	1
723	1	156,521,353	156,522,189	836	1	12.154	14.577	22	29	0	0	1	IQGAP3	20,625	in gene	ActReg chr1 #723	0	1
724	1	156,571,003	156,572,256	1,253	2	9.625	12.075	15	20	0	1	2	APOA1BP, GPATCH4	10071, -359	downstream, upstream	ActReg chr1 #724	1	1
725	1	156,621,343	156,622,266	923	1	10.517	13.931	16	23	0	0	1	BCAN	10,064	in gene	ActReg chr1 #725	0	1
726	1	156,629,678	156,630,745	1,067	2	14.758	16.121	25	28	0	0	2	BCAN, NES	18471, 16978	downstream, downstream	ActReg chr1 #726	1	1
727	1	156,630,750	156,632,673	1,923	2	12.918	15.393	24	34	0	0	2	BCAN, NES	19971, 15478	downstream, downstream	ActReg chr1 #727	1	1
728	1	156,646,307	156,647,581	1,274	1	8.641	14.487	17	19	1	1	1	NES	245	in gene	ActReg chr1 #728	0	1
729	1	156,697,764	156,699,230	1,466	2	13.733	13.044	33	31	1	2	3	ISG20L2, C1orf66, MRPL24	-792, 234, 12426	upstream, in gene, downstream	ActReg chr1 #729	1	1
730	1	156,710,147	156,711,654	1,507	2	14.761	13.468	36	26	1	1	3	C1orf66, MRPL24, HDGF	12637, 23, 11340	downstream, in gene, downstream	ActReg chr1 #730	1	1
731	1	156,717,553	156,719,125	1,572	1	10.347	11.714	15	20	0	1	2	MRPL24, HDGF	-7416, 3901	upstream, in gene	ActReg chr1 #731	0	1
732	1	156,721,361	156,722,401	1,040	2	26.303	28.212	78	81	1	1	1	HDGF	359	in gene	ActReg chr1 #732	1	1
733	1	156,736,120	156,737,894	1,774	2	17.054	19.893	41	45	1	1	1	PRCC	-267	upstream	ActReg chr1 #733	1	1
734	1	156,915,701	156,916,772	1,071	1	10.235	11.853	19	18	0	0	2	ARHGEF11, MIR765	98926, -10200	in gene, upstream	ActReg chr1 #734	0	1
735	1	157,107,533	157,108,913	1,380	2	13.395	12.93	20	24	1	1	1	ETV3	160	in gene	ActReg chr1 #735	1	1
736	1	158,007,446	158,008,265	819	1	13.962	9.615	27	15	0	0	2	KIRREL, LOC100505785	44792, 12510	in gene, downstream	ActReg chr1 #736	1	0
737	1	158,114,580	158,115,483	903	1	8.536	11.857	18	16	0	1	1	hCG_1654703	-4,601	upstream	ActReg chr1 #737	0	1
738	1	158,115,670	158,116,541	871	1	8.296	14.37	14	27	0	1	1	hCG_1654703	-5,675	upstream	ActReg chr1 #738	0	1
739	1	158,150,546	158,151,377	831	1	8.808	13.192	15	20	1	1	1	CD1D	1,224	in gene	ActReg chr1 #739	0	1
740	1	158,969,271	158,970,070	799	2	11.6	11.32	18	22	0	0	1	IFI16	-10,012	upstream	ActReg chr1 #740	1	1
741	1	159,046,261	159,047,577	1,316	1	9.61	13.634	14	24	0	1	1	AIM2	-272	upstream	ActReg chr1 #741	0	1
742	1	159,061,033	159,061,976	943	2	12.414	12.034	16	19	0	0	0				ActReg chr1 #742	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
743	1	159,145,022	159,145,943	921	2	16.035	13.034	34	29	0	0	1	CADM3	4,105	in gene	ActReg chr1 #743	1	1
744	1	159,146,463	159,147,725	1,262	2	23.875	26.625	82	83	0	0	1	CADM3	5,717	in gene	ActReg chr1 #744	1	1
745	1	159,774,403	159,775,410	1,007	2	11.452	13.613	20	25	0	1	1	FCRL6	2,733	in gene	ActReg chr1 #745	1	1
746	1	159,879,929	159,880,746	817	1	6.731	11.423	11	17	0	0	1	TAGLN2	14,947	downstream	ActReg chr1 #746	0	1
747	1	159,893,975	159,895,798	1,823	2	15.105	15.895	33	33	1	1	2	TAGLN2, IGSF9	398, 20500	in gene, downstream	ActReg chr1 #747	1	1
748	1	160,000,771	160,002,245	1,474	2	10.783	13	23	25	1	1	2	PIGM, KCNJ10	275, 38543	in gene, downstream	ActReg chr1 #748	1	1
749	1	160,175,147	160,176,359	1,212	1	8.474	12.447	14	20	1	1	3	CASQ1, PEA15, DCAF8	15468, 628, 56597	downstream, in gene, downstream	ActReg chr1 #749	0	1
750	1	160,231,702	160,232,593	891	2	12.036	13.571	22	20	1	2	3	DCAF8, LOC100287049, LOC100505665	203, 9443, 629	in gene, in gene	ActReg chr1 #750	1	1
751	1	160,254,505	160,255,316	811	2	13.04	11.92	23	26	0	1	2	PEX19, COPA	31, 58444	in gene, downstream	ActReg chr1 #751	1	1
752	1	160,795,809	160,796,495	686	2	11.857	12.524	24	25	0	0	2	LY9, CD244	30224, 36540	in gene, downstream	ActReg chr1 #752	1	1
753	1	161,087,190	161,088,317	1,127	2	12.371	12.771	23	16	1	2	3	PFDN2, NIT1, DEDD	113, -109, 14725	in gene, upstream, downstream	ActReg chr1 #753	1	1
754	1	161,101,934	161,103,158	1,224	2	12.658	13.921	29	26	1	1	2	NIT1, DEDD	14684, -68	downstream, upstream	ActReg chr1 #754	1	1
755	1	161,123,595	161,124,219	624	1	10.79	13.947	18	25	0	2	2	UFC1, USP21	373, -5347	in gene, upstream	ActReg chr1 #755	0	1
756	1	161,128,389	161,129,903	1,514	2	10.766	10.702	18	16	1	2	3	UFC1, USP21, PPOX	5612, -108, 7035	downstream, upstream, upstream	ActReg chr1 #756	1	1
757	1	161,135,469	161,137,078	1,609	2	18.94	22.92	59	63	1	1	4	UFC1, USP21, PPOX, B4GALT3	12739, 7019, 92, 11041	downstream, downstream, in gene, downstream	ActReg chr1 #757	1	1
758	1	161,171,788	161,172,654	866	1	11.482	15.815	16	26	1	1	2	ADAMTS4, NDUFS2	-3376, 3116	upstream, in gene	ActReg chr1 #758	0	1
759	1	161,195,364	161,196,497	1,133	1	7.514	11.943	13	19	0	2	4	FCER1G, APOA2, TOMM40L, NR1I3	10843, -2512, 97, 12070	downstream, upstream, in gene, downstream	ActReg chr1 #759	0	1
760	1	161,348,677	161,349,299	622	2	9.368	9.947	20	21	0	0	0				ActReg chr1 #760	1	1
761	1	161,359,288	161,360,704	1,416	3	10.711	11.644	19	25	1	0	1	LOC100505703	-9,203	upstream	ActReg chr1 #761	1	1
762	1	161,368,779	161,370,163	1,384	2	13.605	14.907	24	24	1	1	1	LOC100505703	272	in gene	ActReg chr1 #762	1	1
763	1	161,391,517	161,392,166	649	2	10.667	9.905	16	21	0	0	1	LOC100505703	22,642	in gene	ActReg chr1 #763	1	1
764	1	161,410,041	161,410,690	649	1	7.143	10	13	18	1	0	0				ActReg chr1 #764	0	1
765	1	161,468,351	161,468,943	592	1	10.579	11.21	18	20	0	1	1	FCGR2A	-6,558	upstream	ActReg chr1 #765	0	1
766	1	161,500,512	161,501,191	679	1	5.955	10.273	14	15	1	0	1	HSPA6	6,815	downstream	ActReg chr1 #766	0	1
767	1	161,509,606	161,510,303	697	2	13.524	16.667	25	33	0	0	1	FCGR3A	10,459	downstream	ActReg chr1 #767	1	1
768	1	161,691,504	161,692,274	770	2	13.083	16.167	32	34	0	1	2	FCRLA, FCRLB	15127, -568	downstream, upstream	ActReg chr1 #768	1	1
769	1	161,695,350	161,696,905	1,555	2	14.082	14.792	29	25	1	0	1	FCRLB	3,670	in gene	ActReg chr1 #769	1	1
770	1	161,699,853	161,700,497	644	1	13.95	9.3	19	13	0	0	1	FCRLB	7,718	downstream	ActReg chr1 #770	1	0
771	1	161,719,114	161,720,391	1,277	2	14.375	15.525	31	29	1	1	1	DUSP12	171	in gene	ActReg chr1 #771	1	1
772	1	161,735,813	161,736,506	693	2	12.524	12.905	21	21	0	1	2	DUSP12, ATF6	16578, 75	downstream, in gene	ActReg chr1 #772	1	1
773	1	161,972,775	161,973,478	703	1	11.682	12.454	15	19	0	0	1	OLFML2B	20,518	in gene	ActReg chr1 #773	0	1
774	1	162,024,817	162,025,428	611	1	6.474	12.737	10	19	0	0	0				ActReg chr1 #774	0	1
775	1	162,279,845	162,280,755	910	2	15.393	14.536	30	33	0	0	1	NOS1AP	240,719	in gene	ActReg chr1 #775	1	1
776	1	162,374,409	162,375,111	702	1	10.773	6.182	19	12	0	0	1	SH2D1B	7,168	in gene	ActReg chr1 #776	1	0
777	1	162,467,487	162,468,437	950	2	12.8	12.433	21	28	1	1	1	UHMK1	998	in gene	ActReg chr1 #777	1	1
778	1	162,530,343	162,532,491	2,148	2	10.746	13.672	20	28	1	1	1	UAP1	121	in gene	ActReg chr1 #778	1	1
779	1	162,575,169	162,575,815	646	1	7.1	10.3	13	16	0	0	1	UAP1	44,196	downstream	ActReg chr1 #779	0	1
780	1	162,602,585	162,603,378	793	1	8.8	10.64	16	17	0	1	1	DDR2	753	in gene	ActReg chr1 #780	0	1
781	1	163,005,438	163,006,123	685	1	10.636	10.046	18	18	0	0	0				ActReg chr1 #781	1	0
782	1	163,017,602	163,018,553	951	1	7.034	10.345	14	16	0	0	0				ActReg chr1 #782	0	1
783	1	163,291,197	163,292,301	1,104	2	21.057	25.657	51	66	1	1	1	NUF2	26	in gene	ActReg chr1 #783	1	1
784	1	164,527,728	164,528,329	601	1	10.632	8.158	17	14	0	1	1	PBX1	-774	upstream	ActReg chr1 #784	1	0
785	1	165,131,967	165,132,734	767	1	13.625	16.375	24	40	0	0	0				ActReg chr1 #785	0	1
786	1	165,508,346	165,509,261	915	2	11.793	10.345	20	21	0	1	2	LOC400794, LRRC52	42538, -4675	in gene, upstream	ActReg chr1 #786	1	1
787	1	165,599,682	165,601,140	1,458	2	10.533	12.556	23	20	1	1	1	MGST3	-39	upstream	ActReg chr1 #787	1	1
788	1	165,667,390	165,668,248	858	1	13.444	11.259	19	19	1	1	1	ALDH9A1	81	in gene	ActReg chr1 #788	1	0
789	1	165,737,712	165,738,582	870	2	13.111	13.148	27	21	1	2	2	TMCO1, LOC100147773	-12, -19	upstream, upstream	ActReg chr1 #789	1	1
790	1	165,797,405	165,797,995	590	1	10.684	8.789	15	13	1	1	1	UCK2	810	in gene	ActReg chr1 #790	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
791	1	165,918,556	165,919,183	627	1	13.65	11.35	22	18	0	0	0				ActReg chr1 #791	1	0
792	1	166,135,923	166,136,959	1,036	2	9.5	9.906	17	19	1	1	1	FAM78B	-483	upstream	ActReg chr1 #792	1	1
793	1	166,139,711	166,141,121	1,410	2	11.889	12.911	21	23	0	1	1	FAM78B	-4,458	upstream	ActReg chr1 #793	1	1
794	1	166,808,127	166,808,872	745	1	9.913	13.125	17	24	1	1	1	POGK	-225	upstream	ActReg chr1 #794	0	1
795	1	166,844,669	166,846,004	1,335	2	15.5	13.976	38	35	1	1	1	TADA1	318	in gene	ActReg chr1 #795	1	1
796	1	166,921,361	166,922,185	824	2	12.769	12.192	23	22	0	0	1	ILDR2	22,788	in gene	ActReg chr1 #796	1	1
797	1	167,105,307	167,106,043	736	1	9.826	12.913	16	22	0	0	1	DUSP27	41,588	downstream	ActReg chr1 #797	0	1
798	1	167,126,242	167,126,834	592	1	8.833	12.389	13	21	0	0	0				ActReg chr1 #798	0	1
799	1	167,164,987	167,165,594	607	1	12.579	7.368	22	11	0	0	0				ActReg chr1 #799	1	0
800	1	167,189,208	167,190,554	1,346	2	13.976	13.405	27	21	1	1	1	POU2F1	-262	upstream	ActReg chr1 #800	1	1
801	1	167,190,944	167,191,914	970	2	10.032	10.516	22	15	1	1	1	POU2F1	1,286	in gene	ActReg chr1 #801	1	1
802	1	167,486,497	167,487,252	755	1	10.652	15.783	17	23	0	1	1	CD247	973	in gene	ActReg chr1 #802	0	1
803	1	167,522,516	167,523,010	494	1	13	11.438	18	18	1	1	1	CREG1	293	in gene	ActReg chr1 #803	1	0
804	1	167,532,377	167,533,555	1,178	1	10.324	13.432	20	22	0	0	1	CREG1	-9,910	upstream	ActReg chr1 #804	0	1
805	1	167,683,273	167,685,154	1,881	2	14.542	15.661	31	39	2	1	2	RCSD1, MPZL1	84739, -6974	downstream, upstream	ActReg chr1 #805	1	1
806	1	167,690,417	167,691,715	1,298	1	12.049	16.024	16	26	1	1	1	MPZL1	-121	upstream	ActReg chr1 #806	0	1
807	1	167,904,597	167,906,862	2,265	2	10	11.409	16	21	1	2	2	BRP44, DCAF6	549, -179	in gene, upstream	ActReg chr1 #807	1	1
808	1	168,147,582	168,149,061	1,479	1	8.66	13.575	13	23	1	1	1	TIPRL	150	in gene	ActReg chr1 #808	0	1
809	1	168,206,137	168,206,841	704	1	11.591	13.182	19	21	0	0	1	SFT2D2	11,234	in gene	ActReg chr1 #809	0	1
810	1	168,290,001	168,290,694	693	1	10.954	10.5	15	18	0	0	1	TBX19	40,069	downstream	ActReg chr1 #810	0	1
811	1	168,435,146	168,435,873	727	1	11.826	10.13	16	18	0	0	0				ActReg chr1 #811	1	0
812	1	168,445,739	168,446,954	1,215	1	10.684	10.342	18	18	0	0	0				ActReg chr1 #812	1	0
813	1	168,592,137	168,592,822	685	1	11.524	8.048	16	14	0	0	0				ActReg chr1 #813	1	0
814	1	168,678,246	168,679,848	1,602	1	10.88	8.12	16	15	0	0	1	DPT	19,395	in gene	ActReg chr1 #814	1	0
815	1	168,688,385	168,689,221	836	2	12.615	10.923	26	21	0	0	1	DPT	9,639	in gene	ActReg chr1 #815	1	1
816	1	169,074,691	169,075,838	1,147	1	8.057	12.886	13	21	1	1	1	ATP1B1	-683	upstream	ActReg chr1 #816	0	1
817	1	169,075,844	169,076,483	639	1	10.15	14.5	18	20	1	1	1	ATP1B1	216	in gene	ActReg chr1 #817	0	1
818	1	169,085,024	169,085,808	784	1	11.32	13.4	20	23	0	0	1	ATP1B1	9,469	in gene	ActReg chr1 #818	0	1
819	1	169,132,229	169,133,005	776	1	10.375	8.75	16	17	0	0	1	NME7	204,569	in gene	ActReg chr1 #819	1	0
820	1	169,280,993	169,281,889	896	2	18.679	26.786	50	73	0	0	1	NME7	55,745	in gene	ActReg chr1 #820	1	1
821	1	169,564,801	169,565,406	605	1	9.611	11.778	19	20	0	0	2	F5, SELP	-9334, 34274	upstream, in gene	ActReg chr1 #821	0	1
822	1	169,763,744	169,764,527	783	2	13.24	12.92	18	23	1	2	2	C1orf156, C1orf112	-104, -415	upstream, upstream	ActReg chr1 #822	1	1
823	1	169,862,846	169,863,568	722	2	12.522	14.783	22	35	1	1	1	SCYL3	-131	upstream	ActReg chr1 #823	1	1
824	1	169,968,348	169,968,975	627	1	5	11.4	9	16	0	0	1	KIFAP3	75,218	in gene	ActReg chr1 #824	0	1
825	1	170,043,180	170,044,246	1,066	2	16.333	13.454	26	23	1	1	1	KIFAP3	166	in gene	ActReg chr1 #825	1	1
826	1	170,083,495	170,084,993	1,498	2	10.468	13.809	31	37	0	0	0				ActReg chr1 #826	1	1
827	1	170,265,755	170,266,250	495	1	10.062	8.938	16	16	0	0	0				ActReg chr1 #827	1	0
828	1	170,489,576	170,490,002	426	1	10.923	8.077	14	14	0	0	0				ActReg chr1 #828	1	0
829	1	170,500,683	170,501,988	1,305	2	14.951	13.561	28	31	0	1	1	GORAB	72	in gene	ActReg chr1 #829	1	1
830	1	170,667,753	170,668,275	522	1	5.625	11.688	10	19	0	0	1	PRRX1	34,701	in gene	ActReg chr1 #830	0	1
831	1	170,677,077	170,677,702	625	1	11	8.3	17	12	0	0	1	PRRX1	44,076	in gene	ActReg chr1 #831	1	0
832	1	170,776,307	170,777,107	800	2	12.12	10.8	25	14	0	0	0				ActReg chr1 #832	1	1
833	1	171,196,818	171,197,252	434	1	10.643	7.929	15	12	0	0	0				ActReg chr1 #833	1	0
834	1	171,282,841	171,283,485	644	1	6.15	11.25	10	18	0	1	1	FMO4	-323	upstream	ActReg chr1 #834	0	1
835	1	171,453,903	171,455,296	1,393	2	11.364	10.204	26	22	1	1	1	BAT2L2	-67	upstream	ActReg chr1 #835	1	1
836	1	171,710,559	171,711,862	1,303	2	18.61	19.659	52	45	1	1	1	VAMP4	169	in gene	ActReg chr1 #836	1	1
837	1	171,763,105	171,763,936	831	2	12.423	10.269	24	23	0	0	1	METTL13	12,759	in gene	ActReg chr1 #837	1	1
838	1	171,810,068	171,811,335	1,267	2	9.775	12.4	18	22	1	1	1	DNM3	80	in gene	ActReg chr1 #838	1	1
839	1	171,813,384	171,814,092	708	1	11.227	6.227	15	8	0	0	1	DNM3	3,117	in gene	ActReg chr1 #839	1	0
840	1	172,412,648	172,413,817	1,169	2	28.444	30.389	74	100	1	1	2	C1orf105, PIGC	23404, -2	in gene, upstream	ActReg chr1 #840	1	1
841	1	172,501,104	172,502,978	1,874	2	15.356	14.763	33	26	1	1	1	C1orf9	-219	upstream	ActReg chr1 #841	1	1
842	1	172,557,781	172,558,543	762	2	13.417	11.458	23	17	0	0	1	C1orf9	55,902	in gene	ActReg chr1 #842	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
843	1	172,578,534	172,579,121	587	1	10.444	5.833	17	9	0	0	1	C1orf9	76,567	in gene	ActReg chr1 #843	1	0
844	1	172,607,748	172,609,165	1,417	2	17.591	14.523	49	35	0	0	0				ActReg chr1 #844	1	1
845	1	172,623,541	172,624,129	588	1	6.368	11.579	9	15	0	1	1	FASLG	-4,350	upstream	ActReg chr1 #845	0	1
846	1	172,668,150	172,668,807	657	1	11.381	7.905	17	14	0	0	0				ActReg chr1 #846	1	0
847	1	172,902,971	172,903,837	866	2	11.741	11.444	17	20	0	0	0				ActReg chr1 #847	1	1
848	1	172,917,404	172,918,151	747	1	8.375	13.542	21	29	0	0	0				ActReg chr1 #848	0	1
849	1	172,968,285	172,968,948	663	1	12.429	6.81	25	12	0	0	0				ActReg chr1 #849	1	0
850	1	173,031,159	173,031,829	670	1	16.095	17.476	32	32	0	0	0				ActReg chr1 #850	0	1
851	1	173,091,990	173,092,599	609	1	11.053	7.263	18	10	0	0	0				ActReg chr1 #851	1	0
852	1	173,238,487	173,239,152	665	1	11.714	9.714	18	13	0	0	1	LOC100506023	207,475	in gene	ActReg chr1 #852	1	0
853	1	173,445,689	173,446,324	635	1	7.8	11	16	16	1	2	2	LOC100506023, PRDX6	288, -480	in gene, upstream	ActReg chr1 #853	0	1
854	1	173,683,646	173,684,610	964	2	14.645	13.129	26	32	1	1	1	KLHL20	48	in gene	ActReg chr1 #854	1	1
855	1	173,793,174	173,794,377	1,203	2	14.71	12.237	26	25	1	2	2	CENPL, DARS2	2, -22	in gene, upstream	ActReg chr1 #855	1	1
856	1	173,836,482	173,837,918	1,436	2	12.409	14.182	21	28	1	12	14	DARS2, LOC100506046, GAS5, SNORD81, SNORD47, SNORD80, SNORD79, SNORD78, SNORD44, SNORD77, SNORD76, SNORD75, SNORD74, ZBTB37	43403, 5910, -75, -3845, -3617, -3159, -2632, -2376, -2034, -1691, -1347, -1124, -317, -293	downstream, downstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr1 #856	1	1
857	1	173,839,390	173,840,072	682	1	7.091	12.409	11	18	0	12	13	LOC100506046, GAS5, SNORD81, SNORD47, SNORD80, SNORD79, SNORD78, SNORD44, SNORD77, SNORD76, SNORD75, SNORD74, ZBTB37	8441, -2606, -6376, -6148, -5690, -5163, -4907, -4565, -4222, -3878, -3655, -2848, 2238	downstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, in gene	ActReg chr1 #857	0	1
858	1	173,990,651	173,991,948	1,297	1	9.878	15.585	22	25	1	0	0				ActReg chr1 #858	0	1
859	1	174,021,092	174,021,703	611	1	7.368	10.684	13	19	0	0	0				ActReg chr1 #859	0	1
860	1	174,128,035	174,129,378	1,343	1	10.524	12.548	18	20	1	1	1	RABGAP1L	72	in gene	ActReg chr1 #860	0	1
861	1	174,367,081	174,367,703	622	1	7.947	10.368	15	14	0	0	1	RABGAP1L	238,758	in gene	ActReg chr1 #861	0	1
862	1	174,628,840	174,629,386	546	1	8.294	10.823	14	17	0	0	1	RABGAP1L	500,479	in gene	ActReg chr1 #862	0	1
863	1	174,968,200	174,969,725	1,525	3	13.085	14.617	30	28	1	1	2	LOC100506087, CACYBP	35057, 391	downstream, in gene	ActReg chr1 #863	1	1
864	1	175,138,263	175,139,739	1,476	2	11.022	12.935	19	19	0	0	1	KIAA0040	23,228	in gene	ActReg chr1 #864	1	1
865	1	175,166,099	175,167,218	1,119	1	10.6	6.229	20	10	0	1	1	KIAA0040	-4,429	upstream	ActReg chr1 #865	1	0
866	1	175,642,214	175,643,280	1,066	1	8.697	12.576	13	22	0	0	1	TNR	70,005	in gene	ActReg chr1 #866	0	1
867	1	175,694,576	175,695,471	893	2	13.25	18.964	34	43	0	0	1	TNR	17,728	in gene	ActReg chr1 #867	1	1
868	1	175,711,949	175,713,154	1,205	2	10.868	11.816	25	22	0	1	1	TNR	201	in gene	ActReg chr1 #868	1	1
869	1	176,175,805	176,177,141	1,336	2	10.929	11.238	18	21	1	1	1	RFWD2	-103	upstream	ActReg chr1 #869	1	1
870	1	176,486,493	176,487,053	560	1	8.167	11.167	11	22	0	0	1	PAPPA2	54,466	in gene	ActReg chr1 #870	0	1
871	1	177,177,954	177,178,993	1,039	2	13.031	14.75	28	33	0	0	1	FAM5B	37,840	in gene	ActReg chr1 #871	1	1
872	1	177,225,308	177,225,989	681	1	11.682	11.091	18	15	0	0	1	FAM5B	85,015	in gene	ActReg chr1 #872	1	0
873	1	177,278,976	177,280,167	1,191	2	11.474	11.579	22	23	0	0	0				ActReg chr1 #873	1	1
874	1	177,568,160	177,568,729	569	2	10.889	9.278	22	17	0	0	0				ActReg chr1 #874	1	1
875	1	178,021,869	178,022,549	680	1	10.667	11.809	15	16	0	0	0				ActReg chr1 #875	0	1
876	1	178,062,114	178,064,182	2,068	2	12.719	14.406	32	31	1	2	2	LOC100302401, RASAL2	-20, 284	upstream, in gene	ActReg chr1 #876	1	1
877	1	178,095,811	178,096,394	583	2	12	11.278	23	18	0	0	1	RASAL2	33,238	in gene	ActReg chr1 #877	1	1
878	1	178,386,919	178,387,601	682	1	14.476	9	26	16	0	0	1	RASAL2	324,396	in gene	ActReg chr1 #878	1	0
879	1	178,505,777	178,506,696	919	1	11.31	8.966	18	17	0	1	1	C1orf220	-5,695	upstream	ActReg chr1 #879	1	0
880	1	178,511,037	178,512,761	1,724	2	11.333	12.537	17	20	1	1	1	C1orf220	-32	upstream	ActReg chr1 #880	1	1
881	1	178,583,413	178,584,084	671	2	10.952	9.905	18	16	0	0	0				ActReg chr1 #881	1	1
882	1	178,693,890	178,694,316	426	1	8.462	11.077	10	17	1	1	1	RALGPS2	-197	upstream	ActReg chr1 #882	0	1
883	1	178,994,553	178,995,054	501	1	11.875	15.5	18	28	1	1	1	FAM20B	-271	upstream	ActReg chr1 #883	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
884	1	178,995,280	178,996,294	1,014	2	9.906	10.062	19	18	1	1	1	FAM20B	713	in gene	ActReg chr1 #884	1	1
885	1	179,050,554	179,051,697	1,143	2	12.167	12.583	19	19	1	1	2	FAM20B, TOR3A	56051, 13	downstream, in gene	ActReg chr1 #885	1	1
886	1	179,262,284	179,263,242	958	2	12.467	11.167	18	17	1	1	1	SOAT1	-254	upstream	ActReg chr1 #886	1	1
887	1	179,334,719	179,335,537	818	1	10.962	12.5	15	25	1	1	1	C1orf125	273	in gene	ActReg chr1 #887	0	1
888	1	179,519,575	179,520,900	1,325	2	11.571	13.309	23	22	0	0	2	C1orf125, NPHS2	185382, 24847	in gene, in gene	ActReg chr1 #888	1	1
889	1	179,850,907	179,852,507	1,600	2	14.98	15.22	29	24	1	2	2	TOR1AIP2, TOR1AIP1	-4766, 287	upstream, in gene	ActReg chr1 #889	1	1
890	1	179,923,541	179,924,600	1,059	1	10.636	15.939	18	30	1	1	1	CEP350	162	in gene	ActReg chr1 #890	0	1
891	1	180,471,077	180,472,434	1,357	2	15.048	18.024	31	35	1	1	1	ACBD6	267	in gene	ActReg chr1 #891	1	1
892	1	180,601,013	180,602,030	1,017	2	10.062	10.969	17	19	1	1	1	XPR1	375	in gene	ActReg chr1 #892	1	1
893	1	180,991,095	180,992,192	1,097	1	9.971	12.829	15	20	2	1	1	STX6	403	in gene	ActReg chr1 #893	0	1
894	1	181,057,215	181,058,628	1,413	2	12.622	14.444	24	32	1	1	1	IER5	283	in gene	ActReg chr1 #894	1	1
895	1	181,058,718	181,059,307	589	1	8	11.474	10	19	1	1	1	IER5	1,374	in gene	ActReg chr1 #895	0	1
896	1	181,074,645	181,075,264	619	1	12	12.05	16	20	1	0	0				ActReg chr1 #896	0	1
897	1	182,204,685	182,205,968	1,283	2	11.65	10.275	16	18	0	0	0				ActReg chr1 #897	1	1
898	1	182,557,924	182,558,779	855	1	7.115	11.846	11	17	0	1	2	RNASEL, RGS16	-2243, 15197	upstream, downstream	ActReg chr1 #898	0	1
899	1	182,572,961	182,573,898	937	2	11.621	14.069	19	24	1	1	1	RGS16	119	in gene	ActReg chr1 #899	1	1
900	1	182,583,784	182,584,621	837	2	10.231	10.231	16	17	1	1	1	LOC284648	-73	upstream	ActReg chr1 #900	1	1
901	1	182,720,925	182,722,548	1,623	2	11.726	12.118	22	23	0	0	0				ActReg chr1 #901	1	1
902	1	182,758,279	182,759,314	1,035	1	9.25	15.094	19	30	1	1	1	NPL	-2,598	upstream	ActReg chr1 #902	0	1
903	1	182,807,877	182,809,247	1,370	1	9.524	11.809	16	18	1	1	2	NPL, DHX9	47168, 123	downstream, in gene	ActReg chr1 #903	0	1
904	1	182,991,214	182,992,225	1,011	1	7.469	11.188	14	18	1	1	1	LAMC1	-876	upstream	ActReg chr1 #904	0	1
905	1	182,992,878	182,993,695	817	2	11.12	13.12	22	22	1	1	1	LAMC1	691	in gene	ActReg chr1 #905	1	1
906	1	183,203,390	183,204,383	993	1	12.29	10.419	19	16	0	0	1	LAMC2	48,712	in gene	ActReg chr1 #906	1	0
907	1	183,246,880	183,249,547	2,667	1	10.607	11.738	19	19	0	0	1	NMNAT2	139,524	in gene	ActReg chr1 #907	0	1
908	1	183,318,152	183,319,579	1,427	1	8.386	11.932	18	20	0	0	1	NMNAT2	68,872	in gene	ActReg chr1 #908	0	1
909	1	183,385,253	183,387,845	2,592	2	14.123	19.407	32	48	1	1	1	NMNAT2	1,188	in gene	ActReg chr1 #909	1	1
910	1	183,439,896	183,442,392	2,496	2	12.218	15.192	23	32	1	2	2	LOC100506298, SMG7	-10, -362	upstream, upstream	ActReg chr1 #910	1	1
911	1	183,569,154	183,569,829	675	1	14.762	11.476	31	20	0	0	1	NCF2	-9,435	upstream	ActReg chr1 #911	1	0
912	1	183,604,457	183,605,660	1,203	2	12.378	12.432	25	20	1	2	4	ARPC5, LOC100292409, RGL1, APOBEC4	-73, 3349, -150, 17390	upstream, downstream, upstream, downstream	ActReg chr1 #912	1	1
913	1	183,912,020	183,912,717	697	1	9.091	11.409	18	18	0	0	1	GLT25D2	94,495	in gene	ActReg chr1 #913	0	1
914	1	184,020,376	184,021,656	1,280	2	10.85	14.8	25	30	1	1	1	TSEN15	205	in gene	ActReg chr1 #914	1	1
915	1	184,168,109	184,169,535	1,426	1	12.159	9.932	18	18	0	0	0				ActReg chr1 #915	1	0
916	1	184,584,259	184,585,024	765	2	10.667	11.125	17	21	0	0	1	C1orf21	228,491	in gene	ActReg chr1 #916	1	1
917	1	184,591,231	184,592,092	861	1	13.37	8.889	22	14	0	0	1	C1orf21	235,511	in gene	ActReg chr1 #917	1	0
918	1	184,723,117	184,724,863	1,746	2	11.944	13.963	20	26	1	1	1	EDEM3	51	in gene	ActReg chr1 #918	1	1
919	1	184,836,197	184,836,705	508	1	11.312	10.438	14	14	0	0	1	FAM129A	107,231	in gene	ActReg chr1 #919	1	0
920	1	185,014,288	185,015,298	1,010	1	10.781	8.406	18	13	1	1	1	RNF2	242	in gene	ActReg chr1 #920	1	0
921	1	185,125,465	185,127,014	1,549	1	10.551	10.959	16	16	1	2	2	C1orf25, C1orf26	-123, 47	upstream, in gene	ActReg chr1 #921	0	1
922	1	185,285,252	185,287,138	1,886	1	9.655	13.407	15	24	1	1	1	IVNS1ABP	266	in gene	ActReg chr1 #922	0	1
923	1	185,342,948	185,343,629	681	1	12.381	10.191	20	15	0	0	0				ActReg chr1 #923	1	0
924	1	185,378,651	185,379,867	1,216	2	11.737	11.816	19	22	0	0	0				ActReg chr1 #924	1	1
925	1	185,452,812	185,454,003	1,191	2	12.405	13.46	23	27	0	0	0				ActReg chr1 #925	1	1
926	1	185,615,215	185,615,753	538	1	8.765	10.941	14	16	0	0	0				ActReg chr1 #926	0	1
927	1	185,703,150	185,703,964	814	1	10.32	15.36	18	31	1	1	1	HMCN1	-126	upstream	ActReg chr1 #927	0	1
928	1	185,759,262	185,760,106	844	1	9.259	10.778	14	16	0	0	1	HMCN1	56,001	in gene	ActReg chr1 #928	0	1
929	1	186,152,199	186,153,143	944	1	10.31	7.793	18	14	0	0	1	HMCN1	448,988	in gene	ActReg chr1 #929	1	0
930	1	186,156,539	186,157,890	1,351	2	15.512	14.721	23	29	0	0	1	HMCN1	453,531	in gene	ActReg chr1 #930	1	1
931	1	186,177,813	186,178,549	736	1	12	10	18	17	0	0	0				ActReg chr1 #931	1	0
932	1	186,205,514	186,206,710	1,196	2	13.297	11.46	25	23	0	0	0				ActReg chr1 #932	1	1
933	1	186,343,998	186,345,178	1,180	2	16.811	16.378	35	23	1	2	2	TPR, C1orf27	-131, -302	upstream, upstream	ActReg chr1 #933	1	1
934	1	186,447,583	186,448,139	556	2	8.222	10.333	17	16	0	0	0				ActReg chr1 #934	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
935	1	186,649,632	186,650,187	555	1	7.444	10.556	12	16	1	1	1	PTGS2	-350	upstream	ActReg chr1 #935	0	1
936	1	187,660,424	187,661,137	713	2	10.727	12	23	20	0	0	0				ActReg chr1 #936	1	1
937	1	187,811,583	187,812,221	638	1	10.6	6.55	16	10	0	0	0				ActReg chr1 #937	1	0
938	1	188,639,781	188,640,490	709	1	11.182	15.136	19	29	0	0	0				ActReg chr1 #938	0	1
939	1	188,856,935	188,858,040	1,105	2	12.353	13.794	21	20	0	0	0				ActReg chr1 #939	1	1
940	1	189,586,015	189,586,350	335	1	10.727	7.273	15	10	0	0	0				ActReg chr1 #940	1	0
941	1	189,627,581	189,627,995	414	1	10.846	8.077	12	12	0	0	0				ActReg chr1 #941	1	0
942	1	189,991,730	189,992,369	639	1	10.1	7.6	20	15	0	0	0				ActReg chr1 #942	1	0
943	1	192,194,946	192,195,455	509	1	10.467	9.333	16	14	0	0	0				ActReg chr1 #943	1	0
944	1	192,500,122	192,500,627	505	1	5.625	10.562	7	18	0	0	0				ActReg chr1 #944	0	1
945	1	192,519,829	192,520,621	792	2	11.72	11	18	25	0	0	0				ActReg chr1 #945	1	1
946	1	192,777,124	192,778,604	1,480	1	9.435	11.891	20	20	1	1	1	RGS2	-305	upstream	ActReg chr1 #946	0	1
947	1	193,027,357	193,029,430	2,073	2	12.8	14.815	34	35	1	2	2	UCHL5, TROVE2	128, -159	in gene, upstream	ActReg chr1 #947	1	1
948	1	193,073,889	193,074,988	1,099	1	8.882	11.588	15	20	1	1	1	GLRX2	806	in gene	ActReg chr1 #948	0	1
949	1	193,090,546	193,091,709	1,163	2	14.194	14.361	25	24	1	1	1	CDC73	39	in gene	ActReg chr1 #949	1	1
950	1	193,427,649	193,428,353	704	1	12	9.455	15	18	0	0	0				ActReg chr1 #950	1	0
951	1	193,527,452	193,528,059	607	1	7.684	10.421	11	14	0	0	0				ActReg chr1 #951	0	1
952	1	195,633,516	195,634,175	659	1	12.55	8.4	24	11	0	0	0				ActReg chr1 #952	1	0
953	1	196,149,657	196,150,854	1,197	1	14.474	10.026	33	19	0	0	0				ActReg chr1 #953	1	0
954	1	196,577,019	196,578,844	1,825	2	10.544	12.737	21	21	1	1	1	KCNT2	-432	upstream	ActReg chr1 #954	1	1
955	1	197,115,134	197,116,335	1,201	2	11.974	15.632	26	28	0	1	2	ASPM, ZBTB41	90, 53938	in gene, downstream	ActReg chr1 #955	1	1
956	1	197,169,911	197,171,123	1,212	1	10.026	15.895	17	37	1	1	1	ZBTB41	-845	upstream	ActReg chr1 #956	0	1
957	1	197,871,326	197,872,391	1,065	2	16.971	16.941	36	39	1	1	2	C1orf53, LHX9	176, -9777	in gene, upstream	ActReg chr1 #957	1	1
958	1	197,987,588	197,988,502	914	1	9.536	12.321	18	21	0	0	0				ActReg chr1 #958	0	1
959	1	198,090,034	198,090,833	799	1	9.88	13.28	17	19	0	0	0				ActReg chr1 #959	0	1
960	1	198,126,312	198,126,861	549	1	5.647	11.471	10	17	1	1	1	NEK7	478	in gene	ActReg chr1 #960	0	1
961	1	198,412,371	198,413,031	660	2	11.238	12.857	21	31	0	0	0				ActReg chr1 #961	1	1
962	1	198,682,298	198,682,787	489	1	4.188	9.25	6	16	0	0	1	PTPRC	74,405	in gene	ActReg chr1 #962	0	1
963	1	198,850,221	198,850,806	585	1	11.556	9.056	20	13	0	0	0				ActReg chr1 #963	1	0
964	1	199,711,466	199,712,323	857	2	14.778	13.963	30	39	0	0	0				ActReg chr1 #964	1	1
965	1	200,008,284	200,008,990	706	1	9.227	12.591	17	17	1	0	1	NR5A2	11,867	in gene	ActReg chr1 #965	0	1
966	1	200,044,600	200,045,064	464	1	10.067	4.4	18	8	0	0	1	NR5A2	48,062	in gene	ActReg chr1 #966	1	0
967	1	200,149,121	200,150,594	1,473	1	6.333	12.022	14	18	0	0	1	NR5A2	153,087	downstream	ActReg chr1 #967	0	1
968	1	200,589,428	200,590,354	926	2	13.828	12.172	24	21	1	1	1	KIF14	-29	upstream	ActReg chr1 #968	1	1
969	1	200,638,343	200,639,558	1,215	2	12.579	17.79	26	32	1	1	1	DDX59	176	in gene	ActReg chr1 #969	1	1
970	1	200,708,059	200,708,793	734	1	8.565	14.87	13	25	1	1	1	CAMSAP1L1	-260	upstream	ActReg chr1 #970	0	1
971	1	200,849,250	200,849,969	719	1	9.182	14.273	18	24	0	0	1	GPR25	7,443	downstream	ActReg chr1 #971	0	1
972	1	200,859,495	200,860,936	1,441	2	14.156	17.156	32	36	1	1	1	C1orf106	-424	upstream	ActReg chr1 #972	1	1
973	1	201,198,824	201,199,844	1,020	2	12.656	9.75	19	17	0	0	1	IGFN1	39,381	downstream	ActReg chr1 #973	1	1
974	1	201,279,551	201,280,587	1,036	1	13.242	12.727	21	17	0	0	1	PKP1	27,489	in gene	ActReg chr1 #974	1	0
975	1	201,419,849	201,420,644	795	1	9.44	13.16	12	20	0	0	0				ActReg chr1 #975	0	1
976	1	201,430,178	201,431,728	1,550	2	14.021	12.435	30	23	0	0	1	PHLDA3	7,346	downstream	ActReg chr1 #976	1	1
977	1	201,437,394	201,439,179	1,785	1	9.518	13.054	19	19	1	1	1	PHLDA3	13	in gene	ActReg chr1 #977	0	1
978	1	201,457,899	201,458,934	1,035	2	10.656	11.406	21	22	0	0	1	CSRP1	17,971	in gene	ActReg chr1 #978	1	1
979	1	201,475,835	201,476,737	902	2	12.207	12.862	23	21	1	2	2	CSRP1, LOC100506590	101, -1113	in gene, upstream	ActReg chr1 #979	1	1
980	1	201,520,814	201,521,560	746	2	12.478	14.739	25	31	0	0	0				ActReg chr1 #980	1	1
981	1	201,562,139	201,563,179	1,040	2	13.333	14.242	27	24	0	0	0				ActReg chr1 #981	1	1
982	1	201,563,219	201,564,846	1,627	1	8.686	13.706	22	25	0	0	0				ActReg chr1 #982	0	1
983	1	201,617,735	201,618,498	763	1	6.917	12.208	12	21	1	1	1	NAV1	666	in gene	ActReg chr1 #983	0	1
984	1	201,682,280	201,683,021	741	1	7.522	13.261	13	23	0	0	1	NAV1	65,200	in gene	ActReg chr1 #984	0	1
985	1	201,797,805	201,798,907	1,102	2	25.235	28.765	72	78	1	1	2	NAV1, IPO9	180906, 68	downstream, in gene	ActReg chr1 #985	1	1
986	1	201,924,126	201,925,327	1,201	2	10.395	11.158	23	21	1	1	2	LMOD1, TIMM17A	-9010, 107	upstream, in gene	ActReg chr1 #986	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
987	1	201,951,741	201,952,800	1,059	1	9.515	13.177	20	23	1	1	1	RNPEP	504	in gene	ActReg chr1 #987	0	1
988	1	202,310,736	202,311,492	756	2	9.958	11.636	16	22	1	2	2	UBE2T, PPP1R12B	-20, -6716	upstream, upstream	ActReg chr1 #988	1	1
989	1	202,317,467	202,318,703	1,236	1	12.769	11.41	20	19	1	2	2	UBE2T, PPP1R12B	-6991, 255	upstream, in gene	ActReg chr1 #989	1	0
990	1	202,625,761	202,627,161	1,400	2	13.186	13.698	26	24	0	0	1	SYT2	53,090	in gene	ActReg chr1 #990	1	1
991	1	202,649,406	202,650,222	816	1	6.154	11.731	15	17	0	0	1	SYT2	29,737	in gene	ActReg chr1 #991	0	1
992	1	202,661,852	202,662,974	1,122	2	19.086	24.286	58	63	0	0	1	SYT2	17,138	in gene	ActReg chr1 #992	1	1
993	1	202,777,008	202,777,846	838	1	9.538	13.269	16	20	1	2	2	KDM5B, LOC100506696	122, -2647	in gene, upstream	ActReg chr1 #993	0	1
994	1	202,779,399	202,780,674	1,275	2	13.1	10.6	23	22	1	2	3	KDM5B, LOC100506696, LOC641515	-2487, -38, 9349	upstream, upstream, upstream	ActReg chr1 #994	1	1
995	1	202,830,472	202,831,364	892	1	11.286	8.607	16	12	1	0	0				ActReg chr1 #995	1	0
996	1	202,895,764	202,896,654	890	1	9.964	13.071	16	21	1	1	1	KLHL12	162	in gene	ActReg chr1 #996	0	1
997	1	202,926,782	202,927,750	968	1	7.548	13.774	15	21	1	1	2	ADIPOR1, CYB5R1	434, 9138	in gene, downstream	ActReg chr1 #997	0	1
998	1	202,976,085	202,977,130	1,045	1	9.727	12.606	22	18	1	1	1	TMEM183A	73	in gene	ActReg chr1 #998	0	1
999	1	203,096,950	203,098,120	1,170	1	10.568	12	18	21	1	1	1	ADORA1	699	in gene	ActReg chr1 #999	0	1
1000	1	203,247,242	203,248,464	1,222	1	8.289	11.342	13	20	0	0	1	LOC100506775	-8,427	upstream	ActReg chr1 #1000	0	1
1001	1	203,456,519	203,457,386	867	1	12.185	11.296	17	15	1	1	2	PRELP, OPTC	12069, -6319	in gene, upstream	ActReg chr1 #1001	1	0
1002	1	203,503,411	203,504,211	800	2	13.44	12.24	25	22	0	0	0				ActReg chr1 #1002	1	1
1003	1	203,527,172	203,528,397	1,225	2	14.895	12.842	33	23	0	0	0				ActReg chr1 #1003	1	1
1004	1	203,559,277	203,560,335	1,058	2	15.152	14.848	33	22	0	0	0				ActReg chr1 #1004	1	1
1005	1	203,830,138	203,831,308	1,170	2	14.568	20.946	35	46	1	1	2	ZC3H11A, SNRPE	65972, -17	downstream, upstream	ActReg chr1 #1005	1	1
1006	1	204,042,651	204,043,925	1,274	2	12.125	10.75	18	17	1	1	1	SOX13	1,042	in gene	ActReg chr1 #1006	1	1
1007	1	204,386,349	204,387,282	933	1	9.483	12.034	13	17	0	1	2	PPP1R15B, PIK3C2B	-5871, 72659	upstream, downstream	ActReg chr1 #1007	0	1
1008	1	204,475,875	204,476,533	658	1	12.45	8.05	24	15	0	0	1	MDM4	-9,307	upstream	ActReg chr1 #1008	1	0
1009	1	204,485,046	204,486,025	979	1	14.323	9.323	23	16	1	1	1	MDM4	24	in gene	ActReg chr1 #1009	1	0
1010	1	204,616,185	204,617,589	1,404	2	20.204	22.454	68	81	0	0	1	LRRN2	37,710	in gene	ActReg chr1 #1010	1	1
1011	1	204,732,693	204,733,469	776	1	9.833	14	14	30	0	0	0				ActReg chr1 #1011	0	1
1012	1	204,806,148	204,807,366	1,218	2	15.132	16.684	32	37	0	0	1	NFASC	8,975	in gene	ActReg chr1 #1012	1	1
1013	1	204,958,236	204,959,610	1,374	1	7.047	11.605	13	21	0	0	1	NFASC	161,141	in gene	ActReg chr1 #1013	0	1
1014	1	205,090,604	205,091,792	1,188	2	19.892	19.919	49	50	0	1	1	RBBP5	-48	upstream	ActReg chr1 #1014	1	1
1015	1	205,179,966	205,181,540	1,574	2	9.66	14.6	18	26	1	1	1	DSTYK	-26	upstream	ActReg chr1 #1015	1	1
1016	1	205,227,610	205,228,419	809	1	9.846	11.846	16	19	0	0	2	TMCC2, LOC100506871	30976, -8622	in gene, upstream	ActReg chr1 #1016	0	1
1017	1	205,252,872	205,254,477	1,605	2	12.76	12.68	19	27	0	0	0				ActReg chr1 #1017	1	1
1018	1	205,417,884	205,418,780	896	1	12.857	9.5	17	14	0	2	3	LOC100506918, MIR135B, LOC284577	6882, -806, 6713	in gene, upstream, upstream	ActReg chr1 #1018	1	0
1019	1	205,426,767	205,428,718	1,951	3	15.312	16.623	36	54	0	2	3	LOC100506918, MIR135B, LOC284577	-2528, -10216, 2697	upstream, upstream, in gene	ActReg chr1 #1019	1	1
1020	1	205,600,776	205,601,703	927	2	11.483	16.345	32	38	1	1	1	ELK4	761	in gene	ActReg chr1 #1020	1	1
1021	1	205,719,194	205,719,821	627	1	8.75	12.55	12	19	1	1	1	NUCKS1	-146	upstream	ActReg chr1 #1021	0	1
1022	1	205,744,000	205,745,050	1,050	2	12.364	14.303	29	26	1	1	1	RAB7L1	85	in gene	ActReg chr1 #1022	1	1
1023	1	205,782,031	205,782,939	908	1	9.143	14.5	16	25	1	2	2	SLC41A1, LOC100131354	-324, 617	upstream, in gene	ActReg chr1 #1023	0	1
1024	1	205,902,243	205,903,553	1,310	2	11.61	13.805	22	24	0	0	1	SLC26A9	9,690	in gene	ActReg chr1 #1024	1	1
1025	1	206,275,444	206,276,072	628	1	6.05	10.75	9	17	0	0	1	LOC100505650	12,441	downstream	ActReg chr1 #1025	0	1
1026	1	206,643,288	206,645,009	1,721	2	13.444	12.093	25	27	0	1	2	SRGAP2, IKBKE	127952, 562	downstream, in gene	ActReg chr1 #1026	1	1
1027	1	206,785,329	206,786,289	960	2	20.067	24.433	51	53	1	1	1	LGTN	95	in gene	ActReg chr1 #1027	1	1
1028	1	206,808,324	206,809,398	1,074	1	10.061	14.333	24	22	1	1	1	DYRK3	-20	upstream	ActReg chr1 #1028	0	1
1029	1	206,857,738	206,858,311	573	1	3.444	10.944	6	22	1	1	1	MAPKAPK2	-265	upstream	ActReg chr1 #1029	0	1
1030	1	207,063,205	207,064,731	1,526	3	12.128	11.234	19	18	0	1	1	IL24	-6,820	upstream	ActReg chr1 #1030	1	1
1031	1	207,194,251	207,195,430	1,179	1	9.081	12.027	14	18	0	0	1	C1orf116	11,261	in gene	ActReg chr1 #1031	0	1
1032	1	207,226,149	207,227,101	952	1	8.345	12.345	14	20	1	2	2	YOD1, PFKFB2	-2203, 5	upstream, in gene	ActReg chr1 #1032	0	1
1033	1	207,377,938	207,379,259	1,321	2	8.463	8.512	15	18	0	0	1	LOC100129101	116,876	in gene	ActReg chr1 #1033	1	1
1034	1	207,392,137	207,392,769	632	1	8.75	10.7	12	18	0	0	1	LOC100129101	103,021	in gene	ActReg chr1 #1034	0	1
1035	1	208,280,911	208,282,034	1,123	2	12.429	11.886	20	16	0	0	1	PLXNA2	136,193	in gene	ActReg chr1 #1035	1	1
1036	1	208,357,380	208,358,213	833	1	7.962	12.269	16	20	0	0	1	PLXNA2	59,869	in gene	ActReg chr1 #1036	0	1
1037	1	208,502,540	208,503,210	670	1	6.938	11.857	14	20	0	0	0				ActReg chr1 #1037	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1038	1	208,648,776	208,649,395	619	1	7.211	11.21	11	20	0	0	0				ActReg chr1 #1038	0	1
1039	1	208,842,096	208,842,945	849	2	13.444	20.926	40	55	0	0	0				ActReg chr1 #1039	1	1
1040	1	208,922,169	208,922,783	614	1	5.737	10.632	11	17	0	0	0				ActReg chr1 #1040	0	1
1041	1	209,212,623	209,213,568	945	2	10.767	12	19	20	0	0	0				ActReg chr1 #1041	1	1
1042	1	209,323,216	209,324,297	1,081	2	16.765	22.882	48	69	0	0	0				ActReg chr1 #1042	1	1
1043	1	209,414,756	209,415,409	653	1	8.5	12.55	14	20	0	0	0				ActReg chr1 #1043	0	1
1044	1	209,491,821	209,492,469	648	1	11.85	9.85	17	15	0	0	0				ActReg chr1 #1044	1	0
1045	1	209,542,005	209,542,888	883	1	7.714	10.75	15	17	0	0	0				ActReg chr1 #1045	0	1
1046	1	209,575,837	209,576,534	697	1	6.409	11.636	10	22	0	0	0				ActReg chr1 #1046	0	1
1047	1	209,824,292	209,825,069	777	1	14.875	11.833	27	21	0	1	1	LAMB3	1,140	in gene	ActReg chr1 #1047	1	0
1048	1	209,826,231	209,827,328	1,097	1	7.4	12.286	13	22	0	1	1	LAMB3	-959	upstream	ActReg chr1 #1048	0	1
1049	1	210,000,966	210,001,763	797	1	11	14.6	17	29	1	1	1	C1orf107	52	in gene	ActReg chr1 #1049	0	1
1050	1	210,013,019	210,013,962	943	2	11.067	11.133	21	22	0	0	1	C1orf107	12,178	in gene	ActReg chr1 #1050	1	1
1051	1	210,052,605	210,053,418	813	2	11.846	11.308	18	21	0	0	0				ActReg chr1 #1051	1	1
1052	1	210,099,180	210,099,803	623	1	5.947	11	9	21	0	0	0				ActReg chr1 #1052	0	1
1053	1	210,110,219	210,112,263	2,044	3	11.547	15.016	48	53	1	1	1	SYT14	-297	upstream	ActReg chr1 #1053	1	1
1054	1	210,247,897	210,248,842	945	2	12.433	13.4	24	23	0	0	1	SYT14	136,831	in gene	ActReg chr1 #1054	1	1
1055	1	210,303,037	210,303,592	555	1	7.222	10.222	11	16	0	0	1	SYT14	191,776	in gene	ActReg chr1 #1055	0	1
1056	1	210,305,791	210,306,507	716	1	11.304	9.13	21	18	0	0	1	SYT14	194,611	in gene	ActReg chr1 #1056	1	0
1057	1	210,386,273	210,387,313	1,040	2	10.938	11.594	18	25	0	0	0				ActReg chr1 #1057	1	1
1058	1	210,406,391	210,407,348	957	1	12.7	11	17	19	2	2	2	C1orf133, SERTAD4	597, 674	in gene, in gene	ActReg chr1 #1058	1	0
1059	1	210,465,624	210,466,467	843	2	11.704	13.407	24	22	1	0	0				ActReg chr1 #1059	1	1
1060	1	210,546,793	210,548,132	1,339	2	14.905	15.024	35	35	0	0	1	HHAT	45,866	in gene	ActReg chr1 #1060	1	1
1061	1	210,566,704	210,567,556	852	1	10.741	13.704	18	25	0	0	1	HHAT	65,534	in gene	ActReg chr1 #1061	0	1
1062	1	210,612,096	210,613,001	905	1	11.483	8.862	18	14	0	0	1	HHAT	110,952	in gene	ActReg chr1 #1062	1	0
1063	1	210,770,732	210,772,046	1,314	2	12.024	15.659	21	26	0	0	1	HHAT	269,793	in gene	ActReg chr1 #1063	1	1
1064	1	210,899,635	210,900,540	905	2	12.429	14.286	21	29	0	0	1	KCNH1	407,370	in gene	ActReg chr1 #1064	1	1
1065	1	210,912,822	210,913,525	703	1	10.5	11.636	18	21	0	0	1	KCNH1	394,284	in gene	ActReg chr1 #1065	0	1
1066	1	211,307,188	211,307,958	770	1	9.083	12.792	16	21	1	1	1	KCNH1	-116	upstream	ActReg chr1 #1066	0	1
1067	1	211,431,837	211,432,603	766	2	11.833	10.625	17	21	1	1	1	RCOR3	-488	upstream	ActReg chr1 #1067	1	1
1068	1	211,433,451	211,434,072	621	1	11.79	8.579	21	13	1	1	1	RCOR3	1,053	in gene	ActReg chr1 #1068	1	0
1069	1	211,750,869	211,753,261	2,392	1	9.213	13.387	15	21	1	1	1	SLC30A1	34	in gene	ActReg chr1 #1069	0	1
1070	1	211,765,189	211,766,126	937	2	9.724	14	19	28	0	0	0				ActReg chr1 #1070	1	1
1071	1	211,848,439	211,849,248	809	1	9.962	12.615	21	22	1	1	1	NEK2	124	in gene	ActReg chr1 #1071	0	1
1072	1	211,908,434	211,909,661	1,227	1	13.816	10	20	13	0	0	1	LPGAT1	95,067	downstream	ActReg chr1 #1072	1	0
1073	1	212,204,074	212,205,255	1,181	2	10.838	12.838	28	32	0	1	2	INTS7, DTL	4220, -4255	in gene, upstream	ActReg chr1 #1073	1	1
1074	1	212,208,440	212,209,478	1,038	1	11.454	13.273	21	21	1	2	2	INTS7, DTL	-75, 40	upstream, in gene	ActReg chr1 #1074	0	1
1075	1	212,457,770	212,460,216	2,446	2	14.487	15.342	30	33	1	1	1	PPP2R5A	114	in gene	ActReg chr1 #1075	1	1
1076	1	212,643,156	212,644,022	866	2	12.926	14.926	26	28	0	0	0				ActReg chr1 #1076	1	1
1077	1	212,655,079	212,656,977	1,898	2	12.864	13.186	30	23	0	0	0				ActReg chr1 #1077	1	1
1078	1	212,658,164	212,659,952	1,788	2	11.679	12.857	20	32	0	0	0				ActReg chr1 #1078	1	1
1079	1	212,732,014	212,732,890	876	1	9.407	14.074	14	25	1	1	1	ATF3	-6,245	upstream	ActReg chr1 #1079	0	1
1080	1	212,781,412	212,782,429	1,017	2	11.484	12.129	17	18	1	0	1	ATF3	43,223	in gene	ActReg chr1 #1080	1	1
1081	1	212,844,716	212,845,607	891	1	13.25	6.607	21	11	0	0	0				ActReg chr1 #1081	1	0
1082	1	212,964,687	212,965,580	893	2	14.607	14.607	28	26	1	2	2	NSL1, TATDN3	6, -37	in gene, upstream	ActReg chr1 #1082	1	1
1083	1	213,030,835	213,032,416	1,581	1	10.58	12.74	14	22	1	2	3	C1orf227, LQK1, FLVCR1	-10634, -145, 28	upstream, upstream, in gene	ActReg chr1 #1083	0	1
1084	1	213,089,942	213,090,590	648	1	8.55	12.6	15	18	0	0	0				ActReg chr1 #1084	0	1
1085	1	213,188,907	213,189,380	473	1	10.933	13.2	16	21	1	1	1	ANGEL2	25	in gene	ActReg chr1 #1085	0	1
1086	1	213,224,012	213,225,225	1,213	1	11.71	13.684	23	28	1	1	1	RPS6KC1	30	in gene	ActReg chr1 #1086	0	1
1087	1	213,500,471	213,501,186	715	2	11.348	11.391	24	22	0	0	0				ActReg chr1 #1087	1	1
1088	1	213,862,473	213,863,039	566	1	11.765	9.647	15	13	0	0	0				ActReg chr1 #1088	1	0
1089	1	214,146,269	214,146,984	715	1	12.696	9.348	20	14	0	1	1	LOC100505832	-7,018	upstream	ActReg chr1 #1089	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1090	1	214,280,491	214,281,128	637	1	5.158	11.35	8	18	0	0	0				ActReg chr1 #1090	0	1
1091	1	214,296,438	214,297,162	724	2	10.478	10.174	18	20	0	0	0				ActReg chr1 #1091	1	1
1092	1	214,454,443	214,455,113	670	1	11.857	11.524	25	20	1	1	1	SMYD2	213	in gene	ActReg chr1 #1092	0	1
1093	1	214,600,804	214,601,765	961	1	13.633	9.6	26	21	0	0	1	PTPN14	123,740	in gene	ActReg chr1 #1093	1	0
1094	1	214,619,983	214,620,845	862	2	10.37	13.074	16	24	0	0	1	PTPN14	104,610	in gene	ActReg chr1 #1094	1	1
1095	1	214,723,871	214,725,118	1,247	1	9.769	10.82	15	17	2	1	1	PTPN14	530	in gene	ActReg chr1 #1095	0	1
1096	1	214,776,138	214,777,179	1,041	1	9.5	17.031	21	32	1	1	2	CENPF, FAM108A4	126, 5925	in gene, downstream	ActReg chr1 #1096	0	1
1097	1	215,631,359	215,632,043	684	1	9.136	11.818	14	25	0	0	0				ActReg chr1 #1097	0	1
1098	1	215,740,277	215,741,447	1,170	2	12.649	10.838	21	22	1	1	1	KCTD3	127	in gene	ActReg chr1 #1098	1	1
1099	1	216,896,474	216,897,234	760	1	15.583	8.708	35	20	0	0	1	ESRRG	414,243	in gene	ActReg chr1 #1099	1	0
1100	1	217,102,890	217,103,564	674	1	5.286	11.667	11	18	0	0	1	ESRRG	207,870	in gene	ActReg chr1 #1100	0	1
1101	1	217,262,802	217,263,423	621	2	9.789	10.263	17	17	1	0	1	ESRRG	47,985	in gene	ActReg chr1 #1101	1	1
1102	1	217,803,966	217,804,913	947	2	12	10.767	20	16	1	2	2	GPATCH2, SPATA17	-30, -256	upstream, upstream	ActReg chr1 #1102	1	1
1103	1	217,833,541	217,834,210	669	2	12	13.143	23	25	0	0	1	SPATA17	29,180	in gene	ActReg chr1 #1103	1	1
1104	1	218,080,572	218,081,358	786	1	9.44	11.92	18	22	0	0	0				ActReg chr1 #1104	0	1
1105	1	218,337,627	218,338,415	788	1	7.28	13	11	18	1	0	0				ActReg chr1 #1105	0	1
1106	1	218,435,405	218,436,130	725	1	9.565	13.87	17	26	0	0	0				ActReg chr1 #1106	0	1
1107	1	218,457,976	218,459,132	1,156	2	14.528	13.583	26	27	1	1	1	RRP15	-75	upstream	ActReg chr1 #1107	1	1
1108	1	218,599,132	218,600,056	924	1	9.862	10.172	18	17	0	0	1	TGFB2	80,203	in gene	ActReg chr1 #1108	0	1
1109	1	218,671,302	218,672,194	892	1	10.964	6.893	17	14	0	0	0				ActReg chr1 #1109	1	0
1110	1	218,758,239	218,760,022	1,783	2	10.339	11.071	17	18	0	0	0				ActReg chr1 #1110	1	1
1111	1	218,833,906	218,834,661	755	2	13.833	9.292	25	18	0	0	0				ActReg chr1 #1111	1	1
1112	1	219,047,453	219,048,112	659	1	10.809	10.048	21	17	0	0	0				ActReg chr1 #1112	1	0
1113	1	219,261,904	219,262,757	853	2	11.889	10.24	24	17	0	0	0				ActReg chr1 #1113	1	1
1114	1	219,346,932	219,348,035	1,103	2	10.886	10.743	24	17	1	1	1	LYPLAL1	291	in gene	ActReg chr1 #1114	1	1
1115	1	219,559,054	219,559,508	454	1	9.929	8.214	15	13	0	0	0				ActReg chr1 #1115	1	0
1116	1	219,634,259	219,635,016	757	2	11.333	11.542	18	24	0	0	0				ActReg chr1 #1116	1	1
1117	1	219,813,231	219,814,700	1,469	1	10.065	11.543	16	20	0	0	0				ActReg chr1 #1117	0	1
1118	1	219,834,977	219,835,625	648	1	7.2	10.8	13	19	0	0	0				ActReg chr1 #1118	0	1
1119	1	219,873,183	219,873,848	665	1	12.571	8.19	21	12	0	0	0				ActReg chr1 #1119	1	0
1120	1	219,943,975	219,944,990	1,015	1	16	13.129	35	31	0	0	0				ActReg chr1 #1120	1	0
1121	1	220,262,810	220,263,733	923	2	11.138	14.724	25	30	0	2	2	BPNT1, IARS2	-80, -4184	upstream, upstream	ActReg chr1 #1121	1	1
1122	1	220,267,079	220,267,949	870	1	6.5	13.926	10	21	1	2	2	BPNT1, IARS2	-4323, 59	upstream, in gene	ActReg chr1 #1122	0	1
1123	1	220,445,105	220,446,235	1,130	1	10.886	13.686	19	23	1	1	1	RAB3GAP2	173	in gene	ActReg chr1 #1123	0	1
1124	1	220,543,302	220,544,010	708	1	9.091	12.818	14	18	0	0	0				ActReg chr1 #1124	0	1
1125	1	220,701,570	220,702,856	1,286	2	12.475	11.025	17	17	1	1	1	MARK1	645	in gene	ActReg chr1 #1125	1	1
1126	1	221,052,997	221,053,784	787	1	9.417	12.292	17	22	1	1	1	HLX	647	in gene	ActReg chr1 #1126	0	1
1127	1	221,290,493	221,291,421	928	1	7.517	12	18	24	0	0	0				ActReg chr1 #1127	0	1
1128	1	221,508,364	221,509,403	1,039	1	11.25	9.625	19	16	0	1	1	LOC400804	755	in gene	ActReg chr1 #1128	1	0
1129	1	221,911,750	221,913,492	1,742	2	14.63	16.074	36	34	0	1	1	DUSP10	2,840	in gene	ActReg chr1 #1129	1	1
1130	1	221,915,412	221,917,127	1,715	2	13.333	11.518	27	22	1	1	1	DUSP10	-808	upstream	ActReg chr1 #1130	1	1
1131	1	221,996,861	221,997,926	1,065	2	10.559	12.853	16	27	0	0	0				ActReg chr1 #1131	1	1
1132	1	222,012,954	222,013,655	701	1	12.727	10.591	24	19	0	0	0				ActReg chr1 #1132	1	0
1133	1	222,031,969	222,032,593	624	1	9.368	10.158	15	20	0	0	0				ActReg chr1 #1133	0	1
1134	1	222,134,928	222,135,649	721	1	11.739	9.783	18	17	0	0	0				ActReg chr1 #1134	1	0
1135	1	222,161,003	222,161,769	766	1	8.25	13.375	17	26	0	0	0				ActReg chr1 #1135	0	1
1136	1	222,167,297	222,168,129	832	1	10.231	15.154	17	22	0	0	0				ActReg chr1 #1136	0	1
1137	1	222,560,471	222,561,271	800	1	5.48	12.08	11	17	0	0	0				ActReg chr1 #1137	0	1
1138	1	222,817,034	222,818,123	1,089	2	14.059	12.088	26	20	1	0	1	MIA3	26,134	in gene	ActReg chr1 #1138	1	1
1139	1	222,885,698	222,887,004	1,306	2	12.975	17.025	25	34	1	2	2	AIDA, C1orf58	-487, 445	upstream, in gene	ActReg chr1 #1139	1	1
1140	1	222,987,145	222,989,116	1,971	2	11.312	12.541	18	22	1	0	0				ActReg chr1 #1140	1	1
1141	1	223,092,127	223,092,952	825	1	9.038	11.423	13	17	0	0	1	DISP1	-9,244	upstream	ActReg chr1 #1141	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1142	1	223,189,537	223,190,294	757	1	11.739	6.826	17	14	0	0	0				ActReg chr1 #1142	1	0
1143	1	223,673,430	223,674,513	1,083	1	8.824	11.559	19	17	0	0	0				ActReg chr1 #1143	0	1
1144	1	223,840,013	223,840,714	701	1	11.818	11.091	24	19	0	0	1	CAPN8	13,073	in gene	ActReg chr1 #1144	1	0
1145	1	223,888,260	223,889,282	1,022	1	12.469	11.719	21	20	0	1	1	CAPN2	-524	upstream	ActReg chr1 #1145	1	0
1146	1	223,894,801	223,895,865	1,064	1	11.121	9.667	15	15	0	0	1	CAPN2	6,038	in gene	ActReg chr1 #1146	1	0
1147	1	223,902,383	223,903,569	1,186	2	11.595	11.216	17	19	0	0	1	CAPN2	13,681	in gene	ActReg chr1 #1147	1	1
1148	1	223,952,666	223,953,443	777	1	8.36	11.68	12	20	0	0	1	CAPN2	63,759	in gene	ActReg chr1 #1148	0	1
1149	1	224,063,908	224,064,679	771	1	11.458	8.917	18	17	0	0	0				ActReg chr1 #1149	1	0
1150	1	224,075,511	224,076,286	775	1	11.625	9.625	18	15	0	0	0				ActReg chr1 #1150	1	0
1151	1	224,180,123	224,180,641	518	1	17.235	10.882	36	21	1	1	1	LOC100288102	-36	upstream	ActReg chr1 #1151	1	0
1152	1	224,301,419	224,302,596	1,177	1	12.892	11.595	21	25	1	1	1	FBXO28	216	in gene	ActReg chr1 #1152	1	0
1153	1	224,370,369	224,371,859	1,490	1	10.891	12.717	16	21	1	1	1	DEGS1	186	in gene	ActReg chr1 #1153	0	1
1154	1	224,517,461	224,518,456	995	2	14.774	16.839	31	30	1	1	1	NVL	-86	upstream	ActReg chr1 #1154	1	1
1155	1	224,544,242	224,545,334	1,092	1	10.618	16.323	16	25	1	1	1	CNIH4	193	in gene	ActReg chr1 #1155	0	1
1156	1	224,621,391	224,622,146	755	1	8	10.583	12	16	1	2	2	WDR26, LOC100506354	233, -846	in gene, upstream	ActReg chr1 #1156	0	1
1157	1	224,622,409	224,623,271	862	2	19.963	23.259	39	47	1	2	2	WDR26, LOC100506354	-839, 226	upstream, in gene	ActReg chr1 #1157	1	1
1158	1	224,685,540	224,686,708	1,168	1	12.583	8.333	24	17	0	0	1	LOC100506354	63,510	in gene	ActReg chr1 #1158	1	0
1159	1	224,752,094	224,753,641	1,547	2	14.429	17.184	32	30	0	0	0				ActReg chr1 #1159	1	1
1160	1	224,895,273	224,896,427	1,154	1	9.778	12.028	17	17	0	0	1	CNIH3	91,671	in gene	ActReg chr1 #1160	0	1
1161	1	224,920,711	224,921,808	1,097	1	8.618	12.118	16	21	0	0	1	CNIH3	117,080	in gene	ActReg chr1 #1161	0	1
1162	1	225,116,986	225,117,912	926	2	12.483	11.172	21	21	1	1	1	DNAH14	93	in gene	ActReg chr1 #1162	1	1
1163	1	225,614,423	225,616,792	2,369	3	10.405	13.527	19	21	1	1	1	LBR	912	in gene	ActReg chr1 #1163	1	1
1164	1	225,844,990	225,845,755	765	1	8.75	10.833	15	18	0	1	1	ENAH	-4,527	upstream	ActReg chr1 #1164	0	1
1165	1	225,857,850	225,859,527	1,677	2	13.321	13.207	22	23	0	0	0				ActReg chr1 #1165	1	1
1166	1	225,954,934	225,956,859	1,925	1	8.5	12.65	13	22	0	0	1	SRP9	-9,619	upstream	ActReg chr1 #1166	0	1
1167	1	225,959,791	225,960,407	616	1	12.526	5.737	21	8	0	1	1	SRP9	-5,416	upstream	ActReg chr1 #1167	1	0
1168	1	225,964,759	225,966,161	1,402	2	16.591	21.727	57	77	1	1	1	SRP9	-55	upstream	ActReg chr1 #1168	1	1
1169	1	226,064,813	226,065,921	1,108	1	7.943	12.886	14	25	0	0	2	TMEM63A, LEFTY1	5053, 11469	in gene, downstream	ActReg chr1 #1169	0	1
1170	1	226,067,535	226,068,618	1,083	1	11.441	7.971	17	13	0	1	2	TMEM63A, LEFTY1	2344, 8760	in gene, downstream	ActReg chr1 #1170	1	0
1171	1	226,069,698	226,071,334	1,636	2	12.196	12.667	18	21	1	1	2	TMEM63A, LEFTY1	-96, 6320	upstream, downstream	ActReg chr1 #1171	1	1
1172	1	226,111,543	226,112,252	709	1	12	12.773	19	23	1	1	1	PYCR2	68	in gene	ActReg chr1 #1172	0	1
1173	1	226,249,290	226,249,944	654	1	12.45	10.7	19	16	1	1	2	H3F3A, LOC100506398	-804, 34803	upstream, downstream	ActReg chr1 #1173	1	0
1174	1	226,270,550	226,272,114	1,564	1	12.02	12.429	19	21	1	0	1	LOC100506398	13,088	in gene	ActReg chr1 #1174	0	1
1175	1	226,298,003	226,298,761	758	1	12.167	10.542	17	15	1	0	0				ActReg chr1 #1175	1	0
1176	1	226,373,832	226,374,877	1,045	2	12.375	11.938	18	16	1	1	1	ACBD3	69	in gene	ActReg chr1 #1176	1	1
1177	1	226,496,262	226,497,193	931	2	9.862	14.414	21	33	1	1	1	LIN9	471	in gene	ActReg chr1 #1177	1	1
1178	1	226,595,304	226,595,984	680	2	11.286	10.429	19	17	1	1	1	PARP1	157	in gene	ActReg chr1 #1178	1	1
1179	1	226,890,645	226,891,577	932	1	8.276	15.621	18	25	1	0	1	ITPKB	35,765	in gene	ActReg chr1 #1179	0	1
1180	1	227,002,585	227,003,389	804	1	15.48	13.6	32	26	0	0	0				ActReg chr1 #1180	1	0
1181	1	227,118,665	227,119,260	595	1	11.889	9.778	22	15	0	0	1	CABC1	-8,976	upstream	ActReg chr1 #1181	1	0
1182	1	227,127,010	227,128,620	1,610	2	12.34	13.82	17	29	1	1	1	CABC1	-123	upstream	ActReg chr1 #1182	1	1
1183	1	227,544,717	227,545,578	861	2	11.741	10.111	19	26	0	0	0				ActReg chr1 #1183	1	1
1184	1	227,566,351	227,567,408	1,057	2	10.667	12.788	17	21	0	0	0				ActReg chr1 #1184	1	1
1185	1	227,729,208	227,730,006	798	1	6.52	11.32	12	17	1	0	0				ActReg chr1 #1185	0	1
1186	1	227,751,075	227,751,844	769	1	9.125	12.667	14	18	1	1	1	ZNF678	239	in gene	ActReg chr1 #1186	0	1
1187	1	227,922,531	227,923,422	891	2	14.333	15.518	26	24	1	2	3	LOC100130093, JMJD4, SNAP47	6736, 136, 279	downstream, in gene, in gene	ActReg chr1 #1187	1	1
1188	1	228,122,177	228,123,282	1,105	2	12.471	12.794	24	22	0	0	1	WNT9A	12,947	in gene	ActReg chr1 #1188	1	1
1189	1	228,269,757	228,271,080	1,323	1	8.286	12.738	20	19	1	2	2	LOC100506571, ARF1	-6167, 57	upstream, in gene	ActReg chr1 #1189	0	1
1190	1	228,290,612	228,291,409	797	1	12.28	15.96	19	30	1	1	4	ARF1, C1orf35, LOC100506628, MRPL55	20649, 12, 13772, 6003	downstream, in gene, downstream, downstream	ActReg chr1 #1190	0	1
1191	1	228,296,585	228,297,476	891	2	11.786	13.929	27	28	1	2	4	ARF1, C1orf35, LOC100506628, MRPL55	26669, -6008, 7752, 17	downstream, upstream, in gene, upstream	ActReg chr1 #1191	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1192	1	228,327,490	228,328,424	934	1	17.103	13.621	25	23	1	1	2	GUK1, GJC2	28, -9596	in gene, upstream	ActReg chr1 #1192	1	0
1193	1	228,353,095	228,354,103	1,008	2	22.258	25.323	54	65	1	2	3	GJC2, LOC100506642, C1orf69	16046, -1050, 170	downstream, upstream, in gene	ActReg chr1 #1193	1	1
1194	1	228,644,747	228,647,277	2,530	2	11.544	14.987	28	27	1	2	2	HIST3H2A, HIST3H2BB	-452, 204	upstream, in gene	ActReg chr1 #1194	1	1
1195	1	228,673,964	228,675,335	1,371	2	27.442	32.279	66	84	1	1	1	RNF187	-419	upstream	ActReg chr1 #1195	1	1
1196	1	228,688,499	228,689,341	842	1	8.769	11.885	14	19	0	0	2	RNF187, LOC100129094	13852, 10738	downstream, downstream	ActReg chr1 #1196	0	1
1197	1	228,782,376	228,784,278	1,902	4	12.034	13	21	23	1	4	5	RN5S13, RN5S14, RN5S15, RN5S16, RN5S17	-10366, -8125, -5894, -3653, -1422	upstream, upstream, upstream, upstream, upstream	ActReg chr1 #1197	1	1
1198	1	228,870,580	228,871,569	989	1	6.968	10.484	17	20	1	1	1	RHOU	205	in gene	ActReg chr1 #1198	0	1
1199	1	228,918,181	228,919,116	935	1	8.862	10.621	13	19	0	0	0				ActReg chr1 #1199	0	1
1200	1	228,977,800	228,978,454	654	1	14.1	10.45	28	15	0	0	0				ActReg chr1 #1200	1	0
1201	1	229,038,647	229,039,671	1,024	1	7.375	11.688	12	19	0	0	0				ActReg chr1 #1201	0	1
1202	1	229,073,422	229,074,293	871	1	8.778	13.482	13	23	0	0	0				ActReg chr1 #1202	0	1
1203	1	229,159,256	229,160,053	797	1	10.96	9.04	17	12	0	0	0				ActReg chr1 #1203	1	0
1204	1	229,230,487	229,231,278	791	1	12.24	8.12	21	16	0	0	0				ActReg chr1 #1204	1	0
1205	1	229,334,912	229,335,882	970	1	8.355	10.387	13	16	0	0	0				ActReg chr1 #1205	0	1
1206	1	229,406,450	229,407,193	743	1	6.391	11.783	11	18	1	1	1	RAB4A	-58	upstream	ActReg chr1 #1206	0	1
1207	1	229,477,971	229,479,095	1,124	1	10.543	14.057	18	22	1	1	1	C1orf96	155	in gene	ActReg chr1 #1207	0	1
1208	1	229,566,149	229,566,961	812	1	13.04	10.12	20	22	0	0	1	ACTA1	3,288	downstream	ActReg chr1 #1208	1	0
1209	1	229,643,589	229,644,554	965	1	10.633	17.333	19	30	1	1	2	NUP133, ABCB10	17, 50371	in gene, downstream	ActReg chr1 #1209	0	1
1210	1	229,694,194	229,695,606	1,412	2	14.886	17.454	32	40	1	1	1	ABCB10	-458	upstream	ActReg chr1 #1210	1	1
1211	1	229,761,595	229,762,418	823	2	15.077	16.923	33	37	1	2	2	TAF5L, URB2	-212, 25	upstream, in gene	ActReg chr1 #1211	1	1
1212	1	229,799,422	229,800,654	1,232	2	15.154	18.077	37	35	0	0	1	URB2	38,057	downstream	ActReg chr1 #1212	1	1
1213	1	229,979,453	229,980,113	660	1	11.429	5.857	18	9	0	0	0				ActReg chr1 #1213	1	0
1214	1	230,208,823	230,209,638	815	1	11.692	8.923	15	13	0	0	1	GALNT2	6,274	in gene	ActReg chr1 #1214	1	0
1215	1	230,240,304	230,241,074	770	1	10.167	14.542	16	22	0	0	1	GALNT2	37,733	in gene	ActReg chr1 #1215	0	1
1216	1	230,439,376	230,440,131	755	1	10.917	13.042	16	26	0	0	0				ActReg chr1 #1216	0	1
1217	1	230,443,626	230,444,368	742	1	12.913	16.087	31	32	0	0	0				ActReg chr1 #1217	0	1
1218	1	230,562,188	230,563,535	1,347	2	12.143	14.429	27	27	1	0	0				ActReg chr1 #1218	1	1
1219	1	230,777,455	230,778,900	1,445	2	60.333	59.867	253	237	1	1	1	COG2	-25	upstream	ActReg chr1 #1219	1	1
1220	1	230,992,426	230,993,425	999	1	9.581	13.226	16	25	0	0	1	C1orf198	12,410	in gene	ActReg chr1 #1220	0	1
1221	1	230,994,455	230,995,269	814	1	8.346	10.538	13	16	0	0	1	C1orf198	10,473	in gene	ActReg chr1 #1221	0	1
1222	1	231,114,323	231,115,308	985	2	16.097	13.839	30	29	1	2	2	TTC13, ARV1	-197, -8	upstream, upstream	ActReg chr1 #1222	1	1
1223	1	231,228,750	231,229,713	963	1	12.3	6.967	17	11	0	0	0				ActReg chr1 #1223	1	0
1224	1	231,274,613	231,276,199	1,586	2	11.46	15.34	23	29	0	0	0				ActReg chr1 #1224	1	1
1225	1	231,297,649	231,299,038	1,389	2	12	16.023	26	35	1	1	1	TRIM67	-331	upstream	ActReg chr1 #1225	1	1
1226	1	231,346,967	231,347,738	771	1	11	9.083	17	18	0	0	1	TRIM67	48,678	in gene	ActReg chr1 #1226	1	0
1227	1	231,472,951	231,474,543	1,592	1	11.22	15.14	28	28	1	2	2	EXOC8, C1orf124	-169, 65	upstream, in gene	ActReg chr1 #1227	0	1
1228	1	231,647,737	231,648,363	626	1	11.85	7.95	21	11	0	0	0				ActReg chr1 #1228	1	0
1229	1	231,663,741	231,664,883	1,142	2	13.028	17.861	25	38	1	2	2	TSNAX-DISC1, TSNAX	-87, -87	upstream, upstream	ActReg chr1 #1229	1	1
1230	1	232,182,071	232,182,964	893	1	10.607	11.143	14	15	0	0	2	TSNAX-DISC1, DISC1	518118, 419956	downstream, downstream	ActReg chr1 #1230	0	1
1231	1	232,505,026	232,506,025	999	1	9.29	12.742	17	19	0	0	0				ActReg chr1 #1231	0	1
1232	1	232,508,138	232,509,357	1,219	1	10.763	15.21	21	26	0	0	0				ActReg chr1 #1232	0	1
1233	1	232,520,664	232,521,551	887	1	10.643	12.143	18	20	0	0	0				ActReg chr1 #1233	0	1
1234	1	232,673,823	232,674,373	550	1	11.556	11.389	17	18	0	0	0				ActReg chr1 #1234	0	1
1235	1	232,839,927	232,841,095	1,168	1	14.946	10.919	26	24	0	0	0				ActReg chr1 #1235	1	0
1236	1	232,902,981	232,903,839	858	1	8.846	11.654	15	19	0	0	0				ActReg chr1 #1236	0	1
1237	1	233,085,609	233,086,659	1,050	1	12.364	9.152	18	14	1	1	1	C1orf57	-236	upstream	ActReg chr1 #1237	1	0
1238	1	233,248,499	233,249,827	1,328	2	13.405	14.833	29	24	0	0	1	PCNXL2	182,296	in gene	ActReg chr1 #1238	1	1
1239	1	233,463,756	233,464,445	689	1	5.333	9.762	11	14	1	1	1	KIAA1804	586	in gene	ActReg chr1 #1239	0	1
1240	1	233,679,162	233,680,036	874	2	14.179	16.143	26	34	0	0	0				ActReg chr1 #1240	1	1
1241	1	234,129,283	234,129,951	668	1	8.684	12.7	13	22	0	0	1	SLC35F3	88,938	in gene	ActReg chr1 #1241	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1242	1	234,321,665	234,322,363	698	1	10.095	11.714	16	19	0	0	1	SLC35F3	281,335	in gene	ActReg chr1 #1242	0	1
1243	1	234,349,663	234,350,207	544	1	5.588	11.765	10	20	1	0	1	SLC35F3	309,256	in gene	ActReg chr1 #1243	0	1
1244	1	234,353,389	234,354,299	910	1	11.429	8.357	16	16	0	0	1	SLC35F3	313,165	in gene	ActReg chr1 #1244	1	0
1245	1	234,508,709	234,509,825	1,116	2	15.314	15.257	36	28	1	2	2	LOC100506778, C1orf31	112, -162	in gene, upstream	ActReg chr1 #1245	1	1
1246	1	234,663,672	234,664,608	936	1	6.321	10.9	9	16	0	0	1	LOC100506795	3,385	in gene	ActReg chr1 #1246	0	1
1247	1	234,792,417	234,794,444	2,027	2	10.857	12.016	23	23	0	0	0				ActReg chr1 #1247	1	1
1248	1	234,857,999	234,859,366	1,367	1	12.209	8	16	13	0	1	1	LOC100506810	-1,107	upstream	ActReg chr1 #1248	1	0
1249	1	235,001,700	235,002,687	987	1	14.567	10.533	19	17	0	0	0				ActReg chr1 #1249	1	0
1250	1	235,068,785	235,069,732	947	1	7.9	13.6	14	25	0	0	0				ActReg chr1 #1250	0	1
1251	1	235,110,018	235,111,467	1,449	2	12.111	13.489	25	23	0	0	0				ActReg chr1 #1251	1	1
1252	1	235,115,899	235,117,323	1,424	2	13.644	13.378	29	21	0	0	0				ActReg chr1 #1252	1	1
1253	1	235,132,866	235,133,623	757	1	13.043	11.217	24	18	0	0	0				ActReg chr1 #1253	1	0
1254	1	235,147,294	235,148,609	1,315	2	12.286	10.095	23	23	0	0	0				ActReg chr1 #1254	1	1
1255	1	235,291,625	235,292,712	1,087	2	14.588	14.618	25	31	1	2	3	TOMM20, SNORA14B, RBM34	88, -916, 32403	in gene, upstream, downstream	ActReg chr1 #1255	1	1
1256	1	235,324,134	235,325,056	922	1	11.966	15.207	19	27	1	1	2	RBM34, ARID4B	-24, 166937	upstream, downstream	ActReg chr1 #1256	0	1
1257	1	235,491,170	235,492,622	1,452	1	10.2	11.956	16	20	1	2	2	ARID4B, GGPS1	-364, 143	upstream, in gene	ActReg chr1 #1257	0	1
1258	1	235,530,408	235,531,480	1,072	1	8.848	11.97	20	17	0	1	1	TBCE	216	in gene	ActReg chr1 #1258	0	1
1259	1	235,667,347	235,668,887	1,540	2	14.438	16.521	28	28	1	1	1	B3GALNT2	-336	upstream	ActReg chr1 #1259	1	1
1260	1	235,804,785	235,806,706	1,921	2	11.833	12.167	21	23	1	0	1	GNG4	8,309	in gene	ActReg chr1 #1260	1	1
1261	1	236,029,361	236,030,922	1,561	2	11.878	11.245	19	16	1	1	1	LYST	79	in gene	ActReg chr1 #1261	1	1
1262	1	236,046,308	236,047,417	1,109	1	9.647	12.647	15	18	0	0	0				ActReg chr1 #1262	0	1
1263	1	236,066,189	236,066,975	786	1	12.125	7.333	20	13	0	0	0				ActReg chr1 #1263	1	0
1264	1	236,081,241	236,081,967	726	1	8.304	12.261	13	16	0	0	0				ActReg chr1 #1264	0	1
1265	1	236,162,152	236,163,535	1,383	2	11.721	11.977	20	20	0	0	1	NID1	65,638	in gene	ActReg chr1 #1265	1	1
1266	1	236,188,960	236,189,833	873	1	7.321	11.857	11	15	0	0	1	NID1	39,085	in gene	ActReg chr1 #1266	0	1
1267	1	236,227,167	236,229,144	1,977	1	10.419	12.806	23	26	1	1	1	NID1	326	in gene	ActReg chr1 #1267	0	1
1268	1	236,291,972	236,292,646	674	1	8.571	11.809	13	21	0	0	0				ActReg chr1 #1268	0	1
1269	1	236,449,704	236,451,015	1,311	2	8.805	13.171	15	23	0	1	1	ERO1LB	-5,020	upstream	ActReg chr1 #1269	1	1
1270	1	236,686,920	236,688,310	1,390	1	9.628	14.488	15	27	1	1	2	LGALS8, LOC100287902	6050, 193	in gene, in gene	ActReg chr1 #1270	0	1
1271	1	236,909,983	236,910,654	671	1	11.524	8.619	21	15	0	0	1	ACTN2	60,548	in gene	ActReg chr1 #1271	1	0
1272	1	236,958,016	236,959,248	1,232	1	10.436	13.513	16	18	1	1	1	MTR	51	in gene	ActReg chr1 #1272	0	1
1273	1	237,922,298	237,923,531	1,233	2	14.897	14.18	35	27	0	0	1	RYR2	717,212	in gene	ActReg chr1 #1273	1	1
1274	1	237,945,908	237,946,616	708	1	4.727	11.091	8	17	0	0	1	RYR2	740,560	in gene	ActReg chr1 #1274	0	1
1275	1	238,036,593	238,037,671	1,078	1	13.588	15.059	27	25	0	0	1	ZP4	17,090	downstream	ActReg chr1 #1275	0	1
1276	1	238,041,905	238,043,138	1,233	1	10.436	6.231	16	13	0	0	1	ZP4	11,701	in gene	ActReg chr1 #1276	1	0
1277	1	238,054,844	238,055,909	1,065	2	11.588	13.118	24	22	0	1	1	ZP4	-1,154	upstream	ActReg chr1 #1277	1	1
1278	1	238,066,986	238,067,769	783	2	13.917	12.125	26	20	0	0	0				ActReg chr1 #1278	1	1
1279	1	238,226,046	238,227,352	1,306	2	13	16.317	35	37	0	0	0				ActReg chr1 #1279	1	1
1280	1	238,251,611	238,252,675	1,064	2	13.588	11.765	23	21	0	0	0				ActReg chr1 #1280	1	1
1281	1	238,571,974	238,573,127	1,153	2	15.278	12.889	30	30	0	0	0				ActReg chr1 #1281	1	1
1282	1	238,769,951	238,770,669	718	1	13.217	10	23	16	0	0	0				ActReg chr1 #1282	1	0
1283	1	238,810,992	238,811,699	707	2	13.864	12.591	22	27	0	0	0				ActReg chr1 #1283	1	1
1284	1	239,977,490	239,978,336	846	1	12.444	9.185	20	16	0	0	1	CHRM3	185,540	in gene	ActReg chr1 #1284	1	0
1285	1	240,021,225	240,021,896	671	2	10.429	11.286	21	23	0	0	1	CHRM3	229,187	in gene	ActReg chr1 #1285	1	1
1286	1	240,255,359	240,256,238	879	1	12.643	7.25	16	11	1	1	1	FMN2	613	in gene	ActReg chr1 #1286	1	0
1287	1	241,319,909	241,320,367	458	1	9.538	12.929	13	20	0	0	1	RGS7	200,340	in gene	ActReg chr1 #1287	0	1
1288	1	241,486,524	241,487,369	845	2	10.963	18.63	22	45	0	0	1	RGS7	33,532	in gene	ActReg chr1 #1288	1	1
1289	1	241,520,078	241,520,640	562	1	8.389	11.778	14	19	1	1	1	RGS7	119	in gene	ActReg chr1 #1289	0	1
1290	1	241,586,857	241,587,742	885	2	12.926	12.815	24	20	1	0	0				ActReg chr1 #1290	1	1
1291	1	241,682,159	241,683,412	1,253	2	10.641	16.231	24	34	1	1	1	FH	300	in gene	ActReg chr1 #1291	1	1
1292	1	241,754,476	241,756,129	1,653	2	9.327	13.885	20	26	0	0	2	KMO, OPN3	59622, 48399	in gene, downstream	ActReg chr1 #1292	1	1
1293	1	241,870,283	241,871,312	1,029	1	7.438	12.219	22	20	0	0	1	WDR64	55,217	in gene	ActReg chr1 #1293	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1294	1	242,010,894	242,011,947	1,053	2	15.424	16.061	28	29	1	1	1	EXO1	-73	upstream	ActReg chr1 #1294	1	1
1295	1	243,010,596	243,011,118	522	2	11.188	10.125	20	14	0	0	0				ActReg chr1 #1295	1	1
1296	1	243,053,314	243,053,836	522	1	10.312	3.312	17	7	1	0	0				ActReg chr1 #1296	1	0
1297	1	243,418,160	243,419,740	1,580	2	10.755	13.837	19	24	1	2	2	CEP170, SDCCAG8	-242, -370	upstream, upstream	ActReg chr1 #1297	1	1
1298	1	243,432,779	243,433,386	607	1	8.421	10.737	11	17	0	0	1	SDCCAG8	13,762	in gene	ActReg chr1 #1298	0	1
1299	1	244,012,128	244,013,206	1,078	1	8.765	10.706	14	17	1	1	1	AKT3	-6,114	upstream	ActReg chr1 #1299	0	1
1300	1	244,014,198	244,015,016	818	1	7.654	10.039	14	14	1	0	1	AKT3	-8,054	upstream	ActReg chr1 #1300	0	1
1301	1	244,067,077	244,067,827	750	2	14.478	12.826	28	28	0	0	0				ActReg chr1 #1301	1	1
1302	1	244,137,500	244,138,614	1,114	2	13.4	17.229	31	35	0	0	1	LOC339529	57,353	in gene	ActReg chr1 #1302	1	1
1303	1	244,327,049	244,327,886	837	1	10.615	12.154	16	17	0	0	0				ActReg chr1 #1303	0	1
1304	1	244,377,245	244,378,083	838	1	13.852	9.741	23	17	0	0	0				ActReg chr1 #1304	1	0
1305	1	244,516,919	244,517,486	567	1	10.056	11.5	16	17	0	1	1	C1orf100	1,265	in gene	ActReg chr1 #1305	0	1
1306	1	244,614,211	244,615,277	1,066	1	10.515	13.788	16	25	1	1	2	ADSS, C1orf101	669, -9929	in gene, upstream	ActReg chr1 #1306	0	1
1307	1	244,997,689	244,998,937	1,248	2	11.051	11.487	19	19	1	1	2	FAM36A, NCRNA00201	-326, 11930	upstream, downstream	ActReg chr1 #1307	1	1
1308	1	245,026,799	245,028,736	1,937	2	11.607	14.262	21	24	1	1	1	HNRNPU	60	in gene	ActReg chr1 #1308	1	1
1309	1	245,132,876	245,134,902	2,026	2	10.095	14.286	22	34	1	1	1	EFCAB2	718	in gene	ActReg chr1 #1309	1	1
1310	1	245,748,495	245,749,206	711	1	12.227	10.454	17	16	0	0	1	KIF26B	430,563	in gene	ActReg chr1 #1310	1	0
1311	1	245,966,001	245,966,843	842	2	9.5	11.5	16	18	0	0	1	SMYD3	704,222	in gene	ActReg chr1 #1311	1	1
1312	1	246,810,372	246,811,126	754	1	13.478	12.174	25	20	0	0	1	CNST	81,110	in gene	ActReg chr1 #1312	1	0
1313	1	247,094,852	247,095,968	1,116	1	11.4	17.686	20	36	1	1	1	AHCTF1	-684	upstream	ActReg chr1 #1313	0	1
1314	1	247,241,501	247,242,338	837	2	11.444	10.259	19	18	1	1	1	ZNF670	196	in gene	ActReg chr1 #1314	1	1
1315	1	247,267,005	247,267,820	815	1	8.385	13.154	18	25	1	1	2	ZNF669, C1orf229	262, 8307	in gene, downstream	ActReg chr1 #1315	0	1
1316	1	247,373,564	247,374,464	900	2	9.517	10.138	20	15	1	0	0				ActReg chr1 #1316	1	1
1317	1	247,494,179	247,496,032	1,853	2	11.448	11.379	25	19	1	1	1	ZNF496	-60	upstream	ActReg chr1 #1317	1	1
1318	1	247,505,781	247,506,521	740	1	4.826	11.435	9	18	0	0	0				ActReg chr1 #1318	0	1
1319	1	247,802,533	247,803,341	808	2	13.04	10.96	20	22	1	1	1	LOC100507070	1,228	in gene	ActReg chr1 #1319	1	1
1320	1	248,020,436	248,021,137	701	2	10.364	11.454	15	16	1	1	1	TRIM58	285	in gene	ActReg chr1 #1320	1	1
1321	1	248,100,314	248,100,845	531	1	8.176	11.647	12	21	1	1	1	OR2L13	86	in gene	ActReg chr1 #1321	0	1
1322	1	249,119,632	249,121,201	1,569	1	10.469	13.347	18	25	1	2	2	SH3BP5L, MIR3124	-262, -160	upstream, upstream	ActReg chr1 #1322	0	1
1323	1	249,131,944	249,133,610	1,666	2	13.538	15.788	25	34	1	1	1	ZNF672	247	in gene	ActReg chr1 #1323	1	1
1324	1	249,151,837	249,153,820	1,983	3	14.823	16.177	36	39	1	1	2	ZNF672, ZNF692	20298, 487	downstream, in gene	ActReg chr1 #1324	1	1
1325	1	249,166,960	249,168,959	1,999	2	15.113	12.903	29	25	1	0	0				ActReg chr1 #1325	1	1
1326	1	249,199,964	249,200,761	797	1	10.8	18.08	17	33	1	1	1	PGBD2	-80	upstream	ActReg chr1 #1326	0	1
1327	10	1,033,819	1,034,707	888	2	14.857	15.071	36	32	1	2	2	LOC100288619, GTPBP4	18, -86	in gene, upstream	ActReg chr10 #1327	1	1
1328	10	1,094,527	1,095,459	932	2	9.433	11.9	14	21	1	2	3	C10orf110, IDI1, WDR37	26416, 68, -7783	downstream, in gene, upstream	ActReg chr10 #1328	1	1
1329	10	2,256,270	2,256,706	436	1	8.429	5.357	14	10	0	0	0				ActReg chr10 #1329	1	0
1330	10	2,274,645	2,275,049	404	1	7.769	13.615	12	23	0	0	0				ActReg chr10 #1330	0	1
1331	10	3,006,602	3,006,993	391	1	5.167	10.583	7	15	0	0	0				ActReg chr10 #1331	0	1
1332	10	3,389,803	3,390,300	497	1	4.067	9.733	8	16	0	0	0				ActReg chr10 #1332	0	1
1333	10	3,966,424	3,966,985	561	1	5.222	9.056	10	17	0	0	0				ActReg chr10 #1333	0	1
1334	10	4,746,238	4,746,688	450	2	9.333	10.6	15	15	0	0	0				ActReg chr10 #1334	1	1
1335	10	4,925,384	4,926,028	644	2	10.55	9.25	18	16	0	0	0				ActReg chr10 #1335	1	1
1336	10	5,359,580	5,360,058	478	1	9.667	5.267	15	8	0	0	0				ActReg chr10 #1336	1	0
1337	10	6,019,336	6,020,084	748	1	11.87	8.043	20	13	1	1	1	IL15RA	432	in gene	ActReg chr10 #1337	1	0
1338	10	6,130,601	6,131,054	453	2	10.357	9.857	17	17	1	1	1	RBM17	-122	upstream	ActReg chr10 #1338	1	1
1339	10	6,755,072	6,756,128	1,056	3	10.059	11.235	23	22	0	0	0				ActReg chr10 #1339	1	1
1340	10	7,029,265	7,029,773	508	1	5.875	12.25	11	17	0	0	0				ActReg chr10 #1340	0	1
1341	10	7,691,885	7,692,384	499	1	8.438	10.438	14	15	0	0	1	ITIH5	16,827	in gene	ActReg chr10 #1341	0	1
1342	10	7,860,107	7,861,055	948	2	13.414	13.172	29	23	1	1	1	TAF3	-92	upstream	ActReg chr10 #1342	1	1
1343	10	12,084,692	12,085,396	704	2	10.046	11.273	20	19	1	1	1	UPF2	-21	upstream	ActReg chr10 #1343	1	1
1344	10	13,203,058	13,203,817	759	2	14.292	9.667	27	18	1	1	1	MCM10	-117	upstream	ActReg chr10 #1344	1	1
1345	10	13,390,169	13,390,619	450	1	6.462	9.214	10	15	0	1	1	SEPHS1	-114	upstream	ActReg chr10 #1345	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1346	10	13,404,664	13,405,058	394	1	8	9.769	13	16	0	0	0				ActReg chr10 #1346	0	1
1347	10	13,628,482	13,629,327	845	2	21.038	24.154	58	69	1	1	1	PRPF18	-35	upstream	ActReg chr10 #1347	1	1
1348	10	13,754,833	13,755,320	487	1	9.067	9.4	12	14	0	0	1	FRMD4A	617,790	in gene	ActReg chr10 #1348	0	1
1349	10	14,035,194	14,035,640	446	1	7.429	10	12	16	0	0	1	FRMD4A	337,449	in gene	ActReg chr10 #1349	0	1
1350	10	14,195,502	14,195,951	449	1	10.786	7.5	13	12	0	0	1	FRMD4A	177,140	in gene	ActReg chr10 #1350	1	0
1351	10	14,286,726	14,287,467	741	2	11.174	10.261	20	20	0	0	1	FRMD4A	85,770	in gene	ActReg chr10 #1351	1	1
1352	10	14,439,028	14,439,486	458	1	10.143	7.643	15	11	0	0	0				ActReg chr10 #1352	1	0
1353	10	15,902,324	15,902,861	537	2	8.824	11.059	13	14	1	1	1	FAM188A	-73	upstream	ActReg chr10 #1353	1	1
1354	10	16,654,242	16,654,635	393	1	9.417	8.5	15	14	0	0	1	RSU1	205,015	in gene	ActReg chr10 #1354	1	0
1355	10	17,155,736	17,156,201	465	1	4.4	10.667	7	15	0	0	1	CUBN	15,848	in gene	ActReg chr10 #1355	0	1
1356	10	17,243,165	17,243,758	593	1	7.947	10.21	15	14	1	1	1	TRDMT1	609	in gene	ActReg chr10 #1356	0	1
1357	10	17,271,152	17,271,755	603	1	6.895	11.263	11	20	1	2	2	LOC100507347, VIM	-2556, 1195	upstream, in gene	ActReg chr10 #1357	0	1
1358	10	17,280,538	17,280,979	441	1	4.643	9.929	8	15	0	0	1	VIM	10,500	downstream	ActReg chr10 #1358	0	1
1359	10	17,685,722	17,686,494	772	2	9.5	12.375	18	22	1	1	1	STAM	-16	upstream	ActReg chr10 #1359	1	1
1360	10	21,814,555	21,815,003	448	1	9.429	6.357	14	13	1	1	2	C10orf140, MLLT10	-168, -8323	upstream, upstream	ActReg chr10 #1360	1	0
1361	10	22,518,018	22,518,741	723	1	9.955	9.136	15	16	1	0	0				ActReg chr10 #1361	1	0
1362	10	24,078,879	24,079,577	698	2	16.364	13.6	41	30	0	0	1	KIAA1217	95,553	in gene	ActReg chr10 #1362	1	1
1363	10	24,115,214	24,115,898	684	1	5.714	11.857	11	26	0	0	1	KIAA1217	131,881	in gene	ActReg chr10 #1363	0	1
1364	10	25,463,158	25,465,096	1,938	4	11.869	16	29	35	1	2	2	LOC100128811, GPR158	1078, -163	in gene, upstream	ActReg chr10 #1364	1	1
1365	10	27,149,528	27,150,033	505	1	5.188	9.625	9	16	1	1	1	ABI1	236	in gene	ActReg chr10 #1365	0	1
1366	10	27,443,095	27,443,492	397	1	9.231	6.538	13	11	1	2	2	YME1L1, MASTL	28, -460	in gene, upstream	ActReg chr10 #1366	1	0
1367	10	27,792,860	27,793,563	703	1	7.545	12.364	12	23	1	1	1	RAB18	-38	upstream	ActReg chr10 #1367	0	1
1368	10	30,092,325	30,092,911	586	1	7.167	10.778	8	18	0	0	0				ActReg chr10 #1368	0	1
1369	10	31,073,845	31,074,447	602	1	6.421	11.316	12	15	1	0	0				ActReg chr10 #1369	0	1
1370	10	31,320,513	31,321,035	522	1	4.062	9.062	9	16	1	1	2	ZNF438, LOC100507663	92, -9028	in gene, upstream	ActReg chr10 #1370	0	1
1371	10	31,893,412	31,893,981	569	1	11.412	7.765	19	9	0	0	0				ActReg chr10 #1371	1	0
1372	10	31,958,394	31,958,793	399	1	7.308	10.846	12	17	0	0	0				ActReg chr10 #1372	0	1
1373	10	32,635,032	32,635,498	466	1	8.867	6.8	13	9	1	1	1	EPC1	848	in gene	ActReg chr10 #1373	1	0
1374	10	34,524,380	34,524,906	526	2	10.353	12	19	25	0	0	1	PARD3	579,610	in gene	ActReg chr10 #1374	1	1
1375	10	34,999,299	34,999,839	540	1	4.312	9.625	7	17	0	0	1	PARD3	104,684	in gene	ActReg chr10 #1375	0	1
1376	10	35,379,082	35,379,927	845	2	17.615	15.269	40	32	1	1	1	CUL2	-210	upstream	ActReg chr10 #1376	1	1
1377	10	35,931,017	35,931,544	527	2	10.625	9.562	15	15	1	1	1	FZD8	-918	upstream	ActReg chr10 #1377	1	1
1378	10	43,277,679	43,278,570	891	2	8.357	11.714	16	19	1	1	1	BMS1	170	in gene	ActReg chr10 #1378	1	1
1379	10	43,778,218	43,779,382	1,164	2	10.5	16.306	21	27	0	0	0				ActReg chr10 #1379	1	1
1380	10	43,779,569	43,780,296	727	2	7.826	12.609	19	28	0	0	0				ActReg chr10 #1380	1	1
1381	10	44,101,733	44,102,123	390	1	6.417	10.417	11	16	1	1	1	ZNF485	73	in gene	ActReg chr10 #1381	0	1
1382	10	44,144,087	44,144,703	616	1	6.579	10.105	9	16	1	1	1	ZNF32	-69	upstream	ActReg chr10 #1382	0	1
1383	10	44,796,582	44,796,993	411	1	5.385	10	7	16	0	0	1	LOC100130539	8,583	downstream	ActReg chr10 #1383	0	1
1384	10	45,202,099	45,202,560	461	1	9.8	10.333	15	17	0	0	0				ActReg chr10 #1384	0	1
1385	10	46,951,196	46,951,663	467	1	7.467	10	10	16	0	1	2	LOC100507539, SYT15	-43, 19172	upstream, downstream	ActReg chr10 #1385	0	1
1386	10	47,594,087	47,594,802	715	1	7.545	11.636	13	18	0	0	0				ActReg chr10 #1386	0	1
1387	10	47,605,931	47,606,452	521	1	9.875	5	16	8	0	0	0				ActReg chr10 #1387	1	0
1388	10	50,605,849	50,606,500	651	2	11.048	9.762	21	17	1	1	1	DRGX	-6,267	upstream	ActReg chr10 #1388	1	1
1389	10	50,814,775	50,815,909	1,134	2	9.5	13.889	26	27	0	2	2	CHAT, SLC18A3	-1799, -3005	upstream, upstream	ActReg chr10 #1389	1	1
1390	10	50,970,270	50,970,724	454	1	8.867	9.867	15	15	1	1	1	OGDHL	-72	upstream	ActReg chr10 #1390	1	0
1391	10	52,383,355	52,383,805	450	1	10.429	6.929	15	11	1	1	1	SGMS1	157	in gene	ActReg chr10 #1391	1	0
1392	10	52,383,975	52,385,289	1,314	2	9.146	12.585	23	30	1	1	1	SGMS1	-895	upstream	ActReg chr10 #1392	1	1
1393	10	53,592,628	53,593,215	587	1	7.667	11.667	12	20	0	0	1	PRKG1	841,976	in gene	ActReg chr10 #1393	0	1
1394	10	59,908,532	59,909,143	611	2	10.737	10.684	16	18	0	0	0				ActReg chr10 #1394	1	1
1395	10	59,935,678	59,936,124	446	1	9.357	10.357	14	17	0	0	0				ActReg chr10 #1395	0	1
1396	10	60,144,967	60,145,519	552	1	5.647	11.412	8	19	1	1	1	TFAM	67	in gene	ActReg chr10 #1396	0	1
1397	10	61,665,810	61,666,851	1,041	2	27.727	31.531	91	98	1	1	1	CCDC6	488	in gene	ActReg chr10 #1397	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1398	10	64,492,639	64,493,078	439	1	10.857	4.5	17	8	0	0	0				ActReg chr10 #1398	1	0
1399	10	64,563,923	64,564,345	422	1	9.769	4.692	15	7	1	1	2	ADO, EGR2	-382, 14793	upstream, downstream	ActReg chr10 #1399	1	0
1400	10	64,675,782	64,676,545	763	1	8.833	10.958	14	20	0	0	0				ActReg chr10 #1400	0	1
1401	10	64,693,983	64,694,458	475	1	6.067	9.4	14	15	0	0	0				ActReg chr10 #1401	0	1
1402	10	66,227,584	66,228,076	492	1	10.438	4.812	16	7	0	0	0				ActReg chr10 #1402	1	0
1403	10	69,523,782	69,524,308	526	1	7.438	11.062	12	15	1	0	0				ActReg chr10 #1403	0	1
1404	10	69,895,958	69,896,571	613	1	9.263	5.368	18	9	0	0	1	MYPN	27,014	in gene	ActReg chr10 #1404	1	0
1405	10	69,913,312	69,913,762	450	1	11.067	5.067	20	9	0	0	1	MYPN	44,287	in gene	ActReg chr10 #1405	1	0
1406	10	70,166,382	70,167,350	968	2	14.067	14.933	29	28	1	1	2	RUFY2, DNA2	185, 65013	in gene, downstream	ActReg chr10 #1406	1	1
1407	10	70,319,973	70,320,420	447	1	10.643	9.143	14	12	1	1	1	TET1	79	in gene	ActReg chr10 #1407	1	0
1408	10	70,715,459	70,716,445	986	2	8.867	9.067	19	18	1	1	2	DDX50, DDX21	54918, 60	downstream, in gene	ActReg chr10 #1408	1	1
1409	10	70,748,293	70,748,936	643	1	5	12.45	9	17	1	1	3	DDX21, LOC100507126, KIAA1279	32722, 14205, 137	downstream, in gene, in gene	ActReg chr10 #1409	0	1
1410	10	70,939,500	70,940,245	745	1	12.957	10.913	24	20	1	1	2	VPS26A, SUPV3L1	55964, -121	downstream, upstream	ActReg chr10 #1410	1	0
1411	10	71,327,437	71,328,025	588	2	10.889	10.611	21	16	0	0	1	NEUROG3	5,479	downstream	ActReg chr10 #1411	1	1
1412	10	71,629,186	71,629,765	579	1	7.444	11.5	10	16	0	0	1	COL13A1	67,831	in gene	ActReg chr10 #1412	0	1
1413	10	72,575,986	72,576,448	462	1	2.714	9.133	6	16	1	1	1	SGPL1	513	in gene	ActReg chr10 #1413	0	1
1414	10	73,554,668	73,555,923	1,255	2	13.282	16.846	32	42	0	0	1	CDH23	398,604	in gene	ActReg chr10 #1414	1	1
1415	10	73,619,978	73,620,564	586	2	10.167	11.111	15	15	0	0	1	PSAP	-9,189	upstream	ActReg chr10 #1415	1	1
1416	10	74,033,033	74,034,054	1,021	1	8.062	9.844	13	22	1	1	1	DDIT4	-134	upstream	ActReg chr10 #1416	0	1
1417	10	74,114,279	74,115,096	817	2	11.2	12.08	17	18	1	1	1	DNAJB12	220	in gene	ActReg chr10 #1417	1	1
1418	10	74,856,250	74,857,123	873	2	12.179	13.75	25	26	1	1	1	P4HA1	46	in gene	ActReg chr10 #1418	1	1
1419	10	74,927,516	74,928,129	613	1	10.85	9.05	18	14	1	2	2	ECD, FAM149B1	31, -55	in gene, upstream	ActReg chr10 #1419	1	0
1420	10	75,255,644	75,256,099	455	1	7	8.733	11	17	1	2	3	PPP3CB, LOC100507259, USP54	-89, 361, 79562	upstream, in gene, downstream	ActReg chr10 #1420	0	1
1421	10	75,489,959	75,490,699	740	2	9.087	12.826	15	24	1	0	0				ActReg chr10 #1421	1	1
1422	10	75,936,164	75,936,800	636	1	8.5	10.2	13	16	1	0	1	ADK	25,517	in gene	ActReg chr10 #1422	0	1
1423	10	76,586,113	76,586,565	452	2	9.429	10.714	15	18	1	1	1	MYST4	-40	upstream	ActReg chr10 #1423	1	1
1424	10	76,969,992	76,970,856	864	2	15.593	13.778	36	26	1	1	1	VDAC2	512	in gene	ActReg chr10 #1424	1	1
1425	10	77,161,328	77,161,842	514	1	6.5	12.25	11	19	1	2	2	ZNF503, C10orf41	-72, 299	upstream, in gene	ActReg chr10 #1425	0	1
1426	10	77,161,851	77,162,390	539	1	6.118	10.118	10	17	1	2	2	ZNF503, C10orf41	-607, 834	upstream, in gene	ActReg chr10 #1426	0	1
1427	10	77,162,859	77,163,263	404	1	5.75	10.75	9	17	1	2	2	ZNF503, C10orf41	-1548, 1775	upstream, in gene	ActReg chr10 #1427	0	1
1428	10	77,533,144	77,533,612	468	1	11.133	7.4	17	11	0	0	1	C10orf11	-9,141	upstream	ActReg chr10 #1428	1	0
1429	10	79,056,910	79,057,600	690	1	8.636	13.182	12	28	0	0	1	KCNMA1	340,322	in gene	ActReg chr10 #1429	0	1
1430	10	79,087,803	79,088,704	901	2	14.241	15.517	30	36	0	0	1	KCNMA1	309,324	in gene	ActReg chr10 #1430	1	1
1431	10	79,110,294	79,110,841	547	1	11.059	9.824	18	18	0	0	1	KCNMA1	287,010	in gene	ActReg chr10 #1431	1	0
1432	10	79,152,260	79,153,086	826	2	11.72	11.32	20	19	0	0	1	KCNMA1	244,904	in gene	ActReg chr10 #1432	1	1
1433	10	79,265,198	79,266,169	971	2	11.467	10.033	21	16	0	0	1	KCNMA1	131,894	in gene	ActReg chr10 #1433	1	1
1434	10	79,273,334	79,274,258	924	1	7.483	10.897	16	16	0	0	1	KCNMA1	123,781	in gene	ActReg chr10 #1434	0	1
1435	10	79,291,039	79,291,988	949	1	14.2	10.533	21	18	0	0	1	KCNMA1	106,064	in gene	ActReg chr10 #1435	1	0
1436	10	79,342,301	79,343,082	781	1	12.04	9.32	20	15	0	0	1	KCNMA1	54,886	in gene	ActReg chr10 #1436	1	0
1437	10	79,421,149	79,421,855	706	2	10.773	12	16	17	0	0	0				ActReg chr10 #1437	1	1
1438	10	79,608,700	79,609,468	768	2	12.167	12.417	20	21	0	0	1	DLG5	77,264	in gene	ActReg chr10 #1438	1	1
1439	10	79,788,913	79,789,951	1,038	2	13.281	13.812	24	23	1	2	2	POLR3A, RPS24	-134, -4086	upstream, upstream	ActReg chr10 #1439	1	1
1440	10	80,015,088	80,016,550	1,462	1	7.196	12.13	18	21	0	0	1	LOC100132987	7,573	downstream	ActReg chr10 #1440	0	1
1441	10	80,023,051	80,023,952	901	1	12.357	8.464	19	16	0	0	0				ActReg chr10 #1441	1	0
1442	10	80,516,268	80,517,324	1,056	2	11.97	12.636	24	19	0	0	0				ActReg chr10 #1442	1	1
1443	10	80,732,043	80,733,537	1,494	2	10.021	12.021	19	19	0	0	1	LOC283050	94,415	in gene	ActReg chr10 #1443	1	1
1444	10	80,827,031	80,827,587	556	1	10.667	12.611	16	19	1	2	2	LOC283050, ZMIZ1	-104, -1483	upstream, upstream	ActReg chr10 #1444	0	1
1445	10	80,841,328	80,841,953	625	1	10.7	12.9	15	17	0	0	1	ZMIZ1	12,848	in gene	ActReg chr10 #1445	0	1
1446	10	80,908,631	80,909,617	986	1	8.71	10.548	15	18	0	0	1	ZMIZ1	80,332	in gene	ActReg chr10 #1446	0	1
1447	10	81,080,446	81,081,765	1,319	2	13.595	17.571	32	36	0	0	1	ZMIZ1	252,313	downstream	ActReg chr10 #1447	1	1
1448	10	81,106,949	81,107,776	827	1	7.154	12.846	12	17	2	1	1	PPIF	142	in gene	ActReg chr10 #1448	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1449	10	81,197,693	81,198,283	590	1	12.526	10.79	18	16	0	0	1	ZCCHC24	7,395	in gene	ActReg chr10 #1449	1	0
1450	10	81,205,323	81,205,969	646	1	13.6	8.05	25	18	1	1	1	ZCCHC24	-263	upstream	ActReg chr10 #1450	1	0
1451	10	81,664,146	81,665,170	1,024	2	11.406	12.406	16	26	1	1	1	LOC100288974	4	in gene	ActReg chr10 #1451	1	1
1452	10	81,838,242	81,838,683	441	1	12.154	7.462	16	12	1	2	2	LOC219347, C10orf57	487, 36	in gene, in gene	ActReg chr10 #1452	1	0
1453	10	81,886,835	81,887,239	404	1	7.615	10.692	10	15	0	1	1	PLAC9	-5,221	upstream	ActReg chr10 #1453	0	1
1454	10	81,965,056	81,965,749	693	1	9.045	12.091	14	16	1	2	2	ANXA11, LOC439990	-74, -2077	upstream, upstream	ActReg chr10 #1454	0	1
1455	10	83,737,858	83,738,539	681	2	11.429	11.714	22	20	0	0	1	NRG3	103,128	in gene	ActReg chr10 #1455	1	1
1456	10	84,972,378	84,973,086	708	1	7.864	10.273	11	16	0	0	0				ActReg chr10 #1456	0	1
1457	10	85,899,002	85,899,829	827	1	10.423	12.462	15	20	1	1	1	GHITM	230	in gene	ActReg chr10 #1457	0	1
1458	10	85,916,560	85,917,016	456	1	7	10.5	12	16	0	0	1	GHITM	17,603	downstream	ActReg chr10 #1458	0	1
1459	10	86,050,979	86,051,773	794	2	19.542	31.208	53	78	0	0	1	LOC170425	11,640	in gene	ActReg chr10 #1459	1	1
1460	10	87,661,202	87,661,761	559	1	7.611	10.611	14	16	0	0	1	GRID1	464,769	in gene	ActReg chr10 #1460	0	1
1461	10	87,963,214	87,964,211	997	1	7.774	9.258	17	16	0	0	1	GRID1	162,538	in gene	ActReg chr10 #1461	0	1
1462	10	88,066,310	88,066,842	532	1	10.25	11.25	17	21	0	0	1	GRID1	59,674	in gene	ActReg chr10 #1462	0	1
1463	10	88,281,085	88,282,109	1,024	1	12.625	10.219	18	21	1	1	1	WAPAL	-56	upstream	ActReg chr10 #1463	1	0
1464	10	88,313,100	88,313,872	772	1	9.208	12.25	18	20	0	0	0				ActReg chr10 #1464	0	1
1465	10	88,515,596	88,516,258	662	1	10.286	8.15	15	11	1	1	1	BMPR1A	-469	upstream	ActReg chr10 #1465	1	0
1466	10	88,730,901	88,731,890	989	1	9.484	14.323	16	27	1	2	4	SNCG, LOC100133190, C10orf116, AGAP11	13107, -327, 3207, 897	downstream, upstream, downstream, in gene	ActReg chr10 #1466	0	1
1467	10	88,854,273	88,854,782	509	2	11	10	19	17	1	2	2	GLUD1, FAM35A	249, -426	in gene, upstream	ActReg chr10 #1467	1	1
1468	10	88,854,928	88,855,691	763	2	10	11.667	18	17	1	2	2	GLUD1, FAM35A	-533, 356	upstream, in gene	ActReg chr10 #1468	1	1
1469	10	89,264,249	89,265,403	1,154	2	11.389	12.194	18	19	1	1	1	MINPP1	603	in gene	ActReg chr10 #1469	1	1
1470	10	89,345,643	89,346,382	739	2	12.261	8.435	22	19	0	0	0				ActReg chr10 #1470	1	1
1471	10	89,395,419	89,396,246	827	1	9.154	11.808	17	17	0	0	0				ActReg chr10 #1471	0	1
1472	10	89,430,960	89,431,713	753	1	11.583	7.625	15	13	0	0	1	PAPSS2	11,860	in gene	ActReg chr10 #1472	1	0
1473	10	89,577,602	89,578,405	803	1	8.68	11.6	15	17	1	1	1	ATAD1	-86	upstream	ActReg chr10 #1473	0	1
1474	10	89,604,808	89,605,393	585	1	6.889	11.111	13	16	0	0	0				ActReg chr10 #1474	0	1
1475	10	89,622,584	89,623,645	1,061	2	11.03	8.636	20	19	1	2	2	KILLIN, PTEN	80, -81	in gene, upstream	ActReg chr10 #1475	1	1
1476	10	89,912,232	89,913,007	775	1	12.875	8.208	23	12	0	0	0				ActReg chr10 #1476	1	0
1477	10	90,145,444	90,145,853	409	1	4.333	10.167	6	16	0	0	1	RNLS	197,434	in gene	ActReg chr10 #1477	0	1
1478	10	90,234,274	90,234,795	521	1	9.375	6.812	14	9	0	0	1	RNLS	108,548	in gene	ActReg chr10 #1478	1	0
1479	10	90,639,861	90,640,960	1,099	2	10.743	13.2	21	21	1	1	1	STAMBPL1	384	in gene	ActReg chr10 #1479	1	1
1480	10	91,111,806	91,112,497	691	2	13.318	14.35	25	33	0	0	1	LOC100507575	-9,735	upstream	ActReg chr10 #1480	1	1
1481	10	91,174,223	91,175,367	1,144	1	8.583	12.722	15	22	1	1	1	IFIT5	470	in gene	ActReg chr10 #1481	0	1
1482	10	91,403,790	91,405,275	1,485	1	6.935	11.109	13	17	1	1	1	PANK1	683	in gene	ActReg chr10 #1482	0	1
1483	10	91,460,788	91,462,346	1,558	2	11.96	11.51	25	29	1	1	1	KIF20B	200	in gene	ActReg chr10 #1483	1	1
1484	10	91,621,423	91,622,106	683	1	9.048	11	14	14	0	0	0				ActReg chr10 #1484	0	1
1485	10	91,664,405	91,665,118	713	1	9.636	11.409	17	20	0	0	0				ActReg chr10 #1485	0	1
1486	10	92,346,899	92,347,527	628	1	8.4	9.9	13	19	0	0	0				ActReg chr10 #1486	0	1
1487	10	92,381,241	92,381,744	503	1	6.375	10.312	10	16	0	0	0				ActReg chr10 #1487	0	1
1488	10	92,534,841	92,535,468	627	1	8.6	11.55	12	21	0	0	1	HTR7	82,517	in gene	ActReg chr10 #1488	0	1
1489	10	92,631,132	92,632,026	894	1	10.143	11.679	19	20	0	1	1	RPP30	-130	upstream	ActReg chr10 #1489	0	1
1490	10	92,887,052	92,887,576	524	1	8.312	11.562	13	17	0	0	0				ActReg chr10 #1490	0	1
1491	10	92,923,087	92,923,551	464	1	5.929	10.071	8	15	0	0	0				ActReg chr10 #1491	0	1
1492	10	92,950,807	92,951,375	568	1	9.778	7.222	15	12	0	0	0				ActReg chr10 #1492	1	0
1493	10	93,169,098	93,169,897	799	1	10.2	10.24	14	15	1	1	2	LOC100188947, HECTD2	129840, -599	in gene, upstream	ActReg chr10 #1493	1	0
1494	10	93,271,017	93,271,877	860	1	4.037	10.667	8	19	0	0	2	LOC100188947, HECTD2	27890, 101351	in gene, in gene	ActReg chr10 #1494	0	1
1495	10	93,334,538	93,335,497	959	1	7.167	12.7	13	21	0	0	0				ActReg chr10 #1495	0	1
1496	10	93,411,947	93,412,699	752	1	7.348	12.913	14	22	0	0	0				ActReg chr10 #1496	0	1
1497	10	93,646,884	93,647,765	881	1	7.704	12.815	11	20	1	0	0				ActReg chr10 #1497	0	1
1498	10	93,667,838	93,669,130	1,292	2	24.854	26.244	79	85	1	1	1	FGFBP3	774	in gene	ActReg chr10 #1498	1	1
1499	10	93,683,182	93,683,956	774	1	12.083	9.917	22	21	1	1	1	BTAF1	-167	upstream	ActReg chr10 #1499	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1500	10	94,050,499	94,051,374	875	2	12.407	12	24	21	1	2	2	CPEB3, MARCH5	-61, 16	upstream, in gene	ActReg chr10 #1500	1	1
1501	10	94,146,941	94,147,756	815	2	13.769	15.577	33	35	0	0	0				ActReg chr10 #1501	1	1
1502	10	94,167,051	94,167,895	844	2	10.577	11.192	15	20	0	0	0				ActReg chr10 #1502	1	1
1503	10	94,351,138	94,351,733	595	2	9.778	10.389	17	15	1	1	1	KIF11	-1,390	upstream	ActReg chr10 #1503	1	1
1504	10	94,449,668	94,450,385	717	1	7.5	12.091	10	17	1	1	1	HHEX	345	in gene	ActReg chr10 #1504	0	1
1505	10	94,651,867	94,652,641	774	1	7.16	12.28	12	23	0	0	1	EXOC6	57,784	in gene	ActReg chr10 #1505	0	1
1506	10	94,968,328	94,969,001	673	2	11.905	10.857	20	20	0	0	0				ActReg chr10 #1506	1	1
1507	10	95,241,678	95,242,592	914	2	14.885	14.483	28	30	0	1	1	MYOF	-61	upstream	ActReg chr10 #1507	1	1
1508	10	95,255,713	95,256,744	1,031	2	10.812	11.312	19	22	1	1	1	CEP55	-141	upstream	ActReg chr10 #1508	1	1
1509	10	95,462,004	95,462,739	735	1	12.652	14.13	24	28	1	1	1	C10orf4	-42	upstream	ActReg chr10 #1509	0	1
1510	10	95,511,586	95,512,130	544	1	9.706	11.412	15	19	0	1	1	LGI1	-5,708	upstream	ActReg chr10 #1510	0	1
1511	10	95,653,236	95,653,903	667	1	8.429	11.905	16	21	1	1	1	TMEM20	-161	upstream	ActReg chr10 #1511	0	1
1512	10	95,751,509	95,752,252	743	2	11.565	10.739	17	22	0	1	1	PLCE1	-1,866	upstream	ActReg chr10 #1512	1	1
1513	10	95,825,935	95,826,805	870	2	16.593	23.148	37	60	0	0	1	PLCE1	72,624	in gene	ActReg chr10 #1513	1	1
1514	10	95,875,340	95,876,113	773	1	9.667	13.875	26	35	0	0	1	PLCE1	121,980	in gene	ActReg chr10 #1514	0	1
1515	10	95,984,271	95,984,827	556	1	8.882	13	14	22	0	0	1	PLCE1	230,803	in gene	ActReg chr10 #1515	0	1
1516	10	96,122,325	96,123,030	705	2	13	12.091	25	18	1	1	1	NOC3L	6	in gene	ActReg chr10 #1516	1	1
1517	10	96,305,531	96,305,995	464	1	8.667	11.733	13	18	1	1	2	TBC1D12, HELLS	143577, 189	downstream, in gene	ActReg chr10 #1517	0	1
1518	10	96,943,026	96,944,021	995	2	12.194	13.742	22	26	1	0	1	C10orf129	-10,434	upstream	ActReg chr10 #1518	1	1
1519	10	97,151,604	97,152,222	618	2	11.579	13.263	19	26	0	0	1	SORBS1	169,258	in gene	ActReg chr10 #1519	1	1
1520	10	97,153,679	97,154,363	684	1	11.667	9.952	22	18	0	0	1	SORBS1	167,150	in gene	ActReg chr10 #1520	1	0
1521	10	97,415,986	97,416,794	808	1	13.2	10	22	15	1	1	2	ALDH18A1, TCTN3	177, 37510	in gene, downstream	ActReg chr10 #1521	1	0
1522	10	97,453,435	97,454,123	688	2	9.818	12.682	17	21	1	1	1	TCTN3	121	in gene	ActReg chr10 #1522	1	1
1523	10	97,667,188	97,668,026	838	1	9.115	12.231	16	21	1	1	1	C10orf131	-115	upstream	ActReg chr10 #1523	0	1
1524	10	97,802,935	97,803,662	727	1	9.739	11.043	14	15	1	1	2	LOC728558, CCNJ	46655, 139	in gene, in gene	ActReg chr10 #1524	0	1
1525	10	97,803,766	97,804,395	629	1	10.65	6.45	16	12	1	1	2	LOC728558, CCNJ	45873, 921	in gene, in gene	ActReg chr10 #1525	1	0
1526	10	97,849,311	97,850,634	1,323	2	11.571	14.762	25	26	1	1	1	LOC728558	-19	upstream	ActReg chr10 #1526	1	1
1527	10	97,889,288	97,890,756	1,468	2	10.348	14.326	19	31	1	1	1	ZNF518A	550	in gene	ActReg chr10 #1527	1	1
1528	10	98,255,690	98,256,682	992	2	12.355	19.742	25	45	0	0	1	TLL2	17,497	in gene	ActReg chr10 #1528	1	1
1529	10	98,273,200	98,273,939	739	1	8.043	11.174	14	18	1	1	2	TLL2, TM9SF3	114, 73240	in gene, downstream	ActReg chr10 #1529	0	1
1530	10	98,841,240	98,842,011	771	1	9.917	14.917	19	30	0	0	1	SLIT1	104,058	in gene	ActReg chr10 #1530	0	1
1531	10	99,078,465	99,079,361	896	2	12.143	12.25	25	20	1	1	1	FRAT1	-109	upstream	ActReg chr10 #1531	1	1
1532	10	99,093,314	99,093,997	683	1	8.4	10.095	12	18	1	1	1	FRAT2	803	in gene	ActReg chr10 #1532	0	1
1533	10	99,094,271	99,094,913	642	2	12.191	10.571	23	19	1	1	1	FRAT2	-134	upstream	ActReg chr10 #1533	1	1
1534	10	99,185,729	99,186,879	1,150	1	6.2	10.857	11	19	1	1	2	PCAM1, EXOSC1	277, 19464	in gene, downstream	ActReg chr10 #1534	0	1
1535	10	99,257,415	99,258,325	910	1	10.893	10.036	14	19	1	2	2	MMS19, UBTD1	496, -898	in gene, upstream	ActReg chr10 #1535	1	0
1536	10	99,301,856	99,303,419	1,563	3	10.225	10.674	18	21	0	0	1	UBTD1	43,869	in gene	ActReg chr10 #1536	1	1
1537	10	99,446,522	99,447,697	1,175	2	12.297	11.784	22	21	1	1	1	AVPI1	-94	upstream	ActReg chr10 #1537	1	1
1538	10	99,473,651	99,474,162	511	1	7.625	11.75	13	20	1	1	2	MARVELD1, LOC100270710	441, 19392	in gene, downstream	ActReg chr10 #1538	0	1
1539	10	99,486,302	99,486,996	694	1	11.909	8.273	18	12	0	0	3	MARVELD1, LOC100270710, ZFYVE27	13184, 6649, -10229	downstream, in gene, upstream	ActReg chr10 #1539	1	0
1540	10	99,496,419	99,497,385	966	2	10.633	11.733	16	18	1	2	2	LOC100270710, ZFYVE27	-3604, 24	upstream, in gene	ActReg chr10 #1540	1	1
1541	10	99,570,162	99,570,873	711	1	8.045	12.636	14	18	0	0	0				ActReg chr10 #1541	0	1
1542	10	99,602,395	99,603,571	1,176	2	10.784	15.081	26	28	0	1	2	LOC100505561, GOLGA7B	6572, -7013	in gene, upstream	ActReg chr10 #1542	1	1
1543	10	99,620,909	99,621,717	808	1	8.48	13.28	15	23	0	1	3	GOLGA7B, CRTAC1, LOC100128300	11317, 169272, -6576	in gene, downstream, upstream	ActReg chr10 #1543	0	1
1544	10	99,641,800	99,643,033	1,233	2	15.79	10.421	29	23	0	0	1	CRTAC1	148,169	in gene	ActReg chr10 #1544	1	1
1545	10	99,649,062	99,649,905	843	1	8.692	14.308	15	26	0	0	1	CRTAC1	141,102	in gene	ActReg chr10 #1545	0	1
1546	10	99,751,447	99,752,176	729	1	8.391	14.087	15	27	0	0	1	CRTAC1	38,774	in gene	ActReg chr10 #1546	0	1
1547	10	99,814,841	99,816,992	2,151	2	19.221	23.073	73	103	0	0	0				ActReg chr10 #1547	1	1
1548	10	99,846,866	99,847,548	682	2	11.095	10.714	21	20	0	0	0				ActReg chr10 #1548	1	1
1549	10	99,894,176	99,894,754	578	2	9.316	9.158	18	14	1	1	1	C10orf28	84	in gene	ActReg chr10 #1549	1	1
1550	10	100,006,635	100,007,480	845	1	7.5	11.269	11	16	0	0	2	C10orf28, LOXL4	112676, 20950	downstream, downstream	ActReg chr10 #1550	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1551	10	100,029,147	100,029,748	601	1	9.947	12.158	15	19	0	1	1	LOXL4	-1,440	upstream	ActReg chr10 #1551	0	1
1552	10	100,059,002	100,059,626	624	1	11.35	7.444	21	13	0	0	0				ActReg chr10 #1552	1	0
1553	10	100,082,439	100,083,582	1,143	1	8.714	13.6	16	31	0	0	0				ActReg chr10 #1553	0	1
1554	10	100,113,066	100,113,904	838	1	6.615	10.654	11	15	0	0	0				ActReg chr10 #1554	0	1
1555	10	100,248,151	100,249,084	933	1	7.414	12.621	12	23	0	0	1	HPSE2	747,015	in gene	ActReg chr10 #1555	0	1
1556	10	101,380,993	101,381,666	673	1	12.762	10	26	19	1	1	1	SLC25A28	-1,108	upstream	ActReg chr10 #1556	1	0
1557	10	101,418,376	101,419,374	998	1	9.806	11.194	16	22	1	1	1	ENTPD7	-388	upstream	ActReg chr10 #1557	0	1
1558	10	101,945,442	101,946,148	706	1	9.714	12.682	14	23	1	1	2	ERLIN1, CHUK	19, 43549	in gene, downstream	ActReg chr10 #1558	0	1
1559	10	102,027,110	102,027,681	571	1	10.833	16.389	16	35	1	1	2	CWF19L1, BLOC1S2	42, 19044	in gene, downstream	ActReg chr10 #1559	0	1
1560	10	102,084,770	102,085,480	710	1	9.591	11.818	21	23	0	0	1	PKD2L1	5,118	in gene	ActReg chr10 #1560	0	1
1561	10	102,105,979	102,107,785	1,806	2	9.491	12.491	22	24	1	1	1	SCD	110	in gene	ActReg chr10 #1561	1	1
1562	10	102,266,302	102,266,943	641	1	5.421	11.7	9	25	0	0	1	SEC31B	12,973	in gene	ActReg chr10 #1562	0	1
1563	10	102,295,195	102,295,978	783	2	16.04	17.56	34	48	0	2	2	NDUFB8, HIF1AN	-5950, -55	upstream, upstream	ActReg chr10 #1563	1	1
1564	10	102,440,193	102,441,001	808	2	10.36	13.12	23	22	1	0	0				ActReg chr10 #1564	1	1
1565	10	102,586,538	102,587,142	604	1	9.368	12.368	14	18	1	0	1	PAX2	81,372	in gene	ActReg chr10 #1565	0	1
1566	10	102,746,366	102,747,555	1,189	2	9.289	12.658	18	22	1	2	4	SEMA4C, MRPL43, C10orf2, LZTS2	14674, 312, 333, -10005	downstream, in gene, upstream, upstream	ActReg chr10 #1566	1	1
1567	10	102,758,293	102,759,311	1,018	1	10.312	12.344	14	18	1	1	2	C10orf2, LZTS2	11509, 1837	downstream, in gene	ActReg chr10 #1567	0	1
1568	10	102,768,346	102,768,923	577	1	6.5	13.167	11	19	0	0	2	LZTS2, PDZD7	11669, 22245	downstream, downstream	ActReg chr10 #1568	0	1
1569	10	102,791,323	102,792,921	1,598	1	12.86	9.94	22	19	1	2	2	PDZD7, SFXN3	-1243, 1126	upstream, in gene	ActReg chr10 #1569	1	0
1570	10	102,840,580	102,841,358	778	2	10.542	13.25	18	22	0	0	1	TLX1NB	49,934	downstream	ActReg chr10 #1570	1	1
1571	10	102,845,475	102,846,253	778	2	10.708	15.792	21	26	0	0	1	TLX1NB	45,039	downstream	ActReg chr10 #1571	1	1
1572	10	103,113,145	103,114,406	1,261	2	13.05	13.525	22	22	1	1	1	BTRC	-50	upstream	ActReg chr10 #1572	1	1
1573	10	103,124,310	103,124,776	466	2	12.933	19.333	25	41	0	0	1	BTRC	10,718	in gene	ActReg chr10 #1573	1	1
1574	10	103,453,722	103,454,839	1,117	1	9.743	10.886	15	18	1	1	1	FBXW4	463	in gene	ActReg chr10 #1574	0	1
1575	10	103,542,744	103,543,669	925	1	9.481	11.655	18	19	1	2	3	FGF8, NPM3, MGEA5	-7447, -36, 35016	upstream, upstream, downstream	ActReg chr10 #1575	0	1
1576	10	103,577,904	103,578,785	881	2	15.607	15.464	34	33	1	2	3	MGEA5, LOC100289509, KCNIP2	-122, -481, 25333	upstream, upstream, downstream	ActReg chr10 #1576	1	1
1577	10	103,600,341	103,601,920	1,579	2	15.22	17.24	37	51	0	1	2	KCNIP2, C10orf76	2547, 214802	in gene, downstream	ActReg chr10 #1577	1	1
1578	10	103,815,446	103,816,412	966	2	15.1	16.433	33	34	1	1	2	C10orf76, HPS6	3, -9218	in gene, upstream	ActReg chr10 #1578	1	1
1579	10	103,824,653	103,825,810	1,157	1	9.472	10.833	14	19	1	1	2	C10orf76, HPS6	-9299, 84	upstream, in gene	ActReg chr10 #1579	0	1
1580	10	103,892,129	103,893,947	1,818	2	12.375	17.089	38	35	1	1	1	PPRC1	251	in gene	ActReg chr10 #1580	1	1
1581	10	103,911,655	103,912,678	1,023	1	8.812	12.469	17	21	1	1	2	PPRC1, NOLC1	19379, 233	downstream, in gene	ActReg chr10 #1581	0	1
1582	10	104,005,019	104,005,561	542	1	11.294	7.235	20	13	1	2	2	PITX3, GBF1	-4059, -19	upstream, upstream	ActReg chr10 #1582	1	0
1583	10	104,121,392	104,121,827	435	1	7.5	10.214	12	18	0	0	1	GBF1	116,300	in gene	ActReg chr10 #1583	0	1
1584	10	104,153,604	104,154,859	1,255	1	9.615	12.59	16	21	1	1	2	NFKB2, PSD	2, 24670	in gene, downstream	ActReg chr10 #1584	0	1
1585	10	104,179,186	104,179,863	677	1	10.619	11.143	21	17	1	2	4	PSD, FBXL15, LOC100286939, CUEDC2	-623, -47, 3369, 12899	upstream, upstream, downstream, downstream	ActReg chr10 #1585	0	1
1586	10	104,180,284	104,181,719	1,435	2	17.511	19.533	47	60	1	3	4	PSD, FBXL15, LOC100286939, CUEDC2	-2100, 1430, 1892, 11422	upstream, in gene, downstream, downstream	ActReg chr10 #1586	1	1
1587	10	104,191,917	104,192,769	852	2	12.704	11.296	21	26	1	2	4	FBXL15, LOC100286939, CUEDC2, MIR146B	12772, -9450, 80, -3926	downstream, upstream, in gene, upstream	ActReg chr10 #1587	1	1
1588	10	104,261,880	104,262,883	1,003	1	9.719	11.562	20	22	1	2	2	ACTR1A, SUFU	131, -1338	in gene, upstream	ActReg chr10 #1588	0	1
1589	10	104,263,342	104,263,967	625	1	13.579	10.842	23	14	1	2	2	ACTR1A, SUFU	-1142, -65	upstream, upstream	ActReg chr10 #1589	1	0
1590	10	104,405,225	104,406,102	877	1	11.852	10.37	20	15	0	1	1	TRIM8	1,411	in gene	ActReg chr10 #1590	1	0
1591	10	104,473,399	104,474,037	638	1	7.85	10.25	13	15	1	2	2	ARL3, SFXN2	472, -580	in gene, upstream	ActReg chr10 #1591	0	1
1592	10	104,613,729	104,614,508	779	1	10.667	16.875	15	34	1	1	1	C10orf32	151	in gene	ActReg chr10 #1592	0	1
1593	10	104,952,440	104,953,029	589	1	7.158	10.105	12	15	1	1	1	NT5C2	322	in gene	ActReg chr10 #1593	0	1
1594	10	105,001,020	105,001,609	589	1	11.316	9.053	16	13	0	1	1	hCG_2024410	-4,330	upstream	ActReg chr10 #1594	1	0
1595	10	105,025,217	105,025,910	693	1	10.714	14.333	15	28	0	0	0				ActReg chr10 #1595	0	1
1596	10	105,032,542	105,033,350	808	2	13.346	15.769	30	42	0	1	1	INA	-3,974	upstream	ActReg chr10 #1596	1	1
1597	10	105,037,854	105,039,072	1,218	2	10.923	15.462	32	37	1	1	1	INA	1,543	in gene	ActReg chr10 #1597	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1598	10	105,110,150	105,111,204	1,054	2	8.818	7.939	16	21	1	1	1	PCGF6	214	in gene	ActReg chr10 #1598	1	1
1599	10	105,127,564	105,128,225	661	1	11.571	13.333	15	19	2	1	1	TAF5	170	in gene	ActReg chr10 #1599	0	1
1600	10	105,419,824	105,421,203	1,379	2	12.116	12.767	22	18	1	0	1	SH3PXD2A	194,651	in gene	ActReg chr10 #1600	1	1
1601	10	105,506,297	105,507,556	1,259	2	10.825	12.85	20	24	0	1	2	SH3PXD2A, LOC100505839	108238, 389	in gene, in gene	ActReg chr10 #1601	1	1
1602	10	105,560,087	105,561,031	944	1	9.367	12.033	18	21	0	0	1	SH3PXD2A	54,605	in gene	ActReg chr10 #1602	0	1
1603	10	105,587,452	105,589,006	1,554	2	9.939	10.408	16	20	0	0	1	SH3PXD2A	26,935	in gene	ActReg chr10 #1603	1	1
1604	10	105,621,090	105,621,825	735	1	6.522	9.652	11	15	0	1	1	SH3PXD2A	-6,293	upstream	ActReg chr10 #1604	0	1
1605	10	105,655,071	105,655,863	792	1	7.12	12.48	12	20	0	0	1	OBFC1	22,578	in gene	ActReg chr10 #1605	0	1
1606	10	105,869,573	105,870,283	710	1	12.182	8.682	18	15	0	0	0				ActReg chr10 #1606	1	0
1607	10	105,881,379	105,881,954	575	1	11.278	11	17	13	1	1	2	C10orf78, C10orf79	-150, 110454	upstream, downstream	ActReg chr10 #1607	1	0
1608	10	105,991,491	105,992,294	803	1	7.28	13.12	11	23	1	1	1	C10orf79	228	in gene	ActReg chr10 #1608	0	1
1609	10	106,014,141	106,015,107	966	1	10.129	10.419	15	15	1	1	1	GSTO1	672	in gene	ActReg chr10 #1609	0	1
1610	10	106,059,323	106,060,697	1,374	1	7.884	11.488	16	18	0	0	1	GSTO2	31,379	downstream	ActReg chr10 #1610	0	1
1611	10	106,088,760	106,089,735	975	2	13.806	13.581	26	21	0	0	2	ITPRIP, LOC100505856	4416, 6125	in gene, downstream	ActReg chr10 #1611	1	1
1612	10	106,097,667	106,098,905	1,238	2	18.763	21.842	52	52	1	1	1	ITPRIP	-4,623	upstream	ActReg chr10 #1612	1	1
1613	10	106,307,718	106,308,341	623	1	10.579	11.79	21	19	0	0	0				ActReg chr10 #1613	0	1
1614	10	106,583,819	106,584,847	1,028	2	20.969	29.406	61	80	0	0	1	SORCS3	183,474	in gene	ActReg chr10 #1614	1	1
1615	10	106,697,218	106,697,847	629	1	10.895	10.474	18	19	0	0	1	SORCS3	296,673	in gene	ActReg chr10 #1615	1	0
1616	10	109,305,332	109,306,010	678	1	10	10.286	12	16	0	0	0				ActReg chr10 #1616	0	1
1617	10	111,694,585	111,695,238	653	1	8.095	11.286	12	17	0	0	0				ActReg chr10 #1617	0	1
1618	10	111,766,552	111,767,526	974	2	10.484	11.258	17	20	1	1	1	ADD3	1,313	in gene	ActReg chr10 #1618	1	1
1619	10	111,836,523	111,836,979	456	1	5	9.714	8	15	0	0	1	ADD3	71,025	in gene	ActReg chr10 #1619	0	1
1620	10	111,966,968	111,967,636	668	1	12.143	6.429	20	13	1	1	1	MXI1	-61	upstream	ActReg chr10 #1620	1	0
1621	10	111,970,139	111,970,803	664	1	9.714	10.714	16	17	1	0	1	MXI1	3,108	in gene	ActReg chr10 #1621	0	1
1622	10	112,167,216	112,168,146	930	1	8.621	9.931	14	14	0	0	0				ActReg chr10 #1622	0	1
1623	10	112,173,781	112,174,803	1,022	2	9.844	9.562	18	19	0	0	0				ActReg chr10 #1623	1	1
1624	10	112,185,493	112,186,211	718	1	11.217	4.652	18	8	0	0	0				ActReg chr10 #1624	1	0
1625	10	112,257,030	112,257,770	740	1	7.826	12.696	11	17	1	1	1	DUSP5	-225	upstream	ActReg chr10 #1625	0	1
1626	10	112,258,112	112,258,717	605	1	7.421	10.842	10	16	1	1	1	DUSP5	789	in gene	ActReg chr10 #1626	0	1
1627	10	112,285,431	112,285,981	550	1	8.294	10.235	13	16	0	0	0				ActReg chr10 #1627	0	1
1628	10	112,295,607	112,296,531	924	2	11.448	12.379	17	17	0	0	0				ActReg chr10 #1628	1	1
1629	10	112,326,787	112,327,923	1,136	2	16.571	19.286	40	43	1	1	1	SMC3	-94	upstream	ActReg chr10 #1629	1	1
1630	10	112,431,689	112,432,672	983	2	13.677	9.967	26	21	1	0	1	RBM20	28,025	in gene	ActReg chr10 #1630	1	1
1631	10	112,533,835	112,534,554	719	2	10.954	11.182	15	23	0	0	1	RBM20	130,039	in gene	ActReg chr10 #1631	1	1
1632	10	112,678,226	112,679,285	1,059	2	13.576	12.939	23	27	1	2	2	NCRNA00081, SHOC2	369, -546	in gene, upstream	ActReg chr10 #1632	1	1
1633	10	112,993,275	112,993,699	424	1	9.214	5.929	14	9	0	0	0				ActReg chr10 #1633	1	0
1634	10	113,515,947	113,516,773	826	1	7.154	12.538	12	23	0	0	0				ActReg chr10 #1634	0	1
1635	10	113,766,498	113,767,490	992	1	10.419	7.645	15	11	0	0	0				ActReg chr10 #1635	1	0
1636	10	113,799,620	113,800,027	407	1	6.417	10.25	8	13	0	0	0				ActReg chr10 #1636	0	1
1637	10	113,943,149	113,944,003	854	2	10.407	13.148	21	26	1	1	1	GPAM	-51	upstream	ActReg chr10 #1637	1	1
1638	10	114,206,132	114,207,244	1,112	2	9.143	12.657	19	17	1	2	2	ZDHHC6, VTI1A	-16, -68	upstream, upstream	ActReg chr10 #1638	1	1
1639	10	114,393,746	114,394,267	521	1	11	4.667	16	8	0	1	2	VTI1A, MIR4295	187250, 77	in gene, in gene	ActReg chr10 #1639	1	0
1640	10	114,719,005	114,719,601	596	1	6.474	9.684	12	16	0	0	1	TCF7L2	9,294	in gene	ActReg chr10 #1640	0	1
1641	10	114,751,309	114,752,380	1,071	2	12.818	10.333	23	20	0	0	1	TCF7L2	41,835	in gene	ActReg chr10 #1641	1	1
1642	10	115,144,819	115,145,357	538	1	10.588	7.765	16	10	0	0	0				ActReg chr10 #1642	1	0
1643	10	115,195,995	115,196,631	636	1	3.3	10.5	9	15	0	0	0				ActReg chr10 #1643	0	1
1644	10	115,438,624	115,440,363	1,739	2	10.618	13.673	17	24	1	1	1	CASP7	558	in gene	ActReg chr10 #1644	1	1
1645	10	115,613,842	115,614,387	545	1	10.765	8.882	15	14	1	2	2	DCLRE1A, NHLRC2	-255, -277	upstream, upstream	ActReg chr10 #1645	1	0
1646	10	115,614,410	115,615,052	642	1	9.95	11.65	14	18	1	2	2	DCLRE1A, NHLRC2	-872, 340	upstream, in gene	ActReg chr10 #1646	0	1
1647	10	115,933,387	115,934,162	775	1	7.958	11.375	15	20	1	3	3	C10orf118, MIR2110, TDRD1	590, 164, -5255	in gene, downstream, upstream	ActReg chr10 #1647	0	1
1648	10	116,105,343	116,106,655	1,312	1	10.268	7.927	16	13	0	0	1	AFAP1L2	58,516	in gene	ActReg chr10 #1648	1	0
1649	10	116,149,058	116,149,635	577	1	12.222	13.167	20	24	0	0	1	AFAP1L2	15,169	in gene	ActReg chr10 #1649	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1650	10	116,154,296	116,155,274	978	1	8.742	10.677	14	14	0	0	1	AFAP1L2	9,730	in gene	ActReg chr10 #1650	0	1
1651	10	116,697,747	116,698,226	479	1	11.8	12.8	16	19	1	1	1	TRUB1	34	in gene	ActReg chr10 #1651	1	0
1652	10	117,943,134	117,943,610	476	1	12.4	11.467	19	15	0	0	1	GFRA1	89,754	in gene	ActReg chr10 #1652	1	0
1653	10	118,764,263	118,764,793	530	1	9.5	11.125	16	15	1	1	1	KIAA1598	560	in gene	ActReg chr10 #1653	0	1
1654	10	118,946,161	118,946,862	701	1	11.727	9.273	22	14	0	0	0				ActReg chr10 #1654	1	0
1655	10	118,976,081	118,976,747	666	1	8.048	12.191	15	20	1	0	1	KCNK18	19,414	downstream	ActReg chr10 #1655	0	1
1656	10	119,134,891	119,135,561	670	1	10.667	12.238	16	21	1	1	1	PDZD8	-289	upstream	ActReg chr10 #1656	0	1
1657	10	119,202,394	119,203,069	675	1	11.191	6	20	10	0	0	0				ActReg chr10 #1657	1	0
1658	10	119,739,800	119,740,301	501	1	5	11.562	8	14	0	0	0				ActReg chr10 #1658	0	1
1659	10	120,011,358	120,011,979	621	2	10.7	10.2	17	16	0	0	0				ActReg chr10 #1659	1	1
1660	10	120,248,149	120,248,639	490	1	9.267	11.667	15	20	0	0	0				ActReg chr10 #1660	0	1
1661	10	120,322,804	120,323,252	448	1	9	9.643	13	14	0	0	0				ActReg chr10 #1661	0	1
1662	10	120,353,723	120,355,217	1,494	2	10.17	13.553	21	24	1	1	1	PRLHR	690	in gene	ActReg chr10 #1662	1	1
1663	10	120,355,296	120,356,048	752	1	9.542	12.917	14	21	1	1	1	PRLHR	-512	upstream	ActReg chr10 #1663	0	1
1664	10	120,513,517	120,514,974	1,457	2	12.311	11.822	20	19	1	1	1	C10orf46	513	in gene	ActReg chr10 #1664	1	1
1665	10	120,839,870	120,840,645	775	1	9.56	10.2	16	13	1	1	1	EIF3A	77	in gene	ActReg chr10 #1665	0	1
1666	10	120,937,826	120,938,488	662	1	11	9.85	17	14	1	1	1	PRDX3	188	in gene	ActReg chr10 #1666	1	0
1667	10	121,258,524	121,259,428	904	1	8.138	11.793	13	17	0	0	1	RGS10	43,246	downstream	ActReg chr10 #1667	0	1
1668	10	121,356,064	121,357,085	1,021	1	8.094	12.812	14	20	1	1	1	TIAL1	-33	upstream	ActReg chr10 #1668	0	1
1669	10	121,427,117	121,428,418	1,301	1	9.829	13.61	16	20	0	0	1	BAG3	16,885	in gene	ActReg chr10 #1669	0	1
1670	10	121,651,620	121,652,509	889	1	12.111	8.778	20	15	1	1	1	SEC23IP	-159	upstream	ActReg chr10 #1670	1	0
1671	10	121,890,675	121,891,274	599	2	9.158	12.368	20	23	0	0	0				ActReg chr10 #1671	1	1
1672	10	122,146,720	122,147,430	710	1	5.87	10.609	12	14	0	0	0				ActReg chr10 #1672	0	1
1673	10	122,220,206	122,220,943	737	1	8.565	13.13	17	25	0	0	1	PPAPDC1A	4,108	in gene	ActReg chr10 #1673	0	1
1674	10	122,267,738	122,268,522	784	2	11.16	10.76	20	23	0	0	1	PPAPDC1A	51,664	in gene	ActReg chr10 #1674	1	1
1675	10	122,273,446	122,273,969	523	1	12	6.875	20	11	0	0	1	PPAPDC1A	57,241	in gene	ActReg chr10 #1675	1	0
1676	10	122,610,482	122,611,330	848	2	9.407	13.63	16	28	1	2	2	LOC283089, WDR11	-215, 219	upstream, in gene	ActReg chr10 #1676	1	1
1677	10	122,802,444	122,803,051	607	1	8.895	11.105	13	20	0	0	0				ActReg chr10 #1677	0	1
1678	10	122,828,428	122,829,246	818	2	9.52	11.72	15	19	0	0	0				ActReg chr10 #1678	1	1
1679	10	123,687,389	123,688,128	739	2	10.542	10.542	21	14	1	2	2	ATE1, LOC100130887	-212, -69	upstream, upstream	ActReg chr10 #1679	1	1
1680	10	123,702,412	123,702,847	435	1	8	12.385	10	17	0	0	1	LOC100130887	14,802	in gene	ActReg chr10 #1680	0	1
1681	10	123,733,717	123,735,323	1,606	2	18.98	21.62	66	74	1	1	1	NSMCE4A	223	in gene	ActReg chr10 #1681	1	1
1682	10	123,872,739	123,873,423	684	1	9.524	12	14	20	1	0	1	TACC2	124,392	in gene	ActReg chr10 #1682	0	1
1683	10	123,900,253	123,901,240	987	2	15.516	13.387	30	26	0	0	1	TACC2	152,057	in gene	ActReg chr10 #1683	1	1
1684	10	124,091,304	124,091,859	555	1	7	12.177	12	18	0	0	1	BTBD16	60,760	in gene	ActReg chr10 #1684	0	1
1685	10	124,228,388	124,229,200	812	1	10.28	13.2	14	20	0	0	1	HTRA1	7,753	in gene	ActReg chr10 #1685	0	1
1686	10	124,254,156	124,254,828	672	1	13.143	9	22	15	0	0	1	HTRA1	33,451	in gene	ActReg chr10 #1686	1	0
1687	10	124,545,607	124,546,357	750	2	12.522	12.043	27	25	0	0	0				ActReg chr10 #1687	1	1
1688	10	124,638,807	124,639,684	877	1	6.786	12.357	9	20	1	1	1	FAM24B	-88	upstream	ActReg chr10 #1688	0	1
1689	10	124,670,853	124,672,221	1,368	2	26.286	31.214	68	95	0	1	1	FAM24A	1,320	in gene	ActReg chr10 #1689	1	1
1690	10	124,713,369	124,714,398	1,029	1	11.75	14.844	23	22	1	1	1	C10orf88	36	in gene	ActReg chr10 #1690	0	1
1691	10	124,739,589	124,740,433	844	2	10.385	10.039	24	21	1	1	1	PSTK	455	in gene	ActReg chr10 #1691	1	1
1692	10	124,767,678	124,768,960	1,282	1	10.244	11.39	18	18	1	2	2	IKZF5, ACADSB	-8, -110	upstream, upstream	ActReg chr10 #1692	0	1
1693	10	124,913,397	124,914,711	1,314	1	8.61	11.317	15	19	1	1	2	HMX2, BUB3	6416, 294	downstream, in gene	ActReg chr10 #1693	0	1
1694	10	125,374,253	125,375,121	868	2	9.963	15.259	22	27	0	0	0				ActReg chr10 #1694	1	1
1695	10	126,479,635	126,480,750	1,115	1	10.086	11.343	17	20	1	1	2	METTL10, FAM175B	247, -10162	in gene, upstream	ActReg chr10 #1695	0	1
1696	10	126,489,982	126,490,631	649	1	8.667	11.238	18	17	1	1	2	METTL10, FAM175B	-9867, -48	upstream, upstream	ActReg chr10 #1696	0	1
1697	10	126,847,288	126,847,813	525	1	6.118	9	10	16	1	1	1	CTBP2	2,074	in gene	ActReg chr10 #1697	0	1
1698	10	126,889,508	126,890,139	631	1	6.842	11.79	14	17	0	0	0				ActReg chr10 #1698	0	1
1699	10	127,511,459	127,512,415	956	2	14.414	19.138	29	47	1	2	2	UROS, BCCIP	-100, -167	upstream, upstream	ActReg chr10 #1699	1	1
1700	10	127,583,420	127,585,558	2,138	1	17.612	20.343	28	38	1	1	1	FANK1	-619	upstream	ActReg chr10 #1700	0	1
1701	10	127,750,850	127,751,853	1,003	1	9.452	11.032	15	16	0	0	1	ADAM12	325,776	in gene	ActReg chr10 #1701	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1702	10	127,887,691	127,888,277	586	1	8.667	14.667	13	29	0	0	1	ADAM12	189,143	in gene	ActReg chr10 #1702	0	1
1703	10	128,148,385	128,149,193	808	1	10.08	13.12	21	22	0	0	1	C10orf90	61,221	in gene	ActReg chr10 #1703	0	1
1704	10	128,330,315	128,330,972	657	1	10.25	7.75	19	14	0	0	0				ActReg chr10 #1704	1	0
1705	10	128,352,570	128,353,128	558	1	6.389	11.722	11	16	0	0	0				ActReg chr10 #1705	0	1
1706	10	128,915,306	128,915,857	551	1	9.529	11.118	18	17	0	0	1	DOCK1	146,616	in gene	ActReg chr10 #1706	0	1
1707	10	129,283,384	129,284,001	617	1	10.1	14.4	22	27	0	0	0				ActReg chr10 #1707	0	1
1708	10	129,355,092	129,355,684	592	2	9.158	9.579	14	19	0	0	1	NPS	7,775	downstream	ActReg chr10 #1708	1	1
1709	10	129,398,489	129,399,359	870	2	13.741	16.815	25	34	0	0	0				ActReg chr10 #1709	1	1
1710	10	131,661,411	131,662,075	664	1	10.15	14.05	19	23	0	0	1	EBF3	100,348	in gene	ActReg chr10 #1710	0	1
1711	10	131,749,420	131,750,134	714	1	11.591	8.591	17	13	0	0	1	EBF3	12,314	in gene	ActReg chr10 #1711	1	0
1712	10	131,820,553	131,821,491	938	1	6	11.862	13	19	0	0	0				ActReg chr10 #1712	0	1
1713	10	131,863,094	131,864,009	915	1	7.241	11.621	13	18	0	0	1	LOC387723	45,530	in gene	ActReg chr10 #1713	0	1
1714	10	131,908,295	131,910,125	1,830	2	12.232	15.053	25	26	1	1	1	LOC387723	-129	upstream	ActReg chr10 #1714	1	1
1715	10	132,098,777	132,100,288	1,511	2	12.396	10.396	19	21	0	0	0				ActReg chr10 #1715	1	1
1716	10	133,152,557	133,153,083	526	1	7.25	10.5	12	17	0	0	0				ActReg chr10 #1716	0	1
1717	10	134,133,519	134,134,188	669	1	4.05	10.952	8	17	0	0	1	LOC100506057	11,520	downstream	ActReg chr10 #1717	0	1
1718	10	134,145,045	134,146,093	1,048	2	9.606	12.182	17	23	1	2	2	LOC100506057, LRRC27	-196, -45	upstream, upstream	ActReg chr10 #1718	1	1
1719	10	134,606,001	134,606,702	701	1	4	13.773	8	25	1	1	2	INPP5A, NKX6-2	254998, -6814	downstream, upstream	ActReg chr10 #1719	0	1
1720	10	134,778,916	134,779,481	565	2	10.059	11	19	18	1	2	2	LOC100289424, LOC399829	-415, 160	upstream, in gene	ActReg chr10 #1720	1	1
1721	10	134,893,323	134,893,927	604	1	9.632	11.263	18	18	1	1	2	LOC100128127, GPR123	6512, -7784	downstream, upstream	ActReg chr10 #1721	0	1
1722	10	135,091,888	135,092,908	1,020	1	10.094	14.469	17	25	0	1	3	ADAM8, LOC100506167, TUBGCP2	-1991, 14835, 30246	upstream, in gene, downstream	ActReg chr10 #1722	0	1
1723	10	135,106,159	135,107,218	1,059	1	8.212	11.546	12	17	0	0	1	TUBGCP2	15,956	in gene	ActReg chr10 #1723	0	1
1724	10	135,207,530	135,208,171	641	1	6.4	11.4	10	20	1	1	2	PAOX, MTG1	15109, 229	downstream, in gene	ActReg chr10 #1724	0	1
1725	11	189,325	190,472	1,147	2	17.889	15.083	31	30	0	2	2	SCGB1C1, ODF3	-3182, -6863	upstream, upstream	ActReg chr11 #1725	1	1
1726	11	364,199	365,035	836	2	16.962	17.038	43	43	0	1	1	B4GALNT4	-5,178	upstream	ActReg chr11 #1726	1	1
1727	11	448,153	448,664	511	1	7.188	10.75	12	16	0	2	2	ANO9, PTDSS2	-6397, -1872	upstream, upstream	ActReg chr11 #1727	0	1
1728	11	449,854	450,711	857	2	9.889	14.111	21	31	1	1	2	ANO9, PTDSS2	-8271, 2	upstream, in gene	ActReg chr11 #1728	1	1
1729	11	536,898	537,624	726	1	8.591	12.318	13	23	1	2	2	HRAS, LRRC56	-1711, -261	upstream, upstream	ActReg chr11 #1729	0	1
1730	11	809,118	810,070	952	2	11.467	9.733	17	17	1	3	4	LRDD, RPLP2, SNORA52, PNPLA2	-4344, -342, -2087, -9307	upstream, upstream, upstream, upstream	ActReg chr11 #1730	1	1
1731	11	834,819	835,367	548	1	11.059	9.118	19	15	0	2	5	PNPLA2, EFCAB4A, CD151, POLR2L, TSPAN4	16192, 7508, 2141, 7436, -7731	downstream, downstream, in gene, downstream, upstream	ActReg chr11 #1731	1	0
1732	11	842,280	843,068	788	2	23.087	23.375	55	54	1	2	3	CD151, POLR2L, TSPAN4	9722, -145, 150	downstream, upstream, upstream	ActReg chr11 #1732	1	1
1733	11	1,246,136	1,246,626	490	1	7.438	11.438	10	15	0	1	1	MUC5B	2,086	in gene	ActReg chr11 #1733	0	1
1734	11	1,330,674	1,331,527	853	1	10.963	7.741	14	15	1	2	2	TOLLIP, LOC255512	-208, 162	upstream, in gene	ActReg chr11 #1734	1	0
1735	11	1,884,351	1,884,964	613	1	5.85	11.2	10	18	0	1	2	LSP1, MIR4298	10457, -3891	in gene, upstream	ActReg chr11 #1735	0	1
1736	11	1,968,269	1,969,355	1,086	2	12.382	18.853	33	51	1	1	2	TNNT3, MRPL23	28013, 310	downstream, in gene	ActReg chr11 #1736	1	1
1737	11	2,421,327	2,422,214	887	2	12	9.607	23	15	1	1	3	CD81, TSSC4, TRPM5	23223, -1753, 22505	downstream, upstream, downstream	ActReg chr11 #1737	1	1
1738	11	2,906,279	2,906,640	361	1	5.455	10.182	8	15	1	1	2	CDKN1C, SLC22A18AS	536, 18716	in gene, downstream	ActReg chr11 #1738	0	1
1739	11	2,950,222	2,950,709	487	1	7.2	13.133	12	19	1	1	2	SLC22A18, PHLDA2	29514, 185	downstream, in gene	ActReg chr11 #1739	0	1
1740	11	3,078,567	3,078,993	426	1	8.462	10.846	12	16	1	1	1	CARS	-99	upstream	ActReg chr11 #1740	0	1
1741	11	3,862,596	3,863,100	504	1	7.467	9.733	12	18	1	1	1	RHOG	-635	upstream	ActReg chr11 #1741	0	1
1742	11	4,115,874	4,116,302	428	1	11.923	9.769	16	13	1	1	2	STIM1, RRM1	239155, 164	downstream, in gene	ActReg chr11 #1742	0	1
1743	11	4,629,020	4,629,513	493	1	3.5	10.75	5	16	1	1	1	TRIM68	171	in gene	ActReg chr11 #1743	0	1
1744	11	6,502,334	6,503,174	840	2	8.481	9.778	14	16	1	3	3	TRIM3, ARFIP2, FXC1	-7549, -159, 77	upstream, upstream, in gene	ActReg chr11 #1744	1	1
1745	11	7,621,404	7,621,966	562	1	5.222	12.889	8	21	0	0	1	PPFIBP2	86,684	in gene	ActReg chr11 #1745	0	1
1746	11	7,672,243	7,672,842	599	1	9.895	5.579	17	10	0	0	1	PPFIBP2	137,541	in gene	ActReg chr11 #1746	1	0
1747	11	8,244,744	8,245,405	661	1	8.7	12	15	18	0	0	1	LMO1	40,332	downstream	ActReg chr11 #1747	0	1
1748	11	8,430,013	8,430,624	611	2	10.7	8.05	19	15	0	0	1	STK33	185,185	in gene	ActReg chr11 #1748	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1749	11	8,703,979	8,704,649	670	1	11.286	6.81	20	14	1	3	3	RPL27A, SNORA3, SNORA45	319, -1460, 2672	in gene, upstream, upstream	ActReg chr11 #1749	1	0
1750	11	9,385,688	9,386,266	578	1	5.944	12.833	10	23	1	0	0				ActReg chr11 #1750	0	1
1751	11	9,481,817	9,482,561	744	1	8.833	10.583	14	13	1	2	2	LOC644656, ZNF143	56, -323	in gene, upstream	ActReg chr11 #1751	0	1
1752	11	9,635,524	9,635,988	464	1	10.786	10.643	16	18	1	0	0				ActReg chr11 #1752	1	0
1753	11	10,325,834	10,326,571	737	2	11.522	15.087	19	30	1	1	1	ADM	-440	upstream	ActReg chr11 #1753	1	1
1754	11	10,511,965	10,512,777	812	1	9.346	11.308	13	14	0	0	1	AMPD3	40,503	in gene	ActReg chr11 #1754	0	1
1755	11	10,562,564	10,563,061	497	1	11.333	10.4	14	15	1	2	2	RNF141, LOC100129827	-38, 25	upstream, in gene	ActReg chr11 #1755	0	1
1756	11	10,746,736	10,747,285	549	1	10.235	5.941	20	9	0	0	0				ActReg chr11 #1756	1	0
1757	11	10,829,698	10,830,223	525	1	5.562	10.25	10	16	1	2	2	EIF4G2, SNORD97	622, -6805	in gene, upstream	ActReg chr11 #1757	0	1
1758	11	11,413,283	11,413,733	450	1	10.5	6.357	18	10	0	0	1	GALNTL4	230,053	in gene	ActReg chr11 #1758	1	0
1759	11	12,309,189	12,309,901	712	1	11.909	7.5	19	11	0	1	1	MICALCL	1,098	in gene	ActReg chr11 #1759	1	0
1760	11	12,695,542	12,696,067	525	1	9.118	8.118	18	12	1	1	1	TEAD1	-165	upstream	ActReg chr11 #1760	1	0
1761	11	13,237,381	13,238,204	823	1	7.6	10.08	13	13	0	0	0				ActReg chr11 #1761	0	1
1762	11	13,299,638	13,300,032	394	1	9.923	9.077	15	13	1	1	1	ARNTL	510	in gene	ActReg chr11 #1762	1	0
1763	11	14,358,619	14,359,108	489	1	8.562	10.188	14	20	0	0	1	RRAS2	27,189	in gene	ActReg chr11 #1763	0	1
1764	11	14,380,389	14,381,289	900	2	13.714	23.464	30	59	1	0	1	RRAS2	5,213	in gene	ActReg chr11 #1764	1	1
1765	11	14,521,153	14,521,617	464	1	8.929	12.643	14	20	0	1	2	COPB1, PSMA1	56, 143795	in gene, downstream	ActReg chr11 #1765	0	1
1766	11	14,541,589	14,542,377	788	2	17.96	18.32	39	39	1	0	1	PSMA1	123,197	in gene	ActReg chr11 #1766	1	1
1767	11	15,900,258	15,900,770	512	1	10.5	11.562	17	23	0	0	0				ActReg chr11 #1767	0	1
1768	11	16,759,848	16,760,510	662	1	7.35	13.25	14	20	1	1	1	C11orf58	31	in gene	ActReg chr11 #1768	0	1
1769	11	18,127,180	18,128,715	1,535	3	15.625	13.271	37	36	1	1	1	SAAL1	-309	upstream	ActReg chr11 #1769	1	1
1770	11	18,132,470	18,133,135	665	1	7.619	11.619	18	18	0	1	2	SAAL1, MRGPRX3	-5164, -9700	upstream, upstream	ActReg chr11 #1770	0	1
1771	11	18,548,082	18,548,748	666	1	12.095	10.286	23	15	1	1	2	TSG101, UEVLD	74, 61866	in gene, downstream	ActReg chr11 #1771	1	0
1772	11	18,655,630	18,656,235	605	1	10.316	8.421	16	14	1	1	1	SPTY2D1	88	in gene	ActReg chr11 #1772	1	0
1773	11	18,857,829	18,858,478	649	1	9.5	6.5	17	14	0	0	0				ActReg chr11 #1773	1	0
1774	11	19,940,655	19,941,357	702	2	10.546	10.454	16	18	0	0	1	NAV2	568,735	in gene	ActReg chr11 #1774	1	1
1775	11	20,133,827	20,134,548	721	1	5.727	11.773	12	16	0	0	1	NAV2	761,916	in gene	ActReg chr11 #1775	0	1
1776	11	20,180,067	20,181,050	983	2	11.533	18.033	26	37	1	1	1	DBX1	1,312	in gene	ActReg chr11 #1776	1	1
1777	11	20,621,073	20,621,755	682	1	6.333	15.905	15	29	0	1	1	SLC6A5	468	in gene	ActReg chr11 #1777	0	1
1778	11	22,358,958	22,359,761	803	1	7.76	14.6	12	30	0	1	1	SLC17A6	-308	upstream	ActReg chr11 #1778	0	1
1779	11	27,255,651	27,256,203	552	1	6.529	10.529	10	18	0	0	0				ActReg chr11 #1779	0	1
1780	11	27,740,595	27,741,283	688	2	10.182	9.842	20	16	1	1	1	BDNF	2,666	in gene	ActReg chr11 #1780	1	1
1781	11	27,741,480	27,742,599	1,119	2	14.543	19.086	32	43	1	1	1	BDNF	1,566	in gene	ActReg chr11 #1781	1	1
1782	11	27,742,912	27,743,383	471	1	5	10.067	7	13	1	1	1	BDNF	458	in gene	ActReg chr11 #1782	0	1
1783	11	27,743,675	27,744,104	429	1	11.357	7	15	13	1	1	1	BDNF	-284	upstream	ActReg chr11 #1783	1	0
1784	11	27,926,045	27,926,486	441	1	7.714	10.714	9	16	0	0	0				ActReg chr11 #1784	0	1
1785	11	28,129,717	28,130,116	399	1	5.769	10.231	8	14	0	2	2	KIF18A, METT5D1	-170, 118	upstream, in gene	ActReg chr11 #1785	0	1
1786	11	28,723,643	28,724,036	393	1	5.385	10.154	8	14	0	0	0				ActReg chr11 #1786	0	1
1787	11	29,303,598	29,304,218	620	2	7.526	13.579	17	29	0	0	0				ActReg chr11 #1787	1	1
1788	11	31,391,112	31,391,683	571	1	7.889	9.556	11	16	1	2	2	DCDC1, DNAJC24	-76, 20	upstream, in gene	ActReg chr11 #1788	0	1
1789	11	31,990,676	31,991,398	722	1	11.783	6.435	17	12	0	0	0				ActReg chr11 #1789	1	0
1790	11	31,996,156	31,996,781	625	2	10.5	8.85	21	19	0	0	0				ActReg chr11 #1790	1	1
1791	11	32,109,430	32,110,407	977	1	10.71	7.258	17	13	0	1	1	RCN1	-2,559	upstream	ActReg chr11 #1791	1	0
1792	11	32,219,407	32,220,378	971	2	9.607	11.5	20	22	0	0	0				ActReg chr11 #1792	1	1
1793	11	32,913,792	32,914,353	561	1	10.833	6.333	21	10	1	1	1	QSER1	-720	upstream	ActReg chr11 #1793	1	0
1794	11	33,036,911	33,037,741	830	2	11.923	9.615	20	19	1	1	1	DEPDC7	-84	upstream	ActReg chr11 #1794	1	1
1795	11	33,060,605	33,061,768	1,163	2	12.297	13.324	19	28	1	1	2	DEPDC7, TCP11L1	23776, 223	downstream, in gene	ActReg chr11 #1795	1	1
1796	11	33,232,964	33,233,651	687	1	10.238	8.286	18	13	0	0	0				ActReg chr11 #1796	1	0
1797	11	33,278,816	33,280,282	1,466	1	9.63	11.109	15	17	1	1	1	HIPK3	381	in gene	ActReg chr11 #1797	0	1
1798	11	33,654,677	33,655,834	1,157	2	10.639	9.389	16	14	0	0	1	C11orf41	91,378	in gene	ActReg chr11 #1798	1	1
1799	11	33,691,751	33,693,031	1,280	2	9.275	8.475	16	13	0	0	1	C11orf41	128,514	in gene	ActReg chr11 #1799	1	1
1800	11	33,703,857	33,704,492	635	1	8.25	12.25	11	19	0	0	1	C11orf41	140,297	downstream	ActReg chr11 #1800	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1801	11	33,742,895	33,744,536	1,641	2	8.039	10.726	14	17	0	0	1	CD59	14,310	in gene	ActReg chr11 #1801	1	1
1802	11	33,758,085	33,758,750	665	1	11.45	6.3	17	8	1	1	2	CD59, FBXO3	-392, 37654	upstream, downstream	ActReg chr11 #1802	1	0
1803	11	33,823,957	33,824,713	756	1	8.458	12.917	12	23	0	0	0				ActReg chr11 #1803	0	1
1804	11	33,933,955	33,934,847	892	2	12.111	15.889	27	29	0	0	0				ActReg chr11 #1804	1	1
1805	11	34,072,908	34,073,533	625	2	12.895	11.368	22	19	1	1	1	CAPRIN1	-10	upstream	ActReg chr11 #1805	1	1
1806	11	34,126,598	34,127,556	958	1	11.767	16.767	24	34	1	1	2	CAPRIN1, NAT10	53847, -34	downstream, upstream	ActReg chr11 #1806	0	1
1807	11	34,236,419	34,236,951	532	1	7.5	12	12	19	0	0	1	ABTB2	142,870	in gene	ActReg chr11 #1807	0	1
1808	11	34,272,635	34,273,166	531	1	9.294	11.294	13	15	0	0	1	ABTB2	106,655	in gene	ActReg chr11 #1808	0	1
1809	11	34,323,729	34,324,610	881	1	6.786	12.464	13	23	0	0	1	ABTB2	55,386	in gene	ActReg chr11 #1809	0	1
1810	11	34,352,605	34,353,487	882	1	15.536	7.857	29	15	0	0	1	ABTB2	26,509	in gene	ActReg chr11 #1810	1	0
1811	11	34,360,671	34,361,231	560	1	10.167	8.056	16	12	0	0	1	ABTB2	18,604	in gene	ActReg chr11 #1811	1	0
1812	11	34,380,291	34,380,918	627	1	11.947	12.053	17	19	1	1	1	ABTB2	-1,049	upstream	ActReg chr11 #1812	0	1
1813	11	34,417,529	34,418,252	723	2	12.087	12.348	18	23	0	0	0				ActReg chr11 #1813	1	1
1814	11	34,675,372	34,676,873	1,501	3	10.362	12.106	18	24	0	0	1	EHF	33,534	in gene	ActReg chr11 #1814	1	1
1815	11	35,124,835	35,125,398	563	1	6.471	10.353	9	14	0	0	0				ActReg chr11 #1815	0	1
1816	11	35,160,112	35,161,534	1,422	1	9.159	11.341	15	25	1	2	2	LOC100507144, CD44	-1249, 406	upstream, in gene	ActReg chr11 #1816	0	1
1817	11	35,187,994	35,188,717	723	2	13.217	12.13	21	23	0	0	1	CD44	27,938	in gene	ActReg chr11 #1817	1	1
1818	11	35,640,473	35,641,704	1,231	2	10.846	11.795	19	20	1	1	1	FJX1	1,353	in gene	ActReg chr11 #1818	1	1
1819	11	35,683,599	35,684,752	1,153	1	9.472	12.778	17	20	1	1	1	TRIM44	-178	upstream	ActReg chr11 #1819	0	1
1820	11	35,747,341	35,748,185	844	2	16.077	15.731	41	39	0	0	1	TRIM44	63,410	in gene	ActReg chr11 #1820	1	1
1821	11	36,013,029	36,013,597	568	1	8.765	10.235	13	18	0	0	1	LDLRAD3	47,701	in gene	ActReg chr11 #1821	0	1
1822	11	36,023,670	36,024,278	608	1	6.789	12.737	12	22	0	0	1	LDLRAD3	58,362	in gene	ActReg chr11 #1822	0	1
1823	11	36,170,919	36,171,798	879	2	13.593	14.482	32	24	0	0	1	LDLRAD3	205,746	in gene	ActReg chr11 #1823	1	1
1824	11	36,310,696	36,311,374	678	1	10.381	12.238	16	20	0	2	2	COMMD9, PRR5L	-36, -6690	upstream, upstream	ActReg chr11 #1824	0	1
1825	11	36,453,060	36,453,861	801	1	8.6	11.92	20	20	0	0	1	PRR5L	135,735	in gene	ActReg chr11 #1825	0	1
1826	11	36,531,001	36,532,299	1,298	2	23.146	30.366	63	93	1	1	1	TRAF6	172	in gene	ActReg chr11 #1826	1	1
1827	11	36,615,753	36,616,333	580	2	10.177	12.333	18	19	0	1	2	RAG2, C11orf74	3786, -50	in gene, upstream	ActReg chr11 #1827	1	1
1828	11	37,525,538	37,526,117	579	2	9.556	9.611	13	19	0	0	0				ActReg chr11 #1828	1	1
1829	11	37,810,043	37,810,479	436	1	8.214	9.857	10	18	0	0	0				ActReg chr11 #1829	0	1
1830	11	40,409,845	40,410,435	590	1	5.316	9.211	9	17	0	0	0				ActReg chr11 #1830	0	1
1831	11	40,898,698	40,899,340	642	1	12.1	6.75	20	10	0	0	1	LOC100507187	582,749	in gene	ActReg chr11 #1831	1	0
1832	11	43,333,087	43,334,069	982	2	33.419	40.484	103	128	1	1	1	API5	73	in gene	ActReg chr11 #1832	1	1
1833	11	43,380,202	43,380,969	767	2	11.083	13.625	25	20	1	1	1	TTC17	150	in gene	ActReg chr11 #1833	1	1
1834	11	43,598,367	43,599,139	772	2	12.8	14.32	32	28	0	2	3	LOC100507261, LOC100131381, MIR129-2	7897, -1776, -4191	downstream, upstream, upstream	ActReg chr11 #1834	1	1
1835	11	43,638,821	43,639,516	695	1	8.143	12.619	13	19	0	0	0				ActReg chr11 #1835	0	1
1836	11	43,665,355	43,666,257	902	2	13.321	17.286	34	36	0	0	0				ActReg chr11 #1836	1	1
1837	11	43,890,302	43,891,055	753	2	12.542	10.917	21	16	0	0	1	LOC100507282	-9,616	upstream	ActReg chr11 #1837	1	1
1838	11	43,901,866	43,902,908	1,042	2	9.774	16.25	19	34	1	1	1	ALKBH3	30	in gene	ActReg chr11 #1838	1	1
1839	11	43,941,977	43,942,809	832	2	12.192	12.115	24	22	0	1	2	ALKBH3, LOC100507300	40036, 83	downstream, in gene	ActReg chr11 #1839	1	1
1840	11	44,087,364	44,088,331	967	2	13	12.633	26	19	1	1	2	ACCSL, ACCS	18316, 118	downstream, in gene	ActReg chr11 #1840	1	1
1841	11	44,116,855	44,117,686	831	1	11.962	8.423	21	17	1	1	1	EXT2	171	in gene	ActReg chr11 #1841	1	0
1842	11	45,119,252	45,120,236	984	2	12.258	15.839	26	29	0	0	1	PRDM11	4,180	in gene	ActReg chr11 #1842	1	1
1843	11	45,280,933	45,281,723	790	1	14.875	6.708	23	13	0	0	1	SYT13	26,556	in gene	ActReg chr11 #1843	1	0
1844	11	45,565,199	45,566,062	863	2	14.852	15.741	35	35	0	0	0				ActReg chr11 #1844	1	1
1845	11	45,601,852	45,602,609	757	2	11.5	11.833	18	22	0	0	0				ActReg chr11 #1845	1	1
1846	11	45,825,546	45,827,583	2,037	3	12.889	9.889	39	22	1	1	1	SLC35C1	941	in gene	ActReg chr11 #1846	1	1
1847	11	45,868,561	45,869,497	936	1	6.148	12.276	10	24	1	1	1	CRY2	360	in gene	ActReg chr11 #1847	0	1
1848	11	45,894,315	45,894,964	649	1	12.4	12.6	20	20	0	0	1	CRY2	25,970	in gene	ActReg chr11 #1848	0	1
1849	11	45,906,501	45,907,143	642	1	8.05	11.95	13	19	1	1	2	CRY2, MAPK8IP1	38153, -360	downstream, upstream	ActReg chr11 #1849	0	1
1850	11	45,920,455	45,921,650	1,195	2	11.838	11.54	25	22	1	0	3	MAPK8IP1, C11orf94, PEX16	13850, 7781, 18622	in gene, downstream, downstream	ActReg chr11 #1850	1	1
1851	11	45,939,132	45,940,466	1,334	2	11.214	11.167	23	17	1	2	2	PEX16, GYLTL1B	-125, -3397	upstream, upstream	ActReg chr11 #1851	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1852	11	46,258,675	46,259,641	966	2	12	11.333	21	18	1	0	0				ActReg chr11 #1852	1	1
1853	11	46,384,143	46,385,670	1,527	2	10.188	11.333	24	18	0	0	1	DGKZ	30,167	in gene	ActReg chr11 #1853	1	1
1854	11	46,410,828	46,412,103	1,275	2	10.55	11.925	20	19	1	1	4	DGKZ, MDK, CHRM4, AMBRA1	56726, 8847, -3358, 201449	downstream, downstream, upstream, downstream	ActReg chr11 #1854	1	1
1855	11	46,413,840	46,415,113	1,273	2	9.175	12.35	21	23	1	1	3	MDK, CHRM4, AMBRA1	11858, -6369, 198438	downstream, upstream, downstream	ActReg chr11 #1855	1	1
1856	11	46,614,990	46,616,141	1,151	2	15.028	18.611	38	49	1	1	2	AMBRA1, HARBI1	-2651, 23212	upstream, downstream	ActReg chr11 #1856	1	1
1857	11	46,638,417	46,639,506	1,089	2	10.559	10.912	19	19	1	2	2	HARBI1, KIAA0652	-184, 135	upstream, in gene	ActReg chr11 #1857	1	1
1858	11	46,721,890	46,722,734	844	2	10.462	14.308	14	23	1	2	2	ARHGAP1, ZNF408	-192, -5	upstream, upstream	ActReg chr11 #1858	1	1
1859	11	46,866,963	46,868,447	1,484	2	14.848	14.457	44	35	1	2	3	CKAP5, LOC100507401, LRP4	138, -252, 72468	in gene, upstream, downstream	ActReg chr11 #1859	1	1
1860	11	47,207,017	47,207,615	598	1	10.278	12.722	14	18	1	1	2	ARFGAP2, PACSIN3	-8897, 694	upstream, in gene	ActReg chr11 #1860	0	1
1861	11	47,208,009	47,208,664	655	1	12.15	7.5	20	12	1	1	2	ARFGAP2, PACSIN3	-9917, -326	upstream, upstream	ActReg chr11 #1861	1	0
1862	11	47,270,114	47,270,889	775	1	10.542	13.375	16	23	1	2	3	DDB2, ACP2, NR1H3	34008, -44, 52	downstream, upstream, in gene	ActReg chr11 #1862	0	1
1863	11	47,290,503	47,291,177	674	1	7.571	11.238	12	15	1	1	2	NR1H3, MADD	20391, -87	downstream, upstream	ActReg chr11 #1863	0	1
1864	11	47,429,555	47,430,099	544	1	13.647	10.647	26	21	1	1	1	SLC39A13	-219	upstream	ActReg chr11 #1864	1	0
1865	11	47,447,539	47,448,574	1,035	1	9.438	10.781	16	16	1	1	2	SLC39A13, PSMC3	18010, -32	downstream, upstream	ActReg chr11 #1865	0	1
1866	11	47,485,952	47,486,475	523	1	7.647	13.294	9	23	0	0	1	CUGBP1	88,579	downstream	ActReg chr11 #1866	0	1
1867	11	47,573,936	47,575,154	1,218	2	10.237	13.158	21	23	1	1	1	CUGBP1	247	in gene	ActReg chr11 #1867	1	1
1868	11	47,600,101	47,600,974	873	2	13.444	13	27	23	1	3	4	PTPMT1, KBTBD4, NDUFS3, FAM180B	13555, 30, -25, -7693	downstream, in gene, upstream, upstream	ActReg chr11 #1868	1	1
1869	11	47,869,425	47,870,318	893	2	9.893	12.893	18	23	1	1	1	NUP160	186	in gene	ActReg chr11 #1869	1	1
1870	11	47,968,433	47,969,322	889	2	11.143	9.893	18	14	0	0	0				ActReg chr11 #1870	1	1
1871	11	48,012,802	48,013,302	500	1	10.267	5.733	18	7	0	0	1	PTPRJ	10,942	in gene	ActReg chr11 #1871	1	0
1872	11	48,014,809	48,015,375	566	1	11.389	8.111	20	11	0	0	1	PTPRJ	12,982	in gene	ActReg chr11 #1872	1	0
1873	11	48,076,677	48,077,833	1,156	1	8.528	10.833	14	16	0	0	1	PTPRJ	75,145	in gene	ActReg chr11 #1873	0	1
1874	11	55,640,074	55,641,127	1,053	2	9.903	10.848	14	20	1	0	1	SPRYD5	-10,173	upstream	ActReg chr11 #1874	1	1
1875	11	56,700,224	56,700,837	613	1	5.6	11.4	9	21	0	0	0				ActReg chr11 #1875	0	1
1876	11	57,092,111	57,093,432	1,321	2	16.171	16.976	46	59	1	1	2	TNKS1BP1, SSRP1	-358, 10580	upstream, downstream	ActReg chr11 #1876	1	1
1877	11	57,102,739	57,103,599	860	1	11.185	9.556	22	15	1	2	2	SSRP1, P2RX3	182, -2780	in gene, upstream	ActReg chr11 #1877	1	0
1878	11	57,146,833	57,147,761	928	2	14.103	15.345	26	27	0	1	3	P2RX3, PRG3, PRG2	41348, 1326, 10833	downstream, in gene, downstream	ActReg chr11 #1878	1	1
1879	11	57,335,248	57,336,045	797	1	7.04	12.04	9	18	1	1	1	UBE2L6	-193	upstream	ActReg chr11 #1879	0	1
1880	11	57,336,777	57,337,330	553	1	10.882	6.529	16	10	0	1	1	UBE2L6	-1,600	upstream	ActReg chr11 #1880	1	0
1881	11	57,424,780	57,425,477	697	1	11.091	13.318	17	24	1	2	4	LOC100507106, YPEL4, CLP1, ZDHHC5	19278, -7711, -88, -10346	downstream, upstream, upstream, upstream	ActReg chr11 #1881	0	1
1882	11	57,508,474	57,509,206	732	2	14.067	15.174	22	30	1	1	3	TMX2, C11orf31, BTBD18	28798, 118, 10413	downstream, in gene, downstream	ActReg chr11 #1882	1	1
1883	11	57,652,516	57,653,492	976	2	15.4	19.7	36	49	0	0	0				ActReg chr11 #1883	1	1
1884	11	58,345,705	58,346,500	795	1	12.68	11.2	22	16	1	3	3	LPXN, ZFP91-CNTF, ZFP91	-463, -485, -485	upstream, upstream, upstream	ActReg chr11 #1884	1	0
1885	11	58,409,240	58,409,786	546	2	13.118	9	25	15	0	0	0				ActReg chr11 #1885	1	1
1886	11	58,672,522	58,673,033	511	1	7.25	11	10	18	1	0	0				ActReg chr11 #1886	0	1
1887	11	58,909,867	58,910,603	736	1	8.043	13.565	11	27	1	1	1	FAM111A	-83	upstream	ActReg chr11 #1887	0	1
1888	11	59,317,677	59,318,616	939	2	10.517	10.793	18	14	0	0	0				ActReg chr11 #1888	1	1
1889	11	59,327,469	59,328,055	586	1	11.056	7	15	11	1	0	0				ActReg chr11 #1889	1	0
1890	11	59,382,958	59,383,821	863	1	10.741	11.963	19	18	2	2	2	OSBP, LOC100507411	228, -246	in gene, upstream	ActReg chr11 #1890	0	1
1891	11	59,521,895	59,523,461	1,566	2	11.122	12.755	22	18	1	1	1	STX3	146	in gene	ActReg chr11 #1891	1	1
1892	11	59,554,384	59,554,988	604	1	10.737	9	21	12	0	0	1	STX3	32,154	in gene	ActReg chr11 #1892	1	0
1893	11	59,577,846	59,578,536	690	1	10.046	10.727	16	19	1	1	2	STX3, MRPL16	55659, 154	downstream, in gene	ActReg chr11 #1893	0	1
1894	11	60,282,509	60,283,143	634	1	11.45	9.85	21	12	1	1	2	MS4A12, MS4A13	22575, -60	downstream, upstream	ActReg chr11 #1894	1	0
1895	11	60,640,347	60,641,108	761	1	8.625	11.792	12	17	0	0	1	ZP1	5,712	in gene	ActReg chr11 #1895	0	1
1896	11	60,673,797	60,674,520	723	1	9	11.273	16	19	1	2	2	PRPF19, TMEM109	-97, -7213	upstream, upstream	ActReg chr11 #1896	0	1
1897	11	60,691,382	60,692,129	747	1	10.125	14.958	24	28	1	1	2	TMEM109, TMEM132A	10384, -158	downstream, upstream	ActReg chr11 #1897	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1898	11	60,928,570	60,929,542	972	2	12.355	7.613	21	18	1	1	1	VPS37C	-140	upstream	ActReg chr11 #1898	1	1
1899	11	61,100,189	61,101,128	939	2	12.9	14.367	33	22	1	2	2	DDB1, DAK	8, 4	in gene, in gene	ActReg chr11 #1899	1	1
1900	11	61,129,193	61,130,272	1,079	1	8.029	11.147	13	16	1	2	2	CYBASC3, TMEM138	23, 259	in gene, in gene	ActReg chr11 #1900	0	1
1901	11	61,159,700	61,160,402	702	1	13.364	11.909	24	18	1	1	2	TMEM216, CPSF7	219, 37413	in gene, downstream	ActReg chr11 #1901	1	0
1902	11	61,197,000	61,197,984	984	2	10.871	12.258	17	18	1	2	2	CPSF7, SDHAF2	-28, -105	upstream, upstream	ActReg chr11 #1902	1	1
1903	11	61,312,403	61,313,651	1,248	2	15.051	16.436	45	37	0	0	1	SYT7	35,271	in gene	ActReg chr11 #1903	1	1
1904	11	61,334,370	61,335,644	1,274	2	20.077	21.897	68	69	1	0	1	SYT7	13,291	in gene	ActReg chr11 #1904	1	1
1905	11	61,348,765	61,349,356	591	2	15.368	18.263	36	38	1	1	1	SYT7	-762	upstream	ActReg chr11 #1905	1	1
1906	11	61,559,745	61,560,710	965	2	15.2	15.6	31	36	1	3	5	C11orf9, C11orf10, MIR611, FEN1, FADS1	40106, -142, -194, 77, 24302	downstream, upstream, upstream, in gene, downstream	ActReg chr11 #1906	1	1
1907	11	61,583,792	61,584,661	869	2	11.63	10.148	17	14	1	2	2	FADS1, MIR1908	303, -1514	in gene, upstream	ActReg chr11 #1907	1	1
1908	11	61,657,993	61,658,951	958	2	8.067	10.933	19	18	1	1	2	FADS3, RAB3IL1	534, 26525	in gene, downstream	ActReg chr11 #1908	1	1
1909	11	61,664,221	61,665,674	1,453	2	10.63	11.696	21	16	0	1	2	FADS3, RAB3IL1	-5941, 20050	upstream, in gene	ActReg chr11 #1909	1	1
1910	11	61,734,807	61,736,022	1,215	2	9.579	10.974	17	16	1	1	2	BEST1, FTH1	18058, -282	downstream, upstream	ActReg chr11 #1910	1	1
1911	11	61,780,169	61,780,895	726	1	10.5	14.364	15	22	0	0	0				ActReg chr11 #1911	0	1
1912	11	61,793,031	61,793,752	721	1	8.364	11.364	15	21	0	0	0				ActReg chr11 #1912	0	1
1913	11	61,890,996	61,891,921	925	1	11.345	8.207	15	14	1	1	1	INCENP	13	in gene	ActReg chr11 #1913	1	0
1914	11	62,012,508	62,013,236	728	2	11.957	12.217	23	23	0	0	1	SCGB1D2	3,148	downstream	ActReg chr11 #1914	1	1
1915	11	62,104,468	62,105,333	865	1	5.259	11.704	11	23	1	1	1	ASRGL1	126	in gene	ActReg chr11 #1915	0	1
1916	11	62,230,584	62,231,193	609	1	5.368	9.474	9	15	0	0	1	AHNAK	83,444	in gene	ActReg chr11 #1916	0	1
1917	11	62,320,441	62,321,890	1,449	1	11.196	10.065	17	15	0	1	2	AHNAK, EEF1G	-6833, 20295	upstream, downstream	ActReg chr11 #1917	1	0
1918	11	62,358,598	62,359,772	1,174	2	20.861	17.778	60	35	1	1	3	TUT1, MTA2, EML3	-76, 10118, 21052	upstream, downstream, downstream	ActReg chr11 #1918	1	1
1919	11	62,368,791	62,369,784	993	1	8.806	11.226	13	18	1	1	3	TUT1, MTA2, EML3	-10178, 16, 10950	upstream, in gene, downstream	ActReg chr11 #1919	0	1
1920	11	62,389,140	62,390,004	864	1	8.519	12.407	12	19	1	1	4	EML3, ROM1, B3GAT3, GANAB	-9335, 9359, -124, 24532	upstream, downstream, upstream, downstream	ActReg chr11 #1920	0	1
1921	11	62,413,431	62,414,407	976	1	7.129	10.355	15	17	1	1	2	GANAB, INTS5	185, 6855	in gene, downstream	ActReg chr11 #1921	0	1
1922	11	62,432,011	62,433,124	1,113	2	10.743	10.086	16	19	1	3	4	C11orf48, METTL12, SNORA57, C11orf83	6674, -212, 327, -6559	in gene, upstream, upstream, upstream	ActReg chr11 #1922	1	1
1923	11	62,433,237	62,434,114	877	1	8.643	12.393	15	19	1	3	5	C11orf48, METTL12, SNORA57, C11orf83, UBXN1	5566, 896, 781, -5451, 12852	in gene, in gene, downstream, upstream, downstream	ActReg chr11 #1923	0	1
1924	11	62,438,607	62,439,901	1,294	2	10.625	11.325	21	18	1	2	5	C11orf48, METTL12, SNORA57, C11orf83, UBXN1	-13, 6475, 6360, 128, 7273	upstream, downstream, downstream, in gene, downstream	ActReg chr11 #1924	1	1
1925	11	62,476,819	62,477,636	817	2	9.192	10	17	14	1	2	3	BSCL2, GNG3, HNRNPUL2	-181, 2113, 17594	upstream, downstream, downstream	ActReg chr11 #1925	1	1
1926	11	62,493,824	62,494,324	500	1	9.25	11.312	14	20	1	2	2	HNRNPUL2, TTC9C	747, -1878	in gene, upstream	ActReg chr11 #1926	0	1
1927	11	62,494,701	62,495,359	658	1	7.8	11.9	11	16	1	2	2	HNRNPUL2, TTC9C	-209, -922	upstream, upstream	ActReg chr11 #1927	0	1
1928	11	62,538,022	62,539,518	1,496	2	11.109	12.804	16	21	1	1	2	POLR2G, TAF6L	9759, -105	downstream, upstream	ActReg chr11 #1928	1	1
1929	11	62,554,375	62,555,487	1,112	2	12.471	12.765	21	21	1	1	4	TAF6L, TMEM179B, TMEM223, NXF1	16056, 57, 4555, 18033	downstream, in gene, downstream, downstream	ActReg chr11 #1929	1	1
1930	11	62,558,900	62,559,985	1,085	2	10.559	13.235	18	28	1	1	4	TAF6L, TMEM179B, TMEM223, NXF1	20567, 4568, 44, 13522	downstream, downstream, in gene, downstream	ActReg chr11 #1930	1	1
1931	11	62,572,473	62,573,286	813	2	13.346	12.154	28	21	1	1	2	NXF1, STX5	85, 26681	in gene, downstream	ActReg chr11 #1931	1	1
1932	11	62,598,632	62,600,157	1,525	3	12.553	11.575	23	24	1	1	3	STX5, WDR74, RNU2-2	166, 8234, 9839	in gene, downstream, downstream	ActReg chr11 #1932	1	1
1933	11	62,606,379	62,607,372	993	1	9.097	12.806	17	18	1	3	3	STX5, WDR74, RNU2-2	-7315, 753, 2358	upstream, in gene, downstream	ActReg chr11 #1933	0	1
1934	11	62,608,862	62,609,727	865	2	23.407	22.222	58	63	0	2	4	STX5, WDR74, RNU2-2, SNHG1	-9734, -1666, -61, 14066	upstream, upstream, upstream, downstream	ActReg chr11 #1934	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1935	11	62,622,968	62,623,959	991	1	9.839	13.774	15	21	1	10	10	SNHG1, SNORD22, SNORD31, SNORD30, SNORD29, SNORD28, SNORD27, SNORD26, SNORD25, SLC3A2	-103, -2956, -2598, -2259, -2023, -1296, -908, -625, -360, -55	upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr11 #1935	0	1
1936	11	62,647,767	62,649,277	1,510	2	16.723	21.894	35	48	1	0	1	SLC3A2	25,004	in gene	ActReg chr11 #1936	1	1
1937	11	62,747,379	62,748,279	900	2	11.857	12.964	24	19	0	0	1	SLC22A6	4,640	in gene	ActReg chr11 #1937	1	1
1938	11	63,334,464	63,335,229	765	1	8.125	10.583	14	15	0	1	2	HRASLS2, PLA2G16	-3991, 47095	upstream, downstream	ActReg chr11 #1938	0	1
1939	11	63,438,682	63,439,532	850	2	12.889	11.148	27	18	1	1	2	ATL3, RTN3	-24, -9815	upstream, upstream	ActReg chr11 #1939	1	1
1940	11	63,449,200	63,450,132	932	1	6.517	10.103	10	19	1	1	1	RTN3	744	in gene	ActReg chr11 #1940	0	1
1941	11	63,741,751	63,742,649	898	1	7.643	13.321	12	24	1	1	1	COX8A	121	in gene	ActReg chr11 #1941	0	1
1942	11	63,753,542	63,754,355	813	2	11.16	12.12	19	19	1	1	2	COX8A, OTUB1	11869, 623	downstream, in gene	ActReg chr11 #1942	1	1
1943	11	63,775,722	63,776,419	697	1	5.682	9.682	10	15	1	0	2	OTUB1, MACROD1	22745, 157515	downstream, in gene	ActReg chr11 #1943	0	1
1944	11	63,952,537	63,953,381	844	1	7.63	11.704	10	20	1	1	1	STIP1	-628	upstream	ActReg chr11 #1944	0	1
1945	11	64,013,146	64,013,761	615	1	11.8	10.3	19	15	1	3	5	VEGFB, FKBP2, PPP1R14B, LOC100507590, PLCB3	11187, 5040, 960, -1158, -5542	downstream, downstream, in gene, upstream, upstream	ActReg chr11 #1945	1	0
1946	11	64,014,440	64,015,287	847	1	9.769	15.115	17	24	1	3	5	VEGFB, FKBP2, PPP1R14B, LOC100507590, PLCB3	12597, 6450, -450, 252, -4132	downstream, downstream, upstream, in gene, upstream	ActReg chr11 #1946	0	1
1947	11	64,036,778	64,037,853	1,075	1	9.879	12.333	15	20	1	0	2	PLCB3, BAD	18320, 14861	downstream, in gene	ActReg chr11 #1947	0	1
1948	11	64,068,084	64,068,870	786	1	7.16	11.24	10	17	1	2	3	KCNK4, C11orf20, ESRRA	9684, 614, -4567	downstream, in gene, upstream	ActReg chr11 #1948	0	1
1949	11	64,084,439	64,085,979	1,540	2	15.333	15.771	32	30	1	2	3	ESRRA, TRMT112, PRDX5	12165, -176, -360	downstream, upstream, upstream	ActReg chr11 #1949	1	1
1950	11	64,577,763	64,578,513	750	1	9.391	12.348	18	25	1	2	2	MAP4K2, MEN1	-7425, 628	upstream, in gene	ActReg chr11 #1950	0	1
1951	11	64,623,628	64,624,499	871	1	10.704	11.741	16	17	0	0	1	EHD1	22,128	in gene	ActReg chr11 #1951	0	1
1952	11	64,645,360	64,646,739	1,379	1	9.721	12.512	15	22	1	1	1	EHD1	142	in gene	ActReg chr11 #1952	0	1
1953	11	64,683,633	64,685,385	1,752	2	9.164	10.782	18	20	1	2	2	ATG2A, PPP2R5B	213, -7634	in gene, upstream	ActReg chr11 #1953	1	1
1954	11	64,691,113	64,692,536	1,423	2	21.023	27.546	49	66	1	2	3	ATG2A, PPP2R5B, GPHA2	-7102, -319, 11536	upstream, upstream, downstream	ActReg chr11 #1954	1	1
1955	11	64,745,029	64,745,610	581	2	9	10.833	18	17	0	1	2	C11orf55, BATF2	-5961, 19198	upstream, downstream	ActReg chr11 #1955	1	1
1956	11	64,780,997	64,782,417	1,420	2	11.909	12.068	17	21	1	1	1	ARL2	121	in gene	ActReg chr11 #1956	1	1
1957	11	64,794,488	64,795,622	1,134	2	37.111	46.444	92	120	1	1	2	ARL2, SNX15	13469, 145	downstream, in gene	ActReg chr11 #1957	1	1
1958	11	64,851,308	64,851,875	567	1	11.056	14.167	16	22	1	2	3	CDCA5, ZFPL1, LOC100130348	24, -103, 4912	in gene, upstream, downstream	ActReg chr11 #1958	0	1
1959	11	64,863,338	64,863,964	626	1	10.947	9.895	17	16	1	2	3	ZFPL1, LOC100130348, C11orf2	11957, -7148, -32	downstream, upstream, upstream	ActReg chr11 #1959	1	0
1960	11	64,884,255	64,885,752	1,497	1	8.681	12.298	16	18	1	2	6	C11orf2, TM7SF2, ZNHIT2, FAU, MRPL49, SYVN1	21320, 5662, 167, 4669, -4725, 17009	downstream, downstream, in gene, downstream, upstream, downstream	ActReg chr11 #1960	0	1
1961	11	64,889,207	64,890,196	989	1	10.258	13.323	14	25	1	3	5	TM7SF2, ZNHIT2, FAU, MRPL49, SYVN1	10360, -4531, -29, -27, 12302	downstream, upstream, upstream, upstream, downstream	ActReg chr11 #1961	0	1
1962	11	64,901,643	64,902,832	1,189	2	11.622	12.811	17	24	1	1	2	MRPL49, SYVN1	12509, -234	downstream, upstream	ActReg chr11 #1962	1	1
1963	11	65,028,822	65,029,584	762	1	7	11.708	10	19	1	1	1	POLA2	-229	upstream	ActReg chr11 #1963	0	1
1964	11	65,082,198	65,082,780	582	1	6	10.869	10	21	1	1	1	CDC42EP2	158	in gene	ActReg chr11 #1964	0	1
1965	11	65,121,402	65,122,087	685	1	7.909	11.454	13	16	1	1	2	DPF2, TIGD3	20398, -538	downstream, upstream	ActReg chr11 #1965	0	1
1966	11	65,149,053	65,150,779	1,726	1	9.63	12.574	16	20	0	2	2	SLC25A45, FRMD8	226, -4125	in gene, upstream	ActReg chr11 #1966	0	1
1967	11	65,153,578	65,154,730	1,152	2	10.694	14.25	25	30	1	2	2	SLC25A45, FRMD8	-4012, 113	upstream, in gene	ActReg chr11 #1967	1	1
1968	11	65,157,678	65,158,594	916	2	10.897	10	22	15	0	0	2	SLC25A45, FRMD8	-7994, 4095	upstream, in gene	ActReg chr11 #1968	1	1
1969	11	65,188,726	65,189,134	408	1	4.308	11.154	6	19	0	1	2	FRMD8, NEAT1	34889, -1339	downstream, upstream	ActReg chr11 #1969	0	1
1970	11	65,189,397	65,191,048	1,651	2	10.904	11.423	20	21	2	1	2	FRMD8, NEAT1	36181, -47	downstream, upstream	ActReg chr11 #1970	1	1
1971	11	65,194,157	65,194,967	810	1	10.92	4.28	15	6	0	0	1	NEAT1	4,293	downstream	ActReg chr11 #1971	1	0
1972	11	65,239,312	65,240,025	713	2	9.955	10.409	20	20	0	0	1	LOC100507645	27,583	in gene	ActReg chr11 #1972	1	1
1973	11	65,244,441	65,245,398	957	1	10.867	12.533	15	16	1	0	1	LOC100507645	22,332	in gene	ActReg chr11 #1973	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
1974	11	65,255,160	65,256,123	963	2	9.6	8.367	14	19	0	0	2	LOC100507645, MALAT1	11610, -9592	in gene, upstream	ActReg chr11 #1974	1	1
1975	11	65,258,884	65,259,675	791	1	12.667	10.667	20	16	0	1	2	LOC100507645, MALAT1	7972, -5954	in gene, upstream	ActReg chr11 #1975	1	0
1976	11	65,264,661	65,265,409	748	2	11.833	14.625	20	25	1	2	2	LOC100507645, MALAT1	2216, -198	in gene, upstream	ActReg chr11 #1976	1	1
1977	11	65,337,178	65,338,330	1,152	2	12	16.778	21	33	1	3	3	SSSCA1, FAM89B, EHBP1L1	-189, -2066, -5755	upstream, upstream, upstream	ActReg chr11 #1977	1	1
1978	11	65,382,301	65,383,257	956	2	20.967	21	60	56	1	2	2	MAP3K11, PCNXL3	-1059, -1004	upstream, upstream	ActReg chr11 #1978	1	1
1979	11	65,430,201	65,430,886	685	1	11.273	7.091	17	13	1	1	1	RELA	-100	upstream	ActReg chr11 #1979	1	0
1980	11	65,479,149	65,480,033	884	1	9.786	14.107	18	25	1	1	2	KAT5, RNASEH2C	102, 8818	in gene, downstream	ActReg chr11 #1980	0	1
1981	11	65,487,301	65,488,454	1,153	2	13.029	13.444	24	25	1	1	2	KAT5, RNASEH2C	8388, 532	downstream, in gene	ActReg chr11 #1981	1	1
1982	11	65,546,492	65,548,168	1,676	2	11.302	13.83	20	26	1	2	3	DKFZp761E198, OVOL1, LOC100507675	492, -7199, 11009	in gene, upstream, downstream	ActReg chr11 #1982	1	1
1983	11	65,600,962	65,602,220	1,258	1	9.667	14	27	28	1	1	1	SNX32	181	in gene	ActReg chr11 #1983	0	1
1984	11	65,624,239	65,626,135	1,896	2	11.881	14.237	27	29	1	2	4	SNX32, CFL1, MUS81, EFEMP2	23777, 617, 2685, 15153	downstream, in gene, upstream, downstream	ActReg chr11 #1984	1	1
1985	11	65,626,487	65,628,861	2,374	2	29.162	32.959	129	133	1	2	4	SNX32, CFL1, MUS81, EFEMP2	26264, -1870, -198, 12666	downstream, upstream, upstream, downstream	ActReg chr11 #1985	1	1
1986	11	65,655,240	65,657,108	1,868	2	11.483	12.966	22	27	1	2	4	CTSW, FIBP, CCDC85B, FOSL1	8890, -164, 1701, 11823	downstream, upstream, upstream, downstream	ActReg chr11 #1986	1	1
1987	11	65,657,943	65,659,380	1,437	2	11.822	13.467	21	23	1	2	4	CTSW, FIBP, CCDC85B, FOSL1	11377, -2651, 786, 9336	downstream, upstream, in gene, downstream	ActReg chr11 #1987	1	1
1988	11	65,666,913	65,668,226	1,313	1	8.244	13.878	14	25	1	1	2	CCDC85B, FOSL1	9694, 428	downstream, in gene	ActReg chr11 #1988	0	1
1989	11	65,670,479	65,671,294	815	1	11.52	10.16	18	14	0	1	1	FOSL1	-2,889	upstream	ActReg chr11 #1989	1	0
1990	11	65,682,289	65,683,780	1,491	2	12.489	11.745	29	21	0	1	2	C11orf68, DRAP1	3497, -3694	downstream, upstream	ActReg chr11 #1990	1	1
1991	11	65,686,409	65,687,412	1,003	2	32.871	35.194	106	113	1	2	2	C11orf68, DRAP1	-379, 182	upstream, in gene	ActReg chr11 #1991	1	1
1992	11	65,728,576	65,729,737	1,161	2	28.946	30.054	103	96	0	1	2	TSGA10IP, SART1	16041, -4	downstream, upstream	ActReg chr11 #1992	1	1
1993	11	65,769,219	65,770,224	1,005	2	14.323	16.516	30	27	1	2	3	EIF1AD, BANF1, CST6	-143, 171, -9741	upstream, in gene, upstream	ActReg chr11 #1993	1	1
1994	11	65,819,351	65,820,381	1,030	2	12.094	11.906	25	20	1	2	2	GAL3ST3, SF3B2	-3215, 50	upstream, in gene	ActReg chr11 #1994	1	1
1995	11	66,024,617	66,026,468	1,851	1	9.069	11.241	17	19	1	1	2	KLC2, RAB1B	777, -10514	in gene, upstream	ActReg chr11 #1995	0	1
1996	11	66,034,343	66,036,141	1,798	1	7.232	10.893	14	15	3	1	3	KLC2, RAB1B, CNIH2	10477, -814, -10454	in gene, upstream, upstream	ActReg chr11 #1996	0	1
1997	11	66,056,000	66,058,043	2,043	2	10.238	13.234	26	24	1	2	3	CNIH2, YIF1A, TMEM151A	11325, -383, -2352	downstream, upstream, upstream	ActReg chr11 #1997	1	1
1998	11	66,103,615	66,104,666	1,051	2	13.97	18.091	33	44	0	1	3	RIN1, BRMS1, B3GNT1	-140, 8442, 11021	upstream, downstream, downstream	ActReg chr11 #1998	1	1
1999	11	66,112,105	66,112,800	695	1	12.546	8.5	20	16	1	2	3	RIN1, BRMS1, B3GNT1	-8452, 130, 2709	upstream, in gene, downstream	ActReg chr11 #1999	1	0
2000	11	66,115,312	66,115,960	648	1	11.8	9.65	21	14	1	2	2	BRMS1, B3GNT1	-3054, -475	upstream, upstream	ActReg chr11 #2000	1	0
2001	11	66,138,420	66,139,368	948	1	8.667	12.1	14	17	1	1	1	SLC29A2	397	in gene	ActReg chr11 #2001	0	1
2002	11	66,176,031	66,176,655	624	1	10.4	7.85	16	18	1	1	1	LOC100505504	-322	upstream	ActReg chr11 #2002	1	0
2003	11	66,185,150	66,190,672	5,522	3	32.272	40.11	235	262	1	1	2	LOC100505504, NPAS4	11246, -564	downstream, upstream	ActReg chr11 #2003	1	1
2004	11	66,205,843	66,206,860	1,017	2	15.625	13.344	34	28	0	1	1	MRPL11	-41	upstream	ActReg chr11 #2004	1	1
2005	11	66,210,897	66,211,483	586	1	9.278	10.611	13	15	0	1	1	MRPL11	-4,880	upstream	ActReg chr11 #2005	0	1
2006	11	66,247,270	66,248,433	1,163	2	12.778	13.5	28	20	1	2	3	PELI3, LOC100505554, DPP3	13515, -145, -29	downstream, upstream, upstream	ActReg chr11 #2006	1	1
2007	11	66,529,460	66,530,312	852	1	7.63	12	11	18	1	0	1	C11orf80	17,679	in gene	ActReg chr11 #2007	0	1
2008	11	66,623,091	66,624,318	1,227	2	9.237	10.395	19	16	1	1	3	RCE1, PC, LRFN4	12821, 102143, -1172	downstream, in gene, upstream	ActReg chr11 #2008	1	1
2009	11	66,659,388	66,660,212	824	2	21.769	22.846	45	57	0	0	1	PC	66,047	in gene	ActReg chr11 #2009	1	1
2010	11	66,725,553	66,726,106	553	1	7.706	13.118	12	22	1	1	1	PC	18	in gene	ActReg chr11 #2010	0	1
2011	11	66,738,203	66,738,793	590	1	12.526	14.158	22	25	0	1	1	C11orf86	-4,256	upstream	ActReg chr11 #2011	0	1
2012	11	67,055,860	67,056,585	725	1	8.087	11.652	11	18	1	1	2	ADRBK1, ANKRD13D	22317, -540	downstream, upstream	ActReg chr11 #2012	0	1
2013	11	67,070,670	67,071,516	846	2	13.154	15.115	27	32	1	1	2	ANKRD13D, SSH3	14331, 174	downstream, in gene	ActReg chr11 #2013	1	1
2014	11	67,141,332	67,142,190	858	2	11.778	12.482	16	21	1	1	2	LOC100130987, CLCF1	56451, -113	in gene, upstream	ActReg chr11 #2014	1	1
2015	11	67,159,014	67,159,657	643	1	8.35	13.4	15	21	1	1	3	LOC100130987, RAD9A, PPP1CA	74025, -88, 10041	downstream, upstream, downstream	ActReg chr11 #2015	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2016	11	67,195,379	67,196,370	991	1	9.29	13.548	13	29	1	1	4	ATPGD1, RPS6KB2, PTPRCAP, CORO1B	12725, -61, 9279, 15389	downstream, upstream, downstream, downstream	ActReg chr11 #2016	0	1
2017	11	67,236,487	67,237,235	748	2	13.217	14	25	29	1	1	2	CABP4, TMEM134	14043, -130	downstream, upstream	ActReg chr11 #2017	1	1
2018	11	67,250,233	67,250,979	746	1	8.25	10.5	20	15	1	1	2	AIP, PITPNM1	101, 22237	in gene, downstream	ActReg chr11 #2018	0	1
2019	11	67,275,039	67,276,419	1,380	2	10.114	10.864	21	16	1	2	3	PITPNM1, CDK2AP2, CABP2	-2886, 373, 15170	upstream, in gene, downstream	ActReg chr11 #2019	1	1
2020	11	67,373,986	67,374,803	817	1	8.8	13.96	20	28	1	2	2	LOC100505621, NDUFV1	-217, 71	upstream, in gene	ActReg chr11 #2020	0	1
2021	11	67,723,209	67,723,558	349	1	3.727	9.364	6	13	1	1	1	LOC100132261	157	in gene	ActReg chr11 #2021	0	1
2022	11	67,777,522	67,778,153	631	1	8.65	11.9	12	22	0	2	2	UNC93B1, ALDH3B1	-6244, 1789	upstream, in gene	ActReg chr11 #2022	0	1
2023	11	67,795,266	67,796,037	771	1	10.333	11.875	21	20	0	1	2	ALDH3B1, NDUFS8	19603, -2433	in gene, upstream	ActReg chr11 #2023	0	1
2024	11	67,960,886	67,961,810	924	2	10.276	10.821	18	27	1	1	1	SUV420H1	-564	upstream	ActReg chr11 #2024	1	1
2025	11	68,039,133	68,039,999	866	1	8.852	11.333	14	20	1	1	1	C11orf24	-97	upstream	ActReg chr11 #2025	0	1
2026	11	68,426,544	68,427,115	571	1	7.5	12.111	11	20	0	0	0				ActReg chr11 #2026	0	1
2027	11	68,670,843	68,671,706	863	2	14.259	15.333	27	31	1	2	2	MRPL21, IGHMBP2	29, -45	in gene, upstream	ActReg chr11 #2027	1	1
2028	11	69,065,621	69,066,923	1,302	1	12.61	11.39	22	17	0	0	1	MYEOV	4,650	downstream	ActReg chr11 #2028	1	0
2029	11	69,068,788	69,069,953	1,165	1	16.622	14.297	30	22	0	0	1	MYEOV	7,748	downstream	ActReg chr11 #2029	1	0
2030	11	69,149,536	69,150,394	858	2	17.846	17.556	43	43	0	0	0				ActReg chr11 #2030	1	1
2031	11	69,167,337	69,167,980	643	1	10.9	8.55	22	15	0	0	0				ActReg chr11 #2031	1	0
2032	11	69,231,682	69,232,331	649	1	7.95	12.95	12	19	0	0	1	LOC100505834	-8,433	upstream	ActReg chr11 #2032	0	1
2033	11	69,489,696	69,490,353	657	1	13.952	13.952	28	28	1	1	1	ORAOV1	141	in gene	ActReg chr11 #2033	0	1
2034	11	70,005,738	70,006,753	1,015	2	9.906	10.062	16	15	0	0	1	ANO1	81,837	in gene	ActReg chr11 #2034	1	1
2035	11	70,079,363	70,080,184	821	2	14.44	10.76	26	20	0	0	0				ActReg chr11 #2035	1	1
2036	11	70,495,877	70,497,593	1,716	2	21.132	26.962	74	91	0	0	1	SHANK2	439,073	in gene	ActReg chr11 #2036	1	1
2037	11	71,072,758	71,074,085	1,327	1	10.881	11.905	17	19	0	0	0				ActReg chr11 #2037	0	1
2038	11	71,639,298	71,640,342	1,044	2	13.312	13.031	20	20	0	1	1	RNF121	52	in gene	ActReg chr11 #2038	1	1
2039	11	71,751,556	71,753,241	1,685	2	15.269	15.154	31	28	0	0	1	NUMA1	39,175	in gene	ActReg chr11 #2039	1	1
2040	11	71,791,646	71,792,292	646	1	6.81	10.809	9	15	1	2	3	NUMA1, MIR3165, LRTOMT	-396, -8621, 587	upstream, upstream, in gene	ActReg chr11 #2040	0	1
2041	11	71,933,932	71,934,697	765	2	12.333	11.083	25	24	1	1	2	FOLR2, INPPL1	6495, -1568	downstream, upstream	ActReg chr11 #2041	1	1
2042	11	72,145,004	72,145,999	995	2	10.194	12.258	22	21	1	1	1	CLPB	67	in gene	ActReg chr11 #2042	1	1
2043	11	72,387,805	72,388,541	736	1	9.696	14	14	28	0	1	2	PDE2A, ARAP1	-2679, 75261	upstream, downstream	ActReg chr11 #2043	0	1
2044	11	72,504,719	72,505,446	727	1	9.391	12.174	17	23	1	1	1	STARD10	-332	upstream	ActReg chr11 #2044	0	1
2045	11	72,524,747	72,526,206	1,459	2	12.956	13.444	28	23	1	1	1	ATG16L2	25	in gene	ActReg chr11 #2045	1	1
2046	11	73,087,805	73,088,508	703	1	9.545	12.818	15	21	1	1	2	ARHGEF17, RELT	68493, 751	downstream, in gene	ActReg chr11 #2046	0	1
2047	11	73,308,774	73,310,026	1,252	2	10.077	10.462	16	20	1	1	1	FAM168A	-172	upstream	ActReg chr11 #2047	1	1
2048	11	73,490,392	73,491,099	707	2	11.046	11.364	22	20	1	0	1	MRPL48	-8,172	upstream	ActReg chr11 #2048	1	1
2049	11	73,498,637	73,499,397	760	2	10.375	12.292	19	25	1	1	1	MRPL48	100	in gene	ActReg chr11 #2049	1	1
2050	11	73,587,411	73,588,484	1,073	1	8.853	11.412	14	17	1	2	2	CHCHD8, PAAF1	-57, -86	upstream, upstream	ActReg chr11 #2050	0	1
2051	11	73,748,228	73,748,883	655	1	8.4	12.3	13	24	0	0	1	C2CD3	133,509	in gene	ActReg chr11 #2051	0	1
2052	11	73,881,671	73,882,848	1,177	2	9.973	14.189	19	24	1	2	2	C2CD3, PPME1	-195, -109	upstream, upstream	ActReg chr11 #2052	1	1
2053	11	73,967,853	73,968,367	514	1	6.688	9.75	8	16	0	0	1	P4HA3	34,589	in gene	ActReg chr11 #2053	0	1
2054	11	74,109,586	74,110,330	744	1	12.522	10.696	23	19	1	1	1	PGM2L1	-456	upstream	ActReg chr11 #2054	1	0
2055	11	74,128,742	74,129,549	807	2	15.84	16.2	26	28	0	0	0				ActReg chr11 #2055	1	1
2056	11	74,204,219	74,204,981	762	2	11.125	10.625	19	19	1	2	2	LIPT2, LOC100287896	155, 115	in gene, in gene	ActReg chr11 #2056	1	1
2057	11	74,459,472	74,460,260	788	2	16.75	16.96	41	39	1	1	1	RNF169	-47	upstream	ActReg chr11 #2057	1	1
2058	11	74,465,570	74,466,132	562	1	11.529	6.235	15	9	0	0	1	RNF169	5,938	in gene	ActReg chr11 #2058	1	0
2059	11	74,560,574	74,561,341	767	1	9.042	12.375	12	18	0	0	2	RNF169, XRRA1	101044, 99275	downstream, in gene	ActReg chr11 #2059	0	1
2060	11	74,659,728	74,660,559	831	1	7.346	15	11	28	1	2	2	XRRA1, SPCS2	89, -149	in gene, upstream	ActReg chr11 #2060	0	1
2061	11	74,925,187	74,926,240	1,053	2	21.788	22.364	66	61	0	0	1	SLCO2B1	63,673	downstream	ActReg chr11 #2061	1	1
2062	11	74,944,543	74,945,554	1,011	2	14.156	17.219	32	40	0	1	1	LOC100507050	-6,374	upstream	ActReg chr11 #2062	1	1
2063	11	75,110,225	75,111,047	822	2	10.423	11.346	18	20	1	3	3	RPS3, SNORD15A, SNORD15B	74, -799, -4829	in gene, upstream, upstream	ActReg chr11 #2063	1	1
2064	11	75,259,661	75,260,359	698	1	10.227	12.318	16	18	0	0	0				ActReg chr11 #2064	0	1
2065	11	75,479,243	75,480,029	786	2	13.542	13.208	27	28	1	1	1	DGAT2	-142	upstream	ActReg chr11 #2065	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2066	11	75,525,360	75,526,590	1,230	1	8.895	11.342	13	20	2	2	2	LOC100506113, UVRAG	-133, -237	upstream, upstream	ActReg chr11 #2066	0	1
2067	11	75,864,137	75,865,036	899	1	7.464	11.179	14	19	0	0	1	UVRAG	338,374	downstream	ActReg chr11 #2067	0	1
2068	11	75,919,704	75,920,713	1,009	2	9.312	12.594	18	19	1	1	1	WNT11	-2,634	upstream	ActReg chr11 #2068	1	1
2069	11	75,946,215	75,947,566	1,351	2	11.786	12.905	22	19	1	0	0				ActReg chr11 #2069	1	1
2070	11	76,090,955	76,092,839	1,884	3	21.152	22.407	93	101	1	2	2	PRKRIR, LOC100506127	-17, -463	upstream, upstream	ActReg chr11 #2070	1	1
2071	11	76,155,303	76,156,302	999	1	9.677	12.677	20	19	1	1	1	C11orf30	-267	upstream	ActReg chr11 #2071	0	1
2072	11	76,288,435	76,289,060	625	1	6.9	10.85	9	17	0	0	0				ActReg chr11 #2072	0	1
2073	11	76,289,311	76,289,949	638	1	9.3	11.55	13	17	0	0	0				ActReg chr11 #2073	0	1
2074	11	76,411,300	76,412,245	945	1	7.828	10.483	15	16	0	0	0				ActReg chr11 #2074	0	1
2075	11	76,435,161	76,435,835	674	2	9.81	11.333	18	20	0	0	0				ActReg chr11 #2075	1	1
2076	11	76,784,208	76,784,998	790	1	6.64	12.2	11	18	0	0	1	CAPN5	6,611	in gene	ActReg chr11 #2076	0	1
2077	11	77,185,264	77,185,786	522	1	10.25	11.5	17	19	1	1	1	PAK1	-417	upstream	ActReg chr11 #2077	0	1
2078	11	77,300,288	77,300,847	559	1	5.667	10.333	9	16	1	1	1	AQP11	-113	upstream	ActReg chr11 #2078	0	1
2079	11	77,348,437	77,349,217	780	2	10.36	11.76	17	22	1	1	1	CLNS1A	24	in gene	ActReg chr11 #2079	1	1
2080	11	77,530,307	77,530,924	617	2	9.158	9.316	16	16	0	2	2	RSF1, C11orf67	1265, -1593	in gene, upstream	ActReg chr11 #2080	1	1
2081	11	77,705,424	77,706,503	1,079	2	11.177	11.765	18	25	1	1	1	INTS4	-246	upstream	ActReg chr11 #2081	1	1
2082	11	77,850,405	77,851,082	677	1	10.714	12.429	18	22	1	1	1	ALG8	-44	upstream	ActReg chr11 #2082	0	1
2083	11	77,899,254	77,900,767	1,513	2	15.106	18.979	47	67	1	2	2	KCTD21, USP35	-346, 152	upstream, in gene	ActReg chr11 #2083	1	1
2084	11	78,285,109	78,286,135	1,026	1	9.312	11.688	14	17	1	1	1	NARS2	287	in gene	ActReg chr11 #2084	0	1
2085	11	82,782,629	82,783,329	700	1	10.954	13.091	15	23	0	2	3	RAB30, LOC100506233, LOC100506259	-95, -140, 7945	upstream, upstream, downstream	ActReg chr11 #2085	0	1
2086	11	82,904,459	82,906,036	1,577	2	9.388	11.388	18	17	1	2	3	PCF11, LOC100506282, ANKRD42	37110, -543, -44	downstream, upstream, upstream	ActReg chr11 #2086	1	1
2087	11	82,996,584	82,997,942	1,358	2	21.357	25.286	58	76	1	1	1	CCDC90B	114	in gene	ActReg chr11 #2087	1	1
2088	11	84,425,217	84,425,760	543	1	12.706	7.529	24	14	0	0	1	DLG2	912,826	in gene	ActReg chr11 #2088	1	0
2089	11	85,339,127	85,339,853	726	1	12.565	7.522	19	13	1	2	2	DLG2, TMEM126B	-1176, -132	upstream, upstream	ActReg chr11 #2089	1	0
2090	11	85,358,669	85,359,251	582	1	10.889	13.722	15	20	1	1	2	TMEM126A, CREBZF	-3, 17222	upstream, downstream	ActReg chr11 #2090	0	1
2091	11	85,429,892	85,430,643	751	2	11.739	14.435	24	26	0	0	1	SYTL2	91,911	in gene	ActReg chr11 #2091	1	1
2092	11	85,565,531	85,566,073	542	1	7.118	11.353	10	22	1	2	2	LOC100506308, CCDC83	184, -342	in gene, upstream	ActReg chr11 #2092	0	1
2093	11	85,601,047	85,601,573	526	1	10.412	7.353	17	11	0	0	1	CCDC83	35,166	in gene	ActReg chr11 #2093	1	0
2094	11	85,779,906	85,780,341	435	1	13.308	8.308	19	11	1	1	1	PICALM	-15	upstream	ActReg chr11 #2094	1	0
2095	11	85,828,012	85,828,550	538	1	10.118	7.059	17	10	0	0	0				ActReg chr11 #2095	1	0
2096	11	85,885,017	85,886,059	1,042	1	9.818	11	15	17	0	0	0				ActReg chr11 #2096	0	1
2097	11	85,955,304	85,956,290	986	2	11.516	16.581	17	29	2	1	1	EED	-18	upstream	ActReg chr11 #2097	1	1
2098	11	86,012,900	86,013,679	779	1	14.625	11.125	25	20	0	1	1	C11orf73	36	in gene	ActReg chr11 #2098	1	0
2099	11	86,170,714	86,171,431	717	1	5	10.826	8	15	0	0	1	ME3	212,606	in gene	ActReg chr11 #2099	0	1
2100	11	86,343,597	86,344,501	904	2	14.464	11.179	29	17	0	0	1	ME3	39,629	in gene	ActReg chr11 #2100	1	1
2101	11	86,382,680	86,383,773	1,093	2	7.824	11.059	15	19	1	1	1	ME3	452	in gene	ActReg chr11 #2101	1	1
2102	11	87,489,120	87,489,813	693	2	8.182	10.909	15	22	0	0	0				ActReg chr11 #2102	1	1
2103	11	88,070,565	88,071,248	683	1	9.667	11.381	15	20	1	1	1	CTSC	35	in gene	ActReg chr11 #2103	0	1
2104	11	88,428,695	88,429,616	921	1	9.286	14.69	15	29	0	0	1	GRM5	367,661	in gene	ActReg chr11 #2104	0	1
2105	11	88,437,499	88,438,135	636	1	10.8	10.15	19	15	0	0	1	GRM5	358,999	in gene	ActReg chr11 #2105	1	0
2106	11	88,442,635	88,443,172	537	1	9.118	9.294	15	16	0	0	1	GRM5	353,913	in gene	ActReg chr11 #2106	0	1
2107	11	88,901,348	88,902,071	723	1	11.954	8.318	19	13	0	0	1	TYR	-9,331	upstream	ActReg chr11 #2107	1	0
2108	11	89,955,906	89,956,851	945	1	7.31	11.966	13	16	1	1	1	CHORDC1	154	in gene	ActReg chr11 #2108	0	1
2109	11	92,930,530	92,931,525	995	1	8.226	11.871	13	19	1	1	1	SLC36A4	68	in gene	ActReg chr11 #2109	0	1
2110	11	93,394,455	93,395,458	1,003	1	8.031	11.469	15	20	1	1	1	KIAA1731	140	in gene	ActReg chr11 #2110	0	1
2111	11	93,474,537	93,475,028	491	1	8.6	10.8	10	16	1	3	9	SNORD6, SNORA1, SNORA8, SNORD5, SNORA18, MIR1304, SNORA40, TAF1D, C11orf54	-10043, -9483, -9117, -8316, -8019, -7852, -6380, -79, -11	upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr11 #2111	0	1
2112	11	93,517,369	93,518,279	910	1	8.172	11.862	13	17	1	1	1	MED17	419	in gene	ActReg chr11 #2112	0	1
2113	11	94,501,079	94,501,911	832	2	16.885	16.385	34	35	1	1	1	AMOTL1	-13	upstream	ActReg chr11 #2113	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2114	11	94,523,567	94,524,283	716	1	11.318	10.182	14	16	0	0	1	AMOTL1	22,417	in gene	ActReg chr11 #2114	1	0
2115	11	94,535,551	94,536,407	856	1	13.444	11.667	23	17	0	0	1	AMOTL1	34,471	in gene	ActReg chr11 #2115	1	0
2116	11	94,612,692	94,613,955	1,263	2	19.7	19.225	74	69	0	0	1	AMOTL1	111,815	downstream	ActReg chr11 #2116	1	1
2117	11	94,800,040	94,801,034	994	1	8.968	10.71	14	19	1	1	1	SFRS2B	481	in gene	ActReg chr11 #2117	0	1
2118	11	94,866,128	94,866,635	507	1	5.438	11.188	8	17	0	0	1	ENDOD1	43,407	downstream	ActReg chr11 #2118	0	1
2119	11	94,883,846	94,884,973	1,127	1	12.8	7.114	23	11	1	0	0				ActReg chr11 #2119	1	0
2120	11	95,289,619	95,290,166	547	1	10.765	6.562	19	12	0	0	0				ActReg chr11 #2120	1	0
2121	11	95,449,484	95,449,930	446	1	10.071	5.571	15	7	0	0	0				ActReg chr11 #2121	1	0
2122	11	95,522,313	95,523,856	1,543	1	9.417	15.083	18	26	1	2	2	FAM76B, CEP57	-130, -558	upstream, upstream	ActReg chr11 #2122	0	1
2123	11	95,656,837	95,657,639	802	2	12.8	14.72	22	33	1	1	1	MTMR2	133	in gene	ActReg chr11 #2123	1	1
2124	11	95,747,130	95,747,734	604	1	10.263	7.316	14	11	0	0	1	MAML2	328,912	in gene	ActReg chr11 #2124	1	0
2125	11	95,855,819	95,856,343	524	1	8.062	11.438	12	16	0	0	1	MAML2	220,263	in gene	ActReg chr11 #2125	0	1
2126	11	95,889,246	95,889,932	686	1	10.091	12.318	17	25	0	0	1	MAML2	186,755	in gene	ActReg chr11 #2126	0	1
2127	11	96,074,358	96,075,193	835	1	11.731	9.077	18	16	0	2	2	MAML2, MIR1260B	1569, 173	in gene, downstream	ActReg chr11 #2127	1	0
2128	11	101,312,422	101,312,871	449	1	5.571	10.714	9	14	0	0	1	TRPC6	142,013	downstream	ActReg chr11 #2128	0	1
2129	11	101,980,725	101,981,405	680	1	7.19	11.571	12	16	1	1	1	YAP1	-127	upstream	ActReg chr11 #2129	0	1
2130	11	102,115,503	102,116,135	632	1	10.7	9.15	19	15	0	0	0				ActReg chr11 #2130	1	0
2131	11	102,217,554	102,218,323	769	1	8.417	12.375	13	19	1	1	2	BIRC3, BIRC2	29744, -28	downstream, upstream	ActReg chr11 #2131	0	1
2132	11	102,323,014	102,323,699	685	2	10.333	9.05	16	16	1	2	2	TMEM123, LOC727869	419, -294	in gene, upstream	ActReg chr11 #2132	1	1
2133	11	102,463,532	102,464,167	635	1	9.45	7.4	16	9	0	0	1	MMP20	32,214	in gene	ActReg chr11 #2133	1	0
2134	11	102,714,050	102,714,718	668	1	10.5	5.4	19	8	0	1	2	LOC100288077, MMP3	59977, -42	downstream, upstream	ActReg chr11 #2134	1	0
2135	11	102,979,807	102,980,480	673	1	10.773	11.182	13	17	0	1	1	DYNC2H1	-17	upstream	ActReg chr11 #2135	0	1
2136	11	103,763,145	103,764,086	941	2	16.207	21.035	36	58	0	0	0				ActReg chr11 #2136	1	1
2137	11	105,228,083	105,228,765	682	1	9.19	11.714	11	19	0	0	0				ActReg chr11 #2137	0	1
2138	11	105,543,652	105,544,384	732	2	11.478	9.217	25	21	0	0	1	GRIA4	63,218	in gene	ActReg chr11 #2138	1	1
2139	11	105,590,008	105,590,549	541	1	4.941	11.118	7	18	0	0	1	GRIA4	109,478	in gene	ActReg chr11 #2139	0	1
2140	11	105,892,528	105,893,491	963	1	8.867	11.233	14	18	1	1	1	KIAA1826	-55	upstream	ActReg chr11 #2140	0	1
2141	11	106,889,305	106,890,331	1,026	2	13.562	22.781	22	44	1	1	1	GUCY1A2	-647	upstream	ActReg chr11 #2141	1	1
2142	11	107,433,504	107,434,099	595	1	11.21	6.842	20	9	0	1	1	ALKBH8	2,660	in gene	ActReg chr11 #2142	1	0
2143	11	107,435,873	107,436,699	826	1	8.44	11.88	13	18	0	1	1	ALKBH8	175	in gene	ActReg chr11 #2143	0	1
2144	11	107,570,022	107,570,807	785	1	7.174	12	13	16	0	0	1	SLN	12,373	downstream	ActReg chr11 #2144	0	1
2145	11	107,799,158	107,799,587	429	1	5.143	10.429	8	14	1	1	1	RAB39	95	in gene	ActReg chr11 #2145	0	1
2146	11	108,093,646	108,094,189	543	1	5.882	9.412	9	15	1	2	2	NPAT, ATM	-552, 358	upstream, in gene	ActReg chr11 #2146	0	1
2147	11	109,512,152	109,512,786	634	2	10.35	11.25	24	22	0	0	0				ActReg chr11 #2147	1	1
2148	11	109,730,008	109,730,611	603	1	7.158	10.632	12	23	0	0	0				ActReg chr11 #2148	0	1
2149	11	111,317,245	111,317,714	469	1	9.6	3.667	17	5	0	0	1	LOC644277	18,256	in gene	ActReg chr11 #2149	1	0
2150	11	111,749,300	111,750,186	886	2	8.214	9.75	18	15	1	3	3	ALG9, FDXACB1, C11orf1	-7438, 410, -205	upstream, in gene, upstream	ActReg chr11 #2150	1	1
2151	11	112,604,626	112,605,444	818	2	13.115	12.077	27	28	0	0	0				ActReg chr11 #2151	1	1
2152	11	112,831,795	112,832,358	563	1	4.944	9.944	8	16	1	1	1	NCAM1	81	in gene	ActReg chr11 #2152	0	1
2153	11	113,185,252	113,185,835	583	1	6.333	13.333	11	21	1	1	1	TTC12	292	in gene	ActReg chr11 #2153	0	1
2154	11	113,316,923	113,317,940	1,017	1	10.781	10.781	18	18	0	0	2	DRD2, MIR4301	28570, 3379	in gene, downstream	ActReg chr11 #2154	0	1
2155	11	113,318,312	113,319,468	1,156	2	13.056	11.722	23	19	0	1	2	DRD2, MIR4301	27111, 1920	in gene, downstream	ActReg chr11 #2155	1	1
2156	11	113,344,372	113,345,907	1,535	2	21.229	25.375	59	74	1	1	1	DRD2	862	in gene	ActReg chr11 #2156	1	1
2157	11	113,535,251	113,536,289	1,038	1	5.879	11.485	14	18	0	0	0				ActReg chr11 #2157	0	1
2158	11	113,545,797	113,546,476	679	1	5.238	11	9	18	0	0	0				ActReg chr11 #2158	0	1
2159	11	113,644,126	113,644,898	772	2	13.48	11.24	32	29	1	2	2	ZW10, CLDN25	-87, -6006	upstream, upstream	ActReg chr11 #2159	1	1
2160	11	113,861,703	113,863,019	1,316	2	11.195	15.39	32	39	0	0	1	HTR3A	16,564	downstream	ActReg chr11 #2160	1	1
2161	11	114,165,676	114,166,204	528	1	5.875	9.875	9	14	0	1	2	NNMT, LOC100506941	-595, 2922	upstream, downstream	ActReg chr11 #2161	0	1
2162	11	114,219,263	114,219,708	445	1	4.769	9.5	6	16	0	0	0				ActReg chr11 #2162	0	1
2163	11	114,270,508	114,271,960	1,452	1	8.444	12.089	14	21	1	2	2	C11orf71, RBM7	-95, -150	upstream, upstream	ActReg chr11 #2163	0	1
2164	11	114,309,834	114,311,070	1,236	2	12.447	15.71	22	32	1	1	1	REXO2	344	in gene	ActReg chr11 #2164	1	1
2165	11	115,093,113	115,093,528	415	1	10.615	6.615	14	9	0	0	1	CADM1	281,921	in gene	ActReg chr11 #2165	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2166	11	115,171,837	115,172,255	418	1	4.231	10.462	6	14	0	0	1	CADM1	203,195	in gene	ActReg chr11 #2166	0	1
2167	11	115,371,294	115,371,758	464	1	10.333	4.6	12	7	0	0	1	CADM1	3,715	in gene	ActReg chr11 #2167	1	0
2168	11	115,373,578	115,374,138	560	1	9.529	10.235	13	19	1	1	1	CADM1	1,383	in gene	ActReg chr11 #2168	0	1
2169	11	115,374,703	115,375,650	947	2	10.533	11.367	20	17	1	1	1	CADM1	65	in gene	ActReg chr11 #2169	1	1
2170	11	115,587,426	115,588,239	813	1	7.12	11.84	13	19	0	0	0				ActReg chr11 #2170	0	1
2171	11	115,812,112	115,812,855	743	1	12.478	10.826	17	16	0	0	0				ActReg chr11 #2171	1	0
2172	11	116,433,483	116,434,776	1,293	1	12.175	12	18	18	0	0	0				ActReg chr11 #2172	1	0
2173	11	116,476,175	116,477,038	863	2	12.407	16.518	26	32	0	0	0				ActReg chr11 #2173	1	1
2174	11	116,897,488	116,898,131	643	1	11.6	8.2	21	13	0	0	1	SIK3	71,184	in gene	ActReg chr11 #2174	1	0
2175	11	116,943,180	116,943,829	649	1	11.35	7	16	10	0	0	1	SIK3	25,489	in gene	ActReg chr11 #2175	1	0
2176	11	117,048,859	117,049,907	1,048	2	20.151	25.485	61	69	1	1	2	PAFAH1B2, SIDT2	34383, -556	downstream, upstream	ActReg chr11 #2176	1	1
2177	11	117,102,319	117,103,588	1,269	2	18.375	17.075	53	54	2	2	2	PCSK7, RNF214	-142, -451	upstream, upstream	ActReg chr11 #2177	1	1
2178	11	117,186,810	117,187,478	668	2	11.667	13.048	21	20	1	1	1	BACE1	-172	upstream	ActReg chr11 #2178	1	1
2179	11	117,196,282	117,199,112	830	1	5.962	11.039	10	18	1	1	2	CEP164, LOC100129201	126, 8650	in gene, downstream	ActReg chr11 #2179	0	1
2180	11	117,467,649	117,468,560	911	2	9.593	10.607	17	16	0	0	1	DSCAML1	199,872	in gene	ActReg chr11 #2180	1	1
2181	11	118,187,170	118,187,940	770	1	9.667	12.75	16	19	0	0	1	CD3E	12,260	downstream	ActReg chr11 #2181	0	1
2182	11	118,229,880	118,230,604	724	1	6.913	14.565	11	30	1	1	2	CD3G, UBE4A	15183, -60	downstream, upstream	ActReg chr11 #2182	0	1
2183	11	118,271,624	118,272,912	1,288	2	10.825	11.4	17	16	1	1	2	UBE4A, ATP5L	41966, 164	downstream, in gene	ActReg chr11 #2183	1	1
2184	11	118,305,241	118,305,892	651	1	8.667	12.143	12	21	1	2	2	MGC13053, MLL	355, -1639	in gene, upstream	ActReg chr11 #2184	0	1
2185	11	118,305,925	118,307,354	1,429	2	14.068	14.227	32	28	1	2	2	MGC13053, MLL	-718, -566	upstream, upstream	ActReg chr11 #2185	1	1
2186	11	118,478,663	118,479,745	1,082	2	13.029	11.941	26	17	1	1	2	ARCN1, PHLDB1	36102, 1991	downstream, in gene	ActReg chr11 #2186	1	1
2187	11	118,560,644	118,561,339	695	1	12.619	7.333	21	13	0	0	0				ActReg chr11 #2187	1	0
2188	11	118,661,843	118,662,382	539	1	5.941	12.177	10	18	1	1	1	DDX6	-140	upstream	ActReg chr11 #2188	0	1
2189	11	118,790,225	118,791,056	831	1	10.962	11.808	19	22	0	0	1	BCL9L	-9,027	upstream	ActReg chr11 #2189	0	1
2190	11	118,796,542	118,797,107	565	1	14.889	10.778	23	18	1	0	0				ActReg chr11 #2190	1	0
2191	11	118,798,663	118,801,141	2,478	2	11.61	13.454	25	24	0	0	0				ActReg chr11 #2191	1	1
2192	11	118,809,116	118,810,060	944	2	8.533	10.9	15	18	0	0	0				ActReg chr11 #2192	1	1
2193	11	118,868,260	118,869,215	955	1	8.483	11.448	14	17	1	1	1	CCDC84	-115	upstream	ActReg chr11 #2193	0	1
2194	11	118,938,055	118,938,970	915	1	9.321	13.536	16	22	1	1	1	VPS11	19	in gene	ActReg chr11 #2194	0	1
2195	11	118,955,238	118,955,899	661	1	12.6	11	18	18	1	1	3	VPS11, HMBS, H2AFX	17075, -19, 10609	downstream, upstream, downstream	ActReg chr11 #2195	1	0
2196	11	118,965,612	118,966,705	1,093	2	13.471	13.471	26	22	1	1	3	HMBS, H2AFX, DPAGT1	10571, 19, 6627	downstream, in gene, downstream	ActReg chr11 #2196	1	1
2197	11	118,972,062	118,973,525	1,463	2	11.457	14.283	19	25	1	3	4	HMBS, H2AFX, DPAGT1, C2CD2L	17206, -6616, -8, -5300	downstream, upstream, upstream, upstream	ActReg chr11 #2197	1	1
2198	11	119,089,169	119,089,668	499	2	9.938	9.4	15	17	0	0	1	CBL	12,428	in gene	ActReg chr11 #2198	1	1
2199	11	119,191,609	119,192,252	643	1	11.65	10.1	17	16	1	1	1	MCAM	-4,090	upstream	ActReg chr11 #2199	1	0
2200	11	119,204,752	119,205,438	686	1	9.333	11.381	15	17	1	1	3	RNF26, MFRP, C1QTNF5	-142, 12288, 12288	upstream, downstream, downstream	ActReg chr11 #2200	0	1
2201	11	119,363,629	119,365,515	1,886	2	14.649	21.305	51	60	0	0	1	LOC100499227	112,084	in gene	ActReg chr11 #2201	1	1
2202	11	119,389,214	119,390,099	885	2	14.107	14.929	27	35	0	0	0				ActReg chr11 #2202	1	1
2203	11	119,438,653	119,439,891	1,238	1	5.359	10.154	11	20	0	0	0				ActReg chr11 #2203	0	1
2204	11	119,599,799	119,600,534	735	1	8	15.043	14	24	1	1	2	PVRL1, LOC100507077	-731, -10255	upstream, upstream	ActReg chr11 #2204	0	1
2205	11	119,644,469	119,645,867	1,398	2	13.454	14.25	30	32	0	0	0				ActReg chr11 #2205	1	1
2206	11	120,081,279	120,082,458	1,179	2	10	11.027	24	20	1	1	1	OAF	121	in gene	ActReg chr11 #2206	1	1
2207	11	120,088,292	120,089,317	1,025	1	11.5	13.188	21	19	0	0	1	OAF	7,057	in gene	ActReg chr11 #2207	0	1
2208	11	120,195,534	120,196,557	1,023	2	18.25	21.469	37	45	1	1	2	POU2F3, TMEM136	85094, 29	downstream, in gene	ActReg chr11 #2208	1	1
2209	11	120,302,691	120,303,322	631	1	10.368	4.222	18	8	0	0	1	ARHGEF12	95,060	in gene	ActReg chr11 #2209	1	0
2210	11	120,953,263	120,953,787	524	1	7.125	12.312	10	20	0	0	1	TBCEL	58,722	in gene	ActReg chr11 #2210	0	1
2211	11	121,964,421	121,964,742	321	1	6.9	12.1	11	16	0	0	3	LOC100507145, LOC399959, MIR125B1	328998, 109189, 5971	in gene, in gene, downstream	ActReg chr11 #2211	0	1
2212	11	122,012,348	122,012,831	483	1	10.267	5.867	17	8	0	0	3	LOC100507145, LOC399959, MIRLET7A2	280990, 61181, 4712	in gene, in gene, downstream	ActReg chr11 #2212	1	0
2213	11	122,073,680	122,074,192	512	1	7.875	10.625	14	15	0	1	2	LOC100507145, LOC399959	219643, -166	in gene, upstream	ActReg chr11 #2213	0	1
2214	11	122,144,184	122,144,798	614	1	10.474	9.053	19	17	0	0	1	LOC100507145	149,088	in gene	ActReg chr11 #2214	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2215	11	122,451,855	122,452,412	557	1	10.118	12.294	16	21	0	0	0				ActReg chr11 #2215	0	1
2216	11	122,526,700	122,527,607	907	1	8.071	10.857	13	14	1	1	1	UBASH3B	755	in gene	ActReg chr11 #2216	0	1
2217	11	122,574,552	122,575,156	604	1	7.684	10.947	12	21	0	0	1	UBASH3B	48,456	in gene	ActReg chr11 #2217	0	1
2218	11	122,851,618	122,853,041	1,423	2	13.454	14.5	29	30	1	1	1	BSX	50	in gene	ActReg chr11 #2218	1	1
2219	11	123,059,378	123,059,894	516	1	11.562	9.25	16	14	0	0	1	ASAM	6,371	in gene	ActReg chr11 #2219	1	0
2220	11	123,524,188	123,525,411	1,223	2	11.359	14.82	28	27	1	1	1	SCN3B	516	in gene	ActReg chr11 #2220	1	1
2221	11	123,611,819	123,612,761	942	2	9.069	10.483	18	18	1	1	1	ZNF202	73	in gene	ActReg chr11 #2221	1	1
2222	11	123,940,000	123,940,614	614	1	9.95	5.15	16	9	0	0	0				ActReg chr11 #2222	1	0
2223	11	124,041,615	124,042,085	470	1	10.467	8.8	14	13	0	0	0				ActReg chr11 #2223	1	0
2224	11	124,471,935	124,472,627	692	2	14.136	13.954	28	34	0	0	1	PANX3	-9,172	upstream	ActReg chr11 #2224	1	1
2225	11	124,492,330	124,493,082	752	2	11.304	11.043	16	18	1	1	2	PANX3, TBRG1	11253, -36	downstream, upstream	ActReg chr11 #2225	1	1
2226	11	124,669,441	124,669,932	491	1	6.667	9.933	13	17	1	2	3	C11orf61, UNQ565, LOC100507283	613, -9721, 638	in gene, upstream, upstream	ActReg chr11 #2226	0	1
2227	11	124,670,076	124,670,598	522	1	8.941	11.706	12	16	1	2	2	C11orf61, LOC100507283	-38, 13	upstream, in gene	ActReg chr11 #2227	0	1
2228	11	124,823,661	124,824,489	828	2	10.115	9.231	16	17	1	1	1	CCDC15	58	in gene	ActReg chr11 #2228	1	1
2229	11	124,940,529	124,941,379	850	1	8.667	12.37	14	18	0	0	1	SLC37A2	7,941	in gene	ActReg chr11 #2229	0	1
2230	11	124,945,413	124,946,288	875	1	6.333	12.407	10	17	0	0	1	SLC37A2	12,837	in gene	ActReg chr11 #2230	0	1
2231	11	125,104,692	125,105,781	1,089	1	7.706	10.471	14	15	0	0	1	PKNOX2	70,677	in gene	ActReg chr11 #2231	0	1
2232	11	125,132,856	125,134,170	1,314	2	9.78	12.488	19	18	0	0	1	PKNOX2	98,954	in gene	ActReg chr11 #2232	1	1
2233	11	125,462,263	125,463,703	1,440	2	10.024	12.044	17	28	1	1	2	EI24, STT3A	23685, 244	downstream, in gene	ActReg chr11 #2233	1	1
2234	11	125,495,216	125,496,087	871	1	11.111	14.37	16	23	1	1	2	STT3A, CHEK1	32912, 615	downstream, in gene	ActReg chr11 #2234	0	1
2235	11	125,932,609	125,933,302	693	2	16.952	13.381	36	27	1	1	1	CDON	232	in gene	ActReg chr11 #2235	1	1
2236	11	126,080,929	126,082,033	1,104	1	8.294	14.353	15	25	1	2	2	RPUSD4, FAM118B	106, -138	in gene, upstream	ActReg chr11 #2236	0	1
2237	11	126,138,488	126,139,369	881	2	9.893	12.893	17	24	1	2	3	FAM118B, SRPR, FOXRED1	57309, -51, 127	downstream, upstream, upstream	ActReg chr11 #2237	1	1
2238	11	126,173,551	126,174,340	789	1	14.68	8.4	23	15	1	1	2	TIRAP, DCPS	20963, 298	downstream, in gene	ActReg chr11 #2238	1	0
2239	11	126,223,227	126,224,116	889	1	10.393	7.286	18	13	0	2	3	DCPS, FLJ39051, ST3GAL4	50024, 1811, -2425	downstream, in gene, upstream	ActReg chr11 #2239	1	0
2240	11	126,413,372	126,416,657	3,285	4	18.126	21.087	63	68	0	0	1	KIRREL3	455,752	in gene	ActReg chr11 #2240	1	1
2241	11	126,430,742	126,432,174	1,432	2	14.578	17.644	32	30	0	0	1	KIRREL3	439,308	in gene	ActReg chr11 #2241	1	1
2242	11	126,462,510	126,463,633	1,123	1	9.514	11.257	16	15	0	0	1	KIRREL3	407,695	in gene	ActReg chr11 #2242	0	1
2243	11	126,588,019	126,588,617	598	1	12.947	11.579	24	17	0	0	1	KIRREL3	282,448	in gene	ActReg chr11 #2243	1	0
2244	11	126,660,474	126,660,976	502	1	5.75	11.688	15	19	0	0	1	KIRREL3	210,041	in gene	ActReg chr11 #2244	0	1
2245	11	126,838,664	126,839,677	1,013	1	6.806	12.355	11	18	0	0	1	KIRREL3	31,596	in gene	ActReg chr11 #2245	0	1
2246	11	126,905,749	126,906,654	905	1	9.536	13.179	17	20	0	0	0				ActReg chr11 #2246	0	1
2247	11	126,968,258	126,969,079	821	2	12	10.56	20	19	0	0	0				ActReg chr11 #2247	1	1
2248	11	127,909,254	127,910,049	795	2	10.16	8.64	18	20	0	0	0				ActReg chr11 #2248	1	1
2249	11	127,931,221	127,931,672	451	1	7.5	10.929	10	13	0	0	0				ActReg chr11 #2249	0	1
2250	11	128,079,980	128,080,815	835	1	12.923	7.038	21	9	0	0	0				ActReg chr11 #2250	1	0
2251	11	128,158,210	128,159,422	1,212	3	11.324	12.486	21	22	0	0	0				ActReg chr11 #2251	1	1
2252	11	128,234,761	128,235,523	762	2	16.792	16.625	38	31	0	0	0				ActReg chr11 #2252	1	1
2253	11	128,391,916	128,393,058	1,142	1	8.333	11.528	14	21	1	0	1	ETS1	64,966	in gene	ActReg chr11 #2253	0	1
2254	11	129,013,112	129,013,748	636	1	10.9	8.25	23	19	0	0	1	RICS	48,663	in gene	ActReg chr11 #2254	1	0
2255	11	129,321,195	129,321,798	603	1	9.526	12.105	16	20	0	0	1	BARX2	75,615	in gene	ActReg chr11 #2255	0	1
2256	11	129,399,999	129,400,919	920	1	6.483	10.241	13	15	0	0	0				ActReg chr11 #2256	0	1
2257	11	129,508,974	129,509,670	696	1	7.273	12.227	13	18	0	0	0				ActReg chr11 #2257	0	1
2258	11	129,512,787	129,513,751	964	1	9.667	11.367	15	18	0	0	0				ActReg chr11 #2258	0	1
2259	11	129,872,152	129,873,121	969	1	11.355	9.097	20	19	1	2	2	PRDM10, NCRNA00167	94, 117	in gene, in gene	ActReg chr11 #2259	1	0
2260	11	130,453,676	130,454,270	594	1	8.944	11.278	12	16	0	0	0				ActReg chr11 #2260	0	1
2261	11	130,500,864	130,501,478	614	1	10.45	6.9	19	13	0	0	0				ActReg chr11 #2261	1	0
2262	11	130,607,527	130,608,232	705	1	8.545	12.773	12	17	0	0	0				ActReg chr11 #2262	0	1
2263	11	130,717,531	130,718,074	543	1	11.118	7.647	22	14	0	0	1	LOC100507431	14,200	in gene	ActReg chr11 #2263	1	0
2264	11	130,785,929	130,786,813	884	2	12	12.296	20	23	1	1	1	SNX19	11	in gene	ActReg chr11 #2264	1	1
2265	11	131,934,180	131,935,508	1,328	2	11.829	12.463	18	22	0	0	1	NTM	694,473	in gene	ActReg chr11 #2265	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2266	11	132,046,765	132,047,953	1,188	2	8.676	12.838	27	26	0	0	1	NTM	806,988	in gene	ActReg chr11 #2266	1	1
2267	11	132,187,969	132,189,024	1,055	2	18.151	25.091	49	65	0	0	1	NTM	948,125	in gene	ActReg chr11 #2267	1	1
2268	11	132,783,761	132,784,936	1,175	1	6.278	12.243	12	21	0	0	2	OPCML, LOC100128095	618055, 257377	in gene, in gene	ActReg chr11 #2268	0	1
2269	11	133,067,202	133,067,961	759	2	11.609	14.043	24	32	0	0	2	OPCML, LOC100128095	334822, 540610	in gene, in gene	ActReg chr11 #2269	1	1
2270	11	133,213,938	133,214,414	476	1	9.867	10.067	15	16	0	0	2	OPCML, LOC100128095	188227, 687205	in gene, in gene	ActReg chr11 #2270	1	0
2271	11	133,804,322	133,805,287	965	1	9.7	14.067	21	24	0	0	1	IGSF9B	22,076	in gene	ActReg chr11 #2271	0	1
2272	11	133,906,892	133,908,020	1,128	1	8.286	10.829	13	20	1	0	1	LOC100128239	5,289	in gene	ActReg chr11 #2272	0	1
2273	11	134,093,461	134,094,890	1,429	1	9.422	11.622	17	17	1	2	2	NCAPD3, VPS26B	251, -386	in gene, upstream	ActReg chr11 #2273	0	1
2274	11	134,122,996	134,123,721	725	2	14.348	12.13	23	22	2	2	3	VPS26B, THYN1, ACAD8	28797, -96, -76	downstream, upstream, upstream	ActReg chr11 #2274	1	1
2275	11	134,288,159	134,288,990	831	2	9.04	12.346	15	27	0	1	1	B3GAT1	-6,762	upstream	ActReg chr11 #2275	1	1
2276	11	134,346,158	134,346,905	747	2	11.143	12.304	23	23	0	0	1	LOC283177	40,155	in gene	ActReg chr11 #2276	1	1
2277	11	134,818,898	134,819,638	740	2	10.261	16.391	17	32	0	0	0				ActReg chr11 #2277	1	1
2278	11	134,897,243	134,897,840	597	1	6.105	11.105	10	20	0	0	0				ActReg chr11 #2278	0	1
2279	12	498,329	499,176	847	1	8.778	12.037	13	21	1	2	2	KDM5A, CCDC77	-132, 236	upstream, in gene	ActReg chr12 #2279	0	1
2280	12	678,839	679,977	1,138	1	13.056	9.444	20	15	1	0	2	B4GALNT3, NINJ2	109865, 93347	downstream, in gene	ActReg chr12 #2280	1	0
2281	12	741,081	741,879	798	1	10.32	4.64	14	9	0	1	2	NINJ2, LOC100049716	31275, 1423	in gene, in gene	ActReg chr12 #2281	1	0
2282	12	861,256	861,910	654	1	12	9.1	26	15	1	1	1	WNK1	-506	upstream	ActReg chr12 #2282	1	0
2283	12	862,306	863,254	948	1	10.414	8	16	16	1	1	1	WNK1	691	in gene	ActReg chr12 #2283	1	0
2284	12	1,058,260	1,059,357	1,097	1	9.176	12.412	18	18	1	1	1	RAD52	55	in gene	ActReg chr12 #2284	0	1
2285	12	1,325,403	1,325,785	382	1	10.833	2.833	18	5	0	0	1	ERC1	225,190	in gene	ActReg chr12 #2285	1	0
2286	12	1,701,877	1,702,613	736	1	11.826	9.957	17	14	1	1	1	FBXL14	1,086	in gene	ActReg chr12 #2286	1	0
2287	12	1,714,224	1,715,377	1,153	2	10.771	10.75	16	17	0	0	0				ActReg chr12 #2287	1	1
2288	12	1,939,938	1,940,823	885	1	10.333	18.963	20	36	0	0	2	CACNA2D4, LRTM2	87490, 10947	in gene, in gene	ActReg chr12 #2288	0	1
2289	12	2,113,041	2,114,118	1,077	2	16	20.677	42	48	1	1	1	DCP1B	98	in gene	ActReg chr12 #2289	1	1
2290	12	2,238,123	2,238,724	601	1	7.211	10.947	12	16	0	0	1	CACNA1C	76,007	in gene	ActReg chr12 #2290	0	1
2291	12	2,861,457	2,862,938	1,481	2	26.065	25.087	90	92	1	0	1	LOC283440	18,638	downstream	ActReg chr12 #2291	1	1
2292	12	2,999,458	3,000,420	962	1	8.333	11.967	15	22	1	1	2	C12orf32, TULP3	13574, -94	downstream, upstream	ActReg chr12 #2292	0	1
2293	12	3,067,477	3,068,156	679	1	7.952	12	18	18	1	1	1	TEAD4	-662	upstream	ActReg chr12 #2293	0	1
2294	12	3,413,440	3,414,395	955	1	9.533	12.633	15	18	0	1	1	LOC100128253	-4,527	upstream	ActReg chr12 #2294	0	1
2295	12	3,441,211	3,441,845	634	1	10.45	10.75	18	18	0	0	0				ActReg chr12 #2295	0	1
2296	12	3,601,116	3,602,012	896	1	7.962	14.036	15	22	1	2	2	LOC100129223, PRMT8	421, 1139	in gene, in gene	ActReg chr12 #2296	0	1
2297	12	4,647,344	4,648,260	916	2	10.724	9.897	16	14	1	2	2	C12orf4, RAD51AP1	-165, -148	upstream, upstream	ActReg chr12 #2297	1	1
2298	12	4,713,756	4,714,447	691	1	7.182	10.318	12	16	0	0	1	DYRK4	14,857	in gene	ActReg chr12 #2298	0	1
2299	12	6,202,055	6,202,876	821	1	10.4	13.44	14	21	0	0	1	VWF	31,371	in gene	ActReg chr12 #2299	0	1
2300	12	6,276,811	6,277,546	735	1	12.783	14.174	19	27	0	0	0				ActReg chr12 #2300	0	1
2301	12	6,338,515	6,339,319	804	1	8.48	11.84	13	19	0	0	1	CD9	29,362	in gene	ActReg chr12 #2301	0	1
2302	12	6,492,699	6,493,859	1,160	1	8.135	12.568	16	20	1	2	2	SCNN1A, LTBR	-6756, -78	upstream, upstream	ActReg chr12 #2302	0	1
2303	12	6,641,481	6,644,162	2,681	2	10.595	14.083	17	26	1	1	3	NCAPD2, GAPDH, IFFO1	39523, -836, 22428	downstream, upstream, downstream	ActReg chr12 #2303	1	1
2304	12	6,646,231	6,647,406	1,175	1	8.703	10.784	15	20	0	0	3	NCAPD2, GAPDH, IFFO1	43520, 3161, 18431	downstream, in gene, downstream	ActReg chr12 #2304	0	1
2305	12	6,772,001	6,772,910	909	2	10.071	9.679	19	19	1	1	2	ING4, ZNF384	-147, 26221	upstream, downstream	ActReg chr12 #2305	1	1
2306	12	6,798,106	6,799,131	1,025	2	11.969	12.312	20	18	1	1	2	ZNF384, C12orf53	58, 11194	in gene, downstream	ActReg chr12 #2306	1	1
2307	12	6,832,856	6,833,729	873	2	14.821	13.786	33	30	1	1	1	COPS7A	142	in gene	ActReg chr12 #2307	1	1
2308	12	6,861,906	6,862,814	908	1	9.5	12.821	17	18	2	1	1	MLF2	276	in gene	ActReg chr12 #2308	0	1
2309	12	6,937,805	6,938,967	1,162	2	12.306	11.306	20	16	1	1	3	CD4, GPR162, LEPREL2	39748, 7423, 814	downstream, downstream, in gene	ActReg chr12 #2309	1	1
2310	12	6,961,166	6,962,100	934	2	15.552	19.517	35	46	1	2	3	GNB3, CDCA3, USP5	12258, -1177, 348	downstream, upstream, in gene	ActReg chr12 #2310	1	1
2311	12	6,982,271	6,983,326	1,055	1	10.636	13.182	17	21	1	1	3	USP5, TPI1, SPSB2	21513, 6214, -277	downstream, downstream, upstream	ActReg chr12 #2311	0	1
2312	12	6,999,704	7,000,568	864	2	10.296	8.926	17	17	1	0	0				ActReg chr12 #2312	1	1
2313	12	7,046,587	7,047,775	1,188	2	28.162	31.189	106	111	1	2	4	ATN1, RNU7, C12orf57, PTPN6	13555, -5798, -6022, -8559	in gene, upstream, upstream, upstream	ActReg chr12 #2313	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2314	12	7,053,030	7,054,096	1,066	2	11.606	11.727	24	20	1	3	4	ATN1, RNU7, C12orf57, PTPN6	19937, 584, 360, -2177	downstream, downstream, in gene, upstream	ActReg chr12 #2314	1	1
2315	12	7,070,230	7,071,771	1,541	2	10.875	11.771	25	18	0	3	7	PTPN6, LOC100507644, MIR200C, MIR141, PHB2, SCARNA12, EMG1	15260, -1409, -1862, -2260, 8916, 5769, -8944	downstream, upstream, upstream, upstream, downstream, downstream, upstream	ActReg chr12 #2315	1	1
2316	12	7,079,091	7,080,354	1,263	2	11.9	12.9	21	22	1	3	8	PTPN6, LOC100507644, MIR200C, MIR141, PHB2, SCARNA12, EMG1, LPCAT3	23982, 7313, 6860, 6462, 194, -2953, -222, 46120	downstream, downstream, downstream, downstream, in gene, upstream, upstream, downstream	ActReg chr12 #2316	1	1
2317	12	7,341,024	7,342,952	1,928	2	11.82	14.148	35	39	2	1	1	PEX5	229	in gene	ActReg chr12 #2317	1	1
2318	12	7,521,836	7,522,391	555	1	7.059	11.588	11	17	0	0	1	CD163L1	74,636	in gene	ActReg chr12 #2318	0	1
2319	12	8,167,349	8,168,057	708	1	8.409	14.546	17	31	0	0	0				ActReg chr12 #2319	0	1
2320	12	8,179,275	8,180,109	834	2	11.308	14.692	24	33	0	1	1	FOXJ2	-5,667	upstream	ActReg chr12 #2320	1	1
2321	12	8,184,798	8,185,256	458	1	7.4	12.667	12	24	1	1	1	FOXJ2	-332	upstream	ActReg chr12 #2321	0	1
2322	12	8,234,200	8,235,283	1,083	2	10.323	16.265	24	25	1	1	1	NECAP1	-66	upstream	ActReg chr12 #2322	1	1
2323	12	9,090,547	9,090,970	423	1	3	8.769	5	12	0	0	2	PHC1, M6PR	23442, 11494	in gene, downstream	ActReg chr12 #2323	0	1
2324	12	9,102,026	9,103,034	1,008	2	9.032	12.774	21	19	1	1	2	PHC1, M6PR	35214, -278	downstream, upstream	ActReg chr12 #2324	1	1
2325	12	9,216,677	9,217,386	709	1	11.773	7.773	19	11	1	2	3	C12orf33, LOC144571, A2M	635, -742, 51527	in gene, upstream, downstream	ActReg chr12 #2325	1	0
2326	12	9,492,927	9,493,465	538	1	11.294	8.765	19	15	0	0	0				ActReg chr12 #2326	1	0
2327	12	9,516,779	9,517,738	959	1	9.167	11.033	14	15	0	0	0				ActReg chr12 #2327	0	1
2328	12	10,765,842	10,766,572	730	2	10.652	14.478	23	29	1	1	2	MAGOHB, STYK1	-24, 60684	upstream, downstream	ActReg chr12 #2328	1	1
2329	12	10,874,406	10,875,562	1,156	2	12.139	9.611	26	16	1	1	1	CSDA	969	in gene	ActReg chr12 #2329	1	1
2330	12	10,902,425	10,902,931	506	1	11.25	9.5	15	12	0	1	1	LOC100506226	-155	upstream	ActReg chr12 #2330	1	0
2331	12	11,652,723	11,654,647	1,924	2	20.617	26.483	91	116	1	0	0				ActReg chr12 #2331	1	1
2332	12	11,801,500	11,802,412	912	2	10	11.138	17	19	1	1	1	ETV6	-832	upstream	ActReg chr12 #2332	1	1
2333	12	11,872,496	11,873,145	649	1	8.15	11.3	13	16	0	0	1	ETV6	70,032	in gene	ActReg chr12 #2333	0	1
2334	12	12,161,679	12,163,916	2,237	2	9.343	11.143	22	18	0	0	0				ActReg chr12 #2334	1	1
2335	12	12,419,623	12,420,540	917	2	10.464	14.107	20	25	1	1	1	LRP6	-270	upstream	ActReg chr12 #2335	1	1
2336	12	12,509,704	12,510,443	739	1	14.043	9.565	26	18	1	3	3	MANSC1, LOH12CR2, LOH12CR1	-6904, -72, 53	upstream, upstream, in gene	ActReg chr12 #2336	1	0
2337	12	12,551,228	12,551,868	640	1	7.5	11.85	12	17	0	0	1	LOH12CR1	41,528	in gene	ActReg chr12 #2337	0	1
2338	12	12,764,394	12,765,051	657	1	11.4	9.25	21	14	1	1	1	CREBL2	-109	upstream	ActReg chr12 #2338	1	0
2339	12	12,836,848	12,838,272	1,424	2	13.333	12.222	21	27	0	0	1	GPR19	11,561	in gene	ActReg chr12 #2339	1	1
2340	12	12,869,834	12,870,647	813	2	10.56	10.04	18	24	1	1	2	CDKN1B, APOLD1	-62, -8611	upstream, upstream	ActReg chr12 #2340	1	1
2341	12	12,877,808	12,879,089	1,281	2	8.3	11.4	19	22	1	1	2	CDKN1B, APOLD1	8146, -403	downstream, upstream	ActReg chr12 #2341	1	1
2342	12	12,879,448	12,879,999	551	1	10.235	6.059	17	11	0	1	2	CDKN1B, APOLD1	9421, 872	downstream, in gene	ActReg chr12 #2342	1	0
2343	12	13,034,373	13,034,960	587	1	8.889	10.944	14	19	0	0	1	GPRC5A	-9,290	upstream	ActReg chr12 #2343	0	1
2344	12	13,043,437	13,044,779	1,342	2	11.214	11.905	16	18	1	1	1	GPRC5A	152	in gene	ActReg chr12 #2344	1	1
2345	12	13,196,945	13,197,987	1,042	2	11.242	12.576	20	24	1	1	1	KIAA1467	151	in gene	ActReg chr12 #2345	1	1
2346	12	13,254,378	13,255,456	1,078	1	7.882	13.677	19	26	1	1	1	GSG1	1,702	in gene	ActReg chr12 #2346	0	1
2347	12	13,880,319	13,881,127	808	2	7.962	10.385	16	16	0	0	1	GRIN2B	252,299	in gene	ActReg chr12 #2347	1	1
2348	12	14,410,373	14,411,297	924	2	16.759	13.69	37	35	0	0	0				ActReg chr12 #2348	1	1
2349	12	14,923,537	14,924,282	745	2	11.043	11.478	22	17	1	2	2	HIST4H4, H2AFJ	156, -3361	in gene, upstream	ActReg chr12 #2349	1	1
2350	12	15,431,842	15,432,697	855	1	8.577	13.577	16	22	0	0	0				ActReg chr12 #2350	0	1
2351	12	15,841,130	15,841,755	625	1	7.947	12.21	11	20	0	0	1	EPS8	101,068	in gene	ActReg chr12 #2351	0	1
2352	12	15,854,092	15,854,676	584	1	6.833	10.389	10	15	0	0	1	EPS8	88,126	in gene	ActReg chr12 #2352	0	1
2353	12	15,910,735	15,911,246	511	1	9.125	10.375	16	20	0	0	1	EPS8	31,520	in gene	ActReg chr12 #2353	0	1
2354	12	15,942,041	15,942,945	904	1	8	12.241	14	16	1	1	1	EPS8	17	in gene	ActReg chr12 #2354	0	1
2355	12	16,034,643	16,035,996	1,353	2	11.357	11.786	20	18	1	1	1	STRAP	31	in gene	ActReg chr12 #2355	1	1
2356	12	18,876,576	18,877,146	570	1	6.278	9.444	11	17	0	0	1	PLCZ1	14,057	in gene	ActReg chr12 #2356	0	1
2357	12	19,002,009	19,002,535	526	1	9.353	4.824	15	9	0	0	0				ActReg chr12 #2357	1	0
2358	12	19,592,653	19,593,268	615	1	5.263	11.421	7	17	1	1	1	AEBP2	352	in gene	ActReg chr12 #2358	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2359	12	19,864,828	19,865,540	712	2	13.609	15.391	27	30	0	0	0				ActReg chr12 #2359	1	1
2360	12	19,948,176	19,948,622	446	1	4.25	9.5	7	13	0	0	0				ActReg chr12 #2360	0	1
2361	12	20,365,409	20,366,212	803	2	13.04	9.6	19	23	0	0	0				ActReg chr12 #2361	1	1
2362	12	22,488,594	22,489,049	455	1	9.286	7.429	16	11	1	1	1	ST8SIA1	-1,173	upstream	ActReg chr12 #2362	1	0
2363	12	22,589,807	22,590,593	786	1	8.24	12.04	14	20	0	0	0				ActReg chr12 #2363	0	1
2364	12	22,696,739	22,697,965	1,226	2	13.947	16.658	28	35	1	1	1	KIAA0528	100	in gene	ActReg chr12 #2364	1	1
2365	12	22,777,896	22,778,965	1,069	1	9.091	11.576	15	16	1	1	1	ETNK1	354	in gene	ActReg chr12 #2365	0	1
2366	12	22,875,058	22,875,654	596	1	4.421	9.737	9	17	0	0	0				ActReg chr12 #2366	0	1
2367	12	24,103,310	24,104,241	931	1	7.241	12.207	16	20	0	0	1	SOX5	611,605	in gene	ActReg chr12 #2367	0	1
2368	12	24,909,561	24,910,265	704	1	8.5	10.364	13	17	0	0	0				ActReg chr12 #2368	0	1
2369	12	25,403,566	25,404,636	1,070	2	12.333	11.697	22	22	0	1	1	KRAS	-247	upstream	ActReg chr12 #2369	1	1
2370	12	25,610,907	25,611,642	735	2	10.043	10.826	21	17	0	0	0				ActReg chr12 #2370	1	1
2371	12	25,619,721	25,620,362	641	1	8.85	10.6	12	18	0	0	1	IFLTD1	181,447	downstream	ActReg chr12 #2371	0	1
2372	12	26,163,137	26,164,077	940	1	10.966	6.069	18	9	0	1	2	RASSF8, LOC100506529	36919, -1104	in gene, upstream	ActReg chr12 #2372	1	0
2373	12	26,279,329	26,279,797	468	1	10.286	11.714	14	15	1	1	1	BHLHE41	-1,560	upstream	ActReg chr12 #2373	0	1
2374	12	26,427,427	26,428,179	752	1	9.261	11.348	18	19	0	0	0				ActReg chr12 #2374	0	1
2375	12	26,470,953	26,471,658	705	2	11.273	11.364	25	17	0	0	0				ActReg chr12 #2375	1	1
2376	12	26,844,345	26,845,000	655	1	11	8.905	21	16	0	0	1	ITPR2	141,459	in gene	ActReg chr12 #2376	1	0
2377	12	26,984,808	26,985,947	1,139	1	7.088	11	13	16	1	1	1	ITPR2	754	in gene	ActReg chr12 #2377	0	1
2378	12	27,175,353	27,175,940	587	1	6.158	10.21	10	17	1	1	2	TM7SF3, MED21	-8307, 163	upstream, in gene	ActReg chr12 #2378	0	1
2379	12	27,396,615	27,397,445	830	1	7.731	12.192	13	26	1	1	1	STK38L	-48	upstream	ActReg chr12 #2379	0	1
2380	12	27,397,472	27,397,944	472	1	4.133	10.933	5	17	1	1	1	STK38L	630	in gene	ActReg chr12 #2380	0	1
2381	12	27,863,403	27,864,222	819	2	14.52	12.72	28	25	1	1	1	MRPS35	106	in gene	ActReg chr12 #2381	1	1
2382	12	28,342,778	28,344,163	1,385	2	12.046	14.091	18	29	1	0	0				ActReg chr12 #2382	1	1
2383	12	28,756,084	28,756,483	399	1	6.077	11.538	9	18	0	0	0				ActReg chr12 #2383	0	1
2384	12	28,912,156	28,912,790	634	1	10.4	11.25	19	17	0	0	0				ActReg chr12 #2384	0	1
2385	12	29,265,153	29,265,753	600	1	5.167	10.5	7	15	0	0	0				ActReg chr12 #2385	0	1
2386	12	29,793,607	29,794,463	856	2	11.846	11.269	18	21	0	0	1	TMTC1	143,657	in gene	ActReg chr12 #2386	1	1
2387	12	29,894,372	29,895,034	662	2	9.55	10.8	18	21	0	0	1	TMTC1	42,989	in gene	ActReg chr12 #2387	1	1
2388	12	30,179,645	30,180,105	460	1	9.933	6.667	15	10	0	0	0				ActReg chr12 #2388	1	0
2389	12	30,948,402	30,949,450	1,048	1	9.97	14	17	22	1	1	1	LOC100287314	949	in gene	ActReg chr12 #2389	0	1
2390	12	30,949,826	30,950,330	504	1	6.8	9.933	8	16	1	1	1	LOC100287314	2,101	in gene	ActReg chr12 #2390	0	1
2391	12	31,079,688	31,080,469	781	1	5.542	12.042	10	18	1	1	1	TSPAN11	240	in gene	ActReg chr12 #2391	0	1
2392	12	31,477,476	31,478,509	1,033	2	10.688	11.344	15	14	1	2	2	FAM60A, FLJ13224	1167, 742	in gene, in gene	ActReg chr12 #2392	1	1
2393	12	31,478,656	31,479,292	636	1	8.75	11.5	12	17	1	2	2	FAM60A, FLJ13224	185, 1724	in gene, downstream	ActReg chr12 #2393	0	1
2394	12	31,811,765	31,812,903	1,138	2	22.222	23.333	50	51	0	0	1	C12orf72	12,240	in gene	ActReg chr12 #2394	1	1
2395	12	31,881,817	31,882,609	792	1	11.52	15.88	19	23	1	1	1	AMN1	-105	upstream	ActReg chr12 #2395	0	1
2396	12	31,902,009	31,902,542	533	1	11.118	8.353	18	13	0	0	0				ActReg chr12 #2396	1	0
2397	12	32,111,935	32,112,619	684	2	10.286	12.364	17	22	1	1	1	C12orf35	-76	upstream	ActReg chr12 #2397	1	1
2398	12	32,204,263	32,204,997	734	2	10.304	10.739	21	17	0	0	0				ActReg chr12 #2398	1	1
2399	12	32,242,433	32,242,999	566	1	9.824	11.412	13	21	0	0	0				ActReg chr12 #2399	0	1
2400	12	32,259,508	32,260,448	940	2	10.5	11.2	19	18	1	1	1	BICD1	-207	upstream	ActReg chr12 #2400	1	1
2401	12	32,552,203	32,553,010	807	1	8.56	13.16	14	21	1	0	0				ActReg chr12 #2401	0	1
2402	12	32,831,849	32,832,944	1,095	2	11.559	13.647	19	20	1	1	1	DNM1L	259	in gene	ActReg chr12 #2402	1	1
2403	12	32,908,082	32,909,347	1,265	1	13.625	8.425	21	14	1	1	2	DNM1L, YARS2	76577, 160	downstream, in gene	ActReg chr12 #2403	1	0
2404	12	34,175,205	34,175,657	452	1	7.786	13.429	14	19	1	1	1	ALG10	215	in gene	ActReg chr12 #2404	0	1
2405	12	38,710,197	38,710,809	612	2	9.105	11.474	18	22	1	1	1	ALG10B	-54	upstream	ActReg chr12 #2405	1	1
2406	12	38,778,357	38,779,123	766	2	13.917	9.5	25	14	0	0	0				ActReg chr12 #2406	1	1
2407	12	39,298,948	39,300,170	1,222	2	11.158	11.947	19	20	1	1	1	CPNE8	-139	upstream	ActReg chr12 #2407	1	1
2408	12	39,835,972	39,837,383	1,411	1	7.318	11.727	14	17	1	1	1	KIF21A	515	in gene	ActReg chr12 #2408	0	1
2409	12	40,410,648	40,411,233	585	1	9.316	12.21	12	24	0	0	1	SLC2A13	88,721	in gene	ActReg chr12 #2409	0	1
2410	12	42,538,265	42,538,779	514	1	7.688	11.688	12	17	1	1	1	GXYLT1	151	in gene	ActReg chr12 #2410	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2411	12	42,630,979	42,631,479	500	1	9.6	7.571	17	13	1	1	1	YAF2	925	in gene	ActReg chr12 #2411	1	0
2412	12	42,982,632	42,983,584	952	2	15.467	18.7	30	35	1	1	1	PRICKLE1	464	in gene	ActReg chr12 #2412	1	1
2413	12	43,253,350	43,253,972	622	1	3.632	10.526	7	16	0	0	0				ActReg chr12 #2413	0	1
2414	12	43,315,578	43,316,173	595	1	11.526	8.947	17	15	0	0	0				ActReg chr12 #2414	1	0
2415	12	44,152,370	44,152,915	545	1	7.294	10.882	12	18	1	2	2	PUS7L, IRAK4	-46, -105	upstream, upstream	ActReg chr12 #2415	0	1
2416	12	44,363,557	44,364,156	599	1	9.556	10.278	14	18	0	0	1	TMEM117	133,894	in gene	ActReg chr12 #2416	0	1
2417	12	45,270,021	45,271,149	1,128	1	7.871	12.429	12	18	1	0	1	NELL2	37,126	in gene	ActReg chr12 #2417	0	1
2418	12	45,609,368	45,610,062	694	2	14	10.409	26	18	1	2	2	PLEKHA9, ANO6	74, -55	in gene, upstream	ActReg chr12 #2418	1	1
2419	12	45,610,078	45,610,859	781	1	11.36	6.6	16	9	1	2	2	PLEKHA9, ANO6	-679, 698	upstream, in gene	ActReg chr12 #2419	1	0
2420	12	45,809,034	45,809,828	794	2	16.48	12.16	36	28	0	0	1	ANO6	199,661	in gene	ActReg chr12 #2420	1	1
2421	12	45,832,666	45,833,258	592	1	7.789	11.895	13	20	0	0	1	ANO6	223,192	in gene	ActReg chr12 #2421	0	1
2422	12	46,031,397	46,031,867	470	1	10.643	5.429	14	7	0	0	0				ActReg chr12 #2422	1	0
2423	12	46,121,088	46,121,810	722	1	10.043	14.696	20	29	1	2	2	LOC400027, ARID2	255, -2171	in gene, upstream	ActReg chr12 #2423	0	1
2424	12	46,122,418	46,122,999	581	1	9.944	10.167	16	18	1	2	2	LOC400027, ARID2	-1004, -912	upstream, upstream	ActReg chr12 #2424	0	1
2425	12	46,333,479	46,333,930	451	1	7.214	10.071	11	15	0	0	1	SFRS2IP	50,697	in gene	ActReg chr12 #2425	0	1
2426	12	46,383,501	46,384,968	1,467	2	13.478	10.891	27	23	1	1	1	SFRS2IP	167	in gene	ActReg chr12 #2426	1	1
2427	12	46,385,362	46,386,092	730	1	12.174	8.957	23	14	1	1	1	SFRS2IP	-1,326	upstream	ActReg chr12 #2427	1	0
2428	12	46,662,255	46,663,271	1,016	1	11.719	13.75	19	23	1	1	1	SLC38A1	445	in gene	ActReg chr12 #2428	0	1
2429	12	46,765,730	46,766,710	980	1	5.933	10.867	9	18	1	1	1	SLC38A2	425	in gene	ActReg chr12 #2429	0	1
2430	12	46,777,240	46,778,139	899	2	13.679	14.643	23	29	1	1	1	LOC100288798	-3,841	upstream	ActReg chr12 #2430	1	1
2431	12	46,917,738	46,918,388	650	1	9	13.2	14	20	0	0	1	LOC100288798	136,533	in gene	ActReg chr12 #2431	0	1
2432	12	46,943,360	46,944,031	671	2	11.191	11.143	20	21	0	0	1	LOC100288798	162,165	in gene	ActReg chr12 #2432	1	1
2433	12	47,479,489	47,479,896	407	1	6.917	11.167	12	15	0	1	1	AMIGO2	-5,958	upstream	ActReg chr12 #2433	0	1
2434	12	48,099,282	48,100,005	723	1	9.696	12.391	16	21	1	1	2	RPAP3, P11	201, 19712	in gene, downstream	ActReg chr12 #2434	0	1
2435	12	48,357,019	48,357,785	766	1	6.417	13.5	10	25	1	1	2	TMEM106C, COL2A1	72, 40883	in gene, downstream	ActReg chr12 #2435	0	1
2436	12	48,499,740	48,500,504	764	1	9.458	11.083	19	19	1	2	2	SENP1, PFKM	-481, 466	upstream, in gene	ActReg chr12 #2436	0	1
2437	12	48,591,514	48,592,363	849	1	8.407	13.185	13	18	1	1	2	DKFZP779L1853, OR10AD1	-208, 5137	upstream, downstream	ActReg chr12 #2437	0	1
2438	12	49,075,415	49,076,260	845	2	10.815	11.778	16	19	1	1	2	C12orf41, LOC144438	198, 10392	in gene, downstream	ActReg chr12 #2438	1	1
2439	12	49,110,100	49,111,327	1,227	1	9.553	12.842	18	19	1	1	2	CCNT1, LOC255411	68, -10505	in gene, upstream	ActReg chr12 #2439	0	1
2440	12	49,245,469	49,246,549	1,080	2	11.735	14.647	25	25	1	1	2	DDX23, RND1	-52, 13644	upstream, downstream	ActReg chr12 #2440	1	1
2441	12	49,297,576	49,298,262	686	2	11.857	11.667	22	23	0	1	1	CCDC65	26	in gene	ActReg chr12 #2441	1	1
2442	12	49,350,899	49,351,723	824	2	12.654	13.462	21	22	1	1	2	ARF3, WNT10B	-59, 14330	upstream, downstream	ActReg chr12 #2442	1	1
2443	12	49,453,954	49,455,258	1,294	2	14.575	17.475	37	35	1	1	2	MLL2, RHEBL1	-5504, 9164	upstream, downstream	ActReg chr12 #2443	1	1
2444	12	49,485,609	49,486,393	784	1	5.083	14.167	9	20	1	1	2	DHH, LMBR1L	2601, 18679	in gene, downstream	ActReg chr12 #2444	0	1
2445	12	49,504,200	49,504,940	740	1	8.478	11.783	15	18	1	1	2	LMBR1L, LOC100288366	110, -9587	in gene, upstream	ActReg chr12 #2445	0	1
2446	12	49,523,934	49,524,736	802	1	11.115	8.385	16	12	1	1	2	LOC100288366, TUBA1B	10178, 969	in gene, in gene	ActReg chr12 #2446	1	0
2447	12	49,627,989	49,628,616	627	1	11.65	8.35	20	14	1	0	1	LOC100293962	30,237	in gene	ActReg chr12 #2447	1	0
2448	12	49,658,305	49,659,691	1,386	2	9.721	11.861	17	19	1	2	2	LOC100293962, TUBA1C	-459, 133	upstream, in gene	ActReg chr12 #2448	1	1
2449	12	49,716,686	49,717,443	757	1	6	11.417	12	17	1	1	2	TROAP, C1QL4	93, 13907	in gene, downstream	ActReg chr12 #2449	0	1
2450	12	49,740,614	49,741,618	1,004	1	9.548	12	14	19	1	1	2	C1QL4, DNAJC22	-10145, 75	upstream, in gene	ActReg chr12 #2450	0	1
2451	12	49,961,468	49,962,129	661	1	6.81	11.095	11	16	1	1	2	KCNH3, MCRS1	28858, 113	downstream, in gene	ActReg chr12 #2451	0	1
2452	12	50,134,820	50,135,604	784	1	11.125	13.125	17	23	1	1	1	TMBIM6	-81	upstream	ActReg chr12 #2452	0	1
2453	12	50,236,031	50,237,262	1,231	2	10.744	10.154	17	21	1	1	2	LOC100286844, BCDIN3D	14320, 266	downstream, in gene	ActReg chr12 #2453	1	1
2454	12	50,360,951	50,361,664	713	1	12.957	11.87	20	16	1	1	3	AQP2, AQP5, AQP6	16783, 6028, -5313	downstream, downstream, upstream	ActReg chr12 #2454	1	0
2455	12	50,450,490	50,451,167	677	1	5.476	11.952	11	18	1	1	1	ACCN2	-659	upstream	ActReg chr12 #2455	0	1
2456	12	50,898,427	50,899,078	651	1	11.857	11.809	16	15	1	1	1	DIP2B	-16	upstream	ActReg chr12 #2456	1	0
2457	12	51,441,409	51,442,499	1,090	2	11.618	12.147	25	22	1	1	1	LETMD1	-130	upstream	ActReg chr12 #2457	1	1
2458	12	51,476,919	51,477,742	823	1	11.923	8.808	21	14	1	1	2	CSRNP2, TFCP2	3, 89596	in gene, downstream	ActReg chr12 #2458	1	0
2459	12	51,566,590	51,567,388	798	1	12.92	11.4	21	18	1	1	1	TFCP2	-63	upstream	ActReg chr12 #2459	1	0
2460	12	51,664,359	51,665,138	779	1	9.667	10.667	16	16	1	1	2	SMAGP, BIN2	-546, 53190	upstream, downstream	ActReg chr12 #2460	0	1
2461	12	51,818,455	51,819,058	603	1	10.947	10.21	20	19	1	1	1	SLC4A8	162	in gene	ActReg chr12 #2461	1	0
2462	12	51,986,536	51,987,689	1,153	2	9.778	13.361	18	31	0	1	1	SCN8A	2,092	in gene	ActReg chr12 #2462	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2463	12	52,444,823	52,445,616	793	2	13.4	10.96	23	23	1	1	2	LOC100506166, NR4A1	18484, 28	in gene, in gene	ActReg chr12 #2463	1	1
2464	12	52,462,802	52,463,969	1,167	2	16.27	14.243	38	27	1	1	2	NR4A1, C12orf44	18194, -373	downstream, upstream	ActReg chr12 #2464	1	1
2465	12	52,540,447	52,541,994	1,547	2	11.98	9.612	22	25	0	0	0				ActReg chr12 #2465	1	1
2466	12	52,585,662	52,586,525	863	1	7.333	13.37	11	28	0	1	1	KRT80	-309	upstream	ActReg chr12 #2466	0	1
2467	12	52,596,606	52,597,465	859	1	10.556	12.074	19	20	0	1	2	LOC283403, LOC283404	7572, -7679	downstream, upstream	ActReg chr12 #2467	0	1
2468	12	52,609,109	52,609,875	766	1	11.667	9.25	20	15	0	1	2	LOC283403, LOC283404	-4885, 4778	upstream, in gene	ActReg chr12 #2468	1	0
2469	12	53,134,995	53,135,916	921	2	14.138	19.172	30	42	0	0	0				ActReg chr12 #2469	1	1
2470	12	53,342,391	53,343,186	795	1	6.84	11.24	10	17	1	1	1	KRT18	133	in gene	ActReg chr12 #2470	0	1
2471	12	53,439,966	53,440,970	984	1	6.484	10.71	10	19	1	1	3	EIF4B, LOC283335, TENC1	40416, 7744, -332	downstream, in gene, upstream	ActReg chr12 #2471	0	1
2472	12	53,573,970	53,574,720	750	1	5.458	11.333	8	19	1	2	2	CSAD, ZNF740	85, -190	in gene, upstream	ActReg chr12 #2472	0	1
2473	12	53,574,766	53,575,318	552	1	6.529	12.529	10	22	1	2	3	CSAD, ZNF740, ITGB7	-612, 507, 25958	upstream, in gene, downstream	ActReg chr12 #2473	0	1
2474	12	53,612,964	53,614,003	1,039	2	11.562	10.281	18	18	1	0	1	RARG	12,553	in gene	ActReg chr12 #2474	1	1
2475	12	53,661,735	53,662,317	582	1	11.722	9.833	16	17	1	1	1	ESPL1	-57	upstream	ActReg chr12 #2475	1	0
2476	12	53,688,991	53,689,698	707	1	7.957	12.435	10	24	1	2	3	ESPL1, PFDN5, C12orf10	27261, 109, 4126	downstream, in gene, upstream	ActReg chr12 #2476	0	1
2477	12	53,693,108	53,694,080	972	1	12.097	14.613	20	28	1	1	4	ESPL1, PFDN5, C12orf10, AAAS	31511, 4359, 124, 21818	downstream, downstream, in gene, downstream	ActReg chr12 #2477	0	1
2478	12	53,714,647	53,715,953	1,306	2	38.171	43.854	138	153	1	1	2	AAAS, SP7	112, 14704	in gene, downstream	ActReg chr12 #2478	1	1
2479	12	53,846,060	53,846,598	538	1	7.647	11	13	19	1	1	2	PRR13, PCBP2	10896, 443	downstream, in gene	ActReg chr12 #2479	0	1
2480	12	53,894,547	53,895,795	1,248	2	13.564	15.462	24	30	1	2	3	MAP3K12, TARBP2, NPFF	-1727, 466, 6251	upstream, in gene, downstream	ActReg chr12 #2480	1	1
2481	12	54,019,640	54,020,473	833	2	12.808	12.192	25	26	1	1	1	ATF7	143	in gene	ActReg chr12 #2481	1	1
2482	12	54,052,707	54,053,238	531	1	7.25	10.375	10	17	0	0	1	ATP5G2	17,540	downstream	ActReg chr12 #2482	0	1
2483	12	54,069,512	54,070,425	913	2	17.571	17.929	33	47	1	1	1	ATP5G2	544	in gene	ActReg chr12 #2483	1	1
2484	12	54,121,004	54,121,918	914	2	12.357	21.393	20	46	0	1	1	CALCOCO1	-154	upstream	ActReg chr12 #2484	1	1
2485	12	54,192,226	54,192,872	646	1	12.9	9.65	21	15	0	0	0				ActReg chr12 #2485	1	0
2486	12	54,332,307	54,333,509	1,202	2	13.553	14.921	22	26	1	1	1	HOXC13	332	in gene	ActReg chr12 #2486	1	1
2487	12	54,391,006	54,391,439	433	1	7.643	11.071	12	14	0	1	3	HOXC10, MIR196A2, HOXC9	12276, 5700, -2655	downstream, downstream, upstream	ActReg chr12 #2487	0	1
2488	12	54,411,673	54,412,532	859	1	6.222	13.593	11	28	1	3	4	HOXC8, HOXC4, HOXC5, HOXC6	9212, 1460, 1460, 1460	downstream, in gene, in gene, in gene	ActReg chr12 #2488	0	1
2489	12	54,426,899	54,427,507	608	1	5.158	11.21	7	16	1	1	4	HOXC4, HOXC5, HOXC6, MIR615	16561, 16561, 16561, -531	in gene, in gene, downstream, upstream	ActReg chr12 #2489	0	1
2490	12	54,519,740	54,520,292	552	1	7.222	11.333	11	15	1	1	2	FLJ12825, LOC400043	67978, 161	downstream, in gene	ActReg chr12 #2490	0	1
2491	12	54,608,297	54,609,192	895	1	8.75	18.821	21	46	0	0	0				ActReg chr12 #2491	0	1
2492	12	54,673,975	54,675,034	1,059	1	13.727	8.576	21	18	1	3	3	CBX5, HNRNPA1, LOC100506653	-589, 16, -5183	upstream, in gene, upstream	ActReg chr12 #2492	1	0
2493	12	54,754,051	54,755,103	1,052	1	7.875	10.438	15	20	0	0	3	COPZ1, GPR84, ZNF385A	35666, 3693, 30506	downstream, downstream, downstream	ActReg chr12 #2493	0	1
2494	12	54,822,229	54,822,853	624	1	6.25	10.55	9	16	0	0	1	ITGA5	-9,491	upstream	ActReg chr12 #2494	0	1
2495	12	54,867,152	54,867,684	532	1	10.823	8.706	17	13	0	1	1	GTSF1	-32	upstream	ActReg chr12 #2495	1	0
2496	12	54,966,845	54,967,414	569	1	6.5	11.667	11	21	0	1	1	PPP1R1A	-4,686	upstream	ActReg chr12 #2496	0	1
2497	12	55,328,948	55,329,574	626	1	9.95	7.2	17	11	0	0	0				ActReg chr12 #2497	1	0
2498	12	55,413,461	55,414,266	805	2	15.04	15.28	33	31	0	1	1	NEUROD4	134	in gene	ActReg chr12 #2498	1	1
2499	12	56,109,482	56,110,113	631	1	10.6	12.65	16	21	1	3	4	ITGA7, BLOC1S1, RDH5, CD63	-3708, -23, -4354, 13113	upstream, upstream, upstream, downstream	ActReg chr12 #2499	0	1
2500	12	56,114,711	56,115,461	750	2	10.875	10.125	19	19	0	2	5	ITGA7, BLOC1S1, RDH5, CD63, LOC100506701	-8997, 5266, 935, 7824, -7802	upstream, downstream, in gene, downstream, upstream	ActReg chr12 #2500	1	1
2501	12	56,121,652	56,122,391	739	1	10.913	9.13	18	15	1	2	4	BLOC1S1, RDH5, CD63, LOC100506701	12201, 7870, 889, -867	downstream, downstream, in gene, upstream	ActReg chr12 #2501	1	0
2502	12	56,223,070	56,224,263	1,193	2	12.605	11.947	20	18	2	2	4	ORMDL2, DNAJC14, LOC440104, MMP19	11860, -246, 274, 13069	downstream, upstream, in gene, downstream	ActReg chr12 #2502	1	1
2503	12	56,320,934	56,321,405	471	1	12.429	8.857	18	12	1	2	2	WBG, DGKA	528, -3777	in gene, upstream	ActReg chr12 #2503	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2504	12	56,367,296	56,368,127	831	1	15.846	12.231	28	19	1	2	4	SILV, CDK2, RAB5B, LOC100131294	-7885, 7155, -151, 7140	upstream, downstream, upstream, downstream	ActReg chr12 #2504	1	0
2505	12	56,400,699	56,401,451	752	2	11.833	11.083	23	22	1	0	1	SUOX	10,032	downstream	ActReg chr12 #2505	1	1
2506	12	56,435,497	56,436,152	655	2	14.1	13.75	21	23	1	1	2	IKZF4, RPS26	21135, 138	downstream, in gene	ActReg chr12 #2506	1	1
2507	12	56,472,739	56,473,995	1,256	1	8.231	12.82	14	21	1	1	1	ERBB3	-525	upstream	ActReg chr12 #2507	0	1
2508	12	56,474,099	56,475,106	1,007	1	9.719	10.375	13	15	1	1	1	ERBB3	710	in gene	ActReg chr12 #2508	0	1
2509	12	56,497,857	56,499,293	1,436	1	11.659	14.523	21	28	1	1	2	ERBB3, PA2G4	24683, 472	downstream, in gene	ActReg chr12 #2509	0	1
2510	12	56,511,659	56,512,411	752	2	10.304	15.478	22	23	1	2	4	PA2G4, RPL41, ZC3H10, ESYT1	13932, 1661, 5, -9951	downstream, downstream, in gene, upstream	ActReg chr12 #2510	1	1
2511	12	56,545,966	56,546,619	653	2	10.9	11.45	21	20	1	2	4	ESYT1, MYL6B, MYL6, SMARCC2	24306, -43, -5808, 37059	downstream, upstream, upstream, downstream	ActReg chr12 #2511	1	1
2512	12	56,583,191	56,584,238	1,047	1	8.97	11.212	16	26	1	1	1	SMARCC2	-363	upstream	ActReg chr12 #2512	0	1
2513	12	56,617,692	56,619,046	1,354	2	12.279	16.023	33	42	1	3	3	RNF41, OBFC2B, SLC39A5	-2634, 244, -5451	upstream, in gene, upstream	ActReg chr12 #2513	1	1
2514	12	56,651,369	56,652,622	1,253	1	7.974	10.564	13	16	1	1	2	ANKRD52, COQ10A	148, -8647	in gene, upstream	ActReg chr12 #2514	0	1
2515	12	56,660,376	56,660,886	510	1	6.875	11.438	12	14	1	1	3	ANKRD52, COQ10A, CS	-8488, -11, 33544	upstream, upstream, downstream	ActReg chr12 #2515	0	1
2516	12	56,709,614	56,710,527	913	1	8.036	12.393	14	19	1	1	2	CNPY2, PAN2	58, 17767	in gene, in gene	ActReg chr12 #2516	0	1
2517	12	56,861,940	56,862,850	910	2	17.931	16.448	45	42	0	1	2	SPRYD4, GLS2	94, 19786	in gene, downstream	ActReg chr12 #2517	1	1
2518	12	56,972,848	56,973,295	447	1	9.714	7.714	15	11	0	0	1	RBMS2	57,462	in gene	ActReg chr12 #2518	1	0
2519	12	57,023,846	57,024,794	948	2	18.69	25	52	68	1	0	2	BAZ2A, ATP5B	5843, 15532	in gene, downstream	ActReg chr12 #2519	1	1
2520	12	57,028,540	57,029,272	732	2	13.435	14.522	30	29	1	1	4	BAZ2A, ATP5B, SNORD59B, SNORD59A	1257, 10946, 8632, 9979	in gene, downstream, downstream, downstream	ActReg chr12 #2520	1	1
2521	12	57,039,372	57,040,196	824	1	7.654	12.846	12	17	1	3	4	BAZ2A, ATP5B, SNORD59B, SNORD59A	-9621, 68, -2246, -899	upstream, in gene, upstream, upstream	ActReg chr12 #2521	0	1
2522	12	57,080,888	57,082,211	1,323	2	7.857	10.905	17	19	1	1	1	PTGES3	529	in gene	ActReg chr12 #2522	1	1
2523	12	57,118,690	57,119,491	801	1	8.28	13.56	16	24	1	1	2	NACA, PRIM1	236, 27056	in gene, downstream	ActReg chr12 #2523	0	1
2524	12	57,443,384	57,444,067	683	1	9.091	12.091	17	18	0	1	2	MYO1A, TMEM194A	168, 26849	in gene, downstream	ActReg chr12 #2524	0	1
2525	12	57,481,608	57,482,570	962	1	9.367	13.767	17	20	1	1	3	TMEM194A, NAB2, STAT6	-9515, -588, 23107	upstream, upstream, downstream	ActReg chr12 #2525	0	1
2526	12	57,632,654	57,633,295	641	2	12.5	13	23	19	1	1	3	SHMT2, NDUFA4L2, STAC3	9618, 1571, 11995	downstream, in gene, downstream	ActReg chr12 #2526	1	1
2527	12	57,635,762	57,637,381	1,619	2	22	25.98	86	85	2	1	3	SHMT2, NDUFA4L2, STAC3	13215, -2026, 8398	downstream, upstream, downstream	ActReg chr12 #2527	1	1
2528	12	57,852,813	57,853,925	1,112	2	9.029	11.029	17	21	1	1	3	INHBC, INHBE, GLI1	24826, 4273, -549	downstream, downstream, upstream	ActReg chr12 #2528	1	1
2529	12	57,881,092	57,882,166	1,074	2	9.939	10.879	16	17	1	2	2	ARHGAP9, MARS	-7996, -222	upstream, upstream	ActReg chr12 #2529	1	1
2530	12	57,913,519	57,914,506	987	1	6.29	11.774	10	17	2	3	5	MARS, DDIT3, MIR616, MBD6, DCTN2	32161, 288, 970, -2647, 26966	downstream, in gene, upstream, upstream, downstream	ActReg chr12 #2530	0	1
2531	12	58,119,975	58,121,250	1,275	2	9.05	10.45	17	13	1	1	3	OS9, AGAP2, hCG_2014417	32874, 15328, 589	downstream, in gene, in gene	ActReg chr12 #2531	1	1
2532	12	58,138,056	58,139,100	1,044	1	10.938	9.031	18	18	0	2	4	AGAP2, TSPAN31, CDK4, MARCH9	-2638, -206, 7586, -10322	upstream, upstream, downstream, upstream	ActReg chr12 #2532	1	0
2533	12	58,159,497	58,160,918	1,421	1	7.636	12.796	14	24	1	2	4	MARCH9, CYP27B1, METTL1, FAM119B	11307, 769, 5707, -6176	downstream, in gene, downstream, upstream	ActReg chr12 #2533	0	1
2534	12	58,165,458	58,166,951	1,493	2	11.872	16.787	28	41	2	3	4	CYP27B1, METTL1, FAM119B, TSFM	-5228, -290, -179, -10324	upstream, upstream, upstream, upstream	ActReg chr12 #2534	1	1
2535	12	58,176,112	58,177,191	1,079	2	41.647	43.824	144	150	0	1	2	FAM119B, TSFM	10268, 123	downstream, in gene	ActReg chr12 #2535	1	1
2536	12	58,239,525	58,240,562	1,037	1	11.781	8.281	17	14	1	1	2	CTDSP2, LOC100506805	704, 9167	in gene, downstream	ActReg chr12 #2536	1	0
2537	12	58,282,290	58,283,111	821	1	7	12.154	13	21	0	0	2	LOC100289282, LOC100289313	9654, 16328	downstream, downstream	ActReg chr12 #2537	0	1
2538	12	58,334,481	58,335,238	757	1	10.958	5.792	17	12	0	2	2	LOC100506844, XRCC6BP1	-4912, -586	upstream, upstream	ActReg chr12 #2538	1	0
2539	12	58,460,859	58,461,728	869	2	13.214	10.107	21	14	0	0	0				ActReg chr12 #2539	1	1
2540	12	58,819,154	58,819,876	722	1	11.174	5.565	19	9	0	0	0				ActReg chr12 #2540	1	0
2541	12	58,894,764	58,895,346	582	1	4.5	11.833	9	16	0	0	0				ActReg chr12 #2541	0	1
2542	12	58,902,851	58,903,267	416	1	10.923	8.077	18	11	0	0	0				ActReg chr12 #2542	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2543	12	59,313,831	59,314,454	623	1	11.421	6.842	17	9	1	1	1	LRIG3	120	in gene	ActReg chr12 #2543	1	0
2544	12	59,430,701	59,431,328	627	1	11.3	8.5	15	14	0	0	0				ActReg chr12 #2544	1	0
2545	12	59,482,419	59,482,971	552	1	9.176	2.214	14	5	0	0	0				ActReg chr12 #2545	1	0
2546	12	59,991,114	59,991,561	447	1	7.429	10.143	12	14	0	0	0				ActReg chr12 #2546	0	1
2547	12	60,366,657	60,367,243	586	1	9	10.111	12	17	0	0	0				ActReg chr12 #2547	0	1
2548	12	62,653,480	62,654,522	1,042	2	49.375	54.5	168	173	1	1	1	USP15	-186	upstream	ActReg chr12 #2548	1	1
2549	12	62,996,016	62,997,763	1,747	2	12.655	12.618	21	22	1	2	3	MON2, C12orf61, MIRLET7I	136292, 325, -577	downstream, in gene, upstream	ActReg chr12 #2549	1	1
2550	12	63,025,499	63,026,857	1,358	1	8.558	12.954	17	29	1	0	0				ActReg chr12 #2550	0	1
2551	12	63,118,627	63,119,242	615	1	7.421	11.263	15	17	0	0	1	PPM1H	209,731	in gene	ActReg chr12 #2551	0	1
2552	12	63,125,673	63,126,408	735	1	12	8.391	20	16	0	0	1	PPM1H	202,625	in gene	ActReg chr12 #2552	1	0
2553	12	63,177,489	63,178,343	854	1	12.704	10.667	23	18	0	0	1	PPM1H	150,749	in gene	ActReg chr12 #2553	1	0
2554	12	63,179,702	63,180,543	841	1	8.577	9.962	15	19	0	0	1	PPM1H	148,543	in gene	ActReg chr12 #2554	0	1
2555	12	63,327,791	63,328,481	690	1	7.727	11.591	13	21	1	1	1	PPM1H	529	in gene	ActReg chr12 #2555	0	1
2556	12	64,173,571	64,174,240	669	1	8.048	12.952	13	22	1	1	1	TMEM5	268	in gene	ActReg chr12 #2556	0	1
2557	12	64,237,321	64,238,581	1,260	2	13.359	11.359	23	14	1	1	1	SRGAP1	-590	upstream	ActReg chr12 #2557	1	1
2558	12	64,615,582	64,616,638	1,056	1	15.576	10.212	25	18	1	1	1	C12orf66	-34	upstream	ActReg chr12 #2558	1	0
2559	12	64,798,274	64,798,765	491	1	10.267	13.733	12	20	1	1	1	XPOT	286	in gene	ActReg chr12 #2559	0	1
2560	12	64,845,542	64,846,442	900	1	10.429	9.179	17	16	1	1	2	XPOT, TBK1	47759, 55	downstream, in gene	ActReg chr12 #2560	1	0
2561	12	65,214,966	65,215,521	555	1	10.667	9.944	16	13	0	0	1	TBC1D30	40,654	in gene	ActReg chr12 #2561	1	0
2562	12	65,219,823	65,220,683	860	2	14.778	15.037	36	28	0	0	1	TBC1D30	45,664	in gene	ActReg chr12 #2562	1	1
2563	12	66,042,783	66,043,205	422	1	10.571	9.5	16	14	0	1	1	LOC100507065	-6,842	upstream	ActReg chr12 #2563	1	0
2564	12	66,088,824	66,089,547	723	1	10.783	7.609	17	12	0	0	0				ActReg chr12 #2564	1	0
2565	12	66,217,178	66,219,192	2,014	3	10.079	12.984	19	29	1	1	1	HMGA2	-55	upstream	ActReg chr12 #2565	1	1
2566	12	66,563,149	66,564,148	999	2	13.161	14.839	26	29	1	1	1	TMBIM4	159	in gene	ActReg chr12 #2566	1	1
2567	12	66,695,963	66,696,763	800	1	5.08	12.04	8	20	0	1	1	HELB	7	in gene	ActReg chr12 #2567	0	1
2568	12	67,027,445	67,028,002	557	2	8.222	11.167	18	20	0	0	1	GRIP1	45,202	in gene	ActReg chr12 #2568	1	1
2569	12	67,134,024	67,134,561	537	1	6.375	9.882	11	15	0	0	0				ActReg chr12 #2569	0	1
2570	12	67,587,224	67,588,246	1,022	2	14.438	20.562	36	50	0	0	0				ActReg chr12 #2570	1	1
2571	12	67,662,496	67,663,809	1,313	2	13.643	11.048	24	23	1	1	1	CAND1	91	in gene	ActReg chr12 #2571	1	1
2572	12	67,828,569	67,829,062	493	1	10.438	10.812	14	15	0	0	0				ActReg chr12 #2572	0	1
2573	12	68,141,438	68,143,212	1,774	2	11.232	10.857	22	21	0	0	0				ActReg chr12 #2573	1	1
2574	12	69,080,311	69,081,200	889	2	13.786	14.964	25	29	1	2	2	LOC100507250, NUP107	-172, 24	upstream, in gene	ActReg chr12 #2574	1	1
2575	12	69,979,037	69,979,636	599	1	10.263	13.053	13	22	1	1	2	FRS2, CCT2	115207, 128	downstream, in gene	ActReg chr12 #2575	0	1
2576	12	70,215,588	70,216,078	490	1	9.933	8.733	17	12	0	1	2	RAB3IP, C12orf28	83202, -3465	in gene, upstream	ActReg chr12 #2576	1	0
2577	12	70,446,661	70,447,189	528	1	7.062	11.062	12	14	0	0	0				ActReg chr12 #2577	0	1
2578	12	70,636,328	70,637,269	941	1	7.966	13.552	12	19	1	2	2	LOC100507317, CNOT2	316, 21	in gene, in gene	ActReg chr12 #2578	0	1
2579	12	71,003,517	71,004,063	546	1	8	11.588	13	19	1	0	1	PTPRB	27,429	in gene	ActReg chr12 #2579	0	1
2580	12	71,313,243	71,314,483	1,240	2	9.667	10.846	16	17	0	1	1	PTPRR	721	in gene	ActReg chr12 #2580	1	1
2581	12	71,833,445	71,834,128	683	1	10.952	11.524	18	20	1	1	1	LGR5	-27	upstream	ActReg chr12 #2581	0	1
2582	12	72,056,615	72,057,809	1,194	1	11.676	9.405	17	17	1	2	2	ZFC3H1, THAP2	537, -572	in gene, upstream	ActReg chr12 #2582	1	0
2583	12	72,079,704	72,080,270	566	1	9.722	12.389	14	21	1	1	2	THAP2, TMEM19	22203, 109	downstream, in gene	ActReg chr12 #2583	0	1
2584	12	72,332,327	72,333,076	749	2	12.826	14.435	26	31	0	1	1	TPH2	75	in gene	ActReg chr12 #2584	1	1
2585	12	72,374,695	72,375,504	809	2	12.44	10.24	21	18	0	0	1	TPH2	42,473	in gene	ActReg chr12 #2585	1	1
2586	12	72,666,343	72,667,016	673	1	12.476	13.238	21	21	1	2	2	LOC283392, TRHDE	610, 150	in gene, in gene	ActReg chr12 #2586	0	1
2587	12	73,993,039	73,993,509	470	1	4.067	9.867	6	14	0	0	0				ActReg chr12 #2587	0	1
2588	12	74,686,260	74,686,920	660	1	6.762	10.857	12	18	0	1	1	LOC100507377	-179	upstream	ActReg chr12 #2588	0	1
2589	12	74,931,454	74,931,917	463	1	9.8	8.867	15	12	1	1	1	LOC552889	134	in gene	ActReg chr12 #2589	1	0
2590	12	75,571,748	75,572,269	521	2	10	9.4	14	16	0	0	1	KCNC2	31,503	in gene	ActReg chr12 #2590	1	1
2591	12	75,602,702	75,603,676	974	1	9.167	12.067	18	20	1	1	1	KCNC2	322	in gene	ActReg chr12 #2591	0	1
2592	12	75,723,610	75,724,465	855	2	13.333	15.482	25	38	1	2	2	CAPS2, GLIPR1L1	-201, -4426	upstream, upstream	ActReg chr12 #2592	1	1
2593	12	75,728,096	75,728,804	708	1	9.739	9.391	18	14	0	2	2	CAPS2, GLIPR1L1	-4614, -13	upstream, upstream	ActReg chr12 #2593	0	1
2594	12	75,904,967	75,905,791	824	2	11	13.2	24	21	1	1	2	GLIPR1, KRR1	30866, 39	downstream, in gene	ActReg chr12 #2594	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2595	12	76,160,460	76,161,091	631	1	5.6	11.05	9	20	0	0	0				ActReg chr12 #2595	0	1
2596	12	76,326,784	76,327,381	597	1	9.947	6.842	20	10	0	1	1	LOC100289143	-5,703	upstream	ActReg chr12 #2596	1	0
2597	12	76,338,081	76,338,773	692	1	12.714	8.524	20	12	0	0	1	LOC100289143	5,642	in gene	ActReg chr12 #2597	1	0
2598	12	76,414,023	76,414,676	653	1	11.55	11.3	17	20	0	0	1	PHLDA1	11,207	downstream	ActReg chr12 #2598	1	0
2599	12	76,424,854	76,426,608	1,754	3	10.055	11.982	18	18	1	1	1	PHLDA1	-175	upstream	ActReg chr12 #2599	1	1
2600	12	76,576,903	76,577,852	949	1	9.897	11.069	17	17	0	0	0				ActReg chr12 #2600	0	1
2601	12	76,953,083	76,953,789	706	1	7.591	11.864	13	15	1	1	1	OSBPL8	153	in gene	ActReg chr12 #2601	0	1
2602	12	77,005,323	77,005,851	528	1	5.25	9.375	9	15	0	0	0				ActReg chr12 #2602	0	1
2603	12	77,272,707	77,273,289	582	1	7	10.556	10	17	1	1	1	CSRP2	-199	upstream	ActReg chr12 #2603	0	1
2604	12	77,336,536	77,337,032	496	1	7.25	11.562	11	16	0	0	0				ActReg chr12 #2604	0	1
2605	12	77,527,122	77,528,043	921	2	15.897	17.724	37	43	0	0	0				ActReg chr12 #2605	1	1
2606	12	78,241,551	78,242,249	698	1	7.682	10.682	10	16	0	0	1	NAV3	16,831	in gene	ActReg chr12 #2606	0	1
2607	12	80,328,244	80,329,604	1,360	2	12.465	15.465	24	32	1	1	1	PPP1R12A	311	in gene	ActReg chr12 #2607	1	1
2608	12	80,457,772	80,458,469	697	1	11.954	5.864	18	9	0	0	0				ActReg chr12 #2608	1	0
2609	12	82,751,781	82,752,874	1,093	2	37.765	35.735	125	107	1	2	2	CCDC59, C12orf26	257, 51	in gene, in gene	ActReg chr12 #2609	1	1
2610	12	83,081,245	83,081,703	458	1	5.8	9.6	8	14	1	1	1	TMTC2	540	in gene	ActReg chr12 #2610	0	1
2611	12	85,305,103	85,306,934	1,831	3	11.561	12.368	19	27	3	1	1	SLC6A15	588	in gene	ActReg chr12 #2611	1	1
2612	12	85,410,097	85,410,683	586	1	11.444	9.529	22	19	0	0	1	TSPAN19	19,665	in gene	ActReg chr12 #2612	1	0
2613	12	85,486,261	85,487,280	1,019	2	13.094	12.438	21	25	0	0	1	LRRIQ1	56,671	in gene	ActReg chr12 #2613	1	1
2614	12	85,673,758	85,674,765	1,007	2	11.875	14.156	24	25	1	1	1	ALX1	225	in gene	ActReg chr12 #2614	1	1
2615	12	87,822,955	87,823,470	515	1	3.75	9.938	7	16	0	0	0				ActReg chr12 #2615	0	1
2616	12	87,833,689	87,834,337	648	2	8.667	11.048	16	17	0	0	0				ActReg chr12 #2616	1	1
2617	12	88,177,921	88,178,631	710	1	6.909	11.046	12	24	0	0	0				ActReg chr12 #2617	0	1
2618	12	88,429,086	88,429,833	747	2	13.417	11.125	23	20	1	2	2	C12orf50, C12orf29	-6283, 191	upstream, in gene	ActReg chr12 #2618	1	1
2619	12	88,535,384	88,536,395	1,011	1	9.906	14.094	16	26	1	2	2	CEP290, TMTC3	104, -184	in gene, upstream	ActReg chr12 #2619	0	1
2620	12	88,692,467	88,693,061	594	1	10.105	10.263	14	17	0	0	0				ActReg chr12 #2620	0	1
2621	12	88,693,195	88,694,007	812	2	10.68	9.68	19	19	0	0	0				ActReg chr12 #2621	1	1
2622	12	88,718,863	88,719,475	612	1	10.947	8.368	14	14	0	0	0				ActReg chr12 #2622	1	0
2623	12	88,814,155	88,814,783	628	2	10.842	10.474	21	18	0	0	0				ActReg chr12 #2623	1	1
2624	12	88,974,112	88,974,637	525	1	9.647	3.667	14	8	1	1	1	KITLG	-124	upstream	ActReg chr12 #2624	1	0
2625	12	89,458,456	89,459,137	681	2	9.636	9.182	20	21	0	0	0				ActReg chr12 #2625	1	1
2626	12	89,511,185	89,511,633	448	1	9	10.929	13	13	0	0	0				ActReg chr12 #2626	0	1
2627	12	89,619,017	89,619,884	867	1	11.815	10.296	18	17	0	0	0				ActReg chr12 #2627	1	0
2628	12	89,744,294	89,744,946	652	1	5.15	9.8	8	17	0	1	1	DUSP6	1,676	in gene	ActReg chr12 #2628	0	1
2629	12	89,745,185	89,746,068	883	2	12.963	11.852	18	20	1	1	1	DUSP6	670	in gene	ActReg chr12 #2629	1	1
2630	12	89,746,251	89,746,933	682	1	12.571	9.286	24	13	1	1	1	DUSP6	-296	upstream	ActReg chr12 #2630	1	0
2631	12	89,784,373	89,785,467	1,094	2	10.941	10.441	16	17	0	0	0				ActReg chr12 #2631	1	1
2632	12	89,833,624	89,834,253	629	1	11	8.65	18	14	0	0	1	WDR51B	85,839	in gene	ActReg chr12 #2632	1	0
2633	12	89,919,240	89,920,347	1,107	2	35.147	30.5	101	90	1	2	2	WDR51B, GALNT4	-16, -1258	upstream, upstream	ActReg chr12 #2633	1	1
2634	12	90,101,249	90,101,672	423	1	4	11.154	5	17	1	1	1	LOC338758	-1,272	upstream	ActReg chr12 #2634	0	1
2635	12	90,103,227	90,103,993	766	2	10.833	12.125	15	18	1	1	1	LOC338758	878	in gene	ActReg chr12 #2635	1	1
2636	12	90,162,805	90,163,544	739	1	12.696	8.304	22	12	0	0	0				ActReg chr12 #2636	1	0
2637	12	90,484,944	90,485,388	444	1	11.571	10.429	15	15	0	0	0				ActReg chr12 #2637	0	1
2638	12	90,727,498	90,728,070	572	1	10	7	15	11	0	0	0				ActReg chr12 #2638	1	0
2639	12	90,904,630	90,905,307	677	1	9.095	11.143	13	21	0	0	0				ActReg chr12 #2639	0	1
2640	12	92,530,644	92,531,516	872	1	10.741	5.519	17	10	0	0	1	BTG1	8,593	downstream	ActReg chr12 #2640	1	0
2641	12	92,539,336	92,540,536	1,200	2	10.351	10.189	16	21	1	1	1	BTG1	-263	upstream	ActReg chr12 #2641	1	1
2642	12	92,683,194	92,683,773	579	1	7.556	9.278	14	15	0	0	0				ActReg chr12 #2642	0	1
2643	12	92,763,382	92,763,978	596	2	7.789	10.737	13	18	0	0	0				ActReg chr12 #2643	1	1
2644	12	92,932,741	92,933,435	694	1	8.286	11.048	12	21	0	0	0				ActReg chr12 #2644	0	1
2645	12	92,952,449	92,953,317	868	1	8.037	10.667	14	18	0	0	0				ActReg chr12 #2645	0	1
2646	12	93,043,441	93,044,080	639	1	7.2	10.9	10	16	0	0	0				ActReg chr12 #2646	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2647	12	93,323,127	93,323,651	524	1	6.882	10.059	11	18	1	1	1	EEA1	-282	upstream	ActReg chr12 #2647	0	1
2648	12	93,547,103	93,547,560	457	1	9.533	4.333	14	7	0	0	0				ActReg chr12 #2648	1	0
2649	12	93,623,139	93,623,958	819	1	9.92	5.32	14	10	0	0	0				ActReg chr12 #2649	1	0
2650	12	93,770,980	93,771,716	736	1	8.348	15.739	14	35	1	1	1	NUDT4	-353	upstream	ActReg chr12 #2650	0	1
2651	12	93,781,564	93,782,037	473	1	9.133	7.533	13	11	0	0	1	NUDT4	10,099	in gene	ActReg chr12 #2651	1	0
2652	12	93,861,145	93,861,793	648	1	9.143	10.524	16	21	1	1	1	MRPL42	199	in gene	ActReg chr12 #2652	0	1
2653	12	93,963,829	93,965,174	1,345	2	13.643	14.071	29	23	1	2	2	LOC144481, SOCS2	1477, 903	in gene, in gene	ActReg chr12 #2653	1	1
2654	12	94,070,792	94,071,932	1,140	2	10.314	10.943	16	15	1	1	1	CRADD	211	in gene	ActReg chr12 #2654	1	1
2655	12	94,212,489	94,213,224	735	1	10	12.13	16	19	0	0	1	CRADD	141,705	in gene	ActReg chr12 #2655	0	1
2656	12	94,358,613	94,359,310	697	1	6.727	11.318	12	18	0	0	0				ActReg chr12 #2656	0	1
2657	12	94,376,337	94,377,319	982	1	11.226	8.355	19	18	0	0	0				ActReg chr12 #2657	1	0
2658	12	94,852,981	94,854,347	1,366	2	12.349	12.767	22	20	1	2	2	CCDC41, LOC144486	100, -115	in gene, upstream	ActReg chr12 #2658	1	1
2659	12	95,009,623	95,010,578	955	2	10.967	10.2	18	16	0	0	1	TMCC3	34,224	in gene	ActReg chr12 #2659	1	1
2660	12	95,038,219	95,038,915	696	1	11.046	8.636	17	15	0	0	1	TMCC3	5,757	in gene	ActReg chr12 #2660	1	0
2661	12	95,397,135	95,397,888	753	2	14.167	10.75	35	19	1	1	1	NDUFA12	0	in gene	ActReg chr12 #2661	1	1
2662	12	95,466,605	95,467,855	1,250	2	12.897	14.667	35	37	1	1	2	NR2C1, FGD6	174, 144010	in gene, downstream	ActReg chr12 #2662	1	1
2663	12	95,610,784	95,612,412	1,628	2	8.314	10.235	17	16	1	2	2	FGD6, VEZT	-358, 76	upstream, in gene	ActReg chr12 #2663	1	1
2664	12	95,805,090	95,805,868	778	2	9.708	9.625	22	15	0	0	0				ActReg chr12 #2664	1	1
2665	12	95,867,486	95,868,211	725	2	12.217	15.261	26	35	1	1	1	METAP2	26	in gene	ActReg chr12 #2665	1	1
2666	12	96,184,965	96,185,428	463	1	10.5	6.857	16	10	1	1	1	NTN4	-660	upstream	ActReg chr12 #2666	1	0
2667	12	96,271,355	96,271,776	421	1	10.5	5.714	14	8	0	0	1	CCDC38	64,863	in gene	ActReg chr12 #2667	1	0
2668	12	96,428,752	96,430,058	1,306	2	10.78	12.878	23	28	1	1	1	LTA4H	-40	upstream	ActReg chr12 #2668	1	1
2669	12	96,529,834	96,530,365	531	1	10.75	12	18	16	0	0	0				ActReg chr12 #2669	0	1
2670	12	96,792,958	96,793,646	688	1	9.545	11.409	15	16	1	1	1	CDK17	1,064	in gene	ActReg chr12 #2670	0	1
2671	12	97,300,682	97,301,442	760	2	10.792	9.375	16	15	1	1	1	NEDD1	61	in gene	ActReg chr12 #2671	1	1
2672	12	98,231,183	98,231,725	542	1	5.882	8.294	12	15	0	0	0				ActReg chr12 #2672	0	1
2673	12	98,690,419	98,691,027	608	1	8.158	9.632	11	19	0	0	0				ActReg chr12 #2673	0	1
2674	12	98,746,131	98,746,712	581	1	6.389	10.611	10	17	0	0	0				ActReg chr12 #2674	0	1
2675	12	98,811,904	98,812,695	791	1	11.56	6.96	17	9	0	0	0				ActReg chr12 #2675	1	0
2676	12	98,896,938	98,897,938	1,000	2	10.645	12.032	26	18	1	1	2	LOC643770, LOC100128191	189, 12566	in gene, downstream	ActReg chr12 #2676	1	1
2677	12	98,908,820	98,910,685	1,865	1	8.983	11.431	16	17	1	2	2	LOC100128191, TMPO	252, 401	in gene, in gene	ActReg chr12 #2677	0	1
2678	12	98,987,086	98,988,138	1,052	1	12.606	10.697	24	21	1	2	2	SLC25A3, SNORA53	209, -5801	in gene, upstream	ActReg chr12 #2678	1	0
2679	12	99,038,550	99,039,369	819	2	10.115	9.769	15	15	1	2	2	IKBIP, APAF1	-370, -119	upstream, upstream	ActReg chr12 #2679	1	1
2680	12	99,207,919	99,208,471	552	1	7.176	10.177	10	15	0	0	1	ANKS1B	1,170,237	in gene	ActReg chr12 #2680	0	1
2681	12	99,290,507	99,291,179	672	1	4.857	10.524	8	14	0	0	1	ANKS1B	1,087,589	in gene	ActReg chr12 #2681	0	1
2682	12	99,848,993	99,849,598	605	1	9.333	8.111	17	12	0	0	1	ANKS1B	529,137	in gene	ActReg chr12 #2682	1	0
2683	12	100,932,866	100,933,647	781	2	12.292	13.25	31	29	0	0	1	NR1H4	65,577	in gene	ActReg chr12 #2683	1	1
2684	12	100,967,032	100,968,116	1,084	1	8.676	11.882	14	20	1	1	2	NR1H4, GAS2L3	99895, 85	downstream, in gene	ActReg chr12 #2684	0	1
2685	12	101,081,910	101,082,826	916	2	8.931	10.517	17	19	0	0	0				ActReg chr12 #2685	1	1
2686	12	101,219,951	101,220,622	671	2	11.238	9.19	19	16	0	0	1	ANO4	31,912	in gene	ActReg chr12 #2686	1	1
2687	12	101,693,774	101,694,205	431	1	9.846	6.308	14	9	0	0	1	UTP20	20,084	in gene	ActReg chr12 #2687	1	0
2688	12	101,801,284	101,801,920	636	1	9.4	12	11	16	1	1	1	ARL1	-30	upstream	ActReg chr12 #2688	0	1
2689	12	102,091,719	102,092,342	623	1	10.368	11.21	15	18	1	1	1	CHPT1	613	in gene	ActReg chr12 #2689	0	1
2690	12	102,270,829	102,271,991	1,162	1	8.278	12.25	16	16	1	1	1	DRAM1	305	in gene	ActReg chr12 #2690	0	1
2691	12	102,329,849	102,330,709	860	2	9.556	13.111	14	21	0	0	0				ActReg chr12 #2691	1	1
2692	12	102,513,414	102,514,276	862	1	10.482	12.778	16	21	1	2	2	NUP37, C12orf48	-1484, -111	upstream, upstream	ActReg chr12 #2692	0	1
2693	12	103,889,498	103,889,950	452	1	3.643	10.5	7	16	1	1	1	C12orf42	25	in gene	ActReg chr12 #2693	0	1
2694	12	103,954,304	103,954,828	524	1	12.765	10.294	26	19	0	0	0				ActReg chr12 #2694	1	0
2695	12	103,968,958	103,969,605	647	2	10.762	11.619	24	21	0	0	0				ActReg chr12 #2695	1	1
2696	12	104,195,673	104,196,633	960	1	10.4	9.267	16	16	0	0	1	NT5DC3	38,822	in gene	ActReg chr12 #2696	1	0
2697	12	104,350,492	104,351,353	861	2	13.074	13.444	23	26	1	1	3	HSP90B1, C12orf73, TDG	26733, 71, -8671	downstream, in gene, upstream	ActReg chr12 #2697	1	1
2698	12	104,359,208	104,360,124	916	2	13.321	16.75	24	37	1	1	2	C12orf73, TDG	-8673, 73	upstream, in gene	ActReg chr12 #2698	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2699	12	104,457,724	104,458,695	971	1	7.935	12.581	13	22	1	1	1	HCFC2	-27	upstream	ActReg chr12 #2699	0	1
2700	12	104,680,353	104,681,062	709	1	7.636	12.091	12	19	1	0	1	TXNRD1	71,148	in gene	ActReg chr12 #2700	0	1
2701	12	104,682,214	104,683,029	815	1	5.04	12.4	8	19	1	0	1	TXNRD1	73,062	in gene	ActReg chr12 #2701	0	1
2702	12	104,850,242	104,850,904	662	2	10.4	10.15	18	19	1	1	1	CHST11	-119	upstream	ActReg chr12 #2702	1	1
2703	12	105,501,145	105,502,001	856	1	11.037	14.333	20	24	1	1	1	KIAA1033	81	in gene	ActReg chr12 #2703	0	1
2704	12	105,651,080	105,651,661	581	1	10.333	11.389	16	22	0	0	0				ActReg chr12 #2704	0	1
2705	12	106,696,139	106,697,286	1,147	2	14.389	15.417	28	30	1	1	1	TCP11L2	131	in gene	ActReg chr12 #2705	1	1
2706	12	106,751,211	106,752,142	931	1	9.69	12.379	20	20	1	1	1	POLR3B	240	in gene	ActReg chr12 #2706	0	1
2707	12	107,167,593	107,168,843	1,250	2	12.359	13.923	23	22	1	2	2	LOC100287944, RIC8B	478, -181	in gene, upstream	ActReg chr12 #2707	1	1
2708	12	107,349,357	107,350,388	1,031	1	7.281	10.844	10	17	1	1	1	C12orf23	328	in gene	ActReg chr12 #2708	0	1
2709	12	107,486,766	107,487,968	1,202	1	6.921	11.579	11	16	1	1	1	CRY1	231	in gene	ActReg chr12 #2709	0	1
2710	12	108,079,364	108,080,094	730	1	9.455	13.046	15	18	1	1	1	PWP1	139	in gene	ActReg chr12 #2710	0	1
2711	12	108,349,887	108,350,474	587	1	8.579	10.632	14	17	0	0	0				ActReg chr12 #2711	0	1
2712	12	108,588,052	108,588,610	558	1	3.611	10.389	5	17	0	0	1	WSCD2	64,820	in gene	ActReg chr12 #2712	0	1
2713	12	108,607,968	108,608,765	797	2	11.88	13.44	20	29	0	0	1	WSCD2	84,855	in gene	ActReg chr12 #2713	1	1
2714	12	108,622,250	108,623,128	878	2	9.481	10.407	14	16	0	0	1	WSCD2	99,178	in gene	ActReg chr12 #2714	1	1
2715	12	108,954,578	108,955,251	673	1	14.809	12.667	22	18	1	2	2	SART3, ISCU	251, -1380	in gene, upstream	ActReg chr12 #2715	1	0
2716	12	109,037,613	109,038,252	639	1	11.85	9	19	16	0	0	2	SELPLG, CORO1C	-10262, 87363	upstream, downstream	ActReg chr12 #2716	1	0
2717	12	109,084,969	109,086,330	1,361	2	9.071	11.976	15	19	0	0	1	CORO1C	39,646	in gene	ActReg chr12 #2717	1	1
2718	12	109,124,608	109,125,313	705	1	6.913	11.087	9	18	1	1	1	CORO1C	335	in gene	ActReg chr12 #2718	0	1
2719	12	109,248,126	109,248,804	678	1	11.182	11.954	17	18	0	0	1	SSH1	2,894	in gene	ActReg chr12 #2719	0	1
2720	12	109,283,922	109,284,492	570	1	10.444	5.056	20	10	0	0	1	DAO	10,350	in gene	ActReg chr12 #2720	1	0
2721	12	109,458,369	109,459,253	884	2	15.148	17.667	32	37	0	0	0				ActReg chr12 #2721	1	1
2722	12	109,489,981	109,491,228	1,247	1	8.077	12.667	20	25	1	2	2	LOC100131733, USP30	1166, 224	in gene, in gene	ActReg chr12 #2722	0	1
2723	12	109,530,951	109,531,751	800	2	18.72	15.68	45	35	1	2	3	USP30, ALKBH2, UNG	40971, -58, 4064	downstream, upstream, upstream	ActReg chr12 #2723	1	1
2724	12	109,535,024	109,536,183	1,159	2	11	11.972	25	23	1	2	3	USP30, ALKBH2, UNG	45223, -4310, 188	downstream, upstream, in gene	ActReg chr12 #2724	1	1
2725	12	109,914,870	109,915,919	1,049	2	12.758	15.333	26	33	1	2	2	KCTD10, UBE3B	-239, -45	upstream, upstream	ActReg chr12 #2725	1	1
2726	12	109,982,573	109,983,398	825	1	11.115	7.654	15	11	0	0	2	UBE3B, MMAB	67546, 28373	downstream, downstream	ActReg chr12 #2726	1	0
2727	12	110,010,697	110,011,572	875	2	14.074	17.074	28	33	1	2	2	MMAB, MVK	224, -366	in gene, upstream	ActReg chr12 #2727	1	1
2728	12	110,148,356	110,149,140	784	1	13.333	10.292	22	14	0	1	1	C12orf34	-3,439	upstream	ActReg chr12 #2728	1	0
2729	12	110,337,609	110,338,727	1,118	2	13.914	17.057	27	41	1	1	1	TCHP	89	in gene	ActReg chr12 #2729	1	1
2730	12	110,384,889	110,385,437	548	1	8.588	11.529	12	16	0	0	1	GIT2	49,031	in gene	ActReg chr12 #2730	0	1
2731	12	110,436,572	110,437,497	925	2	23.276	22.138	64	57	1	2	2	GIT2, ANKRD13A	-2840, -201	upstream, upstream	ActReg chr12 #2731	1	1
2732	12	110,486,125	110,486,672	547	1	9.647	10.647	14	14	1	0	2	ANKRD13A, C12orf76	49163, 19102	downstream, in gene	ActReg chr12 #2732	0	1
2733	12	110,718,387	110,718,898	511	1	12	8.375	19	14	1	1	1	ATP2A2	-390	upstream	ActReg chr12 #2733	1	0
2734	12	110,841,001	110,841,725	724	1	8.136	11.727	12	21	1	1	1	ANAPC7	172	in gene	ActReg chr12 #2734	0	1
2735	12	110,905,830	110,906,480	650	1	9.9	13.9	18	20	1	2	2	GPN3, C12orf24	371, -77	in gene, upstream	ActReg chr12 #2735	0	1
2736	12	110,939,613	110,940,376	763	2	11.083	11.542	16	21	1	2	2	VPS29, RAD9B	-78, -11	upstream, upstream	ActReg chr12 #2736	1	1
2737	12	111,016,373	111,016,973	600	1	11.842	6.474	19	11	0	0	1	PPTC7	4,391	in gene	ActReg chr12 #2737	1	0
2738	12	111,051,549	111,052,296	747	1	12.083	8.917	17	15	1	1	1	TCTN1	90	in gene	ActReg chr12 #2738	1	0
2739	12	111,806,239	111,807,391	1,152	2	15.167	10.889	26	22	1	1	1	FAM109A	110	in gene	ActReg chr12 #2739	1	1
2740	12	111,834,637	111,835,403	766	2	14.917	14.167	33	29	1	0	1	SH2B3	-8,732	upstream	ActReg chr12 #2740	1	1
2741	12	111,836,817	111,837,695	878	1	10.63	8.519	15	17	0	1	1	SH2B3	-6,496	upstream	ActReg chr12 #2741	1	0
2742	12	111,851,157	111,852,336	1,179	1	8.919	12.838	16	18	0	0	1	SH2B3	7,994	in gene	ActReg chr12 #2742	0	1
2743	12	112,035,888	112,036,350	462	1	7.786	10.571	10	14	1	1	1	ATXN2	1,361	in gene	ActReg chr12 #2743	0	1
2744	12	112,037,380	112,037,985	605	1	9.842	8.053	16	11	1	1	1	ATXN2	-202	upstream	ActReg chr12 #2744	1	0
2745	12	112,279,452	112,280,506	1,054	2	11.636	16.303	30	33	1	2	2	C12orf47, MAPKAPK5	727, -300	in gene, upstream	ActReg chr12 #2745	1	1
2746	12	112,450,512	112,451,993	1,481	2	12.826	10.522	21	19	1	2	2	TMEM116, ERP29	-229, 100	upstream, in gene	ActReg chr12 #2746	1	1
2747	12	112,545,977	112,547,047	1,070	1	9.147	13.235	18	26	1	1	1	NAA25	123	in gene	ActReg chr12 #2747	0	1
2748	12	112,554,388	112,554,868	480	2	9.933	10.133	16	15	0	0	2	NAA25, TRAFD1	-7993, -8721	upstream, upstream	ActReg chr12 #2748	1	1
2749	12	112,820,090	112,820,777	687	1	6.636	12.5	13	18	1	1	1	C12orf51	-537	upstream	ActReg chr12 #2749	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2750	12	112,846,786	112,847,577	791	1	8.542	10.875	17	15	1	1	3	LOC100506435, RPL6, PTPN11	8780, 262, -9355	downstream, in gene, upstream	ActReg chr12 #2750	0	1
2751	12	112,856,285	112,856,953	668	1	13.667	8.048	20	12	1	1	2	RPL6, PTPN11	-9176, 83	upstream, in gene	ActReg chr12 #2751	1	0
2752	12	113,102,192	113,102,989	797	2	15.88	16.2	32	34	0	0	0				ActReg chr12 #2752	1	1
2753	12	113,228,922	113,229,987	1,065	2	15	17.235	31	35	0	1	1	RPH3A	-95	upstream	ActReg chr12 #2753	1	1
2754	12	113,306,053	113,306,824	771	2	11.917	12.125	24	22	0	0	1	RPH3A	76,889	in gene	ActReg chr12 #2754	1	1
2755	12	113,622,633	113,623,899	1,266	2	13.59	13.872	29	28	1	2	3	DDX54, C12orf52, IQCD	18, -289, 35614	in gene, upstream, downstream	ActReg chr12 #2755	1	1
2756	12	113,772,810	113,773,412	602	1	10.526	9.789	19	16	1	1	1	SLC24A6	-186	upstream	ActReg chr12 #2756	1	0
2757	12	113,795,967	113,796,960	993	2	13.281	13.906	24	22	1	1	1	PLBD2	92	in gene	ActReg chr12 #2757	1	1
2758	12	113,859,732	113,860,416	684	1	11.909	10.046	24	17	0	1	1	SDSL	-142	upstream	ActReg chr12 #2758	1	0
2759	12	113,917,565	113,918,489	924	2	9.621	12.621	21	25	1	0	2	LHX5, LOC100506452	-8150, 8219	upstream, in gene	ActReg chr12 #2759	1	1
2760	12	114,039,094	114,040,086	992	1	10.097	14.194	17	27	0	0	0				ActReg chr12 #2760	0	1
2761	12	114,403,827	114,404,614	787	1	7.12	11.48	16	17	1	1	1	RBM19	-44	upstream	ActReg chr12 #2761	0	1
2762	12	115,121,791	115,122,479	688	1	9.818	12	14	18	1	1	1	TBX3	-166	upstream	ActReg chr12 #2762	0	1
2763	12	115,211,792	115,212,466	674	1	9.429	11.143	17	17	0	0	0				ActReg chr12 #2763	0	1
2764	12	115,353,742	115,354,355	613	2	11	11.421	20	21	0	0	0				ActReg chr12 #2764	1	1
2765	12	115,371,085	115,371,874	789	2	10.64	12.12	22	25	0	0	0				ActReg chr12 #2765	1	1
2766	12	115,374,587	115,375,351	764	1	5.125	9.875	12	13	0	0	0				ActReg chr12 #2766	0	1
2767	12	115,593,189	115,594,104	915	1	8.929	11.786	14	20	0	0	0				ActReg chr12 #2767	0	1
2768	12	115,779,102	115,779,726	624	1	5.85	10.2	12	18	0	0	0				ActReg chr12 #2768	0	1
2769	12	115,877,994	115,878,684	690	2	12.381	10.952	23	15	0	0	0				ActReg chr12 #2769	1	1
2770	12	117,039,223	117,039,887	664	1	5.476	9.619	10	17	0	0	0				ActReg chr12 #2770	0	1
2771	12	117,175,627	117,176,374	747	1	10.348	13.739	23	34	1	2	2	C12orf49, RNFT2	-157, -96	upstream, upstream	ActReg chr12 #2771	0	1
2772	12	117,250,728	117,251,866	1,138	1	11	15.657	15	22	0	0	1	RNFT2	75,201	in gene	ActReg chr12 #2772	0	1
2773	12	117,256,714	117,257,433	719	1	9.045	11.5	12	16	1	0	1	RNFT2	80,977	in gene	ActReg chr12 #2773	0	1
2774	12	117,295,782	117,296,376	594	2	10.167	12.333	20	21	0	0	2	RNFT2, HRK	119983, 23153	downstream, downstream	ActReg chr12 #2774	1	1
2775	12	117,354,527	117,355,030	503	1	7.312	9.75	11	16	0	0	1	FBXW8	6,017	in gene	ActReg chr12 #2775	0	1
2776	12	118,432,024	118,432,965	941	1	12.033	9.533	18	15	0	0	0				ActReg chr12 #2776	1	0
2777	12	118,573,548	118,574,819	1,271	2	10.55	10.125	15	18	1	1	2	LOC100506570, PEBP1	9204, 313	in gene, in gene	ActReg chr12 #2777	1	1
2778	12	118,810,344	118,811,258	914	2	20.357	13.929	46	29	1	2	2	TAOK3, SUDS3	-51, -3557	upstream, upstream	ActReg chr12 #2778	1	1
2779	12	118,814,072	118,814,589	517	1	8.688	12.5	12	17	1	2	2	TAOK3, SUDS3	-3580, -28	upstream, upstream	ActReg chr12 #2779	0	1
2780	12	119,496,686	119,499,583	897	2	13	16.25	28	36	0	0	1	SRRM4	79,738	in gene	ActReg chr12 #2780	1	1
2781	12	120,314,466	120,315,353	887	1	9	13.926	15	23	1	1	1	CIT	183	in gene	ActReg chr12 #2781	0	1
2782	12	120,427,079	120,427,489	410	1	10.538	9.538	17	16	1	1	1	CCDC64	-364	upstream	ActReg chr12 #2782	1	0
2783	12	120,427,634	120,428,398	764	2	12.625	10.167	18	18	1	1	1	CCDC64	368	in gene	ActReg chr12 #2783	1	1
2784	12	120,524,568	120,525,402	834	2	12.769	12.885	21	18	1	0	2	CCDC64, RAB35	97337, 29658	in gene, downstream	ActReg chr12 #2784	1	1
2785	12	120,632,090	120,633,407	1,317	2	11.512	13.293	25	25	1	2	3	GCN1L1, RPLP0, LOC100506649	-235, 6266, -6363	upstream, downstream, upstream	ActReg chr12 #2785	1	1
2786	12	120,638,325	120,639,635	1,310	2	54.073	61.244	202	217	1	3	4	GCN1L1, RPLP0, LOC100506649, PXN	-6467, 34, -131, 64583	upstream, in gene, upstream, downstream	ActReg chr12 #2786	1	1
2787	12	120,669,053	120,669,937	884	1	11.393	9.714	17	14	0	0	1	PXN	34,068	in gene	ActReg chr12 #2787	1	0
2788	12	120,703,652	120,704,154	502	1	11.6	6.133	15	8	1	1	1	PXN	-340	upstream	ActReg chr12 #2788	1	0
2789	12	120,729,397	120,730,570	1,173	2	14.486	18.973	46	56	0	2	3	RNU4-2, RNU4-1, SIRT4	-277, 1057, -10141	upstream, downstream, upstream	ActReg chr12 #2789	1	1
2790	12	120,730,881	120,731,445	564	1	13.235	9.412	24	13	0	2	3	RNU4-2, RNU4-1, SIRT4	-1457, -123, -8961	upstream, upstream, upstream	ActReg chr12 #2790	1	0
2791	12	120,739,865	120,740,576	711	2	12.043	12.857	28	27	0	1	2	RNU4-1, SIRT4	-9180, 96	upstream, in gene	ActReg chr12 #2791	1	1
2792	12	120,883,856	120,884,666	810	2	11.48	15.84	20	28	1	2	3	COX6A1, TRIAP1, GATC	8357, -46, 20	downstream, upstream, in gene	ActReg chr12 #2792	1	1
2793	12	120,907,227	120,908,053	826	2	13	14.5	27	32	1	2	3	GATC, SFRS9, DYNLL1	23399, -82, -20	downstream, upstream, upstream	ActReg chr12 #2793	1	1
2794	12	120,933,746	120,934,531	785	1	7.28	10	14	17	1	1	3	DYNLL1, LOC100506668, COQ5	26478, -395, 32826	in gene, upstream, downstream	ActReg chr12 #2794	0	1
2795	12	120,966,570	120,967,367	797	1	8.48	12.2	16	18	1	2	2	COQ5, RNF10	-4, -5164	upstream, upstream	ActReg chr12 #2795	0	1
2796	12	120,972,106	120,972,563	457	1	7.5	11.714	14	16	1	2	2	COQ5, RNF10	-5370, 202	upstream, in gene	ActReg chr12 #2796	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2797	12	121,342,102	121,342,575	473	1	9.333	13.4	12	23	1	1	1	UNQ1887	-187	upstream	ActReg chr12 #2797	0	1
2798	12	121,344,754	121,345,683	929	2	7.966	10.552	15	17	0	1	1	UNQ1887	-3,067	upstream	ActReg chr12 #2798	1	1
2799	12	121,476,365	121,477,364	999	2	21.129	16.1	53	35	0	1	1	OASL	-84	upstream	ActReg chr12 #2799	1	1
2800	12	121,789,569	121,790,542	973	2	14	10.3	24	20	1	1	1	ANAPC5	1,957	in gene	ActReg chr12 #2800	1	1
2801	12	121,904,768	121,905,636	868	2	10.5	11.429	25	21	1	0	1	KDM2B	113,718	in gene	ActReg chr12 #2801	1	1
2802	12	122,231,373	122,232,448	1,075	1	9.088	11.941	21	16	1	1	2	RHOF, LOC338799	-316, 9480	upstream, downstream	ActReg chr12 #2802	0	1
2803	12	122,234,779	122,235,560	781	1	13.56	8.56	24	15	1	2	3	RHOF, LOC338799, SETD1B	-3575, 6221, -7469	upstream, in gene, upstream	ActReg chr12 #2803	1	0
2804	12	122,235,655	122,236,340	685	1	7.952	11.524	11	15	0	2	3	RHOF, LOC338799, SETD1B	-4403, 5393, -6641	upstream, in gene, upstream	ActReg chr12 #2804	0	1
2805	12	122,326,150	122,327,177	1,027	2	12.656	11.938	28	21	1	2	2	HPD, PSMD9	-146, 17	upstream, in gene	ActReg chr12 #2805	1	1
2806	12	122,516,021	122,516,644	623	1	9.7	13.1	17	23	1	1	2	LOC100506691, MLXIP	10345, -428	downstream, upstream	ActReg chr12 #2806	0	1
2807	12	122,710,254	122,710,923	669	1	11.381	6.524	19	14	1	1	2	DIABLO, VPS33A	1480, 40480	in gene, downstream	ActReg chr12 #2807	1	0
2808	12	122,750,453	122,751,554	1,101	2	12.257	16.029	28	27	1	1	2	VPS33A, CLIP1	65, 156113	in gene, downstream	ActReg chr12 #2808	1	1
2809	12	123,237,063	123,237,692	629	1	11.158	12.263	15	18	1	1	1	DENR	6	in gene	ActReg chr12 #2809	0	1
2810	12	123,380,380	123,381,196	816	2	12.346	13	27	31	1	1	1	VPS37B	-76	upstream	ActReg chr12 #2810	1	1
2811	12	123,428,923	123,430,181	1,258	2	12.275	11.75	23	21	0	0	1	ABCB9	30,200	in gene	ActReg chr12 #2811	1	1
2812	12	123,458,842	123,460,105	1,263	2	19.025	16.725	33	37	1	3	4	ABCB9, OGFOD2, ARL6IP4, PITPNM2	279, 119, -5407, 135502	in gene, in gene, upstream, downstream	ActReg chr12 #2812	1	1
2813	12	123,570,205	123,571,152	947	1	9.233	9.733	13	17	0	0	2	PITPNM2, LOC100507091	24297, 4747	in gene, downstream	ActReg chr12 #2813	0	1
2814	12	123,573,958	123,574,754	796	2	11.32	10	21	19	0	0	2	PITPNM2, LOC100507091	20619, 8425	in gene, downstream	ActReg chr12 #2814	1	1
2815	12	123,610,908	123,611,755	847	1	13.704	10.111	23	18	0	0	0				ActReg chr12 #2815	1	0
2816	12	123,717,131	123,717,930	799	2	12.28	12.8	22	29	1	1	1	C12orf65	-314	upstream	ActReg chr12 #2816	1	1
2817	12	124,068,664	124,069,540	876	2	14.643	20.214	33	45	1	1	1	TMED2	26	in gene	ActReg chr12 #2817	1	1
2818	12	124,085,962	124,087,043	1,081	2	14.294	12.853	28	25	1	1	3	TMED2, LOC100507130, DDX55	17426, 14062, -170	downstream, in gene, upstream	ActReg chr12 #2818	1	1
2819	12	124,117,793	124,118,718	925	2	12.179	13.821	21	32	1	2	2	EIF2B1, GTF2H3	68, -126	in gene, upstream	ActReg chr12 #2819	1	1
2820	12	124,676,291	124,677,228	937	1	8.759	11.172	14	17	0	0	0				ActReg chr12 #2820	0	1
2821	12	124,773,765	124,774,654	889	1	8.407	12.667	11	21	0	1	1	FAM101A	499	in gene	ActReg chr12 #2821	0	1
2822	12	125,050,986	125,051,633	647	1	6.05	11.4	10	20	1	1	1	NCOR2	701	in gene	ActReg chr12 #2822	0	1
2823	12	125,052,182	125,052,721	539	2	12.706	17.529	24	33	1	1	1	NCOR2	-441	upstream	ActReg chr12 #2823	1	1
2824	12	125,110,682	125,111,401	719	1	7.565	11.217	11	18	0	0	0				ActReg chr12 #2824	0	1
2825	12	125,165,882	125,166,867	985	1	9.484	12.355	16	19	0	0	0				ActReg chr12 #2825	0	1
2826	12	125,211,588	125,212,400	812	2	10.72	12	16	21	0	0	0				ActReg chr12 #2826	1	1
2827	12	125,398,493	125,399,893	1,400	2	16.091	18.204	42	45	1	1	2	LOC100288312, UBC	5110, 384	downstream, in gene	ActReg chr12 #2827	1	1
2828	12	125,401,493	125,402,460	967	1	15.133	8.067	32	19	0	1	2	LOC100288312, UBC	7893, -2399	downstream, upstream	ActReg chr12 #2828	1	0
2829	12	125,412,111	125,412,821	710	1	13.409	8.636	27	14	1	0	0				ActReg chr12 #2829	1	0
2830	12	125,425,124	125,425,866	742	1	11.261	8.217	18	13	0	0	1	DHX37	48,172	downstream	ActReg chr12 #2830	1	0
2831	12	125,533,851	125,534,751	900	1	7.571	11.357	11	18	1	0	0				ActReg chr12 #2831	0	1
2832	12	126,536,139	126,536,648	509	1	10.5	7.688	16	13	0	0	0				ActReg chr12 #2832	1	0
2833	12	126,895,459	126,896,010	551	1	10.529	5.938	18	9	0	0	0				ActReg chr12 #2833	1	0
2834	12	127,544,629	127,545,646	1,017	1	8.5	14.312	14	22	0	0	0				ActReg chr12 #2834	0	1
2835	12	127,610,277	127,610,865	588	1	11.222	9.944	16	19	0	0	0				ActReg chr12 #2835	1	0
2836	12	127,675,615	127,676,053	438	1	9.357	3.615	16	7	0	0	0				ActReg chr12 #2836	1	0
2837	12	127,715,203	127,715,821	618	1	10.158	13.053	13	22	0	0	0				ActReg chr12 #2837	0	1
2838	12	127,874,202	127,875,044	842	2	10.333	13.63	23	29	0	0	0				ActReg chr12 #2838	1	1
2839	12	127,969,950	127,970,552	602	1	8.579	9.789	13	15	0	0	0				ActReg chr12 #2839	0	1
2840	12	128,043,870	128,044,809	939	1	8.233	12.8	14	27	0	0	0				ActReg chr12 #2840	0	1
2841	12	131,260,622	131,261,676	1,054	2	11.727	13.485	24	26	0	0	0				ActReg chr12 #2841	1	1
2842	12	131,355,941	131,356,382	441	1	8.769	10.538	11	15	1	1	1	RAN	-456	upstream	ActReg chr12 #2842	0	1
2843	12	131,468,134	131,468,747	613	1	8.526	11.632	12	19	0	0	2	GPR133, LOC100128840	29968, 6133	in gene, downstream	ActReg chr12 #2843	0	1
2844	12	131,529,097	131,530,098	1,001	2	11.194	13.774	22	26	1	0	1	GPR133	91,145	in gene	ActReg chr12 #2844	1	1
2845	12	132,102,441	132,103,387	946	2	11.172	14.379	26	35	0	0	0				ActReg chr12 #2845	1	1
2846	12	132,194,917	132,196,094	1,177	2	11.639	16.417	26	26	1	1	1	SFRS8	-130	upstream	ActReg chr12 #2846	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2847	12	132,268,372	132,269,341	969	2	11.167	9.586	15	18	0	0	1	SFRS8	73,221	in gene	ActReg chr12 #2847	1	1
2848	12	132,269,393	132,270,028	635	1	8.4	9.85	14	18	0	0	1	SFRS8	74,075	in gene	ActReg chr12 #2848	0	1
2849	12	132,312,498	132,313,167	669	2	14.286	12.737	35	26	1	1	1	MMP17	-109	upstream	ActReg chr12 #2849	1	1
2850	12	132,628,665	132,629,323	658	2	12.526	12.476	24	27	1	2	2	DDX51, NOC4L	-114, 1	upstream, in gene	ActReg chr12 #2850	1	1
2851	12	133,263,713	133,264,478	765	2	14.783	12.409	34	28	1	2	2	POLE, PXMP2	-150, -97	upstream, upstream	ActReg chr12 #2851	1	1
2852	12	133,286,958	133,287,600	642	2	10.444	9.25	16	18	1	1	2	PXMP2, PGAM5	23087, -114	downstream, upstream	ActReg chr12 #2852	1	1
2853	12	133,338,752	133,339,139	387	1	10	7.538	16	11	1	1	2	ANKLE2, GOLGA3	-494, 66481	upstream, downstream	ActReg chr12 #2853	1	0
2854	12	133,405,361	133,405,831	470	1	10.533	13.6	16	24	1	1	1	GOLGA3	-170	upstream	ActReg chr12 #2854	0	1
2855	12	133,464,233	133,464,911	678	2	10.905	9.571	17	14	1	1	1	CHFR	-368	upstream	ActReg chr12 #2855	1	1
2856	12	133,532,642	133,533,209	567	1	6.353	14.765	9	27	1	1	1	ZNF605	-33	upstream	ActReg chr12 #2856	0	1
2857	12	133,562,532	133,563,259	727	1	7.952	12.454	15	21	1	1	1	ZNF26	-161	upstream	ActReg chr12 #2857	0	1
2858	12	133,656,426	133,657,941	1,515	2	11.766	14.319	20	24	1	1	1	ZNF140	146	in gene	ActReg chr12 #2858	1	1
2859	12	133,757,693	133,758,437	744	1	7.217	13.083	13	23	1	1	1	ZNF268	70	in gene	ActReg chr12 #2859	0	1
2860	13	20,160,825	20,161,517	692	1	9.318	12.409	15	21	0	0	0				ActReg chr13 #2860	0	1
2861	13	20,207,887	20,208,617	730	1	8.348	11.13	12	15	1	1	1	MPHOSPH8	464	in gene	ActReg chr13 #2861	0	1
2862	13	20,356,825	20,357,456	631	1	6.3	10	9	15	1	1	1	PSPC1	-57	upstream	ActReg chr13 #2862	0	1
2863	13	20,437,461	20,438,222	761	2	14.875	15.917	29	34	1	2	2	ZMYM5, LOC400099	-65, 717	upstream, in gene	ActReg chr13 #2863	1	1
2864	13	20,531,452	20,532,230	778	1	8.76	10.6	15	15	1	1	1	ZMYM2	-969	upstream	ActReg chr13 #2864	0	1
2865	13	20,735,154	20,736,005	851	1	13.074	6.926	19	11	1	1	1	GJA3	-396	upstream	ActReg chr13 #2865	1	0
2866	13	20,993,789	20,994,677	888	1	9.464	11.857	15	17	0	0	1	CRYL1	105,779	in gene	ActReg chr13 #2866	0	1
2867	13	21,100,112	21,100,781	669	1	7.476	12.191	15	18	1	1	1	CRYL1	-434	upstream	ActReg chr13 #2867	0	1
2868	13	21,347,235	21,348,392	1,157	2	9.417	13.028	18	18	1	1	2	N6AMT2, XPO4	244, 129100	in gene, downstream	ActReg chr13 #2868	1	1
2869	13	21,634,350	21,634,854	504	1	10.875	6.688	16	10	1	1	1	LATS2	1,120	in gene	ActReg chr13 #2869	1	0
2870	13	21,635,266	21,635,988	702	2	11.273	8.727	18	17	1	1	1	LATS2	85	in gene	ActReg chr13 #2870	1	1
2871	13	21,750,084	21,751,217	1,133	2	13.457	14.086	27	29	1	2	2	SKA3, MRP63	91, 278	in gene, in gene	ActReg chr13 #2871	1	1
2872	13	21,871,624	21,873,077	1,453	2	31.133	36.889	141	160	1	1	2	LOC650794, LOC100505610	8, 50510	in gene, downstream	ActReg chr13 #2872	1	1
2873	13	22,177,782	22,178,585	803	1	8.16	13	14	18	1	1	1	EFHA1	172	in gene	ActReg chr13 #2873	0	1
2874	13	24,007,212	24,008,219	1,007	1	10.774	8.355	17	15	0	1	2	SACS, LOC100506680	126, 14605	in gene, downstream	ActReg chr13 #2874	1	0
2875	13	24,041,266	24,041,749	483	1	4.571	12.5	6	19	0	1	1	LOC100506697	-2,134	upstream	ActReg chr13 #2875	0	1
2876	13	24,144,154	24,144,757	603	1	9.368	11.474	14	20	0	1	1	TNFRSF19	-268	upstream	ActReg chr13 #2876	0	1
2877	13	24,153,349	24,153,998	649	1	6.8	13	10	18	1	0	1	TNFRSF19	8,950	in gene	ActReg chr13 #2877	0	1
2878	13	24,462,916	24,464,514	1,598	2	35.82	40.3	176	189	1	2	3	MIPEP, PCOTH, RP11-45B20.2	-128, 687, 7410	upstream, in gene, downstream	ActReg chr13 #2878	1	1
2879	13	24,553,224	24,554,162	938	2	11.069	12.517	18	19	1	0	0				ActReg chr13 #2879	1	1
2880	13	24,734,325	24,735,251	926	1	6	9.862	12	15	1	2	2	SPATA13, MIR2276	-73, -1767	upstream, upstream	ActReg chr13 #2880	0	1
2881	13	25,086,101	25,087,260	1,159	1	13.889	9.889	25	17	1	1	1	PARP4	268	in gene	ActReg chr13 #2881	1	0
2882	13	25,496,364	25,497,459	1,095	1	14.059	11.5	22	17	1	1	1	CENPJ	174	in gene	ActReg chr13 #2882	1	0
2883	13	25,850,849	25,851,308	459	2	13.143	9.071	23	16	0	0	1	MTMR6	10,626	in gene	ActReg chr13 #2883	1	1
2884	13	25,860,649	25,862,156	1,507	2	22.425	25.979	80	90	1	1	1	MTMR6	302	in gene	ActReg chr13 #2884	1	1
2885	13	25,875,278	25,876,484	1,206	2	11.79	12.895	31	28	1	1	1	NUPL1	215	in gene	ActReg chr13 #2885	1	1
2886	13	26,067,985	26,068,444	459	1	9.714	10.571	12	14	0	0	1	ATP8A2	122,005	in gene	ActReg chr13 #2886	0	1
2887	13	26,760,198	26,761,025	827	1	8	13.154	17	25	1	0	0				ActReg chr13 #2887	0	1
2888	13	26,795,777	26,796,856	1,079	2	10.788	13.152	20	24	1	1	1	RNF6	192	in gene	ActReg chr13 #2888	1	1
2889	13	27,062,834	27,063,374	540	1	10.353	11.765	13	24	0	0	0				ActReg chr13 #2889	0	1
2890	13	27,131,360	27,131,726	366	1	10	6.083	15	8	1	0	0				ActReg chr13 #2890	1	0
2891	13	27,609,852	27,610,624	772	1	8.08	13.64	13	21	0	0	0				ActReg chr13 #2891	0	1
2892	13	27,746,045	27,746,644	599	2	9.789	11.263	19	16	0	1	1	USP12	-311	upstream	ActReg chr13 #2892	1	1
2893	13	27,769,385	27,769,909	524	2	10.5	9.938	16	14	0	0	0				ActReg chr13 #2893	1	1
2894	13	27,825,159	27,826,149	990	2	10.194	12.258	19	18	1	3	3	RPL21, SNORD102, SNORA27	-38, -3547, -3884	upstream, upstream, upstream	ActReg chr13 #2894	1	1
2895	13	27,845,075	27,845,643	568	1	7.389	11.222	10	17	1	1	1	RASL11A	895	in gene	ActReg chr13 #2895	0	1
2896	13	28,024,094	28,025,021	927	1	11.724	9.517	19	15	1	1	1	MTIF3	182	in gene	ActReg chr13 #2896	1	0
2897	13	28,366,120	28,367,735	1,615	2	11.02	16.88	35	45	1	1	1	GSX1	147	in gene	ActReg chr13 #2897	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2898	13	29,114,577	29,115,203	626	1	7.95	12	16	20	0	0	0				ActReg chr13 #2898	0	1
2899	13	29,148,617	29,149,236	619	1	9.737	13.526	14	24	0	0	0				ActReg chr13 #2899	0	1
2900	13	29,198,040	29,199,220	1,180	1	8.649	12.243	12	18	0	0	0				ActReg chr13 #2900	0	1
2901	13	30,010,046	30,010,706	660	1	4.81	11.048	9	15	0	0	1	MTUS2	411,628	in gene	ActReg chr13 #2901	0	1
2902	13	30,156,777	30,157,923	1,146	1	6.118	12.917	11	20	0	0	1	SLC7A1	12,475	in gene	ActReg chr13 #2902	0	1
2903	13	30,307,291	30,307,823	532	1	10.765	8.647	14	13	0	0	0				ActReg chr13 #2903	1	0
2904	13	30,963,663	30,964,256	593	1	9.737	9.526	14	15	0	0	0				ActReg chr13 #2904	0	1
2905	13	31,151,433	31,152,046	613	1	6.263	11.684	11	21	0	0	0				ActReg chr13 #2905	0	1
2906	13	31,191,484	31,192,707	1,223	2	10.744	13.333	20	26	1	1	1	USPL1	265	in gene	ActReg chr13 #2906	1	1
2907	13	31,247,687	31,248,855	1,168	2	11.472	12.444	19	19	1	0	0				ActReg chr13 #2907	1	1
2908	13	31,317,117	31,318,286	1,169	2	12.135	14.405	20	31	0	0	1	ALOX5AP	8,032	in gene	ActReg chr13 #2908	1	1
2909	13	31,403,135	31,403,950	815	2	15.885	15.423	31	26	0	0	0				ActReg chr13 #2909	1	1
2910	13	31,735,623	31,736,908	1,285	2	8.65	10.9	18	17	1	1	1	HSPH1	-148	upstream	ActReg chr13 #2910	1	1
2911	13	32,605,465	32,606,033	568	1	9.944	6.167	16	10	1	2	2	LOC100507099, FRY	31, 312	in gene, in gene	ActReg chr13 #2911	1	0
2912	13	32,889,303	32,889,831	528	1	7.647	10.529	11	17	1	2	2	ZAR1L, BRCA2	-3476, -50	upstream, upstream	ActReg chr13 #2912	0	1
2913	13	32,889,841	32,890,287	446	1	10.214	5.857	12	8	1	2	2	ZAR1L, BRCA2	-3973, 447	upstream, in gene	ActReg chr13 #2913	1	0
2914	13	33,112,339	33,113,571	1,232	2	22.615	20.18	59	62	0	1	1	N4BP2L2	-19	upstream	ActReg chr13 #2914	1	1
2915	13	34,021,115	34,021,818	703	2	9.409	11.864	17	24	0	0	0				ActReg chr13 #2915	1	1
2916	13	34,116,736	34,117,301	565	1	10.333	9.5	17	15	1	0	0				ActReg chr13 #2916	1	0
2917	13	34,184,388	34,185,048	660	1	11.1	6.5	19	11	0	0	0				ActReg chr13 #2917	1	0
2918	13	34,391,857	34,392,640	783	2	11.72	11.2	27	21	1	1	1	RFC3	42	in gene	ActReg chr13 #2918	1	1
2919	13	34,730,906	34,731,614	708	1	12.864	9.273	20	15	0	0	0				ActReg chr13 #2919	1	0
2920	13	34,921,775	34,922,545	770	1	12.75	3.75	21	8	0	0	0				ActReg chr13 #2920	1	0
2921	13	35,486,950	35,487,651	701	1	12.636	11.046	25	24	0	0	0				ActReg chr13 #2921	1	0
2922	13	35,500,559	35,501,109	550	2	11.286	14.941	20	26	0	0	0				ActReg chr13 #2922	1	1
2923	13	36,429,576	36,430,279	703	1	6.909	12	14	21	0	0	1	DCLK1	275,537	in gene	ActReg chr13 #2923	0	1
2924	13	36,920,207	36,921,175	968	2	11.586	14.9	24	25	1	1	2	SPG20, LOC100507135	23626, 116	in gene, in gene	ActReg chr13 #2924	1	1
2925	13	37,292,057	37,292,658	601	1	10.632	11.21	15	17	0	0	0				ActReg chr13 #2925	0	1
2926	13	37,393,655	37,394,319	664	1	4.857	10.857	7	17	1	1	1	RFXAP	648	in gene	ActReg chr13 #2926	0	1
2927	13	37,572,841	37,573,946	1,105	2	35.294	37.912	136	126	1	2	3	ALG5, EXOSC8, FAM48A	111, -1285, 60457	in gene, upstream, downstream	ActReg chr13 #2927	1	1
2928	13	37,574,491	37,575,210	719	2	11	11.565	20	19	1	2	3	ALG5, EXOSC8, FAM48A	-1346, 172, 59000	upstream, in gene, downstream	ActReg chr13 #2928	1	1
2929	13	39,248,208	39,248,922	714	2	12.773	9.381	26	21	0	0	0				ActReg chr13 #2929	1	1
2930	13	39,462,483	39,462,958	475	1	9.2	9.667	12	17	0	0	1	FREM2	201,547	downstream	ActReg chr13 #2930	0	1
2931	13	39,611,666	39,612,867	1,181	2	13.324	17.811	32	42	2	2	2	C13orf23, NHLRC3	-24, -179	upstream, upstream	ActReg chr13 #2931	1	1
2932	13	40,414,255	40,414,840	585	1	11.111	8.722	19	13	0	0	0				ActReg chr13 #2932	1	0
2933	13	40,676,890	40,677,423	533	1	5.941	11.529	8	21	0	0	0				ActReg chr13 #2933	0	1
2934	13	40,738,070	40,738,578	508	1	5.133	12.5	8	19	0	0	0				ActReg chr13 #2934	0	1
2935	13	40,742,491	40,743,277	786	1	7.68	10.88	13	17	0	0	0				ActReg chr13 #2935	0	1
2936	13	40,976,402	40,976,923	521	1	10.125	2.875	17	5	0	0	1	LOC646982	78,481	in gene	ActReg chr13 #2936	1	0
2937	13	41,027,648	41,028,320	672	2	9.8	9.682	18	16	0	0	1	LOC646982	27,159	in gene	ActReg chr13 #2937	1	1
2938	13	41,238,698	41,239,959	1,261	2	9.949	11.41	16	22	1	1	1	FOXO1	1,406	in gene	ActReg chr13 #2938	1	1
2939	13	41,344,926	41,345,718	792	2	12.08	11.88	25	25	1	1	1	MRPS31	25	in gene	ActReg chr13 #2939	1	1
2940	13	41,495,333	41,496,213	880	1	9.333	11.111	17	18	1	0	1	ELF1	97,735	downstream	ActReg chr13 #2940	0	1
2941	13	41,634,046	41,636,301	2,255	2	9.859	13.225	29	24	1	1	1	WBP4	-524	upstream	ActReg chr13 #2941	1	1
2942	13	41,706,077	41,707,301	1,224	1	8.59	12.18	25	27	1	1	1	KBTBD6	247	in gene	ActReg chr13 #2942	0	1
2943	13	41,768,212	41,769,062	850	2	10.852	11.037	18	28	1	1	1	KBTBD7	65	in gene	ActReg chr13 #2943	1	1
2944	13	41,884,910	41,886,018	1,108	2	10.857	9.429	21	17	1	1	1	NAA16	123	in gene	ActReg chr13 #2944	1	1
2945	13	42,534,787	42,535,611	824	1	9.32	12.08	18	16	1	2	2	KIAA0564, LOC100507240	22, -106	in gene, upstream	ActReg chr13 #2945	0	1
2946	13	43,294,461	43,294,993	532	1	10.118	9.529	15	17	0	0	0				ActReg chr13 #2946	0	1
2947	13	43,632,070	43,632,767	697	1	9.619	10.476	14	13	0	0	1	DNAJC15	35,056	in gene	ActReg chr13 #2947	0	1
2948	13	44,379,108	44,379,727	619	1	7.412	9	13	18	0	0	0				ActReg chr13 #2948	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2949	13	44,453,120	44,453,633	513	1	10.529	11.118	15	15	1	2	2	CCDC122, C13orf31	450, -44	in gene, upstream	ActReg chr13 #2949	1	0
2950	13	44,706,724	44,707,420	696	1	8.857	12.238	12	22	0	0	1	LOC100507253	-9,392	upstream	ActReg chr13 #2950	0	1
2951	13	44,733,637	44,734,359	722	1	8.273	12.091	18	25	0	0	1	LOC100507253	17,534	downstream	ActReg chr13 #2951	0	1
2952	13	44,817,019	44,817,762	743	1	12.75	9.167	21	13	0	0	0				ActReg chr13 #2952	1	0
2953	13	45,391,080	45,391,604	524	1	5.375	12.062	11	16	0	0	0				ActReg chr13 #2953	0	1
2954	13	45,393,054	45,393,806	752	1	8.583	12.167	13	21	0	0	0				ActReg chr13 #2954	0	1
2955	13	45,491,697	45,493,080	1,383	2	12.628	12.674	20	25	0	0	0				ActReg chr13 #2955	1	1
2956	13	45,563,213	45,564,144	931	2	11.276	9.724	18	18	1	2	2	NUFIP1, KIAA1704	-65, -9	upstream, upstream	ActReg chr13 #2956	1	1
2957	13	45,915,102	45,915,802	700	2	9.818	14.546	18	26	1	3	4	LOC100287803, TPT1, SNORA31, LOC100190939	4451, -155, -3708, -28	in gene, upstream, upstream, upstream	ActReg chr13 #2957	1	1
2958	13	45,991,569	45,992,784	1,215	1	7.763	11.842	13	20	1	2	2	SLC25A30, LOC100507293	340, 217	in gene, in gene	ActReg chr13 #2958	0	1
2959	13	46,038,624	46,039,883	1,259	1	8.4	11.6	16	20	1	1	1	COG3	182	in gene	ActReg chr13 #2959	0	1
2960	13	46,626,546	46,627,213	667	1	9.667	10.667	14	21	1	1	2	ZC3H13, CPB2	15, 52332	in gene, downstream	ActReg chr13 #2960	0	1
2961	13	47,127,709	47,128,460	751	1	12.292	8.042	20	13	1	1	1	LRCH1	788	in gene	ActReg chr13 #2961	1	0
2962	13	47,370,583	47,371,327	744	1	7.696	9.783	12	13	1	1	1	ESD	412	in gene	ActReg chr13 #2962	0	1
2963	13	48,235,068	48,235,679	611	2	8.737	7.842	18	15	0	0	0				ActReg chr13 #2963	1	1
2964	13	48,574,821	48,575,951	1,130	1	7.829	11.543	13	17	1	1	1	SUCLA2	76	in gene	ActReg chr13 #2964	0	1
2965	13	48,611,419	48,612,545	1,126	2	14.556	15.611	26	26	1	1	1	NUDT15	279	in gene	ActReg chr13 #2965	1	1
2966	13	48,668,765	48,669,700	935	2	27.6	33.633	83	99	1	1	1	MED4	8	in gene	ActReg chr13 #2966	1	1
2967	13	48,784,181	48,784,824	643	1	11.4	6.55	20	14	0	0	0				ActReg chr13 #2967	1	0
2968	13	49,020,655	49,021,152	497	1	9.938	4.875	15	9	0	1	2	RB1, LPAR6	143020, -2063	in gene, upstream	ActReg chr13 #2968	1	0
2969	13	49,106,612	49,107,440	828	1	11.731	10.308	18	17	1	1	1	RCBTB2	290	in gene	ActReg chr13 #2969	1	0
2970	13	49,323,696	49,324,360	664	1	6.952	10.714	11	19	0	0	0				ActReg chr13 #2970	0	1
2971	13	49,466,337	49,467,383	1,046	2	15.031	12.344	31	22	0	0	0				ActReg chr13 #2971	1	1
2972	13	50,017,828	50,018,837	1,009	1	9.581	11.613	17	18	1	2	2	CAB39L, SETDB2	-111, -97	upstream, upstream	ActReg chr13 #2972	0	1
2973	13	50,070,232	50,070,810	578	1	7.944	11.556	12	19	1	1	2	SETDB2, PHF11	52092, 720	downstream, in gene	ActReg chr13 #2973	0	1
2974	13	50,366,525	50,367,230	705	2	13.727	14.546	27	28	1	1	1	KPNA3	180	in gene	ActReg chr13 #2974	1	1
2975	13	50,509,809	50,510,931	1,122	2	18.971	24.629	47	75	1	1	1	C13orf1	256	in gene	ActReg chr13 #2975	1	1
2976	13	50,697,948	50,699,390	1,442	3	8.956	12.822	15	29	1	1	1	DLEU2	1,008	in gene	ActReg chr13 #2976	1	1
2977	13	50,985,360	50,985,892	532	1	7.941	10.588	13	13	0	0	0				ActReg chr13 #2977	0	1
2978	13	51,199,982	51,200,580	598	1	4.158	10.632	7	15	0	0	0				ActReg chr13 #2978	0	1
2979	13	51,483,542	51,484,867	1,325	1	7.071	13.857	11	20	1	1	1	RNASEH2B	312	in gene	ActReg chr13 #2979	0	1
2980	13	52,377,513	52,378,130	617	1	7.684	12.21	12	17	1	2	3	DHRS12, LOC100507413, RP11-327P2.4	472, 88, 41465	in gene, in gene, downstream	ActReg chr13 #2980	0	1
2981	13	52,378,135	52,378,750	615	1	8.056	11.263	13	18	1	2	3	DHRS12, LOC100507413, RP11-327P2.4	-149, 709, 40844	upstream, in gene, downstream	ActReg chr13 #2981	0	1
2982	13	53,024,145	53,025,071	926	2	9.655	11.517	15	18	1	2	2	VPS36, CKAP2	155, -4887	in gene, upstream	ActReg chr13 #2982	1	1
2983	13	53,029,077	53,030,285	1,208	1	8.053	10.29	15	17	1	2	2	VPS36, CKAP2	-4918, 186	upstream, in gene	ActReg chr13 #2983	0	1
2984	13	53,191,105	53,192,048	943	1	8.103	11.931	11	21	1	1	1	HNRNPA1L2	-29	upstream	ActReg chr13 #2984	0	1
2985	13	53,226,147	53,227,518	1,371	2	11.333	12.976	24	38	1	1	2	HNRNPA1L2, SUGT1	35227, 1	downstream, in gene	ActReg chr13 #2985	1	1
2986	13	53,424,393	53,425,640	1,247	2	10.256	12.462	15	18	1	1	1	PCDH8	-2,242	upstream	ActReg chr13 #2986	1	1
2987	13	60,737,687	60,738,467	780	1	10.12	12.72	18	27	1	1	1	DIAPH3	42	in gene	ActReg chr13 #2987	0	1
2988	13	62,269,168	62,269,696	528	1	11.235	6.941	18	14	0	0	0				ActReg chr13 #2988	1	0
2989	13	63,216,918	63,217,779	861	2	10.407	13.37	24	24	0	0	0				ActReg chr13 #2989	1	1
2990	13	64,009,795	64,010,330	535	1	7.188	10.688	11	17	0	0	0				ActReg chr13 #2990	0	1
2991	13	64,649,609	64,650,379	770	1	6.917	11.125	14	19	0	0	0				ActReg chr13 #2991	0	1
2992	13	64,651,239	64,651,994	755	1	12.522	9.13	20	14	0	0	0				ActReg chr13 #2992	1	0
2993	13	65,125,879	65,126,427	548	1	7.824	11.412	15	16	0	0	0				ActReg chr13 #2993	0	1
2994	13	66,114,479	66,114,921	442	1	10.643	6.429	19	11	0	0	0				ActReg chr13 #2994	1	0
2995	13	67,804,218	67,805,078	860	2	13.148	12.518	21	18	1	2	2	PCDH9, LOC730236	-180, -67	upstream, upstream	ActReg chr13 #2995	1	1
2996	13	68,343,463	68,344,387	924	1	7.655	10.207	11	18	0	0	0				ActReg chr13 #2996	0	1
2997	13	69,795,905	69,796,301	396	1	9.5	10.167	12	14	0	0	0				ActReg chr13 #2997	0	1
2998	13	72,958,877	72,959,407	530	1	9.235	6.875	16	10	0	0	0				ActReg chr13 #2998	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
2999	13	73,301,088	73,302,331	1,243	2	12.436	13.949	31	30	1	2	2	C13orf37, C13orf34	229, -333	in gene, upstream	ActReg chr13 #2999	1	1
3000	13	73,911,147	73,911,510	363	1	10.182	3.818	15	5	0	0	0				ActReg chr13 #3000	1	0
3001	13	74,707,838	74,708,309	471	1	7.533	9.4	11	15	1	1	1	KLF12	-7	upstream	ActReg chr13 #3001	0	1
3002	13	74,709,791	74,710,545	754	1	7.875	10.292	17	15	1	1	1	KLF12	-2,102	upstream	ActReg chr13 #3002	0	1
3003	13	74,784,917	74,785,532	615	2	11.421	15.053	18	29	0	0	0				ActReg chr13 #3003	1	1
3004	13	76,055,508	76,056,947	1,439	1	9	10.311	16	18	1	1	1	TBC1D4	23	in gene	ActReg chr13 #3004	0	1
3005	13	76,111,575	76,112,575	1,000	2	11.355	14.129	23	32	1	1	1	COMMD6	-84	upstream	ActReg chr13 #3005	1	1
3006	13	76,123,314	76,124,335	1,021	2	10.969	13.844	22	22	1	1	1	UCHL3	-103	upstream	ActReg chr13 #3006	1	1
3007	13	76,210,480	76,211,118	638	1	12.95	8.2	22	11	1	0	1	LMO7	16,229	in gene	ActReg chr13 #3007	1	0
3008	13	76,567,844	76,568,295	451	1	9.714	10.571	16	19	0	0	0				ActReg chr13 #3008	0	1
3009	13	76,593,423	76,594,287	864	1	6.37	12.926	10	18	0	0	0				ActReg chr13 #3009	0	1
3010	13	77,566,073	77,566,645	572	1	10.111	11.833	17	18	1	1	1	CLN5	300	in gene	ActReg chr13 #3010	0	1
3011	13	77,900,404	77,901,627	1,223	1	8.316	11.947	17	25	1	1	1	MYCBP2	162	in gene	ActReg chr13 #3011	0	1
3012	13	77,903,095	77,903,957	862	2	12.889	11.926	20	24	1	1	1	MYCBP2	-2,349	upstream	ActReg chr13 #3012	1	1
3013	13	78,427,829	78,428,468	639	1	10.15	6.4	18	12	0	0	1	LOC100505518	35,076	in gene	ActReg chr13 #3013	1	0
3014	13	78,492,424	78,493,092	668	1	11.333	9.19	18	12	1	1	2	LOC100505518, EDNRB	99686, 208	downstream, in gene	ActReg chr13 #3014	1	0
3015	13	79,702,237	79,702,796	559	2	8.556	8.778	14	17	0	0	0				ActReg chr13 #3015	1	1
3016	13	79,980,137	79,981,070	933	1	6.552	13.069	13	19	1	2	2	RBM26, LOC100505538	-680, 120	upstream, in gene	ActReg chr13 #3016	0	1
3017	13	80,205,323	80,205,726	403	1	5.583	11.667	9	20	0	0	0				ActReg chr13 #3017	0	1
3018	13	80,561,366	80,561,978	612	1	9.947	6.211	16	11	0	0	0				ActReg chr13 #3018	1	0
3019	13	80,563,189	80,563,710	521	1	11.938	9	16	13	0	0	0				ActReg chr13 #3019	1	0
3020	13	80,614,575	80,615,296	721	2	13.13	12.217	23	22	0	0	0				ActReg chr13 #3020	1	1
3021	13	80,916,687	80,917,635	948	1	6.833	9.867	14	18	0	1	1	SPRY2	-2,075	upstream	ActReg chr13 #3021	0	1
3022	13	80,953,480	80,953,914	434	1	10.462	6.923	17	11	0	0	0				ActReg chr13 #3022	1	0
3023	13	81,042,844	81,043,382	538	1	9.529	6.353	15	10	0	0	0				ActReg chr13 #3023	1	0
3024	13	81,622,080	81,622,509	429	1	11	11.214	14	13	0	0	0				ActReg chr13 #3024	1	0
3025	13	84,073,223	84,073,948	725	2	10.318	12.364	15	20	0	0	0				ActReg chr13 #3025	1	1
3026	13	84,453,349	84,454,887	1,538	1	6.792	12.604	14	21	1	1	1	SLITRK1	2,410	in gene	ActReg chr13 #3026	0	1
3027	13	84,455,825	84,456,663	838	2	15.654	21.615	37	50	0	1	1	SLITRK1	284	in gene	ActReg chr13 #3027	1	1
3028	13	84,660,236	84,661,047	811	1	12.64	13.24	19	20	0	0	0				ActReg chr13 #3028	0	1
3029	13	85,439,874	85,440,589	715	1	6.045	10.409	12	17	0	0	0				ActReg chr13 #3029	0	1
3030	13	85,887,709	85,888,400	691	1	8.409	13.409	12	27	0	0	0				ActReg chr13 #3030	0	1
3031	13	85,888,588	85,889,327	739	2	9.043	10.391	17	18	0	0	0				ActReg chr13 #3031	1	1
3032	13	86,160,435	86,161,185	750	1	8	9.583	11	13	0	0	0				ActReg chr13 #3032	0	1
3033	13	86,225,235	86,226,049	814	1	9.846	7.36	16	12	0	0	0				ActReg chr13 #3033	1	0
3034	13	87,233,956	87,234,599	643	1	7.4	11.25	13	19	0	0	0				ActReg chr13 #3034	0	1
3035	13	87,444,042	87,444,852	810	2	22.72	21.08	52	48	0	0	0				ActReg chr13 #3035	1	1
3036	13	87,731,881	87,733,155	1,274	1	11.175	8.6	15	12	0	0	0				ActReg chr13 #3036	1	0
3037	13	88,150,726	88,151,458	732	2	12	13.043	22	26	0	0	1	hCG_1795283	172,126	in gene	ActReg chr13 #3037	1	1
3038	13	88,323,176	88,324,281	1,105	1	10.735	14.559	23	28	1	2	2	hCG_1795283, SLITRK5	-510, -1142	upstream, upstream	ActReg chr13 #3038	0	1
3039	13	88,462,467	88,463,616	1,149	2	11.556	15.611	23	26	0	0	0				ActReg chr13 #3039	1	1
3040	13	88,606,549	88,606,989	440	1	9.5	7.143	15	12	0	0	0				ActReg chr13 #3040	1	0
3041	13	89,815,246	89,815,909	663	1	13.476	11.238	31	21	0	0	0				ActReg chr13 #3041	1	0
3042	13	90,378,847	90,379,437	590	2	10.316	10.895	21	16	0	0	0				ActReg chr13 #3042	1	1
3043	13	92,001,220	92,001,648	428	1	4.846	10.923	7	18	1	7	7	MIR17HG, MIR17, MIR18A, MIR19A, MIR20A, MIR19B1, MIR92A1	1360, -1425, -1571, -1711, -1885, -2012, -2134	in gene, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr13 #3043	0	1
3044	13	93,495,757	93,496,395	638	1	7.25	9.8	11	17	0	0	1	GPC5	1,445,141	in gene	ActReg chr13 #3044	0	1
3045	13	93,803,302	93,804,089	787	1	10.958	9.708	14	14	0	0	0				ActReg chr13 #3045	1	0
3046	13	93,822,155	93,822,887	732	2	14.043	11.565	31	22	0	0	0				ActReg chr13 #3046	1	1
3047	13	93,869,679	93,870,501	822	1	7.231	11.077	17	19	0	0	1	GPC6	-8,988	upstream	ActReg chr13 #3047	0	1
3048	13	93,878,663	93,881,075	2,412	3	11.68	14.4	20	24	1	1	1	GPC6	791	in gene	ActReg chr13 #3048	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3049	13	93,900,744	93,901,331	587	1	7.722	12.778	11	21	0	0	1	GPC6	21,959	in gene	ActReg chr13 #3049	0	1
3050	13	93,901,656	93,902,338	682	1	11	9.864	15	13	0	0	1	GPC6	22,919	in gene	ActReg chr13 #3050	1	0
3051	13	94,016,355	94,016,895	540	1	7.438	13.625	11	25	0	0	1	GPC6	137,547	in gene	ActReg chr13 #3051	0	1
3052	13	94,499,204	94,499,825	621	1	8.947	10.632	16	20	0	0	1	GPC6	620,436	in gene	ActReg chr13 #3052	0	1
3053	13	94,981,893	94,982,582	689	1	7.19	10.714	11	18	0	0	1	GPC6	1,103,159	in gene	ActReg chr13 #3053	0	1
3054	13	95,253,679	95,254,561	882	1	9.679	11.857	14	15	1	2	2	TGDS, GPR180	-5609, 16	upstream, in gene	ActReg chr13 #3054	0	1
3055	13	95,752,590	95,753,418	828	2	10.808	10.808	17	18	0	0	1	ABCC4	200,683	in gene	ActReg chr13 #3055	1	1
3056	13	95,952,873	95,953,791	918	2	11.893	13.714	23	26	1	1	1	ABCC4	355	in gene	ActReg chr13 #3056	1	1
3057	13	96,187,394	96,188,230	836	2	13.615	13.346	23	25	0	0	1	CLDN10	101,959	in gene	ActReg chr13 #3057	1	1
3058	13	96,295,802	96,296,699	897	1	11	11.821	19	16	1	1	1	DZIP1	707	in gene	ActReg chr13 #3058	0	1
3059	13	96,328,718	96,329,855	1,137	2	12.171	14.029	17	25	1	2	2	LOC100289274, DNAJC3	-125, -107	upstream, upstream	ActReg chr13 #3059	1	1
3060	13	97,646,125	97,646,869	744	1	11.478	9.478	23	18	1	1	1	OXGR1	107	in gene	ActReg chr13 #3060	1	0
3061	13	97,655,262	97,655,771	509	1	10.812	5.062	17	9	0	0	1	OXGR1	-8,912	upstream	ActReg chr13 #3061	1	0
3062	13	97,907,021	97,907,504	483	1	10.133	8	17	14	0	0	1	MBNL2	32,688	in gene	ActReg chr13 #3062	1	0
3063	13	97,947,629	97,948,204	575	1	9.944	3.647	15	6	0	0	1	MBNL2	73,342	in gene	ActReg chr13 #3063	1	0
3064	13	98,019,171	98,019,688	517	1	6.625	10.25	12	17	0	0	1	MBNL2	144,855	in gene	ActReg chr13 #3064	0	1
3065	13	98,047,649	98,048,510	861	2	9.692	15.5	18	33	0	0	1	MBNL2	173,505	downstream	ActReg chr13 #3065	1	1
3066	13	98,085,253	98,086,303	1,050	1	12	10.25	21	16	1	1	1	RAP2A	-697	upstream	ActReg chr13 #3066	1	0
3067	13	98,300,898	98,301,365	467	1	11.643	11.143	17	14	0	0	0				ActReg chr13 #3067	1	0
3068	13	98,371,940	98,372,535	595	1	4.5	10.5	7	19	0	0	0				ActReg chr13 #3068	0	1
3069	13	98,432,570	98,433,244	674	2	11.048	11.762	19	17	0	0	0				ActReg chr13 #3069	1	1
3070	13	99,128,582	99,129,260	678	1	11.286	13.619	22	24	0	0	1	STK24	100,475	in gene	ActReg chr13 #3070	0	1
3071	13	99,161,723	99,162,282	559	1	10.389	6.167	18	10	0	0	1	STK24	67,394	in gene	ActReg chr13 #3071	1	0
3072	13	99,739,049	99,739,887	838	1	5.923	13.115	10	20	1	1	1	DOCK9	-808	upstream	ActReg chr13 #3072	0	1
3073	13	99,852,537	99,853,291	754	1	9.708	13.25	15	26	1	2	2	LOC100289373, UBAC2	97, 235	in gene, in gene	ActReg chr13 #3073	0	1
3074	13	100,153,093	100,154,029	936	2	13.793	11.724	26	18	1	1	1	TM9SF2	-167	upstream	ActReg chr13 #3074	1	1
3075	13	100,448,170	100,448,902	732	2	11.87	14.261	21	23	0	0	1	CLYBL	189,617	in gene	ActReg chr13 #3075	1	1
3076	13	100,740,824	100,741,651	827	2	10.5	13.039	24	18	1	2	2	LOC100507636, PCCA	-40, -32	upstream, upstream	ActReg chr13 #3076	1	1
3077	13	101,240,723	101,241,719	996	2	11.968	16.323	36	35	1	1	2	A2LD1, LOC100507654	-175, -8850	upstream, upstream	ActReg chr13 #3077	1	1
3078	13	102,118,098	102,118,719	621	1	9.842	8.158	21	11	0	0	1	ITGBL1	13,442	in gene	ActReg chr13 #3078	1	0
3079	13	102,497,793	102,498,278	485	1	10.933	6.067	16	9	0	0	1	FGF14	556,089	in gene	ActReg chr13 #3079	1	0
3080	13	102,571,681	102,572,305	624	2	8.789	10.947	15	17	0	0	1	FGF14	482,131	in gene	ActReg chr13 #3080	1	1
3081	13	103,052,186	103,053,201	1,015	1	6.875	10.094	14	15	1	2	3	FGF14, LOC283480, LOC283481	1431, -5824, 5765	in gene, upstream, downstream	ActReg chr13 #3081	0	1
3082	13	103,057,853	103,058,496	643	1	6.333	14.905	12	28	0	1	2	FGF14, LOC283481	-4050, 11246	upstream, downstream	ActReg chr13 #3082	0	1
3083	13	103,248,888	103,249,542	654	1	9.381	11.905	15	19	1	1	1	TPP2	-71	upstream	ActReg chr13 #3083	0	1
3084	13	103,425,949	103,426,643	694	1	13.046	8.864	19	14	1	1	2	C13orf27, KDELC1	-147, 25108	upstream, downstream	ActReg chr13 #3084	1	0
3085	13	103,450,913	103,451,711	798	1	8.292	12.75	11	20	1	2	2	KDELC1, BIVM	92, -87	in gene, upstream	ActReg chr13 #3085	0	1
3086	13	103,451,805	103,452,527	722	1	6.565	11.696	10	17	1	2	2	KDELC1, BIVM	-762, 767	upstream, in gene	ActReg chr13 #3086	0	1
3087	13	103,497,764	103,498,580	816	1	12.36	15.52	26	31	1	1	2	BIVM, ERCC5	46773, -2	downstream, upstream	ActReg chr13 #3087	0	1
3088	13	104,038,496	104,039,344	848	2	18.185	21.815	51	58	0	0	0				ActReg chr13 #3088	1	1
3089	13	104,695,312	104,696,062	750	2	10.783	10.391	18	18	0	0	0				ActReg chr13 #3089	1	1
3090	13	105,102,017	105,102,784	767	1	5.25	11.958	10	20	0	0	0				ActReg chr13 #3090	0	1
3091	13	105,311,315	105,312,153	838	2	12	11.577	23	19	0	0	0				ActReg chr13 #3091	1	1
3092	13	105,490,030	105,490,716	686	1	3.579	11.095	7	18	0	0	0				ActReg chr13 #3092	0	1
3093	13	106,239,947	106,240,782	835	2	12.423	14	33	33	0	0	0				ActReg chr13 #3093	1	1
3094	13	106,294,735	106,295,476	743	2	12.652	12.783	21	21	0	0	0				ActReg chr13 #3094	1	1
3095	13	106,426,150	106,427,057	907	1	7.071	12.393	10	19	0	0	0				ActReg chr13 #3095	0	1
3096	13	106,643,582	106,644,575	993	2	11.839	11.452	24	20	0	0	0				ActReg chr13 #3096	1	1
3097	13	106,803,510	106,804,441	931	1	11.586	8.966	19	21	0	0	0				ActReg chr13 #3097	1	0
3098	13	106,828,491	106,829,161	670	1	9.381	10.809	17	16	0	0	0				ActReg chr13 #3098	0	1
3099	13	107,028,180	107,029,739	1,559	1	7.837	12.796	16	22	0	1	1	LOC728192	48	in gene	ActReg chr13 #3099	0	1
3100	13	107,124,161	107,124,905	744	1	6.87	10.652	13	15	0	0	0				ActReg chr13 #3100	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3101	13	107,160,031	107,160,575	544	1	10.941	11.765	17	17	0	0	1	EFNB2	27,034	in gene	ActReg chr13 #3101	0	1
3102	13	107,165,322	107,166,144	822	1	11.615	9.231	17	14	0	0	1	EFNB2	21,604	in gene	ActReg chr13 #3102	1	0
3103	13	107,219,658	107,220,544	886	1	10.464	11.643	18	18	1	1	1	ARGLU1	413	in gene	ActReg chr13 #3103	0	1
3104	13	108,516,698	108,517,749	1,051	2	11.303	12.333	23	24	0	1	1	FAM155A	2,237	in gene	ActReg chr13 #3104	1	1
3105	13	108,772,632	108,773,088	456	1	4.933	9.733	8	14	0	0	0				ActReg chr13 #3105	0	1
3106	13	108,870,295	108,871,205	910	2	10.724	13.138	21	24	1	2	2	LIG4, ABHD13	-34, -13	upstream, upstream	ActReg chr13 #3106	1	1
3107	13	108,929,782	108,930,452	670	1	9	11.238	17	21	0	0	1	TNFSF13B	8,140	in gene	ActReg chr13 #3107	0	1
3108	13	109,554,579	109,555,300	721	1	10.304	11.478	15	17	0	0	1	MYO16	306,439	in gene	ActReg chr13 #3108	0	1
3109	13	109,637,364	109,638,016	652	1	9.333	12.619	18	16	0	0	1	MYO16	389,190	in gene	ActReg chr13 #3109	0	1
3110	13	109,639,549	109,640,351	802	1	9.08	11.92	13	18	0	0	1	MYO16	391,450	in gene	ActReg chr13 #3110	0	1
3111	13	109,833,066	109,833,677	611	1	6.579	11.368	10	17	0	0	1	MYO16	584,871	in gene	ActReg chr13 #3111	0	1
3112	13	109,895,521	109,896,279	758	1	11.913	9	17	12	0	0	0				ActReg chr13 #3112	1	0
3113	13	110,434,259	110,437,041	2,782	2	12.391	14.483	24	22	1	1	1	IRS2	3,264	in gene	ActReg chr13 #3113	1	1
3114	13	110,443,379	110,443,988	609	1	6.632	10.263	12	18	0	1	1	IRS2	-4,769	upstream	ActReg chr13 #3114	0	1
3115	13	110,492,474	110,493,317	843	1	10.926	15.704	19	30	0	0	0				ActReg chr13 #3115	0	1
3116	13	110,650,936	110,651,797	861	1	8.815	12.222	13	20	0	0	0				ActReg chr13 #3116	0	1
3117	13	110,658,267	110,659,222	955	2	12.867	12.933	24	19	0	0	0				ActReg chr13 #3117	1	1
3118	13	110,679,699	110,680,857	1,158	1	14.917	9.083	30	18	0	0	0				ActReg chr13 #3118	1	0
3119	13	110,746,745	110,747,713	968	2	12.613	13.613	23	32	0	0	0				ActReg chr13 #3119	1	1
3120	13	110,760,396	110,761,650	1,254	1	11.154	13.462	17	21	0	0	0				ActReg chr13 #3120	0	1
3121	13	110,790,123	110,790,857	734	1	13.043	14.565	20	25	1	0	0				ActReg chr13 #3121	0	1
3122	13	110,958,614	110,960,684	2,070	2	11.431	11.492	18	18	1	2	2	COL4A1, COL4A2	-153, 18	upstream, in gene	ActReg chr13 #3122	1	1
3123	13	110,971,546	110,973,006	1,460	2	14.652	13.109	26	23	0	0	1	COL4A2	12,645	in gene	ActReg chr13 #3123	1	1
3124	13	111,151,696	111,153,138	1,442	2	10.911	11.4	21	19	0	0	1	COL4A2	192,786	in gene	ActReg chr13 #3124	1	1
3125	13	111,213,308	111,214,113	805	1	7.077	11.5	12	19	1	1	1	RAB20	361	in gene	ActReg chr13 #3125	0	1
3126	13	111,267,412	111,268,850	1,438	2	12.8	12.778	22	19	1	1	1	CARKD	123	in gene	ActReg chr13 #3126	1	1
3127	13	111,365,056	111,366,064	1,008	1	12.062	13	19	20	1	2	2	CARS2, ING1	-7080, 477	upstream, in gene	ActReg chr13 #3127	0	1
3128	13	111,366,979	111,368,119	1,140	1	8.886	10.657	15	13	1	1	2	CARS2, ING1	-9069, 2466	upstream, in gene	ActReg chr13 #3128	0	1
3129	13	111,521,668	111,523,194	1,526	1	10.34	15.234	23	26	0	1	2	C13orf29, ANKRD10	224, 44985	in gene, downstream	ActReg chr13 #3129	0	1
3130	13	111,566,849	111,568,001	1,152	1	10.778	12.222	18	26	1	1	1	ANKRD10	-9	upstream	ActReg chr13 #3130	0	1
3131	13	111,805,372	111,806,885	1,513	2	12.729	15.062	27	30	1	1	2	ARHGEF7, LOC100505533	38504, -204	in gene, upstream	ActReg chr13 #3131	1	1
3132	13	113,241,537	113,242,876	1,339	2	11.341	13.854	16	22	2	1	1	TUBGCP3	275	in gene	ActReg chr13 #3132	1	1
3133	13	113,622,742	113,623,455	713	1	4.955	12.954	9	23	1	2	2	LOC100289410, MCF2L	-146, 341	upstream, in gene	ActReg chr13 #3133	0	1
3134	13	113,718,293	113,719,435	1,142	1	6.556	13.083	11	25	0	0	1	MCF2L	96,107	in gene	ActReg chr13 #3134	0	1
3135	13	113,841,260	113,842,043	783	1	10.458	12.375	15	20	0	1	2	PCID2, LOC100506079	21378, 1659	in gene, downstream	ActReg chr13 #3135	0	1
3136	13	113,842,351	113,843,005	654	1	9.85	11.4	18	22	0	1	2	PCID2, LOC100506079	20351, 632	in gene, in gene	ActReg chr13 #3136	0	1
3137	13	113,862,299	113,863,581	1,282	2	14.65	16.275	33	29	1	2	2	PCID2, CUL4A	89, -146	in gene, upstream	ActReg chr13 #3137	1	1
3138	13	113,950,614	113,951,734	1,120	2	15.229	18.057	37	36	1	1	1	LAMP1	-295	upstream	ActReg chr13 #3138	1	1
3139	13	114,047,550	114,048,452	902	2	9.276	11.414	23	22	1	0	0				ActReg chr13 #3139	1	1
3140	13	114,064,909	114,066,127	1,218	1	11.079	11.395	20	15	0	0	0				ActReg chr13 #3140	0	1
3141	13	114,145,004	114,146,263	1,259	2	10.205	14.462	22	38	2	2	2	DCUN1D2, TMCO3	-610, 325	upstream, in gene	ActReg chr13 #3141	1	1
3142	13	114,487,888	114,488,782	894	2	14.5	12.714	26	26	0	0	1	FAM70B	26,119	in gene	ActReg chr13 #3142	1	1
3143	13	114,523,539	114,525,412	1,873	2	13.203	14.017	24	25	1	0	2	FAM70B, GAS6	62259, 42571	downstream, in gene	ActReg chr13 #3143	1	1
3144	13	114,540,385	114,541,206	821	1	14.28	13.16	20	20	0	1	2	GAS6, FLJ41484	26251, -4498	in gene, upstream	ActReg chr13 #3144	1	0
3145	13	114,829,594	114,831,845	2,251	2	12.113	13.859	24	22	0	0	1	RASA3	67,376	in gene	ActReg chr13 #3145	1	1
3146	13	114,893,841	114,895,021	1,180	2	12.27	11.865	25	24	0	0	1	RASA3	3,664	in gene	ActReg chr13 #3146	1	1
3147	13	114,896,394	114,897,743	1,349	1	10.809	14.905	17	25	1	1	1	RASA3	1,027	in gene	ActReg chr13 #3147	0	1
3148	13	115,000,051	115,001,082	1,031	2	13.25	12.781	24	21	1	1	1	CDC16	204	in gene	ActReg chr13 #3148	1	1
3149	13	115,046,415	115,047,079	664	1	6.762	11.809	18	19	1	1	2	CDC16, UPF3A	46385, -331	downstream, upstream	ActReg chr13 #3149	0	1
3150	13	115,079,469	115,080,439	970	1	10.4	15.833	19	28	1	1	2	UPF3A, ZNF828	32876, -11	downstream, upstream	ActReg chr13 #3150	0	1
3151	14	19,469,010	19,469,497	487	1	6	9.933	11	16	0	0	0				ActReg chr14 #3151	0	1
3152	14	20,773,639	20,774,403	764	2	10.75	20	26	43	0	1	2	TTC5, CCNB1IP1	132, 27436	in gene, downstream	ActReg chr14 #3152	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3153	14	20,811,214	20,811,938	724	1	12.609	9.783	27	20	0	2	3	CCNB1IP1, RPPH1, PARP2	-10119, -6, 197	upstream, upstream, upstream	ActReg chr14 #3153	1	0
3154	14	20,937,398	20,937,982	584	1	7.444	10.278	12	20	0	1	2	TMEM55B, PNP	-8053, 152	upstream, in gene	ActReg chr14 #3154	0	1
3155	14	21,100,054	21,101,005	951	1	7.5	11.333	10	16	1	0	1	OR6S1	9,321	downstream	ActReg chr14 #3155	0	1
3156	14	21,439,460	21,439,975	515	1	6.625	9.875	9	16	1	0	0				ActReg chr14 #3156	0	1
3157	14	21,571,647	21,572,448	801	2	12.769	13.039	27	30	1	1	2	ZNF219, C14orf176	816, 4951	in gene, downstream	ActReg chr14 #3157	1	1
3158	14	21,924,171	21,925,028	857	1	9.148	14.037	15	22	1	0	1	RAB2B	20,533	downstream	ActReg chr14 #3158	0	1
3159	14	21,944,895	21,945,812	917	2	20.172	28.552	54	77	1	2	2	RAB2B, TOX4	-221, 18	upstream, in gene	ActReg chr14 #3159	1	1
3160	14	21,979,170	21,979,940	770	2	12.625	13.167	26	33	1	1	2	METTL3, SALL2	-98, 25782	upstream, downstream	ActReg chr14 #3160	1	1
3161	14	23,005,806	23,006,337	531	1	8.059	9.941	14	19	0	8	18	TRA@, TRAJ17, TRAJ16, TRAJ15, TRAJ14, TRAJ13, TRAJ12, TRAJ11, TRAJ10, TRAJ9, TRAJ8, TRAJ7, TRAJ6, TRAJ5, TRAJ4, TRAJ3, TRAJ2, TRAJ1	916014, 10259, 8584, 7491, 6793, 6045, 5182, 4619, 3626, 1569, 979, -496, -1945, -3119, -5071, -6051, -6944, -7910	in gene, downstream, downstream, downstream, downstream, downstream, downstream, downstream, downstream, downstream, downstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr14 #3161	0	1
3162	14	23,356,251	23,356,929	678	2	10.636	11.727	28	24	1	0	2	LRP10, REM2	15630, 4158	downstream, in gene	ActReg chr14 #3162	1	1
3163	14	23,475,821	23,476,770	949	2	11.1	11.7	19	23	1	0	1	C14orf93	3,065	in gene	ActReg chr14 #3163	1	1
3164	14	23,584,081	23,584,609	528	1	11.118	9.471	15	13	0	0	3	LOC100128908, CEBPE, SLC7A8	-10174, 4129, 68504	upstream, downstream, downstream	ActReg chr14 #3164	1	0
3165	14	23,938,218	23,938,755	537	1	7.125	9.294	14	15	0	1	1	NGDN	-412	upstream	ActReg chr14 #3165	0	1
3166	14	24,422,675	24,423,686	1,011	2	13.844	24	29	57	1	2	2	C14orf167, DHRS4	1118, 215	in gene, in gene	ActReg chr14 #3166	1	1
3167	14	24,505,338	24,506,405	1,067	2	11.765	9.118	23	23	1	1	1	DHRS4L1	161	in gene	ActReg chr14 #3167	1	1
3168	14	24,521,359	24,521,949	590	1	11.333	9.556	15	14	1	1	2	DHRS4L1, LRRC16B	15944, 448	downstream, in gene	ActReg chr14 #3168	1	0
3169	14	24,629,989	24,630,411	422	1	6.846	12.154	10	15	0	1	2	RNF31, IRF9	13541, -222	downstream, upstream	ActReg chr14 #3169	0	1
3170	14	24,684,810	24,685,404	594	1	12.167	8.944	16	14	0	2	4	TSSK4, CHMP4A, MDP1, NEDD8	10181, -1922, 134, 16469	downstream, upstream, in gene, downstream	ActReg chr14 #3170	1	0
3171	14	24,701,656	24,702,164	508	1	7.75	10.312	11	16	1	2	3	NEDD8, GMPR2, TINF2	-334, 262, 9970	upstream, in gene, downstream	ActReg chr14 #3171	0	1
3172	14	24,740,439	24,741,044	605	1	7.842	11.053	11	14	1	1	2	TGM1, RABGGTA	-8325, 62	upstream, in gene	ActReg chr14 #3172	0	1
3173	14	24,768,675	24,769,336	661	2	8.3	11.35	15	24	1	2	3	DHRS1, C14orf21, CIDEB	34, -93, 11571	in gene, upstream, downstream	ActReg chr14 #3173	1	1
3174	14	24,836,221	24,836,972	751	2	10.583	10.375	17	15	1	1	1	NFATC4	451	in gene	ActReg chr14 #3174	1	1
3175	14	24,962,125	24,962,663	538	1	4.294	9.471	7	14	0	1	1	CMA1	-4,923	upstream	ActReg chr14 #3175	0	1
3176	14	27,432,833	27,433,340	507	1	4.067	9.467	6	15	0	0	0				ActReg chr14 #3176	0	1
3177	14	30,692,442	30,693,032	590	1	7.684	11.632	11	21	0	0	0				ActReg chr14 #3177	0	1
3178	14	31,889,473	31,890,224	751	2	17.696	20	44	51	1	0	0				ActReg chr14 #3178	1	1
3179	14	32,670,438	32,671,680	1,242	1	7.538	10.872	12	16	1	0	0				ActReg chr14 #3179	0	1
3180	14	32,672,260	32,672,954	694	1	8.333	14.524	11	26	1	0	0				ActReg chr14 #3180	0	1
3181	14	34,206,486	34,206,997	511	1	7	9.438	11	17	0	0	1	NPAS3	798,282	in gene	ActReg chr14 #3181	0	1
3182	14	34,844,381	34,844,986	605	1	6.556	10.684	14	16	0	0	0				ActReg chr14 #3182	0	1
3183	14	36,003,927	36,005,030	1,103	2	11.714	16.486	27	31	1	1	2	INSM2, RALGAPA1	1230, 273954	in gene, downstream	ActReg chr14 #3183	1	1
3184	14	36,295,069	36,295,722	653	2	11.429	8.55	15	16	1	1	1	BRMS1L	-202	upstream	ActReg chr14 #3184	1	1
3185	14	37,207,462	37,208,010	548	1	9.235	8.235	17	15	0	0	1	SLC25A21	434,129	in gene	ActReg chr14 #3185	1	0
3186	14	39,735,966	39,736,820	854	2	13.741	16.741	29	36	1	1	1	CTAGE5	1,917	in gene	ActReg chr14 #3186	1	1
3187	14	39,901,235	39,902,338	1,103	2	16.343	14.286	43	40	1	1	1	FBXO33	-82	upstream	ActReg chr14 #3187	1	1
3188	14	41,754,335	41,754,919	584	2	9.882	10.053	18	18	0	0	0				ActReg chr14 #3188	1	1
3189	14	42,078,879	42,079,508	629	1	9.95	5.7	18	11	0	1	1	LRFN5	2,429	in gene	ActReg chr14 #3189	1	0
3190	14	45,603,175	45,603,977	802	2	14.13	17.88	36	49	1	2	2	FKBP3, FANCM	156, -1560	in gene, upstream	ActReg chr14 #3190	1	1
3191	14	45,722,205	45,722,938	733	2	11.783	12	22	21	1	1	1	C14orf106	34	in gene	ActReg chr14 #3191	1	1
3192	14	46,517,278	46,517,916	638	1	5.75	12.3	13	24	0	0	0				ActReg chr14 #3192	0	1
3193	14	49,770,467	49,771,212	745	2	13	16.913	28	39	0	0	0				ActReg chr14 #3193	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3194	14	50,065,044	50,066,003	959	1	8.5	14.567	19	29	1	1	1	PPIL5	108	in gene	ActReg chr14 #3194	0	1
3195	14	50,100,640	50,101,373	733	1	11.174	9.043	16	11	1	1	2	C14orf104, POLE2	942, 53929	in gene, downstream	ActReg chr14 #3195	1	0
3196	14	50,159,574	50,160,122	548	1	9.235	12.471	14	22	1	2	2	POLE2, KLHDC1	-4913, 25	upstream, in gene	ActReg chr14 #3196	0	1
3197	14	50,234,383	50,235,167	784	2	18.208	16.833	37	36	1	1	1	KLHDC2	-12	upstream	ActReg chr14 #3197	1	1
3198	14	50,319,366	50,319,934	568	1	11.823	6	20	9	1	1	2	SDCCAG1, RN7SL2	-111, 9917	upstream, downstream	ActReg chr14 #3198	1	0
3199	14	50,359,358	50,359,984	626	1	10.2	10.25	14	15	1	1	1	ARF6	-65	upstream	ActReg chr14 #3199	0	1
3200	14	50,469,773	50,470,385	612	1	9.474	10.105	13	14	1	1	2	C14orf182, LOC100506463	4159, 565	in gene, in gene	ActReg chr14 #3200	0	1
3201	14	50,778,374	50,779,149	775	2	12.542	14.583	26	30	1	2	2	L2HGDH, ATP5S	186, -286	in gene, upstream	ActReg chr14 #3201	1	1
3202	14	51,561,252	51,562,080	828	1	8.038	11.577	15	19	1	1	2	TRIM9, LOC100506566	756, 5991	in gene, downstream	ActReg chr14 #3202	0	1
3203	14	51,605,896	51,606,498	602	1	7.684	9.368	14	17	0	0	0				ActReg chr14 #3203	0	1
3204	14	52,282,700	52,283,560	860	1	4.074	10.593	7	16	0	0	0				ActReg chr14 #3204	0	1
3205	14	52,294,508	52,295,174	666	1	9.048	11.238	16	19	0	0	0				ActReg chr14 #3205	0	1
3206	14	53,427,758	53,428,247	489	1	9.733	4.267	17	9	0	0	1	FERMT2	-10,187	upstream	ActReg chr14 #3206	1	0
3207	14	53,684,115	53,684,564	449	1	5.143	9.857	7	14	0	0	0				ActReg chr14 #3207	0	1
3208	14	54,720,155	54,720,767	612	1	8.947	10.421	12	16	0	0	0				ActReg chr14 #3208	0	1
3209	14	54,955,504	54,955,922	418	1	10.615	9.615	19	14	1	1	1	GMFB	31	in gene	ActReg chr14 #3209	0	1
3210	14	55,016,437	55,017,112	675	1	9.286	10.476	18	17	0	0	0				ActReg chr14 #3210	0	1
3211	14	56,046,436	56,046,979	543	2	8.647	9.059	17	17	1	2	2	C14orf33, KTN1	103, -218	in gene, upstream	ActReg chr14 #3211	1	1
3212	14	56,269,766	56,270,294	528	1	6.875	11.938	9	17	0	1	1	C14orf34	-6,638	upstream	ActReg chr14 #3212	0	1
3213	14	57,045,967	57,047,098	1,131	2	30.771	32.514	67	73	1	1	1	C14orf101	21	in gene	ActReg chr14 #3213	1	1
3214	14	58,666,445	58,667,011	566	2	8.556	10.222	14	21	1	1	1	ACTR10	-105	upstream	ActReg chr14 #3214	1	1
3215	14	59,688,187	59,688,884	697	1	5.091	11	7	16	0	0	1	DAAM1	33,136	in gene	ActReg chr14 #3215	0	1
3216	14	59,950,436	59,951,197	761	1	8.391	12.609	15	20	1	2	2	C14orf149, JKAMP	257, -345	in gene, upstream	ActReg chr14 #3216	0	1
3217	14	60,558,287	60,559,109	822	1	8.192	11.615	13	20	1	1	1	C14orf135	69	in gene	ActReg chr14 #3217	0	1
3218	14	61,115,396	61,116,334	938	1	11.103	7.31	20	11	1	1	1	SIX1	290	in gene	ActReg chr14 #3218	1	0
3219	14	61,123,902	61,124,323	421	1	7.5	9.714	10	14	1	0	1	SIX1	-7,957	upstream	ActReg chr14 #3219	0	1
3220	14	61,619,499	61,619,969	470	1	5.133	10.2	10	14	0	0	0				ActReg chr14 #3220	0	1
3221	14	61,822,548	61,823,193	645	1	10.75	3.7	19	6	0	0	1	PRKCH	34,355	in gene	ActReg chr14 #3221	1	0
3222	14	62,020,274	62,021,278	1,004	1	10.581	12.419	20	19	0	0	1	PRKCH	232,261	downstream	ActReg chr14 #3222	0	1
3223	14	62,029,002	62,030,144	1,142	1	8.167	12.917	14	20	0	1	1	FLJ22447	-7,741	upstream	ActReg chr14 #3223	0	1
3224	14	62,128,878	62,129,649	771	2	12.708	12.792	19	23	0	0	1	FLJ22447	91,949	downstream	ActReg chr14 #3224	1	1
3225	14	62,431,822	62,432,269	447	1	9	9.786	11	12	0	0	0				ActReg chr14 #3225	0	1
3226	14	64,805,494	64,806,062	568	1	3.667	10.889	6	16	1	1	2	ESR2, LOC441687	-510, 8551	upstream, downstream	ActReg chr14 #3226	0	1
3227	14	64,970,712	64,971,181	469	1	9.533	11.667	14	16	1	2	2	ZBTB25, ZBTB1	-392, -346	upstream, upstream	ActReg chr14 #3227	0	1
3228	14	65,273,189	65,273,674	485	1	6.333	10.067	8	16	0	0	1	SPTB	16,435	in gene	ActReg chr14 #3228	0	1
3229	14	65,453,399	65,454,029	630	1	8.75	11.7	13	18	1	1	1	FNTB	207	in gene	ActReg chr14 #3229	0	1
3230	14	66,974,253	66,975,149	896	2	10.286	12.893	17	19	1	1	2	C14orf53, GPHN	21592, 576	downstream, in gene	ActReg chr14 #3230	1	1
3231	14	67,708,148	67,708,764	616	1	7.263	11.316	10	19	1	1	1	MPP5	435	in gene	ActReg chr14 #3231	0	1
3232	14	67,826,327	67,827,347	1,020	2	30.094	30.344	86	71	1	2	2	ATP6V1D, EIF2S1	-246, -197	upstream, upstream	ActReg chr14 #3232	1	1
3233	14	67,880,632	67,881,413	781	1	6.56	9.56	12	17	0	1	1	PLEK2	-2,194	upstream	ActReg chr14 #3233	0	1
3234	14	67,999,613	68,000,157	544	1	4.643	9.412	7	15	1	1	1	PLEKHH1	-123	upstream	ActReg chr14 #3234	0	1
3235	14	68,140,986	68,141,826	840	2	11.556	12.222	20	28	1	1	2	VTI1B, RDH11	196, 21104	in gene, downstream	ActReg chr14 #3235	1	1
3236	14	68,205,505	68,206,281	776	2	7.792	9.875	18	14	0	0	2	RDH12, ZFYVE26	37290, 77413	downstream, downstream	ActReg chr14 #3236	1	1
3237	14	68,644,445	68,644,871	426	1	4.286	9.571	7	15	0	0	1	RAD51L1	358,162	in gene	ActReg chr14 #3237	0	1
3238	14	69,014,806	69,015,468	662	1	7.381	10.381	10	16	0	0	1	RAD51L1	728,641	in gene	ActReg chr14 #3238	0	1
3239	14	69,417,818	69,418,395	577	1	5.778	10.444	8	18	0	0	1	ACTN1	27,977	in gene	ActReg chr14 #3239	0	1
3240	14	69,657,977	69,658,540	563	2	9.667	9.611	15	17	1	1	1	EXD2	64	in gene	ActReg chr14 #3240	1	1
3241	14	70,233,541	70,233,980	439	1	10.692	7.308	15	9	1	2	3	LOC100289511, SFRS5, SLC10A1	670, -69, 30246	in gene, upstream, downstream	ActReg chr14 #3241	1	0
3242	14	70,519,764	70,520,253	489	1	7.733	10.067	12	18	0	0	1	SLC8A3	135,779	in gene	ActReg chr14 #3242	0	1
3243	14	70,826,133	70,826,796	663	2	10.905	11.333	17	20	1	1	2	COX16, SYNJ2BP	-20, 57343	upstream, downstream	ActReg chr14 #3243	1	1
3244	14	71,323,473	71,323,972	499	1	6.625	8.625	13	16	0	0	0				ActReg chr14 #3244	0	1
3245	14	73,074,539	73,075,811	1,272	2	7.975	8.2	15	16	0	0	0				ActReg chr14 #3245	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3246	14	73,493,670	73,494,284	614	1	9.579	8.789	18	15	1	1	1	ZFYVE1	-57	upstream	ActReg chr14 #3246	1	0
3247	14	74,079,126	74,079,694	568	1	9.778	5.444	18	10	1	1	1	ACOT6	-4,138	upstream	ActReg chr14 #3247	1	0
3248	14	74,769,265	74,770,067	802	2	11.68	8.12	21	15	1	1	1	ABCD4	101	in gene	ActReg chr14 #3248	1	1
3249	14	74,892,337	74,892,831	494	1	9.333	9.2	14	12	1	1	1	TMEM90A	221	in gene	ActReg chr14 #3249	1	0
3250	14	75,086,407	75,087,014	607	1	8.526	10.684	13	15	0	1	1	LTBP2	-7,676	upstream	ActReg chr14 #3250	0	1
3251	14	75,348,254	75,348,857	603	2	10.579	9.053	19	16	1	1	1	DLST	-39	upstream	ActReg chr14 #3251	1	1
3252	14	75,725,588	75,726,392	804	2	9.68	11.84	20	16	1	0	0				ActReg chr14 #3252	1	1
3253	14	75,745,044	75,746,028	984	2	13.645	16.452	23	29	1	2	2	FOS, LOC100287415	55, 1295	in gene, in gene	ActReg chr14 #3253	1	1
3254	14	76,451,947	76,452,441	494	1	9.8	7.533	16	13	1	2	2	TGFB3, C14orf179	-4102, 98	upstream, in gene	ActReg chr14 #3254	1	0
3255	14	76,599,133	76,599,953	820	2	10.423	14.423	18	29	0	0	0				ActReg chr14 #3255	1	1
3256	14	77,370,349	77,371,129	780	1	5.667	11.125	9	14	0	0	0				ActReg chr14 #3256	0	1
3257	14	77,498,992	77,499,569	577	1	6.611	9.5	10	15	2	1	1	C14orf4	-4,246	upstream	ActReg chr14 #3257	0	1
3258	14	77,599,547	77,600,714	1,167	2	12.784	21.622	39	53	0	0	1	ZDHHC22	8,004	in gene	ActReg chr14 #3258	1	1
3259	14	77,674,872	77,675,434	562	1	12.111	13.667	21	26	0	0	1	TMEM63C	27,051	in gene	ActReg chr14 #3259	0	1
3260	14	77,708,221	77,709,024	803	1	5.462	9.269	10	15	0	0	1	TMEM63C	60,520	in gene	ActReg chr14 #3260	0	1
3261	14	77,769,293	77,769,773	480	1	7.667	13.067	12	22	0	0	1	POMT2	17,692	in gene	ActReg chr14 #3261	0	1
3262	14	77,784,184	77,784,659	475	1	10.067	2.167	14	3	0	1	2	POMT2, GSTZ1	2804, -2809	in gene, upstream	ActReg chr14 #3262	1	0
3263	14	77,787,251	77,787,903	652	1	6.75	11.9	10	18	1	2	2	POMT2, GSTZ1	-352, 347	upstream, in gene	ActReg chr14 #3263	0	1
3264	14	78,986,026	78,986,724	698	2	10.318	8.864	20	16	0	0	1	NRXN3	116,282	in gene	ActReg chr14 #3264	1	1
3265	14	79,329,437	79,329,960	523	1	11.235	7.353	18	14	0	0	1	NRXN3	459,605	in gene	ActReg chr14 #3265	1	0
3266	14	79,485,230	79,485,711	481	1	6.733	9.133	11	15	0	0	1	NRXN3	615,377	in gene	ActReg chr14 #3266	0	1
3267	14	79,511,635	79,511,973	338	1	10.182	8.8	15	12	0	0	1	NRXN3	641,711	in gene	ActReg chr14 #3267	1	0
3268	14	79,627,806	79,628,432	626	2	9.5	10.45	20	18	0	0	1	NRXN3	758,026	in gene	ActReg chr14 #3268	1	1
3269	14	81,407,699	81,408,533	834	2	9.923	15.039	21	33	1	1	1	C14orf145	-2,232	upstream	ActReg chr14 #3269	1	1
3270	14	81,687,383	81,687,793	410	1	5.615	9.923	8	17	1	2	2	GTF2A1, LOC100506659	-13, 26	upstream, in gene	ActReg chr14 #3270	0	1
3271	14	82,541,878	82,542,330	452	1	9.5	9	17	13	0	0	0				ActReg chr14 #3271	1	0
3272	14	85,997,511	85,998,299	788	1	7.875	11.292	12	14	1	2	2	LOC100506731, FLRT2	-1436, 1417	upstream, in gene	ActReg chr14 #3272	0	1
3273	14	87,598,219	87,598,642	423	1	4.692	9.385	7	16	0	0	0				ActReg chr14 #3273	0	1
3274	14	89,017,491	89,018,247	756	2	12.583	13.217	24	33	1	0	1	PTPN21	3,254	in gene	ActReg chr14 #3274	1	1
3275	14	89,443,999	89,444,699	700	2	11.409	12	23	23	0	0	0				ActReg chr14 #3275	1	1
3276	14	89,448,543	89,449,425	882	2	8.857	13.393	17	26	0	0	0				ActReg chr14 #3276	1	1
3277	14	89,450,162	89,450,610	448	1	5.643	9.286	8	13	0	0	0				ActReg chr14 #3277	0	1
3278	14	89,506,740	89,507,378	638	1	6.85	9.9	12	19	0	0	0				ActReg chr14 #3278	0	1
3279	14	89,603,753	89,604,359	606	1	5.316	9.105	8	17	0	0	0				ActReg chr14 #3279	0	1
3280	14	90,420,817	90,421,705	888	2	10	9.857	17	17	1	2	2	C14orf143, TDP1	-172, -985	upstream, upstream	ActReg chr14 #3280	1	1
3281	14	90,421,779	90,422,661	882	2	10.75	11.679	23	18	1	2	2	C14orf143, TDP1	-1131, -26	upstream, upstream	ActReg chr14 #3281	1	1
3282	14	90,961,194	90,962,435	1,241	2	10.205	17	30	35	0	0	0				ActReg chr14 #3282	1	1
3283	14	91,580,164	91,580,739	575	1	7.778	12.111	13	20	0	1	1	C14orf159	94	in gene	ActReg chr14 #3283	0	1
3284	14	91,976,421	91,977,198	777	2	11.375	11.125	18	18	1	1	1	SMEK1	-165	upstream	ActReg chr14 #3284	1	1
3285	14	92,506,148	92,506,749	601	1	11.111	8.167	18	13	1	1	1	TRIP11	-45	upstream	ActReg chr14 #3285	1	0
3286	14	92,572,786	92,573,464	678	2	12.571	13.095	29	32	1	1	2	ATXN3, NDUFB1	-160, 15028	upstream, downstream	ActReg chr14 #3286	1	1
3287	14	92,587,645	92,588,801	1,156	2	12.46	15.27	34	24	1	2	2	NDUFB1, CPSF2	-70, -106	upstream, upstream	ActReg chr14 #3287	1	1
3288	14	92,980,342	92,980,821	479	1	7	10.733	10	13	1	1	1	RIN3	456	in gene	ActReg chr14 #3288	0	1
3289	14	93,371,935	93,372,465	530	1	12.059	7.647	18	12	0	0	0				ActReg chr14 #3289	1	0
3290	14	93,380,322	93,381,002	680	2	12.571	13.143	26	29	0	0	1	CHGA	-8,783	upstream	ActReg chr14 #3290	1	1
3291	14	93,389,543	93,390,256	713	2	11.046	11.5	20	20	1	1	1	CHGA	454	in gene	ActReg chr14 #3291	1	1
3292	14	94,425,670	94,426,310	640	2	10.9	10.65	15	15	0	1	2	ASB2, LOC100506919	-2223, 2868	upstream, in gene	ActReg chr14 #3292	1	1
3293	14	94,492,311	94,492,883	572	2	13.353	16.611	26	31	1	1	1	OTUB2	-127	upstream	ActReg chr14 #3293	1	1
3294	14	94,808,318	94,808,926	608	1	6.526	11.737	10	18	0	0	0				ActReg chr14 #3294	0	1
3295	14	95,120,410	95,120,990	580	1	5.278	10.111	7	19	0	0	0				ActReg chr14 #3295	0	1
3296	14	95,727,032	95,727,590	558	1	10.111	10.667	14	17	0	0	1	CLMN	58,934	in gene	ActReg chr14 #3296	1	0
3297	14	95,826,567	95,827,043	476	1	10.4	6.867	13	10	1	0	0				ActReg chr14 #3297	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3298	14	95,973,342	95,973,725	383	1	4.833	10.167	7	13	0	0	0				ActReg chr14 #3298	0	1
3299	14	96,328,391	96,329,100	709	2	16.773	19.273	38	49	0	0	0				ActReg chr14 #3299	1	1
3300	14	96,967,929	96,968,675	746	1	4.292	10.917	6	15	1	1	1	PAPOLA	-418	upstream	ActReg chr14 #3300	0	1
3301	14	97,406,324	97,406,879	555	1	6.765	10.353	11	17	0	0	0				ActReg chr14 #3301	0	1
3302	14	98,179,285	98,179,748	463	1	7.2	9.067	12	17	0	0	0				ActReg chr14 #3302	0	1
3303	14	98,565,861	98,566,348	487	1	8.267	10.133	12	13	0	0	0				ActReg chr14 #3303	0	1
3304	14	100,070,738	100,071,388	650	1	12.1	7.2	17	10	1	2	2	CCDC85C, LOC100507108	-336, 170	upstream, in gene	ActReg chr14 #3304	1	0
3305	14	100,224,684	100,225,374	690	1	11.143	7.714	20	13	0	0	0				ActReg chr14 #3305	1	0
3306	14	100,942,617	100,943,221	604	1	11	4.842	19	8	0	1	2	WDR25, LOC100507124	100164, -4374	in gene, upstream	ActReg chr14 #3306	1	0
3307	14	100,952,707	100,953,272	565	1	8.471	11.588	14	17	0	0	2	WDR25, LOC100507124	110234, 5696	in gene, downstream	ActReg chr14 #3307	0	1
3308	14	101,539,453	101,540,084	631	1	11.9	5.55	25	8	0	0	7	MIR541, MIR409, MIR412, MIR369, MIR410, MIR656, LOC100507257	8936, 8131, 7984, 7833, 7519, 6707, 3520	downstream, downstream, downstream, downstream, downstream, downstream, downstream	ActReg chr14 #3308	1	0
3309	14	101,620,005	101,620,503	498	1	8.067	9.733	12	16	0	0	0				ActReg chr14 #3309	0	1
3310	14	102,414,154	102,414,998	844	1	10.462	12.885	21	18	1	0	0				ActReg chr14 #3310	0	1
3311	14	102,771,246	102,771,758	512	1	9.938	5.5	17	8	1	1	1	RAGE	29	in gene	ActReg chr14 #3311	1	0
3312	14	102,780,453	102,781,008	555	1	6.824	10.235	13	16	1	1	2	RAGE, ZNF839	-9199, -5366	upstream, upstream	ActReg chr14 #3312	0	1
3313	14	102,828,986	102,829,535	549	1	4.176	9.588	7	16	1	2	2	CINP, TECPR2	-7, -40	upstream, upstream	ActReg chr14 #3313	0	1
3314	14	102,991,473	102,991,965	492	1	10.6	4.467	17	7	0	0	0				ActReg chr14 #3314	1	0
3315	14	103,996,688	103,997,225	537	1	10.765	9.118	18	12	0	1	2	CKB, TRMT61A	-7786, 1447	upstream, in gene	ActReg chr14 #3315	1	0
3316	14	104,028,528	104,029,263	735	1	6.435	12.304	10	20	1	2	2	BAG5, C14orf153	256, -404	in gene, upstream	ActReg chr14 #3316	0	1
3317	14	104,073,314	104,073,808	494	1	4.733	9.733	6	14	0	0	0				ActReg chr14 #3317	0	1
3318	14	104,387,447	104,388,302	855	2	11.556	12.518	30	21	1	2	2	C14orf2, TDRD9	29, -6943	in gene, upstream	ActReg chr14 #3318	1	1
3319	14	105,282,097	105,282,633	536	1	10.294	15.177	15	30	1	1	1	MGC23270	-5,173	upstream	ActReg chr14 #3319	0	1
3320	14	105,491,164	105,491,545	381	1	11	6.833	16	10	0	1	1	CDCA4	-3,929	upstream	ActReg chr14 #3320	1	0
3321	14	105,957,016	105,957,738	722	2	10.522	10	14	15	1	1	2	CRIP1, C14orf80	4120, 857	downstream, in gene	ActReg chr14 #3321	1	1
3322	14	105,965,582	105,966,103	521	1	8.062	11.312	11	15	0	0	1	C14orf80	9,322	downstream	ActReg chr14 #3322	0	1
3323	14	106,267,238	106,268,088	850	2	15.808	14.731	39	37	0	0	1	IGH@	1,020,388	in gene	ActReg chr14 #3323	1	1
3324	14	106,915,984	106,916,337	353	1	6.909	11.182	9	17	1	0	2	IGH@, IGHV3-43	371891, 10484	in gene, downstream	ActReg chr14 #3324	0	1
3325	14	106,938,338	106,938,766	428	1	9.231	8.077	13	12	1	1	2	IGH@, C14orf98	349499, 97	in gene, in gene	ActReg chr14 #3325	1	0
3326	15	20,851,034	20,851,930	896	1	11.357	15.464	26	33	0	0	0				ActReg chr15 #3326	0	1
3327	15	21,915,889	21,916,570	681	1	12.143	9.095	17	15	0	0	0				ActReg chr15 #3327	1	0
3328	15	22,387,250	22,387,746	496	1	5.25	9.938	9	15	0	0	1	OR4N4	5,025	downstream	ActReg chr15 #3328	0	1
3329	15	22,832,999	22,833,975	976	2	12.6	10.967	18	21	1	1	1	TUBGCP5	92	in gene	ActReg chr15 #3329	1	1
3330	15	25,017,844	25,018,796	952	2	13.333	14.7	29	39	1	0	0				ActReg chr15 #3330	1	1
3331	15	25,123,228	25,123,815	587	1	7.263	10.632	14	17	1	0	1	SNRPN	54,727	in gene	ActReg chr15 #3331	0	1
3332	15	25,749,025	25,750,146	1,121	1	7.971	10.657	17	17	0	0	0				ActReg chr15 #3332	0	1
3333	15	26,327,190	26,327,822	632	1	7.5	12.55	9	20	1	0	0				ActReg chr15 #3333	0	1
3334	15	26,873,985	26,874,588	603	1	5.056	10.778	9	16	1	0	1	GABRB3	144,649	in gene	ActReg chr15 #3334	0	1
3335	15	27,710,087	27,710,711	624	1	11.105	8.895	18	13	0	0	1	GABRG3	493,970	in gene	ActReg chr15 #3335	1	0
3336	15	27,837,234	27,837,909	675	1	10.667	11.191	18	19	0	0	0				ActReg chr15 #3336	0	1
3337	15	28,088,543	28,089,849	1,306	2	8.583	12.366	18	17	0	0	1	OCA2	255,262	in gene	ActReg chr15 #3337	1	1
3338	15	29,269,394	29,270,418	1,024	2	17	18.188	44	43	0	0	1	APBA2	56,066	in gene	ActReg chr15 #3338	1	1
3339	15	29,741,182	29,741,930	748	1	7.125	12.25	14	22	0	0	1	FAM189A1	121,371	in gene	ActReg chr15 #3339	0	1
3340	15	30,114,760	30,115,394	634	1	6.7	12.35	13	21	1	1	1	TJP1	-371	upstream	ActReg chr15 #3340	0	1
3341	15	30,917,759	30,918,100	341	1	9.364	4.545	15	7	0	1	1	ARHGAP11B	-950	upstream	ActReg chr15 #3341	1	0
3342	15	31,195,604	31,196,442	838	2	15.615	23.5	39	52	1	1	1	MTMR15	-32	upstream	ActReg chr15 #3342	1	1
3343	15	32,976,033	32,976,875	842	1	11.115	9.692	15	15	0	0	1	SCG5	42,584	in gene	ActReg chr15 #3343	1	0
3344	15	33,243,850	33,244,620	770	2	10.542	9.917	17	17	0	0	1	FMN1	115,850	in gene	ActReg chr15 #3344	1	1
3345	15	33,446,945	33,447,765	820	1	12.36	7.92	21	14	0	0	1	LOC100506959	39,542	in gene	ActReg chr15 #3345	1	0
3346	15	33,570,857	33,571,531	674	1	11	11.762	15	23	0	0	0				ActReg chr15 #3346	0	1
3347	15	33,840,047	33,840,560	513	1	10.688	10.875	18	17	0	0	1	RYR3	237,126	in gene	ActReg chr15 #3347	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3348	15	34,013,149	34,013,633	484	2	10.25	12.188	17	21	0	0	1	RYR3	410,214	in gene	ActReg chr15 #3348	1	1
3349	15	34,152,854	34,153,436	582	1	12.056	8	21	16	0	0	2	RYR3, AVEN	549968, 178158	in gene, downstream	ActReg chr15 #3349	1	0
3350	15	34,339,580	34,340,577	997	1	9.656	11.438	16	20	0	0	2	AVEN, CHRM5	-8775, 78989	upstream, in gene	ActReg chr15 #3350	0	1
3351	15	34,516,879	34,517,685	806	1	10.6	10.68	16	15	0	1	2	TMEM85, SLC12A6	37, 112983	in gene, downstream	ActReg chr15 #3351	0	1
3352	15	34,634,918	34,635,756	838	2	9.462	11.923	16	22	0	3	3	SLC12A6, NOP10, C15orf55	-5072, 25, -2729	upstream, in gene, upstream	ActReg chr15 #3352	1	1
3353	15	34,659,484	34,660,178	694	2	11.136	10.909	19	18	1	1	2	C15orf55, LPCAT4	21765, -436	downstream, upstream	ActReg chr15 #3353	1	1
3354	15	34,875,832	34,876,681	849	1	7.519	13.667	13	22	1	1	1	GOLGA8B	-485	upstream	ActReg chr15 #3354	0	1
3355	15	35,045,096	35,045,999	903	2	11.821	16.821	25	33	0	1	1	GJD2	1,142	in gene	ActReg chr15 #3355	1	1
3356	15	35,129,335	35,129,810	475	1	10.267	9.267	19	17	0	0	0				ActReg chr15 #3356	1	0
3357	15	35,261,524	35,262,492	968	2	40.1	40.833	124	132	1	1	2	AQR, ZNF770	-13, 18489	upstream, downstream	ActReg chr15 #3357	1	1
3358	15	35,280,162	35,281,207	1,045	2	12.969	12.906	27	23	1	1	1	ZNF770	-187	upstream	ActReg chr15 #3358	1	1
3359	15	35,585,495	35,586,131	636	2	10.05	11.7	19	21	0	0	0				ActReg chr15 #3359	1	1
3360	15	35,837,960	35,838,877	917	2	11.857	11.464	22	17	1	2	2	ATPBD4, LOC100507466	-14, 22	upstream, in gene	ActReg chr15 #3360	1	1
3361	15	36,030,518	36,031,077	559	1	7.333	11.167	11	22	0	0	1	LOC100507466	192,401	in gene	ActReg chr15 #3361	0	1
3362	15	36,166,296	36,166,991	695	1	12.273	8.364	25	13	0	0	0				ActReg chr15 #3362	1	0
3363	15	36,813,729	36,814,471	742	1	6.913	10.826	14	21	0	0	0				ActReg chr15 #3363	0	1
3364	15	36,871,136	36,871,927	791	2	11.04	14.2	16	25	1	1	1	C15orf41	-281	upstream	ActReg chr15 #3364	1	1
3365	15	38,116,951	38,117,455	504	1	10.375	7.312	17	13	0	0	0				ActReg chr15 #3365	1	0
3366	15	38,422,283	38,422,936	653	1	5.7	11	8	15	0	0	0				ActReg chr15 #3366	0	1
3367	15	38,543,938	38,544,729	791	2	10.458	11.708	15	16	1	1	1	SPRED1	-719	upstream	ActReg chr15 #3367	1	1
3368	15	38,746,018	38,746,923	905	2	12.5	14.25	29	31	1	1	1	FAM98B	142	in gene	ActReg chr15 #3368	1	1
3369	15	39,178,636	39,179,343	707	2	12.227	12.682	23	24	0	0	0				ActReg chr15 #3369	1	1
3370	15	39,464,006	39,464,636	630	1	6.842	12.421	12	19	0	0	0				ActReg chr15 #3370	0	1
3371	15	39,464,767	39,465,601	834	1	8.444	12.333	17	23	0	0	0				ActReg chr15 #3371	0	1
3372	15	39,469,311	39,470,205	894	1	7.893	11	14	18	0	0	0				ActReg chr15 #3372	0	1
3373	15	39,487,861	39,488,661	800	1	8.48	11.96	12	21	0	0	0				ActReg chr15 #3373	0	1
3374	15	39,527,457	39,528,055	598	1	9.722	8.167	17	13	0	0	0				ActReg chr15 #3374	1	0
3375	15	39,561,571	39,562,060	489	1	6.533	11.667	10	16	0	0	0				ActReg chr15 #3375	0	1
3376	15	39,696,739	39,697,534	795	2	10.833	13.292	22	25	0	0	0				ActReg chr15 #3376	1	1
3377	15	39,872,877	39,873,742	865	1	10.778	13.518	21	23	1	1	1	THBS1	29	in gene	ActReg chr15 #3377	0	1
3378	15	39,875,942	39,876,813	871	2	14.482	9.519	23	22	0	0	1	THBS1	3,097	in gene	ActReg chr15 #3378	1	1
3379	15	40,069,574	40,070,325	751	2	10.783	12	19	23	0	0	1	FSIP1	5,090	in gene	ActReg chr15 #3379	1	1
3380	15	40,074,742	40,075,344	602	1	5.263	11.474	9	17	1	1	1	FSIP1	-4	upstream	ActReg chr15 #3380	0	1
3381	15	40,212,188	40,213,116	928	1	10.034	11.552	14	18	1	2	2	GPR176, LOC100505534	441, -559	in gene, upstream	ActReg chr15 #3381	0	1
3382	15	40,268,417	40,269,131	714	1	8.955	10.046	13	15	1	0	1	EIF2AK4	42,427	in gene	ActReg chr15 #3382	0	1
3383	15	40,330,651	40,331,775	1,124	1	8.686	10.829	17	17	1	2	3	EIF2AK4, SRP14, LOC100131089	104866, 176, -299	downstream, in gene, upstream	ActReg chr15 #3383	0	1
3384	15	40,390,659	40,391,486	827	1	9.64	10.92	20	17	0	0	1	BMF	10,003	in gene	ActReg chr15 #3384	0	1
3385	15	40,400,969	40,401,674	705	2	17.227	15.546	38	32	1	1	1	BMF	-246	upstream	ActReg chr15 #3385	1	1
3386	15	40,452,837	40,453,761	924	2	17.759	16	34	42	1	1	1	BUB1B	89	in gene	ActReg chr15 #3386	1	1
3387	15	40,574,369	40,575,065	696	1	6.857	12.381	9	21	1	1	3	PAK6, LOC100131244, PLCB2	65088, 70, 25457	downstream, in gene, downstream	ActReg chr15 #3387	0	1
3388	15	40,615,056	40,615,926	870	2	40.556	45.222	109	126	1	1	2	LOC100505573, C15orf52	-1692, 17677	upstream, downstream	ActReg chr15 #3388	1	1
3389	15	40,885,901	40,887,111	1,210	1	8.368	12.079	19	21	1	1	1	CASC5	59	in gene	ActReg chr15 #3389	0	1
3390	15	41,047,229	41,047,688	459	1	8.333	11.133	11	15	1	1	2	FAM82A2, GCHFR	0, -8827	in gene, upstream	ActReg chr15 #3390	0	1
3391	15	41,099,010	41,100,227	1,217	2	11.947	13.71	21	20	1	2	3	DNAJC17, ZFYVE19, PPP1R14D	58, 344, 21289	in gene, in gene, downstream	ActReg chr15 #3391	1	1
3392	15	41,186,088	41,186,897	809	1	12.2	9.56	17	12	1	1	1	VPS18	-136	upstream	ActReg chr15 #3392	1	0
3393	15	41,408,057	41,409,095	1,038	2	26.394	31.182	77	104	1	1	1	INO80	-236	upstream	ActReg chr15 #3393	1	1
3394	15	41,522,611	41,523,904	1,293	2	16.244	22.732	47	55	1	2	2	EXD1, CHP	-362, -180	upstream, upstream	ActReg chr15 #3394	1	1
3395	15	41,575,918	41,576,534	616	1	9.684	11.737	18	17	1	1	2	CHP, LOC729082	52789, 25	downstream, in gene	ActReg chr15 #3395	0	1
3396	15	41,624,194	41,625,447	1,253	2	11.308	13.667	22	21	1	2	2	OIP5, NUSAP1	-1, -106	upstream, upstream	ActReg chr15 #3396	1	1
3397	15	41,694,244	41,694,940	696	2	10.429	10.286	18	19	1	1	1	NDUFAF1	50	in gene	ActReg chr15 #3397	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3398	15	41,877,203	41,877,790	587	1	6.333	10.444	8	17	1	0	1	TYRO3	26,276	downstream	ActReg chr15 #3398	0	1
3399	15	42,186,327	42,187,293	966	1	11.733	7.167	15	11	0	2	3	SPTBN5, LOC100289090, EHD4	-535, 485, 77945	upstream, in gene, downstream	ActReg chr15 #3399	1	0
3400	15	42,349,051	42,350,286	1,235	2	11.026	17	32	38	0	0	1	PLA2G4D	37,084	downstream	ActReg chr15 #3400	1	1
3401	15	42,565,261	42,566,119	858	2	11.593	10.111	17	16	2	2	2	TMEM87A, GANC	65, -676	in gene, upstream	ActReg chr15 #3401	1	1
3402	15	42,782,961	42,783,682	721	1	7.652	10.652	11	13	1	1	1	SNAP23	-4,514	upstream	ActReg chr15 #3402	0	1
3403	15	42,840,658	42,841,297	639	1	11.3	10.85	18	15	1	2	2	LRRC57, HAUS2	25, -34	in gene, upstream	ActReg chr15 #3403	1	0
3404	15	43,212,758	43,213,880	1,122	1	7.086	10.514	14	17	1	1	1	TTBK2	-312	upstream	ActReg chr15 #3404	0	1
3405	15	43,425,440	43,426,460	1,020	2	10.625	10.562	17	18	1	1	1	TMEM62	228	in gene	ActReg chr15 #3405	1	1
3406	15	43,541,877	43,542,318	441	1	11.786	9.143	17	13	0	0	1	TGM5	16,958	in gene	ActReg chr15 #3406	1	0
3407	15	43,621,925	43,622,914	989	1	9.387	11.387	15	17	1	2	2	LCMT2, ADAL	472, -453	in gene, upstream	ActReg chr15 #3407	0	1
3408	15	43,662,307	43,663,958	1,651	2	10.177	10.353	20	17	1	2	2	ZSCAN29, TUBGCP4	-874, -181	upstream, upstream	ActReg chr15 #3408	1	1
3409	15	43,732,989	43,733,549	560	1	9.611	7.118	16	13	0	0	1	TP53BP1	69,438	in gene	ActReg chr15 #3409	1	0
3410	15	43,802,977	43,803,721	744	1	7.87	10.609	9	14	1	2	2	TP53BP1, MAP1A	-642, -6457	upstream, upstream	ActReg chr15 #3410	0	1
3411	15	44,038,719	44,039,137	418	1	6.286	10.857	8	14	1	1	1	PDIA3	338	in gene	ActReg chr15 #3411	0	1
3412	15	44,116,501	44,117,171	670	1	8.714	11.238	17	19	1	2	2	MFAP1, WDR76	115, -2276	in gene, upstream	ActReg chr15 #3412	0	1
3413	15	44,203,278	44,203,837	559	1	8.941	10.471	13	14	0	0	1	FRMD5	283,872	in gene	ActReg chr15 #3413	0	1
3414	15	44,205,309	44,205,973	664	1	9.476	14.095	14	21	0	0	1	FRMD5	281,788	in gene	ActReg chr15 #3414	0	1
3415	15	44,394,597	44,395,522	925	2	12.552	9.759	18	17	0	0	1	FRMD5	92,370	in gene	ActReg chr15 #3415	1	1
3416	15	44,487,276	44,487,921	645	2	12.4	11.7	23	23	1	1	1	FRMD5	-169	upstream	ActReg chr15 #3416	1	1
3417	15	44,781,501	44,782,329	828	2	8.154	10.423	18	21	0	0	1	CTDSPL2	62,336	in gene	ActReg chr15 #3417	1	1
3418	15	44,828,417	44,829,141	724	2	10.909	12.091	20	17	1	2	3	CTDSPL2, LOC645212, EIF3J	109200, 342, -487	downstream, in gene, upstream	ActReg chr15 #3418	1	1
3419	15	44,829,267	44,830,236	969	2	11.367	10.433	16	15	1	2	3	CTDSPL2, LOC645212, EIF3J	110172, -630, 485	downstream, upstream, in gene	ActReg chr15 #3419	1	1
3420	15	44,955,248	44,956,199	951	1	10.833	14.4	16	23	1	1	2	SPG11, PATL2	153, 13363	in gene, downstream	ActReg chr15 #3420	0	1
3421	15	45,003,285	45,004,166	881	2	11.929	13.107	19	25	1	1	1	B2M	40	in gene	ActReg chr15 #3421	1	1
3422	15	45,076,513	45,077,202	689	2	12.667	10.429	23	18	0	0	0				ActReg chr15 #3422	1	1
3423	15	45,145,510	45,145,881	371	1	11.182	7.182	15	10	0	0	0				ActReg chr15 #3423	1	0
3424	15	45,490,509	45,491,320	811	2	12.32	10.96	17	20	1	1	1	SHF	2,459	in gene	ActReg chr15 #3424	1	1
3425	15	45,492,332	45,493,083	751	2	14.174	10.696	26	22	0	1	1	SHF	666	in gene	ActReg chr15 #3425	1	1
3426	15	45,694,011	45,695,345	1,334	1	12.214	11.619	22	19	1	1	1	SPATA5L1	159	in gene	ActReg chr15 #3426	1	0
3427	15	45,748,390	45,749,244	854	1	8.308	13.538	17	20	0	0	0				ActReg chr15 #3427	0	1
3428	15	45,879,053	45,880,052	999	2	13.452	15	26	26	1	1	1	PLDN	135	in gene	ActReg chr15 #3428	1	1
3429	15	48,482,744	48,483,641	897	2	14.964	16.786	32	35	0	1	1	CTXN2	-675	upstream	ActReg chr15 #3429	1	1
3430	15	48,623,217	48,624,648	1,431	3	9.956	14.533	17	30	1	1	1	DUT	311	in gene	ActReg chr15 #3430	1	1
3431	15	48,717,135	48,717,635	500	1	3.812	13.312	6	17	0	0	1	FBN1	220,600	in gene	ActReg chr15 #3431	0	1
3432	15	48,725,666	48,726,318	652	1	10.9	8.3	18	11	0	0	1	FBN1	211,993	in gene	ActReg chr15 #3432	1	0
3433	15	48,937,449	48,938,091	642	1	4.8	11.55	8	18	1	2	2	FBN1, LOC100506059	215, -1084	in gene, upstream	ActReg chr15 #3433	0	1
3434	15	49,015,455	49,015,963	508	1	10.562	8.688	15	13	0	0	0				ActReg chr15 #3434	1	0
3435	15	49,150,940	49,151,433	493	1	2.75	9.188	6	16	0	0	1	SHC4	104,455	in gene	ActReg chr15 #3435	0	1
3436	15	49,169,749	49,170,956	1,207	1	5.921	12.737	13	25	1	1	2	SHC4, EID1	85289, 62	in gene, in gene	ActReg chr15 #3436	0	1
3437	15	49,221,618	49,222,383	765	1	8.208	10.875	13	16	0	0	1	SHC4	33,641	in gene	ActReg chr15 #3437	0	1
3438	15	49,338,412	49,339,130	718	1	12.636	10.091	18	17	1	1	1	SECISBP2L	-11	upstream	ActReg chr15 #3438	1	0
3439	15	49,447,146	49,448,233	1,087	2	9.735	14.265	17	28	1	2	2	COPS2, GALK2	165, -287	in gene, upstream	ActReg chr15 #3439	1	1
3440	15	49,912,823	49,913,605	782	2	10.56	12.48	18	23	1	2	2	C15orf33, DTWD1	-96, -12	upstream, upstream	ActReg chr15 #3440	1	1
3441	15	50,429,423	50,430,081	658	1	12.429	12.571	23	21	0	0	0				ActReg chr15 #3441	0	1
3442	15	50,647,026	50,647,768	742	2	11.348	10.087	16	20	1	3	3	GABPB1, FLJ10038, LOC100129387	208, -321, 1026	in gene, upstream, in gene	ActReg chr15 #3442	1	1
3443	15	50,716,190	50,716,944	754	1	12.875	9.583	23	14	1	1	1	USP8	-12	upstream	ActReg chr15 #3443	1	0
3444	15	51,177,561	51,178,465	904	1	6.241	9.724	13	15	0	0	0				ActReg chr15 #3444	0	1
3445	15	51,200,701	51,201,425	724	1	11.696	8.739	16	14	1	1	1	AP4E1	117	in gene	ActReg chr15 #3445	1	0
3446	15	51,913,931	51,914,657	726	1	7.478	12.435	10	21	1	1	1	DMXL2	673	in gene	ActReg chr15 #3446	0	1
3447	15	51,973,200	51,974,095	895	2	17.357	23.821	47	62	1	1	1	SCG3	97	in gene	ActReg chr15 #3447	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3448	15	52,263,480	52,264,374	894	2	11.429	14.464	25	31	1	1	1	LEO1	31	in gene	ActReg chr15 #3448	1	1
3449	15	52,332,223	52,332,683	460	1	6.4	11.8	10	16	0	0	1	MAPK6	21,042	in gene	ActReg chr15 #3449	0	1
3450	15	52,471,341	52,471,843	502	1	8.562	10.75	13	19	1	1	2	GNB5, LOC100129973	11973, -604	in gene, upstream	ActReg chr15 #3450	0	1
3451	15	52,820,194	52,820,932	738	1	9.217	12.522	15	21	1	1	1	MYO5A	684	in gene	ActReg chr15 #3451	0	1
3452	15	53,363,983	53,365,338	1,355	2	23.476	29.191	89	109	0	0	0				ActReg chr15 #3452	1	1
3453	15	53,484,689	53,485,918	1,229	2	9.289	14.158	28	35	0	0	0				ActReg chr15 #3453	1	1
3454	15	53,600,431	53,600,977	546	1	8.941	13.177	12	19	0	0	0				ActReg chr15 #3454	0	1
3455	15	53,620,183	53,621,086	903	2	12.036	14.464	29	27	0	0	0				ActReg chr15 #3455	1	1
3456	15	55,488,771	55,489,555	784	2	11.25	13.625	23	24	1	1	2	RSL24D1, RAB27A	68, 92838	in gene, downstream	ActReg chr15 #3456	1	1
3457	15	55,571,784	55,572,430	646	1	8.65	11.65	16	21	0	0	1	RAB27A	9,894	in gene	ActReg chr15 #3457	0	1
3458	15	55,610,858	55,611,782	924	2	12.31	13.69	25	25	1	2	2	LOC100506294, PIGB	21, 187	in gene, in gene	ActReg chr15 #3458	1	1
3459	15	55,699,812	55,700,820	1,008	1	8.774	11.065	14	16	1	2	3	CCPG1, FLJ27352, DYX1C1	258, -430, 100116	in gene, upstream, downstream	ActReg chr15 #3459	0	1
3460	15	56,199,835	56,200,483	648	1	8.286	11.857	15	26	0	0	1	NEDD4	85,676	in gene	ActReg chr15 #3460	0	1
3461	15	56,209,044	56,209,516	472	1	9.933	8.067	16	12	0	0	1	NEDD4	76,555	in gene	ActReg chr15 #3461	1	0
3462	15	56,538,122	56,538,543	421	1	5.846	10	8	14	0	1	1	RFX7	-2,849	upstream	ActReg chr15 #3462	0	1
3463	15	57,178,999	57,180,029	1,030	2	11	11.5	19	20	1	0	1	LOC145783	31,183	in gene	ActReg chr15 #3463	1	1
3464	15	57,210,054	57,211,163	1,109	1	9.882	16.206	15	29	1	2	2	LOC145783, TCF12	89, -225	in gene, upstream	ActReg chr15 #3464	0	1
3465	15	57,829,081	57,829,677	596	1	10.053	11.053	18	18	0	0	1	CGNL1	99,196	in gene	ActReg chr15 #3465	0	1
3466	15	57,998,506	57,999,115	609	1	10.526	10.842	16	19	1	1	2	GCOM1, GRINL1A	114708, -91	in gene, upstream	ActReg chr15 #3466	1	0
3467	15	58,472,036	58,472,980	944	1	8.966	11.828	14	17	0	0	1	AQP9	42,100	in gene	ActReg chr15 #3467	0	1
3468	15	59,062,789	59,064,455	1,666	1	7.519	11.923	20	24	1	2	2	LOC100506466, FAM63B	-444, 229	upstream, in gene	ActReg chr15 #3468	0	1
3469	15	59,664,663	59,665,516	853	1	10.37	8.889	15	15	1	1	1	MYO1E	-18	upstream	ActReg chr15 #3469	1	0
3470	15	59,949,300	59,949,907	607	1	10.737	12.526	17	20	1	1	2	GTF2A2, BNIP2	134, 32039	in gene, downstream	ActReg chr15 #3470	0	1
3471	15	59,981,035	59,981,885	850	1	10.923	9.231	15	19	1	1	1	BNIP2	182	in gene	ActReg chr15 #3471	1	0
3472	15	60,184,992	60,185,761	769	1	8.6	13.28	12	21	0	0	0				ActReg chr15 #3472	0	1
3473	15	60,297,426	60,297,874	448	1	7.571	11.429	10	13	1	1	1	FOXB1	1,229	in gene	ActReg chr15 #3473	0	1
3474	15	60,654,776	60,655,308	532	1	6.882	10.706	12	17	0	0	1	ANXA2	35,143	in gene	ActReg chr15 #3474	0	1
3475	15	60,663,150	60,664,138	988	2	11.581	13.258	20	25	0	0	1	ANXA2	26,541	in gene	ActReg chr15 #3475	1	1
3476	15	60,666,009	60,667,349	1,340	1	10.619	8.857	15	20	0	0	1	ANXA2	23,506	in gene	ActReg chr15 #3476	1	0
3477	15	60,685,063	60,685,721	658	1	12.4	7.45	23	12	0	0	1	ANXA2	4,793	in gene	ActReg chr15 #3477	1	0
3478	15	60,700,438	60,701,106	668	2	12.286	11.714	19	21	0	0	0				ActReg chr15 #3478	1	1
3479	15	60,770,881	60,771,770	889	2	10.296	15.518	18	23	1	1	2	NARG2, RORA	19, 750177	in gene, downstream	ActReg chr15 #3479	1	1
3480	15	61,467,222	61,467,735	513	1	6.357	9.125	11	16	0	0	1	RORA	54,024	in gene	ActReg chr15 #3480	0	1
3481	15	61,876,592	61,877,085	493	1	7.8	10.067	11	17	0	0	0				ActReg chr15 #3481	0	1
3482	15	62,411,427	62,412,118	691	2	13.809	12.857	24	24	0	0	0				ActReg chr15 #3482	1	1
3483	15	62,682,678	62,683,009	331	1	9.273	10.454	13	16	1	0	0				ActReg chr15 #3483	0	1
3484	15	62,898,398	62,899,440	1,042	2	12.242	14.939	24	28	0	0	0				ActReg chr15 #3484	1	1
3485	15	62,939,523	62,940,141	618	1	13.526	7.105	24	12	0	2	2	MGC15885, TLN2	-2452, 322	upstream, in gene	ActReg chr15 #3485	1	0
3486	15	63,178,683	63,179,193	510	1	10.25	8.25	18	10	0	0	0				ActReg chr15 #3486	1	0
3487	15	63,310,584	63,311,977	1,393	2	10.477	10.841	15	16	0	0	0				ActReg chr15 #3487	1	1
3488	15	63,413,436	63,414,435	999	2	18	17.75	53	48	1	1	1	LACTB	-97	upstream	ActReg chr15 #3488	1	1
3489	15	63,449,323	63,450,047	724	1	10.364	14.091	13	26	1	1	1	RPS27L	56	in gene	ActReg chr15 #3489	0	1
3490	15	63,478,222	63,478,882	660	1	10.952	8.048	21	14	0	1	1	RAB8B	-3,176	upstream	ActReg chr15 #3490	1	0
3491	15	63,616,061	63,616,905	844	1	9.63	11.963	16	18	0	0	1	CA12	57,592	in gene	ActReg chr15 #3491	0	1
3492	15	63,640,166	63,640,939	773	1	9.125	7.792	14	14	0	0	1	CA12	33,523	in gene	ActReg chr15 #3492	1	0
3493	15	63,796,426	63,797,125	699	2	12.136	13.682	25	28	1	1	1	USP3	-35	upstream	ActReg chr15 #3493	1	1
3494	15	64,162,354	64,163,520	1,166	2	20.514	26.432	62	77	0	1	1	MIR422A	281	downstream	ActReg chr15 #3494	1	1
3495	15	64,385,688	64,386,796	1,108	2	11.343	12.429	22	20	1	2	2	FAM96A, SNX1	-35, -1935	upstream, upstream	ActReg chr15 #3495	1	1
3496	15	64,387,915	64,388,621	706	1	12.091	8.273	20	15	1	2	2	FAM96A, SNX1	-2061, 91	upstream, in gene	ActReg chr15 #3496	1	0
3497	15	64,454,884	64,455,929	1,045	2	15.969	15.469	33	29	1	1	3	SNX22, PPIB, CSNK1G1	11490, -52, 193036	downstream, upstream, downstream	ActReg chr15 #3497	1	1
3498	15	64,647,591	64,648,120	529	1	4.75	12.375	7	22	1	1	2	CSNK1G1, KIAA0101	587, 25847	in gene, downstream	ActReg chr15 #3498	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3499	15	64,648,297	64,648,920	623	1	11.105	7.947	17	11	1	1	2	CSNK1G1, KIAA0101	-166, 25094	upstream, downstream	ActReg chr15 #3499	1	0
3500	15	64,673,118	64,674,033	915	1	7.241	11.655	11	19	0	2	2	KIAA0101, TRIP4	127, -6428	in gene, upstream	ActReg chr15 #3500	0	1
3501	15	64,679,649	64,680,362	713	2	12.727	12.864	23	26	1	2	2	KIAA0101, TRIP4	-6303, 2	upstream, in gene	ActReg chr15 #3501	1	1
3502	15	64,752,263	64,752,988	725	2	10.409	11.909	22	22	1	0	1	TRIP4	72,622	downstream	ActReg chr15 #3502	1	1
3503	15	65,117,284	65,118,389	1,105	1	8.206	11.823	12	24	0	1	1	PIF1	2	in gene	ActReg chr15 #3503	0	1
3504	15	65,127,764	65,128,535	771	2	10.625	9.625	16	15	1	1	2	PIF1, PLEKHO2	-10311, -5933	upstream, upstream	ActReg chr15 #3504	1	1
3505	15	65,176,103	65,176,906	803	1	4.56	10.08	8	18	0	0	0				ActReg chr15 #3505	0	1
3506	15	65,321,515	65,322,111	596	1	11	9.5	16	14	1	1	1	MTFMT	164	in gene	ActReg chr15 #3506	1	0
3507	15	65,361,321	65,361,983	662	1	8.05	11.65	11	17	0	2	2	RASL12, KBTBD13	-1264, -7502	upstream, upstream	ActReg chr15 #3507	0	1
3508	15	65,425,763	65,426,592	829	2	9.115	12.615	19	22	1	1	1	PDCD7	-3	upstream	ActReg chr15 #3508	1	1
3509	15	65,587,904	65,588,612	708	2	19.13	15	46	33	0	1	3	PARP16, RNU5A, RNU5B-1	-9240, -131, -8757	upstream, upstream, upstream	ActReg chr15 #3509	1	1
3510	15	65,596,607	65,597,840	1,233	1	7.974	10.436	15	16	0	1	2	RNU5A, RNU5B-1	8834, 208	downstream, downstream	ActReg chr15 #3510	0	1
3511	15	65,809,237	65,810,616	1,379	2	49.279	53.791	176	189	1	1	1	DPP8	109	in gene	ActReg chr15 #3511	1	1
3512	15	65,903,038	65,904,079	1,041	2	11.424	16.454	24	38	1	1	1	C15orf44	-89	upstream	ActReg chr15 #3512	1	1
3513	15	66,084,515	66,085,256	741	2	18.478	20.522	41	37	1	1	1	DENND4A	-254	upstream	ActReg chr15 #3513	1	1
3514	15	66,125,231	66,125,677	446	1	6.5	11.357	11	15	0	0	0				ActReg chr15 #3514	0	1
3515	15	66,161,273	66,162,054	781	1	10.28	15.96	13	26	1	1	1	RAB11A	-133	upstream	ActReg chr15 #3515	0	1
3516	15	66,244,452	66,247,249	2,797	3	16.977	19.759	50	52	0	0	1	MEGF11	300,225	in gene	ActReg chr15 #3516	1	1
3517	15	66,296,780	66,297,838	1,058	2	15.061	12.152	35	28	0	0	1	MEGF11	248,766	in gene	ActReg chr15 #3517	1	1
3518	15	66,299,158	66,299,974	816	2	13.077	14.577	24	32	0	0	1	MEGF11	246,509	in gene	ActReg chr15 #3518	1	1
3519	15	66,544,900	66,545,547	647	1	4	10.95	7	17	1	1	1	MEGF11	852	in gene	ActReg chr15 #3519	0	1
3520	15	66,678,757	66,679,300	543	1	9.529	12.294	15	21	1	1	1	MAP2K1	-183	upstream	ActReg chr15 #3520	0	1
3521	15	66,789,648	66,790,762	1,114	2	10.229	11.257	16	29	1	2	8	MAP2K1, SNAPC5, RPL4, SNORD18C, SNORD18B, SNORD16, SNORD18A, ZWILCH	110994, -59, 6979, 3451, 4224, 5043, 5447, 7226	downstream, upstream, downstream, downstream, downstream, downstream, downstream, upstream	ActReg chr15 #3521	1	1
3522	15	66,913,213	66,913,665	452	1	4.467	9.667	8	13	0	0	0				ActReg chr15 #3522	0	1
3523	15	66,993,668	66,994,616	948	2	12.138	11.414	22	19	1	1	1	SMAD6	-532	upstream	ActReg chr15 #3523	1	1
3524	15	67,058,129	67,058,810	681	1	9.762	11.714	15	18	0	0	1	SMAD6	63,795	in gene	ActReg chr15 #3524	0	1
3525	15	67,134,111	67,134,678	567	1	5.833	11.611	13	15	1	0	0				ActReg chr15 #3525	0	1
3526	15	67,316,082	67,317,192	1,110	1	10.171	7.286	17	11	0	0	0				ActReg chr15 #3526	1	0
3527	15	67,383,357	67,384,008	651	1	12.191	10.952	19	19	0	0	1	SMAD3	25,487	in gene	ActReg chr15 #3527	1	0
3528	15	67,546,566	67,547,544	978	2	14	16.7	31	38	1	2	2	AAGAB, IQCH	19, -83	in gene, upstream	ActReg chr15 #3528	1	1
3529	15	67,812,981	67,813,476	495	1	9.5	5.188	15	8	1	2	2	LOC100506686, C15orf61	954, -294	in gene, upstream	ActReg chr15 #3529	1	0
3530	15	67,834,667	67,835,096	429	1	10.462	8.385	14	11	1	1	1	MAP2K5	-140	upstream	ActReg chr15 #3530	1	0
3531	15	68,113,180	68,113,797	617	1	8.5	13.4	15	23	1	1	1	LBXCOR1	-4,453	upstream	ActReg chr15 #3531	0	1
3532	15	68,132,394	68,133,216	822	1	11.423	12.462	17	22	1	1	2	LBXCOR1, RNU6-1	14864, -422	downstream, upstream	ActReg chr15 #3532	0	1
3533	15	68,569,538	68,571,241	1,703	2	15.377	15.925	27	32	1	1	1	FEM1B	248	in gene	ActReg chr15 #3533	1	1
3534	15	68,664,591	68,665,177	586	1	11.611	5.667	18	9	0	0	1	ITGA11	59,608	in gene	ActReg chr15 #3534	1	0
3535	15	68,870,344	68,871,043	699	1	11.864	10.954	18	14	1	0	0				ActReg chr15 #3535	0	1
3536	15	69,366,387	69,367,213	826	1	8.962	13.538	14	21	1	1	1	TMEM84	-6,390	upstream	ActReg chr15 #3536	0	1
3537	15	69,706,281	69,707,454	1,173	1	8.444	13.194	14	25	1	2	3	PAQR5, LOC145694, KIF23	115573, 501, 179	downstream, in gene, in gene	ActReg chr15 #3537	0	1
3538	15	69,744,648	69,745,725	1,077	2	10.485	14.939	19	28	1	1	2	KIF23, RPLP1	38498, 27	downstream, in gene	ActReg chr15 #3538	1	1
3539	15	70,006,443	70,007,115	672	1	11.238	10.286	20	14	0	0	0				ActReg chr15 #3539	1	0
3540	15	70,053,067	70,054,099	1,032	2	11.469	13.531	22	25	0	0	0				ActReg chr15 #3540	1	1
3541	15	70,264,757	70,266,189	1,432	2	15.867	21.156	45	66	0	0	0				ActReg chr15 #3541	1	1
3542	15	70,268,103	70,269,552	1,449	2	8.578	14	21	28	0	0	0				ActReg chr15 #3542	1	1
3543	15	70,389,605	70,390,197	592	1	8.056	11.611	12	17	1	1	1	TLE3	355	in gene	ActReg chr15 #3543	0	1
3544	15	70,563,436	70,564,355	919	2	13.241	13.207	26	25	0	0	0				ActReg chr15 #3544	1	1
3545	15	70,667,337	70,667,865	528	1	13.562	11.812	20	17	0	0	0				ActReg chr15 #3545	1	0
3546	15	70,717,518	70,719,393	1,875	2	9.305	11.915	30	27	0	0	0				ActReg chr15 #3546	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3547	15	70,766,630	70,768,620	1,990	2	9.435	12.403	17	23	0	0	0				ActReg chr15 #3547	1	1
3548	15	70,784,634	70,785,487	853	2	12.407	13.63	27	24	0	0	0				ActReg chr15 #3548	1	1
3549	15	70,797,246	70,798,317	1,071	1	6.471	11.177	10	15	0	0	0				ActReg chr15 #3549	0	1
3550	15	71,184,701	71,185,449	748	1	10.75	10.542	16	20	1	2	2	THAP10, LRRC49	-322, 88	upstream, in gene	ActReg chr15 #3550	1	0
3551	15	71,587,241	71,588,222	981	1	6.1	12.067	12	21	0	0	1	THSD4	153,943	in gene	ActReg chr15 #3551	0	1
3552	15	72,522,464	72,524,114	1,650	2	10.673	11.712	17	17	1	1	2	PKM2, PARP6	395, 40339	in gene, downstream	ActReg chr15 #3552	1	1
3553	15	72,564,509	72,565,728	1,219	2	29.333	33.821	118	122	1	1	1	PARP6	-1,490	upstream	ActReg chr15 #3553	1	1
3554	15	72,611,645	72,613,075	1,430	3	10.489	13.622	26	27	1	1	1	BRUNOL6	165	in gene	ActReg chr15 #3554	1	1
3555	15	72,667,936	72,668,772	836	2	14.148	14.815	28	29	1	2	2	HEXA, C15orf34	166, -100	in gene, upstream	ActReg chr15 #3555	1	1
3556	15	72,766,179	72,767,000	821	1	9.76	14.08	14	20	1	1	1	ARIH1	-78	upstream	ActReg chr15 #3556	0	1
3557	15	72,767,205	72,767,917	712	1	7.682	15.682	10	26	1	1	1	ARIH1	894	in gene	ActReg chr15 #3557	0	1
3558	15	72,978,133	72,978,883	750	1	9.417	11.833	15	18	1	1	1	BBS4	-18	upstream	ActReg chr15 #3558	0	1
3559	15	73,075,577	73,076,686	1,109	2	10.143	16.4	25	31	1	1	1	ADPGK	-5	upstream	ActReg chr15 #3559	1	1
3560	15	73,344,006	73,344,594	588	1	4.25	10.389	6	19	1	1	1	NEO1	-525	upstream	ActReg chr15 #3560	0	1
3561	15	73,638,848	73,639,632	784	2	11.76	17.68	22	35	0	0	1	HCN4	22,365	in gene	ActReg chr15 #3561	1	1
3562	15	73,924,972	73,925,408	436	1	4	10.357	7	18	1	1	1	NPTN	563	in gene	ActReg chr15 #3562	0	1
3563	15	74,115,142	74,115,922	780	2	14.417	17.5	36	43	0	0	0				ActReg chr15 #3563	1	1
3564	15	74,143,583	74,144,875	1,292	2	14.415	20.585	37	58	0	0	0				ActReg chr15 #3564	1	1
3565	15	74,189,983	74,190,696	713	1	8.696	13.261	16	21	0	0	1	TBC1D21	24,371	downstream	ActReg chr15 #3565	0	1
3566	15	74,284,313	74,285,408	1,095	2	31.486	30.971	108	111	1	2	2	STOML1, PML	-225, -2154	upstream, upstream	ActReg chr15 #3566	1	1
3567	15	74,471,339	74,472,979	1,640	1	9.314	14.118	18	23	0	0	2	ISLR, STRA6	6072, 29212	downstream, in gene	ActReg chr15 #3567	0	1
3568	15	74,492,975	74,494,075	1,100	1	8.147	11.853	15	18	0	0	1	STRA6	7,846	in gene	ActReg chr15 #3568	0	1
3569	15	74,556,975	74,558,121	1,146	2	11.833	20.194	24	39	0	0	1	CCDC33	28,881	in gene	ActReg chr15 #3569	1	1
3570	15	74,583,375	74,584,733	1,358	2	15.452	19.357	37	36	0	0	1	CCDC33	55,387	in gene	ActReg chr15 #3570	1	1
3571	15	74,665,684	74,666,433	749	1	5.75	10.708	8	14	1	1	2	CYP11A1, LOC729739	-5977, 19261	upstream, downstream	ActReg chr15 #3571	0	1
3572	15	74,906,927	74,908,561	1,634	1	12.863	10.392	19	18	1	0	1	CLK3	7,031	in gene	ActReg chr15 #3572	1	0
3573	15	74,987,941	74,988,692	751	1	14.565	10.261	26	15	1	1	1	EDC3	70	in gene	ActReg chr15 #3573	1	0
3574	15	75,016,206	75,016,833	627	1	6.15	11.75	8	18	0	1	1	CYP1A1	1,358	in gene	ActReg chr15 #3574	0	1
3575	15	75,018,183	75,019,376	1,193	1	10.27	14.649	21	28	1	1	1	CYP1A1	-902	upstream	ActReg chr15 #3575	0	1
3576	15	75,182,011	75,183,223	1,212	1	10.79	9.184	22	16	1	1	2	MPI, C15orf17	207, 16845	in gene, downstream	ActReg chr15 #3576	1	0
3577	15	75,198,811	75,200,007	1,196	2	9.711	10.895	13	21	1	1	2	MPI, C15orf17	16999, 53	downstream, in gene	ActReg chr15 #3577	1	1
3578	15	75,229,783	75,230,874	1,091	2	13.177	11.323	20	19	1	1	1	COX5A	167	in gene	ActReg chr15 #3578	1	1
3579	15	75,248,159	75,250,077	1,918	2	10.467	10.85	22	19	1	1	1	RPP25	657	in gene	ActReg chr15 #3579	1	1
3580	15	75,276,098	75,276,814	716	2	11.909	10	22	19	0	0	0				ActReg chr15 #3580	1	1
3581	15	75,287,338	75,287,890	552	2	13.118	12.412	20	22	1	1	1	SCAMP5	-262	upstream	ActReg chr15 #3581	1	1
3582	15	75,315,664	75,316,308	644	1	8.35	11.35	13	20	1	1	2	SCAMP5, PPCDC	28110, 59	downstream, in gene	ActReg chr15 #3582	0	1
3583	15	75,335,582	75,336,466	884	1	9.286	11.929	17	20	0	0	1	PPCDC	20,097	in gene	ActReg chr15 #3583	0	1
3584	15	75,474,630	75,475,630	1,000	1	6.968	14.71	14	22	0	0	0				ActReg chr15 #3584	0	1
3585	15	75,494,221	75,495,093	872	1	9.259	12.037	13	19	1	1	1	C15orf39	436	in gene	ActReg chr15 #3585	0	1
3586	15	75,660,001	75,661,152	1,151	1	10.528	12.583	20	22	1	1	2	MAN2C1, SIN3A	365, 87548	in gene, downstream	ActReg chr15 #3586	0	1
3587	15	75,917,610	75,918,616	1,006	1	7.774	13.484	11	25	1	1	1	SNUPN	606	in gene	ActReg chr15 #3587	0	1
3588	15	75,931,868	75,932,996	1,128	1	12.139	11.722	18	19	1	1	2	IMP3, SNX33	232, -8916	in gene, upstream	ActReg chr15 #3588	1	0
3589	15	75,987,457	75,988,297	840	1	10.308	10.692	14	14	0	0	1	CSPG4	17,312	in gene	ActReg chr15 #3589	0	1
3590	15	75,988,420	75,989,731	1,311	2	8.756	10.293	20	19	0	0	1	CSPG4	16,114	in gene	ActReg chr15 #3590	1	1
3591	15	76,005,386	76,006,388	1,002	2	11	14.161	18	24	0	1	2	CSPG4, ODF3L1	-698, -10432	upstream, upstream	ActReg chr15 #3591	1	1
3592	15	76,184,117	76,184,644	527	1	9.176	7.647	15	12	0	0	1	UBE2Q2	48,758	in gene	ActReg chr15 #3592	1	0
3593	15	76,195,855	76,196,646	791	1	10.48	12.68	18	18	1	1	2	UBE2Q2, FBXO22	60628, 50	downstream, in gene	ActReg chr15 #3593	0	1
3594	15	76,603,304	76,603,961	657	2	11.6	10.25	16	19	1	1	1	ETFA	178	in gene	ActReg chr15 #3594	1	1
3595	15	77,247,053	77,247,570	517	2	8.5	9.812	17	14	0	1	2	RCN2, LOC100506704	23349, 512	downstream, in gene	ActReg chr15 #3595	1	1
3596	15	77,363,164	77,363,887	723	2	12.696	10.739	25	19	1	1	1	TSPAN3	45	in gene	ActReg chr15 #3596	1	1
3597	15	77,712,152	77,712,548	396	1	2.385	10.077	4	17	1	1	1	HMG20A	-893	upstream	ActReg chr15 #3597	0	1
3598	15	77,835,446	77,836,243	797	2	10.12	13.24	19	21	0	0	0				ActReg chr15 #3598	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3599	15	77,994,503	77,995,471	968	2	13.833	13.667	22	27	0	0	0				ActReg chr15 #3599	1	1
3600	15	78,441,476	78,442,163	687	1	9.667	12.952	16	26	1	1	1	IDH3A	100	in gene	ActReg chr15 #3600	0	1
3601	15	78,591,673	78,592,222	549	1	11.118	10.941	15	14	0	1	1	WDR61	-7	upstream	ActReg chr15 #3601	1	0
3602	15	78,729,852	78,730,644	792	2	10.92	10.92	17	19	1	1	1	IREB2	-270	upstream	ActReg chr15 #3602	1	1
3603	15	79,575,835	79,576,515	680	1	10.727	13.727	21	25	1	2	3	LOC729911, LOC100506846, ANKRD34C	3187, -19, 1029	in gene, upstream, in gene	ActReg chr15 #3603	0	1
3604	15	79,603,391	79,604,088	697	1	8.048	11.773	16	17	1	1	1	TMED3	248	in gene	ActReg chr15 #3604	0	1
3605	15	80,188,909	80,189,948	1,039	2	9.469	12.719	18	21	1	1	2	MTHFS, ST20	-58, 26649	upstream, downstream	ActReg chr15 #3605	1	1
3606	15	80,215,386	80,216,301	915	1	11	11.207	21	16	1	2	2	ST20, C15orf37	234, 730	in gene, in gene	ActReg chr15 #3606	0	1
3607	15	80,303,410	80,304,028	618	1	6.842	10.895	10	17	0	0	0				ActReg chr15 #3607	0	1
3608	15	80,364,553	80,365,141	588	1	9.444	6.333	16	12	0	0	1	ZFAND6	12,826	in gene	ActReg chr15 #3608	1	0
3609	15	80,557,206	80,557,937	731	2	11.391	13.522	19	26	0	0	1	LOC283688	76,576	in gene	ActReg chr15 #3609	1	1
3610	15	80,609,620	80,610,474	854	1	10.111	12.667	17	20	0	0	1	LOC283688	24,100	in gene	ActReg chr15 #3610	0	1
3611	15	80,707,108	80,707,560	452	1	9.143	11.929	11	20	0	0	1	ARNT2	10,642	in gene	ActReg chr15 #3611	0	1
3612	15	80,728,721	80,729,481	760	1	8.833	12	13	17	0	0	2	ARNT2, LOC100133746	32409, 8127	in gene, in gene	ActReg chr15 #3612	0	1
3613	15	80,872,069	80,872,937	868	1	12.704	9.852	24	21	0	0	1	ARNT2	175,811	in gene	ActReg chr15 #3613	1	0
3614	15	81,071,790	81,073,471	1,681	2	11.654	13.538	28	20	1	1	1	KIAA1199	918	in gene	ActReg chr15 #3614	1	1
3615	15	81,247,942	81,248,619	677	1	6.714	12.191	10	21	0	0	1	KIAA1199	176,568	downstream	ActReg chr15 #3615	0	1
3616	15	81,281,506	81,282,283	777	1	7.083	12.083	13	17	1	1	1	MESDC2	311	in gene	ActReg chr15 #3616	0	1
3617	15	81,384,388	81,385,183	795	1	7.042	11.333	12	18	0	0	1	LOC647020	25,707	in gene	ActReg chr15 #3617	0	1
3618	15	81,473,539	81,474,842	1,303	1	8.605	11.85	17	22	0	0	0				ActReg chr15 #3618	0	1
3619	15	81,528,222	81,528,902	680	1	9.636	13.273	13	20	0	0	1	IL16	39,343	in gene	ActReg chr15 #3619	0	1
3620	15	82,180,203	82,180,653	450	1	10.643	6.286	13	9	0	0	0				ActReg chr15 #3620	1	0
3621	15	82,337,414	82,338,203	789	1	6.833	11.792	10	18	1	1	1	MEX3B	553	in gene	ActReg chr15 #3621	0	1
3622	15	82,824,860	82,825,126	266	2	18.444	24.444	27	37	1	1	1	RPS17	-128	upstream	ActReg chr15 #3622	1	1
3623	15	83,316,027	83,316,719	692	1	11.954	8.545	20	15	1	1	1	CPEB1	355	in gene	ActReg chr15 #3623	1	0
3624	15	83,331,456	83,332,895	1,439	2	12.444	17.4	30	36	0	0	1	AP3B2	46,460	in gene	ActReg chr15 #3624	1	1
3625	15	83,378,229	83,379,073	844	2	10.741	13.63	17	26	1	1	2	AP3B2, LOC338963	-16, 4094	upstream, downstream	ActReg chr15 #3625	1	1
3626	15	83,501,775	83,502,554	779	1	10.833	6.667	16	11	0	0	2	WHAMM, LOC100505647	24191, 10032	in gene, downstream	ActReg chr15 #3626	1	0
3627	15	83,679,561	83,680,991	1,430	2	31.136	32.886	99	102	1	1	2	C15orf40, BTBD1	117, 55830	in gene, downstream	ActReg chr15 #3627	1	1
3628	15	83,735,396	83,736,282	886	2	9.815	12.704	14	20	1	1	1	BTBD1	267	in gene	ActReg chr15 #3628	1	1
3629	15	85,113,916	85,114,518	602	1	7.737	11.79	12	22	1	1	1	LOC100506874	-1,206	upstream	ActReg chr15 #3629	0	1
3630	15	85,143,622	85,144,931	1,309	1	6.073	11.049	11	16	1	1	1	ZSCAN2	27	in gene	ActReg chr15 #3630	0	1
3631	15	85,259,027	85,259,632	605	2	12.895	11.632	24	15	1	1	1	SEC11A	345	in gene	ActReg chr15 #3631	1	1
3632	15	85,290,674	85,291,394	720	1	7.348	10.696	10	14	1	1	1	ZNF592	-784	upstream	ActReg chr15 #3632	0	1
3633	15	85,523,353	85,524,999	1,646	2	15.423	18.75	31	41	1	1	1	PDE8A	-1,029	upstream	ActReg chr15 #3633	1	1
3634	15	85,667,136	85,667,785	649	1	3.833	10.191	7	16	0	0	1	PDE8A	142,255	in gene	ActReg chr15 #3634	0	1
3635	15	85,873,192	85,873,742	550	1	5.235	10.235	10	14	0	0	0				ActReg chr15 #3635	0	1
3636	15	87,891,816	87,892,297	481	1	9.733	6.533	20	11	0	0	0				ActReg chr15 #3636	1	0
3637	15	88,709,418	88,710,009	591	1	8.722	12.167	18	20	0	0	1	NTRK3	89,948	in gene	ActReg chr15 #3637	0	1
3638	15	89,010,217	89,011,343	1,126	1	9.4	13.886	17	22	1	2	2	MRPL46, MRPS11	-147, 96	upstream, in gene	ActReg chr15 #3638	0	1
3639	15	89,089,603	89,090,341	738	2	18.565	15.87	42	39	0	1	1	DET1	-60	upstream	ActReg chr15 #3639	1	1
3640	15	89,129,723	89,130,412	689	1	12.182	9.182	24	16	0	0	0				ActReg chr15 #3640	1	0
3641	15	89,148,315	89,149,586	1,271	2	15.1	14.7	33	39	1	2	2	MIR1179, MIR7-2	-2388, -6106	upstream, upstream	ActReg chr15 #3641	1	1
3642	15	89,164,151	89,164,853	702	1	8.273	10.909	14	17	1	1	2	MIR7-2, AEN	9446, -25	downstream, upstream	ActReg chr15 #3642	0	1
3643	15	89,181,705	89,182,611	906	2	14.393	14.393	24	29	0	1	2	AEN, ISG20	17631, 119	downstream, in gene	ActReg chr15 #3643	1	1
3644	15	89,192,465	89,193,237	772	1	8.875	13.542	14	20	0	0	1	ISG20	10,812	in gene	ActReg chr15 #3644	0	1
3645	15	89,333,754	89,334,602	848	1	10.963	7.111	19	12	0	0	0				ActReg chr15 #3645	1	0
3646	15	89,456,320	89,456,836	516	1	10.588	7.824	16	10	1	1	1	MFGE8	85	in gene	ActReg chr15 #3646	1	0
3647	15	89,630,719	89,631,907	1,188	2	10.184	10.947	16	16	1	1	1	ABHD2	-68	upstream	ActReg chr15 #3647	1	1
3648	15	89,710,484	89,711,608	1,124	2	11.657	9.314	20	15	0	0	1	ABHD2	79,665	in gene	ActReg chr15 #3648	1	1
3649	15	89,769,875	89,770,421	546	1	7.941	10.706	12	17	0	1	1	RLBP1	-5,226	upstream	ActReg chr15 #3649	0	1
3650	15	89,877,595	89,878,843	1,248	2	15.769	17.949	35	38	1	2	2	POLG, LOC100506983	-193, -283	upstream, upstream	ActReg chr15 #3650	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3651	15	89,904,535	89,905,759	1,224	2	11.684	15.605	26	29	1	1	1	MIR9-3	-6,101	upstream	ActReg chr15 #3651	1	1
3652	15	89,907,522	89,908,592	1,070	2	11.909	10.212	19	17	0	1	1	MIR9-3	-3,191	upstream	ActReg chr15 #3652	1	1
3653	15	89,962,407	89,963,268	861	1	8.963	13.037	19	25	0	0	0				ActReg chr15 #3653	0	1
3654	15	89,973,669	89,974,423	754	1	9.174	11.652	13	19	1	0	0				ActReg chr15 #3654	0	1
3655	15	90,118,263	90,119,636	1,373	2	10.767	11.233	23	16	1	1	1	C15orf42	131	in gene	ActReg chr15 #3655	1	1
3656	15	90,436,787	90,437,763	976	2	13.839	15.581	34	30	1	1	3	AP3S2, LOC100507010, C15orf38	342, 5480, 18947	in gene, downstream, downstream	ActReg chr15 #3656	1	1
3657	15	90,776,604	90,777,349	745	1	6.208	11	11	16	1	2	3	SEMA4B, CIB1, C15orf58	48824, 303, 511	downstream, in gene, upstream	ActReg chr15 #3657	0	1
3658	15	90,808,375	90,809,204	829	1	10.385	12.654	17	25	1	2	3	TTLL13, NCRN, LOC100507029	16025, -106, -7397	downstream, upstream, upstream	ActReg chr15 #3658	0	1
3659	15	91,445,400	91,445,965	565	1	11	5.625	22	10	1	1	2	FES, MAN2A2	18017, -1738	downstream, upstream	ActReg chr15 #3659	1	0
3660	15	91,474,832	91,476,252	1,420	2	21.523	26.5	61	76	1	2	3	MAN2A2, UNC45A, HDDC3	28122, 2132, 232	downstream, in gene, in gene	ActReg chr15 #3660	1	1
3661	15	91,537,287	91,538,377	1,090	2	9.235	11.152	18	20	1	1	3	PRC1, LOC100507118, VPS33B	-28, 28229, 28001	upstream, downstream, downstream	ActReg chr15 #3661	1	1
3662	15	91,881,892	91,882,559	667	1	7.9	12.8	16	23	0	0	0				ActReg chr15 #3662	0	1
3663	15	92,058,477	92,059,118	641	2	11.05	11.2	20	17	0	0	0				ActReg chr15 #3663	1	1
3664	15	92,395,777	92,396,288	511	1	7.062	11.062	12	14	1	1	1	SLCO3A1	-906	upstream	ActReg chr15 #3664	0	1
3665	15	92,555,047	92,555,665	618	1	8.211	10.632	12	14	0	0	1	SLCO3A1	158,418	in gene	ActReg chr15 #3665	0	1
3666	15	93,352,100	93,353,067	967	2	11.567	12.767	22	22	1	0	0				ActReg chr15 #3666	1	1
3667	15	93,524,495	93,525,024	529	1	11.588	8.882	16	11	0	0	1	CHD2	81,208	in gene	ActReg chr15 #3667	1	0
3668	15	94,372,512	94,373,358	846	1	11.963	12.259	25	21	0	0	0				ActReg chr15 #3668	1	0
3669	15	94,443,416	94,444,599	1,183	1	7.351	12.135	12	16	0	0	0				ActReg chr15 #3669	0	1
3670	15	94,569,538	94,570,165	627	1	10.947	8.895	19	14	0	0	0				ActReg chr15 #3670	1	0
3671	15	95,753,497	95,754,242	745	1	8.417	11	14	24	0	0	0				ActReg chr15 #3671	0	1
3672	15	95,790,154	95,790,976	822	2	10.115	13.731	18	24	0	0	0				ActReg chr15 #3672	1	1
3673	15	96,816,666	96,817,451	785	1	10.04	14.8	19	24	0	0	2	LOC644192, LOC100506754	53532, 53351	in gene, downstream	ActReg chr15 #3673	0	1
3674	15	96,899,998	96,900,698	700	2	9.955	10.864	18	18	1	1	1	LOC728800	-2,545	upstream	ActReg chr15 #3674	1	1
3675	15	98,418,466	98,419,308	842	2	15.692	14.5	30	29	0	1	1	LOC91948	-1,228	upstream	ActReg chr15 #3675	1	1
3676	15	98,503,267	98,504,273	1,006	2	11.968	16.806	25	30	1	1	1	ARRDC4	-163	upstream	ActReg chr15 #3676	1	1
3677	15	99,091,303	99,091,845	542	1	10.529	10.412	13	15	1	0	0				ActReg chr15 #3677	0	1
3678	15	99,396,299	99,396,833	534	1	8.824	10.941	15	19	0	0	1	IGF1R	203,805	in gene	ActReg chr15 #3678	0	1
3679	15	99,439,393	99,440,442	1,049	1	11.438	6.969	18	12	0	0	1	IGF1R	247,156	in gene	ActReg chr15 #3679	1	0
3680	15	99,645,793	99,646,370	577	1	10.556	14.333	15	21	1	1	1	SYNM	795	in gene	ActReg chr15 #3680	0	1
3681	15	99,663,783	99,664,367	584	1	12.389	10.889	19	15	0	0	1	SYNM	18,789	in gene	ActReg chr15 #3681	1	0
3682	15	99,789,543	99,790,107	564	1	10.353	13.235	17	23	0	2	2	TTC23, LRRC28	-10, -1827	upstream, upstream	ActReg chr15 #3682	0	1
3683	15	100,468,645	100,469,165	520	1	12.438	9.75	20	15	0	0	0				ActReg chr15 #3683	1	0
3684	15	100,889,806	100,890,717	911	1	10.107	12.036	18	18	1	1	2	ADAMTS17, FLJ42289	-8078, 662	upstream, in gene	ActReg chr15 #3684	0	1
3685	15	101,226,179	101,227,205	1,026	1	7.219	12.062	16	18	0	0	0				ActReg chr15 #3685	0	1
3686	15	101,261,849	101,262,594	745	1	10.417	11.917	23	20	0	0	0				ActReg chr15 #3686	0	1
3687	15	101,431,083	101,432,386	1,303	1	10.317	14.098	16	21	0	0	2	ALDH1A3, LOC100507452	11725, 27754	in gene, downstream	ActReg chr15 #3687	0	1
3688	15	101,458,101	101,459,466	1,365	1	8.326	11.558	14	19	1	2	3	ALDH1A3, LOC100507452, LRRK1	38774, 705, 677	downstream, in gene, upstream	ActReg chr15 #3688	0	1
3689	15	101,791,943	101,792,918	975	2	11.4	11.667	20	19	1	1	1	CHSY1	-293	upstream	ActReg chr15 #3689	1	1
3690	15	101,834,799	101,836,242	1,443	2	17.267	18.933	42	43	1	1	2	SNRPA1, PCSK6	-60, 194667	upstream, downstream	ActReg chr15 #3690	1	1
3691	15	102,191,885	102,193,091	1,206	1	7.605	11.579	15	17	1	1	2	TM2D3, TARSL2	106, 72157	in gene, downstream	ActReg chr15 #3691	0	1
3692	15	102,351,091	102,351,637	546	1	6.529	9.765	10	17	0	1	2	OR4F6, OR4F15	5441, -7026	downstream, upstream	ActReg chr15 #3692	0	1
3693	16	103,179	103,836	657	1	11.45	11.2	16	19	1	2	3	POLR3K, SNRNP25, RHBDF1	125, -322, 19122	in gene, upstream, downstream	ActReg chr16 #3693	0	1
3694	16	118,151	118,843	692	1	12.619	11.524	18	22	0	0	2	RHBDF1, MPG	4132, -8521	in gene, upstream	ActReg chr16 #3694	1	0
3695	16	122,632	123,394	762	1	7.125	11.417	12	19	1	2	2	RHBDF1, MPG	-384, -4005	upstream, upstream	ActReg chr16 #3695	0	1
3696	16	278,990	279,832	842	2	12.154	13.115	19	24	1	3	3	LUC7L, LOC100129478, ITFG3	38, -1118, -5390	in gene, upstream, upstream	ActReg chr16 #3696	1	1
3697	16	377,057	377,965	908	1	10.464	14.607	15	26	0	0	1	AXIN1	24,953	in gene	ActReg chr16 #3697	0	1
3698	16	474,742	475,616	874	1	12.893	9.929	22	16	1	1	1	RAB11FIP3	-489	upstream	ActReg chr16 #3698	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3699	16	576,580	577,776	1,196	2	12.486	13.108	23	24	1	2	3	RAB11FIP3, C16orf10, SOLH	101510, 229, -678	downstream, in gene, upstream	ActReg chr16 #3699	1	1
3700	16	578,307	579,014	707	1	7.818	11.636	11	15	0	2	4	RAB11FIP3, C16orf10, SOLH, LOC100507047	102992, -1253, 804, -10290	downstream, upstream, in gene, upstream	ActReg chr16 #3700	0	1
3701	16	685,919	687,100	1,181	2	17.676	20.595	43	46	1	3	6	RAB40C, WFIKKN1, C16orf13, LOC100287175, LOC100130285, FAM195A	47152, 5497, -162, -308, 5226, -5340	downstream, downstream, upstream, upstream, downstream, upstream	ActReg chr16 #3701	1	1
3702	16	717,798	718,387	589	1	9.111	13.833	12	24	1	1	4	WDR90, LOC100507167, RHOT2, RHBDL1	18729, 4132, -41, -7983	downstream, downstream, upstream, upstream	ActReg chr16 #3702	0	1
3703	16	733,663	734,724	1,061	1	10.853	11.294	17	22	1	1	6	RHOT2, RHBDL1, STUB1, JMJD8, WDR24, FBXL16	16060, 8118, 4078, 246, 6207, 21632	downstream, downstream, downstream, in gene, downstream, downstream	ActReg chr16 #3703	0	1
3704	16	739,809	740,712	903	1	8.679	12.571	17	22	1	2	4	STUB1, JMJD8, WDR24, FBXL16	10145, -5821, 140, 15565	downstream, upstream, in gene, downstream	ActReg chr16 #3704	0	1
3705	16	770,872	771,526	654	1	10.476	13.857	15	23	1	2	5	METRN, FAM173A, CCDC78, HAGHL, NARFL	6026, 41, 5274, -5759, 19798	downstream, in gene, downstream, upstream, downstream	ActReg chr16 #3705	0	1
3706	16	790,759	791,351	592	1	11.278	11.778	21	18	1	1	1	NARFL	-58	upstream	ActReg chr16 #3706	0	1
3707	16	838,455	839,082	627	1	7.7	12.25	13	26	1	3	4	MSLNL, RPUSD1, CHTF18, GNG13	-5842, -385, 146, 11965	upstream, upstream, in gene, downstream	ActReg chr16 #3707	0	1
3708	16	1,020,168	1,021,126	958	1	8.8	12.233	15	21	1	0	1	LMF1	10,671	in gene	ActReg chr16 #3708	0	1
3709	16	1,358,749	1,359,526	777	2	18.16	17.96	40	33	1	1	1	UBE2I	-43	upstream	ActReg chr16 #3709	1	1
3710	16	1,401,063	1,402,465	1,402	1	9.25	12.659	16	21	1	2	3	BAIAP3, C16orf42, GNPTG	17101, 109, 136	downstream, in gene, upstream	ActReg chr16 #3710	0	1
3711	16	1,470,152	1,471,222	1,070	2	11.485	13.879	27	25	1	1	2	UNKL, C16orf91	-5982, 8658	upstream, in gene	ActReg chr16 #3711	1	1
3712	16	1,524,705	1,525,399	694	1	9.571	13	19	26	1	1	1	CLCN7	33	in gene	ActReg chr16 #3712	0	1
3713	16	1,695,812	1,696,553	741	2	11.478	11.652	17	18	0	0	1	CRAMP1L	31,541	in gene	ActReg chr16 #3713	1	1
3714	16	1,755,502	1,756,739	1,237	2	11.41	12.128	21	19	0	1	2	HN1L, MAPK8IP3	27842, -101	downstream, upstream	ActReg chr16 #3714	1	1
3715	16	1,821,831	1,822,561	730	1	8.609	12.913	13	20	1	3	5	MAPK8IP3, NME3, MRPS34, EME2, SPSB3	65975, -486, 944, -1033, 10385	downstream, upstream, in gene, upstream, downstream	ActReg chr16 #3715	0	1
3716	16	1,822,702	1,823,493	791	1	9.2	15.12	13	30	1	3	6	MAPK8IP3, NME3, MRPS34, EME2, SPSB3, NUBP2	66876, -1387, 43, -132, 9484, -9836	downstream, upstream, in gene, upstream, downstream, upstream	ActReg chr16 #3716	0	1
3717	16	1,832,536	1,833,254	718	1	8.217	14.217	13	26	1	2	5	MRPS34, EME2, SPSB3, NUBP2, IGFALS	-9755, 9666, -314, -38, 12014	upstream, downstream, upstream, upstream, downstream	ActReg chr16 #3717	0	1
3718	16	1,876,704	1,877,694	990	2	11.065	20.097	18	45	1	2	3	HAGH, FAHD1, C16orf73	-4, -26, 44980	upstream, upstream, downstream	ActReg chr16 #3718	1	1
3719	16	2,009,145	2,009,994	849	2	12.407	14.926	26	34	1	6	8	RPL3L, NDUFB10, RPS2, SNORA10, SNORA64, SNHG9, SNORA78, RNF151	-4890, 52, 5258, 2898, 3538, -5428, 5616, -7306	upstream, in gene, downstream, downstream, downstream, upstream, upstream, upstream	ActReg chr16 #3719	1	1
3720	16	2,021,575	2,022,526	951	2	14.345	14.483	28	32	1	2	9	NDUFB10, RPS2, SNORA10, SNORA64, SNHG9, SNORA78, RNF151, TBL3, NOXO1	12533, -7223, -9583, -8943, 7053, 6865, 5175, -14, 9390	downstream, upstream, upstream, upstream, downstream, downstream, downstream, upstream, downstream	ActReg chr16 #3720	1	1
3721	16	2,033,515	2,034,082	567	1	10.889	13.611	18	22	1	3	4	TBL3, NOXO1, GFER, SYNGR3	11734, -2358, -352, -6170	downstream, upstream, upstream, upstream	ActReg chr16 #3721	0	1
3722	16	2,059,809	2,060,621	812	1	12.28	15.44	19	27	1	1	2	ZNF598, NPW	-452, -9306	upstream, upstream	ActReg chr16 #3722	0	1
3723	16	2,072,993	2,073,799	806	1	10.92	9.04	19	15	0	1	2	NPW, SLC9A3R2	3875, -3492	downstream, upstream	ActReg chr16 #3723	1	0
3724	16	2,082,513	2,084,096	1,583	1	10.14	12.46	15	17	0	0	2	SLC9A3R2, NTHL1	6416, 14563	in gene, downstream	ActReg chr16 #3724	0	1
3725	16	2,097,466	2,098,181	715	2	11.609	11.043	17	15	1	2	3	SLC9A3R2, NTHL1, TSC2	20935, 44, -167	downstream, in gene, upstream	ActReg chr16 #3725	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3726	16	2,202,443	2,203,267	824	1	9.192	15.962	16	31	0	3	4	RAB26, LOC100507303, SNORD60, TRAF7	4204, 2504, 2251, -2944	in gene, downstream, downstream, upstream	ActReg chr16 #3726	0	1
3727	16	2,255,030	2,256,328	1,298	2	16.22	16.171	43	35	1	1	4	CASKIN1, MLST8, C16orf79, PGP	-9214, 229, 5332, 9143	upstream, in gene, downstream, downstream	ActReg chr16 #3727	1	1
3728	16	2,264,940	2,265,615	675	1	5.476	10.476	11	14	1	2	4	MLST8, C16orf79, PGP, E4F1	9827, -4266, -455, -8290	downstream, upstream, upstream, upstream	ActReg chr16 #3728	0	1
3729	16	2,317,638	2,318,907	1,269	2	18.103	16.462	43	41	1	2	3	RNPS1, MIR940, ABCA3	-158, -3476, 72475	upstream, upstream, downstream	ActReg chr16 #3729	1	1
3730	16	2,390,776	2,391,242	466	1	10.533	11.133	17	15	1	1	1	ABCA3	-262	upstream	ActReg chr16 #3730	0	1
3731	16	2,517,878	2,518,675	797	1	6.56	10.72	11	17	1	2	4	CCNF, C16orf59, NTN3, TBC1D24	38881, 8161, -3224, -6871	downstream, downstream, upstream, upstream	ActReg chr16 #3731	0	1
3732	16	2,523,981	2,524,590	609	1	8.158	13.105	12	21	1	2	3	C16orf59, NTN3, TBC1D24	14170, 2785, -862	downstream, downstream, upstream	ActReg chr16 #3732	0	1
3733	16	2,653,071	2,654,003	932	2	10.931	14.862	17	24	1	1	2	PDPK1, PRO0461	65567, 152	downstream, in gene	ActReg chr16 #3733	1	1
3734	16	2,732,067	2,732,838	771	2	13.375	12.75	23	20	1	1	2	LOC100507321, KCTD5	-9012, -43	upstream, upstream	ActReg chr16 #3734	1	1
3735	16	2,801,792	2,803,107	1,315	2	10.548	10.286	22	21	1	2	2	LOC100128788, SRRM2	152, 119	in gene, in gene	ActReg chr16 #3735	1	1
3736	16	2,910,802	2,911,629	827	2	11.423	12.962	17	28	0	1	1	PRSS22	-3,044	upstream	ActReg chr16 #3736	1	1
3737	16	2,917,787	2,918,701	914	2	9.552	13.241	17	24	1	0	1	PRSS22	-10,073	upstream	ActReg chr16 #3737	1	1
3738	16	2,961,543	2,962,218	675	2	10.667	12.333	22	22	1	1	1	FLYWCH1	-100	upstream	ActReg chr16 #3738	1	1
3739	16	3,018,510	3,019,446	936	2	13.172	14.448	26	28	1	1	3	KREMEN2, PAQR4, PKMYT1	4761, -364, 11496	downstream, upstream, downstream	ActReg chr16 #3739	1	1
3740	16	3,030,210	3,031,027	817	1	7.32	12.64	9	18	1	1	3	PAQR4, PKMYT1, LOC283875	11276, -144, -8437	downstream, upstream, upstream	ActReg chr16 #3740	0	1
3741	16	3,070,543	3,072,215	1,672	3	9.885	11.558	21	19	1	4	6	CLDN9, CLDN6, TNFRSF12A, HCFC1R1, THOC6, CCDC64B	8922, -3191, 1066, 2908, -2653, 14163	downstream, upstream, in gene, downstream, upstream, downstream	ActReg chr16 #3741	1	1
3742	16	3,073,582	3,074,602	1,020	2	12.531	11.281	21	21	1	3	7	CLDN9, CLDN6, TNFRSF12A, HCFC1R1, THOC6, CCDC64B, LOC100128770	11635, -5904, 3779, 195, 60, 11450, -8390	downstream, upstream, downstream, in gene, in gene, downstream, upstream	ActReg chr16 #3742	1	1
3743	16	3,156,109	3,156,646	537	1	5.765	10	13	15	1	1	2	MGC3771, ZNF205	9222, -6186	downstream, upstream	ActReg chr16 #3743	0	1
3744	16	3,174,106	3,175,133	1,027	2	12.719	12.25	23	21	1	0	4	MGC3771, ZNF205, LOC100507458, ZNF213	-9020, 12056, 10259, -10438	upstream, downstream, downstream, upstream	ActReg chr16 #3744	1	1
3745	16	3,200,307	3,201,168	861	2	13.482	10.37	26	15	1	0	1	ZNF213	15,680	downstream	ActReg chr16 #3745	1	1
3746	16	3,202,337	3,203,234	897	1	8.25	12.357	12	18	0	0	1	ZNF213	17,728	downstream	ActReg chr16 #3746	0	1
3747	16	3,239,282	3,239,871	589	1	11.5	8.222	14	12	1	0	0				ActReg chr16 #3747	1	0
3748	16	3,354,964	3,356,211	1,247	2	8.077	11.59	18	17	1	2	2	TIGD7, ZNF75A	-4187, 154	upstream, in gene	ActReg chr16 #3748	1	1
3749	16	3,414,697	3,415,425	728	1	9.435	11.304	13	15	1	0	2	OR2C1, MTRNR2L4	9172, 7222	downstream, downstream	ActReg chr16 #3749	0	1
3750	16	3,450,552	3,451,700	1,148	2	13.25	13.861	27	30	1	2	2	ZNF434, ZNF174	-101, -64	upstream, upstream	ActReg chr16 #3750	1	1
3751	16	3,507,348	3,508,248	900	2	9.893	10.75	17	19	1	0	1	NAT15	14,130	in gene	ActReg chr16 #3751	1	1
3752	16	3,550,457	3,551,344	887	2	12.893	13.714	24	24	2	2	2	C16orf90, CLUAP1	-5479, -63	upstream, upstream	ActReg chr16 #3752	1	1
3753	16	3,661,222	3,661,756	534	1	11.312	5.438	17	8	1	1	1	BTBD12	96	in gene	ActReg chr16 #3753	1	0
3754	16	3,766,915	3,768,062	1,147	1	9.6	11.914	15	20	1	1	2	TRAP1, CREBBP	110, 162633	in gene, downstream	ActReg chr16 #3754	0	1
3755	16	3,929,261	3,929,807	546	1	9.765	8.765	15	14	1	1	1	CREBBP	587	in gene	ActReg chr16 #3755	1	0
3756	16	4,233,442	4,234,229	787	2	10.833	10.875	17	18	1	0	1	SRL	58,246	downstream	ActReg chr16 #3756	1	1
3757	16	4,303,691	4,304,340	649	1	10.85	11.65	14	18	1	1	2	LOC100507501, TFAP4	-225, 18986	upstream, downstream	ActReg chr16 #3757	0	1
3758	16	4,321,551	4,322,215	664	1	9.905	11.286	17	25	2	1	1	TFAP4	1,118	in gene	ActReg chr16 #3758	0	1
3759	16	4,475,216	4,476,260	1,044	2	13.454	13.727	26	23	1	1	2	CORO7, DNAJA3	-9099, -120	upstream, upstream	ActReg chr16 #3759	1	1
3760	16	4,525,740	4,526,612	872	1	10.667	8.741	14	15	1	2	2	NMRAL1, HMOX2	-1280, 1457	upstream, in gene	ActReg chr16 #3760	1	0
3761	16	4,588,407	4,589,116	709	1	9.045	12.364	13	22	1	1	1	C16orf5	55	in gene	ActReg chr16 #3761	0	1
3762	16	4,664,435	4,665,532	1,097	2	10.412	12.618	22	19	1	1	2	FAM100A, MGRN1	-56, -9843	upstream, upstream	ActReg chr16 #3762	1	1
3763	16	4,665,774	4,666,480	706	1	11.409	10.636	18	16	1	1	2	FAM100A, MGRN1	-1200, -8699	upstream, upstream	ActReg chr16 #3763	1	0
3764	16	4,674,129	4,675,085	956	2	10.233	14.767	16	23	1	1	3	FAM100A, MGRN1, LOC100507570	-9680, -219, 16017	upstream, upstream, downstream	ActReg chr16 #3764	1	1
3765	16	4,783,840	4,784,618	778	1	10.12	11.88	13	17	1	2	2	ANKS3, C16orf71	-66, -60	upstream, upstream	ActReg chr16 #3765	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3766	16	4,816,941	4,817,675	734	2	13.043	16.13	26	26	1	1	2	ZNF500, SEPT12	-142, 21091	upstream, downstream	ActReg chr16 #3766	1	1
3767	16	4,909,156	4,910,456	1,300	2	11.825	12.55	18	24	0	0	1	UBN1	11,894	in gene	ActReg chr16 #3767	1	1
3768	16	4,992,956	4,993,760	804	1	7.615	11.462	14	16	0	1	1	PPL	-6,222	upstream	ActReg chr16 #3768	0	1
3769	16	4,994,380	4,995,191	811	1	9.88	10.76	18	16	0	1	1	PPL	-7,649	upstream	ActReg chr16 #3769	0	1
3770	16	4,995,648	4,996,133	485	1	12.562	3.875	21	8	0	0	1	PPL	-8,754	upstream	ActReg chr16 #3770	1	0
3771	16	8,076,347	8,077,041	694	2	9.1	14.273	17	31	0	0	0				ActReg chr16 #3771	1	1
3772	16	8,241,653	8,242,424	771	2	11.917	11.708	20	24	0	0	0				ActReg chr16 #3772	1	1
3773	16	8,396,142	8,396,810	668	2	9.81	12	18	26	0	0	0				ActReg chr16 #3773	1	1
3774	16	8,891,301	8,892,003	702	1	12.591	15.227	18	27	1	2	2	TMEM186, PMM2	-147, -18	upstream, upstream	ActReg chr16 #3774	0	1
3775	16	9,025,585	9,026,244	659	2	10.191	10.524	24	20	0	0	1	USP7	31,427	in gene	ActReg chr16 #3775	1	1
3776	16	10,837,460	10,838,033	573	1	10.056	13	16	25	1	1	1	NUBP1	48	in gene	ActReg chr16 #3776	0	1
3777	16	10,972,036	10,973,361	1,325	2	9.756	9.683	14	20	1	1	1	CIITA	1,643	in gene	ActReg chr16 #3777	1	1
3778	16	10,988,737	10,989,578	841	1	10.692	8.577	18	14	0	0	1	CIITA	18,102	in gene	ActReg chr16 #3778	1	0
3779	16	11,038,005	11,038,751	746	2	13	11.783	26	22	1	2	3	DEXI, LOC100505564, CLEC16A	-2121, 3802, 33	upstream, downstream, in gene	ActReg chr16 #3779	1	1
3780	16	11,890,887	11,891,935	1,048	2	14.188	17.774	37	48	1	0	0				ActReg chr16 #3780	1	1
3781	16	12,009,392	12,010,414	1,022	2	11.031	11.031	21	18	1	1	1	GSPT1	616	in gene	ActReg chr16 #3781	1	1
3782	16	12,069,978	12,070,697	719	1	8.652	11.261	13	15	1	1	2	TNFRSF17, RUNDC2A	11373, -265	downstream, upstream	ActReg chr16 #3782	0	1
3783	16	12,755,471	12,756,084	613	1	9.421	12.526	15	22	0	0	1	CPPED1	141,967	in gene	ActReg chr16 #3783	0	1
3784	16	12,896,998	12,898,185	1,187	2	12.946	17.081	30	33	1	1	1	CPPED1	153	in gene	ActReg chr16 #3784	1	1
3785	16	13,130,441	13,130,901	460	1	10.071	7.929	17	11	0	0	1	SHISA9	135,194	in gene	ActReg chr16 #3785	1	0
3786	16	13,203,847	13,204,752	905	1	8.679	12.679	13	21	0	0	1	SHISA9	208,822	in gene	ActReg chr16 #3786	0	1
3787	16	13,385,569	13,386,290	701	2	9.727	11.091	15	21	0	0	0				ActReg chr16 #3787	1	1
3788	16	14,051,122	14,052,107	985	2	11.839	10.516	19	16	0	0	1	ERCC4	37,600	downstream	ActReg chr16 #3788	1	1
3789	16	14,164,656	14,165,232	576	1	7.222	11.778	13	16	1	1	1	MKL2	-252	upstream	ActReg chr16 #3789	0	1
3790	16	14,379,117	14,380,233	1,116	2	12.2	12.029	23	27	1	0	0				ActReg chr16 #3790	1	1
3791	16	14,493,325	14,493,857	532	1	9.647	7.059	17	14	0	0	0				ActReg chr16 #3791	1	0
3792	16	14,595,319	14,595,965	646	1	7.8	13.95	12	27	0	0	1	PARN	128,482	in gene	ActReg chr16 #3792	0	1
3793	16	14,605,015	14,605,792	777	1	10.52	7.96	15	11	0	0	1	PARN	118,721	in gene	ActReg chr16 #3793	1	0
3794	16	14,726,414	14,727,418	1,004	1	12.097	9.903	18	16	1	2	2	PARN, BFAR	-2792, 248	upstream, in gene	ActReg chr16 #3794	1	0
3795	16	15,052,485	15,053,248	763	2	12.458	8.75	24	16	0	0	1	NPIP	21,566	downstream	ActReg chr16 #3795	1	1
3796	16	15,489,438	15,490,221	783	2	11.12	7.88	19	18	1	1	1	MPV17L	218	in gene	ActReg chr16 #3796	1	1
3797	16	15,527,991	15,528,633	642	1	7.5	11.65	15	17	1	1	1	C16orf45	-13	upstream	ActReg chr16 #3797	0	1
3798	16	15,684,500	15,685,303	803	2	10.6	10.68	19	21	0	0	2	C16orf45, KIAA0430	156576, 52122	downstream, downstream	ActReg chr16 #3798	1	1
3799	16	15,693,346	15,694,125	779	1	10.25	7.458	16	13	0	0	1	KIAA0430	43,288	in gene	ActReg chr16 #3799	1	0
3800	16	15,766,331	15,767,023	692	1	8.591	12.636	14	20	0	0	1	NDE1	29,553	in gene	ActReg chr16 #3800	0	1
3801	16	15,961,907	15,962,702	795	1	11.08	9.261	19	15	1	1	1	C16orf63	143	in gene	ActReg chr16 #3801	1	0
3802	16	16,326,267	16,326,498	231	1	7.125	11.375	10	16	1	1	2	ABCC6, NOMO3	-9054, -7	upstream, upstream	ActReg chr16 #3802	0	1
3803	16	16,891,120	16,891,689	569	1	10.833	5.833	17	8	0	0	0				ActReg chr16 #3803	1	0
3804	16	16,922,480	16,923,413	933	1	9.862	6.483	14	10	0	0	0				ActReg chr16 #3804	1	0
3805	16	16,951,865	16,952,346	481	1	10	10.933	15	15	0	0	0				ActReg chr16 #3805	0	1
3806	16	17,232,457	17,233,361	904	2	11.929	12.286	25	22	0	0	2	XYLT1, LOC100506171	331829, 4548	in gene, downstream	ActReg chr16 #3806	1	1
3807	16	17,243,544	17,244,437	893	2	17.929	22	49	57	0	0	1	XYLT1	320,748	in gene	ActReg chr16 #3807	1	1
3808	16	17,259,845	17,260,513	668	1	8.762	14.476	18	24	0	0	1	XYLT1	304,559	in gene	ActReg chr16 #3808	0	1
3809	16	17,271,889	17,272,647	758	2	10.292	15.125	27	30	0	0	1	XYLT1	292,470	in gene	ActReg chr16 #3809	1	1
3810	16	17,491,222	17,491,743	521	1	5.562	10	10	17	0	0	1	XYLT1	73,256	in gene	ActReg chr16 #3810	0	1
3811	16	17,498,775	17,499,764	989	1	12.129	11.194	18	23	0	0	1	XYLT1	65,469	in gene	ActReg chr16 #3811	1	0
3812	16	17,877,574	17,878,534	960	2	14.433	11.867	25	23	0	0	0				ActReg chr16 #3812	1	1
3813	16	18,133,723	18,134,350	627	1	5.35	10.1	11	17	0	0	0				ActReg chr16 #3813	0	1
3814	16	18,801,179	18,802,126	947	2	13.367	13.4	23	22	1	1	2	RPS15A, ARL6IP1	4, 11205	in gene, downstream	ActReg chr16 #3814	1	1
3815	16	18,812,284	18,813,721	1,437	2	20.911	28.378	70	85	1	1	2	ARL6IP1, SMG1	-145, 124724	upstream, downstream	ActReg chr16 #3815	1	1
3816	16	19,078,622	19,079,455	833	2	12	11.615	20	18	1	1	2	TMC7, COQ7	83782, 121	downstream, in gene	ActReg chr16 #3816	1	1
3817	16	19,124,723	19,125,542	819	1	8.154	10.654	12	14	1	1	1	ITPRIPL2	-122	upstream	ActReg chr16 #3817	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3818	16	19,125,710	19,126,652	942	1	8.276	14.483	13	23	1	1	1	ITPRIPL2	927	in gene	ActReg chr16 #3818	0	1
3819	16	19,178,892	19,179,522	630	1	7.95	10.9	14	19	1	1	1	SYT17	-431	upstream	ActReg chr16 #3819	0	1
3820	16	19,318,668	19,319,834	1,166	2	17	20.139	43	45	0	0	1	LOC728276	22,146	downstream	ActReg chr16 #3820	1	1
3821	16	19,534,958	19,535,480	522	1	6.625	11.688	11	18	1	2	2	GDE1, CP110	-1769, 40	upstream, in gene	ActReg chr16 #3821	0	1
3822	16	19,566,310	19,567,425	1,115	1	7.914	11.886	15	19	1	1	2	CP110, C16orf62	31688, -173	downstream, upstream	ActReg chr16 #3822	0	1
3823	16	19,728,965	19,729,887	922	1	6.643	13.893	10	23	1	2	2	C16orf88, IQCK	66, 1648	in gene, in gene	ActReg chr16 #3823	0	1
3824	16	20,752,796	20,753,474	678	1	8.636	17.409	20	37	1	1	1	THUMPD1	64	in gene	ActReg chr16 #3824	0	1
3825	16	20,817,290	20,818,849	1,559	2	10.918	9.714	28	18	1	2	3	ACSM3, ERI2, LOC81691	42757, -274, 302	downstream, upstream, in gene	ActReg chr16 #3825	1	1
3826	16	20,911,930	20,912,654	724	1	8.565	10.913	15	20	1	2	3	DCUN1D3, LOC100506372, LYRM1	-731, 13452, 735	upstream, downstream, in gene	ActReg chr16 #3826	0	1
3827	16	21,531,360	21,531,905	545	2	12.056	13.722	17	29	1	0	0				ActReg chr16 #3827	1	1
3828	16	21,610,275	21,611,214	939	2	11.759	13.034	18	28	1	1	1	METTL9	-112	upstream	ActReg chr16 #3828	1	1
3829	16	21,696,308	21,696,800	492	1	6.688	11.375	8	18	0	0	1	OTOA	6,719	in gene	ActReg chr16 #3829	0	1
3830	16	21,964,122	21,965,006	884	2	12.571	13.286	21	21	0	1	1	UQCRC2	-45	upstream	ActReg chr16 #3830	1	1
3831	16	22,017,939	22,019,337	1,398	2	10.568	11.182	18	18	1	2	2	C16orf65, C16orf52	-6207, -818	upstream, upstream	ActReg chr16 #3831	1	1
3832	16	22,201,077	22,201,916	839	1	7.577	13.654	12	26	1	0	1	LOC100288072	24,592	in gene	ActReg chr16 #3832	0	1
3833	16	22,217,176	22,218,759	1,583	2	10.46	15.32	18	31	1	1	1	EEF2K	375	in gene	ActReg chr16 #3833	1	1
3834	16	22,308,160	22,309,925	1,765	2	10.821	12.589	20	22	1	1	2	EEF2K, POLR3E	91450, 301	downstream, in gene	ActReg chr16 #3834	1	1
3835	16	22,625,016	22,626,437	1,421	2	11.089	12.689	20	21	0	0	0				ActReg chr16 #3835	1	1
3836	16	22,651,977	22,653,056	1,079	2	14.059	15.441	22	29	0	0	0				ActReg chr16 #3836	1	1
3837	16	22,899,977	22,900,591	614	1	4.053	10.263	7	14	0	0	1	HS3ST2	74,424	in gene	ActReg chr16 #3837	0	1
3838	16	23,037,910	23,038,709	799	2	11.88	14.76	29	28	0	0	0				ActReg chr16 #3838	1	1
3839	16	23,182,731	23,183,318	587	1	4.278	11.333	6	17	0	0	0				ActReg chr16 #3839	0	1
3840	16	23,185,801	23,186,414	613	1	9.842	11.947	13	18	0	0	1	SCNN1G	-7,933	upstream	ActReg chr16 #3840	0	1
3841	16	23,568,208	23,569,120	912	2	11.69	12.379	23	20	1	2	2	EARS2, UBFD1	32, -198	in gene, upstream	ActReg chr16 #3841	1	1
3842	16	23,606,906	23,608,179	1,273	2	32.075	30.875	122	114	1	1	2	NDUFAB1, PALB2	97, 45136	in gene, downstream	ActReg chr16 #3842	1	1
3843	16	23,652,257	23,653,183	926	2	16.679	21.179	40	48	1	2	2	PALB2, DCTN5	-42, -87	upstream, upstream	ActReg chr16 #3843	1	1
3844	16	23,689,695	23,690,965	1,270	2	11.225	21.525	32	59	1	1	3	DCTN5, LOC100506587, PLK1	37523, 8998, 129	downstream, downstream, in gene	ActReg chr16 #3844	1	1
3845	16	23,985,489	23,986,117	628	1	6.6	10.8	14	16	0	0	1	PRKCB	138,503	in gene	ActReg chr16 #3845	0	1
3846	16	24,189,714	24,190,352	638	1	8.05	10	15	21	0	0	1	PRKCB	342,733	in gene	ActReg chr16 #3846	0	1
3847	16	24,266,991	24,267,735	744	2	12.304	14.478	24	28	1	1	1	CACNG3	487	in gene	ActReg chr16 #3847	1	1
3848	16	24,550,312	24,551,060	748	1	9.435	12.957	15	23	1	1	1	RBBP6	-222	upstream	ActReg chr16 #3848	0	1
3849	16	24,680,487	24,681,251	764	2	8.792	12.696	21	24	0	1	1	FLJ45256	1,514	in gene	ActReg chr16 #3849	1	1
3850	16	24,740,549	24,741,118	569	1	9	10.647	16	17	1	1	1	TNRC6A	-216	upstream	ActReg chr16 #3850	0	1
3851	16	24,869,377	24,870,367	990	2	13.633	13.233	25	29	0	0	1	SLC5A11	12,320	in gene	ActReg chr16 #3851	1	1
3852	16	25,059,702	25,060,625	923	2	11.483	14.897	28	37	0	0	0				ActReg chr16 #3852	1	1
3853	16	25,268,589	25,269,228	639	1	11.15	7.2	16	11	1	1	1	ZKSCAN2	-53	upstream	ActReg chr16 #3853	1	0
3854	16	27,214,403	27,215,793	1,390	2	18.116	17.698	46	63	1	1	1	JMJD5	291	in gene	ActReg chr16 #3854	1	1
3855	16	27,279,867	27,280,696	829	1	8.962	11.192	14	16	1	2	2	NSMCE1, FLJ21408	-168, 114	upstream, in gene	ActReg chr16 #3855	0	1
3856	16	27,738,088	27,738,760	672	1	12.143	11	25	18	0	0	1	KIAA0556	176,956	in gene	ActReg chr16 #3856	1	0
3857	16	27,806,957	27,808,236	1,279	2	15.35	21.8	30	55	0	0	1	GSG1L	267,234	in gene	ActReg chr16 #3857	1	1
3858	16	28,314,940	28,315,977	1,037	2	10.219	14.242	23	28	0	0	1	SBK1	11,618	in gene	ActReg chr16 #3858	1	1
3859	16	28,503,132	28,503,823	691	1	8	11.454	17	22	1	2	3	CLN3, APOB48R, IL27	146, -2516, 14678	in gene, upstream, downstream	ActReg chr16 #3859	0	1
3860	16	28,833,767	28,834,259	492	1	9.467	11.467	15	16	1	1	1	ATXN2L	-401	upstream	ActReg chr16 #3860	0	1
3861	16	28,835,208	28,835,887	679	1	9.048	13.762	13	23	1	1	1	ATXN2L	1,133	in gene	ActReg chr16 #3861	0	1
3862	16	28,857,051	28,858,232	1,181	2	10.189	14	24	30	1	1	2	ATXN2L, TUFM	23227, 88	downstream, in gene	ActReg chr16 #3862	1	1
3863	16	28,874,481	28,875,273	792	1	10.88	12.32	17	19	1	1	1	SH2B1	-201	upstream	ActReg chr16 #3863	0	1
3864	16	28,985,731	28,986,546	815	1	12.76	17.08	22	32	1	1	3	NFATC2IP, SPNS1, LAT	23820, 42, -10009	downstream, in gene, upstream	ActReg chr16 #3864	0	1
3865	16	29,301,768	29,302,499	731	1	8.826	11.217	14	18	0	0	0				ActReg chr16 #3865	0	1
3866	16	29,624,595	29,625,071	476	2	10.2	10	14	15	1	0	0				ActReg chr16 #3866	1	1
3867	16	29,801,273	29,802,710	1,437	2	8.6	12.044	16	19	1	1	2	ZG16, KIF22	12430, -67	downstream, upstream	ActReg chr16 #3867	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3868	16	29,816,428	29,817,177	749	1	10.13	12.652	18	21	1	2	3	KIF22, MAZ, PRRT2	14744, -1053, -6607	downstream, upstream, upstream	ActReg chr16 #3868	0	1
3869	16	29,818,609	29,819,770	1,161	1	10.278	12.861	15	20	1	2	4	KIF22, MAZ, PRRT2, C16orf53	17131, 1334, -4220, -8339	downstream, in gene, upstream, upstream	ActReg chr16 #3869	0	1
3870	16	29,821,195	29,822,080	885	1	9.857	8.214	14	14	0	2	5	KIF22, MAZ, PRRT2, C16orf53, MVP	19579, 3782, -1772, -5891, -10150	downstream, in gene, upstream, upstream, upstream	ActReg chr16 #3870	1	0
3871	16	29,822,286	29,823,403	1,117	1	10.143	11.943	22	17	1	2	5	KIF22, MAZ, PRRT2, C16orf53, MVP	20786, 4989, -565, -4684, -8943	downstream, downstream, upstream, upstream, upstream	ActReg chr16 #3871	0	1
3872	16	29,827,045	29,827,681	636	1	10.65	12.6	17	19	1	2	4	MAZ, PRRT2, C16orf53, MVP	9508, 3954, -165, -4424	downstream, downstream, upstream, upstream	ActReg chr16 #3872	0	1
3873	16	29,873,782	29,875,310	1,528	2	22.708	28.917	61	76	1	2	3	CDIPT, LOC440356, SEZ6L2	32, -458, 36034	in gene, upstream, downstream	ActReg chr16 #3873	1	1
3874	16	29,910,834	29,912,145	1,311	1	6.1	11.22	14	21	1	2	3	SEZ6L2, ASPHD1, KCTD13	-909, -658, 26056	upstream, upstream, downstream	ActReg chr16 #3874	0	1
3875	16	29,937,545	29,938,441	896	1	6.536	10.536	10	18	1	1	1	KCTD13	-448	upstream	ActReg chr16 #3875	0	1
3876	16	30,006,413	30,008,030	1,617	2	9.56	12.46	21	18	1	2	4	TAOK2, HIRIP3, INO80E, DOC2A	21999, 191, -310, 15180	downstream, in gene, upstream, downstream	ActReg chr16 #3876	1	1
3877	16	30,076,196	30,077,354	1,158	2	12.222	11.056	24	18	1	0	1	ALDOA	12,264	in gene	ActReg chr16 #3877	1	1
3878	16	30,102,744	30,104,233	1,489	2	11	13.106	23	33	1	3	5	PPP4C, TBX6, YPEL3, LOC100271831, LOC100506914	16103, -283, 4049, -1577, -4263	downstream, upstream, downstream, upstream, upstream	ActReg chr16 #3878	1	1
3879	16	30,366,278	30,367,526	1,248	2	11.692	11.205	20	19	1	1	2	CD2BP2, TBC1D10B	-220, 14620	upstream, downstream	ActReg chr16 #3879	1	1
3880	16	30,389,518	30,390,272	754	1	4.19	12.125	7	25	1	0	3	TBC1D10B, MYLPF, SEPT1	-8373, 3772, 4276	upstream, downstream, in gene	ActReg chr16 #3880	0	1
3881	16	30,440,945	30,441,543	598	1	10.053	10.368	13	16	1	1	1	DCTPP1	129	in gene	ActReg chr16 #3881	0	1
3882	16	30,456,454	30,457,209	755	1	10.826	13.652	19	21	1	1	1	SEPHS2	393	in gene	ActReg chr16 #3882	0	1
3883	16	30,546,343	30,547,003	660	1	4.1	12.2	7	17	1	2	4	ZNF768, LOC100506960, ZNF747, LOC100506973	-8763, 8526, -479, 282	upstream, downstream, upstream, in gene	ActReg chr16 #3883	0	1
3884	16	30,569,054	30,569,913	859	1	8.074	10.556	13	19	1	1	1	ZNF764	159	in gene	ActReg chr16 #3884	0	1
3885	16	30,620,982	30,622,186	1,204	2	10.737	14.579	22	29	1	1	1	ZNF689	98	in gene	ActReg chr16 #3885	1	1
3886	16	30,661,499	30,662,424	925	2	12.552	12.759	24	25	1	1	2	PRR14, LOC100506988	-280, -9026	upstream, upstream	ActReg chr16 #3886	1	1
3887	16	30,669,010	30,670,913	1,903	2	20.667	17.267	37	35	1	2	3	PRR14, LOC100506988, FBRS	7720, -1026, -5817	downstream, upstream, upstream	ActReg chr16 #3887	1	1
3888	16	30,709,188	30,710,331	1,143	1	10.857	11.571	18	20	1	2	2	LOC730183, SRCAP	51, -703	in gene, upstream	ActReg chr16 #3888	0	1
3889	16	30,786,538	30,787,769	1,231	2	10.46	13.053	19	23	1	0	2	RNF40, ZNF629	13523, 11370	downstream, downstream	ActReg chr16 #3889	1	1
3890	16	30,798,341	30,798,915	574	1	6.611	12	9	19	1	1	1	ZNF629	-105	upstream	ActReg chr16 #3890	0	1
3891	16	30,885,942	30,887,082	1,140	2	13.583	11.914	23	26	1	0	0				ActReg chr16 #3891	1	1
3892	16	30,905,502	30,906,104	602	2	11.474	15.632	22	28	1	3	3	BCL7C, MIR762, CTF1	-404, 579, -2125	upstream, downstream, upstream	ActReg chr16 #3892	1	1
3893	16	30,932,941	30,934,924	1,983	2	11.29	13.581	30	27	1	2	2	NCRNA00095, FBXL19	658, -1964	in gene, upstream	ActReg chr16 #3893	1	1
3894	16	30,968,193	30,969,521	1,328	2	13.195	16.78	36	45	1	1	3	FBXL19, ORAI3, SETD1A	32961, 8452, 242	downstream, downstream, in gene	ActReg chr16 #3894	1	1
3895	16	31,044,185	31,045,013	828	1	12.154	8.423	20	17	1	1	1	STX4	-304	upstream	ActReg chr16 #3895	1	0
3896	16	31,084,170	31,086,049	1,879	2	18.271	24.237	41	53	1	2	3	ZNF668, ZNF646, POL3S	532, -634, 15021	in gene, upstream, downstream	ActReg chr16 #3896	1	1
3897	16	31,119,449	31,120,028	579	1	9.611	12.167	14	21	1	1	3	BCKDK, MYST1, LOC100507092	76, -9247, -9543	in gene, upstream, upstream	ActReg chr16 #3897	0	1
3898	16	31,190,808	31,192,100	1,292	2	12.488	16.073	20	37	1	1	1	FUS	23	in gene	ActReg chr16 #3898	1	1
3899	16	31,453,967	31,454,832	865	1	11.148	13.444	17	26	1	1	2	LOC100507110, ZNF843	11001, -51	in gene, upstream	ActReg chr16 #3899	0	1
3900	16	31,470,117	31,471,264	1,147	2	11.472	10.25	18	20	1	2	2	LOC100507110, ARMC5	-5290, 373	upstream, in gene	ActReg chr16 #3900	1	1
3901	16	31,519,346	31,520,155	809	1	9.28	14.8	14	27	1	1	1	C16orf58	-44	upstream	ActReg chr16 #3901	0	1
3902	16	34,586,723	34,587,168	445	1	6.571	11.143	9	19	1	0	0				ActReg chr16 #3902	0	1
3903	16	46,723,182	46,724,480	1,298	1	6.707	12.878	11	23	1	2	2	VPS35, ORC6L	-687, 273	upstream, in gene	ActReg chr16 #3903	0	1
3904	16	46,823,863	46,824,457	594	2	10.21	10.632	19	19	1	0	0				ActReg chr16 #3904	1	1
3905	16	46,917,579	46,918,475	896	2	9	13.464	16	23	1	1	1	GPT2	-281	upstream	ActReg chr16 #3905	1	1
3906	16	47,494,509	47,495,548	1,039	1	8.969	11.281	13	15	1	2	2	ITFG1, PHKB	-10, -182	upstream, upstream	ActReg chr16 #3906	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3907	16	47,821,520	47,822,069	569	1	9.889	5.222	18	10	0	0	0				ActReg chr16 #3907	1	0
3908	16	48,004,007	48,004,664	657	2	10.1	14.75	19	32	0	0	0				ActReg chr16 #3908	1	1
3909	16	48,047,289	48,047,895	606	1	9.474	12.526	13	21	0	0	0				ActReg chr16 #3909	0	1
3910	16	48,115,408	48,116,462	1,054	1	7.636	10.546	15	20	0	0	1	ABCC12	64,746	downstream	ActReg chr16 #3910	0	1
3911	16	48,156,817	48,157,637	820	1	9.731	14.808	19	29	0	0	1	ABCC12	23,454	in gene	ActReg chr16 #3911	0	1
3912	16	48,160,674	48,161,429	755	1	11.913	9.652	20	15	0	0	1	ABCC12	19,630	in gene	ActReg chr16 #3912	1	0
3913	16	48,277,869	48,278,680	811	2	12.76	17	23	29	1	1	2	ABCC11, LONP2	-9186, 63	upstream, in gene	ActReg chr16 #3913	1	1
3914	16	48,478,475	48,479,498	1,023	2	9.433	12.094	25	25	0	0	0				ActReg chr16 #3914	1	1
3915	16	48,952,288	48,953,015	727	1	8.261	12.696	14	19	0	0	0				ActReg chr16 #3915	0	1
3916	16	49,160,983	49,161,471	488	1	9.133	11.467	13	20	0	0	0				ActReg chr16 #3916	0	1
3917	16	49,191,675	49,192,539	864	2	23.926	25.296	62	70	0	0	0				ActReg chr16 #3917	1	1
3918	16	50,058,615	50,059,631	1,016	2	24.125	23.781	69	66	1	1	1	TMEM188	-66	upstream	ActReg chr16 #3918	1	1
3919	16	50,186,522	50,187,067	545	2	10.882	10.647	18	17	0	2	2	LOC100505488, PAPD5	173, -35	in gene, upstream	ActReg chr16 #3919	1	1
3920	16	50,840,147	50,840,707	560	1	10.111	10.833	14	17	0	0	1	CYLD	64,466	downstream	ActReg chr16 #3920	0	1
3921	16	51,197,904	51,198,671	767	1	13.667	11	25	20	0	0	0				ActReg chr16 #3921	1	0
3922	16	51,534,097	51,534,680	583	1	8.5	10.111	17	19	0	0	0				ActReg chr16 #3922	0	1
3923	16	51,670,569	51,671,411	842	2	12.308	11.5	18	20	0	0	0				ActReg chr16 #3923	1	1
3924	16	51,914,493	51,915,128	635	1	4.95	10.75	11	18	0	0	0				ActReg chr16 #3924	0	1
3925	16	53,068,474	53,069,009	535	1	6.765	10.529	12	17	1	1	1	CHD9	-204	upstream	ActReg chr16 #3925	0	1
3926	16	53,132,778	53,133,317	539	1	10.882	8.706	15	15	0	0	1	CHD9	44,102	in gene	ActReg chr16 #3926	1	0
3927	16	53,164,463	53,165,057	594	1	7.368	12.263	11	19	1	0	1	CHD9	75,815	in gene	ActReg chr16 #3927	0	1
3928	16	53,165,455	53,166,006	551	1	8.941	10.765	16	18	1	0	1	CHD9	76,785	in gene	ActReg chr16 #3928	0	1
3929	16	53,468,069	53,469,186	1,117	2	10.371	12.486	22	18	1	1	1	RBL2	276	in gene	ActReg chr16 #3929	1	1
3930	16	53,537,202	53,537,948	746	1	11.391	8.391	16	18	1	1	1	AKTIP	-405	upstream	ActReg chr16 #3930	1	0
3931	16	53,737,402	53,738,410	1,008	1	8.219	12.438	17	23	1	2	2	RPGRIP1L, FTO	-135, 31	upstream, in gene	ActReg chr16 #3931	0	1
3932	16	54,114,280	54,114,969	689	2	11.667	11.095	17	18	0	0	1	FTO	376,749	in gene	ActReg chr16 #3932	1	1
3933	16	54,319,200	54,319,854	654	1	6.476	11.714	11	19	1	1	1	IRX3	851	in gene	ActReg chr16 #3933	0	1
3934	16	54,320,866	54,321,410	544	1	9.765	5.118	14	7	1	1	1	IRX3	-760	upstream	ActReg chr16 #3934	1	0
3935	16	54,407,435	54,408,244	809	1	10.32	11.2	15	15	0	0	0				ActReg chr16 #3935	0	1
3936	16	55,452,279	55,452,969	690	1	7.318	10.727	13	17	0	0	0				ActReg chr16 #3936	0	1
3937	16	55,572,820	55,573,259	439	1	10.857	4	18	5	0	0	1	LPCAT2	30,126	in gene	ActReg chr16 #3937	1	0
3938	16	56,047,614	56,048,557	943	2	21.633	22.533	63	60	0	0	0				ActReg chr16 #3938	1	1
3939	16	56,484,816	56,485,690	874	1	9.852	10.407	14	14	1	2	2	NUDT21, OGFOD1	8, -171	in gene, upstream	ActReg chr16 #3939	0	1
3940	16	56,640,926	56,641,675	749	1	8.125	11.042	12	17	0	1	1	MT2A	-1,178	upstream	ActReg chr16 #3940	0	1
3941	16	56,641,900	56,642,838	938	1	8.69	13.586	15	24	1	1	1	MT2A	-109	upstream	ActReg chr16 #3941	0	1
3942	16	56,763,956	56,764,497	541	1	11.118	10.412	18	14	1	2	2	LOC100505742, NUP93	-246, 209	upstream, in gene	ActReg chr16 #3942	1	0
3943	16	57,034,127	57,034,847	720	1	12.727	9.5	21	11	0	0	1	NLRC5	11,077	in gene	ActReg chr16 #3943	1	0
3944	16	57,278,449	57,279,351	902	2	13.429	12.893	29	25	1	1	2	RSPRY1, ARL2BP	58659, -138	downstream, upstream	ActReg chr16 #3944	1	1
3945	16	57,334,121	57,335,005	884	1	8.926	16.482	14	32	0	0	0				ActReg chr16 #3945	0	1
3946	16	57,481,158	57,481,861	703	2	11.5	11.773	20	17	1	2	2	CIAPIN1, COQ9	-140, 160	upstream, in gene	ActReg chr16 #3946	1	1
3947	16	57,496,138	57,496,979	841	2	25.154	26.923	72	80	1	1	3	COQ9, POLR2C, DOK4	15209, 7, 23827	downstream, in gene, downstream	ActReg chr16 #3947	1	1
3948	16	57,657,316	57,658,133	817	1	7.44	13.96	14	26	0	0	1	GPR56	3,814	in gene	ActReg chr16 #3948	0	1
3949	16	57,667,778	57,668,705	927	1	11.862	10.517	19	18	0	0	1	GPR56	14,331	in gene	ActReg chr16 #3949	1	0
3950	16	57,836,348	57,837,400	1,052	1	7.364	14.515	16	24	1	2	2	KIFC3, LOC388282	-435, -7675	upstream, upstream	ActReg chr16 #3950	0	1
3951	16	58,162,984	58,163,813	829	1	8.769	14.269	15	23	1	1	1	C16orf80	-102	upstream	ActReg chr16 #3951	0	1
3952	16	58,231,888	58,232,395	507	2	13.812	16.938	26	28	0	1	1	CSNK2A2	-359	upstream	ActReg chr16 #3952	1	1
3953	16	58,425,852	58,427,057	1,205	2	17.368	26.579	51	74	1	1	1	GINS3	156	in gene	ActReg chr16 #3953	1	1
3954	16	58,549,213	58,549,909	696	1	10.091	12.636	17	22	1	1	3	NDRG4, SETD6, CNOT1	52012, 178, 114189	downstream, in gene, downstream	ActReg chr16 #3954	0	1
3955	16	58,718,255	58,718,973	718	1	12.409	12.318	18	19	1	1	1	SLC38A7	60	in gene	ActReg chr16 #3955	1	0
3956	16	58,767,495	58,768,651	1,156	2	19.611	20.611	53	56	1	1	1	GOT2	173	in gene	ActReg chr16 #3956	1	1
3957	16	59,912,321	59,912,928	607	1	6.842	11.79	11	19	0	0	0				ActReg chr16 #3957	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3958	16	60,676,726	60,677,285	559	1	9.889	6.611	17	12	0	0	0				ActReg chr16 #3958	1	0
3959	16	61,162,762	61,163,313	551	1	3.412	8.824	5	17	0	0	0				ActReg chr16 #3959	0	1
3960	16	64,195,157	64,195,826	669	1	11.809	6.571	21	13	0	0	0				ActReg chr16 #3960	1	0
3961	16	65,427,045	65,427,609	564	1	9.118	12.529	16	21	0	0	1	LOC283867	182,876	in gene	ActReg chr16 #3961	0	1
3962	16	66,115,537	66,116,356	819	2	8.038	11.231	17	16	0	0	0				ActReg chr16 #3962	1	1
3963	16	66,164,978	66,165,746	768	2	13.833	17.792	31	38	0	0	0				ActReg chr16 #3963	1	1
3964	16	66,583,499	66,584,310	811	1	9	13.56	14	23	1	2	2	TK2, CKLF	411, -2562	in gene, upstream	ActReg chr16 #3964	0	1
3965	16	66,586,153	66,586,976	823	1	13.192	12.269	23	22	1	2	2	TK2, CKLF	-2249, 98	upstream, in gene	ActReg chr16 #3965	1	0
3966	16	66,864,460	66,865,237	777	1	11.583	9.542	16	13	1	1	1	NAE1	31	in gene	ActReg chr16 #3966	1	0
3967	16	66,906,810	66,907,557	747	1	12.375	10.083	19	17	1	1	1	PDP2	-7,253	upstream	ActReg chr16 #3967	1	0
3968	16	66,914,345	66,914,983	638	1	12.1	14.5	18	26	1	1	2	PDP2, LOC100505926	228, -8003	in gene, upstream	ActReg chr16 #3968	0	1
3969	16	66,967,977	66,968,909	932	1	9.724	11.759	18	19	1	2	3	RRAD, FAM96B, CES2	-9004, -123, 96	upstream, upstream, in gene	ActReg chr16 #3969	0	1
3970	16	67,207,827	67,208,560	733	1	11.348	13.826	17	26	1	0	5	FBXL8, HSF4, NOL3, KIAA0895L, EXOC3L	14302, 10905, 3788, 9690, 15914	downstream, downstream, in gene, downstream, downstream	ActReg chr16 #3970	0	1
3971	16	67,219,138	67,219,756	618	1	11.526	13.632	19	25	1	2	4	NOL3, KIAA0895L, EXOC3L, E2F4	15042, -1564, 4660, 6621	downstream, upstream, in gene, upstream	ActReg chr16 #3971	0	1
3972	16	67,225,495	67,226,779	1,284	1	7.275	12.375	15	24	0	3	5	KIAA0895L, EXOC3L, E2F4, ELMO3, MIR328	-8254, -2030, 69, -6891, 10161	upstream, upstream, in gene, upstream, downstream	ActReg chr16 #3972	0	1
3973	16	67,260,247	67,261,358	1,111	1	9.829	12.914	16	32	1	2	3	LRRC29, TMEM208, FHOD1	99, -214, 20623	in gene, upstream, downstream	ActReg chr16 #3973	0	1
3974	16	67,302,019	67,302,556	537	1	11.5	5.875	21	11	0	0	2	SLC9A5, PLEKHG4	19432, -9126	in gene, upstream	ActReg chr16 #3974	1	0
3975	16	67,312,622	67,314,292	1,670	2	11.404	16.865	37	43	1	1	3	SLC9A5, PLEKHG4, KCTD19	30602, 2044, 47204	downstream, in gene, downstream	ActReg chr16 #3975	1	1
3976	16	67,345,366	67,346,457	1,091	1	8.188	11.118	20	15	0	0	1	KCTD19	14,750	in gene	ActReg chr16 #3976	0	1
3977	16	67,499,532	67,500,168	636	1	9.85	11.3	14	18	0	0	1	ATP6V0D1	15,239	in gene	ActReg chr16 #3977	0	1
3978	16	67,514,709	67,516,164	1,455	1	9.935	12.978	16	23	1	2	2	ATP6V0D1, AGRP	-347, 2280	upstream, downstream	ActReg chr16 #3978	0	1
3979	16	67,554,864	67,555,923	1,059	2	11.364	12.121	20	23	0	1	2	LOC100505942, FAM65A	7158, -7324	in gene, upstream	ActReg chr16 #3979	1	1
3980	16	67,595,871	67,596,572	701	2	11.727	10.409	26	19	1	1	1	CTCF	-89	upstream	ActReg chr16 #3980	1	1
3981	16	67,596,904	67,597,584	680	1	9.25	11.857	14	19	1	1	1	CTCF	934	in gene	ActReg chr16 #3981	0	1
3982	16	67,685,763	67,686,774	1,011	1	6.097	10.935	11	16	1	0	3	RLTPR, ACD, PARD6A	7238, 8450, 8583	in gene, downstream, upstream	ActReg chr16 #3982	0	1
3983	16	67,700,632	67,701,525	893	1	6.643	11.643	12	16	1	3	6	RLTPR, ACD, PARD6A, C16orf48, C16orf86, GFOD2	22048, -6360, 6227, -450, 361, 52195	downstream, upstream, downstream, upstream, in gene, downstream	ActReg chr16 #3983	0	1
3984	16	67,840,199	67,841,252	1,053	2	12.454	13.667	30	25	1	2	2	RANBP10, TSNAXIP1	-170, -285	upstream, upstream	ActReg chr16 #3984	1	1
3985	16	67,867,395	67,868,054	659	1	10.05	12	19	18	1	0	3	TSNAXIP1, CENPT, THAP11	26714, 13637, -8489	downstream, in gene, upstream	ActReg chr16 #3985	0	1
3986	16	67,876,338	67,876,955	617	1	12.632	11.895	21	16	1	2	3	CENPT, THAP11, NUTF2	4715, 433, 4173	in gene, in gene, upstream	ActReg chr16 #3986	1	0
3987	16	67,880,413	67,881,379	966	2	9.032	12.452	20	29	1	2	3	CENPT, THAP11, NUTF2	465, 4683, 77	in gene, downstream, in gene	ActReg chr16 #3987	1	1
3988	16	67,906,592	67,907,384	792	1	6.76	12.04	13	21	1	1	2	NUTF2, EDC4	26169, -11	downstream, upstream	ActReg chr16 #3988	0	1
3989	16	67,969,070	67,970,186	1,116	1	10	11.857	15	18	1	2	5	PSKH1, CTRL, PSMB10, LCAT, SLC12A4	42453, -3863, 1125, 8387, 32969	downstream, upstream, in gene, downstream, downstream	ActReg chr16 #3989	0	1
3990	16	68,056,311	68,057,500	1,189	1	10.703	13.027	25	19	1	2	2	DDX28, DUS2L	865, -299	in gene, upstream	ActReg chr16 #3990	0	1
3991	16	68,118,333	68,119,094	761	1	6.333	11	10	18	1	1	2	DUS2L, NFATC3	61509, -662	downstream, upstream	ActReg chr16 #3991	0	1
3992	16	68,119,326	68,119,881	555	1	9.889	9.5	18	13	1	1	2	DUS2L, NFATC3	62399, 228	downstream, in gene	ActReg chr16 #3992	1	0
3993	16	68,278,637	68,279,668	1,031	2	11.281	15.438	25	28	1	1	2	ESRP2, PLA2G15	-9016, -95	upstream, upstream	ActReg chr16 #3993	1	1
3994	16	68,297,736	68,299,160	1,424	1	7.614	12.136	13	26	1	1	2	PLA2G15, SLC7A6	19201, 25	downstream, in gene	ActReg chr16 #3994	0	1
3995	16	68,344,429	68,345,557	1,128	2	8.571	12.571	18	20	1	2	3	SLC7A6, SLC7A6OS, PRMT7	46570, -125, 116	downstream, upstream, in gene	ActReg chr16 #3995	1	1
3996	16	68,477,807	68,478,506	699	2	12.273	14.454	24	32	0	0	1	SMPD3	4,253	in gene	ActReg chr16 #3996	1	1
3997	16	68,481,760	68,483,458	1,698	2	10.611	15.704	20	28	1	1	1	SMPD3	-200	upstream	ActReg chr16 #3997	1	1
3998	16	68,701,922	68,702,734	812	2	10.88	10.08	19	16	0	0	1	CDH3	24,177	in gene	ActReg chr16 #3998	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
3999	16	69,107,113	69,107,811	698	1	8.364	13.591	13	22	0	0	1	TMCO7	229,953	in gene	ActReg chr16 #3999	0	1
4000	16	69,200,036	69,200,628	592	1	10.444	6.222	16	9	0	0	1	CIRH1A	33,833	in gene	ActReg chr16 #4000	1	0
4001	16	69,220,456	69,221,335	879	2	11.037	10.704	17	20	1	1	1	SNTB2	-155	upstream	ActReg chr16 #4001	1	1
4002	16	69,363,758	69,364,859	1,101	1	11.412	12.941	18	21	1	1	5	VPS4A, LOC100506031, COG8, PDF, NIP7	19021, 12049, 9218, 190, -9238	downstream, in gene, in gene, in gene, upstream	ActReg chr16 #4002	0	1
4003	16	69,372,856	69,374,013	1,157	2	14.833	19.389	42	44	1	3	5	LOC100506031, COG8, PDF, NIP7, TMED6	2923, 92, -8936, -112, 12278	in gene, in gene, upstream, upstream, downstream	ActReg chr16 #4003	1	1
4004	16	69,457,989	69,459,019	1,030	1	7.469	13.875	13	22	1	1	1	CYB5B	6	in gene	ActReg chr16 #4004	0	1
4005	16	69,564,621	69,565,082	461	1	6.786	11.929	11	18	0	0	0				ActReg chr16 #4005	0	1
4006	16	69,599,537	69,599,951	414	1	4.615	10.692	8	14	1	2	2	NFAT5, MIR1538	747, 27	in gene, in gene	ActReg chr16 #4006	0	1
4007	16	69,760,178	69,760,994	816	1	7.5	11.115	13	17	1	1	1	NQO1	-53	upstream	ActReg chr16 #4007	0	1
4008	16	69,788,361	69,789,179	818	1	7.4	14.44	11	28	1	2	2	NOB1, WWP2	59, -7504	in gene, upstream	ActReg chr16 #4008	0	1
4009	16	70,285,417	70,286,361	944	2	27.276	27.517	79	82	1	1	2	EXOSC6, AARS	-56, 37523	upstream, downstream	ActReg chr16 #4009	1	1
4010	16	70,332,862	70,333,480	618	2	9.85	10.35	16	17	0	1	2	AARS, DDX19B	-9759, 99	upstream, in gene	ActReg chr16 #4010	1	1
4011	16	70,380,534	70,381,268	734	2	11.391	12.696	24	21	1	2	2	LOC100506083, DDX19A	-223, 77	upstream, in gene	ActReg chr16 #4011	1	1
4012	16	70,472,891	70,473,767	876	2	15.821	20.821	34	45	1	1	1	ST3GAL2	-338	upstream	ActReg chr16 #4012	1	1
4013	16	70,487,912	70,488,859	947	2	22.793	27.483	49	71	1	1	1	FUK	-113	upstream	ActReg chr16 #4013	1	1
4014	16	70,491,187	70,491,864	677	1	12.286	10.667	19	13	0	0	1	FUK	3,027	in gene	ActReg chr16 #4014	1	0
4015	16	70,557,560	70,558,184	624	1	6.95	10.3	11	16	1	3	3	COG4, SF3B3, SNORD111B	-415, 181, -5533	upstream, in gene, upstream	ActReg chr16 #4015	0	1
4016	16	70,834,643	70,835,377	734	1	10.261	12.087	19	21	1	1	2	VAC14, HYDIN	51, 429559	in gene, downstream	ActReg chr16 #4016	0	1
4017	16	70,895,357	70,896,372	1,015	1	12.031	13.25	23	23	0	0	1	HYDIN	368,705	in gene	ActReg chr16 #4017	0	1
4018	16	71,020,561	71,022,363	1,802	2	16.75	16.321	39	39	0	0	1	HYDIN	243,107	in gene	ActReg chr16 #4018	1	1
4019	16	71,052,828	71,053,688	862	2	14.926	18.704	27	39	0	0	1	HYDIN	211,312	in gene	ActReg chr16 #4019	1	1
4020	16	71,322,742	71,323,451	709	2	11.954	9.864	21	17	1	1	1	FTSJD1	413	in gene	ActReg chr16 #4020	1	1
4021	16	71,349,966	71,350,558	592	1	9.444	11.5	17	22	0	0	0				ActReg chr16 #4021	0	1
4022	16	71,495,601	71,496,623	1,022	2	10	15.656	22	32	1	2	2	ZNF23, LOC100506105	5, -86	in gene, upstream	ActReg chr16 #4022	1	1
4023	16	71,501,025	71,502,309	1,284	2	17.025	19.875	47	52	0	1	3	ZNF23, LOC100506105, ZNF19	-5550, 5469, 21587	upstream, downstream, downstream	ActReg chr16 #4023	1	1
4024	16	71,508,653	71,509,244	591	1	7.667	10.833	11	18	0	0	1	ZNF19	14,306	in gene	ActReg chr16 #4024	0	1
4025	16	71,518,060	71,518,705	645	1	10.8	11.65	15	17	0	0	1	ZNF19	4,872	in gene	ActReg chr16 #4025	0	1
4026	16	71,842,151	71,843,133	982	2	11.9	12.133	21	26	1	1	1	AP1G1	334	in gene	ActReg chr16 #4026	1	1
4027	16	71,879,558	71,880,249	691	1	9.714	13.524	14	19	1	1	1	ATXN1L	4	in gene	ActReg chr16 #4027	0	1
4028	16	71,928,994	71,929,746	752	1	9.826	15.913	14	27	1	1	2	ATXN1L, KIAA0174	49471, -76	downstream, upstream	ActReg chr16 #4028	0	1
4029	16	72,042,293	72,043,114	821	2	11.615	11.115	25	21	1	1	2	PKD1L3, DHODH	-8826, 60	upstream, in gene	ActReg chr16 #4029	1	1
4030	16	72,127,184	72,128,342	1,158	2	10.194	10.833	19	22	1	2	2	TXNL4B, DHX38	452, 148	in gene, in gene	ActReg chr16 #4030	1	1
4031	16	72,325,667	72,326,126	459	1	6.286	11	7	18	0	0	0				ActReg chr16 #4031	0	1
4032	16	72,961,445	72,961,974	529	1	6.467	12.75	10	21	0	0	1	ZFHX3	130,825	in gene	ActReg chr16 #4032	0	1
4033	16	73,054,192	73,054,895	703	2	14.091	10.591	28	24	0	0	2	ZFHX3, LOC100506152	37991, -8265	in gene, upstream	ActReg chr16 #4033	1	1
4034	16	75,181,980	75,182,666	686	1	11.5	13.454	18	25	1	1	1	ZFP1	-98	upstream	ActReg chr16 #4034	0	1
4035	16	75,497,887	75,498,970	1,083	2	10.118	13.147	16	23	1	1	2	TMEM170A, CHST6	156, 30498	in gene, downstream	ActReg chr16 #4035	1	1
4036	16	75,589,582	75,590,544	962	2	10.367	13.667	21	24	1	1	2	TMEM231, GABARAPL2	107, -10186	in gene, upstream	ActReg chr16 #4036	1	1
4037	16	75,681,172	75,682,555	1,383	1	9.116	13.419	14	20	1	2	2	KARS, TERF2IP	-278, 228	upstream, in gene	ActReg chr16 #4037	0	1
4038	16	76,838,882	76,839,535	653	1	11.85	10.25	22	12	0	0	0				ActReg chr16 #4038	1	0
4039	16	76,960,842	76,961,392	550	1	9.059	11.623	11	21	0	0	0				ActReg chr16 #4039	0	1
4040	16	77,247,213	77,247,944	731	1	10.478	13.217	13	23	0	0	1	SYCE1L	14,229	downstream	ActReg chr16 #4040	0	1
4041	16	77,821,897	77,822,893	996	1	7.548	12.097	14	18	1	1	1	VAT1L	-88	upstream	ActReg chr16 #4041	0	1
4042	16	78,079,547	78,080,554	1,007	2	19.375	30.125	53	71	1	0	0				ActReg chr16 #4042	1	1
4043	16	78,133,029	78,134,271	1,242	2	17.842	16.947	38	42	1	1	1	WWOX	99	in gene	ActReg chr16 #4043	1	1
4044	16	79,406,389	79,406,902	513	1	8.188	10.688	14	18	0	0	0				ActReg chr16 #4044	0	1
4045	16	79,634,519	79,635,705	1,186	1	8.568	13.297	12	21	1	1	1	MAF	-490	upstream	ActReg chr16 #4045	0	1
4046	16	79,662,205	79,662,850	645	1	6.238	10.905	9	16	0	0	0				ActReg chr16 #4046	0	1
4047	16	79,681,365	79,682,023	658	1	11.286	9.857	20	16	0	0	0				ActReg chr16 #4047	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4048	16	79,685,061	79,685,782	721	2	11.909	11.046	20	16	0	0	0				ActReg chr16 #4048	1	1
4049	16	79,692,039	79,692,679	640	1	11.05	9.15	17	13	0	0	0				ActReg chr16 #4049	1	0
4050	16	80,039,964	80,040,793	829	1	5.038	10.385	8	15	0	0	0				ActReg chr16 #4050	0	1
4051	16	80,060,821	80,061,596	775	2	9.917	11.667	18	22	0	0	0				ActReg chr16 #4051	1	1
4052	16	80,574,368	80,575,177	809	1	10.077	14.077	20	25	1	1	1	DYNLRB2	-82	upstream	ActReg chr16 #4052	0	1
4053	16	81,039,856	81,041,398	1,542	2	22.792	27.708	93	78	1	2	2	C16orf61, CENPN	-125, 524	upstream, in gene	ActReg chr16 #4053	1	1
4054	16	81,348,185	81,348,850	665	2	9.81	13.809	14	24	1	1	1	GAN	-54	upstream	ActReg chr16 #4054	1	1
4055	16	81,434,607	81,435,519	912	1	10	7.571	16	13	0	0	0				ActReg chr16 #4055	1	0
4056	16	81,779,409	81,780,294	885	2	9.214	11.536	18	20	0	0	0				ActReg chr16 #4056	1	1
4057	16	82,203,343	82,204,232	889	2	10.536	13.107	16	21	1	1	1	MPHOSPH6	42	in gene	ActReg chr16 #4057	1	1
4058	16	82,661,333	82,662,233	900	1	9.214	13.071	16	20	1	1	1	CDH13	1,205	in gene	ActReg chr16 #4058	0	1
4059	16	82,667,567	82,668,232	665	1	11	7.095	18	12	0	0	1	CDH13	7,321	in gene	ActReg chr16 #4059	1	0
4060	16	83,170,633	83,171,294	661	1	5.55	11.45	11	16	0	0	1	CDH13	510,385	in gene	ActReg chr16 #4060	0	1
4061	16	83,546,607	83,547,373	766	1	11.042	7.917	15	11	0	0	2	CDH13, MIR3182	886412, 5039	in gene, downstream	ActReg chr16 #4061	1	0
4062	16	83,595,250	83,596,055	805	2	10.96	16.8	25	34	0	0	1	CDH13	935,074	in gene	ActReg chr16 #4062	1	1
4063	16	83,734,986	83,735,667	681	1	12.524	11.381	22	17	0	0	1	CDH13	1,074,748	in gene	ActReg chr16 #4063	1	0
4064	16	83,751,247	83,752,095	848	1	8	11.577	12	17	0	0	1	CDH13	1,091,093	in gene	ActReg chr16 #4064	0	1
4065	16	83,986,128	83,987,130	1,002	2	16.774	16.613	29	32	0	0	1	OSGIN1	3,957	in gene	ActReg chr16 #4065	1	1
4066	16	84,150,283	84,151,513	1,230	1	7.158	11.5	14	17	1	1	2	MBTPS1, HSDL1	-381, 27902	upstream, downstream	ActReg chr16 #4066	0	1
4067	16	84,220,250	84,220,883	633	1	8.7	14.1	12	19	1	2	4	LRRC50, TAF1C, ADAD2, LOC654780	41701, 96, -4157, 10093	downstream, in gene, upstream, downstream	ActReg chr16 #4067	0	1
4068	16	84,261,806	84,262,734	928	1	8.103	10.828	15	20	0	0	1	KCNG4	11,086	in gene	ActReg chr16 #4068	0	1
4069	16	84,636,568	84,637,594	1,026	1	12.406	9.704	25	18	0	0	1	COTL1	14,588	in gene	ActReg chr16 #4069	1	0
4070	16	84,839,960	84,841,142	1,182	1	7.811	11.054	15	15	0	0	0				ActReg chr16 #4070	0	1
4071	16	84,918,179	84,919,184	1,005	1	6.065	11.484	14	17	0	0	1	CRISPLD2	65,094	in gene	ActReg chr16 #4071	0	1
4072	16	85,586,864	85,588,132	1,268	2	9.5	8.9	18	17	1	0	0				ActReg chr16 #4072	1	1
4073	16	85,643,941	85,644,786	845	1	6	11.731	10	16	2	1	1	KIAA0182	-666	upstream	ActReg chr16 #4073	0	1
4074	16	85,833,027	85,833,729	702	1	13.864	13.227	26	20	1	2	3	COX4NB, LOC100506521, COX4I1	-230, 7357, 182	upstream, downstream, in gene	ActReg chr16 #4074	0	1
4075	16	86,427,373	86,428,048	675	1	6.333	11.905	9	18	0	0	0				ActReg chr16 #4075	0	1
4076	16	86,432,220	86,432,756	536	1	12.177	6.824	18	9	0	0	0				ActReg chr16 #4076	1	0
4077	16	86,524,559	86,525,669	1,110	2	10.514	10.143	18	18	0	0	1	FLJ34515	17,352	in gene	ActReg chr16 #4077	1	1
4078	16	86,697,923	86,699,035	1,112	2	12.029	12.382	20	22	0	0	0				ActReg chr16 #4078	1	1
4079	16	86,805,621	86,806,332	711	1	10.773	5.773	20	10	0	0	0				ActReg chr16 #4079	1	0
4080	16	86,922,336	86,922,875	539	1	5.118	9.882	8	15	0	0	0				ActReg chr16 #4080	0	1
4081	16	86,984,528	86,986,308	1,780	2	13.125	17.5	23	29	0	0	0				ActReg chr16 #4081	1	1
4082	16	87,350,280	87,351,330	1,050	2	10.515	10.606	14	15	1	1	1	LOC100506581	190	in gene	ActReg chr16 #4082	1	1
4083	16	87,417,371	87,417,976	605	1	9.556	12.474	19	23	1	0	2	FBXO31, MAP1LC3B	8035, -8128	in gene, upstream	ActReg chr16 #4083	0	1
4084	16	87,425,045	87,426,251	1,206	2	11.605	11.079	19	21	1	2	2	FBXO31, MAP1LC3B	60, -153	in gene, upstream	ActReg chr16 #4084	1	1
4085	16	87,526,533	87,526,973	440	1	12.077	5.615	19	9	0	1	1	ZCCHC14	-1,293	upstream	ActReg chr16 #4085	1	0
4086	16	87,615,957	87,616,758	801	1	9.08	10.96	14	16	0	0	0				ActReg chr16 #4086	0	1
4087	16	87,641,433	87,642,877	1,444	2	16.022	18.578	35	41	0	0	1	JPH3	5,656	in gene	ActReg chr16 #4087	1	1
4088	16	87,694,749	87,695,744	995	2	9.219	14.406	16	35	0	0	1	JPH3	58,747	in gene	ActReg chr16 #4088	1	1
4089	16	87,823,447	87,824,100	653	1	5.19	10.667	10	18	0	0	0				ActReg chr16 #4089	0	1
4090	16	87,965,090	87,966,143	1,053	1	9.344	11.469	19	17	0	0	1	CA5A	4,496	in gene	ActReg chr16 #4090	0	1
4091	16	87,984,061	87,985,209	1,148	2	9.583	17.417	25	38	1	1	1	BANP	-403	upstream	ActReg chr16 #4091	1	1
4092	16	88,365,510	88,366,942	1,432	2	12.682	13.386	29	25	0	0	0				ActReg chr16 #4092	1	1
4093	16	88,509,337	88,510,159	822	1	7.077	11.115	11	15	0	0	2	ZNF469, ZFPM1	15869, -10266	downstream, upstream	ActReg chr16 #4093	0	1
4094	16	88,626,561	88,628,274	1,713	2	14.226	17.076	37	34	0	0	1	ZC3H18	-9,372	upstream	ActReg chr16 #4094	1	1
4095	16	88,851,705	88,852,462	757	2	11.417	12.208	18	18	1	1	1	FAM38A	-711	upstream	ActReg chr16 #4095	1	1
4096	16	88,869,553	88,870,291	738	2	10.391	13.478	25	24	1	1	3	CDT1, APRT, GALNS	-264, 8420, 53452	upstream, downstream, downstream	ActReg chr16 #4096	1	1
4097	16	88,877,499	88,879,295	1,796	2	16.5	13.571	31	31	1	1	3	CDT1, APRT, GALNS	8211, -55, 44977	downstream, upstream, downstream	ActReg chr16 #4097	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4098	16	88,923,162	88,924,046	884	1	9.464	12.857	13	23	1	2	3	GALNS, TRAPPC2L, PABPN1L	-230, 98, 9410	upstream, in gene, downstream	ActReg chr16 #4098	0	1
4099	16	89,075,675	89,076,575	900	1	8.536	13.143	13	21	0	0	0				ActReg chr16 #4099	0	1
4100	16	89,082,170	89,083,699	1,529	2	13.729	15.375	27	35	0	0	0				ActReg chr16 #4100	1	1
4101	16	89,103,345	89,104,483	1,138	1	8.028	10.667	16	16	0	0	1	LOC100506183	15,459	downstream	ActReg chr16 #4101	0	1
4102	16	89,283,787	89,284,543	756	1	8.609	11.261	14	16	1	1	1	ZNF778	54	in gene	ActReg chr16 #4102	0	1
4103	16	89,306,993	89,307,577	584	2	13.611	16.833	27	30	0	0	0				ActReg chr16 #4103	1	1
4104	16	89,386,319	89,387,474	1,155	1	8.889	12.833	13	22	0	1	2	ANKRD11, LOC100287036	170073, -645	in gene, upstream	ActReg chr16 #4104	0	1
4105	16	89,575,045	89,575,640	595	1	5.222	11.389	8	17	1	1	2	LOC100506268, SPG7	17609, 537	downstream, in gene	ActReg chr16 #4105	0	1
4106	16	89,626,841	89,628,222	1,381	1	8.488	10.698	20	16	1	2	3	SPG7, RPL13, SNORD68	52726, 441, 307	downstream, in gene, upstream	ActReg chr16 #4106	0	1
4107	16	89,631,459	89,632,712	1,253	1	7.769	12.077	15	19	1	0	4	SPG7, RPL13, SNORD68, CPNE7	57280, 4995, 4247, 10091	downstream, downstream, downstream, upstream	ActReg chr16 #4107	0	1
4108	16	89,787,063	89,787,964	901	2	16.286	14.643	36	23	1	2	3	C16orf7, LOC100128881, ZNF276	-119, 9249, 120	upstream, downstream, in gene	ActReg chr16 #4108	1	1
4109	16	89,882,828	89,883,349	521	1	11.125	10.25	16	16	1	1	1	FANCA	-23	upstream	ActReg chr16 #4109	1	0
4110	16	89,894,932	89,895,261	329	1	4.3	10.3	6	15	1	1	1	SPIRE2	189	in gene	ActReg chr16 #4110	0	1
4111	16	89,988,236	89,988,910	674	1	8.048	12.381	13	17	1	1	2	MC1R, TUBB3	4286, -1172	downstream, upstream	ActReg chr16 #4111	0	1
4112	16	90,014,619	90,015,281	662	2	14.571	24.952	38	56	1	1	1	DEF8	-201	upstream	ActReg chr16 #4112	1	1
4113	16	90,087,162	90,087,882	720	2	11.565	10.652	21	15	0	2	3	DBNDD1, GAS8, C16orf3	-1585, -1486, 8787	upstream, upstream, downstream	ActReg chr16 #4113	1	1
4114	17	617,570	618,519	949	2	16.828	13.655	36	28	1	1	1	VPS53	52	in gene	ActReg chr17 #4114	1	1
4115	17	685,083	686,007	924	2	12.759	13.724	19	28	1	2	2	GLOD4, RNMTL1	26, 32	in gene, in gene	ActReg chr17 #4115	1	1
4116	17	899,535	900,681	1,146	1	9.111	13.75	18	24	1	2	3	TIMM22, LOC100506836, ABR	-249, -5699, 190508	upstream, upstream, downstream	ActReg chr17 #4116	0	1
4117	17	1,013,571	1,015,320	1,749	1	10.056	12.056	20	18	0	0	1	ABR	76,171	in gene	ActReg chr17 #4117	0	1
4118	17	1,054,190	1,054,899	709	1	13.091	7.591	30	12	0	0	1	ABR	36,072	in gene	ActReg chr17 #4118	1	0
4119	17	1,090,242	1,090,858	616	1	11.316	9.474	19	14	0	1	1	ABR	66	in gene	ActReg chr17 #4119	1	0
4120	17	1,162,432	1,163,153	721	1	7.87	10.957	13	18	1	0	0				ActReg chr17 #4120	0	1
4121	17	1,226,590	1,227,052	462	1	9.667	12.6	15	24	0	0	0				ActReg chr17 #4121	0	1
4122	17	1,302,888	1,303,539	651	1	6.15	10.35	12	16	1	1	1	YWHAE	343	in gene	ActReg chr17 #4122	0	1
4123	17	1,389,080	1,389,978	898	2	11.607	17.769	28	34	1	0	2	MYO1C, INPP5K	6472, 30653	in gene, downstream	ActReg chr17 #4123	1	1
4124	17	1,466,002	1,466,538	536	2	17.706	15.353	36	30	1	1	2	PITPNA, LOC100507036	-160, 13711	upstream, in gene	ActReg chr17 #4124	1	1
4125	17	1,587,872	1,588,543	671	1	5.333	11.238	9	18	1	1	1	PRPF8	-31	upstream	ActReg chr17 #4125	0	1
4126	17	1,619,152	1,621,220	2,068	2	13.169	15.369	24	28	1	4	4	TLCD2, C17orf91, MIR22, WDR81	-6524, -620, -2905, 369	upstream, upstream, upstream, in gene	ActReg chr17 #4126	1	1
4127	17	1,932,891	1,934,334	1,443	2	19.667	20.622	61	77	1	2	2	RTN4RL1, DPH1	-5434, 181	upstream, in gene	ActReg chr17 #4127	1	1
4128	17	1,944,519	1,945,831	1,312	2	11.878	10.829	21	24	1	1	4	DPH1, OVCA2, MIR132, MIR212	11744, -102, 8127, 8499	in gene, upstream, downstream, downstream	ActReg chr17 #4128	1	1
4129	17	2,262,427	2,263,169	742	1	13	10.542	22	16	0	0	1	SGSM2	21,992	in gene	ActReg chr17 #4129	1	0
4130	17	2,295,616	2,297,196	1,580	1	9.38	13.24	15	21	1	0	1	MNT	7,852	in gene	ActReg chr17 #4130	0	1
4131	17	2,304,047	2,305,502	1,455	2	29.956	36.4	83	116	1	1	2	MNT, LOC284009	-516, 13956	upstream, downstream	ActReg chr17 #4131	1	1
4132	17	2,496,317	2,497,026	709	1	6.348	12.783	13	24	1	1	1	PAFAH1B1	-252	upstream	ActReg chr17 #4132	0	1
4133	17	2,614,832	2,615,552	720	2	11.478	12.348	23	27	1	1	1	KIAA0664	-265	upstream	ActReg chr17 #4133	1	1
4134	17	2,653,102	2,653,636	534	1	9.471	12.941	18	25	1	1	1	MIR1253	-1,893	upstream	ActReg chr17 #4134	0	1
4135	17	2,858,215	2,858,944	729	2	10.261	10.348	23	19	0	0	1	RAP1GAP2	158,847	in gene	ActReg chr17 #4135	1	1
4136	17	2,863,297	2,864,130	833	1	9.333	15.769	17	27	0	0	1	RAP1GAP2	163,981	in gene	ActReg chr17 #4136	0	1
4137	17	2,878,674	2,879,196	522	2	9.625	12	14	19	0	0	1	RAP1GAP2	179,203	in gene	ActReg chr17 #4137	1	1
4138	17	2,951,890	2,952,505	615	1	8.579	11.79	13	17	1	0	0				ActReg chr17 #4138	0	1
4139	17	3,301,158	3,301,595	437	1	9.667	12.154	17	20	0	1	1	OR1E1	328	in gene	ActReg chr17 #4139	0	1
4140	17	3,336,561	3,336,986	425	1	8.462	11.923	14	18	0	1	2	OR1E2, SPATA22	362, 38369	in gene, downstream	ActReg chr17 #4140	0	1
4141	17	3,434,894	3,435,498	604	1	10.053	10.158	18	14	0	0	1	TRPV3	26,093	in gene	ActReg chr17 #4141	1	0
4142	17	3,571,231	3,572,500	1,269	1	9.6	11.675	13	20	1	2	5	CTNS, TAX1BP3, TMEM93, P2RX5, LOC100506618	32103, 108, 225, 27718, 10705	downstream, in gene, upstream, downstream, downstream	ActReg chr17 #4142	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4143	17	3,626,635	3,627,920	1,285	2	19.45	21.825	47	52	1	1	2	ITGAE, GSG2	77260, 80	in gene, in gene	ActReg chr17 #4143	1	1
4144	17	3,749,186	3,749,952	766	1	8.125	12.542	18	23	1	1	1	C17orf85	-29	upstream	ActReg chr17 #4144	0	1
4145	17	4,046,206	4,047,248	1,042	1	9.788	12.636	20	23	1	2	2	ZZEF1, CYB5D2	-474, 265	upstream, in gene	ActReg chr17 #4145	0	1
4146	17	4,395,949	4,397,126	1,177	2	12.351	16.108	30	39	0	1	2	SPNS3, SPNS2	59318, -5592	downstream, upstream	ActReg chr17 #4146	1	1
4147	17	4,606,970	4,607,794	824	1	9	13.039	15	21	1	2	2	PELP1, ARRB2	250, -6407	in gene, upstream	ActReg chr17 #4147	0	1
4148	17	4,634,284	4,635,250	966	2	12.267	11.167	20	19	1	1	4	ARRB2, MED11, CXCL16, ZMYND15	20978, 44, 8456, -8552	downstream, in gene, downstream, upstream	ActReg chr17 #4148	1	1
4149	17	4,692,766	4,694,067	1,301	1	6.854	11.439	13	18	1	4	5	TM4SF5, VMO1, GLTPD2, LOC100288822, PSMB6	18229, -3687, 1162, 459, -6041	downstream, upstream, in gene, in gene, upstream	ActReg chr17 #4149	0	1
4150	17	4,850,897	4,851,859	962	1	10.567	12.033	20	17	1	3	4	SLC25A11, RNF167, PFN1, ENO3	-7916, 7748, 447, 3006	upstream, downstream, in gene, upstream	ActReg chr17 #4150	0	1
4151	17	4,872,095	4,873,094	999	2	11.594	9.656	18	16	0	1	2	SPAG7, CAMTA2	-1462, 18366	upstream, in gene	ActReg chr17 #4151	1	1
4152	17	4,890,180	4,891,314	1,134	2	20.257	19.343	48	48	1	1	3	CAMTA2, INCA1, KIF1C	213, 10158, 10496	in gene, downstream, upstream	ActReg chr17 #4152	1	1
4153	17	4,900,576	4,901,956	1,380	2	18.932	17.091	70	59	1	2	3	CAMTA2, INCA1, KIF1C	-10306, -361, 23	upstream, upstream, in gene	ActReg chr17 #4153	1	1
4154	17	5,014,705	5,015,426	721	2	10.826	10.435	16	18	1	1	2	ZNF232, LOC100506676	11332, 302	in gene, in gene	ActReg chr17 #4154	1	1
4155	17	5,094,691	5,095,921	1,230	2	37.263	41.947	129	145	1	2	2	ZNF594, LOC100130950	-128, -73	upstream, upstream	ActReg chr17 #4155	1	1
4156	17	5,342,000	5,342,919	919	2	12.379	16.759	26	30	1	1	3	RPAIN, C1QBP, DHX33	19498, 12, 29722	downstream, in gene, downstream	ActReg chr17 #4156	1	1
4157	17	5,371,919	5,372,793	874	2	13	13.518	24	24	1	1	2	DHX33, DERL2	-175, 17141	upstream, downstream	ActReg chr17 #4157	1	1
4158	17	5,388,918	5,389,460	542	1	7.294	10.882	10	16	1	2	2	DERL2, MIS12	308, -1058	in gene, upstream	ActReg chr17 #4158	0	1
4159	17	5,389,775	5,390,567	792	1	7.88	11.04	14	17	1	2	2	DERL2, MIS12	-674, -76	upstream, upstream	ActReg chr17 #4159	0	1
4160	17	5,430,032	5,430,627	595	1	9.526	11.79	18	20	0	0	1	NLRP1	57,503	in gene	ActReg chr17 #4160	0	1
4161	17	5,496,651	5,497,433	782	1	8.417	15.667	17	26	0	0	1	NLRP1	-9,210	upstream	ActReg chr17 #4161	0	1
4162	17	5,969,419	5,970,155	736	1	7	11.435	12	24	0	1	1	WSCD1	-4,147	upstream	ActReg chr17 #4162	0	1
4163	17	6,172,618	6,173,415	797	2	13.68	16.48	31	34	0	0	0				ActReg chr17 #4163	1	1
4164	17	6,206,614	6,207,615	1,001	2	17.871	20.839	40	47	0	0	0				ActReg chr17 #4164	1	1
4165	17	6,268,500	6,269,267	767	1	6.167	11.667	10	17	0	0	0				ActReg chr17 #4165	0	1
4166	17	6,429,503	6,430,111	608	1	11.842	11.105	18	17	0	0	1	PITPNM3	30,070	in gene	ActReg chr17 #4166	1	0
4167	17	6,543,854	6,544,778	924	2	15.793	12.862	33	22	1	2	3	KIAA0753, TXNDC17, MED31	-69, 94, 10638	upstream, in gene, downstream	ActReg chr17 #4167	1	1
4168	17	6,554,757	6,555,588	831	1	9.231	11.5	14	14	1	2	3	TXNDC17, MED31, C17orf100	10950, -218, 113	downstream, upstream, in gene	ActReg chr17 #4168	0	1
4169	17	6,572,194	6,573,063	869	1	12.185	11.518	18	19	0	0	0				ActReg chr17 #4169	1	0
4170	17	6,915,374	6,916,323	949	2	13.033	13.867	25	27	1	3	7	LOC100506713, ALOX12, RNASEK, C17orf49, LOC100506755, MIR195, MIR497	-180, 16464, 50, -2225, 7125, 5172, 5493	upstream, downstream, in gene, upstream, downstream, downstream, downstream	ActReg chr17 #4170	1	1
4171	17	6,917,336	6,918,575	1,239	2	12.462	13.256	30	32	1	4	8	LOC100506713, ALOX12, RNASEK, C17orf49, LOC100506755, MIR195, MIR497, BCL6B	-2287, 18571, 2157, -118, 5018, 3065, 3386, -8414	upstream, downstream, downstream, upstream, downstream, downstream, downstream, upstream	ActReg chr17 #4171	1	1
4172	17	6,963,641	6,964,219	578	1	10.278	10.389	18	14	0	0	0				ActReg chr17 #4172	1	0
4173	17	7,117,923	7,118,847	924	1	11.929	15.107	22	26	1	1	4	DLG4, ACADVL, MIR324, DVL2	4984, -4768, 8313, 19478	in gene, upstream, downstream, downstream	ActReg chr17 #4173	0	1
4174	17	7,122,922	7,124,024	1,102	1	9.676	12.559	16	20	1	2	4	DLG4, ACADVL, MIR324, DVL2	-104, 320, 3225, 14390	upstream, in gene, downstream, downstream	ActReg chr17 #4174	0	1
4175	17	7,137,485	7,138,344	859	2	12.556	13.667	19	20	1	1	5	ACADVL, DVL2, PHF23, GABARAP, DULLARD	14761, -51, 4911, 7839, 17345	downstream, upstream, downstream, downstream, downstream	ActReg chr17 #4175	1	1
4176	17	7,142,528	7,143,258	730	1	10.217	12.304	16	20	1	3	4	DVL2, PHF23, GABARAP, DULLARD	-5030, -68, 2860, 12366	upstream, upstream, downstream, downstream	ActReg chr17 #4176	0	1
4177	17	7,154,951	7,156,201	1,250	2	10.231	12.128	18	20	1	2	4	GABARAP, DULLARD, C17orf81, CLDN7	-9823, -317, 204, 10936	upstream, upstream, in gene, downstream	ActReg chr17 #4177	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4178	17	7,210,103	7,211,190	1,087	1	6.412	11.088	9	17	1	1	3	EIF5A, GPS2, NEURL4	328, 8012, 21992	in gene, downstream, downstream	ActReg chr17 #4178	0	1
4179	17	7,217,926	7,218,480	554	1	7.438	14.647	13	28	1	1	3	EIF5A, GPS2, NEURL4	7885, 455, 14435	downstream, in gene, downstream	ActReg chr17 #4179	0	1
4180	17	7,232,619	7,233,372	753	1	9.609	13.043	18	26	1	3	3	NEURL4, LOC390760, ACAP1	-357, -776, -6853	upstream, upstream, upstream	ActReg chr17 #4180	0	1
4181	17	7,254,999	7,255,802	803	2	11.56	15.04	17	25	1	2	3	ACAP1, KCTD11, TMEM95	15552, 192, 3097	downstream, in gene, upstream	ActReg chr17 #4181	1	1
4182	17	7,382,995	7,383,561	566	1	5.5	11.944	9	16	0	2	3	ZBTB4, AMAC1L3, POLR2A	4290, -1443, -4572	in gene, upstream, upstream	ActReg chr17 #4182	0	1
4183	17	7,386,414	7,388,499	2,085	2	35.354	34.892	201	176	1	3	3	ZBTB4, AMAC1L3, POLR2A	112, 2735, -394	in gene, downstream, upstream	ActReg chr17 #4183	1	1
4184	17	7,475,566	7,476,821	1,255	1	8.974	14.718	14	22	1	5	6	SENP3, EIF4A1, SNORA48, SNORD10, SNORA67, CD68	10874, 136, -1838, -3936, -5080, -6612	downstream, in gene, upstream, upstream, upstream, upstream	ActReg chr17 #4184	0	1
4185	17	7,482,512	7,483,647	1,135	1	10.057	11.8	17	18	0	4	8	SENP3, EIF4A1, SNORA48, SNORD10, SNORA67, CD68, MPDU1, SOX15	17760, 7022, 5048, 2950, 1806, 274, -3886, 10409	downstream, downstream, downstream, downstream, downstream, downstream, in gene, upstream, downstream	ActReg chr17 #4185	0	1
4186	17	7,486,658	7,487,965	1,307	1	10.575	11.8	17	22	1	1	8	EIF4A1, SNORA48, SNORD10, SNORA67, CD68, MPDU1, SOX15, FXR2	11254, 9280, 7182, 6038, 4506, 346, 6177, 30904	downstream, downstream, downstream, downstream, downstream, in gene, downstream, downstream	ActReg chr17 #4186	0	1
4187	17	7,553,784	7,554,440	656	1	5.429	10.905	11	20	1	1	1	ATP1B2	-142	upstream	ActReg chr17 #4187	0	1
4188	17	7,589,216	7,590,391	1,175	2	11.108	10.514	16	17	1	3	3	TP53, LOC100506809, WRAP53	1060, -181, 414	in gene, upstream, in gene	ActReg chr17 #4188	1	1
4189	17	7,607,923	7,608,654	731	1	12.435	11.696	25	19	1	1	2	WRAP53, EFNB3	18899, -232	downstream, upstream	ActReg chr17 #4189	1	0
4190	17	7,620,112	7,621,137	1,025	2	14.406	16.812	29	43	1	1	2	EFNB3, DNAH2	12104, -2415	downstream, upstream	ActReg chr17 #4190	1	1
4191	17	7,739,784	7,740,696	912	2	21.143	18.75	52	47	1	1	2	DNAH2, KDM6B	117201, -2995	downstream, upstream	ActReg chr17 #4191	1	1
4192	17	7,744,892	7,746,702	1,810	2	12.491	11.947	22	19	1	1	2	DNAH2, KDM6B	122758, 2562	downstream, in gene	ActReg chr17 #4192	1	1
4193	17	7,746,890	7,748,157	1,267	1	8.333	11.077	16	18	1	0	2	DNAH2, KDM6B	124484, 4288	downstream, in gene	ActReg chr17 #4193	0	1
4194	17	7,760,091	7,762,136	2,045	3	9.219	12.234	21	25	1	3	4	KDM6B, TMEM88, LSMD1, CYB5D1	17878, 2729, 59, 49	downstream, downstream, in gene, in gene	ActReg chr17 #4194	1	1
4195	17	7,788,751	7,789,730	979	2	9.613	9.935	15	22	1	1	1	CHD3	1,117	in gene	ActReg chr17 #4195	1	1
4196	17	7,982,982	7,983,728	746	1	7.435	10.739	10	15	1	0	2	ALOX12B, MIR4314	7666, -8019	in gene, upstream	ActReg chr17 #4196	0	1
4197	17	8,022,702	8,024,524	1,822	2	10.123	8.632	25	19	1	1	2	ALOXE3, HES7	-1379, 3797	upstream, downstream	ActReg chr17 #4197	1	1
4198	17	8,025,757	8,026,530	773	1	7.4	10	12	17	1	2	2	ALOXE3, HES7	-3909, 1267	upstream, in gene	ActReg chr17 #4198	0	1
4199	17	8,028,657	8,029,290	633	1	12.2	7.85	20	15	1	2	2	ALOXE3, HES7	-6739, -1563	upstream, upstream	ActReg chr17 #4199	1	0
4200	17	8,041,867	8,043,122	1,255	2	12.872	9.718	28	18	0	0	1	PER1	13,259	downstream	ActReg chr17 #4200	1	1
4201	17	8,076,489	8,077,475	986	2	13.677	15.258	22	32	0	2	2	TMEM107, SNORD118	2732, -76	in gene, upstream	ActReg chr17 #4201	1	1
4202	17	8,089,211	8,091,492	2,281	2	12.806	11.875	26	27	1	1	2	TMEM107, C17orf59	-10637, 3213	upstream, downstream	ActReg chr17 #4202	1	1
4203	17	8,092,219	8,094,000	1,781	2	10.625	14.643	23	32	1	1	1	C17orf59	455	in gene	ActReg chr17 #4203	1	1
4204	17	8,103,282	8,103,909	627	1	6.1	11.95	10	16	0	0	2	C17orf59, AURKB	-10031, 10288	upstream, downstream	ActReg chr17 #4204	0	1
4205	17	8,123,976	8,125,192	1,216	2	10.342	10.763	18	18	1	1	2	C17orf44, C17orf68	2777, 26829	in gene, downstream	ActReg chr17 #4205	1	1
4206	17	8,125,361	8,127,344	1,983	2	10.855	14.048	23	32	2	1	2	C17orf44, C17orf68	1009, 25061	in gene, downstream	ActReg chr17 #4206	1	1
4207	17	8,191,654	8,192,594	940	1	7	12.103	10	18	1	1	2	SLC25A35, RANGRF	6046, 155	in gene, in gene	ActReg chr17 #4207	0	1
4208	17	8,286,052	8,287,374	1,322	2	43.707	51.463	155	171	1	1	2	RPL26, RNF222	-148, 14431	upstream, downstream	ActReg chr17 #4208	1	1
4209	17	8,762,275	8,763,219	944	2	14.759	12.931	28	29	0	0	1	PIK3R6	8,247	in gene	ActReg chr17 #4209	1	1
4210	17	8,818,721	8,819,530	809	2	12.06	12.8	17	19	0	0	1	PIK3R5	49,899	in gene	ActReg chr17 #4210	1	1
4211	17	9,478,737	9,479,449	712	2	11.273	11.182	18	15	1	2	2	STX8, WDR16	182, -851	in gene, upstream	ActReg chr17 #4211	1	1
4212	17	9,579,917	9,580,566	649	1	12.7	11.1	16	20	0	0	1	USP43	31,291	in gene	ActReg chr17 #4212	1	0
4213	17	9,880,543	9,881,051	508	1	10.938	5.188	20	10	0	0	1	GAS7	221,071	in gene	ActReg chr17 #4213	1	0
4214	17	10,018,273	10,019,156	883	1	7.519	11.222	15	17	0	0	1	GAS7	83,154	in gene	ActReg chr17 #4214	0	1
4215	17	10,173,498	10,174,271	773	2	10.292	12.292	17	21	0	0	0				ActReg chr17 #4215	1	1
4216	17	10,600,449	10,601,322	873	1	8.519	14.963	14	28	1	2	2	SCO1, C17orf48	0, -42	in gene, upstream	ActReg chr17 #4216	0	1
4217	17	11,756,907	11,757,822	915	1	7.357	12.286	15	19	0	0	1	DNAH9	255,616	in gene	ActReg chr17 #4217	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4218	17	11,900,261	11,901,493	1,232	2	11.237	10.974	16	17	1	1	1	ZNF18	-188	upstream	ActReg chr17 #4218	1	1
4219	17	12,920,617	12,921,613	996	2	10.968	12.323	19	22	1	1	1	ELAC2	266	in gene	ActReg chr17 #4219	1	1
4220	17	13,464,895	13,465,839	944	1	10.867	12.7	14	21	0	0	1	HS3ST3A1	39,877	in gene	ActReg chr17 #4220	0	1
4221	17	13,503,719	13,504,307	588	1	6.167	10.778	11	17	1	1	1	HS3ST3A1	1,231	in gene	ActReg chr17 #4221	0	1
4222	17	13,972,329	13,973,246	917	1	9.321	13.321	17	19	1	2	2	LOC100506989, COX10	-12, 68	upstream, in gene	ActReg chr17 #4222	0	1
4223	17	15,009,723	15,010,391	668	1	6.905	11.571	14	27	0	0	0				ActReg chr17 #4223	0	1
4224	17	15,165,499	15,166,831	1,332	1	7.857	11.691	15	16	1	1	1	PMP22	2,479	in gene	ActReg chr17 #4224	0	1
4225	17	15,295,505	15,296,708	1,203	2	8.026	11.947	18	22	0	0	0				ActReg chr17 #4225	1	1
4226	17	15,393,473	15,394,611	1,138	1	10.6	9.8	16	14	0	0	0				ActReg chr17 #4226	1	0
4227	17	15,602,760	15,603,160	400	1	9.25	8	13	12	1	1	1	ZNF286A	69	in gene	ActReg chr17 #4227	1	0
4228	17	15,824,036	15,824,669	633	1	7.789	11.79	11	17	0	0	0				ActReg chr17 #4228	0	1
4229	17	15,902,199	15,903,324	1,125	1	8.971	11.943	21	22	1	2	2	ZSWIM7, TTC19	245, -21	in gene, upstream	ActReg chr17 #4229	0	1
4230	17	16,284,181	16,284,995	814	1	7.269	10.808	12	16	1	1	1	UBB	221	in gene	ActReg chr17 #4230	0	1
4231	17	16,341,520	16,342,585	1,065	1	7.364	12.424	14	19	1	4	6	TRPV2, NCRNA00188, SNORD49B, SNORD49A, SNORD65, C17orf76	23196, -249, -771, -1298, -2488, 53428	downstream, upstream, upstream, upstream, upstream, downstream	ActReg chr17 #4231	0	1
4232	17	16,471,990	16,472,682	692	1	9.5	11.227	15	20	1	1	1	ZNF287	184	in gene	ActReg chr17 #4232	0	1
4233	17	16,556,382	16,557,452	1,070	1	7.912	11.118	19	18	1	1	1	ZNF624	250	in gene	ActReg chr17 #4233	0	1
4234	17	16,946,386	16,947,164	778	1	6.917	10.083	10	14	1	1	1	MPRIP	668	in gene	ActReg chr17 #4234	0	1
4235	17	17,108,813	17,110,054	1,241	1	9.59	13.487	17	24	2	1	2	PLD6, FLCN	213, 31069	in gene, downstream	ActReg chr17 #4235	0	1
4236	17	17,139,628	17,141,369	1,741	2	21.148	26.018	78	86	1	1	2	FLCN, COPS3	4, 44093	in gene, downstream	ActReg chr17 #4236	1	1
4237	17	17,380,214	17,380,788	574	2	12	11.278	19	18	1	1	1	MED9	201	in gene	ActReg chr17 #4237	1	1
4238	17	17,494,085	17,495,589	1,504	2	13.17	15.234	37	36	1	1	1	PEMT	157	in gene	ActReg chr17 #4238	1	1
4239	17	17,596,603	17,597,726	1,123	1	9.353	12.343	16	18	1	0	1	RAI1	12,377	in gene	ActReg chr17 #4239	0	1
4240	17	17,739,685	17,740,287	602	1	11.444	10.944	15	16	1	1	2	SREBF1, TOM1L2	339, 135798	in gene, downstream	ActReg chr17 #4240	1	0
4241	17	17,875,340	17,876,397	1,057	2	12.273	10.121	28	23	1	2	2	TOM1L2, LRRC48	-84, -259	upstream, upstream	ActReg chr17 #4241	1	1
4242	17	17,928,789	17,930,133	1,344	2	13.357	15.119	25	28	0	0	2	LRRC48, ATPAF2	53334, 13019	downstream, in gene	ActReg chr17 #4242	1	1
4243	17	17,936,749	17,937,118	369	1	13.727	11.091	22	15	0	1	2	ATPAF2, C17orf39	5547, -5678	in gene, upstream	ActReg chr17 #4243	1	0
4244	17	17,942,137	17,943,077	940	2	12.133	13.3	22	22	1	2	2	ATPAF2, C17orf39	-127, -4	upstream, upstream	ActReg chr17 #4244	1	1
4245	17	17,990,892	17,991,543	651	2	10.8	12.95	18	26	1	1	1	DRG2	-66	upstream	ActReg chr17 #4245	1	1
4246	17	18,085,865	18,087,369	1,504	2	11.809	10.298	20	19	1	1	2	MYO15A, ALKBH5	74597, -250	downstream, upstream	ActReg chr17 #4246	1	1
4247	17	18,161,309	18,162,247	938	2	11.633	11.7	20	21	1	2	2	FLII, SMCR7	277, -2070	in gene, upstream	ActReg chr17 #4247	1	1
4248	17	18,163,285	18,164,405	1,120	2	13.971	17	35	36	1	2	2	FLII, SMCR7	-1790, -3	upstream, upstream	ActReg chr17 #4248	1	1
4249	17	18,217,703	18,218,877	1,174	1	8.806	14.889	12	27	1	2	2	TOP3A, SMCR8	31, -304	in gene, upstream	ActReg chr17 #4249	0	1
4250	17	19,220,383	19,221,639	1,256	2	15.9	17.55	49	61	0	0	1	EPN2	80,321	in gene	ActReg chr17 #4250	1	1
4251	17	19,551,340	19,552,654	1,314	1	8.976	13.366	14	20	1	1	1	ALDH3A2	-67	upstream	ActReg chr17 #4251	0	1
4252	17	19,655,921	19,656,831	910	1	10.857	13.536	24	24	0	1	1	ALDH3A1	-4,630	upstream	ActReg chr17 #4252	0	1
4253	17	19,967,151	19,968,131	980	2	11.097	10.161	14	19	0	0	0				ActReg chr17 #4253	1	1
4254	17	20,825,543	20,826,022	479	1	7.4	10.933	10	17	0	0	1	LOC100507263	30,120	in gene	ActReg chr17 #4254	0	1
4255	17	20,946,652	20,947,268	616	1	10.2	7.9	20	17	1	1	1	USP22	-608	upstream	ActReg chr17 #4255	1	0
4256	17	21,002,052	21,002,943	891	1	7.481	10.852	12	16	0	0	0				ActReg chr17 #4256	0	1
4257	17	21,029,973	21,030,703	730	1	11.739	10.217	17	16	1	1	1	DHRS7B	80	in gene	ActReg chr17 #4257	1	0
4258	17	21,116,790	21,118,215	1,425	2	14.444	11.689	31	29	1	1	1	TMEM11	406	in gene	ActReg chr17 #4258	1	1
4259	17	21,190,643	21,192,215	1,572	2	13.49	11.612	24	20	0	0	1	MAP2K3	3,461	in gene	ActReg chr17 #4259	1	1
4260	17	21,226,038	21,227,324	1,286	1	15.3	12.325	25	19	0	0	1	MAP2K3	38,713	downstream	ActReg chr17 #4260	1	0
4261	17	21,454,253	21,454,762	509	1	4.5	10.125	7	17	1	1	1	C17orf51	434	in gene	ActReg chr17 #4261	0	1
4262	17	25,620,859	25,621,993	1,134	2	10.722	12.917	18	21	1	1	1	WSB1	320	in gene	ActReg chr17 #4262	1	1
4263	17	25,680,341	25,681,130	789	1	7.8	11.6	19	16	1	0	0				ActReg chr17 #4263	0	1
4264	17	25,798,336	25,799,331	995	2	11.469	12.75	18	20	0	1	1	KSR1	-203	upstream	ActReg chr17 #4264	1	1
4265	17	26,089,719	26,090,504	785	2	8.625	15.88	20	40	0	0	1	NOS2	37,444	in gene	ActReg chr17 #4265	1	1
4266	17	26,104,007	26,104,883	876	2	11.296	11.518	18	21	0	0	1	NOS2	23,110	in gene	ActReg chr17 #4266	1	1
4267	17	26,301,726	26,302,856	1,130	1	9.917	12.139	16	19	0	0	0				ActReg chr17 #4267	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4268	17	26,335,142	26,336,168	1,026	2	19.844	21.219	50	64	0	0	0				ActReg chr17 #4268	1	1
4269	17	26,368,381	26,368,915	534	2	12.059	14.588	24	28	1	1	1	NLK	-1,040	upstream	ActReg chr17 #4269	1	1
4270	17	26,645,238	26,646,774	1,536	2	10.188	13.125	16	22	2	1	2	TMEM97, IFT20	-115, 16489	upstream, downstream	ActReg chr17 #4270	1	1
4271	17	26,661,972	26,663,434	1,462	2	10.935	13.478	20	22	1	2	3	TMEM97, IFT20, TNFAIP1	16582, -208, 155	downstream, upstream, in gene	ActReg chr17 #4271	1	1
4272	17	26,684,092	26,685,104	1,012	2	19.531	22.469	50	54	1	2	4	POLDIP2, TMEM199, SEBOX, VTN	5, -89, 7667, 12775	in gene, upstream, downstream, downstream	ActReg chr17 #4272	1	1
4273	17	26,700,487	26,701,203	716	1	9.045	11.636	13	24	0	2	3	SEBOX, VTN, SARM1	-8580, -3472, 1858	upstream, upstream, in gene	ActReg chr17 #4273	0	1
4274	17	26,732,955	26,733,787	832	1	11.192	8.5	15	12	1	1	2	SARM1, SLC46A1	34384, -143	downstream, upstream	ActReg chr17 #4274	1	0
4275	17	26,925,568	26,927,105	1,537	1	12.674	8.367	20	14	1	2	3	SPAG5, LOC100506436, FLJ25006	-280, 528, 14875	upstream, in gene, downstream	ActReg chr17 #4275	1	0
4276	17	26,988,708	26,989,510	802	1	10	11.36	15	21	1	2	2	SDF2, SUPT6H	-176, -193	upstream, upstream	ActReg chr17 #4276	0	1
4277	17	27,043,909	27,044,868	959	1	9.567	10.7	16	15	1	7	8	PROCA1, RAB34, RPL23A, SNORD42B, SNORD4A, SNORD42A, SNORD4B, TLCD1	-5516, 898, -2612, -3180, -5212, -6060, -6311, 9561	upstream, in gene, upstream, upstream, upstream, upstream, upstream, downstream	ActReg chr17 #4277	0	1
4278	17	27,046,363	27,047,366	1,003	1	11.25	9.969	19	17	1	7	9	PROCA1, RAB34, RPL23A, SNORD42B, SNORD4A, SNORD42A, SNORD4B, TLCD1, NEK8	-7992, -1578, -136, 704, -2736, 3584, -3835, 7085, 8968	upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, downstream, upstream	ActReg chr17 #4278	1	0
4279	17	27,051,364	27,052,682	1,318	1	6.171	10.195	11	15	0	6	8	RAB34, RPL23A, SNORD42B, SNORD4A, SNORD42A, SNORD4B, TLCD1, NEK8	-6737, 5023, 4455, 2423, 1575, 1324, 1926, 3809	upstream, downstream, downstream, downstream, downstream, downstream, downstream, in gene, upstream	ActReg chr17 #4279	0	1
4280	17	27,052,713	27,053,283	570	1	9.471	10.778	16	16	1	5	8	RAB34, RPL23A, SNORD42B, SNORD4A, SNORD42A, SNORD4B, TLCD1, NEK8	-7712, 5998, 5430, 3398, 2550, 2299, 951, -2834	upstream, downstream, downstream, downstream, downstream, downstream, downstream, in gene, upstream	ActReg chr17 #4280	0	1
4281	17	27,053,392	27,054,204	812	1	6.96	11.8	11	21	1	2	8	RAB34, RPL23A, SNORD42B, SNORD4A, SNORD42A, SNORD4B, TLCD1, NEK8	-8512, 6798, 6230, 4198, 3350, 3099, 151, -2034	upstream, downstream, downstream, downstream, downstream, downstream, downstream, in gene, upstream	ActReg chr17 #4281	0	1
4282	17	27,181,389	27,182,577	1,188	2	8.622	16.081	18	27	1	1	3	ERAL1, MIR451, MIR144	-60, 6475, 6653	upstream, downstream, downstream	ActReg chr17 #4282	1	1
4283	17	27,278,343	27,279,730	1,387	1	12.233	9.116	18	20	2	1	2	PHF12, SEZ6	-528, 54045	upstream, downstream	ActReg chr17 #4283	1	0
4284	17	27,331,008	27,331,984	976	1	9.097	11.161	22	16	0	1	1	SEZ6	1,585	in gene	ActReg chr17 #4284	0	1
4285	17	27,332,729	27,333,594	865	2	12.704	14.185	32	31	1	1	1	SEZ6	-80	upstream	ActReg chr17 #4285	1	1
4286	17	27,334,453	27,335,481	1,028	2	13.719	11.469	30	23	0	1	1	SEZ6	-1,886	upstream	ActReg chr17 #4286	1	1
4287	17	27,459,794	27,460,563	769	1	11.625	7.333	20	13	0	0	1	MYO18A	47,229	in gene	ActReg chr17 #4287	1	0
4288	17	27,478,370	27,479,030	660	1	10.95	11.9	18	23	0	0	1	MYO18A	28,707	in gene	ActReg chr17 #4288	0	1
4289	17	27,481,730	27,483,133	1,403	1	8	12.302	13	21	0	0	1	MYO18A	24,976	in gene	ActReg chr17 #4289	0	1
4290	17	27,522,608	27,523,230	622	1	7.316	12	11	20	0	0	0				ActReg chr17 #4290	0	1
4291	17	27,567,765	27,568,719	954	1	6	13.233	11	20	0	1	1	CRYBA1	-5,633	upstream	ActReg chr17 #4291	0	1
4292	17	27,620,786	27,621,707	921	1	9.103	14.034	16	26	1	1	1	NUFIP2	-80	upstream	ActReg chr17 #4292	0	1
4293	17	27,893,034	27,893,938	904	1	4.429	9.893	7	17	1	2	3	ABHD15, TP53I13, GIT1	556, -2253, 23124	in gene, upstream, downstream	ActReg chr17 #4293	0	1
4294	17	27,916,641	27,917,289	648	1	10.1	12.15	17	23	1	2	2	GIT1, ANKRD13B	-355, -3562	upstream, upstream	ActReg chr17 #4294	0	1
4295	17	27,920,769	27,921,823	1,054	1	9.719	11.875	16	18	1	2	2	GIT1, ANKRD13B	-4686, 769	upstream, in gene	ActReg chr17 #4295	0	1
4296	17	28,087,975	28,088,555	580	1	7.889	12.389	16	19	1	0	1	SSH2	168,753	in gene	ActReg chr17 #4296	0	1
4297	17	28,256,632	28,257,620	988	1	7.806	10.194	14	15	1	2	2	SSH2, EFCAB5	-108, 252	upstream, in gene	ActReg chr17 #4297	0	1
4298	17	28,703,655	28,704,482	827	1	6.346	11.385	10	17	0	1	1	CPD	-1,916	upstream	ActReg chr17 #4298	0	1
4299	17	28,705,246	28,706,542	1,296	2	9.366	13.024	18	24	1	1	1	CPD	-90	upstream	ActReg chr17 #4299	1	1
4300	17	28,803,779	28,804,973	1,194	2	31.081	30.676	102	100	1	1	2	CPD, GOSR1	98392, -50	downstream, upstream	ActReg chr17 #4300	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4301	17	28,877,444	28,878,321	877	1	10.444	8.741	15	14	0	0	1	TBC1D29	-8,702	upstream	ActReg chr17 #4301	1	0
4302	17	28,927,009	28,927,868	859	1	9.962	13.615	18	25	1	0	0				ActReg chr17 #4302	0	1
4303	17	29,034,957	29,035,672	715	2	15.636	17	23	30	1	0	0				ActReg chr17 #4303	1	1
4304	17	29,035,687	29,036,143	456	2	14.643	18.857	23	34	1	0	0				ActReg chr17 #4304	1	1
4305	17	29,151,358	29,151,833	475	1	14.4	9.6	22	15	1	2	2	CRLF3, ATAD5	183, -7425	in gene, upstream	ActReg chr17 #4305	1	0
4306	17	29,158,521	29,159,545	1,024	2	12.531	16.562	24	33	1	2	2	CRLF3, ATAD5	-7255, 13	upstream, in gene	ActReg chr17 #4306	1	1
4307	17	29,232,931	29,233,792	861	2	10.593	12	18	19	1	1	1	C17orf42	-75	upstream	ActReg chr17 #4307	1	1
4308	17	29,378,804	29,379,458	654	1	13.762	9.048	20	13	0	0	0				ActReg chr17 #4308	1	0
4309	17	29,740,844	29,741,442	598	1	11.316	10.526	20	17	0	0	1	RAB11FIP4	22,501	in gene	ActReg chr17 #4309	1	0
4310	17	29,799,086	29,799,671	585	1	12.278	9.222	19	13	0	0	1	RAB11FIP4	80,736	in gene	ActReg chr17 #4310	1	0
4311	17	29,826,892	29,827,632	740	1	7.913	11.174	12	14	0	0	1	RAB11FIP4	108,620	in gene	ActReg chr17 #4311	0	1
4312	17	29,876,788	29,877,621	833	2	10.538	17.115	22	34	2	0	1	MIR193A	-9,811	upstream	ActReg chr17 #4312	1	1
4313	17	29,907,328	29,908,454	1,126	1	13.583	8.361	20	14	0	0	1	MIR365-2	5,461	downstream	ActReg chr17 #4313	1	0
4314	17	29,923,191	29,924,755	1,564	1	9.204	11.388	18	20	0	0	0				ActReg chr17 #4314	0	1
4315	17	30,048,794	30,050,367	1,573	2	11.837	12.531	24	19	0	0	0				ActReg chr17 #4315	1	1
4316	17	30,468,867	30,469,710	843	2	11.308	10.808	20	23	1	1	1	RHOT1	-185	upstream	ActReg chr17 #4316	1	1
4317	17	30,601,713	30,602,703	990	2	10.355	11.516	22	20	0	0	1	RHBDL3	9,013	in gene	ActReg chr17 #4317	1	1
4318	17	30,668,953	30,669,501	548	1	7.824	11.823	12	19	1	1	3	C17orf75, MIR632, ZNF207	-38, -7901, -7930	upstream, upstream, upstream	ActReg chr17 #4318	0	1
4319	17	30,771,185	30,772,096	911	1	8.759	10.034	14	18	1	1	1	PSMD11	138	in gene	ActReg chr17 #4319	0	1
4320	17	31,399,376	31,400,397	1,021	1	8.312	13.781	20	27	0	0	1	ACCN1	1,083,939	in gene	ActReg chr17 #4320	0	1
4321	17	31,469,472	31,470,470	998	2	18.188	17.5	38	34	0	0	1	ACCN1	1,013,854	in gene	ActReg chr17 #4321	1	1
4322	17	31,594,099	31,595,215	1,116	2	11.086	10.514	17	17	0	0	1	ACCN1	889,168	in gene	ActReg chr17 #4322	1	1
4323	17	31,654,999	31,655,779	780	2	8.72	12.68	17	28	0	0	1	ACCN1	828,436	in gene	ActReg chr17 #4323	1	1
4324	17	33,030,342	33,031,189	847	2	12.808	11.231	23	21	0	0	0				ActReg chr17 #4324	1	1
4325	17	33,124,556	33,125,210	654	1	5.8	12.2	12	24	0	0	0				ActReg chr17 #4325	0	1
4326	17	33,288,047	33,288,670	623	2	11.462	16.038	19	34	1	2	2	CCT6B, ZNF830	70, -91	in gene, upstream	ActReg chr17 #4326	1	1
4327	17	33,390,497	33,391,036	539	1	10.062	9.062	18	13	0	0	1	RFFL	25,528	in gene	ActReg chr17 #4327	1	0
4328	17	33,446,328	33,447,039	711	1	10.591	10.091	14	13	1	2	2	RAD51L3, FNDC8	205, -1948	in gene, upstream	ActReg chr17 #4328	1	0
4329	17	33,468,670	33,469,702	1,032	2	18.303	14.879	39	35	1	2	2	NLE1, UNC45B	136, -5650	in gene, upstream	ActReg chr17 #4329	1	1
4330	17	33,568,923	33,569,470	547	1	10.882	7.529	16	11	1	1	1	SLFN5	-890	upstream	ActReg chr17 #4330	1	0
4331	17	33,569,470	33,570,277	807	1	5.692	11.385	12	16	1	1	1	SLFN5	-213	upstream	ActReg chr17 #4331	0	1
4332	17	33,570,384	33,571,013	629	1	4.5	11.3	7	21	1	1	1	SLFN5	612	in gene	ActReg chr17 #4332	0	1
4333	17	33,700,589	33,700,986	397	1	10.167	10.083	15	12	2	1	1	SLFN11	-67	upstream	ActReg chr17 #4333	1	0
4334	17	34,070,439	34,071,435	996	2	19.323	17	40	42	0	0	2	RASL10B, GAS2L2	12258, 8960	downstream, downstream	ActReg chr17 #4334	1	1
4335	17	34,135,774	34,136,844	1,070	2	14.206	18.529	27	38	1	1	1	TAF15	-179	upstream	ActReg chr17 #4335	1	1
4336	17	34,819,552	34,820,291	739	2	11.292	14.167	26	30	1	0	0				ActReg chr17 #4336	1	1
4337	17	34,838,329	34,839,360	1,031	1	6.455	11.424	12	17	1	1	1	ZNHIT3	-3,629	upstream	ActReg chr17 #4337	0	1
4338	17	34,842,040	34,843,128	1,088	2	16.794	17.5	46	48	1	1	2	ZNHIT3, MYO19	111, 48721	in gene, downstream	ActReg chr17 #4338	1	1
4339	17	34,890,192	34,891,844	1,652	1	8.077	11.365	19	16	1	2	3	MYO19, PIGW, GGNBP2	287, -385, -9719	in gene, upstream, upstream	ActReg chr17 #4339	0	1
4340	17	34,901,268	34,901,974	706	2	12.227	11.636	25	17	1	1	3	MYO19, PIGW, GGNBP2	-10316, 10218, 884	upstream, downstream, in gene	ActReg chr17 #4340	1	1
4341	17	35,054,180	35,054,820	640	1	7.15	11.55	10	18	0	0	0				ActReg chr17 #4341	0	1
4342	17	35,060,003	35,060,643	640	2	12.462	13.039	23	23	1	0	0				ActReg chr17 #4342	1	1
4343	17	35,134,155	35,135,026	871	2	11.148	13.37	23	21	0	0	0				ActReg chr17 #4343	1	1
4344	17	35,206,896	35,207,513	617	1	8.368	12.842	10	20	0	0	0				ActReg chr17 #4344	0	1
4345	17	35,278,607	35,279,248	641	1	8.6	12.1	12	18	0	0	0				ActReg chr17 #4345	0	1
4346	17	35,305,666	35,306,831	1,165	1	8.611	14.444	14	23	1	1	2	LHX1, AATF	11749, 73	downstream, in gene	ActReg chr17 #4346	0	1
4347	17	35,843,412	35,844,125	713	1	11.5	9.364	17	14	0	1	2	TADA2A, DUSP14	76791, -6183	downstream, upstream	ActReg chr17 #4347	1	0
4348	17	35,969,155	35,969,747	592	1	9.111	11.833	11	17	1	1	2	SYNRG, DDX52	35, 34036	in gene, downstream	ActReg chr17 #4348	0	1
4349	17	36,003,120	36,003,670	550	1	6.941	10.765	9	18	1	1	1	DDX52	92	in gene	ActReg chr17 #4349	0	1
4350	17	36,208,845	36,209,704	859	1	6.296	10.407	11	19	0	0	0				ActReg chr17 #4350	0	1
4351	17	36,507,358	36,507,948	590	1	7.316	10.526	10	21	1	1	2	GPR179, SOCS7	-7960, -352	upstream, upstream	ActReg chr17 #4351	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4352	17	36,830,572	36,831,018	446	1	8.429	10.643	10	17	1	1	1	C17orf96	392	in gene	ActReg chr17 #4352	0	1
4353	17	36,907,940	36,909,809	1,869	2	16.31	15.845	53	49	2	2	2	PCGF2, PSMB3	-4316, -128	upstream, upstream	ActReg chr17 #4353	1	1
4354	17	36,955,005	36,955,886	881	2	7.714	13.821	17	23	1	1	2	PIP4K2B, CWC25	713, 26144	in gene, downstream	ActReg chr17 #4354	1	1
4355	17	36,956,017	36,956,609	592	1	11.632	9.474	23	18	1	1	2	PIP4K2B, CWC25	-155, 25276	upstream, downstream	ActReg chr17 #4355	1	0
4356	17	36,981,332	36,981,976	644	2	13.3	15.05	27	28	1	1	2	CWC25, C17orf98	-65, 15988	upstream, downstream	ActReg chr17 #4356	1	1
4357	17	37,009,353	37,010,488	1,135	1	7.743	13.543	20	24	1	2	2	RPL23, SNORA21	133, -672	in gene, upstream	ActReg chr17 #4357	0	1
4358	17	37,026,013	37,026,933	920	1	7.276	11.586	15	18	1	1	1	LASP1	361	in gene	ActReg chr17 #4358	0	1
4359	17	37,157,880	37,158,778	898	1	12.464	8.929	17	14	0	0	0				ActReg chr17 #4359	1	0
4360	17	37,310,397	37,311,124	727	2	9.957	11.217	17	19	0	1	2	PLXDC1, ARL5C	-2858, 11654	upstream, downstream	ActReg chr17 #4360	1	1
4361	17	37,556,954	37,558,253	1,299	1	11.585	7.561	15	14	1	1	2	FBXL20, MED1	306, 49924	in gene, downstream	ActReg chr17 #4361	1	0
4362	17	37,748,185	37,749,307	1,122	2	9.657	11.771	20	18	0	0	0				ActReg chr17 #4362	1	1
4363	17	37,774,470	37,775,106	636	1	7.3	15.05	14	22	1	0	1	PPP1R1B	-8,391	upstream	ActReg chr17 #4363	0	1
4364	17	37,886,261	37,886,872	611	1	9	11.263	13	16	1	2	3	ERBB2, C17orf37, GRB7	42173, 222, 7621	downstream, in gene, upstream	ActReg chr17 #4364	0	1
4365	17	37,909,790	37,910,914	1,124	2	13.556	12.972	22	27	1	0	1	GRB7	16,165	downstream	ActReg chr17 #4365	1	1
4366	17	38,083,671	38,084,204	533	1	9.176	11.529	14	20	1	1	2	GSDMB, ORMDL3	-9034, -83	upstream, upstream	ActReg chr17 #4366	0	1
4367	17	38,136,454	38,137,548	1,094	2	25.235	29.029	83	85	1	1	2	GSDMA, PSMD3	17775, -59	downstream, upstream	ActReg chr17 #4367	1	1
4368	17	38,219,146	38,219,902	756	2	12.095	12.696	21	25	1	1	2	MED24, THRA	-8635, 1078	upstream, in gene	ActReg chr17 #4368	1	1
4369	17	38,256,277	38,257,138	861	1	12.852	9.815	21	14	1	1	2	THRA, NR1D1	38261, 266	downstream, in gene	ActReg chr17 #4369	1	0
4370	17	38,279,302	38,280,152	850	1	8.615	11.231	15	16	1	1	1	MSL1	937	in gene	ActReg chr17 #4370	0	1
4371	17	38,470,774	38,471,350	576	2	11.889	11.611	18	19	0	0	1	RARA	5,639	in gene	ActReg chr17 #4371	1	1
4372	17	38,573,547	38,574,726	1,179	2	12.054	12.54	20	25	1	1	1	TOP2A	66	in gene	ActReg chr17 #4372	1	1
4373	17	38,803,879	38,804,667	788	1	7.375	10.375	11	15	1	1	2	SMARCE1, KRT222	-170, 17143	upstream, downstream	ActReg chr17 #4373	0	1
4374	17	39,254,677	39,255,143	466	1	2.733	9.4	6	13	0	2	2	KRTAP4-8, KRTAP4-9	-535, -6731	upstream, upstream	ActReg chr17 #4374	0	1
4375	17	39,559,953	39,560,744	791	2	11.16	13.08	18	24	0	2	2	KRT31, LOC100505782	-6504, 1680	upstream, in gene	ActReg chr17 #4375	1	1
4376	17	39,821,747	39,822,676	929	2	10.897	10.483	20	18	1	0	0				ActReg chr17 #4376	1	1
4377	17	39,834,609	39,835,782	1,173	2	14.757	15.081	34	29	0	0	1	EIF1	-9,932	upstream	ActReg chr17 #4377	1	1
4378	17	39,967,480	39,969,221	1,741	2	12.146	18.454	19	36	1	2	2	SC65, FKBP10	101, -612	in gene, upstream	ActReg chr17 #4378	1	1
4379	17	40,020,946	40,021,808	862	1	7.852	11.926	13	18	1	1	2	KLHL11, ACLY	252, 53895	in gene, downstream	ActReg chr17 #4379	0	1
4380	17	40,086,319	40,087,112	793	2	9.56	10.8	14	15	1	1	1	TTC25	-173	upstream	ActReg chr17 #4380	1	1
4381	17	40,168,911	40,170,210	1,299	2	12.659	18.098	33	32	1	2	4	DNAJC7, NKIRAS2, ZNF385C, LOC100507628	155, -34, 11147, 20484	in gene, upstream, downstream, downstream	ActReg chr17 #4381	1	1
4382	17	40,171,520	40,172,494	974	2	31.484	34.419	96	108	1	2	4	DNAJC7, NKIRAS2, ZNF385C, LOC100507628	-2292, 2413, 8700, 18037	upstream, in gene, downstream, downstream	ActReg chr17 #4382	1	1
4383	17	40,306,866	40,307,874	1,008	1	8.031	11.281	13	18	1	1	2	RAB5C, KCNH4	-348, 25926	upstream, downstream	ActReg chr17 #4383	0	1
4384	17	40,331,923	40,333,628	1,705	2	11.509	16.377	26	40	1	1	3	KCNH4, HCRT, GHDC	521, 4695, 13775	in gene, downstream, downstream	ActReg chr17 #4384	1	1
4385	17	40,345,987	40,347,044	1,057	2	23.546	32.364	69	89	0	1	3	HCRT, GHDC, STAT5B	-9045, 35, 81909	upstream, in gene, downstream	ActReg chr17 #4385	1	1
4386	17	40,418,852	40,419,344	492	1	10	9.533	16	15	0	0	1	STAT5B	9,326	in gene	ActReg chr17 #4386	1	0
4387	17	40,439,155	40,439,851	696	1	9.682	11.636	16	26	0	1	1	STAT5A	-62	upstream	ActReg chr17 #4387	0	1
4388	17	40,540,093	40,541,159	1,066	2	19.618	21.118	45	54	1	1	1	STAT3	-113	upstream	ActReg chr17 #4388	1	1
4389	17	40,610,698	40,611,593	895	1	9.071	10.643	16	16	1	1	1	ATP6V0A1	283	in gene	ActReg chr17 #4389	0	1
4390	17	40,705,149	40,705,868	719	1	4.739	12.565	8	21	1	2	4	NAGLU, HSD17B1, LOC100290566, COASY	17557, 1524, 1258, 8584	downstream, in gene, in gene, upstream	ActReg chr17 #4390	0	1
4391	17	40,706,331	40,706,762	431	1	11.214	10.143	14	13	1	3	4	NAGLU, HSD17B1, LOC100290566, COASY	18595, 2562, 220, -7546	downstream, in gene, in gene, upstream	ActReg chr17 #4391	1	0
4392	17	40,718,633	40,719,584	951	1	10	10.933	16	16	1	1	3	COASY, MLX, PSMC3IP	5016, 30, 10639	downstream, in gene, downstream	ActReg chr17 #4392	0	1
4393	17	40,829,056	40,830,341	1,285	1	9	13.268	16	19	0	2	3	PLEKHH3, CCR10, CNTNAP1	-650, 4147, -4934	upstream, downstream, upstream	ActReg chr17 #4393	0	1
4394	17	40,831,506	40,832,488	982	2	14.258	15.935	28	27	1	3	3	PLEKHH3, CCR10, CNTNAP1	-2949, 1848, -2635	upstream, in gene, upstream	ActReg chr17 #4394	1	1
4395	17	40,950,309	40,951,056	747	1	10.609	12	17	21	1	2	3	WNK4, CCDC56, CNTD1	18033, 22, -172	downstream, in gene, upstream	ActReg chr17 #4395	0	1
4396	17	40,975,790	40,976,642	852	1	11.667	10.037	20	16	1	1	2	BECN1, PSME3	94, -9207	in gene, upstream	ActReg chr17 #4396	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4397	17	40,984,780	40,986,238	1,458	2	10.533	10.111	21	15	1	1	2	BECN1, PSME3	-9199, 86	upstream, in gene	ActReg chr17 #4397	1	1
4398	17	41,149,859	41,150,813	954	2	10.552	13.172	24	20	1	1	3	RUNDC1, RPL27, IFI35	17754, -110, -8433	downstream, upstream, upstream	ActReg chr17 #4398	1	1
4399	17	41,162,706	41,163,591	885	1	4.607	9.893	11	14	0	0	3	RPL27, IFI35, VAT1	12702, 4379, 11311	downstream, in gene, downstream	ActReg chr17 #4399	0	1
4400	17	41,173,724	41,174,746	1,022	2	11.656	12.375	24	20	1	2	3	IFI35, VAT1, RND2	15466, 224, 3023	downstream, in gene, upstream	ActReg chr17 #4400	1	1
4401	17	41,392,392	41,393,576	1,184	2	14.946	13.6	30	30	1	0	0				ActReg chr17 #4401	1	1
4402	17	41,438,212	41,439,151	939	2	11.586	13.931	26	29	1	0	1	LOC100130581	27,585	downstream	ActReg chr17 #4402	1	1
4403	17	41,444,834	41,446,022	1,188	2	13.486	15.108	32	36	1	0	1	LOC100130581	20,838	downstream	ActReg chr17 #4403	1	1
4404	17	41,496,139	41,496,923	784	1	10.083	11.583	17	16	0	0	0				ActReg chr17 #4404	0	1
4405	17	41,519,968	41,520,608	640	1	8.667	10.143	15	19	0	1	1	MIR2117	-1,886	upstream	ActReg chr17 #4405	0	1
4406	17	41,560,831	41,561,665	834	2	17.889	15.926	45	37	1	1	1	DHX8	-86	upstream	ActReg chr17 #4406	1	1
4407	17	42,091,955	42,092,712	757	1	10.042	16.042	20	30	2	1	2	NAGS, TMEM101	10301, 12	downstream, in gene	ActReg chr17 #4407	0	1
4408	17	42,200,967	42,201,681	714	2	12.409	9.905	26	15	1	1	1	HDAC5	-310	upstream	ActReg chr17 #4408	1	1
4409	17	42,215,238	42,216,141	903	2	11.464	14.464	21	26	0	1	1	C17orf53	-3,585	upstream	ActReg chr17 #4409	1	1
4410	17	42,219,013	42,219,742	729	2	11.318	14.136	17	26	1	1	1	C17orf53	103	in gene	ActReg chr17 #4410	1	1
4411	17	42,285,717	42,286,411	694	1	7.045	11.409	15	18	0	0	1	UBTF	12,186	in gene	ActReg chr17 #4411	0	1
4412	17	42,298,596	42,299,015	419	1	11.769	7.333	20	11	1	1	1	UBTF	-555	upstream	ActReg chr17 #4412	1	0
4413	17	42,385,587	42,386,237	650	2	12.8	10.55	22	17	1	1	1	RUNDC3A	-15	upstream	ActReg chr17 #4413	1	1
4414	17	42,401,525	42,402,742	1,217	2	13.684	17.237	32	36	2	1	2	RUNDC3A, SLC25A39	16206, 84	downstream, in gene	ActReg chr17 #4414	1	1
4415	17	42,403,997	42,404,735	738	2	17	11.739	43	31	0	1	2	RUNDC3A, SLC25A39	18439, -2149	downstream, upstream	ActReg chr17 #4415	1	1
4416	17	42,580,439	42,581,285	846	1	8.519	12.741	11	19	1	1	1	GPATCH8	95	in gene	ActReg chr17 #4416	0	1
4417	17	42,633,698	42,634,756	1,058	2	10.394	11.121	16	16	1	1	1	FZD2	-698	upstream	ActReg chr17 #4417	1	1
4418	17	42,766,686	42,767,810	1,124	2	10.75	10.861	14	20	1	1	1	CCDC43	-83	upstream	ActReg chr17 #4418	1	1
4419	17	42,785,646	42,786,704	1,058	2	11.606	14.152	19	31	1	1	1	DBF4B	199	in gene	ActReg chr17 #4419	1	1
4420	17	42,976,600	42,977,317	717	1	12.826	12.217	23	20	1	2	3	EFTUD2, CCDC103, GFAP	35, -196, 15956	in gene, upstream, downstream	ActReg chr17 #4420	0	1
4421	17	43,024,706	43,025,642	936	1	9.172	13.621	13	26	1	1	1	KIF18B	-92	upstream	ActReg chr17 #4421	0	1
4422	17	43,138,019	43,138,982	963	1	11.867	12.933	20	23	1	2	2	DCAKD, NMT1	-27, -180	upstream, upstream	ActReg chr17 #4422	0	1
4423	17	43,224,700	43,226,306	1,606	1	10.922	16.216	29	36	1	1	2	ACBD4, HEXIM1	15536, 819	downstream, in gene	ActReg chr17 #4423	0	1
4424	17	43,238,487	43,239,805	1,318	1	12.561	8.341	20	13	1	1	3	HEXIM1, HEXIM2, LOC100505972	14462, 882, 9706	downstream, in gene, downstream	ActReg chr17 #4424	1	0
4425	17	43,247,894	43,248,670	776	1	9.167	12.167	12	23	0	1	2	HEXIM2, LOC100505972	10018, 570	downstream, in gene	ActReg chr17 #4425	0	1
4426	17	43,249,367	43,250,734	1,367	2	12.465	16.977	28	34	0	1	2	HEXIM2, LOC100505972	11786, -1198	downstream, upstream	ActReg chr17 #4426	1	1
4427	17	43,394,487	43,395,154	667	1	11.333	9.762	17	16	1	1	1	MAP3K14	-406	upstream	ActReg chr17 #4427	1	0
4428	17	43,448,829	43,449,515	686	1	9.909	12.318	16	22	1	0	0				ActReg chr17 #4428	0	1
4429	17	43,935,207	43,936,060	853	2	10.423	12.462	24	23	0	0	1	LOC100128977	37,246	in gene	ActReg chr17 #4429	1	1
4430	17	43,971,336	43,972,074	738	2	11.652	10.783	17	20	1	3	3	LOC100128977, MAPT, LOC100130148	1174, -43, -1444	in gene, upstream, upstream	ActReg chr17 #4430	1	1
4431	17	45,000,004	45,000,913	909	2	13.357	16.143	22	34	1	1	1	GOSR2	-28	upstream	ActReg chr17 #4431	1	1
4432	17	45,041,228	45,042,261	1,033	2	9.5	10.594	19	23	0	0	0				ActReg chr17 #4432	1	1
4433	17	45,144,460	45,145,120	660	2	12.905	12.381	26	24	0	1	1	LOC100506214	64	in gene	ActReg chr17 #4433	1	1
4434	17	45,331,110	45,331,744	634	1	10.25	6.65	15	11	1	1	1	ITGB3	219	in gene	ActReg chr17 #4434	1	0
4435	17	45,357,586	45,358,342	756	1	7.875	11.167	13	19	0	0	1	ITGB3	26,756	in gene	ActReg chr17 #4435	0	1
4436	17	45,371,888	45,373,107	1,219	1	6.947	12.447	11	17	0	0	2	ITGB3, LOC100506252	41289, 10554	in gene, downstream	ActReg chr17 #4436	0	1
4437	17	45,400,799	45,401,981	1,182	1	10.946	10.189	19	18	1	1	1	C17orf57	43	in gene	ActReg chr17 #4437	1	0
4438	17	45,862,669	45,863,703	1,034	2	17.344	18.594	45	46	0	0	0				ActReg chr17 #4438	1	1
4439	17	45,898,715	45,899,621	906	2	19.679	18.241	51	41	0	1	4	LOC100506269, OSBPL7, MRPL10, LRRC46	16697, -21, 9735, -9825	in gene, upstream, downstream, upstream	ActReg chr17 #4439	1	1
4440	17	45,972,954	45,974,258	1,304	2	16.244	19.805	44	56	1	2	3	LOC100506295, SP2, LOC100506325	-428, 90, 45119	upstream, in gene, downstream	ActReg chr17 #4440	1	1
4441	17	46,047,930	46,049,273	1,343	1	9.31	13.738	17	20	1	1	1	CDK5RAP3	172	in gene	ActReg chr17 #4441	0	1
4442	17	46,124,825	46,125,785	960	2	10.567	12.933	19	18	1	1	2	COPZ2, NFE2L1	-10153, -381	upstream, upstream	ActReg chr17 #4442	1	1
4443	17	46,178,220	46,179,131	911	1	10.75	9.393	18	15	1	2	2	CBX1, SNX11	208, -6245	in gene, upstream	ActReg chr17 #4443	1	0
4444	17	46,184,413	46,185,446	1,033	1	6.485	10.121	9	14	1	2	2	CBX1, SNX11	-6046, 9	upstream, in gene	ActReg chr17 #4444	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4445	17	46,687,586	46,688,390	804	2	10.8	10	18	16	1	2	4	hCG_2042068, HOXB6, HOXB7, HOXB8	20165, -5654, 395, 4313	downstream, upstream, in gene, downstream	ActReg chr17 #4445	1	1
4446	17	46,800,850	46,801,605	755	1	11.5	9.208	20	19	3	3	4	PRAC, C17orf93, MIR3185, HOXB13	-1345, 685, 610, 4884	upstream, in gene, downstream, downstream	ActReg chr17 #4446	1	0
4447	17	47,021,914	47,022,711	797	1	10.92	12.44	15	20	1	1	1	SNF8	-158	upstream	ActReg chr17 #4447	0	1
4448	17	47,049,526	47,050,261	735	1	7.783	11.609	11	21	0	1	1	GIP	-3,938	upstream	ActReg chr17 #4448	0	1
4449	17	47,269,172	47,270,211	1,039	2	12.727	12.515	26	21	1	0	0				ActReg chr17 #4449	1	1
4450	17	47,337,680	47,338,560	880	1	4.536	12	10	18	1	0	1	FLJ40194	12,515	downstream	ActReg chr17 #4450	0	1
4451	17	47,784,938	47,786,086	1,148	2	22.333	25.194	48	56	0	1	2	SLC35B1, FAM117A	-230, 56006	upstream, downstream	ActReg chr17 #4451	1	1
4452	17	47,865,851	47,866,834	983	1	9.731	13.516	15	21	1	1	1	MYST2	271	in gene	ActReg chr17 #4452	0	1
4453	17	48,004,052	48,004,787	735	2	11.391	11.391	20	22	0	0	0				ActReg chr17 #4453	1	1
4454	17	48,104,644	48,106,241	1,597	1	8.98	13.72	18	23	0	0	0				ActReg chr17 #4454	0	1
4455	17	48,123,821	48,124,838	1,017	1	4.875	10.688	10	15	0	0	2	LOC284080, ITGA3	8774, -9011	downstream, upstream	ActReg chr17 #4455	0	1
4456	17	48,172,177	48,173,532	1,355	2	9	14.833	24	30	1	1	2	ITGA3, PDK2	39514, 158	downstream, in gene	ActReg chr17 #4456	1	1
4457	17	48,228,429	48,229,891	1,462	2	12.13	11.152	30	27	1	1	1	PPP1R9B	-1,283	upstream	ActReg chr17 #4457	1	1
4458	17	48,474,507	48,475,399	892	2	13.857	14	29	24	1	1	1	LRRC59	-39	upstream	ActReg chr17 #4458	1	1
4459	17	48,555,749	48,556,709	960	2	20.533	23.867	55	53	1	1	3	ACSF2, CHAD, RSAD1	52710, -10002, 39	downstream, upstream, in gene	ActReg chr17 #4459	1	1
4460	17	48,559,678	48,560,360	682	2	12.773	11.364	29	26	0	0	2	ACSF2, RSAD1	56500, 3829	downstream, in gene	ActReg chr17 #4460	1	1
4461	17	48,716,004	48,717,114	1,110	1	9.029	15.029	13	23	0	0	1	ABCC3	4,341	in gene	ActReg chr17 #4461	0	1
4462	17	48,796,763	48,797,495	732	1	8.261	10.783	11	16	1	1	1	LUC7L3	203	in gene	ActReg chr17 #4462	0	1
4463	17	48,943,317	48,944,262	945	1	7.414	11.433	15	18	1	2	2	TOB1, LOC400604	-2376, -108	upstream, upstream	ActReg chr17 #4463	0	1
4464	17	48,970,598	48,971,413	815	1	9.417	13.2	19	23	0	0	0				ActReg chr17 #4464	0	1
4465	17	49,010,632	49,011,298	666	1	12	9.238	20	13	0	0	1	LOC100506609	11,109	downstream	ActReg chr17 #4465	1	0
4466	17	49,230,704	49,231,528	824	1	11.308	15.731	23	31	1	2	2	NME1-NME2, NME1	196, 196	in gene, in gene	ActReg chr17 #4466	0	1
4467	17	49,243,545	49,244,906	1,361	1	8.233	11.93	13	20	1	1	4	NME1-NME2, NME1, NME2, MBTD1	13305, 13305, 1334, 93202	in gene, downstream, in gene, downstream	ActReg chr17 #4467	0	1
4468	17	49,337,182	49,338,077	895	2	20.321	16.071	46	40	1	2	2	MBTD1, UTP18	-202, -268	upstream, upstream	ActReg chr17 #4468	1	1
4469	17	49,430,035	49,431,158	1,123	1	6.943	10.714	12	15	0	0	0				ActReg chr17 #4469	0	1
4470	17	50,238,211	50,238,738	527	1	6.875	11.188	12	21	0	1	1	CA10	-1,097	upstream	ActReg chr17 #4470	0	1
4471	17	53,239,401	53,240,084	683	2	10.667	11.238	21	19	0	0	1	STXBP4	193,616	in gene	ActReg chr17 #4471	1	1
4472	17	53,535,811	53,536,803	992	2	11.355	10.323	18	16	0	0	0				ActReg chr17 #4472	1	1
4473	17	54,397,857	54,398,304	447	1	3	10.357	4	15	0	0	1	ANKFN1	167,244	in gene	ActReg chr17 #4473	0	1
4474	17	54,990,620	54,991,823	1,203	1	8.921	11.684	12	17	1	1	1	TRIM25	188	in gene	ActReg chr17 #4474	0	1
4475	17	55,162,022	55,162,526	504	1	9	13.667	12	23	1	1	1	AKAP1	-279	upstream	ActReg chr17 #4475	0	1
4476	17	55,288,899	55,289,514	615	1	7.526	10.737	11	16	0	0	0				ActReg chr17 #4476	0	1
4477	17	55,557,896	55,558,507	611	1	8.368	11.21	14	17	0	0	1	MSI2	224,270	in gene	ActReg chr17 #4477	0	1
4478	17	55,926,952	55,928,139	1,187	2	28.108	31.838	92	88	1	1	1	MRPS23	-146	upstream	ActReg chr17 #4478	1	1
4479	17	56,013,125	56,013,807	682	1	13.048	5.762	25	9	0	0	0				ActReg chr17 #4479	1	0
4480	17	56,083,763	56,085,378	1,615	3	10.451	11.961	20	20	1	1	1	SFRS1	137	in gene	ActReg chr17 #4480	1	1
4481	17	56,190,254	56,190,862	608	1	10.947	6.421	15	9	0	0	0				ActReg chr17 #4481	1	0
4482	17	56,197,351	56,198,149	798	2	16.4	14.56	35	29	0	0	0				ActReg chr17 #4482	1	1
4483	17	56,249,547	56,250,178	631	1	4.7	10.3	10	20	0	0	1	OR4D2	2,845	downstream	ActReg chr17 #4483	0	1
4484	17	56,296,182	56,297,184	1,002	2	10.312	13.531	17	26	1	1	1	MKS1	283	in gene	ActReg chr17 #4484	1	1
4485	17	56,429,120	56,430,455	1,335	2	8.762	10.976	18	19	1	1	3	LOC100506779, SUPT4H1, RNF43	26976, -224, 65144	in gene, upstream, downstream	ActReg chr17 #4485	1	1
4486	17	56,708,893	56,709,801	908	2	13.172	10.138	23	18	0	0	1	TEX14	60,069	in gene	ActReg chr17 #4486	1	1
4487	17	56,736,438	56,737,152	714	2	11.478	12.348	23	22	1	0	1	TEX14	32,621	in gene	ActReg chr17 #4487	1	1
4488	17	56,743,765	56,744,631	866	1	8.222	12.037	17	19	0	0	1	TEX14	25,218	in gene	ActReg chr17 #4488	0	1
4489	17	56,756,613	56,757,497	884	2	10.444	12	21	22	0	0	1	TEX14	12,361	in gene	ActReg chr17 #4489	1	1
4490	17	56,832,618	56,833,410	792	2	11.76	13.24	20	22	1	1	1	PPM1E	-218	upstream	ActReg chr17 #4490	1	1
4491	17	57,183,311	57,183,729	418	1	10.769	5.385	16	8	1	2	3	TRIM37, LOC100506847, SKA2	746, -331, 49280	in gene, upstream, downstream	ActReg chr17 #4491	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4492	17	57,233,797	57,234,238	441	1	5.231	11.538	7	13	0	3	3	SKA2, MIR301A, PRR11	-1217, -5435, 1157	upstream, upstream, in gene	ActReg chr17 #4492	0	1
4493	17	57,297,741	57,298,550	809	1	7.24	10.44	9	14	1	1	2	C17orf71, GDPD1	10774, 317	downstream, in gene	ActReg chr17 #4493	0	1
4494	17	57,432,307	57,433,249	942	1	10.367	11.3	16	16	0	0	1	YPEL2	23,725	in gene	ActReg chr17 #4494	0	1
4495	17	57,642,496	57,643,320	824	2	10.962	12.885	19	25	1	1	1	DHX40	22	in gene	ActReg chr17 #4495	1	1
4496	17	57,696,364	57,697,188	824	2	12.846	11.923	24	16	1	1	1	CLTC	-274	upstream	ActReg chr17 #4496	1	1
4497	17	57,920,405	57,921,224	819	1	10.154	7.385	17	13	0	1	2	TMEM49, MIR21	135951, 2187	downstream, downstream	ActReg chr17 #4497	1	0
4498	17	57,922,957	57,923,422	465	1	11	5.857	17	8	0	0	2	TMEM49, MIR21	138326, 4562	downstream, downstream	ActReg chr17 #4498	1	0
4499	17	57,930,546	57,931,147	601	1	5.789	9.211	10	15	0	0	1	TUBD1	39,460	downstream	ActReg chr17 #4499	0	1
4500	17	57,970,205	57,970,891	686	1	10.954	13.546	23	24	1	2	2	TUBD1, RPS6KB1	-242, 105	upstream, in gene	ActReg chr17 #4500	0	1
4501	17	58,216,796	58,217,785	989	2	11.452	16.484	28	33	1	0	1	CA4	-10,012	upstream	ActReg chr17 #4501	1	1
4502	17	58,218,197	58,219,305	1,108	1	8.176	11.971	15	19	1	0	1	CA4	-8,551	upstream	ActReg chr17 #4502	0	1
4503	17	58,468,631	58,470,259	1,628	1	8.157	11.412	15	17	1	1	1	USP32	141	in gene	ActReg chr17 #4503	0	1
4504	17	58,602,961	58,603,988	1,027	2	11.531	9.719	18	17	1	1	1	APPBP2	106	in gene	ActReg chr17 #4504	1	1
4505	17	58,676,933	58,678,259	1,326	1	7.878	10.854	14	18	1	1	1	PPM1D	42	in gene	ActReg chr17 #4505	0	1
4506	17	59,328,298	59,328,915	617	1	6.421	12.21	8	17	0	0	1	BCAS3	573,434	in gene	ActReg chr17 #4506	0	1
4507	17	59,389,525	59,390,156	631	1	11.15	10.9	14	18	0	0	1	BCAS3	634,668	in gene	ActReg chr17 #4507	0	1
4508	17	59,398,599	59,399,206	607	2	13.105	10.389	22	18	0	0	1	BCAS3	643,730	in gene	ActReg chr17 #4508	1	1
4509	17	59,489,460	59,490,080	620	1	7.95	12	11	17	1	2	3	LOC645722, TBX2, C17orf82	-854, 12513, 658	upstream, downstream, in gene	ActReg chr17 #4509	0	1
4510	17	59,887,134	59,887,705	571	1	5.222	10	8	19	0	0	1	BRIP1	53,501	in gene	ActReg chr17 #4510	0	1
4511	17	60,004,690	60,005,555	865	2	12.815	10.667	23	16	1	1	1	INTS2	255	in gene	ActReg chr17 #4511	1	1
4512	17	60,142,863	60,143,550	687	2	10.952	11.333	20	20	1	1	1	MED13	-563	upstream	ActReg chr17 #4512	1	1
4513	17	60,501,021	60,501,610	589	1	5.263	9.947	10	17	1	1	2	EFCAB3, METTL2A	53736, 69	downstream, in gene	ActReg chr17 #4513	0	1
4514	17	60,704,428	60,705,294	866	1	10.444	10.667	15	13	1	1	1	MRC2	99	in gene	ActReg chr17 #4514	1	0
4515	17	60,771,495	60,772,504	1,009	2	11.29	13.258	18	21	0	0	2	MRC2, MARCH10	67237, 113706	downstream, downstream	ActReg chr17 #4515	1	1
4516	17	60,839,202	60,839,877	675	1	6	11.286	8	19	0	0	1	10-Mar	46,166	in gene	ActReg chr17 #4516	0	1
4517	17	60,869,411	60,869,983	572	1	10.235	15.882	15	26	0	0	1	10-Mar	16,008	in gene	ActReg chr17 #4517	0	1
4518	17	61,352,548	61,353,288	740	2	10.174	11.13	20	24	0	0	1	TANC2	266,020	in gene	ActReg chr17 #4518	1	1
4519	17	61,433,453	61,434,094	641	1	11.05	11.45	21	21	0	0	1	TANC2	346,875	in gene	ActReg chr17 #4519	1	0
4520	17	61,538,074	61,538,600	526	1	7.471	11.823	12	19	0	0	0				ActReg chr17 #4520	0	1
4521	17	61,627,084	61,628,256	1,172	2	10.865	10.919	17	15	1	1	2	KCNH6, DCAF7	26975, -152	downstream, upstream	ActReg chr17 #4521	1	1
4522	17	61,677,796	61,678,543	747	2	12.957	10.348	23	20	1	1	2	DCAF7, TACO1	50347, -62	downstream, upstream	ActReg chr17 #4522	1	1
4523	17	61,850,637	61,851,245	608	1	12.105	12.842	20	19	1	2	2	CCDC47, DDX42	147, -626	in gene, upstream	ActReg chr17 #4523	1	0
4524	17	61,851,334	61,851,834	500	1	10.867	10.667	16	13	1	2	2	CCDC47, DDX42	-496, 17	upstream, in gene	ActReg chr17 #4524	1	0
4525	17	61,904,606	61,905,448	842	1	8.556	13.148	16	22	1	2	4	DDX42, FTSJ3, PSMC5, SMARCD2	53460, 4, 217, 15324	downstream, in gene, in gene, downstream	ActReg chr17 #4525	0	1
4526	17	61,919,937	61,920,529	592	2	12.333	17.222	23	33	1	1	1	SMARCD2	118	in gene	ActReg chr17 #4526	1	1
4527	17	62,051,307	62,052,281	974	2	11.4	12.367	19	17	0	1	1	SCN4A	-1,516	upstream	ActReg chr17 #4527	1	1
4528	17	62,222,845	62,224,251	1,406	2	10.909	15.341	23	27	1	2	3	SNORD104, SNORA76, TEX2	110, -151, 117105	downstream, upstream, downstream	ActReg chr17 #4528	1	1
4529	17	62,340,469	62,341,363	894	2	19.964	26.393	57	71	1	1	1	TEX2	-263	upstream	ActReg chr17 #4529	1	1
4530	17	62,403,371	62,404,196	825	1	8.962	11.231	12	18	0	2	2	LOC100506961, PECAM1	-5742, -2578	upstream, upstream	ActReg chr17 #4530	0	1
4531	17	62,492,926	62,493,640	714	1	5.565	12.261	10	19	1	1	3	POLG2, DDX5, CCDC45	-99, 9201, -9875	upstream, downstream, upstream	ActReg chr17 #4531	0	1
4532	17	62,502,719	62,503,722	1,003	1	7.188	12.969	13	24	1	2	3	POLG2, DDX5, CCDC45	-10036, -736, 62	upstream, upstream, in gene	ActReg chr17 #4532	0	1
4533	17	62,675,815	62,676,380	565	1	12.529	9.588	18	13	0	0	0				ActReg chr17 #4533	1	0
4534	17	62,702,925	62,703,745	820	1	6.538	11.5	14	19	0	0	0				ActReg chr17 #4534	0	1
4535	17	62,971,228	62,972,370	1,142	2	12.833	12.528	25	19	1	0	0				ActReg chr17 #4535	1	1
4536	17	62,986,962	62,987,627	665	1	8.476	14.238	15	26	0	0	0				ActReg chr17 #4536	0	1
4537	17	62,988,404	62,989,036	632	2	11.75	10.6	25	20	0	0	0				ActReg chr17 #4537	1	1
4538	17	63,074,440	63,075,004	564	1	9.118	13.118	13	20	0	0	0				ActReg chr17 #4538	0	1
4539	17	63,084,775	63,085,284	509	1	9.5	11.25	16	15	0	0	0				ActReg chr17 #4539	1	0
4540	17	63,250,238	63,250,787	551	1	7.889	11.222	13	23	0	0	0				ActReg chr17 #4540	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4541	17	64,271,637	64,272,325	688	2	11.273	10.636	24	24	0	0	0				ActReg chr17 #4541	1	1
4542	17	64,489,348	64,490,339	991	1	11.839	8.774	18	16	0	0	1	PRKCA	190,917	in gene	ActReg chr17 #4542	1	0
4543	17	64,505,338	64,505,941	603	1	8.316	10.158	12	15	0	0	1	PRKCA	206,713	in gene	ActReg chr17 #4543	0	1
4544	17	64,536,074	64,536,879	805	2	11.16	11.2	18	26	0	0	1	PRKCA	237,550	in gene	ActReg chr17 #4544	1	1
4545	17	64,825,532	64,826,184	652	1	10.952	15.571	19	35	0	0	0				ActReg chr17 #4545	0	1
4546	17	65,362,172	65,362,918	746	1	10.875	13.417	21	24	1	1	1	PSMD12	176	in gene	ActReg chr17 #4546	0	1
4547	17	65,713,659	65,714,418	759	1	10.042	12.667	19	21	1	2	2	LOC100507049, NOL11	-294, -23	upstream, upstream	ActReg chr17 #4547	0	1
4548	17	65,821,277	65,821,785	508	1	9.938	8.438	16	11	1	1	1	BPTF	-249	upstream	ActReg chr17 #4548	1	0
4549	17	66,015,761	66,016,537	776	2	14.042	14.542	24	29	1	0	0				ActReg chr17 #4549	1	1
4550	17	66,031,605	66,032,509	904	1	9.143	12	14	22	1	1	1	KPNA2	209	in gene	ActReg chr17 #4550	0	1
4551	17	66,376,987	66,377,802	815	2	9.962	10	16	19	0	0	1	ARSG	122,071	in gene	ActReg chr17 #4551	1	1
4552	17	66,395,909	66,396,943	1,034	2	11.469	10.719	18	16	0	0	1	ARSG	141,103	in gene	ActReg chr17 #4552	1	1
4553	17	66,431,723	66,432,585	862	1	10.407	7.037	16	12	0	0	1	WIPI1	21,499	in gene	ActReg chr17 #4553	1	0
4554	17	66,507,945	66,509,066	1,121	2	11.314	15.114	21	26	1	1	1	PRKAR1A	395	in gene	ActReg chr17 #4554	1	1
4555	17	66,690,894	66,691,918	1,024	2	10.625	12.062	18	17	0	0	0				ActReg chr17 #4555	1	1
4556	17	66,694,133	66,694,709	576	1	10.389	4.444	15	7	0	0	0				ActReg chr17 #4556	1	0
4557	17	66,905,089	66,905,582	493	1	9	9.6	14	14	0	0	1	ABCA8	46,198	in gene	ActReg chr17 #4557	0	1
4558	17	67,535,840	67,536,234	394	1	7.154	10.077	11	15	0	0	1	MAP2K6	125,199	in gene	ActReg chr17 #4558	0	1
4559	17	67,759,453	67,760,273	820	2	12.308	11.962	29	30	0	0	0				ActReg chr17 #4559	1	1
4560	17	67,866,161	67,866,753	592	1	10.368	10.79	16	17	0	0	0				ActReg chr17 #4560	0	1
4561	17	68,165,019	68,165,468	449	1	8.357	10.929	11	17	1	2	2	FLJ36644, KCNJ2	300, -433	in gene, upstream	ActReg chr17 #4561	0	1
4562	17	68,192,594	68,193,300	706	2	12.682	14.182	27	27	0	0	0				ActReg chr17 #4562	1	1
4563	17	68,401,727	68,402,312	585	1	12.158	9	22	12	0	0	0				ActReg chr17 #4563	1	0
4564	17	69,067,996	69,068,445	449	1	10.357	11.571	16	16	0	0	0				ActReg chr17 #4564	0	1
4565	17	69,408,900	69,409,403	503	1	5.2	9.667	9	17	0	0	0				ActReg chr17 #4565	0	1
4566	17	69,437,139	69,437,663	524	1	10.562	12.375	15	20	0	0	0				ActReg chr17 #4566	0	1
4567	17	70,026,435	70,026,943	508	1	6.8	10.067	9	15	0	0	0				ActReg chr17 #4567	0	1
4568	17	70,461,597	70,462,116	519	1	9.706	5.824	18	10	0	0	1	LOC100499467	127,087	in gene	ActReg chr17 #4568	1	0
4569	17	70,567,912	70,568,972	1,060	1	11.03	12.061	15	17	0	0	1	LOC100499467	20,501	in gene	ActReg chr17 #4569	0	1
4570	17	70,611,641	70,612,391	750	1	11.417	12.083	19	21	0	0	1	FLJ26484	24,595	in gene	ActReg chr17 #4570	0	1
4571	17	70,613,564	70,615,005	1,441	1	10.556	13.756	17	24	0	0	1	FLJ26484	22,327	in gene	ActReg chr17 #4571	0	1
4572	17	70,627,460	70,628,958	1,498	1	11.717	12.761	18	25	0	0	1	FLJ26484	8,402	in gene	ActReg chr17 #4572	0	1
4573	17	70,651,827	70,652,952	1,125	2	11.8	10.314	19	21	0	0	1	SLC39A11	436,464	in gene	ActReg chr17 #4573	1	1
4574	17	70,657,501	70,658,585	1,084	2	10.719	12.5	20	21	0	0	1	SLC39A11	430,810	in gene	ActReg chr17 #4574	1	1
4575	17	70,680,071	70,680,955	884	2	12	11.296	19	16	0	0	1	SLC39A11	408,340	in gene	ActReg chr17 #4575	1	1
4576	17	70,720,537	70,721,358	821	1	7	9.846	11	14	0	0	1	SLC39A11	367,906	in gene	ActReg chr17 #4576	0	1
4577	17	71,189,125	71,189,663	538	1	7.75	12.25	12	20	1	1	1	COG1	221	in gene	ActReg chr17 #4577	0	1
4578	17	71,287,715	71,288,651	936	1	10.897	12.448	17	20	0	0	1	CDC42EP4	19,960	in gene	ActReg chr17 #4578	0	1
4579	17	72,199,359	72,200,235	876	2	20.607	24.036	53	71	1	1	3	RPL38, MGC16275, TTYH2	2, 9663, -9899	in gene, downstream, upstream	ActReg chr17 #4579	1	1
4580	17	72,606,001	72,606,731	730	1	7.217	13.13	14	20	0	0	1	CD300E	13,435	downstream	ActReg chr17 #4580	0	1
4581	17	72,667,033	72,668,034	1,001	2	26.125	29.125	79	79	1	1	1	RAB37	277	in gene	ActReg chr17 #4581	1	1
4582	17	72,772,205	72,772,874	669	1	7.905	12.095	15	23	1	2	3	SLC9A3R1, NAT9, TMEM104	27776, -69, -83	downstream, upstream, upstream	ActReg chr17 #4582	0	1
4583	17	72,978,069	72,978,984	915	1	8.759	10.69	13	17	1	1	2	C17orf28, CDR2L	-9626, -5201	upstream, upstream	ActReg chr17 #4583	0	1
4584	17	73,008,202	73,009,258	1,056	2	11.758	12.182	19	22	1	1	2	CDR2L, ICT1	25003, -50	downstream, upstream	ActReg chr17 #4584	1	1
4585	17	73,029,645	73,031,660	2,015	2	14.762	14.444	31	24	1	0	1	ATP5H	12,422	downstream	ActReg chr17 #4585	1	1
4586	17	73,042,738	73,043,418	680	1	10.25	10.191	15	15	1	2	2	ATP5H, KCTD2	-4, -201	upstream, upstream	ActReg chr17 #4586	0	1
4587	17	73,120,169	73,120,949	780	1	9.542	11.5	14	18	0	0	2	ARMC7, NT5C	14477, 7318	in gene, downstream	ActReg chr17 #4587	0	1
4588	17	73,127,412	73,128,037	625	1	8.15	12.3	12	19	1	1	3	ARMC7, NT5C, HN1	21642, 153, 23051	downstream, in gene, downstream	ActReg chr17 #4588	0	1
4589	17	73,201,020	73,202,403	1,383	2	18.932	18.454	53	55	1	1	1	NUP85	114	in gene	ActReg chr17 #4589	1	1
4590	17	73,257,055	73,258,322	1,267	2	10.425	11.95	18	18	1	2	4	GGA3, MRPS7, MIF4GD, LOC100287042	756, -61, 9615, -9692	in gene, upstream, downstream, upstream	ActReg chr17 #4590	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4591	17	73,285,009	73,286,041	1,032	2	12.875	9.656	23	14	1	1	1	SLC25A19	5	in gene	ActReg chr17 #4591	1	1
4592	17	73,511,675	73,513,421	1,746	2	13.873	12.982	28	38	1	2	3	CASKIN2, TSEN54, LLGL2	-921, -61, -9235	upstream, upstream, upstream	ActReg chr17 #4592	1	1
4593	17	73,663,021	73,663,700	679	1	11.238	12.571	18	22	1	2	2	RECQL5, SAP30BP	-91, -39	upstream, upstream	ActReg chr17 #4593	0	1
4594	17	73,687,385	73,688,375	990	1	7.806	11.484	11	19	0	0	1	SAP30BP	24,481	in gene	ActReg chr17 #4594	0	1
4595	17	73,775,563	73,776,176	613	2	11.263	11.421	17	21	1	2	2	H3F3B, UNK	-9, -4812	upstream, upstream	ActReg chr17 #4595	1	1
4596	17	73,780,458	73,781,680	1,222	2	15.105	13.842	26	22	1	2	2	H3F3B, UNK	-5209, 388	upstream, in gene	ActReg chr17 #4596	1	1
4597	17	73,851,342	73,852,201	859	1	11.222	9.407	17	15	1	1	1	WBP2	-270	upstream	ActReg chr17 #4597	1	0
4598	17	73,871,624	73,873,092	1,468	1	6.152	12.978	10	20	0	1	1	TRIM47	2,298	in gene	ActReg chr17 #4598	0	1
4599	17	73,873,274	73,874,768	1,494	1	9.045	11.34	20	18	1	1	1	TRIM47	635	in gene	ActReg chr17 #4599	0	1
4600	17	73,936,674	73,937,454	780	1	9.292	11	16	17	1	1	2	FBF1, ACOX1	55, 38451	in gene, downstream	ActReg chr17 #4600	0	1
4601	17	73,974,623	73,975,400	777	1	7.32	9.8	11	14	1	2	2	ACOX1, C17orf106	504, -290	in gene, upstream	ActReg chr17 #4601	0	1
4602	17	74,068,189	74,068,994	805	2	14.154	14.615	29	34	1	3	4	SRP68, GALR2, ZACN, EXOC7	16, -2301, -6672, 31277	in gene, upstream, upstream, downstream	ActReg chr17 #4602	1	1
4603	17	74,236,819	74,237,440	621	2	10.2	9.8	20	18	1	1	1	RNF157	-739	upstream	ActReg chr17 #4603	1	1
4604	17	74,247,931	74,249,557	1,626	2	9.608	14.569	37	44	0	0	0				ActReg chr17 #4604	1	1
4605	17	74,553,332	74,554,484	1,152	2	9.889	9.583	18	17	2	4	6	LOC100507230, LOC100507246, SNORD1C, SNORD1B, SNORD1A, ST6GALNAC2	12208, 62, -966, -3282, -3807, 28237	downstream, in gene, upstream, upstream, upstream, downstream	ActReg chr17 #4605	1	1
4606	17	74,581,730	74,582,321	591	1	9.889	10.944	14	16	1	1	1	ST6GALNAC2	120	in gene	ActReg chr17 #4606	0	1
4607	17	74,721,906	74,722,787	881	1	9.857	13.536	16	24	1	2	4	JMJD6, C17orf95, SFRS2, MIR636	535, -604, 11096, 10284	in gene, upstream, downstream, downstream	ActReg chr17 #4607	0	1
4608	17	74,787,409	74,787,953	544	1	5.882	10.941	10	21	0	0	0				ActReg chr17 #4608	0	1
4609	17	74,868,377	74,869,216	839	2	11.815	12.148	20	25	0	0	1	MGAT5B	3,998	in gene	ActReg chr17 #4609	1	1
4610	17	74,905,828	74,906,729	901	1	9.071	13.25	22	25	0	0	1	MGAT5B	41,480	in gene	ActReg chr17 #4610	0	1
4611	17	75,084,301	75,085,174	873	2	18.296	19.926	38	43	1	2	2	C17orf66, SCARNA16	12, -652	in gene, upstream	ActReg chr17 #4611	1	1
4612	17	75,242,856	75,243,457	601	1	11.632	10.79	19	19	1	0	0				ActReg chr17 #4612	1	0
4613	17	75,250,768	75,251,913	1,145	2	14.083	12.194	25	24	1	0	0				ActReg chr17 #4613	1	1
4614	17	75,281,600	75,282,563	963	1	7.968	12.742	15	24	0	0	1	9-Sep	4,589	in gene	ActReg chr17 #4614	0	1
4615	17	75,282,662	75,283,713	1,051	1	8.485	10.758	14	14	0	0	1	9-Sep	5,695	in gene	ActReg chr17 #4615	0	1
4616	17	75,283,812	75,284,737	925	1	8.793	10.966	13	18	0	0	1	9-Sep	6,782	in gene	ActReg chr17 #4616	0	1
4617	17	75,318,422	75,319,871	1,449	2	11.311	12.044	16	20	0	0	1	9-Sep	41,654	in gene	ActReg chr17 #4617	1	1
4618	17	75,361,554	75,362,267	713	1	13.954	11.409	22	21	0	0	1	9-Sep	84,418	in gene	ActReg chr17 #4618	1	0
4619	17	75,421,765	75,422,760	995	1	10.645	9.548	17	14	0	0	1	9-Sep	144,770	in gene	ActReg chr17 #4619	1	0
4620	17	75,451,210	75,452,722	1,512	1	9.894	12.277	19	19	0	0	2	SEPT9, LOC100507304	174474, 11180	in gene, downstream	ActReg chr17 #4620	0	1
4621	17	75,883,621	75,884,418	797	1	7.48	11.48	14	20	1	1	1	FLJ45079	-3,850	upstream	ActReg chr17 #4621	0	1
4622	17	76,182,788	76,183,559	771	1	9.75	18.75	23	44	1	2	2	TK1, AFMID	112, -225	in gene, upstream	ActReg chr17 #4622	0	1
4623	17	76,209,930	76,210,961	1,031	2	12.562	15.125	23	28	1	1	3	AFMID, BIRC5, EPR1	27047, 168, 10338	downstream, in gene, in gene	ActReg chr17 #4623	1	1
4624	17	76,249,914	76,250,925	1,011	2	11.812	11.5	19	22	1	0	0				ActReg chr17 #4624	1	1
4625	17	76,290,318	76,291,282	964	1	7.333	11.767	10	17	0	0	0				ActReg chr17 #4625	0	1
4626	17	76,356,618	76,357,255	637	1	8.65	11.75	12	21	1	1	1	SOCS3	-778	upstream	ActReg chr17 #4626	0	1
4627	17	76,360,865	76,361,423	558	1	11.823	11.235	19	19	0	1	1	SOCS3	-4,986	upstream	ActReg chr17 #4627	0	1
4628	17	76,462,563	76,463,680	1,117	1	5.914	11.514	13	21	0	0	1	DNAH17	110,355	in gene	ActReg chr17 #4628	0	1
4629	17	76,835,988	76,837,669	1,681	2	23.472	25.358	98	101	1	1	1	USP36	141	in gene	ActReg chr17 #4629	1	1
4630	17	76,879,037	76,880,668	1,631	1	9.431	12.451	15	17	0	0	1	TIMP2	41,620	in gene	ActReg chr17 #4630	0	1
4631	17	76,929,207	76,929,954	747	1	8.206	14.042	12	21	0	0	1	TIMP2	-8,108	upstream	ActReg chr17 #4631	0	1
4632	17	77,188,378	77,189,177	799	1	7.48	14.52	12	26	0	0	1	hCG_1776007	289,786	in gene	ActReg chr17 #4632	0	1
4633	17	77,290,296	77,291,115	819	2	11.577	16.154	25	31	0	0	1	hCG_1776007	187,858	in gene	ActReg chr17 #4633	1	1
4634	17	77,784,724	77,785,722	998	1	7.226	11.774	11	19	1	0	1	LOC100507425	10,826	downstream	ActReg chr17 #4634	0	1
4635	17	78,037,755	78,038,618	863	2	9.704	10.889	24	19	0	0	1	CCDC40	27,751	in gene	ActReg chr17 #4635	1	1
4636	17	78,193,278	78,194,353	1,075	1	6.441	10.794	11	22	1	2	2	SGSH, SLC26A11	384, -385	in gene, upstream	ActReg chr17 #4636	0	1
4637	17	78,235,047	78,235,610	563	1	6.765	9.941	9	15	1	1	2	SLC26A11, RNF213	41128, 661	downstream, in gene	ActReg chr17 #4637	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4638	17	78,388,520	78,390,045	1,525	2	10.021	10.957	19	20	1	3	3	LOC100294362, FLJ35220, LOC100507440	-314, 315, -1935	upstream, in gene, upstream	ActReg chr17 #4638	1	1
4639	17	78,414,717	78,415,447	730	1	8.217	13	12	27	0	0	1	FLJ35220	26,115	downstream	ActReg chr17 #4639	0	1
4640	17	78,428,103	78,429,141	1,038	1	7.844	11.719	12	18	1	0	0				ActReg chr17 #4640	0	1
4641	17	78,518,360	78,519,397	1,037	2	10.788	15.121	25	26	1	1	1	RPTOR	253	in gene	ActReg chr17 #4641	1	1
4642	17	78,623,053	78,624,123	1,070	1	6.455	10.879	11	17	0	0	1	RPTOR	104,963	in gene	ActReg chr17 #4642	0	1
4643	17	78,806,670	78,807,427	757	1	6.208	12.75	10	19	0	0	1	RPTOR	288,423	in gene	ActReg chr17 #4643	0	1
4644	17	78,847,310	78,847,967	657	1	11.8	15.85	22	25	0	0	1	RPTOR	329,013	in gene	ActReg chr17 #4644	0	1
4645	17	78,865,896	78,866,627	731	1	6.87	13.478	10	20	0	0	1	RPTOR	347,636	in gene	ActReg chr17 #4645	0	1
4646	17	79,367,552	79,368,314	762	2	10.417	9.792	21	20	1	2	2	LOC100507520, BAHCC1	-3246, -5607	upstream, upstream	ActReg chr17 #4646	1	1
4647	17	79,368,561	79,369,124	563	1	10.778	6.611	16	9	1	2	2	LOC100507520, BAHCC1	-4155, -4698	upstream, upstream	ActReg chr17 #4647	1	0
4648	17	79,369,738	79,370,720	982	1	7.968	10.484	16	16	1	2	2	LOC100507520, BAHCC1	-5542, -3311	upstream, upstream	ActReg chr17 #4648	0	1
4649	17	79,478,832	79,480,005	1,173	1	5.703	12.243	14	19	1	1	2	LOC100507545, ACTG1	25108, 409	in gene, in gene	ActReg chr17 #4649	0	1
4650	17	79,480,128	79,480,849	721	1	8.652	12.13	15	17	1	1	2	LOC100507545, ACTG1	26178, -661	in gene, upstream	ActReg chr17 #4650	0	1
4651	17	79,633,286	79,634,152	866	1	7.556	13.185	15	21	1	2	3	PDE6G, C17orf90, CCDC137	-10112, -101, -42	upstream, upstream, upstream	ActReg chr17 #4651	0	1
4652	17	79,650,505	79,651,640	1,135	2	10.971	10.4	20	17	1	2	3	CCDC137, ARL16, HGS	17311, -118, 52	downstream, upstream, in gene	ActReg chr17 #4652	1	1
4653	17	79,669,790	79,670,854	1,064	2	12.059	11.147	21	21	1	1	3	HGS, MRPL12, SLC25A10	19302, -85, -9049	downstream, upstream, upstream	ActReg chr17 #4653	1	1
4654	17	79,818,575	79,819,404	829	1	8.577	11.385	13	24	1	1	2	P4HB, ARHGDIA	-445, 10293	upstream, downstream	ActReg chr17 #4654	0	1
4655	17	79,824,744	79,825,655	911	1	5.25	12.036	8	18	0	1	2	P4HB, ARHGDIA	-6655, 4083	upstream, downstream	ActReg chr17 #4655	0	1
4656	17	79,829,126	79,830,646	1,520	2	16.319	15.447	41	40	1	1	1	ARHGDIA	-604	upstream	ActReg chr17 #4656	1	1
4657	17	79,885,472	79,886,022	550	2	10.778	14.778	21	25	1	2	4	SIRT7, MAFG, LOC92659, PYCR1	-9689, -159, 42, 9221	upstream, upstream, in gene, downstream	ActReg chr17 #4657	1	1
4658	17	79,961,245	79,962,072	827	2	11.192	11.923	18	19	1	0	1	ASPSCR1	26,232	in gene	ActReg chr17 #4658	1	1
4659	17	79,988,199	79,988,946	747	1	12.435	12.13	22	24	1	2	4	STRA13, LRRC45, RAC3, DCXR	-7799, 7292, -960, 7001	upstream, in gene, upstream, downstream	ActReg chr17 #4659	0	1
4660	17	79,994,710	79,995,780	1,070	2	9.529	11.206	21	16	1	1	4	LRRC45, RAC3, DCXR, RFNG	13965, 5713, 328, 14405	downstream, downstream, in gene, downstream	ActReg chr17 #4660	1	1
4661	17	80,054,703	80,055,583	880	1	9.926	8.593	15	14	1	1	2	FASN, CCDC57	963, 115546	in gene, downstream	ActReg chr17 #4661	1	0
4662	17	80,170,308	80,171,081	773	1	6.75	12.542	12	21	1	1	1	CCDC57	-5	upstream	ActReg chr17 #4662	0	1
4663	17	80,174,015	80,175,544	1,529	1	9.979	12	15	19	0	1	1	CCDC57	-4,090	upstream	ActReg chr17 #4663	0	1
4664	17	80,254,906	80,256,524	1,618	2	10.667	13.255	18	25	0	0	0				ActReg chr17 #4664	1	1
4665	17	80,376,207	80,376,797	590	2	13.833	15.778	25	31	1	3	3	C17orf101, HEXDC, LOC100505970	11, 250, -6872	in gene, in gene, upstream	ActReg chr17 #4665	1	1
4666	17	80,415,788	80,416,628	840	2	9.923	11.5	14	19	1	2	2	C17orf62, NARF	-7501, 148	upstream, in gene	ActReg chr17 #4666	1	1
4667	17	80,476,779	80,477,637	858	1	5	11.593	9	16	1	1	1	FOXK2	-386	upstream	ActReg chr17 #4667	0	1
4668	17	80,605,807	80,606,535	728	1	7.364	12.739	15	22	1	1	3	WDR45L, LOC100506019, RAB40B	240, 8586, 50427	in gene, downstream, downstream	ActReg chr17 #4668	0	1
4669	17	80,709,620	80,710,252	632	2	13.05	12.85	25	25	1	1	2	FN3K, TBCD	16484, -4	downstream, upstream	ActReg chr17 #4669	1	1
4670	17	80,943,837	80,944,439	602	1	8.5	10	14	16	0	0	1	B3GNTL1	65,548	in gene	ActReg chr17 #4670	0	1
4671	17	81,008,457	81,009,108	651	1	5.05	11.05	8	21	1	1	1	B3GNTL1	904	in gene	ActReg chr17 #4671	0	1
4672	18	267,774	268,310	536	1	8.471	12.118	13	19	1	1	1	THOC1	17	in gene	ActReg chr18 #4672	0	1
4673	18	657,790	658,446	656	1	6.476	11.238	10	20	1	2	3	CLUL1, C18orf56, TYMS	61120, 222, 514	downstream, in gene, in gene	ActReg chr18 #4673	0	1
4674	18	903,552	904,295	743	2	18.708	16.667	39	39	0	1	1	ADCYAP1	-1,021	upstream	ActReg chr18 #4674	1	1
4675	18	1,094,383	1,094,909	526	2	8.062	11.062	16	16	0	0	0				ActReg chr18 #4675	1	1
4676	18	2,571,271	2,571,804	533	1	12.062	13.688	19	22	1	2	2	METTL4, NDC80	-48, 27	upstream, in gene	ActReg chr18 #4676	0	1
4677	18	2,627,871	2,628,336	465	1	5.867	10.133	10	15	0	0	0				ActReg chr18 #4677	0	1
4678	18	2,655,688	2,656,507	819	1	6.458	9.44	10	16	1	2	2	LOC645158, SMCHD1	-2866, 211	upstream, in gene	ActReg chr18 #4678	0	1
4679	18	2,905,822	2,906,378	556	1	4.562	8.833	8	15	1	0	1	EMILIN2	59,072	in gene	ActReg chr18 #4679	0	1
4680	18	3,247,245	3,247,945	700	2	9.364	12.046	20	18	1	1	2	MYL12A, LOC100505577	67, 14250	in gene, downstream	ActReg chr18 #4680	1	1
4681	18	3,261,561	3,262,700	1,139	2	13.472	14.944	26	32	1	2	3	MYL12A, LOC100505577, MYL12B	14602, -285, 19	downstream, upstream, in gene	ActReg chr18 #4681	1	1
4682	18	3,297,097	3,297,848	751	2	21.13	23.174	50	56	0	0	0				ActReg chr18 #4682	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4683	18	3,448,028	3,448,630	602	1	10.263	4.737	18	7	1	0	1	TGIF1	36,257	in gene	ActReg chr18 #4683	1	0
4684	18	5,237,892	5,238,369	477	1	9.133	6.4	14	11	1	2	2	C18orf18, LOC339290	-102, 31	upstream, in gene	ActReg chr18 #4684	1	0
4685	18	8,608,988	8,609,615	627	2	10.65	7.65	17	11	1	1	1	RAB12	-142	upstream	ActReg chr18 #4685	1	1
4686	18	8,685,494	8,686,131	637	1	8.9	12.15	16	24	0	0	0				ActReg chr18 #4686	0	1
4687	18	8,705,579	8,705,860	281	1	2.625	10.667	4	15	1	0	0				ActReg chr18 #4687	0	1
4688	18	9,136,175	9,137,078	903	2	9.214	13.321	17	24	1	1	2	NDUFV2, ANKRD12	33998, -132	downstream, upstream	ActReg chr18 #4688	1	1
4689	18	9,913,905	9,914,255	350	1	10.182	9.818	15	13	1	1	1	VAPA	125	in gene	ActReg chr18 #4689	1	0
4690	18	11,688,963	11,689,378	415	1	7.385	10.692	10	16	1	1	1	GNAL	34	in gene	ActReg chr18 #4690	0	1
4691	18	11,851,035	11,851,710	675	1	11.762	8.095	17	12	1	1	2	GNAL, CHMP1B	162236, -17	in gene, upstream	ActReg chr18 #4691	1	0
4692	18	11,908,382	11,908,921	539	1	7.235	9.412	12	14	1	1	1	MPPE1	-10	upstream	ActReg chr18 #4692	0	1
4693	18	12,307,298	12,307,999	701	1	7.905	12.381	11	18	1	1	1	TUBB6	-609	upstream	ActReg chr18 #4693	0	1
4694	18	12,419,941	12,420,351	410	1	6.083	11.667	10	14	1	0	1	SLMO1	12,251	in gene	ActReg chr18 #4694	0	1
4695	18	12,702,333	12,703,261	928	2	10.552	15.552	24	29	1	2	2	CEP76, PSMG2	-94, -267	upstream, upstream	ActReg chr18 #4695	1	1
4696	18	12,991,209	12,991,719	510	1	8.875	10.125	13	13	1	1	2	SEH1L, CEP192	43481, 103	downstream, in gene	ActReg chr18 #4696	0	1
4697	18	13,726,186	13,726,991	805	1	8.4	14.84	15	28	1	2	2	C18orf19, RNMT	3, -116	in gene, upstream	ActReg chr18 #4697	0	1
4698	18	19,180,193	19,180,944	751	1	8.826	12.435	13	18	1	1	1	ESCO1	125	in gene	ActReg chr18 #4698	0	1
4699	18	19,191,806	19,192,703	897	2	24.571	30	75	75	1	1	1	SNRPD1	-6	upstream	ActReg chr18 #4699	1	1
4700	18	19,731,998	19,732,389	391	1	2.846	10.615	6	18	0	0	0				ActReg chr18 #4700	0	1
4701	18	20,065,545	20,066,221	676	2	11.905	8.19	23	17	0	0	0				ActReg chr18 #4701	1	1
4702	18	20,160,029	20,160,659	630	2	14.05	13.25	34	26	0	0	0				ActReg chr18 #4702	1	1
4703	18	21,017,658	21,018,124	466	1	4.667	9.733	8	16	1	1	1	C18orf45	34	in gene	ActReg chr18 #4703	0	1
4704	18	21,083,099	21,083,751	652	2	13.286	17.286	27	41	1	1	1	C18orf8	-37	upstream	ActReg chr18 #4704	1	1
4705	18	21,296,258	21,297,011	753	2	18.739	16.044	47	36	0	0	1	LAMA3	27,072	in gene	ActReg chr18 #4705	1	1
4706	18	21,656,127	21,656,734	607	1	5.947	10.579	8	20	0	0	1	TTC39C	83,693	in gene	ActReg chr18 #4706	0	1
4707	18	21,977,549	21,978,020	471	1	8.867	11.6	12	15	1	1	1	OSBPL1A	6	in gene	ActReg chr18 #4707	0	1
4708	18	22,006,165	22,006,727	562	1	10.833	7.722	16	10	1	1	1	IMPACT	-163	upstream	ActReg chr18 #4708	1	0
4709	18	23,317,492	23,318,122	630	1	5.15	9.7	9	16	0	0	0				ActReg chr18 #4709	0	1
4710	18	23,670,182	23,671,418	1,236	2	11.816	15	30	25	1	1	1	SS18	-189	upstream	ActReg chr18 #4710	1	1
4711	18	23,806,268	23,807,041	773	1	7.24	9.68	11	14	1	1	1	TAF4B	245	in gene	ActReg chr18 #4711	0	1
4712	18	25,199,084	25,199,574	490	1	10.333	4.867	15	7	0	0	0				ActReg chr18 #4712	1	0
4713	18	28,591,207	28,591,751	544	1	8.706	5.824	16	9	0	0	1	DSC3	31,302	in gene	ActReg chr18 #4713	1	0
4714	18	29,259,209	29,259,730	521	1	7.438	10.25	9	15	0	1	2	B4GALT6, LOC100507120	5217, -5580	in gene, upstream	ActReg chr18 #4714	0	1
4715	18	29,522,754	29,523,238	484	1	4.5	10	6	17	1	1	1	KIAA1012	95	in gene	ActReg chr18 #4715	0	1
4716	18	29,952,314	29,952,912	598	1	8.895	8.053	16	13	0	0	1	FAM59A	97,834	in gene	ActReg chr18 #4716	1	0
4717	18	32,558,824	32,559,459	635	1	10.5	3.55	17	8	0	1	1	MAPRE2	2,249	in gene	ActReg chr18 #4717	1	0
4718	18	32,621,375	32,621,828	453	1	6.133	10	9	16	1	0	1	MAPRE2	64,709	in gene	ActReg chr18 #4718	0	1
4719	18	32,869,882	32,870,730	848	2	15.593	14.889	34	34	1	1	1	ZNF397OS	-110	upstream	ActReg chr18 #4719	1	1
4720	18	32,923,990	32,924,479	489	1	9.933	4	14	5	1	1	1	ZNF24	192	in gene	ActReg chr18 #4720	1	0
4721	18	33,077,354	33,078,143	789	2	10.625	11.458	15	19	1	1	1	INO80C	207	in gene	ActReg chr18 #4721	1	1
4722	18	33,355,910	33,356,396	486	1	10.067	7.933	15	12	0	0	0				ActReg chr18 #4722	1	0
4723	18	33,647,009	33,647,599	590	1	11.833	10.333	17	13	1	1	1	RPRD1A	69	in gene	ActReg chr18 #4723	1	0
4724	18	33,709,048	33,710,148	1,100	2	10.771	17.286	20	29	1	2	2	SLC39A6, ELP2	-241, -289	upstream, upstream	ActReg chr18 #4724	1	1
4725	18	33,756,637	33,757,163	526	1	4.588	8.706	7	15	0	0	1	ELP2	47,013	downstream	ActReg chr18 #4725	0	1
4726	18	34,849,540	34,851,203	1,663	2	14.288	23.827	52	74	0	0	1	BRUNOL4	295,629	in gene	ActReg chr18 #4726	1	1
4727	18	35,063,413	35,063,993	580	2	9.611	10	16	20	0	0	1	BRUNOL4	82,297	in gene	ActReg chr18 #4727	1	1
4728	18	35,144,722	35,145,246	524	1	8.938	10.625	15	16	1	1	1	BRUNOL4	1,016	in gene	ActReg chr18 #4728	0	1
4729	18	36,298,577	36,298,961	384	1	7.583	11.667	11	16	0	0	0				ActReg chr18 #4729	0	1
4730	18	38,448,157	38,448,529	372	1	4.167	10.5	8	18	0	0	0				ActReg chr18 #4730	0	1
4731	18	39,754,865	39,755,544	679	2	10.762	13.809	20	24	0	0	0				ActReg chr18 #4731	1	1
4732	18	40,125,768	40,126,192	424	1	10.154	5.769	17	10	0	0	0				ActReg chr18 #4732	1	0
4733	18	42,747,533	42,748,128	595	1	8.421	5.632	18	8	0	0	0				ActReg chr18 #4733	1	0
4734	18	42,748,991	42,749,982	991	2	11	9.484	16	16	0	0	0				ActReg chr18 #4734	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4735	18	43,062,202	43,062,923	721	1	10.478	6.739	14	13	0	0	0				ActReg chr18 #4735	1	0
4736	18	43,546,936	43,547,480	544	1	13	10.177	22	16	1	1	1	KIAA1632	97	in gene	ActReg chr18 #4736	1	0
4737	18	43,684,164	43,684,690	526	1	3.812	11.062	6	16	1	2	2	ATP5A1, HAUS1	-228, 129	upstream, in gene	ActReg chr18 #4737	0	1
4738	18	43,753,211	43,754,382	1,171	2	22.568	24.054	64	63	1	1	1	C18orf25	-192	upstream	ActReg chr18 #4738	1	1
4739	18	44,076,929	44,077,608	679	2	12.053	10.857	23	21	0	0	1	LOXHD1	159,728	in gene	ActReg chr18 #4739	1	1
4740	18	44,082,317	44,082,911	594	1	7.438	9.889	13	15	0	0	1	LOXHD1	154,382	in gene	ActReg chr18 #4740	0	1
4741	18	44,116,489	44,116,922	433	1	12.308	10.077	17	16	0	0	1	LOXHD1	120,291	in gene	ActReg chr18 #4741	1	0
4742	18	44,212,565	44,213,250	685	2	9.682	7.909	18	17	0	0	1	LOXHD1	24,089	in gene	ActReg chr18 #4742	1	1
4743	18	44,337,279	44,337,800	521	1	6	8.824	11	16	2	1	1	ST8SIA5	-500	upstream	ActReg chr18 #4743	0	1
4744	18	44,519,423	44,520,042	619	1	6.05	9.8	12	19	0	1	1	KATNAL2	-7,055	upstream	ActReg chr18 #4744	0	1
4745	18	45,816,912	45,817,355	443	1	3.571	8.286	6	15	0	0	0				ActReg chr18 #4745	0	1
4746	18	46,067,082	46,067,949	867	1	8	10.704	13	15	1	1	1	KIAA0427	2,088	in gene	ActReg chr18 #4746	0	1
4747	18	47,112,112	47,112,743	631	1	6.25	11.1	8	23	0	0	1	LIPG	24,000	in gene	ActReg chr18 #4747	0	1
4748	18	47,424,660	47,425,393	733	2	10.391	11.636	20	28	0	0	1	MYO5B	296,425	in gene	ActReg chr18 #4748	1	1
4749	18	48,494,286	48,494,787	501	1	10.688	8.688	19	12	1	1	1	ELAC1	149	in gene	ActReg chr18 #4749	1	0
4750	18	48,724,294	48,724,835	541	1	7.941	9.353	12	16	1	1	1	MEX3C	-513	upstream	ActReg chr18 #4750	0	1
4751	18	48,760,355	48,760,856	501	1	3.308	9.2	5	15	0	0	0				ActReg chr18 #4751	0	1
4752	18	49,052,281	49,052,798	517	1	5.938	9.812	9	16	0	0	0				ActReg chr18 #4752	0	1
4753	18	49,686,961	49,687,428	467	1	9.667	7.583	16	13	0	0	0				ActReg chr18 #4753	1	0
4754	18	49,763,823	49,764,390	567	1	10.278	7.167	15	11	0	0	0				ActReg chr18 #4754	1	0
4755	18	51,795,593	51,796,085	492	1	8.133	11.2	11	14	1	1	1	POLI	-10	upstream	ActReg chr18 #4755	0	1
4756	18	51,883,990	51,884,467	477	1	6.2	9.333	10	15	1	2	2	STARD6, C18orf54	-3285, -943	upstream, upstream	ActReg chr18 #4756	0	1
4757	18	52,942,647	52,943,237	590	1	6.211	8.737	10	17	0	0	1	TCF4	312,918	in gene	ActReg chr18 #4757	0	1
4758	18	54,318,259	54,319,006	747	1	10.652	9	16	17	1	2	2	LOC100505499, WDR7	-127, 16	upstream, in gene	ActReg chr18 #4758	1	0
4759	18	55,114,138	55,114,836	698	2	11.182	10.773	21	20	0	0	1	ONECUT2	11,570	in gene	ActReg chr18 #4759	1	1
4760	18	55,289,011	55,289,645	634	1	8.95	4.85	18	10	1	1	2	NARS, LOC100505549	-151, -8254	upstream, upstream	ActReg chr18 #4760	1	0
4761	18	55,852,106	55,852,581	475	1	7.571	11.333	13	18	0	0	1	NEDD4L	140,724	in gene	ActReg chr18 #4761	0	1
4762	18	56,246,368	56,246,868	500	1	10.125	6.812	16	10	0	0	1	ALPK2	49,571	in gene	ActReg chr18 #4762	1	0
4763	18	56,272,693	56,273,248	555	1	4.278	9.5	7	16	0	0	1	ALPK2	23,219	in gene	ActReg chr18 #4763	0	1
4764	18	56,806,739	56,807,833	1,094	1	6.265	11.559	14	18	1	1	1	SEC11C	161	in gene	ActReg chr18 #4764	0	1
4765	18	58,330,309	58,330,895	586	1	6.5	10.944	10	16	0	0	0				ActReg chr18 #4765	0	1
4766	18	60,189,666	60,190,412	746	2	10.826	12.261	18	24	1	1	1	ZCCHC2	-619	upstream	ActReg chr18 #4766	1	1
4767	18	60,381,956	60,382,672	716	2	11.636	10.5	19	21	1	1	1	PHLPP1	-358	upstream	ActReg chr18 #4767	1	1
4768	18	61,034,366	61,035,300	934	2	13.033	11.967	30	22	1	1	1	KDSR	-327	upstream	ActReg chr18 #4768	1	1
4769	18	61,637,187	61,637,694	507	1	10.4	7.067	15	10	1	1	2	HMSD, SERPINB8	20852, 177	downstream, in gene	ActReg chr18 #4769	1	0
4770	18	67,711,884	67,712,311	427	1	5.769	11.231	8	16	0	0	1	RTTN	160,865	in gene	ActReg chr18 #4770	0	1
4771	18	67,872,623	67,873,563	940	2	10.448	15.379	18	29	1	1	1	RTTN	-131	upstream	ActReg chr18 #4771	1	1
4772	18	70,497,144	70,497,905	761	2	9.792	11.292	25	21	0	0	1	NETO1	37,286	in gene	ActReg chr18 #4772	1	1
4773	18	71,575,441	71,576,014	573	2	10.778	10.889	24	22	0	0	0				ActReg chr18 #4773	1	1
4774	18	72,163,468	72,163,907	439	1	11.143	10	15	15	1	1	1	CNDP2	187	in gene	ActReg chr18 #4774	1	0
4775	18	72,264,835	72,265,356	521	1	6.875	10.25	12	15	1	1	1	LOC400657	-24	upstream	ActReg chr18 #4775	0	1
4776	18	72,919,920	72,920,486	566	1	9.722	8.833	17	14	1	2	2	ZADH2, TSHZ1	1078, -2528	in gene, upstream	ActReg chr18 #4776	1	0
4777	18	73,120,759	73,121,371	612	2	11.526	9.737	21	14	0	0	1	C18orf62	18,524	downstream	ActReg chr18 #4777	1	1
4778	18	74,533,799	74,534,223	424	1	3.231	10.385	5	16	1	1	1	ZNF236	-2,105	upstream	ActReg chr18 #4778	0	1
4779	18	77,438,925	77,439,997	1,072	2	13.879	13.212	25	25	1	1	1	CTDP1	-340	upstream	ActReg chr18 #4779	1	1
4780	19	266,931	267,734	803	2	12.4	14.52	22	30	1	0	0				ActReg chr19 #4780	1	1
4781	19	342,545	343,906	1,361	2	9.256	10.721	15	17	0	1	1	MIER2	1,566	in gene	ActReg chr19 #4781	1	1
4782	19	459,566	460,326	760	1	6.667	12.042	12	18	1	1	2	SHC2, ODF3L2	1050, 15037	in gene, downstream	ActReg chr19 #4782	0	1
4783	19	488,461	489,524	1,063	2	12.727	12.333	26	24	1	1	1	MADCAM1	-7,498	upstream	ActReg chr19 #4783	1	1
4784	19	506,524	507,135	611	1	9.421	14.895	15	25	1	1	2	MADCAM1, C19orf20	10339, -668	downstream, upstream	ActReg chr19 #4784	0	1
4785	19	507,147	508,137	990	2	11.226	14.903	19	23	2	1	2	MADCAM1, C19orf20	11152, 145	downstream, in gene	ActReg chr19 #4785	1	1
4786	19	796,626	797,441	815	2	10.731	9.654	20	19	1	1	1	PTBP1	-359	upstream	ActReg chr19 #4786	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4787	19	892,926	893,775	849	2	12.074	12.444	24	18	1	1	2	MED16, C19orf22	-132, 19875	upstream, downstream	ActReg chr19 #4787	1	1
4788	19	925,046	926,033	987	2	11	17.355	20	40	2	1	2	KISS1R, ARID3A	8197, -498	downstream, upstream	ActReg chr19 #4788	1	1
4789	19	1,020,934	1,022,057	1,123	2	12.857	14.257	21	27	1	2	2	C19orf6, CNN2	-354, -4803	upstream, upstream	ActReg chr19 #4789	1	1
4790	19	1,039,632	1,040,376	744	2	10.522	13.304	21	27	1	1	2	CNN2, ABCA7	13706, -98	downstream, upstream	ActReg chr19 #4790	1	1
4791	19	1,095,139	1,095,622	483	1	6.8	10.2	9	16	1	1	3	HMHA1, POLR2E, GPX4	28206, 11, -8556	downstream, in gene, upstream	ActReg chr19 #4791	0	1
4792	19	1,170,419	1,170,925	506	1	10.938	7.25	17	9	0	0	1	SBNO2	3,610	in gene	ActReg chr19 #4792	1	0
4793	19	1,265,841	1,266,512	671	1	9.381	11.048	12	20	1	1	4	MIDN, C19orf23, CIRBP, C19orf24	17624, 4083, -3091, -9344	downstream, downstream, upstream, upstream	ActReg chr19 #4793	0	1
4794	19	1,266,840	1,267,326	486	1	11.6	10.933	19	14	1	1	4	MIDN, C19orf23, CIRBP, C19orf24	18531, 3176, -2184, -8437	downstream, downstream, upstream, upstream	ActReg chr19 #4794	1	0
4795	19	1,383,212	1,384,190	978	2	11.267	12.167	16	22	1	1	2	MUM1, NDUFS7	28725, -182	downstream, upstream	ActReg chr19 #4795	1	1
4796	19	1,437,919	1,438,764	845	2	22.444	25.37	63	75	1	2	3	DAZAP1, RPS15, LOC100506822	30757, -22, -2503	downstream, upstream, upstream	ActReg chr19 #4796	1	1
4797	19	1,507,500	1,508,295	795	2	13.64	19.125	30	44	1	0	2	REEP6, ADAMTSL5	16732, 5291	downstream, in gene	ActReg chr19 #4797	1	1
4798	19	1,652,640	1,653,339	699	1	7.524	12.546	13	24	0	1	1	TCF3	-663	upstream	ActReg chr19 #4798	0	1
4799	19	1,848,406	1,848,838	432	1	11.286	10.786	20	17	1	1	2	REXO1, KLF16	-170, 14942	upstream, downstream	ActReg chr19 #4799	1	0
4800	19	1,875,748	1,876,673	925	2	12.586	12.207	27	24	1	0	1	FAM108A1	9,308	downstream	ActReg chr19 #4800	1	1
4801	19	2,059,424	2,060,224	800	2	11.462	7.846	18	19	0	0	1	MKNK2	-8,581	upstream	ActReg chr19 #4801	1	1
4802	19	2,061,374	2,062,041	667	2	9.476	11.857	16	21	1	0	1	MOBKL2A	34,562	downstream	ActReg chr19 #4802	1	1
4803	19	2,095,930	2,096,673	743	1	8.375	12.25	14	25	1	2	3	MOBKL2A, C19orf36, AP3D1	-32, -567, 55255	upstream, upstream, downstream	ActReg chr19 #4803	0	1
4804	19	2,269,401	2,269,803	402	1	8.615	10	12	13	1	1	2	OAZ1, C19orf35	82, 12579	in gene, downstream	ActReg chr19 #4804	0	1
4805	19	2,427,276	2,427,911	635	1	10.25	9.45	19	12	1	1	3	TMPRSS9, TIMM13, LMNB2	37809, 282, 29365	downstream, in gene, downstream	ActReg chr19 #4805	1	0
4806	19	2,475,923	2,476,805	882	1	5.464	9.857	8	15	1	1	1	GADD45B	241	in gene	ActReg chr19 #4806	0	1
4807	19	2,494,049	2,495,185	1,136	2	8.8	15.143	15	30	1	0	0				ActReg chr19 #4807	1	1
4808	19	2,722,973	2,723,396	423	1	10.214	5	18	8	1	1	2	DIRAS1, SLC39A3	-1794, 16890	upstream, downstream	ActReg chr19 #4808	1	0
4809	19	2,739,951	2,740,614	663	2	11.286	11.667	19	20	1	1	1	SLC39A3	-208	upstream	ActReg chr19 #4809	1	1
4810	19	2,819,421	2,820,235	814	2	29.231	28.885	91	86	1	1	2	THOP1, ZNF554	34322, -44	downstream, upstream	ActReg chr19 #4810	1	1
4811	19	2,840,899	2,841,466	567	2	10.294	11.765	17	16	1	1	2	ZNF554, ZNF555	21310, -251	downstream, upstream	ActReg chr19 #4811	1	1
4812	19	2,944,966	2,945,702	736	2	8.957	10.261	23	19	1	1	1	ZNF77	-365	upstream	ActReg chr19 #4812	1	1
4813	19	3,035,226	3,036,766	1,540	2	7.958	10.979	15	18	2	0	1	TLE2	11,637	in gene	ActReg chr19 #4813	1	1
4814	19	3,171,884	3,172,718	834	1	9.462	12.154	16	20	0	1	2	GNA15, S1PR4	36110, -6435	downstream, upstream	ActReg chr19 #4814	0	1
4815	19	3,243,673	3,244,851	1,178	2	14.703	22.216	32	53	0	0	1	BRUNOL5	19,561	in gene	ActReg chr19 #4815	1	1
4816	19	3,360,441	3,361,240	799	1	11.68	10.44	17	17	1	1	1	NFIC	1,224	in gene	ActReg chr19 #4816	1	0
4817	19	3,396,972	3,398,131	1,159	1	11.917	7.861	16	13	0	0	1	NFIC	37,935	in gene	ActReg chr19 #4817	1	0
4818	19	3,434,465	3,435,602	1,137	2	11.743	11.6	17	25	1	0	1	NFIC	75,417	in gene	ActReg chr19 #4818	1	1
4819	19	3,450,737	3,451,527	790	1	10.68	8.16	16	13	0	0	1	NFIC	91,516	in gene	ActReg chr19 #4819	1	0
4820	19	3,500,188	3,501,325	1,137	2	11.194	17.083	27	36	1	2	2	DOHH, FZR1	182, -5539	in gene, upstream	ActReg chr19 #4820	1	1
4821	19	3,505,572	3,506,233	661	1	13.05	9.45	24	15	1	2	2	DOHH, FZR1	-4964, -393	upstream, upstream	ActReg chr19 #4821	1	0
4822	19	3,557,388	3,558,223	835	2	13.423	14.692	27	27	1	1	1	C19orf28	-234	upstream	ActReg chr19 #4822	1	1
4823	19	3,572,335	3,572,975	640	2	9.45	11	16	24	1	1	1	HMG20B	-288	upstream	ActReg chr19 #4823	1	1
4824	19	3,626,307	3,627,308	1,001	2	16.613	19.742	44	42	1	1	2	C19orf29, PIP5K1C	6, 73638	in gene, downstream	ActReg chr19 #4824	1	1
4825	19	3,721,189	3,721,934	745	2	11.652	12.8	20	24	1	1	1	TJP3	-6,813	upstream	ActReg chr19 #4825	1	1
4826	19	3,876,826	3,877,406	580	2	10.889	17.444	18	36	0	1	2	ZFR2, ATCAY	-8089, -3502	upstream, upstream	ActReg chr19 #4826	1	1
4827	19	3,985,140	3,985,735	595	1	10.263	8.211	15	10	1	2	2	EEF2, SNORD37	24, -2867	in gene, upstream	ActReg chr19 #4827	1	0
4828	19	4,145,566	4,146,281	715	2	12.652	10.696	24	15	0	1	1	CREB3L3	-7,706	upstream	ActReg chr19 #4828	1	1
4829	19	4,181,730	4,182,975	1,245	1	8.553	13.763	13	22	1	2	3	CREB3L3, SIRT6, ANKRD24	28723, 244, 999	downstream, in gene, upstream	ActReg chr19 #4829	0	1
4830	19	4,246,485	4,247,419	934	2	12.448	12.724	29	26	1	1	2	EBI3, CCDC94	17412, -159	downstream, upstream	ActReg chr19 #4830	1	1
4831	19	4,374,218	4,375,353	1,135	2	11.657	11.086	20	25	0	0	1	SH3GL1	25,686	in gene	ActReg chr19 #4831	1	1
4832	19	4,584,001	4,584,578	577	1	8.556	12.111	16	20	1	0	0				ActReg chr19 #4832	0	1
4833	19	4,694,308	4,694,982	674	1	8.714	11.286	17	21	0	0	2	DPP9, LOC100131094	29210, 15351	in gene, downstream	ActReg chr19 #4833	0	1
4834	19	4,722,857	4,724,382	1,525	2	18.565	16.66	43	35	1	1	1	DPP9	236	in gene	ActReg chr19 #4834	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4835	19	4,744,438	4,745,338	900	1	11.036	12.214	21	21	0	0	0				ActReg chr19 #4835	0	1
4836	19	4,768,739	4,771,274	2,535	2	32.279	38.544	179	207	0	2	2	C19orf30, MIR7-3	889, -676	in gene, upstream	ActReg chr19 #4836	1	1
4837	19	4,791,031	4,792,337	1,306	2	22.098	20.512	54	53	1	2	3	LOC100506984, FEM1A, LOC100507004	-432, -44, 9594	upstream, upstream, downstream	ActReg chr19 #4837	1	1
4838	19	4,812,737	4,813,621	884	1	13.185	8.333	20	17	0	0	1	TICAM1	18,558	downstream	ActReg chr19 #4838	1	0
4839	19	4,831,486	4,832,124	638	1	11.8	13.95	20	23	1	1	2	TICAM1, PLIN3	-68, 35975	upstream, downstream	ActReg chr19 #4839	0	1
4840	19	4,869,976	4,870,485	509	1	11.875	8.125	19	13	0	1	1	PLIN3	-2,450	upstream	ActReg chr19 #4840	1	0
4841	19	4,958,359	4,959,198	839	2	12.308	12.538	22	27	1	1	2	UHRF1, KDM4B	59268, -346	downstream, upstream	ActReg chr19 #4841	1	1
4842	19	5,036,769	5,037,453	684	1	11.809	12.905	21	23	1	0	1	KDM4B	67,987	in gene	ActReg chr19 #4842	0	1
4843	19	5,345,725	5,346,534	809	2	13	11.692	20	25	0	1	1	PTPRS	-5,315	upstream	ActReg chr19 #4843	1	1
4844	19	5,403,750	5,404,654	904	2	18.179	21.429	45	58	0	0	0				ActReg chr19 #4844	1	1
4845	19	5,434,830	5,435,828	998	1	13.387	9.323	20	16	0	0	0				ActReg chr19 #4845	1	0
4846	19	5,622,503	5,623,396	893	1	9.179	11.536	16	16	1	2	2	SAFB2, SAFB	-11, -215	upstream, upstream	ActReg chr19 #4846	0	1
4847	19	5,679,958	5,681,079	1,121	2	13.057	13.486	27	21	1	2	3	C19orf70, HSD11B1L, RPL36	393, -517, -9754	in gene, upstream, upstream	ActReg chr19 #4847	1	1
4848	19	5,689,829	5,690,968	1,139	2	15.114	16.2	27	34	1	1	4	C19orf70, HSD11B1L, RPL36, LONP1	-9487, 9363, 126, 29778	upstream, downstream, in gene, downstream	ActReg chr19 #4848	1	1
4849	19	5,719,897	5,720,899	1,002	2	9.875	12.812	20	19	1	2	2	LONP1, TMEM146	-222, -290	upstream, upstream	ActReg chr19 #4849	1	1
4850	19	5,790,328	5,791,578	1,250	2	12.641	14.333	26	27	1	2	2	PRR22, DUS3L	-6177, 296	upstream, in gene	ActReg chr19 #4850	1	1
4851	19	5,827,893	5,828,757	864	2	11.63	10.741	18	18	1	0	2	NRTN, FUT6	4507, 11417	in gene, downstream	ActReg chr19 #4851	1	1
4852	19	5,913,775	5,914,471	696	1	6.682	12.273	13	21	0	1	4	NDUFA11, VMAC, CAPS, RANBP3	-10099, 9271, -70, 64197	upstream, downstream, upstream, downstream	ActReg chr19 #4852	0	1
4853	19	6,087,768	6,088,432	664	1	11.714	8.143	17	13	0	0	1	RFX2	22,564	in gene	ActReg chr19 #4853	1	0
4854	19	6,199,202	6,199,803	601	1	11.667	13.667	16	23	1	1	2	ACSBG2, LOC100507094	63792, 38	downstream, in gene	ActReg chr19 #4854	0	1
4855	19	6,424,708	6,425,672	964	1	10.067	13.433	15	21	2	1	2	KHSRP, SLC25A41	-368, 8600	upstream, downstream	ActReg chr19 #4855	0	1
4856	19	6,459,709	6,460,870	1,161	2	11.73	14.351	25	30	1	2	3	SLC25A23, CRB3, DENND1C	-508, -3971, 21509	upstream, upstream, downstream	ActReg chr19 #4856	1	1
4857	19	6,504,427	6,505,322	895	1	8.357	13.107	21	25	0	1	2	TUBB4, MIR220B	-2544, 8915	upstream, downstream	ActReg chr19 #4857	0	1
4858	19	6,530,784	6,531,421	637	1	10.05	10.45	17	15	1	1	1	TNFSF9	92	in gene	ActReg chr19 #4858	1	0
4859	19	6,564,296	6,564,944	648	2	14.3	11.15	28	18	0	0	0				ActReg chr19 #4859	1	1
4860	19	6,590,682	6,591,260	578	1	11.611	7.333	19	10	1	1	1	CD70	192	in gene	ActReg chr19 #4860	1	0
4861	19	6,737,080	6,738,183	1,103	2	14.771	15.314	26	36	1	2	2	GPR108, TRIP10	2, -2076	in gene, upstream	ActReg chr19 #4861	1	1
4862	19	6,947,621	6,948,153	532	1	10.688	8.812	19	16	0	0	1	EMR1	60,305	downstream	ActReg chr19 #4862	1	0
4863	19	7,196,857	7,197,606	749	2	10.417	13.958	23	24	1	0	1	INSR	96,780	in gene	ActReg chr19 #4863	1	1
4864	19	7,574,358	7,575,097	739	2	11.522	13	16	27	0	1	2	C19orf45, ZNF358	12282, -6277	downstream, upstream	ActReg chr19 #4864	1	1
4865	19	7,587,031	7,587,918	887	2	14.964	18	37	40	1	1	2	ZNF358, MCOLN1	6470, -22	downstream, upstream	ActReg chr19 #4865	1	1
4866	19	7,598,095	7,599,434	1,339	2	9	13.476	25	29	1	1	2	MCOLN1, PNPLA6	11268, -274	in gene, upstream	ActReg chr19 #4866	1	1
4867	19	7,599,876	7,601,098	1,222	2	13.5	16.132	25	33	1	1	2	MCOLN1, PNPLA6	12991, 1449	downstream, in gene	ActReg chr19 #4867	1	1
4868	19	7,627,154	7,628,343	1,189	2	11.027	15.081	23	36	0	0	1	PNPLA6	28,710	downstream	ActReg chr19 #4868	1	1
4869	19	7,894,491	7,895,121	630	2	10.5	10.8	23	18	0	1	1	EVI5L	-355	upstream	ActReg chr19 #4869	1	1
4870	19	7,968,135	7,968,964	829	1	10.5	12.731	17	19	1	1	2	LRRC8E, MAP2K7	15159, -216	downstream, upstream	ActReg chr19 #4870	0	1
4871	19	8,372,367	8,373,738	1,371	2	13.581	13.465	26	23	1	1	2	CD320, NDUFA7	188, 13228	in gene, downstream	ActReg chr19 #4871	1	1
4872	19	8,385,475	8,386,560	1,085	1	9.5	11.618	14	20	1	2	3	NDUFA7, RPS28, KANK3	263, -367, 22129	in gene, upstream, downstream	ActReg chr19 #4872	0	1
4873	19	8,429,076	8,429,733	657	1	9.81	11.143	14	22	1	1	2	ANGPTL4, LOC100507567	393, 26165	in gene, downstream	ActReg chr19 #4873	0	1
4874	19	8,841,605	8,842,288	683	1	6.762	11.476	10	22	0	1	1	OR2Z1	555	in gene	ActReg chr19 #4874	0	1
4875	19	8,942,534	8,943,368	834	2	9.731	17.269	18	31	1	0	2	ZNF558, MBD3L1	-9386, -10318	upstream, upstream	ActReg chr19 #4875	1	1
4876	19	9,084,153	9,084,560	407	1	10	9.615	16	14	0	0	1	MUC16	7,662	in gene	ActReg chr19 #4876	1	0
4877	19	9,186,187	9,186,820	633	2	10.15	11.2	20	23	0	0	0				ActReg chr19 #4877	1	1
4878	19	9,250,820	9,251,519	699	1	4.667	10.762	8	15	1	1	1	ZNF317	113	in gene	ActReg chr19 #4878	0	1
4879	19	9,420,218	9,420,712	494	1	4.75	9.875	6	17	1	1	1	ZNF699	-4,670	upstream	ActReg chr19 #4879	0	1
4880	19	9,517,576	9,518,088	512	1	10.375	5.438	15	9	1	0	1	ZNF266	28,402	downstream	ActReg chr19 #4880	1	0
4881	19	9,545,917	9,546,365	448	1	9.929	6.357	15	11	1	1	1	ZNF266	93	in gene	ActReg chr19 #4881	1	0
4882	19	9,785,348	9,786,139	791	2	12	10.167	21	16	1	1	1	ZNF562	33	in gene	ActReg chr19 #4882	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4883	19	9,878,855	9,879,860	1,005	2	11.323	11.613	20	17	1	1	1	ZNF846	53	in gene	ActReg chr19 #4883	1	1
4884	19	9,929,055	9,929,862	807	2	10.269	11.808	18	23	1	1	2	FBXL12, UBL5	273, -9110	in gene, upstream	ActReg chr19 #4884	1	1
4885	19	10,049,685	10,050,642	957	2	9.5	12.733	16	25	0	1	1	OLFM2	-3,093	upstream	ActReg chr19 #4885	1	1
4886	19	10,172,321	10,173,423	1,102	2	16.382	21.235	34	40	1	0	0				ActReg chr19 #4886	1	1
4887	19	10,224,535	10,225,834	1,299	2	10.683	11.415	18	19	1	1	6	PPAN, PPAN-P2RY11, SNORD105, SNORD105B, P2RY11, EIF3G	8219, 8113, 6857, 4759, 2987, 5415	downstream, in gene, downstream, downstream, in gene, downstream	ActReg chr19 #4887	1	1
4888	19	10,229,966	10,230,965	999	1	10.968	13.032	20	24	1	1	5	PPAN, PPAN-P2RY11, SNORD105B, P2RY11, EIF3G	13500, 13394, 10040, 8268, 134	downstream, downstream, downstream, downstream, in gene	ActReg chr19 #4888	0	1
4889	19	10,304,695	10,306,053	1,358	1	10.302	12.233	17	23	1	1	1	DNMT1	381	in gene	ActReg chr19 #4889	0	1
4890	19	10,337,713	10,338,502	789	1	7.52	12.48	11	23	0	1	2	S1PR2, MIR4322	3841, -2982	in gene, upstream	ActReg chr19 #4890	0	1
4891	19	10,340,638	10,341,736	1,098	2	13.486	13.429	26	23	1	2	2	S1PR2, MIR4322	761, 98	in gene, downstream	ActReg chr19 #4891	1	1
4892	19	10,362,498	10,363,264	766	1	7.083	13.417	12	25	1	1	1	MRPL4	241	in gene	ActReg chr19 #4892	0	1
4893	19	10,380,686	10,381,796	1,110	1	7.943	11.8	14	17	1	1	2	MRPL4, ICAM1	18601, -276	downstream, upstream	ActReg chr19 #4893	0	1
4894	19	10,400,838	10,402,371	1,533	1	10.521	12.688	21	27	1	1	3	ICAM1, ICAM4, ICAM5	20087, 3954, 949	downstream, downstream, in gene	ActReg chr19 #4894	0	1
4895	19	10,443,269	10,446,058	2,789	2	11.943	14.943	20	30	1	1	2	RAVER1, ICAM3	-349, 5682	upstream, in gene	ActReg chr19 #4895	1	1
4896	19	10,490,970	10,491,955	985	1	10.129	12.581	16	19	1	1	2	TYK2, CDC37	-214, 22809	upstream, downstream	ActReg chr19 #4896	0	1
4897	19	10,513,816	10,515,392	1,576	2	14.22	16.1	26	30	1	2	2	CDC37, MIR1181	-333, -390	upstream, upstream	ActReg chr19 #4897	1	1
4898	19	10,526,204	10,527,986	1,782	2	12.732	15.268	27	38	1	1	1	PDE4A	-4,238	upstream	ActReg chr19 #4898	1	1
4899	19	10,530,058	10,531,145	1,087	2	12.765	14.912	24	29	1	1	1	PDE4A	-732	upstream	ActReg chr19 #4899	1	1
4900	19	10,612,460	10,613,947	1,487	2	13.348	14.826	24	26	1	1	2	KEAP1, S1PR5	851, 15465	in gene, downstream	ActReg chr19 #4900	1	1
4901	19	10,676,293	10,676,889	596	1	12.889	12.444	20	20	1	1	3	KRI1, CDKN2D, AP1M2	111, 3064, 21400	in gene, downstream, downstream	ActReg chr19 #4901	0	1
4902	19	10,679,513	10,680,565	1,052	2	13.758	15.182	32	30	1	2	3	KRI1, CDKN2D, AP1M2	-3337, -384, 17952	upstream, upstream, downstream	ActReg chr19 #4902	1	1
4903	19	10,713,112	10,713,705	593	1	11.684	8.889	19	12	1	1	1	SLC44A2	287	in gene	ActReg chr19 #4903	1	0
4904	19	10,764,106	10,765,394	1,288	2	17.2	17.3	44	36	1	2	3	SLC44A2, LOC147727, ILF3	51629, -202, -187	downstream, upstream, upstream	ActReg chr19 #4904	1	1
4905	19	10,805,604	10,807,214	1,610	2	12.52	14.56	20	25	0	1	2	ILF3, QTRT1	41472, -5703	downstream, upstream	ActReg chr19 #4905	1	1
4906	19	10,811,792	10,812,942	1,150	2	10.972	12.333	24	18	1	1	2	ILF3, QTRT1	47430, 255	downstream, in gene	ActReg chr19 #4906	1	1
4907	19	10,827,478	10,828,913	1,435	1	13.2	14.956	25	30	1	2	3	QTRT1, DNM2, MIR638	16083, -534, -885	downstream, upstream, upstream	ActReg chr19 #4907	0	1
4908	19	10,919,362	10,920,435	1,073	2	10.636	12.364	23	23	0	1	3	DNM2, LOC100507081, MIR199A1	91169, -1117, 8274	in gene, upstream, downstream	ActReg chr19 #4908	1	1
4909	19	10,945,835	10,947,700	1,865	2	14.914	15.845	26	31	1	1	2	DNM2, TMED1	118038, 216	downstream, in gene	ActReg chr19 #4909	1	1
4910	19	11,038,864	11,040,142	1,278	2	11.05	13.975	20	30	1	2	3	CARM1, YIPF2, C19orf52	57250, -146, 79	downstream, upstream, in gene	ActReg chr19 #4910	1	1
4911	19	11,070,945	11,071,566	621	1	8.211	13.263	12	25	1	1	1	SMARCA4	-343	upstream	ActReg chr19 #4911	0	1
4912	19	11,199,597	11,200,682	1,085	1	12.059	9.412	19	15	0	1	1	LDLR	82	in gene	ActReg chr19 #4912	1	0
4913	19	11,201,118	11,201,948	830	1	9.962	13.885	21	22	1	1	1	LDLR	1,476	in gene	ActReg chr19 #4913	0	1
4914	19	11,202,072	11,202,893	821	1	10.231	7.769	17	17	0	1	1	LDLR	2,425	in gene	ActReg chr19 #4914	1	0
4915	19	11,249,163	11,250,128	965	2	11.724	13.767	17	23	0	0	2	LDLR, SPC24	49588, 16839	downstream, downstream	ActReg chr19 #4915	1	1
4916	19	11,253,302	11,254,489	1,187	2	13.054	14.432	23	27	0	0	2	LDLR, SPC24	53838, 12589	downstream, downstream	ActReg chr19 #4916	1	1
4917	19	11,265,994	11,266,883	889	1	11.107	16.286	17	32	1	1	2	SPC24, KANK2	46, 41805	in gene, downstream	ActReg chr19 #4917	0	1
4918	19	11,404,342	11,405,035	693	1	7.955	12.727	10	22	1	1	1	TSPAN16	-2,136	upstream	ActReg chr19 #4918	0	1
4919	19	11,480,097	11,481,003	906	1	10.286	15.929	18	29	0	1	3	LPPR2, C19orf39, EPOR	14488, -4833, 14468	downstream, upstream, downstream	ActReg chr19 #4919	0	1
4920	19	11,545,574	11,546,960	1,386	2	12.419	12.395	18	21	1	2	2	CCDC151, PRKCSH	-287, -2	upstream, upstream	ActReg chr19 #4920	1	1
4921	19	11,592,536	11,593,935	1,399	2	12.364	12.5	21	22	1	1	2	ELAVL3, ZNF653	-1432, 23503	upstream, downstream	ActReg chr19 #4921	1	1
4922	19	11,639,262	11,640,321	1,059	2	12.559	11.823	24	16	1	1	2	ECSIT, CNN1	196, -9788	in gene, upstream	ActReg chr19 #4922	1	1
4923	19	11,669,526	11,670,522	996	1	8.71	14	13	24	1	1	2	CNN1, ELOF1	20445, 27	downstream, in gene	ActReg chr19 #4923	0	1
4924	19	11,708,059	11,708,870	811	1	13.846	12.808	25	21	1	1	1	ZNF627	229	in gene	ActReg chr19 #4924	1	0
4925	19	11,805,208	11,806,238	1,030	1	7.5	11.719	14	19	1	0	0				ActReg chr19 #4925	0	1
4926	19	11,877,437	11,878,505	1,068	2	14.588	13.177	25	22	1	1	1	ZNF441	156	in gene	ActReg chr19 #4926	1	1
4927	19	11,908,334	11,908,860	526	1	4.812	11.062	8	16	0	1	1	ZNF491	-794	upstream	ActReg chr19 #4927	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4928	19	11,909,301	11,909,975	674	1	11.619	6.286	17	10	1	1	1	ZNF491	247	in gene	ActReg chr19 #4928	1	0
4929	19	11,998,318	11,999,257	939	2	10.966	12	19	18	1	1	1	ZNF69	117	in gene	ActReg chr19 #4929	1	1
4930	19	12,035,466	12,036,398	932	1	11.31	14.897	19	29	1	1	1	ZNF700	32	in gene	ActReg chr19 #4930	0	1
4931	19	12,163,289	12,163,997	708	2	10.182	11.773	20	18	1	0	2	LOC100507111, ZNF878	65160, 3484	downstream, in gene	ActReg chr19 #4931	1	1
4932	19	12,175,198	12,176,188	990	1	6.806	10.839	13	16	1	1	2	ZNF878, ZNF844	-8566, 147	upstream, in gene	ActReg chr19 #4932	0	1
4933	19	12,266,953	12,267,912	959	1	9.4	11.9	14	17	1	2	2	ZNF625, ZNF136	97, -6440	in gene, upstream	ActReg chr19 #4933	0	1
4934	19	12,476,114	12,477,169	1,055	2	11.273	9.303	18	20	1	1	1	ZNF442	-166	upstream	ActReg chr19 #4934	1	1
4935	19	12,511,235	12,512,247	1,012	1	11.419	10.129	17	14	1	1	1	ZNF799	347	in gene	ActReg chr19 #4935	1	0
4936	19	12,551,529	12,552,115	586	1	12.5	8.444	18	12	1	1	1	ZNF443	104	in gene	ActReg chr19 #4936	1	0
4937	19	12,661,762	12,662,935	1,173	1	14.056	15.611	23	32	1	1	1	ZNF564	8	in gene	ActReg chr19 #4937	0	1
4938	19	12,779,869	12,781,206	1,337	2	12.691	12.905	18	21	1	3	5	MAN2B1, WDR83, C19orf56, DHPS, LOC100507285	-2946, 2919, -72, 12140, -9080	upstream, in gene, upstream, downstream, upstream	ActReg chr19 #4938	1	1
4939	19	12,806,957	12,807,838	881	1	10.889	14.741	20	22	1	1	5	LOC100507285, LOC648044, FBXW9, TNPO2, SNORD41	17780, 8585, 58, 27413, 9935	downstream, downstream, in gene, downstream, downstream	ActReg chr19 #4939	0	1
4940	19	12,833,223	12,833,951	728	1	10.909	14.364	24	26	1	1	2	TNPO2, C19orf43	1223, 11942	in gene, downstream	ActReg chr19 #4940	0	1
4941	19	12,847,761	12,849,019	1,258	2	10.897	15.231	16	34	1	2	2	C19orf43, ASNA1	-2861, 84	upstream, in gene	ActReg chr19 #4941	1	1
4942	19	12,886,140	12,886,763	623	2	20.8	19.15	49	43	1	1	1	HOOK2	-17	upstream	ActReg chr19 #4942	1	1
4943	19	12,888,571	12,889,605	1,034	1	10	12.424	16	21	1	1	1	HOOK2	-2,654	upstream	ActReg chr19 #4943	0	1
4944	19	12,892,529	12,894,135	1,606	2	14.56	17.7	39	54	1	1	2	HOOK2, JUNB	-6898, -8978	upstream, upstream	ActReg chr19 #4944	1	1
4945	19	12,900,578	12,903,960	3,382	4	14.476	13.571	31	26	2	1	2	JUNB, PRDX2	-41, 10425	upstream, downstream	ActReg chr19 #4945	1	1
4946	19	12,904,023	12,905,203	1,180	2	14.189	12.135	22	27	1	1	2	JUNB, PRDX2	2303, 8081	downstream, downstream	ActReg chr19 #4946	1	1
4947	19	12,911,789	12,913,288	1,499	2	16.617	17.311	26	33	1	2	3	JUNB, PRDX2, RNASEH2A	10228, 156, 4890	downstream, in gene, upstream	ActReg chr19 #4947	1	1
4948	19	12,942,702	12,944,069	1,367	2	18.861	22.605	48	63	1	2	3	RTBDN, LOC100507305, MAST1	2845, 6860, 5874	in gene, in gene, upstream	ActReg chr19 #4948	1	1
4949	19	12,946,855	12,947,673	818	1	11.12	15.56	18	34	0	2	3	RTBDN, LOC100507305, MAST1	-1034, 10739, -1995	upstream, downstream, upstream	ActReg chr19 #4949	0	1
4950	19	12,958,009	12,959,083	1,074	1	13.588	10.677	22	16	1	0	1	MAST1	9,287	in gene	ActReg chr19 #4950	1	0
4951	19	12,991,841	12,992,562	721	1	8.455	12.046	14	22	1	1	4	MAST1, DNASE2, KLF1, GCDH	42942, 134, 5816, -9773	downstream, in gene, downstream, upstream	ActReg chr19 #4951	0	1
4952	19	13,001,345	13,003,107	1,762	2	21.709	23.782	83	81	1	2	4	DNASE2, KLF1, GCDH, SYCE2	-9891, -4209, 252, 27860	upstream, upstream, in gene, downstream	ActReg chr19 #4952	1	1
4953	19	13,048,431	13,049,925	1,494	2	15.702	16.319	34	33	1	3	4	FARSA, CALR, LOC100507328, RAD23A	-4620, -236, 29027, -7476	upstream, upstream, downstream, upstream	ActReg chr19 #4953	1	1
4954	19	13,067,078	13,068,416	1,338	2	11.619	11.309	18	20	1	1	3	LOC100507328, RAD23A, GADD45GIP1	10458, 11093, 303	in gene, downstream, in gene	ActReg chr19 #4954	1	1
4955	19	13,095,208	13,096,765	1,557	2	12.312	12.542	19	21	0	0	2	DAND5, NFIX	15554, -10598	downstream, upstream	ActReg chr19 #4955	1	1
4956	19	13,105,360	13,106,352	992	1	11.161	11.484	24	24	0	1	1	NFIX	-728	upstream	ActReg chr19 #4956	1	0
4957	19	13,106,750	13,108,028	1,278	1	8.675	12.275	16	22	1	1	1	NFIX	805	in gene	ActReg chr19 #4957	0	1
4958	19	13,227,041	13,228,080	1,039	2	13.5	17.188	31	35	1	2	2	TRMT1, NACC1	3, -1549	in gene, upstream	ActReg chr19 #4958	1	1
4959	19	13,260,195	13,264,876	4,681	4	18.062	17.294	51	47	1	2	3	NACC1, STX10, IER2	33426, -1548, 1253	downstream, upstream, in gene	ActReg chr19 #4959	1	1
4960	19	13,273,540	13,275,007	1,467	1	9.844	12.467	16	24	1	0	1	IER2	12,991	downstream	ActReg chr19 #4960	0	1
4961	19	13,275,024	13,276,156	1,132	2	12.4	11.6	17	17	0	0	1	IER2	14,308	downstream	ActReg chr19 #4961	1	1
4962	19	13,371,909	13,372,674	765	2	13.708	12	22	21	0	0	1	CACNA1A	244,983	in gene	ActReg chr19 #4962	1	1
4963	19	13,552,404	13,553,659	1,255	2	17.846	21.872	44	55	0	0	1	CACNA1A	64,243	in gene	ActReg chr19 #4963	1	1
4964	19	13,572,526	13,574,971	2,445	3	9.987	16.079	30	47	0	0	1	CACNA1A	43,526	in gene	ActReg chr19 #4964	1	1
4965	19	13,842,190	13,842,857	667	1	7.429	12.476	14	19	0	0	0				ActReg chr19 #4965	0	1
4966	19	13,858,158	13,859,001	843	1	12	13.577	20	22	1	1	1	CCDC130	-174	upstream	ActReg chr19 #4966	0	1
4967	19	13,874,899	13,875,389	490	1	10.933	14.8	14	21	1	1	3	CCDC130, MRI1, C19orf53	16391, -193, -10113	downstream, upstream, upstream	ActReg chr19 #4967	0	1
4968	19	13,884,803	13,886,485	1,682	2	12.635	18.288	41	57	1	1	2	MRI1, C19orf53	10307, 387	downstream, in gene	ActReg chr19 #4968	1	1
4969	19	13,905,393	13,906,466	1,073	1	10.294	12.088	17	21	1	1	1	ZSWIM4	-345	upstream	ActReg chr19 #4969	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
4970	19	13,946,955	13,948,094	1,139	1	12.066	13.629	19	23	0	4	5	ZSWIM4, LOC284454, MIR24-2, MIR27A, MIR23A	41250, -421, -351, -193, -51	downstream, upstream, upstream, upstream, upstream	ActReg chr19 #4970	1	0
4971	19	13,949,551	13,952,719	3,168	2	12.768	13.495	25	23	0	4	5	ZSWIM4, LOC284454, MIR24-2, MIR27A, MIR23A	44861, -4032, -3962, -3804, -3662	downstream, upstream, upstream, upstream, upstream	ActReg chr19 #4971	1	1
4972	19	13,957,099	13,959,103	2,004	2	12.355	13.339	29	20	0	0	4	LOC284454, MIR24-2, MIR27A, MIR23A	-10998, -10928, -10770, -10628	upstream, upstream, upstream, upstream	ActReg chr19 #4972	1	1
4973	19	13,961,579	13,962,749	1,170	2	12.333	14.472	26	27	0	0	0				ActReg chr19 #4973	1	1
4974	19	13,990,828	13,991,539	711	1	13.546	12.909	21	19	1	0	4	MIR181C, MIR181D, NANOS3, C19orf57	5670, 5494, 3233, 25726	downstream, downstream, in gene, downstream	ActReg chr19 #4974	0	1
4975	19	14,013,864	14,014,607	743	2	12.217	14.565	29	31	0	2	2	C19orf57, CC2D1A	2674, -272	in gene, upstream	ActReg chr19 #4975	1	1
4976	19	14,016,799	14,017,682	883	1	12.5	10.786	20	14	1	2	2	C19orf57, CC2D1A	-331, 284	upstream, in gene	ActReg chr19 #4976	0	1
4977	19	14,116,988	14,118,226	1,238	2	15.103	18.538	26	38	1	1	1	RFX1	-473	upstream	ActReg chr19 #4977	1	1
4978	19	14,192,097	14,192,987	890	1	9.148	13.222	23	23	1	0	4	LOC113230, C19orf67, SAMD1, PRKACA	8721, 3897, 8690, 36017	downstream, in gene, downstream, downstream	ActReg chr19 #4978	0	1
4979	19	14,229,212	14,230,020	808	1	9.692	12.192	14	17	1	1	2	PRKACA, ASF1B	-1057, 17824	upstream, downstream	ActReg chr19 #4979	0	1
4980	19	14,246,992	14,248,607	1,615	2	11.7	13.22	21	22	1	2	3	ASF1B, LOC100507373, LPHN1	-359, -181, 69198	upstream, upstream, downstream	ActReg chr19 #4980	1	1
4981	19	14,317,539	14,318,876	1,337	2	20.537	31.317	40	55	1	1	1	LPHN1	-1,210	upstream	ActReg chr19 #4981	1	1
4982	19	14,491,999	14,493,144	1,145	1	7.611	11.278	14	16	0	2	2	CD97, LOC100507396	358, -2460	in gene, upstream	ActReg chr19 #4982	0	1
4983	19	14,544,788	14,545,883	1,095	1	12.706	9.735	22	18	1	1	1	PKN1	1,169	in gene	ActReg chr19 #4983	1	0
4984	19	14,630,287	14,631,377	1,090	2	12.971	13.441	23	24	0	1	3	DNAJB1, MIR639, TECR	-1631, -9523, -9550	upstream, upstream, upstream	ActReg chr19 #4984	1	1
4985	19	14,682,214	14,683,391	1,177	2	26.417	32.25	83	99	1	1	2	TECR, NDUFB7	42420, 84	downstream, in gene	ActReg chr19 #4985	1	1
4986	19	15,126,445	15,127,351	906	1	11.107	19.857	23	37	0	0	1	CCDC105	5,359	in gene	ActReg chr19 #4986	0	1
4987	19	15,197,598	15,198,711	1,113	1	7.029	12.543	18	25	0	1	1	OR111	277	in gene	ActReg chr19 #4987	0	1
4988	19	15,235,845	15,236,863	1,018	1	11.903	15.742	21	25	1	1	1	ILVBL	223	in gene	ActReg chr19 #4988	0	1
4989	19	15,441,691	15,442,509	818	1	9.462	14.039	17	21	1	0	0				ActReg chr19 #4989	0	1
4990	19	15,489,515	15,491,515	2,000	2	10.71	13.677	27	27	1	1	2	AKAP8, AKAP8L	88, 39318	in gene, downstream	ActReg chr19 #4990	1	1
4991	19	15,529,222	15,530,286	1,064	2	16.273	12.939	29	24	1	1	2	AKAP8L, WIZ	79, 31008	in gene, downstream	ActReg chr19 #4991	1	1
4992	19	15,543,438	15,544,097	659	2	18.048	25.333	32	55	1	0	1	WIZ	16,995	in gene	ActReg chr19 #4992	1	1
4993	19	15,666,598	15,667,806	1,208	1	10.108	11.838	20	21	0	0	1	CYP4F22	47,866	downstream	ActReg chr19 #4993	0	1
4994	19	15,687,744	15,688,541	797	1	10.84	15.48	22	27	0	0	0				ActReg chr19 #4994	0	1
4995	19	15,733,954	15,735,149	1,195	2	13.297	15.46	29	41	0	0	1	CYP4F8	8,522	in gene	ActReg chr19 #4995	1	1
4996	19	15,880,213	15,880,958	745	1	9.522	15.13	17	30	0	0	1	LOC388514	10,213	in gene	ActReg chr19 #4996	0	1
4997	19	15,947,337	15,948,082	745	1	10.87	12.957	19	27	1	0	1	UCA1	7,952	downstream	ActReg chr19 #4997	0	1
4998	19	16,161,824	16,162,729	905	2	11.552	10.966	22	19	0	0	1	FLJ25328	18,990	downstream	ActReg chr19 #4998	1	1
4999	19	16,221,881	16,223,022	1,141	2	10.75	11.944	18	23	1	1	2	TPM4, RAB8A	44134, -39	downstream, upstream	ActReg chr19 #4999	1	1
5000	19	16,271,326	16,272,394	1,068	2	13.677	12.647	22	22	0	0	2	HSH2D, CIB3	27022, 12426	downstream, downstream	ActReg chr19 #5000	1	1
5001	19	16,308,178	16,309,134	956	1	13.1	6.6	21	12	1	1	2	FAM32A, AP1M1	12421, -9	downstream, upstream	ActReg chr19 #5001	1	0
5002	19	16,404,306	16,404,992	686	1	11.818	7.773	18	15	0	0	0				ActReg chr19 #5002	1	0
5003	19	16,448,521	16,450,408	1,887	1	10.237	13.441	21	19	0	0	0				ActReg chr19 #5003	0	1
5004	19	16,606,639	16,607,607	968	1	13.667	17.8	24	35	1	2	2	CALR3, C19orf44	-120, -82	upstream, upstream	ActReg chr19 #5004	0	1
5005	19	16,652,769	16,653,842	1,073	2	11.818	13.061	19	25	1	1	2	CHERP, SLC35E1	-42, 29888	upstream, downstream	ActReg chr19 #5005	1	1
5006	19	16,739,074	16,739,913	839	1	9.577	12.769	18	21	1	1	2	MED26, LOC100507522	-478, 17309	upstream, downstream	ActReg chr19 #5006	0	1
5007	19	16,770,530	16,771,946	1,416	2	17.023	13.273	37	31	1	2	2	C19orf42, TMEM38A	-270, -700	upstream, upstream	ActReg chr19 #5007	1	1
5008	19	16,850,203	16,850,929	726	1	7.261	14.304	11	29	0	0	1	NWD1	19,779	in gene	ActReg chr19 #5008	0	1
5009	19	16,869,187	16,870,591	1,404	1	8.093	15.07	16	33	0	0	1	NWD1	39,102	in gene	ActReg chr19 #5009	0	1
5010	19	17,185,198	17,186,779	1,581	2	16.082	23.918	60	80	1	2	2	HAUS8, MYO9B	355, -603	in gene, upstream	ActReg chr19 #5010	1	1
5011	19	17,190,331	17,191,483	1,152	1	9.167	11.167	14	23	0	1	2	HAUS8, MYO9B	-4564, 4316	upstream, in gene	ActReg chr19 #5011	0	1
5012	19	17,218,134	17,219,334	1,200	2	14.421	12.21	22	20	0	0	1	MYO9B	32,143	in gene	ActReg chr19 #5012	1	1
5013	19	17,246,065	17,246,868	803	1	12.72	8.76	20	13	0	0	1	MYO9B	59,875	in gene	ActReg chr19 #5013	1	0
5014	19	17,325,753	17,326,538	785	1	9.56	14.88	18	29	1	1	2	MYO9B, USE1	139554, -10	downstream, upstream	ActReg chr19 #5014	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5015	19	17,336,747	17,337,743	996	2	16.452	16.129	37	38	1	1	3	USE1, OCEL1, NR2F6	11090, 190, 18906	downstream, in gene, downstream	ActReg chr19 #5015	1	1
5016	19	17,346,090	17,346,916	826	2	11.833	14.308	23	28	1	0	2	OCEL1, NR2F6	9448, 9648	downstream, in gene	ActReg chr19 #5016	1	1
5017	19	17,358,994	17,359,702	708	1	7.591	13	11	19	0	1	2	NR2F6, USHBP1	-3197, 16196	upstream, downstream	ActReg chr19 #5017	0	1
5018	19	17,402,573	17,404,271	1,698	1	7.755	10.679	14	17	1	0	2	ANKLE1, ABHD8	10968, 10860	downstream, in gene	ActReg chr19 #5018	0	1
5019	19	17,413,852	17,414,678	826	2	14.5	15.731	33	30	1	3	3	ABHD8, MRPL34, DDA1	17, -2212, -6072	in gene, upstream, upstream	ActReg chr19 #5019	1	1
5020	19	17,416,003	17,417,499	1,496	1	10.022	13.283	19	24	1	3	3	ABHD8, MRPL34, DDA1	-2469, 274, -3586	upstream, in gene, upstream	ActReg chr19 #5020	0	1
5021	19	17,419,970	17,420,753	783	1	7.542	13.125	11	19	1	2	3	ABHD8, MRPL34, DDA1	-6079, 3884, 24	upstream, downstream, in gene	ActReg chr19 #5021	0	1
5022	19	17,444,704	17,446,426	1,722	2	13.537	15.296	36	37	2	2	2	ANO8, GTPBP3	73, -2791	in gene, upstream	ActReg chr19 #5022	1	1
5023	19	17,447,255	17,449,156	1,901	2	10.883	14.783	22	31	2	2	2	ANO8, GTPBP3	-2567, -151	upstream, upstream	ActReg chr19 #5023	1	1
5024	19	17,529,968	17,531,731	1,763	2	11.854	12.782	19	22	1	1	2	LOC100507535, FAM125A	14299, -63	in gene, upstream	ActReg chr19 #5024	1	1
5025	19	17,585,985	17,587,044	1,059	2	11.182	11.394	17	19	0	0	1	SLC27A1	5,214	in gene	ActReg chr19 #5025	1	1
5026	19	17,618,392	17,619,436	1,044	1	9.788	14.121	15	22	0	2	3	SLC27A1, LOC100507551, PGLS	37614, -5641, -3518	downstream, upstream, upstream	ActReg chr19 #5026	0	1
5027	19	17,622,028	17,623,430	1,402	2	16.818	16.386	34	35	1	1	3	SLC27A1, LOC100507551, PGLS	41429, -9456, 297	downstream, upstream, in gene	ActReg chr19 #5027	1	1
5028	19	17,649,528	17,650,862	1,334	2	11.952	12.238	22	19	1	0	1	FAM129C	16,085	in gene	ActReg chr19 #5028	1	1
5029	19	17,665,739	17,667,466	1,727	2	16.444	20.093	37	36	1	1	2	FAM129C, GLT25D1	32492, 91	downstream, in gene	ActReg chr19 #5029	1	1
5030	19	17,716,613	17,717,625	1,012	1	13.581	15.581	28	28	1	0	1	UNC13A	81,889	in gene	ActReg chr19 #5030	0	1
5031	19	17,790,316	17,791,654	1,338	2	11.286	12.595	22	20	1	0	1	UNC13A	8,023	in gene	ActReg chr19 #5031	1	1
5032	19	17,792,134	17,793,615	1,481	2	12.087	13.239	27	25	0	0	1	UNC13A	6,134	in gene	ActReg chr19 #5032	1	1
5033	19	17,797,071	17,799,825	2,754	2	16.384	21.802	34	44	2	1	1	UNC13A	560	in gene	ActReg chr19 #5033	1	1
5034	19	17,829,461	17,830,490	1,029	1	9.875	12.5	16	18	1	1	1	MAP1S	-328	upstream	ActReg chr19 #5034	0	1
5035	19	17,970,145	17,971,432	1,287	2	13.45	13.325	23	24	1	2	2	RPL18A, SNORA68	57, -2609	in gene, upstream	ActReg chr19 #5035	1	1
5036	19	17,999,979	18,001,347	1,368	2	19.861	25.419	60	72	0	0	1	SLC5A5	17,881	in gene	ActReg chr19 #5036	1	1
5037	19	18,043,146	18,044,218	1,072	2	13.939	14.454	23	24	1	1	1	CCDC124	-142	upstream	ActReg chr19 #5037	1	1
5038	19	18,343,206	18,345,360	2,152	2	26.791	33.478	72	81	1	0	1	PDE4C	14,726	in gene	ActReg chr19 #5038	1	1
5039	19	18,385,539	18,386,418	879	1	11.037	13.185	16	21	0	2	3	KIAA1683, JUND, MIR3188	-659, 6454, 6909	upstream, downstream, upstream	ActReg chr19 #5039	0	1
5040	19	18,390,825	18,391,729	904	1	10.84	11.286	17	20	1	3	3	KIAA1683, JUND, MIR3188	-5958, 1155, -1610	upstream, in gene, upstream	ActReg chr19 #5040	0	1
5041	19	18,392,396	18,393,681	1,285	1	12.275	8.4	24	12	1	3	3	KIAA1683, JUND, MIR3188	-7719, -606, 151	upstream, upstream, downstream	ActReg chr19 #5041	1	0
5042	19	18,402,089	18,404,414	2,325	2	12.708	16.25	28	37	1	0	2	JUND, MIR3188	-10819, 10364	upstream, downstream	ActReg chr19 #5042	1	1
5043	19	18,411,708	18,412,502	794	1	10.92	13.44	24	24	0	0	1	LSM4	21,896	downstream	ActReg chr19 #5043	0	1
5044	19	18,433,483	18,434,473	990	1	11.774	11.419	18	21	1	1	1	LSM4	23	in gene	ActReg chr19 #5044	1	0
5045	19	18,439,191	18,439,859	668	1	9.714	12.191	16	20	0	1	1	LSM4	-5,524	upstream	ActReg chr19 #5045	0	1
5046	19	18,484,901	18,485,649	748	1	14	12.435	25	21	0	0	1	PGPEP1	33,867	downstream	ActReg chr19 #5046	1	0
5047	19	18,527,377	18,530,386	3,009	2	11.181	13.149	21	21	1	1	1	SSBP4	-1,340	upstream	ActReg chr19 #5047	1	1
5048	19	18,630,763	18,631,681	918	2	13.828	12.241	26	28	0	1	1	ELL	1,715	in gene	ActReg chr19 #5048	1	1
5049	19	18,632,302	18,633,797	1,495	2	37.766	36.723	125	120	1	1	2	ELL, FKBP8	-112, 21334	upstream, downstream	ActReg chr19 #5049	1	1
5050	19	18,682,219	18,683,217	998	1	12.903	13.806	23	28	1	1	2	C19orf50, UBA52	14146, 104	downstream, in gene	ActReg chr19 #5050	0	1
5051	19	18,698,824	18,700,746	1,922	2	21.433	24.7	69	76	1	1	2	C19orf60, CRLF1	290, 17875	in gene, downstream	ActReg chr19 #5051	1	1
5052	19	18,770,373	18,772,232	1,859	1	10.293	12.672	31	22	1	0	1	KLHL26	23,464	in gene	ActReg chr19 #5052	0	1
5053	19	18,942,202	18,943,213	1,011	2	12.188	9.781	27	15	1	1	1	UPF1	-37	upstream	ActReg chr19 #5053	1	1
5054	19	19,029,649	19,031,037	1,388	2	13.861	13.93	22	26	1	2	3	COPE, DDX49, HOMER3	-144, -141, 21698	upstream, upstream, downstream	ActReg chr19 #5054	1	1
5055	19	19,144,179	19,144,964	785	2	14.8	13.32	26	24	1	2	2	SFRS14, ARMC6	-191, 100	upstream, in gene	ActReg chr19 #5055	1	1
5056	19	19,173,858	19,175,076	1,218	1	9.2	13.895	17	22	1	1	2	ARMC6, SLC25A42	29996, -336	downstream, upstream	ActReg chr19 #5056	0	1
5057	19	19,302,305	19,303,980	1,675	2	19.365	22.365	54	49	2	3	4	LOC729991-MEF2B, LOC729991, RFXANK, NR2C2AP	258, 258, 134, 11096	in gene, in gene, in gene, downstream	ActReg chr19 #5057	1	1
5058	19	19,313,594	19,314,566	972	2	12.742	13.871	24	27	1	1	3	RFXANK, NR2C2AP, NCAN	11072, 158, 8702	downstream, in gene, upstream	ActReg chr19 #5058	1	1
5059	19	19,325,501	19,326,258	757	1	12.917	10.958	27	23	0	0	1	NCAN	3,097	in gene	ActReg chr19 #5059	1	0
5060	19	19,431,012	19,432,215	1,203	2	10.432	18.865	15	27	1	2	2	SF4, KIAA0892	-306, -17	upstream, upstream	ActReg chr19 #5060	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5061	19	19,515,896	19,516,662	766	2	14.583	14	33	32	1	0	1	GATAD2A	19,637	in gene	ActReg chr19 #5061	1	1
5062	19	19,626,678	19,627,669	991	1	9.032	13.613	20	29	1	2	3	GATAD2A, TSSK6, NDUFA13	130531, -704, 154	downstream, upstream, in gene	ActReg chr19 #5062	0	1
5063	19	19,701,701	19,702,788	1,087	2	11.323	12.294	23	25	0	0	1	PBX4	27,195	in gene	ActReg chr19 #5063	1	1
5064	19	19,886,746	19,887,988	1,242	2	15.462	16.923	32	39	0	1	1	LOC284440	-145	upstream	ActReg chr19 #5064	1	1
5065	19	20,149,773	20,150,480	707	1	10.091	11	18	15	1	1	1	ZNF682	151	in gene	ActReg chr19 #5065	0	1
5066	19	20,162,477	20,163,765	1,288	2	11.375	17.35	24	36	1	0	0				ActReg chr19 #5066	1	1
5067	19	21,182,426	21,183,129	703	1	7.273	13.773	11	27	0	0	0				ActReg chr19 #5067	0	1
5068	19	21,203,269	21,204,028	759	1	7.261	14.348	11	26	0	1	1	ZNF430	222	in gene	ActReg chr19 #5068	0	1
5069	19	21,511,704	21,512,419	715	1	11.826	10.217	21	14	0	1	1	ZNF708	151	in gene	ActReg chr19 #5069	1	0
5070	19	21,949,794	21,950,545	751	2	9.13	10.957	19	16	1	1	1	ZNF100	261	in gene	ActReg chr19 #5070	1	1
5071	19	22,604,846	22,605,511	665	1	8.81	10.667	15	17	0	1	1	ZNF98	-30	upstream	ActReg chr19 #5071	0	1
5072	19	23,432,778	23,433,607	829	1	9.615	12.462	16	23	0	0	1	LOC100132815	23,840	downstream	ActReg chr19 #5072	0	1
5073	19	23,945,443	23,946,449	1,006	2	9.742	14	17	21	1	1	1	ZNF681	-4,253	upstream	ActReg chr19 #5073	1	1
5074	19	23,954,709	23,955,881	1,172	1	9.676	14.946	18	23	0	0	0				ActReg chr19 #5074	0	1
5075	19	24,097,305	24,098,183	878	1	7.893	11.429	16	18	0	1	1	ZNF726	60	in gene	ActReg chr19 #5075	0	1
5076	19	24,236,686	24,237,907	1,221	1	10.132	14.842	16	25	0	0	0				ActReg chr19 #5076	0	1
5077	19	28,284,635	28,285,509	874	1	11.429	11	17	14	1	2	2	LOC148189, LOC100506694	-224, 697	upstream, in gene	ActReg chr19 #5077	0	1
5078	19	29,820,146	29,820,988	842	2	12.885	18.654	32	42	0	0	0				ActReg chr19 #5078	1	1
5079	19	30,096,737	30,097,502	765	1	6.043	12.826	10	20	1	1	1	POP4	-51	upstream	ActReg chr19 #5079	0	1
5080	19	30,136,855	30,137,349	494	1	10.812	8.812	18	13	0	0	0				ActReg chr19 #5080	1	0
5081	19	31,118,627	31,119,089	462	1	12.357	7.857	16	10	0	0	0				ActReg chr19 #5081	1	0
5082	19	31,899,202	31,899,675	473	1	7.929	10.5	10	15	0	0	0				ActReg chr19 #5082	0	1
5083	19	32,836,216	32,837,112	896	1	7.214	11.357	13	17	1	1	1	ZNF507	150	in gene	ActReg chr19 #5083	0	1
5084	19	33,071,760	33,072,818	1,058	2	11.879	10.727	17	22	1	1	1	PDCD5	185	in gene	ActReg chr19 #5084	1	1
5085	19	33,182,423	33,182,953	530	1	11.353	9.412	16	13	1	1	1	NUDT19	-179	upstream	ActReg chr19 #5085	1	0
5086	19	33,462,570	33,463,512	942	2	13.138	20.759	33	56	1	2	3	CCDC123, C19orf40, RHPN2	-172, -107, 92783	upstream, upstream, downstream	ActReg chr19 #5086	1	1
5087	19	33,667,538	33,668,814	1,276	2	14.375	14.85	24	27	1	0	1	WDR88	45,178	downstream	ActReg chr19 #5087	1	1
5088	19	33,710,134	33,710,748	614	1	12.158	11.526	16	18	0	0	1	SLC7A10	6,315	in gene	ActReg chr19 #5088	0	1
5089	19	34,174,948	34,175,664	716	1	9.182	12.773	18	23	1	0	1	CHST8	62,445	in gene	ActReg chr19 #5089	0	1
5090	19	34,231,503	34,232,264	761	1	8.458	13.125	13	21	0	0	1	CHST8	119,022	in gene	ActReg chr19 #5090	0	1
5091	19	34,258,423	34,259,271	848	2	12.37	12.593	24	20	0	0	1	CHST8	145,986	in gene	ActReg chr19 #5091	1	1
5092	19	34,310,570	34,312,079	1,509	1	9.638	12.34	16	20	1	0	1	KCTD15	23,573	downstream	ActReg chr19 #5092	0	1
5093	19	34,625,074	34,625,842	768	1	14.333	8.458	28	12	1	0	0				ActReg chr19 #5093	1	0
5094	19	34,662,662	34,663,341	679	1	8.952	12.571	15	19	1	1	1	LSM14A	-351	upstream	ActReg chr19 #5094	0	1
5095	19	34,723,764	34,724,380	616	1	11.947	9.263	17	13	0	0	1	LSM14A	60,720	downstream	ActReg chr19 #5095	1	0
5096	19	34,849,829	34,850,719	890	1	9.815	12.444	19	19	1	1	2	KIAA0355, GPI	104818, -5371	downstream, upstream	ActReg chr19 #5096	0	1
5097	19	34,894,984	34,895,677	693	1	7.905	11.143	14	19	1	1	2	GPI, PDCD2L	39685, 27	downstream, in gene	ActReg chr19 #5097	0	1
5098	19	35,167,620	35,169,055	1,435	2	11.704	14.068	20	20	1	1	1	ZNF302	-230	upstream	ActReg chr19 #5098	1	1
5099	19	35,263,912	35,264,441	529	1	8.5	11.375	13	18	1	1	1	ZNF599	-42	upstream	ActReg chr19 #5099	0	1
5100	19	35,596,067	35,597,612	1,545	2	11.438	11.667	18	21	0	1	2	LOC100128675, FXYD3	369, -9893	in gene, upstream	ActReg chr19 #5100	1	1
5101	19	35,605,833	35,606,477	644	1	4.389	12.55	9	17	0	1	3	LOC100128675, FXYD3, LGI4	-8947, -577, 20023	upstream, upstream, downstream	ActReg chr19 #5101	0	1
5102	19	35,809,540	35,810,439	899	1	13.679	8.964	25	16	0	0	2	MAG, CD22	26951, -10083	downstream, upstream	ActReg chr19 #5102	1	0
5103	19	35,896,139	35,896,606	467	1	4.643	10.643	9	16	0	0	0				ActReg chr19 #5103	0	1
5104	19	36,103,293	36,103,992	699	2	10.091	15.046	19	29	1	1	1	HAUS5	-4	upstream	ActReg chr19 #5104	1	1
5105	19	36,119,535	36,120,274	739	2	13.913	12.435	26	25	1	1	2	HAUS5, RBM42	16258, -76	downstream, upstream	ActReg chr19 #5105	1	1
5106	19	36,192,947	36,193,925	978	2	11.613	13.935	26	24	1	0	1	ZBTB32	-10,394	upstream	ActReg chr19 #5106	1	1
5107	19	36,207,756	36,208,732	976	2	10.967	12	16	19	1	1	2	ZBTB32, MLL4	4414, -677	downstream, upstream	ActReg chr19 #5107	1	1
5108	19	36,319,372	36,320,225	853	2	14.333	16.63	30	39	0	0	1	NPHS1	23,097	in gene	ActReg chr19 #5108	1	1
5109	19	36,370,452	36,371,359	907	2	17.143	18.429	35	41	0	0	2	APLP1, NFKBID	11504, 20647	downstream, downstream	ActReg chr19 #5109	1	1
5110	19	36,454,246	36,454,946	700	1	9.545	13.136	18	25	0	0	0				ActReg chr19 #5110	0	1
5111	19	36,466,251	36,467,192	941	2	12.517	11.414	25	20	0	0	0				ActReg chr19 #5111	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5112	19	36,485,644	36,486,524	880	1	9.074	12.593	13	18	2	1	2	SDHAF1, C19orf46	-6, 13588	upstream, downstream	ActReg chr19 #5112	0	1
5113	19	36,500,050	36,500,957	907	1	10.214	9.964	17	15	1	1	3	C19orf46, ALKBH6, CLIP3	-831, 4638, 23272	upstream, in gene, downstream	ActReg chr19 #5113	1	0
5114	19	36,544,637	36,545,505	868	1	9.286	12.857	15	18	1	2	2	THAP8, WDR62	593, -712	in gene, upstream	ActReg chr19 #5114	0	1
5115	19	36,605,463	36,606,274	811	1	12.346	10.885	23	15	1	2	4	WDR62, LOC728361, POLR2I, TBCB	60085, 3763, 338, -20	downstream, downstream, in gene, upstream	ActReg chr19 #5115	1	0
5116	19	36,630,253	36,631,290	1,037	2	15.625	18.406	38	40	1	1	1	CAPNS1	-147	upstream	ActReg chr19 #5116	1	1
5117	19	36,705,072	36,706,380	1,308	1	9.024	13.293	15	22	1	2	2	ZNF565, ZNF146	260, 222	in gene, in gene	ActReg chr19 #5117	0	1
5118	19	36,869,413	36,870,353	940	2	11.69	11.483	25	16	1	1	1	ZFP14	195	in gene	ActReg chr19 #5118	1	1
5119	19	36,979,715	36,981,028	1,313	1	6.683	11.073	11	16	1	2	2	ZNF566, LOC728752	92, -158	in gene, upstream	ActReg chr19 #5119	0	1
5120	19	37,063,831	37,064,380	549	1	9.647	10.588	16	13	1	0	1	ZNF529	32,073	in gene	ActReg chr19 #5120	1	0
5121	19	37,328,744	37,329,312	568	1	11.167	8.722	16	14	1	1	2	LOC284408, ZNF790	40941, 256	downstream, in gene	ActReg chr19 #5121	1	0
5122	19	37,406,754	37,407,665	911	1	11.929	7.179	16	11	1	2	2	ZNF829, ZNF568	-16, -25	upstream, upstream	ActReg chr19 #5122	1	0
5123	19	37,708,509	37,709,567	1,058	1	10.273	13	15	21	1	1	2	ZNF585B, ZNF383	-7587, -8328	upstream, upstream	ActReg chr19 #5123	0	1
5124	19	37,825,082	37,825,832	750	1	6.333	11.333	9	16	1	1	2	LOC100507342, HKR1	16655, -123	downstream, upstream	ActReg chr19 #5124	0	1
5125	19	37,861,660	37,862,570	910	1	8.655	13.931	15	26	1	1	2	HKR1, ZNF527	36535, 56	downstream, in gene	ActReg chr19 #5125	0	1
5126	19	38,269,681	38,270,578	897	1	13.25	9.429	21	14	1	1	1	ZNF573	101	in gene	ActReg chr19 #5126	1	0
5127	19	38,397,395	38,398,019	624	1	8.5	10.9	17	17	1	2	2	WDR87, SIPA1L3	-390, -161	upstream, upstream	ActReg chr19 #5127	0	1
5128	19	38,864,770	38,865,917	1,147	2	9.143	10.143	19	18	1	1	3	CATSPERG, PSMD8, GGN	38900, 153, 13325	downstream, in gene, downstream	ActReg chr19 #5128	1	1
5129	19	38,893,537	38,894,071	534	1	8.438	10.938	11	15	1	1	3	SPRED3, FAM98C, RASGRP4	12865, 29, 23141	downstream, in gene, downstream	ActReg chr19 #5129	0	1
5130	19	38,945,483	38,946,267	784	2	10.292	14.833	21	33	0	0	1	RYR1	21,535	in gene	ActReg chr19 #5130	1	1
5131	19	39,109,181	39,110,167	986	1	7.71	11.742	14	21	1	2	2	MAP4K1, EIF3K	-1031, -48	upstream, upstream	ActReg chr19 #5131	0	1
5132	19	39,137,879	39,138,600	721	1	10.609	13.87	20	21	1	1	1	ACTN4	-88	upstream	ActReg chr19 #5132	0	1
5133	19	39,148,347	39,148,841	494	1	8	10.688	12	16	0	0	1	ACTN4	10,267	in gene	ActReg chr19 #5133	0	1
5134	19	39,173,926	39,174,864	938	2	12.276	10.552	18	15	0	0	1	ACTN4	36,068	in gene	ActReg chr19 #5134	1	1
5135	19	39,182,237	39,183,320	1,083	2	9.912	10.794	15	14	0	0	1	ACTN4	44,451	in gene	ActReg chr19 #5135	1	1
5136	19	39,342,862	39,343,561	699	1	9.955	12.182	16	21	1	1	1	HNRNPL	-232	upstream	ActReg chr19 #5136	0	1
5137	19	39,360,214	39,361,403	1,189	2	13.811	15.703	35	37	1	0	2	RINL, SIRT2	8086, 29694	in gene, downstream	ActReg chr19 #5137	1	1
5138	19	39,389,802	39,390,790	988	2	10.935	13.129	17	22	1	2	3	SIRT2, NFKBIB, LOC643669	206, -319, 12502	in gene, upstream, downstream	ActReg chr19 #5138	1	1
5139	19	39,561,282	39,562,047	765	2	11.565	14.304	17	25	0	0	0				ActReg chr19 #5139	1	1
5140	19	39,564,074	39,564,790	716	2	13.864	11.091	23	19	0	0	0				ActReg chr19 #5140	1	1
5141	19	39,714,196	39,714,969	773	2	13.708	14.546	31	28	0	0	0				ActReg chr19 #5141	1	1
5142	19	39,832,089	39,833,083	994	2	33.968	33.581	106	116	1	2	2	GMFG, SAMD4B	-5860, -522	upstream, upstream	ActReg chr19 #5142	1	1
5143	19	39,881,258	39,882,566	1,308	2	11.073	13.537	18	22	1	2	3	SAMD4B, PAF1, MED29	48804, -233, -51	downstream, upstream, upstream	ActReg chr19 #5143	1	1
5144	19	39,902,555	39,903,677	1,122	2	13.8	15.314	23	27	1	1	2	ZFP36, PLEKHG2	5629, -634	downstream, upstream	ActReg chr19 #5144	1	1
5145	19	39,926,044	39,926,840	796	1	7.64	12.24	13	21	1	1	3	PLEKHG2, RPS16, SUPT5H	22692, 176, 9744	downstream, in gene, upstream	ActReg chr19 #5145	0	1
5146	19	39,971,237	39,971,882	645	1	13.55	12.9	16	17	1	1	2	SUPT5H, TIMM50	35373, 507	downstream, in gene	ActReg chr19 #5146	1	0
5147	19	40,030,574	40,031,026	452	1	11.357	9.5	15	14	2	2	2	EID2B, EID2	-7306, 38	upstream, in gene	ActReg chr19 #5147	1	0
5148	19	40,089,604	40,090,382	778	2	10.75	12.5	21	22	0	1	1	LGALS13	-3,176	upstream	ActReg chr19 #5148	1	1
5149	19	40,135,715	40,136,955	1,240	2	13.763	16.526	27	36	0	0	1	LGALS16	-10,223	upstream	ActReg chr19 #5149	1	1
5150	19	40,476,546	40,477,340	794	1	8.083	13.042	12	23	1	1	1	PSMC4	-130	upstream	ActReg chr19 #5150	0	1
5151	19	40,596,285	40,597,033	748	1	6.583	11.667	12	23	1	1	1	ZNF780A	186	in gene	ActReg chr19 #5151	0	1
5152	19	40,626,624	40,627,413	789	2	13.24	8.68	28	20	0	0	0				ActReg chr19 #5152	1	1
5153	19	40,725,456	40,726,253	797	1	9.76	13.56	16	23	0	1	4	MAP3K10, TTC9B, CNTD2, AKT2	28203, -1548, 6743, 65411	downstream, upstream, downstream, downstream	ActReg chr19 #5153	0	1
5154	19	40,854,081	40,854,790	709	1	11.227	13.954	20	25	1	2	2	C19orf47, PLD3	-142, 103	upstream, in gene	ActReg chr19 #5154	0	1
5155	19	40,971,295	40,972,943	1,648	1	9.51	11.712	17	21	1	2	2	BLVRB, SPTBN4	-394, -1007	upstream, upstream	ActReg chr19 #5155	0	1
5156	19	41,082,427	41,083,319	892	2	10.607	13.75	21	34	1	1	2	SPTBN4, SHKBP1	109747, 116	downstream, in gene	ActReg chr19 #5156	1	1
5157	19	41,110,954	41,111,957	1,003	1	11.194	9.903	15	15	1	0	1	LTBP4	12,383	in gene	ActReg chr19 #5157	1	0
5158	19	41,116,072	41,117,457	1,385	2	9.744	12.419	21	19	0	0	1	LTBP4	17,692	in gene	ActReg chr19 #5158	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5159	19	41,120,039	41,120,636	597	1	7.944	11.278	11	17	1	0	1	LTBP4	21,265	in gene	ActReg chr19 #5159	0	1
5160	19	41,221,337	41,223,178	1,841	3	10.724	9.586	21	16	2	2	3	ADCK4, ITPKC, LOC100507668	533, -751, 16952	in gene, upstream, downstream	ActReg chr19 #5160	1	1
5161	19	41,769,871	41,770,740	869	1	8.037	13.148	15	21	1	1	2	AXL, HNRNPUL1	45197, 1914	downstream, in gene	ActReg chr19 #5161	0	1
5162	19	41,815,760	41,816,618	858	2	13.074	11.741	24	22	1	1	2	HNRNPUL1, CCDC97	47798, 95	downstream, in gene	ActReg chr19 #5162	1	1
5163	19	41,827,602	41,828,340	738	1	7.739	10.304	11	15	0	0	2	CCDC97, TGFB1	11877, 31860	in gene, downstream	ActReg chr19 #5163	0	1
5164	19	41,828,906	41,830,004	1,098	1	7.735	11.618	14	18	0	0	2	CCDC97, TGFB1	13361, 30376	in gene, downstream	ActReg chr19 #5164	0	1
5165	19	41,869,694	41,870,315	621	1	9.4	10.4	14	16	1	2	3	TGFB1, B9D2, TMEM91	-10173, 74, 133	upstream, in gene, in gene	ActReg chr19 #5165	0	1
5166	19	41,945,292	41,946,411	1,119	2	19.6	21.971	65	61	1	2	3	ATP5SL, C19orf69, LOC100505495	-8, -3212, 60703	upstream, upstream, downstream	ActReg chr19 #5166	1	1
5167	19	42,123,223	42,123,950	727	2	11.261	10.348	18	19	0	0	1	CEACAM4	9,856	downstream	ActReg chr19 #5167	1	1
5168	19	42,317,432	42,317,992	560	2	10.944	12.167	21	23	0	0	1	CEACAM3	17,178	downstream	ActReg chr19 #5168	1	1
5169	19	42,363,491	42,364,460	969	2	11.3	9.167	17	17	1	1	3	DMRTC2, RPS19, LOC100505604	14889, -13, 9306	downstream, upstream, downstream	ActReg chr19 #5169	1	1
5170	19	42,388,010	42,388,749	739	1	7.826	12.652	10	21	1	1	2	CD79A, ARHGEF1	7189, 1112	downstream, in gene	ActReg chr19 #5170	0	1
5171	19	42,391,704	42,392,408	704	1	8.136	12	17	21	0	0	2	CD79A, ARHGEF1	10866, 4789	downstream, in gene	ActReg chr19 #5171	0	1
5172	19	42,500,978	42,501,814	836	1	9.5	15.731	14	31	1	1	2	ATP1A3, GRIK5	-3014, 68561	upstream, downstream	ActReg chr19 #5172	0	1
5173	19	42,644,054	42,644,952	898	2	18.179	18.107	39	41	0	2	3	POU2F2, LOC100505622, MIR4323	-7873, 7796, -6838	upstream, downstream, upstream	ActReg chr19 #5173	1	1
5174	19	42,646,988	42,648,275	1,287	2	19.075	24.125	52	65	0	0	3	LOC100505622, MIR4323, LOC100505639	10924, -9966, -9090	downstream, upstream, upstream	ActReg chr19 #5174	1	1
5175	19	42,720,853	42,721,495	642	1	9.1	10.65	13	21	1	2	2	DEDD2, ZNF526	639, -3318	in gene, upstream	ActReg chr19 #5175	0	1
5176	19	42,722,439	42,723,266	827	1	9.808	8.038	14	13	0	2	2	DEDD2, ZNF526	-1039, -1640	upstream, upstream	ActReg chr19 #5176	1	0
5177	19	42,746,697	42,747,771	1,074	2	15.364	16.636	23	25	1	2	3	GSK3A, LOC100132272, ERF	-498, 307, 12075	upstream, in gene, downstream	ActReg chr19 #5177	1	1
5178	19	42,748,608	42,749,574	966	2	10.581	11.806	16	17	1	2	3	GSK3A, LOC100132272, ERF	-2355, 2164, 10218	upstream, in gene, downstream	ActReg chr19 #5178	1	1
5179	19	42,758,001	42,758,750	749	1	8.391	12.043	13	21	1	1	2	LOC100132272, ERF	11448, 934	downstream, in gene	ActReg chr19 #5179	0	1
5180	19	42,772,608	42,773,462	854	2	11.296	13.111	22	23	1	0	0				ActReg chr19 #5180	1	1
5181	19	42,783,911	42,785,197	1,286	2	13.05	14.925	24	31	1	1	1	CIC	-4,263	upstream	ActReg chr19 #5181	1	1
5182	19	42,787,068	42,788,082	1,014	1	8.406	12.969	17	20	0	1	1	CIC	-1,242	upstream	ActReg chr19 #5182	0	1
5183	19	42,806,212	42,807,039	827	2	12.16	11.88	22	17	1	3	4	CIC, LOC100505682, PAFAH1B3, PRR19	17808, 1657, 327, 341	downstream, in gene, in gene, in gene	ActReg chr19 #5183	1	1
5184	19	42,817,313	42,818,100	787	1	7.083	11.208	9	17	1	1	3	LOC100505682, PRR19, TMEM145	-9424, 11422, 229	upstream, downstream, in gene	ActReg chr19 #5184	0	1
5185	19	42,900,993	42,901,825	832	1	6.538	13.077	10	22	1	1	2	CNFN, LIPE	-6965, 30169	upstream, downstream	ActReg chr19 #5185	0	1
5186	19	42,927,307	42,928,334	1,027	1	6.5	11.938	9	18	1	0	2	LIPE, CXCL17	3758, 19316	in gene, downstream	ActReg chr19 #5186	0	1
5187	19	43,105,666	43,106,590	924	1	9.143	13.964	18	26	0	1	1	CEACAM8	-7,046	upstream	ActReg chr19 #5187	0	1
5188	19	43,469,488	43,469,926	438	1	9	5.714	13	9	0	0	1	PSG11	60,924	in gene	ActReg chr19 #5188	1	0
5189	19	43,624,640	43,625,162	522	2	10.765	9.647	19	14	0	0	0				ActReg chr19 #5189	1	1
5190	19	43,943,080	43,943,581	501	1	12.8	10.933	22	17	0	0	0				ActReg chr19 #5190	1	0
5191	19	44,029,575	44,030,177	602	1	9.368	12.158	13	23	0	2	2	ETHE1, ZNF575	1520, -7464	in gene, upstream	ActReg chr19 #5191	0	1
5192	19	44,030,980	44,031,792	812	2	13.68	12.2	30	24	1	2	2	ETHE1, ZNF575	10, -5954	in gene, upstream	ActReg chr19 #5192	1	1
5193	19	44,036,641	44,037,597	956	1	6.379	11.241	14	18	1	2	3	ETHE1, ZNF575, XRCC1	-5723, -221, 42611	upstream, upstream, downstream	ActReg chr19 #5193	0	1
5194	19	44,099,839	44,101,043	1,204	2	15.921	16.368	37	28	1	2	2	IRGQ, ZNF576	-154, -103	upstream, upstream	ActReg chr19 #5194	1	1
5195	19	44,123,193	44,124,433	1,240	2	12.128	15.205	20	24	1	1	3	ZNF428, SRRM5, CADM4	201, 7560, 20178	in gene, downstream, downstream	ActReg chr19 #5195	1	1
5196	19	44,269,032	44,269,861	829	1	10.731	12.385	14	25	0	0	2	C19orf61, KCNN4	-10304, 15963	upstream, downstream	ActReg chr19 #5196	0	1
5197	19	44,284,741	44,285,946	1,205	1	9.378	11.784	14	18	0	1	1	KCNN4	66	in gene	ActReg chr19 #5197	0	1
5198	19	44,292,960	44,293,734	774	2	16.44	17.8	34	40	0	0	2	KCNN4, LYPD5	-7938, 31461	upstream, downstream	ActReg chr19 #5198	1	1
5199	19	44,405,710	44,406,451	741	1	12	11.13	18	16	1	1	1	LOC100505715	-123	upstream	ActReg chr19 #5199	1	0
5200	19	44,506,689	44,507,691	1,002	1	8.226	12.903	14	21	1	2	3	ZNF155, LOC100505743, ZNF230	18835, -202, 113	downstream, upstream, in gene	ActReg chr19 #5200	0	1
5201	19	44,598,213	44,598,824	611	1	7.474	12.526	11	15	1	1	2	ZNF284, ZNF224	22221, 36	downstream, in gene	ActReg chr19 #5201	0	1
5202	19	44,617,078	44,617,711	633	1	11.35	11.1	19	18	1	2	3	ZNF224, LOC100379224, ZNF225	18912, -58, -154	downstream, upstream, upstream	ActReg chr19 #5202	1	0
5203	19	44,763,802	44,764,441	639	2	17.4	15	37	30	1	1	1	ZNF233	45	in gene	ActReg chr19 #5203	1	1
5204	19	44,808,708	44,809,277	569	1	9.706	10.177	14	16	1	1	1	ZNF235	186	in gene	ActReg chr19 #5204	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5205	19	45,003,988	45,005,040	1,052	2	9.758	14.606	14	24	1	1	2	ZNF180, CEACAM20	60, 29034	in gene, downstream	ActReg chr19 #5205	1	1
5206	19	45,016,774	45,017,438	664	1	5.2	10.4	8	17	0	0	1	CEACAM20	16,442	in gene	ActReg chr19 #5206	0	1
5207	19	45,245,033	45,245,746	713	1	13.591	6.818	24	13	0	1	1	BCL3	-6,589	upstream	ActReg chr19 #5207	1	0
5208	19	45,457,800	45,459,088	1,288	2	10.65	12.6	20	24	1	1	3	APOC4, APOC2, CLPTM1	12949, 9201, -194	downstream, downstream, upstream	ActReg chr19 #5208	1	1
5209	19	45,582,093	45,582,874	781	1	11.917	13.333	22	24	1	2	3	SFRS16, ZNF296, GEMIN7	40185, -2795, -35	downstream, upstream, upstream	ActReg chr19 #5209	0	1
5210	19	45,595,642	45,596,709	1,067	1	6.767	13.677	20	26	1	1	2	GEMIN7, LRRC68	13657, -41	downstream, upstream	ActReg chr19 #5210	0	1
5211	19	45,829,311	45,829,923	612	1	8.5	11.35	12	23	0	1	1	CKM	-3,384	upstream	ActReg chr19 #5211	0	1
5212	19	45,873,335	45,874,354	1,019	2	18.375	18.219	47	47	1	1	2	ERCC2, PPP1R13L	1, 35763	in gene, downstream	ActReg chr19 #5212	1	1
5213	19	45,901,185	45,901,777	592	1	11.389	7.611	20	13	1	0	3	PPP1R13L, CD3EAP, ERCC1	8126, -7986, 25696	in gene, upstream, downstream	ActReg chr19 #5213	1	0
5214	19	45,908,506	45,910,424	1,918	2	32.4	37.617	133	146	2	2	3	PPP1R13L, CD3EAP, ERCC1	142, -2, 17712	in gene, upstream, downstream	ActReg chr19 #5214	1	1
5215	19	45,926,665	45,927,355	690	1	10.191	12.905	14	21	1	1	1	ERCC1	167	in gene	ActReg chr19 #5215	0	1
5216	19	45,953,306	45,954,789	1,483	2	12.957	16.404	29	30	1	0	0				ActReg chr19 #5216	1	1
5217	19	45,958,841	45,959,864	1,023	2	12.594	14.625	22	31	0	0	0				ActReg chr19 #5217	1	1
5218	19	45,981,228	45,982,502	1,274	2	12.75	15.175	32	32	0	0	2	FOSB, RTN2	10612, 18448	downstream, downstream	ActReg chr19 #5218	1	1
5219	19	45,988,400	45,989,045	645	1	11.35	11.65	23	27	0	0	2	FOSB, RTN2	17469, 11591	downstream, in gene	ActReg chr19 #5219	0	1
5220	19	45,998,819	46,000,220	1,401	2	9.535	13.395	20	25	1	2	2	RTN2, FLJ40125	794, -2212	in gene, upstream	ActReg chr19 #5220	1	1
5221	19	46,009,466	46,009,928	462	1	11.867	9.6	14	12	1	1	3	RTN2, FLJ40125, VASP	-9384, 7966, -991	upstream, downstream, upstream	ActReg chr19 #5221	1	0
5222	19	46,010,216	46,011,087	871	2	16.577	21.926	40	50	1	1	3	RTN2, FLJ40125, VASP	-10338, 8920, -37	upstream, downstream, upstream	ActReg chr19 #5222	1	1
5223	19	46,045,490	46,046,168	678	1	8.81	12.381	13	20	0	0	1	OPA3	42,293	in gene	ActReg chr19 #5223	0	1
5224	19	46,047,243	46,047,933	690	1	11	8.286	22	14	0	0	1	OPA3	40,534	in gene	ActReg chr19 #5224	1	0
5225	19	46,064,105	46,065,362	1,257	1	12.128	9.333	18	14	0	0	2	OPA3, GPR4	3389, 20733	in gene, downstream	ActReg chr19 #5225	1	0
5226	19	46,087,716	46,088,659	943	2	15.448	19.069	39	46	1	1	2	OPA3, GPR4	-65, 17279	upstream, downstream	ActReg chr19 #5226	1	1
5227	19	46,145,215	46,145,919	704	1	10.864	13.136	15	19	1	2	3	EML2, MIR330, LOC100287177	3208, -3222, 619	in gene, upstream, in gene	ActReg chr19 #5227	0	1
5228	19	46,194,810	46,196,295	1,485	1	8.936	12.723	13	19	1	2	3	GIPR, SNRPD2, QPCTL	24050, -109, -189	downstream, upstream, upstream	ActReg chr19 #5228	0	1
5229	19	46,220,390	46,221,285	895	2	17.036	17.536	38	42	1	0	1	FBXO46	13,314	in gene	ActReg chr19 #5229	1	1
5230	19	46,365,950	46,367,049	1,099	1	10.057	13.286	18	22	1	2	2	SYMPK, FOXA3	49, -1019	in gene, upstream	ActReg chr19 #5230	0	1
5231	19	46,388,750	46,389,234	484	1	10.067	10.733	15	18	1	1	2	IRF2BP1, MYPOP	384, 16870	in gene, downstream	ActReg chr19 #5231	0	1
5232	19	46,389,310	46,390,450	1,140	2	11.361	14.833	20	27	2	1	2	IRF2BP1, MYPOP	-504, 15982	upstream, downstream	ActReg chr19 #5232	1	1
5233	19	46,405,928	46,406,379	451	1	9.214	10.5	11	13	1	1	1	MYPOP	-291	upstream	ActReg chr19 #5233	0	1
5234	19	46,430,782	46,431,474	692	2	9.955	12.046	27	23	0	0	0				ActReg chr19 #5234	1	1
5235	19	46,455,610	46,456,627	1,017	1	8.125	17.375	17	34	1	0	1	NOVA2	20,539	in gene	ActReg chr19 #5235	0	1
5236	19	46,571,645	46,572,412	767	1	6.167	14	9	24	0	0	0				ActReg chr19 #5236	0	1
5237	19	46,721,198	46,722,011	813	2	16.32	16.8	29	36	0	0	1	DKFZp434J0226	8,105	downstream	ActReg chr19 #5237	1	1
5238	19	47,103,708	47,104,489	781	2	14.68	15.8	28	27	1	2	2	LOC100506012, CALM3	359, -414	in gene, upstream	ActReg chr19 #5238	1	1
5239	19	47,220,299	47,220,904	605	1	11.368	11.632	15	21	1	1	3	PRKD2, MIR320E, STRN4	-217, -7999, 29119	upstream, upstream, downstream	ActReg chr19 #5239	0	1
5240	19	47,287,865	47,288,685	820	2	13.577	13.654	25	24	0	0	1	SLC1A5	3,567	in gene	ActReg chr19 #5240	1	1
5241	19	47,291,558	47,292,149	591	1	9.778	6.722	15	10	1	1	1	SLC1A5	-11	upstream	ActReg chr19 #5241	1	0
5242	19	47,296,446	47,296,967	521	1	11	7.235	19	10	0	1	1	SLC1A5	-4,864	upstream	ActReg chr19 #5242	1	0
5243	19	47,353,993	47,354,640	647	1	9.1	11.35	18	22	1	1	1	AP2S1	-113	upstream	ActReg chr19 #5243	0	1
5244	19	47,359,817	47,360,370	553	1	11.471	9	18	14	0	1	1	AP2S1	-5,890	upstream	ActReg chr19 #5244	1	0
5245	19	47,551,627	47,552,257	630	1	10.95	17	21	36	1	1	2	NPAS1, TMEM160	27799, -60	downstream, upstream	ActReg chr19 #5245	0	1
5246	19	47,615,259	47,615,860	601	1	9.474	9.789	12	16	1	1	1	ZC3H4	1,450	in gene	ActReg chr19 #5246	0	1
5247	19	47,633,728	47,634,431	703	1	11.636	8.682	17	15	1	1	1	SAE1	-1	upstream	ActReg chr19 #5247	1	0
5248	19	47,759,400	47,759,952	552	1	10.471	15.471	15	30	1	1	1	CCDC9	-55	upstream	ActReg chr19 #5248	0	1
5249	19	47,776,454	47,777,102	648	1	10.3	12.85	17	18	1	1	2	CCDC9, PRR24	17047, -1364	downstream, upstream	ActReg chr19 #5249	0	1
5250	19	47,792,674	47,793,104	430	1	12.077	8.077	18	11	0	0	0				ActReg chr19 #5250	1	0
5251	19	47,818,451	47,819,067	616	1	11.053	9.579	16	16	0	0	1	C5AR1	5,655	in gene	ActReg chr19 #5251	1	0
5252	19	47,939,915	47,941,644	1,729	2	11.074	10.37	24	21	0	0	1	SLC8A2	34,528	in gene	ActReg chr19 #5252	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5253	19	47,947,308	47,948,086	778	2	14.625	14.042	25	29	0	0	1	SLC8A2	27,610	in gene	ActReg chr19 #5253	1	1
5254	19	47,987,094	47,987,793	699	1	14.046	14.454	23	27	1	2	3	KPTN, LOC100505681, NAPA	78, -27, 31054	in gene, upstream, downstream	ActReg chr19 #5254	0	1
5255	19	48,017,891	48,018,866	975	1	11.167	11.667	16	18	1	1	2	NAPA, ZNF541	119, 40735	in gene, downstream	ActReg chr19 #5255	0	1
5256	19	48,111,348	48,112,151	803	1	7.48	10.88	15	18	1	1	1	GLTSCR1	296	in gene	ActReg chr19 #5256	0	1
5257	19	48,226,057	48,226,892	835	1	5.077	10.154	8	14	0	0	1	EHD2	9,873	in gene	ActReg chr19 #5257	0	1
5258	19	48,246,249	48,247,327	1,078	2	12.546	13.909	23	23	1	1	2	EHD2, GLTSCR2	30187, -2005	downstream, upstream	ActReg chr19 #5258	1	1
5259	19	48,277,058	48,277,544	486	1	11.333	10.533	15	14	0	2	2	LOC729626, SEPW1	-5204, -4541	upstream, upstream	ActReg chr19 #5259	1	0
5260	19	48,281,206	48,282,194	988	2	13.129	15.516	26	35	1	1	2	LOC729626, SEPW1	-9603, -142	upstream, upstream	ActReg chr19 #5260	1	1
5261	19	48,613,562	48,614,227	665	1	7.762	10.714	13	20	0	1	2	PLA2G4C, LIG1	215, 59666	in gene, downstream	ActReg chr19 #5261	0	1
5262	19	48,673,292	48,674,128	836	2	9.308	13.231	18	24	1	2	2	LIG1, C19orf68	-150, -1500	upstream, upstream	ActReg chr19 #5262	1	1
5263	19	48,824,971	48,825,557	586	1	10.5	13.389	13	21	1	2	2	CCDC114, EMP3	-1932, -3365	upstream, upstream	ActReg chr19 #5263	0	1
5264	19	48,866,187	48,866,871	684	2	14.381	13.095	27	25	1	2	2	TMEM143, SYNGR4	657, -1128	in gene, upstream	ActReg chr19 #5264	1	1
5265	19	48,948,697	48,949,476	779	1	10.32	13.52	16	23	1	1	3	GRIN2D, GRWD1, KCNJ14	50954, 56, -9680	downstream, in gene, upstream	ActReg chr19 #5265	0	1
5266	19	49,121,944	49,123,178	1,234	1	12.231	13.231	18	21	1	3	3	FAM83E, RPL18, SPHK2	-5867, -128, 13	upstream, upstream, in gene	ActReg chr19 #5266	0	1
5267	19	49,140,662	49,141,647	985	2	14.677	16.032	35	33	1	1	3	SPHK2, DBP, CA11	18606, -515, 8297	downstream, upstream, downstream	ActReg chr19 #5267	1	1
5268	19	49,147,904	49,148,632	728	1	10.783	8.609	20	15	0	2	2	DBP, CA11	-7629, 1183	upstream, in gene	ActReg chr19 #5268	1	0
5269	19	49,149,327	49,150,140	813	2	14.4	14.8	29	26	0	1	2	DBP, CA11	-9094, -282	upstream, upstream	ActReg chr19 #5269	1	1
5270	19	49,223,683	49,224,692	1,009	2	12	13.129	20	22	1	1	2	MAMSTR, RASIP1	-1211, 19783	upstream, in gene	ActReg chr19 #5270	1	1
5271	19	49,298,312	49,299,213	901	2	18.808	17.286	46	38	1	0	1	BCAT2	15,558	in gene	ActReg chr19 #5271	1	1
5272	19	49,468,362	49,469,642	1,280	2	10.375	11.925	21	21	1	1	3	BAX, FTL, GYS1	10885, 436, 27608	downstream, in gene, downstream	ActReg chr19 #5272	1	1
5273	19	49,496,599	49,497,377	778	2	14.64	11.92	28	21	1	2	2	GYS1, RUVBL2	-378, -168	upstream, upstream	ActReg chr19 #5273	1	1
5274	19	49,588,267	49,589,255	988	2	11.065	14.065	18	23	1	1	1	SNRNP70	296	in gene	ActReg chr19 #5274	1	1
5275	19	49,621,806	49,622,672	866	2	17.704	17.296	37	34	1	2	4	SNRNP70, LIN7B, C19orf73, PPFIA3	33774, 4621, 158, -424	downstream, downstream, in gene, upstream	ActReg chr19 #5275	1	1
5276	19	49,652,683	49,654,318	1,635	2	14.686	16.569	27	26	1	1	3	PPFIA3, HRC, TRPM4	30837, 5181, -7552	in gene, downstream, upstream	ActReg chr19 #5276	1	1
5277	19	49,946,419	49,947,416	997	2	13.097	9.9	25	21	1	1	3	SLC17A7, PIH1D1, ALDH16A1	-2109, 8198, -9556	upstream, downstream, upstream	ActReg chr19 #5277	1	1
5278	19	49,956,303	49,957,239	936	1	11.448	7.643	24	14	1	2	2	PIH1D1, ALDH16A1	-1656, 298	upstream, in gene	ActReg chr19 #5278	1	0
5279	19	49,981,858	49,982,618	760	2	16.522	20.652	42	53	0	0	3	ALDH16A1, FLT3LG, RPL13A	25765, 4752, -8627	downstream, in gene, upstream	ActReg chr19 #5279	1	1
5280	19	50,116,647	50,118,000	1,353	1	9.143	12.571	17	21	0	0	1	PRR12	22,411	in gene	ActReg chr19 #5280	0	1
5281	19	50,143,080	50,144,315	1,235	2	14.079	12.79	30	25	1	2	2	RRAS, SCAF1	-297, -1685	upstream, upstream	ActReg chr19 #5281	1	1
5282	19	50,144,792	50,145,627	835	2	14.5	10.885	32	20	1	2	2	RRAS, SCAF1	-1809, -173	upstream, upstream	ActReg chr19 #5282	1	1
5283	19	50,220,648	50,221,266	618	2	14.526	14.368	28	30	0	0	1	CPT1C	26,556	downstream	ActReg chr19 #5283	1	1
5284	19	50,316,417	50,317,283	866	2	13.407	12.37	23	24	1	2	3	AP2A1, FUZ, MED25	46670, -283, -4686	downstream, upstream, upstream	ActReg chr19 #5284	1	1
5285	19	50,353,948	50,354,583	635	1	7.7	10.85	14	18	1	2	4	LOC100506033, PTOV1, LOC100506002, PNKP	668, -151, 8279, 16553	in gene, upstream, downstream, downstream	ActReg chr19 #5285	0	1
5286	19	50,379,338	50,381,030	1,692	2	11.264	12.358	21	19	1	2	3	PNKP, AKT1S1, TBC1D17	-9366, 460, -498	upstream, in gene, upstream	ActReg chr19 #5286	1	1
5287	19	50,432,097	50,433,105	1,008	2	10.484	15.258	16	28	1	3	3	IL4I1, NUP62, ATF5	161, 387, 642	in gene, in gene, in gene	ActReg chr19 #5287	1	1
5288	19	50,489,558	50,492,534	2,976	2	39.215	51.849	257	320	0	0	1	VRK3	37,759	in gene	ActReg chr19 #5288	1	1
5289	19	50,836,653	50,837,182	529	1	14.25	9	22	15	1	1	1	KCNC3	-4,283	upstream	ActReg chr19 #5289	1	0
5290	19	51,014,134	51,015,139	1,005	2	12.469	14.062	24	24	1	1	3	JOSD2, ASPDH, LRRC4B	-291, 3311, 56666	upstream, downstream, downstream	ActReg chr19 #5290	1	1
5291	19	51,161,604	51,162,391	787	1	9.417	11.875	13	16	1	0	2	LOC342918, SHANK1	9295, 58198	in gene, downstream	ActReg chr19 #5291	0	1
5292	19	51,307,490	51,308,455	965	2	19.867	26.4	43	62	1	4	5	ACPT, C19orf48, SNORD88B, SNORD88A, SNORD88C	14300, 2, -5590, -5180, -2294	downstream, in gene, upstream, upstream, upstream	ActReg chr19 #5292	1	1
5293	19	51,373,454	51,374,204	750	2	12.391	12.87	19	22	0	1	2	KLK3, KLK2	15658, -2860	downstream, upstream	ActReg chr19 #5293	1	1
5294	19	51,867,404	51,868,100	696	1	7.136	13.909	11	24	0	1	3	ETFB, CLDND2, NKG7	1920, 4505, 8208	in gene, downstream, downstream	ActReg chr19 #5294	0	1
5295	19	51,925,089	51,925,743	654	2	10.8	14.85	23	33	1	1	2	SIGLEC10, LOC100129083	-4359, 6256	upstream, downstream	ActReg chr19 #5295	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5296	19	51,983,594	51,984,402	808	1	7.4	13.56	16	22	0	0	1	CEACAM18	4,160	in gene	ActReg chr19 #5296	0	1
5297	19	52,056,282	52,057,058	776	2	9.92	12.4	25	25	0	0	0				ActReg chr19 #5297	1	1
5298	19	52,074,097	52,074,711	614	1	12.368	9.211	19	14	1	1	1	ZNF175	-127	upstream	ActReg chr19 #5298	1	0
5299	19	52,097,494	52,098,139	645	1	10.55	14.05	18	24	1	1	2	ZNF175, FLJ30403	23285, -183	downstream, upstream	ActReg chr19 #5299	0	1
5300	19	52,111,031	52,111,899	868	2	14.185	16.259	33	37	0	0	1	SIGLEC5	22,262	downstream	ActReg chr19 #5300	1	1
5301	19	52,531,413	52,531,998	585	1	10.5	12.722	15	19	1	1	2	ZNF614, ZNF432	-25, 20368	upstream, downstream	ActReg chr19 #5301	0	1
5302	19	52,800,463	52,801,119	656	1	8.05	10.45	12	18	1	1	2	ZNF766, ZNF480	27967, 365	downstream, in gene	ActReg chr19 #5302	0	1
5303	19	54,023,724	54,024,519	795	1	11.4	9.68	20	14	2	1	1	ZNF331	-56	upstream	ActReg chr19 #5303	1	0
5304	19	54,406,127	54,406,980	853	2	10.482	16.593	21	30	0	0	2	PRKCG, CACNG7	21086, -9518	in gene, upstream	ActReg chr19 #5304	1	1
5305	19	54,430,571	54,431,613	1,042	2	12.25	15.719	25	37	0	0	1	CACNG7	15,021	in gene	ActReg chr19 #5305	1	1
5306	19	54,483,045	54,483,574	529	1	9	12.75	13	21	1	1	2	CACNG8, MIR935	17015, -2252	in gene, upstream	ActReg chr19 #5306	0	1
5307	19	54,605,778	54,606,443	665	1	10.905	12.667	20	24	1	2	3	OSCAR, NDUFA3, TFPT	-1962, -50, 12945	upstream, upstream, downstream	ActReg chr19 #5307	0	1
5308	19	54,618,354	54,619,489	1,135	2	11.583	16.111	24	30	1	2	3	NDUFA3, TFPT, PRPF31	12761, 134, 131	downstream, in gene, in gene	ActReg chr19 #5308	1	1
5309	19	54,662,796	54,663,537	741	1	6.409	12.478	9	19	1	1	3	CNOT3, LENG1, TMC4	21730, 280, 13778	downstream, in gene, downstream	ActReg chr19 #5309	0	1
5310	19	54,815,490	54,816,256	766	2	9.917	11.792	18	18	0	0	1	LILRA5	8,536	downstream	ActReg chr19 #5310	1	1
5311	19	54,959,240	54,961,088	1,848	2	9.31	13.483	16	27	1	1	1	LENG8	99	in gene	ActReg chr19 #5311	1	1
5312	19	54,974,560	54,976,303	1,743	2	11.909	11.146	20	18	1	1	3	LENG8, LENG9, CDC42EP5	15366, -537, 8991	downstream, upstream, downstream	ActReg chr19 #5312	1	1
5313	19	55,028,508	55,029,131	623	2	8.75	14.1	15	29	0	0	1	LAIR2	14,806	downstream	ActReg chr19 #5313	1	1
5314	19	55,195,609	55,196,346	737	2	14	18.609	32	45	0	0	0				ActReg chr19 #5314	1	1
5315	19	55,690,148	55,691,981	1,833	2	9.158	13.702	22	22	1	1	2	SYT5, PTPRH	656, 29810	in gene, downstream	ActReg chr19 #5315	1	1
5316	19	55,700,415	55,701,333	918	2	13.31	12.828	25	22	0	0	2	SYT5, PTPRH	-9154, 20000	upstream, in gene	ActReg chr19 #5316	1	1
5317	19	55,727,551	55,729,019	1,468	2	19.261	23.783	41	48	1	1	2	PTPRH, TMEM86B	-7411, 12347	upstream, downstream	ActReg chr19 #5317	1	1
5318	19	55,769,953	55,771,159	1,206	2	15.784	15.514	25	31	1	1	2	SAPS1, HSPBP1	-518, 21195	upstream, downstream	ActReg chr19 #5318	1	1
5319	19	55,918,867	55,920,085	1,218	2	11	12.237	17	21	1	1	1	UBE2S	-151	upstream	ActReg chr19 #5319	1	1
5320	19	55,948,045	55,949,392	1,347	2	14.167	20.238	45	52	0	0	1	SHISA7	5,512	in gene	ActReg chr19 #5320	1	1
5321	19	55,967,467	55,968,178	711	1	10.454	12.773	18	21	1	1	2	ZNF628, NAT14	123, -8772	in gene, upstream	ActReg chr19 #5321	0	1
5322	19	55,968,205	55,968,909	704	2	16.636	22.909	28	40	1	1	2	ZNF628, NAT14	858, -8037	in gene, upstream	ActReg chr19 #5322	1	1
5323	19	56,030,346	56,031,782	1,436	2	11.222	17.578	19	38	0	0	2	SSC5D, SBK2	31194, 17371	downstream, downstream	ActReg chr19 #5323	1	1
5324	19	56,092,232	56,093,293	1,061	1	6.484	12	12	20	0	1	2	ZNF579, FIZ1	-551, 18131	upstream, downstream	ActReg chr19 #5324	0	1
5325	19	56,110,725	56,111,808	1,083	2	13.032	14.618	32	24	1	2	2	FIZ1, ZNF524	-373, -464	upstream, upstream	ActReg chr19 #5325	1	1
5326	19	56,150,382	56,150,876	494	1	10.867	11.333	17	13	0	2	3	ZNF580, ZNF581, CCDC106	-1763, -4357, -8325	upstream, upstream, upstream	ActReg chr19 #5326	1	0
5327	19	56,154,107	56,155,173	1,066	1	10	10.971	18	23	2	3	3	ZNF580, ZNF581, CCDC106	2248, -346, -4314	in gene, upstream, upstream	ActReg chr19 #5327	0	1
5328	19	56,158,887	56,160,183	1,296	2	18.7	21.9	39	44	1	2	4	ZNF580, ZNF581, CCDC106, U2AF2	7143, 4549, 581, -5881	downstream, downstream, in gene, upstream	ActReg chr19 #5328	1	1
5329	19	56,186,267	56,186,872	605	2	10.421	13.105	21	19	1	1	2	U2AF2, EPN1	21153, 8	downstream, in gene	ActReg chr19 #5329	1	1
5330	19	56,320,429	56,321,137	708	1	12.546	8.227	20	17	0	0	1	NLRP11	27,345	in gene	ActReg chr19 #5330	1	0
5331	19	56,530,219	56,530,641	422	1	6.231	11.538	8	17	0	0	1	NLRP5	19,338	in gene	ActReg chr19 #5331	0	1
5332	19	56,652,091	56,652,687	596	1	8.368	13.947	15	28	1	1	1	ZNF444	-167	upstream	ActReg chr19 #5332	0	1
5333	19	56,763,967	56,764,583	616	1	10.55	7	18	15	0	0	1	ZSCAN5D	12,502	downstream	ActReg chr19 #5333	1	0
5334	19	56,825,876	56,826,851	975	1	10.742	11.484	14	18	1	0	1	LOC100506374	13,058	downstream	ActReg chr19 #5334	0	1
5335	19	57,049,709	57,050,145	436	1	10.154	11.571	15	20	1	1	3	ZNF471, ZFP28, LOC100506419	30715, -390, 28855	downstream, upstream, downstream	ActReg chr19 #5335	0	1
5336	19	57,078,327	57,079,250	923	1	6.483	10.379	11	18	1	2	2	LOC100506419, ZNF470	-6, -102	upstream, upstream	ActReg chr19 #5336	0	1
5337	19	57,106,456	57,107,107	651	1	7.381	9.905	9	18	1	1	1	ZNF71	117	in gene	ActReg chr19 #5337	0	1
5338	19	57,149,041	57,151,160	2,119	2	29.742	35.03	134	144	1	1	1	LOC147670	-4,427	upstream	ActReg chr19 #5338	1	1
5339	19	57,702,365	57,703,183	818	1	6.846	11.5	9	15	1	1	1	ZNF264	-94	upstream	ActReg chr19 #5339	0	1
5340	19	57,751,608	57,752,454	846	2	11.037	11.741	18	23	1	1	2	AURKC, ZNF805	9654, -22	downstream, upstream	ActReg chr19 #5340	1	1
5341	19	57,791,328	57,792,202	874	1	10.286	13.393	17	26	1	1	1	ZNF460	-88	upstream	ActReg chr19 #5341	0	1
5342	19	57,862,241	57,862,901	660	1	11.5	9.55	18	14	1	1	1	ZNF304	-74	upstream	ActReg chr19 #5342	1	0
5343	19	57,874,350	57,875,238	888	2	10.786	11.321	18	23	1	1	2	ZNF304, ZNF547	12149, -97	downstream, upstream	ActReg chr19 #5343	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5344	19	57,900,882	57,901,647	765	2	10.375	11.417	15	16	1	1	2	ZNF547, ZNF548	26373, 46	downstream, in gene	ActReg chr19 #5344	1	1
5345	19	57,922,323	57,923,084	761	1	10.333	11.375	20	15	1	1	2	ZNF548, ZNF17	21485, 174	downstream, in gene	ActReg chr19 #5345	0	1
5346	19	57,946,326	57,946,950	624	1	10.95	12.6	18	21	1	1	1	ZNF749	-55	upstream	ActReg chr19 #5346	0	1
5347	19	58,090,080	58,090,770	690	1	9.952	10.636	15	19	1	2	2	ZNF416, ZIK1	-182, -5203	upstream, upstream	ActReg chr19 #5347	0	1
5348	19	58,094,940	58,095,919	979	1	5.935	10.548	9	18	1	2	2	ZNF416, ZIK1	-5186, -199	upstream, upstream	ActReg chr19 #5348	0	1
5349	19	58,193,134	58,193,827	693	1	8.227	11.227	16	19	1	1	2	ZSCAN4, ZNF551	13177, 123	downstream, in gene	ActReg chr19 #5349	0	1
5350	19	58,458,858	58,459,582	724	2	10.454	9.955	21	22	1	1	1	ZNF256	-143	upstream	ActReg chr19 #5350	1	1
5351	19	58,513,756	58,514,463	707	1	10.182	8.773	15	12	1	2	2	ZNF606, LOC100128398	605, -153	in gene, upstream	ActReg chr19 #5351	1	0
5352	19	58,520,999	58,521,479	480	1	10.867	10.867	15	18	1	1	2	ZNF606, LOC100128398	-6525, 6977	upstream, downstream	ActReg chr19 #5352	0	1
5353	19	58,665,992	58,666,820	828	1	11.039	11.808	17	16	1	1	1	ZNF329	-4,258	upstream	ActReg chr19 #5353	0	1
5354	19	58,739,782	58,740,579	797	1	13.4	9.84	23	14	1	1	1	ZNF544	110	in gene	ActReg chr19 #5354	1	0
5355	19	58,789,839	58,791,267	1,428	1	7.956	11	13	16	1	2	2	LOC100506561, ZNF8	-396, 235	upstream, in gene	ActReg chr19 #5355	0	1
5356	19	58,816,275	58,817,233	958	2	12.5	12.033	23	23	1	1	2	ZNF8, LOC100506584	26436, 11	downstream, in gene	ActReg chr19 #5356	1	1
5357	19	58,838,081	58,839,110	1,029	2	18.562	18.125	34	34	1	1	1	ZSCAN22	210	in gene	ActReg chr19 #5357	1	1
5358	19	58,873,116	58,874,336	1,220	2	12.256	13	22	22	1	1	4	A1BG, NCRNA00181, ZNF497, ZNF837	-8861, 10390, 394, 18663	upstream, downstream, in gene, downstream	ActReg chr19 #5358	1	1
5359	19	58,891,303	58,892,653	1,350	2	9.667	12.548	21	25	1	2	2	ZNF837, RPS5	411, -6658	in gene, upstream	ActReg chr19 #5359	1	1
5360	19	58,897,878	58,898,902	1,024	1	8.938	13	17	20	1	2	3	ZNF837, RPS5, LOC100506612	-6001, -246, -9067	upstream, upstream, upstream	ActReg chr19 #5360	0	1
5361	19	58,912,682	58,913,228	546	1	6.412	10.647	13	18	1	2	5	RPS5, LOC100506612, LOC100506657, LOC100506634, ZNF584	14319, 5498, 314, 5708, -7108	downstream, downstream, in gene, downstream, upstream	ActReg chr19 #5361	0	1
5362	19	58,919,562	58,920,735	1,173	2	14.056	11.944	23	18	1	3	3	LOC100506657, LOC100506634, ZNF584	-6879, -1485, 85	upstream, upstream, in gene	ActReg chr19 #5362	1	1
5363	19	58,962,617	58,963,548	931	1	6.379	10.862	11	17	1	1	1	ZNF324B	111	in gene	ActReg chr19 #5363	0	1
5364	19	59,025,146	59,025,736	590	1	6.895	11.895	13	22	1	1	2	SLC27A5, ZBTB45	-2009, 5480	upstream, in gene	ActReg chr19 #5364	0	1
5365	19	59,030,396	59,031,784	1,388	2	12.727	13.954	25	27	1	2	2	SLC27A5, ZBTB45	-7658, -169	upstream, upstream	ActReg chr19 #5365	1	1
5366	19	59,066,080	59,066,682	602	1	8.947	12.947	16	16	1	2	5	TRIM28, CHMP2A, UBE2M, LOC100131691, MZF1	10545, 105, 3962, -4211, 18561	downstream, in gene, downstream, upstream, downstream	ActReg chr19 #5366	0	1
5367	19	59,069,891	59,070,773	882	1	12.148	7.926	20	14	1	3	5	TRIM28, CHMP2A, UBE2M, LOC100131691, MZF1	14496, -3846, 11, -260, 14610	downstream, upstream, in gene, upstream, downstream	ActReg chr19 #5367	1	0
5368	2	264,614	265,214	600	1	10	6.833	16	12	1	2	2	SH3YL1, ACP1	-846, 45	upstream, in gene	ActReg chr2 #5368	1	0
5369	2	2,332,547	2,333,029	482	1	7.533	10.733	11	19	0	1	2	MYT1L, LOC730811	2257, 9784	in gene, downstream	ActReg chr2 #5369	0	1
5370	2	2,617,039	2,617,548	509	1	11.062	10.938	20	17	0	0	0				ActReg chr2 #5370	0	1
5371	2	3,381,057	3,382,262	1,205	2	10.568	12.351	18	20	1	2	2	TSSC1, TTC15	-6, -1787	upstream, upstream	ActReg chr2 #5371	1	1
5372	2	3,383,243	3,383,975	732	1	10.087	12.609	17	20	1	2	2	TSSC1, TTC15	-1956, 163	upstream, in gene	ActReg chr2 #5372	0	1
5373	2	3,522,522	3,523,640	1,118	1	10.057	12.257	17	20	1	1	1	ADI1	269	in gene	ActReg chr2 #5373	0	1
5374	2	3,584,077	3,584,773	696	1	13.682	9.545	27	20	0	1	2	LOC100506014, RNASEH1	-2628, 21515	upstream, downstream	ActReg chr2 #5374	1	0
5375	2	3,622,442	3,623,250	808	2	13.24	13.96	34	24	1	1	1	RPS7	-7	upstream	ActReg chr2 #5375	1	1
5376	2	6,646,068	6,646,943	875	2	10.259	12.741	17	21	0	0	0				ActReg chr2 #5376	1	1
5377	2	6,696,926	6,697,376	450	1	4.333	10.267	6	14	0	0	0				ActReg chr2 #5377	0	1
5378	2	7,373,174	7,373,810	636	1	6.737	10.2	13	16	0	0	0				ActReg chr2 #5378	0	1
5379	2	7,759,546	7,760,938	1,392	3	8.636	10.159	24	18	0	0	0				ActReg chr2 #5379	1	1
5380	2	7,888,906	7,889,650	744	1	7.217	11	11	18	0	0	0				ActReg chr2 #5380	0	1
5381	2	8,738,222	8,739,416	1,194	2	14.351	12.081	33	29	0	0	0				ActReg chr2 #5381	1	1
5382	2	9,211,008	9,211,705	697	2	13.364	11.046	25	25	0	0	0				ActReg chr2 #5382	1	1
5383	2	9,224,464	9,225,192	728	1	10.652	4.957	15	8	0	0	0				ActReg chr2 #5383	1	0
5384	2	9,252,070	9,252,861	791	2	12.125	13.833	22	22	0	0	0				ActReg chr2 #5384	1	1
5385	2	9,305,606	9,306,174	568	1	9.412	11.412	13	14	0	0	0				ActReg chr2 #5385	0	1
5386	2	9,319,441	9,320,536	1,095	1	8.412	10.677	14	15	0	0	0				ActReg chr2 #5386	0	1
5387	2	9,330,766	9,331,642	876	2	11.333	13.037	22	19	0	0	0				ActReg chr2 #5387	1	1
5388	2	9,374,437	9,375,409	972	1	8.533	12.8	15	20	0	0	1	ASAP2	28,029	in gene	ActReg chr2 #5388	0	1
5389	2	9,375,585	9,376,305	720	1	9.227	11.136	13	15	0	0	1	ASAP2	29,051	in gene	ActReg chr2 #5389	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5390	2	9,427,506	9,428,791	1,285	3	9.55	13.075	20	27	0	0	1	ASAP2	81,254	in gene	ActReg chr2 #5390	1	1
5391	2	9,518,434	9,519,133	699	1	4.571	12.762	7	20	0	0	1	ASAP2	171,889	in gene	ActReg chr2 #5391	0	1
5392	2	9,562,699	9,563,920	1,221	1	10.395	14.605	21	31	1	2	2	ITGB1BP1, CPSF3	334, -559	in gene, upstream	ActReg chr2 #5392	0	1
5393	2	9,695,161	9,696,424	1,263	2	10.6	10.75	17	19	1	1	1	ADAM17	125	in gene	ActReg chr2 #5393	1	1
5394	2	9,770,882	9,771,789	907	2	9.179	10.643	17	16	1	1	1	YWHAQ	-229	upstream	ActReg chr2 #5394	1	1
5395	2	9,778,320	9,778,978	658	1	7.619	11	12	21	0	1	1	YWHAQ	-7,543	upstream	ActReg chr2 #5395	0	1
5396	2	9,892,517	9,893,823	1,306	2	10.95	12.9	15	21	0	0	1	LOC100506386	17,300	downstream	ActReg chr2 #5396	1	1
5397	2	9,983,299	9,984,031	732	1	9.5	13.5	13	22	1	1	1	TAF1B	94	in gene	ActReg chr2 #5397	0	1
5398	2	10,261,895	10,263,478	1,583	2	14.449	20.388	40	53	1	1	1	RRM2	-9	upstream	ActReg chr2 #5398	1	1
5399	2	10,275,735	10,276,666	931	2	12.207	13.897	21	24	0	1	2	RRM2, C2orf48	13505, -5309	downstream, upstream	ActReg chr2 #5399	1	1
5400	2	10,429,822	10,430,622	800	2	11.68	14.04	23	28	0	0	0				ActReg chr2 #5400	1	1
5401	2	10,443,846	10,444,633	787	1	7.5	10.75	12	15	1	1	1	HPCAL1	1,199	in gene	ActReg chr2 #5401	0	1
5402	2	10,451,913	10,453,178	1,265	1	11.256	14.949	17	24	0	0	1	HPCAL1	9,505	in gene	ActReg chr2 #5402	0	1
5403	2	10,545,329	10,546,139	810	1	6.96	12.96	10	21	0	0	1	HPCAL1	102,694	in gene	ActReg chr2 #5403	0	1
5404	2	10,637,770	10,638,478	708	1	8.955	11.727	12	20	0	0	0				ActReg chr2 #5404	0	1
5405	2	10,829,522	10,830,346	824	1	7.615	9.962	14	15	1	1	1	NOL10	178	in gene	ActReg chr2 #5405	0	1
5406	2	10,979,876	10,980,578	702	2	10.954	10.864	15	18	0	0	0				ActReg chr2 #5406	1	1
5407	2	11,041,181	11,041,915	734	1	5.435	11.913	9	17	0	0	0				ActReg chr2 #5407	0	1
5408	2	11,076,151	11,076,785	634	1	11.25	12.9	19	21	0	0	0				ActReg chr2 #5408	0	1
5409	2	11,295,496	11,296,298	802	1	6.68	11.84	13	18	1	1	2	C2orf50, PQLC3	22718, 357	downstream, in gene	ActReg chr2 #5409	0	1
5410	2	11,483,683	11,484,390	707	1	9.045	10.409	13	18	1	2	2	ROCK2, LOC650157	675, -7717	in gene, upstream	ActReg chr2 #5410	0	1
5411	2	11,514,413	11,515,399	986	2	10.258	10.581	15	18	0	0	1	LOC650157	23,153	downstream	ActReg chr2 #5411	1	1
5412	2	11,606,074	11,607,210	1,136	2	8.5	12.306	20	26	1	1	1	E2F6	-345	upstream	ActReg chr2 #5412	1	1
5413	2	11,809,654	11,810,440	786	2	13.96	16.92	34	39	1	1	1	NTSR2	282	in gene	ActReg chr2 #5413	1	1
5414	2	11,883,932	11,884,915	983	2	13.065	12.645	32	21	0	1	1	LPIN1	-2,317	upstream	ActReg chr2 #5414	1	1
5415	2	11,970,060	11,970,688	628	1	8.85	11.9	13	20	0	0	2	LPIN1, MIR4262	83634, 6738	downstream, downstream	ActReg chr2 #5415	0	1
5416	2	12,260,250	12,261,172	922	1	9.517	10.793	14	16	0	0	1	LOC100506457	13,961	in gene	ActReg chr2 #5416	0	1
5417	2	12,309,207	12,310,209	1,002	1	7.656	9.219	12	16	0	0	0				ActReg chr2 #5417	0	1
5418	2	12,647,189	12,647,944	755	2	11.292	12.625	20	23	0	0	0				ActReg chr2 #5418	1	1
5419	2	12,748,082	12,748,566	484	1	9.333	7.2	17	15	0	0	0				ActReg chr2 #5419	1	0
5420	2	15,701,097	15,701,753	656	2	11.2	10.35	17	16	1	1	1	NBAS	29	in gene	ActReg chr2 #5420	1	1
5421	2	15,731,476	15,732,337	861	1	10.259	14.778	16	27	1	1	1	DDX1	136	in gene	ActReg chr2 #5421	0	1
5422	2	16,727,277	16,727,825	548	2	9.765	8.353	19	16	0	0	1	FAM49A	77,736	downstream	ActReg chr2 #5422	1	1
5423	2	17,699,345	17,699,885	540	1	10.177	10.412	16	15	0	1	1	RAD51AP2	91	in gene	ActReg chr2 #5423	1	0
5424	2	17,719,968	17,720,737	769	1	12.48	10.04	26	22	1	1	1	VSNL1	-1,455	upstream	ActReg chr2 #5424	1	0
5425	2	17,721,204	17,721,633	429	1	12	8.571	18	12	1	1	1	VSNL1	-389	upstream	ActReg chr2 #5425	1	0
5426	2	18,741,562	18,742,312	750	2	12.208	11.5	23	23	1	1	2	RDH14, NT5C1B	22, 28901	in gene, downstream	ActReg chr2 #5426	1	1
5427	2	19,278,546	19,279,222	676	1	6.286	11.191	9	15	0	0	0				ActReg chr2 #5427	0	1
5428	2	19,319,018	19,320,027	1,009	1	9.194	12.645	16	20	0	0	0				ActReg chr2 #5428	0	1
5429	2	19,320,558	19,321,393	835	1	12.154	8.192	21	15	0	0	0				ActReg chr2 #5429	1	0
5430	2	19,386,825	19,387,722	897	2	9.714	13.393	21	20	0	0	0				ActReg chr2 #5430	1	1
5431	2	19,547,349	19,548,195	846	2	11.37	10.704	19	15	1	0	1	OSR1	10,600	downstream	ActReg chr2 #5431	1	1
5432	2	19,871,417	19,872,127	710	1	11.409	5.227	14	11	0	0	0				ActReg chr2 #5432	1	0
5433	2	19,902,026	19,902,679	653	1	7.35	13.85	12	21	0	0	0				ActReg chr2 #5433	0	1
5434	2	20,001,056	20,001,679	623	1	12.05	8.4	25	13	0	0	0				ActReg chr2 #5434	1	0
5435	2	20,101,201	20,102,201	1,000	2	14.645	13.516	27	24	1	1	2	TTC32, WDR35	46, 88183	in gene, downstream	ActReg chr2 #5435	1	1
5436	2	20,189,268	20,190,339	1,071	2	10.412	11.5	21	19	1	1	2	WDR35, MATN3	81, 22652	in gene, downstream	ActReg chr2 #5436	1	1
5437	2	20,549,968	20,550,514	546	1	7.118	13.118	14	21	1	0	0				ActReg chr2 #5437	0	1
5438	2	20,550,526	20,551,404	878	1	10	10.393	16	21	1	0	0				ActReg chr2 #5438	1	0
5439	2	20,647,014	20,648,097	1,083	1	8.471	12.5	17	25	1	1	1	RHOB	720	in gene	ActReg chr2 #5439	0	1
5440	2	20,777,307	20,778,199	892	1	8.071	14.607	19	27	0	0	0				ActReg chr2 #5440	0	1
5441	2	20,778,582	20,779,569	987	1	13.452	9.968	23	17	0	0	0				ActReg chr2 #5441	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5442	2	20,850,599	20,851,274	675	1	8.714	12.333	13	20	1	1	1	HS1BP3	-72	upstream	ActReg chr2 #5442	0	1
5443	2	21,022,326	21,023,193	867	2	11.482	14.111	23	27	1	1	1	C2orf43	68	in gene	ActReg chr2 #5443	1	1
5444	2	23,078,251	23,079,125	874	1	4.222	11.704	8	20	0	0	0				ActReg chr2 #5444	0	1
5445	2	23,582,491	23,583,282	791	1	12.2	7.56	20	11	0	0	0				ActReg chr2 #5445	1	0
5446	2	23,747,034	23,747,678	644	2	9.55	9.6	19	18	0	0	1	KLHL29	139,058	in gene	ActReg chr2 #5446	1	1
5447	2	24,149,554	24,150,410	856	1	11.704	14.518	23	24	1	1	1	ATAD2B	-48	upstream	ActReg chr2 #5447	0	1
5448	2	24,298,775	24,299,573	798	2	12.36	12.84	24	24	1	1	2	SF3B14, TP53I3	140, 8554	in gene, downstream	ActReg chr2 #5448	1	1
5449	2	24,306,854	24,308,078	1,224	2	24.395	22.263	52	43	1	1	2	SF3B14, TP53I3	-8152, 262	upstream, in gene	ActReg chr2 #5449	1	1
5450	2	24,345,774	24,346,605	831	2	9.962	11.192	15	19	1	2	2	PFN4, LOC375190	-38, -161	upstream, upstream	ActReg chr2 #5450	1	1
5451	2	24,454,239	24,454,816	577	1	13.158	8.526	19	12	0	1	2	ITSN2, LOC100507630	128870, -5125	in gene, upstream	ActReg chr2 #5451	1	0
5452	2	24,583,016	24,583,771	755	1	10.217	9.696	16	13	1	1	1	ITSN2	4	in gene	ActReg chr2 #5452	0	1
5453	2	24,931,391	24,931,980	589	1	10.053	4.526	19	8	0	0	1	NCOA1	124,339	in gene	ActReg chr2 #5453	1	0
5454	2	25,015,662	25,017,073	1,411	2	9.386	12.341	19	18	1	2	2	C2orf79, CENPO	-116, 34	upstream, in gene	ActReg chr2 #5454	1	1
5455	2	25,326,009	25,326,638	629	1	8.75	11.9	15	19	0	0	1	EFR3B	61,350	in gene	ActReg chr2 #5455	0	1
5456	2	25,565,128	25,565,901	773	2	13.5	14.792	23	29	1	1	1	DNMT3A	-55	upstream	ActReg chr2 #5456	1	1
5457	2	25,896,764	25,897,210	446	1	6.929	10.5	12	15	1	1	1	DTNB	-484	upstream	ActReg chr2 #5457	0	1
5458	2	26,220,426	26,220,981	555	1	8	11.353	12	16	0	0	1	LOC729769	3,099	downstream	ActReg chr2 #5458	0	1
5459	2	26,256,693	26,257,451	758	1	10.083	13.042	16	23	1	2	2	LOC391358, RAB10	-5591, 343	upstream, in gene	ActReg chr2 #5459	0	1
5460	2	26,467,048	26,468,508	1,460	2	11.422	12.556	20	30	2	2	2	HADHA, HADHB	-184, 162	upstream, in gene	ActReg chr2 #5460	1	1
5461	2	26,568,528	26,569,391	863	2	11.704	11.778	18	17	1	2	2	GPR113, SELI	726, 5	in gene, in gene	ActReg chr2 #5461	1	1
5462	2	26,918,914	26,919,734	820	1	12.2	10.28	18	17	0	0	1	KCNK3	3,743	in gene	ActReg chr2 #5462	1	0
5463	2	26,980,689	26,981,130	441	1	10.5	10.643	15	16	0	1	1	C2orf18	-6,233	upstream	ActReg chr2 #5463	0	1
5464	2	27,008,400	27,009,255	855	2	11.963	11.63	24	19	1	1	2	C2orf18, CENPA	21685, -55	downstream, upstream	ActReg chr2 #5464	1	1
5465	2	27,061,148	27,062,239	1,091	2	12.853	15.882	29	33	0	0	1	DPYSL5	-9,276	upstream	ActReg chr2 #5465	1	1
5466	2	27,193,076	27,193,865	789	1	10.44	12.48	17	19	1	1	1	MAPRE3	-55	upstream	ActReg chr2 #5466	0	1
5467	2	27,216,192	27,217,161	969	2	13.387	22.613	27	53	0	0	1	MAPRE3	23,151	in gene	ActReg chr2 #5467	1	1
5468	2	27,255,702	27,256,296	594	1	10	12.737	13	22	1	1	2	MAPRE3, TMEM214	62474, 225	downstream, in gene	ActReg chr2 #5468	0	1
5469	2	27,273,286	27,274,582	1,296	2	15.025	13.525	23	22	2	1	2	TMEM214, AGBL5	18160, -557	downstream, upstream	ActReg chr2 #5469	1	1
5470	2	27,293,983	27,294,867	884	1	9.071	10.607	14	19	1	2	3	AGBL5, LOC100128731, EMILIN1	19934, 142, 7010	downstream, in gene, upstream	ActReg chr2 #5470	0	1
5471	2	27,308,329	27,309,622	1,293	2	9.744	13.525	24	20	1	1	2	EMILIN1, KHK	7540, -636	in gene, upstream	ActReg chr2 #5471	1	1
5472	2	27,357,258	27,357,848	590	2	14.667	12.167	24	21	1	1	3	ABHD1, PREB, C2orf53	10896, -11, 4779	downstream, upstream, downstream	ActReg chr2 #5472	1	1
5473	2	27,434,886	27,435,641	755	2	11	10.652	16	16	1	3	3	SLC5A6, C2orf28, CAD	-88, 364, -4995	upstream, in gene, upstream	ActReg chr2 #5473	1	1
5474	2	27,545,662	27,546,296	634	1	13.55	13	21	20	0	1	2	MPV17, GTF3C2	-10, 33889	upstream, downstream	ActReg chr2 #5474	1	0
5475	2	27,578,967	27,579,760	793	1	10.32	11.72	17	16	1	2	3	GTF3C2, LOC100505605, EIF2B4	505, 250, 13961	in gene, in gene, downstream	ActReg chr2 #5475	0	1
5476	2	27,592,572	27,594,058	1,486	2	20.766	25	66	74	1	2	4	LOC100505605, EIF2B4, SNX17, ZNF513	14202, 9, -74, 10278	downstream, in gene, upstream, downstream	ActReg chr2 #5476	1	1
5477	2	27,851,548	27,852,140	592	1	8.632	11.895	17	21	0	2	3	ZNF512, CCDC121, GPN1	45951, 54, 329	downstream, in gene, in gene	ActReg chr2 #5477	0	1
5478	2	27,942,872	27,943,657	785	2	12	10.4	17	17	0	0	0				ActReg chr2 #5478	1	1
5479	2	27,994,248	27,995,085	837	2	9.462	10.154	15	19	1	1	2	MRPL33, RBKS	82, 118557	in gene, downstream	ActReg chr2 #5479	1	1
5480	2	28,093,289	28,094,229	940	2	15.138	11.552	27	26	0	0	1	RBKS	19,464	in gene	ActReg chr2 #5480	1	1
5481	2	28,236,384	28,237,001	617	2	9.35	10.1	18	17	0	0	1	BRE	123,210	in gene	ActReg chr2 #5481	1	1
5482	2	28,612,866	28,614,166	1,300	1	8	11.55	15	18	1	1	2	FLJ31356, FOSL2	4023, -2263	in gene, upstream	ActReg chr2 #5482	0	1
5483	2	28,615,061	28,615,975	914	2	11.552	12.241	26	23	1	2	2	FLJ31356, FOSL2	2021, -261	in gene, upstream	ActReg chr2 #5483	1	1
5484	2	28,806,658	28,807,933	1,275	1	12.026	10.615	22	19	0	0	1	PLB1	88,357	in gene	ActReg chr2 #5484	1	0
5485	2	28,833,226	28,834,590	1,364	1	9.833	14.309	17	24	0	0	1	PLB1	114,970	in gene	ActReg chr2 #5485	0	1
5486	2	28,940,145	28,941,003	858	2	12.222	14.259	27	30	0	0	1	LOC100505774	18,456	in gene	ActReg chr2 #5486	1	1
5487	2	28,973,780	28,974,920	1,140	2	11.556	13.778	22	32	1	1	1	PPP1CB	-264	upstream	ActReg chr2 #5487	1	1
5488	2	29,092,785	29,093,625	840	2	12.115	12.885	23	24	1	1	1	TRMT61B	-30	upstream	ActReg chr2 #5488	1	1
5489	2	29,116,950	29,117,877	927	2	17.621	22.552	38	47	1	1	1	WDR43	-120	upstream	ActReg chr2 #5489	1	1
5490	2	29,337,248	29,337,976	728	1	6.565	10.565	12	14	1	1	1	CLIP4	-696	upstream	ActReg chr2 #5490	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5491	2	29,338,613	29,339,587	974	1	6.742	10.71	11	15	1	1	1	CLIP4	792	in gene	ActReg chr2 #5491	0	1
5492	2	29,516,591	29,517,301	710	1	13.318	11	30	17	0	0	1	ALK	627,486	in gene	ActReg chr2 #5492	1	0
5493	2	29,970,728	29,971,583	855	2	16.154	14.923	35	35	0	0	1	ALK	173,277	in gene	ActReg chr2 #5493	1	1
5494	2	30,142,388	30,144,507	2,119	2	11.212	18.515	27	41	1	1	1	ALK	985	in gene	ActReg chr2 #5494	1	1
5495	2	30,248,506	30,249,817	1,311	2	16.829	18.488	37	37	0	0	0				ActReg chr2 #5495	1	1
5496	2	30,369,021	30,369,715	694	1	10.818	14.273	22	26	1	1	1	YPEL5	-382	upstream	ActReg chr2 #5496	0	1
5497	2	30,607,960	30,608,839	879	2	12.321	15.964	29	36	0	0	0				ActReg chr2 #5497	1	1
5498	2	30,669,858	30,670,510	652	1	5.45	11.95	9	20	1	1	1	LCLAT1	61	in gene	ActReg chr2 #5498	0	1
5499	2	31,330,232	31,331,049	817	2	14.962	17.385	37	38	0	0	1	GALNT14	30,931	in gene	ActReg chr2 #5499	1	1
5500	2	31,331,533	31,332,131	598	1	6.579	10.737	11	19	0	0	1	GALNT14	29,739	in gene	ActReg chr2 #5500	0	1
5501	2	31,360,969	31,361,784	815	2	11.48	10.4	16	14	1	1	1	GALNT14	195	in gene	ActReg chr2 #5501	1	1
5502	2	31,456,545	31,457,254	709	2	12.864	10.227	25	20	1	1	1	EHD3	19	in gene	ActReg chr2 #5502	1	1
5503	2	32,235,776	32,236,640	864	2	13.714	19.321	27	43	1	1	1	MEMO1	-510	upstream	ActReg chr2 #5503	1	1
5504	2	32,264,641	32,265,221	580	2	10.444	12.722	16	23	1	1	1	DPY30	-87	upstream	ActReg chr2 #5504	1	1
5505	2	32,390,459	32,391,221	762	2	13.042	11.542	25	24	1	1	2	SPAST, SLC30A6	102160, -70	downstream, upstream	ActReg chr2 #5505	1	1
5506	2	32,581,580	32,582,650	1,070	2	10.818	12.394	18	20	1	1	1	BIRC6	19	in gene	ActReg chr2 #5506	1	1
5507	2	33,294,669	33,295,839	1,170	2	8.111	9.361	18	14	0	0	1	LTBP1	122,885	in gene	ActReg chr2 #5507	1	1
5508	2	33,359,175	33,359,709	534	1	10.5	10.688	16	18	0	0	1	LTBP1	187,073	in gene	ActReg chr2 #5508	0	1
5509	2	33,500,683	33,501,269	586	1	8.556	12	17	20	0	0	1	LTBP1	328,607	in gene	ActReg chr2 #5509	0	1
5510	2	33,600,096	33,600,845	749	1	7.375	10.625	14	18	0	0	1	LTBP1	428,101	in gene	ActReg chr2 #5510	0	1
5511	2	33,700,745	33,701,194	449	1	10.786	6.357	18	8	0	0	1	RASGRP3	39,553	in gene	ActReg chr2 #5511	1	0
5512	2	33,823,821	33,825,100	1,279	2	10.45	11.41	17	17	1	1	1	FAM98A	-98	upstream	ActReg chr2 #5512	1	1
5513	2	34,035,156	34,035,604	448	1	7.286	9.929	11	15	0	0	0				ActReg chr2 #5513	0	1
5514	2	34,803,518	34,804,217	699	1	14.046	5.5	29	10	0	0	0				ActReg chr2 #5514	1	0
5515	2	34,877,661	34,878,215	554	1	10.333	7.722	23	13	0	0	0				ActReg chr2 #5515	1	0
5516	2	35,966,465	35,967,172	707	2	10.227	11.727	22	21	0	0	0				ActReg chr2 #5516	1	1
5517	2	36,400,872	36,401,679	807	1	12.24	8.96	18	16	0	0	0				ActReg chr2 #5517	1	0
5518	2	36,584,663	36,585,486	823	1	11.615	10.692	18	15	1	2	2	LOC100288911, CRIM1	-2361, 1677	upstream, in gene	ActReg chr2 #5518	1	0
5519	2	36,654,710	36,655,443	733	1	7.913	13.043	12	22	0	0	1	CRIM1	71,679	in gene	ActReg chr2 #5519	0	1
5520	2	37,458,249	37,459,294	1,045	1	6.812	13.094	12	18	1	2	2	CEBPZ, C2orf56	-31, -3	upstream, upstream	ActReg chr2 #5520	0	1
5521	2	37,552,064	37,552,628	564	1	11	10.278	20	14	1	0	1	PRKD3	-8,124	upstream	ActReg chr2 #5521	1	0
5522	2	37,603,616	37,604,438	822	2	10.039	12.039	19	17	0	0	1	QPCT	32,274	downstream	ActReg chr2 #5522	1	1
5523	2	37,606,855	37,607,413	558	1	8.059	11.118	12	17	0	0	1	QPCT	35,381	downstream	ActReg chr2 #5523	0	1
5524	2	37,797,936	37,798,586	650	1	10.6	9.15	16	13	0	0	0				ActReg chr2 #5524	1	0
5525	2	37,898,927	37,900,290	1,363	2	9.14	11.349	18	18	1	1	1	CDC42EP3	-282	upstream	ActReg chr2 #5525	1	1
5526	2	38,007,268	38,008,138	870	1	8.296	11.963	11	17	0	0	0				ActReg chr2 #5526	0	1
5527	2	38,152,246	38,153,082	836	1	10.615	13.615	16	19	1	1	1	FAM82A1	202	in gene	ActReg chr2 #5527	0	1
5528	2	38,303,884	38,304,570	686	1	10.381	12.905	14	19	1	1	2	FAM82A1, CYP1B1	151765, -904	downstream, upstream	ActReg chr2 #5528	0	1
5529	2	38,373,609	38,374,367	758	1	7.783	10.565	14	15	0	0	1	C2orf58	15,741	in gene	ActReg chr2 #5529	0	1
5530	2	38,429,973	38,430,952	979	2	11.419	11.419	18	18	0	0	0				ActReg chr2 #5530	1	1
5531	2	38,604,038	38,604,811	773	2	11.833	14.125	25	26	1	1	1	ATL2	8	in gene	ActReg chr2 #5531	1	1
5532	2	38,763,005	38,763,592	587	1	7.158	10.842	13	18	1	0	0				ActReg chr2 #5532	0	1
5533	2	38,917,606	38,918,052	446	1	10.571	5.214	16	7	0	0	1	GALM	24,777	in gene	ActReg chr2 #5533	1	0
5534	2	39,102,561	39,103,276	715	2	11.636	13.773	17	24	1	2	2	DHX57, MORN2	103, -185	in gene, upstream	ActReg chr2 #5534	1	1
5535	2	39,347,920	39,348,470	550	1	12.471	12.765	20	21	1	1	1	SOS1	-591	upstream	ActReg chr2 #5535	0	1
5536	2	39,351,170	39,352,046	876	2	18.926	16.074	49	42	1	1	1	SOS1	-4,004	upstream	ActReg chr2 #5536	1	1
5537	2	39,597,132	39,597,661	529	1	10.5	7.438	18	12	0	0	1	MAP4K3	66,823	in gene	ActReg chr2 #5537	1	0
5538	2	40,885,983	40,886,552	569	1	6.778	9.222	13	17	0	0	0				ActReg chr2 #5538	0	1
5539	2	42,018,340	42,019,244	904	2	13.643	17.179	31	36	0	0	0				ActReg chr2 #5539	1	1
5540	2	42,063,835	42,064,815	980	2	20.226	19.613	46	44	0	0	0				ActReg chr2 #5540	1	1
5541	2	42,067,502	42,068,748	1,246	2	20.41	27.872	64	95	2	0	0				ActReg chr2 #5541	1	1
5542	2	42,568,111	42,568,795	684	1	12.381	9.095	22	15	0	0	2	EML4, COX7A2L	171963, 19903	downstream, downstream	ActReg chr2 #5542	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5543	2	42,568,939	42,570,536	1,597	2	11.84	11.02	20	19	0	0	2	EML4, COX7A2L	173247, 18619	downstream, downstream	ActReg chr2 #5543	1	1
5544	2	42,587,961	42,588,799	838	1	10.846	11.846	17	18	1	1	1	COX7A2L	-24	upstream	ActReg chr2 #5544	0	1
5545	2	43,037,312	43,038,697	1,385	2	8.659	14.432	21	24	2	0	0				ActReg chr2 #5545	1	1
5546	2	43,268,433	43,269,207	774	1	8	10.792	13	17	0	0	0				ActReg chr2 #5546	0	1
5547	2	43,446,479	43,447,513	1,034	1	8.812	12.188	19	24	0	1	2	ZFP36L2, LOC100129726	6749, -7354	downstream, upstream	ActReg chr2 #5547	0	1
5548	2	43,452,115	43,453,145	1,030	1	8.688	11.562	14	19	1	2	3	ZFP36L2, LOC100129726, THADA	1115, -1720, 370555	in gene, upstream, downstream	ActReg chr2 #5548	0	1
5549	2	43,454,306	43,455,120	814	1	9.76	10.2	13	13	1	2	3	ZFP36L2, LOC100129726, THADA	-968, 363, 368472	upstream, in gene, downstream	ActReg chr2 #5549	1	0
5550	2	43,520,725	43,521,435	710	2	17.864	13.364	41	25	0	0	1	THADA	302,105	in gene	ActReg chr2 #5550	1	1
5551	2	43,822,771	43,823,697	926	2	11.621	13.069	20	21	1	1	1	THADA	-49	upstream	ActReg chr2 #5551	1	1
5552	2	44,222,535	44,223,753	1,218	2	18.447	15.921	44	32	1	1	1	LRPPRC	0	in gene	ActReg chr2 #5552	1	1
5553	2	44,243,216	44,244,021	805	2	13.68	11.2	29	22	0	0	0				ActReg chr2 #5553	1	1
5554	2	44,327,361	44,328,264	903	1	9.286	14.571	16	27	0	0	0				ActReg chr2 #5554	0	1
5555	2	44,395,328	44,396,330	1,002	1	6.375	10.5	10	15	1	1	1	PPM1B	-171	upstream	ActReg chr2 #5555	0	1
5556	2	44,588,369	44,589,464	1,095	1	12.059	8.088	21	16	1	2	2	PREPL, C2orf34	85, -127	in gene, upstream	ActReg chr2 #5556	1	0
5557	2	45,020,402	45,020,961	559	1	6.375	9.389	11	19	0	0	0				ActReg chr2 #5557	0	1
5558	2	45,186,014	45,186,627	613	1	8.85	11.1	17	17	0	0	0				ActReg chr2 #5558	0	1
5559	2	46,078,621	46,079,424	803	2	11.538	9.077	17	18	0	0	1	PRKCE	199,979	in gene	ActReg chr2 #5559	1	1
5560	2	46,165,964	46,166,808	844	1	10.192	7.923	14	12	0	0	1	PRKCE	287,343	in gene	ActReg chr2 #5560	1	0
5561	2	46,325,614	46,326,449	835	2	8.654	9.692	16	16	0	0	1	PRKCE	446,988	in gene	ActReg chr2 #5561	1	1
5562	2	46,398,365	46,398,930	565	1	7.611	12.056	11	17	0	0	1	PRKCE	519,604	in gene	ActReg chr2 #5562	0	1
5563	2	46,443,452	46,444,046	594	1	5.105	10.526	8	17	0	0	0				ActReg chr2 #5563	0	1
5564	2	46,708,524	46,709,183	659	1	5.75	11.45	9	20	0	1	1	LOC388946	2,149	in gene	ActReg chr2 #5564	0	1
5565	2	46,727,114	46,727,916	802	1	7.696	12.92	15	24	0	0	0				ActReg chr2 #5565	0	1
5566	2	47,136,611	47,137,331	720	1	8.773	12.182	21	21	0	0	2	LOC100506177, MCFD2	10557, 32023	downstream, in gene	ActReg chr2 #5566	0	1
5567	2	47,312,819	47,313,525	706	1	10.591	7.5	17	13	0	0	2	TTC7A, C2orf61	144859, 69345	downstream, downstream	ActReg chr2 #5567	1	0
5568	2	47,403,239	47,404,440	1,201	2	13.297	12.405	20	20	1	1	1	CALM2	-99	upstream	ActReg chr2 #5568	1	1
5569	2	47,425,842	47,426,549	707	1	10.318	13.136	15	20	0	0	0				ActReg chr2 #5569	0	1
5570	2	47,499,128	47,499,911	783	1	12.12	10.68	20	15	1	0	0				ActReg chr2 #5570	1	0
5571	2	47,629,946	47,630,954	1,008	2	10.375	10.906	19	17	1	1	1	MSH2	187	in gene	ActReg chr2 #5571	1	1
5572	2	47,798,042	47,799,199	1,157	2	14.972	17.083	32	32	1	1	1	KCNK12	-1,150	upstream	ActReg chr2 #5572	1	1
5573	2	48,010,137	48,010,696	559	1	8.222	11.222	11	21	1	1	1	MSH6	195	in gene	ActReg chr2 #5573	0	1
5574	2	48,667,357	48,668,059	702	1	9.182	11.682	12	19	1	1	1	KLRAQ1	-200	upstream	ActReg chr2 #5574	0	1
5575	2	48,793,575	48,793,996	421	1	3.846	10.308	6	14	0	1	1	STON1-GTF2A1L	-2,374	upstream	ActReg chr2 #5575	0	1
5576	2	51,180,045	51,180,730	685	1	10.809	6.81	20	9	0	0	1	NRXN1	79,287	in gene	ActReg chr2 #5576	1	0
5577	2	51,258,953	51,259,876	923	2	13.759	20.276	28	53	0	1	1	NRXN1	260	in gene	ActReg chr2 #5577	1	1
5578	2	51,808,778	51,809,511	733	1	12.826	8.043	21	13	0	0	0				ActReg chr2 #5578	1	0
5579	2	52,233,956	52,234,438	482	1	4.133	10.533	6	15	0	0	0				ActReg chr2 #5579	0	1
5580	2	53,580,363	53,580,909	546	1	11.471	8.647	17	13	0	0	0				ActReg chr2 #5580	1	0
5581	2	54,013,641	54,014,664	1,023	1	9.875	13.688	17	21	1	2	3	ASB3, LOC100302652, ERLEC1	-73, 73018, 84	upstream, in gene, in gene	ActReg chr2 #5581	0	1
5582	2	54,330,794	54,331,272	478	1	6.6	8.8	9	13	0	0	0				ActReg chr2 #5582	0	1
5583	2	54,342,383	54,343,247	864	1	8	10.444	14	16	1	1	1	ACYP2	405	in gene	ActReg chr2 #5583	0	1
5584	2	54,709,628	54,710,152	524	1	11.235	7.235	18	10	0	0	1	SPTBN1	26,436	in gene	ActReg chr2 #5584	1	0
5585	2	54,950,241	54,951,302	1,061	1	12.848	11.515	19	15	1	1	1	EML6	-1,378	upstream	ActReg chr2 #5585	1	0
5586	2	55,130,979	55,131,835	856	1	10.154	13.615	16	23	0	0	1	EML6	179,258	in gene	ActReg chr2 #5586	0	1
5587	2	55,275,957	55,276,642	685	2	14.727	11.727	23	20	1	1	1	RTN4	1,435	in gene	ActReg chr2 #5587	1	1
5588	2	55,496,039	55,496,797	758	1	11.565	10.522	18	22	1	1	1	MTIF2	-34	upstream	ActReg chr2 #5588	1	0
5589	2	55,646,622	55,647,362	740	1	12.333	9.75	21	17	1	1	1	CCDC88A	65	in gene	ActReg chr2 #5589	1	0
5590	2	55,844,397	55,845,217	820	2	11.154	12.039	19	21	1	1	1	SMEK2	-11	upstream	ActReg chr2 #5590	1	1
5591	2	58,069,565	58,070,136	571	1	3.444	8.722	5	18	0	0	0				ActReg chr2 #5591	0	1
5592	2	58,273,436	58,274,553	1,117	1	11.657	9.829	18	15	1	1	1	VRK2	217	in gene	ActReg chr2 #5592	1	0
5593	2	58,468,080	58,468,844	764	1	10.458	6.417	15	10	1	1	1	FANCL	53	in gene	ActReg chr2 #5593	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5594	2	58,787,794	58,788,301	507	1	10.625	5.125	15	7	0	0	1	FLJ30838	40,159	in gene	ActReg chr2 #5594	1	0
5595	2	58,828,109	58,828,613	504	1	5.625	10.25	12	16	0	0	1	FLJ30838	80,473	in gene	ActReg chr2 #5595	0	1
5596	2	61,107,949	61,108,986	1,037	1	6.344	10.938	12	19	1	2	2	FLJ16341, REL	-18, -285	upstream, upstream	ActReg chr2 #5596	0	1
5597	2	61,243,882	61,245,291	1,409	2	27.432	25.095	78	65	0	2	2	PUS10, PEX13	779, -226	in gene, upstream	ActReg chr2 #5597	1	1
5598	2	61,403,564	61,404,505	941	2	11.357	12.724	17	31	1	1	1	AHSA2	-521	upstream	ActReg chr2 #5598	1	1
5599	2	61,765,189	61,765,815	626	1	8.947	11.21	12	18	1	1	1	XPO1	-84	upstream	ActReg chr2 #5599	0	1
5600	2	61,991,214	61,991,993	779	1	7.417	12	13	16	1	0	0				ActReg chr2 #5600	0	1
5601	2	62,081,148	62,082,307	1,159	1	9.378	12.351	17	17	1	1	1	FAM161A	-449	upstream	ActReg chr2 #5601	0	1
5602	2	62,115,339	62,116,107	768	2	10.542	11.917	22	19	1	1	1	CCT4	68	in gene	ActReg chr2 #5602	1	1
5603	2	62,132,406	62,133,101	695	2	10.864	10.818	21	18	0	1	1	COMMD1	-50	upstream	ActReg chr2 #5603	1	1
5604	2	62,266,296	62,266,887	591	2	9.789	9.368	21	19	0	0	1	COMMD1	133,788	in gene	ActReg chr2 #5604	1	1
5605	2	62,282,718	62,283,331	613	1	11	13.6	16	21	0	0	1	COMMD1	150,221	in gene	ActReg chr2 #5605	0	1
5606	2	62,932,312	62,932,843	531	1	10.765	9.941	15	14	1	0	1	EHBP1	31,591	in gene	ActReg chr2 #5606	1	0
5607	2	63,815,390	63,816,347	957	2	12.8	10.867	20	22	1	2	2	C2orf86, MDH1	-17, -254	upstream, upstream	ActReg chr2 #5607	1	1
5608	2	64,067,635	64,069,123	1,488	2	11.149	11.575	22	23	1	1	1	UGP2	281	in gene	ActReg chr2 #5608	1	1
5609	2	64,455,001	64,455,992	991	2	22.387	18.355	65	47	0	1	1	LOC100507006	-92	upstream	ActReg chr2 #5609	1	1
5610	2	64,500,560	64,501,480	920	2	11.345	10.586	18	21	0	0	0				ActReg chr2 #5610	1	1
5611	2	64,575,783	64,576,377	594	1	4.389	11.5	6	18	0	0	0				ActReg chr2 #5611	0	1
5612	2	64,586,752	64,587,682	930	1	9.1	12	13	18	0	0	0				ActReg chr2 #5612	0	1
5613	2	64,751,010	64,752,080	1,070	1	8.061	11.697	13	19	1	1	1	AFTPH	106	in gene	ActReg chr2 #5613	0	1
5614	2	64,977,645	64,979,346	1,701	1	8.038	11.377	14	23	1	0	0				ActReg chr2 #5614	0	1
5615	2	65,034,369	65,035,035	666	2	9.25	11.45	20	21	0	0	0				ActReg chr2 #5615	1	1
5616	2	65,058,309	65,059,015	706	1	9.636	11.182	14	15	0	0	0				ActReg chr2 #5616	0	1
5617	2	65,212,249	65,213,144	895	1	10.429	8.536	14	15	0	1	1	SLC1A4	-2,883	upstream	ActReg chr2 #5617	1	0
5618	2	65,356,969	65,357,673	704	2	13.227	9.409	26	20	2	1	1	RAB1A	114	in gene	ActReg chr2 #5618	1	1
5619	2	65,454,897	65,455,452	555	1	7.529	10.941	10	15	1	1	1	ACTR2	345	in gene	ActReg chr2 #5619	0	1
5620	2	65,659,497	65,660,202	705	2	8.773	11.273	20	20	1	1	1	SPRED2	-193	upstream	ActReg chr2 #5620	1	1
5621	2	65,662,667	65,663,376	709	2	11.773	12.091	23	20	1	1	1	SPRED2	-3,365	upstream	ActReg chr2 #5621	1	1
5622	2	66,661,695	66,662,568	873	2	12.357	11.25	23	22	2	2	2	LOC730198, MEIS1	-622, -401	upstream, upstream	ActReg chr2 #5622	1	1
5623	2	67,096,177	67,096,655	479	1	7.2	9.733	11	16	0	0	0				ActReg chr2 #5623	0	1
5624	2	67,115,675	67,116,336	661	1	9.095	10.857	14	18	0	0	0				ActReg chr2 #5624	0	1
5625	2	67,624,488	67,625,084	596	1	7.944	9.556	12	15	1	1	1	ETAA1	344	in gene	ActReg chr2 #5625	0	1
5626	2	67,691,014	67,691,514	500	1	9.4	9.5	16	16	0	0	0				ActReg chr2 #5626	1	0
5627	2	68,289,866	68,290,476	610	1	5.684	11.105	13	17	0	1	1	C1D	-12	upstream	ActReg chr2 #5627	0	1
5628	2	68,383,893	68,385,436	1,543	2	17.792	20.188	60	61	1	2	2	WDR92, PNO1	-8, -341	upstream, upstream	ActReg chr2 #5628	1	1
5629	2	68,547,300	68,547,871	571	1	9.824	13.353	16	22	1	1	1	CNRIP1	-402	upstream	ActReg chr2 #5629	0	1
5630	2	68,694,026	68,695,100	1,074	2	13.758	16.546	21	30	1	2	2	FBXO48, APLF	-173, -128	upstream, upstream	ActReg chr2 #5630	1	1
5631	2	69,056,309	69,056,777	468	1	11.067	7.533	20	10	0	0	1	ARHGAP25	94,630	downstream	ActReg chr2 #5631	1	0
5632	2	69,220,674	69,221,445	771	1	6.167	14.375	8	24	0	0	0				ActReg chr2 #5632	0	1
5633	2	69,405,122	69,405,757	635	2	11.316	10.368	21	20	0	0	1	ANTXR1	165,163	in gene	ActReg chr2 #5633	1	1
5634	2	69,664,148	69,665,026	878	1	9.143	12.036	15	17	1	1	1	NFU1	166	in gene	ActReg chr2 #5634	0	1
5635	2	69,869,433	69,870,232	799	1	6.84	11.04	11	19	1	1	1	AAK1	1,145	in gene	ActReg chr2 #5635	0	1
5636	2	69,871,550	69,872,104	554	1	5.882	10.722	10	17	1	1	1	AAK1	-850	upstream	ActReg chr2 #5636	0	1
5637	2	69,968,690	69,969,685	995	1	10.71	9.677	16	16	1	1	1	ANXA4	60	in gene	ActReg chr2 #5637	1	0
5638	2	70,056,285	70,057,356	1,071	1	11.353	11.177	16	19	1	1	2	ANXA4, GMCL1	87693, 2	downstream, in gene	ActReg chr2 #5638	0	1
5639	2	70,313,248	70,314,676	1,428	2	7.978	10.644	18	17	1	2	2	LOC400960, PCBP1	185, -623	in gene, upstream	ActReg chr2 #5639	1	1
5640	2	70,314,682	70,315,656	974	1	9.484	11.032	15	19	1	2	2	LOC400960, PCBP1	-1022, 584	upstream, in gene	ActReg chr2 #5640	0	1
5641	2	70,369,569	70,370,252	683	1	10.191	12.571	18	26	1	0	1	C2orf42	48,241	downstream	ActReg chr2 #5641	0	1
5642	2	70,417,520	70,418,159	639	1	10.6	11.65	15	17	1	1	1	C2orf42	312	in gene	ActReg chr2 #5642	0	1
5643	2	70,485,170	70,485,828	658	1	7.714	10.381	11	16	1	2	3	TIA1, MIR1285-2, PCYOX1	-9720, -5362, 268	upstream, upstream, in gene	ActReg chr2 #5643	0	1
5644	2	70,520,248	70,521,186	938	2	11.967	8.7	21	17	1	1	2	SNRPG, FAM136A	152, 8503	in gene, downstream	ActReg chr2 #5644	1	1
5645	2	70,528,431	70,529,232	801	1	10.08	15	12	29	1	1	2	SNRPG, FAM136A	-7962, 389	upstream, in gene	ActReg chr2 #5645	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5646	2	70,780,732	70,781,841	1,109	2	13.143	9.029	27	18	1	1	1	TGFA	-181	upstream	ActReg chr2 #5646	1	1
5647	2	70,823,287	70,824,349	1,062	1	10.576	8.182	17	13	0	0	0				ActReg chr2 #5647	1	0
5648	2	70,914,034	70,914,432	398	1	7.692	11.308	9	17	0	0	1	ADD2	81,142	in gene	ActReg chr2 #5648	0	1
5649	2	71,098,625	71,099,297	672	1	10.667	11.238	18	15	1	0	0				ActReg chr2 #5649	0	1
5650	2	71,174,582	71,175,235	653	1	7.524	11.857	11	21	0	0	1	ATP6V1B1	11,910	in gene	ActReg chr2 #5650	0	1
5651	2	71,221,216	71,222,680	1,464	2	21.217	27.413	78	99	1	1	2	ANKRD53, TEX261	16373, 53	downstream, in gene	ActReg chr2 #5651	1	1
5652	2	71,295,084	71,296,143	1,059	2	13.879	13.848	21	24	1	1	1	NAGK	205	in gene	ActReg chr2 #5652	1	1
5653	2	71,356,867	71,357,968	1,101	2	10.941	13.265	23	24	1	2	2	MCEE, MPHOSPH10	-23, -27	upstream, upstream	ActReg chr2 #5653	1	1
5654	2	71,503,449	71,504,177	728	1	10.826	12.652	14	20	1	0	0				ActReg chr2 #5654	1	0
5655	2	71,574,453	71,576,309	1,856	3	11.207	15.793	23	29	0	0	1	ZNF638	16,492	in gene	ActReg chr2 #5655	1	1
5656	2	71,971,176	71,971,828	652	1	10.95	10.6	19	18	0	0	0				ActReg chr2 #5656	1	0
5657	2	72,070,350	72,071,073	723	1	11.609	7.783	23	11	0	0	0				ActReg chr2 #5657	1	0
5658	2	72,083,566	72,084,343	777	1	8.375	11.583	16	19	0	0	0				ActReg chr2 #5658	0	1
5659	2	72,109,520	72,110,687	1,167	2	13.139	14.806	27	25	0	0	0				ActReg chr2 #5659	1	1
5660	2	72,342,431	72,343,421	990	2	9.387	11.71	19	17	0	0	0				ActReg chr2 #5660	1	1
5661	2	73,005,571	73,005,970	399	1	8.167	9.583	12	14	0	0	1	EXOC6B	47,407	in gene	ActReg chr2 #5661	0	1
5662	2	73,052,527	73,053,430	903	2	10.821	12.037	18	25	1	1	1	EXOC6B	199	in gene	ActReg chr2 #5662	1	1
5663	2	73,110,257	73,111,109	852	2	16.222	16.704	34	36	0	1	1	SPR	-3,829	upstream	ActReg chr2 #5663	1	1
5664	2	73,114,238	73,114,932	694	1	8.227	12.727	14	22	1	1	1	SPR	73	in gene	ActReg chr2 #5664	0	1
5665	2	73,297,960	73,298,818	858	1	10.963	8.815	15	13	1	1	2	SFXN5, RAB11FIP5	576, 41757	in gene, downstream	ActReg chr2 #5665	1	0
5666	2	73,441,170	73,442,036	866	2	9.852	10.185	18	18	1	1	2	NOTO, SMYD5	12217, 237	downstream, in gene	ActReg chr2 #5666	1	1
5667	2	73,460,485	73,462,095	1,610	2	10.96	13.1	19	19	1	2	3	SMYD5, C2orf7, CCT7	19924, -934, -74	downstream, upstream, upstream	ActReg chr2 #5667	1	1
5668	2	73,517,949	73,519,428	1,479	2	8.596	14.936	22	28	1	1	2	LOC100507133, EGR4	7035, 2141	downstream, in gene	ActReg chr2 #5668	1	1
5669	2	73,612,995	73,613,589	594	1	6.667	12.833	10	19	1	1	1	ALMS1	406	in gene	ActReg chr2 #5669	0	1
5670	2	73,964,261	73,965,183	922	2	13.25	13.643	23	23	1	1	1	TPRKB	-205	upstream	ActReg chr2 #5670	1	1
5671	2	74,007,001	74,007,593	592	1	9.368	12.579	16	26	1	2	2	DUSP11, C2orf78	-13, -4019	upstream, upstream	ActReg chr2 #5671	0	1
5672	2	74,055,776	74,056,525	749	1	8	11.5	13	18	1	1	1	STAMBP	64	in gene	ActReg chr2 #5672	0	1
5673	2	74,057,924	74,058,374	450	1	12.286	8.929	16	12	0	1	1	STAMBP	2,063	in gene	ActReg chr2 #5673	1	0
5674	2	74,079,117	74,079,780	663	1	11.143	8	17	10	0	0	1	STAMBP	23,362	in gene	ActReg chr2 #5674	1	0
5675	2	74,153,820	74,154,380	560	1	6.765	11.667	11	18	1	1	2	ACTG2, DGUOK	34007, 147	downstream, in gene	ActReg chr2 #5675	0	1
5676	2	74,347,093	74,348,114	1,021	2	27.469	34.312	79	106	1	0	0				ActReg chr2 #5676	1	1
5677	2	74,374,393	74,375,846	1,453	2	27.239	30.848	103	136	1	2	3	BOLA3, LOC100507171, MOBKL1B	-80, -47, 30876	upstream, upstream, downstream	ActReg chr2 #5677	1	1
5678	2	74,425,470	74,426,104	634	1	9.8	10.6	17	18	1	1	1	MTHFD2	97	in gene	ActReg chr2 #5678	0	1
5679	2	74,619,034	74,619,563	529	1	11.471	8	16	16	1	1	2	DCTN1, LOC100189589	-84, 6453	upstream, in gene	ActReg chr2 #5679	1	0
5680	2	74,648,325	74,648,992	667	1	7.571	11.381	12	18	1	3	4	C2orf81, LOC100130009, WDR54, RTKN	-3814, -3089, -227, 20402	upstream, upstream, upstream, downstream	ActReg chr2 #5680	0	1
5681	2	74,666,888	74,668,405	1,517	2	11.83	16.234	29	40	1	1	1	RTKN	1,414	in gene	ActReg chr2 #5681	1	1
5682	2	74,681,780	74,682,672	892	1	10.893	12.464	23	20	1	2	3	INO80B, WBP1, MOGS	27, -3351, 10311	in gene, upstream, downstream	ActReg chr2 #5682	0	1
5683	2	74,699,282	74,700,232	950	2	12.6	10.533	20	22	1	2	4	MOGS, MRPL53, CCDC142, TTC31	-7220, 170, 10600, -10443	upstream, in gene, downstream, upstream	ActReg chr2 #5683	1	1
5684	2	74,709,114	74,710,738	1,624	2	12.922	12.941	19	23	1	2	3	MRPL53, CCDC142, TTC31	-9999, 431, -274	upstream, in gene, upstream	ActReg chr2 #5684	1	1
5685	2	74,734,027	74,735,041	1,014	2	13.562	19	28	38	1	3	4	LBX2, hCG_1811732, PCGF1, TLX2	-4091, 4790, 287, -7062	upstream, downstream, in gene, upstream	ActReg chr2 #5685	1	1
5686	2	74,756,206	74,757,065	859	1	8.889	13.518	16	27	1	3	4	DQX1, AUP1, HTRA2, LOXL3	-3227, 339, 103, 24427	upstream, in gene, in gene, downstream	ActReg chr2 #5686	0	1
5687	2	75,061,530	75,062,527	997	1	9.548	12.677	16	22	1	1	1	HK2	2,246	in gene	ActReg chr2 #5687	0	1
5688	2	75,144,861	75,145,810	949	1	11.2	10.2	18	16	0	0	0				ActReg chr2 #5688	1	0
5689	2	75,274,854	75,275,461	607	1	12.737	8.105	22	16	0	0	1	TACR1	151,488	in gene	ActReg chr2 #5689	1	0
5690	2	75,818,943	75,819,781	838	2	13.259	15.778	29	38	0	0	0				ActReg chr2 #5690	1	1
5691	2	75,833,019	75,833,683	664	1	7.3	11.429	14	17	0	0	0				ActReg chr2 #5691	0	1
5692	2	75,873,486	75,874,293	807	2	9.84	13.36	17	21	1	1	1	MRPL19	-20	upstream	ActReg chr2 #5692	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5693	2	75,937,414	75,938,346	932	1	9.724	11.931	19	23	1	1	1	C2orf3	231	in gene	ActReg chr2 #5693	0	1
5694	2	76,098,824	76,099,898	1,074	2	9.97	11.97	20	20	0	0	0				ActReg chr2 #5694	1	1
5695	2	77,185,601	77,186,344	743	2	9.696	13.13	20	20	0	0	1	LRRTM4	563,530	in gene	ActReg chr2 #5695	1	1
5696	2	78,768,719	78,769,742	1,023	2	14.062	16.344	39	40	0	0	0				ActReg chr2 #5696	1	1
5697	2	81,708,145	81,709,376	1,231	2	9.692	10.615	17	20	0	0	0				ActReg chr2 #5697	1	1
5698	2	81,885,337	81,885,808	471	1	11.2	8.2	19	12	0	0	0				ActReg chr2 #5698	1	0
5699	2	84,541,917	84,542,356	439	1	10	4.071	14	6	0	0	0				ActReg chr2 #5699	1	0
5700	2	84,686,044	84,687,002	958	2	15.6	16.933	40	37	1	1	1	SUCLG1	63	in gene	ActReg chr2 #5700	1	1
5701	2	84,968,026	84,968,928	902	1	6.586	11.414	10	25	0	0	1	DNAH6	224,898	in gene	ActReg chr2 #5701	0	1
5702	2	85,132,396	85,133,696	1,300	1	7	11.366	10	19	2	1	1	TMSB10	283	in gene	ActReg chr2 #5702	0	1
5703	2	85,152,635	85,153,611	976	2	13.419	12.774	21	24	0	0	0				ActReg chr2 #5703	1	1
5704	2	85,153,720	85,154,520	800	1	10.44	8.08	15	11	0	0	0				ActReg chr2 #5704	1	0
5705	2	85,554,843	85,555,657	814	2	11.923	11.577	20	18	1	1	1	TGOLN2	124	in gene	ActReg chr2 #5705	1	1
5706	2	85,580,961	85,582,198	1,237	1	8.289	13.237	14	21	1	2	2	RETSAT, ELMOD3	242, -264	in gene, upstream	ActReg chr2 #5706	0	1
5707	2	85,647,630	85,648,173	543	1	8.059	13.118	11	21	0	0	1	CAPG	-10,225	upstream	ActReg chr2 #5707	0	1
5708	2	85,664,507	85,665,085	578	1	6.333	11.5	11	21	1	0	1	SH2D6	2,878	downstream	ActReg chr2 #5708	0	1
5709	2	85,765,430	85,767,294	1,864	2	10.397	11.345	21	19	1	1	3	MAT2A, LOC100507238, GGCX	74, 7030, 22295	in gene, downstream, downstream	ActReg chr2 #5709	1	1
5710	2	85,822,269	85,823,246	977	1	6.452	11.258	15	17	1	1	4	VAMP5, RNF181, TMEM150A, C2orf68	11226, -80, 7065, 16422	downstream, upstream, downstream, downstream	ActReg chr2 #5710	0	1
5711	2	85,829,489	85,830,405	916	1	9.172	14.379	13	23	1	1	4	VAMP5, RNF181, TMEM150A, C2orf68	18416, 7110, -125, 9232	downstream, downstream, upstream, downstream	ActReg chr2 #5711	0	1
5712	2	85,838,529	85,839,742	1,213	1	8.73	11.108	16	21	1	2	3	TMEM150A, C2orf68, USP39	-9313, 44, -4148	upstream, in gene, upstream	ActReg chr2 #5712	0	1
5713	2	85,889,869	85,890,472	603	1	9.263	14	15	24	0	0	1	SFTPB	5,694	in gene	ActReg chr2 #5713	0	1
5714	2	85,999,303	86,000,021	718	2	11.409	13.773	23	26	0	0	1	ATOH8	18,753	in gene	ActReg chr2 #5714	1	1
5715	2	86,120,534	86,121,223	689	1	8	13	18	19	0	1	1	ST3GAL5	-4,721	upstream	ActReg chr2 #5715	0	1
5716	2	86,129,228	86,129,977	749	1	6.957	10.87	12	13	0	0	0				ActReg chr2 #5716	0	1
5717	2	86,332,397	86,333,662	1,265	2	13.538	14.641	25	28	1	2	2	POLR1A, PTCD3	249, -276	in gene, upstream	ActReg chr2 #5717	1	1
5718	2	86,527,392	86,528,593	1,201	2	13.368	14.895	22	26	0	0	1	REEP1	37,214	in gene	ActReg chr2 #5718	1	1
5719	2	86,667,736	86,668,338	602	1	11.053	10.947	17	16	1	1	1	KDM3A	-234	upstream	ActReg chr2 #5719	1	0
5720	2	86,669,085	86,669,763	678	1	3.4	13.546	9	21	1	1	1	KDM3A	1,153	in gene	ActReg chr2 #5720	0	1
5721	2	86,789,597	86,790,566	969	2	11.935	13.871	29	24	1	1	1	VPS24	539	in gene	ActReg chr2 #5721	1	1
5722	2	88,417,356	88,418,006	650	1	8.8	9.9	17	17	0	0	2	SMYD1, FABP1	50299, 9897	downstream, downstream	ActReg chr2 #5722	0	1
5723	2	88,438,654	88,439,115	461	1	4.8	9.6	6	14	0	0	0				ActReg chr2 #5723	0	1
5724	2	88,927,188	88,927,868	680	1	11.333	10.809	16	14	1	2	2	EIF2AK3, LOC100507360	-434, 489	upstream, in gene	ActReg chr2 #5724	1	0
5725	2	88,990,616	88,991,517	901	2	12.607	12.786	24	25	1	1	1	RPIA	-110	upstream	ActReg chr2 #5725	1	1
5726	2	91,953,923	91,954,933	1,010	2	9.161	9.29	19	16	0	0	0				ActReg chr2 #5726	1	1
5727	2	95,424,981	95,425,512	531	1	10.529	10.294	15	19	0	0	0				ActReg chr2 #5727	0	1
5728	2	95,787,413	95,787,863	450	1	8.929	10.857	12	18	1	1	1	MRPS5	116	in gene	ActReg chr2 #5728	0	1
5729	2	95,831,334	95,831,863	529	1	9.688	10	13	17	1	2	2	ZNF514, ZNF2	-6335, 415	upstream, in gene	ActReg chr2 #5729	0	1
5730	2	95,999,365	95,999,915	550	1	9.941	6.706	18	13	0	0	1	KCNIP3	36,568	in gene	ActReg chr2 #5730	1	0
5731	2	96,068,199	96,068,877	678	1	4.1	10.667	6	21	1	1	1	FAHD2A	90	in gene	ActReg chr2 #5731	0	1
5732	2	96,917,454	96,917,881	427	1	10.538	13.077	18	21	0	0	2	LOC285033, TMEM127	11690, 14084	downstream, in gene	ActReg chr2 #5732	0	1
5733	2	97,001,339	97,001,905	566	2	10.556	9.167	17	15	1	1	2	ITPRIPL1, NCAPH	10560, 138	downstream, in gene	ActReg chr2 #5733	1	1
5734	2	97,073,031	97,073,668	637	1	7.05	11.15	11	16	0	0	0				ActReg chr2 #5734	0	1
5735	2	97,222,462	97,223,151	689	2	11.909	9.682	20	19	0	0	1	ARID5A	20,342	downstream	ActReg chr2 #5735	1	1
5736	2	97,303,851	97,304,517	666	2	11.952	11.238	20	24	1	2	2	KIAA1310, FER1L5	-69, -4390	upstream, upstream	ActReg chr2 #5736	1	1
5737	2	97,481,780	97,482,353	573	1	10.111	6.556	20	10	1	2	3	CNNM4, LOC100506036, CNNM3	55427, -1896, 75	downstream, upstream, in gene	ActReg chr2 #5737	1	0
5738	2	98,280,354	98,280,979	625	1	12.053	7.579	23	15	1	1	1	ACTR1B	-105	upstream	ActReg chr2 #5738	1	0
5739	2	99,224,479	99,225,000	521	1	4.118	10.059	9	16	1	2	2	C2orf64, UNC50	216, -303	in gene, upstream	ActReg chr2 #5739	0	1
5740	2	99,797,280	99,797,796	516	1	9.647	10.471	14	18	1	2	2	MTTD1, MRPL30	-46, -40	upstream, upstream	ActReg chr2 #5740	0	1
5741	2	99,953,555	99,954,101	546	1	13.353	8	20	14	1	2	2	TXNDC9, EIF5B	-968, -6	upstream, upstream	ActReg chr2 #5741	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5742	2	100,498,206	100,498,726	520	1	9	3.235	14	5	0	0	1	AFF3	260,571	in gene	ActReg chr2 #5742	1	0
5743	2	101,087,235	101,087,884	649	2	8.5	9.85	17	18	0	1	1	NMS	615	in gene	ActReg chr2 #5743	1	1
5744	2	101,736,942	101,737,640	698	2	7.818	10	16	17	0	0	1	TBC1D8	30,555	in gene	ActReg chr2 #5744	1	1
5745	2	102,063,223	102,063,841	618	2	10	8.6	23	18	0	0	1	RFX8	27,633	in gene	ActReg chr2 #5745	1	1
5746	2	102,133,629	102,134,234	605	1	11.158	7.842	17	11	0	0	0				ActReg chr2 #5746	1	0
5747	2	105,953,594	105,954,140	546	1	7.824	9.882	12	18	1	3	3	TGFBRAP1, LOC100506473, C2orf49	-7719, -1862, -146	upstream, upstream, upstream	ActReg chr2 #5747	0	1
5748	2	106,535,603	106,536,501	898	1	11.929	8.214	18	21	0	0	0				ActReg chr2 #5748	1	0
5749	2	106,731,226	106,732,328	1,102	2	10.171	11.371	22	19	0	0	1	UXS1	79,018	in gene	ActReg chr2 #5749	1	1
5750	2	109,335,645	109,336,238	593	1	10.79	12	17	20	1	1	1	RANBP2	4	in gene	ActReg chr2 #5750	0	1
5751	2	109,745,156	109,745,746	590	1	3.889	10.833	7	19	1	2	2	LOC100287216, SH3RF3	1124, -546	in gene, upstream	ActReg chr2 #5751	0	1
5752	2	109,830,385	109,830,850	465	1	4.6	11.2	9	17	0	0	1	SH3RF3	84,620	in gene	ActReg chr2 #5752	0	1
5753	2	109,859,436	109,859,895	459	1	5.077	10.214	8	17	0	0	2	SH3RF3, LOC100506574	113668, -8213	in gene, upstream	ActReg chr2 #5753	0	1
5754	2	111,435,420	111,436,021	601	1	6.211	11.368	11	18	2	1	1	BUB1	-36	upstream	ActReg chr2 #5754	0	1
5755	2	111,858,269	111,858,894	625	2	12	12.4	26	24	0	0	2	ACOXL, FLJ44006	368431, 13181	in gene, in gene	ActReg chr2 #5755	1	1
5756	2	112,641,582	112,642,094	512	1	7	10.125	10	15	1	1	1	ANAPC1	-97	upstream	ActReg chr2 #5756	0	1
5757	2	113,032,721	113,033,616	895	1	7.25	11.071	13	19	1	1	1	ZC3H6	-10	upstream	ActReg chr2 #5757	0	1
5758	2	113,299,346	113,300,174	828	1	9.077	10.885	13	17	1	1	2	TTL, POLR1B	60017, 268	downstream, in gene	ActReg chr2 #5758	0	1
5759	2	113,398,164	113,398,872	708	1	8.909	11.136	12	18	0	1	2	FLJ42351, SLC20A1	3239, -5009	downstream, upstream	ActReg chr2 #5759	0	1
5760	2	113,403,322	113,404,227	905	1	6.241	9.552	13	15	1	2	2	FLJ42351, SLC20A1	-2017, 247	upstream, in gene	ActReg chr2 #5760	0	1
5761	2	113,521,895	113,522,572	677	2	8.81	11.286	15	23	1	1	2	CKAP2L, IL1A	21, 20738	in gene, downstream	ActReg chr2 #5761	1	1
5762	2	113,561,452	113,562,021	569	1	11.889	6.444	16	10	0	0	0				ActReg chr2 #5762	1	0
5763	2	113,638,702	113,639,259	557	1	7.882	11.529	13	19	0	0	0				ActReg chr2 #5763	0	1
5764	2	113,678,456	113,679,039	583	1	7.056	10.556	11	17	0	0	1	IL1F7	8,199	downstream	ActReg chr2 #5764	0	1
5765	2	113,998,293	113,998,954	661	2	10.048	12.333	16	21	0	0	3	PAX8, LOC654433, LOC100506707	37875, 4777, 2977	in gene, in gene, downstream	ActReg chr2 #5765	1	1
5766	2	114,340,988	114,341,773	785	2	18.24	18.792	30	33	1	1	2	FAM138B, MIR1302-3	6421, -707	downstream, upstream	ActReg chr2 #5766	1	1
5767	2	115,200,103	115,200,618	515	1	10.188	7.938	14	13	0	1	1	DPP10	461	in gene	ActReg chr2 #5767	1	0
5768	2	118,571,774	118,572,574	800	2	25.12	26.52	69	73	1	1	1	DDX18	-81	upstream	ActReg chr2 #5768	1	1
5769	2	119,863,731	119,864,429	698	1	9.227	11.591	21	23	0	0	0				ActReg chr2 #5769	0	1
5770	2	119,924,613	119,925,014	401	1	10.917	8.417	15	11	0	0	1	C1QL2	-8,342	upstream	ActReg chr2 #5770	1	0
5771	2	120,770,118	120,770,913	795	2	15.64	22.56	38	53	1	1	1	EPB41L5	-89	upstream	ActReg chr2 #5771	1	1
5772	2	120,891,796	120,892,193	397	1	7.385	10.385	11	15	0	0	1	EPB41L5	121,390	in gene	ActReg chr2 #5772	0	1
5773	2	122,287,996	122,288,652	656	2	11.809	12.809	23	23	1	1	3	CLASP1, RNU4ATAC, LOC100506849	118728, -132, 15705	in gene, upstream, downstream	ActReg chr2 #5773	1	1
5774	2	122,512,856	122,513,572	716	2	16.304	13.957	37	29	1	1	1	TSN	93	in gene	ActReg chr2 #5774	1	1
5775	2	127,414,024	127,414,497	473	1	3.818	8.933	5	15	1	1	1	GYPC	576	in gene	ActReg chr2 #5775	0	1
5776	2	127,976,306	127,976,702	396	1	4.833	9.917	7	16	1	0	0				ActReg chr2 #5776	0	1
5777	2	128,848,328	128,849,223	895	2	13.607	11.857	23	25	1	1	1	UGGT1	21	in gene	ActReg chr2 #5777	1	1
5778	2	130,938,776	130,939,422	646	2	8.4	9.7	16	19	1	2	3	SMPD4, FAM128B, TUBA3E	1224, -402, 16935	in gene, upstream, downstream	ActReg chr2 #5778	1	1
5779	2	131,100,091	131,100,856	765	1	8.583	12.292	17	20	1	2	2	CCDC115, IMP4	-551, -16	upstream, upstream	ActReg chr2 #5779	0	1
5780	2	132,250,299	132,250,807	508	1	5.75	10.688	8	14	1	1	2	TUBA3D, FAM128A	16887, -489	downstream, upstream	ActReg chr2 #5780	0	1
5781	2	133,075,887	133,077,101	1,214	2	11.579	11.816	24	20	0	1	1	ZNF806	1,819	downstream	ActReg chr2 #5781	1	1
5782	2	133,104,568	133,105,416	848	2	12.222	11.444	24	21	0	1	1	LOC339742	-1,798	upstream	ActReg chr2 #5782	1	1
5783	2	133,246,524	133,247,155	631	2	11.1	9.1	17	16	0	0	1	GPR39	72,692	in gene	ActReg chr2 #5783	1	1
5784	2	133,784,318	133,784,780	462	1	6.6	8.933	12	13	0	0	1	NCKAP5	541,482	in gene	ActReg chr2 #5784	0	1
5785	2	133,821,293	133,821,800	507	2	11.688	11.875	20	20	0	0	1	NCKAP5	504,485	in gene	ActReg chr2 #5785	1	1
5786	2	134,575,822	134,576,252	430	1	5.769	11.077	9	17	0	0	0				ActReg chr2 #5786	0	1
5787	2	135,788,354	135,788,957	603	2	10.5	10.278	17	18	0	1	1	YSK4	-6,407	upstream	ActReg chr2 #5787	1	1
5788	2	137,285,127	137,285,581	454	1	8.071	14.214	13	25	0	0	0				ActReg chr2 #5788	0	1
5789	2	138,829,727	138,830,425	698	2	12.682	13.046	28	27	0	0	0				ActReg chr2 #5789	1	1
5790	2	139,899,843	139,900,367	524	1	9.562	9.125	16	15	0	0	0				ActReg chr2 #5790	1	0
5791	2	140,879,478	140,880,121	643	2	10.35	11.65	22	24	0	0	0				ActReg chr2 #5791	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5792	2	142,314,936	142,315,328	392	1	9.231	4.308	15	7	0	0	1	LRP1B	574,138	in gene	ActReg chr2 #5792	1	0
5793	2	143,637,716	143,638,156	440	1	10.214	4.857	16	7	0	0	1	KYNU	2,741	in gene	ActReg chr2 #5793	1	0
5794	2	150,444,057	150,444,620	563	1	7.833	10.222	14	19	0	2	2	MMADHC, LOC642340	-8, 466	upstream, in gene	ActReg chr2 #5794	0	1
5795	2	151,061,026	151,061,509	483	1	6	9.867	8	17	0	0	0				ActReg chr2 #5795	0	1
5796	2	151,342,500	151,343,190	690	1	5.381	11.857	9	18	1	1	1	RND3	1,335	in gene	ActReg chr2 #5796	0	1
5797	2	152,265,981	152,266,713	732	2	13.522	14.478	26	31	1	1	1	RIF1	-50	upstream	ActReg chr2 #5797	1	1
5798	2	153,032,144	153,032,836	692	1	11.091	13.046	17	20	1	1	1	STAM2	16	in gene	ActReg chr2 #5798	0	1
5799	2	153,056,962	153,057,605	643	1	12.15	5.474	25	10	0	0	0				ActReg chr2 #5799	1	0
5800	2	153,312,811	153,313,230	419	1	5.462	9.231	8	14	0	0	1	FMNL2	121,269	in gene	ActReg chr2 #5800	0	1
5801	2	153,573,878	153,575,346	1,468	2	15.435	21.13	41	44	1	2	2	PRPF40A, ARL6IP6	-637, 189	upstream, in gene	ActReg chr2 #5801	1	1
5802	2	157,189,058	157,189,596	538	1	10.938	8.938	15	15	1	1	1	NR4A2	-40	upstream	ActReg chr2 #5802	1	0
5803	2	161,098,285	161,098,696	411	1	8.462	11.462	14	16	0	0	0				ActReg chr2 #5803	0	1
5804	2	161,469,803	161,470,344	541	1	7.882	9.588	14	17	0	0	0				ActReg chr2 #5804	0	1
5805	2	162,016,780	162,017,366	586	1	10.944	7.667	18	11	1	0	1	TANK	23,607	in gene	ActReg chr2 #5805	1	0
5806	2	162,164,773	162,165,367	594	1	7	10.5	11	18	1	1	1	PSMD14	284	in gene	ActReg chr2 #5806	0	1
5807	2	163,696,915	163,697,768	853	2	17.074	18.482	43	48	0	1	1	KCNH7	-2,101	upstream	ActReg chr2 #5807	1	1
5808	2	166,810,052	166,810,789	737	2	13.957	9.652	27	16	1	1	2	TTC21B, LOC100506134	-72, 20053	upstream, downstream	ActReg chr2 #5808	1	1
5809	2	170,681,092	170,681,731	639	1	6.1	10.6	10	21	1	2	2	METTL5, UBR3	-58, -2607	upstream, upstream	ActReg chr2 #5809	0	1
5810	2	171,785,247	171,786,038	791	2	11.92	14.4	24	28	1	1	1	GORASP2	-69	upstream	ActReg chr2 #5810	1	1
5811	2	172,949,355	172,949,883	528	1	10.438	7.938	13	12	1	1	2	MAP1D, DLX1	84815, -589	downstream, upstream	ActReg chr2 #5811	1	0
5812	2	172,959,966	172,960,568	602	1	9.737	10.105	14	15	1	0	2	DLX1, DLX2	10059, 7211	downstream, downstream	ActReg chr2 #5812	0	1
5813	2	173,114,540	173,114,984	444	1	9.714	4.5	14	7	0	0	0				ActReg chr2 #5813	1	0
5814	2	174,016,296	174,016,882	586	2	10.167	9.667	19	17	0	0	1	ZAK	76,024	in gene	ActReg chr2 #5814	1	1
5815	2	174,218,864	174,220,362	1,498	2	7.979	15.787	19	40	1	1	1	CDCA7	52	in gene	ActReg chr2 #5815	1	1
5816	2	176,952,846	176,953,445	599	2	10.368	11.947	19	22	1	2	2	EVX2, HOXD13	-4455, -4387	upstream, upstream	ActReg chr2 #5816	1	1
5817	2	176,957,804	176,958,155	351	1	6.455	9.909	11	15	1	2	3	EVX2, HOXD13, HOXD12	-9289, 447, -6551	upstream, in gene, upstream	ActReg chr2 #5817	0	1
5818	2	177,418,754	177,419,340	586	1	3.556	11.333	7	16	0	0	0				ActReg chr2 #5818	0	1
5819	2	178,128,105	178,128,637	532	1	10.438	10.188	19	13	1	2	2	NFE2L2, MIR3128	1488, -7633	in gene, upstream	ActReg chr2 #5819	1	0
5820	2	178,483,244	178,483,972	728	1	7.652	11.522	12	19	1	1	2	TTC30A, PDE11A	86, 489458	in gene, downstream	ActReg chr2 #5820	0	1
5821	2	178,976,630	178,978,026	1,396	2	10.364	16.341	34	35	1	2	2	PDE11A, RBM45	-4262, 146	upstream, in gene	ActReg chr2 #5821	1	1
5822	2	179,269,024	179,269,607	583	1	6.737	8.947	13	20	0	0	2	OSBPL6, LOC100506831	209941, -9337	downstream, upstream	ActReg chr2 #5822	0	1
5823	2	179,278,323	179,278,720	397	1	8.167	10	12	16	1	1	1	LOC100506831	-131	upstream	ActReg chr2 #5823	0	1
5824	2	180,871,697	180,872,219	522	1	11.438	7.125	16	10	1	1	1	CWC22	-178	upstream	ActReg chr2 #5824	1	0
5825	2	180,882,314	180,882,695	381	1	9	4.75	13	9	0	0	0				ActReg chr2 #5825	1	0
5826	2	182,321,702	182,322,276	574	1	10.611	8.333	15	14	1	1	1	ITGA4	370	in gene	ActReg chr2 #5826	1	0
5827	2	182,542,378	182,543,430	1,052	2	12.454	17.333	30	38	0	1	1	NEUROD1	2,477	in gene	ActReg chr2 #5827	1	1
5828	2	182,549,849	182,550,424	575	1	10.111	7.778	15	13	0	1	1	NEUROD1	-4,755	upstream	ActReg chr2 #5828	1	0
5829	2	183,580,738	183,581,251	513	1	12	9.625	15	14	1	1	1	DNAJC10	-5	upstream	ActReg chr2 #5829	1	0
5830	2	187,350,447	187,351,175	728	2	9.522	9.957	21	15	1	1	1	ZC3H15	-74	upstream	ActReg chr2 #5830	1	1
5831	2	187,454,492	187,455,183	691	1	4.682	11.318	6	18	1	1	1	ITGAV	47	in gene	ActReg chr2 #5831	0	1
5832	2	189,156,085	189,156,558	473	1	9.4	7.8	13	10	1	2	2	GULP1, MIR561	-1069, -5898	upstream, upstream	ActReg chr2 #5832	1	0
5833	2	190,627,037	190,627,635	598	1	9.421	10.21	16	14	0	1	2	OSGEPL1, ORMDL1	588, 21761	in gene, downstream	ActReg chr2 #5833	1	0
5834	2	191,184,109	191,185,073	964	2	9.133	13.733	22	28	1	1	1	HIBCH	180	in gene	ActReg chr2 #5834	1	1
5835	2	191,884,950	191,885,596	646	1	11.5	8.65	17	12	1	1	2	STAT1, STAT4	-6297, 130652	upstream, downstream	ActReg chr2 #5835	1	0
5836	2	194,367,095	194,367,450	355	1	6.545	10.273	9	15	0	0	0				ActReg chr2 #5836	0	1
5837	2	196,398,815	196,399,429	614	1	10.05	8.95	16	14	0	0	0				ActReg chr2 #5837	1	0
5838	2	197,503,958	197,504,866	908	2	6.269	10.828	15	17	1	1	1	CCDC150	56	in gene	ActReg chr2 #5838	1	1
5839	2	198,364,314	198,365,039	725	2	13.174	9.87	25	17	1	2	2	HSPD1, HSPE1	322, -45	in gene, upstream	ActReg chr2 #5839	1	1
5840	2	198,380,416	198,381,084	668	1	7.905	12.809	13	23	1	1	1	MOBKL3	430	in gene	ActReg chr2 #5840	0	1
5841	2	200,180,052	200,180,634	582	1	5.222	10.222	9	15	0	0	1	SATB2	155,646	in gene	ActReg chr2 #5841	0	1
5842	2	200,323,541	200,324,791	1,250	2	12.308	15.513	27	32	1	1	3	SATB2, LOC100288092, FLJ32063	11823, 1743, -8655	in gene, in gene, upstream	ActReg chr2 #5842	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5843	2	200,819,985	200,820,922	937	2	11.276	12.69	32	20	1	2	2	C2orf60, C2orf47	6, 413	in gene, in gene	ActReg chr2 #5843	1	1
5844	2	201,374,688	201,375,139	451	1	9.667	8.667	16	11	1	1	1	KCTD18	-121	upstream	ActReg chr2 #5844	1	0
5845	2	201,527,433	201,527,872	439	1	5.143	9.714	8	13	0	0	1	AOX1	76,921	in gene	ActReg chr2 #5845	0	1
5846	2	201,676,195	201,676,818	623	2	11.737	11.263	17	15	1	1	1	BZW1	-141	upstream	ActReg chr2 #5846	1	1
5847	2	201,936,352	201,936,947	595	1	11.421	8.579	20	12	1	2	2	FAM126B, NDUFB3	-257, 187	upstream, in gene	ActReg chr2 #5847	1	0
5848	2	201,980,704	201,981,539	835	1	7.815	10.63	14	18	1	1	1	CFLAR	305	in gene	ActReg chr2 #5848	0	1
5849	2	202,316,040	202,316,491	451	1	12.214	8.857	17	12	1	2	2	TRAK2, STRADB	54, -127	in gene, upstream	ActReg chr2 #5849	1	0
5850	2	202,645,419	202,646,158	739	1	10.696	7.565	15	12	1	1	1	ALS2	107	in gene	ActReg chr2 #5850	1	0
5851	2	202,899,787	202,900,611	824	1	5.731	12.269	8	18	1	1	1	FZD7	889	in gene	ActReg chr2 #5851	0	1
5852	2	203,130,235	203,130,883	648	2	10.667	11.476	16	19	1	1	1	NOP58	44	in gene	ActReg chr2 #5852	1	1
5853	2	203,776,009	203,776,733	724	2	10.864	8.591	15	19	1	2	2	WDR12, ALS2CR8	578, -607	in gene, upstream	ActReg chr2 #5853	1	1
5854	2	204,103,321	204,104,097	776	2	14.12	17.08	27	34	1	2	2	LOC100507265, CYP20A1	-1033, 545	upstream, in gene	ActReg chr2 #5854	1	1
5855	2	204,884,336	204,884,800	464	1	10.333	6.267	16	7	0	0	0				ActReg chr2 #5855	1	0
5856	2	206,514,970	206,515,453	483	1	11	8.6	20	12	0	0	0				ActReg chr2 #5856	1	0
5857	2	206,544,785	206,545,296	511	1	11.062	7.438	21	12	0	1	1	NRP2	-2,184	upstream	ActReg chr2 #5857	1	0
5858	2	206,950,438	206,950,882	444	1	6.429	10.643	9	13	1	2	2	INO80D, LOC729570	246, 1340	in gene, in gene	ActReg chr2 #5858	0	1
5859	2	208,067,187	208,067,873	686	1	10.818	8	24	13	0	0	0				ActReg chr2 #5859	1	0
5860	2	208,352,446	208,353,137	691	2	14.182	13.227	32	27	0	0	0				ActReg chr2 #5860	1	1
5861	2	208,489,440	208,490,326	886	2	10.393	11.143	18	17	1	1	1	FAM119A	90	in gene	ActReg chr2 #5861	1	1
5862	2	209,130,354	209,131,207	853	2	16.889	17.333	47	43	1	1	2	LOC100507475, PIKFYVE	10823, -211	downstream, upstream	ActReg chr2 #5862	1	1
5863	2	210,636,171	210,636,795	624	1	8.211	12.526	12	20	1	1	1	UNC80	-234	upstream	ActReg chr2 #5863	0	1
5864	2	215,275,568	215,276,069	501	1	7.188	13.812	12	26	0	1	2	SPAG16, VWC2L	1126702, -643	downstream, upstream	ActReg chr2 #5864	0	1
5865	2	216,871,036	216,871,512	476	1	4.067	9.533	6	13	0	0	1	MREG	7,072	in gene	ActReg chr2 #5865	0	1
5866	2	217,236,668	217,238,028	1,360	2	11.767	15.558	28	41	1	1	1	4-Mar	-598	upstream	ActReg chr2 #5866	1	1
5867	2	217,238,235	217,238,735	500	2	8.438	11.125	15	20	0	1	1	4-Mar	-1,735	upstream	ActReg chr2 #5867	1	1
5868	2	217,276,717	217,277,612	895	2	11	10.143	16	16	1	1	1	SMARCAL1	27	in gene	ActReg chr2 #5868	1	1
5869	2	217,363,325	217,363,909	584	1	11.684	7.895	24	12	1	2	2	LOC100507554, RPL37A	-148, 97	upstream, in gene	ActReg chr2 #5869	1	0
5870	2	218,142,431	218,142,941	510	1	5.438	10.875	12	17	0	0	1	DIRC3	478,630	downstream	ActReg chr2 #5870	0	1
5871	2	219,260,628	219,261,492	864	2	10.741	18.407	21	37	0	2	3	SLC11A1, CTDSP1, MIR26B	14308, -3418, -6309	in gene, upstream, upstream	ActReg chr2 #5871	1	1
5872	2	219,264,158	219,264,885	727	2	11.043	15.13	30	38	1	2	3	SLC11A1, CTDSP1, MIR26B	17769, 43, -2848	downstream, in gene, upstream	ActReg chr2 #5872	1	1
5873	2	219,773,660	219,774,240	580	1	10.895	9.789	19	15	1	0	0				ActReg chr2 #5873	1	0
5874	2	219,826,631	219,828,303	1,672	2	11.654	16.481	22	28	1	1	1	CDK5R2	3,069	downstream	ActReg chr2 #5874	1	1
5875	2	219,856,379	219,856,908	529	1	9.647	4.706	17	7	0	2	3	FEV, CRYBA2, MIR375	-6264, 1484, 9787	upstream, in gene, downstream	ActReg chr2 #5875	1	0
5876	2	219,910,497	219,911,279	782	2	11.708	11.75	26	24	0	1	2	CCDC108, IHH	-4643, 14350	upstream, downstream	ActReg chr2 #5876	1	1
5877	2	219,989,848	219,990,483	635	2	9.2	10.6	14	18	0	0	1	NHEJ1	35,422	in gene	ActReg chr2 #5877	1	1
5878	2	220,083,177	220,083,918	741	1	7.696	10.522	14	14	1	1	3	ZFAND2B, ABCB6, ATG9A	12009, 125, 10814	downstream, in gene, downstream	ActReg chr2 #5878	0	1
5879	2	220,093,883	220,094,538	655	1	10.857	8.286	17	15	1	2	3	ATG9A, ANKZF1, GLB1L	151, -269, 15921	in gene, upstream, downstream	ActReg chr2 #5879	1	0
5880	2	220,109,923	220,110,585	662	1	6.45	11	9	15	1	2	4	ANKZF1, GLB1L, STK16, TUBA4A	15775, -123, 62, 8384	downstream, upstream, in gene, downstream	ActReg chr2 #5880	0	1
5881	2	220,172,763	220,173,682	919	2	13.414	15.034	24	30	2	1	1	PTPRN	921	in gene	ActReg chr2 #5881	1	1
5882	2	220,196,163	220,196,733	570	1	8.235	11.235	13	19	1	1	1	RESP18	1,451	in gene	ActReg chr2 #5882	0	1
5883	2	220,253,030	220,253,588	558	1	11.118	8.118	20	15	0	1	1	DNPEP	-647	upstream	ActReg chr2 #5883	1	0
5884	2	220,546,343	220,546,834	491	1	11.533	4.267	17	6	0	0	0				ActReg chr2 #5884	1	0
5885	2	220,571,468	220,572,131	663	1	9.05	12.571	15	20	0	0	0				ActReg chr2 #5885	0	1
5886	2	221,989,490	221,990,017	527	1	6.118	9	11	17	0	0	0				ActReg chr2 #5886	0	1
5887	2	223,520,406	223,521,197	791	1	7.36	11.8	15	19	1	1	1	FARSB	26	in gene	ActReg chr2 #5887	0	1
5888	2	223,573,959	223,574,378	419	1	9.462	10.385	11	14	0	0	1	MOGAT1	37,711	in gene	ActReg chr2 #5888	0	1
5889	2	223,725,529	223,726,031	502	1	12.812	7	20	10	1	1	1	ACSL3	48	in gene	ActReg chr2 #5889	1	0
5890	2	224,401,202	224,401,640	438	1	10.357	11.643	14	16	0	0	0				ActReg chr2 #5890	1	0
5891	2	224,760,234	224,760,873	639	1	6.3	9.85	10	21	0	0	1	WDFY1	49,499	in gene	ActReg chr2 #5891	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5892	2	224,809,786	224,810,335	549	2	8.529	11.529	16	21	1	1	1	WDFY1	-8	upstream	ActReg chr2 #5892	1	1
5893	2	224,821,868	224,822,673	805	1	5.208	12.24	13	21	1	1	1	MRPL44	149	in gene	ActReg chr2 #5893	0	1
5894	2	224,907,023	224,907,460	437	1	10.071	9.214	16	14	0	1	1	SERPINE2	-3,205	upstream	ActReg chr2 #5894	1	0
5895	2	225,984,843	225,985,386	543	1	5.824	10.118	10	18	0	0	0				ActReg chr2 #5895	0	1
5896	2	226,785,720	226,786,112	392	1	5.923	9.154	9	13	0	0	0				ActReg chr2 #5896	0	1
5897	2	226,802,316	226,802,960	644	2	12	11.25	20	19	0	0	0				ActReg chr2 #5897	1	1
5898	2	227,675,588	227,676,227	639	2	8.389	13.45	13	23	0	0	0				ActReg chr2 #5898	1	1
5899	2	228,336,365	228,337,261	896	2	29.25	28	89	90	1	1	1	ACFG1	-75	upstream	ActReg chr2 #5899	1	1
5900	2	228,727,402	228,727,930	528	1	7.562	11.188	10	14	0	0	1	WDR69	-8,661	upstream	ActReg chr2 #5900	0	1
5901	2	230,579,443	230,580,270	827	2	9.846	12.808	19	19	1	1	1	DNER	-570	upstream	ActReg chr2 #5901	1	1
5902	2	231,577,168	231,577,763	595	2	17.737	18.684	37	39	1	1	1	CAB39	-92	upstream	ActReg chr2 #5902	1	1
5903	2	231,773,216	231,773,843	627	1	9.95	11.8	12	16	0	0	1	GPR55	16,412	in gene	ActReg chr2 #5903	0	1
5904	2	231,917,368	231,917,981	613	1	7.579	10	10	15	1	1	2	C2orf72, PSMD1	15393, -3904	downstream, upstream	ActReg chr2 #5904	0	1
5905	2	231,920,929	231,922,094	1,165	2	34.583	37.472	113	104	1	1	2	C2orf72, PSMD1	19230, -67	downstream, upstream	ActReg chr2 #5905	1	1
5906	2	232,229,680	232,230,337	657	2	14.381	10.571	24	15	0	0	0				ActReg chr2 #5906	1	1
5907	2	232,252,929	232,253,750	821	2	9.32	9.84	18	13	0	1	1	B3GNT7	-6,996	upstream	ActReg chr2 #5907	1	1
5908	2	232,526,891	232,527,289	398	1	6	10.583	8	15	1	0	0				ActReg chr2 #5908	0	1
5909	2	232,531,019	232,531,597	578	1	6.944	11.444	10	15	0	0	0				ActReg chr2 #5909	0	1
5910	2	232,570,935	232,572,555	1,620	2	11.274	15	28	34	1	1	1	PTMA	-1,490	upstream	ActReg chr2 #5910	1	1
5911	2	232,572,827	232,573,646	819	2	10.538	8.346	13	17	1	1	1	PTMA	1	in gene	ActReg chr2 #5911	1	1
5912	2	232,645,613	232,646,418	805	1	6.4	11.48	10	19	1	2	2	PDE6D, COPS7B	-41, -5147	upstream, upstream	ActReg chr2 #5912	0	1
5913	2	232,650,724	232,651,581	857	2	9.115	14.154	21	22	1	2	2	PDE6D, COPS7B	-5178, -10	upstream, upstream	ActReg chr2 #5913	1	1
5914	2	233,180,028	233,180,760	732	2	8.217	11.174	16	18	0	0	1	DIS3L2	354,101	in gene	ActReg chr2 #5914	1	1
5915	2	234,821,205	234,822,004	799	2	11.2	16.48	23	39	0	1	1	TRPM8	-4,439	upstream	ActReg chr2 #5915	1	1
5916	2	235,087,125	235,087,947	822	2	12.385	14.615	31	30	0	0	0				ActReg chr2 #5916	1	1
5917	2	235,244,267	235,244,650	383	1	5.917	11	8	13	0	0	0				ActReg chr2 #5917	0	1
5918	2	237,195,732	237,196,231	499	1	7.312	9.812	12	19	0	0	0				ActReg chr2 #5918	0	1
5919	2	237,994,126	237,994,827	701	2	9.955	13.546	18	28	1	1	1	COPS8	392	in gene	ActReg chr2 #5919	1	1
5920	2	238,136,104	238,136,721	617	1	9.316	11.053	14	19	0	0	0				ActReg chr2 #5920	0	1
5921	2	238,341,126	238,341,835	709	1	7.182	11.591	10	19	0	0	0				ActReg chr2 #5921	0	1
5922	2	238,383,726	238,384,864	1,138	2	17.111	17.528	46	46	1	0	0				ActReg chr2 #5922	1	1
5923	2	238,472,343	238,472,917	574	1	7.778	11.111	13	17	0	1	2	MLPH, PRLH	76752, -2587	downstream, upstream	ActReg chr2 #5923	0	1
5924	2	238,807,104	238,807,810	706	2	9.87	11.043	20	20	0	0	1	RAMP1	39,270	in gene	ActReg chr2 #5924	1	1
5925	2	238,875,281	238,875,793	512	1	9	6.25	16	10	1	1	1	UBE2F	-163	upstream	ActReg chr2 #5925	1	0
5926	2	238,969,140	238,969,711	571	1	3.889	10.333	7	19	1	1	1	SCLY	-207	upstream	ActReg chr2 #5926	0	1
5927	2	239,165,067	239,165,685	618	2	12.526	16.526	30	32	0	0	1	PER2	31,831	in gene	ActReg chr2 #5927	1	1
5928	2	239,197,300	239,197,839	539	2	9.765	9.647	17	16	1	1	1	PER2	-362	upstream	ActReg chr2 #5928	1	1
5929	2	239,552,609	239,553,111	502	1	10.933	8.6	14	11	0	0	0				ActReg chr2 #5929	1	0
5930	2	239,592,972	239,593,525	553	1	9.941	6.824	16	11	0	0	0				ActReg chr2 #5930	1	0
5931	2	239,670,270	239,670,970	700	2	10.454	11.091	21	19	0	0	0				ActReg chr2 #5931	1	1
5932	2	240,196,687	240,197,298	611	1	6.579	11.684	9	18	1	0	1	HDAC4	125,651	in gene	ActReg chr2 #5932	0	1
5933	2	240,323,064	240,323,610	546	2	11.353	9.353	15	15	1	1	1	HDAC4	-694	upstream	ActReg chr2 #5933	1	1
5934	2	240,964,695	240,965,078	383	1	10	11.333	13	18	1	1	2	NDUFA10, OR6B2	-67, 4960	upstream, downstream	ActReg chr2 #5934	0	1
5935	2	242,041,480	242,042,101	621	1	12.053	9.737	18	18	1	1	3	SNED1, MTERFD2, PASK	103535, -43, 47088	downstream, upstream, downstream	ActReg chr2 #5935	1	0
5936	2	242,211,134	242,211,704	570	2	8.444	8.5	16	16	1	0	1	HDLBP	43,835	in gene	ActReg chr2 #5936	1	1
5937	2	242,254,097	242,255,148	1,051	2	12.727	14	34	27	1	2	2	HDLBP, SEPT2	632, -101	in gene, upstream	ActReg chr2 #5937	1	1
5938	2	242,447,812	242,448,542	730	1	8.727	11.318	15	19	1	1	1	STK25	-143	upstream	ActReg chr2 #5938	0	1
5939	20	304,854	305,671	817	1	8.846	12.615	16	22	1	2	2	LOC100507459, SOX12	634, -977	in gene, upstream	ActReg chr20 #5939	0	1
5940	20	387,823	388,604	781	1	9.958	10.875	22	18	1	1	2	TRIB3, RBCK1	26905, -496	downstream, upstream	ActReg chr20 #5940	0	1
5941	20	411,901	412,598	697	1	11.954	4.318	16	8	0	0	2	RBCK1, TBC1D20	23540, 30938	downstream, downstream	ActReg chr20 #5941	1	0
5942	20	524,001	525,114	1,113	2	12.441	11.735	21	22	1	1	1	CSNK2A1	-75	upstream	ActReg chr20 #5942	1	1
5943	20	655,828	656,654	826	1	8.115	10.423	12	18	1	1	1	SCRT2	582	in gene	ActReg chr20 #5943	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5944	20	813,935	814,759	824	2	13.154	10.385	29	18	1	1	1	FAM110A	-9	upstream	ActReg chr20 #5944	1	1
5945	20	859,347	859,801	454	1	8.357	12.357	12	22	0	0	1	ANGPT4	37,386	in gene	ActReg chr20 #5945	0	1
5946	20	1,098,624	1,099,911	1,287	2	10.537	12.415	23	28	1	0	1	PSMF1	5,361	in gene	ActReg chr20 #5946	1	1
5947	20	1,305,676	1,306,681	1,005	1	6.871	11.194	11	16	1	1	3	SDCBP2, LOC100507495, LOC100288764	3660, 124, 11377	in gene, in gene, downstream	ActReg chr20 #5947	0	1
5948	20	1,396,498	1,397,354	856	1	10.111	13.259	21	22	0	0	0				ActReg chr20 #5948	0	1
5949	20	1,446,885	1,447,966	1,081	2	10.303	13.727	25	25	1	1	2	NSFL1C, SIRPB2	992, 24808	in gene, downstream	ActReg chr20 #5949	1	1
5950	20	1,464,910	1,465,351	441	1	7.286	10.429	10	17	0	0	1	SIRPB2	7,103	in gene	ActReg chr20 #5950	0	1
5951	20	1,757,536	1,758,462	926	2	18.241	20.241	50	55	1	0	1	LOC100289473	4,838	in gene	ActReg chr20 #5951	1	1
5952	20	1,808,461	1,809,173	712	1	6.682	12.136	12	20	0	0	0				ActReg chr20 #5952	0	1
5953	20	1,986,271	1,987,050	779	2	13.36	13.2	29	27	0	0	0				ActReg chr20 #5953	1	1
5954	20	2,082,188	2,084,315	2,127	2	30.909	32.818	97	93	1	1	1	STK35	723	in gene	ActReg chr20 #5954	1	1
5955	20	2,187,968	2,188,686	718	1	7.857	11.304	14	16	1	1	1	LOC388780	361	in gene	ActReg chr20 #5955	0	1
5956	20	2,363,191	2,364,062	871	1	9.185	11.593	16	18	0	1	1	TGM6	2,072	in gene	ActReg chr20 #5956	0	1
5957	20	2,450,800	2,451,767	967	2	12.733	13.633	22	25	1	2	2	SNRPB, SNORD119	216, -7590	in gene, upstream	ActReg chr20 #5957	1	1
5958	20	2,489,129	2,490,008	879	2	11.704	9.963	18	13	2	1	1	ZNF343	210	in gene	ActReg chr20 #5958	1	1
5959	20	2,632,652	2,633,732	1,080	1	9.353	13.677	14	24	1	7	8	NOP56, MIR1292, SNORD110, SNORA51, SNORD86, SNORD56, SNORD57, IDH3B	-62, -231, -1666, -2521, -3551, -4078, -4393, 11651	upstream, upstream, upstream, upstream, upstream, upstream, upstream, downstream	ActReg chr20 #5959	0	1
5960	20	2,644,445	2,645,267	822	1	9.885	12.731	16	23	1	1	7	NOP56, SNORD110, SNORA51, SNORD86, SNORD56, SNORD57, IDH3B	11602, 9998, 9143, 8113, 7586, 7271, -13	downstream, downstream, downstream, downstream, downstream, downstream, upstream	ActReg chr20 #5960	0	1
5961	20	2,851,194	2,851,878	684	1	10.636	7.864	20	12	0	0	2	VPS16, PTPRA	30163, 6695	downstream, in gene	ActReg chr20 #5961	1	0
5962	20	3,049,568	3,050,278	710	2	11.522	10.783	22	24	0	1	1	OXT	-2,343	upstream	ActReg chr20 #5962	1	1
5963	20	3,139,936	3,141,016	1,080	1	15.029	9.471	25	21	1	2	3	UBOX5, FASTKD5, ProSAPiP1	64, 56, 8731	in gene, in gene, downstream	ActReg chr20 #5963	1	0
5964	20	3,154,056	3,155,108	1,052	2	12.909	11.879	30	22	1	1	1	ProSAPiP1	-5,375	upstream	ActReg chr20 #5964	1	1
5965	20	3,219,456	3,220,595	1,139	2	12.528	13.611	21	23	1	1	2	SLC4A11, C20orf194	-138, 168230	upstream, downstream	ActReg chr20 #5965	1	1
5966	20	3,451,047	3,452,278	1,231	2	10.632	13.816	17	25	1	1	2	ATRN, LOC100507610	-3, -8980	upstream, upstream	ActReg chr20 #5966	1	1
5967	20	3,776,045	3,776,911	866	1	9.556	11.889	13	18	2	1	2	CENPB, CDC25B	-9141, 77	upstream, in gene	ActReg chr20 #5967	0	1
5968	20	3,792,163	3,792,988	825	1	15	11.44	26	24	0	0	2	CDC25B, C20orf29	16174, -8628	downstream, upstream	ActReg chr20 #5968	1	0
5969	20	3,800,652	3,801,762	1,110	2	12.114	12.971	21	22	1	1	1	C20orf29	4	in gene	ActReg chr20 #5969	1	1
5970	20	3,826,785	3,827,207	422	1	6.692	10.692	9	14	1	1	1	MAVS	-453	upstream	ActReg chr20 #5970	0	1
5971	20	3,827,223	3,827,962	739	1	8.522	12.522	15	18	1	1	1	MAVS	143	in gene	ActReg chr20 #5971	0	1
5972	20	3,869,292	3,870,247	955	1	8.567	12.7	18	21	1	1	1	PANK2	283	in gene	ActReg chr20 #5972	0	1
5973	20	4,047,930	4,048,600	670	1	8.524	10.905	16	16	0	0	0				ActReg chr20 #5973	0	1
5974	20	4,116,751	4,117,526	775	1	6.708	11.708	12	18	0	0	0				ActReg chr20 #5974	0	1
5975	20	4,387,120	4,387,933	813	1	6.92	13.4	13	23	0	0	0				ActReg chr20 #5975	0	1
5976	20	4,536,008	4,536,638	630	1	12.105	9.684	21	19	0	0	0				ActReg chr20 #5976	1	0
5977	20	4,543,769	4,544,697	928	2	9.897	13.069	23	35	0	0	0				ActReg chr20 #5977	1	1
5978	20	4,646,650	4,647,150	500	1	10.312	6.938	15	10	0	0	0				ActReg chr20 #5978	1	0
5979	20	4,663,860	4,664,484	624	1	6.55	9.9	10	19	0	1	1	PRNP	-2,625	upstream	ActReg chr20 #5979	0	1
5980	20	5,093,330	5,094,282	952	2	14.133	15.3	27	32	1	2	3	C20orf30, PCNA, PCNAAS	-73, 13462, -6426	upstream, downstream, upstream	ActReg chr20 #5980	1	1
5981	20	5,099,795	5,100,855	1,060	1	7.242	12.212	10	22	1	3	4	C20orf30, PCNA, PCNAAS, CDS2	-6592, 6943, 93, -7157	upstream, in gene, in gene, upstream	ActReg chr20 #5981	0	1
5982	20	5,380,533	5,381,366	833	2	11.692	13.462	25	26	0	0	0				ActReg chr20 #5982	1	1
5983	20	5,824,768	5,825,366	598	1	9.368	12.21	16	24	0	0	1	C20orf196	94,024	in gene	ActReg chr20 #5983	0	1
5984	20	5,891,727	5,892,771	1,044	2	17.379	24.212	33	65	1	1	1	CHGB	275	in gene	ActReg chr20 #5984	1	1
5985	20	5,930,812	5,931,399	587	1	10.79	8.684	14	14	1	2	2	TRMT6, MCM8	68, -193	in gene, upstream	ActReg chr20 #5985	1	0
5986	20	6,103,314	6,104,055	741	1	8.957	10.913	15	16	1	1	1	FERMT1	507	in gene	ActReg chr20 #5986	0	1
5987	20	6,472,885	6,473,813	928	1	6.759	13.276	12	21	0	0	0				ActReg chr20 #5987	0	1
5988	20	6,481,489	6,482,331	842	1	13.462	10	21	16	0	0	0				ActReg chr20 #5988	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
5989	20	6,665,490	6,666,151	661	1	9.19	10.429	15	18	0	0	0				ActReg chr20 #5989	0	1
5990	20	6,750,318	6,751,110	792	1	11.52	10.28	24	16	1	1	1	BMP2	1,969	in gene	ActReg chr20 #5990	1	0
5991	20	7,176,216	7,176,751	535	1	6.471	10.765	11	19	0	0	0				ActReg chr20 #5991	0	1
5992	20	7,588,828	7,589,342	514	1	10.188	7.312	16	10	0	0	0				ActReg chr20 #5992	1	0
5993	20	7,831,365	7,832,110	745	1	11.435	7.435	18	13	0	0	0				ActReg chr20 #5993	1	0
5994	20	7,905,295	7,906,038	743	2	10	8.391	21	18	0	0	1	HAO1	15,427	in gene	ActReg chr20 #5994	1	1
5995	20	7,999,809	8,000,825	1,016	2	10.613	11.387	16	18	1	1	1	TMX4	76	in gene	ActReg chr20 #5995	1	1
5996	20	8,054,045	8,054,462	417	1	6.846	11.769	11	16	0	0	0				ActReg chr20 #5996	0	1
5997	20	8,525,745	8,526,417	672	2	10.667	10.429	18	18	0	0	1	PLCB1	412,785	in gene	ActReg chr20 #5997	1	1
5998	20	8,736,952	8,737,501	549	1	8.706	10.941	14	19	0	0	1	PLCB1	623,930	in gene	ActReg chr20 #5998	0	1
5999	20	9,049,715	9,050,261	546	1	9.647	10	16	14	1	1	1	PLCB4	287	in gene	ActReg chr20 #5999	1	0
6000	20	10,020,721	10,021,271	550	1	10.294	12.235	21	19	0	0	2	LOC100131208, ANKRD5	179155, 5299	in gene, in gene	ActReg chr20 #6000	0	1
6001	20	10,040,764	10,041,485	721	2	10.652	10.739	20	16	0	0	2	LOC100131208, ANKRD5	159027, 25427	in gene, downstream	ActReg chr20 #6001	1	1
6002	20	10,073,557	10,074,352	795	1	11.8	7.28	17	12	0	0	1	LOC100131208	126,197	in gene	ActReg chr20 #6002	1	0
6003	20	10,198,354	10,199,089	735	1	7.13	12.609	10	20	1	2	2	LOC100131208, SNAP25	1430, -756	in gene, upstream	ActReg chr20 #6003	0	1
6004	20	10,199,395	10,200,659	1,264	2	18.051	22.769	50	57	1	2	2	LOC100131208, SNAP25	124, 550	in gene, in gene	ActReg chr20 #6004	1	1
6005	20	10,413,997	10,415,580	1,583	2	13.735	13.674	25	27	1	2	2	MKKS, C20orf94	78, -1163	in gene, upstream	ActReg chr20 #6005	1	1
6006	20	10,579,107	10,579,566	459	1	11.214	7.857	14	12	0	0	1	C20orf94	163,385	in gene	ActReg chr20 #6006	1	0
6007	20	10,654,582	10,655,304	722	1	7.783	11.826	15	18	1	1	1	JAG1	-249	upstream	ActReg chr20 #6007	0	1
6008	20	10,686,373	10,687,209	836	2	10.923	11.885	19	21	0	0	0				ActReg chr20 #6008	1	1
6009	20	10,982,325	10,983,023	698	2	9.409	10.409	14	20	0	0	0				ActReg chr20 #6009	1	1
6010	20	11,098,169	11,099,031	862	2	11.259	13.556	21	26	0	0	0				ActReg chr20 #6010	1	1
6011	20	11,159,539	11,160,158	619	1	10.632	4.842	20	9	0	0	0				ActReg chr20 #6011	1	0
6012	20	12,709,856	12,710,517	661	2	10.191	10.333	20	18	0	0	0				ActReg chr20 #6012	1	1
6013	20	13,765,206	13,765,902	696	1	8.773	12.864	15	20	1	2	2	ESF1, C20orf7	-22, -118	upstream, upstream	ActReg chr20 #6013	0	1
6014	20	14,269,114	14,269,859	745	1	11.333	6.417	18	10	0	0	1	MACROD2	293,340	in gene	ActReg chr20 #6014	1	0
6015	20	14,845,604	14,846,261	657	1	5.45	10.25	8	21	0	0	1	MACROD2	869,786	in gene	ActReg chr20 #6015	0	1
6016	20	15,679,947	15,680,616	669	1	14.095	10.714	28	25	0	0	1	MACROD2	1,704,135	in gene	ActReg chr20 #6016	1	0
6017	20	16,197,186	16,197,738	552	1	4.941	10.941	8	16	0	0	0				ActReg chr20 #6017	0	1
6018	20	16,553,818	16,554,469	651	1	10.857	13.238	18	22	1	1	1	KIF16B	-65	upstream	ActReg chr20 #6018	0	1
6019	20	16,555,165	16,555,901	736	1	12.391	9.087	19	12	1	1	1	KIF16B	-1,455	upstream	ActReg chr20 #6019	1	0
6020	20	16,710,195	16,711,121	926	2	21.724	27.483	60	76	1	1	1	SNRPB2	49	in gene	ActReg chr20 #6020	1	1
6021	20	16,844,228	16,845,237	1,009	1	10.484	13.258	17	20	0	0	0				ActReg chr20 #6021	0	1
6022	20	17,010,314	17,011,014	700	1	7.909	11.682	15	17	0	0	0				ActReg chr20 #6022	0	1
6023	20	17,064,245	17,064,856	611	1	8.211	10.526	11	20	0	0	0				ActReg chr20 #6023	0	1
6024	20	17,207,095	17,207,505	410	1	8.769	10.154	14	16	1	1	1	PCSK2	-331	upstream	ActReg chr20 #6024	0	1
6025	20	17,207,811	17,208,847	1,036	2	11.419	15.375	22	30	1	1	1	PCSK2	698	in gene	ActReg chr20 #6025	1	1
6026	20	17,397,735	17,398,480	745	2	11.435	12.696	25	31	0	0	1	PCSK2	190,476	in gene	ActReg chr20 #6026	1	1
6027	20	17,836,678	17,837,153	475	1	8.533	13.733	12	22	0	0	0				ActReg chr20 #6027	0	1
6028	20	17,862,528	17,864,193	1,665	2	10.623	12.377	20	22	0	0	0				ActReg chr20 #6028	1	1
6029	20	17,948,947	17,950,330	1,383	2	12.302	16.309	23	30	1	3	3	SNX5, SNORD17, C20orf72	-148, -6049, -124	upstream, upstream, upstream	ActReg chr20 #6029	1	1
6030	20	18,118,093	18,118,957	864	2	16.963	20.37	44	44	1	2	2	PET117, CSRP2BP	26, -4343	in gene, upstream	ActReg chr20 #6030	1	1
6031	20	18,268,174	18,269,360	1,186	1	7.784	13.108	15	21	1	1	1	ZNF133	-354	upstream	ActReg chr20 #6031	0	1
6032	20	18,393,773	18,394,249	476	1	10.133	7.467	18	10	0	0	1	C20orf12	53,818	in gene	ActReg chr20 #6032	1	0
6033	20	18,447,536	18,448,597	1,061	2	11.697	13.061	24	24	1	3	3	C20orf12, POLR3F, MIR3192	-237, 33, -3193	upstream, in gene, upstream	ActReg chr20 #6033	1	1
6034	20	18,477,507	18,478,101	594	1	6.5	10.944	8	19	1	1	1	RBBP9	83	in gene	ActReg chr20 #6034	0	1
6035	20	18,487,992	18,488,707	715	2	12.609	10.043	21	13	1	1	1	SEC23B	161	in gene	ActReg chr20 #6035	1	1
6036	20	18,568,227	18,568,878	651	1	7.9	8.9	11	16	1	1	1	DTD1	-4	upstream	ActReg chr20 #6036	0	1
6037	20	19,063,514	19,064,347	833	2	13.538	13.154	23	25	0	0	0				ActReg chr20 #6037	1	1
6038	20	19,997,611	19,998,610	999	2	10.194	13.645	25	26	1	1	1	NAA20	173	in gene	ActReg chr20 #6038	1	1
6039	20	20,675,738	20,676,523	785	2	10.8	11.12	25	25	0	0	1	RALGAPA2	17,136	in gene	ActReg chr20 #6039	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6040	20	21,283,539	21,284,684	1,145	2	13.333	9	25	15	1	1	1	XRN2	169	in gene	ActReg chr20 #6040	1	1
6041	20	21,416,628	21,417,144	516	1	7.125	10.75	11	14	0	0	0				ActReg chr20 #6041	0	1
6042	20	22,785,784	22,786,559	775	2	11.042	11.583	21	22	0	0	0				ActReg chr20 #6042	1	1
6043	20	23,238,474	23,239,426	952	1	7.367	12.3	13	20	0	0	0				ActReg chr20 #6043	0	1
6044	20	23,330,650	23,331,574	924	1	7.966	10.724	16	20	1	1	2	NXT1, LOC100505683	-261, 7530	upstream, downstream	ActReg chr20 #6044	0	1
6045	20	23,341,979	23,342,765	786	2	12.48	15.72	25	23	1	2	3	NXT1, LOC100505683, GZF1	10999, -3730, -2649	downstream, upstream, upstream	ActReg chr20 #6045	1	1
6046	20	24,615,412	24,616,116	704	1	4.864	10.273	8	18	0	0	1	TMEM90B	165,929	in gene	ActReg chr20 #6046	0	1
6047	20	24,972,561	24,973,632	1,071	2	13.059	11.353	24	16	1	1	1	C20orf3	329	in gene	ActReg chr20 #6047	1	1
6048	20	25,035,278	25,036,434	1,156	2	13.306	16.278	35	32	0	0	1	ACSS1	3,760	in gene	ActReg chr20 #6048	1	1
6049	20	25,159,360	25,160,155	795	2	10.52	11.32	17	20	0	0	0				ActReg chr20 #6049	1	1
6050	20	25,175,767	25,176,660	893	1	8.071	12.107	13	18	2	1	1	ENTPD6	-126	upstream	ActReg chr20 #6050	0	1
6051	20	25,203,725	25,204,425	700	2	12.227	12.182	19	19	0	0	1	ENTPD6	27,736	in gene	ActReg chr20 #6051	1	1
6052	20	25,218,068	25,218,904	836	1	11.192	13.769	17	27	0	0	1	PYGB	-10,220	upstream	ActReg chr20 #6052	0	1
6053	20	25,290,232	25,290,889	657	1	6.333	11.619	10	18	0	0	1	ABHD12	80,917	in gene	ActReg chr20 #6053	0	1
6054	20	25,387,889	25,388,744	855	1	8.778	13.778	16	26	1	1	1	GINS1	-7	upstream	ActReg chr20 #6054	0	1
6055	20	25,477,552	25,478,323	771	1	13.542	13.042	26	24	0	0	1	NINL	88,216	in gene	ActReg chr20 #6055	1	0
6056	20	25,603,845	25,605,278	1,433	2	11.386	11.614	21	19	1	1	1	NANP	87	in gene	ActReg chr20 #6056	1	1
6057	20	25,676,823	25,677,866	1,043	2	13.03	15.515	27	28	1	1	1	ZNF337	125	in gene	ActReg chr20 #6057	1	1
6058	20	30,101,944	30,102,771	827	2	11.962	11.923	24	17	1	1	1	HM13	116	in gene	ActReg chr20 #6058	1	1
6059	20	30,160,362	30,160,990	628	1	10.421	9.105	21	13	1	0	1	HM13	58,435	downstream	ActReg chr20 #6059	1	0
6060	20	30,180,972	30,181,946	974	1	8.267	11.967	13	19	0	0	0				ActReg chr20 #6060	0	1
6061	20	30,310,886	30,312,070	1,184	2	11.378	13.243	17	21	2	1	1	BCL2L1	-822	upstream	ActReg chr20 #6061	1	1
6062	20	30,326,668	30,327,464	796	2	10.6	10.92	19	18	1	1	1	TPX2	162	in gene	ActReg chr20 #6062	1	1
6063	20	30,457,912	30,458,650	738	1	8.043	11.217	13	17	1	2	2	DUSP15, TTLL9	198, -224	in gene, upstream	ActReg chr20 #6063	0	1
6064	20	30,556,119	30,556,851	732	2	23.391	30.174	56	71	1	1	1	XKR7	680	in gene	ActReg chr20 #6064	1	1
6065	20	30,697,137	30,697,914	777	1	13.458	6.833	22	11	0	1	2	HCK, TM9SF4	57534, 216	downstream, in gene	ActReg chr20 #6065	1	0
6066	20	30,795,490	30,796,279	789	1	10.667	10	16	15	1	2	2	PLAGL2, POFUT1	-338, 188	upstream, in gene	ActReg chr20 #6066	1	0
6067	20	30,945,277	30,946,429	1,152	2	11.611	14.611	23	21	1	2	2	LOC100506402, ASXL1	-5994, -294	upstream, upstream	ActReg chr20 #6067	1	1
6068	20	31,051,068	31,052,205	1,137	2	10.25	14.333	15	26	0	0	1	C20orf112	19,652	in gene	ActReg chr20 #6068	1	1
6069	20	31,070,385	31,070,751	366	1	7.182	11.818	9	17	1	1	2	C20orf112, LOC100506597	720, 53883	in gene, downstream	ActReg chr20 #6069	0	1
6070	20	31,780,664	31,781,339	675	2	12.381	13.048	21	22	0	0	0				ActReg chr20 #6070	1	1
6071	20	31,797,485	31,798,073	588	1	9.333	14.389	17	26	0	1	1	C20orf71	-7,356	upstream	ActReg chr20 #6071	0	1
6072	20	31,968,921	31,969,745	824	2	11.231	11.346	20	21	1	1	2	CDK5RAP1, SNTA1	4, 42365	in gene, downstream	ActReg chr20 #6072	1	1
6073	20	32,254,643	32,256,236	1,593	2	9.94	11.64	15	20	1	1	4	NECAB3, C20orf144, C20orf134, E2F1	6825, 5319, 1135, 18771	in gene, downstream, in gene, downstream	ActReg chr20 #6073	1	1
6074	20	32,307,692	32,308,506	814	1	7.56	14.8	12	31	1	1	1	PXMP4	37	in gene	ActReg chr20 #6074	0	1
6075	20	32,398,638	32,399,356	718	1	11	15.046	27	33	1	1	1	CHMP4B	-113	upstream	ActReg chr20 #6075	0	1
6076	20	32,533,234	32,533,895	661	2	12.143	11.191	21	19	0	0	0				ActReg chr20 #6076	1	1
6077	20	32,581,254	32,582,051	797	1	11	11.44	20	16	1	2	2	LOC100505490, RALY	510, -80	in gene, upstream	ActReg chr20 #6077	0	1
6078	20	32,699,434	32,700,468	1,034	1	8.062	11.531	12	18	1	1	1	EIF2S2	134	in gene	ActReg chr20 #6078	0	1
6079	20	32,890,091	32,891,625	1,534	2	22.688	27.771	76	88	1	0	1	AHCY	8,750	in gene	ActReg chr20 #6079	1	1
6080	20	32,902,138	32,902,952	814	1	9.154	13.308	13	23	0	1	1	AHCY	-2,937	upstream	ActReg chr20 #6080	0	1
6081	20	32,950,845	32,951,483	638	1	10.65	11.1	19	21	1	1	1	ITCH	102	in gene	ActReg chr20 #6081	0	1
6082	20	33,103,145	33,104,870	1,725	1	11.833	13.389	21	21	1	1	2	ITCH, DYNLRB1	152945, -197	downstream, upstream	ActReg chr20 #6082	0	1
6083	20	33,112,993	33,114,312	1,319	2	12.244	13.902	24	31	0	0	1	DYNLRB1	9,448	in gene	ActReg chr20 #6083	1	1
6084	20	33,145,915	33,146,708	793	1	12.04	14.2	21	27	1	0	2	MAP1LC3A, PIGU	11619, 118778	in gene, downstream	ActReg chr20 #6084	0	1
6085	20	33,264,600	33,265,421	821	1	12.039	16.577	18	31	1	1	1	PIGU	79	in gene	ActReg chr20 #6085	0	1
6086	20	33,460,376	33,461,139	763	1	7.833	13.292	12	24	1	2	2	GGT7, ACSS2	-96, -2009	upstream, upstream	ActReg chr20 #6086	0	1
6087	20	33,494,880	33,496,662	1,782	2	9.786	11.569	17	17	0	0	1	ACSS2	33,005	in gene	ActReg chr20 #6087	1	1
6088	20	33,542,988	33,544,231	1,243	2	14.205	14.538	24	27	1	2	2	GSS, MYH7B	-8, -95	upstream, upstream	ActReg chr20 #6088	1	1
6089	20	33,679,866	33,681,331	1,465	2	11.391	12.087	20	21	2	1	1	TRPC4AP	20	in gene	ActReg chr20 #6089	1	1
6090	20	33,786,898	33,787,784	886	1	5.107	10.214	8	15	0	0	0				ActReg chr20 #6090	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6091	20	33,814,889	33,815,892	1,003	2	14.903	16.903	24	33	1	1	1	MMP24	851	in gene	ActReg chr20 #6091	1	1
6092	20	33,871,495	33,873,085	1,590	1	10.775	14.041	23	21	1	1	3	MMP24, EIF6, FAM83C	57751, 304, 7935	downstream, in gene, downstream	ActReg chr20 #6092	0	1
6093	20	33,892,957	33,894,600	1,643	2	13.519	13.692	29	28	0	0	1	UQCC	106,167	in gene	ActReg chr20 #6093	1	1
6094	20	33,895,542	33,896,888	1,346	1	6.905	10.976	10	17	0	0	1	UQCC	103,730	in gene	ActReg chr20 #6094	0	1
6095	20	34,042,876	34,043,710	834	1	11.885	7.5	17	12	1	2	2	MIR1289-1, CEP250	-1374, 70	upstream, in gene	ActReg chr20 #6095	1	0
6096	20	34,203,404	34,204,384	980	2	11.903	12.516	19	23	1	1	2	SPAG4, CPNE1	85, 48954	in gene, downstream	ActReg chr20 #6096	1	1
6097	20	34,286,841	34,287,811	970	1	11.516	15.129	22	23	1	2	3	NFS1, ROMO1, RBM39	-52, 94, 42867	upstream, in gene, downstream	ActReg chr20 #6097	0	1
6098	20	34,329,947	34,330,905	958	1	10.733	12.467	21	22	1	1	1	RBM39	-233	upstream	ActReg chr20 #6098	0	1
6099	20	34,356,931	34,357,626	695	1	11.048	12.333	22	25	0	1	1	PHF20	-2,645	upstream	ActReg chr20 #6099	0	1
6100	20	34,541,441	34,543,028	1,587	2	15.49	15.612	31	27	1	1	2	PHF20, SCAND1	182311, 194	downstream, in gene	ActReg chr20 #6100	1	1
6101	20	34,638,343	34,639,213	870	2	10.185	10.333	17	16	1	1	1	LOC647979	104	in gene	ActReg chr20 #6101	1	1
6102	20	34,673,261	34,674,136	875	1	9.296	11.741	14	16	0	0	0				ActReg chr20 #6102	0	1
6103	20	34,680,761	34,681,940	1,179	1	9	13.081	14	23	1	0	0				ActReg chr20 #6103	0	1
6104	20	34,823,692	34,824,812	1,120	2	11.4	14.971	19	29	1	1	2	EPB41L1, C20orf4	123904, -195	downstream, upstream	ActReg chr20 #6104	1	1
6105	20	34,972,622	34,973,959	1,337	2	10.929	18	24	42	0	0	0				ActReg chr20 #6105	1	1
6106	20	35,011,775	35,014,175	2,400	2	9.137	16.733	44	60	0	0	1	DLGAP4	17,531	in gene	ActReg chr20 #6106	1	1
6107	20	35,233,547	35,234,948	1,401	2	12.727	15.159	26	33	1	1	2	C20orf24, SLA2	80, 40311	in gene, downstream	ActReg chr20 #6107	1	1
6108	20	35,723,497	35,724,964	1,467	2	10.391	13.413	18	24	1	1	2	RBL1, C20orf132	180, 83744	in gene, downstream	ActReg chr20 #6108	1	1
6109	20	35,806,422	35,808,406	1,984	2	24.113	26.855	95	96	1	2	2	C20orf132, RPN2	560, -42	in gene, upstream	ActReg chr20 #6109	1	1
6110	20	35,917,786	35,918,670	884	1	10.607	14.321	21	26	1	1	1	MANBAL	177	in gene	ActReg chr20 #6110	0	1
6111	20	35,971,707	35,972,511	804	1	13.28	15.56	24	30	0	1	1	SRC	-979	upstream	ActReg chr20 #6111	0	1
6112	20	36,155,757	36,157,158	1,401	2	28.432	32.568	82	88	1	1	2	BLCAP, NNAT	-124, 6850	upstream, downstream	ActReg chr20 #6112	1	1
6113	20	36,201,110	36,201,967	857	2	11.593	16.741	23	30	0	0	0				ActReg chr20 #6113	1	1
6114	20	36,254,614	36,256,222	1,608	2	18.64	19.08	63	62	0	0	0				ActReg chr20 #6114	1	1
6115	20	36,529,673	36,530,295	622	2	13.684	13.737	22	18	0	1	1	VSTM2L	-1,515	upstream	ActReg chr20 #6115	1	1
6116	20	36,530,306	36,531,077	771	2	17.917	17.083	31	27	1	1	1	VSTM2L	-808	upstream	ActReg chr20 #6116	1	1
6117	20	36,661,279	36,662,260	981	1	9.065	14.871	15	26	1	2	2	KIAA0406, RPRD1B	64, -179	in gene, upstream	ActReg chr20 #6117	0	1
6118	20	36,780,604	36,781,598	994	1	8.645	13.71	14	20	0	0	1	TGM2	12,599	in gene	ActReg chr20 #6118	0	1
6119	20	36,899,377	36,900,463	1,086	1	12.147	8.794	23	20	0	0	0				ActReg chr20 #6119	1	0
6120	20	36,903,988	36,904,761	773	1	12.583	11.75	22	14	0	0	0				ActReg chr20 #6120	1	0
6121	20	37,063,286	37,064,422	1,136	2	17.528	19.583	44	45	1	4	5	LOC388796, SNORA71B, SNORA71A, SNORA71C, SNORA71D	164, -9876, -7768, -5407, -1212	in gene, upstream, upstream, upstream, upstream	ActReg chr20 #6121	1	1
6122	20	37,074,843	37,075,935	1,092	2	25.323	26.294	69	84	1	3	3	SNHG11, SNORA39, SNORA60	92, -1337, -2623	in gene, upstream, upstream	ActReg chr20 #6122	1	1
6123	20	37,274,543	37,275,601	1,058	1	8.455	11.879	19	23	1	0	1	C20orf95	44,495	in gene	ActReg chr20 #6123	0	1
6124	20	37,308,323	37,309,875	1,552	2	25.396	27.167	79	77	0	0	0				ActReg chr20 #6124	1	1
6125	20	37,314,070	37,315,485	1,415	2	16.318	19.864	49	51	0	0	0				ActReg chr20 #6125	1	1
6126	20	37,320,287	37,322,343	2,056	2	20.246	23.815	62	80	0	0	0				ActReg chr20 #6126	1	1
6127	20	37,376,802	37,377,611	809	1	11.96	13.88	18	20	1	1	1	ACTR5	109	in gene	ActReg chr20 #6127	0	1
6128	20	37,393,157	37,394,043	886	1	7	11.333	14	19	0	0	1	ACTR5	16,503	in gene	ActReg chr20 #6128	0	1
6129	20	37,518,268	37,519,756	1,488	2	13.447	15.255	29	30	0	0	1	PPP1R16B	84,664	in gene	ActReg chr20 #6129	1	1
6130	20	37,525,629	37,526,588	959	1	10.667	13.6	15	19	0	0	1	PPP1R16B	91,760	in gene	ActReg chr20 #6130	0	1
6131	20	37,554,399	37,555,820	1,421	2	11.444	13.578	20	21	1	1	2	PPP1R16B, FAM83D	120761, 154	downstream, in gene	ActReg chr20 #6131	1	1
6132	20	37,590,375	37,591,624	1,249	1	10.923	13.692	20	23	1	1	2	FAM83D, DHX35	36044, 18	downstream, in gene	ActReg chr20 #6132	0	1
6133	20	37,678,257	37,679,207	950	1	7.833	13.133	15	22	1	0	1	DHX35	87,751	downstream	ActReg chr20 #6133	0	1
6134	20	39,193,358	39,194,309	951	1	9.433	12.3	16	20	0	0	0				ActReg chr20 #6134	0	1
6135	20	39,589,923	39,592,002	2,079	2	10.308	12.815	19	20	0	0	0				ActReg chr20 #6135	1	1
6136	20	39,631,557	39,632,828	1,271	1	13.41	10.359	23	17	0	0	1	LOC100128988	22,766	in gene	ActReg chr20 #6136	1	0
6137	20	39,633,173	39,634,194	1,021	1	7.375	10.844	12	15	0	0	1	LOC100128988	24,257	in gene	ActReg chr20 #6137	0	1
6138	20	39,656,933	39,658,660	1,727	2	14.759	13.426	24	27	1	1	2	LOC100128988, TOP1	48370, 334	downstream, in gene	ActReg chr20 #6138	1	1
6139	20	39,700,865	39,701,394	529	1	6.188	12.25	11	20	0	0	1	TOP1	43,667	in gene	ActReg chr20 #6139	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6140	20	39,769,430	39,770,533	1,103	1	9.829	12.057	20	26	0	1	2	LOC100505725, PLCG1	-3341, 3820	upstream, in gene	ActReg chr20 #6140	0	1
6141	20	39,945,207	39,946,169	962	2	13.621	11.9	21	23	1	0	0				ActReg chr20 #6141	1	1
6142	20	39,957,883	39,958,731	848	2	10.462	13.407	21	24	0	0	0				ActReg chr20 #6142	1	1
6143	20	40,272,006	40,272,732	726	1	13.182	6.773	23	13	0	0	0				ActReg chr20 #6143	1	0
6144	20	40,321,199	40,322,637	1,438	2	13.956	17.089	29	32	1	0	0				ActReg chr20 #6144	1	1
6145	20	42,086,189	42,087,080	891	2	12.25	13.821	20	25	1	1	1	SFRS6	130	in gene	ActReg chr20 #6145	1	1
6146	20	42,218,897	42,219,855	958	2	12.9	15.267	31	30	1	1	2	SGK2, IFT52	31690, -203	downstream, upstream	ActReg chr20 #6146	1	1
6147	20	42,285,693	42,286,494	801	1	10.76	16.64	19	30	1	0	2	IFT52, MYBL2	66514, -9616	downstream, upstream	ActReg chr20 #6147	0	1
6148	20	42,553,686	42,554,431	745	1	9.913	12.913	15	24	0	0	1	TOX2	10,566	in gene	ActReg chr20 #6148	0	1
6149	20	42,603,748	42,604,486	738	1	11.067	14.217	19	29	0	0	1	TOX2	60,625	in gene	ActReg chr20 #6149	0	1
6150	20	42,839,005	42,840,008	1,003	1	10.125	12.375	20	21	1	2	2	C20orf111, LOC100505783	-75, -7	upstream, upstream	ActReg chr20 #6150	0	1
6151	20	42,876,295	42,877,456	1,161	2	12	16.361	19	39	1	1	1	GDAP1L1	967	in gene	ActReg chr20 #6151	1	1
6152	20	42,892,556	42,893,925	1,369	2	11.837	14.465	29	31	0	0	1	GDAP1L1	17,332	in gene	ActReg chr20 #6152	1	1
6153	20	42,939,199	42,940,250	1,051	2	15.454	17.333	35	34	1	1	1	FITM2	165	in gene	ActReg chr20 #6153	1	1
6154	20	43,056,770	43,057,841	1,071	2	15.03	21.788	38	48	0	0	1	HNF4A	72,864	in gene	ActReg chr20 #6154	1	1
6155	20	43,104,104	43,105,339	1,235	1	11.29	12.737	21	23	1	1	1	TTPAL	174	in gene	ActReg chr20 #6155	0	1
6156	20	43,124,188	43,125,244	1,056	1	10.848	12.303	16	18	0	0	2	TTPAL, SERINC3	20169, 26010	downstream, downstream	ActReg chr20 #6156	0	1
6157	20	43,150,224	43,150,947	723	1	9.043	13.217	15	22	1	1	2	SERINC3, PKIG	141, -9851	in gene, upstream	ActReg chr20 #6157	0	1
6158	20	43,201,293	43,201,996	703	1	11.046	9.636	16	12	0	0	1	PKIG	41,208	in gene	ActReg chr20 #6158	1	0
6159	20	43,357,315	43,358,141	826	1	14.04	9.36	24	20	0	0	1	WISP2	13,843	downstream	ActReg chr20 #6159	1	0
6160	20	43,405,376	43,406,338	962	2	12.065	17.032	22	40	0	0	1	RIMS4	33,055	in gene	ActReg chr20 #6160	1	1
6161	20	43,407,890	43,409,392	1,502	2	13.936	16.617	44	49	0	0	1	RIMS4	30,271	in gene	ActReg chr20 #6161	1	1
6162	20	43,513,659	43,514,868	1,209	1	8.447	13.868	14	21	1	1	1	YWHAB	-81	upstream	ActReg chr20 #6162	0	1
6163	20	43,538,560	43,539,183	623	1	9.6	13.05	11	20	1	1	2	YWHAB, PABPC1L	24527, 168	downstream, in gene	ActReg chr20 #6163	0	1
6164	20	43,588,586	43,589,462	876	1	8.778	11.778	16	18	1	2	3	TOMM34, LOC100505826, STK4	90, 6075, -6096	in gene, downstream, upstream	ActReg chr20 #6164	0	1
6165	20	43,594,498	43,595,537	1,039	2	11.062	13.938	18	24	1	3	3	TOMM34, LOC100505826, STK4	-5903, 82, -103	upstream, in gene, upstream	ActReg chr20 #6165	1	1
6166	20	43,716,772	43,717,372	600	1	13.722	12.222	22	20	0	0	2	STK4, KCNS1	121952, 12681	downstream, downstream	ActReg chr20 #6166	1	0
6167	20	43,921,742	43,922,680	938	1	10.655	13.069	19	21	1	0	1	MATN4	14,756	in gene	ActReg chr20 #6167	0	1
6168	20	43,976,158	43,977,093	935	1	11.933	9.333	17	17	1	1	1	SDC4	439	in gene	ActReg chr20 #6168	1	0
6169	20	43,991,042	43,992,570	1,528	2	12.894	15.298	24	31	1	2	3	SYS1, SYS1-DBNDD2, TP53TG5	105, -34, 15151	in gene, upstream, downstream	ActReg chr20 #6169	1	1
6170	20	44,409,857	44,410,498	641	1	11.1	9.6	18	15	0	0	1	WFDC3	10,370	in gene	ActReg chr20 #6170	1	0
6171	20	44,420,253	44,420,941	688	1	11.818	14.864	18	28	1	2	2	WFDC3, DNTTIP1	-50, 21	upstream, in gene	ActReg chr20 #6171	0	1
6172	20	44,440,762	44,441,814	1,052	2	14.697	14.667	25	22	1	1	2	DNTTIP1, UBE2C	20712, 33	downstream, in gene	ActReg chr20 #6172	1	1
6173	20	44,461,828	44,463,820	1,992	2	11.194	14.403	19	28	1	2	3	TNNC2, SNX21, ACOT8	-6871, 354, 23211	upstream, in gene, downstream	ActReg chr20 #6173	1	1
6174	20	44,485,428	44,486,518	1,090	2	14.029	12.206	21	22	0	2	2	ACOT8, ZSWIM3	62, -289	in gene, upstream	ActReg chr20 #6174	1	1
6175	20	44,519,117	44,520,716	1,599	2	12.18	12.78	24	25	1	3	5	ZSWIM1, C20orf165, NEURL2, CTSA, PLTP	10068, -3678, -15, 325, 20870	downstream, upstream, upstream, in gene, downstream	ActReg chr20 #6175	1	1
6176	20	44,539,644	44,541,088	1,444	1	9.609	11.696	16	22	2	1	1	PLTP	420	in gene	ActReg chr20 #6176	0	1
6177	20	44,562,849	44,563,753	904	2	12.893	13.679	20	26	1	1	1	PCIF1	-16	upstream	ActReg chr20 #6177	1	1
6178	20	44,599,663	44,601,518	1,855	2	18.965	20.862	35	40	1	1	1	ZNF335	243	in gene	ActReg chr20 #6178	1	1
6179	20	44,655,239	44,658,560	3,321	3	11.173	13.827	30	34	1	1	2	LOC100128028, SLC12A5	-6187, 6570	upstream, in gene	ActReg chr20 #6179	1	1
6180	20	44,668,780	44,670,319	1,539	2	14.521	19.917	39	34	0	0	1	SLC12A5	19,220	in gene	ActReg chr20 #6180	1	1
6181	20	44,717,723	44,718,979	1,256	2	11.9	13.4	20	31	1	1	1	NCOA5	229	in gene	ActReg chr20 #6181	1	1
6182	20	44,857,385	44,860,251	2,866	2	21.281	24.213	61	64	0	0	1	CDH22	21,516	in gene	ActReg chr20 #6182	1	1
6183	20	44,921,498	44,922,347	849	2	12.407	15.815	21	33	0	0	0				ActReg chr20 #6183	1	1
6184	20	44,992,207	44,993,008	801	1	9.64	12.32	13	18	1	1	2	SLC35C2, ELMO2	457, 42664	in gene, downstream	ActReg chr20 #6184	0	1
6185	20	45,034,512	45,035,998	1,486	2	14.739	14.022	24	23	1	1	1	ELMO2	16	in gene	ActReg chr20 #6185	1	1
6186	20	45,141,769	45,142,575	806	1	8.72	12.24	15	21	1	1	1	ZNF334	22	in gene	ActReg chr20 #6186	0	1
6187	20	45,152,503	45,153,080	577	1	11.611	13.056	21	21	0	0	0				ActReg chr20 #6187	0	1
6188	20	45,259,687	45,260,470	783	1	8.667	16.875	17	42	0	0	1	SLC13A3	53,046	in gene	ActReg chr20 #6188	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6189	20	45,959,867	45,960,851	984	1	10.065	14.065	20	26	0	0	1	ZMYND8	25,115	in gene	ActReg chr20 #6189	0	1
6190	20	46,020,712	46,022,101	1,389	2	12.023	11.977	18	20	0	0	0				ActReg chr20 #6190	1	1
6191	20	46,438,234	46,439,408	1,174	1	10.919	14.514	26	32	0	0	0				ActReg chr20 #6191	0	1
6192	20	46,579,710	46,580,863	1,153	1	8.944	12	13	20	1	1	1	LOC100505983	743	in gene	ActReg chr20 #6192	0	1
6193	20	46,958,512	46,959,184	672	1	9.571	11.714	13	20	0	0	0				ActReg chr20 #6193	0	1
6194	20	47,139,473	47,140,785	1,312	2	12.805	14.878	32	37	0	0	0				ActReg chr20 #6194	1	1
6195	20	47,254,971	47,255,730	759	1	9.917	14.042	14	25	0	0	1	PREX1	189,070	in gene	ActReg chr20 #6195	0	1
6196	20	47,470,012	47,471,168	1,156	1	9.333	11.622	17	19	0	0	0				ActReg chr20 #6196	0	1
6197	20	47,803,504	47,804,275	771	1	9.833	11.083	14	16	1	1	1	STAU1	1,015	in gene	ActReg chr20 #6197	0	1
6198	20	47,804,746	47,805,554	808	2	12	14.08	25	26	1	1	1	STAU1	-246	upstream	ActReg chr20 #6198	1	1
6199	20	47,894,301	47,895,657	1,356	2	14.256	14.512	23	34	1	5	5	ZNFX1, C20orf199, SNORD12C, SNORD12B, SNORD12	-223, 264, -503, -1871, -2241	upstream, in gene, upstream, upstream, upstream	ActReg chr20 #6199	1	1
6200	20	48,016,372	48,017,375	1,003	1	7.645	10.677	11	15	0	0	1	KCNB1	82,308	in gene	ActReg chr20 #6200	0	1
6201	20	48,098,613	48,099,750	1,137	2	12.917	15.139	24	32	1	1	1	KCNB1	0	in gene	ActReg chr20 #6201	1	1
6202	20	48,100,698	48,101,306	608	2	12.421	11.316	22	24	1	1	1	KCNB1	-1,821	upstream	ActReg chr20 #6202	1	1
6203	20	48,227,239	48,228,233	994	2	11.871	12.548	20	23	0	1	1	LOC728671	-4,676	upstream	ActReg chr20 #6203	1	1
6204	20	48,278,067	48,278,858	791	1	10	10.76	14	15	0	0	1	B4GALT5	51,959	in gene	ActReg chr20 #6204	0	1
6205	20	48,334,044	48,334,985	941	1	6.9	11.567	16	19	0	1	1	B4GALT5	-4,093	upstream	ActReg chr20 #6205	0	1
6206	20	48,391,461	48,392,311	850	1	14.385	10.154	27	14	0	0	0				ActReg chr20 #6206	1	0
6207	20	48,428,365	48,430,214	1,849	1	9.448	12.741	14	21	1	1	1	SLC9A8	39	in gene	ActReg chr20 #6207	0	1
6208	20	48,503,877	48,505,024	1,147	2	12.722	12.361	22	19	0	0	1	SLC9A8	75,200	in gene	ActReg chr20 #6208	1	1
6209	20	48,531,762	48,532,862	1,100	2	14.765	16.147	34	38	1	1	1	SPATA2	-232	upstream	ActReg chr20 #6209	1	1
6210	20	48,552,466	48,553,767	1,301	2	11.098	12.927	23	19	1	1	1	RNF114	202	in gene	ActReg chr20 #6210	1	1
6211	20	48,605,677	48,606,888	1,211	1	8.184	13.421	14	22	0	0	1	SNAI1	6,769	downstream	ActReg chr20 #6211	0	1
6212	20	48,635,947	48,637,467	1,520	1	9.681	11.681	13	17	0	0	0				ActReg chr20 #6212	0	1
6213	20	48,732,166	48,733,165	999	1	9.839	13.194	16	25	0	1	3	TMEM189-UBE2V1, UBE2V1, TMEM189	37670, -171, 37670	in gene, upstream, downstream	ActReg chr20 #6213	0	1
6214	20	48,754,737	48,756,097	1,360	2	13.442	13.558	23	25	0	0	2	TMEM189-UBE2V1, TMEM189	14918, 14918	in gene, in gene	ActReg chr20 #6214	1	1
6215	20	48,859,215	48,860,154	939	1	18.828	14.724	32	20	0	0	0				ActReg chr20 #6215	1	0
6216	20	48,860,429	48,861,463	1,034	1	10.031	14.281	16	23	0	0	0				ActReg chr20 #6216	0	1
6217	20	48,883,181	48,884,662	1,481	2	10.217	11.674	17	18	0	1	1	LOC100506115	-114	upstream	ActReg chr20 #6217	1	1
6218	20	49,055,487	49,056,548	1,061	1	14.235	13.735	22	23	0	0	0				ActReg chr20 #6218	0	1
6219	20	49,056,898	49,057,775	877	2	13.482	12.37	22	21	0	0	0				ActReg chr20 #6219	1	1
6220	20	49,126,203	49,127,255	1,052	1	11.485	9.424	19	16	1	1	1	PTPN1	-162	upstream	ActReg chr20 #6220	1	0
6221	20	49,177,709	49,178,701	992	1	7.323	13.452	14	24	0	0	2	PTPN1, LOC100506153	51314, 16373	in gene, downstream	ActReg chr20 #6221	0	1
6222	20	49,261,635	49,262,627	992	2	10.194	15.161	18	23	0	1	2	FAM65C, LOC100506175	-8705, 123	upstream, in gene	ActReg chr20 #6222	1	1
6223	20	49,347,543	49,348,429	886	1	10.857	8.179	20	12	1	1	1	PARD6B	-95	upstream	ActReg chr20 #6223	1	0
6224	20	49,547,862	49,548,766	904	2	13.643	14.607	20	28	1	1	2	ADNP, DPM1	-787, 26746	upstream, downstream	ActReg chr20 #6224	1	1
6225	20	49,574,650	49,576,328	1,678	2	13.321	16.66	20	32	1	2	2	DPM1, MOCS3	-429, 126	upstream, in gene	ActReg chr20 #6225	1	1
6226	20	49,596,654	49,597,954	1,300	1	10.22	12.317	18	22	0	0	0				ActReg chr20 #6226	0	1
6227	20	49,638,884	49,640,646	1,762	1	11.236	13.782	16	22	1	1	1	KCNG1	-90	upstream	ActReg chr20 #6227	0	1
6228	20	49,650,116	49,650,667	551	1	13.882	12	30	21	0	0	0				ActReg chr20 #6228	1	0
6229	20	49,923,057	49,923,787	730	1	10.174	12.957	16	18	0	0	0				ActReg chr20 #6229	0	1
6230	20	49,961,165	49,963,120	1,955	1	9.951	11.344	15	23	0	0	0				ActReg chr20 #6230	0	1
6231	20	49,970,906	49,971,860	954	1	9.7	13.467	15	21	0	0	0				ActReg chr20 #6231	0	1
6232	20	49,976,815	49,978,050	1,235	2	12.82	11.282	21	18	0	0	0				ActReg chr20 #6232	1	1
6233	20	49,982,406	49,983,898	1,492	2	11.5	12.065	18	19	0	0	0				ActReg chr20 #6233	1	1
6234	20	49,985,075	49,985,817	742	1	12.652	13.522	19	22	0	0	0				ActReg chr20 #6234	0	1
6235	20	50,041,655	50,042,585	930	2	15.103	18.793	34	47	0	0	1	NFATC2	137,048	in gene	ActReg chr20 #6235	1	1
6236	20	50,053,971	50,054,956	985	2	12.871	13.774	23	24	0	0	1	NFATC2	124,705	in gene	ActReg chr20 #6236	1	1
6237	20	50,113,773	50,115,183	1,410	2	12.659	12.818	23	22	0	0	1	NFATC2	64,690	in gene	ActReg chr20 #6237	1	1
6238	20	50,170,217	50,171,549	1,332	1	8.854	11.366	16	17	0	0	1	NFATC2	8,285	in gene	ActReg chr20 #6238	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6239	20	50,179,878	50,180,930	1,052	2	11.364	11.091	18	21	0	1	1	NFATC2	-1,236	upstream	ActReg chr20 #6239	1	1
6240	20	50,416,635	50,417,220	585	1	7	13.368	10	22	1	1	1	SALL4	2,121	in gene	ActReg chr20 #6240	0	1
6241	20	50,555,298	50,556,079	781	2	12.292	10.917	22	21	0	0	0				ActReg chr20 #6241	1	1
6242	20	50,807,245	50,809,287	2,042	2	12.891	12.516	25	23	1	1	1	ZFP64	258	in gene	ActReg chr20 #6242	1	1
6243	20	52,199,345	52,199,871	526	1	9.5	11.438	14	19	0	1	1	ZNF217	28	in gene	ActReg chr20 #6243	0	1
6244	20	52,515,556	52,516,956	1,400	2	12.093	12.628	20	24	0	0	0				ActReg chr20 #6244	1	1
6245	20	52,523,408	52,524,138	730	1	12.87	8.435	19	14	0	0	0				ActReg chr20 #6245	1	0
6246	20	52,534,095	52,534,822	727	1	9.435	12.435	16	22	0	0	0				ActReg chr20 #6246	0	1
6247	20	52,739,791	52,740,749	958	2	14.433	12.967	27	24	0	0	0				ActReg chr20 #6247	1	1
6248	20	52,749,059	52,750,351	1,292	2	15.7	12.15	27	16	0	0	0				ActReg chr20 #6248	1	1
6249	20	52,755,505	52,756,171	666	2	12.667	11.809	20	18	0	0	0				ActReg chr20 #6249	1	1
6250	20	52,824,071	52,825,189	1,118	2	14.794	19.343	29	45	1	1	1	PFDN4	128	in gene	ActReg chr20 #6250	1	1
6251	20	52,867,339	52,867,879	540	1	12.647	5.647	20	9	0	0	0				ActReg chr20 #6251	1	0
6252	20	52,883,589	52,884,663	1,074	2	17.242	15.182	35	29	0	0	0				ActReg chr20 #6252	1	1
6253	20	52,901,497	52,902,261	764	1	7.375	10.5	13	17	0	0	0				ActReg chr20 #6253	0	1
6254	20	54,686,920	54,687,580	660	1	7.9	12.95	13	23	0	0	0				ActReg chr20 #6254	0	1
6255	20	54,903,690	54,904,586	896	2	14.929	17.821	26	36	0	0	0				ActReg chr20 #6255	1	1
6256	20	54,934,720	54,935,682	962	1	8.387	14.71	14	25	0	1	2	C20orf108, AURKA	1218, 32150	in gene, downstream	ActReg chr20 #6256	0	1
6257	20	54,966,940	54,968,154	1,214	2	20.368	21.105	56	59	1	2	2	AURKA, CSTF1	-196, 120	upstream, in gene	ActReg chr20 #6257	1	1
6258	20	55,043,034	55,044,034	1,000	2	13.688	14.812	34	26	1	1	2	CASS4, C20orf43	56366, -113	downstream, upstream	ActReg chr20 #6258	1	1
6259	20	55,205,076	55,206,937	1,861	1	8.828	13.483	15	24	1	1	1	TFAP2C	1,648	in gene	ActReg chr20 #6259	0	1
6260	20	55,277,513	55,279,237	1,724	1	8.278	14	20	22	0	0	0				ActReg chr20 #6260	0	1
6261	20	55,362,867	55,363,810	943	1	8.167	12.3	13	21	0	0	0				ActReg chr20 #6261	0	1
6262	20	55,574,909	55,576,793	1,884	2	10.305	13.712	16	23	0	0	0				ActReg chr20 #6262	1	1
6263	20	55,605,543	55,606,825	1,282	2	11.725	11.6	24	20	0	0	0				ActReg chr20 #6263	1	1
6264	20	55,613,861	55,614,875	1,014	1	8.968	12.161	12	18	0	0	0				ActReg chr20 #6264	0	1
6265	20	55,622,140	55,623,470	1,330	1	7.786	12.119	14	19	0	0	0				ActReg chr20 #6265	0	1
6266	20	55,651,025	55,651,778	753	1	9.583	13.042	12	21	0	0	0				ActReg chr20 #6266	0	1
6267	20	55,765,455	55,766,565	1,110	1	10.257	12.743	18	19	0	0	1	BMP7	75,697	in gene	ActReg chr20 #6267	0	1
6268	20	55,770,208	55,771,155	947	1	8.7	16.333	19	33	0	0	1	BMP7	71,026	in gene	ActReg chr20 #6268	0	1
6269	20	55,780,599	55,781,403	804	1	14.56	10.6	22	21	0	0	1	BMP7	60,706	in gene	ActReg chr20 #6269	1	0
6270	20	55,926,076	55,926,795	719	1	9.739	12.826	19	22	1	1	3	SPO11, RAE1, MTRNR2L3	21604, 290, 8443	downstream, in gene, downstream	ActReg chr20 #6270	0	1
6271	20	56,010,422	56,011,747	1,325	2	11.61	13.476	17	20	0	0	0				ActReg chr20 #6271	1	1
6272	20	56,175,525	56,176,559	1,034	1	13.562	14.781	22	24	0	0	1	ZBP1	19,590	downstream	ActReg chr20 #6272	0	1
6273	20	56,273,035	56,274,534	1,499	2	10.34	11.447	20	21	0	0	1	PMEPA1	12,757	in gene	ActReg chr20 #6273	1	1
6274	20	56,284,831	56,286,000	1,169	2	19.568	21	47	48	1	1	1	PMEPA1	1,126	in gene	ActReg chr20 #6274	1	1
6275	20	56,293,363	56,294,265	902	2	15.571	16.071	33	31	1	1	1	PMEPA1	-7,273	upstream	ActReg chr20 #6275	1	1
6276	20	56,347,210	56,348,306	1,096	2	13.588	12.588	19	22	0	0	0				ActReg chr20 #6276	1	1
6277	20	56,566,217	56,567,578	1,361	2	14.048	15.191	33	32	0	0	0				ActReg chr20 #6277	1	1
6278	20	56,592,191	56,595,264	3,073	3	13.103	13.196	23	27	0	0	0				ActReg chr20 #6278	1	1
6279	20	56,621,607	56,623,763	2,156	2	20.448	23.597	56	68	0	0	0				ActReg chr20 #6279	1	1
6280	20	56,661,692	56,662,973	1,281	1	8.289	12.025	12	19	0	0	0				ActReg chr20 #6280	0	1
6281	20	56,663,012	56,663,837	825	1	8.84	13.92	16	23	0	0	0				ActReg chr20 #6281	0	1
6282	20	56,677,235	56,678,565	1,330	1	12	13.357	22	22	0	0	0				ActReg chr20 #6282	0	1
6283	20	56,754,316	56,755,178	862	1	11.556	13.074	23	20	1	0	0				ActReg chr20 #6283	0	1
6284	20	57,014,888	57,015,592	704	1	9.955	11.591	14	21	0	0	1	VAPB	50,995	in gene	ActReg chr20 #6284	0	1
6285	20	57,197,578	57,199,446	1,868	1	16.431	12.328	29	25	0	0	1	LOC149773	108,077	downstream	ActReg chr20 #6285	1	0
6286	20	57,220,438	57,221,226	788	1	7.44	12	11	17	0	1	2	MGC4294, STX16	11005, -5496	downstream, upstream	ActReg chr20 #6286	0	1
6287	20	57,225,834	57,227,173	1,339	2	13.405	17	31	42	1	1	1	STX16	175	in gene	ActReg chr20 #6287	1	1
6288	20	57,365,333	57,366,353	1,020	1	10.094	13.75	18	22	0	0	0				ActReg chr20 #6288	0	1
6289	20	57,581,089	57,582,520	1,431	1	8.318	12.114	14	19	1	1	1	CTSZ	505	in gene	ActReg chr20 #6289	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6290	20	57,606,834	57,607,587	753	2	12.208	14.375	25	27	1	1	3	TUBB1, ATP5E, SLMO2	12901, 212, 10691	downstream, in gene, downstream	ActReg chr20 #6290	1	1
6291	20	57,616,881	57,619,280	2,399	2	12.667	12.32	24	18	1	1	2	ATP5E, SLMO2	-10658, -179	upstream, upstream	ActReg chr20 #6291	1	1
6292	20	57,637,959	57,639,366	1,407	1	10.818	7.432	16	14	0	0	0				ActReg chr20 #6292	1	0
6293	20	57,708,617	57,709,993	1,376	2	13.698	16	28	35	0	0	1	LOC100287547	20,599	in gene	ActReg chr20 #6293	1	1
6294	20	57,716,831	57,717,884	1,053	2	13.818	21.303	41	49	0	0	1	LOC100287547	12,547	in gene	ActReg chr20 #6294	1	1
6295	20	57,795,833	57,796,764	931	1	11.069	9.793	15	15	0	0	1	ZNF831	30,223	in gene	ActReg chr20 #6295	1	0
6296	20	57,817,633	57,818,266	633	1	6.368	12.053	10	22	0	0	1	ZNF831	51,874	in gene	ActReg chr20 #6296	0	1
6297	20	57,822,840	57,823,836	996	1	11.677	7.419	17	14	0	0	1	ZNF831	57,263	in gene	ActReg chr20 #6297	1	0
6298	20	58,072,373	58,073,633	1,260	2	11.425	10.9	18	18	0	0	0				ActReg chr20 #6298	1	1
6299	20	58,340,263	58,341,348	1,085	2	14.323	17.147	32	32	0	0	1	PHACTR3	161,202	in gene	ActReg chr20 #6299	1	1
6300	20	58,514,009	58,514,764	755	1	6.083	12.125	9	17	1	2	3	SYCP2, C20orf177, PPP1R3D	-7177, 5567, 966	upstream, in gene, in gene	ActReg chr20 #6300	0	1
6301	20	58,515,100	58,516,251	1,151	2	13.556	12.611	23	18	1	1	3	SYCP2, C20orf177, PPP1R3D	-8466, 6856, -323	upstream, in gene, upstream	ActReg chr20 #6301	1	1
6302	20	58,824,533	58,825,025	492	1	11.562	8.5	19	11	0	0	0				ActReg chr20 #6302	1	0
6303	20	59,087,532	59,088,213	681	1	6.571	13.143	10	25	0	0	0				ActReg chr20 #6303	0	1
6304	20	59,158,478	59,159,353	875	2	12.222	17.222	23	37	0	0	0				ActReg chr20 #6304	1	1
6305	20	59,163,738	59,165,341	1,603	2	8.94	13.46	30	36	0	0	0				ActReg chr20 #6305	1	1
6306	20	60,105,587	60,106,349	762	1	8.75	13.625	16	29	0	0	1	CDH4	278,409	in gene	ActReg chr20 #6306	0	1
6307	20	60,183,181	60,183,946	765	1	10.708	14.167	17	26	0	0	1	CDH4	356,004	in gene	ActReg chr20 #6307	0	1
6308	20	60,545,171	60,545,803	632	1	13.2	10.15	18	17	2	0	1	TAF4	95,379	downstream	ActReg chr20 #6308	1	0
6309	20	60,719,149	60,719,810	661	1	8.684	12.714	16	21	1	2	3	LSM14B, PSMA7, SS18L1	21962, -1005, 657	downstream, upstream, in gene	ActReg chr20 #6309	0	1
6310	20	60,757,448	60,758,606	1,158	2	13.417	16.028	27	30	1	1	2	SS18L1, GTPBP5	39205, -54	downstream, upstream	ActReg chr20 #6310	1	1
6311	20	60,876,885	60,878,244	1,359	2	13.721	14.628	25	39	1	1	3	OSBPL2, ADRM1, LAMA5	63984, -463, 64804	downstream, upstream, downstream	ActReg chr20 #6311	1	1
6312	20	60,878,465	60,880,647	2,182	1	8.397	11.735	15	18	1	1	3	OSBPL2, ADRM1, LAMA5	65976, 1529, 62812	downstream, in gene, downstream	ActReg chr20 #6312	0	1
6313	20	60,961,478	60,962,265	787	1	11.333	12.458	19	20	1	1	2	RPS21, CABLES2	-250, 20468	upstream, downstream	ActReg chr20 #6313	0	1
6314	20	60,962,345	60,963,154	809	2	14.44	19.28	38	42	1	1	2	CABLES2, C20orf151	-410, 19880	upstream, downstream	ActReg chr20 #6314	1	1
6315	20	61,076,612	61,078,153	1,541	1	6.208	12.208	12	18	0	0	0				ActReg chr20 #6315	0	1
6316	20	61,173,348	61,174,664	1,316	2	11.098	15.049	24	27	0	1	2	C20orf166, LOC100131174	26346, 1209	downstream, in gene	ActReg chr20 #6316	1	1
6317	20	61,200,138	61,201,522	1,384	1	7.349	13.628	13	23	1	0	0				ActReg chr20 #6317	0	1
6318	20	61,297,563	61,300,693	3,130	2	11.163	15.99	20	26	0	1	2	SLCO4A1, hCG_2018279	25331, -1155	in gene, upstream	ActReg chr20 #6318	1	1
6319	20	61,334,335	61,336,340	2,005	1	11.048	15.079	21	26	0	1	1	NTSR1	-4,852	upstream	ActReg chr20 #6319	0	1
6320	20	61,370,733	61,373,665	2,932	2	12.413	14.272	24	31	0	0	1	NTSR1	32,010	in gene	ActReg chr20 #6320	1	1
6321	20	61,426,256	61,427,264	1,008	1	10.75	12.938	18	24	1	1	2	C20orf20, OGFR	-1045, -9417	upstream, upstream	ActReg chr20 #6321	0	1
6322	20	61,448,394	61,450,210	1,816	1	9.684	13.281	17	19	1	1	2	OGFR, COL9A3	13125, 888	downstream, in gene	ActReg chr20 #6322	0	1
6323	20	61,556,716	61,557,567	851	1	6.885	10.808	11	16	1	0	1	DIDO1	12,163	in gene	ActReg chr20 #6323	0	1
6324	20	61,568,599	61,569,478	879	2	11.857	10.593	20	18	1	2	2	DIDO1, C20orf11	266, -403	in gene, upstream	ActReg chr20 #6324	1	1
6325	20	61,569,634	61,570,453	819	1	7.68	11.92	12	17	1	2	2	DIDO1, C20orf11	-739, 602	upstream, in gene	ActReg chr20 #6325	0	1
6326	20	61,700,913	61,701,672	759	2	11.833	15.917	21	35	0	0	1	LOC63930	60,557	in gene	ActReg chr20 #6326	1	1
6327	20	61,712,575	61,714,670	2,095	2	14.591	19	43	47	0	0	1	LOC63930	72,887	in gene	ActReg chr20 #6327	1	1
6328	20	61,747,157	61,748,390	1,233	1	8.564	13.128	14	22	0	0	0				ActReg chr20 #6328	0	1
6329	20	62,106,367	62,107,013	646	1	12.191	10.286	21	15	0	1	1	KCNQ2	-2,697	upstream	ActReg chr20 #6329	1	0
6330	20	62,129,156	62,130,054	898	1	10.786	12.571	17	20	0	1	1	EEF1A2	900	in gene	ActReg chr20 #6330	0	1
6331	20	62,258,477	62,259,169	692	1	10.8	12.273	15	20	1	2	2	GMEB2, LOC100505771	-442, 236	upstream, in gene	ActReg chr20 #6331	0	1
6332	20	62,276,469	62,277,097	628	1	9.05	14.15	16	26	0	0	1	STMN3	7,997	in gene	ActReg chr20 #6332	0	1
6333	20	62,284,477	62,285,373	896	1	6.185	12.464	12	26	1	2	2	STMN3, RTEL1	-145, -4722	upstream, upstream	ActReg chr20 #6333	0	1
6334	20	62,289,283	62,290,667	1,384	1	11.07	17.395	21	27	2	2	2	STMN3, RTEL1	-5195, 328	upstream, in gene	ActReg chr20 #6334	0	1
6335	20	62,330,275	62,331,140	865	1	12.222	9.852	20	15	0	0	4	RTEL1, TNFRSF6B, ARFRP1, ZGPAT	41060, 4419, 8648, 8087	downstream, downstream, in gene, upstream	ActReg chr20 #6335	1	0
6336	20	62,338,311	62,339,626	1,315	2	13.171	14.098	32	37	1	2	3	TNFRSF6B, ARFRP1, ZGPAT	12680, 387, 174	downstream, in gene, in gene	ActReg chr20 #6336	1	1
6337	20	62,495,254	62,497,300	2,046	2	10.062	11.984	17	20	1	1	2	C20orf135, TPD52L2	3711, -313	downstream, upstream	ActReg chr20 #6337	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6338	20	62,525,996	62,526,585	589	1	13.944	9.167	24	14	1	1	2	TPD52L2, DNAJC5	29700, -228	downstream, upstream	ActReg chr20 #6338	1	0
6339	20	62,571,449	62,572,055	606	1	6.421	13.947	9	22	1	2	4	DNAJC5, UCKL1, MIR1914, MIR647	45234, 16048, 1145, 2327	downstream, in gene, downstream, downstream	ActReg chr20 #6339	0	1
6340	20	62,586,771	62,588,342	1,571	2	12.326	17.224	29	31	1	2	3	UCKL1, UCKL1AS, ZNF512B	244, 2819, 13662	in gene, in gene, downstream	ActReg chr20 #6340	1	1
6341	20	62,611,377	62,612,984	1,607	2	12.62	19.3	29	47	1	2	2	SAMD10, PRPF6	-1185, -251	upstream, upstream	ActReg chr20 #6341	1	1
6342	20	62,669,637	62,670,578	941	1	8.037	12.793	13	17	1	0	3	PRPF6, NCRNA00176, SOX18	57676, 4410, 10872	downstream, in gene, downstream	ActReg chr20 #6342	0	1
6343	20	62,693,410	62,694,816	1,406	2	10.727	14.704	33	38	1	0	2	TCEA2, RGS19	5674, 17211	in gene, downstream	ActReg chr20 #6343	1	1
6344	20	62,793,004	62,793,822	818	2	12.84	17.24	28	38	0	1	1	MYT1	-2,414	upstream	ActReg chr20 #6344	1	1
6345	20	62,797,834	62,798,664	830	1	5.769	12.808	11	26	0	1	1	MYT1	2,422	in gene	ActReg chr20 #6345	0	1
6346	20	62,823,227	62,824,416	1,189	1	8.421	13.29	19	21	0	0	1	MYT1	27,994	in gene	ActReg chr20 #6346	0	1
6347	20	62,836,379	62,837,670	1,291	1	10.732	13.293	16	20	0	0	1	MYT1	41,197	in gene	ActReg chr20 #6347	0	1
6348	20	62,886,245	62,887,374	1,129	2	14.257	13.4	29	33	1	1	1	PCMTD2	-239	upstream	ActReg chr20 #6348	1	1
6349	21	11,169,834	11,170,646	812	1	15.76	16.28	25	23	0	0	0				ActReg chr21 #6349	0	1
6350	21	16,437,893	16,438,408	515	1	5.562	8.812	10	14	1	1	1	NRIP1	-1,024	upstream	ActReg chr21 #6350	0	1
6351	21	18,835,767	18,836,260	493	1	6.062	8.938	10	16	0	0	0				ActReg chr21 #6351	0	1
6352	21	19,060,933	19,061,725	792	2	8.417	14.792	21	30	0	0	0				ActReg chr21 #6352	1	1
6353	21	19,191,349	19,192,217	868	2	15.741	18.148	48	42	1	1	1	C21orf91	-80	upstream	ActReg chr21 #6353	1	1
6354	21	26,979,501	26,980,090	589	1	11	13.556	14	21	1	1	1	MRPL39	6	in gene	ActReg chr21 #6354	0	1
6355	21	27,512,449	27,513,027	578	1	10.778	6.889	17	12	0	0	1	APP	30,400	in gene	ActReg chr21 #6355	1	0
6356	21	29,186,625	29,187,079	454	1	9	10.143	12	14	0	0	0				ActReg chr21 #6356	0	1
6357	21	30,365,004	30,365,470	466	1	9.286	12	16	19	1	1	1	RNF160	40	in gene	ActReg chr21 #6357	0	1
6358	21	30,445,524	30,446,445	921	1	8.31	14	17	27	1	2	2	CCT8, C21orf7	26, -6889	in gene, upstream	ActReg chr21 #6358	0	1
6359	21	30,672,059	30,672,912	853	1	7.444	10.667	15	18	0	1	1	BACH1	1,265	in gene	ActReg chr21 #6359	0	1
6360	21	31,028,971	31,029,349	378	1	9.833	5.333	14	7	0	0	1	GRIK1	283,122	in gene	ActReg chr21 #6360	1	0
6361	21	33,650,955	33,651,715	760	1	9.75	16.042	20	34	1	1	1	C21orf45	41	in gene	ActReg chr21 #6361	0	1
6362	21	33,941,554	33,942,276	722	1	6.609	10.043	11	13	1	0	1	TCP10L	15,930	downstream	ActReg chr21 #6362	0	1
6363	21	33,969,254	33,970,221	967	2	19.067	16.867	53	40	0	0	1	C21orf59	15,181	downstream	ActReg chr21 #6363	1	1
6364	21	33,984,608	33,985,210	602	1	10.737	11.579	13	17	1	1	1	C21orf59	9	in gene	ActReg chr21 #6364	0	1
6365	21	34,100,459	34,101,157	698	1	8	11.546	13	21	1	2	3	SYNJ1, LOC100506215, C21orf66	-457, 383, 43361	upstream, in gene, downstream	ActReg chr21 #6365	0	1
6366	21	34,143,785	34,144,766	981	2	15.8	18.367	36	46	1	2	2	C21orf66, C21orf49	-106, -136	upstream, upstream	ActReg chr21 #6366	1	1
6367	21	34,696,712	34,697,270	558	1	8.412	11.118	14	18	1	1	1	IFNAR1	-223	upstream	ActReg chr21 #6367	0	1
6368	21	34,752,798	34,753,355	557	1	8.778	7.278	19	13	0	0	0				ActReg chr21 #6368	1	0
6369	21	34,776,396	34,776,900	504	1	5.875	10.875	9	16	1	1	1	IFNGR2	1,446	in gene	ActReg chr21 #6369	0	1
6370	21	34,852,446	34,852,986	540	1	9	6.235	15	12	1	1	2	TMEM50B, DNAJC28	-435, 11307	upstream, downstream	ActReg chr21 #6370	1	0
6371	21	35,395,124	35,395,621	497	1	4.062	11	7	16	0	0	0				ActReg chr21 #6371	0	1
6372	21	35,967,323	35,968,027	704	2	15.909	16.818	33	36	1	1	1	RCAN1	-293	upstream	ActReg chr21 #6372	1	1
6373	21	37,432,532	37,433,027	495	1	10	5.688	16	8	1	1	2	SETD4, CBR1	37, -9506	in gene, upstream	ActReg chr21 #6373	1	0
6374	21	38,445,205	38,446,460	1,255	2	11.026	8.923	22	17	1	2	2	PIGP, TTC3	-374, 261	upstream, in gene	ActReg chr21 #6374	1	1
6375	21	39,649,250	39,650,183	933	1	10	5.586	15	11	0	0	1	KCNJ15	21,052	in gene	ActReg chr21 #6375	1	0
6376	21	40,159,700	40,160,247	547	1	7.647	10.647	13	15	0	0	0				ActReg chr21 #6376	0	1
6377	21	40,817,640	40,818,248	608	1	9.474	6.632	17	13	1	2	2	LCA5L, SH3BGR	-1816, 147	upstream, in gene	ActReg chr21 #6377	1	0
6378	21	43,309,006	43,309,528	522	1	3.688	9.625	8	13	0	0	2	PRDM15, C2CD2	-9676, 64732	upstream, in gene	ActReg chr21 #6378	0	1
6379	21	43,857,721	43,858,563	842	1	9.259	12.593	17	21	0	0	1	UBASH3A	34,123	in gene	ActReg chr21 #6379	0	1
6380	21	44,299,255	44,299,955	700	2	10.636	10.454	20	19	1	1	1	WDR4	73	in gene	ActReg chr21 #6380	1	1
6381	21	44,393,887	44,395,023	1,136	2	13.778	16.639	37	42	1	1	1	PKNOX1	-188	upstream	ActReg chr21 #6381	1	1
6382	21	44,495,160	44,496,031	871	1	10.037	8.074	15	11	1	1	1	CBS	877	in gene	ActReg chr21 #6382	1	0
6383	21	44,630,064	44,630,493	429	1	7.231	10.308	10	13	0	0	0				ActReg chr21 #6383	0	1
6384	21	45,209,132	45,209,715	583	1	4.389	11.278	6	20	1	1	1	RRP1	5	in gene	ActReg chr21 #6384	0	1
6385	21	45,622,428	45,622,992	564	1	9.444	5.167	17	9	1	0	0				ActReg chr21 #6385	1	0
6386	21	45,759,099	45,759,641	542	1	9.941	8.824	16	14	1	1	2	C21orf2, LOC100505684	-85, 3635	upstream, downstream	ActReg chr21 #6386	1	0
6387	21	46,221,275	46,221,972	697	1	6.682	12.318	11	23	1	1	2	UBE2G2, SUMO3	115, 16421	in gene, downstream	ActReg chr21 #6387	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6388	21	46,293,431	46,294,359	928	2	9.793	11.31	18	19	1	1	1	PTTG1IP	-154	upstream	ActReg chr21 #6388	1	1
6389	21	46,359,456	46,360,060	604	1	5.158	9.895	9	17	1	2	3	LOC100505746, C21orf67, C21orf70	18792, 70, -197	downstream, in gene, upstream	ActReg chr21 #6389	0	1
6390	21	46,783,819	46,784,308	489	1	10.8	7.667	13	11	0	0	0				ActReg chr21 #6390	1	0
6391	21	46,975,511	46,976,031	520	1	8.438	11.125	13	15	1	0	0				ActReg chr21 #6391	0	1
6392	21	47,065,536	47,066,235	699	2	13.773	14.364	35	36	0	0	0				ActReg chr21 #6392	1	1
6393	21	47,705,700	47,706,476	776	1	8.917	11.833	13	16	1	2	2	MCM3AP, C21orf57	-852, -179	upstream, upstream	ActReg chr21 #6393	0	1
6394	21	48,055,400	48,056,297	897	2	12.786	9.5	21	20	1	1	1	PRMT2	321	in gene	ActReg chr21 #6394	1	1
6395	22	17,652,113	17,653,158	1,045	2	11.818	15.273	21	34	1	1	3	CECR5, CECR4, CECR1	-6458, 12356, 38144	upstream, downstream, downstream	ActReg chr22 #6395	1	1
6396	22	18,455,392	18,456,063	671	1	6.762	10.333	9	19	0	0	2	MICAL3, MIR648	51598, 8000	in gene, downstream	ActReg chr22 #6396	0	1
6397	22	18,484,002	18,485,046	1,044	2	34.906	32.156	86	75	1	0	1	MICAL3	22,601	in gene	ActReg chr22 #6397	1	1
6398	22	18,560,173	18,561,048	875	1	7.741	13.259	14	19	1	1	1	PEX26	-76	upstream	ActReg chr22 #6398	0	1
6399	22	19,108,897	19,109,471	574	1	3.941	9.471	6	15	1	1	3	DGCR2, DGCR14, TSSK2	783, 23006, 9137	in gene, downstream, upstream	ActReg chr22 #6399	0	1
6400	22	19,158,765	19,159,377	612	1	10.947	10.316	16	13	1	0	2	SLC25A1, CLTCL1	7230, 120168	downstream, downstream	ActReg chr22 #6400	1	0
6401	22	19,189,317	19,190,098	781	2	7.5	13.667	16	24	0	0	1	CLTCL1	89,532	in gene	ActReg chr22 #6401	1	1
6402	22	19,419,677	19,420,335	658	2	9.429	10.191	15	15	1	2	3	HIRA, MRPL40, C22orf39	-787, -30, 15749	upstream, upstream, downstream	ActReg chr22 #6402	1	1
6403	22	19,434,232	19,434,674	442	1	10.714	3.643	14	5	1	2	3	C22orf39, LOC100506503, UFD1L	1302, -963, 32285	in gene, upstream, downstream	ActReg chr22 #6403	1	0
6404	22	19,466,559	19,467,199	640	2	10.35	11.35	17	18	1	2	2	UFD1L, CDC45L	-141, -535	upstream, upstream	ActReg chr22 #6404	1	1
6405	22	19,842,135	19,842,903	768	1	7.792	11.458	12	16	1	2	2	GNB1L, C22orf29	-57, -148	upstream, upstream	ActReg chr22 #6405	0	1
6406	22	20,104,349	20,105,079	730	2	10.957	10.217	24	20	1	2	3	DGCR8, TRMT2A, RANBP1	36959, 54, -310	downstream, in gene, upstream	ActReg chr22 #6406	1	1
6407	22	20,118,313	20,119,055	742	1	7.522	15.348	13	29	1	1	2	RANBP1, ZDHHC8	13660, -680	downstream, upstream	ActReg chr22 #6407	0	1
6408	22	20,861,570	20,862,190	620	2	8.053	11	16	19	1	1	1	MED15	-6	upstream	ActReg chr22 #6408	1	1
6409	22	21,212,833	21,213,458	625	2	11.474	11	25	21	1	2	2	PI4KA, SNAP29	-75, -147	upstream, upstream	ActReg chr22 #6409	1	1
6410	22	21,336,045	21,336,880	835	1	8.269	12.731	15	18	1	1	2	AIFM3, LZTR1	17044, -96	downstream, upstream	ActReg chr22 #6410	0	1
6411	22	21,355,713	21,356,607	894	2	10.148	10.482	18	21	1	2	3	LZTR1, THAP7, FLJ39582	19602, 244, 51	downstream, in gene, upstream	ActReg chr22 #6411	1	1
6412	22	21,363,778	21,364,406	628	1	8.526	12.947	14	21	0	2	3	THAP7, FLJ39582, P2RX6	-7688, 7881, -5350	upstream, in gene, upstream	ActReg chr22 #6412	0	1
6413	22	21,983,289	21,984,700	1,411	2	15.204	17.864	42	38	1	2	3	UBE2L3, YDJC, CCDC116	62037, 346, 3092	downstream, in gene, upstream	ActReg chr22 #6413	1	1
6414	22	22,020,165	22,020,692	527	1	11.875	10.562	17	13	1	1	1	PPIL2	155	in gene	ActReg chr22 #6414	1	0
6415	22	24,359,448	24,360,159	711	1	9.364	12.046	18	19	0	1	1	LOC729832	-7,724	upstream	ActReg chr22 #6415	0	1
6416	22	24,951,461	24,952,134	673	1	6.048	11.524	9	16	1	2	2	C22orf13, SNRPD3	-522, 179	upstream, in gene	ActReg chr22 #6416	0	1
6417	22	25,271,791	25,272,360	569	1	8.111	12.5	14	23	0	0	1	SGSM1	69,939	in gene	ActReg chr22 #6417	0	1
6418	22	26,143,052	26,143,691	639	1	11	7	16	14	0	0	1	MYO18B	5,251	in gene	ActReg chr22 #6418	1	0
6419	22	26,908,196	26,908,701	505	1	9.333	9.867	14	15	1	2	2	TFIP11, LOC100507599	-11, -28	upstream, upstream	ActReg chr22 #6419	0	1
6420	22	27,345,090	27,345,748	658	2	9.1	11.15	20	20	0	0	0				ActReg chr22 #6420	1	1
6421	22	27,471,161	27,471,719	558	1	9.5	8.611	18	16	0	0	0				ActReg chr22 #6421	1	0
6422	22	27,508,990	27,509,610	620	1	12.4	9.1	20	14	0	0	0				ActReg chr22 #6422	1	0
6423	22	27,608,460	27,609,061	601	1	7.789	10.579	12	16	0	0	0				ActReg chr22 #6423	0	1
6424	22	28,122,569	28,123,101	532	1	6.5	10.875	10	18	0	0	0				ActReg chr22 #6424	0	1
6425	22	29,663,633	29,664,581	948	2	14.033	17.833	32	41	1	2	3	EMID1, RHBDD3, EWSR1	62154, -193, 109	downstream, upstream, in gene	ActReg chr22 #6425	1	1
6426	22	29,702,048	29,703,294	1,246	2	9.564	12.692	16	19	1	1	3	EWSR1, GAS2L1, RASL10A	38673, -326, 9077	downstream, upstream, downstream	ActReg chr22 #6426	1	1
6427	22	29,949,402	29,950,173	771	2	12.333	10.208	24	25	1	1	2	THOC5, NIPSNAP1	-51, 27357	upstream, downstream	ActReg chr22 #6427	1	1
6428	22	30,112,050	30,113,531	1,481	2	14.804	19.696	52	55	0	1	1	CABP7	-3,554	upstream	ActReg chr22 #6428	1	1
6429	22	30,162,891	30,163,689	798	1	7.28	12.4	14	24	1	2	2	ZMAT5, UQCR10	-321, -68	upstream, upstream	ActReg chr22 #6429	0	1
6430	22	30,195,085	30,195,636	551	1	10.235	7.235	15	10	0	0	1	ASCC2	38,894	in gene	ActReg chr22 #6430	1	0
6431	22	30,622,162	30,622,619	457	1	3	11.357	5	17	0	0	0				ActReg chr22 #6431	0	1
6432	22	30,752,488	30,753,073	585	1	7.278	10.944	11	19	1	2	2	SF3A1, CCDC157	133, 153	in gene, in gene	ActReg chr22 #6432	0	1
6433	22	30,819,957	30,820,485	528	1	13.882	9.824	21	18	1	1	2	SEC14L2, MTP18	27288, -1499	in gene, upstream	ActReg chr22 #6433	1	0
6434	22	30,855,089	30,855,810	721	2	9.522	12.13	19	20	0	0	1	SEC14L3	12,585	in gene	ActReg chr22 #6434	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6435	22	31,198,467	31,199,287	820	2	15.8	16.28	29	33	1	0	1	OSBP2	108,084	in gene	ActReg chr22 #6435	1	1
6436	22	31,202,127	31,202,929	802	2	14.92	15.32	28	28	0	0	1	OSBP2	111,735	in gene	ActReg chr22 #6436	1	1
6437	22	31,364,852	31,365,672	820	2	11.923	11.808	33	20	1	2	2	MORC2, TUG1	-1075, -372	upstream, upstream	ActReg chr22 #6437	1	1
6438	22	31,885,791	31,886,364	573	1	9.278	11.611	13	19	1	2	2	EIF4ENIF1, SFI1	-203, -6184	upstream, upstream	ActReg chr22 #6438	0	1
6439	22	32,026,690	32,027,319	629	2	9.947	11.105	16	20	1	1	1	PISD	-194	upstream	ActReg chr22 #6439	1	1
6440	22	32,145,632	32,146,537	905	2	10.138	10.655	17	25	1	2	2	C22orf30, DEPDC5	36, -3985	in gene, upstream	ActReg chr22 #6440	1	1
6441	22	32,499,778	32,500,675	897	1	7.857	14.607	15	27	0	0	1	SLC5A1	61,207	in gene	ActReg chr22 #6441	0	1
6442	22	32,502,783	32,503,318	535	1	7	11.412	10	14	0	0	1	SLC5A1	64,031	in gene	ActReg chr22 #6442	0	1
6443	22	32,870,317	32,871,164	847	2	8.808	11.308	14	19	1	1	1	FBXO7	33	in gene	ActReg chr22 #6443	1	1
6444	22	32,928,024	32,929,067	1,043	1	7.152	11.454	16	17	0	0	1	SYN3	525,832	in gene	ActReg chr22 #6444	0	1
6445	22	33,192,741	33,193,345	604	1	10.421	6.474	20	10	0	1	2	SYN3, TIMP3	261334, -3759	in gene, upstream	ActReg chr22 #6445	1	0
6446	22	35,653,077	35,653,887	810	2	8.24	15.4	17	31	1	1	1	HMGXB4	37	in gene	ActReg chr22 #6446	1	1
6447	22	35,695,741	35,696,895	1,154	2	7.667	12.028	13	20	1	1	2	HMGXB4, TOM1	42873, 1050	downstream, in gene	ActReg chr22 #6447	1	1
6448	22	35,772,750	35,773,322	572	1	10.556	5.611	17	9	0	1	1	HMOX1	-4,024	upstream	ActReg chr22 #6448	1	0
6449	22	36,877,287	36,877,753	466	1	9.357	10.143	12	17	0	1	2	TXN2, FOXRED2	167, 25628	in gene, downstream	ActReg chr22 #6449	0	1
6450	22	36,924,924	36,925,434	510	1	9.938	6.812	15	11	1	1	1	EIF3D	98	in gene	ActReg chr22 #6450	1	0
6451	22	36,942,894	36,943,457	563	1	4.833	10.778	9	18	0	0	0				ActReg chr22 #6451	0	1
6452	22	37,039,949	37,040,862	913	2	12.667	18.036	33	36	0	0	1	CACNG2	58,498	in gene	ActReg chr22 #6452	1	1
6453	22	37,055,879	37,056,507	628	1	6.579	11.053	12	18	0	0	1	CACNG2	42,710	in gene	ActReg chr22 #6453	0	1
6454	22	37,099,318	37,099,857	539	2	10.118	8.471	16	17	1	1	1	CACNG2	-684	upstream	ActReg chr22 #6454	1	1
6455	22	38,004,231	38,005,159	928	2	16.483	17.759	32	36	1	1	1	GGA1	214	in gene	ActReg chr22 #6455	1	1
6456	22	38,061,989	38,062,734	745	2	10.913	13.826	23	26	1	1	2	LGALS1, NOL12	10748, 17	downstream, in gene	ActReg chr22 #6456	1	1
6457	22	38,239,927	38,240,691	764	1	8.042	13.292	15	18	1	3	4	ANKRD54, MIR658, MIR659, EIF3L	44, 69, 3472, -5061	in gene, in gene, downstream, upstream	ActReg chr22 #6457	0	1
6458	22	38,245,108	38,245,861	753	1	7.625	11.375	12	19	1	4	4	ANKRD54, MIR658, MIR659, EIF3L	-5131, -5106, -1703, 114	upstream, upstream, upstream, in gene	ActReg chr22 #6458	0	1
6459	22	38,300,846	38,301,769	923	1	11.966	7.828	18	15	1	1	1	MICALL1	-1,039	upstream	ActReg chr22 #6459	1	0
6460	22	38,363,560	38,364,879	1,319	1	11.293	8.951	16	15	0	0	2	POLR2F, SOX10	14545, 16320	in gene, downstream	ActReg chr22 #6460	1	0
6461	22	38,378,834	38,380,206	1,372	1	8.163	10.674	13	16	1	2	2	SOX10, LOC100131530	1019, -2650	in gene, upstream	ActReg chr22 #6461	0	1
6462	22	38,426,407	38,427,956	1,549	1	7.562	13.167	14	22	0	0	0				ActReg chr22 #6462	0	1
6463	22	38,429,498	38,430,882	1,384	1	7.705	11.704	14	18	0	0	0				ActReg chr22 #6463	0	1
6464	22	39,077,420	39,078,404	984	2	35.677	39.645	112	130	1	2	5	CBY1, LOC100506326, TOMM22, LOC100506349, JOSD1	25254, -137, -42, 21129, 18547	downstream, upstream, upstream, downstream, downstream	ActReg chr22 #6464	1	1
6465	22	39,096,775	39,097,303	528	1	11.125	11.375	20	20	1	3	3	LOC100506349, JOSD1, GTPBP1	2002, -580, 4768	in gene, upstream, upstream	ActReg chr22 #6465	0	1
6466	22	39,101,444	39,102,193	749	2	10.826	10.174	19	17	1	3	3	LOC100506349, JOSD1, GTPBP1	-2777, -5359, 11	upstream, upstream, in gene	ActReg chr22 #6466	1	1
6467	22	39,151,340	39,152,640	1,300	3	9.805	8.5	23	20	1	1	1	SUN2	-43	upstream	ActReg chr22 #6467	1	1
6468	22	39,190,079	39,190,597	518	1	8.706	6.294	15	8	1	1	1	DNAL4	-177	upstream	ActReg chr22 #6468	1	0
6469	22	39,220,296	39,221,130	834	2	12.269	15.423	25	27	0	0	1	NPTXR	19,304	in gene	ActReg chr22 #6469	1	1
6470	22	39,227,241	39,227,757	516	1	4.875	11.188	8	16	0	0	1	NPTXR	12,518	in gene	ActReg chr22 #6470	0	1
6471	22	39,268,265	39,268,725	460	1	7.769	10.786	13	18	1	1	2	LOC100506361, CBX6	21306, -237	downstream, upstream	ActReg chr22 #6471	0	1
6472	22	39,312,741	39,313,245	504	1	7	9.467	11	16	0	0	0				ActReg chr22 #6472	0	1
6473	22	39,715,055	39,715,851	796	1	6.32	11.28	10	19	1	5	5	RPL3, SNORD83B, SNORD83A, RNU86, SNORD43	217, -5537, -4141, -2552, -335	in gene, upstream, upstream, upstream, upstream	ActReg chr22 #6473	0	1
6474	22	39,795,378	39,796,092	714	2	15.636	16.364	32	36	1	1	1	MAP3K7IP1	-24	upstream	ActReg chr22 #6474	1	1
6475	22	39,874,025	39,874,922	897	2	10.429	10.75	20	15	0	0	2	MGAT3, LOC100506493	21148, 3027	in gene, downstream	ActReg chr22 #6475	1	1
6476	22	39,924,922	39,925,674	752	1	9.708	6.5	17	11	0	0	2	ATF4, RPS19BP1	8729, 3562	downstream, in gene	ActReg chr22 #6476	1	0
6477	22	39,941,361	39,942,836	1,475	2	11.783	14.522	27	34	0	0	0				ActReg chr22 #6477	1	1
6478	22	40,742,245	40,742,705	460	1	9.929	10.071	12	14	1	1	1	ADSL	-29	upstream	ActReg chr22 #6478	1	0
6479	22	41,032,450	41,033,423	973	2	10.133	10.333	20	17	1	1	1	MKL1	-246	upstream	ActReg chr22 #6479	1	1
6480	22	41,682,042	41,682,640	598	1	8.053	11.684	15	26	1	1	1	RANGAP1	-125	upstream	ActReg chr22 #6480	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6481	22	41,842,518	41,843,319	801	2	10.8	11.6	17	16	1	1	1	TOB2	109	in gene	ActReg chr22 #6481	1	1
6482	22	41,864,542	41,865,443	901	2	10	10.586	16	16	1	2	2	PHF5A, ACO2	-284, -137	upstream, upstream	ActReg chr22 #6482	1	1
6483	22	41,939,915	41,940,521	606	1	12.21	9.895	20	15	1	1	1	POLR3H	261	in gene	ActReg chr22 #6483	1	0
6484	22	42,062,719	42,063,093	374	1	6.833	11.667	10	17	1	0	3	XRCC6, NHP2L1, LOC100506562	45611, 22007, 10346	downstream, downstream, downstream	ActReg chr22 #6484	0	1
6485	22	42,228,373	42,229,345	972	2	18.484	12.194	39	30	1	1	2	CCDC134, SREBF2	32181, -247	downstream, upstream	ActReg chr22 #6485	1	1
6486	22	42,342,573	42,343,478	905	2	13.286	16.786	32	39	1	2	2	CENPM, LOC339674	123, -5166	in gene, upstream	ActReg chr22 #6486	1	1
6487	22	42,567,892	42,568,903	1,011	2	9.406	8.188	14	15	0	0	1	TCF20	43,048	in gene	ActReg chr22 #6487	1	1
6488	22	43,010,624	43,011,745	1,121	2	11.806	12.917	24	22	1	2	3	POLDIP3, RNU12, CYB5R3	-222, -67, 34221	upstream, upstream, downstream	ActReg chr22 #6488	1	1
6489	22	43,150,642	43,151,099	457	1	7.143	10.786	11	15	0	0	0				ActReg chr22 #6489	0	1
6490	22	43,484,698	43,485,674	976	2	15.645	22.258	33	53	1	1	1	TTLL1	248	in gene	ActReg chr22 #6490	1	1
6491	22	44,208,156	44,208,708	552	1	7.222	10.5	10	15	1	1	1	EFCAB6	-215	upstream	ActReg chr22 #6491	0	1
6492	22	44,263,506	44,264,231	725	2	8.87	13.391	20	28	0	1	1	SULT4A1	-5,490	upstream	ActReg chr22 #6492	1	1
6493	22	44,350,938	44,351,622	684	2	7.455	10.046	17	14	1	1	2	PNPLA3, SAMM50	31661, 19	downstream, in gene	ActReg chr22 #6493	1	1
6494	22	45,371,223	45,371,902	679	2	11.714	12.191	21	24	0	1	2	PHF21B, LOC100506695	34247, -3397	in gene, upstream	ActReg chr22 #6494	1	1
6495	22	45,475,874	45,476,537	663	1	8.684	11.7	14	19	0	0	0				ActReg chr22 #6495	0	1
6496	22	46,068,097	46,068,824	727	1	3.773	10.046	6	15	1	1	1	ATXN10	782	in gene	ActReg chr22 #6496	0	1
6497	22	46,364,636	46,365,429	793	1	6.56	11.92	12	18	0	0	2	WNT7B, LOC100506756	7976, 19196	in gene, in gene	ActReg chr22 #6497	0	1
6498	22	46,481,696	46,482,298	602	1	11.684	6.737	17	11	1	1	1	LOC400931	120	in gene	ActReg chr22 #6498	1	0
6499	22	46,692,402	46,693,110	708	2	12.318	11.954	22	20	1	2	3	TTC38, CN5H6.4, GTSE1	28895, -199, 118	downstream, upstream, in gene	ActReg chr22 #6499	1	1
6500	22	46,731,270	46,732,034	764	1	8.167	14.708	14	29	1	1	2	GTSE1, TRMU	39014, 354	downstream, in gene	ActReg chr22 #6500	0	1
6501	22	46,849,931	46,850,514	583	1	8.056	11	10	15	0	0	1	CELSR1	82,845	in gene	ActReg chr22 #6501	0	1
6502	22	47,158,098	47,158,869	771	2	8.792	11.917	17	18	1	1	1	TBC1D22A	-35	upstream	ActReg chr22 #6502	1	1
6503	22	48,027,225	48,027,995	770	1	7.292	11.542	12	23	1	1	1	RP11-191L9.1	-292	upstream	ActReg chr22 #6503	0	1
6504	22	49,039,961	49,040,542	581	1	5.611	10.778	10	18	0	0	1	FAM19A5	154,963	in gene	ActReg chr22 #6504	0	1
6505	22	49,098,193	49,098,938	745	1	11.609	9.261	17	12	0	0	1	FAM19A5	213,277	in gene	ActReg chr22 #6505	1	0
6506	22	50,128,944	50,129,393	449	1	3.929	10.214	7	16	0	0	0				ActReg chr22 #6506	0	1
6507	22	50,465,991	50,466,583	592	1	8.556	12.056	11	17	0	0	1	TTLL8	26,768	in gene	ActReg chr22 #6507	0	1
6508	22	50,683,064	50,683,743	679	1	7.762	12.952	13	19	1	1	3	TUBGCP6, HDAC10, MAPK12	-3, 6431, 16686	upstream, downstream, downstream	ActReg chr22 #6508	0	1
6509	22	50,765,532	50,766,366	834	2	9.538	10.84	19	17	1	1	1	FAM116B	-460	upstream	ActReg chr22 #6509	1	1
6510	22	50,964,473	50,965,236	763	1	8.167	11.25	13	16	1	1	4	NCAPH2, SCO2, TYMP, ODF3B	18209, 14, 3660, 6154	downstream, in gene, in gene, downstream	ActReg chr22 #6510	0	1
6511	22	51,038,174	51,038,947	773	2	10.72	13.04	20	23	1	1	1	MAPK8IP2	-571	upstream	ActReg chr22 #6511	1	1
6512	3	577,429	578,349	920	2	12.862	18.965	35	52	0	0	0				ActReg chr3 #6512	1	1
6513	3	754,952	755,391	439	1	11.308	9.615	14	14	0	0	0				ActReg chr3 #6513	1	0
6514	3	1,220,505	1,221,193	688	1	11.5	7.545	18	12	0	0	1	CNTN6	86,220	in gene	ActReg chr3 #6514	1	0
6515	3	3,168,052	3,169,211	1,159	1	9	13.222	18	27	1	1	1	TRNT1	31	in gene	ActReg chr3 #6515	0	1
6516	3	3,220,867	3,221,929	1,062	2	33.636	43.636	102	127	1	1	1	CRBN	3	in gene	ActReg chr3 #6516	1	1
6517	3	4,344,592	4,345,426	834	1	10.154	7.769	16	13	1	1	1	SETMAR	21	in gene	ActReg chr3 #6517	1	0
6518	3	4,508,493	4,509,219	726	2	15.565	17.13	34	35	1	1	1	SUMF1	110	in gene	ActReg chr3 #6518	1	1
6519	3	4,534,524	4,535,320	796	2	11.56	10.68	19	16	1	1	1	ITPR1	-110	upstream	ActReg chr3 #6519	1	1
6520	3	4,994,591	4,995,438	847	2	11.333	12.37	18	22	0	0	0				ActReg chr3 #6520	1	1
6521	3	5,019,604	5,020,263	659	1	6.714	11.809	11	20	1	1	1	BHLHE40	-1,164	upstream	ActReg chr3 #6521	0	1
6522	3	5,163,429	5,164,785	1,356	2	45.191	51.809	189	203	1	1	1	ARL8B	177	in gene	ActReg chr3 #6522	1	1
6523	3	6,951,983	6,952,733	750	2	9.739	9.435	17	17	0	0	1	GRM7	49,556	in gene	ActReg chr3 #6523	1	1
6524	3	7,031,174	7,031,783	609	1	10.632	7.105	16	11	0	0	1	GRM7	128,676	in gene	ActReg chr3 #6524	1	0
6525	3	7,546,822	7,547,292	470	1	6.5	10.857	12	17	0	0	1	GRM7	644,255	in gene	ActReg chr3 #6525	0	1
6526	3	8,019,565	8,020,441	876	1	10.037	15.889	17	28	0	0	0				ActReg chr3 #6526	0	1
6527	3	8,543,080	8,543,729	649	1	7.75	13.15	11	22	1	2	2	LOC100288428, LMCD1	-60, -107	upstream, upstream	ActReg chr3 #6527	0	1
6528	3	8,671,048	8,671,794	746	2	10.043	15.826	23	32	0	0	1	C3orf32	22,316	in gene	ActReg chr3 #6528	1	1
6529	3	8,834,654	8,835,395	741	1	9.75	14.125	18	27	0	0	0				ActReg chr3 #6529	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6530	3	9,004,623	9,005,437	814	1	13.06	7.92	21	19	1	1	1	RAD18	129	in gene	ActReg chr3 #6530	1	0
6531	3	9,438,114	9,439,208	1,094	1	7.912	13.529	18	21	1	3	4	THUMPD3, LOC440944, LOC100507618, SETD5	33944, 513, 91, -742	downstream, in gene, in gene, upstream	ActReg chr3 #6531	0	1
6532	3	9,464,290	9,464,875	585	1	9.056	6.611	16	13	0	0	1	SETD5	25,179	in gene	ActReg chr3 #6532	1	0
6533	3	9,593,782	9,594,408	626	1	7.75	21.85	13	42	1	1	1	LHFPL4	1,391	in gene	ActReg chr3 #6533	0	1
6534	3	9,773,031	9,773,740	709	1	5.682	10.182	10	16	1	1	2	CPNE9, BRPF1	27875, -49	downstream, upstream	ActReg chr3 #6534	0	1
6535	3	9,833,843	9,834,993	1,150	1	8.972	12.5	15	21	1	2	2	TADA3, ARPC4	2, 191	in gene, in gene	ActReg chr3 #6535	0	1
6536	3	9,932,004	9,932,777	773	2	11.875	15.667	23	29	1	1	1	JAGN1	119	in gene	ActReg chr3 #6536	1	1
6537	3	9,974,627	9,975,821	1,194	2	11.054	15.46	19	36	1	1	2	IL17RC, CRELD1	16460, -300	in gene, upstream	ActReg chr3 #6537	1	1
6538	3	9,987,697	9,989,657	1,960	2	20.377	26.279	59	84	1	0	2	CRELD1, PRRT3	13153, 5401	downstream, in gene	ActReg chr3 #6538	1	1
6539	3	10,027,987	10,028,963	976	2	11.419	14.871	26	31	0	2	2	TMEM111, LOC442075	47, -120	in gene, upstream	ActReg chr3 #6539	1	1
6540	3	10,067,728	10,068,468	740	2	14.739	18.391	33	43	1	1	1	FANCD2	-15	upstream	ActReg chr3 #6540	1	1
6541	3	10,247,195	10,248,252	1,057	1	7.636	11.879	13	17	0	0	1	IRAK2	41,160	in gene	ActReg chr3 #6541	0	1
6542	3	10,362,511	10,363,169	658	1	9.286	13.095	18	29	1	1	3	SEC13, ATP2B2, MIR378B	18, 184428, 9073	in gene, downstream, upstream	ActReg chr3 #6542	0	1
6543	3	10,500,462	10,503,169	2,707	2	20.224	26.671	117	119	0	0	1	ATP2B2	45,453	in gene	ActReg chr3 #6543	1	1
6544	3	10,599,152	10,600,332	1,180	2	10.838	10.865	20	16	0	0	0				ActReg chr3 #6544	1	1
6545	3	10,636,427	10,637,165	738	2	12.652	10.174	27	17	0	0	0				ActReg chr3 #6545	1	1
6546	3	10,641,843	10,643,301	1,458	1	6.739	11.761	11	17	0	0	0				ActReg chr3 #6546	0	1
6547	3	10,683,257	10,684,074	817	2	10.231	11.846	19	17	0	0	0				ActReg chr3 #6547	1	1
6548	3	10,795,436	10,796,235	799	2	10.84	19.48	25	43	0	0	1	LOC285370	10,042	downstream	ActReg chr3 #6548	1	1
6549	3	11,005,769	11,006,751	982	2	12.2	15.967	24	28	0	0	0				ActReg chr3 #6549	1	1
6550	3	11,138,190	11,138,810	620	1	6.474	12.263	15	17	0	0	0				ActReg chr3 #6550	0	1
6551	3	11,609,314	11,610,513	1,199	2	12.892	14.189	26	26	1	1	2	VGLL4, LOC100133039	152307, -3964	in gene, upstream	ActReg chr3 #6551	1	1
6552	3	11,651,350	11,651,852	502	1	8.688	12.562	16	23	0	0	1	VGLL4	110,619	in gene	ActReg chr3 #6552	0	1
6553	3	11,887,586	11,888,927	1,341	2	47.366	46.439	193	174	1	1	1	C3orf31	96	in gene	ActReg chr3 #6553	1	1
6554	3	12,196,797	12,197,886	1,089	2	11.059	10.794	20	25	0	0	2	SYN2, TIMP4	151479, 3306	in gene, in gene	ActReg chr3 #6554	1	1
6555	3	12,437,009	12,437,553	544	1	9.235	4.294	14	7	0	0	1	PPARG	107,932	in gene	ActReg chr3 #6555	1	0
6556	3	12,447,203	12,447,680	477	1	4.933	10.267	7	17	0	0	1	PPARG	118,092	in gene	ActReg chr3 #6556	0	1
6557	3	12,525,501	12,526,448	947	2	10.933	11.7	19	19	1	1	1	TSEN2	43	in gene	ActReg chr3 #6557	1	1
6558	3	12,598,103	12,599,064	961	2	13.433	14.2	22	26	1	1	1	MKRN2	-11	upstream	ActReg chr3 #6558	1	1
6559	3	12,705,033	12,706,207	1,174	2	15.111	17.111	35	45	1	1	1	RAF1	80	in gene	ActReg chr3 #6559	1	1
6560	3	12,882,656	12,883,650	994	1	7.906	15.094	13	28	1	2	3	CAND2, RPL32, SNORA7A	44982, -72, -1204	downstream, upstream, upstream	ActReg chr3 #6560	0	1
6561	3	12,989,820	12,991,265	1,445	1	7.652	11.957	15	18	0	0	1	IQSEC1	124,075	in gene	ActReg chr3 #6561	0	1
6562	3	13,035,973	13,037,072	1,099	2	18.677	22.823	48	71	1	0	1	IQSEC1	78,095	in gene	ActReg chr3 #6562	1	1
6563	3	13,096,040	13,096,939	899	1	8.071	10.75	14	19	0	0	1	IQSEC1	18,128	in gene	ActReg chr3 #6563	0	1
6564	3	13,182,632	13,184,552	1,920	2	11.95	20.117	37	56	0	0	0				ActReg chr3 #6564	1	1
6565	3	14,165,391	14,167,772	2,381	1	8.608	14.351	14	23	1	2	2	CHCHD4, TMEM43	-210, 141	upstream, in gene	ActReg chr3 #6565	0	1
6566	3	14,219,621	14,220,605	984	2	10.4	14.1	21	24	1	2	2	XPC, LSM3	59, -115	in gene, upstream	ActReg chr3 #6566	1	1
6567	3	14,306,626	14,307,390	764	1	6.609	9.739	12	13	0	0	0				ActReg chr3 #6567	0	1
6568	3	14,473,551	14,474,367	816	2	12.8	12	23	15	0	0	1	SLC6A6	29,853	in gene	ActReg chr3 #6568	1	1
6569	3	14,493,507	14,494,878	1,371	1	8.762	12	14	18	0	0	1	SLC6A6	50,086	in gene	ActReg chr3 #6569	0	1
6570	3	14,605,609	14,606,841	1,232	1	8.105	12.105	13	18	0	0	0				ActReg chr3 #6570	0	1
6571	3	14,639,318	14,641,072	1,754	2	23.927	31.927	74	99	0	0	0				ActReg chr3 #6571	1	1
6572	3	14,968,550	14,968,963	413	1	5.846	12.385	8	18	1	3	3	LOC100505673, LOC100505641, NR2C2	1175, 644, -480	in gene, in gene, upstream	ActReg chr3 #6572	0	1
6573	3	15,140,253	15,141,179	926	2	17.172	18.828	46	43	1	1	1	ZFYVE20	-61	upstream	ActReg chr3 #6573	1	1
6574	3	15,247,731	15,248,375	644	1	10.2	13.5	13	23	1	1	1	CAPN7	320	in gene	ActReg chr3 #6574	0	1
6575	3	15,310,760	15,311,540	780	1	12.625	9.792	24	19	0	0	2	LOC100505696, SH3BP5	15991, 71751	downstream, in gene	ActReg chr3 #6575	1	0
6576	3	15,342,072	15,343,131	1,059	2	10.152	14.727	21	29	0	0	1	SH3BP5	40,300	in gene	ActReg chr3 #6576	1	1
6577	3	15,352,112	15,352,689	577	1	7.278	10.722	12	16	0	0	1	SH3BP5	30,501	in gene	ActReg chr3 #6577	0	1
6578	3	15,373,034	15,374,415	1,381	2	14.302	17.395	33	28	1	0	1	SH3BP5	9,177	in gene	ActReg chr3 #6578	1	1
6579	3	15,468,366	15,469,431	1,065	1	7.424	10.424	10	14	1	2	2	METTL6, EAF1	144, -166	in gene, upstream	ActReg chr3 #6579	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6580	3	15,900,424	15,900,969	545	1	9	11.118	14	18	1	1	1	ANKRD28	357	in gene	ActReg chr3 #6580	0	1
6581	3	15,901,441	15,902,029	588	1	9.167	11.333	15	18	1	1	1	ANKRD28	-682	upstream	ActReg chr3 #6581	0	1
6582	3	16,024,444	16,025,160	716	1	11.261	9.957	19	14	0	0	0				ActReg chr3 #6582	1	0
6583	3	16,306,031	16,306,881	850	1	13.741	9.963	24	19	1	2	2	DPH3, OXNAD1	40, -211	in gene, upstream	ActReg chr3 #6583	1	0
6584	3	16,468,632	16,469,164	532	1	10.412	8.294	19	15	0	0	1	RFTN1	86,324	in gene	ActReg chr3 #6584	1	0
6585	3	16,625,005	16,625,562	557	1	11.294	7.941	20	10	0	0	1	DAZL	21,723	downstream	ActReg chr3 #6585	1	0
6586	3	16,930,530	16,931,201	671	1	11.238	5.286	16	9	0	0	1	PLCL2	4,413	in gene	ActReg chr3 #6586	1	0
6587	3	18,960,580	18,961,012	432	1	9.692	10.154	14	14	0	0	0				ActReg chr3 #6587	0	1
6588	3	19,189,326	19,189,848	522	1	8.25	12	13	17	1	1	1	KCNH8	-430	upstream	ActReg chr3 #6588	0	1
6589	3	19,190,030	19,190,705	675	2	10.238	10.238	16	17	1	1	1	KCNH8	350	in gene	ActReg chr3 #6589	1	1
6590	3	19,190,722	19,191,608	886	2	14.37	15.037	29	32	0	1	1	KCNH8	1,148	in gene	ActReg chr3 #6590	1	1
6591	3	19,988,267	19,988,976	709	1	10.182	10.591	17	19	1	1	1	RAB5A	49	in gene	ActReg chr3 #6591	0	1
6592	3	20,227,314	20,227,981	667	1	10.619	12.857	16	23	1	1	1	SCOL1	36	in gene	ActReg chr3 #6592	0	1
6593	3	22,626,869	22,627,555	686	2	11.273	10.136	21	17	0	0	0				ActReg chr3 #6593	1	1
6594	3	23,244,674	23,245,124	450	1	9.143	9.786	14	17	1	2	2	LOC100505877, UBE2E2	-830, 115	upstream, in gene	ActReg chr3 #6594	0	1
6595	3	23,726,972	23,727,733	761	1	10.708	4.958	16	13	0	0	0				ActReg chr3 #6595	1	0
6596	3	23,957,973	23,959,377	1,404	1	9.091	16.046	16	26	1	2	3	NKIRAS1, RPL15, LOC100505901	-138, 36, 23840	upstream, in gene, downstream	ActReg chr3 #6596	0	1
6597	3	23,987,310	23,988,107	797	1	7.44	12.08	14	16	1	2	2	LOC100505901, NR1D2	-5193, 957	upstream, in gene	ActReg chr3 #6597	0	1
6598	3	24,197,862	24,198,524	662	1	12.2	8.9	23	17	0	0	1	THRB	338,120	in gene	ActReg chr3 #6598	1	0
6599	3	24,262,263	24,263,270	1,007	1	8.25	12.094	15	20	0	0	1	THRB	273,547	in gene	ActReg chr3 #6599	0	1
6600	3	24,406,585	24,407,133	548	1	3.412	11	5	19	0	0	1	THRB	129,454	in gene	ActReg chr3 #6600	0	1
6601	3	24,513,716	24,514,326	610	1	5.895	11.579	10	21	0	0	1	THRB	22,292	in gene	ActReg chr3 #6601	0	1
6602	3	24,535,431	24,536,195	764	2	10.667	12.917	18	17	1	1	1	THRB	500	in gene	ActReg chr3 #6602	1	1
6603	3	24,549,748	24,550,346	600	1	9.947	4.789	16	8	0	0	0				ActReg chr3 #6603	1	0
6604	3	24,563,570	24,564,125	555	1	4.529	10	7	15	1	0	0				ActReg chr3 #6604	0	1
6605	3	25,705,519	25,706,059	540	1	8.471	10	16	18	1	1	1	TOP2B	-1	upstream	ActReg chr3 #6605	0	1
6606	3	25,831,193	25,831,945	752	1	11.708	7	16	9	0	2	2	NCLY1, OXSM	-39, 6	upstream, in gene	ActReg chr3 #6606	1	0
6607	3	27,156,121	27,156,673	552	1	10.278	6.706	21	14	0	0	0				ActReg chr3 #6607	1	0
6608	3	27,524,705	27,525,352	647	1	11.25	8.15	16	13	1	0	0				ActReg chr3 #6608	1	0
6609	3	27,525,628	27,526,416	788	1	9.08	11.68	15	15	1	0	0				ActReg chr3 #6609	0	1
6610	3	27,575,111	27,576,375	1,264	2	16.026	16.949	44	42	0	0	0				ActReg chr3 #6610	1	1
6611	3	27,763,393	27,764,084	691	2	11.048	9.19	18	16	1	1	1	EOMES	47	in gene	ActReg chr3 #6611	1	1
6612	3	27,799,389	27,800,145	756	2	10.667	10.333	21	19	0	0	0				ActReg chr3 #6612	1	1
6613	3	30,327,339	30,327,998	659	2	13.75	12.85	27	23	0	0	0				ActReg chr3 #6613	1	1
6614	3	30,389,037	30,389,803	766	1	6.333	11.167	13	16	0	0	0				ActReg chr3 #6614	0	1
6615	3	30,696,691	30,697,460	769	1	7.958	11.75	11	18	0	0	1	TGFBR2	49,081	in gene	ActReg chr3 #6615	0	1
6616	3	31,118,370	31,119,310	940	2	11.483	11.379	21	21	0	0	0				ActReg chr3 #6616	1	1
6617	3	31,329,635	31,330,604	969	1	8.3	11.433	14	19	0	0	0				ActReg chr3 #6617	0	1
6618	3	31,418,532	31,419,063	531	1	6.438	9.312	11	16	0	0	0				ActReg chr3 #6618	0	1
6619	3	31,573,072	31,574,511	1,439	2	10.422	13.178	19	20	1	1	1	STT3B	-700	upstream	ActReg chr3 #6619	1	1
6620	3	31,978,553	31,979,281	728	2	11.565	12.304	19	20	0	0	1	OSBPL10	44,425	in gene	ActReg chr3 #6620	1	1
6621	3	32,022,556	32,023,717	1,161	2	9.541	11.135	17	18	1	2	2	OSBPL10, ZNF860	206, -130	in gene, upstream	ActReg chr3 #6621	1	1
6622	3	32,147,605	32,148,271	666	1	13.381	7.524	21	15	1	1	1	GPD1L	-65	upstream	ActReg chr3 #6622	1	0
6623	3	32,268,294	32,268,846	552	1	11.412	5.588	18	8	0	0	0				ActReg chr3 #6623	1	0
6624	3	32,611,764	32,612,767	1,003	1	8.097	11.355	15	15	1	1	1	DYNC1LI1	101	in gene	ActReg chr3 #6624	0	1
6625	3	32,726,169	32,727,189	1,020	2	8.594	12.844	17	27	1	1	1	CNOT10	-19	upstream	ActReg chr3 #6625	1	1
6626	3	33,137,878	33,139,226	1,348	1	7.405	10.833	13	17	1	2	2	GLB1, TMPPE	142, -259	in gene, upstream	ActReg chr3 #6626	0	1
6627	3	33,155,246	33,156,295	1,049	1	7.121	12.515	12	21	1	1	1	CRTAP	320	in gene	ActReg chr3 #6627	0	1
6628	3	33,481,980	33,482,696	716	1	7.304	12.13	11	16	2	1	1	UBP1	-441	upstream	ActReg chr3 #6628	0	1
6629	3	33,700,205	33,701,280	1,075	2	12.265	11.265	22	17	0	0	1	CLASP2	59,106	in gene	ActReg chr3 #6629	1	1
6630	3	33,759,436	33,760,262	826	2	12.423	10.077	19	18	1	1	1	CLASP2	-1	upstream	ActReg chr3 #6630	1	1
6631	3	33,839,784	33,840,522	738	1	10.609	13.087	13	19	1	1	1	PDCD6IP	87	in gene	ActReg chr3 #6631	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6632	3	36,421,674	36,422,552	878	2	10.296	11.926	14	18	1	1	1	STAC	16	in gene	ActReg chr3 #6632	1	1
6633	3	36,718,712	36,719,439	727	1	11.304	7.739	18	13	0	0	0				ActReg chr3 #6633	1	0
6634	3	37,033,957	37,035,420	1,463	2	11.6	11.733	22	20	1	2	2	EPM2AIP1, MLH1	107, -153	in gene, upstream	ActReg chr3 #6634	1	1
6635	3	37,204,401	37,205,215	814	1	7.04	11.84	13	18	0	0	1	LRRFIP2	13,043	in gene	ActReg chr3 #6635	0	1
6636	3	37,217,307	37,218,391	1,084	2	9.606	13	22	21	1	1	1	LRRFIP2	2	in gene	ActReg chr3 #6636	1	1
6637	3	37,284,308	37,285,242	934	2	12.138	11.207	23	19	1	1	1	GOLGA4	93	in gene	ActReg chr3 #6637	1	1
6638	3	37,661,421	37,662,342	921	2	8.103	14.586	16	30	0	0	1	ITGA9	168,068	in gene	ActReg chr3 #6638	1	1
6639	3	37,734,746	37,735,603	857	1	6.815	10.407	10	16	0	0	1	ITGA9	241,361	in gene	ActReg chr3 #6639	0	1
6640	3	37,903,629	37,904,324	695	2	8.455	10.546	16	19	1	1	1	CTDSPL	307	in gene	ActReg chr3 #6640	1	1
6641	3	37,950,711	37,951,243	532	1	7	13	12	23	0	0	1	CTDSPL	47,308	in gene	ActReg chr3 #6641	0	1
6642	3	37,977,677	37,978,160	483	1	9.2	11.333	14	15	0	0	1	CTDSPL	74,249	in gene	ActReg chr3 #6642	0	1
6643	3	38,178,804	38,179,695	891	1	11.107	8.321	17	18	2	2	2	ACAA1, MYD88	-516, -720	upstream, upstream	ActReg chr3 #6643	1	0
6644	3	38,179,787	38,180,481	694	1	11.136	8.409	17	15	1	2	2	ACAA1, MYD88	-1401, 165	upstream, in gene	ActReg chr3 #6644	1	0
6645	3	38,387,866	38,388,644	778	2	11.84	13.72	22	27	1	1	1	XYLB	4	in gene	ActReg chr3 #6645	1	1
6646	3	38,846,914	38,847,885	971	2	23.433	23.2	60	60	0	0	0				ActReg chr3 #6646	1	1
6647	3	39,079,660	39,080,402	742	1	6.696	10.565	10	15	0	0	0				ActReg chr3 #6647	0	1
6648	3	39,148,799	39,149,826	1,027	2	12.242	10.242	24	21	1	2	2	GORASP1, TTC21A	-182, 160	upstream, in gene	ActReg chr3 #6648	1	1
6649	3	39,188,197	39,189,264	1,067	1	11.303	12.182	23	19	0	0	2	TTC21A, CSRNP1	39578, 6372	downstream, in gene	ActReg chr3 #6649	0	1
6650	3	39,193,204	39,194,798	1,594	2	12.34	12.36	23	29	1	1	1	CSRNP1	1,101	in gene	ActReg chr3 #6650	1	1
6651	3	39,207,556	39,208,373	817	1	8.84	11	13	14	0	0	0				ActReg chr3 #6651	0	1
6652	3	39,424,641	39,425,951	1,310	2	9.65	11.675	17	22	1	1	1	SLC25A38	481	in gene	ActReg chr3 #6652	1	1
6653	3	39,448,029	39,448,527	498	1	11.562	10.75	16	14	1	3	4	SLC25A38, RPSA, SNORA6, SNORA62	23463, 74, -1604, -4267	downstream, in gene, upstream, upstream	ActReg chr3 #6653	1	0
6654	3	39,680,739	39,681,241	502	1	10.933	9.467	21	15	0	0	0				ActReg chr3 #6654	1	0
6655	3	40,300,002	40,300,657	655	1	9.95	7.9	21	14	0	0	2	MYRIP, FLJ33065	449026, 50860	in gene, in gene	ActReg chr3 #6655	1	0
6656	3	40,350,715	40,351,461	746	2	13.25	15.042	25	30	1	2	2	FLJ33065, EIF1B	101, -85	in gene, upstream	ActReg chr3 #6656	1	1
6657	3	40,518,308	40,518,839	531	1	6	12.75	8	19	1	1	1	ZNF619	-31	upstream	ActReg chr3 #6657	0	1
6658	3	40,565,835	40,567,178	1,343	2	12.191	11.476	21	20	1	1	2	ZNF620, ZNF621	18976, 130	downstream, in gene	ActReg chr3 #6658	1	1
6659	3	41,012,730	41,013,721	991	2	9.345	10	17	16	0	0	0				ActReg chr3 #6659	1	1
6660	3	41,240,431	41,241,411	980	2	9.69	10.677	16	18	1	1	1	CTNNB1	-21	upstream	ActReg chr3 #6660	1	1
6661	3	42,003,237	42,004,064	827	2	14.308	14.769	27	28	1	2	2	ULK4, LOC100287063	10, 736	in gene, in gene	ActReg chr3 #6661	1	1
6662	3	42,121,861	42,122,596	735	1	11.348	5.304	15	8	0	0	1	LOC100287063	119,314	in gene	ActReg chr3 #6662	1	0
6663	3	42,341,369	42,342,091	722	1	9.739	14.261	18	26	0	0	0				ActReg chr3 #6663	0	1
6664	3	42,622,981	42,624,253	1,272	2	11.79	12	19	19	1	1	2	SEC22C, SS18L2	-189, -8681	upstream, upstream	ActReg chr3 #6664	1	1
6665	3	42,641,745	42,642,486	741	1	12.391	9.435	17	15	1	1	2	SS18L2, NKTR	9817, -32	downstream, upstream	ActReg chr3 #6665	1	0
6666	3	42,742,472	42,743,586	1,114	2	14.629	11.257	25	22	0	1	3	KBTBD5, HHATL, CCDC13	16018, 1290, 71716	downstream, in gene, downstream	ActReg chr3 #6666	1	1
6667	3	42,814,400	42,815,113	713	1	12.652	7.739	23	14	1	1	2	CCDC13, HIGD1A	-11, 31271	upstream, downstream	ActReg chr3 #6667	1	0
6668	3	42,845,558	42,846,429	871	1	7.481	11.482	11	14	1	2	2	HIGD1A, CCBP2	34, -4971	in gene, upstream	ActReg chr3 #6668	0	1
6669	3	42,860,911	42,861,803	892	1	6.25	9.357	10	15	0	0	1	CCBP2	10,393	in gene	ActReg chr3 #6669	0	1
6670	3	42,921,995	42,923,002	1,007	1	10.516	12.29	13	17	1	1	1	CYP8B1	-4,865	upstream	ActReg chr3 #6670	0	1
6671	3	43,001,677	43,002,323	646	2	12.65	13.85	28	32	0	0	0				ActReg chr3 #6671	1	1
6672	3	43,197,138	43,197,777	639	1	7.4	10.6	13	18	0	0	0				ActReg chr3 #6672	0	1
6673	3	43,673,573	43,674,431	858	2	12.615	11.538	20	21	0	0	0				ActReg chr3 #6673	1	1
6674	3	43,837,470	43,838,060	590	1	7.474	12.421	10	23	0	0	0				ActReg chr3 #6674	0	1
6675	3	43,995,205	43,995,823	618	1	9.316	13.053	15	22	0	0	0				ActReg chr3 #6675	0	1
6676	3	44,040,260	44,041,207	947	1	8.724	11	12	15	1	0	0				ActReg chr3 #6676	0	1
6677	3	44,177,916	44,178,487	571	2	16.667	19.222	28	34	0	0	0				ActReg chr3 #6677	1	1
6678	3	44,379,819	44,380,670	851	1	11.308	10.231	20	18	1	1	2	C3orf77, C3orf23	96866, 633	downstream, in gene	ActReg chr3 #6678	1	0
6679	3	44,519,093	44,519,466	373	1	4	10.083	7	13	1	1	1	ZNF445	-117	upstream	ActReg chr3 #6679	0	1
6680	3	44,551,717	44,552,295	578	1	3.444	11.056	8	19	0	1	1	ZNF852	126	in gene	ActReg chr3 #6680	0	1
6681	3	44,574,029	44,574,876	847	2	9.692	13.538	23	24	0	0	0				ActReg chr3 #6681	1	1
6682	3	44,666,172	44,666,821	649	2	12.524	12	16	20	1	1	1	ZNF197	-15	upstream	ActReg chr3 #6682	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6683	3	44,753,886	44,754,348	462	1	9.8	12.2	13	20	1	1	1	ZNF502	-18	upstream	ActReg chr3 #6683	0	1
6684	3	45,147,182	45,147,884	702	2	11.091	11.182	21	18	0	0	1	CDCP1	40,381	in gene	ActReg chr3 #6684	1	1
6685	3	45,165,274	45,166,189	915	1	10.69	8.31	17	14	0	0	1	CDCP1	22,183	in gene	ActReg chr3 #6685	1	0
6686	3	45,195,715	45,196,860	1,145	1	8.886	14.771	20	22	0	0	1	CDCP1	-8,373	upstream	ActReg chr3 #6686	0	1
6687	3	45,208,290	45,209,436	1,146	2	12.143	14.543	22	30	0	0	0				ActReg chr3 #6687	1	1
6688	3	45,515,403	45,515,859	456	1	6.714	10.714	10	13	0	0	1	LARS2	85,556	in gene	ActReg chr3 #6688	0	1
6689	3	45,550,532	45,551,192	660	1	12.65	10.8	20	15	0	0	1	LARS2	120,787	in gene	ActReg chr3 #6689	1	0
6690	3	45,698,088	45,698,654	566	1	8.824	12.177	12	23	0	0	1	LIMD1	62,048	in gene	ActReg chr3 #6690	0	1
6691	3	45,730,152	45,731,156	1,004	2	13.032	18.484	24	33	2	2	3	LIMD1, LOC644714, SACM1L	94331, -260, -100	downstream, upstream, upstream	ActReg chr3 #6691	1	1
6692	3	45,859,120	45,860,273	1,153	2	10.333	8.5	17	15	0	0	1	LZTFL1	23,925	downstream	ActReg chr3 #6692	1	1
6693	3	45,883,231	45,884,007	776	2	11.56	11.76	17	21	1	1	1	LZTFL1	2	in gene	ActReg chr3 #6693	1	1
6694	3	46,036,988	46,037,694	706	1	11.136	10.364	17	16	1	1	1	FYCO1	-34	upstream	ActReg chr3 #6694	1	0
6695	3	47,017,597	47,018,889	1,292	2	11.366	14.829	25	25	1	2	2	CCDC12, NBEAL2	27, -2930	in gene, upstream	ActReg chr3 #6695	1	1
6696	3	47,205,395	47,206,212	817	2	11.885	14	25	25	1	2	2	SETD2, FLJ39534	-336, -57	upstream, upstream	ActReg chr3 #6696	1	1
6697	3	47,324,008	47,324,670	662	1	11.05	14.1	16	25	1	2	2	KIF9, KLHL18	-2, 9	upstream, in gene	ActReg chr3 #6697	0	1
6698	3	47,421,674	47,423,248	1,574	2	12.122	9.571	16	19	1	1	1	PTPN23	-30	upstream	ActReg chr3 #6698	1	1
6699	3	47,516,873	47,517,851	978	1	7.067	11.467	12	17	1	1	1	SCAP	83	in gene	ActReg chr3 #6699	0	1
6700	3	47,563,541	47,564,206	665	1	10.476	7.667	18	14	0	0	1	C3orf75	-8,674	upstream	ActReg chr3 #6700	1	0
6701	3	47,844,239	47,845,357	1,118	2	10.4	10.486	17	18	1	1	1	DHX30	399	in gene	ActReg chr3 #6701	1	1
6702	3	47,865,937	47,867,225	1,288	2	31.875	39.55	113	117	1	0	1	DHX30	22,182	in gene	ActReg chr3 #6702	1	1
6703	3	47,952,085	47,952,800	715	1	11.957	8.4	25	14	0	0	1	MAP4	178,327	in gene	ActReg chr3 #6703	1	0
6704	3	48,130,289	48,131,028	739	1	10.174	11.957	16	20	1	1	1	MAP4	111	in gene	ActReg chr3 #6704	0	1
6705	3	48,229,500	48,230,333	833	2	10.962	11.115	19	18	1	1	1	CDC25A	-115	upstream	ActReg chr3 #6705	1	1
6706	3	48,282,169	48,282,835	666	1	7.238	14.238	15	23	1	1	1	ZNF589	-94	upstream	ActReg chr3 #6706	0	1
6707	3	48,342,398	48,343,502	1,104	1	9	14.886	15	22	1	1	2	NME6, SPINK8	-102, 26881	upstream, downstream	ActReg chr3 #6707	0	1
6708	3	48,487,631	48,488,480	849	2	13	10.407	21	20	1	2	3	CCDC51, CCDC72, ATRIP	-6526, 6369, -163	upstream, downstream, upstream	ActReg chr3 #6708	1	1
6709	3	48,598,322	48,602,084	3,762	3	10.814	11.873	20	21	0	2	3	PFKFB4, UCN2, COL7A1	-5976, 998, 32390	upstream, in gene, downstream	ActReg chr3 #6709	1	1
6710	3	48,672,150	48,673,583	1,433	2	13.156	13.511	23	21	1	1	2	SLC26A6, CELSR3	60, 27482	in gene, downstream	ActReg chr3 #6710	1	1
6711	3	48,698,015	48,700,041	2,026	2	11.953	16.703	26	44	1	1	1	CELSR3	1,320	in gene	ActReg chr3 #6711	1	1
6712	3	48,700,099	48,701,883	1,784	1	10.655	12.964	17	30	1	1	2	CELSR3, NCKIPSD	-643, 22343	upstream, downstream	ActReg chr3 #6712	0	1
6713	3	48,955,911	48,956,535	624	1	8.895	12.316	13	20	1	2	2	C3orf71, ARIH2	595, -58	in gene, upstream	ActReg chr3 #6713	0	1
6714	3	49,044,490	49,045,286	796	1	10.84	13.44	22	22	1	1	3	P4HTM, WDR6, DALRD3	17547, 251, 13579	downstream, in gene, downstream	ActReg chr3 #6714	0	1
6715	3	49,054,987	49,056,003	1,016	1	8.719	12.906	13	17	1	4	6	WDR6, DALRD3, MIR425, NDUFAF3, MIR191, IMPDH2	10858, 2972, 2172, 2413, 2647, 11380	downstream, in gene, downstream, upstream, downstream, downstream	ActReg chr3 #6715	0	1
6716	3	49,057,815	49,060,702	2,887	2	19.878	26.222	100	144	1	4	7	WDR6, DALRD3, MIR425, NDUFAF3, MIR191, IMPDH2, QRICH1	14621, -791, -1591, 1350, -1116, 7617, 72246	downstream, upstream, upstream, in gene, upstream, downstream, downstream	ActReg chr3 #6716	1	1
6717	3	49,130,794	49,132,810	2,016	2	30.349	40.222	89	117	1	1	2	QRICH1, QARS	-298, 10369	upstream, downstream	ActReg chr3 #6717	1	1
6718	3	49,141,729	49,142,436	707	1	9.136	12.091	14	19	1	1	2	QARS, USP19	89, 16131	in gene, downstream	ActReg chr3 #6718	0	1
6719	3	49,157,543	49,158,546	1,003	1	8.871	13.323	13	21	1	1	2	USP19, LAMB2	169, 12555	in gene, downstream	ActReg chr3 #6719	0	1
6720	3	49,169,889	49,171,439	1,550	1	15.354	11.979	21	25	0	1	1	LAMB2	-65	upstream	ActReg chr3 #6720	1	0
6721	3	49,203,591	49,204,476	885	1	9.889	12.111	18	23	1	2	2	CCDC71, KLHDC8B	-248, 4985	upstream, upstream	ActReg chr3 #6721	0	1
6722	3	49,313,947	49,314,790	843	1	8	10.815	12	16	1	2	3	C3orf62, MIR4271, USP4	140, 2815, 63168	in gene, downstream, downstream	ActReg chr3 #6722	0	1
6723	3	49,377,121	49,378,358	1,237	2	12.526	13.132	26	23	1	2	2	USP4, LOC100289130	-203, -7612	upstream, upstream	ActReg chr3 #6723	1	1
6724	3	49,449,536	49,450,143	607	1	11.895	6.368	20	11	1	2	4	RHOA, TCTA, AMT, NICN1	-313, 200, 10272, 16918	upstream, in gene, downstream, downstream	ActReg chr3 #6724	1	0
6725	3	49,726,652	49,727,380	728	1	9.087	12.913	21	26	1	2	3	APEH, MST1, RNF123	15581, -820, 26	downstream, upstream, in gene	ActReg chr3 #6725	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6726	3	49,761,011	49,762,028	1,017	1	10.344	12.688	19	22	1	2	4	RNF123, AMIGO3, GMPPB, IP6K1	34529, -4281, -135, 62454	downstream, upstream, upstream, downstream	ActReg chr3 #6726	0	1
6727	3	49,839,853	49,840,532	679	1	7.333	13.333	12	24	1	2	3	CDHR4, C3orf54, UBA7	-2938, -495, 11199	upstream, upstream, downstream	ActReg chr3 #6727	0	1
6728	3	49,893,502	49,894,161	659	1	11.524	12.857	20	17	1	1	2	TRAIP, CAMKV	161, 13538	in gene, downstream	ActReg chr3 #6728	0	1
6729	3	49,904,952	49,905,729	777	2	12.96	13.833	25	28	0	1	1	CAMKV	2,029	in gene	ActReg chr3 #6729	1	1
6730	3	49,977,174	49,978,131	957	1	9.567	15.667	16	25	1	1	2	MON1A, RBM6	-10207, 175	upstream, in gene	ActReg chr3 #6730	0	1
6731	3	50,264,297	50,265,403	1,106	2	10.559	13	27	24	1	0	2	SLC38A3, GNAI2	22158, -8797	downstream, upstream	ActReg chr3 #6731	1	1
6732	3	50,329,535	50,330,383	848	2	19.556	23.296	55	55	1	1	5	C3orf45, IFRD2, HYAL3, NAT6, HYAL1	13441, 67, 6940, 6753, 19853	downstream, in gene, downstream, downstream, downstream	ActReg chr3 #6732	1	1
6733	3	50,336,112	50,337,077	965	2	13.267	17.133	36	40	1	3	4	IFRD2, HYAL3, NAT6, HYAL1	-6568, 305, 118, 13218	upstream, in gene, in gene, downstream	ActReg chr3 #6733	1	1
6734	3	50,358,240	50,359,732	1,492	2	34.596	40.957	149	163	2	1	4	HYAL1, HYAL2, TUSC2, RASSF1	-9174, 1295, 6682, 19381	upstream, in gene, downstream, downstream	ActReg chr3 #6734	1	1
6735	3	50,374,164	50,375,323	1,159	1	10.083	13.222	22	23	1	0	4	TUSC2, RASSF1, ZMYND10, TUSC4	-9075, 3624, 8413, 13743	upstream, in gene, downstream, downstream	ActReg chr3 #6735	0	1
6736	3	50,387,803	50,388,970	1,167	2	13.54	15.081	31	29	1	3	5	RASSF1, ZMYND10, TUSC4, CYB561D2, TMEM115	-10019, -5230, 100, 89, 8553	upstream, upstream, in gene, in gene, downstream	ActReg chr3 #6736	1	1
6737	3	50,396,669	50,397,487	818	2	13.923	14.231	23	24	1	3	6	TUSC4, CYB561D2, TMEM115, CACNA2D2, LOC100506825, LOC100506802	-8592, 8781, -139, 143814, -5683, -7855	upstream, downstream, upstream, downstream, upstream, upstream	ActReg chr3 #6737	1	1
6738	3	50,563,199	50,564,053	854	2	17.556	15.889	36	36	0	0	0				ActReg chr3 #6738	1	1
6739	3	50,606,522	50,607,343	821	2	10.885	15.462	24	31	1	2	2	C3orf18, HEMK1	1526, 23	in gene, in gene	ActReg chr3 #6739	1	1
6740	3	50,664,611	50,665,563	952	1	8.414	11.862	14	16	0	0	1	MAPKAPK3	10,486	in gene	ActReg chr3 #6740	0	1
6741	3	51,533,275	51,533,830	555	1	9.167	11.167	14	15	1	1	1	VPRBP	466	in gene	ActReg chr3 #6741	0	1
6742	3	51,572,295	51,572,924	629	2	9	12.158	17	22	1	1	1	RAD54L2	-2,987	upstream	ActReg chr3 #6742	1	1
6743	3	51,870,678	51,871,201	523	1	8.941	10.118	11	15	0	0	2	LOC100506840, IQCF3	19319, 8370	downstream, downstream	ActReg chr3 #6743	0	1
6744	3	51,963,290	51,964,213	923	2	11.793	17.207	26	39	0	0	1	RRP9	12,171	downstream	ActReg chr3 #6744	1	1
6745	3	51,975,841	51,976,771	930	1	13.172	7.724	23	14	1	2	2	RRP9, PARP3	-384, -55	upstream, upstream	ActReg chr3 #6745	1	0
6746	3	52,016,336	52,017,661	1,325	2	15.439	11.488	25	19	1	1	4	ABHD14B, ABHD14A, ACY1, RPL29	-8352, 7956, -565, 12960	upstream, downstream, upstream, downstream	ActReg chr3 #6746	1	1
6747	3	52,029,487	52,030,281	794	2	12.2	12.52	20	22	1	1	2	ACY1, RPL29	12321, 74	downstream, in gene	ActReg chr3 #6747	1	1
6748	3	52,090,576	52,091,590	1,014	2	11.594	16.875	20	26	2	1	2	DUSP7, C3orf74	-622, 8045	upstream, downstream	ActReg chr3 #6748	1	1
6749	3	52,187,956	52,189,318	1,362	2	26.233	27.767	52	76	1	1	1	WDR51A	69	in gene	ActReg chr3 #6749	1	1
6750	3	52,231,635	52,232,527	892	1	10.929	13.464	24	19	1	1	1	ALAS1	-35	upstream	ActReg chr3 #6750	0	1
6751	3	52,311,975	52,313,196	1,221	2	10.184	10.105	17	18	1	1	3	WDR82, MIRLET7G, GLYCTK	74, -10208, 9251	in gene, upstream, upstream	ActReg chr3 #6751	1	1
6752	3	52,321,541	52,322,298	757	2	11.13	10.913	22	22	1	1	3	WDR82, GLYCTK, MIR135A1	-9260, 83, 6405	upstream, in gene, downstream	ActReg chr3 #6752	1	1
6753	3	52,568,124	52,569,008	884	1	8.429	10.571	11	16	1	2	3	STAB1, NT5DC2, LOC440957	39210, 527, 2055	downstream, in gene, upstream	ActReg chr3 #6753	0	1
6754	3	52,570,427	52,571,212	785	1	7.84	12.92	13	21	1	2	3	NT5DC2, LOC440957, PBRM1	-1726, 198, 149047	upstream, in gene, downstream	ActReg chr3 #6754	0	1
6755	3	52,643,383	52,643,829	446	1	9.071	11.214	14	16	0	0	1	PBRM1	76,260	in gene	ActReg chr3 #6755	0	1
6756	3	52,704,626	52,705,283	657	1	6.905	9.952	11	14	0	0	1	PBRM1	14,912	in gene	ActReg chr3 #6756	0	1
6757	3	52,719,738	52,720,439	701	1	8.524	12.046	16	21	1	5	6	PBRM1, GNL3, SNORD19, SNORD19B, SNORD69, GLT8D1	-222, 152, -3168, -4666, -6664, 19960	upstream, in gene, upstream, upstream, upstream, downstream	ActReg chr3 #6757	0	1
6758	3	52,738,849	52,740,590	1,741	2	11.87	12.148	23	25	1	2	3	GLT8D1, SPCS1, NEK4	329, -138, 65246	in gene, upstream, downstream	ActReg chr3 #6758	1	1
6759	3	52,804,593	52,805,446	853	2	10.889	9.519	17	19	1	2	2	NEK4, ITIH1	-54, -6589	upstream, upstream	ActReg chr3 #6759	1	1
6760	3	53,203,009	53,205,652	2,643	1	8.354	12.207	16	27	0	0	1	PRKCD	9,107	in gene	ActReg chr3 #6760	0	1
6761	3	53,272,162	53,272,754	592	1	7.5	12.556	11	19	0	0	1	TKT	17,610	in gene	ActReg chr3 #6761	0	1
6762	3	53,381,155	53,382,106	951	2	15.483	19.035	33	42	1	1	1	DCP1A	24	in gene	ActReg chr3 #6762	1	1
6763	3	53,604,671	53,605,410	739	2	10.542	9.167	14	19	0	0	1	CACNA1D	76,009	in gene	ActReg chr3 #6763	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6764	3	53,915,655	53,916,422	767	2	11.458	11.125	22	24	1	1	2	ACTR8, SELK	191, 9951	in gene, downstream	ActReg chr3 #6764	1	1
6765	3	53,925,415	53,926,397	982	2	12.9	9.6	27	21	1	1	2	ACTR8, SELK	-9677, 83	upstream, in gene	ActReg chr3 #6765	1	1
6766	3	54,004,524	54,005,164	640	2	10.15	11.75	22	23	0	0	0				ActReg chr3 #6766	1	1
6767	3	54,221,426	54,222,898	1,472	2	13.261	18.065	43	57	0	0	1	CACNA2D3	65,469	in gene	ActReg chr3 #6767	1	1
6768	3	54,591,835	54,592,440	605	1	9.842	11.947	16	20	0	0	1	CACNA2D3	435,444	in gene	ActReg chr3 #6768	0	1
6769	3	54,654,962	54,655,570	608	1	9.368	11.737	15	18	0	0	1	CACNA2D3	498,573	in gene	ActReg chr3 #6769	0	1
6770	3	55,201,611	55,202,470	859	1	9.259	10.667	13	15	0	0	0				ActReg chr3 #6770	0	1
6771	3	55,236,078	55,236,585	507	1	13.188	5.875	17	10	0	0	0				ActReg chr3 #6771	1	0
6772	3	55,464,929	55,465,555	626	1	6.632	11.474	11	16	0	0	0				ActReg chr3 #6772	0	1
6773	3	55,520,031	55,520,794	763	1	7.917	12.667	14	26	1	1	1	WNT5A	919	in gene	ActReg chr3 #6773	0	1
6774	3	56,528,475	56,529,238	763	2	17.333	19.083	43	49	0	0	0				ActReg chr3 #6774	1	1
6775	3	56,717,049	56,717,694	645	1	9.15	11.8	12	21	1	1	1	C3orf63	-236	upstream	ActReg chr3 #6775	0	1
6776	3	57,014,596	57,015,279	683	2	10.952	13.65	17	29	0	0	1	ARHGEF3	98,399	in gene	ActReg chr3 #6776	1	1
6777	3	57,051,061	57,051,817	756	1	7.5	10.333	13	13	0	0	1	ARHGEF3	61,897	in gene	ActReg chr3 #6777	0	1
6778	3	57,541,276	57,542,787	1,511	2	10.667	12.146	23	18	1	1	1	PDE12	50	in gene	ActReg chr3 #6778	1	1
6779	3	57,582,505	57,583,534	1,029	2	11.594	13.188	22	22	1	1	1	ARF4	196	in gene	ActReg chr3 #6779	1	1
6780	3	57,741,658	57,743,092	1,434	1	8.4	12.667	15	20	1	2	2	LOC100287789, SLMAP	567, -799	in gene, upstream	ActReg chr3 #6780	0	1
6781	3	57,789,216	57,789,893	677	2	9.273	13.091	19	26	0	0	1	SLMAP	46,380	in gene	ActReg chr3 #6781	1	1
6782	3	57,791,255	57,791,933	678	2	14.667	13.095	35	27	0	0	1	SLMAP	48,420	in gene	ActReg chr3 #6782	1	1
6783	3	58,223,887	58,224,563	676	1	7.524	11.619	11	18	1	1	1	ABHD6	966	in gene	ActReg chr3 #6783	0	1
6784	3	58,291,471	58,292,644	1,173	2	34.568	41.73	110	137	1	1	1	RPP14	85	in gene	ActReg chr3 #6784	1	1
6785	3	58,318,160	58,318,884	724	2	11.565	14.522	25	30	1	1	1	PXK	-95	upstream	ActReg chr3 #6785	1	1
6786	3	58,472,637	58,473,416	779	1	12.4	9.36	27	13	0	1	1	KCTD6	-4,797	upstream	ActReg chr3 #6786	1	0
6787	3	58,477,383	58,477,992	609	2	7.667	9.211	17	22	1	1	1	KCTD6	-136	upstream	ActReg chr3 #6787	1	1
6788	3	58,511,864	58,513,026	1,162	2	13.46	12.351	21	24	0	0	1	ACOX2	10,484	in gene	ActReg chr3 #6788	1	1
6789	3	58,573,183	58,574,577	1,394	2	10.136	14.091	21	27	0	0	1	FAM107A	-10,389	upstream	ActReg chr3 #6789	1	1
6790	3	59,128,182	59,128,687	505	1	3.062	9.625	6	15	0	0	0				ActReg chr3 #6790	0	1
6791	3	59,128,968	59,129,536	568	1	4.389	9.722	8	17	0	0	0				ActReg chr3 #6791	0	1
6792	3	59,545,189	59,546,026	837	2	15.923	15.192	31	35	0	0	0				ActReg chr3 #6792	1	1
6793	3	60,262,944	60,263,546	602	1	3.895	9.947	6	17	0	0	1	FHIT	973,888	in gene	ActReg chr3 #6793	0	1
6794	3	61,546,098	61,546,980	882	1	11.393	8.893	16	13	1	1	1	PTPRG	-704	upstream	ActReg chr3 #6794	1	0
6795	3	62,304,171	62,305,494	1,323	2	11.341	12.829	22	22	1	2	2	LOC100506994, C3orf14	-210, -564	upstream, upstream	ActReg chr3 #6795	1	1
6796	3	62,514,757	62,515,370	613	1	10.79	15.263	21	31	0	0	1	CADPS	346,001	in gene	ActReg chr3 #6796	0	1
6797	3	62,573,074	62,573,764	690	1	5.409	12.318	7	19	0	0	1	CADPS	287,645	in gene	ActReg chr3 #6797	0	1
6798	3	62,589,869	62,590,523	654	1	11.3	10.3	18	15	0	0	1	CADPS	270,868	in gene	ActReg chr3 #6798	1	0
6799	3	62,859,352	62,860,021	669	1	11.714	7.714	16	15	1	1	1	CADPS	1,378	in gene	ActReg chr3 #6799	1	0
6800	3	62,861,572	62,862,315	743	2	12.913	12	27	26	0	1	1	CADPS	-879	upstream	ActReg chr3 #6800	1	1
6801	3	62,907,811	62,908,510	699	2	12.095	12.857	25	20	0	0	0				ActReg chr3 #6801	1	1
6802	3	63,053,530	63,054,462	932	2	12.069	19.586	37	48	0	0	0				ActReg chr3 #6802	1	1
6803	3	63,350,155	63,350,711	556	1	6.059	8.941	10	16	0	0	1	SYNPR	86,519	in gene	ActReg chr3 #6803	0	1
6804	3	63,739,100	63,739,666	566	1	8.833	9.889	14	17	0	0	1	LOC100130345	59,428	in gene	ActReg chr3 #6804	0	1
6805	3	63,795,176	63,795,880	704	1	13.364	8.136	26	11	0	0	2	LOC100130345, C3orf49	3283, -9513	in gene, upstream	ActReg chr3 #6805	1	0
6806	3	63,897,593	63,898,320	727	2	11.217	9.826	18	16	2	0	1	ATXN7	47,723	in gene	ActReg chr3 #6806	1	1
6807	3	63,949,958	63,950,354	396	1	8.75	10.75	11	15	0	0	1	ATXN7	99,923	in gene	ActReg chr3 #6807	0	1
6808	3	64,008,552	64,009,636	1,084	2	35.618	39.088	120	133	1	1	1	PSMD6	26	in gene	ActReg chr3 #6808	1	1
6809	3	64,090,063	64,090,954	891	2	11.071	12.75	18	22	0	0	1	PRICKLE2	120,623	in gene	ActReg chr3 #6809	1	1
6810	3	64,218,228	64,218,964	736	1	8.696	11.217	13	18	0	1	1	PRICKLE2	-7,465	upstream	ActReg chr3 #6810	0	1
6811	3	64,276,610	64,277,504	894	1	11.071	15.607	22	31	0	0	0				ActReg chr3 #6811	0	1
6812	3	64,670,834	64,671,521	687	1	11.364	7	16	11	1	2	2	ADAMTS9, LOC100507098	2188, 631	in gene, in gene	ActReg chr3 #6812	1	0
6813	3	64,673,647	64,674,291	644	2	9.1	10.278	15	18	1	1	2	ADAMTS9, LOC100507098	-604, 3423	upstream, in gene	ActReg chr3 #6813	1	1
6814	3	64,973,813	64,974,440	627	2	11.25	12.3	18	20	0	0	0				ActReg chr3 #6814	1	1
6815	3	65,016,237	65,017,047	810	2	11	10.36	21	21	0	0	0				ActReg chr3 #6815	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6816	3	65,949,580	65,950,261	681	1	8.762	12.333	13	17	0	0	2	MAGI1, LOC151877	74589, -9687	in gene, upstream	ActReg chr3 #6816	0	1
6817	3	65,977,712	65,978,345	633	1	6.9	10.1	12	22	0	0	1	MAGI1	46,481	in gene	ActReg chr3 #6817	0	1
6818	3	66,024,362	66,025,322	960	2	11.833	13.333	20	22	1	1	1	MAGI1	-333	upstream	ActReg chr3 #6818	1	1
6819	3	66,551,068	66,552,009	941	1	10.233	13.8	16	27	1	1	1	LRIG1	-693	upstream	ActReg chr3 #6819	0	1
6820	3	67,068,844	67,069,736	892	2	10.464	9.25	16	17	0	0	1	KBTBD8	20,563	downstream	ActReg chr3 #6820	1	1
6821	3	67,164,071	67,164,732	661	2	18.95	17.25	41	36	0	0	0				ActReg chr3 #6821	1	1
6822	3	67,704,644	67,705,482	838	1	11.692	9.769	17	14	1	1	1	SUCLG2	-25	upstream	ActReg chr3 #6822	1	0
6823	3	68,355,705	68,356,146	441	1	9.857	7	18	11	0	0	1	FAM19A1	302,471	in gene	ActReg chr3 #6823	1	0
6824	3	69,062,502	69,063,300	798	1	8.6	10.56	12	14	1	1	2	C3orf64, TMF1	-127, 38583	upstream, downstream	ActReg chr3 #6824	0	1
6825	3	69,230,720	69,231,465	745	2	10.25	11.625	17	22	0	0	1	FRMD4B	204,338	in gene	ActReg chr3 #6825	1	1
6826	3	69,355,526	69,356,210	684	1	9.571	12.286	17	24	0	0	1	FRMD4B	79,562	in gene	ActReg chr3 #6826	0	1
6827	3	69,788,145	69,789,203	1,058	1	10.394	11.758	17	18	1	1	1	MITF	88	in gene	ActReg chr3 #6827	0	1
6828	3	70,048,361	70,049,540	1,179	1	8.811	11.757	16	23	0	0	0				ActReg chr3 #6828	0	1
6829	3	70,089,582	70,090,160	578	1	4.278	10.056	6	16	0	0	0				ActReg chr3 #6829	0	1
6830	3	70,102,266	70,102,828	562	1	12.5	7.611	20	12	0	0	0				ActReg chr3 #6830	1	0
6831	3	72,031,660	72,032,276	616	1	9.368	11.474	14	21	0	0	0				ActReg chr3 #6831	0	1
6832	3	72,173,129	72,173,746	617	1	10.053	9	19	15	0	0	0				ActReg chr3 #6832	1	0
6833	3	72,387,243	72,389,118	1,875	2	20.569	20.483	48	39	0	0	0				ActReg chr3 #6833	1	1
6834	3	72,710,119	72,710,805	686	1	12.143	4.619	16	8	0	0	1	LOC100506865	2,938	downstream	ActReg chr3 #6834	1	0
6835	3	72,897,125	72,897,863	738	1	7.783	11.87	13	22	1	1	1	SHQ1	104	in gene	ActReg chr3 #6835	0	1
6836	3	72,936,775	72,937,295	520	1	8.562	11.625	14	20	0	1	1	GXYLT2	-350	upstream	ActReg chr3 #6836	0	1
6837	3	72,987,678	72,988,095	417	1	11.308	6.846	16	9	0	0	1	GXYLT2	50,501	in gene	ActReg chr3 #6837	1	0
6838	3	73,143,037	73,143,907	870	1	8.464	10.25	13	14	0	0	0				ActReg chr3 #6838	0	1
6839	3	73,277,374	73,278,146	772	1	7.36	12.96	12	24	0	0	0				ActReg chr3 #6839	0	1
6840	3	73,629,370	73,630,005	635	1	8.65	12.9	11	26	0	0	1	PDZRN3	44,385	in gene	ActReg chr3 #6840	0	1
6841	3	73,673,994	73,674,667	673	1	8.762	12.333	13	19	1	1	1	PDZRN3	-258	upstream	ActReg chr3 #6841	0	1
6842	3	75,273,389	75,274,053	664	1	10.238	12.667	16	21	0	0	0				ActReg chr3 #6842	0	1
6843	3	75,481,987	75,482,563	576	1	9	12.222	16	19	0	0	0				ActReg chr3 #6843	0	1
6844	3	75,690,130	75,690,761	631	1	4.95	12.5	10	22	0	0	0				ActReg chr3 #6844	0	1
6845	3	75,707,368	75,708,491	1,123	2	16.743	17.971	51	43	1	1	2	FRG2C, LOC100506764	-5558, -9450	upstream, upstream	ActReg chr3 #6845	1	1
6846	3	78,599,826	78,600,366	540	2	11.059	9.882	20	16	0	0	0				ActReg chr3 #6846	1	1
6847	3	79,068,075	79,069,239	1,164	2	19.472	22.25	55	47	1	0	1	ROBO1	748,402	in gene	ActReg chr3 #6847	1	1
6848	3	80,281,777	80,282,473	696	1	11.046	7.727	21	13	0	0	0				ActReg chr3 #6848	1	0
6849	3	80,819,681	80,820,313	632	1	7.263	13.684	12	21	1	0	0				ActReg chr3 #6849	0	1
6850	3	81,810,359	81,811,290	931	2	9.276	16.172	19	27	1	1	1	GBE1	126	in gene	ActReg chr3 #6850	1	1
6851	3	83,273,000	83,273,735	735	1	7.739	11.652	12	18	0	0	0				ActReg chr3 #6851	0	1
6852	3	84,597,235	84,598,269	1,034	1	7.188	11.406	12	16	0	0	0				ActReg chr3 #6852	0	1
6853	3	85,609,423	85,609,896	473	1	7	10	10	17	0	0	1	CADM2	601,526	in gene	ActReg chr3 #6853	0	1
6854	3	87,382,510	87,383,052	542	1	9.059	9.176	13	18	0	0	0				ActReg chr3 #6854	0	1
6855	3	88,080,696	88,081,386	690	2	9.955	13.727	20	32	0	0	0				ActReg chr3 #6855	1	1
6856	3	88,087,532	88,088,358	826	2	10.385	14.808	19	28	0	0	0				ActReg chr3 #6856	1	1
6857	3	88,107,549	88,108,814	1,265	1	8.725	11.7	15	21	1	1	1	CGGBP1	-35	upstream	ActReg chr3 #6857	0	1
6858	3	88,198,605	88,199,585	980	2	12.516	12.29	23	22	1	1	2	ZNF654, C3orf38	10833, 202	downstream, in gene	ActReg chr3 #6858	1	1
6859	3	89,156,368	89,157,135	767	1	9.083	13.458	14	24	0	1	1	EPHA3	77	in gene	ActReg chr3 #6859	0	1
6860	3	89,163,359	89,164,182	823	1	8.115	12.154	12	20	1	0	1	EPHA3	7,096	in gene	ActReg chr3 #6860	0	1
6861	3	89,220,772	89,221,353	581	1	6.222	10	9	17	0	0	1	EPHA3	64,388	in gene	ActReg chr3 #6861	0	1
6862	3	89,731,658	89,732,199	541	1	3.353	10.765	7	20	0	0	0				ActReg chr3 #6862	0	1
6863	3	90,234,044	90,234,457	413	1	5.769	9.385	10	15	0	0	0				ActReg chr3 #6863	0	1
6864	3	93,881,404	93,881,971	567	1	8.722	10.667	13	19	0	0	0				ActReg chr3 #6864	0	1
6865	3	94,345,199	94,345,789	590	1	9.5	9.722	14	15	0	0	0				ActReg chr3 #6865	0	1
6866	3	96,532,188	96,533,753	1,565	3	9.082	10.735	17	17	1	1	1	EPHA6	-455	upstream	ActReg chr3 #6866	1	1
6867	3	97,540,767	97,541,657	890	1	6.5	10.607	9	16	1	1	1	CRYBG3	643	in gene	ActReg chr3 #6867	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6868	3	97,691,031	97,691,542	511	1	6.125	11	10	14	1	1	1	MINA	9	in gene	ActReg chr3 #6868	0	1
6869	3	98,241,459	98,242,114	655	1	10.524	11.333	18	15	1	1	2	CLDND1, GPR15	124, -9092	in gene, upstream	ActReg chr3 #6869	1	0
6870	3	98,488,953	98,489,670	717	1	10.13	8.522	16	14	0	0	1	ST3GAL6	37,739	in gene	ActReg chr3 #6870	1	0
6871	3	98,620,089	98,620,670	581	1	9.167	12.278	15	18	1	1	1	DCBLD2	154	in gene	ActReg chr3 #6871	0	1
6872	3	98,696,396	98,696,912	516	1	7.375	9.625	13	15	0	1	1	LOC100506377	-3,248	upstream	ActReg chr3 #6872	0	1
6873	3	98,847,822	98,848,469	647	1	6.8	10.4	13	20	0	0	0				ActReg chr3 #6873	0	1
6874	3	99,280,773	99,281,646	873	1	10.259	15.074	18	31	0	0	0				ActReg chr3 #6874	0	1
6875	3	99,536,012	99,537,026	1,014	2	10.312	14.594	15	33	1	1	1	C3orf26	-159	upstream	ActReg chr3 #6875	1	1
6876	3	99,894,361	99,895,035	674	2	9.095	11.809	17	18	0	0	1	C3orf26	358,020	in gene	ActReg chr3 #6876	1	1
6877	3	99,979,339	99,980,222	883	2	13.111	10.222	24	16	1	1	1	TBC1D23	94	in gene	ActReg chr3 #6877	1	1
6878	3	100,244,466	100,245,526	1,060	1	11.727	8.212	17	16	0	0	1	TMEM45A	33,533	in gene	ActReg chr3 #6878	1	0
6879	3	101,292,256	101,293,806	1,550	2	11.796	14.775	24	28	1	1	2	RG9MTD1, PCNP	12319, -11	downstream, upstream	ActReg chr3 #6879	1	1
6880	3	101,394,484	101,395,121	637	1	4.95	11.55	10	16	1	2	3	ZBTB11, LOC100009676, RPL24	1186, -472, 10761	in gene, upstream, downstream	ActReg chr3 #6880	0	1
6881	3	101,497,539	101,498,879	1,340	1	8.854	11.829	15	19	1	1	1	FAM55C	180	in gene	ActReg chr3 #6881	0	1
6882	3	101,568,155	101,568,848	693	1	8.409	11.636	13	22	1	0	1	NFKBIZ	21,667	in gene	ActReg chr3 #6882	0	1
6883	3	101,809,449	101,810,039	590	1	10.222	5.944	16	9	0	0	0				ActReg chr3 #6883	1	0
6884	3	101,875,388	101,875,958	570	1	10.556	6	17	9	0	0	0				ActReg chr3 #6884	1	0
6885	3	102,914,025	102,914,458	433	1	7.231	10.077	10	14	0	0	0				ActReg chr3 #6885	0	1
6886	3	105,073,919	105,074,679	760	1	10.792	7.75	14	10	0	0	0				ActReg chr3 #6886	1	0
6887	3	105,086,183	105,086,780	597	1	6.667	10.889	12	17	1	1	1	ALCAM	768	in gene	ActReg chr3 #6887	0	1
6888	3	105,088,190	105,088,871	681	1	8.273	11.909	15	18	1	1	1	ALCAM	2,817	in gene	ActReg chr3 #6888	0	1
6889	3	105,587,946	105,588,965	1,019	1	11.406	8.219	17	16	1	1	1	CBLB	-568	upstream	ActReg chr3 #6889	1	0
6890	3	105,715,938	105,717,495	1,557	2	10.854	12.729	27	26	0	0	0				ActReg chr3 #6890	1	1
6891	3	106,147,262	106,147,825	563	1	11.167	8.778	20	16	0	0	0				ActReg chr3 #6891	1	0
6892	3	106,176,076	106,176,720	644	2	8.7	11.95	16	25	0	0	0				ActReg chr3 #6892	1	1
6893	3	106,407,186	106,407,684	498	1	6.688	8.688	11	17	0	0	0				ActReg chr3 #6893	0	1
6894	3	106,484,104	106,484,568	464	1	8.214	12.429	13	17	0	0	0				ActReg chr3 #6894	0	1
6895	3	107,150,373	107,150,995	622	1	6.421	11.21	10	18	1	0	0				ActReg chr3 #6895	0	1
6896	3	107,809,433	107,810,449	1,016	2	8.719	12.031	20	18	1	1	1	CD47	-6	upstream	ActReg chr3 #6896	1	1
6897	3	108,139,698	108,140,251	553	2	12.706	14.706	25	25	0	0	1	MYH15	108,195	in gene	ActReg chr3 #6897	1	1
6898	3	108,308,260	108,308,936	676	1	11.476	8.571	18	15	1	2	2	KIAA1524, DZIP3	-107, 261	upstream, in gene	ActReg chr3 #6898	1	0
6899	3	109,404,014	109,404,544	530	1	10.588	9.471	14	13	0	0	0				ActReg chr3 #6899	1	0
6900	3	110,790,071	110,790,835	764	1	9.667	11.458	15	19	1	2	2	LOC100506555, PVRL3	-2211, -412	upstream, upstream	ActReg chr3 #6900	0	1
6901	3	111,070,086	111,070,584	498	1	9.667	13.2	17	21	0	0	0				ActReg chr3 #6901	0	1
6902	3	111,433,102	111,433,602	500	1	7.5	10.25	13	18	0	0	1	PLCXD2	39,829	in gene	ActReg chr3 #6902	0	1
6903	3	111,577,811	111,578,829	1,018	2	12.469	13.281	27	25	1	0	1	PHLDB2	126,993	in gene	ActReg chr3 #6903	1	1
6904	3	111,918,413	111,919,059	646	1	13.2	7.1	24	11	0	0	1	SLC9A10	94,338	in gene	ActReg chr3 #6904	1	0
6905	3	112,280,284	112,281,566	1,282	2	11.45	12.35	25	21	1	2	2	ATG3, SLC35A5	-440, 30	upstream, in gene	ActReg chr3 #6905	1	1
6906	3	112,359,873	112,360,538	665	1	9.8	13.5	16	21	0	1	1	CCDC80	-228	upstream	ActReg chr3 #6906	0	1
6907	3	112,847,176	112,847,672	496	1	10.067	6.133	19	9	0	0	0				ActReg chr3 #6907	1	0
6908	3	113,415,509	113,416,161	652	1	13.905	10.905	25	23	1	1	2	KIAA2018, LOC100506638	-342, 20735	upstream, downstream	ActReg chr3 #6908	1	0
6909	3	113,465,783	113,466,412	629	1	10.2	6.25	20	11	0	2	2	NAA50, ATP6V1A	-1001, 189	upstream, in gene	ActReg chr3 #6909	1	0
6910	3	113,775,108	113,775,910	802	2	12.8	13.32	25	22	1	2	2	KIAA1407, QTRTD1	-49, -102	upstream, upstream	ActReg chr3 #6910	1	1
6911	3	113,897,381	113,898,188	807	2	12.24	13.96	27	33	0	1	1	DRD3	115	in gene	ActReg chr3 #6911	1	1
6912	3	114,130,945	114,131,677	732	1	11.454	7	17	12	0	0	1	ZBTB20	734,816	in gene	ActReg chr3 #6912	1	0
6913	3	115,044,160	115,044,975	815	2	16.846	17.538	38	42	0	0	0				ActReg chr3 #6913	1	1
6914	3	115,155,276	115,156,208	932	2	12.586	17.621	24	37	0	0	0				ActReg chr3 #6914	1	1
6915	3	115,502,711	115,503,968	1,257	2	10.075	12.3	17	20	1	0	0				ActReg chr3 #6915	1	1
6916	3	115,509,417	115,510,167	750	2	12.739	17.913	28	44	0	0	0				ActReg chr3 #6916	1	1
6917	3	115,604,344	115,604,961	617	2	8.35	12.15	13	21	0	0	1	LSAMP	559,733	in gene	ActReg chr3 #6917	1	1
6918	3	115,719,142	115,719,728	586	1	13.278	9.722	24	14	0	0	1	LSAMP	444,950	in gene	ActReg chr3 #6918	1	0
6919	3	115,867,682	115,868,365	683	1	12.238	9.81	19	14	0	0	1	LSAMP	296,362	in gene	ActReg chr3 #6919	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6920	3	116,298,622	116,299,251	629	1	7.35	9.55	13	18	0	0	0				ActReg chr3 #6920	0	1
6921	3	117,041,487	117,042,223	736	2	7.087	14.13	16	31	0	0	0				ActReg chr3 #6921	1	1
6922	3	117,340,795	117,341,454	659	1	11.191	8.476	17	12	0	0	0				ActReg chr3 #6922	1	0
6923	3	117,454,317	117,454,938	621	1	6.737	10.632	10	17	0	0	0				ActReg chr3 #6923	0	1
6924	3	119,041,669	119,042,628	959	1	6.767	10.233	9	18	1	0	1	CDGAP	28,928	in gene	ActReg chr3 #6924	0	1
6925	3	119,182,073	119,183,253	1,180	1	8.568	12.973	15	28	0	2	2	TMEM39A, KTELC1	-192, -5122	upstream, upstream	ActReg chr3 #6925	0	1
6926	3	119,298,137	119,298,869	732	1	8.565	12.087	12	17	1	1	1	ADPRH	-20	upstream	ActReg chr3 #6926	0	1
6927	3	119,813,830	119,814,684	854	1	10.808	8.538	16	12	1	2	2	GSK3B, LOC100506784	-993, -220	upstream, upstream	ActReg chr3 #6927	1	0
6928	3	120,067,450	120,068,502	1,052	1	9.848	13.273	17	22	1	1	2	LRRC58, LOC100130701	210, -8689	in gene, upstream	ActReg chr3 #6928	0	1
6929	3	120,499,693	120,500,349	656	1	11.7	7.85	25	13	0	0	1	GTF2E1	38,463	in gene	ActReg chr3 #6929	1	0
6930	3	120,626,807	120,627,507	700	1	11.046	14.5	16	30	1	1	1	STXBP5L	107	in gene	ActReg chr3 #6930	0	1
6931	3	121,264,446	121,265,019	573	1	10.778	9.5	17	14	1	1	1	POLQ	121	in gene	ActReg chr3 #6931	1	0
6932	3	122,233,252	122,234,268	1,016	2	9.355	9.613	16	20	1	1	1	KPNA1	26	in gene	ActReg chr3 #6932	1	1
6933	3	122,785,677	122,786,612	935	1	11.69	11.31	17	16	1	1	1	PDIA5	288	in gene	ActReg chr3 #6933	1	0
6934	3	122,991,971	122,992,584	613	1	7.789	10	12	15	0	0	1	SEC22A	71,503	in gene	ActReg chr3 #6934	0	1
6935	3	123,004,908	123,006,227	1,319	2	11.659	20.146	34	41	0	0	1	ADCY5	161,825	in gene	ActReg chr3 #6935	1	1
6936	3	123,303,449	123,304,505	1,056	1	10.091	12.212	16	16	2	2	2	PTPLB, LOC100506826	-53, -426	upstream, upstream	ActReg chr3 #6936	0	1
6937	3	123,936,033	123,937,167	1,134	2	17.971	21.029	42	52	0	0	1	KALRN	123,042	in gene	ActReg chr3 #6937	1	1
6938	3	124,147,589	124,148,438	849	1	11.308	6	22	12	0	0	1	KALRN	334,455	in gene	ActReg chr3 #6938	1	0
6939	3	124,249,065	124,249,576	511	1	8.812	12.125	13	19	0	0	1	KALRN	435,762	in gene	ActReg chr3 #6939	0	1
6940	3	124,249,696	124,250,188	492	1	11.812	6.188	17	9	0	0	1	KALRN	436,384	in gene	ActReg chr3 #6940	1	0
6941	3	124,448,873	124,449,732	859	2	11.667	10.63	16	21	1	2	4	KALRN, LOC100506841, UMPS, MIR544B	635744, 5359, 89, -1984	downstream, downstream, in gene, upstream	ActReg chr3 #6941	1	1
6942	3	124,531,541	124,532,643	1,102	1	6.971	11.657	11	19	0	0	1	ITGB5	74,052	in gene	ActReg chr3 #6942	0	1
6943	3	124,704,967	124,705,583	616	1	10.053	11.632	13	18	0	0	1	HEG1	69,527	in gene	ActReg chr3 #6943	0	1
6944	3	124,802,558	124,803,052	494	1	4.5	11.25	6	17	0	0	1	SLC12A8	128,804	in gene	ActReg chr3 #6944	0	1
6945	3	125,093,915	125,094,612	697	2	13.136	13.046	27	23	1	1	1	ZNF148	-65	upstream	ActReg chr3 #6945	1	1
6946	3	125,238,611	125,239,341	730	1	10.739	6.87	14	13	1	1	2	SNX4, OSBPL11	82, 75405	in gene, downstream	ActReg chr3 #6946	1	0
6947	3	125,694,591	125,695,034	443	1	3.786	10	5	18	0	0	1	ROPN1B	6,784	in gene	ActReg chr3 #6947	0	1
6948	3	125,927,321	125,928,021	700	1	8.955	12.273	13	20	0	0	0				ActReg chr3 #6948	0	1
6949	3	126,074,695	126,075,695	999	1	10.452	11.839	20	19	1	1	2	KLF15, LOC100506907	1041, 37290	in gene, downstream	ActReg chr3 #6949	0	1
6950	3	126,422,665	126,423,833	1,168	1	5.722	14.667	11	24	1	2	2	CHCHD6, LOC100132481	131, -2946	in gene, upstream	ActReg chr3 #6950	0	1
6951	3	126,629,777	126,630,851	1,074	2	13.412	10.265	19	17	0	0	1	CHCHD6	207,196	in gene	ActReg chr3 #6951	1	1
6952	3	126,701,170	126,701,841	671	1	13.095	10.905	22	16	1	1	1	PLXNA1	-5,932	upstream	ActReg chr3 #6952	1	0
6953	3	126,676,876	126,678,222	1,346	2	14.571	22.429	45	76	0	0	0				ActReg chr3 #6953	1	1
6954	3	126,881,659	126,882,346	687	1	7.318	11.318	12	18	0	0	0				ActReg chr3 #6954	0	1
6955	3	127,039,269	127,040,106	837	2	11.346	18.269	25	35	0	0	0				ActReg chr3 #6955	1	1
6956	3	127,177,222	127,177,956	734	1	9.087	13.217	17	22	0	0	0				ActReg chr3 #6956	0	1
6957	3	127,308,901	127,310,314	1,413	2	20.818	20.568	39	45	1	2	2	TPRA1, MCM2	-39, -7646	upstream, upstream	ActReg chr3 #6957	1	1
6958	3	127,316,500	127,317,295	795	2	7.88	12.04	18	16	1	2	2	TPRA1, MCM2	-7329, -356	upstream, upstream	ActReg chr3 #6958	1	1
6959	3	127,468,732	127,470,398	1,666	2	9.942	11.346	16	17	0	0	1	MGLL	72,486	in gene	ActReg chr3 #6959	1	1
6960	3	127,494,408	127,495,027	619	1	8.316	11.21	14	17	0	0	1	MGLL	47,334	in gene	ActReg chr3 #6960	0	1
6961	3	127,770,242	127,771,225	983	2	9.433	8.067	16	18	1	1	1	SEC61A1	-479	upstream	ActReg chr3 #6961	1	1
6962	3	127,842,297	127,843,066	769	1	10.375	12.042	14	17	1	1	1	RUVBL1	-10	upstream	ActReg chr3 #6962	0	1
6963	3	127,871,975	127,872,792	817	2	11	11.76	16	21	1	1	1	EEFSEC	70	in gene	ActReg chr3 #6963	1	1
6964	3	128,206,403	128,207,480	1,077	1	7.576	11.333	11	19	1	1	2	GATA2, LOC100506995	5089, -1011	in gene, upstream	ActReg chr3 #6964	0	1
6965	3	128,336,037	128,337,587	1,550	2	33.083	39.521	110	116	1	0	1	RPN1	32,907	downstream	ActReg chr3 #6965	1	1
6966	3	128,369,249	128,369,932	683	2	12.048	13.286	17	19	1	1	1	RPN1	129	in gene	ActReg chr3 #6966	1	1
6967	3	128,399,254	128,400,386	1,132	1	8.917	13.222	19	24	1	0	0				ActReg chr3 #6967	0	1
6968	3	128,598,029	128,598,944	915	2	12.69	16.345	25	31	1	1	2	LOC653712, ACAD9	-8102, 153	upstream, in gene	ActReg chr3 #6968	1	1
6969	3	128,745,687	128,746,348	661	1	12.476	8.238	22	12	1	0	1	CCDC48	25,545	in gene	ActReg chr3 #6969	1	0
6970	3	128,772,411	128,773,219	808	2	12.808	16.615	30	38	0	1	1	GP9	-6,830	upstream	ActReg chr3 #6970	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
6971	3	128,879,803	128,880,813	1,010	2	12.781	14.469	22	24	1	1	2	ISY1, CNBP	-279, 22502	upstream, downstream	ActReg chr3 #6971	1	1
6972	3	128,945,337	128,946,188	851	1	6.926	10.482	14	15	0	0	0				ActReg chr3 #6972	0	1
6973	3	128,967,949	128,968,854	905	2	11.286	12.893	19	25	1	1	1	COPG	-52	upstream	ActReg chr3 #6973	1	1
6974	3	129,034,949	129,035,872	923	1	9.571	11.31	19	19	1	2	2	H1FX, C3orf47	-290, 296	upstream, in gene	ActReg chr3 #6974	0	1
6975	3	129,117,710	129,118,994	1,284	2	12.65	15.05	38	34	0	1	2	SNORA7B, C3orf25	-2161, 29142	upstream, downstream	ActReg chr3 #6975	1	1
6976	3	129,345,883	129,346,471	588	1	7.789	11.579	11	22	1	0	0				ActReg chr3 #6976	0	1
6977	3	130,539,814	130,540,368	554	1	8.118	11.059	14	16	0	0	0				ActReg chr3 #6977	0	1
6978	3	130,745,056	130,745,896	840	2	10.815	10.407	19	17	1	2	3	ATP2C1, ASTE1, NEK11	132042, 170, -218	downstream, in gene, upstream	ActReg chr3 #6978	1	1
6979	3	131,221,410	131,222,240	830	1	8.615	11.423	15	19	1	1	1	MRPL3	4	in gene	ActReg chr3 #6979	0	1
6980	3	131,753,612	131,754,444	832	2	9.385	10.385	24	22	1	1	1	CPNE4	-184	upstream	ActReg chr3 #6980	1	1
6981	3	132,136,183	132,136,836	653	1	11.809	7.762	20	12	1	1	1	DNAJC13	-44	upstream	ActReg chr3 #6981	1	0
6982	3	132,378,415	132,379,544	1,129	2	10.771	12.629	19	21	2	1	2	ACAD11, UBA5	-4, 5689	upstream, in gene	ActReg chr3 #6982	1	1
6983	3	133,524,373	133,524,991	618	1	10.105	14.263	16	24	1	0	1	SRPRB	21,805	in gene	ActReg chr3 #6983	0	1
6984	3	133,663,528	133,664,510	982	1	6.633	12.1	12	19	0	0	1	SLCO2A1	84,901	in gene	ActReg chr3 #6984	0	1
6985	3	134,034,291	134,034,956	665	1	11.333	9.762	20	15	0	0	0				ActReg chr3 #6985	1	0
6986	3	134,145,978	134,146,727	749	1	14.458	12.333	27	21	0	1	1	LOC100507224	-4,947	upstream	ActReg chr3 #6986	1	0
6987	3	134,204,167	134,205,505	1,338	2	10.095	16.286	22	31	1	2	2	ANAPC13, CEP63	29, 261	in gene, in gene	ActReg chr3 #6987	1	1
6988	3	134,513,409	134,514,680	1,271	1	12.462	8	17	12	1	1	1	EPHB1	-55	upstream	ActReg chr3 #6988	1	0
6989	3	134,825,003	134,825,934	931	2	16.241	17.31	41	34	0	0	1	EPHB1	311,369	in gene	ActReg chr3 #6989	1	1
6990	3	134,843,650	134,844,530	880	2	11.556	12.778	23	23	0	0	1	EPHB1	329,991	in gene	ActReg chr3 #6990	1	1
6991	3	135,471,433	135,472,338	905	2	13	17.607	30	37	0	0	0				ActReg chr3 #6991	1	1
6992	3	135,683,986	135,685,333	1,347	3	9.262	9.905	19	17	1	1	1	PPP2R3A	144	in gene	ActReg chr3 #6992	1	1
6993	3	135,689,419	135,690,130	711	1	8.091	11.5	15	19	0	0	1	PPP2R3A	5,259	in gene	ActReg chr3 #6993	0	1
6994	3	135,914,042	135,914,691	649	1	8.857	12.143	15	21	1	1	1	MSL2	322	in gene	ActReg chr3 #6994	0	1
6995	3	135,914,817	135,916,104	1,287	2	11.55	12.7	22	19	1	1	1	MSL2	-772	upstream	ActReg chr3 #6995	1	1
6996	3	135,968,996	135,969,663	667	1	11.2	10.35	19	17	1	1	1	PCCB	162	in gene	ActReg chr3 #6996	1	0
6997	3	136,537,745	136,539,588	1,843	2	13.983	16.862	24	31	1	1	1	TMEM22	805	in gene	ActReg chr3 #6997	1	1
6998	3	136,580,743	136,581,462	719	1	8.045	11.954	13	19	1	2	3	TMEM22, LOC100507239, NCK1	43241, -200, 52	downstream, upstream, in gene	ActReg chr3 #6998	0	1
6999	3	137,833,803	137,834,737	934	2	10.517	14.034	16	22	1	1	2	DZIP1L, A4GNT	181, 16959	in gene, downstream	ActReg chr3 #6999	1	1
7000	3	137,905,923	137,907,155	1,232	1	8.105	13.184	14	22	1	1	1	ARMC8	391	in gene	ActReg chr3 #7000	0	1
7001	3	138,066,588	138,067,716	1,128	2	9.629	11.944	19	18	1	1	1	MRAS	527	in gene	ActReg chr3 #7001	1	1
7002	3	138,312,722	138,313,741	1,019	1	8.688	11.031	14	15	1	1	1	CEP70	-102	upstream	ActReg chr3 #7002	0	1
7003	3	138,327,194	138,328,010	816	1	10.039	13.423	15	23	1	1	1	FAIM	60	in gene	ActReg chr3 #7003	0	1
7004	3	138,552,358	138,553,782	1,424	2	11.159	14.296	23	26	1	0	0				ActReg chr3 #7004	1	1
7005	3	139,019,890	139,020,697	807	1	8	14.6	11	28	0	0	0				ActReg chr3 #7005	0	1
7006	3	139,048,013	139,048,584	571	1	9.222	10.333	17	19	0	0	0				ActReg chr3 #7006	0	1
7007	3	139,483,717	139,484,267	550	1	11.177	8.941	16	18	0	0	0				ActReg chr3 #7007	1	0
7008	3	139,516,391	139,517,116	725	2	12.454	13.364	24	29	0	0	0				ActReg chr3 #7008	1	1
7009	3	139,925,382	139,926,027	645	1	10.05	8.75	23	15	0	0	1	CLSTN2	271,677	in gene	ActReg chr3 #7009	1	0
7010	3	140,011,570	140,012,451	881	1	7.929	8.929	14	15	0	0	1	CLSTN2	357,983	in gene	ActReg chr3 #7010	0	1
7011	3	140,348,627	140,349,642	1,015	2	10.625	12.781	15	22	0	0	0				ActReg chr3 #7011	1	1
7012	3	140,660,463	140,660,964	501	1	10.125	8.312	13	11	1	1	1	SLC25A36	51	in gene	ActReg chr3 #7012	1	0
7013	3	140,958,925	140,959,579	654	1	6.05	10.85	10	16	0	0	1	ACPL2	8,570	in gene	ActReg chr3 #7013	0	1
7014	3	141,021,119	141,021,972	853	2	10.741	12.556	16	22	0	0	1	ACPL2	70,863	downstream	ActReg chr3 #7014	1	1
7015	3	141,030,244	141,031,097	853	1	9.115	13.692	14	24	1	0	0				ActReg chr3 #7015	0	1
7016	3	141,054,275	141,054,863	588	1	6.5	11.222	8	18	0	0	1	ZBTB38	11,514	in gene	ActReg chr3 #7016	0	1
7017	3	141,085,851	141,087,890	2,039	4	9.984	10.312	18	18	0	0	1	ZBTB38	43,815	in gene	ActReg chr3 #7017	1	1
7018	3	141,206,167	141,206,895	728	1	8.652	10.043	12	13	1	1	1	RASA2	605	in gene	ActReg chr3 #7018	0	1
7019	3	141,456,688	141,458,070	1,382	2	12.463	13.628	23	26	1	1	1	RNF7	328	in gene	ActReg chr3 #7019	1	1
7020	3	141,658,694	141,659,627	933	2	9.241	11.517	21	16	0	0	1	TFDP2	209,226	downstream	ActReg chr3 #7020	1	1
7021	3	141,867,573	141,868,406	833	1	7.731	10.769	11	14	1	1	2	TFDP2, GK5	397, 76460	in gene, downstream	ActReg chr3 #7021	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7022	3	142,297,084	142,298,104	1,020	2	18.875	20.031	49	53	1	1	1	ATR	74	in gene	ActReg chr3 #7022	1	1
7023	3	142,314,698	142,315,551	853	1	11.692	13.115	17	19	1	1	1	PLS1	-105	upstream	ActReg chr3 #7023	0	1
7024	3	142,606,768	142,607,367	599	1	7.632	10.684	12	15	1	1	1	PCOLCE2	978	in gene	ActReg chr3 #7024	0	1
7025	3	142,614,883	142,615,578	695	1	8	12.381	13	18	0	1	1	PCOLCE2	-7,185	upstream	ActReg chr3 #7025	0	1
7026	3	142,695,413	142,695,880	467	1	10.8	9.733	17	14	0	0	0				ActReg chr3 #7026	1	0
7027	3	142,719,653	142,721,030	1,377	2	15.233	15.465	38	42	1	2	2	LOC100289361, SR140	-32, -31	upstream, upstream	ActReg chr3 #7027	1	1
7028	3	143,161,304	143,161,951	647	1	6.3	12.95	10	19	0	0	1	SLC9A9	405,746	in gene	ActReg chr3 #7028	0	1
7029	3	143,405,341	143,406,050	709	2	11.435	9.857	22	16	0	0	1	SLC9A9	161,678	in gene	ActReg chr3 #7029	1	1
7030	3	143,689,620	143,690,154	534	2	10.471	9.176	15	14	1	1	1	C3orf58	-753	upstream	ActReg chr3 #7030	1	1
7031	3	143,690,600	143,692,352	1,752	4	10.036	10.382	16	19	1	1	1	C3orf58	836	in gene	ActReg chr3 #7031	1	1
7032	3	145,849,706	145,850,223	517	1	5.25	10.875	7	16	0	0	1	PLOD2	29,318	in gene	ActReg chr3 #7032	0	1
7033	3	145,968,296	145,968,951	655	1	6.15	10	10	19	1	1	1	PLSCR4	343	in gene	ActReg chr3 #7033	0	1
7034	3	146,221,500	146,222,152	652	1	11.286	9.286	18	13	0	0	1	PLSCR2	-8,104	upstream	ActReg chr3 #7034	1	0
7035	3	147,987,640	147,988,122	482	1	8.067	11.6	11	14	0	0	0				ActReg chr3 #7035	0	1
7036	3	148,728,314	148,728,905	591	1	10.947	8.474	16	14	0	0	1	GYG1	19,414	in gene	ActReg chr3 #7036	1	0
7037	3	148,803,781	148,804,893	1,112	1	8.971	12.765	14	21	1	1	1	HLTF	4	in gene	ActReg chr3 #7037	0	1
7038	3	148,847,058	148,847,981	923	1	9.138	13.655	17	23	1	1	1	HPS3	148	in gene	ActReg chr3 #7038	0	1
7039	3	148,897,665	148,898,375	710	1	8.227	13.636	13	19	0	0	2	HPS3, CP	50649, 41812	downstream, in gene	ActReg chr3 #7039	0	1
7040	3	149,104,059	149,105,065	1,006	1	12.219	9.781	19	17	0	0	1	TM4SF1	-8,994	upstream	ActReg chr3 #7040	1	0
7041	3	149,375,261	149,376,290	1,029	1	12.091	9.636	16	15	1	0	1	WWTR1	45,285	in gene	ActReg chr3 #7041	1	0
7042	3	149,395,944	149,396,702	758	2	9.957	13.261	17	23	0	0	1	WWTR1	24,737	in gene	ActReg chr3 #7042	1	1
7043	3	149,469,911	149,470,591	680	2	11.381	11.714	20	21	1	1	2	COMMD2, C3orf16	35, 40359	in gene, downstream	ActReg chr3 #7043	1	1
7044	3	149,530,505	149,532,216	1,711	2	10.283	12.34	16	21	1	1	1	RNF13	885	in gene	ActReg chr3 #7044	1	1
7045	3	149,688,732	149,689,595	863	2	8.704	11.556	16	18	1	2	4	RNF13, PFN2, LOC646903, TMEM183B	158688, -422, 97, 11990	downstream, upstream, in gene, downstream	ActReg chr3 #7045	1	1
7046	3	149,812,039	149,812,703	664	1	7.6	11.55	10	19	0	0	0				ActReg chr3 #7046	0	1
7047	3	149,864,751	149,865,456	705	1	7.455	10	14	13	0	0	0				ActReg chr3 #7047	0	1
7048	3	150,125,989	150,127,347	1,358	2	11.571	10.667	17	17	1	1	1	TSC22D2	-120	upstream	ActReg chr3 #7048	1	1
7049	3	150,263,672	150,264,806	1,134	2	10.639	11.194	18	23	1	2	2	SERP1, EIF2A	189, -335	in gene, upstream	ActReg chr3 #7049	1	1
7050	3	150,320,604	150,321,831	1,227	2	11.436	13.949	22	26	1	1	1	SELT	151	in gene	ActReg chr3 #7050	1	1
7051	3	150,481,315	150,481,863	548	1	10.177	10.412	14	15	1	1	1	SIAH2	-326	upstream	ActReg chr3 #7051	0	1
7052	3	151,113,411	151,114,100	689	2	12.191	10.238	24	22	0	0	1	MED12L	309,079	in gene	ActReg chr3 #7052	1	1
7053	3	151,162,917	151,163,831	914	1	7.179	11.357	11	19	0	0	2	MED12L, IGSF10	358698, 13123	downstream, in gene	ActReg chr3 #7053	0	1
7054	3	151,693,999	151,694,515	516	1	9.812	9.125	16	16	0	0	0				ActReg chr3 #7054	1	0
7055	3	151,739,363	151,740,299	936	1	8.034	11.724	13	16	0	0	0				ActReg chr3 #7055	0	1
7056	3	151,976,106	151,976,789	683	1	13.095	8	23	13	0	0	2	hCG_1806964, MBNL1	10968, -9382	downstream, upstream	ActReg chr3 #7056	1	0
7057	3	151,984,195	151,984,992	797	1	7.76	11.48	11	19	0	2	2	hCG_1806964, MBNL1	2822, -1236	in gene, upstream	ActReg chr3 #7057	0	1
7058	3	151,986,680	151,987,311	631	1	6.85	11.2	10	16	1	2	2	hCG_1806964, MBNL1	420, 1166	in gene, in gene	ActReg chr3 #7058	0	1
7059	3	152,339,122	152,339,585	463	1	10.533	9.133	14	12	0	0	0				ActReg chr3 #7059	1	0
7060	3	152,436,677	152,437,518	841	2	10.615	9.385	14	15	0	0	0				ActReg chr3 #7060	1	1
7061	3	152,552,711	152,553,378	667	1	8.143	12.143	12	17	1	1	1	P2RY1	308	in gene	ActReg chr3 #7061	0	1
7062	3	152,878,090	152,880,350	2,260	2	11.971	14.671	27	29	1	1	1	RAP2B	-809	upstream	ActReg chr3 #7062	1	1
7063	3	153,066,444	153,066,835	391	1	10.833	8.917	15	13	0	0	0				ActReg chr3 #7063	1	0
7064	3	154,138,705	154,139,389	684	2	12.619	13.714	28	30	0	0	1	GPR149	8,457	in gene	ActReg chr3 #7064	1	1
7065	3	155,462,367	155,463,090	723	1	10.261	11.391	19	16	1	1	1	LOC100507556	-1,213	upstream	ActReg chr3 #7065	0	1
7066	3	155,588,757	155,589,522	765	1	9.125	10.625	12	14	1	1	1	GMPS	814	in gene	ActReg chr3 #7066	0	1
7067	3	156,252,919	156,253,513	594	1	8.737	9.895	12	18	0	0	2	KCNAB1, SSR3	414879, 19757	in gene, downstream	ActReg chr3 #7067	0	1
7068	3	156,391,560	156,392,871	1,311	2	12.805	14.293	27	29	1	2	2	LOC100287227, TIPARP	1287, 10	in gene, in gene	ActReg chr3 #7068	1	1
7069	3	156,505,826	156,506,543	717	2	10.546	12.273	20	20	0	0	1	LOC730091	28,639	in gene	ActReg chr3 #7069	1	1
7070	3	156,533,761	156,535,241	1,480	2	11.5	13.522	23	28	1	1	2	LOC730091, LEKR1	322, -9595	in gene, upstream	ActReg chr3 #7070	1	1
7071	3	156,799,277	156,799,936	659	1	7.714	10.476	11	17	0	0	2	LOC339894, LOC100498859	41185, -8064	in gene, upstream	ActReg chr3 #7071	0	1
7072	3	156,806,619	156,807,332	713	1	8.739	13.609	14	24	1	1	2	LOC339894, LOC100498859	33816, -695	in gene, upstream	ActReg chr3 #7072	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7073	3	156,845,803	156,846,562	759	1	10.25	13.125	17	25	0	1	1	LOC339894	-5,391	upstream	ActReg chr3 #7073	0	1
7074	3	156,877,623	156,878,465	842	2	16.63	14.852	35	28	1	1	1	CCNL1	438	in gene	ActReg chr3 #7074	1	1
7075	3	156,892,409	156,893,325	916	2	11.034	14.414	24	28	1	0	0				ActReg chr3 #7075	1	1
7076	3	156,966,492	156,967,000	508	1	9.125	12.875	14	18	0	0	0				ActReg chr3 #7076	0	1
7077	3	157,772,849	157,773,508	659	1	10.809	10.048	21	20	0	0	0				ActReg chr3 #7077	1	0
7078	3	157,827,496	157,828,587	1,091	2	19.235	18.559	40	49	1	2	2	SHOX2, RSRC1	-4089, 149	upstream, in gene	ActReg chr3 #7078	1	1
7079	3	157,845,668	157,845,964	296	1	10.333	12.444	14	17	0	0	1	RSRC1	17,924	in gene	ActReg chr3 #7079	0	1
7080	3	158,288,556	158,289,173	617	1	5.789	12.421	9	19	1	1	1	MLF1	-89	upstream	ActReg chr3 #7080	0	1
7081	3	158,361,808	158,362,882	1,074	2	48.706	53.235	180	177	1	1	1	GFM1	28	in gene	ActReg chr3 #7081	1	1
7082	3	158,800,280	158,800,771	491	1	8.688	8.375	13	14	0	0	1	IQCJ	13,408	in gene	ActReg chr3 #7082	0	1
7083	3	158,846,114	158,846,754	640	1	7.7	11.95	15	19	0	0	1	IQCJ	59,317	in gene	ActReg chr3 #7083	0	1
7084	3	158,991,261	158,991,859	598	2	11.895	10.579	25	20	0	1	2	IQCJ, SCHIP1	204443, 16	downstream, in gene	ActReg chr3 #7084	1	1
7085	3	159,482,455	159,483,829	1,374	2	11.279	11.674	20	21	1	0	1	SCHIP1	491,596	in gene	ActReg chr3 #7085	1	1
7086	3	159,847,201	159,848,228	1,027	1	4.938	10.781	9	19	0	0	0				ActReg chr3 #7086	0	1
7087	3	160,097,922	160,098,567	645	1	8.25	11.75	13	19	0	0	1	IFT80	19,076	in gene	ActReg chr3 #7087	0	1
7088	3	160,117,162	160,118,331	1,169	1	7.639	12.083	18	23	1	4	4	IFT80, SMC4, MIR15B, MIR16-2	-426, 316, -4630, -4787	upstream, in gene, upstream, upstream	ActReg chr3 #7088	0	1
7089	3	160,213,761	160,214,268	507	1	2.385	10.267	4	17	0	1	2	LOC100507647, KPNA4	1698, 69362	in gene, downstream	ActReg chr3 #7089	0	1
7090	3	160,472,090	160,473,578	1,488	2	16.277	21.83	42	53	1	1	1	PPM1L	-1,162	upstream	ActReg chr3 #7090	1	1
7091	3	162,108,758	162,109,138	380	1	5.667	11.5	8	18	0	0	0				ActReg chr3 #7091	0	1
7092	3	167,813,308	167,813,889	581	1	6.053	11	10	21	1	1	1	GOLIM4	-181	upstream	ActReg chr3 #7092	0	1
7093	3	167,967,112	167,968,195	1,083	1	7.059	10.941	10	19	1	1	1	C3orf50	343	in gene	ActReg chr3 #7093	0	1
7094	3	167,990,218	167,990,672	454	1	9.643	7.714	16	12	0	0	1	C3orf50	23,135	in gene	ActReg chr3 #7094	1	0
7095	3	169,939,699	169,940,409	710	2	15.591	17	32	36	1	1	1	PRKCI	-166	upstream	ActReg chr3 #7095	1	1
7096	3	170,302,253	170,302,895	642	2	11.65	12	21	20	1	1	1	SLC7A14	1,289	in gene	ActReg chr3 #7096	1	1
7097	3	170,310,519	170,310,957	438	1	8.857	10.571	12	15	0	1	1	SLC7A14	-6,875	upstream	ActReg chr3 #7097	0	1
7098	3	172,167,106	172,168,086	980	2	16.167	13.967	25	30	1	1	1	GHSR	-1,350	upstream	ActReg chr3 #7098	1	1
7099	3	172,428,479	172,429,271	792	2	12.24	12.56	28	23	1	2	2	NCEH1, LOC100505528	133, 1088	in gene, in gene	ActReg chr3 #7099	1	1
7100	3	172,468,200	172,468,629	429	1	10.462	5.692	16	8	1	1	1	ECT2	-3,885	upstream	ActReg chr3 #7100	1	0
7101	3	173,115,355	173,115,901	546	1	9.353	3.529	17	6	1	1	1	NLGN1	-616	upstream	ActReg chr3 #7101	1	0
7102	3	177,077,483	177,078,164	681	2	12.762	8.81	23	16	0	0	0				ActReg chr3 #7102	1	1
7103	3	178,402,510	178,403,264	754	2	11.292	11.167	23	25	0	0	1	KCNMB2	148,663	in gene	ActReg chr3 #7103	1	1
7104	3	178,408,266	178,408,707	441	1	9	9.571	15	14	0	0	1	KCNMB2	154,262	in gene	ActReg chr3 #7104	0	1
7105	3	180,707,124	180,707,654	530	1	9.412	8.235	18	14	1	1	2	FXR1, DNAJC19	77155, 173	downstream, in gene	ActReg chr3 #7105	1	0
7106	3	181,034,408	181,034,848	440	1	10.714	6.846	14	13	0	0	0				ActReg chr3 #7106	1	0
7107	3	181,900,251	181,900,844	593	1	6.526	9.474	13	22	0	0	0				ActReg chr3 #7107	0	1
7108	3	182,816,705	182,817,620	915	1	5.071	10.893	8	17	1	1	1	MCCC1	203	in gene	ActReg chr3 #7108	0	1
7109	3	183,602,391	183,603,108	717	2	10.13	11.913	19	23	1	1	1	PARL	-56	upstream	ActReg chr3 #7109	1	1
7110	3	183,852,750	183,853,562	812	2	9.88	11.52	23	14	1	1	1	EIF2B5	346	in gene	ActReg chr3 #7110	1	1
7111	3	183,892,456	183,893,036	580	1	7.833	9.778	14	17	1	1	2	DVL3, AP2M1	19462, 112	downstream, in gene	ActReg chr3 #7111	0	1
7112	3	183,966,340	183,967,047	707	1	11.636	9.682	22	15	0	2	5	VWA5B2, MIR1224, ALG3, ECE2, CAMK2N2	18376, 7500, 620, -752, 12558	downstream, downstream, in gene, upstream, downstream	ActReg chr3 #7112	1	0
7113	3	184,267,583	184,268,121	538	1	4.294	10.823	8	16	0	0	0				ActReg chr3 #7113	0	1
7114	3	184,279,361	184,279,943	582	1	5.944	9.556	10	15	1	1	1	EPHB3	65	in gene	ActReg chr3 #7114	0	1
7115	3	184,893,224	184,893,726	502	1	7.333	10	9	15	0	0	0				ActReg chr3 #7115	0	1
7116	3	185,216,448	185,217,136	688	1	10.591	10.5	20	16	1	1	2	TMEM41A, LIPH	53, 53577	in gene, downstream	ActReg chr3 #7116	1	0
7117	3	185,826,731	185,827,333	602	2	11.79	10.158	21	13	1	1	1	ETV5	-131	upstream	ActReg chr3 #7117	1	1
7118	3	185,938,097	185,938,455	358	1	4.545	11	7	16	0	0	1	DGKG	141,747	in gene	ActReg chr3 #7118	0	1
7119	3	186,025,244	186,025,914	670	2	12.238	9.143	26	16	0	0	1	DGKG	54,444	in gene	ActReg chr3 #7119	1	1
7120	3	186,284,665	186,285,327	662	1	11.191	7.619	16	12	1	1	2	TBCCD1, DNAJB11	3336, -3471	in gene, upstream	ActReg chr3 #7120	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7121	3	186,501,044	186,501,620	576	1	6.611	10.333	9	15	1	5	6	EIF4A2, SNORD2, SNORA81, SNORA63, SNORA4, RFC4	-29, -1253, -3132, -3756, -4070, 23152	upstream, upstream, upstream, upstream, upstream, downstream	ActReg chr3 #7121	0	1
7122	3	186,523,959	186,524,789	830	1	8.615	13.269	17	21	1	1	1	RFC4	110	in gene	ActReg chr3 #7122	0	1
7123	3	187,387,259	187,388,019	760	2	11.958	15.375	21	31	1	1	1	SST	562	in gene	ActReg chr3 #7123	1	1
7124	3	187,463,055	187,463,869	814	2	11.952	11	23	22	0	1	1	BCL6	51	in gene	ActReg chr3 #7124	1	1
7125	3	187,770,107	187,770,674	567	2	8	12.389	14	21	0	0	0				ActReg chr3 #7125	1	1
7126	3	190,231,164	190,231,866	702	1	6.636	10.5	11	13	1	1	1	IL1RAP	-325	upstream	ActReg chr3 #7126	0	1
7127	3	190,303,633	190,304,088	455	1	10.286	7.143	16	10	0	0	1	IL1RAP	72,020	in gene	ActReg chr3 #7127	1	0
7128	3	190,557,951	190,558,404	453	1	6.733	10.467	13	17	0	0	0				ActReg chr3 #7128	0	1
7129	3	191,905,349	191,905,932	583	1	5.167	10.111	10	17	0	0	1	FGF12	539,748	in gene	ActReg chr3 #7129	0	1
7130	3	192,675,168	192,675,732	564	1	5.5	10.222	7	15	0	0	0				ActReg chr3 #7130	0	1
7131	3	193,310,549	193,311,297	748	2	11.083	12.75	25	26	1	1	1	OPA1	-10	upstream	ActReg chr3 #7131	1	1
7132	3	193,587,042	193,587,577	535	1	11.562	9.688	15	12	1	0	0				ActReg chr3 #7132	1	0
7133	3	193,601,356	193,601,874	518	1	10.688	6.438	14	10	0	0	0				ActReg chr3 #7133	1	0
7134	3	193,721,034	193,721,852	818	2	12.92	10	20	20	1	1	2	LOC647323, LOC100505902	5, 67298	in gene, downstream	ActReg chr3 #7134	1	1
7135	3	193,852,546	193,853,204	658	1	11.45	6.45	19	11	1	1	1	HES1	-1,059	upstream	ActReg chr3 #7135	1	0
7136	3	194,392,771	194,393,588	817	2	13.52	11.56	28	20	1	1	1	LSG1	27	in gene	ActReg chr3 #7136	1	1
7137	3	194,461,371	194,461,979	608	1	7.474	9.579	12	16	0	0	1	LOC100507391	32,525	in gene	ActReg chr3 #7137	0	1
7138	3	194,707,152	194,707,733	581	1	9.778	6.278	15	11	0	0	0				ActReg chr3 #7138	1	0
7139	3	194,991,671	194,992,480	809	2	11.346	12.192	20	26	1	1	2	C3orf21, ACAP2	-180, 171742	upstream, downstream	ActReg chr3 #7139	1	1
7140	3	196,006,245	196,006,692	447	1	10.929	4.714	18	8	0	0	1	PCYT1A	8,116	in gene	ActReg chr3 #7140	1	0
7141	3	196,668,944	196,669,627	683	1	6.952	11.286	10	17	1	2	4	SENP5, NCBP2, LOC152217, PIGZ	74558, 179, 209, 26419	downstream, in gene, upstream, downstream	ActReg chr3 #7141	0	1
7142	3	196,755,245	196,755,831	586	1	6.222	11.5	9	18	1	1	1	MFI2	1,149	in gene	ActReg chr3 #7142	0	1
7143	3	196,756,352	196,758,893	541	1	11.941	9.176	21	16	0	1	1	MFI2	-1,935	upstream	ActReg chr3 #7143	1	0
7144	3	197,281,542	197,282,326	784	1	7.042	9.833	11	15	1	0	1	BDH1	18,260	in gene	ActReg chr3 #7144	0	1
7145	4	52,648	55,108	2,460	2	13.714	15.649	34	35	1	1	1	ZNF595	651	in gene	ActReg chr4 #7145	1	1
7146	4	206,135	206,673	538	1	9.706	7.294	16	12	1	0	0				ActReg chr4 #7146	1	0
7147	4	467,242	468,203	961	1	9.2	12.567	16	19	1	0	1	ZNF721	25,720	in gene	ActReg chr4 #7147	0	1
7148	4	492,672	493,365	693	2	11.046	11.546	25	19	1	2	2	ZNF721, PIGG	424, 29	in gene, in gene	ActReg chr4 #7148	1	1
7149	4	575,282	575,933	651	1	6.95	10.95	10	18	0	0	0				ActReg chr4 #7149	0	1
7150	4	667,916	668,808	892	1	9.857	9.964	16	16	1	2	4	PDE6B, ATP5I, MYL5, MFSD7	48999, -235, -3349, 14611	downstream, upstream, upstream, downstream	ActReg chr4 #7150	0	1
7151	4	774,872	775,709	837	1	8	11.039	14	18	1	1	2	LOC100129917, CPLX1	346, 44655	in gene, downstream	ActReg chr4 #7151	0	1
7152	4	925,533	926,263	730	1	9.609	12.957	16	19	1	2	2	GAK, TMEM175	276, -364	in gene, upstream	ActReg chr4 #7152	0	1
7153	4	980,480	981,349	869	1	5.786	11.036	11	15	2	1	2	SLC26A1, IDUA	6310, 129	in gene, in gene	ActReg chr4 #7153	0	1
7154	4	1,037,083	1,037,945	862	2	14.593	14	30	27	0	0	0				ActReg chr4 #7154	1	1
7155	4	1,075,794	1,076,487	693	1	11.773	10.864	18	18	0	0	1	RNF212	31,442	in gene	ActReg chr4 #7155	1	0
7156	4	1,340,233	1,341,021	788	2	9.917	15.833	16	29	1	1	2	MAEA, KIAA1530	56955, -477	downstream, upstream	ActReg chr4 #7156	1	1
7157	4	1,403,421	1,405,819	2,398	2	20.507	27.493	91	119	1	1	1	NKX1-1	-4,501	upstream	ActReg chr4 #7157	1	1
7158	4	1,713,927	1,715,034	1,107	2	12.706	13.823	20	19	1	1	3	SLBP, TMEM129, TACC3	-450, 8604, 8786	upstream, downstream, upstream	ActReg chr4 #7158	1	1
7159	4	1,716,012	1,716,983	971	2	17.567	18.1	50	39	0	2	3	SLBP, TMEM129, TACC3	-2467, 6587, -6769	upstream, downstream, upstream	ActReg chr4 #7159	1	1
7160	4	1,857,671	1,858,603	932	2	12.862	13.966	24	29	1	1	1	LETM1	-163	upstream	ActReg chr4 #7160	1	1
7161	4	2,010,277	2,010,982	705	1	9.545	11.773	13	21	1	1	1	WHSC2	330	in gene	ActReg chr4 #7161	0	1
7162	4	2,243,407	2,244,178	771	1	7.25	12.875	13	21	1	1	2	HAUS3, MXD4	68, 19947	in gene, downstream	ActReg chr4 #7162	0	1
7163	4	2,414,978	2,415,616	638	1	5.895	9.3	13	16	0	1	2	ZFYVE28, LOC402160	5073, -5404	in gene, upstream	ActReg chr4 #7163	0	1
7164	4	2,845,125	2,845,618	493	1	12.267	9.867	20	14	1	1	2	SH3BP2, ADD1	50621, -213	downstream, upstream	ActReg chr4 #7164	1	0
7165	4	2,936,463	2,937,064	601	1	8.316	13.421	15	21	1	2	4	ADD1, MFSD10, C4orf10, NOP14	91179, -177, -510, 28355	downstream, upstream, upstream, downstream	ActReg chr4 #7165	0	1
7166	4	2,964,411	2,965,591	1,180	1	10.324	13.135	15	23	1	2	2	NOP14, GRK4	117, -342	in gene, upstream	ActReg chr4 #7166	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7167	4	3,793,381	3,794,281	900	1	12.679	15.5	26	29	0	0	0				ActReg chr4 #7167	0	1
7168	4	3,956,289	3,956,990	701	1	11	5.81	18	13	1	0	0				ActReg chr4 #7168	1	0
7169	4	4,249,337	4,250,399	1,062	2	9.545	11.97	17	21	1	2	2	TMEM128, LOC100507225	66, 2387	in gene, downstream	ActReg chr4 #7169	1	1
7170	4	4,543,379	4,544,204	825	2	15.654	16.308	38	36	1	2	2	STX18, LOC100507266	-16, -67	upstream, upstream	ActReg chr4 #7170	1	1
7171	4	4,992,509	4,993,711	1,202	2	10.105	11.763	18	25	0	0	0				ActReg chr4 #7171	1	1
7172	4	5,039,583	5,040,161	578	1	10.316	8.158	18	13	0	0	0				ActReg chr4 #7172	1	0
7173	4	5,207,834	5,208,720	886	1	12.321	8.607	19	15	0	0	1	STK32B	154,750	in gene	ActReg chr4 #7173	1	0
7174	4	5,221,687	5,222,201	514	1	9.938	13	17	25	0	0	1	STK32B	168,417	in gene	ActReg chr4 #7174	0	1
7175	4	5,339,992	5,340,606	616	2	9.2	10	16	15	0	0	1	STK32B	286,773	in gene	ActReg chr4 #7175	1	1
7176	4	5,367,264	5,367,967	703	1	9.227	12.773	18	21	0	0	1	STK32B	314,088	in gene	ActReg chr4 #7176	0	1
7177	4	5,713,865	5,714,983	1,118	1	7	11.029	11	16	0	2	2	EVC2, EVC	-3149, 1500	upstream, in gene	ActReg chr4 #7177	0	1
7178	4	5,882,559	5,883,606	1,047	1	6.182	13.97	13	32	0	0	2	CRMP1, LOC100507292	11703, 8876	in gene, in gene	ActReg chr4 #7178	0	1
7179	4	6,226,834	6,227,693	859	2	12.444	9.222	28	15	0	0	1	LOC285484	24,803	in gene	ActReg chr4 #7179	1	1
7180	4	6,345,518	6,346,142	624	1	12.947	9.684	22	16	0	0	1	PPP2R2C	128,496	in gene	ActReg chr4 #7180	1	0
7181	4	6,364,025	6,365,166	1,141	2	12.611	17.889	32	48	0	0	1	PPP2R2C	109,731	in gene	ActReg chr4 #7181	1	1
7182	4	6,479,527	6,480,146	619	1	7.211	9.842	13	15	0	1	1	PPP2R2C	-5,510	upstream	ActReg chr4 #7182	0	1
7183	4	6,576,459	6,577,332	873	1	12.667	7.444	19	10	1	1	1	MAN2B2	-7	upstream	ActReg chr4 #7183	1	0
7184	4	6,710,810	6,711,445	635	1	7.9	11.15	11	21	1	2	2	MRFAP1L1, CNO	479, -6715	in gene, upstream	ActReg chr4 #7184	0	1
7185	4	6,717,512	6,718,640	1,128	2	12.829	11.771	21	22	1	2	2	MRFAP1L1, CNO	-6470, 234	upstream, in gene	ActReg chr4 #7185	1	1
7186	4	6,728,560	6,729,344	784	1	3.88	11.48	6	18	1	0	1	CNO	11,110	downstream	ActReg chr4 #7186	0	1
7187	4	6,910,764	6,911,493	729	2	11.609	14.565	23	33	1	1	1	TBC1D14	-43	upstream	ActReg chr4 #7187	1	1
7188	4	6,917,831	6,918,971	1,140	2	12.914	13.429	19	28	0	0	1	TBC1D14	7,230	in gene	ActReg chr4 #7188	1	1
7189	4	6,988,532	6,989,544	1,012	2	16.125	12.719	27	20	1	0	1	TBC1D14	77,867	in gene	ActReg chr4 #7189	1	1
7190	4	7,069,062	7,069,978	916	1	10.357	12.143	21	19	1	1	2	TADA2B, GRPEL1	24364, 280	downstream, in gene	ActReg chr4 #7190	0	1
7191	4	7,207,926	7,208,996	1,070	2	10.323	10	17	14	0	0	1	SORCS2	14,087	in gene	ActReg chr4 #7191	1	1
7192	4	7,297,153	7,297,894	741	1	13.217	6.304	20	10	0	0	1	SORCS2	103,149	in gene	ActReg chr4 #7192	1	0
7193	4	7,651,098	7,652,058	960	1	12.433	14.5	19	27	0	0	1	SORCS2	457,204	in gene	ActReg chr4 #7193	0	1
7194	4	7,738,280	7,739,561	1,281	2	11.25	20.175	40	56	0	0	1	SORCS2	544,546	in gene	ActReg chr4 #7194	1	1
7195	4	7,940,532	7,941,648	1,116	2	12.286	15.486	22	24	1	1	1	AFAP1	563	in gene	ActReg chr4 #7195	1	1
7196	4	7,957,821	7,958,709	888	2	11.464	12.464	20	21	0	0	1	ABLIM2	202,294	downstream	ActReg chr4 #7196	1	1
7197	4	8,429,756	8,430,514	758	1	12.333	8.417	20	17	1	0	1	ACOX3	12,317	in gene	ActReg chr4 #7197	1	0
7198	4	8,442,089	8,442,964	875	2	10.037	10.556	16	16	1	2	2	ACOX3, C4orf23	-74, -6	upstream, upstream	ActReg chr4 #7198	1	1
7199	4	8,540,326	8,541,075	749	1	9.478	12.217	18	19	0	0	0				ActReg chr4 #7199	0	1
7200	4	8,676,910	8,678,055	1,145	2	10.833	14.389	24	33	0	0	0				ActReg chr4 #7200	1	1
7201	4	11,166,626	11,167,028	402	1	5.917	10.5	8	16	0	0	0				ActReg chr4 #7201	0	1
7202	4	11,368,883	11,369,603	720	2	10.391	11.174	19	17	0	2	2	MIR572, LOC643446	-1208, -1292	upstream, upstream	ActReg chr4 #7202	1	1
7203	4	11,545,201	11,545,795	594	1	9.316	9.895	16	18	0	0	0				ActReg chr4 #7203	0	1
7204	4	13,485,821	13,486,372	551	1	11.278	11.556	19	21	1	1	1	RAB28	-107	upstream	ActReg chr4 #7204	0	1
7205	4	13,629,138	13,629,763	625	1	12.15	9.45	22	13	1	1	1	BOD1L	-122	upstream	ActReg chr4 #7205	1	0
7206	4	13,641,684	13,642,367	683	2	12.238	10.667	23	24	0	0	0				ActReg chr4 #7206	1	1
7207	4	13,655,825	13,656,485	660	1	7.714	12.524	12	22	0	0	0				ActReg chr4 #7207	0	1
7208	4	13,703,368	13,703,863	495	1	8.133	11	13	17	0	0	0				ActReg chr4 #7208	0	1
7209	4	13,908,392	13,909,531	1,139	2	14.061	17.171	43	44	0	0	0				ActReg chr4 #7209	1	1
7210	4	13,922,349	13,923,119	770	2	12.5	12.833	23	28	0	0	0				ActReg chr4 #7210	1	1
7211	4	14,197,585	14,198,319	734	2	14.217	12.913	28	29	0	0	0				ActReg chr4 #7211	1	1
7212	4	14,857,981	14,858,560	579	1	9.368	11.21	18	17	0	0	0				ActReg chr4 #7212	0	1
7213	4	15,003,260	15,005,031	1,771	2	9.5	11.143	17	21	1	2	2	LOC441009, CPEB2	-181, -153	upstream, upstream	ActReg chr4 #7213	1	1
7214	4	15,563,697	15,564,374	677	1	11.381	12.857	17	24	0	0	1	CC2D2A	92,546	in gene	ActReg chr4 #7214	0	1
7215	4	15,682,767	15,683,896	1,129	1	9.171	13.257	14	19	1	1	1	LOC285550	-21	upstream	ActReg chr4 #7215	0	1
7216	4	15,696,711	15,697,699	988	2	12.129	10.613	19	20	0	1	2	LOC285550, BST1	13853, -7368	downstream, upstream	ActReg chr4 #7216	1	1
7217	4	15,922,714	15,923,559	845	2	12.518	10	23	21	0	0	0				ActReg chr4 #7217	1	1
7218	4	16,142,441	16,143,154	713	1	9.227	10.773	19	16	0	0	0				ActReg chr4 #7218	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7219	4	16,574,772	16,575,347	575	1	8.778	4.278	18	8	0	0	1	LDB2	325,365	in gene	ActReg chr4 #7219	1	0
7220	4	17,513,114	17,514,285	1,171	2	11.46	15.568	24	36	1	2	2	QDPR, CLRN2	158, -3089	in gene, upstream	ActReg chr4 #7220	1	1
7221	4	17,615,911	17,616,645	734	1	8.652	11.348	13	17	1	1	2	LAP3, MED28	37351, 5	downstream, in gene	ActReg chr4 #7221	0	1
7222	4	17,688,982	17,690,121	1,139	2	10.75	13.611	21	27	0	0	1	FAM184B	93,584	in gene	ActReg chr4 #7222	1	1
7223	4	17,692,245	17,693,071	826	2	12.423	14.5	24	29	0	0	1	FAM184B	90,477	in gene	ActReg chr4 #7223	1	1
7224	4	17,811,758	17,813,080	1,322	2	11.439	11.146	18	18	1	2	2	DCAF16, NCAPG	-38, -106	upstream, upstream	ActReg chr4 #7224	1	1
7225	4	18,023,331	18,024,182	851	2	12	11.231	17	22	1	1	1	LCORL	-273	upstream	ActReg chr4 #7225	1	1
7226	4	20,253,358	20,254,174	816	1	7.68	10.32	12	15	1	1	1	SLIT2	-1,469	upstream	ActReg chr4 #7226	0	1
7227	4	20,475,634	20,476,290	656	2	8.476	9.19	13	18	0	0	1	SLIT2	220,727	in gene	ActReg chr4 #7227	1	1
7228	4	20,880,266	20,881,098	832	2	16.423	13.846	38	33	0	0	1	KCNIP4	1,069,692	in gene	ActReg chr4 #7228	1	1
7229	4	21,014,693	21,015,506	813	1	8.8	11.12	15	16	0	0	1	KCNIP4	935,275	in gene	ActReg chr4 #7229	0	1
7230	4	21,889,946	21,890,560	614	1	6.05	11.3	11	16	0	0	1	KCNIP4	60,121	in gene	ActReg chr4 #7230	0	1
7231	4	21,901,967	21,902,403	436	1	8.786	3.286	13	5	0	0	1	KCNIP4	48,189	in gene	ActReg chr4 #7231	1	0
7232	4	22,171,901	22,172,408	507	1	10.625	7.786	16	11	0	0	0				ActReg chr4 #7232	1	0
7233	4	22,180,703	22,181,122	419	2	9.786	9.714	15	13	0	0	0				ActReg chr4 #7233	1	1
7234	4	23,325,749	23,326,567	818	1	6.692	12.577	12	20	0	0	0				ActReg chr4 #7234	0	1
7235	4	23,708,801	23,709,434	633	1	8.316	11	15	18	0	0	0				ActReg chr4 #7235	0	1
7236	4	23,729,989	23,730,619	630	2	7.526	12.368	15	22	0	0	0				ActReg chr4 #7236	1	1
7237	4	23,857,814	23,858,533	719	1	12.13	10.435	19	15	0	0	1	PPARGC1A	33,527	in gene	ActReg chr4 #7237	1	0
7238	4	23,946,966	23,947,688	722	1	9.957	5.348	14	9	0	0	0				ActReg chr4 #7238	1	0
7239	4	24,474,579	24,475,419	840	1	9.231	12.077	15	21	1	0	1	LOC729175	9,503	in gene	ActReg chr4 #7239	0	1
7240	4	24,585,752	24,586,513	761	1	8.167	12.333	13	18	1	1	1	DHX15	52	in gene	ActReg chr4 #7240	0	1
7241	4	24,770,656	24,772,272	1,616	1	9.196	11.902	16	20	0	0	0				ActReg chr4 #7241	0	1
7242	4	25,161,669	25,162,355	686	1	8.857	12.809	15	18	1	2	2	SEPSECS, LOC285540	192, -282	in gene, upstream	ActReg chr4 #7242	0	1
7243	4	25,174,839	25,175,672	833	1	7.269	13.769	18	25	0	0	1	LOC285540	12,961	in gene	ActReg chr4 #7243	0	1
7244	4	25,235,592	25,236,365	773	1	5.458	10.958	8	15	1	1	1	PI4K2B	325	in gene	ActReg chr4 #7244	0	1
7245	4	25,313,921	25,314,856	935	2	24.828	30.862	71	88	1	1	1	ZCCHC4	-8	upstream	ActReg chr4 #7245	1	1
7246	4	25,378,858	25,379,477	619	1	9.053	10.842	14	16	1	1	2	ZCCHC4, ANAPC4	64771, 319	downstream, in gene	ActReg chr4 #7246	0	1
7247	4	25,910,044	25,910,787	743	2	12.375	11.292	18	18	0	2	2	LOC100506024, C4orf52	-1953, -5399	upstream, upstream	ActReg chr4 #7247	1	1
7248	4	26,060,078	26,060,652	574	1	11.778	12	19	22	0	0	0				ActReg chr4 #7248	0	1
7249	4	26,067,375	26,068,027	652	1	15.55	12.35	28	23	0	0	0				ActReg chr4 #7249	1	0
7250	4	26,198,711	26,199,412	701	1	9.5	12.682	15	19	0	0	0				ActReg chr4 #7250	0	1
7251	4	26,320,602	26,322,749	2,147	3	12.552	12.638	26	36	2	1	1	RBPJ	343	in gene	ActReg chr4 #7251	1	1
7252	4	26,585,203	26,586,135	932	2	10.759	14.069	23	26	1	1	1	TBC1D19	123	in gene	ActReg chr4 #7252	1	1
7253	4	26,858,904	26,859,810	906	2	10	12.069	16	17	1	2	2	LOC100506048, STIM2	2864, -2956	downstream, upstream	ActReg chr4 #7253	1	1
7254	4	26,861,789	26,862,374	585	1	10.579	8.632	18	12	1	2	2	LOC100506048, STIM2	140, -232	in gene, upstream	ActReg chr4 #7254	1	0
7255	4	27,156,159	27,156,779	620	1	12.85	9.15	21	15	0	0	0				ActReg chr4 #7255	1	0
7256	4	27,218,883	27,219,566	683	1	8.19	11.191	14	20	0	0	0				ActReg chr4 #7256	0	1
7257	4	27,280,020	27,280,801	781	2	10.72	12.84	27	22	0	0	0				ActReg chr4 #7257	1	1
7258	4	27,351,678	27,352,362	684	2	11.182	9.545	18	15	0	0	0				ActReg chr4 #7258	1	1
7259	4	29,590,203	29,590,671	468	1	6.867	9.667	11	18	0	0	0				ActReg chr4 #7259	0	1
7260	4	29,719,291	29,719,787	496	1	9.75	7	15	12	0	0	0				ActReg chr4 #7260	1	0
7261	4	30,601,785	30,602,324	539	1	5.471	8.706	10	13	0	0	0				ActReg chr4 #7261	0	1
7262	4	30,718,965	30,719,450	485	1	5.6	10.8	9	15	1	1	1	PCDH7	-2,830	upstream	ActReg chr4 #7262	0	1
7263	4	31,463,115	31,463,515	400	1	9.25	10.167	13	16	0	0	0				ActReg chr4 #7263	0	1
7264	4	32,011,576	32,012,238	662	1	10.619	9.381	17	13	0	0	0				ActReg chr4 #7264	1	0
7265	4	32,849,029	32,849,581	552	2	11.353	10.471	22	18	0	0	0				ActReg chr4 #7265	1	1
7266	4	35,526,653	35,527,700	1,047	2	8.576	13.091	21	26	0	0	0				ActReg chr4 #7266	1	1
7267	4	36,717,960	36,719,053	1,093	2	9.147	14.029	19	29	0	0	0				ActReg chr4 #7267	1	1
7268	4	37,478,702	37,479,211	509	1	9.562	9.188	15	15	0	0	1	C4orf19	23,404	in gene	ActReg chr4 #7268	1	0
7269	4	37,630,496	37,631,084	588	1	8.632	11.21	17	23	0	0	1	RELL1	57,209	in gene	ActReg chr4 #7269	0	1
7270	4	37,649,561	37,650,295	734	1	7.364	14.478	14	27	0	0	1	RELL1	38,071	in gene	ActReg chr4 #7270	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7271	4	37,687,336	37,688,034	698	1	8.545	12.409	13	23	1	1	1	RELL1	314	in gene	ActReg chr4 #7271	0	1
7272	4	37,731,091	37,731,626	535	1	5.176	9.941	9	16	0	0	0				ActReg chr4 #7272	0	1
7273	4	37,827,877	37,828,614	737	1	11.391	7.652	14	12	1	1	1	PGM2	-37	upstream	ActReg chr4 #7273	1	0
7274	4	38,192,255	38,192,895	640	1	10.75	10.1	17	17	0	0	0				ActReg chr4 #7274	1	0
7275	4	38,622,275	38,622,953	678	1	7.905	11.524	12	17	0	0	1	FLJ13197	43,635	in gene	ActReg chr4 #7275	0	1
7276	4	38,753,482	38,754,167	685	1	5.833	11.714	9	19	0	0	0				ActReg chr4 #7276	0	1
7277	4	39,367,457	39,368,215	758	1	9.087	11.522	16	15	1	1	1	RFC1	159	in gene	ActReg chr4 #7277	0	1
7278	4	39,460,094	39,460,956	862	2	13.482	14.333	31	28	1	2	3	KLB, RPL9, LIAS	52052, 43, -140	downstream, in gene, upstream	ActReg chr4 #7278	1	1
7279	4	39,528,603	39,529,882	1,279	2	10.5	13.5	20	27	1	1	1	UGDH	-24	upstream	ActReg chr4 #7279	1	1
7280	4	39,640,628	39,641,541	913	1	9.483	9.517	15	14	1	1	1	C4orf34	-603	upstream	ActReg chr4 #7280	1	0
7281	4	39,979,214	39,979,991	777	2	18.792	17	45	42	1	1	1	PDS5A	-26	upstream	ActReg chr4 #7281	1	1
7282	4	40,057,378	40,058,041	663	2	11.7	11.3	17	19	1	1	1	N4BP2	-815	upstream	ActReg chr4 #7282	1	1
7283	4	40,256,614	40,257,492	878	2	10	12.074	18	21	0	0	0				ActReg chr4 #7283	1	1
7284	4	40,631,467	40,632,068	601	1	7.737	11.158	14	18	1	1	1	RBM47	116	in gene	ActReg chr4 #7284	0	1
7285	4	40,899,417	40,900,012	595	1	10.842	12.421	21	23	0	0	1	APBB2	316,921	in gene	ActReg chr4 #7285	0	1
7286	4	40,910,793	40,911,623	830	1	10.308	8.5	17	11	0	0	1	APBB2	305,427	in gene	ActReg chr4 #7286	1	0
7287	4	41,216,220	41,216,934	714	1	10.783	13.696	14	27	1	1	1	APBB2	58	in gene	ActReg chr4 #7287	0	1
7288	4	41,218,484	41,219,047	563	1	8	10.222	15	16	1	1	1	APBB2	-2,130	upstream	ActReg chr4 #7288	0	1
7289	4	41,736,305	41,736,872	567	1	9.278	9.944	16	15	0	0	1	PHOX2B	14,399	downstream	ActReg chr4 #7289	1	0
7290	4	41,992,150	41,992,947	797	1	9.48	12.76	21	20	1	1	2	DCAF4L1, SLC30A9	8835, 25	downstream, in gene	ActReg chr4 #7290	0	1
7291	4	42,658,979	42,659,939	960	2	14.633	15.733	37	27	1	1	1	ATP8A1	-337	upstream	ActReg chr4 #7291	1	1
7292	4	43,341,305	43,341,879	574	1	9.722	6	15	12	0	0	0				ActReg chr4 #7292	1	0
7293	4	44,680,193	44,680,859	666	1	8.15	11.2	13	20	1	1	1	GUF1	93	in gene	ActReg chr4 #7293	0	1
7294	4	47,465,229	47,465,874	645	1	8.6	12.6	13	22	1	1	1	COMMD8	125	in gene	ActReg chr4 #7294	0	1
7295	4	48,781,072	48,782,706	1,634	2	9.471	13.157	19	20	1	1	1	FRYL	427	in gene	ActReg chr4 #7295	1	1
7296	4	48,832,630	48,833,613	983	2	11.355	12.516	18	22	1	1	1	OCIAD1	61	in gene	ActReg chr4 #7296	1	1
7297	4	52,788,976	52,789,625	649	1	4.4	10.35	11	15	0	0	1	DCUN1D4	80,024	downstream	ActReg chr4 #7297	0	1
7298	4	53,578,378	53,579,047	669	1	5.905	12.191	10	16	1	2	2	KIAA0114, SNORA26	91, -704	in gene, upstream	ActReg chr4 #7298	0	1
7299	4	53,703,968	53,704,632	664	1	13.048	10	25	16	0	0	0				ActReg chr4 #7299	1	0
7300	4	54,231,287	54,232,577	1,290	2	9.39	11.951	19	20	1	1	1	SCFD2	310	in gene	ActReg chr4 #7300	1	1
7301	4	54,243,624	54,244,482	858	2	10.185	12.482	12	18	1	1	1	FIP1L1	233	in gene	ActReg chr4 #7301	1	1
7302	4	54,373,858	54,375,016	1,158	1	6.806	11.75	12	18	0	0	1	LNX1	83,287	in gene	ActReg chr4 #7302	0	1
7303	4	54,568,710	54,569,653	943	2	10.241	12.172	17	19	0	0	1	LOC100506444	7,113	in gene	ActReg chr4 #7303	1	1
7304	4	54,720,952	54,722,011	1,059	1	6.727	12.424	11	18	0	0	0				ActReg chr4 #7304	0	1
7305	4	54,853,964	54,854,572	608	1	9.474	6.789	18	12	0	0	0				ActReg chr4 #7305	1	0
7306	4	55,452,369	55,453,028	659	1	10.809	10.476	16	14	0	0	0				ActReg chr4 #7306	1	0
7307	4	56,261,560	56,262,542	982	2	7.161	11.387	16	22	1	1	2	LOC100506462, TMEM165	-10304, -39	upstream, upstream	ActReg chr4 #7307	1	1
7308	4	56,458,129	56,458,693	564	1	8.824	11.778	17	24	0	1	2	PDCL2, NMU	-32, 44054	upstream, downstream	ActReg chr4 #7308	0	1
7309	4	56,719,544	56,720,223	679	1	8.905	10.952	14	20	1	1	1	EXOC1	67	in gene	ActReg chr4 #7309	0	1
7310	4	56,814,589	56,815,797	1,208	1	8.789	11.395	18	19	1	1	1	CEP135	156	in gene	ActReg chr4 #7310	0	1
7311	4	56,914,660	56,915,241	581	1	8.278	11.389	11	19	1	0	0				ActReg chr4 #7311	0	1
7312	4	57,301,748	57,302,621	873	1	8.63	10.852	13	18	1	2	2	PPAT, PAICS	-339, 269	upstream, in gene	ActReg chr4 #7312	0	1
7313	4	57,397,621	57,398,261	640	1	8.65	11.1	15	15	0	1	2	ARL9, LOC100506564	26566, 1098	downstream, in gene	ActReg chr4 #7313	0	1
7314	4	57,774,120	57,775,062	942	2	11.207	11.103	17	18	1	1	1	REST	549	in gene	ActReg chr4 #7314	1	1
7315	4	57,775,207	57,775,757	550	1	11.706	9	16	16	1	1	1	REST	1,440	in gene	ActReg chr4 #7315	1	0
7316	4	57,886,875	57,887,386	511	1	10	9.562	17	14	0	0	2	POLR2B, IGFBP7	42021, 89409	in gene, downstream	ActReg chr4 #7316	0	1
7317	4	58,029,694	58,030,747	1,053	1	10.788	7.879	17	15	1	0	1	LOC255130	54,292	in gene	ActReg chr4 #7317	1	0
7318	4	58,276,081	58,277,022	941	1	7.793	14.207	14	24	0	0	0				ActReg chr4 #7318	0	1
7319	4	60,463,639	60,464,404	765	1	7.333	11.5	11	17	0	0	0				ActReg chr4 #7319	0	1
7320	4	71,553,815	71,554,485	670	1	13.381	7.19	20	10	1	1	1	UTP3	-46	upstream	ActReg chr4 #7320	1	0
7321	4	72,322,515	72,322,928	413	1	10	3.846	16	5	0	0	1	SLC4A4	269,718	in gene	ActReg chr4 #7321	1	0
7322	4	72,978,133	72,978,628	495	2	8.875	9.25	15	15	0	0	1	NPFFR2	80,859	in gene	ActReg chr4 #7322	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7323	4	73,935,210	73,935,856	646	1	7	11.3	11	21	1	1	2	COX18, ANKRD17	-61, 188969	upstream, downstream	ActReg chr4 #7323	0	1
7324	4	74,570,107	74,570,692	585	1	8.632	10.947	15	17	0	0	0				ActReg chr4 #7324	0	1
7325	4	74,974,686	74,975,711	1,025	1	7.188	12.594	11	23	0	0	1	CXCL2	-10,201	upstream	ActReg chr4 #7325	0	1
7326	4	75,023,419	75,024,026	607	2	8.105	10	14	18	1	1	1	MTHFD2L	-107	upstream	ActReg chr4 #7326	1	1
7327	4	75,607,739	75,608,287	548	1	6.882	11.529	9	19	0	0	0				ActReg chr4 #7327	0	1
7328	4	76,439,320	76,440,051	731	2	10.391	9.826	17	14	1	2	2	RCHY1, THAP6	-57, 31	upstream, in gene	ActReg chr4 #7328	1	1
7329	4	76,597,808	76,598,552	744	1	5.87	10.522	9	16	1	1	1	G3BP2	487	in gene	ActReg chr4 #7329	0	1
7330	4	77,068,964	77,069,900	936	2	9.034	9.31	20	19	1	1	2	NUP54, SCARB2	223, 65603	in gene, downstream	ActReg chr4 #7330	1	1
7331	4	77,625,330	77,625,764	434	1	4.357	10	5	14	0	0	1	SHROOM3	269,294	in gene	ActReg chr4 #7331	0	1
7332	4	77,997,082	77,997,601	519	1	8.412	12.353	12	18	1	1	1	CCNI	-216	upstream	ActReg chr4 #7332	0	1
7333	4	78,557,936	78,558,370	434	1	5.5	9.286	8	14	0	0	0				ActReg chr4 #7333	0	1
7334	4	83,295,363	83,295,753	390	1	10.583	10.417	17	17	1	1	1	HNRNPD	-409	upstream	ActReg chr4 #7334	0	1
7335	4	83,569,196	83,569,820	624	1	10.526	5.474	16	10	0	0	1	SCD5	150,502	in gene	ActReg chr4 #7335	1	0
7336	4	83,821,721	83,822,480	759	2	10.739	13.542	22	29	1	2	3	SEC31A, LOC100499177, THAP9	-9681, -31, 263	upstream, upstream, in gene	ActReg chr4 #7336	1	1
7337	4	83,933,953	83,934,609	656	2	12.05	9.55	18	18	1	1	1	LIN54	-241	upstream	ActReg chr4 #7337	1	1
7338	4	83,955,797	83,956,478	681	2	13.238	14.714	27	32	0	1	1	COPS4	-102	upstream	ActReg chr4 #7338	1	1
7339	4	84,205,530	84,206,196	666	1	7.952	12.429	11	20	1	1	1	COQ2	204	in gene	ActReg chr4 #7339	0	1
7340	4	84,376,912	84,377,412	500	1	10.75	8	17	12	1	2	3	HELQ, MRPS18C, FAM175A	-137, 44, 29128	upstream, in gene, downstream	ActReg chr4 #7340	1	0
7341	4	84,405,657	84,406,183	526	1	6	9.941	9	14	1	1	1	FAM175A	370	in gene	ActReg chr4 #7341	0	1
7342	4	84,469,667	84,470,124	457	1	9.571	9.857	14	14	0	0	1	AGPAT9	12,242	in gene	ActReg chr4 #7342	0	1
7343	4	86,697,684	86,698,117	433	1	10.429	7.571	15	13	0	0	1	ARHGAP24	301,616	in gene	ActReg chr4 #7343	1	0
7344	4	87,927,856	87,928,684	828	1	8.269	11.5	15	18	1	0	1	AFF1	72,116	in gene	ActReg chr4 #7344	0	1
7345	4	88,343,400	88,344,085	685	2	10.048	12.286	14	22	1	1	1	NUDT9	7	in gene	ActReg chr4 #7345	1	1
7346	4	88,764,884	88,765,364	480	1	7.2	9	10	15	0	0	1	MEPE	22,561	in gene	ActReg chr4 #7346	0	1
7347	4	89,204,675	89,205,199	524	1	7.75	9.812	14	17	1	1	1	PPM1K	951	in gene	ActReg chr4 #7347	0	1
7348	4	89,299,923	89,300,757	834	1	10.192	9.15	15	15	1	1	1	HERC6	449	in gene	ActReg chr4 #7348	1	0
7349	4	89,444,626	89,445,049	423	1	9.308	11.769	15	15	1	1	1	PIGY	118	in gene	ActReg chr4 #7349	0	1
7350	4	89,686,882	89,687,387	505	1	10.467	13.067	20	20	0	0	1	FAM13A	291,189	in gene	ActReg chr4 #7350	1	0
7351	4	90,031,888	90,032,432	544	1	6.706	11.588	12	16	1	2	2	LOC731282, TIGD2	296, -1808	in gene, upstream	ActReg chr4 #7351	0	1
7352	4	96,577,212	96,577,703	491	1	8.812	8.938	16	13	0	0	1	C4orf37	486,934	in gene	ActReg chr4 #7352	0	1
7353	4	99,916,200	99,916,631	431	1	10.538	8.308	17	13	1	1	1	METAP1	-373	upstream	ActReg chr4 #7353	1	0
7354	4	100,815,175	100,815,588	413	1	5.308	10.385	8	16	0	1	2	MAPKSP1, DNAJB14	322, 52498	in gene, downstream	ActReg chr4 #7354	0	1
7355	4	103,138,982	103,139,398	416	1	9.308	9.077	15	15	0	0	0				ActReg chr4 #7355	1	0
7356	4	103,563,039	103,563,500	461	1	7.333	9.333	11	15	0	0	1	MANBA	118,882	in gene	ActReg chr4 #7356	0	1
7357	4	104,119,038	104,120,038	1,000	2	10.469	14.875	24	29	1	1	1	CENPE	28	in gene	ActReg chr4 #7357	1	1
7358	4	106,394,901	106,395,411	510	1	10.5	11.688	16	17	1	1	1	PPA2	71	in gene	ActReg chr4 #7358	0	1
7359	4	106,844,487	106,844,937	450	1	11	6	18	11	0	0	1	NPNT	28,115	in gene	ActReg chr4 #7359	1	0
7360	4	108,132,036	108,132,559	523	1	5.267	10.062	10	17	0	0	0				ActReg chr4 #7360	0	1
7361	4	108,910,757	108,911,370	613	1	8.316	11.474	13	18	1	1	1	HADH	193	in gene	ActReg chr4 #7361	0	1
7362	4	109,282,247	109,282,637	390	1	7.417	10.167	10	14	0	0	0				ActReg chr4 #7362	0	1
7363	4	109,571,424	109,572,013	589	1	6.526	11	9	16	1	1	1	OSTC	-23	upstream	ActReg chr4 #7363	0	1
7364	4	109,782,387	109,782,837	450	1	7.286	9.643	10	13	0	0	1	COL25A1	441,187	in gene	ActReg chr4 #7364	0	1
7365	4	109,802,392	109,802,797	405	1	10.692	5.615	16	9	0	0	1	COL25A1	421,205	in gene	ActReg chr4 #7365	1	0
7366	4	110,331,896	110,332,419	523	1	6.294	9.294	10	19	0	0	0				ActReg chr4 #7366	0	1
7367	4	110,354,780	110,355,122	342	1	9.091	6.182	13	10	1	1	1	SEC24B	-20	upstream	ActReg chr4 #7367	1	0
7368	4	111,544,047	111,544,791	744	2	8.957	13.391	18	23	1	0	1	PITX2	14,089	in gene	ActReg chr4 #7368	1	1
7369	4	114,613,419	114,613,966	547	1	11.118	5.353	16	10	0	0	1	CAMK2D	69,391	in gene	ActReg chr4 #7369	1	0
7370	4	115,068,036	115,068,767	731	1	8.864	11.364	13	16	0	0	0				ActReg chr4 #7370	0	1
7371	4	115,280,971	115,281,474	503	1	4.062	9.312	6	14	0	0	0				ActReg chr4 #7371	0	1
7372	4	120,130,109	120,130,674	565	1	7.167	10.722	12	17	0	1	1	USP53	-3,391	upstream	ActReg chr4 #7372	0	1
7373	4	120,375,497	120,376,289	792	2	16.04	24.04	45	67	1	2	2	LOC100507306, LOC645513	-109, -51	upstream, upstream	ActReg chr4 #7373	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7374	4	123,748,417	123,748,977	560	1	4.706	9.941	7	17	1	1	1	FGF2	834	in gene	ActReg chr4 #7374	0	1
7375	4	123,843,486	123,844,603	1,117	3	10.514	11.829	22	23	2	2	2	NUDT6, SPATA5	79, -181	in gene, upstream	ActReg chr4 #7375	1	1
7376	4	125,552,828	125,553,431	603	2	7.647	11.053	17	21	0	0	0				ActReg chr4 #7376	1	1
7377	4	126,238,575	126,239,110	535	1	8.529	10.118	14	15	1	1	1	FAT4	1,275	in gene	ActReg chr4 #7377	0	1
7378	4	127,771,246	127,771,969	723	2	11.13	9.857	24	24	0	0	0				ActReg chr4 #7378	1	1
7379	4	129,438,769	129,439,426	657	1	10	5.714	18	9	0	1	1	LOC100507487	2,065	in gene	ActReg chr4 #7379	1	0
7380	4	130,014,464	130,015,085	621	1	5.45	11.1	9	18	1	2	2	SCLT1, C4orf33	-10, -55	upstream, upstream	ActReg chr4 #7380	0	1
7381	4	135,248,121	135,248,556	435	1	5.429	9.929	10	14	0	0	0				ActReg chr4 #7381	0	1
7382	4	135,252,245	135,252,960	715	2	11.261	10.478	19	23	0	0	0				ActReg chr4 #7382	1	1
7383	4	139,936,470	139,936,936	466	1	7.2	11.067	10	14	1	1	1	CCRN4L	-240	upstream	ActReg chr4 #7383	0	1
7384	4	140,222,498	140,223,052	554	1	6.529	12.294	9	21	1	2	2	NDUFC1, NAA15	930, 99	in gene, in gene	ActReg chr4 #7384	0	1
7385	4	140,477,123	140,477,688	565	1	7.529	11.118	11	16	1	1	1	SETD7	172	in gene	ActReg chr4 #7385	0	1
7386	4	141,016,979	141,017,611	632	1	11.15	5.25	17	9	0	0	1	MAML3	57,938	in gene	ActReg chr4 #7386	1	0
7387	4	141,072,049	141,072,570	521	1	9.312	10.438	12	16	1	0	1	MAML3	2,924	in gene	ActReg chr4 #7387	0	1
7388	4	141,074,877	141,075,729	852	2	8.296	10.296	17	18	1	1	1	MAML3	-70	upstream	ActReg chr4 #7388	1	1
7389	4	141,677,566	141,678,114	548	1	12.722	8.556	17	12	1	1	1	TBC1D9	-369	upstream	ActReg chr4 #7389	1	0
7390	4	143,484,715	143,485,346	631	2	12.05	8.5	21	14	0	0	1	INPP4B	282,574	in gene	ActReg chr4 #7390	1	1
7391	4	144,105,562	144,106,019	457	1	7.5	9.6	13	12	1	1	1	USP38	-280	upstream	ActReg chr4 #7391	0	1
7392	4	146,101,434	146,102,077	643	1	9.25	5.65	20	11	1	1	1	OTUD4	-923	upstream	ActReg chr4 #7392	1	0
7393	4	146,540,122	146,540,607	485	1	6.333	10.667	12	16	1	1	1	MMAA	-176	upstream	ActReg chr4 #7393	0	1
7394	4	146,655,720	146,656,461	741	1	7.696	9.826	13	16	0	0	1	C4orf51	54,734	downstream	ActReg chr4 #7394	0	1
7395	4	147,442,791	147,443,939	1,148	2	11.917	13.694	21	30	1	1	1	SLC10A7	-242	upstream	ActReg chr4 #7395	1	1
7396	4	147,557,878	147,558,620	742	2	8	12.565	16	27	1	1	1	POU4F2	-1,796	upstream	ActReg chr4 #7396	1	1
7397	4	147,564,891	147,565,453	562	1	10.833	7	19	13	0	0	1	POU4F2	5,127	downstream	ActReg chr4 #7397	1	0
7398	4	148,261,314	148,261,805	491	1	11.067	6	19	9	0	0	0				ActReg chr4 #7398	1	0
7399	4	150,330,205	150,330,667	462	1	4.8	9.2	8	16	0	0	0				ActReg chr4 #7399	0	1
7400	4	151,422,156	151,422,509	353	1	8.091	10.546	11	16	0	0	1	LRBA	514,547	in gene	ActReg chr4 #7400	0	1
7401	4	152,020,371	152,021,141	770	1	8.417	13.792	15	27	1	2	2	RPS3A, SNORD73A	2, -4223	in gene, upstream	ActReg chr4 #7401	0	1
7402	4	152,329,736	152,330,175	439	1	11	6.154	14	10	1	1	1	FAM160A1	-443	upstream	ActReg chr4 #7402	1	0
7403	4	152,681,884	152,682,459	575	1	11.889	7.278	21	11	1	1	1	PET112L	4	in gene	ActReg chr4 #7403	1	0
7404	4	153,535,465	153,536,170	705	1	12.046	5.909	24	9	0	0	0				ActReg chr4 #7404	1	0
7405	4	153,700,905	153,701,537	632	1	12.2	9.55	20	12	1	2	2	TIGD4, ARFIP1	-344, 109	upstream, in gene	ActReg chr4 #7405	1	0
7406	4	153,904,308	153,905,498	1,190	2	13.135	17.081	22	32	0	0	1	FHDC1	40,768	downstream	ActReg chr4 #7406	1	1
7407	4	155,254,026	155,254,544	518	1	2.357	9.125	3	15	1	0	1	DCHS2	158,645	in gene	ActReg chr4 #7407	0	1
7408	4	158,141,158	158,141,906	748	1	9.565	13.609	22	26	1	1	1	GRIA2	-204	upstream	ActReg chr4 #7408	0	1
7409	4	159,015,808	159,016,297	489	1	3.375	8.25	5	15	0	0	0				ActReg chr4 #7409	0	1
7410	4	159,592,755	159,594,094	1,339	2	29.762	35.857	119	124	1	2	2	C4orf46, ETFDH	-222, 147	upstream, in gene	ActReg chr4 #7410	1	1
7411	4	159,644,164	159,644,844	680	1	5.667	9.905	8	14	1	1	1	PPID	48	in gene	ActReg chr4 #7411	0	1
7412	4	160,843,646	160,844,196	550	1	8.5	6.278	16	9	0	0	0				ActReg chr4 #7412	1	0
7413	4	163,084,866	163,085,524	658	2	11.85	13.9	22	28	0	1	1	FSTL5	-9	upstream	ActReg chr4 #7413	1	1
7414	4	164,415,379	164,416,042	663	2	7.571	11.191	14	19	1	1	1	C4orf43	37	in gene	ActReg chr4 #7414	1	1
7415	4	165,431,118	165,431,559	441	1	8.857	3.429	14	5	0	0	0				ActReg chr4 #7415	1	0
7416	4	169,194,938	169,195,425	487	1	6.733	9.562	13	16	0	0	1	DDX60	44,777	in gene	ActReg chr4 #7416	0	1
7417	4	170,744,649	170,745,455	806	2	13.24	17.16	28	43	0	0	0				ActReg chr4 #7417	1	1
7418	4	170,948,397	170,948,951	554	2	11.706	11.647	20	20	1	1	1	MFAP3L	-1,245	upstream	ActReg chr4 #7418	1	1
7419	4	171,900,064	171,900,623	559	2	9.722	9.167	18	16	0	0	0				ActReg chr4 #7419	1	1
7420	4	174,173,311	174,173,921	610	2	10.3	15.368	18	29	0	0	1	GALNT7	83,712	in gene	ActReg chr4 #7420	1	1
7421	4	174,255,347	174,256,180	833	1	10.154	13.769	15	27	1	1	1	HMGB2	-168	upstream	ActReg chr4 #7421	0	1
7422	4	174,382,126	174,382,586	460	1	5.214	9.571	7	16	0	0	0				ActReg chr4 #7422	0	1
7423	4	174,780,601	174,781,009	408	1	9.769	4.846	15	7	0	0	0				ActReg chr4 #7423	1	0
7424	4	175,204,820	175,205,416	596	1	8.053	11.947	15	18	1	2	2	FBXO8, KIAA1712	284, 290	in gene, in gene	ActReg chr4 #7424	0	1
7425	4	175,749,701	175,750,456	755	2	13.565	15.652	25	29	1	1	1	GLRA3	387	in gene	ActReg chr4 #7425	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7426	4	175,750,589	175,750,970	381	1	10.583	4.5	13	6	1	1	1	GLRA3	-314	upstream	ActReg chr4 #7426	1	0
7427	4	177,191,766	177,192,264	498	1	8.562	10.125	13	16	0	1	1	ASB5	-1,642	upstream	ActReg chr4 #7427	0	1
7428	4	177,459,299	177,459,856	557	1	4.25	10.706	7	16	0	0	0				ActReg chr4 #7428	0	1
7429	4	177,909,293	177,909,876	583	1	7.444	10.944	12	19	0	0	0				ActReg chr4 #7429	0	1
7430	4	178,362,773	178,363,832	1,059	1	6.818	13.97	13	23	1	1	1	AGA	355	in gene	ActReg chr4 #7430	0	1
7431	4	178,365,921	178,366,432	511	1	12.125	8.688	15	12	0	1	1	AGA	-2,519	upstream	ActReg chr4 #7431	1	0
7432	4	180,016,874	180,017,489	615	2	8.947	10.842	17	15	0	0	0				ActReg chr4 #7432	1	1
7433	4	180,018,014	180,019,371	1,357	2	7.512	13.439	15	24	0	0	0				ActReg chr4 #7433	1	1
7434	4	180,146,592	180,148,137	1,545	2	10.878	9.735	18	18	0	0	0				ActReg chr4 #7434	1	1
7435	4	180,979,375	180,979,817	442	1	9.214	4	14	9	1	0	0				ActReg chr4 #7435	1	0
7436	4	181,463,360	181,464,072	712	2	12.609	10.261	27	19	0	0	0				ActReg chr4 #7436	1	1
7437	4	182,102,511	182,103,109	598	1	9.474	11.79	14	21	0	0	0				ActReg chr4 #7437	0	1
7438	4	182,609,611	182,610,436	825	1	8.5	9.962	14	16	0	0	0				ActReg chr4 #7438	0	1
7439	4	182,775,245	182,775,845	600	2	9.105	10.947	15	21	0	0	0				ActReg chr4 #7439	1	1
7440	4	182,871,511	182,871,990	479	1	6.933	11.667	10	18	0	0	0				ActReg chr4 #7440	0	1
7441	4	182,873,471	182,874,073	602	1	12.053	11	21	19	0	0	0				ActReg chr4 #7441	1	0
7442	4	183,182,556	183,183,365	809	2	11.769	18.654	29	48	0	0	0				ActReg chr4 #7442	1	1
7443	4	183,288,316	183,289,004	688	1	7.182	12.682	14	24	0	0	1	ODZ3	43,523	in gene	ActReg chr4 #7443	0	1
7444	4	183,369,120	183,370,247	1,127	1	8.25	12.972	11	21	1	0	1	ODZ3	124,546	in gene	ActReg chr4 #7444	0	1
7445	4	184,019,506	184,020,588	1,082	2	14.941	10.088	32	17	1	2	2	C4orf38, WWC2	305, -416	in gene, upstream	ActReg chr4 #7445	1	1
7446	4	184,364,876	184,366,301	1,425	2	10.636	9.955	17	16	1	1	1	CDKN2AIP	-201	upstream	ActReg chr4 #7446	1	1
7447	4	184,425,383	184,426,238	855	2	15.885	18.192	33	40	1	2	2	LOC389247, ING2	-142, -410	upstream, upstream	ActReg chr4 #7447	1	1
7448	4	184,427,047	184,427,775	728	1	9.909	11.818	17	17	1	2	2	LOC389247, ING2	-1743, 1191	upstream, in gene	ActReg chr4 #7448	0	1
7449	4	184,580,199	184,580,644	445	1	8.286	9.5	11	13	1	2	2	RWDD4A, C4orf41	-90, -25	upstream, upstream	ActReg chr4 #7449	0	1
7450	4	185,339,013	185,339,524	511	1	9.875	14.188	17	24	0	0	1	IRF2	56,458	in gene	ActReg chr4 #7450	0	1
7451	4	185,395,891	185,396,688	797	1	7.8	12.36	11	19	1	1	1	IRF2	-563	upstream	ActReg chr4 #7451	0	1
7452	4	185,654,686	185,655,808	1,122	2	16.361	22.667	49	59	1	1	1	MLF1IP	39	in gene	ActReg chr4 #7452	1	1
7453	4	185,734,256	185,735,184	928	2	11.483	11.172	24	19	0	0	1	ACSL1	12,495	in gene	ActReg chr4 #7453	1	1
7454	4	185,746,157	185,746,816	659	1	6.333	12.048	9	21	1	1	1	ACSL1	729	in gene	ActReg chr4 #7454	0	1
7455	4	185,832,392	185,832,982	590	1	9.056	11.056	11	18	0	0	0				ActReg chr4 #7455	0	1
7456	4	186,063,924	186,064,694	770	1	11.542	13.333	19	20	1	1	1	SLC25A4	-108	upstream	ActReg chr4 #7456	0	1
7457	4	186,227,094	186,227,758	664	1	11.667	6.619	20	12	0	0	1	SNX25	96,142	in gene	ActReg chr4 #7457	1	0
7458	4	186,316,968	186,317,814	846	1	12	14.692	20	23	1	1	2	ANKRD37, UFSP2	-449, 29748	upstream, downstream	ActReg chr4 #7458	0	1
7459	4	186,346,634	186,347,824	1,190	2	14.243	15.811	27	33	1	2	2	UFSP2, C4orf47	-90, -3316	upstream, upstream	ActReg chr4 #7459	1	1
7460	4	186,456,163	186,456,812	649	1	11.05	6.6	17	11	1	1	1	PDLIM3	225	in gene	ActReg chr4 #7460	1	0
7461	4	186,494,781	186,495,428	647	1	5.238	11.762	8	23	0	0	0				ActReg chr4 #7461	0	1
7462	4	186,760,149	186,760,899	750	2	11	12.333	19	23	0	0	1	SORBS2	117,346	in gene	ActReg chr4 #7462	1	1
7463	4	186,768,379	186,769,091	712	1	12.391	5.478	27	11	0	0	1	SORBS2	109,135	in gene	ActReg chr4 #7463	1	0
7464	4	186,853,982	186,854,726	744	1	9.625	12.792	13	26	0	0	1	SORBS2	23,516	in gene	ActReg chr4 #7464	0	1
7465	4	187,112,177	187,113,739	1,562	2	10.633	12.796	17	22	1	1	1	CYP4V2	284	in gene	ActReg chr4 #7465	1	1
7466	4	187,644,155	187,644,781	626	1	7.7	10.7	11	16	1	1	1	FAT1	519	in gene	ActReg chr4 #7466	0	1
7467	4	187,646,874	187,648,317	1,443	1	7.156	11.733	12	17	1	1	1	FAT1	-2,608	upstream	ActReg chr4 #7467	0	1
7468	4	187,764,584	187,764,978	394	1	2.667	9.75	4	13	0	0	0				ActReg chr4 #7468	0	1
7469	4	187,766,176	187,766,737	561	1	11.444	9.611	22	16	0	0	0				ActReg chr4 #7469	1	0
7470	4	188,735,719	188,736,571	852	1	8.731	13.308	18	20	0	0	0				ActReg chr4 #7470	0	1
7471	4	189,338,348	189,339,062	714	1	8.227	12.546	15	17	0	0	0				ActReg chr4 #7471	0	1
7472	4	189,581,877	189,582,391	514	1	8.133	11.312	10	16	0	0	0				ActReg chr4 #7472	0	1
7473	4	190,695,103	190,695,535	432	1	5.714	10.786	9	18	0	0	0				ActReg chr4 #7473	0	1
7474	4	190,861,061	190,862,597	1,536	2	13.333	16.917	23	34	1	1	1	FRG1	-145	upstream	ActReg chr4 #7474	1	1
7475	4	190,958,718	190,959,143	425	2	12.857	8.5	23	17	1	0	0				ActReg chr4 #7475	1	1
7476	5	56,658	57,690	1,032	2	9.312	12.156	16	22	0	0	0				ActReg chr5 #7476	1	1
7477	5	218,935	219,427	492	1	6.375	10.938	10	17	1	2	2	CCDC127, SDHA	-884, 825	upstream, in gene	ActReg chr5 #7477	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7478	5	271,218	272,064	846	1	6.963	13.444	13	26	2	2	2	LOC100507671, PDCD6	-30, -95	upstream, upstream	ActReg chr5 #7478	0	1
7479	5	372,842	373,696	854	1	8	10.518	11	16	1	0	1	AHRR	68,978	in gene	ActReg chr5 #7479	0	1
7480	5	398,416	399,203	787	1	9.88	6.76	16	10	0	0	1	AHRR	94,518	in gene	ActReg chr5 #7480	1	0
7481	5	911,965	913,154	1,189	2	14.763	15.079	36	46	1	0	1	TRIP13	19,590	in gene	ActReg chr5 #7481	1	1
7482	5	1,246,792	1,247,862	1,070	2	11.242	13.576	20	27	1	0	2	SLC6A18, TERT	21857, 47835	downstream, downstream	ActReg chr5 #7482	1	1
7483	5	1,633,891	1,634,515	624	1	6.842	11.737	12	17	1	0	0				ActReg chr5 #7483	0	1
7484	5	3,310,906	3,311,614	708	1	10.773	14.364	16	28	0	0	0				ActReg chr5 #7484	0	1
7485	5	3,320,371	3,321,094	723	1	6.696	12.174	10	21	0	0	0				ActReg chr5 #7485	0	1
7486	5	3,324,807	3,325,716	909	1	10.679	13.929	18	24	1	0	0				ActReg chr5 #7486	0	1
7487	5	5,126,505	5,127,099	594	1	6.111	10.667	8	15	0	0	0				ActReg chr5 #7487	0	1
7488	5	5,271,408	5,271,970	562	1	5.444	11.722	13	18	0	0	1	ADAMTS16	131,246	in gene	ActReg chr5 #7488	0	1
7489	5	5,340,168	5,341,000	832	1	14.615	11.192	27	18	0	0	0				ActReg chr5 #7489	1	0
7490	5	5,421,906	5,422,955	1,049	2	13.546	12.182	22	25	1	1	1	KIAA0947	-377	upstream	ActReg chr5 #7490	1	1
7491	5	6,302,580	6,303,307	727	1	5.043	9.826	10	17	0	0	1	FLJ33360	34,462	downstream	ActReg chr5 #7491	0	1
7492	5	6,328,089	6,328,786	697	1	8.818	10.954	17	25	0	0	1	FLJ33360	8,968	in gene	ActReg chr5 #7492	0	1
7493	5	6,365,466	6,366,124	658	1	9.429	10.238	14	14	0	0	1	MED10	12,844	downstream	ActReg chr5 #7493	0	1
7494	5	6,377,908	6,378,710	802	1	7.68	11.76	10	18	1	1	1	MED10	330	in gene	ActReg chr5 #7494	0	1
7495	5	6,633,287	6,634,041	754	1	9.783	10.522	17	16	1	2	2	NSUN2, SRD5A1	-191, 164	upstream, in gene	ActReg chr5 #7495	0	1
7496	5	6,712,111	6,713,230	1,119	1	9.4	12.286	14	23	1	2	2	LOC100505625, PAPD7	-4846, -2048	upstream, upstream	ActReg chr5 #7496	0	1
7497	5	7,868,889	7,869,517	628	2	12.1	13.95	18	25	1	2	3	LOC100288963, FASTKD3, MTRR	18284, -53, 14	downstream, upstream, upstream	ActReg chr5 #7497	1	1
7498	5	8,828,836	8,829,788	952	2	10.379	11.379	19	17	0	0	0				ActReg chr5 #7498	1	1
7499	5	9,244,425	9,244,984	559	1	7.706	10.177	13	14	0	0	1	SEMA5A	301,529	in gene	ActReg chr5 #7499	0	1
7500	5	10,249,518	10,250,008	490	1	11.533	9	17	12	1	2	2	FAM173B, CCT5	251, -519	in gene, upstream	ActReg chr5 #7500	1	0
7501	5	10,250,211	10,251,176	965	1	9	10.8	14	16	1	2	2	FAM173B, CCT5	-679, 411	upstream, in gene	ActReg chr5 #7501	0	1
7502	5	10,353,213	10,353,994	781	1	9.24	13.8	15	23	1	1	1	6-Mar	-225	upstream	ActReg chr5 #7502	0	1
7503	5	10,724,819	10,725,787	968	1	7.633	10.3	14	17	0	0	1	DAP	36,084	in gene	ActReg chr5 #7503	0	1
7504	5	10,761,539	10,762,073	534	1	5	12.375	8	19	1	1	1	DAP	-419	upstream	ActReg chr5 #7504	0	1
7505	5	10,859,514	10,860,621	1,107	1	9.686	9.943	17	14	0	0	0				ActReg chr5 #7505	0	1
7506	5	13,553,867	13,554,429	562	1	6.059	11.882	11	25	0	0	0				ActReg chr5 #7506	0	1
7507	5	13,866,970	13,867,365	395	1	7.231	9.846	11	16	0	0	1	DNAH5	77,422	in gene	ActReg chr5 #7507	0	1
7508	5	14,039,156	14,039,821	665	1	12.238	7.524	18	11	0	0	0				ActReg chr5 #7508	1	0
7509	5	14,178,448	14,179,340	892	1	5.857	12.321	9	19	0	0	1	TRIO	35,065	in gene	ActReg chr5 #7509	0	1
7510	5	14,268,229	14,269,208	979	1	8.833	10.2	19	19	0	0	1	TRIO	124,889	in gene	ActReg chr5 #7510	0	1
7511	5	14,628,296	14,628,968	672	2	10.333	13.667	17	28	0	0	0				ActReg chr5 #7511	1	1
7512	5	14,664,140	14,664,984	844	2	12.346	10.808	18	14	1	1	1	FAM105B	-221	upstream	ActReg chr5 #7512	1	1
7513	5	14,775,690	14,776,385	695	1	7.318	11.046	11	15	0	1	2	ANKH, LOC100128508	95850, 1104	in gene, in gene	ActReg chr5 #7513	0	1
7514	5	14,880,256	14,881,332	1,076	2	10.853	11.294	17	24	0	0	1	ANKH	-8,907	upstream	ActReg chr5 #7514	1	1
7515	5	14,937,392	14,938,009	617	1	6.842	10.368	12	16	0	0	0				ActReg chr5 #7515	0	1
7516	5	15,008,412	15,009,114	702	1	13.227	9.409	29	19	0	0	0				ActReg chr5 #7516	1	0
7517	5	16,178,862	16,179,318	456	1	6	11.357	10	19	1	2	2	MARCH11, LOC401176	807, -1257	in gene, upstream	ActReg chr5 #7517	0	1
7518	5	16,465,385	16,466,497	1,112	2	11.657	11.371	18	17	1	1	2	ZNF622, FAM134B	-47, 151177	upstream, downstream	ActReg chr5 #7518	1	1
7519	5	16,502,824	16,503,486	662	1	6	11	8	17	0	0	1	FAM134B	113,963	in gene	ActReg chr5 #7519	0	1
7520	5	20,276,273	20,276,968	695	1	7.955	10.727	14	16	0	0	0				ActReg chr5 #7520	0	1
7521	5	20,679,063	20,679,629	566	1	7.611	10.444	14	19	0	0	0				ActReg chr5 #7521	0	1
7522	5	21,459,127	21,459,891	764	2	44.391	45.875	133	129	1	0	0				ActReg chr5 #7522	1	1
7523	5	21,551,954	21,552,695	741	1	7.87	12	11	19	0	0	0				ActReg chr5 #7523	0	1
7524	5	22,372,162	22,372,833	671	2	10.143	11.095	13	18	0	0	1	CDH12	481,234	in gene	ActReg chr5 #7524	1	1
7525	5	23,084,785	23,085,512	727	1	7.739	13.478	13	20	0	0	0				ActReg chr5 #7525	0	1
7526	5	27,241,848	27,242,497	649	1	10.286	6.143	20	9	0	0	0				ActReg chr5 #7526	1	0
7527	5	27,706,775	27,707,446	671	1	8.095	10.476	15	20	0	0	0				ActReg chr5 #7527	0	1
7528	5	28,077,693	28,078,273	580	1	9.211	10.053	13	14	0	0	0				ActReg chr5 #7528	0	1
7529	5	28,808,965	28,810,938	1,973	2	10.852	13.41	27	27	1	0	0				ActReg chr5 #7529	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7530	5	31,532,000	31,532,994	994	1	6.688	11.969	12	20	1	2	2	RNASEN, C5orf22	-215, 124	upstream, in gene	ActReg chr5 #7530	0	1
7531	5	32,173,831	32,174,887	1,056	1	8.394	13.121	17	24	1	1	1	GOLPH3	66	in gene	ActReg chr5 #7531	0	1
7532	5	32,390,930	32,391,571	641	1	7.1	12.15	16	20	0	0	2	ZFR, MIR579	53594, 3331	in gene, downstream	ActReg chr5 #7532	0	1
7533	5	33,049,767	33,050,528	761	1	8.208	12.958	11	23	0	0	0				ActReg chr5 #7533	0	1
7534	5	33,440,372	33,441,703	1,331	1	8.238	10.024	16	17	1	1	1	TARS	139	in gene	ActReg chr5 #7534	0	1
7535	5	33,690,884	33,691,336	452	1	7.714	10.571	12	17	0	0	1	ADAMTS12	201,014	in gene	ActReg chr5 #7535	0	1
7536	5	33,935,957	33,938,305	2,348	2	11.662	14.608	33	29	1	1	2	RXFP3, SLC45A2	640, 47649	in gene, downstream	ActReg chr5 #7536	1	1
7537	5	34,001,308	34,001,838	530	1	6.176	10.823	9	15	0	0	1	AMACR	6,647	in gene	ActReg chr5 #7537	0	1
7538	5	34,007,823	34,008,517	694	1	9.864	12	13	17	1	1	2	AMACR, C1QTNF3	50, 35147	in gene, downstream	ActReg chr5 #7538	0	1
7539	5	34,047,104	34,047,781	677	1	11.273	8.909	19	13	0	1	1	C1QTNF3	-4,125	upstream	ActReg chr5 #7539	1	0
7540	5	34,053,186	34,053,847	661	1	11.9	6.8	16	12	0	0	1	C1QTNF3	-10,199	upstream	ActReg chr5 #7540	1	0
7541	5	34,839,038	34,839,764	726	1	6.565	11.13	12	19	1	1	2	RAI14, TTC23L	182968, 132	downstream, in gene	ActReg chr5 #7541	0	1
7542	5	34,914,873	34,916,231	1,358	2	10.279	15.884	21	34	1	2	2	RAD1, BRIX1	228, -268	in gene, upstream	ActReg chr5 #7542	1	1
7543	5	35,247,503	35,248,273	770	1	7.5	11.167	12	18	0	0	0				ActReg chr5 #7543	0	1
7544	5	35,617,433	35,618,623	1,190	2	28.514	34.838	94	96	1	1	1	SPEF2	39	in gene	ActReg chr5 #7544	1	1
7545	5	36,151,570	36,152,818	1,248	1	8.359	10.923	16	18	1	3	3	LMBRD2, MIR580, SKP2	-179, -4104, 5	upstream, upstream, in gene	ActReg chr5 #7545	0	1
7546	5	36,241,024	36,241,756	732	1	7.739	10.261	10	14	1	1	2	C5orf33, RANBP3L	868, 60621	in gene, downstream	ActReg chr5 #7546	0	1
7547	5	36,241,807	36,242,700	893	2	15.214	14.214	29	21	1	1	2	C5orf33, RANBP3L	5, 59758	in gene, downstream	ActReg chr5 #7547	1	1
7548	5	36,657,500	36,658,167	667	1	8.667	15.762	12	27	0	0	1	SLC1A3	51,376	in gene	ActReg chr5 #7548	0	1
7549	5	37,370,861	37,371,809	948	2	11.6	14.5	22	26	1	1	2	NUP155, WDR70	-138, -8077	upstream, upstream	ActReg chr5 #7549	1	1
7550	5	37,378,865	37,379,795	930	2	43.241	50.035	160	166	1	1	2	NUP155, WDR70	-8133, -82	upstream, upstream	ActReg chr5 #7550	1	1
7551	5	37,722,929	37,723,484	555	1	11.765	6.765	20	10	0	0	1	WDR70	343,794	in gene	ActReg chr5 #7551	1	0
7552	5	37,786,913	37,787,621	708	1	8.227	11.091	13	17	0	0	0				ActReg chr5 #7552	0	1
7553	5	37,889,674	37,890,618	944	2	11.724	13.069	18	21	0	0	0				ActReg chr5 #7553	1	1
7554	5	38,601,757	38,602,450	693	2	11.364	10.318	16	20	0	1	2	LIFR, LOC100506495	-6596, 45239	upstream, in gene	ActReg chr5 #7554	1	1
7555	5	38,772,472	38,772,941	469	1	6.667	10.933	10	17	0	0	0				ActReg chr5 #7555	0	1
7556	5	38,782,952	38,783,782	830	1	7.154	11.269	13	16	0	0	0				ActReg chr5 #7556	0	1
7557	5	38,921,228	38,921,674	446	1	8.857	9.429	14	16	0	0	1	OSMR	75,491	in gene	ActReg chr5 #7557	0	1
7558	5	39,074,427	39,075,105	678	1	12.591	7.909	22	15	1	1	1	RICTOR	-265	upstream	ActReg chr5 #7558	1	0
7559	5	39,196,536	39,197,122	586	1	5.789	9.105	9	16	0	0	1	FYB	22,838	in gene	ActReg chr5 #7559	0	1
7560	5	39,399,551	39,400,118	567	1	6.5	10.611	11	19	0	0	1	DAB2	25,501	in gene	ActReg chr5 #7560	0	1
7561	5	39,424,903	39,425,699	796	1	9.28	12.4	16	18	1	1	1	DAB2	34	in gene	ActReg chr5 #7561	0	1
7562	5	40,410,321	40,410,921	600	1	10.79	10.368	13	16	0	0	0				ActReg chr5 #7562	0	1
7563	5	40,518,482	40,518,994	512	1	10.438	13.25	19	24	0	0	0				ActReg chr5 #7563	0	1
7564	5	40,755,069	40,756,473	1,404	2	12.659	12.796	20	18	1	1	2	TTC33, PRKAA1	301, 42526	in gene, downstream	ActReg chr5 #7564	1	1
7565	5	40,834,950	40,836,080	1,130	2	10.143	12.943	23	20	1	4	4	LOC100506548, RPL37, SNORD72, CARD6	-4959, -128, -2678, -5895	upstream, upstream, upstream, upstream	ActReg chr5 #7565	1	1
7566	5	41,095,011	41,095,400	389	1	11.083	5.083	17	7	0	0	0				ActReg chr5 #7566	1	0
7567	5	41,870,106	41,870,918	812	1	13.808	9.231	21	13	1	1	1	OXCT1	279	in gene	ActReg chr5 #7567	1	0
7568	5	41,903,788	41,904,760	972	1	11.067	9.667	16	14	1	1	1	C5orf51	-196	upstream	ActReg chr5 #7568	1	0
7569	5	41,924,931	41,926,088	1,157	2	11.833	13.861	23	29	1	1	2	C5orf51, FBXO4	21039, 153	downstream, in gene	ActReg chr5 #7569	1	1
7570	5	42,423,482	42,423,923	441	1	7.214	11.786	10	16	1	1	1	GHR	-324	upstream	ActReg chr5 #7570	0	1
7571	5	42,531,604	42,532,206	602	1	5.842	9.421	9	16	0	0	1	GHR	107,879	in gene	ActReg chr5 #7571	0	1
7572	5	42,950,512	42,951,129	617	1	10.684	6.211	17	10	1	0	0				ActReg chr5 #7572	1	0
7573	5	42,982,147	42,982,500	353	1	5.364	9	9	15	0	0	1	FLJ32255	11,145	downstream	ActReg chr5 #7573	0	1
7574	5	42,991,892	42,992,714	822	2	11.308	11.615	17	22	1	1	1	FLJ32255	1,165	in gene	ActReg chr5 #7574	1	1
7575	5	43,017,846	43,018,851	1,005	2	16	11.844	31	30	1	1	1	LOC648987	565	in gene	ActReg chr5 #7575	1	1
7576	5	43,064,599	43,065,351	752	1	13.292	9.708	24	21	0	2	2	hCG_2039148, LOC100506639	2098, -2153	downstream, upstream	ActReg chr5 #7576	1	0
7577	5	43,105,312	43,106,132	820	2	13.192	12.269	30	22	0	0	0				ActReg chr5 #7577	1	1
7578	5	43,190,870	43,191,380	510	1	8.625	11.812	13	17	0	1	1	MGC42105	-1,202	upstream	ActReg chr5 #7578	0	1
7579	5	43,191,875	43,193,226	1,351	1	6.333	11.691	11	14	1	1	1	MGC42105	223	in gene	ActReg chr5 #7579	0	1
7580	5	43,193,629	43,194,088	459	1	8.133	10.867	12	15	0	1	1	MGC42105	1,531	in gene	ActReg chr5 #7580	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7581	5	43,396,870	43,397,414	544	1	12.471	12.823	16	20	1	0	1	CCL28	15,346	in gene	ActReg chr5 #7581	0	1
7582	5	43,483,398	43,484,533	1,135	2	10.486	15.543	16	29	1	1	2	C5orf28, C5orf34	27, 31222	in gene, downstream	ActReg chr5 #7582	1	1
7583	5	43,556,247	43,557,564	1,317	3	15.878	20.366	52	61	1	1	1	PAIP1	616	in gene	ActReg chr5 #7583	1	1
7584	5	44,808,509	44,809,949	1,440	2	16.622	16.578	39	37	1	2	2	LOC100506674, MRPS30	-367, 202	upstream, in gene	ActReg chr5 #7584	1	1
7585	5	45,694,262	45,694,972	710	2	10.727	11.364	18	22	0	1	1	HCN1	1,603	in gene	ActReg chr5 #7585	1	1
7586	5	50,678,643	50,679,541	898	1	9.429	12.571	14	18	1	2	2	LOC642366, ISL1	396, 134	in gene, in gene	ActReg chr5 #7586	0	1
7587	5	52,023,466	52,023,960	494	1	10.933	4.6	20	8	0	0	0				ActReg chr5 #7587	1	0
7588	5	52,053,748	52,054,323	575	2	9.333	11.278	15	16	0	0	0				ActReg chr5 #7588	1	1
7589	5	52,083,533	52,084,430	897	1	9.893	11.214	16	19	1	2	2	PELO, ITGA1	207, -155	in gene, upstream	ActReg chr5 #7589	0	1
7590	5	52,284,631	52,286,035	1,404	1	8.614	11.046	17	20	1	1	1	ITGA2	177	in gene	ActReg chr5 #7590	0	1
7591	5	52,319,642	52,320,097	455	1	12.267	7.733	20	9	0	0	1	ITGA2	34,713	in gene	ActReg chr5 #7591	1	0
7592	5	52,405,229	52,405,931	702	1	8.727	12.727	15	20	1	2	2	MOCS2, LOC257396	18, -107	in gene, upstream	ActReg chr5 #7592	0	1
7593	5	53,388,679	53,389,471	792	1	9.833	12.917	16	23	0	0	1	ARL15	217,328	in gene	ActReg chr5 #7593	0	1
7594	5	53,606,238	53,607,058	820	2	12.538	10.885	18	16	1	1	1	ARL15	-245	upstream	ActReg chr5 #7594	1	1
7595	5	53,813,028	53,813,867	839	2	16.962	16.269	37	42	1	1	1	SNX18	-142	upstream	ActReg chr5 #7595	1	1
7596	5	53,953,740	53,954,150	410	1	10.077	5.769	15	9	0	0	0				ActReg chr5 #7596	1	0
7597	5	53,998,827	53,999,781	954	1	7.5	11.033	13	23	0	0	0				ActReg chr5 #7597	0	1
7598	5	54,039,440	54,040,185	745	1	3.609	10.739	5	13	0	0	0				ActReg chr5 #7598	0	1
7599	5	54,280,964	54,281,663	699	1	11.857	9.286	18	13	0	1	1	ESM1	101	in gene	ActReg chr5 #7599	1	0
7600	5	54,528,101	54,529,783	1,682	1	9.808	11.039	17	16	2	2	2	LOC345643, CCNO	-5799, 566	upstream, in gene	ActReg chr5 #7600	0	1
7601	5	54,603,075	54,604,083	1,008	1	12.097	8.806	20	15	1	2	2	DHX29, SKIV2L2	-58, 3	upstream, in gene	ActReg chr5 #7601	1	0
7602	5	54,829,965	54,831,174	1,209	2	11.895	11.974	22	18	1	1	1	PPAP2A	304	in gene	ActReg chr5 #7602	1	1
7603	5	55,068,811	55,069,212	401	1	11.417	7	17	10	0	0	1	DDX4	35,166	in gene	ActReg chr5 #7603	1	0
7604	5	55,290,649	55,291,410	761	2	10.875	10.667	17	15	1	2	2	IL6ST, FLJ31104	-208, 40	upstream, in gene	ActReg chr5 #7604	1	1
7605	5	55,408,278	55,408,837	559	1	8.611	10.111	13	15	0	0	1	ANKRD55	120,629	in gene	ActReg chr5 #7605	0	1
7606	5	55,419,394	55,420,159	765	1	12.087	7.87	21	13	0	0	1	ANKRD55	109,410	in gene	ActReg chr5 #7606	1	0
7607	5	55,479,163	55,480,377	1,214	1	10.526	10.263	17	15	0	0	1	ANKRD55	49,416	in gene	ActReg chr5 #7607	1	0
7608	5	55,744,770	55,745,827	1,057	1	11.515	12.273	21	27	0	0	0				ActReg chr5 #7608	0	1
7609	5	56,006,956	56,007,559	603	1	10.158	11.947	17	19	0	0	0				ActReg chr5 #7609	0	1
7610	5	56,327,836	56,328,592	756	2	16.792	13	36	31	0	0	0				ActReg chr5 #7610	1	1
7611	5	56,682,578	56,683,171	593	1	6.263	10.158	8	15	0	0	0				ActReg chr5 #7611	0	1
7612	5	56,744,531	56,745,136	605	1	6.211	10	8	17	0	0	0				ActReg chr5 #7612	0	1
7613	5	57,031,062	57,031,831	769	1	11.5	10.583	17	19	0	0	0				ActReg chr5 #7613	0	1
7614	5	57,389,721	57,390,413	692	1	7.591	11.136	15	16	0	0	0				ActReg chr5 #7614	0	1
7615	5	57,610,283	57,610,871	588	1	11.111	12.944	16	22	0	0	0				ActReg chr5 #7615	0	1
7616	5	57,755,442	57,757,091	1,649	2	10.673	11.654	19	22	1	2	2	PLK2, LOC100289379	-353, 500	upstream, in gene	ActReg chr5 #7616	1	1
7617	5	57,878,433	57,879,579	1,146	2	17.971	21.314	39	45	1	1	1	RAB3C	67	in gene	ActReg chr5 #7617	1	1
7618	5	58,334,996	58,335,483	487	1	10.8	9.933	13	14	1	1	2	PDE4D, LOC642781	1448686, 204	in gene, in gene	ActReg chr5 #7618	1	0
7619	5	58,423,281	58,423,900	619	2	12.158	10.579	18	17	0	0	1	PDE4D	1,360,335	in gene	ActReg chr5 #7619	1	1
7620	5	58,489,597	58,490,240	643	1	6.667	13.667	13	23	0	0	1	PDE4D	1,294,007	in gene	ActReg chr5 #7620	0	1
7621	5	58,594,889	58,595,339	450	1	10.143	4.857	15	7	0	0	1	PDE4D	1,188,811	in gene	ActReg chr5 #7621	1	0
7622	5	59,189,275	59,190,459	1,184	2	15.243	19.838	32	44	1	0	1	PDE4D	594,058	in gene	ActReg chr5 #7622	1	1
7623	5	59,388,339	59,389,071	732	1	7.043	11.739	15	20	0	0	1	PDE4D	395,220	in gene	ActReg chr5 #7623	0	1
7624	5	59,492,098	59,492,581	483	1	9.667	8.133	14	14	0	0	1	PDE4D	291,586	in gene	ActReg chr5 #7624	1	0
7625	5	59,628,482	59,628,986	504	1	10.4	8.467	16	13	0	0	1	PDE4D	155,191	in gene	ActReg chr5 #7625	1	0
7626	5	59,995,634	59,996,758	1,124	1	7.171	12.629	14	24	1	1	1	DEPDC1B	-203	upstream	ActReg chr5 #7626	0	1
7627	5	60,457,657	60,459,129	1,472	2	12.587	11.043	20	17	1	1	2	NDUFAF2, C5orf43	217437, -91	downstream, upstream	ActReg chr5 #7627	1	1
7628	5	60,623,918	60,624,355	437	1	8.071	11.143	12	17	0	1	1	ZSWIM6	-3,964	upstream	ActReg chr5 #7628	0	1
7629	5	60,626,754	60,627,624	870	2	11.482	14.815	20	22	1	1	1	ZSWIM6	-911	upstream	ActReg chr5 #7629	1	1
7630	5	60,627,633	60,628,168	535	2	17.765	17.353	34	35	1	1	1	ZSWIM6	-200	upstream	ActReg chr5 #7630	1	1
7631	5	60,940,838	60,941,647	809	1	13.36	7.52	20	12	0	0	1	FLJ37543	7,606	in gene	ActReg chr5 #7631	1	0
7632	5	61,699,011	61,699,939	928	1	9.179	12.345	14	16	1	1	2	DIMT1L, IPO11	253, -9098	in gene, upstream	ActReg chr5 #7632	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7633	5	61,708,308	61,709,063	755	1	10.833	13.583	19	28	1	1	2	DIMT1L, IPO11	-8957, 112	upstream, in gene	ActReg chr5 #7633	0	1
7634	5	63,258,852	63,259,404	552	2	10.177	12.882	18	23	0	1	1	HTR1A	-1,582	upstream	ActReg chr5 #7634	1	1
7635	5	64,064,011	64,065,031	1,020	2	19.438	16.5	44	35	1	2	2	SFRS12IP1, CWC27	-25, -234	upstream, upstream	ActReg chr5 #7635	1	1
7636	5	64,494,350	64,494,872	522	1	9.562	5.688	15	9	0	0	1	ADAMTS6	283,093	in gene	ActReg chr5 #7636	1	0
7637	5	64,858,603	64,859,505	902	1	7.5	13.857	13	24	1	2	2	CENPK, PPWD1	-59, -77	upstream, upstream	ActReg chr5 #7637	0	1
7638	5	65,439,619	65,440,807	1,188	2	8.892	12.73	14	19	1	1	1	SFRS12	128	in gene	ActReg chr5 #7638	1	1
7639	5	65,528,426	65,529,169	743	1	12.261	10.87	23	18	0	0	1	FLJ46010	36,680	in gene	ActReg chr5 #7639	1	0
7640	5	67,510,833	67,512,295	1,462	1	9.087	10.891	14	17	1	0	0				ActReg chr5 #7640	0	1
7641	5	67,640,139	67,640,736	597	1	8.263	11.105	12	15	0	0	0				ActReg chr5 #7641	0	1
7642	5	67,729,869	67,730,562	693	1	10.454	14.136	16	30	0	0	0				ActReg chr5 #7642	0	1
7643	5	67,850,688	67,851,401	713	1	8.043	13.13	15	30	0	0	0				ActReg chr5 #7643	0	1
7644	5	67,979,349	67,980,003	654	1	10.429	12.714	19	24	0	0	0				ActReg chr5 #7644	0	1
7645	5	68,194,983	68,195,899	916	1	6.393	9.071	12	14	0	0	0				ActReg chr5 #7645	0	1
7646	5	68,462,526	68,463,451	925	1	9.241	13.621	15	24	1	1	1	CCNB1	75	in gene	ActReg chr5 #7646	0	1
7647	5	68,484,850	68,485,875	1,025	1	6.5	11.344	12	21	1	1	1	CENPH	-13	upstream	ActReg chr5 #7647	0	1
7648	5	68,628,363	68,629,065	702	1	5.773	11.546	9	15	1	0	0				ActReg chr5 #7648	0	1
7649	5	68,665,063	68,666,023	960	2	10.633	13.767	21	23	1	2	2	TAF9, RAD17	297, 419	in gene, in gene	ActReg chr5 #7649	1	1
7650	5	68,745,845	68,746,449	604	1	10.737	7	19	10	0	0	1	MARVELD2	35,208	downstream	ActReg chr5 #7650	1	0
7651	5	70,751,121	70,752,055	934	2	10.448	9.621	18	17	1	1	2	LOC100505674, BDP1	-9419, 146	upstream, in gene	ActReg chr5 #7651	1	1
7652	5	71,014,642	71,015,936	1,294	2	12.537	16.415	25	28	1	1	1	CARTPT	299	in gene	ActReg chr5 #7652	1	1
7653	5	71,228,676	71,229,199	523	1	10.875	7.875	16	11	0	0	0				ActReg chr5 #7653	1	0
7654	5	71,358,637	71,359,629	992	2	12.323	12.774	25	27	0	0	0				ActReg chr5 #7654	1	1
7655	5	71,363,159	71,363,946	787	1	9.8	14.28	20	26	0	0	0				ActReg chr5 #7655	0	1
7656	5	71,403,213	71,404,097	884	1	11.714	10.214	16	14	1	1	1	MAP1B	537	in gene	ActReg chr5 #7656	1	0
7657	5	71,603,767	71,604,712	945	2	10.667	13.033	21	22	1	1	2	MRPS27, LOC100130998	11845, -38	in gene, upstream	ActReg chr5 #7657	1	1
7658	5	71,761,285	71,762,071	786	1	11.833	9.958	17	17	0	0	1	ZNF366	41,571	in gene	ActReg chr5 #7658	1	0
7659	5	72,111,834	72,112,274	440	1	3.857	11.714	10	14	1	1	1	TNPO1	-364	upstream	ActReg chr5 #7659	0	1
7660	5	72,143,617	72,144,452	835	2	13.039	15.808	30	34	1	0	1	TNPO1	31,616	in gene	ActReg chr5 #7660	1	1
7661	5	72,250,994	72,251,942	948	1	6.8	10.433	12	18	1	1	1	FCHO2	-340	upstream	ActReg chr5 #7661	0	1
7662	5	72,511,812	72,512,584	772	2	11.708	11.792	21	18	1	0	0				ActReg chr5 #7662	1	1
7663	5	72,606,898	72,607,867	969	1	8.567	12.067	18	16	0	0	0				ActReg chr5 #7663	0	1
7664	5	72,793,809	72,794,948	1,139	2	11.111	12.306	20	22	1	1	1	BTF3	128	in gene	ActReg chr5 #7664	1	1
7665	5	72,860,936	72,861,420	484	1	7.8	11.533	13	15	1	2	2	ANKRA2, UTP15	333, -420	in gene, upstream	ActReg chr5 #7665	0	1
7666	5	73,313,487	73,314,348	861	1	9.222	14	14	23	0	0	0				ActReg chr5 #7666	0	1
7667	5	73,411,993	73,412,558	565	2	10.278	9.556	21	15	0	0	0				ActReg chr5 #7667	1	1
7668	5	73,496,977	73,497,700	723	1	10.174	13.565	14	25	0	0	0				ActReg chr5 #7668	0	1
7669	5	74,062,501	74,063,494	993	2	21	17.29	51	49	1	2	3	GFM2, NSA2, FAM169A	45, -106, 99618	in gene, upstream, downstream	ActReg chr5 #7669	1	1
7670	5	74,632,294	74,633,125	831	1	8.231	12.615	16	18	1	1	1	HMGCR	-284	upstream	ActReg chr5 #7670	0	1
7671	5	74,806,479	74,808,123	1,644	2	10.294	10.882	20	23	1	2	2	COL4A3BP, POLK	505, -356	in gene, upstream	ActReg chr5 #7671	1	1
7672	5	74,959,309	74,960,157	848	1	10.192	7.692	17	15	0	0	2	ANKDD1B, C5orf37	52273, 53580	in gene, downstream	ActReg chr5 #7672	1	0
7673	5	75,012,901	75,013,452	551	2	11	11.529	17	20	1	1	1	C5orf37	137	in gene	ActReg chr5 #7673	1	1
7674	5	75,181,622	75,182,241	619	1	10.1	10.85	14	17	0	0	0				ActReg chr5 #7674	0	1
7675	5	75,337,437	75,338,167	730	1	5.909	10.087	10	16	0	0	0				ActReg chr5 #7675	0	1
7676	5	75,399,612	75,400,491	879	2	15.393	24.643	41	65	0	0	1	SV2C	20,746	in gene	ActReg chr5 #7676	1	1
7677	5	76,086,381	76,087,040	659	1	10.619	12.524	17	24	0	0	0				ActReg chr5 #7677	0	1
7678	5	76,134,611	76,135,194	583	1	9.056	10.722	15	20	0	0	1	F2RL1	20,069	downstream	ActReg chr5 #7678	0	1
7679	5	76,169,994	76,170,461	467	1	9.643	7.571	16	12	0	0	1	S100Z	24,401	in gene	ActReg chr5 #7679	1	0
7680	5	76,382,498	76,383,448	950	2	11.517	12.241	18	19	1	3	3	ZBED3, SNORA47, LOC728723	57, -6577, 350	in gene, upstream, in gene	ActReg chr5 #7680	1	1
7681	5	76,428,971	76,429,471	500	1	10.733	8.533	14	13	0	0	1	LOC728723	46,598	in gene	ActReg chr5 #7681	1	0
7682	5	76,463,933	76,464,837	904	1	5.655	10.414	13	18	0	0	0				ActReg chr5 #7682	0	1
7683	5	76,787,612	76,788,605	993	2	11.258	11.548	17	15	1	1	1	WDR41	224	in gene	ActReg chr5 #7683	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7684	5	77,189,103	77,189,776	673	2	8.952	11.571	18	21	0	0	0				ActReg chr5 #7684	1	1
7685	5	77,590,321	77,590,998	677	1	11.619	9.333	16	17	1	1	1	AP3B1	-131	upstream	ActReg chr5 #7685	1	0
7686	5	77,655,340	77,656,868	1,528	2	14.083	16.646	24	29	1	2	2	LOC728769, SCAMP1	2630, -235	in gene, upstream	ActReg chr5 #7686	1	1
7687	5	77,881,811	77,882,608	797	2	11.4	10.72	18	15	0	0	1	LHFPL2	62,439	in gene	ActReg chr5 #7687	1	1
7688	5	77,892,997	77,893,631	634	1	10.895	5.526	18	10	0	0	1	LHFPL2	51,334	in gene	ActReg chr5 #7688	1	0
7689	5	77,943,155	77,943,716	561	1	9.222	6.278	16	10	1	1	1	LHFPL2	1,213	in gene	ActReg chr5 #7689	1	0
7690	5	77,995,227	77,996,146	919	1	14.69	10.207	31	16	0	0	0				ActReg chr5 #7690	1	0
7691	5	78,641,936	78,642,847	911	2	10.786	12.393	22	20	0	0	0				ActReg chr5 #7691	1	1
7692	5	78,809,483	78,810,727	1,244	2	12.128	11.897	25	20	1	1	1	HOMER1	-405	upstream	ActReg chr5 #7692	1	1
7693	5	78,908,218	78,908,677	459	1	11.467	7.267	18	12	1	1	1	PAPD4	204	in gene	ActReg chr5 #7693	1	0
7694	5	79,141,170	79,141,940	770	2	10.792	13.25	18	22	0	0	0				ActReg chr5 #7694	1	1
7695	5	79,252,033	79,252,777	744	1	10.087	12	16	20	0	0	0				ActReg chr5 #7695	0	1
7696	5	79,421,708	79,422,276	568	1	7.222	10.556	10	14	0	0	1	SERINC5	129,906	in gene	ActReg chr5 #7696	0	1
7697	5	79,695,253	79,695,772	519	1	11	7.562	16	12	0	0	1	ZFYVE16	-8,326	upstream	ActReg chr5 #7697	1	0
7698	5	80,596,894	80,597,884	990	2	13.161	13.613	23	28	1	2	2	LOC100131067, ZCCHC9	-1, -13	upstream, upstream	ActReg chr5 #7698	1	1
7699	5	80,715,920	80,716,376	456	1	3.357	9.5	5	15	0	0	1	SSBP2	330,924	in gene	ActReg chr5 #7699	0	1
7700	5	81,046,466	81,047,631	1,165	2	12.139	12.194	21	27	1	1	1	SSBP2	24	in gene	ActReg chr5 #7700	1	1
7701	5	81,147,450	81,148,031	581	2	11.5	11.389	20	20	0	0	0				ActReg chr5 #7701	1	1
7702	5	81,267,647	81,268,088	441	1	7.857	9.071	11	14	1	1	1	ATG10	23	in gene	ActReg chr5 #7702	0	1
7703	5	81,573,809	81,574,540	731	1	6.652	12.652	10	21	1	1	1	RPS23	61	in gene	ActReg chr5 #7703	0	1
7704	5	82,020,132	82,020,676	544	2	10.235	10.177	17	19	0	0	0				ActReg chr5 #7704	1	1
7705	5	82,248,047	82,248,536	489	1	7.6	10	13	14	0	0	0				ActReg chr5 #7705	0	1
7706	5	82,633,054	82,633,823	769	1	6.625	11.667	16	16	0	0	1	XRCC4	260,121	in gene	ActReg chr5 #7706	0	1
7707	5	82,769,253	82,769,811	558	1	11.235	12.529	16	23	1	1	1	VCAN	2,039	in gene	ActReg chr5 #7707	0	1
7708	5	83,267,891	83,268,555	664	1	12.905	5.15	22	10	0	0	1	EDIL3	412,388	in gene	ActReg chr5 #7708	1	0
7709	5	83,804,805	83,805,194	389	1	8	10.333	10	15	0	0	0				ActReg chr5 #7709	0	1
7710	5	86,212,665	86,213,370	705	2	11.909	12.318	21	23	0	0	0				ActReg chr5 #7710	1	1
7711	5	86,563,188	86,563,734	546	2	11.177	10.765	22	19	0	1	1	RASA1	-690	upstream	ActReg chr5 #7711	1	1
7712	5	86,596,496	86,597,120	624	1	8.95	7.105	19	14	0	0	1	RASA1	32,657	in gene	ActReg chr5 #7712	1	0
7713	5	86,708,443	86,709,342	899	2	8.214	12.107	20	17	1	1	1	CCNH	-56	upstream	ActReg chr5 #7713	1	1
7714	5	87,195,558	87,196,119	561	1	9.824	7.471	15	11	0	0	0				ActReg chr5 #7714	1	0
7715	5	87,436,721	87,437,534	813	2	13.08	14.8	29	31	1	0	0				ActReg chr5 #7715	1	1
7716	5	87,748,665	87,749,124	459	1	6.733	9.6	11	16	0	0	0				ActReg chr5 #7716	0	1
7717	5	87,956,672	87,957,492	820	1	6.769	13.615	13	22	1	0	2	LOC645323, MIR9-2	23538, 5675	in gene, downstream	ActReg chr5 #7717	0	1
7718	5	87,970,078	87,972,159	2,081	3	10.892	12.231	22	18	1	1	2	LOC645323, MIR9-2	9502, -8361	in gene, upstream	ActReg chr5 #7718	1	1
7719	5	87,976,090	87,976,914	824	2	9.269	8.346	13	16	1	0	1	LOC645323	4,118	in gene	ActReg chr5 #7719	1	1
7720	5	88,080,476	88,081,195	719	2	11.609	9.478	21	17	0	0	1	MEF2C	119,087	in gene	ActReg chr5 #7720	1	1
7721	5	89,769,734	89,770,951	1,217	2	13.29	14.158	21	24	1	2	2	MBLAC2, POLR3G	243, -339	in gene, upstream	ActReg chr5 #7721	1	1
7722	5	89,842,982	89,843,546	564	2	9.588	8.375	15	14	0	0	0				ActReg chr5 #7722	1	1
7723	5	89,854,063	89,854,998	935	2	19.724	17.552	52	42	1	1	1	GPR98	-87	upstream	ActReg chr5 #7723	1	1
7724	5	90,575,692	90,576,883	1,191	1	8.676	11.973	17	17	1	1	1	LOC729040	672	in gene	ActReg chr5 #7724	0	1
7725	5	90,678,959	90,679,740	781	1	12.583	8.458	17	13	0	1	2	ARRDC3, LOC100129716	-200, 3185	upstream, in gene	ActReg chr5 #7725	1	0
7726	5	91,144,148	91,144,849	701	1	13.046	8.818	28	16	0	0	0				ActReg chr5 #7726	1	0
7727	5	91,714,568	91,715,321	753	1	7.522	12.522	9	19	0	0	0				ActReg chr5 #7727	0	1
7728	5	92,304,824	92,305,379	555	1	4.471	9.222	8	15	0	0	0				ActReg chr5 #7728	0	1
7729	5	92,414,138	92,414,767	629	2	9	11.5	18	22	0	0	0				ActReg chr5 #7729	1	1
7730	5	92,527,605	92,528,329	724	1	12.739	7.478	19	11	0	0	0				ActReg chr5 #7730	1	0
7731	5	92,915,750	92,916,446	696	1	9.333	11.381	12	20	1	2	2	FLJ42709, NR2F1	905, -2945	in gene, upstream	ActReg chr5 #7731	0	1
7732	5	92,916,913	92,917,412	499	2	17.375	17.312	33	31	1	2	2	FLJ42709, NR2F1	-159, -1881	upstream, upstream	ActReg chr5 #7732	1	1
7733	5	92,947,502	92,948,349	847	1	7.577	13.769	12	24	0	0	2	FAM172A, MIR2277	499479, 8569	downstream, downstream	ActReg chr5 #7733	0	1
7734	5	92,948,361	92,948,785	424	1	5.231	9.615	6	14	0	0	2	FAM172A, MIR2277	498831, 7921	downstream, downstream	ActReg chr5 #7734	0	1
7735	5	92,956,043	92,956,984	941	1	7.429	13.276	15	25	1	1	2	FAM172A, MIR2277	490891, -19	in gene, upstream	ActReg chr5 #7735	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7736	5	92,956,991	92,957,537	546	1	8.611	11.778	15	21	1	1	2	FAM172A, MIR2277	490140, -770	in gene, upstream	ActReg chr5 #7736	0	1
7737	5	93,356,992	93,357,509	517	1	11	11.118	17	16	0	0	1	FAM172A	90,154	in gene	ActReg chr5 #7737	0	1
7738	5	93,446,937	93,447,812	875	2	9.28	11.286	17	17	1	1	1	FAM172A	30	in gene	ActReg chr5 #7738	1	1
7739	5	93,954,008	93,954,978	970	2	10.161	8.774	16	14	1	2	2	C5orf36, ANKRD32	-184, 102	upstream, in gene	ActReg chr5 #7739	1	1
7740	5	94,128,973	94,129,472	499	1	8.938	5	15	7	0	0	1	MCTP1	491,057	in gene	ActReg chr5 #7740	1	0
7741	5	94,753,680	94,754,181	501	1	9.125	3.375	16	6	0	0	1	FAM81B	26,882	in gene	ActReg chr5 #7741	1	0
7742	5	94,890,339	94,891,331	992	2	16.774	15.452	33	26	1	2	2	TTC37, ARSK	-126, 10	upstream, in gene	ActReg chr5 #7742	1	1
7743	5	95,047,895	95,048,482	587	1	6.579	11.158	12	17	0	0	0				ActReg chr5 #7743	0	1
7744	5	95,067,225	95,067,875	650	1	6.143	12.143	11	20	1	1	1	RHOBTB3	700	in gene	ActReg chr5 #7744	0	1
7745	5	95,194,308	95,195,036	728	1	7.591	10.864	11	18	0	0	1	C5orf27	6,736	in gene	ActReg chr5 #7745	0	1
7746	5	95,719,848	95,720,518	670	1	7.714	11.762	10	19	0	0	1	PCSK1	48,802	downstream	ActReg chr5 #7746	0	1
7747	5	95,766,996	95,769,273	2,277	2	13.634	14.324	30	27	1	1	1	PCSK1	851	in gene	ActReg chr5 #7747	1	1
7748	5	95,769,527	95,770,510	983	2	18.645	24.452	46	62	0	1	1	PCSK1	-1,033	upstream	ActReg chr5 #7748	1	1
7749	5	95,819,358	95,820,191	833	2	9.115	17.615	20	40	0	0	0				ActReg chr5 #7749	1	1
7750	5	95,908,443	95,909,183	740	1	12.652	9.174	20	15	0	0	0				ActReg chr5 #7750	1	0
7751	5	95,997,438	95,998,169	731	1	10.348	12.478	16	20	1	1	1	CAST	62	in gene	ActReg chr5 #7751	0	1
7752	5	95,998,340	95,999,147	807	1	7.92	12.48	13	17	1	1	1	CAST	1,002	in gene	ActReg chr5 #7752	0	1
7753	5	96,038,120	96,038,715	595	1	11.556	12.556	17	17	1	0	1	CAST	40,676	in gene	ActReg chr5 #7753	1	0
7754	5	96,142,905	96,143,798	893	2	10.143	13.893	15	28	1	1	1	ERAP1	541	in gene	ActReg chr5 #7754	1	1
7755	5	96,270,376	96,272,075	1,699	2	18.358	16.226	38	30	1	1	1	LNPEP	-121	upstream	ActReg chr5 #7755	1	1
7756	5	96,518,657	96,519,542	885	2	12.815	11.185	17	17	1	1	1	RIOK2	-94	upstream	ActReg chr5 #7756	1	1
7757	5	98,108,833	98,110,112	1,279	1	10.8	11.05	16	16	1	1	2	RGMB, FLJ35946	4473, -684	in gene, upstream	ActReg chr5 #7757	0	1
7758	5	98,264,220	98,265,600	1,380	2	10.227	10.75	17	20	1	2	2	CHD1, LOC100289230	-2672, 72	upstream, in gene	ActReg chr5 #7758	1	1
7759	5	98,652,760	98,653,361	601	1	7.158	10.053	11	18	0	0	0				ActReg chr5 #7759	0	1
7760	5	100,176,022	100,176,505	483	1	3.714	9.867	5	16	0	0	1	ST8SIA4	62,724	in gene	ActReg chr5 #7760	0	1
7761	5	100,236,007	100,237,006	999	1	5.655	11.839	10	22	1	1	1	ST8SIA4	2,481	in gene	ActReg chr5 #7761	0	1
7762	5	101,631,392	101,632,618	1,226	2	10.333	11.974	27	23	1	1	1	SLCO4C1	248	in gene	ActReg chr5 #7762	1	1
7763	5	102,170,099	102,170,746	647	1	4.1	10.75	7	18	0	0	0				ActReg chr5 #7763	0	1
7764	5	102,201,414	102,202,198	784	1	10.708	8.083	16	15	1	1	1	PAM	279	in gene	ActReg chr5 #7764	1	0
7765	5	102,455,355	102,456,552	1,197	2	10.895	13.132	28	30	1	1	2	GIN1, PPIP5K2	-111, -9304	upstream, upstream	ActReg chr5 #7765	1	1
7766	5	102,898,056	102,898,514	458	1	7.857	11.286	10	18	0	1	1	NUDT12	205	in gene	ActReg chr5 #7766	0	1
7767	5	103,425,006	103,425,622	616	2	9.667	10.474	17	17	0	0	0				ActReg chr5 #7767	1	1
7768	5	103,680,756	103,681,239	483	1	4.533	10.6	7	14	0	0	0				ActReg chr5 #7768	0	1
7769	5	104,482,621	104,482,982	361	1	9.167	10.25	12	15	0	0	0				ActReg chr5 #7769	0	1
7770	5	106,724,745	106,725,320	575	1	7.944	9.278	13	17	0	0	1	EFNA5	281,564	in gene	ActReg chr5 #7770	0	1
7771	5	106,804,984	106,805,577	593	1	10.053	12.526	16	23	0	0	1	EFNA5	201,316	in gene	ActReg chr5 #7771	0	1
7772	5	107,006,825	107,007,286	461	1	7.786	11.643	12	14	1	1	1	EFNA5	-459	upstream	ActReg chr5 #7772	0	1
7773	5	107,007,650	107,008,316	666	1	6.2	12	9	23	1	1	1	EFNA5	-1,387	upstream	ActReg chr5 #7773	0	1
7774	5	107,008,330	107,008,818	488	1	10.133	8.933	17	14	1	1	1	EFNA5	-1,978	upstream	ActReg chr5 #7774	1	0
7775	5	107,155,860	107,156,622	762	2	12.208	10.917	16	16	0	0	0				ActReg chr5 #7775	1	1
7776	5	107,717,374	107,717,852	478	1	9.8	11.733	13	15	1	1	1	FBXL17	186	in gene	ActReg chr5 #7776	0	1
7777	5	108,063,511	108,064,326	815	2	11.731	13.308	20	23	1	0	0				ActReg chr5 #7777	1	1
7778	5	110,074,076	110,075,154	1,078	1	7.706	11.529	15	16	1	1	1	SLC25A46	-139	upstream	ActReg chr5 #7778	0	1
7779	5	110,427,659	110,428,366	707	2	12.864	16.046	21	31	1	1	1	WDR36	142	in gene	ActReg chr5 #7779	1	1
7780	5	110,559,327	110,560,217	890	1	8.857	10.464	13	14	1	1	1	CAMK4	-310	upstream	ActReg chr5 #7780	0	1
7781	5	110,700,461	110,701,535	1,074	2	11.788	19.576	21	42	0	0	1	CAMK4	140,916	in gene	ActReg chr5 #7781	1	1
7782	5	110,702,585	110,703,275	690	2	11.454	8.955	21	15	0	0	1	CAMK4	142,848	in gene	ActReg chr5 #7782	1	1
7783	5	110,719,337	110,719,805	468	1	7.714	10.429	12	15	0	0	1	CAMK4	159,489	in gene	ActReg chr5 #7783	0	1
7784	5	110,847,374	110,848,561	1,187	1	11.405	7.027	17	11	1	2	2	STARD4, LOC100505678	190, 43	in gene, in gene	ActReg chr5 #7784	1	0
7785	5	111,495,965	111,497,069	1,104	2	34.143	36.371	113	126	1	2	3	NCRNA00219, SNORA13, EPB41L4A	294, -665, 258493	in gene, upstream, downstream	ActReg chr5 #7785	1	1
7786	5	111,884,193	111,884,696	503	1	11.133	5.067	21	9	0	0	0				ActReg chr5 #7786	1	0
7787	5	112,042,709	112,043,750	1,041	1	10.939	13.273	17	20	1	1	1	APC	11	in gene	ActReg chr5 #7787	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7788	5	112,257,339	112,258,017	678	1	8.455	12.546	13	18	1	1	1	REEP5	353	in gene	ActReg chr5 #7788	0	1
7789	5	112,311,913	112,312,934	1,021	2	11.312	11.531	20	19	1	1	2	LOC100287967, DCP2	15515, -10	in gene, upstream	ActReg chr5 #7789	1	1
7790	5	112,538,766	112,539,561	795	1	11.52	10.84	16	19	0	0	1	MCC	285,364	in gene	ActReg chr5 #7790	1	0
7791	5	112,823,542	112,824,531	989	2	9.645	11.097	17	18	1	1	1	MCC	491	in gene	ActReg chr5 #7791	1	1
7792	5	112,849,239	112,849,980	741	1	12.478	9.522	20	11	1	1	1	YTHDC2	218	in gene	ActReg chr5 #7792	1	0
7793	5	114,598,198	114,598,909	711	1	9.864	11.864	14	18	1	1	2	PGGT1B, CCDC112	16, 33905	in gene, downstream	ActReg chr5 #7793	0	1
7794	5	114,790,873	114,791,803	930	2	13.241	16.724	23	33	0	0	0				ActReg chr5 #7794	1	1
7795	5	114,961,334	114,962,100	766	1	6.625	11.208	11	14	1	2	3	TMED7-TICAM2, LOC100505719, TMED7	159, 23875, 159	in gene, downstream, in gene	ActReg chr5 #7795	0	1
7796	5	115,177,022	115,177,762	740	2	11.583	14.917	28	30	1	2	2	ATG12, AP3S1	156, -227	in gene, upstream	ActReg chr5 #7796	1	1
7797	5	115,910,303	115,911,033	730	1	11.174	15.348	22	28	1	1	1	SEMA6A	-117	upstream	ActReg chr5 #7797	0	1
7798	5	118,323,594	118,324,527	933	2	10.586	12.931	19	23	1	1	1	DTWD2	180	in gene	ActReg chr5 #7798	1	1
7799	5	118,603,885	118,604,416	531	1	12.059	8.294	19	11	1	1	1	TNFAIP8	-268	upstream	ActReg chr5 #7799	1	0
7800	5	119,495,664	119,496,329	665	1	10.381	6.048	22	11	0	0	0				ActReg chr5 #7800	1	0
7801	5	121,297,341	121,298,035	694	2	12.046	10.591	26	18	1	1	1	SRFBP1	32	in gene	ActReg chr5 #7801	1	1
7802	5	121,602,774	121,603,290	516	1	6.438	10.188	10	15	0	0	0				ActReg chr5 #7802	0	1
7803	5	121,686,282	121,686,705	423	1	9.769	7.385	16	13	0	0	1	SNCAIP	38,673	in gene	ActReg chr5 #7803	1	0
7804	5	122,372,089	122,373,091	1,002	1	11.625	9.062	18	18	1	1	1	PPIC	-165	upstream	ActReg chr5 #7804	1	0
7805	5	122,544,897	122,545,823	926	1	12.929	8.821	23	14	0	0	0				ActReg chr5 #7805	1	0
7806	5	122,758,608	122,759,787	1,179	2	23.757	24.486	78	74	1	1	1	CEP120	89	in gene	ActReg chr5 #7806	1	1
7807	5	122,847,249	122,848,212	963	1	9.6	11.433	14	15	1	1	1	CSNK1G3	-63	upstream	ActReg chr5 #7807	0	1
7808	5	123,043,721	123,044,215	494	1	9.6	8.533	16	14	0	0	0				ActReg chr5 #7808	1	0
7809	5	123,088,216	123,088,682	466	1	10.467	8.6	14	13	0	0	0				ActReg chr5 #7809	1	0
7810	5	123,882,208	123,882,884	676	2	11.909	11.682	26	26	0	0	0				ActReg chr5 #7810	1	1
7811	5	123,987,284	123,987,971	687	1	6.636	13	13	25	1	0	1	ZNF608	93,178	in gene	ActReg chr5 #7811	0	1
7812	5	123,996,964	123,997,708	744	1	10.696	5.522	14	9	0	0	1	ZNF608	83,469	in gene	ActReg chr5 #7812	1	0
7813	5	124,125,553	124,127,060	1,507	1	7.872	11.255	16	20	0	0	0				ActReg chr5 #7813	0	1
7814	5	124,396,223	124,397,053	830	2	13.577	13.077	28	21	0	0	0				ActReg chr5 #7814	1	1
7815	5	124,470,302	124,470,688	386	1	7.692	10.692	9	16	0	0	0				ActReg chr5 #7815	0	1
7816	5	125,789,598	125,790,218	620	1	10	5.9	16	13	0	0	1	GRAMD3	94,120	in gene	ActReg chr5 #7816	1	0
7817	5	125,930,486	125,931,404	918	2	11.931	14.414	28	23	1	2	2	ALDH7A1, PHAX	137, -5662	in gene, upstream	ActReg chr5 #7817	1	1
7818	5	125,936,136	125,937,296	1,160	2	29.389	32.611	64	89	1	2	2	ALDH7A1, PHAX	-5634, 109	upstream, in gene	ActReg chr5 #7818	1	1
7819	5	126,112,052	126,112,826	774	2	12.333	10.875	21	21	1	1	1	LMNB1	-394	upstream	ActReg chr5 #7819	1	1
7820	5	126,113,183	126,114,677	1,494	1	6.511	11.511	12	16	1	1	1	LMNB1	1,097	in gene	ActReg chr5 #7820	0	1
7821	5	126,365,226	126,366,748	1,522	1	8.106	11.553	19	15	1	1	1	3-Mar	453	in gene	ActReg chr5 #7821	0	1
7822	5	127,292,925	127,293,342	417	1	10.077	10.769	15	20	0	0	0				ActReg chr5 #7822	0	1
7823	5	127,418,349	127,419,348	999	2	11.742	12.419	20	20	1	2	2	FLJ33630, SLC12A2	-82, -635	upstream, upstream	ActReg chr5 #7823	1	1
7824	5	128,005,415	128,005,842	427	1	10.769	6.154	15	8	0	0	0				ActReg chr5 #7824	1	0
7825	5	130,970,306	130,971,309	1,003	1	9.129	13.806	19	23	1	1	2	RAPGEF6, FNIP1	122, 161949	in gene, downstream	ActReg chr5 #7825	0	1
7826	5	131,132,279	131,133,095	816	1	10.577	12.231	13	18	1	1	2	FNIP1, LOC100505572	69, 59934	in gene, downstream	ActReg chr5 #7826	0	1
7827	5	131,347,773	131,348,898	1,125	2	10.229	17.389	19	31	1	1	1	ACSL6	-986	upstream	ActReg chr5 #7827	1	1
7828	5	131,425,531	131,426,368	837	1	5.296	12.185	10	19	0	0	0				ActReg chr5 #7828	0	1
7829	5	131,438,472	131,439,227	755	1	5.739	11.348	9	16	0	0	0				ActReg chr5 #7829	0	1
7830	5	131,628,954	131,630,277	1,323	1	11.738	9.857	15	16	1	1	1	SLC22A4	-530	upstream	ActReg chr5 #7830	1	0
7831	5	131,725,162	131,726,182	1,020	2	11.062	11.531	16	20	0	0	1	SLC22A5	20,271	in gene	ActReg chr5 #7831	1	1
7832	5	131,825,579	131,827,110	1,531	2	9.479	12.167	20	20	1	1	1	IRF1	121	in gene	ActReg chr5 #7832	1	1
7833	5	131,832,104	131,832,807	703	1	7.591	11.954	12	18	1	1	1	IRF1	-5,990	upstream	ActReg chr5 #7833	0	1
7834	5	131,892,276	131,893,016	740	1	11.261	12.652	19	20	1	1	1	RAD50	30	in gene	ActReg chr5 #7834	0	1
7835	5	132,072,567	132,073,510	943	1	6.9	9.933	12	16	1	1	2	KIF3A, CCNI2	227, -10099	in gene, upstream	ActReg chr5 #7835	0	1
7836	5	132,201,960	132,202,855	875	2	13.143	13.179	19	20	1	3	4	GDF9, UQCRQ, LEAP2, AFF4	-1940, 98, -6941, 96937	upstream, in gene, upstream, downstream	ActReg chr5 #7836	1	1
7837	5	132,298,920	132,299,832	912	2	12.679	11.643	20	19	1	2	2	AFF4, LOC100506073	-22, -2098	upstream, upstream	ActReg chr5 #7837	1	1
7838	5	132,576,044	132,576,692	648	1	11.35	13.55	20	27	0	0	1	FSTL4	371,855	in gene	ActReg chr5 #7838	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7839	5	132,580,836	132,581,724	888	2	11.704	11.518	30	21	0	0	1	FSTL4	366,943	in gene	ActReg chr5 #7839	1	1
7840	5	132,582,959	132,583,676	717	1	11.046	6.182	13	10	0	0	1	FSTL4	364,906	in gene	ActReg chr5 #7840	1	0
7841	5	132,631,045	132,631,870	825	2	12.64	14.88	28	30	0	0	1	FSTL4	316,766	in gene	ActReg chr5 #7841	1	1
7842	5	132,901,585	132,902,218	633	2	9.35	11.6	16	20	0	0	1	FSTL4	46,322	in gene	ActReg chr5 #7842	1	1
7843	5	133,166,691	133,167,403	712	1	6.909	11.364	11	14	0	0	0				ActReg chr5 #7843	0	1
7844	5	133,339,572	133,340,264	692	1	7.545	13.136	11	19	1	1	1	VDAC1	515	in gene	ActReg chr5 #7844	0	1
7845	5	133,340,466	133,341,237	771	1	12.292	10	20	16	1	1	1	VDAC1	-418	upstream	ActReg chr5 #7845	1	0
7846	5	133,394,425	133,395,390	965	1	10.833	8.3	18	15	0	0	0				ActReg chr5 #7846	1	0
7847	5	133,512,226	133,513,016	790	2	12.522	14.833	20	26	1	1	1	SKP1	103	in gene	ActReg chr5 #7847	1	1
7848	5	133,561,435	133,562,540	1,105	2	10.057	9.714	19	20	1	1	1	PPP2CA	-37	upstream	ActReg chr5 #7848	1	1
7849	5	133,706,475	133,707,387	912	2	12.821	12.357	22	24	1	2	2	CDKL3, UBE2B	-4166, 61	upstream, in gene	ActReg chr5 #7849	1	1
7850	5	133,747,151	133,748,189	1,038	2	20.438	23.688	52	61	1	1	2	LOC100506132, CDKN2AIPNL	16239, -72	downstream, upstream	ActReg chr5 #7850	1	1
7851	5	133,877,198	133,877,743	545	1	7.133	12.412	12	21	0	0	1	PHF15	15,672	in gene	ActReg chr5 #7851	0	1
7852	5	134,073,767	134,075,006	1,239	2	13.895	11.21	24	29	1	1	1	CAMLG	180	in gene	ActReg chr5 #7852	1	1
7853	5	134,093,906	134,095,094	1,188	2	40.649	41.73	139	132	1	1	2	CAMLG, DDX46	20294, 39	downstream, in gene	ActReg chr5 #7853	1	1
7854	5	134,181,286	134,182,174	888	1	8.111	14.037	13	24	1	1	1	C5orf24	360	in gene	ActReg chr5 #7854	0	1
7855	5	134,210,570	134,211,353	783	1	11.125	10.417	18	14	1	1	1	TXNDC15	1,501	in gene	ActReg chr5 #7855	1	0
7856	5	134,240,191	134,240,857	666	2	9.905	10.952	15	17	1	1	2	TXNDC15, PCBD2	31064, -286	downstream, upstream	ActReg chr5 #7856	1	1
7857	5	134,543,576	134,545,055	1,479	1	8.978	11.696	16	21	0	0	0				ActReg chr5 #7857	0	1
7858	5	134,734,687	134,735,408	721	1	7.174	11.478	12	19	1	1	1	H2AFY	530	in gene	ActReg chr5 #7858	0	1
7859	5	135,355,982	135,356,994	1,012	2	10.188	9.75	16	20	0	0	1	TGFBI	-8,096	upstream	ActReg chr5 #7859	1	1
7860	5	135,389,187	135,389,852	665	2	12.4	12.5	20	20	0	0	1	TGFBI	24,935	in gene	ActReg chr5 #7860	1	1
7861	5	135,468,113	135,469,055	942	2	11.138	11.552	24	17	1	2	2	SMAD5OS, SMAD5	1995, 48	in gene, in gene	ActReg chr5 #7861	1	1
7862	5	135,700,658	135,701,494	836	2	15.615	17.154	35	43	0	1	1	TRPC7	88	in gene	ActReg chr5 #7862	1	1
7863	5	136,478,232	136,478,985	753	1	12.417	7.042	20	10	0	0	1	SPOCK1	356,410	in gene	ActReg chr5 #7863	1	0
7864	5	136,788,936	136,789,806	870	2	14.518	16.963	32	37	0	0	1	SPOCK1	45,647	in gene	ActReg chr5 #7864	1	1
7865	5	136,805,977	136,806,998	1,021	2	14.75	17.656	24	36	0	0	1	SPOCK1	28,531	in gene	ActReg chr5 #7865	1	1
7866	5	137,089,614	137,090,444	830	1	11.231	13.923	16	23	1	1	1	HNRNPA0	10	in gene	ActReg chr5 #7866	0	1
7867	5	137,367,997	137,368,592	595	1	5.789	11.632	10	17	1	2	2	FAM13B, LOC100130172	508, -188	in gene, upstream	ActReg chr5 #7867	0	1
7868	5	137,667,220	137,667,732	512	1	11.5	10.688	21	13	1	2	2	CDC25C, FAM53C	40, -5748	in gene, upstream	ActReg chr5 #7868	1	0
7869	5	137,672,947	137,674,322	1,375	2	44.256	55.465	121	164	1	2	2	CDC25C, FAM53C	-6118, 410	upstream, in gene	ActReg chr5 #7869	1	1
7870	5	137,687,808	137,689,544	1,736	3	12.527	10.546	32	31	1	1	2	FAM53C, KDM3B	15452, 391	downstream, in gene	ActReg chr5 #7870	1	1
7871	5	137,800,281	137,801,466	1,185	2	18.649	22.324	36	43	1	1	1	EGR1	-308	upstream	ActReg chr5 #7871	1	1
7872	5	137,827,463	137,828,032	569	1	13.056	10	20	15	1	0	0				ActReg chr5 #7872	1	0
7873	5	137,878,330	137,879,625	1,295	2	11.512	15.463	18	26	1	1	1	ETF1	-45	upstream	ActReg chr5 #7873	1	1
7874	5	137,910,694	137,911,654	960	2	11.867	17.533	24	31	1	1	1	HSPA9	144	in gene	ActReg chr5 #7874	1	1
7875	5	137,991,535	137,992,503	968	1	10.233	8.867	15	13	0	0	0				ActReg chr5 #7875	1	0
7876	5	137,998,154	137,999,096	942	1	10.483	11.966	22	18	0	0	0				ActReg chr5 #7876	0	1
7877	5	138,060,728	138,061,510	782	2	12.4	10.92	22	20	0	0	0				ActReg chr5 #7877	1	1
7878	5	138,609,317	138,610,303	986	1	11.767	10.2	17	16	1	3	3	MATR3, SNHG4, SNORA74A	369, 369, -4659	in gene, in gene, upstream	ActReg chr5 #7878	1	0
7879	5	138,677,174	138,678,159	985	1	10.903	11.935	15	19	1	1	2	MATR3, PAIP2	68225, 147	downstream, in gene	ActReg chr5 #7879	0	1
7880	5	138,739,405	138,740,233	828	1	12	12.077	17	20	1	1	3	LOC389333, SPATA24, DNAJC18	-8934, -43, 35395	upstream, upstream, downstream	ActReg chr5 #7880	0	1
7881	5	138,774,861	138,775,583	722	1	11.364	9.136	18	14	0	1	2	DNAJC18, ECSCR	-8, 9641	upstream, downstream	ActReg chr5 #7881	1	0
7882	5	139,016,881	139,017,620	739	1	7.783	12.435	17	32	1	0	1	UBE2D2	76,499	downstream	ActReg chr5 #7882	0	1
7883	5	139,076,466	139,077,141	675	1	9.381	13.191	14	20	1	0	0				ActReg chr5 #7883	0	1
7884	5	139,365,062	139,365,818	756	2	10.739	11.261	18	17	0	0	1	NRG2	57,444	in gene	ActReg chr5 #7884	1	1
7885	5	139,422,696	139,423,589	893	2	11.321	10.321	17	19	1	1	1	NRG2	-258	upstream	ActReg chr5 #7885	1	1
7886	5	139,487,052	139,487,708	656	1	11.55	9.85	16	13	1	2	2	LOC100505636, PURA	770, -6328	in gene, upstream	ActReg chr5 #7886	1	0
7887	5	139,492,776	139,493,616	840	1	6.654	10.769	10	15	2	2	2	LOC100505636, PURA	-5046, -512	upstream, upstream	ActReg chr5 #7887	0	1
7888	5	139,493,865	139,494,798	933	2	9.897	12.414	15	22	1	2	2	LOC100505636, PURA	-6161, 623	upstream, in gene	ActReg chr5 #7888	1	1
7889	5	139,601,269	139,601,944	675	1	7	10.857	13	17	0	0	1	C5orf32	46,953	in gene	ActReg chr5 #7889	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7890	5	139,779,971	139,782,233	2,262	2	14.9	15.471	30	34	1	2	2	ANKHD1-EIF4EBP3, ANKHD1	-327, -327	upstream, upstream	ActReg chr5 #7890	1	1
7891	5	139,943,609	139,944,661	1,052	2	12.606	18.727	33	39	1	3	4	SRA1, APBB3, SLC35A4, LOC100505798	-6457, 54, -285, 27542	upstream, in gene, upstream, downstream	ActReg chr5 #7891	1	1
7892	5	140,018,751	140,019,743	992	1	7.032	11.71	13	16	1	2	4	CD14, TMCO6, NDUFA2, IK	-5961, 235, 8123, -8137	upstream, in gene, downstream, upstream	ActReg chr5 #7892	0	1
7893	5	140,026,714	140,027,469	755	1	13.125	11.667	18	16	1	2	3	TMCO6, NDUFA2, IK	8079, 279, -293	downstream, in gene, upstream	ActReg chr5 #7893	1	0
7894	5	140,043,775	140,044,780	1,005	2	10.625	10.812	17	23	1	1	4	IK, WDR55, DND1, HARS	16893, -107, 8694, 26694	downstream, upstream, downstream, downstream	ActReg chr5 #7894	1	1
7895	5	140,070,517	140,071,486	969	1	13.167	9.267	21	16	1	2	3	HARS, HARS2, ZMAT2	-30, -17, -9031	upstream, upstream, upstream	ActReg chr5 #7895	1	0
7896	5	140,090,329	140,091,240	911	2	13.897	14.448	29	26	0	0	1	ZMAT2	10,752	downstream	ActReg chr5 #7896	1	1
7897	5	140,098,014	140,098,898	884	2	13.25	12.964	23	25	0	0	0				ActReg chr5 #7897	1	1
7898	5	140,105,259	140,106,105	846	2	13	12.846	25	25	0	0	0				ActReg chr5 #7898	1	1
7899	5	140,305,840	140,306,637	797	1	10.96	11.96	16	18	1	1	15	PCDHA@, PCDHA1, PCDHA2, PCDHA3, PCDHA4, PCDHA5, PCDHA6, PCDHA7, PCDHA8, PCDHA9, PCDHA10, PCDHA11, PCDHA12, PCDHA13, PCDHAC1	140362, 140362, 131794, 125455, 119566, 104877, 98588, 92269, 85331, 78881, 70604, 58407, 51307, 44384, -64	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	ActReg chr5 #7899	0	1
7900	5	140,420,203	140,421,132	929	2	13.759	12.828	25	23	0	0	2	PCDHB@, PCDHB1	-10312, -10312	upstream, upstream	ActReg chr5 #7900	1	1
7901	5	140,430,886	140,431,480	594	1	5.278	12.056	9	19	0	2	2	PCDHB@, PCDHB1	204, 204	in gene, in gene	ActReg chr5 #7901	0	1
7902	5	140,473,878	140,474,559	681	1	8.286	11.809	14	19	0	2	3	PCDHB@, PCDHB2, PCDHB3	43239, -19, -6016	in gene, upstream, upstream	ActReg chr5 #7902	0	1
7903	5	140,855,174	140,856,500	1,326	1	8.049	10.561	14	17	1	1	21	PCDHGA1, PCDHGA2, PCDHGA3, PCDHGB1, PCDHGA4, PCDHGB2, PCDHGA5, PCDHGB3, PCDHGA6, PCDHGA7, PCDHGB4, PCDHGA8, PCDHGB5, PCDHGA9, PCDHGB6, PCDHGA10, PCDHGB7, PCDHGA11, PCDHGA12, PCDHGC3, PCDHGC4	145585, 137483, 132236, 126009, 121069, 116134, 111939, 105875, 102186, 93370, 88385, 84354, 78142, 73317, 68067, 63094, 58555, 55300, 45679, 268, 8904	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	ActReg chr5 #7903	0	1
7904	5	140,892,966	140,893,795	829	1	7.808	10.808	12	16	1	0	23	PCDHGA1, PCDHGA2, PCDHGA3, PCDHGB1, PCDHGA4, PCDHGB2, PCDHGA5, PCDHGB3, PCDHGA6, PCDHGA7, PCDHGB4, PCDHGA8, PCDHGB5, PCDHGA9, PCDHGB6, PCDHGA10, PCDHGB7, PCDHGA11, PCDHGA12, PCDHGC3, PCDHGC4, PCDHGC5, DIAPH1	183128, 175026, 169779, 163552, 158612, 153677, 149482, 143418, 139729, 130913, 125928, 121897, 115685, 110860, 105610, 100637, 96098, 92843, 83222, 37811, 28639, 24572, 105242	downstream, downstream	ActReg chr5 #7904	0	1
7905	5	140,904,102	140,904,811	709	1	11.273	5.818	18	9	0	0	1	DIAPH1	94,166	in gene	ActReg chr5 #7905	1	0
7906	5	140,936,990	140,937,729	739	2	11.917	14.125	30	36	0	1	2	DIAPH1, LOC100505658	61263, -519	in gene, upstream	ActReg chr5 #7906	1	1
7907	5	140,943,389	140,944,307	918	2	33.586	32.207	111	92	0	0	2	DIAPH1, LOC100505658	54774, 5970	in gene, in gene	ActReg chr5 #7907	1	1
7908	5	140,998,310	140,999,170	860	2	19.741	17.556	47	43	1	1	2	DIAPH1, HDAC3	-118, 17683	upstream, downstream	ActReg chr5 #7908	1	1
7909	5	141,017,159	141,018,248	1,089	2	12.118	12.823	20	29	1	2	3	HDAC3, RELL2, FCHSD1	-1280, 1186, 13283	upstream, in gene, downstream	ActReg chr5 #7909	1	1
7910	5	141,037,514	141,038,211	697	2	11.546	11.954	17	23	0	1	2	FCHSD1, ARAP3	-6876, 23938	upstream, in gene	ActReg chr5 #7910	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7911	5	141,061,624	141,062,391	767	1	8.125	11.792	13	18	0	1	1	ARAP3	-207	upstream	ActReg chr5 #7911	0	1
7912	5	141,071,476	141,073,252	1,776	2	16.357	18.643	42	43	1	0	1	ARAP3	-10,564	upstream	ActReg chr5 #7912	1	1
7913	5	141,075,007	141,076,589	1,582	1	9.74	10.74	16	17	0	0	0				ActReg chr5 #7913	0	1
7914	5	141,093,132	141,093,948	816	1	8.68	15.32	14	27	0	0	0				ActReg chr5 #7914	0	1
7915	5	141,113,839	141,114,991	1,152	2	14.833	17.389	35	40	0	0	0				ActReg chr5 #7915	1	1
7916	5	141,121,834	141,123,840	2,006	2	14.127	21.032	47	69	0	0	0				ActReg chr5 #7916	1	1
7917	5	141,133,244	141,134,733	1,489	2	10.128	15.213	20	30	1	0	0				ActReg chr5 #7917	1	1
7918	5	141,229,499	141,230,092	593	1	10.579	7.25	16	12	1	0	1	PCDH1	28,149	downstream	ActReg chr5 #7918	1	0
7919	5	141,256,201	141,256,932	731	1	11.043	8.043	15	12	1	1	1	PCDH1	1,378	in gene	ActReg chr5 #7919	1	0
7920	5	141,258,235	141,259,140	905	1	10	13.069	16	20	1	1	1	PCDH1	-743	upstream	ActReg chr5 #7920	0	1
7921	5	141,261,975	141,263,697	1,722	2	12.778	15.759	28	32	1	1	1	PCDH1	-4,892	upstream	ActReg chr5 #7921	1	1
7922	5	141,432,907	141,433,347	440	1	9.929	10.214	14	15	0	0	0				ActReg chr5 #7922	0	1
7923	5	141,488,003	141,488,692	689	1	8.286	10.714	13	14	1	1	1	NDFIP1	23	in gene	ActReg chr5 #7923	0	1
7924	5	141,655,032	141,655,747	715	1	3.957	10.435	7	19	0	0	0				ActReg chr5 #7924	0	1
7925	5	141,693,627	141,694,064	437	1	6	10.714	10	15	0	0	1	SPRY4	10,775	in gene	ActReg chr5 #7925	0	1
7926	5	141,736,279	141,736,877	598	1	9.684	10.526	13	18	1	0	0				ActReg chr5 #7926	0	1
7927	5	141,851,644	141,852,396	752	2	11.083	11.917	19	23	0	0	0				ActReg chr5 #7927	1	1
7928	5	141,854,238	141,854,820	582	1	14.579	12.526	23	19	0	0	0				ActReg chr5 #7928	1	0
7929	5	142,150,453	142,151,201	748	1	10.208	11.625	17	17	1	1	1	ARHGAP26	535	in gene	ActReg chr5 #7929	0	1
7930	5	142,201,102	142,202,209	1,107	2	12.486	14.114	27	33	0	0	1	ARHGAP26	51,363	in gene	ActReg chr5 #7930	1	1
7931	5	142,206,557	142,207,377	820	1	11.769	10.538	19	19	0	0	1	ARHGAP26	56,675	in gene	ActReg chr5 #7931	1	0
7932	5	142,625,238	142,626,132	894	2	14.107	10.964	25	19	0	0	0				ActReg chr5 #7932	1	1
7933	5	142,782,691	142,783,468	777	1	8.792	11.5	20	16	1	0	1	NR3C1	31,998	in gene	ActReg chr5 #7933	0	1
7934	5	142,783,579	142,784,171	592	1	8.684	10.895	14	18	1	0	1	NR3C1	31,202	in gene	ActReg chr5 #7934	0	1
7935	5	142,784,596	142,785,480	884	1	8.821	11.786	11	21	1	0	1	NR3C1	30,039	in gene	ActReg chr5 #7935	0	1
7936	5	145,325,553	145,326,430	877	1	7.222	10.444	14	16	0	0	1	SH3RF2	9,865	in gene	ActReg chr5 #7936	0	1
7937	5	145,561,843	145,562,763	920	2	14.69	15.621	26	36	0	1	1	LARS	-9	upstream	ActReg chr5 #7937	1	1
7938	5	145,582,514	145,583,478	964	2	15.533	15.467	32	36	1	1	1	RBM27	-167	upstream	ActReg chr5 #7938	1	1
7939	5	145,826,293	145,827,529	1,236	2	21.256	21.308	58	50	1	1	1	TCERG1	38	in gene	ActReg chr5 #7939	1	1
7940	5	146,204,333	146,205,229	896	2	14.321	22.393	33	59	0	0	1	PPP2R2B	256,252	in gene	ActReg chr5 #7940	1	1
7941	5	146,888,732	146,889,743	1,011	1	9.094	11.906	15	18	1	0	0				ActReg chr5 #7941	0	1
7942	5	148,381,309	148,382,043	734	2	11	11.043	16	16	0	0	1	SH3TC2	61,061	in gene	ActReg chr5 #7942	1	1
7943	5	148,441,657	148,442,807	1,150	2	13.833	13.111	28	22	0	3	3	SH3TC2, MIR584, hCG_1980447	505, -260, -834	in gene, upstream, upstream	ActReg chr5 #7943	1	1
7944	5	148,513,440	148,514,531	1,091	1	12.257	8.343	23	14	0	1	1	ABLIM3	-7,069	upstream	ActReg chr5 #7944	1	0
7945	5	148,542,090	148,542,965	875	1	7.37	11	13	17	0	0	1	ABLIM3	21,473	in gene	ActReg chr5 #7945	0	1
7946	5	148,724,653	148,725,663	1,010	1	12.161	9.968	17	16	1	1	2	AFAP1L1, GRPEL2	73757, 181	downstream, in gene	ActReg chr5 #7946	1	0
7947	5	148,784,172	148,784,784	612	1	12.947	11.684	23	15	0	1	1	LOC728264	-1,962	upstream	ActReg chr5 #7947	1	0
7948	5	148,825,346	148,825,889	543	1	13.706	9.059	23	15	0	0	0				ActReg chr5 #7948	1	0
7949	5	148,835,139	148,836,154	1,015	1	12.613	9.839	22	16	0	0	0				ActReg chr5 #7949	1	0
7950	5	148,845,697	148,846,801	1,104	2	12.706	13.471	19	28	0	0	0				ActReg chr5 #7950	1	1
7951	5	148,865,552	148,866,398	846	1	9.077	10.692	17	17	0	0	1	CSNK1A1	65,032	downstream	ActReg chr5 #7951	0	1
7952	5	148,930,501	148,931,610	1,109	2	11.088	9.206	20	18	1	1	1	CSNK1A1	-48	upstream	ActReg chr5 #7952	1	1
7953	5	149,339,929	149,340,915	986	1	9.194	13.097	16	17	1	1	1	SLC26A2	122	in gene	ActReg chr5 #7953	0	1
7954	5	149,379,603	149,381,007	1,404	2	13.886	13.409	24	24	1	2	2	TIGD6, HMGXB3	-88, 136	upstream, in gene	ActReg chr5 #7954	1	1
7955	5	149,415,970	149,416,638	668	1	13.2	5.75	26	10	0	0	1	HMGXB3	36,135	in gene	ActReg chr5 #7955	1	0
7956	5	149,696,392	149,697,342	950	2	12.586	12.034	27	21	0	0	0				ActReg chr5 #7956	1	1
7957	5	149,736,951	149,738,364	1,413	1	7.841	13.614	16	20	1	1	1	TCOF1	455	in gene	ActReg chr5 #7957	0	1
7958	5	149,828,841	149,829,963	1,122	2	13.686	18.371	31	51	1	1	1	RPS14	-83	upstream	ActReg chr5 #7958	1	1
7959	5	149,880,082	149,880,928	846	1	13.518	7.963	23	13	0	1	1	NDST1	-7,169	upstream	ActReg chr5 #7959	1	0
7960	5	150,019,832	150,020,639	807	1	8.56	10.92	13	15	0	0	1	SYNPO	39,593	in gene	ActReg chr5 #7960	0	1
7961	5	150,079,781	150,081,025	1,244	2	10.692	13.051	21	20	1	1	2	RBM22, DCTN4	266, 58254	in gene, downstream	ActReg chr5 #7961	1	1
7962	5	150,137,919	150,138,907	988	1	10.742	8.097	17	15	1	1	1	DCTN4	244	in gene	ActReg chr5 #7962	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
7963	5	150,180,699	150,181,257	558	1	6.667	12.222	11	19	0	0	1	C5orf62	23,470	downstream	ActReg chr5 #7963	0	1
7964	5	150,284,106	150,285,099	993	2	16.581	20.9	38	52	1	1	1	ZNF300	-57	upstream	ActReg chr5 #7964	1	1
7965	5	150,325,728	150,326,539	811	1	10.077	12.577	22	22	1	0	0				ActReg chr5 #7965	0	1
7966	5	150,632,446	150,633,087	641	1	9.35	11.85	19	17	0	1	1	GM2A	153	in gene	ActReg chr5 #7966	0	1
7967	5	150,826,946	150,827,709	763	1	9.609	13.957	17	21	1	1	1	SLC36A1	164	in gene	ActReg chr5 #7967	0	1
7968	5	151,122,204	151,122,936	732	1	12.783	6.609	21	13	0	0	1	ATOX1	15,640	in gene	ActReg chr5 #7968	1	0
7969	5	151,124,380	151,125,634	1,254	1	14.75	11.175	22	20	0	0	1	ATOX1	13,203	in gene	ActReg chr5 #7969	1	0
7970	5	151,151,096	151,151,729	633	1	11.9	7.75	19	15	1	1	1	G3BP1	-64	upstream	ActReg chr5 #7970	1	0
7971	5	151,303,896	151,305,033	1,137	2	16.25	22.306	48	67	1	1	1	GLRA1	-67	upstream	ActReg chr5 #7971	1	1
7972	5	153,418,180	153,418,855	675	1	9.81	13.143	16	25	1	2	2	FAM114A2, MFAP3	-20, -2	upstream, upstream	ActReg chr5 #7972	0	1
7973	5	153,569,564	153,570,192	628	1	10.55	9.7	17	15	1	1	1	GALNT10	-417	upstream	ActReg chr5 #7973	1	0
7974	5	153,577,488	153,578,224	736	1	9.957	11.087	15	21	0	0	1	GALNT10	7,561	in gene	ActReg chr5 #7974	0	1
7975	5	153,656,456	153,656,937	481	1	11.8	11.867	17	15	0	0	1	GALNT10	86,401	in gene	ActReg chr5 #7975	0	1
7976	5	154,134,147	154,134,820	673	2	11.524	16.333	21	29	1	1	2	LARP1, LOC100505847	42021, -652	in gene, upstream	ActReg chr5 #7976	1	1
7977	5	154,237,702	154,238,501	799	2	10	11.88	23	21	1	2	2	C5orf4, CNOT8	-7888, -97	upstream, upstream	ActReg chr5 #7977	1	1
7978	5	154,317,512	154,318,214	702	2	10.136	11.682	21	23	1	2	2	GEMIN5, MRPL22	-87, -2770	upstream, upstream	ActReg chr5 #7978	1	1
7979	5	154,320,316	154,320,930	614	1	8.75	11.55	13	20	0	2	2	GEMIN5, MRPL22	-2847, -10	upstream, upstream	ActReg chr5 #7979	0	1
7980	5	154,461,905	154,462,527	622	1	8.737	11.632	13	21	0	0	0				ActReg chr5 #7980	0	1
7981	5	157,158,085	157,159,046	961	2	19.233	18.6	44	43	1	1	1	THG1L	242	in gene	ActReg chr5 #7981	1	1
7982	5	157,170,304	157,170,987	683	1	6.636	11.318	11	15	1	1	2	THG1L, LSM11	12322, -110	downstream, upstream	ActReg chr5 #7982	0	1
7983	5	157,562,499	157,563,273	774	1	7.542	12.833	12	22	0	0	0				ActReg chr5 #7983	0	1
7984	5	157,569,072	157,569,830	758	1	10.625	8.625	15	14	0	0	0				ActReg chr5 #7984	1	0
7985	5	157,817,504	157,818,117	613	1	6.5	12.2	9	23	0	0	0				ActReg chr5 #7985	0	1
7986	5	158,143,566	158,144,227	661	1	8.952	7.905	18	11	0	0	1	EBF1	382,892	in gene	ActReg chr5 #7986	1	0
7987	5	158,153,755	158,154,580	825	2	10.731	11.269	19	14	0	0	1	EBF1	372,621	in gene	ActReg chr5 #7987	1	1
7988	5	158,527,164	158,528,155	991	1	10.742	7.129	16	14	1	1	1	EBF1	-871	upstream	ActReg chr5 #7988	1	0
7989	5	159,008,748	159,009,349	601	1	10.474	10.947	16	20	0	0	0				ActReg chr5 #7989	0	1
7990	5	159,199,980	159,200,657	677	1	8.714	11.095	14	16	1	0	0				ActReg chr5 #7990	0	1
7991	5	159,329,339	159,330,207	868	2	13.852	13.593	28	21	0	0	0				ActReg chr5 #7991	1	1
7992	5	159,354,984	159,355,684	700	1	7.773	12.682	12	19	0	0	1	ADRA1B	11,594	in gene	ActReg chr5 #7992	0	1
7993	5	159,435,894	159,436,458	564	1	8.444	11.5	12	19	0	1	1	TTC1	-4	upstream	ActReg chr5 #7993	0	1
7994	5	159,545,717	159,547,022	1,305	1	8.366	11.122	14	15	1	1	1	PWWP2A	83	in gene	ActReg chr5 #7994	0	1
7995	5	159,591,901	159,592,872	971	2	10.323	11.774	20	19	0	0	0				ActReg chr5 #7995	1	1
7996	5	159,848,694	159,849,272	578	1	6.778	12.056	12	18	1	2	2	SLU7, PTTG1	-2815, 118	upstream, in gene	ActReg chr5 #7996	0	1
7997	5	159,890,483	159,891,151	668	1	8	10.048	12	15	0	0	0				ActReg chr5 #7997	0	1
7998	5	159,894,803	159,895,456	653	1	8.952	10.429	17	15	0	1	1	MIR3142	-6,322	upstream	ActReg chr5 #7998	0	1
7999	5	161,495,229	161,496,074	845	2	17.444	23.963	51	64	0	1	1	GABRG2	1,003	in gene	ActReg chr5 #7999	1	1
8000	5	162,886,732	162,887,227	495	1	8.667	13.4	14	17	1	2	2	NUDCD2, HMMR	164, -538	in gene, upstream	ActReg chr5 #8000	0	1
8001	5	162,932,218	162,933,226	1,008	2	10.719	14.781	24	32	1	1	1	MAT2B	2,491	in gene	ActReg chr5 #8001	1	1
8002	5	164,027,267	164,027,899	632	1	5.263	11.263	9	16	0	0	1	LOC100507193	303,526	in gene	ActReg chr5 #8002	0	1
8003	5	165,935,934	165,936,518	584	1	7.579	10.947	11	17	0	0	0				ActReg chr5 #8003	0	1
8004	5	165,989,001	165,989,826	825	2	10	14.308	19	28	0	0	0				ActReg chr5 #8004	1	1
8005	5	166,149,941	166,150,431	490	1	10.333	6.067	16	10	0	0	0				ActReg chr5 #8005	1	0
8006	5	167,913,053	167,913,944	891	2	31.286	28.25	95	76	1	1	1	RARS	35	in gene	ActReg chr5 #8006	1	1
8007	5	167,955,478	167,956,386	908	1	8.31	10.31	14	18	1	0	1	RARS	42,469	downstream	ActReg chr5 #8007	0	1
8008	5	168,083,210	168,083,805	595	1	7.722	11.833	10	19	0	0	1	SLIT3	644,626	downstream	ActReg chr5 #8008	0	1
8009	5	168,601,759	168,602,479	720	2	11.826	13.87	24	30	0	0	1	SLIT3	126,014	in gene	ActReg chr5 #8009	1	1
8010	5	169,077,649	169,078,459	810	1	11.52	6.84	15	12	0	0	1	DOCK2	13,803	in gene	ActReg chr5 #8010	1	0
8011	5	169,646,422	169,647,065	643	1	11.4	8.7	19	15	0	0	0				ActReg chr5 #8011	1	0
8012	5	169,878,876	169,879,460	584	1	7	10.737	13	17	0	0	1	KCNIP1	98,287	in gene	ActReg chr5 #8012	0	1
8013	5	169,919,999	169,920,692	693	1	5	11.682	8	20	0	0	1	KCNIP1	139,464	in gene	ActReg chr5 #8013	0	1
8014	5	170,024,006	170,024,778	772	1	13.583	8.917	19	16	0	0	1	KCNIP1	243,511	in gene	ActReg chr5 #8014	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8015	5	170,107,945	170,108,716	771	1	8.706	11.958	18	21	0	0	1	KCNIP1	327,449	in gene	ActReg chr5 #8015	0	1
8016	5	171,433,069	171,434,361	1,292	1	12.2	18.275	27	42	1	1	1	FBXW11	162	in gene	ActReg chr5 #8016	0	1
8017	5	171,615,117	171,616,086	969	2	10.933	12.1	17	20	1	2	2	STK10, EFCAB9	-255, -5575	upstream, upstream	ActReg chr5 #8017	1	1
8018	5	171,701,934	171,702,376	442	1	9.643	3.071	14	4	0	0	1	UBTD2	8,640	in gene	ActReg chr5 #8018	1	0
8019	5	172,197,286	172,198,683	1,397	2	9.279	12.605	16	21	1	1	1	DUSP1	219	in gene	ActReg chr5 #8019	1	1
8020	5	172,385,941	172,386,902	961	2	43.067	42.467	149	141	3	2	3	ERGIC1, LOC100288168, RPL26L1	125198, -50, -18	downstream, upstream, upstream	ActReg chr5 #8020	1	1
8021	5	172,410,429	172,411,168	739	2	10.542	10.75	19	19	1	1	1	ATP6V0E1	35	in gene	ActReg chr5 #8021	1	1
8022	5	172,571,148	172,571,985	837	2	14.692	12.154	28	28	0	1	2	C5orf41, BNIP1	88211, 121	downstream, in gene	ActReg chr5 #8022	1	1
8023	5	172,661,783	172,662,952	1,169	1	8.514	10.568	15	22	1	1	1	NKX2-5	-52	upstream	ActReg chr5 #8023	0	1
8024	5	172,685,214	172,685,761	547	1	11.444	9.444	17	13	0	0	0				ActReg chr5 #8024	1	0
8025	5	172,710,641	172,711,319	678	1	4.905	11.048	9	16	1	0	0				ActReg chr5 #8025	0	1
8026	5	172,883,547	172,884,383	836	2	10.885	10.808	17	17	0	0	0				ActReg chr5 #8026	1	1
8027	5	173,043,381	173,044,154	773	2	16	13.708	45	35	1	1	1	BOD1	-101	upstream	ActReg chr5 #8027	1	1
8028	5	173,344,816	173,345,467	651	1	15.15	9.85	31	17	0	0	1	CPEB4	29,810	in gene	ActReg chr5 #8028	1	0
8029	5	173,472,383	173,473,063	680	2	15.909	13.409	32	26	0	1	1	HMP19	-1	upstream	ActReg chr5 #8029	1	1
8030	5	173,509,087	173,509,815	728	1	12	7.913	19	13	0	0	1	HMP19	36,727	in gene	ActReg chr5 #8030	1	0
8031	5	173,656,795	173,657,269	474	1	10.733	7.267	18	12	0	0	0				ActReg chr5 #8031	1	0
8032	5	174,748,706	174,749,367	661	2	9.75	13.25	16	25	0	0	0				ActReg chr5 #8032	1	1
8033	5	174,944,469	174,945,375	906	1	13.143	5.429	20	9	0	0	1	SFXN1	39,408	in gene	ActReg chr5 #8033	1	0
8034	5	175,222,777	175,225,151	2,374	2	19.459	24.703	93	99	1	1	1	CPLX2	354	in gene	ActReg chr5 #8034	1	1
8035	5	175,238,356	175,239,068	712	1	6.611	10.227	14	16	0	0	1	CPLX2	15,102	in gene	ActReg chr5 #8035	0	1
8036	5	175,298,405	175,299,624	1,219	2	17.763	15.053	44	44	1	0	1	CPLX2	75,404	in gene	ActReg chr5 #8036	1	1
8037	5	175,815,096	175,816,706	1,610	2	11.706	13.235	21	25	2	2	3	NOP16, HIGD2A, CLTB	-361, 117, 27639	upstream, in gene, downstream	ActReg chr5 #8037	1	1
8038	5	175,843,427	175,844,159	732	2	14.318	15.727	31	38	1	1	1	CLTB	-253	upstream	ActReg chr5 #8038	1	1
8039	5	175,874,943	175,875,663	720	1	11.652	10.391	16	14	1	1	1	FAF2	-53	upstream	ActReg chr5 #8039	1	0
8040	5	175,963,345	175,965,433	2,088	2	15.2	15.354	27	28	1	2	2	RNF44, CDHR2	32, -5123	in gene, upstream	ActReg chr5 #8040	1	1
8041	5	176,037,818	176,038,231	413	1	4.333	12.077	7	20	0	1	2	GPRIN1, SNCB	-893, 19533	upstream, downstream	ActReg chr5 #8041	0	1
8042	5	176,038,351	176,038,935	584	2	10.833	12.167	20	22	0	1	2	GPRIN1, SNCB	-1512, 18914	upstream, downstream	ActReg chr5 #8042	1	1
8043	5	176,103,208	176,103,826	618	1	13.053	7.105	21	13	0	0	0				ActReg chr5 #8043	1	0
8044	5	176,216,705	176,217,404	699	1	11.429	6.286	22	12	0	0	0				ActReg chr5 #8044	1	0
8045	5	176,230,793	176,231,600	807	2	11.6	16.88	19	35	0	1	1	UNC5A	-6,364	upstream	ActReg chr5 #8045	1	1
8046	5	176,232,325	176,234,103	1,778	3	12.673	14.2	38	47	0	1	1	UNC5A	-4,346	upstream	ActReg chr5 #8046	1	1
8047	5	176,264,062	176,265,442	1,380	2	23.046	32.409	92	117	0	0	1	UNC5A	27,192	in gene	ActReg chr5 #8047	1	1
8048	5	176,433,384	176,434,172	788	2	11.208	12.708	16	21	1	1	1	UIMC1	-335	upstream	ActReg chr5 #8048	1	1
8049	5	176,729,894	176,731,129	1,235	1	8.316	11.658	14	20	1	2	4	NSD1, RAB24, PRELID1, MXD3	170431, 233, -324, 8781	downstream, in gene, upstream, downstream	ActReg chr5 #8049	0	1
8050	5	176,736,246	176,737,067	821	1	4.5	10.269	7	14	0	2	4	NSD1, RAB24, PRELID1, MXD3	176576, -5912, 5821, 2636	downstream, upstream, downstream, in gene	ActReg chr5 #8050	0	1
8051	5	176,776,257	176,779,239	982	2	11.742	13.226	22	26	1	2	2	LMAN2, RGS14	137, -6096	in gene, upstream	ActReg chr5 #8051	1	1
8052	5	176,874,559	176,875,986	1,427	1	11.378	8.2	16	20	1	1	3	GRK6, PRR7, DBN1	21585, 1476, 25422	downstream, in gene, downstream	ActReg chr5 #8052	1	0
8053	5	176,923,377	176,924,089	712	1	7.227	11.954	10	21	1	1	2	PDLIM7, DOK3	869, 13694	in gene, downstream	ActReg chr5 #8053	0	1
8054	5	176,943,302	176,944,518	1,216	2	13.579	17.895	32	40	1	2	3	DOK3, DDX41, FAM193B	-6483, 57, 37638	upstream, in gene, downstream	ActReg chr5 #8054	1	1
8055	5	176,972,993	176,974,015	1,022	1	10.097	12.742	17	21	0	0	1	FAM193B	8,044	in gene	ActReg chr5 #8055	0	1
8056	5	177,631,173	177,631,767	594	1	8.778	12.222	14	17	1	1	2	HNRNPAB, AGXT2L2	-38, 28333	upstream, downstream	ActReg chr5 #8056	0	1
8057	5	177,633,071	177,633,648	577	1	5.611	10.944	7	16	0	1	2	HNRNPAB, AGXT2L2	1851, 26444	in gene, downstream	ActReg chr5 #8057	0	1
8058	5	178,053,085	178,053,867	782	2	8.16	10.4	18	16	1	1	1	CLK4	578	in gene	ActReg chr5 #8058	1	1
8059	5	178,286,615	178,287,249	634	1	12.05	7.95	18	11	1	1	1	ZNF354B	-22	upstream	ActReg chr5 #8059	1	0
8060	5	178,322,645	178,323,127	482	1	9	10.667	12	13	1	1	1	ZFP2	-30	upstream	ActReg chr5 #8060	0	1
8061	5	178,486,929	178,487,867	938	2	9.552	17.069	18	34	1	1	1	ZNF354C	-209	upstream	ActReg chr5 #8061	1	1
8062	5	179,050,233	179,051,834	1,601	1	9	11.38	17	21	1	1	1	HNRNPH1	-311	upstream	ActReg chr5 #8062	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8063	5	179,105,146	179,106,253	1,107	1	13.229	10.714	21	19	1	1	1	CBY3	2,276	in gene	ActReg chr5 #8063	1	0
8064	5	179,234,169	179,234,919	750	1	8.958	10.333	12	13	1	2	3	MGAT4B, MIR1229, SQSTM1	-592, -9198, 1156	upstream, upstream, in gene	ActReg chr5 #8064	0	1
8065	5	179,245,818	179,247,129	1,311	2	13.195	10.488	26	17	0	0	1	SQSTM1	13,085	in gene	ActReg chr5 #8065	1	1
8066	5	179,247,299	179,248,336	1,037	2	12.844	14.062	25	23	1	0	1	SQSTM1	14,429	in gene	ActReg chr5 #8066	1	1
8067	5	179,497,783	179,498,765	982	1	7.3	10.419	14	19	1	1	1	RNF130	835	in gene	ActReg chr5 #8067	0	1
8068	5	179,779,467	179,780,557	1,090	2	9.853	10.941	20	20	1	1	1	CPT2	303	in gene	ActReg chr5 #8068	1	1
8069	5	179,920,943	179,921,640	697	2	10.636	16.182	25	35	1	1	1	CNOT6	-126	upstream	ActReg chr5 #8069	1	1
8070	5	180,237,151	180,238,154	1,003	2	9.188	11.719	16	18	1	1	1	MGAT1	-515	upstream	ActReg chr5 #8070	1	1
8071	5	180,287,776	180,288,881	1,105	2	9.543	12.286	18	19	1	1	1	ZFP62	-42	upstream	ActReg chr5 #8071	1	1
8072	5	180,527,455	180,527,867	412	1	4	10.615	6	18	1	0	0				ActReg chr5 #8072	0	1
8073	5	180,596,776	180,597,269	493	1	10.6	11.933	15	20	1	0	0				ActReg chr5 #8073	0	1
8074	5	180,614,292	180,615,020	728	1	7.87	12.435	12	19	0	0	1	TRIM7	17,521	downstream	ActReg chr5 #8074	0	1
8075	5	180,618,091	180,619,174	1,083	2	11.265	14.235	23	22	1	1	2	TRIM7, LOC100507546	13545, -6570	downstream, upstream	ActReg chr5 #8075	1	1
8076	5	180,631,794	180,632,510	716	1	6.318	12.364	11	23	1	1	2	TRIM7, LOC100507546	25, 6950	in gene, downstream	ActReg chr5 #8076	0	1
8077	5	180,644,627	180,645,673	1,046	1	13.576	10.394	23	15	1	1	1	TRIM41	-5,156	upstream	ActReg chr5 #8077	1	0
8078	5	180,648,488	180,649,792	1,304	2	12.39	14.366	20	29	1	1	1	TRIM41	-1,166	upstream	ActReg chr5 #8078	1	1
8079	5	180,649,926	180,650,968	1,042	2	12.562	11.938	20	23	3	1	1	TRIM41	141	in gene	ActReg chr5 #8079	1	1
8080	5	180,670,490	180,671,278	788	1	11	8.32	19	12	1	5	6	TRIM41, GNB2L1, SNORD96A, LOC100289627, SNORD95, LOC100507619	20578, 22, -1995, 1919, 508, -2623	downstream, in gene, upstream, in gene, upstream, upstream	ActReg chr5 #8080	1	0
8081	5	180,687,687	180,689,213	1,526	2	12.979	10.596	26	18	1	2	3	LOC100507619, TRIM52, LOC100507602	14943, -331, 237	downstream, upstream, in gene	ActReg chr5 #8081	1	1
8082	6	292,096	292,748	652	1	8.476	11.619	15	16	1	1	1	DUSP22	321	in gene	ActReg chr6 #8082	0	1
8083	6	692,699	693,546	847	2	17.741	15.667	37	40	1	1	1	EXOC2	-13	upstream	ActReg chr6 #8083	1	1
8084	6	711,032	711,525	493	1	5.75	11.125	9	18	1	0	0				ActReg chr6 #8084	0	1
8085	6	1,335,633	1,336,081	448	1	6.429	9.357	8	15	0	0	0				ActReg chr6 #8085	0	1
8086	6	2,658,894	2,659,518	624	1	8.053	11.474	15	21	0	0	1	MYLK4	91,948	downstream	ActReg chr6 #8086	0	1
8087	6	2,765,450	2,765,922	472	2	9.6	12.733	15	23	1	1	1	WRNIP1	20	in gene	ActReg chr6 #8087	1	1
8088	6	2,989,617	2,990,089	472	1	9.333	10.2	13	13	1	1	2	DKFZP686I15217, NQO2	1652, -10214	in gene, downstream	ActReg chr6 #8088	0	1
8089	6	3,069,102	3,069,564	462	1	7.571	9.857	11	12	1	1	1	RIPK1	-7,725	upstream	ActReg chr6 #8089	0	1
8090	6	3,258,903	3,259,540	637	2	11.15	13.45	18	27	1	1	3	LOC100507294, PSMG4, SLC22A23	31062, 59, 197572	in gene, in gene, downstream	ActReg chr6 #8090	1	1
8091	6	3,324,249	3,325,076	827	1	7.269	10.769	12	17	0	0	1	SLC22A23	132,131	in gene	ActReg chr6 #8091	0	1
8092	6	3,808,914	3,809,510	596	1	7.895	10.842	12	19	0	0	0				ActReg chr6 #8092	0	1
8093	6	5,003,778	5,004,321	543	1	8	10.588	10	15	1	1	1	RPP40	222	in gene	ActReg chr6 #8093	0	1
8094	6	5,261,285	5,261,973	688	1	5.333	10.952	8	20	1	2	2	LYRM4, FARS2	-457, 45	upstream, in gene	ActReg chr6 #8094	0	1
8095	6	7,312,986	7,313,663	677	1	7.571	11.333	14	14	1	1	1	SSR1	217	in gene	ActReg chr6 #8095	0	1
8096	6	10,694,641	10,695,089	448	1	10.143	7.714	14	10	1	2	2	C6orf52, PAK1IP1	165, -323	in gene, upstream	ActReg chr6 #8096	1	0
8097	6	10,722,773	10,723,549	776	2	10.333	11.25	22	21	1	1	1	TMEM14C	13	in gene	ActReg chr6 #8097	1	1
8098	6	10,747,452	10,748,116	664	2	9.667	10.238	16	19	1	2	2	LOC100506379, TMEM14B	112, -211	in gene, upstream	ActReg chr6 #8098	1	1
8099	6	10,886,828	10,887,594	766	2	14.792	14.458	36	33	1	2	2	GCM2, SYCP2L	-5113, 147	upstream, in gene	ActReg chr6 #8099	1	1
8100	6	11,093,612	11,094,416	804	2	8.08	11.4	18	17	1	1	2	LOC221710, HERV-FRD	-252, 18057	upstream, downstream	ActReg chr6 #8100	1	1
8101	6	11,143,826	11,144,425	599	2	16.474	12.158	32	27	0	0	1	LOC221710	49,859	downstream	ActReg chr6 #8101	1	1
8102	6	11,207,316	11,207,729	413	1	11.462	7.769	17	12	0	0	2	NEDD9, LOC100506431	175059, -7814	in gene, upstream	ActReg chr6 #8102	1	0
8103	6	11,535,762	11,536,366	604	2	8.842	11.526	18	23	0	1	1	TMEM170B	-2,447	upstream	ActReg chr6 #8103	1	1
8104	6	12,441,257	12,441,763	506	1	8.188	10.938	12	20	0	0	0				ActReg chr6 #8104	0	1
8105	6	13,328,492	13,329,148	656	1	5.05	10.9	9	17	1	1	1	TBC1D7	-33	upstream	ActReg chr6 #8105	0	1
8106	6	13,575,171	13,575,560	389	1	7.833	10.083	11	12	1	1	1	SIRT5	573	in gene	ActReg chr6 #8106	0	1
8107	6	13,614,726	13,616,092	1,366	2	21.262	22.619	77	76	1	1	3	SIRT5, NOL7, RANBP9	40617, -150, 96387	downstream, upstream, downstream	ActReg chr6 #8107	1	1
8108	6	13,712,228	13,712,706	478	1	9.8	8.2	17	11	1	1	1	RANBP9	-671	upstream	ActReg chr6 #8108	1	0
8109	6	14,001,583	14,002,453	870	1	11.111	6.444	17	9	0	0	0				ActReg chr6 #8109	1	0
8110	6	15,245,591	15,246,363	772	2	11.333	12.125	24	21	1	1	2	JARID2, LOC100506681	-550, 2910	upstream, downstream	ActReg chr6 #8110	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8111	6	15,691,462	15,691,992	530	1	8.75	6.875	16	13	0	0	0				ActReg chr6 #8111	1	0
8112	6	16,334,829	16,335,392	563	2	10.389	10	15	18	0	0	1	ATXN1	426,611	in gene	ActReg chr6 #8112	1	1
8113	6	16,681,657	16,682,197	540	2	9.235	9.588	14	17	0	0	1	ATXN1	79,794	in gene	ActReg chr6 #8113	1	1
8114	6	16,766,392	16,766,797	405	1	9.385	4.462	15	6	0	1	1	ATXN1	-4,873	upstream	ActReg chr6 #8114	1	0
8115	6	17,706,862	17,707,527	665	1	7.762	12.286	16	26	1	1	1	NUP153	-376	upstream	ActReg chr6 #8115	0	1
8116	6	17,907,904	17,908,435	531	1	7.235	12.059	11	20	0	0	1	KIF13A	79,630	in gene	ActReg chr6 #8116	0	1
8117	6	18,122,580	18,123,011	431	1	9.929	7.429	14	12	1	1	2	NHLRC1, TPMT	56, 32579	in gene, downstream	ActReg chr6 #8117	1	0
8118	6	19,988,816	19,989,285	469	2	9.533	8.867	15	17	0	0	0				ActReg chr6 #8118	1	1
8119	6	20,534,365	20,534,879	514	1	10.438	6.625	15	10	0	1	1	CDKAL1	-66	upstream	ActReg chr6 #8119	1	0
8120	6	20,877,559	20,878,234	675	2	10.191	9.381	17	16	0	0	1	CDKAL1	343,208	in gene	ActReg chr6 #8120	1	1
8121	6	21,022,608	21,023,069	461	1	9.714	9.929	15	13	0	0	1	CDKAL1	488,150	in gene	ActReg chr6 #8121	1	0
8122	6	24,126,905	24,127,497	592	1	6	10.737	12	17	0	1	1	NRSN1	787	in gene	ActReg chr6 #8122	0	1
8123	6	24,402,867	24,403,650	783	2	9.8	13.16	16	21	1	1	1	MRS2	105	in gene	ActReg chr6 #8123	1	1
8124	6	24,494,867	24,495,500	633	1	11.2	6.05	22	11	1	2	2	GPLD1, ALDH5A1	-5333, -14	upstream, upstream	ActReg chr6 #8124	1	0
8125	6	24,666,910	24,667,542	632	1	8.1	10.6	12	16	1	2	2	TTRAP, ACOT13	-111, -37	upstream, upstream	ActReg chr6 #8125	0	1
8126	6	24,775,054	24,775,839	785	1	6.917	9.667	11	13	1	1	1	GMNN	282	in gene	ActReg chr6 #8126	0	1
8127	6	25,138,459	25,138,985	526	1	7.882	9.353	11	15	0	0	0				ActReg chr6 #8127	0	1
8128	6	25,652,064	25,652,962	898	2	16.483	13.931	37	33	1	1	1	SCGN	84	in gene	ActReg chr6 #8128	1	1
8129	6	25,660,631	25,661,214	583	2	9	9.111	17	20	0	0	1	SCGN	8,493	in gene	ActReg chr6 #8129	1	1
8130	6	26,020,714	26,021,161	447	1	10.286	6	15	9	1	3	4	HIST1H1A, HIST1H3A, HIST1H4A, HIST1H4B	-2897, 219, -970, 6543	upstream, in gene, upstream, downstream	ActReg chr6 #8130	1	0
8131	6	26,031,881	26,032,369	488	1	7.2	11.667	11	14	1	3	4	HIST1H4A, HIST1H4B, HIST1H3B, HIST1H2AB	10218, -4645, 163, 1671	downstream, upstream, in gene, downstream	ActReg chr6 #8131	0	1
8132	6	26,033,254	26,033,685	431	1	2.923	10.385	6	14	1	3	4	HIST1H4B, HIST1H3B, HIST1H2AB, HIST1H2BB	-5989, -1181, 327, 10416	upstream, upstream, in gene, downstream	ActReg chr6 #8132	0	1
8133	6	26,056,446	26,056,838	392	1	3.615	10.308	4	14	1	1	1	HIST1H1C	57	in gene	ActReg chr6 #8133	0	1
8134	6	26,220,548	26,220,963	415	1	10.231	9.385	15	13	0	2	3	HIST1H2BG, HIST1H2AE, HIST1H3E	-3883, 3607, -4628	upstream, downstream, upstream	ActReg chr6 #8134	1	0
8135	6	26,240,538	26,241,069	531	1	8.706	9.412	12	15	1	2	4	HIST1H1D, HIST1H4F, HIST1H4G, HIST1H3F	-5587, 149, 6402, 10032	upstream, in gene, downstream, downstream	ActReg chr6 #8135	0	1
8136	6	26,285,224	26,285,853	629	1	8.947	10.737	13	19	1	2	2	LOC100507025, HIST1H4H	225, 189	in gene, in gene	ActReg chr6 #8136	0	1
8137	6	26,522,167	26,522,714	547	1	7.765	10.235	12	16	1	1	1	HCG11	506	in gene	ActReg chr6 #8137	0	1
8138	6	26,538,167	26,538,734	567	1	7.222	10.278	10	16	1	1	1	HMGN4	-122	upstream	ActReg chr6 #8138	0	1
8139	6	26,554,141	26,554,698	557	1	4.889	9.333	9	16	0	0	1	HMGN4	15,847	downstream	ActReg chr6 #8139	0	1
8140	6	27,560,386	27,560,839	453	1	10.5	8.429	15	13	0	0	0				ActReg chr6 #8140	1	0
8141	6	27,636,244	27,636,665	421	1	6	9.923	9	16	0	0	0				ActReg chr6 #8141	0	1
8142	6	27,720,902	27,721,355	453	1	4.167	10.571	6	16	0	0	0				ActReg chr6 #8142	0	1
8143	6	27,804,675	27,805,497	822	1	6.12	12.04	13	23	0	3	3	HIST1H4K, HIST1H2AK, HIST1H2BN	-5781, 1038, -1278	upstream, downstream, upstream	ActReg chr6 #8143	0	1
8144	6	27,860,677	27,861,420	743	1	11.522	9.565	19	15	2	3	3	HIST1H3J, HIST1H2AM, HIST1H2BO	-2478, -85, 155	upstream, upstream, upstream	ActReg chr6 #8144	1	0
8145	6	28,048,440	28,049,033	593	1	8.579	7.789	15	12	0	2	3	LOC100507241, ZNF165, LOC100129195	221, 254, 56335	in gene, in gene, downstream	ActReg chr6 #8145	1	0
8146	6	28,092,240	28,092,848	608	1	6.211	10.105	11	18	0	1	2	LOC100129195, ZSCAN16	12527, 157	in gene, in gene	ActReg chr6 #8146	0	1
8147	6	28,109,306	28,109,997	691	2	11.364	11.682	19	18	1	2	2	LOC100129195, ZNF192	-4580, -65	upstream, upstream	ActReg chr6 #8147	1	1
8148	6	28,323,552	28,324,013	461	1	4.467	9.867	6	14	0	1	2	ZNF323, ZKSCAN3	266, 6091	in gene, in gene	ActReg chr6 #8148	0	1
8149	6	28,554,768	28,555,366	598	1	6.158	9.105	10	18	1	1	1	SCAND3	45	in gene	ActReg chr6 #8149	0	1
8150	6	28,574,207	28,574,753	546	1	4.333	9.556	6	15	0	0	0				ActReg chr6 #8150	0	1
8151	6	28,834,197	28,834,726	529	1	6.471	9.529	9	16	0	1	1	LOC401242	-3,007	upstream	ActReg chr6 #8151	0	1
8152	6	29,759,792	29,760,313	521	1	9.25	7.938	14	13	1	0	0				ActReg chr6 #8152	1	0
8153	6	30,294,837	30,295,229	392	1	5.5	10.583	8	16	1	2	2	HCG18, TRIM39	-106, 412	upstream, in gene	ActReg chr6 #8153	0	1
8154	6	30,345,871	30,346,516	645	2	9.25	9.25	19	15	0	0	0				ActReg chr6 #8154	1	1
8155	6	30,523,856	30,524,627	771	1	8.167	11.75	13	22	1	2	2	GNL1, PRR3	1130, -245	in gene, upstream	ActReg chr6 #8155	0	1
8156	6	30,640,513	30,641,236	723	2	14.773	13.273	32	30	1	1	2	DHX16, KIAA1949	-44, 14798	upstream, downstream	ActReg chr6 #8156	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8157	6	30,875,346	30,876,026	680	1	9.286	14.429	17	24	1	2	3	DDR1, GTF2H4, VARS2	23825, -291, -6296	downstream, upstream, upstream	ActReg chr6 #8157	0	1
8158	6	30,881,876	30,882,673	797	1	6.08	9.6	11	13	1	1	2	GTF2H4, VARS2	6297, 292	downstream, in gene	ActReg chr6 #8158	0	1
8159	6	31,261,020	31,261,637	617	2	7.8	11.2	15	24	0	0	0				ActReg chr6 #8159	1	1
8160	6	31,509,325	31,510,521	1,196	2	9.892	12	18	20	1	4	5	BAT1, SNORD117, SNORD84, ATP6V1G2, NFKBIL1	302, -5697, -968, 4704, -4705	in gene, upstream, upstream, downstream, upstream	ActReg chr6 #8160	1	1
8161	6	31,633,388	31,633,871	483	1	5.733	11	8	15	1	4	5	APOM, C6orf47, BAT4, CSNK2B, LY6G5B	9958, -5080, -466, -28, -5099	downstream, upstream, upstream, upstream, upstream	ActReg chr6 #8161	0	1
8162	6	31,707,417	31,707,971	554	1	7.444	10.556	10	15	1	2	3	DDAH2, CLIC1, MSH5	-9655, -3353, -31	upstream, upstream, upstream	ActReg chr6 #8162	0	1
8163	6	31,830,623	31,831,063	440	1	9.214	9.5	13	14	1	1	2	NEU1, SLC44A4	-134, 15980	upstream, downstream	ActReg chr6 #8163	0	1
8164	6	31,939,551	31,940,418	867	2	9.071	13.679	18	19	1	2	4	SKIV2L, DOM3Z, STK19, C4A	13403, 48, 1032, -9850	downstream, in gene, in gene, upstream	ActReg chr6 #8164	1	1
8165	6	32,073,122	32,073,575	453	1	4.429	10.429	7	17	0	0	2	TNXB, ATF6B	3805, 22682	in gene, downstream	ActReg chr6 #8165	0	1
8166	6	32,097,832	32,098,591	759	2	12.957	14.13	24	28	1	2	2	ATF6B, FKBPL	-2181, -144	upstream, upstream	ActReg chr6 #8166	1	1
8167	6	32,787,381	32,787,913	532	1	10.235	11.882	15	24	0	1	2	HLA-DOB, TAP2	-2822, 18900	upstream, downstream	ActReg chr6 #8167	0	1
8168	6	32,937,466	32,937,943	477	1	9.867	4	13	6	0	1	1	BRD2	1,267	in gene	ActReg chr6 #8168	1	0
8169	6	33,175,923	33,176,474	551	1	13.353	9.118	25	14	1	3	5	RXRB, SLC39A7, HSD17B8, MIR219-1, RING1	-7766, 7595, 3779, 586, -88	upstream, downstream, downstream, downstream, upstream	ActReg chr6 #8169	1	0
8170	6	33,218,470	33,218,978	508	1	9.062	3.438	15	7	0	0	1	VPS52	20,938	in gene	ActReg chr6 #8170	1	0
8171	6	33,239,484	33,240,310	826	2	10.615	7.038	17	17	1	3	4	VPS52, RPS18, B3GALT4, WDR46	-235, 45, -5020, 17407	upstream, in gene, upstream, downstream	ActReg chr6 #8171	1	1
8172	6	33,266,628	33,267,783	1,155	2	11.25	11.583	23	15	1	1	4	WDR46, PFDN6, RGL2, TAPBP	-9901, 9827, -29, 14959	upstream, downstream, upstream, downstream	ActReg chr6 #8172	1	1
8173	6	33,285,349	33,286,012	663	2	13.9	14.45	26	25	1	2	3	TAPBP, ZBTB22, DAXX	-3516, 39, 5113	upstream, in gene, downstream	ActReg chr6 #8173	1	1
8174	6	33,290,910	33,291,688	778	1	6.56	11.12	11	21	1	2	3	TAPBP, ZBTB22, DAXX	-9135, -5580, -506	upstream, upstream, upstream	ActReg chr6 #8174	0	1
8175	6	33,756,722	33,757,139	417	1	10.846	8.231	16	12	1	1	2	LEMD2, MLN	-24, 14863	upstream, downstream	ActReg chr6 #8175	1	0
8176	6	33,780,259	33,780,880	621	2	10.474	10.895	19	23	0	0	1	MLN	-8,776	upstream	ActReg chr6 #8176	1	1
8177	6	34,083,052	34,083,599	547	1	5.353	9.941	8	14	0	0	1	GRM4	18,118	in gene	ActReg chr6 #8177	0	1
8178	6	34,100,154	34,101,306	1,152	2	10.556	13.917	21	31	0	1	1	GRM4	713	in gene	ActReg chr6 #8178	1	1
8179	6	34,855,519	34,856,152	633	1	6.1	9.8	13	17	1	2	2	TAF11, ANKS1A	-16, -1203	upstream, upstream	ActReg chr6 #8179	0	1
8180	6	35,435,826	35,436,465	639	2	12.65	11.05	17	14	1	1	3	FANCE, RPL10A, TEAD3	16007, -33, 28716	downstream, upstream, downstream	ActReg chr6 #8180	1	1
8181	6	35,772,802	35,773,551	749	2	10.696	11.609	22	17	1	1	2	CLPS, LHFPL5	-8074, 105	upstream, in gene	ActReg chr6 #8181	1	1
8182	6	35,995,013	35,995,631	618	2	8.842	9.526	17	16	1	2	2	SLC26A8, MAPK14	-2909, -132	upstream, upstream	ActReg chr6 #8182	1	1
8183	6	36,647,822	36,648,721	899	2	8.964	10.643	22	17	1	1	1	CDKN1A	1,812	in gene	ActReg chr6 #8183	1	1
8184	6	36,953,753	36,954,242	489	1	9.625	10.688	14	15	1	1	1	MTCH1	-48	upstream	ActReg chr6 #8184	0	1
8185	6	37,321,637	37,322,096	459	1	9.571	8.429	13	11	1	1	1	RNF8	118	in gene	ActReg chr6 #8185	1	0
8186	6	37,493,251	37,494,070	819	2	12.32	15.72	21	28	0	0	0				ActReg chr6 #8186	1	1
8187	6	37,597,898	37,598,735	837	1	11.808	13.769	17	23	0	0	1	MDGA1	67,450	downstream	ActReg chr6 #8187	0	1
8188	6	37,786,585	37,787,600	1,015	2	10.344	14.312	17	23	1	1	1	ZFAND3	-215	upstream	ActReg chr6 #8188	1	1
8189	6	38,197,267	38,198,039	752	1	6.913	15.087	15	33	0	0	1	BTBD9	410,261	in gene	ActReg chr6 #8189	0	1
8190	6	38,325,734	38,326,262	528	1	3.562	10.062	7	14	0	0	1	BTBD9	281,926	in gene	ActReg chr6 #8190	0	1
8191	6	38,670,613	38,671,297	684	2	9.409	12.227	22	27	1	1	1	GLO1	-3	upstream	ActReg chr6 #8191	1	1
8192	6	39,056,121	39,056,571	450	1	2.308	10.214	4	17	0	0	1	GLP1R	39,789	downstream	ActReg chr6 #8192	0	1
8193	6	39,104,994	39,105,499	505	1	7.533	10.467	14	17	0	0	0				ActReg chr6 #8193	0	1
8194	6	39,196,810	39,197,287	477	1	8.6	10.333	14	17	1	1	1	KCNK5	203	in gene	ActReg chr6 #8194	0	1
8195	6	41,086,833	41,087,225	392	1	9.083	10.5	14	15	0	0	0				ActReg chr6 #8195	0	1
8196	6	41,134,509	41,135,245	736	1	5	9.87	9	15	0	1	1	TREM2	-3,955	upstream	ActReg chr6 #8196	0	1
8197	6	41,703,104	41,703,748	644	2	14.889	11.905	31	29	1	1	2	TFEB, PGC	571, 11713	in gene, downstream	ActReg chr6 #8197	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8198	6	41,754,643	41,755,628	985	2	11.935	10.774	21	22	1	2	4	FRS3, PRICKLE4, TOMM6, USP49	-7505, 6635, -46, 107964	upstream, downstream, upstream, downstream	ActReg chr6 #8198	1	1
8199	6	41,888,643	41,889,643	1,000	2	17.774	20.742	39	46	1	2	2	MED20, BYSL	-266, 178	upstream, in gene	ActReg chr6 #8199	1	1
8200	6	42,066,986	42,067,434	448	1	6.571	10.643	12	17	0	0	1	C6orf132	43,505	downstream	ActReg chr6 #8200	0	1
8201	6	42,419,388	42,419,823	435	1	11.214	7.286	17	12	1	1	1	TRERF1	178	in gene	ActReg chr6 #8201	1	0
8202	6	42,713,563	42,713,977	414	1	4.846	9.923	8	14	1	1	1	TBCC	114	in gene	ActReg chr6 #8202	0	1
8203	6	42,847,104	42,847,856	752	1	9.625	11.75	19	22	0	1	1	RPL7L1	-191	upstream	ActReg chr6 #8203	0	1
8204	6	42,858,505	42,858,928	423	1	10	10.077	12	12	1	1	2	RPL7L1, C6orf226	11045, -162	downstream, upstream	ActReg chr6 #8204	0	1
8205	6	43,149,663	43,150,178	515	1	7.882	10.118	11	17	1	1	2	SRF, CUL9	11000, -2	downstream, upstream	ActReg chr6 #8205	0	1
8206	6	43,394,844	43,395,495	651	1	14.143	4.81	23	9	1	1	1	ABCC10	-4,320	upstream	ActReg chr6 #8206	1	0
8207	6	43,476,922	43,477,527	605	1	9.263	6.579	16	12	1	2	4	TJAP1, C6orf154, YIPF3, POLR1C	31963, 1200, 7504, 7567	downstream, in gene, downstream, upstream	ActReg chr6 #8207	1	0
8208	6	43,603,350	43,604,000	650	1	4.19	10.095	6	18	1	1	3	GTPBP2, MAD2L1BP, RSPH9	-6739, 6396, -9092	upstream, in gene, upstream	ActReg chr6 #8208	0	1
8209	6	43,607,991	43,608,427	436	1	3.571	9.714	5	14	0	1	2	MAD2L1BP, RSPH9	10930, -4558	in gene, upstream	ActReg chr6 #8209	0	1
8210	6	44,213,939	44,215,206	1,267	2	15.1	14.975	31	31	1	1	3	LOC100505819, HSP90AB1, SLC35B2	7048, -277, 10711	in gene, upstream, downstream	ActReg chr6 #8210	1	1
8211	6	44,224,672	44,225,501	829	1	7.769	13.538	13	21	1	2	4	LOC100505819, HSP90AB1, SLC35B2, NFKBIE	-3466, 10237, 197, 8439	upstream, downstream, in gene, downstream	ActReg chr6 #8211	0	1
8212	6	44,253,178	44,254,194	1,016	2	10	11.75	20	21	1	0	2	TMEM151B, TCTE1	15206, 11772	downstream, in gene	ActReg chr6 #8212	1	1
8213	6	44,280,530	44,281,535	1,005	2	27.323	31.645	82	88	1	1	1	AARS2	31	in gene	ActReg chr6 #8213	1	1
8214	6	46,620,741	46,621,283	542	2	8.059	8.647	15	14	1	2	2	CYP39A1, SLC25A27	-489, 333	upstream, in gene	ActReg chr6 #8214	1	1
8215	6	47,135,918	47,136,416	498	1	9.188	8.5	16	13	0	0	0				ActReg chr6 #8215	1	0
8216	6	47,148,299	47,148,915	616	2	10.263	10.158	20	20	0	0	0				ActReg chr6 #8216	1	1
8217	6	48,396,618	48,397,111	493	1	10.733	7.467	16	11	0	0	0				ActReg chr6 #8217	1	0
8218	6	50,273,266	50,273,930	664	2	8.7	10.143	20	22	0	0	0				ActReg chr6 #8218	1	1
8219	6	50,688,222	50,688,652	430	1	6.643	9.786	9	17	0	0	1	TFAP2D	7,180	in gene	ActReg chr6 #8219	0	1
8220	6	51,263,026	51,263,706	680	1	11.905	7.524	21	14	0	0	0				ActReg chr6 #8220	1	0
8221	6	52,288,700	52,289,222	522	1	3.882	10.647	6	18	0	0	1	EFHC1	3,967	in gene	ActReg chr6 #8221	0	1
8222	6	52,859,837	52,860,196	359	1	7.917	10.583	10	14	1	2	3	GSTA4, RN7SK, ICK	162, -402, 66584	in gene, upstream, downstream	ActReg chr6 #8222	0	1
8223	6	52,929,314	52,929,977	663	2	9.9	10.2	18	21	1	2	2	ICK, FBXO9	-3045, -151	upstream, upstream	ActReg chr6 #8223	1	1
8224	6	53,213,146	53,213,885	739	1	10.87	9.087	16	15	1	1	1	ELOVL5	427	in gene	ActReg chr6 #8224	1	0
8225	6	53,223,785	53,224,873	1,088	2	12.147	11.177	21	22	1	0	1	ELOVL5	-10,387	upstream	ActReg chr6 #8225	1	1
8226	6	53,408,929	53,410,294	1,365	2	12.833	13.429	31	29	1	1	1	GCLC	220	in gene	ActReg chr6 #8226	1	1
8227	6	53,412,416	53,413,285	869	2	14.857	15.286	38	30	1	1	1	GCLC	-3,019	upstream	ActReg chr6 #8227	1	1
8228	6	53,659,304	53,660,220	916	1	5.893	10.75	9	16	1	1	1	LRRC1	-16	upstream	ActReg chr6 #8228	0	1
8229	6	53,849,074	53,849,518	444	1	9.929	10.071	13	15	0	0	0				ActReg chr6 #8229	0	1
8230	6	55,041,556	55,042,370	814	2	13.654	10.308	29	19	0	1	1	HCRTR2	2,892	in gene	ActReg chr6 #8230	1	1
8231	6	56,200,487	56,201,049	562	1	8.118	9.941	13	16	0	0	0				ActReg chr6 #8231	0	1
8232	6	58,287,335	58,288,168	833	2	25.654	34.875	80	107	1	0	0				ActReg chr6 #8232	1	1
8233	6	62,995,867	62,996,532	665	2	13.809	12.048	28	21	1	1	1	KHDRBS2	-99	upstream	ActReg chr6 #8233	1	1
8234	6	64,281,569	64,282,245	676	1	15.095	10	24	14	1	1	1	PTP4A1	-13	upstream	ActReg chr6 #8234	1	0
8235	6	64,282,965	64,283,875	910	1	7.483	12.552	12	21	1	1	1	PTP4A1	1,500	in gene	ActReg chr6 #8235	0	1
8236	6	64,284,079	64,284,782	703	2	12.5	9.273	28	18	0	1	1	PTP4A1	2,510	in gene	ActReg chr6 #8236	1	1
8237	6	64,308,163	64,309,074	911	2	15.214	16.556	37	42	0	0	0				ActReg chr6 #8237	1	1
8238	6	64,345,470	64,346,423	953	2	13.767	15.567	25	31	1	0	0				ActReg chr6 #8238	1	1
8239	6	66,470,006	66,470,717	711	2	13.091	13.046	31	31	0	0	0				ActReg chr6 #8239	1	1
8240	6	67,846,224	67,846,839	615	1	9.474	9.211	15	15	0	0	0				ActReg chr6 #8240	1	0
8241	6	68,789,797	68,790,567	770	2	16.417	13.208	42	29	0	0	0				ActReg chr6 #8241	1	1
8242	6	69,942,588	69,943,252	664	2	11.762	14.571	27	35	0	0	1	BAI3	597,288	in gene	ActReg chr6 #8242	1	1
8243	6	70,627,682	70,628,251	569	1	10.529	7.529	16	10	0	0	1	COL19A1	51,518	in gene	ActReg chr6 #8243	1	0
8244	6	73,831,042	73,831,907	865	2	10.538	14.63	21	28	0	0	1	KCNQ5	499,903	in gene	ActReg chr6 #8244	1	1
8245	6	74,230,359	74,231,208	849	2	10.926	9.074	20	17	1	1	1	EEF1A1	-28	upstream	ActReg chr6 #8245	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8246	6	74,405,322	74,406,143	821	2	8.64	9.8	13	14	1	2	2	LOC100506740, CD109	122, 224	in gene, in gene	ActReg chr6 #8246	1	1
8247	6	81,481,551	81,482,133	582	1	4.25	10.222	7	19	0	0	0				ActReg chr6 #8247	0	1
8248	6	82,462,733	82,463,397	664	1	11.429	9.762	24	13	1	1	1	FAM46A	-637	upstream	ActReg chr6 #8248	1	0
8249	6	84,568,505	84,569,680	1,175	2	13.027	21.757	45	62	1	1	2	RIPPLY2, CYB5R4	6107, -278	downstream, upstream	ActReg chr6 #8249	1	1
8250	6	85,231,769	85,232,341	572	1	8.167	8.944	12	14	0	0	0				ActReg chr6 #8250	0	1
8251	6	85,474,181	85,474,638	457	1	5.786	10.857	10	16	1	1	1	TBX18	-510	upstream	ActReg chr6 #8251	0	1
8252	6	85,484,267	85,484,870	603	1	4.526	10.421	8	17	1	0	0				ActReg chr6 #8252	0	1
8253	6	86,174,358	86,174,948	590	1	8.368	10.579	13	17	0	0	1	NT5E	15,351	in gene	ActReg chr6 #8253	0	1
8254	6	86,388,118	86,388,790	672	2	10.476	11.143	16	18	1	3	3	SNHG5, SNORD50A, SNORD50B	-3, -1368, -1077	upstream, upstream, upstream	ActReg chr6 #8254	1	1
8255	6	88,031,783	88,032,733	950	2	24.759	27.517	64	82	1	1	2	GJB7, C6orf162	6738, -48	in gene, upstream	ActReg chr6 #8255	1	1
8256	6	88,145,867	88,146,757	890	2	14.679	18.778	41	54	0	0	1	C6orf165	28,622	in gene	ActReg chr6 #8256	1	1
8257	6	88,182,139	88,182,921	782	2	11.64	12.64	19	20	1	1	2	C6orf165, SLC35A1	64840, -113	downstream, upstream	ActReg chr6 #8257	1	1
8258	6	88,433,045	88,433,385	340	1	10.182	4.727	16	7	0	0	0				ActReg chr6 #8258	1	0
8259	6	89,247,782	89,248,226	444	1	7.786	10.571	11	19	0	0	0				ActReg chr6 #8259	0	1
8260	6	90,062,020	90,062,807	787	1	7.833	10.875	11	15	1	1	1	UBE2J1	206	in gene	ActReg chr6 #8260	0	1
8261	6	90,528,849	90,529,866	1,017	1	6.781	11.875	12	18	1	1	2	MDN1, CASP8AP2	85, -10262	in gene, upstream	ActReg chr6 #8261	0	1
8262	6	90,604,658	90,605,650	992	2	16.645	22	43	56	0	1	1	GJA10	966	in gene	ActReg chr6 #8262	1	1
8263	6	90,932,365	90,932,939	574	1	6.333	10.5	14	20	0	0	1	BACH2	73,975	in gene	ActReg chr6 #8263	0	1
8264	6	91,296,811	91,297,360	549	1	8.294	13.294	15	25	1	1	1	MAP3K7	-178	upstream	ActReg chr6 #8264	0	1
8265	6	93,550,060	93,550,530	470	1	8.8	10.533	14	15	0	0	0				ActReg chr6 #8265	0	1
8266	6	97,345,401	97,346,063	662	2	20.905	18.809	46	40	1	1	1	NDUFAF4	35	in gene	ActReg chr6 #8266	1	1
8267	6	99,105,524	99,106,210	686	2	11.048	7.273	21	18	0	0	0				ActReg chr6 #8267	1	1
8268	6	99,800,974	99,801,457	483	2	11.067	10.933	14	16	0	1	1	C6orf168	-3,684	upstream	ActReg chr6 #8268	1	1
8269	6	99,962,946	99,963,440	494	1	5.667	9.933	9	15	1	1	1	USP45	59	in gene	ActReg chr6 #8269	0	1
8270	6	101,841,166	101,841,701	535	2	10.059	11.353	20	19	1	1	1	GRIK2	-5,428	upstream	ActReg chr6 #8270	1	1
8271	6	102,062,488	102,063,098	610	1	10.316	4.316	17	10	0	0	1	GRIK2	215,932	in gene	ActReg chr6 #8271	1	0
8272	6	102,114,085	102,114,517	432	1	5.077	13	7	21	0	0	1	GRIK2	267,440	in gene	ActReg chr6 #8272	0	1
8273	6	105,307,275	105,307,760	485	1	7.4	10.733	15	17	1	1	1	HACE1	277	in gene	ActReg chr6 #8273	0	1
8274	6	105,335,070	105,335,645	575	1	6.889	9.944	13	16	0	0	0				ActReg chr6 #8274	0	1
8275	6	105,391,529	105,392,118	589	1	5.556	10.056	10	17	0	0	0				ActReg chr6 #8275	0	1
8276	6	105,850,661	105,851,651	990	2	8.645	9.355	22	14	1	1	2	PREP, LOC100506148	-157, 25896	upstream, downstream	ActReg chr6 #8276	1	1
8277	6	106,533,996	106,534,466	470	1	6.6	9.467	10	13	1	1	1	PRDM1	36	in gene	ActReg chr6 #8277	0	1
8278	6	106,773,327	106,773,765	438	1	7.929	11.429	13	13	1	1	1	ATG5	149	in gene	ActReg chr6 #8278	0	1
8279	6	106,958,403	106,958,849	446	1	7.286	12.429	12	23	1	1	1	AIM1	-1,104	upstream	ActReg chr6 #8279	0	1
8280	6	107,077,137	107,077,729	592	1	6.263	10.421	9	20	0	2	2	RTN4IP1, QRSL1	-60, -8	upstream, upstream	ActReg chr6 #8280	0	1
8281	6	107,348,924	107,349,892	968	2	20.71	26.613	57	72	1	1	1	C6orf203	1	in gene	ActReg chr6 #8281	1	1
8282	6	107,435,273	107,435,825	552	1	4.941	11.235	9	19	1	1	1	BEND3	87	in gene	ActReg chr6 #8282	0	1
8283	6	107,810,622	107,811,092	470	1	4.067	8.8	7	15	1	1	1	SOBP	-460	upstream	ActReg chr6 #8283	0	1
8284	6	109,703,554	109,704,159	605	1	6.944	11.944	12	20	1	1	2	CD164, PPIL6	-94, 58518	upstream, downstream	ActReg chr6 #8284	0	1
8285	6	110,299,572	110,300,207	635	2	10.1	12.65	18	22	1	1	1	GPR6	-409	upstream	ActReg chr6 #8285	1	1
8286	6	110,494,744	110,495,070	326	1	6.7	10.7	9	16	0	1	2	WASF1, CDC40	6300, -6717	in gene, upstream	ActReg chr6 #8286	0	1
8287	6	110,500,721	110,501,441	720	1	7	10.565	10	18	2	2	2	WASF1, CDC40	126, -543	in gene, upstream	ActReg chr6 #8287	0	1
8288	6	110,576,393	110,576,993	600	2	10.526	10.737	20	24	0	0	1	C6orf186	102,782	in gene	ActReg chr6 #8288	1	1
8289	6	110,868,475	110,868,998	523	1	6.133	9.059	9	14	0	0	0				ActReg chr6 #8289	0	1
8290	6	111,135,805	111,136,245	440	1	6.643	9	10	14	1	1	1	CDK19	387	in gene	ActReg chr6 #8290	0	1
8291	6	111,136,387	111,137,072	685	1	7.429	11.524	15	15	1	1	1	CDK19	-317	upstream	ActReg chr6 #8291	0	1
8292	6	111,303,011	111,303,695	684	1	5.05	11.095	10	16	1	1	1	RPF2	62	in gene	ActReg chr6 #8292	0	1
8293	6	111,804,331	111,804,888	557	2	10.412	8.882	14	17	1	2	2	REV3L, LOC643749	-195, -66	upstream, upstream	ActReg chr6 #8293	1	1
8294	6	112,364,119	112,364,626	507	2	11	9.562	19	15	0	0	0				ActReg chr6 #8294	1	1
8295	6	112,576,252	112,576,684	432	1	3.214	10.214	6	15	0	1	2	LAMA4, LOC100506430	-640, 18671	upstream, in gene	ActReg chr6 #8295	0	1
8296	6	113,768,212	113,768,551	339	1	3.75	10.454	6	14	0	0	0				ActReg chr6 #8296	0	1
8297	6	114,291,876	114,292,850	974	2	10.333	14.067	21	25	1	1	1	HDAC2	-4	upstream	ActReg chr6 #8297	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8298	6	116,892,007	116,893,013	1,006	2	19.613	23.161	52	63	1	1	1	RWDD1	-73	upstream	ActReg chr6 #8298	1	1
8299	6	116,917,939	116,918,484	545	2	9.471	8.059	16	13	0	0	1	RWDD1	25,628	downstream	ActReg chr6 #8299	1	1
8300	6	116,989,592	116,990,008	416	1	8.385	10.385	13	13	0	1	1	ZUFSP	173	in gene	ActReg chr6 #8300	0	1
8301	6	117,996,030	117,996,846	816	2	37.952	48.846	116	137	1	1	1	NUS1	-179	upstream	ActReg chr6 #8301	1	1
8302	6	118,816,797	118,817,305	508	1	9.25	9.5	14	18	0	0	1	C6orf204	214,187	in gene	ActReg chr6 #8302	0	1
8303	6	118,971,641	118,972,307	666	1	8.095	10.905	13	16	1	0	1	C6orf204	59,264	in gene	ActReg chr6 #8303	0	1
8304	6	119,030,967	119,031,706	739	1	13.043	9.478	30	15	0	1	1	C6orf204	-98	upstream	ActReg chr6 #8304	1	0
8305	6	119,214,835	119,215,755	920	2	26.241	26.793	81	80	1	1	1	ASF1A	54	in gene	ActReg chr6 #8305	1	1
8306	6	121,655,469	121,655,964	495	1	6.133	9	10	13	1	1	1	C6orf170	-72	upstream	ActReg chr6 #8306	0	1
8307	6	125,474,713	125,475,112	399	1	9.692	8	14	12	1	1	1	TPD52L1	33	in gene	ActReg chr6 #8307	1	0
8308	6	125,622,599	125,623,339	740	1	5.783	11.087	13	17	1	1	1	HDDC2	313	in gene	ActReg chr6 #8308	0	1
8309	6	126,133,594	126,134,239	645	2	10.1	10.75	15	19	0	0	1	NCOA7	21,915	in gene	ActReg chr6 #8309	1	1
8310	6	126,277,637	126,278,294	657	2	13	13.9	28	27	1	1	1	HINT3	104	in gene	ActReg chr6 #8310	1	1
8311	6	126,860,039	126,860,638	599	1	10.5	6.889	20	13	0	0	0				ActReg chr6 #8311	1	0
8312	6	126,946,040	126,946,711	671	2	12.7	10.952	28	22	0	0	0				ActReg chr6 #8312	1	1
8313	6	127,587,564	127,588,530	966	1	8.7	10.433	13	17	1	1	1	RNF146	27	in gene	ActReg chr6 #8313	0	1
8314	6	127,836,993	127,838,232	1,239	2	9.5	13.105	15	20	1	1	1	C6orf174	2,888	in gene	ActReg chr6 #8314	1	1
8315	6	131,949,037	131,949,831	794	2	14.32	17.36	29	47	1	1	2	MED23, ENPP3	-71, -9008	upstream, upstream	ActReg chr6 #8315	1	1
8316	6	132,271,443	132,272,072	629	1	10.2	10.7	17	16	2	1	2	LOC100131774, CTGF	5127, 761	downstream, in gene	ActReg chr6 #8316	0	1
8317	6	133,135,076	133,135,915	839	2	19.192	15	37	32	1	4	4	RPS12, SNORD101, SNORD100, SNORA33	-213, -951, -2446, -2863	upstream, upstream, upstream, upstream	ActReg chr6 #8317	1	1
8318	6	134,273,099	134,273,658	559	1	12.118	8.412	20	12	1	1	1	TBPL1	-923	upstream	ActReg chr6 #8318	1	0
8319	6	134,743,834	134,744,445	611	1	10.368	7	16	13	0	0	0				ActReg chr6 #8319	1	0
8320	6	135,491,155	135,491,718	563	1	10.333	5.778	18	10	0	0	0				ActReg chr6 #8320	1	0
8321	6	135,818,460	135,819,177	717	2	8.739	10.522	18	17	1	2	2	AHI1, C6orf217	85, -121	in gene, upstream	ActReg chr6 #8321	1	1
8322	6	136,043,984	136,044,450	466	1	5.867	10.867	12	16	0	0	0				ActReg chr6 #8322	0	1
8323	6	136,571,166	136,571,828	662	1	7.762	12.143	12	22	1	1	2	FAM54A, BCLAF1	-48, 39492	upstream, downstream	ActReg chr6 #8323	0	1
8324	6	139,309,116	139,309,559	443	1	9.929	10.357	13	15	1	1	1	REPS1	61	in gene	ActReg chr6 #8324	0	1
8325	6	139,695,510	139,696,943	1,433	2	12.622	14.133	25	31	1	1	1	CITED2	-441	upstream	ActReg chr6 #8325	1	1
8326	6	140,123,031	140,123,463	432	1	7.571	9.143	14	15	0	0	0				ActReg chr6 #8326	0	1
8327	6	140,364,399	140,364,997	598	1	6.889	10.316	13	23	0	0	0				ActReg chr6 #8327	0	1
8328	6	142,467,985	142,468,766	781	2	8.917	14.292	18	25	1	1	1	VTA1	-35	upstream	ActReg chr6 #8328	1	1
8329	6	142,622,828	142,623,358	530	1	10	10.375	16	15	1	1	1	GPR126	37	in gene	ActReg chr6 #8329	1	0
8330	6	143,771,551	143,772,249	698	2	10.636	12.909	18	23	1	2	2	ADAT2, PEX3	-59, -18	upstream, upstream	ActReg chr6 #8330	1	1
8331	6	146,055,899	146,056,426	527	1	5.882	10.823	9	16	1	2	2	EPM2A, LOC100507557	829, 154	in gene, in gene	ActReg chr6 #8331	0	1
8332	6	146,349,272	146,349,930	658	2	8.095	13.619	15	29	0	1	1	GRM1	819	in gene	ActReg chr6 #8332	1	1
8333	6	148,663,581	148,664,106	525	1	4.824	8.941	8	15	1	1	1	SASH1	114	in gene	ActReg chr6 #8333	0	1
8334	6	149,256,865	149,257,231	366	1	10.091	4.091	15	6	0	0	1	UST	188,777	in gene	ActReg chr6 #8334	1	0
8335	6	149,333,090	149,333,654	564	2	8.882	11.177	17	19	0	0	1	UST	265,101	in gene	ActReg chr6 #8335	1	1
8336	6	149,638,186	149,638,697	511	1	7.812	9.375	14	18	1	1	1	MAP3K7IP2	-995	upstream	ActReg chr6 #8336	0	1
8337	6	149,866,861	149,867,586	725	2	10.174	11.609	19	22	1	1	1	PPIL4	-52	upstream	ActReg chr6 #8337	1	1
8338	6	150,070,777	150,071,272	495	1	6.5	9.5	9	14	1	2	2	NUP43, PCMT1	-3336, 193	upstream, in gene	ActReg chr6 #8338	0	1
8339	6	151,772,988	151,773,782	794	1	11.2	8.16	21	14	1	2	2	RMND1, C6orf211	-69, -37	upstream, upstream	ActReg chr6 #8339	1	0
8340	6	152,168,186	152,168,597	411	1	10.308	8.25	19	12	0	0	1	ESR1	156,760	in gene	ActReg chr6 #8340	1	0
8341	6	153,071,719	153,072,201	482	1	10.2	7.6	14	13	0	1	1	VIP	27	in gene	ActReg chr6 #8341	1	0
8342	6	154,360,100	154,361,204	1,104	2	18.235	26.088	45	76	1	0	1	OPRM1	29,016	in gene	ActReg chr6 #8342	1	1
8343	6	155,054,156	155,055,008	852	1	9.593	10.444	17	15	1	1	1	RBM16	70	in gene	ActReg chr6 #8343	0	1
8344	6	155,447,980	155,448,743	763	1	14.5	6.083	26	11	0	0	1	TIAM2	36,938	in gene	ActReg chr6 #8344	1	0
8345	6	155,492,223	155,492,728	505	1	7.062	9.938	11	18	0	0	1	TIAM2	81,052	in gene	ActReg chr6 #8345	0	1
8346	6	157,342,411	157,343,003	592	1	6.389	11.667	12	15	1	0	1	ARID1B	243,643	in gene	ActReg chr6 #8346	0	1
8347	6	157,469,852	157,470,285	433	1	9.929	7	13	12	0	0	1	ARID1B	371,004	in gene	ActReg chr6 #8347	1	0
8348	6	157,744,117	157,744,830	713	1	9.045	12.091	16	22	1	1	1	C6orf35	780	in gene	ActReg chr6 #8348	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8349	6	157,876,784	157,877,394	610	1	7.684	9.947	12	17	0	0	1	ZDHHC14	74,532	in gene	ActReg chr6 #8349	0	1
8350	6	157,950,295	157,950,809	514	1	9.688	6.125	17	9	0	0	1	ZDHHC14	147,995	in gene	ActReg chr6 #8350	1	0
8351	6	158,185,337	158,186,042	705	2	9.5	11.318	14	21	0	0	0				ActReg chr6 #8351	1	1
8352	6	158,956,867	158,957,737	870	2	12.63	14.148	24	27	1	1	1	TMEM181	-166	upstream	ActReg chr6 #8352	1	1
8353	6	159,065,410	159,065,949	539	1	9.938	6.75	17	9	1	2	3	TMEM181, DYNLT1, SYTL3	108211, 125, -5367	downstream, in gene, upstream	ActReg chr6 #8353	1	0
8354	6	159,420,809	159,421,218	409	1	7.692	9.769	11	11	1	1	1	RSPH3	185	in gene	ActReg chr6 #8354	0	1
8355	6	160,113,614	160,114,328	714	1	7.409	11	12	16	1	1	1	SOD2	382	in gene	ActReg chr6 #8355	0	1
8356	6	160,114,374	160,114,753	379	1	9.583	11.5	14	19	1	1	1	SOD2	-210	upstream	ActReg chr6 #8356	0	1
8357	6	160,147,921	160,148,389	468	1	9.067	5.933	13	12	1	1	1	WTAP	3	in gene	ActReg chr6 #8357	1	0
8358	6	160,183,156	160,183,604	448	1	8.214	9.214	11	10	1	2	3	WTAP, LOC100129518, ACAT2	35228, -16, 391	downstream, upstream, in gene	ActReg chr6 #8358	0	1
8359	6	161,412,441	161,413,056	615	1	10.65	9.6	16	15	1	1	1	MAP3K4	-74	upstream	ActReg chr6 #8359	1	0
8360	6	161,458,980	161,459,502	522	1	8.625	11	15	19	0	0	1	MAP3K4	46,419	in gene	ActReg chr6 #8360	0	1
8361	6	163,834,223	163,834,863	640	1	10.8	10.4	16	19	0	1	1	QKI	-1,132	upstream	ActReg chr6 #8361	0	1
8362	6	164,235,546	164,236,095	549	1	6.353	9.294	11	16	0	0	0				ActReg chr6 #8362	0	1
8363	6	164,668,235	164,668,703	468	1	5.286	10.071	9	15	0	0	0				ActReg chr6 #8363	0	1
8364	6	166,308,785	166,309,482	697	2	8.818	10.954	18	22	0	1	1	LOC100505705	592	in gene	ActReg chr6 #8364	1	1
8365	6	166,400,903	166,401,751	848	2	10.423	10.231	17	15	1	2	2	C6orf176, LOC441177	200, 288	in gene, in gene	ActReg chr6 #8365	1	1
8366	6	166,795,569	166,796,235	666	1	8.619	11.762	13	16	1	1	1	BRP44L	584	in gene	ActReg chr6 #8366	0	1
8367	6	167,412,731	167,413,144	413	1	7.385	11.923	11	19	1	1	1	FGFR1OP	121	in gene	ActReg chr6 #8367	0	1
8368	6	168,083,620	168,084,165	545	1	5.824	11.529	11	15	0	1	1	LOC401286	-3,989	upstream	ActReg chr6 #8368	0	1
8369	6	169,470,682	169,471,197	515	1	5.875	9.875	7	15	0	0	0				ActReg chr6 #8369	0	1
8370	6	169,692,532	169,692,958	426	1	6.615	10.538	11	14	0	0	0				ActReg chr6 #8370	0	1
8371	6	170,101,827	170,102,902	1,075	2	10.212	12.454	14	20	1	2	3	WDR27, C6orf120, PHF10	-205, 107, 21742	upstream, in gene, downstream	ActReg chr6 #8371	1	1
8372	6	170,151,521	170,152,461	940	1	5.552	10.69	13	16	1	2	2	TCTE3, C6orf70	-353, 270	upstream, in gene	ActReg chr6 #8372	0	1
8373	6	170,747,383	170,747,789	406	1	7.308	9.538	13	12	0	0	0				ActReg chr6 #8373	0	1
8374	6	170,863,154	170,864,000	846	2	7.741	10	15	16	1	2	2	PSMB1, TBP	-1160, 156	upstream, in gene	ActReg chr6 #8374	1	1
8375	7	101,699	102,479	780	1	7.13	12.375	17	17	0	0	0				ActReg chr7 #8375	0	1
8376	7	558,347	558,922	575	1	4.5	11.222	7	20	1	2	2	PDGFA, FLJ44511	847, -1394	in gene, upstream	ActReg chr7 #8376	0	1
8377	7	915,582	916,525	943	2	11.367	12.633	24	23	1	2	3	SUN1, C7orf20, LOC100505531	60859, -138, -3533	downstream, upstream, upstream	ActReg chr7 #8377	1	1
8378	7	1,014,489	1,015,967	1,478	2	13.109	16.717	40	43	1	2	2	COX19, CYP2W1	7, -7607	in gene, upstream	ActReg chr7 #8378	1	1
8379	7	1,199,454	1,200,248	794	1	10.48	9.56	15	16	1	1	1	ZFAND2A	4	in gene	ActReg chr7 #8379	1	0
8380	7	1,498,467	1,499,097	630	1	12.684	8.789	25	12	1	1	1	MICALL2	327	in gene	ActReg chr7 #8380	1	0
8381	7	1,543,477	1,544,590	1,113	2	27.647	32.971	86	107	1	1	1	INTS1	-15	upstream	ActReg chr7 #8381	1	1
8382	7	1,552,735	1,553,407	672	1	7.476	12.095	11	22	0	0	1	INTS1	-9,053	upstream	ActReg chr7 #8382	0	1
8383	7	1,571,972	1,572,659	687	1	4.81	10.809	7	19	0	2	3	MAFK, LOC100128653, TMEM184A	1947, 2201, 23751	in gene, in gene, downstream	ActReg chr7 #8383	0	1
8384	7	1,609,264	1,610,177	913	1	9.241	12.276	14	21	1	2	2	PSMG3, KIAA1908	-52, 11	upstream, in gene	ActReg chr7 #8384	0	1
8385	7	2,272,271	2,273,008	737	1	16.261	11.913	28	18	1	1	3	MAD1L1, FTSJ2, NUDT1	-56, 9194, -9218	upstream, downstream, upstream	ActReg chr7 #8385	1	0
8386	7	2,393,342	2,394,666	1,324	2	21.881	27.143	52	59	1	1	1	EIF3B	-470	upstream	ActReg chr7 #8386	1	1
8387	7	2,594,811	2,595,440	629	2	12.35	13.1	18	20	1	2	2	C7orf27, IQCE	21, -3507	in gene, upstream	ActReg chr7 #8387	1	1
8388	7	2,598,245	2,598,942	697	2	11.333	11.762	17	26	1	2	2	C7orf27, IQCE	-3447, -39	upstream, upstream	ActReg chr7 #8388	1	1
8389	7	2,672,910	2,674,115	1,205	1	9.395	10.947	16	18	0	1	1	TTYH3	1,909	in gene	ActReg chr7 #8389	0	1
8390	7	2,913,246	2,914,458	1,212	2	10.974	9.342	19	17	0	0	0				ActReg chr7 #8390	1	1
8391	7	3,067,627	3,068,136	509	2	9.688	9.438	15	17	0	0	1	CARD11	15,698	in gene	ActReg chr7 #8391	1	1
8392	7	4,509,851	4,510,411	560	1	6.389	10.167	10	15	0	0	0				ActReg chr7 #8392	0	1
8393	7	4,606,238	4,606,843	605	2	10.947	10.526	18	21	0	0	0				ActReg chr7 #8393	1	1
8394	7	4,659,929	4,660,381	452	1	5.143	9.357	8	14	0	0	0				ActReg chr7 #8394	0	1
8395	7	4,681,132	4,682,021	889	1	10.679	16.25	16	29	1	0	0				ActReg chr7 #8395	0	1
8396	7	4,814,885	4,815,554	669	2	11.619	12.286	22	19	1	1	2	FOXK1, KIAA0415	93289, -45	downstream, upstream	ActReg chr7 #8396	1	1
8397	7	4,991,395	4,992,487	1,092	2	11.912	15.235	23	30	0	0	1	MMD2	6,903	in gene	ActReg chr7 #8397	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8398	7	5,085,075	5,085,712	637	1	11.75	12.4	22	22	1	1	1	RBAK	-160	upstream	ActReg chr7 #8398	1	0
8399	7	5,553,075	5,553,984	909	2	13.379	9.655	25	21	1	1	1	FBXL18	-130	upstream	ActReg chr7 #8399	1	1
8400	7	5,601,735	5,602,591	856	1	9.731	13.346	15	22	2	0	0				ActReg chr7 #8400	0	1
8401	7	5,603,030	5,603,645	615	1	8.474	11.842	14	15	0	0	0				ActReg chr7 #8401	0	1
8402	7	5,609,581	5,610,099	518	1	13.562	11.875	17	17	1	0	0				ActReg chr7 #8402	0	1
8403	7	5,632,328	5,633,825	1,497	1	8.617	11.723	14	18	1	1	1	FSCN1	622	in gene	ActReg chr7 #8403	0	1
8404	7	5,820,891	5,821,971	1,080	1	7.588	12.971	15	22	1	1	1	RNF216	-139	upstream	ActReg chr7 #8404	0	1
8405	7	5,862,482	5,862,902	420	1	11.692	9.692	17	13	1	0	0				ActReg chr7 #8405	1	0
8406	7	6,048,285	6,049,254	969	1	6.129	10.871	12	20	1	2	2	PMS2, AIMP2	-32, -113	upstream, upstream	ActReg chr7 #8406	0	1
8407	7	6,120,573	6,121,378	805	1	9.038	13	14	21	1	0	0				ActReg chr7 #8407	0	1
8408	7	6,143,862	6,144,519	657	2	12.333	12.2	23	17	1	1	1	USP42	-360	upstream	ActReg chr7 #8408	1	1
8409	7	6,486,892	6,487,704	812	1	11.36	10.12	16	14	1	1	1	DAGLB	345	in gene	ActReg chr7 #8409	1	0
8410	7	6,629,278	6,630,399	1,121	2	13.429	14.314	24	27	1	1	2	ZDHHC4, C7orf26	12773, -77	downstream, upstream	ActReg chr7 #8410	1	1
8411	7	7,222,384	7,223,046	662	1	7.714	11.809	15	18	1	1	1	C1GALT1	469	in gene	ActReg chr7 #8411	0	1
8412	7	7,261,259	7,261,855	596	1	9.722	10.222	16	15	0	0	1	C1GALT1	39,311	in gene	ActReg chr7 #8412	1	0
8413	7	7,466,828	7,467,359	531	1	10.25	6.438	15	9	0	0	1	COL28A1	108,367	in gene	ActReg chr7 #8413	1	0
8414	7	7,478,402	7,478,941	539	1	8.75	9.75	12	19	0	0	1	COL28A1	96,789	in gene	ActReg chr7 #8414	0	1
8415	7	7,802,070	7,802,472	402	1	6.462	9.769	10	16	0	0	1	tcag7.903	121,929	in gene	ActReg chr7 #8415	0	1
8416	7	7,835,091	7,835,643	552	1	10.471	6.588	16	9	0	0	1	tcag7.903	155,025	in gene	ActReg chr7 #8416	1	0
8417	7	8,007,957	8,008,765	808	1	8.64	11.64	13	16	1	1	2	LOC100505921, GLCCI1	-10150, -62	upstream, upstream	ActReg chr7 #8417	0	1
8418	7	8,473,290	8,474,320	1,030	2	9.312	10.656	17	21	1	1	1	NXPH1	220	in gene	ActReg chr7 #8418	1	1
8419	7	8,482,140	8,482,960	820	1	7.385	11.885	16	20	2	0	1	NXPH1	8,955	in gene	ActReg chr7 #8419	0	1
8420	7	10,276,879	10,277,395	516	1	5.75	9.688	10	16	0	0	0				ActReg chr7 #8420	0	1
8421	7	10,979,309	10,980,428	1,119	2	13.114	14.371	24	24	1	1	1	NDUFA4	-55	upstream	ActReg chr7 #8421	1	1
8422	7	11,359,038	11,359,654	616	1	5.25	10.55	9	17	0	0	0				ActReg chr7 #8422	0	1
8423	7	12,250,330	12,251,528	1,198	2	12.132	11.553	18	19	1	1	1	TMEM106B	81	in gene	ActReg chr7 #8423	1	1
8424	7	12,726,648	12,727,482	834	1	7.538	13.077	12	19	1	1	1	ARL4A	584	in gene	ActReg chr7 #8424	0	1
8425	7	13,591,016	13,591,446	430	1	10.615	5.308	15	8	0	0	0				ActReg chr7 #8425	1	0
8426	7	13,818,337	13,819,128	791	1	8.125	12.542	15	24	0	0	0				ActReg chr7 #8426	0	1
8427	7	13,919,540	13,920,150	610	1	7.842	11.474	11	15	0	0	0				ActReg chr7 #8427	0	1
8428	7	14,272,501	14,273,136	635	1	10	7.9	17	13	0	0	1	DGKB	608,257	in gene	ActReg chr7 #8428	1	0
8429	7	15,238,153	15,238,683	530	1	9.5	10.688	16	18	0	0	1	TMEM195	363,222	downstream	ActReg chr7 #8429	0	1
8430	7	16,358,584	16,359,443	859	2	10.111	10.704	17	14	0	0	1	ISPD	101,934	in gene	ActReg chr7 #8430	1	1
8431	7	16,460,158	16,461,531	1,373	2	10.558	11.046	22	16	1	1	1	ISPD	103	in gene	ActReg chr7 #8431	1	1
8432	7	16,524,138	16,525,011	873	1	12.148	6.519	19	15	0	0	0				ActReg chr7 #8432	1	0
8433	7	16,684,760	16,686,325	1,565	2	16.674	19.674	56	48	2	2	2	ANKMY2, BZW2	-100, -217	upstream, upstream	ActReg chr7 #8433	1	1
8434	7	16,707,606	16,708,121	515	1	10.5	7.562	17	11	0	0	1	BZW2	22,104	in gene	ActReg chr7 #8434	1	0
8435	7	16,793,521	16,794,398	877	1	7.222	11.296	13	17	1	1	1	TSPAN13	608	in gene	ActReg chr7 #8435	0	1
8436	7	17,134,391	17,135,441	1,050	2	12.758	11.939	24	21	0	0	0				ActReg chr7 #8436	1	1
8437	7	17,273,445	17,273,977	532	1	5.125	10.438	7	16	0	0	0				ActReg chr7 #8437	0	1
8438	7	17,338,239	17,338,811	572	1	8.889	12	11	18	1	1	1	AHR	249	in gene	ActReg chr7 #8438	0	1
8439	7	17,411,591	17,412,277	686	1	11.905	9.316	19	17	0	0	0				ActReg chr7 #8439	1	0
8440	7	17,586,132	17,586,729	597	1	11.263	8.895	19	16	0	0	0				ActReg chr7 #8440	1	0
8441	7	17,728,927	17,729,889	962	2	11	10.774	19	18	0	0	0				ActReg chr7 #8441	1	1
8442	7	17,735,946	17,736,583	637	2	10.15	10.85	17	19	0	0	0				ActReg chr7 #8442	1	1
8443	7	17,979,188	17,980,559	1,371	1	9.605	12.419	15	20	1	1	1	SNX13	258	in gene	ActReg chr7 #8443	0	1
8444	7	18,498,353	18,498,820	467	1	8.867	9.067	14	16	0	0	0				ActReg chr7 #8444	0	1
8445	7	18,906,161	18,906,776	615	1	6.158	11.842	9	23	0	0	1	HDAC9	371,099	in gene	ActReg chr7 #8445	0	1
8446	7	19,748,247	19,749,011	764	1	9.167	12.208	16	20	1	2	3	TWISTNB, MIR3146, TMEM196	31, -3570, 63775	in gene, upstream, downstream	ActReg chr7 #8446	0	1
8447	7	19,812,035	19,813,230	1,195	2	11.351	14.676	22	21	1	1	1	TMEM196	-228	upstream	ActReg chr7 #8447	1	1
8448	7	19,997,878	19,998,399	521	1	9.875	9.562	17	14	0	0	0				ActReg chr7 #8448	1	0
8449	7	20,123,466	20,123,939	453	1	6.533	10.333	11	17	0	0	0				ActReg chr7 #8449	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8450	7	20,198,755	20,199,336	581	1	10.778	7.778	19	15	0	0	1	MACC1	57,968	in gene	ActReg chr7 #8450	1	0
8451	7	20,258,920	20,260,159	1,239	2	13	13.368	22	22	0	2	2	MACC1, LOC100506098	-2526, 2339	upstream, in gene	ActReg chr7 #8451	1	1
8452	7	20,369,694	20,370,998	1,304	2	10.951	10.585	16	19	1	2	2	LOC100506130, ITGB8	1024, -379	in gene, upstream	ActReg chr7 #8452	1	1
8453	7	20,392,232	20,392,919	687	1	10.762	10.286	17	14	0	0	1	ITGB8	21,850	in gene	ActReg chr7 #8453	0	1
8454	7	20,636,198	20,637,444	1,246	2	10.564	11.051	20	23	0	0	0				ActReg chr7 #8454	1	1
8455	7	20,824,395	20,825,088	693	1	6.227	10.409	10	18	1	1	1	SP8	1,767	in gene	ActReg chr7 #8455	0	1
8456	7	21,806,871	21,807,353	482	1	9.8	4.214	15	7	0	0	1	DNAH11	224,279	in gene	ActReg chr7 #8456	1	0
8457	7	21,985,036	21,986,116	1,080	2	18.118	19.529	45	58	1	1	1	CDCA7L	-34	upstream	ActReg chr7 #8457	1	1
8458	7	22,122,159	22,122,799	640	1	7.75	10.35	13	15	1	0	0				ActReg chr7 #8458	0	1
8459	7	22,539,609	22,540,030	421	1	8.692	10.923	14	16	1	1	1	MGC87042	82	in gene	ActReg chr7 #8459	0	1
8460	7	22,862,101	22,862,768	667	1	8.286	11.809	14	20	1	1	1	TOMM7	-13	upstream	ActReg chr7 #8460	0	1
8461	7	22,897,912	22,899,258	1,346	2	10.786	11.548	19	21	0	1	1	SNORD93	2,353	downstream	ActReg chr7 #8461	1	1
8462	7	23,060,339	23,061,194	855	1	11	9.444	16	17	0	1	1	FAM126A	-6,996	upstream	ActReg chr7 #8462	1	0
8463	7	23,101,944	23,102,589	645	1	9.95	11.65	16	19	0	0	0				ActReg chr7 #8463	0	1
8464	7	23,145,054	23,146,016	962	2	10.613	10.581	20	17	1	1	2	LOC100506198, KLHL7	18864, 182	downstream, in gene	ActReg chr7 #8464	1	1
8465	7	23,221,099	23,222,038	939	2	13.517	13.517	24	24	1	1	2	KLHL7, NUPL2	76215, 122	downstream, in gene	ActReg chr7 #8465	1	1
8466	7	23,286,556	23,287,647	1,091	1	6.412	11.353	11	18	1	1	1	GPNMB	785	in gene	ActReg chr7 #8466	0	1
8467	7	23,338,669	23,339,370	701	1	11.773	9.864	19	19	1	1	1	C7orf30	79	in gene	ActReg chr7 #8467	1	0
8468	7	23,510,763	23,511,208	445	1	11.143	7.071	16	10	0	1	1	IGF2BP3	-990	upstream	ActReg chr7 #8468	1	0
8469	7	23,513,568	23,514,613	1,045	1	9.364	11.091	17	18	1	1	1	IGF2BP3	-4,095	upstream	ActReg chr7 #8469	0	1
8470	7	24,797,173	24,797,866	693	2	9.318	9.591	17	15	1	1	1	DFNA5	120	in gene	ActReg chr7 #8470	1	1
8471	7	24,826,478	24,827,023	545	1	11.353	9.941	22	14	0	0	1	OSBPL3	193,010	downstream	ActReg chr7 #8471	1	0
8472	7	24,861,013	24,861,579	566	1	11.833	7.944	19	11	0	0	1	OSBPL3	158,464	in gene	ActReg chr7 #8472	1	0
8473	7	25,019,395	25,020,415	1,020	1	9.645	11.387	13	17	1	1	1	OSBPL3	-145	upstream	ActReg chr7 #8473	0	1
8474	7	25,164,698	25,165,628	930	2	14.586	15.138	28	25	1	1	2	CYCS, C7orf31	-183, 54654	upstream, downstream	ActReg chr7 #8474	1	1
8475	7	25,901,917	25,902,635	718	2	10.957	11.087	19	20	1	0	0				ActReg chr7 #8475	1	1
8476	7	26,241,277	26,241,748	471	1	8.267	10.4	15	14	1	2	2	HNRNPA2B1, CBX3	-1099, 413	upstream, in gene	ActReg chr7 #8476	0	1
8477	7	26,998,254	26,999,274	1,020	2	12	12.562	21	21	0	0	0				ActReg chr7 #8477	1	1
8478	7	27,189,934	27,190,924	990	1	11.645	13.29	16	23	1	2	4	LOC100133311, HOXA5, HOXA6, HOXA7	10446, -7142, -3061, 5867	in gene, upstream, upstream, downstream	ActReg chr7 #8478	0	1
8479	7	27,702,128	27,703,033	905	2	18.429	16.571	44	34	1	1	1	HIBADH	40	in gene	ActReg chr7 #8479	1	1
8480	7	27,779,235	27,780,203	968	1	8.2	13.4	11	24	1	1	1	TAX1BP1	-19	upstream	ActReg chr7 #8480	0	1
8481	7	28,101,798	28,102,472	674	2	11.714	10.524	18	22	0	0	1	JAZF1	118,302	in gene	ActReg chr7 #8481	1	1
8482	7	28,725,349	28,726,010	661	1	5.45	11.05	9	16	0	0	1	CREB5	386,739	in gene	ActReg chr7 #8482	0	1
8483	7	28,895,322	28,896,105	783	2	11.24	10.88	17	19	0	0	0				ActReg chr7 #8483	1	1
8484	7	29,074,801	29,075,685	884	1	8.25	14.536	14	26	0	0	1	CPVL	110,910	in gene	ActReg chr7 #8484	0	1
8485	7	30,028,610	30,029,222	612	1	6.632	10.421	9	14	1	1	1	SCRN1	989	in gene	ActReg chr7 #8485	0	1
8486	7	30,065,956	30,066,850	894	2	16.75	17.321	34	43	1	2	2	FKBP14, PLEKHA8	-135, -1885	upstream, upstream	ActReg chr7 #8486	1	1
8487	7	30,067,505	30,068,466	961	2	17.467	18.7	38	43	1	2	2	FKBP14, PLEKHA8	-1717, -303	upstream, upstream	ActReg chr7 #8487	1	1
8488	7	30,324,125	30,324,723	598	1	7.579	12.158	10	15	1	2	2	ZNRF2, MIR550-1	501, -4986	in gene, upstream	ActReg chr7 #8488	0	1
8489	7	30,325,402	30,325,910	508	1	8.625	10.625	14	14	1	2	2	ZNRF2, MIR550-1	1733, -3754	in gene, upstream	ActReg chr7 #8489	0	1
8490	7	30,517,924	30,518,732	808	1	8.12	10.36	11	14	1	1	1	NOD1	65	in gene	ActReg chr7 #8490	0	1
8491	7	30,590,494	30,591,030	536	1	6.882	10.588	12	16	0	0	1	LOC401320	26,613	in gene	ActReg chr7 #8491	0	1
8492	7	30,634,061	30,634,793	732	1	10	15.174	15	29	1	1	1	GARS	246	in gene	ActReg chr7 #8492	0	1
8493	7	30,710,901	30,712,864	1,963	2	23.098	34.516	110	139	0	0	1	CRHR2	10,258	in gene	ActReg chr7 #8493	1	1
8494	7	30,756,531	30,757,133	602	1	12	11.316	21	20	0	0	0				ActReg chr7 #8494	1	0
8495	7	30,839,203	30,839,854	651	1	9.55	12.55	14	24	0	0	1	FAM188B	28,495	in gene	ActReg chr7 #8495	0	1
8496	7	31,154,022	31,155,447	1,425	2	16.182	25.318	51	98	0	0	1	ADCYAP1R1	62,592	downstream	ActReg chr7 #8496	1	1
8497	7	31,900,376	31,900,989	613	1	5.158	11.947	11	24	0	0	1	PDE1C	437,701	in gene	ActReg chr7 #8497	0	1
8498	7	32,090,610	32,091,099	489	1	11.933	11.067	16	16	0	0	1	PDE1C	247,529	in gene	ActReg chr7 #8498	1	0
8499	7	32,374,586	32,375,245	659	1	7.714	10.524	14	19	0	0	0				ActReg chr7 #8499	0	1
8500	7	32,467,017	32,467,937	920	2	14.034	16.862	35	37	1	0	0				ActReg chr7 #8500	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8501	7	32,529,426	32,530,419	993	2	17.606	18.355	42	49	1	1	2	LSM5, AVL9	4948, -5254	in gene, upstream	ActReg chr7 #8501	1	1
8502	7	32,981,832	32,982,769	937	1	7.621	11.345	10	18	1	0	0				ActReg chr7 #8502	0	1
8503	7	32,996,774	32,997,839	1,065	2	12.394	12.152	17	21	1	1	1	FKBP9	301	in gene	ActReg chr7 #8503	1	1
8504	7	33,101,782	33,103,035	1,253	1	10	12.41	15	21	1	1	1	NT5C3	1	in gene	ActReg chr7 #8504	0	1
8505	7	33,147,217	33,147,768	551	1	10	8.176	16	11	0	1	1	RP9	1,510	in gene	ActReg chr7 #8505	1	0
8506	7	33,148,445	33,149,624	1,179	3	16.135	19.838	39	61	1	1	1	RP9	-32	upstream	ActReg chr7 #8506	1	1
8507	7	33,168,893	33,169,569	676	1	5.727	12.091	10	21	1	1	1	BBS9	79	in gene	ActReg chr7 #8507	0	1
8508	7	34,026,398	34,027,448	1,050	2	11.152	9.909	20	27	0	0	1	BMPER	81,811	in gene	ActReg chr7 #8508	1	1
8509	7	35,043,307	35,043,887	580	1	9.167	11.444	15	19	0	0	1	DPY19L1	34,056	in gene	ActReg chr7 #8509	0	1
8510	7	35,637,828	35,638,274	446	1	10.286	10.071	14	16	0	0	0				ActReg chr7 #8510	0	1
8511	7	35,733,784	35,735,245	1,461	2	12.13	13.152	26	25	1	1	1	HERPUD2	258	in gene	ActReg chr7 #8511	1	1
8512	7	35,841,244	35,841,777	533	1	6.529	11.118	11	17	1	1	1	7-Sep	883	in gene	ActReg chr7 #8512	0	1
8513	7	36,076,046	36,077,417	1,371	1	6	11.628	10	19	0	0	0				ActReg chr7 #8513	0	1
8514	7	36,154,986	36,155,685	699	1	9.545	10.864	18	23	0	0	0				ActReg chr7 #8514	0	1
8515	7	36,406,432	36,407,295	863	2	10.963	12.852	18	23	1	0	1	KIAA0895	22,871	in gene	ActReg chr7 #8515	1	1
8516	7	36,546,357	36,546,963	606	1	10.053	8.053	17	15	0	0	1	AOAH	217,494	downstream	ActReg chr7 #8516	1	0
8517	7	37,071,429	37,072,412	983	1	9.233	9.6	18	16	0	0	1	ELMO1	416,591	in gene	ActReg chr7 #8517	0	1
8518	7	37,092,140	37,092,839	699	2	8.455	13.5	19	23	0	0	1	ELMO1	396,022	in gene	ActReg chr7 #8518	1	1
8519	7	37,394,412	37,394,915	503	1	11.25	9.375	15	12	0	0	1	ELMO1	93,848	in gene	ActReg chr7 #8519	1	0
8520	7	37,487,267	37,487,791	524	1	10.312	8.625	13	12	1	1	1	ELMO1	982	in gene	ActReg chr7 #8520	1	0
8521	7	37,488,284	37,488,909	625	1	6.4	10.7	11	18	1	1	1	ELMO1	-85	upstream	ActReg chr7 #8521	0	1
8522	7	39,044,879	39,045,524	645	2	9.6	8.8	19	18	0	0	1	POU6F2	27,592	in gene	ActReg chr7 #8522	1	1
8523	7	39,453,327	39,454,456	1,129	2	7.943	10.714	20	19	1	0	1	POU6F2	436,282	in gene	ActReg chr7 #8523	1	1
8524	7	39,605,655	39,606,458	803	1	9.32	13.16	12	24	1	1	1	C7orf36	53	in gene	ActReg chr7 #8524	0	1
8525	7	39,662,797	39,663,476	679	1	12.095	10	17	16	1	1	1	RALA	-26	upstream	ActReg chr7 #8525	1	0
8526	7	39,850,363	39,850,804	441	1	10.429	3.5	13	7	0	0	0				ActReg chr7 #8526	1	0
8527	7	39,989,443	39,990,063	620	1	10.895	8.579	20	13	1	1	1	CDK13	-206	upstream	ActReg chr7 #8527	1	0
8528	7	40,174,019	40,174,820	801	2	11.08	11.92	15	19	1	2	2	C7orf11, C7orf10	-168, -156	upstream, upstream	ActReg chr7 #8528	1	1
8529	7	40,591,097	40,591,836	739	2	9.609	10.13	18	18	0	0	1	C7orf10	416,891	in gene	ActReg chr7 #8529	1	1
8530	7	41,068,534	41,069,190	656	2	11.381	10.762	18	19	0	0	0				ActReg chr7 #8530	1	1
8531	7	41,147,121	41,147,886	765	1	8.333	12.833	16	18	0	0	0				ActReg chr7 #8531	0	1
8532	7	41,229,260	41,229,928	668	1	9.905	12	15	21	0	0	0				ActReg chr7 #8532	0	1
8533	7	41,413,728	41,414,538	810	1	6.731	11.923	9	19	0	0	0				ActReg chr7 #8533	0	1
8534	7	41,465,406	41,466,107	701	2	10.682	8.455	21	17	0	0	0				ActReg chr7 #8534	1	1
8535	7	42,271,739	42,272,279	540	1	9	11.588	17	18	0	0	1	GLI3	4,609	in gene	ActReg chr7 #8535	0	1
8536	7	42,971,683	42,972,335	652	1	7.2	11.5	11	18	1	2	2	PSMA2, MRPL32	-204, 70	upstream, in gene	ActReg chr7 #8536	0	1
8537	7	43,057,903	43,058,541	638	1	9.8	8.3	22	12	0	0	0				ActReg chr7 #8537	1	0
8538	7	43,259,761	43,260,431	670	1	12.857	9.762	24	17	0	0	1	HECW1	107,898	in gene	ActReg chr7 #8538	1	0
8539	7	43,608,907	43,609,645	738	1	9.174	11.217	14	21	0	0	1	HECW1	457,078	downstream	ActReg chr7 #8539	0	1
8540	7	43,622,828	43,623,460	632	1	7.3	10.75	11	22	1	1	1	STK17A	452	in gene	ActReg chr7 #8540	0	1
8541	7	43,687,373	43,688,060	687	1	13.571	10.619	20	14	0	0	1	C7orf44	81,367	in gene	ActReg chr7 #8541	1	0
8542	7	43,713,950	43,714,586	636	1	7.35	11.1	16	18	0	0	1	C7orf44	54,815	in gene	ActReg chr7 #8542	0	1
8543	7	43,768,626	43,769,552	926	2	12.379	16.862	20	33	1	1	1	C7orf44	-6	upstream	ActReg chr7 #8543	1	1
8544	7	43,908,874	43,909,780	906	1	9.429	11.786	15	20	1	1	2	MRPS24, URGCP	-182, 56669	upstream, downstream	ActReg chr7 #8544	0	1
8545	7	43,965,557	43,966,023	466	1	9.8	9.267	16	14	1	2	2	URGCP, UBE2D4	206, -245	in gene, upstream	ActReg chr7 #8545	1	0
8546	7	44,058,411	44,059,210	799	2	42.92	51.6	134	147	1	0	2	SPDYE1, LOC100287164	18321, 7142	downstream, downstream	ActReg chr7 #8546	1	1
8547	7	44,082,530	44,082,954	424	1	10.846	9.538	15	17	0	1	2	FLJ35390, DBNL	4044, -1497	downstream, upstream	ActReg chr7 #8547	1	0
8548	7	44,083,786	44,084,479	693	1	10.905	9.619	18	13	1	1	2	FLJ35390, DBNL	5434, -107	downstream, upstream	ActReg chr7 #8548	1	0
8549	7	44,240,446	44,241,042	596	1	11.684	8.158	22	13	1	1	1	YKT6	166	in gene	ActReg chr7 #8549	1	0
8550	7	44,613,188	44,613,959	771	1	7.917	13.292	13	23	1	1	2	DDX56, TMED4	564, 8254	in gene, downstream	ActReg chr7 #8550	0	1
8551	7	44,621,320	44,622,707	1,387	1	11.698	10.372	20	16	1	2	2	DDX56, TMED4	-7876, -166	upstream, upstream	ActReg chr7 #8551	1	0
8552	7	44,645,851	44,646,595	744	1	11.25	12.667	16	21	1	1	1	OGDH	102	in gene	ActReg chr7 #8552	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8553	7	44,678,410	44,679,824	1,414	1	9.045	12.704	16	20	0	0	1	OGDH	32,996	in gene	ActReg chr7 #8553	0	1
8554	7	44,787,958	44,789,347	1,389	2	12.477	18.326	41	50	2	1	1	ZMIZ2	122	in gene	ActReg chr7 #8554	1	1
8555	7	44,835,728	44,836,599	871	1	9.852	11.556	19	15	1	1	1	PPIA	-78	upstream	ActReg chr7 #8555	0	1
8556	7	44,924,067	44,924,556	489	1	4.786	10.267	10	12	0	1	1	PURB	649	in gene	ActReg chr7 #8556	0	1
8557	7	44,925,049	44,925,802	753	1	10.792	13.042	21	22	0	1	1	PURB	-465	upstream	ActReg chr7 #8557	0	1
8558	7	45,025,799	45,026,665	866	1	9.63	11.556	17	21	1	3	3	MYO1G, C7orf40, SNORA9	-7528, 27, -1123	upstream, in gene, upstream	ActReg chr7 #8558	0	1
8559	7	45,150,759	45,151,823	1,064	2	10.152	16.485	18	24	1	4	4	TBRG4, SNORA5A, SNORA5C, SNORA5B	26, -7210, -6650, -5593	in gene, upstream, upstream, upstream	ActReg chr7 #8559	1	1
8560	7	45,306,773	45,307,431	658	2	11.333	14.333	28	31	0	0	0				ActReg chr7 #8560	1	1
8561	7	45,387,353	45,387,883	530	1	7.882	10.294	13	18	0	0	0				ActReg chr7 #8561	0	1
8562	7	45,808,377	45,808,923	546	2	12.823	12.823	23	23	1	0	0				ActReg chr7 #8562	1	1
8563	7	45,960,240	45,961,088	848	1	8.444	10.963	13	18	1	1	1	IGFBP3	207	in gene	ActReg chr7 #8563	0	1
8564	7	46,013,320	46,014,155	835	1	10.731	10.962	16	17	0	0	0				ActReg chr7 #8564	1	0
8565	7	46,017,535	46,018,263	728	1	9.87	12.609	15	23	0	0	0				ActReg chr7 #8565	0	1
8566	7	46,043,497	46,044,400	903	1	10.786	12	15	21	0	0	0				ActReg chr7 #8566	0	1
8567	7	46,046,576	46,047,178	602	1	7.789	11.579	11	17	0	0	0				ActReg chr7 #8567	0	1
8568	7	46,793,761	46,794,266	505	1	6	11.2	9	17	0	0	0				ActReg chr7 #8568	0	1
8569	7	46,850,485	46,851,642	1,157	2	10.583	10.833	19	18	0	0	0				ActReg chr7 #8569	1	1
8570	7	46,899,513	46,900,355	842	1	6.556	10.518	13	17	0	0	0				ActReg chr7 #8570	0	1
8571	7	47,330,921	47,331,612	691	2	11.857	9.952	19	17	0	0	1	TNS3	247,933	in gene	ActReg chr7 #8571	1	1
8572	7	47,339,970	47,340,713	743	1	12.043	11.087	19	15	0	0	1	TNS3	238,858	in gene	ActReg chr7 #8572	1	0
8573	7	47,367,054	47,367,893	839	1	8.423	12.654	15	23	0	0	1	TNS3	211,726	in gene	ActReg chr7 #8573	0	1
8574	7	47,402,136	47,403,113	977	1	8.484	12.097	16	20	0	0	1	TNS3	176,575	in gene	ActReg chr7 #8574	0	1
8575	7	47,514,467	47,515,305	838	1	14.462	13.808	26	29	0	0	1	TNS3	64,313	in gene	ActReg chr7 #8575	0	1
8576	7	47,640,004	47,640,864	860	1	11.852	9.407	19	15	0	0	0				ActReg chr7 #8576	1	0
8577	7	47,660,663	47,661,756	1,093	1	11.765	7.765	17	16	0	0	0				ActReg chr7 #8577	1	0
8578	7	47,826,005	47,826,638	633	1	6.95	11.9	10	19	0	0	2	PKD1L1, C7orf69	161716, -8568	in gene, upstream	ActReg chr7 #8578	0	1
8579	7	48,018,908	48,019,507	599	2	9.105	10.737	19	18	1	1	2	HUS1, SUN3	39, 49509	in gene, downstream	ActReg chr7 #8579	1	1
8580	7	48,074,876	48,075,766	890	1	5.321	10.679	10	15	1	2	2	SUN3, C7orf57	-6605, 204	upstream, in gene	ActReg chr7 #8580	0	1
8581	7	48,124,184	48,124,855	671	1	8.048	10.857	13	16	0	1	1	UPP1	-3,836	upstream	ActReg chr7 #8581	0	1
8582	7	48,284,229	48,284,868	639	1	7.95	12.5	14	25	0	0	1	ABCA13	73,491	in gene	ActReg chr7 #8582	0	1
8583	7	50,517,662	50,518,888	1,226	2	9.103	11.538	19	22	1	1	2	FIGNL1, DDC	-187, 114879	upstream, downstream	ActReg chr7 #8583	1	1
8584	7	50,602,360	50,603,052	692	2	12.864	12.818	28	23	0	0	2	DDC, LOC100129427	30448, 3249	in gene, in gene	ActReg chr7 #8584	1	1
8585	7	50,620,217	50,621,203	986	2	13.065	16.129	36	34	0	0	2	DDC, LOC100129427	12444, 21253	in gene, downstream	ActReg chr7 #8585	1	1
8586	7	50,894,219	50,895,620	1,401	2	10.591	10.318	22	17	0	0	0				ActReg chr7 #8586	1	1
8587	7	50,919,460	50,920,451	991	1	10.452	6.935	17	12	0	0	0				ActReg chr7 #8587	1	0
8588	7	51,191,131	51,192,006	875	2	13.393	13.964	31	25	0	0	1	COBL	192,947	in gene	ActReg chr7 #8588	1	1
8589	7	51,612,898	51,613,341	443	1	10.308	6.154	14	8	0	0	0				ActReg chr7 #8589	1	0
8590	7	52,341,912	52,342,436	524	1	4.941	12.235	9	17	1	0	0				ActReg chr7 #8590	0	1
8591	7	53,879,358	53,879,882	524	1	7.059	12.882	10	20	0	1	1	FLJ45974	4	in gene	ActReg chr7 #8591	0	1
8592	7	54,082,859	54,083,455	596	1	6.833	12.722	14	25	0	0	0				ActReg chr7 #8592	0	1
8593	7	54,609,836	54,610,518	682	1	4.762	12.286	7	20	1	1	1	VSTM2A	158	in gene	ActReg chr7 #8593	0	1
8594	7	54,610,680	54,611,418	738	1	3.957	12.565	9	23	0	1	1	VSTM2A	1,030	in gene	ActReg chr7 #8594	0	1
8595	7	54,826,695	54,827,440	745	1	13.261	10.87	24	21	1	1	1	SEC61G	-128	upstream	ActReg chr7 #8595	1	0
8596	7	55,200,205	55,201,220	1,015	2	10.688	13.062	19	20	0	0	1	EGFR	113,987	in gene	ActReg chr7 #8596	1	1
8597	7	55,322,144	55,322,985	841	1	6.926	13.667	12	22	1	0	0				ActReg chr7 #8597	0	1
8598	7	55,433,105	55,434,373	1,268	2	14	15.1	28	29	1	1	1	LANCL2	598	in gene	ActReg chr7 #8598	1	1
8599	7	56,019,180	56,019,937	757	2	11.083	13.917	17	22	1	1	1	MRPS17	-53	upstream	ActReg chr7 #8599	1	1
8600	7	56,131,682	56,132,413	731	1	10.227	11.909	16	23	1	1	3	CCT6A, SNORA15, SUMF2	12669, 3884, 130	downstream, downstream, in gene	ActReg chr7 #8600	0	1
8601	7	56,173,799	56,174,547	748	1	10.304	11.826	17	19	1	1	2	CHCHD2, LOC389493	14, 9917	in gene, downstream	ActReg chr7 #8601	0	1
8602	7	56,515,481	56,516,011	530	1	7.706	10.177	11	15	1	0	0				ActReg chr7 #8602	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8603	7	56,605,529	56,606,177	648	2	9	9.81	17	18	0	0	0				ActReg chr7 #8603	1	1
8604	7	63,360,996	63,361,919	923	1	7.429	10.25	12	15	1	0	0				ActReg chr7 #8604	0	1
8605	7	63,386,255	63,387,422	1,167	2	11.389	13.778	23	28	1	0	0				ActReg chr7 #8605	1	1
8606	7	64,712,092	64,712,682	590	1	9.474	11.842	16	16	1	0	0				ActReg chr7 #8606	0	1
8607	7	64,790,610	64,791,114	504	1	10.062	6.125	16	8	0	0	0				ActReg chr7 #8607	1	0
8608	7	64,838,531	64,839,159	628	1	9.368	11	13	20	1	1	1	ZNF92	77	in gene	ActReg chr7 #8608	0	1
8609	7	65,215,327	65,216,368	1,041	1	8.333	13.303	12	21	1	1	1	SNORA22	-4,666	upstream	ActReg chr7 #8609	0	1
8610	7	65,297,114	65,297,719	605	1	11.21	9.579	24	19	0	1	1	DKFZp434F142	-7,782	upstream	ActReg chr7 #8610	1	0
8611	7	65,579,587	65,580,476	889	2	13.556	13.259	20	23	1	1	1	CRCP	226	in gene	ActReg chr7 #8611	1	1
8612	7	65,958,265	65,959,268	1,003	2	10.156	11.906	19	21	1	1	1	LOC100289098	73	in gene	ActReg chr7 #8612	1	1
8613	7	66,056,926	66,057,581	655	1	8.524	14.333	13	24	1	0	0				ActReg chr7 #8613	0	1
8614	7	66,119,012	66,119,883	871	1	7.741	12.963	11	17	1	0	0				ActReg chr7 #8614	0	1
8615	7	66,146,695	66,147,561	866	1	9.111	11.296	16	16	1	0	0				ActReg chr7 #8615	0	1
8616	7	66,205,310	66,206,355	1,045	1	8.455	12.061	15	16	1	1	1	RABGEF1	189	in gene	ActReg chr7 #8616	0	1
8617	7	66,309,426	66,310,273	847	2	11.667	15.482	25	34	1	0	0				ActReg chr7 #8617	1	1
8618	7	66,359,464	66,360,095	631	1	9.316	11.105	19	19	0	0	1	LOC644794	-8,665	upstream	ActReg chr7 #8618	0	1
8619	7	66,385,654	66,386,380	726	1	15.261	10.217	28	23	1	1	1	C7orf42	-186	upstream	ActReg chr7 #8619	1	0
8620	7	66,459,423	66,460,059	636	1	6.7	10.9	15	18	1	2	2	SBDS, TYW1	847, -2076	in gene, upstream	ActReg chr7 #8620	0	1
8621	7	72,299,819	72,300,325	506	1	8.812	10.812	11	15	1	1	1	TYW1B	-1,259	upstream	ActReg chr7 #8621	0	1
8622	7	72,395,234	72,396,105	871	1	7.481	10.37	11	15	1	0	1	POM121	45,733	in gene	ActReg chr7 #8622	0	1
8623	7	72,847,722	72,848,233	511	1	8.688	15.938	16	29	1	1	2	FZD9, BAZ1B	-132, 88638	upstream, downstream	ActReg chr7 #8623	0	1
8624	7	72,936,314	72,937,338	1,024	2	11.094	13.875	19	27	1	1	1	BAZ1B	-211	upstream	ActReg chr7 #8624	1	1
8625	7	73,129,657	73,130,631	974	2	14.258	12.613	27	26	0	0	2	STX1A, MIR4284	3873, 4497	in gene, downstream	ActReg chr7 #8625	1	1
8626	7	73,132,010	73,132,842	832	1	11.808	8.692	19	14	0	1	2	STX1A, MIR4284	1591, 6779	in gene, downstream	ActReg chr7 #8626	1	0
8627	7	73,417,989	73,418,581	592	1	10.5	8.778	16	13	0	0	0				ActReg chr7 #8627	1	0
8628	7	73,508,535	73,509,380	845	1	10.074	6.37	12	13	0	0	1	LIMK1	10,801	in gene	ActReg chr7 #8628	1	0
8629	7	73,512,074	73,512,842	768	1	6.25	11.583	8	17	0	0	1	LIMK1	14,302	in gene	ActReg chr7 #8629	0	1
8630	7	73,668,277	73,669,316	1,039	2	15.212	12.061	26	22	1	1	1	RFC2	-58	upstream	ActReg chr7 #8630	1	1
8631	7	73,720,656	73,721,374	718	1	12.546	8.773	18	12	1	0	1	CLIP2	17,210	in gene	ActReg chr7 #8631	1	0
8632	7	73,892,300	73,893,051	751	1	13.783	12.696	22	21	0	0	1	GTF2IRD1	24,555	in gene	ActReg chr7 #8632	1	0
8633	7	74,071,386	74,072,471	1,085	2	10	11.647	18	17	1	1	1	GTF2I	-102	upstream	ActReg chr7 #8633	1	1
8634	7	74,489,195	74,489,878	683	1	7.714	11.857	13	20	1	1	1	WBSCR16	163	in gene	ActReg chr7 #8634	0	1
8635	7	75,156,835	75,157,814	979	1	7.367	12.6	15	20	1	0	1	HIP1	210,955	downstream	ActReg chr7 #8635	0	1
8636	7	75,368,448	75,369,209	761	1	12.917	8.583	23	12	1	1	1	HIP1	-549	upstream	ActReg chr7 #8636	1	0
8637	7	75,543,734	75,544,922	1,188	2	17.351	19.919	45	57	1	1	1	POR	-92	upstream	ActReg chr7 #8637	1	1
8638	7	75,677,039	75,677,729	690	1	8.909	11.909	12	19	1	2	2	STYXL1, MDH2	-63, -9	upstream, upstream	ActReg chr7 #8638	0	1
8639	7	75,795,736	75,796,468	732	1	8.348	13.522	13	24	1	0	0				ActReg chr7 #8639	0	1
8640	7	75,830,839	75,832,055	1,216	2	9.486	13.974	27	43	1	1	1	SRRM3	231	in gene	ActReg chr7 #8640	1	1
8641	7	76,009,176	76,009,956	780	2	12.6	11.88	27	18	1	0	1	SRCRB4D	29,446	downstream	ActReg chr7 #8641	1	1
8642	7	76,022,556	76,023,114	558	1	11.222	11.556	17	19	1	1	2	SRCRB4D, ZP3	16177, -4006	in gene, upstream	ActReg chr7 #8642	1	0
8643	7	76,751,464	76,752,029	565	2	8.412	8.412	17	17	1	1	1	CCDC146	-188	upstream	ActReg chr7 #8643	1	1
8644	7	77,165,617	77,166,387	770	1	7.625	12.125	15	22	1	1	1	PTPN12	-771	upstream	ActReg chr7 #8644	0	1
8645	7	77,325,470	77,326,198	728	1	9.957	11.391	15	16	1	2	2	LOC100505854, RSBN1L	1123, 91	in gene, in gene	ActReg chr7 #8645	0	1
8646	7	77,768,690	77,769,083	393	1	9.417	10	14	14	0	0	1	MAGI2	1,314,004	in gene	ActReg chr7 #8646	0	1
8647	7	77,780,583	77,781,236	653	1	7.2	11.35	14	19	0	0	1	MAGI2	1,301,981	in gene	ActReg chr7 #8647	0	1
8648	7	77,807,491	77,808,076	585	1	5.889	10.556	10	19	0	0	1	MAGI2	1,275,107	in gene	ActReg chr7 #8648	0	1
8649	7	78,250,115	78,250,810	695	2	10.667	14.048	25	29	0	0	1	MAGI2	832,428	in gene	ActReg chr7 #8649	1	1
8650	7	78,946,912	78,947,335	423	1	9.714	9.071	14	16	0	0	1	MAGI2	135,767	in gene	ActReg chr7 #8650	0	1
8651	7	79,082,731	79,083,754	1,023	2	10.625	14.031	18	21	1	2	2	MAGI2, LOC100505881	-352, -66	upstream, upstream	ActReg chr7 #8651	1	1
8652	7	79,161,399	79,161,837	438	1	4.1	10.357	6	16	0	0	0				ActReg chr7 #8652	0	1
8653	7	79,764,258	79,764,891	633	1	9.947	11.368	14	18	1	1	1	GNAI1	434	in gene	ActReg chr7 #8653	0	1
8654	7	80,741,054	80,741,649	595	1	5.263	11.737	9	20	0	0	0				ActReg chr7 #8654	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8655	7	80,820,283	80,820,753	470	1	11.533	6.8	18	9	0	0	0				ActReg chr7 #8655	1	0
8656	7	81,314,165	81,314,760	595	1	11.053	9.789	16	18	0	0	0				ActReg chr7 #8656	1	0
8657	7	81,823,427	81,823,843	416	1	4.615	10.308	10	18	0	0	1	CACNA2D1	249,396	in gene	ActReg chr7 #8657	0	1
8658	7	82,434,745	82,435,297	552	1	5.944	11	12	17	0	0	1	PCLO	357,176	in gene	ActReg chr7 #8658	0	1
8659	7	82,790,432	82,791,046	614	2	8.8	11.1	19	22	0	1	1	PCLO	1,458	in gene	ActReg chr7 #8659	1	1
8660	7	82,791,249	82,792,832	1,583	2	15.92	16.92	37	31	1	1	1	PCLO	157	in gene	ActReg chr7 #8660	1	1
8661	7	83,097,360	83,098,126	766	2	13.375	11.833	28	29	0	0	1	SEMA3E	180,736	in gene	ActReg chr7 #8661	1	1
8662	7	83,306,387	83,306,956	569	1	10.611	4	16	9	0	0	0				ActReg chr7 #8662	1	0
8663	7	83,866,732	83,867,392	660	1	11.429	6.667	22	10	0	0	0				ActReg chr7 #8663	1	0
8664	7	83,880,689	83,881,130	441	1	6.571	9.929	9	17	0	0	0				ActReg chr7 #8664	0	1
8665	7	84,815,331	84,816,365	1,034	1	9	11.531	13	15	1	0	0				ActReg chr7 #8665	0	1
8666	7	86,729,526	86,730,212	686	1	7.409	12.546	17	28	0	0	0				ActReg chr7 #8666	0	1
8667	7	86,781,200	86,782,317	1,117	1	8.914	12.086	18	21	1	3	3	LOC100505932, DMTF1, LOC100505951	-102, 81, -7078	upstream, in gene, upstream	ActReg chr7 #8667	0	1
8668	7	86,848,747	86,850,354	1,607	2	9.44	12.92	16	25	1	1	1	C7orf23	-519	upstream	ActReg chr7 #8668	1	1
8669	7	86,974,262	86,975,088	826	2	10.615	11.154	13	19	1	2	2	TP53TG1, CROT	133, -276	in gene, upstream	ActReg chr7 #8669	1	1
8670	7	87,257,128	87,257,933	805	2	10.6	10.16	19	16	1	1	2	ABCB1, RUNDC3B	85034, -199	in gene, upstream	ActReg chr7 #8670	1	1
8671	7	87,563,062	87,564,073	1,011	1	8.906	12.031	12	22	1	1	1	ADAM22	-135	upstream	ActReg chr7 #8671	0	1
8672	7	87,814,014	87,814,569	555	1	8.944	10	18	16	0	0	1	ADAM22	250,589	in gene	ActReg chr7 #8672	0	1
8673	7	87,849,115	87,849,868	753	2	11.063	16	20	31	1	0	1	SRI	6,817	in gene	ActReg chr7 #8673	1	1
8674	7	87,908,061	87,908,658	597	1	9.737	4.158	17	7	0	0	1	STEAP4	27,850	in gene	ActReg chr7 #8674	1	0
8675	7	89,975,635	89,976,388	753	2	12.375	9.417	23	16	1	1	1	GTPBP10	21	in gene	ActReg chr7 #8675	1	1
8676	7	90,394,120	90,394,610	490	1	5.133	9.6	8	14	0	0	1	CDK14	55,653	in gene	ActReg chr7 #8676	0	1
8677	7	90,893,313	90,894,101	788	1	14.375	9.417	30	14	1	1	1	FZD1	-76	upstream	ActReg chr7 #8677	1	0
8678	7	91,509,298	91,510,609	1,311	2	16.78	20.634	47	61	1	1	1	MTERF	63	in gene	ActReg chr7 #8678	1	1
8679	7	91,569,731	91,570,629	898	1	12.964	6.704	19	15	1	1	1	AKAP9	-9	upstream	ActReg chr7 #8679	1	0
8680	7	91,762,900	91,764,463	1,563	2	12.062	14.102	20	23	1	2	3	CYP51A1, LOC613126, LOC401387	378, 505, 30909	in gene, in gene, downstream	ActReg chr7 #8680	1	1
8681	7	91,874,658	91,875,629	971	1	8.033	12.033	13	17	1	2	2	KRIT1, ANKIB1	271, -405	in gene, upstream	ActReg chr7 #8681	0	1
8682	7	92,076,668	92,077,184	516	1	9.882	10.588	14	16	1	1	1	GATAD1	161	in gene	ActReg chr7 #8682	0	1
8683	7	92,157,404	92,158,680	1,276	2	32.3	34.925	112	120	1	2	3	PEX1, C7orf64, MGC16142	-197, -45, -9747	upstream, upstream, upstream	ActReg chr7 #8683	1	1
8684	7	92,218,800	92,220,182	1,382	2	34.186	44.767	135	159	1	1	1	FAM133B	215	in gene	ActReg chr7 #8684	1	1
8685	7	92,462,217	92,462,843	626	1	11.684	10.737	18	12	1	0	1	CDK6	3,411	in gene	ActReg chr7 #8685	1	0
8686	7	92,462,983	92,463,804	821	1	6.52	10.8	10	16	1	1	1	CDK6	2,548	in gene	ActReg chr7 #8686	0	1
8687	7	92,464,712	92,465,375	663	1	10.25	9	15	13	1	1	1	CDK6	898	in gene	ActReg chr7 #8687	1	0
8688	7	92,861,112	92,861,988	876	2	10.571	14.393	23	32	0	2	2	HEPACAM2, CCDC132	-5768, -103	upstream, upstream	ActReg chr7 #8688	1	1
8689	7	93,519,713	93,520,325	612	1	5.632	10.632	7	17	1	1	1	TFPI2	46	in gene	ActReg chr7 #8689	0	1
8690	7	93,633,381	93,634,116	735	1	9.391	11.739	15	19	1	1	1	BET1	-58	upstream	ActReg chr7 #8690	0	1
8691	7	94,139,199	94,140,263	1,064	2	9.5	10.235	17	21	1	1	1	CASD1	561	in gene	ActReg chr7 #8691	1	1
8692	7	94,249,989	94,250,786	797	1	12.2	9.36	22	13	0	0	1	SCCE	35,134	in gene	ActReg chr7 #8692	1	0
8693	7	94,536,501	94,537,184	683	2	8.909	11.318	16	24	1	1	1	PPP1R9A	-107	upstream	ActReg chr7 #8693	1	1
8694	7	94,603,038	94,603,655	617	1	9.35	11.85	15	18	0	0	1	PPP1R9A	66,397	in gene	ActReg chr7 #8694	0	1
8695	7	95,064,058	95,064,519	461	1	11.133	7.067	16	9	1	1	1	PON2	96	in gene	ActReg chr7 #8695	1	0
8696	7	95,130,729	95,131,230	501	1	10.6	6.4	14	10	0	0	1	ASB4	15,695	in gene	ActReg chr7 #8696	1	0
8697	7	95,179,101	95,179,880	779	1	9.16	10.32	14	14	0	0	1	LOC100506064	8,033	downstream	ActReg chr7 #8697	0	1
8698	7	95,950,783	95,951,939	1,156	2	13.764	14.243	26	27	1	1	1	SLC25A13	98	in gene	ActReg chr7 #8698	1	1
8699	7	96,338,671	96,339,390	719	1	9.909	11.682	14	17	1	1	1	SHFM1	173	in gene	ActReg chr7 #8699	0	1
8700	7	96,452,159	96,453,133	974	2	16.903	14.419	36	34	0	0	0				ActReg chr7 #8700	1	1
8701	7	96,746,522	96,747,436	914	2	9.966	15.103	22	27	1	1	1	ACN9	1,074	in gene	ActReg chr7 #8701	1	1
8702	7	97,735,825	97,736,680	855	2	9.889	11.148	16	29	1	1	1	LMTK2	55	in gene	ActReg chr7 #8702	1	1
8703	7	97,881,144	97,881,994	850	1	10.37	12.37	21	18	1	1	1	TECPR1	-101	upstream	ActReg chr7 #8703	0	1
8704	7	98,048,016	98,049,189	1,173	2	12.757	9.351	28	22	0	0	0				ActReg chr7 #8704	1	1
8705	7	98,475,963	98,477,047	1,084	2	12.088	17.5	30	39	1	1	2	TMEM130, TRRAP	-8832, 392	upstream, in gene	ActReg chr7 #8705	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8706	7	98,864,924	98,866,004	1,080	1	8.853	13.794	15	23	0	0	0				ActReg chr7 #8706	0	1
8707	7	98,971,771	98,972,425	654	1	8.667	9.762	15	14	1	1	2	ARPC1A, ARPC1B	48602, -231	downstream, upstream	ActReg chr7 #8707	0	1
8708	7	99,005,558	99,006,867	1,309	2	12.439	10.854	19	29	1	2	3	PDAP1, BUD31, PTCD1	80, -389, 30207	in gene, upstream, downstream	ActReg chr7 #8708	1	1
8709	7	99,036,043	99,037,040	997	2	22.742	23.194	69	66	1	2	2	PTCD1, CPSF4	-122, -22	upstream, upstream	ActReg chr7 #8709	1	1
8710	7	99,097,455	99,098,247	792	2	10.6	12.52	18	21	1	2	2	ZNF394, ZKSCAN5	26, -4422	in gene, upstream	ActReg chr7 #8710	1	1
8711	7	99,149,334	99,150,037	703	2	11.773	13.318	29	25	1	2	2	C7orf38, ZNF655	72, -6360	in gene, upstream	ActReg chr7 #8711	1	1
8712	7	99,213,883	99,215,162	1,279	2	20.675	26.95	54	68	1	1	2	LOC100506199, ZNF498	18674, -49	downstream, upstream	ActReg chr7 #8712	1	1
8713	7	99,457,697	99,458,317	620	1	9.789	11.158	13	17	0	0	2	CYP3A, CYP3A43	6166, 32371	in gene, in gene	ActReg chr7 #8713	0	1
8714	7	99,516,684	99,517,747	1,063	2	11.758	9.97	17	21	1	1	2	TRIM4, GJC3	8, 10028	in gene, downstream	ActReg chr7 #8714	1	1
8715	7	99,612,760	99,613,534	774	2	9.625	13.208	22	30	1	1	1	ZKSCAN1	-72	upstream	ActReg chr7 #8715	1	1
8716	7	99,647,193	99,647,789	596	1	10.474	7.684	17	14	0	1	1	ZSCAN21	74	in gene	ActReg chr7 #8716	1	0
8717	7	99,678,894	99,679,766	872	2	11.518	12.482	17	20	1	2	2	ZNF3, COPS6	41, -7253	in gene, upstream	ActReg chr7 #8717	1	1
8718	7	99,697,915	99,699,437	1,522	3	9.511	13.583	22	28	1	5	7	COPS6, MCM7, MIR25, MIR93, MIR106B, AP4M1, TAF6	12093, 751, 7410, -7206, -6979, -454, 18805	downstream, in gene, upstream, upstream, upstream, upstream, downstream	ActReg chr7 #8718	1	1
8719	7	99,716,577	99,717,730	1,153	2	15.444	13.917	23	26	0	3	3	TAF6, CNPY4, MBLAC1	328, -112, -7164	in gene, upstream, upstream	ActReg chr7 #8719	1	1
8720	7	99,724,448	99,725,795	1,347	2	11.256	11.721	22	17	1	2	3	TAF6, CNPY4, MBLAC1	-7640, 7856, 804	upstream, downstream, in gene	ActReg chr7 #8720	1	1
8721	7	100,025,572	100,027,212	1,640	2	12.784	12.137	19	18	1	2	3	ZCWPW1, MEPCE, C7orf47	-90, -21, 7702	upstream, upstream, downstream	ActReg chr7 #8721	1	1
8722	7	100,136,211	100,137,071	860	1	8.963	12	14	17	1	1	1	AGFG2	-193	upstream	ActReg chr7 #8722	0	1
8723	7	100,183,424	100,184,366	942	2	13.2	14.2	20	26	1	2	3	LRCH4, FBXO24, LOC100129845	-119, -61, 17766	upstream, upstream, downstream	ActReg chr7 #8723	1	1
8724	7	100,253,642	100,254,475	833	2	8.923	9.96	19	19	1	1	1	ACTL6B	26	in gene	ActReg chr7 #8724	1	1
8725	7	100,270,915	100,271,465	550	1	11.812	14.235	21	28	1	1	2	GNB2, GIGYF1	-173, 15680	upstream, downstream	ActReg chr7 #8725	0	1
8726	7	100,302,789	100,304,462	1,673	2	9.865	10.308	16	19	1	1	1	POP7	-51	upstream	ActReg chr7 #8726	1	1
8727	7	100,434,679	100,435,420	741	1	9.174	13.087	14	24	1	0	1	EPHB4	-9,906	upstream	ActReg chr7 #8727	0	1
8728	7	100,472,136	100,473,009	873	1	7.296	13	17	20	1	1	3	SLC12A9, TRIP6, SRRT	22214, 7622, -129	downstream, downstream, upstream	ActReg chr7 #8728	0	1
8729	7	100,701,469	100,702,071	602	2	14.21	13.421	27	26	0	0	1	MUC17	38,406	in gene	ActReg chr7 #8729	1	1
8730	7	100,743,316	100,744,230	914	1	7.103	11.931	13	18	0	0	1	TRIM56	14,987	downstream	ActReg chr7 #8730	0	1
8731	7	100,781,695	100,782,168	473	1	8.933	10.667	13	17	0	0	1	SERPINE1	11,552	in gene	ActReg chr7 #8731	0	1
8732	7	100,806,827	100,808,158	1,331	2	10.659	10.024	18	19	1	1	3	AP1S1, VGF, C7orf52	9806, 1360, 16065	downstream, in gene, downstream	ActReg chr7 #8732	1	1
8733	7	100,808,202	100,809,260	1,058	2	16.273	12.333	29	23	1	1	3	AP1S1, VGF, C7orf52	11045, 121, 14826	downstream, in gene, downstream	ActReg chr7 #8733	1	1
8734	7	100,812,308	100,813,489	1,181	1	11.973	10.162	15	17	0	1	3	AP1S1, VGF, C7orf52	15212, -4046, 10659	downstream, upstream, downstream	ActReg chr7 #8734	1	0
8735	7	100,816,293	100,817,028	735	1	7.043	10.478	12	16	1	1	2	VGF, C7orf52	-7808, 6897	upstream, in gene	ActReg chr7 #8735	0	1
8736	7	100,887,211	100,888,717	1,506	2	11.894	11.702	24	25	1	2	2	CLDN15, FIS1	-5863, 407	upstream, in gene	ActReg chr7 #8736	1	1
8737	7	100,895,105	100,895,944	839	2	11.769	15.308	22	32	1	1	1	FIS1	-7,153	upstream	ActReg chr7 #8737	1	1
8738	7	101,457,404	101,458,094	690	2	9.727	10.682	17	21	1	1	1	CUX1	-1,543	upstream	ActReg chr7 #8738	1	1
8739	7	101,458,427	101,458,896	469	1	11.467	11.6	17	16	1	1	1	CUX1	-631	upstream	ActReg chr7 #8739	1	0
8740	7	101,459,099	101,459,410	311	1	5.444	11.3	7	17	1	1	1	CUX1	-38	upstream	ActReg chr7 #8740	0	1
8741	7	101,762,306	101,762,871	565	1	8.647	10.588	12	19	0	0	1	CUX1	303,296	in gene	ActReg chr7 #8741	0	1
8742	7	102,003,937	102,004,501	564	2	13.412	10.529	25	18	1	1	1	SPDYE6	-7,330	upstream	ActReg chr7 #8742	1	1
8743	7	102,036,196	102,037,183	987	2	12	14	25	25	1	1	2	PRKRIP1, MIR548O	-115, 9613	upstream, downstream	ActReg chr7 #8743	1	1
8744	7	102,119,182	102,119,530	348	2	29	39.545	46	64	1	1	4	LRWD1, POLR2J, LOC100506726, RASA4B	13966, 25, 4157, 38868	downstream, in gene, downstream, downstream	ActReg chr7 #8744	1	1
8745	7	102,515,897	102,516,764	867	2	9.667	13.963	24	26	0	0	1	FBXL13	198,958	in gene	ActReg chr7 #8745	1	1
8746	7	102,632,016	102,632,594	578	1	10.333	8.5	18	14	0	0	1	FBXL13	82,983	in gene	ActReg chr7 #8746	1	0
8747	7	102,789,253	102,790,341	1,088	2	8.559	11.471	15	17	1	1	1	NAPEPLD	-228	upstream	ActReg chr7 #8747	1	1
8748	7	102,984,795	102,985,472	677	2	10.727	12.046	20	19	1	2	3	DNAJC2, PSMC2, SLC26A5	187, -2956, 101491	in gene, upstream, downstream	ActReg chr7 #8748	1	1
8749	7	103,276,553	103,277,140	587	2	10.278	13.833	16	24	0	0	1	RELN	353,117	in gene	ActReg chr7 #8749	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8750	7	103,848,046	103,848,851	805	2	10.92	12.48	23	22	0	1	1	ORC5L	15	in gene	ActReg chr7 #8750	1	1
8751	7	104,192,395	104,193,100	705	1	10.056	13.5	21	27	0	0	1	LHFPL3	223,643	in gene	ActReg chr7 #8751	0	1
8752	7	104,267,793	104,268,388	595	2	10.158	13.947	16	25	0	0	1	LHFPL3	298,986	in gene	ActReg chr7 #8752	1	1
8753	7	104,652,991	104,654,138	1,147	1	8.833	11.944	16	16	1	2	2	LOC100216545, MLL5	1024, -1073	in gene, upstream	ActReg chr7 #8753	0	1
8754	7	104,944,530	104,945,286	756	1	8.333	10.625	15	15	0	0	1	SRPK2	84,433	in gene	ActReg chr7 #8754	0	1
8755	7	105,172,330	105,173,112	782	2	13.917	14.125	23	31	1	1	2	PUS7, RINT1	-10036, 189	upstream, in gene	ActReg chr7 #8755	1	1
8756	7	105,415,940	105,417,096	1,156	2	10.5	13.441	28	36	0	0	1	ATXN7L1	100,513	in gene	ActReg chr7 #8756	1	1
8757	7	105,698,992	105,699,507	515	1	11.75	13.438	18	23	0	0	0				ActReg chr7 #8757	0	1
8758	7	105,752,063	105,753,353	1,290	2	9.463	9.61	18	15	1	1	1	SYPL1	349	in gene	ActReg chr7 #8758	1	1
8759	7	106,300,490	106,300,907	417	1	7.833	11.538	12	17	1	1	1	FLJ36031	893	in gene	ActReg chr7 #8759	0	1
8760	7	106,463,994	106,465,441	1,447	2	11.348	12.783	17	24	0	0	0				ActReg chr7 #8760	1	1
8761	7	106,968,446	106,968,995	549	1	9.167	7.222	17	11	0	0	1	COG5	236,239	in gene	ActReg chr7 #8761	1	0
8762	7	107,204,010	107,205,022	1,012	2	14.29	17.839	30	41	1	2	2	COG5, DUS4L	443, 84	in gene, in gene	ActReg chr7 #8762	1	1
8763	7	107,383,552	107,385,069	1,517	1	10.104	13.625	17	20	1	2	2	LOC100128737, CBLL1	716, 31	in gene, in gene	ActReg chr7 #8763	0	1
8764	7	107,988,042	107,988,571	529	1	7.312	10.25	14	19	0	0	1	NRCAM	108,535	in gene	ActReg chr7 #8764	0	1
8765	7	108,071,333	108,072,202	869	1	11.037	14.111	18	26	0	0	1	NRCAM	25,074	in gene	ActReg chr7 #8765	0	1
8766	7	108,082,482	108,082,934	452	1	10.286	6.071	13	10	0	0	1	NRCAM	14,133	in gene	ActReg chr7 #8766	1	0
8767	7	108,094,989	108,096,040	1,051	1	11.061	12.242	16	20	1	1	1	NRCAM	1,327	in gene	ActReg chr7 #8767	0	1
8768	7	108,166,088	108,167,154	1,066	1	8.636	11.152	15	15	1	1	1	PNPLA8	17	in gene	ActReg chr7 #8768	0	1
8769	7	108,209,727	108,210,614	887	2	10.821	12	16	19	1	2	2	THAP5, DNAJB9	-3, -186	upstream, upstream	ActReg chr7 #8769	1	1
8770	7	111,202,068	111,202,928	860	1	10.148	7.889	16	11	1	1	1	IMMP2L	-151	upstream	ActReg chr7 #8770	1	0
8771	7	111,640,837	111,641,487	650	1	7.15	11.35	10	15	0	0	1	DOCK4	205,300	in gene	ActReg chr7 #8771	0	1
8772	7	111,846,101	111,847,121	1,020	2	11.156	11.688	19	23	1	2	2	DOCK4, ZNF277	-149, -32	upstream, upstream	ActReg chr7 #8772	1	1
8773	7	112,090,075	112,091,489	1,414	2	12.556	12.711	21	25	1	0	1	IFRD1	27,556	in gene	ActReg chr7 #8773	1	1
8774	7	112,121,758	112,122,516	758	1	10.5	5.083	16	9	0	1	2	IFRD1, C7orf53	58911, 1229	downstream, in gene	ActReg chr7 #8774	1	0
8775	7	112,124,670	112,125,196	526	1	7.059	11.471	9	17	0	0	2	IFRD1, C7orf53	61707, 4025	downstream, in gene	ActReg chr7 #8775	0	1
8776	7	112,429,747	112,430,928	1,181	1	12.649	7.432	19	12	1	1	1	TMEM168	141	in gene	ActReg chr7 #8776	1	0
8777	7	112,758,458	112,758,862	404	1	9.308	11	13	14	0	1	1	LOC401397	-23	upstream	ActReg chr7 #8777	0	1
8778	7	112,907,834	112,908,492	658	1	8.524	12.714	12	18	0	0	0				ActReg chr7 #8778	0	1
8779	7	114,025,551	114,026,000	449	1	4.571	10.143	7	14	0	0	1	FOXP2	299,410	in gene	ActReg chr7 #8779	0	1
8780	7	114,529,603	114,530,253	650	2	11.35	11.5	27	19	0	0	0				ActReg chr7 #8780	1	1
8781	7	114,871,074	114,871,573	499	1	11.533	9.733	18	18	0	0	0				ActReg chr7 #8781	1	0
8782	7	114,980,914	114,981,441	527	2	9.059	8.647	19	16	0	0	0				ActReg chr7 #8782	1	1
8783	7	115,911,820	115,912,351	531	1	9.875	8.875	15	13	0	0	0				ActReg chr7 #8783	1	0
8784	7	116,166,216	116,167,119	903	2	14.714	12.607	27	19	1	1	1	CAV1	1,828	in gene	ActReg chr7 #8784	1	1
8785	7	116,216,680	116,217,660	980	2	10.133	8.9	16	16	0	0	0				ActReg chr7 #8785	1	1
8786	7	116,256,619	116,257,247	628	1	11.421	9.316	24	18	0	0	0				ActReg chr7 #8786	1	0
8787	7	116,356,558	116,357,132	574	1	14.111	11.611	24	19	0	0	1	MET	44,386	in gene	ActReg chr7 #8787	1	0
8788	7	116,416,390	116,416,805	415	1	9.846	6.154	12	10	0	0	1	MET	104,138	in gene	ActReg chr7 #8788	1	0
8789	7	116,593,984	116,594,568	584	1	9.895	9.789	15	13	1	3	3	ST7OT1, ST7, ST7OT4	112, 895, 323	in gene, in gene, in gene	ActReg chr7 #8789	1	0
8790	7	116,909,300	116,910,036	736	2	13.826	10.261	28	23	0	0	1	WNT2	53,675	downstream	ActReg chr7 #8790	1	1
8791	7	120,590,335	120,591,261	926	2	13.034	10.345	22	22	1	1	1	ING3	-19	upstream	ActReg chr7 #8791	1	1
8792	7	120,844,641	120,845,027	386	1	10.5	7.167	15	11	0	0	1	C7orf58	216,083	in gene	ActReg chr7 #8792	1	0
8793	7	121,035,882	121,036,903	1,021	2	11.875	16.719	28	41	1	1	1	FAM3C	30	in gene	ActReg chr7 #8793	1	1
8794	7	121,783,845	121,784,851	1,006	1	11.032	6.355	15	14	1	1	1	AASS	-4	upstream	ActReg chr7 #8794	1	0
8795	7	122,675,741	122,676,311	570	1	3.056	9.667	5	19	0	0	0				ActReg chr7 #8795	0	1
8796	7	123,197,473	123,198,406	933	2	15.138	13.345	29	24	1	1	1	NDUFA5	19	in gene	ActReg chr7 #8796	1	1
8797	7	123,388,545	123,389,756	1,211	2	10.135	11.135	18	19	1	1	1	WASL	-34	upstream	ActReg chr7 #8797	1	1
8798	7	123,672,509	123,673,077	568	1	10.294	11.167	14	18	1	1	1	TMEM229A	730	in gene	ActReg chr7 #8798	0	1
8799	7	124,362,880	124,363,526	646	2	8.905	9.905	18	18	0	0	0				ActReg chr7 #8799	1	1
8800	7	124,405,583	124,406,212	629	2	9.45	12.158	16	22	1	1	1	GPR37	-216	upstream	ActReg chr7 #8800	1	1
8801	7	125,203,534	125,204,510	976	2	12.036	9.667	24	15	0	0	0				ActReg chr7 #8801	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8802	7	125,666,718	125,667,049	331	1	5	10.182	7	14	0	0	0				ActReg chr7 #8802	0	1
8803	7	126,747,361	126,748,402	1,041	2	18.645	21.438	43	52	0	0	1	GRM8	144,547	in gene	ActReg chr7 #8803	1	1
8804	7	126,893,682	126,894,229	547	1	10.588	7.765	14	15	1	1	1	GRM8	-1,527	upstream	ActReg chr7 #8804	1	0
8805	7	127,031,954	127,032,517	563	1	8.222	10	12	14	1	1	1	ZNF800	532	in gene	ActReg chr7 #8805	0	1
8806	7	127,032,534	127,033,362	828	1	8.115	11.731	16	17	1	1	1	ZNF800	-181	upstream	ActReg chr7 #8806	0	1
8807	7	127,114,349	127,114,991	642	1	9	11.95	15	23	0	1	1	LOC100506682	-2,262	upstream	ActReg chr7 #8807	0	1
8808	7	127,291,550	127,292,296	746	2	11.917	11.25	18	15	1	1	1	SND1	-279	upstream	ActReg chr7 #8808	1	1
8809	7	127,803,683	127,805,032	1,349	1	9.048	11.429	14	17	0	0	0				ActReg chr7 #8809	0	1
8810	7	127,808,248	127,809,075	827	1	8.038	12.538	11	21	1	0	0				ActReg chr7 #8810	0	1
8811	7	127,983,545	127,984,247	702	1	9.227	11.636	16	23	1	1	2	RBM28, PRRT4	66, 17843	in gene, downstream	ActReg chr7 #8811	0	1
8812	7	128,095,539	128,096,319	780	1	9.5	12.125	13	16	1	1	1	C7orf68	45	in gene	ActReg chr7 #8812	0	1
8813	7	128,116,554	128,117,010	456	1	9.214	13.214	13	19	1	1	1	METTL2B	-1	upstream	ActReg chr7 #8813	0	1
8814	7	128,694,255	128,695,556	1,301	2	13.61	13.659	20	24	1	1	1	TNPO3	322	in gene	ActReg chr7 #8814	1	1
8815	7	129,251,228	129,251,744	516	1	7.824	12.412	13	20	1	2	2	LOC100127891, NRF1	9, -69	in gene, upstream	ActReg chr7 #8815	0	1
8816	7	129,609,577	129,610,296	719	1	5.5	11.182	11	15	0	0	0				ActReg chr7 #8816	0	1
8817	7	129,648,685	129,650,654	1,969	2	9.508	12.213	22	22	0	0	1	ZC3HC1	41,564	downstream	ActReg chr7 #8817	1	1
8818	7	129,709,800	129,710,582	782	2	19.083	15.5	44	34	1	1	1	KLHDC10	-158	upstream	ActReg chr7 #8818	1	1
8819	7	129,918,963	129,919,678	715	1	8	11.046	13	16	0	0	1	CPA2	12,617	in gene	ActReg chr7 #8819	0	1
8820	7	129,996,701	129,997,349	648	1	10.714	9.571	17	15	0	0	1	CPA5	12,395	in gene	ActReg chr7 #8820	1	0
8821	7	130,549,682	130,550,778	1,096	2	11.5	15.794	26	31	0	0	1	LOC100506860	11,751	in gene	ActReg chr7 #8821	1	1
8822	7	130,645,065	130,645,664	599	1	8.842	10.316	15	17	0	0	1	FLJ43663	148,198	in gene	ActReg chr7 #8822	0	1
8823	7	130,756,804	130,757,198	394	1	14.25	9.25	22	15	0	0	1	FLJ43663	36,561	in gene	ActReg chr7 #8823	1	0
8824	7	130,873,011	130,873,856	845	1	9.37	11.259	15	16	0	0	1	MKLN1	78,578	in gene	ActReg chr7 #8824	0	1
8825	7	130,896,684	130,897,369	685	2	12.95	11.809	24	21	0	0	1	MKLN1	102,171	in gene	ActReg chr7 #8825	1	1
8826	7	131,011,946	131,013,278	1,332	2	12.829	14.341	21	30	1	1	2	MKLN1, LOC100506881	217757, -74	in gene, upstream	ActReg chr7 #8826	1	1
8827	7	131,292,220	131,293,245	1,025	2	11.438	10.406	24	19	0	0	0				ActReg chr7 #8827	1	1
8828	7	131,430,115	131,431,073	958	2	10.067	16.367	18	34	0	0	0				ActReg chr7 #8828	1	1
8829	7	131,580,314	131,581,154	840	1	8.889	11.778	15	20	0	0	0				ActReg chr7 #8829	0	1
8830	7	131,581,888	131,582,733	845	1	11.667	6.815	20	10	0	0	0				ActReg chr7 #8830	1	0
8831	7	131,977,504	131,978,114	610	1	6.1	10.25	11	17	0	0	1	PLXNA4	355,638	in gene	ActReg chr7 #8831	0	1
8832	7	132,468,522	132,469,140	618	1	10.158	7.421	19	14	0	0	1	CHCHD3	298,002	downstream	ActReg chr7 #8832	1	0
8833	7	132,766,527	132,767,321	794	2	9.96	11.24	18	18	1	1	1	CHCHD3	-91	upstream	ActReg chr7 #8833	1	1
8834	7	132,823,898	132,824,773	875	1	10.321	17.179	21	37	0	0	0				ActReg chr7 #8834	0	1
8835	7	133,597,834	133,598,401	567	1	9.778	10.278	15	15	0	0	1	EXOC4	660,294	in gene	ActReg chr7 #8835	0	1
8836	7	134,000,981	134,002,112	1,131	2	12.528	10.639	20	21	1	1	1	SLC35B4	281	in gene	ActReg chr7 #8836	1	1
8837	7	134,142,974	134,144,359	1,385	2	14.591	14.273	25	37	1	1	1	AKR1B1	222	in gene	ActReg chr7 #8837	1	1
8838	7	134,155,461	134,156,115	654	1	9.8	11.45	19	18	0	0	0				ActReg chr7 #8838	0	1
8839	7	134,331,162	134,332,098	936	2	19.767	21.3	56	54	0	1	1	BPGM	99	in gene	ActReg chr7 #8839	1	1
8840	7	134,832,762	134,833,197	435	1	8.071	10.357	12	15	0	2	2	LOC653739, TMEM140	66, 213	in gene, in gene	ActReg chr7 #8840	0	1
8841	7	134,854,949	134,855,883	934	2	11.103	11.931	16	19	1	1	2	TMEM140, C7orf49	22650, 116	downstream, in gene	ActReg chr7 #8841	1	1
8842	7	134,895,743	134,896,484	741	1	7.417	10.125	11	17	1	1	1	WDR91	203	in gene	ActReg chr7 #8842	0	1
8843	7	135,019,911	135,021,247	1,336	2	12.122	17.561	37	45	0	0	0				ActReg chr7 #8843	1	1
8844	7	135,126,492	135,127,044	552	1	8.944	6.556	16	15	0	0	1	CNOT4	68,107	in gene	ActReg chr7 #8844	1	0
8845	7	135,194,636	135,195,419	783	1	8.625	12.708	18	21	1	1	1	CNOT4	-152	upstream	ActReg chr7 #8845	0	1
8846	7	135,242,241	135,243,142	901	2	12.714	11.607	24	24	0	1	1	NUP205	29	in gene	ActReg chr7 #8846	1	1
8847	7	135,346,662	135,347,700	1,038	2	11.781	12.531	22	21	1	1	1	PL-5283	-40	upstream	ActReg chr7 #8847	1	1
8848	7	135,487,401	135,488,249	848	1	8.038	11.192	17	17	0	0	0				ActReg chr7 #8848	0	1
8849	7	135,819,240	135,819,681	441	1	8.143	9.286	12	14	0	0	0				ActReg chr7 #8849	0	1
8850	7	136,541,924	136,542,898	974	2	13.033	14.967	23	44	0	0	0				ActReg chr7 #8850	1	1
8851	7	137,223,228	137,223,696	468	1	3.867	9.667	6	15	0	0	1	DGKI	308,147	in gene	ActReg chr7 #8851	0	1
8852	7	137,326,652	137,327,478	826	2	11.385	14.808	20	28	0	0	1	DGKI	204,544	in gene	ActReg chr7 #8852	1	1
8853	7	137,366,722	137,367,324	602	1	10.333	9.333	17	12	0	0	1	DGKI	164,586	in gene	ActReg chr7 #8853	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8854	7	137,663,255	137,663,819	564	1	10.167	10.833	13	15	0	0	1	CREB3L2	23,309	in gene	ActReg chr7 #8854	0	1
8855	7	138,437,059	138,437,784	725	1	12.318	10	22	19	0	0	1	ATP6V0A4	45,520	in gene	ActReg chr7 #8855	1	0
8856	7	138,440,131	138,440,978	847	1	10.5	7.615	15	14	0	0	1	ATP6V0A4	42,387	in gene	ActReg chr7 #8856	1	0
8857	7	138,549,251	138,549,942	691	1	9.952	13.381	16	23	0	0	1	KIAA1549	71,033	in gene	ActReg chr7 #8857	0	1
8858	7	138,575,479	138,576,220	741	1	10.217	12.348	17	20	0	0	1	KIAA1549	44,780	in gene	ActReg chr7 #8858	0	1
8859	7	138,793,500	138,794,353	853	1	10.778	11.185	15	15	1	1	1	ZC3HAV1	539	in gene	ActReg chr7 #8859	0	1
8860	7	138,915,411	138,916,387	976	2	9.839	8.613	16	21	1	1	1	UBN2	-332	upstream	ActReg chr7 #8860	1	1
8861	7	139,024,566	139,026,425	1,859	2	12.19	12.638	28	19	1	1	1	C7orf55	-402	upstream	ActReg chr7 #8861	1	1
8862	7	139,365,473	139,366,026	553	1	11.588	15.118	17	28	0	0	0				ActReg chr7 #8862	0	1
8863	7	139,471,023	139,471,773	750	2	8.87	9.435	18	16	0	1	2	LOC100505582, TBXAS1	6295, -6649	in gene, upstream	ActReg chr7 #8863	1	1
8864	7	139,477,867	139,478,651	784	1	7.833	12.375	13	18	1	2	2	LOC100505582, TBXAS1	-566, 212	upstream, in gene	ActReg chr7 #8864	0	1
8865	7	139,762,579	139,763,245	666	1	4.9	10.476	9	19	1	1	1	PARP12	609	in gene	ActReg chr7 #8865	0	1
8866	7	140,178,792	140,179,521	729	1	6.913	10.565	13	16	1	1	1	MKRN1	213	in gene	ActReg chr7 #8866	0	1
8867	7	140,264,379	140,264,938	559	1	11.944	6.611	19	10	0	0	1	DENND2A	37,684	in gene	ActReg chr7 #8867	1	0
8868	7	140,307,134	140,307,859	725	1	10.565	10.043	15	16	0	1	1	DENND2A	-5,154	upstream	ActReg chr7 #8868	1	0
8869	7	140,339,569	140,340,374	805	1	5.958	11.52	9	23	1	0	0				ActReg chr7 #8869	0	1
8870	7	140,396,221	140,397,128	907	2	10	14.586	15	26	1	2	3	ADCK2, LOC100134713, NDUFB2	23721, 203, 193	downstream, in gene, in gene	ActReg chr7 #8870	1	1
8871	7	140,623,724	140,624,538	814	1	12.04	10.24	20	20	1	1	1	BRAF	433	in gene	ActReg chr7 #8871	1	0
8872	7	140,624,752	140,625,225	473	1	6.333	11.267	13	18	1	1	1	BRAF	-424	upstream	ActReg chr7 #8872	0	1
8873	7	140,714,295	140,715,254	959	2	13.533	17.033	29	35	1	1	1	MRPS33	7	in gene	ActReg chr7 #8873	1	1
8874	7	140,772,064	140,773,504	1,440	2	11.587	13.109	19	25	1	1	1	LOC100507421	-1,040	upstream	ActReg chr7 #8874	1	1
8875	7	140,796,958	140,797,811	853	2	12.556	16.037	31	41	0	0	1	LOC100507421	23,560	in gene	ActReg chr7 #8875	1	1
8876	7	140,828,126	140,828,776	650	1	9.286	11.286	13	17	0	0	1	LOC100507421	54,627	in gene	ActReg chr7 #8876	0	1
8877	7	140,844,428	140,845,221	793	1	9.36	11.72	16	17	0	0	1	LOC100507421	71,000	in gene	ActReg chr7 #8877	0	1
8878	7	140,920,561	140,921,447	886	2	11.179	13.107	27	26	0	0	1	LOC100507421	147,180	in gene	ActReg chr7 #8878	1	1
8879	7	141,250,776	141,251,633	857	2	10.889	10.222	17	13	1	1	1	AGK	126	in gene	ActReg chr7 #8879	1	1
8880	7	141,437,544	141,438,574	1,030	2	19.938	21.75	46	60	1	2	3	FLJ40852, WEE2, SSBP1	-29, 29906, 117	upstream, downstream, upstream	ActReg chr7 #8880	1	1
8881	7	142,026,156	142,026,933	777	2	9.375	14.375	18	24	0	1	3	TRB@, TRBV5-1, TRBV6-1	27693, 5650, -1634	in gene, downstream, upstream	ActReg chr7 #8881	1	1
8882	7	142,913,166	142,913,635	469	1	4.6	10.667	9	19	0	1	1	TAS2R40	-5,772	upstream	ActReg chr7 #8882	0	1
8883	7	142,984,699	142,985,277	578	1	8	10.667	15	17	1	1	2	TMEM139, CASP2	2925, -414	in gene, upstream	ActReg chr7 #8883	0	1
8884	7	142,985,316	142,985,909	593	1	7.722	10.889	12	19	1	1	2	TMEM139, CASP2	3549, 210	downstream, in gene	ActReg chr7 #8884	0	1
8885	7	143,077,587	143,078,297	710	1	7.409	12.682	12	23	1	2	3	LOC100507507, ZYX, EPHA1	-354, -418, 28043	upstream, upstream, downstream	ActReg chr7 #8885	0	1
8886	7	144,532,732	144,533,561	829	2	12.731	17.615	22	45	1	1	1	TPK1	0	in gene	ActReg chr7 #8886	1	1
8887	7	144,706,885	144,707,925	1,040	2	9.75	9.969	20	21	0	0	0				ActReg chr7 #8887	1	1
8888	7	144,909,013	144,909,753	740	2	10.783	15.13	24	38	0	0	0				ActReg chr7 #8888	1	1
8889	7	145,341,106	145,342,154	1,048	1	7.091	12.212	12	21	0	0	0				ActReg chr7 #8889	0	1
8890	7	145,812,511	145,814,386	1,875	2	11.373	15.576	22	39	1	1	1	CNTNAP2	-5	upstream	ActReg chr7 #8890	1	1
8891	7	147,530,451	147,530,846	395	1	4.75	10.333	7	14	0	0	1	CNTNAP2	1,717,195	in gene	ActReg chr7 #8891	0	1
8892	7	148,637,694	148,638,573	879	2	11.357	10.536	18	18	1	1	1	RNY5	-447	upstream	ActReg chr7 #8892	1	1
8893	7	148,680,467	148,680,964	497	1	11.188	10.125	17	14	0	1	2	RNY3, RNY1	-132, 3625	upstream, downstream	ActReg chr7 #8893	1	0
8894	7	148,684,013	148,684,917	904	2	12.643	9.679	19	16	0	1	2	RNY3, RNY1	3618, -125	downstream, upstream	ActReg chr7 #8894	1	1
8895	7	148,762,069	148,763,508	1,439	2	14.136	18.067	43	47	1	0	1	ZNF786	25,081	downstream	ActReg chr7 #8895	1	1
8896	7	148,787,341	148,788,488	1,147	1	7.444	12.167	12	23	1	1	1	ZNF786	-45	upstream	ActReg chr7 #8896	0	1
8897	7	148,822,814	148,824,165	1,351	2	17.372	18.605	48	43	1	2	2	ZNF425, ZNF398	-51, -19	upstream, upstream	ActReg chr7 #8897	1	1
8898	7	148,844,080	148,845,737	1,657	1	7.712	12.962	14	21	1	0	1	ZNF398	21,400	in gene	ActReg chr7 #8898	0	1
8899	7	148,892,256	148,892,966	710	2	19.652	30.091	46	70	1	1	1	ZNF282	34	in gene	ActReg chr7 #8899	1	1
8900	7	148,936,050	148,937,351	1,301	2	40.317	47.268	156	160	1	1	1	ZNF212	-42	upstream	ActReg chr7 #8900	1	1
8901	7	148,958,381	148,960,002	1,621	2	11.784	12.549	27	30	1	1	2	ZNF212, LOC100507573	22449, -71	downstream, upstream	ActReg chr7 #8901	1	1
8902	7	149,157,539	149,158,344	805	2	31.92	32	85	81	1	1	1	ZNF777	112	in gene	ActReg chr7 #8902	1	1
8903	7	149,321,348	149,322,446	1,098	2	37.471	36.824	120	114	1	0	0				ActReg chr7 #8903	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8904	7	149,387,985	149,388,539	554	1	9.824	11.529	12	17	0	0	0				ActReg chr7 #8904	0	1
8905	7	150,065,589	150,066,911	1,322	1	5.537	11.512	10	19	1	1	2	REPIN1, ZNF775	371, -10156	in gene, upstream	ActReg chr7 #8905	0	1
8906	7	150,101,941	150,102,687	746	2	15.435	18	35	36	1	1	2	ZNF775, tcag7.1196	25908, -526	downstream, upstream	ActReg chr7 #8906	1	1
8907	7	150,680,778	150,681,644	866	2	14.259	15.037	30	29	0	2	2	KCNH2, NOS3	-6197, -5933	upstream, upstream	ActReg chr7 #8907	1	1
8908	7	150,725,313	150,726,080	767	2	11.083	10.375	17	19	1	2	3	ATG9B, ABCB8, LOC100507614	-4110, 186, 5990	upstream, in gene, in gene	ActReg chr7 #8908	1	1
8909	7	150,736,027	150,737,371	1,344	1	7.976	11.976	14	19	0	1	3	ABCB8, LOC100507614, ACCN3	11189, -5013, -8906	in gene, upstream, upstream	ActReg chr7 #8909	0	1
8910	7	150,754,744	150,755,611	867	2	12.518	13.593	24	28	1	2	4	ABCB8, ACCN3, CDK5, SLC4A2	29667, 9572, -125, 1480	downstream, downstream, upstream, upstream	ActReg chr7 #8910	1	1
8911	7	150,757,469	150,758,259	790	1	7.32	10.48	11	15	1	2	3	ACCN3, CDK5, SLC4A2	12259, -2812, 1207	downstream, upstream, in gene	ActReg chr7 #8911	0	1
8912	7	150,777,054	150,778,074	1,020	1	8.406	12.094	16	22	1	2	4	SLC4A2, FASTK, TMUB1, AGAP3	20907, 387, 3056, -6262	downstream, in gene, downstream, upstream	ActReg chr7 #8912	0	1
8913	7	150,786,306	150,787,129	823	1	10.04	12.32	14	21	0	2	3	FASTK, TMUB1, AGAP3	-8766, -6097, 2891	upstream, upstream, in gene	ActReg chr7 #8913	0	1
8914	7	150,924,009	150,924,797	788	2	12.792	13.542	24	23	1	2	2	ABCF2, CHPF2	-86, -5182	upstream, upstream	ActReg chr7 #8914	1	1
8915	7	151,165,091	151,165,872	781	1	11.375	8.75	16	14	0	0	1	RHEB	51,529	in gene	ActReg chr7 #8915	1	0
8916	7	151,168,746	151,169,370	624	1	11.421	8.368	22	16	0	0	1	RHEB	47,952	in gene	ActReg chr7 #8916	1	0
8917	7	151,442,130	151,442,728	598	1	7.211	11.421	12	17	0	0	1	PRKAG2	131,887	in gene	ActReg chr7 #8917	0	1
8918	7	151,479,970	151,480,556	586	1	12.278	8.278	22	14	1	0	1	PRKAG2	94,053	in gene	ActReg chr7 #8918	1	0
8919	7	151,493,160	151,494,096	936	2	11.31	12.897	20	21	0	0	1	PRKAG2	80,688	in gene	ActReg chr7 #8919	1	1
8920	7	151,722,247	151,722,717	470	1	9.786	11	16	16	1	1	2	GALNTL5, GALNT11	69018, -296	downstream, upstream	ActReg chr7 #8920	0	1
8921	7	152,133,521	152,134,669	1,148	2	10.389	10.667	22	30	0	1	1	MLL3	-1,005	upstream	ActReg chr7 #8921	1	1
8922	7	152,160,878	152,162,743	1,865	2	21.086	17.828	39	32	1	1	1	LOC100128822	601	in gene	ActReg chr7 #8922	1	1
8923	7	152,217,175	152,219,811	2,636	1	9.024	13.614	19	23	0	0	0				ActReg chr7 #8923	0	1
8924	7	152,406,613	152,407,203	590	1	10.263	8.842	16	11	0	0	0				ActReg chr7 #8924	1	0
8925	7	152,758,903	152,759,594	691	2	11.682	11.591	19	27	0	0	0				ActReg chr7 #8925	1	1
8926	7	153,752,456	153,753,043	587	1	6.647	10.222	11	18	0	0	1	DPP6	168,330	in gene	ActReg chr7 #8926	0	1
8927	7	154,794,710	154,795,629	919	2	13.923	13.31	24	27	1	2	2	PAXIP1, LOC202781	-487, 26	upstream, in gene	ActReg chr7 #8927	1	1
8928	7	154,844,487	154,845,559	1,072	2	28.849	37.576	89	110	0	0	0				ActReg chr7 #8928	1	1
8929	7	154,858,184	154,858,670	486	1	9.267	12.4	14	20	0	1	2	LOC100128264, HTR5A	4840, -4119	downstream, upstream	ActReg chr7 #8929	0	1
8930	7	154,861,136	154,862,561	1,425	2	37.133	48.178	133	194	2	2	2	LOC100128264, HTR5A	1419, -698	in gene, upstream	ActReg chr7 #8930	1	1
8931	7	154,862,720	154,863,398	678	1	8.545	10.273	14	14	1	2	2	LOC100128264, HTR5A	208, 513	in gene, in gene	ActReg chr7 #8931	0	1
8932	7	155,088,206	155,089,250	1,044	1	12.273	8.394	17	16	1	1	1	INSIG1	-758	upstream	ActReg chr7 #8932	1	0
8933	7	155,249,452	155,250,369	917	2	19.862	23.172	44	49	1	1	1	EN2	-914	upstream	ActReg chr7 #8933	1	1
8934	7	155,436,637	155,437,996	1,359	3	10.721	8.86	19	20	1	2	2	LOC100506302, RBM33	-242, 113	upstream, in gene	ActReg chr7 #8934	1	1
8935	7	155,452,867	155,453,644	777	1	10.667	7.958	21	12	0	0	1	RBM33	16,052	in gene	ActReg chr7 #8935	1	0
8936	7	155,743,655	155,744,964	1,309	2	9.488	10.902	18	16	0	0	0				ActReg chr7 #8936	1	1
8937	7	155,754,168	155,754,906	738	1	11.522	11.348	16	16	0	1	1	tcag7.1275	-714	upstream	ActReg chr7 #8937	0	1
8938	7	156,432,887	156,433,848	961	1	7.533	12.6	13	18	1	2	2	C7orf13, RNF32	-19, -34	upstream, upstream	ActReg chr7 #8938	0	1
8939	7	156,742,040	156,743,010	970	2	17.194	16.516	47	33	2	1	1	NOM1	108	in gene	ActReg chr7 #8939	1	1
8940	7	157,197,505	157,198,228	723	2	11.682	11.318	18	21	0	0	1	DNAJB6	68,156	in gene	ActReg chr7 #8940	1	1
8941	7	157,357,248	157,358,252	1,004	2	13.594	16.062	27	33	0	0	2	PTPRN2, MIR153-2	1022732, 9364	in gene, downstream	ActReg chr7 #8941	1	1
8942	7	158,346,650	158,347,420	770	2	13.458	12.042	26	28	0	0	1	PTPRN2	33,447	in gene	ActReg chr7 #8942	1	1
8943	7	158,610,999	158,611,840	841	2	8.741	11.185	16	23	0	0	1	ESYT2	10,900	in gene	ActReg chr7 #8943	1	1
8944	7	158,622,140	158,622,810	670	1	13.571	10.667	22	19	1	1	1	ESYT2	-156	upstream	ActReg chr7 #8944	1	0
8945	7	158,648,656	158,649,595	939	2	20.172	20.138	46	55	1	1	1	WDR60	-144	upstream	ActReg chr7 #8945	1	1
8946	8	1,703,509	1,704,132	623	1	6.7	10.45	12	16	0	0	2	LOC100507448, CLN8	8930, -8050	downstream, upstream	ActReg chr8 #8946	0	1
8947	8	1,711,120	1,711,511	391	1	9.833	4.727	14	7	1	2	2	LOC100507448, CLN8	1435, -555	in gene, upstream	ActReg chr8 #8947	1	0
8948	8	3,040,435	3,040,747	312	1	8.1	10.8	11	16	0	0	1	CSMD1	1,811,737	in gene	ActReg chr8 #8948	0	1
8949	8	8,125,695	8,126,664	969	1	7.742	12.419	14	19	0	0	0				ActReg chr8 #8949	0	1
8950	8	8,167,944	8,168,957	1,013	2	9.871	13.065	18	19	0	0	1	PRAGMIN	70,807	downstream	ActReg chr8 #8950	1	1
8951	8	8,209,697	8,210,231	534	2	10.062	9.312	16	16	0	0	1	PRAGMIN	29,293	in gene	ActReg chr8 #8951	1	1
8952	8	9,807,193	9,807,969	776	2	13.52	17.48	33	40	0	0	0				ActReg chr8 #8952	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
8953	8	10,697,086	10,697,569	483	1	5.467	10	9	15	1	1	1	PINX1	-28	upstream	ActReg chr8 #8953	0	1
8954	8	10,847,285	10,849,279	1,994	2	16.468	22.29	51	55	0	0	1	XKR6	210,593	in gene	ActReg chr8 #8954	1	1
8955	8	10,949,900	10,950,512	612	2	11.474	11.79	17	20	0	0	1	XKR6	108,669	in gene	ActReg chr8 #8955	1	1
8956	8	11,058,912	11,059,702	790	2	12	22.32	28	45	2	1	1	XKR6	-432	upstream	ActReg chr8 #8956	1	1
8957	8	11,141,455	11,142,301	846	2	9.346	12.346	19	17	1	1	1	MTMR9	-122	upstream	ActReg chr8 #8957	1	1
8958	8	11,324,241	11,324,876	635	1	7.55	10.8	9	15	1	1	1	FAM167A	-282	upstream	ActReg chr8 #8958	0	1
8959	8	11,339,312	11,339,741	429	1	8.154	9.846	10	16	0	0	0				ActReg chr8 #8959	0	1
8960	8	11,462,820	11,464,154	1,334	2	20.707	24.78	48	60	0	0	0				ActReg chr8 #8960	1	1
8961	8	12,417,627	12,417,982	355	1	3.8	9.636	6	15	0	0	1	LOC100506990	123,255	downstream	ActReg chr8 #8961	0	1
8962	8	17,013,183	17,013,711	528	1	9.294	7.059	16	13	1	1	1	ZDHHC2	-389	upstream	ActReg chr8 #8962	1	0
8963	8	17,480,655	17,481,163	508	1	9.625	6.625	15	9	0	0	1	PDGFRL	46,967	in gene	ActReg chr8 #8963	1	0
8964	8	17,779,978	17,780,635	657	2	10.6	10.25	16	14	1	1	1	PCM1	-60	upstream	ActReg chr8 #8964	1	1
8965	8	17,941,303	17,941,933	630	1	8.3	11.35	13	15	1	1	1	ASAH1	889	in gene	ActReg chr8 #8965	0	1
8966	8	18,998,664	18,999,113	449	1	6.714	10.429	9	15	0	0	0				ActReg chr8 #8966	0	1
8967	8	19,362,869	19,363,309	440	1	5.571	10.143	8	16	0	0	1	CSGALNACT1	177,172	in gene	ActReg chr8 #8967	0	1
8968	8	19,614,864	19,615,377	513	1	6.062	9.438	9	13	1	0	0				ActReg chr8 #8968	0	1
8969	8	19,674,488	19,675,238	750	2	11.191	13.292	24	27	1	1	1	INTS10	-55	upstream	ActReg chr8 #8969	1	1
8970	8	20,054,316	20,054,931	615	1	10.684	11.474	20	16	1	1	1	ATP6V1B2	-81	upstream	ActReg chr8 #8970	1	0
8971	8	21,999,187	21,999,854	667	2	11.381	11.809	22	19	1	1	2	REEP4, LGI3	-72, 14824	upstream, downstream	ActReg chr8 #8971	1	1
8972	8	22,102,218	22,102,924	706	1	7.818	11	13	14	1	2	3	MIR320A, POLR3D, LOC100507071	-15, -48, 30104	upstream, upstream, downstream	ActReg chr8 #8972	0	1
8973	8	22,250,575	22,251,141	566	1	9.833	11.278	15	21	0	0	1	SLC39A14	26,096	in gene	ActReg chr8 #8973	0	1
8974	8	22,526,127	22,526,915	788	1	7.6	12.32	12	23	1	1	1	BIN3	140	in gene	ActReg chr8 #8974	0	1
8975	8	22,602,034	22,602,815	781	1	7	10.125	10	13	0	0	2	PEBP4, LOC100507139	182997, -9899	in gene, upstream	ActReg chr8 #8975	0	1
8976	8	22,608,436	22,608,813	377	1	5.833	11.25	8	17	0	1	2	PEBP4, LOC100507139	176797, -3699	in gene, upstream	ActReg chr8 #8976	0	1
8977	8	23,145,303	23,146,027	724	2	10	9.435	22	22	1	1	2	R3HCC1, LOXL2	53, 116057	in gene, downstream	ActReg chr8 #8977	1	1
8978	8	23,398,782	23,399,557	775	1	10.76	8.36	19	13	0	0	1	SLC25A37	12,806	in gene	ActReg chr8 #8978	1	0
8979	8	24,050,273	24,050,880	607	1	7.105	10.105	12	16	0	0	0				ActReg chr8 #8979	0	1
8980	8	25,045,100	25,045,751	651	1	6.7	11.6	9	18	0	0	1	DOCK5	3,138	in gene	ActReg chr8 #8980	0	1
8981	8	25,316,182	25,317,153	971	2	13.194	17.806	33	38	1	2	2	KCTD9, CDCA2	-683, 154	upstream, in gene	ActReg chr8 #8981	1	1
8982	8	26,240,177	26,240,749	572	1	11.167	10.667	17	15	1	1	2	PPP2R2A, BNIP3L	91456, -60	downstream, upstream	ActReg chr8 #8982	1	0
8983	8	26,434,168	26,434,797	629	1	3.45	10.3	5	18	1	1	1	DPYSL2	-939	upstream	ActReg chr8 #8983	0	1
8984	8	27,695,007	27,695,590	583	2	10.21	11.316	23	20	1	1	1	PBK	51	in gene	ActReg chr8 #8984	1	1
8985	8	27,729,827	27,730,587	760	1	7.087	10.348	10	16	0	0	1	SCARA5	119,991	in gene	ActReg chr8 #8985	0	1
8986	8	28,258,463	28,259,339	876	2	9.643	10.857	17	21	1	0	0				ActReg chr8 #8986	1	1
8987	8	28,514,553	28,515,274	721	2	12.391	13.391	24	30	0	0	0				ActReg chr8 #8987	1	1
8988	8	28,747,218	28,748,139	921	2	9.448	13.966	18	24	1	2	2	INTS9, HMBOX1	20, -233	in gene, upstream	ActReg chr8 #8988	1	1
8989	8	29,206,275	29,206,985	710	1	6.091	10.454	8	15	1	1	1	DUSP4	1,555	in gene	ActReg chr8 #8989	0	1
8990	8	29,370,885	29,371,335	450	1	9.5	5.286	14	13	0	0	0				ActReg chr8 #8990	1	0
8991	8	29,705,709	29,706,085	376	1	10.083	7.583	15	10	0	0	0				ActReg chr8 #8991	1	0
8992	8	29,848,424	29,848,919	495	1	10.733	6.667	15	12	0	0	0				ActReg chr8 #8992	1	0
8993	8	30,013,569	30,014,195	626	2	12.79	9.684	22	18	1	1	1	DCTN6	69	in gene	ActReg chr8 #8993	1	1
8994	8	30,670,011	30,670,726	715	2	16.826	22.714	38	52	1	1	1	PPP2CB	-16	upstream	ActReg chr8 #8994	1	1
8995	8	33,330,361	33,331,079	718	2	10	12.043	22	23	1	1	1	FUT10	-56	upstream	ActReg chr8 #8995	1	1
8996	8	33,370,466	33,371,402	936	2	21.483	19.172	51	40	0	2	2	C8orf41, SNORD13	-231, -59	upstream, upstream	ActReg chr8 #8996	1	1
8997	8	33,579,603	33,580,110	507	1	10.938	9.688	17	12	0	0	0				ActReg chr8 #8997	1	0
8998	8	37,552,923	37,553,509	586	2	10.368	11.263	21	20	1	1	1	ZNF703	-85	upstream	ActReg chr8 #8998	1	1
8999	8	37,707,128	37,707,797	669	2	8.667	9.857	17	19	1	1	3	GPR124, BRF2, RAB11FIP1	53081, -31, 49553	downstream, upstream, downstream	ActReg chr8 #8999	1	1
9000	8	37,962,656	37,963,396	740	2	12.333	13.917	22	24	1	1	1	ASH2L	15	in gene	ActReg chr8 #9000	1	1
9001	8	38,068,745	38,069,472	727	2	10.739	10.957	20	21	1	1	1	DDHD2	99	in gene	ActReg chr8 #9001	1	1
9002	8	38,325,896	38,326,408	512	1	7.938	10.125	11	15	1	1	1	FGFR1	200	in gene	ActReg chr8 #9002	0	1
9003	8	40,030,370	40,030,841	471	1	9.286	4.786	17	9	0	0	0				ActReg chr8 #9003	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9004	8	40,977,797	40,978,430	633	2	8.789	10.474	15	16	0	0	0				ActReg chr8 #9004	1	1
9005	8	41,250,661	41,251,561	900	2	8.714	10.464	15	19	0	0	0				ActReg chr8 #9005	1	1
9006	8	41,575,116	41,575,783	667	1	11.571	6.714	20	11	0	0	1	ANK1	178,831	in gene	ActReg chr8 #9006	1	0
9007	8	41,753,231	41,754,016	785	2	12.84	14.24	24	26	1	1	1	ANK1	657	in gene	ActReg chr8 #9007	1	1
9008	8	42,195,720	42,196,186	466	1	10.857	5.929	15	10	1	1	2	IKBKB, POLB	67133, -77	downstream, upstream	ActReg chr8 #9008	1	0
9009	8	42,948,300	42,949,410	1,110	2	10.914	12.457	21	23	1	1	2	FNTA, SGK196	37413, 198	downstream, in gene	ActReg chr8 #9009	1	1
9010	8	48,650,936	48,651,728	792	1	6.4	11.32	9	18	1	1	2	KIAA0146, CEBPD	477790, -606	downstream, upstream	ActReg chr8 #9010	0	1
9011	8	48,872,996	48,874,080	1,084	1	10.912	15.5	23	38	1	2	2	PRKDC, MCM4	-795, 44	upstream, in gene	ActReg chr8 #9011	0	1
9012	8	48,920,655	48,921,245	590	1	12.5	13	21	19	1	1	1	UBE2V2	-45	upstream	ActReg chr8 #9012	1	0
9013	8	49,320,308	49,320,861	553	1	6.941	9.824	9	15	0	0	0				ActReg chr8 #9013	0	1
9014	8	49,665,931	49,666,710	779	1	6.083	9.792	12	15	0	0	0				ActReg chr8 #9014	0	1
9015	8	49,812,297	49,813,011	714	2	12.091	12.364	25	23	0	1	1	LOC644334	-7,540	upstream	ActReg chr8 #9015	1	1
9016	8	49,833,637	49,834,588	951	1	5.897	10	11	15	0	1	2	LOC644334, SNAI2	13918, -124	downstream, upstream	ActReg chr8 #9016	0	1
9017	8	50,823,925	50,824,636	711	2	9.455	14.409	23	33	0	1	1	SNTG1	-317	upstream	ActReg chr8 #9017	1	1
9018	8	50,969,074	50,969,568	494	1	4.625	11.312	7	17	0	0	1	SNTG1	144,724	in gene	ActReg chr8 #9018	0	1
9019	8	51,475,791	51,476,298	507	1	7.231	10.812	11	19	0	0	1	SNTG1	651,447	in gene	ActReg chr8 #9019	0	1
9020	8	52,307,032	52,308,017	985	2	10.645	13.323	24	23	0	0	1	PXDNL	414,481	in gene	ActReg chr8 #9020	1	1
9021	8	52,811,358	52,812,673	1,315	1	8.738	10.381	14	16	1	2	2	PCMTD1, LOC100287313	-280, 173	upstream, in gene	ActReg chr8 #9021	0	1
9022	8	53,448,521	53,449,118	597	1	7.111	10.056	11	19	0	0	1	FAM150A	29,202	in gene	ActReg chr8 #9022	0	1
9023	8	53,625,567	53,626,219	652	1	10.333	13.048	15	21	1	1	1	RB1CC1	1,133	in gene	ActReg chr8 #9023	0	1
9024	8	53,626,990	53,627,724	734	1	7.87	11.217	11	18	1	1	1	RB1CC1	-331	upstream	ActReg chr8 #9024	0	1
9025	8	53,676,708	53,677,401	693	2	12.857	14.143	21	26	0	0	0				ActReg chr8 #9025	1	1
9026	8	54,792,836	54,793,434	598	1	6.389	10.556	8	14	1	0	1	RGS20	28,767	in gene	ActReg chr8 #9026	0	1
9027	8	54,793,439	54,794,497	1,058	2	10.559	9.735	19	18	1	0	1	RGS20	29,600	in gene	ActReg chr8 #9027	1	1
9028	8	54,934,515	54,935,358	843	2	21.269	24	63	65	1	1	1	TCEA1	72	in gene	ActReg chr8 #9028	1	1
9029	8	55,065,529	55,066,441	912	2	13.103	10.552	26	17	0	0	1	MRPL15	18,204	downstream	ActReg chr8 #9029	1	1
9030	8	55,913,723	55,914,330	607	1	10.474	7.895	19	13	0	0	0				ActReg chr8 #9030	1	0
9031	8	56,015,309	56,015,974	665	2	16.238	23.619	32	46	1	1	1	XKR4	624	in gene	ActReg chr8 #9031	1	1
9032	8	56,685,353	56,686,421	1,068	2	11.273	13.788	18	21	1	2	2	TMEM68, TGS1	-2, 96	upstream, in gene	ActReg chr8 #9032	1	1
9033	8	56,986,637	56,987,800	1,163	2	35.333	39.75	130	143	1	2	2	RPS20, SNORD54	-78, -758	upstream, upstream	ActReg chr8 #9033	1	1
9034	8	57,124,195	57,124,956	761	1	7.261	9.609	10	13	1	2	2	PLAG1, CHCHD7	-716, 260	upstream, in gene	ActReg chr8 #9034	0	1
9035	8	57,357,870	57,358,444	574	1	6.056	12.333	8	21	1	1	1	PENK	1,125	in gene	ActReg chr8 #9035	0	1
9036	8	57,802,399	57,803,062	663	1	10.619	9	20	18	0	0	0				ActReg chr8 #9036	1	0
9037	8	59,323,589	59,324,436	847	1	4.462	12.346	8	18	1	1	1	UBXN2B	189	in gene	ActReg chr8 #9037	0	1
9038	8	59,571,210	59,572,170	960	1	8.793	10.8	18	18	1	1	1	NSMAF	714	in gene	ActReg chr8 #9038	0	1
9039	8	59,671,841	59,672,336	495	1	7.6	11.667	12	20	0	0	0				ActReg chr8 #9039	0	1
9040	8	59,714,026	59,714,576	550	1	9.882	8.471	14	16	0	0	1	TOX	317,466	downstream	ActReg chr8 #9040	1	0
9041	8	61,325,971	61,326,390	419	1	11.769	9.077	16	12	0	1	1	LOC100505532	197	in gene	ActReg chr8 #9041	1	0
9042	8	61,328,611	61,329,335	724	1	6.045	11.046	12	18	0	1	1	LOC100505532	-2,596	upstream	ActReg chr8 #9042	0	1
9043	8	61,564,086	61,565,398	1,312	2	13.39	11.293	30	32	1	0	0				ActReg chr8 #9043	1	1
9044	8	61,863,210	61,864,139	929	2	11.517	13.931	22	24	0	0	0				ActReg chr8 #9044	1	1
9045	8	62,200,402	62,201,291	889	2	13.536	17.714	24	38	0	1	1	CLVS1	321	in gene	ActReg chr8 #9045	1	1
9046	8	62,408,323	62,409,303	980	2	15.867	20.5	40	43	0	0	2	CLVS1, ASPH	206288, 218386	in gene, downstream	ActReg chr8 #9046	1	1
9047	8	62,503,991	62,504,528	537	2	8.235	9.588	17	16	0	0	1	ASPH	122,940	in gene	ActReg chr8 #9047	1	1
9048	8	62,626,686	62,627,555	869	1	6.714	11.679	13	19	1	1	1	ASPH	79	in gene	ActReg chr8 #9048	0	1
9049	8	62,633,920	62,634,457	537	1	11.823	7.118	21	12	0	1	1	ASPH	-6,989	upstream	ActReg chr8 #9049	1	0
9050	8	62,672,101	62,673,305	1,204	2	11.811	11.243	19	18	0	0	0				ActReg chr8 #9050	1	1
9051	8	62,702,264	62,702,984	720	1	10.174	9.304	20	12	0	0	0				ActReg chr8 #9051	1	0
9052	8	64,080,341	64,081,486	1,145	1	6.917	12.139	11	17	1	1	1	YTHDF3	-208	upstream	ActReg chr8 #9052	0	1
9053	8	64,132,850	64,133,355	505	1	9.562	10.875	18	21	0	0	1	YTHDF3	51,981	downstream	ActReg chr8 #9053	0	1
9054	8	65,292,255	65,292,960	705	2	10.261	12.304	18	26	0	1	2	LOC100130155, MIR124-2	6832, 901	downstream, downstream	ActReg chr8 #9054	1	1
9055	8	66,064,882	66,065,592	710	2	10	10.046	15	17	0	0	0				ActReg chr8 #9055	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9056	8	66,546,031	66,546,812	781	2	11.583	11.792	17	20	1	1	1	ARMC1	31	in gene	ActReg chr8 #9056	1	1
9057	8	66,753,995	66,755,063	1,068	2	10.909	10.091	19	18	1	1	1	PDE7A	-774	upstream	ActReg chr8 #9057	1	1
9058	8	66,860,730	66,861,133	403	1	10.923	11.615	15	17	0	0	0				ActReg chr8 #9058	0	1
9059	8	66,938,635	66,939,133	498	1	12.4	8.467	22	12	0	0	1	DNAJC5B	5,093	in gene	ActReg chr8 #9059	1	0
9060	8	67,024,815	67,025,953	1,138	2	12.306	13.75	18	25	2	0	0				ActReg chr8 #9060	1	1
9061	8	67,036,051	67,036,717	666	1	7.333	13.667	12	24	0	1	1	TRIM55	-2,894	upstream	ActReg chr8 #9061	0	1
9062	8	67,089,070	67,090,644	1,574	2	17.388	18.694	53	53	1	1	2	TRIM55, CRH	50579, 989	downstream, in gene	ActReg chr8 #9062	1	1
9063	8	67,340,781	67,342,184	1,403	2	10.667	12.523	19	26	1	3	3	LOC100505676, RRS1, ADHFE1	-270, 219, -3236	upstream, in gene, upstream	ActReg chr8 #9063	1	1
9064	8	67,524,807	67,525,931	1,124	2	11.4	10.771	17	20	1	1	1	MYBL1	111	in gene	ActReg chr8 #9064	1	1
9065	8	67,578,777	67,579,973	1,196	2	13.342	13.237	22	29	1	1	2	VCPIP1, C8orf44	77, -9079	in gene, upstream	ActReg chr8 #9065	1	1
9066	8	67,624,408	67,625,027	619	1	8.333	10.4	12	19	1	1	1	SGK3	-174	upstream	ActReg chr8 #9066	0	1
9067	8	67,837,385	67,838,123	738	1	11.261	9.913	19	14	1	2	3	C8orf45, SNHG6, SNORD87	54770, 23, -2970	downstream, in gene, upstream	ActReg chr8 #9067	1	0
9068	8	67,919,515	67,920,112	597	1	8.895	11	12	20	0	0	1	LRRC67	20,973	in gene	ActReg chr8 #9068	0	1
9069	8	67,974,197	67,974,857	660	1	7.81	12.476	11	18	0	2	2	COPS5, CSPP1	35, -2076	in gene, upstream	ActReg chr8 #9069	0	1
9070	8	67,976,078	67,976,953	875	2	28.654	33.593	82	94	1	2	2	COPS5, CSPP1	-1953, -88	upstream, upstream	ActReg chr8 #9070	1	1
9071	8	67,976,993	67,977,582	589	1	3.778	9.556	7	18	1	2	2	COPS5, CSPP1	-2725, 684	upstream, in gene	ActReg chr8 #9071	0	1
9072	8	68,255,555	68,256,116	561	1	5.412	12.059	8	18	1	1	1	ARFGEF1	77	in gene	ActReg chr8 #9072	0	1
9073	8	70,693,207	70,693,720	513	1	7.562	10.25	14	15	0	0	1	SLCO5A1	53,836	in gene	ActReg chr8 #9073	0	1
9074	8	71,000,591	71,001,021	430	1	3.462	10.231	5	14	0	0	0				ActReg chr8 #9074	0	1
9075	8	71,038,892	71,039,466	574	1	4.889	10.111	7	19	0	0	1	NCOA2	276,841	in gene	ActReg chr8 #9075	0	1
9076	8	71,313,897	71,314,927	1,030	1	8.125	11.156	11	19	1	1	1	NCOA2	1,608	in gene	ActReg chr8 #9076	0	1
9077	8	71,520,150	71,521,112	962	2	23.2	24	61	66	1	1	1	TRAM1	63	in gene	ActReg chr8 #9077	1	1
9078	8	71,580,930	71,581,641	711	2	9.818	10	18	16	1	2	2	LACTB2, XKR9	162, -315	in gene, upstream	ActReg chr8 #9078	1	1
9079	8	72,177,953	72,178,697	744	2	12.478	11.826	29	25	0	0	1	EYA1	96,142	in gene	ActReg chr8 #9079	1	1
9080	8	72,703,939	72,704,510	571	1	6.471	10.941	9	20	0	0	0				ActReg chr8 #9080	0	1
9081	8	72,755,732	72,756,818	1,086	1	10.559	13.471	21	23	1	2	2	MSC, LOC100132891	456, 917	in gene, in gene	ActReg chr8 #9081	0	1
9082	8	74,205,443	74,206,717	1,274	2	12.128	11.077	17	21	1	2	2	RPL7, RDH10	-211, -1185	upstream, upstream	ActReg chr8 #9082	1	1
9083	8	74,207,416	74,208,080	664	1	5.095	11.476	9	16	1	2	2	RPL7, RDH10	-1879, 483	upstream, in gene	ActReg chr8 #9083	0	1
9084	8	74,371,676	74,372,476	800	1	6.92	11.4	12	16	0	0	1	STAU2	287,867	in gene	ActReg chr8 #9084	0	1
9085	8	74,432,696	74,433,272	576	1	7.056	10.222	14	17	0	0	1	STAU2	226,959	in gene	ActReg chr8 #9085	0	1
9086	8	74,790,511	74,791,263	752	1	11.478	9.043	16	15	1	1	1	UBE2W	223	in gene	ActReg chr8 #9086	1	0
9087	8	74,883,921	74,885,089	1,168	2	12.081	11.324	26	18	1	2	2	TCEB1, TMEM70	-159, -3872	upstream, upstream	ActReg chr8 #9087	1	1
9088	8	75,232,609	75,233,220	611	1	12.21	7.789	18	12	1	1	1	JPH1	648	in gene	ActReg chr8 #9088	1	0
9089	8	75,262,295	75,263,282	987	2	13.194	25.194	34	62	1	1	1	GDAP1	170	in gene	ActReg chr8 #9089	1	1
9090	8	75,514,118	75,514,699	581	1	10.833	3.889	17	7	0	1	1	FLJ39080	2,307	in gene	ActReg chr8 #9090	1	0
9091	8	75,734,750	75,735,321	571	1	11.667	3.167	21	5	0	1	1	PI15	-1,737	upstream	ActReg chr8 #9091	1	0
9092	8	75,737,273	75,737,863	590	1	5.632	9.263	10	16	0	1	1	PI15	796	in gene	ActReg chr8 #9092	0	1
9093	8	75,988,681	75,989,154	473	2	10.2	10.6	18	18	0	0	0				ActReg chr8 #9093	1	1
9094	8	77,599,072	77,599,987	915	2	13.828	8.448	24	20	0	1	2	LOC100192378, ZFHX4	-4019, 6014	upstream, in gene	ActReg chr8 #9094	1	1
9095	8	79,428,049	79,429,016	967	1	9.733	15.267	23	32	1	1	1	PKIA	196	in gene	ActReg chr8 #9095	0	1
9096	8	79,578,010	79,578,779	769	1	9.417	11.625	12	20	1	1	1	FAM164A	112	in gene	ActReg chr8 #9096	0	1
9097	8	80,200,190	80,200,945	755	1	8.583	11.25	12	15	0	0	0				ActReg chr8 #9097	0	1
9098	8	80,361,419	80,362,077	658	2	10.45	12.9	20	25	0	0	0				ActReg chr8 #9098	1	1
9099	8	80,520,930	80,521,896	966	2	13.4	12.5	25	23	0	1	1	STMN2	-1,967	upstream	ActReg chr8 #9099	1	1
9100	8	80,522,156	80,523,104	948	1	5.433	11.433	8	15	0	1	1	STMN2	-750	upstream	ActReg chr8 #9100	0	1
9101	8	80,524,592	80,525,384	792	1	4.08	11.36	7	19	1	1	1	STMN2	1,608	in gene	ActReg chr8 #9101	0	1
9102	8	80,677,336	80,678,310	974	2	7.968	14.903	17	33	1	2	2	HEY1, LOC100507186	2275, -2554	in gene, upstream	ActReg chr8 #9102	1	1
9103	8	80,941,789	80,942,443	654	1	5.429	11.143	12	18	1	1	2	MRPS28, TPD52	390, 141720	in gene, downstream	ActReg chr8 #9103	0	1
9104	8	81,083,183	81,083,896	713	1	6.5	12.046	8	19	1	1	1	TPD52	297	in gene	ActReg chr8 #9104	0	1
9105	8	81,602,908	81,603,716	808	2	13.192	14.231	36	26	0	0	1	ZNF704	183,704	in gene	ActReg chr8 #9105	1	1
9106	8	81,785,396	81,786,097	701	1	5.636	10.591	12	17	2	1	1	ZNF704	1,270	in gene	ActReg chr8 #9106	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9107	8	81,938,404	81,939,195	791	1	9.458	14.875	21	27	0	0	1	PAG1	85,504	in gene	ActReg chr8 #9107	0	1
9108	8	82,193,051	82,193,880	829	1	8.808	10.885	15	16	1	1	1	FABP5	680	in gene	ActReg chr8 #9108	0	1
9109	8	82,598,102	82,598,686	584	1	6	12.167	8	20	1	1	2	IMPA1, SLC10A5	195, 8813	in gene, downstream	ActReg chr8 #9109	0	1
9110	8	82,633,313	82,634,078	765	1	7.13	10.435	13	15	1	1	1	ZFAND1	-156	upstream	ActReg chr8 #9110	0	1
9111	8	82,753,801	82,755,205	1,404	2	12.5	13.546	34	29	1	1	1	SNX16	18	in gene	ActReg chr8 #9111	1	1
9112	8	82,771,012	82,771,544	532	1	11.688	9	16	14	0	0	0				ActReg chr8 #9112	1	0
9113	8	87,317,560	87,317,994	434	2	9.643	10.857	17	20	0	0	0				ActReg chr8 #9113	1	1
9114	8	87,354,106	87,354,867	761	2	13.75	12.826	27	21	1	1	1	WWP1	-508	upstream	ActReg chr8 #9114	1	1
9115	8	88,986,281	88,986,829	548	1	6.706	10.882	11	15	0	0	0				ActReg chr8 #9115	0	1
9116	8	88,987,185	88,987,771	586	1	7.944	11.889	13	18	0	0	0				ActReg chr8 #9116	0	1
9117	8	89,252,021	89,252,696	675	2	13.857	9.81	26	19	0	0	1	MMP16	87,359	in gene	ActReg chr8 #9117	1	1
9118	8	89,314,917	89,315,520	603	1	7.421	10.737	10	16	0	0	1	MMP16	24,499	in gene	ActReg chr8 #9118	0	1
9119	8	90,623,879	90,624,514	635	1	6.05	10.85	10	15	0	0	0				ActReg chr8 #9119	0	1
9120	8	90,769,715	90,770,490	775	1	9.792	13.292	18	20	1	1	1	RIPK2	127	in gene	ActReg chr8 #9120	0	1
9121	8	90,996,006	90,997,171	1,165	2	15.528	21.389	36	52	1	1	1	NBN	311	in gene	ActReg chr8 #9121	1	1
9122	8	91,094,662	91,095,450	788	2	14.083	17.667	31	43	0	1	1	CALB1	51	in gene	ActReg chr8 #9122	1	1
9123	8	91,479,896	91,480,561	665	1	11.667	14.381	18	23	0	0	0				ActReg chr8 #9123	0	1
9124	8	91,873,264	91,873,809	545	1	6.176	9.588	12	15	0	0	1	NECAB1	69,615	in gene	ActReg chr8 #9124	0	1
9125	8	92,612,489	92,612,915	426	1	11.308	4.538	16	6	0	0	0				ActReg chr8 #9125	1	0
9126	8	92,692,802	92,693,294	492	1	7.067	10.4	12	17	0	0	0				ActReg chr8 #9126	0	1
9127	8	93,935,221	93,935,687	466	1	10	7.667	14	13	0	0	1	C8orf83	42,918	in gene	ActReg chr8 #9127	1	0
9128	8	93,977,739	93,978,518	779	1	11.792	9.708	21	13	1	1	1	C8orf83	244	in gene	ActReg chr8 #9128	1	0
9129	8	94,599,662	94,600,189	527	1	6.562	12.375	11	20	0	0	1	LOC642924	112,736	in gene	ActReg chr8 #9129	0	1
9130	8	94,817,966	94,818,458	492	1	9.733	3.133	13	8	0	0	1	TMEM67	51,140	in gene	ActReg chr8 #9130	1	0
9131	8	95,084,349	95,084,845	496	2	9.562	9.125	17	15	0	0	0				ActReg chr8 #9131	1	1
9132	8	95,254,066	95,254,825	759	1	13.167	10.708	22	18	0	0	1	GEM	20,102	downstream	ActReg chr8 #9132	1	0
9133	8	95,486,959	95,487,628	669	1	8.905	11.048	14	16	1	1	1	RAD54B	17	in gene	ActReg chr8 #9133	0	1
9134	8	95,565,453	95,566,208	755	2	13.25	12.458	24	29	1	1	1	KIAA1429	-142	upstream	ActReg chr8 #9134	1	1
9135	8	95,731,588	95,732,526	938	2	10.655	12.31	14	18	1	1	1	DPY19L4	-46	upstream	ActReg chr8 #9135	1	1
9136	8	95,834,952	95,835,704	752	1	8.957	12.391	12	20	1	1	1	INTS8	-206	upstream	ActReg chr8 #9136	0	1
9137	8	96,036,905	96,037,514	609	1	11.526	12.421	18	18	1	1	1	C8orf38	-12	upstream	ActReg chr8 #9137	0	1
9138	8	96,281,004	96,282,540	1,536	2	9.062	13.625	16	22	1	1	1	C8orf37	-335	upstream	ActReg chr8 #9138	1	1
9139	8	97,273,419	97,274,756	1,337	2	16.548	16.952	43	38	1	2	2	MTERFD1, PTDSS1	-291, -80	upstream, upstream	ActReg chr8 #9139	1	1
9140	8	98,305,781	98,306,353	572	1	7	8.889	13	15	0	0	0				ActReg chr8 #9140	0	1
9141	8	98,656,131	98,656,835	704	1	10.546	11.273	15	18	1	1	1	MTDH	76	in gene	ActReg chr8 #9141	0	1
9142	8	98,787,572	98,788,071	499	1	6.375	9.75	9	15	1	1	1	LAPTM4B	12	in gene	ActReg chr8 #9142	0	1
9143	8	99,057,585	99,058,260	675	1	11.667	9	19	12	2	2	3	MATN2, RPL30, SNORA72	176611, -149, -3477	downstream, upstream, upstream	ActReg chr8 #9143	1	0
9144	8	99,305,939	99,306,861	922	1	8.069	10.483	14	18	1	1	1	NIPAL2	221	in gene	ActReg chr8 #9144	0	1
9145	8	99,956,193	99,957,093	900	2	12.071	11.393	18	22	1	1	1	OSR2	12	in gene	ActReg chr8 #9145	1	1
9146	8	100,024,770	100,025,747	977	1	11.667	10.733	18	17	1	1	1	VPS13B	-236	upstream	ActReg chr8 #9146	1	0
9147	8	100,905,453	100,906,336	883	2	9.786	10.929	18	17	1	1	1	COX6C	348	in gene	ActReg chr8 #9147	1	1
9148	8	101,169,896	101,170,623	727	1	11	7.5	14	12	1	1	2	POLR2K, SPAG1	7420, -4	downstream, upstream	ActReg chr8 #9148	1	0
9149	8	101,321,762	101,322,418	656	1	10.3	10.75	13	14	1	1	1	RNF19A	237	in gene	ActReg chr8 #9149	0	1
9150	8	101,494,420	101,495,069	649	1	6.6	12.25	15	21	0	0	0				ActReg chr8 #9150	0	1
9151	8	101,514,339	101,515,443	1,104	2	10.941	10.059	16	16	0	0	0				ActReg chr8 #9151	1	1
9152	8	101,571,498	101,572,392	894	2	13.179	12.714	28	23	1	1	1	ANKRD46	67	in gene	ActReg chr8 #9152	1	1
9153	8	101,734,507	101,735,290	783	1	7.792	12.125	11	28	1	1	1	PABPC1	-583	upstream	ActReg chr8 #9153	0	1
9154	8	101,962,694	101,963,227	533	1	12.25	8.875	20	12	1	1	1	YWHAZ	2,663	in gene	ActReg chr8 #9154	1	0
9155	8	101,963,670	101,964,642	972	2	12.548	12.839	22	18	1	1	1	YWHAZ	1,467	in gene	ActReg chr8 #9155	1	1
9156	8	101,998,408	101,999,025	617	1	10.526	10.632	16	19	0	0	0				ActReg chr8 #9156	0	1
9157	8	102,038,284	102,038,995	711	1	12.273	8.545	23	16	0	0	0				ActReg chr8 #9157	1	0
9158	8	102,075,949	102,076,498	549	1	6.471	11.706	10	16	0	0	1	FLJ42969	11,941	in gene	ActReg chr8 #9158	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9159	8	102,109,717	102,111,190	1,473	1	9.935	14.587	23	23	0	0	0				ActReg chr8 #9159	0	1
9160	8	102,120,760	102,122,150	1,390	2	11.659	9.545	21	22	0	0	0				ActReg chr8 #9160	1	1
9161	8	102,138,206	102,139,438	1,232	2	12.026	11.692	27	21	1	0	0				ActReg chr8 #9161	1	1
9162	8	102,255,700	102,256,848	1,148	2	12.778	15.25	29	32	0	0	0				ActReg chr8 #9162	1	1
9163	8	103,024,495	103,025,217	722	1	10.696	6.957	20	11	0	0	1	NCALD	112,279	in gene	ActReg chr8 #9163	1	0
9164	8	103,187,847	103,188,355	508	1	9.062	13.375	15	25	0	0	0				ActReg chr8 #9164	0	1
9165	8	103,549,607	103,550,399	792	1	11.542	5.375	14	9	0	0	0				ActReg chr8 #9165	1	0
9166	8	103,580,041	103,580,612	571	1	7.444	9.778	10	18	0	0	1	ODF1	16,478	downstream	ActReg chr8 #9166	0	1
9167	8	103,768,738	103,769,416	678	1	8.095	12.333	16	23	0	0	0				ActReg chr8 #9167	0	1
9168	8	103,819,062	103,820,384	1,322	1	12.333	9.952	20	17	1	1	1	FLJ45248	673	in gene	ActReg chr8 #9168	1	0
9169	8	103,876,362	103,877,065	703	1	10.818	11.682	15	16	1	2	2	AZIN1, LOC100506753	-316, 148	upstream, in gene	ActReg chr8 #9169	0	1
9170	8	104,032,976	104,033,748	772	1	10.458	12.958	15	24	1	1	1	ATP6V1C1	114	in gene	ActReg chr8 #9170	0	1
9171	8	104,293,194	104,293,952	758	2	11.458	11.167	17	17	0	0	0				ActReg chr8 #9171	1	1
9172	8	104,311,025	104,311,848	823	1	7	11.308	14	18	1	1	1	FZD6	775	in gene	ActReg chr8 #9172	0	1
9173	8	104,360,968	104,361,984	1,016	1	10.875	7.781	19	13	0	0	0				ActReg chr8 #9173	1	0
9174	8	104,383,656	104,384,816	1,160	1	8.167	12.306	14	17	1	1	1	CTHRC1	450	in gene	ActReg chr8 #9174	0	1
9175	8	104,426,765	104,427,869	1,104	2	13.206	11.735	20	19	1	2	2	SLC25A32, DCAF13	151, 375	in gene, in gene	ActReg chr8 #9175	1	1
9176	8	104,497,669	104,498,421	752	2	13.391	15.391	23	33	0	0	0				ActReg chr8 #9176	1	1
9177	8	104,513,465	104,514,510	1,045	2	10.091	13.576	18	24	1	1	1	RIMS2	1,011	in gene	ActReg chr8 #9177	1	1
9178	8	104,992,336	104,993,231	895	1	9.786	12.893	17	26	0	0	1	RIMS2	479,807	in gene	ActReg chr8 #9178	0	1
9179	8	105,235,185	105,235,990	805	1	6.6	12.12	9	19	1	0	1	RIMS2	722,611	in gene	ActReg chr8 #9179	0	1
9180	8	105,349,064	105,349,701	637	1	13	9.65	21	15	0	1	1	TM7SF4	-2,672	upstream	ActReg chr8 #9180	1	0
9181	8	105,601,122	105,602,234	1,112	2	16.029	15.118	47	36	1	1	1	LRP12	-426	upstream	ActReg chr8 #9181	1	1
9182	8	107,072,100	107,073,104	1,004	1	8.903	13.29	18	27	0	0	0				ActReg chr8 #9182	0	1
9183	8	107,218,488	107,219,076	588	1	6.526	9.947	9	17	0	0	0				ActReg chr8 #9183	0	1
9184	8	107,257,763	107,258,455	692	2	9.762	12.048	13	20	0	0	0				ActReg chr8 #9184	1	1
9185	8	107,282,070	107,283,351	1,281	1	10.425	11.975	18	21	1	1	1	OXR1	237	in gene	ActReg chr8 #9185	0	1
9186	8	107,669,550	107,670,412	862	2	16.778	18.074	41	45	1	0	1	OXR1	387,508	in gene	ActReg chr8 #9186	1	1
9187	8	108,513,356	108,513,905	549	1	8.529	13.412	15	27	0	1	1	ANGPT1	-3,376	upstream	ActReg chr8 #9187	0	1
9188	8	109,132,276	109,133,052	776	2	13.375	10.125	23	18	0	0	0				ActReg chr8 #9188	1	1
9189	8	109,260,499	109,261,336	837	2	10.115	13.615	14	19	1	1	1	EIF3E	42	in gene	ActReg chr8 #9189	1	1
9190	8	110,345,804	110,346,826	1,022	2	12.625	16.719	26	37	1	2	2	NUDCD1, ENY2	35, -237	in gene, upstream	ActReg chr8 #9190	1	1
9191	8	110,698,112	110,698,804	692	2	8.955	11.136	19	22	0	0	1	GOLSYN	5,562	in gene	ActReg chr8 #9191	1	1
9192	8	111,906,504	111,907,358	854	2	13.385	14	26	24	0	0	0				ActReg chr8 #9192	1	1
9193	8	113,628,606	113,629,177	571	1	7.833	11.611	13	21	0	0	1	CSMD3	820,351	in gene	ActReg chr8 #9193	0	1
9194	8	114,449,875	114,450,643	768	1	12.375	9.083	19	14	0	1	1	CSMD3	-1,017	upstream	ActReg chr8 #9194	1	0
9195	8	116,068,105	116,068,990	885	1	11.556	8.407	19	13	0	0	0				ActReg chr8 #9195	1	0
9196	8	116,088,676	116,089,218	542	1	10.529	6	17	10	0	0	0				ActReg chr8 #9196	1	0
9197	8	116,660,305	116,660,961	656	1	7.762	10.952	14	21	1	0	1	TRPS1	20,595	in gene	ActReg chr8 #9197	0	1
9198	8	116,791,399	116,792,147	748	1	9.304	10.652	19	15	0	0	0				ActReg chr8 #9198	0	1
9199	8	117,435,797	117,436,572	775	1	8.292	10.833	14	15	0	0	0				ActReg chr8 #9199	0	1
9200	8	117,778,430	117,779,278	848	1	11.482	12.185	18	23	1	1	1	UTP23	112	in gene	ActReg chr8 #9200	1	0
9201	8	118,532,569	118,533,507	938	2	10.733	12.067	19	20	1	1	1	MED30	73	in gene	ActReg chr8 #9201	1	1
9202	8	119,207,988	119,208,724	736	2	10.783	10.957	22	19	0	0	1	SAMD12	425,828	in gene	ActReg chr8 #9202	1	1
9203	8	119,451,919	119,452,418	499	1	10	10.312	16	16	0	0	1	SAMD12	182,016	in gene	ActReg chr8 #9203	1	0
9204	8	119,914,197	119,914,685	488	1	8	10.133	11	16	0	0	0				ActReg chr8 #9204	0	1
9205	8	120,058,179	120,058,766	587	1	9.611	5.167	18	8	0	0	0				ActReg chr8 #9205	1	0
9206	8	120,867,502	120,868,987	1,485	1	12.348	9.957	20	21	1	1	1	DSCC1	-74	upstream	ActReg chr8 #9206	1	0
9207	8	120,885,839	120,886,725	886	1	10.964	15.357	18	28	1	1	1	DEPDC6	382	in gene	ActReg chr8 #9207	0	1
9208	8	121,270,326	121,270,770	444	2	10.429	10	12	13	0	0	1	COL14A1	133,196	in gene	ActReg chr8 #9208	1	1
9209	8	121,745,190	121,745,799	609	1	10.316	10	13	16	0	0	1	SNTB1	78,815	in gene	ActReg chr8 #9209	0	1
9210	8	121,839,692	121,840,684	992	2	11.774	15.161	20	24	0	0	0				ActReg chr8 #9210	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9211	8	121,850,114	121,850,750	636	1	10.632	8.368	18	15	0	0	0				ActReg chr8 #9211	1	0
9212	8	121,869,583	121,870,290	707	1	10.182	13.364	14	18	0	0	0				ActReg chr8 #9212	0	1
9213	8	121,918,863	121,919,526	663	1	11	11.286	18	23	0	0	0				ActReg chr8 #9213	0	1
9214	8	121,944,843	121,945,409	566	1	6	11.167	9	20	0	0	0				ActReg chr8 #9214	0	1
9215	8	122,514,538	122,515,363	825	1	12.231	8.923	23	18	0	0	0				ActReg chr8 #9215	1	0
9216	8	122,542,637	122,543,104	467	1	8.2	12.2	13	15	0	0	0				ActReg chr8 #9216	0	1
9217	8	122,612,276	122,612,905	629	1	10.05	7.35	19	13	0	0	0				ActReg chr8 #9217	1	0
9218	8	122,972,511	122,973,056	545	1	10.111	5.222	20	8	0	0	0				ActReg chr8 #9218	1	0
9219	8	123,330,815	123,331,349	534	1	11.588	10.177	21	21	0	0	0				ActReg chr8 #9219	1	0
9220	8	123,501,602	123,502,297	695	1	10.429	10.952	17	16	0	0	0				ActReg chr8 #9220	1	0
9221	8	123,587,486	123,588,569	1,083	1	9.206	12.735	22	21	0	0	0				ActReg chr8 #9221	0	1
9222	8	123,649,567	123,650,215	648	1	12.191	7.952	24	11	0	0	0				ActReg chr8 #9222	1	0
9223	8	124,053,762	124,055,058	1,296	2	13.55	14.8	30	24	1	1	1	DERL1	238	in gene	ActReg chr8 #9223	1	1
9224	8	124,084,682	124,085,350	668	1	8.619	10.952	12	20	1	1	1	WDR67	96	in gene	ActReg chr8 #9224	0	1
9225	8	124,169,055	124,170,048	993	1	11.156	15.719	20	27	1	0	1	WDR67	84,631	downstream	ActReg chr8 #9225	0	1
9226	8	124,407,862	124,409,329	1,467	2	22.022	30.196	64	101	1	1	1	ATAD2	110	in gene	ActReg chr8 #9226	1	1
9227	8	124,780,411	124,781,130	719	2	9.826	11.522	20	20	1	1	1	FAM91A1	-112	upstream	ActReg chr8 #9227	1	1
9228	8	125,212,107	125,212,986	879	1	11.593	14.259	19	22	0	0	0				ActReg chr8 #9228	0	1
9229	8	125,462,270	125,462,959	689	1	8.864	11.546	19	22	0	1	1	TRMT12	-434	upstream	ActReg chr8 #9229	0	1
9230	8	125,486,592	125,487,331	739	1	8.667	12.75	12	23	1	2	2	LOC100507018, RNF139	-177, -47	upstream, upstream	ActReg chr8 #9230	0	1
9231	8	125,763,773	125,764,444	671	1	11.619	6.571	19	11	0	0	0				ActReg chr8 #9231	1	0
9232	8	125,784,226	125,784,828	602	1	9.889	14	15	20	0	0	0				ActReg chr8 #9232	0	1
9233	8	125,985,177	125,986,110	933	1	9.172	12.621	21	23	0	1	1	ZNF572	104	in gene	ActReg chr8 #9233	0	1
9234	8	126,103,621	126,104,376	755	1	6.478	12.957	10	23	1	2	2	KIAA0196, NSMCE2	63, -85	in gene, upstream	ActReg chr8 #9234	0	1
9235	8	126,346,198	126,346,926	728	1	7.739	12.304	12	21	0	0	1	NSMCE2	242,479	in gene	ActReg chr8 #9235	0	1
9236	8	126,424,158	126,425,465	1,307	2	10.049	11.049	16	20	0	0	0				ActReg chr8 #9236	1	1
9237	8	126,425,687	126,426,262	575	1	10.111	13.444	15	23	0	0	0				ActReg chr8 #9237	0	1
9238	8	126,442,106	126,443,152	1,046	2	9.576	13.485	19	21	1	1	1	TRIB1	66	in gene	ActReg chr8 #9238	1	1
9239	8	126,496,499	126,497,062	563	1	8.444	10.278	12	16	0	0	0				ActReg chr8 #9239	0	1
9240	8	126,524,973	126,525,840	867	2	11.593	13.259	24	25	0	0	0				ActReg chr8 #9240	1	1
9241	8	126,568,201	126,569,492	1,291	1	7.725	11.025	11	17	0	0	0				ActReg chr8 #9241	0	1
9242	8	127,509,411	127,510,136	725	2	10.727	9.636	14	16	0	0	0				ActReg chr8 #9242	1	1
9243	8	127,512,051	127,512,862	811	1	9.04	11.76	12	17	0	0	0				ActReg chr8 #9243	0	1
9244	8	127,559,028	127,560,064	1,036	2	12.909	11.879	19	17	0	0	1	FAM84B	10,920	downstream	ActReg chr8 #9244	1	1
9245	8	127,568,400	127,569,723	1,323	2	12.366	13.61	20	20	1	1	1	FAM84B	1,405	in gene	ActReg chr8 #9245	1	1
9246	8	127,570,136	127,571,170	1,034	2	17.182	15.697	40	41	1	1	1	FAM84B	-187	upstream	ActReg chr8 #9246	1	1
9247	8	127,584,131	127,584,637	506	1	11	3.867	16	8	0	0	0				ActReg chr8 #9247	1	0
9248	8	127,963,256	127,964,005	749	1	12.042	10.083	21	12	0	0	0				ActReg chr8 #9248	1	0
9249	8	128,047,844	128,048,438	594	1	9.833	11.167	15	19	0	0	0				ActReg chr8 #9249	0	1
9250	8	128,747,244	128,748,143	899	2	12.786	13	30	22	1	1	1	MYC	-622	upstream	ActReg chr8 #9250	1	1
9251	8	128,748,229	128,748,767	538	1	5.25	10.75	9	17	1	1	1	MYC	183	in gene	ActReg chr8 #9251	0	1
9252	8	128,821,787	128,822,451	664	1	9.81	9.095	15	13	0	0	2	PVT1, LOC100507101	15340, 15340	in gene, in gene	ActReg chr8 #9252	1	0
9253	8	128,843,453	128,844,789	1,336	2	9.214	11.238	20	22	0	0	2	PVT1, LOC100507101	37342, 37342	in gene, in gene	ActReg chr8 #9253	1	1
9254	8	128,863,682	128,865,233	1,551	1	9.875	13.5	19	21	0	0	2	PVT1, LOC100507101	57678, 57678	in gene, in gene	ActReg chr8 #9254	0	1
9255	8	128,871,926	128,872,602	676	1	8.238	12.809	16	20	0	0	2	PVT1, LOC100507101	65485, 65485	in gene, in gene	ActReg chr8 #9255	0	1
9256	8	128,929,787	128,930,397	610	1	9.368	10.421	14	18	0	0	2	PVT1, LOC100507101	123313, 123313	in gene, in gene	ActReg chr8 #9256	0	1
9257	8	129,157,001	129,157,808	807	2	16.72	12.88	40	28	0	1	1	MIR1208	-4,958	upstream	ActReg chr8 #9257	1	1
9258	8	129,481,748	129,482,490	742	1	10.478	8.13	17	12	0	0	0				ActReg chr8 #9258	1	0
9259	8	129,799,677	129,800,293	616	1	11.45	7.7	18	15	0	0	0				ActReg chr8 #9259	1	0
9260	8	129,970,054	129,970,677	623	1	4.316	11.474	9	22	0	0	0				ActReg chr8 #9260	0	1
9261	8	130,640,424	130,641,497	1,073	1	8.242	12.424	17	17	0	0	0				ActReg chr8 #9261	0	1
9262	8	130,719,777	130,720,925	1,148	2	10.057	8.743	16	15	0	0	0				ActReg chr8 #9262	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9263	8	130,765,686	130,766,188	502	1	9.188	8.75	15	13	0	0	1	GSDMC	33,197	in gene	ActReg chr8 #9263	1	0
9264	8	130,951,944	130,952,744	800	2	12.12	12.96	20	22	1	1	1	FAM49B	-344	upstream	ActReg chr8 #9264	1	1
9265	8	131,007,240	131,008,171	931	1	7.655	10.241	12	19	0	0	0				ActReg chr8 #9265	0	1
9266	8	131,740,094	131,740,732	638	1	7.7	9.75	17	16	0	0	0				ActReg chr8 #9266	0	1
9267	8	131,820,778	131,821,479	701	1	7.727	13.091	15	21	0	0	1	ADCY8	231,707	in gene	ActReg chr8 #9267	0	1
9268	8	131,892,612	131,893,557	945	2	11.621	14.759	26	27	0	0	1	ADCY8	159,751	in gene	ActReg chr8 #9268	1	1
9269	8	132,047,418	132,047,862	444	1	9.571	4.714	14	7	0	0	1	ADCY8	5,195	in gene	ActReg chr8 #9269	1	0
9270	8	132,049,032	132,049,611	579	2	10.611	11.389	17	19	0	0	1	ADCY8	3,514	in gene	ActReg chr8 #9270	1	1
9271	8	132,868,712	132,869,547	835	1	10.731	13.154	18	23	0	0	0				ActReg chr8 #9271	0	1
9272	8	133,082,567	133,083,582	1,015	2	12.871	12.613	19	23	0	0	1	HHLA1	34,438	in gene	ActReg chr8 #9272	1	1
9273	8	133,687,401	133,688,236	835	2	10.115	11.077	15	20	1	1	1	LRRC6	-5	upstream	ActReg chr8 #9273	1	1
9274	8	134,229,962	134,230,649	687	1	8.857	12.619	13	18	0	0	1	WISP1	26,993	in gene	ActReg chr8 #9274	0	1
9275	8	134,309,115	134,310,583	1,468	1	7.696	13.196	16	19	1	1	1	NDRG1	-302	upstream	ActReg chr8 #9275	0	1
9276	8	134,397,349	134,398,542	1,193	1	8.703	14.784	16	31	0	0	0				ActReg chr8 #9276	0	1
9277	8	134,403,018	134,403,666	648	1	9.4	12.7	18	24	0	0	0				ActReg chr8 #9277	0	1
9278	8	134,582,442	134,583,569	1,127	1	10.114	12.257	15	19	1	2	2	ST3GAL1, LOC100129104	1178, -1099	in gene, upstream	ActReg chr8 #9278	0	1
9279	8	134,583,996	134,584,953	957	1	5.667	10.333	12	15	1	2	2	ST3GAL1, LOC100129104	-291, 370	upstream, in gene	ActReg chr8 #9279	0	1
9280	8	135,421,320	135,422,431	1,111	2	17.941	21.912	46	55	0	0	0				ActReg chr8 #9280	1	1
9281	8	135,542,548	135,543,058	510	1	5.125	11.125	9	21	0	0	1	ZFAT	182,489	in gene	ActReg chr8 #9281	0	1
9282	8	135,752,265	135,752,917	652	1	6.15	11.55	10	19	0	0	0				ActReg chr8 #9282	0	1
9283	8	135,844,322	135,845,372	1,050	2	8.406	10.031	16	20	1	0	0				ActReg chr8 #9283	1	1
9284	8	135,909,410	135,910,370	960	1	11.533	11.633	18	16	0	0	0				ActReg chr8 #9284	1	0
9285	8	136,097,896	136,098,546	650	1	6.611	11.1	9	21	0	0	0				ActReg chr8 #9285	0	1
9286	8	136,201,888	136,202,597	709	2	11.348	11.043	20	21	0	0	0				ActReg chr8 #9286	1	1
9287	8	136,247,259	136,248,236	977	1	7.226	10.194	13	17	0	1	1	LOC286094	1,373	in gene	ActReg chr8 #9287	0	1
9288	8	136,332,477	136,333,143	666	1	9.19	11.429	13	20	0	0	0				ActReg chr8 #9288	0	1
9289	8	137,801,608	137,802,075	467	1	5.769	10.071	10	16	0	0	0				ActReg chr8 #9289	0	1
9290	8	138,334,234	138,334,653	419	1	9.615	9.923	14	13	0	0	0				ActReg chr8 #9290	0	1
9291	8	139,548,982	139,549,758	776	1	9.208	13.375	14	25	0	0	0				ActReg chr8 #9291	0	1
9292	8	139,653,993	139,654,776	783	2	9.792	13.917	20	29	0	0	1	COL22A1	271,852	in gene	ActReg chr8 #9292	1	1
9293	8	139,843,065	139,843,701	636	1	9.95	11.95	15	17	0	0	1	COL22A1	82,853	in gene	ActReg chr8 #9293	0	1
9294	8	139,988,070	139,988,612	542	1	8.706	6.882	16	13	0	0	0				ActReg chr8 #9294	1	0
9295	8	140,221,380	140,221,881	501	1	8.4	11.2	13	15	0	0	0				ActReg chr8 #9295	0	1
9296	8	140,227,833	140,228,538	705	2	10.409	10.227	16	16	0	0	0				ActReg chr8 #9296	1	1
9297	8	140,256,081	140,256,904	823	2	9.64	17.72	16	36	0	0	0				ActReg chr8 #9297	1	1
9298	8	140,670,781	140,671,422	641	1	10.45	12.65	16	25	0	0	1	KCNK9	44,198	in gene	ActReg chr8 #9298	0	1
9299	8	140,717,912	140,718,617	705	1	5.955	9.5	11	13	1	1	1	KCNK9	-2,965	upstream	ActReg chr8 #9299	0	1
9300	8	140,732,143	140,732,963	820	2	14.731	18.923	34	45	0	0	1	TRAPPC9	736,125	downstream	ActReg chr8 #9300	1	1
9301	8	140,908,680	140,909,456	776	2	10.75	14.417	23	25	0	0	1	TRAPPC9	559,610	in gene	ActReg chr8 #9301	1	1
9302	8	141,319,220	141,320,633	1,413	2	13.477	13.046	33	34	0	0	1	TRAPPC9	148,752	in gene	ActReg chr8 #9302	1	1
9303	8	141,403,760	141,404,407	647	1	5.65	10.7	8	16	0	0	1	TRAPPC9	64,595	in gene	ActReg chr8 #9303	0	1
9304	8	141,467,388	141,468,216	828	2	13.5	13.423	30	29	1	1	1	TRAPPC9	876	in gene	ActReg chr8 #9304	1	1
9305	8	141,474,004	141,475,240	1,236	2	15.641	14.359	33	25	1	1	1	TRAPPC9	-5,944	upstream	ActReg chr8 #9305	1	1
9306	8	141,520,744	141,521,369	625	1	10	11.21	14	17	1	1	1	CHRAC1	-345	upstream	ActReg chr8 #9306	0	1
9307	8	141,521,950	141,522,823	873	1	6.036	10.143	12	15	1	1	1	CHRAC1	985	in gene	ActReg chr8 #9307	0	1
9308	8	141,598,926	141,600,186	1,260	1	6.897	9.897	15	15	0	0	1	EIF2C2	46,090	in gene	ActReg chr8 #9308	0	1
9309	8	141,631,135	141,631,860	725	2	10.304	11.913	17	21	0	0	1	EIF2C2	14,149	in gene	ActReg chr8 #9309	1	1
9310	8	141,644,095	141,644,873	778	1	8.72	10.84	16	15	1	1	1	EIF2C2	1,162	in gene	ActReg chr8 #9310	0	1
9311	8	142,036,641	142,037,539	898	2	12.607	12.821	22	24	0	0	0				ActReg chr8 #9311	1	1
9312	8	142,045,278	142,045,952	674	1	9.364	11.091	16	21	0	0	0				ActReg chr8 #9312	0	1
9313	8	142,053,174	142,053,872	698	1	10.727	9.636	18	18	0	0	0				ActReg chr8 #9313	1	0
9314	8	142,163,652	142,164,705	1,053	1	7.515	9.485	13	14	0	0	1	DENND3	25,458	in gene	ActReg chr8 #9314	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9315	8	142,525,627	142,527,835	2,208	2	12.696	17.536	37	47	0	0	1	FLJ43860	-9,401	upstream	ActReg chr8 #9315	1	1
9316	8	142,576,842	142,577,947	1,105	2	12.647	16.118	22	35	0	0	0				ActReg chr8 #9316	1	1
9317	8	142,725,776	142,727,004	1,228	2	18.868	23.079	45	67	0	0	0				ActReg chr8 #9317	1	1
9318	8	142,970,567	142,971,193	626	1	8.158	11.632	16	17	0	0	0				ActReg chr8 #9318	0	1
9319	8	143,296,625	143,299,306	681	1	7.429	13.905	14	24	0	0	2	NCRNA00051, TSNARE1	19248, 185578	downstream, in gene	ActReg chr8 #9319	0	1
9320	8	143,331,973	143,332,649	676	2	10.762	11.762	19	23	0	0	1	TSNARE1	152,232	in gene	ActReg chr8 #9320	1	1
9321	8	143,464,504	143,465,223	719	1	10.391	14.304	21	27	0	0	1	TSNARE1	19,680	in gene	ActReg chr8 #9321	0	1
9322	8	143,751,260	143,751,714	454	1	10.733	16	20	33	1	2	2	JRK, PSCA	-86, -239	upstream, upstream	ActReg chr8 #9322	0	1
9323	8	143,762,711	143,763,681	970	1	10.742	12.742	17	22	0	0	1	PSCA	11,470	in gene	ActReg chr8 #9323	0	1
9324	8	143,799,265	143,799,962	697	2	14.762	11.857	30	22	0	0	2	LOC100288181, C8orf55	8778, -9008	in gene, upstream	ActReg chr8 #9324	1	1
9325	8	143,819,865	143,821,063	1,198	1	8.842	13	19	20	1	0	2	C8orf55, SLURP1	11843, 3365	downstream, downstream	ActReg chr8 #9325	0	1
9326	8	143,993,112	143,993,829	717	1	8.043	11.783	13	21	0	0	1	CYP11B2	5,789	in gene	ActReg chr8 #9326	0	1
9327	8	144,024,759	144,025,648	889	2	13.714	16.036	30	36	0	0	0				ActReg chr8 #9327	1	1
9328	8	144,183,001	144,183,866	865	2	11.462	13.296	23	25	0	0	0				ActReg chr8 #9328	1	1
9329	8	144,317,585	144,318,524	939	1	7.379	10.69	11	15	0	0	0				ActReg chr8 #9329	0	1
9330	8	144,348,923	144,349,962	1,039	2	15.273	12	30	33	1	1	2	ZFP41, GLI4	20333, -165	downstream, upstream	ActReg chr8 #9330	1	1
9331	8	144,362,904	144,364,553	1,649	2	32.038	34.923	133	150	0	1	3	GLI4, LOC100507316, ZNF696	14121, 132, 9831	downstream, in gene, upstream	ActReg chr8 #9331	1	1
9332	8	144,372,945	144,373,979	1,034	2	16.062	14.688	32	27	1	1	2	LOC100507316, ZNF696	-9602, -97	upstream, upstream	ActReg chr8 #9332	1	1
9333	8	144,623,433	144,624,157	724	1	9.364	12.409	14	28	1	1	1	ZC3H3	-175	upstream	ActReg chr8 #9333	0	1
9334	8	144,678,971	144,680,051	1,080	2	21.033	20.912	49	54	1	2	3	EEF1D, TIGD5, PYCRL	334, -563, 12273	in gene, upstream, downstream	ActReg chr8 #9334	1	1
9335	8	144,680,171	144,680,664	493	1	6.667	15.467	12	26	1	2	3	EEF1D, TIGD5, PYCRL	-572, 343, 11367	upstream, in gene, downstream	ActReg chr8 #9335	0	1
9336	8	144,700,158	144,700,585	427	1	9.357	10.786	13	18	1	1	2	PYCRL, TSTA3	-8587, -639	upstream, upstream	ActReg chr8 #9336	0	1
9337	8	144,717,606	144,718,595	989	2	9.613	11.452	16	18	1	1	1	ZNF623	-273	upstream	ActReg chr8 #9337	1	1
9338	8	144,766,244	144,767,053	809	2	12.44	13.56	19	23	1	1	1	ZNF707	26	in gene	ActReg chr8 #9338	1	1
9339	8	144,911,130	144,912,022	892	1	10.071	12.786	16	19	1	1	2	PUF60, NRBP2	-39, 11570	upstream, downstream	ActReg chr8 #9339	0	1
9340	8	145,010,409	145,011,319	910	1	13.893	11.071	24	16	0	0	2	PLEC1, MIR661	40049, 8583	in gene, downstream	ActReg chr8 #9340	1	0
9341	8	145,016,332	145,018,450	2,118	2	10.53	12.742	24	26	2	1	2	PLEC1, MIR661	33522, 2056	in gene, downstream	ActReg chr8 #9341	1	1
9342	8	145,021,995	145,023,349	1,354	2	12.881	12.429	22	23	0	1	2	PLEC1, MIR661	28241, -3225	in gene, upstream	ActReg chr8 #9342	1	1
9343	8	145,023,356	145,025,118	1,762	1	8.836	13.127	17	24	1	1	2	PLEC1, MIR661	26676, -4790	in gene, upstream	ActReg chr8 #9343	0	1
9344	8	145,048,862	145,049,663	801	2	10.84	13.52	17	28	1	1	2	PLEC1, PARP10	1651, 11373	in gene, downstream	ActReg chr8 #9344	1	1
9345	8	145,133,070	145,134,330	1,260	2	12.128	13.462	18	22	1	2	2	EXOSC4, GPAA1	178, -3824	in gene, upstream	ActReg chr8 #9345	1	1
9346	8	145,158,228	145,160,193	1,965	2	14.129	17.71	36	40	1	4	5	CYC1, LOC100507382, SHARPIN, MAF1, KIAA1875	9250, -7267, -70, -95, -3419	downstream, upstream, upstream, upstream, upstream	ActReg chr8 #9346	1	1
9347	8	145,550,233	145,551,121	888	2	12.857	13	23	20	1	1	2	DGAT1, SCRT1	-110, 9266	upstream, downstream	ActReg chr8 #9347	1	1
9348	8	145,558,535	145,560,218	1,683	1	7.962	12.788	16	18	1	1	2	DGAT1, SCRT1	-8809, 567	upstream, in gene	ActReg chr8 #9348	0	1
9349	8	145,581,902	145,582,737	835	1	11.423	13.192	25	20	1	3	3	C8ORFK29, FBXL6, GPR172A	-3814, -187, 94	upstream, upstream, in gene	ActReg chr8 #9349	0	1
9350	8	145,597,234	145,597,928	694	1	6.455	11.454	8	16	1	1	1	ADCK5	-150	upstream	ActReg chr8 #9350	0	1
9351	8	145,653,367	145,654,266	899	2	19.107	15.5	37	34	1	1	2	VPS28, NFKBIL2	111, 15996	in gene, downstream	ActReg chr8 #9351	1	1
9352	8	145,690,537	145,690,926	389	1	6.75	11.333	10	17	1	2	3	CYHR1, KIFC2, FOXH1	300, -1007, 10987	in gene, upstream, downstream	ActReg chr8 #9352	0	1
9353	8	145,733,874	145,735,565	1,691	1	10.207	13.057	18	23	1	1	5	PPP1R16A, GPT, MFSD3, RECQL4, LRRC14	12610, 5254, 167, 8491, -8672	downstream, downstream, in gene, downstream, upstream	ActReg chr8 #9353	0	1
9354	8	145,754,092	145,754,706	614	1	11.737	9.263	20	14	1	2	4	LRRC14, LRRC24, C8orf82, KIAA1688	11008, -1983, 59, 84492	downstream, upstream, in gene, downstream	ActReg chr8 #9354	1	0
9355	8	145,980,645	145,981,392	747	2	10.696	11	18	18	1	1	1	ZNF251	-48	upstream	ActReg chr8 #9355	1	1
9356	8	146,012,085	146,013,038	953	1	8.333	11.7	14	17	1	1	2	ZNF34, RPL8	164, 5244	in gene, downstream	ActReg chr8 #9356	0	1
9357	8	146,017,088	146,018,513	1,425	2	10.2	12.644	16	22	1	3	3	ZNF34, RPL8, ZNF517	-5075, 5, -6461	upstream, in gene, upstream	ActReg chr8 #9357	1	1
9358	8	146,052,695	146,053,397	702	2	10.4	14.682	18	27	1	3	3	LOC100130027, LOC100129596, ZNF7	-621, -6897, 143	upstream, upstream, in gene	ActReg chr8 #9358	1	1
9359	8	146,078,025	146,078,859	834	2	11.615	11.269	16	18	1	1	2	ZNF7, COMMD5	25539, 490	downstream, in gene	ActReg chr8 #9359	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9360	8	146,126,423	146,127,853	1,430	2	12.2	14.6	24	28	1	1	1	ZNF250	-292	upstream	ActReg chr8 #9360	1	1
9361	8	146,227,878	146,228,522	644	1	8.95	12.4	14	19	1	1	1	C8orf77	3	in gene	ActReg chr8 #9361	0	1
9362	8	146,277,748	146,278,185	437	1	8.643	12.429	15	21	1	1	1	C8orf33	142	in gene	ActReg chr8 #9362	0	1
9363	9	694,285	695,332	1,047	1	11.939	15.273	16	25	0	0	1	KANK1	190,105	in gene	ActReg chr9 #9363	0	1
9364	9	712,693	713,247	554	1	6.471	12.235	10	19	0	0	1	KANK1	208,267	in gene	ActReg chr9 #9364	0	1
9365	9	738,261	739,141	880	1	8	11.464	13	17	0	0	1	KANK1	233,998	in gene	ActReg chr9 #9365	0	1
9366	9	751,091	752,378	1,287	1	12.475	9.8	18	18	0	0	1	KANK1	247,031	downstream	ActReg chr9 #9366	1	0
9367	9	755,530	756,482	952	2	12.933	14.867	22	25	0	0	1	KANK1	251,303	downstream	ActReg chr9 #9367	1	1
9368	9	2,014,652	2,015,748	1,096	1	9.171	11.486	15	18	1	1	1	SMARCA2	-142	upstream	ActReg chr9 #9368	0	1
9369	9	2,015,767	2,017,983	2,216	1	8.116	14.232	15	19	1	1	1	SMARCA2	1,533	in gene	ActReg chr9 #9369	0	1
9370	9	2,241,643	2,242,714	1,071	2	13.273	18.091	35	43	2	0	0				ActReg chr9 #9370	1	1
9371	9	2,260,689	2,261,295	606	1	7.105	11.105	9	18	0	0	0				ActReg chr9 #9371	0	1
9372	9	2,559,407	2,560,252	845	1	9.385	12.5	14	16	0	0	1	FLJ35024	62,544	in gene	ActReg chr9 #9372	0	1
9373	9	2,574,148	2,574,608	460	1	10.5	6.429	13	9	0	0	1	FLJ35024	47,995	in gene	ActReg chr9 #9373	1	0
9374	9	2,655,212	2,656,118	906	1	8.429	12.75	13	21	0	0	1	VLDLR	33,872	downstream	ActReg chr9 #9374	0	1
9375	9	2,843,827	2,844,566	739	2	11.174	12.391	17	22	1	1	1	KIAA0020	-66	upstream	ActReg chr9 #9375	1	1
9376	9	3,525,901	3,527,460	1,559	2	14.061	16.143	21	32	1	1	1	RFX3	-697	upstream	ActReg chr9 #9376	1	1
9377	9	3,862,950	3,863,675	725	1	9.318	12.364	16	16	0	0	1	GLIS3	436,723	in gene	ActReg chr9 #9377	0	1
9378	9	3,906,331	3,907,413	1,082	2	10.823	9.529	17	14	0	0	2	GLIS3, C9orf70	393163, 8226	in gene, downstream	ActReg chr9 #9378	1	1
9379	9	3,932,332	3,932,972	640	1	11.6	7.55	18	9	0	0	1	GLIS3	367,383	in gene	ActReg chr9 #9379	1	0
9380	9	3,968,754	3,969,322	568	1	10.111	12.056	18	20	0	0	1	GLIS3	330,997	in gene	ActReg chr9 #9380	0	1
9381	9	4,084,326	4,084,925	599	1	10.333	14.056	14	26	0	0	1	GLIS3	215,410	in gene	ActReg chr9 #9381	0	1
9382	9	4,238,363	4,239,059	696	1	7.955	11.5	16	19	0	0	1	GLIS3	61,324	in gene	ActReg chr9 #9382	0	1
9383	9	4,261,401	4,262,015	614	1	10.263	5.158	15	7	0	0	1	GLIS3	38,327	in gene	ActReg chr9 #9383	1	0
9384	9	4,290,456	4,290,910	454	1	5.571	11.429	8	16	0	1	2	GLIS3, LOC100287493	9352, -3541	in gene, upstream	ActReg chr9 #9384	0	1
9385	9	4,293,426	4,294,171	745	2	11.435	12.565	18	22	0	1	2	GLIS3, LOC100287493	6237, -426	in gene, upstream	ActReg chr9 #9385	1	1
9386	9	4,296,978	4,298,178	1,200	1	9.5	13.053	17	24	1	1	2	GLIS3, LOC100287493	2457, 3354	in gene, in gene	ActReg chr9 #9386	0	1
9387	9	4,298,187	4,299,426	1,239	2	10.154	11.026	19	16	1	1	2	GLIS3, LOC100287493	1229, 4582	in gene, in gene	ActReg chr9 #9387	1	1
9388	9	4,299,531	4,300,298	767	1	7.917	12.5	13	25	1	1	2	GLIS3, LOC100287493	121, 5690	in gene, in gene	ActReg chr9 #9388	0	1
9389	9	4,334,291	4,334,970	679	2	11.381	10.952	15	19	0	0	0				ActReg chr9 #9389	1	1
9390	9	4,489,912	4,491,590	1,678	2	14.396	14.925	29	26	2	1	1	SLC1A1	324	in gene	ActReg chr9 #9390	1	1
9391	9	4,530,186	4,531,143	957	1	8.067	12.3	13	21	0	0	1	SLC1A1	40,237	in gene	ActReg chr9 #9391	0	1
9392	9	4,661,960	4,663,299	1,339	2	12.048	11.929	18	20	1	1	2	C9orf68, PPAPDC2	4045, 331	in gene, in gene	ActReg chr9 #9392	1	1
9393	9	4,666,162	4,666,690	528	1	7.938	14.353	13	23	0	1	2	C9orf68, PPAPDC2	248, 4128	in gene, downstream	ActReg chr9 #9393	0	1
9394	9	4,679,136	4,680,307	1,171	2	11.405	13.054	20	20	1	1	1	CDC37L1	155	in gene	ActReg chr9 #9394	1	1
9395	9	4,740,629	4,741,581	952	2	11.567	13.967	17	26	1	1	1	AK3	122	in gene	ActReg chr9 #9395	1	1
9396	9	4,792,235	4,793,573	1,338	1	13.524	11.476	24	17	1	1	1	RCL1	70	in gene	ActReg chr9 #9396	1	0
9397	9	4,984,289	4,985,652	1,363	2	16.191	14.524	27	23	1	1	1	JAK2	-275	upstream	ActReg chr9 #9397	1	1
9398	9	5,437,356	5,438,214	858	1	9.889	12.963	15	25	1	1	1	C9orf46	75	in gene	ActReg chr9 #9398	0	1
9399	9	5,440,818	5,441,609	791	1	13.08	9.16	28	19	0	1	2	C9orf46, CD274	-3353, -9290	upstream, upstream	ActReg chr9 #9399	1	0
9400	9	5,450,194	5,450,987	793	2	12	12.182	18	28	1	1	1	CD274	87	in gene	ActReg chr9 #9400	1	1
9401	9	5,832,313	5,833,336	1,023	1	12.5	11.219	23	18	1	1	1	ERMP1	257	in gene	ActReg chr9 #9401	1	0
9402	9	6,015,159	6,016,164	1,005	1	9.594	15.25	17	28	0	2	2	KIAA2026, RANBP6	-7658, -21	upstream, upstream	ActReg chr9 #9402	0	1
9403	9	6,102,218	6,103,456	1,238	1	11.41	18.615	27	43	0	0	0				ActReg chr9 #9403	0	1
9404	9	6,364,158	6,364,808	650	1	12.095	7.524	16	13	0	0	0				ActReg chr9 #9404	1	0
9405	9	6,412,727	6,413,484	757	1	12.042	12.083	17	18	1	1	1	UHRF2	-46	upstream	ActReg chr9 #9405	1	0
9406	9	6,538,199	6,539,020	821	2	12.115	9.923	24	19	0	0	1	GLDC	107,083	in gene	ActReg chr9 #9406	1	1
9407	9	6,566,896	6,567,677	781	1	13.042	8.625	16	13	0	0	1	GLDC	78,406	in gene	ActReg chr9 #9407	1	0
9408	9	6,645,455	6,646,294	839	1	13.077	8.462	27	15	1	1	1	GLDC	-182	upstream	ActReg chr9 #9408	1	0
9409	9	6,680,624	6,681,985	1,361	2	14.209	13.256	23	24	1	0	0				ActReg chr9 #9409	1	1
9410	9	6,756,889	6,759,230	2,341	2	14.575	11.945	27	25	1	0	1	KDM4C	37,196	in gene	ActReg chr9 #9410	1	1
9411	9	7,266,808	7,268,047	1,239	1	8.821	13.333	13	21	0	0	0				ActReg chr9 #9411	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9412	9	7,319,932	7,320,714	782	2	11.28	14.24	25	25	0	0	0				ActReg chr9 #9412	1	1
9413	9	7,799,509	7,800,006	497	1	7.875	12.875	12	21	1	1	1	C9orf123	42	in gene	ActReg chr9 #9413	0	1
9414	9	11,064,775	11,065,453	678	2	10.714	10.762	18	16	0	0	0				ActReg chr9 #9414	1	1
9415	9	12,708,513	12,709,141	628	1	7.105	11.79	15	17	0	0	2	TYRP1, LOC100506267	15441, 105545	in gene, in gene	ActReg chr9 #9415	0	1
9416	9	12,774,720	12,776,943	2,223	2	13.714	13.929	31	30	1	1	2	LOC100506267, C9orf150	38541, 819	in gene, in gene	ActReg chr9 #9416	1	1
9417	9	12,784,281	12,785,003	722	1	10.174	14.217	17	31	0	0	2	LOC100506267, C9orf150	29730, 9630	in gene, in gene	ActReg chr9 #9417	0	1
9418	9	12,817,404	12,818,129	725	2	10.522	11.13	18	19	0	1	2	LOC100506267, C9orf150	-3394, 42754	upstream, in gene	ActReg chr9 #9418	1	1
9419	9	12,859,337	12,860,102	765	1	11.125	8.208	14	13	0	0	0				ActReg chr9 #9419	1	0
9420	9	12,933,908	12,934,494	586	1	5.667	12.389	10	17	0	0	0				ActReg chr9 #9420	0	1
9421	9	13,082,840	13,083,328	488	1	9.562	2.8	18	5	0	0	0				ActReg chr9 #9421	1	0
9422	9	13,278,147	13,278,944	797	1	12.12	11.28	18	16	1	0	0				ActReg chr9 #9422	1	0
9423	9	13,942,596	13,943,332	736	1	9.304	13.304	17	26	0	0	0				ActReg chr9 #9423	0	1
9424	9	14,238,095	14,238,630	535	1	8.824	14.294	14	25	0	0	1	NFIB	160,620	in gene	ActReg chr9 #9424	0	1
9425	9	14,277,810	14,278,742	932	1	8.724	11.207	14	18	0	0	1	NFIB	120,706	in gene	ActReg chr9 #9425	0	1
9426	9	14,322,113	14,323,258	1,145	2	16.029	23.8	40	52	1	0	1	NFIB	76,297	in gene	ActReg chr9 #9426	1	1
9427	9	14,693,126	14,694,056	930	2	9.345	14.655	17	31	1	1	1	ZDHHC21	-111	upstream	ActReg chr9 #9427	1	1
9428	9	15,422,212	15,423,465	1,253	2	12.667	14.974	28	30	1	1	1	SNAPC3	56	in gene	ActReg chr9 #9428	1	1
9429	9	15,510,385	15,511,529	1,144	2	11.056	15.528	25	30	1	1	1	PSIP1	46	in gene	ActReg chr9 #9429	1	1
9430	9	15,552,531	15,553,910	1,379	2	12.163	11.326	21	18	1	1	1	C9orf93	123	in gene	ActReg chr9 #9430	1	1
9431	9	15,697,465	15,698,136	671	1	10.524	12.667	17	21	0	0	1	C9orf93	144,703	in gene	ActReg chr9 #9431	0	1
9432	9	16,111,603	16,112,789	1,186	2	11.892	14.811	26	23	0	0	0				ActReg chr9 #9432	1	1
9433	9	16,336,840	16,338,103	1,263	2	11.436	12.231	16	18	0	0	0				ActReg chr9 #9433	1	1
9434	9	16,367,920	16,368,623	703	1	8.955	13.273	12	27	0	0	0				ActReg chr9 #9434	0	1
9435	9	16,626,436	16,627,213	777	1	12.083	8.958	21	19	0	0	1	BNC2	243,962	in gene	ActReg chr9 #9435	1	0
9436	9	16,726,657	16,727,365	708	1	10.5	12.5	17	21	1	0	1	BNC2	143,775	in gene	ActReg chr9 #9436	0	1
9437	9	16,870,388	16,871,085	697	1	11.909	9.545	17	17	1	1	1	BNC2	50	in gene	ActReg chr9 #9437	1	0
9438	9	16,963,882	16,964,676	794	1	12.76	12.48	20	20	0	0	0				ActReg chr9 #9438	1	0
9439	9	17,017,812	17,018,752	940	2	17.8	20.6	42	44	0	0	0				ActReg chr9 #9439	1	1
9440	9	17,134,242	17,135,887	1,645	2	12.686	11.118	18	26	1	1	1	CNTLN	26	in gene	ActReg chr9 #9440	1	1
9441	9	17,744,660	17,745,249	589	2	10.21	13.947	19	26	0	0	1	SH3GL2	166,001	in gene	ActReg chr9 #9441	1	1
9442	9	18,268,320	18,268,893	573	1	10.333	8.556	19	16	0	0	0				ActReg chr9 #9442	1	0
9443	9	18,393,053	18,394,088	1,035	2	18.849	15.485	44	32	0	0	0				ActReg chr9 #9443	1	1
9444	9	18,459,803	18,460,498	695	1	10.727	7.591	17	14	0	0	0				ActReg chr9 #9444	1	0
9445	9	19,048,628	19,050,235	1,607	2	11.8	14.24	21	23	1	1	2	RRAGA, HAUS6	59, 53471	in gene, downstream	ActReg chr9 #9445	1	1
9446	9	19,102,678	19,103,294	616	1	10.21	16.895	20	30	1	1	1	HAUS6	-84	upstream	ActReg chr9 #9446	0	1
9447	9	19,127,010	19,127,780	770	1	11.542	14.583	17	23	1	1	1	PLIN2	178	in gene	ActReg chr9 #9447	0	1
9448	9	19,161,514	19,162,214	700	2	14.909	14.818	29	35	0	0	0				ActReg chr9 #9448	1	1
9449	9	19,231,530	19,232,477	947	1	10.276	6.172	16	10	0	0	0				ActReg chr9 #9449	1	0
9450	9	19,379,663	19,380,941	1,278	2	18.15	16.175	36	35	1	1	2	DENND4C, RPS6	89553, -67	downstream, upstream	ActReg chr9 #9450	1	1
9451	9	19,408,101	19,409,546	1,445	1	7.311	12.911	12	24	1	1	1	ACER2	-102	upstream	ActReg chr9 #9451	0	1
9452	9	19,720,151	19,720,796	645	1	6.75	10.85	15	22	0	0	1	SLC24A2	68,118	in gene	ActReg chr9 #9452	0	1
9453	9	19,748,124	19,749,077	953	2	11.867	11.133	21	18	0	0	1	SLC24A2	39,991	in gene	ActReg chr9 #9453	1	1
9454	9	19,999,335	20,000,062	727	1	12.5	11.227	22	20	0	0	0				ActReg chr9 #9454	1	0
9455	9	20,033,365	20,034,111	746	1	13.304	7.304	20	11	0	0	0				ActReg chr9 #9455	1	0
9456	9	20,558,168	20,559,196	1,028	1	10.875	7.219	22	15	0	0	1	MLLT3	63,832	in gene	ActReg chr9 #9456	1	0
9457	9	20,622,097	20,623,642	1,545	2	10.25	12.875	16	20	0	1	1	MLLT3	-355	upstream	ActReg chr9 #9457	1	1
9458	9	20,683,648	20,685,001	1,353	2	11.419	10.372	18	22	1	0	1	KIAA1797	26,015	in gene	ActReg chr9 #9458	1	1
9459	9	21,334,603	21,335,635	1,032	1	10.406	15.375	21	26	1	1	1	KLHL9	310	in gene	ActReg chr9 #9459	0	1
9460	9	21,454,888	21,455,785	897	1	6.5	10.536	10	17	0	0	1	LOC554202	104,361	in gene	ActReg chr9 #9460	0	1
9461	9	21,505,266	21,505,941	675	2	12.191	12.809	25	27	0	0	2	LOC554202, MIR31	54094, 6581	in gene, downstream	ActReg chr9 #9461	1	1
9462	9	21,549,435	21,550,004	569	1	7.333	10.944	11	19	0	0	1	LOC554202	9,978	in gene	ActReg chr9 #9462	0	1
9463	9	21,559,341	21,559,894	553	1	8.118	11.294	12	16	1	1	1	LOC554202	80	in gene	ActReg chr9 #9463	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9464	9	21,591,429	21,592,329	900	2	10.893	13.821	21	26	0	0	0				ActReg chr9 #9464	1	1
9465	9	21,684,714	21,685,395	681	1	13.429	10.571	23	17	0	0	0				ActReg chr9 #9465	1	0
9466	9	21,688,193	21,689,063	870	1	10.518	7.296	16	12	0	0	0				ActReg chr9 #9466	1	0
9467	9	21,801,983	21,803,102	1,119	2	11.543	13.371	23	34	1	1	1	MTAP	-93	upstream	ActReg chr9 #9467	1	1
9468	9	21,836,363	21,837,242	879	1	14.296	11.259	27	18	0	0	1	MTAP	34,167	in gene	ActReg chr9 #9468	1	0
9469	9	22,147,810	22,148,682	872	1	12.037	9.593	19	19	0	0	0				ActReg chr9 #9469	1	0
9470	9	22,216,710	22,217,536	826	1	8.731	12.615	14	18	0	0	0				ActReg chr9 #9470	0	1
9471	9	22,342,455	22,342,950	495	1	11.188	7.562	16	10	0	0	0				ActReg chr9 #9471	1	0
9472	9	23,621,050	23,621,786	736	1	12.478	9.652	20	16	0	0	0				ActReg chr9 #9472	1	0
9473	9	23,824,080	23,827,014	2,934	2	15.924	20.489	50	64	0	1	1	ELAVL2	516	in gene	ActReg chr9 #9473	1	1
9474	9	23,829,340	23,830,288	948	2	14.133	10.833	29	19	0	1	1	ELAVL2	-3,751	upstream	ActReg chr9 #9474	1	1
9475	9	25,677,197	25,678,729	1,532	2	11.021	12.979	16	22	1	1	1	TUSC1	893	in gene	ActReg chr9 #9475	1	1
9476	9	25,700,958	25,701,323	365	1	2.417	10.5	4	15	0	0	0				ActReg chr9 #9476	0	1
9477	9	26,747,258	26,748,064	806	2	9.808	9.923	16	14	0	0	0				ActReg chr9 #9477	1	1
9478	9	26,748,164	26,749,113	949	1	7.966	9.828	14	16	0	0	0				ActReg chr9 #9478	0	1
9479	9	26,892,022	26,893,191	1,169	2	14.919	17.378	25	36	1	1	1	C9orf82	220	in gene	ActReg chr9 #9479	1	1
9480	9	26,946,674	26,947,889	1,215	2	15.447	18.868	24	36	1	2	2	PLAA, IFT74	187, 244	in gene, in gene	ActReg chr9 #9480	1	1
9481	9	26,955,694	26,957,039	1,345	2	10.524	12.309	20	17	1	0	2	PLAA, IFT74	-8898, 9329	upstream, in gene	ActReg chr9 #9481	1	1
9482	9	27,094,491	27,095,463	972	1	8.677	9.613	19	18	0	0	0				ActReg chr9 #9482	0	1
9483	9	27,124,900	27,126,251	1,351	2	12.833	12.548	25	33	0	0	1	TEK	16,428	in gene	ActReg chr9 #9483	1	1
9484	9	27,154,622	27,155,455	833	1	7.769	11.077	12	16	0	0	1	TEK	45,891	in gene	ActReg chr9 #9484	0	1
9485	9	27,194,276	27,195,022	746	1	9.522	14.652	22	30	0	0	1	TEK	85,502	in gene	ActReg chr9 #9485	0	1
9486	9	27,227,116	27,227,739	623	1	11.263	5.895	17	9	0	0	1	TEK	118,280	in gene	ActReg chr9 #9486	1	0
9487	9	27,572,518	27,573,222	704	1	5.727	11.409	11	19	1	1	1	C9orf72	972	in gene	ActReg chr9 #9487	0	1
9488	9	27,573,528	27,574,305	777	2	10	10.2	19	16	2	1	1	C9orf72	-74	upstream	ActReg chr9 #9488	1	1
9489	9	29,213,424	29,214,507	1,083	1	9.529	12.853	22	21	1	0	0				ActReg chr9 #9489	0	1
9490	9	29,564,588	29,565,004	416	1	11.769	8.538	15	11	0	0	0				ActReg chr9 #9490	1	0
9491	9	30,574,651	30,575,055	404	1	10.154	9.231	14	11	0	0	0				ActReg chr9 #9491	1	0
9492	9	32,384,324	32,385,103	779	1	12.833	11.333	19	17	1	1	1	ACO1	112	in gene	ActReg chr9 #9492	1	0
9493	9	32,552,104	32,552,740	636	2	11.4	10.8	20	19	1	2	3	TOPORS, LOC100129250, NDUFB6	200, 1280, 20760	in gene, in gene, downstream	ActReg chr9 #9493	1	1
9494	9	32,572,931	32,573,550	619	1	12.842	11.368	22	21	1	1	1	NDUFB6	-58	upstream	ActReg chr9 #9494	1	0
9495	9	33,001,204	33,001,968	764	1	12.292	9.375	20	13	1	1	1	APTX	40	in gene	ActReg chr9 #9495	1	0
9496	9	33,024,903	33,025,669	766	2	11.375	11.875	21	19	1	1	1	DNAJA1	77	in gene	ActReg chr9 #9496	1	1
9497	9	33,076,207	33,077,060	853	2	12.074	12.778	22	25	1	1	1	SMU1	81	in gene	ActReg chr9 #9497	1	1
9498	9	33,233,641	33,234,787	1,146	2	11.306	14.667	23	33	0	1	1	SPINK4	-5,982	upstream	ActReg chr9 #9498	1	1
9499	9	33,290,002	33,290,934	932	2	16.379	15.138	36	34	1	1	2	CHMP5, NFX1	25591, 50	downstream, in gene	ActReg chr9 #9499	1	1
9500	9	33,523,297	33,524,279	982	1	9.4	10.733	17	19	1	1	1	ANKRD18B	-139	upstream	ActReg chr9 #9500	0	1
9501	9	34,048,513	34,049,750	1,237	2	11.053	13.184	19	25	1	1	1	UBAP2	-184	upstream	ActReg chr9 #9501	1	1
9502	9	34,126,207	34,127,097	890	1	7.167	11.393	12	14	1	1	1	DCAF12	119	in gene	ActReg chr9 #9502	0	1
9503	9	34,412,825	34,413,855	1,030	2	14.5	12.156	29	30	0	0	1	C9orf25	45,228	in gene	ActReg chr9 #9503	1	1
9504	9	34,430,614	34,431,361	747	2	8.583	11.583	19	21	0	0	1	C9orf25	27,581	in gene	ActReg chr9 #9504	1	1
9505	9	34,458,272	34,458,950	678	2	14.136	10.273	38	20	1	2	2	C9orf25, DNAI1	-43, -200	upstream, upstream	ActReg chr9 #9505	1	1
9506	9	34,493,533	34,494,907	1,374	2	14.814	14.581	33	36	0	0	1	DNAI1	35,409	in gene	ActReg chr9 #9506	1	1
9507	9	34,637,080	34,638,166	1,086	1	11.412	14.706	20	23	1	1	3	ARID3C, SIGMAR1, GALT	-9612, 145, 9012	upstream, in gene, upstream	ActReg chr9 #9507	0	1
9508	9	34,646,262	34,647,058	796	1	10.12	10.76	22	14	1	2	3	SIGMAR1, GALT, IL11RA	-8892, 25, 5522	upstream, in gene, upstream	ActReg chr9 #9508	0	1
9509	9	34,983,677	34,984,643	966	2	11.161	15.194	25	30	0	1	2	KIAA1045, DNAJB5	25968, -5565	downstream, upstream	ActReg chr9 #9509	1	1
9510	9	35,071,735	35,072,876	1,141	2	11.778	9.972	20	18	1	1	2	VCP, FANCG	434, 7708	in gene, downstream	ActReg chr9 #9510	1	1
9511	9	35,079,166	35,080,210	1,044	1	8.303	12.364	12	24	1	2	3	VCP, FANCG, PIGO	-6949, 325, 16891	upstream, in gene, downstream	ActReg chr9 #9511	0	1
9512	9	35,095,957	35,096,935	978	2	15.29	13.613	30	28	1	1	3	PIGO, STOML2, KIAA1539	133, 6708, 19447	in gene, downstream, downstream	ActReg chr9 #9512	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9513	9	35,102,499	35,103,521	1,022	2	10.719	12.781	23	18	1	2	3	PIGO, STOML2, KIAA1539	-6431, 144, 12883	upstream, in gene, downstream	ActReg chr9 #9513	1	1
9514	9	35,161,797	35,162,634	837	2	11.154	13.423	20	26	1	2	2	LOC730110, UNC13B	-52, 226	upstream, in gene	ActReg chr9 #9514	1	1
9515	9	35,489,795	35,491,004	1,209	1	9.486	11.568	15	16	1	1	1	RUSC2	392	in gene	ActReg chr9 #9515	0	1
9516	9	35,603,770	35,604,670	900	1	11.357	9.893	17	15	1	1	2	TESK1, CD72	-1061, 14204	upstream, downstream	ActReg chr9 #9516	1	0
9517	9	35,657,234	35,658,931	1,697	2	16.566	16.679	35	24	1	3	4	SIT1, RMRP, CCDC107, C9orf100	-7135, -67, -229, 7196	upstream, upstream, upstream, downstream	ActReg chr9 #9517	1	1
9518	9	35,731,975	35,732,979	1,004	1	9.032	11.129	17	18	1	2	3	TLN1, CREB3, GBA2	-85, 160, 16748	upstream, in gene, downstream	ActReg chr9 #9518	0	1
9519	9	35,945,642	35,946,077	435	1	10.615	9.462	17	13	0	0	0				ActReg chr9 #9519	1	0
9520	9	36,258,132	36,259,241	1,109	2	17.971	15.743	46	36	1	0	1	GNE	18,367	in gene	ActReg chr9 #9520	1	1
9521	9	36,317,563	36,318,070	507	1	9.75	11.375	14	16	0	0	0				ActReg chr9 #9521	0	1
9522	9	36,327,823	36,328,471	648	1	6.7	10.95	11	18	0	0	1	RNF38	73,048	downstream	ActReg chr9 #9522	0	1
9523	9	36,400,256	36,400,717	461	1	11.2	8.333	15	11	1	1	1	RNF38	709	in gene	ActReg chr9 #9523	1	0
9524	9	36,486,758	36,487,297	539	1	5.588	12.059	11	20	1	0	0				ActReg chr9 #9524	0	1
9525	9	36,572,206	36,573,127	921	1	6.207	11.552	12	18	1	1	1	MELK	-239	upstream	ActReg chr9 #9525	0	1
9526	9	36,748,148	36,749,433	1,285	2	12.925	17.325	34	42	0	0	0				ActReg chr9 #9526	1	1
9527	9	36,772,287	36,773,206	919	2	11.966	13.655	20	21	0	0	0				ActReg chr9 #9527	1	1
9528	9	36,923,952	36,924,487	535	1	11.765	8.235	22	13	0	0	1	PAX5	110,257	in gene	ActReg chr9 #9528	1	0
9529	9	37,027,309	37,028,113	804	2	11.92	15.32	21	30	1	0	2	PAX5, LOC100130458	6765, -8352	in gene, upstream	ActReg chr9 #9529	1	1
9530	9	37,422,325	37,422,955	630	2	11.8	10.8	20	17	1	1	1	GRHPR	-67	upstream	ActReg chr9 #9530	1	1
9531	9	37,464,503	37,465,385	882	1	4.885	10.071	11	14	1	1	1	ZBTB5	463	in gene	ActReg chr9 #9531	0	1
9532	9	37,592,119	37,592,954	835	1	12.308	9.231	18	14	1	1	1	TOMM5	100	in gene	ActReg chr9 #9532	1	0
9533	9	37,594,495	37,595,255	760	1	3.25	9.458	7	13	0	1	1	TOMM5	-2,239	upstream	ActReg chr9 #9533	0	1
9534	9	37,784,535	37,785,597	1,062	2	10.727	13.333	20	25	1	2	3	RG9MTD3, EXOSC3, MIR3159	31264, 1, -4387	downstream, in gene, upstream	ActReg chr9 #9534	1	1
9535	9	37,800,257	37,801,592	1,335	2	10.244	15.317	23	31	1	1	2	MIR3159, DCAF10	11471, 134	in gene, in gene	ActReg chr9 #9535	1	1
9536	9	38,069,387	38,070,117	730	1	10.435	11.826	16	22	2	1	1	SHB	-542	upstream	ActReg chr9 #9536	0	1
9537	9	38,620,363	38,621,225	862	2	12.815	14.704	21	26	1	2	2	ANKRD18A, C9orf122	-434, -291	upstream, upstream	ActReg chr9 #9537	1	1
9538	9	44,227,312	44,227,740	428	1	7.231	10.692	11	18	1	0	0				ActReg chr9 #9538	0	1
9539	9	45,729,021	45,729,532	511	1	3.938	9.938	6	17	0	2	2	FAM27A, FAM27E2	2247, -4312	downstream, upstream	ActReg chr9 #9539	0	1
9540	9	66,457,909	66,458,751	842	1	16.115	17.538	29	36	1	2	2	LOC100287759, LOC100505956	-316, 1041	upstream, in gene	ActReg chr9 #9540	0	1
9541	9	68,454,940	68,456,041	1,101	1	9.314	13.771	19	25	1	1	1	LOC642236	-1,115	upstream	ActReg chr9 #9541	0	1
9542	9	71,394,472	71,395,627	1,155	2	11.056	9.667	14	17	1	1	2	PIP5K1B, FAM122A	74433, 85	in gene, in gene	ActReg chr9 #9542	1	1
9543	9	71,795,356	71,796,058	702	1	7.045	11.136	10	22	0	0	1	TJP2	59,483	in gene	ActReg chr9 #9543	0	1
9544	9	72,400,331	72,401,184	853	2	9.444	13.667	24	29	0	0	0				ActReg chr9 #9544	1	1
9545	9	72,627,896	72,628,523	627	1	4	11.1	7	20	0	0	0				ActReg chr9 #9545	0	1
9546	9	72,699,950	72,700,679	729	2	14.318	14.696	31	27	0	0	1	MAMDC2	41,817	in gene	ActReg chr9 #9546	1	1
9547	9	72,873,524	72,874,558	1,034	1	9.875	11.531	15	16	1	2	2	LOC100507299, SMC5	-259, 163	upstream, in gene	ActReg chr9 #9547	0	1
9548	9	73,004,384	73,005,148	764	1	8.417	12.833	11	20	0	0	1	KLF9	24,807	in gene	ActReg chr9 #9548	0	1
9549	9	73,028,624	73,029,601	977	2	17.645	14.903	40	31	1	1	1	KLF9	461	in gene	ActReg chr9 #9549	1	1
9550	9	73,033,273	73,034,800	1,527	2	14.896	13.979	28	26	1	1	1	KLF9	-4,463	upstream	ActReg chr9 #9550	1	1
9551	9	73,215,983	73,216,829	846	1	11.962	10.962	18	15	0	0	1	TRPM3	520,108	in gene	ActReg chr9 #9551	1	0
9552	9	73,517,708	73,518,199	491	1	8.333	10.533	11	15	0	0	1	TRPM3	218,561	in gene	ActReg chr9 #9552	0	1
9553	9	74,060,985	74,062,320	1,335	2	15.738	20.476	34	42	1	0	0				ActReg chr9 #9553	1	1
9554	9	74,121,659	74,122,263	604	2	10.158	11.579	21	25	0	0	0				ActReg chr9 #9554	1	1
9555	9	74,383,921	74,384,557	636	1	9.6	11.6	14	16	1	1	1	TMEM2	-439	upstream	ActReg chr9 #9555	0	1
9556	9	74,397,697	74,398,592	895	1	11.75	15.536	22	32	0	0	0				ActReg chr9 #9556	0	1
9557	9	74,525,628	74,526,250	622	1	11.35	12.5	16	20	1	2	2	FAM108B1, C9orf85	209, -484	in gene, upstream	ActReg chr9 #9557	0	1
9558	9	74,602,291	74,603,299	1,008	2	8.875	10.312	17	21	0	0	0				ActReg chr9 #9558	1	1
9559	9	74,763,991	74,764,951	960	1	10.7	11.933	19	17	1	1	1	GDA	178	in gene	ActReg chr9 #9559	0	1
9560	9	74,979,724	74,980,833	1,109	2	9.229	11.286	22	19	1	1	1	ZFAND5	-115	upstream	ActReg chr9 #9560	1	1
9561	9	75,172,359	75,172,905	546	1	10.235	8.706	16	12	0	0	1	TMC1	35,915	in gene	ActReg chr9 #9561	1	0
9562	9	75,201,323	75,201,859	536	1	12.059	8.765	19	12	0	0	1	TMC1	64,874	in gene	ActReg chr9 #9562	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9563	9	75,748,771	75,749,342	571	1	9.824	10.882	16	18	0	0	0				ActReg chr9 #9563	0	1
9564	9	75,834,571	75,835,686	1,115	2	9.171	12.057	19	25	0	0	0				ActReg chr9 #9564	1	1
9565	9	76,358,599	76,359,061	462	1	7.143	10.857	12	14	0	0	0				ActReg chr9 #9565	0	1
9566	9	77,567,060	77,568,113	1,053	2	9.091	10.576	15	18	1	1	1	C9orf40	216	in gene	ActReg chr9 #9566	1	1
9567	9	77,642,682	77,643,552	870	1	9.964	11.929	15	17	1	1	1	C9orf41	193	in gene	ActReg chr9 #9567	0	1
9568	9	77,702,454	77,703,121	667	1	11.476	7.095	15	11	1	2	2	C9orf95, OSTF1	346, -611	in gene, upstream	ActReg chr9 #9568	1	0
9569	9	78,505,216	78,506,362	1,146	1	8.944	11.472	16	17	2	1	1	PCSK5	229	in gene	ActReg chr9 #9569	0	1
9570	9	78,608,120	78,608,888	768	1	8.5	11.667	17	18	0	0	1	PCSK5	102,944	in gene	ActReg chr9 #9570	0	1
9571	9	78,830,857	78,831,614	757	2	10.217	14.696	20	28	0	0	1	PCSK5	325,675	in gene	ActReg chr9 #9571	1	1
9572	9	79,008,456	79,009,636	1,180	2	10.73	11.324	17	21	1	1	1	RFK	398	in gene	ActReg chr9 #9572	1	1
9573	9	79,191,102	79,191,610	508	1	9.5	7	14	13	0	0	0				ActReg chr9 #9573	1	0
9574	9	79,206,108	79,206,790	682	1	6.455	11.818	13	17	0	0	0				ActReg chr9 #9574	0	1
9575	9	79,302,828	79,303,572	744	1	8.217	13.826	16	22	0	0	1	PRUNE2	217,803	in gene	ActReg chr9 #9575	0	1
9576	9	79,432,993	79,433,578	585	2	11	10.111	18	16	0	0	1	PRUNE2	87,718	in gene	ActReg chr9 #9576	1	1
9577	9	79,520,874	79,521,868	994	2	15.581	17.806	32	37	1	1	1	PRUNE2	-368	upstream	ActReg chr9 #9577	1	1
9578	9	79,792,165	79,792,875	710	1	6.955	11.864	11	18	1	2	2	RP11-470P4.2, VPS13A	313, 159	in gene, in gene	ActReg chr9 #9578	0	1
9579	9	80,190,540	80,191,177	637	2	8.95	13.05	17	24	0	0	1	GNA14	72,374	in gene	ActReg chr9 #9579	1	1
9580	9	80,911,602	80,912,933	1,331	1	8.119	12.429	16	19	1	1	1	PSAT1	208	in gene	ActReg chr9 #9580	0	1
9581	9	81,167,920	81,168,734	814	1	4.92	12.6	7	19	0	0	0				ActReg chr9 #9581	0	1
9582	9	81,400,640	81,401,392	752	1	5.625	11	11	20	0	0	0				ActReg chr9 #9582	0	1
9583	9	82,186,205	82,187,085	880	1	10.929	9.714	19	19	1	1	1	TLE4	-233	upstream	ActReg chr9 #9583	1	0
9584	9	85,425,918	85,426,334	416	1	10.538	6.538	14	11	0	0	0				ActReg chr9 #9584	1	0
9585	9	85,914,318	85,915,003	685	2	11.476	10.619	22	21	0	0	1	FRMD3	238,688	in gene	ActReg chr9 #9585	1	1
9586	9	86,136,223	86,136,944	721	1	8.087	10.957	16	19	0	0	1	FRMD3	16,765	in gene	ActReg chr9 #9586	0	1
9587	9	86,152,672	86,153,962	1,290	2	8.756	11.195	14	24	1	1	1	FRMD3	31	in gene	ActReg chr9 #9587	1	1
9588	9	86,571,306	86,572,043	737	1	10.348	7.565	14	12	1	1	1	C9orf64	-11	upstream	ActReg chr9 #9588	1	0
9589	9	86,594,388	86,595,361	973	1	10.194	13.419	14	20	1	2	3	HNRNPK, MIR7-1, RMI1	695, -10102, -763	in gene, upstream, upstream	ActReg chr9 #9589	0	1
9590	9	88,721,787	88,722,292	505	1	12.5	9.938	25	14	0	1	1	GOLM1	-6,923	upstream	ActReg chr9 #9590	1	0
9591	9	88,800,059	88,801,110	1,051	1	11.061	7.848	15	13	0	0	0				ActReg chr9 #9591	1	0
9592	9	88,896,673	88,897,451	778	1	10.708	10.708	17	19	1	1	2	ISCA1, ZCCHC6	428, 72340	in gene, downstream	ActReg chr9 #9592	0	1
9593	9	88,968,678	88,969,765	1,087	2	15.794	12.853	32	21	1	1	1	ZCCHC6	181	in gene	ActReg chr9 #9593	1	1
9594	9	89,381,618	89,382,306	688	1	6.273	11.773	9	21	0	0	0				ActReg chr9 #9594	0	1
9595	9	89,563,175	89,563,887	712	1	8.909	11.864	17	24	1	2	2	GAS1, LOC100506834	-1427, 730	upstream, in gene	ActReg chr9 #9595	0	1
9596	9	89,813,522	89,814,002	480	1	11	6	15	9	0	0	0				ActReg chr9 #9596	1	0
9597	9	90,328,167	90,328,964	797	2	9.16	12.68	22	22	0	0	1	DAPK1	215,809	downstream	ActReg chr9 #9597	1	1
9598	9	90,340,437	90,341,783	1,346	1	9.048	11.762	19	18	1	1	1	CTSL1	136	in gene	ActReg chr9 #9598	0	1
9599	9	90,407,489	90,408,589	1,100	2	9.529	13.823	19	28	0	0	0				ActReg chr9 #9599	1	1
9600	9	90,589,182	90,589,932	750	1	12.042	11.667	20	17	1	1	1	CDK20	138	in gene	ActReg chr9 #9600	0	1
9601	9	90,691,200	90,691,676	476	1	5.4	10.133	9	15	1	0	0				ActReg chr9 #9601	0	1
9602	9	91,794,646	91,795,561	915	2	10.552	11.759	17	16	0	1	1	SHC3	-1,421	upstream	ActReg chr9 #9602	1	1
9603	9	91,932,906	91,934,030	1,124	2	8.943	13.457	19	23	1	1	3	CKS2, MIR3153, SECISBP2	7355, 6328, 56	downstream, downstream, in gene	ActReg chr9 #9603	1	1
9604	9	92,134,116	92,134,753	637	1	7.85	11.35	12	19	0	0	0				ActReg chr9 #9604	0	1
9605	9	93,926,830	93,927,482	652	1	9.4	10.95	14	20	0	1	1	LOC100128909	-1,616	upstream	ActReg chr9 #9605	0	1
9606	9	93,959,394	93,960,447	1,053	1	10.969	11.188	23	20	0	0	1	LOC100507137	12,669	downstream	ActReg chr9 #9606	0	1
9607	9	94,123,407	94,124,256	849	1	5.741	11.333	9	18	1	1	1	AUH	375	in gene	ActReg chr9 #9607	0	1
9608	9	94,181,430	94,182,127	697	2	11.227	10.136	20	17	0	0	1	NFIL3	4,366	in gene	ActReg chr9 #9608	1	1
9609	9	94,186,292	94,187,133	841	1	6.885	12.577	11	21	1	1	1	NFIL3	-568	upstream	ActReg chr9 #9609	0	1
9610	9	94,877,312	94,878,040	728	2	11.957	13.522	23	27	1	1	1	SPTLC1	14	in gene	ActReg chr9 #9610	1	1
9611	9	94,909,349	94,910,161	812	1	11.64	8.24	15	12	0	0	2	LOC100507197, C9orf44	6034, 6006	in gene, in gene	ActReg chr9 #9611	1	0
9612	9	95,055,712	95,056,454	742	2	13.25	12.917	29	27	1	2	3	IARS, SNORA84, NOL8	-45, -1208, 31793	upstream, upstream, downstream	ActReg chr9 #9612	1	1
9613	9	95,087,258	95,088,766	1,508	2	23.255	31.83	71	107	1	2	2	NOL8, CENPP	-136, 271	upstream, in gene	ActReg chr9 #9613	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9614	9	95,287,378	95,287,989	611	1	10.21	8.789	17	13	0	0	2	CENPP, ECM2	199942, 10569	in gene, in gene	ActReg chr9 #9614	1	0
9615	9	95,432,037	95,432,988	951	1	9.759	14.069	16	22	1	1	1	IPPK	35	in gene	ActReg chr9 #9615	0	1
9616	9	95,527,000	95,528,061	1,061	2	12.242	12.454	19	25	1	1	1	BICD2	-447	upstream	ActReg chr9 #9616	1	1
9617	9	95,858,441	95,859,273	832	1	8.077	10.5	12	15	1	1	1	C9orf89	407	in gene	ActReg chr9 #9617	0	1
9618	9	95,859,634	95,860,388	754	1	6.083	11.333	11	16	0	1	1	C9orf89	1,561	in gene	ActReg chr9 #9618	0	1
9619	9	95,860,411	95,861,314	903	2	11.069	9.759	20	16	0	1	1	C9orf89	2,412	in gene	ActReg chr9 #9619	1	1
9620	9	96,328,654	96,329,188	534	1	7.647	9.706	10	14	1	0	2	FAM120A, PHF2	114748, -9988	downstream, upstream	ActReg chr9 #9620	0	1
9621	9	96,792,575	96,793,404	829	1	9.885	9.654	14	15	1	1	1	PTPDC1	-87	upstream	ActReg chr9 #9621	1	0
9622	9	96,928,134	96,928,891	757	1	6.545	10.522	14	16	1	0	2	MIRLET7A1, MIRLET7F1	-9727, -10117	upstream, upstream	ActReg chr9 #9622	0	1
9623	9	97,021,263	97,021,994	731	1	7.043	13.435	14	23	1	1	1	ZNF169	50	in gene	ActReg chr9 #9623	0	1
9624	9	97,488,633	97,489,347	714	1	10.391	12	15	22	1	1	1	C9orf3	104	in gene	ActReg chr9 #9624	0	1
9625	9	97,545,268	97,546,101	833	2	13.615	21.538	38	52	0	0	1	C9orf3	56,798	in gene	ActReg chr9 #9625	1	1
9626	9	97,691,331	97,692,193	862	1	7.444	12	13	17	0	0	1	C9orf3	202,876	in gene	ActReg chr9 #9626	0	1
9627	9	98,269,148	98,270,496	1,348	2	12.302	12.698	25	21	1	0	1	PTCH1	9,425	in gene	ActReg chr9 #9627	1	1
9628	9	98,272,727	98,273,324	597	1	4.947	9.632	10	17	1	0	1	PTCH1	6,222	in gene	ActReg chr9 #9628	0	1
9629	9	98,637,093	98,638,621	1,528	2	9.723	12.064	26	24	1	2	2	C9orf130, C9orf102	402, -43	in gene, upstream	ActReg chr9 #9629	1	1
9630	9	98,810,998	98,812,102	1,104	2	8.743	9.743	18	18	0	0	0				ActReg chr9 #9630	1	1
9631	9	99,019,006	99,019,434	428	1	9.857	9.071	18	13	0	0	1	HSD17B3	45,214	in gene	ActReg chr9 #9631	1	0
9632	9	99,179,306	99,179,857	551	1	11.294	7	21	9	1	1	1	ZNF367	1,088	in gene	ActReg chr9 #9632	1	0
9633	9	99,180,243	99,180,936	693	2	11.682	11.046	16	19	1	1	1	ZNF367	80	in gene	ActReg chr9 #9633	1	1
9634	9	99,416,818	99,417,403	585	1	8.056	11.389	12	16	1	1	1	C9orf21	489	in gene	ActReg chr9 #9634	0	1
9635	9	100,149,265	100,149,842	577	1	9.056	15.889	15	26	0	0	3	KIAA1529, C9orf174, hCG_2045089	148845, 79643, 9420	downstream, downstream, downstream	ActReg chr9 #9635	0	1
9636	9	100,173,822	100,174,569	747	2	14.625	12.167	34	30	1	1	1	TDRD7	-107	upstream	ActReg chr9 #9636	1	1
9637	9	100,287,763	100,288,597	834	1	6.692	9.154	12	13	0	0	1	TMOD1	24,718	in gene	ActReg chr9 #9637	0	1
9638	9	100,395,281	100,396,428	1,147	1	10.806	12.556	16	18	1	2	2	TSTD2, NCBP1	108, 149	in gene, in gene	ActReg chr9 #9638	0	1
9639	9	100,458,991	100,459,792	801	2	10.2	11.76	17	19	1	1	1	XPA	300	in gene	ActReg chr9 #9639	1	1
9640	9	100,638,976	100,639,581	605	1	10.105	12	14	21	0	0	0				ActReg chr9 #9640	0	1
9641	9	100,684,202	100,685,154	952	2	17.333	19.933	36	45	1	1	2	C9orf156, HEMGN	174, 22456	in gene, downstream	ActReg chr9 #9641	1	1
9642	9	100,743,222	100,743,855	633	1	9	12.15	14	21	0	1	1	ANP32B	-1,951	upstream	ActReg chr9 #9642	0	1
9643	9	100,745,134	100,746,277	1,143	2	9.361	10.639	15	20	1	1	1	ANP32B	216	in gene	ActReg chr9 #9643	1	1
9644	9	100,746,931	100,747,337	406	1	9.769	10.692	13	17	1	1	1	ANP32B	1,645	in gene	ActReg chr9 #9644	0	1
9645	9	100,880,822	100,881,583	761	1	10.333	13	18	22	1	1	2	TRIM14, CORO2A	286, 73754	in gene, downstream	ActReg chr9 #9645	0	1
9646	9	100,955,128	100,955,889	761	1	7.667	10.708	12	16	1	1	2	CORO2A, TBC1D2	-552, 62495	upstream, downstream	ActReg chr9 #9646	0	1
9647	9	101,017,882	101,018,500	618	1	9.4	13	17	26	1	1	1	TBC1D2	-188	upstream	ActReg chr9 #9647	0	1
9648	9	101,337,830	101,338,500	670	1	10.333	11.524	19	18	0	0	1	GABBR2	133,314	in gene	ActReg chr9 #9648	0	1
9649	9	101,472,317	101,473,307	990	1	7.161	13.839	14	24	1	1	1	GABBR2	-1,333	upstream	ActReg chr9 #9649	0	1
9650	9	101,983,593	101,984,676	1,083	2	11.765	14.441	18	33	1	2	2	ALG2, SEC61B	112, -436	in gene, upstream	ActReg chr9 #9650	1	1
9651	9	102,195,696	102,196,274	578	1	11.778	9	21	15	0	0	0				ActReg chr9 #9651	1	0
9652	9	102,318,975	102,319,736	761	1	6.542	10.542	10	16	0	0	0				ActReg chr9 #9652	0	1
9653	9	102,581,562	102,582,134	572	1	7.944	10.278	14	19	1	1	1	NR4A3	-2,289	upstream	ActReg chr9 #9653	0	1
9654	9	102,583,394	102,584,435	1,041	1	9	11.938	15	19	1	1	1	NR4A3	-223	upstream	ActReg chr9 #9654	0	1
9655	9	102,635,774	102,636,485	711	2	10.522	11.478	17	18	0	0	1	NR4A3	51,992	downstream	ActReg chr9 #9655	1	1
9656	9	102,668,905	102,669,537	632	1	10.35	9.35	15	12	1	1	1	STX17	306	in gene	ActReg chr9 #9656	1	0
9657	9	102,860,777	102,862,132	1,355	2	12.143	14.405	25	28	1	2	2	ERP44, INVS	-124, -57	upstream, upstream	ActReg chr9 #9657	1	1
9658	9	103,114,638	103,115,499	861	1	8.704	10.963	14	15	1	2	2	TEX10, LOC100507449	191, -250	in gene, upstream	ActReg chr9 #9658	0	1
9659	9	103,191,448	103,192,090	642	1	8.35	10.8	11	14	0	1	1	C9orf30	2,127	in gene	ActReg chr9 #9659	0	1
9660	9	104,160,562	104,161,246	684	1	9.619	13.524	12	21	1	2	2	MRPL50, ZNF189	15, -259	in gene, upstream	ActReg chr9 #9660	0	1
9661	9	104,248,495	104,249,245	750	1	9.87	11.348	19	15	1	1	2	LOC100507465, C9orf125	17209, 605	downstream, in gene	ActReg chr9 #9661	0	1
9662	9	104,299,016	104,299,535	519	1	6.938	11.938	13	20	0	0	1	RNF20	3,142	in gene	ActReg chr9 #9662	0	1
9663	9	104,390,321	104,390,868	547	2	9	10	17	17	0	0	1	GRIN3A	110,268	in gene	ActReg chr9 #9663	1	1
9664	9	104,498,933	104,499,845	912	2	8.586	13.862	17	29	1	1	1	GRIN3A	1,473	in gene	ActReg chr9 #9664	1	1
9665	9	104,757,461	104,758,107	646	2	10.889	12.65	20	25	0	0	0				ActReg chr9 #9665	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9666	9	105,241,479	105,241,991	512	1	7	10.562	13	16	0	0	0				ActReg chr9 #9666	0	1
9667	9	106,856,021	106,856,835	814	2	9.654	12.577	15	23	1	1	1	SMC2	-113	upstream	ActReg chr9 #9667	1	1
9668	9	106,994,788	106,995,331	543	1	6.353	10.882	9	21	0	0	0				ActReg chr9 #9668	0	1
9669	9	107,509,535	107,510,186	651	1	6.19	10.809	11	17	1	1	1	NIPSNAP3A	-109	upstream	ActReg chr9 #9669	0	1
9670	9	107,730,196	107,731,054	858	2	15.32	16.778	36	41	1	0	0				ActReg chr9 #9670	1	1
9671	9	108,006,354	108,007,080	726	2	8.478	12.522	14	24	1	1	1	SLC44A1	-212	upstream	ActReg chr9 #9671	1	1
9672	9	108,209,685	108,210,741	1,056	2	8.879	11.364	17	19	1	1	1	FSD1L	-102	upstream	ActReg chr9 #9672	1	1
9673	9	108,874,910	108,875,310	400	1	10.692	4.833	18	9	0	0	0				ActReg chr9 #9673	1	0
9674	9	109,182,735	109,183,438	703	1	3.5	12.318	7	22	0	0	0				ActReg chr9 #9674	0	1
9675	9	109,801,684	109,802,295	611	1	12.053	5.579	20	11	0	0	0				ActReg chr9 #9675	1	0
9676	9	109,931,982	109,932,764	782	1	9.583	12.208	15	17	0	0	0				ActReg chr9 #9676	0	1
9677	9	110,045,189	110,045,855	666	1	8.9	13.7	13	23	1	1	1	RAD23B	-22	upstream	ActReg chr9 #9677	0	1
9678	9	110,045,896	110,046,498	602	1	7.316	11.105	12	19	1	1	1	RAD23B	653	in gene	ActReg chr9 #9678	0	1
9679	9	110,250,834	110,251,352	518	1	11.812	9.75	14	12	1	1	1	KLF4	954	in gene	ActReg chr9 #9679	1	0
9680	9	110,803,677	110,804,484	807	1	9.038	12.115	11	20	0	0	0				ActReg chr9 #9680	0	1
9681	9	110,811,383	110,812,018	635	1	7.6	10.5	11	18	0	0	0				ActReg chr9 #9681	0	1
9682	9	110,819,581	110,820,196	615	1	10.15	9.9	19	14	0	0	0				ActReg chr9 #9682	1	0
9683	9	110,918,703	110,919,208	505	1	9.75	10	13	15	0	0	0				ActReg chr9 #9683	0	1
9684	9	111,207,810	111,208,371	561	1	11.059	9.118	16	11	0	0	0				ActReg chr9 #9684	1	0
9685	9	111,305,475	111,306,261	786	1	7.292	11.417	11	17	0	0	0				ActReg chr9 #9685	0	1
9686	9	111,313,326	111,314,185	859	1	9.481	12.185	14	18	0	0	0				ActReg chr9 #9686	0	1
9687	9	111,342,034	111,342,934	900	2	14.536	12.607	30	22	0	0	0				ActReg chr9 #9687	1	1
9688	9	111,597,524	111,598,655	1,131	2	9.943	12.286	22	20	0	0	0				ActReg chr9 #9688	1	1
9689	9	111,647,787	111,648,614	827	2	12	12.5	19	26	0	0	1	IKBKAP	48,408	in gene	ActReg chr9 #9689	1	1
9690	9	111,696,005	111,697,034	1,029	1	9.031	10.875	17	18	1	2	3	IKBKAP, C9orf6, CTNNAL1	89, -154, 79245	in gene, upstream, downstream	ActReg chr9 #9690	0	1
9691	9	111,881,411	111,882,642	1,231	1	7.526	13	12	28	1	1	1	C9orf5	199	in gene	ActReg chr9 #9691	0	1
9692	9	112,006,829	112,007,350	521	1	4.875	9.812	8	16	0	0	1	EPB41L4B	75,932	in gene	ActReg chr9 #9692	0	1
9693	9	112,209,390	112,210,711	1,321	2	9.927	12.024	21	21	0	0	1	PTPN3	50,543	in gene	ActReg chr9 #9693	1	1
9694	9	112,231,980	112,232,868	888	2	10.393	10.964	17	16	0	0	1	PTPN3	28,169	in gene	ActReg chr9 #9694	1	1
9695	9	112,528,247	112,529,168	921	2	12.345	13.621	27	24	0	0	1	PALM2	125,639	in gene	ActReg chr9 #9695	1	1
9696	9	112,578,469	112,579,409	940	1	13.897	10.414	22	21	0	0	2	PALM2, PALM2-AKAP2	175871, 36362	in gene, in gene	ActReg chr9 #9696	1	0
9697	9	113,017,699	113,018,894	1,195	2	9.865	11.622	20	17	1	1	1	TXN	482	in gene	ActReg chr9 #9697	1	1
9698	9	113,341,203	113,341,838	635	2	11	14.15	20	26	1	1	1	SVEP1	640	in gene	ActReg chr9 #9698	1	1
9699	9	113,507,200	113,507,755	555	1	11.056	5.444	18	9	0	0	1	MUSK	76,426	in gene	ActReg chr9 #9699	1	0
9700	9	114,393,032	114,394,367	1,335	2	11.878	11.561	32	17	1	2	2	DNAJC25, DNAJC25-GNG10	67, 33	in gene, in gene	ActReg chr9 #9700	1	1
9701	9	114,505,470	114,505,976	506	1	7.438	10.938	13	20	0	0	1	C9orf84	40,056	in gene	ActReg chr9 #9701	0	1
9702	9	114,658,663	114,659,017	354	1	11.454	8.636	18	13	1	1	1	UGCG	-366	upstream	ActReg chr9 #9702	1	0
9703	9	115,141,553	115,142,416	863	1	7	10.704	11	18	1	1	1	HSDL2	-367	upstream	ActReg chr9 #9703	0	1
9704	9	115,479,968	115,480,599	631	1	9.35	10.85	13	17	1	1	1	C9orf80	104	in gene	ActReg chr9 #9704	0	1
9705	9	115,512,461	115,513,034	573	1	11	9.167	16	15	1	1	1	SNX30	-387	upstream	ActReg chr9 #9705	1	0
9706	9	115,893,708	115,894,721	1,013	2	18	16.219	37	39	0	0	0				ActReg chr9 #9706	1	1
9707	9	115,983,198	115,983,884	686	1	7.091	10.818	11	21	1	2	2	FKBP15, SLC31A1	100, -267	in gene, upstream	ActReg chr9 #9707	0	1
9708	9	116,037,460	116,038,218	758	1	13.375	13.458	23	22	1	2	2	CDC26, PRPF4	30, -135	in gene, upstream	ActReg chr9 #9708	0	1
9709	9	116,102,207	116,102,995	788	1	8.84	12.36	16	23	1	1	2	WDR31, BSPRY	19, -9211	in gene, upstream	ActReg chr9 #9709	0	1
9710	9	116,172,282	116,173,245	963	2	14.267	16.433	29	33	1	2	3	ALAD, POLE3, C9orf43	-9145, 266, 259	upstream, in gene, upstream	ActReg chr9 #9710	1	1
9711	9	116,457,921	116,458,867	946	1	10.517	14.207	20	22	0	0	0				ActReg chr9 #9711	0	1
9712	9	116,939,642	116,940,436	794	1	7.24	9.72	13	14	0	0	1	COL27A1	21,808	in gene	ActReg chr9 #9712	0	1
9713	9	116,985,632	116,986,612	980	1	9.742	5.548	17	8	0	0	1	COL27A1	67,891	in gene	ActReg chr9 #9713	1	0
9714	9	117,314,003	117,314,673	670	1	11.333	9.19	22	12	0	0	0				ActReg chr9 #9714	1	0
9715	9	117,655,966	117,656,576	610	1	8.5	10.85	11	18	0	1	2	LOC100505521, TNFSF8	-3276, 36499	upstream, downstream	ActReg chr9 #9715	0	1
9716	9	117,871,220	117,872,416	1,196	2	17.947	20.605	47	51	0	0	1	TNC	8,668	in gene	ActReg chr9 #9716	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9717	9	117,880,006	117,880,813	807	1	9.04	12.04	14	18	0	1	1	TNC	77	in gene	ActReg chr9 #9717	0	1
9718	9	118,024,583	118,025,165	582	1	6.944	11.056	11	19	0	0	1	1-Dec	120,777	in gene	ActReg chr9 #9718	0	1
9719	9	118,135,296	118,136,132	836	2	11.222	8.68	19	19	0	0	1	1-Dec	231,617	in gene	ActReg chr9 #9719	1	1
9720	9	118,453,056	118,453,894	838	1	8.407	10.889	16	18	0	0	0				ActReg chr9 #9720	0	1
9721	9	118,706,265	118,707,436	1,171	2	9.973	11.73	19	19	0	0	0				ActReg chr9 #9721	1	1
9722	9	118,863,414	118,864,249	835	1	11.538	6.885	17	10	0	0	0				ActReg chr9 #9722	1	0
9723	9	119,459,922	119,461,029	1,107	1	8.4	10.4	13	15	0	0	2	ASTN2, TRIM32	716842, 10894	in gene, in gene	ActReg chr9 #9723	0	1
9724	9	119,568,324	119,568,903	579	2	10.611	8.778	17	16	0	0	1	ASTN2	608,704	in gene	ActReg chr9 #9724	1	1
9725	9	120,434,573	120,435,164	591	1	9.833	7.611	18	12	0	0	0				ActReg chr9 #9725	1	0
9726	9	120,465,707	120,466,182	475	1	10.533	8.133	17	10	0	1	1	TLR4	-516	upstream	ActReg chr9 #9726	1	0
9727	9	120,534,962	120,535,647	685	1	11.048	7.429	16	15	0	0	0				ActReg chr9 #9727	1	0
9728	9	120,821,558	120,822,255	697	2	13.546	12.727	26	29	0	0	0				ActReg chr9 #9728	1	1
9729	9	122,132,977	122,133,533	556	1	6.353	9.647	9	14	0	1	1	DBC1	-1,516	upstream	ActReg chr9 #9729	0	1
9730	9	123,164,404	123,166,346	1,942	2	16.607	20.344	44	49	0	0	1	CDK5RAP2	177,062	in gene	ActReg chr9 #9730	1	1
9731	9	123,604,836	123,605,821	985	2	10.567	10.267	18	18	1	2	2	PSMD5, LOC253039	-122, 8	upstream, in gene	ActReg chr9 #9731	1	1
9732	9	123,638,012	123,639,139	1,127	2	9.611	10.583	15	19	1	1	1	PHF19	1,031	in gene	ActReg chr9 #9732	1	1
9733	9	123,639,799	123,640,566	767	1	8.083	11.083	12	18	1	1	1	PHF19	-576	upstream	ActReg chr9 #9733	0	1
9734	9	123,675,322	123,676,972	1,650	2	9.885	12.808	26	27	0	0	1	TRAF1	15,304	in gene	ActReg chr9 #9734	1	1
9735	9	123,681,479	123,682,113	634	2	12.05	12.15	20	18	0	0	1	TRAF1	9,655	in gene	ActReg chr9 #9735	1	1
9736	9	123,712,823	123,713,425	602	1	6.316	12.316	10	17	0	0	1	C5	99,430	downstream	ActReg chr9 #9736	0	1
9737	9	123,837,174	123,837,807	633	1	7.95	11.9	12	17	1	0	0				ActReg chr9 #9737	0	1
9738	9	123,963,936	123,964,845	909	1	13.897	11.759	24	18	1	1	1	RAB14	-25	upstream	ActReg chr9 #9738	1	0
9739	9	123,996,354	123,997,466	1,112	2	9.765	12.441	16	17	0	0	0				ActReg chr9 #9739	1	1
9740	9	124,009,263	124,009,994	731	1	11.522	9.348	18	14	0	0	0				ActReg chr9 #9740	1	0
9741	9	124,040,715	124,041,474	759	1	11.042	10.792	18	15	0	0	2	GSN, LOC100128064	10714, 8025	in gene, downstream	ActReg chr9 #9741	1	0
9742	9	124,044,200	124,045,427	1,227	1	7.658	11.263	14	18	0	0	2	GSN, LOC100128064	14433, 4306	in gene, in gene	ActReg chr9 #9742	0	1
9743	9	124,132,556	124,134,482	1,926	2	21.233	18.183	93	65	1	1	1	STOM	-974	upstream	ActReg chr9 #9743	1	1
9744	9	124,734,569	124,735,097	528	2	10.562	11.062	20	14	0	0	2	TTLL11, C9orf148	121052, -8835	in gene, upstream	ActReg chr9 #9744	1	1
9745	9	124,854,617	124,855,971	1,354	2	11.163	15.023	25	24	1	1	1	TTLL11	591	in gene	ActReg chr9 #9745	1	1
9746	9	125,164,627	125,165,318	691	2	10.273	9.227	19	18	0	0	1	PTGS1	31,743	downstream	ActReg chr9 #9746	1	1
9747	9	125,225,819	125,227,090	1,271	2	18.175	20.95	54	64	0	0	0				ActReg chr9 #9747	1	1
9748	9	125,667,466	125,668,115	649	2	9.35	11.2	17	17	1	1	2	RC3H2, ZBTB6	-228, 7819	upstream, downstream	ActReg chr9 #9748	1	1
9749	9	125,693,563	125,694,309	746	2	10.667	12.542	19	25	1	1	2	ZBTB26, RABGAP1	-157, -9352	upstream, upstream	ActReg chr9 #9749	1	1
9750	9	126,689,913	126,690,849	936	2	11.367	12	19	17	0	1	1	DENND1A	2,036	in gene	ActReg chr9 #9750	1	1
9751	9	126,816,833	126,817,564	731	1	8.045	13.273	17	26	0	0	0				ActReg chr9 #9751	0	1
9752	9	126,871,284	126,873,972	2,688	2	18.548	23.833	100	119	0	0	0				ActReg chr9 #9752	1	1
9753	9	126,911,904	126,912,789	885	1	6.964	13.179	18	22	0	0	0				ActReg chr9 #9753	0	1
9754	9	127,155,085	127,155,717	632	1	12	7.35	21	10	0	0	1	PSMB7	22,320	in gene	ActReg chr9 #9754	1	0
9755	9	127,177,143	127,178,176	1,033	2	9.909	10	19	18	1	1	1	PSMB7	62	in gene	ActReg chr9 #9755	1	1
9756	9	127,533,002	127,534,203	1,201	2	14.946	15.108	48	38	1	3	3	NR6A1, LOC100505607, OLFML2A	-26, 1200, -5835	upstream, in gene, upstream	ActReg chr9 #9756	1	1
9757	9	127,623,809	127,624,916	1,107	2	12.559	12.647	21	21	1	2	3	WDR38, RPL35, ARPC5L	8607, -122, 7122	downstream, upstream, upstream	ActReg chr9 #9757	1	1
9758	9	127,702,966	127,704,194	1,228	2	10.256	11.436	19	17	1	1	2	GOLGA1, SCAI	-194, 202258	upstream, downstream	ActReg chr9 #9758	1	1
9759	9	127,951,493	127,952,563	1,070	2	12.454	11.758	21	20	1	1	1	PPP6C	190	in gene	ActReg chr9 #9759	1	1
9760	9	128,003,009	128,003,810	801	1	10.08	13.04	16	21	1	1	2	RABEPK, HSPA5	40588, 252	downstream, in gene	ActReg chr9 #9760	0	1
9761	9	128,023,632	128,024,816	1,184	2	9.946	10.838	18	20	1	1	1	GAPVD1	113	in gene	ActReg chr9 #9761	1	1
9762	9	128,508,139	128,509,007	868	1	7.556	9.741	12	14	1	2	2	LOC51145, PBX3	252, -1044	in gene, upstream	ActReg chr9 #9762	0	1
9763	9	128,672,673	128,673,242	569	1	6.294	10.588	11	17	0	0	1	PBX3	163,340	in gene	ActReg chr9 #9763	0	1
9764	9	128,844,067	128,845,988	1,921	2	11.083	15.783	44	50	0	0	0				ActReg chr9 #9764	1	1
9765	9	128,870,263	128,871,573	1,310	2	15.463	18.146	40	50	0	0	0				ActReg chr9 #9765	1	1
9766	9	129,279,016	129,279,850	834	1	8	10.692	12	16	0	0	1	FAM125B	190,305	downstream	ActReg chr9 #9766	0	1
9767	9	129,811,359	129,811,912	553	1	7.722	12.444	12	25	0	0	1	RALGPS1	134,582	in gene	ActReg chr9 #9767	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9768	9	129,884,255	129,885,593	1,338	1	8.833	11.714	14	19	0	1	2	RALGPS1, ANGPTL2	207871, 129	in gene, in gene	ActReg chr9 #9768	0	1
9769	9	129,986,486	129,987,063	577	1	9.056	10.5	11	14	1	0	1	RALGPS1	309,721	downstream	ActReg chr9 #9769	0	1
9770	9	130,186,509	130,187,136	627	1	8.05	12.1	11	21	1	1	1	ZNF79	169	in gene	ActReg chr9 #9770	0	1
9771	9	130,321,044	130,321,834	790	1	5.28	11.64	10	20	0	1	2	FAM129B, LOC100506005	19829, -2498	in gene, upstream	ActReg chr9 #9771	0	1
9772	9	130,329,460	130,330,178	718	1	8.261	11.348	12	18	0	0	1	FAM129B	11,449	in gene	ActReg chr9 #9772	0	1
9773	9	130,477,533	130,478,337	804	1	10.962	8.038	16	12	1	2	3	C9orf117, PTRH1, TTC16	8664, 1, -423	downstream, in gene, upstream	ActReg chr9 #9773	1	0
9774	9	130,513,592	130,514,348	756	2	11.625	14.208	17	29	0	0	1	SH2D3C	27,078	in gene	ActReg chr9 #9774	1	1
9775	9	130,699,510	130,700,566	1,056	1	9	11.576	13	17	1	2	3	PIP5KL1, DPM2, FAM102A	-6962, 725, 42774	upstream, in gene, downstream	ActReg chr9 #9775	0	1
9776	9	130,829,084	130,830,084	1,000	1	8.5	11.438	13	16	1	2	2	NAIF1, SLC25A25	15, -895	in gene, upstream	ActReg chr9 #9776	0	1
9777	9	130,889,617	130,891,006	1,389	2	15.442	17.861	32	33	1	2	3	LOC100289019, PTGES2, LOC389791	-9298, 401, -497	upstream, in gene, upstream	ActReg chr9 #9777	1	1
9778	9	130,952,848	130,954,441	1,593	2	16.36	19.98	59	61	1	0	1	CIZ1	13,018	in gene	ActReg chr9 #9778	1	1
9779	9	130,954,921	130,955,842	921	2	12.379	10.207	18	23	1	0	2	CIZ1, DNM1	11281, -10262	in gene, upstream	ActReg chr9 #9779	1	1
9780	9	131,069,452	131,070,392	940	2	12.621	10.379	18	13	0	0	1	TRUB2	14,775	downstream	ActReg chr9 #9780	1	1
9781	9	131,084,425	131,085,524	1,099	2	15.559	16.529	32	37	1	2	2	TRUB2, COQ4	-277, 183	upstream, in gene	ActReg chr9 #9781	1	1
9782	9	131,182,261	131,182,886	625	1	11.75	11.7	14	17	1	1	2	LOC100506065, CERCAM	8719, -186	downstream, upstream	ActReg chr9 #9782	0	1
9783	9	131,314,778	131,315,459	681	1	9.091	11.136	13	17	1	1	1	SPTAN1	252	in gene	ActReg chr9 #9783	0	1
9784	9	131,533,952	131,534,839	887	2	10.5	10.25	17	22	1	1	1	ZER1	-197	upstream	ActReg chr9 #9784	1	1
9785	9	131,549,158	131,549,882	724	1	10.909	15.046	18	27	1	1	1	TBC1D13	10	in gene	ActReg chr9 #9785	0	1
9786	9	131,580,420	131,581,050	630	1	13.526	8.105	25	14	1	1	3	TBC1D13, ENDOG, C9orf114	31225, -44, 11350	downstream, upstream, downstream	ActReg chr9 #9786	1	0
9787	9	131,591,714	131,592,317	603	1	9.333	14.111	13	23	1	1	3	ENDOG, C9orf114, CCBL1	11236, 70, 52339	downstream, in gene, downstream	ActReg chr9 #9787	0	1
9788	9	131,643,716	131,644,615	899	2	21.357	20.214	48	44	1	2	2	CCBL1, LRRC8A	189, -226	in gene, upstream	ActReg chr9 #9788	1	1
9789	9	131,654,506	131,655,233	727	1	12.13	9.391	18	16	0	0	1	LRRC8A	10,478	in gene	ActReg chr9 #9789	1	0
9790	9	131,709,556	131,710,621	1,065	2	13.424	11.667	21	21	1	2	3	PHYHD1, DOLK, NUP188	26914, -76, 111	downstream, upstream, in gene	ActReg chr9 #9790	1	1
9791	9	131,798,359	131,799,373	1,014	1	8.531	12.531	18	21	1	1	2	SH3GLB2, FAM73B	-8287, -387	upstream, upstream	ActReg chr9 #9791	0	1
9792	9	131,842,803	131,843,734	931	1	7.655	11.69	10	17	1	1	2	FAM73B, DOLPP1	44015, -115	downstream, upstream	ActReg chr9 #9792	0	1
9793	9	131,935,617	131,936,839	1,222	1	10.026	12.605	23	19	1	0	1	IER5L	4,312	downstream	ActReg chr9 #9793	0	1
9794	9	131,964,806	131,965,532	726	1	7.182	12.773	11	19	1	0	0				ActReg chr9 #9794	0	1
9795	9	132,236,115	132,237,052	937	1	4.276	10.483	8	16	0	0	1	LOC100506190	-9,147	upstream	ActReg chr9 #9795	0	1
9796	9	132,251,627	132,252,989	1,362	1	8.524	11.595	18	19	0	1	2	LOC100506190, LOC100128077	6578, -452	in gene, upstream	ActReg chr9 #9796	0	1
9797	9	132,257,966	132,259,177	1,211	1	10.21	11.737	16	15	1	0	2	LOC100506190, LOC100128077	12841, 5811	in gene, downstream	ActReg chr9 #9797	0	1
9798	9	132,403,448	132,405,118	1,670	2	44.038	49.615	213	204	1	1	2	METTL11A, ASB6	15848, 161	downstream, in gene	ActReg chr9 #9798	1	1
9799	9	132,474,999	132,475,742	743	1	7.478	12.348	11	17	0	0	2	PRRX2, LOC100506231	47450, 5587	in gene, in gene	ActReg chr9 #9799	0	1
9800	9	132,539,188	132,539,929	741	2	11.957	13.913	19	25	0	0	0				ActReg chr9 #9800	1	1
9801	9	132,552,547	132,553,211	664	2	11.65	15.9	19	29	0	0	0				ActReg chr9 #9801	1	1
9802	9	132,565,285	132,565,731	446	1	6.214	11.357	10	20	1	1	2	TOR1B, TOR1A	76, 20933	in gene, downstream	ActReg chr9 #9802	0	1
9803	9	132,586,005	132,586,705	700	2	10.429	12.409	21	27	1	1	2	TOR1A, C9orf78	86, 11217	in gene, downstream	ActReg chr9 #9803	1	1
9804	9	133,060,531	133,061,876	1,345	2	13.381	16	29	40	0	0	1	LOC100289200	33,042	in gene	ActReg chr9 #9804	1	1
9805	9	133,641,318	133,641,923	605	1	11.684	9.105	19	15	0	0	1	ABL1	52,352	in gene	ActReg chr9 #9805	1	0
9806	9	133,709,976	133,710,625	649	1	5.81	11.048	12	17	1	0	1	ABL1	121,032	in gene	ActReg chr9 #9806	0	1
9807	9	134,000,622	134,001,466	844	2	16.692	15.615	29	32	1	1	2	AIF1L, NUP214	29181, 63	downstream, in gene	ActReg chr9 #9807	1	1
9808	9	134,248,394	134,249,323	929	2	10.552	12.379	17	20	1	0	0				ActReg chr9 #9808	1	1
9809	9	134,377,926	134,379,125	1,199	2	14.649	16.73	37	45	1	1	2	BAT2L1, POMT1	73048, 236	downstream, in gene	ActReg chr9 #9809	1	1
9810	9	134,649,088	134,650,607	1,519	2	9.688	13.021	22	27	0	0	0				ActReg chr9 #9810	1	1
9811	9	134,650,749	134,651,807	1,058	1	6.545	11.546	10	17	0	0	0				ActReg chr9 #9811	0	1
9812	9	134,651,816	134,652,457	641	1	8.15	13.2	14	23	0	0	0				ActReg chr9 #9812	0	1
9813	9	134,673,841	134,675,221	1,380	2	12	15.046	28	32	0	0	0				ActReg chr9 #9813	1	1
9814	9	134,835,581	134,836,963	1,382	1	7.818	10.636	15	17	0	0	1	MED27	118,981	in gene	ActReg chr9 #9814	0	1
9815	9	134,954,662	134,955,605	943	1	5.828	11	11	21	1	1	1	MED27	120	in gene	ActReg chr9 #9815	0	1
9816	9	134,989,187	134,990,212	1,025	2	10.844	14.656	29	29	0	0	0				ActReg chr9 #9816	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9817	9	135,229,917	135,230,522	605	1	13.105	8.263	20	13	1	1	1	SETX	153	in gene	ActReg chr9 #9817	1	0
9818	9	135,457,194	135,458,135	941	2	23.965	28.828	64	82	1	1	2	C9orf171, BARHL1	172053, -329	downstream, upstream	ActReg chr9 #9818	1	1
9819	9	135,544,883	135,546,195	1,312	1	9.463	12.756	13	19	1	2	2	DDX31, GTF3C4	249, -189	in gene, upstream	ActReg chr9 #9819	0	1
9820	9	135,906,099	135,906,753	654	1	11.762	7.905	21	15	1	1	1	GTF3C5	364	in gene	ActReg chr9 #9820	1	0
9821	9	136,202,600	136,203,509	909	2	26.179	29.036	80	86	1	1	2	SURF6, MED22	-7, 11918	upstream, downstream	ActReg chr9 #9821	1	1
9822	9	136,214,746	136,215,520	774	2	16.48	17.68	28	40	1	6	8	MED22, RPL7A, SNORD24, SNORD36B, SNORD36A, SNORD36C, SURF1, SURF2	-161, 64, -1118, -1816, -2178, -2568, 8228, 8288	upstream, in gene, upstream, upstream, upstream, upstream, downstream, upstream	ActReg chr9 #9822	1	1
9823	9	136,241,697	136,243,619	1,922	3	17.517	17.033	51	58	1	2	2	SURF4, C9orf96	312, -626	in gene, upstream	ActReg chr9 #9823	1	1
9824	9	136,282,899	136,283,716	817	2	11	14.577	20	29	1	1	2	REXO4, ADAMTS13	-143, 3848	upstream, in gene	ActReg chr9 #9824	1	1
9825	9	136,423,845	136,424,406	561	1	7.118	9.647	13	17	0	0	1	ADAMTSL2	26,839	in gene	ActReg chr9 #9825	0	1
9826	9	136,739,174	136,740,198	1,024	1	6.375	12.5	10	20	0	0	1	VAV2	117,760	in gene	ActReg chr9 #9826	0	1
9827	9	136,855,948	136,856,733	785	2	8.333	11.75	16	21	1	1	1	VAV2	1,106	in gene	ActReg chr9 #9827	1	1
9828	9	136,890,234	136,890,936	702	2	21.381	23.773	52	62	1	1	2	NCRNA00094, BRD3	24, 42556	in gene, downstream	ActReg chr9 #9828	1	1
9829	9	137,000,403	137,001,285	882	2	13.321	15.321	23	29	1	1	1	WDR5	-366	upstream	ActReg chr9 #9829	1	1
9830	9	137,029,376	137,030,784	1,408	2	12.511	12.333	22	22	1	1	2	WDR5, RNU6ATAC	28870, -394	downstream, upstream	ActReg chr9 #9830	1	1
9831	9	137,969,163	137,969,815	652	1	6.7	11.45	11	18	0	1	1	OLFM1	2,400	in gene	ActReg chr9 #9831	0	1
9832	9	137,982,251	137,982,942	691	1	8.857	12.381	16	22	0	0	1	OLFM1	15,507	in gene	ActReg chr9 #9832	0	1
9833	9	137,989,967	137,990,811	844	2	11.192	14.231	24	29	0	0	1	OLFM1	23,300	in gene	ActReg chr9 #9833	1	1
9834	9	138,048,204	138,049,016	812	2	13.44	16.12	28	32	0	0	0				ActReg chr9 #9834	1	1
9835	9	138,366,697	138,367,327	630	2	13.947	11.421	33	22	0	2	2	LOC100506599, KIAA0649	-2917, -4636	upstream, upstream	ActReg chr9 #9835	1	1
9836	9	138,391,364	138,393,484	2,120	2	30.515	38.667	125	149	1	2	2	C9orf116, MRPS2	-663, -59	upstream, upstream	ActReg chr9 #9836	1	1
9837	9	138,863,629	138,864,386	757	2	14.167	16.458	32	41	0	0	0				ActReg chr9 #9837	1	1
9838	9	139,001,312	139,002,348	1,036	1	7.455	12.485	13	21	0	0	2	LOC402382, C9orf69	13707, 8901	downstream, downstream	ActReg chr9 #9838	0	1
9839	9	139,006,387	139,007,068	681	1	6.714	11.857	11	17	0	1	2	C9orf69, LOC100129999	4004, -7640	in gene, upstream	ActReg chr9 #9839	0	1
9840	9	139,009,907	139,011,021	1,114	1	10.529	10.514	18	23	1	2	2	C9orf69, LOC100129999	267, -3903	in gene, upstream	ActReg chr9 #9840	0	1
9841	9	139,239,300	139,240,998	1,698	1	8.151	14.415	16	23	1	0	1	GPSM1	18,217	in gene	ActReg chr9 #9841	0	1
9842	9	139,294,423	139,295,233	810	1	9.192	12	14	18	1	1	3	SNAPC4, SDCCAG3, PMPCA	-1939, 10226, -10288	upstream, downstream, upstream	ActReg chr9 #9842	0	1
9843	9	139,333,423	139,334,735	1,312	2	11.171	14.244	20	24	1	1	2	INPP5E, SEC16A	177, 43428	in gene, downstream	ActReg chr9 #9843	1	1
9844	9	139,620,639	139,621,612	973	1	6.774	11	11	16	0	3	4	FAM69B, SNHG7, SNORA43, SNORA17	14101, 1511, -436, 206	downstream, in gene, upstream, downstream	ActReg chr9 #9844	0	1
9845	9	139,622,333	139,623,713	1,380	2	12.454	17.091	26	34	1	3	5	FAM69B, SNHG7, SNORA43, SNORA17, LCN10	15999, -387, -2334, -1692, 14388	downstream, upstream, upstream, upstream, downstream	ActReg chr9 #9845	1	1
9846	9	139,736,306	139,737,452	1,146	2	6.806	10.917	16	19	0	2	4	C9orf86, C9orf172, PHPT1, MAMDC4	34505, -1988, -6377, -9940	downstream, upstream, upstream, upstream	ActReg chr9 #9846	1	1
9847	9	139,742,029	139,742,853	824	2	11.577	12.462	19	21	1	2	4	C9orf86, C9orf172, PHPT1, MAMDC4	40067, 3574, -815, -4378	downstream, downstream, upstream, upstream	ActReg chr9 #9847	1	1
9848	9	139,743,414	139,744,122	708	2	17.227	13.727	33	24	1	2	4	C9orf86, C9orf172, PHPT1, MAMDC4	41394, 4901, 512, -3051	downstream, downstream, in gene, upstream	ActReg chr9 #9848	1	1
9849	9	139,760,677	139,761,009	332	1	9.2	14.4	14	21	1	1	2	MAMDC4, EDF1	14024, -105	downstream, upstream	ActReg chr9 #9849	0	1
9850	9	139,776,489	139,777,395	906	1	9.75	12.679	15	17	0	1	1	TRAF2	-4,023	upstream	ActReg chr9 #9850	0	1
9851	9	139,796,061	139,796,864	803	1	8.192	11.808	14	18	0	0	1	TRAF2	15,497	in gene	ActReg chr9 #9851	0	1
9852	9	139,838,819	139,839,546	727	2	13.046	11.591	27	23	1	3	3	FBXW5, C8G, LCN12	-9, -516, -7586	upstream, upstream, upstream	ActReg chr9 #9852	1	1
9853	9	139,844,339	139,845,079	740	1	7.522	11.652	11	20	1	2	3	FBXW5, C8G, LCN12	-5536, 5011, -2059	upstream, downstream, upstream	ActReg chr9 #9853	0	1
9854	9	139,922,918	139,924,340	1,422	1	7.659	12.023	13	19	1	2	4	ABCA2, C9orf139, FUT7, NPDC1	-255, 1713, 3663, 17047	upstream, in gene, downstream, downstream	ActReg chr9 #9854	0	1
9855	9	139,940,433	139,941,306	873	1	10.593	11.037	18	17	1	1	3	C9orf139, NPDC1, ENTPD2	18953, -193, 7636	downstream, upstream, downstream	ActReg chr9 #9855	0	1
9856	9	139,964,608	139,965,171	563	1	5.444	13.056	9	19	1	2	2	C9orf140, UAP1L1	139, -7064	in gene, upstream	ActReg chr9 #9856	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9857	9	140,082,558	140,083,891	1,333	2	15.262	15.476	46	29	1	2	3	ANAPC2, SSNA1, C9orf75	-167, 170, 11756	upstream, in gene, downstream	ActReg chr9 #9857	1	1
9858	9	140,134,596	140,135,909	1,313	2	9.683	12.805	20	23	1	1	5	SLC34A3, TUBB2C, FAM166A, LOC100129722, C9orf173	10043, -459, 6970, 12697, -10478	downstream, upstream, downstream, downstream, upstream	ActReg chr9 #9858	1	1
9859	9	140,148,988	140,149,786	798	1	11.84	8.64	17	15	1	3	4	FAM166A, LOC100129722, C9orf173, COBRA1	-7165, -1438, 3657, 372	upstream, upstream, downstream, upstream	ActReg chr9 #9859	1	0
9860	9	140,222,489	140,223,085	596	1	15.316	10	37	17	0	0	1	EXD3	94,927	in gene	ActReg chr9 #9860	1	0
9861	9	140,472,837	140,473,850	1,013	2	24.194	25.806	62	76	1	1	2	WDR85, ZMYND19	44, 11594	in gene, downstream	ActReg chr9 #9861	1	1
9862	9	140,778,255	140,780,942	2,687	1	13.774	17.048	38	45	0	0	2	LOC100133077, CACNA1B	7424, 7357	in gene, in gene	ActReg chr9 #9862	0	1
9863	9	140,784,544	140,785,841	1,297	2	12.39	16	28	37	0	1	2	LOC100133077, CACNA1B	1830, 12951	in gene, in gene	ActReg chr9 #9863	1	1
9864	X	3,615,757	3,616,325	568	1	4.667	10.444	9	16	0	0	1	PRKX	15,634	in gene	ActReg chrX #9864	0	1
9865	X	3,732,708	3,733,383	675	1	7.762	11.048	12	16	1	0	1	LOC389906	28,890	downstream	ActReg chrX #9865	0	1
9866	X	3,908,490	3,909,050	560	2	8.294	10.529	14	18	0	0	0				ActReg chrX #9866	1	1
9867	X	9,098,976	9,099,599	623	2	8.95	11.35	16	17	0	0	0				ActReg chrX #9867	1	1
9868	X	9,121,834	9,122,274	440	1	5.786	9.786	9	15	0	0	0				ActReg chrX #9868	0	1
9869	X	9,430,860	9,431,503	643	2	16.15	15.9	36	37	0	1	1	TBL1X	-154	upstream	ActReg chrX #9869	1	1
9870	X	10,602,673	10,603,112	439	1	11	5.143	16	8	0	0	1	MID1	248,917	in gene	ActReg chrX #9870	1	0
9871	X	11,775,773	11,776,175	402	1	6.273	9.308	10	12	1	1	1	MSL3	-304	upstream	ActReg chrX #9871	0	1
9872	X	12,083,196	12,083,883	687	2	15.046	15.864	36	35	0	0	0				ActReg chrX #9872	1	1
9873	X	12,566,506	12,567,324	818	2	7.6	14.68	14	28	0	0	1	FRMPD4	410,330	in gene	ActReg chrX #9873	1	1
9874	X	12,722,681	12,723,320	639	1	1.312	9.8	2	15	0	0	1	FRMPD4	566,415	in gene	ActReg chrX #9874	0	1
9875	X	12,738,899	12,739,839	940	2	11	18.517	28	41	0	0	1	FRMPD4	582,784	in gene	ActReg chrX #9875	1	1
9876	X	14,047,841	14,048,369	528	1	8.812	10.875	13	17	1	1	1	GEMIN8	-70	upstream	ActReg chrX #9876	0	1
9877	X	14,082,952	14,083,599	647	1	4.6	9.7	7	19	0	0	0				ActReg chrX #9877	0	1
9878	X	14,547,394	14,547,756	362	1	10.636	9.273	17	12	0	1	1	GLRA2	155	in gene	ActReg chrX #9878	1	0
9879	X	15,189,303	15,189,784	481	1	9.533	6.067	14	9	0	0	0				ActReg chrX #9879	1	0
9880	X	15,251,784	15,252,269	485	1	9.8	4.333	14	8	0	0	1	ASB9	36,563	downstream	ActReg chrX #9880	1	0
9881	X	15,692,758	15,693,737	979	2	9.933	10.29	14	17	1	0	1	TMEM27	-10,093	upstream	ActReg chrX #9881	1	1
9882	X	16,203,753	16,204,155	402	1	8.5	9.667	13	14	0	0	0				ActReg chrX #9882	0	1
9883	X	16,789,761	16,790,400	639	2	8.75	9.05	18	17	0	0	1	SYAP1	52,373	downstream	ActReg chrX #9883	1	1
9884	X	16,803,985	16,804,488	503	1	11.562	9.875	17	17	1	1	1	CXorf15	-319	upstream	ActReg chrX #9884	1	0
9885	X	19,002,742	19,003,083	341	1	8.364	10.273	11	13	1	1	2	PHKA2, GPR64	-432, 137843	upstream, downstream	ActReg chrX #9885	0	1
9886	X	20,532,365	20,533,104	739	2	10.261	13	22	27	0	0	0				ActReg chrX #9886	1	1
9887	X	21,788,755	21,789,672	917	2	14.724	18.241	36	43	0	0	0				ActReg chrX #9887	1	1
9888	X	21,816,939	21,817,394	455	2	10.071	10	15	15	0	0	0				ActReg chrX #9888	1	1
9889	X	21,857,448	21,858,155	707	1	10.136	14.046	15	27	1	1	1	MBTPS2	145	in gene	ActReg chrX #9889	0	1
9890	X	22,332,543	22,333,153	610	1	11.15	9.85	18	19	0	0	0				ActReg chrX #9890	0	1
9891	X	22,760,236	22,760,682	446	1	10.071	5.429	15	8	0	0	0				ActReg chrX #9891	1	0
9892	X	23,802,949	23,803,412	463	1	1.923	9.714	3	13	0	1	1	SAT1	1,905	in gene	ActReg chrX #9892	0	1
9893	X	24,072,652	24,073,224	572	1	12.167	10.056	19	15	1	1	1	EIF2S3	-127	upstream	ActReg chrX #9893	1	0
9894	X	27,010,385	27,010,805	420	1	7.077	10	10	16	0	0	0				ActReg chrX #9894	0	1
9895	X	27,031,025	27,031,931	906	2	21.286	17	47	41	0	0	0				ActReg chrX #9895	1	1
9896	X	30,907,280	30,907,800	520	1	10.688	8.267	15	12	1	1	1	MAP3K7IP3	-29	upstream	ActReg chrX #9896	1	0
9897	X	37,764,991	37,765,526	535	2	9.765	10.118	16	20	1	0	0				ActReg chrX #9897	1	1
9898	X	38,186,514	38,187,295	781	2	17.792	17.208	47	41	1	1	1	RPGR	-116	upstream	ActReg chrX #9898	1	1
9899	X	38,664,060	38,664,832	772	1	6.12	10.6	12	14	1	0	1	MID1IP1	3,761	in gene	ActReg chrX #9899	0	1
9900	X	40,034,674	40,035,792	1,118	1	7.4	11.457	13	16	1	1	1	BCOR	1,349	in gene	ActReg chrX #9900	0	1
9901	X	40,943,569	40,944,238	669	1	10.762	12.619	13	18	1	1	1	USP9X	-985	upstream	ActReg chrX #9901	0	1
9902	X	43,513,797	43,514,365	568	2	12.177	11.235	21	22	1	1	1	MAOA	-1,328	upstream	ActReg chrX #9902	1	1
9903	X	43,871,846	43,872,364	518	1	10.562	6.625	17	10	0	0	0				ActReg chrX #9903	1	0
9904	X	46,039,701	46,040,122	421	1	8	10.692	13	15	0	0	0				ActReg chrX #9904	0	1
9905	X	46,127,711	46,128,344	633	1	11.7	5.85	18	12	0	0	0				ActReg chrX #9905	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9906	X	47,049,782	47,050,464	682	2	13.864	16.136	32	37	1	1	2	RBM10, UBA1	45492, -76	downstream, upstream	ActReg chrX #9906	1	1
9907	X	47,052,249	47,053,416	1,167	2	12.595	11.811	21	27	1	1	2	RBM10, UBA1	48201, 2633	downstream, in gene	ActReg chrX #9907	1	1
9908	X	47,077,620	47,078,304	684	2	10.591	13.318	17	29	1	1	2	UBA1, CDK16	27763, 434	downstream, in gene	ActReg chrX #9908	1	1
9909	X	47,124,328	47,124,799	471	1	9.929	4.143	15	6	0	0	0				ActReg chrX #9909	1	0
9910	X	47,342,383	47,342,855	472	1	10.6	6.133	16	9	1	1	2	ZNF41, CXorf24	-274, 8653	upstream, in gene	ActReg chrX #9910	1	0
9911	X	47,382,605	47,383,071	466	1	10.643	5.357	19	9	1	0	0				ActReg chrX #9911	1	0
9912	X	47,441,660	47,442,036	376	1	10.417	9.5	13	13	0	1	2	SYN1, TIMP1	37408, 158	in gene, in gene	ActReg chrX #9912	1	0
9913	X	47,478,928	47,479,807	879	2	10.518	16.667	25	37	1	1	2	SYN1, CFP	-111, 10337	upstream, downstream	ActReg chrX #9913	1	1
9914	X	47,880,456	47,881,420	964	2	13.733	18.667	28	41	0	0	0				ActReg chrX #9914	1	1
9915	X	48,432,467	48,433,060	593	1	5.421	10.158	7	14	1	1	2	RBM3, LOC100506703	-73, 6787	upstream, downstream	ActReg chrX #9915	0	1
9916	X	48,455,679	48,456,146	467	1	11.067	6.467	17	10	1	1	1	WDR13	32	in gene	ActReg chrX #9916	1	0
9917	X	48,979,862	48,980,393	531	2	9.824	8.647	16	13	1	1	1	GPKOW	-48	upstream	ActReg chrX #9917	1	1
9918	X	49,022,563	49,023,176	613	1	10.79	8.211	17	13	1	1	3	MAGIX, PLP2, PRICKLE3	3688, -5315, 19907	in gene, upstream, downstream	ActReg chrX #9918	1	0
9919	X	49,056,280	49,057,002	722	2	11.304	13.783	22	27	1	1	2	SYP, CACNA1F	20, 33192	in gene, downstream	ActReg chrX #9919	1	1
9920	X	50,557,250	50,558,581	1,331	1	7	11.268	11	17	1	1	1	SHROOM4	-871	upstream	ActReg chrX #9920	0	1
9921	X	51,486,104	51,486,813	709	2	8.909	12	15	17	1	1	1	GSPT2	-23	upstream	ActReg chrX #9921	1	1
9922	X	51,545,721	51,546,197	476	1	9.2	6.933	14	13	0	1	1	MAGED1	-196	upstream	ActReg chrX #9922	1	0
9923	X	52,963,732	52,964,263	531	1	7.824	12.941	10	18	1	0	0				ActReg chrX #9923	0	1
9924	X	52,964,275	52,964,858	583	1	6.056	10.222	10	18	1	0	0				ActReg chrX #9924	0	1
9925	X	53,254,008	53,254,695	687	1	7.091	11.864	9	19	1	1	2	KDM5C, IQSEC2	253, 96171	in gene, downstream	ActReg chrX #9925	0	1
9926	X	53,292,675	53,293,170	495	1	7.4	11.467	13	15	0	0	1	IQSEC2	57,600	in gene	ActReg chrX #9926	0	1
9927	X	53,710,782	53,711,301	519	1	3.118	12	5	19	1	1	1	HUWE1	2,632	in gene	ActReg chrX #9927	0	1
9928	X	54,466,534	54,466,972	438	1	8	11.769	12	14	0	1	2	TSR2, FGD1	-100, 55846	upstream, downstream	ActReg chrX #9928	0	1
9929	X	54,666,004	54,666,514	510	1	6.188	9.312	9	16	1	0	0				ActReg chrX #9929	0	1
9930	X	57,021,555	57,022,011	456	1	8.286	9.786	11	13	1	1	1	SPIN3	205	in gene	ActReg chrX #9930	0	1
9931	X	63,425,421	63,426,090	669	2	12.048	11.238	22	18	1	1	1	FAM123B	-131	upstream	ActReg chrX #9931	1	1
9932	X	68,048,645	68,049,091	446	1	6.571	10.571	11	14	1	1	1	EFNB1	28	in gene	ActReg chrX #9932	0	1
9933	X	69,664,327	69,664,863	536	1	9.938	8.062	17	12	0	1	1	DLG3	-110	upstream	ActReg chrX #9933	1	0
9934	X	69,697,091	69,697,582	491	1	9.933	8	17	13	0	0	1	DLG3	32,631	in gene	ActReg chrX #9934	1	0
9935	X	70,288,027	70,288,650	623	2	10.8	10.65	23	19	1	1	1	SNX12	-107	upstream	ActReg chrX #9935	1	1
9936	X	70,473,660	70,474,503	843	2	13.593	13.259	29	28	1	1	1	ZMYM3	966	in gene	ActReg chrX #9936	1	1
9937	X	71,401,236	71,401,829	593	1	7.895	11.474	12	17	0	1	1	PIN4	6	in gene	ActReg chrX #9937	0	1
9938	X	71,496,660	71,497,479	819	2	18.654	21.462	45	52	1	1	1	RPS4X	72	in gene	ActReg chrX #9938	1	1
9939	X	71,526,583	71,527,292	709	2	10.773	12.182	22	23	1	1	1	CITED1	100	in gene	ActReg chrX #9939	1	1
9940	X	71,681,614	71,682,015	401	1	5.333	10.417	9	17	0	0	1	HDAC8	111,139	in gene	ActReg chrX #9940	0	1
9941	X	73,163,796	73,164,417	621	2	9.4	9.412	17	20	1	0	0				ActReg chrX #9941	1	1
9942	X	74,375,678	74,376,271	593	1	11.421	8.421	20	14	0	1	1	ABCB7	158	in gene	ActReg chrX #9942	1	0
9943	X	74,493,677	74,494,219	542	1	5.647	9.647	9	18	0	1	1	UPRT	54	in gene	ActReg chrX #9943	0	1
9944	X	77,359,530	77,359,957	427	1	10.538	8.385	14	12	1	1	1	PGK1	77	in gene	ActReg chrX #9944	1	0
9945	X	100,645,544	100,646,305	761	2	10.875	14.708	23	30	1	2	3	BTK, RPL36A, GLA	-4712, -24, 17077	upstream, upstream, downstream	ActReg chrX #9945	1	1
9946	X	103,401,239	103,401,954	715	2	10.391	13.727	22	32	1	1	2	MCART6, CXorf39	112, -9705	in gene, upstream	ActReg chrX #9946	1	1
9947	X	103,410,513	103,411,476	963	2	11.3	12	18	24	1	1	2	MCART6, CXorf39	-9286, -307	upstream, upstream	ActReg chrX #9947	1	1
9948	X	106,567,833	106,568,456	623	1	6.65	10.8	9	18	0	0	0				ActReg chrX #9948	0	1
9949	X	107,334,710	107,335,150	440	1	10.286	8.357	14	12	1	2	2	PSMD10, ATG4A	-82, -4	upstream, upstream	ActReg chrX #9949	1	0
9950	X	109,638,122	109,638,527	405	1	3.182	9.5	6	15	0	0	1	AMMECR1	45,137	in gene	ActReg chrX #9950	0	1
9951	X	118,925,114	118,925,731	617	1	8.7	11.15	12	14	1	2	2	RPL39, SNORA69	184, -3975	in gene, upstream	ActReg chrX #9951	0	1
9952	X	119,005,438	119,006,147	709	1	6.348	10.913	11	14	1	2	2	RNF113A, NDUFA1	-1, 58	upstream, in gene	ActReg chrX #9952	0	1
9953	X	119,077,406	119,077,915	509	1	9.875	9	14	13	1	1	1	NKAP	75	in gene	ActReg chrX #9953	1	0
9954	X	119,763,623	119,764,141	518	1	3.188	11	6	17	1	1	2	MCTS1, C1GALT1C1	26138, 123	downstream, in gene	ActReg chrX #9954	0	1
9955	X	128,673,979	128,674,572	593	2	15.947	13.316	34	28	1	1	1	OCRL	23	in gene	ActReg chrX #9955	1	1
9956	X	129,299,341	129,300,515	1,174	2	9.946	12.649	24	26	1	2	2	AIFM1, RAB33A	-67, -5845	upstream, upstream	ActReg chrX #9956	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA::1 Avg Value	2_A375_pNL97_plus_lncRNA::1 Avg Value	1_A375_pNL7_minus_lncRNA::1 Peak Value	2_A375_pNL97_plus_lncRNA::1 Peak Value	CG Island Count	Promoter Count	Gene Count	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA::1 Present	2_A375_pNL97_plus_lncRNA::1 Present
9957	X	134,049,081	134,049,485	404	1	10.077	6.846	15	16	1	1	1	MOSPD1	14	in gene	ActReg chrX #9957	1	0
9958	X	134,654,125	134,654,963	838	1	6.846	10.923	17	20	1	1	1	DDX26B	-11	upstream	ActReg chrX #9958	0	1
9959	X	134,909,298	134,909,746	448	1	7.571	9.571	9	15	0	0	0				ActReg chrX #9959	0	1
9960	X	134,975,396	134,976,025	629	1	7.211	13.053	13	23	0	2	2	CT45A6, SAGE1	-4466, -75	upstream, upstream	ActReg chrX #9960	0	1
9961	X	135,067,263	135,068,034	771	1	5.64	11.84	10	20	1	1	1	SLC9A6	65	in gene	ActReg chrX #9961	0	1
9962	X	140,846,084	140,846,672	588	1	9.389	7.167	15	12	0	0	0				ActReg chrX #9962	1	0
9963	X	144,691,322	144,691,775	453	1	10.857	1.929	17	4	0	0	0				ActReg chrX #9963	1	0
9964	X	149,369,101	149,369,691	590	2	11	10.667	18	16	0	0	0				ActReg chrX #9964	1	1
9965	X	150,151,319	150,151,905	586	2	13.684	13	27	28	1	1	1	HMGB3	-151	upstream	ActReg chrX #9965	1	1
9966	X	150,921,753	150,922,268	515	1	6.438	11.438	12	18	0	0	1	CNGA2	18,792	downstream	ActReg chrX #9966	0	1
9967	X	151,999,274	151,999,708	434	1	5.692	10	10	14	1	2	2	CETN2, NSDHL	-190, -20	upstream, upstream	ActReg chrX #9967	0	1
9968	X	153,140,610	153,141,378	768	2	13.125	21.417	29	46	0	1	1	L1CAM	405	in gene	ActReg chrX #9968	1	1
9969	X	153,599,088	153,600,001	913	2	11.207	14.552	24	27	1	0	2	FLNA, EMD	3462, -8053	in gene, upstream	ActReg chrX #9969	1	1
9970	X	153,626,290	153,626,991	701	2	9.636	12.091	16	24	1	3	4	LOC100507387, RPL10, SNORA70, DNASE1L1	721, 69, -1982, 13787	in gene, in gene, upstream, downstream	ActReg chrX #9970	1	1
9971	X	153,639,563	153,640,087	524	1	6.812	11.438	10	15	1	2	3	RPL10, DNASE1L1, TAZ	13254, 602, 52	downstream, in gene, upstream	ActReg chrX #9971	0	1
9972	X	154,493,388	154,494,108	720	2	7.81	11.727	17	21	1	1	1	RAB39B	104	in gene	ActReg chrX #9972	1	1
9973	X	154,841,940	154,842,419	479	1	9.267	9.933	14	14	1	1	1	TMLHE	443	in gene	ActReg chrX #9973	0	1
9974	Y	10,037,604	10,037,979	375	2	53.818	55.909	92	94	0	0	0				ActReg chrY #9974	1	1

Table 8. AR active regions as determined via AR ChIP-Seq

Table 8

Intervals per Sample/Rep

Intervals per Sample/Rep (converted only)

Rep\Sample	1_A375_pNL7_minus_lncRNA	2_A375_pNL97_plus_lncRNA
1	5,749	8,274

Interval Correlations
Intervals (rows) that are in ActRegs containing Intervals of Sample/Rep (columns)

Sample		1_A375_pNL7_minus_lncRNA	2_A375_pNL97_plus_lncRNA
	Rep	1	1
1_A375_pNL7_minus_lncRNA	1	5,749	4,014
2_A375_pNL97_plus_lncRNA	1	4,017	8,274

Interval Correlations Percent of Total (converted) Intervals in a Sample/Rep
Intervals (rows) that are in ActRegs containing Intervals of Sample/Rep (columns)

Sample		1_A375_pNL7_minus_lncRNA	2_A375_pNL97_plus_lncRNA
	Rep	1	1
1_A375_pNL7_minus_lncRNA	1	100.00%	69.82%
2_A375_pNL97_plus_lncRNA	1	48.55%	100.00%

Active Region Correlations
Active Regions containing Intervals of Any Two Sample/Rep

Sample		1_A375_pNL7_minus_lncRNA	2_A375_pNL97_plus_lncRNA
	Rep	1	1
1_A375_pNL7_minus_lncRNA	1	5,717	3,982
2_A375_pNL97_plus_lncRNA	1	3,982	8,239

Active Region Correlations Percent of Total ActReg containing Sample/Rep
Active Regions containing Intervals of Any Two Sample/Rep

Sample		1_A375_pNL7_minus_lncRNA	2_A375_pNL97_plus_lncRNA
	Rep	1	1
1_A375_pNL7_minus_lncRNA	1	100.00%	69.65%
2_A375_pNL97_plus_lncRNA	1	48.33%	100.00%

Sample/Rep Present in each Active Region

Sample::Rep		
1_A375_pNL7_minus_lncRNA::1	2_A375_pNL97_pl	# Act Regs
1	0	1,735
0	1	4,257
1	1	3,982
5,717	8,239	9,974

Description	Act Regions	1_A375_pNL7_minus_lncRNA::1	1_A375_pNL7_minus_lncRNA::1 %	2_A375_pNL97_plus_lncRNA::1	2_A375_pNL97_plus_lncRNA::1 %
Total Number of Intervals in Build 37_2		5749		8274	
Number of Intervals Converted to Build 37_2	9974	5749	100.00%	8274	100.00%
Number of Intervals within -10000/+10000 bp of NCBI Genes	7753	4522	78.66%	6547	79.13%
Number of Intervals NOT within -10000/+10000 bp of NCBI Genes	2221	1227	21.34%	1727	20.87%
Number of NCBI Genes with Intervals within -10000/+10000 bp	9139	5916		8164	
Number of Intervals within Promoter Region (-7500/+2500 bp of NCBI Gene Start)	5407	3214	55.91%	4697	56.77%
Number of Intervals 500 bp of NCBI Tx Start	4048	2478	43.10%	3556	42.98%
Number of NCBI Genes with UCSC CpGs and intervals in Promoters (-7500/2500 bp of start)	6418	3971		5704	
Number of NCBI Genes with intervals in Promoters (-7500/2500 bp of start)	6985	4297		6162	
Number of Intervals within 200 bp of UCSC CpG Islands	5236	3088	53.71%	4623	55.87%
Avg Interval Length	862.5218	802.6182		852.7109	
Max Interval Length	5522	5185		5465	
Min Interval Length	231	250		201	
Avg Probe Value		2.545192426		2.58005946	
Max Probe Value		402		448	
Total Probe Count		68807537		67877669	

Chromosome	Length (bp)	Active Regions	Total Intervals	1_A375_pNL7_minus_lncRNA::1 Intervals	2_A375_pNL97_plus_lncRNA::1 Intervals	# CpG Islands	# Genes	# RNAs
1	249,250,621	1,326	1,919	814	1,105	2,462	2,502	3,708
2	243,199,373	571	799	339	460	1,688	1,641	2,326
3	198,022,430	633	889	366	523	1,163	1,325	2,072
4	191,154,276	331	441	177	264	1,031	933	1,380
5	180,915,260	606	835	348	487	1,229	1,088	1,611
6	171,115,067	293	396	154	242	1,253	1,256	1,840
7	159,138,663	571	798	332	466	1,578	1,237	1,784
8	146,364,022	417	576	228	348	1,037	886	1,334
9	141,213,431	501	707	291	416	1,226	1,027	1,437
X	155,270,560	110	150	66	84	896	1,052	1,745
Y	59,373,566	1	2	1	1	181	130	180
10	135,534,747	398	540	210	330	1,143	967	1,509
11	135,006,516	554	792	330	462	1,367	1,505	2,236
12	133,851,895	581	807	338	469	1,221	1,232	1,926
13	115,169,878	291	396	160	236	605	432	597
14	107,349,540	175	233	91	142	788	1,046	1,235
15	102,531,392	367	514	212	302	792	868	1,265
16	90,354,753	421	596	231	365	1,491	1,026	1,489
17	81,195,210	558	793	305	488	1,634	1,382	2,090
18	78,077,248	108	142	60	82	507	360	524
19	59,128,983	588	879	371	508	2,541	1,675	2,416
20	63,025,520	410	594	233	361	801	680	1,027

21	48,129,895	46	57	22	35	365	309	473
22	51,304,566	117	168	70	98	719	614	868

Generated Statistics

Database

Number of CDS entries in NCBI seq_gene	312,377
Number of GENE entries in NCBI seq_ger	36,074
Number of PSEUDO entries in NCBI seq_	10,839
Number of RNA entries in NCBI seq_gene	37,997
Number of UTR entries in NCBI seq_gene	104,241
Number of NCBI Genes (GENE) with CpG	16,435
Number of NCBI Genes (PSEUDO) with C	1,742

Program Settings

NCBI Build for Affymetrix Arrays	37_2
NCBI Build for Analysis after conversion	37_2
Experiment Label	'CSeq 0018 DFCI'
Sample Name #1	1_A375_pNL7_minus_lncRNA::1
Sample Name #2	2_A375_pNL97_plus_lncRNA::1
Intervals File for 1_A375_pNL7_minus_lnc	MACS/1_A375_pNL7_minus_lncRNA_AR_hs_peaks_filtered.bed
Intervals File for 2_A375_pNL97_plus_lnc	MACS/2_A375_pNL97_plus_lncRNA_AR_hs_peaks_filtered.bed
BAR File for Sample 1_A375_pNL7_minu	SEQ/1_0018DFCI_A375_pNL7_minus_lncRNA_AR_hs_i80_uniqnorm_signal.txt
BAR File for Sample 2_A375_pNL97_plus	SEQ/2_0018DFCI_A375_pNL97_plus_lncRNA_AR_hs_i81_uniqnorm_signal.txt
Promoter Start	-7,500
Promoter End	2,500
Intragenic Region Start	1,000
Max Distance between Intervals in an Acti	0
Gene Margin Upstream of gene	10,000
Gene Margin Downstream of gene	10,000
CpG Island Margin	200
Promoter Start Margin	-7,500
Promoter End Margin	2,500
Output File Base Name	Analysis/0018DFCI_AR
Gene Tx Start Margin for NCBI Genes	500

Statistics

Total Number of Intervals in Analysis	14,023
Number of Active Regions	9,974
Number of Active Regions Near UCSC Cp	5,236
Number of Active Regions Near NCBI Ger	5,446
Number of Intervals Near UCSC CpG Islar	7,711
Number of Intervals Near NCBI Promoters	7,976
Distribution of Active Region Sizes	Number of Active Regions
Number of Active Regions with 4 Intervals	7
Number of Active Regions with 3 Intervals	53
Number of Active Regions with 2 Intervals	3,922
Number of Active Regions with 1 Intervals	5,992

Input Parameters

1_A375_pNL7_minus_lncRNA::1::BarFile	SEQ/1_0018DFCI_A375_pNL7_minus_lncRNA_AR_hs_i80_uniqnorm_signal.txt
1_A375_pNL7_minus_lncRNA::1::IntFile	MACS/1_A375_pNL7_minus_lncRNA_AR_hs_peaks_filtered.bed
2_A375_pNL97_plus_lncRNA::1::BarFile	SEQ/2_0018DFCI_A375_pNL97_plus_lncRNA_AR_hs_i81_uniqnorm_signal.txt
2_A375_pNL97_plus_lncRNA::1::IntFile	MACS/2_A375_pNL97_plus_lncRNA_AR_hs_peaks_filtered.bed
AffyBuild	37.2
AllowedContigReference	GRCh37.p2-Primary Assembly
AnnotateList	CpG
BaseDir	/Users/paullabhart/Genpathway/Systems/CSeq/DFCI/0018
BlatDB	hg19
Build	37.2
ClusterMargin	0
CombinedWorkbook	2
CpGMargin	200
CSeq	1
CSeqBGWindowSize	20000
CSeqBinSize	32
CSeqFiles	SEQ/1_0018DFCI_A375_pNL7_minus_lncRNA_AR_hs_i80_uniqnorm, SEQ/2_0018DFCI_A375_pNL97_plus_lncRNA_AR_hs_i81_uniqnorm, SEQ/3_0018DFCI_Pooled_Input_hs_i82_uniqnorm
CSeqFragSize	200
CSeqMachine	bed
CSeqMaxGap	100
CSeqMinRun	2
Experiment	CSeq 0018 DFCI
FactorPath	1
FTPpassword	An5%24ezS%3f
FTPserver	ftp.activemotif.com
FTPusername	gp_chovina
GeneMarginDown	10000
GeneMarginUp	10000
GeneStartMargin	500
MACS2MFold	10 30
MACSBandwidth	200
MACSControlFiles	SEQ/3_0018DFCI_Pooled_Input_hs_i82_uniqnorm_hits.bed, SEQ/3_0018DFCI_Pooled_Input_hs_i82_uniqnorm_hits.bed
MACSGenomeSize	hs
MACSMFold	10,30
MACSName	1_A375_pNL7_minus_lncRNA_AR_hs, 2_A375_pNL97_plus_lncRNA_AR_hs
MACSNoLambda	0
MACSNoModel	0
MACSPValue	0.0000001
MACSTagSize	75
MACSTreatmentFiles	SEQ/1_0018DFCI_A375_pNL7_minus_lncRNA_AR_hs_i80_uniqnorm_hits.bed, SEQ/2_0018DFCI_A375_pNL97_plus_lncRNA_AR_hs_i81_uniqnorm_hits.bed
NoTranslation	1
OutFileBase	Analysis/0018DFCI_AR
OutTableList	intervals, genes, clusters
PeakCallTool	MACS
PeakHoodLength	60
PeakHoodMaxNum	1000
PeakSamples	1_A375_pNL7_minus_lncRNA::1, 2_A375_pNL97_plus_lncRNA::1
PrintList	intervals, genes, chromosomes, stats, clusters
ProbeLength	1
PromoterEnd	2500
PromoterStart	-7500
RNAStartMargin	500
Samples	1_A375_pNL7_minus_lncRNA::1, 2_A375_pNL97_plus_lncRNA::1
StandardChromosomes	T
TaxID	hs

[EXPERIMENTAL DATA]

File name	1_0018DFCI_A37	2_0018DFCI_A375_pNL97_plus_li	3_0018DFCI_Pooled_Input_hs_i82
Total number of reads	33,463,732	32,100,557	33,477,412
Total number of alignments (hg19)	31,354,236	30,379,608	31,555,690
Unique alignments (-q 25)	28,398,072	27,508,140	28,287,244
Unique alignments (without duplicate read	25,499,392	25,035,898	27,121,739
Final number of tags (-chrM, >chromsize)	25,480,655	25,018,346	27,101,479
Normalized tags	25,018,346	25,018,346	25,018,346
Input tags used for peak calling	25,018,346	25,018,346	
[PEAK CALLING]			
MACS 1.4.2			
# effective genome size = 2.70e+09			
# band width = 200			
# model fold = 10,30			
# pvalue cutoff = 1.00e-07			
Paired peaks	927	1,359	
Predicted fragment length	141	135	
Final MACS peak	5,768	8,298	
Negative peaks	33	34	
Empirical FDR	0.57%	0.41%	
ENCODE blacklisted	19	24	
Filtered peaks	5,749	8,274	

MACS diff	1_pNL7_minus_vs	2_pNL97_plus_vs_pNL7_minus
# effective genome size = 2.70e+09		
# band width = 200		
# model fold = 10,30		
# pvalue cutoff = 1.00e-07		
Final MACS peak	16	96
Negative peaks	87	17
ENCODE blacklisted	0	0
Filtered peaks	16	96

Table 9A. AR active genes as determined via AR ChIP-Seq

Table 9A lists the AR active genes as determined via AR ChIP-SEQ.

1_A375_pNL7_minus_lncRNA_AR = vector control

2_A375_pNL97_plus_lncRNA_AR = SLNCR1-expressing vector

Annotations:

[A] 1_A375_pNL7_minus_lncRNA::1 Present

[B] 2_A375_pNL97_plus_lncRNA::1 Present

[C] 1_A375_pNL7_minus_lncRNA::1 AvgPeak

[D] 2_A375_pNL97_plus_lncRNA::1 AvgPeak

Table 9A

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100288069	LOC100288069	1	700,245	714,068	13,823	-	2	1_A375_pNL7_minus_lncRNA::1::0, 2_A375_pNL97_plus_lncRNA::1::0	20, -44	in gene, upstream	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100288069		hypothetical LOC100288069	NR_033908		
GeneID:100287934	LOC100287934	1	721,320	722,513	1,193	+	2	1_A375_pNL7_minus_lncRNA::1::0, 2_A375_pNL97_plus_lncRNA::1::0	-7272, -7208	upstream, upstream	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100287934		hypothetical LOC100287934	XR_112047, XR_108279, XR_115170		
GeneID:26155	NOC2L	1	879,583	894,679	15,096	-	2	2_A375_pNL97_plus_lncRNA::1::1, 2_A375_pNL97_plus_lncRNA::1::2	55, -1241	in gene, upstream	0	1	18	23.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene NOC2L	FLJ35172, NET7, NET15, NIR, NOC2L, DKFZp564C186	nucleolar complex associated 2 homolog (S. cerevisiae)	NM_015658, hCT2275821.0, hCT2275823.0, hCT2275826.0	1559139_at, 202115_s_at	NP_056473.2, EAW56304.1, EAW56305.1, EAW56306.1
GeneID:339451	KLHL17	1	895,967	901,095	5,128	+	2	2_A375_pNL97_plus_lncRNA::1::1, 2_A375_pNL97_plus_lncRNA::1::2	-1343, -47	upstream, upstream	0	1	18	23.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene KLHL17	KLHL17, RP11-54O7.6	kelch-like 17 (Drosophila)	NM_198317, hCT1954985.2, hCT22913.4, hCT2341075.0, hCT2353011.0	1555650_at, 229792_at	NP_938073.1, EAW56300.1, EAW56301.1, EAW56302.1, EAW56303.1
GeneID:84069	PLEKHN1	1	901,877	910,488	8,611	+	2	2_A375_pNL97_plus_lncRNA::1::1, 2_A375_pNL97_plus_lncRNA::1::2	-7253, -5957	upstream, upstream	0	1	18	23.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene PLEKHN1	DKFZp434H2010, MGC120616, MGC120613, PLEKHN1, RP11-54O7.7	pleckstrin homology domain containing, family N member 1	NM_032129, NM_001160184, hCT22914.2	224125_at	NP_115505.2, NP_001153656.1, EAW56299.1
GeneID:57801	HES4	1	934,342	935,552	1,210	-	2	1_A375_pNL7_minus_lncRNA::1::1, 2_A375_pNL97_plus_lncRNA::1::3	-560, -608	upstream, upstream	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene HES4	bHLHb42, HES4	hairy and enhancer of split 4 (Drosophila)	NM_021170, NM_001142467, hCT1809955.2	227347_x_at	NP_066993.1, NP_001135939.1, EAW56296.1
GeneID:375790	AGRN	1	955,503	991,492	35,989	+	2	1_A375_pNL7_minus_lncRNA::1::2, 2_A375_pNL97_plus_lncRNA::1::4	39473, 39457	downstream, downstream	1	1	24	23	1	1_A375_pNL7_minus_lncRNA::1	24	Gene AGRN	FLJ45064, AGRN	agrin	NM_198576, hCT1809981.2	212283_at, 212285_s_at, 217410_at, 217419_x_at	NP_940978.2, EAW56293.1
GeneID:54991	C1orf159	1	1,017,198	1,051,736	34,538	-	2	1_A375_pNL7_minus_lncRNA::1::3, 2_A375_pNL97_plus_lncRNA::1::5	120, 136	in gene, in gene	1	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene C1orf159	FLJ36119, FLJ20584, C1orf159, FLJ21143	chromosome 1 open reading frame 159	NM_017891, hCT1809957.2, hCT1954964.1, hCT1954966.1, hCT2275800.0	219337_at	NP_060361.4, EAW56288.1, EAW56289.1, EAW56290.1, EAW56291.1
GeneID:406984	MIR200B	1	1,102,484	1,102,578	94	+	1	2_A375_pNL97_plus_lncRNA::1::6	-8964	upstream	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MIR200B	MIR200B, MIRN200B	microRNA 200b	NR_029639		
GeneID:406983	MIR200A	1	1,103,243	1,103,332	89	+	1	2_A375_pNL97_plus_lncRNA::1::6	-9723	upstream	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MIR200A	MIRN200A, MIR200A	microRNA 200a	NR_029834		
GeneID:51150	SDF4	1	1,152,288	1,167,447	15,159	-	1	2_A375_pNL97_plus_lncRNA::1::7	-6313	upstream	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SDF4	Cab45, SDF4	stromal cell derived factor 4	NM_016176, NM_016547, hCT10259.3, hCT1954881.1, hCT1954882.1, hCT1954883.1, hCT1954884.1, hCT1954885.1, hCT2275778.0	217855_x_at, 221972_s_at, 224472_x_at, 232032_x_at	NP_057260.2, NP_057631.1, EAW56272.1, EAW56275.1, EAW56276.1, EAW56277.1, EAW56271.1, EAW56273.1, EAW56274.1
GeneID:126792	B3GALT6	1	1,167,629	1,170,421	2,792	+	1	2_A375_pNL97_plus_lncRNA::1::7	6131	downstream	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene B3GALT6	B3GALT6, beta3GalT6	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6	NM_080605, hCT1642223.3	1553959_a_at, 225733_at, 226427_s_at	NP_542172.2, EAW56269.1
GeneID:388581	FAM132A	1	1,177,833	1,182,102	4,269	-	1	2_A375_pNL97_plus_lncRNA::1::7	8342	downstream	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FAM132A	MGC105127, C1QTNF12, FAM132A, C1QDC2	family with sequence similarity 132, member A	NM_001014980	243292_at	NP_001014980.1
GeneID:6339	SCNN1D	1	1,217,489	1,227,409	9,920	+	2	1_A375_pNL7_minus_lncRNA::1::4, 2_A375_pNL97_plus_lncRNA::1::8	17071, 17071	downstream, downstream	1	1	23	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene SCNN1D	MGC149711, SCNN1D, SCNED, dNaCh, MGC149710, ENaCd, ENaCdelta	sodium channel, nonvoltage-gated 1, delta	NM_002978, NM_001130413, hCT1954887.1, hCT1954888.1, hCT1954889.1, hCT1954890.0	208458_at	NP_002969.2, NP_001123885.1, EAW56251.1, EAW56252.1, EAW56253.1, EAW56254.1
GeneID:116983	ACAP3	1	1,227,764	1,243,269	15,505	-	4	1_A375_pNL7_minus_lncRNA::1::4, 1_A375_pNL7_minus_lncRNA::1::5, 2_A375_pNL97_plus_lncRNA::1::8, 2_A375_pNL97_plus_lncRNA::1::9	8709, -331, 8709, -443	in gene, upstream, in gene, upstream	1	1	23	26	2	2_A375_pNL97_plus_lncRNA::1	30	Gene ACAP3	ACAP3, KIAA1716, CENTB5	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3	NM_030649, hCT2275759.0, hCT2275761.0, hCT2275762.0, hCT2275763.0, hCT2275764.0	225529_at, 225542_at	NP_085152.2, EAW56246.1, EAW56247.1, EAW56248.1, EAW56249.1, EAW56250.1
GeneID:126789	PUSL1	1	1,243,994	1,247,057	3,063	+	4	1_A375_pNL7_minus_lncRNA::1::4, 1_A375_pNL7_minus_lncRNA::1::5, 2_A375_pNL97_plus_lncRNA::1::8, 2_A375_pNL97_plus_lncRNA::1::9	-9434, -394, -9434, -282	upstream, upstream, upstream, upstream	1	1	23	26	2	2_A375_pNL97_plus_lncRNA::1	30	Gene PUSL1	FLJ90811, PUSL1	pseudouridylate synthase-like 1	NM_153339, hCT11500.4	228733_at	NP_699170.1, EAW56245.1
GeneID:54973	CPSF3L	1	1,246,965	1,260,046	13,081	-	2	1_A375_pNL7_minus_lncRNA::1::5, 2_A375_pNL97_plus_lncRNA::1::9	16446, 16334	downstream, downstream	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene CPSF3L	RC-68, RC68, FLJ20542, INTS11, FLJ13294, INT11, CPSF73L, CPSF3L	cleavage and polyadenylation specific factor 3-like	NM_017871, hCT11501.2, hCT1954913.1, hCT1954914.1, hCT1954916.1, hCT1954920.1, hCT1968942.1, hCT1968943.1, hCT2353001.0, hCT2353002.0, hCT2353003.0, hCT2353004.0, hCT2353005.0, hCT2353006.0	217994_x_at, 224312_x_at, 232437_at, 233563_s_at, 233625_x_at	NP_060341.2, EAW56234.1, EAW56232.1, EAW56235.1, EAW56236.1, EAW56242.1, EAW56233.1, EAW56237.1, EAW56238.1, EAW56239.1, EAW56240.1, EAW56241.1, EAW56243.1, EAW56244.1
GeneID:100506404	LOC100506404	1	1,303,575	1,322,851	19,276	+	2	1_A375_pNL7_minus_lncRNA::1::6, 2_A375_pNL97_plus_lncRNA::1::10	7061, 7049	in gene, in gene	1	1	46	49	1	2_A375_pNL97_plus_lncRNA::1	49	Gene LOC100506404		hypothetical LOC100506404	XR_112082, XR_108283		
GeneID:54998	AURKAIP1	1	1,309,110	1,310,818	1,708	-	2	1_A375_pNL7_minus_lncRNA::1::6, 2_A375_pNL97_plus_lncRNA::1::10	162, 194	in gene, in gene	1	1	46	49	1	2_A375_pNL97_plus_lncRNA::1	49	Gene AURKAIP1	FLJ20608, AKIP, AURKAIP1, AIP	aurora kinase A interacting protein 1	NM_017900, NM_001127229, NM_001127230, hCT11495.3, hCT1954896.0	215550_x_at, 225552_x_at, 227546_x_at, 228600_x_at	NP_060370.1, NP_001120701.1, NP_001120702.1, EAW56218.1, EAW56219.1
GeneID:81669	CCNL2	1	1,321,091	1,334,718	13,627	-	4	1_A375_pNL7_minus_lncRNA::1::6, 2_A375_pNL97_plus_lncRNA::1::10, 2_A375_pNL97_plus_lncRNA::1::11, 2_A375_pNL97_plus_lncRNA::1::12	24062, 24094, -130, -8066	downstream, downstream, upstream, upstream	1	1	24.67	32	3	2_A375_pNL97_plus_lncRNA::1	49	Gene CCNL2	HLA-ISO, ANIA-6B, CCNM, SB138, PCEE, DKFZp761A1210, HCLA-ISO, DKFZp762O195, CCNL2	cyclin L2	NM_030937, NM_001039577, hCT11502.3, hCT1809975.2, hCT1954921.1, hCT1954922.1, hCT1954923.1, hCT2275736.0, hCT2275739.0	225555_x_at	NP_112199.2, NP_001034666.1, EAW56212.1, EAW56213.1, EAW56215.1, EAW56217.1, EAW56211.1, EAW56214.1, EAW56216.1
GeneID:148413	LOC148413	1	1,334,910	1,337,426	2,516	+	2	2_A375_pNL97_plus_lncRNA::1::11, 2_A375_pNL97_plus_lncRNA::1::12	-62, 7874	upstream, downstream	0	1	14	23.5	2	2_A375_pNL97_plus_lncRNA::1	30	Gene LOC148413		hypothetical LOC148413	NR_015434	225920_at, 225934_at	
GeneID:55052	MRPL20	1	1,337,276	1,342,693	5,417	-	2	2_A375_pNL97_plus_lncRNA::1::11, 2_A375_pNL97_plus_lncRNA::1::12	7845, -91	downstream, upstream	0	1	14	23.5	2	2_A375_pNL97_plus_lncRNA::1	30	Gene MRPL20	MGC74465, MRP-L20, MGC4779, L20mt, MRPL20	mitochondrial ribosomal protein L20	NM_017971, hCT11496.3, hCT1954901.1, hCT1954902.1	220526_s_at, 220527_at, 224603_s_at	NP_060441.2, EAW56206.1, EAW56207.1, EAW56208.1
GeneID:219293	ATAD3C	1	1,385,069	1,405,538	20,469	+	1	2_A375_pNL97_plus_lncRNA::1::13	21971	downstream	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ATAD3C	FLJ34599, ATAD3C, FLJ37183	ATPase family, AAA domain containing 3C	NM_001039211	240210_at	NP_001034300.2
GeneID:83858	ATAD3B	1	1,407,164	1,431,582	24,418	+	1	2_A375_pNL97_plus_lncRNA::1::13	-124	upstream	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ATAD3B	KIAA1273, AAA-TOB3, ATAD3B, TOB3	ATPase family, AAA domain containing 3B	NM_031921, hCT2276508.1, hCT2276509.1, hCT2276510.1	223617_x_at, 227237_x_at, 233091_at	NP_114127.3, EAW56192.1, EAW56193.1, EAW56194.1
GeneID:55210	ATAD3A	1	1,447,523	1,470,067	22,544	+	2	1_A375_pNL7_minus_lncRNA::1::7, 2_A375_pNL97_plus_lncRNA::1::14	-67, -35	upstream, upstream	1	1	20	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene ATAD3A	FLJ35514, ATAD3A, FLJ10709	ATPase family, AAA domain containing 3A	NM_018188, NM_001170535, NM_001170536, hCT1809953.2, hCT1962112.1, hCT1962113.1, hCT1962114.1, hCT2352989.0, hCT2352990.0	219068_x_at, 227700_x_at	NP_060658.3, NP_001164006.1, NP_001164007.1, EAW56186.1, EAW56187.1, EAW56189.1, EAW56188.1, EAW56190.1, EAW56191.1
GeneID:29101	SSU72	1	1,477,053	1,510,262	33,209	-	2	1_A375_pNL7_minus_lncRNA::1::8, 2_A375_pNL97_plus_lncRNA::1::15	-106, -42	upstream, upstream	1	1	22	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SSU72	PNAS-120, FLJ13048, SSU72, HSPC182	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	NM_014188, hCT10254.2, hCT2275838.0	223051_at, 223052_x_at, 223053_x_at, 226229_s_at, 227244_s_at, 229329_s_at, 229330_at	NP_054907.1, EAW56183.1, EAW56182.1
GeneID:984	CDK11B	1	1,571,100	1,590,473	19,373	-	2	1_A375_pNL7_minus_lncRNA::1::9, 2_A375_pNL97_plus_lncRNA::1::16	-23, -135	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene CDK11B	CDC2L1, FLJ59152, CDC2L2, p58CDC2L1, p58, CDK11-p58, p58CLK-1, PK58, CDK11B, CDK11, CLK-1, CDK11-p110, CDK11-p46	cyclin-dependent kinase 11B	NM_033486, NM_033487, NM_033488, NM_033489, NM_033492, NM_033493, hCT2340548.0, hCT2340549.0, hCT2340550.0, hCT2340551.0	211289_x_at	NP_277021.1, NP_277022.1, NP_277023.1, NP_277024.1, NP_277027.1, NP_277028.1, EAW56170.1, EAW56171.1, EAW56172.1, EAW56173.1
GeneID:728661	RP11-345P4.4	1	1,592,939	1,624,243	31,304	-	4	1_A375_pNL7_minus_lncRNA::1::9, 1_A375_pNL7_minus_lncRNA::1::10, 2_A375_pNL97_plus_lncRNA::1::16, 2_A375_pNL97_plus_lncRNA::1::17	33747, -349, 33635, -237	downstream, upstream, downstream, upstream	1	1	20.5	22	2	2_A375_pNL97_plus_lncRNA::1	27	Gene RP11-345P4.4	SLC35E2B, MGC117254, KIAA0447, DKFZp564C093, MGC104754, DKFZp686M0869, FLJ43631, SLC35E2, LOC728661	similar to solute carrier family 35, member E2	NM_001110781	217122_s_at	NP_001104251.1
GeneID:728642	CDK11A	1	1,634,169	1,655,791	21,622	-	2	1_A375_pNL7_minus_lncRNA::1::10, 2_A375_pNL97_plus_lncRNA::1::17	31199, 31311	downstream, downstream	1	1	23	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene CDK11A	MGC131975, CDK11A, p58GTA, CDC2L2, PITSLRE, CDK11-p58, CDC2L3, CDK11-p110, CDK11-p46	cyclin-dependent kinase 11A	NM_033529, NM_024011	207425_x_at, 210474_s_at, 212401_s_at, 215329_s_at	NP_277071.2, NP_076916.2
GeneID:5590	PRKCZ	1	1,981,909	2,116,834	134,925	+	3	1_A375_pNL7_minus_lncRNA::1::11, 1_A375_pNL7_minus_lncRNA::1::12, 2_A375_pNL97_plus_lncRNA::1::18	84619, 139371, 85611	in gene, downstream, in gene	1	1	18	18	2	2_A375_pNL97_plus_lncRNA::1	24	Gene PRKCZ	PRKCZ, PKC2, PKC-ZETA	protein kinase C, zeta	NM_002744, NM_001033581, NM_001033582, hCT15713.3, hCT2345155.0	1569748_at, 202178_at, 220646_s_at	NP_002735.3, NP_001028753.1, NP_001028754.1, EAW56130.1, EAW56131.1
GeneID:100506504	LOC100506504	1	2,113,246	2,115,492	2,246	-	1	1_A375_pNL7_minus_lncRNA::1::12	-5788	upstream	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100506504		hypothetical protein LOC100506504	XM_003119801, XM_003118494, XM_003120338		XP_003119849.1, XP_003118542.1, XP_003120386.1
GeneID:199990	C1orf86	1	2,115,899	2,139,172	23,273	-	1	1_A375_pNL7_minus_lncRNA::1::12	17892	in gene	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene C1orf86	FP7162, C1orf86, FLJ31031, MGC120153	chromosome 1 open reading frame 86	NM_182533, NM_001146310, hCT1809286.4, hCT2336603.2, hCT2343773.1, hCT2344476.1, hCT2350220.0	1556309_s_at, 1558544_at, 1562675_at, 229113_s_at, 230649_at, 236498_s_at, 236499_at, 236584_at	NP_872339.2, NP_001139782.1, EAW56125.1, EAW56127.1, EAW56128.1, EAW56129.1, EAW56126.1
GeneID:100128003	LOC100128003	1	2,120,482	2,125,024	4,542	-	1	1_A375_pNL7_minus_lncRNA::1::12	3744	in gene	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100128003	FLJ43456, FLJ30256, FLJ46660	hypothetical LOC100128003	NR_024445		
GeneID:6497	SKI	1	2,160,134	2,241,652	81,518	+	1	1_A375_pNL7_minus_lncRNA::1::13	2522	in gene	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SKI	SKI, SKV	v-ski sarcoma viral oncogene homolog (avian)	NM_003036, hCT14250.3, hCT1965410.1	204270_at	NP_003027.1, EAW56117.1, EAW56118.1
GeneID:11079	RER1	1	2,323,214	2,336,883	13,669	+	1	2_A375_pNL97_plus_lncRNA::1::19	21250	downstream	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene RER1	RER1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	NM_007033, hCT15722.4, hCT2336643.1, hCT2336644.1, hCT2336645.1, hCT2336646.1, hCT2345156.0	202296_s_at, 202297_s_at, 213296_at	NP_008964.3, EAW56109.1, EAW56110.1, EAW56112.1, EAW56113.1, EAW56114.1, EAW56111.1
GeneID:5192	PEX10	1	2,336,241	2,344,010	7,769	-	1	2_A375_pNL97_plus_lncRNA::1::19	-454	upstream	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene PEX10	MGC1998, NALD, RNF69, PEX10	peroxisomal biogenesis factor 10	NM_002617, NM_153818, hCT1809271.3, hCT1961950.1, hCT1961951.1, hCT2353009.0	206351_s_at, 206352_s_at	NP_002608.1, NP_722540.1, EAW56105.1, EAW56106.1, EAW56107.1, EAW56108.1
GeneID:55229	PANK4	1	2,439,975	2,458,035	18,060	-	2	1_A375_pNL7_minus_lncRNA::1::14, 2_A375_pNL97_plus_lncRNA::1::20	419, 19	in gene, in gene	1	1	35	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene PANK4	FLJ10782, PANK4, DKFZp547M242	pantothenate kinase 4	NM_018216, hCT15719.3, hCT2336585.0, hCT2336586.0	218771_at	NP_060686.1, EAW56097.1, EAW56098.1, EAW56099.1
GeneID:388585	HES5	1	2,460,184	2,461,684	1,500	-	2	1_A375_pNL7_minus_lncRNA::1::14, 2_A375_pNL97_plus_lncRNA::1::20	4068, 3658	downstream, downstream	1	1	35	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene HES5	HES5, bHLHb38	hairy and enhancer of split 5 (Drosophila)	NM_001010926, hCT1965454.1	239230_at	NP_001010926.1, EAW56096.1
GeneID:79258	MMEL1	1	2,522,081	2,564,481	42,400	-	1	1_A375_pNL7_minus_lncRNA::1::15	-9759	upstream	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene MMEL1	NL2, MGC119456, NEP2, SEP, NEPII, MMEL2, MGC119455, MMEL1, MGC119454, NL1	membrane metallo-endopeptidase-like 1	NM_033467, hCT15720.4, hCT2336578.0, hCT2336579.0	1552930_at	NP_258428.2, EAW56080.1, EAW56081.1, EAW56082.1
GeneID:100287898	LOC100287898	1	2,572,807	2,706,230	133,423	-	1	1_A375_pNL7_minus_lncRNA::1::15	131990	in gene	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100287898	TTC34		XM_002342015, XM_003119811, XM_003120448		XP_002342056.1, XP_003119859.1, XP_003120496.1
GeneID:57470	LRRC47	1	3,696,784	3,713,068	16,284	-	2	1_A375_pNL7_minus_lncRNA::1::16, 2_A375_pNL97_plus_lncRNA::1::21	12, 12	in gene, in gene	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LRRC47	LRRC47, KIAA1185	leucine rich repeat containing 47	NM_020710, hCT2291873.0, hCT11152.3	212904_at	NP_065761.1, EAW71479.1, EAW71478.1
GeneID:9731	KIAA0562	1	3,728,645	3,773,797	45,152	-	1	1_A375_pNL7_minus_lncRNA::1::17	101	in gene	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene KIAA0562	KIAA0562, GlyBP	KIAA0562	NM_014704, hCT1967875.1, hCT2291866.0, hCT2291869.0, hCT11151.4	204074_s_at, 204075_s_at, 243696_at	NP_055519.1, EAW71481.1, EAW71482.1, EAW71483.1, EAW71484.1
GeneID:1677	DFFB	1	3,773,845	3,801,993	28,148	+	1	1_A375_pNL7_minus_lncRNA::1::17	-149	upstream	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene DFFB	DFF-40, DFF40, DFF2, DFFB, CAD, CPAN	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	NM_004402, hCT22751.3, hCT2291526.0, hCT2291529.0, hCT2291531.0, hCT2354959.0, hCT1950426.1, hCT1950427.1	206752_s_at	NP_004393.1, EAW71486.1, EAW71487.1, EAW71488.1, EAW71489.1, EAW71490.1, EAW71485.1, EAW71491.1
GeneID:339448	C1orf174	1	3,805,697	3,816,857	11,160	-	1	2_A375_pNL97_plus_lncRNA::1::22	-807	upstream	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C1orf174	C1orf174, RP13-531C17.2	chromosome 1 open reading frame 174	NM_207356, hCT2354933.0, hCT1762202.2	222000_at, 238010_at	NP_997239.2, EAW71493.1, EAW71492.1
GeneID:100133612	LOC100133612	1	3,816,968	3,832,011	15,043	+	1	2_A375_pNL97_plus_lncRNA::1::22	696	in gene	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100133612	FLJ26663	similar to hCG1815312	NR_024455		
GeneID:261734	NPHP4	1	5,922,870	6,052,531	129,661	-	2	1_A375_pNL7_minus_lncRNA::1::18, 2_A375_pNL97_plus_lncRNA::1::26	-45, 355	upstream, in gene	1	1	23	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene NPHP4	KIAA0673, SLSN4, POC10, FLJ46306, NPHP4	nephronophthisis 4	NM_015102, hCT2296807.0, hCT2354934.0, hCT2354935.0, hCT2354936.0, hCT13736.2	213471_at, 216344_at	NP_055917.1, EAW71511.1, EAW71507.1, EAW71508.1, EAW71509.1, EAW71510.1
GeneID:8514	KCNAB2	1	6,086,380	6,160,523	74,143	+	3	1_A375_pNL7_minus_lncRNA::1::19, 2_A375_pNL97_plus_lncRNA::1::27, 2_A375_pNL97_plus_lncRNA::1::28	26292, -10044, 26308	in gene, upstream, in gene	1	1	19	19	2	1_A375_pNL7_minus_lncRNA::1	27	Gene KCNAB2	KV-BETA-2, AKR6A5, HKvbeta2.1, MGC117289, KCNAB2, HKvbeta2.2, KCNA2B, HKvbeta2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	NM_003636, NM_172130, hCT2296126.0, hCT2296128.0, hCT2296130.0, hCT1957603.1	203402_at, 211791_s_at	NP_003627.1, NP_742128.1, EAW71512.1, EAW71513.1, EAW71514.1, EAW71515.1
GeneID:26038	CHD5	1	6,161,847	6,240,194	78,347	-	4	1_A375_pNL7_minus_lncRNA::1::20, 1_A375_pNL7_minus_lncRNA::1::21, 2_A375_pNL97_plus_lncRNA::1::29, 2_A375_pNL97_plus_lncRNA::1::30	22162, 18370, 22338, 18306	in gene, in gene, in gene, in gene	1	1	27.5	32.5	2	2_A375_pNL97_plus_lncRNA::1	42	Gene CHD5	DKFZp434N231, KIAA0444, CHD5	chromodomain helicase DNA binding protein 5	NM_015557, hCT13728.3	213965_s_at, 217250_s_at	NP_056372.1, EAW71516.1
GeneID:6146	RPL22	1	6,245,080	6,259,679	14,599	-	3	1_A375_pNL7_minus_lncRNA::1::22, 2_A375_pNL97_plus_lncRNA::1::31, 2_A375_pNL97_plus_lncRNA::1::32	-33, -49, -9729	upstream, upstream, upstream	1	1	51.5	67.5	2	2_A375_pNL97_plus_lncRNA::1	108	Gene RPL22	RPL22, HBP15/L22, HBP15, EAP, L22	ribosomal protein L22	NM_000983, hCT2296799.0, hCT2296800.0, hCT2296801.0	208768_x_at, 214042_s_at, 220960_x_at, 221726_at, 221775_x_at	NP_000974.1, EAW71520.1, EAW71518.1, EAW71519.1
GeneID:388591	RNF207	1	6,266,189	6,281,359	15,170	+	3	1_A375_pNL7_minus_lncRNA::1::22, 2_A375_pNL97_plus_lncRNA::1::31, 2_A375_pNL97_plus_lncRNA::1::32	-6477, -6461, 3219	upstream, upstream, in gene	1	1	51.5	67.5	2	2_A375_pNL97_plus_lncRNA::1	108	Gene RNF207	C1orf188, RNF207, FLJ32096, FLJ46380, FLJ46593	ring finger protein 207	NM_207396	1555870_at, 233065_at, 242882_at	NP_997279.2

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:23463	ICMT	1	6,281,253	6,296,044	14,791	-	3	1_A375_pNL7_minus_lncRNA::1::23, 2_A375_pNL97_plus_lncRNA::1::33, 2_A375_pNL97_plus_lncRNA::1::34	-9300, -468, -9364	upstream, upstream, upstream	1	1	21	21	2	1_A375_pNL7_minus_lncRNA::1	36	Gene ICMT	PPMT, PCMT, MSTP098, ICMT, PCCMT, HSTE14, MST098, MGC39955	isoprenylcysteine carboxyl methyltransferase	NM_012405, hCT13725.3, hCT1957602.1	1568726_s_at, 201609_x_at, 201610_at, 201611_s_at, 244591_x_at, 244759_x_at	NP_036537.1, EAW71523.1, EAW71522.1
GeneID:148645	C1orf211	1	6,297,866	6,299,504	1,638	+	3	1_A375_pNL7_minus_lncRNA::1::23, 2_A375_pNL97_plus_lncRNA::1::33, 2_A375_pNL97_plus_lncRNA::1::34	7476, -1356, 7540	downstream, upstream, downstream	1	1	21	21	2	1_A375_pNL7_minus_lncRNA::1	36	Gene C1orf211	C1orf211, MGC40166	chromosome 1 open reading frame 211	XR_111921, XR_109862, XR_114045, hCT1960051.2	1553741_at	EAW71524.1
GeneID:390992	HES3	1	6,304,252	6,305,638	1,386	+	3	1_A375_pNL7_minus_lncRNA::1::23, 2_A375_pNL97_plus_lncRNA::1::33, 2_A375_pNL97_plus_lncRNA::1::34	1092, -7740, 1156	in gene, upstream, in gene	1	1	21	21	2	1_A375_pNL7_minus_lncRNA::1	36	Gene HES3	HES3, bHLHb43	hairy and enhancer of split 3 (Drosophila)	NM_001024598, hCT13735.2		NP_001019769.1, EAW71525.1
GeneID:387509	GPR153	1	6,307,406	6,321,035	13,629	-	2	1_A375_pNL7_minus_lncRNA::1::23, 2_A375_pNL97_plus_lncRNA::1::34	15691, 15627	downstream, downstream	1	1	36	27	1	1_A375_pNL7_minus_lncRNA::1	36	Gene GPR153	DKFZp762B2210, GPR153, PGR1	G protein-coupled receptor 153	NM_207370, hCT2343799.0	221902_at, 64942_at	NP_997253.2, EAW71526.1
GeneID:11332	ACOT7	1	6,324,332	6,453,826	129,494	-	1	2_A375_pNL97_plus_lncRNA::1::35	120106	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ACOT7	BACH, ACOT7, RP1-120G22.10, ACT, hBACH, ACH1, LACH, MGC1126, CTE-II, LACH1	acyl-CoA thioesterase 7	NM_007274, NM_181864, NM_181865, NM_181866, hCT2354960.0, hCT2354961.0, hCT13726.2, hCT1686494.2, hCT1960100.1, hCT1960101.1	208002_s_at, 215726_s_at	NP_009205.3, NP_863654.1, NP_863655.1, NP_863656.1, EAW71527.1, EAW71532.1, EAW71528.1, EAW71529.1, EAW71530.1, EAW71531.1
GeneID:100130071	UNQ6193	1	6,326,515	6,327,292	777	+	1	2_A375_pNL97_plus_lncRNA::1::35	7205	downstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene UNQ6193	LOC100130071	GSQS6193	XR_111922, XR_109863, XR_114046		
GeneID:83715	ESPN	1	6,484,848	6,521,004	36,156	+	1	2_A375_pNL97_plus_lncRNA::1::36	22480	in gene	0	1	14	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene ESPN	DKFZp434A196, DFNB36, ESPN, DKFZp434G2126	espin	NM_031475, hCT2291642.0, hCT2291643.0, hCT2291644.0, hCT2291647.0	223549_s_at, 233979_s_at	NP_113663.2, EAW71538.1, EAW71535.1, EAW71536.1, EAW71537.1
GeneID:79707	NOL9	1	6,581,407	6,614,658	33,251	-	2	1_A375_pNL7_minus_lncRNA::1::24, 2_A375_pNL97_plus_lncRNA::1::37	66, 98	in gene, in gene	1	1	93	110	1	2_A375_pNL97_plus_lncRNA::1	110	Gene NOL9	MGC138483, NET6, MGC131821, NOL9, FLJ23323	nucleolar protein 9	NM_024654, hCT2292165.0	1554062_s_at, 1554064_a_at, 218754_at	NP_078930.3, EAW71550.1
GeneID:80835	TAS1R1	1	6,615,338	6,639,817	24,479	+	2	1_A375_pNL7_minus_lncRNA::1::24, 2_A375_pNL97_plus_lncRNA::1::37	-746, -778	upstream, upstream	1	1	93	110	1	2_A375_pNL97_plus_lncRNA::1	110	Gene TAS1R1	TR1, TAS1R1, GPR70, T1R1, gm148	taste receptor, type 1, member 1	NM_138697, NM_177540, hCT2291651.0, hCT2291656.0, hCT2291658.0, hCT13729.2	1555417_a_at, 1564663_a_at	NP_619642.2, NP_803884.1, EAW71551.1, EAW71552.1, EAW71553.1, EAW71554.1
GeneID:9903	KLHL21	1	6,650,784	6,662,929	12,145	-	1	1_A375_pNL7_minus_lncRNA::1::25	145	in gene	1	0	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene KLHL21	MGC99635, KLHL21, KIAA0469	kelch-like 21 (Drosophila)	NM_014851, hCT2354938.0, hCT12174.2	203068_at	NP_055666.2, EAW71559.1, EAW71558.1
GeneID:148479	PHF13	1	6,673,756	6,684,093	10,337	+	1	2_A375_pNL97_plus_lncRNA::1::38	-124	upstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PHF13	PHF5, SPOC1, MGC43399, PHF13	PHD finger protein 13	NM_153812, hCT13731.3	225005_at	NP_722519.2, EAW71561.1
GeneID:55735	DNAJC11	1	6,694,228	6,761,966	67,738	-	2	1_A375_pNL7_minus_lncRNA::1::26, 2_A375_pNL97_plus_lncRNA::1::39	142, 142	in gene, in gene	1	1	169	181	1	2_A375_pNL97_plus_lncRNA::1	181	Gene DNAJC11	DNAJC11, FLJ10737, dJ126A5.1	DnaJ (Hsp40) homolog, subfamily C, member 11	NM_018198, hCT1967919.1, hCT2292160.0, hCT13722.2	1555360_a_at, 215792_s_at	NP_060668.2, EAW71571.1, EAW71570.1, EAW71572.1
GeneID:23261	CAMTA1	1	6,845,384	7,829,764	984,380	+	8	1_A375_pNL7_minus_lncRNA::1::27, 1_A375_pNL7_minus_lncRNA::1::28, 1_A375_pNL7_minus_lncRNA::1::29, 2_A375_pNL97_plus_lncRNA::1::40, 2_A375_pNL97_plus_lncRNA::1::41, 2_A375_pNL97_plus_lncRNA::1::42, 2_A375_pNL97_plus_lncRNA::1::43, 2_A375_pNL97_plus_lncRNA::1::44	290216, 480792, 831208, 261048, 290296, 480760, 528018, 831192	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	23.6	23.4	5	1_A375_pNL7_minus_lncRNA::1	39	Gene CAMTA1	CAMTA1, KIAA0833	calmodulin binding transcription activator 1	NM_015215	1555370_a_at, 213268_at, 225692_at, 225693_s_at, 227328_at, 241882_at	NP_056030.1
GeneID:100505910	LOC100505910	1	7,110,002	7,111,764	1,762	-	1	2_A375_pNL97_plus_lncRNA::1::40	5332	downstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100505910		hypothetical protein LOC100505910	XM_003119755, XM_003118842, XM_003120578		XP_003119803.1, XP_003118890.1, XP_003120626.1
GeneID:11315	PARK7	1	8,021,714	8,045,342	23,628	+	3	1_A375_pNL7_minus_lncRNA::1::30, 1_A375_pNL7_minus_lncRNA::1::31, 2_A375_pNL97_plus_lncRNA::1::45	-7314, -50, 14	upstream, upstream, in gene	1	1	27	29.5	2	2_A375_pNL97_plus_lncRNA::1	47	Gene PARK7	FLJ92274, FLJ27376, FLJ34360, DJ-1, PARK7, DJ1	Parkinson disease (autosomal recessive, early onset) 7	NM_007262, NM_001123377, hCT2293691.0	200006_at	NP_009193.2, NP_001116849.1, EAW71591.1
GeneID:54206	ERRFI1	1	8,071,779	8,086,393	14,614	-	2	1_A375_pNL7_minus_lncRNA::1::32, 2_A375_pNL97_plus_lncRNA::1::46	-39, -23	upstream, upstream	1	1	25	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene ERRFI1	MIG-6, ERRFI1, MIG6, GENE-33, RALT	ERBB receptor feedback inhibitor 1	NM_018948, hCT1967917.1, hCT2354956.0, hCT12911.3	224657_at	NP_061821.1, EAW71593.1, EAW71592.1, EAW71594.1
GeneID:50651	SLC45A1	1	8,384,390	8,404,227	19,837	+	1	2_A375_pNL97_plus_lncRNA::1::50	-6342	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SLC45A1	SLC45A1, FLJ26758, KIAA0458	solute carrier family 45, member 1	NM_001080397	230458_at	NP_001073866.1
GeneID:473	RERE	1	8,412,464	8,877,699	465,235	-	5	1_A375_pNL7_minus_lncRNA::1::35, 1_A375_pNL7_minus_lncRNA::1::36, 2_A375_pNL97_plus_lncRNA::1::51, 2_A375_pNL97_plus_lncRNA::1::52, 2_A375_pNL97_plus_lncRNA::1::53	393315, 77411, 392963, 114147, 77395	in gene, in gene, in gene, in gene, in gene	1	1	15.33	22	3	2_A375_pNL97_plus_lncRNA::1	23	Gene RERE	ARP, FLJ38775, DNB1, RERE, ATN1L, ARG, KIAA0458	arginine-glutamic acid dipeptide (RE) repeats	NM_012102, NM_001042681, NM_001042682, hCT2297542.2, hCT2350683.0, hCT2350684.0, hCT2354944.0	1557349_at, 200938_s_at, 200939_s_at, 200940_s_at, 221643_s_at	NP_036234.3, NP_001036146.1, NP_001036147.1, EAW71598.1, EAW71599.1, EAW71601.1, EAW71600.1
GeneID:2023	ENO1	1	8,921,063	8,938,780	17,717	-	3	1_A375_pNL7_minus_lncRNA::1::37, 1_A375_pNL7_minus_lncRNA::1::38, 2_A375_pNL97_plus_lncRNA::1::54	636, -196, 92	in gene, upstream, in gene	1	1	18.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	21	Gene ENO1	NNE, PPH, ENO1L1, ENO1, MPB1, MBP-1	enolase 1, (alpha)	NM_001428, hCT2292830.0, hCT2292832.0	201231_s_at, 217294_s_at, 240258_at	NP_001419.1, EAW71605.1, EAW71604.1
GeneID:100505975	LOC100505975	1	8,938,894	8,939,944	1,050	+	3	1_A375_pNL7_minus_lncRNA::1::37, 1_A375_pNL7_minus_lncRNA::1::38, 2_A375_pNL97_plus_lncRNA::1::54	-750, 82, -206	upstream, in gene, upstream	1	1	18.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	21	Gene LOC100505975		hypothetical LOC100505975	XR_111929, XR_109869, XR_114052		
GeneID:727721	LOC727721	1	9,241,898	9,257,040	15,142	-	1	1_A375_pNL7_minus_lncRNA::1::39	14576	in gene	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC727721		hypothetical LOC727721	XR_111923, XR_109875, XR_114057		
GeneID:100506022	LOC100506022	1	9,466,715	9,469,055	2,340	-	1	2_A375_pNL97_plus_lncRNA::1::55	31	in gene	0	1	21	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100506022		hypothetical LOC100506022	XR_111932, XR_109872		
GeneID:56998	CTNNBIP1	1	9,908,334	9,970,316	61,982	-	1	2_A375_pNL97_plus_lncRNA::1::56	-628	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CTNNBIP1	CTNNBIP1, MGC15093, ICAT	catenin, beta interacting protein 1	NM_020248, NM_001012329, hCT2294612.0, hCT9723.3	203081_at	NP_064633.1, NP_001012329.1, EAW71631.1, EAW71632.1
GeneID:84328	LZIC	1	9,989,776	10,002,826	13,050	-	2	1_A375_pNL7_minus_lncRNA::1::40, 2_A375_pNL97_plus_lncRNA::1::57	-694, -630	upstream, upstream	1	1	25	22	1	1_A375_pNL7_minus_lncRNA::1	25	Gene LZIC	MGC15436, LZIC	leucine zipper and CTNNBIP1 domain containing	NM_032368, hCT2294605.0, hCT10119.3	226081_at, 226087_at	NP_115744.2, EAW71634.1, EAW71633.1
GeneID:64802	NMNAT1	1	10,003,486	10,045,556	42,070	+	2	1_A375_pNL7_minus_lncRNA::1::40, 2_A375_pNL97_plus_lncRNA::1::57	34, -30	in gene, upstream	1	1	25	22	1	1_A375_pNL7_minus_lncRNA::1	25	Gene NMNAT1	PNAT1, NMNAT, NMNAT1	nicotinamide nucleotide adenylyltransferase 1	NM_022787, hCT1971598.1, hCT2354939.0	1569631_at, 223692_at, 229852_at	NP_073624.2, EAW71635.1, EAW71636.1
GeneID:23095	KIF1B	1	10,270,764	10,441,661	170,897	+	1	1_A375_pNL7_minus_lncRNA::1::41	-172	upstream	1	0	15	9	1	1_A375_pNL7_minus_lncRNA::1	15	Gene KIF1B	CMT2, KIAA1448, HMSNII, KLP, KIAA0591, CMT2A1, FLJ23699, CMT2A, NBLST1, KIF1B, MGC134844	kinesin family member 1B	NM_015074, NM_183416, hCT2293208.0, hCT2293210.0, hCT2293211.0, hCT2293212.0, hCT16410.4	209234_at, 225878_at, 226968_at	NP_055889.2, NP_904325.2, EAW71641.1, EAW71642.1, EAW71644.1, EAW71645.1, EAW71643.1
GeneID:100287506	LOC100287506	1	10,436,657	10,456,955	20,298	-	2	1_A375_pNL7_minus_lncRNA::1::42, 2_A375_pNL97_plus_lncRNA::1::58	11, 27	in gene, in gene	1	1	28	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene LOC100287506		hypothetical LOC100287506	XR_111920, XR_109874, XR_114056		
GeneID:5226	PGD	1	10,459,085	10,480,201	21,116	+	4	1_A375_pNL7_minus_lncRNA::1::42, 1_A375_pNL7_minus_lncRNA::1::43, 2_A375_pNL97_plus_lncRNA::1::58, 2_A375_pNL97_plus_lncRNA::1::59	-141, 31379, -157, 31411	upstream, downstream, upstream, downstream	1	1	30.5	35.5	2	2_A375_pNL97_plus_lncRNA::1	38	Gene PGD	6PGD, PGD	phosphogluconate dehydrogenase	NM_002631, hCT2293214.0, hCT2293215.0	201118_at	NP_002622.2, EAW71647.1, EAW71648.1
GeneID:378708	APITD1	1	10,490,159	10,512,060	21,901	+	2	1_A375_pNL7_minus_lncRNA::1::43, 2_A375_pNL97_plus_lncRNA::1::59	305, 337	in gene, in gene	1	1	33	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene APITD1	MGC32686, CENPS, APITD1, CENP-S, MHF1	apoptosis-inducing, TAF9-like domain 1	NR_036462, NM_199294, NM_198544, NM_199006	213454_at	NP_954988.1, NP_940946.1, NP_950171.2
GeneID:1676	DFFA	1	10,520,588	10,532,613	12,025	-	4	1_A375_pNL7_minus_lncRNA::1::44, 1_A375_pNL7_minus_lncRNA::1::45, 2_A375_pNL97_plus_lncRNA::1::60, 2_A375_pNL97_plus_lncRNA::1::61	-11, -2363, -59, -2299	upstream, upstream, upstream, upstream	1	1	25.5	28	2	2_A375_pNL97_plus_lncRNA::1	34	Gene DFFA	DFF1, DFFA, ICAD, DFF-45	DNA fragmentation factor, 45kDa, alpha polypeptide	NM_004401, NM_213566, hCT16405.2, hCT1950343.1, hCT1962553.1, hCT1962555.1	203277_at, 223518_at	NP_004392.1, NP_998731.1, EAW71655.1, EAW71656.1, EAW71657.1, EAW71658.1
GeneID:5195	PEX14	1	10,535,003	10,690,815	155,812	+	4	1_A375_pNL7_minus_lncRNA::1::44, 1_A375_pNL7_minus_lncRNA::1::45, 2_A375_pNL97_plus_lncRNA::1::60, 2_A375_pNL97_plus_lncRNA::1::61	-2379, -27, -2331, -91	upstream, upstream, upstream, upstream	1	1	25.5	28	2	2_A375_pNL97_plus_lncRNA::1	34	Gene PEX14	Pex14p, MGC12767, dJ734G22.2, PEX14, NAPP2	peroxisomal biogenesis factor 14	NM_004565, hCT1964433.1, hCT1964434.1, hCT1964436.1	1556915_a_at, 203503_s_at, 33760_at	NP_004556.1, EAW71659.1, EAW71660.1, EAW71661.1
GeneID:54897	CASZ1	1	10,696,661	10,856,707	160,046	-	2	1_A375_pNL7_minus_lncRNA::1::46, 2_A375_pNL97_plus_lncRNA::1::62	-93, -77	upstream, upstream	1	1	33	32	1	1_A375_pNL7_minus_lncRNA::1	33	Gene CASZ1	ZNF693, dJ734G22.1, CST, FLJ12223, SRG, FLJ20321, CASZ1	castor zinc finger 1	NM_017766, NM_001079843, hCT2294619.0, hCT2294620.0	220015_at, 230420_at, 233863_at, 235605_at, 243386_at	NP_060236.3, NP_001073312.1, EAW71662.1, EAW71663.1
GeneID:148345	C1orf127	1	11,006,530	11,042,094	35,564	-	1	1_A375_pNL7_minus_lncRNA::1::47	2414	in gene	1	0	19	10	1	1_A375_pNL7_minus_lncRNA::1	19	Gene C1orf127	FLJ37118, C1orf127, FLJ37833	chromosome 1 open reading frame 127	NM_001170754, hCT2292950.1, hCT2341015.0	1553444_a_at	NP_001164225.1, EAW71667.1, EAW71666.1
GeneID:23435	TARDBP	1	11,072,679	11,085,549	12,870	+	2	1_A375_pNL7_minus_lncRNA::1::48, 2_A375_pNL97_plus_lncRNA::1::63	-71, -87	upstream, upstream	1	1	33	31	1	1_A375_pNL7_minus_lncRNA::1	33	Gene TARDBP	TARDBP, TDP-43, ALS10	TAR DNA binding protein	NM_007375, hCT2292403.0, hCT2292404.0, hCT2292408.0, hCT2292409.0, hCT2292411.0	200020_at, 221264_s_at	NP_031401.1, EAW71670.1, EAW71669.1, EAW71671.1, EAW71672.1, EAW71673.1
GeneID:5394	EXOSC10	1	11,126,675	11,159,938	33,263	-	1	2_A375_pNL97_plus_lncRNA::1::64	178	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene EXOSC10	p4, PMSCL2, Rrp6p, EXOSC10, RRP6, PMSCL, PM-Scl, p2, PM/Scl-100, p3	exosome component 10	NM_001001998, NM_002685, hCT2292938.0, hCT2292940.0, hCT2292943.0	1559031_at, 207541_s_at	NP_001001998.1, NP_002676.1, EAW71677.1, EAW71678.1, EAW71679.1
GeneID:2475	MTOR	1	11,166,588	11,322,608	156,020	-	1	2_A375_pNL97_plus_lncRNA::1::64	162848	downstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MTOR	RAFT1, RAPT1, MTOR, FRAP1, FRAP, FLJ44809, FRAP2	mechanistic target of rapamycin (serine/threonine kinase)	NM_004958, hCT2292935.0, hCT2292936.0, hCT15901.3	202288_at, 215381_at	NP_004949.1, EAW71682.1, EAW71681.1, EAW71683.1
GeneID:29914	UBIAD1	1	11,333,255	11,348,491	15,236	+	2	1_A375_pNL7_minus_lncRNA::1::49, 2_A375_pNL97_plus_lncRNA::1::65	569, 121	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene UBIAD1	TERE1, UBIAD1, RP4-796F18.1, SCCD	UbiA prenyltransferase domain containing 1	NM_013319, hCT15895.3	219131_at, 230474_at	NP_037451.1, EAW71686.1
GeneID:57540	PTCHD2	1	11,539,295	11,597,640	58,345	+	4	1_A375_pNL7_minus_lncRNA::1::50, 1_A375_pNL7_minus_lncRNA::1::51, 2_A375_pNL97_plus_lncRNA::1::66, 2_A375_pNL97_plus_lncRNA::1::67	-5439, -303, -255, 1057	upstream, upstream, upstream, in gene	1	1	17.67	20.33	3	2_A375_pNL97_plus_lncRNA::1	22	Gene PTCHD2	DISP3, PTCHD2, KIAA1337	patched domain containing 2	NM_020780	230019_s_at, 234355_s_at	NP_065831.1
GeneID:26270	FBXO6	1	11,724,150	11,734,411	10,261	+	1	2_A375_pNL97_plus_lncRNA::1::70	17018	downstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene FBXO6	FBS2, FBG2, Fbx6b, FBX6, FBXO6	F-box protein 6	NM_018438, hCT15898.3	231769_at	NP_060908.1, EAW71696.1
GeneID:10459	MAD2L2	1	11,734,537	11,751,678	17,141	-	1	2_A375_pNL97_plus_lncRNA::1::70	10510	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MAD2L2	REV7, MAD2L2, MAD2B	MAD2 mitotic arrest deficient-like 2 (yeast)	NM_006341, NM_001127325, hCT15896.3, hCT1950340.1, hCT1956193.1	223234_at	NP_006332.3, NP_001120797.1, EAW71697.1, EAW71698.1, EAW71699.1
GeneID:4524	MTHFR	1	11,845,787	11,866,160	20,373	-	1	1_A375_pNL7_minus_lncRNA::1::54	48	in gene	1	0	25	14	1	1_A375_pNL7_minus_lncRNA::1	25	Gene MTHFR	MTHFR		NM_005957, hCT2292919.0, hCT2292920.0	206600_at, 217070_at, 217071_s_at, 226929_at, 239035_at	NP_005948.3, EAW71708.1, EAW71709.1
GeneID:1185	CLCN6	1	11,866,207	11,903,201	36,994	+	1	1_A375_pNL7_minus_lncRNA::1::54	-95	upstream	1	0	25	14	1	1_A375_pNL7_minus_lncRNA::1	25	Gene CLCN6	KIAA0046, CLCN6, CLC-6	chloride channel 6	NM_001286, NM_021736, NM_021735, NM_021737, hCT2292429.0, hCT2292430.0, hCT2292431.0, hCT2292432.0, hCT2292434.0, hCT16183.3, hCT1778342.2	203950_s_at	NP_001277.1, NP_068504.1, NP_068503.1, NP_068505.1, EAW71710.1, EAW71712.1, EAW71711.1, EAW71713.1, EAW71714.1, EAW71715.1, EAW71716.1
GeneID:4879	NPPB	1	11,917,521	11,918,992	1,471	-	2	1_A375_pNL7_minus_lncRNA::1::55, 2_A375_pNL97_plus_lncRNA::1::71	-576, -544	upstream, upstream	1	1	27	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene NPPB	NPPB, BNP	natriuretic peptide B	NM_002521, hCT2292912.0, hCT16182.2	206801_at	NP_002512.1, EAW71719.1, EAW71718.1
GeneID:26829	RNU5E	1	11,968,211	11,968,329	118	+	4	1_A375_pNL7_minus_lncRNA::1::56, 1_A375_pNL7_minus_lncRNA::1::57, 2_A375_pNL97_plus_lncRNA::1::72, 2_A375_pNL97_plus_lncRNA::1::73	-115, 1837, -179, 1885	upstream, downstream, upstream, downstream	1	1	31	25.5	2	1_A375_pNL7_minus_lncRNA::1	38	Gene RNU5E	RNU5E, U5E	RNA, U5E small nuclear	NR_002754		
GeneID:90231	KIAA2013	1	11,980,122	11,986,480	6,358	-	3	1_A375_pNL7_minus_lncRNA::1::57, 2_A375_pNL97_plus_lncRNA::1::73, 2_A375_pNL97_plus_lncRNA::1::74	16432, 16384, -3488	downstream, downstream, upstream	1	1	20.5	21.5	2	1_A375_pNL7_minus_lncRNA::1	24	Gene KIAA2013	KIAA2013, MGC33867	KIAA2013	NM_138346, hCT2292499.0, hCT2292500.0, hCT2354957.0, hCT16188.3	1555933_at, 224706_at, 224708_at	NP_612355.1, EAW71722.1, EAW71720.1, EAW71721.1, EAW71723.1
GeneID:5351	PLOD1	1	11,994,746	12,035,594	40,848	+	2	2_A375_pNL97_plus_lncRNA::1::74, 2_A375_pNL97_plus_lncRNA::1::75	-4778, 45702	upstream, downstream	0	1	17	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene PLOD1	LH, FLJ42041, LLH, PLOD, PLOD1, LH1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	NM_000302, hCT2292291.0, hCT16181.3	200827_at	NP_000293.2, EAW71725.1, EAW71724.1
GeneID:9927	MFN2	1	12,040,238	12,073,572	33,334	+	1	2_A375_pNL97_plus_lncRNA::1::75	210	in gene	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MFN2	CMT2A2, MARF, HSG, CMT2A, MFN2, CPRP1, KIAA0214	mitofusin 2	NM_014874, NM_001127660, hCT2292293.0, hCT16180.3	1566105_at, 201155_s_at, 216205_s_at	NP_055689.1, NP_001121132.1, EAW71726.1, EAW71727.1
GeneID:390998	LOC390998	1	12,280,784	12,281,164	380	-	3	1_A375_pNL7_minus_lncRNA::1::58, 2_A375_pNL97_plus_lncRNA::1::76, 2_A375_pNL97_plus_lncRNA::1::77	-8916, -8852, -9588	upstream, upstream, upstream	1	1	21	27.5	2	2_A375_pNL97_plus_lncRNA::1	39	Gene LOC390998		ribosomal protein L10 pseudogene		216589_at	

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:55187	VPS13D	1	12,290,113	12,572,099	281,986	+	4	1_A375_pNL7_minus_lncRNA::1::58, 1_A375_pNL7_minus_lncRNA::1::59, 2_A375_pNL97_plus_lncRNA::1::76, 2_A375_pNL97_plus_lncRNA::1::77	-33, 248895, -97, 639	upstream, in gene, upstream, in gene	1	1	20	22	3	2_A375_pNL97_plus_lncRNA::1	39	Gene VPS13D	VPS13D, FLJ23066	vacuolar protein sorting 13 homolog D (S. cerevisiae)	NM_015378, NM_018156, hCT2292306.0, hCT2292307.0, hCT2292309.0	1557571_at, 212323_s_at, 212324_s_at, 212326_at, 220221_at	NP_056193.2, NP_060626.2, EAW71737.1, EAW71738.1, EAW71739.1
GeneID:9249	DHRS3	1	12,627,939	12,677,820	49,881	-	2	2_A375_pNL97_plus_lncRNA::1::79, 2_A375_pNL97_plus_lncRNA::1::80	21724, 700	in gene, in gene	0	1	9.5	21	2	2_A375_pNL97_plus_lncRNA::1	23	Gene DHRS3	RDH17, DHRS3, Rsdr1, retSDR1, SDR16C1, SDR1	dehydrogenase/reductase (SDR family) member 3	NM_004753, hCT1776689.1	202481_at	NP_004744.2, EAW71743.1
GeneID:114827	FHAD1	1	15,573,768	15,724,622	150,854	+	2	2_A375_pNL97_plus_lncRNA::1::81, 2_A375_pNL97_plus_lncRNA::1::82	90616, 105368	in gene, in gene	0	1	19	21	2	2_A375_pNL97_plus_lncRNA::1	27	Gene FHAD1	DKFZp686P19183, DKFZp686G2134, FHAD1, KIAA1937, FLJ31291	forkhead-associated (FHA) phosphopeptide binding domain 1	NM_052929	1557771_at, 1560097_at, 1563639_a_at, 1563830_a_at, 1563961_at, 1564635_a_at	NP_443161.1
GeneID:842	CASP9	1	15,818,791	15,850,790	31,999	-	2	1_A375_pNL7_minus_lncRNA::1::60, 2_A375_pNL97_plus_lncRNA::1::83	-2426, -2378	upstream, upstream	1	1	35	28	1	1_A375_pNL7_minus_lncRNA::1	35	Gene CASP9	APAF3, MCH6, APAF-3, ICE-LAP6, CASP9, CASPASE-9c	caspase 9, apoptosis-related cysteine peptidase	NM_001229, NM_032996, hCT16492.3, hCT1966726.1	203984_s_at, 210775_x_at	NP_001220.2, NP_127463.1, EAW51730.1, EAW51731.1
GeneID:23341	DNAJC16	1	15,853,352	15,898,228	44,876	+	2	1_A375_pNL7_minus_lncRNA::1::60, 2_A375_pNL97_plus_lncRNA::1::83	-136, -184	upstream, upstream	1	1	35	28	1	1_A375_pNL7_minus_lncRNA::1	35	Gene DNAJC16	DKFZp686N0387, DNAJC16, DKFZp686G1298, DKFZp781I1547, KIAA0962	DnaJ (Hsp40) homolog, subfamily C, member 16	NM_015291, hCT2295815.0, hCT2352487.0, hCT2352488.0	212908_at, 212911_at, 217356_at	NP_056106.1, EAW51733.1, EAW51732.1, EAW51734.1
GeneID:348487	FAM131C	1	16,384,264	16,400,127	15,863	-	2	1_A375_pNL7_minus_lncRNA::1::61, 2_A375_pNL97_plus_lncRNA::1::84	-2433, -3233	upstream, upstream	1	1	19	22	1	1_A375_pNL7_minus_lncRNA::1	19	Gene FAM131C	C1orf117, RP11-5P18.9, FAM131C, FLJ36766	family with sequence similarity 131, member C	NM_182623, hCT15838.3, hCT2296328.0	235455_at	NP_872429.2, EAW51766.1, EAW51767.1
GeneID:1969	EPHA2	1	16,450,832	16,482,582	31,750	-	2	1_A375_pNL7_minus_lncRNA::1::62, 1_A375_pNL7_minus_lncRNA::1::63	33078, 54	downstream, in gene	1	0	21	16.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene EPHA2	ARCC2, EPHA2, ECK	EPH receptor A2	NM_004431, hCT15831.2, hCT2296325.0	203499_at	NP_004422.2, EAW51769.1, EAW51770.1
GeneID:100506484	LOC100506484	1	16,481,730	16,483,824	2,094	+	1	1_A375_pNL7_minus_lncRNA::1::63	798	in gene	1	0	16	16	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100506484		hypothetical LOC100506484	XR_108364		
GeneID:54455	FBXO42	1	16,576,559	16,678,948	102,389	-	2	1_A375_pNL7_minus_lncRNA::1::64, 2_A375_pNL97_plus_lncRNA::1::86	-204, 228	upstream, in gene	1	1	24	15	1	1_A375_pNL7_minus_lncRNA::1	24	Gene FBXO42	JFK, FBXO42, Fbx42, KIAA1332	F-box protein 42	NM_018994, hCT15835.3, hCT2296319.0	1559566_at, 221812_at, 221813_at, 47773_at	NP_061867.1, EAW51774.1, EAW51775.1
GeneID:26099	C1orf144	1	16,693,583	16,724,640	31,057	+	2	1_A375_pNL7_minus_lncRNA::1::65, 2_A375_pNL97_plus_lncRNA::1::87	337, 305	in gene, in gene	1	1	36	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene C1orf144	C1orf144, DKFZp566C0424, MGC70432	chromosome 1 open reading frame 144	NM_015609, NM_001114600, hCT2295884.1	212003_at, 212004_at	NP_056424.1, NP_001108072.1, EAW51777.1
GeneID:374955	SPATA21	1	16,725,138	16,763,919	38,781	-	2	1_A375_pNL7_minus_lncRNA::1::66, 2_A375_pNL97_plus_lncRNA::1::88	-3217, -3185	upstream, upstream	1	1	36	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene SPATA21	spergen-2, spergen2, MGC27074, SPATA21	spermatogenesis associated 21	NM_198546, hCT1642372.2	1570241_at, 1570242_x_at	NP_940948.1, EAW51779.1
GeneID:55707	NECAP2	1	16,767,167	16,786,585	19,418	+	2	1_A375_pNL7_minus_lncRNA::1::66, 2_A375_pNL97_plus_lncRNA::1::88	-31, -63	upstream, upstream	1	1	36	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene NECAP2	NECAP2, FLJ10420	NECAP endocytosis associated 2	NM_001145277, NM_001145278, NM_018090, hCT15840.4, hCT1961738.1, hCT1961739.1, hCT1961740.1, hCT1961742.1	220731_s_at	NP_001138749.1, NP_001138750.1, NP_060560.1, EAW51780.1, EAW51783.1, EAW51784.1, EAW51781.1, EAW51782.1
GeneID:55672	NBPF1	1	16,890,412	16,939,982	49,570	-	1	2_A375_pNL97_plus_lncRNA::1::89	78	in gene	0	1	53	59	1	2_A375_pNL97_plus_lncRNA::1	59	Gene NBPF1	NBG, AB14, AB13, AB23, AD2, KIAA1693, FLJ20719, NBPF, NBPF1	neuroblastoma breakpoint family, member 1	NM_017940	230712_at	NP_060410.2
GeneID:100506687	LOC100506687	1	17,215,034	17,216,161	1,127	-	1	2_A375_pNL97_plus_lncRNA::1::92	-6591	upstream	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100506687		hypothetical LOC100506687	XR_108365		
GeneID:26870	RNU1-2	1	17,222,475	17,222,638	163	+	3	1_A375_pNL7_minus_lncRNA::1::69, 2_A375_pNL97_plus_lncRNA::1::92, 2_A375_pNL97_plus_lncRNA::1::93	9077, 277, 9109	downstream, downstream, downstream	1	1	53	67.5	2	2_A375_pNL97_plus_lncRNA::1	112	Gene RNU1-2	RNU1C2, U1C21, U1C1, RNU1C1, RNU1-2	RNA, U1 small nuclear 2	NR_004427		
GeneID:9696	CROCC	1	17,248,445	17,299,474	51,029	+	2	1_A375_pNL7_minus_lncRNA::1::70, 2_A375_pNL97_plus_lncRNA::1::94	-8269, -7613	upstream, upstream	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene CROCC	CROCC, ROLT, KIAA0445	ciliary rootlet coiled-coil, rootletin	NM_014675, hCT2253457.0, hCT2253458.0, hCT2253459.0, hCT2253460.0	206274_s_at, 216419_at	NP_055490.3, EAW94814.1, EAW94815.1, EAW94816.1, EAW94817.1
GeneID:51702	PADI3	1	17,575,593	17,610,728	35,135	+	1	2_A375_pNL97_plus_lncRNA::1::95	44919	downstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene PADI3	MGC126306, PAD3, PADI3, PDI3, MGC126307	peptidyl arginine deiminase, type III	NM_016233, hCT16246.2	220779_at	NP_057317.2, EAW94834.1
GeneID:55920	RCC2	1	17,733,251	17,766,220	32,969	-	1	2_A375_pNL97_plus_lncRNA::1::96	124	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene RCC2	DKFZp762N0610, KIAA1470, RCC2, TD-60	regulator of chromosome condensation 2	NM_018715, NM_001136204, hCT16253.3, hCT2255232.1	224578_at	NP_061185.1, NP_001129676.1, EAW94838.1, EAW94839.1
GeneID:55160	ARHGEF10L	1	17,866,330	18,024,370	158,040	+	1	1_A375_pNL7_minus_lncRNA::1::71	5798	in gene	1	0	20	11	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ARHGEF10L	GrinchGEF, ARHGEF10L, FLJ10521, RP11-473A10.1, KIAA1626	Rho guanine nucleotide exchange factor (GEF) 10-like	NM_018125, NM_001011722, hCT1955046.1, hCT2253470.0, hCT2253471.0, hCT2253474.0, hCT2253475.0	1570511_at, 221656_s_at	NP_060595.3, NP_001011722.2, EAW94840.1, EAW94841.1, EAW94842.1, EAW94843.1, EAW94844.1
GeneID:81569	ACTL8	1	18,149,477	18,153,558	4,081	+	2	1_A375_pNL7_minus_lncRNA::1::72, 2_A375_pNL97_plus_lncRNA::1::97	8811, 8811	downstream, downstream	1	1	28	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene ACTL8	ACTL8, CT57	actin-like 8	NM_030812, hCT16251.3	214957_at	NP_110439.2, EAW94846.1
GeneID:8659	ALDH4A1	1	19,197,924	19,229,293	31,369	-	1	1_A375_pNL7_minus_lncRNA::1::74	77	in gene	1	0	21	14	1	1_A375_pNL7_minus_lncRNA::1	21	Gene ALDH4A1	ALDH4, P5CDh, DKFZp779M035, ALDH4A1, P5CD	aldehyde dehydrogenase 4 family, member A1	NM_003748, NM_170726, NM_001161504, hCT16232.3, hCT1955043.1, hCT2252965.0	203722_at, 211552_s_at	NP_003739.2, NP_733844.1, NP_001154976.1, EAW94858.1, EAW94859.1, EAW94860.1
GeneID:100302276	MIR1290	1	19,223,565	19,223,642	77	-	1	1_A375_pNL7_minus_lncRNA::1::74	-5574	upstream	1	0	21	14	1	1_A375_pNL7_minus_lncRNA::1	21	Gene MIR1290	MIRN1290, hsa-mir-1290, MIR1290	microRNA 1290	NR_031622		
GeneID:126917	IFFO2	1	19,230,774	19,282,826	52,052	-	5	1_A375_pNL7_minus_lncRNA::1::74, 1_A375_pNL7_minus_lncRNA::1::75, 2_A375_pNL97_plus_lncRNA::1::99, 2_A375_pNL97_plus_lncRNA::1::100, 2_A375_pNL97_plus_lncRNA::1::101	53610, 23722, 29941, 23626, 1050	downstream, in gene, in gene, in gene, in gene	1	1	16	17.25	4	2_A375_pNL97_plus_lncRNA::1	22	Gene IFFO2	IFFO2	intermediate filament family orphan 2	NM_001136265	225615_at	NP_001129737.1
GeneID:23352	UBR4	1	19,401,000	19,536,746	135,746	-	2	1_A375_pNL7_minus_lncRNA::1::76, 2_A375_pNL97_plus_lncRNA::1::102	-102, -214	upstream, upstream	1	1	28	19	1	1_A375_pNL7_minus_lncRNA::1	28	Gene UBR4	KIAA0462, FLJ41863, KIAA1307, ZUBR1, p600, UBR4, RBAF600	ubiquitin protein ligase E3 component n-recognin 4	NM_020765, hCT2256791.0, hCT2256792.0, hCT2256793.0, hCT2256794.0, hCT2256795.0, hCT2357800.0	1563113_at, 211950_at, 215636_at, 231669_at, 232907_at	NP_065816.2, EAW94865.1, EAW94864.1, EAW94866.1, EAW94867.1, EAW94868.1, EAW94869.1
GeneID:23065	KIAA0090	1	19,544,584	19,578,046	33,462	-	4	1_A375_pNL7_minus_lncRNA::1::76, 1_A375_pNL7_minus_lncRNA::1::77, 2_A375_pNL97_plus_lncRNA::1::102, 2_A375_pNL97_plus_lncRNA::1::103	41198, -162, 41086, -66	downstream, upstream, downstream, upstream	1	1	32	27.5	2	2_A375_pNL97_plus_lncRNA::1	36	Gene KIAA0090	RP1-43E13.1, KIAA0090	KIAA0090	NM_015047, hCT1955051.1, hCT2357806.0, hCT32353.3	1556186_s_at, 212394_at, 212395_s_at, 212396_s_at, 215991_s_at	NP_055862.1, EAW94872.1, EAW94870.1, EAW94871.1
GeneID:51154	MRTO4	1	19,578,075	19,586,622	8,547	+	2	1_A375_pNL7_minus_lncRNA::1::77, 2_A375_pNL97_plus_lncRNA::1::103	133, 37	in gene, in gene	1	1	36	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene MRTO4	MRT4, dJ657E11.4, MRTO4, C1orf33	mRNA turnover 4 homolog (S. cerevisiae)	NM_016183, hCT1955050.1, hCT1966273.1, hCT32350.3	220668_s_at, 235763_at	NP_057267.2, EAW94873.1, EAW94874.1, EAW94875.1
GeneID:3362	HTR6	1	19,991,780	20,006,055	14,275	+	2	1_A375_pNL7_minus_lncRNA::1::78, 2_A375_pNL97_plus_lncRNA::1::104	11324, 11372	in gene, in gene	1	1	39	50	1	2_A375_pNL97_plus_lncRNA::1	50	Gene HTR6	HTR6, 5-HT6R, 5-HT6	5-hydroxytryptamine (serotonin) receptor 6	NM_000871, hCT29015.2	1552857_a_at, 206944_at	NP_000862.1, EAW94896.1
GeneID:255104	TMCO4	1	20,008,706	20,126,410	117,704	-	2	1_A375_pNL7_minus_lncRNA::1::78, 2_A375_pNL97_plus_lncRNA::1::104	123306, 123258	downstream, downstream	1	1	39	50	1	2_A375_pNL97_plus_lncRNA::1	50	Gene TMCO4	TMCO4, DKFZp686C23231, RP5-1056L3.6	transmembrane and coiled-coil domains 4	NM_181719, hCT1955765.1, hCT2258747.0, hCT2258749.0, hCT2357818.0, hCT2357819.0, hCT2357820.0, hCT29016.3	1560292_a_at, 227007_at	NP_859070.3, EAW94899.1, EAW94897.1, EAW94898.1, EAW94900.1, EAW94901.1, EAW94902.1, EAW94903.1
GeneID:127731	VWA5B1	1	20,617,412	20,681,387	63,975	+	2	1_A375_pNL7_minus_lncRNA::1::79, 2_A375_pNL97_plus_lncRNA::1::105	68220, 67996	downstream, downstream	1	1	24	13	1	1_A375_pNL7_minus_lncRNA::1	24	Gene VWA5B1	FLJ32784, FLJ43845, VWA5B1	von Willebrand factor A domain containing 5B1	NM_001039500	1552853_at, 1552854_a_at	NP_001034589.2
GeneID:339505	LOC339505	1	20,686,294	20,755,287	68,993	-	5	1_A375_pNL7_minus_lncRNA::1::79, 1_A375_pNL7_minus_lncRNA::1::80, 2_A375_pNL97_plus_lncRNA::1::105, 2_A375_pNL97_plus_lncRNA::1::106, 2_A375_pNL97_plus_lncRNA::1::107	69655, 57207, 69879, 57207, 17262	downstream, in gene, downstream, in gene, in gene	1	1	24	24.33	3	2_A375_pNL97_plus_lncRNA::1	42	Gene LOC339505		hypothetical LOC339505	NR_033887	1557373_at	
GeneID:55450	CAMK2N1	1	20,808,884	20,812,728	3,844	-	1	2_A375_pNL97_plus_lncRNA::1::106	-8456	upstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CAMK2N1	RP11-401M16.1, CAMK2N1, MGC22256, PRO1489	calcium/calmodulin-dependent protein kinase II inhibitor 1	NM_018584, hCT1955770.2, hCT29420.4	218309_at, 226302_x_at, 229163_at	NP_061054.2, EAW94924.1, EAW94923.1
GeneID:79594	MUL1	1	20,825,941	20,834,674	8,733	-	3	1_A375_pNL7_minus_lncRNA::1::81, 2_A375_pNL97_plus_lncRNA::1::108, 2_A375_pNL97_plus_lncRNA::1::109	82, 13490, 146	in gene, downstream, in gene	1	1	19	18.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene MUL1	MAPL, RNF218, MULAN, C1orf166, FLJ12875, MUL1, RP11-401M16.2, GIDE	mitochondrial E3 ubiquitin ligase 1	NM_024544, hCT2258548.0, hCT2258550.0, hCT2357795.0, hCT29419.2	218246_at	NP_078820.2, EAW94928.1, EAW94926.1, EAW94927.1, EAW94929.1
GeneID:65018	PINK1	1	20,959,948	20,978,004	18,056	+	1	2_A375_pNL97_plus_lncRNA::1::110	27748	downstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PINK1	FLJ27236, PARK6, BRPK, PINK1	PTEN induced putative kinase 1	NM_032409, hCT2357824.0, hCT30119.3	209018_s_at, 209019_s_at	NP_115785.1, EAW94934.1, EAW94935.1
GeneID:1650	DDOST	1	20,978,260	20,988,037	9,777	-	1	2_A375_pNL97_plus_lncRNA::1::110	341	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene DDOST	AGER1, DDOST, AGE-R1, MGC2191, OST48, OKSW-cl.45, WBP1, OST, OKSWcl45, KIAA0115	dolichyl-diphosphooligosaccharide--protein glycosyltransferase	NM_005216, hCT1955779.1, hCT1955780.1, hCT1955781.1, hCT2258547.0, hCT30117.3	208674_x_at, 208675_s_at	NP_005207.2, EAW94937.1, EAW94936.1, EAW94938.1, EAW94939.1, EAW94940.1
GeneID:57576	KIF17	1	20,990,507	21,044,317	53,810	-	1	2_A375_pNL97_plus_lncRNA::1::110	56621	downstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene KIF17	KIF3X, KIAA1405, KIF17B, KIF17	kinesin family member 17	NM_020816, NM_001122819, hCT1955782.1, hCT2258539.0, hCT2258541.0, hCT2258542.0, hCT2357823.0, hCT30118.3	222144_at	NP_065867.2, NP_001116291.1, EAW94941.1, EAW94942.1, EAW94944.1, EAW94946.1, EAW94943.1, EAW94945.1
GeneID:50809	HP1BP3	1	21,069,171	21,113,181	44,010	-	1	1_A375_pNL7_minus_lncRNA::1::82	221	in gene	1	0	21	17	1	1_A375_pNL7_minus_lncRNA::1	21	Gene HP1BP3	HP1BP3, MGC43701	heterochromatin protein 1, binding protein 3	NM_016287, hCT2258531.0, hCT2258534.0, hCT2258535.0, hCT30116.2	1554251_at, 220633_s_at, 224591_at, 224592_x_at, 229204_at	NP_057371.2, EAW94953.1, EAW94950.1, EAW94951.1, EAW94952.1
GeneID:1889	ECE1	1	21,543,740	21,672,034	128,294	-	1	2_A375_pNL97_plus_lncRNA::1::111	83682	in gene	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ECE1	ECE, ECE1	endothelin converting enzyme 1	NM_001397, NM_001113347, NM_001113348, NM_001113349, hCT1686617.1, hCT1955776.0, hCT1955777.1, hCT1955778.1, hCT2254416.0, hCT2254420.0, hCT2254422.0, hCT2254423.0, hCT2254425.0, hCT2254428.0	201749_at, 201750_s_at	NP_001388.1, NP_001106818.1, NP_001106819.1, NP_001106820.1, EAW94958.1, EAW94963.1, EAW94957.1, EAW94959.1, EAW94960.1, EAW94961.1, EAW94962.1, EAW94964.1, EAW94965.1, EAW94966.1
GeneID:100506824	LOC100506824	1	21,592,575	21,593,744	1,169	+	1	2_A375_pNL97_plus_lncRNA::1::111	-4223	upstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506824		hypothetical LOC100506824	XR_112046, XR_108370, XR_115632		
GeneID:84224	NBPF3	1	21,766,631	21,811,393	44,762	+	2	1_A375_pNL7_minus_lncRNA::1::83, 2_A375_pNL97_plus_lncRNA::1::112	13993, 13961	in gene, in gene	1	1	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene NBPF3	AE2, DKFZp434D177, NBPF3	neuroblastoma breakpoint family, member 3	NM_032264, hCT1955783.1, hCT2253622.0, hCT2253623.0	1558825_s_at, 223638_at	NP_115640.1, EAW94973.1, EAW94971.1, EAW94972.1
GeneID:5909	RAP1GAP	1	21,922,708	21,995,856	73,148	-	4	1_A375_pNL7_minus_lncRNA::1::84, 1_A375_pNL7_minus_lncRNA::1::85, 2_A375_pNL97_plus_lncRNA::1::113, 2_A375_pNL97_plus_lncRNA::1::114	21296, 10048, 21328, 10064	in gene, in gene, in gene, in gene	1	1	26.5	30	2	1_A375_pNL7_minus_lncRNA::1	34	Gene RAP1GAP	RAP1GAP, RAPGAP, RAP1GAP1, RAP1GA1, KIAA0474, RAP1GAPII	RAP1 GTPase activating protein	NM_001145657, NM_001145658, NM_002885, hCT1848938.2, hCT2254405.1, hCT2254407.1, hCT2254408.1, hCT2254409.1, hCT2254410.1, hCT2357816.0, hCT28619.4	203911_at, 210618_at	NP_001139129.1, NP_001139130.1, NP_002876.2, EAW94979.1, EAW94980.1, EAW94986.1, EAW94981.1, EAW94982.1, EAW94983.1, EAW94984.1, EAW94985.1
GeneID:84196	USP48	1	22,004,791	22,109,688	104,897	-	3	1_A375_pNL7_minus_lncRNA::1::86, 1_A375_pNL7_minus_lncRNA::1::87, 2_A375_pNL97_plus_lncRNA::1::115	76520, 120, 152	in gene, in gene, in gene	1	1	21	17.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene USP48	USP31, MGC14879, RAP1GA1, DKFZp762M1713, USP48, MGC132556	ubiquitin specific peptidase 48	NM_032236, NM_001032730, hCT1955736.1, hCT2254397.0, hCT2254398.0, hCT2254402.0, hCT2254403.0, hCT2254404.0	220078_at, 220079_s_at, 225925_s_at, 229812_at, 232621_at	NP_115612.4, NP_001027902.1, EAW94987.1, EAW94990.1, EAW94991.1, EAW94992.1, EAW94988.1, EAW94989.1
GeneID:29092	HSPC157	1	22,351,707	22,357,716	6,009	+	1	2_A375_pNL97_plus_lncRNA::1::117	-187	upstream	0	1	18	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene HSPC157		hypothetical LOC29092	NR_023918, NR_023919	219865_at	
GeneID:9923	ZBTB40	1	22,778,344	22,857,650	79,306	+	1	2_A375_pNL97_plus_lncRNA::1::118	504	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZBTB40	ZNF923, MGC133098, KIAA0478, ZBTB40	zinc finger and BTB domain containing 40	NM_014870, NM_001083621, hCT1957953.1, hCT1957954.1	1559726_at, 203958_s_at, 203959_s_at	NP_055685.3, NP_001077090.1, EAW95011.1, EAW95012.1
GeneID:2046	EPHA8	1	22,890,004	22,930,087	40,083	+	2	1_A375_pNL7_minus_lncRNA::1::90, 2_A375_pNL97_plus_lncRNA::1::119	48140, 48108	downstream, downstream	1	1	72	79	1	2_A375_pNL97_plus_lncRNA::1	79	Gene EPHA8	EK3, EEK, EPHA8, HEK3, KIAA1459	EPH receptor A8	NM_001006943, NM_020526, hCT31226.3	1554069_at, 231796_at	NP_001006944.1, NP_065387.1, EAW95013.1
GeneID:729059	LOC729059	1	23,337,327	23,342,343	5,016	-	2	1_A375_pNL7_minus_lncRNA::1::91, 2_A375_pNL97_plus_lncRNA::1::120	-3385, -3529	upstream, upstream	1	1	22	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC729059		hypothetical LOC729059	XR_112037, XR_108371, XR_115633	231551_at	
GeneID:23028	KDM1A	1	23,345,941	23,410,184	64,243	+	2	1_A375_pNL7_minus_lncRNA::1::91, 2_A375_pNL97_plus_lncRNA::1::120	-213, -69	upstream, upstream	1	1	22	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene KDM1A	KIAA0601, BHC110, KDM1A, LSD1, AOF2, KDM1	lysine (K)-specific demethylase 1A	NM_015013, NM_001009999, hCT1955774.1, hCT2254191.0, hCT30093.2	1555897_at, 212348_s_at, 235652_at	NP_055828.2, NP_001009999.1, EAW95031.1, EAW95032.1, EAW95033.1
GeneID:10236	HNRNPR	1	23,636,276	23,670,853	34,577	-	1	2_A375_pNL97_plus_lncRNA::1::121	-347	upstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene HNRNPR	HNRPR, hnRNP R, FLJ25714, HNRNPR, hnRNP-R	heterogeneous nuclear ribonucleoprotein R	NM_005826, NM_001102397, NM_001102398, NM_001102399, hCT1955785.1, hCT1955786.1, hCT30153.3	208765_s_at, 208766_s_at, 232004_at	NP_005817.1, NP_001095867.1, NP_001095868.1, NP_001095869.1, EAW95040.1, EAW95042.1, EAW95041.1
GeneID:80818	ZNF436	1	23,685,941	23,696,357	10,416	-	2	1_A375_pNL7_minus_lncRNA::1::92, 2_A375_pNL97_plus_lncRNA::1::122	869, -7403	in gene, upstream	1	1	18.5	19	2	1_A375_pNL7_minus_lncRNA::1	20	Gene ZNF436	ZNF, ZNF436, Zfp46, KIAA1710	zinc finger protein 436	NM_001077195, NM_030634, hCT1955772.2, hCT2349676.0, hCT30089.4	226113_at, 226114_at	NP_001070663.1, NP_085137.1, EAW95043.1, EAW95044.1, EAW95045.1
GeneID:148898	C1orf213	1	23,695,464	23,698,332	2,868	+	2	1_A375_pNL7_minus_lncRNA::1::92, 2_A375_pNL97_plus_lncRNA::1::122	24, 8296	in gene, downstream	1	1	18.5	19	2	1_A375_pNL7_minus_lncRNA::1	20	Gene C1orf213	C1orf213, FLJ90508	chromosome 1 open reading frame 213	NR_033690, NR_033691, hCT2254703.0	229086_at	EAW95046.1
GeneID:6920	TCEA3	1	23,707,555	23,751,261	43,706	-	1	2_A375_pNL97_plus_lncRNA::1::122	47501	downstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TCEA3	TFIIS, TCEA3, TFIIS.H	transcription elongation factor A (SII), 3	NM_003196, hCT1955773.1, hCT30092.3	226388_at, 241976_at	NP_003187.1, EAW95048.1, EAW95049.1
GeneID:1870	E2F2	1	23,832,922	23,857,713	24,791	-	2	2_A375_pNL97_plus_lncRNA::1::123, 2_A375_pNL97_plus_lncRNA::1::124	-223, -8623	upstream, upstream	0	1	13	18	2	2_A375_pNL97_plus_lncRNA::1	20	Gene E2F2	E2F-2, E2F2	E2F transcription factor 2	NM_004091, hCT2256381.0, hCT2350480.0, hCT2350481.0, hCT28817.3	207042_at, 228361_at, 235582_at	NP_004082.1, EAW95057.1, EAW95055.1, EAW95056.1, EAW95058.1
GeneID:729856	LOC729856	1	23,997,268	23,997,735	467	+	2	1_A375_pNL7_minus_lncRNA::1::93, 2_A375_pNL97_plus_lncRNA::1::125	2444, 2508	downstream, downstream	1	1	32	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene LOC729856		elongation factor 1-alpha-like	XM_001130188, XM_001131535, XM_001715078		XP_001130188.2, XP_001131535.2, XP_001715130.2
GeneID:6135	RPL11	1	24,018,294	24,022,915	4,621	+	1	2_A375_pNL97_plus_lncRNA::1::126	10	in gene	0	1	19	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene RPL11	L11, DBA7, GIG34, RPL11	ribosomal protein L11	NM_000975, hCT1777320.1, hCT1955732.1	200010_at	NP_000966.2, EAW95068.1, EAW95067.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:6924	TCEB3	1	24,069,856	24,088,549	18,693	+	1	2_A375_pNL97_plus_lncRNA::1::127	96	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene TCEB3	SIII, FLJ38760, FLJ42649, TCEB3, EloA, SIII p110, TCEB3A	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	NM_003198, hCT2254721.0, hCT28764.3	1570625_at, 1570627_at, 202818_s_at, 202819_s_at	NP_003189.2, EAW95070.1, EAW95071.1
GeneID:11313	LYPLA2	1	24,117,646	24,122,029	4,383	+	2	1_A375_pNL7_minus_lncRNA::1::94, 2_A375_pNL97_plus_lncRNA::1::128	8722, 9634	downstream, downstream	1	1	20	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene LYPLA2	APT-2, LYPLA2, DJ886K2.4	lysophospholipase II	NM_007260, hCT2254733.0, hCT2254734.0, hCT2254736.0, hCT2254737.0, hCT2254739.0, hCT2254740.0	202292_x_at, 215568_x_at	NP_009191.1, EAW95077.1, EAW95078.1, EAW95079.1, EAW95080.1, EAW95081.1, EAW95082.1
GeneID:2582	GALE	1	24,122,089	24,127,294	5,205	-	2	1_A375_pNL7_minus_lncRNA::1::94, 2_A375_pNL97_plus_lncRNA::1::128	926, 14	in gene, in gene	1	1	20	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene GALE	FLJ95174, FLJ97302, SDR1E1, GALE	UDP-galactose-4-epimerase	NM_001008216, NM_000403, NM_001127621, hCT1955752.1, hCT1955753.1, hCT1955754.1, hCT1955755.1, hCT2256363.0, hCT2256364.0, hCT2256367.0, hCT2256370.0, hCT2256371.0, hCT2256373.0, hCT28915.3	1557649_at, 1557651_x_at, 202528_at	NP_001008217.1, NP_000394.2, NP_001121093.1, EAW95083.1, EAW95085.1, EAW95092.1, EAW95084.1, EAW95086.1, EAW95087.1, EAW95088.1, EAW95089.1, EAW95090.1, EAW95091.1, EAW95093.1
GeneID:3155	HMGCL	1	24,128,367	24,151,949	23,582	-	2	1_A375_pNL7_minus_lncRNA::1::94, 2_A375_pNL97_plus_lncRNA::1::128	25581, 24669	downstream, downstream	1	1	20	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene HMGCL	HL, HMGCL	3-hydroxymethyl-3-methylglutaryl-CoA lyase	NM_000191, NM_001166059, hCT1955761.1, hCT1955764.1, hCT2357817.0, hCT28917.2	202772_at	NP_000182.2, NP_001159531.1, EAW95094.1, EAW95095.1, EAW95096.1, EAW95097.1
GeneID:10772	SFRS13A	1	24,292,935	24,306,953	14,018	-	2	1_A375_pNL7_minus_lncRNA::1::95, 2_A375_pNL97_plus_lncRNA::1::129	329, 137	in gene, in gene	1	1	23	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene SFRS13A	SRrp40, SRp38, FLJ43846, SFRS13A, TASR1, NSSR, TASR2, FUSIP2, DKFZp686H0644, FLJ30749, SRSF10, FUSIP1, SFRS13, TASR	serine/arginine-rich splicing factor 10	NM_001191005, NM_001191006, NM_001191007, NM_001191009, NM_006625, NM_054016, NR_034035, hCT2256349.0, hCT2256351.0, hCT2256352.0, hCT2256354.0, hCT2357805.0	204299_at, 206095_s_at, 210178_x_at, 213594_x_at	NP_001177934.1, NP_001177935.1, NP_473357.1, NP_006616.1, NP_001177936.1, NP_001177938.1, EAW95103.1, EAW95104.1, EAW95105.1, EAW95106.1, EAW95107.1
GeneID:127294	MYOM3	1	24,382,531	24,438,665	56,134	-	1	2_A375_pNL97_plus_lncRNA::1::130	60585	downstream	0	1	16	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MYOM3	FLJ35961, MYOM3, MGC71483, RP11-293P20.1	myomesin family, member 3	NM_152372, hCT1955726.2, hCT2256346.0, hCT2357798.0	230264_at, 238124_at	NP_689585.3, EAW95108.1, EAW95109.1, EAW95110.1
GeneID:57822	GRHL3	1	24,645,812	24,690,972	45,160	+	2	1_A375_pNL7_minus_lncRNA::1::97, 2_A375_pNL97_plus_lncRNA::1::132	46186, 46060	downstream, downstream	1	1	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene GRHL3	GRHL3, SOM, TFCP2L4, MGC46624	grainyhead-like 3 (Drosophila)	NM_021180, NM_198173, NM_198174, NM_001195010, hCT1813422.3, hCT2348170.1, hCT2348171.0, hCT2348172.0	232116_at	NP_067003.2, NP_937816.1, NP_937817.3, NP_001181939.1, EAW95120.1, EAW95121.1, EAW95122.1, EAW95123.1
GeneID:90529	C1orf201	1	24,683,489	24,727,949	44,460	-	2	1_A375_pNL7_minus_lncRNA::1::97, 2_A375_pNL97_plus_lncRNA::1::132	35949, 36077	in gene, in gene	1	1	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene C1orf201	FLJ33340, C1orf201	chromosome 1 open reading frame 201	NM_178122, hCT11082.2, hCT1955745.1, hCT2256340.0, hCT2256341.0, hCT2357811.0, hCT2357812.0	227694_at, 233693_at	NP_835223.1, EAW95125.1, EAW95124.1, EAW95126.1, EAW95128.1, EAW95129.1, EAW95127.1
GeneID:57185	NIPAL3	1	24,742,245	24,799,473	57,228	+	2	1_A375_pNL7_minus_lncRNA::1::98, 2_A375_pNL97_plus_lncRNA::1::133	-69, -165	upstream, upstream	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene NIPAL3	DKFZp686E22155, DJ462O23.2, NIPAL3, NPAL3	NIPA-like domain containing 3	NM_020448, hCT11061.3	210267_at, 214579_at, 225875_s_at, 225876_at, 229735_s_at	NP_065181.1, EAW95130.1
GeneID:864	RUNX3	1	25,226,002	25,291,501	65,499	-	2	1_A375_pNL7_minus_lncRNA::1::99, 2_A375_pNL97_plus_lncRNA::1::134	15437, 5165	in gene, in gene	1	1	16.5	17.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene RUNX3	AML2, RUNX3, MGC16070, CBFA3, FLJ34510, PEBP2aC	runt-related transcription factor 3	NM_001031680, NM_004350, hCT1955718.1, hCT1955719.1, hCT2254122.0	204197_s_at, 204198_s_at, 234928_x_at	NP_001026850.1, NP_004341.1, EAW95147.1, EAW95148.1, EAW95149.1
GeneID:57035	C1orf63	1	25,568,740	25,573,985	5,245	-	2	2_A375_pNL97_plus_lncRNA::1::137, 2_A375_pNL97_plus_lncRNA::1::138	865, 84	in gene, in gene	0	1	13.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene C1orf63	RP3-465N24.4, DJ465N24.2.1, C1orf63, NPD014	chromosome 1 open reading frame 63	NM_020317, hCT2254136.0, hCT2254137.0, hCT2254138.0, hCT2254139.0, hCT2357821.0	209006_s_at, 209007_s_at	NP_064713.3, EAW95159.1, EAW95157.1, EAW95158.1, EAW95160.1, EAW95161.1
GeneID:26119	LDLRAP1	1	25,870,076	25,895,377	25,301	+	2	1_A375_pNL7_minus_lncRNA::1::101, 2_A375_pNL97_plus_lncRNA::1::139	26372, 25412	downstream, downstream	1	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LDLRAP1	MGC34705, ARH, FHCB1, DKFZp586D0624, FHCB2, LDLRAP1, ARH1, ARH2	low density lipoprotein receptor adaptor protein 1	NM_015627, hCT1777234.2, hCT2334511.1, hCT2334512.1, hCT2334514.0	221790_s_at, 57082_at	NP_056442.2, EAX07873.1, EAX07872.1, EAX07874.1, EAX07875.1
GeneID:57190	SEPN1	1	26,126,667	26,144,713	18,046	+	1	1_A375_pNL7_minus_lncRNA::1::102	19669	downstream	1	0	17	18	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SEPN1	SELN, RSMD1, FLJ24021, MDRS1, SEPN1, RSS	selenoprotein N, 1	NM_020451, NM_206926	224659_at	NP_065184.2, NP_996809.1
GeneID:56181	FAM54B	1	26,146,397	26,159,433	13,036	+	1	1_A375_pNL7_minus_lncRNA::1::102	-61	upstream	1	0	17	18	1	1_A375_pNL7_minus_lncRNA::1	17	Gene FAM54B	MST116, HYST1888, MSTP116, FAM54B	family with sequence similarity 54, member B	NM_019557, NM_001099625, NM_001099626, NM_001099627	224280_s_at	NP_062457.3, NP_001093095.1, NP_001093096.1, NP_001093097.1
GeneID:646471	LOC646471	1	26,146,445	26,150,097	3,652	-	1	1_A375_pNL7_minus_lncRNA::1::102	3761	downstream	1	0	17	18	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC646471		hypothetical LOC646471	NR_024498		
GeneID:5051	PAFAH2	1	26,286,258	26,324,648	38,390	-	2	1_A375_pNL7_minus_lncRNA::1::103, 2_A375_pNL97_plus_lncRNA::1::140	-24, -56	upstream, upstream	1	1	26	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene PAFAH2	FLJ26025, PAFAH2, HSD-PLA2	platelet-activating factor acetylhydrolase 2, 40kDa	NM_000437, hCT14858.2, hCT2359170.0	205232_s_at, 205233_s_at	NP_000428.2, EAX07852.1, EAX07853.1
GeneID:2134	EXTL1	1	26,348,271	26,362,955	14,684	+	4	1_A375_pNL7_minus_lncRNA::1::104, 1_A375_pNL7_minus_lncRNA::1::105, 2_A375_pNL97_plus_lncRNA::1::141, 2_A375_pNL97_plus_lncRNA::1::142	7185, 13617, 7121, 13617	in gene, in gene, in gene, in gene	1	1	25.5	24	2	1_A375_pNL7_minus_lncRNA::1	33	Gene EXTL1	MGC70794, EXTL1, EXTL	exostoses (multiple)-like 1	NM_004455, hCT13943.2	206329_at	NP_004446.2, EAX07851.1
GeneID:7780	SLC30A2	1	26,364,514	26,372,604	8,090	-	4	1_A375_pNL7_minus_lncRNA::1::104, 1_A375_pNL7_minus_lncRNA::1::105, 2_A375_pNL97_plus_lncRNA::1::141, 2_A375_pNL97_plus_lncRNA::1::142	17148, 10716, 17212, 10716	downstream, downstream, downstream, downstream	1	1	25.5	24	2	1_A375_pNL7_minus_lncRNA::1	33	Gene SLC30A2	ZNT2, FLJ36708, SLC30A2, ZnT-2, PP12488, MGC11303	solute carrier family 30 (zinc transporter), member 2	NM_001004434, NM_032513, hCT1641076.2, hCT2334144.0	224485_s_at, 230084_at	NP_001004434.1, NP_115902.1, EAX07849.1, EAX07850.1
GeneID:149420	PDIK1L	1	26,437,656	26,452,034	14,378	+	2	1_A375_pNL7_minus_lncRNA::1::106, 2_A375_pNL97_plus_lncRNA::1::143	72, -56	in gene, upstream	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene PDIK1L	PDIK1L, RP11-96L14.4, STK35L2, CLIK1L	PDLIM1 interacting kinase 1 like	NM_152835, NR_026685, NR_026686, hCT1643508.3, hCT2334496.1, hCT2346889.0	227255_at	NP_690048.1, EAX07846.1, EAX07845.1, EAX07847.1
GeneID:79927	GRRP1	1	26,465,511	26,469,119	3,608	+	2	1_A375_pNL7_minus_lncRNA::1::107, 2_A375_pNL97_plus_lncRNA::1::144	10841, 10841	downstream, downstream	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene GRRP1	RP11-96L14.5, FLJ14050, FAM110D, GRRP1	glycine/arginine rich protein 1	NM_024869, hCT1777226.1	220430_at	NP_079145.2, EAX07844.1
GeneID:100128346	LOC100128346	1	26,496,007	26,498,312	2,305	-	2	1_A375_pNL7_minus_lncRNA::1::107, 2_A375_pNL97_plus_lncRNA::1::144	1960, 1960	in gene, in gene	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100128346		hypothetical LOC100128346	XR_112049, XR_108377, XR_113337		
GeneID:51042	ZNF593	1	26,496,388	26,497,364	976	+	2	1_A375_pNL7_minus_lncRNA::1::107, 2_A375_pNL97_plus_lncRNA::1::144	-36, -36	upstream, upstream	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ZNF593	ZT86, ZNF593	zinc finger protein 593	NM_015871, hCT31846.2	204175_at	NP_056955.2, EAX07843.1
GeneID:10256	CNKSR1	1	26,503,981	26,516,375	12,394	+	2	1_A375_pNL7_minus_lncRNA::1::107, 2_A375_pNL97_plus_lncRNA::1::144	-7629, -7629	upstream, upstream	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene CNKSR1	CNK, CNK1, KSR, CNKSR1	connector enhancer of kinase suppressor of Ras 1	NM_006314, NR_023345, hCT2334500.0, hCT2359169.0, hCT31952.3	204740_at	NP_006305.2, EAX07842.1, EAX07840.1, EAX07841.1
GeneID:64793	CCDC21	1	26,560,693	26,605,299	44,606	+	3	1_A375_pNL7_minus_lncRNA::1::108, 1_A375_pNL7_minus_lncRNA::1::109, 2_A375_pNL97_plus_lncRNA::1::145	-101, 42123, 45667	upstream, in gene, downstream	1	1	16	16.67	3	1_A375_pNL7_minus_lncRNA::1	19	Gene CCDC21	DKFZp434P232, DKFZp434L0117, FLJ13976, CCDC21, FLJ22000	coiled-coil domain containing 21	NM_022778, hCT1777221.1, hCT1964454.1, hCT1964455.1, hCT2359061.0	219611_s_at, 227818_at	NP_073615.2, EAX07836.1, EAX07833.1, EAX07834.1, EAX07835.1
GeneID:83442	SH3BGRL3	1	26,606,213	26,608,013	1,800	+	2	1_A375_pNL7_minus_lncRNA::1::109, 2_A375_pNL97_plus_lncRNA::1::145	-3397, 347	upstream, in gene	1	1	16.5	17.5	2	1_A375_pNL7_minus_lncRNA::1	19	Gene SH3BGRL3	SH3BGRL3, TIP-B1, SH3BP-1	SH3 domain binding glutamic acid-rich protein like 3	NM_031286, hCT1777223.2, hCT1957528.1	221269_s_at	NP_112576.1, EAX07831.1, EAX07832.1
GeneID:91544	UBXN11	1	26,608,773	26,644,756	35,983	-	2	1_A375_pNL7_minus_lncRNA::1::109, 2_A375_pNL97_plus_lncRNA::1::145	41940, 38196	downstream, downstream	1	1	16.5	17.5	2	1_A375_pNL7_minus_lncRNA::1	19	Gene UBXN11	COA-1, PP2243, UBXD5, SOCI, DKFZp686F04228, SOC, UBXN11	UBX domain protein 11	NM_183008, NM_145345, NM_001077262, hCT1777235.1, hCT1964276.1, hCT1964280.1, hCT1964282.1, hCT2359148.0, hCT2359149.0, hCT2359150.0, hCT2359151.0	227716_at	NP_892120.2, NP_663320.2, NP_001070730.1, EAX07825.1, EAX07826.1, EAX07830.1, EAX07823.1, EAX07824.1, EAX07827.1, EAX07828.1, EAX07829.1
GeneID:79727	LIN28	1	26,737,269	26,756,219	18,950	+	4	1_A375_pNL7_minus_lncRNA::1::110, 1_A375_pNL7_minus_lncRNA::1::111, 2_A375_pNL97_plus_lncRNA::1::146, 2_A375_pNL97_plus_lncRNA::1::147	-2069, 21419, -2101, 21463	upstream, downstream, upstream, downstream	1	1	40	50	2	2_A375_pNL97_plus_lncRNA::1	71	Gene LIN28	LIN28, LIN-28, LIN28A, CSDD1, ZCCHC1, FLJ12457	lin-28 homolog (C. elegans)	NM_024674, hCT1950346.1, hCT2334852.0	219623_at	NP_078950.1, EAX07815.1, EAX07814.1
GeneID:79947	DHDDS	1	26,758,802	26,797,797	38,995	+	4	1_A375_pNL7_minus_lncRNA::1::111, 1_A375_pNL7_minus_lncRNA::1::112, 2_A375_pNL97_plus_lncRNA::1::147, 2_A375_pNL97_plus_lncRNA::1::148	-114, 39534, -50, 39470	upstream, downstream, upstream, downstream	1	1	23.5	24.5	2	1_A375_pNL7_minus_lncRNA::1	30	Gene DHDDS	CPT, CIT, DS, FLJ13102, HDS, DHDDS	dehydrodolichyl diphosphate synthase	NM_205861, NM_024887, hCT11293.2, hCT1957534.1, hCT2334856.0, hCT2359101.0, hCT2359102.0, hCT2359103.0, hCT2359104.0	218547_at, 224064_s_at	NP_995583.1, NP_079163.2, EAX07808.1, EAX07810.1, EAX07811.1, EAX07812.1, EAX07806.1, EAX07807.1, EAX07809.1
GeneID:3151	HMGN2	1	26,798,902	26,803,133	4,231	+	2	1_A375_pNL7_minus_lncRNA::1::112, 2_A375_pNL97_plus_lncRNA::1::148	-566, -630	upstream, upstream	1	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene HMGN2	HMG17, MGC88718, MGC5629, HMGN2	high mobility group nucleosomal binding domain 2	NM_005517, hCT2334857.1, hCT2334858.1, hCT2334859.1, hCT2334860.1	208668_x_at	NP_005508.1, EAX07804.1, EAX07802.1, EAX07803.1, EAX07805.1
GeneID:6195	RPS6KA1	1	26,856,249	26,901,520	45,271	+	1	2_A375_pNL97_plus_lncRNA::1::150	26023	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene RPS6KA1	MAPKAPK1A, RSK, RSK1, HU-1, RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	NM_001006665, NM_002953, hCT10675.3, hCT2334862.0, hCT2334863.0	203379_at	NP_001006666.1, NP_002944.2, EAX07798.1, EAX07799.1, EAX07800.1
GeneID:100302190	MIR1976	1	26,881,033	26,881,084	51	+	1	2_A375_pNL97_plus_lncRNA::1::150	1239	downstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MIR1976	hsa-mir-1976, MIR1976	microRNA 1976	NR_031740		
GeneID:8289	ARID1A	1	27,022,522	27,108,601	86,079	+	4	1_A375_pNL7_minus_lncRNA::1::115, 1_A375_pNL7_minus_lncRNA::1::116, 2_A375_pNL97_plus_lncRNA::1::152, 2_A375_pNL97_plus_lncRNA::1::153	-2906, -346, -2906, -410	upstream, upstream, upstream, upstream	1	1	35	51.5	2	2_A375_pNL97_plus_lncRNA::1	58	Gene ARID1A	P270, B120, C1orf4, ARID1A, BAF250a, BM029, BAF250, SMARCF1	AT rich interactive domain 1A (SWI-like)	NM_139135, NM_006015, hCT10522.3, hCT2334864.0, hCT2334866.0, hCT2334867.0, hCT2334868.0	207591_s_at, 210649_s_at, 212152_x_at, 216917_s_at	NP_624361.1, NP_006006.3, EAX07793.1, EAX07794.1, EAX07795.1, EAX07796.1, EAX07797.1
GeneID:84243	ZDHHC18	1	27,153,201	27,182,211	29,010	+	1	2_A375_pNL97_plus_lncRNA::1::154	38207	downstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZDHHC18	DKFZp667O2416, DHHC18, ZDHHC18	zinc finger, DHHC-type containing 18	NM_032283, hCT10530.3, hCT2359066.0	1558327_at, 212860_at, 231900_at	NP_115659.1, EAX07789.1, EAX07788.1
GeneID:2810	SFN	1	27,189,633	27,190,947	1,314	+	1	2_A375_pNL97_plus_lncRNA::1::154	1775	downstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SFN	SFN, YWHAS	stratifin	NM_006142, hCT2334836.0, hCT9437.2	209260_at, 33322_i_at, 33323_r_at	NP_006133.1, EAX07787.1, EAX07786.1
GeneID:54707	GPN2	1	27,205,873	27,216,869	10,996	-	2	1_A375_pNL7_minus_lncRNA::1::117, 2_A375_pNL97_plus_lncRNA::1::155	405, 325	in gene, in gene	1	1	23	19	1	1_A375_pNL7_minus_lncRNA::1	23	Gene GPN2	FLJ10349, ATPBD1B, GPN2	GPN-loop GTPase 2	NM_018066, hCT2344287.0	218799_at	NP_060536.3, EAX07784.1
GeneID:63906	GPATCH3	1	27,216,979	27,226,962	9,983	-	2	1_A375_pNL7_minus_lncRNA::1::117, 2_A375_pNL97_plus_lncRNA::1::155	10498, 10418	downstream, downstream	1	1	23	19	1	1_A375_pNL7_minus_lncRNA::1	23	Gene GPATCH3	GPATC3, FLJ12455, DKFZp686E0221, GPATCH3	G patch domain containing 3	NM_022078, hCT2334041.1	218695_at	NP_071361.2, EAX07783.1
GeneID:8431	NR0B2	1	27,237,975	27,240,567	2,592	-	1	2_A375_pNL97_plus_lncRNA::1::156	-7753	upstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene NR0B2	NR0B2, SHP, SHP1, FLJ17090	nuclear receptor subfamily 0, group B, member 2	NM_021969, hCT10526.3	206410_at	NP_068804.1, EAX07781.1
GeneID:10726	NUDC	1	27,248,224	27,272,887	24,663	+	1	2_A375_pNL97_plus_lncRNA::1::156	96	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene NUDC	NUDC, MNUDC, NPD011, HNUDC	nuclear distribution gene C homolog (A. nidulans)	NM_006600, hCT10523.3	201173_x_at, 210574_s_at, 210575_at	NP_006591.1, EAX07780.1
GeneID:388610	TRNP1	1	27,320,195	27,327,377	7,182	+	2	2_A375_pNL97_plus_lncRNA::1::157, 2_A375_pNL97_plus_lncRNA::1::158	8413, 15837	downstream, downstream	0	1	15.5	20	2	2_A375_pNL97_plus_lncRNA::1	26	Gene TRNP1	C1orf225, TNRP, TRNP1	TMF1-regulated nuclear protein 1	NM_001013642, hCT2347375.0	227862_at, 236052_at	NP_001013664.1, EAX07778.1
GeneID:115572	FAM46B	1	27,331,511	27,339,333	7,822	-	2	2_A375_pNL97_plus_lncRNA::1::157, 2_A375_pNL97_plus_lncRNA::1::158	10725, 3301	downstream, in gene	0	1	15.5	20	2	2_A375_pNL97_plus_lncRNA::1	26	Gene FAM46B	RP11-344H11.6, MGC20645, FAM46B, MGC16491	family with sequence similarity 46, member B	NM_052943, hCT10525.3	229518_at	NP_443175.2, EAX07777.1
GeneID:23038	WDTC1	1	27,561,007	27,635,110	74,103	+	1	1_A375_pNL7_minus_lncRNA::1::118	65	in gene	1	0	21	12	1	1_A375_pNL7_minus_lncRNA::1	21	Gene WDTC1	WDTC1, DCAF9, KIAA1037, ADP	WD and tetratricopeptide repeats 1	NM_015023, hCT2334646.0, hCT2334647.0, hCT2334649.0, hCT2334650.0	215497_s_at, 216036_x_at, 40829_at	NP_055838.2, EAX07770.1, EAX07769.1, EAX07771.1, EAX07772.1
GeneID:84065	TMEM222	1	27,648,636	27,662,891	14,255	+	2	1_A375_pNL7_minus_lncRNA::1::119, 2_A375_pNL97_plus_lncRNA::1::159	36, -28	in gene, upstream	1	1	27	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene TMEM222	C1orf160, TMEM222, MGC111002, DKFZp564D0478	transmembrane protein 222	NM_032125, hCT1970905.1, hCT2359136.0, hCT2359137.0, hCT2359138.0, hCT2359139.0, hCT67687.2	221512_at, 52078_at	NP_115501.2, EAX07764.1, EAX07763.1, EAX07765.1, EAX07767.1, EAX07768.1, EAX07766.1
GeneID:644961	LOC644961	1	27,650,365	27,653,016	2,651	+	2	1_A375_pNL7_minus_lncRNA::1::119, 2_A375_pNL97_plus_lncRNA::1::159	-1693, -1757	upstream, upstream	1	1	27	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene LOC644961		actin, gamma 1 pseudogene	NR_033926		
GeneID:84958	SYTL1	1	27,668,483	27,680,423	11,940	+	1	2_A375_pNL97_plus_lncRNA::1::160	7709	in gene	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SYTL1	JFC1, SYTL1, FLJ14996, SLP1	synaptotagmin-like 1	NM_032872, NM_001193308, hCT10703.3, hCT2334616.0, hCT2334617.0, hCT2359056.0	227134_at	NP_116261.1, NP_001180237.1, EAX07759.1, EAX07760.1, EAX07761.1, EAX07762.1
GeneID:9064	MAP3K6	1	27,681,670	27,693,337	11,667	-	1	2_A375_pNL97_plus_lncRNA::1::160	17145	downstream	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MAP3K6	MAP3K6, ASK2, MEKK6, MAPKKK6, MGC20114, MGC125653	mitogen-activated protein kinase kinase kinase 6	NM_004672, hCT10368.3	1552631_a_at, 219278_at, 229960_at	NP_004663.3, EAX07758.1
GeneID:388611	CD164L2	1	27,705,596	27,709,805	4,209	-	1	2_A375_pNL97_plus_lncRNA::1::161	-9203	upstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CD164L2	UNQ6122, CD164L2	CD164 sialomucin-like 2	NM_207397, hCT10704.2		NP_997280.1, EAX07755.1
GeneID:2827	GPR3	1	27,719,152	27,722,318	3,166	+	1	2_A375_pNL97_plus_lncRNA::1::161	-144	upstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GPR3	GPR3, ACCA	G protein-coupled receptor 3	NM_005281, hCT2334618.1	214613_at	NP_005272.1, EAX07754.1
GeneID:10163	WASF2	1	27,732,126	27,816,669	84,543	-	2	1_A375_pNL7_minus_lncRNA::1::120, 2_A375_pNL97_plus_lncRNA::1::162	-46, -227	upstream, upstream	1	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene WASF2	WASF2, dJ393P12.2, WAVE2, SCAR2	WAS protein family, member 2	NM_006990, hCT10702.3	224562_at, 224563_at	NP_008921.1, EAX07753.1
GeneID:2537	IFI6	1	27,992,572	27,998,724	6,152	-	1	2_A375_pNL97_plus_lncRNA::1::163	36	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene IFI6	IFI616, 6-16, IFI-6-16, G1P3, IFI6, FAM14C	interferon, alpha-inducible protein 6	NM_002038, NM_022872, NM_022873, hCT1764852.1, hCT2334360.0, hCT2334362.0	204415_at, 224533_s_at	NP_002029.3, NP_075010.1, NP_075011.1, EAX07744.1, EAX07745.1, EAX07746.1
GeneID:5724	PTAFR	1	28,473,677	28,520,447	46,770	-	2	1_A375_pNL7_minus_lncRNA::1::121, 2_A375_pNL97_plus_lncRNA::1::164	49343, 49183	downstream, downstream	1	1	20	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene PTAFR	PAFR, PTAFR	platelet-activating factor receptor	NM_001164721, NM_000952, NM_001164722, NM_001164723	206278_at, 211661_x_at	NP_001158193.1, NP_000943.1, NP_001158194.1, NP_001158195.1
GeneID:85028	SNHG12	1	28,905,050	28,908,366	3,316	-	1	2_A375_pNL97_plus_lncRNA::1::167	-82	upstream	0	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SNHG12	C1orf79, RP4-669K10.5, NCRNA00100, SNHG12	small nucleolar RNA host gene 12 (non-protein coding)	NR_024127	223773_s_at, 223774_at, 228990_at	
GeneID:692212	SNORD99	1	28,905,255	28,905,334	79	-	1	2_A375_pNL97_plus_lncRNA::1::167	-3114	upstream	0	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SNORD99	HBII-420, SNORD99	small nucleolar RNA, C/D box 99	NR_003077		
GeneID:677838	SNORA61	1	28,906,276	28,906,405	129	-	1	2_A375_pNL97_plus_lncRNA::1::167	-2043	upstream	0	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SNORA61	ACA61, SNORA61	small nucleolar RNA, H/ACA box 61	NR_002987		
GeneID:677825	SNORA44	1	28,906,893	28,907,024	131	-	1	2_A375_pNL97_plus_lncRNA::1::167	-1424	upstream	0	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SNORA44	SNORA44, ACA44	small nucleolar RNA, H/ACA box 44	NR_002976		
GeneID:692073	SNORA16A	1	28,907,432	28,907,565	133	-	1	2_A375_pNL97_plus_lncRNA::1::167	-883	upstream	0	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SNORA16A	SNORA16A, ACA16	small nucleolar RNA, H/ACA box 16A	NR_003035		
GeneID:115273	RAB42	1	28,918,712	28,921,098	2,386	+	1	2_A375_pNL97_plus_lncRNA::1::167	-10264	upstream	0	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene RAB42	RP4-669K10.6, MGC45806, RAB42	RAB42, member RAS oncogene family	NM_152304, NM_001193532, hCT1640543.4, hCT2349536.0	1552646_s_at	NP_689517.1, NP_001180461.1, EAX07684.1, EAX07685.1
GeneID:6883	TAF12	1	28,929,608	28,969,604	39,996	-	2	1_A375_pNL7_minus_lncRNA::1::123, 2_A375_pNL97_plus_lncRNA::1::168	-5468, -5340	upstream, upstream	1	1	28	23	1	1_A375_pNL7_minus_lncRNA::1	28	Gene TAF12	TAF12, TAF2J, TAFII20	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa	NM_005644, NM_001135218, hCT1785638.3, hCT1960721.2, hCT2334004.1, hCT2343721.0	209463_s_at	NP_005635.1, NP_001128690.1, EAX07680.1, EAX07681.1, EAX07682.1, EAX07683.1
GeneID:26824	RNU11	1	28,975,112	28,975,246	134	+	2	1_A375_pNL7_minus_lncRNA::1::123, 2_A375_pNL97_plus_lncRNA::1::168	-40, -168	upstream, upstream	1	1	28	23	1	1_A375_pNL7_minus_lncRNA::1	28	Gene RNU11	RNU11, U11	RNA, U11 small nuclear	NR_004407		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:10691	GMEB1	1	28,995,244	29,041,398	46,154	+	1	1_A375_pNL7_minus_lncRNA::1::124	-108	upstream	1	0	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene GMEB1	GMEB1, P96PIF, PIF96	glucocorticoid modulatory element binding protein 1	NM_024482, NM_006582, hCT1826638.2, hCT1962963.1, hCT2334298.0, hCT2359202.0	220936_s_at	NP_077808.1, NP_006573.2, EAX07676.1, EAX07677.1, EAX07678.1, EAX07679.1
GeneID:51441	YTHDF2	1	29,063,133	29,096,287	33,154	+	2	1_A375_pNL7_minus_lncRNA::1::125, 2_A375_pNL97_plus_lncRNA::1::169	131, 115	in gene, in gene	1	1	54	35	1	1_A375_pNL7_minus_lncRNA::1	54	Gene YTHDF2	YTHDF2, NY-REN-2, HGRG8	YTH domain family, member 2	NM_016258, NM_001173128, NM_001172828, hCT1826635.1, hCT1971476.1, hCT2334299.0	217812_at, 222430_s_at	NP_057342.2, NP_001166599.1, NP_001166299.1, EAX07673.1, EAX07674.1, EAX07675.1
GeneID:2035	EPB41	1	29,213,603	29,446,558	232,955	+	1	2_A375_pNL97_plus_lncRNA::1::170	29	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene EPB41	EPB41, 4.1R, EL1, HE	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	NM_001166005, NM_203343, NM_001166006, NM_203342, NM_001166007, NM_004437, hCT1953986.1, hCT1953987.1, hCT2334303.0, hCT2334305.0, hCT2334309.0, hCT2334310.0, hCT2334311.0	1554481_a_at, 207793_s_at, 214530_x_at, 225051_at	NP_001159477.1, NP_976218.1, NP_001159478.1, NP_001159479.1, NP_004428.1, NP_976217.1, EAX07662.1, EAX07663.1, EAX07664.1, EAX07665.1, EAX07666.1, EAX07667.1, EAX07668.1
GeneID:6429	SFRS4	1	29,474,250	29,508,637	34,387	-	1	2_A375_pNL97_plus_lncRNA::1::171	210	in gene	0	1	14	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SFRS4	SRP75, SRSF4, SFRS4	serine/arginine-rich splicing factor 4	NM_005626, hCT14590.2, hCT1953988.0, hCT1961896.1	201696_at, 239511_s_at, 239512_at, 241245_at, 242837_at	NP_005617.2, EAX07658.1, EAX07657.1, EAX07659.1
GeneID:51102	MECR	1	29,519,385	29,557,454	38,069	-	1	2_A375_pNL97_plus_lncRNA::1::172	-66	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MECR	OGI-63, NRBF1, FASN2B, MECR	mitochondrial trans-2-enoyl-CoA reductase	NM_016011, NM_001024732, hCT15150.2, hCT1953989.1, hCT2333991.0, hCT2359130.0	218664_at	NP_057095.2, NP_001019903.1, EAX07653.1, EAX07654.1, EAX07655.1, EAX07656.1
GeneID:10076	PTPRU	1	29,563,028	29,653,325	90,297	+	1	2_A375_pNL97_plus_lncRNA::1::172	-5508	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PTPRU	hPTP-J, FLJ37530, PTP-PI, PCP-2, PTP, GLEPP1, PTP-J, PTPRO, PTPPSI, R-PTP-PSI, PTPU2, PTPRU, FMI	protein tyrosine phosphatase, receptor type, U	NM_133178, NM_133177, NM_005704, NM_001195001, hCT1953979.1, hCT2334314.0, hCT2334315.0	211320_s_at	NP_573439.2, NP_573438.3, NP_005695.3, NP_001181930.1, EAX07650.1, EAX07651.1, EAX07652.1
GeneID:4146	MATN1	1	31,184,124	31,196,432	12,308	-	2	1_A375_pNL7_minus_lncRNA::1::128, 2_A375_pNL97_plus_lncRNA::1::179	4640, -8360	in gene, upstream	1	1	16.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene MATN1	CMP, MATN1, CRTM	matrilin 1, cartilage matrix protein	NM_002379, hCT2336084.1, hCT6942.4	206904_at, 206905_s_at	NP_002370.1, EAX07643.1, EAX07642.1
GeneID:100129196	LOC100129196	1	31,191,619	31,199,593	7,974	+	2	1_A375_pNL7_minus_lncRNA::1::128, 2_A375_pNL97_plus_lncRNA::1::179	173, 14173	in gene, downstream	1	1	16.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100129196	FLJ46197	hypothetical LOC100129196	NR_034182		
GeneID:7805	LAPTM5	1	31,205,315	31,230,683	25,368	-	3	1_A375_pNL7_minus_lncRNA::1::130, 2_A375_pNL97_plus_lncRNA::1::179, 2_A375_pNL97_plus_lncRNA::1::180	955, 24891, 1019	in gene, in gene, in gene	1	1	22.5	23.5	2	1_A375_pNL7_minus_lncRNA::1	32	Gene LAPTM5	FLJ61683, MGC125860, CLAST6, MGC125861, LAPTM5, FLJ97251	lysosomal protein transmembrane 5	NM_006762, hCT2336080.0, hCT6100.2	201720_s_at, 201721_s_at	NP_006753.1, EAX07640.1, EAX07641.1
GeneID:79570	NKAIN1	1	31,652,592	31,712,734	60,142	-	2	1_A375_pNL7_minus_lncRNA::1::133, 2_A375_pNL97_plus_lncRNA::1::185	57342, 57470	in gene, in gene	1	1	27	26	1	1_A375_pNL7_minus_lncRNA::1	27	Gene NKAIN1	NKAIN1, FAM77C, FLJ12650	Na+/K+ transporting ATPase interacting 1	NM_024522, hCT2336069.0, hCT2336070.0	219436_at	NP_078798.2, EAX07628.1, EAX07629.1
GeneID:9410	SNRNP40	1	31,732,415	31,769,644	37,229	-	1	2_A375_pNL97_plus_lncRNA::1::186	156	in gene	0	1	9	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene SNRNP40	WDR57, 40K, HPRP8BP, MGC1910, RP11-490K7.3, PRPF8BP, PRP8BP, SNRNP40, FLJ41108, SPF38	small nuclear ribonucleoprotein 40kDa (U5)	NM_004814, hCT11113.3, hCT2336066.0	215905_s_at	NP_004805.2, EAX07626.1, EAX07627.1
GeneID:51538	ZCCHC17	1	31,769,842	31,837,780	67,938	+	1	2_A375_pNL97_plus_lncRNA::1::186	-354	upstream	0	1	9	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene ZCCHC17	HSPC251, ZCCHC17, PS1D, pNO40, RP11-266K22.1	zinc finger, CCHC domain containing 17	NM_016505, hCT11112.3, hCT1953984.1, hCT2336089.0, hCT2336091.0, hCT2359157.0, hCT2359158.0	223107_s_at, 223108_s_at	NP_057589.2, EAX07621.1, EAX07620.1, EAX07622.1, EAX07624.1, EAX07625.1, EAX07623.1
GeneID:347735	SERINC2	1	31,885,963	31,907,525	21,562	+	2	1_A375_pNL7_minus_lncRNA::1::135, 2_A375_pNL97_plus_lncRNA::1::187	21413, 21397	in gene, in gene	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene SERINC2	SERINC2, TDE2L, PRO0899, TDE2, FKSG84, MGC90340	serine incorporator 2	NM_178865, hCT11114.4, hCT1953985.2, hCT2334534.1, hCT2340522.0, hCT2340523.0, hCT2359163.0	224762_at	NP_849196.2, EAX07615.1, EAX07611.1, EAX07612.1, EAX07613.1, EAX07616.1, EAX07614.1
GeneID:553115	PEF1	1	32,095,463	32,110,838	15,375	-	2	1_A375_pNL7_minus_lncRNA::1::136, 2_A375_pNL97_plus_lncRNA::1::188	438, 566	in gene, in gene	1	1	21	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene PEF1	PEF1A, PEFLIN, ABP32, PEF1	penta-EF-hand domain containing 1	NM_012392, NR_033686, NR_033688, hCT1953990.1, hCT2334194.0	217923_at	NP_036524.1, EAX07598.1, EAX07599.1
GeneID:1307	COL16A1	1	32,117,848	32,169,768	51,920	-	3	1_A375_pNL7_minus_lncRNA::1::136, 2_A375_pNL97_plus_lncRNA::1::188, 2_A375_pNL97_plus_lncRNA::1::189	59368, 59496, 14120	downstream, downstream, in gene	1	1	17	26.5	2	2_A375_pNL97_plus_lncRNA::1	33	Gene COL16A1	COL16A1, 447AA, FP1572	collagen, type XVI, alpha 1	NM_001856, hCT2334191.0, hCT2334193.0, hCT32885.2	204345_at	NP_001847.3, EAX07595.1, EAX07596.1, EAX07597.1
GeneID:576	BAI2	1	32,192,718	32,229,648	36,930	-	3	1_A375_pNL7_minus_lncRNA::1::138, 2_A375_pNL97_plus_lncRNA::1::190, 2_A375_pNL97_plus_lncRNA::1::191	40112, 46704, 40080	downstream, downstream, downstream	1	1	28	31.5	2	2_A375_pNL97_plus_lncRNA::1	42	Gene BAI2	BAI2	brain-specific angiogenesis inhibitor 2	NM_001703, hCT1962977.1, hCT1962978.1, hCT1964552.1, hCT2334185.0, hCT2334189.0, hCT32874.3	204966_at	NP_001694.2, EAX07594.1, EAX07589.1, EAX07590.1, EAX07591.1, EAX07592.1, EAX07593.1
GeneID:90853	SPOCD1	1	32,256,025	32,281,580	25,555	-	2	1_A375_pNL7_minus_lncRNA::1::139, 2_A375_pNL97_plus_lncRNA::1::192	27676, 27671	downstream, downstream	1	1	39	26	1	1_A375_pNL7_minus_lncRNA::1	39	Gene SPOCD1	FLJ39908, RP11-84A19.1, SPOCD1, FLJ25348	SPOC domain containing 1	NM_144569, hCT2349554.0, hCT2359076.0, hCT32893.4	1562415_a_at, 235417_at	NP_653170.3, EAX07586.1, EAX07587.1, EAX07588.1
GeneID:8073	PTP4A2	1	32,372,022	32,403,988	31,966	-	1	1_A375_pNL7_minus_lncRNA::1::140	-252	upstream	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene PTP4A2	OV-1, PTP4A, PRL2, PTPCAAX2, HH7-2, ptp-IV1b, ptp-IV1a, PTP4A2, HH13, PRL-2, HU-PP-1	protein tyrosine phosphatase type IVA, member 2	NM_080391, NM_001195100, NM_001195101, hCT2334175.1, hCT2334176.1, hCT2334177.1, hCT2334178.1, hCT2334179.1, hCT2334181.1, hCT32877.4	208615_s_at, 208616_s_at, 208617_s_at, 216988_s_at	NP_536316.1, NP_001182029.1, NP_001182030.1, EAX07578.1, EAX07579.1, EAX07580.1, EAX07581.1, EAX07582.1, EAX07583.1, EAX07584.1
GeneID:55116	TMEM39B	1	32,538,503	32,568,467	29,964	+	3	1_A375_pNL7_minus_lncRNA::1::141, 2_A375_pNL97_plus_lncRNA::1::193, 2_A375_pNL97_plus_lncRNA::1::194	-183, -231, 35161	upstream, upstream, downstream	1	1	17.5	20.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene TMEM39B	FLJ10315, TMEM39B	transmembrane protein 39B	NM_018056, hCT2334556.0, hCT2359078.0, hCT2359079.0, hCT32894.3	218770_s_at	NP_060526.2, EAX07573.1, EAX07570.1, EAX07571.1, EAX07572.1
GeneID:23633	KPNA6	1	32,573,644	32,642,169	68,525	+	2	1_A375_pNL7_minus_lncRNA::1::142, 2_A375_pNL97_plus_lncRNA::1::194	72020, 20	downstream, in gene	1	1	15.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	20	Gene KPNA6	KPNA7, KPNA6, FLJ11249, IPOA7, MGC17918	karyopherin alpha 6 (importin alpha 7)	NM_012316, hCT2334559.0, hCT2359204.0, hCT32879.3	212101_at, 212102_s_at, 212103_at, 226976_at	NP_036448.1, EAX07567.1, EAX07568.1, EAX07569.1
GeneID:200081	TXLNA	1	32,645,345	32,663,886	18,541	+	2	1_A375_pNL7_minus_lncRNA::1::142, 1_A375_pNL7_minus_lncRNA::1::143	319, 25743	in gene, downstream	1	0	16.5	16	2	1_A375_pNL7_minus_lncRNA::1	18	Gene TXLNA	MGC118870, TXLNA, TXLN, DKFZp451J0118, IL14, MGC118871, RP4-622L5.4	taxilin alpha	NM_175852, hCT2340721.0, hCT2340722.0	1561358_at, 212300_at, 231169_at, 240739_at	NP_787048.1, EAX07566.1, EAX07565.1
GeneID:79140	CCDC28B	1	32,666,202	32,670,991	4,789	+	1	1_A375_pNL7_minus_lncRNA::1::143	4886	downstream	1	0	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene CCDC28B	CCDC28B, MGC1203, MGC16441, RP4-622L5.5	coiled-coil domain containing 28B	NM_024296, hCT1953994.1, hCT2359156.0	219585_at, 221912_s_at	NP_077272.2, EAX07563.1, EAX07564.1
GeneID:55721	IQCC	1	32,671,236	32,674,288	3,052	+	1	1_A375_pNL7_minus_lncRNA::1::143	-148	upstream	1	0	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene IQCC	FLJ10547, MGC120341, RP4-622L5.6, IQCC	IQ motif containing C	NM_018134, NM_001160042, hCT32886.2	206650_at	NP_060604.2, NP_001153514.1, EAX07562.1
GeneID:149069	DCDC2B	1	32,674,695	32,681,797	7,102	+	1	1_A375_pNL7_minus_lncRNA::1::143	-3607	upstream	1	0	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene DCDC2B	DCDC2B	doublecortin domain containing 2B	NM_001099434	233918_at	NP_001092904.1
GeneID:100507457	LOC100507457	1	32,674,970	32,681,058	6,088	-	1	1_A375_pNL7_minus_lncRNA::1::143	9970	downstream	1	0	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene LOC100507457		hypothetical LOC100507457	XR_110509, XR_110508		
GeneID:56063	C1orf91	1	32,681,798	32,687,926	6,128	-	1	1_A375_pNL7_minus_lncRNA::1::143	16838	downstream	1	0	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene C1orf91	AASL548, C1orf91, dJ622L5.7, RP4-622L5, TMEM234, PRO1105, FLJ90779	chromosome 1 open reading frame 91	NM_019118, hCT1953997.1, hCT2334172.0, hCT2359237.0, hCT2359238.0, hCT32890.2	223656_s_at, 223676_at, 234006_s_at	NP_061991.3, EAX07557.1, EAX07556.1, EAX07558.1, EAX07559.1, EAX07560.1
GeneID:8668	EIF3I	1	32,687,971	32,697,205	9,234	+	2	1_A375_pNL7_minus_lncRNA::1::144, 2_A375_pNL97_plus_lncRNA::1::195	13917, 13949	downstream, downstream	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene EIF3I	PRO2242, EIF3I, TRIP1, EIF3S2, eIF3-p36, eIF3-beta, TRIP-1	eukaryotic translation initiation factor 3, subunit I	NM_003757, hCT1953992.1, hCT1962979.2, hCT1962980.1, hCT32880.3	208756_at	NP_003748.1, EAX07555.1, EAX07552.1, EAX07553.1, EAX07554.1
GeneID:3932	LCK	1	32,716,840	32,751,766	34,926	+	1	2_A375_pNL97_plus_lncRNA::1::196	41064	downstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LCK	LSK, pp58lck, p56lck, LCK, YT16	lymphocyte-specific protein tyrosine kinase	NM_005356, NM_001042771, hCT1953993.1, hCT2334571.0, hCT2334573.0, hCT2334574.0, hCT32881.3	204890_s_at, 204891_s_at	NP_005347.3, NP_001036236.1, EAX07542.1, EAX07544.1, EAX07545.1, EAX07546.1, EAX07543.1
GeneID:3065	HDAC1	1	32,757,708	32,799,224	41,516	+	1	2_A375_pNL97_plus_lncRNA::1::196	196	in gene	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene HDAC1	HDAC1, GON-10, DKFZp686H12203, RPD3, RPD3L1, HD1	histone deacetylase 1	NM_004964, hCT2334578.0, hCT32882.3	201209_at	NP_004955.2, EAX07541.1, EAX07540.1
GeneID:100128071	LOC100128071	1	32,826,871	32,827,844	973	-	1	2_A375_pNL97_plus_lncRNA::1::197	10372	downstream	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100128071		hypothetical LOC100128071	NM_001167676		NP_001161148.1
GeneID:55108	BSDC1	1	32,830,704	32,860,062	29,358	-	1	2_A375_pNL97_plus_lncRNA::1::198	254	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene BSDC1	DKFZp686B09139, BSDC1, FLJ10276	BSD domain containing 1	NM_018045, NM_001143888, NM_001143889, NM_001143890, hCT1954822.1, hCT1971530.1, hCT1971531.1, hCT2359081.0, hCT2359082.0, hCT32895.3	1559971_at, 218004_at, 222200_s_at	NP_060515.3, NP_001137360.1, NP_001137361.1, NP_001137362.1, EAX07528.1, EAX07529.1, EAX07525.1, EAX07526.1, EAX07527.1, EAX07530.1
GeneID:8565	YARS	1	33,240,840	33,283,633	42,793	-	2	1_A375_pNL7_minus_lncRNA::1::145, 2_A375_pNL97_plus_lncRNA::1::199	657, 657	in gene, in gene	1	1	68	86	1	2_A375_pNL97_plus_lncRNA::1	86	Gene YARS	YTS, YRS, YARS, CMTDIC, TYRRS	tyrosyl-tRNA synthetase	NM_003680, hCT2334127.0, hCT2334128.0, hCT30941.3	212048_s_at, 238760_at	NP_003671.1, EAX07508.1, EAX07506.1, EAX07507.1
GeneID:64766	S100PBP	1	33,283,176	33,324,476	41,300	+	2	1_A375_pNL7_minus_lncRNA::1::145, 2_A375_pNL97_plus_lncRNA::1::199	-200, -200	upstream, upstream	1	1	68	86	1	2_A375_pNL97_plus_lncRNA::1	86	Gene S100PBP	S100PBP, FLJ12903, S100PBPR, DKFZp313K2325	S100P binding protein	NM_022753, NM_001017406, hCT2334726.0, hCT2334727.0, hCT30940.3	218370_s_at, 222610_s_at	NP_073590.2, NP_001017406.1, EAX07503.1, EAX07504.1, EAX07505.1
GeneID:127544	RNF19B	1	33,402,050	33,430,286	28,236	-	1	2_A375_pNL97_plus_lncRNA::1::200	-8242	upstream	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene RNF19B	IBRDC3, RNF19B, FLJ90005, NKLAM	ring finger protein 19B	NM_153341, NM_001127361, hCT2359216.0, hCT2359217.0, hCT30945.3	213038_at, 36564_at	NP_699172.2, NP_001120833.1, EAX07489.1, EAX07490.1, EAX07491.1
GeneID:113451	ADC	1	33,546,714	33,585,995	39,281	+	3	1_A375_pNL7_minus_lncRNA::1::146, 2_A375_pNL97_plus_lncRNA::1::201, 2_A375_pNL97_plus_lncRNA::1::202	46246, 18566, 46246	downstream, in gene, downstream	1	1	52.5	65.5	2	2_A375_pNL97_plus_lncRNA::1	114	Gene ADC	AZI2, ODC1L, KIAA1945, ADC, ODC-p	arginine decarboxylase	NM_052998, hCT1954821.1, hCT2334739.0, hCT2334741.0, hCT2334742.0, hCT2334743.0, hCT2334745.0, hCT2334747.0, hCT2359172.0, hCT2359173.0, hCT2359174.0, hCT2359175.0, hCT2359176.0, hCT2359177.0, hCT30937.3	1554393_a_at, 228000_at	NP_443724.1, EAX07481.1, EAX07469.1, EAX07471.1, EAX07475.1, EAX07479.1, EAX07470.1, EAX07472.1, EAX07473.1, EAX07474.1, EAX07476.1, EAX07477.1, EAX07478.1, EAX07480.1, EAX07482.1
GeneID:55223	TRIM62	1	33,611,003	33,647,671	36,668	-	1	2_A375_pNL97_plus_lncRNA::1::203	20439	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TRIM62	FLJ10759, FLJ16558, TRIM62, DEAR1	tripartite motif containing 62	NM_018207, hCT2334112.0, hCT2334113.0, hCT30936.3	219272_at, 236845_at, 58308_at	NP_060677.2, EAX07465.1, EAX07466.1, EAX07467.1
GeneID:149076	ZNF362	1	33,722,174	33,766,320	44,146	+	1	1_A375_pNL7_minus_lncRNA::1::148	-8190	upstream	1	0	25	19	1	1_A375_pNL7_minus_lncRNA::1	25	Gene ZNF362	FLJ25476, RN, MGC138318, ZNF362, lin-29	zinc finger protein 362	NM_152493, hCT30939.3	214915_at, 226820_at, 228957_at	NP_689706.2, EAX07464.1
GeneID:2707	GJB3	1	35,246,790	35,251,967	5,177	+	1	2_A375_pNL97_plus_lncRNA::1::205	378	in gene	0	1	10	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene GJB3	MGC102938, GJB3, DFNA2, DFNA2B, FLJ22486, EKV, CX31	gap junction protein, beta 3, 31kDa	NM_024009, NM_001005752	205490_x_at, 205491_s_at, 215243_s_at	NP_076872.1, NP_001005752.1
GeneID:113444	C1orf212	1	35,315,963	35,325,417	9,454	-	2	1_A375_pNL7_minus_lncRNA::1::153, 2_A375_pNL97_plus_lncRNA::1::206	-55, -55	upstream, upstream	1	1	133	136	1	2_A375_pNL97_plus_lncRNA::1	136	Gene C1orf212	MGC138436, FLJ90372, C1orf212	chromosome 1 open reading frame 212	NM_138428, NM_001164824, NM_001164825, hCT1641834.4, hCT1957658.2, hCT2349537.0	225404_at, 239510_at	NP_612437.3, NP_001158296.1, NP_001158297.1, EAX07437.1, EAX07438.1, EAX07439.1
GeneID:58512	DLGAP3	1	35,331,037	35,370,984	39,947	-	2	1_A375_pNL7_minus_lncRNA::1::153, 2_A375_pNL97_plus_lncRNA::1::206	45512, 45512	downstream, downstream	1	1	133	136	1	2_A375_pNL97_plus_lncRNA::1	136	Gene DLGAP3	DLGAP3, DAP3, SAPAP3	discs, large (Drosophila) homolog-associated protein 3	NM_001080418	1559630_at, 231151_at	NP_001073887.1
GeneID:100506144	LOC100506144	1	35,447,134	35,450,948	3,814	-	2	1_A375_pNL7_minus_lncRNA::1::155, 2_A375_pNL97_plus_lncRNA::1::208	4, 196	in gene, in gene	1	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506144	FLJ26314	hypothetical protein LOC100506144	XM_003119787, XM_003118961, XM_003120354		XP_003119835.1, XP_003119009.1, XP_003120402.1
GeneID:9204	ZMYM6	1	35,451,766	35,497,569	45,803	-	4	1_A375_pNL7_minus_lncRNA::1::155, 1_A375_pNL7_minus_lncRNA::1::156, 2_A375_pNL97_plus_lncRNA::1::208, 2_A375_pNL97_plus_lncRNA::1::209	46625, 145, 46817, 49	downstream, in gene, downstream, in gene	1	1	15.5	19	2	2_A375_pNL97_plus_lncRNA::1	20	Gene ZMYM6	ZNF258, ZNF198L4, MYM, ZMYM6, Buster2	zinc finger, MYM-type 6	NM_007167, hCT2333809.0, hCT2333811.0	1552969_a_at, 1552970_s_at, 1561892_at, 213698_at, 219924_s_at, 219925_at, 227594_at, 227595_at	NP_009098.3, EAX07432.1, EAX07433.1
GeneID:6421	SFPQ	1	35,649,201	35,658,743	9,542	-	2	1_A375_pNL7_minus_lncRNA::1::157, 2_A375_pNL97_plus_lncRNA::1::210	263, 23	in gene, in gene	1	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SFPQ	POMP100, PSF, SFPQ	splicing factor proline/glutamine-rich	NM_005066, hCT1642639.4, hCT1961259.2, hCT2333806.1, hCT2350049.0, hCT2350052.0, hCT28291.3	201585_s_at, 201586_s_at, 214016_s_at, 221768_at, 226898_s_at	NP_005057.1, EAX07422.1, EAX07421.1, EAX07423.1, EAX07424.1, EAX07425.1, EAX07426.1
GeneID:79932	KIAA0319L	1	35,899,091	36,023,037	123,946	-	1	2_A375_pNL97_plus_lncRNA::1::211	-179	upstream	0	1	15	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene KIAA0319L	FLJ44532, KIAA0319L, KIAA1837	KIAA0319-like	NM_024874, hCT2333798.0, hCT2333800.0, hCT2333801.0, hCT29527.3	217929_s_at, 222468_at	NP_079150.3, EAX07413.1, EAX07414.1, EAX07415.1, EAX07416.1
GeneID:23154	NCDN	1	36,023,393	36,032,380	8,987	+	1	2_A375_pNL97_plus_lncRNA::1::211	-177	upstream	0	1	15	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene NCDN	NCDN, KIAA0607	neurochondrin	NM_014284, NM_001014839, NM_001014841, hCT1957663.1, hCT2359067.0, hCT29531.3	209556_at, 209557_s_at, 237002_at	NP_055099.1, NP_001014839.1, NP_001014841.1, EAX07410.1, EAX07411.1, EAX07412.1
GeneID:5690	PSMB2	1	36,068,739	36,107,143	38,404	-	3	1_A375_pNL7_minus_lncRNA::1::158, 2_A375_pNL97_plus_lncRNA::1::212, 2_A375_pNL97_plus_lncRNA::1::213	71, -25, -9380	in gene, upstream, upstream	1	1	18	16.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene PSMB2	MGC126885, MGC104215, PSMB2, HC7-I	proteasome (prosome, macropain) subunit, beta type, 2	NM_002794, hCT1957661.2, hCT2333795.1, hCT2359225.0	200039_s_at, 201404_x_at, 231323_at	NP_002785.1, EAX07408.1, EAX07406.1, EAX07407.1
GeneID:127703	C1orf216	1	36,179,477	36,184,790	5,313	-	1	2_A375_pNL97_plus_lncRNA::1::215	390	in gene	0	1	14	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene C1orf216	FLJ38984, C1orf216	chromosome 1 open reading frame 216	NM_152374, hCT2333792.1, hCT29533.5	212791_at	NP_689587.1, EAX07404.1, EAX07403.1
GeneID:26523	EIF2C1	1	36,348,810	36,389,899	41,089	+	3	1_A375_pNL7_minus_lncRNA::1::160, 2_A375_pNL97_plus_lncRNA::1::216, 2_A375_pNL97_plus_lncRNA::1::217	-6058, -6026, 48022	upstream, upstream, downstream	1	1	14	19	2	2_A375_pNL97_plus_lncRNA::1	22	Gene EIF2C1	EIF2C1, AGO1, DKFZp686M13167, EIF2C, Q99, GERP95	eukaryotic translation initiation factor 2C, 1	NM_012199, hCT29522.1	218287_s_at, 222576_s_at	NP_036331.1, EAX07396.1
GeneID:192669	EIF2C3	1	36,396,772	36,522,063	125,291	+	1	2_A375_pNL97_plus_lncRNA::1::217	60	in gene	0	1	9	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene EIF2C3	AGO3, FLJ12765, EIF2C3, MGC86946	eukaryotic translation initiation factor 2C, 3	NM_024852, NM_177422, hCT2333926.0, hCT2333927.0	219426_at	NP_079128.2, NP_803171.1, EAX07394.1, EAX07395.1
GeneID:27285	TEKT2	1	36,549,676	36,553,876	4,200	+	2	1_A375_pNL7_minus_lncRNA::1::161, 2_A375_pNL97_plus_lncRNA::1::218	4724, 4788	downstream, downstream	1	1	51	54	1	2_A375_pNL97_plus_lncRNA::1	54	Gene TEKT2	h-tektin-t, TEKTB1, TEKT2, TEKTIN-T	tektin 2 (testicular)	NM_014466, hCT2359229.0, hCT29521.1	210323_at	NP_055281.2, EAX07391.1, EAX07392.1
GeneID:54936	ADPRHL2	1	36,554,453	36,559,533	5,080	+	2	1_A375_pNL7_minus_lncRNA::1::161, 2_A375_pNL97_plus_lncRNA::1::218	-53, 11	upstream, in gene	1	1	51	54	1	2_A375_pNL97_plus_lncRNA::1	54	Gene ADPRHL2	ARH3, FLJ20446, ADPRHL2	ADP-ribosylhydrolase like 2	NM_017825, hCT1956315.1, hCT29529.3	223097_at	NP_060295.1, EAX07389.1, EAX07390.1
GeneID:1296	COL8A2	1	36,560,842	36,565,850	5,008	-	2	1_A375_pNL7_minus_lncRNA::1::161, 2_A375_pNL97_plus_lncRNA::1::218	11450, 11386	downstream, downstream	1	1	51	54	1	2_A375_pNL97_plus_lncRNA::1	54	Gene COL8A2	PPCD2, FECD, FECD1, COL8A2, FLJ00201, MGC116972, PPCD, MGC116970	collagen, type VIII, alpha 2	NM_005202, hCT1826785.2	221900_at, 52651_at	NP_005193.1, EAX07388.1
GeneID:27095	TRAPPC3	1	36,602,173	36,615,067	12,894	-	1	2_A375_pNL97_plus_lncRNA::1::219	-1541	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TRAPPC3	TRAPPC3, BET3	trafficking protein particle complex 3	NM_014408, hCT1956313.1, hCT1971621.1, hCT29519.2	203511_s_at, 203512_at	NP_055223.1, EAX07385.1, EAX07386.1, EAX07387.1
GeneID:55700	MAP7D1	1	36,621,803	36,646,441	24,638	+	1	2_A375_pNL97_plus_lncRNA::1::219	-5195	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MAP7D1	PARCC1, FLJ39022, FLJ10350, RPRC1, MAP7D1, MGC117315	MAP7 domain containing 1	NM_018067, hCT1956314.1, hCT2333933.0, hCT2333936.0, hCT29520.2	217943_s_at	NP_060537.3, EAX07381.1, EAX07382.1, EAX07383.1, EAX07384.1
GeneID:9967	THRAP3	1	36,690,017	36,770,958	80,941	+	3	1_A375_pNL7_minus_lncRNA::1::162, 1_A375_pNL7_minus_lncRNA::1::163, 2_A375_pNL97_plus_lncRNA::1::220	-97, 75791, -129	upstream, in gene, upstream	1	1	20	17.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene THRAP3	FLJ22082, MGC133082, MGC133083, TRAP150, THRAP3	thyroid hormone receptor associated protein 3	NM_005119, hCT2333938.0, hCT28292.3	217847_s_at, 222439_s_at, 222440_s_at, 242163_at	NP_005110.2, EAX07379.1, EAX07380.1
GeneID:79729	C1orf113	1	36,771,994	36,786,848	14,854	+	1	1_A375_pNL7_minus_lncRNA::1::163	-6186	upstream	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene C1orf113	FLJ22938, C1orf113, SH3D21	SH3 domain containing 21	NM_024676, NM_001162530, hCT2333940.0, hCT2333942.0, hCT2333943.0	220193_at	NP_078952.4, NP_001156002.1, EAX07374.1, EAX07375.1, EAX07376.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:83931	STK40	1	36,805,225	36,851,485	46,260	-	5	1_A375_pNL7_minus_lncRNA::1::164, 1_A375_pNL7_minus_lncRNA::1::165, 2_A375_pNL97_plus_lncRNA::1::221, 2_A375_pNL97_plus_lncRNA::1::222, 2_A375_pNL97_plus_lncRNA::1::223	11357, -739, 33005, 11101, -771	in gene, upstream, in gene, in gene, upstream	1	1	18	21.33	3	2_A375_pNL97_plus_lncRNA::1	25	Gene STK40	STK40, MGC4796, RP11-268J15.4, SHIK, SgK495	serine/threonine kinase 40	NM_032017, hCT1826784.2, hCT2333774.0, hCT2333776.0, hCT2359198.0, hCT2359199.0, hCT2359200.0	223852_s_at, 225015_s_at	NP_114406.1, EAX07368.1, EAX07369.1, EAX07370.1, EAX07372.1, EAX07373.1, EAX07371.1
GeneID:100506594	LOC100506594	1	36,832,620	36,843,420	10,800	+	4	1_A375_pNL7_minus_lncRNA::1::164, 1_A375_pNL7_minus_lncRNA::1::165, 2_A375_pNL97_plus_lncRNA::1::222, 2_A375_pNL97_plus_lncRNA::1::223	7508, 19604, 7764, 19636	in gene, downstream, in gene, downstream	1	1	19.5	23	2	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100506594		hypothetical LOC100506594	XR_112061, XR_110496, XR_113341		
GeneID:84967	LSM10	1	36,859,031	36,863,493	4,462	-	4	1_A375_pNL7_minus_lncRNA::1::165, 1_A375_pNL7_minus_lncRNA::1::166, 2_A375_pNL97_plus_lncRNA::1::223, 2_A375_pNL97_plus_lncRNA::1::224	11269, 101, 11237, 101	downstream, in gene, downstream, in gene	1	1	21	22	2	2_A375_pNL97_plus_lncRNA::1	25	Gene LSM10	LSM10, MGC15749, MSTP074, MST074	LSM10, U7 small nuclear RNA associated	NM_032881, hCT1826789.1	225593_at	NP_116270.1, EAX07367.1
GeneID:64960	MRPS15	1	36,921,362	36,930,040	8,678	-	2	1_A375_pNL7_minus_lncRNA::1::167, 2_A375_pNL97_plus_lncRNA::1::225	88, 88	in gene, in gene	1	1	47	55	1	2_A375_pNL97_plus_lncRNA::1	55	Gene MRPS15	S15mt, DC37, FLJ11564, MRPS15, MPR-S15, RPMS15	mitochondrial ribosomal protein S15	NM_031280, hCT15524.3, hCT1956305.1, hCT1956306.1, hCT1961897.1, hCT2359197.0	221437_s_at, 223291_at, 223292_s_at, 226296_s_at	NP_112570.2, EAX07359.1, EAX07360.1, EAX07361.1, EAX07362.1, EAX07363.1
GeneID:1441	CSF3R	1	36,931,644	36,948,915	17,271	-	2	1_A375_pNL7_minus_lncRNA::1::167, 2_A375_pNL97_plus_lncRNA::1::225	18963, 18963	downstream, downstream	1	1	47	55	1	2_A375_pNL97_plus_lncRNA::1	55	Gene CSF3R	CSF3R, CD114, GCSFR	colony stimulating factor 3 receptor (granulocyte)	NM_000760, NM_156039, NM_172313, hCT1958919.1, hCT1958920.1, hCT1958921.1, hCT2333765.0, hCT2333767.0	1553297_a_at, 203591_s_at	NP_000751.1, NP_724781.1, NP_758519.1, EAX07356.1, EAX07357.1, EAX07358.1, EAX07354.1, EAX07355.1
GeneID:2899	GRIK3	1	37,261,128	37,499,844	238,716	-	5	1_A375_pNL7_minus_lncRNA::1::168, 1_A375_pNL7_minus_lncRNA::1::169, 2_A375_pNL97_plus_lncRNA::1::227, 2_A375_pNL97_plus_lncRNA::1::228, 2_A375_pNL97_plus_lncRNA::1::229	67844, 13364, 109924, 67828, 13364	in gene, in gene, in gene, in gene, in gene	1	1	21	31.67	3	2_A375_pNL97_plus_lncRNA::1	47	Gene GRIK3	GLR7, GLUR7, GRIK3, GluR7a, EAA5	glutamate receptor, ionotropic, kainate 3	NM_000831, hCT14246.3, hCT2333451.0	207454_at	NP_000822.2, EAX07351.1, EAX07350.1
GeneID:728431	LOC728431	1	37,920,480	37,940,047	19,567	-	1	2_A375_pNL97_plus_lncRNA::1::232	-5377	upstream	0	1	18	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC728431		hypothetical LOC728431	XR_112060, XR_112059, XR_110498, XR_110497, XR_113343, XR_113342	229676_at	
GeneID:80149	ZC3H12A	1	37,940,119	37,949,978	9,859	+	1	2_A375_pNL97_plus_lncRNA::1::232	5305	in gene	0	1	18	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ZC3H12A	MCPIP, RP3-423B22.1, ZC3H12A, dJ423B22.1, MCPIP1, FLJ23231	zinc finger CCCH-type containing 12A	NM_025079, hCT16805.1, hCT1956308.0, hCT2333501.0	218810_at	NP_079355.2, EAX07347.1, EAX07346.1, EAX07348.1
GeneID:54955	C1orf109	1	38,147,242	38,156,192	8,950	-	2	1_A375_pNL7_minus_lncRNA::1::170, 2_A375_pNL97_plus_lncRNA::1::233	-1632, -1152	upstream, upstream	1	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene C1orf109	FLJ20508, C1orf109	chromosome 1 open reading frame 109	NM_017850, hCT16813.3, hCT2333535.0, hCT2333536.0, hCT2333537.0, hCT2333540.0	218712_at	NP_060320.1, EAX07330.1, EAX07326.1, EAX07327.1, EAX07328.1, EAX07329.1
GeneID:55143	CDCA8	1	38,158,159	38,175,391	17,232	+	2	1_A375_pNL7_minus_lncRNA::1::170, 2_A375_pNL97_plus_lncRNA::1::233	-335, -815	upstream, upstream	1	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CDCA8	DasraB, FLJ10468, BOR, CDCA8, FLJ12042, MESRGP, BOREALIN	cell division cycle associated 8	NM_018101, hCT16808.3, hCT1822581.2	221520_s_at	NP_060571.1, EAX07325.1, EAX07324.1
GeneID:284656	EPHA10	1	38,181,646	38,230,824	49,178	-	2	1_A375_pNL7_minus_lncRNA::1::171, 2_A375_pNL97_plus_lncRNA::1::234	648, 744	in gene, in gene	1	1	25	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene EPHA10	FLJ16103, MGC43817, FLJ33655, EPHA10	EPH receptor A10	NM_001099439, NM_173641, hCT2345924.1, hCT2348645.0, hCT2348646.1	1553371_at, 236073_at, 243717_at	NP_001092909.1, NP_775912.2, EAX07321.1, EAX07322.1, EAX07323.1
GeneID:149175	MANEAL	1	38,259,774	38,267,278	7,504	+	2	1_A375_pNL7_minus_lncRNA::1::172, 2_A375_pNL97_plus_lncRNA::1::235	14082, 14082	downstream, downstream	1	1	22	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene MANEAL	FLJ31434, RP11-109P14.3, MANEAL, MGC78681	mannosidase, endo-alpha-like	NM_152496, NM_001031740, NM_001113482, hCT16806.4, hCT2333583.1	226132_s_at, 231564_at	NP_689709.1, NP_001026910.1, NP_001106954.1, EAX07319.1, EAX07320.1
GeneID:79693	YRDC	1	38,268,614	38,273,865	5,251	-	2	1_A375_pNL7_minus_lncRNA::1::172, 2_A375_pNL97_plus_lncRNA::1::235	9, 9	in gene, in gene	1	1	22	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene YRDC	IRIP, DRIP3, YRDC, SUA5, RP11-109P14.4, FLJ23476, FLJ26165	yrdC domain containing (E. coli)	NM_024640, hCT16812.3, hCT2333528.0	218647_s_at, 222703_s_at	NP_078916.3, EAX07317.1, EAX07318.1
GeneID:127687	C1orf122	1	38,273,473	38,275,126	1,653	+	2	1_A375_pNL7_minus_lncRNA::1::172, 2_A375_pNL97_plus_lncRNA::1::235	383, 383	in gene, in gene	1	1	22	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene C1orf122	C1orf122, ALAESM, FLJ45459, FLJ23476	chromosome 1 open reading frame 122	NM_198446, NM_001142726, hCT16811.3, hCT2348647.0, hCT2348648.0, hCT2348649.0	225480_at	NP_940848.2, NP_001136198.1, EAX07313.1, EAX07314.1, EAX07315.1, EAX07316.1
GeneID:4520	MTF1	1	38,275,239	38,325,292	50,053	-	4	1_A375_pNL7_minus_lncRNA::1::172, 1_A375_pNL7_minus_lncRNA::1::173, 2_A375_pNL97_plus_lncRNA::1::235, 2_A375_pNL97_plus_lncRNA::1::236	51436, 60, 51436, -169	downstream, in gene, downstream, upstream	1	1	20.5	26	2	2_A375_pNL97_plus_lncRNA::1	30	Gene MTF1	MTF-1, MGC23036, ZRF, MTF1	metal-regulatory transcription factor 1	NM_005955, hCT14235.3	205322_s_at, 205323_s_at, 227150_at	NP_005946.2, EAX07312.1
GeneID:3633	INPP5B	1	38,326,369	38,412,729	86,360	-	2	1_A375_pNL7_minus_lncRNA::1::173, 2_A375_pNL97_plus_lncRNA::1::236	87497, 87266	downstream, downstream	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene INPP5B	MGC65156, 5PTase, MGC71303, INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	NM_005540, hCT1956307.1, hCT2333524.0, hCT2359090.0, hCT2359091.0, hCT2359092.0	1563565_at, 213643_s_at, 213804_at	NP_005531.2, EAX07308.1, EAX07307.1, EAX07309.1, EAX07310.1, EAX07311.1
GeneID:10946	SF3A3	1	38,422,647	38,455,761	33,114	-	2	1_A375_pNL7_minus_lncRNA::1::174, 2_A375_pNL97_plus_lncRNA::1::237	-15, -15	upstream, upstream	1	1	172	183	1	2_A375_pNL97_plus_lncRNA::1	183	Gene SF3A3	SAP61, SF3a60, PRP9, SF3A3, PRPF9	splicing factor 3a, subunit 3, 60kDa	NM_006802, hCT2333520.0, hCT2333521.0, hCT2333522.0	203818_s_at	NP_006793.1, EAX07306.1, EAX07304.1, EAX07305.1
GeneID:2275	FHL3	1	38,462,442	38,471,234	8,792	-	4	1_A375_pNL7_minus_lncRNA::1::174, 1_A375_pNL7_minus_lncRNA::1::175, 2_A375_pNL97_plus_lncRNA::1::237, 2_A375_pNL97_plus_lncRNA::1::238	15456, -7342, 15456, -6910	downstream, upstream, downstream, upstream	1	1	94.5	103	2	2_A375_pNL97_plus_lncRNA::1	183	Gene FHL3	MGC19547, FHL3, SLIM2, MGC8696, MGC23614	four and a half LIM domains 3	NM_004468, hCT2333517.0, hCT2333519.0	218818_at	NP_004459.2, EAX07301.1, EAX07302.1
GeneID:51118	UTP11L	1	38,478,384	38,490,497	12,113	+	2	1_A375_pNL7_minus_lncRNA::1::175, 2_A375_pNL97_plus_lncRNA::1::238	192, -240	in gene, upstream	1	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene UTP11L	UTP11L, CGI94, CGI-94	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	NM_016037, hCT2333591.0, hCT2333592.0	218235_s_at, 233760_at	NP_057121.2, EAX07299.1, EAX07300.1
GeneID:79647	AKIRIN1	1	39,456,916	39,471,737	14,821	+	1	2_A375_pNL97_plus_lncRNA::1::241	28	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene AKIRIN1	RP11-781D11.2, FLJ12666, STRF2, AKIRIN1, C1orf108	akirin 1	NM_024595, NM_001136275, hCT1961812.1, hCT2333874.0, hCT32344.3	217893_s_at, 222456_s_at, 222459_at	NP_078871.1, NP_001129747.1, EAX07283.1, EAX07284.1, EAX07285.1
GeneID:8761	PABPC4	1	40,026,485	40,042,521	16,036	-	2	1_A375_pNL7_minus_lncRNA::1::177, 2_A375_pNL97_plus_lncRNA::1::242	-231, -231	upstream, upstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PABPC4	PABPC4, PABP4, APP1, iPABP, FLJ43938, APP-1	poly(A) binding protein, cytoplasmic 4 (inducible form)	NM_001135653, NM_003819, NM_001135654, hCT2333644.0, hCT2333645.0, hCT2333646.0, hCT2333647.0, hCT2333648.0, hCT2333649.0, hCT2333650.0, hCT2359171.0	201064_s_at	NP_001129125.1, NP_003810.1, NP_001129126.1, EAX07261.1, EAX07264.1, EAX07268.1, EAX07262.1, EAX07263.1, EAX07265.1, EAX07266.1, EAX07267.1
GeneID:100506950	LOC100506950	1	40,030,769	40,038,875	8,106	+	2	1_A375_pNL7_minus_lncRNA::1::177, 2_A375_pNL97_plus_lncRNA::1::242	11953, 11953	downstream, downstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100506950		hypothetical LOC100506950	XR_112057, XR_110500, XR_113345		
GeneID:677834	SNORA55	1	40,033,046	40,033,182	136	-	2	1_A375_pNL7_minus_lncRNA::1::177, 2_A375_pNL97_plus_lncRNA::1::242	-9570, -9570	upstream, upstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SNORA55	ACA55, SNORA55	small nucleolar RNA, H/ACA box 55	NR_002983		
GeneID:100287437	LOC100287437	1	40,254,654	40,255,843	1,189	+	1	1_A375_pNL7_minus_lncRNA::1::178	10306	downstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100287437		hypothetical protein LOC100287437	XM_002342076, XM_003120356		XP_002342117.1, XP_003120404.1
GeneID:54802	TRIT1	1	40,306,703	40,349,177	42,474	-	1	2_A375_pNL97_plus_lncRNA::1::243	57	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TRIT1	MOD5, MGC149243, FLJ20061, MGC149242, TRIT1, IPT	tRNA isopentenyltransferase 1	NM_017646, hCT1957526.1, hCT6901.3	218617_at	NP_060116.2, EAX07252.1, EAX07253.1
GeneID:84879	MFSD2A	1	40,420,784	40,435,628	14,844	+	1	2_A375_pNL97_plus_lncRNA::1::244	272	in gene	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene MFSD2A	FLJ14490, MFSD2A, FLJ35904, MFSD2	major facilitator superfamily domain containing 2A	NM_032793, NM_001136493, hCT1654625.2, hCT2336003.0, hCT2359161.0, hCT2359162.0	1553356_at, 225316_at	NP_116182.2, NP_001129965.1, EAX07246.1, EAX07247.1, EAX07248.1, EAX07249.1
GeneID:6018	RLF	1	40,627,041	40,706,593	79,552	+	2	1_A375_pNL7_minus_lncRNA::1::179, 2_A375_pNL97_plus_lncRNA::1::245	-1, -1	upstream, upstream	1	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene RLF	RLF, ZN-15L, MGC142226, ZNF292L	rearranged L-myc fusion	NM_012421, hCT6699.3	204243_at	NP_036553.2, EAX07236.1
GeneID:127391	TMCO2	1	40,713,573	40,717,365	3,792	+	2	1_A375_pNL7_minus_lncRNA::1::180, 2_A375_pNL97_plus_lncRNA::1::246	10263, 10331	downstream, downstream	1	1	28	26	1	1_A375_pNL7_minus_lncRNA::1	28	Gene TMCO2	TMCO2, dJ39G22.2, MGC131705	transmembrane and coiled-coil domains 2	NM_001008740, hCT1815123.1	231264_at	NP_001008740.1, EAX07235.1
GeneID:10269	ZMPSTE24	1	40,723,733	40,759,856	36,123	+	2	1_A375_pNL7_minus_lncRNA::1::180, 2_A375_pNL97_plus_lncRNA::1::246	123, 171	in gene, in gene	1	1	28	26	1	1_A375_pNL7_minus_lncRNA::1	28	Gene ZMPSTE24	FACE-1, PRO1, FACE1, FLJ14968, ZMPSTE24, Ste24p, HGPS, STE24	zinc metallopeptidase (STE24 homolog, S. cerevisiae)	NM_005857, hCT2336014.0, hCT6274.2	202939_at	NP_005848.2, EAX07233.1, EAX07234.1
GeneID:100286968	LOC100286968	1	40,839,353	40,872,543	33,190	-	2	1_A375_pNL7_minus_lncRNA::1::181, 2_A375_pNL97_plus_lncRNA::1::247	32564, 32063	in gene, in gene	1	1	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100286968		hypothetical LOC100286968	XR_112056, XR_110501, XR_113346		
GeneID:64744	SMAP2	1	40,839,728	40,888,994	49,266	+	2	1_A375_pNL7_minus_lncRNA::1::181, 2_A375_pNL97_plus_lncRNA::1::247	251, 752	in gene, in gene	1	1	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SMAP2	SMAP2, RP1-228H13.3, SMAP1L	small ArfGAP2	NM_022733, hCT1965929.1, hCT2359248.0, hCT2359249.0	225262_at	NP_073570.1, EAX07220.1, EAX07221.1, EAX07222.1
GeneID:65243	ZNF643	1	40,916,337	40,929,390	13,053	+	1	2_A375_pNL97_plus_lncRNA::1::248	-465	upstream	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ZNF643	RP11-656D10.1, ZNF643, FLJ34293	zinc finger protein 643	NM_023070, hCT1965928.1, hCT2336019.0, hCT2359247.0, hCT6697.3	207219_at	NP_075558.2, EAX07219.1, EAX07216.1, EAX07217.1, EAX07218.1
GeneID:339559	ZNF642	1	40,943,302	40,962,015	18,713	+	1	1_A375_pNL7_minus_lncRNA::1::182	-198	upstream	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene ZNF642	ZNF642, FLJ16030, Zfp69, RP11-656D10.2	zinc finger protein 642	NM_198494, hCT1659865.3	1569107_s_at	NP_940896.2, EAX07215.1
GeneID:64789	DEM1	1	40,974,433	40,982,228	7,795	+	2	1_A375_pNL7_minus_lncRNA::1::183, 2_A375_pNL97_plus_lncRNA::1::249	-49, 159	upstream, in gene	1	1	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene DEM1	FLJ13183, Exo V, C1orf176, DEM1, FLJ11445, FLJ21144	defects in morphology 1 homolog (S. cerevisiae)	NM_022774, hCT1814661.1, hCT1966173.1, hCT1966174.0, hCT1966176.1, hCT2359077.0	219567_s_at, 222902_s_at	NP_073611.1, EAX07214.1, EAX07210.1, EAX07211.1, EAX07212.1, EAX07213.1
GeneID:127396	ZNF684	1	40,997,233	41,013,841	16,608	+	1	2_A375_pNL97_plus_lncRNA::1::250	127	in gene	0	1	9	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZNF684	ZNF684, MGC27466	zinc finger protein 684	NM_152373, hCT13963.3, hCT2335995.0	232563_at, 244398_x_at	NP_689586.3, EAX07208.1, EAX07209.1
GeneID:9783	RIMS3	1	41,086,352	41,131,324	44,972	-	1	2_A375_pNL97_plus_lncRNA::1::251	39420	in gene	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RIMS3	RIM3, KIAA0237, RIMS3, NIM3	regulating synaptic membrane exocytosis 3	NM_014747, hCT12798.2, hCT1967774.1	204730_at, 210991_s_at	NP_055562.2, EAX07206.1, EAX07207.1
GeneID:100130557	LOC100130557	1	41,154,752	41,157,933	3,181	-	1	2_A375_pNL97_plus_lncRNA::1::252	301	in gene	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100130557		hypothetical LOC100130557	NR_024567		
GeneID:4802	NFYC	1	41,157,242	41,237,275	80,033	+	1	2_A375_pNL97_plus_lncRNA::1::252	390	in gene	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene NFYC	H1TF2A, HAP5, NFYC, NF-YC, FLJ45775, DKFZp667G242, CBFC, HSM, CBF-C	nuclear transcription factor Y, gamma	NM_014223, NM_001142587, NM_001142588, NM_001142589, NM_001142590, hCT13965.4, hCT1956196.1, hCT2333481.0, hCT2333482.0, hCT2359112.0, hCT2359113.0	1556762_a_at, 1559218_s_at, 202215_s_at, 202216_x_at, 211251_x_at, 211797_s_at, 236231_at	NP_055038.2, NP_001136059.1, NP_001136060.1, NP_001136061.1, NP_001136062.1, EAX07202.1, EAX07198.1, EAX07199.1, EAX07200.1, EAX07201.1, EAX07203.1
GeneID:1503	CTPS	1	41,445,007	41,478,235	33,228	+	1	2_A375_pNL97_plus_lncRNA::1::253	145	in gene	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CTPS	CTPS		NM_001905, hCT13966.2, hCT2359116.0	202613_at	NP_001896.2, EAX07193.1, EAX07192.1
GeneID:59269	HIVEP3	1	41,975,684	42,384,496	408,812	-	10	2_A375_pNL97_plus_lncRNA::1::254, 1_A375_pNL7_minus_lncRNA::1::185, 1_A375_pNL7_minus_lncRNA::1::186, 1_A375_pNL7_minus_lncRNA::1::187, 1_A375_pNL7_minus_lncRNA::1::188, 1_A375_pNL7_minus_lncRNA::1::189, 2_A375_pNL97_plus_lncRNA::1::255, 2_A375_pNL97_plus_lncRNA::1::256, 2_A375_pNL97_plus_lncRNA::1::257, 2_A375_pNL97_plus_lncRNA	404336, 135344, 108224, 71973, 48528, -1936, 108272, 107472, 67104, 384	in gene, in gene, in gene, in gene, in gene, upstream, in gene, in gene, in gene, in gene	1	1	18.88	16.13	8	1_A375_pNL7_minus_lncRNA::1	32	Gene HIVEP3	KRC, Schnurri-3, FLJ16752, KIAA1555, KBP1, KBP-1, SHN3, ZNF40C, HIVEP3, ZAS3	human immunodeficiency virus type I enhancer binding protein 3	NM_024503, NM_001127714, hCT1827034.1	220042_x_at, 232581_x_at	NP_078779.2, NP_001121186.1, EAX07173.1
GeneID:100507198	LOC100507198	1	42,312,860	42,337,890	25,030	-	3	1_A375_pNL7_minus_lncRNA::1::187, 1_A375_pNL7_minus_lncRNA::1::188, 2_A375_pNL97_plus_lncRNA::1::257	25367, 1922, 20498	downstream, in gene, in gene	1	1	18	13.67	3	1_A375_pNL7_minus_lncRNA::1	21	Gene LOC100507198		hypothetical LOC100507198	XR_112054, XR_110503, XR_113348		
GeneID:22887	FOXJ3	1	42,642,210	42,800,903	158,693	-	1	2_A375_pNL97_plus_lncRNA::1::260	-153	upstream	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene FOXJ3	MGC176686, FOXJ3, MGC165036	forkhead box J3	NM_014947, hCT12801.2, hCT2333469.0, hCT2333471.0, hCT2359140.0, hCT2359141.0, hCT2359142.0	206015_s_at, 217310_s_at	NP_055762.3, EAX07164.1, EAX07162.1, EAX07163.1, EAX07165.1, EAX07167.1, EAX07166.1
GeneID:284716	RIMKLA	1	42,846,468	42,889,900	43,432	+	2	1_A375_pNL7_minus_lncRNA::1::191, 2_A375_pNL97_plus_lncRNA::1::261	-760, -772	upstream, upstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RIMKLA	RIMKLA, NAAGS, MGC47816, FAM80A	ribosomal modification protein rimK-like family member A	NM_173642, hCT1955231.1	235946_at	NP_775913.2, EAX07161.1
GeneID:84217	ZMYND12	1	42,896,000	42,921,936	25,936	-	1	2_A375_pNL97_plus_lncRNA::1::262	-302	upstream	0	1	14	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ZMYND12	DKFZp434N2435, ZMYND12	zinc finger, MYND-type containing 12	NM_032257, NM_001146192, hCT14099.3, hCT1966146.1	223636_at	NP_115633.3, NP_001139664.1, EAX07159.1, EAX07160.1
GeneID:79717	PPCS	1	42,922,173	42,926,086	3,913	+	1	2_A375_pNL97_plus_lncRNA::1::262	67	in gene	0	1	14	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PPCS	MGC117357, PPCS, MGC138220, FLJ11838	phosphopantothenoylcysteine synthetase	NM_024664, NM_001077447, hCT2344266.0	218341_at	NP_078940.2, NP_001070915.1, EAX07158.1
GeneID:100507214	LOC100507214	1	42,928,957	42,939,088	10,131	+	1	2_A375_pNL97_plus_lncRNA::1::262	-6717	upstream	0	1	14	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100507214		hypothetical LOC100507214	XR_112053, XR_110504, XR_113349		
GeneID:728621	CCDC30	1	43,000,560	43,120,335	119,775	+	3	1_A375_pNL7_minus_lncRNA::1::192, 1_A375_pNL7_minus_lncRNA::1::193, 2_A375_pNL97_plus_lncRNA::1::263	-4784, 123440, 123632	upstream, downstream, downstream	1	1	24.5	22.5	2	1_A375_pNL7_minus_lncRNA::1	29	Gene CCDC30	PFD6L, CCDC30, FLJ20972, PFDN6L	coiled-coil domain containing 30	NM_001080850	221171_at, 230897_at	NP_001074319.1
GeneID:10465	PPIH	1	43,124,048	43,142,429	18,381	+	2	1_A375_pNL7_minus_lncRNA::1::193, 2_A375_pNL97_plus_lncRNA::1::263	-48, 144	upstream, in gene	1	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PPIH	USA-CYP, MGC5016, SnuCyp-20, CYP-20, PPIH, CYPH	peptidylprolyl isomerase H (cyclophilin H)	NM_006347, hCT12839.2, hCT1963346.1, hCT1963347.1, hCT1963348.1, hCT1963349.1, hCT1967880.1	204228_at, 236142_at	NP_006338.1, EAX07153.1, EAX07151.1, EAX07152.1, EAX07155.1, EAX07156.1, EAX07154.1
GeneID:114625	ERMAP	1	43,282,776	43,310,660	27,884	+	1	2_A375_pNL97_plus_lncRNA::1::264	29352	downstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ERMAP	MGC118812, MGC118813, SC, PRO2801, MGC118810, RD, MGC118811, ERMAP	erythroblast membrane-associated protein (Scianna blood group)	NM_018538, NM_001017922, hCT2333831.0, hCT2333832.0, hCT2359099.0, hCT2359100.0	219905_at	NP_061008.2, NP_001017922.1, EAX07130.1, EAX07131.1, EAX07132.1, EAX07133.1
GeneID:51058	ZNF691	1	43,312,280	43,318,146	5,866	+	1	2_A375_pNL97_plus_lncRNA::1::264	-152	upstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ZNF691	Zfp691, ZNF691, RP11-342M1.5	zinc finger protein 691	NM_015911	232780_s_at	NP_056995.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:6513	SLC2A1	1	43,391,046	43,424,847	33,801	-	2	1_A375_pNL7_minus_lncRNA::1::194, 2_A375_pNL97_plus_lncRNA::1::266	143, 111	in gene, in gene	1	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC2A1	MGC141896, MGC141895, DYT18, PED, GLUT1, GLUT1DS, DYT17, SLC2A1, GLUT	solute carrier family 2 (facilitated glucose transporter), member 1	NM_006516, hCT14262.2, hCT2333584.0	201249_at, 201250_s_at	NP_006507.2, EAX07124.1, EAX07123.1
GeneID:440584	FLJ32224	1	43,424,720	43,449,029	24,309	+	2	1_A375_pNL7_minus_lncRNA::1::194, 2_A375_pNL97_plus_lncRNA::1::266	-16, 16	upstream, in gene	1	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FLJ32224		hypothetical LOC440584	NR_033967	1556832_at	
GeneID:4352	MPL	1	43,803,475	43,820,135	16,660	+	1	2_A375_pNL97_plus_lncRNA::1::267	11565	in gene	0	1	11	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene MPL	CD110, TPOR, C-MPL, MPLV, MPL	myeloproliferative leukemia virus oncogene	NM_005373, hCT14266.2, hCT2333849.0, hCT2333850.0	207550_at, 211903_s_at, 216825_s_at	NP_005364.1, EAX07103.1, EAX07104.1, EAX07105.1
GeneID:991	CDC20	1	43,824,626	43,828,874	4,248	+	1	2_A375_pNL97_plus_lncRNA::1::267	-8586	upstream	0	1	11	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CDC20	CDC20, CDC20A, bA276H19.3, p55CDC, MGC102824	cell division cycle 20 homolog (S. cerevisiae)	NM_001255, hCT14269.3, hCT1960860.0	202870_s_at	NP_001246.2, EAX07101.1, EAX07102.1
GeneID:112950	MED8	1	43,849,588	43,855,483	5,895	-	2	1_A375_pNL7_minus_lncRNA::1::195, 2_A375_pNL97_plus_lncRNA::1::268	59, -165	in gene, upstream	1	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene MED8	MGC17544, MED8, ARC32, MGC19641	mediator complex subunit 8	NM_052877, NM_201542, hCT2333564.0	213126_at, 213127_s_at, 213696_s_at	NP_443109.2, NP_963836.2, EAX07099.1
GeneID:149469	C1orf84	1	43,855,556	43,872,565	17,009	+	2	1_A375_pNL7_minus_lncRNA::1::195, 2_A375_pNL97_plus_lncRNA::1::268	-132, 92	upstream, in gene	1	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene C1orf84	FLJ34502, C1orf84, SZT2A	chromosome 1 open reading frame 84	NM_001012961	1569709_at	NP_001012979.1
GeneID:5792	PTPRF	1	43,996,547	44,089,343	92,796	+	2	1_A375_pNL7_minus_lncRNA::1::196, 2_A375_pNL97_plus_lncRNA::1::269	-7523, -7539	upstream, upstream	1	1	30	30	1	1_A375_pNL7_minus_lncRNA::1	30	Gene PTPRF	FLJ45062, FLJ43335, PTPRF, LAR, FLJ45567	protein tyrosine phosphatase, receptor type, F	NM_130440, NM_002840, hCT16333.2, hCT2333861.0, hCT2333862.0, hCT2333863.0	200635_s_at, 200636_s_at, 200637_s_at, 215066_at	NP_569707.2, NP_002831.2, EAX07086.1, EAX07087.1, EAX07088.1, EAX07089.1
GeneID:6487	ST3GAL3	1	44,173,218	44,396,831	223,613	+	4	1_A375_pNL7_minus_lncRNA::1::197, 1_A375_pNL7_minus_lncRNA::1::198, 2_A375_pNL97_plus_lncRNA::1::270, 2_A375_pNL97_plus_lncRNA::1::271	127070, 222206, 127262, 128302	in gene, in gene, in gene, in gene	1	1	22.5	20	2	1_A375_pNL7_minus_lncRNA::1	24	Gene ST3GAL3	ST3GalIII, ST3N, ST3GAL3, ST3GALII, SIAT6	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	NM_006279, NM_174964, NM_174965, NM_174966, NM_174967, NM_174969, NM_174970, NM_174968, NM_174971, NM_174963, hCT16328.3, hCT2333700.0, hCT2333703.0	1555171_at, 1555181_a_at, 1555678_at, 1555702_a_at, 1555703_at, 225905_s_at, 231659_at	NP_006270.1, NP_777624.1, NP_777625.1, NP_777626.1, NP_777627.1, NP_777629.1, NP_777630.1, NP_777628.2, NP_777631.2, NP_777623.2, EAX07082.1, EAX07083.1, EAX07084.1
GeneID:9048	ARTN	1	44,398,992	44,402,912	3,920	+	3	1_A375_pNL7_minus_lncRNA::1::198, 1_A375_pNL7_minus_lncRNA::1::199, 2_A375_pNL97_plus_lncRNA::1::272	-3568, 13424, 13424	upstream, downstream, downstream	1	1	24.5	23.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene ARTN	ARTN, EVN, ENOVIN, NBN	artemin	NM_057090, NM_057091, NM_001136215, hCT16325.2, hCT1963729.1, hCT1963730.0, hCT1963731.0, hCT2333704.0, hCT2333705.0, hCT2333707.0, hCT2333712.0	207675_x_at, 210237_at, 216052_x_at	NP_476431.2, NP_476432.2, NP_001129687.1, EAX07074.1, EAX07077.1, EAX07078.1, EAX07075.1, EAX07076.1, EAX07079.1, EAX07080.1, EAX07081.1
GeneID:9670	IPO13	1	44,412,478	44,433,694	21,216	+	3	1_A375_pNL7_minus_lncRNA::1::199, 1_A375_pNL7_minus_lncRNA::1::200, 2_A375_pNL97_plus_lncRNA::1::272	-62, 21730, -62	upstream, downstream, upstream	1	1	24.5	21	2	2_A375_pNL97_plus_lncRNA::1	25	Gene IPO13	IPO13, KIAA0724, RANBP13, IMP13, KAP13, LGL2	importin 13	NM_014652, hCT16322.2, hCT2333714.0	203546_at	NP_055467.3, EAX07072.1, EAX07073.1
GeneID:1802	DPH2	1	44,435,653	44,439,043	3,390	+	1	1_A375_pNL7_minus_lncRNA::1::200	-1445	upstream	1	0	24	17	1	1_A375_pNL7_minus_lncRNA::1	24	Gene DPH2	DPH2, DPH2L2	DPH2 homolog (S. cerevisiae)	NM_001039589, NM_001384, hCT16323.2, hCT2359106.0	204514_at	NP_001034678.1, NP_001375.2, EAX07070.1, EAX07071.1
GeneID:533	ATP6V0B	1	44,440,602	44,443,972	3,370	+	1	1_A375_pNL7_minus_lncRNA::1::200	-6394	upstream	1	0	24	17	1	1_A375_pNL7_minus_lncRNA::1	24	Gene ATP6V0B	HATPL, ATP6V0B, VMA16, ATP6F	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	NM_001039457, NM_004047, hCT16324.2, hCT1963712.1, hCT2359110.0, hCT2359111.0	200078_s_at	NP_001034546.1, NP_004038.1, EAX07066.1, EAX07067.1, EAX07068.1, EAX07069.1
GeneID:6536	SLC6A9	1	44,462,155	44,497,134	34,979	-	1	2_A375_pNL97_plus_lncRNA::1::273	830	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SLC6A9	GLYT1, DKFZp547A1118, SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	NM_006934, NM_201649, NM_001024845, hCT16326.2, hCT1953759.1, hCT2333436.0, hCT2359186.0	207043_s_at	NP_008865.2, NP_964012.2, NP_001020016.1, EAX07054.1, EAX07055.1, EAX07057.1, EAX07056.1
GeneID:55929	DMAP1	1	44,679,125	44,686,351	7,226	+	1	1_A375_pNL7_minus_lncRNA::1::201	-5	upstream	1	0	30	25	1	1_A375_pNL7_minus_lncRNA::1	30	Gene DMAP1	FLJ11543, DMAP1, DKFZp686L09142, SWC4, KIAA1425, DNMAP1, DNMTAP1, MEAF2, EAF2	DNA methyltransferase 1 associated protein 1	NM_019100, NM_001034023, NM_001034024, hCT16329.3, hCT1968158.1, hCT1968162.1, hCT1968165.1, hCT2359190.0, hCT2359191.0	224163_s_at	NP_061973.1, NP_001029195.1, NP_001029196.1, EAX07046.1, EAX07048.1, EAX07049.1, EAX07047.1, EAX07050.1, EAX07051.1
GeneID:79033	ERI3	1	44,686,742	44,820,939	134,197	-	2	1_A375_pNL7_minus_lncRNA::1::201, 1_A375_pNL7_minus_lncRNA::1::202	141819, 27435	downstream, in gene	1	0	23.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	30	Gene ERI3	MGC2683, FLJ22943, PRNPIP, PINT1, ERI3	ERI1 exoribonuclease family member 3	NM_024066, hCT16331.2, hCT2333427.0, hCT2333429.0, hCT2359196.0	208973_at	NP_076971.1, EAX07043.1, EAX07042.1, EAX07044.1, EAX07045.1
GeneID:55182	RNF220	1	44,870,960	45,117,396	246,436	+	2	1_A375_pNL7_minus_lncRNA::1::203, 2_A375_pNL97_plus_lncRNA::1::274	126912, 126960	in gene, in gene	1	1	26	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene RNF220	FLJ10597, RNF220, C1orf164	ring finger protein 220	NM_018150	219988_s_at	NP_060620.2
GeneID:339541	C1orf228	1	45,140,394	45,191,263	50,869	+	4	1_A375_pNL7_minus_lncRNA::1::204, 1_A375_pNL7_minus_lncRNA::1::205, 2_A375_pNL97_plus_lncRNA::1::275, 2_A375_pNL97_plus_lncRNA::1::276	47286, 56566, 47446, 56582	in gene, downstream, in gene, downstream	1	1	24	30.5	2	2_A375_pNL97_plus_lncRNA::1	34	Gene C1orf228	p40, NCRNA00082, MGC33556, C1orf228	chromosome 1 open reading frame 228	NM_001145636, hCT13275.3, hCT2359131.0	238365_s_at, 238366_at, 238367_s_at, 239644_x_at, 242520_s_at	NP_001139108.1, EAX07026.1, EAX07027.1
GeneID:26830	RNU5D	1	45,196,741	45,196,840	99	-	4	1_A375_pNL7_minus_lncRNA::1::204, 1_A375_pNL7_minus_lncRNA::1::205, 2_A375_pNL97_plus_lncRNA::1::275, 2_A375_pNL97_plus_lncRNA::1::276	9160, -120, 9000, -136	downstream, upstream, downstream, upstream	1	1	24	30.5	2	2_A375_pNL97_plus_lncRNA::1	34	Gene RNU5D	U5DS, RNU5D, U5DL	RNA, U5D small nuclear	NR_002755		
GeneID:11004	KIF2C	1	45,205,490	45,233,439	27,949	+	4	1_A375_pNL7_minus_lncRNA::1::205, 1_A375_pNL7_minus_lncRNA::1::206, 2_A375_pNL97_plus_lncRNA::1::276, 2_A375_pNL97_plus_lncRNA::1::277	-8530, 35598, -8514, 35614	upstream, downstream, upstream, downstream	1	1	22	29	2	2_A375_pNL97_plus_lncRNA::1	34	Gene KIF2C	KNSL6, KIF2C, MCAK	kinesin family member 2C	NM_006845, hCT1814808.3	209408_at, 211519_s_at	NP_006836.2, EAX07025.1
GeneID:6202	RPS8	1	45,241,246	45,244,412	3,166	+	2	1_A375_pNL7_minus_lncRNA::1::206, 2_A375_pNL97_plus_lncRNA::1::277	-158, -142	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene RPS8	RPS8, S8		NM_001012, hCT2333696.0, hCT2333697.0	200858_s_at	NP_001003.1, EAX07024.1, EAX07023.1
GeneID:26811	SNORD55	1	45,241,537	45,241,610	73	+	2	1_A375_pNL7_minus_lncRNA::1::206, 2_A375_pNL97_plus_lncRNA::1::277	-449, -433	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SNORD55	SNORD55, RNU39, U39, U55, RNU55, SNORD39	small nucleolar RNA, C/D box 55	NR_000015		
GeneID:94161	SNORD46	1	45,242,164	45,242,261	97	+	2	1_A375_pNL7_minus_lncRNA::1::206, 2_A375_pNL97_plus_lncRNA::1::277	-1076, -1060	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SNORD46	U46, RNU46, SNORD46, U40, RNU40	small nucleolar RNA, C/D box 46	NR_000024		
GeneID:94162	SNORD38A	1	45,243,514	45,243,584	70	+	2	1_A375_pNL7_minus_lncRNA::1::206, 2_A375_pNL97_plus_lncRNA::1::277	-2426, -2410	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SNORD38A	RNU38A, SNORD38A, U38A	small nucleolar RNA, C/D box 38A	NR_001456		
GeneID:94163	SNORD38B	1	45,244,062	45,244,130	68	+	2	1_A375_pNL7_minus_lncRNA::1::206, 2_A375_pNL97_plus_lncRNA::1::277	-2974, -2958	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SNORD38B	U38B, SNORD38B, RNU38B	small nucleolar RNA, C/D box 38B	NR_001457		
GeneID:266675	BEST4	1	45,249,257	45,253,426	4,169	-	2	1_A375_pNL7_minus_lncRNA::1::206, 2_A375_pNL97_plus_lncRNA::1::277	12338, 12322	downstream, downstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene BEST4	BEST4, VMD2L2, MGC126872	bestrophin 4	NM_153274, hCT2341150.0	1552296_at	NP_695006.1, EAX07022.1
GeneID:149478	BTBD19	1	45,274,154	45,279,801	5,647	+	2	1_A375_pNL7_minus_lncRNA::1::207, 2_A375_pNL97_plus_lncRNA::1::278	11606, 11606	downstream, downstream	1	1	31	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene BTBD19	BTBD19	BTB (POZ) domain containing 19	NM_001136537	1557049_at, 238102_s_at	NP_001130009.1
GeneID:8643	PTCH2	1	45,285,516	45,308,616	23,100	-	2	1_A375_pNL7_minus_lncRNA::1::207, 2_A375_pNL97_plus_lncRNA::1::278	22656, 22656	in gene, in gene	1	1	31	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene PTCH2	PTCH2, PTC2	patched homolog 2 (Drosophila)	NM_003738, NM_001166292, hCT9661.3	221292_at	NP_003729.3, NP_001159764.1, EAX07017.1
GeneID:8891	EIF2B3	1	45,316,194	45,452,361	136,167	-	2	1_A375_pNL7_minus_lncRNA::1::208, 2_A375_pNL97_plus_lncRNA::1::279	9, 73	in gene, in gene	1	1	47	57	1	2_A375_pNL97_plus_lncRNA::1	57	Gene EIF2B3	EIF-2B, EIF2Bgamma, EIF2B3	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	NM_020365, NM_001166588, hCT2333987.0, hCT2333988.0, hCT2359221.0, hCT2359222.0, hCT2359223.0, hCT9665.3	218488_at	NP_065098.1, NP_001160060.1, EAX07011.1, EAX07012.1, EAX07013.1, EAX07016.1, EAX07014.1, EAX07015.1
GeneID:79654	HECTD3	1	45,468,220	45,477,027	8,807	-	2	1_A375_pNL7_minus_lncRNA::1::209, 2_A375_pNL97_plus_lncRNA::1::280	-733, -701	upstream, upstream	1	1	46	43	1	1_A375_pNL7_minus_lncRNA::1	46	Gene HECTD3	MGC161630, RP11-69J16.1, FLJ31983, HECTD3, FLJ21156	HECT domain containing 3	NM_024602, hCT1815098.1, hCT2333985.0	218632_at	NP_078878.3, EAX07009.1, EAX07010.1
GeneID:7389	UROD	1	45,477,805	45,481,341	3,536	+	2	1_A375_pNL7_minus_lncRNA::1::209, 2_A375_pNL97_plus_lncRNA::1::280	-45, -77	upstream, upstream	1	1	46	43	1	1_A375_pNL7_minus_lncRNA::1	46	Gene UROD	PCT, UROD	uroporphyrinogen decarboxylase	NM_000374, NR_036510, hCT2359228.0, hCT8898.2	208970_s_at, 208971_at, 222074_at	NP_000365.3, EAX07008.1, EAX07007.1
GeneID:57643	ZSWIM5	1	45,482,074	45,672,250	190,176	-	2	1_A375_pNL7_minus_lncRNA::1::209, 2_A375_pNL97_plus_lncRNA::1::280	194490, 194522	downstream, downstream	1	1	46	43	1	1_A375_pNL7_minus_lncRNA::1	46	Gene ZSWIM5	KIAA1511, ZSWIM5	zinc finger, SWIM-type containing 5	NM_020883	232336_at	NP_065934.1
GeneID:84842	HPDL	1	45,792,545	45,794,347	1,802	+	1	2_A375_pNL97_plus_lncRNA::1::281	479	in gene	0	1	8	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene HPDL	MGC15668, HPDL, RP4-534D1.1, GLOXD1, 4-HPPD-L	4-hydroxyphenylpyruvate dioxygenase-like	NM_032756, hCT1833603.1	229332_at	NP_116145.1, EAX07002.1
GeneID:4595	MUTYH	1	45,794,914	45,806,142	11,228	-	1	2_A375_pNL97_plus_lncRNA::1::281	13118	downstream	0	1	8	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MUTYH	MYH, MGC4416, CYP2C, MUTYH	mutY homolog (E. coli)	NM_012222, NM_001048171, NM_001048172, NM_001048173, NM_001048174, NM_001128425, hCT1818872.3, hCT1966772.1, hCT2359120.0, hCT2359121.0, hCT2359122.0, hCT2359123.0, hCT2359124.0, hCT2359125.0, hCT2359126.0, hCT2359127.0, hCT2359128.0	207727_s_at	NP_036354.1, NP_001041636.1, NP_001041637.1, NP_001041638.1, NP_001041639.1, NP_001121897.1, EAX06991.1, EAX06992.1, EAX06993.1, EAX06994.1, EAX06995.1, EAX06996.1, EAX06997.1, EAX07001.1, EAX06998.1, EAX06999.1, EAX07000.1
GeneID:10420	TESK2	1	45,809,555	45,956,840	147,285	-	2	1_A375_pNL7_minus_lncRNA::1::210, 2_A375_pNL97_plus_lncRNA::1::282	-8952, -9016	upstream, upstream	1	1	32	32	1	1_A375_pNL7_minus_lncRNA::1	32	Gene TESK2	TESK2		NM_007170, hCT2333975.0, hCT2333976.0, hCT2333977.0, hCT2333978.0	205486_at	NP_009101.2, EAX06989.1, EAX06986.1, EAX06987.1, EAX06988.1
GeneID:126661	CCDC163P	1	45,959,598	45,965,751	6,153	-	2	1_A375_pNL7_minus_lncRNA::1::210, 2_A375_pNL97_plus_lncRNA::1::282	-41, -105	upstream, upstream	1	1	32	32	1	1_A375_pNL7_minus_lncRNA::1	32	Gene CCDC163P	C1orf231, CCDC163P	coiled-coil domain containing 163, pseudogene	NR_033296, NR_033297, NR_033298	1559003_a_at, 236900_x_at	
GeneID:25974	MMACHC	1	45,965,856	45,976,739	10,883	+	2	1_A375_pNL7_minus_lncRNA::1::210, 2_A375_pNL97_plus_lncRNA::1::282	-64, 0	upstream, in gene	1	1	32	32	1	1_A375_pNL7_minus_lncRNA::1	32	Gene MMACHC	DKFZp564I122, MMACHC, cblC, FLJ25671, RP11-291L19.3	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	NM_015506, hCT1818880.1	211774_s_at	NP_056321.2, EAX06983.1
GeneID:5052	PRDX1	1	45,976,707	45,987,609	10,902	-	1	2_A375_pNL97_plus_lncRNA::1::283	25	in gene	0	1	17	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene PRDX1	PAGB, PRXI, PRDX1, PRX1, MSP23, TDPX2, NKEFA, PAGA, PAG	peroxiredoxin 1	NM_181696, NM_181697, NM_002574, hCT1818876.2, hCT1962879.1, hCT1962880.1, hCT1966792.1, hCT2333966.0, hCT2333971.0, hCT2359180.0, hCT2359181.0	208680_at	NP_859047.1, NP_859048.1, NP_002565.1, EAX06979.1, EAX06980.1, EAX06982.1, EAX06975.1, EAX06976.1, EAX06977.1, EAX06978.1, EAX06981.1
GeneID:4678	NASP	1	46,049,717	46,084,567	34,850	+	2	1_A375_pNL7_minus_lncRNA::1::211, 2_A375_pNL97_plus_lncRNA::1::284	-117, -85	upstream, upstream	1	1	28	18	1	1_A375_pNL7_minus_lncRNA::1	28	Gene NASP	PRO1999, MGC20372, MGC2297, DKFZp547F162, FLJ31599, MGC19722, FLJ35510, NASP, FLB7527	nuclear autoantigenic sperm protein (histone-binding)	NM_002482, NM_152298, hCT1963736.1, hCT2334446.0, hCT2334448.0, hCT2334450.0, hCT2359218.0, hCT32147.3	201969_at, 201970_s_at, 242918_at	NP_002473.2, NP_689511.2, EAX06964.1, EAX06965.1, EAX06966.1, EAX06969.1, EAX06967.1, EAX06968.1
GeneID:60313	GPBP1L1	1	46,092,976	46,152,302	59,326	-	3	1_A375_pNL7_minus_lncRNA::1::212, 2_A375_pNL97_plus_lncRNA::1::285, 2_A375_pNL97_plus_lncRNA::1::286	-786, 94, -1490	upstream, in gene, upstream	1	1	15	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene GPBP1L1	RP11-767N6.1, GPBP1L1, SP192	GC-rich promoter binding protein 1-like 1	NM_021639, hCT2333960.0, hCT2333961.0, hCT2333962.0, hCT2333963.0, hCT2333964.0	1569320_at, 217877_s_at, 222452_s_at	NP_067652.1, EAX06958.1, EAX06956.1, EAX06957.1, EAX06959.1, EAX06960.1
GeneID:51249	TMEM69	1	46,153,847	46,160,108	6,261	+	3	1_A375_pNL7_minus_lncRNA::1::212, 2_A375_pNL97_plus_lncRNA::1::285, 2_A375_pNL97_plus_lncRNA::1::286	-759, -1639, -55	upstream, upstream, upstream	1	1	15	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene TMEM69	MGC104183, C1orf154, RP11-767N6.4, FLJ21029, TMEM69	transmembrane protein 69	NM_016486, hCT2334451.0, hCT2334452.0	223335_at	NP_057570.2, EAX06954.1, EAX06953.1
GeneID:3652	IPP	1	46,159,996	46,216,485	56,489	-	4	1_A375_pNL7_minus_lncRNA::1::212, 2_A375_pNL97_plus_lncRNA::1::285, 2_A375_pNL97_plus_lncRNA::1::286, 2_A375_pNL97_plus_lncRNA::1::287	63397, 64277, 62693, 261	downstream, downstream, downstream, in gene	1	1	15.33	19	3	2_A375_pNL97_plus_lncRNA::1	21	Gene IPP	KLHL27, IPP	intracisternal A particle-promoted polypeptide	NM_005897, NM_001145349, hCT1644595.3, hCT2333956.0, hCT2333959.0	1554739_at, 1554740_a_at, 219843_at, 241393_at	NP_005888.1, NP_001138821.1, EAX06950.1, EAX06951.1, EAX06952.1
GeneID:8503	PIK3R3	1	46,505,812	46,598,708	92,896	-	3	1_A375_pNL7_minus_lncRNA::1::213, 2_A375_pNL97_plus_lncRNA::1::288, 2_A375_pNL97_plus_lncRNA::1::289	180, 244, -1868	in gene, in gene, upstream	1	1	25	29	2	2_A375_pNL97_plus_lncRNA::1	42	Gene PIK3R3	FLJ41892, DKFZp686P05226, p55, PIK3R3, p55-GAMMA	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_003629, NM_001114172, hCT1819329.2, hCT1961473.1, hCT2333951.0, hCT2333952.0, hCT2359213.0	202743_at, 211580_s_at	NP_003620.3, NP_001107644.1, EAX06944.1, EAX06945.1, EAX06946.1, EAX06947.1, EAX06943.1
GeneID:8438	RAD54L	1	46,713,367	46,744,145	30,778	+	2	1_A375_pNL7_minus_lncRNA::1::214, 2_A375_pNL97_plus_lncRNA::1::290	-7, 9	upstream, in gene	1	1	29	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene RAD54L	hHR54, hRAD54, RAD54A, HR54, RAD54L	RAD54-like (S. cerevisiae)	NM_003579, NM_001142548, hCT13183.2, hCT2333345.0	204558_at	NP_003570.2, NP_001136020.1, EAX06929.1, EAX06930.1
GeneID:10489	LRRC41	1	46,744,072	46,769,038	24,966	-	3	1_A375_pNL7_minus_lncRNA::1::215, 1_A375_pNL7_minus_lncRNA::1::216, 2_A375_pNL97_plus_lncRNA::1::291	846, -210, 1390	in gene, upstream, in gene	1	1	19.5	19.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene LRRC41	MUF1, PP7759, RP4-636H5.2, LRRC41, MGC126571, MGC126573	leucine rich repeat containing 41	NM_006369, hCT2333318.0, hCT2333320.0	1555831_s_at, 1558983_at, 201932_at, 215765_at	NP_006360.3, EAX06928.1, EAX06927.1
GeneID:7388	UQCRH	1	46,769,380	46,782,448	13,068	+	3	1_A375_pNL7_minus_lncRNA::1::215, 1_A375_pNL7_minus_lncRNA::1::216, 2_A375_pNL97_plus_lncRNA::1::291	-1188, -132, -1732	upstream, upstream, upstream	1	1	19.5	19.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene UQCRH	QCR6, UQCR8, UQCRH, MGC111572	ubiquinol-cytochrome c reductase hinge protein	NM_006004, hCT13184.2, hCT1963362.1, hCT1963363.1, hCT2333348.0, hCT2333351.0	202233_s_at	NP_005995.2, EAX06924.1, EAX06922.1, EAX06923.1, EAX06925.1, EAX06926.1
GeneID:9813	KIAA0494	1	47,140,831	47,184,736	43,905	-	2	1_A375_pNL7_minus_lncRNA::1::217, 2_A375_pNL97_plus_lncRNA::1::292	-128, -144	upstream, upstream	1	1	45	41	1	1_A375_pNL7_minus_lncRNA::1	45	Gene KIAA0494	KIAA0494, RP11-8J9.3	KIAA0494	NM_014774, hCT1819315.1, hCT2333304.1	1559022_at, 201775_s_at, 201776_s_at, 201777_s_at, 201778_s_at	NP_055589.1, EAX06894.1, EAX06893.1
GeneID:10158	PDZK1IP1	1	47,649,261	47,655,771	6,510	-	1	2_A375_pNL97_plus_lncRNA::1::294	10779	downstream	0	1	7	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PDZK1IP1	PDZK1IP1, RP1-18D14.5, MAP17, DD96, SPAP	PDZK1 interacting protein 1	NM_005764, hCT2344285.0	1553589_a_at, 219630_at	NP_005755.1, EAX06878.1
GeneID:6491	STIL	1	47,715,811	47,779,819	64,008	-	2	1_A375_pNL7_minus_lncRNA::1::219, 2_A375_pNL97_plus_lncRNA::1::295	59, 75	in gene, in gene	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene STIL	SIL, STIL, MCPH7, DKFZp686O09161	SCL/TAL1 interrupting locus	NM_003035, NM_001048166, hCT11418.2, hCT2333157.0, hCT2359220.0	205339_at	NP_003026.2, NP_001041631.1, EAX06872.1, EAX06873.1, EAX06874.1
GeneID:84793	MGC12982	1	47,897,805	47,900,313	2,508	-	1	2_A375_pNL97_plus_lncRNA::1::296	-3271	upstream	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MGC12982		hypothetical protein MGC12982	NR_026676	224456_s_at, 224457_at	

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:2306	FOXD2	1	47,901,689	47,906,363	4,674	+	1	2_A375_pNL97_plus_lncRNA::1::296	1695	in gene	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene FOXD2	FKHL17, FOXD2, FREAC-9, FREAC9	forkhead box D2	NM_004474, hCT1819195.2	207653_at	NP_004465.3, EAX06866.1
GeneID:200010	SLC5A9	1	48,688,357	48,714,316	25,959	+	1	2_A375_pNL97_plus_lncRNA::1::298	-6821	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SLC5A9	SGLT4, SLC5A9, MGC132517, MGC132523	solute carrier family 5 (sodium/glucose cotransporter), member 9	NM_001011547, NM_001135181, hCT1951464.2, hCT2359178.0, hCT2359179.0	1569337_at, 232378_at	NP_001011547.2, NP_001128653.1, EAX06857.1, EAX06858.1, EAX06859.1
GeneID:54558	SPATA6	1	48,761,044	48,937,876	176,832	-	1	1_A375_pNL7_minus_lncRNA::1::221	404	in gene	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SPATA6	SRF-1, SPATA6, SRF1, FLJ10007	spermatogenesis associated 6	NM_019073, hCT1639992.3, hCT2333120.0	220298_s_at, 220299_at, 238459_x_at	NP_061946.1, EAX06854.1, EAX06855.1
GeneID:84871	AGBL4	1	48,998,527	50,489,626	1,491,099	-	6	1_A375_pNL7_minus_lncRNA::1::223, 1_A375_pNL7_minus_lncRNA::1::224, 1_A375_pNL7_minus_lncRNA::1::225, 2_A375_pNL97_plus_lncRNA::1::300, 2_A375_pNL97_plus_lncRNA::1::301, 2_A375_pNL97_plus_lncRNA::1::302	1492986, 1170714, 671994, 1492954, 1404410, 1170842	downstream, in gene, in gene, downstream, in gene, in gene	1	1	21.75	22	4	2_A375_pNL97_plus_lncRNA::1	37	Gene AGBL4	AGBL4, CCP6, FLJ14442	ATP/GTP binding protein-like 4	NM_032785, hCT1819300.2	1553412_at, 1569570_at	NP_116174.3, EAX06847.1
GeneID:11124	FAF1	1	50,906,935	51,425,936	519,001	-	3	1_A375_pNL7_minus_lncRNA::1::229, 2_A375_pNL97_plus_lncRNA::1::306, 2_A375_pNL97_plus_lncRNA::1::307	-16, -64, -8752	upstream, upstream, upstream	1	1	15.5	22	2	2_A375_pNL97_plus_lncRNA::1	23	Gene FAF1	UBXD12, FAF1, CGI-03, FLJ37524, hFAF1, UBXN3A, HFAF1s	Fas (TNFRSF6) associated factor 1	NM_007051, hCT2333197.0, hCT30149.3	218080_x_at, 222511_x_at, 224217_s_at, 239749_at	NP_008982.1, EAX06836.1, EAX06837.1
GeneID:1031	CDKN2C	1	51,434,367	51,440,309	5,942	+	3	1_A375_pNL7_minus_lncRNA::1::229, 2_A375_pNL97_plus_lncRNA::1::306, 2_A375_pNL97_plus_lncRNA::1::307	-8415, -8367, 321	upstream, upstream, in gene	1	1	15.5	22	2	2_A375_pNL97_plus_lncRNA::1	23	Gene CDKN2C	p18, INK4C, p18-INK4C, CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	NM_001262, NM_078626, hCT2333207.0, hCT2333209.0, hCT2333210.0, hCT31544.2	204159_at, 211792_s_at	NP_001253.1, NP_523240.1, EAX06833.1, EAX06834.1, EAX06835.1, EAX06836.1
GeneID:26994	RNF11	1	51,701,945	51,739,119	37,174	+	1	1_A375_pNL7_minus_lncRNA::1::230	7	in gene	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene RNF11	MGC51169, RNF11, CGI-123, SID1669	ring finger protein 11	NM_014372, hCT1963406.1, hCT2333213.0	208924_at	NP_055187.1, EAX06830.1, EAX06831.1
GeneID:114883	OSBPL9	1	52,082,547	52,254,891	172,344	+	2	1_A375_pNL7_minus_lncRNA::1::233, 2_A375_pNL97_plus_lncRNA::1::308	893, 112621	in gene, in gene	1	1	16.5	17	2	1_A375_pNL7_minus_lncRNA::1	22	Gene OSBPL9	OSBPL9, FLJ14629, FLJ34384, FLJ12492, MGC15035, FLJ32055, ORP9, FLJ14801	oxysterol binding protein-like 9	NM_148906, NM_024586, NM_148904, NM_148905, NM_148907, NM_148908, NM_148909, hCT1819784.3, hCT1951469.2, hCT2333339.1, hCT2333340.1, hCT2351145.0, hCT2351146.0, hCT2351147.0, hCT2351148.0, hCT2359243.0, hCT2359244.0	218047_at	NP_683704.1, NP_078862.3, NP_683702.1, NP_683703.1, NP_683705.1, NP_683706.2, NP_683707.2, EAX06810.1, EAX06811.1, EAX06812.1, EAX06813.1, EAX06814.1, EAX06815.1, EAX06816.1, EAX06817.1, EAX06818.1, EAX06819.1
GeneID:51060	TXNDC12	1	52,485,803	52,521,047	35,244	-	5	1_A375_pNL7_minus_lncRNA::1::234, 1_A375_pNL7_minus_lncRNA::1::235, 2_A375_pNL97_plus_lncRNA::1::309, 2_A375_pNL97_plus_lncRNA::1::310, 2_A375_pNL97_plus_lncRNA::1::311	21911, -937, 21687, 55, -969	in gene, upstream, in gene, in gene, upstream	1	1	16	20.67	3	2_A375_pNL97_plus_lncRNA::1	21	Gene TXNDC12	TXNDC12, ERP18, PDIA16, hAG-1, AGR1, TLP19, AG1, ERP19	thioredoxin domain containing 12 (endoplasmic reticulum)	NM_015913, hCT23906.3	223017_at	NP_056997.1, EAX06800.1
GeneID:112970	KTI12	1	52,497,777	52,499,472	1,695	-	2	1_A375_pNL7_minus_lncRNA::1::234, 2_A375_pNL97_plus_lncRNA::1::309	336, 112	in gene, in gene	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene KTI12	SBBI81, MGC20419, TOT4, RP11-91A18.3, KTI12	KTI12 homolog, chromatin associated (S. cerevisiae)	NM_138417, hCT2344288.0	225642_at	NP_612426.1, EAX06801.1
GeneID:91408	BTF3L4	1	52,521,857	52,554,090	32,233	+	3	1_A375_pNL7_minus_lncRNA::1::235, 2_A375_pNL97_plus_lncRNA::1::310, 2_A375_pNL97_plus_lncRNA::1::311	127, -865, 159	in gene, upstream, in gene	1	1	15.5	20.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene BTF3L4	RP4-800M22.5, BTF3L4, MGC23908, MGC88389	basic transcription factor 3-like 4	NM_152265, NM_001136497, NR_024350, hCT2333326.0, hCT2333327.0, hCT2359093.0, hCT2359094.0, hCT2359095.0	225976_at, 226963_at	NP_689478.1, NP_001129969.1, EAX06795.1, EAX06797.1, EAX06798.1, EAX06799.1, EAX06796.1
GeneID:4998	ORC1L	1	52,838,501	52,870,143	31,642	-	2	1_A375_pNL7_minus_lncRNA::1::236, 2_A375_pNL97_plus_lncRNA::1::312	431, 543	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ORC1L	HSORC1, PARC1, ORC1, ORC1L	origin recognition complex, subunit 1-like (S. cerevisiae)	NM_001190818, NM_001190819, NM_004153, hCT2359205.0, hCT23665.3	205085_at	NP_001177747.1, NP_001177748.1, NP_004144.2, EAX06783.1, EAX06784.1
GeneID:84950	PRPF38A	1	52,870,219	52,883,992	13,773	+	2	1_A375_pNL7_minus_lncRNA::1::236, 2_A375_pNL97_plus_lncRNA::1::312	-507, -619	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene PRPF38A	MGC3320, RP5-965L7.1, FLJ14936, PRPF38A, Prp38	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	NM_032864, hCT1968037.1, hCT23909.3	1553709_a_at, 223230_at	NP_116253.2, EAX06781.1, EAX06782.1
GeneID:6342	SCP2	1	53,392,901	53,517,289	124,388	+	2	1_A375_pNL7_minus_lncRNA::1::237, 2_A375_pNL97_plus_lncRNA::1::313	87643, 87691	in gene, in gene	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SCP2	NLTP, DKFZp686D11188, SCPX, SCP-CHI, DKFZp686C12188, SCP2, NSL-TP	sterol carrier protein 2	NM_001007098, NM_001007099, NM_001007100, NM_001007250, NM_002979, NM_001193599, NM_001193600, NM_001193617, hCT2333901.0, hCT2333903.0, hCT24596.3	201339_s_at, 211733_x_at	NP_001007099.1, NP_001007100.1, NP_002970.2, NP_001007101.1, NP_001007251.1, NP_001180528.1, NP_001180529.1, NP_001180546.1, EAX06760.1, EAX06761.1, EAX06762.1
GeneID:1376	CPT2	1	53,662,101	53,679,869	17,768	+	3	1_A375_pNL7_minus_lncRNA::1::238, 2_A375_pNL97_plus_lncRNA::1::314, 2_A375_pNL97_plus_lncRNA::1::315	24043, 635, 24043	downstream, in gene, downstream	1	1	13.5	19	2	2_A375_pNL97_plus_lncRNA::1	22	Gene CPT2	CPTASE, CPT2, CPT1	carnitine palmitoyltransferase 2	NM_000098, hCT23664.2	204263_s_at, 204264_at	NP_000089.1, EAX06753.1
GeneID:54987	C1orf123	1	53,679,771	53,686,289	6,518	-	2	1_A375_pNL7_minus_lncRNA::1::238, 2_A375_pNL97_plus_lncRNA::1::315	145, 145	in gene, in gene	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene C1orf123	C1orf123, FLJ20580	chromosome 1 open reading frame 123	NM_017887, hCT1956388.1, hCT1968038.1, hCT2359105.0, hCT24588.2	203197_s_at	NP_060357.1, EAX06749.1, EAX06750.1, EAX06751.1, EAX06752.1
GeneID:4116	MAGOH	1	53,692,564	53,704,207	11,643	-	4	1_A375_pNL7_minus_lncRNA::1::238, 1_A375_pNL7_minus_lncRNA::1::239, 2_A375_pNL97_plus_lncRNA::1::315, 2_A375_pNL97_plus_lncRNA::1::316	18063, -49, 18063, -6	downstream, upstream, downstream, upstream	1	1	17	24.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene MAGOH	MAGOHA, MAGOH1, MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)	NM_002370, hCT1956389.1, hCT24590.2	210092_at, 210093_s_at	NP_002361.1, EAX06747.1, EAX06748.1
GeneID:100507564	LOC100507564	1	53,704,282	53,708,790	4,508	+	2	1_A375_pNL7_minus_lncRNA::1::239, 2_A375_pNL97_plus_lncRNA::1::316	-26, -69	upstream, upstream	1	1	15	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene LOC100507564		hypothetical LOC100507564	XR_110511		
GeneID:7804	LRP8	1	53,711,212	53,793,821	82,609	-	3	1_A375_pNL7_minus_lncRNA::1::239, 2_A375_pNL97_plus_lncRNA::1::316, 2_A375_pNL97_plus_lncRNA::1::317	89565, 89608, 1661	downstream, downstream, in gene	1	1	16.5	24	2	2_A375_pNL97_plus_lncRNA::1	27	Gene LRP8	LRP8, APOER2, MCI1, HSZ75190	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	NM_017522, NM_004631, NM_001018054, NM_033300, hCT1951474.1, hCT2333365.0, hCT2333367.0, hCT2359107.0, hCT2359108.0, hCT24589.3	205282_at, 208433_s_at	NP_059992.3, NP_004622.2, NP_001018064.1, NP_150643.2, EAX06744.1, EAX06745.1, EAX06740.1, EAX06741.1, EAX06742.1, EAX06743.1
GeneID:55706	TMEM48	1	54,231,133	54,304,225	73,092	-	2	1_A375_pNL7_minus_lncRNA::1::240, 2_A375_pNL97_plus_lncRNA::1::318	97, 97	in gene, in gene	1	1	50	78	1	2_A375_pNL97_plus_lncRNA::1	78	Gene TMEM48	FLJ12556, FLJ10407, NET3, TMEM48, NDC1, FLJ34120	transmembrane protein 48	NR_033142, NM_018087, NM_001168551, hCT1972688.1, hCT2359189.0, hCT24896.4	218073_s_at, 234672_s_at	NP_060557.3, NP_001162023.1, EAX06731.1, EAX06732.1, EAX06733.1
GeneID:54432	YIPF1	1	54,317,406	54,355,453	38,047	-	2	1_A375_pNL7_minus_lncRNA::1::241, 2_A375_pNL97_plus_lncRNA::1::319	-89, -67	upstream, upstream	1	1	46	56	1	2_A375_pNL97_plus_lncRNA::1	56	Gene YIPF1	YIPF1, FinGER1, DJ167A19.1	Yip1 domain family, member 1	NM_018982, hCT1951476.1, hCT1955450.1, hCT1955451.1, hCT24898.3	214733_s_at	NP_061855.1, EAX06730.1, EAX06727.1, EAX06728.1, EAX06729.1
GeneID:1733	DIO1	1	54,359,861	54,376,759	16,898	+	2	1_A375_pNL7_minus_lncRNA::1::241, 2_A375_pNL97_plus_lncRNA::1::319	-4309, -4341	upstream, upstream	1	1	46	56	1	2_A375_pNL97_plus_lncRNA::1	56	Gene DIO1	MGC130050, 5DI, TXDI1, DIO1, MGC130051	deiodinase, iodothyronine, type I	NM_000792, NM_001039715, NM_213593, NM_001039716, hCT1829566.2, hCT1958349.1, hCT2334255.0, hCT2359057.0, hCT2359058.0, hCT2359059.0, hCT2359060.0	206457_s_at	NP_000783.2, NP_001034804.1, NP_998758.1, NP_001034805.1, EAX06721.1, EAX06725.1, EAX06720.1, EAX06722.1, EAX06723.1, EAX06724.1, EAX06726.1
GeneID:93528	TMEM59	1	54,497,349	54,519,111	21,762	-	2	1_A375_pNL7_minus_lncRNA::1::242, 2_A375_pNL97_plus_lncRNA::1::320	-121, 210	upstream, in gene	1	1	22	20	1	1_A375_pNL7_minus_lncRNA::1	22	Gene TMEM59	HSPC001, FLJ42977, C1orf8, TMEM59	transmembrane protein 59	NM_004872, hCT1961870.1, hCT1961871.1, hCT1961873.1, hCT1961874.1, hCT1961875.1, hCT2334222.0, hCT2359185.0, hCT24892.3	200620_at, 241018_at	NP_004863.2, EAX06704.1, EAX06705.1, EAX06706.1, EAX06708.1, EAX06711.1, EAX06707.1, EAX06709.1, EAX06710.1
GeneID:127428	C1orf83	1	54,519,274	54,565,416	46,142	+	2	1_A375_pNL7_minus_lncRNA::1::242, 2_A375_pNL97_plus_lncRNA::1::320	-42, -373	upstream, upstream	1	1	22	20	1	1_A375_pNL7_minus_lncRNA::1	22	Gene C1orf83	FLJ32112, C1orf83, FLJ39169, RP4-758J24.3, TCEANC2	chromosome 1 open reading frame 83	NM_153035, hCT24900.3	1562470_at, 238737_at	NP_694580.1, EAX06703.1
GeneID:606495	CYB5RL	1	54,638,009	54,665,746	27,737	-	1	2_A375_pNL97_plus_lncRNA::1::321	-398	upstream	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CYB5RL	CYB5RL, FLJ16295	cytochrome b5 reductase-like	NM_001031672	229605_at, 235981_at, 235992_s_at	NP_001026842.2
GeneID:51253	MRPL37	1	54,665,840	54,684,056	18,216	+	1	2_A375_pNL97_plus_lncRNA::1::321	304	in gene	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene MRPL37	MRPL37, L37mt, MRP-L37, MRPL2, MRP-L2, MGC878, RPML2	mitochondrial ribosomal protein L37	NM_016491, hCT1956283.1, hCT1956284.1, hCT1956285.1, hCT2334241.0, hCT24894.3	222993_at	NP_057575.2, EAX06694.1, EAX06695.1, EAX06696.1, EAX06697.1, EAX06698.1
GeneID:23648	SSBP3	1	54,692,195	54,872,092	179,897	-	1	2_A375_pNL97_plus_lncRNA::1::322	41212	in gene	0	1	13	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene SSBP3	SSBP3, FLJ10355, SSDP, SSDP1, CSDP	single stranded DNA binding protein 3	NM_018070, NM_145716, NM_001009955, hCT2334205.0, hCT2334206.0, hCT2334208.0, hCT2334209.0, hCT2334210.0, hCT2334211.0	222482_at	NP_060540.2, NP_663768.1, NP_001009955.1, EAX06688.1, EAX06689.1, EAX06692.1, EAX06690.1, EAX06691.1, EAX06693.1
GeneID:374977	C1orf175	1	55,107,427	55,175,939	68,512	+	1	2_A375_pNL97_plus_lncRNA::1::323	74077	downstream	0	1	14	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene C1orf175	DKFZp686L2332, HEATR8, FLJ46354, C1orf175, DKFZp781B0622, DKFZp434K085, FLJ45063	HEAT repeat containing 8	NM_001039464, NR_026782	214147_at	NP_001034553.2
GeneID:7268	TTC4	1	55,181,495	55,208,330	26,835	+	1	2_A375_pNL97_plus_lncRNA::1::323	9	in gene	0	1	14	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene TTC4	TTC4, FLJ41930, MGC5097, DKFZp781B0622	tetratricopeptide repeat domain 4	NM_004623, hCT1956282.2, hCT1968036.1, hCT1972665.1, hCT2359239.0, hCT23662.3	218442_at	NP_004614.3, EAX06673.1, EAX06670.1, EAX06671.1, EAX06672.1, EAX06674.1
GeneID:55001	TTC22	1	55,246,752	55,266,941	20,189	-	1	2_A375_pNL97_plus_lncRNA::1::324	-2595	upstream	0	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TTC22	TTC22, FLJ20619	tetratricopeptide repeat domain 22	NM_017904, NM_001114108, hCT1958387.1, hCT24220.2	215106_at, 215107_s_at, 220309_at	NP_060374.2, NP_001107580.1, EAX06667.1, EAX06668.1
GeneID:163747	C1orf177	1	55,271,736	55,307,937	36,201	+	1	2_A375_pNL97_plus_lncRNA::1::324	-2200	upstream	0	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene C1orf177	C1orf177, FLJ40201	chromosome 1 open reading frame 177	NM_152607, NM_001110533, hCT1690450.2, hCT2349541.0	1557016_a_at	NP_689820.2, NP_001104003.1, EAX06665.1, EAX06666.1
GeneID:23358	USP24	1	55,532,032	55,681,039	149,007	-	1	2_A375_pNL97_plus_lncRNA::1::325	-129	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene USP24	USP24, FLJ31309, KIAA1057	ubiquitin specific peptidase 24	NM_015306	212381_at, 212388_at, 230004_at	NP_056121.2
GeneID:100507634	LOC100507634	1	55,681,080	55,682,795	1,715	+	1	2_A375_pNL97_plus_lncRNA::1::325	68	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100507634		hypothetical LOC100507634	XR_112073, XR_110513, XR_113330		
GeneID:5563	PRKAA2	1	57,110,990	57,181,008	70,018	+	1	2_A375_pNL97_plus_lncRNA::1::328	31602	in gene	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PRKAA2	AMPK2, AMPK, PRKAA, PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	NM_006252, hCT13256.2	207709_at, 240349_at	NP_006243.2, EAX06650.1
GeneID:115209	OMA1	1	58,946,391	59,012,446	66,055	-	1	2_A375_pNL97_plus_lncRNA::1::329	-98	upstream	0	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene OMA1	OMA1, MPRP-1, YKR087C, ZMPOMA1, DAB1, 2010001O09Rik, FLJ33782	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	NM_145243, hCT14324.3, hCT1955447.2, hCT1972650.1, hCT2336111.0	226019_at	NP_660286.1, EAX06631.1, EAX06632.1, EAX06633.1, EAX06634.1
GeneID:3725	JUN	1	59,246,463	59,249,785	3,322	-	3	1_A375_pNL7_minus_lncRNA::1::246, 1_A375_pNL7_minus_lncRNA::1::247, 2_A375_pNL97_plus_lncRNA::1::333	2137, 217, -455	in gene, in gene, upstream	1	1	18	17.5	2	2_A375_pNL97_plus_lncRNA::1	20	Gene JUN	AP-1, AP1, c-Jun, JUN	jun oncogene	NM_002228, hCT1819109.1	201464_x_at, 201465_s_at, 201466_s_at, 213281_at	NP_002219.1, EAX06628.1
GeneID:100131060	LOC100131060	1	59,250,823	59,365,384	114,561	+	5	1_A375_pNL7_minus_lncRNA::1::246, 1_A375_pNL7_minus_lncRNA::1::247, 1_A375_pNL7_minus_lncRNA::1::248, 2_A375_pNL97_plus_lncRNA::1::333, 2_A375_pNL97_plus_lncRNA::1::334	-3175, -1255, 64089, -583, 63769	upstream, upstream, in gene, upstream, in gene	1	1	17	20	3	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100131060		hypothetical LOC100131060	NR_034014, NR_034015		
GeneID:729467	LOC729467	1	59,597,608	59,612,479	14,871	-	1	2_A375_pNL97_plus_lncRNA::1::335	-4609	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC729467	HSD52	hypothetical LOC729467	NR_027120		
GeneID:55277	FGGY	1	59,762,625	60,228,402	465,777	+	6	1_A375_pNL7_minus_lncRNA::1::249, 2_A375_pNL97_plus_lncRNA::1::336, 1_A375_pNL7_minus_lncRNA::1::250, 1_A375_pNL7_minus_lncRNA::1::251, 2_A375_pNL97_plus_lncRNA::1::337, 2_A375_pNL97_plus_lncRNA::1::338	158079, 180463, 382015, 434047, 372991, 434047	in gene, in gene, in gene, in gene, in gene, in gene	1	1	15.8	17.6	5	1_A375_pNL7_minus_lncRNA::1	25	Gene FGGY	FGGY, FLJ10986	FGGY carbohydrate kinase domain containing	NM_018291, NM_001113411, hCT1955444.1, hCT1955445.1, hCT2332921.0, hCT2332923.0, hCT2332925.0, hCT2332926.0	219718_at, 232380_at	NP_060761.3, NP_001106882.1, EAX06619.1, EAX06620.1, EAX06622.1, EAX06624.1, EAX06621.1, EAX06623.1
GeneID:83941	TM2D1	1	62,146,719	62,191,095	44,376	-	2	1_A375_pNL7_minus_lncRNA::1::252, 2_A375_pNL97_plus_lncRNA::1::339	311, 327	in gene, in gene	1	1	32	30	1	1_A375_pNL7_minus_lncRNA::1	32	Gene TM2D1	BBP, TM2D1	TM2 domain containing 1	NM_032027, hCT1819834.1, hCT1969316.0, hCT2333009.0	211703_s_at, 212963_at, 213882_at, 213883_s_at	NP_114416.1, EAX06599.1, EAX06597.1, EAX06598.1
GeneID:10207	INADL	1	62,208,149	62,629,592	421,443	+	1	2_A375_pNL97_plus_lncRNA::1::340	250955	in gene	0	1	8	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene INADL	INADL, FLJ26982, PATJ, hINADL, Cipp	InaD-like (Drosophila)	NM_176877, hCT1951994.2, hCT2334414.1, hCT2334417.1, hCT2334418.1	214493_s_at, 214705_at, 223681_s_at, 232041_at, 239173_at	NP_795352.2, EAX06596.1, EAX06593.1, EAX06594.1, EAX06595.1
GeneID:7398	USP1	1	62,901,975	62,917,475	15,500	+	1	2_A375_pNL97_plus_lncRNA::1::341	745	in gene	0	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene USP1	UBP, USP1	ubiquitin specific peptidase 1	NM_003368, NM_001017415, NM_001017416, hCT1815474.1, hCT2333076.0	202412_s_at, 202413_s_at	NP_003359.3, NP_001017415.1, NP_001017416.1, EAX06585.1, EAX06586.1
GeneID:85440	DOCK7	1	62,920,397	63,153,969	233,572	-	1	2_A375_pNL97_plus_lncRNA::1::342	-431	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DOCK7	ZIR2, KIAA1771, DOCK7	dedicator of cytokinesis 7	NM_033407	225384_at, 237470_at	NP_212132.2
GeneID:29929	ALG6	1	63,833,261	63,904,233	70,972	+	1	2_A375_pNL97_plus_lncRNA::1::343	147	in gene	0	1	11	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ALG6	CDG1C, ALG6		NM_013339, hCT1640685.3, hCT1959431.2, hCT1959432.2, hCT1959433.2	219649_at	NP_037471.2, EAX06571.1, EAX06572.1, EAX06573.1, EAX06574.1
GeneID:23421	ITGB3BP	1	63,906,462	63,988,835	82,373	-	2	1_A375_pNL7_minus_lncRNA::1::253, 2_A375_pNL97_plus_lncRNA::1::344	-157, -141	upstream, upstream	1	1	39	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene ITGB3BP	CENPR, HSU37139, NRIF3, TAP20, CENP-R, ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	NM_014288, hCT13270.2, hCT1953050.1, hCT1953051.1, hCT1953052.1, hCT1953053.1, hCT2332959.0, hCT2332961.0	205176_s_at	NP_055103.3, EAX06565.1, EAX06561.1, EAX06562.1, EAX06563.1, EAX06566.1, EAX06564.1, EAX06567.1
GeneID:84455	EFCAB7	1	63,989,013	64,038,364	49,351	+	2	1_A375_pNL7_minus_lncRNA::1::253, 2_A375_pNL97_plus_lncRNA::1::344	-21, -37	upstream, upstream	1	1	39	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene EFCAB7	EFCAB7, RP4-534K7.1, DKFZp666D225, KIAA1799	EF-hand calcium binding domain 7	NM_032437, hCT14559.3, hCT2333109.0, hCT2359154.0	226800_at	NP_115813.2, EAX06568.1, EAX06569.1, EAX06570.1
GeneID:5236	PGM1	1	64,058,947	64,125,916	66,969	+	3	1_A375_pNL7_minus_lncRNA::1::254, 1_A375_pNL7_minus_lncRNA::1::255, 2_A375_pNL97_plus_lncRNA::1::345	237, 69805, 109	in gene, downstream, in gene	1	1	17.5	18	2	2_A375_pNL97_plus_lncRNA::1	22	Gene PGM1	GSD14, PGM1	phosphoglucomutase 1	NM_002633, NM_001172818, NM_001172819, hCT14555.2, hCT2333115.0	201968_s_at	NP_002624.2, NP_001166289.1, NP_001166290.1, EAX06559.1, EAX06560.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:4919	ROR1	1	64,239,690	64,644,707	405,017	+	5	1_A375_pNL7_minus_lncRNA::1::256, 1_A375_pNL7_minus_lncRNA::1::257, 2_A375_pNL97_plus_lncRNA::1::346, 2_A375_pNL97_plus_lncRNA::1::347, 2_A375_pNL97_plus_lncRNA::1::348	195526, 270150, 195414, 303542, 359350	in gene, in gene, in gene, in gene, in gene	1	1	16.5	17.5	4	2_A375_pNL97_plus_lncRNA::1	21	Gene ROR1	MGC99659, dJ537F10.1, NTRKR1, ROR1	receptor tyrosine kinase-like orphan receptor 1	NM_001083592, NM_005012, hCT1955442.1, hCT2359062.0, hCT2359063.0	205805_s_at, 211057_at	NP_001077061.1, NP_005003.2, EAX06555.1, EAX06556.1, EAX06557.1
GeneID:57685	CACHD1	1	64,936,476	65,158,741	222,265	+	1	2_A375_pNL97_plus_lncRNA::1::349	-812	upstream	0	1	12	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene CACHD1	CACHD1, KIAA1573, RP4-655E10.1	cache domain containing 1	NM_020925, hCT15341.3	225627_s_at, 234888_at	NP_065976.2, EAX06551.1
GeneID:55225	RAVER2	1	65,210,778	65,298,915	88,137	+	1	1_A375_pNL7_minus_lncRNA::1::258	342	in gene	1	0	15	9	1	1_A375_pNL7_minus_lncRNA::1	15	Gene RAVER2	KIAA1579, DKFZp762D1011, RAVER2, FLJ10770	ribonucleoprotein, PTB-binding 2	NM_018211, hCT14091.3, hCT2333660.0	220660_at, 231851_at	NP_060681.2, EAX06549.1, EAX06550.1
GeneID:406893	MIR101-1	1	65,524,117	65,524,191	74	-	1	2_A375_pNL97_plus_lncRNA::1::350	-9457	upstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MIR101-1	MIRN101-1, MIR101-1	microRNA 101-1	NR_029516		
GeneID:205	AK3L1	1	65,613,232	65,697,828	84,596	+	1	2_A375_pNL97_plus_lncRNA::1::351	27152	in gene	0	1	9	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene AK3L1	AK3, MGC166959, AK4, AK3L2, AK3L1	adenylate kinase 3-like 1	NM_001005353, NM_013410, NM_203464	204348_s_at, 225342_at	NP_001005353.1, NP_037542.1, NP_982289.1
GeneID:9829	DNAJC6	1	65,730,430	65,881,552	151,122	+	4	1_A375_pNL7_minus_lncRNA::1::259, 1_A375_pNL7_minus_lncRNA::1::260, 2_A375_pNL97_plus_lncRNA::1::352, 2_A375_pNL97_plus_lncRNA::1::353	-62, 45186, -30, 45234	upstream, in gene, upstream, in gene	1	1	24	21.5	2	1_A375_pNL7_minus_lncRNA::1	30	Gene DNAJC6	KIAA0473, MGC48436, MGC129914, DJC6, MGC129915, DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	NM_014787, hCT11248.3, hCT2333677.0, hCT2333678.0, hCT2333679.0, hCT2359250.0	204720_s_at, 204721_s_at	NP_055602.1, EAX06533.1, EAX06534.1, EAX06535.1, EAX06536.1, EAX06537.1
GeneID:100505510	LOC100505510	1	65,764,286	65,765,746	1,460	+	2	1_A375_pNL7_minus_lncRNA::1::260, 2_A375_pNL97_plus_lncRNA::1::353	11330, 11378	downstream, downstream	1	1	30	24	1	1_A375_pNL7_minus_lncRNA::1	30	Gene LOC100505510		hypothetical protein LOC100505510	XM_003118976		XP_003119024.1
GeneID:3953	LEPR	1	65,886,248	66,103,176	216,928	+	2	1_A375_pNL7_minus_lncRNA::1::261, 2_A375_pNL97_plus_lncRNA::1::354	38680, 38787	in gene, in gene	1	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LEPR	OBR, LEPR, DKFZp686B1731, CD295	leptin receptor	NM_002303, NM_001003680, NM_001003679	202377_at	NP_002294.2, NP_001003680.1, NP_001003679.1
GeneID:5142	PDE4B	1	66,258,193	66,840,262	582,069	+	5	1_A375_pNL7_minus_lncRNA::1::262, 1_A375_pNL7_minus_lncRNA::1::263, 1_A375_pNL7_minus_lncRNA::1::264, 2_A375_pNL97_plus_lncRNA::1::355, 2_A375_pNL97_plus_lncRNA::1::356	230639, 469903, 478831, 230607, 469967	in gene, in gene, in gene, in gene, in gene	1	1	20.67	16.67	3	1_A375_pNL7_minus_lncRNA::1	23	Gene PDE4B	PDE4B5, PDEIVB, MGC126529, PDE4B, DKFZp686F2182, DPDE4	phosphodiesterase 4B, cAMP-specific	NM_002600, NM_001037339, NM_001037340, NM_001037341, hCT1951996.1, hCT2333029.0	203708_at, 211302_s_at, 215671_at	NP_002591.2, NP_001032416.1, NP_001032417.1, NP_001032418.1, EAX06524.1, EAX06525.1
GeneID:79819	WDR78	1	67,278,568	67,390,570	112,002	-	1	2_A375_pNL97_plus_lncRNA::1::358	-246	upstream	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene WDR78	WDR78, FLJ23129, RP11-342H21.1	WD repeat domain 78	NM_207014, NM_024763, hCT13951.4, hCT1963743.1, hCT1963744.1	1554140_at, 1554141_s_at, 1559576_at, 220769_s_at, 229816_at	NP_996897.2, NP_079039.4, EAX06513.1, EAX06514.1, EAX06515.1
GeneID:57708	MIER1	1	67,390,578	67,454,302	63,724	+	1	2_A375_pNL97_plus_lncRNA::1::358	238	in gene	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MIER1	KIAA1610, DKFZp781G0451, hMI-ER1, RP5-944N15.1, MIER1, ER1, MGC131940, MGC150641, MI-ER1, MGC150640	mesoderm induction early response 1 homolog (Xenopus laevis)	NM_020948, NM_001077700, NM_001077701, NM_001077702, NM_001077703, NM_001077704, NM_001146110, NM_001146112, NM_001146113, NM_001146111, hCT1951995.2, hCT1972630.2, hCT2349255.0, hCT2349256.0, hCT2349257.0, hCT2349258.0, hCT2359071.0, hCT2359072.0	1555105_a_at, 225475_at, 240227_at	NP_065999.2, NP_001071168.2, NP_001071169.1, NP_001071172.1, NP_001071170.2, NP_001071171.2, NP_001139582.1, NP_001139584.1, NP_001139585.1, NP_001139583.1, EAX06505.1, EAX06506.1, EAX06507.1, EAX06508.1, EAX06509.1, EAX06510.1, EAX06511.1, EAX06512.1
GeneID:23169	SLC35D1	1	67,465,015	67,520,080	55,065	-	1	1_A375_pNL7_minus_lncRNA::1::265	293	in gene	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SLC35D1	KIAA0260, SLC35D1, UGTREL7, MGC138236	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	NM_015139, hCT14234.3	209711_at, 209712_at, 209713_s_at	NP_055954.1, EAX06504.1
GeneID:3595	IL12RB2	1	67,773,047	67,862,583	89,536	+	1	1_A375_pNL7_minus_lncRNA::1::266	92633	downstream	1	0	22	16	1	1_A375_pNL7_minus_lncRNA::1	22	Gene IL12RB2	IL12RB2		NM_001559, hCT14231.2, hCT1972662.1	206999_at	NP_001550.1, EAX06499.1, EAX06500.1
GeneID:26135	SERBP1	1	67,873,493	67,896,123	22,630	-	3	1_A375_pNL7_minus_lncRNA::1::266, 1_A375_pNL7_minus_lncRNA::1::267, 2_A375_pNL97_plus_lncRNA::1::359	30443, -69, -26	downstream, upstream, upstream	1	1	24.5	15.5	2	1_A375_pNL7_minus_lncRNA::1	27	Gene SERBP1	SERBP1, HABP4L, DKFZp564M2423, PAI-RBP1, PAIRBP1, CHD3IP, FLJ90489, CGI-55	SERPINE1 mRNA binding protein 1	NM_001018067, NM_001018068, NM_001018069, NM_015640, hCT2334018.0, hCT2334019.0, hCT2334020.0, hCT2334021.0, hCT2334022.0, hCT2334023.0, hCT2334024.0, hCT2334025.0, hCT2334026.0	209669_s_at, 210076_x_at, 210466_s_at, 217724_at, 217725_x_at, 227369_at, 228129_at	NP_001018077.1, NP_001018078.1, NP_001018079.1, NP_056455.3, EAX06489.1, EAX06494.1, EAX06490.1, EAX06491.1, EAX06492.1, EAX06493.1, EAX06495.1, EAX06496.1, EAX06497.1
GeneID:55970	GNG12	1	68,167,149	68,299,155	132,006	-	2	2_A375_pNL97_plus_lncRNA::1::360, 2_A375_pNL97_plus_lncRNA::1::361	579, -269	in gene, upstream	0	1	12	16	2	2_A375_pNL97_plus_lncRNA::1	16	Gene GNG12	FLJ34695, FLJ31352, GNG12	guanine nucleotide binding protein (G protein), gamma 12	NM_018841, hCT1641053.3, hCT2334015.0, hCT2334017.0	1555240_s_at, 212294_at, 222834_s_at	NP_061329.3, EAX06484.1, EAX06485.1, EAX06486.1
GeneID:100289178	LOC100289178	1	68,297,986	68,668,670	370,684	+	5	1_A375_pNL7_minus_lncRNA::1::268, 1_A375_pNL7_minus_lncRNA::1::269, 2_A375_pNL97_plus_lncRNA::1::360, 2_A375_pNL97_plus_lncRNA::1::361, 2_A375_pNL97_plus_lncRNA::1::362	56222, 280798, 590, 1438, 56158	in gene, in gene, in gene, in gene, in gene	1	1	19	19.25	4	1_A375_pNL7_minus_lncRNA::1	32	Gene LOC100289178		hypothetical protein LOC100289178	XM_002342111, XM_002346366		XP_002342152.1, XP_002346409.1
GeneID:79971	GPR177	1	68,564,142	68,698,284	134,142	-	1	1_A375_pNL7_minus_lncRNA::1::269	119500	in gene	1	0	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene GPR177	MGC131760, EVI, MGC14878, C1orf139, FLJ23091, GPR177, MRP, DKFZp686I0788, WLS	G protein-coupled receptor 177	NM_001002292, NM_024911, NM_001193334, hCT1951997.1, hCT1972631.1, hCT2359073.0	221958_s_at, 228949_at, 228950_s_at	NP_001002292.3, NP_079187.3, NP_001180263.1, EAX06479.1, EAX06480.1, EAX06481.1
GeneID:55635	DEPDC1	1	68,939,835	68,962,799	22,964	-	1	2_A375_pNL97_plus_lncRNA::1::365	79	in gene	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene DEPDC1	DEPDC1-V2, DEP.8, DEPDC1, SDP35, DEPDC1A, FLJ20354	DEP domain containing 1	NM_017779, NM_001114120, hCT13831.3, hCT1951999.1, hCT1972642.1, hCT1972643.1, hCT2332814.0, hCT2332816.0, hCT2332817.0	222958_s_at, 232278_s_at	NP_060249.2, NP_001107592.1, EAX06471.1, EAX06473.1, EAX06474.1, EAX06476.1, EAX06472.1, EAX06475.1, EAX06477.1
GeneID:57554	LRRC7	1	70,225,858	70,589,171	363,313	+	1	1_A375_pNL7_minus_lncRNA::1::271	278014	in gene	1	0	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene LRRC7	LRRC7, KIAA1365, MGC144918, DKFZp686I1147	leucine rich repeat containing 7	NM_020794, hCT1951998.1, hCT2332740.0, hCT2332741.0, hCT2332742.0, hCT2332743.0	1552666_a_at, 233499_at, 242050_at	NP_065845.1, EAX06461.1, EAX06462.1, EAX06463.1, EAX06464.1, EAX06465.1
GeneID:55631	LRRC40	1	70,610,485	70,671,361	60,876	-	1	2_A375_pNL97_plus_lncRNA::1::367	65	in gene	0	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LRRC40	FLJ20331, LRRC40, RP4-677H15.1, dJ677H15.1	leucine rich repeat containing 40	NM_017768, hCT13938.3	1566449_at, 215063_x_at, 218577_at	NP_060238.3, EAX06460.1
GeneID:9295	SFRS11	1	70,671,365	70,717,703	46,338	+	2	2_A375_pNL97_plus_lncRNA::1::367, 2_A375_pNL97_plus_lncRNA::1::368	-69, 15739	upstream, in gene	0	1	16	20	2	2_A375_pNL97_plus_lncRNA::1	22	Gene SFRS11	FLJ16226, DKFZp686M13204, SFRS11, dJ677H15.2, NET2, p54, SRSF11	serine/arginine-rich splicing factor 11	NM_001190987, NM_004768, hCT13935.4, hCT2359167.0	200685_at, 200686_s_at, 213742_at, 236946_x_at, 237746_at	NP_001177916.1, NP_004759.1, EAX06458.1, EAX06459.1
GeneID:81573	ANKRD13C	1	70,724,685	70,820,417	95,732	-	2	1_A375_pNL7_minus_lncRNA::1::272, 2_A375_pNL97_plus_lncRNA::1::369	129, -127	in gene, upstream	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ANKRD13C	RP4-677H15.5, ANKRD13C, dJ677H15.3, DKFZp566D1346, FLJ14998	ankyrin repeat domain 13C	NM_030816, hCT13937.3, hCT1972648.1	1554471_a_at, 1556361_s_at, 223418_x_at, 227375_at, 238597_at	NP_110443.3, EAX06456.1, EAX06457.1
GeneID:11147	HHLA3	1	70,820,493	70,833,706	13,213	+	2	1_A375_pNL7_minus_lncRNA::1::272, 2_A375_pNL97_plus_lncRNA::1::369	-205, 51	upstream, in gene	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene HHLA3	HHLA3		NM_001031693, NM_001036645, NM_001036646, NR_027404, hCT1818979.2, hCT1963386.1, hCT1965957.1, hCT2331167.0	220387_s_at, 234665_x_at, 234703_at	NP_001026863.1, NP_001031722.1, NP_001031723.1, EAX06453.1, EAX06454.1, EAX06455.1, EAX06452.1
GeneID:1491	CTH	1	70,876,901	70,905,534	28,633	+	1	2_A375_pNL97_plus_lncRNA::1::370	-53	upstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CTH	MGC9471, CTH	cystathionase (cystathionine gamma-lyase)	NM_001190463, NM_001902, NM_153742, hCT12775.3, hCT1962917.1	206085_s_at, 217127_at	NP_001177392.1, NP_001893.2, NP_714964.2, EAX06450.1, EAX06451.1
GeneID:9406	ZRANB2	1	71,528,974	71,546,972	17,998	-	2	1_A375_pNL7_minus_lncRNA::1::273, 2_A375_pNL97_plus_lncRNA::1::371	60, 92	in gene, in gene	1	1	32	30	1	1_A375_pNL7_minus_lncRNA::1	32	Gene ZRANB2	ZIS, ZIS2, DKFZp686J1831, FLJ41119, ZIS1, ZNF265, ZRANB2, DKFZp686N09117	zinc finger, RAN-binding domain containing 2	NM_005455, NM_203350, hCT1644643.3, hCT1815428.1, hCT1958911.1, hCT2333052.0	223016_x_at, 223716_s_at, 241345_at	NP_005446.2, NP_976225.1, EAX06432.1, EAX06433.1, EAX06434.1, EAX06435.1
GeneID:257194	NEGR1	1	71,868,625	72,748,277	879,652	-	1	1_A375_pNL7_minus_lncRNA::1::274	-1067	upstream	1	0	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene NEGR1	DMML2433, Ntra, KILON, IGLON4, MGC46680, NEGR1	neuronal growth regulator 1	NM_173808, hCT1640140.4, hCT2347990.0, hCT2347991.0	1553194_at, 229461_x_at, 239546_at, 243357_at	NP_776169.2, EAX06429.1, EAX06428.1, EAX06430.1
GeneID:51086	TNNI3K	1	74,663,947	75,010,108	346,161	+	2	1_A375_pNL7_minus_lncRNA::1::275, 2_A375_pNL97_plus_lncRNA::1::372	304373, 304373	in gene, in gene	1	1	43	62	1	2_A375_pNL97_plus_lncRNA::1	62	Gene TNNI3K	TNNI3K, MGC33828, CARK, MGC142099	TNNI3 interacting kinase	NM_015978, NM_001112808, hCT2332706.0	220415_at	NP_057062.1, NP_001106279.1, EAX06415.1
GeneID:34	ACADM	1	76,190,043	76,229,355	39,312	+	1	2_A375_pNL97_plus_lncRNA::1::374	229	in gene	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ACADM	FLJ18227, FLJ99884, ACAD1, MCADH, FLJ93013, MCAD, ACADM	acyl-CoA dehydrogenase, C-4 to C-12 straight chain	NM_000016, NM_001127328, hCT14015.3, hCT1962226.1, hCT2359207.0	202502_at	NP_000007.1, NP_001120800.1, EAX06399.1, EAX06400.1, EAX06401.1
GeneID:5876	RABGGTB	1	76,251,886	76,260,764	8,878	+	1	2_A375_pNL97_plus_lncRNA::1::375	50	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene RABGGTB	GGTB, RABGGTB	Rab geranylgeranyltransferase, beta subunit	NM_004582, hCT13954.3, hCT1969200.1, hCT2332711.0, hCT2359245.0, hCT2359246.0	209180_at, 209181_s_at, 213704_at	NP_004573.2, EAX06395.1, EAX06394.1, EAX06396.1, EAX06397.1, EAX06398.1
GeneID:692085	SNORD45C	1	76,252,757	76,252,834	77	+	1	2_A375_pNL97_plus_lncRNA::1::375	-821	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORD45C	SNORD45C, U45C	small nucleolar RNA, C/D box 45C	NR_003042		
GeneID:26805	SNORD45A	1	76,253,574	76,253,657	83	+	1	2_A375_pNL97_plus_lncRNA::1::375	-1638	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORD45A	U45a, SNORD45A, RNU45A	small nucleolar RNA, C/D box 45A	NR_002749		
GeneID:26804	SNORD45B	1	76,255,162	76,255,232	70	+	1	2_A375_pNL97_plus_lncRNA::1::375	-3226	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORD45B	U45b, RNU45B, SNORD45B	small nucleolar RNA, C/D box 45B	NR_002748		
GeneID:81849	ST6GALNAC5	1	77,333,186	77,529,737	196,551	+	3	1_A375_pNL7_minus_lncRNA::1::276, 2_A375_pNL97_plus_lncRNA::1::376, 2_A375_pNL97_plus_lncRNA::1::377	172478, 990, 169214	in gene, in gene, in gene	1	1	18.67	18	3	1_A375_pNL7_minus_lncRNA::1	29	Gene ST6GALNAC5	ST6GALNAC5, SIAT7E, ST6GalNAcV, MGC3184	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	NM_030965, hCT1957977.1	1562753_at, 220979_s_at, 230462_at	NP_112227.1, EAX06386.1
GeneID:10026	PIGK	1	77,554,666	77,685,132	130,466	-	1	2_A375_pNL97_plus_lncRNA::1::378	108	in gene	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PIGK	PIGK, GPI8, MGC22559	phosphatidylinositol glycan anchor biosynthesis, class K	NM_005482, hCT13908.3, hCT1969199.1, hCT2332697.0, hCT2359232.0	1555394_at, 209707_at, 227639_at	NP_005473.1, EAX06380.1, EAX06381.1, EAX06382.1, EAX06383.1
GeneID:26009	ZZZ3	1	78,030,190	78,148,343	118,153	-	2	2_A375_pNL97_plus_lncRNA::1::379, 2_A375_pNL97_plus_lncRNA::1::380	23, -841	in gene, upstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene ZZZ3	FLJ10362, ATAC1, DKFZp564I052, DKFZp313N0119, ZZZ3	zinc finger, ZZ-type containing 3	NM_015534, hCT2332693.0, hCT2332694.0, hCT2332695.0, hCT2359087.0, hCT2359088.0	212893_at, 229325_at	NP_056349.1, EAX06373.1, EAX06372.1, EAX06374.1, EAX06375.1, EAX06376.1
GeneID:374986	FAM73A	1	78,245,309	78,344,077	98,768	+	1	1_A375_pNL7_minus_lncRNA::1::277	17219	in gene	1	0	13	9	1	1_A375_pNL7_minus_lncRNA::1	13	Gene FAM73A	DKFZp686M07166, FLJ35093, FAM73A	family with sequence similarity 73, member A	NM_198549, hCT2348643.0	235125_x_at, 243042_at	NP_940951.1, EAX06364.1
GeneID:11080	DNAJB4	1	78,470,636	78,482,998	12,362	+	1	2_A375_pNL97_plus_lncRNA::1::381	-348	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DNAJB4	DNAJB4, HLJ1, DNAJW, DjB4	DnaJ (Hsp40) homolog, subfamily B, member 4	NM_007034, hCT2332683.1, hCT2332684.0	203810_at, 203811_s_at	NP_008965.2, EAX06355.1, EAX06354.1
GeneID:23266	LPHN2	1	82,266,082	82,458,107	192,025	+	2	2_A375_pNL97_plus_lncRNA::1::384, 2_A375_pNL97_plus_lncRNA::1::385	974, 120014	in gene, in gene	0	1	11.5	17	2	2_A375_pNL97_plus_lncRNA::1	20	Gene LPHN2	LPHN2, CL2, LPHH1, CIRL2, LEC1	latrophilin 2	NM_012302, hCT1950476.1, hCT2332929.0, hCT2332930.0, hCT2332931.0, hCT2332932.0, hCT2332933.0, hCT2332934.0, hCT2332935.0, hCT2332937.0, hCT2332938.0, hCT2332939.0, hCT2332941.0, hCT2332942.0, hCT2332943.0, hCT2332944.0, hCT2332945.0, hCT2332946.0, hCT233	206953_s_at	NP_036434.1, EAX06333.1, EAX06321.1, EAX06322.1, EAX06323.1, EAX06335.1, EAX06324.1, EAX06325.1, EAX06326.1, EAX06327.1, EAX06328.1, EAX06329.1, EAX06334.1, EAX06337.1, EAX06330.1, EAX06331.1, EAX06332.1, EAX06336.1, EAX06338.1, EAX06339.1, EAX06340.1, EA
GeneID:79739	TTLL7	1	84,335,057	84,464,833	129,776	-	2	1_A375_pNL7_minus_lncRNA::1::279, 2_A375_pNL97_plus_lncRNA::1::386	33, -63	in gene, upstream	1	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TTLL7	FLJ36855, FLJ23033, TTLL7, RP5-836J3.2	tubulin tyrosine ligase-like family, member 7	NM_024686, hCT1953615.1, hCT1953616.1	219882_at	NP_078962.4, EAW73251.1, EAW73252.1
GeneID:80135	RPF1	1	84,944,920	84,964,033	19,113	+	1	2_A375_pNL97_plus_lncRNA::1::387	-184	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene RPF1	RPF1, RP11-118B23.1, FLJ12475, BXDC5, DKFZp761M0215, DKFZp761G0415	ribosome production factor 1 homolog (S. cerevisiae)	NM_025065, hCT16212.2	218462_at, 234243_at, 234244_at	NP_079341.2, EAW73237.1
GeneID:23576	DDAH1	1	85,784,168	86,044,046	259,878	-	2	1_A375_pNL7_minus_lncRNA::1::280, 2_A375_pNL97_plus_lncRNA::1::388	57198, 57102	in gene, in gene	1	1	22	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene DDAH1	FLJ25539, DDAH, FLJ21264, DDAH1	dimethylarginine dimethylaminohydrolase 1	NM_012137, NM_001134445, hCT2328980.2, hCT2328981.1, hCT2340526.1, hCT2350179.0	1553565_s_at, 209094_at, 229456_s_at, 243711_at	NP_036269.1, NP_001127917.1, EAW73199.1, EAW73200.1, EAW73201.1, EAW73202.1
GeneID:1179	CLCA1	1	86,934,526	86,965,977	31,451	+	2	1_A375_pNL7_minus_lncRNA::1::281, 2_A375_pNL97_plus_lncRNA::1::389	18466, 18210	in gene, in gene	1	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CLCA1	CLCRG1, hCaCC-1, CaCC-1, GOB5, FLJ95147, CACC1, hCLCA1, CACC, CLCA1	chloride channel accessory 1	NM_001285, hCT16357.2	210107_at	NP_001276.2, EAW73186.1
GeneID:9403	15-Sep	1	87,328,128	87,380,107	51,979	-	1	2_A375_pNL97_plus_lncRNA::1::390	315	in gene	0	1	9	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene SEP15		15 kDa selenoprotein	NM_004261, NM_203341, hCT16354.3, hCT1953622.2, hCT1953623.1, hCT1969175.1, hCT2355122.0	200902_at	NP_004252.2, NP_976086.1, EAW73176.1, EAW73177.1, EAW73178.1, EAW73180.1, EAW73179.1
GeneID:9653	HS2ST1	1	87,380,335	87,575,681	195,346	+	1	2_A375_pNL97_plus_lncRNA::1::390	-543	upstream	0	1	9	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene HS2ST1	MGC131986, KIAA0448, dJ604K5.2, FLJ11317, HS2ST1	heparan sulfate 2-O-sulfotransferase 1	NM_012262, NM_001134492, hCT1959963.1, hCT1959964.1, hCT2328970.0, hCT2328972.0	203283_s_at, 203284_s_at, 203285_s_at, 230465_at	NP_036394.1, NP_001127964.1, EAW73170.1, EAW73171.1, EAW73172.1, EAW73173.1
GeneID:5586	PKN2	1	89,149,922	89,301,938	152,016	+	1	2_A375_pNL97_plus_lncRNA::1::392	-74	upstream	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene PKN2	PRKCL2, Pak-2, PRK2, MGC150606, PAK2, PKN2, PRO2042, MGC71074	protein kinase N2	NM_006256, hCT14845.3, hCT2328928.0, hCT2328930.0, hCT2328931.0, hCT2355130.0	210969_at, 212628_at, 212629_s_at, 230400_s_at	NP_006247.1, EAW73161.1, EAW73162.1, EAW73163.1, EAW73164.1, EAW73165.1
GeneID:2959	GTF2B	1	89,318,321	89,357,301	38,980	-	1	2_A375_pNL97_plus_lncRNA::1::393	53	in gene	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene GTF2B	TF2B, TFIIB, GTF2B	general transcription factor IIB	NM_001514, hCT15997.2, hCT1969170.1	208066_s_at	NP_001505.1, EAW73159.1, EAW73160.1
GeneID:56267	CCBL2	1	89,401,456	89,458,643	57,187	-	1	2_A375_pNL97_plus_lncRNA::1::394	427	in gene	0	1	8	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CCBL2	DKFZp547N1117, KAT3, MGC9398, CCBL2, RP4-531M19.2, DKFZp667D0223, KATIII	cysteine conjugate-beta lyase 2	NM_001008662, NM_001008661	209472_at, 227746_at	NP_001008662.1, NP_001008661.1
GeneID:494115	RBMXL1	1	89,445,139	89,458,643	13,504	-	1	2_A375_pNL97_plus_lncRNA::1::394	427	in gene	0	1	8	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene RBMXL1	FLJ32614, DKFZp547N1117, RBMXL1, RBM1, DKFZp667D0223	RNA binding motif protein, X-linked-like 1	NM_019610, NM_001162536		NP_062556.2, NP_001156008.1
GeneID:284695	ZNF326	1	90,460,678	90,494,094	33,416	+	2	1_A375_pNL7_minus_lncRNA::1::282, 2_A375_pNL97_plus_lncRNA::1::395	90, 26	in gene, in gene	1	1	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ZNF326	FLJ20403, MGC61591, ZNF326, ZAN75, dJ871E2.1, Zfp326	zinc finger protein 326	NM_182976, NM_182975, hCT13957.3, hCT1952356.1, hCT2328538.0, hCT2355147.0	227680_at, 234093_at, 241720_at	NP_892021.1, NP_892020.1, EAW73125.1, EAW73126.1, EAW73127.1, EAW73128.1
GeneID:164045	HFM1	1	91,726,323	91,870,426	144,103	-	2	1_A375_pNL7_minus_lncRNA::1::283, 2_A375_pNL97_plus_lncRNA::1::396	122, 90	in gene, in gene	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene HFM1	helicase, MGC163287, FLJ39011, SEC63D1, Si-11-6, FLJ36760, RP11-539G11.1, MER3, Si-11, HFM1	HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)	NM_001017975, hCT2325398.0	1564263_at, 241469_at	NP_001017975.3, EAW73116.1
GeneID:7049	TGFBR3	1	92,145,900	92,351,767	205,867	-	2	1_A375_pNL7_minus_lncRNA::1::284, 2_A375_pNL97_plus_lncRNA::1::397	55539, 567	in gene, in gene	0	1	11.5	16	2	2_A375_pNL97_plus_lncRNA::1	22	Gene TGFBR3	betaglycan, BGCAN, TGFBR3	transforming growth factor, beta receptor III	NM_003243, hCT1280043	204731_at	NP_003234.2, EAW73112.1, EAW73112.1
GeneID:646517	LOC646517	1	92,540,092	92,540,966	875	-	1	2_A375_pNL97_plus_lncRNA::1::399	-5176	upstream	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC646517		SET nuclear oncogene pseudogene			
GeneID:284697	BTBD8	1	92,545,862	92,613,267	67,505	+	1	2_A375_pNL97_plus_lncRNA::1::399	262	in gene	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene BTBD8	BTBD8		NM_183242, hCT1637705.5, hCT1812983.3, hCT2355139.0	1569993_at	NP_899065.2, EAW73104.1, EAW73102.1
GeneID:11146	GLMN	1	92,711,933	92,764,566	52,611	-	2	1_A375_pNL7_minus_lncRNA::1::284, 2_A375_pNL97_plus_lncRNA::1::400	310, 162	in gene, in gene	1	1	15	17	1	1_A375_pNL7_minus_lncRNA::1	17	Gene GLMN	FAP68, GLMN, GVM, GLML, VMGLOM, FAP, FAP48, FKBPAP	glomulin, FKBP associated protein	NM_053274, hCT13658.2, hCT1952355.1	207153_s_at, 236924_at, 237285_at	NP_444504.1, EAW73097.1, EAW73095.1
GeneID:79871	RPAP2	1	92,764,522	92,853,732	89,210	+	2	1_A375_pNL7_minus_lncRNA::1::284, 2_A375_pNL97_plus_lncRNA::1::400	-266, -138	upstream, upstream	1	1	15	17	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RPAP2	C1orf82, RPAP2, FLJ13150	RNA polymerase II associated protein 2	NM_024813, hCT13655.2, hCT2355109.0	219804_s_at, 222893_s_at	NP_079089.2, EAW73096.1
GeneID:6125	RPL5	1	93,297,594	93,307,481	9,887	+	2	1_A375_pNL7_minus_lncRNA::1::285, 2_A375_pNL97_plus_lncRNA::1::401	-90, -90	upstream, upstream	1	1	156	156	1	2_A375_pNL97_plus_lncRNA::1	156	Gene RPL5	L5, MGC117339, DBA6, MSTP030, [illegible]	ribosomal protein L5	NM_000969, hCT2329247.0, hCT2329248.0, hCT2355115.0	1556495_at, 200937_s_at, 213080_x_at, 213969_x_at	NP_000960.2, EAW73085.1, EAW73087.1, [illegible]

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:6083	SNORD21	1	93,302,846	93,302,940	94	+	2	1_A375_pNL7_minus_lncRNA::1::285, 2_A375_pNL97_plus_lncRNA::1::401	-5342, -5342	upstream, upstream	1	1	156	158	1	2_A375_pNL97_plus_lncRNA::1	158	Gene SNORD21	SNORD21, U21, RNU21	small nucleolar RNA, C/D box 21	NR_000006		
GeneID:26782	SNORA66	1	93,306,276	93,306,408	132	+	2	1_A375_pNL7_minus_lncRNA::1::285, 2_A375_pNL97_plus_lncRNA::1::401	-8772, -8772	upstream, upstream	1	1	156	158	1	2_A375_pNL97_plus_lncRNA::1	158	Gene SNORA66	RNU66, SNORA66, U66	small nucleolar RNA, H/ACA box 66	NR_002444	210035_s_at	
GeneID:388650	FAM69A	1	93,307,721	93,427,079	119,358	-	2	1_A375_pNL7_minus_lncRNA::1::285, 2_A375_pNL97_plus_lncRNA::1::401	129575, 129575	downstream, downstream	1	1	156	158	1	2_A375_pNL97_plus_lncRNA::1	158	Gene FAM69A	FLJ23493, FAM69A	family with sequence similarity 69, member A	NM_001006605, hCT13993.2	216044_x_at	NP_001006606.2, EAW73086.1
GeneID:22823	MTF2	1	93,544,792	93,604,638	59,846	+	1	2_A375_pNL97_plus_lncRNA::1::402	-88	upstream	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene MTF2	PCL2, RP5-976O13.1, dJ976O13.2, MTF2, M96	metal response element binding transcription factor 2	NM_007358, NM_001164391, NM_001164392, NM_001164393, hCT23129.3, hCT2355144.0, hCT2355145.0	203345_s_at, 203346_s_at, 203347_s_at, 209705_at	NP_031384.1, NP_001157863.1, NP_001157864.1, NP_001157865.1, EAW73084.1, EAW73085.1, EAW73083.1
GeneID:50999	TMED5	1	93,615,299	93,646,246	30,947	-	2	1_A375_pNL7_minus_lncRNA::1::286, 2_A375_pNL97_plus_lncRNA::1::403	150, 134	in gene, in gene	1	1	21	21	1	1_A375_pNL7_minus_lncRNA::1	21	Gene TMED5	TMED5, DKFZp781B2246, CGI-100	transmembrane emp24 protein transport domain containing 5	NM_016040, NR_030761, NM_001167830, hCT22667.3, hCT2329069.0	1556813_at, 1556814_s_at, 202194_at, 202195_s_at, 239283_at, 242263_at	NP_057124.3, NP_001161302.1, EAW73081.1, EAW73082.1
GeneID:343099	CCDC18	1	93,645,920	93,744,270	98,350	+	2	1_A375_pNL7_minus_lncRNA::1::286, 2_A375_pNL97_plus_lncRNA::1::403	176, 192	in gene, in gene	1	1	21	21	1	1_A375_pNL7_minus_lncRNA::1	21	Gene CCDC18	CCDC18, RP4-717I23.1, NY-SAR-41, dJ717I23.1	coiled-coil domain containing 18	NM_206886, hCT2329251.0, hCT2329252.0, hCT2329253.0	228022_at, 232362_at, 236665_at	NP_996769.2, EAW73080.1, EAW73078.1, EAW73079.1
GeneID:8412	BCAR3	1	94,027,348	94,147,385	120,037	-	2	1_A375_pNL7_minus_lncRNA::1::287, 1_A375_pNL7_minus_lncRNA::1::288	75769, 1113	in gene, in gene	1	0	16.5	13	2	1_A375_pNL7_minus_lncRNA::1	16	Gene BCAR3	SH2D3B, BCAR3, KIAA0554, NSP2	breast cancer anti-estrogen resistance 3	NM_003567, hCT2329063.1, hCT2329064.1, hCT2329065.1, hCT2329066.1	204032_at	NP_003558.1, EAW73067.1, EAW73065.1, EAW73066.1, EAW73068.1
GeneID:100129046	LOC100129046	1	94,057,525	94,065,587	8,062	+	1	1_A375_pNL7_minus_lncRNA::1::287	14091	downstream	1	0	18	14	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100129046		hypothetical LOC100129046	NR_034091		
GeneID:100505940	LOC100505940	1	94,713,414	94,800,404	86,990	+	2	1_A375_pNL7_minus_lncRNA::1::289, 2_A375_pNL97_plus_lncRNA::1::404	77690, 78010	in gene, in gene	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC100505940		hypothetical LOC100505940	XR_112091, XR_110477, XR_113517		
GeneID:199857	ALG14	1	95,448,279	95,538,507	90,228	-	1	2_A375_pNL97_plus_lncRNA::1::406	-5	upstream	0	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ALG14	MGC19780, ALG14	asparagine-linked glycosylation 14 homolog (S. cerevisiae)	NM_144988, hCT1952372.1, hCT23096.2	1553954_at	NP_659425.1, EAW73026.1, EAW73027.1
GeneID:1806	DPYD	1	97,543,299	98,386,615	843,316	-	2	1_A375_pNL7_minus_lncRNA::1::294, 2_A375_pNL97_plus_lncRNA::1::409	231, 343	in gene, in gene	1	1	22	20	1	1_A375_pNL7_minus_lncRNA::1	22	Gene DPYD	MGC132008, DPYD, DHP, MGC70799, DHPDHASE, DPD	dihydropyrimidine dehydrogenase	NM_000110, NM_001160301, hCT1952369.1, hCT2326187.0	1554534_at, 1554536_at, 204646_at	NP_000101.2, NP_001153773.1, EAW73002.1, EAW73003.1
GeneID:400765	FLJ35409	1	98,508,712	98,511,014	2,302	-	4	1_A375_pNL7_minus_lncRNA::1::295, 2_A375_pNL97_plus_lncRNA::1::410, 2_A375_pNL97_plus_lncRNA::1::411, 2_A375_pNL97_plus_lncRNA::1::412	-2906, 102, -970, -2906	upstream, in gene, upstream, upstream	1	1	19.67	31.33	3	2_A375_pNL97_plus_lncRNA::1	60	Gene FLJ35409		FLJ35409 protein	XR_112090, XR_110478, XR_113505	1559504_at, 1559506_x_at	
GeneID:406928	MIR137	1	98,511,626	98,511,727	101	-	4	1_A375_pNL7_minus_lncRNA::1::295, 2_A375_pNL97_plus_lncRNA::1::410, 2_A375_pNL97_plus_lncRNA::1::411, 2_A375_pNL97_plus_lncRNA::1::412	-2193, 815, -257, -2193	upstream, downstream, upstream, upstream	1	1	19.67	31.33	3	2_A375_pNL97_plus_lncRNA::1	60	Gene MIR137	MIR137, MIRN137	microRNA 137	NR_029679		
GeneID:54873	PALMD	1	100,111,431	100,160,097	48,666	+	1	2_A375_pNL97_plus_lncRNA::1::415	36681	in gene	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene PALMD	C1orf11, FLJ20271, PALMD, PALML	palmdelphin	NM_017734, hCT23067.3, hCT2355148.0	218736_s_at, 222725_s_at, 232187_at	NP_060204.1, EAW72990.1, EAW72989.1
GeneID:178	AGL	1	100,315,640	100,389,579	73,939	+	2	1_A375_pNL7_minus_lncRNA::1::296, 2_A375_pNL97_plus_lncRNA::1::416	-56, 72	upstream, in gene	1	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene AGL	GDE, AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase	NM_000028, NM_000645, NM_000643, NM_000646, NM_000644, NM_000642, hCT1814575.1, hCT22678.2, hCT23064.2, hCT23065.2, hCT2328473.0, hCT2328477.0, hCT2328478.0, hCT2328479.0	203566_s_at	NP_000019.2, NP_000636.2, NP_000634.2, NP_000637.2, NP_000635.2, NP_000633.2, EAW72980.1, EAW72981.1, EAW72982.1, EAW72983.1, EAW72984.1, EAW72985.1, EAW72986.1, EAW72987.1
GeneID:730081	LOC730081	1	100,433,942	100,435,838	1,896	-	1	2_A375_pNL97_plus_lncRNA::1::417	382	in gene	0	1	23	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene LOC730081		hypothetical LOC730081	XR_112089, XR_110479, XR_113506		
GeneID:23443	SLC35A3	1	100,435,540	100,489,006	53,466	+	1	2_A375_pNL97_plus_lncRNA::1::417	-84	upstream	0	1	23	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene SLC35A3	SLC35A3, DKFZp781P1297	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3	NM_012243, hCT22676.2, hCT2328480.0, hCT2328481.0	206770_s_at, 209865_at, 226894_at	NP_036375.1, EAW72978.1, EAW72977.1, EAW72979.1
GeneID:64645	HIAT1	1	100,503,789	100,548,933	45,144	+	2	1_A375_pNL7_minus_lncRNA::1::297, 2_A375_pNL97_plus_lncRNA::1::418	-120, -237	upstream, upstream	1	1	19	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene HIAT1	HIAT1, DKFZp564L0864	hippocampus abundant transcript 1	NM_033055, hCT23019.2	225222_at	NP_149044.2, EAW72976.1
GeneID:163786	SASS6	1	100,549,100	100,598,511	49,411	-	2	1_A375_pNL7_minus_lncRNA::1::298, 2_A375_pNL97_plus_lncRNA::1::419	-161, 31	upstream, in gene	1	1	17	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene SASS6	SAS-6, SAS6, MGC119440, FLJ22097, SASS6	spindle assembly 6 homolog (C. elegans)	NM_194292, hCT2328214.0, hCT2328215.0	231895_at	NP_919268.1, EAW72974.1, EAW72975.1
GeneID:54482	CCDC76	1	100,598,706	100,616,054	17,348	+	2	1_A375_pNL7_minus_lncRNA::1::298, 2_A375_pNL97_plus_lncRNA::1::419	-34, -226	upstream, upstream	1	1	17	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene CCDC76	FLJ11219, FLJ10287, CCDC76	coiled-coil domain containing 76	NM_019083, hCT23017.3, hCT2328485.0, hCT2328486.0, hCT2355134.0	219130_at, 232489_at	NP_061956.2, EAW72971.1, EAW72970.1, EAW72972.1, EAW72973.1
GeneID:8556	CDC14A	1	100,818,023	100,985,833	167,810	+	2	1_A375_pNL7_minus_lncRNA::1::299, 2_A375_pNL97_plus_lncRNA::1::420	169, 345	in gene, in gene	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene CDC14A	hCDC14, CDC14A, cdc14	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	NM_033312, NM_003672, NM_033313, hCT1967649.1, hCT2328492.0, hCT2328493.0, hCT2355140.0, hCT24042.3	205288_at, 210440_s_at, 210441_at, 210742_at, 210743_s_at	NP_201569.1, NP_003663.2, NP_201570.1, EAW72956.1, EAW72958.1, EAW72960.1, EAW72957.1, EAW72959.1
GeneID:51611	DPH5	1	101,455,179	101,491,362	36,183	-	1	2_A375_pNL97_plus_lncRNA::1::422	-254	upstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DPH5	HSPC143, NPD015, AD-018, CGI-30, MGC61450, DPH5	DPH5 homolog (S. cerevisiae)	NM_015958, NM_001077395, NM_001077394, hCT1962725.2, hCT1962726.1, hCT1962728.2, hCT1962729.2, hCT1967646.2, hCT2328227.1, hCT2355150.0, hCT2355151.0, hCT2355152.0, hCT24041.4	219590_x_at, 222360_at, 223671_x_at, 224060_s_at, 224196_x_at	NP_057042.2, NP_001070863.1, NP_001070862.1, EAW72935.1, EAW72938.1, EAW72940.1, EAW72932.1, EAW72933.1, EAW72934.1, EAW72936.1, EAW72937.1, EAW72939.1, EAW72941.1
GeneID:100506051	LOC100506051	1	101,491,434	101,546,991	55,557	+	1	2_A375_pNL97_plus_lncRNA::1::422	182	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506051		hypothetical LOC100506051	XR_110482		
GeneID:118427	OLFM3	1	102,268,127	102,462,790	194,663	-	3	1_A375_pNL7_minus_lncRNA::1::302, 2_A375_pNL97_plus_lncRNA::1::423, 2_A375_pNL97_plus_lncRNA::1::424	230, 91910, 230	in gene, in gene, in gene	1	1	23.5	35	2	2_A375_pNL97_plus_lncRNA::1	52	Gene OLFM3	NOELIN3_V6, NOELIN3_V2, NOELIN3_V1, NOELIN3_V3, OPTIMEDIN, NOELIN3_V5, NOELIN3_V4, OLFM3, NOELIN3, NOE3	olfactomedin 3	NM_058170, hCT2328217.0, hCT2328219.0, hCT24249.2	1554524_a_at, 1554526_at	NP_477518.2, EAW72922.1, EAW72921.1, EAW72923.1
GeneID:55170	PRMT6	1	107,599,267	107,601,916	2,649	+	2	1_A375_pNL7_minus_lncRNA::1::305, 2_A375_pNL97_plus_lncRNA::1::426	109, 317	in gene, in gene	1	1	16	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene PRMT6	PRMT6, FLJ10559, FLJ51477, HRMT1L6	protein arginine methyltransferase 6	NM_018137, hCT1644369.3	223275_at	NP_060607.2, EAW51248.1
GeneID:22854	NTNG1	1	107,682,629	108,024,475	341,846	+	2	1_A375_pNL7_minus_lncRNA::1::306, 2_A375_pNL97_plus_lncRNA::1::427	-4369, -4341	upstream, upstream	1	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene NTNG1	KIAA0976, NTNG1, Lmnt1	netrin G1	NM_014917, NM_001113226, NM_001113228, hCT1951529.1, hCT2294772.0	206713_at, 236088_at	NP_055732.2, NP_001106697.1, NP_001106699.1, EAW51249.1, EAW51250.1
GeneID:29957	SLC25A24	1	108,677,445	108,742,974	65,529	-	1	2_A375_pNL97_plus_lncRNA::1::430	-514	upstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SLC25A24	SCAMC-1, DKFZp586G0123, SLC25A24, APC1	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	NM_213651, NM_013386, hCT2294436.0, hCT2352452.0	1569121_at, 204342_at, 244461_at	NP_998816.1, NP_037518.3, EAW51254.1, EAW51255.1
GeneID:29899	GPSM2	1	109,419,603	109,473,044	53,441	+	2	1_A375_pNL7_minus_lncRNA::1::307, 2_A375_pNL97_plus_lncRNA::1::431	13, -53	in gene, upstream	1	1	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene GPSM2	LGN, Pins, PINS, GPSM2, DFNB82	G-protein signaling modulator 2	NM_013296, hCT1960757.2, hCT2279235.1, hCT2279237.1, hCT2279238.1, hCT31165.4	205240_at, 221922_at	NP_037428.3, EAW56340.1, EAW56341.1, EAW56342.1, EAW56343.1, EAW56344.1
GeneID:22911	WDR47	1	109,512,636	109,584,650	72,014	-	1	1_A375_pNL7_minus_lncRNA::1::308	242	in gene	1	0	17	18	1	1_A375_pNL7_minus_lncRNA::1	17	Gene WDR47	KIAA0893, FLJ90135, WDR47	WD repeat domain 47	NM_014969, NM_001142550, NM_001142551, hCT2353064.0, hCT29400.2	203655_at	NP_055784.3, NP_001136022.1, NP_001136023.1, EAW56350.1, EAW56351.1
GeneID:6884	TAF13	1	109,606,998	109,618,624	11,626	-	2	1_A375_pNL7_minus_lncRNA::1::309, 2_A375_pNL97_plus_lncRNA::1::432	-80, 32	upstream, in gene	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TAF13	TAF13, TAFII18, MGC22425, TAF2K	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	NM_005645, hCT2297498.0, hCT29999.2	205966_at	NP_005636.1, EAW56354.1, EAW56355.1
GeneID:56900	TMEM167B	1	109,633,403	109,639,554	6,151	+	4	1_A375_pNL7_minus_lncRNA::1::310, 1_A375_pNL7_minus_lncRNA::1::311, 2_A375_pNL97_plus_lncRNA::1::433, 2_A375_pNL97_plus_lncRNA::1::434	-75, 9253, -91, 9265	upstream, downstream, upstream, downstream	1	1	52.5	54.5	2	1_A375_pNL7_minus_lncRNA::1	66	Gene TMEM167B	AD-020, FLJ90710, C1orf119, TMEM167B	transmembrane protein 167B	NM_020141, hCT2279245.0, hCT31169.3	222495_at	NP_064526.1, EAW56357.1, EAW56356.1
GeneID:677766	SCARNA2	1	109,642,815	109,643,234	419	+	4	1_A375_pNL7_minus_lncRNA::1::310, 1_A375_pNL7_minus_lncRNA::1::311, 2_A375_pNL97_plus_lncRNA::1::433, 2_A375_pNL97_plus_lncRNA::1::434	-9487, -159, -9503, -127	upstream, upstream, upstream, upstream	1	1	52.5	54.5	2	1_A375_pNL7_minus_lncRNA::1	66	Gene SCARNA2	SCARNA2, HBII-382, mgU2-25/61	small Cajal body-specific RNA 2	NR_003023	237137_at	
GeneID:127003	C1orf194	1	109,648,573	109,656,479	7,906	-	2	1_A375_pNL7_minus_lncRNA::1::311, 2_A375_pNL97_plus_lncRNA::1::434	13823, 13791	downstream, downstream	1	1	39	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene C1orf194	C1orf194	chromosome 1 open reading frame 194	NM_001122961	231044_at	NP_001116433.1
GeneID:343263	MYBPHL	1	109,834,987	109,849,663	14,676	-	1	2_A375_pNL97_plus_lncRNA::1::435	7215	in gene	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MYBPHL	MYBPHL	myosin binding protein H-like	NM_001010985, hCT2353061.0, hCT31170.2		NP_001010985.2, EAW56379.1, EAW56378.1
GeneID:6272	SORT1	1	109,852,192	109,940,563	88,371	-	1	2_A375_pNL97_plus_lncRNA::1::435	98115	downstream	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SORT1	LDLCQ6, NT3, Gp95, SORT1	sortilin 1	NM_002959, hCT31181.3	212797_at, 212807_s_at, 224818_at	NP_002950.3, EAW56380.1
GeneID:284612	SYPL2	1	110,009,100	110,024,764	15,664	+	4	1_A375_pNL7_minus_lncRNA::1::312, 1_A375_pNL7_minus_lncRNA::1::313, 1_A375_pNL7_minus_lncRNA::1::314, 2_A375_pNL97_plus_lncRNA::1::436	-55, 16980, 17828, 17780	upstream, downstream, downstream, downstream	1	1	42.5	49	2	2_A375_pNL97_plus_lncRNA::1	84	Gene SYPL2	MG29, SYPL2	synaptophysin-like 2	NM_001040709, hCT2279442.0	230611_at	NP_001035799.1, EAW56385.1
GeneID:127002	ATXN7L2	1	110,026,561	110,035,426	8,865	+	5	1_A375_pNL7_minus_lncRNA::1::313, 1_A375_pNL7_minus_lncRNA::1::314, 1_A375_pNL7_minus_lncRNA::1::315, 2_A375_pNL97_plus_lncRNA::1::436, 2_A375_pNL97_plus_lncRNA::1::437	-481, 367, 10111, 319, 10143	upstream, in gene, downstream, in gene, downstream	1	1	68.5	79.5	2	2_A375_pNL97_plus_lncRNA::1	84	Gene ATXN7L2	MGC46534, ATXN7L2, FLJ00381	ataxin 7-like 2	NM_153340	230038_at	NP_699171.3
GeneID:284613	CYB561D1	1	110,036,658	110,043,063	6,405	+	4	1_A375_pNL7_minus_lncRNA::1::314, 1_A375_pNL7_minus_lncRNA::1::315, 2_A375_pNL97_plus_lncRNA::1::436, 2_A375_pNL97_plus_lncRNA::1::437	-9730, 14, -9778, 46	upstream, in gene, upstream, in gene	1	1	68.5	79.5	2	2_A375_pNL97_plus_lncRNA::1	84	Gene CYB561D1	CYB561D1, FLJ44753, FLJ39035, MGC138204	cytochrome b-561 domain containing 1	NM_182580, NM_001134400, NM_001134402, NM_001134403, NM_001134404		NP_872386.1, NP_001127872.1, NP_001127874.1, NP_001127875.1, NP_001127876.1
GeneID:10768	AHCYL1	1	110,527,308	110,566,364	39,056	+	2	1_A375_pNL7_minus_lncRNA::1::317, 2_A375_pNL97_plus_lncRNA::1::439	295, -44	in gene, upstream	1	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene AHCYL1	PRO0233, IRBIT, DCAL, XPVKONA, AHCYL1	adenosylhomocysteinase-like 1	NM_006621, hCT1960758.1, hCT2279405.0, hCT2279408.0, hCT2279409.0, hCT2279410.0, hCT31502.3	200848_at, 200849_s_at, 200850_s_at, 207464_at	NP_006612.2, EAW56423.1, EAW56422.1, EAW56424.1, EAW56425.1, EAW56426.1, EAW56427.1
GeneID:388662	SLC6A17	1	110,693,132	110,744,824	51,692	+	2	1_A375_pNL7_minus_lncRNA::1::318, 2_A375_pNL97_plus_lncRNA::1::440	5604, 5604	in gene, in gene	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SLC6A17	NTT4, SLC6A17	solute carrier family 6, member 17	NM_001010898, hCT31513.3	229925_at, 233287_at	NP_001010898.1, EAW56432.1
GeneID:64783	RBM15	1	110,881,945	110,889,303	7,358	+	3	1_A375_pNL7_minus_lncRNA::1::319, 2_A375_pNL97_plus_lncRNA::1::441, 2_A375_pNL97_plus_lncRNA::1::442	-425, -713, 2071	upstream, upstream, in gene	1	1	19.5	17	2	1_A375_pNL7_minus_lncRNA::1	28	Gene RBM15	FLJ21943, OTT1, MGC119584, SPEN, RBM15, OTT, FLJ12479	RNA binding motif protein 15	NM_022768, hCT1642035.3, hCT2279432.0, hCT2279434.0	1555760_a_at, 1555761_x_at, 1555762_s_at, 219286_s_at, 226455_at, 232971_at	NP_073605.4, EAW56438.1, EAW56439.1, EAW56440.1
GeneID:10542	HBXIP	1	110,943,875	110,950,546	6,671	-	1	2_A375_pNL97_plus_lncRNA::1::443	306	in gene	0	1	14	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene HBXIP	XIP, HBXIP, MGC71071	hepatitis B virus x interacting protein	NM_006402, hCT31507.3	202299_s_at, 202300_at	NP_006393.2, EAW56447.1
GeneID:55791	C1orf103	1	111,489,812	111,506,566	16,754	-	1	2_A375_pNL97_plus_lncRNA::1::447	-346	upstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene C1orf103	RIF1, FLJ11269, LRIF1, C1orf103, RP11-96K19.1	chromosome 1 open reading frame 103	NM_018372, NM_001006945, hCT2278599.1, hCT31239.4	220235_s_at	NP_060842.3, NP_001006946.1, EAW56460.1, EAW56461.1
GeneID:128338	DRAM2	1	111,659,954	111,682,838	22,884	-	1	2_A375_pNL97_plus_lncRNA::1::448	-410	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene DRAM2	RP5-1180E21.1, MGC54289, TMEM77, DRAM2, WWFQ154, PRO180	DNA-damage regulated autophagy modulator 2	NM_178454, hCT2353067.0, hCT2353068.0, hCT2353069.0, hCT2353070.0, hCT31243.3	225228_at, 225230_at	NP_848549.3, EAW56468.1, EAW56464.1, EAW56465.1, EAW56466.1, EAW56467.1
GeneID:10390	CEPT1	1	111,682,249	111,727,724	45,475	+	1	2_A375_pNL97_plus_lncRNA::1::448	999	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CEPT1	MGC45223, CEPT1, DKFZp313G0615	choline/ethanolamine phosphotransferase 1	NM_001007794, NM_006090, hCT2278193.0, hCT2278197.0, hCT2278201.0, hCT31234.3	1561884_at, 219375_at	NP_001007795.1, NP_006081.1, EAW56469.1, EAW56470.1, EAW56471.1, EAW56472.1
GeneID:55924	C1orf183	1	112,264,686	112,298,419	33,733	-	2	1_A375_pNL7_minus_lncRNA::1::323, 2_A375_pNL97_plus_lncRNA::1::449	51, 275	in gene, in gene	1	1	25	23	1	1_A375_pNL7_minus_lncRNA::1	25	Gene C1orf183	C1orf183, FLJ31105	chromosome 1 open reading frame 183	NM_019099, NM_198926, hCT2278297.0, hCT31333.3	220476_s_at, 229382_at, 229608_at, 241809_at	NP_061972.1, NP_945120.1, EAW56504.1, EAW56505.1
GeneID:100506343	LOC100506343	1	112,282,463	112,290,420	7,957	+	2	1_A375_pNL7_minus_lncRNA::1::323, 2_A375_pNL97_plus_lncRNA::1::449	15905, 15681	downstream, downstream	1	1	25	23	1	1_A375_pNL7_minus_lncRNA::1	25	Gene LOC100506343		hypothetical LOC100506343	XR_112100, XR_110488, XR_113708		
GeneID:11218	DDX20	1	112,298,190	112,310,199	12,009	+	2	1_A375_pNL7_minus_lncRNA::1::323, 2_A375_pNL97_plus_lncRNA::1::449	178, -46	in gene, upstream	1	1	25	23	1	1_A375_pNL7_minus_lncRNA::1	25	Gene DDX20	DKFZp434H052, GEMIN3, DP103, DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	NM_007204, hCT2277976.1, hCT31332.3	223331_s_at, 224315_at	NP_009135.4, EAW56507.1, EAW56508.1
GeneID:3752	KCND3	1	112,318,454	112,531,777	213,323	-	3	1_A375_pNL7_minus_lncRNA::1::324, 2_A375_pNL97_plus_lncRNA::1::450, 2_A375_pNL97_plus_lncRNA::1::451	155633, 155617, 124161	in gene, in gene, in gene	1	1	23	27.5	2	2_A375_pNL97_plus_lncRNA::1	32	Gene KCND3	KSHIVB, KCND3, MGC142035, KCND3L, MGC142037, KV4.3, KCND3S	potassium voltage-gated channel, Shal-related subfamily, member 3	NM_004980, NM_172198, hCT2278294.0, hCT2353022.0, hCT31335.2	211301_at, 211827_s_at	NP_004971.2, NP_751948.1, EAW56510.1, EAW56511.1, EAW56512.1
GeneID:54879	ST7L	1	113,066,140	113,162,040	95,900	-	2	1_A375_pNL7_minus_lncRNA::1::327, 2_A375_pNL97_plus_lncRNA::1::454	-264, 259	upstream, in gene	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ST7L	ST7R, FAM4B, ST7L, FLJ20284, STLR, FLJ11657	suppression of tumorigenicity 7 like	NM_017744, NM_138727, NM_138728, NM_138729, hCT2278286.0, hCT2278288.0, hCT2278289.0, hCT2278291.0, hCT29705.3	1552736_a_at, 1552739_s_at, 219964_at, 230079_at, 233141_s_at, 236123_at	NP_060214.2, NP_620055.1, NP_620056.1, NP_620057.1, EAW56520.1, EAW56521.1, EAW56522.1, EAW56523.1, EAW56524.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Identifier Count	Identifiers	Identifier Outcome	Identifier Position	[A]	[B]	[C]	[D]	Active Regulatory Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:29	CAPZA1	1	113,782,075	113,214,241	62,166	+	3	1_A270_sNU37_dhrsx_locRNA:1:-327,2_A270_sNU37_glrs_locRNA:1:-454,2_A270_sNU37_glrs_locRNA:1:-488	229, -294, 55349	at gene, upstream, downstream	1	1	16.5	20.5	2	2_A270_sNU37_glrs_locRNA:1	23	Gene:CAPZA1	CAPPA1, CAPZA1, CAPZ, CAZ1	Capping protein (actin filament) muscle Z-line, alpha 1	RNA_008135, XCT227974.0, XCT235304.0, XCT26787.3	NM_006135.4	208374_s_at, 217282_at, 231275_at	NP_006126.1, EAW69529.1, EAW69526.1, EAW69527.1
Gene:ID:343	MOVI0	1	113,217,046	113,243,268	26,320	+	3	1_A270_sNU37_dhrsx_locRNA:1:-326,2_A270_sNU37_glrs_locRNA:1:-455,2_A270_sNU37_glrs_locRNA:1:-489	33296, 376, 30382	downstream, at gene, downstream	1	1	16	20.5	2	2_A270_sNU37_glrs_locRNA:1	23	Gene:MOVI0	FLJ32791, MOVI0, DKFZp667O1423, p3(10), KIAA1631, ITSAP1	Movi0, Moloney leukemia virus 10, homolog (murine)	NM_020963, NM_001130078, XCT227537.0, XCT227539.0, XCT235400.0, XCT26706.2	222659_s_at, 233917_s_at	NP_065710.1, NP_001123551.1, EAW56528.1, EAW56529.1, EAW56530.1, EAW56531.1
Gene:ID:59	RHOC	1	113,243,749	113,250,025	6,276	+	2	1_A270_sNU37_dhrsx_locRNA:1:-326,2_A270_sNU37_glrs_locRNA:1:-488	2681, 2681	at gene, us gene	1	1	19	15	1	1_A270_sNU37_dhrsx_loc:RNA:1	19	Gene:RHOC	ARHC, MGC61427, MGC1666, RHOC, ARH9, RHOH9, H9	ras homolog gene family, member C	NM_001042678, NM_175744, NM_001042678	208955_at, 235742_at	NP_001036143.1, NP_786056.1, NP_001036144.1
Gene:ID:33826	PFN1J	1	113,282,616	113,287,890	5,334	+	2	1_A270_sNU37_dhrsx_locRNA:1:-326,2_A270_sNU37_glrs_locRNA:1:-488	10609, 10610	downstream, downstream	1	1	19	16	1	1_A270_sNU37_dhrsx_loc:RNA:1	19	Gene:PFN1J	PFN5-J, PFP2CZ, DKFZp434P1514, MGC90146, PP2Cbeta, MGC16531, PP2CZ, PLJ3B61	profilin 1 pseudogene 1J (PF2C domain containing)	NM_006167	224664_at	NP_006158.5
Gene:ID:566	SLC16A1	1	113,454,969	113,498,975	44,006	-	3	1_A270_sNU37_dhrsx_locRNA:1:-328,2_A270_sNU37_glrs_locRNA:1:-457	271, 287	at gene, us gene	1	1	21	30	1	2_A270_sNU37_glrs_locRNA:1	30	Gene:SLC16A1	MCT1, SLC16A1, MGC48875, HHF7, MCT, PLJB7A5	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	NM_003051, NM_001166496, XCT235702.0, XCT235323.0, XCT26666.4	1307916_s_at, 202234_s_at, 202235_at, 202236_s_at, 202237_s_at	NP_003042.2, NP_001138966.1, EAW56531.1, EAW56532.1, EAW56533.1
Gene:ID:3005638	LOC100506392	1	113,499,020	113,511,609	12,589	+	2	1_A270_sNU37_dhrsx_locRNA:1:-329,2_A270_sNU37_glrs_locRNA:1:-457	-316, -322	upstream, upstream	1	1	21	30	1	2_A270_sNU37_glrs_locRNA:1	30	Gene:LOC100506392		hypothetical LOC100506392	XR_110090		
Gene:ID:990	UFIG2	1	113,515,531	113,567,342	51,811	+	2	1_A270_sNU37_dhrsx_locRNA:1:-330,2_A270_sNU37_glrs_locRNA:1:-458	169, 169	at gene, us gene	1	1	25	40	1	2_A270_sNU37_glrs_locRNA:1	40	Gene:UFIG2	KIAA0599, LEG2, DKFZp451C161, LRIG2	leucine-rich repeats and immunoglobulin-like domains 2	NM_014813, XCT227545.0, XCT26309.2	205853_at, 242164_s_at, 321163_at	NP_055628.1, EAW56556.1, EAW56557.1
Gene:ID:80424	MAGI3	1	113,933,476	114,226,845	293,370	+	1	1_A270_sNU37_glrs_locRNA:1:-459	66171	at gene	0	1	12	14	1	2_A270_sNU37_glrs_locRNA:1	14	Gene:MAGI3	KIAA1709L2.1, MAGI3, MAGI-3, DJ730K2.2, MGC162281	membrane associated guanylate kinase, WW and PDZ domain containing 3	NM_152900, NM_001142762, XCT234989.0, XCT235966.0, XCT26966.0, XCT235966.0, XCT235966.0	224307_s_at, 226770_at	NP_690864.2, NP_001136254.1, EAW56539.1, EAW56540.1, EAW56542.1, EAW56543.1, EAW56541.1
Gene:ID:6745	PHTF1	1	114,230,624	114,301,777	61,953	-	1	2_A270_sNU37_glrs_locRNA:1:-460	-60	upstream	0	1	7	13	1	2_A270_sNU37_glrs_locRNA:1	13	Gene:PHTF1	PHTF, PHTF1	putative homeodomain transcription factor 1	NM_006605, XCT227559.2, XCT227556.0, XCT227564.0, XCT26662.2	203702_at, 210191_s_at, 213255_s_at, 226664_at	NP_006589.2, EAW56567.1, EAW56566.1, EAW56565.1, EAW56569.1
Gene:ID:4665	RSBN1	1	114,304,454	114,355,070	50,616	-	1	2_A270_sNU37_glrs_locRNA:1:-460	53203	downstream	0	1	7	13	1	2_A270_sNU37_glrs_locRNA:1	13	Gene:RSBN1	DKFZp761E2130, RP11-324J2.1, RSBBN, RSBN1	round spermatid basic protein 1	NM_018364, XCT227559.0, XCT235047.0, XCT26564.2	203564_at, 227765_s_at, 227766_at, 227767_s_at, 231281_at	NP_060834.2, EAW56572.1, EAW56570.1, EAW56571.1
Gene:ID:100287220	LOC100287220	1	114,399,257	114,443,859	44,602	+	2	1_A270_sNU37_dhrsx_locRNA:1:-331,2_A270_sNU37_glrs_locRNA:1:-461	46647, 46647	downstream, downstream	1	1	23	29	1	1_A270_sNU37_dhrsx_loc:RNA:1	33	Gene:LOC100287220		hypothetical LOC100287220	XR_112103, XR_110491, XR_112711		
Gene:ID:7717	AFAP1	1	114,437,677	114,447,741	10,064	-	2	1_A270_sNU37_dhrsx_locRNA:1:-331,2_A270_sNU37_glrs_locRNA:1:-461	-163, -163	upstream, upstream	1	1	23	29	1	1_A270_sNU37_dhrsx_loc:RNA:1	33	Gene:AFAP1	BETA-4, AFAP1	adaptin-related protein complex 4, beta 1 subunit	NM_006384	231714_s_at, 231962_at, 235221_at	NP_006365.2
Gene:ID:4658	DCLRE1B	1	114,447,915	114,496,705	8,791	+	2	1_A270_sNU37_dhrsx_locRNA:1:-331,2_A270_sNU37_glrs_locRNA:1:-461	-11, -11	upstream, upstream	1	1	23	29	1	1_A270_sNU37_dhrsx_loc:RNA:1	33	Gene:DCLRE1B	APOLLO, DCLRE1B, FLJ13995, SNM1B, DKFZp686C24187, FLJ12510, SNM1B, DKFZp686C24187	DNA cross-link repair 1B	NM_022836, XCT233330.0, XCT26861.2	219490_s_at, 223689_at	NP_073747.1, EAW56553.1, EAW56552.1
Gene:ID:84551	HIPK1	1	114,471,998	114,530,422	58,425	+	2	1_A270_sNU37_dhrsx_locRNA:1:-332,2_A270_sNU37_glrs_locRNA:1:-462	165, 164	at gene, us gene	1	1	20	21	1	1_A270_sNU37_dhrsx_loc:RNA:1	30	Gene:HIPK1	KIAA0630, Nbla2, Myak, HIPK1	homeodomain interacting protein kinase 1	NM_152696, NM_198166, NM_198268, NM_198269, NM_181358, XCT227559.2, XCT227556.0, XCT227559.0, XCT227560.0, XCT227559.0, XCT233330.0, XCT233332.0, XCT26657.2	1552513_at, 1552516_at_at, 212281_at, 212283_at	NP_689809.2, NP_938038.1, NP_938010.1, NP_938013.1, EAW56561.1, EAW56563.1, EAW56564.1, EAW56562.1, EAW56560.1
Gene:ID:5172	SYT6	1	114,631,914	114,699,472	64,868	-	2	1_A270_sNU37_dhrsx_locRNA:1:-333,2_A270_sNU37_glrs_locRNA:1:-463	39072, 23334	at gene, us gene	1	1	13.5	14.5	2	1_A270_sNU37_dhrsx_loc:RNA:1	16	Gene:SYT6	SYT6		NM_058048, XCT233356.0, XCT233355.0, XCT26858.2	244227_at	NP_996320.1, EAW56596.1, EAW56597.1, EAW56598.1
Gene:ID:512	CSDE1	1	115,258,537	115,300,671	41,134	+	1	2_A270_sNU37_glrs_locRNA:1:-463	255	at gene	0	1	14	19	1	2_A270_sNU37_glrs_locRNA:1	19	Gene:CSDE1	UNR, CSDE1, DKFZp779J1455, DJ313I5E, RP5-1005E10.2, DKFZp779B0247, FLJ26552	cold shock domain containing E1, RNA-binding	NM_007156, NM_001007553, NM_001130523, XCT227555.0, XCT227559.0, XCT227560.4, XCT227559.0, XCT227557.0, XCT227559.0, XCT233328.0, XCT26870.2	202495_s_at, 202496_s_at, 225975_s_at	NP_008954.6, NP_001007554.1, NP_001123995.1, EAW56613.1, EAW56614.1, EAW56615.1, EAW56612.1, EAW56616.1, EAW56617.1, EAW56618.1, EAW56619.1
Gene:ID:4193	SIX2	1	115,312,100	115,323,205	11,106	-	1	1_A270_sNU37_dhrsx_loc:RNA:1	140	at gene	1	0	24	14	1	1_A270_sNU37_dhrsx_loc:RNA:1	24	Gene:SIX2	DKFZp686A0765, SIX2, SIX1, FLJ21166	suppression of HBXE 1	NM_016370, NM_001162396, XCT26762.3	204953_at, 204956_s_at, 221703_s_at	NP_079548.2, NP_001080566.1, EAW56620.1
Gene:ID:4934	NSP	1	115,826,837	115,880,857	52,320	-	1	1_A270_sNU37_dhrsx_loc:RNA:1	27657	at gene	1	0	17	12	1	1_A270_sNU37_dhrsx_loc:RNA:1	17	Gene:NSP	NSP8, MGC161426, HSA9, MGC161428, Beta-NSP, NSP	sieve growth factor (beta polypeptide)	NM_002506, XCT26307.2	209814_at	NP_002497.2, EAW56629.1
Gene:ID:45	CASQ2	1	116,242,624	116,311,826	68,802	-	2	1_A270_sNU37_dhrsx_locRNA:1:-337,1_A270_sNU37_dhrsx_locRNA:1:-336	41122, 40349	at gene, us gene	1	0	16	11.5	2	2_A270_sNU37_glrs_locRNA:1	16	Gene:CASQ2	PDIB2, PLN3214, PLJD5321, CASQ2	calsequestrin 2 (cardiac muscle)	NM_001232, XCT27286.0, XCT27285.1	205317_s_at	NP_001222.2, EAW56638.1, EAW56636.1
Gene:ID:26958	C1orf61	1	116,654,376	116,677,861	23,485	+	1	1_A270_sNU37_dhrsx_loc:RNA:1:-466	11320	at gene	0	1	7	16	1	2_A270_sNU37_glrs_locRNA:1	16	Gene:C1orf61	MKB21-LS, PLJ33716, RP5-1155H19.1, Chr1f61	chromosome 1 open reading frame 161	NM_152367, XCT227553.1, XCT234852.0	1553333_at	NP_689502.2, EAW56640.1, EAW56642.1
Gene:ID:3005648	LOC100506489	1	117,035,636	117,041,834	6,196	-	2	1_A270_sNU37_dhrsx_locRNA:1:-339,2_A270_sNU37_glrs_locRNA:1:-471	-3526, -10070	upstream, upstream	1	1	15	15.5	2	1_A270_sNU37_dhrsx_loc:RNA:1	16	Gene:LOC100506489		hypothetical LOC100506489	XR_112104, XR_110662, XR_112712		
Gene:ID:63	CD58	1	117,057,156	117,113,715	56,559	-	3	1_A270_sNU37_dhrsx_locRNA:1:-339,2_A270_sNU37_glrs_locRNA:1:-471,2_A270_sNU37_glrs_locRNA:1:-472	66355, 61511, 66	downstream, downstream, at gene	1	1	14.33	17	3	2_A270_sNU37_glrs_locRNA:1	20	Gene:CD58	FLJ23161, CD58, FLJ43722, LFA3, LFA-3	CD58 molecule	NM_001144922, NM_001779, NR_026993, XCT19810751.1, XCT226216.0, XCT226219.0, XCT233263.0, XCT26359.2	208173_s_at, 211744_s_at, 216222_at, 216842_s_at, 220061_at	NP_001130294.1, NP_001770.1, EAW56952.1, EAW56954.1, EAW56953.1, EAW56955.1, EAW56956.1, EAW56953.1
Gene:ID:321	ICBP3	1	117,117,031	117,210,314	93,283	-	1	2_A270_sNU37_dhrsx_loc:RNA:1:-472	66698	downstream	0	1	13	20	1	2_A270_sNU37_glrs_locRNA:1	20	Gene:ICBP3	EWH3, MGC117164, V8, ICBP3	immunoglobulin superfamily, member 3	NM_001542, NM_001007237, XCT226216.0, XCT226215.0, XCT226166.0	1552672_s_at, 1554162_at, 1554163_at, 1554164_s_at	NP_001533.2, NP_001007238.1, EAW56937.1, EAW56938.1, EAW56939.1
Gene:ID:1	CD2	1	117,297,556	117,311,551	13,763	+	1	2_A270_sNU37_dhrsx_loc:RNA:1:-473	23555	downstream	0	1	8	16	1	2_A270_sNU37_glrs_locRNA:1	16	Gene:CD2	SRBC, T11, FLJ49032, CD2	CD2 molecule	NM_001767, XCT26313.2	205831_at	NP_001758.2, EAW56661.1
Gene:ID:9878	VTCN1	1	117,656,209	117,753,549	97,340	+	1	2_A270_sNU37_dhrsx_locRNA:1:-474	39025	at gene	0	1	9	19	1	2_A270_sNU37_glrs_locRNA:1	19	Gene:VTCN1	B7-H, B7-H4, RP11-232A16.4, B7H4, VCTN1, VTCN1, B7x, VCTN, B7S1, PRO1291, VTCN1, B7x, UCTN, B7S1, FLJ20486	V-set domain containing T cell activation inhibitor 1	NM_024626, XCT19304.0, XCT19862.25.1, XCT233634.0	219780_at	NP_078902.2, EAW56972.1, EAW56971.1, EAW56973.1
Gene:ID:913	TBX15	1	119,425,666	119,532,179	106,513	-	2	1_A270_sNU37_dhrsx_locRNA:1:-342,2_A270_sNU37_glrs_locRNA:1:-476	65931, 65967	at gene, us gene	1	1	16	20	1	2_A270_sNU37_glrs_locRNA:1	20	Gene:TBX15	TBX15, TBX1d	T-box 15	NM_152382, XCT229803.3	230458_at	NP_689943.2, EAW56991.1
Gene:ID:440420	LOC440420	1	120,140,325	120,141,814	1,589	-	1	1_A270_sNU37_dhrsx_loc:RNA:1:-477	4390	upstream	0	1	8	15	1	2_A270_sNU37_glrs_locRNA:1	15	Gene:LOC440420	FLJ41113	hypothetical LOC440420	NR_036340	1556404_at	
Gene:ID:9874	ZNF687	1	120,162,000	120,190,390	28,390	-	1	2_A270_sNU37_glrs_locRNA:1:-478	714	upstream	0	1	12	16	1	2_A270_sNU37_glrs_locRNA:1	16	Gene:ZNF687	ZNF687, MGC40701	Zinc finger protein 687	NM_001080470	1553702_at	NP_001073939.1
Gene:ID:653	NOTCH2	1	120,454,176	120,612,276	158,100	+	1	2_A270_sNU37_dhrsx_locRNA:1:-478	132	at gene	0	1	18	16	1	2_A270_sNU37_glrs_locRNA:1	16	Gene:NOTCH2	NOTCH2, hN2, XCL2	Notch homolog 2 (Drosophila)	NM_024408, XCT227537.1, XCT19880.2	202443_s_at, 202445_s_at, 210756_s_at, 212277_s_at	NP_077718.2, EAW56716.1, EAW56719.1
Gene:ID:939	PDE4DIP	1	144,651,427	145,076,079	224,652	+	3	1_A270_sNU37_dhrsx_locRNA:1:-338,1_A270_sNU37_glrs_locRNA:1:-346,1_A270_sNU37_glrs_locRNA:1:-350,1_A270_sNU37_glrs_locRNA:1:-462,2_A270_sNU37_glrs_locRNA:1:-483	143756, 66311, 22135, 164567, 143781	at gene, us gene, upstream, downstream, at gene, us gene	1	1	33	33.75	4	1_A270_sNU37_dhrsx_loc:RNA:1	42	Gene:PDE4DIP	DKFZp761X09, MGC75680, PDE4DIP, myomegalin	phosphodiesterase 4D interacting protein	NM_001002212, NM_001002811, NM_022339, NM_001082610, NM_014644	206672_s_at, 206700_s_at, 210305_at, 211751_at, 215579_at, 232099_at	NP_001002212.1, NP_001002811.1, NP_055459.4, NP_077730.3, NP_001002610.1
Gene:ID:3005697	LOC100506497	1	148,016,473	148,018,899	2,426	+	1	1_A270_sNU37_dhrsx_loc:RNA:1:-346	49805	upstream	1	0	32	35	1	1_A270_sNU37_dhrsx_loc:RNA:1	32	Gene:LOC100506497		hypothetical LOC100506971	XR_110632		
Gene:ID:554	SEC22B	1	149,095,407	149,116,622	20,310	+	1	2_A270_sNU37_glrs_locRNA:1:-464	2767	upstream	0	1	29	38	1	2_A270_sNU37_glrs_locRNA:1	38	Gene:SEC22B	SEC22B, ERS-24, SEC22U	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	NM_004892	209206_at, 209207_s_at, 214237_s_at	NP_004883.2
Gene:ID:3005698	LOC100506988	1	149,376,716	149,382,396	5,680	-	2	1_A270_sNU37_dhrsx_locRNA:1:-351,2_A270_sNU37_glrs_locRNA:1:-483	-260, -260	upstream, upstream	1	1	26	35	1	2_A270_sNU37_glrs_locRNA:1	35	Gene:LOC100506988		hypothetical LOC100506988	XR_110633		
Gene:ID:4265	POLR2GL	1	149,686,236	149,700,397	14,161	-	1	2_A270_sNU37_glrs_locRNA:1:-488	-237	upstream	0	1	18	23	1	2_A270_sNU37_glrs_locRNA:1	23	Gene:POLR2GL	POLR2L, RPC12/HOM, hRPC12/22, MGC2332, FLJ34880	polymerase (RNA) III (DNA directed) polypeptide G (32/33kD)	NM_032305, XCT235492.0, XCT234872.0, XCT26911.2	223269_at	NP_115651.1, EAW71412.1, EAW71412.1, EAW71413.1
Gene:ID:84618	ANKRD34A	1	149,470,566	149,479,647	9,138	+	1	2_A270_sNU37_glrs_locRNA:1:-488	116	at gene	0	1	18	23	1	2_A270_sNU37_glrs_locRNA:1	23	Gene:ANKRD34A	ANKRD34, ANKRD34, DKFZp761F252	ankyrin repeat domain 34A	NM_001039555	232733_at	NP_001034977.1
Gene:ID:28077	LIX1L	1	149,477,055	149,499,091	22,036	+	3	1_A270_sNU37_dhrsx_locRNA:1:-335,2_A270_sNU37_glrs_locRNA:1:-459,2_A270_sNU37_glrs_locRNA:1:-480	50691, 6461, 50387	downstream, downstream, downstream	1	1	20.5	20	2	2_A270_sNU37_glrs_locRNA:1	23	Gene:LIX1L	MGC40719, DKFZp762F237, LIX1L	Lix1 homolog (mouse) like	NM_133713, XCT229109.0, XCT19907.1	235793_at, 238636_at	NP_714824.1, EAW71417.1, EAW71416.1
Gene:ID:928	RBM8A	1	149,507,635	149,511,444	3,809	+	4	1_A270_sNU37_dhrsx_locRNA:1:-335,1_A270_sNU37_glrs_locRNA:1:-339,2_A270_sNU37_glrs_locRNA:1:-480,2_A270_sNU37_glrs_locRNA:1:-484	138, 5198, 166, 5668	at gene, downstream, upstream, downstream	1	1	23	16	2	2_A270_sNU37_glrs_locRNA:1	24	Gene:RBM8A	BOV1C, BOV1A, RBM8B, RBME, BOV-1B, ZRNP1, RBM8A, ZNRP, MDS014, Y14	RNA binding motif protein 8A	NM_005105, XCT229109F.1, XCT23901.0.0	1804602_at, 212652_at, 214113_s_at, 217896_at, 217897_s_at, 222443_s_at	NP_003080.1, EAW71418.1, EAW71418.1
Gene:ID:7998	PEX11B	1	149,516,165	149,523,732	7,567	+	4	1_A270_sNU37_dhrsx_locRNA:1:-335,1_A270_sNU37_glrs_locRNA:1:-339,2_A270_sNU37_glrs_locRNA:1:-480,2_A270_sNU37_glrs_locRNA:1:-484	4309, 59, 8693, 171	upstream, at gene, upstream, at gene	1	1	23	16	2	1_A270_sNU37_dhrsx_loc:RNA:1	24	Gene:PEX11B	PEX11B, PEX11-BETA	peroxisomal biogenesis factor 11 beta	NM_001164785, NM_003846, XCT229110.1, XCT26904.3	202858_at	NP_001157724.1, NP_003527.1, EAW71422.1, EAW71423.1
Gene:ID:3675	ITGA10	1	149,524,990	149,543,868	18,878	-	2	1_A270_sNU37_dhrsx_locRNA:1:-339,2_A270_sNU37_glrs_locRNA:1:-480	-4766, 8654	upstream, upstream	1	1	24	19	1	1_A270_sNU37_dhrsx_loc:RNA:1	24	Gene:ITGA10	FRG27, ITGA10	integrin, alpha 10	NM_003637, XCT229110.0, XCT26906.2	206766_at	NP_003626.2, EAW71424.1, EAW71429.1
Gene:ID:84741	ANKRD33	1	149,549,209	149,565,526	16,317	+	1	2_A270_sNU37_glrs_locRNA:1:-482	26539	downstream	0	1	16	23	1	2_A270_sNU37_glrs_locRNA:1	23	Gene:ANKRD33	MGC136857, ANKRD33, MGC129668, ANKRD33	ankyrin repeat domain 33	NM_148568, XCT234419.1, XCT235221.0	231116_at	NP_683299.3, EAW71427.1, EAW71426.1
Gene:ID:5401	PIAS3	1	149,575,565	149,586,546	10,982	+	2	1_A270_sNU37_dhrsx_locRNA:1:-337,2_A270_sNU37_glrs_locRNA:1:-482	13464, 60	downstream, at gene	1	1	16	21	2	2_A270_sNU37_glrs_locRNA:1	23	Gene:PIAS3	DKFZp761A1121, PIAS3, PIAS1	protein inhibitor of activated STAT, 3	NM_006099, XCT229110.0, XCT229110.1, XCT26139.0	203033_s_at	NP_006082.2, EAW71430.1, EAW71429.1, EAW71431.1
Gene:ID:9231	NUDT17	1	149,586,491	149,589,435	2,944	-	1	1_A270_sNU37_dhrsx_loc:RNA:1:-337	-37	upstream	1	0	16	19	1	1_A270_sNU37_dhrsx_loc:RNA:1	19	Gene:NUDT17	NUDT17, FLJ34433	nudix (nucleoside diphosphate linked moiety X)-type motif 17	NM_001012756, XCT19965.7.1, XCT19965.7.2	1561687_at, 221884_at	NP_001012756.1, EAW71432.1, EAW71432.1
Gene:ID:5423	POLR3C	1	149,592,805	149,610,864	18,279	+	3	1_A270_sNU37_dhrsx_locRNA:1:-339,2_A270_sNU37_glrs_locRNA:1:-480,2_A270_sNU37_glrs_locRNA:1:-484	21412, -25, -188	downstream, upstream, upstream	1	1	16.5	23.5	2	2_A270_sNU37_glrs_locRNA:1	24	Gene:POLR3C	RPC3, RPC62, POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	NM_006466, XCT19979.67.1, XCT235131.0, XCT26932.3	208362_at, 210573_s_at	NP_006454.2, EAW71436.1, EAW71434.1, EAW71433.1
Gene:ID:7246	RNF115	1	149,611,036	149,668,776	57,740	+	2	1_A270_sNU37_dhrsx_locRNA:1:-339,2_A270_sNU37_glrs_locRNA:1:-480	-124, 36	upstream, at gene	1	1	21	26	1	2_A270_sNU37_glrs_locRNA:1	26	Gene:RNF115	BCA2, ZNF364, RNF115	ring finger protein 115	NM_014455, XCT235490.0, XCT19815.2	212742_at	NP_055270.1, EAW71437.1, EAW71438.1
Gene:ID:3005972	LOC100506972	1	149,673,522	149,674,203	671	-	1	2_A270_sNU37_glrs_locRNA:1:-484	865	at gene	0	1	7	16	1	2_A270_sNU37_glrs_locRNA:1	16	Gene:LOC100506972		hypothetical LOC100506722	XR_110630, XR_110621		
Gene:ID:3005975	LOC100506975	1	149,673,555	149,674,529	10,974	+	1	2_A270_sNU37_glrs_locRNA:1:-484	173	at gene	0	1	7	16	1	2_A270_sNU37_glrs_locRNA:1	16	Gene:LOC100506975		hypothetical LOC100506752	XR_110622		
Gene:ID:955	PRKAB2	1	149,828,655	149,844,129	17,464	-	2	1_A270_sNU37_dhrsx_locRNA:1:-390,2_A270_sNU37_glrs_locRNA:1:-488	463, -191	upstream, upstream	1	1	27	29	1	2_A270_sNU37_glrs_locRNA:1	29	Gene:PRKAB2	PRKAB2, MGC61466	protein kinase, AMP-activated, beta 2 non-catalytic subunit	NM_005399, XCT12322.2	1555027_s_at, 214479_s_at, 226276_at	NP_005390.1, EAW69845.1
Gene:ID:3005976	LOC100506976	1	149,844,326	149,851,643	37,317	+	2	1_A270_sNU37_dhrsx_locRNA:1:-390,2_A270_sNU37_glrs_locRNA:1:-488	-134, -4	upstream, upstream	1	1	27	29	1	2_A270_sNU37_glrs_locRNA:1	29	Gene:LOC100506976		hypothetical LOC100506794	XR_110623, XR_110624		
Gene:ID:330	FMO5	1	149,855,554	149,897,230	41,396	+	1	2_A270_sNU37_glrs_locRNA:1:-347	236	at gene	0	1	16	14	1	2_A270_sNU37_glrs_locRNA:1	14	Gene:FMO5	FMO5		NM_001461, NM_001144629, NM_001144630, XCT23997.0, XCT23949.0.1, XCT23949.0.2, XCT23949.0.3	1569655_at, 1570776_at, 1570777_s_at, 1570778_at, 1570779_at	NP_001452.2, NP_001130301.1, NP_001130302.1, EAW56840.1, EAW56841.1, EAW56842.1, EAW56839.1, EAW56842.1
Gene:ID:557	CHD1L	1	149,714,291	149,797,843	83,152	+	2	1_A270_sNU37_dhrsx_locRNA:1:-390,2_A270_sNU37_glrs_locRNA:1:-488	-51, 13	upstream, at gene	1	1	21	24	1	2_A270_sNU37_glrs_locRNA:1	24	Gene:CHD1L	ALC1, CHD1L, PLJ22533, CHD1L	Chromodomain helicase DNA binding protein 1-like	NM_004284, XCT235592.0, XCT235593.0	1559555_s_at, 207643_s_at, 212539_at, 226570_at, 244548_at	NP_004275.3, EAW69836.1, EAW69837.1, EAW69838.1
Gene:ID:27	BCL8	1	147,013,152	147,098,017	84,865	+	3	1_A270_sNU37_dhrsx_locRNA:1:-392,2_A270_sNU37_glrs_locRNA:1:-499,2_A270_sNU37_glrs_locRNA:1:-500	56226, -6810, 58194	at gene, upstream, at gene	1	1	16	26	2	2_A270_sNU37_glrs_locRNA:1	27	Gene:BCL8	BCL9, LGS, MGC131991	B-cell CLL/lymphoma 8	NM_004326, XCT235596.0, XCT26963.2	208129_at	NP_004317.2, EAW69932.1, EAW69933.1
Gene:ID:1203	ACP6	1	147,119,165	147,142,634	23,486	-	2	1_A270_sNU37_dhrsx_locRNA:1:-394,2_A270_sNU37_glrs_locRNA:1:-501,2_A270_sNU37_glrs_locRNA:1:-505	-26, -54, 6422	upstream, upstream, upstream	1	1	16.5	20.5	2	2_A270_sNU37_glrs_locRNA:1	25	Gene:ACP6	ACP6, ACPL1, PACPL1, LPAP	acid phosphatase 6, lysophosphatidic	NM_015361, XCT235270.5	218793_at	NP_056145.3, EAW69931.1
Gene:ID:702	GJA5	1	147,226,332	147,249,484	17,152	-	2	1_A270_sNU37_dhrsx_locRNA:1:-395,2_A270_sNU37_glrs_locRNA:1:-503	22556, 22639	downstream, downstream	1	1	30	41	1	2_A270_sNU37_glrs_locRNA:1	41	Gene:GJA5	GJA5, CX40, MGC111165	gap junction protein, alpha 5, 40kDa	NM_005266, NM_181703, XCT23948.2.0, XCT19900.4.2	214695_at, 236101_at	NP_005257.2, NP_859064.1, EAW69829.1, EAW69830.1
Gene:ID:5832	NBPF14	1	148,003,642	148,025,848	22,206	+	2	1_A270_sNU37_dhrsx_locRNA:1:-396,2_A270_sNU37_glrs_locRNA:1:-506	28112, 28120	downstream, downstream	1	1	30	34	1	2_A270_sNU37_glrs_locRNA:1	34	Gene:NBPF14	FLJ38032, FLJ60320, DJ326E19.C1.1, NBPF14, NBPF	neuroblastoma breakpoint family, member 14	NM_015362		NP_056189.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:6281	S100A10	1	151,955,386	151,966,714	11,328	-	2	2_A375_pNL97_plus_lncRNA::1::541, 2_A375_pNL97_plus_lncRNA::1::542	13786, 1818	downstream, in gene	0	1	14.5	25	2	2_A375_pNL97_plus_lncRNA::1	32	Gene S100A10	42C, Cal[1], CLP11, MGC111133, ANX2L, CAL1L, p10, P11, GP11, S100A10, ANX2LG	S100 calcium binding protein A10	NM_002966, hCT1812305.1, hCT1816945.1, hCT7961.2	200872_at, 238909_at	NP_002957.1, EAW53398.1, EAW53397.1, EAW53399.1
GeneID:6282	S100A11	1	152,004,982	152,009,511	4,529	-	2	2_A375_pNL97_plus_lncRNA::1::543, 2_A375_pNL97_plus_lncRNA::1::544	7763, 2247	downstream, in gene	0	1	10.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene S100A11	S100A11, MLN70, S100C	S100 calcium binding protein A11	NM_005620, hCT7962.2	200660_at	NP_005611.1, EAW53392.1
GeneID:6704	SPRR2E	1	153,065,611	153,067,001	1,390	-	1	1_A375_pNL7_minus_lncRNA::1::395	-5895	upstream	1	0	19	13	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SPRR2E	SPRR2E		NM_001024209		NP_001019380.2
GeneID:338324	S100A7A	1	153,389,000	153,395,701	6,701	+	2	1_A375_pNL7_minus_lncRNA::1::396, 2_A375_pNL97_plus_lncRNA::1::548	6168, 6136	in gene, in gene	1	1	30	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene S100A7A	NICE-2, S100A7L1, S100A15, S100A7A, S100A7f	S100 calcium binding protein A7A	NM_176823	232170_at	NP_789793.1
GeneID:6278	S100A7	1	153,430,220	153,433,137	2,917	-	2	1_A375_pNL7_minus_lncRNA::1::397, 2_A375_pNL97_plus_lncRNA::1::549	8065, 8145	downstream, downstream	1	1	30	27	1	1_A375_pNL7_minus_lncRNA::1	30	Gene S100A7	S100A7, S100A7c, PSOR1	S100 calcium binding protein A7	NM_002963, hCT87242.3	205916_at	NP_002954.2, EAW53327.1
GeneID:100505623	LOC100505623	1	153,506,062	153,507,593	1,531	+	5	1_A375_pNL7_minus_lncRNA::1::398, 1_A375_pNL7_minus_lncRNA::1::399, 2_A375_pNL97_plus_lncRNA::1::551, 2_A375_pNL97_plus_lncRNA::1::552, 2_A375_pNL97_plus_lncRNA::1::553	418, 2226, 466, 2258, 11762	in gene, downstream, in gene, downstream, downstream	1	1	22	23.67	3	2_A375_pNL97_plus_lncRNA::1	29	Gene LOC100505623		hypothetical LOC100505623	XR_111941, XR_108353, XR_114806		
GeneID:6277	S100A6	1	153,507,076	153,508,717	1,641	-	5	1_A375_pNL7_minus_lncRNA::1::398, 1_A375_pNL7_minus_lncRNA::1::399, 2_A375_pNL97_plus_lncRNA::1::551, 2_A375_pNL97_plus_lncRNA::1::552, 2_A375_pNL97_plus_lncRNA::1::553	2237, 429, 2189, 397, -9107	downstream, in gene, downstream, in gene, upstream	1	1	22	23.67	3	2_A375_pNL97_plus_lncRNA::1	29	Gene S100A6	5B10, PRA, 2A9, CACY, CABP, S100A6	S100 calcium binding protein A6	NM_014624, hCT1952276.1, hCT1952279.2, hCT2343687.0, hCT2343688.0, hCT2343689.0, hCT2343690.0, hCT2343691.0, hCT2343692.0, hCT2343693.0	217728_at, 228923_at	NP_055439.1, EAW53318.1, EAW53319.1, EAW53320.1, EAW53324.1, EAW53326.1, EAW53321.1, EAW53322.1, EAW53323.1, EAW53325.1
GeneID:6276	S100A5	1	153,509,623	153,514,241	4,618	-	5	1_A375_pNL7_minus_lncRNA::1::398, 1_A375_pNL7_minus_lncRNA::1::399, 2_A375_pNL97_plus_lncRNA::1::551, 2_A375_pNL97_plus_lncRNA::1::552, 2_A375_pNL97_plus_lncRNA::1::553	7761, 5953, 7713, 5921, -3583	downstream, downstream, downstream, downstream, upstream	1	1	22	23.67	3	2_A375_pNL97_plus_lncRNA::1	29	Gene S100A5	S100A5, S100D	S100 calcium binding protein A5	NM_002962, hCT1809062.0, hCT6490.0	207763_at	NP_002953.2, EAW53316.1, EAW53317.1
GeneID:6275	S100A4	1	153,516,095	153,518,282	2,187	-	5	1_A375_pNL7_minus_lncRNA::1::398, 1_A375_pNL7_minus_lncRNA::1::399, 2_A375_pNL97_plus_lncRNA::1::551, 2_A375_pNL97_plus_lncRNA::1::552, 2_A375_pNL97_plus_lncRNA::1::553	11802, 9994, 11754, 9962, 458	downstream, downstream, downstream, downstream, in gene	1	1	22	23.67	3	2_A375_pNL97_plus_lncRNA::1	29	Gene S100A4	S100A4, CAPL, PEL98, FSP1, 42A, 18A2, MTS1, P9KA	S100 calcium binding protein A4	NM_002961, NM_019554, hCT2344333.0, hCT2344335.0, hCT2344338.0, hCT2344339.0, hCT2344340.0, hCT2344341.0	203186_s_at	NP_002952.1, NP_062427.1, EAW53310.1, EAW53311.1, EAW53312.1, EAW53315.1, EAW53313.1, EAW53314.1
GeneID:6274	S100A3	1	153,519,809	153,521,734	1,925	-	1	2_A375_pNL97_plus_lncRNA::1::553	3910	downstream	0	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene S100A3	S100E, S100A3	S100 calcium binding protein A3	NM_002960, hCT2344332.0, hCT2344334.0, hCT2344336.0, hCT2344337.0	206027_at	NP_002951.1, EAW53307.1, EAW53306.1, EAW53308.1, EAW53309.1
GeneID:6273	S100A2	1	153,533,584	153,538,306	4,722	-	4	1_A375_pNL7_minus_lncRNA::1::400, 1_A375_pNL7_minus_lncRNA::1::401, 2_A375_pNL97_plus_lncRNA::1::554, 2_A375_pNL97_plus_lncRNA::1::555	-766, -2782, -62, -2462	upstream, upstream, upstream, upstream	1	1	22.5	20.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene S100A2	MGC111539, S100A2, CAN19, S100L	S100 calcium binding protein A2	NM_005978, hCT6496.3	204268_at	NP_005969.1, EAW53305.1
GeneID:140576	S100A16	1	153,579,367	153,585,514	6,147	-	2	1_A375_pNL7_minus_lncRNA::1::402, 2_A375_pNL97_plus_lncRNA::1::556	4266, 4058	in gene, in gene	1	1	21	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene S100A16	MGC17528, DT1P1A7, S100F, AAG13, S100A16	S100 calcium binding protein A16	NM_080388, hCT1781988.2, hCT2276710.0	227998_at	NP_525127.1, EAW53303.1, EAW53304.1
GeneID:57402	S100A14	1	153,586,731	153,588,790	2,059	-	2	1_A375_pNL7_minus_lncRNA::1::402, 2_A375_pNL97_plus_lncRNA::1::556	7542, 7334	downstream, downstream	1	1	21	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene S100A14	S100A15, BCMP84, S100A14	S100 calcium binding protein A14	NM_020672	218677_at	NP_065723.1
GeneID:6284	S100A13	1	153,591,275	153,606,568	15,293	-	4	1_A375_pNL7_minus_lncRNA::1::402, 1_A375_pNL7_minus_lncRNA::1::403, 2_A375_pNL97_plus_lncRNA::1::556, 2_A375_pNL97_plus_lncRNA::1::557	25320, 7048, 25112, -88	downstream, in gene, downstream, upstream	1	1	17.33	21.33	3	2_A375_pNL97_plus_lncRNA::1	27	Gene S100A13	S100A13		NM_005979, NM_001024210, NM_001024211, NM_001024212, NM_001024213, hCT1781970.3, hCT1952280.1, hCT1952281.1, hCT1952282.2, hCT1952283.2	202598_at, 213461_at	NP_005970.1, NP_001019381.1, NP_001019382.1, NP_001019383.1, NP_001019384.1, EAW53299.1, EAW53296.1, EAW53297.1, EAW53298.1, EAW53300.1
GeneID:6271	S100A1	1	153,600,873	153,604,512	3,639	+	2	1_A375_pNL7_minus_lncRNA::1::403, 2_A375_pNL97_plus_lncRNA::1::557	-1353, 5783	upstream, downstream	1	1	15.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene S100A1	S100A1, S100-alpha, S100A, S100	S100 calcium binding protein A1	NM_006271, hCT1952273.1, hCT6494.2	205334_at	NP_006262.1, EAW53301.1, EAW53302.1
GeneID:26097	C1orf77	1	153,606,525	153,617,979	11,454	+	2	1_A375_pNL7_minus_lncRNA::1::403, 2_A375_pNL97_plus_lncRNA::1::557	-7005, 131	upstream, in gene	1	1	15.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene C1orf77	FLJ40551, pp7704, MGC131924, RP1-178F15.2, C1orf77, MGC86949, SRAG, CHTOP, DKFZp547E1010, FOP	chromatin target of PRMT1	NM_015607, hCT1812976.2, hCT2277539.0, hCT2277543.1, hCT2352625.0, hCT2352626.0, hCT6493.2	202559_x_at, 202560_s_at, 209927_s_at	NP_056422.2, EAW53295.1, EAW53290.1, EAW53291.1, EAW53293.1, EAW53294.1, EAW53292.1
GeneID:65123	INTS3	1	153,700,567	153,746,555	45,988	+	2	1_A375_pNL7_minus_lncRNA::1::404, 2_A375_pNL97_plus_lncRNA::1::558	-375, -391	upstream, upstream	1	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene INTS3	DKFZp761I1253, FLJ44549, SOSS-A, C1orf193, C1orf60, INTS3, DKFZp686E1950, FLJ21919, DKFZp686O20115, INT3	integrator complex subunit 3	NM_023015, hCT2277561.0, hCT2277567.0, hCT2277570.0, hCT2277572.0, hCT2277574.0	202809_s_at	NP_075391.3, EAW53279.1, EAW53280.1, EAW53281.1, EAW53282.1, EAW53283.1
GeneID:9909	DENND4B	1	153,901,977	153,919,154	17,177	-	2	1_A375_pNL7_minus_lncRNA::1::405, 2_A375_pNL97_plus_lncRNA::1::559	-110, -46	upstream, upstream	1	1	55	56	1	2_A375_pNL97_plus_lncRNA::1	56	Gene DENND4B	FLJ26202, KIAA0476, DKFZp762N174, DENND4B	DENN/MADD domain containing 4B	NM_014856	202860_at	NP_055671.2
GeneID:200186	CRTC2	1	153,920,151	153,931,043	10,892	-	5	1_A375_pNL7_minus_lncRNA::1::405, 1_A375_pNL7_minus_lncRNA::1::406, 2_A375_pNL97_plus_lncRNA::1::559, 2_A375_pNL97_plus_lncRNA::1::560, 2_A375_pNL97_plus_lncRNA::1::561	11779, -125, 11843, -109, -4845	downstream, upstream, downstream, upstream, upstream	1	1	33.33	31	3	2_A375_pNL97_plus_lncRNA::1	56	Gene CRTC2	TORC2, RP11-422P24.6, CRTC2	CREB regulated transcription coactivator 2	NM_181715	226307_at	NP_859066.1
GeneID:27173	SLC39A1	1	153,931,568	153,940,168	8,600	-	5	1_A375_pNL7_minus_lncRNA::1::406, 1_A375_pNL7_minus_lncRNA::1::407, 2_A375_pNL97_plus_lncRNA::1::560, 2_A375_pNL97_plus_lncRNA::1::561, 2_A375_pNL97_plus_lncRNA::1::562	9020, -10084, 9036, 4300, -10063	downstream, upstream, downstream, in gene, upstream	1	1	22.33	18	3	1_A375_pNL7_minus_lncRNA::1	27	Gene SLC39A1	ZIRTL, SLC39A1, ZIP1	solute carrier family 39 (zinc transporter), member 1	NM_014437	217778_at	NP_055252.2
GeneID:148327	CREB3L4	1	153,940,397	153,946,832	6,435	+	5	1_A375_pNL7_minus_lncRNA::1::406, 1_A375_pNL7_minus_lncRNA::1::407, 2_A375_pNL97_plus_lncRNA::1::560, 2_A375_pNL97_plus_lncRNA::1::561, 2_A375_pNL97_plus_lncRNA::1::562	-9229, 9875, -9245, -4509, 9654	upstream, downstream, upstream, upstream, downstream	1	1	22.33	18	3	1_A375_pNL7_minus_lncRNA::1	27	Gene CREB3L4	hJAL, CREB3, CREB4, AIBZIP, JAL, CREB3L4, ATCE1	cAMP responsive element binding protein 3-like 4	NM_130898, hCT1964212.1, hCT1964213.0, hCT2277563.0, hCT2277564.0, hCT2352671.0, hCT2352672.0, hCT2352673.0, hCT88033.3	226455_at	NP_570968.1, EAW53251.1, EAW53253.1, EAW53254.1, EAW53255.1, EAW53258.1, EAW53252.1, EAW53256.1, EAW53257.1
GeneID:10899	JTB	1	153,946,745	153,950,451	3,706	-	2	1_A375_pNL7_minus_lncRNA::1::407, 2_A375_pNL97_plus_lncRNA::1::562	179, 200	in gene, in gene	1	1	22	18	1	1_A375_pNL7_minus_lncRNA::1	22	Gene JTB	HSPC222, HJTB, JTB, hJT, PAR	jumping translocation breakpoint	NM_006694	200048_s_at, 210434_x_at, 210927_x_at	NP_006685.1
GeneID:5872	RAB13	1	153,954,127	153,958,806	4,679	-	3	1_A375_pNL7_minus_lncRNA::1::407, 2_A375_pNL97_plus_lncRNA::1::562, 2_A375_pNL97_plus_lncRNA::1::563	8534, 8555, -4346	downstream, downstream, upstream	1	1	18	20	2	1_A375_pNL7_minus_lncRNA::1	22	Gene RAB13	RAB13, GIG4	RAB13, member RAS oncogene family	NM_002870	202252_at	NP_002861.1
GeneID:6232	RPS27	1	153,963,239	153,964,631	1,392	+	1	2_A375_pNL97_plus_lncRNA::1::563	-67	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene RPS27	MPS-1, RPS27, S27, MPS1	ribosomal protein S27	NM_001030, hCT1765054.2, hCT1964201.0	200741_s_at, 236621_at	NP_001021.1, EAW53239.1, EAW53240.1
GeneID:91181	NUP210L	1	153,965,166	154,127,592	162,426	-	1	2_A375_pNL97_plus_lncRNA::1::563	164440	downstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene NUP210L	NUP210L, RP11-144B19.1	nucleoporin 210kDa-like	NM_207308, NM_001159484, hCT1765057.2	232598_at	NP_997191.2, NP_001152956.1, EAW53238.1
GeneID:7170	TPM3	1	154,127,780	154,164,609	36,829	-	2	1_A375_pNL7_minus_lncRNA::1::408, 2_A375_pNL97_plus_lncRNA::1::564	8665, 9165	in gene, in gene	1	1	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene TPM3	TPM3, OK/SW-cl.5, TPMsk3, MGC14582, MGC3261, MGC72094, TM3, TM30nm, TM30, TM-5, hscp30, NEM1, TRK, FLJ41118	tropomyosin 3	NM_153649, NM_152263, NM_001043351, NM_001043352, NM_001043353, hCT2278510.0, hCT2278511.0, hCT2278512.0, hCT2278513.0, hCT2278514.0, hCT2278515.0, hCT2278516.0, hCT2278517.0, hCT2278518.0	214365_at, 222976_s_at, 224164_at, 238065_at, 238079_at	NP_705935.1, NP_689476.2, NP_001036816.1, NP_001036817.1, NP_001036818.1, EAW53234.1, EAW53229.1, EAW53230.1, EAW53231.1, EAW53232.1, EAW53233.1, EAW53235.1, EAW53236.1, EAW53237.1
GeneID:100126346	MIR190B	1	154,166,141	154,166,219	78	-	1	1_A375_pNL7_minus_lncRNA::1::408	10475	downstream	1	0	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene MIR190B	MIRN190B, MIR190B	microRNA 190b	NR_030600		
GeneID:25912	C1orf43	1	154,179,183	154,193,273	14,090	-	1	2_A375_pNL97_plus_lncRNA::1::565	25	in gene	0	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C1orf43	S863-3, MGC111001, HSPC012, C1orf43, NS5ATP4, NICE-3, DKFZp586G1722	chromosome 1 open reading frame 43	NM_001098616, NM_015449, NM_138740, hCT1960948.1, hCT2278506.0, hCT2278507.0, hCT2278508.0, hCT2352680.0, hCT2352681.0, hCT2352682.0	1555225_at, 1555226_s_at, 223034_s_at	NP_001092086.1, NP_056264.1, NP_620077.1, EAW53222.1, EAW53223.1, EAW53227.1, EAW53221.1, EAW53224.1, EAW53225.1, EAW53226.1
GeneID:9898	UBAP2L	1	154,192,655	154,243,329	50,674	+	1	2_A375_pNL97_plus_lncRNA::1::565	593	in gene	0	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene UBAP2L	FLJ42300, UBAP2L, NICE-4, KIAA0144	ubiquitin associated protein 2-like	NM_001127320, NM_014847, hCT1950715.1, hCT2260175.0, hCT2260177.0, hCT2260178.0, hCT2260180.0, hCT2260181.0, hCT2352610.0, hCT29534.2	201377_at, 201378_s_at, 209947_at, 214695_at	NP_001120792.1, NP_055662.3, EAW53213.1, EAW53214.1, EAW53219.1, EAW53220.1, EAW53215.1, EAW53216.1, EAW53217.1, EAW53218.1
GeneID:89872	AQP10	1	154,293,592	154,297,801	4,209	+	1	2_A375_pNL97_plus_lncRNA::1::566	4989	downstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene AQP10	AQP10, AQPA_HUMAN	aquaporin 10	NM_080429, hCT1967451.1, hCT2260183.0, hCT29536.2	1555338_s_at	NP_536354.2, EAW53211.1, EAW53209.1, EAW53210.1
GeneID:57198	ATP8B2	1	154,298,036	154,323,780	25,744	+	1	2_A375_pNL97_plus_lncRNA::1::566	545	in gene	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ATP8B2	DKFZp434M0219, ATP8B2, KIAA1137, ATPID	ATPase, class I, type 8B, member 2	NM_001005855, NM_020452, hCT2260188.0, hCT2260189.0, hCT2352613.0, hCT2352614.0, hCT29537.2	216873_s_at, 226771_at	NP_001005855.1, NP_065185.1, EAW53204.1, EAW53205.1, EAW53207.1, EAW53208.1, EAW53206.1
GeneID:3570	IL6R	1	154,377,669	154,440,188	62,519	+	1	2_A375_pNL97_plus_lncRNA::1::567	1115	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene IL6R	IL-6R-1, CD126, MGC104991, IL6RA, IL-6R-alpha, IL6R	interleukin 6 receptor	NM_181359, NM_000565, hCT1950712.1, hCT2260196.0, hCT2352647.0	205945_at, 217489_s_at, 226333_at	NP_852004.1, NP_000556.1, EAW53199.1, EAW53200.1, EAW53201.1
GeneID:55585	UBE2Q1	1	154,521,051	154,531,120	10,069	-	4	1_A375_pNL7_minus_lncRNA::1::409, 1_A375_pNL7_minus_lncRNA::1::410, 2_A375_pNL97_plus_lncRNA::1::568, 2_A375_pNL97_plus_lncRNA::1::569	-256, -9296, -304, -9296	upstream, upstream, upstream, upstream	1	1	27	31	2	2_A375_pNL97_plus_lncRNA::1	40	Gene UBE2Q1	UBE2Q1, PRO3094, UBE2Q, GTAP, NICE-5	ubiquitin-conjugating enzyme E2Q family member 1	NM_017582, hCT22719.2	217978_s_at, 222480_at, 231816_s_at	NP_060052.3, EAW53193.1
GeneID:1141	CHRNB2	1	154,540,257	154,552,354	12,097	+	4	1_A375_pNL7_minus_lncRNA::1::409, 1_A375_pNL7_minus_lncRNA::1::410, 2_A375_pNL97_plus_lncRNA::1::568, 2_A375_pNL97_plus_lncRNA::1::569	-8881, 159, -8833, 159	upstream, in gene, upstream, in gene	1	1	27	31	2	2_A375_pNL97_plus_lncRNA::1	40	Gene CHRNB2	CHRNB2, nAChRB2, EFNL3	cholinergic receptor, nicotinic, beta 2 (neuronal)	NM_000748, hCT8794.3	206635_at, 241389_at	NP_000739.1, EAW53192.1
GeneID:103	ADAR	1	154,554,533	154,600,456	45,923	-	2	2_A375_pNL97_plus_lncRNA::1::570, 2_A375_pNL97_plus_lncRNA::1::571	19880, 168	in gene, in gene	0	1	16.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene ADAR	DSRAD, DRADA, K88dsRBP, P136, IFI4, G1P1, p136, K88DSRBP, ADAR, DSH, ADAR1, IFI-4	adenosine deaminase, RNA-specific	NM_001111, NM_001025107, NM_015840, NM_015841, NM_001193495, hCT1962283.1, hCT2278483.0, hCT2278484.0, hCT2278485.0, hCT2278487.0, hCT2278489.0, hCT2352674.0, hCT9875.2	201786_s_at	NP_001102.2, NP_001020278.1, NP_056655.2, NP_056656.2, NP_001180424.1, EAW53189.1, EAW53183.1, EAW53184.1, EAW53185.1, EAW53186.1, EAW53187.1, EAW53188.1, EAW53190.1
GeneID:10654	PMVK	1	154,897,208	154,909,484	12,276	-	2	1_A375_pNL7_minus_lncRNA::1::411, 2_A375_pNL97_plus_lncRNA::1::572	172, 124	in gene, in gene	1	1	40	41	1	2_A375_pNL97_plus_lncRNA::1	41	Gene PMVK	PMVK, HUMPMKI, PMKA, PMKASE, PMK	phosphomevalonate kinase	NM_006556, hCT1777356.2, hCT1964606.1	203515_s_at	NP_006547.1, EAW53177.1, EAW53178.1
GeneID:57326	PBXIP1	1	154,916,556	154,928,567	12,011	-	4	1_A375_pNL7_minus_lncRNA::1::411, 1_A375_pNL7_minus_lncRNA::1::412, 2_A375_pNL97_plus_lncRNA::1::572, 2_A375_pNL97_plus_lncRNA::1::573	19255, -5769, 19207, -5769	downstream, upstream, downstream, upstream	1	1	33.5	39.5	2	2_A375_pNL97_plus_lncRNA::1	41	Gene PBXIP1	HPIP, PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	NM_020524, hCT2278476.1, hCT2278478.0, hCT2352750.0	207838_x_at, 212259_s_at, 214176_s_at, 214177_s_at	NP_065385.2, EAW53174.1, EAW53175.1, EAW53176.1
GeneID:90780	PYGO2	1	154,929,502	154,934,258	4,756	-	3	1_A375_pNL7_minus_lncRNA::1::412, 2_A375_pNL97_plus_lncRNA::1::573, 2_A375_pNL97_plus_lncRNA::1::574	-78, -78, -8582	upstream, upstream, upstream	1	1	23.5	31	2	2_A375_pNL97_plus_lncRNA::1	38	Gene PYGO2	1190004M21Rik, FLJ33226, PYGO2	pygopus homolog 2 (Drosophila)	NM_138300, hCT2344269.0, hCT2344270.0	225370_at, 239666_at	NP_612157.1, EAW53172.1, EAW53173.1
GeneID:6464	SHC1	1	154,934,774	154,946,959	12,185	-	4	1_A375_pNL7_minus_lncRNA::1::412, 2_A375_pNL97_plus_lncRNA::1::573, 2_A375_pNL97_plus_lncRNA::1::574, 2_A375_pNL97_plus_lncRNA::1::575	12623, 12623, 3119, -8721	downstream, downstream, in gene, upstream	1	1	22.33	32.67	3	2_A375_pNL97_plus_lncRNA::1	38	Gene SHC1	SHC1, SHCA, FLJ26504, SHC	SHC (Src homology 2 domain containing) transforming protein 1	NM_003029, NM_183001, NM_001130040, NM_001130041, hCT2278470.1, hCT2278473.1, hCT2278477.0, hCT2352636.0, hCT2352637.0	201469_s_at, 214853_s_at	NP_003020.2, NP_892113.4, NP_001123512.1, NP_001123513.1, EAW53168.1, EAW53170.1, EAW53167.1, EAW53169.1, EAW53171.1
GeneID:1163	CKS1B	1	154,947,118	154,951,725	4,607	+	2	2_A375_pNL97_plus_lncRNA::1::574, 2_A375_pNL97_plus_lncRNA::1::575	-3278, 8562	upstream, downstream	0	1	20	30	2	2_A375_pNL97_plus_lncRNA::1	36	Gene CKS1B	PNAS-16, CKS1B, CKS1, PNAS-18, ckshs1	CDC28 protein kinase regulatory subunit 1B	NM_001826, NR_024163, hCT1777359.3, hCT1963031.2, hCT2351530.0, hCT2351531.0, hCT2351532.0, hCT2351533.0, hCT2351534.0	201897_s_at	NP_001817.1, EAW53165.1, EAW53160.1, EAW53161.1, EAW53164.1, EAW53166.1, EAW53162.1, EAW53163.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100423020	MIR4256	1	154,946,169	154,946,259	90	+	2	2_A375_pNL97_plus_lncRNA::1::574, 2_A375_pNL97_plus_lncRNA::1::575	-4329, 7511	upstream, downstream	0	1	20	30	2	2_A375_pNL97_plus_lncRNA::1	36	Gene MIR4256	MIR4256	microRNA 4256	NR_036212		
GeneID:80308	FLAD1	1	154,955,770	154,965,587	9,817	+	4	1_A375_pNL7_minus_lncRNA::1::413, 1_A375_pNL7_minus_lncRNA::1::414, 2_A375_pNL97_plus_lncRNA::1::575, 2_A375_pNL97_plus_lncRNA::1::576	17702, 18886, -90, 17638	downstream, downstream, upstream, downstream	1	1	28	33.5	2	2_A375_pNL97_plus_lncRNA::1	36	Gene FLAD1	FAD1, MGC31803, FADS, FLAD1, RP11-307C12.7, MGC40255, PP591	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	NM_001184891, NM_001184892, NM_025207, NM_201398, hCT11091.2, hCT1953595.1, hCT1953596.1, hCT1953598.1, hCT2352696.0, hCT2352697.0, hCT2352698.0	205661_s_at, 212541_at	NP_001171820.1, NP_001171821.1, NP_079483.3, NP_958800.1, EAW53154.1, EAW53155.1, EAW53153.1, EAW53156.1, EAW53157.1, EAW53158.1, EAW53159.1
GeneID:55891	LENEP	1	154,966,062	154,966,791	729	+	4	1_A375_pNL7_minus_lncRNA::1::413, 1_A375_pNL7_minus_lncRNA::1::414, 1_A375_pNL7_minus_lncRNA::1::415, 2_A375_pNL97_plus_lncRNA::1::576	7410, 8594, 10514, 7346	downstream, downstream, downstream, downstream	1	1	28	25	2	1_A375_pNL7_minus_lncRNA::1	36	Gene LENEP	LENEP, LEP503	lens epithelial protein	NM_018655, hCT1783402.1	221115_s_at	NP_061125.1, EAW53152.1
GeneID:51043	ZBTB7B	1	154,975,112	154,990,999	15,887	+	4	1_A375_pNL7_minus_lncRNA::1::413, 1_A375_pNL7_minus_lncRNA::1::414, 1_A375_pNL7_minus_lncRNA::1::415, 2_A375_pNL97_plus_lncRNA::1::576	-1640, -456, 1464, -1704	upstream, upstream, in gene, upstream	1	1	28	25	2	1_A375_pNL7_minus_lncRNA::1	36	Gene ZBTB7B	ZNF857B, THPOK, ZFP67, ZBTB15, ZBTB7B, c-Krox, hcKrox, DKFZp686G01254	zinc finger and BTB domain containing 7B	NM_015872, hCT2280155.0, hCT2280156.0, hCT2280157.0	205853_at, 235145_at	NP_056956.2, EAW53150.1, EAW53149.1, EAW53151.1
GeneID:149095	DCST1	1	155,006,300	155,023,406	17,106	+	1	1_A375_pNL7_minus_lncRNA::1::416	17044	in gene	1	0	32	24	1	1_A375_pNL7_minus_lncRNA::1	32	Gene DCST1	FLJ32785, RP11-307C12.10, DCST1	DC-STAMP domain containing 1	NM_152494, NM_001143687	1553860_at	NP_689707.2, NP_001137159.1
GeneID:100505666	LOC100505666	1	155,017,667	155,036,419	18,752	-	2	1_A375_pNL7_minus_lncRNA::1::416, 2_A375_pNL97_plus_lncRNA::1::577	13075, 195	in gene, in gene	1	1	24	25	2	1_A375_pNL7_minus_lncRNA::1	32	Gene LOC100505666		hypothetical LOC100505666	XR_111946, XR_111947, XR_108354, XR_108356, XR_108355, XR_114811, XR_114813, XR_114812		
GeneID:8751	ADAM15	1	155,023,762	155,035,252	11,490	+	2	1_A375_pNL7_minus_lncRNA::1::416, 2_A375_pNL97_plus_lncRNA::1::577	-418, 12462	upstream, downstream	1	1	24	25	2	1_A375_pNL7_minus_lncRNA::1	32	Gene ADAM15	MDC15, ADAM15	ADAM metallopeptidase domain 15	NM_003815, NM_207191, NM_207194, NM_207195, NM_207196, NM_207197	1555896_a_at, 217007_s_at	NP_003806.3, NP_997074.1, NP_997077.1, NP_997078.1, NP_997079.1, NP_997080.1
GeneID:1945	EFNA4	1	155,036,213	155,042,029	5,816	+	1	2_A375_pNL97_plus_lncRNA::1::577	11	in gene	0	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene EFNA4	EFNA4, FLJ57652, EPLG4, MGC125826, EFL4, LERK4	ephrin-A4	NM_005227, NM_182689, NM_182690, hCT11095.2, hCT2280163.0, hCT2352737.0	205107_s_at	NP_005218.1, NP_872631.1, NP_872632.2, EAW53138.1, EAW53139.1, EAW53140.1
GeneID:1942	EFNA1	1	155,100,349	155,107,386	7,037	+	4	1_A375_pNL7_minus_lncRNA::1::417, 2_A375_pNL97_plus_lncRNA::1::578, 2_A375_pNL97_plus_lncRNA::1::579, 2_A375_pNL97_plus_lncRNA::1::580	1251, -477, 8195, 12739	in gene, upstream, downstream, downstream	1	1	17.25	19.5	4	2_A375_pNL97_plus_lncRNA::1	23	Gene EFNA1	TNFAIP4, EFNA1, ECKLG, B61, EFL1, EPLG1, LERK1	ephrin-A1	NM_182685, NM_004428, hCT1783408.2, hCT2280166.0, hCT2280167.0, hCT2280168.0, hCT2352708.0	202023_at	NP_872626.1, NP_004419.2, EAW53131.1, EAW53132.1, EAW53133.1, EAW53134.1, EAW53135.1
GeneID:55974	RAG1AP1	1	155,108,288	155,111,334	3,046	+	4	1_A375_pNL7_minus_lncRNA::1::417, 2_A375_pNL97_plus_lncRNA::1::578, 2_A375_pNL97_plus_lncRNA::1::579, 2_A375_pNL97_plus_lncRNA::1::580	-6688, -8416, 256, 4800	upstream, upstream, in gene, downstream	1	1	17.25	19.5	4	2_A375_pNL97_plus_lncRNA::1	23	Gene RAG1AP1	HsSWEET1, RAG1AP1, SLC50A1, SWEET1, slv, SCP	recombination activating gene 1 activating protein 1	NM_018845, NM_001122837, NM_001122839, hCT1950804.1, hCT2280170.0, hCT2280173.0, hCT90560.3	219125_s_at	NP_061333.2, NP_001116309.1, NP_001116311.1, EAW53127.1, EAW53128.1, EAW53129.1, EAW53130.1
GeneID:54344	DPM3	1	155,112,367	155,112,996	629	-	2	2_A375_pNL97_plus_lncRNA::1::579, 2_A375_pNL97_plus_lncRNA::1::580	4452, -92	downstream, upstream	0	1	17.5	19.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene DPM3	MGC125904, DPM3, MGC34275, CDG1O, MGC125905	dolichyl-phosphate mannosyltransferase polypeptide 3	NM_018973, NM_153741, hCT1640883.3, hCT1953578.1	219373_at	NP_061846.2, NP_714963.1, EAW53125.1, EAW53126.1
GeneID:200185	KRTCAP2	1	155,141,884	155,145,804	3,920	-	2	1_A375_pNL7_minus_lncRNA::1::418, 2_A375_pNL97_plus_lncRNA::1::581	-52, -20	upstream, upstream	1	1	156	142	1	1_A375_pNL7_minus_lncRNA::1	156	Gene KRTCAP2	KCP2, KRTCAP2	keratinocyte associated protein 2	NM_173852	224885_s_at	NP_776251.1
GeneID:80128	TRIM46	1	155,146,360	155,157,445	11,085	+	4	1_A375_pNL7_minus_lncRNA::1::418, 1_A375_pNL7_minus_lncRNA::1::419, 2_A375_pNL97_plus_lncRNA::1::581, 2_A375_pNL97_plus_lncRNA::1::582	-504, 17944, -536, 18440	upstream, downstream, upstream, downstream	1	1	88	81.5	2	1_A375_pNL7_minus_lncRNA::1	156	Gene TRIM46	TRIM46, TRIFIC, FLJ23229, GENEY	tripartite motif containing 46	NM_025058, hCT2278820.0, hCT2278821.0, hCT2278822.0, hCT2352717.0	220909_at, 238147_at	NP_079334.3, EAW53123.1, EAW53120.1, EAW53121.1, EAW53122.1
GeneID:4582	MUC1	1	155,158,300	155,162,700	4,400	-	2	1_A375_pNL7_minus_lncRNA::1::419, 2_A375_pNL97_plus_lncRNA::1::582	-1604, -2100	upstream, upstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MUC1	H23AG, PEMT, PEM, MUC1, EMA, CD227, PUM, KL-6, MAM6	mucin 1, cell surface associated	NM_002456, NM_001018016, NM_001018017, NM_001044390, NM_001044391, NM_001044392, NM_001044393	207847_s_at, 211695_x_at, 213693_s_at	NP_002447.4, NP_001018016.1, NP_001037855.1, NP_001037856.1, NP_001037857.1, NP_001018017.1, NP_001037858.1
GeneID:693235	MIR92B	1	155,164,968	155,165,063	95	+	2	1_A375_pNL7_minus_lncRNA::1::419, 2_A375_pNL97_plus_lncRNA::1::582	-664, -168	upstream, upstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MIR92B	MIRN92B, hsa-mir-92b, MIR92B	microRNA 92b	NR_030281		
GeneID:7059	THBS3	1	155,165,379	155,177,690	12,311	-	2	1_A375_pNL7_minus_lncRNA::1::419, 2_A375_pNL97_plus_lncRNA::1::582	13386, 12890	downstream, downstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene THBS3	MGC119565, MGC119564, TSP3, THBS3	thrombospondin 3	NM_007112, hCT1954408.1, hCT7162.2	209561_at	NP_009043.1, EAW53109.1, EAW53110.1
GeneID:100129268	LOC100129268	1	155,170,593	155,175,575	4,982	+	2	1_A375_pNL7_minus_lncRNA::1::419, 2_A375_pNL97_plus_lncRNA::1::582	-6289, -5793	upstream, upstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100129268		hypothetical LOC100129268	XR_111944, XR_111943, XR_111945, XR_108358, XR_108357, XR_114815, XR_114814		
GeneID:2629	GBA	1	155,204,239	155,214,653	10,414	-	4	1_A375_pNL7_minus_lncRNA::1::420, 2_A375_pNL97_plus_lncRNA::1::583, 2_A375_pNL97_plus_lncRNA::1::584, 2_A375_pNL97_plus_lncRNA::1::585	29, 17789, -35, -5891	in gene, downstream, upstream, upstream	1	1	17.67	23.67	3	2_A375_pNL97_plus_lncRNA::1	26	Gene GBA	GBA1, GBA, GLUC, GCB	glucosidase, beta, acid	NM_001005742, NM_001005741, NM_000157, NM_001171811, NM_001171812, hCT2277266.1, hCT2277267.2, hCT2277268.2, hCT2352748.0	209093_s_at, 210589_s_at, 216400_at	NP_001005742.1, NP_001005741.1, NP_000148.2, NP_001165282.1, NP_001165283.1, EAW53101.1, EAW53100.1, EAW53102.1, EAW53103.1
GeneID:10712	FAM189B	1	155,216,996	155,225,274	8,278	-	4	1_A375_pNL7_minus_lncRNA::1::420, 2_A375_pNL97_plus_lncRNA::1::584, 2_A375_pNL97_plus_lncRNA::1::585, 2_A375_pNL97_plus_lncRNA::1::586	10650, 10586, 4730, -6854	downstream, downstream, in gene, upstream	1	1	17.33	25.67	3	2_A375_pNL97_plus_lncRNA::1	26	Gene FAM189B	FAM189B, COTE1, C1orf2	family with sequence similarity 189, member B	NM_006589, NM_198264, hCT1954396.1, hCT1954397.1, hCT2352633.0, hCT2352634.0, hCT2352635.0, hCT7149.2	1555515_a_at, 203550_s_at	NP_006580.2, NP_937995.1, EAW53094.1, EAW53095.1, EAW53097.1, EAW53099.1, EAW53096.1, EAW53098.1
GeneID:10067	SCAMP3	1	155,225,770	155,232,195	6,425	-	2	2_A375_pNL97_plus_lncRNA::1::585, 2_A375_pNL97_plus_lncRNA::1::586	11651, 67	downstream, in gene	0	1	14.5	24.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene SCAMP3	SCAMP3, C1orf3	secretory carrier membrane protein 3	NM_005698, NM_052837, hCT1963120.1, hCT1963122.1, hCT1963123.1, hCT1963124.1	201771_at	NP_005689.2, NP_443069.1, EAW53090.1, EAW53091.1, EAW53092.1, EAW53093.1
GeneID:1196	CLK2	1	155,232,659	155,243,281	10,622	-	2	2_A375_pNL97_plus_lncRNA::1::586, 2_A375_pNL97_plus_lncRNA::1::587	11153, -4143	downstream, upstream	0	1	15	24	2	2_A375_pNL97_plus_lncRNA::1	27	Gene CLK2	CLK2, hCLK2, MGC61500	CDC-like kinase 2	NM_003993, hCT2277258.0, hCT7150.2, hCT7151.2	203229_s_at	NP_003984.2, EAW53089.1, EAW53087.1, EAW53088.1
GeneID:57657	HCN3	1	155,247,374	155,259,638	12,264	+	1	2_A375_pNL97_plus_lncRNA::1::587	50	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene HCN3	KIAA1535, HCN3, MGC131493	hyperpolarization activated cyclic nucleotide-gated potassium channel 3	NM_020897, hCT2278829.1, hCT2278830.1, hCT2278831.1, hCT2352638.0, hCT2352639.0, hCT7160.3	228741_s_at	NP_065948.1, EAW53082.1, EAW53081.1, EAW53083.1, EAW53084.1, EAW53085.1, EAW53086.1
GeneID:5313	PKLR	1	155,259,084	155,271,225	12,141	-	2	1_A375_pNL7_minus_lncRNA::1::421, 2_A375_pNL97_plus_lncRNA::1::588	-7399, -7367	upstream, upstream	1	1	22	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene PKLR	PKLR, PKR, PKL, PKRL, PK1, RPK	pyruvate kinase, liver and RBC	NM_000298, NM_181871, hCT1954411.2, hCT7165.3	207858_s_at, 210451_at	NP_000289.1, NP_870986.1, EAW53079.1, EAW53080.1
GeneID:2224	FDPS	1	155,278,539	155,290,457	11,918	+	3	1_A375_pNL7_minus_lncRNA::1::421, 2_A375_pNL97_plus_lncRNA::1::588, 2_A375_pNL97_plus_lncRNA::1::589	85, 53, 15957	in gene, in gene, downstream	1	1	18.5	23.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene FDPS	FPPS, FDPS, FPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)	NM_002004, NM_001135821, NM_001135822, hCT2278837.0, hCT2278838.1, hCT2278840.1, hCT2352749.0	201275_at	NP_001995.1, NP_001129293.1, NP_001129294.1, EAW53075.1, EAW53076.1, EAW53078.1, EAW53077.1
GeneID:284618	C1orf104	1	155,290,251	155,293,938	3,687	-	1	2_A375_pNL97_plus_lncRNA::1::589	-558	upstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C1orf104	C1orf104, FLJ35976, RP11-21N7.3	chromosome 1 open reading frame 104	NM_001039517	1552862_at	NP_001034606.1
GeneID:23623	RUSC1	1	155,290,640	155,300,909	10,269	+	1	2_A375_pNL97_plus_lncRNA::1::589	3856	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RUSC1	DKFZp761A1822, NESCA, RUSC1	RUN and SH3 domain containing 1	NM_014328, NM_001105203, NM_001105204, NM_001105205, hCT2278834.1, hCT2278835.1, hCT2278836.1, hCT2344271.0	206949_s_at	NP_055143.2, NP_001098673.1, NP_001098674.1, NP_001098675.1, EAW53070.1, EAW53071.1, EAW53069.1, EAW53072.1
GeneID:55870	ASH1L	1	155,305,052	155,532,324	227,272	-	2	1_A375_pNL7_minus_lncRNA::1::422, 2_A375_pNL97_plus_lncRNA::1::590	-572, -540	upstream, upstream	1	1	46	48	1	2_A375_pNL97_plus_lncRNA::1	48	Gene ASH1L	KMT2H, ASH1, FLJ10504, ASH1L1, ASH1L, KIAA1420	ash1 (absent, small, or homeotic)-like (Drosophila)	NM_018489, hCT7158.3	218554_s_at, 222667_s_at, 226447_at	NP_060959.2, EAW53068.1
GeneID:645676	LOC645676	1	155,531,772	155,533,735	1,963	+	2	1_A375_pNL7_minus_lncRNA::1::422, 2_A375_pNL97_plus_lncRNA::1::590	1124, 1092	in gene, in gene	1	1	46	48	1	2_A375_pNL97_plus_lncRNA::1	48	Gene LOC645676	FLJ44595	hypothetical LOC645676	NR_027023	1554057_at	
GeneID:55249	YY1AP1	1	155,629,233	155,658,791	29,558	-	2	1_A375_pNL7_minus_lncRNA::1::423, 2_A375_pNL97_plus_lncRNA::1::591	71, 71	in gene, in gene	1	1	53	70	1	2_A375_pNL97_plus_lncRNA::1	70	Gene YY1AP1	YY1AP1, FLJ13914, YAP, HCCA2, HCCA1, FLJ10875, YY1AP	YY1 associated protein 1	NM_139118, NM_139119, hCT2277245.0, hCT2277246.0, hCT2277247.0, hCT2352711.0, hCT2352712.0, hCT2352713.0, hCT2352714.0, hCT2352715.0, hCT2352716.0	217636_s_at, 227608_at, 232516_x_at	NP_620829.1, NP_620830.1, EAW53052.1, EAW53056.1, EAW53058.1, EAW53060.1, EAW53053.1, EAW53054.1, EAW53055.1, EAW53057.1, EAW53059.1
GeneID:7818	DAP3	1	155,658,874	155,708,320	49,446	+	3	1_A375_pNL7_minus_lncRNA::1::423, 2_A375_pNL97_plus_lncRNA::1::591, 2_A375_pNL97_plus_lncRNA::1::592	-154, -154, 56486	upstream, upstream, downstream	1	1	35	47.5	2	2_A375_pNL97_plus_lncRNA::1	70	Gene DAP3	DAP-3, MRP-S29, FLJ12617, bMRP-10, DKFZp686G12159, MRPS29, DAP3, MGC126058, MGC126059	death associated protein 3	NM_033657, NM_004632, hCT1954429.1, hCT1966078.1, hCT1966079.1, hCT1966080.1, hCT1966081.1, hCT1966082.1, hCT2278846.0, hCT2278848.0, hCT6225.3	208822_s_at	NP_387506.1, NP_004623.1, EAW53043.1, EAW53048.1, EAW53049.1, EAW53051.1, EAW53044.1, EAW53045.1, EAW53046.1, EAW53047.1, EAW53050.1
GeneID:100505728	LOC100505728	1	155,714,903	155,715,773	870	-	1	2_A375_pNL97_plus_lncRNA::1::592	413	in gene	0	1	17	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100505728		hypothetical LOC100505728	XR_111942, XR_108359, XR_114816		
GeneID:54856	GON4L	1	155,719,510	155,826,972	107,462	-	4	1_A375_pNL7_minus_lncRNA::1::424, 2_A375_pNL97_plus_lncRNA::1::592, 2_A375_pNL97_plus_lncRNA::1::593, 2_A375_pNL97_plus_lncRNA::1::594	-132, 111612, -68, -3236	upstream, downstream, upstream, upstream	1	1	26.67	37.67	3	2_A375_pNL97_plus_lncRNA::1	66	Gene GON4L	RP11-101O6.1, MGC138817, GON4L, GON-4, RP11-243J18.4, FLJ20203, MGC138818, GON4, KIAA1606, FLJ12923, FLJ23040, DKFZp761I241	gon-4-like (C. elegans)	NM_001037533, NM_032292, hCT2349480.0, hCT2349481.0, hCT2349482.0, hCT2349483.0, hCT2349484.0, hCT2349485.0, hCT2352622.0, hCT2352623.0	1555913_at, 218873_at, 219846_at, 223555_at	NP_001032622.1, NP_115668.4, EAW53029.1, EAW53030.1, EAW53031.1, EAW53035.1, EAW53032.1, EAW53033.1, EAW53034.1, EAW53036.1
GeneID:23208	SYT11	1	155,829,260	155,854,990	25,730	+	3	1_A375_pNL7_minus_lncRNA::1::424, 2_A375_pNL97_plus_lncRNA::1::593, 2_A375_pNL97_plus_lncRNA::1::594	-2156, -2220, 948	upstream, upstream, in gene	1	1	31.5	44	2	2_A375_pNL97_plus_lncRNA::1	66	Gene SYT11	MGC17226, SYT12, MGC10881, KIAA0080, DKFZp781D015, SYT11	synaptotagmin XI	NM_152280, hCT2278860.0, hCT8241.3	209197_at, 209198_s_at	NP_689493.3, EAW53026.1, EAW53025.1
GeneID:22889	KIAA0907	1	155,882,836	155,904,188	21,352	-	2	1_A375_pNL7_minus_lncRNA::1::425, 2_A375_pNL97_plus_lncRNA::1::595	28, 44	in gene, in gene	1	1	27	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene KIAA0907	KIAA0907, BLOM7, RP11-336K24.1	KIAA0907	NM_014949, hCT1954423.2, hCT2351511.0, hCT8219.3	202220_at, 230028_at	NP_055764.2, EAW53023.1, EAW53021.1, EAW53022.1
GeneID:677771	SCARNA4	1	155,895,749	155,895,877	128	-	2	1_A375_pNL7_minus_lncRNA::1::425, 2_A375_pNL97_plus_lncRNA::1::595	-8283, -8267	upstream, upstream	1	1	27	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene SCARNA4	ACA26, SCARNA4	small Cajal body-specific RNA 4	NR_003005		
GeneID:339403	RXFP4	1	155,911,480	155,912,625	1,145	+	2	1_A375_pNL7_minus_lncRNA::1::425, 2_A375_pNL97_plus_lncRNA::1::595	-7320, -7336	upstream, upstream	1	1	27	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene RXFP4	MGC126556, GPCR142, RLN3R2, RXFP4, RXFPR4, GPR100, MGC126558	relaxin/insulin-like family peptide receptor 4	NM_181885, hCT2351614.0		NP_871001.1, EAW53020.1
GeneID:9181	ARHGEF2	1	155,916,630	155,948,336	31,706	-	1	1_A375_pNL7_minus_lncRNA::1::426	7856	in gene	1	0	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ARHGEF2	GEFH1, DKFZp547P1516, ARHGEF2, DKFZp547L106, P40, FLJ45440, GEF-H1, GEF, LFP40, KIAA0651	Rho/Rac guanine nucleotide exchange factor (GEF) 2	NM_004723, NM_001162383, NM_001162384, hCT2277223.1, hCT2277224.1, hCT2277225.1, hCT2277226.1, hCT2277227.1, hCT2351567.0, hCT2351568.0	1554783_s_at, 207629_s_at, 209435_s_at, 235595_at	NP_004714.2, NP_001155855.1, NP_001155856.1, EAW53014.1, EAW53015.1, EAW53016.1, EAW53012.1, EAW53013.1, EAW53017.1, EAW53018.1
GeneID:56893	UBQLN4	1	156,005,092	156,023,516	18,424	-	2	1_A375_pNL7_minus_lncRNA::1::427, 2_A375_pNL97_plus_lncRNA::1::596	-964, -1028	upstream, upstream	1	1	26	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene UBQLN4	CIP75, UBQLN4, UBIN, A1U, C1orf6	ubiquilin 4	NM_020131, hCT1954431.1, hCT2277217.0, hCT2277218.0, hCT2277219.0, hCT2352651.0	222252_x_at, 224513_s_at	NP_064516.2, EAW53005.1, EAW53006.1, EAW53007.1, EAW53008.1, EAW53009.1
GeneID:28956	ROBLD3	1	156,024,517	156,028,301	3,784	+	2	1_A375_pNL7_minus_lncRNA::1::427, 2_A375_pNL97_plus_lncRNA::1::596	-37, 27	upstream, in gene	1	1	26	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene ROBLD3	ROBLD3, Ragulator2, MAPKSP1AP, ENDAP, LAMTOR2, HSPC003, p14, MAPBPIP	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	NM_014017, NM_001145264, hCT1963147.1	218291_at	NP_054736.1, NP_001138736.1, EAW53004.1
GeneID:57111	RAB25	1	156,030,966	156,040,295	9,329	+	2	1_A375_pNL7_minus_lncRNA::1::427, 2_A375_pNL97_plus_lncRNA::1::596	-6486, -6422	upstream, upstream	1	1	26	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene RAB25	RAB25, CATX-8, RAB11C	RAB25, member RAS oncogene family	NM_020387, hCT8238.2	218186_at	NP_065120.2, EAW53003.1
GeneID:4000	LMNA	1	156,084,461	156,109,878	25,417	+	6	1_A375_pNL7_minus_lncRNA::1::428, 1_A375_pNL7_minus_lncRNA::1::429, 2_A375_pNL97_plus_lncRNA::1::597, 2_A375_pNL97_plus_lncRNA::1::598, 2_A375_pNL97_plus_lncRNA::1::599, 2_A375_pNL97_plus_lncRNA::1::600	-365, 12419, -9357, 451, 8051, 12595	upstream, in gene, upstream, in gene, in gene, in gene	1	1	18.25	19.75	4	2_A375_pNL97_plus_lncRNA::1	26	Gene LMNA	IDC, FPL, LMNA, LMNL1, LGMD1B, LMNC, PRO1, LFP, CMT2B1, EMD2, FPLD, LMN1, HGPS, LDP1, CMD1A, CDDC, CDCD1	lamin A/C	NM_005572, NM_170707, NM_170708, hCT2278868.0, hCT2278869.0, hCT2278870.0, hCT2278871.0, hCT2278873.0	1554600_s_at, 203411_s_at, 212086_x_at, 212089_at, 214213_x_at	NP_005563.1, NP_733821.1, NP_733822.1, EAW52996.1, EAW52997.1, EAW52998.1, EAW52999.1, EAW53000.1
GeneID:9673	SLC25A44	1	156,163,730	156,182,587	18,857	+	1	2_A375_pNL97_plus_lncRNA::1::601	302	in gene	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC25A44	RP11-54H19.3, FLJ90431, SLC25A44, KIAA0446	solute carrier family 25, member 44	NM_014655, hCT1963145.2	212663_at, 32091_at	NP_055470.1, EAW52991.1
GeneID:23381	SMG5	1	156,219,015	156,252,620	33,605	-	1	2_A375_pNL97_plus_lncRNA::1::602	21772	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SMG5	LPTS-RP1, RP11-54H19.7, FLJ12287, LPTSRP1, SMG-5, EST1B, FLJ34864, SMG5, KIAA1089	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	NM_015327, hCT2281930.0, hCT8240.3	212147_at, 34868_at	NP_056142.2, EAW52973.1, EAW52974.1
GeneID:7203	CCT3	1	156,278,752	156,308,195	29,443	-	1	2_A375_pNL97_plus_lncRNA::1::603	-285	upstream	0	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CCT3	TRIC5, PIG48, CCT-gamma, TCP-1-gamma, CCT3, CCTG	chaperonin containing TCP1, subunit 3 (gamma)	NM_001008800, NM_005998, hCT8218.3	200910_at	NP_001008800.1, NP_005989.3, EAW52967.1
GeneID:100505747	LOC100505747	1	156,305,717	156,307,029	1,312	-	1	2_A375_pNL97_plus_lncRNA::1::603	-1451	upstream	0	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100505747		hypothetical LOC100505747	XR_111956, XR_108360, XR_114817		
GeneID:128229	C1orf182	1	156,307,105	156,316,786	9,681	+	1	2_A375_pNL97_plus_lncRNA::1::603	1375	in gene	0	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C1orf182	RP11-443G18.5, C1orf182, MGC26877, SSTK-IP	chromosome 1 open reading frame 182	NM_144627, hCT2282110.0, hCT2352709.0, hCT2352710.0	230608_at	NP_653228.1, EAW52964.1, EAW52965.1, EAW52966.1

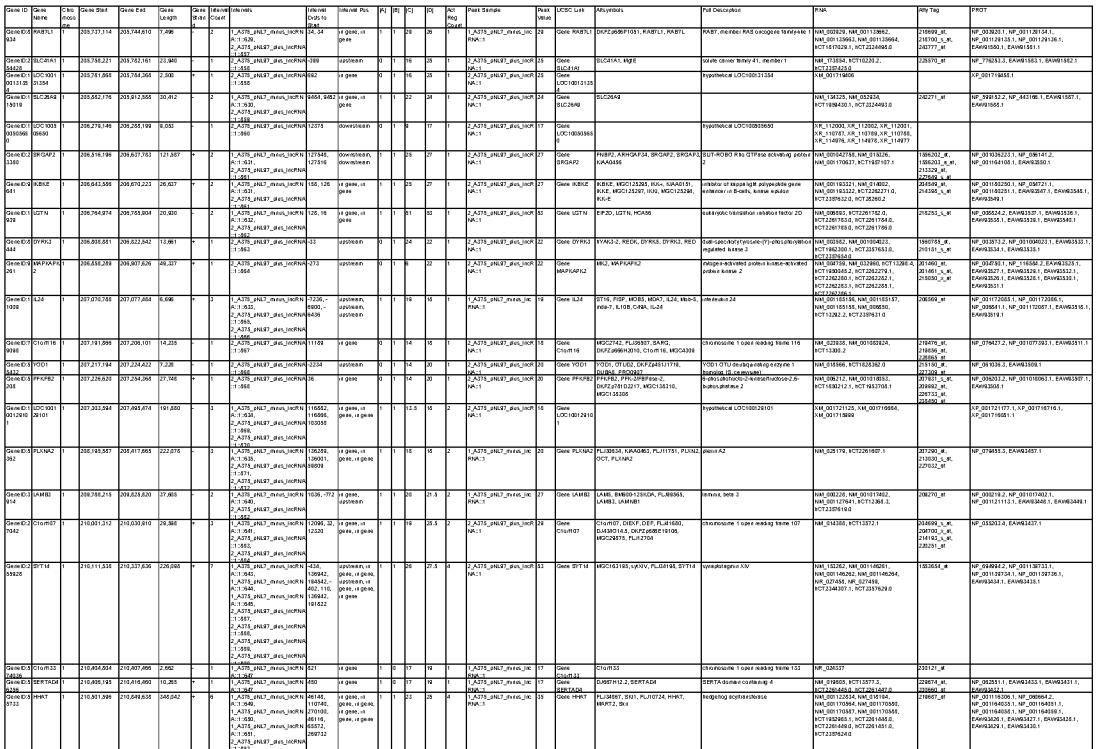
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervals	Intervals Count	Intervals	Intervel Outside Gene	Intervel Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:1 0463	C1orf61	1	156,374,055	156,399,164	25,129	+	3	1_A275_shL7_dhrus_lncRNA:1:430,2_A275_shL97_glus_lncRNA:1:664,2_A275_shL97_glus_lncRNA:1:665	1664, 16752, 7728	si gene, ut gene, rt gene	1	1	23.5	23.5	2	2_A275_shL97_glus_lncRNA:1	26	Gene:C1orf61	FLJ38353, C1orf61, CROC4	chromosome 1 open reading frame 61	NM_006365, XM_6215213.1	1559402_at_st, 1570451_at, 206103_at, 222301_at	NP_0006356.1, EAW62656.1
Gene:ID:1 0350578 5	LOC1003 35765	1	156,378,749	156,382,685	3,936	-	2	1_A275_shL7_dhrus_lncRNA:1:430,2_A275_shL97_glus_lncRNA:1:664,2_A275_shL97_glus_lncRNA:1:665	-6535, -1747, -3771	upstream, upstream, upstream	1	1	23.5	23.5	2	2_A275_shL97_glus_lncRNA:1	26	Gene:LOC100505765		hypothetical LOC100505765	XR_111933, XR_150301, XR_114618		
Gene:ID:4 07046	MIR9-1	1	156,380,133	156,380,221	88	-	3	1_A275_shL7_dhrus_lncRNA:1:430,2_A275_shL97_glus_lncRNA:1:664,2_A275_shL97_glus_lncRNA:1:665	-1289, -5769, -1233	upstream, downstream, upstream	1	1	23.5	23.5	2	2_A275_shL97_glus_lncRNA:1	26	Gene:MIR9-1	MIR9-1, MIRN9-1, hsa-mir-9-1, mirRNA9-1	microRNA 9-1	NR_029691		
Gene:ID:4 209	MEF2D	1	156,422,518	156,470,529	37,010	-	7	1_A275_shL7_dhrus_lncRNA:1:431,1_A275_shL7_dhrus_lncRNA:1:432,1_A275_shL7_dhrus_lncRNA:1:432,2_A275_shL97_glus_lncRNA:1:666,2_A275_shL97_glus_lncRNA:1:667,2_A275_shL97_glus_lncRNA:1:668,2_A275_shL97_glus_lncRNA:1:669	44065, -1551, -43791, -551, -2751, -4767	downstream, 5'UTR, upstream, upstream, upstream, upstream, upstream	1	1	32.25	28.25	4	1_A275_shL7_dhrus_lncRNA:1	32	Gene:MEF2D	DKFZp686I1535, MEF2D	myocyte enhancer factor 2D	NM_005920, NCT02016495.0, NCT02016103.0, NCT02016130.0, NCT02016183.0	202003_at, 202004_s_at, 226431_at	NP_0059911.1, EAW62649.1, EAW62648.1, EAW62650.1, EAW62651.1, EAW62642.1
Gene:ID:1 58239	IQGAP3	1	156,495,197	156,542,396	47,199	-	1	2_A275_shL97_glus_lncRNA:1:1610	20665	si gene	0	1	22	29	1	2_A275_shL97_glus_lncRNA:1	29	Gene:IQGAP3	MGC19477, IQGAP3, MGC10170, MGC10831	IQ motif containing GTPase activating protein 3	NM_178229, NCT01854441.2, NCT02484690.0, NCT02537703.0	1560961_at, 1560962_s_at, 236535_s_at, 241829_at	NP_5396432.2, EAW62645.1, EAW62645.1, EAW62647.1
Gene:ID:1 58240	APOA1BP	1	156,561,556	156,564,091	2,533	+	2	1_A275_shL7_dhrus_lncRNA:1:430,2_A275_shL97_glus_lncRNA:1:1611	15010, 9558	downstream, downstream	1	1	15	20	1	2_A275_shL97_glus_lncRNA:1	20	Gene:APOA1BP	APOA1BP, MGC119140, A1BP, MGC119139, MGC119140, YJEFN1	apolipoprotein A-I binding protein	NM_145772, NCT02394691.0, NCT02526522.0, NCT0231.2	228427_s_at	NP_6598452.2, EAW62681.1, EAW62682.1, EAW62643.1
Gene:ID:5 4966	GPATCH8	1	156,564,279	156,577,270	12,991	-	2	1_A275_shL7_dhrus_lncRNA:1:430,2_A275_shL97_glus_lncRNA:1:1611	4992, -166	upstream, upstream	1	1	15	20	1	2_A275_shL97_glus_lncRNA:1	20	Gene:GPATCH8	GPATCH8, GPATC8	G patch domain containing 8	NM_152679, NM_015189, NCT02016502.0, NCT02016999.0, NCT02527102.0, NCT02527103.0	1553596_at, 227123_s_at, 227124_at, 234622_at, 234623_s_at, 234624_at	NP_6780.2, NP_0557.1, NP_0557.2, EAW62627.1, EAW62628.1, EAW62629.1, EAW62631.1, EAW62630.1
Gene:ID:8 3627	BCAN	1	156,611,740	156,629,220	17,480	+	5	1_A275_shL7_dhrus_lncRNA:1:430,1_A275_shL7_dhrus_lncRNA:1:431,1_A275_shL7_dhrus_lncRNA:1:432,2_A275_shL97_glus_lncRNA:1:912,2_A275_shL97_glus_lncRNA:1:913	18500, 18524, 19212, 19436, 20164	downstream, downstream, si gene, downstream, downstream	1	1	21.67	25.33	3	2_A275_shL97_glus_lncRNA:1	34	Gene:BCAN	BCAN, CSPG7, BEHAB, MGC10035	brevican	NM_198427, NM_021948, NCT01997465.1, NCT02621203.0, NCT02621213.0, NCT02621248.0, NCT02.30.3	1554707_at, 221625_at, 223632_s_at, 223633_s_at, 242563_at, 971025_at	NP_9408191, NP_0557072, EAW62627.1, EAW62628.1, EAW62629.1, EAW62631.1, EAW62630.1
Gene:ID:1 0783	NES	1	156,635,555	156,647,182	6,634	-	5	1_A275_shL7_dhrus_lncRNA:1:430,1_A275_shL7_dhrus_lncRNA:1:431,1_A275_shL7_dhrus_lncRNA:1:432,1_A275_shL7_dhrus_lncRNA:1:813,1_A275_shL7_dhrus_lncRNA:1:814,2_A275_shL97_glus_lncRNA:1:915	16949, 16923, 17013, 15283, 61	downstream, downstream, downstream, downstream, si gene	1	1	22	27	3	2_A275_shL97_glus_lncRNA:1	34	Gene:NES	NM400170, NES, FLJ21541	nestin	NM_006617, NCT02016090.0, NCT02016924.0, NCT02526503.0	218576_at, 226396_at	NP_0096001, EAW62623.1, EAW62624.1, EAW62625.1, EAW62626.1
Gene:ID:5 1870	ISG20L2	1	156,692,813	156,697,705	5,292	+	2	1_A275_shL7_dhrus_lncRNA:1:437,2_A275_shL97_glus_lncRNA:1:916	-419, -467	upstream, upstream	1	1	23	31	1	1_A275_shL7_dhrus_lnc RNA:1	33	Gene:ISG20L2	FLJ12671, ISG20J2	interferon stimulated exonuclease gene 20kDa-like 2	NM_030900, NCT01135681.2, NCT02016840.0	208116_s_at, 212796_s_at, 216502_at, 222138_at	NP_1123427.1, EAW62619.1, EAW62620.1
Gene:ID:5 1093	C1orf66	1	156,695,263	156,709,752	6,490	+	4	1_A275_shL7_dhrus_lncRNA:1:437,1_A275_shL7_dhrus_lncRNA:1:438,2_A275_shL97_glus_lncRNA:1:916,2_A275_shL97_glus_lncRNA:1:917	261, 12748, 329, 12583	si gene, downstream, si gene, downstream	1	1	24.5	25.5	2	1_A275_shL7_dhrus_lnc RNA:1	36	Gene:C1orf66	CG1-41, C1orf66, RRNADI	chromosome 1 open reading frame 66	NM_018997, NM_001142660, NCT02521270.0, NCT02521218.0, NCT02521260, NCT02527.0	218516_at	NP_0570513, NP_001136032.1, EAW62619.1, EAW62616.1, EAW62617.1, EAW62618.1
Gene:ID:7 9340	MRPL24	1	156,707,094	156,710,823	3,829	-	5	1_A275_shL7_dhrus_lncRNA:1:437,1_A275_shL7_dhrus_lncRNA:1:438,2_A275_shL97_glus_lncRNA:1:916,2_A275_shL97_glus_lncRNA:1:917,2_A275_shL97_glus_lncRNA:1:918	12299, -53, 12331, 107, -1561	downstream, upstream, downstream, si gene, upstream	1	1	28	29.67	3	1_A275_shL7_dhrus_lnc RNA:1	36	Gene:MRPL24	MRPL24, FLJ39917, MGC39831, MGC22737, MRP-L24, MRP-L18, L24mt	ribonucleoside-diphosphate reductase subunit M2	NM_148729, NM_024540, NCT01135681.1, NCT 1666813.1	218270_at	NP_0670111, NP_0705816.2, EAW62613.1, EAW62614.1
Gene:ID:3 066	HDGF	1	156,711,899	156,722,240	10,341	-	5	1_A275_shL7_dhrus_lncRNA:1:438,1_A275_shL7_dhrus_lncRNA:1:439,2_A275_shL97_glus_lncRNA:1:915,2_A275_shL97_glus_lncRNA:1:917,2_A275_shL97_glus_lncRNA:1:918	11232, 960, 11424, 3456, 376	downstream, si gene, downstream, si gene, si gene	1	1	40	42.33	3	2_A275_shL97_glus_lncRNA:1	41	Gene:HDGF	HDGF, PL98580, HRP3, HRP3L2, DKFZp686J1764	hepatoma-derived growth factor (high-mobility group protein 1-like)	NM_004494, NM_001129050, NM_001129051, NCT01135681.1, NCT02016896.1, NCT02016760, NCT02526900.0	200990_s_at, 216484_s_at	NP_0044551, NP_001119522.1, NP_001119523.1, EAW62610.1, EAW62611.1, EAW62612.1
Gene:ID:5 546	PRCC	1	156,737,274	156,770,609	33,335	+	2	1_A275_shL7_dhrus_lncRNA:1:440,2_A275_shL97_glus_lncRNA:1:921	-234, -154	upstream, upstream	1	1	41	45	1	2_A275_shL97_glus_lncRNA:1	45	Gene:PRCC	KCCP1, MGC17176, TPRC, MGC47225, PRCC	papillary renal cell carcinoma (translocation-associated)	NM_005137, NCT01997879.1, NCT31963.2	208936_at	NP_0059904.3, EAW62609.1, EAW62608.1
Gene:ID:1 526	ARHGEF11	1	156,904,632	157,015,162	110,530	-	1	2_A275_shL97_glus_lncRNA:1:921	95510	si gene	0	1	19	16	1	2_A275_shL97_glus_lncRNA:1	16	Gene:ARHGEF11	GTRAP48, PDZ-RHOGEF, ARHGEF11, DKFZp667F1223, KIAA0380	Rho guanine nucleotide exchange factor (GEF) 11	NM_014784, NM_198235, NCT02016710.0, NCT02527004.0, NCT02465.2	202913_at, 202914_s_at, 236730_at	NP_0559991.1, NP_937678.1, EAW62602.1, EAW62603.1, EAW62604.1
Gene:ID:7 58220	MIR765	1	156,905,923	156,906,036	113	-	1	2_A275_shL97_glus_lncRNA:1:923	-16316	si gene	0	1	16	16	1	2_A275_shL97_glus_lncRNA:1	16	Gene:MIR765	MIRN765, MIR765, hsa-mir-765	microRNA 765	NR_030377		
Gene:ID:2 117	ETV3	1	157,094,459	157,106,283	12,824	+	2	1_A275_shL7_dhrus_lncRNA:1:441,2_A275_shL97_glus_lncRNA:1:922	-272, 48	upstream, si gene	1	1	20	24	1	2_A275_shL97_glus_lncRNA:1	24	Gene:ETV3	PE-1, PE1, METS, SAH10J1.4, METSV, ETV3	ets variant 3	NM_004240, NM_001145512, NCT02016617.1, NCT02016.3	1552433_at, 214600_at	NP_0533211, NP_0011387561, EAW62588.1, EAW62589.1
Gene:ID:3 5243	KIRREL	1	157,993,063	158,065,696	102,763	+	1	2_A275_shL97_glus_lncRNA:1:682	68745	si gene	1	0	27	15	1	2_A275_shL97_glus_lnc RNA:1	27	Gene:KIRREL	MGC129543, MGC129542, NEPH1, FLJ10545, KIRREL	kin of IRRE like (Drosophila)	NM_018240, NCT02725270.0, NCT02725272.0, NCT31205.3	226525_s_at, 226303_at, 242667_at	NP_0607162, EAW62553.1, EAW62555.1, EAW62555.1
Gene:ID:1 0350578 5	LOC1003 35765	1	157,995,349	158,001,811	6,296	+	1	1_A275_shL7_dhrus_lncRNA:1:442	12462	downstream	1	0	27	15	1	1_A275_shL7_dhrus_lnc RNA:1	27	Gene:LOC100505765		hypothetical LOC100505765	XR_108362		
Gene:ID:1 96266	SCG_163 4703	1	158,101,634	158,110,430	8,796	-	2	2_A275_shL97_glus_lncRNA:1:923,2_A275_shL97_glus_lncRNA:1:924	-4642, 3696	upstream, upstream	0	1	16	21.3	2	2_A275_shL97_glus_lncRNA:1	27	Gene:SCG_1634703		SCG1634703	NR_033849	1557743_at, 1565746_a_at	
Gene:ID:2 12	CD1D	1	158,149,737	158,156,217	6,480	+	1	2_A275_shL97_glus_lncRNA:1:925	1111	si gene	0	1	16	20	1	2_A275_shL97_glus_lncRNA:1	20	Gene:CD1D	R3, CD1A, CD1D, MGC34622	CD1d molecule	NM_001766, NCT02725353.0, NCT02725370.0, NCT31167.2	203702_at	NP_0017371, EAW62587.1, EAW62588.1, EAW62589.1
Gene:ID:3 826	IFI16	1	158,979,682	159,024,845	45,163	+	2	1_A275_shL7_dhrus_lncRNA:1:445,2_A275_shL97_glus_lncRNA:1:926	-10030, 10015	upstream, upstream	1	1	18	22	1	2_A275_shL97_glus_lncRNA:1	22	Gene:IFI16	IFI16, MGC34986, PYHIN2, IFNGIP1	interferon, gamma-inducible protein 16	NM_005531, NCT02725171.1, NCT02725172.0, NCT02725173.0, NCT02725174.1, NCT02725176.1, NCT02725177.0, NCT02526842.0	208332_s_at, 208965_s_at, 208966_x_at	NP_0055322, EAW62769.1, EAW62787.1, EAW62800.1, EAW62801.1, EAW62803.1, EAW62798.1, EAW62802.1
Gene:ID:1 447	AIM2	1	159,032,276	159,046,647	14,372	-	1	2_A275_shL97_glus_lncRNA:1:927	421	upstream	0	1	14	24	1	2_A275_shL97_glus_lncRNA:1	24	Gene:AIM2	PYHIN4, AIM2	absent in melanoma 2	NM_004833, NCT01445561.1	206513_at	NP_0048241, EAW62798.1
Gene:ID:5 1563	CADM3	1	159,141,277	159,172,812	31,355	+	4	1_A275_shL7_dhrus_lncRNA:1:445,1_A275_shL7_dhrus_lncRNA:1:446,2_A275_shL97_glus_lncRNA:1:926,2_A275_shL97_glus_lncRNA:1:928	4111, 9555, 4199, 8555	si gene, si gene, rt gene, si gene	1	1	56	56	2	2_A275_shL97_glus_lncRNA:1	63	Gene:CADM3	IGSF4B, NECL1, TSLL1, Nkl-1, synCAM3, BIgR, FLJ10868, CADM3	cell adhesion molecule 3	NM_021189, NM_001127713, NCT19870751.1, NCT27351.0, NCT30962.2	211677_x_at, 212685_s_at, 219533_at, 221621_s_at	NP_0676121, NP_0012.29451.1, EAW62782.1, EAW62783.1, EAW62784.1
Gene:ID:3 0717	DCAF6	1	160,163,503	160,232,290	69,848	-	3	1_A275_shL7_dhrus_lncRNA:1:480,1_A275_shL7_dhrus_lncRNA:1:635,2_A275_shL97_glus_lncRNA:1:936	126, 56702, 155	si gene, downstream, si gene	1	1	16	20	2	2_A275_shL97_glus_lncRNA:1	22	Gene:DCAF6	DCAF6, HIG26, WDR42A, MGC117276, MGC116891, FLJ35697, MGC99645, DKFZp761G1096	DDB1 and CUL4 associated factor 6	NM_015726, NR_028103, NR_028104, NR_028105, NR_028106, NCT27356363, NCT27356370, NCT30992.3	1554049_at, 1554048_s_at, 212293_s_at, 212294_at, 215653_s_at, 222329_at, 223627_at, 225390_at, 941316_at	NP_0568412, EAW62732.1, EAW62733.1, EAW62721.1
Gene:ID:1 0023734 0	LOC1003 87049	1	160,222,704	160,232,565	9,862	+	2	1_A275_shL7_dhrus_lncRNA:1:480,2_A275_shL97_glus_lncRNA:1:936	8520, 6465	si gene, ut gene	1	1	22	20	1	1_A275_shL7_dhrus_lnc RNA:1	22	Gene:LOC100287049		hypothetical LOC100287049	XM_002342146, XM_003116757, XM_003120795		XP_002342187.1, XP_003116803.1, XP_003120546.1
Gene:ID:1 0350596 6	LOC1003 89665	1	160,231,516	160,232,567	1,048	+	2	1_A275_shL7_dhrus_lncRNA:1:480,2_A275_shL97_glus_lncRNA:1:936	706, 674	si gene, ut gene	1	1	22	20	1	1_A275_shL7_dhrus_lnc RNA:1	22	Gene:LOC100505665		hypothetical LOC100505665	XR_108292		
Gene:ID:5 524	PEX19	1	160,248,599	160,254,841	6,242	-	2	1_A275_shL7_dhrus_lncRNA:1:481,2_A275_shL97_glus_lncRNA:1:937	58, 61	si gene, ut gene	1	1	23	26	1	2_A275_shL97_glus_lncRNA:1	26	Gene:PEX19	PXMP1, HK32, PLI55289, PEX19, DKFZp223E, PMP1, PXF, PMP1	peroxisomal biogenesis factor 19	NM_002857, NM_001160644, NR_036492, NR_036493, NCT27356332.0, NCT27356372.0, NCT30992.3	201709_s_at, 201707_at	NP_0028461, NP_001160972.1, EAW62727.1, EAW62728.1, EAW62729.1
Gene:ID:1 314	COPA	1	160,268,377	160,313,254	50,877	-	2	1_A275_shL7_dhrus_lncRNA:1:481,2_A275_shL97_glus_lncRNA:1:937	58482, 56474	downstream, downstream	1	1	23	26	1	2_A275_shL97_glus_lncRNA:1	26	Gene:COPA	FLJ36320, HEP-COP, COPA	coatomer protein complex, subunit alpha	NM_004371, NM_001098398, NCT27356310.0, NCT27356319.0, NCT30993.3	1559562_at, 200664_at, 214306_s_at, 244307_at	NP_0043622, NP_001091065.1, EAW62732.1, EAW62724.1, EAW62725.1
Gene:ID:8 062	LY9	1	160,765,926	160,798,048	32,117	+	2	1_A275_shL7_dhrus_lncRNA:1:482,2_A275_shL97_glus_lncRNA:1:938	28232, 28264	si gene, si gene	1	1	24	25	1	2_A275_shL97_glus_lncRNA:1	25	Gene:LY9	Ly9, SLAMF3, mLY9, CD229, LY9	lymphocyte antigen 9	NM_002348, NM_001033867, NCT15984.2, NCT27356310.0, NCT27356322.0, NCT31205653.0, NCT31205660.0, NCT31205665.0, NCT31205668.0	205379_s_at, 215907_s_at, 231124_x_at	NP_0023392, NP_0010338391, EAW62698.1, EAW62699.1, EAW62700.1, EAW62697.1, EAW62701.1
Gene:ID:5 1744	CD244	1	160,799,950	160,832,892	32,742	-	2	1_A275_shL7_dhrus_lncRNA:1:482,2_A275_shL97_glus_lncRNA:1:939	28532, 36900	downstream, downstream	1	1	24	25	1	2_A275_shL97_glus_lnc RNA:1	25	Gene:CD244	NAIL, Ny9-3, 2B4, NKR2B4, SLAMF4, CD244	CD244 molecule, natural killer cell receptor 2B4	NM_001166664, NCT15983.2, NM_001166663, NM_001166664, NCT15984.2, NCT27356310.0, NCT27356319.0, NCT27356322.0, NCT31205653.0, NCT31205660.0	1553892_at, 235207_at, 244220_at	NP_0011660.1, EAW62698.1, EAW62699.1, EAW62700.1, EAW62697.1, EAW62701.1
Gene:ID:5 202	PFDN2	1	161,070,346	161,087,866	17,520	-	2	1_A275_shL7_dhrus_lncRNA:1:483,2_A275_shL97_glus_lncRNA:1:939	106, 140	si gene, ut gene	1	1	23	16	1	1_A275_shL7_dhrus_lnc RNA:1	23	Gene:PFDN2	PFDN2, PFD2	prefoldin subunit 2	NM_012394, NCT27354844.0	218336_at	NP_0363262, EAW62636.1
Gene:ID:4 617	NIT1	1	161,087,662	161,095,235	7,573	+	4	1_A275_shL7_dhrus_lncRNA:1:483,1_A275_shL7_dhrus_lncRNA:1:484,1_A275_shL7_dhrus_lncRNA:1:636,2_A275_shL97_glus_lncRNA:1:939,2_A275_shL97_glus_lncRNA:1:940	-162, 16794, 108, 1482	upstream, downstream, upstream, downstream	1	1	26	21	2	1_A275_shL7_dhrus_lnc RNA:1	24	Gene:NIT1	NIT1, MGC57670	nitrilase 1	NM_001165092, NM_001165093, NM_001165094, NM_003800, NCT19870751.1, NCT27354844.0, NCT27355540.0, NCT27356390.0	202691_at, 241265_at	NP_0011720211, NP_0011720221, NP_0035911, NP_0011720231, EAW62634.1, EAW62635.1, EAW62636.1, EAW62637.1
Gene:ID:1 101	DEDD	1	161,090,767	161,102,878	11,711	+	4	1_A275_shL7_dhrus_lncRNA:1:483,1_A275_shL7_dhrus_lncRNA:1:484,1_A275_shL7_dhrus_lncRNA:1:636,2_A275_shL97_glus_lncRNA:1:939,2_A275_shL97_glus_lncRNA:1:940	14715, 176, 14782, 226	upstream, downstream, upstream, upstream	1	1	26	21	2	1_A275_shL7_dhrus_lnc RNA:1	24	Gene:DEDD	FLJ20611, DEDD, DEDD1, CASP8FP1, DEFT, KIS5	death effector domain-containing	NM_032999, NM_001039711, NM_001039712, NCT11927.3, NCT19870751.1, NCT27354844.0, NCT27354900.0, NCT27354911.0	202460_s_at, 211233_s_at, 215158_s_at	NP_1749911, NP_0010349001, NP_0010349011, EAW62640.1, EAW62641.1, EAW62642.1, EAW62643.1, EAW62644.1, EAW62651.1, EAW62652.1
Gene:ID:3 1506	UPC1	1	161,123,534	161,126,646	3,112	+	5	1_A275_shL7_dhrus_lncRNA:1:485,1_A275_shL7_dhrus_lncRNA:1:486,1_A275_shL7_dhrus_lncRNA:1:641,2_A275_shL97_glus_lncRNA:1:942,2_A275_shL97_glus_lncRNA:1:943	5554, 12594, 370, 5615, 12562	downstream, downstream, si gene, downstream, downstream	1	1	31.67	34.67	3	2_A275_shL97_glus_lncRNA:1	43	Gene:UPC1	UPC1, HSPC153	ubiquitin-like modifier conjugating enzyme 1	NM_015406, NCT27355882.2, NCT23484670.0	217797_at	NP_0378982.2, EAW62646.1, EAW62647.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:27005	USP21	1	161,129,254	161,135,516	6,262	+	5	1_A375_pNL7_minus_lncRNA::1::455, 1_A375_pNL7_minus_lncRNA::1::456, 2_A375_pNL97_plus_lncRNA::1::641, 2_A375_pNL97_plus_lncRNA::1::642, 2_A375_pNL97_plus_lncRNA::1::643	-166, 6874, -5350, -102, 6842	upstream, downstream, upstream, upstream, downstream	1	1	31.67	34.67	3	2_A375_pNL97_plus_lncRNA::1	63	Gene USP21	USP21, USP23, USP16, MGC3394	ubiquitin specific peptidase 21	NM_012475, NM_001014443, hCT1804993.2, hCT2276594.0, hCT2276595.0, hCT2276596.1	218367_x_at, 232219_x_at, 234735_s_at	NP_036607.3, NP_001014443.1, EAW52642.1, EAW52643.1, EAW52644.1, EAW52645.1
GeneID:5498	PPOX	1	161,136,181	161,141,010	4,829	+	4	1_A375_pNL7_minus_lncRNA::1::455, 1_A375_pNL7_minus_lncRNA::1::456, 2_A375_pNL97_plus_lncRNA::1::642, 2_A375_pNL97_plus_lncRNA::1::643	-7093, -53, -7029, -85	upstream, upstream, upstream, upstream	1	1	38.5	39.5	2	2_A375_pNL97_plus_lncRNA::1	63	Gene PPOX	MGC8485, V290M, PPOX, PPO, VP	protoporphyrinogen oxidase	NM_000309, NM_001122764, hCT1804992.2, hCT1950444.1, hCT1966807.1, hCT2276597.0, hCT2276598.0, hCT2276599.0, hCT2352675.0	204768_s_at, 238117_at, 238118_s_at	NP_000300.1, NP_001116236.1, EAW52636.1, EAW52637.1, EAW52638.1, EAW52641.1, EAW52635.1, EAW52639.1, EAW52640.1
GeneID:8703	B4GALT3	1	161,141,101	161,147,314	6,213	-	2	1_A375_pNL7_minus_lncRNA::1::456, 2_A375_pNL97_plus_lncRNA::1::643	11186, 11218	downstream, downstream	1	1	59	63	1	2_A375_pNL97_plus_lncRNA::1	63	Gene B4GALT3	beta4Gal-T3, B4GALT3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	NM_003779, hCT1805014.2, hCT2275484.1, hCT2275485.0, hCT2343741.0, hCT2343742.0, hCT2352620.0, hCT2352621.0	210243_s_at, 238312_s_at	NP_003770.1, EAW52628.1, EAW52629.1, EAW52630.1, EAW52631.1, EAW52633.1, EAW52632.1, EAW52634.1
GeneID:9507	ADAMTS4	1	161,159,538	161,168,845	9,307	-	1	2_A375_pNL97_plus_lncRNA::1::644	-3379	upstream	0	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ADAMTS4	KIAA0688, ADAMTS-2, ADAMTS4, ADMP-1, ADAMTS-4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	NM_005099, hCT8887.3	1555350_at	NP_005090.3, EAW52627.1
GeneID:4720	NDUFS2	1	161,169,105	161,184,185	15,080	+	1	2_A375_pNL97_plus_lncRNA::1::644	3119	in gene	0	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene NDUFS2	CI-49, NDUFS2		NM_004550, NM_001166159, hCT2276604.0, hCT8911.4	201966_at	NP_004541.1, NP_001159631.1, EAW52625.1, EAW52626.1
GeneID:2207	FCER1G	1	161,185,087	161,189,038	3,951	+	1	2_A375_pNL97_plus_lncRNA::1::645	10849	downstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene FCER1G	FCRG, FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	NM_004106, hCT2276607.0, hCT2276608.0	1554899_s_at, 204232_at	NP_004097.1, EAW52623.1, EAW52624.1
GeneID:336	APOA2	1	161,192,083	161,193,418	1,335	-	1	2_A375_pNL97_plus_lncRNA::1::645	-2518	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene APOA2	ApoA-II, APOA2, apoAII, Apo-AII		NM_001643, hCT2275480.1, hCT2343743.0, hCT2345694.0, hCT2345696.0, hCT2345697.0	219465_at, 219466_s_at	NP_001634.1, EAW52622.1, EAW52618.1, EAW52619.1, EAW52620.1, EAW52621.1
GeneID:84134	TOMM40L	1	161,195,833	161,200,408	4,575	+	1	2_A375_pNL97_plus_lncRNA::1::645	103	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TOMM40L	TOMM40B, FLJ12770, RP11-297K8.10, TOMM40L	translocase of outer mitochondrial membrane 40 homolog (yeast)-like	NM_032174, hCT2276609.0, hCT2344327.0, hCT2344328.0, hCT2344329.0, hCT2344330.0, hCT2344331.0, hCT2352707.0	226059_at	NP_115550.2, EAW52611.1, EAW52613.1, EAW52614.1, EAW52615.1, EAW52617.1, EAW52612.1, EAW52616.1
GeneID:9970	NR1I3	1	161,199,456	161,208,000	8,544	-	1	2_A375_pNL97_plus_lncRNA::1::645	12064	downstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene NR1I3	MGC97144, MGC97209, NR1I3, CAR, MB67, MGC150433, CAR1	nuclear receptor subfamily 1, group I, member 3	NM_001077469, NM_005122, NM_001077470, NM_001077471, NM_001077472, NM_001077473, NM_001077474, NM_001077475, NM_001077476, NM_001077478, NM_001077477, NM_001077479, NM_001077480, NM_001077481, NM_001077482, hCT1805016.1, hCT2352640.0, hCT2352641.0	1570188_at, 207007_at	NP_001070937.1, NP_005113.1, NP_001070938.1, NP_001070939.1, NP_001070940.1, NP_001070941.1, NP_001070942.1, NP_001070943.1, NP_001070944.1, NP_001070946.1, NP_001070945.1, NP_001070947.1, NP_001070948.1, NP_001070949.1, NP_001070950.1, EAW52608.1, EAW526
GeneID:100505703	LOC100505703	1	161,369,199	161,392,630	23,431	+	7	1_A375_pNL7_minus_lncRNA::1::458, 1_A375_pNL7_minus_lncRNA::1::459, 1_A375_pNL7_minus_lncRNA::1::460, 2_A375_pNL97_plus_lncRNA::1::647, 2_A375_pNL97_plus_lncRNA::1::648, 2_A375_pNL97_plus_lncRNA::1::649, 2_A375_pNL97_plus_lncRNA::1::650	-9039, 401, 22737, -9615, -8991, 401, 22641	upstream, in gene, in gene, upstream, upstream, in gene, in gene	1	1	19.67	23.33	3	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100505703		hypothetical LOC100505703	XR_108294, XR_114825		
GeneID:2212	FCGR2A	1	161,475,205	161,489,360	14,155	+	1	2_A375_pNL97_plus_lncRNA::1::652	-6565	upstream	0	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FCGR2A	CDw32, FCGR2A1, FCGR2A, CD32, MGC30032, FCG2, IGFR2, FCGR2, CD32A, MGC23887, FcGR	Fc fragment of IgG, low affinity IIa, receptor (CD32)	NM_021642, NM_001136219	1565673_at, 1565674_at, 203561_at	NP_067674.2, NP_001129691.1
GeneID:3310	HSPA6	1	161,494,036	161,496,687	2,651	+	1	2_A375_pNL97_plus_lncRNA::1::653	6780	downstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene HSPA6	HSPA6		NM_002155	117_at, 213418_at	NP_002146.2
GeneID:2214	FCGR3A	1	161,511,549	161,520,413	8,864	-	2	1_A375_pNL7_minus_lncRNA::1::461, 2_A375_pNL97_plus_lncRNA::1::654	10301, 10349	downstream, downstream	1	1	25	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene FCGR3A	FCG3, FCGR3, IGFR3, FCR-10, FCRIII, FCGR3A, CD16, FCRIIIA, CD16A, FCGRIII	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	NM_000569, NM_001127592, NM_001127593, NM_001127595, NM_001127596	204006_s_at	NP_000560.5, NP_001121064.1, NP_001121065.1, NP_001121067.1, NP_001121068.1
GeneID:84824	FCRLA	1	161,676,762	161,684,142	7,380	+	2	1_A375_pNL7_minus_lncRNA::1::462, 2_A375_pNL97_plus_lncRNA::1::655	15174, 15158	downstream, downstream	1	1	32	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene FCRLA	FCRX, FCRLe, FCRLc2, FREB, FCRLA, FCRL, FCRLd, FCRLM1, FCRL1, FCRLb, RP11-474I16.5, MGC4595, FCRLc1, FCRLX	Fc receptor-like A	NM_032738, NM_001184866, NM_001184867, NM_001184870, NM_001184871, NM_001184872, NM_001184873, hCT1641704.2, hCT1951537.1, hCT1960931.1, hCT1960932.1, hCT1960933.1, hCT2357410.0, hCT2357411.0	235372_at, 235400_at, 235401_s_at	NP_116127.3, NP_001171795.1, NP_001171796.1, NP_001171799.1, NP_001171800.1, NP_001171801.1, NP_001171802.1, EAW90683.1, EAW90684.1, EAW90685.1, EAW90686.1, EAW90687.1, EAW90688.1, EAW90689.1
GeneID:127943	FCRLB	1	161,692,457	161,697,933	5,476	+	5	1_A375_pNL7_minus_lncRNA::1::462, 1_A375_pNL7_minus_lncRNA::1::463, 1_A375_pNL7_minus_lncRNA::1::464, 2_A375_pNL97_plus_lncRNA::1::655, 2_A375_pNL97_plus_lncRNA::1::656	-521, 3959, 7671, -537, 3863	upstream, in gene, downstream, upstream, in gene	1	1	26.67	24	3	2_A375_pNL97_plus_lncRNA::1	34	Gene FCRLB	FCRLM2, FCRLB, FCRL2, RP11-474I16.6, FCRLY, FREB-2, FcRY, FLJ31052	Fc receptor-like B	NM_001002901, hCT1642726.2, hCT2357414.0	238452_at	NP_001002901.1, EAW90690.1, EAW90691.1
GeneID:11266	DUSP12	1	161,719,581	161,726,952	7,371	+	4	1_A375_pNL7_minus_lncRNA::1::465, 1_A375_pNL7_minus_lncRNA::1::466, 2_A375_pNL97_plus_lncRNA::1::657, 2_A375_pNL97_plus_lncRNA::1::658	-29, 16547, -61, 16547	upstream, downstream, upstream, downstream	1	1	26	25	2	1_A375_pNL7_minus_lncRNA::1	31	Gene DUSP12	DUSP12, YVH1, DUSP1	dual specificity phosphatase 12	NM_007240, hCT6880.3	218576_s_at	NP_009171.1, EAW90692.1
GeneID:22926	ATF6	1	161,736,084	161,928,852	192,768	+	2	1_A375_pNL7_minus_lncRNA::1::466, 2_A375_pNL97_plus_lncRNA::1::658	44, 44	in gene, in gene	1	1	21	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ATF6	ATF6, ATF6A	activating transcription factor 6	NM_007348, hCT6878.2	203952_at, 217550_at, 231927_at	NP_031374.2, EAW90694.1
GeneID:25903	OLFML2B	1	161,952,982	161,993,644	40,662	-	1	2_A375_pNL97_plus_lncRNA::1::659	20460	in gene	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene OLFML2B	RP11-227F8.1, MGC51337, OLFML2B	olfactomedin-like 2B	NM_015441, hCT1806448.1, hCT2323229.0, hCT6881.2	213125_at	NP_056256.1, EAW90696.1, EAW90697.1, EAW90698.1
GeneID:9722	NOS1AP	1	162,039,581	162,339,813	300,232	+	2	1_A375_pNL7_minus_lncRNA::1::467, 2_A375_pNL97_plus_lncRNA::1::661	240739, 240771	in gene, in gene	1	1	30	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene NOS1AP	6330408P19Rik, NOS1AP, MGC138500, CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	NM_001126060, NM_014697, NM_001164757, hCT6884.3	1563512_at, 215153_at	NP_001119532.2, NP_055512.1, NP_001158229.1, EAW90700.1
GeneID:117157	SH2D1B	1	162,365,056	162,381,928	16,872	-	1	1_A375_pNL7_minus_lncRNA::1::468	7144	in gene	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SH2D1B	SH2D1B, EAT2	SH2 domain containing 1B	NM_053282, hCT1642725.3, hCT1964702.2, hCT2344769.0	1553176_at, 1553177_at	NP_444512.2, EAW90703.1, EAW90704.1, EAW90705.1
GeneID:127933	UHMK1	1	162,466,964	162,499,419	32,455	+	2	1_A375_pNL7_minus_lncRNA::1::469, 2_A375_pNL97_plus_lncRNA::1::662	812, 748	in gene, in gene	1	1	21	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene UHMK1	FLJ23015, UHMK1, KIS, DKFZp434C1613, KIST	U2AF homology motif (UHM) kinase 1	NM_001184763, NM_144624, NM_175866, hCT2323214.1, hCT2323215.1, hCT2349335.0, hCT6882.4	1552656_s_at, 227740_at, 235003_at	NP_001171692.1, NP_653225.2, NP_787062.1, EAW90706.1, EAW90707.1, EAW90708.1, EAW90709.1
GeneID:6675	UAP1	1	162,531,296	162,569,633	38,337	+	3	1_A375_pNL7_minus_lncRNA::1::470, 2_A375_pNL97_plus_lncRNA::1::663, 2_A375_pNL97_plus_lncRNA::1::664	448, 400, 44208	in gene, in gene, downstream	1	1	16.5	22	2	2_A375_pNL97_plus_lncRNA::1	28	Gene UAP1	AGX, UAP1, SPAG2, AGX2, AGX1	UDP-N-acteylglucosamine pyrophosphorylase 1	NM_003115, hCT1951536.1, hCT2323218.0, hCT6879.3	209340_at	NP_003106.3, EAW90712.1, EAW90710.1, EAW90711.1
GeneID:4921	DDR2	1	162,602,228	162,750,255	148,027	+	1	2_A375_pNL97_plus_lncRNA::1::665	540	in gene	0	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene DDR2	TKT, TYRO10, MIG20a, DDR2, NTRKR3	discoidin domain receptor tyrosine kinase 2	NM_006182, NM_001014796, hCT2357443.0, hCT5718.3	205168_at, 225442_at, 227561_at, 235631_at	NP_006173.2, NP_001014796.1, EAW90713.1, EAW90714.1
GeneID:83540	NUF2	1	163,291,723	163,325,553	33,830	+	2	1_A375_pNL7_minus_lncRNA::1::472, 2_A375_pNL97_plus_lncRNA::1::667	-43, 21	upstream, in gene	1	1	51	66	1	2_A375_pNL97_plus_lncRNA::1	66	Gene NUF2	NUF2R, CT106, NUF2, CDCA1	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	NM_031423, NM_145697, hCT1957725.1, hCT2357422.0, hCT6216.2	223381_at	NP_113611.2, NP_663735.2, EAW90735.1, EAW90736.1, EAW90737.1
GeneID:5087	PBX1	1	164,528,802	164,821,045	292,243	+	1	1_A375_pNL7_minus_lncRNA::1::473	-834	upstream	1	0	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene PBX1	MGC126627, DKFZp686B09108, PBX1	pre-B-cell leukemia homeobox 1	NM_002585, hCT14111.3, hCT1951556.2, hCT2326852.0, hCT2326854.1	205253_at, 212148_at, 212151_at	NP_002576.1, EAW90740.1, EAW90738.1, EAW90739.1, EAW90741.1
GeneID:400794	LOC400794	1	165,446,079	165,551,341	105,262	-	2	1_A375_pNL7_minus_lncRNA::1::474, 2_A375_pNL97_plus_lncRNA::1::669	42605, 42637	in gene, in gene	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC400794		hypothetical LOC400794	NR_026744	1556601_at, 1557761_s_at, 1561693_at	
GeneID:440699	LRRC52	1	165,513,478	165,533,185	19,707	+	2	1_A375_pNL7_minus_lncRNA::1::474, 2_A375_pNL97_plus_lncRNA::1::669	-4742, -4774	upstream, upstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LRRC52	LRRC52, FLJ25811	leucine rich repeat containing 52	NM_001005214	1556484_at	NP_001005214.2
GeneID:4259	MGST3	1	165,600,450	165,624,857	24,407	+	2	1_A375_pNL7_minus_lncRNA::1::475, 2_A375_pNL97_plus_lncRNA::1::670	-290, 174	upstream, in gene	1	1	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene MGST3	MGST3, GST-III	microsomal glutathione S-transferase 3	NM_004528, hCT1808738.3, hCT1951549.2, hCT2345060.0, hCT2345061.0, hCT2345062.0, hCT2357427.0	201403_s_at, 244122_at	NP_004519.1, EAW90756.1, EAW90752.1, EAW90753.1, EAW90755.1, EAW90757.1, EAW90754.1
GeneID:223	ALDH9A1	1	165,631,449	165,667,900	36,451	-	1	1_A375_pNL7_minus_lncRNA::1::476	177	in gene	1	0	19	19	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ALDH9A1	E3, TMABADH, ALDH9A1, ALDH9, ALDH4, ALDH7	aldehyde dehydrogenase 9 family, member A1	NM_000696, hCT12838.3	201612_at	NP_000687.3, EAW90758.1
GeneID:54499	TMCO1	1	165,693,528	165,738,135	44,607	-	2	1_A375_pNL7_minus_lncRNA::1::477, 2_A375_pNL97_plus_lncRNA::1::671	87, -105	in gene, upstream	1	1	27	21	1	1_A375_pNL7_minus_lncRNA::1	27	Gene TMCO1	RP11-466F5.7, PNAS-136, TMCC4, PCIA3, TMCO1, HP10122	transmembrane and coiled-coil domains 1	NM_019026, hCT1804924.3, hCT2345057.0, hCT2345058.0, hCT2345059.0	208715_at, 208716_s_at, 210768_x_at, 211098_x_at	NP_061899.1, EAW90763.1, EAW90762.1, EAW90764.1, EAW90765.1
GeneID:100147773	LOC100147773	1	165,738,166	165,744,844	6,678	+	2	1_A375_pNL7_minus_lncRNA::1::477, 2_A375_pNL97_plus_lncRNA::1::671	-118, 74	upstream, in gene	1	1	27	21	1	1_A375_pNL7_minus_lncRNA::1	27	Gene LOC100147773	FLJ42974	hypothetical LOC100147773	XR_111961, XR_108300, XR_114979		
GeneID:7371	UCK2	1	165,796,890	165,877,343	80,453	+	1	1_A375_pNL7_minus_lncRNA::1::478	731	in gene	1	0	15	13	1	1_A375_pNL7_minus_lncRNA::1	15	Gene UCK2	TSA903, DKFZp686M04245, UCK2, UMPK, UK	uridine-cytidine kinase 2	NM_012474, hCT13761.2, hCT1951554.1, hCT1951555.1	209825_s_at	NP_036606.2, EAW90768.1, EAW90767.1, EAW90769.1
GeneID:149297	FAM78B	1	166,039,256	166,135,958	96,702	-	4	1_A375_pNL7_minus_lncRNA::1::480, 1_A375_pNL7_minus_lncRNA::1::481, 2_A375_pNL97_plus_lncRNA::1::672, 2_A375_pNL97_plus_lncRNA::1::673	-634, -4234, -618, -4170	upstream, upstream, upstream, upstream	1	1	19	21	2	2_A375_pNL97_plus_lncRNA::1	23	Gene FAM78B	MGC131653, FAM78B	family with sequence similarity 78, member B	NM_001017961, hCT1951557.1	1558113_at	NP_001017961.1, EAW90771.1
GeneID:57645	POGK	1	166,808,724	166,823,709	14,985	+	1	2_A375_pNL97_plus_lncRNA::1::674	-308	upstream	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene POGK	LST003, KRBOX2, BASS2, KIAA1513, POGK, KIAA15131	pogo transposable element with KRAB domain	NM_017542, hCT2322790.0, hCT2322791.0, hCT2322793.0	218229_s_at, 222564_at	NP_060012.3, EAW90777.1, EAW90775.1, EAW90776.1
GeneID:117143	TADA1	1	166,825,747	166,845,654	19,907	-	2	1_A375_pNL7_minus_lncRNA::1::482, 2_A375_pNL97_plus_lncRNA::1::675	54, 38	in gene, in gene	1	1	38	35	1	1_A375_pNL7_minus_lncRNA::1	38	Gene TADA1	hADA1, ADA1, HFI1, RP1-9E21.4, TADA1L, TADA1, STAF42	transcriptional adaptor 1	NM_053053, hCT29232.3	1559269_at, 225455_at	NP_444281.1, EAW90778.1
GeneID:387597	ILDR2	1	166,887,996	166,944,561	56,565	-	2	1_A375_pNL7_minus_lncRNA::1::483, 2_A375_pNL97_plus_lncRNA::1::676	22737, 22737	in gene, in gene	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene ILDR2	ILDR2, dJ782G3.1, RP4-782G3.2, C1orf32	immunoglobulin-like domain containing receptor 2	NM_199351, hCT29230.3		NP_955383.1, EAW90779.1
GeneID:92235	DUSP27	1	167,064,087	167,098,402	34,315	+	1	2_A375_pNL97_plus_lncRNA::1::677	41545	downstream	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene DUSP27	DUSP27		NM_001080426	232252_at	NP_001073895.1
GeneID:5451	POU2F1	1	167,190,143	167,385,342	195,199	+	4	1_A375_pNL7_minus_lncRNA::1::485, 1_A375_pNL7_minus_lncRNA::1::486, 2_A375_pNL97_plus_lncRNA::1::679, 2_A375_pNL97_plus_lncRNA::1::680	161, 1345, -266, 1521	in gene, in gene, upstream, in gene	1	1	24.5	18	2	1_A375_pNL7_minus_lncRNA::1	27	Gene POU2F1	POU2F1, FLJ42836, OCT1, OTF1	POU class 2 homeobox 1	NM_002697, hCT1951562.1, hCT2324115.0, hCT29227.3	206789_s_at	NP_002688.2, EAW90787.1, EAW90786.1, EAW90788.1
GeneID:919	CD247	1	167,399,877	167,487,847	87,970	-	1	2_A375_pNL97_plus_lncRNA::1::681	903	in gene	0	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CD247	T3Z, CD247, CD3H, CD3Q, CD3-ZETA, TCRZ, CD3Z	CD247 molecule	NM_198053, NM_000734, hCT1807549.2, hCT1962038.1, hCT2357440.0	210031_at	NP_932170.1, NP_000725.1, EAW90790.1, EAW90791.1, EAW90792.1
GeneID:8804	CREG1	1	167,510,250	167,523,056	12,806	-	2	1_A375_pNL7_minus_lncRNA::1::487, 2_A375_pNL97_plus_lncRNA::1::682	320, -10032	in gene, upstream	1	1	19	20	2	2_A375_pNL97_plus_lncRNA::1	22	Gene CREG1	CREG, CREG1	cellular repressor of E1A-stimulated genes 1	NM_003851, hCT2324200.0, hCT32589.3	201200_at	NP_003842.1, EAW90794.1, EAW90795.1
GeneID:92241	RCSD1	1	167,599,474	167,675,486	76,012	+	2	1_A375_pNL7_minus_lncRNA::1::488, 2_A375_pNL97_plus_lncRNA::1::683	84430, 84366	downstream, downstream	1	1	31	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene RCSD1	MK2S4, MGC126611, MGC21854, CAPZIP, RCSD1, MGC126585	RCSD domain containing 1	NM_052862, hCT2324121.1, hCT2324122.1, hCT2349443.0, hCT33673.4	225763_at	NP_443094.3, EAW90799.1, EAW90796.1, EAW90797.1, EAW90798.1
GeneID:9019	MPZL1	1	167,691,187	167,761,156	69,969	+	3	1_A375_pNL7_minus_lncRNA::1::488, 2_A375_pNL97_plus_lncRNA::1::683, 2_A375_pNL97_plus_lncRNA::1::684	-7283, -7347, 45	upstream, upstream, in gene	1	1	23.5	32.5	2	2_A375_pNL97_plus_lncRNA::1	39	Gene MPZL1	FLJ21047, PZR, PZRa, PZRb, MPZL1, MPZL1b, PZR1b	myelin protein zero-like 1	NM_003953, NM_024569, NM_001146191, hCT1962098.1, hCT1962099.1, hCT2324127.0, hCT33667.3	201874_at, 201875_s_at, 210087_s_at, 210210_at, 210594_x_at	NP_003944.1, NP_078845.3, NP_001139663.1, EAW90800.1, EAW90801.1, EAW90802.1, EAW90803.1
GeneID:25874	BRP44	1	167,887,310	167,906,278	18,968	-	2	1_A375_pNL7_minus_lncRNA::1::489, 2_A375_pNL97_plus_lncRNA::1::685	-378, 1126	upstream, in gene	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene BRP44	MGC125753, MGC125752, DKFZp564B167, BRP44	brain protein 44	NM_015415, NM_001143674, NR_026550, hCT2324191.0, hCT2324192.0, hCT2357430.0, hCT2357431.0	202427_s_at, 227669_at	NP_056230.1, NP_001137146.1, EAW90813.1, EAW90814.1, EAW90815.1, EAW90816.1
GeneID:55827	DCAF6	1	167,905,908	168,045,081	139,173	+	2	1_A375_pNL7_minus_lncRNA::1::489, 2_A375_pNL97_plus_lncRNA::1::685	748, -756	in gene, upstream	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene DCAF6	1200006M05Rik, FLJ23798, MSTP055, ARCAP, IQWD1, DCAF6, PC326, NRIP	DDB1 and CUL4 associated factor 6	NM_018442, NM_001017977, hCT2324129.0, hCT2324130.0, hCT2324131.0, hCT2324132.0, hCT2324133.0	217908_s_at, 232349_x_at, 241209_at	NP_060912.2, NP_001017977.1, EAW90808.1, EAW90809.1, EAW90811.1, EAW90812.1, EAW90810.1
GeneID:261726	TIPRL	1	168,148,171	168,171,352	23,181	+	1	2_A375_pNL97_plus_lncRNA::1::686	245	in gene	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene TIPRL	dJ69E11.3, MGC3794, TIP, TIP41, TIPRL	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	NM_152902, NM_001031800, hCT2357379.0, hCT33676.2	1553677_a_at, 1554351_a_at, 214773_x_at, 226619_x_at	NP_690866.1, NP_001026970.1, EAW90820.1, EAW90821.1
GeneID:375035	SFT2D2	1	168,195,255	168,212,088	16,833	+	1	2_A375_pNL97_plus_lncRNA::1::687	11145	in gene	0	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SFT2D2	dJ747L4.C1.2, FLJ34085, SFT2D2, UNQ512	SFT2 domain containing 2	NM_199344, hCT33671.3	214838_at	NP_955376.1, EAW90822.1
GeneID:9095	TBX19	1	168,250,278	168,283,664	33,386	+	1	2_A375_pNL97_plus_lncRNA::1::688	40058	downstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TBX19	FLJ34543, dJ747L4.1, TBS19, FLJ34085, TBX19, FLJ26302, TPIT	T-box 19	NM_005149, hCT33670.2	206838_at	NP_005140.1, EAW90824.1
GeneID:1805	DPT	1	168,664,695	168,698,442	33,747	-	3	1_A375_pNL7_minus_lncRNA::1::493, 1_A375_pNL7_minus_lncRNA::1::494, 2_A375_pNL97_plus_lncRNA::1::689	19978, 9626, 9762	in gene, in gene, in gene	1	1	21	18	2	1_A375_pNL7_minus_lncRNA::1	26	Gene DPT	TRAMP, DPT	dermatopontin	NM_001937, hCT29035.3	207977_s_at, 213068_at, 213071_at	NP_001928.2, EAW90830.1
GeneID:481	ATP1B1	1	169,075,947	169,101,960	26,013	+	3	2_A375_pNL97_plus_lncRNA::1::690, 2_A375_pNL97_plus_lncRNA::1::691, 2_A375_pNL97_plus_lncRNA::1::692	-363, 181, 9461	upstream, in gene, in gene	0	1	17	21.33	3	2_A375_pNL97_plus_lncRNA::1	23	Gene ATP1B1	MGC1798, ATP1B1, ATP1B	ATPase, Na+/K+ transporting, beta 1 polypeptide	NM_001677, hCT1951559.1, hCT29032.3	201242_s_at, 201243_s_at	NP_001668.1, EAW90833.1, EAW90832.1
GeneID:29922	NME7	1	169,101,769	169,337,186	235,417	-	3	1_A375_pNL7_minus_lncRNA::1::495, 1_A375_pNL7_minus_lncRNA::1::496, 2_A375_pNL97_plus_lncRNA::1::693	204450, 55746, 55714	in gene, in gene, in gene	1	1	33	45	2	2_A375_pNL97_plus_lncRNA::1	73	Gene NME7	nm23-H7, FLJ37194, MN23H7, NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	NM_197972, NM_013330, hCT2322848.0, hCT2357408.0, hCT29033.3	219553_at, 227556_at	NP_932076.1, NP_037462.1, EAW90834.1, EAW90835.1, EAW90836.1

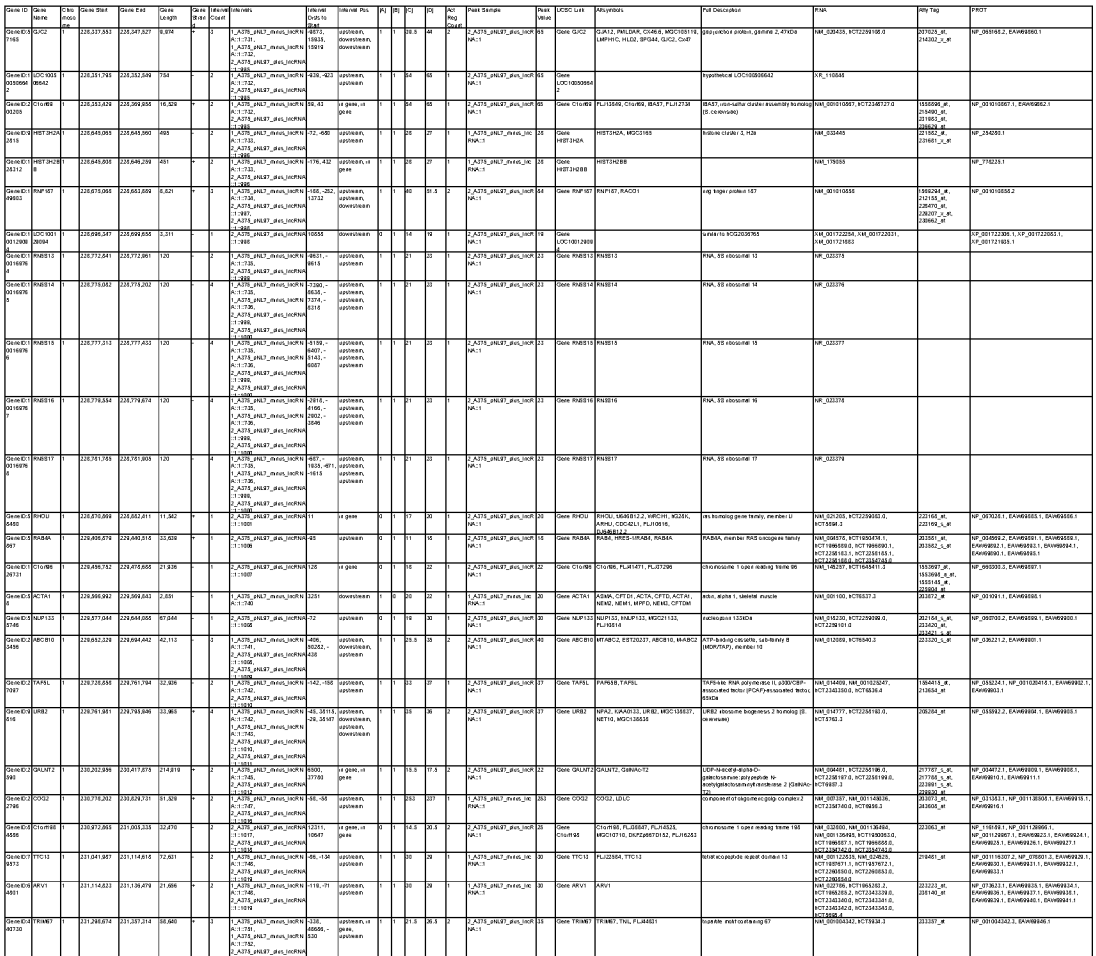
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervening Features	Intervening Counts	Intervening Positions	[A]	[B]	[C]	[D]	Acc Reg Count	Peak Sample	Peak Value	UCSC Link	Attributes	Full Description	RNA	Affy Tag	PROT
Gene:ID:2153	PS	1	169,451,192	169,553,769	74,577	+	1	2_A275_chL97_dtcs_lncRNA:1:1684	4355	upstream	0	1	19	20	1	2_A275_chL97_dtcs_lncRNA:1	20	Gene: PS	PCCP, PS, PVL	Endogenous factor V (procoagulant, latent factor)	NM_000130, NCT02246413	204713_s_at, 206714_s_at, 231029_at	NP_000121.2, EAW93549.1
Gene:ID:6breast	SELP	1	169,556,057	169,599,377	41,320	-	1	2_A275_chL97_dtcs_lncRNA:1:1684	14300	st gene	0	1	19	20	1	2_A275_chL97_dtcs_lncRNA:1	20	Gene: SELP	FLJ45153, GMP140, GRMP, CD62, PSEL, SELP, PADGEM, LECAM6, CD62P	selectin P (granule membrane protein 140kDa, antigen CD62)	NM_003005, NCT02226639, NCT02226861, NCT02246413, NCT02246426	206049_at	NP_002996.2, EAW93550.1, EAW93552.1, EAW93553.1, EAW93554.1
Gene:ID:2342	C1orf156	1	169,761,670	169,764,031	2,361	-	2	1_A275_chL97_dtcs_lncRNA:1:1687, 2_A275_chL97_dtcs_lncRNA:1:1687	-177, -129	upstream, upstream	1	1	16	23	1	2_A275_chL97_dtcs_lncRNA:1	23	Gene: C1orf156	chromosome 1 open reading frame 156	MGC9034, C1orf156, ALTF2, METTL18, RP1-117720.4	NM_032416, NCT01642753.2, NCT01915940.1	213328_at	NP_219655.1, EAW93562.1, EAW93561.1
Gene:ID:5712	C1orf112	1	169,764,550	169,822,229	57,679	+	2	1_A275_chL97_dtcs_lncRNA:1:1687, 2_A275_chL97_dtcs_lncRNA:1:1687	-242, -360	upstream, upstream	1	1	16	23	1	2_A275_chL97_dtcs_lncRNA:1	23	Gene: C1orf112	MGC130019, FLJ13470, C1orf112, FLJ10706, RP1-97F20.1, MGC130016	chromosome 1 open reading frame 112	NM_018186, NCT01915896.0, NCT02574002.0, NCT02989.2	220640_s_at	NP_060656.2, EAW93594.1, EAW93563.1, EAW93565.1, EAW93566.1
Gene:ID:7147	SCYL2	1	169,821,804	169,863,076	41,272	-	2	1_A275_chL97_dtcs_lncRNA:1:1686, 2_A275_chL97_dtcs_lncRNA:1:1686	-220, -124	upstream, upstream	1	1	22	28	1	2_A275_chL97_dtcs_lncRNA:1	28	Gene: SCYL2	FACE-1, SCYL3, FACE1, RP14P20.2	SCY1-like 2 (S. cerevisiae)	NM_020423, NM_181093, NCT02380410.0, NCT02382.0	203407_s_at, 40126_at	NP_065156.5, NP_851607.2, EAW93567.1, EAW93568.1
Gene:ID:2420	IGFAP3	1	169,890,870	170,043,879	153,009	-	3	1_A275_chL97_dtcs_lncRNA:1:1692, 2_A275_chL97_dtcs_lncRNA:1:1687, 3_A275_chL97_dtcs_lncRNA:1:1688	-37, 73167, -41	upstream, st gene, upstream	1	1	17.5	19.5	2	3_A275_chL97_dtcs_lncRNA:1	26	Gene: IGFAP3	IGFAP3, KIAA0, dJ160H16.1, SWAP, Sng-1-like	neurexin-associated protein 3	NM_018370, NCT01955558.1, NCT02053602.0, NCT02572992.0, NCT02572700.0, NCT02246.2	202333_at	NP_055182.2, EAW93570.1, EAW93569.1, EAW93571.1, EAW93572.1, EAW93573.1
Gene:ID:2344	GORAB	1	170,561,263	170,622,874	61,711	+	2	1_A275_chL97_dtcs_lncRNA:1:1692, 2_A275_chL97_dtcs_lncRNA:1:1692	-79, -51	upstream, st gene	1	1	20	31	1	2_A275_chL97_dtcs_lncRNA:1	31	Gene: GORAB	MGC51262, MGC70512, GORAB, FLJ11752, MTMLBP1, SCYL1BP1, GCI	golgin, RAB6-interacting	NM_152281, NM_027397, NM_001146238, NCT01951957.1, NCT01955665.1, NCT02733.2	226327_at	NP_689494.2, NP_001138911.1, EAW93576.1, EAW93577.1, EAW93578.1, EAW93580.1
Gene:ID:5398	PRRX1	1	170,633,313	170,706,841	73,528	+	2	1_A275_chL97_dtcs_lncRNA:1:1694, 2_A275_chL97_dtcs_lncRNA:1:1691	40015, 24653	st gene, st gene	1	1	12.5	15.5	2	2_A275_chL97_dtcs_lncRNA:1	19	Gene: PRRX1	PRX1, PHOX1, PMX1, PRRX1	paired related homeobox 1	NM_022716, NM_006902, NCT00587612, NCT02726.2	206991_s_at, 236683_at	NP_072207.1, NP_008832.1, EAW93582.1, EAW93583.1
Gene:ID:3215	FAM34	1	171,283,456	171,311,223	27,767	+	1	2_A275_chL97_dtcs_lncRNA:1:1693	-350	upstream	0	1	10	16	1	2_A275_chL97_dtcs_lncRNA:1	16	Gene: FAM34	FAM32, FAM34	three cluster-ring microoxygenase 4	NM_052022, NCT02340816.0, NCT02312.4	208263_at	NP_003013.1, EAW93597.1, EAW93598.1
Gene:ID:674	BAT2L2	1	171,454,999	171,562,650	107,664	+	2	1_A275_chL97_dtcs_lncRNA:1:1697, 2_A275_chL97_dtcs_lncRNA:1:1704	-106, -74	upstream, upstream	1	1	26	22	1	2_A275_chL97_dtcs_lncRNA:1	26	Gene: BAT2L2	ATP2, BAT2L2, BAT2D1, PRKCQC, BAT2-rss	HLA-B associated transcript 2-like 2	NM_015172, NCT02334836.0, NCT02340836.0, NCT02340840.0, NCT02353950.0, NCT.09057.3	211944_at, 211945_s_at, 211947_s_at, 211948_s_at, 214652_x_at, 214653_x_at, 214654_x_at	NP_055977.2, EAW93599.1, EAW93599.1, EAW93600.1, EAW93601.1, EAW93602.1
Gene:ID:674	VAMP4	1	171,699,298	171,711,279	42,083	-	2	1_A275_chL97_dtcs_lncRNA:1:1695, 2_A275_chL97_dtcs_lncRNA:1:1703	131, 165	st gene, st gene	1	1	32	45	1	2_A275_chL97_dtcs_lncRNA:1	32	Gene: VAMP4	VAMP4, VAMP-4, VAMP24	vesicle-associated membrane protein 4	NM_001130127, NM_052962, NM_032704, NCT01951961.3, NCT01952667.2, NCT01955554.2, NCT02353910.0, NCT02373262.0, NCT02953.2	207700_s_at, 211760_s_at, 211761_s_at, 214691_x_at	NP_001172266.1, NP_002753.2, EAW93602.1, EAW93607.1, EAW93605.1, EAW93606.1, EAW93603.1, EAW93606.1
Gene:ID:1603	METTL13	1	171,780,761	171,799,896	19,095	+	2	1_A275_chL97_dtcs_lncRNA:1:1699, 2_A275_chL97_dtcs_lncRNA:1:1699	12727, 12693	st gene, st gene	1	1	24	23	1	2_A275_chL97_dtcs_lncRNA:1	24	Gene: METTL13	METTL13, CSD-01, fcbl, KIAA0859, FLJ10310, bb2d001024fm	methyltransferase like 13	NM_025007238, NM_014953, NM_015935, NCT01955552.1, NCT02354840.0, NCT02373307.0, NCT02953.2	206465_s_at, 212403_s_at, 212407_s_at	NP_001007240.1, NP_038770.1, NP_057019.2, EAW93612.1, EAW93612.1, EAW93614.1, EAW93611.1
Gene:ID:6652	DNM3	1	171,810,621	172,081,857	271,236	-	3	1_A275_chL97_dtcs_lncRNA:1:1510, 2_A275_chL97_dtcs_lncRNA:1:1511, 3_A275_chL97_dtcs_lncRNA:1:1697	-283, 3373, 69	upstream, st gene, st gene	1	1	16.5	15	2	2_A275_chL97_dtcs_lncRNA:1	22	Gene: DNM3	KIAA0820, MGC70433, DNM3	dynamin 3	NM_015947, NCT01955627, NCT02246461.1, NCT02246122, NCT02246513.0, NCT02353610.0, NCT02373564.0, NCT02353610, NCT.09059.3	1555501_at, 1555502_s_at, 1555503_at, 205032_at	NP_001129391.1, NP_036354.2, EAW93616.1, EAW93617.1, EAW93618.1, EAW93621.1, EAW93615.1, EAW93619.1, EAW93623.1, EAW93622.1
Gene:ID:2346	C1orf105	1	172,359,526	172,437,999	46,141	+	2	1_A275_chL97_dtcs_lncRNA:1:1512, 2_A275_chL97_dtcs_lncRNA:1:1698	23372, 23355	st gene, st gene	1	1	74	100	1	2_A275_chL97_dtcs_lncRNA:1	100	Gene: C1orf105	RP1-109H8.1, C1orf105	chromosome 1 open reading frame 105	NM__132240, NCT01091226.2	214337_at	NP_640333.2, EAW93624.1
Gene:ID:278	PIGC	1	172,410,997	172,413,230	2,633	-	2	1_A275_chL97_dtcs_lncRNA:1:1512, 2_A275_chL97_dtcs_lncRNA:1:1698	10, 14	st gene, st gene	1	1	74	100	1	2_A275_chL97_dtcs_lncRNA:1	100	Gene: PIGC	PIGC, GPI2, MGC2049	phosphatidylinositol glycan anchor biosynthesis, class C	NM_182747, NM_002642, NCT02353410.0, NCT02373081.0, NCT02353610.0, NCT.09054.2	202649_s_at, 215242_at, 215382_x_at	NP_714969.1, NP_002633.1, EAW93625.1, EAW93626.1, EAW93627.1, EAW93628.1
Gene:ID:1430	C1orf9	1	172,502,260	172,509,873	70,713	+	6	1_A275_chL97_dtcs_lncRNA:1:1510, 2_A275_chL97_dtcs_lncRNA:1:1511, 3_A275_chL97_dtcs_lncRNA:1:1516, 4_A275_chL97_dtcs_lncRNA:1:1512, 5_A275_chL97_dtcs_lncRNA:1:1698, 6_A275_chL97_dtcs_lncRNA:1:1712	-386, 55765, 76524, 372, 55922	upstream, st gene, st gene, upstream, st gene	1	1	24.33	17.33	3	1_A275_chL97_dtcs_lncRNA:1	33	Gene: C1orf9	CIPT, CH1, C1orf9, ELF1	chromosome 1 open reading frame 9	NM_014283, NM_016227, NCT02326940.0, NCT02326993.0, NCT02326960.0, NCT02327007.0, NCT.09218.3, NCT.09059.3	202429_s_at	NP_055081.1, NP_057311.2, EAW93629.1, EAW93632.1, EAW93633.1, EAW93634.1, EAW93630.1, EAW93631.1
Gene:ID:3	PASG	1	172,835,165	172,839,013	7,828	+	1	2_A275_chL97_dtcs_lncRNA:1:1712	4324	upstream	0	1	9	15	1	2_A275_chL97_dtcs_lncRNA:1	15	Gene: PASG2	APT1LG1, CD174, TMPSF6, CD69L, CD69-L, PASLG, PASL	Pas ligand (TNF superfamily, member 6)	NM_006839, NCT02322601.0, NCT.09077.2	210569_at, 211333_s_at	NP_009630.1, EAW93635.1, EAW93636.1
Gene:ID:5936982	LOC1005360	1	172,204,198	172,446,264	242,066	-	2	1_A275_chL97_dtcs_lncRNA:1:1516, 2_A275_chL97_dtcs_lncRNA:1:1516	207382, 264	st gene, st gene	1	1	17	14.5	2	2_A275_chL97_dtcs_lncRNA:1	16	Gene: LOC100396623	hypothetical LOC100396623	XR_100308, XR_114839			
Gene:ID:552	PRDX6	1	172,446,486	172,457,626	11,140	+	1	2_A275_chL97_dtcs_lncRNA:1:1516, 2_A275_chL97_dtcs_lncRNA:1:1516	-466	upstream	0	1	16	16	1	2_A275_chL97_dtcs_lncRNA:1	16	Gene: PRDX6	AOP2, KIAA0106.1-Cys, p29, PRX, MGC26132, MSGPx, aiPLA2, PRDX6	peroxiredoxin 6	NM_004905, NCT01951552.1, NCT02326920.0	200584_s_at, 200585_s_at	NP_004896.1, EAW93640.1, EAW93643.1
Gene:ID:7252	KLHL20	1	172,654,080	172,753,830	71,750	+	2	1_A275_chL97_dtcs_lncRNA:1:1522, 2_A275_chL97_dtcs_lncRNA:1:1517	144, 48	st gene, st gene	1	1	26	32	1	2_A275_chL97_dtcs_lncRNA:1	32	Gene: KLHL20	KHLH5, KLHL5, KLHL20, RP3-383.8.3, KLEP	kelch-like 20 (Drosophila)	NM_014458, NCT01480091.1, NCT01953110.0, NCT02326710.0, NCT02326720.0	204179_at, 204177_s_at, 219634_at, 219635_s_at	NP_055733.2, EAW93653.1, EAW93652.1, EAW93654.1, EAW93655.1
Gene:ID:1657	CENPL	1	172,766,656	172,793,777	25,089	+	2	1_A275_chL97_dtcs_lncRNA:1:1522, 2_A275_chL97_dtcs_lncRNA:1:1518	-207, 145	upstream, st gene	1	1	26	25	1	1_A275_chL97_dtcs_lncRNA:1	26	Gene: CENPL	CENP-L, C1orf135, FLJ31004, FLJ30786, CENPL, RP5-1024.1, dJ354J4.2	centromere protein L	NM_033319, NM_001127181, NM_001171162, NCT.09053.2, NCT01921051.1, NCT02326910.0, NCT02326940.0	1554271_a_at, 221063_s_at	NP_201576.1, NP_001120553.1, NP_201566553.1, EAW93656.1, EAW00957.1, EAW93659.1, EAW93658.1
Gene:ID:5137	DARS2	1	172,793,797	172,827,662	33,865	+	4	1_A275_chL97_dtcs_lncRNA:1:1522, 2_A275_chL97_dtcs_lncRNA:1:1520, 3_A275_chL97_dtcs_lncRNA:1:1716, 4_A275_chL97_dtcs_lncRNA:1:1716	187, 43953, 163, 43967	st gene, downstream, downstream, downstream	1	1	23.5	26.5	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: DARS2	MT-ASPRS, ASPRS, PLO1014, RP3-383.4.2, DARS2, LBSL	aspartyl-tRNA synthetase 2, mitochondrial	NM_018122, NCT01921130.1, NCT02262310, NCT02326230.0	218363_s_at	NP_060992.2, EAW93662.1, EAW93660.1, EAW93661.1
Gene:ID:5359569	LOC1005360	1	172,831,290	172,833,079	1,789	+	3	1_A275_chL97_dtcs_lncRNA:1:1520, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1716	6310, 5974, 6454	downstream, downstream, downstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: LOC100359569	hypothetical LOC100359569	XR_111994, XR_105309, XR_110980			
Gene:ID:9674	GK5	1	172,833,038	172,837,125	4,088	-	2	1_A275_chL97_dtcs_lncRNA:1:1520, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1716	470, 281, 2619	upstream, st gene, upstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: GK5	GK5B, NCRNA00030, SNH22	glycerol kinase 5 (putative) pseudogene	NR_002976	1560402_at, 229741_s_at, 236561_s_at, 237617_s_at, 236235_at, 238317_at	
Gene:ID:6769	SNORD61	1	172,833,313	172,833,355	42	-	3	1_A275_chL97_dtcs_lncRNA:1:1520, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1520	-4245, 3509, 5289	upstream, upstream, upstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: SNORD61	U61, RNU104, SNORD61, Z33	small nucleolar RNA, C/D box 61	NR_003035		
Gene:ID:6652	SNORD47	1	172,833,501	172,833,563	76	-	3	1_A275_chL97_dtcs_lncRNA:1:1524, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1520	-4017, 3261, 6161	upstream, upstream, upstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: SNORD47	U47, RNU47, SNORD47	small nucleolar RNA, C/D box 47	NR_002746		
Gene:ID:6774	SNORD60	1	172,833,971	172,834,041	70	-	3	1_A275_chL97_dtcs_lncRNA:1:1524, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1520	-3559, 2623, 5703	upstream, upstream, upstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: SNORD60	SNORD60, U60, RNU100, Z15	small nucleolar RNA, C/D box 60	NR_003040		
Gene:ID:6770	SNORD79	1	172,834,465	172,834,566	80	-	3	1_A275_chL97_dtcs_lncRNA:1:1524, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1520	-3832, 2296, 6176	upstream, upstream, upstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: SNORD79	U79, RNU103, Z22, SNORD79	small nucleolar RNA, C/D box 79	NR_003979		
Gene:ID:92165	SNORD76	1	172,834,771	172,834,824	53	-	3	1_A275_chL97_dtcs_lncRNA:1:1524, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1520	-4276, 2049, 4820	upstream, upstream, upstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: SNORD76	SNORD76, U76	small nucleolar RNA, C/D box 76	NR_003944		
Gene:ID:6606	SNORD44	1	172,835,106	172,835,166	60	-	3	1_A275_chL97_dtcs_lncRNA:1:1524, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1520	-4434, 1666, 4578	upstream, upstream, upstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: SNORD44	U44, RNU68, SNORD44	small nucleolar RNA, C/D box 44	NR_002750		
Gene:ID:92167	SNORD77	1	172,835,448	172,835,509	60	-	3	1_A275_chL97_dtcs_lncRNA:1:1524, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1520	-2691, 1355, 4235	upstream, upstream, upstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: SNORD77	SNORD77, U77	small nucleolar RNA, C/D box 77	NR_003943		
Gene:ID:92166	SNORD75	1	172,835,773	172,835,833	60	-	3	1_A275_chL97_dtcs_lncRNA:1:1524, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1520	-1747, 1011, 2891	upstream, upstream, upstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: SNORD75	SNORD75, U75	small nucleolar RNA, C/D box 75	NR_003941		
Gene:ID:19466	SNORD74	1	172,835,812	172,835,883	71	-	3	1_A275_chL97_dtcs_lncRNA:1:1524, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1520	-717, 19, 3961	upstream, st gene, upstream	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: SNORD74	U74, Z16, SNORD74	small nucleolar RNA, C/D box 74	NR_002979		
Gene:ID:9814	ZBTB37	1	173,537,493	173,553,774	16,281	-	3	1_A275_chL97_dtcs_lncRNA:1:1524, 2_A275_chL97_dtcs_lncRNA:1:1716, 3_A275_chL97_dtcs_lncRNA:1:1520	107, 429, 2251	st gene, upstream, st gene	1	1	16	23	2	2_A275_chL97_dtcs_lncRNA:1	26	Gene: ZBTB37	ZNF936, ZBTB37, MGC2629, D430036B05Rik	zinc finger and BTB domain containing 37	NM_032522, NM_001122770, NCT01640446.2, NCT.09229.0	220853_s_at, 231547_at	NP_115911.1, NP_001116242.1, EAW93667.1, EAW93665.1
Gene:ID:9910	RASGAP1L	1	174,126,634	174,327,327	196,693	+	4	1_A275_chL97_dtcs_lncRNA:1:1523, 2_A275_chL97_dtcs_lncRNA:1:1524, 3_A275_chL97_dtcs_lncRNA:1:1526, 4_A275_chL97_dtcs_lncRNA:1:1529	70, 230726, 630454	st gene, st gene, st gene, st gene	0	1	15.67	17	2	2_A275_chL97_dtcs_lncRNA:1	20	Gene: RASGAP1L	FLJ76254, TBC1D16, RASGAP1L, HRL, DKFZp686E1492, FLJ55037, FLJ79114	RAS GTPase activating protein 1-like	NM_014557, NM_001033230	1554725_at, 202020_s_at, 213982_s_at, 215242_s_at, 232702_at	NP_059672.2, NP_001030307.1
Gene:ID:7	LOC1005360	1	174,933,905	174,954,445	20,540	-	3	1_A275_chL97_dtcs_lncRNA:1:1526, 2_A275_chL97_dtcs_lncRNA:1:1529, 3_A275_chL97_dtcs_lncRNA:1:1529	54719, 34703, 35515	downstream, downstream, downstream	1	1	30	26	1	1_A275_chL97_dtcs_lncRNA:1	30	Gene: LOC100359687		ras GTPase-activating protein 1-like	XM_003119767, XM_003116486, XM_003120840		XP_003119815.1, XP_003116544.1, XP_003120866.1
Gene:ID:7101	CACYBP	1	174,968,371	174,981,163	12,792	+	3	1_A275_chL97_dtcs_lncRNA:1:1526, 2_A275_chL97_dtcs_lncRNA:1:1526, 3_A275_chL97_dtcs_lncRNA:1:1529	53, 37, 869	st gene, st gene, st gene	1	1	30	26	1	1_A275_chL97_dtcs_lncRNA:1	30	Gene: CACYBP	MGC07971, GIG5, SIP, PNAS-107, RP1-152G20.6, CACYBP, S100A6BP	calcyclin binding protein	NM_014412, NM_001007214, NCT03220010.0, NCT02220004.0	201301_s_at, 201302_at, 216561_x_at, 217761_s_at	NP_055237.1, NP_001007215.1, EAW93682.1, EAW93683.1
Gene:ID:674	KIAA0560	1	175,126,123	175,162,229	36,106	-	3	1_A275_chL97_dtcs_lncRNA:1:1526, 2_A275_chL97_dtcs_lncRNA:1:1527, 3_A275_chL97_dtcs_lncRNA:1:1529	23845, 4651, 22197	st gene, upstream, st gene	1	1	19.5	18.5	2	1_A275_chL97_dtcs_lncRNA:1	20	Gene: KIAA0560	FLJ75522, KIAA0560, MGC133301	KIAA0560	NM_014556, NM_001162682, NM_001162594, NM_001162595, NCT01886291.1, NCT01886.1, NCT01961241.1, NCT.09013.3, NCT02220214	202163_s_at, 202164_s_at	NP_055571.2, NP_001136355.1, NP_001136356.1, NP_001136357.1, EAW93687.1, EAW93688.1, EAW93686.1, EAW93690.1, EAW93691.1
Gene:ID:143	TNR	1	175,291,935	175,712,752	420,817	+	9	1_A275_chL97_dtcs_lncRNA:1:1526, 2_A275_chL97_dtcs_lncRNA:1:1526, 3_A275_chL97_dtcs_lncRNA:1:1526, 4_A275_chL97_dtcs_lncRNA:1:1532, 5_A275_chL97_dtcs_lncRNA:1:1526, 6_A275_chL97_dtcs_lncRNA:1:1530, 7_A275_chL97_dtcs_lncRNA:1:1530, 8_A275_chL97_dtcs_lncRNA:1:1530, 9_A275_chL97_dtcs_lncRNA:1:1530	177744, 416, 99804, 17792, 403	st gene, st gene, st gene, st gene, st gene	1	1	24	29	3	2_A275_chL97_dtcs_lncRNA:1	43	Gene: TNR	TN-R, TNR, MGC148826	tenascin R (restrictin, janusin)	NM_003285, NCT01513.2, NCT02330140	206990_at	NP_003276.3, EAW93694.1, EAW93693.1
Gene:ID:4226	RPWD2	1	176,913,967	176,176,370	262,403	-	2	1_A275_chL97_dtcs_lncRNA:1:1530, 2_A275_chL97_dtcs_lncRNA:1:1532	-414, -94	upstream, upstream	1	1	16	21	1	2_A275_chL97_dtcs_lncRNA:1	21	Gene: RPWD2	RPWD2, RNF200, FLJ10816, COP1	wd repeat and WD repeat domain 2	NM_001001740, NM_022057, NCT01957951.1, NCT02219211.0, NCT02329110.0, NCT02219.0	1552617_a_at, 229590_s_at	NP_001001740.1, NP_071902.2, EAW93699.1, EAW93700.1, EAW93701.1, EAW93702.1
Gene:ID:9676	PAPPA2	1	176,432,307	176,511,972	379,665	+	1	2_A275_chL97_dtcs_lncRNA:1:1733	54477	st gene	0	1	11	22	1	2_A275_chL97_dtcs_lncRNA:1	22	Gene: PAPPA2	PAPPE, PAPPA2, PAPPA2, PLAC3	pappalysin 2	NM_021939, NM_020318, NCT02677703.1, NCT02486603.0	211916_s_at, 213332_at, 214659_at, 226237_at	NP_068757.2, NP_064714.2, EAW91003.1, EAW91004.1
Gene:ID:7783	FAM69	1	177,140,633	177,251,556	110,923	+	3	1_A275_chL97_dtcs_lncRNA:1:1531, 2_A275_chL97_dtcs_lncRNA:1:1532, 3_A275_chL97_dtcs_lncRNA:1:1516	27959, 58999, 35007	st gene, st gene, st gene	1	1	23	38	2	2_A275_chL97_dtcs_lncRNA:1	33	Gene: FAM69	RP5-1026E2.1, BRINP2, FAM69, DBCCR1L2, FLJ41342, KIAA1747	family with sequence similarity 5, member B	NM_021163, NCT.09057.3	214822_at	NP_066956.1, EAW91009.1
Gene:ID:9330248	LOC1003302481	1	178,060,643	176,063,126	2,485	-	2	1_A275_chL97_dtcs_lncRNA:1:1530, 2_A275_chL97_dtcs_lncRNA:1:1536	512, 260	st gene, st gene	1	1	32	31	1	1_A275_chL97_dtcs_lncRNA:1	32	Gene: LOC100330248 1	FLJ42473	hypothetical LOC100302481	NR_027952		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9462	RASAL2	1	178,062,864	178,448,649	385,785	+	5	1_A375_pNL7_minus_lncRNA::1::535, 1_A375_pNL7_minus_lncRNA::1::536, 1_A375_pNL7_minus_lncRNA::1::537, 2_A375_pNL97_plus_lncRNA::1::738, 2_A375_pNL97_plus_lncRNA::1::739	-48, 33232, 324336, -16, 33280	upstream, in gene, in gene, upstream, in gene	1	1	27	21.67	3	1_A375_pNL7_minus_lncRNA::1	32	Gene RASAL2	NGAP, RASAL2, MGC129919	RAS protein activator like 2	NM_004841, NM_170692, hCT2323139.1, hCT2323140.1, hCT2323141.1	1557432_at, 217194_at, 217201_at, 219026_s_at, 222810_s_at, 234343_s_at, 234910_at	NP_004832.1, NP_733793.2, EAW91017.1, EAW91018.1, EAW91019.1
GeneID:400796	C1orf220	1	178,511,931	178,518,024	6,093	+	3	1_A375_pNL7_minus_lncRNA::1::538, 1_A375_pNL7_minus_lncRNA::1::539, 2_A375_pNL97_plus_lncRNA::1::740	-5531, 5, -27	upstream, in gene, upstream	1	1	17.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	20	Gene C1orf220	C1orf220, DKFZp564J047, FLJ40199, FLJ35530	chromosome 1 open reading frame 220	NR_033186, hCT2342662.0	1563876_at	EAW91026.1
GeneID:55103	RALGPS2	1	178,694,300	178,889,238	194,938	+	1	2_A375_pNL97_plus_lncRNA::1::742	-220	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene RALGPS2	dJ595C2.1, FLJ25604, FLJ10244, KIAA0351, RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	NM_152663, hCT1801372.2, hCT2323136.0, hCT2323137.0, hCT2323138.0	220338_at, 227224_at, 232112_at, 242458_at	NP_689876.2, EAW91028.1, EAW91027.1, EAW91029.1, EAW91030.1
GeneID:9917	FAM20B	1	178,995,074	179,045,702	50,628	+	5	1_A375_pNL7_minus_lncRNA::1::541, 1_A375_pNL7_minus_lncRNA::1::542, 2_A375_pNL97_plus_lncRNA::1::743, 2_A375_pNL97_plus_lncRNA::1::744, 2_A375_pNL97_plus_lncRNA::1::745	846, 56158, -226, 414, 56201	in gene, downstream, upstream, in gene, downstream	1	1	18.67	21.67	3	2_A375_pNL97_plus_lncRNA::1	28	Gene FAM20B	gxk1, FAM20B	family with sequence similarity 20, member B	NM_014864, hCT14669.3, hCT2323047.0, hCT2323048.0	202915_s_at, 202916_s_at, 217320_at	NP_055679.1, EAW91036.1, EAW91034.1, EAW91035.1
GeneID:64222	TOR3A	1	179,051,112	179,065,131	14,019	+	2	1_A375_pNL7_minus_lncRNA::1::542, 2_A375_pNL97_plus_lncRNA::1::745	120, 163	in gene, in gene	1	1	19	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TOR3A	ADIR2, TOR3A, FLJ22345, MGC111104, ADIR	torsin family 3, member A	NM_022371, hCT14670.2, hCT1958735.1, hCT1958736.1	218459_at, 233851_s_at	NP_071766.2, EAW91038.1, EAW91037.1, EAW91039.1
GeneID:6646	SOAT1	1	179,263,017	179,324,453	61,436	+	2	1_A375_pNL7_minus_lncRNA::1::543, 2_A375_pNL97_plus_lncRNA::1::746	-265, -41	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SOAT1	STAT, RP11-215I23.2, SOAT1, ACAT, ACACT, SOAT, ACAT1	sterol O-acyltransferase 1	NM_003101, hCT14671.3, hCT2323056.0	221561_at	NP_003092.4, EAW91043.1, EAW91044.1
GeneID:126859	C1orf125	1	179,334,855	179,523,870	189,015	+	3	1_A375_pNL7_minus_lncRNA::1::544, 2_A375_pNL97_plus_lncRNA::1::747, 2_A375_pNL97_plus_lncRNA::1::748	185742, 313, 185305	in gene, in gene, in gene	1	1	19	23.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene C1orf125	FLJ32940, RP11-215I23.2, FLJ25438, DKFZp686H1423, AXDND1, C1orf125	axonemal dynein light chain domain containing 1	NM_144696, hCT1659791.3, hCT2323058.1, hCT2349360.0, hCT2357432.0	1552870_s_at, 1553376_a_at	NP_653297.3, EAW91047.1, EAW91045.1, EAW91046.1, EAW91048.1
GeneID:7827	NPHS2	1	179,519,674	179,545,084	25,410	-	2	1_A375_pNL7_minus_lncRNA::1::544, 2_A375_pNL97_plus_lncRNA::1::748	24487, 24924	in gene, in gene	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene NPHS2	PDCN, SRN1, NPHS2	nephrosis 2, idiopathic, steroid-resistant (podocin)	NM_014625, hCT1640032.3, hCT2357405.0	220424_at	NP_055440.1, EAW91049.1, EAW91050.1
GeneID:163590	TOR1AIP2	1	179,813,066	179,846,941	33,875	-	2	1_A375_pNL7_minus_lncRNA::1::545, 2_A375_pNL97_plus_lncRNA::1::749	-4851, -4979	upstream, upstream	1	1	29	24	1	1_A375_pNL7_minus_lncRNA::1	29	Gene TOR1AIP2	IFRG15, MGC120076, LULL1, TOR1AIP2, MGC120074, MGC120075, MGC138430, RP11-12M5.5, MGC126581, NET9, MGC120077, FLJ77012	torsin A interacting protein 2	NM_145034, NM_022347, hCT2344722.1, hCT2349386.0, hCT2349387.0, hCT2349388.0, hCT2349389.0, hCT2349390.0	1569676_at, 235453_at, 240700_at	NP_659471.1, NP_071742.1, EAW91058.1, EAW91059.1, EAW91060.1, EAW91062.1, EAW91061.1, EAW91063.1
GeneID:26092	TOR1AIP1	1	179,851,420	179,889,211	37,791	+	2	1_A375_pNL7_minus_lncRNA::1::545, 2_A375_pNL97_plus_lncRNA::1::749	372, 500	in gene, in gene	1	1	29	24	1	1_A375_pNL7_minus_lncRNA::1	29	Gene TOR1AIP1	LAP1B, MGC3413, TOR1AIP1, FLJ13142, DKFZp586G011	torsin A interacting protein 1	NM_015602, hCT15598.3, hCT2323064.0	212408_at, 212409_s_at, 216100_s_at	NP_056417.2, EAW91068.1, EAW91067.1
GeneID:9857	CEP350	1	179,923,908	180,084,015	160,107	+	1	2_A375_pNL97_plus_lncRNA::1::750	28	in gene	0	1	18	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene CEP350	GM133, FLJ44058, KIAA0480, FLJ38282, CAP350, CEP350	centrosomal protein 350kDa	NM_014810, hCT2323036.1, hCT2323038.0, hCT2323039.1, hCT2323040.0	204373_s_at, 213165_at, 213956_at, 213957_s_at	NP_055625.4, EAW91071.1, EAW91070.1, EAW91072.1, EAW91073.1
GeneID:84320	ACBD6	1	180,257,352	180,472,022	214,670	-	2	1_A375_pNL7_minus_lncRNA::1::546, 2_A375_pNL97_plus_lncRNA::1::751	374, 374	in gene, in gene	1	1	31	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene ACBD6	MGC2404, ACBD6	acyl-CoA binding domain containing 6	NM_032360, hCT15599.2, hCT2323079.0, hCT2323082.0	225317_at	NP_115736.1, EAW91083.1, EAW91082.1, EAW91084.1
GeneID:9213	XPR1	1	180,601,146	180,859,415	258,269	+	2	1_A375_pNL7_minus_lncRNA::1::547, 2_A375_pNL97_plus_lncRNA::1::752	550, 150	in gene, in gene	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene XPR1	XPR1, SYG1, X3, FLJ90308	xenotropic and polytropic retrovirus receptor	NM_004736, NM_001135669, hCT13751.3, hCT2323030.0	222581_at	NP_004727.2, NP_001129141.1, EAW91086.1, EAW91087.1
GeneID:10228	STX6	1	180,942,175	180,992,046	49,871	-	1	2_A375_pNL97_plus_lncRNA::1::753	46	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene STX6	STX6	syntaxin 6	NM_005819, hCT15282.3, hCT2323076.0, hCT2323077.0	1552618_at, 212799_at, 212800_at, 214441_at, 244041_at	NP_005810.1, EAW91093.1, EAW91091.1, EAW91092.1
GeneID:51278	IER5	1	181,057,638	181,059,979	2,341	+	3	1_A375_pNL7_minus_lncRNA::1::548, 2_A375_pNL97_plus_lncRNA::1::754, 2_A375_pNL97_plus_lncRNA::1::755	-38, 90, 1274	upstream, in gene, in gene	1	1	17	25.5	2	2_A375_pNL97_plus_lncRNA::1	32	Gene IER5	IER5, SBBI48, MGC102760	immediate early response 5	NM_016545, hCT1805206.2	218611_at	NP_057629.2, EAW91099.1
GeneID:6041	RNASEL	1	182,542,772	182,556,108	13,336	-	1	2_A375_pNL97_plus_lncRNA::1::756	-2372	upstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene RNASEL	RNS4, MGC133329, RNASEL, PRCA1, DKFZp781D08126, MGC104972	ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	NM_021133, hCT15509.3	221287_at, 229285_at	NP_066956.1, EAW91128.1
GeneID:6004	RGS16	1	182,567,758	182,573,548	5,790	-	3	1_A375_pNL7_minus_lncRNA::1::550, 2_A375_pNL97_plus_lncRNA::1::758, 2_A375_pNL97_plus_lncRNA::1::759	60, 15068, 140	in gene, downstream, in gene	1	1	15	20.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene RGS16	RGS-R, A28-RGS14, RGS16, A28-RGS14P	regulator of G-protein signaling 16	NM_002928, hCT14189.2	209324_s_at, 209325_s_at	NP_002919.3, EAW91129.1
GeneID:284648	LOC284648	1	182,564,275	182,565,764	1,489	+	2	1_A375_pNL7_minus_lncRNA::1::551, 2_A375_pNL97_plus_lncRNA::1::760	-115, 109	upstream, in gene	1	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC284648		hypothetical LOC284648	NR_036490	231427_at	
GeneID:80896	NPL	1	182,761,394	182,798,588	37,194	+	2	2_A375_pNL97_plus_lncRNA::1::762, 2_A375_pNL97_plus_lncRNA::1::763	-2450, 47534	upstream, downstream	0	1	17.5	24	2	2_A375_pNL97_plus_lncRNA::1	30	Gene NPL	NAL, NPL, C112, C1orf13, MGC149582, MGC61869, DHDPS1, NPL1, c112	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	NM_030769, hCT1964339.1, hCT1964340.1, hCT2323122.0, hCT2323124.0	221210_s_at, 223405_at, 240440_at, 243066_at	NP_110396.1, EAW91134.1, EAW91132.1, EAW91133.1, EAW91135.1
GeneID:1660	DHX9	1	182,808,439	182,857,117	48,678	+	1	2_A375_pNL97_plus_lncRNA::1::763	489	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DHX9	RHA, NDHII, DDX9, LKP, FLJ17406, NDH2, DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	NM_001357, NR_033302, hCT15513.3, hCT2323127.0	202420_s_at, 212105_s_at, 212107_s_at	NP_001348.2, EAW91138.1, EAW91137.1
GeneID:3915	LAMC1	1	182,992,595	183,114,727	122,132	+	3	1_A375_pNL7_minus_lncRNA::1::553, 2_A375_pNL97_plus_lncRNA::1::764, 2_A375_pNL97_plus_lncRNA::1::765	525, -755, 525	in gene, upstream, in gene	1	1	18	20	2	2_A375_pNL97_plus_lncRNA::1	22	Gene LAMC1	LAMB2, MGC87297, LAMC1	laminin, gamma 1 (formerly LAMB2)	NM_002293, hCT2323130.0, hCT31990.2	200770_s_at, 200771_at	NP_002284.3, EAW91145.1, EAW91144.1
GeneID:3918	LAMC2	1	183,155,174	183,214,262	59,088	+	1	1_A375_pNL7_minus_lncRNA::1::554	48938	in gene	1	0	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene LAMC2	MGC141938, CSF, BZT, LAMC2, LAMNB2, BM600, LAMB2T, EBR2, MGC138491, EBR2A	laminin, gamma 2	NM_005562, NM_018891, hCT1686601.2, hCT31991.3	202267_at, 207517_at	NP_005553.2, NP_061486.2, EAW91146.1, EAW91147.1
GeneID:23057	NMNAT2	1	183,217,379	183,387,737	170,358	-	4	1_A375_pNL7_minus_lncRNA::1::555, 2_A375_pNL97_plus_lncRNA::1::766, 2_A375_pNL97_plus_lncRNA::1::767, 2_A375_pNL97_plus_lncRNA::1::768	1753, 138537, 69257, 1721	in gene, in gene, in gene, in gene	1	1	23	29	3	2_A375_pNL97_plus_lncRNA::1	46	Gene NMNAT2	PNAT2, MGC2756, KIAA0479, NMNAT2, C1orf15	nicotinamide nucleotide adenylyltransferase 2	NM_015039, NM_170706, hCT2344443.0, hCT2344444.0, hCT2344445.0, hCT2357406.0	1552712_a_at, 1556029_s_at, 1562818_at, 209755_at	NP_055854.1, NP_733820.1, EAW91148.1, EAW91149.1, EAW91150.1, EAW91151.1
GeneID:100506298	LOC100506298	1	183,430,009	183,441,134	11,125	-	2	1_A375_pNL7_minus_lncRNA::1::556, 2_A375_pNL97_plus_lncRNA::1::769	686, 654	in gene, in gene	1	1	23	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene LOC100506298		hypothetical LOC100506298	XR_111984, XR_108318, XR_114950		
GeneID:9887	SMG7	1	183,441,506	183,523,328	81,822	+	2	1_A375_pNL7_minus_lncRNA::1::556, 2_A375_pNL97_plus_lncRNA::1::769	-1058, -1026	upstream, upstream	1	1	23	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene SMG7	SMG7, KIAA0250, FLJ23717, EST1C, C1orf16, SMG-7, SGA56M	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	NM_001174061, NM_173156, NM_201568, NM_201569, hCT1959865.1, hCT1959866.1, hCT2323343.0, hCT2323352.0, hCT2323354.0, hCT31114.3	201793_x_at, 201794_s_at, 217189_s_at	NP_001167532.1, NP_775179.1, NP_963862.1, NP_963863.2, EAW91156.1, EAW91159.1, EAW91154.1, EAW91155.1, EAW91157.1, EAW91158.1
GeneID:4688	NCF2	1	183,524,697	183,560,056	35,359	-	1	1_A375_pNL7_minus_lncRNA::1::557	-9416	upstream	1	0	31	20	1	1_A375_pNL7_minus_lncRNA::1	31	Gene NCF2	P67PHOX, NCF-2, P67-PHOX, NOXA2, NCF2, FLJ93058	neutrophil cytosolic factor 2	NM_000433, NM_001127651, NM_001190789, NM_001190794, hCT2323458.0, hCT2357404.0, hCT31989.3	209949_at	NP_000424.2, NP_001121123.1, NP_001177718.1, NP_001177723.1, EAW91160.1, EAW91162.1, EAW91161.1
GeneID:10092	ARPC5	1	183,595,332	183,604,985	9,653	-	2	1_A375_pNL7_minus_lncRNA::1::558, 2_A375_pNL97_plus_lncRNA::1::770	-7, 233	upstream, in gene	1	1	25	20	1	1_A375_pNL7_minus_lncRNA::1	25	Gene ARPC5	ARPC5, ARC16, p16-Arc, dJ127C7.3, MGC88523	actin related protein 2/3 complex, subunit 5, 16kDa	NM_005717, hCT1959944.2, hCT2357372.1	1555797_a_at, 1569325_at, 211963_s_at	NP_005708.1, EAW91164.1, EAW91163.1
GeneID:100292409	LOC100292409	1	183,601,709	183,604,939	3,230	+	2	1_A375_pNL7_minus_lncRNA::1::558, 2_A375_pNL97_plus_lncRNA::1::770	3263, 3043	downstream, in gene	1	1	25	20	1	1_A375_pNL7_minus_lncRNA::1	25	Gene LOC100292409		hypothetical LOC100292409	XR_111983, XR_108319, XR_114951		
GeneID:23179	RGL1	1	183,605,208	183,897,666	292,458	+	2	1_A375_pNL7_minus_lncRNA::1::558, 2_A375_pNL97_plus_lncRNA::1::770	-216, -456	upstream, upstream	1	1	25	20	1	1_A375_pNL7_minus_lncRNA::1	25	Gene RGL1	KIAA0959, RGL1, RGL	ral guanine nucleotide dissociation stimulator-like 1	NM_015149, hCT2323357.0, hCT2323359.0, hCT2323363.0, hCT2323364.0	209568_s_at	NP_055964.3, EAW91168.1, EAW91165.1, EAW91166.1, EAW91167.1
GeneID:403314	APOBEC4	1	183,615,410	183,622,448	7,038	-	2	1_A375_pNL7_minus_lncRNA::1::558, 2_A375_pNL97_plus_lncRNA::1::770	17456, 17696	downstream, downstream	1	1	25	20	1	1_A375_pNL7_minus_lncRNA::1	25	Gene APOBEC4	APOBEC4, C1orf169, MGC26594	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 4 (putative)	NM_203454, hCT1645984.1	1554545_at	NP_982279.1, EAW91169.1
GeneID:23127	GLT25D2	1	183,904,966	184,006,863	101,897	-	1	2_A375_pNL97_plus_lncRNA::1::771	94575	in gene	0	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene GLT25D2	GLT25D2, KIAA0584, FLJ37673, C1orf17, FLJ37771	glycosyltransferase 25 domain containing 2	NM_015101, hCT2323454.0, hCT2357398.0, hCT32170.4	209883_at	NP_055916.1, EAW91170.1, EAW91171.1, EAW91172.1
GeneID:116461	TSEN15	1	184,020,811	184,043,346	22,535	+	2	1_A375_pNL7_minus_lncRNA::1::559, 2_A375_pNL97_plus_lncRNA::1::772	37, 21	in gene, in gene	1	1	25	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene TSEN15	sen15, TSEN15, C1orf19	tRNA splicing endonuclease 15 homolog (S. cerevisiae)	NM_052965, NR_023349, NM_001127394, hCT2323368.0, hCT2357396.0, hCT32169.2	225399_at, 225400_at, 230257_s_at	NP_443197.1, NP_001120866.1, EAW91173.1, EAW91174.1, EAW91175.1
GeneID:81563	C1orf21	1	184,356,150	184,598,155	242,005	+	3	1_A375_pNL7_minus_lncRNA::1::561, 1_A375_pNL7_minus_lncRNA::1::562, 2_A375_pNL97_plus_lncRNA::1::773	228554, 235498, 228474	in gene, in gene, in gene	1	1	19.5	17.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene C1orf21	C1orf21, PIG13	chromosome 1 open reading frame 21	NM_030806, hCT2323370.0, hCT32171.3	221272_s_at, 223125_s_at, 223126_s_at, 223127_s_at, 237098_at	NP_110433.1, EAW91176.1, EAW91177.1
GeneID:80267	EDEM3	1	184,659,625	184,724,041	64,416	-	2	1_A375_pNL7_minus_lncRNA::1::563, 2_A375_pNL97_plus_lncRNA::1::774	-439, 201	upstream, in gene	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene EDEM3	C1orf22, EDEM3	ER degradation enhancer, mannosidase alpha-like 3	NM_025191, hCT2323268.0, hCT2323269.0, hCT2323270.0, hCT2323271.0, hCT2323272.0, hCT2323273.0	220342_x_at, 220926_s_at, 223243_s_at	NP_079467.3, EAW91182.1, EAW91178.1, EAW91179.1, EAW91180.1, EAW91181.1, EAW91183.1
GeneID:116496	FAM129A	1	184,760,166	184,943,682	183,516	-	1	1_A375_pNL7_minus_lncRNA::1::564	107218	in gene	1	0	14	14	1	1_A375_pNL7_minus_lncRNA::1	14	Gene FAM129A	FLJ38228, FAM129A, GIG39, NIBAN, C1orf24	family with sequence similarity 129, member A	NM_052966, hCT2323265.0, hCT32161.2	217966_s_at, 217967_s_at	NP_443198.1, EAW91184.1, EAW91185.1
GeneID:6045	RNF2	1	185,014,551	185,071,740	57,189	+	1	1_A375_pNL7_minus_lncRNA::1::565	89	in gene	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene RNF2	RING2, DING, BAP1, RNF2, RING1B, BAP-1, HIPI3	ring finger protein 2	NM_007212, hCT2357352.0, hCT31139.3	205215_at	NP_009143.1, EAW91187.1, EAW91186.1
GeneID:81627	C1orf25	1	185,087,217	185,126,116	38,899	-	1	2_A375_pNL97_plus_lncRNA::1::775	356	in gene	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C1orf25	C1orf25, bG120K12.3, MSTP070, MST070, MGC25112, MGC57134, TRMT1L, TRM1L	TRM1 tRNA methyltransferase 1-like	NM_030934, hCT2357353.0, hCT32164.3	220992_s_at, 223404_s_at, 233750_s_at	NP_112196.3, EAW91189.1, EAW91190.1
GeneID:54823	C1orf26	1	185,126,192	185,260,913	134,721	+	1	2_A375_pNL97_plus_lncRNA::1::775	-432	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C1orf26	C1orf26, HsSwt1, FLJ35944, SWT1, FLJ20121	SWT1 RNA endoribonuclease homolog (S. cerevisiae)	NM_017673, NM_001105518, hCT1951760.1	223548_at	NP_060143.4, NP_001098988.1, EAW91191.1
GeneID:10625	IVNS1ABP	1	185,265,520	185,286,461	20,941	-	1	2_A375_pNL97_plus_lncRNA::1::776	141	in gene	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene IVNS1ABP	NS1-BP, NS1BP, KIAA0850, FLJ10962, FLJ35593, FLJ36593, FLARA3, IVNS1ABP, HSPC068, FLJ10411, ND1, DKFZp686K06216, KLHL39, NS-1, FLJ10069	influenza virus NS1A binding protein	NM_006469, hCT2357351.0, hCT31138.3	201362_at, 201363_s_at, 206245_s_at, 239152_at, 244235_at	NP_006460.2, EAW91193.1, EAW91194.1
GeneID:83872	HMCN1	1	185,703,683	186,160,085	456,402	+	5	2_A375_pNL97_plus_lncRNA::1::780, 2_A375_pNL97_plus_lncRNA::1::781, 1_A375_pNL7_minus_lncRNA::1::569, 1_A375_pNL7_minus_lncRNA::1::570, 2_A375_pNL97_plus_lncRNA::1::782	-99, 55933, 448797, 453501, 453677	upstream, in gene, in gene, in gene, in gene	1	1	18.25	22.5	4	2_A375_pNL97_plus_lncRNA::1	31	Gene HMCN1	FIBL6, ARMD1, FIBL-6, FBLN6, HMCN1	hemicentin 1	NM_031935, hCT2323083.0, hCT2323085.0, hCT2323086.0	235944_at	NP_114141.2, EAW91198.1, EAW91199.1, EAW91200.1
GeneID:7175	TPR	1	186,280,784	186,344,457	63,673	-	2	1_A375_pNL7_minus_lncRNA::1::573, 2_A375_pNL97_plus_lncRNA::1::784	-343, -183	upstream, upstream	1	1	35	23	1	1_A375_pNL7_minus_lncRNA::1	35	Gene TPR	TPR		NM_003292, hCT2323238.0, hCT2323239.0, hCT2357439.0, hCT32452.3	1557227_s_at, 201730_s_at, 201731_s_at, 215220_s_at, 228709_at	NP_003283.2, EAW91204.1, EAW91203.1, EAW91205.1, EAW91206.1
GeneID:54953	C1orf27	1	186,344,890	186,390,503	45,613	+	2	1_A375_pNL7_minus_lncRNA::1::573, 2_A375_pNL97_plus_lncRNA::1::784	-90, -250	upstream, upstream	1	1	35	23	1	1_A375_pNL7_minus_lncRNA::1	35	Gene C1orf27	ODR4, odr-4, FLJ20505, TTG1, C1orf27	chromosome 1 open reading frame 27	NM_017847, NM_001164245, NM_001164246, hCT2323094.0, hCT2323095.0, hCT32454.3	218721_s_at, 222720_x_at	NP_060317.3, NP_001157717.1, NP_001157718.1, EAW91207.1, EAW91208.1, EAW91209.1
GeneID:5743	PTGS2	1	186,640,944	186,649,559	8,615	-	1	2_A375_pNL97_plus_lncRNA::1::786	-361	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene PTGS2	COX-2, PGHS-2, hCox-2, PTGS2, GRIPGHS, PHS-2, PGG/HS, COX2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	NM_000963, hCT31137.3	1554997_a_at, 204748_at	NP_000954.1, EAW91216.1
GeneID:5997	RGS2	1	192,778,169	192,781,407	3,238	+	1	2_A375_pNL97_plus_lncRNA::1::792	55	in gene	0	1	20	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RGS2	RGS2, G0S8	regulator of G-protein signaling 2, 24kDa	NM_002923, hCT2323326.0, hCT31156.3	202388_at	NP_002914.1, EAW91231.1, EAW91232.1
GeneID:51377	UCHL5	1	192,984,899	193,028,521	43,622	-	2	1_A375_pNL7_minus_lncRNA::1::583, 2_A375_pNL97_plus_lncRNA::1::793	-23, 9	upstream, in gene	1	1	34	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene UCHL5	UCH37, CGI-70, INO80R, UCHL5	ubiquitin carboxyl-terminal hydrolase L5	NM_015984, hCT1798536.1, hCT1813150.1, hCT1814584.1, hCT2357420.0, hCT2357421.0, hCT32322.2	1570145_at, 219960_s_at, 220083_x_at	NP_057068.1, EAW91238.1, EAW91234.1, EAW91235.1, EAW91236.1, EAW91237.1, EAW91233.1
GeneID:6738	TROVE2	1	193,028,552	193,060,907	32,355	+	2	1_A375_pNL7_minus_lncRNA::1::583, 2_A375_pNL97_plus_lncRNA::1::793	-8, -40	upstream, upstream	1	1	34	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene TROVE2	SSA2, RORNP, RO60, TROVE2	TROVE domain family, member 2	NM_001042369, NM_001042370, NM_001173524, NM_001173525, NM_004600, NR_033393, hCT2323332.1, hCT2323333.1, hCT2349435.0, hCT2349436.0, hCT2349437.0, hCT2349438.0, hCT2349439.0, hCT2349440.0, hCT32323.4	207520_at, 210435_x_at, 212839_s_at, 212852_s_at, 213027_at	NP_001035828.1, NP_001035829.2, NP_004591.2, NP_001166995.1, NP_001166996.1, EAW91240.1, EAW91239.1, EAW91241.1, EAW91242.1, EAW91243.1, EAW91244.1, EAW91245.1, EAW91246.1, EAW91247.1
GeneID:51022	GLRX2	1	193,065,600	193,075,244	9,644	-	1	2_A375_pNL97_plus_lncRNA::1::794	892	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GLRX2	GLRX2, bA101E13.1, GRX2	glutaredoxin 2	NM_016066, NM_197962, hCT2323424.0, hCT32324.2	219933_at	NP_057150.2, NP_932066.1, EAW91248.1, EAW91249.1
GeneID:79577	CDC73	1	193,091,088	193,223,945	132,857	+	2	1_A375_pNL7_minus_lncRNA::1::584, 2_A375_pNL97_plus_lncRNA::1::795	112, 48	in gene, in gene	1	1	25	24	1	1_A375_pNL7_minus_lncRNA::1	25	Gene CDC73	C1orf28, FLJ23316, HRPT2, HYX, HPTJT, CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	NM_024529, hCT32327.3	218578_at	NP_078805.3, EAW91250.1
GeneID:343450	KCNT2	1	196,194,913	196,577,499	382,586	-	2	1_A375_pNL7_minus_lncRNA::1::588, 2_A375_pNL97_plus_lncRNA::1::797	-709, -357	upstream, upstream	1	1	21	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene KCNT2	MGC119610, KCNT2, KCa4.2, MGC119613, SLO2.1, SLICK, MGC119611, MGC119612	potassium channel, subfamily T, member 2	NM_198503, hCT1951764.2, hCT2323329.1	234103_at, 244455_at	NP_940905.2, EAW91256.1, EAW91255.1
GeneID:259266	ASPM	1	197,053,257	197,115,824	62,567	-	2	1_A375_pNL7_minus_lncRNA::1::589, 2_A375_pNL97_plus_lncRNA::1::798	48, -48	in gene, upstream	1	1	26	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ASPM	FLJ43117, FLJ10549, Calmbp1, FLJ10517, MCPH5, ASP, DKFZp686N06184, ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	NM_018136, hCT2344429.0, hCT2344431.0, hCT2344432.0, hCT2357375.0, hCT2357376.0	219918_s_at, 232238_at, 239002_at	NP_060606.3, EAW91272.1, EAW91270.1, EAW91271.1, EAW91273.1, EAW91274.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervals	Intervals	Intervals Count	Intervals Pct.	[A]	[R]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
Gene ID:23 60023	ZBTB41	1	197,122,614	197,169,872	49,259	+	3	1_A270_shL7_chr(n A:1:599, 1_A270_shL97_glo(n 1:795, 1_A270_shL97_glo(n 1:598	N:53599, 53800, 1016	downstream, downstream, upstream	1	1	21.5	32.5	2	2_A270_shL97_glo(_blcR NA:1	37	Gene ZBTB41	FR3E1, ZBTB41, DKFZp686C06132, RP11-469L3.1, FLJ36189, ZNF624	BAC trigger and BTB domain containing 41	NM_194314, NCT02333976.0		Z26952_at	NP_919299.2, EAW61275.1
Gene ID:55 55722	C1orf63	1	197,571,662	197,576,497	4,815	+	2	1_A270_shL7_chr(n A:1:590, 2_A270_shL97_glo(n 1:595	1258, 126	up gene, un gene	1	1	36	39	1	2_A270_shL97_glo(_blcR NA:1	39	Gene C1orf63	C1orf63	chromosome 1 open reading frame 63	NM_001024594, NCT17089802.2		1555307_at, 1555305_s_at	NP_001019763.1, EAW61266.1
Gene ID:53 6936	UXS1	1	197,661,635	197,699,273	37,639	+	2	1_A270_shL7_chr(n A:1:590, 2_A270_shL97_glo(n 1:595	48992, 8827	upstream, upstream	1	1	36	39	1	2_A270_shL97_glo(_blcR NA:1	39	Gene UXS1	UXS1		NM_020304, NM_001018434, NCT02329691.1, NCT02329690.1, NCT02364122.0, NCT02364122.0, NCT01841242.0		1560252_at, 1560736_at, 1560809_s_at, 1560807_at	NP_064589.2, NP_001018434.1, EAW61247.1, EAW61255.1, EAW61260.1, EAW61262.1, EAW61259.1, EAW61261.1
Gene ID:11 49609	NEK7	1	198,126,108	198,291,550	165,442	+	1	1_A270_shL97_glo(n 1:853	458	up gene	0	1	10	17	1	2_A270_shL97_glo(_blcR NA:1	37	Gene NEK7	NEK7		NM_133494, NCT02329691.0, NCT02329690.1, NCT01922971.1		2125530_at	NP_149031.1, EAW61260.1, EAW61264.1, EAW61263.1, EAW61266.1
Gene ID:53 788	PTPRC	1	198,695,137	198,729,549	114,408	+	1	1_A270_shL97_glo(n 1:868	74423	up gene	0	1	9	16	1	2_A270_shL97_glo(_blcR NA:1	16	Gene PTPRC	LY5, CD45, T200, B220, GP180, CD45R, LCA, PTPRC	protein tyrosine phosphatase, receptor type, C	NM_080921, NM_080922, NM_002838, NCT19307660.1, NCT19307660.1, NCT02329697.0, NCT02337700.0		1552580_s_at, 1560830_at, 2072106_s_at, 212567_s_at, 212568_at	NP_563597.1, NP_563598.1, NP_002829.2, EAW61300.1, EAW61301.1, EAW61303.1, EAW61302.1
Gene ID:2 494	NRSA2	1	199,996,770	200,146,552	149,782	+	3	1_A270_shL7_chr(n A:1:590, 2_A270_shL97_glo(n A:1:597, 2_A270_shL97_glo(n 1:868	47996, 11684, 152655	up gene, un gene, downstream	1	1	16.33	14.33	3	1_A270_shL7_chr(n_blc RNA:1	16	Gene NRSA2	PF2-P1beta, PF7, NR3A2, bB1F, LRH-1, bB1F-2, LRH1, CPF, B1F2, B1F, PTC-P1	nuclear receptor subfamily 5, group A, member 2	NM_003822, NM_205860, NCT16323.3, NCT19357710.1, NCT02329811.0, NCT02329812.0		1560692_at, 2060377_s_at, 2060343_s_at, 219174_at	NP_003813.1, NP_995562.1, EAW61303.1, EAW61306.1, EAW61307.1, EAW61308.1
Gene ID:9 828	KIP14	1	200,520,625	200,569,662	49,237	-	2	1_A270_shL7_chr(n A:1:590, 2_A270_shL97_glo(n 1:868	16, -90	up gene, un gene	1	1	24	21	1	1_A270_shL7_chr(n_blc RNA:1	24	Gene KIP14	MGC142302, KIAAD042, KIP14	kinase family member 14	NM_014679, NCT16539663.1, NCT02341833, NCT02341834		2060364_at, 2060441_at	NP_055993.1, EAW61315.1, EAW61316.1, EAW61317.1
Gene ID:5 3478	DDX58	1	200,613,165	200,639,126	25,961	-	2	1_A270_shL7_chr(n A:1:590, 2_A270_shL97_glo(n 1:1418	186, 246	up gene, un gene	1	1	26	32	1	2_A270_shL97_glo(_blcR NA:1	32	Gene DDX58	ZNFHT5, DDX58, DKFZp564B1623	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	NM_001031725, NCT19309621.1, NCT02341833.0		2226662_s_at, 226383_at, 226366_s_at	NP_001019763.1, EAW61316.1, EAW61318.1
Gene ID:2 3271	CAMSAP1 1	1	200,705,686	200,829,632	121,146	+	1	2_A270_shL97_glo(n 1:1411	-238	upstream	0	1	13	25	1	2_A270_shL97_glo(_blcR NA:1	25	Gene CAMSAP1L1	KIAA1078, MGC130681, MGC130680, CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	NM_020459, NCT16539665.2, NCT02340421.0		212763_at, 212765_at, 212766_s_at	NP_064854.2, EAW61321.1, EAW61320.1
Gene ID:2 646	GPR25	1	200,842,166	200,843,251	1,085	+	1	2_A270_shL97_glo(n 1:812	1495	downstream	0	1	16	24	1	2_A270_shL97_glo(_blcR NA:1	24	Gene GPR25	GPR25	G protein-coupled receptor 25	NM_003566, NCT16555593.0		221953_s_at	NP_003566.2, EAW61322.1
Gene ID:5 5763	C1orf106	1	200,860,639	200,884,864	24,225	+	2	1_A270_shL7_chr(n A:1:597, 2_A270_shL97_glo(n 1:868	-159, -127	upstream, upstream	1	1	32	36	1	2_A270_shL97_glo(_blcR NA:1	36	Gene C1orf106	FLJ10901, C1orf106, MGC125666	chromosome 1 open reading frame 106	NM_018265, NM_001142569, NCT02329620		219010_at	NP_060735.2, NP_001138041.1, EAW61323.1
Gene ID:9 1196	IGFN1	1	201,150,953	201,195,080	35,127	+	2	1_A270_shL7_chr(n A:1:590, 2_A270_shL97_glo(n 1:848	39215, 39339	downstream, downstream	1	1	19	17	1	1_A270_shL7_chr(n_blc RNA:1	19	Gene IGFN1	IGFN1, DKFZp434B1231, EEP1A2BP1	immunoglobulin-like and fibronectin type III domain containing 1	NM_001164585, NCT02329632.1, NCT02329634.1, NCT02340811.0		1553092_at, 229279_at	NP_001158057.1, EAW61349.1, EAW61347.1, EAW61348.1
Gene ID:3 317	PKP1	1	201,252,560	201,302,121	49,561	+	1	1_A270_shL7_chr(n A:1:599	27482	up gene	1	0	21	17	1	1_A270_shL7_chr(n_blc RNA:1	21	Gene PKP1	MGC135629, PKP1, B6P	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	NM_000299, NM_001005337, NCT02329630.0, NCT02329629.0, NCT02341833.0		203724_at, 221564_at	NP_000290.2, NP_001005337.1, EAW61330.1, EAW61331.1, EAW61332.1
Gene ID:2 3612	PHLDA3	1	201,434,622	201,438,299	3,677	-	3	1_A270_shL7_chr(n A:1:600, 1_A270_shL97_glo(n 1:816, 2_A270_shL97_glo(n 1:819	7092, 7131, -293	downstream, downstream, upstream	1	1	24.5	21	2	1_A270_shL7_chr(n_blc RNA:1	30	Gene PHLDA3	TIH1, PHLDA3	pleckstrin homology-like domain, family A, member 3	NM_012396, NCT67731.2		218554_at	NP_036528.1, EAW61358.1
Gene ID:1 465	CSRP1	1	201,482,658	201,499,267	23,729	-	4	1_A270_shL7_chr(n A:1:591, 1_A270_shL97_glo(n A:1:592, 1_A270_shL97_glo(n 1:816, 2_A270_shL97_glo(n 1:818	17691, 163, 17691, 27	up gene, un gene, un gene, downstream	1	1	22	21.5	2	1_A270_shL7_chr(n_blc RNA:1	23	Gene CSRP1	CRP, CSRP1, CYRP, CSRP, DIS181.E, DKFZp686H146, CRP1	cysteine and glycine-rich protein 1	NM_198578, NM_001195570, NM_001163571, NM_001163572, NCT19353845.0, NCT67330.3		206521_at	NP_003469.1, NP_001182492.1, NP_001163051.1, NP_001163051.1, EAW61370.1, EAW61371.1
Gene ID:5 4796	NAV1	1	201,617,450	201,796,102	178,652	+	4	1_A270_shL7_chr(n A:1:591, 1_A270_shL97_glo(n A:1:592, 1_A270_shL97_glo(n 1:823, 2_A270_shL97_glo(n 1:826	160760, 552, 89180, 160726	up gene, un gene, un gene, downstream	1	1	32.33	40.67	3	2_A270_shL97_glo(_blcR NA:1	16	Gene NAV1	STEERIN1, DKFZp547I0314, FLJ12993, neuron navigator 1 POMFIL2, FLJ14283, NAV1, KIAA1151, UNC53H1, MGC14991		NM_020443, NM_001167136, NCT02329665.1, NCT02329690.1, NCT02329693.1		2307710_s_at, 236771_at, 236772_at, 236773_at, 236774_s_at, 243997_at, 233570_at	NP_065176.3, NP_001161210.1, EAW61372.1, EAW61374.1
Gene ID:3 3705	IFI30	1	201,797,268	201,833,422	55,154	+	2	1_A270_shL7_chr(n A:1:592, 2_A270_shL97_glo(n 1:825	-48, -112	upstream, upstream	1	1	12	16	1	2_A270_shL97_glo(_blcR NA:1	16	Gene IFI30	FLJ10402, DKFZp761M1547, IFI30, IFI30	gilysin II	NM_006332, NCT02329618.1, NCT02329620.1, NCT02337429.0		213765_at, 213583_at, 240361_at, 240362_s_at	NP_006323.2, EAW61376.1, EAW61378.1, EAW61377.1
Gene ID:2 5502	MYOD1	1	201,865,564	201,913,716	50,152	-	3	1_A270_shL7_chr(n A:1:592, 1_A270_shL97_glo(n 1:826	47122, -, 8764	downstream, upstream	1	1	23	21	1	1_A270_shL7_chr(n_blc RNA:1	23	Gene MYOD1	FLJ38669, 6A3D, D1, BHLHC0, 1D, MYOD1	myomatin 1 (smooth muscle)	NM_012134, NCT02327677.0, NCT62362.2		203766_s_at, 203767_s_at, 211062_s_at	NP_036266.2, EAW61380.1, EAW61381.1
Gene ID:1 0440	TMMI17A	1	201,924,619	201,929,769	15,170	+	2	1_A270_shL7_chr(n A:1:606, 1_A270_shL97_glo(n 1:824	-171, -139	upstream, upstream	1	1	23	21	1	1_A270_shL7_chr(n_blc RNA:1	23	Gene TMMI17A	TMMI17A, TIMI7, TMI7A	transducer of erbb-2 interacting protein 17 homolog A (rabbit)	NM_006333, NCT16539634.1, NCT19357710.1, NCT67326.2		201621_s_at, 201622_at, 219166_at, 219167_s_at	NP_006324.1, EAW61383.1, EAW61384.1, EAW61385.1
Gene ID:9 551	RAPEP	1	201,951,798	201,979,275	23,309	+	1	2_A270_shL97_glo(n 1:827	120	up gene	0	1	20	23	1	2_A270_shL97_glo(_blcR NA:1	23	Gene RAPEP	RNPEP, DKFZp547H084	arginyl aminopeptidase (aminopeptidase B)	NM_020216, NCT16475166.2, NCT02354930.0		2052703_s_at	NP_064601.3, EAW61386.1, EAW61387.1
Gene ID:2 9688	UBE2T	1	202,300,765	202,311,094	10,329	-	3	1_A270_shL7_chr(n A:1:597, 1_A270_shL97_glo(n 1:606, 1_A270_shL97_glo(n 1:828	6, -7306, 10	up gene, un gene, upstream	1	1	16	20.5	2	2_A270_shL97_glo(_blcR NA:1	22	Gene UBE2T	UBE2T, PIG50, HSPC150	ubiquitin-conjugating enzyme E2T (putative)	NM_014176, NCT02327690.0, NCT02329703.0, NCT02329702.0, NCT02329753.0, NCT02329754.0		2332229_at	NP_054993.1, EAW61414.1, EAW61411.1, EAW61412.1, EAW61413.1, EAW61415.1
Gene ID:4 990	FPR1R12 8	1	202,317,830	202,337,697	239,867	+	3	1_A270_shL7_chr(n A:1:597, 1_A270_shL97_glo(n 1:808, 2_A270_shL97_glo(n 1:828	47422, 670, 4026	upstream, un gene, upstream	1	1	16	20.5	2	2_A270_shL97_glo(_blcR NA:1	22	Gene FPR1R128	FLJ40962, MYP72, MGC87656, MGC131660, FPR1R128	protein phosphatase 1, regulatory (inhibitor) subunit 12B	NM_002481, NM_032103, NM_032104, NM_001167537, NM_001167536, NCT23257240.0, NCT23257239.0, NCT23257227.0, NCT23257226.0, NCT23257230.0, NCT23257231.0, NCT23257232.0, NCT23257233.0		1555444_a_at, 1557553_at, 201957_at, 201955_s_at	NP_002472.2, NP_115286.1, NP_115287.1, NP_001161229.1, NP_001161230.1, EAW61409.1, EAW61410.1, EAW61417.1, EAW61418.1, EAW61419.1, EAW61420.1, EAW61421.1, EAW61422.1, EAW61423.1, EAW61424.1, EAW61425.1, EAW61426.1
Gene ID:1 27832	SYT2	1	202,558,724	202,679,551	119,827	-	5	1_A270_shL7_chr(n A:1:599, 1_A270_shL97_glo(n A:1:610, 1_A270_shL97_glo(n 1:829, 2_A270_shL97_glo(n 1:830, 2_A270_shL97_glo(n 1:834	53071, 17279, 53231, 26705, 17263	up gene, un gene, un gene, un gene, un gene	1	1	33	34.67	3	2_A270_shL97_glo(_blcR NA:1	63	Gene SYT2	FLJ42519, SYT2, SytII	synaptotagmin II	NM_177402, NM_001135854, NCT22812.4, NCT23494068.0			NP_795792.2, NP_001128976.1, EAW61429.1, EAW61430.1
Gene ID:1 0765	KDM5B	1	202,696,532	202,777,599	81,067	-	3	1_A270_shL7_chr(n A:1:611, 1_A270_shL97_glo(n 1:832, 2_A270_shL97_glo(n 1:834	-2419, 93, 2403	upstream, un gene, upstream	1	1	16.5	21	2	1_A270_shL7_chr(n_blc RNA:1	23	Gene KDM5B	FLJ10330, PLU1, KDM5B, CT31, FLJ12459, PLU1, JARID1B, FLJ23970, FLJ12481, RBBP2H1A, PLU1-, FLJ16261	lysine (K)-specific demethylase 5B	NM_006618, NCT23257242.0, NCT23257450.0, NCT23257449.0, NCT23257210.0		2051547_at, 2015545_s_at, 2015546_s_at, 211202_s_at	NP_006609.3, EAW61433.1, EAW61432.1, EAW61434.1, EAW61435.1
Gene ID:1 0356698	LOC1003 86696	1	202,760,074	202,761,040	966	+	3	1_A270_shL7_chr(n A:1:611, 2_A270_shL97_glo(n 1:832, 2_A270_shL97_glo(n 1:834	-106, -, 2616, -122	upstream, upstream, upstream	1	1	16.5	21	2	1_A270_shL7_chr(n_blc RNA:1	23	Gene LOC1003 86696		hypothetical LOC100696696	XR_111976, XR_111979, XR_108330, XR_108329, XR_114963, XR_114964			
Gene ID:6 41515	LOC6415 15	1	202,769,365	202,790,253	6,968	+	2	1_A270_shL7_chr(n A:1:611, 1_A270_shL97_glo(n 1:833	-6417, -, 6433	upstream, upstream	1	1	23	22	1	1_A270_shL7_chr(n_blc RNA:1	23	Gene LOC641515		hypothetical LOC641515	XR_108331, XR_114966			
Gene ID:5 4349	KLHL12	1	202,860,230	202,896,271	36,141	-	1	2_A270_shL97_glo(n 1:838	41	upstream	0	1	16	21	1	2_A270_shL97_glo(_blcR NA:1	21	Gene KLHL12	C3IP1, KLHL12, DKIP, FLJ27152	kelch-like 12 (Drosophila)	NM_021633, NCT16422.3, NCT22480001.0, NCT22480002.0, NCT23514916.0		219831_s_at, 219832_at	NP_067646.1, EAW61445.1, EAW61446.1, EAW61446.1, EAW61447.1, EAW61448.1
Gene ID:3 1094	ADIPOR1	1	202,909,995	202,927,700	17,706	-	1	2_A270_shL97_glo(n 1:838	840	up gene	0	1	18	21	1	2_A270_shL97_glo(_blcR NA:1	21	Gene ADIPOR1	ACDCR1, CGI45, CGI-45, PLI25355, ADIPOR1, PLI42464, TESBP1A, PAQR1	adiponectin receptor 1	NM_015999, NM_001129827, NCT19354721.2, NCT19357710.1, NCT19357721.1		2137748_at	NP_057083.2, NP_001121193.1, EAW61449.1, EAW61450.1
Gene ID:3 1706	CYB5R1	1	202,931,001	202,939,404	8,403	-	1	2_A270_shL97_glo(n 1:838	8544	downstream	0	1	18	21	1	2_A270_shL97_glo(_blcR NA:1	21	Gene CYB5R1	B5R1, NCO3A2, B5R.1, CYB5R1, Hs4B3A2	cytochrome b5 reductase 1	NM_016243, NCT19994719.1, NCT23229849.0, NCT19357710.1, NCT19357721.1		1560043_at, 201262_at	NP_057327.2, EAW61454.1, EAW61451.1, EAW61452.1, EAW61453.1
Gene ID:9 1796	TMEM163	1	202,976,534	202,993,197	16,663	+	1	2_A270_shL97_glo(n 1:838	-166	upstream	0	1	22	16	1	2_A270_shL97_glo(_blcR NA:1	16	Gene TMEM163A	TMEM163A, C1or67	transmembrane protein 163A	NM_139281, NCT23237760.0, NCT23237710.0, NCT19357760.0		212164_at	NP_612830.2, EAW61456.1, EAW61457.1, EAW61458.1
Gene ID:1 54	ADORA1	1	203,098,636	203,136,533	39,897	+	1	2_A270_shL97_glo(n 1:837	858	up gene	0	1	16	21	1	2_A270_shL97_glo(_blcR NA:1	21	Gene ADORA1	RDC7, ADORA1	adenosine A1 receptor	NM_000674, NM_009758, NCT14022.2		205681_at, 216220_s_at	NP_000665.1, EAW61465.1, EAW61466.1
Gene ID:1 0356677	LOC1005 36775	1	203,256,260	203,257,826	1,646	+	1	2_A270_shL97_glo(n 1:838	-5164	upstream	0	1	13	20	1	2_A270_shL97_glo(_blcR NA:1	20	Gene LOC1005367 75		hypothetical LOC100367775	NR_111974, XR_108333, XR_108332, XR_114967			
Gene ID:5 549	PRELP	1	203,444,663	203,460,460	15,797	+	1	1_A270_shL7_chr(n A:1:610	11965	up gene	1	0	17	15	1	1_A270_shL7_chr(n_blc RNA:1	17	Gene PRELP	MST161, SLRR2A, MSTP161, PRELP, MGC45322	proline/arginine-rich end leucine-rich repeat protein	NM_002725, NM_201246, NCT15446.2, NCT19357710.1, NCT67326.2		204222_at, 225224_at, 225225_at	NP_002716.1, NP_958808.1, EAW61481.1
Gene ID:2 4254	OPTC	1	203,463,271	203,474,077	14,806	+	1	2_A270_shL97_glo(n 1:833	6423	upstream	1	0	17	15	1	2_A270_shL97_glo(_blcR NA:1	17	Gene OPTC	OPT, OPTC	opticin	NM_014359, NCT19344.2		210694_at	NP_055174.1, EAW61482.1
Gene ID:9 577	ZCSH11A	1	203,784,751	203,823,296	38,545	+	2	1_A270_shL7_chr(n A:1:617, 2_A270_shL97_glo(n 1:842	65873, 65999	downstream, downstream	1	1	28	46	1	2_A270_shL97_glo(_blcR NA:1	46	Gene ZCSH11A	ZCSH11A, DKFZp27611I2455, DKFZp686D03108, ZCSH0C11A, DKFZp686F14109, KIAA0963	BAC trigger CCCH-type containing 11A	NM_014627, NCT16176001.1, NCT23237620.0		1565997_at, 208787_s_at, 208788_s_at	NP_055442.2, EAW61492.1, EAW61492.1
Gene ID:9 535	SNRPE	1	203,830,740	203,840,280	9,540	+	2	1_A270_shL7_chr(n A:1:617, 2_A270_shL97_glo(n 1:842	-116, -30	upstream, upstream	1	1	28	46	1	2_A270_shL97_glo(_blcR NA:1	46	Gene SNRPE	SME, Sm-E, SNRPE, B-raf	small nuclear ribonucleoprotein polypeptide E	NM_003094, NCT23237766.1, NCT23237767.1		202316_s_at, 231112_at	NP_003084.1, EAW61494.1, EAW61488.1
Gene ID:9 552	SOX12	1	204,042,246	204,098,871	54,625	+	2	1_A270_shL7_chr(n A:1:616, 2_A270_shL97_glo(n 1:842	782, 886	up gene, un gene	1	1	16	17	1	1_A270_shL7_chr(n_blc RNA:1	16	Gene SOX12	MGC117216, Sox-12, SOX12, ICA12	SRY (sex determining region Y)-box 12	NM_006946, NCT23373985.0, NCT67325.2		1560111_at, 206796_at, 38615_at	NP_008877.2, EAW61499.1, EAW61500.1
Gene ID:5 4818	PPP1R15 B	1	204,272,492	204,280,844	8,452	+	1	2_A270_shL97_glo(n 1:842	4712	upstream	0	1	13	17	1	2_A270_shL97_glo(_blcR NA:1	17	Gene PPP1R15B	CREP, FLJ11494, PPP1R15B	protein phosphatase 1, regulatory (inhibitor) subunit 15B	NM_032833, NCT16161.2		224662_at	NP_116222.2, EAW61511.1
Gene ID:5 787	PIK3CB	1	204,291,755	204,459,474	167,719	+	1	2_A270_shL97_glo(n 1:842	72618	downstream	0	1	13	17	1	2_A270_shL97_glo(_blcR NA:1	17	Gene PIK3CB	PIK3CB, DKFZp686G11623I, CLOPIN, PIK3CB	phosphoinositide-3-kinase, class 2, beta polypeptide	NM_006219, NCT23247596.0, NCT67346.2		204454_at	NP_006203.2, EAW61513.1, EAW61514.1
Gene ID:4 194	MDM4	1	204,485,511	204,527,248	41,737	+	2	1_A270_shL7_chr(n A:1:619, 2_A270_shL97_glo(n 1:842	42319, 121	upstream, un gene	1	0	23.5	15.5	2	2_A270_shL97_glo(_blcR NA:1	24	Gene MDM4	MGC13279, DKFZp781B1623, HDMX, MDM5, MRP1, MDM4	MDM4, p53 binding protein homolog (mouse)	NM_002393, NM_031971, NCT23241458.0, NCT67460.3		202553_s_at, 228569_s_at, 236614_at, 236615_at	NP_002384.2, EAW61515.1, EAW61516.1
Gene ID:1 0446	URRA2	1	204,586,301	204,634,597	48,296	-	2	1_A270_shL7_chr(n A:1:627, 2_A270_shL97_glo(n 1:843	27624, 37733	up gene, un gene	1	1	66	61	1	2_A270_shL97_glo(_blcR NA:1	61	Gene URRA2	LRRN5, GAC1, LRANK3, LRRN2, RGLER7	leucine rich repeat neuronal 2	NM_006138, NM_201630, NCT23287010.0, NCT23373960.0, NCT67446.1		208154_at, 219164_at, 219167_at	NP_006129.1, EAW61521.1, EAW61522.1
Gene ID:2 3114	NPAS2	1	204,797,742	204,901,850	104,168	+	3	1_A270_shL7_chr(n A:1:622, 2_A270_shL97_glo(n 1:847, 2_A270_shL97_glo(n 1:848	8034, 8884, 161450	up gene, un gene, un gene	1	1	22.5	29	2	2_A270_shL97_glo(_blcR NA:1	37	Gene NPAS2	DKFZp686P2250, KIAA0756, NP, NPCANL, FLJ36556, NPAS2	neuronal PAS domain protein 2	NM_001005399, NM_016080, NM_001005388, NM_001160331, NM_001160332, NM_001160333		213438_at, 216799_at, 230242_at, 240643_at	NP_001005399.2, NP_057953.2, NP_001005388.2, NP_001153051.1, NP_001153052.1, NP_001153053.1
Gene ID:5 828	RBBP5	1	205,055,270	205,091,150	35,880	-	2	1_A270_shL7_chr(n A:1:622, 2_A270_shL97_glo(n 1:848	-164, -262	upstream, upstream	1	1	49	50	1	2_A270_shL97_glo(_blcR NA:1	50	Gene RBBP5	RBBP5, SWD1, RBQ3	retinoblastoma binding protein 5	NM_005057, NM_001192272, NM_001161273, NCT19963442.2, NCT23285220.0, NCT23573610.0, NCT67466.3		205169_at	NP_005048.2, NP_001160241.1, NP_001160250.1, EAW61535.1, EAW61537.1, EAW61536.1, EAW61538.1
Gene ID:2 9776	DSTYK	1	205,111,631	205,160,727	49,096	+	2	1_A270_shL7_chr(n A:1:626, 2_A270_shL97_glo(n 1:850	407, -73	upstream, upstream	1	1	16	26	1	2_A270_shL97_glo(_blcR NA:1	26	Gene DSTYK	RIPS, HOCM0305F, DustyPK, DSTYK, KIAA0472, RIPK3	dual serine/threonine and tyrosine protein kinase	NM_015375, NM_199462, NCT23481910.0, NCT23248316.0, NCT23481910.0, NCT23248320.0, NCT23248321.0		211514_at, 211515_s_at, 211516_at, 214663_at, 226612_s_at	NP_056190.1, NP_955748.1, EAW61540.1, EAW61541.1, EAW61542.1, EAW61543.1, EAW61544.1
Gene ID:9 911	TMCC2	1	205,197,036	205,242,671	45,635	+	1	2_A270_shL97_glo(n 1:851	20930	up gene	0	1	16	19	1	2_A270_shL97_glo(_blcR NA:1	19	Gene TMCC2	FLJ38497, TMCC2, HUCEP1, KIAA0461	transmembrane and coiled-coil domain family 2	NM_014855, NCT16534491.1, NCT16534492.1, NCT23248316.0, NCT67544.3		1555553_s_at, 213696_at	NP_055670.2, EAW61545.1, EAW61546.1, EAW61547.1, EAW61548.1
Gene ID:1 0356687	LOC1003 86671	1	205,236,636	205,236,992	356	+	1	2_A270_shL97_glo(n 1:851	-5665	upstream	0	1	16	19	1	2_A270_shL97_glo(_blcR NA:1	19	Gene LOC1003 86687		hypothetical protein LOC100367671	NR_033178760, NM_002315852, XM_003120647			NP_002315852.1, XP_003116550.1, XP_003120695.1
Gene ID:1 0356699 6	LOC1005 36616	1	205,454,013	205,525,214	21,201	+	4	1_A270_shL7_chr(n A:1:626, 1_A270_shL97_glo(n A:1:627, 2_A270_shL97_glo(n 1:853, 2_A270_shL97_glo(n 1:854	6795, -, 3010, -, 2016, -, 3106	up gene, upstream, upstream, upstream	1	1	26.5	34	2	2_A270_shL97_glo(_blcR NA:1	34	Gene LOC1005366 16		hypothetical LOC100366616	XR_111965, XR_108337, XR_114972			
Gene ID:4 82691	MIR1338	1	205,517,430	205,517,526	96	-	3	1_A270_shL7_chr(n A:1:626, 1_A270_shL97_glo(n A:1:627, 2_A270_shL97_glo(n 1:853	-690, -, 10696, 3706	upstream, un gene, upstream	1	1	26.5	34	2	2_A270_shL97_glo(_blcR NA:1	34	Gene MIR1338	MIRN1338, MIR1338	microRNA 1338	NR_036691			
Gene ID:2 84577	LOC2845 77	1	205,525,045	205,535,152	10,107	+	4	1_A270_shL7_chr(n A:1:626, 1_A270_shL97_glo(n A:1:627, 1_A270_shL97_glo(n 1:853, 1_A270_shL97_glo(n 1:854	4529, 2179, 2187, 3275	up gene, upstream, un gene, upstream	1	1	26.5	34	2	2_A270_shL97_glo(_blcR NA:1	34	Gene LOC284577		hypothetical LOC284577	XR_111970, XR_108338, XR_114974			
Gene ID:2 005	ELK4	1	205,583,235	205,602,000	18,765	-	2	1_A270_shL7_chr(n A:1:626, 2_A270_shL97_glo(n 1:855	648, 816	up gene, un gene	1	1	22	38	1	2_A270_shL97_glo(_blcR NA:1	38	Gene ELK4	SAP1, ELG4	ELK4, ETS-domain protein (SRF accessory protein 1)	NM_001973, NM_021795, NCT17809651.1, NCT23245908.0, NCT23245909.0, NCT23245907.0, NCT67645.2		206894_at, 206919_at, 235949_at	NP_001964.2, NP_068367.1, EAW61570.1, EAW61571.1, EAW61572.1, EAW61574.1, EAW61573.1
Gene ID:6 4710	NUCKS1	1	205,661,947	205,719,261	57,314	+	1	2_A270_shL97_glo(n 1:856	-21	upstream	0	1	12	19	1	2_A270_shL97_glo(_blcR NA:1	19	Gene NUCKS1	FLJ32016, FLJ21480, FLJ35536, NUCKS, JC7, NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	NM_022731, NCT23224898.0, NCT23285500.0		219302_s_at, 220227_at, 222424_s_at, 236690_at, 236353_s_at	NP_073562.2, EAW61578.1, EAW61579.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:10380	BPNT1	1	220,230,824	220,263,191	32,367	-	3	1_A375_pNL7_minus_lncRNA::1::687, 2_A375_pNL97_plus_lncRNA::1::941, 2_A375_pNL97_plus_lncRNA::1::942	-73, 55, -4441	upstream, in gene, upstream	1	1	17.5	25.5	2	2_A375_pNL97_plus_lncRNA::1	30	Gene BPNT1	PIP, BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	NM_006085, hCT16866.2, hCT1962395.1, hCT1962396.1	1554575_a_at, 219391_at, 232103_at	NP_006076.4, EAW93306.1, EAW93307.1, EAW93308.1
GeneID:55699	IARS2	1	220,267,455	220,321,383	53,928	+	3	1_A375_pNL7_minus_lncRNA::1::687, 2_A375_pNL97_plus_lncRNA::1::941, 2_A375_pNL97_plus_lncRNA::1::942	-4191, -4319, 177	upstream, upstream, in gene	1	1	17.5	25.5	2	2_A375_pNL97_plus_lncRNA::1	30	Gene IARS2	FLJ10326, ILERS, IARS2	isoleucyl-tRNA synthetase 2, mitochondrial	NM_018060, hCT16867.3	217900_at	NP_060530.3, EAW93305.1
GeneID:25782	RAB3GAP2	1	220,321,610	220,445,843	124,233	-	1	2_A375_pNL97_plus_lncRNA::1::943	-13	upstream	0	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RAB3GAP2	FLJ14579, DKFZp434D245, RAB3GAP150, KIAA0839, RAB3-GAP150, RAB3GAP2, p150	RAB3 GTPase activating protein subunit 2 (non-catalytic)	NM_012414, hCT2260874.0	202373_s_at, 202374_s_at, 216057_at, 243851_at	NP_036546.2, EAW93304.1
GeneID:4139	MARK1	1	220,701,568	220,837,799	136,231	+	2	1_A375_pNL7_minus_lncRNA::1::688, 2_A375_pNL97_plus_lncRNA::1::945	256, 448	in gene, in gene	1	1	17	17	1	1_A375_pNL7_minus_lncRNA::1	17	Gene MARK1	MARK, MGC126513, MARK1, MGC126512, KIAA1477	MAP/microtubule affinity-regulating kinase 1	NM_018650, hCT16244.3, hCT2262343.0, hCT2262345.0, hCT2262346.0, hCT2357618.0	1560407_at, 221047_s_at, 226653_at, 231613_at	NP_061120.3, EAW93302.1, EAW93298.1, EAW93299.1, EAW93300.1, EAW93301.1
GeneID:3142	HLX	1	221,052,743	221,058,401	5,658	+	1	2_A375_pNL97_plus_lncRNA::1::946	697	in gene	0	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene HLX	HLX, HB24, HLX1	H2.0-like homeobox	NM_021958, hCT16243.3, hCT2260235.0	214438_at	NP_068777.1, EAW93289.1, EAW93288.1
GeneID:400804	LOC400804	1	221,503,270	221,509,638	6,368	-	1	1_A375_pNL7_minus_lncRNA::1::689	598	in gene	1	0	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene LOC400804	FLJ46636, MGC176608, C1orf140	hypothetical LOC400804	NR_024236		
GeneID:11221	DUSP10	1	221,874,766	221,915,461	40,695	-	4	1_A375_pNL7_minus_lncRNA::1::690, 1_A375_pNL7_minus_lncRNA::1::691, 2_A375_pNL97_plus_lncRNA::1::948, 2_A375_pNL97_plus_lncRNA::1::949	2917, -347, 2917, -347	in gene, upstream, in gene, upstream	1	1	31.5	28	2	1_A375_pNL7_minus_lncRNA::1	36	Gene DUSP10	MKP5, MKP-5, DUSP10	dual specificity phosphatase 10	NM_144728, NM_144729, NM_007207, hCT16153.3, hCT1957420.2, hCT2351374.0, hCT2351375.0, hCT2351376.0	215501_s_at, 221563_at	NP_653329.1, NP_653330.1, NP_009138.1, EAW93284.1, EAW93286.1, EAW93287.1, EAW93283.1, EAW93285.1
GeneID:375056	MIA3	1	222,791,444	222,841,351	49,907	+	2	1_A375_pNL7_minus_lncRNA::1::695, 2_A375_pNL97_plus_lncRNA::1::955	26252, 25996	in gene, in gene	1	1	26	20	1	1_A375_pNL7_minus_lncRNA::1	26	Gene MIA3	KIAA0268, ARNT, FLJ21469, MIA3, TANGO, FLJ39207, UNQ6077, D320, TANGO1	melanoma inhibitory activity family, member 3	NM_198551	1569057_s_at, 212305_s_at, 212310_at	NP_940953.2
GeneID:64853	AIDA	1	222,841,355	222,885,864	44,509	-	2	1_A375_pNL7_minus_lncRNA::1::696, 2_A375_pNL97_plus_lncRNA::1::956	-696, -696	upstream, upstream	1	1	25	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene AIDA	RP11-378J18.7, C1orf80, FLJ32421, FLJ12806, AIDA	axin interactor, dorsalization associated	NM_022831, hCT1782862.1	220199_s_at, 226801_s_at	NP_073742.2, EAX06366.1
GeneID:148362	C1orf58	1	222,885,906	222,906,109	20,203	+	2	1_A375_pNL7_minus_lncRNA::1::696, 2_A375_pNL97_plus_lncRNA::1::956	654, 654	in gene, in gene	1	1	25	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene C1orf58	Brox, MGC142197, BROX, MGC142195, FLJ32421, RP11-452F19.1, C1orf58	BRO1 domain and CAAX motif containing	NM_144695, hCT16461.3	226128_at, 239078_at, 241908_at	NP_653296.2, EAW93265.1
GeneID:84976	DISP1	1	223,101,783	223,179,335	77,552	+	1	2_A375_pNL97_plus_lncRNA::1::958	-9079	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene DISP1	DISPA, DKFZp434I0428, DISP1, FLJ43740, MGC13130, MGC104180, MGC16796	dispatched homolog 1 (Drosophila)	NM_032890, hCT1641075.3	228184_at, 235466_s_at	NP_116279.2, EAW93264.1
GeneID:388743	CAPN8	1	223,714,972	223,853,436	138,464	-	1	1_A375_pNL7_minus_lncRNA::1::699	13116	in gene	1	0	24	19	1	1_A375_pNL7_minus_lncRNA::1	24	Gene CAPN8	CAPN8, nCL-2	calpain 8	NM_001143962	229030_at	NP_001137434.1
GeneID:824	CAPN2	1	223,889,295	223,963,720	74,425	+	5	1_A375_pNL7_minus_lncRNA::1::700, 1_A375_pNL7_minus_lncRNA::1::701, 1_A375_pNL7_minus_lncRNA::1::702, 2_A375_pNL97_plus_lncRNA::1::960, 2_A375_pNL97_plus_lncRNA::1::961	-287, 5761, 13841, 13969, 63697	upstream, in gene, in gene, in gene, in gene	1	1	16.25	18.5	4	1_A375_pNL7_minus_lncRNA::1	21	Gene CAPN2	CANP2, CAPN2, CANPL2, CANPml, FLJ39928, mCANP	calpain 2, (m/II) large subunit	NM_001748, NM_001146068, hCT2260559.0, hCT2260561.0, hCT30148.3	208683_at, 214888_at	NP_001739.2, NP_001139540.1, EAW93249.1, EAW93250.1, EAW93251.1
GeneID:100288102	LOC100288102	1	224,170,752	224,180,346	9,594	-	1	1_A375_pNL7_minus_lncRNA::1::705	-6	upstream	1	0	36	21	1	1_A375_pNL7_minus_lncRNA::1	36	Gene LOC100288102		hypothetical LOC100288102	XR_110840		
GeneID:23219	FBXO28	1	224,301,791	224,349,749	47,958	+	1	1_A375_pNL7_minus_lncRNA::1::706	1	in gene	1	0	21	25	1	1_A375_pNL7_minus_lncRNA::1	21	Gene FBXO28	FLJ10766, FBXO28, KIAA0483, Fbx28	F-box protein 28	NM_015176, NM_001136115, hCT1794077.2, hCT1960196.1	1555970_at, 1555971_s_at, 1555972_s_at, 202271_at, 202272_s_at	NP_055991.1, NP_001129587.1, EAW69709.1, EAW69710.1
GeneID:8560	DEGS1	1	224,370,928	224,381,143	10,215	+	1	2_A375_pNL97_plus_lncRNA::1::962	448	in gene	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene DEGS1	FADS7, Des-1, DEGS1, MLD, MGC5079, DES1, DEGS, MIG15	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	NM_003676, hCT1774769.2, hCT1954054.1	207431_s_at, 209250_at	NP_003667.1, EAW69712.1, EAW69711.1
GeneID:4931	NVL	1	224,415,036	224,517,872	102,836	-	2	1_A375_pNL7_minus_lncRNA::1::707, 2_A375_pNL97_plus_lncRNA::1::963	-176, -160	upstream, upstream	1	1	31	30	1	1_A375_pNL7_minus_lncRNA::1	31	Gene NVL	NVL		NM_002533, NM_206840, hCT1953259.1, hCT2354732.0, hCT87707.2	207877_s_at	NP_002524.2, NP_996671.1, EAW69714.1, EAW69715.1, EAW69716.1
GeneID:29097	CNIH4	1	224,544,595	224,563,691	19,096	+	1	2_A375_pNL97_plus_lncRNA::1::964	221	in gene	0	1	16	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene CNIH4	HSPC163, CNIH4	cornichon homolog 4 (Drosophila)	NM_014184, hCT1953177.1, hCT2354714.0, hCT2354715.0	218728_s_at, 223993_s_at, 228306_at, 228437_at, 243051_at	NP_054903.1, EAW69717.1, EAW69718.1, EAW69719.1
GeneID:80232	WDR26	1	224,572,845	224,622,001	49,156	-	3	1_A375_pNL7_minus_lncRNA::1::708, 2_A375_pNL97_plus_lncRNA::1::965, 2_A375_pNL97_plus_lncRNA::1::966	-591, 177, -623	upstream, in gene, upstream	1	1	25.5	31.5	2	2_A375_pNL97_plus_lncRNA::1	47	Gene WDR26	CDW2, MIP2, FLJ21016, WDR26	WD repeat domain 26	NM_001115113, NM_025160, hCT1774767.3, hCT1953172.2, hCT1953173.2, hCT2272984.1, hCT2354713.0	218107_at, 223863_at, 224897_at, 224898_at, 224905_at	NP_001108585.2, NP_079436.4, EAW69720.1, EAW69721.1, EAW69723.1, EAW69724.1, EAW69722.1
GeneID:100506354	LOC100506354	1	224,622,614	224,709,707	87,093	+	4	1_A375_pNL7_minus_lncRNA::1::708, 1_A375_pNL7_minus_lncRNA::1::709, 2_A375_pNL97_plus_lncRNA::1::965, 2_A375_pNL97_plus_lncRNA::1::966	-22, 63210, -790, 10	upstream, in gene, upstream, in gene	1	1	25	26.67	3	2_A375_pNL97_plus_lncRNA::1	47	Gene LOC100506354		hypothetical LOC100506354	XR_112019, XR_110841, XR_115194		
GeneID:149111	CNIH3	1	224,804,179	224,928,249	124,070	+	2	2_A375_pNL97_plus_lncRNA::1::968, 2_A375_pNL97_plus_lncRNA::1::969	91533, 117293	in gene, in gene	0	1	16.5	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene CNIH3	FLJ38993, CNIH-3, CNIH3	cornichon homolog 3 (Drosophila)	NM_152495	214841_at, 236503_at	NP_689708.1
GeneID:127602	DNAH14	1	225,117,356	225,586,996	469,640	+	2	1_A375_pNL7_minus_lncRNA::1::711, 2_A375_pNL97_plus_lncRNA::1::970	164, 196	in gene, in gene	1	1	21	21	1	1_A375_pNL7_minus_lncRNA::1	21	Gene DNAH14	MGC149666, C1orf67, HL18, DNAH14, MGC149665, Dnahc14, MGC51214, DKFZp781B1548, MGC27277, HL-18	dynein, axonemal, heavy chain 14	NM_144989, NM_001145154, NM_001373	1567862_at	NP_659426.2, NP_001138626.1, NP_001364.1
GeneID:3930	LBR	1	225,589,204	225,616,519	27,315	-	3	1_A375_pNL7_minus_lncRNA::1::712, 2_A375_pNL97_plus_lncRNA::1::971, 2_A375_pNL97_plus_lncRNA::1::972	71, 1415, 519	in gene, in gene, in gene	1	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LBR	LMN2R, PHA, DHCR14B, MGC9041, LBR, FLJ43126	lamin B receptor	NM_002296, NM_194442, hCT1963515.1, hCT2272349.0, hCT23976.3	201795_at	NP_002287.2, NP_919424.1, EAW69741.1, EAW69742.1, EAW69743.1
GeneID:55740	ENAH	1	225,674,534	225,840,845	166,311	-	1	2_A375_pNL97_plus_lncRNA::1::973	-4531	upstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ENAH	ENA, MENA, NDPP1, ENAH	enabled homolog (Drosophila)	NM_018212, NM_001008493, hCT1953161.1	1553672_at, 217820_s_at, 222433_at, 222434_at, 228310_at, 228553_at	NP_060682.2, NP_001008493.1, EAW69747.1
GeneID:6726	SRP9	1	225,965,515	225,978,168	12,653	+	4	1_A375_pNL7_minus_lncRNA::1::714, 1_A375_pNL7_minus_lncRNA::1::715, 2_A375_pNL97_plus_lncRNA::1::975, 2_A375_pNL97_plus_lncRNA::1::976	-5323, -139, -5987, -107	upstream, upstream, upstream, upstream	1	1	30.33	35.67	3	2_A375_pNL97_plus_lncRNA::1	77	Gene SRP9	ALURBP, MGC110981, SRP9	signal recognition particle 9kDa	NM_001130440, NM_003133, hCT2258515.2, hCT2344143.1, hCT2344144.1, hCT2348687.0	201273_s_at	NP_001123912.1, NP_003124.1, EAW69750.1, EAW69751.1, EAW69752.1, EAW69753.1
GeneID:9725	TMEM63A	1	226,033,233	226,070,420	37,187	-	4	1_A375_pNL7_minus_lncRNA::1::716, 1_A375_pNL7_minus_lncRNA::1::717, 2_A375_pNL97_plus_lncRNA::1::977, 2_A375_pNL97_plus_lncRNA::1::978	2516, -284, 4946, 212	in gene, upstream, in gene, in gene	1	1	16.33	19.67	3	2_A375_pNL97_plus_lncRNA::1	25	Gene TMEM63A	KIAA0792, KIAA0489, TMEM63A	transmembrane protein 63A	NM_014698, hCT2272341.0, hCT23463.3	202699_s_at, 202700_s_at, 214833_at, 215583_at	NP_055513.2, EAW69758.1, EAW69759.1
GeneID:10637	LEFTY1	1	226,073,982	226,076,836	2,854	-	4	1_A375_pNL7_minus_lncRNA::1::716, 1_A375_pNL7_minus_lncRNA::1::717, 2_A375_pNL97_plus_lncRNA::1::977, 2_A375_pNL97_plus_lncRNA::1::978	8932, 6132, 11364, 6628	downstream, downstream, downstream, downstream	1	1	16.33	19.67	3	2_A375_pNL97_plus_lncRNA::1	25	Gene LEFTY1	LEFTYB, LEFTY1, LEFTB	left-right determination factor 1	NM_020997, hCT1775773.2	206268_at	NP_066277.1, EAW69760.1
GeneID:29920	PYCR2	1	226,107,580	226,111,965	4,385	-	1	2_A375_pNL97_plus_lncRNA::1::979	77	in gene	0	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene PYCR2	P5CR2, PYCR2, FLJ54750	pyrroline-5-carboxylate reductase family, member 2	NM_013328, hCT1953219.1, hCT1953221.1, hCT1953222.1, hCT2354741.0, hCT23974.2	224855_at, 231715_s_at	NP_037460.2, EAW69764.1, EAW69761.1, EAW69762.1, EAW69763.1, EAW69765.1
GeneID:3020	H3F3A	1	226,250,421	226,259,703	9,282	+	1	1_A375_pNL7_minus_lncRNA::1::718	-693	upstream	1	0	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene H3F3A	H3.3A, MGC87782, H3F3A, H3F3B, H3F3, MGC87783	H3 histone, family 3A	NM_002107, hCT2256679.1, hCT2256680.0, hCT2256681.1, hCT2354700.0	200080_s_at	NP_002098.1, EAW69772.1, EAW69770.1, EAW69771.1, EAW69773.1
GeneID:100506398	LOC100506398	1	226,259,263	226,284,420	25,157	-	2	1_A375_pNL7_minus_lncRNA::1::718, 2_A375_pNL97_plus_lncRNA::1::980	34692, 12900	downstream, in gene	1	1	19	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100506398		hypothetical LOC100506398	XR_112017, XR_112018, XR_110842, XR_115195		
GeneID:64746	ACBD3	1	226,332,380	226,374,423	42,043	-	2	1_A375_pNL7_minus_lncRNA::1::720, 2_A375_pNL97_plus_lncRNA::1::981	-9, -73	upstream, upstream	1	1	18	16	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ACBD3	GOLPH1, PAP7, GCP60, ACBD3, GOCAP1	acyl-CoA binding domain containing 3	NM_022735, hCT1775776.0, hCT2262177.0	202323_s_at, 202324_s_at	NP_073572.2, EAW69776.1, EAW69775.1
GeneID:286826	LIN9	1	226,418,861	226,497,198	78,337	-	2	1_A375_pNL7_minus_lncRNA::1::721, 2_A375_pNL97_plus_lncRNA::1::982	414, 398	in gene, in gene	1	1	21	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene LIN9	BARPsv, TGS, Lin-9, LIN9, BARA, TGS1	lin-9 homolog (C. elegans)	NM_173083, hCT2349292.0, hCT2349293.0, hCT2354717.0	1552771_a_at, 230365_at, 235039_x_at	NP_775106.2, EAW69781.1, EAW69780.1, EAW69782.1
GeneID:142	PARP1	1	226,548,392	226,595,801	47,409	-	2	1_A375_pNL7_minus_lncRNA::1::722, 2_A375_pNL97_plus_lncRNA::1::983	121, 164	in gene, in gene	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene PARP1	PARP, pADPRT-1, ADPRT, PARP-1, PPOL, PARP1, ADPRT 1, ADPRT1	poly (ADP-ribose) polymerase 1	NM_001618, hCT2262172.0, hCT2262173.0, hCT5767.3	208644_at	NP_001609.2, EAW69783.1, EAW69784.1, EAW69785.1
GeneID:3707	ITPKB	1	226,819,391	226,926,876	107,485	-	1	2_A375_pNL97_plus_lncRNA::1::984	35804	in gene	0	1	18	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene ITPKB	ITPKB, IP3K-B, IP3K, IP3KB, IP3-3KB, PIG37	inositol 1,4,5-trisphosphate 3-kinase B	NM_002221, hCT2262168.0	1554306_at, 203723_at, 232499_at, 232526_at, 235213_at	NP_002212.3, EAW69793.1
GeneID:56997	CABC1	1	227,127,938	227,175,246	47,308	+	3	1_A375_pNL7_minus_lncRNA::1::724, 1_A375_pNL7_minus_lncRNA::1::725, 2_A375_pNL97_plus_lncRNA::1::985	-9058, -370, -386	upstream, upstream, upstream	1	1	19.5	22	2	2_A375_pNL97_plus_lncRNA::1	29	Gene CABC1	MGC4849, COQ8, CABC1, ARCA2, SCAR9, ADCK3	aarF domain containing kinase 3	NM_020247, hCT1776120.1, hCT1953180.1, hCT1953181.1, hCT1953182.1, hCT1953183.1	218168_s_at, 222542_x_at	NP_064632.2, EAW69801.1, EAW69802.1, EAW69803.1, EAW69804.1, EAW69805.1
GeneID:339500	ZNF678	1	227,751,220	227,850,164	98,944	+	1	2_A375_pNL97_plus_lncRNA::1::989	244	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF678	MGC15634, MGC42493, FLJ18355, ZNF678, FLJ22822	zinc finger protein 678	NM_178549, NR_033184, hCT2354701.0, hCT33518.4	1554922_at, 232028_at, 242923_at	NP_848644.2, EAW69813.1, EAW69812.1
GeneID:100130093	LOC100130093	1	227,916,240	227,922,078	5,838	+	2	1_A375_pNL7_minus_lncRNA::1::728, 2_A375_pNL97_plus_lncRNA::1::990	6736, 6768	downstream, downstream	1	1	26	24	1	1_A375_pNL7_minus_lncRNA::1	26	Gene LOC100130093		hypothetical LOC100130093	NR_024485, NR_024486		
GeneID:65094	JMJD4	1	227,918,890	227,923,112	4,222	-	2	1_A375_pNL7_minus_lncRNA::1::728, 2_A375_pNL97_plus_lncRNA::1::990	136, 104	in gene, in gene	1	1	26	24	1	1_A375_pNL7_minus_lncRNA::1	26	Gene JMJD4	MGC129896, JMJD4, FLJ12517	jumonji domain containing 4	NM_023007, NM_001161465, hCT1953247.1, hCT33524.3	218560_s_at, 222671_s_at	NP_075383.2, NP_001154937.1, EAW69818.1, EAW69819.1
GeneID:116841	SNAP47	1	227,922,697	227,968,932	46,235	+	2	1_A375_pNL7_minus_lncRNA::1::728, 2_A375_pNL97_plus_lncRNA::1::990	279, 311	in gene, in gene	1	1	26	24	1	1_A375_pNL7_minus_lncRNA::1	26	Gene SNAP47	HEL170, DKFZp686M10160, FLJ12517, C1orf142, SVAP1, SNAP47, SNAP-47	synaptosomal-associated protein, 47kDa	NM_053052, hCT1953253.1, hCT33525.3	225244_at, 230810_at	NP_444280.2, EAW69816.1, EAW69817.1
GeneID:7483	WNT9A	1	228,109,165	228,135,676	26,511	-	2	1_A375_pNL7_minus_lncRNA::1::729, 2_A375_pNL97_plus_lncRNA::1::991	13116, 13100	in gene, in gene	1	1	24	22	1	1_A375_pNL7_minus_lncRNA::1	24	Gene WNT9A	MGC138165, WNT9A, WNT14, MGC141991	wingless-type MMTV integration site family, member 9A	NM_003395, hCT33515.3	1553045_at, 230643_at	NP_003386.1, EAW69821.1
GeneID:100506571	LOC100506571	1	228,261,610	228,264,251	2,641	-	1	2_A375_pNL97_plus_lncRNA::1::992	-5917	upstream	0	1	20	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506571		hypothetical protein LOC100506571	XM_003119777, XM_003119160, XM_003120910		XP_003119825.1, XP_003119208.1, XP_003120958.1
GeneID:375	ARF1	1	228,270,361	228,286,913	16,552	+	4	1_A375_pNL7_minus_lncRNA::1::730, 2_A375_pNL97_plus_lncRNA::1::992, 2_A375_pNL97_plus_lncRNA::1::993, 2_A375_pNL97_plus_lncRNA::1::994	26599, -193, 20615, 26599	downstream, upstream, downstream, downstream	1	1	22	25.67	3	2_A375_pNL97_plus_lncRNA::1	30	Gene ARF1	ARF1	ADP-ribosylation factor 1	NM_001658, NM_001024226, NM_001024227, NM_001024228, hCT1685515.0, hCT1685516.0, hCT1777164.1, hCT1953232.1, hCT2354728.0, hCT2354729.0	1565651_at, 200065_s_at, 208750_s_at, 232175_at, 244504_x_at	NP_001649.1, NP_001019397.1, NP_001019398.1, NP_001019399.1, EAW69832.1, EAW69834.1, EAW69831.1, EAW69833.1, EAW69835.1, EAW69836.1
GeneID:79169	C1orf35	1	228,288,428	228,291,022	2,594	-	3	1_A375_pNL7_minus_lncRNA::1::730, 2_A375_pNL97_plus_lncRNA::1::993, 2_A375_pNL97_plus_lncRNA::1::994	-5938, 46, -5938	upstream, in gene, upstream	1	1	23	29	2	2_A375_pNL97_plus_lncRNA::1	30	Gene C1orf35	MGC4174, MMTAG2, hMMTAG2, C1orf35	chromosome 1 open reading frame 35	NM_024319, hCT1953255.1, hCT2354726.0, hCT2354727.0	219063_at	NP_077295.1, EAW69838.1, EAW69837.1, EAW69839.1
GeneID:100506628	LOC100506628	1	228,291,253	228,304,782	13,529	-	3	1_A375_pNL7_minus_lncRNA::1::730, 2_A375_pNL97_plus_lncRNA::1::993, 2_A375_pNL97_plus_lncRNA::1::994	7622, 13806, 7622	in gene, downstream, in gene	1	1	23	29	2	2_A375_pNL97_plus_lncRNA::1	30	Gene LOC100506628		hypothetical LOC100506628	XR_112020, XR_110847, XR_115199		
GeneID:128308	MRPL55	1	228,294,380	228,297,013	2,633	-	3	1_A375_pNL7_minus_lncRNA::1::730, 2_A375_pNL97_plus_lncRNA::1::993, 2_A375_pNL97_plus_lncRNA::1::994	53, 6037, 53	in gene, downstream, in gene	1	1	23	29	2	2_A375_pNL97_plus_lncRNA::1	30	Gene MRPL55	MRPL55, L55nt, AAVG5835, MGC61802, MRP-L55, PRO19675, DKFZp686D1387	mitochondrial ribosomal protein L55	NM_181463, NM_181454, NM_181455, NM_181456, NM_181462, NM_181464, NM_181465, NM_181441, hCT1953244.1, hCT2354703.0, hCT2354704.0, hCT2354705.0, hCT2354706.0, hCT2354707.0, hCT2354708.0, hCT2354709.0, hCT2354710.0, hCT2354711.0	225719_s_at, 227024_s_at	NP_852128.1, NP_852119.1, NP_852127.2, NP_852120.1, NP_852121.1, NP_852129.1, NP_852106.1, NP_852130.1, EAW69840.1, EAW69841.1, EAW69842.1, EAW69843.1, EAW69844.1, EAW69845.1, EAW69846.1, EAW69847.1, EAW69848.1, EAW69849.1
GeneID:2987	GUK1	1	228,327,929	228,336,656	8,727	+	1	1_A375_pNL7_minus_lncRNA::1::731	-249	upstream	1	0	25	23	1	1_A375_pNL7_minus_lncRNA::1	25	Gene GUK1	FLJ42686, GUK1, FLJ43710, GMK	guanylate kinase 1	NM_000858, NM_001159390, NM_001159391, hCT2259103.1, hCT2259104.0, hCT2259107.1, hCT2259110.1, hCT2259113.1, hCT2340512.0, hCT2340513.0, hCT2350107.0, hCT2350108.0	200075_s_at, 213621_s_at	NP_000849.1, NP_001152862.1, NP_001152863.1, EAW69854.1, EAW69856.1, EAW69859.1, EAW69851.1, EAW69852.1, EAW69853.1, EAW69855.1, EAW69857.1, EAW69858.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Internal Transcripts	Internal Outside Gene	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
GeneID:4611	ND1	1	236,128,130	236,228,481	99,351	-	4	1_A375_shN37_shrut_lncRNA:1:1733, 2_A375_shN37_shrLncRNA:1:1652, 3_A375_shN37_shrLncRNA:1:1653, 4_A375_shN37_shrLncRNA:1:1654	89953, 89281, 89182, 851	u gene, ut gene, nt gene, u gene	1	1	16	20.33	3	1_A375_shN37_shct_lncRNA:1	26	Gene ND1	NI3, MD1	Antigen 1	NM_002505, NCT01652.2, NCT22986630, NCT23547370	1361052_at, 202007_at, 202008_s_at	NP_0034992.2, EAW70338.1, EAW70340.1, EAW70341.1
GeneID:5603	ERO1LB	1	236,316,422	236,445,339	96,917	-	2	1_A375_shN37_shrLncRNA:1:1716, 2_A375_shN37_shrLncRNA:1:1716	-9529, -5593	upstream, upstream	1	1	1	15	23	1_A375_shN37_shct_lncRNA:1	23	Gene ERO1LB	DKFZp779O0341, ERO1L-B, DKFZp779O1642, FLJ11003	ERO1-like beta (S. cerevisiae)	NM_019891, NCT01930453.1, NCT22985870	230012_at, 231644_at	NP_063944.3, EAW70345.1, EAW70346.1
GeneID:9564	LGALS8	1	236,661,993	236,712,998	51,431	+	1	1_A375_shN37_shrLncRNA:1:1697	8663	u gene	0	1	16	27	1	1_A375_shN37_shct_lncRNA:1	27	Gene LGALS8	GAL8, PCTA-1, PIG6-CBP, LGALS8L, PCTA1	lectin, galactoside-binding, soluble, 8	NM_006499, NM_201542, NM_201544, NM_201545, NCT14554.4, NCT19680017.1, NCT19680068.1, NCT23540102.0	208933_s_at, 208934_s_at, 208935_s_at, 208936_s_at, 210731_s_at, 227213_s_at	NP_0064902.2, NP_963837.1, NP_963838.1, NP_963839.1, EAW70333.1, EAW70334.1, EAW70336.1, EAW70337.1
GeneID:9776	LOC100216982	1	238,686,398	238,687,836	1,438	-	1	1_A375_shN37_shct_lncRNA:1:1697	960	u gene	0	1	16	27	1	2_A375_shN37_shct_lncRNA:1:1	27	Gene LOC100216982	LOC100287992	hypothetical LOC100287992	NR_034040	1561552_at	NP_0010984.1, EAW70355.1, EAW70358.1
GeneID:55	ACTN2	1	236,848,775	236,927,555	77,788	+	1	1_A375_shN37_shrLncRNA:1:1775	60554	u gene	1	0	21	15	1	1_A375_shN37_shrLncRNA:1:1	21	Gene ACTN2	ACTN2, CMD1AA	actinin, alpha 2	NM_001103, NCT01930460.1, NCT19860226.1	203661_s_at, 203662_s_at, 203663_at, 203664_s_at	NP_0010984.1, EAW70355.1, EAW70358.1
GeneID:4170	MTR	1	236,935,561	237,067,261	106,700	+	1	2_A375_shN37_shct_lncRNA:1:1699	75	u gene	0	1	16	15	1	2_A375_shN37_shct_lncRNA:1:1	16	Gene MTR	MS, PLI45356, MTR_cbrG, FLJ43216, FLJ45356	5-methyltetrahydrofolate-homocysteine methyltransferase	NM_000254, NCT01930491.1, NCT21967250.0	203774_at	NP_0002455.2, EAW70366.1, EAW70367.1
GeneID:262	RYR2	1	237,205,702	237,997,255	791,555	+	2	1_A375_shN37_shrLncRNA:1:1776, 2_A375_shN37_shrLncRNA:1:1699, 3_A375_shN37_shrLncRNA:1:1697	711114, 711216, 749634	u gene, ut gene, nt gene	1	1	21.5	22	2	1_A375_shN37_shrnds_lnc:1	35	Gene RYR2	ARVD2, ARVC2, VTSIP, RYR2	ryanodine receptor 2 (cardiac)	NM_001035, NCT19947.5, NCT22647450.0, NCT22614660.0	207557_s_at, 214044_at	NP_0010262, EAW70369.1, EAW70370.1, EAW70371.1
GeneID:7828	ZFH4	1	238,041,164	238,054,222	13,058	-	4	1_A375_shN37_shrut_lncRNA:1:1777, 2_A375_shN37_shrLncRNA:1:1776, 3_A375_shN37_shrLncRNA:1:1699, 4_A375_shN37_shrLncRNA:1:1697	12076, 1262, 17294, 1642	u gene, upstream, downstream, upstream	1	1	22.33	20	3	2_A375_shN37_shct_lncRNA:1	25	Gene ZFH4	ZFB, Zp-4, ZFH, ZBP, ZFP1	zinc finger homeodomain 4	NM_024189, NCT19869.3	231796_at	NP_0070091, EAW70372.1
GeneID:131	CHRM3	1	239,792,373	240,072,720	280,247	+	3	1_A375_shN37_shrLncRNA:1:1795, 2_A375_shN37_shrLncRNA:1:1796, 3_A375_shN37_shrLncRNA:1:1697	155515, 229211, 229099	u gene, ut gene, nt gene	1	1	30.5	19.5	2	1_A375_shN37_shct_lncRNA:1	23	Gene CHRM3	CHRM3, HM3	cholinergic receptor, muscarinic 3	NM_000740, NCT01641656.4, NCT22962791.1, NCT23473991.1	1864633_s_at, 1864639_s_at	NP_0007311, EAW70376.1, EAW70377.1, EAW70378.1
GeneID:9776	FHN2	1	240,256,165	240,638,469	383,304	+	1	1_A375_shN37_shrLncRNA:1:1797	511	u gene	1	0	16	11	1	1_A375_shN37_shrnds_lnc:1	16	Gene FHN2	FHN2		NM_020666, NCT01693481.1	1555471_s_at, 1868244_at, 233616_at, 233686_at	NP_0644863, EAW70382.1
GeneID:993	RGS7	1	240,638,617	241,020,276	381,661	-	4	1_A375_shN37_shrut_lncRNA:1:1795, 2_A375_shN37_shrLncRNA:1:1699, 3_A375_shN37_shrLncRNA:1:1676, 4_A375_shN37_shrLncRNA:1:1633	33534, 280395, 33534, 222	u gene, ut gene, nt gene, u gene	1	1	16.33	26	3	2_A375_shN37_shct_lncRNA:1	45	Gene RGS7	RGS7		NM_002923, NCT01693490.1, NCT22851352, NCT23111370, NCT22611400.0	1554900_s_at, 206240_s_at, 216570_at	NP_0029131, EAW70389.1, EAW70390.1, EAW70391.1, EAW70392.1
GeneID:1271	FH	1	241,660,637	241,663,055	22,326	-	2	1_A375_shN37_shrLncRNA:1:1791, 2_A375_shN37_shrLncRNA:1:1697	205, 173	u gene, ut gene	1	1	24	34	1	2_A375_shN37_shct_lncRNA:1	34	Gene FH	FH, HLRCC, MCULT, LRCC, MCL	fumarate hydratase	NM_000143, NCT19955641.1, NCT19862421, NCT22863530.0, NCT23153622.4	202032_s_at, 202033_s_at, 214170_s_at	NP_0001342, EAW70393.1, EAW70394.1, EAW70395.1
GeneID:3564	IMPG2	1	241,693,650	241,756,844	63,264	+	2	1_A375_shN37_shrLncRNA:1:1791, 2_A375_shN37_shrLncRNA:1:1634	60032, 60064	u gene, ut gene	1	1	33	26	1	2_A375_shN37_shct_lncRNA:1	26	Gene IMPG2	IMPG1, GU17G22.1	interphotoreceptor matrix proteoglycan 2	NM_016247, NCT22567420.0, NCT23987480.0, NCT23183.2	205206_s_at, 205207_s_at, 211135_s_at	NP_0156750.2, EAW70398.1, EAW70399.1
GeneID:3386	OPN3	1	241,756,452	241,803,701	47,249	+	1	1_A375_shN37_shrLncRNA:1:1791, 2_A375_shN37_shrLncRNA:1:1634	47599, 47537	downstream, downstream	1	1	20	26	1	2_A375_shN37_shct_lncRNA:1	26	Gene OPN3	EOPN, OPN3	opsin 3	NM_014322, NCT22965485.1, NCT23863466.0, NCT23547716.0	219832_s_at, 224352_s_at	NP_0143172, EAW70399.1, EAW70397.1, EAW70398.1
GeneID:10533	WDR64	1	241,515,550	241,965,635	149,655	+	1	2_A375_shN37_shct_lncRNA:1:1679	54554	u gene	0	1	22	20	1	2_A375_shN37_shct_lncRNA:1:1	20	Gene WDR64	FLJ32970, WDR64	WD repeat domain 64	NM_144625, NCT23293352.1, NCT23153072.0	1553372_at	NP_6332264, EAW70102.1, EAW70101.1
GeneID:199	EXO1	1	242,011,493	242,053,241	41,748	+	2	1_A375_shN37_shrLncRNA:1:1792, 2_A375_shN37_shrLncRNA:1:1679	-165, -283	upstream, upstream	1	1	28	29	1	2_A375_shN37_shct_lncRNA:1	29	Gene EXO1	HEX1, EXO1, hEx1	exonuclease 1	NM_003686, NM_006027, NM_130398, NCT19824993, NCT23587572, NCT23967840, NCT23587645.0	204603_at	NP_0036774, NP_0060165.6, NP_5936522, EAW70103.1, EAW70104.1, EAW70105.1, EAW70106.1
GeneID:539	CEP170	1	243,257,730	243,415,705	158,976	-	2	1_A375_shN37_shrLncRNA:1:1795, 2_A375_shN37_shrLncRNA:1:1699	-8226, 26	upstream, ut gene	1	1	18	24	1	2_A375_shN37_shct_lncRNA:1	24	Gene CEP170	CEP170, PAM65A, KIAB, KIAA0470	centrosomal protein 170kDa	NM_014812, NM_001042468, NM_001042469, NCT29872.3	207719_s_at, 212785_s_at	NP_0156272, NP_0010305651.1, NP_9010358641, EAW69476.1
GeneID:9806	SDCCAG8	1	243,419,330	243,663,293	244,073	+	3	1_A375_shN37_shrLncRNA:1:1795, 2_A375_shN37_shrLncRNA:1:1679, 3_A375_shN37_shrLncRNA:1:1699	-68, -632, 13736	upstream, upstream, ut gene	1	1	18	20.5	2	2_A375_shN37_shct_lncRNA:1	24	Gene SDCCAG8	HEPCS65, SDCCAG8, CCCAP, BBS16, NY-CO-8, BLUB7, NPHP10	serologically defined colon cancer antigen 8	NM_006642, NCT19503661.1, NCT23593770.0, NCT23593692.0, NCT23593670.0, NCT23593770.0, NCT19641.2	1803034_at, 1804237_at, 227155_at, 240772_at, 240963_at	NP_0066331, EAW70369.1, EAW70384.1, EAW70387.1, EAW70388.1, EAW70389.1, EAW70390.1
GeneID:9000	AKT3	1	243,651,535	244,096,553	353,018	+	2	1_A375_shN37_shrLncRNA:1:1680, 2_A375_shN37_shrLncRNA:1:1681	4391, -7015	upstream, upstream	0	1	14	15.5	2	2_A375_shN37_shct_lncRNA:1	17	Gene AKT3	AKT3, PKBG, PRKBG, RAC-PK-gamma, RAC-gamma, DKFZp434N0250, PKB-GAMMA, STS-2	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	NM_181690, NM_005465, NCT22907980.0, NCT6401.2	212607_at, 212609_s_at, 216393_s_at, 222680_at, 236229_s_at, 241676_at	NP_5936291, NP_0053461, EAW70393.1, EAW70394.1
GeneID:3982	LOC339829	1	244,060,704	244,210,619	149,915	+	2	1_A375_shN37_shrLncRNA:1:1797, 2_A375_shN37_shrLncRNA:1:1697	57405, 57424	u gene, ut gene	1	1	21	35	1	2_A375_shN37_shct_lncRNA:1	35	Gene LOC339829		hypothetical LOC339829	NR_033551		
GeneID:1660	C10orf100	1	244,315,937	244,352,293	36,356	+	1	1_A375_shN37_shrLncRNA:1:1698	1311	u gene	0	1	16	17	1	2_A375_shN37_shct_lncRNA:1	17	Gene C10orf100	C10orf100	chromosome 10 open reading frame 100	NM_001012970, NCT19820280.1, NCT19820281.1	227603_at	NP_0010126851, EAW77100.1, EAW77101.1
GeneID:159	ADSS	1	244,371,796	244,615,412	243,617	-	1	1_A375_shN37_shrLncRNA:1:1696	459	u gene	0	1	16	25	1	2_A375_shN37_shct_lncRNA:1	25	Gene ADSS	ADSS, ADEH, MPCD3454	adenylosuccinate synthase	NM_001126, NCT01693521.1, NCT6411.3	221761_at, 227310_at	NP_0011172, EAW77103.1, EAW77102.1
GeneID:57604	C10orf101	1	244,624,673	244,803,662	178,989	+	1	1_A375_shN37_shrLncRNA:1:1696	-59299	upstream	0	1	16	25	1	2_A375_shN37_shct_lncRNA:1	25	Gene C10orf101	MGC33170, RP11-523K2.1, C10orf101	chromosome 10 open reading frame 101	NM_173697, NM_001113697	231978_at, 240771_at	NP_7765871, NP_0011304291
GeneID:16226	RAB39A	1	244,998,639	245,008,259	9,720	-	2	1_A375_shN37_shrLncRNA:1:1799, 2_A375_shN37_shrLncRNA:1:1695	-407, -363	upstream, upstream	1	1	19	19	1	2_A375_shN37_shct_lncRNA:1	19	Gene RAB39A	FLJ42269, RAB39A	RAB39A, member RAS oncogene family	NM_198076, NCT19439232.1, NCT19803051.1, NCT19803390.1, NCT22070640.0, NCT23556669.0	1554060_at, 1554061_s_at, 224624_at	NP_9233421, EAW77122.1, EAW77120.1, EAW77121.1, EAW77123.1, EAW77124.1
GeneID:54702	NCRNA00201	1	245,003,940	245,010,243	6,302	-	2	1_A375_shN37_shrLncRNA:1:1792, 2_A375_shN37_shrLncRNA:1:1698	12011, 11927	downstream, downstream	1	1	19	19	1	2_A375_shN37_shct_lncRNA:1	19	Gene NCRNA00201	FLJ30202, NCRNA00201, C10orf98	non-protein coding RNA 201	NR_026778	235706_at	
GeneID:142	HNRNPU	1	245,013,602	245,027,827	14,226	-	2	1_A375_shN37_shrLncRNA:1:1693, 2_A375_shN37_shrLncRNA:1:1698	18, 418	u gene, ut gene	1	1	21	24	1	2_A375_shN37_shct_lncRNA:1	24	Gene HNRNPU	HNRNP U, SAF-A, HNRNPU, HNRPU, U21.1	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	NM_031844, NM_004501, NCT13382.3, NCT19804111.1	200892_s_at, 200893_s_at, 216653_s_at, 216654_x_at, 225605_at, 225662_at, 236264_at	NP_1140122, NP_0044922.2, EAW77126.1, EAW77127.1
GeneID:8396	EFCAB2	1	245,133,171	245,268,530	135,359	+	2	1_A375_shN37_shrLncRNA:1:1691, 2_A375_shN37_shrLncRNA:1:1699	1165, 1133	u gene, ut gene	1	1	22	34	1	2_A375_shN37_shct_lncRNA:1	34	Gene EFCAB2	FLJ32605, NIR, MGC12456, EFCAB2	EF-hand calcium binding domain 2	NM_032328, NR_026586, NR_026587, NM_001143943, NR_026585	1557674_s_at, 211200_s_at, 225606_at, 231279_at	NP_1115931, NP_0011370415.1
GeneID:4754	SMYD2	1	245,912,642	246,070,644	158,002	+	2	1_A375_shN37_shrLncRNA:1:1693, 2_A375_shN37_shrLncRNA:1:1699	164148, 164148	u gene, ut gene	1	1	16	15	1	2_A375_shN37_shct_lncRNA:1	16	Gene SMYD2	ZNFN4SA1, KMT3E, MGC19181, ZNFN4SA1, SMYD2, MGC104124, FLJ10160	SET and MYND domain containing 2	NM_020742, NM_001167740, NCT19803872.2, NCT19835562.2, NCT19803882.2, NCT23553599.1, NCT23553671.1, NCT23553672.1	219768_s_at	NP_0157553, NP_0011612121, EAW77129.1, EAW77141.1, EAW77142.1, EAW77143.1, EAW77140.1, EAW77144.1
GeneID:63362	CNBT	1	246,729,639	246,831,884	102,245	+	1	1_A375_shN37_shrLncRNA:1:1694	81017	u gene	0	1	28	30	1	1_A375_shN37_shrnds_lnc:1	25	Gene CNBT	FLJ32001, MGC16089, CNBT, C10orf71	centractin, centrosome sorting protein	NM_152699, NM_001134459, NCT19803621.1, NCT23539269.0, NCT23539277.0, NCT23539713.0, NCT23967740, NCT23967742.0	1554990_at, 1554991_s_at, 1554992_at	NP_6898222, NP_0011129231.1, EAW77154.1, EAW77155.1, EAW77156.1, EAW77157.1, EAW77158.1
GeneID:9908	AHCTF1	1	247,002,493	247,094,726	92,326	-	1	2_A375_shN37_shrLncRNA:1:1698	-656	upstream	0	1	20	36	1	2_A375_shN37_shct_lncRNA:1	36	Gene AHCTF1	AHCTF1, MSTP108, DKFZp434N093, TMB362, MSTP105, ELYS	AT hook cut-like nucleoporation factor 1	NM_015496, NCT16422.4, NCT22966601.1, NCT23193810.0	1555234_at, 214766_s_at, 229115_at	NP_0564214, EAW77163.1, EAW77166.1, EAW77167.1, EAW77168.1
GeneID:3474	ZNFN1A3	1	247,199,700	247,282,115	82,415	-	2	1_A375_shN37_shrLncRNA:1:1693, 2_A375_shN37_shrLncRNA:1:1699	131, 163	u gene, ut gene	1	1	16	15	1	1_A375_shN37_shrnds_lnc:1	19	Gene ZNFN1A3	MGC12466, FLJ12606, ZNFN1A3	ikaros family zinc finger 3 (Aiolos)	NM_032213	223695_at	NP_1809921
GeneID:4862	ZNFN1A4	1	247,263,264	247,267,674	4,410	-	1	1_A375_shN37_shrLncRNA:1:1699	214	u gene	0	1	16	25	1	2_A375_shN37_shct_lncRNA:1	25	Gene ZNFN1A4	FLJ12606, ZNFN1A4	ikaros family zinc finger 1A4	NM_024504, NM_001142572	220215_at	NP_0795552, NP_0011360841.1
GeneID:55739	C10orf229	1	247,272,952	247,275,712	2,257	-	1	1_A375_shN37_shrLncRNA:1:1699	6359	downstream	0	1	16	25	1	2_A375_shN37_shct_lncRNA:1	25	Gene C10orf229	FLJ45717, C10orf229	chromosome 10 open reading frame 229	NM_207401		NP_9975541
GeneID:4638	ZNF486	1	247,463,622	247,495,045	31,423	-	2	1_A375_shN37_shrLncRNA:1:1697, 2_A375_shN37_shrLncRNA:1:1698	453, -59	u gene, upstream	1	1	25	19	1	1_A375_shN37_shrnds_lnc:1	25	Gene ZNF486	MGC15546, ZXSCAN17, NEF1, ZNF486	zinc finger protein 486	NM_032752, NCT11951.3, NCT22985790.0, NCT23565651.0, NCT23563702.0, NCT23539671.0	1557618_at, 225332_at, 225333_at, 231339_at	NP_1165411, EAW77179.1, EAW77176.1, EAW77160.1, EAW77161.1, EAW77162.1
GeneID:101060707	LOC100507070	1	247,728,216	247,804,165	74,950	-	2	1_A375_shN37_shrLncRNA:1:1698, 2_A375_shN37_shrLncRNA:1:1697	1197, 1253	u gene, ut gene	1	1	20	22	1	2_A375_shN37_shct_lncRNA:1	22	Gene LOC100507070		hypothetical LOC100507070	XR_112032, XR_110560, XR_115447		
GeneID:5563	TRIM58	1	248,030,501	248,043,490	22,929	-	2	1_A375_shN37_shrLncRNA:1:1699, 2_A375_shN37_shrLncRNA:1:1696	171, 107	u gene, ut gene	1	1	15	16	1	2_A375_shN37_shct_lncRNA:1	16	Gene TRIM58	TRIM58, DKFZp666N0166, DKFZp434C091, BIA2	tripartite motif-containing 58	NM_015431	215047_at	NP_0562463
GeneID:84521	OR2L13	1	248,160,992	248,264,224	103,231	+	1	1_A375_shN37_shrLncRNA:1:1699	118	u gene	0	1	12	21	1	2_A375_shN37_shct_lncRNA:1	21	Gene OR2L13	MGC40347, OR2L13, OR2L14	olfactory receptor, family 2, subfamily L, member 13	NM_178911, NCT16317.2	1554700_at	NP_8711071, EAW77210.1
GeneID:3551	SH3BP5L	1	248,164,651	248,170,154	15,503	+	1	1_A375_shN37_shrLncRNA:1:1700	425	upstream	0	1	16	25	1	2_A375_shN37_shct_lncRNA:1	25	Gene SH3BP5L	SH3BP5L, KIAA1720, PLJ03545	SH3-binding domain protein 5-like	NM_030645, NCT17626.2, NCT23521150.0, NCT23521210.0	221263_at	NP_0054851, EAW77534.1, EAW77535.1, EAW77536.1
GeneID:1004228703	MIR3124	1	248,170,576	248,170,642	66	+	1	2_A375_shN37_shrLncRNA:1:1100	203	downstream	0	1	16	25	1	2_A375_shN37_shct_lncRNA:1	25	Gene MIR3124	MIR3124	microRNA 3124	NR_036070		
GeneID:5697	ZNFN1Z	1	248,132,530	248,143,714	11,184	+	5	1_A375_shN37_shrLncRNA:1:1610, 2_A375_shN37_shrLncRNA:1:1611, 3_A375_shN37_shrLncRNA:1:1612, 4_A375_shN37_shrLncRNA:1:1100, 5_A375_shN37_shrLncRNA:1:1697	446, 19994, 20790, 562, 20791	up gene, downstream, downstream, up gene, downstream	1	1	30.8	36.5	2	2_A375_shN37_shct_lncRNA:1	28	Gene ZNFN1Z	FLJ22301, ZNF672	zinc finger protein 672	NM_024836, NCT16422.4	218065_s_at, 222509_s_at, 227011_at	NP_0788121, EAW78535.1
GeneID:9637	ZNFN2A2	1	248,144,203	248,153,315	9,112	-	2	1_A375_shN37_shrLncRNA:1:1611, 2_A375_shN37_shrLncRNA:1:1612, 3_A375_shN37_shrLncRNA:1:1697	619, 35, 24	u gene, ut gene, nt gene	1	1	26	32	1	2_A375_shN37_shct_lncRNA:1	32	Gene ZNFN2A2	FLJ30531, ZNF692, ZNF692_AREBP	zinc finger protein 692	NM_001136036, NM_015665, NM_001193326, NCT22907.0, NCT23487012.0, NCT23522200.0	226561_s_at	NP_0011245551, NP_0063352, NP_0011602297.1, EAW78529.1, EAW78541.1, EAW78542.1, EAW78540.1
GeneID:67002	PDE8D	1	248,200,442	248,213,345	12,903	+	1	2_A375_shN37_shrLncRNA:1:1104	58	u gene	0	1	17	33	1	2_A375_shN37_shct_lncRNA:1	33	Gene PDE8D	PDE8D	poly(rC)-binding protein interacting protein 1	NM_139243, NM_001017434, NCT22809860.0, NCT23410999.0, NCT23951020.0	238004_at	NP_1138431, NP_0010174341, EAW78540.1, EAW78544.1, EAW78545.1
GeneID:1002550991	LOC100216614	10	1,017,086	1,034,261	17,195	-	2	1_A375_shN37_shrLncRNA:1:1616, 2_A375_shN37_shrLncRNA:1:1108	9, 9	ut gene, nt gene	1	1	36	32	1	1_A375_shN37_shrnds_lnc:1	36	Gene LOC100216614		hypothetical LOC100216614	XR_111033, XR_109866, XR_113326		
GeneID:5980	GTF8PA	10	1,034,249	1,060,708	26,459	+	2	1_A375_shN37_shrLncRNA:1:1616, 2_A375_shN37_shrLncRNA:1:1108	-77, -77	upstream, upstream	1	1	36	32	1	1_A375_shN37_shrnds_lnc:1	36	Gene GTF8PA	GTF8PA, NOG1, FLJ10595, FLJ20774, MDS, FLJ10992, CPPG	GTP binding protein 8	NM_012341, NCT23117940.0, NCT23117935.0, NCT15517.2	217631_at	NP_0366732, EAW65526.1, EAW65526.1, EAW66527.1
GeneID:5553	C10orf110	10	1,056,577	1,060,141	21,564	+	2	1_A375_shN37_shrLncRNA:1:1616, 2_A375_shN37_shrLncRNA:1:1108	26570, 26535	downstream, downstream	1	1	14	21	1	2_A375_shN37_shct_lncRNA:1	21	Gene C10orf110	IDI2-AS1, IDI2-AS, C10orf110, HT009	IDI2 antisense RNA 1 (non-protein coding)	NR_026626, NR_024626, NR_027706, NR_027709, NCT23867013.0, NCT16126640.1, NCT16550404.1	230703_at	EAW66523.1, EAW66522.1, EAW66524.1
GeneID:422	IDI1	10	1,059,863	1,069,961	9,098	-	2	1_A375_shN37_shrLncRNA:1:1616, 2_A375_shN37_shrLncRNA:1:1108	486, 149	upstream, ut gene	1	1	14	21	1	2_A375_shN37_shct_lncRNA:1	21	Gene IDI1	IPP1, IPPI1, IDI1	isopentenyl-diphosphate delta isomerase 1	NM_004508, NCT23116680.0, NCT16816.2	208615_s_at, 208616_s_at, 242063_x_at	NP_0044992, EAW65520.1, EAW65521.1
GeneID:3564	WDR37	10	1,102,776	1,176,237	73,461	+	2	1_A375_shN37_shrLncRNA:1:1616, 2_A375_shN37_shrLncRNA:1:1108	-7629, -7664	upstream, upstream	1	1	14	21	1	2_A375_shN37_shct_lncRNA:1	21	Gene WDR37	RP11-526J15.2, KIAA0662, WDR37, FLJ40334	WD repeat domain 37	NM_014023, NCT23117990.0, NCT23116931.0, NCT23116922.0, NCT23967680.0, NCT19515652.1	1560692_at, 201383_s_at, 230195_at, 231556_at	NP_0550432, EAW65513.1, EAW65514.1, EAW65513.1, EAW65516.1, EAW65517.1
GeneID:601	IL15RA	10	5,994,534	6,020,162	25,628	-	1	1_A375_shN37_shrLncRNA:1:1620	462	u gene	1	0	20	13	1	1_A375_shN37_shrnds_lnc:1	20	Gene IL15RA	IL15RA, MGC104179	interleukin 15 receptor, alpha	NM_002189, NM_172200, NM_033924, NCT23456711.0, NCT23456722.0, NCT23456733.0, NCT23456774.0, NCT23456779.0, NCT19522.2, NCT19826162.2	207375_s_at	NP_0021501, NP_7615802, EAW65417.1, EAW65416.1, EAW65421.1, EAW65422.1, EAW65415.1, EAW65416.1, EAW65420.1
GeneID:4991	RBM17	10	6,130,849	6,159,422	28,573	+	2	1_A375_shN37_shrLncRNA:1:1621, 2_A375_shN37_shrLncRNA:1:1112	-149, -101	upstream, upstream	1	1	17	17	1	1_A375_shN37_shrnds_lnc:1	17	Gene RBM17	DKFZp686F11121, RBM17, SPF45, MGC14439	RNA binding motif protein 17	NM_032903, NM_001143547, NCT23481440.0, NCT23481453.0, NCT23481467.0, NCT23481485.0, NCT23481490.0, NCT23481496.0	221209_at, 224700_at, 224701_s_at, 225701_at	NP_1162941, NP_0011380119.1, EAW66496.1, EAW66507.1, EAW66510.1, EAW66511.1, EAW66503.1, EAW66508.1, EAW66509.1
GeneID:3700	ITIH6	10	7,601,232	7,708,961	107,729	+	1	2_A375_shN37_shrLncRNA:1:1117	16765	u gene	0	1	14	15	1	2_A375_shN37_shct_lncRNA:1	15	Gene ITIH6	pp14736, ITIH6, MGC16585, DKFZp686P0165	inter-alpha (globulin) inhibitor H6	NM_001001851, NM_030569, NM_032517, NCT23113187.1, NCT23115190.1, NCT23567724, NCT19513590.1	1553243_at, 1553244_s_at, 230864_at	NP_0010018511, NP_0850364, NP_1162963, EAW66379.1, EAW66383.1, EAW66383.1, EAW66382.1
GeneID:5560	TAF3	10	7,690,673	8,056,714	196,041	+	2	1_A375_shN37_shrLncRNA:1:1622, 2_A375_shN37_shrLncRNA:1:1112	-225, -266	upstream, upstream	1	1	24	23	1	2_A375_shN37_shct_lncRNA:1	24	Gene TAF3	TAF3160, TAF3-160, TAF3-60, TAF3, MGC29382	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa	NM_031923	235119_at, 235194_at	NP_1161291
GeneID:9018	UPF2	10	11,962,021	12,065,823	123,802	-	2	1_A375_shN37_shrLncRNA:1:1634, 2_A375_shN37_shrLncRNA:1:1118	15, -51	up gene, upstream	1	1	20	19	1	1_A375_shN37_shrnds_lnc:1	20	Gene UPF2	HUPF2, RENT2, smg-2, DKFZp685M0222, KIAA1008	UPF2 regulator of nonsense transcripts homolog (yeast)	NM_015542, NM_080599, NCT23113079.0, NCT23113010.0, NCT23113084.0, NCT23565812.0, NCT19507.2	203152_s_at	NP_0561571, NP_5421961, EAW66325.1, EAW66329.1, EAW66331.1, EAW66332.1, EAW66330.1, EAW66332.1
GeneID:5398	MCM10	10	13,203,554	13,253,164	49,660	+	1	1_A375_shN37_shrLncRNA:1:1635, 2_A375_shN37_shrLncRNA:1:1112	-130, -46	upstream, upstream	1	1	27	16	1	1_A375_shN37_shrnds_lnc:1	27	Gene MCM10	FP032249, MCM10, DNA43, CNH43, MGC126776	mini-chromosome maintenance complex component 10	NM_018518, NM_182751, NCT23113733.0, NCT23544.3	220651_s_at, 223962_s_at, 223570_at	NP_0608533, NP_8773281.1, EAW66297.1, EAW66298.1

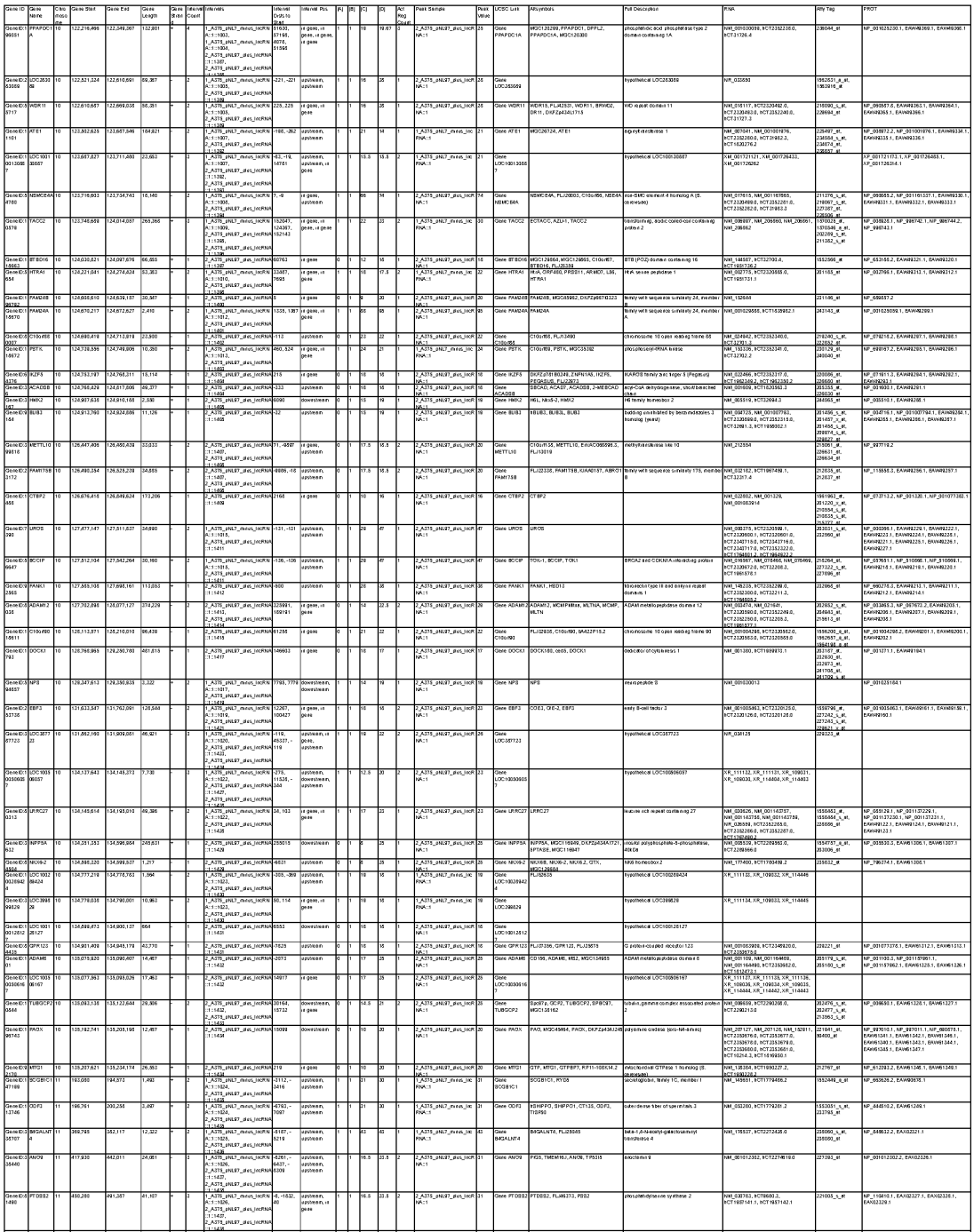
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:22929	SEPHS1	10	13,360,080	13,390,280	30,200	-	1	2_A375_pNL97_plus_lncRNA::1::1121	-88	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SEPHS1	SELD, SPS, MGC4980, SPS1, SEPHS1	selenophosphate synthetase 1	NM_012247, hCT2311246.0, hCT2311247.0, hCT2311248.0, hCT2311249.0, hCT2311250.0	208939_at, 208940_at, 208941_s_at	NP_036379.2, EAW86293.1, EAW86289.1, EAW86290.1, EAW86291.1, EAW86292.1
GeneID:8559	PRPF18	10	13,628,939	13,672,868	43,929	+	2	1_A375_pNL7_minus_lncRNA::1::826, 2_A375_pNL97_plus_lncRNA::1::1123	-75, -27	upstream, upstream	1	1	58	69	1	2_A375_pNL97_plus_lncRNA::1	69	Gene PRPF18	PRP18, PRPF18, hPrp18, FLJ10210	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	NM_003675, hCT1967846.2, hCT2350297.0, hCT2350298.0, hCT31034.3	221546_at, 221547_at, 223685_s_at, 232473_at	NP_003666.1, EAW86280.1, EAW86281.1, EAW86282.1, EAW86283.1
GeneID:55691	FRMD4A	10	13,685,706	14,372,866	687,160	-	5	1_A375_pNL7_minus_lncRNA::1::827, 1_A375_pNL7_minus_lncRNA::1::828, 2_A375_pNL97_plus_lncRNA::1::1124, 2_A375_pNL97_plus_lncRNA::1::1125, 2_A375_pNL97_plus_lncRNA::1::1126	176946, 85714, 617826, 337506, 85762	in gene, in gene, in gene, in gene, in gene	1	1	14.25	15.5	4	1_A375_pNL7_minus_lncRNA::1	20	Gene FRMD4A	KIAA1294, bA295P9.4, FRMD4, FLJ10210, FRMD4A	FERM domain containing 4A	NM_018027, hCT2311237.0, hCT2356813.0, hCT1952487.1	1554033_at, 1554034_a_at, 1560031_at, 208475_at, 208476_s_at, 225163_at, 225167_at, 225168_at	NP_060497.3, EAW86276.1, EAW86275.1, EAW86277.1
GeneID:80013	FAM188A	10	15,820,175	15,902,519	82,344	-	2	1_A375_pNL7_minus_lncRNA::1::830, 2_A375_pNL97_plus_lncRNA::1::1127	-73, -9	upstream, upstream	1	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene FAM188A	my042, C10orf97, RP11-384I23.1, DERP5, FLJ13397, FAM188A, CARP, MST126, MSTP126	family with sequence similarity 188, member A	NM_024948, hCT2311201.0, hCT15276.3	1554509_a_at, 218297_at	NP_079224.1, EAW86233.1, EAW86234.1
GeneID:6251	RSU1	10	16,632,615	16,859,453	226,838	-	1	1_A375_pNL7_minus_lncRNA::1::831	205085	in gene	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene RSU1	RSP-1, FLJ31034, RSU1	Ras suppressor protein 1	NM_152724, NM_012425, hCT2311535.0, hCT2311537.0, hCT2356799.0	1560937_at, 1569543_at, 201980_s_at, 215618_at, 230490_x_at	NP_689937.2, NP_036557.1, EAW86222.1, EAW86223.1, EAW86224.1
GeneID:8029	CUBN	10	16,865,965	17,171,816	305,851	-	1	2_A375_pNL97_plus_lncRNA::1::1128	15848	in gene	0	1	7	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene CUBN	CUBN, FLJ90747, gp280, MGA1, IFCR, FLJ90055	cubilin (intrinsic factor-cobalamin receptor)	NM_001081, hCT1821886.2	206775_at	NP_001072.2, EAW86221.1
GeneID:1787	TRDMT1	10	17,184,982	17,244,070	59,088	-	1	2_A375_pNL97_plus_lncRNA::1::1129	614	in gene	0	1	15	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene TRDMT1	RNMT1, MHSAIIP, TRDMT1, PuMet, DNMT2, DMNT2, PUMET, M.HsaIIP	tRNA aspartic acid methyltransferase 1	NM_004412	206308_at, 232121_at	NP_004403.1
GeneID:100507347	LOC100507347	10	17,256,245	17,268,897	12,652	-	1	2_A375_pNL97_plus_lncRNA::1::1130	-2495	upstream	0	1	11	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100507347		hypothetical LOC100507347	XR_111052, XR_109013, XR_114342		
GeneID:7431	VIM	10	17,270,258	17,279,592	9,334	+	2	2_A375_pNL97_plus_lncRNA::1::1130, 2_A375_pNL97_plus_lncRNA::1::1131	1134, 10478	in gene, downstream	0	1	9.5	17.5	2	2_A375_pNL97_plus_lncRNA::1	20	Gene VIM	VIM, FLJ36605	vimentin	NM_003380, hCT13718.2, hCT1964478.1	1555938_x_at, 201426_s_at	NP_003371.2, EAW86215.1, EAW86216.1
GeneID:8027	STAM	10	17,686,124	17,757,907	71,783	+	2	1_A375_pNL7_minus_lncRNA::1::832, 2_A375_pNL97_plus_lncRNA::1::1132	-44, -44	upstream, upstream	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene STAM	STAM1, STAM, DKFZp686J2352	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	NM_003473, hCT2356797.0, hCT12506.2, hCT1964292.1	203544_s_at	NP_003464.1, EAW86208.1, EAW86207.1, EAW86209.1
GeneID:387640	C10orf140	10	21,802,407	21,814,611	12,204	-	1	1_A375_pNL7_minus_lncRNA::1::833	-141	upstream	1	0	14	13	1	1_A375_pNL7_minus_lncRNA::1	14	Gene C10orf140	FLJ45187, C10orf140, DKFZp761J229, DLN-1	chromosome 10 open reading frame 140	NM_207371, hCT2360305.0	1559265_at, 1559266_s_at	NP_997254.3, EAW86167.1
GeneID:8028	MLLT10	10	21,823,102	22,032,554	209,452	+	1	1_A375_pNL7_minus_lncRNA::1::833	-8350	upstream	1	0	14	13	1	1_A375_pNL7_minus_lncRNA::1	14	Gene MLLT10	DKFZp686E10210, MLLT10, MGC75086, AF10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	NM_004641, hCT1967491.1, hCT2311272.0, hCT2311273.0, hCT2311275.0, hCT1964505.1	1563321_s_at, 205408_at, 216460_x_at, 216503_s_at, 216506_x_at, 216509_x_at, 225992_at, 230122_at, 238257_at	NP_004632.1, EAW86163.1, EAW86161.1, EAW86162.1, EAW86164.1, EAW86165.1
GeneID:56243	KIAA1217	10	23,983,675	24,836,772	853,097	+	3	1_A375_pNL7_minus_lncRNA::1::835, 2_A375_pNL97_plus_lncRNA::1::1133, 2_A375_pNL97_plus_lncRNA::1::1134	95557, 95541, 131893	in gene, in gene, in gene	1	1	26	28	2	1_A375_pNL7_minus_lncRNA::1	41	Gene KIAA1217	SKT, DKFZp761L0424, MGC31990, KIAA1217	KIAA1217	NM_001098500, NM_001098501, NM_019590, hCT2348746.0, hCT2348747.0, hCT2356803.0	1554438_at, 1560115_a_at, 1562966_at, 231807_at, 232046_at, 232762_at	NP_001091970.1, NP_001091971.1, NP_062536.2, EAW86123.1, EAW86124.1, EAW86125.1
GeneID:100128811	LOC100128811	10	25,447,001	25,465,205	18,204	-	4	1_A375_pNL7_minus_lncRNA::1::836, 1_A375_pNL7_minus_lncRNA::1::837, 2_A375_pNL97_plus_lncRNA::1::1135, 2_A375_pNL97_plus_lncRNA::1::1136	1621, 357, 1621, 501	in gene, in gene, in gene, in gene	1	1	29	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene LOC100128811		hypothetical LOC100128811	NR_027333		
GeneID:57512	GPR158	10	25,464,290	25,891,158	426,868	+	4	1_A375_pNL7_minus_lncRNA::1::836, 1_A375_pNL7_minus_lncRNA::1::837, 2_A375_pNL97_plus_lncRNA::1::1135, 2_A375_pNL97_plus_lncRNA::1::1136	-706, 558, -706, 414	upstream, in gene, upstream, in gene	1	1	29	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene GPR158	GPR158, FLJ37801, RP11-59G22.1, KIAA1136	G protein-coupled receptor 158	NM_020752	232195_at	NP_065803.2
GeneID:10006	ABI1	10	27,035,525	27,150,016	114,491	-	1	2_A375_pNL97_plus_lncRNA::1::1137	240	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ABI1	SSH3BP1, E3B1, NAP1BP, SSH3BP, ABI1, ABI-1	abl-interactor 1	NM_001012750, NM_001012751, NM_001012752, NM_001178116, NM_001178119, NM_001178120, NM_001178121, NM_001178122, NM_001178123, NM_001178124, NM_001178125, NM_005470, hCT2311440.0, hCT2311441.0, hCT2311443.0, hCT2311444.0, hCT2311445.0, hCT2356812.0, hCT163	1559890_a_at, 209027_s_at, 209028_s_at	NP_001012768.1, NP_001012769.1, NP_001012770.1, NP_001171587.1, NP_001171590.1, NP_001171591.1, NP_005461.2, NP_001171592.1, NP_001171593.1, NP_001171594.1, NP_001171595.1, NP_001171596.1, EAW86077.1, EAW86078.1, EAW86079.1, EAW86080.1, EAW86081.1, EAW860
GeneID:10730	YME1L1	10	27,399,383	27,443,321	43,938	-	1	1_A375_pNL7_minus_lncRNA::1::838	-71	upstream	1	0	13	11	1	1_A375_pNL7_minus_lncRNA::1	13	Gene YME1L1	PAMP, MEG4, FTSH, YME1L, YME1L1	YME1-like 1 (S. cerevisiae)	NM_014263, NM_139312, hCT16365.3, hCT1962986.1, hCT1962987.1, hCT1962988.1, hCT1962989.1	201351_s_at, 201352_at, 216304_x_at, 232216_at	NP_055078.1, NP_647473.1, EAW86068.1, EAW86069.1, EAW86071.1, EAW86072.1, EAW86070.1
GeneID:84930	MASTL	10	27,443,753	27,475,848	32,095	+	1	1_A375_pNL7_minus_lncRNA::1::838	-361	upstream	1	0	13	11	1	1_A375_pNL7_minus_lncRNA::1	13	Gene MASTL	GWL, RP11-85G18.2, FLJ14813, THC2, MASTL, GREATWALL	microtubule associated serine/threonine kinase-like	NM_001172303, NM_032844, NM_001172304, hCT2311496.0, hCT2311498.0, hCT2356780.0, hCT16367.2	228468_at	NP_001165774.1, NP_116233.2, NP_001165775.1, EAW86064.1, EAW86065.1, EAW86066.1, EAW86067.1
GeneID:22931	RAB18	10	27,793,249	27,829,099	35,850	+	1	2_A375_pNL97_plus_lncRNA::1::1138	-33	upstream	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RAB18	RAB18LI1, RAB18	RAB18, member RAS oncogene family	NM_021252, hCT2311501.0, hCT15904.3	223336_s_at, 224377_s_at, 224787_s_at, 228395_at	NP_067075.1, EAW86055.1, EAW86054.1
GeneID:220929	ZNF438	10	31,133,563	31,320,866	187,303	-	1	2_A375_pNL97_plus_lncRNA::1::1141	98	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZNF438	bA330O11.1, ZNF438, MGC126671, FLJ32761	zinc finger protein 438	NM_182755, NM_001143766, NM_001143767, NM_001143768, NM_001143769, NM_001143770, NM_001143771, NR_026560, hCT2356816.0, hCT1822494.2, hCT1964410.1, hCT1964411.1	229743_at, 244752_at	NP_877432.1, NP_001137238.1, NP_001137239.1, NP_001137240.1, NP_001137241.1, NP_001137242.1, NP_001137243.1, EAW85995.1, EAW85996.1, EAW85997.1, EAW85998.1
GeneID:100507663	LOC100507663	10	31,310,000	31,311,746	1,746	-	1	2_A375_pNL97_plus_lncRNA::1::1141	-9022	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100507663		hypothetical protein LOC100507663	XM_003119464, XM_003118621, XM_003120653		XP_003119512.1, XP_003118669.1, XP_003120701.1
GeneID:80314	EPC1	10	32,557,859	32,636,113	78,254	-	1	1_A375_pNL7_minus_lncRNA::1::840	945	in gene	1	0	13	9	1	1_A375_pNL7_minus_lncRNA::1	13	Gene EPC1	Epl1, EPC1, DKFZp781P2312	enhancer of polycomb homolog 1 (Drosophila)	NM_025209, hCT2310903.0, hCT2310904.0, hCT2356814.0, hCT2356815.0	223875_s_at, 225417_at, 234969_s_at, 238633_at	NP_079485.1, EAW85972.1, EAW85973.1, EAW85974.1, EAW85975.1
GeneID:56288	PARD3	10	34,398,488	35,104,253	705,765	-	3	1_A375_pNL7_minus_lncRNA::1::841, 2_A375_pNL97_plus_lncRNA::1::1143, 2_A375_pNL97_plus_lncRNA::1::1144	579613, 579597, 104765	in gene, in gene, in gene	1	1	13	21	2	2_A375_pNL97_plus_lncRNA::1	25	Gene PARD3	SE2-5LT1, ASIP, Bazooka, SE2-5L16, PAR3, SE2-5T2, FLJ21015, PARD3A, PARD3, Baz, PAR3alpha	par-3 partitioning defective 3 homolog (C. elegans)	NM_001184785, NM_001184786, NM_001184787, NM_001184788, NM_001184789, NM_001184790, NM_001184791, NM_001184792, NM_001184793, NM_001184794, NM_019619, hCT2356794.0, hCT12902.3, hCT1955362.1	210094_s_at, 221280_s_at, 221526_x_at, 221527_s_at	NP_001171714.1, NP_001171715.1, NP_001171716.1, NP_001171717.1, NP_001171718.1, NP_001171719.1, NP_062565.2, NP_001171720.1, NP_001171721.1, NP_001171722.1, NP_001171723.1, EAW85932.1, EAW85933.1, EAW85934.1
GeneID:8453	CUL2	10	35,298,798	35,379,294	80,496	-	2	1_A375_pNL7_minus_lncRNA::1::842, 2_A375_pNL97_plus_lncRNA::1::1145	-194, -162	upstream, upstream	1	1	40	32	1	1_A375_pNL7_minus_lncRNA::1	40	Gene CUL2	MGC131970, CUL2	cullin 2	NM_003591	203078_at, 203079_s_at	NP_003582.2
GeneID:8325	FZD8	10	35,927,177	35,930,362	3,185	-	2	1_A375_pNL7_minus_lncRNA::1::843, 2_A375_pNL97_plus_lncRNA::1::1146	-1038, -950	upstream, upstream	1	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene FZD8	FZD8, hFZ8, FZ-8	frizzled homolog 8 (Drosophila)	NM_031866, hCT16417.2	216587_s_at, 224325_at, 227405_s_at	NP_114072.1, EAW85909.1
GeneID:9790	BMS1	10	43,277,954	43,330,385	52,431	+	2	1_A375_pNL7_minus_lncRNA::1::844, 2_A375_pNL97_plus_lncRNA::1::1147	286, 238	in gene, in gene	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene BMS1	BMS1L, BMS1, KIAA0187	BMS1 homolog, ribosome assembly protein (yeast)	NM_014753, hCT2294229.0, hCT2294231.0, hCT2294232.0	203082_at	NP_055568.3, EAW86572.1, EAW86571.1, EAW86573.1
GeneID:220992	ZNF485	10	44,101,855	44,113,352	11,497	+	1	2_A375_pNL97_plus_lncRNA::1::1150	33	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZNF485	ZNF485		NM_145312, hCT2294208.2, hCT1778956.3	1552427_at	NP_660355.2, EAW86606.1, EAW86605.1
GeneID:7580	ZNF32	10	44,139,307	44,144,326	5,019	-	1	2_A375_pNL97_plus_lncRNA::1::1151	-10	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZNF32	KOX30, ZNF32	zinc finger protein 32	NM_006973, NM_001005368, hCT2356831.0, hCT1767013.3, hCT1965882.1	209538_at	NP_008904.1, NP_001005368.1, EAW86609.1, EAW86610.1, EAW86611.1
GeneID:100130539	LOC100130539	10	44,788,204	44,790,179	1,975	+	1	2_A375_pNL97_plus_lncRNA::1::1152	5564	downstream	0	1	7	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100130539		hypothetical protein LOC100130539	XM_001724322, XM_001716390		XP_001724374.2, XP_001716442.2
GeneID:100507539	LOC100507539	10	46,951,472	46,966,835	15,363	+	1	2_A375_pNL97_plus_lncRNA::1::1154	-16	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100507539		hypothetical LOC100507539	XR_110467		
GeneID:83849	SYT15	10	46,955,444	46,970,601	15,157	-	1	2_A375_pNL97_plus_lncRNA::1::1154	19145	downstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SYT15	SYT15, CHR10SYT, sytXV	synaptotagmin XV	NM_031912, NM_181519, hCT1773017.3	1560878_at, 1560879_a_at	NP_114118.2, NP_852660.1, EAW54662.1
GeneID:644168	DRGX	10	50,574,161	50,599,907	25,746	-	2	1_A375_pNL7_minus_lncRNA::1::848, 2_A375_pNL97_plus_lncRNA::1::1156	-6269, -6301	upstream, upstream	1	1	21	17	1	1_A375_pNL7_minus_lncRNA::1	21	Gene DRGX	PRRXL1, DRG11, DRGX	dorsal root ganglia homeobox	NM_001080520		NP_001073989.1
GeneID:1103	CHAT	10	50,817,141	50,873,150	56,009	+	2	1_A375_pNL7_minus_lncRNA::1::849, 2_A375_pNL97_plus_lncRNA::1::1157	-1973, -1909	upstream, upstream	1	1	26	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene CHAT	CMS1A, CHAT, CHOACTASE, CMS1A2	choline acetyltransferase	NM_020984, NM_020549, NM_020985, NM_020986, NM_001142929, NM_001142933, NM_001142934, hCT2277816.0, hCT2277817.0, hCT2277818.0, hCT2277819.0, hCT2277821.0, hCT2349376.0, hCT2349377.0	221197_s_at	NP_066264.3, NP_065574.3, NP_066265.3, NP_066266.3, NP_001136401.1, NP_001136405.1, NP_001136406.1, EAW93086.1, EAW93087.1, EAW93088.1, EAW93089.1, EAW93090.1, EAW93091.1, EAW93092.1
GeneID:6572	SLC18A3	10	50,818,347	50,820,766	2,419	+	2	1_A375_pNL7_minus_lncRNA::1::849, 2_A375_pNL97_plus_lncRNA::1::1157	-3179, -3115	upstream, upstream	1	1	26	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SLC18A3	MGC12716, SLC18A3, VACHT	solute carrier family 18 (vesicular acetylcholine), member 3	NM_003055, hCT23548.3	207150_at	NP_003046.2, EAW93093.1
GeneID:55753	OGDHL	10	50,942,687	50,970,425	27,738	-	1	1_A375_pNL7_minus_lncRNA::1::850	-71	upstream	1	0	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene OGDHL	OGDHL		NM_018245, NM_001143996, NM_001143997, hCT2277591.0, hCT23932.3, hCT1966504.1	219277_s_at	NP_060715.2, NP_001137468.1, NP_001137469.1, EAW93080.1, EAW93081.1, EAW93082.1
GeneID:259230	SGMS1	10	52,065,345	52,383,737	318,392	-	3	1_A375_pNL7_minus_lncRNA::1::851, 1_A375_pNL7_minus_lncRNA::1::852, 2_A375_pNL97_plus_lncRNA::1::1158	153, -679, -695	in gene, upstream, upstream	1	1	19	20.5	2	2_A375_pNL97_plus_lncRNA::1	30	Gene SGMS1	SGMS1, MOB1, TMEM23, hmob33, SMS1, MGC17342, MOB	sphingomyelin synthase 1	NM_147156, hCT2340901.0, hCT23547.4, hCT1655438.4, hCT1950129.1	212989_at	NP_671512.1, EAW80431.1, EAW80429.1, EAW80430.1, EAW80432.1
GeneID:5592	PRKG1	10	52,750,945	54,055,274	1,304,329	+	1	2_A375_pNL97_plus_lncRNA::1::1159	842015	in gene	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PRKG1	PGK, CGKI, cGKI-alpha, cGKI-BETA, DKFZp686K042, PRKG1B, PRKG1, FLJ36117, MGC71944, PRKGR1B, PKG	protein kinase, cGMP-dependent, type I	NM_001098512, NM_006258, hCT2350053.0, hCT2350054.0	207119_at, 211380_s_at	NP_001091982.1, NP_006249.1, EAW54140.1, EAW54141.1
GeneID:7019	TFAM	10	60,145,176	60,155,897	10,721	+	1	2_A375_pNL97_plus_lncRNA::1::1162	72	in gene	0	1	8	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TFAM	TFAM, TCF6L2, TCF6, MtTF1, TCF6L1, mtTFA, TCF6L3	transcription factor A, mitochondrial	NM_003201, hCT2322020.0, hCT2322021.0, hCT31464.2, hCT1686512.1, hCT1957619.1	203176_s_at, 203177_x_at, 208541_x_at	NP_003192.1, EAW54172.1, EAW54171.1, EAW54173.1, EAW54174.1, EAW54175.1
GeneID:8030	CCDC6	10	61,548,521	61,666,818	118,297	-	2	1_A375_pNL7_minus_lncRNA::1::854, 2_A375_pNL97_plus_lncRNA::1::1163	482, 482	in gene, in gene	1	1	91	98	1	2_A375_pNL97_plus_lncRNA::1	98	Gene CCDC6	FLJ32286, H4, PTC, TPC, CCDC6, TST1, D10S170	coiled-coil domain containing 6	NM_005436, hCT2322339.0, hCT2322340.0	204716_at, 225010_at	NP_005427.2, EAW54196.1, EAW54197.1
GeneID:84890	ADO	10	64,564,516	64,568,239	3,723	+	1	1_A375_pNL7_minus_lncRNA::1::856	-324	upstream	1	0	15	7	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ADO	DKFZp564C046, ADO, FLJ14547, C10orf22	2-aminoethanethiol (cysteamine) dioxygenase	NM_032804, hCT2322461.0, hCT2322463.0, hCT1641864.3	212500_at, 212502_at, 229409_s_at	NP_116193.2, EAW54237.1, EAW54235.1, EAW54236.1
GeneID:1959	EGR2	10	64,571,756	64,578,927	7,171	-	1	1_A375_pNL7_minus_lncRNA::1::856	14735	downstream	1	0	15	7	1	1_A375_pNL7_minus_lncRNA::1	15	Gene EGR2	KROX20, AT591, FLJ14547, CMT4E, DKFZp686J1957, CMT1D, EGR2	early growth response 2	NM_000399, NM_001136177, NM_001136178, NM_001136179, hCT2352833.0, hCT31488.1	205249_at	NP_000390.2, NP_001129649.1, NP_001129650.1, NP_001129651.1, EAW54238.1, EAW54239.1
GeneID:84665	MYPN	10	69,869,250	69,971,774	102,524	+	2	1_A375_pNL7_minus_lncRNA::1::858, 1_A375_pNL7_minus_lncRNA::1::859	26974, 44286	in gene, in gene	1	0	19	9	2	1_A375_pNL7_minus_lncRNA::1	20	Gene MYPN	MYOP, MYPN	myopalladin	NM_032578, hCT2322199.0, hCT24046.3	235367_at	NP_115967.2, EAW54266.1, EAW54267.1
GeneID:55680	RUFY2	10	70,103,275	70,167,051	63,776	-	2	1_A375_pNL7_minus_lncRNA::1::860, 2_A375_pNL97_plus_lncRNA::1::1167	107, 107	in gene, in gene	1	1	29	28	1	1_A375_pNL7_minus_lncRNA::1	29	Gene RUFY2	ZFYVE13, FLJ10063, RABIP4R, KIAA1537, RUFY2	RUN and FYVE domain containing 2	NM_001042417, NM_017987, hCT2322274.0, hCT2322276.0, hCT2352816.0, hCT2352817.0, hCT1958442.1, hCT1958443.1	1554133_at, 1569630_a_at, 219957_at, 233191_at, 233192_s_at, 235345_at, 238550_at	NP_001035882.1, NP_060457.4, EAW54291.1, EAW54292.1, EAW54293.1, EAW54294.1, EAW54290.1, EAW54295.1
GeneID:1763	DNA2	10	70,173,821	70,231,879	58,058	-	2	1_A375_pNL7_minus_lncRNA::1::860, 2_A375_pNL97_plus_lncRNA::1::1167	64935, 64935	downstream, downstream	1	1	29	28	1	1_A375_pNL7_minus_lncRNA::1	29	Gene DNA2	DNA2L, MGC133297, DNA2, KIAA0083, FLJ10063	DNA replication helicase 2 homolog (yeast)	NM_001080449	213647_at	NP_001073918.1
GeneID:80312	TET1	10	70,320,117	70,454,239	134,122	+	1	1_A375_pNL7_minus_lncRNA::1::861	171	in gene	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene TET1	FLJ10839, KIAA1676, CXXC6, FLJ41442, LCX, bA119F7.1, TET1	tet oncogene 1	NM_030625, hCT2348106.0	228906_at	NP_085128.2, EAW54299.1
GeneID:79009	DDX50	10	70,661,034	70,706,603	45,569	+	2	1_A375_pNL7_minus_lncRNA::1::862, 2_A375_pNL97_plus_lncRNA::1::1168	54742, 54774	downstream, downstream	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene DDX50	DDX50, GUB, GU2, MGC3199, RH-II/GuB	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	NM_024045, hCT10434.2	1568614_at, 1568615_a_at, 221699_s_at	NP_076950.1, EAW54304.1
GeneID:9188	DDX21	10	70,715,892	70,744,279	28,387	+	3	1_A375_pNL7_minus_lncRNA::1::862, 2_A375_pNL97_plus_lncRNA::1::1168, 2_A375_pNL97_plus_lncRNA::1::1169	-116, -84, 32620	upstream, upstream, downstream	1	1	14	17.5	2	1_A375_pNL7_minus_lncRNA::1	19	Gene DDX21	RH-II/GU, DDX21, GURDB, GUA, DKFZp686F21172, RH-II/GuA	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	NM_004728, hCT2322659.1, hCT2350250.0, hCT9884.3	208152_s_at, 224654_at	NP_004719.2, EAW54307.1, EAW54305.1, EAW54306.1
GeneID:100507126	LOC100507126	10	70,744,076	70,762,819	18,743	-	1	2_A375_pNL97_plus_lncRNA::1::1169	14307	in gene	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100507126		hypothetical LOC100507126	XR_111072, XR_110410, XR_114373		
GeneID:26128	KIAA1279	10	70,748,477	70,776,739	28,262	+	1	2_A375_pNL97_plus_lncRNA::1::1169	35	in gene	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene KIAA1279	KBP, DKFZp586B0923, TTC20, KIAA1279	KIAA1279	NM_015634, hCT9885.2	212453_at	NP_056449.1, EAW54308.1
GeneID:9559	VPS26A	10	70,883,908	70,932,617	48,709	+	1	1_A375_pNL7_minus_lncRNA::1::863	56028	downstream	1	0	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene VPS26A	PEP8A, VPS26A, HB58, FLJ12930, VPS26, Hbeta58	vacuolar protein sorting 26 homolog A (S. pombe)	NM_004896, NM_001035260, hCT2322666.0, hCT16384.3, hCT1961898.1	201807_at, 243316_x_at	NP_004887.2, NP_001030337.1, EAW54311.1, EAW54312.1, EAW54313.1
GeneID:6832	SUPV3L1	10	70,939,993	70,968,849	28,856	+	1	1_A375_pNL7_minus_lncRNA::1::863	-57	upstream	1	0	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene SUPV3L1	SUPV3L1, SUV3	suppressor of var1, 3-like 1 (S. cerevisiae)	NM_003171, hCT2322671.0, hCT16382.3	212894_at	NP_003162.2, EAW54314.1, EAW54315.1
GeneID:50674	NEUROG3	10	71,331,791	71,333,210	1,419	-	2	1_A375_pNL7_minus_lncRNA::1::864, 2_A375_pNL97_plus_lncRNA::1::1170	5498, 5514	downstream, downstream	1	1	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene NEUROG3	ngn3, NEUROG3, Atoh5, Math4B, bHLHa7	neurogenin 3	NM_020999, hCT1826614.0	207965_at	NP_066279.2, EAW54326.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:1305	COL13A1	10	71,561,644	71,718,904	157,260	+	1	2_A375_pNL97_plus_lncRNA::1::1171	67746	in gene	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene COL13A1	COL13A1, FLJ42485, COLXIIIA1	collagen, type XIII, alpha 1	NM_001130103, NM_080798, NM_080800, NM_080801, NM_080802, NM_080805, hCT2322618.0, hCT2322619.0, hCT2322620.0, hCT2322621.0, hCT2322622.0, hCT2322623.0, hCT2322624.0, hCT2322625.0, hCT2322626.0, hCT2322627.0, hCT2322628.0, hCT2322629.0, hCT2322630.0, hCT2	205535_x_at, 211343_s_at, 211809_x_at	NP_001123575.1, NP_542988.3, NP_542990.3, NP_542991.3, NP_542992.3, NP_542995.3, EAW54334.1, EAW54335.1, EAW54336.1, EAW54342.1, EAW54343.1, EAW54344.1, EAW54345.1, EAW54346.1, EAW54333.1, EAW54337.1, EAW54338.1, EAW54339.1, EAW54340.1, EAW54341.1, EAW543
GeneID:8879	SGPL1	10	72,575,704	72,640,946	65,242	+	1	2_A375_pNL97_plus_lncRNA::1::1172	520	in gene	0	1	6	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SGPL1	SPL, KIAA1252, SGPL1, FLJ13811	sphingosine-1-phosphate lyase 1	NM_003901, hCT14890.3	205381_s_at, 212321_at, 212322_at	NP_003892.2, EAW54414.1
GeneID:64072	CDH23	10	73,156,691	73,575,704	419,013	+	2	1_A375_pNL7_minus_lncRNA::1::865, 2_A375_pNL97_plus_lncRNA::1::1173	398509, 398477	in gene, in gene	1	1	32	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene CDH23	KIAA1774, DKFZp434P2350, CDHR23, FLJ00233, KIAA1812, FLJ36499, MGC102761, USH1D, CDH23	cadherin-related 23	NM_022124, NM_052836, NM_001171930, NM_001171931, NM_001171932, NM_001171933, NM_001171934, NM_001171935, NM_001171936, hCT2322700.0, hCT2322701.0, hCT2322702.0, hCT2322703.0, hCT2322704.0, hCT2322705.0, hCT2322706.0	1552436_a_at, 224527_at, 232845_at, 232846_s_at	NP_071407.4, NP_443068.1, NP_001165401.1, NP_001165402.1, NP_001165403.1, NP_001165404.1, NP_001165405.1, NP_001165406.1, NP_001165407.1, EAW54426.1, EAW54427.1, EAW54428.1, EAW54429.1, EAW54430.1, EAW54431.1, EAW54432.1
GeneID:5660	PSAP	10	73,576,055	73,611,082	35,027	-	2	1_A375_pNL7_minus_lncRNA::1::866, 2_A375_pNL97_plus_lncRNA::1::1174	-9190, -9334	upstream, upstream	1	1	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene PSAP	FLJ00245, SAP1, MGC110993, PSAP, GLBA	prosaposin	NM_001042465, NM_002778, NM_001042466, hCT2322980.0, hCT2352843.0, hCT1826905.2	200866_s_at, 200871_s_at	NP_001035930.1, NP_002769.1, NP_001035931.1, EAW54436.1, EAW54437.1, EAW54438.1
GeneID:54541	DDIT4	10	74,033,677	74,035,797	2,120	+	1	2_A375_pNL97_plus_lncRNA::1::1175	19	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene DDIT4	REDD-1, Dig2, RP11-442H21.1, DDIT4, REDD1, FLJ20500	DNA-damage-inducible transcript 4	NM_019058, hCT2322317.0, hCT2322318.0	202887_s_at	NP_061931.1, EAW54452.1, EAW54453.1
GeneID:54788	DNAJB12	10	74,092,568	74,114,907	22,319	-	2	1_A375_pNL7_minus_lncRNA::1::867, 2_A375_pNL97_plus_lncRNA::1::1176	299, 235	in gene, in gene	1	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DNAJB12	DKFZp586B2023, DJ10, DNAJB12	DnaJ (Hsp40) homolog, subfamily B, member 12	NM_001002762, NM_017626, hCT2322558.0, hCT2322559.0, hCT2352847.0	202865_at, 202866_at, 202867_s_at, 214338_at	NP_001002762.2, NP_060096.3, EAW54454.1, EAW54455.1, EAW54456.1
GeneID:5033	P4HA1	10	74,766,975	74,856,732	89,757	-	2	1_A375_pNL7_minus_lncRNA::1::868, 2_A375_pNL97_plus_lncRNA::1::1177	28, -20	in gene, upstream	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene P4HA1	P4HA, P4HA1	prolyl 4-hydroxylase, alpha polypeptide I	NM_001017962, NM_001142595, NM_001142596, NM_000917, hCT2322548.0, hCT2322549.0, hCT2352812.0, hCT10344.3	207543_s_at	NP_001017962.1, NP_001136067.1, NP_001136068.1, NP_000908.2, EAW54468.1, EAW54470.1, EAW54467.1, EAW54469.1
GeneID:11319	ECD	10	74,894,282	74,927,853	33,571	-	1	1_A375_pNL7_minus_lncRNA::1::869	61	in gene	1	0	18	14	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ECD	GCR2, HSGT1, ECD	ecdysoneless homolog (Drosophila)	NM_007265, NM_001135752, NM_001135753, NR_024203, hCT2322545.0, hCT10333.3	203013_at	NP_009196.1, NP_001129224.1, NP_001129225.1, EAW54477.1, EAW54478.1
GeneID:317662	FAM149B1	10	74,927,877	75,001,939	74,062	+	1	1_A375_pNL7_minus_lncRNA::1::869	-65	upstream	1	0	18	14	1	1_A375_pNL7_minus_lncRNA::1	18	Gene FAM149B1	KIAA0974, FAM149B1	family with sequence similarity 149, member B1	NM_173348	1560755_at, 213456_at, 213463_s_at, 213696_x_at, 235859_at	NP_775483.1
GeneID:5532	PPP3CB	10	75,196,563	75,255,782	59,219	-	1	2_A375_pNL97_plus_lncRNA::1::1178	-90	upstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PPP3CB	CNA2, CALNB, CALNA2, PP2Bbeta, PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	NM_021132, NM_001142353, NM_001142354, hCT2322526.0, hCT2322529.0, hCT2352823.0, hCT9391.2, hCT1963001.1	202432_at, 209817_at	NP_066955.1, NP_001135825.1, NP_001135826.1, EAW54497.1, EAW54499.1, EAW54500.1, EAW54496.1, EAW54498.1
GeneID:100507259	LOC100507259	10	75,255,510	75,256,414	904	+	1	2_A375_pNL97_plus_lncRNA::1::1178	362	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100507259		hypothetical LOC100507259	XR_110417, XR_114380		
GeneID:159195	USP54	10	75,257,296	75,335,433	78,137	-	1	2_A375_pNL97_plus_lncRNA::1::1178	79561	downstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene USP54	C10orf29, bA137L10.3, bA137L10.4, FLJ37318, USP54	ubiquitin specific peptidase 54	NM_152586, hCT2322525.1, hCT1767859.4, hCT1767870.4	227334_at, 238522_at	NP_689799.3, EAW54504.1, EAW54502.1, EAW54503.1
GeneID:132	ADK	10	75,910,965	76,469,060	558,095	+	1	2_A375_pNL97_plus_lncRNA::1::1180	25499	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ADK	AK, ADK	adenosine kinase	NM_001123, NM_006721, hCT2322563.2, hCT2322564.2	204119_s_at, 204120_s_at	NP_001114.2, NP_006712.2, EAW54555.1, EAW54556.1
GeneID:23522	MYST4	10	76,586,379	76,792,639	206,260	+	2	1_A375_pNL7_minus_lncRNA::1::871, 2_A375_pNL97_plus_lncRNA::1::1181	-11, -139	upstream, upstream	1	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MYST4	FLJ90335, qkf, KAT6B, MORF, KIAA0383, MYST4, MOZ2, DKFZp313G1618, querkopf	MYST histone acetyltransferase (monocytic leukemia) 4	NM_012330, hCT2326393.0, hCT2326395.0, hCT1950422.1	1562236_at, 211874_s_at, 212452_x_at, 212462_at, 214496_x_at	NP_036462.2, EAW54559.1, EAW54557.1, EAW54558.1
GeneID:7417	VDAC2	10	76,969,912	76,991,206	21,294	+	2	1_A375_pNL7_minus_lncRNA::1::872, 2_A375_pNL97_plus_lncRNA::1::1182	520, 392	in gene, in gene	1	1	36	26	1	1_A375_pNL7_minus_lncRNA::1	36	Gene VDAC2	POR, FLJ23841, VDAC2	voltage-dependent anion channel 2	NM_001184783, NM_001184823, NM_003375, NR_033675, hCT2326401.0, hCT2326405.0, hCT2326406.0, hCT15098.3, hCT1950424.1, hCT1950425.1	211662_s_at	NP_001171712.1, NP_001171752.1, NP_003366.2, EAW54571.1, EAW54572.1, EAW54573.1, EAW54569.1, EAW54570.1, EAW54574.1
GeneID:84858	ZNF503	10	77,157,602	77,161,513	3,911	-	3	2_A375_pNL97_plus_lncRNA::1::1183, 2_A375_pNL97_plus_lncRNA::1::1184, 2_A375_pNL97_plus_lncRNA::1::1185	-103, -563, -1543	upstream, upstream, upstream	0	1	10	17.67	3	2_A375_pNL97_plus_lncRNA::1	19	Gene ZNF503	MGC2555, FLJ45745, NOLZ-1, ZNF503	zinc finger protein 503	NM_032772, hCT2326432.0, hCT1950019.1, hCT1950020.0	227195_at, 228684_at, 232178_at	NP_116161.2, EAW54580.1, EAW54579.1, EAW54581.1
GeneID:100131213	C10orf41	10	77,161,286	77,168,740	7,454	+	3	2_A375_pNL97_plus_lncRNA::1::1183, 2_A375_pNL97_plus_lncRNA::1::1184, 2_A375_pNL97_plus_lncRNA::1::1185	330, 810, 1770	in gene, in gene, in gene	0	1	10	17.67	3	2_A375_pNL97_plus_lncRNA::1	19	Gene C10orf41	FLJ00096, C10orf41, NCRNA00245	chromosome 10 open reading frame 41	NR_024421, NR_024422		
GeneID:83938	C10orf11	10	77,542,519	78,317,130	774,611	+	1	1_A375_pNL7_minus_lncRNA::1::873	-9175	upstream	1	0	17	11	1	1_A375_pNL7_minus_lncRNA::1	17	Gene C10orf11	CDA017, C10orf11	chromosome 10 open reading frame 11	NM_032024, hCT2345276.0, hCT2345277.0, hCT13604.4	223703_at, 244186_at	NP_114413.1, EAW54586.1, EAW54585.1, EAW54587.1
GeneID:3778	KCNMA1	10	78,629,359	79,397,577	768,218	-	11	1_A375_pNL7_minus_lncRNA::1::874, 1_A375_pNL7_minus_lncRNA::1::875, 1_A375_pNL7_minus_lncRNA::1::876, 1_A375_pNL7_minus_lncRNA::1::877, 1_A375_pNL7_minus_lncRNA::1::878, 1_A375_pNL7_minus_lncRNA::1::879, 2_A375_pNL97_plus_lncRNA::1::1186, 2_A375_pNL97_plus_lncRNA::1::1187, 2_A375_pNL97_plus_lncRNA::1::1188, 2_A375_pNL97_plus_lncRNA::1::1189, 2_A375_pNL97_plus_lncRNA	309257, 286953, 245001, 131753, 106057, 54868, 340361, 309289, 244969, 131625, 124009	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	19.75	20.75	8	2_A375_pNL97_plus_lncRNA::1	36	Gene KCNMA1	SLO, MaxiK, MGC71881, SAKCA, mSLO1, BKTM, SLO1, bA205K10.1, KCa1.1, SLO-ALPHA, DKFZp686K1437, KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	NM_002247, NM_001014797, NM_001161352, NM_001161353, hCT2322401.1, hCT2322405.1, hCT2352850.0, hCT16404.4, hCT1963373.2, hCT1963374.2	214921_at, 221583_s_at, 221584_s_at, 228414_at	NP_002238.2, NP_001014797.1, NP_001154824.1, NP_001154825.1, EAW54601.1, EAW54602.1, EAW54597.1, EAW54598.1, EAW54599.1, EAW54600.1
GeneID:9231	DLG5	10	79,550,549	79,686,348	135,799	-	2	1_A375_pNL7_minus_lncRNA::1::881, 2_A375_pNL97_plus_lncRNA::1::1192	77300, 77324	in gene, in gene	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene DLG5	KIAA0583, P-DLG5, DLG5, LP-DLG, PDLG	discs, large homolog 5 (Drosophila)	NM_004747, hCT2322734.0, hCT2352818.0, hCT2352819.0, hCT13706.3	201681_s_at, 210469_at	NP_004738.3, EAW54609.1, EAW54610.1, EAW54611.1, EAW54612.1
GeneID:11128	POLR3A	10	79,734,907	79,789,298	54,391	-	2	1_A375_pNL7_minus_lncRNA::1::882, 2_A375_pNL97_plus_lncRNA::1::1193	18, 18	in gene, in gene	1	1	24	23	1	1_A375_pNL7_minus_lncRNA::1	24	Gene POLR3A	RPC155, RPC1, POLR3A, hRPC155	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	NM_007055, hCT15953.3	1564318_at, 227872_at, 231763_at	NP_008986.2, EAW54617.1
GeneID:6229	RPS24	10	79,793,518	79,816,571	23,053	+	2	1_A375_pNL7_minus_lncRNA::1::882, 2_A375_pNL97_plus_lncRNA::1::1193	-4236, -4238	upstream, upstream	1	1	24	23	1	1_A375_pNL7_minus_lncRNA::1	24	Gene RPS24	DBA3, RPS24, DKFZp686N1586, S24	ribosomal protein S24	NM_001142283, NM_001142282, NM_001142285, NM_033022, NM_001026, NM_001142284, hCT2322490.0, hCT2322492.0, hCT2322493.0, hCT2322494.0, hCT2322496.0, hCT2322497.0, hCT2322498.0, hCT13707.2, hCT1950418.1, hCT1950419.1	1555878_at, 200061_s_at	NP_001135755.1, NP_001135754.1, NP_148982.1, NP_001135757.1, NP_001135756.1, NP_001017.1, EAW54618.1, EAW54619.1, EAW54620.1, EAW54621.1, EAW54622.1, EAW54623.1, EAW54626.1, EAW54627.1, EAW54624.1, EAW54625.1
GeneID:100132987	LOC100132987	10	80,008,246	80,012,402	4,156	+	1	2_A375_pNL97_plus_lncRNA::1::1194	7658	downstream	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100132987	FLJ33712	hypothetical LOC100132987	XR_111079, XR_110424, XR_114387		
GeneID:283050	LOC283050	10	80,703,083	80,827,205	124,122	-	3	1_A375_pNL7_minus_lncRNA::1::885, 2_A375_pNL97_plus_lncRNA::1::1196, 2_A375_pNL97_plus_lncRNA::1::1197	94325, 93893, -27	in gene, in gene, upstream	1	1	17.5	19	2	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC283050	MGC125551, FLJ44323	hypothetical LOC283050	NR_015429, NR_024429, NR_024431	1563745_a_at	
GeneID:57178	ZMIZ1	10	80,828,792	81,076,285	247,493	+	5	2_A375_pNL97_plus_lncRNA::1::1197, 2_A375_pNL97_plus_lncRNA::1::1198, 2_A375_pNL97_plus_lncRNA::1::1199, 1_A375_pNL7_minus_lncRNA::1::886, 2_A375_pNL97_plus_lncRNA::1::1200	-1560, 12936, 80200, 252264, 252200	upstream, in gene, in gene, downstream, downstream	1	1	19.5	22.5	4	2_A375_pNL97_plus_lncRNA::1	36	Gene ZMIZ1	hZIMP10, ZMIZ1, ZIMP10, Zimp10, KIAA1224, TRAFIP10, RAI17, MIZ, FLJ13541	zinc finger, MIZ-type containing 1	NM_020338, hCT2323399.0, hCT2323402.0, hCT2323403.0, hCT2352849.0, hCT14876.3, hCT1950421.1	212124_at, 232508_at, 233060_at	NP_065071.1, EAW54641.1, EAW54639.1, EAW54640.1, EAW54642.1, EAW54644.1, EAW54643.1
GeneID:10105	PPIF	10	81,107,220	81,115,090	7,870	+	1	2_A375_pNL97_plus_lncRNA::1::1201	-52	upstream	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PPIF	CYP3, PPIF, MGC117207, Cyp-D, FLJ90798	peptidylprolyl isomerase F	NM_005729, hCT2323408.0, hCT2323409.0, hCT2323410.0, hCT13708.1	201489_at, 201490_s_at	NP_005720.1, EAW54645.1, EAW54646.1, EAW54647.1, EAW54648.1
GeneID:219654	ZCCHC24	10	81,142,081	81,205,383	63,302	-	2	1_A375_pNL7_minus_lncRNA::1::887, 1_A375_pNL7_minus_lncRNA::1::888	7447, -249	in gene, upstream	1	0	21.5	17	2	1_A375_pNL7_minus_lncRNA::1	25	Gene ZCCHC24	ZCCHC24, C10orf56, FLJ90798	zinc finger, CCHC domain containing 24	NM_153367, hCT2323474.0, hCT14877.2	212419_at, 212423_at	NP_699198.2, EAW54650.1, EAW54649.1
GeneID:100288974	LOC100288974	10	81,664,654	81,691,557	26,903	+	2	1_A375_pNL7_minus_lncRNA::1::889, 2_A375_pNL97_plus_lncRNA::1::1202	242, -110	in gene, upstream	1	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100288974	MGC88084, FLJ97799	BMS1 homolog, ribosome assembly protein (yeast) pseudogene	NR_033857		
GeneID:219347	LOC219347	10	81,805,989	81,838,949	32,960	-	1	1_A375_pNL7_minus_lncRNA::1::890	357	in gene	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC219347	FLJ99695, FLJ98652, FLJ17303, FLJ17224	hypothetical LOC219347	NR_027428, NR_027429, NR_027430, NR_027432, NR_027431	232294_at	
GeneID:80195	C10orf57	10	81,838,426	81,852,307	13,881	+	1	1_A375_pNL7_minus_lncRNA::1::890	166	in gene	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene C10orf57	bA369J21.6, FLJ13263, C10orf57	chromosome 10 open reading frame 57	NM_025125, hCT1968103.1, hCT1968106.1, hCT2356021.0, hCT2356022.0, hCT2356023.0, hCT2356024.0	218174_s_at, 222545_s_at	NP_079401.2, EAW80412.1, EAW80409.1, EAW80410.1, EAW80413.1, EAW80414.1, EAW80411.1
GeneID:219348	PLAC9	10	81,892,258	81,904,784	12,526	+	1	2_A375_pNL97_plus_lncRNA::1::1203	-5250	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PLAC9	MGC104710, PLAC9	placenta-specific 9	NM_001012973, hCT2340459.0, hCT2340460.0, hCT13785.3	227419_x_at	NP_001012991.1, EAW80408.1, EAW80406.1, EAW80407.1
GeneID:311	ANXA11	10	81,914,880	81,965,328	50,448	-	1	2_A375_pNL97_plus_lncRNA::1::1204	-80	upstream	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ANXA11	ANXA11, ANX11, CAP50	annexin A11	NM_001157, NM_145868, NM_145869, hCT2272864.0, hCT2272867.0, hCT2356015.0, hCT2356016.0, hCT2356017.0, hCT2356018.0, hCT13589.2	206200_s_at, 214783_s_at	NP_001148.1, NP_665875.1, NP_665876.1, EAW80399.1, EAW80403.1, EAW80405.1, EAW80400.1, EAW80401.1, EAW80402.1, EAW80404.1
GeneID:439990	LOC439990	10	81,967,479	81,979,413	11,934	+	1	2_A375_pNL97_plus_lncRNA::1::1204	-2071	upstream	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC439990		hypothetical LOC439990	XR_111093, XR_110426, XR_114392	1569322_at	
GeneID:10718	NRG3	10	83,635,070	84,746,935	1,111,865	+	2	1_A375_pNL7_minus_lncRNA::1::891, 2_A375_pNL97_plus_lncRNA::1::1205	103186, 103159	in gene, in gene	1	1	22	20	1	1_A375_pNL7_minus_lncRNA::1	22	Gene NRG3	pro-NRG3, HRG3, NRG3	neuregulin 3	NM_001010848, NM_001165972, NM_001165973, hCT1642057.3	229233_at	NP_001010848.2, NP_001159444.1, NP_001159445.1, EAW80374.1
GeneID:27069	GHITM	10	85,899,185	85,913,311	14,126	+	2	2_A375_pNL97_plus_lncRNA::1::1207, 2_A375_pNL97_plus_lncRNA::1::1208	271, 17503	in gene, downstream	0	1	13.5	18	2	2_A375_pNL97_plus_lncRNA::1	20	Gene GHITM	PTD010, My021, HSPC282, MICS1, DERP2, GHITM, TMBIM5, FLJ26584, DKFZp566C0746	growth hormone inducible transmembrane protein	NM_014394, hCT2273086.0, hCT2273087.0, hCT2356012.0, hCT10013.3	1554510_s_at, 209248_at, 209249_s_at	NP_055209.2, EAW80369.1, EAW80367.1, EAW80368.1, EAW80370.1
GeneID:170425	LOC170425	10	86,039,736	86,054,415	14,679	+	2	1_A375_pNL7_minus_lncRNA::1::892, 2_A375_pNL97_plus_lncRNA::1::1209	11624, 11560	in gene, in gene	1	1	53	78	1	2_A375_pNL97_plus_lncRNA::1	78	Gene LOC170425		hypothetical LOC170425	XR_111091, XR_110428, XR_114388	1563821_at	
GeneID:2894	GRID1	10	87,359,312	88,126,250	766,938	-	3	2_A375_pNL97_plus_lncRNA::1::1210, 2_A375_pNL97_plus_lncRNA::1::1211, 2_A375_pNL97_plus_lncRNA::1::1212	464874, 162762, 59626	in gene, in gene, in gene	0	1	16	17.67	3	2_A375_pNL97_plus_lncRNA::1	21	Gene GRID1	GRID1, KIAA1220	glutamate receptor, ionotropic, delta 1	NM_017551, hCT2273073.1, hCT2273074.0, hCT2345002.0, hCT1963696.2	1555267_at, 1555268_a_at, 231977_at	NP_060021.1, EAW80338.1, EAW80339.1, EAW80340.1, EAW80341.1
GeneID:23063	WAPAL	10	88,195,013	88,281,541	86,528	-	1	1_A375_pNL7_minus_lncRNA::1::893	69	in gene	1	0	18	21	1	1_A375_pNL7_minus_lncRNA::1	18	Gene WAPAL	KIAA0261, FOE, WAPAL, WAPL	wings apart-like homolog (Drosophila)	NM_015045, hCT2273071.0, hCT2356026.0, hCT2356027.0, hCT14354.2	1554441_a_at, 212264_s_at, 212267_at, 217218_at	NP_055860.1, EAW80335.1, EAW80334.1, EAW80336.1, EAW80337.1
GeneID:657	BMPR1A	10	88,516,396	88,684,945	168,549	+	1	1_A375_pNL7_minus_lncRNA::1::894	-481	upstream	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene BMPR1A	CD292, 10q23del, ALK3, ACVRLK3, SKR5, BMPR1A	bone morphogenetic protein receptor, type IA	NM_004329, hCT2273472.0	204832_s_at, 213578_at	NP_004320.2, EAW80320.1
GeneID:6623	SNCG	10	88,718,288	88,723,017	4,729	+	1	2_A375_pNL97_plus_lncRNA::1::1214	12976	downstream	0	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SNCG	BCSG1, SNCG, SR	synuclein, gamma (breast cancer-specific protein 1)	NM_003087, hCT2273473.0, hCT2273475.0, hCT14368.3, hCT1950840.1	208584_at, 209877_at	NP_003078.2, EAW80317.1, EAW80315.1, EAW80316.1, EAW80318.1
GeneID:100133190	LOC100133190	10	88,725,498	88,731,068	5,570	-	1	2_A375_pNL97_plus_lncRNA::1::1214	-196	upstream	0	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene LOC100133190		hypothetical LOC100133190	XR_111094, XR_110430, XR_114391		
GeneID:10974	C10orf116	10	88,728,188	88,730,666	2,478	+	1	2_A375_pNL97_plus_lncRNA::1::1214	3076	downstream	0	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene C10orf116	APM2, C10orf116	chromosome 10 open reading frame 116	NM_006829	203571_s_at	NP_006820.1
GeneID:119385	AGAP11	10	88,730,498	88,769,960	39,462	+	1	2_A375_pNL97_plus_lncRNA::1::1214	766	in gene	0	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene AGAP11	AGAP11, KIAA1975	ankyrin repeat and GTPase domain Arf GTPase activating protein 11	NM_133447	1557380_at, 1557382_x_at	NP_597704.1
GeneID:2746	GLUD1	10	88,809,959	88,854,776	44,817	-	4	1_A375_pNL7_minus_lncRNA::1::895, 1_A375_pNL7_minus_lncRNA::1::896, 2_A375_pNL97_plus_lncRNA::1::1215, 2_A375_pNL97_plus_lncRNA::1::1216	216, -584, 200, -632	in gene, upstream, in gene, upstream	1	1	18.5	17	2	1_A375_pNL7_minus_lncRNA::1	19	Gene GLUD1	GLUD1, GDH1, MGC132003, GLUD, GDH	glutamate dehydrogenase 1	NM_005271, hCT2273052.1, hCT2273053.1, hCT2273055.1, hCT2273057.1, hCT2356025.0	200946_x_at, 200947_s_at, 244802_at	NP_005262.1, EAW80301.1, EAW80300.1, EAW80302.1, EAW80303.1, EAW80304.1
GeneID:54537	FAM35A	10	88,854,953	88,951,222	96,269	+	4	1_A375_pNL7_minus_lncRNA::1::895, 1_A375_pNL7_minus_lncRNA::1::896, 2_A375_pNL97_plus_lncRNA::1::1215, 2_A375_pNL97_plus_lncRNA::1::1216	-393, 407, -377, 455	upstream, in gene, upstream, in gene	1	1	18.5	17	2	1_A375_pNL7_minus_lncRNA::1	19	Gene FAM35A	bA163M19.1, FAM35A, FAM35A1, MGC5560	family with sequence similarity 35, member A	NM_019054, hCT2329308.0, hCT2329309.0	220547_s_at	NP_061927.2, EAW81363.1, EAW81364.1
GeneID:9562	MINPP1	10	89,264,223	89,313,218	48,995	+	2	1_A375_pNL7_minus_lncRNA::1::897, 2_A375_pNL97_plus_lncRNA::1::1217	396, 513	in gene, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MINPP1	MINPP2, HIPER1, MIPP, MINPP1, DKFZp564L2016	multiple inositol polyphosphate histidine phosphatase, 1	NM_001178117, NM_001178118, NM_004897, hCT2322243.0, hCT2322244.0	209585_s_at	NP_001171588.1, NP_001171589.1, NP_004888.2, EAW50185.1, EAW50186.1
GeneID:9060	PAPSS2	10	89,419,476	89,507,462	87,986	+	1	1_A375_pNL7_minus_lncRNA::1::899	11980	in gene	1	0	15	13	1	1_A375_pNL7_minus_lncRNA::1	15	Gene PAPSS2	ATPSK2, PAPSS2, SK2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	NM_004670, NM_001015880, hCT2322247.0, hCT2322248.0, hCT14436.3	203058_s_at, 203059_s_at, 203060_s_at	NP_004661.2, NP_001015880.1, EAW50181.1, EAW50182.1, EAW50183.1
GeneID:84896	ATAD1	10	89,512,875	89,577,917	65,042	-	1	2_A375_pNL97_plus_lncRNA::1::1220	-195	upstream	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ATAD1	FLJ14600, FNP001, ATAD1, AFDC1	ATPase family, AAA domain containing 1	NM_032810, hCT2321836.1, hCT14439.3, hCT1957990.1, hCT1957991.1	224850_at	NP_116199.2, EAW50178.1, EAW50177.1, EAW50179.1, EAW50180.1
GeneID:100144748	KILLIN	10	89,618,918	89,623,194	4,276	-	2	1_A375_pNL7_minus_lncRNA::1::900, 2_A375_pNL97_plus_lncRNA::1::1222	250, -150	in gene, upstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene KILLIN	KILLIN, KLLN	killin protein	NM_001126049		NP_001119521.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:5728	PTEN	10	89,623,195	89,728,532	105,337	+	2	1_A375_pNL7_minus_lncRNA::1::900, 2_A375_pNL97_plus_lncRNA::1::1222	-251, 149	upstream, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene PTEN	BZS, MHAM, 10q23del, MMAC1, PTEN1, GLM2, MGC11227, DEC, PTEN, TEP1	phosphatase and tensin homolog	NM_000314, hCT2322251.1, hCT2322253.1, hCT2352333.0, hCT1775386.2	204053_x_at, 204054_at, 211711_s_at, 222176_at, 225363_at, 227469_at, 233254_x_at, 233314_at, 242622_x_at	NP_000305.3, EAW50173.1, EAW50172.1, EAW50174.1, EAW50175.1
GeneID:55328	RNLS	10	90,033,621	90,343,082	309,461	-	2	1_A375_pNL7_minus_lncRNA::1::902, 2_A375_pNL97_plus_lncRNA::1::1223	108490, 197450	in gene, in gene	1	1	10	12.5	2	2_A375_pNL97_plus_lncRNA::1	16	Gene RNLS	RENALASE, C10orf59, FLJ11218, RNLS	renalase, FAD-dependent amine oxidase	NM_001031709, NM_018363, hCT2321715.0, hCT2321716.0, hCT2321719.0, hCT2352292.0, hCT1950707.1	220564_at, 223824_at	NP_001026879.2, NP_060833.1, EAW50167.1, EAW50169.1, EAW50170.1, EAW50171.1, EAW50168.1
GeneID:57559	STAMBPL1	10	90,640,026	90,683,244	43,218	+	2	1_A375_pNL7_minus_lncRNA::1::903, 2_A375_pNL97_plus_lncRNA::1::1224	566, 278	in gene, in gene	1	1	21	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene STAMBPL1	ALMalpha, KIAA1373, AMSH-LP, STAMBPL1, FLJ31524, bA399O19.2, AMSH-FP	STAM binding protein-like 1	NM_020799, hCT2321818.0, hCT2321819.1, hCT2321820.1	220603_at, 227606_s_at, 227607_at, 231891_at	NP_065850.1, EAW50156.1, EAW50157.1, EAW50158.1
GeneID:100507575	LOC100507575	10	91,094,411	91,102,416	8,005	-	2	1_A375_pNL7_minus_lncRNA::1::904, 2_A375_pNL97_plus_lncRNA::1::1225	-9744, -9744	upstream, upstream	1	1	25	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene LOC100507575		hypothetical LOC100507575	XR_110434		
GeneID:24138	IFIT5	10	91,174,325	91,180,759	6,434	+	1	2_A375_pNL97_plus_lncRNA::1::1226	555	in gene	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene IFIT5	FLJ53857, FLJ92678, RI58, IFIT5	interferon-induced protein with tetratricopeptide repeats 5	NM_012420, hCT15690.2	203595_s_at, 203596_s_at	NP_036552.1, EAW50135.1
GeneID:53354	PANK1	10	91,342,749	91,405,215	62,466	-	1	2_A375_pNL97_plus_lncRNA::1::1227	767	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PANK1	PANK1a, PANK1, PANK1b, PANK, MGC24596	pantothenate kinase 1	NM_138316, NM_148977, NM_148978, hCT2321552.0, hCT2321553.0, hCT2352251.0, hCT15693.3	226649_at	NP_612189.2, NP_683878.1, NP_683879.1, EAW50130.1, EAW50132.1, EAW50133.1, EAW50131.1
GeneID:9585	KIF20B	10	91,461,367	91,534,700	73,333	+	2	1_A375_pNL7_minus_lncRNA::1::905, 2_A375_pNL97_plus_lncRNA::1::1228	73, 9	in gene, in gene	1	1	25	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene KIF20B	KRMP1, KIF20B, MPP1, MPHOSPH1, DKFZp434P0810, MPP-1, DKFZp434B0435, CT90	kinesin family member 20B	NM_016195, hCT2321614.0, hCT2321616.0, hCT14856.3	205235_s_at	NP_057279.2, EAW50126.1, EAW50127.1, EAW50128.1
GeneID:3363	HTR7	10	92,500,575	92,617,671	117,096	-	1	2_A375_pNL97_plus_lncRNA::1::1233	82471	in gene	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene HTR7	5-HT7, HTR7	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	NM_000872, NM_019859, NM_019860, hCT2321442.1, hCT2321444.1, hCT1826965.3	216098_s_at	NP_000863.1, NP_062873.1, NP_062874.1, EAW50118.1, EAW50119.1, EAW50120.1
GeneID:10556	RPP30	10	92,631,709	92,668,312	36,603	+	1	2_A375_pNL97_plus_lncRNA::1::1234	35	in gene	0	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RPP30	TSG15, RPP30, FLJ36491	ribonuclease P/MRP 30kDa subunit	NM_006413, NM_001104546	203436_at	NP_006404.1, NP_001098016.1
GeneID:100188947	LOC100188947	10	93,066,719	93,299,337	232,618	-	2	1_A375_pNL7_minus_lncRNA::1::907, 2_A375_pNL97_plus_lncRNA::1::1237	129684, 27721	in gene, in gene	1	1	11	17	2	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100188947		hypothetical LOC100188947	NR_024467		
GeneID:143279	HECTD2	10	93,170,096	93,274,520	104,424	+	2	1_A375_pNL7_minus_lncRNA::1::907, 2_A375_pNL97_plus_lncRNA::1::1237	-443, 101520	upstream, in gene	1	1	11	17	2	2_A375_pNL97_plus_lncRNA::1	19	Gene HECTD2	HECTD2, FLJ16050	HECT domain containing 2	NM_173497, NM_182765, hCT2346069.1, hCT2351051.0, hCT2352328.0	1565699_at, 227568_at, 238803_at	NP_775768.2, NP_877497.2, EAW50109.1, EAW50110.1, EAW50111.1
GeneID:143282	FGFBP3	10	93,666,345	93,669,258	2,913	-	2	1_A375_pNL7_minus_lncRNA::1::908, 2_A375_pNL97_plus_lncRNA::1::1241	586, 586	in gene, in gene	1	1	79	85	1	2_A375_pNL97_plus_lncRNA::1	85	Gene FGFBP3	MGC39320, FGFBP3, C10orf13, FGF-BP3	fibroblast growth factor binding protein 3	NM_152429, hCT1819921.2	238453_at	NP_689642.3, EAW50104.1
GeneID:9044	BTAF1	10	93,683,736	93,790,082	106,346	+	1	1_A375_pNL7_minus_lncRNA::1::909	-120	upstream	1	0	22	21	1	1_A375_pNL7_minus_lncRNA::1	22	Gene BTAF1	TAF(II)170, BTAF1, TAFII170, MOT1, TAF172, MGC138406, KIAA0940	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)	NM_003972, hCT2352265.0, hCT10355.3	209430_at	NP_003963.1, EAW50103.1, EAW50102.1
GeneID:22849	CPEB3	10	93,808,397	94,050,875	242,478	-	2	1_A375_pNL7_minus_lncRNA::1::910, 2_A375_pNL97_plus_lncRNA::1::1242	-101, 91	upstream, in gene	1	1	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene CPEB3	CPEB3		NM_001178137, NM_014912, hCT2352361.0, hCT11393.3	1555250_a_at, 205773_at, 243651_at	NP_001171608.1, NP_055727.3, EAW50097.1, EAW50098.1
GeneID:54708	5-Mar	10	94,050,920	94,113,721	62,801	+	2	1_A375_pNL7_minus_lncRNA::1::910, 2_A375_pNL97_plus_lncRNA::1::1242	56, -136	in gene, upstream	1	1	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene MARCH5	FLJ20445, RNF153, MITOL, MARCH5, MARCH-V	membrane-associated ring finger (C3HC4) 5	NM_017824, hCT2321931.0, hCT2321933.0, hCT11396.3	218582_at, 226394_at	NP_060294.1, EAW50096.1, EAW50094.1, EAW50095.1
GeneID:3832	KIF11	10	94,352,825	94,415,152	62,327	+	2	1_A375_pNL7_minus_lncRNA::1::913, 2_A375_pNL97_plus_lncRNA::1::1245	-1401, -1417	upstream, upstream	1	1	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene KIF11	TRIP5, KNSL1, KIF11, HKSP, EG5	kinesin family member 11	NM_004523, hCT201239.3	204444_at	NP_004514.2, EAW50089.1
GeneID:3087	HHEX	10	94,449,681	94,455,408	5,727	+	1	2_A375_pNL97_plus_lncRNA::1::1246	271	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene HHEX	HOX11L-PEN, PRH, HMPH, PRHX, HEX, HHEX	hematopoietically expressed homeobox	NM_002729, hCT2321540.0, hCT1820031.1	204689_at, 215933_s_at	NP_002720.1, EAW50088.1, EAW50087.1
GeneID:54536	EXOC6	10	94,594,470	94,819,251	224,781	+	1	2_A375_pNL97_plus_lncRNA::1::1247	57786	in gene	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene EXOC6	EXOC6, SEC15L3, SEC15L, DKFZp761I2124, FLJ1125, Sec15p, FLJ11251, MGC33397, SEC15L1, EXOC6A, SEC15	exocyst complex component 6	NM_001013848, NM_019053, hCT2321542.0, hCT2321544.0, hCT2352283.0, hCT2352284.0, hCT30768.3	226259_at, 232599_at, 233924_s_at	NP_001013870.1, NP_061926.3, EAW50082.1, EAW50083.1, EAW50084.1, EAW50085.1, EAW50086.1
GeneID:26509	MYOF	10	95,066,186	95,242,074	175,888	-	2	1_A375_pNL7_minus_lncRNA::1::915, 2_A375_pNL97_plus_lncRNA::1::1249	-118, -70	upstream, upstream	1	1	28	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene MYOF	FLJ90777, MYOF, FER1L3, FLJ36571	myoferlin	NM_013451, NM_133337, hCT2321494.0, hCT2352269.0, hCT2352270.0, hCT30781.3	201798_s_at, 211864_s_at, 217518_at	NP_038479.1, NP_579899.1, EAW50073.1, EAW50074.1, EAW50075.1, EAW50076.1
GeneID:55165	CEP55	10	95,256,369	95,288,849	32,480	+	2	1_A375_pNL7_minus_lncRNA::1::916, 2_A375_pNL97_plus_lncRNA::1::1250	79, 15	in gene, in gene	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene CEP55	C10orf3, CEP55, URCC6, FLJ10540, CT111	centrosomal protein 55kDa	NM_018131, NM_001127182, hCT2352272.0, hCT30784.3	218542_at	NP_060601.3, NP_001120654.1, EAW50071.1, EAW50072.1
GeneID:118924	C10orf4	10	95,427,640	95,462,329	34,689	-	1	2_A375_pNL97_plus_lncRNA::1::1251	-39	upstream	0	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene C10orf4	F26C11.1-like, FRA10A, FRA10AC1, C10orf4	chromosome 10 open reading frame 4	NM_145246, hCT2321363.1, hCT2349230.0, hCT2352288.0, hCT2352289.0, hCT2352290.0, hCT2352291.0, hCT30789.4	226398_s_at, 238596_at	NP_660289.2, EAW50056.1, EAW50055.1, EAW50057.1, EAW50058.1, EAW50060.1, EAW50059.1, EAW50061.1
GeneID:9211	LGI1	10	95,517,566	95,557,916	40,350	+	1	2_A375_pNL97_plus_lncRNA::1::1252	-5737	upstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LGI1	IB1099, ETL1, EPITEMPIN, LGI1, EPT	leucine-rich, glioma inactivated 1	NM_005097, hCT2322063.0, hCT2322064.0, hCT2322065.0	206349_at	NP_005088.1, EAW50051.1, EAW50052.1, EAW50053.1
GeneID:159371	TMEM20	10	95,653,730	95,662,491	8,761	+	1	2_A375_pNL97_plus_lncRNA::1::1253	-146	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TMEM20	C10orf60, FLJ33990, TMEM20	transmembrane protein 20	NM_153226, NM_001134658, hCT2344324.0, hCT2344325.0, hCT1646014.4, hCT1627097.3	231012_at, 239265_at	NP_694958.1, NP_001128130.1, EAW50046.1, EAW50047.1, EAW50048.1, EAW50049.1
GeneID:51196	PLCE1	10	95,753,746	96,088,149	334,403	+	6	1_A375_pNL7_minus_lncRNA::1::917, 1_A375_pNL7_minus_lncRNA::1::918, 2_A375_pNL97_plus_lncRNA::1::1254, 2_A375_pNL97_plus_lncRNA::1::1255, 2_A375_pNL97_plus_lncRNA::1::1256, 2_A375_pNL97_plus_lncRNA::1::1257	-1778, 72574, -1938, 72622, 121998, 230646	upstream, in gene, upstream, in gene, in gene, in gene	1	1	23.5	34.75	4	2_A375_pNL97_plus_lncRNA::1	60	Gene PLCE1	KIAA1516, NPHS3, PLCE, MGC167842, PLCE1, PPLC, FLJ23659	phospholipase C, epsilon 1	NM_016341, NM_001165979, hCT2322071.0, hCT1813992.1	1566739_at, 1566740_at, 205111_s_at, 205112_at, 214159_at, 239904_at	NP_057425.3, NP_001159451.1, EAW50042.1, EAW50043.1
GeneID:64318	NOC3L	10	96,092,989	96,122,683	29,694	-	2	1_A375_pNL7_minus_lncRNA::1::919, 2_A375_pNL97_plus_lncRNA::1::1258	27, 123	in gene, in gene	1	1	25	16	1	1_A375_pNL7_minus_lncRNA::1	25	Gene NOC3L	FLJ12820, FAD24, AD24, C10orf117, NOC3L	nucleolar complex associated 3 homolog (S. cerevisiae)	NM_022451, hCT30416.3	218889_at	NP_071896.8, EAW50041.1
GeneID:23232	TBC1D12	10	96,162,186	96,296,089	133,903	+	1	2_A375_pNL97_plus_lncRNA::1::1259	143510	downstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TBC1D12	TBC1D12, FLJ12820, KIAA0608, FLJ10339	TBC1 domain family, member 12	NM_015188	1557609_s_at, 221858_at	NP_056003.1
GeneID:3070	HELLS	10	96,305,574	96,361,856	56,282	+	1	2_A375_pNL97_plus_lncRNA::1::1259	122	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene HELLS	SMARCA6, LSH, Nbla10143, FLJ10339, PASG, HELLS	helicase, lymphoid-specific	NM_018063, hCT2322073.0, hCT2322074.0, hCT2322076.0, hCT2352259.0, hCT2352260.0, hCT2352261.0, hCT2352262.0, hCT2352263.0, hCT2352264.0, hCT2352265.0, hCT2352266.0, hCT2352267.0, hCT30418.3	220085_at, 223556_at, 234040_at	NP_060533.2, EAW50038.1, EAW50026.1, EAW50027.1, EAW50034.1, EAW50037.1, EAW50028.1, EAW50029.1, EAW50030.1, EAW50031.1, EAW50032.1, EAW50033.1, EAW50035.1, EAW50036.1
GeneID:142827	C10orf129	10	96,953,957	96,988,686	34,729	+	1	2_A375_pNL97_plus_lncRNA::1::1260	-10421	upstream	0	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene C10orf129	ACSM6, C10orf129, bA310E22.3	chromosome 10 open reading frame 129	NM_207321, hCT1833044.2		NP_997204.2, EAW50014.1
GeneID:10580	SORBS1	10	97,071,530	97,321,171	249,641	-	3	1_A375_pNL7_minus_lncRNA::1::921, 1_A375_pNL7_minus_lncRNA::1::922, 2_A375_pNL97_plus_lncRNA::1::1261	169315, 167091, 169315	in gene, in gene, in gene	1	1	20.5	22	2	2_A375_pNL97_plus_lncRNA::1	26	Gene SORBS1	KIAA1296, SORBS1, DKFZp451C066, FLAF2, SH3D5, SH3P12, DKFZp586P1422, R85FL, SORB1, CAP, FLJ12406	sorbin and SH3 domain containing 1	NM_006434, NM_015385, NM_001034954, NM_001034955, NM_001034956, NM_024991, NM_001034957, hCT2323641.0, hCT2323644.0, hCT2323646.0, hCT2323649.0, hCT2323651.0, hCT2323654.0, hCT2323657.0, hCT2323659.0, hCT30741.2, hCT1830018.1, hCT1830019.1	211705_s_at, 211819_s_at, 218087_s_at, 222513_s_at	NP_006425.2, NP_056200.1, NP_001030126.1, NP_001030127.1, NP_001030128.1, NP_079267.1, NP_001030129.1, EAW49999.1, EAW50000.1, EAW50001.1, EAW50002.1, EAW50003.1, EAW50004.1, EAW50005.1, EAW50006.1, EAW50007.1, EAW50008.1
GeneID:5832	ALDH18A1	10	97,365,686	97,416,567	50,881	-	1	1_A375_pNL7_minus_lncRNA::1::923	183	in gene	1	0	22	15	1	1_A375_pNL7_minus_lncRNA::1	22	Gene ALDH18A1	PYCS, MGC117316, P5CS, ALDH18A1, GSAS	aldehyde dehydrogenase 18 family, member A1	NM_002860, NM_001017423, hCT2323635.0, hCT2323637.0, hCT2352239.0, hCT29199.3	217791_s_at, 222416_at	NP_002851.2, NP_001017423.1, EAW49994.1, EAW49995.1, EAW49996.1, EAW49997.1
GeneID:26123	TCTN3	10	97,423,153	97,453,900	30,747	-	3	1_A375_pNL7_minus_lncRNA::1::923, 1_A375_pNL7_minus_lncRNA::1::924, 2_A375_pNL97_plus_lncRNA::1::1262	37516, 172, 172	downstream, in gene, in gene	1	1	19.5	16	2	1_A375_pNL7_minus_lncRNA::1	22	Gene TCTN3	C10orf61, TCTN3, DKFZp564D116, TECT3	tectonic family member 3	NM_015631, NM_001143973, hCT30742.3	212121_at, 212123_at	NP_056446.4, NP_001137445.1, EAW49993.1
GeneID:100127889	C10orf131	10	97,667,722	97,698,415	30,693	+	1	2_A375_pNL97_plus_lncRNA::1::1263	-202	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene C10orf131	bA690P14.3, C10orf131, FLJ10895	chromosome 10 open reading frame 131	NM_001130446		NP_001123918.2
GeneID:728558	LOC728558	10	97,780,957	97,849,953	68,996	-	4	1_A375_pNL7_minus_lncRNA::1::925, 1_A375_pNL7_minus_lncRNA::1::926, 2_A375_pNL97_plus_lncRNA::1::1264, 2_A375_pNL97_plus_lncRNA::1::1265	45905, -127, 46657, 33	in gene, upstream, in gene, in gene	1	1	18.33	17.67	3	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC728558	FLJ34077, MGC10764	hypothetical LOC728558	XR_111097, XR_110439, XR_114413		
GeneID:54619	CCNJ	10	97,803,159	97,820,627	17,468	+	2	1_A375_pNL7_minus_lncRNA::1::925, 2_A375_pNL97_plus_lncRNA::1::1264	889, 137	in gene, in gene	1	1	15	13.5	2	1_A375_pNL7_minus_lncRNA::1	16	Gene CCNJ	CCNJ, bA690P14.1	cyclin J	NM_019084, NM_001134375, NM_001134376, hCT2321580.0	219470_x_at, 222688_at, 229091_s_at	NP_061957.2, NP_001127847.1, NP_001127848.1, EAW49984.1
GeneID:9849	ZNF518A	10	97,889,472	97,923,517	34,045	+	2	1_A375_pNL7_minus_lncRNA::1::927, 2_A375_pNL97_plus_lncRNA::1::1266	192, 256	in gene, in gene	1	1	19	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene ZNF518A	MGC125710, ZNF518, MGC125707, ZNF518A, DKFZp781O2147	zinc finger protein 518A	NM_014803, hCT2321584.0	204291_at, 215644_at, 244132_x_at	NP_055518.2, EAW49983.1
GeneID:7093	TLL2	10	98,124,363	98,273,683	149,320	-	3	1_A375_pNL7_minus_lncRNA::1::928, 2_A375_pNL97_plus_lncRNA::1::1267, 2_A375_pNL97_plus_lncRNA::1::1268	17619, 17491, 115	in gene, in gene, in gene	1	1	19.5	31.5	2	2_A375_pNL97_plus_lncRNA::1	45	Gene TLL2	MGC133313, TLL2, KIAA0932, MGC133312	tolloid-like 2	NM_012465, hCT2349223.0, hCT14422.4	208027_s_at, 215008_at, 215843_s_at	NP_036597.1, EAW49976.1, EAW49975.1
GeneID:56889	TM9SF3	10	98,277,867	98,346,809	68,942	-	1	2_A375_pNL97_plus_lncRNA::1::1268	73241	downstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TM9SF3	TM9SF3, RP11-34E5.1, EP70-P-iso, SMBP	transmembrane 9 superfamily member 3	NM_020123, hCT2321398.0, hCT2321399.0, hCT16908.3	217758_s_at, 222399_s_at, 228610_at, 239626_x_at	NP_064508.3, EAW49974.1, EAW49972.1, EAW49973.1
GeneID:6585	SLIT1	10	98,757,795	98,945,683	187,888	-	1	2_A375_pNL97_plus_lncRNA::1::1269	104083	in gene	0	1	19	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene SLIT1	SLIL1, SLIT1, MEGF4, Slit-1, MGC164811, SLIT3, SLIT-1	slit homolog 1 (Drosophila)	NM_003061, hCT2322084.1, hCT2322086.1, hCT2340271.0, hCT16912.4	1557615_a_at, 208221_s_at, 213601_at	NP_003052.2, EAW49956.1, EAW49957.1, EAW49958.1, EAW49959.1
GeneID:10023	FRAT1	10	99,079,022	99,081,672	2,650	+	2	1_A375_pNL7_minus_lncRNA::1::929, 2_A375_pNL97_plus_lncRNA::1::1270	-110, -142	upstream, upstream	1	1	25	20	1	1_A375_pNL7_minus_lncRNA::1	25	Gene FRAT1	FRAT1, FLJ97193	frequently rearranged in advanced T-cell lymphomas	NM_005479, hCT2322413.1, hCT14420.3	219889_at	NP_005470.2, EAW49951.1, EAW49950.1
GeneID:23401	FRAT2	10	99,092,254	99,094,458	2,204	-	3	1_A375_pNL7_minus_lncRNA::1::930, 2_A375_pNL97_plus_lncRNA::1::1271, 2_A375_pNL97_plus_lncRNA::1::1272	-150, 826, -134	upstream, in gene, upstream	1	1	17.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene FRAT2	FRAT2, MGC10562	frequently rearranged in advanced T-cell lymphomas 2	NM_012083, hCT1830634.2	209864_at	NP_036215.1, EAW49949.1
GeneID:5223	PGAM1	10	99,186,027	99,193,198	7,171	+	1	2_A375_pNL97_plus_lncRNA::1::1273	5	in gene	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PGAM1	PGAMA, PGAM1, PGAM-B	phosphoglycerate mutase 1 (brain)	NM_002629, hCT1967406.1, hCT2322418.0, hCT2322421.0, hCT2322422.0, hCT2322423.0, hCT2322425.0, hCT2352271.0, hCT1827142.2	200886_s_at	NP_002620.1, EAW49938.1, EAW49939.1, EAW49941.1, EAW49942.1, EAW49943.1, EAW49937.1, EAW49940.1, EAW49944.1
GeneID:51013	EXOSC1	10	99,195,666	99,205,768	10,102	-	1	2_A375_pNL97_plus_lncRNA::1::1273	19736	downstream	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene EXOSC1	EXOSC1, SKI4, Csl4p, Ski4p, CGI-108, CSL4, hCsl4p, p13	exosome component 1	NM_016046, hCT16904.3	1559044_at, 218369_s_at, 222609_s_at	NP_057130.1, EAW49936.1
GeneID:64210	MMS19	10	99,218,081	99,258,366	40,285	-	1	1_A375_pNL7_minus_lncRNA::1::931	585	in gene	1	0	14	19	1	1_A375_pNL7_minus_lncRNA::1	14	Gene MMS19	FLJ34167, hMMS19, MGC99604, MMS19, MET18, MMS19L, FLJ95146	MMS19 nucleotide excision repair homolog (S. cerevisiae)	NM_022362, hCT2322103.0, hCT2322104.0, hCT2322105.0, hCT2322106.0, hCT2322107.0, hCT2352311.0, hCT2352312.0, hCT16910.3	202167_s_at	NP_071757.4, EAW49922.1, EAW49921.1, EAW49925.1, EAW49926.1, EAW49927.1, EAW49923.1, EAW49924.1, EAW49928.1
GeneID:80019	UBTD1	10	99,258,768	99,330,960	72,192	+	4	1_A375_pNL7_minus_lncRNA::1::931, 1_A375_pNL7_minus_lncRNA::1::932, 2_A375_pNL97_plus_lncRNA::1::1274, 2_A375_pNL97_plus_lncRNA::1::1275	-987, 44048, 43648, 44176	upstream, in gene, in gene, in gene	1	1	16	20	2	2_A375_pNL97_plus_lncRNA::1	21	Gene UBTD1	UBTD1, FLJ11807	ubiquitin domain containing 1	NM_024954, hCT2322437.0, hCT2322440.0, hCT1641196.2	219172_at	NP_079230.1, EAW49920.1, EAW49918.1, EAW49919.1
GeneID:60370	AVPI1	10	99,437,181	99,447,015	9,834	-	2	1_A375_pNL7_minus_lncRNA::1::933, 2_A375_pNL97_plus_lncRNA::1::1276	-217, -249	upstream, upstream	1	1	22	21	1	1_A375_pNL7_minus_lncRNA::1	22	Gene AVPI1	VIP32, RP11-548K23.7, PP5395, VIT32, AVPI1	arginine vasopressin-induced 1	NM_021732, hCT2341102.0, hCT1642887.3	218631_at	NP_068378.2, EAW49905.1, EAW49904.1
GeneID:83742	MARVELD1	10	99,473,465	99,477,909	4,444	+	2	1_A375_pNL7_minus_lncRNA::1::934, 2_A375_pNL97_plus_lncRNA::1::1277	13223, 423	downstream, in gene	1	1	15.5	16	2	2_A375_pNL97_plus_lncRNA::1	20	Gene MARVELD1	FLJ22343, MARVELD1, MARVD1, MGC4415, bA548K23.8, GB14, FLJ23440, RP11-548K23.8, MRVLDC1	MARVEL domain containing 1	NM_031484, hCT1642886.3	223095_at, 234917_at	NP_113672.1, EAW49903.1
GeneID:100270710	LOC100270710	10	99,477,217	99,493,298	16,081	-	4	1_A375_pNL7_minus_lncRNA::1::934, 1_A375_pNL7_minus_lncRNA::1::935, 2_A375_pNL97_plus_lncRNA::1::1277, 2_A375_pNL97_plus_lncRNA::1::1278	6610, -3758, 19410, -3470	in gene, upstream, downstream, upstream	1	1	15.67	16.67	3	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100270710		hypothetical LOC100270710	NR_026754		
GeneID:118813	ZFYVE27	10	99,496,878	99,520,664	23,786	+	3	1_A375_pNL7_minus_lncRNA::1::934, 1_A375_pNL7_minus_lncRNA::1::935, 2_A375_pNL97_plus_lncRNA::1::1278	-10190, 178, -110	upstream, in gene, upstream	1	1	17	15	2	1_A375_pNL7_minus_lncRNA::1	18	Gene ZFYVE27	RP11-459F3.2, ZFYVE27, PROTRUDIN, SPG33	zinc finger, FYVE domain containing 27	NM_001002261, NM_001002262, NM_001174119, NM_001174120, NM_001174121, NM_001174122, NM_144588, hCT2322453.0, hCT2352274.0, hCT2352275.0, hCT2352276.0, hCT2352277.0, hCT2352278.0, hCT2352279.0, hCT16785.2	225218_at	NP_001002261.1, NP_001002262.1, NP_001167590.1, NP_001167591.1, NP_001167592.1, NP_001167593.1, NP_653189.3, EAW49895.1, EAW49896.1, EAW49897.1, EAW49898.1, EAW49899.1, EAW49900.1, EAW49901.1, EAW49902.1
GeneID:100505561	LOC100505561	10	99,588,235	99,609,555	21,320	-	2	1_A375_pNL7_minus_lncRNA::1::936, 2_A375_pNL97_plus_lncRNA::1::1280	6435, 6371	in gene, in gene	1	1	26	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100505561		hypothetical LOC100505561	XR_110441		
GeneID:401647	GOLGA7B	10	99,609,996	99,627,782	17,786	+	3	1_A375_pNL7_minus_lncRNA::1::936, 2_A375_pNL97_plus_lncRNA::1::1280, 2_A375_pNL97_plus_lncRNA::1::1281	-6876, -6812, 11252	upstream, upstream, in gene	1	1	20.5	25.5	2	2_A375_pNL97_plus_lncRNA::1	26	Gene GOLGA7B	bA459F3.4, bA451M19.3, C10orf132, GOLGA7B, MGC131701, C10orf133	golgi autoantigen, golgin subfamily a, 7B	NM_001010917, hCT16286.3	228068_at	NP_001010917.1, EAW49893.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:55118	CRTAC1	10	99,624,758	99,790,585	165,827	-	5	1_A375_pNL7_minus_lncRNA::1::937, 2_A375_pNL97_plus_lncRNA::1::1281, 2_A375_pNL97_plus_lncRNA::1::1282, 2_A375_pNL97_plus_lncRNA::1::1283, 2_A375_pNL97_plus_lncRNA::1::1284	148153, 169337, 148153, 141081, 38777	in gene, downstream, in gene, in gene, in gene	1	1	18.5	24.75	4	1_A375_pNL7_minus_lncRNA::1	29	Gene CRTAC1	FLJ10320, CRTAC1, CEP-68, ASPIC1	cartilage acidic protein 1	NM_018058, hCT2322092.0, hCT2322093.0, hCT16260.3	1555958_at, 221204_s_at	NP_060528.3, EAW49892.1, EAW49890.1, EAW49891.1
GeneID:100128300	LOC100128300	10	99,627,889	99,631,335	3,446	+	1	2_A375_pNL97_plus_lncRNA::1::1281	-6641	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100128300		hypothetical LOC100128300	XR_111108, XR_110442, XR_114417		
GeneID:27291	C10orf28	10	99,894,381	100,004,654	110,273	+	3	1_A375_pNL7_minus_lncRNA::1::940, 2_A375_pNL97_plus_lncRNA::1::1287, 2_A375_pNL97_plus_lncRNA::1::1288	115, 30, 112531	in gene, in gene, downstream	1	1	14.5	15	2	1_A375_pNL7_minus_lncRNA::1	16	Gene C10orf28	C10orf28, GIDRP88, FLJ25458, GIDRP86, FLJ37160, PSORT	chromosome 10 open reading frame 28	NM_014472, hCT2349214.0, hCT2349215.0, hCT2349216.0	210455_at, 228374_at	NP_055287.4, EAW49889.1, EAW49887.1, EAW49888.1
GeneID:84171	LOXL4	10	100,007,443	100,028,007	20,564	-	2	2_A375_pNL97_plus_lncRNA::1::1288, 2_A375_pNL97_plus_lncRNA::1::1289	21095, -1465	downstream, upstream	0	1	13	17.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene LOXL4	FLJ21889, LOXL4, LOXC	lysyl oxidase-like 4	NM_032211, hCT16279.4	1570219_at, 227145_at	NP_115587.6, EAW49886.1
GeneID:60495	HPSE2	10	100,216,834	100,995,632	778,798	-	1	2_A375_pNL97_plus_lncRNA::1::1292	747104	in gene	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene HPSE2	FLJ11684, MGC133234, HPSE2, UFS, HPA2, FLJ44022, HPR2	heparanase 2	NM_021828, NM_001166244, NM_001166245, NM_001166246, hCT2344370.0, hCT2344371.0, hCT2344372.0	220927_s_at	NP_068600.4, NP_001159716.1, NP_001159717.1, NP_001159718.1, EAW49873.1, EAW49874.1, EAW49872.1
GeneID:81894	SLC25A28	10	101,370,275	101,380,221	9,946	-	1	1_A375_pNL7_minus_lncRNA::1::942	-1027	upstream	1	0	26	19	1	1_A375_pNL7_minus_lncRNA::1	26	Gene SLC25A28	NPD016, MFRN2, MRS4L, SLC25A28, DKFZp547C109, MRS3/4	solute carrier family 25, member 28	NM_031212, hCT2321465.0, hCT9464.3, hCT1962278.1, hCT1962279.1	221432_s_at, 223192_at	NP_112489.3, EAW49864.1, EAW49863.1, EAW49865.1, EAW49866.1
GeneID:57089	ENTPD7	10	101,419,263	101,471,002	51,739	+	1	2_A375_pNL97_plus_lncRNA::1::1293	-223	upstream	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ENTPD7	ENTPD7, DKFZp667O124, FLJ30978, LALP1, FLJ31830, MGC141913, FLJ95364, FLJ41522, RP11-483F11.1	ectonucleoside triphosphate diphosphohydrolase 7	NM_020354, hCT2321583.0, hCT2352247.0, hCT9467.3	220153_at	NP_065087.1, EAW49862.1, EAW49860.1, EAW49861.1
GeneID:10613	ERLIN1	10	101,909,847	101,945,814	35,967	-	1	2_A375_pNL97_plus_lncRNA::1::1294	86	in gene	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ERLIN1	KE04, KEO4, C10orf69, ERLIN1, SPFH1, Erlin-1	ER lipid raft associated 1	NM_006459, NM_001100626, hCT2321455.0, hCT9419.3	202441_at, 202444_s_at	NP_006450.2, NP_001094096.1, EAW49846.1, EAW49847.1
GeneID:1147	CHUK	10	101,948,124	101,989,344	41,220	-	1	2_A375_pNL97_plus_lncRNA::1::1294	43616	downstream	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CHUK	IKK1, IKBKA, CHUK, NFKBIKA, IKK-alpha, IKKA, TCF16	conserved helix-loop-helix ubiquitous kinase	NM_001278, hCT10488.3	209666_s_at	NP_001269.3, EAW49845.1
GeneID:55280	CWF19L1	10	101,992,055	102,027,437	35,382	-	1	2_A375_pNL97_plus_lncRNA::1::1295	45	in gene	0	1	16	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene CWF19L1	CWF19L1, FLJ10998	CWF19-like 1, cell cycle control (S. pombe)	NM_018294, hCT1967371.1, hCT1967372.1, hCT2352357.0, hCT2352358.0, hCT2352359.0, hCT2352360.0, hCT10485.3	218787_x_at, 229038_at, 233588_x_at	NP_060764.3, EAW49844.1, EAW49839.1, EAW49841.1, EAW49842.1, EAW49843.1, EAW49838.1, EAW49840.1
GeneID:282991	BLOC1S2	10	102,033,713	102,046,439	12,726	-	1	2_A375_pNL97_plus_lncRNA::1::1295	19047	downstream	0	1	16	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene BLOC1S2	BLOS2, BLOC1S2, MGC10120, RP11-316M21.4, FLJ30135	biogenesis of lysosomal organelles complex-1, subunit 2	NM_173809, NM_001001342, hCT2350919.0, hCT2350920.0, hCT10487.5	225049_at	NP_776170.2, NP_001001342.1, EAW49835.1, EAW49836.1, EAW49837.1
GeneID:9033	PKD2L1	10	102,047,903	102,090,243	42,340	-	1	2_A375_pNL97_plus_lncRNA::1::1296	5187	in gene	0	1	21	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene PKD2L1	PCL, PKDL, PKD2L1, TRPP3, PKD2L	polycystic kidney disease 2-like 1	NM_016112, hCT2321447.0, hCT10483.2	221061_at	NP_057196.2, EAW49834.1, EAW49833.1
GeneID:6319	SCD	10	102,106,772	102,124,588	17,816	+	2	1_A375_pNL7_minus_lncRNA::1::943, 2_A375_pNL97_plus_lncRNA::1::1297	236, 300	in gene, in gene	1	1	22	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SCD	FADS5, SCDOS, SCD, MSTP008, SCD1	stearoyl-CoA desaturase (delta-9-desaturase)	NM_005063, hCT2322391.0, hCT2322393.0, hCT2322394.0, hCT10464.3	200831_s_at, 200832_s_at, 211162_x_at, 211708_s_at	NP_005054.3, EAW49827.1, EAW49828.1, EAW49829.1, EAW49830.1
GeneID:25956	SEC31B	10	102,246,403	102,279,595	33,192	-	1	2_A375_pNL97_plus_lncRNA::1::1298	13035	in gene	0	1	9	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene SEC31B	SEC31L2, DKFZp434M183, SEC31B-1, SEC31B	SEC31 homolog B (S. cerevisiae)	NM_015490, hCT2321308.0, hCT2352224.0, hCT2352225.0, hCT1951248.0	209689_at	NP_056305.1, EAW49821.1, EAW49822.1, EAW49823.1, EAW49824.1
GeneID:4714	NDUFB8	10	102,283,497	102,289,636	6,139	-	2	1_A375_pNL7_minus_lncRNA::1::944, 2_A375_pNL97_plus_lncRNA::1::1299	-5948, -5916	upstream, upstream	1	1	34	48	1	2_A375_pNL97_plus_lncRNA::1	48	Gene NDUFB8	CI-ASHI, ASHI, NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	NM_005004, hCT15775.3, hCT1957994.0	201226_at, 201227_s_at, 214241_at	NP_004995.1, EAW49820.1, EAW49819.1
GeneID:55662	HIF1AN	10	102,295,641	102,313,681	18,040	+	2	1_A375_pNL7_minus_lncRNA::1::944, 2_A375_pNL97_plus_lncRNA::1::1299	-57, -89	upstream, upstream	1	1	34	48	1	2_A375_pNL97_plus_lncRNA::1	48	Gene HIF1AN	FIH1, DKFZp762F1811, FLJ20615, FLJ22027, HIF1AN	hypoxia inducible factor 1, alpha subunit inhibitor	NM_017902, hCT2322355.0, hCT15783.3	218525_s_at, 59999_at	NP_060372.2, EAW49818.1, EAW49817.1
GeneID:5076	PAX2	10	102,505,468	102,589,698	84,230	+	1	2_A375_pNL97_plus_lncRNA::1::1301	81316	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PAX2	PAX2		NM_003990, NM_003988, NM_003987, NM_000278, NM_003989, hCT1967382.1, hCT1967383.1, hCT2322363.0, hCT2322364.0, hCT2322368.0, hCT15776.2, hCT15777.2, hCT1962304.1	206228_at, 206229_x_at	NP_003981.2, NP_003979.2, NP_003978.2, NP_000269.2, NP_003980.2, EAW49816.1, EAW49809.1, EAW49810.1, EAW49811.1, EAW49812.1, EAW49813.1, EAW49814.1, EAW49815.1
GeneID:57715	SEMA4G	10	102,732,286	102,745,372	13,086	+	2	1_A375_pNL7_minus_lncRNA::1::946, 2_A375_pNL97_plus_lncRNA::1::1302	14914, 14850	downstream, downstream	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SEMA4G	SEMA4G, MGC102867, KIAA1619, FLJ20590	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	NM_017893, hCT2322374.0, hCT2322375.0, hCT2352326.0, hCT15787.3	203483_at, 219194_at	NP_060363.2, EAW49802.1, EAW49801.1, EAW49803.1, EAW49804.1
GeneID:84545	MRPL43	10	102,737,579	102,747,272	9,693	-	2	1_A375_pNL7_minus_lncRNA::1::946, 2_A375_pNL97_plus_lncRNA::1::1302	72, 136	in gene, in gene	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MRPL43	bMRP36a, MRPL43, MGC48892, MGC17989	mitochondrial ribosomal protein L43	NM_032112, NM_176793, NM_176794, NM_176792, hCT2321301.0, hCT2352355.0, hCT2352356.0, hCT15789.1, hCT1951249.1, hCT1951250.1	224332_s_at, 230026_at, 230027_s_at	NP_115488.2, NP_789763.1, NP_789762.1, NP_789764.1, EAW49796.1, EAW49797.1, EAW49795.1, EAW49798.1, EAW49799.1, EAW49800.1
GeneID:56652	C10orf2	10	102,747,293	102,754,158	6,865	+	3	1_A375_pNL7_minus_lncRNA::1::946, 2_A375_pNL97_plus_lncRNA::1::1302, 2_A375_pNL97_plus_lncRNA::1::1303	-93, -157, 11235	upstream, upstream, downstream	1	1	16	20	2	2_A375_pNL97_plus_lncRNA::1	22	Gene C10orf2	C10orf2, ATXN8, FLJ21832, PEOA3, IOSCA, MTDPS7, TWINL, PEO, PEO1, SANDO, SCA8	chromosome 10 open reading frame 2	NM_021830, NM_001163812, NM_001163813, NM_001163814, hCT2352324.0, hCT15786.3	218590_at	NP_068602.2, NP_001157284.1, NP_001157285.1, NP_001157286.1, EAW49793.1, EAW49794.1
GeneID:84445	LZTS2	10	102,756,965	102,767,590	10,625	+	4	1_A375_pNL7_minus_lncRNA::1::946, 2_A375_pNL97_plus_lncRNA::1::1302, 2_A375_pNL97_plus_lncRNA::1::1303, 2_A375_pNL97_plus_lncRNA::1::1304	-9765, -9829, 1563, 11611	upstream, upstream, in gene, downstream	1	1	14.33	19.67	3	2_A375_pNL97_plus_lncRNA::1	22	Gene LZTS2	LAPSER1, KIAA1813, LZTS2	leucine zipper, putative tumor suppressor 2	NM_032429, hCT2322379.0, hCT2352327.0, hCT15788.3	1555851_s_at, 224473_x_at, 225013_at, 232129_s_at	NP_115805.1, EAW49792.1, EAW49790.1, EAW49791.1
GeneID:79955	PDZD7	10	102,777,089	102,790,879	13,790	-	2	1_A375_pNL7_minus_lncRNA::1::947, 2_A375_pNL97_plus_lncRNA::1::1304	-1633, 22303	upstream, downstream	1	1	16.5	19	2	1_A375_pNL7_minus_lncRNA::1	22	Gene PDZD7	PDZD7, PDZK7	PDZ domain containing 7	NM_024895, hCT15790.3	220555_s_at	NP_079171.1, EAW49788.1
GeneID:81855	SFXN3	10	102,790,996	102,800,998	10,002	+	1	1_A375_pNL7_minus_lncRNA::1::947	1516	in gene	1	0	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene SFXN3	SFXN3, BA108L7.2, SFX3	sideroflexin 3	NM_030971, hCT2322381.0	1559993_at, 217226_s_at, 220974_x_at	NP_112233.2, EAW49787.1
GeneID:100038246	TLX1NB	10	102,849,078	102,890,903	41,825	-	4	1_A375_pNL7_minus_lncRNA::1::948, 1_A375_pNL7_minus_lncRNA::1::949, 2_A375_pNL97_plus_lncRNA::1::1305, 2_A375_pNL97_plus_lncRNA::1::1306	49975, 45047, 50039, 45111	downstream, downstream, downstream, downstream	1	1	19.5	24	2	2_A375_pNL97_plus_lncRNA::1	26	Gene TLX1NB	TDI, TLX1NB, APT-B7, TD1	TLX1 neighbor	NM_001085398		NP_001078867.1
GeneID:8945	BTRC	10	103,113,825	103,317,070	203,245	+	4	1_A375_pNL7_minus_lncRNA::1::950, 1_A375_pNL7_minus_lncRNA::1::951, 2_A375_pNL97_plus_lncRNA::1::1307, 2_A375_pNL97_plus_lncRNA::1::1308	-145, 10799, -177, 10783	upstream, in gene, upstream, in gene	1	1	23.5	31.5	2	2_A375_pNL97_plus_lncRNA::1	41	Gene BTRC	betaTrCP, FBXW1, FWD1, BETA-TRCP, bTrCP1, FBW1A, FBXW1A, bTrCP, BTRC, MGC4643	beta-transducin repeat containing	NM_033637, NM_003939, hCT2322296.1, hCT2322297.1, hCT2322299.1, hCT2352363.0, hCT1951242.1	1563620_at, 204901_at, 216091_s_at, 222374_at, 224471_s_at	NP_378663.1, NP_003930.1, EAW49770.1, EAW49771.1, EAW49773.1, EAW49774.1, EAW49772.1
GeneID:6468	FBXW4	10	103,370,421	103,454,743	84,322	-	1	2_A375_pNL97_plus_lncRNA::1::1309	663	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FBXW4	SHSF3, FBWD4, DAC, SHFM3, FBXW4, FBW4	F-box and WD repeat domain containing 4	NM_022039, hCT2321971.1, hCT2348003.0, hCT1814001.2	221519_at	NP_071322.1, EAW49751.1, EAW49752.1, EAW49753.1
GeneID:2253	FGF8	10	103,529,887	103,535,759	5,872	-	1	2_A375_pNL97_plus_lncRNA::1::1310	-7601	upstream	0	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene FGF8	AIGF, HBGF-8, FGF8, MGC149376, KAL6	fibroblast growth factor 8 (androgen-induced)	NM_006119, NM_033163, NM_033164, NM_033165, hCT1967402.1, hCT2321966.0, hCT2321968.0, hCT2352296.0, hCT16758.3	208449_s_at	NP_006110.1, NP_149353.1, NP_149354.1, NP_149355.1, EAW49746.1, EAW49749.1, EAW49747.1, EAW49748.1, EAW49750.1
GeneID:10360	NPM3	10	103,541,082	103,543,170	2,088	-	1	2_A375_pNL97_plus_lncRNA::1::1310	-190	upstream	0	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene NPM3	PORMIN, TMEM123, NPM3	nucleophosmin/nucleoplasmin 3	NM_006993, hCT16757.3	205129_at	NP_008924.1, EAW49745.1
GeneID:10724	MGEA5	10	103,544,200	103,578,222	34,022	-	3	1_A375_pNL7_minus_lncRNA::1::952, 2_A375_pNL97_plus_lncRNA::1::1310, 2_A375_pNL97_plus_lncRNA::1::1311	-82, 34862, -178	upstream, downstream, upstream	1	1	26	26	2	1_A375_pNL7_minus_lncRNA::1	34	Gene MGEA5	OGA, NCOAT, FLJ11229, KIAA0679, MGEA5, MEA5, FLJ23355	meningioma expressed antigen 5 (hyaluronidase)	NM_012215, NM_001142434, hCT2321962.0, hCT2321964.0, hCT2352323.0, hCT16770.3	200898_s_at, 200899_s_at, 214972_at, 223494_at, 235868_at	NP_036347.1, NP_001135906.1, EAW49741.1, EAW49742.1, EAW49743.1, EAW49744.1
GeneID:100289509	LOC100289509	10	103,578,825	103,588,646	9,821	+	2	1_A375_pNL7_minus_lncRNA::1::952, 2_A375_pNL97_plus_lncRNA::1::1311	-521, -425	upstream, upstream	1	1	34	33	1	1_A375_pNL7_minus_lncRNA::1	34	Gene LOC100289509		hypothetical LOC100289509	XR_111126, XR_110447, XR_114422		
GeneID:30819	KCNIP2	10	103,585,731	103,603,677	17,946	-	4	1_A375_pNL7_minus_lncRNA::1::952, 1_A375_pNL7_minus_lncRNA::1::953, 2_A375_pNL97_plus_lncRNA::1::1311, 2_A375_pNL97_plus_lncRNA::1::1312	25373, 2557, 25277, 2557	downstream, in gene, downstream, in gene	1	1	35.5	42	2	2_A375_pNL97_plus_lncRNA::1	51	Gene KCNIP2	MGC17241, KCHIP2, KCNIP2, DKFZp566L1246	Kv channel interacting protein 2	NM_173192, NM_173195, NM_173194, NM_173197, NM_173191, NM_014591, NM_173193, hCT2321950.0, hCT2321952.0, hCT2321953.0, hCT2321955.0, hCT2321956.0, hCT2321957.0, hCT2321958.0, hCT16759.3, hCT1951251.2, hCT1951252.2, hCT1951253.2	1555230_a_at, 221321_s_at, 223727_at, 224528_s_at	NP_775284.1, NP_775287.1, NP_055406.2, NP_775283.1, NP_775286.1, NP_775289.1, NP_775285.1, EAW49730.1, EAW49731.1, EAW49732.1, EAW49733.1, EAW49734.1, EAW49735.1, EAW49740.1, EAW49736.1, EAW49737.1, EAW49738.1, EAW49739.1
GeneID:79591	C10orf76	10	103,605,356	103,815,932	210,576	-	5	1_A375_pNL7_minus_lncRNA::1::953, 1_A375_pNL7_minus_lncRNA::1::954, 2_A375_pNL97_plus_lncRNA::1::1312, 2_A375_pNL97_plus_lncRNA::1::1313, 2_A375_pNL97_plus_lncRNA::1::1314	214812, 28, 214812, -4, -9092	downstream, in gene, downstream, upstream, upstream	1	1	28	34.67	3	2_A375_pNL97_plus_lncRNA::1	51	Gene C10orf76	FLJ13114, MGC125927, C10orf76	chromosome 10 open reading frame 76	NM_024541, hCT2321946.0, hCT2321948.0, hCT1951256.1	1566733_at, 218891_at, 55662_at	NP_078817.2, EAW49728.1, EAW49727.1, EAW49729.1
GeneID:79803	HPS6	10	103,825,147	103,827,793	2,646	+	3	1_A375_pNL7_minus_lncRNA::1::954, 2_A375_pNL97_plus_lncRNA::1::1313, 2_A375_pNL97_plus_lncRNA::1::1314	-9243, -9211, -123	upstream, upstream, upstream	1	1	23.5	26.5	2	2_A375_pNL97_plus_lncRNA::1	34	Gene HPS6	FLJ22501, HPS6, MGC20522, RP11-302K17.1	Hermansky-Pudlak syndrome 6	NM_024747, hCT2322306.0, hCT2322307.0	219052_at, 230371_at	NP_079023.2, EAW49725.1, EAW49726.1
GeneID:23082	PPRC1	10	103,892,787	103,910,090	17,303	+	3	1_A375_pNL7_minus_lncRNA::1::955, 2_A375_pNL97_plus_lncRNA::1::1315, 2_A375_pNL97_plus_lncRNA::1::1316	-147, -115, 19117	upstream, upstream, downstream	1	1	27.5	28	2	1_A375_pNL7_minus_lncRNA::1	38	Gene PPRC1	MGC74642, PPRC1, PRC, RP11-302K17.6, KIAA0595	peroxisome proliferator-activated receptor gamma, coactivator-related 1	NM_015062, hCT2322309.0, hCT2352320.0, hCT16766.3	203737_s_at	NP_055877.3, EAW49719.1, EAW49720.1, EAW49721.1
GeneID:9221	NOLC1	10	103,911,933	103,923,627	11,694	+	1	2_A375_pNL97_plus_lncRNA::1::1316	-29	upstream	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene NOLC1	NOPP130, KIAA0035, NOPP140, NOLC1, NS5ATP13, P130	nucleolar and coiled-body phosphoprotein 1	NM_004741, hCT1967404.1, hCT1967405.1, hCT2352302.0, hCT2352303.0, hCT2352304.0, hCT16761.3	205895_s_at, 211949_s_at, 211951_at	NP_004732.2, EAW49715.1, EAW49713.1, EAW49716.1, EAW49717.1, EAW49718.1, EAW49714.1
GeneID:5309	PITX3	10	103,989,946	104,001,231	11,285	-	1	1_A375_pNL7_minus_lncRNA::1::956	-4081	upstream	1	0	20	13	1	1_A375_pNL7_minus_lncRNA::1	20	Gene PITX3	MGC12766, PTX3, PITX3, CTPP4	paired-like homeodomain 3	NM_005029, hCT2321942.0, hCT16763.3	208277_at	NP_005020.1, EAW49709.1, EAW49710.1
GeneID:8729	GBF1	10	104,005,309	104,142,649	137,340	+	2	1_A375_pNL7_minus_lncRNA::1::956, 2_A375_pNL97_plus_lncRNA::1::1317	3, 116291	in gene, in gene	1	1	16	15.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene GBF1	KIAA0248, FLJ21263, MGC134878, ARF1GEF, MGC134877, FLJ21500, GBF1	golgi brefeldin A resistant guanine nucleotide exchange factor 1	NM_004193, hCT2344326.1	201439_at	NP_004184.1, EAW49707.1
GeneID:4791	NFKB2	10	104,154,229	104,162,281	8,052	+	1	2_A375_pNL97_plus_lncRNA::1::1318	-85	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene NFKB2	NFKB2, p52, LYT10, LYT-10	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NM_002502, NM_001077494, NM_001077493, hCT2322137.0, hCT2322138.0, hCT2322139.0, hCT2322140.0, hCT2352307.0, hCT1686444.2, hCT1820469.1	207535_s_at, 209636_at, 211524_at	NP_002493.3, NP_001070962.1, NP_001070961.1, EAW49701.1, EAW49702.1, EAW49704.1, EAW49700.1, EAW49703.1, EAW49705.1, EAW49706.1
GeneID:5662	PSD	10	104,162,376	104,178,901	16,525	-	4	1_A375_pNL7_minus_lncRNA::1::957, 2_A375_pNL97_plus_lncRNA::1::1318, 2_A375_pNL97_plus_lncRNA::1::1319, 2_A375_pNL97_plus_lncRNA::1::1320	-1867, 24757, -603, -1867	upstream, downstream, upstream, upstream	1	1	28	32.67	3	2_A375_pNL97_plus_lncRNA::1	60	Gene PSD	TYL, KIAA2011, PSD1, PSD	pleckstrin and Sec7 domain containing	NM_002779, hCT2321910.0, hCT2321911.0, hCT16771.3	208102_s_at	NP_002770.3, EAW49693.1, EAW49694.1, EAW49695.1
GeneID:79176	FBXL15	10	104,179,571	104,182,893	3,322	+	5	1_A375_pNL7_minus_lncRNA::1::957, 1_A375_pNL7_minus_lncRNA::1::958, 2_A375_pNL97_plus_lncRNA::1::1319, 2_A375_pNL97_plus_lncRNA::1::1320, 2_A375_pNL97_plus_lncRNA::1::1321	1197, 12877, -67, 1197, 12781	in gene, downstream, upstream, in gene, downstream	1	1	29.67	34.33	3	2_A375_pNL97_plus_lncRNA::1	60	Gene FBXL15	FLJ16137, Fbl15, FBXO37, FBXL15, MGC11279, JET, PSD	F-box and leucine-rich repeat protein 15	NM_024326, hCT16772.3	218938_at	NP_077302.3, EAW49699.1
GeneID:100286939	LOC100286939	10	104,181,242	104,182,893	1,651	-	5	1_A375_pNL7_minus_lncRNA::1::957, 1_A375_pNL7_minus_lncRNA::1::958, 2_A375_pNL97_plus_lncRNA::1::1319, 2_A375_pNL97_plus_lncRNA::1::1320, 2_A375_pNL97_plus_lncRNA::1::1321	2125, -9555, 3389, 2125, -9459	downstream, upstream, downstream, downstream, upstream	1	1	29.67	34.33	3	2_A375_pNL97_plus_lncRNA::1	60	Gene LOC100286939		hypothetical protein LOC100286939	XM_003119474, XM_002343013, XM_003120659		XP_003119522.1, XP_002343054.1, XP_003120707.1
GeneID:79004	CUEDC2	10	104,183,002	104,192,423	9,421	-	5	1_A375_pNL7_minus_lncRNA::1::957, 1_A375_pNL7_minus_lncRNA::1::958, 2_A375_pNL97_plus_lncRNA::1::1319, 2_A375_pNL97_plus_lncRNA::1::1320, 2_A375_pNL97_plus_lncRNA::1::1321	11655, -25, 12919, 11655, 71	downstream, upstream, downstream, downstream, in gene	1	1	29.67	34.33	3	2_A375_pNL97_plus_lncRNA::1	60	Gene CUEDC2	CUEDC2, MGC2491, C10orf66, bA18I14.5	CUE domain containing 2	NM_024040, hCT2321907.0, hCT2321908.0, hCT16773.3	218097_s_at	NP_076945.2, EAW49698.1, EAW49696.1, EAW49697.1
GeneID:574447	MIR146B	10	104,196,269	104,196,341	72	+	2	1_A375_pNL7_minus_lncRNA::1::958, 2_A375_pNL97_plus_lncRNA::1::1321	-3821, -3917	upstream, upstream	1	1	21	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene MIR146B	MIRN146B, miRNA146B, MIR146B	microRNA 146b	NR_030169		
GeneID:10121	ACTR1A	10	104,238,986	104,262,512	23,526	-	2	1_A375_pNL7_minus_lncRNA::1::959, 2_A375_pNL97_plus_lncRNA::1::1322	-1136, -112	upstream, upstream	1	1	21.5	18	2	1_A375_pNL7_minus_lncRNA::1	23	Gene ACTR1A	CTRN1, ACTR1A, ARP1, FLJ52800, FLJ55002, FLJ52695	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	NM_005736, hCT2321901.1, hCT2321902.1, hCT2340897.0, hCT14106.2	200720_s_at, 200721_s_at, 236713_at	NP_005727.1, EAW49686.1, EAW49685.1, EAW49687.1, EAW49688.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:51684	SUFU	10	104,263,719	104,393,214	129,495	+	2	1_A375_pNL7_minus_lncRNA::1::959, 2_A375_pNL97_plus_lncRNA::1::1322	-71, -1095	upstream, upstream	1	1	21.5	18	2	1_A375_pNL7_minus_lncRNA::1	23	Gene SUFU	PRO1280, SUFUXL, SUFUH, SUFU	suppressor of fused homolog (Drosophila)	NM_001178133, NM_016169, hCT2322155.0, hCT2322156.0, hCT2322157.0, hCT2352308.0	222749_at, 224201_s_at, 224202_at, 224203_at	NP_001171604.1, NP_057253.2, EAW49681.1, EAW49682.1, EAW49683.1, EAW49684.1
GeneID:81603	TRIM8	10	104,404,252	104,418,076	13,824	+	1	1_A375_pNL7_minus_lncRNA::1::960	1508	in gene	1	0	20	15	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TRIM8	RNF27, TRIM8, GERP	tripartite motif containing 8	NM_030912, hCT2322158.0, hCT13680.2	221012_s_at, 223131_s_at, 223132_s_at, 226015_s_at	NP_112174.2, EAW49679.1, EAW49680.1
GeneID:403	ARL3	10	104,433,468	104,474,190	40,702	-	1	2_A375_pNL97_plus_lncRNA::1::1323	462	in gene	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ARL3	ARL3, ARFL3	ADP-ribosylation factor-like 3	NM_004311, hCT13675.1	1566590_at, 202641_at, 213433_at	NP_004302.1, EAW49678.1
GeneID:118980	SFXN2	10	104,474,298	104,498,946	24,648	+	1	2_A375_pNL97_plus_lncRNA::1::1323	-570	upstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SFXN2	SFXN2	sideroflexin 2	NM_178858, hCT2322162.1, hCT2349219.0, hCT13681.4	227560_at	NP_849189.1, EAW49676.1, EAW49675.1, EAW49677.1
GeneID:119032	C10orf32	10	104,613,967	104,624,718	10,751	+	1	2_A375_pNL97_plus_lncRNA::1::1324	209	in gene	0	1	15	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene C10orf32	FLJ40752, MGC27171, C10orf32, DKFZp686B2219, RP11-753C18.6	chromosome 10 open reading frame 32	NM_144591, NM_001136200	225334_at	NP_653192.2, NP_001129672.1
GeneID:22978	NT5C2	10	104,845,940	104,953,056	107,116	-	1	2_A375_pNL97_plus_lncRNA::1::1325	336	in gene	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene NT5C2	NT5C2, cN-II, PNT5, NT5B, GMP	5'-nucleotidase, cytosolic II	NM_012229, NM_001134373, hCT2321894.0, hCT12939.3	209155_s_at, 241778_at	NP_036361.1, NP_001127845.1, EAW49656.1, EAW49657.1
GeneID:729020	hCG_2024410	10	105,005,644	105,007,773	2,129	+	1	1_A375_pNL7_minus_lncRNA::1::961	-4252	upstream	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene hCG_2024410	LOC729020	rCRPE	NM_001143909		NP_001137381.1
GeneID:9118	INA	10	105,036,920	105,050,108	13,188	+	4	1_A375_pNL7_minus_lncRNA::1::962, 1_A375_pNL7_minus_lncRNA::1::963, 2_A375_pNL97_plus_lncRNA::1::1327, 2_A375_pNL97_plus_lncRNA::1::1328	-3992, 1736, -3992, 1768	upstream, in gene, upstream, in gene	1	1	31	38.5	2	2_A375_pNL97_plus_lncRNA::1	42	Gene INA	NF-66, MGC12702, FLJ57501, FLJ18662, TXBP-1, INA, NEF5	internexin neuronal intermediate filament protein, alpha	NM_032727, hCT2322182.0, hCT15249.2	204465_s_at	NP_116116.1, EAW49653.1, EAW49654.1
GeneID:84108	PCGF6	10	105,062,553	105,110,891	48,338	-	2	1_A375_pNL7_minus_lncRNA::1::964, 2_A375_pNL97_plus_lncRNA::1::1329	459, 43	in gene, in gene	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PCGF6	PCGF6, MGC17541, RNF134, MBLR, MGC15678	polycomb group ring finger 6	NM_032154, NM_001011663, hCT1967341.1, hCT2321887.0, hCT2321889.0, hCT2352365.0, hCT2352366.0, hCT1951243.1	224326_s_at	NP_115530.2, NP_001011663.1, EAW49648.1, EAW49649.1, EAW49650.1, EAW49652.1, EAW49647.1, EAW49651.1
GeneID:6877	TAF5	10	105,127,724	105,148,822	21,098	+	1	2_A375_pNL97_plus_lncRNA::1::1330	148	in gene	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TAF5	TAF5, TAF2D, TAFII100	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	NM_006951, hCT2352226.0, hCT15246.3	1553528_a_at, 210053_at	NP_008882.2, EAW49646.1, EAW49645.1
GeneID:9644	SH3PXD2A	10	105,353,784	105,615,164	261,380	-	8	1_A375_pNL7_minus_lncRNA::1::965, 1_A375_pNL7_minus_lncRNA::1::966, 1_A375_pNL7_minus_lncRNA::1::967, 2_A375_pNL97_plus_lncRNA::1::1331, 2_A375_pNL97_plus_lncRNA::1::1332, 2_A375_pNL97_plus_lncRNA::1::1333, 2_A375_pNL97_plus_lncRNA::1::1334, 2_A375_pNL97_plus_lncRNA	194908, 108188, 27116, 194812, 108060, 54444, 26556, -6372	in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	1	1	17.4	19.6	5	2_A375_pNL97_plus_lncRNA::1	24	Gene SH3PXD2A	SH3MD1, FISH, SH3PXD2A, TSK5	SH3 and PX domains 2A	NM_014631, hCT2321414.0, hCT2321415.0, hCT2321416.0, hCT1951241.1	207661_s_at, 213252_at, 224817_at	NP_055446.2, EAW49625.1, EAW49622.1, EAW49623.1, EAW49624.1
GeneID:100505839	LOC100505839	10	105,506,537	105,515,167	8,630	+	2	1_A375_pNL7_minus_lncRNA::1::966, 2_A375_pNL97_plus_lncRNA::1::1332	439, 567	in gene, in gene	1	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100505839		hypothetical LOC100505839	XR_110452		
GeneID:79991	OBFC1	10	105,637,316	105,678,045	40,729	-	1	2_A375_pNL97_plus_lncRNA::1::1336	22461	in gene	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene OBFC1	STN1, bA541N10.2, RPA-32, AAF-44, OBFC1, RP11-541N10.2, AAF44, FLJ22559	oligonucleotide/oligosaccharide-binding fold containing 1	NM_024928, hCT15252.3, hCT1957992.1	219100_at	NP_079204.2, EAW49620.1, EAW49619.1
GeneID:119392	C10orf78	10	105,881,816	105,886,143	4,327	+	1	1_A375_pNL7_minus_lncRNA::1::969	-248	upstream	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene C10orf78	MEIR5, bA373N18.1, MEI5, FLJ41960, C10orf78	MEI5 meiotic recombination protein homolog (S. cerevisiae)	NM_145247, NM_001002759, hCT1647813.3, hCT1951235.1	236027_at, 238794_at	NP_660290.3, NP_001002759.1, EAW49610.1, EAW49611.1
GeneID:80217	C10orf79	10	105,889,646	105,992,120	102,474	-	2	1_A375_pNL7_minus_lncRNA::1::969, 2_A375_pNL97_plus_lncRNA::1::1337	110552, 152	downstream, in gene	1	1	14	18	2	2_A375_pNL97_plus_lncRNA::1	23	Gene C10orf79	bA373N18.2, FLJ22944, C10orf79, FLJ36006, WDR96	WD repeat domain 96	NM_025145, hCT2349220.1, hCT2349221.0, hCT2349222.1, hCT14247.4, hCT1961047.2	220919_s_at, 224251_at, 231084_at, 243896_at	NP_079421.5, EAW49608.1, EAW49605.1, EAW49606.1, EAW49607.1, EAW49609.1
GeneID:9446	GSTO1	10	106,013,952	106,027,222	13,270	+	1	2_A375_pNL97_plus_lncRNA::1::1338	512	in gene	0	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene GSTO1	DKFZp686H13163, GSTTLp28, GSTO1, P28	glutathione S-transferase omega 1	NM_001191002, NM_001191003, NM_004832, hCT12937.3, hCT1962309.1, hCT1962310.0, hCT1962311.0	1557915_s_at, 201470_at	NP_001177931.1, NP_001177932.1, NP_004823.1, EAW49601.1, EAW49602.1, EAW49604.1, EAW49603.1
GeneID:119391	GSTO2	10	106,028,631	106,059,176	30,545	+	1	2_A375_pNL97_plus_lncRNA::1::1339	31721	downstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene GSTO2	bA127L20.1, GSTO2	glutathione S-transferase omega 2	NM_183239, NM_001191013, NM_001191014, NM_001191015, hCT1960706.2, hCT1964896.1, hCT1964897.1	227163_at	NP_899062.1, NP_001177942.1, NP_001177943.1, NP_001177944.1, EAW49598.1, EAW49600.1, EAW49599.1
GeneID:85450	ITPRIP	10	106,071,899	106,093,663	21,764	-	4	1_A375_pNL7_minus_lncRNA::1::970, 1_A375_pNL7_minus_lncRNA::1::971, 2_A375_pNL97_plus_lncRNA::1::1340, 2_A375_pNL97_plus_lncRNA::1::1341	4415, -4769, 4415, -4769	in gene, upstream, in gene, upstream	1	1	39	36.5	2	2_A375_pNL97_plus_lncRNA::1	52	Gene ITPRIP	DANGER, KIAA1754, bA127L20.2, ITPRIP, bA127L20	inositol 1,4,5-triphosphate receptor interacting protein	NM_033397, hCT1657457.3, hCT1952594.1	225582_at	NP_203755.1, EAW49597.1, EAW49596.1
GeneID:100505856	LOC100505856	10	106,083,122	106,086,762	3,640	+	2	1_A375_pNL7_minus_lncRNA::1::970, 2_A375_pNL97_plus_lncRNA::1::1340	6126, 6126	downstream, downstream	1	1	26	21	1	1_A375_pNL7_minus_lncRNA::1	26	Gene LOC100505856		hypothetical LOC100505856	XR_111119, XR_110453, XR_114428		
GeneID:22986	SORCS3	10	106,400,859	107,024,993	624,134	+	3	1_A375_pNL7_minus_lncRNA::1::972, 1_A375_pNL7_minus_lncRNA::1::973, 2_A375_pNL97_plus_lncRNA::1::1343	183493, 296629, 183461	in gene, in gene, in gene	1	1	39.5	49.5	2	2_A375_pNL97_plus_lncRNA::1	60	Gene SORCS3	SORCS3, SORCS	sortilin-related VPS10 domain containing receptor 3	NM_014978, hCT2344376.2, hCT2351174.0	215522_at	NP_055793.1, EAW49590.1, EAW49589.1
GeneID:120	ADD3	10	111,765,726	111,895,323	129,597	+	3	1_A375_pNL7_minus_lncRNA::1::974, 2_A375_pNL97_plus_lncRNA::1::1346, 2_A375_pNL97_plus_lncRNA::1::1347	1394, 1442, 71042	in gene, in gene, in gene	1	1	12.5	17.5	2	2_A375_pNL97_plus_lncRNA::1	20	Gene ADD3	ADDL, ADD3	adducin 3 (gamma)	NM_016824, NM_001121, NM_019903, hCT2321217.0, hCT2321219.0, hCT2321221.0, hCT1964113.1	201034_at, 201752_s_at, 201753_s_at, 205882_x_at	NP_058432.1, NP_001112.2, NP_063968.1, EAW49571.1, EAW49572.1, EAW49574.1, EAW49573.1
GeneID:4601	MXI1	10	111,967,363	112,047,123	79,760	+	2	1_A375_pNL7_minus_lncRNA::1::975, 2_A375_pNL97_plus_lncRNA::1::1348	-67, 3117	upstream, in gene	1	1	18	15	2	1_A375_pNL7_minus_lncRNA::1	20	Gene MXI1	bHLHc11, MXI1, MXD2, MGC43220, MXI, MAD2	MAX interactor 1	NM_130439, NM_005962, NM_001008541, hCT2321200.0, hCT2321201.0, hCT2321203.0, hCT2321204.0, hCT1951738.1, hCT1951739.1	202364_at	NP_569157.2, NP_005953.4, NP_001008541.1, EAW49565.1, EAW49567.1, EAW49568.1, EAW49566.1, EAW49569.1, EAW49570.1
GeneID:1847	DUSP5	10	112,257,625	112,271,302	13,677	+	2	2_A375_pNL97_plus_lncRNA::1::1351, 2_A375_pNL97_plus_lncRNA::1::1352	-217, 791	upstream, in gene	0	1	10.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene DUSP5	DUSP5, HVH3, DUSP	dual specificity phosphatase 5	NM_004419, hCT2321209.0, hCT1951740.1	209457_at	NP_004410.3, EAW49560.1, EAW49559.1
GeneID:9126	SMC3	10	112,327,449	112,364,392	36,943	+	2	1_A375_pNL7_minus_lncRNA::1::979, 2_A375_pNL97_plus_lncRNA::1::1355	-217, -153	upstream, upstream	1	1	40	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene SMC3	HCAP, BAM, SMC3, CSPG6, SMC3L1, CDLS3, BMH	structural maintenance of chromosomes 3	NM_005445, hCT2321211.0, hCT2321212.0	1556925_at, 209257_s_at, 209258_s_at, 209259_s_at	NP_005436.1, EAW49558.1, EAW49557.1
GeneID:282996	RBM20	10	112,404,155	112,599,227	195,072	+	4	1_A375_pNL7_minus_lncRNA::1::980, 1_A375_pNL7_minus_lncRNA::1::981, 2_A375_pNL97_plus_lncRNA::1::1356, 2_A375_pNL97_plus_lncRNA::1::1357	28101, 130032, 28133, 129973	in gene, in gene, in gene, in gene	1	1	20.5	22	2	1_A375_pNL7_minus_lncRNA::1	26	Gene RBM20	RBM20		NM_001134363	238763_at	NP_001127835.1
GeneID:92482	NCRNA00081	10	112,658,488	112,679,124	20,636	-	2	1_A375_pNL7_minus_lncRNA::1::982, 2_A375_pNL97_plus_lncRNA::1::1358	100, 116	in gene, in gene	1	1	23	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene NCRNA00081	bA348N5.3, BBIP10, BBIP1, NCRNA00081	BBSome interacting protein 1	NR_024141	213220_at, 213224_s_at, 228993_s_at, 232885_at, 232910_at, 236043_at, 238664_at	
GeneID:8036	SHOC2	10	112,679,301	112,773,425	94,124	+	2	1_A375_pNL7_minus_lncRNA::1::982, 2_A375_pNL97_plus_lncRNA::1::1358	-277, -293	upstream, upstream	1	1	23	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SHOC2	SUR8, SIAA0862, KIAA0862, SOC-2, FLJ60412, SOC2, SHOC2, SUR-8	soc-2 suppressor of clear homolog (C. elegans)	NM_007373, hCT2352294.0, hCT31986.3, hCT1962345.0	202777_at	NP_031399.2, EAW49550.1, EAW49548.1, EAW49549.1
GeneID:57678	GPAM	10	113,909,622	113,943,525	33,903	-	2	1_A375_pNL7_minus_lncRNA::1::985, 2_A375_pNL97_plus_lncRNA::1::1361	-91, -59	upstream, upstream	1	1	21	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene GPAM	RP11-426E5.2, KIAA1560, GPAM, GPAT1, MGC26846, GPAT	glycerol-3-phosphate acyltransferase, mitochondrial	NM_020918, hCT2352255.0, hCT2352256.0, hCT32243.3	225420_at, 225424_at	NP_065969.3, EAW49544.1, EAW49543.1, EAW49545.1
GeneID:64429	ZDHHC6	10	114,190,058	114,206,672	16,614	-	2	1_A375_pNL7_minus_lncRNA::1::986, 2_A375_pNL97_plus_lncRNA::1::1362	-128, 64	upstream, in gene	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ZDHHC6	ZNF376, ZDHHC6, FLJ21952	zinc finger, DHHC-type containing 6	NM_022494, hCT2320967.0, hCT2352257.0, hCT2352258.0, hCT32244.3, hCT1955000.1, hCT1955001.1	216249_at	NP_071939.1, EAW49528.1, EAW49526.1, EAW49529.1, EAW49530.1, EAW49531.1, EAW49527.1
GeneID:143187	VTI1A	10	114,206,756	114,578,503	371,747	+	3	1_A375_pNL7_minus_lncRNA::1::986, 1_A375_pNL7_minus_lncRNA::1::987, 2_A375_pNL97_plus_lncRNA::1::1362	44, 167260, -148	in gene, in gene, upstream	1	1	17.5	12.5	2	1_A375_pNL7_minus_lncRNA::1	19	Gene VTI1A	Vti1-rp2, VTI1A, MVti1	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	NM_145206, hCT2349195.0, hCT1951726.1	1552536_at, 235034_at, 235923_at, 236849_at, 242356_at	NP_660207.2, EAW49525.1, EAW49524.1
GeneID:100422909	MIR4295	10	114,393,929	114,394,013	84	+	1	1_A375_pNL7_minus_lncRNA::1::987	87	downstream	1	0	16	8	1	1_A375_pNL7_minus_lncRNA::1	16	Gene MIR4295	MIR4295	microRNA 4295	NR_036177		
GeneID:6934	TCF7L2	10	114,710,009	114,927,437	217,428	+	3	1_A375_pNL7_minus_lncRNA::1::988, 2_A375_pNL97_plus_lncRNA::1::1363, 2_A375_pNL97_plus_lncRNA::1::1364	41991, 9255, 41991	in gene, in gene, in gene	1	1	17.5	18	2	1_A375_pNL7_minus_lncRNA::1	23	Gene TCF7L2	TCF4, TCF-4, TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	NM_001146283, NM_001146284, NM_001146285, NM_001146286, NM_030756, NM_001146274, hCT2322954.0, hCT2322955.0, hCT2322956.0, hCT2322957.0, hCT2322958.0, hCT2322959.0, hCT2322960.0, hCT2322961.0, hCT2322963.0, hCT2352336.0, hCT2352337.0, hCT32266.3	212759_s_at, 212761_at, 212762_s_at, 216035_x_at, 216037_x_at, 216511_s_at, 236094_at	NP_001139755.1, NP_001139756.1, NP_110383.2, NP_001139757.1, NP_001139758.1, NP_001139746.1, EAW49506.1, EAW49507.1, EAW49508.1, EAW49509.1, EAW49510.1, EAW49511.1, EAW49513.1, EAW49516.1, EAW49512.1, EAW49514.1, EAW49515.1, EAW49517.1
GeneID:840	CASP7	10	115,438,935	115,490,664	51,729	+	2	1_A375_pNL7_minus_lncRNA::1::990, 2_A375_pNL97_plus_lncRNA::1::1366	521, 137	in gene, in gene	1	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CASP7	CMH-1, CASP7, MCH3, ICE-LAP3	caspase 7, apoptosis-related cysteine peptidase	NM_033340, NM_001227, NM_033339, NM_033338, hCT2322972.0, hCT2352293.0, hCT1820339.2, hCT1957988.1, hCT1962044.1	207181_s_at	NP_203126.1, NP_001218.1, NP_203124.1, NP_203125.1, EAW49495.1, EAW49496.1, EAW49494.1, EAW49497.1, EAW49498.1
GeneID:9937	DCLRE1A	10	115,594,484	115,613,859	19,375	-	2	1_A375_pNL7_minus_lncRNA::1::991, 2_A375_pNL97_plus_lncRNA::1::1367	-205, -893	upstream, upstream	1	1	14.5	16	2	2_A375_pNL97_plus_lncRNA::1	18	Gene DCLRE1A	SNM1, KIAA0086, PSO2, SNM1A, DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)	NM_014881, hCT2320951.0, hCT32263.2	209804_at	NP_055696.3, EAW49489.1, EAW49490.1
GeneID:374354	NHLRC2	10	115,614,391	115,672,265	57,874	+	2	1_A375_pNL7_minus_lncRNA::1::991, 2_A375_pNL97_plus_lncRNA::1::1367	-327, 361	upstream, in gene	1	1	14.5	16	2	2_A375_pNL97_plus_lncRNA::1	18	Gene NHLRC2	FLJ20147, FLJ33312, NHLRC2, DKFZp779F115, FLJ25621, MGC45492	NHL repeat containing 2	NM_198514, hCT2352329.0, hCT32264.2	219353_at, 235356_at, 236185_at, 244320_at	NP_940916.2, EAW49488.1, EAW49487.1
GeneID:55088	C10orf118	10	115,881,974	115,934,364	52,390	-	1	2_A375_pNL97_plus_lncRNA::1::1368	604	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C10orf118	MGC118918, C10orf118, FLJ35301, MGC129699, FLJ10188	chromosome 10 open reading frame 118	NM_018017	219544_at, 227701_at, 229399_at	NP_060487.2
GeneID:100302224	MIR2110	10	115,933,864	115,933,938	74	-	1	2_A375_pNL97_plus_lncRNA::1::1368	178	downstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene MIR2110	MIR2110, hsa-mir-2110	microRNA 2110	NR_031747		
GeneID:56165	TDRD1	10	115,939,029	115,992,063	53,034	+	1	2_A375_pNL97_plus_lncRNA::1::1368	-5269	upstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TDRD1	CT41.1, FLJ21082, TDRD1	tudor domain containing 1	NM_198795, hCT2321168.1, hCT2321169.1, hCT2343996.1, hCT2352301.0, hCT32213.4	221018_s_at	NP_942090.1, EAW49477.1, EAW49476.1, EAW49478.1, EAW49479.1, EAW49480.1
GeneID:84632	AFAP1L2	10	116,054,583	116,164,515	109,932	-	3	1_A375_pNL7_minus_lncRNA::1::992, 2_A375_pNL97_plus_lncRNA::1::1369, 2_A375_pNL97_plus_lncRNA::1::1370	58947, 15187, 9571	in gene, in gene, in gene	1	1	16.67	17	3	2_A375_pNL97_plus_lncRNA::1	24	Gene AFAP1L2	FLJ14564, AFAP1L2, XB130, KIAA1914	actin filament associated protein 1-like 2	NM_032550, NM_001001936, hCT2321075.1, hCT2349237.0, hCT2352305.0, hCT2352306.0, hCT32214.2	226829_at	NP_115939.1, NP_001001936.1, EAW49470.1, EAW49472.1, EAW49473.1, EAW49474.1, EAW49471.1
GeneID:142940	TRUB1	10	116,697,952	116,737,439	39,487	+	1	1_A375_pNL7_minus_lncRNA::1::993	32	in gene	1	0	16	19	1	1_A375_pNL7_minus_lncRNA::1	16	Gene TRUB1	TRUB1, PUS4	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	NM_139169, hCT32217.3	226339_at, 235447_at, 236020_s_at, 241605_at, 241606_s_at	NP_631908.1, EAW49463.1
GeneID:2674	GFRA1	10	117,816,436	118,033,126	216,690	-	1	1_A375_pNL7_minus_lncRNA::1::994	89734	in gene	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene GFRA1	MGC23045, TRNR1, FLJ10561, GFR-ALPHA-1, DKFZp313E1012, RET1L, FLJ31546, GFRA1, GDNFRA, DKFZp686J0156, GDNFR, RETL1	GDNF family receptor alpha 1	NM_005264, NM_145793, NM_001145453, hCT2320985.0, hCT2352362.0, hCT32231.2	205696_s_at	NP_005255.1, NP_665736.1, NP_001138925.1, EAW49456.1, EAW49457.1, EAW49458.1
GeneID:57698	KIAA1598	10	118,644,306	118,765,088	120,782	-	1	2_A375_pNL97_plus_lncRNA::1::1371	533	in gene	0	1	16	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene KIAA1598	SHOOTIN1, shootin-1, KIAA1598, MGC40476, DKFZp686A0439	KIAA1598	NM_001127211, NM_018330, hCT2321181.1, hCT2321182.1, hCT2321183.0, hCT2321184.1, hCT2352367.0	221802_s_at	NP_001120683.1, NP_060800.2, EAW49434.1, EAW49435.1, EAW49436.1, EAW49438.1, EAW49437.1
GeneID:338567	KCNK18	10	118,957,000	118,969,810	12,810	+	1	2_A375_pNL97_plus_lncRNA::1::1372	19384	downstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene KCNK18	KCNK18, TRESK, TRESK-2, TRIK, MGR13, TRESK2, K2p18.1	potassium channel, subfamily K, member 18	NM_181840		NP_862823.1
GeneID:118987	PDZD8	10	119,042,606	119,134,937	92,331	-	1	2_A375_pNL97_plus_lncRNA::1::1373	-263	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PDZD8	FLJ25412, PDZK8, PDZD8, FLJ34427, bA129M16.2	PDZ domain containing 8	NM_173791, hCT32179.3	225829_at, 225830_at	NP_776152.1, EAW49427.1
GeneID:2834	PRLHR	10	120,352,916	120,355,160	2,244	-	3	1_A375_pNL7_minus_lncRNA::1::998, 2_A375_pNL97_plus_lncRNA::1::1378, 2_A375_pNL97_plus_lncRNA::1::1379	856, 824, -584	in gene, in gene, upstream	1	1	17.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene PRLHR	GPR10, MGC126541, PrRPR, PRLHR, GR3, MGC126539	prolactin releasing hormone receptor	NM_004248, hCT2321565.0, hCT32412.2	231805_at	NP_004239.1, EAW49413.1, EAW49414.1
GeneID:143384	C10orf46	10	120,440,494	120,514,758	74,264	-	2	1_A375_pNL7_minus_lncRNA::1::999, 2_A375_pNL97_plus_lncRNA::1::1380	198, 198	in gene, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene C10orf46	MGC33215, C10orf46, FLJ40409	chromosome 10 open reading frame 46	NM_153810, hCT2350941.0, hCT32414.5	225192_at, 227136_s_at, 227137_at, 227257_s_at, 227258_at	NP_722517.3, EAW49412.1, EAW49411.1
GeneID:8661	EIF3A	10	120,794,541	120,840,334	45,793	-	1	2_A375_pNL97_plus_lncRNA::1::1381	-114	upstream	0	1	16	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene EIF3A	p180, EIF3A, P167, EIF3S10, eIF3-theta, EIF3, p185, TIF32, KIAA0139, eIF3-p170	eukaryotic translation initiation factor 3, subunit A	NM_003750, hCT32413.3	200595_s_at, 200596_s_at, 200597_at	NP_003741.1, EAW49408.1
GeneID:10935	PRDX3	10	120,927,215	120,938,345	11,130	-	1	1_A375_pNL7_minus_lncRNA::1::1000	169	in gene	1	0	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene PRDX3	SP-22, MGC104387, MER5, PRO1748, PRDX3, AOP-1, AOP1, MGC24293	peroxiredoxin 3	NM_014098, NM_006793, hCT1967449.1, hCT2352254.0, hCT29133.3, hCT1962340.1	201619_at, 209766_at	NP_054817.2, NP_006784.1, EAW49396.1, EAW49397.1, EAW49398.1, EAW49399.1
GeneID:6001	RGS10	10	121,259,339	121,302,222	42,883	-	1	2_A375_pNL97_plus_lncRNA::1::1382	43182	downstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene RGS10	RGS10	regulator of G-protein signaling 10	NM_002925, NM_001005339, hCT2320854.0, hCT31868.2, hCT1814002.1	204316_at, 204319_s_at, 214000_s_at	NP_002916.1, NP_001005339.1, EAW49389.1, EAW49390.1, EAW49391.1
GeneID:7073	TIAL1	10	121,332,977	121,356,541	23,564	-	1	2_A375_pNL97_plus_lncRNA::1::1383	-195	upstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TIAL1	MGC33401, TCBP, TIAL1, TIAR	TIA1 cytotoxic granule-associated RNA binding protein-like 1	NM_003252, NM_001033925, hCT2320851.0, hCT2320852.0, hCT31863.3, hCT1955843.1	202405_at, 202406_s_at, 217500_at	NP_003243.1, NP_001029097.1, EAW49385.1, EAW49386.1, EAW49387.1, EAW49388.1
GeneID:9531	BAG3	10	121,410,882	121,437,331	26,449	+	1	2_A375_pNL97_plus_lncRNA::1::1384	16862	in gene	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene BAG3	BAG3, BAG-3, MGC104307, CAIR-1, BIS	BCL2-associated athanogene 3	NM_004281, hCT1967457.1, hCT31862.3	217911_s_at	NP_004272.2, EAW49382.1, EAW49383.1
GeneID:11196	SEC23IP	10	121,652,223	121,701,245	49,022	+	1	1_A375_pNL7_minus_lncRNA::1::1001	-191	upstream	1	0	20	15	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SEC23IP	SEC23IP, P125, P125A, MSTP053	SEC23 interacting protein	NM_007190, hCT2320944.0, hCT2352230.0, hCT31865.3	209175_at, 209176_at, 216392_s_at	NP_009121.1, EAW49374.1, EAW49371.1, EAW49372.1, EAW49373.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:7106	TSPAN4	11	842,824	867,116	24,292	+	3	1_A375_pNL7_minus_lncRNA::1::1028, 1_A375_pNL7_minus_lncRNA::1::1029, 2_A375_pNL97_plus_lncRNA::1::1441	-7656, -104, -136	upstream, upstream, upstream	1	1	37	34.5	2	1_A375_pNL7_minus_lncRNA::1	55	Gene TSPAN4	TSPAN4, TETRASPAN, NAG-2, NAG2, TM4SF7, TSPAN-4	tetraspanin 4	NM_003271, NM_001025234, NM_001025235, NM_001025236, NM_001025237, NM_001025238, NM_001025239, hCT2272492.0, hCT2272493.0, hCT2272495.0	209263_x_at, 209264_s_at	NP_003262.1, NP_001020405.1, NP_001020406.1, NP_001020407.1, NP_001020408.1, NP_001020409.1, NP_001020410.1, EAX02409.1, EAX02410.1, EAX02411.1
GeneID:727897	MUC5B	11	1,244,295	1,283,406	39,111	+	1	2_A375_pNL97_plus_lncRNA::1::1442	2121	in gene	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MUC5B	MUC5B, MUC5, MUC9, MG1	mucin 5B, oligomeric mucus/gel-forming	NM_002458	213432_at, 222268_x_at	NP_002449.2
GeneID:54472	TOLLIP	11	1,295,598	1,330,892	35,294	-	1	1_A375_pNL7_minus_lncRNA::1::1030	-180	upstream	1	0	14	15	1	1_A375_pNL7_minus_lncRNA::1	14	Gene TOLLIP	TOLLIP, FLJ33531, IL-1RAcPIP	toll interacting protein	NM_019009, hCT2358641.0, hCT31638.3, hCT1952266.1	217930_s_at, 222469_s_at, 233881_s_at	NP_061882.2, EAX02435.1, EAX02433.1, EAX02434.1
GeneID:255512	LOC255512	11	1,330,938	1,331,937	999	+	1	1_A375_pNL7_minus_lncRNA::1::1030	134	in gene	1	0	14	15	1	1_A375_pNL7_minus_lncRNA::1	14	Gene LOC255512		hypothetical LOC255512	NR_029409	1555865_at	
GeneID:4046	LSP1	11	1,874,200	1,913,493	39,293	+	1	2_A375_pNL97_plus_lncRNA::1::1443	10440	in gene	0	1	10	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LSP1	LSP1, pp52, WP34	lymphocyte-specific protein 1	NM_002339, NM_001013253, NM_001013254, NM_001013255, hCT2271483.0, hCT2271484.0	203523_at	NP_002330.1, NP_001013271.1, NP_001013272.1, NP_001013273.1, EAX02470.1, EAX02471.1
GeneID:100423021	MIR4298	11	1,880,694	1,880,766	72	-	1	2_A375_pNL97_plus_lncRNA::1::1443	-3874	upstream	0	1	10	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIR4298	MIR4298	microRNA 4298	NR_036185		
GeneID:7140	TNNT3	11	1,940,799	1,959,936	19,137	+	2	1_A375_pNL7_minus_lncRNA::1::1031, 2_A375_pNL97_plus_lncRNA::1::1444	27783, 27809	downstream, downstream	1	1	33	51	1	2_A375_pNL97_plus_lncRNA::1	51	Gene TNNT3	DKFZp779M2348, TNNT3, TNTF	troponin T type 3 (skeletal, fast)	NM_001042782, NM_006757, NM_001042780, NM_001042781, hCT1952151.1	1569956_x_at, 205693_at	NP_001036247.1, NP_006748.1, NP_001036245.1, NP_001036246.1, EAW50569.1
GeneID:6150	MRPL23	11	1,968,502	1,977,839	9,337	+	2	1_A375_pNL7_minus_lncRNA::1::1031, 2_A375_pNL97_plus_lncRNA::1::1444	90, 106	in gene, in gene	1	1	33	51	1	2_A375_pNL97_plus_lncRNA::1	51	Gene MRPL23	RPL23, RPL23L, FLJ45367, L23MRP, MRPL23	mitochondrial ribosomal protein L23	NM_021134, hCT2271488.0, hCT2271489.0	1562392_at, 213897_s_at	NP_066957.3, EAX02472.1, EAX02473.1
GeneID:975	CD81	11	2,398,547	2,418,649	20,102	+	2	1_A375_pNL7_minus_lncRNA::1::1032, 2_A375_pNL97_plus_lncRNA::1::1445	23277, 23277	downstream, downstream	1	1	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene CD81	CD81, CVID6, TSPAN28, S5.7, TAPA1	CD81 molecule	NM_004356, hCT6502.2, hCT1952146.1	200675_at	NP_004347.1, EAX02507.1, EAX02508.1
GeneID:10078	TSSC4	11	2,423,523	2,425,106	1,583	+	2	1_A375_pNL7_minus_lncRNA::1::1032, 2_A375_pNL97_plus_lncRNA::1::1445	-1699, -1699	upstream, upstream	1	1	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene TSSC4	TSSC4		NM_005706, hCT5693.3, hCT1952140.1, hCT1952141.0, hCT1952142.1	218612_s_at	NP_005697.2, EAX02513.1, EAX02510.1, EAX02511.1, EAX02512.1
GeneID:29850	TRPM5	11	2,425,745	2,444,275	18,530	-	2	1_A375_pNL7_minus_lncRNA::1::1032, 2_A375_pNL97_plus_lncRNA::1::1445	22451, 22451	downstream, downstream	1	1	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene TRPM5	TRPM5, LTRPC5, MTR1	transient receptor potential cation channel, subfamily M, member 5	NM_014555, hCT2276358.0, hCT2358654.0, hCT7476.2	223935_at	NP_055370.1, EAX02515.1, EAX02514.1, EAX02516.1
GeneID:1028	CDKN1C	11	2,904,448	2,906,995	2,547	-	1	2_A375_pNL97_plus_lncRNA::1::1446	531	in gene	0	1	8	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene CDKN1C	KIP2, WBS, CDKN1C, BWS, p57, BWCR	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	NM_000076, NM_001122630, NM_001122631, hCT1821915.1, hCT1952649.1	213182_x_at, 213183_s_at, 213348_at, 216894_x_at, 219533_at, 219534_x_at	NP_000067.1, NP_001116102.1, NP_001116103.1, EAX02524.1, EAX02525.1
GeneID:5003	SLC22A18AS	11	2,909,327	2,925,175	15,848	-	1	2_A375_pNL97_plus_lncRNA::1::1446	18711	downstream	0	1	8	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SLC22A18AS	SLC22A18AS, SLC22A1LS, BWR1B, BWSCR1B, ORCTL2S, p27-BWR1B	solute carrier family 22 (organic cation transporter), member 18 antisense	NM_007105, hCT7473.2, hCT1952637.0	206097_at	NP_009036.2, EAX02527.1, EAX02526.1
GeneID:5002	SLC22A18	11	2,920,951	2,946,476	25,525	+	1	2_A375_pNL97_plus_lncRNA::1::1447	29561	downstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SLC22A18	BWSCR1A, IMPT1, TSSC5, SLC22A1L, p45-BWR1A, BWR1A, ITM, ORCTL2, SLC22A18, DKFZp667A184, HET	solute carrier family 22, member 18	NM_183233, NM_002555, hCT2358645.0, hCT7471.2, hCT1952636.1	204981_at	NP_899056.2, NP_002546.3, EAX02528.1, EAX02529.1, EAX02530.1
GeneID:7262	PHLDA2	11	2,949,503	2,950,650	1,147	-	1	2_A375_pNL97_plus_lncRNA::1::1447	138	in gene	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PHLDA2	IPL, BRW1C, HLDA2, PHLDA2, TSSC3, BWR1C	pleckstrin homology-like domain, family A, member 2	NM_003311, hCT7470.2	209802_at, 209803_s_at, 229494_s_at	NP_003302.1, EAX02531.1
GeneID:833	CARS	11	3,022,152	3,078,681	56,529	-	1	2_A375_pNL97_plus_lncRNA::1::1448	-119	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CARS	CARS1, CYSRS, CARS, MGC:11246	cysteinyl-tRNA synthetase	NM_001014437, NM_139273, NM_001751, NM_001194997, NR_036542, hCT2358646.0, hCT2358647.0, hCT7479.3, hCT1821926.2, hCT1952643.1, hCT1952645.1	1562436_at, 202402_s_at, 212971_at, 240982_at, 240983_s_at	NP_001014437.1, NP_644802.1, NP_001742.1, NP_001181926.1, EAX02537.1, EAX02538.1, EAX02536.1, EAX02539.1, EAX02540.1, EAX02541.1
GeneID:391	RHOG	11	3,848,208	3,862,213	14,005	-	1	2_A375_pNL97_plus_lncRNA::1::1449	-635	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene RHOG	MGC125836, RHOG, ARHG, MGC125835	ras homolog gene family, member G (rho G)	NM_001665, hCT2273843.0, hCT2273845.0, hCT2273846.0	203175_at	NP_001656.2, EAX02577.1, EAX02575.1, EAX02576.1
GeneID:6786	STIM1	11	3,876,933	4,114,440	237,507	+	1	2_A375_pNL97_plus_lncRNA::1::1450	239067	downstream	0	1	16	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene STIM1	STIM1, GOK, D11S4896E	stromal interaction molecule 1	NM_003156, hCT6247.3, hCT1950089.1	202764_at	NP_003147.2, EAX02581.1, EAX02580.1
GeneID:6240	RRM1	11	4,115,924	4,160,106	44,182	+	1	2_A375_pNL97_plus_lncRNA::1::1450	76	in gene	0	1	16	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene RRM1	RR1, RRM1, R1, RIR1	ribonucleotide reductase M1	NM_001033, hCT7193.3	201476_s_at, 201477_s_at	NP_001024.1, EAX02583.1
GeneID:55128	TRIM68	11	4,619,902	4,629,437	9,535	-	1	2_A375_pNL97_plus_lncRNA::1::1451	189	in gene	0	1	5	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TRIM68	MGC126176, SS-56, FLJ10369, TRIM68, SS56, RNF137, GC109	tripartite motif containing 68	NM_018073, hCT2270464.0, hCT13687.3	219405_at	NP_060543.5, EAW68834.1, EAW68835.1
GeneID:10612	TRIM3	11	6,469,843	6,495,205	25,362	-	2	1_A375_pNL7_minus_lncRNA::1::1033, 2_A375_pNL97_plus_lncRNA::1::1452	-7403, -7579	upstream, upstream	1	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TRIM3	BERP, TRIM3, RNF97, FLJ16135, RNF22, HAC1	tripartite motif containing 3	NM_033278, NM_006458, hCT2271163.0, hCT2271164.0, hCT2271165.0, hCT2271167.0, hCT2271169.0, hCT2271170.0, hCT2271171.0, hCT2271176.0, hCT1877198.1	204910_s_at, 204911_s_at, 213884_s_at, 213885_at	NP_150594.2, NP_006449.2, EAW68709.1, EAW68710.1, EAW68712.1, EAW68716.1, EAW68711.1, EAW68713.1, EAW68714.1, EAW68715.1, EAW68717.1
GeneID:23647	ARFIP2	11	6,496,910	6,502,595	5,685	-	2	1_A375_pNL7_minus_lncRNA::1::1033, 2_A375_pNL97_plus_lncRNA::1::1452	-13, -189	upstream, upstream	1	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ARFIP2	POR1, ARFIP2	ADP-ribosylation factor interacting protein 2	NM_012402, hCT2271162.0, hCT15191.3	202109_at	NP_036534.1, EAW68708.1, EAW68707.1
GeneID:26515	FXC1	11	6,502,677	6,505,911	3,234	+	2	1_A375_pNL7_minus_lncRNA::1::1033, 2_A375_pNL97_plus_lncRNA::1::1452	-69, 107	upstream, in gene	1	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene FXC1	Tim9b, FXC1, TIMM10B, TIM10B	fracture callus 1 homolog (rat)	NM_012192, hCT2271690.0	217981_s_at, 222481_at	NP_036324.1, EAW68706.1
GeneID:8495	PPFIBP2	11	7,535,001	7,674,991	139,990	+	2	1_A375_pNL7_minus_lncRNA::1::1034, 2_A375_pNL97_plus_lncRNA::1::1453	137495, 86663	in gene, in gene	1	1	12.5	15.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene PPFIBP2	Cclp1, PPFIBP2, DKFZp781K06126, MGC42541	PTPRF interacting protein, binding protein 2 (liprin beta 2)	NM_003621, hCT2270376.0, hCT2270377.0, hCT13846.3	212841_s_at, 215959_at	NP_003612.2, EAW68654.1, EAW68652.1, EAW68653.1
GeneID:4004	LMO1	11	8,245,857	8,285,406	39,549	-	1	2_A375_pNL97_plus_lncRNA::1::1454	40398	downstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LMO1	RHOM1, TTG1, RBTN1, LMO1, MGC116692	LIM domain only 1 (rhombotin 1)	NM_002315, hCT13380.3	206718_at	NP_002306.1, EAW68626.1
GeneID:65975	STK33	11	8,413,418	8,615,503	202,085	-	2	1_A375_pNL7_minus_lncRNA::1::1035, 2_A375_pNL97_plus_lncRNA::1::1455	185231, 185103	in gene, in gene	1	1	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene STK33	STK33		NM_030906, hCT2354542.0, hCT2354543.0, hCT15008.3	226035_at, 226066_at	NP_112168.1, EAW68624.1, EAW68623.1, EAW68625.1
GeneID:6157	RPL27A	11	8,703,995	8,711,419	7,424	+	1	1_A375_pNL7_minus_lncRNA::1::1036	325	in gene	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene RPL27A	MGC87238, FLJ43464, RPL27A, MGC10850, L27A, MGC17878	ribosomal protein L27a	NM_000990, hCT15000.4	212044_s_at	NP_000981.1, EAW68619.1
GeneID:619562	SNORA3	11	8,705,774	8,705,903	129	+	1	1_A375_pNL7_minus_lncRNA::1::1036	-1454	upstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SNORA3	ACA3, SNORA3	small nucleolar RNA, H/ACA box 3	NR_002580		
GeneID:677826	SNORA45	11	8,706,986	8,707,116	130	+	1	1_A375_pNL7_minus_lncRNA::1::1036	-2666	upstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SNORA45	SNORA45, ACA3-2	small nucleolar RNA, H/ACA box 45	NR_002977		
GeneID:644656	LOC644656	11	9,481,103	9,482,245	1,142	-	1	2_A375_pNL97_plus_lncRNA::1::1457	69	in gene	0	1	14	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene LOC644656		hypothetical LOC644656	NR_036539	229870_at	
GeneID:7702	ZNF143	11	9,482,512	9,550,071	67,559	+	1	2_A375_pNL97_plus_lncRNA::1::1457	-336	upstream	0	1	14	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene ZNF143	ZNF143, STAF, SBF, pHZ-1	zinc finger protein 143	NM_003442, hCT1958746.2	206428_s_at, 221873_at	NP_003433.3, EAW68569.1
GeneID:133	ADM	11	10,326,642	10,328,923	2,281	+	2	1_A375_pNL7_minus_lncRNA::1::1038, 2_A375_pNL97_plus_lncRNA::1::1458	-391, -402	upstream, upstream	1	1	19	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene ADM	ADM, AM	adrenomedullin	NM_001124, hCT15103.2, hCT1958745.1	202912_at	NP_001115.1, EAW68572.1, EAW68571.1
GeneID:272	AMPD3	11	10,471,868	10,529,126	57,258	+	1	2_A375_pNL97_plus_lncRNA::1::1459	40708	in gene	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene AMPD3	AMPD3		NM_000480, NM_001025389, NM_001025390, NM_001172430, NM_001172431, hCT13549.2, hCT1686490.2, hCT1686491.2	207992_s_at, 209491_s_at	NP_000471.1, NP_001020560.1, NP_001020561.1, NP_001165901.1, NP_001165902.1, EAW68568.1, EAW68567.1, EAW68569.1
GeneID:50862	RNF141	11	10,533,225	10,562,774	29,549	-	1	2_A375_pNL97_plus_lncRNA::1::1460	-74	upstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene RNF141	ZFP26, MGC8715, RNF141, ZNF230	ring finger protein 141	NM_016422, hCT14255.3	1565544_at, 1565546_at, 219104_at, 226106_at	NP_057506.2, EAW68566.1
GeneID:100129827	LOC100129827	11	10,562,787	10,621,479	58,692	+	1	2_A375_pNL97_plus_lncRNA::1::1460	61	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100129827		hypothetical LOC100129827	NR_034093, NR_034094		
GeneID:1982	EIF4G2	11	10,818,593	10,830,582	11,989	-	1	2_A375_pNL97_plus_lncRNA::1::1461	662	in gene	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene EIF4G2	P97, p97, NAT1, AAG1, DAP5, FLJ41344, EIF4G2	eukaryotic translation initiation factor 4 gamma, 2	NM_001042559, NM_001418, NM_001172705, hCT2269853.1, hCT2269854.1, hCT2354518.0, hCT2354519.0	1557964_at, 200004_at, 217607_x_at	NP_001036024.3, NP_001409.3, NP_001166176.1, EAW68552.1, EAW68553.1, EAW68555.1, EAW68554.1
GeneID:692223	SNORD97	11	10,823,014	10,823,155	141	-	1	2_A375_pNL97_plus_lncRNA::1::1461	-6765	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORD97	SNORD97, U97	small nucleolar RNA, C/D box 97	NR_004403		
GeneID:374378	GALNTL4	11	11,292,421	11,643,561	351,140	-	1	1_A375_pNL7_minus_lncRNA::1::1040	230089	in gene	1	0	18	10	1	1_A375_pNL7_minus_lncRNA::1	18	Gene GALNTL4	MGC71806, GalNAc-T15, GALNT18, GALNTL4, GALNT15	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	NM_198516, hCT2269944.0	1554079_at, 233186_at	NP_940918.2, EAW68545.1
GeneID:84953	MICALCL	11	12,308,447	12,380,691	72,244	+	1	1_A375_pNL7_minus_lncRNA::1::1041	1121	in gene	1	0	19	11	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MICALCL	Ebitein1, MICALCL, FLJ14966	MICAL C-terminal like	NM_032867, hCT1951292.1	243611_at	NP_116256.2, EAW68527.1
GeneID:7003	TEAD1	11	12,695,969	12,966,284	270,315	+	1	1_A375_pNL7_minus_lncRNA::1::1042	-193	upstream	1	0	18	12	1	1_A375_pNL7_minus_lncRNA::1	18	Gene TEAD1	TEAD1, TCF13, AA, FLJ17970, REF1, TEF-1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	NM_021961, hCT2274322.0, hCT2274325.0	1553322_s_at, 214600_at, 224955_at	NP_068780.2, EAW68520.1, EAW68521.1
GeneID:406	ARNTL	11	13,299,325	13,408,813	109,488	+	1	1_A375_pNL7_minus_lncRNA::1::1043	515	in gene	1	0	15	13	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ARNTL	MGC47515, TIC, PASD3, BMAL1, BMAL1c, bHLHe5, MOP3, JAP3, ARNTL	aryl hydrocarbon receptor nuclear translocator-like	NM_001178, NM_001030272, NM_001030273, hCT2274303.0, hCT2274304.0, hCT2274305.0, hCT2274309.0, hCT2354532.0, hCT2354533.0, hCT2354534.0, hCT2354535.0, hCT1963619.1, hCT1963620.1, hCT1963621.1	209824_s_at, 210971_s_at	NP_001169.3, NP_001025443.1, NP_001025444.1, EAW68508.1, EAW68509.1, EAW68512.1, EAW68503.1, EAW68504.1, EAW68505.1, EAW68506.1, EAW68507.1, EAW68510.1, EAW68511.1, EAW68513.1
GeneID:22800	RRAS2	11	14,299,466	14,386,052	86,586	-	3	1_A375_pNL7_minus_lncRNA::1::1044, 2_A375_pNL97_plus_lncRNA::1::1463, 2_A375_pNL97_plus_lncRNA::1::1464	5264, 27204, 5300	in gene, in gene, in gene	1	1	22	39.5	2	2_A375_pNL97_plus_lncRNA::1	59	Gene RRAS2	TC21, RRAS2	related RAS viral (r-ras) oncogene homolog 2	NM_001102669, NM_001177314, NM_001177315, NM_012250, hCT2270114.0, hCT2270115.0	208456_s_at, 212589_at, 212590_at	NP_001096139.1, NP_001170785.1, NP_036382.2, NP_001170786.1, EAW68486.1, EAW68487.1
GeneID:1315	COPB1	11	14,479,049	14,521,441	42,392	-	1	2_A375_pNL97_plus_lncRNA::1::1465	97	in gene	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene COPB1	FLJ46444, COPB, DKFZp761K102, FLJ10341, FLJ57957, COPB1	coatomer protein complex, subunit beta 1	NM_016451, NM_001144061, NM_001144062, hCT2270112.0, hCT2354530.0, hCT1823423.1, hCT1966300.1, hCT1966301.1	201358_s_at, 201359_at, 233308_at	NP_057535.1, NP_001137533.1, NP_001137534.1, EAW68483.1, EAW68484.1, EAW68485.1, EAW68481.1, EAW68482.1
GeneID:5682	PSMA1	11	14,526,422	14,665,180	138,758	-	3	1_A375_pNL7_minus_lncRNA::1::1045, 2_A375_pNL97_plus_lncRNA::1::1465, 2_A375_pNL97_plus_lncRNA::1::1466	123196, 143836, 123292	in gene, downstream, in gene	1	1	26.5	29.5	2	1_A375_pNL7_minus_lncRNA::1	39	Gene PSMA1	HC2, MGC21459, MGC1667, MGC14751, MGC23915, MGC14542, MGC22853, PSMA1, PROS30, MGC14575, NU	proteasome (prosome, macropain) subunit, alpha type, 1	NM_148976, NM_002786, NM_001143937, hCT2270106.0, hCT2270107.0, hCT2270109.0, hCT14544.3	201676_x_at, 210759_s_at, 211746_x_at	NP_683877.1, NP_002777.1, NP_001137409.1, EAW68476.1, EAW68477.1, EAW68479.1, EAW68478.1
GeneID:10944	C11orf58	11	16,760,148	16,779,901	19,753	+	1	2_A375_pNL97_plus_lncRNA::1::1468	-52	upstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C11orf58	IMAGE145052, DKFZp686N0232, C11orf58, SMAP, MGC117265	chromosome 11 open reading frame 58	NM_014267, NM_001142705, hCT2350084.0, hCT2350085.0, hCT2354526.0	200084_at, 201784_s_at	NP_055082.1, NP_001136177.1, EAW68455.1, EAW68456.1, EAW68457.1
GeneID:113174	SAAL1	11	18,101,890	18,127,638	25,748	-	4	1_A375_pNL7_minus_lncRNA::1::1046, 2_A375_pNL97_plus_lncRNA::1::1469, 2_A375_pNL97_plus_lncRNA::1::1470, 2_A375_pNL97_plus_lncRNA::1::1471	-10, 22, -778, -5162	upstream, in gene, upstream, upstream	1	1	27.5	27	2	1_A375_pNL7_minus_lncRNA::1	37	Gene SAAL1	FLJ41463, SAAL1	serum amyloid A-like 1	NM_138421, hCT2354514.0, hCT6565.2	225614_at	NP_612430.2, EAW68418.1, EAW68419.1
GeneID:117195	MRGPRX3	11	18,142,502	18,160,027	17,525	+	1	2_A375_pNL97_plus_lncRNA::1::1471	-9702	upstream	0	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MRGPRX3	SNSR1, GPCR, SNSR2, MRGX3, MRGPRX3	MAS-related GPR, member X3	NM_054031, hCT6562.3	1553293_at	NP_473372.3, EAW68417.1
GeneID:7251	TSG101	11	18,501,858	18,548,489	46,631	-	1	1_A375_pNL7_minus_lncRNA::1::1047	41	in gene	1	0	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene TSG101	TSG101, VPS23, TSG10	tumor susceptibility gene 101	NM_006292, hCT2269453.1, hCT2269454.1, hCT2348756.0, hCT2348757.0, hCT2348758.0, hCT2354513.0	201758_at	NP_006283.1, EAW68385.1, EAW68381.1, EAW68383.1, EAW68384.1, EAW68386.1, EAW68382.1
GeneID:55293	UEVLD	11	18,553,244	18,610,281	57,037	-	1	1_A375_pNL7_minus_lncRNA::1::1047	61833	downstream	1	0	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene UEVLD	UEV3, UEVLD, ATTP, FLJ11068	UEV and lactate/malate dehyrogenase domains	NM_001040697, NM_018314, hCT2269451.0, hCT2269452.0, hCT2354544.0, hCT2354545.0, hCT1645592.3	1554396_at, 1554397_s_at, 220775_s_at	NP_001035787.1, NP_060784.3, EAW68377.1, EAW68378.1, EAW68379.1, EAW68380.1, EAW68376.1
GeneID:144108	SPTY2D1	11	18,627,948	18,656,020	28,072	-	1	1_A375_pNL7_minus_lncRNA::1::1048	116	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SPTY2D1	FLJ39441, DKFZp686F1942, SPTY2D1, DKFZp686I068	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	NM_194285, hCT6566.3	229594_at, 235440_at	NP_919261.2, EAW68374.1
GeneID:89797	NAV2	11	19,372,271	20,143,147	770,876	+	3	1_A375_pNL7_minus_lncRNA::1::1050, 2_A375_pNL97_plus_lncRNA::1::1472, 2_A375_pNL97_plus_lncRNA::1::1473	568737, 568721, 761921	in gene, in gene, in gene	1	1	14	17	2	2_A375_pNL97_plus_lncRNA::1	18	Gene NAV2	FLJ77876, NAV2, UNC53H2, FLJ23707, HELAD1, KIAA1419, RAINB1, STEERIN2, FLJ10633, POMFIL2, FLJ11030	neuron navigator 2	NM_145117, NM_182964, NM_001111018, NM_001111019, hCT2270156.1, hCT2270157.1, hCT2270160.1, hCT2270161.1, hCT2270162.1, hCT2348690.0	1556606_at, 1567357_at, 1567358_at, 218330_s_at, 222599_s_at, 239141_at	NP_660093.2, NP_892009.3, NP_001104488.1, NP_001104489.1, EAW68345.1, EAW68348.1, EAW68343.1, EAW68344.1, EAW68346.1, EAW68347.1
GeneID:120237	DBX1	11	20,177,760	20,181,870	4,110	-	2	1_A375_pNL7_minus_lncRNA::1::1051, 2_A375_pNL97_plus_lncRNA::1::1474	1486, 1454	in gene, in gene	1	1	26	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene DBX1	DBX1		NM_001029865, hCT5910.1		NP_001025036.1, EAW68342.1
GeneID:9152	SLC6A5	11	20,620,946	20,676,610	55,664	+	1	2_A375_pNL97_plus_lncRNA::1::1475	494	in gene	0	1	15	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene SLC6A5	SLC6A5, GLYT-2, GLYT2, NET1	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	NM_004211, hCT14449.3	210810_s_at	NP_004202.2, EAW68330.1
GeneID:57084	SLC17A6	11	22,359,667	22,401,049	41,382	+	1	2_A375_pNL97_plus_lncRNA::1::1476	-371	upstream	0	1	12	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene SLC17A6	SLC17A6, VGLUT2, DNPI	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	NM_020346, hCT23683.3	220551_at	NP_065079.1, EAW68324.1
GeneID:627	BDNF	11	27,676,440	27,743,605	67,165	-	6	1_A375_pNL7_minus_lncRNA::1::1052, 1_A375_pNL7_minus_lncRNA::1::1053, 1_A375_pNL7_minus_lncRNA::1::1054, 2_A375_pNL97_plus_lncRNA::1::1478, 2_A375_pNL97_plus_lncRNA::1::1479, 2_A375_pNL97_plus_lncRNA::1::1480	2645, 1541, -443, 2709, 1429, 485	in gene, in gene, upstream, in gene, in gene, in gene	1	1	18.5	21.25	4	2_A375_pNL97_plus_lncRNA::1	43	Gene BDNF	MGC34632, BDNF	brain-derived neurotrophic factor	NM_170731, NM_170732, NM_170733, NM_001709, NM_170734, NM_170735, NM_001143805, NM_001143806, NM_001143807, NM_001143808, NM_001143809, NM_001143810, NM_001143811, NM_001143812, NM_001143813, NM_001143814, NM_001143816, hCT2269104.1, hCT2269107.1, hCT2348	206382_s_at, 239367_at	NP_733927.1, NP_733928.1, NP_733929.1, NP_733930.1, NP_733931.1, NP_001700.2, NP_001137277.1, NP_001137278.1, NP_001137279.1, NP_001137280.1, NP_001137281.1, NP_001137282.1, NP_001137283.1, NP_001137284.1, NP_001137285.1, NP_001137286.1, NP_001137288.1, E
GeneID:81930	KIF18A	11	28,042,163	28,129,746	87,583	-	1	2_A375_pNL97_plus_lncRNA::1::1482	-158	upstream	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene KIF18A	DKFZp434G2226, KIF18A, MS-KIF18A	kinesin family member 18A	NM_031217, hCT18535.3	221258_s_at	NP_112494.3, EAW68271.1
GeneID:196074	METT5D1	11	28,129,798	28,355,054	225,256	+	1	2_A375_pNL97_plus_lncRNA::1::1482	106	in gene	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene METT5D1	FLJ33979, METTL15, METT5D1	methyltransferase 5 domain containing 1	NM_152636, NM_001113528, hCT2269228.1, hCT2269230.1, hCT2349306.0, hCT2354573.0	1562830_at, 1565898_at, 1565900_at, 238773_at, 242247_at	NP_689849.2, NP_001107000.1, EAW68266.1, EAW68267.1, EAW68268.1, EAW68269.1
GeneID:341019	DCDC1	11	31,284,171	31,391,321	107,150	-	1	2_A375_pNL97_plus_lncRNA::1::1485	-87	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DCDC1	DCDC1, FLJ44076	doublecortin domain containing 1	NM_181807, hCT1648343.3		NP_861523.2, EAW68248.1
GeneID:120526	DNAJC24	11	31,391,377	31,454,382	63,005	+	1	2_A375_pNL97_plus_lncRNA::1::1485	31	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DNAJC24	ZCSL3, DPH4, DNAJC24, JJJ3	DnaJ (Hsp40) homolog, subfamily C, member 24	NM_181706, hCT2348798.0, hCT2348799.0, hCT2348800.0, hCT2348886.0, hCT2348887.0, hCT2348888.0, hCT18998.5	1570048_at, 213853_at, 242562_at	NP_859057.4, EAW68247.1, EAW68241.1, EAW68242.1, EAW68243.1, EAW68246.1, EAW68244.1, EAW68245.1
GeneID:5954	RCN1	11	32,112,477	32,127,272	14,795	+	1	1_A375_pNL7_minus_lncRNA::1::1058	-2781	upstream	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RCN1	FLJ55835, RCN1, RCAL, PIG20, RCN, FLJ37041	reticulocalbin 1, EF-hand calcium binding domain	NM_002901, hCT2268698.0, hCT18996.3	201063_at	NP_002892.1, EAW68228.1, EAW68227.1
GeneID:79832	QSER1	11	32,914,792	33,001,816	87,024	+	1	1_A375_pNL7_minus_lncRNA::1::1060	-744	upstream	1	0	21	10	1	1_A375_pNL7_minus_lncRNA::1	21	Gene QSER1	FLJ21924, QSER1	glutamine and serine rich 1	NM_001076786, hCT1823778.3	219705_at, 226265_at, 229982_at, 244563_at	NP_001070254.1, EAW68214.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:91614	DEPDC7	11	33,037,410	33,055,126	17,716	+	4	1_A375_pNL7_minus_lncRNA::1::1061, 1_A375_pNL7_minus_lncRNA::1::1062, 2_A375_pNL97_plus_lncRNA::1::1488, 2_A375_pNL97_plus_lncRNA::1::1489	-98, 23806, 30, 23518	upstream, downstream, in gene, downstream	1	1	19.5	23.5	2	2_A375_pNL97_plus_lncRNA::1	26	Gene DEPDC7	DEPDC7, TR2, dJ85M6.4	DEP domain containing 7	NM_001077242, NM_139160, hCT2336460.0, hCT18458.2	226293_at	NP_001070710.1, NP_631899.2, EAW68212.1, EAW68213.1
GeneID:55346	TCP11L1	11	33,060,963	33,095,109	34,146	+	2	1_A375_pNL7_minus_lncRNA::1::1062, 2_A375_pNL97_plus_lncRNA::1::1489	253, -35	in gene, upstream	1	1	19	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene TCP11L1	dJ85M6.3, FLJ11336, FLJ11386, TCP11L1	t-complex 11 (mouse)-like 1	NM_001145541, NM_018393, hCT2336461.0, hCT2336462.0, hCT2336463.0, hCT2336464.0, hCT2336465.0, hCT18459.1	205796_at, 205797_s_at, 233472_at	NP_001139013.1, NP_060863.3, EAW68205.1, EAW68206.1, EAW68208.1, EAW68210.1, EAW68207.1, EAW68209.1
GeneID:10114	HIPK3	11	33,279,168	33,375,939	96,771	+	1	2_A375_pNL97_plus_lncRNA::1::1490	-64	upstream	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene HIPK3	YAK1, FIST3, DYRK6, PKY, HIPK3	homeodomain interacting protein kinase 3	NM_005734, NM_001048200, hCT2336446.0, hCT2336447.0	207764_s_at, 210148_at, 213697_at, 226297_at	NP_005725.3, NP_001041665.1, EAW68198.1, EAW68199.1
GeneID:25758	C11orf41	11	33,563,877	33,695,648	131,771	+	5	1_A375_pNL7_minus_lncRNA::1::1064, 1_A375_pNL7_minus_lncRNA::1::1065, 2_A375_pNL97_plus_lncRNA::1::1491, 2_A375_pNL97_plus_lncRNA::1::1492, 2_A375_pNL97_plus_lncRNA::1::1493	91483, 128763, 91206, 128371, 140395	in gene, in gene, in gene, in gene, downstream	1	1	14.33	15.33	3	2_A375_pNL97_plus_lncRNA::1	19	Gene C11orf41	C11orf69, FLJ36988, G2, MGC34830, C11orf41	chromosome 11 open reading frame 41	NM_012194	214772_at, 244584_at	NP_036326.2
GeneID:966	CD59	11	33,724,556	33,758,025	33,469	-	3	1_A375_pNL7_minus_lncRNA::1::1066, 1_A375_pNL7_minus_lncRNA::1::1067, 2_A375_pNL97_plus_lncRNA::1::1494	13756, -455, 14025	in gene, upstream, in gene	1	1	15.5	12.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene CD59	MIRL, MACIF, MGC2354, CD59, HRF-20, MIN2, MEM43, MIC11, MIN1, EJ30, MIN3, EL32, G344, 1F5, FLJ92039, MSK21, 16.3A5, EJ16, HRF20, p18-20, FLJ38134, MAC-IP	CD59 molecule, complement regulatory protein	NM_001127223, NM_203330, NM_203329, NM_001127225, NM_203331, NM_000611, NM_001127226, NM_001127227, hCT2336233.0, hCT2336234.0	200983_x_at, 200984_s_at, 200985_s_at, 212463_at, 228748_at	NP_001120695.1, NP_976075.1, NP_000602.1, NP_001120697.1, NP_976076.1, NP_976074.1, NP_001120698.1, NP_001120699.1, EAW68192.1, EAW68193.1
GeneID:26273	FBXO3	11	33,762,490	33,796,071	33,581	-	1	1_A375_pNL7_minus_lncRNA::1::1067	37591	downstream	1	0	17	8	1	1_A375_pNL7_minus_lncRNA::1	17	Gene FBXO3	FBA, FBX3, DKFZp564B092, FBXO3	F-box protein 3	NM_033406, NM_012175, hCT1969181.1, hCT2336229.0, hCT2354546.0, hCT2354547.0, hCT2354548.0, hCT18708.3	218432_at, 229955_at, 232815_at, 232851_at, 235686_at, 242791_at	NP_208385.1, NP_036307.2, EAW68187.1, EAW68188.1, EAW68189.1, EAW68190.1, EAW68186.1, EAW68191.1
GeneID:4076	CAPRIN1	11	34,073,230	34,124,157	50,927	+	3	1_A375_pNL7_minus_lncRNA::1::1069, 2_A375_pNL97_plus_lncRNA::1::1497, 2_A375_pNL97_plus_lncRNA::1::1498	82, -78, 53938	in gene, upstream, downstream	1	1	23	26.5	2	2_A375_pNL97_plus_lncRNA::1	34	Gene CAPRIN1	RNG105, CAPRIN1, M11S1, GPIP137, caprin-1, p137GPI, GPIAP1	cell cycle associated protein 1	NM_005898, NM_203364, hCT2268993.0, hCT2268994.0, hCT2354576.0, hCT2354577.0, hCT18711.3	200722_s_at, 200723_s_at, 225340_s_at, 226285_at, 226289_at, 226990_at, 243370_at	NP_005889.3, NP_976240.1, EAW68176.1, EAW68177.1, EAW68178.1, EAW68180.1, EAW68179.1
GeneID:55226	NAT10	11	34,127,111	34,168,458	41,347	+	1	2_A375_pNL97_plus_lncRNA::1::1498	57	in gene	0	1	24	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene NAT10	KIAA1709, NET43, DKFZp434C116, ALP, FLJ10774, FLJ23850, FLJ12179, NAT10	N-acetyltransferase 10 (GCN5-related)	NM_024662, NM_001144030, hCT2268997.0, hCT18707.3	217584_at	NP_078938.2, NP_001137502.1, EAW68174.1, EAW68175.1
GeneID:25841	ABTB2	11	34,172,534	34,379,555	207,021	-	6	1_A375_pNL7_minus_lncRNA::1::1070, 1_A375_pNL7_minus_lncRNA::1::1071, 2_A375_pNL97_plus_lncRNA::1::1499, 2_A375_pNL97_plus_lncRNA::1::1500, 2_A375_pNL97_plus_lncRNA::1::1501, 2_A375_pNL97_plus_lncRNA::1::1502	26499, 18595, 142915, 106659, 55411, -1053	in gene, in gene, in gene, in gene, in gene, upstream	1	1	16.67	17.17	6	1_A375_pNL7_minus_lncRNA::1	29	Gene ABTB2	ABTB2, DKFZp586C1619	ankyrin repeat and BTB (POZ) domain containing 2	NM_145804, hCT2354561.0, hCT1951779.1	213497_at, 232624_at	NP_665803.2, EAW68172.1, EAW68173.1
GeneID:26298	EHF	11	34,642,588	34,684,835	42,247	+	3	1_A375_pNL7_minus_lncRNA::1::1073, 1_A375_pNL7_minus_lncRNA::1::1074, 2_A375_pNL97_plus_lncRNA::1::1504	33092, 33956, 33316	in gene, in gene, in gene	1	1	18	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene EHF	EHF, ESE3, ESEJ	ets homologous factor	NM_012153, hCT1969193.1, hCT19738.3, hCT2269004.0, hCT2354555.0, hCT2354556.0	219850_s_at, 222932_at, 224189_x_at, 225645_at, 232360_at, 232361_s_at, 241397_at	NP_036285.2, EAW68162.1, EAW68163.1, EAW68164.1, EAW68165.1, EAW68166.1
GeneID:100507144	LOC100507144	11	35,154,197	35,159,574	5,377	-	1	2_A375_pNL97_plus_lncRNA::1::1506	-1226	upstream	0	1	15	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100507144		hypothetical LOC100507144	XR_111155, XR_109039, XR_114478		
GeneID:960	CD44	11	35,160,417	35,253,949	93,532	+	3	1_A375_pNL7_minus_lncRNA::1::1075, 2_A375_pNL97_plus_lncRNA::1::1506, 2_A375_pNL97_plus_lncRNA::1::1507	28031, 383, 28095	in gene, in gene, in gene	1	1	18	24	2	2_A375_pNL97_plus_lncRNA::1	25	Gene CD44	MIC4, ECMR-III, Pgp1, MUTCH-I, HCELL, MC56, CSPG8, IN, MDU3, CD44, CDW44, LHR, MGC10468, MDU2	CD44 molecule (Indian blood group)	NM_000610, NM_001001389, NM_001001390, NM_001001391, NM_001001392, hCT2297697.0, hCT2297698.0, hCT2297699.0, hCT2297700.0, hCT2297701.0, hCT2297702.0, hCT2297703.0, hCT2297704.0, hCT2297705.0, hCT2354552.0, hCT2354553.0, hCT1951772.1	1557905_s_at, 1565868_at, 204489_s_at, 204490_s_at, 209835_x_at, 210916_s_at, 212014_x_at, 212063_at, 216056_at, 217523_at, 234411_x_at, 234418_x_at	NP_000601.3, NP_001001389.1, NP_001001390.1, NP_001001391.1, NP_001001392.1, EAW68152.1, EAW68144.1, EAW68145.1, EAW68146.1, EAW68147.1, EAW68148.1, EAW68149.1, EAW68150.1, EAW68151.1, EAW68153.1, EAW68154.1, EAW68155.1
GeneID:24147	FJX1	11	35,639,735	35,642,421	2,686	+	2	1_A375_pNL7_minus_lncRNA::1::1076, 2_A375_pNL97_plus_lncRNA::1::1508	1113, 1449	in gene, in gene	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FJX1	FLJ22416, FLJ25593, FJX1	four jointed box 1 (Drosophila)	NM_014344, hCT19093.2	219522_at	NP_055159.2, EAW68138.1
GeneID:54765	TRIM44	11	35,684,353	35,830,930	146,577	+	3	1_A375_pNL7_minus_lncRNA::1::1077, 2_A375_pNL97_plus_lncRNA::1::1509, 2_A375_pNL97_plus_lncRNA::1::1510	63327, 47, 63359	in gene, in gene, in gene	1	1	29	29.5	2	1_A375_pNL7_minus_lncRNA::1	41	Gene TRIM44	DIPB, TRIM44, HSA249128, MGC3490, MC7	tripartite motif containing 44	NM_017583, hCT2297711.0, hCT2297712.0, hCT19094.3	217759_at, 217760_at	NP_060053.2, EAW68134.1, EAW68133.1, EAW68135.1
GeneID:143458	LDLRAD3	11	35,965,612	36,252,841	287,229	+	4	1_A375_pNL7_minus_lncRNA::1::1078, 2_A375_pNL97_plus_lncRNA::1::1511, 2_A375_pNL97_plus_lncRNA::1::1512, 2_A375_pNL97_plus_lncRNA::1::1513	205780, 47700, 58356, 205812	in gene, in gene, in gene, in gene	1	1	19	21.33	3	1_A375_pNL7_minus_lncRNA::1	32	Gene LDLRAD3	LDLRAD3	low density lipoprotein receptor class A domain containing 3	NM_174902, hCT2268389.1, hCT2348688.0, hCT2348689.0	234985_at, 244338_at	NP_777562.1, EAW68127.1, EAW68125.1, EAW68126.1
GeneID:29099	COMMD9	11	36,293,842	36,310,999	17,157	-	1	2_A375_pNL97_plus_lncRNA::1::1514	-73	upstream	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene COMMD9	COMMD9, HSPC166, FLJ31106	COMM domain containing 9	NM_014186, NM_001101653, hCT2354527.0, hCT17639.2, hCT1814572.1	218072_at	NP_054905.2, NP_001095123.1, EAW68128.1, EAW68129.1, EAW68130.1
GeneID:79899	PRR5L	11	36,317,725	36,486,754	169,029	+	2	2_A375_pNL97_plus_lncRNA::1::1514, 2_A375_pNL97_plus_lncRNA::1::1515	-6653, 135715	upstream, in gene	0	1	18	20	2	2_A375_pNL97_plus_lncRNA::1	20	Gene PRR5L	PROTOR2, FLJ22630, MGC16218, FLJ14213, PRR5L	proline rich 5 like	NM_024841, NM_001160167, NM_001160168, NM_001160169, hCT1823920.2, hCT1958672.1	1555486_a_at, 219383_at, 233119_at, 233379_at	NP_079117.3, NP_001153639.1, NP_001153640.1, NP_001153641.1, EAW68123.1, EAW68124.1
GeneID:7189	TRAF6	11	36,510,723	36,531,822	21,099	-	2	1_A375_pNL7_minus_lncRNA::1::1079, 2_A375_pNL97_plus_lncRNA::1::1516	78, 46	in gene, in gene	1	1	63	93	1	2_A375_pNL97_plus_lncRNA::1	93	Gene TRAF6	RNF85, TRAF6, MGC:3310	TNF receptor-associated factor 6	NM_004620, NM_145803, hCT2268155.0, hCT2268156.0, hCT2268158.0, hCT2354539.0	205558_at	NP_004611.1, NP_665802.1, EAW68119.1, EAW68120.1, EAW68121.1, EAW68122.1
GeneID:5897	RAG2	11	36,613,493	36,619,829	6,336	-	2	1_A375_pNL7_minus_lncRNA::1::1080, 2_A375_pNL97_plus_lncRNA::1::1517	3765, 3925	in gene, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RAG2	RAG-2, RAG2	recombination activating gene 2	NM_000536, NR_033666, hCT1643134.1	215117_at	NP_000527.2, EAW68117.1
GeneID:119710	C11orf74	11	36,616,093	36,680,817	64,724	+	2	1_A375_pNL7_minus_lncRNA::1::1080, 2_A375_pNL97_plus_lncRNA::1::1517	-29, -189	upstream, upstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C11orf74	C11orf74, FLJ38678	chromosome 11 open reading frame 74	NM_138787, hCT1969187.1, hCT1969189.1, hCT2354524.0, hCT2354525.0, hCT19032.2	226249_at	NP_620142.2, EAW68114.1, EAW68112.1, EAW68113.1, EAW68115.1, EAW68116.1
GeneID:100507187	LOC100507187	11	40,669,774	41,481,768	811,994	-	1	1_A375_pNL7_minus_lncRNA::1::1082	582760	in gene	1	0	20	10	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100507187		hypothetical LOC100507187	XR_109041		
GeneID:8539	API5	11	43,333,505	43,366,080	32,575	+	2	1_A375_pNL7_minus_lncRNA::1::1083, 2_A375_pNL97_plus_lncRNA::1::1521	-1, -33	upstream, upstream	1	1	103	128	1	2_A375_pNL97_plus_lncRNA::1	128	Gene API5	API5, AAC-11, AAC11	apoptosis inhibitor 5	NR_024625, NM_006595, NM_001142930, NM_001142931, hCT2268328.0, hCT2268329.0	201686_x_at, 201687_s_at, 214959_s_at, 214960_at, 233076_at	NP_006586.1, NP_001136402.1, NP_001136403.1, EAW68098.1, EAW68099.1
GeneID:55761	TTC17	11	43,380,435	43,516,483	136,048	+	2	1_A375_pNL7_minus_lncRNA::1::1084, 2_A375_pNL97_plus_lncRNA::1::1522	141, 77	in gene, in gene	1	1	25	20	1	1_A375_pNL7_minus_lncRNA::1	25	Gene TTC17	DKFZp686D20222, FLJ13099, TTC17, FLJ10890, FLJ23673	tetratricopeptide repeat domain 17	NM_018259, hCT2268335.0, hCT2354506.0, hCT6161.3, hCT1951775.2, hCT1961086.1	218972_at, 224649_at, 224652_at, 232323_s_at, 232646_at, 244416_at	NP_060729.2, EAW68095.1, EAW68092.1, EAW68093.1, EAW68094.1, EAW68096.1
GeneID:100507261	LOC100507261	11	43,590,856	43,591,945	1,089	+	2	1_A375_pNL7_minus_lncRNA::1::1085, 2_A375_pNL97_plus_lncRNA::1::1523	7896, 7864	downstream, downstream	1	1	32	28	1	1_A375_pNL7_minus_lncRNA::1	32	Gene LOC100507261		hypothetical LOC100507261	XR_111178, XR_109044, XR_114482		
GeneID:100131381	LOC100131381	11	43,600,529	43,606,151	5,622	+	2	1_A375_pNL7_minus_lncRNA::1::1085, 2_A375_pNL97_plus_lncRNA::1::1523	-1777, -1809	upstream, upstream	1	1	32	28	1	1_A375_pNL7_minus_lncRNA::1	32	Gene LOC100131381		hypothetical LOC100131381	XM_001716729, XM_001717461, XM_001717697		XP_001716781.3, XP_001717513.2, XP_001717949.2
GeneID:406918	MIR129-2	11	43,602,944	43,603,033	89	+	2	1_A375_pNL7_minus_lncRNA::1::1085, 2_A375_pNL97_plus_lncRNA::1::1523	-4192, -4224	upstream, upstream	1	1	32	28	1	1_A375_pNL7_minus_lncRNA::1	32	Gene MIR129-2	mir-129-2, MIR129-2, MIRN129-2, MIR-129b	microRNA 129-2	NR_029697		
GeneID:100507282	LOC100507282	11	43,880,281	43,881,062	781	-	2	1_A375_pNL7_minus_lncRNA::1::1087, 2_A375_pNL97_plus_lncRNA::1::1526	-9562, -9450	upstream, upstream	1	1	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene LOC100507282		hypothetical LOC100507282	XR_109045		
GeneID:221120	ALKBH3	11	43,902,357	43,941,825	39,468	+	4	1_A375_pNL7_minus_lncRNA::1::1088, 1_A375_pNL7_minus_lncRNA::1::1089, 2_A375_pNL97_plus_lncRNA::1::1527, 2_A375_pNL97_plus_lncRNA::1::1528	-117, 40027, -69, 39995	upstream, downstream, upstream, downstream	1	1	21.5	28	2	2_A375_pNL97_plus_lncRNA::1	34	Gene ALKBH3	DEPC-1, ALKBH3, PCA1, MGC118792, MGC118793, ABH3, MGC118790, DEPC1, FLJ43614	alkB, alkylation repair homolog 3 (E. coli)	NM_139178, hCT2354501.0, hCT1824049.2	226127_at	NP_631917.1, EAW68078.1, EAW68079.1
GeneID:100507300	LOC100507300	11	43,930,839	43,942,476	11,637	-	2	1_A375_pNL7_minus_lncRNA::1::1089, 2_A375_pNL97_plus_lncRNA::1::1528	92, 124	in gene, in gene	1	1	24	22	1	1_A375_pNL7_minus_lncRNA::1	24	Gene LOC100507300		hypothetical LOC100507300	XR_109046, XR_114484		
GeneID:390110	ACCSL	11	44,069,531	44,081,527	11,996	+	2	1_A375_pNL7_minus_lncRNA::1::1090, 2_A375_pNL97_plus_lncRNA::1::1529	18341, 18149	downstream, downstream	1	1	26	19	1	1_A375_pNL7_minus_lncRNA::1	26	Gene ACCSL	ACCSL		NM_001031854, hCT2347802.0		NP_001027025.2, EAW68074.1
GeneID:84680	ACCS	11	44,087,729	44,105,569	17,840	+	2	1_A375_pNL7_minus_lncRNA::1::1090, 2_A375_pNL97_plus_lncRNA::1::1529	143, -49	in gene, upstream	1	1	26	19	1	1_A375_pNL7_minus_lncRNA::1	26	Gene ACCS	ACS, PHACS, ACCS	1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)	NM_032592, NM_001127219, hCT1824050.2, hCT1958674.1	226264_at	NP_115981.1, NP_001120691.1, EAW68072.1, EAW68073.1
GeneID:2132	EXT2	11	44,117,099	44,266,980	149,881	+	1	1_A375_pNL7_minus_lncRNA::1::1091	149	in gene	1	0	21	17	1	1_A375_pNL7_minus_lncRNA::1	21	Gene EXT2	EXT2, SOTV	exostoses (multiple) 2	NM_207122, NM_000401, NM_001178083, hCT2268354.0, hCT2354557.0, hCT2354558.0, hCT2354559.0, hCT1951773.1	202012_s_at, 202013_s_at	NP_997005.1, NP_000392.3, NP_001171554.1, EAW68068.1, EAW68069.1, EAW68070.1, EAW68067.1, EAW68071.1
GeneID:56981	PRDM11	11	45,115,564	45,246,903	131,339	+	2	1_A375_pNL7_minus_lncRNA::1::1092, 2_A375_pNL97_plus_lncRNA::1::1530	4116, 4148	in gene, in gene	1	1	26	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene PRDM11	PFM8, PRDM11	PR domain containing 11	NM_020229, hCT2269236.0, hCT1951771.0	220571_at, 239763_at	NP_064614.2, EAW68049.1, EAW68048.1
GeneID:57586	SYT13	11	45,261,853	45,307,884	46,031	-	1	1_A375_pNL7_minus_lncRNA::1::1093	26551	in gene	1	0	23	13	1	1_A375_pNL7_minus_lncRNA::1	23	Gene SYT13	KIAA1427, SYT13	synaptotagmin XIII	NM_020826, hCT2268766.0, hCT16513.2	221859_at, 226086_at	NP_065877.1, EAW68044.1, EAW68043.1
GeneID:55343	SLC35C1	11	45,825,623	45,834,567	8,944	+	3	1_A375_pNL7_minus_lncRNA::1::1096, 2_A375_pNL97_plus_lncRNA::1::1533, 2_A375_pNL97_plus_lncRNA::1::1534	969, 190, 969	in gene, in gene, in gene	1	1	39	22	1	1_A375_pNL7_minus_lncRNA::1	39	Gene SLC35C1	FUCT1, FLJ11320, CDG2C, FLJ14841, SLC35C1	solute carrier family 35, member C1	NM_018389, NM_001145265, NM_001145266, hCT1824261.3, hCT1966308.1, hCT1966309.1	218485_s_at, 222647_at	NP_060859.4, NP_001138737.1, NP_001138738.1, EAW68031.1, EAW68032.1, EAW68033.1
GeneID:1408	CRY2	11	45,868,669	45,904,799	36,130	+	3	2_A375_pNL97_plus_lncRNA::1::1535, 2_A375_pNL97_plus_lncRNA::1::1536, 2_A375_pNL97_plus_lncRNA::1::1537	419, 26003, 36243	in gene, in gene, downstream	0	1	14.33	21	3	2_A375_pNL97_plus_lncRNA::1	24	Gene CRY2	PHLL2, FLJ10332, KIAA0658, HCRY2, CRY2	cryptochrome 2 (photolyase-like)	NM_021117, NM_001127457, hCT2268665.0, hCT16897.2	212695_at	NP_066940.2, NP_001120929.1, EAW68029.1, EAW68030.1
GeneID:9479	MAPK8IP1	11	45,907,202	45,928,016	20,814	+	3	1_A375_pNL7_minus_lncRNA::1::1097, 2_A375_pNL97_plus_lncRNA::1::1537, 2_A375_pNL97_plus_lncRNA::1::1538	13886, -290, 13856	in gene, upstream, in gene	1	1	19	20.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene MAPK8IP1	PRKM8IP, JIP-1, MAPK8IP1, IB1, JIP1	mitogen-activated protein kinase 8 interacting protein 1	NM_005456, hCT2268668.0, hCT2354570.0	213013_at, 213014_at	NP_005447.1, EAW68027.1, EAW68028.1
GeneID:143678	C11orf94	11	45,928,085	45,928,833	748	-	2	1_A375_pNL7_minus_lncRNA::1::1097, 2_A375_pNL97_plus_lncRNA::1::1538	7745, 7745	downstream, downstream	1	1	25	22	1	1_A375_pNL7_minus_lncRNA::1	25	Gene C11orf94	C11orf94	chromosome 11 open reading frame 94	NM_001080446	240029_at	NP_001073915.2
GeneID:9409	PEX16	11	45,931,220	45,939,674	8,454	-	4	1_A375_pNL7_minus_lncRNA::1::1097, 1_A375_pNL7_minus_lncRNA::1::1098, 2_A375_pNL97_plus_lncRNA::1::1538, 2_A375_pNL97_plus_lncRNA::1::1539	18586, -70, 18586, 218	downstream, upstream, downstream, in gene	1	1	24	19.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene PEX16	PEX16		NM_057174, NM_004813, hCT16893.3, hCT1814566.1, hCT1951762.1	221603_at, 221604_s_at, 49878_at	NP_476515.1, NP_004804.1, EAW68022.1, EAW68023.1, EAW68024.1
GeneID:120071	GYLTL1B	11	45,943,196	45,950,647	7,451	+	2	1_A375_pNL7_minus_lncRNA::1::1098, 2_A375_pNL97_plus_lncRNA::1::1539	-3452, -3740	upstream, upstream	1	1	23	17	1	1_A375_pNL7_minus_lncRNA::1	23	Gene GYLTL1B	PP5656, LARGE2, GYLTL1B, FLJ35207	glycosyltransferase-like 1B	NM_152312, hCT2354504.0, hCT16898.3	227829_at	NP_689525.3, EAW68021.1, EAW68020.1
GeneID:8525	DGKZ	11	46,354,739	46,402,104	47,365	+	4	1_A375_pNL7_minus_lncRNA::1::1100, 1_A375_pNL7_minus_lncRNA::1::1101, 2_A375_pNL97_plus_lncRNA::1::1541, 2_A375_pNL97_plus_lncRNA::1::1542	30413, 56765, 30573, 56365	in gene, downstream, in gene, downstream	1	1	22	18.5	2	1_A375_pNL7_minus_lncRNA::1	24	Gene DGKZ	hDGKzeta, DGKZ, DAGK6, DAGK5, DGK-ZETA	diacylglycerol kinase, zeta	NM_201532, NM_201533, NM_003646, NM_001105540, hCT2268637.0, hCT2268638.0, hCT2268640.0, hCT2354515.0	207556_s_at, 239342_at	NP_963290.1, NP_963291.1, NP_001099010.1, NP_003637.2, EAW68006.1, EAW68009.1, EAW68007.1, EAW68008.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:4192	MDK	11	46,402,618	46,405,375	2,757	+	4	1_A375_pNL7_minus_lncRNA::1::1101, 1_A375_pNL7_minus_lncRNA::1::1102, 2_A375_pNL97_plus_lncRNA::1::1542, 2_A375_pNL97_plus_lncRNA::1::1543	8886, 11590, 8486, 11686	downstream, downstream, downstream, downstream	1	1	20.5	21	2	2_A375_pNL97_plus_lncRNA::1	23	Gene MDK	MK, FLJ27379, MDK, NEGF2	midkine (neurite growth-promoting factor 2)	NM_001012334, NM_002391, NM_001012333, hCT16892.4	209035_at	NP_001012334.1, NP_002382.1, NP_001012333.1, EAW68005.1
GeneID:1132	CHRM4	11	46,406,640	46,408,107	1,467	-	4	1_A375_pNL7_minus_lncRNA::1::1101, 1_A375_pNL7_minus_lncRNA::1::1102, 2_A375_pNL97_plus_lncRNA::1::1542, 2_A375_pNL97_plus_lncRNA::1::1543	-3397, -6101, -2997, -6197	upstream, upstream, upstream, upstream	1	1	20.5	21	2	2_A375_pNL97_plus_lncRNA::1	23	Gene CHRM4	HM4, M4R, CHRM4	cholinergic receptor, muscarinic 4	NM_000741, hCT1823058.2	221357_at	NP_000732.2, EAW68004.1
GeneID:55626	AMBRA1	11	46,417,964	46,612,914	194,950	-	6	1_A375_pNL7_minus_lncRNA::1::1101, 1_A375_pNL7_minus_lncRNA::1::1102, 1_A375_pNL7_minus_lncRNA::1::1103, 2_A375_pNL97_plus_lncRNA::1::1542, 2_A375_pNL97_plus_lncRNA::1::1543, 2_A375_pNL97_plus_lncRNA::1::1544	201410, 198706, -2734, 201810, 198610, -2670	downstream, downstream, upstream, downstream, downstream, upstream	1	1	26.33	30.33	3	2_A375_pNL97_plus_lncRNA::1	49	Gene AMBRA1	AMBRA1, DCAF3, FLJ20294, MGC33725, KIAA1736, WDR94	autophagy/beclin-1 regulator 1	NM_017749, hCT2269673.0, hCT2269674.0, hCT2269675.0, hCT2269676.0, hCT2269677.0, hCT2354593.0, hCT2354594.0	219141_s_at, 234236_at, 234237_s_at, 52731_at	NP_060219.2, EAW68002.1, EAW67996.1, EAW67997.1, EAW67998.1, EAW68000.1, EAW67999.1, EAW68001.1
GeneID:283254	HARBI1	11	46,624,856	46,638,777	13,921	-	4	1_A375_pNL7_minus_lncRNA::1::1103, 1_A375_pNL7_minus_lncRNA::1::1104, 2_A375_pNL97_plus_lncRNA::1::1544, 2_A375_pNL97_plus_lncRNA::1::1545	23129, -71, 23193, -55	downstream, upstream, downstream, upstream	1	1	28.5	34	2	2_A375_pNL97_plus_lncRNA::1	49	Gene HARBI1	HARBI1, C11orf77, FLJ32675	harbinger transposase derived 1	NM_173811, hCT1966867.1, hCT2346942.0, hCT1768221.4	241498_at	NP_776172.1, EAW67992.1, EAW67993.1, EAW67994.1
GeneID:9776	KIAA0652	11	46,638,826	46,696,368	57,542	+	2	1_A375_pNL7_minus_lncRNA::1::1104, 2_A375_pNL97_plus_lncRNA::1::1545	22, 6	in gene, in gene	1	1	19	19	1	1_A375_pNL7_minus_lncRNA::1	19	Gene KIAA0652	FLJ20698, ATG13, KIAA0652	ATG13 autophagy related 13 homolog (S. cerevisiae)	NM_014741, NM_001142673, NR_024587, NR_024586, NR_024589, hCT2270680.0, hCT2270681.0, hCT2270683.0, hCT2354479.0, hCT2354480.0, hCT10779.3, hCT1954002.0	203363_s_at, 203364_s_at, 209021_x_at	NP_055556.2, NP_001136145.1, EAW67985.1, EAW67986.1, EAW67987.1, EAW67988.1, EAW67989.1, EAW67990.1, EAW67991.1
GeneID:392	ARHGAP1	11	46,698,630	46,722,120	23,490	-	2	1_A375_pNL7_minus_lncRNA::1::1105, 2_A375_pNL97_plus_lncRNA::1::1546	-296, -152	upstream, upstream	1	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ARHGAP1	RHOGAP1, ARHGAP1, CDC42GAP, p50rhoGAP, RHOGAP	Rho GTPase activating protein 1	NM_004308, hCT2269667.0, hCT2269669.0, hCT1768216.2	202117_at, 216689_x_at, 217153_at, 241419_at	NP_004299.1, EAW67982.1, EAW67983.1, EAW67984.1
GeneID:79797	ZNF408	11	46,722,317	46,727,466	5,149	+	2	1_A375_pNL7_minus_lncRNA::1::1105, 2_A375_pNL97_plus_lncRNA::1::1546	99, -45	in gene, upstream	1	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ZNF408	ZNF408, FLJ12827	zinc finger protein 408	NM_001184751, NM_024741, hCT1768219.0	219224_x_at	NP_001171680.1, NP_079017.1, EAW67981.1
GeneID:9793	CKAP5	11	46,765,084	46,867,843	102,759	-	2	1_A375_pNL7_minus_lncRNA::1::1106, 2_A375_pNL97_plus_lncRNA::1::1547	-61, 3	upstream, in gene	1	1	44	35	1	1_A375_pNL7_minus_lncRNA::1	44	Gene CKAP5	CKAP5, FLJ35359, TOG, CHTOG, ch-TOG, MSPS, KIAA0097, TOGp	cytoskeleton associated protein 5	NM_001008938, NM_014756, hCT1954003.1	1555278_a_at, 212832_s_at	NP_001008938.1, NP_055571.2, EAW67976.1
GeneID:100507401	LOC100507401	11	46,867,957	46,895,967	28,010	+	2	1_A375_pNL7_minus_lncRNA::1::1106, 2_A375_pNL97_plus_lncRNA::1::1547	-53, -117	upstream, upstream	1	1	44	35	1	1_A375_pNL7_minus_lncRNA::1	44	Gene LOC100507401		hypothetical LOC100507401	XR_111173, XR_109049, XR_114487		
GeneID:4038	LRP4	11	46,878,268	46,940,173	61,905	-	2	1_A375_pNL7_minus_lncRNA::1::1106, 2_A375_pNL97_plus_lncRNA::1::1547	72269, 72333	downstream, downstream	1	1	44	35	1	1_A375_pNL7_minus_lncRNA::1	44	Gene LRP4	MEGF7, CLSS, KIAA0816, LRP4, LRP10	low density lipoprotein receptor-related protein 4	NM_002334, hCT2269663.0, hCT10393.3	212850_s_at	NP_002325.2, EAW67975.1, EAW67974.1
GeneID:84364	ARFGAP2	11	47,185,852	47,198,419	12,567	-	2	1_A375_pNL7_minus_lncRNA::1::1107, 2_A375_pNL97_plus_lncRNA::1::1548	-9537, -8941	upstream, upstream	1	1	17	15	2	1_A375_pNL7_minus_lncRNA::1	20	Gene ARFGAP2	FLJ14576, ARFGAP2, FLJ26000, ZNF289, Zfp289, IRZ, Nbla10535	ADP-ribosylation factor GTPase activating protein 2	NM_032389, hCT1966892.1, hCT1966893.1, hCT1966896.1, hCT2354582.0, hCT1768220.3, hCT1953056.1	211975_at	NP_115765.2, EAW67965.1, EAW67963.1, EAW67964.1, EAW67966.1, EAW67967.1, EAW67968.1
GeneID:29763	PACSIN3	11	47,199,073	47,208,010	8,937	-	2	1_A375_pNL7_minus_lncRNA::1::1107, 2_A375_pNL97_plus_lncRNA::1::1548	-246, 650	upstream, in gene	1	1	17	15	2	1_A375_pNL7_minus_lncRNA::1	20	Gene PACSIN3	SDPIII, PACSIN3, FLJ17861	protein kinase C and casein kinase substrate in neurons 3	NM_001184974, NM_001184975, NM_016223, hCT1966897.1, hCT2354563.0, hCT2354564.0	218744_s_at	NP_001171903.1, NP_001171904.1, NP_057307.2, EAW67960.1, EAW67961.1, EAW67962.1
GeneID:1643	DDB2	11	47,236,493	47,260,769	24,276	+	1	2_A375_pNL97_plus_lncRNA::1::1549	33907	downstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene DDB2	UV-DDB2, DDB2, FLJ34321, DDBB	damage-specific DNA binding protein 2, 48kDa	NM_000107, hCT1966899.1, hCT1966900.2, hCT2354565.0, hCT2354566.0, hCT2354567.0, hCT2354568.0, hCT2354569.0, hCT16302.3	203409_at	NP_000098.1, EAW67959.1, EAW67953.1, EAW67954.1, EAW67957.1, EAW67958.1, EAW67952.1, EAW67955.1, EAW67956.1
GeneID:53	ACP2	11	47,260,853	47,270,457	9,604	-	1	2_A375_pNL97_plus_lncRNA::1::1549	57	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ACP2	ACP2		NM_001610, NM_001131064, hCT2269705.1, hCT14655.4	202767_at	NP_001601.1, NP_001124536.1, EAW67950.1, EAW67951.1
GeneID:10062	NR1H3	11	47,270,449	47,290,401	19,952	+	2	2_A375_pNL97_plus_lncRNA::1::1549, 2_A375_pNL97_plus_lncRNA::1::1550	-49, 20415	upstream, downstream	0	1	14	19	2	2_A375_pNL97_plus_lncRNA::1	23	Gene NR1H3	RLD-1, LXR-a, NR1H3, LXRA	nuclear receptor subfamily 1, group H, member 3	NM_005693, NM_001130102, NM_001130101, hCT2270705.0, hCT2270707.0, hCT2270710.0, hCT2348711.0, hCT2348712.0, hCT2348713.0, hCT2348714.0, hCT1953087.0	203920_at	NP_005684.2, NP_001123574.1, NP_001123573.1, EAW67942.1, EAW67944.1, EAW67949.1, EAW67943.1, EAW67945.1, EAW67946.1, EAW67947.1, EAW67948.1
GeneID:8567	MADD	11	47,290,927	47,351,582	60,655	+	1	2_A375_pNL97_plus_lncRNA::1::1550	-63	upstream	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MADD	FLJ35600, RAB3GEP, KIAA0358, MADD, IG20, FLJ36300, DENN	MAP-kinase activating death domain	NM_130476, NM_130470, NM_130471, NM_130472, NM_130473, NM_130474, NM_130475, NM_003682, NM_001135943, NM_001135944, hCT1970591.1, hCT1970592.1, hCT1970593.1, hCT1970594.1, hCT1970595.1, hCT2270716.0, hCT2270720.0, hCT2270723.0, hCT2354587.0, hCT2354588.0,	210252_s_at, 38398_at	NP_569832.2, NP_569826.2, NP_569827.2, NP_569828.2, NP_569829.2, NP_569830.2, NP_569831.1, NP_003673.3, NP_001129415.1, NP_001129416.1, EAW67930.1, EAW67931.1, EAW67932.1, EAW67933.1, EAW67934.1, EAW67935.1, EAW67936.1, EAW67937.1, EAW67938.1, EAW67939.1,
GeneID:91252	SLC39A13	11	47,430,046	47,438,051	8,005	+	2	1_A375_pNL7_minus_lncRNA::1::1108, 2_A375_pNL97_plus_lncRNA::1::1551	-254, 17922	upstream, downstream	1	1	21	18.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene SLC39A13	FLJ25785, SLC39A13	solute carrier family 39 (zinc transporter), member 13	NM_001128225, NM_152264, hCT2270734.0, hCT2270739.0, hCT2348963.0, hCT2354494.0, hCT1768374.2, hCT1953084.1, hCT1953085.1	1552295_a_at, 225277_at	NP_001121697.1, NP_689477.2, EAW67917.1, EAW67918.1, EAW67922.1, EAW67923.1, EAW67919.1, EAW67920.1, EAW67921.1
GeneID:5702	PSMC3	11	47,440,320	47,448,024	7,704	-	1	2_A375_pNL97_plus_lncRNA::1::1551	56	in gene	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene PSMC3	MGC8487, TBP1, PSMC3	proteasome (prosome, macropain) 26S subunit, ATPase, 3	NM_002804, hCT16310.3	201267_s_at	NP_002795.2, EAW67916.1
GeneID:10658	CUGBP1	11	47,487,489	47,574,792	87,303	-	3	1_A375_pNL7_minus_lncRNA::1::1109, 2_A375_pNL97_plus_lncRNA::1::1552, 2_A375_pNL97_plus_lncRNA::1::1553	24, 88648, 8	in gene, downstream, in gene	1	1	15	23	2	2_A375_pNL97_plus_lncRNA::1	23	Gene CUGBP1	NAB50, CELF1, CUGBP, hNab50, CUG-BP, NAPOR, BRUNOL2, EDEN-BP, CUGBP1	CUG triplet repeat, RNA binding protein 1	NM_006560, NM_001025596, NM_001172639, NM_001172640, NM_198700, hCT2269686.0, hCT2269687.0, hCT2269688.0, hCT2354583.0, hCT16308.3, hCT1953089.1, hCT1953090.1	1555467_a_at, 204113_at, 209489_at, 221742_at, 221743_at, 235297_at, 235865_at	NP_006551.1, NP_001020767.1, NP_941989.1, NP_001166110.1, NP_001166111.1, EAW67909.1, EAW67906.1, EAW67907.1, EAW67908.1, EAW67910.1, EAW67911.1, EAW67912.1
GeneID:114971	PTPMT1	11	47,586,982	47,595,013	8,031	+	2	1_A375_pNL7_minus_lncRNA::1::1110, 2_A375_pNL97_plus_lncRNA::1::1554	13530, 13594	downstream, downstream	1	1	27	23	1	1_A375_pNL7_minus_lncRNA::1	27	Gene PTPMT1	PTPMT1, FLJ46081, PLIP, PNAS-129, DUSP23, MOSP	protein tyrosine phosphatase, mitochondrial 1	NM_175732, NM_001143984	223808_s_at, 225901_at, 229535_at	NP_783859.1, NP_001137456.1
GeneID:55709	KBTBD4	11	47,593,749	47,600,567	6,818	-	2	1_A375_pNL7_minus_lncRNA::1::1110, 2_A375_pNL97_plus_lncRNA::1::1554	55, -9	in gene, upstream	1	1	27	23	1	1_A375_pNL7_minus_lncRNA::1	27	Gene KBTBD4	KBTBD4, BKLHD4, FLJ10450, HSPC252	kelch repeat and BTB (POZ) domain containing 4	NM_016095, NM_018506, NR_024222, hCT2354521.0, hCT2354522.0, hCT1952030.1, hCT1952031.1, hCT1952032.1	218569_s_at, 218570_at, 223765_s_at	NP_060565.4, NP_057590.3, EAW67898.1, EAW67899.1, EAW67900.1, EAW67902.1, EAW67901.1
GeneID:4722	NDUFS3	11	47,600,562	47,606,115	5,553	+	2	1_A375_pNL7_minus_lncRNA::1::1110, 2_A375_pNL97_plus_lncRNA::1::1554	-50, 14	upstream, in gene	1	1	27	23	1	1_A375_pNL7_minus_lncRNA::1	27	Gene NDUFS3	CI-30, NDUFS3		NM_004551, hCT16309.2, hCT1952033.1, hCT1952034.1	201740_at	NP_004542.1, EAW67895.1, EAW67896.1, EAW67897.1
GeneID:399888	FAM180B	11	47,608,230	47,610,746	2,516	+	2	1_A375_pNL7_minus_lncRNA::1::1110, 2_A375_pNL97_plus_lncRNA::1::1554	-7718, -7654	upstream, upstream	1	1	27	23	1	1_A375_pNL7_minus_lncRNA::1	27	Gene FAM180B	FAM180B	family with sequence similarity 180, member B	NM_001164379		NP_001157851.1
GeneID:23279	NUP160	11	47,799,670	47,870,057	70,387	-	2	1_A375_pNL7_minus_lncRNA::1::1111, 2_A375_pNL97_plus_lncRNA::1::1555	297, 105	in gene, in gene	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene NUP160	MGC150678, NUP160, MGC150679, DKFZp686M14102	nucleoporin 160kDa	NM_015231, hCT1970598.1, hCT1970599.1, hCT1970600.1, hCT2354499.0, hCT2354500.0, hCT16316.3	212709_at, 214962_s_at, 214963_at	NP_056046.1, EAW67878.1, EAW67879.1, EAW67880.1, EAW67881.1, EAW67882.1, EAW67883.1
GeneID:5795	PTPRJ	11	48,002,110	48,192,394	190,284	+	3	1_A375_pNL7_minus_lncRNA::1::1113, 1_A375_pNL7_minus_lncRNA::1::1114, 2_A375_pNL97_plus_lncRNA::1::1557	10978, 12882, 75138	in gene, in gene, in gene	1	1	17.33	11.33	3	1_A375_pNL7_minus_lncRNA::1	20	Gene PTPRJ	R-PTP-ETA, PTPRJ, HPTPeta, DEP1, CD148, SCC1	protein tyrosine phosphatase, receptor type, J	NM_001098503, NM_002843, hCT2265644.0, hCT2265650.0, hCT2265655.0, hCT14332.3	210173_at, 214137_at	NP_001091973.1, NP_002834.3, EAW67873.1, EAW67874.1, EAW67875.1, EAW67876.1
GeneID:84767	SPRYD5	11	55,650,773	55,659,286	8,513	+	2	1_A375_pNL7_minus_lncRNA::1::1115, 2_A375_pNL97_plus_lncRNA::1::1558	-9962, -10122	upstream, upstream	1	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SPRYD5	TRIM51, MGC10977, SPRYD5	SPRY domain containing 5	NM_032681, hCT1967468.1, hCT2309153.0	223975_at	NP_116070.2, EAW73688.1, EAW73689.1
GeneID:85456	TNKS1BP1	11	57,067,103	57,092,413	25,310	-	2	1_A375_pNL7_minus_lncRNA::1::1116, 2_A375_pNL97_plus_lncRNA::1::1560	-99, -99	upstream, upstream	1	1	46	59	1	2_A375_pNL97_plus_lncRNA::1	59	Gene TNKS1BP1	KIAA1741, TNKS1BP1, FLJ45975, TAB182	tankyrase 1 binding protein 1, 182kDa	NM_033396, hCT2355229.0, hCT2355230.0, hCT1953657.1	224792_at	NP_203754.2, EAW73732.1, EAW73731.1, EAW73733.1
GeneID:6749	SSRP1	11	57,093,459	57,103,351	9,892	-	3	1_A375_pNL7_minus_lncRNA::1::1116, 1_A375_pNL7_minus_lncRNA::1::1117, 2_A375_pNL97_plus_lncRNA::1::1560	10839, -41, 10839	downstream, upstream, downstream	1	1	34	37	2	2_A375_pNL97_plus_lncRNA::1	59	Gene SSRP1	FACT80, T160, FACT, SSRP1	structure specific recognition protein 1	NM_003146, hCT2309792.0, hCT1953645.1	200956_s_at, 200957_s_at	NP_003137.1, EAW73735.1, EAW73734.1
GeneID:5024	P2RX3	11	57,105,949	57,137,549	31,600	+	3	1_A375_pNL7_minus_lncRNA::1::1117, 1_A375_pNL7_minus_lncRNA::1::1118, 2_A375_pNL97_plus_lncRNA::1::1561	-2557, 41251, 41411	upstream, downstream, downstream	1	1	24	21	2	2_A375_pNL97_plus_lncRNA::1	27	Gene P2RX3	P2RX3, P2X3, MGC129956	purinergic receptor P2X, ligand-gated ion channel, 3	NM_002559, hCT2309297.1, hCT1953653.2	206338_at	NP_002550.2, EAW73737.1, EAW73736.1
GeneID:10394	PRG3	11	57,144,242	57,148,623	4,381	-	2	1_A375_pNL7_minus_lncRNA::1::1118, 2_A375_pNL97_plus_lncRNA::1::1561	1423, 1263	in gene, in gene	1	1	26	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene PRG3	MBPH, MGC141971, MGC126662, MBP2, PRG3	proteoglycan 3	NM_006093, hCT31013.1	220811_at	NP_006084.2, EAW73738.1
GeneID:5553	PRG2	11	57,154,834	57,158,130	3,296	-	2	1_A375_pNL7_minus_lncRNA::1::1118, 2_A375_pNL97_plus_lncRNA::1::1561	10930, 10770	downstream, downstream	1	1	26	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene PRG2	MGC14537, MBP, BMPG, MBP1, PRG2	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	NM_002728	211743_s_at	NP_002719.3
GeneID:9246	UBE2L6	11	57,319,129	57,335,453	16,324	-	2	1_A375_pNL7_minus_lncRNA::1::1119, 2_A375_pNL97_plus_lncRNA::1::1562	-1603, -179	upstream, upstream	1	1	12.5	14	2	2_A375_pNL97_plus_lncRNA::1	18	Gene UBE2L6	RIG-B, UBCH8, UBE2L6, MGC40331	ubiquitin-conjugating enzyme E2L 6	NM_004223, NM_198183, hCT1953646.1, hCT2355310.0, hCT2355311.0, hCT2355312.0, hCT31010.2	201649_at	NP_004214.1, NP_937826.1, EAW73755.1, EAW73756.1, EAW73758.1, EAW73759.1, EAW73757.1
GeneID:100507106	LOC100507106	11	57,405,850	57,420,606	14,756	+	1	2_A375_pNL97_plus_lncRNA::1::1563	19238	downstream	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100507106		hypothetical LOC100507106	XR_111179, XR_110907, XR_114489		
GeneID:219539	YPEL4	11	57,412,560	57,417,417	4,857	-	1	2_A375_pNL97_plus_lncRNA::1::1563	-7671	upstream	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene YPEL4	YPEL4, MGC138324, FLJ30213, MGC102723	yippee-like 4 (Drosophila)	NM_145008, hCT1966315.1, hCT1966316.1, hCT2355207.0, hCT2355208.0, hCT2355209.0	235916_at	NP_659445.1, EAW73768.1, EAW73765.1, EAW73766.1, EAW73767.1, EAW73769.1
GeneID:10978	CLP1	11	57,425,216	57,429,337	4,121	+	1	2_A375_pNL97_plus_lncRNA::1::1563	-128	upstream	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CLP1	HEAB, hClp1, CLP1	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	NM_006831, NM_001142597, hCT31016.1	204370_at, 229496_at	NP_006822.1, NP_001136069.1, EAW73770.1
GeneID:25921	ZDHHC5	11	57,435,474	57,468,659	33,185	+	1	2_A375_pNL97_plus_lncRNA::1::1563	-10386	upstream	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ZDHHC5	ZNF375, KIAA1748, DKFZp586K0524, ZDHHC5	zinc finger, DHHC-type containing 5	NM_015457, hCT2355394.0, hCT2355395.0, hCT31024.3	224858_at, 224868_at	NP_056272.2, EAW73771.1, EAW73772.1, EAW73773.1
GeneID:51075	TMX2	11	57,480,042	57,508,445	28,403	+	2	1_A375_pNL7_minus_lncRNA::1::1120, 2_A375_pNL97_plus_lncRNA::1::1564	28758, 28726	downstream, downstream	1	1	22	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene TMX2	PIG26, DKFZp781O2021, CGI-31, PDIA12, TXNDC14, TMX2, MGC111151	thioredoxin-related transmembrane protein 2	NM_015959, NM_001144012, NR_026593, hCT2355364.0, hCT2355365.0, hCT2355366.0, hCT31017.2	201175_at	NP_057043.1, NP_001137484.1, EAW73777.1, EAW73778.1, EAW73779.1, EAW73780.1
GeneID:280636	C11orf31	11	57,508,722	57,510,883	2,161	+	2	1_A375_pNL7_minus_lncRNA::1::1120, 2_A375_pNL97_plus_lncRNA::1::1564	78, 46	in gene, in gene	1	1	22	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene C11orf31	SELH, C17orf10, C11orf31	chromosome 11 open reading frame 31	NM_170746, hCT2340231.0, hCT2341134.1	1557799_at, 1557801_x_at, 224677_x_at, 226331_at, 226332_s_at, 231045_x_at	NP_734467.1, EAW73782.1, EAW73781.1
GeneID:643376	BTBD18	11	57,510,986	57,519,253	8,267	-	2	1_A375_pNL7_minus_lncRNA::1::1120, 2_A375_pNL97_plus_lncRNA::1::1564	10453, 10485	downstream, downstream	1	1	22	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene BTBD18	BTBD18	BTB (POZ) domain containing 18	NM_001145101	215349_at	NP_001138573.1
GeneID:9404	LPXN	11	58,294,344	58,345,639	51,295	-	1	1_A375_pNL7_minus_lncRNA::1::1122	-393	upstream	1	0	22	16	1	1_A375_pNL7_minus_lncRNA::1	22	Gene LPXN	LPXN, LDPL	leupaxin	NM_004811, NM_001143995, hCT2309080.0, hCT2355219.0, hCT29051.2	216250_s_at, 242778_at	NP_004802.1, NP_001137467.1, EAW73807.1, EAW73808.1, EAW73809.1
GeneID:80829	ZFP91	11	58,346,587	58,388,515	41,928	+	1	1_A375_pNL7_minus_lncRNA::1::1122	-555	upstream	1	0	22	16	1	1_A375_pNL7_minus_lncRNA::1	22	Gene ZFP91	FKSG11, DSM-6, ZFP91, ZNF757, ZFP-91, DMS-6, FLJ57065, PZF	zinc finger protein 91 homolog (mouse)	NM_053023	224631_at, 224636_at	NP_444251.1
GeneID:386607	ZFP91-CNTF	11	58,346,587	58,393,206	46,619	+	1	1_A375_pNL7_minus_lncRNA::1::1122	-555	upstream	1	0	22	16	1	1_A375_pNL7_minus_lncRNA::1	22	Gene ZFP91-CNTF	MGC51126	ZFP91-CNTF readthrough	NR_024091		
GeneID:63901	FAM111A	11	58,910,318	58,922,512	12,194	+	1	2_A375_pNL97_plus_lncRNA::1::1566	-78	upstream	0	1	11	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene FAM111A	FAM111A, FLJ22794, DKFZp686A06175, KIAA1895	family with sequence similarity 111, member A	NM_022074, NM_198847, NM_001142519, NM_001142520, NM_001142521, hCT2309181.0, hCT2309183.0, hCT2355406.0, hCT2355407.0	218248_at, 229196_at, 239368_at	NP_071357.2, NP_942144.1, NP_001135991.1, NP_001135992.1, NP_001135993.1, EAW73836.1, EAW73834.1, EAW73835.1, EAW73837.1
GeneID:5007	OSBP	11	59,341,871	59,383,617	41,746	-	1	2_A375_pNL97_plus_lncRNA::1::1570	65	in gene	0	1	19	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene OSBP	OSBP, OSBP1	oxysterol binding protein	NM_002556, hCT2309274.0	1563051_at, 201799_s_at, 201800_s_at	NP_002547.1, EAW73849.1
GeneID:100507411	LOC100507411	11	59,383,635	59,407,353	23,718	+	1	2_A375_pNL97_plus_lncRNA::1::1570	-83	upstream	0	1	19	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100507411		hypothetical LOC100507411	XR_111180, XR_111181, XR_110908, XR_110909, XR_114490, XR_114491		
GeneID:6809	STX3	11	59,522,532	59,573,355	50,823	+	4	1_A375_pNL7_minus_lncRNA::1::1126, 1_A375_pNL7_minus_lncRNA::1::1127, 2_A375_pNL97_plus_lncRNA::1::1571, 2_A375_pNL97_plus_lncRNA::1::1572	108, 32188, 60, 55676	in gene, in gene, in gene, downstream	1	1	19.67	16.33	3	1_A375_pNL7_minus_lncRNA::1	22	Gene STX3	STX3, FLJ30906, STX3A	syntaxin 3	NM_001178040, NM_004177, hCT2309171.1, hCT2309173.1, hCT2309175.1, hCT2355388.0, hCT32188.3	209238_at, 216985_s_at	NP_001171511.1, NP_004168.1, EAW73853.1, EAW73854.1, EAW73856.1, EAW73857.1, EAW73855.1
GeneID:54948	MRPL16	11	59,573,608	59,578,345	4,737	-	1	2_A375_pNL97_plus_lncRNA::1::1572	137	in gene	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MRPL16	L16mt, FLJ20484, MRP-L16, MRPL16, PNAS-111	mitochondrial ribosomal protein L16	NM_017840, hCT2347556.1, hCT32193.4	217980_s_at	NP_060310.1, EAW73859.1, EAW73858.1
GeneID:54860	MS4A12	11	60,260,251	60,274,903	14,652	+	1	1_A375_pNL7_minus_lncRNA::1::1128	22629	downstream	1	0	21	12	1	1_A375_pNL7_minus_lncRNA::1	21	Gene MS4A12	Ms4a10, MS4A12	membrane-spanning 4-domains, subfamily A, member 12	NM_017716, NM_001164470, hCT31665.2	220834_at	NP_060186.2, NP_001157942.1, EAW73893.1
GeneID:503497	MS4A13	11	60,282,886	60,310,194	27,308	+	1	1_A375_pNL7_minus_lncRNA::1::1128	-6	upstream	1	0	21	12	1	1_A375_pNL7_minus_lncRNA::1	21	Gene MS4A13	MS4A13		NM_001012417, NM_001100909		NP_001012417.2, NP_001094379.1
GeneID:22917	ZP1	11	60,635,015	60,643,164	8,149	+	1	2_A375_pNL97_plus_lncRNA::1::1573	5721	in gene	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ZP1	MGC87693, ZP1	zona pellucida glycoprotein 1 (sperm receptor)	NM_207341, hCT31654.2	237335_at	NP_997224.2, EAW73903.1
GeneID:27339	PRPF19	11	60,658,019	60,674,061	16,042	-	1	2_A375_pNL97_plus_lncRNA::1::1574	13	in gene	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PRPF19	SNEV, PRPF19, hPSO4, UBOX4, NMP200, PRP19, PSO4	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	NM_014502, hCT2309574.0, hCT2309575.0	203103_s_at	NP_055317.1, EAW73904.1, EAW73905.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Count	Intervals	Internal Gaps to Next	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ENSG00000139372	TMEM109	11	99,661,271	99,680,815	9,544	+	2	2_A275_shL97_gtex_lockRNA:1-1574, 2_A275_shL97_gtex_lockRNA:1-1575	7223, 16869	upstream, downstream	0	1	20	23.5	2	2_A275_shL97_gtex_lockRNA:1	26	Gene TMEM109	MGC33505, TMEM109	transmembrane protein 109	NM_034092, XCT2009435.0	201361_at	NP_078997.1, EAW73696.1
Gene:ENSG00000149212	TMEM132A	11	99,691,913	99,704,831	12,718	+	1	1_A275_shL97_gtex_lockRNA:1-1575	73	upstream	0	1	24	28	1	2_A275_shL97_gtex_lockRNA:1	26	Gene TMEM132A	MGC135869, FLJ20538, TMEM132A, DKFZp547E214, HSPASBP1, GBP	transmembrane protein 132A	NM_017870, NM_178031, XCT1956536.1, XCT2009431.0, XCT2009432.0, XCT2009433.0, XCT2009434.0, XCT2009436.0, XCT19569.2	218334_s_at, 222755_s_at, 224405_s_at, 232419_at	NP_060342.2, NP_821174.1, EAW73695.1, EAW73910.1, EAW73912.1, EAW73911.1, EAW73912.1
Gene:ENSG00000139346	VPS37C	11	99,697,725	99,825,816	31,168	-	2	1_A275_shL1_rhinus_lockRNA:1-1529, 2_A275_shL97_gtex_lockRNA:1-1576	-140, -12	upstream, upstream	1	1	21	16	1	1_A275_shL1_rhinus_lockRNA:1	21	Gene VPS37C	VPS37C, FLJ35497	vacuolar protein sorting 37 homolog C (S. cerevisiae)	NM_017966, XCT1765185.1, XCT2039254.0, XCT2129.2	1560352_at, 1560392_s_at, 219053_s_at	NP_060436.0, EAW73826.1, EAW73825.1, EAW73827.1
Gene:ENSG00000139370	DDB1	11	61,099,919	61,160,866	22,747	-	2	1_A275_shL1_rhinus_lockRNA:1-1530, 2_A275_shL97_gtex_lockRNA:1-1577	80, 135	e gene, upstream	1	1	33	22	1	1_A275_shL1_rhinus_lockRNA:1	33	Gene DDB1	XPE, XPE-BP, XAP1, DDBA, DDB1, UV-DDB1, XPCE	damage-specific DNA binding protein 1, 127kDa	NM_001923, XCT2311633.0, XCT2311634.0, XCT2311635.0, XCT2311637.0, XCT2126.3	205919_at	NP_001914.3, EAW73832.1, EAW73834.1, EAW73833.1, EAW73836.1, EAW73837.1
Gene:ENSG00000139354	DAK	11	61,103,634	61,116,231	13,877	+	2	1_A275_shL1_rhinus_lockRNA:1-1530, 2_A275_shL97_gtex_lockRNA:1-1577	-76, -126	upstream, upstream	1	1	33	22	1	1_A275_shL1_rhinus_lockRNA:1	33	Gene DAK	MGC39621, DAK, NET45, DKFZp586B1621	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	NM_018133, XCT2310282.1, XCT2312684.1, XCT2312.1	218955_at, 244627_at	NP_060594.2, EAW73835.1, EAW73839.1, EAW73840.1
Gene:ENSG00000139326	CYB5R3	11	61,116,220	61,129,755	13,535	-	1	2_A275_shL97_gtex_lockRNA:1-1576	-229	upstream	0	1	13	16	1	2_A275_shL97_gtex_lockRNA:1	16	Gene CYB5R3	CYB5R3, FLJ39724, LCYT5, MGC20446	cytochrome b5 reductase-dependent 3	NM_130511, NM_001166456, NM_001161452, XCT2311631.1, XCT2126.3	224735_at	NP_705839.3, NP_001156626.1, NP_001154624.1, EAW73841.1, EAW73842.1
Gene:ENSG00000139344	TMEM136	11	61,129,473	61,139,877	7,594	+	1	2_A275_shL97_gtex_lockRNA:1-1578	511	e gene	0	1	13	16	1	2_A275_shL97_gtex_lockRNA:1	16	Gene TMEM136	TMEM136, HSPC196	transmembrane protein 136	NM_018464, NM_025472, XCT22122.3	223112_at	NP_057546.1, EAW73840.1
Gene:ENSG00000139349	TMEM216	11	61,139,632	61,166,223	6,491	+	1	2_A275_shL1_rhinus_lockRNA:1-1531	152	e gene	1	0	24	16	1	1_A275_shL1_rhinus_lockRNA:1	24	Gene TMEM216	TMEM216, JBTS8, CORS2, JBTS2, MKS13-216, MKS2	transmembrane protein 216	NM_001173992, NM_001173991, NM_018463, XCT2311.0	223303_at	NP_001167461.1, NP_001167462.1, NP_060933.2, EAW73843.1
Gene:ENSG00000139370	CPSF7	11	61,170,120	61,197,664	27,544	-	3	1_A275_shL1_rhinus_lockRNA:1-1531, 2_A275_shL97_gtex_lockRNA:1-1532, 2_A275_shL97_gtex_lockRNA:1-1578	27460, 90, 130	downstream, e gene, ut gene	1	1	20.5	16	2	1_A275_shL1_rhinus_lockRNA:1	24	Gene CPSF7	CPSF7d, MGC9215, FLJ39924, CPSF7, FLJ12529	cleavage and polyadenylation specific factor 7, 59kDa	NM_024511, NM_001130540, NM_001142965, XCT1965327.1	217595_at	NP_079057.2, NP_001120312.1, NP_001136027.1, EAW73845.1
Gene:ENSG00000139368	SDHAF2	11	61,197,997	61,214,239	16,842	+	2	1_A275_shL1_rhinus_lockRNA:1-1532, 2_A275_shL97_gtex_lockRNA:1-1578	-169, -283	upstream, upstream	1	1	17	16	1	2_A275_shL97_gtex_lockRNA:1	16	Gene SDHAF2	SDH5, FOZ, FLJ20487, SDHAF2, C11orf9	succinate dehydrogenase complex assembly factor 2	NM_017841	223058_at	NP_060311.1
Gene:ENSG00000139355	SYT7	11	61,282,765	61,349,298	65,513	+	9	1_A275_shL1_rhinus_lockRNA:1-1533, 1_A275_shL1_rhinus_lockRNA:1-1534, 1_A275_shL1_rhinus_lockRNA:1-1535, 1_A275_shL1_rhinus_lockRNA:1-1580, 2_A275_shL97_gtex_lockRNA:1-1581	23335, 1, 5982, 726, 35234, 13682, 662	e gene, upstream, us gene, ut gene, upstream	1	1	49.67	66	3	2_A275_shL97_gtex_lockRNA:1	99	Gene SYT7	SYT-VII, MGC150517, SYT7, IPCA-7, PCANAP7	synaptotagmin VII	NM_004200, XCT2311632.0, XCT2311633.0, XCT2311634.0, XCT2311635.0, XCT2311637.0, XCT2130.3	1559392_s_at, 1559393_at, 226167_at, 232029_at	NP_004191.2, EAW73853.1, EAW73854.1, EAW73855.1, EAW73856.1, EAW73857.1
Gene:ENSG00000139359	C11orf46	11	61,320,121	61,353,689	33,568	+	2	1_A275_shL1_rhinus_lockRNA:1-1536, 2_A275_shL97_gtex_lockRNA:1-1582	40103, 40119	downstream, downstream	1	1	31	36	1	2_A275_shL97_gtex_lockRNA:1	36	Gene C11orf46	MGC10761, N865, MRF, KIAA0854, C11orf46	chromosome 11 open reading frame 46	NM_001127392, NM_012279, XCT2310307.0, XCT2310308.0, XCT2310310.0, XCT2310311.0, XCT2310312.0, XCT2310313.0	204073_s_at, 217462_at, 217463_s_at	NP_001120864.1, NP_037411.1, EAW73862.1, EAW73864.1, EAW73865.1, EAW73866.1, EAW73867.1
Gene:ENSG00000139352	C11orf46	11	61,339,602	61,360,085	3,483	-	2	1_A275_shL1_rhinus_lockRNA:1-1536, 2_A275_shL97_gtex_lockRNA:1-1582	-139, -155	upstream, upstream	1	1	21	36	1	2_A275_shL97_gtex_lockRNA:1	36	Gene C11orf46	C11orf46	chromosome 11 open reading frame 10	NM_014356, XCT2311581.0, XCT2127.1	218212_s_at	NP_055921.1, EAW73870.1, EAW73870.1
Gene:ENSG00000139356	MRVI1	11	61,359,967	61,360,633	66	-	2	1_A275_shL1_rhinus_lockRNA:1-1536, 2_A275_shL97_gtex_lockRNA:1-1582	-191, -207	upstream, upstream	1	1	21	36	1	2_A275_shL97_gtex_lockRNA:1	36	Gene MRVI1	MRVI1, MIRN611, hsa-mir-611	microRNA 611	NR_030342		
Gene:ENSG00000139351	PEX1	11	61,369,150	61,384,710	8,560	+	2	1_A275_shL1_rhinus_lockRNA:1-1536, 2_A275_shL97_gtex_lockRNA:1-1582	74, 90	ut gene, ut gene	1	1	31	36	1	2_A275_shL97_gtex_lockRNA:1	36	Gene PEX1	PEX1, MP1, PEN1, RAD2	Mg2 chaperone-specific exteroreceptor 1	NM_004111, XCT2311.2	204767_s_at, 204768_s_at	NP_000462.1, EAW73872.1
Gene:ENSG00000139350	PAOD1	11	61,387,097	61,564,529	17,432	+	4	1_A275_shL1_rhinus_lockRNA:1-1536, 1_A275_shL1_rhinus_lockRNA:1-1537, 2_A275_shL97_gtex_lockRNA:1-1582, 2_A275_shL97_gtex_lockRNA:1-1583	23003, 91, 24289, 113	e gene, downstream, ut gene, downstream, ut gene	1	1	24	25	2	2_A275_shL97_gtex_lockRNA:1	26	Gene PAOD1	PAOD6, PAOD3, PAOD1, DSD, LLCDL1, FLJ90273, FLJ35936, TUH2	fatty acid desaturase 1	NM_013402, XCT2311614.0	205952_s_at, 205953_at, 205954_s_at	NP_037534.2, EAW73873.1
Gene:ENSG00000207606	MIR1908	11	61,562,833	61,562,712	79	-	2	1_A275_shL1_rhinus_lockRNA:1-1537, 2_A275_shL97_gtex_lockRNA:1-1583	-1126, -1704	upstream, upstream	1	1	17	14	1	1_A275_shL1_rhinus_lockRNA:1	17	Gene MIR1908	MIR1908, hsa-mir-1908, MIRN1908	microRNA 1908	NR_031729		
Gene:ENSG00000139343	PAOD2	11	61,640,998	61,659,006	16,008	+	4	1_A275_shL1_rhinus_lockRNA:1-1538, 1_A275_shL1_rhinus_lockRNA:1-1539, 2_A275_shL97_gtex_lockRNA:1-1584, 2_A275_shL97_gtex_lockRNA:1-1585	542, -5556, 670, -5586	e gene, upstream, ut gene, upstream	1	1	20	17	2	1_A275_shL1_rhinus_lockRNA:1	21	Gene PAOD2	PAOD2, LCCDL3, CYB5RP	fatty acid desaturase 2	NM_021727, XCT2311698.0, XCT2311699.0, XCT2116.2	204297_at, 240393_s_at	NP_068370.2, EAW73876.1, EAW73877.1, EAW73878.1
Gene:ENSG00000139345	RABSL1	11	61,664,773	61,664,997	20,224	+	4	1_A275_shL1_rhinus_lockRNA:1-1538, 1_A275_shL1_rhinus_lockRNA:1-1539, 2_A275_shL97_gtex_lockRNA:1-1585, 2_A275_shL97_gtex_lockRNA:1-1586	26533, 20133, 26661, 20403	downstream, e gene, downstream, downstream	1	1	20	17	2	1_A275_shL1_rhinus_lockRNA:1	21	Gene RABSL1	RABSL1, GRAB	RABSA interacting protein (ubx2)-like 1	NM_013401, XCT1669491.1, XCT1799219.1, XCT2355359.0	219379_at	NP_037532.2, EAW73881.1, EAW73879.1, EAW73880.1
Gene:ENSG00000139343	BEST1	11	61,717,396	61,731,835	14,879	+	2	1_A275_shL1_rhinus_lockRNA:1-1540, 2_A275_shL97_gtex_lockRNA:1-1587	17700, 16524	downstream, downstream	1	1	17	16	1	1_A275_shL1_rhinus_lockRNA:1	17	Gene BEST1	TU159, RP30, BMD, BEST, BEST1, ARB, VMD2	bestrophin 1	NM_004183, NM_001139443, XCT1669511.1, XCT2155320.0, XCT2310321.0, XCT2355361.0, XCT2355362.0, XCT2355363.0, XCT2355364.0	1554442_at, 1554443_s_at, 207671_s_at	NP_004174.1, NP_001132915.1, EAW73882.1, EAW73883.1, EAW73885.1, EAW73887.1, EAW73884.1, EAW73886.1
Gene:ENSG00000139354	PTH1	11	61,731,797	61,735,132	3,376	-	2	1_A275_shL1_rhinus_lockRNA:1-1540, 2_A275_shL97_gtex_lockRNA:1-1587	176, -548	e gene, upstream	1	1	17	16	1	1_A275_shL1_rhinus_lockRNA:1	17	Gene PTH1	PTH1, PUP, MGC102426, PTH, PTG15, PTHLH, PHC	broker, tearing polypeptide 1	NM_002822, XCT1614521.1, XCT2311605.1, XCT2345253.0, XCT2345258.0, XCT2345259.0, XCT2345260.0, XCT2345267.0, XCT2345268.0, XCT2345289.0, XCT2345290.0, XCT2345291.0, XCT2345292.0, XCT2355365.0	203758_s_at, 214211_at	NP_002813.2, EAW73888.1, EAW73889.1, EAW73890.1, EAW73891.1, EAW73892.1, EAW73893.1, EAW73894.1, EAW73895.1, EAW73896.1, EAW74000.1, EAW74001.1
Gene:ENSG00000139329	INCENP	11	61,891,448	61,920,635	28,188	+	1	1_A275_shL1_rhinus_lockRNA:1-1541	11	e gene	1	0	10	14	1	1_A275_shL1_rhinus_lockRNA:1	16	Gene INCENP	INCENP, MGC111393, FLJ31633	inner centromere protein antigens 135/155kDa	NM_001040694, NM_020238, XCT2310324.0, XCT2310328.0, XCT2310329.0	218769_at, 242707_at	NP_001033764.1, NP_064823.2, EAW74002.1, EAW74004.1, EAW74005.1
Gene:ENSG00000139337	SCGB1D2	11	62,009,724	62,012,260	2,536	+	2	1_A275_shL1_rhinus_lockRNA:1-1542, 2_A275_shL97_gtex_lockRNA:1-1588	3300, 3208	downstream, downstream	1	1	23	23	1	2_A275_shL97_gtex_lockRNA:1	23	Gene SCGB1D2	LIPB, LPHB, SCGB1D2	secretoglobin, family 1D, member 2	NM_006551, XCT2310062.2	206799_at	NP_006542.2, EAW74009.1
Gene:ENSG00000139329	ASRGL1	11	62,104,774	62,160,687	56,113	+	1	2_A275_shL97_gtex_lockRNA:1-1589	166	e gene	0	1	11	23	1	2_A275_shL97_gtex_lockRNA:1	23	Gene ASRGL1	FLJ22316, CRASH, ALP, ALP1, ASRGL1	asparaginase like 1	NM_025080, NM_001083626, XCT1966555.1, XCT1993529.1, XCT2309903.0, XCT2309904.0, XCT2309905.0, XCT2309906.0, XCT2309907.0, XCT2355302.0, XCT2355303.0, XCT2355304.0, XCT2355305.0	218837_s_at, 227764_at	NP_079263.2, NP_001077293.1, EAW74012.1, EAW74013.1, EAW74016.1, EAW74017.1, EAW74014.1, EAW74015.1
Gene:ENSG00000139326	AHNAK	11	62,201,016	62,314,232	113,216	+	2	1_A275_shL1_rhinus_lockRNA:1-1543, 2_A275_shL97_gtex_lockRNA:1-1592	4546, 53420	upstream, us gene	1	1	12	15	2	1_A275_shL1_rhinus_lockRNA:1	17	Gene AHNAK	AHNAK, AHNAX93, MGC3093	AHNAK nucleoprotein	NM_024060, NM_001620, XCT1799081.1	1553992_at, 201999_at, 220016_at, 231291_s_at, 235554_at	NP_078955.2, NP_001611.1, EAW74019.1
Gene:ENSG00000139318	EEF1G	11	62,327,072	62,341,460	14,387	-	1	1_A275_shL1_rhinus_lockRNA:1-1543	20550	downstream	1	0	17	15	1	1_A275_shL1_rhinus_lockRNA:1	17	Gene EEF1G	GIG35, EF1G, EEF1G	eukaryotic translation elongation factor 1 gamma	NM_001404, XCT2315395.1, XCT2315397.1, XCT2315310.1, XCT2315313.1, XCT2315314.1, XCT2355306.0	200969_s_at, 211345_s_at, 211927_s_at	NP_001395.1, EAW74023.1, EAW74024.1, EAW74026.1, EAW74027.1, EAW74028.1, EAW74029.1
Gene:ENSG00000139324	TUT1	11	62,342,517	62,359,109	16,592	+	2	1_A275_shL1_rhinus_lockRNA:1-1543, 2_A275_shL97_gtex_lockRNA:1-1593, 2_A275_shL97_gtex_lockRNA:1-1594	-76, -21, 10043	upstream, upstream	1	1	36.5	26.5	2	2_A275_shL97_gtex_lockRNA:1	60	Gene TUT1	FLJ22347, MGC149899, STAR-PAP, FLJ22267, RBM21, TUT1, PAPD2, FLJ21650, TUTase, MGC131997	terminal uridylyl transferase 1, U6 snRNA-specific	NM_022630, XCT2315339.1	218965_s_at	NP_072741.2, EAW74038.1
Gene:ENSG00000139314	MTA2	11	62,360,675	62,369,303	8,628	+	3	1_A275_shL1_rhinus_lockRNA:1-1544, 1_A275_shL97_gtex_lockRNA:1-1595, 2_A275_shL97_gtex_lockRNA:1-1596	10119, 10167, 151	downstream, downstream, e gene	1	1	36.5	26.5	2	1_A275_shL1_rhinus_lockRNA:1	60	Gene MTA2	MTA1L1, DKFZp686F2251, MTA2, PID	metastasis associated 1 family, member 2	NM_004739, XCT1714613.3, XCT2315304.0	202464_s_at	NP_004730.2, EAW74032.1, EAW74031.1
Gene:ENSG00000139308	EML2	11	62,369,691	62,380,237	10,546	-	3	1_A275_shL1_rhinus_lockRNA:1-1544, 2_A275_shL97_gtex_lockRNA:1-1595, 2_A275_shL97_gtex_lockRNA:1-1596	21053, 13585, 8331	downstream, downstream, upstream	1	1	36.33	24	3	1_A275_shL1_rhinus_lockRNA:1	60	Gene EML2	FLJ38627, MGC111422, ELP66, EML2	echinoderm microtubule associated protein like 2	NM_152265, XCT1714612.2, XCT1969772.1, XCT1969772.2, XCT2315300.0, XCT2315301.0, XCT2315302.0, XCT2355352.0, XCT2355353.0	202442_at, 202443_at, 212669_s_at	NP_694972.2, EAW74033.1, EAW74034.1, EAW74035.1, EAW74036.1, EAW74037.1, EAW74038.1
Gene:ENSG00000139304	ROM1	11	62,380,213	62,382,592	2,379	+	1	2_A275_shL97_gtex_lockRNA:1-1598	8355	downstream	0	1	12	19	1	2_A275_shL97_gtex_lockRNA:1	19	Gene ROM1	ROM, ROSP1, ROM1, RP7, TSPAN23	retinal outer segment membrane protein 1	NM_000327, XCT2309690.0	203606_at	NP_000318.1, EAW74041.1
Gene:ENSG00000139297	B3GAT3	11	62,382,765	62,399,646	16,882	-	1	2_A275_shL97_gtex_lockRNA:1-1598	-120	upstream	0	1	12	19	1	2_A275_shL97_gtex_lockRNA:1	19	Gene B3GAT3	B3GAT3, GLCAT1	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	NM_012300, XCT2315296.1, XCT2352750.0, XCT2427.4	203552_at, 241179_at	NP_036332.2, EAW74043.1, EAW74042.1, EAW74044.1
Gene:ENSG00000139289	QKI	11	62,392,294	62,614,104	21,806	-	3	2_A275_shL97_gtex_lockRNA:1-1598	24536, 38	downstream, e gene	0	1	13.5	16	2	2_A275_shL97_gtex_lockRNA:1	19	Gene QKI	Q3NA, NAA0068, QLI1, QKI, QKI6	quaking homolog, KH domain RNA binding (mouse)	NM_138433, NM_138435, XCT1962.4, XCT1981126.2, XCT1981127.2, XCT1981457.2, XCT2355374.0, XCT2355375.0	213534_s_at, 214626_s_at	NP_620181.1, NP_620183.1, EAW74045.1, EAW74046.1, EAW74047.1, EAW74050.1, EAW74048.1
Gene:ENSG00000139278	INTS5	11	62,614,320	62,620,774	6,454	-	1	2_A275_shL97_gtex_lockRNA:1-1598	8694	downstream	0	1	15	17	1	2_A275_shL97_gtex_lockRNA:1	17	Gene INTS5	INTS, INTS5, KIAA1945	integrator complex subunit 5	NM_020748, XCT2315291.1	221515_at, 221516_s_at	NP_065801.1, EAW74051.1
Gene:ENSG00000139269	C11orf46	11	62,630,268	62,639,241	8,982	-	5	1_A275_shL1_rhinus_lockRNA:1-1545, 1_A275_shL1_rhinus_lockRNA:1-1546, 1_A275_shL1_rhinus_lockRNA:1-1547, 1_A275_shL1_rhinus_lockRNA:1-1548, 1_A275_shL1_rhinus_lockRNA:1-1549, 2_A275_shL97_gtex_lockRNA:1-1599	8637, -279, 5417, -7	e gene, upstream, ut gene, ut gene, upstream	1	1	17.33	16.67	3	1_A275_shL1_rhinus_lockRNA:1	21	Gene C11orf46	MGC24777, C11orf46	chromosome 11 open reading frame 46	NM_024099, XCT1772811.3, XCT1857210.1, XCT2345229.0, XCT2345256.0, XCT2345277.0, XCT2345286.0, XCT2355354.0	217637_s_at	NP_077004.2, EAW74056.1, EAW74052.1, EAW74054.1, EAW74055.1, EAW74058.1, EAW74053.1, EAW74057.1
Gene:ENSG00000139291	METTL12	11	62,632,779	62,634,823	2,164	+	5	1_A275_shL1_rhinus_lockRNA:1-1545, 1_A275_shL1_rhinus_lockRNA:1-1546, 1_A275_shL1_rhinus_lockRNA:1-1547, 1_A275_shL1_rhinus_lockRNA:1-1548, 1_A275_shL1_rhinus_lockRNA:1-1549, 2_A275_shL97_gtex_lockRNA:1-1599	-475, 6341, -10, 1045, 6469	upstream, downstream, upstream, e gene, downstream	1	1	17.33	16.67	3	1_A275_shL1_rhinus_lockRNA:1	21	Gene METTL12	METTL12		NM_030943229	235690_at, 238316_at	NP_001036584.1
Gene:ENSG00000207552	SNORA57	11	62,632,894	62,633,042	148	+	5	1_A275_shL1_rhinus_lockRNA:1-1545, 1_A275_shL1_rhinus_lockRNA:1-1546, 1_A275_shL1_rhinus_lockRNA:1-1547, 1_A275_shL1_rhinus_lockRNA:1-1548, 1_A275_shL1_rhinus_lockRNA:1-1549, 2_A275_shL97_gtex_lockRNA:1-1599	-590, 6629, -190, 930, 6354	upstream, downstream, downstream, upstream, downstream	1	1	17.33	16.67	3	1_A275_shL1_rhinus_lockRNA:1	21	Gene SNORA57	U69, SNORA57	small nucleolar RNA, H/ACA box 57	NR_006390		
Gene:ENSG00000139289	C11orf83	11	62,639,126	62,639,852	726	+	5	1_A275_shL1_rhinus_lockRNA:1-1545, 1_A275_shL1_rhinus_lockRNA:1-1546, 1_A275_shL1_rhinus_lockRNA:1-1547, 1_A275_shL1_rhinus_lockRNA:1-1548, 1_A275_shL1_rhinus_lockRNA:1-1549, 2_A275_shL97_gtex_lockRNA:1-1599	4822, 394, 4422, -, 5282, 12	upstream, us gene, upstream, upstream, us gene	1	1	17.33	16.67	3	1_A275_shL1_rhinus_lockRNA:1	21	Gene C11orf83	C11orf83, UNQ655, CCDS41658.1, MGC87549	chromosome 11 open reading frame 83	NM_001085372	236099_at	NP_001076841.1
Gene:ENSG00000139288	UBXN6	11	62,641,872	62,648,827	2,930	-	3	1_A275_shL1_rhinus_lockRNA:1-1549, 2_A275_shL97_gtex_lockRNA:1-1598	7807, 12703, 1279	downstream, downstream, downstream	1	1	16	16.5	2	1_A275_shL1_rhinus_lockRNA:1	21	Gene UBXN6	ZB2B, SAKS1, UBXN1, UBXD10	UBX domain protein 6	NM_014562, XCT1969780.1, XCT2315295.0, XCT2315297.0, XCT2315298.0, XCT2355314.0, XCT2355315.0, XCT2355316.0	201671_s_at, 219523_at	NP_055737.2, EAW74067.1, EAW74063.1, EAW74064.1, EAW74065.1, EAW74066.1, EAW74061.1, EAW74062.1
Gene:ENSG00000139284	BSCL2	11	62,657,747	62,677,046	19,299	-	2	1_A275_shL1_rhinus_lockRNA:1-1547, 2_A275_shL97_gtex_lockRNA:1-1600	-170, -106	upstream, upstream	1	1	17	14	1	1_A275_shL1_rhinus_lockRNA:1	17	Gene BSCL2	MGC34934, FLJ19551, BSCL2, HMNB, GMG3LG, SPG17	Berardinelli-Seip congenital lipodystrophy 2 (seipin)	NM_032667, NM_001130702, NM_001122955		NP_116096.2, NP_001124174.1, NP_001116527.1
Gene:ENSG00000139278	GNG3	11	62,675,114	62,676,676	1,566	+	2	1_A275_shL1_rhinus_lockRNA:1-1547, 2_A275_shL97_gtex_lockRNA:1-1600	2102, 2035	downstream, downstream	1	1	17	14	1	1_A275_shL1_rhinus_lockRNA:1	17	Gene GNG3	GMG3		NM_012302, XCT1772693.1	222003_s_at	NP_036334.1, EAW74082.1
Gene:ENSG00000139274	HNRNPU L2	11	62,682,220	62,694,821	12,601	+	4	1_A275_shL1_rhinus_lockRNA:1-1547, 2_A275_shL97_gtex_lockRNA:1-1600, 2_A275_shL97_gtex_lockRNA:1-1601, 2_A275_shL97_gtex_lockRNA:1-1602	17605, 17669, 655, -198	downstream, downstream, e gene, upstream	1	1	14	16.67	3	2_A275_shL97_gtex_lockRNA:1	20	Gene HNRNPUL2	HNRNPUL2, DKFZp762N1910, HNRPUL2	heterogeneous nuclear ribonucleoprotein U-like 2	NM_001078556	222264_at, 236053_at	NP_001073027.1
Gene:ENSG00000153227	TTC9C	11	62,693,652	62,696,108	10,156	+	2	2_A275_shL97_gtex_lockRNA:1-1602, 2_A275_shL97_gtex_lockRNA:1-1603	-1836, -453	upstream, upstream	0	1	12.5	16	2	2_A275_shL97_gtex_lockRNA:1	20	Gene TTC9C	MGC29648, TTC9C	tetratricopeptide repeat domain 9C	NM_173510, XCT2309698.0, XCT2355356.0	1560199_at, 226179_at	NP_776711.1, EAW74086.1, EAW74087.1
Gene:ENSG00000139257	POLR2G	11	62,529,011	62,534,187	5,176	+	3	1_A275_shL1_rhinus_lockRNA:1-1545, 2_A275_shL97_gtex_lockRNA:1-1602	9656, 19077	downstream, downstream	1	1	16	21	1	2_A275_shL97_gtex_lockRNA:1	21	Gene POLR2G	MGC135367, RPB19, hRPB19, hsRPB7, RPB7, POLR2G, MGC105269	polymerase (RNA) II (DNA directed) polypeptide G	NM_002695, XCT2309695.0, XCT2309696.0, XCT2355359.0	202206_at	NP_002677.1, EAW74091.1, EAW74090.1, EAW74092.1

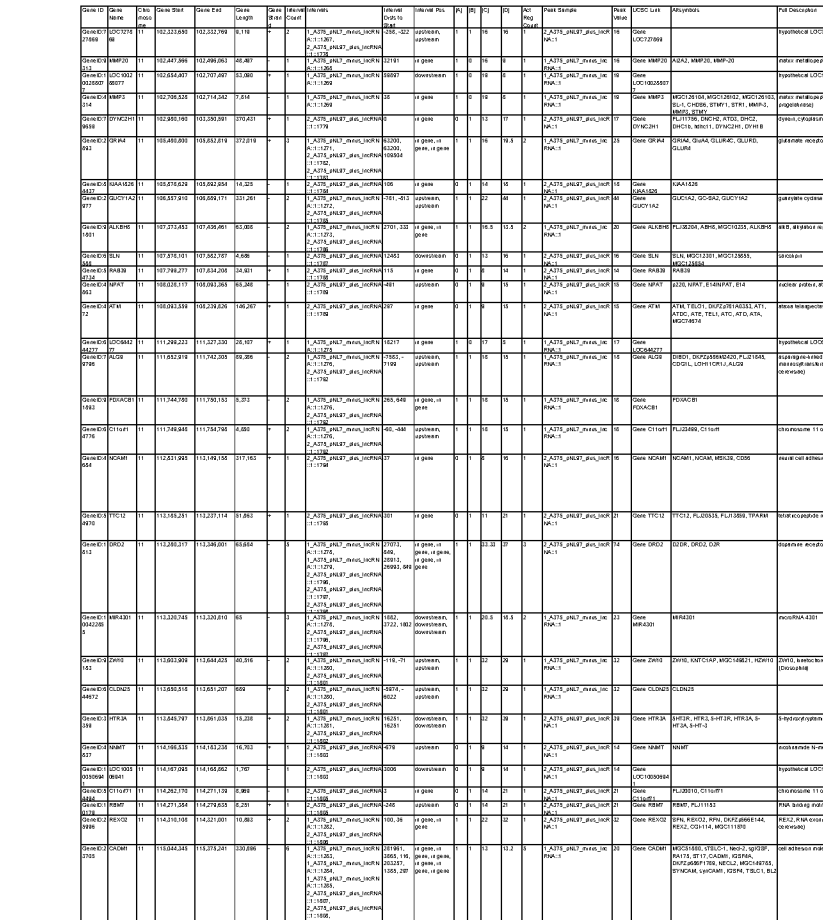
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:10629	TAF6L	11	62,538,875	62,554,814	15,939	+	6	1_A375_pNL7_minus_lncRNA::1::1148, 1_A375_pNL7_minus_lncRNA::1::1149, 1_A375_pNL7_minus_lncRNA::1::1150, 2_A375_pNL97_plus_lncRNA::1::1603, 2_A375_pNL97_plus_lncRNA::1::1604, 2_A375_pNL97_plus_lncRNA::1::1605	-208, 16133, 20421, 213, 15861, 20453	upstream, downstream, downstream, in gene, in gene, downstream	1	1	18.33	23.33	3	2_A375_pNL97_plus_lncRNA::1	28	Gene TAF6L	PAF65A, FLJ11136, MGC4288, TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	NM_006473, hCT2309607.1, hCT2309608.1, hCT2309609.1, hCT2344938.0	213209_at, 213210_at, 213211_s_at, 222053_at, 230049_at	NP_006464.1, EAW74094.1, EAW74093.1, EAW74095.1, EAW74096.1
GeneID:374395	TMEM179B	11	62,554,874	62,557,872	2,998	+	4	1_A375_pNL7_minus_lncRNA::1::1149, 1_A375_pNL7_minus_lncRNA::1::1150, 2_A375_pNL97_plus_lncRNA::1::1604, 2_A375_pNL97_plus_lncRNA::1::1605	134, 4422, -136, 4454	in gene, downstream, upstream, downstream	1	1	19.5	24.5	2	2_A375_pNL97_plus_lncRNA::1	28	Gene TMEM179B	TMEM179B	transmembrane protein 179B	NM_199337, hCT2309610.0, hCT2309612.0, hCT2309614.0	226089_x_at	NP_955369.1, EAW74098.1, EAW74099.1, EAW74100.1
GeneID:79064	TMEM223	11	62,557,767	62,559,466	1,699	-	4	1_A375_pNL7_minus_lncRNA::1::1149, 1_A375_pNL7_minus_lncRNA::1::1150, 2_A375_pNL97_plus_lncRNA::1::1604, 2_A375_pNL97_plus_lncRNA::1::1605	4476, 190, 4750, 158	downstream, in gene, downstream, in gene	1	1	19.5	24.5	2	2_A375_pNL97_plus_lncRNA::1	28	Gene TMEM223	TMEM223, MGC3196	transmembrane protein 223	NM_001080501	220934_s_at, 238981_at	NP_001073970.1
GeneID:10482	NXF1	11	62,559,598	62,572,964	13,366	-	6	1_A375_pNL7_minus_lncRNA::1::1149, 1_A375_pNL7_minus_lncRNA::1::1150, 1_A375_pNL7_minus_lncRNA::1::1151, 2_A375_pNL97_plus_lncRNA::1::1604, 2_A375_pNL97_plus_lncRNA::1::1605, 2_A375_pNL97_plus_lncRNA::1::1606	17956, 13668, 100, 18228, 13636, 52	downstream, downstream, in gene, downstream, downstream, in gene	1	1	22.33	23.33	3	2_A375_pNL97_plus_lncRNA::1	28	Gene NXF1	NXF1, MEX67, DKFZp667O0311, TAP	nuclear RNA export factor 1	NM_001081491, NM_006362, hCT2315263.1, hCT2315264.1, hCT2315265.1, hCT2315266.1, hCT2344940.0	208922_s_at	NP_001074960.1, NP_006353.2, EAW74103.1, EAW74104.1, EAW74106.1, EAW74107.1, EAW74105.1
GeneID:6811	STX5	11	62,574,369	62,599,560	25,191	-	8	1_A375_pNL7_minus_lncRNA::1::1151, 1_A375_pNL7_minus_lncRNA::1::1152, 1_A375_pNL7_minus_lncRNA::1::1153, 1_A375_pNL7_minus_lncRNA::1::1154, 2_A375_pNL97_plus_lncRNA::1::1606, 2_A375_pNL97_plus_lncRNA::1::1607, 2_A375_pNL97_plus_lncRNA::1::1608, 2_A375_pNL97_plus_lncRNA::1::1609	26696, 552, -152, -9688, 26648, 584, -7331, -9688	downstream, in gene, upstream, upstream, downstream, in gene, upstream, upstream	1	1	31.5	31.5	4	2_A375_pNL97_plus_lncRNA::1	63	Gene STX5	SED5, STX5, STX5A	syntaxin 5	NM_003164, hCT1772907.1, hCT2315259.1, hCT2315260.1	203330_s_at	NP_003155.2, EAW74110.1, EAW74108.1, EAW74109.1
GeneID:54663	WDR74	11	62,600,383	62,607,628	7,245	-	6	1_A375_pNL7_minus_lncRNA::1::1152, 1_A375_pNL7_minus_lncRNA::1::1153, 1_A375_pNL7_minus_lncRNA::1::1154, 2_A375_pNL97_plus_lncRNA::1::1607, 2_A375_pNL97_plus_lncRNA::1::1608, 2_A375_pNL97_plus_lncRNA::1::1609	8620, 7916, -1620, 8652, 737, -1620	downstream, downstream, upstream, downstream, in gene, upstream	1	1	32.67	35	3	2_A375_pNL97_plus_lncRNA::1	63	Gene WDR74	WDR74, FLJ21730, FLJ10439	WD repeat domain 74	NM_018093, hCT1764836.2, hCT2340857.0	218278_at, 221712_s_at	NP_060563.2, EAW74111.1, EAW74112.1
GeneID:26855	RNU2-2	11	62,609,096	62,609,233	137	-	6	1_A375_pNL7_minus_lncRNA::1::1152, 1_A375_pNL7_minus_lncRNA::1::1153, 1_A375_pNL7_minus_lncRNA::1::1154, 2_A375_pNL97_plus_lncRNA::1::1607, 2_A375_pNL97_plus_lncRNA::1::1608, 2_A375_pNL97_plus_lncRNA::1::1609	10225, 9521, -15, 10257, 2342, -15	downstream, downstream, upstream, downstream, downstream, upstream	1	1	32.67	35	3	2_A375_pNL97_plus_lncRNA::1	63	Gene RNU2-2	U2, RNU2B, RNU2-2	RNA, U2 small nuclear 2	NR_002761		
GeneID:23642	SNHG1	11	62,619,460	62,623,360	3,900	-	3	1_A375_pNL7_minus_lncRNA::1::1154, 2_A375_pNL97_plus_lncRNA::1::1609, 2_A375_pNL97_plus_lncRNA::1::1610	14112, 14112, -224	downstream, downstream, upstream	1	1	36.5	42	2	2_A375_pNL97_plus_lncRNA::1	63	Gene SNHG1	NCRNA00057, U22HG, SNHG1, UHG	small nucleolar RNA host gene 1 (non-protein coding)	NR_003098	224610_at	
GeneID:9304	SNORD22	11	62,620,382	62,620,507	125	-	1	2_A375_pNL97_plus_lncRNA::1::1610	-3077	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD22	U22, RNU22, SNORD22	small nucleolar RNA, C/D box 22	NR_000008		
GeneID:9298	SNORD31	11	62,620,798	62,620,865	67	-	1	2_A375_pNL97_plus_lncRNA::1::1610	-2719	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD31	SNORD31, RNU31, U31	small nucleolar RNA, C/D box 31	NR_002560		
GeneID:9299	SNORD30	11	62,621,135	62,621,204	69	-	1	2_A375_pNL97_plus_lncRNA::1::1610	-2380	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD30	SNORD30, RNU30, U30	small nucleolar RNA, C/D box 30	NR_002561		
GeneID:9297	SNORD29	11	62,621,376	62,621,440	64	-	1	2_A375_pNL97_plus_lncRNA::1::1610	-2144	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD29	U29, RNU29, SNORD29	small nucleolar RNA, C/D box 29	NR_002559		
GeneID:9300	SNORD28	11	62,622,093	62,622,167	74	-	1	2_A375_pNL97_plus_lncRNA::1::1610	-1417	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD28	SNORD28, U28, RNU28	small nucleolar RNA, C/D box 28	NR_002562		
GeneID:9301	SNORD27	11	62,622,484	62,622,555	71	-	1	2_A375_pNL97_plus_lncRNA::1::1610	-1029	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD27	RNU27, U27, SNORD27	small nucleolar RNA, C/D box 27	NR_002563		
GeneID:9302	SNORD26	11	62,622,764	62,622,838	74	-	1	2_A375_pNL97_plus_lncRNA::1::1610	-746	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD26	U26, SNORD26, RNU26	small nucleolar RNA, C/D box 26	NR_002564		
GeneID:9303	SNORD25	11	62,623,037	62,623,103	66	-	1	2_A375_pNL97_plus_lncRNA::1::1610	-481	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD25	SNORD25, U25, RNU25	small nucleolar RNA, C/D box 25	NR_002565		
GeneID:6520	SLC3A2	11	62,623,518	62,656,353	32,835	+	3	1_A375_pNL7_minus_lncRNA::1::1155, 2_A375_pNL97_plus_lncRNA::1::1610, 2_A375_pNL97_plus_lncRNA::1::1611	25282, 66, 25314	in gene, in gene, in gene	1	1	25	34.5	2	2_A375_pNL97_plus_lncRNA::1	48	Gene SLC3A2	4F2, 4T2HC, NACAE, MDU1, CD98, 4F2HC, CD98HC, SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	NM_001012661, NM_001012662, NM_001012663, NM_001012664, NM_001013251, NM_002394, hCT2309580.0, hCT2309581.0, hCT2309582.0, hCT2309583.0, hCT2355337.0, hCT2355338.0	200924_s_at	NP_001012679.1, NP_001012680.1, NP_001012681.1, NP_001012682.1, NP_001013269.1, NP_002385.3, EAW74118.1, EAW74119.1, EAW74120.1, EAW74121.1, EAW74122.1, EAW74123.1
GeneID:9356	SLC22A6	11	62,744,069	62,752,469	8,400	-	2	1_A375_pNL7_minus_lncRNA::1::1156, 2_A375_pNL97_plus_lncRNA::1::1612	4693, 4725	in gene, in gene	1	1	24	19	1	1_A375_pNL7_minus_lncRNA::1	24	Gene SLC22A6	FLJ55736, SLC22A6, MGC45260, HOAT1, ROAT1, PAHT, OAT1	solute carrier family 22 (organic anion transporter), member 6	NM_004790, NM_153276, NM_153277, NM_153278, hCT12402.2, hCT2315246.0, hCT2315247.0, hCT2315248.0	210343_s_at, 216599_x_at	NP_004781.2, NP_695008.1, NP_695009.1, NP_695010.1, EAW74130.1, EAW74131.1, EAW74129.1, EAW74132.1
GeneID:54979	HRASLS2	11	63,320,242	63,330,855	10,613	-	1	2_A375_pNL97_plus_lncRNA::1::1613	-4004	upstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene HRASLS2	PLA1/2-2, FLJ20556, HRASLS2	HRAS-like suppressor 2	NM_017878, hCT1641002.1	216759_at, 216760_at, 221122_at	NP_060348.1, EAW74157.1
GeneID:11145	PLA2G16	11	63,341,934	63,381,941	40,007	-	1	2_A375_pNL97_plus_lncRNA::1::1613	47082	downstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PLA2G16	MGC118754, HRASLS3, HREV107-3, PLA2G16, AdPLA, H-REV107-1, HREV107	phospholipase A2, group XVI	NM_007069, NM_001128203, hCT2310772.0, hCT2310773.0, hCT2355212.0	209581_at, 235110_at	NP_009000.2, NP_001121675.1, EAW74158.1, EAW74159.1, EAW74160.1
GeneID:25923	ATL3	11	63,396,437	63,439,083	42,646	-	2	1_A375_pNL7_minus_lncRNA::1::1157, 2_A375_pNL97_plus_lncRNA::1::1614	-53, 11	upstream, in gene	1	1	27	18	1	1_A375_pNL7_minus_lncRNA::1	27	Gene ATL3	DKFZp564J0863, ATL3	atlastin GTPase 3	NM_015459, hCT2310774.1, hCT2310775.1, hCT2355297.0	223452_s_at, 223453_s_at	NP_056274.3, EAW74163.1, EAW74161.1, EAW74162.1
GeneID:10313	RTN3	11	63,448,922	63,527,363	78,441	+	3	1_A375_pNL7_minus_lncRNA::1::1157, 2_A375_pNL97_plus_lncRNA::1::1614, 2_A375_pNL97_plus_lncRNA::1::1615	-9786, -9850, 518	upstream, upstream, in gene	1	1	18.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	27	Gene RTN3	ASYIP, NSPLII, RTN3-A1, HAP, RTN3, NSPL2	reticulon 3	NM_201429, NM_201430, NM_201428, NM_006054, hCT1814006.2, hCT2310251.0, hCT2310252.0, hCT2355355.0, hCT2355356.0, hCT2355357.0, hCT2355358.0	219549_s_at, 224564_s_at	NP_958832.1, NP_958833.1, NP_006045.1, NP_958831.1, EAW74167.1, EAW74169.1, EAW74164.1, EAW74165.1, EAW74166.1, EAW74168.1, EAW74170.1
GeneID:1351	COX8A	11	63,742,079	63,744,015	1,936	+	3	1_A375_pNL7_minus_lncRNA::1::1158, 2_A375_pNL97_plus_lncRNA::1::1616, 2_A375_pNL97_plus_lncRNA::1::1617	11937, 33, 11905	downstream, in gene, downstream	1	1	15.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene COX8A	COX8L, COX8-2, COX, COX8, VIII-L, VIII, COX8A	cytochrome c oxidase subunit 8A (ubiquitous)	NM_004074, hCT18291.3	201119_s_at	NP_004065.1, EAW74186.1
GeneID:55611	OTUB1	11	63,753,325	63,765,892	12,567	+	3	1_A375_pNL7_minus_lncRNA::1::1158, 2_A375_pNL97_plus_lncRNA::1::1617, 2_A375_pNL97_plus_lncRNA::1::1618	691, 659, 22771	in gene, in gene, downstream	1	1	14.5	17	2	2_A375_pNL97_plus_lncRNA::1	19	Gene OTUB1	FLJ20113, OTB1, OTUB1, MGC111158, MGC4584, OTU1, HSPC263, FLJ40710	OTU domain, ubiquitin aldehyde binding 1	NM_017670, NR_003089, hCT1965468.1, hCT2355298.0, hCT2355299.0, hCT2355300.0, hCT2355301.0	201245_s_at, 201246_s_at, 38710_at	NP_060140.2, EAW74189.1, EAW74187.1, EAW74188.1, EAW74190.1, EAW74191.1
GeneID:28992	MACROD1	11	63,766,030	63,933,585	167,555	-	1	2_A375_pNL97_plus_lncRNA::1::1618	157489	in gene	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MACROD1	LRP16, MACROD1	MACRO domain containing 1	NM_014067, hCT12453.3, hCT1957095.1	1559731_x_at, 219188_s_at	NP_054786.2, EAW74193.1, EAW74192.1
GeneID:10963	STIP1	11	63,953,587	63,972,020	18,433	+	1	2_A375_pNL97_plus_lncRNA::1::1619	-579	upstream	0	1	10	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene STIP1	HOP, P60, STIP1, STI1L, IEF-SSP-3521, STI1	stress-induced-phosphoprotein 1	NM_006819, hCT12456.3, hCT2310214.0, hCT2355361.0	212009_s_at, 213330_s_at	NP_006810.1, EAW74196.1, EAW74197.1, EAW74198.1
GeneID:7423	VEGFB	11	64,002,266	64,006,259	3,993	+	2	1_A375_pNL7_minus_lncRNA::1::1159, 2_A375_pNL97_plus_lncRNA::1::1620	11142, 12598	downstream, downstream	1	1	18	19.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene VEGFB	VEGFL, VEGFB, VRF	vascular endothelial growth factor B	NM_003377, hCT12451.5, hCT1954867.2, hCT1957094.3	203683_s_at	NP_003368.1, EAW74222.1, EAW74221.1, EAW74223.1
GeneID:2286	FKBP2	11	64,008,413	64,011,607	3,194	+	2	1_A375_pNL7_minus_lncRNA::1::1159, 2_A375_pNL97_plus_lncRNA::1::1620	4995, 6451	downstream, downstream	1	1	18	19.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene FKBP2	PPIase, FKBP-13, FKBP2	FK506 binding protein 2, 13kDa	NM_004470, NM_057092, NM_001135208, hCT12452.3, hCT1961959.1	203391_at	NP_004461.2, NP_476433.1, NP_001128680.1, EAW74224.1, EAW74225.1
GeneID:26472	PPP1R14B	11	64,011,951	64,014,413	2,462	-	2	1_A375_pNL7_minus_lncRNA::1::1159, 2_A375_pNL97_plus_lncRNA::1::1620	1005, -451	in gene, upstream	1	1	18	19.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene PPP1R14B	PPP1R14B, PHI-1, PLCB3N, PNG, SOM172	protein phosphatase 1, regulatory (inhibitor) subunit 14B	NM_138689, hCT2310784.0, hCT2310786.0	212680_x_at, 226138_s_at, 230374_at	NP_619634.1, EAW74226.1, EAW74227.1
GeneID:100507590	LOC100507590	11	64,014,611	64,015,679	1,068	+	2	1_A375_pNL7_minus_lncRNA::1::1159, 2_A375_pNL97_plus_lncRNA::1::1620	-1203, 253	upstream, in gene	1	1	18	19.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100507590		hypothetical LOC100507590	XR_110912		
GeneID:5331	PLCB3	11	64,018,995	64,036,924	17,929	+	3	1_A375_pNL7_minus_lncRNA::1::1159, 2_A375_pNL97_plus_lncRNA::1::1620, 2_A375_pNL97_plus_lncRNA::1::1621	-5587, -4131, 18477	upstream, upstream, downstream	1	1	17	19.67	3	2_A375_pNL97_plus_lncRNA::1	24	Gene PLCB3	FLJ37084, PLCB3	phospholipase C, beta 3 (phosphatidylinositol-specific)	NM_000932, NM_001184883, hCT12464.4, hCT2355218.0	213384_x_at	NP_000923.1, NP_001171812.1, EAW74230.1, EAW74231.1
GeneID:572	BAD	11	64,037,300	64,052,176	14,876	-	1	2_A375_pNL97_plus_lncRNA::1::1621	14704	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene BAD	BAD, BCL2L8, BBC2	BCL2-associated agonist of cell death	NM_004322, NM_032989, hCT12460.2, hCT2311041.0, hCT2311042.0, hCT2355215.0	1861_at, 209364_at, 232660_at	NP_004313.1, NP_116784.1, EAW74233.1, EAW74234.1, EAW74235.1, EAW74236.1
GeneID:50801	KCNK4	11	64,058,793	64,067,503	8,710	+	1	2_A375_pNL97_plus_lncRNA::1::1622	9719	downstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene KCNK4	KCNK4, TRAAK1, K2p4.1	potassium channel, subfamily K, member 4	NM_033310	224552_s_at	NP_201567.1
GeneID:25858	C11orf20	11	64,067,863	64,072,239	4,376	+	1	2_A375_pNL97_plus_lncRNA::1::1622	649	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C11orf20	C11orf20, DKFZp566E164	chromosome 11 open reading frame 20	NM_001039496		NP_001034585.1
GeneID:2101	ESRRA	11	64,073,044	64,084,210	11,166	+	3	1_A375_pNL7_minus_lncRNA::1::1160, 2_A375_pNL97_plus_lncRNA::1::1622, 2_A375_pNL97_plus_lncRNA::1::1623	12236, -4532, 12108	downstream, upstream, downstream	1	1	21	23.5	2	1_A375_pNL7_minus_lncRNA::1	32	Gene ESRRA	ERRa, ESRL1, ERRalpha, ERR1, ESRRA, NR3B1	estrogen-related receptor alpha	NM_004451	1487_at, 203193_at	NP_004442.3
GeneID:51504	TRMT112	11	64,084,163	64,085,033	870	-	2	1_A375_pNL7_minus_lncRNA::1::1160, 2_A375_pNL97_plus_lncRNA::1::1623	-247, -119	upstream, upstream	1	1	32	30	1	1_A375_pNL7_minus_lncRNA::1	32	Gene TRMT112	TRM112, HSPC170, HSPC152, TRMT112, TRMT11-2	tRNA methyltransferase 11-2 homolog (S. cerevisiae)	NM_016404, hCT14490.3, hCT1957102.1, hCT1957103.1	217774_s_at	NP_057488.1, EAW74252.1, EAW74251.1, EAW74253.1
GeneID:25824	PRDX5	11	64,085,569	64,089,283	3,714	+	2	1_A375_pNL7_minus_lncRNA::1::1160, 2_A375_pNL97_plus_lncRNA::1::1623	-289, -417	upstream, upstream	1	1	32	30	1	1_A375_pNL7_minus_lncRNA::1	32	Gene PRDX5	PRXV, MGC142285, AOEB166, MGC117264, MGC142283, PLP, PMP20, SBBI10, PRDX5, PRDX6, B166, ACR1	peroxiredoxin 5	NM_012094, NM_181651, NM_181652	1560587_s_at, 222994_at	NP_036226.1, NP_857634.1, NP_857635.1
GeneID:5871	MAP4K2	11	64,556,609	64,570,713	14,104	-	1	2_A375_pNL97_plus_lncRNA::1::1624	-7431	upstream	0	1	18	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MAP4K2	MAP4K2, RAB8IP, BL44, GCK	mitogen-activated protein kinase kinase kinase kinase 2	NM_004579, hCT14486.3, hCT1957100.1, hCT1957101.1, hCT2355249.0	204936_at	NP_004570.2, EAW74299.1, EAW74300.1, EAW74301.1, EAW74302.1
GeneID:4221	MEN1	11	64,570,986	64,578,766	7,780	-	1	2_A375_pNL97_plus_lncRNA::1::1624	622	in gene	0	1	18	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MEN1	MEN1, MEAI, SCG2, MENIN	multiple endocrine neoplasia I	NM_130799, NM_000244, NM_130802, NM_130800, NM_130801, NM_130803, NM_130804, hCT2311000.0, hCT2311001.0, hCT2311002.0, hCT2311003.0, hCT2311004.0, hCT2311005.0, hCT2311006.0, hCT2311007.0, hCT2311009.0, hCT2311011.0, hCT2311012.0, hCT2311013.0, hCT2355264	202645_s_at	NP_570711.1, NP_000235.2, NP_570712.1, NP_570713.1, NP_570714.1, NP_570715.1, NP_570716.1, EAW74303.1, EAW74304.1, EAW74305.1, EAW74306.1, EAW74307.1, EAW74308.1, EAW74309.1, EAW74310.1, EAW74311.1, EAW74312.1, EAW74313.1, EAW74314.1, EAW74315.1
GeneID:10938	EHD1	11	64,620,208	64,646,191	25,983	-	2	2_A375_pNL97_plus_lncRNA::1::1625, 2_A375_pNL97_plus_lncRNA::1::1626	22223, 191	in gene, in gene	0	1	15.5	19.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene EHD1	FLJ42622, PAST1, HPAST1, H-PAST, FLJ44618, PAST, EHD1	EH-domain containing 1	NM_006795, hCT14493.2, hCT1963042.1, hCT1963043.1, hCT2310995.0, hCT2355302.0	208112_x_at, 209037_s_at, 209038_s_at, 209039_x_at, 222221_x_at	NP_006786.2, EAW74319.1, EAW74317.1, EAW74318.1, EAW74320.1, EAW74321.1
GeneID:23130	ATG2A	11	64,662,004	64,684,722	22,718	-	4	1_A375_pNL7_minus_lncRNA::1::1161, 1_A375_pNL7_minus_lncRNA::1::1162, 2_A375_pNL97_plus_lncRNA::1::1627, 2_A375_pNL97_plus_lncRNA::1::1628	-270, -6958, 114, -6990	upstream, upstream, in gene, upstream	1	1	33.5	43	2	2_A375_pNL97_plus_lncRNA::1	66	Gene ATG2A	MGC117153, ATG2A, KIAA0404	ATG2 autophagy related 2 homolog A (S. cerevisiae)	NM_015104, hCT2311010.0	213300_at	NP_055919.2, EAW74323.1
GeneID:5526	PPP2R5B	11	64,692,143	64,701,950	9,807	+	4	1_A375_pNL7_minus_lncRNA::1::1161, 1_A375_pNL7_minus_lncRNA::1::1162, 2_A375_pNL97_plus_lncRNA::1::1627, 2_A375_pNL97_plus_lncRNA::1::1628	-7151, -463, -7535, -431	upstream, upstream, upstream, upstream	1	1	33.5	43	2	2_A375_pNL97_plus_lncRNA::1	66	Gene PPP2R5B	B56B, PPP2R5B, PR61B, FLJ35411	protein phosphatase 2, regulatory subunit B', beta	NM_006244, hCT14484.3, hCT2310061.0	204611_s_at, 635_s_at	NP_006235.1, EAW74324.1, EAW74325.1
GeneID:170589	GPHA2	11	64,701,943	64,703,360	1,417	-	2	1_A375_pNL7_minus_lncRNA::1::1162, 2_A375_pNL97_plus_lncRNA::1::1628	11680, 11648	downstream, downstream	1	1	49	66	1	2_A375_pNL97_plus_lncRNA::1	66	Gene GPHA2	MGC126572, GPHA2, ZSIG51, A2, GPA2	glycoprotein hormone alpha 2	NM_130769, hCT2310991.0, hCT2310993.0	237230_at	NP_570125.1, EAW74327.1, EAW74326.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Count	Internal Intervals	Internal Outside Start	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:253129	C11orf65	11	64,703,929	64,739,356	35,428	+	2	1_A2TS_shL7_chr(c(...)N:1:1163,2_A2TS_shL7_glo(c(...)N:1:1632	6822, 3690	up/down/in, up/down	1	1	16	17	1	1_A2TS_shL7_chr(c(...)N:1	16	Gene C11orf65	MGC129364, C11orf65	Chromosome 11 open reading frame 65	NM_001037225, NM_001349612.1	231210_at	NP_001032202.1, EAW74228.1
Gene:ID:116071	BATF2	11	64,753,417	64,764,317	10,180	-	2	1_A2TS_shL7_chr(c(...)N:1:1163,2_A2TS_shL7_glo(c(...)N:1:1632	18237, 19269	downstream, downstream	1	1	16	17	1	1_A2TS_shL7_chr(c(...)N:1	16	Gene BATF2	SARI, BATF2, MGC20410	Basic leucine zipper transcription factor, ATF-like 2	NM_138456, NM_001349780.3, NM_001349781.1	228439_at	NP_612865.2, EAW74231.1, EAW74230.1
Gene:ID:4402	ARL2	11	64,761,566	64,769,656	8,070	+	4	1_A2TS_shL7_chr(c(...)N:1:1164,2_A2TS_shL7_glo(c(...)N:1:1163,2_A2TS_shL7_glo(c(...)N:1:1632,2_A2TS_shL7_glo(c(...)N:1:1633	386, 13550, 206, 1082	up gene, downstream, up/down, downstream	1	1	64.5	70.5	2	2_A2TS_shL97_glo(c(...)N:1	120	Gene ARL2	ARL2, ARPL2	ADP-ribosylation factor-like 2	NM_001667	202564_s_at	NP_001658.2
Gene:ID:59027	SNX15	11	64,794,910	64,808,044	13,134	+	2	1_A2TS_shL7_chr(c(...)N:1:1163,2_A2TS_shL7_glo(c(...)N:1:1632	226, 256	up gene, up gene	1	1	92	120	1	2_A2TS_shL97_glo(c(...)N:1	120	Gene SNX15	HSAP001403, SNX15	sorting nexin 15	NM_013306, NM_147777	203462_x_at	NP_037438.2, NP_680088.2
Gene:ID:23130	CDCA3	11	64,844,927	64,851,815	6,888	-	1	2_A2TS_shL7_glo(c(...)N:1:1632	31	up gene	0	1	16	22	1	2_A2TS_shL97_glo(c(...)N:1	22	Gene CDCA3	MGC16386, CDCA3, SORORIN	cell division cycle associated 3	NM_031966, NM_001349013.1, NM_001349012.1	230753_at	NP_542399.1, EAW74243.1, EAW74242.1
Gene:ID:342	ZFP1	11	64,851,694	64,855,874	4,180	+	2	1_A2TS_shL7_chr(c(...)N:1:1166,2_A2TS_shL7_glo(c(...)N:1:1632	12015, 110	down/in, up/down	1	1	16.5	19	2	2_A2TS_shL97_glo(c(...)N:1	22	Gene ZFP1	MCG4, DKFZp686O24166, ZFP1	zinc finger protein-like 1	NM_030762, NCT14479.2, NCT23107010, NCT21507310	208426_s_at, 214310_s_at, 214311_at	NP_009773.2, EAW74244.1, EAW74245.1, EAW74246.1
Gene:ID:100133983	UDCMS1	11	64,855,644	64,856,503	859	-	2	1_A2TS_shL7_chr(c(...)N:1:1166,2_A2TS_shL7_glo(c(...)N:1:1632	-2209, 4919	up/down, down/in	1	1	16.5	19	2	2_A2TS_shL97_glo(c(...)N:1	22	Gene UDCMS1	LOC100133983	uncharacterized LOC645629	XM_002119855, XM_001716097, XM_002120715		XP_002119855.1, XP_001716109.3, XP_002120761.1
Gene:ID:3818	C11orf42	11	64,863,653	64,879,160	15,487	+	2	1_A2TS_shL7_chr(c(...)N:1:1166,2_A2TS_shL7_glo(c(...)N:1:1632	28, 20828	up gene, downstream	1	1	16.5	17	2	2_A2TS_shL97_glo(c(...)N:1	16	Gene C11orf42	C11orf2, FFK, C11orf2, FLJ10679, AIM23, AIM22, FLJ39472	Chromosome 11 open reading frame 2	NM_012269, NCT14477.2	217869_at	NP_037097.2, EAW74247.1
Gene:ID:1105	TMTBP2	11	64,879,241	64,883,707	4,266	+	2	1_A2TS_shL7_chr(c(...)N:1:1632,2_A2TS_shL7_glo(c(...)N:1:1634	5267, 16387	down/in, down/in	0	1	13	21.5	2	2_A2TS_shL97_glo(c(...)N:1	25	Gene TMTBP2	AAG3, NET47, TMTBP2, CHCR18A	transmembrane 7 superfamily member 2	NM_003273, NCT14474.2, NCT14819817.1, NCT23585353.0, NCT23585356.0	218130_s_at	NP_003264.2, EAW74230.1, EAW74248.1, EAW74249.1, EAW74251.1
Gene:ID:1111	ZNHIT2	11	64,883,675	64,885,170	1,295	-	2	1_A2TS_shL7_chr(c(...)N:1:1632,2_A2TS_shL7_glo(c(...)N:1:1634	562, -4555	up gene, down/in	0	1	15	21.5	2	2_A2TS_shL97_glo(c(...)N:1	25	Gene ZNHIT2	FON, ZNHIT2, C11orf8, MGC120285, MGC120286	zinc finger, HIT type 2	NM_014620, NCT14476.3	214090_s_at, 222614_s_at, 227734_s_at	NP_055626.1, EAW74252.1
Gene:ID:197	PAU	11	64,885,099	64,889,872	1,973	-	2	1_A2TS_shL7_chr(c(...)N:1:1632,2_A2TS_shL7_glo(c(...)N:1:1634	9064, -96	down/in, down/in	1	1	15	21.5	2	2_A2TS_shL97_glo(c(...)N:1	25	Gene PAU	Fetb, RPS30, FAU, FLJ22895, rps1, FAU1, MNSFbeta, Fubi1, S30	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed	NM_001997, NCT23107010.0	200919_s_at	NP_001955.1, EAW74250.1
Gene:ID:1900	MRPL49	11	64,889,728	64,894,841	5,113	+	4	1_A2TS_shL7_chr(c(...)N:1:1167,2_A2TS_shL7_glo(c(...)N:1:1633,2_A2TS_shL7_glo(c(...)N:1:1634,2_A2TS_shL7_glo(c(...)N:1:1635	12704, 5120, 0, 1365	up/down, up/down, in gene, up/down	1	1	15.67	22.33	3	2_A2TS_shL97_glo(c(...)N:1	25	Gene MRPL49	C11orf6, MGC10696, MRPL49, NOF, L49mt, NOF1	mitochondrial ribosomal protein L49	NM_056827, NCT14473.5, NCT19818692.2, NCT23585387.0	209777_at	NP_060161.1, EAW74236.1, EAW74354.1, EAW74355.1
Gene:ID:4447	SYVN1	11	64,894,751	64,902,203	7,232	-	4	1_A2TS_shL7_chr(c(...)N:1:1167,2_A2TS_shL7_glo(c(...)N:1:1633,2_A2TS_shL7_glo(c(...)N:1:1634,2_A2TS_shL7_glo(c(...)N:1:1635	-429, 17295, 12775, 173	up/down, down/down, down/down, up/down	1	1	15.67	22.33	3	2_A2TS_shL97_glo(c(...)N:1	25	Gene SYVN1	SYVN1, HRD1, RAM1610, MGC48372	synovial apoptosis inhibitor 1, synoviolin	NM_032431, NM_172230, NCT14869.4, NCT19884496.2, NCT19884496.2, NCT23585350.0, NCT23585352.0	228590_at, 240522_at	NP_115977.1, NP_757338.1, EAW74357.1, EAW74359.1, EAW74360.1, EAW74362.1, EAW74358.1, EAW74361.1
Gene:ID:5427	POLA2	11	65,029,432	65,063,058	33,626	+	1	2_A2TS_shL7_glo(c(...)N:1:1638	-260	up/down	0	1	10	19	1	2_A2TS_shL97_glo(c(...)N:1	19	Gene POLA2	FLJ37250, FLJ21662, POLA2	polymerase (DNA directed), alpha 2 (70kD subunit)	NM_002689, NCT23109360.0	204431_s_at, 244573_at	NP_002680.2, EAW74373.1
Gene:ID:4435	CDC42EP1	11	65,052,331	65,059,800	7,569	+	1	2_A2TS_shL7_glo(c(...)N:1:1637	133	up gene	0	1	10	21	1	2_A2TS_shL97_glo(c(...)N:1	21	Gene CDC42EP2	BORG1, CEP2, CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2	NM_006779, NCT23109362.0	209530_s_at, 240514_at	NP_006760.1, EAW74374.1
Gene:ID:377	DPF2	11	65,101,346	65,120,451	19,105	+	1	2_A2TS_shL7_glo(c(...)N:1:1638	20542	down/in	0	1	12	16	1	2_A2TS_shL97_glo(c(...)N:1	16	Gene DPF2	UBI3A, ubi-d4, MGC10180, REQ, DPF2	D4, zinc and double PHD fingers family 2	NM_006268, NCT19854311.1, NCT19854312.1, NCT23585289.0	202116_at	NP_006259.1, EAW74375.1, EAW74376.1, EAW74377.1
Gene:ID:29150	TIGD3	11	65,122,282	65,123,684	2,002	+	1	2_A2TS_shL7_glo(c(...)N:1:1638	-284	upstream	0	1	12	16	1	2_A2TS_shL97_glo(c(...)N:1	16	Gene TIGD3	TIGD3	tigger transposable element derived 3	NM_145716, NCT16433091.3	224709_at	NP_852771.1, EAW74378.1
Gene:ID:53130	SLC25A40	11	65,142,663	65,150,142	7,479	-	6	1_A2TS_shL7_chr(c(...)N:1:1165,2_A2TS_shL7_glo(c(...)N:1:1669,2_A2TS_shL7_glo(c(...)N:1:1670,2_A2TS_shL7_glo(c(...)N:1:1632,2_A2TS_shL97_glo(c(...)N:1:1640,2_A2TS_shL97_glo(c(...)N:1:1650,2_A2TS_shL97_glo(c(...)N:1:1642	-3810, -8052, 269, -2716, -7662	upstream, up/down, up gene, downstream, up/down, up gene, up/down	1	1	21	21.67	3	2_A2TS_shL97_glo(c(...)N:1	30	Gene SLC25A40	SLC25A40	solute carrier family 25, member 40	NM_152586, NM_001077241, NCT23145513.1, NCT23585390.0, NCT23585387.0, NCT23585390.0	1563268_s_at, 236436_at	NP_872362.2, NP_001070709.1, EAW74380.1, EAW74351.1, EAW74352.1, EAW74353.1
Gene:ID:7766	FRMD8	11	65,154,041	65,160,896	26,983	+	8	1_A2TS_shL7_chr(c(...)N:1:1166,2_A2TS_shL7_glo(c(...)N:1:1669,2_A2TS_shL7_glo(c(...)N:1:1670,2_A2TS_shL7_glo(c(...)N:1:1632,2_A2TS_shL97_glo(c(...)N:1:1640,2_A2TS_shL97_glo(c(...)N:1:1650,2_A2TS_shL97_glo(c(...)N:1:1642,2_A2TS_shL97_glo(c(...)N:1:1643	-69, -5163, 38135, -, 4260, -121, 3763, -, 34555, 38103	up/down, in gene, up/down, up/down, up/down, up/down, up gene, up/down, up/down, up/down	1	1	17.6	21	5	2_A2TS_shL97_glo(c(...)N:1	30	Gene FRMD8	FRMD8, FLJ32216, MGC131765, FLJ40366	FERM domain containing 8	NM_031904, NCT23131401.0, NCT23585350.0, NCT23585289.0	1554903_at, 1554903_s_at, 210053_at, 227964_at	NP_114103.1, EAW74384.1, EAW74385.1, EAW74386.1
Gene:ID:53131	NEAT1	11	65,190,269	65,194,003	3,734	+	4	1_A2TS_shL7_chr(c(...)N:1:1170,2_A2TS_shL7_glo(c(...)N:1:1171,2_A2TS_shL97_glo(c(...)N:1:1642,2_A2TS_shL97_glo(c(...)N:1:1643	-83, 4227, 1272, -123	up/down, down/down, up/down, up/down	1	1	13.67	19.33	3	2_A2TS_shL97_glo(c(...)N:1	21	Gene NEAT1	TncRNA, NCRNA00094, NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	NR_028272	214697_s_at, 226953_at, 226999_at, 227062_at, 234869_at, 238320_at	
Gene:ID:100507845	LOC100507845	11	65,239,991	65,267,291	20,380	-	6	1_A2TS_shL7_chr(c(...)N:1:1172,2_A2TS_shL7_glo(c(...)N:1:1172,2_A2TS_shL7_glo(c(...)N:1:1174,2_A2TS_shL7_glo(c(...)N:1:1173,2_A2TS_shL97_glo(c(...)N:1:1646,2_A2TS_shL97_glo(c(...)N:1:1649,2_A2TS_shL97_glo(c(...)N:1:1646,2_A2TS_shL97_glo(c(...)N:1:1647	27539, 11699, 7891, 2323, 27903, 22396, 11627, 2227	up gene, in gene, in gene, up gene, in gene, up gene, in gene, in gene	1	1	17.6	19.2	5	2_A2TS_shL97_glo(c(...)N:1	25	Gene LOC100507845		hypothetical LOC100507845	XR_111190, XR_111191, XR_110915, XR_110916, XR_110917, XR_114497, XR_114498, XR_114499		
Gene:ID:54102	EHBP1L1	11	65,340,809	65,360,116	19,307	+	2	1_A2TS_shL7_chr(c(...)N:1:1170,2_A2TS_shL7_glo(c(...)N:1:1632	4653, -5309	up/down, up/down	1	1	21	33	1	2_A2TS_shL97_glo(c(...)N:1	33	Gene EHBP1L1	EHBP1L1, FLJ33401, DKFZp762C186	EH-domain binding protein 1-like 1	NM_001039408	1557228_at, 1557748_at, 221753_at	NP_001192879.1
Gene:ID:29126	MAP3K11	11	65,365,226	65,381,720	16,494	-	2	1_A2TS_shL7_chr(c(...)N:1:1177,2_A2TS_shL7_glo(c(...)N:1:1648	-1032, 1045	up/down, up/down	1	1	60	96	1	1_A2TS_shL7_chr(c(...)N:1	60	Gene MAP3K11	PTK1, MLK2, MEKK11, SPRK, MLK-3, MRK3K11, MGC17114	mitogen-activated protein kinase kinase kinase 11	NM_002419, NCT14583.3, NCT23145522.0	1555683_at, 205652_at	NP_002410.1, EAW74416.1, EAW74417.1
Gene:ID:99899	PCNXL3	11	65,393,763	65,404,810	21,127	+	2	1_A2TS_shL7_chr(c(...)N:1:1177,2_A2TS_shL7_glo(c(...)N:1:1648	-1031, 1015	up/down, up/down	1	1	60	96	1	1_A2TS_shL7_chr(c(...)N:1	60	Gene PCNXL3	PCNDL3, FLJ22427	pecanex-like 3 (Drosophila)	NM_022223	221656_at	NP_115992.2
Gene:ID:6310	SESCA1	11	65,337,843	65,339,239	1,396	+	2	1_A2TS_shL7_chr(c(...)N:1:1179,2_A2TS_shL97_glo(c(...)N:1:1650	-47, -23	up/down, up/down	0	1	21	33	1	2_A2TS_shL97_glo(c(...)N:1	33	Gene SESCA1	SESCA1, p27	Sjogren's syndrome/scleroderma autoantigen 1	NM_006396, NCT14563.2, NCT23130810.0, NCT23130812.0	202114_at	NP_006387.1, EAW74406.1, EAW74407.1, EAW74408.1
Gene:ID:3625	PANX1	11	65,339,620	65,341,669	1,849	+	2	1_A2TS_shL7_chr(c(...)N:1:1179,2_A2TS_shL7_glo(c(...)N:1:1650	-1064, 1000	up/down, up/down	1	1	21	33	1	2_A2TS_shL97_glo(c(...)N:1	33	Gene PANX1	MTVR1, PANX1	pannexin 1	NM_015368, NM_001098425, NM_001098765	212464_at, 222099_at	NP_056243.1, NP_001092254.1, NP_001092255.1
Gene:ID:54102	EHBP1L1	11	65,340,809	65,360,116	19,307	+	2	1_A2TS_shL7_chr(c(...)N:1:1170,2_A2TS_shL7_glo(c(...)N:1:1632	4653, -5309	up/down, up/down	1	1	21	33	1	2_A2TS_shL97_glo(c(...)N:1	33	Gene EHBP1L1	EHBP1L1, FLJ33401, DKFZp762C186	EH-domain binding protein 1-like 1	NM_001039408	1557228_at, 1557748_at, 221753_at	NP_001192879.1
Gene:ID:29126	MAP3K11	11	65,365,226	65,381,720	16,494	-	2	1_A2TS_shL7_chr(c(...)N:1:1177,2_A2TS_shL7_glo(c(...)N:1:1648	-1032, 1045	up/down, up/down	1	1	60	96	1	1_A2TS_shL7_chr(c(...)N:1	60	Gene MAP3K11	PTK1, MLK2, MEKK11, SPRK, MLK-3, MRK3K11, MGC17114	mitogen-activated protein kinase kinase kinase 11	NM_002419, NCT14583.3, NCT23145522.0	1555683_at, 205652_at	NP_002410.1, EAW74416.1, EAW74417.1
Gene:ID:6310	SESCA1	11	65,337,843	65,339,239	1,396	+	2	1_A2TS_shL7_chr(c(...)N:1:1179,2_A2TS_shL97_glo(c(...)N:1:1650	-47, -23	up/down, up/down	0	1	21	33	1	2_A2TS_shL97_glo(c(...)N:1	33	Gene SESCA1	SESCA1, p27	Sjogren's syndrome/scleroderma autoantigen 1	NM_006396, NCT14563.2, NCT23130810.0, NCT23130812.0	202114_at	NP_006387.1, EAW74406.1, EAW74407.1, EAW74408.1
Gene:ID:3625	PANX1	11	65,339,620	65,341,669	1,849	+	2	1_A2TS_shL7_chr(c(...)N:1:1179,2_A2TS_shL7_glo(c(...)N:1:1650	-1064, 1000	up/down, up/down	1	1	21	33	1	2_A2TS_shL97_glo(c(...)N:1	33	Gene PANX1	MTVR1, PANX1	pannexin 1	NM_015368, NM_001098425, NM_001098765	212464_at, 222099_at	NP_056243.1, NP_001092254.1, NP_001092255.1
Gene:ID:54122	SNX32	11	65,601,410	65,621,172	19,762	+	5	1_A2TS_shL7_chr(c(...)N:1:1181,2_A2TS_shL7_glo(c(...)N:1:1632,2_A2TS_shL7_glo(c(...)N:1:1632,2_A2TS_shL97_glo(c(...)N:1:1632,2_A2TS_shL97_glo(c(...)N:1:1634	26552, 26452, 120, 24254, 26430	down/in, down/down, up/down, down/down, down/down	1	1	61	80.33	3	2_A2TS_shL97_glo(c(...)N:1	133	Gene SNX32	MGC42112, SNX6B, PLI20834, DKFZp761P1120, SNX32, MGC87276	sorting nexin 32	NM_152760, NCT14403.2, NCT19795991.1, NCT19795997.1, NCT19796981.1, NCT19796991.1, NCT23131048.0, NCT23131051.0	1554151_at, 231184_at	NP_689772.2, EAW74441.1, EAW74442.1, EAW74443.1, EAW74445.1, EAW74446.1, EAW74444.1, EAW74447.1
Gene:ID:1312	CPL1	11	65,622,262	65,625,894	3,532	+	4	1_A2TS_shL7_chr(c(...)N:1:1181,2_A2TS_shL7_glo(c(...)N:1:1182,2_A2TS_shL97_glo(c(...)N:1:1634,2_A2TS_shL97_glo(c(...)N:1:1635	12, -3066, 140, -2929	up gene, up/down, in gene, up/down	1	1	76	91	2	2_A2TS_shL97_glo(c(...)N:1	133	Gene CPL1	CPL1, CPL	cofilin 1 (non-muscle)	NM_005507, NCT23145090.0, NCT23145113.0, NCT23585387.0, NCT23585390.0, NCT23585393.0	1555730_a_at, 200021_at	NP_005489.1, EAW74466.1, EAW74469.1, EAW74460.1, EAW74451.1, EAW74452.1
Gene:ID:9186	MUSS1	11	65,627,672	65,633,814	6,042	+	4	1_A2TS_shL7_chr(c(...)N:1:1181,2_A2TS_shL7_glo(c(...)N:1:1182,2_A2TS_shL7_glo(c(...)N:1:1634,2_A2TS_shL7_glo(c(...)N:1:1635	-2000, -2208, -2	up/down, in gene, up/down, up/down	1	1	76	91	2	2_A2TS_shL97_glo(c(...)N:1	133	Gene MUSS1	SLI3, MUSS1, FLJ21012, FLJ46572	MUSS1 cardiomyocyte homolog (S. cerevisiae)	NM_025126, NCT19469.3, NCT19684268.1	218463_s_at, 238670_at	NP_079404.2, EAW74454.1, EAW74453.1
Gene:ID:6000	EFEMP2	11	65,633,912	65,640,346	6,435	+	4	1_A2TS_shL7_chr(c(...)N:1:1181,2_A2TS_shL7_glo(c(...)N:1:1182,2_A2TS_shL7_glo(c(...)N:1:1634,2_A2TS_shL7_glo(c(...)N:1:1635	18546, 12466, 10676, 12900	down/down, down/down, down/down, down/down	1	1	76	91	2	2_A2TS_shL97_glo(c(...)N:1	133	Gene EFEMP2	FBLN4, UPH1, MBP1, EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	NM_016938, NCT23145110.0, NCT23145113.0, NCT23145200.0, NCT23585345.0, NCT23585348.0, NCT23585387.0, NCT23585390.0	208560_s_at, 208399_s_at	NP_058634.2, EAW74459.1, EAW74455.1, EAW74456.1, EAW74461.1, EAW74462.1, EAW74458.1, EAW74457.1, EAW74463.1
Gene:ID:521	CTSW	11	65,647,264	65,651,212	3,928	+	4	1_A2TS_shL7_chr(c(...)N:1:1183,2_A2TS_shL7_glo(c(...)N:1:1184,2_A2TS_shL7_glo(c(...)N:1:1636,2_A2TS_shL7_glo(c(...)N:1:1637	8652, 11052, 8504, 11054	down/down, down/down, down/down, down/down	1	1	21.5	25	2	2_A2TS_shL97_glo(c(...)N:1	27	Gene CTSW	CTSW, LYPN	cathepsin W	NM_001335, NCT14399.2, NCT23131112.0	214450_at	NP_001326.2, EAW74464.1, EAW74462.1
Gene:ID:155	FBP	11	65,651,211	65,656,010	4,799	+	4	1_A2TS_shL7_chr(c(...)N:1:1183,2_A2TS_shL7_glo(c(...)N:1:1184,2_A2TS_shL7_glo(c(...)N:1:1636,2_A2TS_shL7_glo(c(...)N:1:1637	14, -2126, 122, -2355	up gene, up/down, in gene, up/down	1	1	21.5	25	2	2_A2TS_shL97_glo(c(...)N:1	27	Gene FBP	FDP/BP, FBP-1, FBP	fibroblast growth factor (acidic) intracellular binding protein	NM_006214, NM_195597, NCT14380.4, NCT19818693.1, NCT19818964.1	202041_s_at	NP_006205.2, NP_942908.1, EAW74465.1, EAW74466.1, EAW74467.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Count	Internal Infos	Internal Dists to Start	Internal Pos.	[A]	[R]	[C]	[G]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
Gene:ENSG00000171007	CCDC85B	11	63,657,073	63,699,108	1,231	+	5	1_A275_shL7_chrus_IncRNA:1:1163, 1_A275_shL7_chrus_IncRNA:1:1164, 1_A275_shL97_chrus_IncRNA:1:1636, 2_A275_shL97_chrus_IncRNA:1:1637, 2_A275_shL97_chrus_IncRNA:1:1638	-1939, -861, -1907, -893, 9773	upstream, utr gene, upstream, utr gene, downstream	1	1	19	25	3	2_A275_shL97_chrus_IncRNA:1	27	Gene CCDC85B	CDPA	Coiled-coil domain-containing 85B	NM_033545, NCT14366.2	264609_at, 204610_s_at, 213290_at	NP_0936539.2, EAW74466.1
Gene:ENSG00000164961	POSLD1	11	63,699,692	63,867,897	8,308	-	9	1_A275_shL7_chrus_IncRNA:1:1162, 1_A275_shL7_chrus_IncRNA:1:1163, 1_A275_shL7_chrus_IncRNA:1:1164, 1_A275_shL7_chrus_IncRNA:1:1165, 2_A275_shL97_chrus_IncRNA:1:1636, 2_A275_shL97_chrus_IncRNA:1:1637, 2_A275_shL97_chrus_IncRNA:1:1638	12061, 8661, -2663, 12109, 8629, 349	downstream, downstream, upstream, downstream, downstream, u gene	1	1	16.78	22.23	4	2_A275_shL97_chrus_IncRNA:1	27	Gene POSLD1	PRA, PRA1, POSL1, hb-1	POsplA-like antigen 1	NM_003438, NCT22145808	264420_at	NP_0934281, EAW74488.1
Gene:ENSG00000179935	C11orf65	11	63,664,261	63,686,631	2,230	-	4	1_A275_shL7_chrus_IncRNA:1:1166, 1_A275_shL7_chrus_IncRNA:1:1167, 2_A275_shL97_chrus_IncRNA:1:1639, 2_A275_shL97_chrus_IncRNA:1:1640	2171, -353, 2075, -317	downstream, upstream, downstream, upstream	1	1	67.5	67	2	2_A275_shL97_chrus_IncRNA:1	113	Gene C11orf65	BLES03, PS3Z6, C11orf65	chromosome 11 open reading frame 65	NM_031450, NM_001139835, NCT16402482, NCT22145803.0	221534_at	NP_1136362, NP_001126107.1, EAW74470.1, EAW74471.1
Gene:ENSG00000179588	DRAP1	11	63,686,726	63,689,048	2,320	+	4	1_A275_shL7_chrus_IncRNA:1:1166, 1_A275_shL7_chrus_IncRNA:1:1167, 2_A275_shL97_chrus_IncRNA:1:1639, 2_A275_shL97_chrus_IncRNA:1:1640	-2360, 88, -3272, 120	upstream, utr gene, upstream, utr gene	1	1	67.5	67	2	2_A275_shL97_chrus_IncRNA:1	113	Gene DRAP1	DRAP1, NC2-alpha	DR1-associated protein 1 (negative cofactor 2 alpha)	NM_006642, NCT14292.3	203258_at, 203160_s_at	NP_0066333.2, EAW74472.1
Gene:ENSG00000154161	TSGA10IP	11	63,712,115	63,727,634	15,519	+	2	1_A275_shL7_chrus_IncRNA:1:1166, 2_A275_shL97_chrus_IncRNA:1:1639	16021, 16037	downstream, downstream	1	1	100	96	1	1_A275_shL7_chrus_IncRNA:1	103	Gene TSGA10IP	FLJ22550, MGC120486, TSGA10IP, FAM161C, MGC120486, MGC120486	testis specific, 10 interacting protein	NM_152762, ENST00001 90.2	1553652_at	NP_6899752, EAW74473.1
Gene:ENSG00000092621	SART1	11	63,729,160	63,747,607	18,447	+	2	1_A275_shL7_chrus_IncRNA:1:1166, 2_A275_shL97_chrus_IncRNA:1:1640	-24, -6	upstream, upstream	1	1	100	96	1	1_A275_shL7_chrus_IncRNA:1	103	Gene SART1	MGC2035, Sart66, SNRNP110, SART1, Ala1, SART1299, HOM81	squamous cell carcinoma antigen recognized by T cells	NM_005146, NCT14413.2, NCT23121118.0	206051_at	NP_0035137.1, EAW74475.1, EAW74474.1
Gene:ENSG00000134324	EIF4AD	11	63,764,017	63,769,976	5,961	-	2	1_A275_shL7_chrus_IncRNA:1:1169, 2_A275_shL97_chrus_IncRNA:1:1642	-182, -32	upstream, upstream	1	1	33	27	1	1_A275_shL7_chrus_IncRNA:1	33	Gene EIF4AD	MGC11102, EIF4AD, triosinx	eukaryotic translation initiation factor 1A domain containing	NM_032235, NCT14412.2, NCT23149971.1, NCT23149969.1, NCT23149550.1, NCT23149909.2	228662_s_at, 238377_at	NP_1137012, EAW74479.1, EAW74476.1, EAW74480.1, EAW74481.1, EAW74482.1
Gene:ENSG00000179515	BANP1	11	63,769,550	63,771,617	2,067	+	2	1_A275_shL7_chrus_IncRNA:1:1169, 2_A275_shL97_chrus_IncRNA:1:1642	210, 61	ua gene, ua gene	1	1	33	27	1	1_A275_shL7_chrus_IncRNA:1	33	Gene BANP1	BAP, BANP1, MGC111161, BCRP1, DKFZp434B1428	basic nuclear autoantigen factor 1	NM_032560, NM_001145925, NCT14382.4, NCT23131118.1, NCT23131121.1, NCT23131122.1	218125_s_at	NP_0035511, NP_001137457.1, EAW74483.1, EAW74484.1, EAW74485.1, EAW74486.1
Gene:ENSG00000174474	CST6	11	63,779,462	63,780,976	1,514	+	2	1_A275_shL7_chrus_IncRNA:1:1169, 2_A275_shL97_chrus_IncRNA:1:1642	8702, 8651	downstream, upstream	1	1	33	27	1	1_A275_shL7_chrus_IncRNA:1	33	Gene CST6	CST6		NM_001323, NCT14391.3	205593_at, 231246_at	NP_0013141.1, EAW74487.1
Gene:ENSG00000149782	GALJST3	11	63,800,236	63,816,681	16,445	+	2	1_A275_shL7_chrus_IncRNA:1:1160, 2_A275_shL97_chrus_IncRNA:1:1642	3125, 3189	upstream, upstream	1	1	29	30	1	1_A275_shL7_chrus_IncRNA:1	25	Gene GALJST3	GALJST2, GALJST3, MGC142112, MGC142110, GALJST-3	galactose-3-O-sulfotransferase 3	NM_033036, NCT14399.4	1553237_at	NP_1480351, EAW74490.1
Gene:ENSG00000110092	SF3B2	11	63,819,816	63,836,252	16,366	+	2	1_A275_shL7_chrus_IncRNA:1:1160, 2_A275_shL97_chrus_IncRNA:1:1642	-40, 164	upstream, ua gene	1	1	29	30	1	1_A275_shL7_chrus_IncRNA:1	25	Gene SF3B2	SF3b1, SF3B145, SF3B2, SAP145, SF3b150, Cus1	splicing factor 3b, subunit 2, 145kDa	NM_006842, NCT14393.2, NCT23302650.0, NCT23302660.0, NCT23302670.0, NCT23302680.0, NCT23302700.0, NCT23302710.0, NCT23302720.0, NCT23302730.0, NCT23302740.0	1555230_at, 200619_at	NP_0068332.2, EAW74492.1, EAW74496.1, EAW74499.1, EAW74500.1, EAW74493.1, EAW74494.1, EAW74495.1, EAW74497.1, EAW74498.1, EAW74501.1
Gene:ENSG00000164734	SLC2	11	65,024,765	65,035,332	10,567	+	2	2_A275_shL97_chrus_IncRNA:1:1664, 2_A275_shL97_chrus_IncRNA:1:1665	465, 10461	ua gene, ua gene	0	1	16.5	17	2	2_A275_shL97_chrus_IncRNA:1	19	Gene SLC2	SLC2, FLJ12357	kelene light chain 2	NM_022822, NM_001134714, NM_001134775, NM_001134776, NCT23095750.0	219906_s_at	NP_0707331, NP_001128249.1, NP_001128247.1, NP_001128246.1, EAW74507.1
Gene:ENSG00000151876	RAB18	11	66,039,099	66,044,983	5,907	+	2	2_A275_shL97_chrus_IncRNA:1:1664, 2_A275_shL97_chrus_IncRNA:1:1665	-10555, -830	upstream, upstream	0	1	16.5	17	2	2_A275_shL97_chrus_IncRNA:1	19	Gene RAB18	RAB18		NM_020801	220864_s_at	NP_112243.1
Gene:ENSG00000134243	CNIH2	11	66,048,696	66,051,663	2,967	+	3	1_A275_shL7_chrus_IncRNA:1:1161, 2_A275_shL97_chrus_IncRNA:1:1665, 2_A275_shL97_chrus_IncRNA:1:1666	11424, 10870, 11645	downstream, downstream, downstream	1	1	20	19.5	2	1_A275_shL7_chrus_IncRNA:1	26	Gene CNIH2	CNIH2, Cni, MGC50899, CNIH-2	cornichon homolog 2 (Drosophila)	NM_182553, NCT23309.14	233070_at	NP_8723391, EAW74508.1
Gene:ENSG00000111371	YIPF1A	11	66,052,051	66,056,635	4,587	-	2	1_A275_shL7_chrus_IncRNA:1:1161, 2_A275_shL97_chrus_IncRNA:1:1666	-852, -706	upstream, upstream	1	1	26	24	1	1_A275_shL7_chrus_IncRNA:1	26	Gene YIPF1A	YIP1P, SdTM, FinGER7, YIP1A, YIP1	Yip1 interacting factor homolog A (S. cerevisiae)	NM_020470, NCT23148402.0	202416_at	NP_0652012, EAW74509.1
Gene:ENSG00000164776	TMEM151A	11	66,059,373	66,064,135	4,762	+	2	1_A275_shL7_chrus_IncRNA:1:1161, 2_A275_shL97_chrus_IncRNA:1:1666	-2253, 2629	upstream, downstream	1	1	26	24	1	1_A275_shL7_chrus_IncRNA:1	26	Gene TMEM151A	TMEM151, MGC33456, TMEM151A	transmembrane protein 151A	NM_152266, NCT11563.5	235614_at	NP_6999951, EAW74510.1
Gene:ENSG00000149656	KIN1	11	66,099,542	66,104,000	4,458	-	3	1_A275_shL7_chrus_IncRNA:1:1162, 1_A275_shL7_chrus_IncRNA:1:1163, 2_A275_shL97_chrus_IncRNA:1:1666	-64, -6382, 66	upstream, upstream, upstream	1	1	26.5	30	2	2_A275_shL97_chrus_IncRNA:1	44	Gene KIN1	KIN1		NM_004782, NCT11562.2	205211_s_at	NP_0043513.2, EAW74512.1
Gene:ENSG00000135558	BRMS1	11	66,104,603	66,112,582	7,776	+	4	1_A275_shL7_chrus_IncRNA:1:1162, 1_A275_shL7_chrus_IncRNA:1:1163, 1_A275_shL7_chrus_IncRNA:1:1164, 2_A275_shL97_chrus_IncRNA:1:1666	6515, 230, 2970, 6455	downstream, ua gene, upstream, downstream	1	1	24.67	24.67	3	2_A275_shL97_chrus_IncRNA:1	44	Gene BRMS1	DKFZp566A063, BRMS1	breast cancer metastasis-suppressor 1	NM_015399, NM_001032837, NCT10815.4, NCT19986857.1, NCT19966955.1, NCT19949999.1	218631_s_at	NP_0562141, NP_001035126.1, EAW74513.1, EAW74514.1, EAW74515.1, EAW74516.1
Gene:ENSG00000143179	B3GNT1	11	66,112,643	66,113,161	2,518	+	4	1_A275_shL7_chrus_IncRNA:1:1162, 1_A275_shL7_chrus_IncRNA:1:1163, 1_A275_shL7_chrus_IncRNA:1:1164, 2_A275_shL97_chrus_IncRNA:1:1666	11097, 2609, -391, 11061	downstream, downstream, upstream, downstream	1	1	24.67	24.67	3	2_A275_shL97_chrus_IncRNA:1	44	Gene B3GNT1	IGNT, B3GNT1, IGAT, BETA3GNT1, B3GNT6, B3GN-T1	UDP-GlcNAc betaGal beta-1,3-N-acetylglucosaminyltransferase 1	NM_006876, NCT11247.2, NCT23309.0	230156_at, 235203_at	NP_0068697.1, EAW74517.1, EAW74518.1
Gene:ENSG00000164983	SLC29A2	11	66,129,992	66,139,291	9,299	-	1	1_A275_shL97_chrus_IncRNA:1:1666	671	ua gene	0	1	14	17	1	2_A275_shL97_chrus_IncRNA:1	17	Gene SLC29A2	DER12, ENT2, SLC29A2, HNP36	solute carrier family 29 (nucleoside transporters), member 2	NM_001332, NCT11364.3, NCT23305250, NCT23106260, NCT23309260	1553580_a_at, 1560962_at, 1560149_at, 1560151_s_at, 204113_s_at	NP_0013222, EAW74519.1, EAW74520.1, EAW74521.1, EAW74522.1
Gene:ENSG00000260583	LOC10033 5554	11	66,178,663	66,184,606	7,943	+	4	1_A275_shL7_chrus_IncRNA:1:1169, 1_A275_shL7_chrus_IncRNA:1:1196, 1_A275_shL7_chrus_IncRNA:1:1197, 2_A275_shL97_chrus_IncRNA:1:1669	-212, 9871, 12967, 12563	upstream, downstream, downstream, downstream	1	1	129.5	140	2	2_A275_shL97_chrus_IncRNA:1	262	Gene LOC100335554		hypothetical LOC100335554	XR_110921		
Gene:ENSG00000204944	NPAS4	11	66,185,675	66,194,177	8,702	+	3	1_A275_shL7_chrus_IncRNA:1:1196, 1_A275_shL7_chrus_IncRNA:1:1197, 2_A275_shL97_chrus_IncRNA:1:1669	-2139, 787, 773	upstream, ua gene, ua gene	1	1	239	262	1	2_A275_shL97_chrus_IncRNA:1	262	Gene NPAS4	bHLHE70, NXF, bHLHe70, PASD10	aryl-hydrocarbon receptor nuclear translocator-like protein 4	NM_178864, NCT18139.2	1554299_at, 206769_at	NP_8491852, EAW74525.1
Gene:ENSG00000149809	MRPL11	11	66,202,550	66,209,210	6,660	-	2	1_A275_shL7_chrus_IncRNA:1:1168, 1_A275_shL7_chrus_IncRNA:1:1670, 2_A275_shL97_chrus_IncRNA:1:1672	-122, -154, 4622	upstream, upstream, upstream	1	1	23.5	21.5	2	1_A275_shL7_chrus_IncRNA:1	34	Gene MRPL11	L11MT, CGI-113, MRPL11, MRP-L11, MGC11024	mitochondrial ribosomal protein L11	NM_016050, NM_170730, NM_170729, NCT23309210.0, NCT23309220.0, NCT23309230.0, NCT23309240.0, NCT23309250.0, NCT23309260.0	218162_s_at	NP_0571541, NP_733938.1, NP_733933.1, EAW74526.1, EAW74526.1, EAW74532.1, EAW74527.1, EAW74531.1, EAW74533.1
Gene:ENSG00000149380	PELI3	11	66,234,336	66,244,606	10,472	+	2	1_A275_shL7_chrus_IncRNA:1:1169, 2_A275_shL97_chrus_IncRNA:1:1672	13726, 13564	downstream, downstream	1	1	28	30	1	1_A275_shL7_chrus_IncRNA:1	26	Gene PELI3	MGC33521, PELI3	pellino homolog 3 (Drosophila)	NM_145983, NM_001098810, NCT11743.4, NCT23101261.1, NCT23101271.1, NCT23101421.1, NCT23101501.0	238431_s_at, 244214_at	NP_6589022, NP_001091850.1, EAW74532.1, EAW74533.1, EAW74534.1, EAW74536.1, EAW74535.1
Gene:ENSG00000260583	LOC10033 5554	11	66,244,017	66,247,706	3,689	-	2	1_A275_shL7_chrus_IncRNA:1:1169, 2_A275_shL97_chrus_IncRNA:1:1672	-258, -218	upstream, upstream	1	1	28	30	1	1_A275_shL7_chrus_IncRNA:1	26	Gene LOC100335554		hypothetical LOC100335554	XR_111186, XR_110922, XR_114391		
Gene:ENSG00000100372	DPP3	11	66,247,880	66,277,130	29,250	+	2	1_A275_shL7_chrus_IncRNA:1:1169, 2_A275_shL97_chrus_IncRNA:1:1672	184, 40	ua gene, ua gene	1	1	28	30	1	1_A275_shL7_chrus_IncRNA:1	26	Gene DPP3	FLJ11327, FLJ22331, DPP3, DPP3	dipeptidyl-peptidase 3	NM_005700, NM_130463	216567_s_at, 223510_s_at	NP_0056912, NP_569710.2
Gene:ENSG00000179344	C11orf80	11	66,512,207	66,610,687	98,780	+	1	2_A275_shL97_chrus_IncRNA:1:1673	17555	ua gene	0	1	11	15	1	2_A275_shL97_chrus_IncRNA:1	16	Gene C11orf80	C11orf80, FLJ22531	chromosome 11 open reading frame 80	NM_024690, NCT23107750.0, NCT23107760.0	226622_at, 226393_at	NP_0788262, EAW74562.1, EAW74563.1
Gene:ENSG00000149968	RCE1	11	66,610,653	66,614,003	3,130	+	2	1_A275_shL7_chrus_IncRNA:1:1200, 2_A275_shL97_chrus_IncRNA:1:1674	12117, 12909	downstream, downstream	1	1	19	16	1	1_A275_shL7_chrus_IncRNA:1	18	Gene RCE1	RCE1B, FACE2, RCE1A, RCE1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	NM_020120, NM_001032279, NCT23107160.0, NCT23107170.0, NCT23107180.0	1553532_at, 209333_s_at	NP_0010241, NP_001027490.1, EAW74565.1, EAW74566.1, EAW74567.1
Gene:ENSG00000038427	PC	11	66,615,897	66,723,647	109,750	-	5	1_A275_shL7_chrus_IncRNA:1:1200, 1_A275_shL7_chrus_IncRNA:1:1201, 2_A275_shL97_chrus_IncRNA:1:1674, 2_A275_shL97_chrus_IncRNA:1:1675, 2_A275_shL97_chrus_IncRNA:1:1676	108547, 86539, 101975, 95007, 119	ua gene, utr gene, ua gene, utr gene	1	1	28.33	31.67	3	2_A275_shL97_chrus_IncRNA:1	57	Gene PC	PC, PCB	pyruvate carboxylase	NM_022172, NM_000920, NM_001040716, NCT19866221.0, NCT19866231.1, NCT23105900.0, NCT23106003.0	1570042_a_at, 209301_at	NP_0010042.2, NP_000911.2, NP_001033596.1, EAW74564.1, EAW74570.1, EAW74572.1, EAW74569.1, EAW74571.1
Gene:ENSG00000179979	UFM1	11	66,624,076	66,627,946	3,870	+	2	1_A275_shL7_chrus_IncRNA:1:1200, 2_A275_shL97_chrus_IncRNA:1:1674	476, -1004	upstream, upstream	1	1	19	16	1	1_A275_shL7_chrus_IncRNA:1	18	Gene UFM1	SALM2, MGC3103, PIGLER6, SALM2, LRFN4	leucine rich repeat and fibronectin type III domain containing 4	NM_206936, NCT11699.2, NCT23101612.0	219491_at	NP_0788412, EAW74573.1, EAW74574.1
Gene:ENSG00000164338	C11orf86	11	66,742,734	66,744,479	1,726	+	1	2_A275_shL97_chrus_IncRNA:1:1677	4386	upstream	0	1	22	28	1	2_A275_shL97_chrus_IncRNA:1	29	Gene C11orf86	FLJ22679, C11orf86	chromosome 11 open reading frame 86	NM_001136455	233838_at	NP_0011298897.1
Gene:ENSG00000137796	ADRBK1	11	67,033,903	67,053,929	20,124	+	1	2_A275_shL97_chrus_IncRNA:1:1678	22319	downstream	0	1	11	15	1	2_A275_shL97_chrus_IncRNA:1	16	Gene ADRBK1	BARK1, FLJ16718, BETA-ARK1, GRK2, ADRBK1	adrenergic, beta, receptor kinase 1	NM_001619, NCT11216.2, NCT23101162.0	209401_s_at, 209402_at, 209407_at	NP_0016102.2, EAW74581.1, EAW74582.1
Gene:ENSG00000166135	ANKRD13D	11	67,056,762	67,069,855	13,093	+	3	1_A275_shL7_chrus_IncRNA:1:1202, 1_A275_shL7_chrus_IncRNA:1:1678, 2_A275_shL97_chrus_IncRNA:1:1679	16355, 535, 14278	downstream, upstream, downstream	1	1	19	25	2	2_A275_shL97_chrus_IncRNA:1	32	Gene ANKRD13D	MGC30628, ANKRD13D	ankyrin repeat domain 13 family, member D	NM_206538, NM_030767, NCT12499.2, NCT23101470.0, NCT23553170.0, NCT23553180.0	1553555_s_at, 236205_at, 236156_at	NP_9423372, EAW74585.1, EAW74583.1, EAW74584.1, EAW74585.1
Gene:ENSG00000143961	SSH3	11	67,070,019	67,080,076	9,158	+	2	1_A275_shL7_chrus_IncRNA:1:1202, 2_A275_shL97_chrus_IncRNA:1:1679	201, 121	ua gene, ua gene	1	1	27	32	2	2_A275_shL97_chrus_IncRNA:1	32	Gene SSH3	SSH3L, FLJ42240, SSH2, FLJ30515, FLJ10826	slingshot homolog 3 (Drosophila)	NM_017557, NCT12147.3, NCT19894852.1, NCT23102300.0, NCT23102310.0, NCT23102320.0, NCT23102330.0, NCT23102340.0, NCT23553000.0, NCT23553010.0	219241_s_at, 219819_s_at, 51162_at	NP_0933272, EAW74592.1, EAW74587.1, EAW74588.1, EAW74591.1, EAW74594.1, EAW74589.1, EAW74590.1, EAW74592.1, EAW74593.1, EAW74596.1
Gene:ENSG00000260583	LOC10033 5554	11	67,085,210	67,199,158	113,949	-	3	1_A275_shL7_chrus_IncRNA:1:1202, 2_A275_shL97_chrus_IncRNA:1:1680, 2_A275_shL97_chrus_IncRNA:1:1681	86418, 86662, 72870	ua gene, ua gene, downstream	1	1	19.5	21	2	2_A275_shL97_chrus_IncRNA:1	21	Gene LOC100133555	FLJ38536	hypothetical LOC100133555	NR_024069		
Gene:ENSG00000179526	CLCF1	11	67,131,639	67,141,648	10,009	-	2	1_A275_shL7_chrus_IncRNA:1:1202, 2_A275_shL97_chrus_IncRNA:1:1680	-66, -148	upstream, upstream	1	1	16	21	1	2_A275_shL97_chrus_IncRNA:1	21	Gene CLCF1	CISS2, CLCF1, NNT1, CLC, BSF-3, NNP1	cardiotrophin-like cytokine factor 1	NM_013246, NM_001166212, NCT12132.4, NCT19852661	218000_at	NP_0370781, NP_001138664.1, EAW74601.1, EAW74602.1
Gene:ENSG00000164326	RADBA	11	67,161,423	67,165,883	6,460	+	1	2_A275_shL97_chrus_IncRNA:1:1681	142	upstream	0	1	19	21	1	2_A275_shL97_chrus_IncRNA:1	21	Gene RADBA	RADBA, RAD8	RAD8 homolog A (S. pombe)	NM_204854, NCT12133.4, NCT19852451.1, NCT19852452.1	1562022_s_at, 204626_at	NP_0548751, EAW74603.1, EAW74604.1, EAW74606.1
Gene:ENSG00000149948	PPP1CA	11	67,165,852	67,169,276	3,424	+	1	2_A275_shL97_chrus_IncRNA:1:1681	10295	downstream	0	1	19	21	1	2_A275_shL97_chrus_IncRNA:1	21	Gene PPP1CA	PPP1ALPHA, MGC15877, PP-1A, PPP1CA, PPP1A, MGC1614	protein phosphatase 1, catalytic subunit, alpha isoform	NM_002705, NM_206873, NM_001008709, NCT12142.4, NCT19853521.1, NCT19853341.1, NCT19852472.1	200585_s_at	NP_2029991, NP_2957961, NP_001008709.1, EAW74608.1, EAW74609.1, EAW74610.1, EAW74607.1
Gene:ENSG00000137311	ATPGD1	11	67,167,149	67,193,078	8,929	+	1	2_A275_shL97_chrus_IncRNA:1:1682	12767	ua gene	0	1	12	29	1	2_A275_shL97_chrus_IncRNA:1	29	Gene ATPGD1	CARVS1, ATPGD1, KIAA1394	ATP-gated channel 1	NM_020811, NM_001166222	226664_at	NP_0555921, NP_001138694.1
Gene:ENSG00000149923	RPS6KB2	11	67,193,833	67,202,879	9,046	+	1	2_A275_shL97_chrus_IncRNA:1:1682	1	ua gene	0	1	12	29	1	2_A275_shL97_chrus_IncRNA:1	29	Gene RPS6KB2	P70-beta-1, S6K-beta2, p70S6Kb, STK14B, dJ3L8, P70-beta, S6K, S6K2, RPS6KB2, P70-beta-2, p70(S6K)-beta	ribosomal protein S6 kinase, 70kDa, polypeptide 2	NM_003952, NCT12180.2, NCT19852621.1, NCT23104370.0, NCT23104380.0	203777_s_at	NP_0039432, EAW74620.1, EAW74618.1, EAW74621.1
Gene:ENSG00000164744	PTPRCAP	11	67,202,951	67,205,153	2,172	-	1	2_A275_shL97_chrus_IncRNA:1:1682	8217	downstream	0	1	13	29	1	2_A275_shL97_chrus_IncRNA:1	29	Gene PTPRCAP	MGC133662, PTPRCAP, MGC133663, CD45-AP, LPAP	protein tyrosine phosphatase, receptor-type, C-associated protein	NM_006608, NCT23125551.1	204960_at	NP_0035991, EAW74622.1
Gene:ENSG00000110719	CORO1B	11	67,205,514	67,211,263	5,749	-	1	2_A275_shL97_chrus_IncRNA:1:1682	13227	downstream	0	1	13	29	1	2_A275_shL97_chrus_IncRNA:1	29	Gene CORO1B	DKFZp762H196, CORONIN2, CORO1B	coronin, actin binding protein, 1B	NM_032461, NM_001018070, NCT23125530.0, NCT23125540.0, NCT23125550.0	221754_s_at, 64496_at	NP_0035754, NP_001018060.1, EAW74623.1, EAW74624.1, EAW74625.1, EAW74626.1
Gene:ENSG00000137801	CABP4	11	67,222,916	67,229,245	6,329	+	2	1_A275_shL7_chrus_IncRNA:1:1204, 2_A275_shL97_chrus_IncRNA:1:1682	18549, 14014	downstream, downstream	1	1	23	29	2	2_A275_shL97_chrus_IncRNA:1	29	Gene CABP4	CABP4, CSNB2B	calcium binding protein 4	NM_145200, NCT19853514, NCT23104312.1, NCT23104334.1, NCT23104338.1	1552690_a_at, 1554201_at, 1554202_s_at	NP_6602011, EAW74627.1, EAW74628.1, EAW74630.1
Gene:ENSG00000260184	TMEM134	11	67,231,619	67,236,731	4,912	+	2	1_A275_shL7_chrus_IncRNA:1:1204, 2_A275_shL97_chrus_IncRNA:1:1682	-132, -101	upstream, upstream	1	1	23	29	2	2_A275_shL97_chrus_IncRNA:1	29	Gene TMEM134	TMEM134, FLJ21169, MGC149691	transmembrane protein 134	NM__025124, NM_001079851, NM_001079856, NCT19885516.1, NCT19885518.1, NCT19885521.1, NCT23553690.0, NCT23553700.0	1555712_at, 215531_at, 231018_at	NP_0794901, NP_001072119.1, NP_001072118.1, EAW74632.1, EAW74633.1, EAW74634.1, EAW74635.1, EAW74636.1
Gene:ENSG00000149948	AIP	11	67,250,503	67,258,579	8,076	+	1	2_A275_shL97_chrus_IncRNA:1:1684	283	ua gene	0	1	20	15	1	2_A275_shL97_chrus_IncRNA:1	15	Gene AIP	SMTPHN, XAP2, FKBP16, AIP, FKBP37, ARA9	aryl hydrocarbon receptor interacting protein	NM_003977, NCT12134.2	201781_s_at, 201782_s_at	NP_0039662, EAW74637.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9600	PITPNM1	11	67,259,239	67,272,843	13,604	-	3	1_A375_pNL7_minus_lncRNA::1::1205, 2_A375_pNL97_plus_lncRNA::1::1684, 2_A375_pNL97_plus_lncRNA::1::1685	-3253, 22043, -2549	upstream, downstream, upstream	1	1	20.5	15.5	2	1_A375_pNL7_minus_lncRNA::1	21	Gene PITPNM1	PITPNM1, Rd9, NIR2, PITPNM, DRES9, RDGB, RDGBA1, RDGBA, RDGB1, FLJ44997	phosphatidylinositol transfer protein, membrane-associated 1	NM_004910, NM_001130848, hCT12137.4, hCT1965344.1, hCT1965345.1, hCT2312499.0, hCT2355251.0, hCT2355252.0	203826_s_at	NP_004901.2, NP_001124320.1, EAW74638.1, EAW74639.1, EAW74642.1, EAW74643.1, EAW74640.1, EAW74641.1
GeneID:10263	CDK2AP2	11	67,273,968	67,276,102	2,134	-	2	1_A375_pNL7_minus_lncRNA::1::1205, 2_A375_pNL97_plus_lncRNA::1::1685	6, 710	in gene, in gene	1	1	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene CDK2AP2	FLJ10636, CDK2AP2, DOC-1R, p14	cyclin-dependent kinase 2 associated protein 2	NM_005851, hCT12138.2	203252_at	NP_005842.1, EAW74644.1
GeneID:51475	CABP2	11	67,286,418	67,290,899	4,481	-	1	1_A375_pNL7_minus_lncRNA::1::1205	14803	downstream	1	0	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene CABP2	CABP2	calcium binding protein 2	NM_016366, NM_031204, hCT12144.2, hCT1964057.0, hCT2355272.0	207745_at	NP_057450.2, NP_112481.2, EAW74645.1, EAW74646.1, EAW74647.1
GeneID:100505621	LOC100505621	11	67,370,351	67,374,177	3,826	-	1	2_A375_pNL97_plus_lncRNA::1::1686	-191	upstream	0	1	20	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene LOC100505621	MGC129825, C11orf72, MGC129824, FLJ90834	chromosome 11 open reading frame 72	XM_003119502, XM_003119187, XM_003120707		XP_003119550.1, XP_003119235.1, XP_003120755.1
GeneID:4723	NDUFV1	11	67,374,323	67,380,012	5,689	+	1	2_A375_pNL97_plus_lncRNA::1::1686	45	in gene	0	1	20	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene NDUFV1	CI-51K, NDUFV1, FLJ59059, CI51KD, UQOR1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	NM_007103, NM_001166102, hCT12143.3, hCT1964053.1, hCT1964054.1, hCT1964055.1, hCT2310443.0	208714_at, 227785_at	NP_009034.2, NP_001159574.1, EAW74652.1, EAW74654.1, EAW74655.1, EAW74656.1, EAW74653.1
GeneID:100132261	LOC100132261	11	67,722,755	67,723,540	785	-	1	2_A375_pNL97_plus_lncRNA::1::1687	148	in gene	0	1	6	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene LOC100132261		hypothetical LOC100132261			
GeneID:81622	UNC93B1	11	67,758,575	67,771,593	13,018	-	1	2_A375_pNL97_plus_lncRNA::1::1688	-6263	upstream	0	1	12	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene UNC93B1	UNC93, MGC126617, Unc-93B1, UNC93B1, UNC93B	unc-93 homolog B1 (C. elegans)	NM_030930, hCT2312531.0, hCT2312532.0	220998_s_at, 225869_s_at	NP_112192.2, EAW74677.1, EAW74676.1
GeneID:221	ALDH3B1	11	67,776,048	67,796,743	20,695	+	2	2_A375_pNL97_plus_lncRNA::1::1688, 2_A375_pNL97_plus_lncRNA::1::1689	1808, 19632	in gene, in gene	0	1	16.5	21	2	2_A375_pNL97_plus_lncRNA::1	22	Gene ALDH3B1	ALDH4, ALDH3B1, FLJ26433, ALDH7, FLJ34710	aldehyde dehydrogenase 3 family, member B1	NM_000694, NM_001030010, NM_001161473, hCT11332.2, hCT2310452.0, hCT2310453.0, hCT2310454.0, hCT2355273.0, hCT2355274.0	1565731_at, 205640_at, 211004_s_at	NP_000685.1, NP_001025181.1, NP_001154945.1, EAW74678.1, EAW74680.1, EAW74681.1, EAW74679.1, EAW74682.1, EAW74683.1
GeneID:4728	NDUFS8	11	67,798,084	67,804,114	6,030	+	1	2_A375_pNL97_plus_lncRNA::1::1689	-2404	upstream	0	1	21	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene NDUFS8	CI23KD, NDUFS8, TYKY, CI-23k	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	NM_002496, hCT11335.1, hCT1813721.1, hCT2310458.0, hCT2355275.0	203189_s_at, 203190_at, 232169_x_at	NP_002487.1, EAW74686.1, EAW74685.1, EAW74687.1, EAW74688.1
GeneID:51111	SUV420H1	11	67,923,507	67,980,784	57,277	-	2	1_A375_pNL7_minus_lncRNA::1::1206, 2_A375_pNL97_plus_lncRNA::1::1690	-400, -464	upstream, upstream	1	1	18	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SUV420H1	KMT5B, CGI85, SUV420H1, MGC21161, MGC118906, MGC703, MGC118909, CGI-85	suppressor of variegation 4-20 homolog 1 (Drosophila)	NM_017635, NM_016028, hCT1954046.1, hCT1956038.1, hCT2312523.0, hCT2312524.0, hCT2312525.0	218242_s_at, 222566_at, 222759_at, 242646_at	NP_060105.3, NP_057112.3, EAW74697.1, EAW74698.1, EAW74700.1, EAW74701.1, EAW74699.1
GeneID:53838	C11orf24	11	68,028,803	68,039,469	10,666	-	1	2_A375_pNL97_plus_lncRNA::1::1691	-275	upstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C11orf24	C11orf24, DM4E3	chromosome 11 open reading frame 24	NM_022338, hCT18327.2, hCT2312518.0, hCT2355263.0	218299_at, 52164_at	NP_071733.1, EAW74702.1, EAW74703.1, EAW74704.1
GeneID:219927	MRPL21	11	68,658,746	68,671,303	12,557	-	2	1_A375_pNL7_minus_lncRNA::1::1207, 2_A375_pNL97_plus_lncRNA::1::1693	-25, 39	upstream, in gene	1	1	27	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene MRPL21	L21mt, MGC62013, MRPL21, MRP-L21	mitochondrial ribosomal protein L21	NM_181514, NM_181515, hCT18318.3, hCT2309551.0, hCT2355400.0, hCT2355401.0, hCT2355402.0	225315_at	NP_852615.1, NP_852616.1, EAW74724.1, EAW74725.1, EAW74727.1, EAW74728.1, EAW74726.1
GeneID:3508	IGHMBP2	11	68,671,319	68,708,069	36,750	+	2	1_A375_pNL7_minus_lncRNA::1::1207, 2_A375_pNL97_plus_lncRNA::1::1693	8, -55	in gene, upstream	1	1	27	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene IGHMBP2	IGHMBP2, FLJ34220, SMUBP2, SMARD1, HCSA, HMN6, FLJ41171, CATF1	immunoglobulin mu binding protein 2	NM_002180, hCT18316.2	215980_s_at, 31861_at	NP_002171.2, EAW74729.1
GeneID:26579	MYEOV	11	69,061,622	69,064,754	3,132	+	2	1_A375_pNL7_minus_lncRNA::1::1208, 1_A375_pNL7_minus_lncRNA::1::1209	4522, 7706	downstream, downstream	1	0	26	19.5	2	1_A375_pNL7_minus_lncRNA::1	30	Gene MYEOV	OCIM, MYEOV	myeloma overexpressed (in a subset of t(11;14) positive multiple myelomas)	NM_138768, hCT1970719.1, hCT2355296.0	227342_s_at, 227343_at	NP_620123.2, EAW74741.1, EAW74740.1
GeneID:100505834	LOC100505834	11	69,240,439	69,244,389	3,950	+	1	2_A375_pNL97_plus_lncRNA::1::1695	-8567	upstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100505834		hypothetical LOC100505834	XR_111194, XR_110888, XR_114502		
GeneID:220064	ORAOV1	11	69,480,331	69,490,165	9,834	-	1	2_A375_pNL97_plus_lncRNA::1::1696	197	in gene	0	1	28	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ORAOV1	TAOS1, ORAOV1	oral cancer overexpressed 1	NM_153451, hCT19137.2, hCT2355295.0	226676_at, 243531_at	NP_703152.1, EAW74749.1, EAW74750.1
GeneID:55107	ANO1	11	69,924,408	70,035,651	111,243	+	2	1_A375_pNL7_minus_lncRNA::1::1212, 2_A375_pNL97_plus_lncRNA::1::1697	81896, 81736	in gene, in gene	1	1	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ANO1	ORAOV2, ANO1, TAOS2, FLJ10261, TMEM16A, DOG1	anoctamin 1, calcium activated chloride channel	NM_018043, NR_030691, hCT16223.3, hCT2309663.0, hCT2309664.0	1555269_a_at, 218804_at	NP_060513.5, EAW74758.1, EAW74757.1, EAW74759.1
GeneID:22941	SHANK2	11	70,313,961	70,935,808	621,847	-	2	1_A375_pNL7_minus_lncRNA::1::1214, 2_A375_pNL97_plus_lncRNA::1::1699	439168, 439232	in gene, in gene	1	1	74	91	1	2_A375_pNL97_plus_lncRNA::1	91	Gene SHANK2	CORTBP1, ProSAP1, SHANK2, SPANK-3, AUTS17, CTTNBP1, SHANK	SH3 and multiple ankyrin repeat domains 2	NM_012309, NM_133266, hCT2344128.0, hCT2344129.0, hCT2344130.0, hCT2344131.0, hCT2344132.0, hCT2344133.0, hCT2344134.0, hCT2344135.0, hCT2355340.0	1564377_at, 213307_at, 213308_at, 215829_at, 215830_at, 243681_at	NP_036441.2, NP_573573.2, EAW74771.1, EAW74772.1, EAW74773.1, EAW74775.1, EAW74774.1, EAW74776.1, EAW74777.1, EAW74778.1, EAW74779.1
GeneID:55298	RNF121	11	71,639,768	71,708,643	68,875	+	2	1_A375_pNL7_minus_lncRNA::1::1215, 2_A375_pNL97_plus_lncRNA::1::1701	136, 232	in gene, in gene	1	1	20	20	1	1_A375_pNL7_minus_lncRNA::1	20	Gene RNF121	RNF121, FLJ11099	ring finger protein 121	NM_018320, NR_024147, NR_024148, hCT1952428.1, hCT1952429.1, hCT1969225.1, hCT2355353.0, hCT2355354.0	219021_at	NP_060790.2, EAW74809.1, EAW74807.1, EAW74808.1, EAW74810.1, EAW74811.1
GeneID:4926	NUMA1	11	71,713,911	71,791,573	77,662	-	3	1_A375_pNL7_minus_lncRNA::1::1216, 2_A375_pNL97_plus_lncRNA::1::1702, 2_A375_pNL97_plus_lncRNA::1::1703	38837, 38789, -387	in gene, in gene, upstream	1	1	20	21.5	2	1_A375_pNL7_minus_lncRNA::1	31	Gene NUMA1	NUMA, NUMA1	nuclear mitotic apparatus protein 1	NM_006185, hCT2310492.0, hCT2310493.0, hCT2310494.0, hCT2310495.0, hCT2310496.0, hCT2310497.0, hCT2310498.0, hCT2310499.0, hCT2310500.0, hCT2355290.0, hCT2355291.0	1554663_a_at, 200747_s_at, 214250_at, 214251_s_at	NP_006176.2, EAW74827.1, EAW74821.1, EAW74822.1, EAW74823.1, EAW74828.1, EAW74824.1, EAW74825.1, EAW74826.1, EAW74829.1, EAW74830.1, EAW74831.1
GeneID:100422953	MIR3165	11	71,783,274	71,783,348	74	-	1	2_A375_pNL97_plus_lncRNA::1::1703	-8612	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MIR3165	MIR3165	microRNA 3165	NR_036123		
GeneID:220074	LRTOMT	11	71,791,382	71,821,828	30,446	+	1	2_A375_pNL97_plus_lncRNA::1::1703	578	in gene	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LRTOMT	LRTOMT1, DFNB63, LRRC51, LRTOMT2, FLJ52451, COMT2, LRTOMT	leucine rich transmembrane and 0-methyltransferase domain containing	NM_145309, NM_001145307, NR_026686, NM_001145308, NM_001145309, NM_001145310, hCT2309910.1, hCT2351777.0, hCT2355322.0	1568882_at, 226717_at	NP_660352.1, NP_001138779.1, NP_001138780.1, NP_001138781.1, NP_001138782.1, EAW74832.1, EAW74833.1, EAW74834.1
GeneID:2350	FOLR2	11	71,927,819	71,932,994	5,175	+	2	1_A375_pNL7_minus_lncRNA::1::1217, 2_A375_pNL97_plus_lncRNA::1::1704	6469, 6485	downstream, downstream	1	1	25	24	1	1_A375_pNL7_minus_lncRNA::1	25	Gene FOLR2	FOLR2, BETA-HFR, FR-P3, FR-BETA, FBP/PL-1	folate receptor 2 (fetal)	NM_000803, NM_001113534, NM_001113535, NM_001113536, hCT1813794.2	204829_s_at, 229619_at	NP_000794.3, NP_001107006.1, NP_001107007.1, NP_001107008.1, EAW74853.1
GeneID:3636	INPPL1	11	71,935,882	71,950,191	14,309	+	2	1_A375_pNL7_minus_lncRNA::1::1217, 2_A375_pNL97_plus_lncRNA::1::1704	-1594, -1578	upstream, upstream	1	1	25	24	1	1_A375_pNL7_minus_lncRNA::1	25	Gene INPPL1	INPPL1, SHIP2	inositol polyphosphate phosphatase-like 1	NM_001567, hCT14337.2, hCT2309787.0	201598_s_at	NP_001558.3, EAW74855.1, EAW74854.1
GeneID:81570	CLPB	11	72,003,469	72,145,568	142,099	-	2	1_A375_pNL7_minus_lncRNA::1::1218, 2_A375_pNL97_plus_lncRNA::1::1705	-32, -64	upstream, upstream	1	1	22	21	1	1_A375_pNL7_minus_lncRNA::1	22	Gene CLPB	CLPB, SKD3, FLJ13152, HSP78	ClpB caseinolytic peptidase B homolog (E. coli)	NM_030813, hCT15212.2, hCT1952436.1, hCT2310117.0	221845_s_at, 224510_s_at	NP_110440.1, EAW74860.1, EAW74858.1, EAW74859.1
GeneID:5138	PDE2A	11	72,287,185	72,385,494	98,309	-	1	2_A375_pNL97_plus_lncRNA::1::1706	-2570	upstream	0	1	14	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene PDE2A	PDE2A, PDE2A1, PED2A4	phosphodiesterase 2A, cGMP-stimulated	NM_002599, NM_001143839, NR_026572, NM_001146209, hCT1952437.1, hCT2310110.0	204134_at	NP_002590.1, NP_001137311.1, NP_001139681.1, EAW74861.1, EAW74862.1
GeneID:116985	ARAP1	11	72,396,114	72,463,434	67,320	-	1	2_A375_pNL97_plus_lncRNA::1::1706	75370	downstream	0	1	14	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ARAP1	KIAA0782, CENTD2, ARAP1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1	NM_001040118, NM_015242, NM_001135190, hCT15211.2, hCT2310105.0, hCT2310107.0, hCT2310108.0	212516_at, 242039_at, 34206_at	NP_001035207.1, NP_056057.2, NP_001128662.1, EAW74863.1, EAW74864.1, EAW74865.1, EAW74866.1
GeneID:10809	STARD10	11	72,465,774	72,504,750	38,976	-	1	2_A375_pNL97_plus_lncRNA::1::1707	-338	upstream	0	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene STARD10	NY-CO-28, STARD10, SDCCAG28, CGI-52, PCTP2, MGC14401	StAR-related lipid transfer (START) domain containing 10	NM_006645, hCT15215.3, hCT1957419.1, hCT1960880.1, hCT1960881.1, hCT2310098.0, hCT2310099.0	223103_at, 232322_x_at, 238911_at	NP_006636.2, EAW74868.1, EAW74867.1, EAW74869.1, EAW74870.1, EAW74871.1, EAW74872.1
GeneID:89849	ATG16L2	11	72,525,451	72,540,680	15,229	+	2	1_A375_pNL7_minus_lncRNA::1::1219, 2_A375_pNL97_plus_lncRNA::1::1708	-235, -219	upstream, upstream	1	1	28	23	1	1_A375_pNL7_minus_lncRNA::1	28	Gene ATG16L2	FLJ00012, WDR80, ATG16L2, ATG16B	ATG16 autophagy related 16-like 2 (S. cerevisiae)	NM_033388, hCT15216.3, hCT2309769.0, hCT2309771.0, hCT2309772.0, hCT2355270.0, hCT2355271.0	225883_at, 229389_at	NP_203746.1, EAW74874.1, EAW74875.1, EAW74876.1, EAW74878.1, EAW74879.1, EAW74877.1
GeneID:9828	ARHGEF17	11	73,019,663	73,080,425	60,762	+	1	2_A375_pNL97_plus_lncRNA::1::1709	68497	downstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ARHGEF17	KIAA0337, p164-RhoGEF, ARHGEF17, FLJ90019, TEM4, P164RHOGEF	Rho guanine nucleotide exchange factor (GEF) 17	NM_014786, hCT13878.2	203756_at	NP_055601.2, EAW74891.1
GeneID:84957	RELT	11	73,087,405	73,108,519	21,114	+	1	2_A375_pNL97_plus_lncRNA::1::1709	755	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene RELT	RELT, TNFRSF19L, FLJ14993	RELT tumor necrosis factor receptor	NM_032871, NM_152222, hCT14437.3, hCT1952434.1, hCT1952435.1, hCT2309933.0, hCT2309934.0, hCT2309936.0, hCT2355214.0	227060_at	NP_116260.2, NP_689405.1, EAW74892.1, EAW74893.1, EAW74894.1, EAW74898.1, EAW74895.1, EAW74896.1, EAW74897.1
GeneID:23201	FAM168A	11	73,117,028	73,309,228	192,200	-	2	1_A375_pNL7_minus_lncRNA::1::1220, 2_A375_pNL97_plus_lncRNA::1::1710	-292, -164	upstream, upstream	1	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FAM168A	FAM168A, KIAA0280, TCRP1	family with sequence similarity 168, member A	NM_015159	212357_at, 36612_at	NP_055974.1
GeneID:51642	MRPL48	11	73,498,917	73,575,656	76,739	+	4	1_A375_pNL7_minus_lncRNA::1::1221, 1_A375_pNL7_minus_lncRNA::1::1222, 2_A375_pNL97_plus_lncRNA::1::1711, 2_A375_pNL97_plus_lncRNA::1::1712	-8165, 91, -8261, 91	upstream, in gene, upstream, in gene	1	1	20.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene MRPL48	FLJ17047, L48MT, MRPL48, MGC13323, HSPC290, MRP-L48, FLJ99260, CGI-118	mitochondrial ribosomal protein L48	NM_016055, hCT18476.2	218281_at	NP_057139.1, EAW74913.1
GeneID:51287	CHCHD8	11	73,583,712	73,587,890	4,178	-	1	2_A375_pNL97_plus_lncRNA::1::1713	82	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CHCHD8	E2IG2, MGC117205, CHCHD8, DKFZp762H1711	coiled-coil-helix-coiled-coil-helix domain containing 8	NM_016565, hCT18473.2, hCT1956000.0, hCT2316379.0	220647_s_at	NP_057649.2, EAW74915.1, EAW74914.1, EAW74916.1
GeneID:80227	PAAF1	11	73,586,033	73,636,779	50,746	+	1	2_A375_pNL97_plus_lncRNA::1::1713	-225	upstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PAAF1	Rpn14, WDR71, FLJ11848, PAAF, PAAF1	proteasomal ATPase-associated factor 1	NM_025155, hCT2309949.0, hCT2355210.0, hCT2355211.0	1566702_a_at, 218957_s_at	NP_079431.1, EAW74918.1, EAW74917.1, EAW74919.1
GeneID:26005	C2CD3	11	73,745,480	73,882,064	136,584	-	3	1_A375_pNL7_minus_lncRNA::1::1223, 2_A375_pNL97_plus_lncRNA::1::1714, 2_A375_pNL97_plus_lncRNA::1::1715	-304, 133520, -368	upstream, in gene, upstream	1	1	16	24	2	2_A375_pNL97_plus_lncRNA::1	24	Gene C2CD3	DKFZp586P0123, FLJ34770, C2CD3	C2 calcium-dependent domain containing 3	NM_015531	1556756_at, 213199_at, 231705_at, 36552_at	NP_056346.3
GeneID:51400	PPME1	11	73,882,368	73,965,748	83,380	+	2	1_A375_pNL7_minus_lncRNA::1::1223, 2_A375_pNL97_plus_lncRNA::1::1715	0, 64	in gene, in gene	1	1	19	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene PPME1	PME-1, FLJ22226, PPME1	protein phosphatase methylesterase 1	NM_016147, hCT17598.3	217841_s_at, 49077_at	NP_057231.1, EAW74932.1
GeneID:283208	P4HA3	11	73,977,702	74,022,699	44,997	-	1	2_A375_pNL97_plus_lncRNA::1::1716	34635	in gene	0	1	6	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene P4HA3	P4HA3		NM_182904, hCT18477.3, hCT2355260.0, hCT2355261.0	1560715_at, 228703_at	NP_878907.1, EAW74934.1, EAW74935.1, EAW74936.1
GeneID:283209	PGM2L1	11	74,041,361	74,109,502	68,141	-	1	1_A375_pNL7_minus_lncRNA::1::1224	-462	upstream	1	0	23	19	1	1_A375_pNL7_minus_lncRNA::1	23	Gene PGM2L1	PGM2L1, FLJ32029, BM32A	phosphoglucomutase 2-like 1	NM_173582, hCT18470.4	1569448_at, 229256_at, 229553_at, 235149_at, 238417_at	NP_775853.2, EAW74937.1
GeneID:387787	LIPT2	11	74,202,923	74,204,755	1,832	-	2	1_A375_pNL7_minus_lncRNA::1::1226, 2_A375_pNL97_plus_lncRNA::1::1718	131, 147	in gene, in gene	1	1	19	19	1	1_A375_pNL7_minus_lncRNA::1	19	Gene LIPT2	LIPT2		NM_001144869		NP_001138341.1
GeneID:100287896	LOC100287896	11	74,204,485	74,209,287	4,802	+	2	1_A375_pNL7_minus_lncRNA::1::1226, 2_A375_pNL97_plus_lncRNA::1::1718	139, 123	in gene, in gene	1	1	19	19	1	1_A375_pNL7_minus_lncRNA::1	19	Gene LOC100287896		hypothetical protein LOC100287896	XM_002343118, XM_003119510, XM_003120708		XP_002343159.1, XP_003119558.1, XP_003120756.1
GeneID:254225	RNF169	11	74,459,913	74,553,458	93,545	+	4	1_A375_pNL7_minus_lncRNA::1::1227, 1_A375_pNL7_minus_lncRNA::1::1228, 2_A375_pNL97_plus_lncRNA::1::1719, 2_A375_pNL97_plus_lncRNA::1::1720	-73, 5927, -73, 101111	upstream, in gene, upstream, downstream	1	1	22.67	22	3	1_A375_pNL7_minus_lncRNA::1	41	Gene RNF169	KIAA1991, RNF169	ring finger protein 169	NM_001098638	226739_at	NP_001092108.1
GeneID:143570	XRRA1	11	74,551,955	74,660,232	108,277	-	2	2_A375_pNL97_plus_lncRNA::1::1720, 2_A375_pNL97_plus_lncRNA::1::1721	99208, 24	in gene, in gene	0	1	11.5	23	2	2_A375_pNL97_plus_lncRNA::1	28	Gene XRRA1	XRRA1	X-ray radiation resistance associated 1	NM_182969	230557_at, 237666_at	NP_892014.1
GeneID:9789	SPCS2	11	74,660,292	74,690,076	29,784	+	1	2_A375_pNL97_plus_lncRNA::1::1721	-84	upstream	0	1	11	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene SPCS2	MGC117366, SPCS2, KIAA0102	signal peptidase complex subunit 2 homolog (S.cerevisiae)	NM_014752, hCT1971010.1	201240_s_at	NP_055567.2, EAW74952.1
GeneID:11309	SLCO2B1	11	74,862,040	74,917,445	55,405	+	2	1_A375_pNL7_minus_lncRNA::1::1229, 2_A375_pNL97_plus_lncRNA::1::1722	63560, 63592	downstream, downstream	1	1	66	61	1	1_A375_pNL7_minus_lncRNA::1	66	Gene SLCO2B1	OATP-B, OATPB, SLCO2B1, DKFZp686E0517, OATP2B1, SLC21A9, KIAA0880	solute carrier organic anion transporter family, member 2B1	NM_007256, NM_001145211, NM_001145212, hCT16542.2, hCT2309843.0, hCT2309844.0	203472_s_at, 203473_at, 211557_x_at	NP_009187.1, NP_001138683.1, NP_001138684.1, EAW74956.1, EAW74957.1, EAW74958.1
GeneID:100507050	LOC100507050	11	74,951,422	74,953,243	1,821	+	2	1_A375_pNL7_minus_lncRNA::1::1230, 2_A375_pNL97_plus_lncRNA::1::1723	-6462, -6462	upstream, upstream	1	1	32	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene LOC100507050		hypothetical protein LOC100507050	XM_003119180, XM_003120716		XP_003119228.1, XP_003120764.1
GeneID:6188	RPS3	11	75,110,562	75,116,733	6,171	+	2	1_A375_pNL7_minus_lncRNA::1::1231, 2_A375_pNL97_plus_lncRNA::1::1724	30, 158	in gene, in gene	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RPS3	RPS3, FLJ26283, S3, MGC87870, FLJ27450	ribosomal protein S3	NM_001005, hCT2310640.0	208692_at	NP_000996.2, EAW74963.1
GeneID:6079	SNORD15A	11	75,111,435	75,111,582	147	+	2	1_A375_pNL7_minus_lncRNA::1::1231, 2_A375_pNL97_plus_lncRNA::1::1724	-843, -715	upstream, upstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SNORD15A	SNORD15A, U15A, SNORNA, RNU15A	small nucleolar RNA, C/D box 15A	NR_000005		
GeneID:114599	SNORD15B	11	75,115,465	75,115,610	145	+	2	1_A375_pNL7_minus_lncRNA::1::1231, 2_A375_pNL97_plus_lncRNA::1::1724	-4873, -4745	upstream, upstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SNORD15B	RNU15B, U15B, SNORD15B	small nucleolar RNA, C/D box 15B	NR_000025		
GeneID:84649	DGAT2	11	75,479,778	75,512,579	32,801	+	2	1_A375_pNL7_minus_lncRNA::1::1232, 2_A375_pNL97_plus_lncRNA::1::1726	-114, -162	upstream, upstream	1	1	27	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene DGAT2	DKFZp686A15125, GS1999FULL, DGAT2, HMFN1045	diacylglycerol O-acyltransferase homolog 2 (mouse)	NM_032564, hCT19005.3, hCT2310649.0	224327_s_at, 226064_s_at	NP_115953.2, EAW74984.1, EAW74985.1
GeneID:100506113	LOC100506113	11	75,524,424	75,525,842	1,418	-	1	2_A375_pNL97_plus_lncRNA::1::1727	226	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100506113		hypothetical LOC100506113	XR_111204, XR_110893, XR_114507		
GeneID:7405	UVRAG	11	75,526,212	75,855,282	329,070	+	2	2_A375_pNL97_plus_lncRNA::1::1727, 2_A375_pNL97_plus_lncRNA::1::1728	-596, 338556	upstream, downstream	0	1	13.5	19.5	2	2_A375_pNL97_plus_lncRNA::1	20	Gene UVRAG	UVRAG, p63, DHTX, VPS38	UV radiation resistance associated gene	NM_003369, hCT19008.3, hCT2310651.0	203241_at	NP_003360.2, EAW74986.1, EAW74987.1
GeneID:7481	WNT11	11	75,897,370	75,917,574	20,204	-	2	1_A375_pNL7_minus_lncRNA::1::1233, 2_A375_pNL97_plus_lncRNA::1::1729	-2618, -2554	upstream, upstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene WNT11	MGC141948, HWNT11, MGC141946, WNT11	wingless-type MMTV integration site family, member 11	NM_004626, hCT19002.1, hCT1971015.1	206737_at	NP_004617.2, EAW74989.1, EAW74988.1
GeneID:5612	PRKRIR	11	76,061,004	76,091,880	30,876	-	3	1_A375_pNL7_minus_lncRNA::1::1235, 2_A375_pNL97_plus_lncRNA::1::1731, 2_A375_pNL97_plus_lncRNA::1::1732	-248, 248, -248	upstream, in gene, upstream	1	1	93	101	1	2_A375_pNL97_plus_lncRNA::1	101	Gene PRKRIR	MGC102750, DAP4, PRKRIR, P52rIPK, THAP0	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	NM_004705, hCT2310834.0, hCT2310835.0, hCT2310837.0	209323_at	NP_004696.2, EAW74993.1, EAW74991.1, EAW74992.1
GeneID:100506127	LOC100506127	11	76,092,360	76,119,176	26,816	+	3	1_A375_pNL7_minus_lncRNA::1::1235, 2_A375_pNL97_plus_lncRNA::1::1731, 2_A375_pNL97_plus_lncRNA::1::1732	-232, -728, -232	upstream, upstream, upstream	1	1	93	101	1	2_A375_pNL97_plus_lncRNA::1	101	Gene LOC100506127	FLJ43633, FLJ37770	putative uncharacterized protein FLJ37770-like	XM_003119509, XM_003119508, XM_003119507, XM_003119174, XM_003119173, XM_003119172, XM_003120711, XM_003120710, XM_003120709		XP_003119557.1, XP_003119556.1, XP_003119555.1, XP_003119222.1, XP_003119221.1, XP_003119220.1, XP_003120759.1, XP_003120758.1, XP_003120757.1
GeneID:56946	C11orf30	11	76,156,069	76,262,589	106,520	+	1	2_A375_pNL97_plus_lncRNA::1::1733	-208	upstream	0	1	20	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C11orf30	EMSY, GL002, C11orf30, FLJ90741	chromosome 11 open reading frame 30	NM_020193, hCT2312764.0, hCT2312765.0, hCT2312766.0, hCT2312767.0, hCT2312769.0	1569349_at, 219012_s_at, 222806_s_at, 222807_at, 234669_x_at, 242847_at	NP_064578.2, EAW74998.1, EAW74996.1, EAW74997.1, EAW74999.1, EAW75000.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:726	CAPN5	11	76,777,992	76,837,201	59,209	+	1	2_A375_pNL97_plus_lncRNA::1::1738	6632	in gene	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CAPN5	nCL-3, FLJ46245, CAPN5, HTRA3	calpain 5	NM_004055, hCT2312787.1, hCT2351381.0, hCT33143.3	205166_at, 226292_at	NP_004046.2, EAW75015.1, EAW75014.1, EAW75016.1
GeneID:5058	PAK1	11	77,033,060	77,185,108	152,048	-	1	2_A375_pNL97_plus_lncRNA::1::1739	-396	upstream	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PAK1	MGC130001, MGC130000, PAKalpha, PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	NM_002576, NM_001128620, hCT1954872.1, hCT2313054.0, hCT2313056.0, hCT33146.3	1565772_at, 209615_s_at, 226507_at, 230100_x_at	NP_002567.3, NP_001122092.1, EAW75026.1, EAW75027.1, EAW75028.1, EAW75029.1
GeneID:282679	AQP11	11	77,300,680	77,321,401	20,721	+	1	2_A375_pNL97_plus_lncRNA::1::1740	-136	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene AQP11	AQP11, AQPX1	aquaporin 11	NM_173039, hCT2309957.1, hCT2355277.0	229526_at	NP_766627.1, EAW75031.1, EAW75030.1
GeneID:1207	CLNS1A	11	77,327,196	77,348,851	21,655	-	2	1_A375_pNL7_minus_lncRNA::1::1237, 2_A375_pNL97_plus_lncRNA::1::1741	-29, 19	upstream, in gene	1	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene CLNS1A	CLNS1A, CLNS1B, CLCI, ICln	chloride channel, nucleotide-sensitive, 1A	NM_001293, hCT18250.3	209143_s_at	NP_001284.1, EAW75032.1
GeneID:51773	RSF1	11	77,377,274	77,531,880	154,606	-	2	1_A375_pNL7_minus_lncRNA::1::1238, 2_A375_pNL97_plus_lncRNA::1::1742	1288, 1384	in gene, in gene	1	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene RSF1	RSF1, HBXAP, XAP8, RSF-1, p325	remodeling and spacing factor 1	NM_016578, hCT2344877.0, hCT2344878.0, hCT2344880.0	218166_s_at, 222540_s_at, 222541_at, 223818_s_at	NP_057662.3, EAW75033.1, EAW75034.1, EAW75035.1
GeneID:26971	C11orf67	11	77,532,208	77,583,398	51,190	+	2	1_A375_pNL7_minus_lncRNA::1::1238, 2_A375_pNL97_plus_lncRNA::1::1742	-1616, -1712	upstream, upstream	1	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C11orf67	PTD015, CK067, FLJ21035, C11orf67, MGC3367	chromosome 11 open reading frame 67	NM_024684, hCT18251.2, hCT2309959.0, hCT2309960.0, hCT2309961.0	220266_at, 221599_at, 221600_s_at	NP_078960.1, EAW75036.1, EAW75037.1, EAW75038.1, EAW75039.1
GeneID:92105	INTS4	11	77,589,766	77,705,717	115,951	-	2	1_A375_pNL7_minus_lncRNA::1::1239, 2_A375_pNL97_plus_lncRNA::1::1743	-331, -139	upstream, upstream	1	1	18	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene INTS4	MGC16733, INTS4, MST093, INT4	integrator complex subunit 4	NM_033547	1553670_at, 1569253_at, 1569254_s_at, 225169_at, 233193_x_at	NP_291025.3
GeneID:79053	ALG8	11	77,811,988	77,850,699	38,711	-	1	2_A375_pNL97_plus_lncRNA::1::1744	-53	upstream	0	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ALG8	CDG1H, ALG8, MGC2840	asparagine-linked glycosylation 8, alpha-1,3-glucosyltransferase homolog (S. cerevisiae)	NM_024079, NM_001007027, hCT1969009.1, hCT2310401.0, hCT2310403.0, hCT2355341.0	203545_at	NP_076984.2, NP_001007028.1, EAW75048.1, EAW75049.1, EAW75050.1, EAW75051.1
GeneID:283219	KCTD21	11	77,882,298	77,899,664	17,366	-	2	1_A375_pNL7_minus_lncRNA::1::1240, 2_A375_pNL97_plus_lncRNA::1::1745	-144, -112	upstream, upstream	1	1	47	67	1	2_A375_pNL97_plus_lncRNA::1	67	Gene KCTD21	KCTD21	potassium channel tetramerisation domain containing 21	NM_001029859, hCT1644284.2, hCT2310399.0	229873_at	NP_001025030.1, EAW75054.1, EAW75053.1
GeneID:57558	USP35	11	77,899,858	77,925,757	25,899	+	2	1_A375_pNL7_minus_lncRNA::1::1240, 2_A375_pNL97_plus_lncRNA::1::1745	-50, -82	upstream, upstream	1	1	47	67	1	2_A375_pNL97_plus_lncRNA::1	67	Gene USP35	USP35		NM_020798	229198_at	NP_065849.1
GeneID:79731	NARS2	11	78,147,016	78,285,909	138,893	-	1	2_A375_pNL97_plus_lncRNA::1::1746	101	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NARS2	FLJ23441, SLM5, NARS2	asparaginyl-tRNA synthetase 2, mitochondrial (putative)	NM_024678, NR_027479, hCT17605.3, hCT2310394.0, hCT2310396.0	219217_at	NP_078954.4, EAW75062.1, EAW75061.1, EAW75063.1
GeneID:27314	RAB30	11	82,692,478	82,782,884	90,406	-	1	2_A375_pNL97_plus_lncRNA::1::1747	-28	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RAB30	RAB30	RAB30, member RAS oncogene family	NM_014488, hCT18425.3, hCT2310547.0, hCT2310548.0, hCT2310549.0	206530_at, 227842_at, 228003_at	NP_055303.2, EAW75080.1, EAW75078.1, EAW75079.1, EAW75081.1
GeneID:100506233	LOC100506233	11	82,783,119	82,785,008	1,889	+	1	2_A375_pNL97_plus_lncRNA::1::1747	-207	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100506233		hypothetical LOC100506233	XR_111200, XR_111201, XR_110896, XR_110897, XR_114510, XR_114511		
GeneID:100506259	LOC100506259	11	82,789,752	82,790,924	1,172	-	1	2_A375_pNL97_plus_lncRNA::1::1747	8012	downstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100506259		hypothetical LOC100506259	XR_111199, XR_110898, XR_114512		
GeneID:51585	PCF11	11	82,868,137	82,896,836	28,699	+	2	1_A375_pNL7_minus_lncRNA::1::1241, 2_A375_pNL97_plus_lncRNA::1::1748	37623, 37303	downstream, downstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene PCF11	KIAA0824, PCF11	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)	NM_015885, hCT17609.2, hCT2310335.0	203378_at, 227622_at	NP_056969.2, EAW75083.1, EAW75084.1
GeneID:100506282	LOC100506282	11	82,902,887	82,904,704	1,817	-	2	1_A375_pNL7_minus_lncRNA::1::1241, 2_A375_pNL97_plus_lncRNA::1::1748	-1056, -736	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100506282		hypothetical LOC100506282	XR_110899		
GeneID:338699	ANKRD42	11	82,905,291	82,960,013	54,722	+	2	1_A375_pNL7_minus_lncRNA::1::1241, 2_A375_pNL97_plus_lncRNA::1::1748	469, 149	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ANKRD42	SARP, ANKRD42, FLJ37874	ankyrin repeat domain 42	NM_182603, hCT1644122.2, hCT2355231.0	232600_at, 243151_at	NP_872409.2, EAW75086.1, EAW75087.1
GeneID:60492	CCDC90B	11	82,972,506	82,997,377	24,871	-	2	1_A375_pNL7_minus_lncRNA::1::1242, 2_A375_pNL97_plus_lncRNA::1::1749	-127, -127	upstream, upstream	1	1	58	76	1	2_A375_pNL97_plus_lncRNA::1	76	Gene CCDC90B	MGC104239, MDS025, MDS011, CCDC90B	coiled-coil domain containing 90B	NM_021825, hCT18488.3, hCT1964122.1, hCT2355324.0, hCT2355325.0	1568834_s_at, 218288_s_at, 222577_at	NP_068597.2, EAW75090.1, EAW75088.1, EAW75089.1, EAW75091.1
GeneID:1740	DLG2	11	83,166,055	85,338,314	2,172,259	-	2	1_A375_pNL7_minus_lncRNA::1::1243, 1_A375_pNL7_minus_lncRNA::1::1244	912842, -1302	in gene, upstream	1	0	21.5	13.5	2	1_A375_pNL7_minus_lncRNA::1	24	Gene DLG2	PSD93, PSD-93, MGC131811, DKFZp781D1854, FLJ37266, DLG2, DKFZp781E0954	discs, large homolog 2 (Drosophila)	NM_001142702, NM_001364, NM_001142699, NM_001142700, hCT18487.4, hCT2310272.1, hCT2310538.1	206253_at, 228973_at	NP_001136174.1, NP_001355.2, NP_001136171.1, NP_001136172.1, EAW75093.1, EAW75094.1, EAW75095.1
GeneID:55863	TMEM126B	11	85,339,622	85,347,583	7,961	+	1	1_A375_pNL7_minus_lncRNA::1::1244	-6	upstream	1	0	19	13	1	1_A375_pNL7_minus_lncRNA::1	19	Gene TMEM126B	MGC111203, HT007, TMEM126B	transmembrane protein 126B	NM_018480, NM_001193537, NM_001193538, NR_036465, hCT1641097.3, hCT1962027.0, hCT2310346.0, hCT2310347.0, hCT2355404.0, hCT2355405.0	1554537_at, 221622_s_at	NP_060950.3, NP_001180466.1, NP_001180467.1, EAW75099.1, EAW75100.1, EAW75101.1, EAW75096.1, EAW75097.1, EAW75098.1
GeneID:84233	TMEM126A	11	85,358,963	85,367,597	8,634	+	1	2_A375_pNL97_plus_lncRNA::1::1750	-99	upstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TMEM126A	OPA7, DKFZp586C1924, TMEM126A	transmembrane protein 126A	NM_032273, hCT18815.3	223334_at	NP_115649.1, EAW75102.1
GeneID:58487	CREBZF	11	85,368,608	85,376,182	7,574	-	1	2_A375_pNL97_plus_lncRNA::1::1750	17316	downstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CREBZF	ZF, FLJ94018, SMILE, CREBZF	CREB/ATF bZIP transcription factor	NM_001039618, NR_028024, NR_028025, NR_028026, NR_028027, hCT1641884.2	202977_s_at, 202978_s_at, 202979_s_at, 213584_s_at, 225584_at, 225585_at	NP_001034707.1, EAW75103.1
GeneID:54843	SYTL2	11	85,405,264	85,522,178	116,914	-	2	1_A375_pNL7_minus_lncRNA::1::1245, 2_A375_pNL97_plus_lncRNA::1::1751	91949, 91986	in gene, in gene	1	1	24	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene SYTL2	SGA72M, FLJ45597, EXO4, MGC102768, FLJ34602, KIAA1597, SLP2, SLP2A, FLJ42764, CHR11SYT, SYTL2, FLJ21219	synaptotagmin-like 2	NM_032379, NM_206927, NM_206928, NM_206929, NM_206930, NM_001162951, NM_001162952, NM_001162953, NM_032943, hCT18812.3, hCT2310576.0, hCT2310577.0, hCT2310578.0, hCT2310580.0, hCT2310581.0, hCT2310582.0	220613_s_at, 225496_s_at, 232914_s_at	NP_115755.2, NP_996810.1, NP_001156423.1, NP_996811.1, NP_996812.1, NP_996813.1, NP_116561.1, NP_001156424.1, NP_001156425.1, EAW75107.1, EAW75108.1, EAW75109.1, EAW75110.1, EAW75111.1, EAW75112.1, EAW75113.1
GeneID:100506308	LOC100506308	11	85,563,600	85,565,986	2,386	-	1	2_A375_pNL97_plus_lncRNA::1::1752	130	in gene	0	1	10	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100506308		hypothetical protein LOC100506308	XM_003119506, XM_003119175, XM_003120712		XP_003119554.1, XP_003119223.1, XP_003120760.1
GeneID:220047	CCDC83	11	85,566,144	85,631,051	64,907	+	2	1_A375_pNL7_minus_lncRNA::1::1246, 2_A375_pNL97_plus_lncRNA::1::1752	35120, -288	in gene, upstream	1	1	13.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene CCDC83	FLJ42119, HSD9, MGC34732, CCDC83	coiled-coil domain containing 83	NM_173556, hCT1641883.4, hCT2355323.0	237160_at	NP_775827.2, EAW75114.1, EAW75115.1
GeneID:8301	PICALM	11	85,668,485	85,780,108	111,623	-	1	1_A375_pNL7_minus_lncRNA::1::1247	12	in gene	1	0	19	11	1	1_A375_pNL7_minus_lncRNA::1	19	Gene PICALM	PICALM, CALM, CLTH, LAP	phosphatidylinositol binding clathrin assembly protein	NM_007166, NM_001008660, hCT1767873.2, hCT1767874.2, hCT1767875.2, hCT1964108.1, hCT2310563.0, hCT2310564.0, hCT2310566.0, hCT2310567.0, hCT2310568.0, hCT2310570.0, hCT2355378.0	203134_at, 212506_at, 212511_at, 215236_s_at, 215632_x_at	NP_009097.2, NP_001008660.1, EAW75124.1, EAW75125.1, EAW75126.1, EAW75128.1, EAW75118.1, EAW75119.1, EAW75120.1, EAW75121.1, EAW75122.1, EAW75123.1, EAW75127.1
GeneID:8726	EED	11	85,955,815	85,989,781	33,966	+	2	1_A375_pNL7_minus_lncRNA::1::1249, 2_A375_pNL97_plus_lncRNA::1::1754	121, -135	in gene, upstream	1	1	17	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene EED	WAIT1, HEED, EED	embryonic ectoderm development	NM_003797, NM_152991, hCT18942.3, hCT2355265.0, hCT2355266.0	209572_s_at, 210656_at	NP_003788.2, NP_694536.1, EAW75129.1, EAW75130.1, EAW75131.1
GeneID:51501	C11orf73	11	86,013,253	86,056,985	43,732	+	1	1_A375_pNL7_minus_lncRNA::1::1250	-85	upstream	1	0	25	20	1	1_A375_pNL7_minus_lncRNA::1	25	Gene C11orf73	HSPC179, C11orf73, FLJ43020, HSPC138, L7RN6	chromosome 11 open reading frame 73	NM_016401, NR_024596, NR_024597, NR_024598, hCT2310361.0, hCT2310362.0, hCT2310363.0, hCT2355227.0, hCT2355228.0	219979_s_at, 230326_s_at	NP_057485.2, EAW75133.1, EAW75134.1, EAW75135.1, EAW75136.1, EAW75137.1
GeneID:10873	ME3	11	86,152,150	86,383,678	231,528	-	5	1_A375_pNL7_minus_lncRNA::1::1251, 1_A375_pNL7_minus_lncRNA::1::1252, 2_A375_pNL97_plus_lncRNA::1::1755, 2_A375_pNL97_plus_lncRNA::1::1756, 2_A375_pNL97_plus_lncRNA::1::1757	39646, 606, 212542, 39774, 329	in gene, in gene, in gene, in gene, in gene	1	1	17.33	17	3	1_A375_pNL7_minus_lncRNA::1	29	Gene ME3	ME3, FLJ34862	malic enzyme 3, NADP(+)-dependent, mitochondrial	NM_006680, NM_001014811, NM_001161586, hCT18939.3, hCT2310557.0, hCT2310559.0, hCT2310561.0, hCT2310562.0	204663_at, 231295_at	NP_006671.2, NP_001014811.1, NP_001155058.1, EAW75138.1, EAW75139.1, EAW75141.1, EAW75140.1, EAW75142.1
GeneID:1075	CTSC	11	88,026,760	88,070,941	44,181	-	1	2_A375_pNL97_plus_lncRNA::1::1759	29	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CTSC	CTSC, HMS, JP, PALS, DPPI, CPPI, PLS, JPD, DPP1	cathepsin C	NM_148170, NM_001114173, NM_001814, hCT11863.1, hCT2353414.0	201487_at, 225646_at, 225647_s_at, 231234_at	NP_680475.1, NP_001107645.1, NP_001805.3, EAW59363.1, EAW59364.1
GeneID:2915	GRM5	11	88,237,744	88,796,816	559,072	-	3	1_A375_pNL7_minus_lncRNA::1::1254, 2_A375_pNL97_plus_lncRNA::1::1760, 2_A375_pNL97_plus_lncRNA::1::1761	359024, 367760, 353936	in gene, in gene, in gene	1	1	16.33	20	3	2_A375_pNL97_plus_lncRNA::1	29	Gene GRM5	MGLUR5, GPRC1E, GRM5, mGlu5	glutamate receptor, metabotropic 5	NM_000842, NM_001143831, hCT2348962.0, hCT2348963.0	1565389_s_at, 207235_s_at, 214217_at	NP_000833.1, NP_001137303.1, EAW59358.1, EAW59359.1
GeneID:7299	TYR	11	88,911,040	89,028,927	117,887	+	1	1_A375_pNL7_minus_lncRNA::1::1255	-9344	upstream	1	0	19	13	1	1_A375_pNL7_minus_lncRNA::1	19	Gene TYR	OCAIA, TYR, OCA1A, CMM8, SHEP3	tyrosinase (oculocutaneous albinism IA)	NM_000372, hCT10762.4, hCT2258943.1	1555504_at, 1555505_a_at, 206630_at	NP_000363.1, EAW59356.1, EAW59357.1
GeneID:26973	CHORDC1	11	89,933,597	89,956,532	22,935	-	1	2_A375_pNL97_plus_lncRNA::1::1762	308	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CHORDC1	FLJ37289, CHP1, CHORDC1	cysteine and histidine-rich domain (CHORD) containing 1	NM_012124, NM_001144073, hCT2334896.0, hCT2334897.0, hCT2334898.0, hCT2334899.0, hCT2354466.0	218566_s_at, 239436_at	NP_036256.2, NP_001137545.1, EAW66867.1, EAW66869.1, EAW66870.1, EAW66871.1, EAW66868.1
GeneID:120103	SLC36A4	11	92,880,850	92,931,095	50,245	-	1	2_A375_pNL97_plus_lncRNA::1::1763	311	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SLC36A4	PAT4, FLJ38932, SLC36A4	solute carrier family 36 (proton/amino acid symporter), member 4	NM_152313, hCT1768097.2, hCT2354455.0, hCT2354456.0	234978_at	NP_689526.2, EAW66895.1, EAW66896.1, EAW66897.1
GeneID:85459	KIAA1731	11	93,394,816	93,463,522	68,706	+	1	2_A375_pNL97_plus_lncRNA::1::1764	320	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene KIAA1731	KIAA1731, FLJ40913	KIAA1731	NM_033395	1565829_at, 1569302_at, 215018_at, 229878_at	NP_203753.1
GeneID:692075	SNORD6	11	93,464,669	93,464,739	70	-	1	2_A375_pNL97_plus_lncRNA::1::1765	-9917	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORD6	SNORD6, mgh28S-2412	small nucleolar RNA, C/D box 6	NR_003036		
GeneID:677792	SNORA1	11	93,465,170	93,465,299	129	-	1	2_A375_pNL97_plus_lncRNA::1::1765	-9357	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORA1	SNORA1, ACA1	small nucleolar RNA, H/ACA box 1	NR_003026		
GeneID:654320	SNORA8	11	93,465,527	93,465,665	138	-	1	2_A375_pNL97_plus_lncRNA::1::1765	-8991	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORA8	SNORA8, ACA8	small nucleolar RNA, H/ACA box 8	NR_002920		
GeneID:692072	SNORD5	11	93,466,394	93,466,466	72	-	1	2_A375_pNL97_plus_lncRNA::1::1765	-8190	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORD5	SNORD5, mgh28S-2410	small nucleolar RNA, C/D box 5	NR_003033		
GeneID:677805	SNORA18	11	93,466,632	93,466,763	131	-	1	2_A375_pNL97_plus_lncRNA::1::1765	-7893	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORA18	ACA18, SNORA18	small nucleolar RNA, H/ACA box 18	NR_002959		
GeneID:100302240	MIR1304	11	93,466,840	93,466,930	90	-	1	2_A375_pNL97_plus_lncRNA::1::1765	-7726	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MIR1304	MIRN1304, MIR1304, hsa-mir-1304	microRNA 1304	NR_031639		
GeneID:677822	SNORA40	11	93,468,276	93,468,402	126	-	1	2_A375_pNL97_plus_lncRNA::1::1765	-6254	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORA40	ACA40, SNORA40	small nucleolar RNA, H/ACA box 40	NR_002973		
GeneID:79101	TAF1D	11	93,469,095	93,474,703	5,608	-	1	2_A375_pNL97_plus_lncRNA::1::1765	47	in gene	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TAF1D	TAF1D, MGC5306, JOSD3, TAF(I)41, RAFI41	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	NM_024116, hCT2334474.0, hCT2334476.0, hCT2334477.0	218750_at, 221580_s_at, 222728_s_at	NP_077021.1, EAW66912.1, EAW66913.1, EAW66914.1
GeneID:25970	C11orf54	11	93,474,793	93,496,247	21,454	+	1	2_A375_pNL97_plus_lncRNA::1::1765	-137	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C11orf54	PTD012, C11orf54	chromosome 11 open reading frame 54	NM_014039, hCT10870.3, hCT1965782.1, hCT2334391.0, hCT2334392.0, hCT2354464.0	1559623_at, 223268_at, 229851_s_at	NP_054758.2, EAW66915.1, EAW66916.1, EAW66917.1, EAW66918.1, EAW66919.1
GeneID:9440	MED17	11	93,517,405	93,546,496	29,091	+	1	2_A375_pNL97_plus_lncRNA::1::1766	547	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MED17	CRSP77, DRIP80, TRAP80, MED17, CRSP6, FLJ10812	mediator complex subunit 17	NM_004268, hCT12014.3, hCT2334393.0	221517_s_at, 223115_at, 232483_at	NP_004259.3, EAW66920.1, EAW66921.1
GeneID:154810	AMOTL1	11	94,501,508	94,609,918	108,410	+	6	1_A375_pNL7_minus_lncRNA::1::1256, 1_A375_pNL7_minus_lncRNA::1::1257, 1_A375_pNL7_minus_lncRNA::1::1258, 1_A375_pNL7_minus_lncRNA::1::1259, 2_A375_pNL97_plus_lncRNA::1::1767, 2_A375_pNL97_plus_lncRNA::1::1768	-84, 22556, 34492, 112028, -164, 112028	upstream, in gene, in gene, downstream, upstream, downstream	1	1	36.25	34.25	4	1_A375_pNL7_minus_lncRNA::1	74	Gene AMOTL1	JEAP, AMOTL1	angiomotin like 1	NM_130847, hCT12585.3, hCT2334662.1, hCT2354397.0	225450_at, 225459_at, 226840_at, 235277_at	NP_570899.1, EAW66945.1, EAW66943.1, EAW66944.1
GeneID:10929	SFRS2B	11	94,800,056	94,804,388	4,332	+	1	2_A375_pNL97_plus_lncRNA::1::1769	275	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SFRS2B	SRSF8, SRP46, SFRS2B	serine/arginine-rich splicing factor 8	NM_032102, hCT1812374.1, hCT1813985.1, hCT2334671.0	213152_s_at, 214789_x_at, 226760_at, 229471_s_at, 238929_at	NP_115285.1, EAW66954.1, EAW66955.1, EAW66956.1
GeneID:23052	ENDOD1	11	94,822,974	94,865,815	42,841	+	1	2_A375_pNL97_plus_lncRNA::1::1770	43330	downstream	0	1	8	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ENDOD1	KIAA0830, MGC88092, ENDOD1	endonuclease domain containing 1	NM_015036	212570_at, 212573_at	NP_055851.1
GeneID:143684	FAM76B	11	95,502,106	95,522,954	20,848	-	1	2_A375_pNL97_plus_lncRNA::1::1771	-150	upstream	0	1	18	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene FAM76B	MGC33371, FAM76B	family with sequence similarity 76, member B	NM_144664, hCT12543.3, hCT2354386.0, hCT2354387.0	1553749_at, 1553750_a_at, 226753_at, 232048_at	NP_653265.3, EAW66964.1, EAW66962.1, EAW66963.1
GeneID:9702	CEP57	11	95,523,642	95,565,854	42,212	+	1	2_A375_pNL97_plus_lncRNA::1::1771	-538	upstream	0	1	18	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene CEP57	KIAA0092, PIG8, TSP57, CEP57	centrosomal protein 57kDa	NM_014679, hCT12544.3, hCT1965785.1, hCT2334325.0, hCT2334326.0, hCT2354388.0, hCT2354389.0	203491_s_at, 203492_x_at, 203493_s_at, 203494_s_at, 209862_s_at	NP_055494.2, EAW66968.1, EAW66965.1, EAW66966.1, EAW66969.1, EAW66970.1, EAW66967.1
GeneID:8898	MTMR2	11	95,566,044	95,657,371	91,327	-	2	1_A375_pNL7_minus_lncRNA::1::1263, 2_A375_pNL97_plus_lncRNA::1::1772	203, 155	in gene, in gene	1	1	22	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene MTMR2	CMT4B1, CMT4B, MTMR2, KIAA1073	myotubularin related protein 2	NR_023356, NM_016156, NM_201278, NM_201281, hCT12542.3, hCT2354383.0, hCT2354384.0, hCT2354385.0	203211_s_at, 203212_s_at, 214649_s_at	NP_057240.3, NP_958435.1, NP_958438.1, EAW66972.1, EAW66973.1, EAW66974.1, EAW66971.1
GeneID:84441	MAML2	11	95,711,440	96,076,344	364,904	-	4	1_A375_pNL7_minus_lncRNA::1::1264, 2_A375_pNL97_plus_lncRNA::1::1773, 2_A375_pNL97_plus_lncRNA::1::1774, 1_A375_pNL7_minus_lncRNA::1::1265	328888, 220312, 186776, 1528	in gene, in gene, in gene, in gene	1	1	15.25	17	4	2_A375_pNL97_plus_lncRNA::1	25	Gene MAML2	MAML2, MAM3, KIAA1819, MGC176701, MAM-3, MAM2, MLL-MAML2, DKFZp686N0150	mastermind-like 2 (Drosophila)	NM_032427, hCT2348993.0	235106_at, 235457_at	NP_115803.1, EAW66975.1
GeneID:100422991	MIR1260B	11	96,074,602	96,074,690	88	+	1	1_A375_pNL7_minus_lncRNA::1::1265	214	downstream	1	0	18	16	1	1_A375_pNL7_minus_lncRNA::1	18	Gene MIR1260B	MIR1260B	microRNA 1260b	NR_036125		
GeneID:7225	TRPC6	11	101,322,295	101,454,659	132,364	-	1	2_A375_pNL97_plus_lncRNA::1::1775	141998	downstream	0	1	9	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene TRPC6	FLJ14863, FSGS2, TRP6, FLJ11098, TRPC6	transient receptor potential cation channel, subfamily C, member 6	NM_004621, hCT2335292.0, hCT2335293.0, hCT32167.2	206528_at, 217287_s_at	NP_004612.2, EAW67004.1, EAW67003.1, EAW67005.1
GeneID:10413	YAP1	11	101,981,192	102,104,154	122,962	+	1	2_A375_pNL97_plus_lncRNA::1::1776	-72	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene YAP1	YKI, YAP2, YAP1, YAP65, YAP	Yes-associated protein 1	NM_001130145, NM_006106, NM_001195044, NM_001195045, hCT1957216.1, hCT2354472.0, hCT2354473.0, hCT2354474.0, hCT32749.2	213342_at, 224894_at, 224895_at	NP_001123617.1, NP_006097.2, NP_001181973.1, NP_001181974.1, EAW67012.1, EAW67013.1, EAW67011.1, EAW67014.1, EAW67015.1
GeneID:330	BIRC3	11	102,188,194	102,208,465	20,271	+	1	2_A375_pNL97_plus_lncRNA::1::1777	29790	downstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene BIRC3	CIAP2, HIAP1, AIP1, RNF49, c-IAP2, API2, HAIP1, BIRC3, MIHC, MALT2	baculoviral IAP repeat containing 3	NM_001165, NM_182962, hCT32748.3	210538_s_at	NP_001156.1, NP_892007.1, EAW67017.1
GeneID:329	BIRC2	11	102,217,966	102,249,401	31,435	+	1	2_A375_pNL97_plus_lncRNA::1::1777	18	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene BIRC2	Hiap-2, cIAP1, RNF48, API1, BIRC2, HIAP2, c-IAP1, MIHB	baculoviral IAP repeat containing 2	NM_001166, hCT2334468.0	202076_at	NP_001157.1, EAW67018.1
GeneID:114908	TMEM123	11	102,267,056	102,323,775	56,719	-	2	1_A375_pNL7_minus_lncRNA::1::1267, 2_A375_pNL97_plus_lncRNA::1::1778	363, 447	in gene, in gene	1	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TMEM123	KCT3, PORMIN, PORIMIN, TMEM123	transmembrane protein 123	NM_052932, hCT2335287.0, hCT2354475.0, hCT32750.2	211967_at	NP_443164.2, EAW67019.1, EAW67020.1, EAW67021.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervening Features	Intervening Count	Intervening Info	Intervening Pos.	[A]	[R]	[C]	[D]	Acc Reg Count	Peak Sample	Peak Value	UCSC Link	Attributes	Full Description	RNA	Ally Tag	PROT
Gene:ENSG00000227869	LOC727698	11	102,323,650	102,332,769	9,119	+	2	1_A270_shL7_dhrus_lncRNA:1-1307, 2_A270_shL97_dhs_lncRNA:1-1278	1305, -322	upstream, upstream	1	1	16	16	1	2_A270_shL97_dhs_lncRNA:1	16	Gene: LOC727698	hypothetical LOC727698	XR_111211, XR_110918, XR_114518	226241_at	
Gene:ENSG00000213	MMP20	11	102,447,996	102,499,863	51,867	-	1	1_A270_shL7_dhrus_lncRNA:1-1305	12191	st gene	1	0	16	8	1	1_A270_shL7_dhrus_lnc RNA:1	16	Gene: MMP20	AGA2, MMP20, MMP-20	matrix metallopeptidase 20	NM_004771, XM_017027481.2	207599_at	NP_004762.2, EAW67638.1
Gene:ENSG00000260776	LOC10022 56077	11	102,654,907	102,707,287	53,380	+	1	1_A270_shL7_dhrus_lncRNA:1-1269	56897	downstream	1	0	16	8	1	1_A270_shL7_dhrus_lnc RNA:1	16	Gene: LOC100225577	hypothetical LOC100225077	XR_111210, XR_110916, XR_114520			
Gene:ENSG00000314	MMP3	11	102,706,535	102,714,342	7,814	-	1	1_A270_shL7_dhrus_lncRNA:1-1269	56	st gene	1	0	16	8	1	1_A270_shL7_dhrus_lnc RNA:1	16	Gene: MMP3	MGC126100, MGC126102, MGC126103, SL-1, CHS5b, STMY1, STR1, MMP-3, stromelysin-1	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	NM_002422, XR_001727464.3	205828_at	NP_002413.1, EAW67632.1
Gene:ENSG00009658	DYNC2H1	11	102,980,160	103,330,091	370,431	+	1	1_A270_shL7_dhrus_lncRNA:1-1279	8	st gene	0	1	13	17	1	2_A270_shL97_dhs_lncRNA:1	17	Gene: DYNC2H1	DHC1B2, DHC1B, KIAA0553, DHC2, DHC2, DHC8, bithci1, DYNC2HH, DYHI B	dynein, cytoplasmic 2, heavy chain 1	NM_001080463, NM_003777	1561939_at, 1560148_at, 242699_at	NP_001073932.1, NP_001065.2
Gene:ENSG00000693	GRIA4	11	103,480,800	103,653,819	372,019	+	3	1_A270_shL7_dhrus_lncRNA:1-1271, 2_A270_shL97_dhs_lncRNA:1-1702, 2_A270_shL97_dhs_lncRNA:1-1705	63200, 63200, 159304	st gene, st gene, st gene	1	1	16	19.3	2	2_A270_shL97_dhs_lncRNA:1	25	Gene: GRIA4	GRIA4, GluA4, GLUR4C, GLUR3, GLUR4	glutamate receptor, ionotropic, AMPA 4	NM_000777244, NM_000828, NM_001077243, NM_001112812, NCT23478767.0, NCT23479867.0, NCT23479867.0	1569178_at, 206864_at, 206863_s_at	NP_001707121.1, NP_000820.3, NP_001707121.2, NP_000106283.1, EAW67667.1, EAW67666.1, EAW67666.1, EAW67666.1
Gene:ENSG00004437	KIAA1626	11	103,576,629	103,592,854	16,225	-	1	1_A270_shL7_dhrus_lncRNA:1-1704	106	st gene	0	1	14	15	1	2_A270_shL97_dhs_lncRNA:1	15	Gene: KIAA1626	KIAA1626		NM_032424, NCT23173962	223792_at, 223816_at	NP_115930.1, EAW67671.1
Gene:ENSG00000277	GUCY1A2	11	106,557,916	106,589,171	231,261	-	2	1_A270_shL7_dhrus_lncRNA:1-1272, 2_A270_shL97_dhs_lncRNA:1-1699	-781, -813	upstream, upstream	1	1	22	44	1	2_A270_shL97_dhs_lncRNA:1	44	Gene: GUCY1A2	GUCY1A2, GC-SA2, GUCY1A2	guanylate cyclase 1, soluble, alpha 2	NM_000855, NCT23173673	206527_s_at	NP_0005845.1, EAW67681.1
Gene:ENSG00001651	ALX8H6	11	107,373,453	107,436,461	63,008	-	2	1_A270_shL7_dhrus_lncRNA:1-1272, 2_A270_shL97_dhs_lncRNA:1-1696	2701, 330	st gene, st gene	1	1	16.5	12.5	2	1_A270_shL97_dhs_lnc RNA:1	20	Gene: ALX8H6	FLJ38204, ABH8, MGC10255, ALX8H6	alkB, alkylation repair homolog 6 (E. coli)	NM_138779, NCT23548525.1, NCT23544140, NCT23560.4	235610_at, 235713_at	NP_620130.2, EAW67666.1, EAW67659.1, EAW67690.1
Gene:ENSG00000466	SLN	11	107,570,101	107,582,707	6,606	-	1	2_A270_shL97_dhs_lncRNA:1-1697	12451	downstream	0	1	12	16	1	2_A270_shL97_dhs_lncRNA:1	16	Gene: SLN	SLN, MGC12301, MGC126555, MGC126554	sarcolipin	NM_003063, NCT23562.1	203374_at	NP_003054.1, EAW67694.1
Gene:ENSG00004732	RAB39	11	107,799,277	107,834,208	34,931	+	1	2_A270_shL97_dhs_lncRNA:1-1706	118	st gene	0	1	8	14	1	2_A270_shL97_dhs_lncRNA:1	14	Gene: RAB39	RAB39		NM_015716, NCT21640102.2	1554000_at	NP_056995.1, EAW67100.1
Gene:ENSG00005631	NPAT	11	108,026,117	108,093,263	93,240	-	1	2_A270_shL97_dhs_lncRNA:1-1709	491	upstream	0	1	9	15	1	2_A270_shL97_dhs_lncRNA:1	15	Gene: NPAT	p220, NPAT, E14/NPAT, E14	nuclear protein, ataxia-telangiectasia locus	NM_002519, NCT23548690.0, NCT30350.3	203798_at, 211564_s_at, 211565_at	NP_0025102, EAW67107.1, EAW67106.1
Gene:ENSG00007212	ATM	11	108,093,559	108,239,826	146,267	+	1	2_A270_shL97_dhs_lncRNA:1-1708	287	st gene	0	1	9	15	1	2_A270_shL97_dhs_lncRNA:1	15	Gene: ATM	ATM, TELO1, DKFZp761A0313, AT1, ATDC, ATE, TEL1, ATC, ATD, ATA, MGC74674	ataxia telangiectasia mutated	NM_000051, NCT23548596.1, NCT23548558.1, NCT23548559.1, NCT23548593.1, NCT23548591.1, NCT23548787.0, NCT23548668.0, NCT23548.3	1554537_at, 1554631_at, 1570352_at, 208666_s_at, 208322_at	NP_0000437.3, EAW67111.1, EAW67108.1, EAW67109.1, EAW67109.1, EAW67112.1, EAW67113.1, EAW67114.1, EAW67115.1
Gene:ENSG00004427	LOC5442 77	11	111,299,223	111,327,330	28,107	-	1	1_A270_shL7_dhrus_lncRNA:1-1274	18217	st gene	1	0	17	0	1	2_A270_shL97_dhs_lnc RNA:1	17	Gene: LOC644277	hypothetical LOC644277	XR_110541, XR_114507			
Gene:ENSG00004795	ALG9	11	111,652,918	111,742,305	89,388	-	2	1_A270_shL7_dhrus_lncRNA:1-1279, 2_A270_shL97_dhs_lncRNA:1-1702	-7553, 7199	upstream, upstream	1	1	16	15	1	2_A270_shL97_dhs_lnc RNA:1	16	Gene: ALG9	DIBD1, DKFZp586H0320, FLJ21585, CDG1L, LCH1/CRI1, ALG9	dolichyl-phosphate (glucosyltransferase) 9, alpha-1,2 glucosyltransferase homolog (S. cerevisiae)	NM_024740, NM_001077900, NM_001077902, NCT23286260.0, NCT23286270.0, NCT23286290.0, NCT23286300.0, NCT23544110.0, NCT23544312.0	219274_s_at, 226817_at	NP_0789116.2, NP_001071151.1, NP_001071150.1, NP_079116.2, EAW67152.1, EAW67156.1, EAW67153.1, EAW67154.1, EAW67155.1, EAW67157.1, EAW67158.1
Gene:ENSG00001692	FDXACB1	11	111,744,760	111,750,153	5,373	-	2	1_A270_shL7_dhrus_lncRNA:1-1276, 2_A270_shL97_dhs_lncRNA:1-1702	265, 649	st gene, st gene	1	1	16	15	1	1_A270_shL7_dhrus_lnc RNA:1	16	Gene: FDXACB1	FDXACB1		NM_138378	229669_at	NP_612367.1
Gene:ENSG00004776	C11orf1	11	111,749,946	111,754,795	4,850	+	2	1_A270_shL7_dhrus_lncRNA:1-1276, 2_A270_shL97_dhs_lncRNA:1-1702	-460, -946	upstream, upstream	1	1	16	15	1	2_A270_shL97_dhs_lnc RNA:1	16	Gene: C11orf1	FLJ23499, C11orf1	chromosome 11 open reading frame 1	NM_022761, NCT23072.2	219225_s_at, 227765_s_at, 231530_s_at, 1511558_at	NP_0729561, EAW67160.1
Gene:ENSG00004554	NCAM1	11	112,531,925	112,149,156	317,165	+	1	2_A270_shL97_dhs_lncRNA:1-1704	27	st gene	0	1	8	16	1	2_A270_shL97_dhs_lncRNA:1	16	Gene: NCAM1	NCAM1, NCAM, MSK39, CD56	neural cell adhesion molecule 1	NM_000615, NM_001076682, NM_181351, NCT23548648.1, NCT23548545.1, NCT23548496.1, NCT23548497.1, NCT23548498.1, NCT23548500.0, NCT23548470.0, NCT23548771.0	1552699_at, 209566_s_at, 212643_at, 214652_at, 207309_s_at, 221586_at, 229799_s_at, 1510322_at	NP_0006062, NP_001070150.1, NP_551008.2, EAW67201.1, EAW67202.1, EAW67201.1, EAW67202.1, EAW67204.1, EAW67205.1, EAW67209.1, EAW67208.1
Gene:ENSG00004970	TTC12	11	113,165,231	113,237,114	51,883	+	1	2_A270_shL97_dhs_lncRNA:1-1708	681	st gene	0	1	11	21	1	2_A270_shL97_dhs_lncRNA:1	21	Gene: TTC12	TTC12, FLJ20535, FLJ13859, TPARM	tetratricopeptide repeat domain 12	NM_017868, NCT23490032.0, NCT23490033.0, NCT23490034.0, NCT23546427.0, NCT23546426.0	1554531_at, 215568_at, 216567_at, 1554521_s_at	NP_0603350, EAW67214.1, EAW67210.1, EAW67211.1, EAW67212.1, EAW67212.1
Gene:ENSG00005513	DRD2	11	113,280,217	113,346,091	65,874	-	3	1_A270_shL7_dhrus_lncRNA:1-1276, 1_A270_shL7_dhrus_lncRNA:1-1279, 2_A270_shL97_dhs_lncRNA:1-1796, 2_A270_shL97_dhs_lncRNA:1-1797, 2_A270_shL97_dhs_lncRNA:1-1798	27073, 649, 28912, 26993, 649	st gene, st gene, st gene, st gene, st gene	1	1	33.33	27	3	2_A270_shL97_dhs_lnc RNA:1	74	Gene: DRD2	D2DR, DRD2, D2R	dopamine receptor D2	NM_000795, NM_016574, NCT19655442.2, NCT23548665.0, NCT23548667.0, NCT23548668.0, NCT23548991.0, NCT30845.3	206990_s_at, 211626_s_at, 216624_s_at, 216630_s_at	NP_000785.1, NP_057630.2, EAW67219.1, EAW67222.1, EAW67224.1, EAW67225.1, EAW67220.1, EAW67221.1, EAW67223.1
Gene:ENSG00004992	MIR4301	11	113,320,745	113,320,810	65	-	3	1_A270_shL7_dhrus_lncRNA:1-1276, 1_A270_shL7_dhrus_lncRNA:1-1279, 2_A270_shL97_dhs_lncRNA:1-1698	1662, 3722, 1802	downstream, downstream, downstream	1	1	20.5	16.5	2	1_A270_shL7_dhrus_lnc RNA:1	23	Gene: MIR4301	MIR4301	rhoxis RNA 4301	NR_036163		
Gene:ENSG00001651	ZW10	11	113,693,909	113,694,025	80,316	-	2	1_A270_shL7_dhrus_lncRNA:1-1280, 2_A270_shL97_dhs_lncRNA:1-1699	-1110, -71	upstream, upstream	1	1	22	29	1	1_A270_shL7_dhrus_lnc RNA:1	32	Gene: ZW10	ZW10, KNTC1AP, MGC148821, NDW10	ZW10, kinetochore associated, homolog (Drosophila)	NM_004724, NCT23564.2	204812_at	NP_0037151, EAW67229.1
Gene:ENSG00004467	CLDN25	11	113,850,516	113,851,207	692	-	2	1_A270_shL7_dhrus_lncRNA:1-1280, 2_A270_shL97_dhs_lncRNA:1-1699	-5974, -6622	upstream, upstream	1	1	22	29	1	1_A270_shL7_dhrus_lnc RNA:1	32	Gene: CLDN25	CLDN25		NM_001013589		NP_0010245591
Gene:ENSG00003398	HTR3A	11	113,949,797	113,991,035	15,238	-	2	1_A270_shL7_dhrus_lncRNA:1-1281, 2_A270_shL97_dhs_lncRNA:1-1692	16251, 16251	downstream, downstream	1	1	22	29	1	2_A270_shL97_dhs_lnc RNA:1	29	Gene: HTR3A	5HT3R, HTR3, 5-HT3R, HTR3A, 5-HT3A, 5-HT-3	5-hydroxytryptamine (serotonin) receptor 3A	NM_000869, NM_213621, NM_001161772, ECT19715136.1, ECT19715138.1, ECT23548672.0, ECT30852.2	216613_s_at, 217002_s_at	NP_0008691, NP_998786.2, NP_001155246.1, EAW67237.1, EAW67236.1, EAW67238.1, EAW67239.1, EAW67240.1
Gene:ENSG00005577	NNMT	11	114,166,535	114,183,238	16,703	+	1	2_A270_shL97_dhs_lncRNA:1-1692	479	upstream	0	1	9	14	1	2_A270_shL97_dhs_lncRNA:1	14	Gene: NNMT	NNMT	Acetylserotonin N-methyltransferase	NM_006169, NCT23349172, NCT30965.2	202237_at, 202235_s_at, 221839_at	NP_0061601, EAW67243.1, EAW67242.1
Gene:ENSG00009684	LOC1005 96841	11	114,167,095	114,168,062	1,767	-	1	2_A270_shL97_dhs_lncRNA:1-1693	2006	downstream	0	1	9	14	1	2_A270_shL97_dhs_lnc RNA:1	14	Gene: LOC100309684	hypothetical LOC100309841	XR_111222, XR_110521, XR_114526			
Gene:ENSG00004866	C11orf11	11	114,262,170	114,271,139	8,969	-	1	2_A270_shL97_dhs_lncRNA:1-1696	2	st gene	0	1	14	21	1	2_A270_shL97_dhs_lnc RNA:1	21	Gene: C11orf11	FLJ30110, C11orf11	chromosome 11 open reading frame 11	NM_019021, NCT23548693.0	219799_s_at, 1557284_at	NP_0610442, EAW67249.1
Gene:ENSG00004178	RBM7	11	114,271,354	114,279,633	8,291	+	1	2_A270_shL97_dhs_lncRNA:1-1696	-246	upstream	0	1	14	21	1	2_A270_shL97_dhs_lnc RNA:1	21	Gene: RBM7	RBM7, PCJ11153	RNA binding motif protein 7	NM_016090, NCT23548163.0, NCT23561804, NCT23548703.0	1555279_at, 1555284_at	NP_0161541, EAW67247.1, EAW67246.1, EAW67244.1
Gene:ENSG00004996	KEX02	11	114,310,105	114,321,001	10,893	+	2	2_A270_shL97_dhs_lncRNA:1-1692, 2_A270_shL97_dhs_lncRNA:1-1699	100, 39	st gene, st gene	1	1	22	32	1	2_A270_shL97_dhs_lnc RNA:1	32	Gene: KEX02	SPN, KEX02, RPH, DKFZp666E144, KEX2, CGI-114, MGC111850	KEX2, RNA convertase-like 2 homolog (S. cerevisiae)	NM_015923, NCT23548793.0, NCT30283.2	218164_at, 223993_s_at, 239616_at	NP_0569382, EAW67249.1, EAW67250.1
Gene:ENSG00003703	CADM1	11	113,044,345	113,378,241	330,896	+	9	1_A270_shL7_dhrus_lncRNA:1-1283, 1_A270_shL7_dhrus_lncRNA:1-1284, 1_A270_shL7_dhrus_lncRNA:1-1285, 2_A270_shL97_dhs_lncRNA:1-1697, 2_A270_shL97_dhs_lncRNA:1-1698, 2_A270_shL97_dhs_lncRNA:1-1699	281961, 3865, 116, 203257, 1055, 295	st gene, st gene, st gene, st gene, st gene, st gene	1	1	13	13.2	5	1_A270_shL7_dhrus_lnc RNA:1	30	Gene: CADM1	MGC131550, sTSLC1, Necl-2, IgSF3/P, RA175, ST17, CADM1, IGSF4A, DKFZp686F1769, NECL2, MGC149763, SYNCAM, cpiCAM1, IGSF4, TSLC1, SL2	cell adhesion molecule 1	NM_014333, NM_001098617, NCT23562362.0, NCT23562364.0, NCT23563850.0, NCT23564366.0, NCT23562.2	208030_s_at, 208031_at, 208032_s_at, 227951_at, 240348_at	NP_0553482, NP_001091607.1, EAW67236.1, EAW67237.1, EAW67238.1, EAW67250.1, EAW67239.1
Gene:ENSG00003387	SIK3	11	116,714,118	116,966,893	254,875	-	2	1_A270_shL7_dhrus_lncRNA:1-1289, 1_A270_shL7_dhrus_lncRNA:1-1290	71201, 39441	st gene, st gene	1	0	16.5	11.5	2	1_A270_shL7_dhrus_lnc RNA:1	21	Gene: SIK3	FLJ12240, LI9, KIAA0999, SIK3, QSK	SIK family kinase 3	NM_025164, NCT23537.0, NCT23563.3	1554929_at, 1563433_at, 206155_s_at, 206156_at, 206157_s_at, 1553548_at	NP_0789402, EAW67276.1, EAW67276.1
Gene:ENSG00003492	RAFAH1B2	11	117,015,000	117,047,610	32,610	+	2	1_A270_shL7_dhrus_lncRNA:1-1281, 2_A270_shL97_dhs_lncRNA:1-1612	12072, 34580	downstream, downstream	1	1	9.1	19	1	2_A270_shL97_dhs_lnc RNA:1	19	Gene: RAFAH1B2	RAFAH1B2		NM_001167745, NM_001164747, NM_001164746, NM_002572, NCT19965306.1, NCT30121.2	1569631_at, 203160_at, 224777_s_at	NP_0011716751, NP_0011716761, NP_0025631, NP_0011716771, EAW67281.1, EAW67282.1
Gene:ENSG00001092	SIDT2	11	117,049,939	117,066,161	16,222	+	2	1_A270_shL7_dhrus_lncRNA:1-1281, 2_A270_shL97_dhs_lncRNA:1-1612	-467, -480	upstream, upstream	1	1	9.1	19	1	2_A270_shL97_dhs_lnc RNA:1	19	Gene: SIDT2	FLJ90656, CGI-60, DKFZp686L17232, SIDT2	SID1 transmembrane family, member 2	NM_001040455, NCT23548681.1, NCT23548682.0, NCT23548683.0, NCT23548518.0, NCT23548519.0, NCT23548520.0, NCT23548521.0, NCT23548522.0, NCT23548523.0, NCT23548524.0, NCT23548525.0, NCT23548526.0, NCT23548527.0, NCT23548528.0	218765_at, 36256_at	NP_0010355451, EAW67284.1, EAW67283.1, EAW67284.1, EAW67285.1, EAW67286.1, EAW67287.1, EAW67288.1, EAW67289.1, EAW67290.1, EAW67292.1, EAW67293.1, EAW67295.1, EAW67295.1
Gene:ENSG00001598	PCSK7	11	117,075,788	117,102,811	27,023	-	2	1_A270_shL7_dhrus_lncRNA:1-1282, 2_A270_shL97_dhs_lncRNA:1-1693	-337, -357	upstream, upstream	1	1	9.1	19	1	2_A270_shL97_dhs_lnc RNA:1	19	Gene: PCSK7	SPC7, LPC, PC8, FLJ31900, PCSK7, FLJ45329, PC7	proprotein convertase subtilisin/kexin type 7	NM_004716, NCT23337160, NCT23337161, NCT23337162, NCT23337163	203116_at, 232521_at	NP_0047072, EAW67303.1, EAW67303.1, EAW67303.1, EAW67305.1
Gene:ENSG00005716	RNF214	11	117,103,864	117,196,464	93,000	+	2	1_A270_shL7_dhrus_lncRNA:1-1282, 2_A270_shL97_dhs_lncRNA:1-1693	-236, -256	upstream, upstream	1	1	9.1	19	1	2_A270_shL97_dhs_lnc RNA:1	19	Gene: RNF214	DKFZp547C193, RNF214	ring finger protein 214	NM_207343, NM_001077236, NCT23563445.0, NCT23564.2	227116_at	NP_9972362, NP_001070707.1, EAW67306.1, EAW67307.1
Gene:ENSG00003621	BACE1	11	117,196,614	117,199,272	30,658	-	2	1_A270_shL7_dhrus_lncRNA:1-1282, 2_A270_shL97_dhs_lncRNA:1-1614	-47, -100	upstream, upstream	1	1	9.1	21	1	2_A270_shL97_dhs_lnc RNA:1	21	Gene: BACE1	BACE1, HSPC168, ASP2, BACE, FLJ90566, KIAA1149	beta-site APP-cleaving enzyme 1	NM_012104, NM_138971, NM_138972, NM_138973, NCT19655595.1, NCT23370100, NCT23370111.0, NCT23370112.0, NCT23370113.0, NCT23564433.0, NCT23564436.0, NCT23564437.0, NCT23564.2	217604_s_at, 222462_s_at, 224462_s_at, 224463_s_at, 224333_s_at	NP_0362361, NP_620427.1, NP_620426.1, NP_620428.1, EAW67312.1, EAW67312.1, EAW67309.1, EAW67309.1, EAW67310.1, EAW67311.1, EAW67314.1, EAW67315.1, EAW67316.1, EAW67317.1
Gene:ENSG00001717	CEP164	11	117,195,971	117,263,862	68,411	+	1	2_A270_shL97_dhs_lncRNA:1-1615	277	st gene	0	1	10	16	1	2_A270_shL97_dhs_lnc RNA:1	16	Gene: CEP164	KIAA1052, FLJ45767, CEP164	centrosomal protein 164kDa	NM_014956, NCT19693917.1, NCT23564150, NCT23564151, NCT23564152	1555893_s_at, 1564290_s_at, 245231_s_at	NP_0149781, EAW67321.1, EAW67318.1, EAW67319.1, EAW67320.1
Gene:ENSG00001292	LOC1001 26201	11	117,206,917	117,207,247	330	-	1	2_A270_shL97_dhs_lncRNA:1-1615	5899	downstream	0	1	10	16	1	2_A270_shL97_dhs_lnc RNA:1	16	Gene: LOC100126201	hypothetical protein LOC100126201	XM_001732843, XM_002116861, XM_003120765.1			NP_9031135951, NP_9031165261, NP_9031205651.1
Gene:ENSG00007453	DSCAML1	11	117,295,659	117,667,976	369,667	+	2	1_A270_shL7_dhrus_lncRNA:1-1284, 2_A270_shL97_dhs_lncRNA:1-1697	169276, 169944	st gene, st gene	1	1	17	16	1	1_A270_shL7_dhrus_lnc RNA:1	17	Gene: DSCAML1	DSCAML1, KIAA1152	Down syndrome cell adhesion molecule like 1	NM_020693, NCT19909331.0, NCT23544560.0	232059_at, 234903_s_at	NP_0037454.2, EAW67323.1, EAW67322.1
Gene:ENSG00001116	CD3E	11	118,176,295	118,189,890	11,595	+	1	2_A270_shL97_dhs_lncRNA:1-1617	12223	downstream	0	1	16	19	1	2_A270_shL97_dhs_lnc RNA:1	19	Gene: CD3E	CD3E, TCRE, T3E, FLJ19663	CD3e molecule, epsilon (CD3-TCR complex)	NM_000733, NCT19634161.1, NCT19634171.1, NCT19634181.1, NCT23172.2	205456_at	NP_0007241, EAW67361.1, EAW67360.1, EAW67362.1, EAW67363.1, EAW67364.1
Gene:ENSG00001177	CD3G	11	118,215,039	118,224,897	9,838	+	1	2_A270_shL97_dhs_lncRNA:1-1618	1517	downstream	0	1	11	20	1	2_A270_shL97_dhs_lnc RNA:1	20	Gene: CD3G	MGC126597, CD3-GAMMA, CD3G, FLJ18762, T3G, FLJ17664, FLJ40612, FLJ75364	CD3g molecule, gamma (CD3-TCR complex)	NM_000073, NCT19670307.3	206804_at	NP_0000651, EAW67368.1
Gene:ENSG00003543	UBE4A	11	118,230,302	118,269,926	39,624	+	3	1_A270_shL7_dhrus_lncRNA:1-1283, 1_A270_shL7_dhrus_lncRNA:1-1618, 2_A270_shL97_dhs_lncRNA:1-1629	61954, 126, 42082	downstream, upstream, downstream	1	1	14	22	2	2_A270_shL97_dhs_lnc RNA:1	22	Gene: UBE4A	UFD2, E4, UBOX2, UBE4A, MGC132315, KIAA0126	ubiquitination factor E4A (UFD2 homolog, yeast)	NM_004788	202035_at	NP_0047791.2
Gene:ENSG00003754	ATP8IL	11	118,272,104	118,293,562	8,496	+	2	1_A270_shL7_dhrus_lncRNA:1-1283, 2_A270_shL97_dhs_lncRNA:1-1612	182, 269	st gene, st gene	1	1	17	16	1	1_A270_shL7_dhrus_lnc RNA:1	17	Gene: ATP8IL	ATP8IL2, ATP9L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	NM_006476, NP_0132759	207572_s_at, 208748_at, 208749_s_at, 240553_s_at	NP_0396974
Gene:ENSG00004796	MGC13033 3	11	118,303,656	118,309,821	7,066	-	3	1_A270_shL7_dhrus_lncRNA:1-1286, 2_A270_shL97_dhs_lncRNA:1-1630, 2_A270_shL97_dhs_lncRNA:1-1631	1119, 383, 1071	upstream, st gene, upstream	1	1	22	24.5	2	1_A270_shL7_dhrus_lnc RNA:1	32	Gene: MGC13033	hypothetical MGC13033	XR_111217, XR_110526, XR_114531	211773_s_at	
Gene:ENSG00000297	MLL	11	118,307,203	118,393,836	86,721	+	3	1_A270_shL7_dhrus_lncRNA:1-1286, 2_A270_shL97_dhs_lncRNA:1-1630, 2_A270_shL97_dhs_lncRNA:1-1631	-165, 1669, -213	upstream, upstream, upstream	1	1	22	24.5	2	1_A270_shL7_dhrus_lnc RNA:1	32	Gene: MLL	FLJ11783, CXXC7, KMT2A, MLLIGA937, HTRX1, MLL, TRX1, TET1-MLL, ALL-1, MLL1A, HRX	ytwisty(trithorax) or mixed-lineage leukemia (trithorax homolog, Drosophila)	NM_005933, NCT19362NT.2, NCT19362062.2, NCT23357611.1, NCT23357643, NCT30555.4	1555536_s_at, 1563439_s_at, 212076_at, 212076_s_at, 212079_s_at, 212080_at, 216624_s_at, 236991_at, 244100_at	NP_0059332, EAW67383.1, EAW67380.1, EAW67381.1, EAW67382.1, EAW67384.1
Gene:ENSG00001272	ARCN1	11	118,443,102	118,473,748	30,646	+	2	1_A270_shL7_dhrus_lncRNA:1-1287, 2_A270_shL97_dhs_lncRNA:1-1622	36194, 36389	downstream, downstream	1	1	28	17	1	2_A270_shL97_dhs_lnc RNA:1	26	Gene: ARCN1	ARCN1, COPD	archain 1	NM_001655, NM_001142281, NCT23357722.0, NCT23544112.0, NCT30.2	201196_s_at	NP_0016462, NP_001135753.1, EAW67397.1, EAW67398.1, EAW67399.1
Gene:ENSG00001687	PHLDB1	11	118,877,213	118,936,741	51,528	+	2	1_A270_shL7_dhrus_lncRNA:1-1287, 2_A270_shL97_dhs_lncRNA:1-1622	2083, 2213	st gene, st gene	1	1	28	17	1	2_A270_shL97_dhs_lnc RNA:1	26	Gene: PHLDB1	MGC111531, FLJ90181, DKFZp686H029, DKFZp686O22410, LL5A, FLJ90266, PHLDB1, KIAA0630	pleckstrin homology-like domain, family B, member 1	NM_015157, NM_001142458, NM_001164759, ECT19930291.1, ECT23357753.0, ECT23544161.0, ECT23544162.0, ECT23544163.0, ECT23544164.0, ECT23544165.0, ECT30.2	212138_at, 218019_s_at, 218102_at	NP_0551572, NP_001128230.1, NP_001135231.1, EAW67401.1, EAW67406.1, EAW67407.1, EAW67408.1, EAW67402.1, EAW67403.1, EAW67404.1, EAW67405.1
Gene:ENSG00005556	DDX6	11	118,616,872	118,661,972	43,550	+	1	2_A270_shL97_dhs_lncRNA:1-1623	-160	upstream	0	1	10	16	1	2_A270_shL97_dhs_lnc RNA:1	16	Gene: DDX6	RLR2, RCK, P54, FLJ36338, DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	NM_004397, NCT23359870.0, NCT23666.2	204809_at	NP_0043382, EAW67413.1, EAW67412.1
Gene:ENSG00005148	BCL9L	11	118,766,549	118,781,813	15,264	-	1	2_A270_shL97_dhs_lncRNA:1-1628	4075	upstream	0	1	19	22	1	2_A270_shL97_dhs_lnc RNA:1	22	Gene: BCL9L	BLNB11, BCL9L, BCL9-2	B-cell CLL/lymphoma 9-like	NM_182557	227616_at, 1555565_at	NP_872353.1
Gene:ENSG00005637	CCDC64	11	118,868,552	118,886,455	17,903	+	1	2_A270_shL97_dhs_lncRNA:1-1629	-372	upstream	0	1	14	17	1	2_A270_shL97_dhs_lnc RNA:1	17	Gene: CCDC64	CCDC64, DUNB16	coiled-coil domain containing 64	NM_194569, NCT23356961.0, NCT23560210.0, NCT23560402.0	227205_at	NP_9409411, EAW67428.1, EAW67427.1, EAW67429.1
Gene:ENSG00005523	VPS11	11	118,935,491	118,953,665	18,185	+	2	1_A270_shL7_dhrus_lncRNA:1-1302, 2_A270_shL97_dhs_lncRNA:1-1625	17099, 38	downstream, st gene	1	1	17	20	2	2_A270_shL97_dhs_lnc RNA:1	22	Gene: VPS11	END1, RVPS11, VPS11, RNP108, PEP3	vacuolar protein sorting 11 homolog (S. cerevisiae)	NM_021729, NCT23357700.0, NCT23357701.0, NCT30550.4	201292_s_at	NP_0662732, EAW67446.1, EAW67445.1, EAW67446.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervals Count	Intervals	Intervals Dists to Start	Intervals Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:3148	HMBS	11	118,955,557	118,964,299	8,872	+	5	1_A275_sNL37_dhrus_loKRNA:1:1302, 1_A275_sNL37_dhrus_loKRNA:1:1303, 1_A275_sNL37_dhrus_loKRNA:1:1304, 2_A275_sNL37_glus_loKRNA:1:1626, 2_A275_sNL37_glus_loKRNA:1:1627	535, 10523, 17149, 10297, 17055	upstream, downstream, downstream, downstream, downstream	1	1	21	21.67	3	1_A275_sNL7_dhrus_loKRNA:1	26	Gene: HMBS	PBGD, PBGD, HMBS, PORC, UPS	Hydroxymethylbilane synthase	NM_000190, NM_001024382, NCT19809277.1, NCT23544000.0, NCT23546092.0, NCT30698.2	202640_s_at	NP_000181.2, NP_001018553.1, EAW67447.1, EAW67446.1, EAW67446.1, EAW67450.1
Gene:ID:3014	HDAFX	11	118,964,554	118,999,177	1,992	-	5	1_A275_sNL7_dhrus_loKRNA:1:1302, 1_A275_sNL7_dhrus_loKRNA:1:1303, 1_A275_sNL7_dhrus_loKRNA:1:1304, 2_A275_sNL37_glus_loKRNA:1:1626, 2_A275_sNL37_glus_loKRNA:1:1627	10623, 68, 9559, 192, 6293	downstream, st gene, upstream, st gene, upstream	1	1	21	21.67	3	1_A275_sNL7_dhrus_loKRNA:1	26	Gene: HDAFX	HDAX, HZAX, HZA.X, HDAFX	HZA histone family, member X	NM_002105, NCT20547.2	203436_s_at, 212524_s_at, 212525_s_at, 212344_s_at	NP_002096.1, EAW67491.1
Gene:ID:7925	DPAGT1	11	118,967,213	118,972,765	5,572	-	4	1_A275_sNL7_dhrus_loKRNA:1:1302, 1_A275_sNL7_dhrus_loKRNA:1:1304, 2_A275_sNL37_glus_loKRNA:1:1626, 2_A275_sNL37_glus_loKRNA:1:1627	8673, 49, 6501, 113	downstream, st gene, downstream, st gene	1	1	22.5	23.5	2	1_A275_sNL7_dhrus_loKRNA:1	26	Gene: DPAGT1	UGAT, ALG7, DPAGT2, DGPT, G115366, DPAGT1, CDG-I, CDG1I, DPAGT, GPT, GPT, UAGT	diacylglycerophosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (dolichol-P-N-acetylsu	NM_001382, NCT16909231.1, NCT19856503.1, NCT23539920.0, NCT30946.2	208509_s_at	NP_001372.2, EAW67488.1, EAW67482.1, EAW67483.1, EAW67484.1
Gene:ID:8540	C2CD2L	11	118,976,093	118,987,827	8,734	+	2	1_A275_sNL37_glus_loKRNA:1:1304, 2_A275_sNL37_glus_loKRNA:1:1626	4337, -1821	upstream, upstream	1	1	18	20	1	2_A275_sNL37_glus_loKRNA:1	25	Gene: C2CD2L	DKFZp686B1233, KIAA0286, TMEM24, C2CD2L	C2CD2-like	NM_014937, NCT16909815.1, NCT16909816.1, NCT23539660.0, NCT23566630	204737_s_at, 230758_s_at	NP_055622.3, EAW67497.1, EAW67496.1, EAW67498.1, EAW67498.1
Gene:ID:8507	CBL	11	119,076,990	119,178,859	101,869	+	2	1_A275_sNL37_glus_loKRNA:1:1303, 1_A275_sNL37_glus_loKRNA:1:1631	12386, 12002	st gene, st gene	1	1	18	17	1	2_A275_sNL37_glus_loKRNA:1	17	Gene: CBL	RNF55, C-CBL, CBL2, CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	NM_005188, NCT16270.2	206077_at, 235231_at, 235234_at, 236010_at, 240479_at	NP_005179.2, EAW67479.1, EAW67476.1
Gene:ID:4162	MCAM	11	119,179,234	119,187,840	8,606	-	1	1_A275_sNL7_dhrus_loKRNA:1:1306	-4182	upstream	1	0	17	16	1	1_A275_sNL7_dhrus_loKRNA:1	17	Gene: MCAM	CD146, MCAM, MUC18	melanoma cell adhesion molecule	NM_006500, NCT23539930.0, NCT6231.2	202735_s_at, 209099_x_at, 209097_s_at, 209098_s_at, 211062_x_at, 211063_s_at	NP_006491.2, EAW67476.1, EAW67477.1
Gene:ID:8182	RNF26	11	119,203,237	119,205,022	2,785	+	1	1_A275_sNL37_glus_loKRNA:1:1632	-161	upstream	0	1	18	17	1	2_A275_sNL37_glus_loKRNA:1	17	Gene: RNF26	MGC2642, RNF26	ring finger protein 26	NM_032015, NCT16466548.2	224335_s_at, 224337_at	NP_114604.1, EAW67479.1
Gene:ID:5332	MPRP	11	119,209,652	119,217,383	7,731	-	1	2_A275_sNL37_glus_loKRNA:1:1632	12327	downstream	0	1	18	17	1	2_A275_sNL37_glus_loKRNA:1	17	Gene: MPRP	MPRP, PSB, PLSB370, MGC31938, PIP5K3/MBP621, bMIP3, MCOPS	phosphoinositide-binding protein	NM_031433, NCT17669196.2	224286_at	NP_113621.1, EAW67483.1
Gene:ID:1486	C1QTNF5	11	119,209,652	119,217,383	7,731	+	1	2_A275_sNL37_glus_loKRNA:1:1632	12327	downstream	0	1	18	17	1	2_A275_sNL37_glus_loKRNA:1	17	Gene: C1QTNF5	FLJ33570, DKFZp686B0621, C1QTNF5, CTRP5, UCEP1	C1q and tumor necrosis factor related protein 5	NM_015645, NCT23539649.0, NCT6729.2	223489_at	NP_056460.1, EAW67482.1, EAW67481.1
Gene:ID:3948627	LOC1004 96227	11	119,257,455	119,399,844	117,456	+	2	1_A275_sNL37_glus_loKRNA:1:1307, 2_A275_sNL37_glus_loKRNA:1:1632	112120, 112055	st gene, st gene	1	1	51	60	1	2_A275_sNL37_glus_loKRNA:1	60	Gene: LOC100499227	hypothetical LOC100499227	hypothetical LOC100499227	NM_034160		
Gene:ID:818	PVRL1	11	119,506,606	119,599,433	90,827	-	1	2_A275_sNL37_glus_loKRNA:1:1638	-461	upstream	0	1	16	24	1	2_A275_sNL37_glus_loKRNA:1	24	Gene: PVRL1	CPC1, SK-12, PRR1, CD111, PRR, HVEC, PVRR, MGC148231, nectin-1, CLPED1, MGC16207, PVRL1, HSJP, PVRR1, EC6	poliovirus receptor-related 1 (herpesvirus entry mediator C)	NM_002855, NM_203266, NM_022555, NCT19825551.1, NCT19825561.1, NCT23539811.0, NCT23539811.0	205553_at, 211505_at, 211506_s_at, 211511_at	NP_976030.1, NP_976031.1, NP_002846.2, EAW67502.1, EAW67502.1, EAW67504.1
Gene:ID:3936707	LOC1005 05077	11	119,610,421	119,617,424	7,003	+	1	2_A275_sNL37_glus_loKRNA:1:1639	-10225	upstream	0	1	14	24	1	2_A275_sNL37_glus_loKRNA:1	24	Gene: LOC100507077	hypothetical LOC100507077	hypothetical LOC100507077	XR_110527		
Gene:ID:20323	OAP	11	120,051,747	120,100,690	16,963	+	3	1_A275_sNL37_glus_loKRNA:1:1310, 2_A275_sNL37_glus_loKRNA:1:1636, 2_A275_sNL37_glus_loKRNA:1:1638	1497, 429, 7266	upstream, st gene, st gene	1	1	22.5	19.5	2	1_A275_sNL7_dhrus_loKRNA:1	24	Gene: OAP	NESATF1/ZTF2, MGC62117, OAP	OAP homolog (Drosophila)	NM_178307, NCT23539930.1	1553999_at, 1553570_s_at	NP_848922.1, EAW67502.1
Gene:ID:5533	POU2F2	11	120,110,951	120,190,653	79,702	+	2	1_A275_sNL37_glus_loKRNA:1:1311, 2_A275_sNL37_glus_loKRNA:1:1640	65033, 65017	downstream, downstream	1	1	17	15	1	2_A275_sNL37_glus_loKRNA:1	15	Gene: POU2F2	MGC126698, Epoc-1, Ste-1a, FLJ40063, OCT11, POU2F2, PLA-4	POU class 2 homeobox 2	NM_014352, NCT16529911.1	207109_at, 215355_at	NP_035167.2, EAW67503.1
Gene:ID:19952	TMEM136	11	120,195,016	120,201,247	6,231	+	2	1_A275_sNL37_glus_loKRNA:1:1311, 2_A275_sNL37_glus_loKRNA:1:1640	-52, -65	upstream, upstream	1	1	17	15	1	2_A275_sNL37_glus_loKRNA:1	15	Gene: TMEM136	TMEM136, MGC17639	transmembrane protein 136	NM_174929, NCT23543923.0, NCT7235.2	1554076_s_at, 235166_at, 235497_at	NP_777556.1, EAW67505.1, EAW67506.1
Gene:ID:3369	ARHGEF12	11	120,227,946	120,360,648	132,699	+	1	1_A275_sNL37_glus_loKRNA:1:1312	93094	st gene	1	0	16	8	1	1_A275_sNL7_dhrus_loKRNA:1	16	Gene: ARHGEF12	LARG, ARHGEF12, PRO2762, KIAA0382, DKFZp686O0272	Rho guanine nucleotide exchange factor (GEF) 12	NM_015313, NCT23539838.0, NCT23560360.0, NCT9851.3	1555833_at, 1566093_at, 1570471_at, 201333_s_at, 201334_s_at, 201335_s_at, 210741_at, 231620_at, 233621_s_at, 234126_at, 234541_s_at, 234542_at, 234544_at	NP_056139.1, EAW67509.1, EAW67508.1, EAW67510.1
Gene:ID:19599	TBCEL	11	120,644,503	120,960,296	65,553	+	1	2_A275_sNL37_glus_loKRNA:1:1641	59765	st gene	0	1	16	20	1	2_A275_sNL37_glus_loKRNA:1	20	Gene: TBCEL	tt, TBCEL, LRRC55, FLJ14177, MGC10233	tubulin folding cofactor E-like	NM_152715, NM_001130047, NCT19825407.1, NCT23546434.0, NCT27277.2	211697_at	NP_689926.2, NP_001122519.1, EAW67512.1, EAW67514.1, EAW67515.1
Gene:ID:3930745	LOC1005 97145	11	121,936,635	122,293,979	356,841	+	4	1_A275_sNL37_glus_loKRNA:1:1313, 1_A275_sNL37_glus_loKRNA:1:1314, 2_A275_sNL37_glus_loKRNA:1:1642, 2_A275_sNL37_glus_loKRNA:1:1643	280971, 149098, 329035, 219643	st gene, st gene, st gene, st gene	1	1	19.25	14	4	1_A275_sNL7_dhrus_loKRNA:1	19	Gene: LOC100507145	hypothetical LOC100507145	hypothetical LOC100507145	XR_110529		
Gene:ID:89939	LOC3999 58	11	121,959,811	122,073,770	113,959	+	3	1_A275_sNL37_glus_loKRNA:1:1313, 2_A275_sNL37_glus_loKRNA:1:1642, 2_A275_sNL37_glus_loKRNA:1:1643	61162, 105226, 166	st gene, st gene, st gene	1	1	14	13	3	1_A275_sNL7_dhrus_loKRNA:1	17	Gene: LOC399959	MIR100HG, FLJ21653, FLJ10331, DKFZp686G0115, DKFZp686L04156, FLJ11480, FLJ34394	hypothetical LOC399959	NR_036430	225351_at, 238540_at, 241679_at	
Gene:ID:29311	MIR125B1	11	121,970,465	121,970,552	87	-	1	2_A275_sNL37_glus_loKRNA:1:1642	8005	downstream	0	1	11	16	1	2_A275_sNL37_glus_loKRNA:1	16	Gene: MIR125B1	MIRN125B1, MIR125B1	microRNA 125b-1	NR_029671		
Gene:ID:26554	MIRLET7A1	11	122,017,230	122,017,301	71	-	1	2_A275_sNL37_glus_loKRNA:1:1642	4693	downstream	1	0	17	8	1	2_A275_sNL37_glus_loKRNA:1	17	Gene: MIRLET7A1	MIRLET7A2, LET7A2, let-7a-2, MIRNLET7A2	microRNA let-7a-2	NR_029477		
Gene:ID:4998	UBASH3B	11	122,326,398	122,655,167	156,769	+	2	1_A275_sNL37_glus_loKRNA:1:1646, 2_A275_sNL37_glus_loKRNA:1:1646	664, 46366	st gene, st gene	0	1	12.5	17.5	2	2_A275_sNL37_glus_loKRNA:1	21	Gene: UBASH3B	MGC31437, STS1, KIAA1959, p70, UBASH3B, STS-1, TULA-2	ubiquitin associated and SH3 domain containing B	NM_032873, NCT10147.2	226353_x_at, 226359_at, 226362_at, 226507_at, 241267_at	NP_116262.2, EAW67531.1
Gene:ID:30258	IBSX	11	122,846,337	122,852,379	6,022	-	2	1_A275_sNL37_glus_loKRNA:1:1315, 1_A275_sNL37_glus_loKRNA:1:1647	-163, -329	upstream, upstream	1	1	28	30	1	2_A275_sNL37_glus_loKRNA:1	30	Gene: IBSX	IBSX, IBSX1	brain-specific homeobox	NM_001098169		NP_001091639.1
Gene:ID:8227	ADAM	11	122,943,030	123,066,007	122,887	-	1	2_A275_sNL37_glus_loKRNA:1:1316	6295	st gene	1	0	16	14	1	1_A275_sNL7_dhrus_loKRNA:1	16	Gene: ADAM	FLJ22415, CLM/F, ACAM, ADAM	CXADR-like membrane protein	NM_024769, NCT23539490.0, NCT23546429.0, NCT23546512.0	226552_at	NP_079045.1, EAW67540.1, EAW67544.1, EAW67545.1
Gene:ID:5500	SCN2B	11	123,998,595	123,329,315	25,420	-	2	1_A275_sNL37_glus_loKRNA:1:1317, 1_A275_sNL37_glus_loKRNA:1:1650	499, 451	st gene, st gene	1	1	20	27	1	1_A275_sNL7_dhrus_loKRNA:1	28	Gene: SCN2B	HBA2/3390, SCNB2, SCN2B	sodium channel, voltage-gated, type III, beta	NM_000100151, NM_019400, NCT23546602.0, NCT23547014.0, NCT31147.3	204722_at, 204723_at	NP_001332201.1, NP_066970.1, EAW67530.1, EAW67531.1, EAW67532.1
Gene:ID:7553	ZNF202	11	123,594,997	123,612,265	17,268	-	2	1_A275_sNL37_glus_loKRNA:1:1316, 2_A275_sNL37_glus_loKRNA:1:1650	27, -21	upstream, upstream	1	1	16	16	1	2_A275_sNL37_glus_loKRNA:1	16	Gene: ZNF202	ZNSCAN10, ZNF202	zinc finger protein 202	NM_003459, NCT01962186.2, NCT19821682.2	204227_s_at, 204228_s_at	NP_003449.2, EAW67553.1, EAW67554.1
Gene:ID:19255	PANX2	11	124,451,453	124,490,252	6,798	+	4	1_A275_sNL37_glus_loKRNA:1:1321, 1_A275_sNL37_glus_loKRNA:1:1322, 1_A275_sNL37_glus_loKRNA:1:1636, 2_A275_sNL37_glus_loKRNA:1:1651	4181, 11240, 8197, 11219	downstream, downstream, upstream, downstream	1	1	22	26	2	2_A275_sNL37_glus_loKRNA:1	34	Gene: PANX2	FKS2, PANX3	pannexin 3	NM_052899, NCT31056.1	240853_at	NP_443191.1, EAW67565.1
Gene:ID:4893	TBRG1	11	124,922,742	124,935,822	12,080	+	2	1_A275_sNL37_glus_loKRNA:1:1322, 2_A275_sNL37_glus_loKRNA:1:1651	-49, -70	upstream, upstream	1	1	16	16	1	2_A275_sNL37_glus_loKRNA:1	16	Gene: TBRG1	FLJ90112, FLJ23620, NRIM, MGC126690, TBRG1, TB-3, FLJ14621	transforming growth factor beta regulator 1	NM_032611, NR_016021, NCT23539466.0, NCT31651.3	226515_s_at, 226516_at, 226518_at, 235120_at, 235681_at, 241200_at	NP_116200.2, EAW67560.1, EAW67559.1
Gene:ID:9664	C11orf61	11	124,936,294	124,970,299	33,805	+	2	1_A275_sNL37_glus_loKRNA:1:1652, 2_A275_sNL37_glus_loKRNA:1:1652	835, 27	st gene, st gene	0	1	12.5	16.5	2	2_A275_sNL37_glus_loKRNA:1	17	Gene: C11orf61	C11orf61, FLJ23342	Chromosome 11 open reading frame 61	NM_024631, NCT23544468.0, NCT31699.2	221356_s_at	NP_078907.2, EAW67600.1, EAW67601.1
Gene:ID:3001042	LOC1005 03	11	124,939,136	124,939,865	629	-	1	1_A275_sNL37_glus_loKRNA:1:1652	-8699	upstream	0	1	13	17	1	1_A275_sNL37_glus_loKRNA:1	17	Gene: LOC345063	LOC100130428	KIY1365	XR_111238, XR_110533, XR_114536		
Gene:ID:3003728	LOC1005 03	11	124,670,324	124,679,657	9,333	+	2	2_A275_sNL37_glus_loKRNA:1:1652, 2_A275_sNL37_glus_loKRNA:1:1650	-460, -62	upstream, upstream	0	1	12.5	16.5	2	2_A275_sNL37_glus_loKRNA:1	17	Gene: LOC100507263	hypothetical LOC100507263	hypothetical LOC100507263	XR_110534		
Gene:ID:9371	CCDC15	11	124,624,017	124,911,365	67,366	+	2	1_A275_sNL37_glus_loKRNA:1:1323, 2_A275_sNL37_glus_loKRNA:1:1652	76, -17	st gene, upstream	1	1	16	17	1	2_A275_sNL37_glus_loKRNA:1	17	Gene: CCDC15	FLJ13215, CCDC15	coiled-coil domain containing 15	NM_025004, NCT23559620.0, NCT31080.2	220495_at, 241360_at	NP_079280.2, EAW67617.1, EAW67616.1
Gene:ID:19855	SLC37A2	11	124,933,013	124,990,412	27,398	+	2	1_A275_sNL37_glus_loKRNA:1:1636, 1_A275_sNL37_glus_loKRNA:1:1636	7879, 13533	st gene, st gene	0	1	12	17.5	2	2_A275_sNL37_glus_loKRNA:1	18	Gene: SLC37A2	sp11682, MGC71430, FLJ00171, SLC37A2	solute carrier family 37 (glucose-6-phosphate transporter), member 2	NM_198277, NM_001142900, NCT23539440.0, NCT23546008.0, NCT30165.3	238638_at	NP_938018.1, NP_001130762.1, EAW67619.1, EAW67620.1, EAW67621.1, EAW67622.1
Gene:ID:3876	PKNOX2	11	125,034,559	125,303,265	268,726	+	3	1_A275_sNL37_glus_loKRNA:1:1324, 2_A275_sNL37_glus_loKRNA:1:1650, 2_A275_sNL37_glus_loKRNA:1:1651	89009, 78625, 89041	st gene, st gene, st gene	1	1	16.5	16.5	3	1_A275_sNL7_dhrus_loKRNA:1	19	Gene: PKNOX2	FLJ13074, PKNOX2, PREP2	PBX/knotted 1 homeobox 2	NM_022062, NCT23551260.0, NCT23551270.0, NCT30164.3	216096_s_at, 222171_s_at, 222165_at, 242093_at	NP_071345.2, EAW67632.1, EAW67631.1, EAW67633.1
Gene:ID:9271	EI24	11	125,439,295	125,454,975	15,277	+	2	1_A275_sNL37_glus_loKRNA:1:1324, 2_A275_sNL37_glus_loKRNA:1:1650	24014, 23196	downstream, downstream	1	1	17	16	1	2_A275_sNL37_glus_loKRNA:1	25	Gene: EI24	PIG8, EI24, EPG4, TP53I8	etoposide induced 2.4 mRNA	NM_004879, NR_001027277, NCT19821861.1, NCT30159.3	208289_s_at, 219390_s_at	NP_004870.3, NP_001007275.1, EAW67641.1, EAW67642.1
Gene:ID:703	STT3A	11	125,482,738	125,491,260	26,941	+	3	1_A275_sNL37_glus_loKRNA:1:1325, 1_A275_sNL37_glus_loKRNA:1:1636, 2_A275_sNL37_glus_loKRNA:1:1650	672, -245, 33021	st gene, upstream, downstream	1	1	16.5	20.5	2	2_A275_sNL37_glus_loKRNA:1	26	Gene: STT3A	STT3A, STT3A, IT41, MGC9042, FLJ27035, TMC	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	NM_152713	202223_at	NP_689926.1
Gene:ID:1113	CHEK1	11	125,693,036	125,849,150	51,114	+	1	2_A275_sNL37_glus_loKRNA:1:1650	724	st gene	0	1	16	23	1	2_A275_sNL37_glus_loKRNA:1	23	Gene: CHEK1	CHK1, CHEK1	CHK1 checkpoint homolog (S. pombe)	NM_001274, NM_001114121, NM_001114122	205393_s_at, 209144_at	NP_001265.2, NP_001107593.1, NP_001107594.1
Gene:ID:9427	CDON	11	125,826,713	125,933,187	106,474	+	2	1_A275_sNL37_glus_loKRNA:1:1326, 2_A275_sNL37_glus_loKRNA:1:1650	88, 227	st gene, st gene	1	1	16	27	1	1_A275_sNL7_dhrus_loKRNA:1	36	Gene: CDON	MGC111524, ORCAM, CDON, CDO	Cdon homolog (mouse)	NM_016952, NCT3037?.4	207732_at, 227526_at	NP_058648.4, EAW67672.1
Gene:ID:4551	RPUSD4	11	126,071,959	126,081,557	9,598	-	1	2_A275_sNL37_glus_loKRNA:1:1652	61	st gene	0	1	16	25	1	2_A275_sNL37_glus_loKRNA:1	25	Gene: RPUSD4	FLJ14954	RNA pseudouridylate synthase domain containing 4	NM_032765, NM_001144827, NCT23552120, NCT30160.2	225768_at, 225769_at	NP_116154.2, NP_001138292.1, EAW67678.1, EAW67679.1
Gene:ID:9907	FAM115B	11	126,081,619	126,132,879	51,260	+	2	1_A275_sNL37_glus_loKRNA:1:1327, 2_A275_sNL37_glus_loKRNA:1:1652, 2_A275_sNL37_glus_loKRNA:1:1652	57229, -63, 57293	downstream, downstream, upstream, downstream	1	1	16	20.5	2	2_A275_sNL37_glus_loKRNA:1	25	Gene: FAM115B	FAM115B, FLJ21103	family with sequence similarity 115, member B	NM_024599, NCT19532482.1, NCT23552280.0, NCT23552300.0, NCT23552320.0	224996_at, 230009_at, 236316_at	NP_078812.2, EAW67677.1, EAW67678.1, EAW67680.1, EAW67679.1, EAW67680.1
Gene:ID:734	SRFR	11	126,132,614	126,135,877	6,060	-	2	1_A275_sNL37_glus_loKRNA:1:1327, 2_A275_sNL37_glus_loKRNA:1:1652	-28, -55	st gene, upstream	1	1	17	24	1	2_A275_sNL37_glus_loKRNA:1	24	Gene: SRFR	MGC9371, MGC17358, MGC3660, SRF-alpha, DP, SRFR, Sidpha	signal recognition particle receptor (docking protein)	NM_001177542, NM_003139, NCT23539080.0, NCT23539090.0, NCT30215.3	200817_s_at, 200816_s_at	NP_001171213.1, NP_003130.2, EAW67684.1, EAW67685.1, EAW67686.1
Gene:ID:5372	PDXRED1	11	126,139,055	126,148,027	8,972	+	2	1_A275_sNL37_glus_loKRNA:1:1327, 2_A275_sNL37_glus_loKRNA:1:1652	-207, -143	upstream, upstream	1	1	17	24	1	2_A275_sNL37_glus_loKRNA:1	24	Gene: PDXRED1	H17, PDXRED1, PRN14	PHD-dependent carboxreductase domain containing 1	NM_017427, NCT01962181.1, NCT19821621.1, NCT30178.2	223128_at	NP_059517.1, EAW67681.1, EAW67682.1, EAW67683.1
Gene:ID:14609	TIRAP	11	126,152,982	126,164,628	11,586	+	1	2_A275_sNL37_glus_loKRNA:1:1328	21034	downstream	1	0	22	15	1	1_A275_sNL7_dhrus_loKRNA:1	23	Gene: TIRAP	Mal, FLJ42203, TIRAP, wyatt	Toll-interleukin 1 receptor (TIR) domain containing adaptor protein	NM_001039661, NM_148910, NCT23552360.0, NCT23552370.0, NCT23565320.0	1552360_a_at, 1552004_a_at, 1554091_x_at, 1554092_s_at	NP_001034750.1, NP_683705.1, EAW67687.1, EAW67688.1, EAW67688.1
Gene:ID:5969	DCPS	11	126,173,647	126,215,644	41,997	+	2	1_A275_sNL37_glus_loKRNA:1:1328, 1_A275_sNL37_glus_loKRNA:1:1329	369, 49745	st gene, downstream	1	0	20.5	14	2	1_A275_sNL7_dhrus_loKRNA:1	23	Gene: DCPS	HSPC015, DCPS, HNIT-5, HSL1	decapping enzyme, scavenger	NM_016026, NCT23537?4.2	218774_at	NP_057451.1, EAW67690.1
Gene:ID:29372	FLJ39811	11	126,211,611	126,229,452	17,871	+	1	2_A275_sNL37_glus_loKRNA:1:1329	2090	st gene	1	0	16	13	1	1_A275_sNL7_dhrus_loKRNA:1	16	Gene: FLJ39811	FLJ39811	hypothetical LOC339872	NR_038039	237825_at, 237899_at	
Gene:ID:464	STX3A	11	126,226,096	126,264,533	38,437	+	1	2_A275_sNL37_glus_loKRNA:1:1329	-2104	upstream	1	0	16	13	1	1_A275_sNL7_dhrus_loKRNA:1	16	Gene: STX3A	STZ, COD23, FLJ40764, SYA1C, STA1A, STX3, STX3A, STX3ALA, SYA1, FLJ11957, MAINT-3	STX3 beta-galactoside alpha-2,3-sialyltransferase 4	NM_004177, NCT23539218.0, NCT23552410.0, NCT23552420.0, NCT23552440.0, NCT30624.2	203799_at, 203710_at	NP_004168.1, EAW67693.1, EAW67692.1, EAW67691.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:84623	KIRREL3	11	126,293,396	126,870,766	577,370	-	10	1_A375_pNL7_minus_lncRNA::1::1330, 1_A375_pNL7_minus_lncRNA::1::1331, 1_A375_pNL7_minus_lncRNA::1::1332, 1_A375_pNL7_minus_lncRNA::1::1333, 2_A375_pNL97_plus_lncRNA::1::1864, 2_A375_pNL97_plus_lncRNA::1::1865, 2_A375_pNL97_plus_lncRNA::1::1866, 2_A375_pNL97_plus_lncRNA::1::1867, 2_A375_pNL97_plus_lncRNA::1::1868, 2_A375_pNL97_plus_lncRNA	456062, 454542, 439310, 282510, 456030, 454494, 439358, 407790, 210094, 31582	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	26.83	27.83	6	2_A375_pNL97_plus_lncRNA::1	68	Gene KIRREL3	NEPH2, PRO4502, KIRREL3, MGC126824, KIRRE, MRD4, MGC126850, KIAA1867	kin of IRRE like 3 (Drosophila)	NM_032531, NM_001161707, hCT2335321.1, hCT2335322.1, hCT2335323.1		NP_115920.1, NP_001155179.1, EAW67698.1, EAW67699.1, EAW67700.1
GeneID:2113	ETS1	11	128,328,656	128,457,453	128,797	-	1	2_A375_pNL97_plus_lncRNA::1::1876	64749	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ETS1	EWSR2, FLJ10768, ETS1, ETS-1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	NM_005238, NM_001143820, NM_001162422, hCT1769897.3, hCT1952993.2, hCT2335367.1, hCT2354391.0	1555355_a_at, 214447_at, 224833_at	NP_005229.1, NP_001137292.1, NP_001155894.1, EAW67710.1, EAW67711.1, EAW67712.1, EAW67709.1
GeneID:9743	RICS	11	128,834,955	129,062,093	227,138	-	1	1_A375_pNL7_minus_lncRNA::1::1340	48653	in gene	1	0	23	19	1	1_A375_pNL7_minus_lncRNA::1	23	Gene RICS	GRIT, GC-GAP, ARHGAP32, p200RhoGAP, PX-RICS, RICS, p250GAP, MGC1892, KIAA0712	Rho GTPase activating protein 32	NM_014715, NM_001142685, hCT2348801.1, hCT2348802.1, hCT2348803.1, hCT2348804.1, hCT2348805.1, hCT2349132.0, hCT2349133.0, hCT2349134.0, hCT2349135.0, hCT2349136.0, hCT2354352.0	203431_s_at, 210791_s_at	NP_055530.2, NP_001136157.1, EAW67732.1, EAW67733.1, EAW67737.1, EAW67738.1, EAW67734.1, EAW67735.1, EAW67736.1, EAW67739.1, EAW67740.1, EAW67741.1, EAW67742.1
GeneID:8538	BARX2	11	129,245,881	129,322,174	76,293	+	1	2_A375_pNL97_plus_lncRNA::1::1877	75655	in gene	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene BARX2	MGC133369, BARX2, MGC133368	BARX homeobox 2	NM_003658, hCT29846.1	210419_at	NP_003649.2, EAW67743.1
GeneID:56980	PRDM10	11	129,769,601	129,872,730	103,129	-	1	1_A375_pNL7_minus_lncRNA::1::1341	410	in gene	1	0	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene PRDM10	KIAA1231, PFM7, MGC131802, PRDM10	PR domain containing 10	NM_020228, NM_199437, NM_199438, NM_199439	214158_s_at, 219515_at	NP_064613.2, NP_955469.1, NP_955470.1, NP_955471.1
GeneID:440072	NCRNA00167	11	129,872,519	129,875,381	2,862	+	1	1_A375_pNL7_minus_lncRNA::1::1341	-199	upstream	1	0	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene NCRNA00167	MGC168927, MGC168926, NCRNA00167, C11orf37, FLJ31394	non-protein coding RNA 167	NR_024233	1562413_at	
GeneID:100507431	LOC100507431	11	130,714,088	130,732,002	17,914	-	1	1_A375_pNL7_minus_lncRNA::1::1343	14242	in gene	1	0	22	14	1	1_A375_pNL7_minus_lncRNA::1	22	Gene LOC100507431		hypothetical protein LOC100507431	XM_003119517, XM_003118983, XM_003120722		XP_003119565.1, XP_003119031.1, XP_003120770.1
GeneID:399979	SNX19	11	130,745,766	130,786,382	40,616	-	2	1_A375_pNL7_minus_lncRNA::1::1344, 2_A375_pNL97_plus_lncRNA::1::1883	78, 46	in gene, in gene	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SNX19	DKFZp667I205, KIAA0254, SNX19, CHET8	sorting nexin 19	NM_014758, hCT31674.2	1554986_a_at, 1561710_at, 202358_s_at, 202359_s_at	NP_055573.2, EAW67794.1
GeneID:50863	NTM	11	131,240,371	132,206,716	966,345	+	6	1_A375_pNL7_minus_lncRNA::1::1345, 2_A375_pNL97_plus_lncRNA::1::1884, 1_A375_pNL7_minus_lncRNA::1::1346, 1_A375_pNL7_minus_lncRNA::1::1347, 2_A375_pNL97_plus_lncRNA::1::1885, 2_A375_pNL97_plus_lncRNA::1::1886	694765, 694562, 806861, 948173, 806829, 948109	in gene, in gene, in gene, in gene, in gene, in gene	1	1	31.33	37.67	3	2_A375_pNL97_plus_lncRNA::1	65	Gene NTM	IGLON2, MGC60329, NTM, HNT, NTRI	neurotrimin	NM_016522, NM_001048209, NM_001144058, NM_001144059, hCT1953783.1, hCT2335272.0, hCT2335273.0	222020_s_at, 227566_at	NP_057606.1, NP_001041674.1, NP_001137530.1, NP_001137531.1, EAW67801.1, EAW67802.1, EAW67800.1
GeneID:4978	OPCML	11	132,284,875	133,402,403	1,117,528	-	4	1_A375_pNL7_minus_lncRNA::1::1348, 1_A375_pNL7_minus_lncRNA::1::1349, 2_A375_pNL97_plus_lncRNA::1::1887, 2_A375_pNL97_plus_lncRNA::1::1888	334835, 188195, 616008, 334851	in gene, in gene, in gene, in gene	1	1	17	23	3	2_A375_pNL97_plus_lncRNA::1	32	Gene OPCML	OPCM, OBCAM, IGLON1, OPCML	opioid binding protein/cell adhesion molecule-like	NM_002545, NM_001012393, hCT1953785.1, hCT2335283.0	206215_at, 214111_at	NP_002536.1, NP_001012393.1, EAW67804.1, EAW67805.1
GeneID:100128095	LOC100128095	11	132,526,971	133,402,878	875,907	+	4	1_A375_pNL7_minus_lncRNA::1::1348, 1_A375_pNL7_minus_lncRNA::1::1349, 2_A375_pNL97_plus_lncRNA::1::1887, 2_A375_pNL97_plus_lncRNA::1::1888	540597, 687237, 257424, 540561	in gene, in gene, in gene, in gene	1	1	17	23	3	2_A375_pNL97_plus_lncRNA::1	32	Gene LOC100128095		hypothetical LOC100128095	XR_110538, XR_114543		
GeneID:22997	IGSF9B	11	133,785,185	133,826,880	41,695	-	1	2_A375_pNL97_plus_lncRNA::1::1889	21856	in gene	0	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene IGSF9B	KIAA1030, IGSF9B	immunoglobulin superfamily, member 9B	NM_014987	215166_at, 215255_at	NP_055802.1
GeneID:100128239	LOC100128239	11	133,902,167	133,911,236	9,069	+	1	2_A375_pNL97_plus_lncRNA::1::1890	5065	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100128239		hypothetical LOC100128239	NR_027276		
GeneID:23310	NCAPD3	11	134,022,337	134,094,426	72,089	-	1	2_A375_pNL97_plus_lncRNA::1::1891	-6	upstream	0	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NCAPD3	NCAPD3, MGC104671, KIAA0056, hHCP6, hCAP-D3, FLJ42888, CAP-D3, hcp-6	non-SMC condensin II complex, subunit D3	NM_015261, hCT1963567.1, hCT2354380.0, hCT2354381.0, hCT28841.3	212789_at	NP_056076.1, EAW67821.1, EAW67822.1, EAW67823.1, EAW67824.1
GeneID:112936	VPS26B	11	134,094,561	134,117,686	23,125	+	3	1_A375_pNL7_minus_lncRNA::1::1350, 2_A375_pNL97_plus_lncRNA::1::1891, 2_A375_pNL97_plus_lncRNA::1::1892	28815, -129, 28767	downstream, upstream, downstream	1	1	20	19.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene VPS26B	MGC10485, VPS26B, Pep8b	vacuolar protein sorting 26 homolog B (S. pombe)	NM_052875, hCT2335647.0, hCT2335649.0, hCT28842.2	225483_at, 230306_at	NP_443107.1, EAW67826.1, EAW67825.1, EAW67827.1
GeneID:29087	THYN1	11	134,118,173	134,123,260	5,087	-	2	1_A375_pNL7_minus_lncRNA::1::1350, 2_A375_pNL97_plus_lncRNA::1::1892	-116, -68	upstream, upstream	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene THYN1	THY28, THY28KD, MY105, THYN1, MGC12187, HSPC144, MDS012	thymocyte nuclear protein 1	NM_014174, NM_199297, NM_199298, NM_001037304, NM_001037305, hCT1954617.2, hCT1963079.2, hCT1963080.2, hCT2354373.0, hCT28837.2	218491_s_at, 223711_s_at	NP_054893.1, NP_954994.1, NP_954995.1, NP_001032381.1, NP_001032382.1, EAW67831.1, EAW67828.1, EAW67829.1, EAW67830.1, EAW67832.1
GeneID:27034	ACAD8	11	134,123,434	134,135,749	12,315	+	2	1_A375_pNL7_minus_lncRNA::1::1350, 2_A375_pNL97_plus_lncRNA::1::1892	-58, -106	upstream, upstream	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene ACAD8	ACAD-8, ARC42, FLJ22590, ACAD8	acyl-CoA dehydrogenase family, member 8	NM_014384, hCT2354420.0, hCT2354421.0, hCT28491.1	221669_s_at	NP_055199.1, EAW67833.1, EAW67834.1, EAW67835.1
GeneID:27087	B3GAT1	11	134,248,398	134,281,812	33,414	-	2	1_A375_pNL7_minus_lncRNA::1::1351, 2_A375_pNL97_plus_lncRNA::1::1893	-6668, -6764	upstream, upstream	1	1	15	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene B3GAT1	GLCATP, HNK1, LEU7, NK1, B3GAT1, GLCUATP, NK-1, CD57	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	NM_018644, NM_054025	219521_at	NP_061114.2, NP_473366.1
GeneID:283177	LOC283177	11	134,306,376	134,375,555	69,179	+	2	1_A375_pNL7_minus_lncRNA::1::1352, 2_A375_pNL97_plus_lncRNA::1::1894	40136, 40152	in gene, in gene	1	1	23	23	1	1_A375_pNL7_minus_lncRNA::1	23	Gene LOC283177		hypothetical LOC283177	NR_033852	1557207_s_at, 236112_at	
GeneID:5927	KDM5A	12	389,223	498,620	109,397	-	1	2_A375_pNL97_plus_lncRNA::1::1897	-36	upstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene KDM5A	RBP2, RBBP-2, KDM5A, JARID1A, RBBP2	lysine (K)-specific demethylase 5A	NM_001042603, hCT16395.4, hCT2285595.1	202040_s_at, 215698_at, 226367_at, 226371_at, 230226_s_at	NP_001036068.1, EAW88971.1, EAW88970.1
GeneID:84318	CCDC77	12	498,516	551,808	53,292	+	1	2_A375_pNL97_plus_lncRNA::1::1897	140	in gene	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CCDC77	MGC13183, CCDC77	coiled-coil domain containing 77	NM_001130148, NM_032358, NM_001130146, NM_001130147, hCT16400.2, hCT1955085.1, hCT2286278.0	224521_s_at	NP_001123620.1, NP_115734.1, NP_001123618.1, NP_001123619.1, EAW88967.1, EAW88969.1, EAW88968.1
GeneID:283358	B4GALNT3	12	569,543	671,058	101,515	+	1	1_A375_pNL7_minus_lncRNA::1::1354	109977	downstream	1	0	20	15	1	1_A375_pNL7_minus_lncRNA::1	20	Gene B4GALNT3	FLJ40362, B4GALNT3, FLJ16224	beta-1,4-N-acetyl-galactosaminyl transferase 3	NM_173593, hCT1769241.2, hCT2286286.1, hCT2286287.1, hCT2357116.0	1553727_at, 229203_at, 229909_at	NP_775864.3, EAW88962.1, EAW88963.1, EAW88964.1, EAW88965.1
GeneID:4815	NINJ2	12	673,462	772,755	99,293	-	2	1_A375_pNL7_minus_lncRNA::1::1354, 1_A375_pNL7_minus_lncRNA::1::1355	93235, 31091	in gene, in gene	1	0	17	12	2	1_A375_pNL7_minus_lncRNA::1	20	Gene NINJ2	FLJ56349, NINJ2	ninjurin 2	NM_016533, hCT16399.2, hCT2285667.0	219594_at	NP_057617.2, EAW88959.1, EAW88960.1
GeneID:100049716	LOC100049716	12	740,057	755,046	14,989	+	1	1_A375_pNL7_minus_lncRNA::1::1355	1607	in gene	1	0	14	9	1	1_A375_pNL7_minus_lncRNA::1	14	Gene LOC100049716		hypothetical LOC100049716	XR_111248, XR_109114, XR_114550		
GeneID:65125	WNK1	12	862,089	1,020,618	158,529	+	2	1_A375_pNL7_minus_lncRNA::1::1356, 1_A375_pNL7_minus_lncRNA::1::1357	-521, 439	upstream, in gene	1	0	21	15.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene WNK1	KIAA0344, PSK, PRKWNK1, HSAN2, WNK1, MGC163341, PHA2C, HSN2, MGC163339, KDP	WNK lysine deficient protein kinase 1	NM_001184985, NM_014823, NM_018979, NM_213655, hCT16396.2, hCT1640957.2, hCT1968990.1, hCT2286297.0, hCT2286299.0, hCT2286302.0, hCT2286305.0, hCT2357123.0	1555068_at, 202940_at, 211992_at, 211993_at, 211994_at, 228712_at, 39313_at	NP_001171914.1, NP_055638.2, NP_061852.3, NP_998820.3, EAW88951.1, EAW88954.1, EAW88952.1, EAW88953.1, EAW88955.1, EAW88956.1, EAW88957.1, EAW88958.1
GeneID:5893	RAD52	12	1,021,255	1,058,863	37,608	-	1	2_A375_pNL97_plus_lncRNA::1::1898	175	in gene	0	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene RAD52	RAD52		NM_134424, hCT1686440.2, hCT2285631.0, hCT2285634.0, hCT2285639.0, hCT2285647.0, hCT2285650.0, hCT2285653.0, hCT2285658.0, hCT2357126.0	205647_at, 210630_s_at, 211904_x_at, 236042_at	NP_602296.2, EAW88943.1, EAW88944.1, EAW88945.1, EAW88949.1, EAW88950.1, EAW88942.1, EAW88946.1, EAW88947.1, EAW88948.1
GeneID:23085	ERC1	12	1,100,404	1,605,099	504,695	+	1	1_A375_pNL7_minus_lncRNA::1::1358	225164	in gene	1	0	18	5	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ERC1	RAB6IP2, Cast2, FLJ31750, MGC12974, ELKS, ERC1, KIAA1081	ELKS/RAB6-interacting/CAST family member 1	NR_027946, NM_178039, NM_178040, NR_027948, NR_027949, hCT1955084.1, hCT2288928.0, hCT2288930.0, hCT2288931.0, hCT2288932.0, hCT2288933.0, hCT2288934.0, hCT2357134.0, hCT2357135.0	1552663_a_at, 1555294_a_at, 1563947_a_at, 215606_s_at, 216440_at	NP_829883.1, NP_829884.1, EAW88932.1, EAW88933.1, EAW88934.1, EAW88939.1, EAW88935.1, EAW88936.1, EAW88937.1, EAW88938.1, EAW88940.1
GeneID:144699	FBXL14	12	1,675,159	1,703,331	28,172	-	1	1_A375_pNL7_minus_lncRNA::1::1359	1091	in gene	1	0	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene FBXL14	FBXL14, Fbl14, MGC40195	F-box and leucine-rich repeat protein 14	NM_152441, hCT1970530.1, hCT2286726.2, hCT2350918.0	1553682_at, 1553683_s_at, 213145_at	NP_689654.1, EAW88930.1, EAW88928.1, EAW88929.1
GeneID:93589	CACNA2D4	12	1,901,123	2,027,870	126,747	-	1	2_A375_pNL97_plus_lncRNA::1::1900	87454	in gene	0	1	20	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene CACNA2D4	RCD4, CACNA2D4	calcium channel, voltage-dependent, alpha 2/delta subunit 4	NM_172364, hCT1951286.0, hCT1964495.1, hCT2286697.0	1552690_a_at, 228063_at	NP_758952.4, EAW88918.1, EAW88919.1, EAW88920.1
GeneID:654429	LRTM2	12	1,929,433	1,945,918	16,485	+	1	2_A375_pNL97_plus_lncRNA::1::1900	10953	in gene	0	1	20	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene LRTM2	FLJ42697, LRTM2	leucine-rich repeats and transmembrane domains 2	NM_001039029, NM_001163925, NM_001163926	1556530_at	NP_001034118.1, NP_001157397.1, NP_001157398.1
GeneID:196513	DCP1B	12	2,055,214	2,113,677	58,463	-	2	1_A375_pNL7_minus_lncRNA::1::1361, 2_A375_pNL97_plus_lncRNA::1::1901	45, -19	in gene, upstream	1	1	42	48	1	2_A375_pNL97_plus_lncRNA::1	48	Gene DCP1B	hDcp1b, DCP1B, DCP1	DCP1 decapping enzyme homolog B (S. cerevisiae)	NM_152640, hCT15334.2, hCT2285686.0	226093_at	NP_689853.3, EAW88916.1, EAW88915.1
GeneID:775	CACNA1C	12	2,162,416	2,807,115	644,699	+	1	2_A375_pNL97_plus_lncRNA::1::1902	75888	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CACNA1C	CACNL1A1, MGC120730, CCHL1A1, CACNA1C, CACN2, CaV1.2, TS, CACH2	calcium channel, voltage-dependent, L type, alpha 1C subunit	NM_001129832, NM_001129834, NM_001129835, NM_001129837, NM_001129838, NM_001129840, NM_001129841, NM_001129842, NM_001129843, NM_001129844, NM_001129846, NM_000719, NM_199460, NM_001129827, NM_001129829, NM_001129830, NM_001129831, NM_001129833, NM_001129	208020_s_at, 211592_s_at, 238636_at, 242973_at	NP_001123304.1, NP_001123306.1, NP_001123307.1, NP_001123309.1, NP_001123310.1, NP_001123312.1, NP_000710.5, NP_001123313.1, NP_001123314.1, NP_001123315.1, NP_001123316.1, NP_001123318.1, NP_955630.2, NP_001123299.1, NP_001123301.1, NP_001123302.1, NP_00
GeneID:283440	LOC283440	12	2,870,366	2,880,835	10,469	-	2	1_A375_pNL7_minus_lncRNA::1::1362, 2_A375_pNL97_plus_lncRNA::1::1903	18883, 18851	downstream, downstream	1	1	90	92	1	2_A375_pNL97_plus_lncRNA::1	92	Gene LOC283440		similar to hCG2045467	NR_033958		
GeneID:83695	C12orf32	12	2,986,365	2,998,626	12,261	+	1	2_A375_pNL97_plus_lncRNA::1::1904	13699	downstream	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene C12orf32	MGC13204, HKMT1188, C12orf32	chromosome 12 open reading frame 32	NR_027363, NR_027364, NR_027365, hCT18175.3	211632_at, 211639_x_at, 225836_s_at, 225837_at, 241074_at	EAW88879.1
GeneID:7289	TULP3	12	3,000,033	3,050,306	50,273	+	1	2_A375_pNL97_plus_lncRNA::1::1904	31	in gene	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene TULP3	MGC45295, TULP3, TUBL3	tubby like protein 3	NM_003324, NM_001160408, hCT18170.3, hCT2357124.0, hCT2357125.0	205854_at, 221964_at	NP_003315.2, NP_001153880.1, EAW88876.1, EAW88877.1, EAW88878.1
GeneID:7004	TEAD4	12	3,068,478	3,149,842	81,364	+	1	2_A375_pNL97_plus_lncRNA::1::1905	-606	upstream	0	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TEAD4	TEF3, MGC9014, TEF-3, TEAD4, hRTEF-1B, TEFR-1, EFTR-2, RTEF1, TCF13L1	TEA domain family member 4	NM_003213, NM_201441, NM_201443, hCT18169.2, hCT1967436.1, hCT2357121.0, hCT2357122.0	204281_at, 41037_at	NP_003204.2, NP_958849.1, NP_958851.1, EAW88873.1, EAW88874.1, EAW88875.1, EAW88872.1
GeneID:100128253	LOC100128253	12	3,405,217	3,409,390	4,173	-	1	2_A375_pNL97_plus_lncRNA::1::1906	-4306	upstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100128253		hypothetical LOC100128253	XR_111244, XR_109118, XR_114554		
GeneID:100129223	LOC100129223	12	3,592,878	3,601,985	9,107	-	1	2_A375_pNL97_plus_lncRNA::1::1908	257	in gene	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100129223		hypothetical LOC100129223	XR_111243, XR_109119, XR_114555		
GeneID:56341	PRMT8	12	3,600,425	3,703,139	102,714	+	1	2_A375_pNL97_plus_lncRNA::1::1908	1303	in gene	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PRMT8	HRMT1L3, PRMT8, HRMT1L4	protein arginine methyltransferase 8	NM_019854, hCT15563.3, hCT2326640.0	207772_s_at, 230839_at	NP_062828.3, EAW88861.1, EAW88862.1
GeneID:57102	C12orf4	12	4,596,901	4,647,637	50,736	-	2	1_A375_pNL7_minus_lncRNA::1::1363, 2_A375_pNL97_plus_lncRNA::1::1909	-331, -91	upstream, upstream	1	1	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene C12orf4	C12orf4, FLJ21158, FLJ23899	chromosome 12 open reading frame 4	NM_020374, hCT16083.3, hCT2357082.0	218374_s_at, 222613_at	NP_065107.1, EAW88846.1, EAW88845.1
GeneID:10635	RAD51AP1	12	4,647,950	4,669,213	21,263	+	2	1_A375_pNL7_minus_lncRNA::1::1363, 2_A375_pNL97_plus_lncRNA::1::1909	18, -222	in gene, upstream	1	1	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene RAD51AP1	PIR51, RAD51AP1	RAD51 associated protein 1	NM_001130862, NM_006479, hCT16075.3, hCT2285076.0	204146_at	NP_001124334.1, NP_006470.1, EAW88843.1, EAW88844.1
GeneID:8798	DYRK4	12	4,699,244	4,723,041	23,797	+	1	2_A375_pNL97_plus_lncRNA::1::1910	14953	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DYRK4	DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	NM_003845, hCT16080.4, hCT2340536.0	212954_at	NP_003836.1, EAW88842.1, EAW88841.1
GeneID:7450	VWF	12	6,058,040	6,233,836	175,796	-	1	2_A375_pNL97_plus_lncRNA::1::1911	31436	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene VWF	F8VWF, VWF, VWD	von Willebrand factor	NM_000552, hCT2286544.0, hCT2286545.0, hCT2286546.0, hCT2286547.0, hCT2357120.0	202112_at, 233980_s_at	NP_000543.2, EAW88814.1, EAW88815.1, EAW88816.1, EAW88817.1, EAW88818.1
GeneID:928	CD9	12	6,309,555	6,347,427	37,872	+	1	2_A375_pNL97_plus_lncRNA::1::1913	29261	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CD9	MIC3, GIG2, MRP-1, 5H9, DRAP-27, FLJ99568, TSPAN-29, TSPAN29, CD9, BTCC-1, BA2, P24	CD9 molecule	NM_001769, hCT12726.2, hCT2292614.0	201005_at, 233317_at, 233322_at	NP_001760.1, EAW88813.1, EAW88812.1
GeneID:6337	SCNN1A	12	6,456,009	6,486,523	30,514	-	1	2_A375_pNL97_plus_lncRNA::1::1914	-6949	upstream	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SCNN1A	ENaCalpha, FLJ21883, SCNEA, ENaCa, SCNN1, SCNN1A, BESC2	sodium channel, nonvoltage-gated 1 alpha	NM_001038, NM_001159575, NM_001159576, hCT15428.2, hCT2357094.0	203453_at, 215026_x_at, 217264_s_at	NP_001029.1, NP_001153047.1, NP_001153048.1, EAW88803.1, EAW88804.1
GeneID:4055	LTBR	12	6,493,357	6,500,734	7,377	+	1	2_A375_pNL97_plus_lncRNA::1::1914	115	in gene	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LTBR	LTBR, TNFR2-RP, TNF-R-III, TNFRSF3, TNFR-RP, LT-BETA-R, CD18, TNFCR, D12S370	lymphotoxin beta receptor (TNFR superfamily, member 3)	NM_002342, hCT15427.2, hCT1967387.1	203005_at, 232819_s_at, 243400_x_at	NP_002333.1, EAW88801.1, EAW88802.1
GeneID:9918	NCAPD2	12	6,603,298	6,641,132	37,834	+	3	1_A375_pNL7_minus_lncRNA::1::1364, 2_A375_pNL97_plus_lncRNA::1::1915, 2_A375_pNL97_plus_lncRNA::1::1916	40007, 40446, 43742	downstream, downstream, downstream	1	1	16	23	2	2_A375_pNL97_plus_lncRNA::1	26	Gene NCAPD2	CAP-D2, KIAA0159, CNAP1, NCAPD2, hCAP-D2	non-SMC condensin I complex, subunit D2	NM_014865, hCT15429.3, hCT2292603.0, hCT2357095.0	201774_s_at	NP_055680.3, EAW88788.1, EAW88789.1, EAW88790.1
GeneID:2597	GAPDH	12	6,643,657	6,647,536	3,879	+	3	1_A375_pNL7_minus_lncRNA::1::1364, 2_A375_pNL97_plus_lncRNA::1::1915, 2_A375_pNL97_plus_lncRNA::1::1916	-352, 87, 3383	upstream, in gene, in gene	1	1	16	23	2	2_A375_pNL97_plus_lncRNA::1	26	Gene GAPDH	MGC88685, GAPDH, G3PD, GAPD	glyceraldehyde-3-phosphate dehydrogenase	NM_002046, hCT2292605.0, hCT2357101.0	212581_x_at, 213453_x_at, 217398_x_at, AFFX-HUMGAPDH/M33197_3_at, AFFX-HUMGAPDH/M33197_5_at, AFFX-HUMGAPDH/M33197_M_at	NP_002037.2, EAW88787.1, EAW88786.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:25900	IFFO1	12	6,648,694	6,665,249	16,555	-	3	1_A375_pNL7_minus_lncRNA::1::1364, 2_A375_pNL97_plus_lncRNA::1::1915, 2_A375_pNL97_plus_lncRNA::1::1916	21944, 21505, 18209	downstream, downstream, downstream	1	1	16	23	2	2_A375_pNL97_plus_lncRNA::1	26	Gene IFFO1	MGC117359, IFFO, DKFZp586I2223, HOM-TES-103, IFFO1, FLJ20703	intermediate filament family orphan 1	NM_001039670, NM_001193457, NM_080730, NR_036467, hCT17083.2, hCT2286567.0, hCT2286568.0, hCT2286570.0, hCT2286574.0	209721_s_at, 36030_at	NP_001034759.1, NP_001180386.1, NP_542768.2, EAW88781.1, EAW88784.1, EAW88785.1, EAW88782.1, EAW88783.1
GeneID:51147	ING4	12	6,759,704	6,772,308	12,604	-	2	1_A375_pNL7_minus_lncRNA::1::1365, 2_A375_pNL97_plus_lncRNA::1::1917	-124, -220	upstream, upstream	1	1	19	19	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ING4	ING4, p29ING4, my036, MGC12557	inhibitor of growth family, member 4	NM_001127582, NM_016162, NM_001127583, NM_001127584, NM_001127585, NM_001127586, hCT17055.4, hCT1967418.1, hCT1967419.1, hCT2357083.0, hCT2357084.0, hCT2357085.0, hCT2357086.0, hCT2357087.0, hCT2357088.0, hCT2357089.0, hCT2357090.0, hCT2357091.0	218234_at, 48825_at	NP_001121054.1, NP_057246.2, NP_001121055.1, NP_001121056.1, NP_001121057.1, NP_001121058.1, EAW88762.1, EAW88763.1, EAW88764.1, EAW88765.1, EAW88766.1, EAW88767.1, EAW88768.1, EAW88770.1, EAW88769.1, EAW88771.1, EAW88772.1, EAW88773.1
GeneID:171017	ZNF384	12	6,775,643	6,798,676	23,033	-	4	1_A375_pNL7_minus_lncRNA::1::1365, 1_A375_pNL7_minus_lncRNA::1::1366, 2_A375_pNL97_plus_lncRNA::1::1917, 2_A375_pNL97_plus_lncRNA::1::1918	26244, -76, 26148, 212	downstream, upstream, downstream, in gene	1	1	19.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene ZNF384	CAGH1A, TNRC1, ZNF384, NP, ERDA2, FLJ59043, CAGH1, NMP4, CIZ	zinc finger protein 384	NM_133476, NM_001039916, NM_001039917, NM_001039918, NM_001039919, NM_001039920, NM_001135734, hCT17062.3, hCT1954390.1, hCT2286963.0, hCT2286965.0, hCT2357109.0, hCT2357110.0	212369_at	NP_597733.2, NP_001035005.1, NP_001035006.1, NP_001035007.1, NP_001035008.1, NP_001035009.1, NP_001129206.1, EAW88755.1, EAW88756.1, EAW88757.1, EAW88758.1, EAW88759.1, EAW88760.1
GeneID:196500	C12orf53	12	6,802,957	6,809,812	6,855	-	2	1_A375_pNL7_minus_lncRNA::1::1366, 2_A375_pNL97_plus_lncRNA::1::1918	11060, 11348	downstream, downstream	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene C12orf53	C12orf53, DKFZp547D2210, PANP	chromosome 12 open reading frame 53	NM_153685, hCT17061.4, hCT2349154.0, hCT2349155.0, hCT2349156.0, hCT2357108.0	1553566_at, 228165_at	NP_710152.1, EAW88751.1, EAW88750.1, EAW88752.1, EAW88753.1, EAW88754.1
GeneID:50813	COPS7A	12	6,833,150	6,841,041	7,891	+	2	1_A375_pNL7_minus_lncRNA::1::1367, 2_A375_pNL97_plus_lncRNA::1::1919	146, 226	in gene, in gene	1	1	33	30	1	1_A375_pNL7_minus_lncRNA::1	33	Gene COPS7A	COPS7A, CSN7A, MGC110877	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	NM_001164095, NM_016319, NM_001164093, NM_001164094, hCT1967410.1, hCT1967412.1, hCT2357079.0, hCT2357080.0, hCT2357081.0	209029_at	NP_001157567.1, NP_057403.1, NP_001157565.1, NP_001157566.1, EAW88745.1, EAW88747.1, EAW88746.1, EAW88748.1, EAW88749.1
GeneID:8079	MLF2	12	6,857,158	6,862,636	5,478	-	1	2_A375_pNL97_plus_lncRNA::1::1920	236	in gene	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MLF2	NTN4, MLF2	myeloid leukemia factor 2	NM_005439, NR_026581, hCT17056.2, hCT2286958.0	200948_at	NP_005430.1, EAW88743.1, EAW88744.1
GeneID:920	CD4	12	6,898,638	6,929,976	31,338	+	2	1_A375_pNL7_minus_lncRNA::1::1368, 2_A375_pNL97_plus_lncRNA::1::1921	39986, 39570	downstream, downstream	1	1	20	16	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CD4	CD4mut, CD4	CD4 molecule	NM_000616, NM_001195014, NM_001195015, NM_001195016, NM_001195017, NR_036545, hCT17077.3, hCT2286501.0	203547_at, 216424_at	NP_000607.1, NP_001181943.1, NP_001181944.1, NP_001181945.1, NP_001181946.1, EAW88738.1, EAW88739.1
GeneID:27239	GPR162	12	6,930,963	6,936,583	5,620	+	2	1_A375_pNL7_minus_lncRNA::1::1368, 2_A375_pNL97_plus_lncRNA::1::1921	7661, 7245	downstream, downstream	1	1	20	16	1	1_A375_pNL7_minus_lncRNA::1	20	Gene GPR162	FLJ78837, A-2, GRCA, GPR162	G protein-coupled receptor 162	NM_014449, NM_019858, hCT2286506.1, hCT2286514.0, hCT2286516.0	205056_s_at	NP_055264.1, NP_062832.1, EAW88735.1, EAW88736.1, EAW88737.1
GeneID:10536	LEPREL2	12	6,937,572	6,949,018	11,446	+	2	1_A375_pNL7_minus_lncRNA::1::1368, 2_A375_pNL97_plus_lncRNA::1::1921	1052, 636	in gene, in gene	1	1	20	16	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LEPREL2	HSU47926, GRCB, P3H3, LEPREL2	leprecan-like 2	NM_014262, hCT2286503.1, hCT2357130.0, hCT2357131.0, hCT2357132.0	204854_at	NP_055077.2, EAW88731.1, EAW88732.1, EAW88733.1, EAW88734.1
GeneID:2784	GNB3	12	6,949,375	6,956,557	7,182	+	2	1_A375_pNL7_minus_lncRNA::1::1369, 2_A375_pNL97_plus_lncRNA::1::1922	12289, 12289	downstream, downstream	1	1	35	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene GNB3	GNB3		NM_002075, hCT17063.3	206047_at	NP_002066.1, EAW88730.1
GeneID:83461	CDCA3	12	6,957,972	6,960,456	2,484	-	2	1_A375_pNL7_minus_lncRNA::1::1369, 2_A375_pNL97_plus_lncRNA::1::1922	-1208, -1208	upstream, upstream	1	1	35	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene CDCA3	GRCC8, CDCA3, FBXO52, TOME-1, MGC2577	cell division cycle associated 3	NM_031299, hCT17078.2, hCT1954389.1	221436_s_at, 223307_at	NP_112589.1, EAW88729.1, EAW88728.1
GeneID:8078	USP5	12	6,961,285	6,975,796	14,511	+	3	1_A375_pNL7_minus_lncRNA::1::1369, 2_A375_pNL97_plus_lncRNA::1::1922, 2_A375_pNL97_plus_lncRNA::1::1923	379, 379, 21627	in gene, in gene, downstream	1	1	26	33.5	2	2_A375_pNL97_plus_lncRNA::1	46	Gene USP5	ISOT, USP5	ubiquitin specific peptidase 5 (isopeptidase T)	NM_003481, NM_001098536, hCT17062.2, hCT1967428.1, hCT2286522.0, hCT2357106.0	206031_s_at	NP_003472.2, NP_001092006.1, EAW88724.1, EAW88725.1, EAW88726.1, EAW88727.1
GeneID:7167	TPI1	12	6,976,584	6,980,110	3,526	+	1	2_A375_pNL97_plus_lncRNA::1::1923	6328	downstream	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TPI1	TPI, MGC88108, TPI1	triosephosphate isomerase 1	NM_000365, NM_001159287, NR_027483, hCT17064.4, hCT1967429.1, hCT1967430.1	200822_x_at, 210050_at, 213011_s_at	NP_000356.1, NP_001152759.1, EAW88721.1, EAW88722.1, EAW88723.1
GeneID:84727	SPSB2	12	6,980,099	6,982,521	2,422	-	1	2_A375_pNL97_plus_lncRNA::1::1923	-391	upstream	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SPSB2	MGC2519, GRCC9, FLJ17395, SSB2, SPSB2	splA/ryanodine receptor domain and SOCS box containing 2	NM_001146316, NM_032641, hCT17085.3, hCT2286940.0	223580_at	NP_001139788.1, NP_116030.1, EAW88719.1, EAW88720.1
GeneID:1822	ATN1	12	7,033,626	7,051,484	17,858	+	4	1_A375_pNL7_minus_lncRNA::1::1371, 1_A375_pNL7_minus_lncRNA::1::1372, 2_A375_pNL97_plus_lncRNA::1::1925, 2_A375_pNL97_plus_lncRNA::1::1926	13670, 20166, 13670, 20086	in gene, downstream, in gene, downstream	1	1	65	65.5	2	2_A375_pNL97_plus_lncRNA::1	111	Gene ATN1	B37, D12S755E, HRS, ATN1, DRPLA, NOD	atrophin 1	NM_001940, NM_001007026, hCT17086.2, hCT2286462.0, hCT2286464.0	1555754_s_at, 208871_at, 211076_x_at, 229265_at, 40489_at	NP_001931.2, NP_001007027.1, EAW88706.1, EAW88707.1, EAW88708.1
GeneID:100147744	RNU7	12	7,052,979	7,053,041	62	+	4	1_A375_pNL7_minus_lncRNA::1::1371, 1_A375_pNL7_minus_lncRNA::1::1372, 2_A375_pNL97_plus_lncRNA::1::1925, 2_A375_pNL97_plus_lncRNA::1::1926	-5683, 813, -5683, 733	upstream, downstream, upstream, downstream	1	1	65	65.5	2	2_A375_pNL97_plus_lncRNA::1	111	Gene RNU7	RNU7-1, U7.1, RNU7	RNA, U7 small nuclear	NR_023317		
GeneID:113246	C12orf57	12	7,053,203	7,055,165	1,962	+	4	1_A375_pNL7_minus_lncRNA::1::1371, 1_A375_pNL7_minus_lncRNA::1::1372, 2_A375_pNL97_plus_lncRNA::1::1925, 2_A375_pNL97_plus_lncRNA::1::1926	-5907, 589, -5907, 509	upstream, in gene, upstream, in gene	1	1	65	65.5	2	2_A375_pNL97_plus_lncRNA::1	111	Gene C12orf57	FLJ17306, GRCC10, C12orf57	chromosome 12 open reading frame 57	NM_138425, hCT1967433.1	224719_s_at	NP_612434.1, EAW88705.1
GeneID:5777	PTPN6	12	7,055,740	7,070,479	14,739	+	8	1_A375_pNL7_minus_lncRNA::1::1371, 1_A375_pNL7_minus_lncRNA::1::1372, 1_A375_pNL7_minus_lncRNA::1::1373, 1_A375_pNL7_minus_lncRNA::1::1374, 2_A375_pNL97_plus_lncRNA::1::1925, 2_A375_pNL97_plus_lncRNA::1::1926, 2_A375_pNL97_plus_lncRNA::1::1927, 2_A375_pNL97_plus_lncRNA::1::1928	-8444, -1948, 14884, 24180, -8444, -2028, 14820, 23993	upstream, upstream, downstream, downstream, upstream, upstream, downstream, downstream	1	1	44	42.75	4	2_A375_pNL97_plus_lncRNA::1	111	Gene PTPN6	SHP-1L, SH-PTP1, SHP-1, HCPH, HCP, PTP-1C, SHP1, HPTP1C, PTPN6	protein tyrosine phosphatase, non-receptor type 6	NM_080548, NM_002831, NM_080549, hCT17069.3, hCT2286467.0, hCT2286469.0, hCT2286470.0, hCT2286471.0	206687_s_at	NP_536858.1, NP_002822.2, NP_536859.1, EAW88700.1, EAW88701.1, EAW88703.1, EAW88702.1, EAW88704.1
GeneID:100507644	LOC100507644	12	7,072,409	7,073,610	1,201	+	4	1_A375_pNL7_minus_lncRNA::1::1373, 1_A375_pNL7_minus_lncRNA::1::1374, 2_A375_pNL97_plus_lncRNA::1::1927, 2_A375_pNL97_plus_lncRNA::1::1928	-1765, 7511, -1849, 7324	upstream, downstream, upstream, downstream	1	1	23	20	2	1_A375_pNL7_minus_lncRNA::1	25	Gene LOC100507644		hypothetical LOC100507644	XR_111251, XR_109127, XR_114564		
GeneID:406985	MIR200C	12	7,072,862	7,072,929	67	+	4	1_A375_pNL7_minus_lncRNA::1::1373, 1_A375_pNL7_minus_lncRNA::1::1374, 2_A375_pNL97_plus_lncRNA::1::1927, 2_A375_pNL97_plus_lncRNA::1::1928	-2238, 7058, -2302, 6871	upstream, downstream, upstream, downstream	1	1	23	20	2	1_A375_pNL7_minus_lncRNA::1	25	Gene MIR200C	MIRN200C, MIR200C	microRNA 200c	NR_029779		
GeneID:406933	MIR141	12	7,073,260	7,073,354	94	+	4	1_A375_pNL7_minus_lncRNA::1::1373, 1_A375_pNL7_minus_lncRNA::1::1374, 2_A375_pNL97_plus_lncRNA::1::1927, 2_A375_pNL97_plus_lncRNA::1::1928	-2636, 6660, -2700, 6473	upstream, downstream, upstream, downstream	1	1	23	20	2	1_A375_pNL7_minus_lncRNA::1	25	Gene MIR141	MIRN141, MIR141	microRNA 141	NR_029682		
GeneID:11331	PHB2	12	7,074,515	7,079,916	5,401	-	4	1_A375_pNL7_minus_lncRNA::1::1373, 1_A375_pNL7_minus_lncRNA::1::1374, 2_A375_pNL97_plus_lncRNA::1::1927, 2_A375_pNL97_plus_lncRNA::1::1928	9292, -4, 9356, 183	downstream, upstream, downstream, in gene	1	1	23	20	2	1_A375_pNL7_minus_lncRNA::1	25	Gene PHB2	p22, REA, BAP, Bap37, BCAP37, PHB2, MGC117268, PNAS-141	prohibitin 2	NM_007273, NM_001144831, hCT17067.3	201600_at	NP_009204.1, NP_001138303.1, EAW88699.1
GeneID:677777	SCARNA12	12	7,076,500	7,076,769	269	-	4	1_A375_pNL7_minus_lncRNA::1::1373, 1_A375_pNL7_minus_lncRNA::1::1374, 2_A375_pNL97_plus_lncRNA::1::1927, 2_A375_pNL97_plus_lncRNA::1::1928	6145, -3151, 6209, -2964	downstream, upstream, downstream, upstream	1	1	23	20	2	1_A375_pNL7_minus_lncRNA::1	25	Gene SCARNA12	SCARNA12, U89	small Cajal body-specific RNA 12	NR_003010		
GeneID:10436	EMG1	12	7,079,944	7,085,165	5,221	+	4	1_A375_pNL7_minus_lncRNA::1::1373, 1_A375_pNL7_minus_lncRNA::1::1374, 2_A375_pNL97_plus_lncRNA::1::1927, 2_A375_pNL97_plus_lncRNA::1::1928	-9320, -24, -9384, -211	upstream, upstream, upstream, upstream	1	1	23	20	2	1_A375_pNL7_minus_lncRNA::1	25	Gene EMG1	EMG1, NEP1, FLJ60792, C2F, Grcc2f, BWCNS	EMG1 nucleolar protein homolog (S. cerevisiae)	NM_006331, hCT17084.4, hCT1967435.2, hCT2349157.0, hCT2349158.0, hCT2349159.0	209233_at	NP_006322.4, EAW88696.1, EAW88694.1, EAW88695.1, EAW88697.1, EAW88698.1
GeneID:10162	LPCAT3	12	7,085,347	7,125,842	40,495	-	2	1_A375_pNL7_minus_lncRNA::1::1374, 2_A375_pNL97_plus_lncRNA::1::1928	45922, 46109	downstream, downstream	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LPCAT3	LPLAT 5, MBOAT5, LPCAT, OACT5, nessy, LPCAT3, C3F, LPSAT	lysophosphatidylcholine acyltransferase 3	NM_005768, hCT17070.3, hCT1954387.1, hCT2286932.0	202793_at, 213615_at	NP_005759.4, EAW88692.1, EAW88691.1, EAW88693.1
GeneID:5830	PEX5	12	7,341,759	7,371,170	29,411	+	2	1_A375_pNL7_minus_lncRNA::1::1375, 2_A375_pNL97_plus_lncRNA::1::1929	353, 365	in gene, in gene	1	1	35	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene PEX5	FLJ50721, PTS1R, PEX5, FLJ50634, PXR1, FLJ51948, PTS1-BP	peroxisomal biogenesis factor 5	NM_000319, NM_001131023, NM_001131024, NM_001131025, NM_001131026, hCT1967432.1, hCT2288485.0, hCT2288486.0, hCT2288487.0, hCT2288488.0, hCT2288491.0	203244_at, 215481_s_at	NP_000310.2, NP_001124495.1, NP_001124496.1, NP_001124497.1, NP_001124498.1, EAW88675.1, EAW88670.1, EAW88671.1, EAW88672.1, EAW88673.1, EAW88674.1
GeneID:283316	CD163L1	12	7,507,556	7,596,749	89,193	-	1	2_A375_pNL97_plus_lncRNA::1::1930	74605	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CD163L1	CD163B, CD163L1, M160	CD163 molecule-like 1	NM_174941, hCT17074.2, hCT2357093.0	223655_at	NP_777601.2, EAW88667.1, EAW88668.1
GeneID:55810	FOXJ2	12	8,185,359	8,208,118	22,759	+	3	1_A375_pNL7_minus_lncRNA::1::1376, 2_A375_pNL97_plus_lncRNA::1::1932, 2_A375_pNL97_plus_lncRNA::1::1933	-5647, -5647, -303	upstream, upstream, upstream	1	1	18	28.5	2	2_A375_pNL97_plus_lncRNA::1	33	Gene FOXJ2	FOXJ2, FHX	forkhead box J2	NM_018416, hCT13317.2, hCT2292340.0	1555305_at, 203734_at	NP_060886.1, EAW88642.1, EAW88643.1
GeneID:25977	NECAP1	12	8,234,807	8,250,373	15,566	+	2	1_A375_pNL7_minus_lncRNA::1::1377, 2_A375_pNL97_plus_lncRNA::1::1934	-119, -119	upstream, upstream	1	1	24	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene NECAP1	NECAP1, DKFZP566B183, MGC131900	NECAP endocytosis associated 1	NM_015509, NR_024260, hCT13312.3, hCT1967352.1, hCT2292342.0, hCT2357105.0	209300_s_at	NP_056324.2, EAW88638.1, EAW88636.1, EAW88637.1, EAW88639.1
GeneID:1911	PHC1	12	9,067,316	9,094,063	26,747	+	3	1_A375_pNL7_minus_lncRNA::1::1378, 2_A375_pNL97_plus_lncRNA::1::1935, 2_A375_pNL97_plus_lncRNA::1::1936	35372, 23356, 35340	downstream, in gene, downstream	1	1	13	15.5	2	1_A375_pNL7_minus_lncRNA::1	21	Gene PHC1	HPH1, EDR1, PHC1, RAE28	polyhomeotic homolog 1 (Drosophila)	NM_004426, hCT2289395.1, hCT2289396.1	225958_at	NP_004417.2, EAW88600.1, EAW88601.1
GeneID:4074	M6PR	12	9,092,964	9,102,252	9,288	-	3	1_A375_pNL7_minus_lncRNA::1::1378, 2_A375_pNL97_plus_lncRNA::1::1935, 2_A375_pNL97_plus_lncRNA::1::1936	-436, 11580, -404	upstream, downstream, upstream	1	1	13	15.5	2	1_A375_pNL7_minus_lncRNA::1	21	Gene M6PR	CD-MPR, MPR46, FLJ32994, SMPR, M6PR	mannose-6-phosphate receptor (cation dependent)	NM_002355, hCT16338.4, hCT1961746.2, hCT1961747.2, hCT1961749.2	200900_s_at, 200901_s_at	NP_002346.1, EAW88598.1, EAW88596.1, EAW88597.1, EAW88599.1
GeneID:253128	C12orf33	12	9,208,185	9,217,666	9,481	-	1	1_A375_pNL7_minus_lncRNA::1::1379	674	in gene	1	0	19	11	1	1_A375_pNL7_minus_lncRNA::1	19	Gene C12orf33	FLJ41814, C12orf33, MGC40170	chromosome 12 open reading frame 33	NR_034140	1555040_at	
GeneID:144571	LOC144571	12	9,217,773	9,220,651	2,878	+	1	1_A375_pNL7_minus_lncRNA::1::1379	-781	upstream	1	0	19	11	1	1_A375_pNL7_minus_lncRNA::1	19	Gene LOC144571		hypothetical LOC144571	NR_026971	1564139_at	
GeneID:2	A2M	12	9,220,304	9,268,558	48,254	-	1	1_A375_pNL7_minus_lncRNA::1::1379	51566	downstream	1	0	19	11	1	1_A375_pNL7_minus_lncRNA::1	19	Gene A2M	DKFZp779B086, CPAMD5, S863-7, FWP007, A2M	alpha-2-macroglobulin	NM_000014, hCT16340.4	1558450_at, 217757_at	NP_000005.2, EAW88590.1
GeneID:55110	MAGOHB	12	10,756,794	10,766,183	9,389	-	2	1_A375_pNL7_minus_lncRNA::1::1381, 2_A375_pNL97_plus_lncRNA::1::1938	71, 39	in gene, in gene	1	1	23	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene MAGOHB	MGN2, magoh, MAGOHB, FLJ10292, mago	mago-nashi homolog B (Drosophila)	NM_018048, hCT1812470.2, hCT1950856.1, hCT2349784.0, hCT2349785.0	218894_s_at, 222776_at, 241806_at	NP_060518.1, EAW96198.1, EAW96196.1, EAW96197.1, EAW96199.1
GeneID:55359	STYK1	12	10,771,538	10,826,891	55,353	-	2	1_A375_pNL7_minus_lncRNA::1::1381, 2_A375_pNL97_plus_lncRNA::1::1938	60779, 60747	downstream, downstream	1	1	23	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene STYK1	DKFZp761P1010, STYK1, SuRTK106, NOK	serine/threonine/tyrosine kinase 1	NM_018423, hCT18559.1	220030_at, 221696_s_at	NP_060893.2, EAW96200.1
GeneID:8531	CSDA	12	10,851,676	10,875,953	24,277	-	2	1_A375_pNL7_minus_lncRNA::1::1382, 2_A375_pNL97_plus_lncRNA::1::1939	1073, 673	in gene, in gene	1	1	26	16	1	1_A375_pNL7_minus_lncRNA::1	26	Gene CSDA	CSDA, DBPA, ZONAB, CSDA1	cold shock domain protein A	NM_003651, NM_001145426, hCT1815415.1, hCT18561.3, hCT1950865.1, hCT2298187.0, hCT2298188.0	201160_s_at, 201161_s_at, 213319_s_at, 228634_s_at	NP_003642.3, NP_001138898.1, EAW96201.1, EAW96202.1, EAW96204.1, EAW96205.1, EAW96203.1
GeneID:100506226	LOC100506226	12	10,902,833	10,930,043	27,210	+	1	1_A375_pNL7_minus_lncRNA::1::1383	-161	upstream	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene LOC100506226		hypothetical LOC100506226	XR_111272, XR_111271, XR_109085, XR_109084, XR_114569, XR_114568		
GeneID:2120	ETV6	12	11,802,788	12,048,336	245,548	+	3	1_A375_pNL7_minus_lncRNA::1::1385, 2_A375_pNL97_plus_lncRNA::1::1941, 2_A375_pNL97_plus_lncRNA::1::1942	-868, -804, 70108	upstream, upstream, in gene	1	1	15	17.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene ETV6	TEL/ABL, TEL, ETV6	ets variant 6	NM_001987, hCT18464.3	205585_at, 225764_at, 235056_at, 239740_at	NP_001978.1, EAW96240.1
GeneID:4040	LRP6	12	12,268,959	12,419,811	150,852	-	2	1_A375_pNL7_minus_lncRNA::1::1387, 2_A375_pNL97_plus_lncRNA::1::1944	-221, -285	upstream, upstream	1	1	20	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LRP6	FLJ90421, LRP6, FLJ90062, ADCAD2	low density lipoprotein receptor-related protein 6	NM_002336, hCT17703.3	205606_at, 225745_at, 34697_at	NP_002327.2, EAW96253.1
GeneID:54682	MANSC1	12	12,482,218	12,503,169	20,951	-	1	1_A375_pNL7_minus_lncRNA::1::1388	-6879	upstream	1	0	26	18	1	1_A375_pNL7_minus_lncRNA::1	26	Gene MANSC1	MANSC1, 9130403P13Rik, LOH12CR3, FLJ10298	MANSC domain containing 1	NM_018050, hCT1643554.3, hCT1950843.1	220945_x_at	NP_060520.2, EAW96254.1, EAW96255.1
GeneID:503693	LOH12CR2	12	12,508,342	12,510,001	1,659	-	1	1_A375_pNL7_minus_lncRNA::1::1388	-47	upstream	1	0	26	18	1	1_A375_pNL7_minus_lncRNA::1	26	Gene LOH12CR2	LOH2CR12, LOH12CR2	loss of heterozygosity, 12, chromosomal region 2	NR_024061	236311_at	
GeneID:118426	LOH12CR1	12	12,510,020	12,619,838	109,818	+	2	1_A375_pNL7_minus_lncRNA::1::1388, 2_A375_pNL97_plus_lncRNA::1::1945	28, 41468	in gene, in gene	1	1	19	17.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene LOH12CR1	LOH1CR12, LOH12CR1	loss of heterozygosity, 12, chromosomal region 1	NM_058169, hCT18841.4, hCT1951414.2, hCT2349803.0, hCT2357936.0	227723_at	NP_477517.1, EAW96257.1, EAW96258.1, EAW96259.1, EAW96260.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:1389	CREBL2	12	12,764,831	12,798,041	33,210	+	1	1_A375_pNL7_minus_lncRNA::1::1389	-95	upstream	1	0	21	14	1	1_A375_pNL7_minus_lncRNA::1	21	Gene CREBL2	MGC117311, MGC138362, CREBL2	cAMP responsive element binding protein-like 2	NM_001310, hCT18833.3, hCT1951411.1, hCT2298173.0	201988_s_at, 201989_s_at, 201990_s_at	NP_001301.1, EAW96269.1, EAW96268.1, EAW96270.1
GeneID:2842	GPR19	12	12,813,995	12,849,121	35,126	-	2	1_A375_pNL7_minus_lncRNA::1::1390, 2_A375_pNL97_plus_lncRNA::1::1946	11457, 11281	in gene, in gene	1	1	21	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene GPR19	GPR19		NM_006143	207183_at	NP_006134.1
GeneID:1027	CDKN1B	12	12,870,302	12,875,305	5,003	+	5	1_A375_pNL7_minus_lncRNA::1::1391, 1_A375_pNL7_minus_lncRNA::1::1392, 1_A375_pNL7_minus_lncRNA::1::1393, 2_A375_pNL97_plus_lncRNA::1::1947, 2_A375_pNL97_plus_lncRNA::1::1948	2, 8034, 9378, -158, 8098	in gene, downstream, downstream, upstream, downstream	1	1	18	19	3	2_A375_pNL97_plus_lncRNA::1	24	Gene CDKN1B	KIP1, CDKN1B, CDKN4, MEN4, P27KIP1, MEN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	NM_004064, hCT18834.2, hCT1951412.1	209112_at	NP_004055.1, EAW96275.1, EAW96276.1
GeneID:81575	APOLD1	12	12,878,851	12,944,400	65,549	+	5	1_A375_pNL7_minus_lncRNA::1::1391, 1_A375_pNL7_minus_lncRNA::1::1392, 1_A375_pNL7_minus_lncRNA::1::1393, 2_A375_pNL97_plus_lncRNA::1::1947, 2_A375_pNL97_plus_lncRNA::1::1948	-8547, -515, 829, -8707, -451	upstream, upstream, in gene, upstream, upstream	1	1	18	19	3	2_A375_pNL97_plus_lncRNA::1	24	Gene APOLD1	DKFZp434F0318, FLJ25138, VERGE, APOLD1, FLJ95166	apolipoprotein L domain containing 1	NM_030817, NM_001130415	221031_s_at	NP_110444.3, NP_001123887.1
GeneID:9052	GPRC5A	12	13,043,956	13,066,600	22,644	+	3	1_A375_pNL7_minus_lncRNA::1::1394, 2_A375_pNL97_plus_lncRNA::1::1949, 2_A375_pNL97_plus_lncRNA::1::1950	76, -9332, 556	in gene, upstream, in gene	1	1	15	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene GPRC5A	RAI3, GPCR5A, GPRC5A, RAIG1	G protein-coupled receptor, family C, group 5, member A	NM_003979, hCT18835.3	203108_at	NP_003970.1, EAW96289.1
GeneID:57613	KIAA1467	12	13,197,315	13,236,383	39,068	+	2	1_A375_pNL7_minus_lncRNA::1::1395, 2_A375_pNL97_plus_lncRNA::1::1951	-99, 141	upstream, in gene	1	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene KIAA1467	DKFZp781O012, KIAA1467	KIAA1467	NM_020853, hCT19368.2	1559302_at, 213232_at, 213234_at	NP_065904.1, EAW96298.1
GeneID:83445	GSG1	12	13,237,042	13,256,619	19,577	-	1	2_A375_pNL97_plus_lncRNA::1::1952	1463	in gene	0	1	19	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene GSG1	MGC111023, GSG1, MGC3146	germ cell associated 1	NM_031289, NM_153823, NM_001080554, NM_001080555, hCT19369.3, hCT1951415.1, hCT2299029.0, hCT2357939.0, hCT2357940.0	221252_s_at, 241553_at	NP_112579.2, NP_722545.2, NP_001074023.1, NP_001074024.1, EAW96299.1, EAW96300.1, EAW96301.1, EAW96302.1, EAW96303.1
GeneID:2904	GRIN2B	12	13,714,410	14,133,022	418,612	-	2	1_A375_pNL7_minus_lncRNA::1::1396, 2_A375_pNL97_plus_lncRNA::1::1953	252094, 252446	in gene, in gene	1	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene GRIN2B	NR2B, MGC142178, NMDAR2B, GRIN2B, hNR3, MGC142180	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	NM_000834, hCT1951423.0	210411_s_at, 210412_at	NP_000825.2, EAW96311.1
GeneID:121504	HIST4H4	12	14,923,654	14,924,065	411	-	2	1_A375_pNL7_minus_lncRNA::1::1398, 2_A375_pNL97_plus_lncRNA::1::1955	161, 209	in gene, in gene	1	1	22	17	1	1_A375_pNL7_minus_lncRNA::1	22	Gene HIST4H4	HIST1H4D, HIST1H4H, HIST1H4E, HIST1H4B, HIST2H4A, HIST2H4B, HIST1H4A, HIST1H4L, HIST1H4J, H4/p, MGC24116, HIST1H4C, HIST4H4, HIST1H4I, HIST1H4F, HIST1H4K	histone cluster 4, H4	NM_175054		NP_778224.1
GeneID:55766	H2AFJ	12	14,927,270	14,930,936	3,666	+	2	1_A375_pNL7_minus_lncRNA::1::1398, 2_A375_pNL97_plus_lncRNA::1::1955	-3366, -3414	upstream, upstream	1	1	22	17	1	1_A375_pNL7_minus_lncRNA::1	22	Gene H2AFJ	FLJ52230, H2AJ, H2AFJ, MGC921, FLJ10903	H2A histone family, member J	NM_177925, NR_027716, hCT1639889.4, hCT2350491.0	220936_s_at, 224301_x_at, 225245_x_at, 226213_at	NP_808760.1, EAW96327.1, EAW96326.1
GeneID:2059	EPS8	12	15,773,075	15,942,510	169,435	-	4	2_A375_pNL97_plus_lncRNA::1::1957, 2_A375_pNL97_plus_lncRNA::1::1958, 2_A375_pNL97_plus_lncRNA::1::1959, 2_A375_pNL97_plus_lncRNA::1::1960	101086, 88142, 31518, -66	in gene, in gene, in gene, upstream	0	1	12.75	17.75	4	2_A375_pNL97_plus_lncRNA::1	20	Gene EPS8	EPS8	epidermal growth factor receptor pathway substrate 8	NM_004447, hCT1951425.2, hCT2357930.0	202609_at	NP_004438.3, EAW96354.1, EAW96355.1
GeneID:11171	STRAP	12	16,035,288	16,056,412	21,124	+	2	1_A375_pNL7_minus_lncRNA::1::1399, 2_A375_pNL97_plus_lncRNA::1::1961	-88, 328	upstream, in gene	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene STRAP	STRAP, PT-WD, MAWD, UNRIP	serine/threonine kinase receptor associated protein	NM_007178, hCT16290.3	1558002_at, 200870_at	NP_009109.3, EAW96356.1
GeneID:89869	PLCZ1	12	18,836,116	18,890,918	54,802	-	1	2_A375_pNL97_plus_lncRNA::1::1962	14054	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PLCZ1	PLCzeta, PLCZ1, MGC149885, NYD-SP27	phospholipase C, zeta 1	NM_033123, hCT15321.3, hCT1951397.1, hCT1971450.1	231425_at	NP_149114.2, EAW96389.1, EAW96388.1, EAW96390.1
GeneID:121536	AEBP2	12	19,592,608	19,675,173	82,565	+	1	2_A375_pNL97_plus_lncRNA::1::1963	224	in gene	0	1	7	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene AEBP2	AEBP2, MGC17922	AE binding protein 2	NM_153207, NM_001114176, hCT1951424.2, hCT2298434.1, hCT2344967.0	225889_at, 235184_at	NP_694939.2, NP_001107648.1, EAW96398.1, EAW96399.1, EAW96400.1
GeneID:6489	ST8SIA1	12	22,346,325	22,487,648	141,323	-	1	1_A375_pNL7_minus_lncRNA::1::1403	-1104	upstream	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ST8SIA1	SIAT8A, SIAT8, ST8SiaI, ST8SIA1, GD3S	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	NM_003034, hCT15906.3, hCT2298835.0, hCT2357914.0, hCT2357915.0	1569788_at, 210073_at	NP_003025.1, EAW96468.1, EAW96469.1, EAW96470.1, EAW96471.1
GeneID:9847	KIAA0528	12	22,601,517	22,697,452	95,935	-	2	1_A375_pNL7_minus_lncRNA::1::1404, 2_A375_pNL97_plus_lncRNA::1::1968	-20, -20	upstream, upstream	1	1	28	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene KIAA0528	DKFZp779N2044, KIAA0528	KIAA0528	NM_014802, hCT15907.2, hCT2298832.0, hCT2298833.0, hCT2357919.0	212943_at	NP_055617.1, EAW96474.1, EAW96473.1, EAW96475.1, EAW96476.1
GeneID:55500	ETNK1	12	22,778,076	22,843,608	65,532	+	1	2_A375_pNL97_plus_lncRNA::1::1969	196	in gene	0	1	15	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ETNK1	EKI1, Nbla10396, EKI, ETNK1, EKI 1	ethanolamine kinase 1	NM_018638, NM_001039481, hCT13824.3, hCT1967884.1, hCT2357934.0	219017_at, 222262_s_at, 224453_s_at, 224454_at, 225290_at, 226432_at, 231576_at	NP_061108.2, NP_001034570.1, EAW96478.1, EAW96479.1, EAW96480.1
GeneID:6660	SOX5	12	23,685,231	24,715,380	1,030,149	-	1	2_A375_pNL97_plus_lncRNA::1::1971	611508	in gene	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SOX5	L-SOX5, MGC35153, SOX5	SRY (sex determining region Y)-box 5	NM_178010, NM_006940, NM_152989, hCT1951385.2, hCT2298450.1, hCT2298451.1, hCT2349788.0, hCT2349789.0, hCT2349790.0, hCT2357933.0	1569638_at, 207336_at, 238285_at	NP_821078.1, NP_008871.3, NP_694534.1, EAW96486.1, EAW96488.1, EAW96491.1, EAW96487.1, EAW96489.1, EAW96490.1, EAW96492.1
GeneID:3845	KRAS	12	25,358,180	25,403,854	45,674	-	2	1_A375_pNL7_minus_lncRNA::1::1405, 2_A375_pNL97_plus_lncRNA::1::1973	-402, -466	upstream, upstream	1	1	22	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene KRAS	K-RAS4A, KRAS, C-K-RAS, KI-RAS, KRAS1, K-RAS4B, NS3, KRAS2, NS, K-RAS2B, RASK2, K-RAS2A	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	NM_004985, NM_033360, hCT1965959.1, hCT2300689.0, hCT2300691.0, hCT5752.3	1559203_s_at, 1559204_x_at, 204009_s_at, 204010_s_at, 214352_s_at	NP_004976.2, NP_203524.1, EAW96511.1, EAW96512.1, EAW96513.1, EAW96514.1
GeneID:160492	IFLTD1	12	25,629,016	25,801,488	172,472	-	1	2_A375_pNL97_plus_lncRNA::1::1975	181440	downstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene IFLTD1	IFLTD1, FLJ36004, Pas1c1	intermediate filament tail domain containing 1	NM_152590, NM_001145727, NM_001145728, NM_001145729, NR_027296, hCT1650229.4, hCT2349782.0, hCT2349783.0	1552865_a_at	NP_689803.2, NP_001139199.1, NP_001139200.1, NP_001139201.1, EAW96516.1, EAW96518.1, EAW96517.1
GeneID:11228	RASSF8	12	26,126,688	26,232,825	106,137	+	1	1_A375_pNL7_minus_lncRNA::1::1407	36704	in gene	1	0	18	9	1	1_A375_pNL7_minus_lncRNA::1	18	Gene RASSF8	RASSF8, DKFZp434O0227, FLJ11542, HOJ1, C12orf2	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	NM_007211, NM_001164746, NM_001164747, NM_001164748, hCT1951417.2, hCT2299045.1, hCT2299047.1, hCT29271.4	207754_at, 225946_at, 235996_at	NP_009142.2, NP_001158218.1, NP_001158219.1, NP_001158220.1, EAW96522.1, EAW96524.1, EAW96523.1, EAW96525.1
GeneID:100506529	LOC100506529	12	26,164,711	26,173,442	8,731	+	1	1_A375_pNL7_minus_lncRNA::1::1407	-1319	upstream	1	0	18	9	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100506529		hypothetical LOC100506529	XR_111265, XR_109094, XR_114579		
GeneID:79365	BHLHE41	12	26,272,959	26,278,003	5,044	-	1	2_A375_pNL97_plus_lncRNA::1::1976	-1517	upstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene BHLHE41	BHLHE41, SHARP1, BHLHB3, DEC2, SHARP-1	basic helix-loop-helix family, member e41	NM_030762, hCT2298786.0, hCT29273.3	221530_s_at, 223165_s_at, 231242_at, 231243_s_at	NP_110389.1, EAW96528.1, EAW96527.1
GeneID:3709	ITPR2	12	26,488,285	26,986,131	497,846	-	2	1_A375_pNL7_minus_lncRNA::1::1409, 2_A375_pNL97_plus_lncRNA::1::1979	141523, 579	in gene, in gene	1	1	17	16	2	1_A375_pNL7_minus_lncRNA::1	21	Gene ITPR2	ITPR2, IP3R2	inositol 1,4,5-triphosphate receptor, type 2	NM_002223, hCT2298779.1, hCT2298780.1	202660_at, 202661_at, 202662_s_at, 211360_s_at	NP_002214.2, EAW96534.1, EAW96535.1
GeneID:51768	TM7SF3	12	27,124,503	27,167,339	42,836	-	1	2_A375_pNL97_plus_lncRNA::1::1980	-8325	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TM7SF3	TM7SF3		NM_016551, hCT29587.3	1563598_at, 217974_at, 222477_s_at, 226478_at	NP_057635.1, EAW96542.1
GeneID:9412	MED21	12	27,175,463	27,182,662	7,199	+	1	2_A375_pNL97_plus_lncRNA::1::1980	161	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MED21	SRB7, MED21, SURB7	mediator complex subunit 21	NM_004264, hCT2298552.0, hCT2298553.0, hCT2298554.0, hCT2298555.0	209362_at, 209363_s_at	NP_004255.2, EAW96546.1, EAW96544.1, EAW96545.1, EAW96547.1
GeneID:23012	STK38L	12	27,397,078	27,478,892	81,814	+	2	2_A375_pNL97_plus_lncRNA::1::1981, 2_A375_pNL97_plus_lncRNA::1::1982	-54, 634	upstream, in gene	0	1	9	21.5	2	2_A375_pNL97_plus_lncRNA::1	26	Gene STK38L	NDR2, KIAA0965, STK38L	serine/threonine kinase 38 like	NM_015000, hCT2299822.0, hCT2357943.0, hCT30012.2	212565_at, 212572_at	NP_055815.1, EAW96551.1, EAW96549.1, EAW96550.1
GeneID:60488	MRPS35	12	27,863,706	27,909,237	45,531	+	2	1_A375_pNL7_minus_lncRNA::1::1410, 2_A375_pNL97_plus_lncRNA::1::1983	102, 102	in gene, in gene	1	1	28	25	1	1_A375_pNL7_minus_lncRNA::1	28	Gene MRPS35	MDS023, MRPS35, MRPS28, MGC104278, MRP-S28, HDCMD11P, DKFZp762P093	mitochondrial ribosomal protein S35	NM_001190864, NM_021821, hCT2357942.0, hCT30011.3	217942_at	NP_001177793.1, NP_068593.2, EAW96567.1, EAW96568.1
GeneID:83857	TMTC1	12	29,653,746	29,937,692	283,946	-	4	1_A375_pNL7_minus_lncRNA::1::1412, 1_A375_pNL7_minus_lncRNA::1::1413, 2_A375_pNL97_plus_lncRNA::1::1988, 2_A375_pNL97_plus_lncRNA::1::1989	143580, 43036, 143708, 43004	in gene, in gene, in gene, in gene	1	1	18	21	2	2_A375_pNL97_plus_lncRNA::1	21	Gene TMTC1	FLJ41625, ARG99, OLF, TMTC1A, TMTC1, FLJ31400	transmembrane and tetratricopeptide repeat containing 1	NM_001193451, NM_175861	224397_s_at, 226322_at, 226931_at, 244506_at	NP_001180380.1, NP_787057.2
GeneID:100287314	LOC100287314	12	30,947,977	30,955,645	7,668	+	2	2_A375_pNL97_plus_lncRNA::1::1990, 2_A375_pNL97_plus_lncRNA::1::1991	631, 2023	in gene, in gene	0	1	12.5	19	2	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100287314		hypothetical LOC100287314	XR_111267, XR_109096, XR_114581		
GeneID:441631	TSPAN11	12	31,079,838	31,149,537	69,699	+	1	2_A375_pNL97_plus_lncRNA::1::1992	226	in gene	0	1	10	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TSPAN11	TSPAN11, VSSW1971	tetraspanin 11	NM_001080509	227610_at	NP_001073978.1
GeneID:58516	FAM60A	12	31,433,518	31,479,159	45,641	-	3	1_A375_pNL7_minus_lncRNA::1::1415, 2_A375_pNL97_plus_lncRNA::1::1993, 2_A375_pNL97_plus_lncRNA::1::1994	1159, 1159, 135	in gene, in gene, in gene	1	1	13.5	15.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene FAM60A	L4, FAM60A, C12orf14, TERA	family with sequence similarity 60, member A	NM_021238, NM_001135811, NM_001135812, hCT2289014.0, hCT2289016.0, hCT2289017.0, hCT2289018.0, hCT2289020.0, hCT2289022.0, hCT2289023.0	220147_s_at	NP_067061.1, NP_001129283.1, NP_001129284.1, EAW88561.1, EAW88562.1, EAW88567.1, EAW88563.1, EAW88564.1, EAW88565.1, EAW88566.1
GeneID:79857	FLJ13224	12	31,477,250	31,478,879	1,629	+	3	1_A375_pNL7_minus_lncRNA::1::1415, 2_A375_pNL97_plus_lncRNA::1::1993, 2_A375_pNL97_plus_lncRNA::1::1994	750, 750, 1774	in gene, in gene, downstream	1	1	13.5	15.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene FLJ13224		hypothetical LOC79857	NR_026806	220211_at	
GeneID:254013	C12orf72	12	31,800,094	31,822,016	21,922	+	2	1_A375_pNL7_minus_lncRNA::1::1416, 2_A375_pNL97_plus_lncRNA::1::1995	12098, 12194	in gene, in gene	1	1	50	51	1	2_A375_pNL97_plus_lncRNA::1	51	Gene C12orf72	C12orf72, METTL20, MGC50559	chromosome 12 open reading frame 72	NM_173802, NM_001135863, NM_001135864, hCT2349176.0, hCT2349177.0, hCT2349178.0, hCT30426.4	1554582_a_at, 1554583_a_at, 1563474_at, 1563475_s_at, 1569792_a_at	NP_776163.1, NP_001129335.1, NP_001129336.1, EAW88545.1, EAW88546.1, EAW88547.1, EAW88548.1
GeneID:196394	AMN1	12	31,824,071	31,882,108	58,037	-	1	2_A375_pNL97_plus_lncRNA::1::1996	124	in gene	0	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene AMN1	AMN1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	NM_001113402, NR_004854, hCT1950877.2, hCT2357117.0	226258_at	NP_001106873.1, EAW88544.1, EAW88543.1
GeneID:55196	C12orf35	12	32,112,353	32,146,041	33,688	+	2	1_A375_pNL7_minus_lncRNA::1::1418, 2_A375_pNL97_plus_lncRNA::1::1997	-113, -97	upstream, upstream	1	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene C12orf35	FLJ20696, C12orf35, FLJ10652	chromosome 12 open reading frame 35	NM_018169, hCT1950844.1, hCT1950845.1	218614_at, 227152_at	NP_060639.3, EAW88538.1, EAW88537.1
GeneID:636	BICD1	12	32,260,185	32,531,141	270,956	+	2	1_A375_pNL7_minus_lncRNA::1::1420, 2_A375_pNL97_plus_lncRNA::1::2000	-345, -25	upstream, upstream	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene BICD1	BICD, BICD1	bicaudal D homolog 1 (Drosophila)	NM_001714, NM_001003398, hCT2284941.0, hCT2284944.0, hCT31230.2	1554020_at, 1556051_a_at, 204741_at, 214806_at, 226691_at	NP_001705.2, NP_001003398.1, EAW88532.1, EAW88533.1, EAW88534.1
GeneID:10059	DNM1L	12	32,832,137	32,898,584	66,447	+	3	1_A375_pNL7_minus_lncRNA::1::1421, 1_A375_pNL7_minus_lncRNA::1::1422, 2_A375_pNL97_plus_lncRNA::1::2002	-41, 76639, 2	upstream, downstream, in gene	1	1	20	17	2	1_A375_pNL7_minus_lncRNA::1	21	Gene DNM1L	DNM1L, FLJ41912, DYMPLE, DVLP, DRP1, DYNIV-11, HDYNIV, DLP1, VPS1	dynamin 1-like	NM_012062, NM_012063, NM_005690, hCT1950884.2, hCT1950885.2, hCT1950886.2, hCT2284632.0, hCT2284634.0, hCT2284635.0, hCT2284636.0, hCT2284637.0, hCT2284638.0	203105_s_at, 226154_at, 237797_at	NP_036192.2, NP_036193.2, NP_005681.2, EAW88523.1, EAW88525.1, EAW88526.1, EAW88519.1, EAW88520.1, EAW88521.1, EAW88522.1, EAW88524.1, EAW88527.1
GeneID:51067	YARS2	12	32,899,459	32,908,874	9,415	-	1	1_A375_pNL7_minus_lncRNA::1::1422	-102	upstream	1	0	21	14	1	1_A375_pNL7_minus_lncRNA::1	21	Gene YARS2	CGI-04, mt-TyrRS, MLASA2, YARS2, MT-TYRRS, FLJ13995, TYRRS	tyrosyl-tRNA synthetase 2, mitochondrial	NM_001040436, hCT2284347.0, hCT2284348.0	218470_at	NP_001035526.1, EAW88517.1, EAW88518.1
GeneID:84920	ALG10	12	34,175,216	34,181,237	6,021	+	1	2_A375_pNL97_plus_lncRNA::1::2003	144	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ALG10	ALG10, KCR1, FLJ14751, DIE2	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog (S. pombe)	NM_032834, hCT1826583.2	1552304_at, 1552306_at	NP_116223.3, EAW88508.1
GeneID:144245	ALG10B	12	38,710,557	38,723,528	12,971	+	2	1_A375_pNL7_minus_lncRNA::1::1423, 2_A375_pNL97_plus_lncRNA::1::2004	-77, -61	upstream, upstream	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ALG10B	ALG10, KCR1, ALG10B	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog B (yeast)	NM_001013620, hCT1766333.1		NP_001013642.1, EAW57795.1
GeneID:144402	CPNE8	12	39,046,002	39,299,420	253,418	-	2	1_A375_pNL7_minus_lncRNA::1::1425, 2_A375_pNL97_plus_lncRNA::1::2006	-276, -356	upstream, upstream	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CPNE8	MGC129645, CPNE8, MGC129646	copine VIII	NM_153634, hCT2353256.0, hCT29499.2	228365_at, 241706_at, 243727_at	NP_705898.1, EAW57799.1, EAW57798.1
GeneID:55605	KIF21A	12	39,687,030	39,837,192	150,162	-	1	2_A375_pNL97_plus_lncRNA::1::2007	200	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene KIF21A	KIF21A, CFEOM, FEOM1, KIAA1708, CFEOM3B, CFEOM1, FEOM3A, DKFZp779C159, FLJ20052, FEOM	kinesin family member 21A	NM_001173463, NM_001173464, NM_001173465, NM_017641, hCT1950723.1, hCT2279134.0, hCT2279136.0, hCT2279137.0, hCT30434.3	226003_at, 231875_at	NP_001166934.1, NP_001166935.1, NP_060111.2, NP_001166936.1, EAW57803.1, EAW57805.1, EAW57802.1, EAW57804.1, EAW57806.1
GeneID:114134	SLC2A13	12	40,148,823	40,499,661	350,838	-	1	2_A375_pNL97_plus_lncRNA::1::2008	88717	in gene	0	1	12	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SLC2A13	HMIT, MGC48624, SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	NM_052885, hCT29500.3	1552694_at, 1552695_a_at, 227176_at, 234268_at, 234561_at	NP_443117.3, EAW57811.1
GeneID:283464	GXYLT1	12	42,475,647	42,538,673	63,026	-	1	2_A375_pNL97_plus_lncRNA::1::2009	241	in gene	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene GXYLT1	GLT8D3, GXYLT1, FLJ43151	glucoside xylosyltransferase 1	NM_001099650, NM_173601	226868_at, 232021_at	NP_001093120.1, NP_775872.1
GeneID:10138	YAF2	12	42,550,906	42,632,154	81,248	-	1	1_A375_pNL7_minus_lncRNA::1::1426	890	in gene	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene YAF2	MGC41856, DKFZp779H1820, YAF2	YY1 associated factor 2	NM_001190977, NM_001190979, NM_001190980, NM_005748, NR_034000, hCT2279386.2, hCT2279387.2, hCT2345213.1, hCT2349845.0, hCT2349846.0, hCT2353290.0, hCT2353291.0	206238_s_at, 244783_at	NP_001177906.1, NP_001177908.1, NP_005739.2, NP_001177909.1, EAW57834.1, EAW57839.1, EAW57835.1, EAW57836.1, EAW57837.1, EAW57838.1, EAW57840.1
GeneID:144165	PRICKLE1	12	42,852,140	42,983,572	131,432	-	2	1_A375_pNL7_minus_lncRNA::1::1427, 2_A375_pNL97_plus_lncRNA::1::2010	468, 596	in gene, in gene	1	1	30	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene PRICKLE1	EPM1B, RILP, FLJ31937, PRICKLE1, MGC138903, FLJ31627, MGC138902	prickle homolog 1 (Drosophila)	NM_153026, NM_001144881, NM_001144882, NM_001144883, hCT2353294.0, hCT30697.3	226065_at, 226069_at, 230708_at, 232811_x_at	NP_694571.2, NP_001138353.1, NP_001138354.1, NP_001138355.1, EAW57854.1, EAW57855.1
GeneID:83448	PUS7L	12	44,122,410	44,152,596	30,186	-	1	2_A375_pNL97_plus_lncRNA::1::2012	-44	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PUS7L	DKFZp434G1415, PUS7L, FLJ40012, DKFZp781B2386, FLJ34711	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	NM_001098614, NM_031292, NM_001098615, hCT30749.3	221025_x_at, 229751_s_at	NP_001092084.1, NP_112582.3, NP_001092085.1, EAW57866.1
GeneID:51135	IRAK4	12	44,152,747	44,183,346	30,599	+	1	2_A375_pNL97_plus_lncRNA::1::2012	-107	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene IRAK4	IRAK4, NY-REN-64, IPD1, REN64	interleukin-1 receptor-associated kinase 4	NM_001114182, NM_016123, NM_001145256, NM_001145257, NM_001145258, hCT30745.3	219618_at	NP_001107654.1, NP_057207.2, NP_001138728.1, NP_001138729.1, NP_001138730.1, EAW57867.1
GeneID:84216	TMEM117	12	44,229,962	44,783,541	553,579	+	1	2_A375_pNL97_plus_lncRNA::1::2013	133910	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TMEM117	DKFZp434K2435, TMEM117	transmembrane protein 117	NM_032256, hCT2279098.0, hCT2279100.0	223594_at	NP_115632.1, EAW57871.1, EAW57872.1
GeneID:4753	NELL2	12	44,902,058	45,307,711	405,653	-	1	2_A375_pNL97_plus_lncRNA::1::2014	37151	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene NELL2	NELL2, NRP2	NEL-like 2 (chicken)	NM_006159, NM_001145107, NM_001145108, NM_001145109, NM_001145110, hCT1967266.0, hCT2353304.0, hCT29542.3	203413_at	NP_006150.1, NP_001138579.1, NP_001138580.1, NP_001138581.1, NP_001138582.1, EAW57873.1, EAW57874.1, EAW57875.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervals	Intervals	Intervals Count	Intervals Pos.	[A]	[R]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:31054	FLEKHA8	12	48,399,647	48,609,769	42,962	+	3	1_A375_shN7_shrus_lncRNA:1:1429,1_A375_shN7_shrus_lncRNA:1:1430,1_A375_shN37_gfus_lncRNA:1:3035	561,-643,61	up gene, upstream, us gene	1	1	21	12.5	2	1_A375_shN7_shrus_lncRNA:1	26	Gene FLEKHA8	FLEKHA8, FLJ14196, FLEKHA8P1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	NM_019099, XCT1937982.1, XCT1962533.1, XCT.3116.3	235197_x_at	NP_0998531, EAW87678.1, EAW87678.1, EAW87680.1
Gene:ID:95527	ANO6	12	48,609,770	48,634,187	224,417	+	6	1_A375_shN7_shrus_lncRNA:1:1429,1_A375_shN7_shrus_lncRNA:1:1430,1_A375_shN7_shrus_lncRNA:1:1431,2_A375_shN37_gfus_lncRNA:1:3035,2_A375_shN37_gfus_lncRNA:1:3036,2_A375_shN37_gfus_lncRNA:1:3037	-42,662,199522,-42,199374,222390	upstream, us gene, us gene, upstream, us gene, us gene	1	1	22.29	18.75	4	1_A375_shN7_shrus_lncRNA:1	36	Gene ANO6	ANO6, MGC102731, TMEM16F	anoctamin 6	NM_001025356, NM_001142676, NM_001142676, NM_001142650	238606_at, 240947_at	NP_001026527.2, NP_001136150.1, NP_001136151.1, NP_001136152.1
Gene:ID:9169	SPRED2IP	12	48,612,814	48,664,601	71,487	-	4	1_A375_shN7_shrus_lncRNA:1:1433,1_A375_shN7_shrus_lncRNA:1:1434,2_A375_shN37_gfus_lncRNA:1:3026,2_A375_shN37_gfus_lncRNA:1:3027	-143,-1293,509573,-175	upstream, upstream, us gene, upstream	1	1	20.33	17.33	3	1_A375_shN7_shrus_lncRNA:1	27	Gene SPRED2IP	SPRY129, CASP11, SCAP11, SPSP2IP, SPRED2IP, SPRED2IP	SPR-related CTD-associated factor 11	NM_058719, XCT2293747.0, XCT.3352359, XCT.39443.3	206909_s_at, 206379_x_at, 210590_s_at, 235390_at, 232597_x_at, 235379_at	NP_0047192.2, EAW87692.1, EAW87692.1, EAW87694.1
Gene:ID:1539	SLC35A1	12	48,976,838	49,663,208	66,370	-	1	2_A375_shN37_gfus_lncRNA:1:3022	616	up gene	0	1	18	23	1	2_A375_shN37_gfus_lncRNA:1	23	Gene SLC35A1	SAT1, NAT2, SNAT1, ATA1, SLC35A1	solute carrier family 35, member 1	NM_030972, NM_001077654, XCT.2387485.1, XCT.2387396.1, XCT.2392560.0, XCT.2552269.0, XCT.39763.3	218277_s_at, 226579_at, 236560_at, 236557_at	NP_109993.3, NP_001076653.1, EAW87689.1, EAW87686.1, EAW87687.1, EAW87686.1, EAW87699.1
Gene:ID:4407	SLC35A2	12	48,751,971	49,799,645	14,674	-	1	2_A375_shN37_gfus_lncRNA:1:3023	149	up gene	0	1	9	15	1	2_A375_shN37_gfus_lncRNA:1:3023	15	Gene SLC35A2	KIAA1352, ATA2, SAT2, SLC35A2, SNAT2, PRO1066	solute carrier family 35, member 2	NM_005660, XCT.1950270.1, XCT.2387422.0, XCT.39761.3	210581_s_at, 229424_s_at, 229552_x_at	NP_0056492, EAW87900.1, EAW87901.1, EAW87902.1
Gene:ID:6026878	LOC100276816	12	48,761,830	47,266,854	467,224	+	3	1_A375_shN7_shrus_lncRNA:1:1429,1_A375_shN7_shrus_lncRNA:1:1430,2_A375_shN37_gfus_lncRNA:1:3026,2_A375_shN37_gfus_lncRNA:1:3027,2_A375_shN37_gfus_lncRNA:1:3028	-3896,162190,-3634,135932,162130	upstream, us gene, upstream, us gene, us gene	1	1	19	23.33	3	1_A375_shN7_shrus_lncRNA:1	28	Gene LOC100276816		hypothetical LOC100276816	XR_111276, XR_110373, XR_114557		
Gene:ID:260	COL2A1	12	48,366,748	48,399,283	31,327	-	1	2_A375_shN37_gfus_lncRNA:1:3029	40877	up gene	0	1	10	25	1	2_A375_shN37_gfus_lncRNA:1:3029	25	Gene COL2A1	ACH4, SEDC, ANFH, COL2A1, COLL11A2, OSMED	collagen, type II, alpha 1	NM_033150, NM_001844, XCT.1864E3.2, XCT.1962553.1, XCT.2521252.0, XCT.2521513.0, XCT.2521515.0	213292_at, 217404_s_at	NP_1489162.2, NP_0011638.2, EAW87666.1, EAW87667.1, EAW87669.1, EAW87670.1, EAW87666.1
Gene:ID:213	SENP1	12	48,436,737	48,499,641	62,864	-	1	2_A375_shN37_gfus_lncRNA:1:3030	455	up gene	0	1	19	19	1	2_A375_shN37_gfus_lncRNA:1:3030	19	Gene SENP1	SuPr-2, SENP1	SUMO/sentrin specific peptidase 1	NM_014554, XCT.1907258.1, XCT.2392147.0	1552012_s_at, 236619_at	NP_0135599.1, EAW87671.1, EAW87672.1
Gene:ID:213	PPKAR	12	48,499,696	48,540,187	40,531	+	1	2_A375_shN37_gfus_lncRNA:1:3030	440	up gene	0	1	19	19	1	2_A375_shN37_gfus_lncRNA:1:3030	19	Gene PPKAR	PPK1, PPK1, PPKA, PPKAR, PPK-1, MGC99998, CSD7	phosphotidylkinase, mutate	NM_001199556, NM_002959, NM_001199557, NM_001199555, XCT.2385559.0, XCT.2385557.0, XCT.2385558.0	210976_s_at	NP_0011991561, NP_0029501, NP_0011991591, NP_0011991601, EAW87673.1, EAW87674.1, EAW87678.1
Gene:ID:9169	DKFZP779L1653	12	48,502,146	48,593,814	3,666	+	1	2_A375_shN37_gfus_lncRNA:1:3031	370	upstream	0	1	13	16	1	2_A375_shN37_gfus_lncRNA:1:3031	16	Gene DKFZP779L1653	FLJ40937	hypothetical LOC643762	XR_111277, XR_110335, XR_114558		
Gene:ID:41275	OR10A5	12	48,595,122	48,597,075	953	-	1	2_A375_shN37_gfus_lncRNA:1:3032	6299	downstream	0	1	13	16	1	2_A375_shN37_gfus_lncRNA:1:3032	16	Gene OR10A5	OR10AD1P, OR12-1, OR10AD1	olfactory receptor, family 10, subfamily AD, member 1	NM_001004134, XCT.1613363.3		NP_0010041341, EAW87678.1
Gene:ID:9434	C12orf41	12	48,649,994	49,076,035	29,041	-	2	2_A375_shN37_gfus_lncRNA:1:3027,2_A375_shN37_gfus_lncRNA:1:3028	131, 99	up gene, us gene	1	1	16	19	1	2_A375_shN37_gfus_lncRNA:1:3027	19	Gene C12orf41	FLJ20436, FLJ12670, C12orf41	chromosome 12 open reading frame 41	NM_017622, XCT.1810999.2, XCT.1985499.0, XCT.1985500.0, XCT.2321777.0, XCT.2521716.0, XCT.2521950.0	221821_s_at	NP_0602923.2, EAW87686.1, EAW87691.1, EAW87693.1, EAW87694.1, EAW87696.1, EAW87692.1
Gene:ID:44435	LOC144638	12	48,662,288	49,096,229	3,956	-	2	2_A375_shN37_gfus_lncRNA:1:3027,2_A375_shN37_gfus_lncRNA:1:3028	10525, 10293	downstream, downstream	1	1	16	19	1	2_A375_shN37_gfus_lncRNA:1:3027	19	Gene LOC144638		hypothetical LOC144638	NR_024268	235693_at	
Gene:ID:94	CCNT1	12	48,699,752	49,110,761	24,029	-	1	2_A375_shN37_gfus_lncRNA:1:3028	173	up gene	0	1	16	19	1	2_A375_shN37_gfus_lncRNA:1:3028	19	Gene CCNT1	HIV81, CYCT1, CCNT, CCNT1	cyclin T1	NM_001240, XCT.1810141822.2	209807_at	NP_0012312, EAW87696.1
Gene:ID:54411	LOC26541	12	48,721,216	49,159,569	55,281	+	1	2_A375_shN37_gfus_lncRNA:1:3028	10610	upstream	0	1	16	19	1	2_A375_shN37_gfus_lncRNA:1:3028	19	Gene LOC26541	FLJ27495	hypothetical LOC26541	NR_026445, NR_029449	1565619_at	
Gene:ID:416	DDX23	12	48,723,539	49,249,897	22,416	-	2	2_A375_shN37_gfus_lncRNA:1:3027,2_A375_shN37_gfus_lncRNA:1:3028	443, -107	upstream, us gene	1	1	19	25	1	2_A375_shN37_gfus_lncRNA:1:3027	25	Gene DDX23	PRP28, DDX23, U5-100KD, MGC5416, prp28, U5-100KD	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	NM_004818, XCT.17699.2, XCT.2321683.1, XCT.2321684.1, XCT.2392369.0, XCT.2392369.0, XCT.2392370.0, XCT.2552370.0, XCT.2552372.0	201440_at, 40469_at	NP_0048092.2, EAW85013.1, EAW85010.1, EAW85012.1, EAW85017.1, EAW85014.1, EAW85016.1, EAW85018.1
Gene:ID:7288	RND1	12	48,760,916	49,299,653	8,737	-	2	2_A375_shN37_gfus_lncRNA:1:1435,2_A375_shN37_gfus_lncRNA:1:3034	12653, 12559	downstream, downstream	1	1	23	25	1	2_A375_shN37_gfus_lncRNA:1:3034	25	Gene RND1	RHO6, ARH8, RHO6, RND1, FLJ42264	Rho family GTPase 1	NM_014470, XCT.2282164.0	210096_at	NP_0052651, EAW85019.1
Gene:ID:5476	CCDC65	12	48,797,693	49,215,359	17,666	+	2	2_A375_shN37_gfus_lncRNA:1:1429,2_A375_shN37_gfus_lncRNA:1:3028	-492, 27	upstream, us gene	1	1	22	23	1	2_A375_shN37_gfus_lncRNA:1:3028	23	Gene CCDC65	FLJ35663, NY-SP28, FLJ33732, CCDC65	coiled-coil domain containing 65	NM_033124, XCT.1603228.1, XCT.2288111.3	1552330_a_at, 1552321_s_at, 1561623_at	NP_1491152, EAW85020.1, EAW85021.1
Gene:ID:77	ARF3	12	48,329,662	49,351,252	21,260	-	2	2_A375_shN37_gfus_lncRNA:1:1440,2_A375_shN37_gfus_lncRNA:1:3029	26, -44	upstream, us gene	1	1	21	22	1	2_A375_shN37_gfus_lncRNA:1:3029	22	Gene ARF3	ARF3	ADP-ribosylation factor 3	NM_001659, XCT.1962255.1, XCT.2392264.0, XCT.2516845.2	200011_s_at, 200734_s_at, 211625_s_at	NP_001650.1, EAW85027.1, EAW85025.1, EAW85026.1
Gene:ID:480	WNT10B	12	48,339,123	49,363,641	6,518	-	2	2_A375_shN37_gfus_lncRNA:1:1440,2_A375_shN37_gfus_lncRNA:1:3029	18428, 14349	downstream, downstream	1	1	21	22	1	2_A375_shN37_gfus_lncRNA:1:3029	22	Gene WNT10B	WNT-12, SHFM6, WNT10B	wingless-type MMTV integration site family, member 10B	NM_003394, XCT.2282196.0, XCT.32764.2	206213_at	NP_0033853.2, EAW85029.1, EAW85028.1
Gene:ID:4297	MLL2	12	49,012,758	49,099,107	36,389	-	2	2_A375_shN37_gfus_lncRNA:1:1441,2_A375_shN37_gfus_lncRNA:1:3029	-5581, 5613	upstream, upstream	1	1	27	35	1	1_A375_shN7_shrus_lncRNA:1	37	Gene MLL2	KMT2D, KMS, MLL2, CAGL114, ALR, TNRC21, MLL2, AAD10, KMT2B	myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482, XCT.2300482.0, XCT.2300483.0, XCT.2300484.0, XCT.32763.3	217191_s_at, 227527_at, 227526_s_at, 231674_at	NP_0034733.2, EAW85033.1, EAW85034.1, EAW85036.1
Gene:ID:21266	RHEBL1	12	49,056,868	49,063,775	6,307	+	2	2_A375_shN37_gfus_lncRNA:1:1441,2_A375_shN37_gfus_lncRNA:1:3029	6087, 6053	downstream, downstream	1	1	27	35	1	1_A375_shN7_shrus_lncRNA:1	37	Gene RHEBL1	FLJ35797, RHEBL1, MGC34699, RHEBL1c	Ras homolog enriched in brain like 1	NM_145563, XCT.2353282.0, XCT.32776.2	1553713_s_at, 1570253_at	NP_6539481, EAW85037.1, EAW85038.1
Gene:ID:4646	DHH	12	49,063,264	49,065,662	8,398	-	1	2_A375_shN37_gfus_lncRNA:1:3029	3815	upstream	0	1	9	20	1	2_A375_shN37_gfus_lncRNA:1:3029	20	Gene DHH	DHH, MGC39145, HHG-2	desert hedgehog homolog (Drosophila)	NM_021044, XCT.32771.4	1552730_at	NP_0953421, EAW85039.1
Gene:ID:3716	LMBR1L	12	49,490,922	49,504,660	13,758	-	2	2_A375_shN37_gfus_lncRNA:1:2038,2_A375_shN37_gfus_lncRNA:1:2039	18699, 6	downstream, us gene	1	1	12	19	2	2_A375_shN37_gfus_lncRNA:1:2038	20	Gene LMBR1L	FLJ39231, LMBR1L, NAA1174, LMR, FLJ14494	limb region 1 homolog (chicken)-like	NM_018112, XCT.2300463.0, XCT.2300464.0, XCT.2300465.0, XCT.2300466.0, XCT.2300467.0, XCT.2300468.0, XCT.2552266.0, XCT.2552267.0	220039_s_at	NP_0603612.2, EAW85040.1, EAW85041.1, EAW85044.1, EAW85046.1, EAW85047.1, EAW85042.1, EAW85043.1
Gene:ID:6026836	LOC100276816	12	49,514,197	49,527,171	13,014	+	2	2_A375_shN37_gfus_lncRNA:1:1442,2_A375_shN37_gfus_lncRNA:1:3029	10053, 9853	up gene, downstream	1	1	18.5	15	2	2_A375_shN37_gfus_lncRNA:1:3029	16	Gene LOC100276816		hypothetical LOC100276816	XR_111283, XR_111280, XR_110343, XR_110342, XR_110341, XR_114591		
Gene:ID:3376	TUBA1B	12	49,521,563	49,525,304	3,738	-	1	2_A375_shN37_gfus_lncRNA:1:1442	1148	up gene	1	0	16	12	1	1_A375_shN7_shrus_lncRNA:1	16	Gene TUBA1B	K-ALPHA-1, TUBA1B	tubulin, alpha 1b	NM_006082, XCT.2300465.1, XCT.2300462.3	1565665_at, 201090_x_at, 211056_x_at, 211072_x_at, 212624_x_at, 213480_x_at	NP_0060732, EAW85048.1, EAW85049.1
Gene:ID:6026396	LOC100276816	12	49,529,973	49,656,539	31,986	-	2	2_A375_shN37_gfus_lncRNA:1:1442,2_A375_shN37_gfus_lncRNA:1:1443,2_A375_shN37_gfus_lncRNA:1:3029	10157, -993, -998	up gene, upstream, upstream	1	1	16.5	16.5	2	1_A375_shN7_shrus_lncRNA:1	20	Gene LOC100276816		hypothetical LOC100283962	XR_111287, XR_110349, XR_114597		
Gene:ID:4740	TUBA1C	12	49,656,893	49,667,113	6,248	-	2	2_A375_shN37_gfus_lncRNA:1:1443,2_A375_shN37_gfus_lncRNA:1:3029	387, 479	up gene, us gene	1	1	17	19	1	2_A375_shN37_gfus_lncRNA:1:3029	19	Gene TUBA1C	MGC10551, MGC14580, TUBA1C, bm498, TUBA6	tubulin, alpha 1c	NM_032704, XCT.1810141772.2	209251_s_at, 211700_s_at	NP_1160731, EAW85037.1
Gene:ID:9224	TROAP	12	49,716,971	49,725,514	8,543	+	1	2_A375_shN37_gfus_lncRNA:1:3031	133	up gene	0	1	12	17	1	2_A375_shN37_gfus_lncRNA:1:3031	17	Gene TROAP	TROAP, TASTIN	trophinin associated protein (tastin)	NM_005480, NM_001100620, XCT.2300484.1, XCT.2385215.0, XCT.32773.2	1565590_at, 204569_at	NP_0054712, NP_0010006901, EAW85062.1, EAW85063.1, EAW85064.1
Gene:ID:35781	C1QL4	12	49,726,200	49,730,971	4,771	-	2	2_A375_shN37_gfus_lncRNA:1:3041,2_A375_shN37_gfus_lncRNA:1:3042	13997, 13853	downstream, downstream	0	1	13	16	2	2_A375_shN37_gfus_lncRNA:1:3042	19	Gene C1QL4	C1QL4, C1QTNF11, MGC131705	complement component 1, q subcomponent like 4	NM_001005223, XCT.32965.2		NP_0010052241, EAW85065.1
Gene:ID:9892	DNAJC22	12	48,741,041	49,749,697	4,836	+	1	2_A375_shN37_gfus_lncRNA:1:3042	177	upstream	0	1	14	19	1	2_A375_shN37_gfus_lncRNA:1:3042	19	Gene DNAJC22	wrs, FLJ12236, DNAJC22	DnaJ (Hsp40) homolog, subfamily C, member 22	NM_024892, XCT.2281648.1, XCT.32784.4	220441_at, 244192_at	NP_0789162, EAW85067.1, EAW85066.1
Gene:ID:4416	KCNK6	12	49,932,840	49,952,077	19,137	+	1	2_A375_shN37_gfus_lncRNA:1:3043	25509	downstream	0	1	11	16	1	2_A375_shN37_gfus_lncRNA:1:3043	16	Gene KCNK6	KAA1252, ELK2, KCNK6, BEC1, Kv12.2	potassium inwardly-rectifying channel, subfamily K, member 6	NM_0012354, XCT.1912304.4, XCT.1985221.1	220376_at	NP_0394161, EAW85070.1, EAW85074.1
Gene:ID:9448	MCRS1	12	49,952,055	49,961,811	8,826	-	1	2_A375_shN37_gfus_lncRNA:1:3043	162	up gene	0	1	11	16	1	2_A375_shN37_gfus_lncRNA:1:3043	16	Gene MCRS1	KIF23PP, bM360G, P78, MSP58, MCRS1, MCRS2	kinesin family member 23 pseudogene	NM_006337, NM_001012300, XCT.1.215.4, XCT.1810F336.1, XCT.1962719.1, XCT.2300466.0, XCT.2300467.0, XCT.2300468.0, XCT.2300472.0	202595_s_at	NP_0063282, NP_0010123001, EAW85078.1, EAW85079.1, EAW85080.1, EAW85077.1, EAW85079.1
Gene:ID:9309	TMEM66	12	50,135,293	50,150,717	23,424	+	1	2_A375_shN37_gfus_lncRNA:1:3044	28	up gene	0	1	17	23	1	2_A375_shN37_gfus_lncRNA:1:3044	23	Gene TMEM66	TEGT, TMEM66, Bi-1, BAX1	transmembrane BAX inhibitor motif containing 6	NM_001005376, NM_003217, XCT.1.214.3, XCT.1962117.1, XCT.2281655.0, XCT.2281659.2, XCT.2281661.0	200803_s_at, 200804_at	NP_0010023661, NP_003208.2, EAW85089.1, EAW85091.1, EAW85092.1, EAW85093.1
Gene:ID:44232	SCO1	12	50,222,526	50,234,837	12,611	-	2	2_A375_shN37_gfus_lncRNA:1:1445,2_A375_shN37_gfus_lncRNA:1:3046	14595, 14186	downstream, downstream	1	1	17	21	2	2_A375_shN37_gfus_lncRNA:1:3046	21	Gene LOC100276864	FLJ30560	hypothetical LOC100276864	NR_027092, NR_027593, NR_027501		
Gene:ID:9535	BCDIN3D	12	50,229,626	50,239,812	7,095	-	2	2_A375_shN37_gfus_lncRNA:1:1445,2_A375_shN37_gfus_lncRNA:1:3046	4112, 490	upstream, us gene	1	1	17	21	2	2_A375_shN37_gfus_lncRNA:1:3046	21	Gene BCDIN3D	BCDIN3D		NM_181705, XCT.2300459.0	234979_at	NP_5595912, EAW85101.1
Gene:ID:9637	AQP2	12	50,344,524	50,352,864	8,148	+	1	2_A375_shN37_gfus_lncRNA:1:1446	19755	downstream	1	0	20	16	1	1_A375_shN7_shrus_lncRNA:1	20	Gene AQP2	MGC34501, AQP2, AQP-CD, WCH-CD	aquaporin 2 (collecting duct)	NM_000486, XCT.1712704.4	206672_at, 236630_at, 240268_at	NP_0394771, EAW85109.1
Gene:ID:9252	AQP5	12	50,353,279	50,359,461	4,182	+	1	2_A375_shN37_gfus_lncRNA:1:1446	6033	downstream	1	0	20	16	1	1_A375_shN7_shrus_lncRNA:1	20	Gene AQP5	AQP5		NM_001651, XCT.1603307.3	213611_at	NP_0016421, EAW85110.1
Gene:ID:9253	AQP6	12	50,366,620	50,370,922	4,302	+	1	2_A375_shN37_gfus_lncRNA:1:1446	-5306	upstream	1	0	20	16	1	1_A375_shN7_shrus_lncRNA:1	20	Gene AQP6	KID, AQP2L, AQP6	aquaporin 6, kidney specific	NM_001652	205435_s_at, 216218_at	NP_0016422
Gene:ID:7917	ACCN2	12	50,451,687	50,477,384	25,967	+	1	2_A375_shN37_gfus_lncRNA:1:3046	-733	upstream	0	1	11	16	1	2_A375_shN37_gfus_lncRNA:1:3046	16	Gene ACCN2	BNaC2, ASIC, ASIC1, ASIC1A, hBNaC2, ACCN2	amiloride-sensitive cation channel 2, neuronal	NM_001095, NM_020039, XCT.1962443.1, XCT.2252327.0, XCT.2252329.0, XCT.32852.3	203156_s_at, 37455_s_at	NP_0010862, NP_0664222, EAW85116.1, EAW85117.1, EAW85115.1, EAW85119.1
Gene:ID:9208	DIP2B	12	50,598,765	51,142,490	543,662	+	1	2_A375_shN37_gfus_lncRNA:1:1447	16	up gene	0	1	16	15	1	2_A375_shN37_gfus_lncRNA:1:3047	16	Gene DIP2B	MGC104855, DIP2B, KIAA1960	DIP2 disco-interacting protein 2 homolog B (Drosophila)	NM_173602, XCT.2322348.1, XCT.2282346.1	1553271_at, 224572_at, 242070_at	NP_7738732, EAW85160.1, EAW85159.1
Gene:ID:5878	LETMD1	12	51,442,054	51,454,207	12,123	+	2	2_A375_shN37_gfus_lncRNA:1:1449,2_A375_shN37_gfus_lncRNA:1:3047	-292, -276	upstream, upstream	1	1	23	22	1	2_A375_shN37_gfus_lncRNA:1:3047	25	Gene LETMD1	DKFZp686A0111, HCR-2, 1110190123Rik, HCCR1, HCCR-1, HCCR-2, LETMD1	LETM1 domain containing 1	NM_015479, NM_001024866, XCT.1962112.2, XCT.2346754.0, XCT.2352290.0, XCT.2352291.0, XCT.2352292.0, XCT.32154.2	201170_s_at	NP_0562315, NP_0010185291, EAW85190.1, EAW85189.1, EAW85187.1, EAW85185.1, EAW85170.1, EAW85171.1
Gene:ID:1966	C12orf42	12	51,454,990	51,477,333	22,343	+	1	2_A375_shN37_gfus_lncRNA:1:1449	21	up gene	1	0	16	12	1	1_A375_shN7_shrus_lncRNA:1	21	Gene C12orf42	C12orf42, FLJ20576, C12orf42, TAIP-12, CSRNP2	cysteine-rich with nuclear localization signal protein 2	NM_020939, XCT.1962122.1	221260_s_at, 225042_s_at	NP_1160361, EAW85173.1
Gene:ID:624	TFCP2	12	51,487,339	51,566,826	79,387	-	2	2_A375_shN37_gfus_lncRNA:1:1450,2_A375_shN37_gfus_lncRNA:1:3048	69614, -48	downstream, upstream	1	0	21	16	2	2_A375_shN37_gfus_lncRNA:1:3048	21	Gene TFCP2	TFCP2C, TFCP2, LBP1D, CP2, SEF, LBP1C, LBP-1C, LSF	transcription factor CP2	NM_001173452, NM_001173453, NM_005653, XCT.2251187.0, XCT.2351160.0, XCT.2351173.0, XCT.2352358.0, XCT.32136.3	207627_s_at, 207627_x_at	NP_0011668231, NP_0011669231, NP_005644.2, EAW85174.1, EAW85175.1, EAW85176.1, EAW85177.1, EAW85178.1
Gene:ID:7226	SMAGP	12	51,539,133	51,564,202	25,069	+	1	2_A375_shN37_gfus_lncRNA:1:3046	430	upstream	0	1	16	16	1	2_A375_shN37_gfus_lncRNA:1:3046	16	Gene SMAGP	KIAAGP, MGC148054, MGC148052, SMAGP	small cell adhesion glycoprotein	NM_0058314, NM_001033573, XCT.1621494.2, XCT.1967160.1, XCT.2352372.0	209579_s_at	NP_0012978451, NP_0010295651, EAW85163.1, EAW85164.1, EAW85165.1
Gene:ID:4431	BIN2	12	51,674,622	51,717,835	43,116	+	1	2_A375_shN37_gfus_lncRNA:1:3046	53105	downstream	0	1	16	16	1	2_A375_shN37_gfus_lncRNA:1:3046	16	Gene BIN2	BRAP-1, BIN2	bridging integrator 2	NM_0092263, XCT.1853416.0, XCT.2281519.0, XCT.2352370.0	218191_s_at	NP_0973772, EAW85186.1, EAW85187.1, EAW85188.1
Gene:ID:4998	SLC4A8	12	51,816,994	51,902,860	64,386	+	1	2_A375_shN37_gfus_lncRNA:1:1451	180	up gene	1	0	20	16	1	1_A375_shN7_shrus_lncRNA:1	20	Gene SLC4A8	NCBE, NBC2, SLC4A8, FLJ46462, DKFZp781B2316	solute carrier family 4, sodium bicarbonate cotransporter, member 8	NM_0010039980, NM_0048361, XCT.1962422.1, XCT.2278870.0, XCT.32.3	1554113_a_at, 207096_s_at, 221833_at	NP_0010035491, NP_0045492, EAW85191.1, EAW85192.1, EAW85193.1
Gene:ID:334	SCN4A	12	51,965,820	52,002,207	217,287	+	2	2_A375_shN37_gfus_lncRNA:1:1452,2_A375_shN37_gfus_lncRNA:1:3049	2340, 2404	up gene, us gene	1	1	16	21	1	2_A375_shN37_gfus_lncRNA:1:3049	21	Gene SCN4A	MED, PNI, CEIII, hNv1.4, SCN4A, NaCh6, Osrlt	sodium channel, voltage gated, type V81, alpha subunit	NM_014191, NM_0011779561, XCT.1962117.1, XCT.1969340.1, XCT.2278572.0, XCT.2278573.0, XCT.2278574.0, XCT.2352382.2	1561630_at, 207049_at	NP_0330001, NP_0011174551.1, EAW85197.1, EAW85199.1, EAW85200.1, EAW85201.1, EAW85196.1
Gene:ID:9355	LOC100505618	12	51,965,733	52,047,359	20,624	+	2	2_A375_shN37_gfus_lncRNA:1:1452,2_A375_shN37_gfus_lncRNA:1:3049	1653.1, 1653.1	up gene, us gene	1	1	23	23	1	2_A375_shN37_gfus_lncRNA:1:3049	23	Gene LOC100505618		hypothetical protein LOC100505618	XM_0031149334, XM_0031149485, XM_0031207335		XP_0031149682.1, XP_0031169931.1, XP_0031207821.1
Gene:ID:164	NR4A1	12	52,045,191	52,053,287	8,096	+	4	1_A375_shN37_gfus_lncRNA:1:1453,1_A375_shN37_gfus_lncRNA:1:1454,1_A375_shN37_gfus_lncRNA:1:3050,2_A375_shN37_gfus_lncRNA:1:3050	57, 16329, 57, 16329	up gene, downstream, us gene, downstream	1	1	20.5	25	2	1_A375_shN7_shrus_lncRNA:1	36	Gene NR4A1	NGFIB, NP10, TR3, HMR, NAK1, NUR77, NR4A1, N10, MGC34489, GFRP1	nuclear receptor subfamily 4, group A, member 1	NM_002133, NM_173157, XCT.2278564.1, XCT.2278569.0, XCT.2392706.0, XCT.2392707.0, XCT.2392708.0, XCT.2392709.0, XCT.2392.3	202340_x_at, 216236_s_at, 211143_s_at	NP_0021262, NP_7751.0, EAW85223.1, EAW85224.1, EAW85225.1, EAW85226.1, EAW85222.1, EAW85227.1, EAW85228.1
Gene:ID:9672	C12orf44	12	52,463,756	52,471,279	7,521	+	2	1_A375_shN37_gfus_lncRNA:1:1454,2_A375_shN37_gfus_lncRNA:1:3050	-238, -180	upstream, upstream	1	1	18	27	1	1_A375_shN7_shrus_lncRNA:1	36	Gene C12orf44	ATG101, FLJ11772, C12orf44	chromosome 12 open reading frame 44	NM_027834, NM_0010098873, XCT.1966227.1, XCT.2621.0	218214_at	NP_0078532, NP_0010021433.1, EAW85239.1, EAW85230.1
Gene:ID:84501	KIF7	12	52,562,760	52,583,764	23,004	-	1	2_A375_shN37_gfus_lncRNA:1:3052	405	upstream	0	1	11	25	1	2_A375_shN37_gfus_lncRNA:1:3052	25	Gene KIF7	KIF7, hJS2	kinesin 82	NM_0059824, NM_1625?, XCT.1212.3, XCT.2346.0, XCT.2352.2	231692_at	NP_0019749.1, NP_6723.2, EAW85238.1, EAW85236.1, EAW85237.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervals/Intervals Count	Intervals	Intervals/Distance to gene	Intervals Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:2:63463	LOC26340	12	52,999,395	52,994,807	4,239	+	2	1_A375_shL37_shcs_lncRNA:1:1496,1_A375_shL37_shcs_lncRNA:1:2694	4697,1455	upstream, downstream	1	1	16.5	17.5	2	2_A375_shL37_shcs_lncRNA:1	20	Gene LOC263463		hypothetical LOC263463	XR_111290, XR_110354, XR_114930	1560279_at, 1560277_s_at	
Gene:ID:2:63464	LOC26340	12	52,994,714	52,917,997	12,883	+	2	1_A375_shL37_shcs_lncRNA:1:1496,1_A375_shL37_shcs_lncRNA:1:2694	4790,-7562	at gene, upstream	1	1	16.5	17.5	2	2_A375_shL37_shcs_lncRNA:1	20	Gene LOC263464		hypothetical LOC263464	NR_027334	1558193_at	
Gene:ID:3:815	KRT16	12	52,342,655	52,346,655	4,030	+	1	2_A375_shL37_shcs_lncRNA:1:2696	209	at gene	0	1	10	17	1	2_A375_shL37_shcs_lncRNA:1	17	Gene KRT16	KRT16, CYK16, K16	keratin 16	NM_005224, NM_194187, ENST00000340, ENST00000	201595_s_at	NP_005215.1, NP_954637.1, EAW96655.1, EAW96656.1
Gene:ID:1:976	EIF4B	12	53,900,062	53,433,993	35,931	+	1	2_A375_shL37_shcs_lncRNA:1:2697	48706	downstream	0	1	10	19	1	2_A375_shL37_shcs_lncRNA:1	19	Gene EIF4B	EIF-4B, EIF4B, PRO1645	eukaryotic translation initiation factor 4B	NM_001417, ENST00000	201627_at, 201626_at	NP_001408.2, EAW96657.1
Gene:ID:2:63135	LOC26331	12	53,436,973	53,448,222	11,249	+	1	2_A375_shL37_shcs_lncRNA:1:2697	7454	at gene	0	1	10	19	1	2_A375_shL37_shcs_lncRNA:1	19	Gene LOC263135		hypothetical LOC263135	NR_033654	243265_at	
Gene:ID:2:3371	TENC1	12	53,440,810	53,458,163	17,353	+	1	2_A375_shL37_shcs_lncRNA:1:2697	-42	upstream	0	1	10	19	1	2_A375_shL37_shcs_lncRNA:1	19	Gene TENC1	DKFZp686D13234, TNS2, TENC1, PLI-TN3220, CTEN, C1-TEN, KIAA1078	tensin like C1 domain-containing phosphatase (tensin 2)	NM_015318, NM_170754, NM_198216, NM_001308177, ENST00000	212464_at	NP_056134.2, NP_739510.2, NP_939072.1, EAW96555.1, EAW96556.1, EAW96557.1
Gene:ID:3:1380	CSAD	12	53,551,447	53,574,020	22,573	-	2	1_A375_shL37_shcs_lncRNA:1:2696,1_A375_shL37_shcs_lncRNA:1:2539	84, -514	at gene, upstream	0	1	9	20.5	2	2_A375_shL37_shcs_lncRNA:1	22	Gene CSAD	CSD, MGC119354, PCAP, MGC119355, CSAD, PLA49987, PLA49987, MGC119357	cysteine sulfinic acid decarboxylase	NM_015908, ENST00000	1565630_at, 221139_s_at	NP_057072.4, EAW96571.1, EAW96666.1, EAW96669.1, EAW96670.1, EAW96672.1, EAW96667.1, EAW96668.1
Gene:ID:2:53337	ZNF740	12	53,574,535	53,564,864	10,119	-	2	1_A375_shL37_shcs_lncRNA:1:2696,1_A375_shL37_shcs_lncRNA:1:2539	-199, -839	upstream, at gene	0	1	9	20.5	2	2_A375_shL37_shcs_lncRNA:1	22	Gene ZNF740	dJ921M3, MGC61706, ZNF740	zinc finger protein 740	NM_001003434, ENST00000	1555277_at	NP_001003434.1, EAW96673.1, EAW96674.1
Gene:ID:3:916	ITGB7	12	53,555,107	53,601,000	15,893	+	1	2_A375_shL37_shcs_lncRNA:1:2539	26056	downstream	0	1	10	22	1	2_A375_shL37_shcs_lncRNA:1	22	Gene ITGB7	ITGB7		NM_000889, ENST00000	203715_at	NP_000880.1, EAW96675.1
Gene:ID:3:916	RARG	12	53,604,553	53,626,035	21,483	+	2	1_A375_shL37_shcs_lncRNA:1:1456,1_A375_shL37_shcs_lncRNA:1:2690	12244, 12626	at gene, at gene	1	1	10	15	1	1_A375_shL37_shcs_bkRNA:1	16	Gene RARG	NR1B3, RARG, RARC	retinoic acid receptor, gamma	NM_000966, NM_001042726, ENST00000	204853_s_at, 204102_at, 211716_at	NP_000957.1, NP_001018121.1, EAW96676.1, EAW96677.1, EAW96678.1
Gene:ID:3:700	ESPL1	12	53,662,063	53,687,427	25,364	+	3	1_A375_shL37_shcs_lncRNA:1:1459,1_A375_shL37_shcs_lncRNA:1:2695,1_A375_shL37_shcs_lncRNA:1:2692	169, 27282, 21561	at gene, downstream, downstream, downstream	1	1	10.33	23	3	2_A375_shL37_shcs_lncRNA:1	23	Gene ESPL1	ESP1, KIAA0165, FLJ46482, ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	NM_012291, ENST00000	206017_at, 59156_at	NP_039234.2, EAW96682.1, EAW96681.1
Gene:ID:3:204	PFDN6	12	53,669,233	53,692,234	3,998	+	2	1_A375_shL37_shcs_lncRNA:1:2695,1_A375_shL37_shcs_lncRNA:1:2692	141, 4429	at gene, downstream	0	1	10	26	2	2_A375_shL37_shcs_lncRNA:1	26	Gene PFDN6	MM1, MM1, MGC71907, PFD3, PFDN6, MGC5328	prefoldin subunit 6	NM_002624, NM_145697, ENST00000	207122_s_at, 210505_s_at	NP_002615.2, NP_663804.1, EAW96683.1, EAW96684.1, EAW96685.1
Gene:ID:3:3314	C12orf10	12	53,693,470	53,700,965	7,495	+	2	1_A375_shL37_shcs_lncRNA:1:2695,1_A375_shL37_shcs_lncRNA:1:2692	4094, 164	upstream, at gene	0	1	10	26	2	2_A375_shL37_shcs_lncRNA:1	26	Gene C12orf10	MSTP024, MYG, MYG1, MSTO36, C12orf10	chromosome 12 open reading frame 10	NM_025040, ENST00000	218220_at	NP_079313.2, EAW96686.1, EAW96687.1, EAW96689.1, EAW96690.1
Gene:ID:3:556	AAAS	12	53,701,240	53,715,812	14,172	-	3	1_A375_shL37_shcs_lncRNA:1:1460,1_A375_shL37_shcs_lncRNA:1:2692,1_A375_shL37_shcs_lncRNA:1:2690	92, 21746, 12	at gene, downstream, upstream	1	1	7.5	20.5	2	2_A375_shL37_shcs_lncRNA:1	153	Gene AAAS	ADRACALA, AAAS, AAA, GLO32, DKFZp686G1624, ALADIN, ADRACALIN, AAAS9	adrenocortical dysplasia, achalasia, alacrimia	NM_015665, NM_001173466, ENST00000	218075_at	NP_056551.1, NP_001166137.1, EAW96692.1, EAW96693.1
Gene:ID:1:1340	SP7	12	53,720,559	53,730,004	9,445	+	2	1_A375_shL37_shcs_lncRNA:1:1460,1_A375_shL37_shcs_lncRNA:1:2692	14644, 14593	downstream, downstream	1	1	13.5	15.5	1	2_A375_shL37_shcs_lncRNA:1	15.5	Gene SP7	SP7, OSX, MGC126596	Sp7 transcription factor	NM_152860, NM_001173467, ENST00000	1552340_at	NP_690599.1, NP_001166535.1, EAW96695.1, EAW96696.1, EAW96697.1
Gene:ID:3:4656	PRR13	12	53,835,833	53,840,427	4,594	+	1	2_A375_shL37_shcs_lncRNA:1:2694	16655	downstream	0	1	13	19	1	2_A375_shL37_shcs_lncRNA:1	19	Gene PRR13	DUF2, bA511I7, PRR13, PL-J33016, PL-B4576, TXR1	proline rich 13	NM_015437, NM_001003334, ENST00000	217794_at	NP_056271.1, NP_001003334.1, EAW96702.1, EAW96703.1, EAW96704.1, EAW96705.1
Gene:ID:3:264	PCBP2	12	53,849,586	53,874,646	29,060	+	1	2_A375_shL37_shcs_lncRNA:1:2694	462	at gene	0	1	13	19	1	2_A375_shL37_shcs_lncRNA:1	19	Gene PCBP2	hnRNP-E2, HNRPE2, PCBP2, MGC110095	poly(rC) binding protein 2	NM_005016026, NM_030516, NM_031989, NM_001128911, NM_001129912, NM_001129913, NM_001129914, NM_001129915, NM_001129916, NM_001129917, ENST00000	204631_s_at, 212953_s_at, 212954_at, 229467_at	NP_001092090.1, NP_005007.2, NP_114396.1, NP_001122353.1, NP_001122354.1, NP_001122355.1, NP_001122356.1, EAW96706.1, EAW96707.1, EAW96708.1, EAW96709.1, EAW96710.1, EAW96711.1
Gene:ID:6:155	MKRN3C12	12	53,874,276	53,893,464	19,188	-	2	1_A375_shL37_shcs_lncRNA:1:1461,1_A375_shL37_shcs_lncRNA:1:2695	-1852, -1555	upstream, downstream	1	1	24	30	1	2_A375_shL37_shcs_lncRNA:1	30	Gene MKRN3C12	MEKK12, DUL, ZFK, MUK, ZFP2P1, MKP3C12	mitogen-activated protein kinase kinase kinase 12	NM_005381, NM_001163811, ENST00000	205407_s_at, 205408_s_at	NP_005372.2, NP_001150493.1, EAW96712.1, EAW96713.1, EAW96714.1, EAW96716.1, EAW96715.1
Gene:ID:6:595	TARBP2	12	53,894,703	53,900,215	5,513	+	2	1_A375_shL37_shcs_lncRNA:1:1461,1_A375_shL37_shcs_lncRNA:1:2695	581, 527	at gene, at gene	1	1	24	30	1	2_A375_shL37_shcs_lncRNA:1	30	Gene TARBP2	TARBP2, TRBP2, TRBP1, TRBP, LOQ3	TAR (HIV-1) RNA binding protein 2	NM_134323, NM_134324, NM_004178, ENST00000	203677_s_at	NP_891551.1, NP__599151.2, NP_004169.2, EAW96717.1, EAW96718.1, EAW96720.1, EAW96719.1
Gene:ID:6:620	NPPF	12	53,900,674	53,901,622	948	-	2	1_A375_shL37_shcs_lncRNA:1:1461,1_A375_shL37_shcs_lncRNA:1:2695	6126, 6193	downstream, downstream	1	1	24	30	1	2_A375_shL37_shcs_lncRNA:1	30	Gene NPPF	PMRFRFL, NPFF	neuropeptide FF-amide peptide precursor	NM_022117, ENST00000	206402_s_at, 214164_at	NP_072054.1, EAW96721.1, EAW96722.1
Gene:ID:1:1016	ATF7	12	53,905,643	54,020,199	114,556	+	2	1_A375_shL37_shcs_lncRNA:1:1462,1_A375_shL37_shcs_lncRNA:1:2696	135, 119	at gene, at gene	1	1	25	26	1	2_A375_shL37_shcs_lncRNA:1	26	Gene ATF7	ATPA, ATF7, MGC57152	activating transcription factor 7	NM_001130059, NM_006856, NM_001130060, NCT14464-4, NCT12132054	206554_s_at, 226529_at, 226530_s_at	NP_001123531.1, NP_006847.1, NP_001123532.1, EAW96723.1, EAW96724.1
Gene:ID:3:17	ATF7IP2	12	54,056,844	54,070,512	11,668	-	3	1_A375_shL37_shcs_lncRNA:1:1462,1_A375_shL37_shcs_lncRNA:1:2697,1_A375_shL37_shcs_lncRNA:1:2696	606, 17520, 360	at gene, downstream, at gene	1	1	21.5	32	2	2_A375_shL37_shcs_lncRNA:1	47	Gene ATF7IP2	ATF7IP2		NM_018179, NM_001003531, NCT14462-2, NCT12120510	207552_at, 208764_s_at	NP_060649.2, NP_001002531.1, EAW96726.1
Gene:ID:7:655	CALCOCO1	12	54,104,902	54,121,307	16,405	-	2	1_A375_shL37_shcs_lncRNA:1:1464,1_A375_shL37_shcs_lncRNA:1:2698	-101, -101	upstream, upstream	1	1	20	46	1	2_A375_shL37_shcs_lncRNA:1	46	Gene CALCOCO1	FP13270, Cocoa, calcilogrin, CALCOCO1, KIAA1536	calcium binding and coiled-coil domain 1	NM_025080, NM_001145662, NR_026554, NCT14467-4, NCT12120460, NCT12120464, NCT12060760, NCT12060772, NCT12060780, NCT12060790, NCT12060810, NCT12060820	209002_s_at	NP_079249.1, NP_001131154.1, EAW96727.1, EAW96728.1, EAW96732.1, EAW96731.1, EAW96730.1, EAW96729.1, EAW96733.1, EAW96732.1
Gene:ID:3:228	HOXC13	12	54,332,976	54,340,326	7,792	+	2	1_A375_shL37_shcs_lncRNA:1:1466,1_A375_shL37_shcs_lncRNA:1:2672	160, 160	at gene, at gene	1	1	22	26	1	2_A375_shL37_shcs_lncRNA:1	26	Gene HOXC13	HOX13, MGC5239, HOXC10	homeobox C13	NM_017410, NCT14454-2	218632_s_at	NP_059106.2, EAW96734.1
Gene:ID:3:226	HOXC10	12	54,378,846	54,384,963	6,117	+	1	2_A375_shL37_shcs_lncRNA:1:2672	12254	downstream	0	1	12	14	1	2_A375_shL37_shcs_lncRNA:1	14	Gene HOXC10	HOX31, MGC5239, HOXC10	homeobox C10	NM_017409, NCT14461-2, NCT12132430, NCT12132440	218899_at	NP_059105.2, EAW96736.1, EAW96740.1
Gene:ID:4:6972.1	MIR199A2	12	54,383,522	54,383,631	109	+	1	2_A375_shL37_shcs_lncRNA:1:2672	5675	downstream	0	1	12	14	1	2_A375_shL37_shcs_lncRNA:1	14	Gene MIR199A2	MIRN199-2, MIR199A2, MIRN199A2	microRNA 199b-2	NR_029617		
Gene:ID:3:215	HOXC9	12	54,392,877	54,397,121	3,244	+	1	2_A375_shL37_shcs_lncRNA:1:2672	-2677	upstream	0	1	12	14	1	2_A375_shL37_shcs_lncRNA:1	14	Gene HOXC9	HOX2, HOXC9, HOX38	homeobox C9	NM_006897, NCT14462-4, NCT12132410	221636_at	NP_008828.1, EAW96742.1, EAW96741.1
Gene:ID:3:224	HOXC8	12	54,402,890	54,406,547	3,657	+	1	2_A375_shL37_shcs_lncRNA:1:2672	8206	downstream	0	1	11	26	1	2_A375_shL37_shcs_lncRNA:1	26	Gene HOXC8	HOX1A, HOX2, HOXC8	homeobox C8	NM_022658, NCT14451681-2	221100_at	NP_073749.1, EAW96743.1
Gene:ID:3:222	HOXC5	12	54,410,642	54,429,145	18,503	+	2	1_A375_shL37_shcs_lncRNA:1:2672,1_A375_shL37_shcs_lncRNA:1:2672	1454, 16534	at gene, downstream	0	1	9	22	2	2_A375_shL37_shcs_lncRNA:1	26	Gene HOXC5	HOX3C, CP11, HOX3, HOX3D	homeobox C5	NM_018953, NR_003064, NCT14463-1	206709_at	NP_061826.1, EAW96746.1
Gene:ID:3:223	HOXC6	12	54,410,642	54,424,607	13,965	+	2	1_A375_shL37_shcs_lncRNA:1:2672,1_A375_shL37_shcs_lncRNA:1:2672	1454, 16534	at gene, downstream	0	1	9	22	2	2_A375_shL37_shcs_lncRNA:1	26	Gene HOXC6	HOX3C, HOX3, CP25, HOX3.C, HOXC6	homeobox C6	NM_004503, NM_153693, NCT12112042, NCT12132242	206555_s_at	NP_004494.1, NP__710160.1, EAW96749.1, EAW96747.1
Gene:ID:3:221	HOXC4	12	54,410,642	54,449,614	39,172	+	2	1_A375_shL37_shcs_lncRNA:1:2672,1_A375_shL37_shcs_lncRNA:1:2672	1454, 16534	at gene, at gene	0	1	9	22	2	2_A375_shL37_shcs_lncRNA:1	26	Gene HOXC4	HOX3, HOXC4, HOX3E, cp19	homeobox C4	NM_153633, NM_014620	206194_at	NP__705977.1, NP__035439.2
Gene:ID:3:3946	MRN18	12	54,427,734	54,427,829	95	+	1	2_A375_shL37_shcs_lncRNA:1:2673	556	upstream	0	1	7	16	1	2_A375_shL37_shcs_lncRNA:1	16	Gene MIR615	MIRN18, bladder-t65, MIRN615	microRNA 615	NR_030753		
Gene:ID:4:84101	FLJ12825	12	54,452,035	54,516,018	63,983	+	1	2_A375_shL37_shcs_lncRNA:1:2674	67949	downstream	0	1	11	15	1	2_A375_shL37_shcs_lncRNA:1	15	Gene FLJ12825	FLJ12825	hypothetical LOC440031	NR_038655	1557299_at, 233008_at	
Gene:ID:3:90043	LOC44003	12	54,519,655	54,526,677	6,772	+	1	2_A375_shL37_shcs_lncRNA:1:2674	129	at gene	0	1	11	15	1	2_A375_shL37_shcs_lncRNA:1	15	Gene LOC440043		hypothetical LOC440043	NR_038656	236382_at	
Gene:ID:3:3466	CBX3	12	54,624,730	54,673,815	49,185	+	1	2_A375_shL37_shcs_lncRNA:1:1467	4645	upstream	1	0	21	16	1	1_A375_shL7_shcs_bkRNA:1	21	Gene CBX3	HP1A, CBX3, HP1	chromobox homolog 3	NM_007276, ENST00000	209715_at, 242669_at	NP_009207.1, EAW96750.1, EAW96751.1, EAW96752.1, EAW96753.1, EAW96754.1, EAW96755.1, EAW96756.1, EAW96757.1, EAW96758.1
Gene:ID:3:178	HNRNPA1	12	54,674,468	54,679,630	5,542	+	1	2_A375_shL37_shcs_lncRNA:1:1467	72	at gene	1	0	21	16	1	1_A375_shL7_shcs_bkRNA:1	21	Gene HNRNPA1	HNRNPA1, hnRNP-A1, hnRNPA1, HNRPA1L2, HNRPA1, MGC102825	heterogeneous nuclear ribonucleoprotein A1	NM_002136, NM_031157, NM_001242806, NM_001242807, NM_001242808, NM_001242809, NM_001242810, NM_001242811, NM_001242812, NM_001242813, NM_001242814, NM_001242815, NM_001242816, NM_001242817, NM_001242818, NM_001242819, NM_001242820	200016_s_at, 214290_s_at	NP_002127.7, NP__112420.1, EAW96761.1, EAW96762.1, EAW96763.1, EAW96764.1, EAW96765.1, EAW96766.1, EAW96767.1, EAW96768.1, EAW96769.1
Gene:ID:1:678	ITGA7	12	56,016,552	56,109,589	27,737	-	3	1_A375_shL37_shcs_lncRNA:1:1471,1_A375_shL37_shcs_lncRNA:1:2690,1_A375_shL37_shcs_lncRNA:1:2689	4972, 2703, 1647	upstream, downstream, upstream	1	1	17.5	20	2	2_A375_shL37_shcs_lncRNA:1	21	Gene ITGA7	ITGA7, FLJ23220	integrin, alpha 7	NM_002206, NM_001144896, NM_001144897, NCT11823-1, NCT11807150-1, NCT12069370, NCT12069530	208663_s_at, 216231_at	NP_002197.2, NP_001138466.1, NP_001138469.1, EAW96819.1, EAW96820.1, EAW96821.1, EAW96822.1, EAW96823.1
Gene:ID:2:647	BLOC1S1	12	56,109,620	56,112,497	2,897	+	4	1_A375_shL37_shcs_lncRNA:1:1471,1_A375_shL37_shcs_lncRNA:1:1472,1_A375_shL37_shcs_lncRNA:1:2690,1_A375_shL37_shcs_lncRNA:1:2689	5241, 12262, -25, 5316	downstream, downstream, upstream, upstream	1	1	17.67	18.33	3	2_A375_shL37_shcs_lncRNA:1	21	Gene BLOC1S1	MGC07458, MKGA, RT14, BLOS1, FLJ90569, GCN5L1, FLJ90337, BLOC1S1	biogenesis of lysosome-related organelles complex-1 subunit 1	NM_001497, ENST00000	202582_at	NP_001478.1, EAW96824.1
Gene:ID:3:856	RDH5	12	56,114,151	56,116,526	4,375	+	4	1_A375_shL37_shcs_lncRNA:1:1471,1_A375_shL37_shcs_lncRNA:1:1472,1_A375_shL37_shcs_lncRNA:1:2690,1_A375_shL37_shcs_lncRNA:1:2689	810, 7981, 4539, 855	at gene, downstream, upstream, at gene	1	1	17.67	18.33	3	2_A375_shL37_shcs_lncRNA:1	21	Gene RDH5	RDH5, SDR9C9, RDH1, FLJ97089, FLJ32337, HSD17B9	retinol dehydrogenase 5 (11-cis/9-cis)	NM_002905, ENST00000	210106_at, 238291_at	NP_002896.2, EAW96826.1, EAW96829.1
Gene:ID:6:9230	CD63	12	56,119,230	56,122,910	3,680	+	4	1_A375_shL37_shcs_lncRNA:1:1471,1_A375_shL37_shcs_lncRNA:1:1472,1_A375_shL37_shcs_lncRNA:1:2690,1_A375_shL37_shcs_lncRNA:1:2689	1589, 196, 1315, 7774	at gene, downstream, upstream, at gene	1	1	17.67	18.33	3	2_A375_shL37_shcs_lncRNA:1	21	Gene CD63	MLA1, ONA5H1, MS1R1, LAMP-3, TSPAN30, CD63	CD63 molecule	NM_001780, NM_001040034, NCT11822-2, NCT11822135-1, NCT11807164-1	208963_at	NP_077711.1, NP_001035123.1, EAW96827.1, EAW96828.1, EAW96829.1
Gene:ID:1:1355	LOC10050	12	56,122,666	56,124,636	1,746	+	3	1_A375_shL37_shcs_lncRNA:1:1471,1_A375_shL37_shcs_lncRNA:1:1472,1_A375_shL37_shcs_lncRNA:1:2690	-7627, -778, -7752	upstream, upstream, upstream	1	1	16.5	17	2	1_A375_shL7_shcs_bkRNA:1	18	Gene LOC100506701		hypothetical LOC100506701	XR_111297, XR_110355, XR_114641		
Gene:ID:2:9093	ORMDL2	12	56,211,009	56,214,859	3,150	+	2	1_A375_shL37_shcs_lncRNA:1:1472,1_A375_shL37_shcs_lncRNA:1:2692	11714, 11538	downstream, downstream	1	1	20	16	1	1_A375_shL7_shcs_bkRNA:1	20	Gene ORMDL2	6tbdn-2, ORMDL2, HSPC190, MSTP083, MSTP093	ORM1-like 2 (S. cerevisiae)	NM_014182, ENST00000	218596_at	NP_054901.1, EAW96840.1
Gene:ID:5:5800	DNAJC14	12	56,214,744	56,223,620	8,876	+	2	1_A375_shL37_shcs_lncRNA:1:1472,1_A375_shL37_shcs_lncRNA:1:2692	-100, 76	upstream, at gene	1	1	20	16	1	1_A375_shL7_shcs_bkRNA:1	20	Gene DNAJC14	DRIP76, DNAJC14, DNAJ, LIP6, HDJ3	DnaJ (Hsp40) homolog, subfamily C, member 14	NM_022364	223420_at	NP__115740.5
Gene:ID:4:4106	LOC4401 04	12	56,223,092	56,230,830	6,838	+	2	1_A375_shL37_shcs_lncRNA:1:1472,1_A375_shL37_shcs_lncRNA:1:2692	126, -46	at gene, upstream	1	1	20	16	1	1_A375_shL7_shcs_bkRNA:1	20	Gene LOC440104		1100012D05Rik pseudogene	NR_036476, NR_036477, NR_036478, NR_036479	1557124_at, 227106_at	
Gene:ID:4:327	MMP19	12	56,229,214	56,236,735	7,521	+	2	1_A375_shL37_shcs_lncRNA:1:1472,1_A375_shL37_shcs_lncRNA:1:2692	13215, 10201	downstream, downstream	1	1	20	16	1	1_A375_shL7_shcs_bkRNA:1	20	Gene MMP19	RASI-1, MMP19, MMP15	matrix metallopeptidase 19	NM_002429, ENST00000	206574_s_at	NP_002420.1, EAW96844.1, EAW96845.1
Gene:ID:3:4305	WIBG	12	56,293,197	56,321,697	28,500	+	1	2_A375_shL37_shcs_lncRNA:1:1474	481	at gene	1	0	18	12	1	1_A375_shL7_shcs_bkRNA:1	18	Gene WIBG	PYM, MGC13064, WIBG	partner of Y14 and mago homolog (Drosophila)	NM_032345, NM_001143853, ENST00000	1569433_at, 224563_s_at, 228353_at	NP_115731.1, NP_001137325.1, EAW96847.1, EAW96848.1
Gene:ID:1:998	DGKA	12	56,324,846	56,347,607	22,761	+	1	2_A375_shL37_shcs_lncRNA:1:1474	-2730	upstream	1	0	18	12	1	1_A375_shL7_shcs_bkRNA:1	18	Gene DGKA	MGC43256, DAGK, DAGK, DGKA, MGC12521, DGKalpha	diacylglycerol kinase, alpha 80kDa	NM_001345, NM_201444, NM_201445, NM_201556, ENST00000	202353_at, 211272_s_at	NP_001336.2, NP_958353.2, NP_958354.1, NP_963461.1, EAW96849.1, EAW96850.1, EAW96851.1
Gene:ID:6:493	SILV	12	56,347,659	56,359,826	11,927	-	1	2_A375_shL37_shcs_lncRNA:1:1474	-7854	upstream	1	0	28	16	2	1_A375_shL7_shcs_bkRNA:1	28	Gene SILV	SIL, SI, PMEL, SILV, gp100, ME20, D12S53E, PMEL17	premelanosome protein	NM_006928, ENST00000	205665_s_at	NP_008859.2, EAW96852.1, EAW96853.1, EAW96854.1, EAW96855.1
Gene:ID:1:617	CDK2	12	56,360,598	56,366,866	6,012	+	1	2_A375_shL37_shcs_lncRNA:1:1473	7124	downstream	1	0	28	16	1	1_A375_shL7_shcs_bkRNA:1	28	Gene CDK2	p33CDK2, CDK2	cyclin-dependent kinase 2	NM_052827, NM_001798, ENST00000	204252_at, 211653_at, 211654_s_at	NP_439902.2, NP_001789.2, EAW96856.1, EAW96857.1, EAW96858.1, EAW96860.1, EAW96859.1
Gene:ID:3:5909	RAB5B	12	56,397,662	56,398,490	20,828	+	1	2_A375_shL37_shcs_lncRNA:1:1473	-182	upstream	1	0	28	16	1	1_A375_shL7_shcs_bkRNA:1	28	Gene RAB5B	RAB5B	RAB5B, member RAS oncogene family	NM_002868, ENST00000	201279_at	NP_002859.1, EAW96862.1, EAW96863.1, EAW96864.1
Gene:ID:1:5321	LOC1001 00131126	12	56,373,755	56,374,851	1,096	-	1	2_A375_shL37_shcs_lncRNA:1:1474	1171	downstream	1	0	28	16	1	1_A375_shL7_shcs_bkRNA:1	28	Gene LOC100131126		RAB13, member RAS oncogene family pseudogene	NR_003927, ENST00000	1553032_a_at, 224907_at	NP_001027555.1, NP_001273391.1, EAW96857.1, EAW96859.1, EAW96870.1, EAW96866.1, EAW96871.1
Gene:ID:6:521	SUOX	12	56,391,683	56,399,209	8,296	+	2	1_A375_shL37_shcs_lncRNA:1:1474,1_A375_shL37_shcs_lncRNA:1:2692	10012, 10012	downstream, downstream	1	1	23	22	1	1_A375_shL7_shcs_bkRNA:1	23	Gene SUOX	SUOX	sulfite oxidase	NM_000456, NM_001032386, NM_001032387, NCT14111-2, NCT11850116-1, NCT12076550, NCT12076568, NCT12082112	1553030_a_at, 224907_at	NP_000447.2, NP_001027555.1, NP_001273391.1, EAW96857.1, EAW96859.1, EAW96870.1, EAW96866.1, EAW96871.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:64375	IKZF4	12	56,414,689	56,432,219	17,530	+	2	1_A375_pNL7_minus_lncRNA::1::1477, 2_A375_pNL97_plus_lncRNA::1::2084	21023, 20991	downstream, downstream	1	1	21	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene IKZF4	ZNFN1A4, EOS, IKZF4, KIAA1782	IKAROS family zinc finger 4 (Eos)	NM_022465, hCT16119.4, hCT2307662.1, hCT2349797.0	208472_at, 226759_at, 226761_at, 229752_at	NP_071910.3, EAW96874.1, EAW96872.1, EAW96873.1
GeneID:6231	RPS26	12	56,435,686	56,438,007	2,321	+	2	1_A375_pNL7_minus_lncRNA::1::1477, 2_A375_pNL97_plus_lncRNA::1::2084	26, -6	in gene, upstream	1	1	21	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RPS26	DBA10, MGC104292, S26, RPS26	ribosomal protein S26	NM_001029, hCT2307666.0, hCT2307670.0, hCT2307671.0	217753_s_at	NP_001020.2, EAW96876.1, EAW96877.1, EAW96878.1
GeneID:2065	ERBB3	12	56,473,892	56,497,128	23,236	+	3	2_A375_pNL97_plus_lncRNA::1::2085, 2_A375_pNL97_plus_lncRNA::1::2086, 2_A375_pNL97_plus_lncRNA::1::2087	-804, 924, 24346	upstream, in gene, downstream	0	1	16	21.33	3	2_A375_pNL97_plus_lncRNA::1	26	Gene ERBB3	ERBB3, MDA-BF-1, c-erbB-3, c-erbB3, erbB3-S, MGC88033, HER3, p45-sErbB3, p85-sErbB3, p180-ErbB3, ErbB-3, LCCS2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	NM_001982, NM_001005915, hCT16106.2, hCT2307676.0, hCT2307678.0, hCT2307680.0, hCT2307681.0	1563252_at, 1563253_s_at, 202454_s_at, 215638_at, 226213_at	NP_001973.2, NP_001005915.1, EAW96879.1, EAW96880.1, EAW96881.1, EAW96883.1, EAW96882.1
GeneID:5036	PA2G4	12	56,498,103	56,507,694	9,591	+	3	1_A375_pNL7_minus_lncRNA::1::1478, 2_A375_pNL97_plus_lncRNA::1::2087, 2_A375_pNL97_plus_lncRNA::1::2088	13929, 137, 13977	downstream, in gene, downstream	1	1	21.5	25.5	2	2_A375_pNL97_plus_lncRNA::1	26	Gene PA2G4	PA2G4, p38-2G4, EBP1, HG4-1	proliferation-associated 2G4, 38kDa	NM_006191, hCT2307685.0, hCT2307687.0	208676_s_at, 214794_at	NP_006182.2, EAW96884.1, EAW96885.1
GeneID:6171	RPL41	12	56,510,374	56,511,616	1,242	+	2	1_A375_pNL7_minus_lncRNA::1::1478, 2_A375_pNL97_plus_lncRNA::1::2088	1656, 1706	downstream, downstream	1	1	22	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RPL41	RPL41, L41		NM_021104, NM_001035267, hCT2307689.1, hCT2348770.0	201492_s_at	NP_066927.1, NP_001030344.1, EAW96886.1, EAW96887.1
GeneID:84872	ZC3H10	12	56,512,030	56,516,278	4,248	+	2	1_A375_pNL7_minus_lncRNA::1::1478, 2_A375_pNL97_plus_lncRNA::1::2088	2, 50	in gene, in gene	1	1	22	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ZC3H10	FLJ14451, ZC3H10, ZC3HDC10	zinc finger CCCH-type containing 10	NM_032786, hCT1823165.2, hCT2307691.2	227430_at	NP_116175.1, EAW96888.1, EAW96889.1
GeneID:23344	ESYT1	12	56,521,986	56,538,460	16,474	+	4	1_A375_pNL7_minus_lncRNA::1::1478, 1_A375_pNL7_minus_lncRNA::1::1479, 2_A375_pNL97_plus_lncRNA::1::2088, 2_A375_pNL97_plus_lncRNA::1::2089	-9854, 24302, -9906, 24318	upstream, downstream, upstream, downstream	1	1	21.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene ESYT1	KIAA0747, MBC2, ESYT1, FAM62A	extended synaptotagmin-like protein 1	NM_001184796, NM_015292, hCT16123.2, hCT2307695.0, hCT2307696.0, hCT2307697.0	208858_s_at, 244234_at	NP_001171725.1, NP_056107.1, EAW96890.1, EAW96891.1, EAW96892.1, EAW96893.1
GeneID:140465	MYL6B	12	56,546,335	56,551,771	5,436	+	2	1_A375_pNL7_minus_lncRNA::1::1479, 2_A375_pNL97_plus_lncRNA::1::2089	-47, -31	upstream, upstream	1	1	21	20	1	1_A375_pNL7_minus_lncRNA::1	21	Gene MYL6B	MLC1SA, MYL6B	myosin, light chain 6B, alkali, smooth muscle and non-muscle	NM_002475, hCT2307700.1, hCT2307702.1, hCT2307704.1, hCT2358106.0, hCT2358107.0	204173_at	NP_002466.1, EAW96894.1, EAW96895.1, EAW96896.1, EAW96897.1, EAW96898.1
GeneID:4637	MYL6	12	56,552,100	56,555,366	3,266	+	2	1_A375_pNL7_minus_lncRNA::1::1479, 2_A375_pNL97_plus_lncRNA::1::2089	-5812, -5796	upstream, upstream	1	1	21	20	1	1_A375_pNL7_minus_lncRNA::1	21	Gene MYL6	MLC3SM, LC17A, ESMLC, LC17B, MLC3NM, MYL6, MLC1SM, LC17-GI, LC17-NM	myosin, light chain 6, alkali, smooth muscle and non-muscle	NM_021019, NM_079423, hCT2307699.1, hCT2307701.1, hCT2307703.1, hCT2307705.1, hCT2307706.1, hCT2307707.1, hCT2344311.0	212082_s_at, 214002_at	NP_066299.2, NP_524147.2, EAW96899.1, EAW96900.1, EAW96901.1, EAW96904.1, EAW96902.1, EAW96903.1, EAW96905.1
GeneID:6601	SMARCC2	12	56,555,636	56,583,351	27,715	-	3	1_A375_pNL7_minus_lncRNA::1::1479, 2_A375_pNL97_plus_lncRNA::1::2089, 2_A375_pNL97_plus_lncRNA::1::2090	37063, 37047, -185	downstream, downstream, upstream	1	1	18.5	23	2	2_A375_pNL97_plus_lncRNA::1	26	Gene SMARCC2	Rsc8, CRACC2, BAF170, SMARCC2, DKFZp313D0632	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	NM_001130420, NM_003075, NM_139067, hCT16125.3, hCT2308912.0, hCT2308914.0	1561973_at, 201320_at, 201321_s_at	NP_001123892.1, NP_003066.2, NP_620706.1, EAW96906.1, EAW96907.1, EAW96908.1
GeneID:10193	RNF41	12	56,598,285	56,615,735	17,450	-	2	1_A375_pNL7_minus_lncRNA::1::1480, 2_A375_pNL97_plus_lncRNA::1::2091	-2345, -2409	upstream, upstream	1	1	33	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene RNF41	MGC45228, NRDP1, RNF41, SBBI03	ring finger protein 41	NM_005785, NM_194358, NM_194359, hCT16105.4, hCT2308909.1, hCT2308910.1	201961_s_at, 201962_s_at	NP_005776.1, NP_919339.1, NP_919340.1, EAW96909.1, EAW96910.1, EAW96911.1
GeneID:79035	OBFC2B	12	56,618,125	56,623,638	5,513	+	2	1_A375_pNL7_minus_lncRNA::1::1480, 2_A375_pNL97_plus_lncRNA::1::2091	-45, 19	upstream, in gene	1	1	33	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene OBFC2B	hSSB1, SSB1, MGC2731, OBFC2B, SOSS-B1	oligonucleotide/oligosaccharide-binding fold containing 2B	NM_024068, hCT16129.3, hCT2307709.1, hCT2350545.0, hCT2350546.0	218903_s_at	NP_076973.1, EAW96912.1, EAW96913.1, EAW96914.1, EAW96915.1
GeneID:283375	SLC39A5	12	56,623,820	56,631,630	7,810	+	2	1_A375_pNL7_minus_lncRNA::1::1480, 2_A375_pNL97_plus_lncRNA::1::2091	-5740, -5676	upstream, upstream	1	1	33	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene SLC39A5	LZT-Hs7, SLC39A5, MGC34778, ZIP5	solute carrier family 39 (metal ion transporter), member 5	NM_173596, NM_001135195, hCT16131.3, hCT2307710.1, hCT2307711.1	1552281_at, 231667_at	NP_775867.2, NP_001128667.1, EAW96916.1, EAW96917.1, EAW96918.1
GeneID:283373	ANKRD52	12	56,631,591	56,652,143	20,552	-	2	2_A375_pNL97_plus_lncRNA::1::2092, 2_A375_pNL97_plus_lncRNA::1::2093	-209, -8561	upstream, upstream	0	1	12.5	15	2	2_A375_pNL97_plus_lncRNA::1	16	Gene ANKRD52	ANKRD33, FLJ34236, ANKRD52	ankyrin repeat domain 52	NM_173595	226257_at	NP_775866.2
GeneID:93058	COQ10A	12	56,660,642	56,664,750	4,108	+	2	2_A375_pNL97_plus_lncRNA::1::2092, 2_A375_pNL97_plus_lncRNA::1::2093	-8290, 62	upstream, in gene	0	1	12.5	15	2	2_A375_pNL97_plus_lncRNA::1	16	Gene COQ10A	COQ10A, FLJ32452	coenzyme Q10 homolog A (S. cerevisiae)	NM_144576, NM_001099337, hCT16128.4, hCT2307715.1, hCT2307716.1	225747_at	NP_653177.3, NP_001092807.1, EAW96920.1, EAW96921.1, EAW96922.1
GeneID:1431	CS	12	56,665,483	56,694,175	28,692	-	1	2_A375_pNL97_plus_lncRNA::1::2093	33471	downstream	0	1	12	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene CS	CS	citrate synthase	NM_004077, hCT2308904.0, hCT2308905.0	208660_at	NP_004068.2, EAW96923.1, EAW96924.1
GeneID:10330	CNPY2	12	56,704,212	56,710,128	5,916	-	1	2_A375_pNL97_plus_lncRNA::1::2094	144	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CNPY2	CNPY2, ZSIG9, TMEM4, HP10390, MSAP	canopy 2 homolog (zebrafish)	NM_001190991, NM_014255, hCT2308895.2, hCT2349793.0, hCT2349794.0	1557798_at, 202857_at, 209796_s_at, 209797_at	NP_001177920.1, NP_055070.1, EAW96925.1, EAW96926.1, EAW96927.1
GeneID:9924	PAN2	12	56,710,007	56,727,637	17,630	-	1	2_A375_pNL97_plus_lncRNA::1::2094	17653	downstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PAN2	KIAA0710, PAN2, USP52, FLJ39360	PAN2 poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	NM_014871, NM_001166279, NM_001127460, hCT2308894.1, hCT2308898.1, hCT2308901.1, hCT2358058.0, hCT2358059.0	203117_s_at	NP_055686.3, NP_001159751.1, NP_001120932.1, EAW96928.1, EAW96930.1, EAW96931.1, EAW96929.1, EAW96932.1
GeneID:283377	SPRYD4	12	56,862,301	56,864,769	2,468	+	2	1_A375_pNL7_minus_lncRNA::1::1481, 2_A375_pNL97_plus_lncRNA::1::2095	67, 83	in gene, in gene	1	1	45	42	1	1_A375_pNL7_minus_lncRNA::1	45	Gene SPRYD4	DKFZp686N0877, SPRYD4	SPRY domain containing 4	NM_207344, hCT16124.2	225616_at	NP_997227.1, EAW96941.1
GeneID:27165	GLS2	12	56,864,736	56,882,181	17,445	-	2	1_A375_pNL7_minus_lncRNA::1::1481, 2_A375_pNL97_plus_lncRNA::1::2095	19813, 19797	downstream, downstream	1	1	45	42	1	1_A375_pNL7_minus_lncRNA::1	45	Gene GLS2	MGC71567, GLS2, LGA, hLGA, GLS, GA	glutaminase 2 (liver, mitochondrial)	NM_013267, hCT16103.2, hCT2308884.0, hCT2358164.0, hCT2358165.0	1564705_at, 1564706_s_at, 1564707_x_at, 205531_s_at	NP_037399.2, EAW96943.1, EAW96942.1, EAW96944.1, EAW96945.1
GeneID:5939	RBMS2	12	56,915,609	56,989,980	74,371	+	1	1_A375_pNL7_minus_lncRNA::1::1482	57479	in gene	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene RBMS2	FLJ39093, FLJ43262, FLJ40023, RBMS2, SCR3	RNA binding motif, single stranded interacting protein 2	NM_002898, hCT1955009.1, hCT2307726.0	205228_at, 34187_at	NP_002889.1, EAW96947.1, EAW96948.1
GeneID:11176	BAZ2A	12	56,989,380	57,030,163	40,783	-	5	1_A375_pNL7_minus_lncRNA::1::1463, 1_A375_pNL7_minus_lncRNA::1::1464, 2_A375_pNL97_plus_lncRNA::1::2096, 2_A375_pNL97_plus_lncRNA::1::2097, 2_A375_pNL97_plus_lncRNA::1::2098	5939, 1235, 5971, 1235, -9645	in gene, in gene, in gene, in gene, upstream	1	1	31.33	38	3	2_A375_pNL97_plus_lncRNA::1	68	Gene BAZ2A	FLJ13768, FLJ45876, BAZ2A, DKFZp781B109, FLJ13780, KIAA0314, TIP5, WALp3	bromodomain adjacent to zinc finger domain, 2A	NM_013449, hCT16115.4, hCT2308879.0, hCT2308881.0	201353_s_at, 201354_s_at, 201355_s_at, 215437_x_at	NP_038477.2, EAW96949.1, EAW96950.1, EAW96951.1
GeneID:506	ATP5B	12	57,031,959	57,039,852	7,893	-	5	1_A375_pNL7_minus_lncRNA::1::1463, 1_A375_pNL7_minus_lncRNA::1::1464, 2_A375_pNL97_plus_lncRNA::1::2096, 2_A375_pNL97_plus_lncRNA::1::2097, 2_A375_pNL97_plus_lncRNA::1::2098	15628, 10924, 15660, 10924, 44	downstream, downstream, downstream, downstream, in gene	1	1	31.33	38	3	2_A375_pNL97_plus_lncRNA::1	68	Gene ATP5B	ATPMB, ATP5B, MGC5231, ATPSB	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	NM_001686, hCT16121.3	201322_at	NP_001677.2, EAW96952.1
GeneID:692090	SNORD59B	12	57,037,464	57,037,538	74	-	3	1_A375_pNL7_minus_lncRNA::1::1464, 2_A375_pNL97_plus_lncRNA::1::2097, 2_A375_pNL97_plus_lncRNA::1::2098	8610, 8610, -2270	downstream, downstream, upstream	1	1	21	23	2	1_A375_pNL7_minus_lncRNA::1	30	Gene SNORD59B	SNORD59B, U59B	small nucleolar RNA, C/D box 59B	NR_003046		
GeneID:26769	SNORD59A	12	57,038,811	57,038,885	74	-	3	1_A375_pNL7_minus_lncRNA::1::1464, 2_A375_pNL97_plus_lncRNA::1::2097, 2_A375_pNL97_plus_lncRNA::1::2098	9957, 9957, -923	downstream, downstream, upstream	1	1	21	23	2	1_A375_pNL7_minus_lncRNA::1	30	Gene SNORD59A	SNORD59A, RNU59, U59	small nucleolar RNA, C/D box 59A	NR_002737		
GeneID:10728	PTGES3	12	57,057,125	57,082,078	24,953	-	2	1_A375_pNL7_minus_lncRNA::1::1465, 2_A375_pNL97_plus_lncRNA::1::2099	190, 254	in gene, in gene	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PTGES3	P23, TEBP, cPGES, PTGES3	prostaglandin E synthase 3 (cytosolic)	NM_006601, hCT2309388.0, hCT2309389.0, hCT2309390.0, hCT2309391.0, hCT2358182.0, hCT2358183.0	200627_at	NP_006592.3, EAW96956.1, EAW96953.1, EAW96954.1, EAW96955.1, EAW96957.1, EAW96958.1
GeneID:4666	NACA	12	57,106,211	57,119,326	13,115	-	1	2_A375_pNL97_plus_lncRNA::1::2100	254	in gene	0	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene NACA	HSD48, NACA, NACA1, MGC117224	nascent polypeptide-associated complex alpha subunit	NM_005594, NM_001113201, NM_001113202, NM_001113203	200735_x_at, 208635_x_at	NP_005585.1, NP_001106672.1, NP_001106673.1, NP_001106674.1
GeneID:5557	PRIM1	12	57,125,364	57,146,146	20,782	-	1	2_A375_pNL97_plus_lncRNA::1::2100	27074	downstream	0	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene PRIM1	p49, PRIM1, MGC12308	primase, DNA, polypeptide 1 (49kDa)	NM_000946	205053_at	NP_000937.1
GeneID:4640	MYO1A	12	57,422,301	57,443,893	21,592	-	1	2_A375_pNL97_plus_lncRNA::1::2101	229	in gene	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MYO1A	DFNA48, MYHL, MYO1A, MIHC, BBMI	myosin IA	NM_005379, hCT2309372.1, hCT2309373.0, hCT2309375.1	211916_s_at	NP_005370.1, EAW96983.1, EAW96981.1, EAW96982.1
GeneID:23306	TMEM194A	12	57,449,426	57,472,574	23,148	-	2	2_A375_pNL97_plus_lncRNA::1::2101, 2_A375_pNL97_plus_lncRNA::1::2102	26910, -9762	downstream, upstream	0	1	17	19	2	2_A375_pNL97_plus_lncRNA::1	20	Gene TMEM194A	TMEM194, KIAA0286, DKFZp686N1768, TMEM194A	transmembrane protein 194A	NM_015257, NM_001130963, hCT2348776.0, hCT2348777.0, hCT32503.4	212619_at, 212621_at	NP_056072.2, NP_001124435.1, EAW96984.1, EAW96985.1, EAW96986.1
GeneID:4665	NAB2	12	57,482,677	57,489,259	6,582	+	1	2_A375_pNL97_plus_lncRNA::1::2102	-341	upstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene NAB2	MADER, NAB2, MGC75085	NGFI-A binding protein 2 (EGR1 binding protein 2)	NM_005967, hCT2308501.0, hCT2308505.0, hCT32497.3	212803_at, 216017_s_at	NP_005958.1, EAW96987.1, EAW96988.1, EAW96989.1
GeneID:6778	STAT6	12	57,489,187	57,505,196	16,009	-	1	2_A375_pNL97_plus_lncRNA::1::2102	22660	downstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene STAT6	STAT6C, STAT6B, D12S1644, STAT6, IL-4-STAT	signal transducer and activator of transcription 6, interleukin-4 induced	NM_001178078, NM_001178079, NM_001178080, NM_001178081, NM_003153, NR_033659	201331_s_at, 201332_s_at	NP_001171549.1, NP_001171550.1, NP_003144.3, NP_001171551.1, NP_001171552.1
GeneID:6472	SHMT2	12	57,623,356	57,628,718	5,362	+	4	1_A375_pNL7_minus_lncRNA::1::1486, 1_A375_pNL7_minus_lncRNA::1::1487, 2_A375_pNL97_plus_lncRNA::1::2103, 2_A375_pNL97_plus_lncRNA::1::2104	9700, 13252, 9652, 13252	downstream, downstream, downstream, downstream	1	1	54.5	52	2	1_A375_pNL7_minus_lncRNA::1	86	Gene SHMT2	GLYA, SHMT, SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	NM_005412, NM_001166356, NM_001166357, NM_001166358, NM_001166359, NR_029415, NR_029416, NR_029417, hCT1817523.0, hCT1955024.1, hCT2308515.0, hCT2358159.0, hCT2358160.0, hCT2358161.0, hCT2358162.0, hCT2358163.0, hCT32501.2	214095_at, 214096_s_at, 214437_s_at	NP_005403.2, NP_001159828.1, NP_001159829.1, NP_001159830.1, NP_001159831.1, EAW96993.1, EAW96994.1, EAW96995.1, EAW96996.1, EAW96997.1, EAW96998.1, EAW96999.1, EAW97000.1, EAW97001.1
GeneID:56901	NDUFA4L2	12	57,628,686	57,634,545	5,859	-	4	1_A375_pNL7_minus_lncRNA::1::1486, 1_A375_pNL7_minus_lncRNA::1::1487, 2_A375_pNL97_plus_lncRNA::1::2103, 2_A375_pNL97_plus_lncRNA::1::2104	1489, -2063, 1537, -2063	in gene, upstream, in gene, upstream	1	1	54.5	52	2	1_A375_pNL7_minus_lncRNA::1	86	Gene NDUFA4L2	NUOMS, NDUFA4L2, FLJ26118	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	NM_020142, hCT2309362.0, hCT32506.2	218484_at	NP_064527.1, EAW97002.1, EAW97003.1
GeneID:246329	STAC3	12	57,637,242	57,644,969	7,727	-	4	1_A375_pNL7_minus_lncRNA::1::1486, 1_A375_pNL7_minus_lncRNA::1::1487, 2_A375_pNL97_plus_lncRNA::1::2103, 2_A375_pNL97_plus_lncRNA::1::2104	11913, 8361, 11961, 8361	downstream, downstream, downstream, downstream	1	1	54.5	52	2	1_A375_pNL7_minus_lncRNA::1	86	Gene STAC3	STAC3, MGC2793	SH3 and cysteine rich domain 3	NM_145064, hCT2309361.0, hCT2358167.0, hCT2358168.0, hCT32507.3	230652_at	NP_659501.1, EAW97005.1, EAW97004.1, EAW97006.1, EAW97007.1
GeneID:3626	INHBC	12	57,828,543	57,844,609	16,066	+	2	1_A375_pNL7_minus_lncRNA::1::1488, 2_A375_pNL97_plus_lncRNA::1::2105	24961, 24961	downstream, downstream	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene INHBC	INHBC, IHBC	inhibin, beta C	NM_005538, hCT1961147.1	207687_at, 207688_s_at	NP_005529.1, EAW97011.1
GeneID:83729	INHBE	12	57,849,096	57,851,791	2,695	+	2	1_A375_pNL7_minus_lncRNA::1::1488, 2_A375_pNL97_plus_lncRNA::1::2105	4408, 4408	downstream, downstream	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene INHBE	MGC4638, INHBE	inhibin, beta E	NM_031479, hCT1961148.1	210587_at	NP_113667.1, EAW97012.1
GeneID:2735	GLI1	12	57,853,918	57,866,051	12,133	+	2	1_A375_pNL7_minus_lncRNA::1::1488, 2_A375_pNL97_plus_lncRNA::1::2105	-414, -414	upstream, upstream	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene GLI1	GLI1, GLI	GLI family zinc finger 1	NM_005269, NM_001160045, NM_001167609, hCT2308523.0	206646_at	NP_005260.1, NP_001153517.1, NP_001161081.1, EAW97013.1
GeneID:64333	ARHGAP9	12	57,866,038	57,873,633	7,595	-	2	1_A375_pNL7_minus_lncRNA::1::1489, 2_A375_pNL97_plus_lncRNA::1::2106	-8095, -8127	upstream, upstream	1	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ARHGAP9	FLJ16525, RGL1, 10C, ARHGAP9, MGC1295	Rho GTPase activating protein 9	NM_032496, NM_001080156, NM_001080157, hCT2309354.0, hCT2309355.0, hCT2309356.0, hCT2358108.0, hCT30920.4	224451_x_at, 226906_s_at, 232543_x_at	NP_115885.2, NP_001073625.1, NP_001073626.1, EAW97014.1, EAW97015.1, EAW97018.1, EAW97016.1, EAW97017.1
GeneID:4141	MARS	12	57,881,851	57,910,433	28,582	+	3	1_A375_pNL7_minus_lncRNA::1::1489, 2_A375_pNL97_plus_lncRNA::1::2106, 2_A375_pNL97_plus_lncRNA::1::2107	-123, -91, 32117	upstream, upstream, downstream	1	1	13	17	2	2_A375_pNL97_plus_lncRNA::1	17	Gene MARS	FLJ35667, MARS, MRS, MTRNS, METRS	methionyl-tRNA synthetase	NM_004990, hCT2344312.1, hCT2344313.1	201475_x_at, 213671_s_at, 213672_at	NP_004981.2, EAW97019.1, EAW97020.1
GeneID:1649	DDIT3	12	57,910,371	57,914,300	3,929	-	1	2_A375_pNL97_plus_lncRNA::1::2107	332	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene DDIT3	CHOP10, CHOP, CHOP-10, CEBPZ, MGC4154, DDIT3, GADD153	DNA-damage-inducible transcript 3	NM_001195053, NM_001195054, NM_001195055, NM_001195056, NM_004083, NM_001195057, hCT1955021.1, hCT1955022.1, hCT30913.3	209383_at	NP_001181982.1, NP_001181983.1, NP_004074.2, NP_001181984.1, NP_001181985.1, NP_001181986.1, EAW97021.1, EAW97022.1, EAW97023.1
GeneID:693201	MIR616	12	57,912,946	57,913,042	96	-	1	2_A375_pNL97_plus_lncRNA::1::2107	-926	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MIR616	MIR616, hsa-mir-616, MIRN616	microRNA 616	NR_030346		
GeneID:114785	MBD6	12	57,916,659	57,923,931	7,272	+	1	2_A375_pNL97_plus_lncRNA::1::2107	-2691	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MBD6	KIAA1887, MBD6	methyl-CpG binding domain protein 6	NM_052897, hCT2308524.1, hCT2308525.1, hCT2308526.1	214384_s_at, 226076_s_at, 227832_at, 227833_s_at	NP_443129.3, EAW97024.1, EAW97025.1, EAW97026.1
GeneID:10540	DCTN2	12	57,924,094	57,940,978	16,884	-	1	2_A375_pNL97_plus_lncRNA::1::2107	27010	downstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene DCTN2	DYNAMITIN, RBP50, DCTN2, DCTN50	dynactin 2 (p50)	NM_006400, hCT2309348.0, hCT2309349.0, hCT2309350.0	200932_s_at, 232505_at	NP_006391.1, EAW97028.1, EAW97027.1, EAW97029.1
GeneID:10956	OS9	12	58,087,738	58,115,340	27,602	+	2	1_A375_pNL7_minus_lncRNA::1::1490, 2_A375_pNL97_plus_lncRNA::1::2108	32550, 33403	downstream, downstream	1	1	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene OS9	OS-9, ERLEC2, OS9	osteosarcoma amplified 9, endoplasmic reticulum lectin	NM_006812, NM_001017956, NM_001017957, NM_001017958, hCT2358203.0, hCT2358204.0, hCT2358205.0, hCT31404.3	200714_x_at, 215399_s_at	NP_006803.1, NP_001017956.1, NP_001017957.1, NP_001017958.1, EAW97044.1, EAW97047.1, EAW97045.1, EAW97046.1
GeneID:116986	AGAP2	12	58,118,994	58,135,940	16,946	-	3	1_A375_pNL7_minus_lncRNA::1::1490, 1_A375_pNL7_minus_lncRNA::1::1491, 2_A375_pNL97_plus_lncRNA::1::2108	15652, -2396, 14799	in gene, upstream, in gene	1	1	17.5	15.5	2	1_A375_pNL7_minus_lncRNA::1	18	Gene AGAP2	KIAA0167, AGAP2, FLJ16430, GGAP2, PIKE, CENTG1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	NM_014770, NM_001122772, hCT1971571.1, hCT2306333.0, hCT2306334.0, hCT31393.3	206152_at, 215080_s_at	NP_055585.1, NP_001116244.1, EAW97048.1, EAW97049.1, EAW97050.1, EAW97051.1
GeneID:100130776	hCG_2014417	12	58,120,023	58,122,139	2,116	+	2	1_A375_pNL7_minus_lncRNA::1::1490, 2_A375_pNL97_plus_lncRNA::1::2108	265, 1118	in gene, in gene	1	1	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene hCG_2014417	LOC100130776	hypothetical LOC100130776	NR_027032		
GeneID:6302	TSPAN31	12	58,138,784	58,142,026	3,242	+	1	1_A375_pNL7_minus_lncRNA::1::1491	-448	upstream	1	0	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene TSPAN31	TSPAN31, SAS	tetraspanin 31	NM_005981, hCT2306078.1, hCT2306079.1, hCT2341417.0, hCT31394.4	203226_s_at, 203227_s_at	NP_005972.1, EAW97054.1, EAW97055.1, EAW97056.1, EAW97057.1
GeneID:1019	CDK4	12	58,142,003	58,146,164	4,161	-	1	1_A375_pNL7_minus_lncRNA::1::1491	7828	downstream	1	0	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene CDK4	PSK-J3, MGC14458, CMM3, CDK4	cyclin-dependent kinase 4	NM_000075, hCT1971572.1, hCT2306328.0, hCT2306330.0, hCT2306331.0, hCT31395.2	202246_s_at	NP_000066.1, EAW97059.1, EAW97058.1, EAW97060.1, EAW97061.1, EAW97062.1
GeneID:92979	9-Mar	12	58,148,900	58,153,689	4,789	+	2	1_A375_pNL7_minus_lncRNA::1::1491, 2_A375_pNL97_plus_lncRNA::1::2109	-10564, 11676	upstream, downstream	1	1	16	21	2	2_A375_pNL97_plus_lncRNA::1	24	Gene MARCH9	FLJ36578, RNF179, MARCH-IX, MARCH9	membrane-associated ring finger (C3HC4) 9	NM_138396, hCT2306085.0, hCT2358185.0, hCT31403.1	226454_at, 230001_at	NP_612405.2, EAW97065.1, EAW97063.1, EAW97064.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:1594	CYP27B1	12	58,156,117	58,160,976	4,859	-	3	1_A375_pNL7_minus_lncRNA::1::1492, 2_A375_pNL97_plus_lncRNA::1::2109, 2_A375_pNL97_plus_lncRNA::1::2110	-4976, 400, -4944	upstream, in gene, upstream	1	1	21	32.5	2	2_A375_pNL97_plus_lncRNA::1	41	Gene CYP27B1	PDDR, CYP27B, VDD1, VDDRI, CYP27B1, P450c1, VDR, CP2B, VDDR, CYP1, CYP1alpha	cytochrome P450, family 27, subfamily B, polypeptide 1	NM_000785	205676_at	NP_000776.1
GeneID:4234	METTL1	12	58,162,351	58,165,914	3,563	-	3	1_A375_pNL7_minus_lncRNA::1::1492, 2_A375_pNL97_plus_lncRNA::1::2109, 2_A375_pNL97_plus_lncRNA::1::2110	-38, 5338, -6	upstream, downstream, upstream	1	1	21	32.5	2	2_A375_pNL97_plus_lncRNA::1	41	Gene METTL1	C12orf1, FLJ95748, METTL1, YDL201w, TRM8	methyltransferase like 1	NM_005371, NM_023033	204027_s_at	NP_005362.3, NP_075422.3
GeneID:25895	FAM119B	12	58,166,363	58,176,324	9,941	+	5	1_A375_pNL7_minus_lncRNA::1::1492, 1_A375_pNL7_minus_lncRNA::1::1493, 2_A375_pNL97_plus_lncRNA::1::2109, 2_A375_pNL97_plus_lncRNA::1::2110, 2_A375_pNL97_plus_lncRNA::1::2111	-431, 10129, -5807, -463, 10129	upstream, downstream, upstream, upstream, downstream	1	1	62	71.67	3	2_A375_pNL97_plus_lncRNA::1	150	Gene FAM119B	DKFZp586D0919, FAM119B, METTL21B	family with sequence similarity 119, member B	NM_015433, NM_206914, hCT2306087.1, hCT2306090.1, hCT31400.4	213861_s_at	NP_056248.2, NP_996797.1, EAW97072.1, EAW97073.1, EAW97074.1
GeneID:10102	TSFM	12	58,176,528	58,196,639	20,111	+	3	1_A375_pNL7_minus_lncRNA::1::1493, 2_A375_pNL97_plus_lncRNA::1::2110, 2_A375_pNL97_plus_lncRNA::1::2111	-16, -10608, -16	upstream, upstream, upstream	1	1	86	85.5	2	2_A375_pNL97_plus_lncRNA::1	150	Gene TSFM	EFTS, COXPD3, EF-TS, EF-Tsmt, TSFM, EFTSMT	Ts translation elongation factor, mitochondrial	NM_001172695, NM_001172696, NM_001172697, NM_005726, hCT1971573.1, hCT2306094.1, hCT2356184.0, hCT31398.3	212656_at, 214331_at, 214332_s_at	NP_001166166.1, NP_001166167.1, NP_005717.3, NP_001166168.1, EAW97077.1, EAW97078.1, EAW97075.1, EAW97076.1
GeneID:10106	CTDSP2	12	58,213,710	58,240,747	27,037	-	1	1_A375_pNL7_minus_lncRNA::1::1494	923	in gene	1	0	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene CTDSP2	OS4, PSR2, SCP2, CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	NM_005730, hCT1962527.1, hCT1971574.1, hCT1971575.1, hCT2306312.0, hCT2306314.0, hCT2306317.0, hCT2358209.0, hCT2358210.0, hCT31406.4	203445_s_at, 208735_s_at	NP_005721.3, EAW97086.1, EAW97082.1, EAW97083.1, EAW97087.1, EAW97089.1, EAW97081.1, EAW97084.1, EAW97085.1, EAW97088.1
GeneID:100506805	LOC100506805	12	58,230,876	58,237,544	6,668	+	1	1_A375_pNL7_minus_lncRNA::1::1494	5946	downstream	1	0	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC100506805		hypothetical LOC100506805	XR_110363		
GeneID:100289282	LOC100289282	12	58,273,046	58,273,873	827	+	1	2_A375_pNL97_plus_lncRNA::1::2112	9626	downstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100289282		hypothetical protein LOC100289282	XM_002343174, XM_003120739		XP_002343215.1, XP_003120787.1
GeneID:100289313	LOC100289313	12	58,289,528	58,299,028	9,500	-	1	2_A375_pNL97_plus_lncRNA::1::2112	16356	downstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100289313		hypothetical LOC100289313	XR_111317, XR_110364, XR_114646		
GeneID:100506644	LOC100506644	12	58,325,232	58,329,947	4,715	-	1	1_A375_pNL7_minus_lncRNA::1::1495	-5061	upstream	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC100506644		hypothetical LOC100506644	XR_111314, XR_111316, XR_111315, XR_110365, XR_110366, XR_114647, XR_114648, XR_114649		
GeneID:91419	XRCC6BP1	12	58,335,445	58,351,052	15,607	+	1	1_A375_pNL7_minus_lncRNA::1::1495	-437	upstream	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene XRCC6BP1	MGC134818, XRCC6BP1, KUB3, MGC134817	XRCC6 binding protein 1	NM_033276, hCT1816507.2	1554349_at, 227678_at	NP_150592.1, EAW97091.1
GeneID:121227	LRIG3	12	59,265,937	59,314,262	48,325	-	1	1_A375_pNL7_minus_lncRNA::1::1499	70	in gene	1	0	17	9	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LRIG3	LRIG3, FLJ90440, KIAA3016, FLJ26573, LIG3	leucine-rich repeats and immunoglobulin-like domains 3	NM_153377, NM_001136051, hCT2358180.0, hCT30356.2	226908_at	NP_700356.2, NP_001129523.1, EAW97094.1, EAW97095.1
GeneID:9958	USP15	12	62,654,187	62,799,898	145,711	+	2	1_A375_pNL7_minus_lncRNA::1::1502, 2_A375_pNL97_plus_lncRNA::1::2117	-139, -171	upstream, upstream	1	1	168	173	1	2_A375_pNL97_plus_lncRNA::1	173	Gene USP15	UNPH4, MGC131982, MGC149838, KIAA0529, USP15, MGC74854	ubiquitin specific peptidase 15	NM_006313, hCT1821360.2, hCT2306163.0, hCT2306164.0	209475_at, 210681_s_at, 231990_at	NP_006304.1, EAW97104.1, EAW97105.1, EAW97106.1
GeneID:23041	MON2	12	62,860,597	62,991,363	130,766	+	2	1_A375_pNL7_minus_lncRNA::1::1503, 2_A375_pNL97_plus_lncRNA::1::2118	136491, 135883	downstream, downstream	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MON2	MGC35493, MON2, KIAA1040	MON2 homolog (S. cerevisiae)	NM_015026	212754_s_at, 212755_at	NP_055841.2
GeneID:283416	C12orf61	12	62,995,531	62,997,214	1,683	-	2	1_A375_pNL7_minus_lncRNA::1::1503, 2_A375_pNL97_plus_lncRNA::1::2118	126, 734	in gene, in gene	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene C12orf61	FLJ25590, C12orf61	chromosome 12 open reading frame 61	NM_175895, hCT2306301.1	1557312_at	NP_787091.1, EAW97110.1
GeneID:406891	MIRLET7I	12	62,997,466	62,997,549	83	+	2	1_A375_pNL7_minus_lncRNA::1::1503, 2_A375_pNL97_plus_lncRNA::1::2118	-378, -986	upstream, upstream	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MIRLET7I	MIRLET7I, hsa-let-7i, LET7I, MIRNLET7I	microRNA let-7i	NR_029661		
GeneID:57460	PPM1H	12	63,037,762	63,328,665	290,903	-	5	1_A375_pNL7_minus_lncRNA::1::1504, 1_A375_pNL7_minus_lncRNA::1::1505, 2_A375_pNL97_plus_lncRNA::1::2120, 2_A375_pNL97_plus_lncRNA::1::2121, 2_A375_pNL97_plus_lncRNA::1::2122	202665, 150873, 209833, 148697, 441	in gene, in gene, in gene, in gene, in gene	1	1	17.2	18.2	5	1_A375_pNL7_minus_lncRNA::1	23	Gene PPM1H	NERPP-2C, KIAA1157, FLJ13253, ARHCL1, PPM1H, URCC2	protein phosphatase 1H (PP2C domain containing)	NM_020700	1558654_at, 212686_at, 233911_s_at	NP_065751.1
GeneID:10329	TMEM5	12	64,173,637	64,202,887	29,250	+	1	2_A375_pNL97_plus_lncRNA::1::2123	123	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene TMEM5	TMEM5, HP10481	transmembrane protein 5	NM_014254, hCT2358177.0, hCT23758.2	204807_at, 204808_s_at	NP_055069.1, EAW97120.1, EAW97121.1
GeneID:57522	SRGAP1	12	64,238,541	64,541,613	303,072	+	2	1_A375_pNL7_minus_lncRNA::1::1506, 2_A375_pNL97_plus_lncRNA::1::2124	-717, -717	upstream, upstream	1	1	23	14	1	1_A375_pNL7_minus_lncRNA::1	23	Gene SRGAP1	FLJ22166, SRGAP1, ARHGAP13, KIAA1304	SLIT-ROBO Rho GTPase activating protein 1	NM_020762, hCT1960834.1, hCT2306181.0	1554473_at, 1569269_s_at, 233858_s_at	NP_065813.1, EAW97122.1, EAW97123.1
GeneID:144577	C12orf66	12	64,586,419	64,616,076	29,657	-	1	1_A375_pNL7_minus_lncRNA::1::1507	-244	upstream	1	0	25	18	1	1_A375_pNL7_minus_lncRNA::1	25	Gene C12orf66	C12orf66, FLJ32549	chromosome 12 open reading frame 66	NM_152440, hCT23965.2	1554067_at, 1554068_s_at, 235026_at	NP_689653.3, EAW97124.1
GeneID:11260	XPOT	12	64,798,233	64,842,464	44,231	+	2	1_A375_pNL7_minus_lncRNA::1::1508, 2_A375_pNL97_plus_lncRNA::1::2125	47943, 231	downstream, in gene	1	1	14.5	18	2	2_A375_pNL97_plus_lncRNA::1	20	Gene XPOT	XPO3, XPOT	exportin, tRNA (nuclear export receptor for tRNAs)	NM_007235, hCT2306512.0, hCT2306513.0, hCT2306514.0, hCT2306515.0, hCT2306516.0	212160_at	NP_009166.2, EAW97132.1, EAW97128.1, EAW97129.1, EAW97130.1, EAW97131.1
GeneID:29110	TBK1	12	64,845,937	64,895,891	49,954	+	1	1_A375_pNL7_minus_lncRNA::1::1508	239	in gene	1	0	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TBK1	T2K, FLJ11330, NAK, TBK1	TANK-binding kinase 1	NM_013254, hCT31928.3	1554391_at, 218520_at	NP_037386.1, EAW97133.1
GeneID:23329	TBC1D30	12	65,174,589	65,272,411	97,822	+	3	1_A375_pNL7_minus_lncRNA::1::1509, 1_A375_pNL7_minus_lncRNA::1::1510, 2_A375_pNL97_plus_lncRNA::1::2126	40547, 45635, 45651	in gene, in gene, in gene	1	1	26	20.5	2	1_A375_pNL7_minus_lncRNA::1	36	Gene TBC1D30	KIAA0984, TBC1D30	TBC1 domain family, member 30	XM_003119536, XM_003119539, XM_003119538, XM_001716833, XM_003119537, XM_003118950, XM_003118948, XM_003118951, XM_037557, XM_003118949, XM_003120747, XM_003120745, XM_003120748, XM_939476, XM_003120746	213912_at, 213913_s_at, 215186_at	XP_003119584.1, XP_003119587.1, XP_001716885.2, XP_003119586.1, XP_003119585.1, XP_003118998.1, XP_037557.5, XP_944569.2, XP_003118996.1, XP_003118999.1, XP_003118997.1, XP_003120795.1, XP_003120793.1, XP_003120796.1, XP_003120794.1
GeneID:100507065	LOC100507065	12	65,860,597	66,036,152	175,555	-	1	1_A375_pNL7_minus_lncRNA::1::1511	-6952	upstream	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100507065		hypothetical LOC100507065	XR_111309, XR_111311, XR_111310, XR_110370, XR_110369, XR_110371, XR_114653, XR_114652, XR_114654		
GeneID:8091	HMGA2	12	66,218,240	66,360,071	141,831	+	3	1_A375_pNL7_minus_lncRNA::1::1513, 2_A375_pNL97_plus_lncRNA::1::2127, 2_A375_pNL97_plus_lncRNA::1::2128	-400, -672, 128	upstream, upstream, in gene	1	1	19	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene HMGA2	BABL, HMGI-C, HMGA2, HMGIC, LIPO, STQTL9	high mobility group AT-hook 2	NM_003483, NM_003484, hCT1963920.1	1558682_at, 1558683_a_at, 1559891_at, 1561633_at, 1567223_at, 1567224_at, 1568286_at, 1568287_at, 208025_s_at	NP_003474.1, NP_003475.1, EAW97152.1
GeneID:51643	TMBIM4	12	66,530,717	66,563,807	33,090	-	2	1_A375_pNL7_minus_lncRNA::1::1514, 2_A375_pNL97_plus_lncRNA::1::2129	31, 127	in gene, in gene	1	1	26	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene TMBIM4	S1R, GAAP, TMBIM4, ZPRO, LFG4, CGI-119	transmembrane BAX inhibitor motif containing 4	NM_016056, hCT1951633.1, hCT2306884.0, hCT2358016.0, hCT2358017.0, hCT7747.3	219206_x_at, 222845_x_at, 223892_s_at	NP_057140.2, EAW97158.1, EAW97159.1, EAW97160.1, EAW97161.1, EAW97162.1
GeneID:92797	HELB	12	66,696,356	66,731,958	35,602	+	1	2_A375_pNL97_plus_lncRNA::1::2130	-52	upstream	0	1	8	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene HELB	HELB		NM_033647, hCT1813162.1, hCT1813163.1, hCT2357966.0	1552767_at, 1552768_s_at, 1570200_at	NP_387467.2, EAW97165.1, EAW97166.1, EAW97167.1
GeneID:23426	GRIP1	12	66,741,211	67,072,925	331,714	-	2	1_A375_pNL7_minus_lncRNA::1::1515, 2_A375_pNL97_plus_lncRNA::1::2131	45293, 45245	in gene, in gene	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GRIP1	GRIP, GRIP1	glutamate receptor interacting protein 1	NM_001178074, NM_021150	214018_at	NP_001171545.1, NP_066973.2
GeneID:55832	CAND1	12	67,663,061	67,708,388	45,327	+	2	1_A375_pNL7_minus_lncRNA::1::1517, 2_A375_pNL97_plus_lncRNA::1::2134	139, 203	in gene, in gene	1	1	24	23	1	1_A375_pNL7_minus_lncRNA::1	24	Gene CAND1	FLJ10929, KIAA0829, CAND1, FLJ38691, FLJ10114, FLJ90441, TIP120A, TIP120, DKFZp434M1414	cullin-associated and neddylation-dissociated 1	NM_018448, hCT2306402.0, hCT7623.3	207483_s_at, 208838_at, 208839_s_at, 238771_at	NP_060918.2, EAW97171.1, EAW97172.1
GeneID:100507250	LOC100507250	12	69,068,151	69,080,583	12,432	-	2	1_A375_pNL7_minus_lncRNA::1::1519, 2_A375_pNL97_plus_lncRNA::1::2137	-153, -121	upstream, upstream	1	1	25	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene LOC100507250		hypothetical LOC100507250	XR_111306, XR_110376, XR_114658		
GeneID:57122	NUP107	12	69,080,731	69,136,473	55,742	+	2	1_A375_pNL7_minus_lncRNA::1::1519, 2_A375_pNL97_plus_lncRNA::1::2137	5, -27	in gene, upstream	1	1	25	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene NUP107	NUP84, NUP107	nucleoporin 107kDa	NM_020401, hCT12522.2, hCT1957147.1	218768_at	NP_065134.1, EAW97194.1, EAW97195.1
GeneID:10818	FRS2	12	69,864,129	69,973,562	109,433	+	1	2_A375_pNL97_plus_lncRNA::1::2138	115263	downstream	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene FRS2	SNT1, FRS2A, FRS2, SNT-1, FRS2alpha, SNT	fibroblast growth factor receptor substrate 2	NM_006654, NM_001042555, hCT1951647.1, hCT2307036.0, hCT2307039.0	221308_at, 226045_at, 238486_at	NP_006645.3, NP_001036020.1, EAW97225.1, EAW97226.1, EAW97227.1
GeneID:10576	CCT2	12	69,979,208	69,995,357	16,149	+	1	2_A375_pNL97_plus_lncRNA::1::2138	184	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene CCT2	TCP-1-beta, CCT2, 99D8.1, CCT-beta, MGC142074, CCTB, PRO1633, MGC142076	chaperonin containing TCP1, subunit 2 (beta)	NM_006431, hCT15577.3, hCT1951648.1, hCT2306490.0	201946_s_at, 201947_s_at	NP_006422.1, EAW97229.1, EAW97228.1, EAW97230.1
GeneID:117177	RAB3IP	12	70,132,631	70,216,984	84,353	+	1	1_A375_pNL7_minus_lncRNA::1::1520	83241	in gene	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RAB3IP	RABIN3, FLJ14660, FLJ22548, RAB3IP, MGC71495	RAB3A interacting protein (rabin3)	NM_175624, NM_175623, NM_001024647, NM_175625, NM_022456, hCT15582.3, hCT1951655.1, hCT2306494.0, hCT2358147.0, hCT2358148.0, hCT2358149.0	1565799_at, 1565800_x_at, 223471_at, 228432_at, 231399_at, 238526_at, 238853_at	NP_783323.1, NP_783322.1, NP_071901.2, NP_783324.1, NP_001019818.1, EAW97237.1, EAW97238.1, EAW97239.1, EAW97240.1, EAW97241.1, EAW97242.1
GeneID:196446	C12orf28	12	70,219,298	70,352,504	133,206	+	1	1_A375_pNL7_minus_lncRNA::1::1520	-3426	upstream	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene C12orf28	FLJ25056, C12orf15, MGC126869, bcm1377, C12orf28	chromosome 12 open reading frame 28	XM_001718058, XM_001718908, XM_001716650, hCT1640476.3	1556267_at	XP_001718110.2, XP_001718960.1, XP_001716702.2, EAW97243.1
GeneID:100507317	LOC100507317	12	70,636,086	70,637,114	1,028	-	1	2_A375_pNL97_plus_lncRNA::1::2140	410	in gene	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100507317		hypothetical LOC100507317	XR_111305, XR_110378, XR_114659		
GeneID:4848	CNOT2	12	70,636,777	70,748,773	111,996	+	1	2_A375_pNL97_plus_lncRNA::1::2140	-73	upstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CNOT2	NOT2, FLJ26456, CDC36, NOT2H, CNOT2, HSPC131	CCR4-NOT transcription complex, subunit 2	NM_014515, hCT16269.3, hCT1951656.1, hCT1951657.1, hCT1951658.1, hCT2358215.0	217798_at, 222181_at, 222182_s_at, 233054_at	NP_055330.1, EAW97249.1, EAW97245.1, EAW97246.1, EAW97247.1, EAW97248.1
GeneID:5787	PTPRB	12	70,910,630	71,031,219	120,589	-	1	2_A375_pNL97_plus_lncRNA::1::2141	27379	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PTPRB	HPTP-BETA, PTPB, R-PTP-BETA, DKFZp686E2262, HPTPB, PTPRB, MGC142023, FLJ44133, DKFZp686H15164, VEPTP, MGC59935	protein tyrosine phosphatase, receptor type, B	NM_002837, NM_001109754, hCT16271.3, hCT1951659.2	1560105_at, 205846_at, 230250_at	NP_002828.3, NP_001103224.1, EAW97253.1, EAW97254.1
GeneID:5801	PTPRR	12	71,031,862	71,314,584	282,722	-	2	1_A375_pNL7_minus_lncRNA::1::1521, 2_A375_pNL97_plus_lncRNA::1::2142	1027, 888	in gene, in gene	1	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PTPRR	PCPTP1, PTPRQ, MGC131968, PTPBR7, FLJ34328, DKFZp781C1038, PTP-SL, MGC148170, EC-PTP, PTPRR	protein tyrosine phosphatase, receptor type, R	NM_002849, NM_130846, hCT16535.3, hCT1957864.1	206084_at, 210675_s_at	NP_002840.1, NP_570897.1, EAW97255.1, EAW97256.1
GeneID:8549	LGR5	12	71,833,813	71,978,622	144,809	+	1	2_A375_pNL97_plus_lncRNA::1::2143	43	in gene	0	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LGR5	GRP49, GPR67, HG38, LGR5, FEX, GPR49, MGC117008	leucine-rich repeat containing G protein-coupled receptor 5	NM_003667, hCT14878.3, hCT2358225.0	210393_at, 213880_at	NP_003658.1, EAW97259.1, EAW97258.1
GeneID:196441	ZFC3H1	12	72,003,379	72,057,749	54,370	-	1	1_A375_pNL7_minus_lncRNA::1::1522	501	in gene	1	0	17	17	1	1_A375_pNL7_minus_lncRNA::1	17	Gene ZFC3H1	MGC90200, PSRC2, MGC23401, DKFZp686A0722, CCDC131, ZFC3H1, KIAA0546	zinc finger, C3H1-type containing	NM_144982, hCT16536.4, hCT2306448.1, hCT2306450.1, hCT2349799.0, hCT2358169.0	1553736_at, 213065_at	NP_659419.3, EAW97261.1, EAW97260.1, EAW97262.1, EAW97263.1, EAW97264.1
GeneID:83591	THAP2	12	72,057,784	72,074,419	16,635	+	2	1_A375_pNL7_minus_lncRNA::1::1522, 2_A375_pNL97_plus_lncRNA::1::2144	-536, 22152	upstream, downstream	1	1	15.5	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene THAP2	DKFZp564I0422, THAP2	THAP domain containing, apoptosis associated protein 2	NM_031435, hCT16534.2	223588_at, 230380_at	NP_113623.1, EAW97265.1
GeneID:55266	TMEM19	12	72,079,878	72,097,840	17,962	+	1	2_A375_pNL97_plus_lncRNA::1::2144	58	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TMEM19	FLJ10936, TMEM19	transmembrane protein 19	NM_018279, hCT1812612.2, hCT1951636.1, hCT1951637.1, hCT2306530.0	219941_at, 226860_at, 229126_at, 230676_s_at	NP_060749.2, EAW97269.1, EAW97266.1, EAW97267.1, EAW97268.1
GeneID:121278	TPH2	12	72,332,626	72,426,221	93,595	+	4	1_A375_pNL7_minus_lncRNA::1::1523, 1_A375_pNL7_minus_lncRNA::1::1524, 2_A375_pNL97_plus_lncRNA::1::2145, 2_A375_pNL97_plus_lncRNA::1::2146	46, 42510, 30, 42494	in gene, in gene, in gene, in gene	1	1	23.5	24.5	2	2_A375_pNL97_plus_lncRNA::1	31	Gene TPH2	ADHD7, MGC138872, NTPH, TPH2, MGC138871, FLJ37295	tryptophan hydroxylase 2	NM_173353, hCT16299.4, hCT2349798.0, hCT2358055.0	1555332_at	NP_775489.2, EAW97278.1, EAW97277.1, EAW97279.1
GeneID:283392	LOC283392	12	72,647,287	72,667,289	20,002	-	1	2_A375_pNL97_plus_lncRNA::1::2147	601	in gene	0	1	21	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC283392		hypothetical LOC283392	NR_026836, NR_026837		
GeneID:29953	TRHDE	12	72,666,529	73,059,422	392,893	+	1	2_A375_pNL97_plus_lncRNA::1::2147	159	in gene	0	1	21	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TRHDE	TRH-DE, TRHDE, PAP-II, FLJ22381, PGPEP2	thyrotropin-releasing hormone degrading enzyme	NM_013381, hCT14873.2	1560697_at, 1560698_a_at, 219937_at	NP_037513.1, EAW97281.1
GeneID:100507377	LOC100507377	12	74,526,953	74,686,411	159,458	-	1	2_A375_pNL97_plus_lncRNA::1::2149	-133	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100507377		hypothetical protein LOC100507377	XM_003118937		XP_003118985.1
GeneID:552889	LOC552889	12	74,931,551	74,935,232	3,681	+	1	1_A375_pNL7_minus_lncRNA::1::1525	81	in gene	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene LOC552889	FLJ32060, MGC17296, ATXN7L3B	ataxin 7-like 3B	NM_001136262	212113_at, 212114_at	NP_001129734.1
GeneID:3747	KCNC2	12	75,433,896	75,603,511	169,615	-	3	1_A375_pNL7_minus_lncRNA::1::1526, 2_A375_pNL97_plus_lncRNA::1::2150, 2_A375_pNL97_plus_lncRNA::1::2151	31527, 31511, 39	in gene, in gene, in gene	1	1	16	18	2	2_A375_pNL97_plus_lncRNA::1	20	Gene KCNC2	KCNC2, KV3.2, MGC138196	potassium voltage-gated channel, Shaw-related subfamily, member 2	NM_139137, NM_139136, NM_153748, hCT2306868.0, hCT2306869.0, hCT2306870.0, hCT2306871.0, hCT2357970.0, hCT2357971.0, hCT2357972.0, hCT2357973.0	222269_at, 240614_at	NP_631875.1, NP_631874.1, NP_715624.1, EAW97287.1, EAW97288.1, EAW97292.1, EAW97289.1, EAW97290.1, EAW97291.1, EAW97293.1, EAW97294.1
GeneID:84698	CAPS2	12	75,669,759	75,723,836	54,077	-	3	1_A375_pNL7_minus_lncRNA::1::1527, 2_A375_pNL97_plus_lncRNA::1::2152, 2_A375_pNL97_plus_lncRNA::1::2153	-196, -228, -4724	upstream, upstream, upstream	1	1	21.5	26	2	2_A375_pNL97_plus_lncRNA::1	38	Gene CAPS2	FLJ34520, CAPS2, UG0636c06	calcyphosine 2	NM_032606, hCT2347873.1, hCT2349895.0, hCT2349896.0, hCT2349897.0, hCT2349898.0	1560458_s_at, 224370_s_at	NP_115995.2, EAW97296.1, EAW97297.1, EAW97298.1, EAW97299.1, EAW97300.1
GeneID:256710	GLIPR1L1	12	75,728,463	75,764,170	35,707	+	3	1_A375_pNL7_minus_lncRNA::1::1527, 2_A375_pNL97_plus_lncRNA::1::2152, 2_A375_pNL97_plus_lncRNA::1::2153	-4431, -4399, 97	upstream, upstream, in gene	1	1	21.5	26	2	2_A375_pNL97_plus_lncRNA::1	38	Gene GLIPR1L1	PRO7434, MGC26856, GLIPR1L1, ALKN2972	GLI pathogenesis-related 1 like 1	NM_152779, hCT1656549.2, hCT1966187.1	238296_at	NP_689992.1, EAW97301.1, EAW97302.1
GeneID:11010	GLIPR1	12	75,874,513	75,895,716	21,203	+	2	1_A375_pNL7_minus_lncRNA::1::1528, 2_A375_pNL97_plus_lncRNA::1::2154	30927, 30911	downstream, downstream	1	1	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene GLIPR1	RTVP1, GLIPR1, CRISP7, GLIPR	GLI pathogenesis-related 1	NM_006851, hCT17644.4, hCT2306701.1, hCT2306702.1	204221_x_at, 204222_s_at, 214085_x_at, 226136_at, 226142_at	NP_006842.2, EAW97305.1, EAW97306.1, EAW97307.1
GeneID:11103	KRR1	12	75,891,419	75,905,418	13,999	-	2	1_A375_pNL7_minus_lncRNA::1::1528, 2_A375_pNL97_plus_lncRNA::1::2154	-22, -6	upstream, upstream	1	1	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene KRR1	HRB2, RIP-1, KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	NM_007043, hCT19040.4	203202_at, 203203_s_at, 232441_at, 235038_at	NP_008974.5, EAW97309.1
GeneID:100289143	LOC100289143	12	76,332,785	76,371,830	39,045	+	2	1_A375_pNL7_minus_lncRNA::1::1529, 1_A375_pNL7_minus_lncRNA::1::1530	-5681, 5647	upstream, in gene	1	0	20	11	2	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100289143		similar to nucleolar protein family A, member 3	XM_002343200, XM_003120750		XP_002343241.1, XP_003120798.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:22822	PHLDA1	12	76,419,227	76,425,556	6,329	-	4	1_A375_pNL7_minus_lncRNA::1::1531, 1_A375_pNL7_minus_lncRNA::1::1532, 2_A375_pNL97_plus_lncRNA::1::2156, 2_A375_pNL97_plus_lncRNA::1::2157	11220, 164, 180, -780	downstream, in gene, in gene, upstream	1	1	17.5	19	2	2_A375_pNL97_plus_lncRNA::1	18	Gene PHLDA1	TDAG51, PHRIP, PHLDA1, DT1P1B11, MGC131738	pleckstrin homology-like domain, family A, member 1	NM_007350, hCT17650.3, hCT2307103.0	217996_at	NP_031376.3, EAW97313.1, EAW97312.1
GeneID:114882	OSBPL8	12	76,745,577	76,953,589	208,012	-	1	2_A375_pNL97_plus_lncRNA::1::2159	117	in gene	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene OSBPL8	MGC133203, MSTP120, OSBPL8, DKFZp686A11164, OSBP10, MST120, ORP8, MGC126578	oxysterol binding protein-like 8	NM_020841, NM_001003712, hCT18565.3, hCT1951665.1, hCT2307087.0, hCT2358062.0	212582_at, 212585_at, 226986_at	NP_065892.1, NP_001003712.1, EAW97324.1, EAW97325.1, EAW97326.1, EAW97327.1
GeneID:1466	CSRP2	12	77,252,496	77,272,799	20,303	-	1	2_A375_pNL97_plus_lncRNA::1::2161	-257	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CSRP2	LMO5, SmLIM, CSRP2, CRP2	cysteine and glycine-rich protein 2	NM_001321, hCT18369.2, hCT1961392.1	207030_s_at, 211126_s_at	NP_001312.1, EAW97336.1, EAW97337.1
GeneID:89795	NAV3	12	78,225,069	78,606,790	381,721	+	1	2_A375_pNL97_plus_lncRNA::1::2164	16755	in gene	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene NAV3	NAV3, POMFIL1, unc53H3, KIAA0938, STEERIN3	neuron navigator 3	NM_014903, hCT2344319.0, hCT2344320.0	1552658_a_at, 204823_at, 216466_at, 216632_at	NP_055718.4, EAW97342.1, EAW97341.1
GeneID:4659	PPP1R12A	12	80,167,343	80,329,235	161,892	-	2	1_A375_pNL7_minus_lncRNA::1::1534, 2_A375_pNL97_plus_lncRNA::1::2165	403, 275	in gene, in gene	1	1	24	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene PPP1R12A	MGC133042, PPP1R12A, MBS, MYPT1	protein phosphatase 1, regulatory (inhibitor) subunit 12A	NM_002480, NM_001143885, NM_001143886, hCT1951671.1, hCT1951672.1, hCT1951673.1, hCT2358043.0, hCT2358044.0, hCT2358045.0	201602_s_at, 201603_at, 201604_s_at	NP_002471.1, NP_001137357.1, NP_001137358.1, EAW97351.1, EAW97353.1, EAW97354.1, EAW97352.1, EAW97355.1, EAW97356.1
GeneID:29080	CCDC59	12	82,746,083	82,752,584	6,501	-	2	1_A375_pNL7_minus_lncRNA::1::1536, 2_A375_pNL97_plus_lncRNA::1::2166	328, 328	in gene, in gene	1	1	125	107	1	1_A375_pNL7_minus_lncRNA::1	125	Gene CCDC59	HSPC128, TAP26, DKFZp686K1021, BR22, CCDC59, FLJ10294	coiled-coil domain containing 59	NM_014167, NR_033192, hCT14843.3, hCT2358141.0	218936_s_at, 222792_s_at	NP_054886.2, EAW97380.1, EAW97379.1
GeneID:84190	C12orf26	12	82,752,276	82,873,018	120,742	+	2	1_A375_pNL7_minus_lncRNA::1::1536, 2_A375_pNL97_plus_lncRNA::1::2166	-20, -20	upstream, upstream	1	1	125	107	1	1_A375_pNL7_minus_lncRNA::1	125	Gene C12orf26	C12orf26, FLJ22789	chromosome 12 open reading frame 26	NM_032230, hCT1971605.1, hCT1971606.1	229018_at	NP_115606.2, EAW97381.1, EAW97382.1
GeneID:160335	TMTC2	12	83,080,934	83,528,065	447,131	+	1	2_A375_pNL97_plus_lncRNA::1::2167	506	in gene	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene TMTC2	DKFZp762A217, TMTC2	transmembrane and tetratricopeptide repeat containing 2	NM_152588, hCT1768129.4, hCT2350663.0	226574_at, 235775_at	NP_689801.1, EAW97384.1, EAW97385.1
GeneID:55117	SLC6A15	12	85,253,267	85,306,606	53,339	-	3	1_A375_pNL7_minus_lncRNA::1::1537, 1_A375_pNL7_minus_lncRNA::1::1538, 2_A375_pNL97_plus_lncRNA::1::2168	1102, -18, 78	in gene, upstream, in gene	1	1	19	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SLC6A15	V7-3, SBAT1, NTT73, FLJ10316, MGC87066, DKFZp761I0921, hv7-3, SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	NM_182767, NM_018057, NM_001146335, hCT17662.3, hCT2306905.0, hCT2306907.0	206376_at, 232263_at, 239352_at, 240419_at	NP_877499.1, NP_060527.2, NP_001139807.1, EAW97388.1, EAW97389.1, EAW97390.1
GeneID:144448	TSPAN19	12	85,408,094	85,430,055	21,961	-	1	1_A375_pNL7_minus_lncRNA::1::1539	19687	in gene	1	0	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene TSPAN19	FLJ44351, TSPAN19	tetraspanin 19	NM_001100917		NP_001094387.1
GeneID:84125	LRRIQ1	12	85,430,099	85,638,863	208,764	+	2	1_A375_pNL7_minus_lncRNA::1::1540, 2_A375_pNL97_plus_lncRNA::1::2169	56589, 56653	in gene, in gene	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LRRIQ1	FLJ12303, LRRIQ1	leucine-rich repeats and IQ motif containing 1	NM_032165, NM_001079910, hCT18716.3, hCT2306897.1, hCT2306900.1, hCT2349942.0	223617_at	NP_115541.3, NP_001073379.1, EAW97393.1, EAW97394.1, EAW97395.1, EAW97396.1
GeneID:8092	ALX1	12	85,674,036	85,695,562	21,526	+	2	1_A375_pNL7_minus_lncRNA::1::1541, 2_A375_pNL97_plus_lncRNA::1::2170	428, 236	in gene, in gene	1	1	24	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene ALX1	ALX1, CART1, FND3	ALX homeobox 1	NM_006982, hCT17665.3	206837_at	NP_008913.2, EAW97398.1
GeneID:160419	C12orf50	12	88,373,816	88,423,176	49,360	-	2	1_A375_pNL7_minus_lncRNA::1::1543, 2_A375_pNL97_plus_lncRNA::1::2174	-6216, -6232	upstream, upstream	1	1	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene C12orf50	C12orf50, FLJ35821	chromosome 12 open reading frame 50	NM_152589, hCT1644321.3, hCT2349889.0, hCT2349890.0	238219_at	NP_689802.1, EAW97406.1, EAW97407.1, EAW97408.1
GeneID:91298	C12orf29	12	88,429,268	88,443,937	14,669	+	2	1_A375_pNL7_minus_lncRNA::1::1543, 2_A375_pNL97_plus_lncRNA::1::2174	124, 140	in gene, in gene	1	1	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene C12orf29	FLJ38158, DKFZp686L04169, DKFZp434N2030, MGC102978, DKFZp313K0436, C12orf29	chromosome 12 open reading frame 29	NM_001009894, hCT1967801.2, hCT2346772.0, hCT2346773.0, hCT2346774.0	213701_at, 228378_at	NP_001009894.2, EAW97412.1, EAW97409.1, EAW97410.1, EAW97411.1
GeneID:80184	CEP290	12	88,442,790	88,535,993	93,203	-	1	2_A375_pNL97_plus_lncRNA::1::2175	41	in gene	0	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene CEP290	BBS14, LCA10, FLJ21979, JBTS6, rd16, SLSN6, 3H11Ag, CEP290, MKS4, JBTS5, CT87, POC3, FLJ13615, NPHP6, KIAA0373	centrosomal protein 290kDa	NM_025114, hCT18446.3, hCT2307123.0	1556850_at, 205250_s_at, 221683_s_at	NP_079390.3, EAW97413.1, EAW97414.1
GeneID:160418	TMTC3	12	88,536,073	88,593,664	57,591	+	1	2_A375_pNL97_plus_lncRNA::1::2175	-121	upstream	0	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene TMTC3	FLJ90492, SMILE, TMTC3, DKFZp686O22167, DKFZp686M1969, DKFZp686C0968, DKFZp686O2342	transmembrane and tetratricopeptide repeat containing 3	NM_181783, hCT18444.4	1560017_at, 226600_at, 226604_at	NP_861448.2, EAW97415.1
GeneID:4254	KITLG	12	88,886,570	88,974,250	87,680	-	1	1_A375_pNL7_minus_lncRNA::1::1547	-118	upstream	1	0	14	8	1	1_A375_pNL7_minus_lncRNA::1	14	Gene KITLG	Kitl, KITLG, SF, KL-1, SCF, MGF, SHEP7, FPH2, DKFZp686F2250	KIT ligand	NM_000899, NM_003994, hCT18442.3, hCT18443.3, hCT2307114.0, hCT2307116.0	207029_at, 211124_s_at, 226534_at	NP_000890.1, NP_003985.2, EAW97416.1, EAW97417.1, EAW97418.1, EAW97419.1
GeneID:1848	DUSP6	12	89,741,837	89,746,296	4,459	-	4	1_A375_pNL7_minus_lncRNA::1::1550, 1_A375_pNL7_minus_lncRNA::1::1551, 2_A375_pNL97_plus_lncRNA::1::2181, 2_A375_pNL97_plus_lncRNA::1::2182	648, -296, 1688, 776	in gene, upstream, in gene, in gene	1	1	16.67	16.67	3	1_A375_pNL7_minus_lncRNA::1	24	Gene DUSP6	DUSP6, MKP3, PYST1	dual specificity phosphatase 6	NM_001946, NM_022652, hCT17735.3, hCT2307454.0, hCT2307456.0	208891_at, 208892_s_at, 208893_s_at	NP_001937.2, NP_073143.2, EAW97422.1, EAW97423.1, EAW97424.1
GeneID:282809	WDR51B	12	89,813,501	89,919,777	106,276	-	3	1_A375_pNL7_minus_lncRNA::1::1553, 1_A375_pNL7_minus_lncRNA::1::1554, 2_A375_pNL97_plus_lncRNA::1::2184	85889, -95, -127	in gene, upstream, upstream	1	1	59.5	52	2	1_A375_pNL7_minus_lncRNA::1	101	Gene WDR51B	PIX1, FLJ41111, WDR51B, POC1B, FLJ14923	POC1 centriolar protein homolog B (Chlamydomonas)	NM_172240, hCT18747.3, hCT2358198.0, hCT2358199.0	226263_at	NP_758440.1, EAW97426.1, EAW97425.1, EAW97427.1
GeneID:8693	GALNT4	12	89,913,189	89,918,535	5,346	-	2	1_A375_pNL7_minus_lncRNA::1::1554, 2_A375_pNL97_plus_lncRNA::1::2184	-1337, -1369	upstream, upstream	1	1	101	90	1	1_A375_pNL7_minus_lncRNA::1	101	Gene GALNT4	GALNACT4, GALNT4, FLJ93314, GALNAC-T4, GalNAcT4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)	NM_003774, hCT1805815.2	220442_at, 231632_at	NP_003765.2, EAW97428.1
GeneID:338758	LOC338758	12	90,102,732	90,105,729	2,997	+	3	1_A375_pNL7_minus_lncRNA::1::1555, 2_A375_pNL97_plus_lncRNA::1::2185, 2_A375_pNL97_plus_lncRNA::1::2186	858, -1276, 836	in gene, upstream, in gene	1	1	10	17.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC338758		hypothetical LOC338758	NR_026136	238693_at	
GeneID:694	BTG1	12	92,534,054	92,539,673	5,619	-	3	1_A375_pNL7_minus_lncRNA::1::1558, 1_A375_pNL7_minus_lncRNA::1::1559, 2_A375_pNL97_plus_lncRNA::1::2189	8457, -519, 153	downstream, upstream, in gene	1	1	16.5	15.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene BTG1	BTG1		NM_001731, hCT12274.3, hCT2307173.0	1559975_at, 200920_s_at, 200921_s_at	NP_001722.1, EAW97467.1, EAW97466.1
GeneID:8411	EEA1	12	93,166,285	93,323,107	156,822	-	1	2_A375_pNL97_plus_lncRNA::1::2195	-253	upstream	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene EEA1	ZFYVE2, MST105, MSTP105, EEA1	early endosome antigen 1	NM_003566, hCT11229.5, hCT2307219.1	204840_s_at, 204841_s_at, 225865_at	NP_003557.2, EAW97471.1, EAW97472.1
GeneID:11163	NUDT4	12	93,771,701	93,797,024	25,323	+	2	1_A375_pNL7_minus_lncRNA::1::1563, 2_A375_pNL97_plus_lncRNA::1::2196	10075, -389	in gene, upstream	1	1	13.5	23	2	2_A375_pNL97_plus_lncRNA::1	35	Gene NUDT4	HDCMB47P, DIPP2beta, DIPP2alpha, KIAA0487, NUDT4, DKFZp686I1281, DIPP2	nudix (nucleoside diphosphate linked moiety X)-type motif 4	NM_019094, NM_199040, hCT2307198.0, hCT2307199.0, hCT2307200.0, hCT2307201.0, hCT2307202.0	212181_s_at, 212183_at	NP_061967.3, NP_950241.1, EAW97476.1, EAW97477.1, EAW97478.1, EAW97479.1, EAW97475.1
GeneID:28977	MRPL42	12	93,861,270	93,896,432	35,162	+	1	2_A375_pNL97_plus_lncRNA::1::2197	170	in gene	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MRPL42	MRPL31, MRP-L31, L31MT, S32MT, MRPL42, MRPS32, L42MT, HSPC204, RPML31, PTD007	mitochondrial ribosomal protein L42	NM_014050, NM_172177, NM_172178, hCT1647281.3, hCT1951360.1, hCT1951361.1, hCT2307203.0, hCT2307207.0, hCT2358118.0, hCT2358119.0	217919_s_at, 222466_s_at	NP_054769.1, NP_751917.1, NP_751918.1, EAW97483.1, EAW97485.1, EAW97486.1, EAW97484.1, EAW97487.1, EAW97488.1, EAW97489.1
GeneID:144481	LOC144481	12	93,959,404	93,965,978	6,574	-	2	1_A375_pNL7_minus_lncRNA::1::1564, 2_A375_pNL97_plus_lncRNA::1::2198	1786, 1349	in gene, in gene	1	1	29	23	1	1_A375_pNL7_minus_lncRNA::1	29	Gene LOC144481		hypothetical protein LOC144481	XM_003118939, XM_003118940, XM_003120753, XM_003120754	1559315_s_at	XP_003118987.1, XP_003118988.1, XP_003120801.1, XP_003120802.1
GeneID:8835	SOCS2	12	93,963,598	93,969,978	6,380	+	2	1_A375_pNL7_minus_lncRNA::1::1564, 2_A375_pNL97_plus_lncRNA::1::2198	594, 1031	in gene, in gene	1	1	29	23	1	1_A375_pNL7_minus_lncRNA::1	29	Gene SOCS2	SOCS2, SSI-2, SSI2, Cish2, CIS2, STATI2, SOCS-2	suppressor of cytokine signaling 2	NM_003877, hCT2307205.0, hCT31344.2	203372_s_at, 203373_at	NP_003868.1, EAW97492.1, EAW97493.1
GeneID:8738	CRADD	12	94,071,151	94,244,532	173,381	+	3	1_A375_pNL7_minus_lncRNA::1::1565, 2_A375_pNL97_plus_lncRNA::1::2199, 2_A375_pNL97_plus_lncRNA::1::2200	369, 529, 141713	in gene, in gene, in gene	1	1	16	17	2	2_A375_pNL97_plus_lncRNA::1	19	Gene CRADD	MGC9163, RAIDD, CRADD	CASP2 and RIPK1 domain containing adaptor with death domain	NM_003805, hCT31343.3	209833_at	NP_003796.1, EAW97497.1
GeneID:51134	CCDC41	12	94,702,056	94,853,764	151,708	-	2	1_A375_pNL7_minus_lncRNA::1::1567, 2_A375_pNL97_plus_lncRNA::1::2202	180, 196	in gene, in gene	1	1	22	20	1	1_A375_pNL7_minus_lncRNA::1	22	Gene CCDC41	CCDC41, MGC149726, NY-REN-58	coiled-coil domain containing 41	NM_001042399, NM_016122, hCT2307261.0, hCT2307263.0, hCT2307264.0, hCT2358214.0, hCT31348.3	219644_at, 239282_at	NP_001035858.1, NP_057206.2, EAW97501.1, EAW97502.1, EAW97504.1, EAW97505.1, EAW97503.1
GeneID:144486	LOC144486	12	94,853,779	94,856,346	2,567	+	2	1_A375_pNL7_minus_lncRNA::1::1567, 2_A375_pNL97_plus_lncRNA::1::2202	-195, -211	upstream, upstream	1	1	22	20	1	1_A375_pNL7_minus_lncRNA::1	22	Gene LOC144486		hypothetical LOC144486	NR_027035	237021_at	
GeneID:57458	TMCC3	12	94,960,900	95,044,324	83,424	-	3	1_A375_pNL7_minus_lncRNA::1::1568, 1_A375_pNL7_minus_lncRNA::1::1569, 2_A375_pNL97_plus_lncRNA::1::2203	34132, 5700, 34532	in gene, in gene, in gene	1	1	17.5	15.5	2	1_A375_pNL7_minus_lncRNA::1	18	Gene TMCC3	KIAA1145, TMCC3	transmembrane and coiled-coil domain family 3	NM_020698, hCT2307256.0, hCT2307257.0, hCT9961.3	226489_at	NP_065749.2, EAW97512.1, EAW97510.1, EAW97511.1
GeneID:55967	NDUFA12	12	95,365,109	95,397,511	32,402	-	2	1_A375_pNL7_minus_lncRNA::1::1570, 2_A375_pNL97_plus_lncRNA::1::2204	39, 60	in gene, in gene	1	1	35	19	1	1_A375_pNL7_minus_lncRNA::1	35	Gene NDUFA12	B17.2, DAP13, NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	NM_018838, hCT1829952.2, hCT2307253.0	223244_s_at	NP_061326.1, EAW97515.1, EAW97516.1
GeneID:7181	NR2C1	12	95,414,057	95,467,404	53,347	-	2	1_A375_pNL7_minus_lncRNA::1::1571, 2_A375_pNL97_plus_lncRNA::1::2205	-4, -52	upstream, upstream	1	1	35	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene NR2C1	NR2C1, TR2	nuclear receptor subfamily 2, group C, member 1	NM_001032287, NM_003297, NM_001127362, hCT1686317.2, hCT2358060.0, hCT2358061.0, hCT9229.2	204791_at, 210530_s_at, 210531_at	NP_001027458.1, NP_003288.2, NP_001120834.1, EAW97517.1, EAW97518.1, EAW97520.1, EAW97519.1
GeneID:55785	FGD6	12	95,470,525	95,611,240	140,715	-	4	1_A375_pNL7_minus_lncRNA::1::1571, 1_A375_pNL7_minus_lncRNA::1::1572, 2_A375_pNL97_plus_lncRNA::1::2205, 2_A375_pNL97_plus_lncRNA::1::2206	143832, -888, 143784, -288	downstream, upstream, downstream, upstream	1	1	26	26.5	2	2_A375_pNL97_plus_lncRNA::1	37	Gene FGD6	FGD6, ZFYVE24	FYVE, RhoGEF and PH domain containing 6	NM_018351, hCT24308.3	1555136_at, 1555137_a_at, 219901_at	NP_060821.3, EAW97521.1
GeneID:55591	VEZT	12	95,611,522	95,696,566	85,044	+	2	1_A375_pNL7_minus_lncRNA::1::1572, 2_A375_pNL97_plus_lncRNA::1::2206	606, 6	in gene, in gene	1	1	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene VEZT	VEZATIN, VEZT, DKFZp761C241	vezatin, adherens junctions transmembrane protein	NM_017599, hCT1951880.2, hCT2307163.1, hCT2307164.1, hCT2307166.1, hCT2307167.1, hCT2307169.1, hCT2358035.0, hCT2358036.0, hCT2358037.0, hCT2358038.0, hCT2358039.0, hCT2358040.0, hCT24309.4	207263_x_at, 223089_at, 223090_x_at, 223675_s_at	NP_060069.3, EAW97525.1, EAW97526.1, EAW97527.1, EAW97530.1, EAW97533.1, EAW97524.1, EAW97528.1, EAW97529.1, EAW97531.1, EAW97532.1, EAW97534.1, EAW97535.1, EAW97536.1
GeneID:10988	METAP2	12	95,867,822	95,909,615	41,793	+	2	1_A375_pNL7_minus_lncRNA::1::1574, 2_A375_pNL97_plus_lncRNA::1::2208	-14, 18	upstream, in gene	1	1	26	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene METAP2	METAP2, MNPEP, MAP2, p67eIF2, p67	methionyl aminopeptidase 2	NM_006838, hCT2307236.0, hCT2358206.0, hCT2358207.0	209861_s_at, 213899_at, 227993_at	NP_006829.1, EAW97537.1, EAW97538.1, EAW97539.1
GeneID:59277	NTN4	12	96,051,583	96,184,536	132,953	-	1	1_A375_pNL7_minus_lncRNA::1::1575	-680	upstream	1	0	16	10	1	1_A375_pNL7_minus_lncRNA::1	16	Gene NTN4	PRO3091, FLJ23180, NTN4	netrin 4	NM_021229, hCT1963695.1, hCT2358024.0	223315_at	NP_067052.2, EAW97544.1, EAW97545.1
GeneID:120935	CCDC38	12	96,260,826	96,336,428	75,602	-	1	1_A375_pNL7_minus_lncRNA::1::1576	64860	in gene	1	0	14	8	1	1_A375_pNL7_minus_lncRNA::1	14	Gene CCDC38	CCDC38, FLJ40089	coiled-coil domain containing 38	NM_182496, hCT2343967.0, hCT24311.3	1557620_a_at	NP_872302.2, EAW97551.1, EAW97550.1
GeneID:4048	LTA4H	12	96,394,611	96,429,365	34,754	-	2	1_A375_pNL7_minus_lncRNA::1::1577, 2_A375_pNL97_plus_lncRNA::1::2209	-43, 5	upstream, in gene	1	1	23	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene LTA4H	LTA4H		NM_000895, hCT1951930.1, hCT1951932.1, hCT2307318.0, hCT2307320.0	208771_s_at	NP_000886.1, EAW97560.1, EAW97557.1, EAW97558.1, EAW97559.1
GeneID:5128	CDK17	12	96,672,039	96,794,366	122,327	-	1	2_A375_pNL97_plus_lncRNA::1::2211	1118	in gene	0	1	15	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CDK17	CDK17, PCTK2, PCTAIRE2	cyclin-dependent kinase 17	NM_001170464, NM_002595, hCT2307330.0, hCT2307331.0, hCT2358070.0, hCT24315.3	206474_at, 221918_at	NP_001163935.1, NP_002586.2, EAW97566.1, EAW97567.1, EAW97568.1, EAW97569.1
GeneID:121441	NEDD1	12	97,301,001	97,347,469	46,468	+	2	1_A375_pNL7_minus_lncRNA::1::1578, 2_A375_pNL97_plus_lncRNA::1::2212	55, 167	in gene, in gene	1	1	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene NEDD1	GCP-WD, NEDD1, TUBGCP7, FLJ35902	neural precursor cell expressed, developmentally down-regulated 1	NM_001135175, NM_152905, NM_001135176, NM_001135177, hCT2307136.0, hCT2358071.0, hCT2358072.0, hCT24316.3	1552417_a_at, 1560116_a_at, 234964_at	NP_001128647.1, NP_690869.1, NP_001128648.1, NP_001128649.1, EAW97578.1, EAW97579.1, EAW97577.1, EAW97580.1
GeneID:643770	LOC643770	12	98,879,322	98,897,627	18,305	-	2	1_A375_pNL7_minus_lncRNA::1::1580, 2_A375_pNL97_plus_lncRNA::1::2216	411, 443	in gene, in gene	1	1	26	18	1	1_A375_pNL7_minus_lncRNA::1	26	Gene LOC643770		hypothetical LOC643770	XR_111325, XR_110331, XR_114602		
GeneID:100128191	LOC100128191	12	98,906,751	98,910,004	3,253	-	3	1_A375_pNL7_minus_lncRNA::1::1580, 2_A375_pNL97_plus_lncRNA::1::2216, 2_A375_pNL97_plus_lncRNA::1::2217	12788, 12820, 276	downstream, downstream, in gene	1	1	21	17.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene LOC100128191		hypothetical LOC100128191	NR_027157		
GeneID:7112	TMPO	12	98,909,351	98,944,157	34,806	+	1	2_A375_pNL97_plus_lncRNA::1::2217	377	in gene	0	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TMPO	LEMD4, TMPO, MGC61508, PRO0868, TP, LAP2, CMD1T	thymopoietin	NM_001032283, NM_001032284, NM_003276, hCT2307591.0, hCT2307592.0, hCT2307593.0, hCT2358189.0, hCT2358190.0, hCT2358191.0	203432_at, 209753_s_at, 209754_s_at, 224944_at	NP_001027454.1, NP_001027455.1, NP_003267.1, EAW97590.1, EAW97591.1, EAW97594.1, EAW97589.1, EAW97592.1, EAW97593.1
GeneID:5250	SLC25A3	12	98,987,403	98,995,778	8,375	+	1	1_A375_pNL7_minus_lncRNA::1::1581	5	in gene	1	0	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene SLC25A3	SLC25A3, OK/SW-cl.48, PHC	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	NM_213611, NM_002635, NM_005888, hCT1952509.1, hCT1952510.1, hCT1958300.1, hCT1961345.1, hCT1965545.1, hCT2307595.0	200030_s_at	NP_998776.1, NP_002626.1, NP_005879.1, EAW97595.1, EAW97598.1, EAW97599.1, EAW97596.1, EAW97597.1, EAW97600.1
GeneID:677832	SNORA53	12	98,993,413	98,993,662	249	+	1	1_A375_pNL7_minus_lncRNA::1::1581	-6005	upstream	1	0	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene SNORA53	SNORA53, ACA53	small nucleolar RNA, H/ACA box 53	NR_003015		
GeneID:121457	IKBIP	12	99,007,162	99,038,569	31,407	-	2	1_A375_pNL7_minus_lncRNA::1::1582, 2_A375_pNL97_plus_lncRNA::1::2218	-179, -323	upstream, upstream	1	1	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene IKBIP	FLJ31051, IKIP, IKBIP	IKBKB interacting protein	NM_201613, NM_201612, NM_153687, hCT2307751.0, hCT27953.2	227295_at, 235202_x_at, 236249_at	NP_963907.1, NP_963906.1, NP_710154.1, EAW97601.1, EAW97602.1
GeneID:317	APAF1	12	99,039,078	99,129,211	90,133	+	2	1_A375_pNL7_minus_lncRNA::1::1582, 2_A375_pNL97_plus_lncRNA::1::2218	-310, -166	upstream, upstream	1	1	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene APAF1	APAF1, APAF-1, CED4, DKFZp781B1145	apoptotic peptidase activating factor 1	NM_181861, NM_181868, NM_181869, NM_001160, NM_013229, hCT2307601.0, hCT2307602.0, hCT2307604.0, hCT2307606.0, hCT2307607.0, hCT2357967.0, hCT2357968.0, hCT27948.2, hCT27949.2	204859_s_at, 211553_x_at, 211554_s_at	NP_863651.1, NP_863658.1, NP_001151.1, NP_037361.1, NP_863659.1, EAW97610.1, EAW97603.1, EAW97604.1, EAW97605.1, EAW97606.1, EAW97607.1, EAW97608.1, EAW97609.1, EAW97611.1
GeneID:56899	ANKS1B	12	99,129,071	100,378,432	1,249,361	-	3	1_A375_pNL7_minus_lncRNA::1::1583, 2_A375_pNL97_plus_lncRNA::1::2219, 2_A375_pNL97_plus_lncRNA::1::2220	529136, 1170272, 1087504	in gene, in gene, in gene	1	1	11.67	13.67	3	1_A375_pNL7_minus_lncRNA::1	17	Gene ANKS1B	MGC26087, AIDA-1, EB-1, EB1, ANKS1B, ANKS2, AIDA, cajalin-2	ankyrin repeat and sterile alpha motif domain containing 1B	NM_152788, NM_181670, NM_020140	219869_s_at, 227439_at, 227440_at, 227441_s_at, 240292_x_at	NP_690001.3, NP_858056.2, NP_064525.1
GeneID:9971	NR1H4	12	100,867,679	100,957,643	89,964	+	3	1_A375_pNL7_minus_lncRNA::1::1584, 2_A375_pNL97_plus_lncRNA::1::2221, 2_A375_pNL97_plus_lncRNA::1::2222	65505, 65537, 100097	in gene, in gene, downstream	1	1	22.5	24.5	2	1_A375_pNL7_minus_lncRNA::1	31	Gene NR1H4	FXR, RIP14, MGC163445, BAR, HRR-1, HRR1, NR1H4	nuclear receptor subfamily 1, group H, member 4	NM_005123, hCT11975.2, hCT2307277.0, hCT2358104.0	1554375_a_at, 206340_at, 243800_at	NP_005114.1, EAW97638.1, EAW97639.1, EAW97640.1
GeneID:283431	GAS2L3	12	100,967,489	101,018,690	51,201	+	1	2_A375_pNL97_plus_lncRNA::1::2222	287	in gene	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GAS2L3	GAS2L3		NM_174942, hCT12698.3, hCT2349938.0, hCT2349939.0, hCT2349940.0	235709_at, 238756_at	NP_777602.1, EAW97642.1, EAW97641.1, EAW97643.1, EAW97644.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:121601	ANO4	12	101,188,374	101,522,419	334,045	+	2	1_A375_pNL7_minus_lncRNA::1::1586, 2_A375_pNL97_plus_lncRNA::1::2224	31930, 31898	in gene, in gene	1	1	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ANO4	TMEM16D, MGC130026, FLJ35277, ANO4, FLJ34272, FLJ34221	anoctamin 4	NM_178826, hCT1645123.3, hCT1958540.2, hCT2345377.1	229749_at, 236420_s_at, 239883_s_at	NP_849148.2, EAW97645.1, EAW97646.1, EAW97647.1
GeneID:27340	UTP20	12	101,673,905	101,780,397	106,492	+	1	1_A375_pNL7_minus_lncRNA::1::1587	19963	in gene	1	0	14	9	1	1_A375_pNL7_minus_lncRNA::1	14	Gene UTP20	DRIM, UTP20	UTP20, small subunit (SSU) processome component, homolog (yeast)	NM_014503, hCT12933.3, hCT2307229.0, hCT2307231.0, hCT2307232.0, hCT2307233.0	209725_at	NP_055318.2, EAW97654.1, EAW97652.1, EAW97653.1, EAW97655.1, EAW97656.1
GeneID:400	ARL1	12	101,786,914	101,801,572	14,658	-	1	2_A375_pNL97_plus_lncRNA::1::2225	-12	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ARL1	ARFL1, ARL1	ADP-ribosylation factor-like 1	NM_001177, hCT1820920.1, hCT1957557.1, hCT1960841.1, hCT1961824.1	201657_at, 201658_at, 201659_s_at	NP_001168.1, EAW97657.1, EAW97658.1, EAW97659.1, EAW97660.1
GeneID:56994	CHPT1	12	102,091,417	102,122,846	31,429	+	1	2_A375_pNL97_plus_lncRNA::1::2226	711	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CHPT1	CPT, CPT1, CHPT1	choline phosphotransferase 1	NM_020244, hCT12934.2, hCT1953881.1, hCT1953882.1, hCT2356137.0, hCT2356138.0	1559739_at, 221675_s_at, 230364_at	NP_064629.2, EAW97675.1, EAW97673.1, EAW97674.1, EAW97676.1, EAW97677.1
GeneID:55332	DRAM1	12	102,271,105	102,317,401	46,296	+	1	2_A375_pNL97_plus_lncRNA::1::2227	255	in gene	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DRAM1	DRAM, FLJ11259, DRAM1	DNA-damage regulated autophagy modulator 1	NM_018370, hCT2307389.0, hCT2307390.0	218627_at, 241992_at	NP_060840.2, EAW97686.1, EAW97685.1
GeneID:79023	NUP37	12	102,467,970	102,512,361	44,391	-	1	2_A375_pNL97_plus_lncRNA::1::2228	-1431	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene NUP37	NUP37, FLJ22618, MGC5585, p37	nucleoporin 37kDa	NM_024057, hCT12966.1, hCT1953887.1	218622_at	NP_076962.2, EAW97689.1, EAW97688.1
GeneID:55010	C12orf48	12	102,513,956	102,591,298	77,342	+	1	2_A375_pNL97_plus_lncRNA::1::2229	-164	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene C12orf48	FLJ20641, AROM, PARPBP, C12orf48	chromosome 12 open reading frame 48	NM_017915, hCT1820890.1, hCT2307392.0, hCT2356150.0	220060_s_at, 224147_at, 227928_at	NP_060385.3, EAW97690.1, EAW97691.1, EAW97692.1
GeneID:374470	C12orf42	12	103,695,733	103,889,749	194,016	-	1	2_A375_pNL97_plus_lncRNA::1::2230	21	in gene	0	1	7	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C12orf42	MGC43592, MGC57409, C12orf42, FLJ25323	chromosome 12 open reading frame 42	NM_001099336, NM_198521, hCT2340694.0, hCT2340695.0, hCT2340696.0, hCT2340697.0, hCT2340698.0, hCT2340699.0	1561378_at, 239977_at	NP_001092806.1, NP_940923.2, EAW97704.1, EAW97706.1, EAW97707.1, EAW97709.1, EAW97705.1, EAW97708.1
GeneID:51559	NT5DC3	12	104,166,081	104,234,975	68,894	-	1	1_A375_pNL7_minus_lncRNA::1::1591	38975	in gene	1	0	16	16	1	1_A375_pNL7_minus_lncRNA::1	16	Gene NT5DC3	FLJ11266, GNN, TU12B1-TY, TU12B1TY, NT5DC3	5'-nucleotidase domain containing 3	NM_001031701, hCT1960352.1, hCT2307434.0, hCT2307435.0, hCT2307436.0	218786_at, 234737_at	NP_001026871.1, EAW97718.1, EAW97715.1, EAW97716.1, EAW97717.1
GeneID:7184	HSP90B1	12	104,324,189	104,341,703	17,514	+	2	1_A375_pNL7_minus_lncRNA::1::1592, 2_A375_pNL97_plus_lncRNA::1::2232	26819, 26691	downstream, downstream	1	1	23	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene HSP90B1	GRP94, GP96, ECGP, TRA1, HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	NM_003299, hCT12957.2, hCT2344688.0	200598_s_at, 200599_s_at, 216449_x_at, 216450_x_at	NP_003290.1, EAW97724.1, EAW97723.1
GeneID:728568	C12orf73	12	104,343,980	104,350,993	7,013	-	4	1_A375_pNL7_minus_lncRNA::1::1592, 1_A375_pNL7_minus_lncRNA::1::1593, 2_A375_pNL97_plus_lncRNA::1::2232, 2_A375_pNL97_plus_lncRNA::1::2233	-15, -8815, 113, -8591	upstream, upstream, in gene, upstream	1	1	23.5	31.5	2	2_A375_pNL97_plus_lncRNA::1	37	Gene C12orf73	C12orf73, DKFZp547P055, FLJ13975	chromosome 12 open reading frame 73	NM_001135570	226927_at, 226943_at	NP_001129042.1
GeneID:6996	TDG	12	104,359,593	104,382,656	23,063	+	4	1_A375_pNL7_minus_lncRNA::1::1592, 1_A375_pNL7_minus_lncRNA::1::1593, 2_A375_pNL97_plus_lncRNA::1::2232, 2_A375_pNL97_plus_lncRNA::1::2233	-8585, 215, -8713, -9	upstream, in gene, upstream, upstream	1	1	23.5	31.5	2	2_A375_pNL97_plus_lncRNA::1	37	Gene TDG	TDG		NM_003211, hCT2307503.1, hCT2307505.1, hCT2356224.0	203743_s_at	NP_003202.3, EAW97727.1, EAW97728.1, EAW97729.1
GeneID:29915	HCFC2	12	104,458,236	104,500,302	42,066	+	1	2_A375_pNL97_plus_lncRNA::1::2234	100	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene HCFC2	HCFC2, HCF2, HCF-2, FLJ94012	host cell factor C2	NM_013320, hCT11979.2, hCT2356109.0	219464_at	NP_037452.1, EAW97737.1, EAW97736.1
GeneID:7296	TXNRD1	12	104,609,559	104,744,062	134,503	+	2	2_A375_pNL97_plus_lncRNA::1::2235, 2_A375_pNL97_plus_lncRNA::1::2236	71081, 73033	in gene, in gene	0	1	10	19	2	2_A375_pNL97_plus_lncRNA::1	19	Gene TXNRD1	GRIM-12, TR1, TR, TRXR1, TXNRD1, MGC9145, TXNR	thioredoxin reductase 1	NM_182729, NM_182742, NM_182743, NM_003330, NM_001093771, hCT1957554.2, hCT2307512.0, hCT2357954.0	201266_at	NP_877393.1, NP_877419.1, NP_003321.3, NP_001087240.1, NP_877420.1, EAW97743.1, EAW97744.1, EAW97745.1
GeneID:50515	CHST11	12	104,850,692	105,155,792	305,100	+	2	1_A375_pNL7_minus_lncRNA::1::1594, 2_A375_pNL97_plus_lncRNA::1::2237	-116, -132	upstream, upstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CHST11	DKFZp667A035, CHST11, C4ST1, C4ST, C4ST-1, HSA269537, FLJ41682	carbohydrate (chondroitin 4) sulfotransferase 11	NM_001173982, NM_018413, hCT2307515.1, hCT2307516.1, hCT2351951.0	219634_at, 226368_at, 226372_at	NP_001167453.1, NP_060883.1, EAW97748.1, EAW97749.1, EAW97750.1
GeneID:23325	KIAA1033	12	105,501,492	105,562,908	61,416	+	1	2_A375_pNL97_plus_lncRNA::1::2238	44	in gene	0	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene KIAA1033	KIAA1033		NM_015275, hCT1953867.1, hCT2356170.0, hCT2356171.0, hCT6531.3	212794_s_at, 212795_at, 215936_s_at	NP_056090.1, EAW97761.1, EAW97758.1, EAW97759.1, EAW97760.1
GeneID:255394	TCP11L2	12	106,696,581	106,740,793	44,212	+	2	1_A375_pNL7_minus_lncRNA::1::1595, 2_A375_pNL97_plus_lncRNA::1::2240	-197, -229	upstream, upstream	1	1	28	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene TCP11L2	TCP11L2, MGC40368	t-complex 11 (mouse)-like 2	NM_152772, hCT1958539.2, hCT2349908.0, hCT2349909.0, hCT2349910.0, hCT2349911.0, hCT2349912.0	1553861_at, 1559413_at, 1565000_a_at, 1565525_a_at, 1565527_x_at, 1569206_at, 1569207_s_at, 244249_at	NP_689985.1, EAW97778.1, EAW97774.1, EAW97776.1, EAW97777.1, EAW97779.1, EAW97775.1
GeneID:55703	POLR3B	12	106,751,436	106,903,976	152,540	+	1	2_A375_pNL97_plus_lncRNA::1::2241	20	in gene	0	1	20	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene POLR3B	POLR3B, DKFZp686B10117, FLJ10388, RPC2, C128	polymerase (RNA) III (DNA directed) polypeptide B	NM_018082, NM_001160708, hCT1955536.1, hCT2307477.0	1556603_at, 1556604_s_at, 219459_at	NP_060552.4, NP_001154180.1, EAW97780.1, EAW97781.1
GeneID:100287944	LOC100287944	12	106,889,736	107,168,696	278,960	-	2	1_A375_pNL7_minus_lncRNA::1::1596, 2_A375_pNL97_plus_lncRNA::1::2242	760, 680	in gene, in gene	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene LOC100287944		hypothetical protein LOC100287944	XM_002343183		XP_002343224.1
GeneID:55188	RIC8B	12	107,168,399	107,283,094	114,695	+	2	1_A375_pNL7_minus_lncRNA::1::1596, 2_A375_pNL97_plus_lncRNA::1::2242	-463, -383	upstream, upstream	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene RIC8B	FLJ10620, MGC39476, RIC8, RIC8B, hSyn	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	NM_018157, hCT2307484.0, hCT2358208.0, hCT7135.2	219446_at, 229637_at	NP_060627.2, EAW97785.1, EAW97786.1, EAW97787.1
GeneID:90488	C12orf23	12	107,349,544	107,367,813	18,269	+	1	2_A375_pNL97_plus_lncRNA::1::2243	184	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C12orf23	FLJ11721, MGC17943, C12orf23, FLJ13859	chromosome 12 open reading frame 23	NM_152261, hCT2307465.0, hCT7550.3	224759_s_at	NP_689474.1, EAW97790.1, EAW97791.1
GeneID:1407	CRY1	12	107,385,142	107,487,598	102,456	-	1	2_A375_pNL97_plus_lncRNA::1::2244	52	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CRY1	PHLL1, CRY1	cryptochrome 1 (photolyase-like)	NM_004075, hCT1953871.1, hCT2307573.0, hCT2307575.0	209674_at	NP_004066.1, EAW97796.1, EAW97795.1, EAW97797.1
GeneID:11137	PWP1	12	108,079,590	108,106,257	26,667	+	1	2_A375_pNL97_plus_lncRNA::1::2245	26	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PWP1	IEF-SSP-9502, PWP1	PWP1 homolog (S. cerevisiae)	NM_007062, hCT2307409.0, hCT7547.1	201606_s_at, 201607_at, 201608_s_at	NP_008993.1, EAW97803.1, EAW97802.1
GeneID:9671	WSCD2	12	108,523,511	108,644,314	120,803	+	5	1_A375_pNL7_minus_lncRNA::1::1597, 1_A375_pNL7_minus_lncRNA::1::1598, 2_A375_pNL97_plus_lncRNA::1::2247, 2_A375_pNL97_plus_lncRNA::1::2248, 2_A375_pNL97_plus_lncRNA::1::2249	64665, 98921, 64641, 64937, 99273	in gene, in gene, in gene, in gene, in gene	1	1	13	20.67	3	2_A375_pNL97_plus_lncRNA::1	29	Gene WSCD2	WSCD2, MGC117165, KIAA0789	WSC domain containing 2	NM_014653, hCT2307398.0, hCT2307399.0, hCT2307400.0	207637_at, 229032_at	NP_055468.2, EAW97807.1, EAW97808.1, EAW97809.1
GeneID:9733	SART3	12	108,915,991	108,955,165	39,174	-	1	1_A375_pNL7_minus_lncRNA::1::1599	413	in gene	1	0	22	18	1	1_A375_pNL7_minus_lncRNA::1	22	Gene SART3	DSAP1, SART3, KIAA0156, P100, p110, RP11-13G14, p110(nrb), TIP110, MGC138188	squamous cell carcinoma antigen recognized by T cells 3	NM_014706, hCT2358025.0, hCT6722.3	1554276_at, 200069_at, 209127_s_at, 209128_s_at	NP_055521.1, EAW97816.1, EAW97817.1
GeneID:23479	ISCU	12	108,956,294	108,963,160	6,866	+	1	1_A375_pNL7_minus_lncRNA::1::1599	-1542	upstream	1	0	22	18	1	1_A375_pNL7_minus_lncRNA::1	22	Gene ISCU	NIFU, 2310020H20Rik, MGC74517, hnifU, NIFUN, ISCU, HML, ISU2	iron-sulfur cluster scaffold homolog (E. coli)	NM_014301, NM_213595, hCT2307549.0, hCT2358084.0, hCT2358085.0, hCT2358086.0, hCT6727.2	209075_s_at	NP_055116.1, NP_998760.1, EAW97818.1, EAW97819.1, EAW97820.1, EAW97822.1, EAW97821.1
GeneID:6404	SELPLG	12	109,015,671	109,027,670	11,999	-	1	1_A375_pNL7_minus_lncRNA::1::1600	-10154	upstream	1	0	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SELPLG	CD162, PSGL-1, CLA, PSGL1, SELPLG	selectin P ligand	NM_003006, hCT1953870.1, hCT2358018.0	209879_at, 209880_s_at	NP_002997.1, EAW97824.1, EAW97825.1
GeneID:23603	CORO1C	12	109,038,885	109,125,295	86,410	-	4	1_A375_pNL7_minus_lncRNA::1::1600, 1_A375_pNL7_minus_lncRNA::1::1601, 2_A375_pNL97_plus_lncRNA::1::2250, 2_A375_pNL97_plus_lncRNA::1::2251	87471, 39887, 39951, 415	downstream, in gene, in gene, in gene	1	1	14.33	17.67	3	1_A375_pNL7_minus_lncRNA::1	19	Gene CORO1C	CORO1C, HCRNN4	coronin, actin binding protein, 1C	NM_014325, hCT1953869.2, hCT2308005.1, hCT2308008.1, hCT6720.3	221676_s_at, 222409_at	NP_055140.1, EAW97826.1, EAW97827.1, EAW97828.1, EAW97829.1
GeneID:54434	SSH1	12	109,176,466	109,251,359	74,893	-	1	2_A375_pNL97_plus_lncRNA::1::2252	2911	in gene	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SSH1	FLJ21928, SSH1, KIAA1298, SSH1L, FLJ38102	slingshot homolog 1 (Drosophila)	NM_018984, NM_001161330, NM_001161331, hCT2307998.0, hCT2307999.0, hCT2308003.0, hCT6725.3	1554274_a_at, 1555624_a_at, 221752_at, 221753_at	NP_061857.3, NP_001154802.1, NP_001154803.1, EAW97830.1, EAW97832.1, EAW97833.1, EAW97831.1
GeneID:1610	DAO	12	109,273,857	109,294,710	20,853	+	1	1_A375_pNL7_minus_lncRNA::1::1602	10287	in gene	1	0	20	10	1	1_A375_pNL7_minus_lncRNA::1	20	Gene DAO	DAO, OXDA, MGC35381, DAAO, DAMOX	D-amino-acid oxidase	NM_001917, hCT1970725.1, hCT2307559.0, hCT2357974.0, hCT2357975.0, hCT5901.2	206878_at	NP_001908.3, EAW97838.1, EAW97834.1, EAW97835.1, EAW97836.1, EAW97837.1
GeneID:100131733	LOC100131733	12	109,490,163	109,491,770	1,607	-	1	2_A375_pNL97_plus_lncRNA::1::2254	1370	in gene	0	1	20	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100131733		hypothetical LOC100131733	XR_111335, XR_109138, XR_114609		
GeneID:84749	USP30	12	109,490,380	109,525,831	35,451	+	5	1_A375_pNL7_minus_lncRNA::1::1604, 1_A375_pNL7_minus_lncRNA::1::1605, 2_A375_pNL97_plus_lncRNA::1::2254, 2_A375_pNL97_plus_lncRNA::1::2255, 2_A375_pNL97_plus_lncRNA::1::2256	40980, 45364, 20, 40946, 45380	downstream, downstream, in gene, downstream, downstream	1	1	30	27.67	3	1_A375_pNL7_minus_lncRNA::1	45	Gene USP30	FLJ40511, MGC10702, USP30	ubiquitin specific peptidase 30	NM_032663, hCT2307562.0, hCT2357991.0, hCT31584.3	223602_at, 227572_at	NP_116052.2, EAW97842.1, EAW97843.1, EAW97844.1
GeneID:121642	ALKBH2	12	109,525,993	109,531,293	5,300	-	4	1_A375_pNL7_minus_lncRNA::1::1604, 1_A375_pNL7_minus_lncRNA::1::1605, 2_A375_pNL97_plus_lncRNA::1::2255, 2_A375_pNL97_plus_lncRNA::1::2256	-67, -4451, -35, -4467	upstream, upstream, upstream, upstream	1	1	35	29	2	1_A375_pNL7_minus_lncRNA::1	45	Gene ALKBH2	ABH2, FLJ99103, ALKBH2, MGC90512	alkB, alkylation repair homolog 2 (E. coli)	NM_001145374, NM_001001655, NM_001145375, NR_026930, NR_026931, hCT31589.3	225625_at	NP_001138846.1, NP_001001655.1, NP_001138847.1, EAW97845.1
GeneID:7374	UNG	12	109,535,415	109,548,798	13,383	+	4	1_A375_pNL7_minus_lncRNA::1::1604, 1_A375_pNL7_minus_lncRNA::1::1605, 2_A375_pNL97_plus_lncRNA::1::2255, 2_A375_pNL97_plus_lncRNA::1::2256	-4055, 329, -4087, 345	upstream, in gene, upstream, in gene	1	1	35	29	2	1_A375_pNL7_minus_lncRNA::1	45	Gene UNG	UNG15, UNG2, UDG, DGU, UNG1, DKFZp781L1143, UNG, HIGM4	uracil-DNA glycosylase	NM_003362, NM_080911, hCT2307563.0, hCT2307565.0, hCT2307566.0, hCT2307567.0, hCT29737.3	202330_s_at	NP_003353.1, NP_550433.1, EAW97846.1, EAW97847.1, EAW97849.1, EAW97850.1, EAW97848.1
GeneID:83892	KCTD10	12	109,886,460	109,915,155	28,695	-	2	1_A375_pNL7_minus_lncRNA::1::1606, 2_A375_pNL97_plus_lncRNA::1::2257	-141, -109	upstream, upstream	1	1	26	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene KCTD10	ULR061, MSTP028, FLJ41739, KCTD10	potassium channel tetramerisation domain containing 10	NM_031954, hCT2308337.0, hCT2308339.1, hCT2349955.0, hCT2357979.0, hCT31579.3	223208_at, 226518_at	NP_114160.1, EAW97861.1, EAW97860.1, EAW97862.1, EAW97863.1, EAW97864.1
GeneID:89910	UBE3B	12	109,915,439	109,974,507	59,068	+	3	1_A375_pNL7_minus_lncRNA::1::1606, 1_A375_pNL7_minus_lncRNA::1::1607, 2_A375_pNL97_plus_lncRNA::1::2257	-143, 67441, -175	upstream, downstream, upstream	1	1	20.5	22	2	2_A375_pNL97_plus_lncRNA::1	33	Gene UBE3B	DKFZp686A1051, MGC131858, DKFZp586K2123, MGC78388, FLJ45294, UBE3B	ubiquitin protein ligase E3B	NM_183415, NM_130466, hCT2307617.0, hCT2307618.0, hCT2358030.0, hCT31586.3	212403_at, 212404_s_at, 213822_s_at, 227914_s_at, 228860_at, 232301_at	NP_904324.1, NP_569733.2, EAW97865.1, EAW97866.1, EAW97867.1, EAW97868.1
GeneID:326625	MMAB	12	109,991,520	110,011,358	19,838	-	3	1_A375_pNL7_minus_lncRNA::1::1607, 1_A375_pNL7_minus_lncRNA::1::1608, 2_A375_pNL97_plus_lncRNA::1::2258	28478, 222, 254	downstream, in gene, in gene	1	1	21.5	22	2	2_A375_pNL97_plus_lncRNA::1	33	Gene MMAB	ATR, MGC20496, cob, MMAB, cblB	methylmalonic aciduria (cobalamin deficiency) cblB type	NM_052845, hCT31587.3	225826_at, 238975_at, 242082_at	NP_443077.1, EAW97869.1
GeneID:4598	MVK	12	110,011,500	110,035,071	23,571	+	2	1_A375_pNL7_minus_lncRNA::1::1608, 2_A375_pNL97_plus_lncRNA::1::2258	-364, -396	upstream, upstream	1	1	28	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene MVK	MK, MVK, LRBP, MVLK, FLJ96772	mevalonate kinase	NM_000431, NM_001114185, hCT1955422.1, hCT2357976.0, hCT2357977.0, hCT31576.3	204056_s_at, 215649_s_at, 236686_at, 36907_at	NP_000422.1, NP_001107657.1, EAW97870.1, EAW97871.1, EAW97872.1, EAW97873.1
GeneID:84915	C12orf34	12	110,152,187	110,208,312	56,125	+	1	1_A375_pNL7_minus_lncRNA::1::1609	-3419	upstream	1	0	22	14	1	1_A375_pNL7_minus_lncRNA::1	22	Gene C12orf34	C12orf34, FLJ14721	chromosome 12 open reading frame 34	NM_032829, hCT1644630.3, hCT1964706.1	226487_at	NP_116218.2, EAW97874.1, EAW97875.1
GeneID:84260	TCHP	12	110,338,079	110,355,874	17,795	+	2	1_A375_pNL7_minus_lncRNA::1::1610, 2_A375_pNL97_plus_lncRNA::1::2259	-95, -63	upstream, upstream	1	1	27	41	1	2_A375_pNL97_plus_lncRNA::1	41	Gene TCHP	MGC10854, TCHP	trichoplein, keratin filament binding	NM_032300, NM_001143852, hCT2358041.0, hCT31568.4	223455_at, 223456_s_at	NP_115676.1, NP_001137324.1, EAW97883.1, EAW97884.1
GeneID:9815	GIT2	12	110,367,607	110,434,194	66,587	-	3	1_A375_pNL7_minus_lncRNA::1::1611, 2_A375_pNL97_plus_lncRNA::1::2260, 2_A375_pNL97_plus_lncRNA::1::2261	-2894, 49074, -2830	upstream, in gene, upstream	1	1	38	36.5	2	1_A375_pNL7_minus_lncRNA::1	64	Gene GIT2	GIT2, KIAA0148, MGC760, CAT-2, DKFZp686G01261, CAT2	G protein-coupled receptor kinase interacting ArfGAP 2	NM_139201, NM_057170, NM_057169, NM_014776, NM_001135213, NM_001135214, hCT2308310.0, hCT2308313.0, hCT2308316.0, hCT2358155.0, hCT2358156.0, hCT29739.4	204982_at, 209876_at, 225558_at	NP_631940.2, NP_476511.1, NP_476510.1, NP_055591.2, NP_001128685.1, NP_001128686.1, EAW97885.1, EAW97886.1, EAW97887.1, EAW97888.1, EAW97889.1, EAW97890.1
GeneID:88455	ANKRD13A	12	110,437,235	110,477,237	40,002	+	3	1_A375_pNL7_minus_lncRNA::1::1611, 2_A375_pNL97_plus_lncRNA::1::2261, 2_A375_pNL97_plus_lncRNA::1::2262	-147, -211, 49037	upstream, upstream, downstream	1	1	39	35.5	2	1_A375_pNL7_minus_lncRNA::1	64	Gene ANKRD13A	ANKRD13A, NY-REN-25, ANKRD13	ankyrin repeat domain 13A	NM_033121, hCT2307626.0, hCT2307628.0, hCT30298.3	224810_s_at, 238851_at	NP_149112.1, EAW97893.1, EAW97891.1, EAW97892.1
GeneID:400073	C12orf76	12	110,478,983	110,505,500	26,517	-	1	2_A375_pNL97_plus_lncRNA::1::2262	19228	in gene	0	1	14	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene C12orf76	FLJ40142, FLJ11385, C12orf76	chromosome 12 open reading frame 76	NM_207435	1556299_s_at, 226583_at	NP_997318.1
GeneID:488	ATP2A2	12	110,719,032	110,788,898	69,866	+	1	1_A375_pNL7_minus_lncRNA::1::1612	-344	upstream	1	0	19	14	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ATP2A2	ATP2B, DD, FLJ20293, DAR, MGC45367, DKFZp686P0211, ATP2A2, FLJ38063, SERCA2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	NM_170665, NM_001681, NM_001135765, hCT1686592.2, hCT2307838.0, hCT2307839.0, hCT2358201.0, hCT2358202.0, hCT30296.2	209186_at, 212361_s_at, 212362_at, 239996_x_at	NP_733765.1, NP_001672.1, NP_001129237.1, EAW97902.1, EAW97905.1, EAW97907.1, EAW97903.1, EAW97904.1, EAW97906.1
GeneID:51434	ANAPC7	12	110,810,705	110,841,535	30,830	-	1	2_A375_pNL97_plus_lncRNA::1::2263	191	in gene	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ANAPC7	APC7, ANAPC7	anaphase promoting complex subunit 7	NM_016238, NM_001137664, hCT2308302.0, hCT2308303.0, hCT2357980.0	225521_at, 225554_s_at	NP_057322.2, NP_001131136.1, EAW97909.1, EAW97910.1, EAW97911.1
GeneID:51184	GPN3	12	110,890,291	110,906,526	16,235	-	1	2_A375_pNL97_plus_lncRNA::1::2264	438	in gene	0	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GPN3	GPN3, MGC14560, ATPBD1C, MGC32610	GPN-loop GTPase 3	NM_016301, NM_001164372, NM_001164373, hCT2308295.0	218461_at	NP_057385.3, NP_001157844.1, NP_001157845.1, EAW97914.1
GeneID:29902	C12orf24	12	110,906,232	110,928,192	21,960	+	1	2_A375_pNL97_plus_lncRNA::1::2264	-144	upstream	0	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C12orf24	HSU79274, C12orf24	chromosome 12 open reading frame 24	NM_013300, hCT1826922.2, hCT1961846.1, hCT2358003.0	204521_at	NP_037432.2, EAW97915.1, EAW97916.1, EAW97917.1
GeneID:51699	VPS29	12	110,929,330	110,939,916	10,586	-	2	1_A375_pNL7_minus_lncRNA::1::1613, 2_A375_pNL97_plus_lncRNA::1::2265	-52, -36	upstream, upstream	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene VPS29	FLJ20492, DKFZp564F0223, DC7, VPS29, DC15, PEP11	vacuolar protein sorting 29 homolog (S. cerevisiae)	NM_057180, NM_016226, hCT2308290.0, hCT2308292.0	1554368_at, 223026_s_at	NP_476528.1, NP_057310.1, EAW97918.1, EAW97919.1
GeneID:144715	RAD9B	12	110,940,005	110,969,891	29,886	+	2	1_A375_pNL7_minus_lncRNA::1::1613, 2_A375_pNL97_plus_lncRNA::1::2265	-37, -53	upstream, upstream	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene RAD9B	RAD9B, MGC75426, FLJ40346	RAD9 homolog B (S. pombe)	NM_152442, hCT2307845.1, hCT2349957.0, hCT2358090.0, hCT2358091.0, hCT2358092.0, hCT2358093.0, hCT32562.3	1553285_s_at, 1564688_a_at	NP_689655.3, EAW97920.1, EAW97921.1, EAW97922.1, EAW97923.1, EAW97926.1, EAW97924.1, EAW97925.1
GeneID:160760	PPTC7	12	110,972,237	111,021,064	48,827	-	1	1_A375_pNL7_minus_lncRNA::1::1614	4488	in gene	1	0	19	11	1	1_A375_pNL7_minus_lncRNA::1	19	Gene PPTC7	TA-PP2C, DKFZp686M07120, MGC133072, PPTC7, TAPP2C	PTC7 protein phosphatase homolog (S. cerevisiae)	NM_139283, hCT2349956.0, hCT32557.4	225204_at, 225213_at, 235744_at	NP_644812.1, EAW97927.1, EAW97928.1
GeneID:79600	TCTN1	12	111,051,832	111,086,935	35,103	+	1	1_A375_pNL7_minus_lncRNA::1::1615	-24	upstream	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TCTN1	TECT1, FLJ21127, TCTN1	tectonic family member 1	NM_001082537, NM_001082538, NM_001173975, NM_001173976, NM_024549, hCT2307522.0, hCT2307523.0, hCT2358057.0, hCT32558.3	1556864_at, 218584_at	NP_001076006.1, NP_001076007.1, NP_078825.2, NP_001167446.1, NP_001167447.1, EAW97929.1, EAW97930.1, EAW97931.1, EAW97932.1
GeneID:144717	FAM109A	12	111,798,455	111,806,925	8,470	-	2	1_A375_pNL7_minus_lncRNA::1::1616, 2_A375_pNL97_plus_lncRNA::1::2266	109, 13	in gene, in gene	1	1	26	22	1	1_A375_pNL7_minus_lncRNA::1	26	Gene FAM109A	SES1, IPIP27A, FLJ32356, FAM109A	family with sequence similarity 109, member A	NM_001177996, NM_001177997, NM_144671, hCT2307785.1, hCT2349951.0, hCT2349952.0, hCT2349953.0, hCT31468.4	229690_at	NP_001171467.1, NP_001171468.1, NP_653272.2, EAW97950.1, EAW97951.1, EAW97952.1, EAW97949.1, EAW97953.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:10019	SH2B3	12	111,843,752	111,889,427	45,675	+	4	1_A375_pNL7_minus_lncRNA::1::1617, 1_A375_pNL7_minus_lncRNA::1::1618, 2_A375_pNL97_plus_lncRNA::1::2267, 2_A375_pNL97_plus_lncRNA::1::2268	-8760, -6696, -8760, 7576	upstream, upstream, upstream, in gene	1	1	21.33	21.33	3	1_A375_pNL7_minus_lncRNA::1	33	Gene SH2B3	LNK, SH2B3, IDDM20	SH2B adaptor protein 3	NM_005475, hCT2307537.0, hCT31465.3	203320_at	NP_005466.1, EAW97955.1, EAW97956.1
GeneID:6311	ATXN2	12	111,890,018	112,037,480	147,462	-	2	1_A375_pNL7_minus_lncRNA::1::1619, 2_A375_pNL97_plus_lncRNA::1::2269	-152, 1336	upstream, in gene	1	1	13	12.5	2	1_A375_pNL7_minus_lncRNA::1	16	Gene ATXN2	FLJ46772, SCA2, ATX2, TNRC13, ATXN2	ataxin 2	NM_002973, hCT1956212.1, hCT2307761.0, hCT2357959.0, hCT29789.2	202622_s_at	NP_002964.3, EAW97960.1, EAW97957.1, EAW97958.1, EAW97959.1
GeneID:51275	C12orf47	12	112,277,573	112,280,706	3,133	-	2	1_A375_pNL7_minus_lncRNA::1::1620, 2_A375_pNL97_plus_lncRNA::1::2270	866, 898	in gene, in gene	1	1	30	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene C12orf47	FLJ39616, C12orf47	chromosome 12 open reading frame 47	NR_015404, hCT1961819.1, hCT1961820.1	1553987_at, 212868_x_at, 219817_at, 64432_at	EAW97977.1, EAW97978.1
GeneID:8550	MAPKAPK5	12	112,280,279	112,331,228	50,949	+	2	1_A375_pNL7_minus_lncRNA::1::1620, 2_A375_pNL97_plus_lncRNA::1::2270	-439, -471	upstream, upstream	1	1	30	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene MAPKAPK5	PRAK, MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	NM_003668, NM_139078, hCT2309110.0, hCT2358154.0, hCT31402.3	1561937_x_at, 212871_at, 217083_at, 217084_at	NP_003659.2, NP_620777.1, EAW97979.1, EAW97980.1, EAW97981.1
GeneID:89894	TMEM116	12	112,369,086	112,451,023	81,937	-	2	1_A375_pNL7_minus_lncRNA::1::1621, 2_A375_pNL97_plus_lncRNA::1::2271	63, -273	in gene, upstream	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene TMEM116	TMEM116, FLJ90167	transmembrane protein 116	NM_001193453, NM_001193531, NM_138341, hCT1956216.2, hCT2349901.0, hCT2349903.0, hCT2349904.0, hCT2349905.0, hCT2349906.0, hCT2349907.0, hCT31415.4	227172_at	NP_001180382.1, NP_001180460.1, NP_612350.1, EAW97983.1, EAW97987.1, EAW97988.1, EAW97982.1, EAW97984.1, EAW97985.1, EAW97986.1, EAW97989.1
GeneID:10961	ERP29	12	112,451,152	112,461,024	9,872	+	2	1_A375_pNL7_minus_lncRNA::1::1621, 2_A375_pNL97_plus_lncRNA::1::2271	-192, 144	upstream, in gene	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene ERP29	ERp28, C12orf8, PDI-DB, ERP29, ERp31, PDIA9	endoplasmic reticulum protein 29	NM_006817, NM_001034025, hCT1956215.1, hCT2309114.0, hCT31396.2	201216_at	NP_006808.1, NP_001029197.1, EAW97990.1, EAW97991.1, EAW97992.1
GeneID:80018	NAA25	12	112,464,493	112,546,635	82,142	-	3	1_A375_pNL7_minus_lncRNA::1::1622, 2_A375_pNL97_plus_lncRNA::1::2272, 2_A375_pNL97_plus_lncRNA::1::2273	-7969, -69, -7941	upstream, upstream, upstream	1	1	17	20.5	2	2_A375_pNL97_plus_lncRNA::1	26	Gene NAA25	MDM20, DKFZp667K2112, NAP1, NAA25, FLJ13089, C12orf30	N(alpha)-acetyltransferase 25, NatB auxiliary subunit	NM_024953, hCT1956209.1, hCT2358216.0	225886_at, 227245_at, 236816_at	NP_079229.2, EAW97994.1, EAW97993.1
GeneID:10906	TRAFD1	12	112,563,349	112,591,408	28,059	+	2	1_A375_pNL7_minus_lncRNA::1::1622, 2_A375_pNL97_plus_lncRNA::1::2273	-8725, -8773	upstream, upstream	1	1	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene TRAFD1	FLN29, TRAFD1	TRAF-type zinc finger domain containing 1	NM_006700, NM_001143906, hCT1957560.1, hCT2309117.0, hCT2357955.0	202837_at, 242497_at, 243196_s_at, 35254_at	NP_006691.1, NP_001137378.1, EAW97995.1, EAW97996.1, EAW97997.1
GeneID:283450	C12orf51	12	112,597,992	112,819,896	221,904	-	1	2_A375_pNL97_plus_lncRNA::1::2274	-424	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C12orf51	FLJ10510, FLJ30092, FLJ34154, FLJ30208, DKFZp586O1022, C12orf51, MGC126531, KIAA0614	chromosome 12 open reading frame 51	NM_001109662, hCT2344300.1, hCT2349931.0, hCT2349932.0	1557529_at, 1561130_at, 230216_at, 244378_at	NP_001103132.2, EAW97998.1, EAW97999.1, EAW98000.1
GeneID:100506435	LOC100506435	12	112,838,401	112,843,526	5,125	+	1	2_A375_pNL97_plus_lncRNA::1::2275	8799	downstream	0	1	17	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100506435		hypothetical LOC100506435	XR_109130, XR_114614		
GeneID:6128	RPL6	12	112,842,994	112,847,443	4,449	-	2	1_A375_pNL7_minus_lncRNA::1::1623, 2_A375_pNL97_plus_lncRNA::1::2275	-9165, 243	upstream, in gene	1	1	18.5	13.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene RPL6	SHUJUN-2, L6, TXREB1, TAXREB107, RPL6	ribosomal protein L6	NM_000970, NM_001024662, hCT1963979.1, hCT1963980.1, hCT1963981.1, hCT1963982.1, hCT1963983.1, hCT1963984.1, hCT29780.2	200034_s_at	NP_000961.2, NP_001019833.1, EAW98004.1, EAW98007.1, EAW98008.1, EAW98010.1, EAW98005.1, EAW98006.1, EAW98009.1
GeneID:5781	PTPN11	12	112,856,536	112,947,717	91,181	+	2	1_A375_pNL7_minus_lncRNA::1::1623, 2_A375_pNL97_plus_lncRNA::1::2275	72, -9336	in gene, upstream	1	1	18.5	13.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene PTPN11	SH-PTP2, CFC, PTP-1D, MGC14433, NS1, BPTP3, PTP2C, SHP2, SH-PTP3, PTPN11	protein tyrosine phosphatase, non-receptor type 11	NM_002834, hCT2309121.2, hCT2350670.0	1552637_at, 205867_at, 205868_s_at, 209895_at, 209896_s_at, 212610_at	NP_002825.3, EAW98012.1, EAW98011.1
GeneID:22895	RPH3A	12	113,229,549	113,336,686	107,137	+	4	1_A375_pNL7_minus_lncRNA::1::1625, 1_A375_pNL7_minus_lncRNA::1::1626, 2_A375_pNL97_plus_lncRNA::1::2277, 2_A375_pNL97_plus_lncRNA::1::2278	-141, 76947, -141, 76883	upstream, in gene, upstream, in gene	1	1	27.5	28.5	2	2_A375_pNL97_plus_lncRNA::1	35	Gene RPH3A	KIAA0985, RPH3A	rabphilin 3A homolog (mouse)	NM_014954, NM_001143854, hCT2307886.0, hCT2307888.0, hCT2358187.0, hCT2358188.0, hCT31627.4	205230_at	NP_055769.2, NP_001137326.1, EAW98014.1, EAW98016.1, EAW98017.1, EAW98018.1, EAW98015.1
GeneID:79039	DDX54	12	113,594,978	113,623,284	28,306	-	2	1_A375_pNL7_minus_lncRNA::1::1627, 2_A375_pNL97_plus_lncRNA::1::2279	-108, -108	upstream, upstream	1	1	29	28	1	1_A375_pNL7_minus_lncRNA::1	29	Gene DDX54	MGC2835, DDX54, DP97	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	NM_024072, NM_001111322, hCT2307983.0, hCT2358223.0	219111_s_at, 224433_s_at, 225428_s_at	NP_076977.3, NP_001104792.1, EAW98039.1, EAW98040.1
GeneID:84934	C12orf52	12	113,623,555	113,630,119	6,564	+	2	1_A375_pNL7_minus_lncRNA::1::1627, 2_A375_pNL97_plus_lncRNA::1::2279	-163, -163	upstream, upstream	1	1	29	28	1	1_A375_pNL7_minus_lncRNA::1	29	Gene C12orf52	C12orf52, RITA, FLJ14827	chromosome 12 open reading frame 52	NM_032848, hCT2307876.0, hCT31637.3	221777_at, 44065_at	NP_116237.1, EAW98042.1, EAW98041.1
GeneID:115811	IQCD	12	113,633,246	113,658,880	25,634	-	2	1_A375_pNL7_minus_lncRNA::1::1627, 2_A375_pNL97_plus_lncRNA::1::2279	35488, 35488	downstream, downstream	1	1	29	28	1	1_A375_pNL7_minus_lncRNA::1	29	Gene IQCD	4933433C09Rik, IQCD	IQ motif containing D	NM_138451, hCT1956208.1, hCT2307980.0, hCT2307982.0	1552540_s_at	NP_612460.1, EAW98044.1, EAW98043.1, EAW98045.1
GeneID:80024	SLC24A6	12	113,736,571	113,772,925	36,354	-	1	1_A375_pNL7_minus_lncRNA::1::1628	-211	upstream	1	0	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SLC24A6	SLC24A6, FLJ22233, NCLX, NCKX6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	NM_024959, hCT2307974.0, hCT2307975.0, hCT2307977.0, hCT31635.3	218749_s_at, 222727_s_at	NP_079235.2, EAW98049.1, EAW98048.1, EAW98050.1, EAW98051.1
GeneID:196463	PLBD2	12	113,796,371	113,827,458	31,087	+	2	1_A375_pNL7_minus_lncRNA::1::1629, 2_A375_pNL97_plus_lncRNA::1::2280	98, 109	in gene, in gene	1	1	24	22	1	1_A375_pNL7_minus_lncRNA::1	24	Gene PLBD2	P76, PLBD2	phospholipase B domain containing 2	NM_001159727, NM_173542, hCT2358193.0, hCT31634.3	226845_at	NP_001153199.1, NP_775813.2, EAW98052.1, EAW98053.1
GeneID:113675	SDSL	12	113,860,216	113,876,081	15,865	+	1	1_A375_pNL7_minus_lncRNA::1::1630	-152	upstream	1	0	24	17	1	1_A375_pNL7_minus_lncRNA::1	24	Gene SDSL	SDH 2, TDH, SDS-RS1, SDSL	serine dehydratase-like	NM_138432, hCT2307882.0, hCT2307883.0, hCT31633.1	226274_at	NP_612441.1, EAW98057.1, EAW98058.1, EAW98059.1
GeneID:64211	LHX5	12	113,900,694	113,909,877	9,183	-	2	1_A375_pNL7_minus_lncRNA::1::1631, 2_A375_pNL97_plus_lncRNA::1::2281	-8187, -8171	upstream, upstream	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LHX5	MGC129689, LHX5	LIM homeobox 5	NM_022363, hCT31631.1	208333_at	NP_071758.1, EAW98060.1
GeneID:100506452	LOC100506452	12	113,909,808	113,918,286	8,478	+	2	1_A375_pNL7_minus_lncRNA::1::1631, 2_A375_pNL97_plus_lncRNA::1::2281	8256, 8240	in gene, in gene	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100506452		hypothetical LOC100506452	XR_111339, XR_109131, XR_114615		
GeneID:9904	RBM19	12	114,254,543	114,404,176	149,633	-	1	2_A375_pNL97_plus_lncRNA::1::2283	-16	upstream	0	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene RBM19	RBM19, KIAA0682, DKFZp586F1023	RNA binding motif protein 19	NM_016196, NM_001146698, NM_001146699, hCT31594.2, hCT31595.2	205115_s_at, 206019_at	NP_057280.2, NP_001140170.1, NP_001140171.1, EAW98062.1, EAW98063.1
GeneID:6926	TBX3	12	115,108,059	115,121,969	13,910	-	1	2_A375_pNL97_plus_lncRNA::1::2284	-111	upstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TBX3	TBX3, UMS, TBX3-ISO, XHL	T-box 3	NM_005996, NM_016569, hCT1956047.0, hCT1959859.1, hCT2307500.0, hCT2307501.0, hCT2358073.0, hCT31596.2	219682_s_at, 222917_s_at, 225544_at, 228344_s_at, 229565_x_at, 229576_s_at, 243234_at	NP_005987.3, NP_057653.3, EAW98069.1, EAW98070.1, EAW98072.1, EAW98073.1, EAW98071.1, EAW98074.1
GeneID:79794	C12orf49	12	117,153,596	117,175,843	22,247	-	1	2_A375_pNL97_plus_lncRNA::1::2293	-125	upstream	0	1	23	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene C12orf49	C12orf49, FLJ21415	chromosome 12 open reading frame 49	NM_024738, hCT1956214.1, hCT30979.2	218867_s_at, 222767_s_at	NP_079014.1, EAW98088.1, EAW98089.1
GeneID:84900	RNFT2	12	117,176,096	117,291,436	115,340	+	5	1_A375_pNL7_minus_lncRNA::1::1635, 2_A375_pNL97_plus_lncRNA::1::2293, 2_A375_pNL97_plus_lncRNA::1::2294, 2_A375_pNL97_plus_lncRNA::1::2295, 2_A375_pNL97_plus_lncRNA::1::2296	120032, -128, 75265, 81200, 119920	downstream, upstream, in gene, in gene, downstream	1	1	17.5	23.25	4	2_A375_pNL97_plus_lncRNA::1	34	Gene RNFT2	RNFT2, TMEM118, FLJ14627	ring finger protein, transmembrane 2	NM_032814, NM_001109903, hCT1820423.3, hCT2307626.0, hCT2358053.0	1553209_at, 221908_at, 221909_at	NP_116203.2, NP_001103373.1, EAW98090.1, EAW98091.1, EAW98092.1
GeneID:8739	HRK	12	117,299,027	117,319,232	20,205	-	2	1_A375_pNL7_minus_lncRNA::1::1635, 2_A375_pNL97_plus_lncRNA::1::2296	23104, 23216	downstream, downstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene HRK	DP5, HRK, HARAKIRI	harakiri, BCL2 interacting protein (contains only BH3 domain)	NM_003806, hCT29775.2	206864_s_at, 206865_at	NP_003797.1, EAW98093.1
GeneID:26259	FBXW8	12	117,348,761	117,468,953	120,192	+	1	2_A375_pNL97_plus_lncRNA::1::2297	5927	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene FBXW8	FBW6, FBXW8, FBW8, FBXO29, FBXW6, FBX29, MGC33534	F-box and WD repeat domain containing 8	NM_012174, NM_153348, hCT2307629.0, hCT2307630.0, hCT2358124.0, hCT31608.3	231683_at	NP_036306.1, NP_699179.2, EAW98094.1, EAW98095.1, EAW98096.1, EAW98097.1
GeneID:100506570	LOC100506570	12	118,570,053	118,583,387	13,334	-	2	1_A375_pNL7_minus_lncRNA::1::1637, 2_A375_pNL97_plus_lncRNA::1::2298	8795, 9419	in gene, in gene	1	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506570		hypothetical LOC100506570	XR_111344, XR_109137, XR_109136, XR_114620		
GeneID:5037	PEBP1	12	118,573,870	118,583,390	9,520	+	2	1_A375_pNL7_minus_lncRNA::1::1637, 2_A375_pNL97_plus_lncRNA::1::2298	722, 98	in gene, in gene	1	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PEBP1	PEBP, PBP, RKIP, HCNP, PEBP1	phosphatidylethanolamine binding protein 1	NM_002567, hCT2309027.0, hCT2309028.0	205353_s_at, 210825_s_at, 211941_s_at	NP_002558.1, EAW98122.1, EAW98123.1
GeneID:51347	TAOK3	12	118,587,606	118,810,750	223,144	-	3	1_A375_pNL7_minus_lncRNA::1::1638, 2_A375_pNL97_plus_lncRNA::1::2299, 2_A375_pNL97_plus_lncRNA::1::2300	-130, -130, -3554	upstream, upstream, upstream	1	1	29	23	2	1_A375_pNL7_minus_lncRNA::1	46	Gene TAOK3	FLJ31808, JIK, DPK, MAP3K18, DKFZp666H245, TAOK3	TAO kinase 3	NM_016281, hCT1815220.1, hCT1957568.1	220761_s_at, 221508_at	NP_057365.3, EAW98124.1, EAW98125.1
GeneID:64426	SUDS3	12	118,814,358	118,855,840	41,482	+	3	1_A375_pNL7_minus_lncRNA::1::1638, 2_A375_pNL97_plus_lncRNA::1::2299, 2_A375_pNL97_plus_lncRNA::1::2300	-3478, -3478, -54	upstream, upstream, upstream	1	1	29	23	2	1_A375_pNL7_minus_lncRNA::1	46	Gene SUDS3	SAP45, SUDS3, MGC104711, FLJ00052, SDS3	suppressor of defective silencing 3 homolog (S. cerevisiae)	NM_022491, hCT1956213.1, hCT2309040.0, hCT2309043.0, hCT2358054.0, hCT30906.3	224974_at, 233541_s_at	NP_071936.2, EAW98137.1, EAW98138.1, EAW98139.1, EAW98140.1, EAW98141.1
GeneID:84530	SRRM4	12	119,419,396	119,600,857	181,461	+	2	1_A375_pNL7_minus_lncRNA::1::1639, 2_A375_pNL97_plus_lncRNA::1::2301	79708, 79772	in gene, in gene	1	1	28	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene SRRM4	nSR100, SRRM4, MGC176729, MU-MB-2.76, KIAA1853	serine/arginine repetitive matrix 4	NM_194286, hCT18345.3	230010_at, 236151_at, 237828_at	NP_919262.2, EAW98142.1
GeneID:11113	CIT	12	120,123,598	120,315,092	191,494	-	1	2_A375_pNL97_plus_lncRNA::1::2302	212	in gene	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CIT	CIT, CRIK, KIAA0949, STK21	citron (rho-interacting, serine/threonine kinase 21)	NM_007174, hCT18924.4, hCT2349943.0, hCT2349944.0, hCT2349945.0	212801_at, 242872_at	NP_009105.1, EAW98155.1, EAW98156.1, EAW98157.1, EAW98158.1
GeneID:92558	CCDC64	12	120,427,648	120,532,299	104,651	+	5	1_A375_pNL7_minus_lncRNA::1::1640, 1_A375_pNL7_minus_lncRNA::1::1641, 1_A375_pNL7_minus_lncRNA::1::1642, 2_A375_pNL97_plus_lncRNA::1::2303, 2_A375_pNL97_plus_lncRNA::1::2304	-336, 352, 97120, 128, 97131	upstream, in gene, in gene, in gene, in gene	1	1	18.67	17.33	3	1_A375_pNL7_minus_lncRNA::1	21	Gene CCDC64	H_267D11.1, CCDC64, FLJ26450, BICDR-1	coiled-coil domain containing 64	NM_207311, hCT2307915.0, hCT2307916.0, hCT2307917.0, hCT2358056.0	215015_at, 228320_x_at	NP_997194.2, EAW98160.1, EAW98159.1, EAW98161.1, EAW98162.1
GeneID:11021	RAB35	12	120,532,899	120,554,643	21,744	-	2	1_A375_pNL7_minus_lncRNA::1::1642, 2_A375_pNL97_plus_lncRNA::1::2304	29875, 29864	downstream, downstream	1	1	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene RAB35	RAB1C, RAY, H-ray, RAB35	RAB35, member RAS oncogene family	NM_001167606, NM_006861, hCT2308872.0, hCT2358001.0, hCT2358002.0	205461_at, 221819_at, 225620_at	NP_001161078.1, NP_006852.1, EAW98163.1, EAW98164.1, EAW98165.1
GeneID:10985	GCN1L1	12	120,565,014	120,632,513	67,499	-	4	1_A375_pNL7_minus_lncRNA::1::1643, 1_A375_pNL7_minus_lncRNA::1::1644, 2_A375_pNL97_plus_lncRNA::1::2305, 2_A375_pNL97_plus_lncRNA::1::2306	1, -6559, 65, -6559	in gene, upstream, in gene, upstream	1	1	113.5	121	2	2_A375_pNL97_plus_lncRNA::1	217	Gene GCN1L1	PRIC295, GCN1L, GCN1, KIAA0219, GCN1L1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	NM_006836, hCT18923.3, hCT2308865.0, hCT2308866.0	212139_at, 216232_s_at	NP_006827.1, EAW98169.1, EAW98167.1, EAW98168.1
GeneID:6175	RPLP0	12	120,634,503	120,639,014	4,511	-	4	1_A375_pNL7_minus_lncRNA::1::1643, 1_A375_pNL7_minus_lncRNA::1::1644, 2_A375_pNL97_plus_lncRNA::1::2305, 2_A375_pNL97_plus_lncRNA::1::2306	6502, -58, 6566, -58	downstream, upstream, downstream, upstream	1	1	113.5	121	2	2_A375_pNL97_plus_lncRNA::1	217	Gene RPLP0	MGC111226, PRLP0, LP0, L10E, RPLP0, P0, RPP0, MGC88175	ribosomal protein, large, P0	NM_053275, NM_001002, hCT2308860.1, hCT2308861.0, hCT2308862.1, hCT2308863.1, hCT2358000.1	201033_x_at, 208856_x_at, 211720_x_at, 211972_x_at	NP_444505.1, NP_000993.1, EAW98170.1, EAW98171.1, EAW98173.1, EAW98174.1, EAW98172.1
GeneID:100506649	LOC100506649	12	120,639,111	120,651,201	12,090	+	4	1_A375_pNL7_minus_lncRNA::1::1643, 1_A375_pNL7_minus_lncRNA::1::1644, 2_A375_pNL97_plus_lncRNA::1::2305, 2_A375_pNL97_plus_lncRNA::1::2306	-6599, -39, -6663, -39	upstream, upstream, upstream, upstream	1	1	113.5	121	2	2_A375_pNL97_plus_lncRNA::1	217	Gene LOC100506649		hypothetical LOC100506649	XR_111345, XR_111346, XR_109139, XR_109140, XR_114621, XR_114622		
GeneID:5829	PXN	12	120,648,250	120,703,563	55,313	-	4	1_A375_pNL7_minus_lncRNA::1::1644, 1_A375_pNL7_minus_lncRNA::1::1645, 1_A375_pNL7_minus_lncRNA::1::1646, 2_A375_pNL97_plus_lncRNA::1::2306	64491, 33979, -213, 64491	downstream, in gene, upstream, downstream	1	1	78	79.67	3	2_A375_pNL97_plus_lncRNA::1	217	Gene PXN	FLJ16691, PXN	paxillin	NM_001080855, NM_002859, NM_025157, hCT18914.3, hCT1955415.2, hCT2308854.1, hCT2308857.1, hCT2308858.1	201087_at, 211823_s_at	NP_001074324.1, NP_002850.2, NP_079433.3, EAW98175.1, EAW98177.1, EAW98178.1, EAW98176.1, EAW98179.1
GeneID:26834	RNU4-2	12	120,729,566	120,729,706	140	-	3	1_A375_pNL7_minus_lncRNA::1::1647, 1_A375_pNL7_minus_lncRNA::1::1648, 2_A375_pNL97_plus_lncRNA::1::2307	-54, -1366, -102	upstream, upstream, upstream	1	1	35	34.5	2	2_A375_pNL97_plus_lncRNA::1	56	Gene RNU4-2	RNU4C, RNU4-1B, U4A, U4b, RNU4B1, U4c, RNU4-2	RNA, U4 small nuclear 2	NR_003137		
GeneID:26835	RNU4-1	12	120,730,897	120,731,040	143	-	5	1_A375_pNL7_minus_lncRNA::1::1647, 1_A375_pNL7_minus_lncRNA::1::1648, 1_A375_pNL7_minus_lncRNA::1::1649, 2_A375_pNL97_plus_lncRNA::1::2307, 2_A375_pNL97_plus_lncRNA::1::2308	1280, -32, -9120, 1232, -9152	downstream, upstream, upstream, downstream, upstream	1	1	32.67	32	3	2_A375_pNL97_plus_lncRNA::1	56	Gene RNU4-1	U4BL, U4, RNU4-1, RNU4A, RNU4B2	RNA, U4 small nuclear 1	NR_003925		
GeneID:23409	SIRT4	12	120,740,124	120,751,045	10,921	+	5	1_A375_pNL7_minus_lncRNA::1::1647, 1_A375_pNL7_minus_lncRNA::1::1648, 1_A375_pNL7_minus_lncRNA::1::1649, 2_A375_pNL97_plus_lncRNA::1::2307, 2_A375_pNL97_plus_lncRNA::1::2308	-10364, -9052, 36, -10316, 68	upstream, upstream, in gene, upstream, in gene	1	1	32.67	32	3	2_A375_pNL97_plus_lncRNA::1	56	Gene SIRT4	MGC130047, SIR2L4, MGC130046, SIRT4, MGC57437	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	NM_012240, hCT18916.2, hCT2308058.0	220047_at, 222248_s_at	NP_036372.1, EAW98182.1, EAW98183.1
GeneID:1337	COX6A1	12	120,875,904	120,878,532	2,628	+	2	1_A375_pNL7_minus_lncRNA::1::1650, 2_A375_pNL97_plus_lncRNA::1::2309	8304, 8352	downstream, downstream	1	1	20	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene COX6A1	COX6AL, COX6A1, MGC104500, COX6A	cytochrome c oxidase subunit VIa polypeptide 1	NM_004373, hCT1816775.1, hCT2308018.0	200925_at, 224344_at, 234676_at	NP_004364.2, EAW98190.1, EAW98191.1

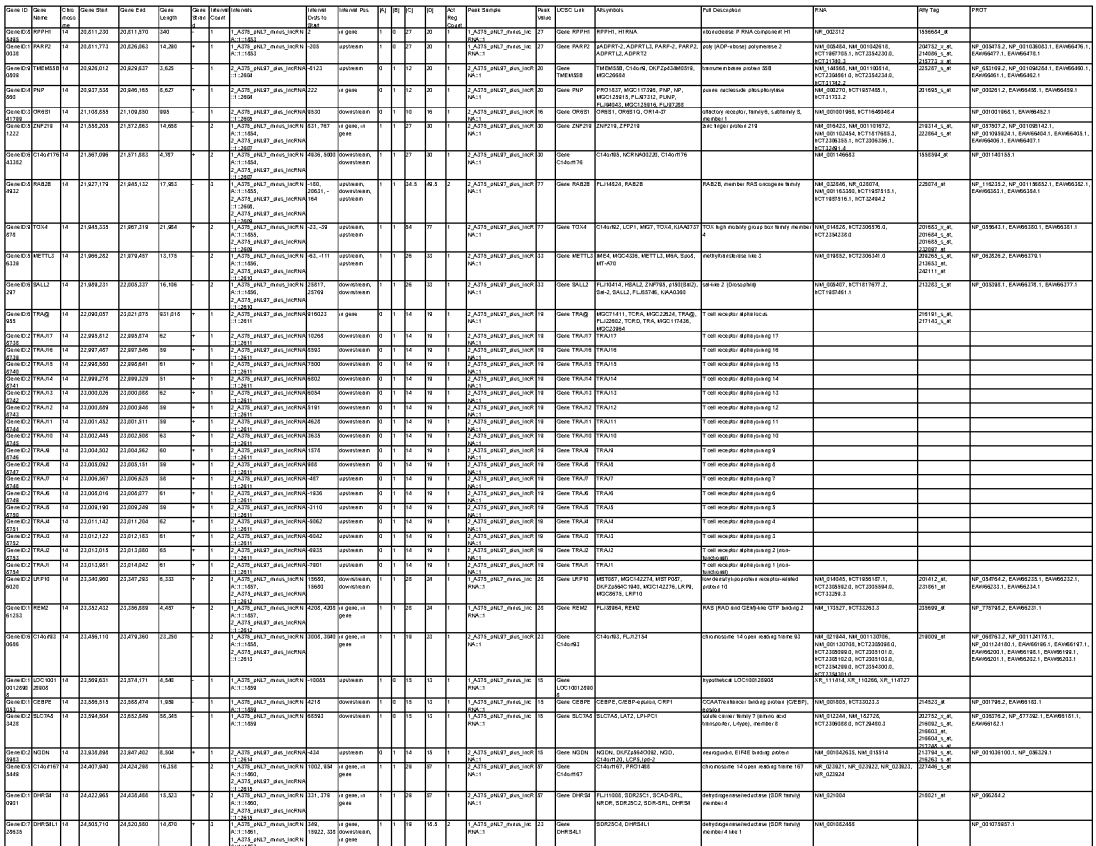
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:51499	TRIAP1	12	120,881,764	120,884,215	2,451	-	2	1_A375_pNL7_minus_lncRNA::1::1650, 2_A375_pNL97_plus_lncRNA::1::2309	7, -41	in gene, upstream	1	1	20	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene TRIAP1	WF-1, P53CSV, TRIAP1, HSPC132	TP53 regulated inhibitor of apoptosis 1	NM_016399, hCT17663.1	218403_at	NP_057483.1, EAW98192.1
GeneID:283459	GATC	12	120,884,241	120,901,556	17,315	+	4	1_A375_pNL7_minus_lncRNA::1::1650, 1_A375_pNL7_minus_lncRNA::1::1651, 2_A375_pNL97_plus_lncRNA::1::2309, 2_A375_pNL97_plus_lncRNA::1::2310	-33, 23343, 15, 23423	upstream, downstream, in gene, downstream	1	1	23.5	30	2	2_A375_pNL97_plus_lncRNA::1	32	Gene GATC	FLJ37000, GATC, 15E1.2, MGC129936	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)	NM_176818, NR_033684, hCT18921.2	214711_at	NP_789788.1, EAW98193.1
GeneID:8683	SFRS9	12	120,899,471	120,907,558	8,087	-	2	1_A375_pNL7_minus_lncRNA::1::1651, 2_A375_pNL97_plus_lncRNA::1::2310	-26, -106	upstream, upstream	1	1	27	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene SFRS9	SFRS9, SRp30c, SRSF9	serine/arginine-rich splicing factor 9	NM_003769, hCT18913.2	200044_at, 201698_s_at, 225430_at	NP_003760.1, EAW98194.1
GeneID:8655	DYNLL1	12	120,907,660	120,936,298	28,638	+	3	1_A375_pNL7_minus_lncRNA::1::1651, 2_A375_pNL97_plus_lncRNA::1::2310, 2_A375_pNL97_plus_lncRNA::1::2311	-76, 4, 26644	upstream, in gene, in gene	1	1	20.5	24.5	2	2_A375_pNL97_plus_lncRNA::1	32	Gene DYNLL1	DYNLL1, LC8, DNCLC1, DNCL1, PIN, DLC1, LC8a, MGC126138, DLC8, MGC126137, hdlc1	dynein, light chain, LC8-type 1	NM_001037494, NM_001037495, NM_003746, hCT18909.1, hCT2308021.0, hCT2308022.0	200703_at	NP_001032583.1, NP_001032584.1, NP_003737.1, EAW98195.1, EAW98196.1, EAW98197.1
GeneID:100506668	LOC100506668	12	120,925,095	120,933,743	8,648	-	1	2_A375_pNL97_plus_lncRNA::1::2311	-561	upstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100506668		hypothetical LOC100506668	XR_111348, XR_111347, XR_109142, XR_109141, XR_114624, XR_114623		
GeneID:84274	COQ5	12	120,941,082	120,966,964	25,882	-	3	2_A375_pNL97_plus_lncRNA::1::2311, 2_A375_pNL97_plus_lncRNA::1::2312, 2_A375_pNL97_plus_lncRNA::1::2313	32660, 100, -5372	downstream, in gene, upstream	0	1	14.67	17	3	2_A375_pNL97_plus_lncRNA::1	18	Gene COQ5	MGC4767, MGC104303, COQ5	coenzyme Q5 homolog, methyltransferase (S. cerevisiae)	NM_032314, hCT1816781.2, hCT18920.2	223114_at	NP_115690.3, EAW98199.1, EAW98198.1
GeneID:9921	RNF10	12	120,972,132	121,015,397	43,265	+	2	2_A375_pNL97_plus_lncRNA::1::2312, 2_A375_pNL97_plus_lncRNA::1::2313	-5268, 204	upstream, in gene	0	1	15	17	2	2_A375_pNL97_plus_lncRNA::1	18	Gene RNF10	RIE2, MGC126758, RNF10, KIAA0262, MGC126764	ring finger protein 10	NM_014868, hCT18912.2, hCT2308024.0, hCT2308025.0, hCT2357989.0, hCT2357990.0	207801_s_at, 208632_at	NP_055683.3, EAW98201.1, EAW98200.1, EAW98202.1, EAW98203.1, EAW98204.1
GeneID:121665	UNQ1887	12	121,201,035	121,342,151	141,116	-	3	1_A375_pNL7_minus_lncRNA::1::1652, 2_A375_pNL97_plus_lncRNA::1::2314, 2_A375_pNL97_plus_lncRNA::1::2315	-3321, -121, -2873	upstream, upstream, upstream	1	1	13.5	20	2	2_A375_pNL97_plus_lncRNA::1	23	Gene UNQ1887	MGC126676, PRO4332, SPPL3, DKFZp586C1324, MGC126674, PSL4, IMP2, MGC90402, MDHV1887	signal peptide peptidase 3	NM_139015, hCT1816783.4, hCT1966205.2, hCT1966206.2, hCT2351278.0	1554564_a_at, 1554565_x_at, 1566896_at, 1566897_at, 224638_at, 224639_at, 224640_at	NP_620584.2, EAW98220.1, EAW98221.1, EAW98222.1, EAW98223.1
GeneID:8638	OASL	12	121,458,095	121,476,780	18,685	-	2	1_A375_pNL7_minus_lncRNA::1::1653, 2_A375_pNL97_plus_lncRNA::1::2316	-116, -180	upstream, upstream	1	1	53	35	1	1_A375_pNL7_minus_lncRNA::1	53	Gene OASL	OASL, p59OASL, TRIP14	2'-5'-oligoadenylate synthetase-like	NM_198213, NM_003733, hCT18501.2, hCT1955413.1, hCT2309626.0, hCT2309629.0	205660_at, 210797_s_at	NP_937856.1, NP_003724.1, EAW98235.1, EAW98236.1, EAW98237.1, EAW98238.1
GeneID:51433	ANAPC5	12	121,746,048	121,792,012	45,964	-	2	1_A375_pNL7_minus_lncRNA::1::1654, 2_A375_pNL97_plus_lncRNA::1::2317	1676, 1676	in gene, in gene	1	1	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene ANAPC5	APC5, ANAPC5	anaphase promoting complex subunit 5	NM_016237, NM_001137559, hCT17651.4, hCT2345157.1, hCT2358219.0	200098_s_at, 208721_s_at, 208722_s_at, 211036_x_at, 238651_at	NP_057321.2, NP_001131031.1, EAW98259.1, EAW98260.1, EAW98261.1
GeneID:84678	KDM2B	12	121,866,899	122,018,920	152,021	-	2	1_A375_pNL7_minus_lncRNA::1::1655, 2_A375_pNL97_plus_lncRNA::1::2318	113672, 113960	in gene, in gene	1	1	25	21	1	1_A375_pNL7_minus_lncRNA::1	25	Gene KDM2B	JHDM1B, CXXC2, PCCX2, FBXL10, KDM2B, Fbl10	lysine (K)-specific demethylase 2B	NM_001005366, NM_032590, hCT18489.3, hCT2309709.0, hCT2309710.0	226215_s_at	NP_001005366.1, NP_115979.3, EAW98266.1, EAW98267.1, EAW98268.1
GeneID:54509	RHOF	12	122,215,660	122,231,594	15,934	-	3	1_A375_pNL7_minus_lncRNA::1::1656, 2_A375_pNL97_plus_lncRNA::1::2319, 2_A375_pNL97_plus_lncRNA::1::2320	-3542, -406, -4454	upstream, upstream, upstream	1	1	18.67	15.33	3	1_A375_pNL7_minus_lncRNA::1	24	Gene RHOF	RIF, FLJ20247, ARHF, RHOF	ras homolog gene family, member F (in filopodia)	NM_019034, hCT10568.2, hCT2309705.0	1554538_at, 1554539_a_at, 219045_at, 219154_at, 222812_s_at, 236667_at	NP_061907.2, EAW98278.1, EAW98279.1
GeneID:338799	LOC338799	12	122,233,173	122,241,390	8,217	-	3	1_A375_pNL7_minus_lncRNA::1::1656, 2_A375_pNL97_plus_lncRNA::1::2319, 2_A375_pNL97_plus_lncRNA::1::2320	6254, 9390, 5342	in gene, downstream, in gene	1	1	18.67	15.33	3	1_A375_pNL7_minus_lncRNA::1	24	Gene LOC338799	FLJ37163	hypothetical LOC338799	NR_002809	1556042_s_at, 226369_at	
GeneID:23067	SETD1B	12	122,242,638	122,270,562	27,924	+	2	1_A375_pNL7_minus_lncRNA::1::1656, 2_A375_pNL97_plus_lncRNA::1::2320	-7502, -6590	upstream, upstream	1	1	17.5	15	2	1_A375_pNL7_minus_lncRNA::1	24	Gene SETD1B	KMT2G, KIAA1076, FLJ20803, SETD1B, Set1B	SET domain containing 1B	NM_015048	213153_at	NP_055863.1
GeneID:3242	HPD	12	122,277,433	122,326,517	49,084	-	2	1_A375_pNL7_minus_lncRNA::1::1657, 2_A375_pNL97_plus_lncRNA::1::2321	53, -107	in gene, upstream	1	1	28	21	1	1_A375_pNL7_minus_lncRNA::1	28	Gene HPD	4-HPPD, HPD, PPD, GLOD3, HPPDASE, 4HPPD	4-hydroxyphenylpyruvate dioxygenase	NM_002150, NM_001171993, hCT1957563.2, hCT9657.2	206024_at	NP_002141.1, NP_001165464.1, EAW98291.1, EAW98292.1
GeneID:5715	PSMD9	12	122,326,646	122,355,771	29,125	+	2	1_A375_pNL7_minus_lncRNA::1::1657, 2_A375_pNL97_plus_lncRNA::1::2321	-182, -22	upstream, upstream	1	1	28	21	1	1_A375_pNL7_minus_lncRNA::1	28	Gene PSMD9	PSMD9, MGC8644, Rpn4, p27	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	NM_002813, hCT2309314.0, hCT2309315.0, hCT2309316.0, hCT2358019.0, hCT2358020.0	207805_s_at, 209334_s_at	NP_002804.2, EAW98295.1, EAW98293.1, EAW98294.1, EAW98296.1, EAW98297.1
GeneID:100506691	LOC100506691	12	122,505,987	122,506,670	683	+	1	2_A375_pNL97_plus_lncRNA::1::2322	10429	downstream	0	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100506691		hypothetical LOC100506691	XR_109143		
GeneID:22877	MLXIP	12	122,516,760	122,517,172	412	+	1	2_A375_pNL97_plus_lncRNA::1::2322	-344	upstream	0	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene MLXIP	MONDOA, bHLHe36, MIR, MLXIP, KIAA0867	MLX interacting protein	NM_014938, hCT1957558.2, hCT2309320.1, hCT2309321.1	1554866_a_at, 202519_at, 211789_s_at, 225157_at	NP_055753.3, EAW98304.1, EAW98305.1, EAW98306.1
GeneID:56616	DIABLO	12	122,692,209	122,712,068	19,859	-	1	1_A375_pNL7_minus_lncRNA::1::1658	1556	in gene	1	0	19	14	1	1_A375_pNL7_minus_lncRNA::1	19	Gene DIABLO	FLJ10537, FLJ25049, SMAC, DIABLO, DIABLO-S, SMAC3	diablo homolog (Drosophila)	NM_019887, NM_138929, NR_024600, NR_024601	219350_s_at	NP_063940.1, NP_620307.1
GeneID:65082	VPS33A	12	122,716,094	122,751,068	34,974	-	3	1_A375_pNL7_minus_lncRNA::1::1658, 1_A375_pNL7_minus_lncRNA::1::1659, 2_A375_pNL97_plus_lncRNA::1::2323	40556, -4, 124	downstream, upstream, in gene	1	1	23.5	20.5	2	1_A375_pNL7_minus_lncRNA::1	28	Gene VPS33A	FLJ23187, FLJ22395, VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	NM_022916	204590_x_at, 244400_at	NP_075067.2
GeneID:6249	CLIP1	12	122,755,981	122,907,116	151,135	-	2	1_A375_pNL7_minus_lncRNA::1::1659, 2_A375_pNL97_plus_lncRNA::1::2323	156044, 156172	downstream, downstream	1	1	28	27	1	1_A375_pNL7_minus_lncRNA::1	28	Gene CLIP1	CLIP-170, MGC131604, RSN, CLIP170, CLIP, CLIP1, CYLN1	CAP-GLY domain containing linker protein 1	NM_002956, NM_198240, hCT2309714.0, hCT2309715.0, hCT2309716.0, hCT2309718.0	1556924_s_at, 1568012_at, 201975_at, 210716_s_at, 240444_x_at	NP_002947.1, NP_937883.1, EAW98320.1, EAW98321.1, EAW98322.1, EAW98323.1
GeneID:8562	DENR	12	123,237,371	123,255,953	18,582	+	1	2_A375_pNL97_plus_lncRNA::1::2324	5	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DENR	DRP1, DRP, SMAP-3, DENR	density-regulated protein	NM_003677, hCT2349948.0, hCT2349949.0, hCT2358050.0, hCT2358051.0, hCT2358052.0, hCT24384.4	221509_at, 231896_s_at, 234347_s_at, 234915_s_at	NP_003668.2, EAW98341.1, EAW98339.1, EAW98340.1, EAW98342.1, EAW98343.1, EAW98338.1
GeneID:79720	VPS37B	12	123,349,875	123,380,712	30,837	-	2	1_A375_pNL7_minus_lncRNA::1::1660, 2_A375_pNL97_plus_lncRNA::1::2325	-24, -88	upstream, upstream	1	1	27	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene VPS37B	VPS37B, FLJ12750	vacuolar protein sorting 37 homolog B (S. cerevisiae)	NM_024667, hCT1963699.1, hCT1963700.1, hCT2309220.0, hCT24379.2	221704_s_at	NP_078943.1, EAW98348.1, EAW98349.1, EAW98350.1, EAW98351.1
GeneID:23457	ABCB9	12	123,413,539	123,459,752	46,213	-	4	1_A375_pNL7_minus_lncRNA::1::1661, 1_A375_pNL7_minus_lncRNA::1::1662, 2_A375_pNL97_plus_lncRNA::1::2326, 2_A375_pNL97_plus_lncRNA::1::2327	30376, 477, 30600, 456	in gene, in gene, in gene, in gene	1	1	28	29	2	2_A375_pNL97_plus_lncRNA::1	37	Gene ABCB9	ABCB9, hABCB9, KIAA1520, TAPL, EST122234	ATP-binding cassette, sub-family B (MDR/TAP), member 9	NM_203444, NM_019625, NM_019624, hCT1821103.3, hCT2309208.1, hCT2309209.1, hCT2309210.0, hCT2309211.0, hCT2309212.1, hCT2309214.1, hCT2343638.0, hCT2343639.0, hCT2358049.0, hCT24383.4	1555323_at, 207321_s_at, 214209_s_at	NP_982269.1, NP_062571.1, NP_062570.1, EAW98353.1, EAW98354.1, EAW98358.1, EAW98355.1, EAW98356.1, EAW98357.1, EAW98359.1, EAW98360.1, EAW98361.1, EAW98362.1, EAW98363.1
GeneID:79676	OGFOD2	12	123,459,354	123,464,588	5,234	+	2	1_A375_pNL7_minus_lncRNA::1::1662, 2_A375_pNL97_plus_lncRNA::1::2327	-79, -58	upstream, upstream	1	1	33	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene OGFOD2	OGFOD2, DKFZp686H15154, MGC120434, FLJ13491, MGC120436, FLJ37501	2-oxoglutarate and iron-dependent oxygenase domain containing 2	NM_024623, hCT2308155.0, hCT2358008.0, hCT2358009.0, hCT2358010.0, hCT2358011.0, hCT2358012.0, hCT2358013.0, hCT2358014.0, hCT24381.2	219245_s_at, 219246_s_at, 44617_at	NP_078899.1, EAW98367.1, EAW98364.1, EAW98365.1, EAW98371.1, EAW98372.1, EAW98366.1, EAW98368.1, EAW98369.1, EAW98370.1
GeneID:51329	ARL6IP4	12	123,464,880	123,467,460	2,580	+	2	1_A375_pNL7_minus_lncRNA::1::1662, 2_A375_pNL97_plus_lncRNA::1::2327	-5605, -5584	upstream, upstream	1	1	33	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene ARL6IP4	SRp37, SFRS20, SRp25, SR-25, ARL6IP4, MGC814	ADP-ribosylation-like factor 6 interacting protein 4	NM_001002252, NM_016638, NM_001002251, NM_018694, hCT1821106.2, hCT2308128.0, hCT2308129.0, hCT2308130.0, hCT2308131.0, hCT2308132.0, hCT2308134.0, hCT2308135.0, hCT2357994.0, hCT24373.2	218216_x_at, 220597_s_at	NP_001002252.1, NP_057722.2, NP_001002251.1, NP_061164.2, EAW98378.1, EAW98381.1, EAW98373.1, EAW98374.1, EAW98375.1, EAW98376.1, EAW98377.1, EAW98379.1, EAW98380.1, EAW98382.1
GeneID:57605	PITPNM2	12	123,468,027	123,594,975	126,948	-	5	1_A375_pNL7_minus_lncRNA::1::1662, 1_A375_pNL7_minus_lncRNA::1::1663, 2_A375_pNL97_plus_lncRNA::1::2327, 2_A375_pNL97_plus_lncRNA::1::2328, 2_A375_pNL97_plus_lncRNA::1::2329	135700, 20575, 135679, 24511, 20703	downstream, in gene, downstream, in gene, in gene	1	1	22.33	24.33	3	2_A375_pNL97_plus_lncRNA::1	37	Gene PITPNM2	PITPNM2, RDGBA2, KIAA1457, RDGB2, NIR3	phosphatidylinositol transfer protein, membrane-associated 2	NM_020845, hCT2309204.0, hCT2309205.0, hCT2309206.0, hCT24380.3	1552923_a_at, 1552924_a_at, 232950_s_at	NP_065896.1, EAW98386.1, EAW98383.1, EAW98384.1, EAW98385.1
GeneID:100507091	LOC100507091	12	123,565,931	123,569,291	3,360	+	3	1_A375_pNL7_minus_lncRNA::1::1663, 2_A375_pNL97_plus_lncRNA::1::2328, 2_A375_pNL97_plus_lncRNA::1::2329	8469, 4533, 8341	downstream, downstream, downstream	1	1	17	18	2	1_A375_pNL7_minus_lncRNA::1	21	Gene LOC100507091		hypothetical LOC100507091	XR_111356, XR_109101, XR_114628		
GeneID:91574	C12orf65	12	123,717,844	123,742,506	24,662	+	2	1_A375_pNL7_minus_lncRNA::1::1665, 2_A375_pNL97_plus_lncRNA::1::2330	-212, -297	upstream, upstream	1	1	22	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene C12orf65	FLJ38663, C12orf65, COXPD7	chromosome 12 open reading frame 65	NM_001143905, NM_152269, NM_001194995, hCT2308139.0, hCT2308140.0	223476_s_at, 223477_s_at, 232650_at	NP_001137377.1, NP_689482.1, NP_001181924.1, EAW98395.1, EAW98396.1
GeneID:10959	TMED2	12	124,069,076	124,082,688	13,612	+	4	1_A375_pNL7_minus_lncRNA::1::1666, 1_A375_pNL7_minus_lncRNA::1::1667, 2_A375_pNL97_plus_lncRNA::1::2331, 2_A375_pNL97_plus_lncRNA::1::2332	-84, 17420, -20, 17452	upstream, downstream, upstream, downstream	1	1	30.5	35	2	2_A375_pNL97_plus_lncRNA::1	45	Gene TMED2	FLJ21323, RNP24, P24A, TMED2	transmembrane emp24 domain trafficking protein 2	NM_006815, hCT1781768.2, hCT2336930.0	200087_s_at, 204426_at, 204427_s_at	NP_006806.1, EAW98417.1, EAW98418.1
GeneID:100507130	LOC100507130	12	124,082,395	124,100,564	18,169	-	2	1_A375_pNL7_minus_lncRNA::1::1667, 2_A375_pNL97_plus_lncRNA::1::2332	14068, 14036	in gene, in gene	1	1	28	25	1	1_A375_pNL7_minus_lncRNA::1	28	Gene LOC100507130		hypothetical LOC100507130	XR_109103, XR_114630		
GeneID:57696	DDX55	12	124,086,672	124,105,482	18,810	+	2	1_A375_pNL7_minus_lncRNA::1::1667, 2_A375_pNL97_plus_lncRNA::1::2332	-176, -144	upstream, upstream	1	1	28	25	1	1_A375_pNL7_minus_lncRNA::1	28	Gene DDX55	MGC33209, KIAA1595, DDX55, FLJ16577	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	NM_020936, hCT2336931.0, hCT2336932.0, hCT2336933.0, hCT2358152.0, hCT2358153.0	231843_at	NP_065987.1, EAW98422.1, EAW98419.1, EAW98420.1, EAW98421.1, EAW98423.1
GeneID:1967	EIF2B1	12	124,105,570	124,118,323	12,753	-	2	1_A375_pNL7_minus_lncRNA::1::1668, 2_A375_pNL97_plus_lncRNA::1::2333	147, 147	in gene, in gene	1	1	21	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene EIF2B1	MGC125868, EIF2B1, MGC117409, EIF2BA, MGC125869, EIF2B	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa	NM_001414, hCT1825252.2, hCT1966872.1	201632_at	NP_001405.1, EAW98425.1, EAW98424.1
GeneID:2967	GTF2H3	12	124,118,381	124,145,334	26,953	+	2	1_A375_pNL7_minus_lncRNA::1::1668, 2_A375_pNL97_plus_lncRNA::1::2333	-205, -205	upstream, upstream	1	1	21	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene GTF2H3	GTF2H3, TFB4, BTF2, TFIIH	general transcription factor IIH, polypeptide 3, 34kDa	NM_001516, hCT2336936.0, hCT2336937.0, hCT2336939.0, hCT2336940.0	222104_x_at	NP_001507.2, EAW98426.1, EAW98427.1, EAW98428.1, EAW98429.1
GeneID:144347	FAM101A	12	124,773,710	124,800,568	26,858	+	1	2_A375_pNL97_plus_lncRNA::1::2335	642	in gene	0	1	11	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene FAM101A	FAM101A, FLJ44614	family with sequence similarity 101, member A	NM_181709, hCT16429.3	227320_at	NP_859060.3, EAW98447.1
GeneID:9612	NCOR2	12	124,808,961	125,052,010	243,049	-	3	1_A375_pNL7_minus_lncRNA::1::1669, 2_A375_pNL97_plus_lncRNA::1::2336, 2_A375_pNL97_plus_lncRNA::1::2337	-374, 714, -342	upstream, in gene, upstream	1	1	17	26.5	2	2_A375_pNL97_plus_lncRNA::1	33	Gene NCOR2	TRAC-1, SMRTE, FLJ25011, CTG26, NCOR2, SMRTE-tau, SMRT, TNRC14, TRAC1	nuclear receptor co-repressor 2	NM_001077261, NM_006312, hCT16428.3, hCT1962322.1, hCT1962323.1, hCT2336974.0, hCT2336976.0, hCT2336977.0	207760_s_at, 208888_s_at, 208889_s_at, 215205_x_at	NP_001070729.1, NP_006303.3, EAW98448.1, EAW98449.1, EAW98452.1, EAW98453.1, EAW98450.1, EAW98451.1
GeneID:100288312	LOC100288312	12	125,394,083	125,397,359	3,276	+	3	1_A375_pNL7_minus_lncRNA::1::1671, 1_A375_pNL7_minus_lncRNA::1::1672, 2_A375_pNL97_plus_lncRNA::1::2341	5245, 7773, 5341	downstream, downstream, downstream	1	1	37	32	2	2_A375_pNL97_plus_lncRNA::1	45	Gene LOC100288312		hypothetical LOC100288312	XR_109105, XR_109104		
GeneID:7316	UBC	12	125,396,192	125,399,577	3,385	-	3	1_A375_pNL7_minus_lncRNA::1::1671, 1_A375_pNL7_minus_lncRNA::1::1672, 2_A375_pNL97_plus_lncRNA::1::2341	249, -2279, 153	in gene, upstream, in gene	1	1	37	32	2	2_A375_pNL97_plus_lncRNA::1	45	Gene UBC	UBC, HMG20	ubiquitin C	NM_021009, hCT1782398.3, hCT2308461.1, hCT2308464.1, hCT2343718.0	208980_s_at, 211296_x_at	NP_066289.2, EAW98463.1, EAW98464.1, EAW98465.1, EAW98466.1
GeneID:57647	DHX37	12	125,431,372	125,473,667	42,295	-	1	1_A375_pNL7_minus_lncRNA::1::1674	48227	downstream	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene DHX37	MGC2695, DHX37, DDX37, FLJ41974, MGC46245, KIAA1517, MGC4322	DEAH (Asp-Glu-Ala-His) box polypeptide 37	NM_032656, hCT1955088.1, hCT2308448.0, hCT2308451.0	223364_s_at, 223365_at	NP_116045.2, EAW98468.1, EAW98467.1, EAW98469.1
GeneID:5901	RAN	12	131,356,617	131,360,826	4,209	+	1	2_A375_pNL97_plus_lncRNA::1::2349	-489	upstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene RAN	TC4, Gsp1, ARA24, RAN	RAN, member RAS oncogene family	NM_006325, hCT1782813.3, hCT2308101.1, hCT2308103.1	200749_at, 200750_s_at	NP_006316.1, EAW98516.1, EAW98515.1, EAW98517.1
GeneID:283383	GPR133	12	131,438,452	131,626,010	187,558	+	3	1_A375_pNL7_minus_lncRNA::1::1681, 2_A375_pNL97_plus_lncRNA::1::2350, 2_A375_pNL97_plus_lncRNA::1::2351	90924, 29996, 91180	in gene, in gene, in gene	1	1	17	22.5	2	2_A375_pNL97_plus_lncRNA::1	26	Gene GPR133	GPR133, MGC138512, MGC138514, FLJ16770, PGR25, DKFZp434B1272	G protein-coupled receptor 133	NM_198827	232267_at	NP_942122.2
GeneID:100128840	LOC100128840	12	131,472,857	131,474,573	1,716	-	1	2_A375_pNL97_plus_lncRNA::1::2350	6125	downstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100128840		hypothetical LOC100128840	XR_111360, XR_109110, XR_114635		
GeneID:6433	SFRS8	12	132,195,635	132,284,282	88,647	+	5	1_A375_pNL7_minus_lncRNA::1::1683, 1_A375_pNL7_minus_lncRNA::1::1684, 2_A375_pNL97_plus_lncRNA::1::2353, 2_A375_pNL97_plus_lncRNA::1::2354, 2_A375_pNL97_plus_lncRNA::1::2355	-147, 72941, -19, 73112, 74093	upstream, in gene, upstream, in gene, in gene	1	1	18.33	20.67	3	2_A375_pNL97_plus_lncRNA::1	26	Gene SFRS8	SWAP, SFRS8, SFSWAP, MGC167082	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	NM_004592, hCT1955081.1, hCT2358211.0	202773_s_at, 202774_s_at, 202775_s_at, 240078_at	NP_004583.2, EAW98526.1, EAW98527.1
GeneID:4326	MMP17	12	132,312,941	132,336,316	23,375	+	2	1_A375_pNL7_minus_lncRNA::1::1685, 2_A375_pNL97_plus_lncRNA::1::2356	-109, -125	upstream, upstream	1	1	35	26	1	1_A375_pNL7_minus_lncRNA::1	35	Gene MMP17	MMP17, MT4-MMP	matrix metallopeptidase 17 (membrane-inserted)	NM_016155, hCT22762.3	206234_s_at	NP_057239.4, EAW98528.1
GeneID:317781	DDX51	12	132,621,139	132,628,880	7,741	-	2	1_A375_pNL7_minus_lncRNA::1::1686, 2_A375_pNL97_plus_lncRNA::1::2357	-112, -32	upstream, upstream	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene DDX51	DKFZp686N2081, DDX51, MGC42193	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	NM_175066, hCT87975.3	1554085_at, 214968_at, 229462_at	NP_778236.2, EAW98543.1
GeneID:79050	NOC4L	12	132,628,993	132,636,986	7,993	+	2	1_A375_pNL7_minus_lncRNA::1::1686, 2_A375_pNL97_plus_lncRNA::1::2357	-1, -51	upstream, upstream	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene NOC4L	NOC4L, MGC3162, NET49, NOC4	nucleolar complex associated 4 homolog (S. cerevisiae)	NM_024078, hCT1967461.1, hCT88123.2	218560_at	NP_076983.1, EAW98545.1, EAW98544.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:5426	POLE	12	133,200,348	133,263,945	63,597	-	2	1_A375_pNL7_minus_lncRNA::1::1687, 2_A375_pNL97_plus_lncRNA::1::2358	-55, -135	upstream, upstream	1	1	34	28	1	1_A375_pNL7_minus_lncRNA::1	34	Gene POLE	DKFZp434F222, FLJ21434, POLE, POLE1	polymerase (DNA directed), epsilon	NM_006231, hCT1950438.1, hCT2295109.0, hCT2295111.0, hCT2295112.0, hCT2352677.0	1561940_at, 216026_s_at	NP_006222.2, EAW54834.1, EAW54830.1, EAW54831.1, EAW54832.1, EAW54833.1
GeneID:5827	PXMP2	12	133,264,192	133,281,577	17,385	+	4	1_A375_pNL7_minus_lncRNA::1::1687, 1_A375_pNL7_minus_lncRNA::1::1688, 2_A375_pNL97_plus_lncRNA::1::2358, 2_A375_pNL97_plus_lncRNA::1::2359	-192, 23072, -112, 23088	upstream, downstream, upstream, downstream	1	1	25	23	2	1_A375_pNL7_minus_lncRNA::1	34	Gene PXMP2	PXMP2, FLJ54922, PMP22	peroxisomal membrane protein 2, 22kDa	NM_018663, hCT1827340.2, hCT2350249.0	219076_s_at	NP_061133.1, EAW54828.1, EAW54829.1
GeneID:192111	PGAM5	12	133,287,393	133,299,323	11,930	+	2	1_A375_pNL7_minus_lncRNA::1::1688, 2_A375_pNL97_plus_lncRNA::1::2359	-129, -113	upstream, upstream	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PGAM5	MGC5352, PGAM5, BXLBV68	phosphoglycerate mutase family member 5	NM_001170543, NM_001170544, NM_138575, hCT1827346.4, hCT2350916.0, hCT2350917.0	1553637_at, 1555943_at	NP_001164014.1, NP_001164015.1, NP_612642.2, EAW54825.1, EAW54826.1, EAW54827.1
GeneID:23141	ANKLE2	12	133,302,254	133,338,451	36,197	-	1	1_A375_pNL7_minus_lncRNA::1::1689	-461	upstream	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ANKLE2	LEMD7, KIAA0692, FLJ36132, ANKLE2, FLJ22280	ankyrin repeat and LEM domain containing 2	NM_015114	212200_at, 212201_at, 213962_s_at	NP_055929.1
GeneID:2802	GOLGA3	12	133,345,495	133,405,426	59,931	-	2	1_A375_pNL7_minus_lncRNA::1::1689, 2_A375_pNL97_plus_lncRNA::1::2360	66514, -110	downstream, upstream	1	1	16	17.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene GOLGA3	GOLGA3, MEA-2, GCP170	golgi autoantigen, golgin subfamily a, 3	NM_005895, NM_001172557, hCT10025.3, hCT2295104.0, hCT2352871.0, hCT2352872.0	1554987_at, 202106_at, 226949_at	NP_005886.2, NP_001166028.1, EAW54817.1, EAW54818.1, EAW54819.1, EAW54820.1
GeneID:55743	CHFR	12	133,416,938	133,464,204	47,266	-	2	1_A375_pNL7_minus_lncRNA::1::1690, 2_A375_pNL97_plus_lncRNA::1::2361	-276, -340	upstream, upstream	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene CHFR	FLJ10796, CHFR, RNF116, FLJ33629, RNF196	checkpoint with forkhead and ring finger domains	NM_001161344, NM_001161345, NM_001161346, NM_018223, NM_001161347, hCT13335.4, hCT1966697.1, hCT2295099.0, hCT2295101.0, hCT2352866.0, hCT2352867.0, hCT2352868.0	218803_at, 223931_s_at	NP_001154816.1, NP_001154817.1, NP_001154818.1, NP_060693.2, NP_001154819.1, EAW54810.1, EAW54809.1, EAW54811.1, EAW54812.1, EAW54813.1, EAW54814.1, EAW54815.1
GeneID:100289635	ZNF605	12	133,498,019	133,532,892	34,873	-	1	2_A375_pNL97_plus_lncRNA::1::2362	60	in gene	0	1	9	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene ZNF605	DKFZp686B222, ZNF605, DKFZp451B1818, FLJ16520, FLJ14967	zinc finger protein 605	NM_183238, NM_001164715		NP_899061.1, NP_001158187.1
GeneID:7574	ZNF26	12	133,563,056	133,589,153	26,097	+	1	2_A375_pNL97_plus_lncRNA::1::2363	-96	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZNF26	ZNF26, FLJ20755, KOX20	zinc finger protein 26	NM_019591, hCT1950434.1, hCT2296056.0	1555325_s_at, 219595_at	NP_062537.2, EAW54803.1, EAW54804.1
GeneID:7699	ZNF140	12	133,657,037	133,684,260	27,223	+	2	1_A375_pNL7_minus_lncRNA::1::1691, 2_A375_pNL97_plus_lncRNA::1::2364	-45, 328	upstream, in gene	1	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ZNF140	ZNF140, pHZ-39	zinc finger protein 140	NM_003440, hCT13332.3, hCT1961713.1, hCT2352873.0, hCT2352874.0, hCT2352875.0	204523_at, 238631_at	NP_003431.2, EAW54797.1, EAW54794.1, EAW54795.1, EAW54796.1, EAW54798.1
GeneID:10795	ZNF268	12	133,757,995	133,783,698	25,703	+	1	2_A375_pNL97_plus_lncRNA::1::2365	21	in gene	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ZNF268	HZF3, ZNF268, MGC126498	zinc finger protein 268	NM_003415, NM_152943, NM_001165883, NM_001165885, NM_001165886, NM_001165887, NM_001165881, NM_001165882, NM_001165884, hCT1827672.3, hCT2352878.0, hCT2352879.0, hCT2352880.0	1565768_at, 209969_at, 238030_at	NP_003406.1, NP_694422.2, NP_001159355.1, NP_001159357.1, NP_001159358.1, NP_001159359.1, NP_001159353.1, NP_001159354.1, NP_001159356.2, EAW54786.1, EAW54787.1, EAW54788.1, EAW54789.1
GeneID:54737	MPHOSPH8	13	20,207,788	20,247,599	39,811	+	1	2_A375_pNL97_plus_lncRNA::1::2367	788	in gene	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MPHOSPH8	MPHOSPH8, TWA3, HSMPP8, FLJ35237, mpp8	M-phase phosphoprotein 8	NM_017520, hCT1812942.2, hCT2314358.0, hCT2359290.0	221771_s_at, 225041_at, 227026_at, 240942_at	NP_059990.2, EAX08230.1, EAX08228.1, EAX08229.1
GeneID:55269	PSPC1	13	20,248,896	20,357,083	108,187	-	1	2_A375_pNL97_plus_lncRNA::1::2368	-85	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PSPC1	PSPC1, PSP1, FLJ10955, DKFZp566B1447	paraspeckle component 1	NM_001042414, NR_003272, hCT2314782.1, hCT2314783.1, hCT2314785.1	218371_s_at, 222611_s_at, 222612_at, 226574_at, 226724_s_at	NP_001035879.1, EAX08234.1, EAX08232.1, EAX08233.1
GeneID:9205	ZMYM5	13	20,397,624	20,437,776	40,152	-	2	1_A375_pNL7_minus_lncRNA::1::1692, 2_A375_pNL97_plus_lncRNA::1::2369	-80, -80	upstream, upstream	1	1	29	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene ZMYM5	ZNF237, MYM, HSPC050, ZMYM5, ZNF198L1	zinc finger, MYM-type 5	NM_001039650, NM_001039649, NM_001142684, hCT2314768.0, hCT2314770.0, hCT2314771.0, hCT2314773.0, hCT2314774.0, hCT2314776.0, hCT2314778.0	206652_at, 206744_s_at, 215948_x_at, 235620_x_at	NP_001034739.1, NP_001034738.1, NP_001136156.1, EAX08236.1, EAX08237.1, EAX08240.1, EAX08235.1, EAX08238.1, EAX08239.1, EAX08241.1
GeneID:400099	LOC400099	13	20,437,124	20,439,190	2,066	+	2	1_A375_pNL7_minus_lncRNA::1::1692, 2_A375_pNL97_plus_lncRNA::1::2369	732, 732	in gene, in gene	1	1	29	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene LOC400099		hypothetical LOC400099	XR_110132	230136_at	
GeneID:7750	ZMYM2	13	20,532,810	20,665,968	133,158	+	1	2_A375_pNL97_plus_lncRNA::1::2370	-986	upstream	0	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ZMYM2	ZNF198, SCLL, MYM, ZMYM2, RAMP, FIM	zinc finger, MYM-type 2	NM_001190964, NM_001190965, NM_003453, NM_197968, hCT11575.3, hCT1968000.1, hCT2314366.0, hCT2359321.0, hCT2359322.0, hCT2359323.0	202778_s_at, 210281_s_at, 210282_at	NP_001177893.1, NP_001177894.1, NP_003444.1, NP_932072.1, EAX08243.1, EAX08246.1, EAX08244.1, EAX08245.1, EAX08247.1, EAX08248.1
GeneID:2700	GJA3	13	20,712,394	20,735,183	22,789	-	1	1_A375_pNL7_minus_lncRNA::1::1693	-401	upstream	1	0	19	11	1	1_A375_pNL7_minus_lncRNA::1	19	Gene GJA3	CZP3, GJA3, CX46	gap junction protein, alpha 3, 46kDa	NM_021954, hCT11573.1	206590_x_at, 239572_at	NP_068773.2, EAX08251.1
GeneID:51084	CRYL1	13	20,977,806	21,100,012	122,206	-	2	2_A375_pNL97_plus_lncRNA::1::2371, 2_A375_pNL97_plus_lncRNA::1::2372	105740, -484	in gene, upstream	0	1	15	17.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene CRYL1	lambda-CRY, MGC149525, CRYL1, MGC149526, GDH	crystallin, lambda 1	NM_015974, hCT11574.3, hCT1816114.1, hCT2314733.0, hCT2314735.0, hCT2314736.0, hCT2314738.0, hCT2314740.0	220753_s_at	NP_057058.2, EAX08260.1, EAX08259.1, EAX08261.1, EAX08262.1, EAX08263.1, EAX08264.1, EAX08265.1
GeneID:221143	N6AMT2	13	21,303,073	21,348,057	44,984	-	2	1_A375_pNL7_minus_lncRNA::1::1694, 2_A375_pNL97_plus_lncRNA::1::2373	249, -71	in gene, upstream	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene N6AMT2	N6AMT2, ESP13	N-6 adenine-specific DNA methyltransferase 2 (putative)	NM_174928, hCT1816116.2, hCT1966389.1, hCT22284.4, hCT2359313.0	227054_at	NP_777588.1, EAX08279.1, EAX08277.1, EAX08278.1, EAX08280.1
GeneID:64328	XPO4	13	21,351,468	21,476,913	125,445	-	2	1_A375_pNL7_minus_lncRNA::1::1694, 2_A375_pNL97_plus_lncRNA::1::2373	129105, 128785	downstream, downstream	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene XPO4	XPO4, KIAA1721, FLJ13046	exportin 4	NM_022459, hCT1812975.3, hCT2359326.0, hCT2359327.0	218479_s_at, 222649_at	NP_071904.4, EAX08282.1, EAX08281.1, EAX08283.1
GeneID:26524	LATS2	13	21,547,175	21,635,722	88,547	-	3	1_A375_pNL7_minus_lncRNA::1::1695, 1_A375_pNL7_minus_lncRNA::1::1696, 2_A375_pNL97_plus_lncRNA::1::2374	1146, 138, 74	in gene, in gene, in gene	1	1	17	13.5	2	1_A375_pNL7_minus_lncRNA::1	18	Gene LATS2	FLJ13161, LATS2, KPM	LATS, large tumor suppressor, homolog 2 (Drosophila)	NM_014572, hCT1812979.2, hCT2314659.0	223379_s_at, 223380_s_at, 227013_at, 230348_at	NP_055387.2, EAX08287.1, EAX08286.1
GeneID:221150	SKA3	13	21,727,734	21,750,741	23,007	-	2	1_A375_pNL7_minus_lncRNA::1::1697, 2_A375_pNL97_plus_lncRNA::1::2375	181, 261	in gene, in gene	1	1	27	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene SKA3	SKA3, MGC4832, C13orf3, RAMA1	spindle and kinetochore associated complex subunit 3	NM_145061, NM_001166017, hCT1965390.2, hCT22288.5, hCT2314652.1	227165_at	NP_659498.4, NP_001159489.1, EAX08293.1, EAX08294.1, EAX08295.1
GeneID:78988	MRP63	13	21,750,372	21,753,223	2,851	+	2	1_A375_pNL7_minus_lncRNA::1::1697, 2_A375_pNL97_plus_lncRNA::1::2375	188, 108	in gene, in gene	1	1	27	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene MRP63	bMRP63, MRP63, MGC3243	mitochondrial ribosomal protein 63	NM_024026, hCT1812972.1, hCT1816115.1, hCT2314419.0	204386_s_at, 204387_x_at, 224535_s_at	NP_076931.1, EAX08298.1, EAX08296.1, EAX08297.1
GeneID:650794	LOC650794	13	21,872,342	21,879,657	7,315	+	2	1_A375_pNL7_minus_lncRNA::1::1698, 2_A375_pNL97_plus_lncRNA::1::2376	-150, -150	upstream, upstream	1	1	141	160	1	2_A375_pNL97_plus_lncRNA::1	160	Gene LOC650794		hypothetical LOC650794	XR_111367, XR_110104, XR_114662	236637_x_at, 243760_at	
GeneID:100505610	LOC100505610	13	21,877,510	21,922,860	45,350	-	2	1_A375_pNL7_minus_lncRNA::1::1698, 2_A375_pNL97_plus_lncRNA::1::2376	50668, 50668	downstream, downstream	1	1	141	160	1	2_A375_pNL97_plus_lncRNA::1	160	Gene LOC100505610		hypothetical LOC100505610	XR_111365, XR_111366, XR_110133, XR_110134, XR_114660, XR_114661		
GeneID:221154	EFHA1	13	22,066,828	22,178,355	111,527	-	1	2_A375_pNL97_plus_lncRNA::1::2377	115	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene EFHA1	1110008L20Rik, EFHA1, FLJ25016, FLJ34588	EF-hand domain family, member A1	NM_152726, hCT22255.3, hCT2359287.0	212410_at	NP_689939.1, EAX08313.1, EAX08312.1
GeneID:26278	SACS	13	23,902,965	24,007,841	104,876	-	1	1_A375_pNL7_minus_lncRNA::1::1699	-95	upstream	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SACS	SACS, ARSACS, DNAJC29, DKFZp686B15167	spastic ataxia of Charlevoix-Saguenay (sacsin)	NM_014363, hCT1958120.1	213262_at	NP_055178.3, EAX08323.1
GeneID:100506680	LOC100506680	13	23,993,110	24,003,008	9,898	+	1	1_A375_pNL7_minus_lncRNA::1::1699	14826	downstream	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC100506680	SACS-AS1	SACS antisense RNA 1 (non-protein coding)	XR_110106		
GeneID:100506697	LOC100506697	13	24,043,651	24,061,603	17,952	+	1	2_A375_pNL97_plus_lncRNA::1::2378	-2195	upstream	0	1	6	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506697		hypothetical LOC100506697	XR_111370, XR_110107, XR_114665		
GeneID:55504	TNFRSF19	13	24,144,723	24,250,232	105,509	+	2	2_A375_pNL97_plus_lncRNA::1::2379, 2_A375_pNL97_plus_lncRNA::1::2380	-275, 8973	upstream, in gene	0	1	12	19	2	2_A375_pNL97_plus_lncRNA::1	20	Gene TNFRSF19	TAJ, TNFRSF19, TRADE, TAJ-alpha, TROY	tumor necrosis factor receptor superfamily, member 19	NM_018647, NM_148957, hCT15301.3, hCT2314686.0, hCT2314687.0	223827_at, 224090_s_at, 227812_at	NP_061117.2, NP_683760.1, EAX08325.1, EAX08326.1, EAX08327.1
GeneID:4285	MIPEP	13	24,304,328	24,463,587	159,259	-	2	1_A375_pNL7_minus_lncRNA::1::1700, 2_A375_pNL97_plus_lncRNA::1::2381	-29, -29	upstream, upstream	1	1	176	189	1	2_A375_pNL97_plus_lncRNA::1	189	Gene MIPEP	MIP, MIPEP, HMIP	mitochondrial intermediate peptidase	NM_005932, hCT13848.2, hCT2314777.0	204305_at, 36830_at	NP_005923.2, EAX08329.1, EAX08328.1
GeneID:542767	PCOTH	13	24,463,028	24,466,242	3,214	+	2	1_A375_pNL7_minus_lncRNA::1::1700, 2_A375_pNL97_plus_lncRNA::1::2381	588, 588	in gene, in gene	1	1	176	189	1	2_A375_pNL97_plus_lncRNA::1	189	Gene PCOTH		prostate collagen triple helix	NM_001014442, NM_001135816	222277_at	NP_001014442.2, NP_001129288.1
GeneID:387911	RP11-45B20.2	13	24,465,428	24,471,125	5,697	-	2	1_A375_pNL7_minus_lncRNA::1::1700, 2_A375_pNL97_plus_lncRNA::1::2381	7509, 7509	downstream, downstream	1	1	176	189	1	2_A375_pNL97_plus_lncRNA::1	189	Gene RP11-45B20.2	C1QTNF9B, CTRP9B, MGC117159	C1q and tumor necrosis factor related protein 9B	NM_001007537		NP_001007538.1
GeneID:221178	SPATA13	13	24,734,861	24,881,212	146,351	+	1	2_A375_pNL97_plus_lncRNA::1::2383	115	in gene	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SPATA13	ASEF2, MGC129959, ARHGEF29, FLJ31208, MGC129958, SPATA13, FLJ35435	spermatogenesis associated 13	NM_153023, NM_001166271, hCT2336161.1, hCT2341359.0	1556601_a_at, 1557470_at, 225564_at	NP_694568.1, NP_001159743.1, EAX08331.1, EAX08332.1
GeneID:100313842	MIR2276	13	24,736,555	24,736,643	88	+	1	2_A375_pNL97_plus_lncRNA::1::2383	-1579	upstream	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MIR2276	MIR2276	microRNA 2276	NR_031753		
GeneID:143	PARP4	13	24,995,069	25,086,948	91,879	-	1	1_A375_pNL7_minus_lncRNA::1::1702	100	in gene	1	0	25	17	1	1_A375_pNL7_minus_lncRNA::1	25	Gene PARP4	PH5P, PARP4, VWA5C, PARPL, PARP-4, ADPRTL1, VPARP, p193, VAULT3	poly (ADP-ribose) polymerase family, member 4	NM_006437, hCT1957374.1	202239_at	NP_006428.2, EAX08336.1
GeneID:55835	CENPJ	13	25,456,412	25,497,085	40,673	-	1	1_A375_pNL7_minus_lncRNA::1::1703	317	in gene	1	0	22	17	1	1_A375_pNL7_minus_lncRNA::1	22	Gene CENPJ	MGC142222, MGC142224, BM032, LAP, SASS4, SCKL4, CENPJ, Sas-4, MGC131581, LIP1, MCPH6, MGC131582, CPAP	centromere protein J	NM_018451, hCT2336278.0, hCT2336279.0, hCT2336280.0, hCT2359304.0	220885_s_at, 223513_at, 234023_s_at	NP_060921.3, EAX08352.1, EAX08351.1, EAX08353.1, EAX08354.1
GeneID:9107	MTMR6	13	25,820,339	25,861,704	41,365	-	4	1_A375_pNL7_minus_lncRNA::1::1704, 1_A375_pNL7_minus_lncRNA::1::1705, 2_A375_pNL97_plus_lncRNA::1::2384, 2_A375_pNL97_plus_lncRNA::1::2385	10600, 72, 10616, 104	in gene, in gene, in gene, in gene	1	1	51.5	53	2	2_A375_pNL97_plus_lncRNA::1	90	Gene MTMR6	MTMR6	myotubularin related protein 6	NM_004685, hCT2316000.0	214429_at, 226789_at	NP_004676.3, EAX08367.1
GeneID:9818	NUPL1	13	25,875,666	25,916,561	40,895	+	2	1_A375_pNL7_minus_lncRNA::1::1706, 2_A375_pNL97_plus_lncRNA::1::2386	-34, -50	upstream, upstream	1	1	31	28	1	1_A375_pNL7_minus_lncRNA::1	31	Gene NUPL1	PRO2463, KIAA0410, NUPL1	nucleoporin like 1	NM_014089, NM_001008564, hCT1957888.2, hCT20992.3, hCT2351969.0, hCT2359324.0	204435_at, 223984_s_at, 225047_at, 241425_at	NP_054808.1, NP_001008564.1, EAX08368.1, EAX08369.1, EAX08370.1, EAX08371.1
GeneID:51761	ATP8A2	13	25,946,209	26,595,420	649,211	+	1	2_A375_pNL97_plus_lncRNA::1::2387	121983	in gene	0	1	12	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene ATP8A2	IB, ML-1, ATP, ATPIB, DKFZp434B1913, ATP8A2	ATPase, aminophospholipid transporter, class I, type 8A, member 2	NM_016529, hCT19364.3, hCT2315376.0, hCT2315378.0, hCT2315379.0, hCT2315380.0	219659_at, 219660_s_at	NP_057613.4, EAX08376.1, EAX08372.1, EAX08373.1, EAX08374.1, EAX08375.1
GeneID:6049	RNF6	13	26,786,905	26,796,508	9,603	-	2	1_A375_pNL7_minus_lncRNA::1::1707, 2_A375_pNL97_plus_lncRNA::1::2389	-4, 28	upstream, in gene	1	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene RNF6	DKFZp686P0776, RNF6	ring finger protein (C3H2C3 type) 6	NM_183044, NM_005977, NM_183043, hCT19365.2, hCT2359345.0, hCT2359346.0, hCT2359347.0	203403_s_at, 210931_at, 210932_s_at	NP_898865.1, NP_005968.1, NP_898864.1, EAX08380.1, EAX08381.1, EAX08382.1, EAX08383.1
GeneID:219333	USP12	13	27,640,287	27,746,033	105,746	-	2	1_A375_pNL7_minus_lncRNA::1::1709, 2_A375_pNL97_plus_lncRNA::1::2392	-175, -367	upstream, upstream	1	1	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene USP12	USP12L1, USP12, UBH1	ubiquitin specific peptidase 12	NM_182488, hCT1812874.2, hCT2316787.0	213327_s_at, 215886_x_at	NP_872294.2, EAX08392.1, EAX08393.1
GeneID:6144	RPL21	13	27,825,692	27,830,705	5,013	+	2	1_A375_pNL7_minus_lncRNA::1::1711, 2_A375_pNL97_plus_lncRNA::1::2394	-156, -188	upstream, upstream	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene RPL21	FLJ27458, L21, DKFZp686C06101, MGC71252, MGC104274, RPL21, MGC104275	ribosomal protein L21	NM_000982, hCT2315079.0, hCT2315080.0, hCT2315081.0, hCT2315082.0, hCT2315083.0, hCT2315084.0, hCT2315085.0	200012_x_at	NP_000973.2, EAX08396.1, EAX08397.1, EAX08398.1, EAX08399.1, EAX08401.1, EAX08395.1, EAX08400.1
GeneID:26771	SNORD102	13	27,829,201	27,829,272	71	+	2	1_A375_pNL7_minus_lncRNA::1::1711, 2_A375_pNL97_plus_lncRNA::1::2394	-3665, -3697	upstream, upstream	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SNORD102	Z18, SNORD102, RNU102	small nucleolar RNA, C/D box 102	NR_002574		
GeneID:619499	SNORA27	13	27,829,538	27,829,663	125	+	2	1_A375_pNL7_minus_lncRNA::1::1711, 2_A375_pNL97_plus_lncRNA::1::2394	-4002, -4034	upstream, upstream	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SNORA27	SNORA27, ACA27	small nucleolar RNA, H/ACA box 27	NR_002575		
GeneID:387496	RASL11A	13	27,844,464	27,847,827	3,363	+	1	2_A375_pNL97_plus_lncRNA::1::2395	920	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene RASL11A	RASL11A	RAS-like, family 11, member A	NM_206827, hCT21992.3	238353_at	NP_996563.1, EAX08402.1
GeneID:219402	MTIF3	13	28,009,776	28,024,739	14,963	-	1	1_A375_pNL7_minus_lncRNA::1::1712	35	in gene	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MTIF3	FLJ33676, IF3mt, MTIF3	mitochondrial translational initiation factor 3	NM_152912, NM_001166261, NM_001166262, NM_001166263, hCT1957897.1, hCT21997.3, hCT2315234.0, hCT2359293.0, hCT2359294.0, hCT2359295.0, hCT2359296.0	223356_s_at, 223357_s_at	NP_690876.3, NP_001159733.1, NP_001159734.1, NP_001159735.1, EAX08406.1, EAX08409.1, EAX08407.1, EAX08408.1, EAX08410.1, EAX08411.1, EAX08412.1
GeneID:219409	GSX1	13	28,366,780	28,368,089	1,309	+	2	1_A375_pNL7_minus_lncRNA::1::1713, 2_A375_pNL97_plus_lncRNA::1::2396	-124, -204	upstream, upstream	1	1	35	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene GSX1	GSX1, GSH1, Gsh-1	GS homeobox 1	NM_145657, hCT21994.3	1555676_s_at, 234791_at	NP_663632.1, EAX08418.1
GeneID:23281	MTUS2	13	29,598,748	30,080,084	481,336	+	1	2_A375_pNL97_plus_lncRNA::1::2400	411748	in gene	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MTUS2	MTUS2, TIP150, CAZIP, KIAA0774	microtubule associated tumor suppressor candidate 2	NM_001033602, NM_015233, hCT20314.4, hCT2314828.1	1554755_a_at, 214961_at	NP_001028774.2, NP_056048.1, EAX08439.1, EAX08440.1
GeneID:6541	SLC7A1	13	30,083,551	30,169,825	86,274	-	1	2_A375_pNL97_plus_lncRNA::1::2401	12241	in gene	0	1	11	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC7A1	REC1L, ATRC1, CAT-1, SLC7A1, HCAT1, ERR	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	NM_003045, hCT18944.3, hCT1957870.1	206566_at, 212290_at, 212292_at, 212295_s_at, 215979_s_at	NP_003036.1, EAX08444.1, EAX08443.1
GeneID:10208	USPL1	13	31,191,830	31,233,686	41,856	+	2	1_A375_pNL7_minus_lncRNA::1::1715, 2_A375_pNL97_plus_lncRNA::1::2404	122, 74	in gene, in gene	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene USPL1	D13S106E, USPL1, C13orf22, RP11-121O19.1, bA121O19.1, DKFZp781K2286, FLJ32952	ubiquitin specific peptidase like 1	NM_005800, hCT18945.2	1562238_at, 204190_at	NP_005791.3, EAX08466.1
GeneID:241	ALOX5AP	13	31,309,669	31,338,556	28,887	+	2	1_A375_pNL7_minus_lncRNA::1::1717, 2_A375_pNL97_plus_lncRNA::1::2406	8107, 8203	in gene, in gene	1	1	20	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene ALOX5AP	ALOX5AP, FLAP	arachidonate 5-lipoxygenase-activating protein	NM_001629, hCT19452.2	204174_at	NP_001620.2, EAX08467.1
GeneID:10808	HSPH1	13	31,710,762	31,736,117	25,355	-	2	1_A375_pNL7_minus_lncRNA::1::1719, 2_A375_pNL97_plus_lncRNA::1::2408	-427, 165	upstream, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene HSPH1	HSP105, DKFZp686M05240, KIAA0201, HSP105A, NY-CO-25, HSP105B, HSPH1	heat shock 105kDa/110kDa protein 1	NM_006644, hCT1957643.1, hCT2314897.0, hCT2314899.0, hCT23356.3, hCT2359302.0, hCT2359303.0	206976_s_at, 208744_x_at	NP_006635.2, EAX08477.1, EAX08478.1, EAX08479.1, EAX08480.1, EAX08481.1, EAX08482.1
GeneID:100507099	LOC100507099	13	32,598,183	32,605,780	7,597	-	1	1_A375_pNL7_minus_lncRNA::1::1720	52	in gene	1	0	16	10	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100507099	FRY-AS1	hypothetical LOC100507099	XR_111377, XR_110114, XR_114692		
GeneID:10129	FRY	13	32,605,437	32,870,776	265,339	+	1	1_A375_pNL7_minus_lncRNA::1::1720	291	in gene	1	0	16	10	1	1_A375_pNL7_minus_lncRNA::1	16	Gene FRY	FRY, 214K23.2, bA207N4.2, bA37E23.1, C13orf14, CG003, 13CDNA73	furry homolog (Drosophila)	NM_023037, hCT2315163.0, hCT2315164.0, hCT2315165.0, hCT2315166.0, hCT2315167.0, hCT2359289.0, hCT24323.3	204072_s_at, 214318_s_at, 214319_at	NP_075463.2, EAX08490.1, EAX08491.1, EAX08492.1, EAX08494.1, EAX08495.1, EAX08489.1, EAX08493.1
GeneID:646799	ZAR1L	13	32,877,908	32,886,091	8,183	-	2	1_A375_pNL7_minus_lncRNA::1::1721, 2_A375_pNL97_plus_lncRNA::1::2409	-3561, -3461	upstream, upstream	1	1	11.5	12.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene ZAR1L	ZAR2, ZAR1L		NM_001136571		NP_001130043.1
GeneID:675	BRCA2	13	32,889,617	32,973,809	84,192	+	2	1_A375_pNL7_minus_lncRNA::1::1721, 2_A375_pNL97_plus_lncRNA::1::2409	335, -65	in gene, upstream	1	1	11.5	12.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene BRCA2	FANCB, FACD, FAD1, FANCD1, BROVCA2, BRCC2, FAD, BRCA2, FANCD, GLM3, PNCA2	breast cancer 2, early onset	NM_000059, hCT2315170.0, hCT2315171.0, hCT24319.2	208368_s_at, 214727_at	NP_000050.2, EAX08501.1, EAX08499.1, EAX08500.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Identical Transcripts	Identical Details	Identical Pos.	[A]	[R]	[C]	[D]	Acc Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:10443	NAIP2/L2	13	33,009,930	33,112,806	106,876	+	2	1_A375_shL7_dhrus_UcKrN A:1:1722, 2_A375_shL97_dhrs_UcKrNA :1:2410	-152, -120	upstream, upstream	1	1	89	82	1	2_A375_shL97_dhrs_UcKrNA:1	62	Gene NAIP2,L2	E2MI5.2, FLJ41009, FLJ59193, NAIP2,L2	NEDD4 binding protein 2-like 2	NM_033111, NM_014697	202255_s_at, 202299_s_at, 216753_at, 221699_at, 228947_at, 1569296_a_at	NP_149102.2, NP_055702.1
Gene:ID:3951	RPC3	13	34,392,206	34,540,685	148,480	+	2	1_A375_shL7_dhrus_UcKrN A:1:1726, 2_A375_shL97_dhrs_UcKrNA :1:2414	-50, 90	at gene, at gene	1	1	1	27	21	1	2_A375_shL97_dhrs_UcKrNA:1	27	Gene RPC3	MGC3276, RPC38, RPC3	depolarization factor C (activator 1) 3, 38kDa	NM_002913, NM_181555, NCT23149110, NCT23352.2	204127_at, 204126_s_at, 221119_at	NP_002904.1, NP_853536.2, EAX05537.1, EAX05535.1
Gene:ID:201	DCLK1	13	36,343,122	36,705,364	362,242	+	1	1_A375_shL97_dhrs_UcKrNA :1:2414	2755512	at gene	0	1	64	21	1	2_A375_shL97_dhrs_UcKrNA:1	21	Gene DCLK1	DCLK1, DCAMKL1, CLICK1, CLI, DCLK, doublecortin-like kinase 1	NM_004734, NCT23152300.0, NCT23352.2	205356_at, 205357_s_at, 1568690_at	NP_004725.1, EAX05551.1, EAX05550.1
Gene:ID:3111	SPG20	13	36,815,775	36,844,317	66,562	+	2	1_A375_shL7_dhrus_UcKrN A:1:1731, 2_A375_shL97_dhrs_UcKrNA :1:2415	23677, 23709	at gene, at gene	1	1	24	25	1	2_A375_shL97_dhrs_UcKrNA:1	25	Gene SPG20	SPG20, TAHCCP1, KIAA0610, SPARTIN	spastic paraplegia 20 (Troyer syndrome)	NM_001142294, NM_001142295, NM_001142296, NM_018007, NCT19458114.1, NCT19458113.1, NCT23151760.0, NCT23151940.0, NCT23152357.0	212529_at, 219965_s_at, 239603_at	NP_001133766.1, NP_001133767.1, NP_059021.1, NP_001120765.1, EAX05555.1, EAX05553.1, EAX05560.1, EAX05561.1, EAX05562.1, EAX05563.1
Gene:ID:3000713	LOC10033 07135	13	36,930,975	36,943,872	23,397	+	2	1_A375_shL7_dhrus_UcKrN A:1:1731, 2_A375_shL97_dhrs_UcKrNA :1:2415	65, 33	at gene, at gene	1	1	24	25	1	2_A375_shL97_dhrs_UcKrNA:1	25	Gene LOC100307137	C13orf43, KIAA0610	Chromosome 13 open reading frame 43	NM_001178552, NM_032118881, XM_003120766	1554111_s_at	XP_003119600.1, NP_003120814.1
Gene:ID:9509	RPAP	13	37,393,339	37,403,740	10,401	+	1	1_A375_shL97_dhrs_UcKrNA :1:2417	613	at gene	0	1	7	17	1	2_A375_shL97_dhrs_UcKrNA:1	17	Gene RPAP	RPAP		NM_006308, NCT23150000.0, NCT24001.2	205692_at, 224501_at	NP_006259.1, EAX05574.1, EAX05575.1
Gene:ID:9500	ALG9	13	37,523,907	37,573,904	49,997	+	4	1_A375_shL7_dhrus_UcKrN A:1:1732, 1_A375_shL7_dhrus_UcKrN A:1:1733, 1_A375_shL97_dhrs_UcKrNA :1:2416, 2_A375_shL97_dhrs_UcKrNA :1:2418	32, -1246, 0, -1360	at gene, upstream, at gene, upstream	1	1	76	72.5	2	2_A375_shL97_dhrs_UcKrNA:1	136	Gene ALG9	ALG9, bA421P11.2, KIF1-421P11.2	dolichyl-pyrophosphate (glucosyl)3-N-acetylchitobiose alpha-glucosyltransferase homolog (S. cerevisiae)	NM_013339, NM_001142864, NCT19565040.0, NCT23179.2	1560731_at, 218203_at, 223596_at	NP_037470.1, NP_001136839.1, EAX05577.1, EAX05576.1
Gene:ID:1340	EXOSC8	13	37,974,975	37,983,791	8,873	+	4	1_A375_shL7_dhrus_UcKrN A:1:1732, 1_A375_shL7_dhrus_UcKrN A:1:1733, 1_A375_shL97_dhrs_UcKrNA :1:2416, 2_A375_shL97_dhrs_UcKrNA :1:2418	-1209, 34, 1174, 186	upstream, at gene, upstream, at gene	1	1	76	72.5	2	2_A375_shL97_dhrs_UcKrNA:1	136	Gene EXOSC8	EXOSC8, CIP2, RRP42, CIP2, bA421P11.3, KIF11-421P11.3, p9, Rrp42p, EXP2	exosome component 8	NM_181503, NCT16400355.2, NCT19899800.1, NCT23593150.0	219139_s_at	NP_034900.1, EAX05581.1, EAX05579.1, EAX05580.1
Gene:ID:9268	C13orf23	13	38,564,002	39,617,252	28,250	+	2	1_A375_shL7_dhrus_UcKrN A:1:1733, 2_A375_shL97_dhrs_UcKrNA :1:2422	140, 124	at gene, at gene	1	1	32	42	1	2_A375_shL97_dhrs_UcKrNA:1	42	Gene C13orf23	C13orf23, BA3019.2, FLJ23780, FLJ31661	Chromosome 13 open reading frame 23	NM_025135, NM_170719, NCT19749162.2, NCT19457716.1	218420_s_at, 221697_at	NP_079414.2, NP_733637.2, EAX05610.1, EAX05611.1
Gene:ID:67521	NHLRC3	13	39,612,855	39,624,246	11,791	+	2	1_A375_shL7_dhrus_UcKrN A:1:1733, 2_A375_shL97_dhrs_UcKrNA :1:2422	-343, -327	upstream, upstream	1	1	32	42	1	2_A375_shL97_dhrs_UcKrNA:1	42	Gene NHLRC3	NHLRC3, DKFZp313H1221, DKFZp686E1148	NHL repeat containing 3	NM_030117154, NM_001017370, NCT16825822.2, NCT19457716.1, NCT23593000.0, NCT23593090.0	227060_at, 229583_s_at, 229314_at	NP_001017372.1, NP_001017370.1, EAX06121.1, EAX06120.1, EAX06119.1, EAX06118.1, EAX06115.1
Gene:ID:49302	LOC6499 62	13	40,921,269	41,055,143	133,874	+	3	1_A375_shL7_dhrus_UcKrN A:1:1727, 1_A375_shL7_dhrus_UcKrN A:1:1728, 2_A375_shL97_dhrs_UcKrNA :1:2426	76471, 27111, 27207	at gene, at gene	1	1	17.5	10.5	2	2_A375_shL7_dhrus_UcKrNA:1	16	Gene LOC649652	FLJ21437, TTL	tubulin tyrosine ligase	NR_024093, NR_024596, NR_024097	1554927_at, 1555264_s_at, 233432_at	
Gene:ID:368	FOXO1	13	41,129,601	41,240,734	110,833	+	2	1_A375_shL7_dhrus_UcKrN A:1:1729, 2_A375_shL97_dhrs_UcKrNA :1:2427	1214, 1685	at gene, at gene	1	1	16	22	1	2_A375_shL97_dhrs_UcKrNA:1	22	Gene FOXO1	FKHR, FOXO1, FKH1, FOXO1A	forkhead box O1	NM_002015, NCT23372.2	202723_s_at, 202724_s_at, 238464_s_at	NP_002006.2, EAX06627.1
Gene:ID:5340	MRPS31	13	41,303,432	41,349,247	41,916	+	2	1_A375_shL7_dhrus_UcKrN A:1:1730, 2_A375_shL97_dhrs_UcKrNA :1:2426	118, 35	at gene, at gene	1	1	23	25	1	2_A375_shL97_dhrs_UcKrNA:1	25	Gene MRPS31	MRPS31, MRP63/38, S31 rit, MRP-S31	mitochondrial ribosomal protein S31	NM_006630, NCT23084.2	212603_at, 212604_s_at, 240521_at	NP_006621.2, EAX06629.1
Gene:ID:597	ELF1	13	41,395,033	41,563,806	67,463	+	1	1_A375_shL97_dhrs_UcKrNA :1:2428	87505	downstream	0	1	17	16	1	2_A375_shL97_dhrs_UcKrNA:1	16	Gene ELF1	ELF1		NM_001145153, NM_172373, NCT23155810.0, NCT23852.2	212416_at, 212420_at	NP_001138825.1, NP_796961.1, EAX06640.1, EAX06641.1
Gene:ID:1183	WIBP4	13	41,615,697	41,655,129	22,462	+	2	1_A375_shL7_dhrus_UcKrN A:1:1731, 2_A375_shL97_dhrs_UcKrNA :1:2428	-765, -17	at gene, at gene	1	1	24	24	1	2_A375_shL97_dhrs_UcKrNA:1	24	Gene WIBP4	WIBP4, MGC117202, FBP21	WW domain binding protein 4 (formin binding protein 21)	NM_025167, NCT23151592.0, NCT23852.2	203307_s_at, 203308_s_at, 203593_s_at	NP_079165.1, EAX06643.1, EAX06644.1
Gene:ID:4076	KBTBD7	13	41,765,511	41,765,702	2,991	+	2	1_A375_shL7_dhrus_UcKrN A:1:1742, 2_A375_shL97_dhrs_UcKrNA :1:2440	-16, -2	upstream, upstream	1	1	16	26	1	2_A375_shL97_dhrs_UcKrNA:1	26	Gene KBTBD7	KBTBD7, DKFZp434E2316	kelch repeat and BTB (POZ) domain containing 7	NM_032130, NCT16444438.2	223812_at	NP_115514.2, EAX06647.1
Gene:ID:9612	NAA16	13	41,885,341	41,891,166	60,825	+	2	1_A375_shL7_dhrus_UcKrN A:1:1743, 2_A375_shL97_dhrs_UcKrNA :1:2433	-141, -39	upstream, upstream	1	1	21	17	1	2_A375_shL97_dhrs_UcKrNA:1	21	Gene NAA16	MGC40612, NAA16, DKFZp686O05147, NARG1L	N(alpha)-acetyltransferase 16, NatA hisiliary subunit	NM_018127, NM_024561, NM_001110798, NCT23152040.0, NCT23152106.1, NCT23152207.0, NCT23152208.1, NCT23152209.1, NCT23152211.0, NCT23852209.0	1555850_at, 218378_at	NP_060997.2, NP_078837.2, NP_001104298.1, EAX06643.1, EAX06577.1, EAX06636.1, EAX06635.1, EAX06636.1, EAX06639.1, EAX06640.1
Gene:ID:9370	KIAA0664	13	42,140,961	42,533,231	384,260	+	1	2_A375_shL97_dhrs_UcKrNA :1:2434	-139	upstream	0	1	16	16	1	2_A375_shL97_dhrs_UcKrNA:1	16	Gene KIAA0664	KIAA0664		NM_015050, NM_001009814, NCT23154600.0, NCT23154602.0, NCT24929.2	212690_at, 214231_s_at	NP_055873.1, NP_001008814.1, EAX06663.1, EAX06666.1, EAX06667.1
Gene:ID:9369	LOC1003 07240	13	42,533,305	42,555,701	20,396	+	1	2_A375_shL97_dhrs_UcKrNA :1:2434	83	at gene	0	1	16	16	1	2_A375_shL97_dhrs_UcKrNA:1	16	Gene LOC100307240		hypothetical LOC100307240	XR_111555, XR_110117, XR_110693		
Gene:ID:96857	CCDC132	13	44,410,455	44,455,626	45,338	+	1	1_A375_shL7_dhrus_UcKrN A:1:1744	546	at gene	0	15	15	1	1	2_A375_shL7_dhrus_UcKrNA:1	15	Gene CCDC132	CCDC132, FLJ51646	coiled-coil domain containing 132	NM_144974, NCT23155593.1, NCT23155962.1, NCT23154609.0, NCT23852.2	1554111_s_at, 1554112_at	NP_659111.2, EAX06797.1, EAX06798.1, EAX06799.1, EAX06798.1
Gene:ID:84611	C13orf31	13	44,453,420	44,466,266	14,846	+	1	1_A375_shL97_dhrs_UcKrNA :1:1744	-140	upstream	0	1	15	15	1	2_A375_shL97_dhrs_UcKrNA:1	15	Gene C13orf31	C13orf31, DKFZp686D11116, FLJ35725	Chromosome 13 open reading frame 31	NM_152216, NM_001123033, NCT23612.2	1553141_at, 1553142_s_at, 229827_at	NP_689430.2, NP_001121775.1, EAX06761.1
Gene:ID:3000728	LOC1003 07253	13	44,716,464	44,726,215	11,751	+	2	2_A375_shL97_dhrs_UcKrNA :1:2436, 2_A375_shL97_dhrs_UcKrNA :1:2438	-6424, 17520	upstream, upstream	0	1	15	23.5	2	2_A375_shL97_dhrs_UcKrNA:1	25	Gene LOC100307253		hypothetical LOC100307253	XR_111354, XR_110116, XR_110698		
Gene:ID:6147	NUP91	13	45,512,054	45,563,813	50,229	+	2	2_A375_shL97_dhrs_UcKrNA :1:2440, 2_A375_shL97_dhrs_UcKrNA :1:2442	83, -131	at gene, upstream	1	1	16	16	1	2_A375_shL97_dhrs_UcKrNA:1	16	Gene NUP91	NUP91, MAB0N85.1, NUP1P	nuclear trigle K inverted interactions protein unlinking protein 1	NM_032345, NCT19749552.2	203134_s_at, 203135_s_at, 203136_s_at	NP_039477.2, EAX07119.1
Gene:ID:5425	KIAA1704	13	45,563,657	45,602,469	38,716	+	2	2_A375_shL97_dhrs_UcKrNA :1:2440, 2_A375_shL97_dhrs_UcKrNA :1:2442	-1167, 57	upstream, at gene	0	1	16	16	1	2_A375_shL97_dhrs_UcKrNA:1	16	Gene KIAA1704	KIAA1704, RP11-245H20.2, KIDE29, bA245H20.2, LSR7	KIAA1704	NM_015599, NCT19104080.0, NCT23155590.0, NCT23593140.0, NCT23965.1	1207171_s_at, 223606_s_at, 226429_at, 229075_s_at, 229081_s_at	NP_056729.2, EAX07222.1, EAX07220.1, EAX07221.1, EAX07222.1
Gene:ID:3007983	LOC1002 87603	13	45,911,001	45,916,722	5,721	+	2	1_A375_shL7_dhrus_UcKrN A:1:1745, 2_A375_shL97_dhrs_UcKrNA :1:2446	4339, 4315	at gene, at gene	1	1	16	26	1	2_A375_shL97_dhrs_UcKrNA:1	26	Gene LOC100287603		hypothetical LOC100287603	XR_111393, XR_111381, XR_110120, XR_110121, XR_114696, XR_110702		
Gene:ID:7175	TPT1	13	45,911,304	45,913,297	3,992	+	2	1_A375_shL7_dhrus_UcKrN A:1:1745, 2_A375_shL97_dhrs_UcKrNA :1:2446	43, -79	upstream, upstream	1	1	16	26	1	2_A375_shL97_dhrs_UcKrNA:1	26	Gene TPT1	TCTP, HRF, p22, TPT1, FLJ27337	tumor protein, translationally-controlled 1	NM_003295, NCT16036539.1, NCT16731090.1, NCT16731182.1, NCT23852.2	213663_x_at, 213664_s_at, 213699_s_at, 214327_x_at, 216520_s_at	NP_003286.1, EAX07235.1, EAX07231.1, EAX07232.1, EAX07233.1
Gene:ID:77814	SNORA31	13	45,911,615	45,911,744	129	+	2	1_A375_shL7_dhrus_UcKrN A:1:1745, 2_A375_shL97_dhrs_UcKrNA :1:2446	-3816, 3632	upstream, upstream	1	1	16	26	1	2_A375_shL97_dhrs_UcKrNA:1	26	Gene SNORA31	SNORA31, ACA31	small nucleolar RNA, H/ACA box 31	NR_002987		
Gene:ID:3001609 3	LOC1003 09329	13	45,913,480	45,963,616	50,136	+	2	1_A375_shL7_dhrus_UcKrN A:1:1745, 2_A375_shL97_dhrs_UcKrNA :1:2446	-120, -104	upstream, upstream	1	1	16	26	1	2_A375_shL97_dhrs_UcKrNA:1	26	Gene LOC100309329	FLJ42341, FLJ43662	hypothetical LOC100309329	NM_024455		
Gene:ID:53512	SLC25A30	13	45,967,431	45,992,816	25,065	+	1	2_A375_shL97_dhrs_UcKrNA :1:2445	680	at gene	0	1	12	20	1	2_A375_shL97_dhrs_UcKrNA:1	20	Gene SLC25A30	KMCP1, SLC25A30	solute carrier family 25, member 30	NM_001010873, NCT19812241.1	218712_at, 218721_at, 228762_at, 228717_at	NP_001010873.1, EAX07339.1
Gene:ID:3007236	LOC1003 87293	13	45,991,939	45,994,506	2,567	+	1	2_A375_shL97_dhrs_UcKrNA :1:2445	-23	upstream	0	1	12	20	1	2_A375_shL97_dhrs_UcKrNA:1	20	Gene LOC100287236		hypothetical protein LOC100287293	NM_033116553, NM_002111582, XM_003120765		XP_003119601.1, NP_002110840.1, XP_003120816.1
Gene:ID:5345	CCG2	13	46,039,071	46,110,760	71,689	+	1	2_A375_shL97_dhrs_UcKrNA :1:2446	813	at gene	0	1	16	20	1	2_A375_shL97_dhrs_UcKrNA:1	20	Gene CCG2	SEC34, CCG2	component of oligomeric golgi complex 2	NM_021431, NCT23154453.2, NCT23155600.0, NCT23852.2	1554338_s_at, 224580_s_at	NP_113619.1, EAX07431.1, EAX07432.1, EAX07433.1
Gene:ID:3091	ZCSH13	13	46,539,314	46,629,884	90,570	+	1	2_A375_shL97_dhrs_UcKrNA :1:2447	48	at gene	0	1	14	21	1	2_A375_shL97_dhrs_UcKrNA:1	21	Gene ZCSH13	DKFZp434G1612, ZC3H13, KIAA0853, FLJ35669	zinc finger CCCH-type containing 13	NM_015070, NCT19605582.1, NCT23446.1, NCT23159404.0	1554033_at, 212402_at, 227126_at	NP_055885.2, EAX07503.1, EAX07501.1, EAX07502.1
Gene:ID:5161	CPB2	13	46,677,322	46,679,211	51,889	+	1	2_A375_shL97_dhrs_UcKrNA :1:2447	52363	downstream	0	1	14	21	1	2_A375_shL97_dhrs_UcKrNA:1	21	Gene CPB2	TAFI, PCPB, CPB2, CPU	carboxypeptidase B2 (plasma)	NM_016413, NM_001672, NCT23642.3, NCT23852.2	209651_s_at	NP_057497.2, NP_001662.2, EAX08754.1, EAX07345.1
Gene:ID:9183	UROH	13	47,127,298	47,137,176	199,880	+	1	2_A375_shL97_dhrs_UcKrNA :1:2448	720	at gene	0	20	13	1	1	2_A375_shL97_dhrs_UcKrNA:1	20	Gene UROH	KIAA1016, FLJ41960, NP61, UROH1, CHDC	uroporphyrinogen III synthase (congenital erythropoietic porphyria)	NM_015116, NM_001164211, NM_001164213, NCT23154630.0	209436_at, 209437_s_at	NP_055931.1, NP_001157653.1, NP_001157654.1, NP_001157655.1, EAX07566.1
Gene:ID:998	EDD	13	47,345,291	47,371,367	25,976	+	1	2_A375_shL97_dhrs_UcKrNA :1:2448	583	at gene	0	1	12	13	1	2_A375_shL97_dhrs_UcKrNA:1	13	Gene EDD	PDH, FLJ11763, EDD	ubiquitin protein ligase E3 component n-recognin 5 (putative)	NM_015902, NCT19654998.1, NCT19865033.1, NCT23159.2	209009_s_at, 210095_s_at, 226162_at, 1565995_at	NP_057986.2, EAX07767.1, EAX07768.1, EAX07769.1
Gene:ID:6603	SUCLA2	13	48,516,791	48,573,662	56,871	+	2	2_A375_shL97_dhrs_UcKrNA :1:2450, 2_A375_shL97_dhrs_UcKrNA :1:2452	-262	upstream, upstream	0	1	12	17	1	2_A375_shL97_dhrs_UcKrNA:1	17	Gene SUCLA2	A-BETA, SCS-betaA, MTDPS5, SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	NM_003850, NCT19547972.2, NCT19547986.2, NCT21525.2, NCT23852.2	202563_s_at	NP_003841.2, EAX07776.1, EAX07775.1, EAX07777.1, EAX07776.1
Gene:ID:5270	NUDT15	13	48,611,703	48,621,282	9,579	+	2	1_A375_shL7_dhrus_UcKrN A:1:1751, 2_A375_shL97_dhrs_UcKrNA :1:2460	16, 105	at gene, at gene	1	1	26	26	1	2_A375_shL97_dhrs_UcKrNA:1	26	Gene NUDT15	RP11-190M22.1, MTH2, NUDT15, FLJ16939, MGC104282	nudix (nucleoside diphosphate linked moiety X)-type motif 15	NM_018283, NCT19410982.2	219347_at	NP_060753.2, EAX07852.1
Gene:ID:9378	MED4	13	48,690,092	48,699,240	19,148	+	2	1_A375_shL7_dhrus_UcKrN A:1:1752, 2_A375_shL97_dhrs_UcKrNA :1:2452	-8, -72	upstream, upstream	1	1	82	89	1	2_A375_shL97_dhrs_UcKrNA:1	89	Gene MED4	RP11-190M22.2, MED4, FLJ10986, HSPC126, DRIP36, VDRIP, TRAP36	vitamin D receptor interacting protein complex subunit 4	NM_014166, NCT19749942.2, NCT19867180.1, NCT19882420.1, NCT23923550.0	217643_s_at, 217644_at	NP_054853.1, EAX07953.1, EAX07953.2, EAX07954.1, EAX07955.1
Gene:ID:5161	RB1	13	48,877,883	49,056,026	178,143	+	1	2_A375_shL97_dhrs_UcKrNA :1:2454	1430312	at gene	1	0	16	8	1	2_A375_shL97_dhrs_UcKrNA:1	15	Gene RB1	OSRC, RB, p105-RB, pRb, RB1, pp110	retinoblastoma 1	NM_000321, NCT23162.2, NCT23155700.0	203132_at, 211300_s_at	NP_000312.2, EAX07963.1, EAX07964.1
Gene:ID:5161	LPAR6	13	48,955,151	49,016,840	33,689	+	1	2_A375_shL97_dhrs_UcKrNA :1:2454	-2036	upstream	0	1	8	9	1	2_A375_shL97_dhrs_UcKrNA:1	15	Gene LPAR6	MGC120358, P2RY5, ARHHY1, LPAR6, P2Y5, LAH3	lysophosphatidic acid receptor 6	NM_022987, NM_001142497, NM_001162498	1557762_at, 1557763_s_at, 1561558_at	NP_001135970.1, NP_001135971.1, NP_074388.2
Gene:ID:102	RCBTB2	13	49,063,099	49,107,216	44,217	+	1	2_A375_shL97_dhrs_UcKrNA :1:2455	458	at gene	1	0	16	17	1	2_A375_shL97_dhrs_UcKrNA:1	16	Gene RCBTB2	RCBTB2, CHC1L	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	NM_001270, NCT21215.0, NCT23152.2	209744_s_at	NP_001253.2, EAX07990.1
Gene:ID:3852	CABZ3L	13	49,552,786	50,018,221	135,435	+	1	2_A375_shL97_dhrs_UcKrNA :1:2458	45	at gene	0	1	17	15	1	2_A375_shL97_dhrs_UcKrNA:1	15	Gene CABZ3L	MGC2L, bA453.6.6.3, FLJ31277, RP11-453.6.6.2, MGC25-BETA, CAB3BL	Calcium binding protein 39-like	NM_001079879, NM_030625, NCT21213.2, NCT21545710.0, NCT21545720.0, NCT23852.2	219163_s_at, 229814_s_at, 229815_at	NP_001073347.1, NP_109601.2, EAX08520.1, EAX08521.1, EAX08522.1, EAX08523.1
Gene:ID:3852	SETD8L2	13	50,018,429	50,069,139	50,710	+	2	2_A375_shL97_dhrs_UcKrNA :1:2458, 2_A375_shL97_dhrs_UcKrNA :1:2460	-253, 52635	upstream, downstream	0	1	14.5	16.5	2	2_A375_shL97_dhrs_UcKrNA:1	19	Gene SETD8L2	DKFZp586G0123, C13orf6, SETD8L2, CLL06, DKFZp761J1217, KMT5F, CLL12	SET domain, bifurcated 2	NM_019815, NM_001190305, NCT20465.3, NCT23963150.0, NCT23963350.0	1554979_at, 1554972_x_at, 1554973_s_at, 225339_at, 1570331_at	NP_001171240.1, NP_062788.2, EAX08524.1, EAX08525.1, EAX08526.1
Gene:ID:1131	PHF11	13	50,069,801	50,103,117	33,316	+	1	2_A375_shL97_dhrs_UcKrNA :1:2458	663	at gene	0	1	12	19	1	2_A375_shL97_dhrs_UcKrNA:1	19	Gene PHF11	PHF11, NY-REN-58, APY, NYRENZ4, KIEL, SCAP, HDHEB, EDET	PHD finger protein 11	NM_001040443, NM_001040444, NCT19567911.1, NCT19567921.1	221616_s_at, 221617_at, 241060_at	NP_001033533.1, NP_001033534.1, EAX08527.1, EAX08528.1
Gene:ID:839	KPNA2	13	50,273,843	50,367,697	93,914	+	2	1_A375_shL7_dhrus_UcKrN A:1:1757, 2_A375_shL97_dhrs_UcKrNA :1:2460	113, 145	at gene, at gene	1	1	27	28	1	2_A375_shL97_dhrs_UcKrNA:1	28	Gene KPNA2	ERP1, KPNA2, RBRP1, SRP1gamma, IPOA2, SRP2	karyopherin alpha 2 (importin alpha 1)	NM_002267, NCT23158590.0, NCT23155570.0, NCT23155550.0	221502_at, 221503_s_at	NP_002258.2, EAX08538.1, EAX08537.1, EAX08539.1
Gene:ID:7212	C13orf1	13	50,666,642	50,910,826	23,764	+	2	2_A375_shL97_dhrs_UcKrNA :1:2460, 2_A375_shL97_dhrs_UcKrNA :1:2462	164, 162	at gene, at gene	1	1	47	35	1	2_A375_shL97_dhrs_UcKrNA:1	35	Gene C13orf1	CLL06, C13orf1	chromosome 13 open reading frame 1	NM_020456, NM_001127682, NM_022351, NCT19862451.1, NCT19862491.1, NCT23159830.0, NCT23159832.0	218665_at, 230191_at	NP_065189.1, NP_001120654.1, EAX05440.1, EAX05441.1, EAX05442.1, EAX05443.1
Gene:ID:647	DLEU2	13	50,599,655	50,699,877	142,689	+	3	1_A375_shL7_dhrus_UcKrN A:1:1759, 2_A375_shL97_dhrs_UcKrNA :1:2458, 2_A375_shL97_dhrs_UcKrNA :1:2460	653, 1457, 701	at gene, at gene	1	1	15	29	1	2_A375_shL97_dhrs_UcKrNA:1	29	Gene DLEU2	DLEU2, FP22/23, BCMS3U, MGC95357, MIR13AHG, NCRNA00022, TRIM13OS, 18d, DLB2, LEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	NR_002612	1556520_at, 1556521_s_at, 1563229_at, 1564041_at, 1569600_at, 1569770_s_at, 1569936_at	
Gene:ID:9621	RNASEN2	13	51,463,092	51,548,596	60,764	+	1	2_A375_shL97_dhrs_UcKrNA :1:2462	268	at gene	0	1	11	20	1	2_A375_shL97_dhrs_UcKrNA:1	20	Gene RNASEN2B	FLJ11712, DLEU8, AGS2, RNASEN2B	ribonuclease H2, subunit B	NM_024570, NM_001142279, NCT19587843.1, NCT16851.2	1555080_at, 1555081_s_at, 226210_at, 1570190_at	NP_079846.2, NP_001127751.1, EAX05563.1, EAX05564.1
Gene:ID:9736	DHRS12	13	52,342,131	52,370,293	28,162	+	2	2_A375_shL97_dhrs_UcKrNA :1:2464, 2_A375_shL97_dhrs_UcKrNA :1:2466	-359, -21	at gene, at gene	0	1	12.5	17.5	2	2_A375_shL97_dhrs_UcKrNA:1	16	Gene DHRS12	DHRS12, SDR4DC1, FLJ13639	dehydrogenase/reductase (SDR family) member 12	NM_024705, NM_001031710, NCT19547850.0, NCT19547961.1, NCT19862472.0, NCT23852.2, NCT23852.3	224503_s_at, 224501_s_at, 231348_s_at	NP_078951.1, NP_001026859.1, EAX05558.1, EAX05555.1, EAX05556.1, EAX05559.1, EAX05557.1
Gene:ID:8655	LOC1003 07413	13	52,377,733	52,387,356	9,623	+	2	2_A375_shL97_dhrs_UcKrNA :1:2464, 2_A375_shL97_dhrs_UcKrNA :1:2466	171, 651	at gene, at gene	0	1	12.5	17.5	2	2_A375_shL97_dhrs_UcKrNA:1	16	Gene LOC100307413		hypothetical LOC100307413	NR_027049		
Gene:ID:83321	RP11-327P2.4	13	52,387,483	52,419,266	31,803	+	2	2_A375_shL97_dhrs_UcKrNA :1:2464, 2_A375_shL97_dhrs_UcKrNA :1:2466	41582, 40902	downstream, downstream	0	1	12.5	17.5	2	2_A375_shL97_dhrs_UcKrNA:1	16	Gene RP11-327P2.4	FLJ27307, NCRNA00262	hypothetical LOC283521	NR_027047, NR_027048	1557483_at	
Gene:ID:1026	VPS36	13	52,569,737	53,024,763	35,026	+	3	1_A375_shL7_dhrus_UcKrN A:1:1760, 2_A375_shL97_dhrs_UcKrNA :1:2466, 2_A375_shL97_dhrs_UcKrNA :1:2467	483, 291, 4669	at gene, upstream	1	1	15	17.5	2	2_A375_shL97_dhrs_UcKrNA:1	16	Gene VPS36	EAP45, CGI-145, C13orf6, DKFZp761E0571, VPS36	vacuolar protein sorting 36 homolog (S. cerevisiae)	NM_016079	222478_at, 240006_at	NP_057159.2
Gene:ID:6598	CHAP2	13	53,029,695	53,050,763	21,268	+	3	1_A375_shL7_dhrus_UcKrN A:1:1760, 2_A375_shL97_dhrs_UcKrNA :1:2466, 2_A375_shL97_dhrs_UcKrNA :1:2467	5175, 4663, 137	upstream, upstream, at gene	1	1	15	17.5	2	2_A375_shL97_dhrs_UcKrNA:1	16	Gene CHAP2	gc30-10, DKFZp686L1235, LB1, FLJ10749, TMAP, CHAP2	cytoskeleton associated protein 2	NM_001008525, NM_018256, NCT19936061.1, NCT23517440.0	230764_x_at	NP_001018083.1, NP_060674.2, EAX05589.1, EAX05590.1

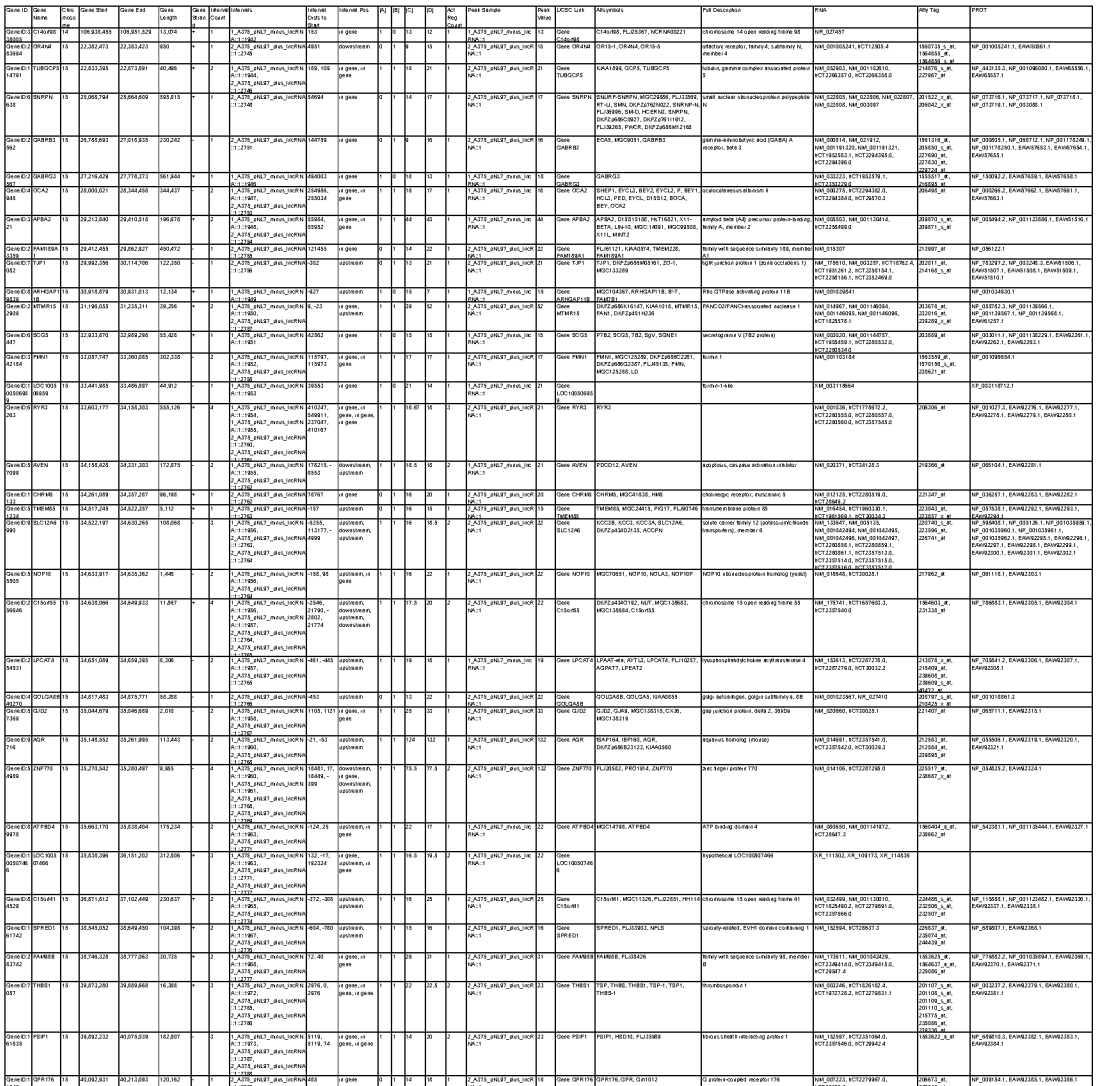
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:144983	HNRNPA1L2	13	53,191,605	53,217,919	26,314	+	3	1_A375_pNL7_minus_lncRNA::1::1761, 2_A375_pNL97_plus_lncRNA::1::2468, 2_A375_pNL97_plus_lncRNA::1::2469	35275, 43, 35323	downstream, in gene, downstream	1	1	17.5	29.5	2	2_A375_pNL97_plus_lncRNA::1	38	Gene HNRNPA1L2	HNRNPA1L2, MGC102957	heterogeneous nuclear ribonucleoprotein A1 like 2	NM_001011724, NM_001011725, hCT2254988.0, hCT2254989.0, hCT2254990.0	238696_at	NP_001011724.1, NP_001011725.1, EAW52040.1, EAW52041.1, EAW52042.1
GeneID:10910	SUGT1	13	53,226,831	53,262,433	35,602	+	2	1_A375_pNL7_minus_lncRNA::1::1761, 2_A375_pNL97_plus_lncRNA::1::2469	49, 97	in gene, in gene	1	1	24	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene SUGT1	SGT1, SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	NM_006704, NM_001130912, hCT1967573.1, hCT20731.3, hCT2254995.0, hCT2352518.0	234686_at	NP_006695.1, NP_001124384.1, EAW52043.1, EAW52044.1, EAW52045.1, EAW52046.1
GeneID:5100	PCDH8	13	53,418,109	53,422,774	4,665	-	2	1_A375_pNL7_minus_lncRNA::1::1762, 2_A375_pNL97_plus_lncRNA::1::2470	-2197, -2106	upstream, upstream	1	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDH8	ARCADLIN, PCDH8, PAPC	protocadherin 8	NM_002590, NM_032949, hCT18643.4, hCT1968177.1, hCT2255127.0	206935_at	NP_002581.2, NP_116567.1, EAW52049.1, EAW52050.1, EAW52051.1
GeneID:81624	DIAPH3	13	60,239,717	60,738,119	498,402	-	1	2_A375_pNL97_plus_lncRNA::1::2471	71	in gene	0	1	18	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene DIAPH3	NSDAN, DRF3, diap3, mDia2, AUNA1, DIAPH3, AN, FLJ34705, DKFZp686A13178, DKFZp434C0931	diaphanous homolog 3 (Drosophila)	NM_030932, NM_001042517, hCT2254691.0, hCT2254692.0, hCT2254694.0, hCT2254695.1, hCT2254696.0, hCT2254697.0	220997_s_at, 229097_at, 232596_at	NP_112194.2, NP_001035982.1, EAW52069.1, EAW52070.1, EAW52072.1, EAW52074.1, EAW52071.1, EAW52073.1
GeneID:5101	PCDH9	13	66,876,966	67,804,468	927,502	-	2	1_A375_pNL7_minus_lncRNA::1::1767, 2_A375_pNL97_plus_lncRNA::1::2476	-140, -268	upstream, upstream	1	1	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene PCDH9	PCDH9		NM_020403, NM_203487, hCT2325676.0	219737_s_at, 219738_s_at	NP_065136.1, NP_982354.1, EAW80499.1
GeneID:730236	LOC730236	13	67,804,715	67,805,815	1,100	+	2	1_A375_pNL7_minus_lncRNA::1::1767, 2_A375_pNL97_plus_lncRNA::1::2476	-107, 21	upstream, in gene	1	1	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene LOC730236		hypothetical LOC730236	XM_001715647, XM_001133153, XM_001714412	241471_at	XP_001715699.1, XP_001133153.1, XP_001714464.1
GeneID:440145	C13orf37	13	73,282,495	73,301,938	19,443	-	2	1_A375_pNL7_minus_lncRNA::1::1769, 2_A375_pNL97_plus_lncRNA::1::2479	18, 2	in gene, in gene	1	1	31	30	1	1_A375_pNL7_minus_lncRNA::1	31	Gene C13orf37	MOZART1, MZT1, MGC150539, C13orf37, FLJ21869	chromosome 13 open reading frame 37	NM_001071775	225578_at, 226530_at	NP_001065243.1
GeneID:79866	C13orf34	13	73,302,042	73,330,328	28,286	+	2	1_A375_pNL7_minus_lncRNA::1::1769, 2_A375_pNL97_plus_lncRNA::1::2479	-122, -106	upstream, upstream	1	1	31	30	1	1_A375_pNL7_minus_lncRNA::1	31	Gene C13orf34	C13orf34, BORA, FLJ22624	chromosome 13 open reading frame 34	NM_024808, hCT1819879.2, hCT1953045.1	219544_at	NP_079084.2, EAW80514.1, EAW80515.1
GeneID:11278	KLF12	13	74,260,149	74,708,066	447,917	-	2	2_A375_pNL97_plus_lncRNA::1::2480, 2_A375_pNL97_plus_lncRNA::1::2481	-30, -2142	upstream, upstream	0	1	14	15	2	2_A375_pNL97_plus_lncRNA::1	15	Gene KLF12	HSPC122, KLF12, AP2REP, AP-2rep	Kruppel-like factor 12	NM_007249, hCT1960115.1, hCT23987.3	206965_at, 206966_s_at, 208467_at, 214276_at, 227261_at, 229881_at, 238940_at, 239019_at	NP_009180.3, EAW80529.1, EAW80528.1
GeneID:9882	TBC1D4	13	75,858,809	76,056,250	197,441	-	1	2_A375_pNL97_plus_lncRNA::1::2483	-358	upstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TBC1D4	TBC1D4, AS160, DKFZp779C0666	TBC1 domain family, member 4	NM_014832, hCT19319.3, hCT1958914.1, hCT2326169.0	203386_at, 203387_s_at	NP_055647.2, EAW80538.1, EAW80536.1, EAW80537.1
GeneID:170622	COMMD6	13	76,099,350	76,111,991	12,641	-	2	1_A375_pNL7_minus_lncRNA::1::1772, 2_A375_pNL97_plus_lncRNA::1::2484	-105, -169	upstream, upstream	1	1	23	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene COMMD6	Acrg, COMMD6	COMM domain containing 6	NM_203495, NM_203497, hCT1640004.3, hCT1965964.1, hCT1965965.1	225312_at, 240030_at	NP_987091.1, NP_987093.1, EAW80539.1, EAW80540.1, EAW80541.1
GeneID:7347	UCHL3	13	76,123,927	76,180,069	56,142	+	2	1_A375_pNL7_minus_lncRNA::1::1773, 2_A375_pNL97_plus_lncRNA::1::2485	-215, -236	upstream, upstream	1	1	22	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene UCHL3	UCH-L3, UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	NM_006002, hCT1968021.1, hCT20736.3, hCT2325769.0, hCT2325770.0, hCT2325771.0, hCT2325772.0	204616_at	NP_005993.1, EAW80546.1, EAW80542.1, EAW80543.1, EAW80544.1, EAW80547.1, EAW80545.1
GeneID:4008	LMO7	13	76,194,570	76,434,006	239,436	+	1	1_A375_pNL7_minus_lncRNA::1::1774	16278	in gene	1	0	22	11	1	1_A375_pNL7_minus_lncRNA::1	22	Gene LMO7	FBXO20, KIAA0858, LOMP, FBX20, LMO7	LIM domain 7	NM_005358, NM_015842, hCT2325775.0, hCT2325778.0, hCT2325782.0, hCT2325784.0, hCT2325785.0, hCT2325787.0, hCT2325788.0	1556377_s_at, 202674_s_at, 241140_at, 242722_at	NP_005349.3, NP_056667.2, EAW80550.1, EAW80552.1, EAW80554.1, EAW80555.1, EAW80549.1, EAW80551.1, EAW80553.1
GeneID:1203	CLN5	13	77,566,059	77,576,652	10,593	+	1	2_A375_pNL97_plus_lncRNA::1::2488	261	in gene	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CLN5	FLJ90628, CLN5, NCL	ceroid-lipofuscinosis, neuronal 5	NM_006493, hCT19323.2, hCT2325688.0	204084_s_at, 204085_s_at, 214252_s_at	NP_006484.1, EAW80562.1, EAW80561.1
GeneID:23077	MYCBP2	13	77,618,792	77,901,177	282,385	-	3	1_A375_pNL7_minus_lncRNA::1::1775, 2_A375_pNL97_plus_lncRNA::1::2489, 2_A375_pNL97_plus_lncRNA::1::2490	-2295, -135, -2247	upstream, upstream, upstream	1	1	18.5	24.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene MYCBP2	PAM, DKFZp686M08244, MYCBP2, FLJ21646, FLJ10106, FLJ21597, FLJ13826, KIAA0916	MYC binding protein 2	NM_015057, hCT1953047.0, hCT2325946.0, hCT2325948.0, hCT2325949.0	1557370_s_at, 201959_s_at, 201960_s_at	NP_055872.4, EAW80565.1, EAW80564.1, EAW80566.1, EAW80567.1
GeneID:100505518	LOC100505518	13	78,393,072	78,482,818	89,746	+	2	1_A375_pNL7_minus_lncRNA::1::1776, 1_A375_pNL7_minus_lncRNA::1::1777	35088, 89664	in gene, downstream	1	0	18	12	2	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100505518		hypothetical LOC100505518	XR_110130		
GeneID:1910	EDNRB	13	78,469,616	78,492,966	23,350	-	1	1_A375_pNL7_minus_lncRNA::1::1777	230	in gene	1	0	18	12	1	1_A375_pNL7_minus_lncRNA::1	18	Gene EDNRB	HSCR, ETRB, WS4A, ETB, HSCR2, ABCDS, ETBR, EDNRB	endothelin receptor type B	NM_003991, NM_000115, NM_001122659, hCT2325937.0, hCT2325938.0, hCT2325939.0, hCT2325940.0, hCT2325941.0, hCT2325942.0	204271_s_at, 204273_at, 206701_x_at	NP_003982.1, NP_000106.1, NP_001116131.1, EAW80573.1, EAW80574.1, EAW80575.1, EAW80576.1, EAW80577.1, EAW80578.1
GeneID:64062	RBM26	13	79,894,089	79,979,923	85,834	-	1	2_A375_pNL97_plus_lncRNA::1::2492	-637	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RBM26	FLJ20957, PRO1777, ZC3H17, C13orf10, MGC133295, RBM26, SE70-2, RP11-255E21.1, ARRS2, MGC133296	RNA binding motif protein 26	NM_022118, hCT1960102.1, hCT2326781.0, hCT2326782.0, hCT2326785.0	215647_at, 215751_at, 218422_s_at, 220509_at, 222626_at, 227355_at, 229433_at	NP_071401.3, EAW80593.1, EAW80591.1, EAW80592.1, EAW80594.1
GeneID:100505538	LOC100505538	13	79,980,483	79,998,471	17,988	+	1	2_A375_pNL97_plus_lncRNA::1::2492	77	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100505538	RBM26-AS1	hypothetical LOC100505538	XR_111394, XR_110131, XR_114702		
GeneID:10253	SPRY2	13	80,910,111	80,915,086	4,975	-	1	2_A375_pNL97_plus_lncRNA::1::2495	-2290	upstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SPRY2	SPRY2, hSPRY2, MGC23039	sprouty homolog 2 (Drosophila)	NM_005842, hCT23425.3	204011_at	NP_005833.1, EAW80601.1
GeneID:114798	SLITRK1	13	84,451,343	84,456,528	5,185	-	3	1_A375_pNL7_minus_lncRNA::1::1786, 2_A375_pNL97_plus_lncRNA::1::2497, 2_A375_pNL97_plus_lncRNA::1::2498	256, 2416, 368	in gene, in gene, in gene	1	1	25.5	35.5	2	2_A375_pNL97_plus_lncRNA::1	50	Gene SLITRK1	TTM, LRRC12, KIAA1910, SLITRK1, RP11-395N17.1, FLJ54428, KIAA0918	SLIT and NTRK-like family, member 1	NM_052910, hCT1647464.1	236734_at	NP_443142.1, EAW80608.1
GeneID:642345	hCG_1795283	13	88,096,242	88,323,218	226,976	-	3	1_A375_pNL7_minus_lncRNA::1::1791, 2_A375_pNL97_plus_lncRNA::1::2506, 2_A375_pNL97_plus_lncRNA::1::2507	172098, 172050, -302	in gene, in gene, upstream	1	1	22.5	27	2	2_A375_pNL97_plus_lncRNA::1	28	Gene hCG_1795283	LOC642345	hCG1818123	NR_033829	232648_at	
GeneID:26050	SLITRK5	13	88,324,870	88,331,871	7,001	+	1	2_A375_pNL97_plus_lncRNA::1::2507	-1350	upstream	0	1	23	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene SLITRK5	bA364G4.2, SLITRK5, LRRC11, FLJ58374, KIAA0918	SLIT and NTRK-like family, member 5	NM_015567	214930_at	NP_056382.1
GeneID:407975	MIR17HG	13	92,000,074	92,006,829	6,755	+	1	2_A375_pNL97_plus_lncRNA::1::2510	1334	in gene	0	1	7	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIR17HG	FLJ14178, MGC126270, MIHG1, NCRNA00048, miR-17-92, MIRHG1, MIRH1, C13orf25, MIR17HG	MIR17 host gene (non-protein coding)	NR_027349, NR_027350	232291_at, 233636_at	
GeneID:406952	MIR17	13	92,002,859	92,002,942	83	+	1	2_A375_pNL97_plus_lncRNA::1::2510	-1451	upstream	0	1	7	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIR17	miRNA17, MIR17, MIRN91, miR17-3p, MIR91, hsa-mir-17, MIRN17, miR-17, miRNA91, MIR17-5p	microRNA 17	NR_029487		
GeneID:406953	MIR18A	13	92,003,005	92,003,075	70	+	1	2_A375_pNL97_plus_lncRNA::1::2510	-1597	upstream	0	1	7	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIR18A	MIRN18, MIR18A, MIRN18A, hsa-mir-18a, miR-18, MIR18, miRNA18A, hsa-mir-18	microRNA 18a	NR_029488		
GeneID:406979	MIR19A	13	92,003,145	92,003,226	81	+	1	2_A375_pNL97_plus_lncRNA::1::2510	-1737	upstream	0	1	7	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIR19A	miR-19a, hsa-mir-19a, MIRN19A, miRNA19A, MIR19A	microRNA 19a	NR_029489		
GeneID:406982	MIR20A	13	92,003,319	92,003,389	70	+	1	2_A375_pNL97_plus_lncRNA::1::2510	-1911	upstream	0	1	7	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIR20A	miRNA20A, MIR20, hsa-mir-20a, hsa-mir-20, MIR20A, MIRN20A, MIRN20, miR-20	microRNA 20a	NR_029492		
GeneID:406980	MIR19B1	13	92,003,446	92,003,532	86	+	1	2_A375_pNL97_plus_lncRNA::1::2510	-2038	upstream	0	1	7	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIR19B1	MIRN19B1, MIR19B1, miR-19b-1, miRNA19B1	microRNA 19b-1	NR_029490		
GeneID:407048	MIR92A1	13	92,003,568	92,003,645	77	+	1	2_A375_pNL97_plus_lncRNA::1::2510	-2160	upstream	0	1	7	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIR92A1	MIR92A1, MIRN92A1, MIRN92-1, MIR92-1, miRNA92-1, MIRN92A-1	microRNA 92a-1	NR_029508		
GeneID:2262	GPC5	13	92,050,935	93,519,490	1,468,555	+	1	2_A375_pNL97_plus_lncRNA::1::2511	1445065	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene GPC5	GPC5		NM_004466, hCT23420.4	207174_at	NP_004457.1, EAX08927.1
GeneID:10082	GPC6	13	93,879,078	95,060,274	1,181,196	+	9	1_A375_pNL7_minus_lncRNA::1::1798, 1_A375_pNL7_minus_lncRNA::1::1799, 2_A375_pNL97_plus_lncRNA::1::2513, 2_A375_pNL97_plus_lncRNA::1::2514, 2_A375_pNL97_plus_lncRNA::1::2515, 2_A375_pNL97_plus_lncRNA::1::2516, 2_A375_pNL97_plus_lncRNA::1::2517, 2_A375_pNL97_plus_lncRNA::1::2518, 2_A375_pNL97_plus_lncRNA	122, 22949, -8950, 90, 954, 22042, 137546, 620410, 1103162	in gene, in gene, upstream, in gene, in gene, in gene, in gene, in gene, in gene	1	1	14.43	20	7	2_A375_pNL97_plus_lncRNA::1	25	Gene GPC6	GPC6, MGC126288, OMIMD1	glypican 6	NM_005708, hCT2344420.0, hCT2344421.0, hCT2344422.0, hCT2344423.0	223730_at, 227059_at	NP_005699.1, EAX08933.1, EAX08931.1, EAX08932.1, EAX08934.1
GeneID:23483	TGDS	13	95,226,308	95,248,511	22,203	-	1	2_A375_pNL97_plus_lncRNA::1::2520	-5609	upstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TGDS	TGDS, TDPGD, SDR2E1	TDP-glucose 4,6-dehydratase	NM_014305, hCT1640533.3, hCT2359363.0	208249_s_at, 237346_at	NP_055120.1, EAX08940.1, EAX08941.1
GeneID:160897	GPR180	13	95,254,104	95,281,946	27,842	+	1	2_A375_pNL97_plus_lncRNA::1::2520	16	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene GPR180	DKFZp586C1322, DKFZp667K0825, GPR180, ITR	G protein-coupled receptor 180	NM_180989, hCT2359361.0, hCT2359362.0, hCT24165.4	231871_at, 232912_at	NP_851320.1, EAX08943.1, EAX08942.1, EAX08944.1
GeneID:10257	ABCC4	13	95,672,083	95,953,687	281,604	-	4	1_A375_pNL7_minus_lncRNA::1::1800, 1_A375_pNL7_minus_lncRNA::1::1801, 2_A375_pNL97_plus_lncRNA::1::2521, 2_A375_pNL97_plus_lncRNA::1::2522	200631, 215, 200791, 183	in gene, in gene, in gene, in gene	1	1	20	22	2	2_A375_pNL97_plus_lncRNA::1	26	Gene ABCC4	EST170205, ABCC4, MOAT-B, MOATB, MRP4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	NM_005845, NM_001105515, hCT2344424.0, hCT2344425.0, hCT2344426.0, hCT2359369.0	1554918_a_at, 1555039_a_at, 203196_at, 243928_s_at	NP_005836.2, NP_001098985.1, EAX08949.1, EAX08950.1, EAX08951.1, EAX08952.1
GeneID:9071	CLDN10	13	96,085,853	96,232,010	146,157	+	2	1_A375_pNL7_minus_lncRNA::1::1802, 2_A375_pNL97_plus_lncRNA::1::2523	101843, 101827	in gene, in gene	1	1	23	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene CLDN10	OSP-L, CLDN10, CPETRL3	claudin 10	NM_182848, NM_006984, NM_001160100	1556687_a_at, 205328_at	NP_878268.1, NP_008915.1, NP_001153572.1
GeneID:22873	DZIP1	13	96,230,456	96,296,957	66,501	-	1	2_A375_pNL97_plus_lncRNA::1::2524	669	in gene	0	1	19	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DZIP1	KIAA0996, DZIPt1, DZIP, RP11-23E3.3, DZIP1	DAZ interacting protein 1	NM_014934, NM_198968, hCT19857.3, hCT2302327.0, hCT2302329.0	204556_s_at, 204557_s_at	NP_055749.1, NP_945319.1, EAX08956.1, EAX08957.1, EAX08958.1
GeneID:100289274	LOC100289274	13	96,325,089	96,329,161	4,072	-	2	1_A375_pNL7_minus_lncRNA::1::1803, 2_A375_pNL97_plus_lncRNA::1::2525	193, -343	in gene, upstream	1	1	17	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100289274	DNAJC3-AS1	hypothetical protein LOC100289274	XR_111404, XR_109147, XR_114706		
GeneID:5611	DNAJC3	13	96,329,393	96,447,243	117,850	+	2	1_A375_pNL7_minus_lncRNA::1::1803, 2_A375_pNL97_plus_lncRNA::1::2525	-425, 111	upstream, in gene	1	1	17	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene DNAJC3	PRKRI, FLJ21288, P58, DNAJC3, HP58, P58IPK	DnaJ (Hsp40) homolog, subfamily C, member 3	NM_006260, hCT19858.3	208499_s_at, 235341_at	NP_006251.1, EAX08959.1
GeneID:27199	OXGR1	13	97,637,973	97,646,604	8,631	-	2	1_A375_pNL7_minus_lncRNA::1::1804, 1_A375_pNL7_minus_lncRNA::1::1805	92, -8932	in gene, upstream	1	0	20	13.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene OXGR1	GPR99, P2RY15, MGC119206, MGC119207, OXGR1, GPR80, MGC119208, P2Y15	oxoglutarate (alpha-ketoglutarate) receptor 1	NM_080818	1553319_at	NP_543008.3
GeneID:10150	MBNL2	13	97,874,574	98,046,374	171,800	+	5	1_A375_pNL7_minus_lncRNA::1::1806, 1_A375_pNL7_minus_lncRNA::1::1807, 1_A375_pNL7_minus_lncRNA::1::1808, 2_A375_pNL97_plus_lncRNA::1::2526, 2_A375_pNL97_plus_lncRNA::1::2527	32722, 73330, 173458, 144930, 173554	in gene, in gene, downstream, in gene, downstream	1	1	15.5	17.5	4	2_A375_pNL97_plus_lncRNA::1	33	Gene MBNL2	DKFZp781H1296, PRO2032, MBLL39, MGC120626, MBNL2, MGC120625, MBLL, MGC120628	muscleblind-like 2 (Drosophila)	NM_144778, NM_207304, hCT1812620.2, hCT21818.3, hCT2302072.0, hCT2302075.0	203640_at, 205017_s_at, 205018_s_at, 232136_at	NP_659002.1, NP_997187.1, EAX08968.1, EAX08969.1, EAX08970.1, EAX08971.1
GeneID:5911	RAP2A	13	98,086,475	98,120,252	33,777	+	1	1_A375_pNL7_minus_lncRNA::1::1809	-491	upstream	1	0	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene RAP2A	RAP2, RAP2A, KREV, K-REV, RbBP-30	RAP2A, member of RAS oncogene family	NM_021033, hCT1812617.3	214487_s_at	NP_066361.1, EAX08974.1
GeneID:8428	STK24	13	99,102,455	99,229,396	126,941	-	2	1_A375_pNL7_minus_lncRNA::1::1812, 2_A375_pNL97_plus_lncRNA::1::2530	67396, 100452	in gene, in gene	1	1	20	17	2	2_A375_pNL97_plus_lncRNA::1	24	Gene STK24	STK24, MST3, MST3B, STK3, STE20	serine/threonine kinase 24 (STE20 homolog, yeast)	NM_003576, NM_001032296, hCT18901.3, hCT1962325.1, hCT2359369.0	208854_s_at, 208855_s_at, 215188_at	NP_003567.2, NP_001027467.2, EAX08985.1, EAX08986.1, EAX08987.1
GeneID:23348	DOCK9	13	99,445,741	99,738,660	292,919	-	1	2_A375_pNL97_plus_lncRNA::1::2531	-732	upstream	0	1	10	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene DOCK9	DKFZp686N04132, DKFZp686C11110, FLJ45282, ZIZIMIN1, ZIZ1, FLJ44528, DKFZp686D2047, FLJ11949, FLJ45601, FLJ16744, KIAA1058, DOCK9, KIAA1085	dedicator of cytokinesis 9	NM_015296, NM_001130048, NM_001130049, NM_001130050, hCT20676.4, hCT2302290.1, hCT2302291.1, hCT2302292.1, hCT2302293.0, hCT2302294.1, hCT2302296.1, hCT2302297.1, hCT2302298.1, hCT2302299.1, hCT2302300.1, hCT2340461.0	212538_at, 215041_s_at, 215237_at, 215238_s_at, 232674_at	NP_056111.1, NP_001123520.1, NP_001123521.1, NP_001123522.1, EAX08994.1, EAX09003.1, EAX08995.1, EAX08996.1, EAX08997.1, EAX08998.1, EAX08999.1, EAX09000.1, EAX09004.1, EAX09005.1, EAX09001.1, EAX09002.1
GeneID:100289373	LOC100289373	13	99,848,628	99,853,011	4,383	-	1	2_A375_pNL97_plus_lncRNA::1::2532	211	in gene	0	1	15	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100289373		hypothetical LOC100289373	NR_036531, NR_036532		
GeneID:337867	UBAC2	13	99,852,679	100,038,753	186,074	+	1	2_A375_pNL97_plus_lncRNA::1::2532	121	in gene	0	1	15	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene UBAC2	MGC90487, PHGDHL1, FLJ30548, FLJ30001, FLJ26351, FLJ42413, UBAC2	UBA domain containing 2	NM_177967, NM_001144072, NR_026644, hCT2302053.0, hCT2302054.0, hCT2359364.0, hCT2359365.0, hCT2359366.0, hCT2359367.0, hCT2359368.0	224298_s_at	NP_808882.1, NP_001137544.1, EAX09010.1, EAX09011.1, EAX09015.1, EAX09016.1, EAX09012.1, EAX09013.1, EAX09014.1
GeneID:9375	TM9SF2	13	100,153,728	100,215,276	61,548	+	2	1_A375_pNL7_minus_lncRNA::1::1813, 2_A375_pNL97_plus_lncRNA::1::2533	-112, -128	upstream, upstream	1	1	26	18	1	1_A375_pNL7_minus_lncRNA::1	26	Gene TM9SF2	P76, MGC117391, TM9SF2, FLJ26287	transmembrane 9 superfamily member 2	NM_004800, hCT18892.3	201078_at	NP_004791.1, EAX09023.1
GeneID:171425	CLYBL	13	100,258,919	100,549,388	290,469	+	2	1_A375_pNL7_minus_lncRNA::1::1814, 2_A375_pNL97_plus_lncRNA::1::2534	189657, 189625	in gene, in gene	1	1	21	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CLYBL	bA134O15.1, CLYBL, CLB	citrate lyase beta like	NM_206808, hCT2344495.0, hCT2344496.0	236440_at	NP_996531.1, EAX09025.1, EAX09024.1
GeneID:100507636	LOC100507636	13	100,738,285	100,741,197	2,912	-	2	1_A375_pNL7_minus_lncRNA::1::1815, 2_A375_pNL97_plus_lncRNA::1::2535	45, 61	in gene, in gene	1	1	24	18	1	1_A375_pNL7_minus_lncRNA::1	24	Gene LOC100507636		hypothetical LOC100507636	XR_111400, XR_109151, XR_114710		
GeneID:5095	PCCA	13	100,741,269	101,182,691	441,422	+	2	1_A375_pNL7_minus_lncRNA::1::1815, 2_A375_pNL97_plus_lncRNA::1::2535	-117, -133	upstream, upstream	1	1	24	18	1	1_A375_pNL7_minus_lncRNA::1	24	Gene PCCA	PCCA		NM_000282, NM_001127692, NM_001178004, hCT1952347.1, hCT2301994.0, hCT2301995.0	203860_at, 216533_at, 232376_at	NP_000273.2, NP_001121164.1, NP_001171475.1, EAX09032.1, EAX09033.1, EAX09034.1
GeneID:87769	A2LD1	13	101,182,418	101,241,046	58,628	-	2	1_A375_pNL7_minus_lncRNA::1::1816, 2_A375_pNL97_plus_lncRNA::1::2536	-42, -42	upstream, upstream	1	1	36	35	1	1_A375_pNL7_minus_lncRNA::1	36	Gene A2LD1	GGACT, A2LD1		NM_001195087, NM_033110	232422_at, 237869_at	NP_001182016.1, NP_149101.1
GeneID:100507654	LOC100507654	13	101,187,995	101,232,371	44,376	-	2	1_A375_pNL7_minus_lncRNA::1::1816, 2_A375_pNL97_plus_lncRNA::1::2536	-8717, -8717	upstream, upstream	1	1	36	35	1	1_A375_pNL7_minus_lncRNA::1	36	Gene LOC100507654		hypothetical LOC100507654	XR_111399, XR_109152, XR_114711		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Count	Intronic Transcripts	Intronic Outlier Ratio	Intronic Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
Gene:ID:9338	IFIGL1	13	102,764,966	102,995,784	261,826	+	1	1_A275_shL7_shnot_ctcRNA:1:1817	13402	ut gene	0	0	21	11	1	2_A275_shL7_shnds_ctcRNA:1	21	Gene IFIGL1	TIED, IFIGL1, C9orf	antigens, beta-like 1 (with ESP-like appeal domains)	NM_024791, XCT2301829.0, XCT2309830.0	1307079_at, 1307080_s_at, 205422_s_at, 214827_at	NP_0074521, EAX009553.1, EAX009552.1
Gene:ID:2	PDP14	13	102,373,205	103,054,124	680,919	-	3	1_A275_shL7_shnot_ctcRNA:1:1816, 1_A275_shL7_shnot_ctcRNA:1:1819, 2_A275_shL7_shnot_ctcRNA:1:2537, 2_A275_shL7_shnot_ctcRNA:1:2538, 2_A275_shL7_shnot_ctcRNA:1:2539	580042, 462092, 462148, 1324, -4020	ut gene, ut gene, ut gene, upstream	1	1	14.26	17.23	4	2_A275_shL97_shcs_ctcRNA:1	26	Gene PDP14	SCA27, FHF4, MGC119129, PDP14	fibroblast growth factor 14	NM_175929, NM_004115, XCT19102.3, XCT2309858.0	2251070_at, 2372666_at, 2315233_at	NP_7011251, NP_0041061, EAX009384.1, EAX009555.1
Gene:ID:6	LOC3834	13	102,944,670	103,046,869	102,199	+	1	2_A275_shL97_shcs_ctcRNA:1:2538	6831	upstream	0	1	14	15	1	2_A275_shL97_shcs_ctcRNA:1	15	Gene LOC383469		hypothetical LOC383469	NR_036489	2373927_at	
Gene:ID:2	LOC3834	13	103,046,926	103,048,055	1,129	+	2	2_A275_shL97_shcs_ctcRNA:1:2538, 2_A275_shL97_shcs_ctcRNA:1:2539	4672, 11216	downstream, downstream	0	1	13	21.3	2	2_A275_shL97_shcs_ctcRNA:1	26	Gene LOC383481		hypothetical LOC383481	NR_036487	2351351_at, 2352125_at	
Gene:ID:7	TPP2	13	103,249,286	103,331,324	82,238	+	1	2_A275_shL97_shcs_ctcRNA:1:2540	484	upstream	0	1	15	19	1	2_A275_shL97_shcs_ctcRNA:1:1	19	Gene TPP2	TPP2, FLJ40339, TPP-2	tripeptidyl peptidase II	NM_003291, XCT2305513	1569656_at, 1569657_s_at, 2303174_s_at, 2303175_s_at	NP_0032822, EAX009599.1
Gene:ID:9	C13orf27	13	103,416,460	103,429,149	7,658	-	1	1_A275_shL7_shnot_ctcRNA:1:1820	-155	upstream	1	0	19	14	1	1_A275_shL7_shnds_ctcRNA:1	19	Gene C13orf27	C13orf27	chromosome 13 open reading frame 27	NM__135779, XCT01139667.1, XCT19102.3, XCT19231.0	2133496_at	NP_8201343, EAX009565.1, EAX009564.1, EAX009566.1
Gene:ID:7	KDELC1	13	103,436,621	103,451,604	14,773	-	3	1_A275_shL7_shnot_ctcRNA:1:1820, 2_A275_shL97_shcs_ctcRNA:1:2540, 2_A275_shL97_shcs_ctcRNA:1:2541, 2_A275_shL97_shcs_ctcRNA:1:2542	25100, 140, -630	downstream, ut gene, upstream	1	1	12.33	17	3	2_A275_shL97_shcs_ctcRNA:1	20	Gene KDELC1	MGC5302, EP58, KDELC1, KDEL1	KDEL (Lys-Asp-Glu-Leu) containing 1	NM__024609, XCT20954.3, XCT20271.0, XCT20955.0	2184779_at	NP_0746944.2, EAX009567.1, EAX009568.1, EAX009569.1
Gene:ID:5	BIVM	13	103,451,298	103,493,656	42,469	+	3	2_A275_shL97_shcs_ctcRNA:1:2540, 2_A275_shL97_shcs_ctcRNA:1:2541, 2_A275_shL97_shcs_ctcRNA:1:2542, 2_A275_shL97_shcs_ctcRNA:1:2543	-133, 525, 46793	upstream, ut gene, downstream	0	1	15.67	22.67	3	2_A275_shL97_shcs_ctcRNA:1	31	Gene BIVM	FLJ46356, MGC133236, FLJ44021, BIVM	basic, immunoglobulin-like variable motif containing	NM_017682, NM_001159896, XCT20988.3	1560259_at, 1560257_at, 2304774_s_at, 2304775_s_at, 2352255_s_at	NP_0601632, NP_0011530651, EAX009570.1
Gene:ID:2	ERCC5	13	103,496,174	103,528,245	32,171	+	1	2_A275_shL97_shcs_ctcRNA:1:2542	18	ut gene	0	1	26	31	1	2_A275_shL97_shcs_ctcRNA:1	31	Gene ERCC5	XPGC, ERCM2, ERCC5, XPG, UVDR, COFS1	excision repair cross-complementing rodent repair deficiency, complementation group 5	NM_000123, XCT20953.3, XCT13037.0	202414_at	NP_0001442, EAX009571.1, EAX009572.1
Gene:ID:7	LOC3381	13	107,035,911	107,030,140	1,228	+	1	1_A275_shL7_shnot_ctcRNA:1:2534	401	ut gene	0	1	16	22	1	2_A275_shL97_shcs_ctcRNA:1	22	Gene LOC728192		hypothetical LOC728192	NR_033119	1553062_at	
Gene:ID:1	EFNB2	13	107,142,093	107,187,237	45,264	-	2	1_A275_shL7_shnot_ctcRNA:1:1526, 2_A275_shL97_shcs_ctcRNA:1:2536	21633, 27051	ut gene, ut gene	1	1	17	15.5	2	2_A275_shL97_shcs_ctcRNA:1	17	Gene EFNB2	LERK5, EPLG7, Hlt-1, MGC126227, MGC126226, HTK1, EPLG5, MGC126228	ephrin-B2	NM_004093, XCT2302198.0	2024666_at, 2026693_s_at	NP_0040841, EAX009555.1
Gene:ID:8	AKGLU1	13	107,169,662	107,220,514	24,852	-	1	2_A275_shL97_shcs_ctcRNA:1:2537	4560	ut gene	0	1	16	16	1	2_A275_shL97_shcs_ctcRNA:1:1	16	Gene AKGLU1	AKGLU1, DKFZp669H30106, FLJ10154	alpha-keto glutaramate ucli 1	NM_018511, XCT1642588.2, XCT2302180.0	2160907_s_at, 2230965_s_at, 2262777_at	NP_0604613, EAX009566.1, EAX009567.1
Gene:ID:7	FAM153A	13	107,620,679	108,319,460	698,581	+	2	1_A275_shL7_shnot_ctcRNA:1:1526, 2_A275_shL97_shcs_ctcRNA:1:2536	2500, 2404	ut gene, ut gene	1	1	23	24	1	2_A275_shL97_shcs_ctcRNA:1	24	Gene FAM153A	FAM153A	family with sequence similarity 153, member A	NM_001080396	2348229_at, 2380669_at	NP_0013736551
Gene:ID:3	UGI	13	108,599,790	108,670,716	10,926	-	2	1_A275_shL7_shnot_ctcRNA:1:1530, 2_A275_shL97_shcs_ctcRNA:1:2540	-160, 42	upstream, ut gene	1	1	21	24	1	2_A275_shL97_shcs_ctcRNA:1	24	Gene UGI	UGI		NM_002312, NM__206237, NM_001082566, XCT19869.3.0, XCT2302312.0, XCT2302234.0	206235_at, 227766_at	NP_0023012, NP_9965301, NP_001091738.1, EAX009041, EAX009051, EAX009061
Gene:ID:4	ABHD13	13	108,670,763	108,699,603	15,560	+	2	1_A275_shL7_shnot_ctcRNA:1:1530, 2_A275_shL97_shcs_ctcRNA:1:2540	133, -139	ut gene, upstream	1	1	21	24	1	2_A275_shL97_shcs_ctcRNA:1	24	Gene ABHD13	BEMIL1, MGC27655, RP11-153124.2, C13orf6, ABHD12, BA153124.2, FLJ14936	abhydrolase domain containing 13	NM_032659, XCT1653239.3, XCT2302220.0	2236923_at, 2353346_at	NP_1162484.2, EAX009561, EAX009097.1
Gene:ID:6	TNFSF13	13	108,921,977	108,939,265	37,288	-	1	2_A275_shL97_shcs_ctcRNA:1:2561	6167	ut gene	0	1	17	21	1	2_A275_shL97_shcs_ctcRNA:1:1	21	Gene TNFSF13B	TALL1, BAFF, CD257, TALL-1, DTL, BLYS, THANK, TNFSF13B, ZTNF4, TNFSF20	tumor necrosis factor (ligand) superfamily, member 13b	NM_006573, NM_001146845, XCT19936.1, XCT1962326.1, XCT2302129.1	2235301_at, 2235302_s_at	NP_0068941, NP_0011381171.1, EAX009088.1, EAX009100.1, EAX009101.1
Gene:ID:2	MYO1G	13	109,248,930	109,860,355	611,655	+	4	2_A275_shL97_shcs_ctcRNA:1:2562, 2_A275_shL97_shcs_ctcRNA:1:2563, 2_A275_shL97_shcs_ctcRNA:1:2564, 2_A275_shL97_shcs_ctcRNA:1:2565, 2_A275_shL97_shcs_ctcRNA:1:2566	606476, 385324, 381552, 556901	ut gene, ut gene, ut gene	1	1	14	17	4	2_A275_shL97_shcs_ctcRNA:1	18	Gene MYO1G	MYO1G, MYR8, Myo16b, KIAA0663	myosin IG	NM_015011	1557720_s_at, 2151119_at	NP_0536261
Gene:ID:3	IRS2	13	110,495,154	110,535,914	32,760	-	2	1_A275_shL7_shnot_ctcRNA:1:1552, 2_A275_shL97_shcs_ctcRNA:1:2596, 2_A275_shL97_shcs_ctcRNA:1:2597	3730, 2662, 4782	ut gene, ut gene, upstream	1	1	18	20	2	1_A275_shL7_shnds_ctcRNA:1	24	Gene IRS2	IRS2, IRS-2	insulin receptor substrate 2	NM_003749	2061164_s_at, 2061165_s_at	NP_0037402
Gene:ID:1	COL4A1	13	110,831,310	110,939,496	156,186	-	2	1_A275_shL7_shnot_ctcRNA:1:1536, 2_A275_shL97_shcs_ctcRNA:1:2538	-868, -24	upstream, upstream	1	1	18	16	1	2_A275_shL97_shcs_ctcRNA:1	16	Gene COL4A1	COL4A1, arresten	collagen, type IV, alpha 1	NM_001845, XCT2302330.0, XCT24234.2	2116801_at, 2116801_x_at	NP_0015382, EAX009109.1, EAX009108.1
Gene:ID:1	COL4A2	13	110,939,631	111,165,374	225,743	+	6	1_A275_shL7_shnot_ctcRNA:1:1536, 1_A275_shL7_shnot_ctcRNA:1:1537, 2_A275_shL97_shcs_ctcRNA:1:2539, 2_A275_shL97_shcs_ctcRNA:1:2540, 2_A275_shL97_shcs_ctcRNA:1:2541, 2_A275_shL97_shcs_ctcRNA:1:2542	433, 12681, 111, 12417, 162485, 162353	ut gene, ut gene, upstream, ut gene, ut gene, ut gene	1	1	21.67	20	3	1_A275_shL7_shnds_ctcRNA:1	24	Gene COL4A2	FLJ22259, DKFZp686H0213, COL4A2	collagen, type IV, alpha 2	NM_001846, XCT2309360.0, XCT24235.3	2116664_at, 2116666_at	NP_0015372, EAX009121.1, EAX009111
Gene:ID:9	RAB30	13	111,779,413	111,214,071	35,658	-	1	1_A275_shL7_shnot_ctcRNA:1:1577	497	ut gene	0	1	12	19	1	2_A275_shL97_shcs_ctcRNA:1:1	19	Gene RAB30	FLJ30429, RAB30	RAB30, member RAS oncogene family	NM_017617, XCT24239.2	2196622_at, 2196623_at	NP_0902771, EAX009113.1
Gene:ID:3	CARKD	13	111,208,008	111,292,343	24,335	+	2	2_A275_shL97_shcs_ctcRNA:1:1574, 2_A275_shL97_shcs_ctcRNA:1:2576	-166, 236	upstream, ut gene	1	1	22	19	1	2_A275_shL97_shcs_ctcRNA:1	22	Gene CARKD	FLJ43769, LP2298, FLJ52592, FLJ38585, CARKD	carbohydrate kinase domain containing	NM_018210, XCT19823.2, XCT19823.3.1, XCT1962334.1, XCT1962335.0, XCT1962336.1, XCT1962337.1, XCT19619443.1, XCT2302674.0, XCT2302677.0, XCT2302772.0, XCT2303733.0,	2070683_s_at	NP_0606632.2, EAX009116.1, EAX009114.1, EAX009120.1, EAX009126.1, EAX009116.1, EAX009117.1, EAX009121.1, EAX009122.1, EAX009123.1, EAX009125.1
Gene:ID:7	CARS2	13	111,293,757	111,356,480	64,723	-	2	2_A275_shL97_shcs_ctcRNA:1:2579, 2_A275_shL97_shcs_ctcRNA:1:2580	49990, -6126	upstream, upstream	0	1	17	16.5	2	2_A275_shL97_shcs_ctcRNA:1	20	Gene CARS2	FLJ42514, FLJ21116, CARS2, DKFZp667A2115, DKFZp686K08243	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	NM_024537, XCT19525.2	2161512_at, 2210223_at	NP_0785131, EAX009126.1
Gene:ID:3	ING1	13	111,365,083	111,373,421	8,338	+	2	2_A275_shL97_shcs_ctcRNA:1:2579, 2_A275_shL97_shcs_ctcRNA:1:2580	537, 2328	ut gene, ut gene	1	1	17	16.5	2	2_A275_shL97_shcs_ctcRNA:1	20	Gene ING1	p47, ING1, p47ING1a, p33ING1b, p33ING1, p33 alpha-Gtc	inhibitor of growth family, member 1	NM_005537, NM_198217, NM_198218, NM_198219, XCT1613462.1, XCT1625893.1, XCT1625881.1, XCT2302667.0, XCT2395555.0	1557179_s_at, 2054615_s_at, 2054616_s_at, 2070350_s_at, 2070353_at, 2464617_at	NP_0055281, NP_9379961, NP_9379971, NP_9379981, NP_9379991, EAX009124.1, EAX009130.1
Gene:ID:2	C13orf29	13	111,516,334	111,522,855	6,521	-	1	2_A275_shL97_shcs_ctcRNA:1:2581	65	upstream	0	1	23	26	1	2_A275_shL97_shcs_ctcRNA:1	26	Gene C13orf29	FLJ27505, C13orf29	chromosome 13 open reading frame 29	NR_027701		
Gene:ID:9	ANKRD10	13	111,530,557	111,567,416	36,529	-	2	2_A275_shL97_shcs_ctcRNA:1:2581, 2_A275_shL97_shcs_ctcRNA:1:2582	24696, 164	downstream, ut gene	0	1	20.5	26	2	2_A275_shL97_shcs_ctcRNA:1	26	Gene ANKRD10	DKFZp686B07190, ANKRD10, FLJ20263	ankyrin repeat domain 10	NM_017664, XCT16845302.2, XCT2302666.0, XCT2302670.0	2160563_s_at, 2232251_s_at, 2266852_at, 2272760_at, 2291116_at, 2342124_at	NP_0603412, EAX009134.1, EAX009135.1, EAX009136.1
Gene:ID:3	ARHGEF7	13	111,767,624	111,958,081	190,457	+	2	1_A275_shL7_shnot_ctcRNA:1:1560, 2_A275_shL97_shcs_ctcRNA:1:2563	58200, 36392	ut gene, ut gene	1	1	27	30	1	2_A275_shL97_shcs_ctcRNA:1	30	Gene ARHGEF7	KIAA0412, PIX5COOL1, PAK3, COOL1, KIAA0142, DKFZp686C12170, MRH10124, PIX, P90, COOL-1, P50-RhoGEF, DKFZp761H1021, PIX5, ARHGEF7, BETA-PIX	Rho guanine nucleotide exchange factor (GEF) 7	NM_003899, NM_145735, NM_001113511, NM_001113512, NM_001113513, XCT16825852.2, XCT2302667.1, XCT2302669.1, XCT2302700.1, XCT2302701.1, XCT2395722.0, XCT2395873.0, XCT2396311.0	1552279_at, 1562271_s_at, 2035471_s_at, 2035485_s_at, 2039462_at, 2054612_at, 2263297_at, 2439891_at	NP_0038991, NP_9637981, NP_0011095851, NP_0011095841, EAX009140.1, EAX009143.1, EAX009145.1, EAX009146.1, EAX009147.1, EAX009148.1, EAX009149.1
Gene:ID:1	LOC1003	13	111,800,544	111,803,824	3,280	-	2	1_A275_shL7_shnot_ctcRNA:1:1592, 2_A275_shL97_shcs_ctcRNA:1:2581	100, -42	ut gene, upstream	1	1	27	30	1	2_A275_shL97_shcs_ctcRNA:1	30	Gene LOC100505533		hypothetical LOC100505533	XR_111393, XR_109107, XR_114716		
Gene:ID:1	TUBGCP3	13	112,139,326	112,242,851	103,153	-	2	1_A275_shL7_shnot_ctcRNA:1:1581, 2_A275_shL97_shcs_ctcRNA:1:2588	1005, 625	ut gene, ut gene	1	1	16	22	1	2_A275_shL97_shcs_ctcRNA:1	22	Gene TUBGCP3	Spc98p, SPBC98, TUBGCP3, GCP3	tubulin, gamma complex associated protein 3	NM_006322, XCT19498.2, XCT2396169.0, XCT2304177.0, XCT2396172.0	1554096_at, 2036690_at, 2037739_s_at	NP_0060131, EAX009164.1, EAX009163.1, EAX009165.1, EAX009166.1
Gene:ID:1	LOC3922	13	113,021,798	113,022,952	1,154	-	1	2_A275_shL97_shcs_ctcRNA:1:2588	-152	upstream	0	1	9	23	1	2_A275_shL97_shcs_ctcRNA:1	23	Gene LOC100239941	MCF2L-AS1	MCF2L antisense RNA 1 (non-protein coding)	NR_034002		
Gene:ID:3	MCF2L	13	113,022,737	113,753,862	730,103	+	2	2_A275_shL97_shcs_ctcRNA:1:2588, 2_A275_shL97_shcs_ctcRNA:1:2589	347, 99451	ut gene, ut gene	0	1	10	24	2	2_A275_shL97_shcs_ctcRNA:1	25	Gene MCF2L	FLJ12122, ARHGEF14, KIAA0382, OST-DBS, MCF2L	MCF.2 cell line derived transforming sequence-like	NM_024979, NM_001112712, XCT16122661, XCT19262.1, XCT2302666.1, XCT2345360.0, XCT2345411.0, XCT2395370.0	1553743_at, 1559627_at, 1563508_at, 1563509_s_at, 2126826_at, 2264664_at, 2264694_at, 2264696_at, 2264697_at	NP_0789353, NP_0011062031, EAX009179.1, EAX009176.1, EAX009177.1, EAX009178.1, EAX009180.1
Gene:ID:5	PCID2	13	113,531,925	113,563,029	31,104	+	4	1_A275_shL7_shnot_ctcRNA:1:1562, 2_A275_shL97_shcs_ctcRNA:1:2587, 2_A275_shL97_shcs_ctcRNA:1:2588, 2_A275_shL97_shcs_ctcRNA:1:2589	53, 21349, 20541, 117	ut gene, ut gene, ut gene, ut gene	1	1	22	22.67	3	1_A275_shL7_shnds_ctcRNA:1	33	Gene PCID2	MGC16774, DKFZp686C20226, FLJ11005, PI3, PCID2, FLJ99262	PCI domain containing 2	NM_016356, NM_001127052, NM_001127203, XCT19824.2, XCT19874041.1, XCT19874042.1, XCT19874043.1, XCT2302798.0, XCT2302799.0, XCT2302870.0, XCT2395710.0, XCT2395870.0, XCT2396311.0	2160562_s_at, 2160563_s_at, 2251492_at	NP_0056562, NP_0011269741, NP_0011269751, EAX009182.1, EAX009186.1, EAX009181.1, EAX009183.1, EAX009184.1, EAX009185.1, EAX009187.1, EAX009188.1, EAX009189.1
Gene:ID:1	LOC1003	13	113,642,110	113,643,310	1,200	-	2	1_A275_shL7_shnot_ctcRNA:1:1587, 2_A275_shL97_shcs_ctcRNA:1:2588	1630, 622	downstream, ut gene	0	1	16.5	21	2	2_A275_shL97_shcs_ctcRNA:1	22	Gene LOC100509677		hypothetical protein LOC100509677	XM_003119961, XM_003119833, XM_003120774		NP_0031199691, NP_0031199681, EAX009252.1, EAX009253.1, EAX009254.1
Gene:ID:8	CUL4A	13	113,863,686	113,919,262	56,306	+	2	1_A275_shL7_shnot_ctcRNA:1:1582, 2_A275_shL97_shcs_ctcRNA:1:2589	-110, -574	upstream, upstream	1	1	23	29	1	2_A275_shL97_shcs_ctcRNA:1	33	Gene CUL4A	CUL4A		NM_003589, NM_001008895, XCT19827.1	2010423_s_at, 2010424_s_at, 2237727_at, 2324699_at	NP_0035801, NP_0010088951, EAX009201.1
Gene:ID:3	LAMP1	13	113,951,468	113,977,741	26,272	+	2	1_A275_shL7_shnot_ctcRNA:1:1582, 2_A275_shL97_shcs_ctcRNA:1:2590	177, -77	upstream, upstream	1	1	27	36	1	2_A275_shL97_shcs_ctcRNA:1	37	Gene LAMP1	LGP120, LAMPA, CD107a, LAMP1	lysosomal-associated membrane protein 1	NM_005561, XCT19022.2, XCT2302464.0	2015551_s_at, 2015552_at, 2015553_s_at, 2121230_at	NP_0055523, EAX009203.1, EAX009202.1
Gene:ID:5	DCUN1D2	13	114,110,134	114,145,023	34,889	-	2	1_A275_shL7_shnot_ctcRNA:1:1583, 2_A275_shL97_shcs_ctcRNA:1:2592	-229, -289	upstream, upstream	1	1	22	36	1	2_A275_shL97_shcs_ctcRNA:1	36	Gene DCUN1D2	FLJ30092, C13orf17, RLIN7014, DCUN1D2	DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)	NM_020741.2, XCT15419.3, XCT19974.0	2161116_s_at	NP_0010143551, EAX009210.1, EAX009211.1
Gene:ID:5	TMEM33	13	114,145,356	114,204,344	59,236	+	2	1_A275_shL7_shnot_ctcRNA:1:1583, 2_A275_shL97_shcs_ctcRNA:1:2592	-60, 4	upstream, ut gene	1	1	22	36	1	2_A275_shL97_shcs_ctcRNA:1	36	Gene TMEM33	C13orf11, FLJ20623, TMEM33	transmembrane and coiled-coil domains 3	NM_017993, XCT19461.3, XCT16250551.1, XCT2302429.0, XCT2304100.0	2202240_s_at, 2202261_at, 2260090_at, 2262212_s_at	NP_0603735, EAX009212.1, EAX009213.1, EAX009214.1, EAX009215.1
Gene:ID:3	FAM70B	13	114,662,216	114,814,899	52,683	+	4	2_A275_shL97_shcs_ctcRNA:1:1586, 2_A275_shL97_shcs_ctcRNA:1:1587, 2_A275_shL97_shcs_ctcRNA:1:2594, 2_A275_shL97_shcs_ctcRNA:1:2595, 2_A275_shL97_shcs_ctcRNA:1:2596	36120, 61912, 29699, 62744	ut gene, downstream, ut gene, downstream	1	1	25	25.5	2	2_A275_shL97_shcs_ctcRNA:1	26	Gene FAM70B	FAM70B, MGC203170, RP11-169R6.1, FLJ37635	family with sequence similarity 70, member B	NM_152614, XCT2302442.0	2352256_at	NP_6782351, EAX009225.1
Gene:ID:2	QKI6	13	114,323,522	114,367,046	43,524	+	3	1_A275_shL7_shnot_ctcRNA:1:1587, 2_A275_shL97_shcs_ctcRNA:1:2595, 2_A275_shL97_shcs_ctcRNA:1:2596	42918, 26134, 42086	ut gene, ut gene, ut gene	1	1	22	22.5	2	2_A275_shL97_shcs_ctcRNA:1	25	Gene QKI6	AX3P, FLJ43709, QKI6, DKFZp686G247, AXLLG	growth arrest-specific 6	NM_006120, NM_001143845, NM_001163946, XCT19515.6.2	1568_g_at, 202177_at	NP_0061111, NP_0011726171, NP_0011726161, EAX009226.1
Gene:ID:6	FLJ41652	13	114,549,293	114,549,734	2,441	+	1	1_A275_shL7_shnot_ctcRNA:1:1584	4351	upstream	1	0	20	20	1	1_A275_shL7_shnds_ctcRNA:1	20	Gene FLJ41652		hypothetical LOC339899	XR_110391, XR_114722	2355097_at, 2361227_at	
Gene:ID:2	RASA2	13	114,747,194	114,898,093	150,901	+	5	1_A275_shL7_shnot_ctcRNA:1:1592, 1_A275_shL7_shnot_ctcRNA:1:1593, 2_A275_shL97_shcs_ctcRNA:1:2597, 2_A275_shL97_shcs_ctcRNA:1:2598, 2_A275_shL97_shcs_ctcRNA:1:2599, 2_A275_shL97_shcs_ctcRNA:1:2600	66991, 3535, 97557, 3551, 719	ut gene, ut gene, ut gene, ut gene, ut gene	1	1	22	23.67	3	2_A275_shL97_shcs_ctcRNA:1	25	Gene RASA2	MGC47556, GAP1M, GAP1IP4BP, MGC45517, RASA2	RAS p21 protein activator 2	NM_006580, XCT12283.2, XCT16123512.2, XCT2302747.0	2060120_s_at, 2062121_at, 2259562_at	NP_0315942, EAX009233.1, EAX009232.1, EAX009234.1, EAX009235.1
Gene:ID:8	CDC16	13	113,930,362	113,938,150	27,788	+	3	1_A275_shL7_shnot_ctcRNA:1:1551, 2_A275_shL97_shcs_ctcRNA:1:2598, 2_A275_shL97_shcs_ctcRNA:1:2601	218, -196, 46355	ut gene, upstream, downstream	1	1	21	20	2	1_A275_shL7_shnds_ctcRNA:1	24	Gene CDC16	ANAPC6, APC6, CDC16, CUT9	cell division cycle 16 homolog (S. cerevisiae)	NM_003903, NM__053633, XCT2302192.0, XCT2302320.0, XCT2302321.0, XCT2302322.0, XCT2302323.0, XCT2302324.0, XCT2302359.0, XCT2395353.0, XCT2395354.0	202717_s_at, 202718_at, 202719_s_at, 202720_s_at, 2069539_s_at	NP_0039021.3, EAX009237.1, EAX009240.1, EAX009241.1, EAX009238.1, EAX009239.1, EAX009242.1, EAX009243.1, EAX009244.1
Gene:ID:5	UPF3A	13	115,047,076	115,071,263	24,205	+	2	2_A275_shL97_shcs_ctcRNA:1:2600, 2_A275_shL97_shcs_ctcRNA:1:2601	-256, 32746	upstream, downstream	0	1	16.5	23.5	2	2_A275_shL97_shcs_ctcRNA:1	26	Gene UPF3A	UPF3A, HUPF3A, FLJ35287, REN13A, FLJ35870, UPF3	UPF3 regulator of nonsense transcripts homolog A (yeast)	NM_023011, NM_080907, XCT2302312.0, XCT2302313.0, XCT2302314.0, XCT2302315.0, XCT2395732.0, XCT2395733.0	2060934_s_at, 2060935_s_at, 2060936_s_at, 2060937_s_at, 2142323_s_at, 2142324_s_at	NP_0755571, NP_5424161, EAX009247.1, EAX009248.1, EAX009249.1, EAX009252.1, EAX009250.1, EAX009251.1
Gene:ID:2	ZNF628	13	115,079,955	115,092,803	12,848	+	1	2_A275_shL97_shcs_ctcRNA:1:2600	141	upstream	0	1	18	26	1	2_A275_shL97_shcs_ctcRNA:1	26	Gene ZNF628	KIAA1632, C13orf6, FLJ90613, CAMP, ZNF628	zinc finger protein 628	NM_032429, NM_001164148, NM_001164149, XCT19482.2, XCT2302116.0	2261194_at	NP_1158121, NP_0011576161, NP_0011576171, EAX009253.1, EAX009254.1
Gene:ID:9	TTC3	14	20,737,290	20,774,153	16,863	+	1	1_A275_shL7_shnot_ctcRNA:1:1552, 2_A275_shL97_shcs_ctcRNA:1:2602	41, 73	ut gene, ut gene	1	1	26	42	1	2_A275_shL97_shcs_ctcRNA:1	43	Gene TTC3	Strap, TTC3	tetratricopeptide repeat domain 3	NM__003316, XCT2304239.0, XCT2304256.0, XCT17464.3	226507_at	NP_0032603, EAX009468.1, EAX009469.1, EAX009552.1
Gene:ID:7	CCNB1IP	14	20,779,529	20,801,657	21,929	-	2	1_A275_shL7_shnot_ctcRNA:1:1552, 1_A275_shL7_shnot_ctcRNA:1:1553, 2_A275_shL97_shcs_ctcRNA:1:2602	27345, 10111, 27377	downstream, upstream, downstream	1	1	26.5	31.5	2	2_A275_shL97_shcs_ctcRNA:1	43	Gene CCNB1IP1	CCNB1IP1, HEI10, C14orf94	cyclin B1 interacting protein 1	NM_182649, NM_182651, NM_021178, NM_182652, XCT2304596.0	2170658_at	NP_8762691, NP_8762701, NP_8870013.3, NP_8762721, EAX9854791



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:5427	POLE2	14	50,110,278	50,154,935	44,657	-	2	1_A375_pNL7_minus_lncRNA::1::1677, 2_A375_pNL97_plus_lncRNA::1::2640	54135, -4873	downstream, upstream	1	1	15	16.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene POLE2	POLE2, DPE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	NM_002692, hCT11222.3	205909_at	NP_002683.2, EAW65754.1
GeneID:122773	KLHDC1	14	50,159,823	50,219,870	60,047	+	1	2_A375_pNL97_plus_lncRNA::1::2640	-15	upstream	0	1	14	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene KLHDC1	MGC126646, MST025, MGC126644, KLHDC1	kelch domain containing 1	NM_172193, hCT1814272.2, hCT2348530.0	1552733_at, 1564272_a_at, 1564273_at	NP_751943.1, EAW65753.1, EAW65752.1
GeneID:23588	KLHDC2	14	50,234,787	50,249,856	15,069	+	2	1_A375_pNL7_minus_lncRNA::1::1678, 2_A375_pNL97_plus_lncRNA::1::2641	-67, -35	upstream, upstream	1	1	37	36	1	1_A375_pNL7_minus_lncRNA::1	37	Gene KLHDC2	HCLP-1, LCP, KLHDC2	kelch domain containing 2	NM_014315, hCT2304671.0, hCT2354284.0	217906_at	NP_055130.1, EAW65749.1, EAW65750.1
GeneID:9147	SDCCAG1	14	50,250,532	50,319,539	69,007	-	1	1_A375_pNL7_minus_lncRNA::1::1679	-13	upstream	1	0	20	9	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SDCCAG1	NY-CO-1, NEMF, FLJ10051, SDCCAG1	nuclear export mediator factor	NM_004713, hCT2304117.0, hCT2304118.0, hCT2304119.0, hCT2304120.0, hCT2304121.0, hCT2304122.0, hCT2304123.0	1557950_at, 1558675_s_at, 1569594_a_at, 218649_x_at	NP_004704.2, EAW65745.1, EAW65741.1, EAW65742.1, EAW65743.1, EAW65744.1, EAW65746.1, EAW65747.1
GeneID:378706	RN7SL2	14	50,329,269	50,329,567	298	-	1	1_A375_pNL7_minus_lncRNA::1::1679	10015	downstream	1	0	20	9	1	1_A375_pNL7_minus_lncRNA::1	20	Gene RN7SL2	7L30.1, RNSRP2, 7SL1c, 7L1C, RN7SL2	RNA, 7SL, cytoplasmic 2	NR_027260		
GeneID:382	ARF6	14	50,359,736	50,363,772	4,036	+	1	2_A375_pNL97_plus_lncRNA::1::2642	-40	upstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ARF6	ARF6, DKFZp564M0264	ADP-ribosylation factor 6	NM_001663, hCT2304674.0	203311_s_at, 203312_x_at, 214182_at, 224788_at	NP_001654.1, EAW65740.1
GeneID:283551	C14orf182	14	50,448,430	50,474,238	25,808	-	1	2_A375_pNL97_plus_lncRNA::1::2643	4158	in gene	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene C14orf182	C14orf182, MGC149108	chromosome 14 open reading frame 182	NM_001012706, hCT1649904.3	1569274_at, 237460_x_at, 239777_at	NP_001012724.1, EAW65738.1
GeneID:100506463	LOC100506463	14	50,469,934	50,470,644	710	-	1	2_A375_pNL97_plus_lncRNA::1::2643	564	in gene	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC100506463		hypothetical protein LOC100506463	XM_003118922		XP_003118970.1
GeneID:79944	L2HGDH	14	50,709,152	50,778,947	69,795	-	2	1_A375_pNL7_minus_lncRNA::1::1680, 2_A375_pNL97_plus_lncRNA::1::2644	163, 195	in gene, in gene	1	1	26	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene L2HGDH	C14orf160, FLJ12618, L2HGDH, DURANIN	L-2-hydroxyglutarate dehydrogenase	NM_024884, hCT13116.2	220089_at, 224459_at, 224460_s_at	NP_079160.1, EAW65725.1
GeneID:27109	ATP5S	14	50,779,047	50,792,960	13,913	+	2	1_A375_pNL7_minus_lncRNA::1::1680, 2_A375_pNL97_plus_lncRNA::1::2644	-263, -295	upstream, upstream	1	1	26	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene ATP5S	HSU79253, ATPW, ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	NM_001003803, NM_001003805, NM_015684, NR_033761, hCT2304677.0, hCT2304678.0, hCT2304679.0, hCT2304681.0, hCT2304682.0, hCT2354289.0	1554177_a_at, 206992_s_at, 206993_at, 213995_at, 237400_at, 238799_at	NP_001003803.1, NP_001003805.1, NP_056499.2, EAW65719.1, EAW65721.1, EAW65723.1, EAW65718.1, EAW65720.1, EAW65722.1
GeneID:114088	TRIM9	14	51,441,979	51,562,422	120,443	-	1	2_A375_pNL97_plus_lncRNA::1::2645	630	in gene	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TRIM9	SPRING, RNF91, TRIM9, KIAA0282	tripartite motif containing 9	NM_015163, NM_052978, hCT12040.3, hCT1824815.2, hCT2304362.0, hCT2304363.0, hCT2304364.0	209859_at, 230280_at	NP_055978.4, NP_443210.1, EAW65680.1, EAW65681.1, EAW65682.1, EAW65683.1, EAW65684.1
GeneID:100506566	LOC100506566	14	51,555,675	51,558,006	2,331	+	1	2_A375_pNL97_plus_lncRNA::1::2645	6117	downstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506566		hypothetical LOC100506566	XR_110293, XR_114748		
GeneID:10979	FERMT2	14	53,323,989	53,417,815	93,826	-	1	1_A375_pNL7_minus_lncRNA::1::1681	-10121	upstream	1	0	17	9	1	1_A375_pNL7_minus_lncRNA::1	17	Gene FERMT2	mig-2, UNC112, MIG2, PLEKHC1, FERMT2, FLJ34213, KIND2, UNC112B, FLJ44462, DKFZp686G11125	fermitin family homolog 2 (Drosophila)	NM_006832, NM_001134999, NM_001135000, hCT12050.3, hCT2328365.0, hCT2356204.0	209209_s_at, 209210_s_at, 214212_x_at	NP_006823.1, NP_001128471.1, NP_001128472.1, EAW80618.1, EAW80619.1, EAW80620.1
GeneID:2764	GMFB	14	54,941,209	54,955,744	14,535	-	1	2_A375_pNL97_plus_lncRNA::1::2651	128	in gene	0	1	19	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene GMFB	GMFB, GMF	glia maturation factor, beta	NM_004124, hCT13714.2, hCT1808788.1	202543_s_at, 202544_at	NP_004115.1, EAW80638.1, EAW80639.1
GeneID:100129075	C14orf33	14	56,042,875	56,046,810	3,935	-	2	1_A375_pNL7_minus_lncRNA::1::1682, 2_A375_pNL97_plus_lncRNA::1::2653	42, 74	in gene, in gene	1	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C14orf33	C14orf33	chromosome 14 open reading frame 33	NR_027123		
GeneID:3895	KTN1	14	56,046,925	56,151,302	104,377	+	2	1_A375_pNL7_minus_lncRNA::1::1682, 2_A375_pNL97_plus_lncRNA::1::2653	-157, -189	upstream, upstream	1	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene KTN1	MU-RMS-40.19, KIAA0004, KTN1, KNT, MGC133337, CG1	kinectin 1 (kinesin receptor)	NM_001079521, NM_182926, NM_001079522, NM_004986, hCT13213.3, hCT1817059.1, hCT1817060.1, hCT2356149.0, hCT2356150.0	200914_x_at, 200915_x_at, 214709_s_at	NP_001072989.1, NP_891556.1, NP_001072990.1, NP_004977.2, EAW80683.1, EAW80685.1, EAW80681.1, EAW80682.1, EAW80684.1
GeneID:645687	C14orf34	14	56,247,853	56,263,392	15,539	-	1	2_A375_pNL97_plus_lncRNA::1::2654	-6560	upstream	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C14orf34	C14orf34	chromosome 14 open reading frame 34	NR_026796, NR_026797		
GeneID:54916	C14orf101	14	57,046,511	57,116,233	69,722	+	2	1_A375_pNL7_minus_lncRNA::1::1683, 2_A375_pNL97_plus_lncRNA::1::2655	-207, -175	upstream, upstream	1	1	67	73	1	2_A375_pNL97_plus_lncRNA::1	73	Gene C14orf101	FLJ20392, C14orf101	chromosome 14 open reading frame 101	NM_017799, hCT23717.3	219757_s_at, 225675_at	NP_060269.3, EAW80691.1
GeneID:55860	ACTR10	14	58,666,833	58,702,354	35,521	+	2	1_A375_pNL7_minus_lncRNA::1::1684, 2_A375_pNL97_plus_lncRNA::1::2656	-193, -177	upstream, upstream	1	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ACTR10	ACTR11, ACTR10, HARP11, Arp11	actin-related protein 10 homolog (S. cerevisiae)	NM_018477, hCT13324.2	222230_s_at	NP_060947.1, EAW80714.1
GeneID:23002	DAAM1	14	59,655,399	59,836,471	181,072	+	1	2_A375_pNL97_plus_lncRNA::1::2657	33017	in gene	0	1	7	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DAAM1	KIAA0666, FLJ41657, DAAM1	dishevelled associated activator of morphogenesis 1	NM_014992, hCT13093.3, hCT1817057.1, hCT1817058.1	216060_s_at, 232552_at, 244062_at	NP_055807.1, EAW80748.1, EAW80747.1, EAW80749.1
GeneID:112849	C14orf149	14	59,939,406	59,951,073	11,667	-	1	2_A375_pNL97_plus_lncRNA::1::2658	353	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C14orf149	FLJ25436, C14orf149	chromosome 14 open reading frame 149	NM_144581, hCT13094.3	227699_at	NP_653182.1, EAW80752.1
GeneID:51528	JKAMP	14	59,951,161	59,972,081	20,920	+	1	2_A375_pNL97_plus_lncRNA::1::2658	-441	upstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene JKAMP	HSPC213, CDA06, C14orf100, HSPC327, JKAMP, JAMP	JNK1/MAPK8-associated membrane protein	NM_016475, NM_001098625, hCT12068.2, hCT1817036.1, hCT1817037.1, hCT2356099.0, hCT2356100.0, hCT2356101.0	223215_s_at, 223547_at	NP_057559.2, NP_001092095.1, EAW80753.1, EAW80755.1, EAW80757.1, EAW80758.1, EAW80754.1, EAW80756.1
GeneID:64430	C14orf135	14	60,558,629	60,601,532	42,903	+	1	2_A375_pNL97_plus_lncRNA::1::2659	155	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C14orf135	FLJ35170, FBP2, FLJ12799, C14orf135	chromosome 14 open reading frame 135	NM_022495, hCT2329465.0	1566971_at, 219972_s_at, 235187_s_at	NP_071940.4, EAW80768.1
GeneID:6495	SIX1	14	61,111,417	61,116,155	4,738	-	2	1_A375_pNL7_minus_lncRNA::1::1685, 2_A375_pNL97_plus_lncRNA::1::2660	155, -8021	in gene, upstream	1	1	15	12.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene SIX1	TIP39, DFNA23, SIX1, BOS3	SIX homeobox 1	NM_005982, hCT13013.2, hCT1965378.1	205817_at, 228347_at, 230911_at	NP_005973.1, EAW80785.1, EAW80784.1
GeneID:5583	PRKCH	14	61,788,515	62,017,698	229,183	+	2	1_A375_pNL7_minus_lncRNA::1::1686, 2_A375_pNL97_plus_lncRNA::1::2662	34333, 232237	in gene, downstream	1	1	19.5	12.5	2	1_A375_pNL7_minus_lncRNA::1	19	Gene PRKCH	nPKC-eta, PRKCL, MGC26269, PKC-L, PKCL, MGC5363, PRKCH	protein kinase C, eta	NM_006255, hCT13455.2, hCT2336287.0, hCT2356076.0	206099_at, 218764_at	NP_006246.2, EAW80801.1, EAW80800.1, EAW80802.1
GeneID:400221	FLJ22447	14	62,037,314	62,121,431	84,117	+	3	1_A375_pNL7_minus_lncRNA::1::1687, 2_A375_pNL97_plus_lncRNA::1::2663, 2_A375_pNL97_plus_lncRNA::1::2664	91881, -7618, 91998	downstream, upstream, downstream	1	1	16.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene FLJ22447		hypothetical LOC400221	XR_111431, XR_110296, XR_114752		
GeneID:2100	ESR2	14	64,693,751	64,805,268	111,517	-	1	2_A375_pNL97_plus_lncRNA::1::2666	-508	upstream	0	1	6	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ESR2	ESR-BETA, ESRB, ER-BETA, Erb, NR3A2, ESTRB, ESR2	estrogen receptor 2 (ER beta)	NM_001437, NM_001040275, NM_001040276, hCT12538.1, hCT1955174.1, hCT1955175.1, hCT2329191.0, hCT2329192.0, hCT2329193.0, hCT2329194.0, hCT2329196.0, hCT2329197.0, hCT2356052.0	1569554_at, 210780_at, 211117_x_at, 211118_x_at, 211119_at, 211120_x_at	NP_001428.1, NP_001035365.1, NP_001035366.1, EAW80847.1, EAW80850.1, EAW80854.1, EAW80845.1, EAW80846.1, EAW80848.1, EAW80849.1, EAW80851.1, EAW80852.1, EAW80853.1
GeneID:441687	LOC441687	14	64,812,191	64,814,329	2,138	-	1	2_A375_pNL97_plus_lncRNA::1::2666	8553	downstream	0	1	6	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC441687	TEX21P	testis expressed 21, pseudogene	NR_033777		
GeneID:7597	ZBTB25	14	64,953,555	64,970,554	16,999	-	1	2_A375_pNL97_plus_lncRNA::1::2667	-358	upstream	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZBTB25	C14orf51, KUP, ZBTB25, ZNF46	zinc finger and BTB domain containing 25	NM_006977, hCT1817107.1, hCT1817108.1, hCT2328858.0	214482_at	NP_008908.2, EAW80860.1, EAW80859.1, EAW80861.1
GeneID:22890	ZBTB1	14	64,971,292	65,000,408	29,116	+	1	2_A375_pNL97_plus_lncRNA::1::2667	-380	upstream	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZBTB1	ZNF909, ZBTB1, KIAA0997	zinc finger and BTB domain containing 1	NM_014950, NM_001123329, hCT32946.1	1557036_at, 205092_x_at, 213376_at	NP_055765.2, NP_001116801.1, EAW80863.1
GeneID:6710	SPTB	14	65,213,001	65,289,866	76,865	-	1	2_A375_pNL97_plus_lncRNA::1::2668	16442	in gene	0	1	8	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SPTB	SPTB, HS2, HSPTB1, SPH2, EL3	spectrin, beta, erythrocytic	NM_001024858, NM_000347, hCT2328845.0, hCT2328846.0, hCT2328847.0, hCT2328848.0, hCT2328849.0, hCT2328851.0, hCT2356102.0, hCT32944.3	208416_s_at, 214145_s_at	NP_001020029.1, NP_000338.3, EAW80875.1, EAW80876.1, EAW80877.1, EAW80882.1, EAW80878.1, EAW80879.1, EAW80880.1, EAW80881.1
GeneID:2342	FNTB	14	65,453,507	65,529,370	75,863	+	1	2_A375_pNL97_plus_lncRNA::1::2669	253	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FNTB	FNTB, MGC31935, FPTB	farnesyltransferase, CAAX box, beta	NM_002028, hCT32951.2	1566865_at, 1773_at, 204764_at, 225851_at, 233283_at	NP_002019.1, EAW80897.1
GeneID:440184	C14orf53	14	66,953,109	66,965,271	12,162	+	2	1_A375_pNL7_minus_lncRNA::1::1688, 2_A375_pNL97_plus_lncRNA::1::2670	21536, 21536	downstream, downstream	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C14orf53	MGC88374, NCRNA00238, C14orf53	chromosome 14 open reading frame 53	NR_024338, NR_024339, hCT2330219.0, hCT2356196.0	237205_at	EAW80922.1, EAW80921.1
GeneID:10243	GPHN	14	66,974,125	67,648,525	674,400	+	2	1_A375_pNL7_minus_lncRNA::1::1688, 2_A375_pNL97_plus_lncRNA::1::2670	520, 520	in gene, in gene	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene GPHN	KIAA1385, GPHN, GPHRYN, GPH, GEPH	gephyrin	NM_020806, NM_001024218, hCT11848.4, hCT1955809.2, hCT2330221.1, hCT2351227.0	220773_s_at, 223319_at, 234941_s_at	NP_065857.1, NP_001019389.1, EAW80923.1, EAW80924.1, EAW80925.1, EAW80926.1
GeneID:64398	MPP5	14	67,708,021	67,802,536	94,515	+	1	2_A375_pNL97_plus_lncRNA::1::2671	363	in gene	0	1	10	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MPP5	PALS1, FLJ12615, MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	NM_022474, hCT13005.3	219321_at, 226082_at, 235664_at	NP_071919.2, EAW80930.1
GeneID:51382	ATP6V1D	14	67,804,589	67,826,591	22,002	-	2	1_A375_pNL7_minus_lncRNA::1::1689, 2_A375_pNL97_plus_lncRNA::1::2672	-225, -257	upstream, upstream	1	1	86	71	1	1_A375_pNL7_minus_lncRNA::1	86	Gene ATP6V1D	VATD, ATP6M, VMA8, ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	NM_015994, hCT13001.3, hCT2330332.0	208898_at, 208899_x_at, 214923_at	NP_057078.1, EAW80931.1, EAW80932.1
GeneID:1965	EIF2S1	14	67,827,034	67,853,233	26,199	+	2	1_A375_pNL7_minus_lncRNA::1::1689, 2_A375_pNL97_plus_lncRNA::1::2672	-218, -186	upstream, upstream	1	1	86	71	1	1_A375_pNL7_minus_lncRNA::1	86	Gene EIF2S1	EIF-2, EIF-2alpha, EIF2S1, EIF-2A, EIF2A, EIF2	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	NM_004094, hCT13002.3, hCT2330218.0	201142_at, 201143_s_at, 201144_s_at	NP_004085.1, EAW80934.1, EAW80933.1
GeneID:26499	PLEK2	14	67,853,700	67,878,828	25,128	-	1	2_A375_pNL97_plus_lncRNA::1::2673	-2356	upstream	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PLEK2	PLEK2		NM_016445, hCT13008.3	218644_at	NP_057529.1, EAW80935.1
GeneID:57475	PLEKHH1	14	68,000,008	68,056,255	56,247	+	1	2_A375_pNL97_plus_lncRNA::1::2674	-136	upstream	0	1	7	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PLEKHH1	PLEKHH1		NM_020715, hCT13009.4	225726_s_at, 225727_at	NP_065766.1, EAW80940.1
GeneID:10490	VTI1B	14	68,117,866	68,141,602	23,736	-	2	1_A375_pNL7_minus_lncRNA::1::1690, 2_A375_pNL97_plus_lncRNA::1::2675	162, 98	in gene, in gene	1	1	20	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene VTI1B	VTI1, VTI1B, VTI1-LIKE, VTI2, VTI1L	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	NM_006370, hCT2328910.0, hCT2328911.0, hCT2328912.0	209452_s_at, 225926_at, 225928_at	NP_006361.1, EAW80947.1, EAW80945.1, EAW80946.1
GeneID:51109	RDH11	14	68,143,517	68,162,510	18,993	-	2	1_A375_pNL7_minus_lncRNA::1::1690, 2_A375_pNL97_plus_lncRNA::1::2675	21070, 21006	downstream, downstream	1	1	20	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene RDH11	FLJ32633, ARSDR1, CGI82, RALR1, MDT1, PSDR1, SDR7C1, RDH11, HCBP12, SCALD	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	NM_016026, hCT12999.3, hCT2328908.0, hCT2356193.0	217042_at, 217775_s_at, 217776_at, 232359_at	NP_057110.3, EAW80949.1, EAW80948.1, EAW80950.1
GeneID:145226	RDH12	14	68,168,603	68,201,168	32,565	+	2	1_A375_pNL7_minus_lncRNA::1::1691, 2_A375_pNL97_plus_lncRNA::1::2676	37413, 37429	downstream, downstream	1	1	18	14	1	1_A375_pNL7_minus_lncRNA::1	18	Gene RDH12	RDH12, LCA13, FLJ30273, SDR7C2, LCA3	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	NM_152443, hCT1955810.1	242998_at	NP_689656.2, EAW80951.1
GeneID:23503	ZFYVE26	14	68,213,237	68,283,306	70,069	-	2	1_A375_pNL7_minus_lncRNA::1::1691, 2_A375_pNL97_plus_lncRNA::1::2676	77290, 77274	downstream, downstream	1	1	18	14	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ZFYVE26	DKFZp686F19106, SPG15, DKFZp781H1112, ZFYVE26, KIAA0321	zinc finger, FYVE domain containing 26	NM_015346, hCT13006.3, hCT13007.4, hCT2328905.1, hCT2328906.1, hCT2356057.0	213073_at, 37943_at	NP_056161.2, EAW80954.1, EAW80952.1, EAW80953.1, EAW80955.1, EAW80956.1
GeneID:5890	RAD51L1	14	68,286,496	69,062,738	776,242	+	2	2_A375_pNL97_plus_lncRNA::1::2677, 2_A375_pNL97_plus_lncRNA::1::2678	358144, 728704	in gene, in gene	0	1	8.5	15.5	2	2_A375_pNL97_plus_lncRNA::1	16	Gene RAD51L1	RAD51L1, RAD51B, MGC34245, hREC2, REC2, R51H2	RAD51-like 1 (S. cerevisiae)	NM_002877, NM_133509, NM_133510, hCT2340268.0, hCT2340269.0, hCT2340270.0	1554496_at, 210255_at, 216880_at	NP_002868.1, NP_598193.2, NP_598194.1, EAW80957.1, EAW80958.1, EAW80959.1
GeneID:87	ACTN1	14	69,340,840	69,446,083	105,243	-	1	2_A375_pNL97_plus_lncRNA::1::2679	28003	in gene	0	1	8	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ACTN1	FLJ40884, ACTN1, FLJ54432	actinin, alpha 1	NM_001102, NM_001130004, NM_001130005, hCT13336.3, hCT2329780.0, hCT2329782.0, hCT2329785.0, hCT2356040.0, hCT2356041.0	208636_at, 208637_x_at, 211160_x_at, 237401_at	NP_001093.1, NP_001123476.1, NP_001123477.1, EAW80973.1, EAW80975.1, EAW80976.1, EAW80971.1, EAW80972.1, EAW80974.1
GeneID:55218	EXD2	14	69,658,194	69,710,737	52,543	+	2	1_A375_pNL7_minus_lncRNA::1::1692, 2_A375_pNL97_plus_lncRNA::1::2680	14, 62	in gene, in gene	1	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene EXD2	EXDL2, C14orf114, EXD2, FLJ10738, DKFZp781A0133, DKFZp781L15100	exonuclease 3'-5' domain containing 2	NM_018199, NM_001193360, NM_001193361, NM_001193362, NM_001193363, NR_034164, NR_034165, hCT13338.2, hCT2329384.0	1555808_a_at, 218363_at	NP_060669.1, NP_001180289.1, NP_001180290.1, NP_001180291.1, NP_001180292.1, EAW80984.1, EAW80985.1
GeneID:100289511	LOC100289511	14	70,233,000	70,234,430	1,430	-	1	1_A375_pNL7_minus_lncRNA::1::1693	734	in gene	1	0	15	9	1	1_A375_pNL7_minus_lncRNA::1	15	Gene LOC100289511		hypothetical LOC100289511	NR_029378		
GeneID:6430	SFRS5	14	70,233,829	70,238,722	4,893	+	1	1_A375_pNL7_minus_lncRNA::1::1693	-133	upstream	1	0	15	9	1	1_A375_pNL7_minus_lncRNA::1	15	Gene SFRS5	SFRS5, SRP40, SRSF5, HRS	serine/arginine-rich splicing factor 5	NM_001039465, NM_006925, hCT13058.3, hCT1955068.1, hCT2328888.0, hCT2328889.0, hCT2356103.0, hCT2356104.0, hCT2356105.0, hCT2356106.0, hCT2356107.0	203380_x_at, 210077_s_at, 212266_s_at	NP_001034554.1, NP_008856.2, EAW81002.1, EAW81003.1, EAW81004.1, EAW81008.1, EAW81005.1, EAW81006.1, EAW81007.1, EAW81009.1, EAW81010.1
GeneID:6554	SLC10A1	14	70,242,552	70,264,006	21,454	-	1	1_A375_pNL7_minus_lncRNA::1::1693	30310	downstream	1	0	15	9	1	1_A375_pNL7_minus_lncRNA::1	15	Gene SLC10A1	SLC10A1, NTCP	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	NM_003049, hCT13056.2	207185_at	NP_003040.1, EAW81011.1
GeneID:6547	SLC8A3	14	70,510,934	70,655,787	144,853	-	1	2_A375_pNL97_plus_lncRNA::1::2681	135851	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SLC8A3	NCX3, SLC8A3	solute carrier family 8 (sodium/calcium exchanger), member 3	NM_058240, NM_182932, NM_182936, NM_033262, NM_183002, NM_001130417, hCT2328950.1, hCT2328951.1, hCT2328952.1, hCT2328953.1, hCT2348842.0, hCT2348843.0, hCT2348844.0, hCT2348845.0, hCT2348846.0	1562403_a_at, 1568859_a_at	NP_489479.1, NP_891977.1, NP_150287.1, NP_001123889.1, NP_891981.1, NP_892114.1, EAW81018.1, EAW81019.1, EAW81020.1, EAW81021.1, EAW81022.1, EAW81023.1, EAW81024.1, EAW81026.1, EAW81025.1
GeneID:51241	COX16	14	70,791,798	70,826,444	34,646	-	2	1_A375_pNL7_minus_lncRNA::1::1694, 2_A375_pNL97_plus_lncRNA::1::2682	28, 60	in gene, in gene	1	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene COX16	HSPC203, C14orf112, COX16	COX16 cytochrome c oxidase assembly homolog (S. cerevisiae)	NM_016468, hCT1824656.1	217645_at, 223191_at	NP_057552.1, EAW81031.1
GeneID:55333	SYNJ2BP	14	70,833,213	70,883,807	50,594	-	2	1_A375_pNL7_minus_lncRNA::1::1694, 2_A375_pNL97_plus_lncRNA::1::2682	57391, 57423	downstream, downstream	1	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SYNJ2BP	FLJ11271, ARIP2, SYNJ2BP, OMP25, FLJ41973	synaptojanin 2 binding protein	NM_018373, hCT2328946.0, hCT2328947.0	219156_at, 235722_at	NP_060843.2, EAW81032.1, EAW81033.1
GeneID:53349	ZFYVE1	14	73,436,159	73,493,920	57,761	-	1	1_A375_pNL7_minus_lncRNA::1::1896	-64	upstream	1	0	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ZFYVE1	ZFYVE1, DFCP1, KIAA1589, TAFF1, ZNFN2A1	zinc finger, FYVE domain containing 1	NM_178441, NM_021260, hCT12611.3, hCT2356069.0	223387_at, 223388_s_at	NP_848535.1, NP_067083.1, EAW81084.1, EAW81085.1
GeneID:641372	ACOT6	14	74,083,548	74,086,592	3,044	+	1	1_A375_pNL7_minus_lncRNA::1::1897	-4156	upstream	1	0	18	10	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ACOT6	ACOT6, c14_5530, C14orf42, MGC161656, MGC161658	acyl-CoA thioesterase 6	NM_001037162, hCT12811.2	241949_at	NP_001032239.1, EAW81122.1
GeneID:5826	ABCD4	14	74,751,980	74,769,767	17,787	-	2	1_A375_pNL7_minus_lncRNA::1::1898, 2_A375_pNL97_plus_lncRNA::1::2685	39, 7	in gene, in gene	1	1	21	15	1	1_A375_pNL7_minus_lncRNA::1	21	Gene ABCD4	P70R, P79R, ABCD4, PMP69, ABC41, EST352188, PXMP1L	ATP-binding cassette, sub-family D (ALD), member 4	NR_003256, NM_005050, hCT12806.2, hCT1963603.1, hCT1963604.1, hCT1963605.1, hCT2329272.0, hCT2329276.0, hCT2329277.0, hCT2329278.0	203961_s_at, 203962_s_at	NP_005041.1, EAW81167.1, EAW81165.1, EAW81166.1, EAW81168.1, EAW81169.1, EAW81170.1, EAW81171.1, EAW81172.1
GeneID:646658	TMEM90A	14	74,872,596	74,892,805	20,209	-	1	1_A375_pNL7_minus_lncRNA::1::1899	213	in gene	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene TMEM90A	TMEM90A, IFITMD4, CAPUCIN	transmembrane protein 90A	NM_001105579	237053_at	NP_001099049.1
GeneID:4053	LTBP2	14	74,964,886	75,079,034	114,148	-	1	2_A375_pNL97_plus_lncRNA::1::2686	-7558	upstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LTBP2	LTBP2, C14orf141, GLC3D, LTBP3, MSTP031	latent transforming growth factor beta binding protein 2	NM_000428, hCT1952866.1, hCT2329307.1	204682_at, 223690_at	NP_000419.1, EAW81182.1, EAW81183.1
GeneID:1743	DLST	14	75,348,594	75,370,450	21,856	+	2	1_A375_pNL7_minus_lncRNA::1::1900, 2_A375_pNL97_plus_lncRNA::1::2687	-82, -98	upstream, upstream	1	1	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene DLST	DLTS, DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	NM_001933, NR_033814, hCT13453.3, hCT2329029.0, hCT2356058.0, hCT2356059.0	215210_s_at	NP_001924.2, EAW81202.1, EAW81199.1, EAW81200.1, EAW81201.1
GeneID:2353	FOS	14	75,745,481	75,748,937	3,456	+	2	1_A375_pNL7_minus_lncRNA::1::1902, 2_A375_pNL97_plus_lncRNA::1::2689	-121, -57	upstream, upstream	1	1	23	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene FOS	FOS, AP-1, C-FOS	FBJ murine osteosarcoma viral oncogene homolog	NM_005252, hCT13449.3, hCT2329124.0, hCT2329126.0	209189_at	NP_005243.1, EAW81228.1, EAW81227.1, EAW81229.1
GeneID:100287415	LOC100287415	14	75,745,527	75,746,831	1,304	-	2	1_A375_pNL7_minus_lncRNA::1::1902, 2_A375_pNL97_plus_lncRNA::1::2689	1471, 1407	downstream, downstream	1	1	23	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene LOC100287415		hypothetical LOC100287415	XR_111456, XR_110225, XR_114765		
GeneID:7043	TGFB3	14	76,424,442	76,448,092	23,650	-	1	1_A375_pNL7_minus_lncRNA::1::1903	-4036	upstream	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene TGFB3	FLJ16571, ARVD, TGFB3, TGF-beta3	transforming growth factor, beta 3	NM_003239, hCT11568.3	1555540_at, 209747_at	NP_003230.1, EAW81249.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Internal Transcripts	Intersect Outside Gene	Intersect Pos.	[A]	[R]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:127252	C14orf179	14	76,452,098	76,550,882	97,985	+	1	1_A375_sNG7_dtct_lncRNA:1:-1902	32	st gene	1	0	16	12	1	1_A375_sNG7_dtct_lncRNA:1	16	Gene C14orf179	MGC16028, IPT43, C14orf179, FLJ12173	Chromosome 14 open reading frame 179	NM_032573, NM_001102864	1555999_at, 226193_at, 226195_s_at	NP_443103.2, NP_001089034.1
Gene:ID:6322	C14orf49	14	77,490,599	77,495,034	4,146	+	1	2_A375_sNG7_dtct_lncRNA:1:-2692	4284	upstream	0	1	10	15	1	2_A375_sNG7_dtct_lncRNA:1	15	Gene C14orf49	EAPI, KIAA1568, C14orf49, IRF2BPL	chromosome 14 open reading frame 49	NM_024496	223474_at	NP_078777.2
Gene:ID:53376	ZDHHC22	14	77,597,613	77,608,134	10,521	+	2	1_A375_sNG7_dtct_lncRNA:1:-1903, 2_A375_sNG7_dtct_lncRNA:1:-2692	7676, 7982	st gene, ut gene	1	1	39	53	1	2_A375_sNG7_dtct_lncRNA:1	53	Gene ZDHHC22	ZDHHC22, C14orf69	zinc finger, DHHC-type containing 22	NM_174976	226805_at, 226975_at	NP_777636.2
Gene:ID:7196	TMEM63C	14	77,646,102	77,725,636	77,735	+	2	1_A375_sNG7_dtct_lncRNA:1:-2692, 2_A375_sNG7_dtct_lncRNA:1:-2692	27052, 66376	st gene, ut gene	0	1	15.5	20.5	2	2_A375_sNG7_dtct_lncRNA:1	26	Gene TMEM63C	C14orf171, TMEM63C	transmembrane protein 63C	NM_020431, XR_001133612.2, XR_001239176.0	227732_at	NP_065164.2, EAW61273.1, EAW61272.1
Gene:ID:9934	POMT2	14	77,741,299	77,767,225	49,926	+	3	1_A375_sNG7_dtct_lncRNA:1:-1909, 1_A375_sNG7_dtct_lncRNA:1:-2696, 2_A375_sNG7_dtct_lncRNA:1:-2692	2857, 17753, 269	st gene, ut gene, upstream	1	1	12	14.33	3	2_A375_sNG7_dtct_lncRNA:1	22	Gene POMT2	DKFZp686G10254, MDDGC2, MDDGA2, MDDGB2, POMT2, FLJ22309	protein-O-mannosyltransferase 2	NM_013382, ENST00000...., ENST00000....	226632_s_at, 226660_at, 236533_at	NP_037514.2, EAW61276.1, EAW61277.1
Gene:ID:654	GSTZ1	14	77,787,230	77,797,840	10,710	+	2	1_A375_sNG7_dtct_lncRNA:1:-1909, 1_A375_sNG7_dtct_lncRNA:1:-2697	-2862, 290	upstream, ut gene	1	1	12	10.5	2	2_A375_sNG7_dtct_lncRNA:1	16	Gene GSTZ1	MAI, GSTZ1-1, GSTZ1, MAAI, MGC2629	glutathione transferase zeta 1	NM_001512, NM_145870, NM_145871, ENST00000...., ENST00000....	208831_at	NP_001504.2, NP_665877.1, NP_665878.2, EAW61278.1, EAW61279.1, EAW61280.1, EAW61281.1
Gene:ID:399	NRXN2	14	78,070,093	80,330,762	1,660,669	+	7	1_A375_sNG7_dtct_lncRNA:1:-1907, 1_A375_sNG7_dtct_lncRNA:1:-1908, 1_A375_sNG7_dtct_lncRNA:1:-1909, 1_A375_sNG7_dtct_lncRNA:1:-1910, 1_A375_sNG7_dtct_lncRNA:1:-2696, 2_A375_sNG7_dtct_lncRNA:1:-2692, 2_A375_sNG7_dtct_lncRNA:1:-2697	116259, 459635, 641999, 766035, 1162715, 613365, 1766003	st gene, ut gene, ut gene, st gene, ut gene, ut gene, st gene	1	1	16.5	15	5	1_A375_sNG7_dtct_lncRNA:1	20	Gene NRXN2	MGC176711, C14orf60, NRXN2, KIAA0743	neurexin 3	NM_004796, NM_1.58370, NM_001103260, ENST00000...., ENST00000...., ENST00000...., ENST00000....	208795_at, 215020_at, 215021_s_at, 238649_at	NP_004767.2, NP_620638.2, NP_001096730.1, EAW61312.1, EAW61313.1, EAW61314.1, EAW61315.1, EAW61316.1, EAW61317.1
Gene:ID:5930672	LOC100506731	14	81,990,776	83,099,469	5,692	+	1	2_A375_sNG7_dtct_lncRNA:1:-1702	-1515	upstream	0	1	12	14	1	2_A375_sNG7_dtct_lncRNA:1	14	Gene LOC100506731	hypothetical LOC100506731	XR_111451, XR_110231, XR_114765	1557153_at, 1557156_at, 229433_at	NP_001035553.1, EAW61555.1
Gene:ID:4555	C14orf143	14	82,962,821	81,403,884	-843,063	-	2	1_A375_sNG7_dtct_lncRNA:1:-1911, 2_A375_sNG7_dtct_lncRNA:1:-1702	-2264, -2195	upstream, upstream	1	1	21	33	1	2_A375_sNG7_dtct_lncRNA:1	33	Gene C14orf143	C14orf143, C14orf61	chromosome 14 open reading frame 143	NM_152486	1557733_at, 1557756_a_at, 229435_at, 233699_at, 240013_at	NP_689699.2
Gene:ID:6317	GTF2A1	14	81,646,284	81,667,975	41,161	+	1	2_A375_sNG7_dtct_lncRNA:1:-1702	7	st gene	0	1	9	17	1	2_A375_sNG7_dtct_lncRNA:1	17	Gene GTF2A1	TF2A1, TF1A, GTF2A1, MGC129970, MGC129969	general transcription factor IIA, 1, 19/37kDa	NM_.201569, NM_015559, ENST00000...., ENST00000....	209521_s_at, 221433_at	NP_.983597.1, NP_056940.1, EAW61334.1, EAW61555.1
Gene:ID:5930666	LOC100506666	14	81,667,562	81,668,804	1,242	+	1	2_A375_sNG7_dtct_lncRNA:1:-1702	8	st gene	0	1	9	17	1	2_A375_sNG7_dtct_lncRNA:1	17	Gene LOC100506666	hypothetical LOC100506666	XR_111453, XR_110228, XR_114765	1557155_at	NP_.111453.1, XR_110228, XR_114765
Gene:ID:5930672	LOC100506731	14	81,990,776	83,099,469	5,692	+	1	2_A375_sNG7_dtct_lncRNA:1:-1702	-1515	upstream	0	1	12	14	1	2_A375_sNG7_dtct_lncRNA:1	14	Gene LOC100506731	hypothetical LOC100506731	XR_111451, XR_110231, XR_114771	1557153_at	NP_001035553.1, EAW61555.1
Gene:ID:3746	FLRT2	14	85,999,688	86,099,270	97,782	+	1	2_A375_sNG7_dtct_lncRNA:1:-1702	-1696	upstream	0	1	12	14	1	2_A375_sNG7_dtct_lncRNA:1	14	Gene FLRT2	KIAA0493, FLRT2	fibronectin leucine rich transmembrane protein 2	NM_013231	204355_s_at, 204356_at	NP_037363.1
Gene:ID:1092	PTPN21	14	88,932,122	89,021,123	89,001	+	2	1_A375_sNG7_dtct_lncRNA:1:-1910, 2_A375_sNG7_dtct_lncRNA:1:-2709	3299, 3299	st gene, ut gene	0	1	24	32	1	2_A375_sNG7_dtct_lncRNA:1	33	Gene PTPN21	PTPN21, PTPD1, PTPRL10	protein tyrosine phosphatase, non-receptor type 21	NM_007039, ENST11101.3, ENST00230156.0	1235_at, 203436_at, 221092_at, 40124_at	NP_.009070.2, EAW61353.1, EAW61352.1
Gene:ID:6141	C14orf143	14	90,263,469	90,421,689	157,820	+	4	1_A375_sNG7_dtct_lncRNA:1:-1916, 1_A375_sNG7_dtct_lncRNA:1:-1917, 1_A375_sNG7_dtct_lncRNA:1:-2711, 2_A375_sNG7_dtct_lncRNA:1:-2712	-127, -1039, -127, -1053	upstream, upstream, upstream, upstream	1	1	20	17.5	2	1_A375_sNG7_dtct_lncRNA:1	23	Gene C14orf143	DKFZp547I415, FLJ31529, C14orf143, EPCAB11	EF-hand calcium binding domain 11	NM_148231, ENST00145501.4, ENST00234124.2	1555525_s_at, 214264_s_at	NP_.992274.1, EAW61411.1, EAW61412.1
Gene:ID:5715	TDP1	14	90,422,246	90,511,168	88,862	+	4	1_A375_sNG7_dtct_lncRNA:1:-1916, 1_A375_sNG7_dtct_lncRNA:1:-1917, 1_A375_sNG7_dtct_lncRNA:1:-2711, 2_A375_sNG7_dtct_lncRNA:1:-2712	-1030, -118, -1030, -152	upstream, upstream, upstream, upstream	1	1	20	17.5	2	1_A375_sNG7_dtct_lncRNA:1	23	Gene TDP1	MGC104252, TDP1, PLJ11093	tyrosyl-DNA phosphodiesterase 1	NM_018319, NM_001008744, NCT12866.2, NCT19823.61, NCT22246660.0	218713_s_at, 226044_at, 240622_at	NP_.060789.2, NP_001008744.1, EAW61434.1, EAW61435.1, EAW61436.1
Gene:ID:6317	C14orf159	14	91,580,287	91,691,703	111,246	+	1	2_A375_sNG7_dtct_lncRNA:1:-2714	38	st gene	0	1	10	20	1	2_A375_sNG7_dtct_lncRNA:1	20	Gene C14orf159	C14orf159, PLJ20942, C14orf159, DKFZp686G2126, PLJ20979, PLJ20980	chromosome 14 open reading frame 159	NM_.024932, NM_001102366, NM_001102367, NM_001102366, NM_001102368, ENST00234313.1, ENST00230603.0, ENST00230605.0, ENST00230606.0	1554039_at, 219295_s_at	NP_.078833.4, NP_001089536.1, NP_001095837.1, NP_001095836.1, NP_001095839.1, EAW61440.1, EAW61441.1, EAW61442.1, EAW61444.1
Gene:ID:5671	SMEK2	14	91,823,855	91,879,624	52,469	+	2	1_A375_sNG7_dtct_lncRNA:1:-1919, 2_A375_sNG7_dtct_lncRNA:1:-2715	-172, -252	upstream, upstream	1	1	10	16	1	2_A375_sNG7_dtct_lncRNA:1	16	Gene SMEK2	smk1, FNIP3A, FLFL1, smk1, SMEK1, KIAA2010, MSTP033	SMEK homolog 1, suppressor of clb1+1 (Dictyostelium)	NM_.032860, ENST00230...., ENST00230...., ENST00230...., ENST00230...., ENST00230....	220365_s_at, 220369_at, 221092_s_at	NP_.116049.2, EAW61454.1, EAW61452.1, EAW61453.1, EAW61456.1, EAW61457.1, EAW61463.1
Gene:ID:321	TRIP11	14	92,434,243	92,506,403	72,160	+	1	2_A375_sNG7_dtct_lncRNA:1:-1920	-61	upstream	1	1	10	13	1	1_A375_sNG7_dtct_lncRNA:1	16	Gene TRIP11	CEV14, TRIP230, TRIP11, GMAP-210, AGG14	thyroid hormone receptor interactor 11	NM_.004239, ENST00230...., ENST00230....	209770_at, 242760_s_at	NP_.004230.2, EAW61466.1, EAW61468.1
Gene:ID:287	ATXN3	14	92,534,696	92,572,865	40,069	+	2	1_A375_sNG7_dtct_lncRNA:1:-1921, 2_A375_sNG7_dtct_lncRNA:1:-2719	-187, -155	upstream, upstream	1	1	26	32	1	2_A375_sNG7_dtct_lncRNA:1	32	Gene ATXN3	JOS, MJD, MJD, ATAX3, ATX3, ATX3_, SCA3	ataxin 3	NM_.004993, NM_.030660, NM_001127696, NM_.025656, NM_.025657, NM_.025436, NM_.025439, NM_.025460, NM_.025462, NM_.025661, NM_.025464, NM_.025463, NM_.025466, NM_.025467, NM_.025665, NM_.025469, NM_.025470, NM_001127697, NM_001164774, NM_001164776, NM_001164778	205815_s_at, 205816_s_at, 216697_at, 217221_s_at, 231162_x_at, 231163_s_at, 231164_s_at, 231165_s_at, 231166_s_at, 231167_s_at, 231168_s_at, 231169_s_at, 231170_s_at, 231171_s_at, 231172_s_at, 231173_s_at, 231174_s_at, 231175_s_at, 231176_s_at, 231177_s_at, 231178_s_at, 231179_s_at, 231180_s_at, 231181_s_at, 231182_s_at, 231183_s_at, 231184_s_at, 231185_s_at, 231186_s_at, 231187_s_at, 231188_s_at, 231189_s_at, 231190_s_at, 231191_s_at, 231192_s_at, 231193_s_at, 231194_s_at, 231195_s_at, 231196_s_at, 231197_s_at, 231198_s_at, 231199_s_at, 231200_at, 231723_at	NP_.004984.2, NP_.109776.1, NP_001121166.1, NP_001121169.2, NP_001155246.1, NP_001155245.1, NP_001155249.1, NP_001155251.1, NP_001155252.1, NP_001155253.1, NP_001155254.1, EAW61471.1, EAW61472.1, EAW61473.1, EAW61474.1, EAW61475.1
Gene:ID:4707	NDUFB1	14	92,562,867	92,568,153	5,686	+	4	1_A375_sNG7_dtct_lncRNA:1:-1921, 1_A375_sNG7_dtct_lncRNA:1:-1922, 2_A375_sNG7_dtct_lncRNA:1:-2719, 2_A375_sNG7_dtct_lncRNA:1:-2720	15001, 25, 15033, -169	downstream, st gene, downstream, downstream	1	1	31.5	26	2	1_A375_sNG7_dtct_lncRNA:1	34	Gene NDUFB1	MNLL, NDUFB1, CI-SGDH, CHMNLL	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	NM_.004545, ENST00234...., ENST00230...., ENST00230....	208790_s_at, 208830_at	NP_.004536.2, EAW61476.1, EAW61478.1, EAW61477.1, EAW61479.1
Gene:ID:3951	CPSF2	14	92,555,529	92,630,543	42,214	+	2	1_A375_sNG7_dtct_lncRNA:1:-1922, 2_A375_sNG7_dtct_lncRNA:1:-2719	-201, 23	upstream, ut gene	1	1	24	24	1	1_A375_sNG7_dtct_lncRNA:1	24	Gene CPSF2	CPSF2, KIAA1367, CPSF100	cleavage and polyadenylation specific factor 2, 100kDa	NM_.017437, ENST00234...., ENST00230...., ENST00230....	235695_s_at, 235694_at, 235705_s_at	NP_.059133.1, EAW61463.1, EAW61460.1, EAW61461.1, EAW61462.1
Gene:ID:9890	RIN3	14	92,985,125	93,153,336	179,211	+	1	2_A375_sNG7_dtct_lncRNA:1:-2716	467	st gene	0	1	10	13	1	2_A375_sNG7_dtct_lncRNA:1	13	Gene RIN3	DKFZp762H913, FLJ11700, RIN3, FLJ22439	Ras and Rab interactor 3	NM_.024832, ENST00230...., ENST00230...., ENST00230...., ENST00230...., ENST00230...., ENST00230...., ENST00230....	1562008_at, 218486_s_at, 218487_s_at, 220439_at, 40471_at	NP_.079183.2, EAW61480.1, EAW61481.1, EAW61459.1, EAW61466.1, EAW61468.1, EAW61462.1, EAW61463.1, EAW61464.1, EAW61466.1, EAW61467.1
Gene:ID:112	CHGA	14	93,389,633	93,401,838	12,183	+	4	1_A375_sNG7_dtct_lncRNA:1:-1923, 1_A375_sNG7_dtct_lncRNA:1:-2716, 1_A375_sNG7_dtct_lncRNA:1:-2720	-6637, -83, -6709, -675	upstream, ut gene, upstream, ut gene	1	1	23	28.5	2	2_A375_sNG7_dtct_lncRNA:1	29	Gene CHGA	CHGA, CGA	chromogranin A (parathyroid secretory protein 1)	NM_.001275, ENST00230...., ENST00230....	208697_s_at	NP_.001266.1, EAW61508.1, EAW61509.1
Gene:ID:1678	AEBP2	14	94,400,313	94,423,767	23,254	+	2	1_A375_sNG7_dtct_lncRNA:1:-1926, 2_A375_sNG7_dtct_lncRNA:1:-2721	-2121, -2249	upstream, upstream	1	1	10	15	1	1_A375_sNG7_dtct_lncRNA:1	15	Gene AEBP2	AEBP2, ASB2, MGC40044	AE binding protein 2	NM_.015100, ENST00234...., ENST00230....	227913_at, 233697_s_at	NP_.055934.2, EAW61543.1, EAW61540.1, EAW61541.1, EAW61542.1
Gene:ID:5930691	LOC100506691	14	94,423,122	94,443,137	20,015	+	2	1_A375_sNG7_dtct_lncRNA:1:-1926, 2_A375_sNG7_dtct_lncRNA:1:-2721	-2766, -2884	st gene, ut gene	1	1	15	15	1	1_A375_sNG7_dtct_lncRNA:1	15	Gene LOC100506691	hypothetical LOC100506691	XR_110238, XR_110238		
Gene:ID:5990	OTUB2	14	94,692,724	94,813,276	22,382	+	2	1_A375_sNG7_dtct_lncRNA:1:-1927, 2_A375_sNG7_dtct_lncRNA:1:-2723	-122, -68	upstream, ut gene	1	1	24	21	1	2_A375_sNG7_dtct_lncRNA:1	31	Gene OTUB2	OTB2, OTUB2, OTU2, MGC13102, C14orf137, PLJ21916	OTU domain, ubiquitin aldehyde binding 2	NM_.023112, ENST00234...., ENST00230....	1555552_at, 219269_s_at, 220976_s_at	NP_.075601.1, EAW61549.1, EAW61548.1
Gene:ID:9768	CLMN	14	93,846,276	93,766,245	137,969	-	1	1_A375_sNG7_dtct_lncRNA:1:-1928	59949	st gene	1	0	14	17	1	1_A375_sNG7_dtct_lncRNA:1	14	Gene CLMN	KIAA1105, FLJ43995, CLMN, KIAA0593,	calmin (calponin-like, transmembrane)	NM_.024734, ENST00235...., ENST00230....	1557552_s_at, 229797_s_at, 229798_at	NP_.079010.2, EAW61585.1, EAW61587.1
Gene:ID:6914	PAFOLA	14	99,965,720	97,031,446	-64,726	-	1	2_A375_sNG7_dtct_lncRNA:1:-2727	-432	upstream	0	1	9	15	1	2_A375_sNG7_dtct_lncRNA:1	15	Gene PAFOLA	MGC53376, PAF, PAFOLA	poly(A) polymerase alpha	NM_.032632, ENST00232...., ENST00236614.1, ENST00230616.1, ENST00230619.1, ENST00230620.1, ENST00230169.0	1555556_at, 212715_at, 212720_at, 215374_at, 223035_s_at, 224599_at	NP_.116027.2, EAW61642.1, EAW61643.1, EAW61644.1, EAW61645.1, EAW61646.1, EAW61647.1, EAW61648.1
Gene:ID:17762	CCDC85C	14	99,977,603	100,070,727	93,124	+	1	1_A375_sNG7_dtct_lncRNA:1:-1931	-213	upstream	1	0	17	10	1	1_A375_sNG7_dtct_lncRNA:1	17	Gene CCDC85C	MGC117453, CCDC85C, PLJ22556	coiled-coil domain containing 85C	NM_.020.1.69993	219015_s_at	NP_.001138567.1
Gene:ID:5930716	LOC100506716	14	100,070,693	100,092,077	21,184	+	1	2_A375_sNG7_dtct_lncRNA:1:-1931	-147	st gene	1	0	17	10	1	1_A375_sNG7_dtct_lncRNA:1	17	Gene LOC100506716	hypothetical LOC100506716	XR_111471, XR_110247, XR_114786		
Gene:ID:9448	WDR25	14	100,642,755	100,996,600	153,845	+	2	1_A375_sNG7_dtct_lncRNA:1:-1932, 2_A375_sNG7_dtct_lncRNA:1:-2730	100237, 110293	st gene, ut gene	1	1	16.5	12.5	2	2_A375_sNG7_dtct_lncRNA:1	19	Gene WDR25	WDR25, MGC20645	WD repeat domain 25	NM_.001161476, NM_.025615, ENST00231...., ENST00230....	219609_at	NP_.001154686.1, NP_.078791.3, EAW61708.1, EAW61709.1, EAW61705.1
Gene:ID:5930712	LOC100506712	14	100,947,293	100,947,604	311	+	2	1_A375_sNG7_dtct_lncRNA:1:-1933, 2_A375_sNG7_dtct_lncRNA:1:-2731	-4301, 3715	upstream, downstream	1	1	16.5	12.5	2	2_A375_sNG7_dtct_lncRNA:1	19	Gene LOC100506712	HMGN1P25	high mobility group nucleosome binding domain 1 pseudogene 25	XM_.003119854, XM_.003118915, XM_.003120780		XP_.003119902.1, XP_.003118953.1, XP_.003120835.1
Gene:ID:5930736	MIR541	14	101,330,632	101,330,815	83	+	1	1_A375_sNG7_dtct_lncRNA:1:-1934	6812	downstream	1	0	25	8	1	1_A375_sNG7_dtct_lncRNA:1	25	Gene MIR541	MIRN541, MIR541, hsa-mir-541	microRNA 541	NR_.030594		
Gene:ID:74613	MIR409	14	101,331,627	101,331,715	76	+	1	1_A375_sNG7_dtct_lncRNA:1:-1934	5107	downstream	1	0	25	8	1	1_A375_sNG7_dtct_lncRNA:1	25	Gene MIR409	MIRN409, MIR409, hsa-mir-409	microRNA 409	NR_.029978		
Gene:ID:74622	MIR412	14	101,331,764	101,331,874	90	+	1	1_A375_sNG7_dtct_lncRNA:1:-1934	7960	downstream	1	0	25	8	1	1_A375_sNG7_dtct_lncRNA:1	25	Gene MIR412	MIRN412, hsa-mir-412, MIR412	microRNA 412	NR_.030153		
Gene:ID:432516	MIR368	14	101,331,935	101,332,004	69	+	1	1_A375_sNG7_dtct_lncRNA:1:-1934	7809	downstream	1	0	25	8	1	1_A375_sNG7_dtct_lncRNA:1	25	Gene MIR368	MIRN368, hsa-mir-368, MIR368, MIRN368-3, MIR368-3	microRNA 368	NR_.029982		
Gene:ID:74656	MIR410	14	101,332,249	101,332,326	78	+	1	1_A375_sNG7_dtct_lncRNA:1:-1934	7495	downstream	1	0	25	8	1	1_A375_sNG7_dtct_lncRNA:1	25	Gene MIR410	MIRN410, MIR410, hsa-mir-410, MIR410, MIRN410	microRNA 410	NR_.030156		
Gene:ID:406226	MIR656	14	101,333,061	101,333,138	77	+	1	1_A375_sNG7_dtct_lncRNA:1:-1934	6663	downstream	1	0	25	8	1	1_A375_sNG7_dtct_lncRNA:1	25	Gene MIR656	MIRN656, MIRN656, hsa-mir-656	microRNA 656	NR_.030342		
Gene:ID:5930725	LOC100506725	14	101,336,248	101,339,274	3,026	+	1	1_A375_sNG7_dtct_lncRNA:1:-1934	3266	downstream	1	0	25	8	1	1_A375_sNG7_dtct_lncRNA:1	25	Gene LOC100506725	hypothetical LOC100507257	XR_111467, XR_110251, XR_114790	1557157_at, 1557160_at	NP_.001035553.1, EAW61555.1
Gene:ID:693	TECPR2	14	102,026,300	102,966,616	129,516	+	1	2_A375_sNG7_dtct_lncRNA:1:-2728	-52	upstream	1	1	16	16	1	2_A375_sNG7_dtct_lncRNA:1	16	Gene TECPR2	KIAA0297, TECPR2, KIAA0226	tectonin beta-propeller repeat containing 2	NM_.014844, NM_001172631, ENST00230...., ENST00230....	204307_at, 204308_s_at	NP_.055859.2, NP_001160102.1, EAW61737.1, EAW61738.1, EAW61739.1
Gene:ID:152	CKB	14	103,955,996	103,959,170	3,174	+	1	1_A375_sNG7_dtct_lncRNA:1:-1937	-7606	upstream	1	0	16	12	1	1_A375_sNG7_dtct_lncRNA:1	16	Gene CKB	CKB, B-CK, CKBB	Creatine kinase, brain	NM_.001823, ENST00229...., ENST00230....	203554_at	NP_.001814.2, EAW61622.1, EAW61620.1, EAW61621.1
Gene:ID:15706	TRMT61A	14	103,995,509	104,003,410	7,901	+	1	1_A375_sNG7_dtct_lncRNA:1:-1937	1467	st gene	1	0	16	12	1	1_A375_sNG7_dtct_lncRNA:1	16	Gene TRMT61A	TRMT61A, GCD14, RTRMB1, TRMB1, TRMT61A	RNA methyltransferase 61 homolog A (S. cerevisiae)	NM_.152307, ENST00235...., ENST00230....	1554317_s_at, 221607_at, 40124_at	NP_.689514.2, EAW61625.1, EAW61622.1, EAW61624.1
Gene:ID:329	BAG3	14	104,022,559	104,029,181	6,262	+	1	2_A375_sNG7_dtct_lncRNA:1:-2736	423	st gene	1	0	10	20	1	2_A375_sNG7_dtct_lncRNA:1	20	Gene BAG3	BAG3, BAG-3	BCL2-associated athanogene 3	NM_.004.973, NM_.001013616, NM_.001013649, NCT16824.3, NCT16825.1, NCT19829.1, NCT19829.2	202464_s_at, 202465_s_at, 202467_s_at	NP_.004094.1, NP_.001010585.1, NP_.001010616.1, EAW61626.1, EAW61627.1, EAW61628.1
Gene:ID:4224	C14orf133	14	104,029,299	104,037,236	27,937	+	1	2_A375_sNG7_dtct_lncRNA:1:-2736	271	upstream	1	1	10	20	1	2_A375_sNG7_dtct_lncRNA:1	20	Gene C14orf133	C14orf133, APOF1, MGC23562	chromosome 14 open reading frame 133	NM_.032374, NCT16823.3, NCT19822.61, NCT19829.2	1555844_at, 222614_s_at	NP_.115783.2, EAW61631.1, EAW61629.1, EAW61630.1
Gene:ID:555	C14orf2	14	104,370,625	104,387,803	16,274	+	2	1_A375_sNG7_dtct_lncRNA:1:-1938, 2_A375_sNG7_dtct_lncRNA:1:-2737	-17, -1	upstream, upstream	1	1	30	21	1	1_A375_sNG7_dtct_lncRNA:1	30	Gene C14orf2	MP65, PLPM, C14orf2	chromosome 14 open reading frame 2	NM_.001127342, NM_.004854, NCT16826.2, NCT19812.76.1, NCT19812.60.0, NCT23304570	202278_at, 210532_s_at	NP_.001120814.1, NP_.004845.1, EAW61636.1, EAW61635.1, EAW61637.1
Gene:ID:22402	TDRD9	14	104,394,517	104,519,004	124,187	+	2	1_A375_sNG7_dtct_lncRNA:1:-1938, 2_A375_sNG7_dtct_lncRNA:1:-2738	4697, 4813	upstream, downstream	1	1	30	21	1	1_A375_sNG7_dtct_lncRNA:1	30	Gene TDRD9	TDRD9, MGC133925, FLJ20194, C14orf9, HIG-1, NET54, DKFZp434K0620	Tudor domain containing 9	NM_.153046	226265_at	NP_.694921.2
Gene:ID:9638	MGC22277	14	103,287,535	105,290,055	2,517	+	1	2_A375_sNG7_dtct_lncRNA:1:-1939	4202	upstream	0	1	10	20	1	2_A375_sNG7_dtct_lncRNA:1	20	Gene MGC22277	MGC22277	hypothetical LOC116672	NM_.024299	1553780_at	
Gene:ID:9030	CDCA4	14	105,479,910	105,487,825	11,915	-	1	1_A375_sNG7_dtct_lncRNA:1:-1939	-2603	upstream	1	0	16	10	1	1_A375_sNG7_dtct_lncRNA:1	16	Gene CDCA4	FLJ20764, MGC116517, SEI-3/HEPP, FLJ32816, HEPP, CCDC4	cell division cycle associated 4	NM_.145701, NM_.017955, NCT12.83137.0, NCT23305239.0, NCT23305240.0, NCT23305241.0	218399_s_at	NP_.663749.1, NP_.060425.2, EAW61690.1, EAW61689.1, EAW61687.1
Gene:ID:396	CRIP1	14	105,953,287	105,955,126	1,839	+	2	1_A375_sNG7_dtct_lncRNA:1:-1940, 2_A375_sNG7_dtct_lncRNA:1:-2740	4592, 4383	downstream, downstream	1	1	14	15	1	2_A375_sNG7_dtct_lncRNA:1	15	Gene CRIP1	CRIP1, PLJ40971, CRHP, CRP1, CRIP	cysteine-rich protein 1 (intestinal)	NM_.001311	203001_at	NP_.001302.1
Gene:ID:53643	C14orf80	14	105,956,520	105,963,555	6,965	+	2	1_A375_sNG7_dtct_lncRNA:1:-1940, 2_A375_sNG7_dtct_lncRNA:1:-2740, 2_A375_sNG7_dtct_lncRNA:1:-2741	788, 1680, 6256	st gene, ut gene, downstream	1	1	12.5	15	2	2_A375_sNG7_dtct_lncRNA:1	15	Gene C14orf80	C14orf80, MGC16771	chromosome 14 open reading frame 80	NM_.001134578, NM_.001134577, NM_.001134577	1555558_at	NP_.001128347.1, NP_.001128345.1, NP_.001128349.1
Gene:ID:492	IGHJ6	14	106,032,614	107,288,051	1,255,437	+	4	1_A375_sNG7_dtct_lncRNA:1:-1941, 1_A375_sNG7_dtct_lncRNA:1:-1942, 2_A375_sNG7_dtct_lncRNA:1:-2742, 2_A375_sNG7_dtct_lncRNA:1:-2743	1020357, 349442, 1020323, 271907	st gene, ut gene, ut gene, st gene	1	1	20.33	22	3	1_A375_sNG7_dtct_lncRNA:1	39	Gene IGHJ6	IGH1@, MGC68754, IGH, IGH@, MGC72071, DKFZp686C15213, IGHDY1	immunoglobulin heavy locus		205816_at	
Gene:ID:5426	IGHV3-43	14	106,326,167	106,326,644	477	+	1	2_A375_sNG7_dtct_lncRNA:1:-2743	10500	downstream	0	1	9	17	1	2_A375_sNG7_dtct_lncRNA:1	17	Gene IGHV3-43	VH, IGHV3-53, IGHV3-43	immunoglobulin heavy variable 3-43			



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:729082	LOC729082	15	41,576,201	41,591,795	15,594	+	1	2_A375_pNL97_plus_lncRNA::1::2802	-9	upstream	0	1	18	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC729082		hypothetical LOC729082	NR_026757		
GeneID:11339	OIP5	15	41,601,466	41,624,819	23,353	-	2	1_A375_pNL7_minus_lncRNA::1::1981, 2_A375_pNL97_plus_lncRNA::1::2803	243, 259	in gene, in gene	1	1	22	21	1	1_A375_pNL7_minus_lncRNA::1	22	Gene OIP5	MIS18B, CT86, hMIS18beta, LINT-25, OIP5, MIS18beta, 5730547N13Rik	Opa interacting protein 5	NM_007280, hCT1642461.1, hCT2281706.0	213599_at	NP_009211.1, EAW92481.1, EAW92480.1
GeneID:51203	NUSAP1	15	41,624,926	41,673,248	48,322	+	2	1_A375_pNL7_minus_lncRNA::1::1981, 2_A375_pNL97_plus_lncRNA::1::2803	-350, -366	upstream, upstream	1	1	22	21	1	1_A375_pNL7_minus_lncRNA::1	22	Gene NUSAP1	PRO0310p1, LNP, Q0310, FLJ13421, ANKT, SAPL, BM037, NUSAP1, NUSAP	nucleolar and spindle associated protein 1	NM_018454, NM_016359, NM_001129897, hCT2281019.0, hCT2281021.0, hCT2357530.0, hCT2357531.0, hCT30536.3	218039_at, 219978_s_at	NP_060924.4, NP_057443.2, NP_001123369.1, EAW92482.1, EAW92484.1, EAW92485.1, EAW92483.1, EAW92486.1
GeneID:51103	NDUFAF1	15	41,679,551	41,694,642	15,091	-	2	1_A375_pNL7_minus_lncRNA::1::1982, 2_A375_pNL97_plus_lncRNA::1::2804	-30, 50	upstream, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene NDUFAF1	CGI65, CIA30, NDUFAF1, CGI-65	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	NM_016013, hCT1825835.2, hCT2281704.0, hCT2281705.0	204125_at	NP_057097.2, EAW92487.1, EAW92488.1, EAW92489.1
GeneID:7301	TYRO3	15	41,851,220	41,871,536	20,316	+	1	2_A375_pNL97_plus_lncRNA::1::2805	26346	downstream	0	1	6	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TYRO3	FLJ16467, Dtk, BYK, TYRO3, RSE, Sky, Tif, Brt	TYRO3 protein tyrosine kinase	NM_006293, hCT2281030.0, hCT2281032.0, hCT28664.3	211431_s_at, 211432_s_at	NP_006284.2, EAW92507.1, EAW92506.1, EAW92508.1
GeneID:51332	SPTBN5	15	42,140,344	42,186,275	45,931	-	1	1_A375_pNL7_minus_lncRNA::1::1983	-797	upstream	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene SPTBN5	HUSPECV, BSPECV, SPTBN5, HUBSPECV	spectrin, beta, non-erythrocytic 5	NM_016642, hCT29402.3	220067_at, 237097_at	NP_057726.3, EAW92523.1
GeneID:100289090	LOC100289090	15	42,186,325	42,187,530	1,205	+	1	1_A375_pNL7_minus_lncRNA::1::1983	747	in gene	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene LOC100289090		hypothetical protein LOC100289090	XM_002343339		XP_002343380.2
GeneID:30844	EHD4	15	42,191,636	42,264,755	73,117	-	1	1_A375_pNL7_minus_lncRNA::1::1983	77663	downstream	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene EHD4	PAST4, EHD4	EH-domain containing 4	NM_139265, hCT2281688.0, hCT31682.3	1556607_at, 1556608_a_at, 209536_s_at, 233660_at	NP_644670.1, EAW92525.1, EAW92526.1
GeneID:283748	PLA2G4D	15	42,359,881	42,386,752	26,871	-	2	1_A375_pNL7_minus_lncRNA::1::1984, 2_A375_pNL97_plus_lncRNA::1::2806	36926, 36896	downstream, downstream	1	1	32	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene PLA2G4D	PLA2G4D, cPLA2delta	phospholipase A2, group IVD (cytosolic)	NM_178034, hCT2340772.1, hCT2348477.1	1554914_at	NP_828848.3, EAW92529.1, EAW92530.1
GeneID:25963	TMEM87A	15	42,502,726	42,565,755	63,029	-	2	1_A375_pNL7_minus_lncRNA::1::1985, 2_A375_pNL97_plus_lncRNA::1::2807	-85, 155	upstream, in gene	1	1	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TMEM87A	DKFZp564G2022, TMEM87A	transmembrane protein 87A	NM_015497, NM_001110503, hCT2282221.0, hCT2282222.0, hCT31659.2	212202_s_at, 212204_at, 223771_at, 223772_s_at	NP_056312.2, NP_001103973.1, EAW92540.1, EAW92541.1, EAW92542.1
GeneID:2595	GANC	15	42,566,366	42,645,864	79,498	+	2	1_A375_pNL7_minus_lncRNA::1::1985, 2_A375_pNL97_plus_lncRNA::1::2807	-526, -766	upstream, upstream	1	1	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene GANC	GANC, MGC138256, FLJ40082	glucosidase, alpha; neutral C	NM_198141	235340_at, 236077_at	NP_937784.2
GeneID:8773	SNAP23	15	42,787,835	42,825,256	37,421	+	1	2_A375_pNL97_plus_lncRNA::1::2808	-4459	upstream	0	1	11	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene SNAP23	SNAP23B, SNAP23, HsT17016, SNAP23A	synaptosomal-associated protein, 23kDa	NM_003825, NM_130798, hCT1957923.1, hCT1957924.1, hCT2280601.0, hCT29862.1	209130_at, 209131_s_at, 214544_s_at	NP_003816.2, NP_570710.1, EAW92556.1, EAW92557.1, EAW92558.1, EAW92559.1
GeneID:255252	LRRC57	15	42,834,720	42,841,002	6,282	-	1	1_A375_pNL7_minus_lncRNA::1::1986	74	in gene	1	0	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LRRC57	DKFZp686H1865, LRRC57, FLJ36812	leucine rich repeat containing 57	NM_153260, hCT1641577.4, hCT2349338.0, hCT2349339.0, hCT2349340.0, hCT2349341.0, hCT2349342.0	229232_at	NP_694992.2, EAW92562.1, EAW92560.1, EAW92563.1, EAW92564.1, EAW92565.1, EAW92561.1
GeneID:55142	HAUS2	15	42,841,011	42,862,192	21,181	+	1	1_A375_pNL7_minus_lncRNA::1::1986	-83	upstream	1	0	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene HAUS2	HAUS2, C15orf25, FLJ10460, CEP27, HsT17025	HAUS augmin-like complex, subunit 2	NM_018097, NM_001130447, hCT1971615.1, hCT1971616.1, hCT1971617.1, hCT1971618.1, hCT2280603.0, hCT2357522.0, hCT31692.2	220071_x_at, 229181_s_at, 229208_at	NP_060567.1, NP_001123919.1, EAW92566.1, EAW92567.1, EAW92569.1, EAW92572.1, EAW92568.1, EAW92570.1, EAW92571.1
GeneID:146057	TTBK2	15	43,036,536	43,213,007	176,471	-	1	2_A375_pNL97_plus_lncRNA::1::2809	-657	upstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TTBK2	KIAA0847, TTBK2, SCA11, TTBK	tau tubulin kinase 2	NM_173500, hCT1957925.2, hCT2282207.1, hCT2357520.0	1554293_at, 1554294_s_at, 1554295_x_at, 1557073_s_at, 213922_at, 231610_at, 240011_at	NP_775771.3, EAW92581.1, EAW92582.1, EAW92583.1
GeneID:80021	TMEM62	15	43,425,722	43,477,342	51,620	+	2	1_A375_pNL7_minus_lncRNA::1::1987, 2_A375_pNL97_plus_lncRNA::1::2810	422, -5	in gene, upstream	1	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TMEM62	TMEM62, FLJ23375	transmembrane protein 62	NM_024956, hCT2280191.0, hCT30967.2	218776_s_at, 222739_at	NP_079232.3, EAW92586.1, EAW92587.1
GeneID:9333	TGM5	15	43,524,793	43,559,055	34,262	-	1	1_A375_pNL7_minus_lncRNA::1::1988	16991	in gene	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TGM5	TGX, TGASEX, MGC141907, TGM5, TGASE5, TGMX, TGM6	transglutaminase 5	NM_201631, NM_004245, hCT1957921.1, hCT2281076.0, hCT2281077.0, hCT30960.3	207911_s_at	NP_963925.2, NP_004236.1, EAW92593.1, EAW92594.1, EAW92595.1, EAW92596.1
GeneID:9836	LCMT2	15	43,619,974	43,622,891	2,917	-	1	2_A375_pNL97_plus_lncRNA::1::2811	267	in gene	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LCMT2	MGC9534, FLJ51321, TYW4, KIAA0547, LCMT2, PPM2	leucine carboxyl methyltransferase 2	NM_014793	204012_s_at, 204013_s_at	NP_055608.2
GeneID:161823	ADAL	15	43,622,872	43,646,096	23,224	+	1	2_A375_pNL97_plus_lncRNA::1::2811	-248	upstream	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ADAL	FLJ44620, DKFZp313B2137, ADAL	adenosine deaminase-like	NM_001012969, NM_001159280, hCT2280197.0, hCT2280198.1	238424_at, 239711_at	NP_001012987.1, NP_001152752.1, EAW92598.1, EAW92599.1
GeneID:146050	ZSCAN29	15	43,650,370	43,662,258	11,888	-	2	1_A375_pNL7_minus_lncRNA::1::1989, 2_A375_pNL97_plus_lncRNA::1::2812	-1134, -590	upstream, upstream	1	1	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ZSCAN29	ZNF690, ZSCAN29, MGC129895, MGC129894, Zfp690, FLJ35867	zinc finger and SCAN domain containing 29	NM_152455, hCT2357524.0, hCT2357525.0, hCT30963.2	226562_at	NP_689668.3, EAW92600.1, EAW92601.1, EAW92602.1
GeneID:27229	TUBGCP4	15	43,663,313	43,698,258	34,945	+	2	1_A375_pNL7_minus_lncRNA::1::1989, 2_A375_pNL97_plus_lncRNA::1::2812	79, -465	in gene, upstream	1	1	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TUBGCP4	76P, GCP4, TUBGCP4, FLJ14797	tubulin, gamma complex associated protein 4	NM_014444, hCT30961.2	211337_s_at, 213266_at	NP_055259.2, EAW92603.1
GeneID:7158	TP53BP1	15	43,699,412	43,802,707	103,295	-	2	1_A375_pNL7_minus_lncRNA::1::1990, 2_A375_pNL97_plus_lncRNA::1::2813	69459, -605	in gene, upstream	1	1	12.5	13.5	2	1_A375_pNL7_minus_lncRNA::1	16	Gene TP53BP1	TP53BP1, p202, MGC138366, 53BP1, FLJ41424	tumor protein p53 binding protein 1	NM_005657, NM_001141979, NM_001141980, hCT2357526.0, hCT30955.3	1569097_at, 1569098_s_at, 203050_at	NP_005648.1, NP_001135451.1, NP_001135452.1, EAW92604.1, EAW92605.1
GeneID:4130	MAP1A	15	43,809,806	43,823,818	14,012	+	1	2_A375_pNL97_plus_lncRNA::1::2813	-6494	upstream	0	1	9	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene MAP1A	MAP1A, MAP1L, FLJ77111, MTAP1A	microtubule-associated protein 1A	NM_002373, hCT1828441.3, hCT2280207.0, hCT30962.4	203151_at, 215384_s_at, 215391_at	NP_002364.5, EAW92606.1, EAW92607.1, EAW92608.1
GeneID:2923	PDIA3	15	44,038,590	44,064,804	26,214	+	1	2_A375_pNL97_plus_lncRNA::1::2814	366	in gene	0	1	6	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene PDIA3	ERp61, GRP57, ERp57, P58, PDIA3, HsT17083, ER60, PI-PLC, ERp60, GRP58	protein disulfide isomerase family A, member 3	NM_005313, hCT2355689.0, hCT2355690.0, hCT29238.3	208612_at, 227033_at, 229453_at	NP_005304.3, EAW77234.1, EAW77235.1, EAW77236.1
GeneID:4236	MFAP1	15	44,096,733	44,116,951	20,218	-	1	2_A375_pNL97_plus_lncRNA::1::2815	151	in gene	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MFAP1	MFAP1	microfibrillar-associated protein 1	NM_005926, hCT28966.3	203406_at	NP_005917.2, EAW77247.1
GeneID:79968	WDR76	15	44,119,112	44,160,617	41,505	+	1	2_A375_pNL97_plus_lncRNA::1::2815	-2312	upstream	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene WDR76	WDR76, CDW14, FLJ12973	WD repeat domain 76	NM_024908, NM_001167941, hCT29237.4	205519_at	NP_079184.2, NP_001161413.1, EAW77246.1
GeneID:84978	FRMD5	15	44,165,730	44,487,429	321,699	-	6	1_A375_pNL7_minus_lncRNA::1::1991, 1_A375_pNL7_minus_lncRNA::1::1992, 2_A375_pNL97_plus_lncRNA::1::2816, 2_A375_pNL97_plus_lncRNA::1::2817, 2_A375_pNL97_plus_lncRNA::1::2818, 2_A375_pNL97_plus_lncRNA::1::2819	92363, -112, 283693, 281765, 92133, -155	in gene, upstream, in gene, in gene, in gene, upstream	1	1	17	18.75	4	1_A375_pNL7_minus_lncRNA::1	23	Gene FRMD5	MGC14161, FRMD5, FLJ41022	FERM domain containing 5	NM_032892, hCT1644764.3, hCT2290090.0, hCT2290091.0, hCT2290092.0, hCT2355744.0, hCT2355745.0, hCT2355746.0	1569470_a_at	NP_116281.2, EAW77250.1, EAW77249.1, EAW77251.1, EAW77253.1, EAW77254.1, EAW77252.1, EAW77255.1
GeneID:51496	CTDSPL2	15	44,719,579	44,819,430	99,851	+	5	1_A375_pNL7_minus_lncRNA::1::1993, 1_A375_pNL7_minus_lncRNA::1::1994, 1_A375_pNL7_minus_lncRNA::1::1995, 2_A375_pNL97_plus_lncRNA::1::2820, 2_A375_pNL97_plus_lncRNA::1::2821	62213, 109349, 109877, 62341, 109157	in gene, downstream, downstream, in gene, downstream	1	1	18	17.67	3	2_A375_pNL97_plus_lncRNA::1	21	Gene CTDSPL2	FLJ10523, HSPC129, CTDSPL2, HSPC058	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	NM_016396, hCT1958152.1, hCT29021.3	1555106_a_at, 223270_at, 223271_s_at, 239133_at	NP_057480.2, EAW77265.1, EAW77266.1
GeneID:645212	LOC645212	15	44,826,703	44,829,121	2,418	-	4	1_A375_pNL7_minus_lncRNA::1::1994, 1_A375_pNL7_minus_lncRNA::1::1995, 2_A375_pNL97_plus_lncRNA::1::2821, 2_A375_pNL97_plus_lncRNA::1::2822	193, -335, 365, -719	in gene, upstream, in gene, upstream	1	1	18	16	2	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC645212		hypothetical LOC645212	NR_034170, NR_034171		
GeneID:8669	EIF3J	15	44,829,266	44,855,001	25,735	+	4	1_A375_pNL7_minus_lncRNA::1::1994, 1_A375_pNL7_minus_lncRNA::1::1995, 2_A375_pNL97_plus_lncRNA::1::2821, 2_A375_pNL97_plus_lncRNA::1::2822	-338, 190, -530, 574	upstream, in gene, upstream, in gene	1	1	18	16	2	1_A375_pNL7_minus_lncRNA::1	20	Gene EIF3J	eIF3-p35, EIF3J, eIF3-alpha, EIF3S1	eukaryotic translation initiation factor 3, subunit J	NM_003758, hCT1971218.1, hCT1971219.1, hCT2289527.0, hCT30575.4	208264_s_at, 208985_s_at	NP_003749.2, EAW77268.1, EAW77269.1, EAW77270.1, EAW77271.1
GeneID:80208	SPG11	15	44,854,894	44,955,876	100,982	-	1	2_A375_pNL97_plus_lncRNA::1::2823	132	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SPG11	SPG11, DKFZp762B1512, FLJ21439, KIAA1840	spastic paraplegia 11 (autosomal recessive)	NM_025137, NM_001160227, hCT2290081.0, hCT2290083.0	1559747_at, 203513_at, 232403_at, 241920_x_at	NP_079413.3, NP_001153699.1, EAW77272.1, EAW77273.1
GeneID:197135	PATL2	15	44,957,930	44,969,086	11,156	-	1	2_A375_pNL97_plus_lncRNA::1::2823	13342	downstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene PATL2	Pat1a, PATL2, hPat1a	protein associated with topoisomerase II homolog 2 (yeast)	NM_001145112	230753_at	NP_001138584.1
GeneID:567	B2M	15	45,003,685	45,010,357	6,672	+	2	1_A375_pNL7_minus_lncRNA::1::1996, 2_A375_pNL97_plus_lncRNA::1::2824	91, -5	in gene, upstream	1	1	19	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene B2M	B2M		NM_004048, hCT1825753.4, hCT1971070.2, hCT2340882.0	201891_s_at, 216231_s_at, 232311_at	NP_004039.1, EAW77277.1, EAW77276.1, EAW77278.1
GeneID:90525	SHF	15	45,459,412	45,493,373	33,961	-	4	1_A375_pNL7_minus_lncRNA::1::1999, 1_A375_pNL7_minus_lncRNA::1::2000, 2_A375_pNL97_plus_lncRNA::1::2826, 2_A375_pNL97_plus_lncRNA::1::2827	2445, 701, 2493, 733	in gene, in gene, in gene, in gene	1	1	21.5	21	2	1_A375_pNL7_minus_lncRNA::1	26	Gene SHF	SHF, MGC126650, MGC126652	Src homology 2 domain containing F	NM_138356, hCT2286684.0, hCT2355680.0, hCT2355681.0, hCT30246.2	228922_at	NP_612365.2, EAW77301.1, EAW77298.1, EAW77299.1, EAW77300.1
GeneID:79029	SPATA5L1	15	45,694,519	45,713,617	19,098	+	1	1_A375_pNL7_minus_lncRNA::1::2001	-135	upstream	1	0	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene SPATA5L1	FLJ12286, SPATA5L1, MGC5347	spermatogenesis associated 5-like 1	NM_024063, NR_027635, hCT2285471.0, hCT30974.3	215694_at, 218933_at, 222163_s_at	NP_076968.2, EAW77310.1, EAW77311.1
GeneID:26256	PLDN	15	45,879,417	45,901,909	22,492	+	2	1_A375_pNL7_minus_lncRNA::1::2002, 2_A375_pNL97_plus_lncRNA::1::2829	103, 199	in gene, in gene	1	1	26	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene PLDN	PA, PLDN, PALLID	pallidin homolog (mouse)	NM_012388	222826_at, 224883_at, 224892_at	NP_036520.1
GeneID:399697	CTXN2	15	48,483,867	48,495,951	12,084	+	2	1_A375_pNL7_minus_lncRNA::1::2003, 2_A375_pNL97_plus_lncRNA::1::2830	-667, -699	upstream, upstream	1	1	32	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene CTXN2	CTXN2, DKFZp781M2440	cortexin 2	NM_001145668		NP_001139140.1
GeneID:1854	DUT	15	48,623,621	48,635,570	11,949	+	3	1_A375_pNL7_minus_lncRNA::1::2004, 1_A375_pNL7_minus_lncRNA::1::2005, 2_A375_pNL97_plus_lncRNA::1::2831	-5, 763, 635	upstream, in gene, in gene	1	1	17	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene DUT	FLJ20622, DUT, dUTPase	deoxyuridine triphosphatase	NM_001025248, NM_001948, NM_001025249, hCT1951321.1, hCT1962503.1, hCT1962504.1, hCT2355774.0	208955_at, 208956_x_at, 209932_s_at	NP_001020419.1, NP_001939.1, NP_001020420.1, EAW77349.1, EAW77350.1, EAW77352.1, EAW77351.1
GeneID:2200	FBN1	15	48,700,503	48,937,985	237,482	-	3	1_A375_pNL7_minus_lncRNA::1::2006, 2_A375_pNL97_plus_lncRNA::1::2832, 2_A375_pNL97_plus_lncRNA::1::2833	211969, 220641, 241	in gene, in gene, in gene	1	1	10.67	15.33	3	1_A375_pNL7_minus_lncRNA::1	18	Gene FBN1	SSKS, MASS, FBN, MFS1, WMS, SGS, FBN1, OCTD	fibrillin 1	NM_000138, hCT2286994.0, hCT29990.2	202765_s_at, 202766_s_at, 235318_at	NP_000129.3, EAW77354.1, EAW77353.1
GeneID:100506059	LOC100506059	15	48,938,854	48,944,213	5,359	+	1	2_A375_pNL97_plus_lncRNA::1::2833	-1110	upstream	0	1	6	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506059		hypothetical LOC100506059	XR_109187		
GeneID:399694	SHC4	15	49,115,934	49,255,641	139,707	-	3	2_A375_pNL97_plus_lncRNA::1::2834, 2_A375_pNL97_plus_lncRNA::1::2835, 2_A375_pNL97_plus_lncRNA::1::2836	104469, 65305, 33577	in gene, in gene, in gene	0	1	10.67	19	3	2_A375_pNL97_plus_lncRNA::1	25	Gene SHC4	RaLP, SHCD, SHC4, MGC34023	SHC (Src homology 2 domain containing) family, member 4	NM_203349	230538_at, 235238_at	NP_976224.3
GeneID:23741	EID1	15	49,170,290	49,172,380	2,090	+	1	2_A375_pNL97_plus_lncRNA::1::2835	46	in gene	0	1	13	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene EID1	RBP21, MGC138884, C15orf3, IRO45620, MGC138883, PTD014, EID1, CRI1, EID-1, PNAS-22	EP300 interacting inhibitor of differentiation 1	NM_014335, hCT33058.2	208669_s_at, 208670_s_at, 211698_at	NP_055150.1, EAW77357.1
GeneID:9728	SECISBP2L	15	49,280,835	49,338,760	57,925	-	1	1_A375_pNL7_minus_lncRNA::1::2008	61	in gene	1	0	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SECISBP2L	SECISBP2L, KIAA0256	SECIS binding protein 2-like	NM_001193489, NM_014701, hCT2286874.0, hCT2286876.0, hCT33062.3	212450_at, 212451_at	NP_001180418.1, NP_055516.2, EAW77360.1, EAW77361.1, EAW77362.1
GeneID:9318	COPS2	15	49,417,471	49,447,854	30,383	-	2	1_A375_pNL7_minus_lncRNA::1::2009, 2_A375_pNL97_plus_lncRNA::1::2837	78, -18	in gene, upstream	1	1	17	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene COPS2	TRIP15, SGN2, CSN2, COPS2, ALIEN	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	NM_004236, NM_001143887, hCT2286870.0, hCT2355678.0, hCT33059.3	202467_s_at, 209838_at	NP_004227.1, NP_001137359.1, EAW77364.1, EAW77365.1, EAW77366.1
GeneID:2585	GALK2	15	49,447,976	49,622,002	174,026	+	2	1_A375_pNL7_minus_lncRNA::1::2009, 2_A375_pNL97_plus_lncRNA::1::2837	-200, -104	upstream, upstream	1	1	17	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene GALK2	GALK2, MGC1745, GK2	galactokinase 2	NM_002044, NM_001001556, hCT1955463.1	1557429_s_at, 205219_s_at, 216411_s_at	NP_002035.1, NP_001001556.1, EAW77367.1
GeneID:196951	C15orf33	15	49,620,590	49,913,118	292,528	-	2	1_A375_pNL7_minus_lncRNA::1::2010, 2_A375_pNL97_plus_lncRNA::1::2838	-66, -162	upstream, upstream	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene C15orf33	MGC57432, FLJ32800, C15orf33	chromosome 15 open reading frame 33	NM_152647, hCT1644268.4, hCT2286658.1, hCT2344040.0, hCT2344041.0, hCT2344042.0, hCT2344043.0	1553799_at	NP_689860.2, EAW77369.1, EAW77370.1, EAW77371.1, EAW77372.1, EAW77373.1, EAW77374.1
GeneID:56986	DTWD1	15	49,913,226	49,937,333	24,107	+	2	1_A375_pNL7_minus_lncRNA::1::2010, 2_A375_pNL97_plus_lncRNA::1::2838	-42, 54	upstream, in gene	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene DTWD1	DTWD1, MDS009, MGC111207	DTW domain containing 1	NM_020234, NM_001144955, hCT2286249.0, hCT2286250.0, hCT31071.3	1555210_at, 219291_at, 236649_at, 244146_at	NP_064619.2, NP_001138427.1, EAW77377.1, EAW77378.1, EAW77379.1
GeneID:2553	GABPB1	15	50,569,389	50,647,605	78,216	-	2	1_A375_pNL7_minus_lncRNA::1::2011, 2_A375_pNL97_plus_lncRNA::1::2840	298, 325	in gene, in gene	1	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GABPB1	GABPB, E4TF1B, E4TF1-53, NRF2B2, GABPB1, E4TF1, E4TF1-47, GABPB2, BABPB2, NRF2B1	GA binding protein transcription factor, beta subunit 1	NM_016655, NM_002041, NM_181427, NM_016654, NM_005254, hCT2287251.0, hCT2287252.1, hCT2287256.1, hCT2287257.0, hCT2287258.0, hCT2287259.1, hCT2287262.1, hCT2355712.0	204618_s_at, 206173_x_at, 226900_at, 227406_at	NP_057739.1, NP_002032.2, NP_005245.2, NP_057738.1, NP_852092.1, EAW77393.1, EAW77388.1, EAW77389.1, EAW77390.1, EAW77391.1, EAW77392.1, EAW77394.1, EAW77395.1
GeneID:55056	FLJ10038	15	50,641,133	50,647,076	5,943	-	2	1_A375_pNL7_minus_lncRNA::1::2011, 2_A375_pNL97_plus_lncRNA::1::2840	-231, -204	upstream, upstream	1	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FLJ10038		hypothetical protein FLJ10038	NR_026891	205510_s_at, 205511_at	
GeneID:100129387	LOC100129387	15	50,646,371	50,650,509	4,138	+	2	1_A375_pNL7_minus_lncRNA::1::2011, 2_A375_pNL97_plus_lncRNA::1::2840	936, 909	in gene, in gene	1	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100129387	MGC33732, DKFZp686O15152	hypothetical LOC100129387	NR_024490		
GeneID:9101	USP8	15	50,716,579	50,793,277	76,698	+	1	1_A375_pNL7_minus_lncRNA::1::2012	-67	upstream	1	0	23	14	1	1_A375_pNL7_minus_lncRNA::1	23	Gene USP8	UBPY, USP8, MGC129718, KIAA0055, FLJ34456, HumORF8	ubiquitin specific peptidase 8	NM_005154, NM_001128610, NM_001128611, hCT2286659.0, hCT2286660.0, hCT2355703.0, hCT29993.3	202745_at, 229501_s_at	NP_005145.3, NP_001122082.1, NP_001122083.1, EAW77399.1, EAW77400.1, EAW77402.1, EAW77401.1
GeneID:23431	AP4E1	15	51,200,946	51,298,097	97,151	+	1	1_A375_pNL7_minus_lncRNA::1::2013	46	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene AP4E1	AP4E1, DKFZp686L12167	adaptor-related protein complex 4, epsilon 1 subunit	NM_007347, hCT31108.2	220228_at, 220229_s_at, 228164_at, 241174_at	NP_031373.2, EAW77411.1
GeneID:23312	DMXL2	15	51,739,921	51,914,967	175,046	-	1	2_A375_pNL97_plus_lncRNA::1::2842	791	in gene	0	1	10	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene DMXL2	FLJ26672, KIAA0856, RC3, DMXL2	Dmx-like 2	NM_001174116, NM_001174117, NM_015263, hCT1825416.2, hCT2288126.0, hCT2288132.0, hCT2288133.0, hCT2288136.0	212820_at, 215761_at	NP_001167587.1, NP_001167588.1, NP_056078.2, EAW77420.1, EAW77421.1, EAW77424.1, EAW77422.1, EAW77423.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervening Count	Intervening	Intervening Dist to start	Intervening Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:29106	SCG3	15	51,973,590	52,013,223	39,673	+	2	1_A375_shN7_shrus_lncRNA:1:2014, 2_A375_shN7_shrs_lncRNA:1:2640	1148, 1486	up gene, within gene	1	1	47	62	1	2_A375_shN7_shrs_lncRNA:1	62	Gene:SCG3	SCG3, SG16, FLJ00033	secretogranin III	NM_031243, NM_001166357, XCT:9731206.1, XCT:29986.3	218199_at	NP_037075.2, NP_001158729.1, EAW77428.1, EAW77426.1
Gene:ID:21169	LEO1	15	52,230,222	52,263,856	33,706	+	2	1_A375_shN7_shrus_lncRNA:1:1812, 2_A375_shN7_shrs_lncRNA:1:2648	1812, 54	up gene, within gene	1	1	28	31	1	2_A375_shN7_shrs_lncRNA:1	31	Gene:LEO1	RDL1, LEO1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	NM_138782, XCT:2556999.0, XCT:31361.2	238099_at	NP_620147.1, EAW77432.1, EAW77432.1
Gene:ID:367	MAPK6	15	52,311,411	52,356,462	47,051	+	1	2_A375_shN7_shrs_lncRNA:1:2648	21153	up gene	0	1	10	16	1	2_A375_shN7_shrs_lncRNA:1	16	Gene:MAPK6	ERK3, DUF2,dj656M21.002, MAPK6, p97MAPK6, HLT17250, PRKM6	extracellular-signal-regulated kinase 6	NM_002748, XCT:240227.2	207121_s_at	NP_002739.1, EAW74354.1
Gene:ID:9661	GNB5	15	52,413,123	52,453,565	70,462	-	1	2_A375_shN7_shrs_lncRNA:1:2648	11949	up gene	0	1	13	19	1	2_A375_shN7_shrs_lncRNA:1	19	Gene:GNB5	FLJ43714, FLJ43857, GNB5_ORS	guanine nucleotide binding protein (G protein), beta 5	NM_016194, NM_006578, XCT:9731246.1, XCT:9731291.1, XCT:2986719.0, XCT:2986976.0, XCT:2401052.0, XCT:2401053.0, XCT:1363.1	1554546_at, 204600_at, 207124_s_at, 215871_x_at	NP_057278.2, NP_006568.1, EAW74436.1, EAW74437.1, EAW74438.1, EAW74439.1, EAW74440.1, EAW74441.1, EAW74443.1, EAW74444.1
Gene:ID:101126997	LOC10011	15	52,472,196	52,498,071	25,876	+	1	2_A375_shN7_shrs_lncRNA:1:2648	-860	upstream	0	1	13	19	1	2_A375_shN7_shrs_lncRNA:1	19	Gene:LOC10012997		hypothetical LOC100129973	XR_111528, XR_109194, XR_114551		
Gene:ID:644	MYO5A	15	52,599,650	52,821,247	221,767	+	1	2_A375_shN7_shrs_lncRNA:1:2647	671	up gene	0	1	10	21	1	2_A375_shN7_shrs_lncRNA:1	21	Gene:MYO5A	MYH12, QS1, MYR12, MYO5A, MYO5	myosin VA (heavy chain 12, myosin)	NM_000259, NM_001134865, XCT:1626577.2, XCT:2883807.0, XCT:2883808.0, XCT:2883900.0, XCT:2883910.0, XCT:2883912.0, XCT:2883913.0	204627_at, 217409_at, 217417_at, 227761_at, 241066_at	NP_000250.2, NP_001121065.1, EAW77447.1, EAW77448.1, EAW77449.1, EAW77453.1, EAW77455.1, EAW77457.1
Gene:ID:11877	RSL24D1	15	52,672,512	52,689,231	16,719	-	2	1_A375_shN7_shrus_lncRNA:1:2019, 2_A375_shN7_shrs_lncRNA:1:2652	111, -17	up gene, upstream	1	1	23	34	1	2_A375_shN7_shrs_lncRNA:1	34	Gene:RSL24D1	RPL24, RLP24, C15orf15, RSL24D1, HRPL24-like, TVAS3, RPL24L, L20	ribosomal L24 domain containing 1	NM_015343, XCT:1671229.1, XCT:1671230.1, XCT:1368.2	217915_s_at	NP_057365.1, EAW74374.1, EAW74372.1, EAW74373.1
Gene:ID:5873	RAB27A	15	52,695,792	52,862,001	66,209	-	3	1_A375_shN7_shrus_lncRNA:1:2019, 2_A375_shN7_shrs_lncRNA:1:2652, 2_A375_shN7_shrs_lncRNA:1:2653	62561, 62763, 8637	downstream, downstream, up gene	1	1	19.5	22.5	2	2_A375_shN7_shrs_lncRNA:1	24	Gene:RAB27A	RAB27, RAB27A, GS2, HsT16676, RAM, MGC117249	RAB27A, member RAS oncogene family	NM_183234, NM_004580, NM_183235, NM_183236, XCT:1962489.1, XCT:2870849.0, XCT:2870849.0, XCT:2911.4	208514_s_at, 208513_s_at, 208513_s_at, 210551_x_at	NP_004571.1, NP_004571.2, NP_599058.1, NP_599059.1, EAW74476.1, EAW74477.1, EAW74478.1
Gene:ID:451852	DYX1C1	15	53,709,853	53,800,432	90,479	+	1	2_A375_shN7_shrs_lncRNA:1:2658	100255	downstream	0	1	14	16	1	2_A375_shN7_shrs_lncRNA:1	16	Gene:DYX1C1	DYX1C1, MGC70916, FLJ37602, DYX1, EKAI, RD, DYXC1	dyslexia susceptibility 1 candidate 1	NM_030933.3, NM_130810, XCT:9731351.2, XCT:29989.1, XCT:2986966.0	235272_at, 241713_s_at	NP_001027731.1, NP_570722.2, NP_001257121.1, EAW74980.1, EAW74981.1
Gene:ID:734	NEDD4	15	56,119,120	56,283,835	166,715	-	2	1_A375_shN7_shrs_lncRNA:1:2021, 2_A375_shN7_shrs_lncRNA:1:2658	76533, 63707	up gene, within gene	0	1	10.5	19	2	2_A375_shN7_shrs_lncRNA:1	26	Gene:NEDD4	KIAA0093, RIFF1, MGC119703, NEDD4, NEDD4-1	neural precursor cell expressed, developmentally down-regulated 4	NM_198400, NM_006154, XCT:2986572.0, XCT:2985723.0, XCT:31367.2	213012_at	NP_849562.2, NP_006146.2, EAW74985.1, EAW74987.1, EAW74987.1
Gene:ID:4864	RPX7	15	56,382,731	56,535,883	153,152	-	1	2_A375_shN7_shrs_lncRNA:1:2657	-2653	upstream	0	1	8	14	1	2_A375_shN7_shrs_lncRNA:1	14	Gene:RPX7	FLJ12993, MGC131636, FLJ21164, RPX7, RPX7DC2	regulatory factor X, 7	NM_022561, XCT:2556596.0, XCT:2556597.0	218530_s_at, 223520_at	NP_072172.5, EAW74986.1, EAW74989.1
Gene:ID:45783	LOC1057	15	57,176,366	57,210,697	32,329	-	2	1_A375_shN7_shrs_lncRNA:1:2022, 2_A375_shN7_shrs_lncRNA:1:2658, 2_A375_shN7_shrs_lncRNA:1:2659	31401, 21097, -55	up gene, within gene, upstream	1	1	17	28.5	2	2_A375_shN7_shrs_lncRNA:1	28	Gene:LOC1057	FLJ32544	hypothetical LOC145783	NR_015819	1555252_at, 1555570_at, 236012_at	
Gene:ID:836	TCF12	15	57,210,633	57,560,716	349,883	+	1	2_A375_shN7_shrs_lncRNA:1:2658	-31	upstream	0	1	19	29	1	2_A375_shN7_shrs_lncRNA:1	29	Gene:TCF12	HEB, HLT17399, TCF12, bHLHb20, HTF4	helix-loop-helix factor 12	NM_003205, NM_207036, NM_207037, NM_207038, NM_207040, XCT:2987628.0, XCT:2987629.0, XCT:3537709.0, XCT:3537710.0, XCT:3537711.0, XCT:31967.2	205899_at, 215611_at, 235625_at	NP_003189.1, NP_996818.1, NP_996820.1, NP_996821.1, NP_996822.1, EAW75316.1, EAW75317.1, EAW75312.1, EAW75313.1, EAW75314.1, EAW75315.1, EAW75317.1
Gene:ID:4602	CGNL1	15	57,730,163	57,842,821	112,738	+	1	2_A375_shN7_shrs_lncRNA:1:2660	89129	up gene	0	1	16	16	1	2_A375_shN7_shrs_lncRNA:1	16	Gene:CGNL1	CGNL1, KIAA1794, JACOP, MGC136258, FLJ14897	cingulin-like 1	NM_032866, XCT:2987632.0	1555547_at, 235617_at	NP_116253.2, EAW75321.1
Gene:ID:45761	GCOM1	15	57,854,102	58,009,753	155,651	+	1	2_A375_shN7_shrs_lncRNA:1:2023	114998	up gene	1	0	16	19	1	2_A375_shN7_shrs_lncRNA:1	19	Gene:GCOM1	MGC116393, GCOM1, Gas2, Gas, FLJ30972, MGC126696, MYO2AP, GCOM1, GRINL1A, Gas1	GRINL1A complex locus	NM_001010100, NM_001010099, NM_001010091, NM_152851	212241_at, 212243_at, 212248_at	NP_001010110.1, NP_001010100.1, NP_001010091.1, NP_689654.3, NP_001010101.1
Gene:ID:1458	GRINL1A	15	57,995,001	58,009,753	10,852	+	1	2_A375_shN7_shrs_lncRNA:1:2023	-101	upstream	1	0	16	19	1	2_A375_shN7_shrs_lncRNA:1	19	Gene:GRINL1A	DUF2,bS6F816, GRINL1A	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	NM_015532, NM_001010102, NM_152199	205347_s_at	NP_001010112.1, NP_001010101.1, NP_689654.3
Gene:ID:5346	AQP4	15	58,430,866	58,478,110	47,782	+	1	2_A375_shN7_shrs_lncRNA:1:2660	42232	up gene	0	1	14	17	1	2_A375_shN7_shrs_lncRNA:1	17	Gene:AQP4	MIWC1, AQP4, HLT17257, AQP4	aquaporin 4	NM_004028, XCT:9731225.1, XCT:2985900.0, XCT:31246.4	205565_at	NP_0991902, EAW75336.1, EAW75332.1, EAW75332.1
Gene:ID:5322	LOC1005	15	59,060,271	59,063,176	2,907	-	1	2_A375_shN7_shrs_lncRNA:1:2662	-635	upstream	0	1	20	24	1	2_A375_shN7_shrs_lncRNA:1	24	Gene:LOC1003094		hypothetical LOC100306466	XR_109293		
Gene:ID:4628	PAM82B	15	59,062,093	59,149,754	66,381	+	1	2_A375_shN7_shrs_lncRNA:1:2662	223	up gene	0	1	20	24	1	2_A375_shN7_shrs_lncRNA:1	24	Gene:PAM82B	KIAA1164, PAM82B	family with sequence similarity 63, member B	NM_001040450, NM_001040451, XCT:2985480.0, XCT:2985778.0, XCT:2985779.0, XCT:3537710.0, XCT:3537711.0, XCT:31961.1	214691_s_at, 215052_x_at	NP_001035540.1, NP_001035542.1, EAW75840.1, EAW75843.1, EAW75847.1, EAW75846.1
Gene:ID:4611	MYO1E	15	59,438,963	59,663,071	236,808	+	1	2_A375_shN7_shrs_lncRNA:1:2024	-129	upstream	1	0	15	15	1	2_A375_shN7_shrs_lncRNA:1	15	Gene:MYO1E	MYO1E, MGC104635, MYO1C, Heavy-O	myosin IE	NM_004998, XCT:2556615.0		NP_004989.2, EAW75964.1
Gene:ID:2335	GTP2A2	15	59,930,261	59,949,737	19,476	+	1	2_A375_shN7_shrs_lncRNA:1:2662	169	up gene	0	1	17	20	1	2_A375_shN7_shrs_lncRNA:1	20	Gene:GTP2A2	TP2A2, HLT15743, GTP2A2, TP4A	guanylate binding protein family, member 2, 12/34	NM_004482, XCT:1962466.1, XCT:1972.2	202670_at	NP_004463.1, EAW75973.1, EAW75974.1
Gene:ID:63	BNIP2	15	59,933,061	59,991,642	26,581	+	2	1_A375_shN7_shrs_lncRNA:1:2025, 2_A375_shN7_shrs_lncRNA:1:2662	106, 32074	up gene, downstream	1	1	16	19.5	2	2_A375_shN7_shrs_lncRNA:1	20	Gene:BNIP2	NIP2, BNIP2, BNIP-2	BCL2/adenovirus E1B 19kDa interacting protein 2	NM_004330, XCT:1971136.1, XCT:24803.2	209300_s_at	NP_004321.2, EAW75976.1, EAW77979.1
Gene:ID:2252	FOXB1	15	60,296,421	60,298,142	1,721	+	1	2_A375_shN7_shrs_lncRNA:1:2666	1243	up gene	0	1	10	13	1	2_A375_shN7_shrs_lncRNA:1	13	Gene:FOXB1	HFH9-5, FOXB1, FKH5	forkhead box B1	NM_012162, XCT:1641747.2	205512_at	NP_036314.2, EAW77581.1
Gene:ID:302	ANXA2	15	60,639,350	60,690,165	50,815	-	5	1_A375_shN7_shrs_lncRNA:1:2026, 1_A375_shN7_shrs_lncRNA:1:2027, 1_A375_shN7_shrs_lncRNA:1:2028, 2_A375_shN7_shrs_lncRNA:1:2666, 2_A375_shN7_shrs_lncRNA:1:2676	26348, 4512, 4777, 39177, 26505	up gene, in gene, in gene, in gene, within gene	1	1	17.5	18.5	4	2_A375_shN7_shrs_lncRNA:1	25	Gene:ANXA2	LIP2, PAP-IV, ANX02, P36, CAL1H, ANX2, LPC2D, LPC2, ANX2LG	annexin A2	NM_001002857, NM_004039, NM_001136015, NM_001002556, XCT:2986467.0, XCT:2986469.0, XCT:2986471.0, XCT:2986472.0, XCT:2986473.0, XCT:2986475.0	1560126_at, 201590_x_at, 210427_x_at, 213503_x_at	NP_001002857.1, NP_004030.1, NP_001126557.1, NP_001002555.1, EAW75562.1, EAW75565.1, EAW75566.1, EAW75567.1, EAW75565.1, EAW75567.1
Gene:ID:9904	NARG2	15	60,711,006	60,771,344	59,326	-	2	1_A375_shN7_shrs_lncRNA:1:2030, 2_A375_shN7_shrs_lncRNA:1:2666	-60, -240	upstream, upstream	1	1	16	23	1	2_A375_shN7_shrs_lncRNA:1	23	Gene:NARG2	NARG2, BRCC1	NMDA receptor-regulated 2	NM_024611, NM_001018059, XCT:2986453.1, XCT:2986454.1, XCT:2986455.1	218713_at, 228960_at, 228169_at	NP_078887.2, NP_001150099.1, EAW77580.1, EAW77589.1, EAW77590.1
Gene:ID:093	RORA	15	60,760,663	61,521,302	760,639	+	2	1_A375_shN7_shrs_lncRNA:1:2030, 2_A375_shN7_shrs_lncRNA:1:2666, 2_A375_shN7_shrs_lncRNA:1:2676	760376, 760396, 43562	downstream, downstream, up gene	1	1	14.5	19.5	2	2_A375_shN7_shrs_lncRNA:1	23	Gene:RORA	RORQ, NR1F1, MGC119329, RZRA, RZR-ALPHA, DKFZp686M2414, ROR1, RORQ, MGC116226, RORA	RAR-related orphan receptor A	NM_134261, NM_134262, NM_002943, NM_134260, NM_134263, NM_134264, XCT:1629698.1, XCT:1629699.2, XCT:1963125.2, XCT:2986461.0	216426_x_at, 216476_s_at, 202434_s_at, 228390_at	NP_599022.1, NP_599022.1, NP_599024.1, NP_002934.1, EAW77982.1, EAW77983.1, EAW77984.1, EAW77985.1
Gene:ID:91703053	MGC1556	15	62,929,271	62,937,350	8,080	-	1	2_A375_shN7_shrs_lncRNA:1:2033	-2524	upstream	1	0	24	12	1	2_A375_shN7_shrs_lncRNA:1	24	Gene:MGC1556	MGC115665	hypothetical protein MGC115665	NR_026997	1569293_at	
Gene:ID:3960	TLN2	15	62,939,810	63,139,830	197,120	+	1	2_A375_shN7_shrs_lncRNA:1:2033	384	up gene	1	0	24	12	1	2_A375_shN7_shrs_lncRNA:1	24	Gene:TLN2	DKFZp686I0978, KIAA0320, TLN2, DKFZp686I0976, DKFZp451B1011, LIVED	talin 2	NM_015059, XCT:1971178.2, XCT:2985375.1, XCT:2985790.0	212703_at, 232629_at	NP_055874.2, EAW77616.1, EAW77618.1, EAW77617.1
Gene:ID:16294	LACTB	15	63,414,033	63,534,260	20,228	+	2	1_A375_shN7_shrs_lncRNA:1:2030, 1_A375_shN7_shrs_lncRNA:1:2676	-144, -144	upstream, upstream	1	1	53	46	1	2_A375_shN7_shrs_lncRNA:1	53	Gene:LACTB	LACTB, MRPL56, FLJ14802, Q24	lactamase, beta	NM_032637, NM_171846, XCT:2985330.0, XCT:29940.3	1552483_at, 1552484_at, 226354_at	NP_116246.2, NP_741982.1, EAW77637.1, EAW77636.1
Gene:ID:1093	RPS27L	15	63,445,539	63,449,741	4,202	-	1	2_A375_shN7_shrs_lncRNA:1:2677	-19	upstream	0	1	13	26	1	2_A375_shN7_shrs_lncRNA:1	26	Gene:RPS27L	RPS27L	ribosomal protein S27-like	NM_015920, XCT:2556922.0, XCT:24668.2	218007_s_at, 221467_s_at, 228505_at	NP_057004.1, EAW77639.1, EAW77640.1
Gene:ID:1762	RASSF	15	63,461,725	63,559,875	70,367	+	1	2_A375_shN7_shrs_lncRNA:1:2037	-3200	upstream	1	0	21	14	1	2_A375_shN7_shrs_lncRNA:1	21	Gene:RASSF	FLJ36125, RASSF	RASSF, member RAS oncogene family	NM_016335, XCT:2556536.0, XCT:24666.3	219210_s_at, 222696_at, 228522_at	NP_057419.1, EAW77642.1, EAW77641.1
Gene:ID:771	CA12	15	63,615,730	63,674,078	56,348	-	2	1_A375_shN7_shrs_lncRNA:1:2038, 2_A375_shN7_shrs_lncRNA:1:2676	32339, 15099	up gene, within gene	1	1	13	19	2	2_A375_shN7_shrs_lncRNA:1	19	Gene:CA12	HLT15516, FLJ20151, CA12, CAXII	carbonic anhydrase XII	NM_001218, NM_206925, XCT:2985812.0, XCT:2985812.0, XCT:2985815.1, XCT:2985816.1	203963_at, 204589_s_at, 204509_at, 210735_s_at, 214164_x_at, 231466_x_at	NP_001209.1, NP_996906.1, EAW77646.1, EAW77648.1, EAW77650.1, EAW77647.1
Gene:ID:990	USP3	15	63,796,610	63,863,663	66,853	+	2	1_A375_shN7_shrs_lncRNA:1:2026, 2_A375_shN7_shrs_lncRNA:1:2676	22, -10	up gene, within gene	1	1	25	26	1	2_A375_shN7_shrs_lncRNA:1	26	Gene:USP3	UBP, SHH03, MGC129876, MGC129879, USP3	ubiquitin specific peptidase 3	NM_006537, XCT:1655466.1	221654_s_at, 226632_at	NP_006528.2, EAW77651.1
Gene:ID:94324	MIR422A	15	64,163,129	64,163,216	69	+	2	1_A375_shN7_shrs_lncRNA:1:2040, 2_A375_shN7_shrs_lncRNA:1:2680	336, 336	downstream, downstream	1	1	82	77	1	2_A375_shN7_shrs_lncRNA:1	77	Gene:MIR422A	MIRN422A, MIRN422A	microRNA 422a	NR_029844		
Gene:ID:4191	PAM86A	15	64,364,761	64,386,207	21,446	-	3	1_A375_shN7_shrs_lncRNA:1:2041, 1_A375_shN7_shrs_lncRN A:1:2042, 2_A375_shN7_shrs_lncRNA:1:2680	93, -3217, 321	up gene, upstream, upstream	1	1	21	17.5	2	2_A375_shN7_shrs_lncRNA:1	22	Gene:PAM86A	PAM86A, FLJ22875	family with sequence similarity 96, member A	NM_032231, NM_001018612, XCT:2556691.0, XCT:2556692.0, XCT:24948.2	226792_s_at	NP_1156071, NP_001018612.1, EAW77660.1, EAW77661.1, EAW77662.1
Gene:ID:642	SNX1	15	64,386,177	64,436,633	50,256	+	3	1_A375_shN7_shrs_lncRNA:1:2041, 1_A375_shN7_shrs_lncRN A:1:2042, 2_A375_shN7_shrs_lncRNA:1:2680	-2663, -2, 1699	upstream, up gene, upstream	1	1	21	17.5	2	2_A375_shN7_shrs_lncRNA:1	22	Gene:SNX1	SNX1, HLT1379, SNX1A, MGC8662, Vps5	sorting nexin 1	NM_003099, NM_148935, NM_152626, XCT:2985780.0, XCT:2985790.0, XCT:2985791.0, XCT:24948.2	200716_at, 213364_s_at, 214551_s_at, 216357_at	NP_003090.2, NP_683736.1, NP_689039.1, EAW77664.1, EAW77665.1, EAW77666.1, EAW77667.1
Gene:ID:9581	SNX22	15	64,443,916	64,469,680	5,764	+	2	1_A375_shN7_shrs_lncRNA:1:2043, 2_A375_shN7_shrs_lncRNA:1:2682	11484, 11426	downstream, downstream	1	1	22	29	1	2_A375_shN7_shrs_lncRNA:1	33	Gene:SNX22	FLJ13852, SNX22	sorting nexin 22	NM_024760, XCT:1961665.1, XCT:24949.2	1565851_s_at, 230309_at, 238490_at	NP_079074.2, EAW77668.1, EAW77667.1
Gene:ID:478	PPIB	15	64,468,014	64,483,354	15,340	+	2	1_A375_shN7_shrs_lncRNA:1:2043, 2_A375_shN7_shrs_lncRNA:1:2682	-4, 10	upstream, in gene	1	1	23	29	1	2_A375_shN7_shrs_lncRNA:1	33	Gene:PPIB	CYN, SCYLP, MGC2230, CYPB, CYP-S1, CYP-23	peptidylprolyl isomerase B (cyclophilin B)	NM_000942, XCT:24543.4	200907_at, 200965_s_at	NP_000933.1, EAW77669.1
Gene:ID:3944	CSNK1G1	15	64,487,716	64,648,442	160,726	+	4	1_A375_shN7_shrs_lncRNA:1:2043, 1_A375_shN7_shrs_lncRN A:1:2044, 1_A375_shN7_shrs_lncRNA:1:2045, 2_A375_shN7_shrs_lncRNA:1:2682, 2_A375_shN7_shrs_lncRNA:1:2686	183032, -262, 183032, 666	downstream, upstream, downstream, up gene	1	1	19	20.67	3	2_A375_shN7_shrs_lncRNA:1	33	Gene:CSNK1G1			NM_022048	209640_at, 221671_s_at, 236508_at, 231620_s_at	NP_073331.2
Gene:ID:766	KIAA0101	15	64,657,193	64,672,702	15,509	+	3	1_A375_shN7_shrs_lncRNA:1:2044, 1_A375_shN7_shrs_lncRN A:1:2045, 1_A375_shN7_shrs_lncRNA:1:2046, 2_A375_shN7_shrs_lncRNA:1:2682, 2_A375_shN7_shrs_lncRNA:1:2686, 2_A375_shN7_shrs_lncRNA:1:2687, 2_A375_shN7_shrs_lncRNA:1:2688	29992, 8252, 29926, 6, -8296	downstream, upstream, downstream, upstream, downstream, up gene	1	1	14.5	19.5	4	2_A375_shN7_shrs_lncRNA:1	26	Gene:KIAA0101	FLJ36702, L5, KIAA0101, OEATC1, OEATC-1, p15(PAF), PAF, MDS4TP2	KIAA0101	NM_014736, NM_001029889	202503_s_at, 211713_x_at	NP_055551.1, NP_001025160.1
Gene:ID:3118	RIF1	15	65,107,631	65,117,638	10,007	-	3	1_A375_shN7_shrs_lncRN A:1:2047, 2_A375_shN7_shrs_lncRNA:1:2686, 2_A375_shN7_shrs_lncRNA:1:2687, 2_A375_shN7_shrs_lncRNA:1:2688	-10290, -274, 10255	upstream, upstream, upstream	1	1	14	19.5	2	2_A375_shN7_shrs_lncRNA:1	24	Gene:RIF1	C1orf20, PIP1, PIF	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	NM_018151, XCT:2986998.2, XCT:2986117.0, XCT:2986819.0	1555991_at, 226252_at	NP_060621.2, EAW77684.1, EAW77685.1, EAW77686.1
Gene:ID:9301	FLEKHO2	15	65,134,052	65,160,201	26,149	+	2	1_A375_shN7_shrs_lncRNA:1:2047, 2_A375_shN7_shrs_lncRNA:1:2686	-8934, 9666	upstream, downstream	1	1	16	15	1	2_A375_shN7_shrs_lncRNA:1	16	Gene:FLEKHO2	FLJ38560, DKFZp761J2312, FP1626, FLEKHO1, FLEKHO2, pp9999	pleckstrin homology domain containing, family O member 2	NM_025201, NM_001193858, XCT:2985870.0, XCT:2985872.0, XCT:2985954.0, XCT:3537610.0	208436_at	NP_079577.2, NP_001180851.1, EAW77697.1, EAW77698.1, EAW77699.1, EAW77700.1
Gene:ID:2260	MTFMT	15	65,293,650	65,321,977	28,127	-	1	2_A375_shN7_shrs_lncRNA:1:2048	165	up gene	1	0	16	14	1	2_A375_shN7_shrs_lncRNA:1	16	Gene:MTFMT	MTFMT, FMT1	mitochondrial methionyl-tRNA formyltransferase	NM_139242, XCT:1671775.8, XCT:1972374.1	235692_at	NP_640333.2, EAW77706.1, EAW77707.1
Gene:ID:1265	RASLL2	15	65,349,673	65,360,356	14,713	+	1	2_A375_shN7_shrs_lncRNA:1:2048	-1372	upstream	0	1	11	17	1	2_A375_shN7_shrs_lncRNA:1	17	Gene:RASL12	RASL12, R1S	RAS-like, family 12	NM_052933, XCT:1674723.4, XCT:1972372.1	218167_at	NP_439647.1, EAW77710.1, EAW77709.1
Gene:ID:90566	KBTBD13	15	65,399,154	65,572,276	5,122	+	1	2_A375_shN7_shrs_lncRNA:1:2048	-7284	upstream	0	1	11	17	1	2_A375_shN7_shrs_lncRNA:1	17	Gene:KBTBD13	KBTBD13, HCG1645727, NEM9	kelch repeat and BTB (POZ) domain containing 13	NM_0901052	NM_001104552.1	
Gene:ID:5501	PDCD7	15	65,809,717	65,826,174	16,457	-	2	1_A375_shN7_shrs_lncRNA:1:2049, 2_A375_shN7_shrs_lncRNA:1:2688	1110, 142	up gene, up gene	1	1	19	22	1	2_A375_shN7_shrs_lncRNA:1	22	Gene:PDCD7	HES16, PDCD7, FLJ36213, ES16, MGC22015	programmed cell death 7	NM_005707, XCT:1677925.1, XCT:1970680.1	220152_at, 231609_s_at	NP_0059261.1, EAW77713.1, EAW77716.1
Gene:ID:4696	PARP16	15	65,830,437	65,879,816	20,381	-	2	1_A375_shN7_shrs_lncRNA:1:2050, 2_A375_shN7_shrs_lncRNA:1:2688	4002, 9302	upstream, upstream	1	1	11	66	33	1	2_A375_shN7_shrs_lncRNA:1	66	Gene:PARP16	C15orf30, FLJ23281, PARP16, FLJ30909, pART15	poly (ADP-ribose) polymerase family, member 16	NM_017651, XCT:1677942.2, XCT:1981331.1, XCT:2535707.0, XCT:2535709.0	219034_at	NP_060321.2, EAW77730.1, EAW77716.1, EAW77719.1, EAW77721.1
Gene:ID:6531	RNU5A	15	65,565,359	65,565,505	116	+	2	1_A375_shN7_shrs_lncRNA:1:2050, 2_A375_shN7_shrs_lncRNA:1:2692, 2_A375_shN7_shrs_lncRNA:1:2693	-656, -656, 5707	upstream, downstream	1	1	30.5	28.5	2	2_A375_shN7_shrs_lncRNA:1	46	Gene:RNU5A	U5A, RNU5A, RNU5C, U5SP1, RNU5	RNA, U5A small nuclear	NR_002756		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Internal Transcripts	Internal Dists to Start	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Loci	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:26 6532	RNU6B-1	15	93,397,013	93,397,131	116	+	3	1_A270_shN37_dhrot_lncRNA:1-2690, 2_A270_shN37_dhrs_lncRNA:1-2692, 3_A270_shN37_dhrs_lncRNA:1-2691	46693, 46695, 61	upstream, upstream, ut gene	1	1	30.5	24.5	2	2_A270_shN37_dhrsb_lncRNA:1	46	Gene RNU6B-1	RNU6B, U6B1, RNU6B-1, RNU6B-1P	RNA, U6B small nuclear 1	NR_002737		
Gene:ID:33 4676	DPP8	15	93,727,995	93,810,035	72,027	-	2	1_A270_shN37_dhrot_lncRNA:1-2691, 2_A270_shN37_dhrs_lncRNA:1-2694	-13, -13	upstream, upstream	1	1	176	169	1	2_A270_shN37_dhrs_lncRNA:1	169	Gene DPP8	MGC26191, FLJ14820, DP8, DPP8, FLJ22053, MSTP141, DPRP1	dipeptidyl-peptidase 8	NM_130439, NM_197961, NM_017742, NM_197960, XCT145778.3, XCT187073.1, XCT187076.1, XCT229159.0, XCT229160.0, XCT229164.0, XCT233713.0, XCT233714.0, XCT233715.0	226529_x_at, 227016_at	NP_569118.1, NP_932098.1, NP_060213.2, NP_932094.1, EAW77726.1, EAW77727.1, EAW77728.1, EAW77729.1, EAW77730.1, EAW77731.1, EAW77732.1, EAW77733.1, EAW77734.1
Gene:ID:5 1596	C15orf44	15	93,871,116	93,901,469	22,353	-	2	1_A270_shN37_dhrot_lncRNA:1-2692, 2_A270_shN37_dhrs_lncRNA:1-2695	-11, -29	upstream, ut gene	1	1	24	35	1	2_A270_shN37_dhrs_lncRNA:1	35	Gene C15orf44	DKFZp566O1664, C15orf44	chromosome 15 open reading frame 44	NM_020600, NM_001128643, XCT14777.3, XCT229155.0	1565551_at, 221263_s_at	NP_115927.1, NP_001128313.1, EAW77737.1, EAW77738.1
Gene:ID:1 0260	DENND4A	15	93,932,834	94,054,831	131,877	-	2	1_A270_shN37_dhrot_lncRNA:1-2693, 2_A270_shN37_dhrs_lncRNA:1-2696	-103, -72	upstream, upstream	1	1	41	37	1	1_A270_shN37_dhrot_lncRNA:1	41	Gene DENND4A	DENND4A, KIAA0476, MYCPBP, FLJ32649, IRLB	DENN/MADD domain containing 4A	NM_005848, NM_001144622	1554332_s_at, 214707_at	NP_005839.3, NP_001138293.1
Gene:ID:3 766	RAB11A	15	96,161,796	96,181,762	19,966	+	1	2_A270_shN37_dhrs_lncRNA:1-2696	All	ut gene	0	1	13	26	1	2_A270_shN37_dhrs_lncRNA:1	26	Gene RAB11A	YL6, MGC1680, RAB11A	RAB11A, member RAS oncogene family	NM_004663, XCT135616.6, XCT145246.5	200863_s_at, 200864_s_at	NP_004654.1, EAW77753.1, EAW77752.1
Gene:ID:5 4465	MEGF11	15	96,187,634	96,596,075	356,681	+	6	1_A270_shN37_dhrot_lncRNA:1-2694, 1_A270_shN37_dhrot_lncRNA:1-2695, 1_A270_shN37_dhrot_lncRNA:1-2696, 1_A270_shN37_dhrot_lncRNA:1-2697, 1_A270_shN37_dhrot_lncRNA:1-2698, 1_A270_shN37_dhrot_lncRNA:1-2699, 2_A270_shN37_dhrs_lncRNA:1-2697, 2_A270_shN37_dhrs_lncRNA:1-2698	331147, 289355, 249593, 246567, 201147, 246967, 246522, 939	ut gene, ut gene, ut gene, ut gene, ut gene, ut gene, ut gene	1	1	29	32.25	4	2_A270_shN37_dhrs_lncRNA:1	52	Gene MEGF11	DKFZp434L121, MEGF11, KIAA1761	multiple EGF-like-domains 11	NM_032445, XCT185547.1, XCT229113.0, XCT229114.0, XCT233656.0	1552439_s_at, 1560334_at, 1560874_a_at	NP_115621.2, EAW77751.1, EAW77754.1, EAW77755.1, EAW77756.1
Gene:ID:5 604	MAP2K1	15	66,679,211	66,763,682	104,671	+	3	1_A270_shN37_dhrot_lncRNA:1-2695, 2_A270_shN37_dhrs_lncRNA:1-2692, 2_A270_shN37_dhrs_lncRNA:1-2693	110737, -202, 110933	downstream, upstream, downstream	1	1	16.5	25	2	2_A270_shN37_dhrs_lncRNA:1	29	Gene MAP2K1	MAP2K1, MEK1, MKK1, MAPK33, PRKMK1	mitogen-activated protein kinase kinase 1	NM_002755, XCT135627.5, XCT197055.2, XCT229121.1, XCT234659.0, XCT234660.0	202670_at	NP_002746.1, EAW77765.1, EAW77766.1, EAW77767.1, EAW77769.1
Gene:ID:1 0302	SNAPC5	15	66,742,666	66,760,146	17,480	-	2	1_A270_shN37_dhrot_lncRNA:1-2696, 2_A270_shN37_dhrs_lncRNA:1-2699	170, 2	ut gene, ut gene	1	1	16	29	1	2_A270_shN37_dhrs_lncRNA:1	29	Gene SNAPC5	SNAPC5, SNAP19	small nuclear RNA activating complex, polypeptide 5, 19kDa	NM_006240, XCT135939.6, XCT198242.1, XCT229129.0	1554932_a_at, 213203_at, 214592_s_at	NP_006840.1, EAW77770.1, EAW77771.1, EAW77772.1
Gene:ID:6 124	RPL4	15	66,791,653	66,797,164	5,531	-	2	1_A270_shN37_dhrot_lncRNA:1-2698, 2_A270_shN37_dhrs_lncRNA:1-2699	7216, 7040	downstream, downstream	1	1	16	29	1	2_A270_shN37_dhrs_lncRNA:1	29	Gene RPL4	L4, RPL4		NM_000968, XCT229239.7, XCT229239.1, XCT229239.2	200003_s_at, 201154_x_at, 217110_s_at	NP_000959.2, EAW77775.1, EAW77772.1, EAW77774.1, EAW77776.1
Gene:ID:6 85100	SNORD16 C	15	66,792,590	66,793,656	66	-	2	1_A270_shN37_dhrot_lncRNA:1-2695, 2_A270_shN37_dhrs_lncRNA:1-2699	3656, 3812	downstream, downstream	1	1	16	29	1	2_A270_shN37_dhrs_lncRNA:1	29	Gene SNORD16C	SNORD16C, U16C	small nucleolar RNA, C/D box 16C	NR_002443		
Gene:ID:6 85099	SNORD16 B	15	66,794,360	66,794,429	69	-	2	1_A270_shN37_dhrot_lncRNA:1-2695, 2_A270_shN37_dhrs_lncRNA:1-2699	4661, 4265	downstream, downstream	1	1	16	29	1	2_A270_shN37_dhrs_lncRNA:1	29	Gene SNORD16B	U16B, SNORD16B	small nucleolar RNA, C/D box 16B	NR_002442		
Gene:ID:6 85097	SNORD16	15	66,795,149	66,795,248	99	-	2	1_A270_shN37_dhrot_lncRNA:1-2695, 2_A270_shN37_dhrs_lncRNA:1-2699	5260, 5104	downstream, downstream	1	1	16	29	1	2_A270_shN37_dhrs_lncRNA:1	29	Gene SNORD16	SNORD16, U16	small nucleolar RNA, C/D box 16	NR_002440		
Gene:ID:6 85096	SNORD16 A	15	66,795,553	66,795,652	99	-	2	1_A270_shN37_dhrot_lncRNA:1-2695, 2_A270_shN37_dhrs_lncRNA:1-2699	5664, 5508	downstream, downstream	1	1	16	29	1	2_A270_shN37_dhrs_lncRNA:1	29	Gene SNORD16A	SNORD16A, U16A	small nucleolar RNA, C/D box 16A	NR_002441		
Gene:ID:5 5555	ZW10CH1	15	66,797,451	66,841,823	44,372	+	2	1_A270_shN37_dhrot_lncRNA:1-2695, 2_A270_shN37_dhrs_lncRNA:1-2699	-7463, -7267	upstream, downstream	1	1	16	29	1	2_A270_shN37_dhrs_lncRNA:1	29	Gene ZW10CH1	KNTC1AP, ZWILCH, MGC11354, FLJ10306, FLJ10340, bZwilch	Zwilch, kinetochore associated, homolog (Drosophila)	NR_052105, NM_017975, XCT185972.2, XCT229123.0, XCT229124.0	218349_s_at, 222606_at	NP_060445.3, EAW77777.1, EAW77776.1, EAW77779.1
Gene:ID:4 291	SMAD6	15	66,994,674	67,074,336	79,664	+	2	1_A270_shN37_dhrot_lncRNA:1-2693, 1_A270_shN37_dhrot_lncRNA:1-2696, 2_A270_shN37_dhrs_lncRNA:1-2697	466, -660	upstream, upstream, ut gene	1	1	16.5	15.5	2	2_A270_shN37_dhrs_lncRNA:1	22	Gene SMAD6	MADH6, SMAD6, HsT17432, MADH7	SMAD family member 6	NM_001242691, NR_027654, NM_005585, XCT185349.1, XCT229113.0, XCT233772.0	207069_s_at, 208600_s_at, 208601_at, 213563_s_at	NP_001139353.1, NP_005579.2, EAW77758.1, EAW77755.1, EAW77756.1
Gene:ID:4 088	SMAD3	15	67,356,193	67,487,833	129,336	+	1	1_A270_shN37_dhrot_lncRNA:1-2691	23533	ut gene	1	0	19	19	1	1_A270_shN37_dhrot_lncRNA:1	19	Gene SMAD3	MGC90396, HsT17436, DKFZp686J10186, MADH3, SMAD3, DKFZp686N0721, JV15-2, HSPC193	SMAD family member 3	NM_005902, NM_001145102, NM_001145103, NM_001145104, XCT135612.3, XCT229115.0, XCT229116.0	206398_s_at, 206397_x_at, 206398_s_at, 212865_s_at	NP_005893.1, NP_001138374.1, NP_001138373.1, NP_001138375.1, EAW77783.1, EAW77784.1, EAW77785.1
Gene:ID:7 9719	AAGAB	15	67,992,366	67,047,074	53,708	-	2	1_A270_shN37_dhrot_lncRNA:1-2692, 2_A270_shN37_dhrs_lncRNA:1-2699	2, -62	ut gene, upstream	1	1	21	35	1	2_A270_shN37_dhrs_lncRNA:1	35	Gene AAGAB	p34, AAGAB, DKFZp686G08116, DKFZp687D2317, FLJ11506	alpha- and gamma-adaptin binding protein	NM_024666, XCT135873.4, XCT233726.0	202551_at, 202552_s_at, 242264_at	NP_078942.2, EAW77821.1, EAW77792.1
Gene:ID:6 4799	IQCH	15	67,047,135	67,094,142	247,004	+	2	1_A270_shN37_dhrot_lncRNA:1-2692, 2_A270_shN37_dhrs_lncRNA:1-2699	-66, -2	upstream, upstream	1	1	21	35	1	2_A270_shN37_dhrs_lncRNA:1	35	Gene IQCH	NYD-SP3, FLJ12476, IQCH, DKFZp434P2314	IQ motif containing H	NM_032154, NM_001031715, XCT198033.2, XCT229167.0, XCT229749.0, XCT229750.0	1569610_at, 1569611_a_at, 226361_at, 226165_s_at, 236812_s_at, 236514_at	NP_073621.2, NP_001028655.1, EAW77796.1, EAW77795.1, EAW77797.1
Gene:ID:1 55513	LOC1005 66695	15	67,093,850	67,814,182	116,232	-	1	1_A270_shN37_dhrot_lncRNA:1-2693	654	ut gene	1	0	13	6	1	1_A270_shN37_dhrot_lncRNA:1	15	Gene LOC100506695		hypothetical LOC100506695	XR_111515, XR_111514, XR_109209, XR_109208, XR_114865, XR_114864		
Gene:ID:5 997	C15orf61	15	67,813,522	67,818,641	6,119	+	1	1_A270_shN37_dhrot_lncRNA:1-2693	-274	upstream	1	0	13	6	1	1_A270_shN37_dhrot_lncRNA:1	15	Gene C15orf61	C15orf61, FLJ90357	chromosome 15 open reading frame 61	NM_001143939	229742_at	NP_001137405.1
Gene:ID:5 997	MAP2K5	15	67,835,021	68,099,652	264,631	+	1	1_A270_shN37_dhrot_lncRNA:1-2694	-109	upstream	1	0	14	11	1	1_A270_shN37_dhrot_lncRNA:1	14	Gene MAP2K5	Hs71458A, MAP2K5, PRKMK5, MAPKK5, MEK5	mitogen-activated protein kinase kinase 5	NM_002757, NM_145160, XCT135623.1, XCT229230.0, XCT229231.0, XCT229252.0	206795_at, 216462_x_at, 211370_x_at, 211371_s_at, 216403_at, 224303_at	NP_002745.1, NP_660140.1, EAW77799.1, EAW77800.1, EAW77801.1, EAW77802.1
Gene:ID:3 90566	LBXCOR1	15	68,117,641	68,129,174	6,233	+	2	2_A270_shN37_dhrs_lncRNA:1-2816, 2_A270_shN37_dhrs_lncRNA:1-2820	4605, 14627	upstream, downstream	0	1	16	22.5	2	2_A270_shN37_dhrs_lncRNA:1	23	Gene LBXCOR1	FLJ35815, LBXCOR1, SXOR1, CORL1	Ladybird homeobox (mouse)	NM_001031697		NP_001026977.1
Gene:ID:2 6427	RNU6-1	15	68,132,276	68,132,393	105	-	1	2_A270_shN37_dhrs_lncRNA:1-2811	-265	upstream	0	1	17	22	1	2_A270_shN37_dhrs_lncRNA:1	22	Gene RNU6-1	RNU6-1, U6, RNU6A, RNU6	RNA, U6 small nuclear 1	NR_004394		
Gene:ID:1 0116	FEMT1	15	68,370,141	68,563,840	12,489	+	2	1_A270_shN37_dhrot_lncRNA:1-2693, 1_A270_shN37_dhrot_lncRNA:1-2697	-157, -173	upstream, upstream	1	1	27	32	1	1_A270_shN37_dhrot_lncRNA:1	32	Gene FEMT1	FEMT1, FHA, DKFZp451B0710, FYA-ALPHA	fem-1 homolog b (C. elegans)	NM_015322, XCT135617.2, XCT229626.0	212267_at, 212373_at, 212374_at	NP_056137.1, EAW77816.1, EAW77819.1
Gene:ID:2 3301	ITGA11	15	68,564,042	68,724,662	130,600	-	1	1_A270_shN37_dhrot_lncRNA:1-2696	58648	ut gene	1	0	16	8	1	1_A270_shN37_dhrot_lncRNA:1	16	Gene ITGA11	Hs71894K, ITGA11	integrin, alpha 11	NM_001004439, XCT145821.3, XCT229146.0	1564819_a_at, 222599_at	NP_001004439.1, EAW77821.1, EAW77820.1
Gene:ID:2 63673	TMEM64	15	68,373,190	68,395,164	14,974	+	1	1_A270_shN37_dhrot_lncRNA:1-2814	4449	upstream	0	1	14	21	1	1_A270_shN37_dhrot_lncRNA:1	21	Gene TMEM64	MGC13645, FLJ33766, MGC129643, NCRNA00277, TMEM64	mis-positor coding RNA 277	NR_038949, XCT234116.0, XCT234117.0, XCT234118.0, XCT234119.0	240812_x_at	EAW78533.1, EAW78535.1, EAW77834.1
Gene:ID:5 4552	PAQR5	15	68,591,294	69,099,976	508,682	+	1	2_A270_shN37_dhrs_lncRNA:1-2815	113234	downstream	0	1	14	25	1	2_A270_shN37_dhrs_lncRNA:1	25	Gene PAQR5	MPRG, PAQR5, FLJ20190	progestin and adipoQ receptor family member V	NM_001135554, NM_017703, XCT229165.0, XCT233213.0	230333_at, 241071_at	NP_001129026.1, NP_060173.2, EAW78538.1, EAW78539.1
Gene:ID:1 55558	LOC1055 58	15	68,659,243	69,707,356	16,125	+	1	2_A270_shN37_dhrs_lncRNA:1-2815	540	ut gene	0	1	14	25	1	2_A270_shN37_dhrs_lncRNA:1	25	Gene LOC105558		hypothetical LOC105558	XR_111513, XR_109210, XR_114866	243622_at	
Gene:ID:9 492	IQF23	15	68,709,658	69,740,764	34,076	+	3	1_A270_shN37_dhrot_lncRNA:1-2697, 2_A270_shN37_dhrs_lncRNA:1-2815, 2_A270_shN37_dhrs_lncRNA:1-2816	30592, 160, 30624	downstream, upstream, downstream	1	1	16.5	26.5	2	2_A270_shN37_dhrs_lncRNA:1	26	Gene IQF23	MKLP-1, KNSL5, MKLP1, CHO1, KIF23	kinesin family member 23	NM_004856, NM_138555, XCT229169.0, XCT23522.2	206709_s_at, 244627_at	NP_004847.2, NP_612565.1, EAW77841.1, EAW77842.1
Gene:ID:6 176	RPLP1	15	68,745,159	68,747,864	2,725	+	2	1_A270_shN37_dhrot_lncRNA:1-2697, 1_A270_shN37_dhrot_lncRNA:1-2816	121, 153	ut gene, ut gene	1	1	16	35	1	2_A270_shN37_dhrs_lncRNA:1	35	Gene RPLP1	RPLP1, MGC5215, LP1, RPP1, P1, FLJ25486	ribosomal protein, large, P1	NM_001003, NM_213729, XCT187216.1, XCT233773.0, XCT30044.3	200763_s_at, 244191_at	NP_000994.1, NP_998967.1, EAW77843.1, EAW77844.1, EAW77842.1
Gene:ID:7 590	TLE3	15	68,340,543	70,090,256	49,712	+	2	2_A270_shN37_dhrs_lncRNA:1-2692	368	ut gene	0	1	12	17	1	2_A270_shN37_dhrs_lncRNA:1	17	Gene TLE3	KIAA1547, HsT16976, E(SG), GRG3, FLJ36460, TLE2, ESG3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	NM_005078, NM_020908, NM_001165162, XCT229551.0, XCT229552.0, XCT229553.0, XCT229561.0	208472_s_at, 212769_at, 212770_at, 212771_at	NP_003909.2, NP_065958.1, NP_001159562.1, EAW77845.1, EAW77846.1, EAW77850.1, EAW77851.1
Gene:ID:5 4836	THAP10	15	71,172,651	71,184,753	11,972	-	1	1_A270_shN37_dhrot_lncRNA:1-2677	-863	upstream	1	0	16	20	1	1_A270_shN37_dhrot_lncRNA:1	20	Gene THAP10	THAP10	THAP domain containing 10	NM_032417, XCT231903.2	219599_at	NP_065822.1, EAW77862.1
Gene:ID:7 9578	LRRC49	15	71,184,667	71,242,836	157,469	+	1	1_A270_shN37_dhrot_lncRNA:1-2677	229	ut gene	1	0	16	20	1	1_A270_shN37_dhrot_lncRNA:1	20	Gene LRRC49	LRRC49, FLJ20196	leucine rich repeat containing 49	NM_017691, XCT235598.0, XCT235599.0, XCT235600.0, XCT235601.0	218255_s_at	NP_060161.2, EAW77865.1, EAW77866.1, EAW77867.1
Gene:ID:7 9579	THSD4	15	71,433,766	72,079,722	641,934	+	1	1_A270_shN37_dhrot_lncRNA:1-2678	154052	ut gene	0	1	12	21	1	1_A270_shN37_dhrot_lncRNA:1	21	Gene THSD4	FVES1934, FKIA3405, FLJ13710, ADAMTSL6, THSD4	thrombospondin, type I, domain containing 4	NM_024517, XCT185347.1, XCT229550.0, XCT229555.0	219182_s_at, 225535_at, 226506_at, 241223_at	NP_078932.2, EAW77874.1, EAW77873.1, EAW77875.1
Gene:ID:3 319	PKM2	15	72,491,370	72,523,880	32,314	-	2	1_A270_shN37_dhrot_lncRNA:1-2676, 2_A270_shN37_dhrs_lncRNA:1-2677	164, 356	ut gene, ut gene	1	1	17	17	1	1_A270_shN37_dhrot_lncRNA:1	17	Gene PKM2	TCB, PKM, THBP1, PK2, MGC3933, PKM2, OIP2, CTHBP	pyruvate kinase, muscle	NM_002654, NM_182470, NM_182471, XCT229524.0, XCT229163.0, XCT229167.0, XCT229168.0, XCT229169.0, XCT229170.0, XCT233752.0	201251_at	NP_002643.3, NP_872270.1, NP_872271.1, EAW77884.1, EAW77885.1, EAW77887.1, EAW77886.1, EAW77888.1, EAW77889.1, EAW77890.1
Gene:ID:5 6965	PARP6	15	72,533,522	72,563,828	30,106	+	4	1_A270_shN37_dhrot_lncRNA:1-2676, 1_A270_shN37_dhrot_lncRNA:1-2679, 2_A270_shN37_dhrs_lncRNA:1-2677, 2_A270_shN37_dhrs_lncRNA:1-2678	30105, 1555, 30093, 1556	downstream, upstream, downstream, upstream	1	1	67.5	69.5	2	2_A270_shN37_dhrs_lncRNA:1	122	Gene PARP6	pART17, MSTO31971, PARP6	poly (ADP-ribose) polymerase family, member 6	NM_138718, XCT185133.1, XCT229165.0, XCT229166.0, XCT229167.0, XCT229168.0, XCT229169.0, XCT229170.0, XCT37123.0	219539_x_at, 232663_s_at, 236710_s_at	NP_064599.2, EAW77891.1, EAW77892.1, EAW77893.1, EAW77894.1, EAW77895.1, EAW77896.1, EAW77897.1, EAW77898.1
Gene:ID:9 0677	BRUNOL6	15	72,977,066	72,812,329	39,487	-	2	1_A270_shN37_dhrot_lncRNA:1-2692, 1_A270_shN37_dhrot_lncRNA:1-2691, 2_A270_shN37_dhrs_lncRNA:1-2824	449, -231, 287	ut gene, upstream, ut gene	1	1	26	27	1	2_A270_shN37_dhrs_lncRNA:1	27	Gene BRUNOL6	CUGBP, Elav-like family member 6	CUGBP, Elav-like family member 6	NM_032940, NM_001172654, NM_001172655, XCT235956.0, XCT1720.3	227779_at	NP_443712.2, NP_001166153.1, NP_001166156.1, EAW77900.1, EAW77901.1
Gene:ID:3 073	HEXA	15	72,633,776	72,668,520	32,742	-	2	1_A270_shN37_dhrot_lncRNA:1-2692, 2_A270_shN37_dhrs_lncRNA:1-2693	104, 104	ut gene, ut gene	1	1	28	29	1	2_A270_shN37_dhrs_lncRNA:1	29	Gene HEXA	MGC99658, HEXA, TSD	hexosaminidase A (alpha polypeptide)	NM_000520, XCT17116.4	1553424_at, 201765_s_at, 213193_at	NP_000511.2, EAW77902.1
Gene:ID:3 0372	C15orf34	15	72,668,434	72,671,129	2,676	+	2	1_A270_shN37_dhrot_lncRNA:1-2692, 2_A270_shN37_dhrs_lncRNA:1-2693	-28, -28	ut gene, ut gene	1	1	28	29	1	2_A270_shN37_dhrs_lncRNA:1	29	Gene C15orf34	FLJ13315, C15orf34	chromosome 15 open reading frame 34	NP_077262, XCT135679.3	220715_at	EAW77903.1
Gene:ID:2 5620	ARIH1	15	72,799,667	72,876,896	112,229	+	2	2_A270_shN37_dhrs_lncRNA:1-2820, 2_A270_shN37_dhrs_lncRNA:1-2824	-139, 725	upstream, ut gene	0	1	12	23	2	2_A270_shN37_dhrs_lncRNA:1	26	Gene ARIH1	HARI, UBCHTBP, FLJ20329, ARI1, ARIH1, DKFZp686O13126, FLJ30116, HHR21	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	NM_005744, XCT229094.0, XCT29307.2	201670_at, 201679_at, 201680_at, 201681_s_at	NP_005735.2, EAW77905.1, EAW77907.1
Gene:ID:3 93	BBS4	15	72,916,526	73,030,817	92,291	+	1	1_A270_shN37_dhrot_lncRNA:1-2693	162	ut gene	0	1	15	16	1	1_A270_shN37_dhrot_lncRNA:1	16	Gene BBS4	BBS4	Bardet-Biedl syndrome 4	NM_033028, XCT185519.1, XCT31722.3	212744_at, 212745_s_at	NP_149017.2, EAW77913.1, EAW77912.1
Gene:ID:8 3440	ADPGK	15	73,043,708	73,079,126	32,418	-	2	1_A270_shN37_dhrot_lncRNA:1-2693, 2_A270_shN37_dhrs_lncRNA:1-2694	64, 14	ut gene, ut gene	1	1	25	31	1	2_A270_shN37_dhrs_lncRNA:1	31	Gene ADPGK	ADPGK, DKFZp434G1615, ADPGK, 2610019G08Rik	ADP-dependent glucokinase	NM_031284, NR_023318, NR_023319, XCT185460.2, XCT198239.1, XCT198241.1, XCT233720.0, XCT233721.0, XCT233722.0, XCT233723.0	220693_s_at, 224453_s_at	NP_112574.2, EAW77914.1, EAW77917.1, EAW77916.1, EAW77915.1, EAW77921.1, EAW77918.1, EAW77919.1
Gene:ID:4 756	NEO1	15	73,344,623	73,597,547	252,722	+	1	1_A270_shN37_dhrot_lncRNA:1-2693	-661	upstream	0	1	8	19	1	1_A270_shN37_dhrot_lncRNA:1	19	Gene NEO1	Hs71753A, NEO1, IGDCC2, DKFZp547E146, DKFZp547H096, NGN	neogenin 1	NM_002499, NM_001172626, XCT229844.0, XCT229845.0	206321_at, 226270_at, 226677_at	NP_002490.2, NP_001160093.1, EAW77923.1, EAW77924.1
Gene:ID:1 0021	HCN4	15	73,612,200	73,661,805	49,605	+	2	1_A270_shN37_dhrot_lncRNA:1-2694, 2_A270_shN37_dhrs_lncRNA:1-2830	22589, 22589	ut gene, ut gene	1	1	22	35	1	2_A270_shN37_dhrs_lncRNA:1	35	Gene HCN4	HCN4, BBS2	hyperpolarization activated cyclic nucleotide-gated potassium channel 4	NM_005477, XCT229013.3	205698_at	NP_005465.1, EAW77925.1
Gene:ID:2 7020	NPTN	15	73,652,344	73,823,752	72,409	+	1	1_A270_shN37_dhrot_lncRNA:1-2677	8681	ut gene	0	1	7	16	1	1_A270_shN37_dhrot_lncRNA:1	16	Gene NPTN	DKFZp686K2477, MGC10303, GPNB, KS55, SDFR1, np55, NPTN, GP55, SDR1	neuroplastin	NM_012428, NM_017455, NM_001161363, NM_001161364, XCT187214.1, XCT30886.3, XCT30892.2	202226_s_at	NP_036993.1, NP_059428.1, NP_001154638.1, NP_001154639.1, EAW77930.1, EAW77932.1, EAW77931.1
Gene:ID:1 61514	TBC1D21	15	74,163,998	74,181,555	19,367	+	1	2_A270_shN37_dhrs_lncRNA:1-2840	22279	downstream	0	1	16	21	1	2_A270_shN37_dhrs_lncRNA:1	21	Gene TBC1D21	TBC1D21, MGC34741	TBC1 domain family, member 21	NM_153356, XCT233709.0, XCT30962.2	231473_at	NP_699187.1, EAW77938.1, EAW77937.1
Gene:ID:9 398	STOML1	15	74,275,990	74,284,635	8,675	-	2	1_A270_shN37_dhrot_lncRNA:1-2697, 2_A270_shN37_dhrs_lncRNA:1-2840	-101, -101	upstream, upstream	1	1	100	111	1	1_A270_shN37_dhrot_lncRNA:1	111	Gene STOML1	STOML1, hUNC-24, SLP-1, STORP, FLJ30370	stomatin (EPB72)-like 1	NM_004809, NM_198563.2, XCT185298.1, XCT198237.1, XCT198238.1, XCT198239.1, XCT198240.1, XCT233699.0, XCT30972.2	1554320_at, 204701_s_at, 53195_at	NP_004800.2, EAW77943.1, EAW77940.1, EAW77941.1, EAW77942.1, EAW77945.1, EAW77943.1
Gene:ID:5 371	PML	15	74,287,014	74,340,160	53,146	+	2	1_A270_shN37_dhrot_lncRNA:1-2697, 2_A270_shN37_dhrs_lncRNA:1-2840	-2276, -2276	upstream, upstream	1	1	100	111	1	2_A270_shN37_dhrs_lncRNA:1	111	Gene PML	TRIM19, RNF71, PML, MYL, PP8675	promyelocytic leukemia	NM_033238, NM_033240, NM_033244, NM_033246, NM_002675, NM_033247, NM_033239, NM_033240, NM_033250, NM_033244, XCT185249.2, XCT197.1.4.4.1	208353_x_at, 208350_at, 210352_x_at, 210353_x_at, 211568_s_at, 211569_at, 225558_at, 225560_at	NP_150241.2, NP_150252.1, NP_150243.1, NP_150242.1, NP_150244.1, NP_002666.1, NP_150250.2, NP_150247.2, NP_150253.2, EAW77946.1, EAW77947.1
Gene:ID:3 971	SLK	15	74,499,087	74,499,212	3,126	+	1	2_A270_shN37_dhrs_lncRNA:1-2840	8645	downstream	0	1	16	23	1	2_A270_shN37_dhrs_lncRNA:1	23	Gene SLK	SLK, MGC102816, HsT17563	ste20-like kinase (yeast)	NM_014720, XCT185493.1, XCT197.1.4.2.2, XCT234694.0	1555391_at, 1555392_a_at	NP_055391.1, NP_998034.1, EAW69257.1, EAW69258.1
Gene:ID:6 4220	STRA6	15	74,671,807	74,801,371	29,564	-	2	2_A270_shN37_dhrs_lncRNA:1-2842, 2_A270_shN37_dhrs_lncRNA:1-2840	26339, 6039	ut gene, ut gene	0	1	16.5	20.5	2	2_A270_shN37_dhrs_lncRNA:1	23	Gene STRA6	FLJ12541, PP14296, STRA6, MCOPS9	stimulated by retinoic acid gene 6 homolog (mouse)	NM_022369, NM_001142617, NM_001142618, NM_001142619, NM_001142620, XCT229165.0, XCT229166.0, XCT229167.0, XCT229168.0, XCT229169.0	1555334_at, 1555335_s_at, 221701_s_at	NP_071764.3, NP_001136059.1, NP_001136060.1, NP_001136061.1, NP_001136062.1, EAW69350.1, EAW69351.1, EAW69352.1, EAW69353.1
Gene:ID:8 0125	CCDC33	15	74,838,667	74,839,482	99,815	+	4	1_A270_shN37_dhrot_lncRNA:1-2695, 1_A270_shN37_dhrot_lncRNA:1-2699, 1_A270_shN37_dhrot_lncRNA:1-2840, 1_A270_shN37_dhrot_lncRNA:1-2841	28917, 85332, 28959, 85461	ut gene, ut gene, ut gene	1	1	30.5	27.5	2	2_A270_shN37_dhrs_lncRNA:1	28	Gene CCDC33	FLJ23160, MGC34145, FLJ23658, CCDC33, CT61	coiled-coil domain containing 33	NM_152791, NM_029055, XCT229097.0, XCT229098.0, XCT229271.0, XCT233299.0, XCT33660.2	1563090_at, 235905_at	NP_877932.2, NP_076331.2, EAW69343.1, EAW69344.1, EAW69345.1, EAW69346.1, EAW69347.1
Gene:ID:1 563	CYP11A1	15	74,930,103	74,960,081	29,978	-	1	1_A270_shN37_dhrot_lncRNA:1-2840	4143	upstream	0	1	8	14	1	2_A270_shN37_dhrs_lncRNA:1	14	Gene CYP11A1	CYP11A, P450SCC, CYP11A1	cytochrome P450, family 11, subfamily A, polypeptide 1	NM_000781, NM_001099773, XCT229165.1, XCT29378.3	204309_at	NP_000772.2, NP_001092242.1, EAW69340.1, EAW69342.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:729739	LOC729739	15	74,646,797	74,656,961	10,164	+	1	2_A375_pNL97_plus_lncRNA::1::2946	19427	downstream	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC729739		hypothetical LOC729739	XR_111533, XR_109164, XR_114671		
GeneID:1198	CLK3	15	74,900,713	74,922,542	21,829	+	1	1_A375_pNL7_minus_lncRNA::1::2090	7351	in gene	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene CLK3	PHCLK3, CLK3, PHCLK3/152, FLJ22858	CDC-like kinase 3	NM_003992, NM_001130028, hCT1777101.1, hCT1952449.0, hCT1952450.0, hCT1952451.1, hCT1952452.0, hCT1952453.1	202140_s_at	NP_003983.2, NP_001123500.1, EAW99320.1, EAW99321.1, EAW99322.1, EAW99323.1, EAW99324.1, EAW99325.1
GeneID:80153	EDC3	15	74,922,899	74,988,386	65,487	-	1	1_A375_pNL7_minus_lncRNA::1::2091	66	in gene	1	0	26	15	1	1_A375_pNL7_minus_lncRNA::1	26	Gene EDC3	FLJ31777, FLJ21128, YJEFN2, YJDC, LSM16, EDC3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	NM_025083, NM_001142443, NM_001142444, hCT2291067.0, hCT2291068.0, hCT2291069.0, hCT2358317.0	219207_at, 226042_at	NP_079359.2, NP_001135915.1, NP_001135916.1, EAW99316.1, EAW99317.1, EAW99319.1, EAW99318.1
GeneID:1543	CYP1A1	15	75,011,883	75,017,877	5,994	-	2	2_A375_pNL97_plus_lncRNA::1::2947, 2_A375_pNL97_plus_lncRNA::1::2948	1461, -1099	in gene, upstream	0	1	14.5	23	2	2_A375_pNL97_plus_lncRNA::1	28	Gene CYP1A1	AHRR, P450DX, CYP1A1, AHH, CP11, P450-C, CYP1, P1-450	cytochrome P450, family 1, subfamily A, polypeptide 1	NM_000499, hCT2343624.0, hCT29959.4	205749_at	NP_000490.1, EAW99315.1, EAW99314.1
GeneID:4351	MPI	15	75,182,410	75,190,565	8,155	+	3	1_A375_pNL7_minus_lncRNA::1::2092, 1_A375_pNL7_minus_lncRNA::1::2093, 2_A375_pNL97_plus_lncRNA::1::2949	-10, 17161, 16982	upstream, downstream, downstream	1	1	17.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene MPI	MPI, PMI, PMI1, CDG1B, FLJ39201	mannose phosphate isomerase	NM_002435, hCT2294520.0, hCT2294522.0, hCT2294523.0, hCT2294526.0	202472_at, 230524_at	NP_002426.1, EAW99295.1, EAW99296.1, EAW99297.1, EAW99298.1
GeneID:57184	C15orf17	15	75,192,328	75,199,462	7,134	-	3	1_A375_pNL7_minus_lncRNA::1::2092, 1_A375_pNL7_minus_lncRNA::1::2093, 2_A375_pNL97_plus_lncRNA::1::2949	17062, -109, 70	downstream, upstream, in gene	1	1	17.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene C15orf17	FLJ00005, C15orf17	chromosome 15 open reading frame 17	NM_020447, hCT1777494.2, hCT1953012.2, hCT2348818.0, hCT2348819.0, hCT2348820.0, hCT2358290.0	224798_s_at, 224804_s_at, 224805_s_at	NP_065180.1, EAW99291.1, EAW99289.1, EAW99292.1, EAW99293.1, EAW99294.1, EAW99290.1
GeneID:9377	COX5A	15	75,212,616	75,230,495	17,879	-	2	1_A375_pNL7_minus_lncRNA::1::2094, 2_A375_pNL97_plus_lncRNA::1::2950	146, 31	in gene, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene COX5A	VA, COX, COX-VA, COX5A	cytochrome c oxidase subunit Va	NM_004255, hCT2292220.0, hCT2292221.0	203663_s_at, 217451_at, 229426_at	NP_004246.2, EAW99287.1, EAW99288.1
GeneID:54913	RPP25	15	75,247,443	75,249,775	2,332	-	2	1_A375_pNL7_minus_lncRNA::1::2095, 2_A375_pNL97_plus_lncRNA::1::2951	-113, 847	upstream, in gene	1	1	22	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RPP25	FLJ20374, RPP25	ribonuclease P/MRP 25kDa subunit	NM_017793, hCT1643355.3, hCT2292218.0	219143_s_at, 223415_at	NP_060263.2, EAW99285.1, EAW99286.1
GeneID:192683	SCAMP5	15	75,287,876	75,313,836	25,960	+	3	1_A375_pNL7_minus_lncRNA::1::2097, 2_A375_pNL97_plus_lncRNA::1::2953, 2_A375_pNL97_plus_lncRNA::1::2954	-180, -196, 26124	upstream, upstream, downstream	1	1	16.5	21	2	2_A375_pNL97_plus_lncRNA::1	22	Gene SCAMP5	DKFZp686L1799, MGC24969, SCAMP5	secretory carrier membrane protein 5	NM_001178111, NM_001178112, NM_138967, NR_033660, hCT13164.2, hCT2294530.0, hCT2294532.0, hCT2358320.0, hCT2358321.0, hCT2358322.0, hCT2358323.0, hCT2358324.0	212699_at, 234568_at	NP_001171582.1, NP_001171583.1, NP_620417.1, EAW99277.1, EAW99278.1, EAW99279.1, EAW99280.1, EAW99281.1, EAW99282.1, EAW99283.1, EAW99284.1
GeneID:60490	PPCDC	15	75,315,927	75,343,067	27,140	+	2	2_A375_pNL97_plus_lncRNA::1::2954, 2_A375_pNL97_plus_lncRNA::1::2955	73, 20137	in gene, in gene	0	1	15	20	2	2_A375_pNL97_plus_lncRNA::1	20	Gene PPCDC	MDS018, FLJ14585, PPCDC	phosphopantothenoylcysteine decarboxylase	NM_021823, hCT13010.3, hCT1961703.1	219066_at	NP_068595.3, EAW99276.1, EAW99275.1
GeneID:56905	C15orf39	15	75,494,221	75,504,510	10,289	+	1	2_A375_pNL97_plus_lncRNA::1::2957	147	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C15orf39	FLJ46337, C15orf39, DKFZp434H132, MGC117209	chromosome 15 open reading frame 39	NM_015492, hCT2294539.0, hCT2294540.0	204494_s_at, 204495_s_at, 215087_at	NP_056307.2, EAW99272.1, EAW99273.1
GeneID:4123	MAN2C1	15	75,648,133	75,660,941	12,808	-	1	2_A375_pNL97_plus_lncRNA::1::2958	621	in gene	0	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MAN2C1	MAN2C1, MAN6A8, MANA, MGC67979, MANA1, DKFZp686E23167	mannosidase, alpha, class 2C, member 1	NM_006715, hCT1777486.2, hCT1962646.1, hCT2358312.0	203666_at, 236089_at, 236230_x_at	NP_006706.2, EAW99254.1, EAW99252.1, EAW99253.1
GeneID:25942	SIN3A	15	75,661,720	75,748,124	86,404	-	1	2_A375_pNL97_plus_lncRNA::1::2958	87804	downstream	0	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SIN3A	SIN3A, FLJ90319, DKFZp434K2235, KIAA0700	SIN3 homolog A, transcription regulator (yeast)	NM_001145357, NM_001145358, NM_015477, hCT2292207.0, hCT2292208.1, hCT2292209.1	225135_at, 236189_at	NP_001138829.1, NP_001138830.1, NP_056292.1, EAW99249.1, EAW99250.1, EAW99251.1
GeneID:10073	SNUPN	15	75,890,424	75,918,719	28,295	-	1	2_A375_pNL97_plus_lncRNA::1::2959	735	in gene	0	1	11	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene SNUPN	Snurportin1, SNUPN, RNUT1, KPNBL	snurportin 1	NM_005701, NM_001042581, NM_001042588, hCT2292202.0, hCT2292203.0	207436_s_at	NP_005692.1, NP_001036046.1, NP_001036053.1, EAW99245.1, EAW99246.1
GeneID:55272	IMP3	15	75,931,426	75,932,664	1,238	-	1	1_A375_pNL7_minus_lncRNA::1::2098	456	in gene	1	0	18	19	1	1_A375_pNL7_minus_lncRNA::1	18	Gene IMP3	MRPS4, BRMS2, C15orf12, DKFZp586L0118, FLJ10968, IMP3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	NM_018285	221688_s_at	NP_060755.1
GeneID:257364	SNX33	15	75,941,348	75,950,968	9,620	+	1	1_A375_pNL7_minus_lncRNA::1::2098	-9140	upstream	1	0	18	19	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SNX33	SNX33, SNX30, MGC32065, SH3PXD3C, SH3PX3	sorting nexin 33	NM_153271, hCT1768890.1	227151_at	NP_695003.1, EAW99243.1
GeneID:1464	CSPG4	15	75,966,663	76,005,189	38,526	-	5	1_A375_pNL7_minus_lncRNA::1::2099, 1_A375_pNL7_minus_lncRNA::1::2100, 2_A375_pNL97_plus_lncRNA::1::2960, 2_A375_pNL97_plus_lncRNA::1::2961, 2_A375_pNL97_plus_lncRNA::1::2962	16437, -731, 17525, 15781, -747	in gene, upstream, in gene, in gene, upstream	1	1	17.33	19	3	2_A375_pNL97_plus_lncRNA::1	24	Gene CSPG4	CSPG4, HMW-MAA, MCSPG, MCSP, MSK16, NG2, MEL-CSPG	chondroitin sulfate proteoglycan 4	NM_001897, hCT1777484.2, hCT2292200.0	204736_s_at, 214297_at	NP_001888.2, EAW99239.1, EAW99240.1
GeneID:161753	ODF3L1	15	76,016,319	76,020,027	3,708	+	1	2_A375_pNL97_plus_lncRNA::1::2962	-10383	upstream	0	1	18	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ODF3L1	ODF3L1, MGC48986	outer dense fiber of sperm tails 3-like 1	NM_175881, hCT1777492.1	236245_at	NP_787077.1, EAW99238.1
GeneID:92912	UBE2Q2	15	76,135,622	76,193,388	57,766	+	2	1_A375_pNL7_minus_lncRNA::1::2101, 2_A375_pNL97_plus_lncRNA::1::2963	48778, 60666	in gene, downstream	1	1	16.5	15	2	2_A375_pNL97_plus_lncRNA::1	18	Gene UBE2Q2	UBE2Q2, DKFZp762C143	ubiquitin-conjugating enzyme E2Q family member 2	NM_173469, NM_001145335, hCT2294568.0, hCT2294569.0	224747_at	NP_775740.1, NP_001138807.1, EAW99233.1, EAW99234.1
GeneID:26263	FBXO22	15	76,196,200	76,226,944	30,744	+	1	2_A375_pNL97_plus_lncRNA::1::2963	88	in gene	0	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FBXO22	FISTC1, FLJ13986, MGC31799, FBX22, FBXO22	F-box protein 22	NM_012170, NM_147188, hCT1961786.2, hCT1961787.2, hCT2358315.0, hCT29550.4	219638_at, 225734_at, 225736_at, 225737_s_at	NP_036302.1, NP_671717.1, EAW99229.1, EAW99230.1, EAW99231.1, EAW99232.1
GeneID:2108	ETFA	15	76,508,628	76,603,810	95,182	-	2	1_A375_pNL7_minus_lncRNA::1::2102, 2_A375_pNL97_plus_lncRNA::1::2964	226, 226	in gene, in gene	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ETFA	GA2, EMA, MADD, ETFA	electron-transfer-flavoprotein, alpha polypeptide	NM_000126, NM_001127716, hCT1961802.1, hCT30665.2	201931_at	NP_000117.1, NP_001121188.1, EAW99221.1, EAW99222.1
GeneID:5955	RCN2	15	77,223,962	77,242,601	18,639	+	2	1_A375_pNL7_minus_lncRNA::1::2103, 2_A375_pNL97_plus_lncRNA::1::2965	23270, 23318	downstream, downstream	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RCN2	ERC-55, RCN2, E6BP, TCBP49, ERC55	reticulocalbin 2, EF-hand calcium binding domain	NM_002902, hCT32061.2	201485_s_at, 201486_at	NP_002893.1, EAW99216.1
GeneID:100506704	LOC100506704	15	77,241,494	77,247,823	6,329	-	2	1_A375_pNL7_minus_lncRNA::1::2103, 2_A375_pNL97_plus_lncRNA::1::2965	591, 543	in gene, in gene	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC100506704		hypothetical LOC100506704	XR_111535, XR_109166, XR_114670		
GeneID:10099	TSPAN3	15	77,336,359	77,363,570	27,211	-	2	1_A375_pNL7_minus_lncRNA::1::2104, 2_A375_pNL97_plus_lncRNA::1::2966	18, 18	in gene, in gene	1	1	25	19	1	1_A375_pNL7_minus_lncRNA::1	25	Gene TSPAN3	TM4-A, TSPAN-3, TSPAN3, TM4SF8	tetraspanin 3	NM_005724, NM_198902, NM_001168412, hCT2290907.1, hCT2290908.0, hCT32062.3	200972_at, 200973_s_at	NP_005715.1, NP_944492.1, NP_001161884.1, EAW99209.1, EAW99210.1, EAW99211.1
GeneID:10363	HMG20A	15	77,713,243	77,777,945	64,702	+	1	2_A375_pNL97_plus_lncRNA::1::2967	-907	upstream	0	1	4	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene HMG20A	HMG20A, HMGXB1, FLJ10739, HMGX1	high mobility group 20A	NM_018200, hCT1769190.1, hCT1953852.1, hCT2358308.0	218152_at	NP_060670.1, EAW99201.1, EAW99202.1, EAW99203.1
GeneID:3419	IDH3A	15	78,441,719	78,462,884	21,165	+	1	2_A375_pNL97_plus_lncRNA::1::2970	137	in gene	0	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene IDH3A	IDH3A		NM_005530, hCT2293520.0, hCT29234.3	202069_s_at, 202070_s_at	NP_005521.1, EAW99181.1, EAW99182.1
GeneID:80349	WDR61	15	78,575,577	78,591,940	16,363	-	1	1_A375_pNL7_minus_lncRNA::1::2107	66	in gene	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene WDR61	WDR61, SKI8, REC14	WD repeat domain 61	NM_025234, hCT2292529.0, hCT2292530.0, hCT2292532.0	215156_at, 221531_at, 221532_s_at, 232075_at, 237208_at	NP_079510.1, EAW99175.1, EAW99173.1, EAW99174.1
GeneID:3658	IREB2	15	78,730,518	78,793,798	63,280	+	2	1_A375_pNL7_minus_lncRNA::1::2106, 2_A375_pNL97_plus_lncRNA::1::2971	-294, -278	upstream, upstream	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene IREB2	IREB2, ACO3, FLJ23381, IRP2, IRP2AD	iron-responsive element binding protein 2	NM_004136, hCT2292060.0, hCT2292062.0, hCT30184.3	1555476_at, 214666_x_at, 225892_at	NP_004127.1, EAW99170.1, EAW99169.1, EAW99171.1
GeneID:729911	LOC729911	15	79,484,049	79,579,362	95,313	-	1	2_A375_pNL97_plus_lncRNA::1::2972	3266	in gene	0	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC729911		hypothetical LOC729911	XM_001130603, XM_001134184, XM_001719815		XP_001130603.2, XP_001134184.2, XP_001719867.2
GeneID:100506846	LOC100506846	15	79,505,439	79,576,156	70,717	-	1	2_A375_pNL97_plus_lncRNA::1::2972	60	in gene	0	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100506846		hypothetical protein LOC100506846	XM_003119613, XM_003118662, XM_003120815		XP_003119661.1, XP_003118710.1, XP_003120863.1
GeneID:390616	ANKRD34C	15	79,575,146	79,590,581	15,435	+	1	2_A375_pNL97_plus_lncRNA::1::2972	950	in gene	0	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene ANKRD34C	FLJ45093, ANKRD34C, FLJ33346	ankyrin repeat domain 34C	NM_001146341	216073_at	NP_001139813.1
GeneID:23423	TMED3	15	79,603,491	79,615,189	11,698	+	1	2_A375_pNL97_plus_lncRNA::1::2973	253	in gene	0	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TMED3	TMED3, C15orf22, P24B, MGC133022	transmembrane emp24 protein transport domain containing 3	NM_007364, hCT15948.2, hCT2358318.0	208837_at	NP_031390.1, EAW99138.1, EAW99139.1
GeneID:10588	MTHFS	15	80,137,318	80,189,370	52,052	-	2	1_A375_pNL7_minus_lncRNA::1::2108, 2_A375_pNL97_plus_lncRNA::1::2974	58, 122	in gene, in gene	1	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MTHFS	MTHFS, FLJ30410, HsT19268	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	NM_006441, hCT15949.1	203433_at, 210242_x_at	NP_006432.1, EAW99132.1
GeneID:400410	ST20	15	80,191,182	80,216,077	24,895	-	3	1_A375_pNL7_minus_lncRNA::1::2109, 2_A375_pNL97_plus_lncRNA::1::2974, 2_A375_pNL97_plus_lncRNA::1::2975	26765, 26829, 189	downstream, downstream, in gene	1	1	19.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene ST20	ST20, HCCS-1	suppressor of tumorigenicity 20	NM_001100879, NM_001100880	217104_at	NP_001094349.1, NP_001094350.1
GeneID:283687	C15orf37	15	80,215,113	80,217,196	2,083	+	1	2_A375_pNL97_plus_lncRNA::1::2975	775	in gene	0	1	21	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C15orf37	C15orf37, FLJ33788	chromosome 15 open reading frame 37	NR_026330	1556588_at	
GeneID:54469	ZFAND6	15	80,352,021	80,430,710	78,689	+	1	1_A375_pNL7_minus_lncRNA::1::2110	12779	in gene	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ZFAND6	ZA20D3, ZFAND5B, AWP1, ZFAND6	zinc finger, AN1-type domain 6	NM_019006, hCT2290828.0, hCT2290829.0, hCT2290830.0, hCT2358292.0, hCT2358293.0, hCT2358294.0	221613_s_at, 222186_at, 238757_at	NP_061879.2, EAW99126.1, EAW99122.1, EAW99123.1, EAW99124.1, EAW99127.1, EAW99125.1
GeneID:283688	LOC283688	15	80,555,410	80,634,147	78,737	-	3	1_A375_pNL7_minus_lncRNA::1::2111, 2_A375_pNL97_plus_lncRNA::1::2977, 2_A375_pNL97_plus_lncRNA::1::2978	76563, 76595, 24067	in gene, in gene, in gene	1	1	18	23	2	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC283688		hypothetical LOC283688	NR_033833	1559579_at, 1566526_at	
GeneID:9915	ARNT2	15	80,696,692	80,890,278	193,586	+	3	1_A375_pNL7_minus_lncRNA::1::2112, 2_A375_pNL97_plus_lncRNA::1::2979, 2_A375_pNL97_plus_lncRNA::1::2980	175884, 10620, 32572	in gene, in gene, in gene	1	1	16	19.33	3	1_A375_pNL7_minus_lncRNA::1	24	Gene ARNT2	ARNT2, KIAA0307, bHLHe1	aryl-hydrocarbon receptor nuclear translocator 2	NM_014862, hCT19223.4	202986_at	NP_055677.3, EAW99114.1
GeneID:100133746	LOC100133746	15	80,728,655	80,737,228	8,573	-	1	2_A375_pNL97_plus_lncRNA::1::2980	7964	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100133746		hypothetical LOC100133746	XR_109169, XR_114873		
GeneID:57214	KIAA1199	15	81,071,712	81,243,999	172,287	+	3	1_A375_pNL7_minus_lncRNA::1::2113, 2_A375_pNL97_plus_lncRNA::1::2981, 2_A375_pNL97_plus_lncRNA::1::2982	1408, 944, 176608	in gene, in gene, downstream	1	1	19	20.5	2	1_A375_pNL7_minus_lncRNA::1	28	Gene KIAA1199	CCSP1, KIAA1199, TMEM2L	KIAA1199	NM_018689, hCT19222.2	1554685_a_at, 212942_s_at	NP_061159.1, EAW99111.1
GeneID:23184	MESDC2	15	81,268,095	81,282,205	14,110	-	1	2_A375_pNL97_plus_lncRNA::1::2983	429	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MESDC2	MESD, MESDC2, KIAA0081, BOCA	mesoderm development candidate 2	NM_015154, hCT19225.3, hCT2290495.1	224672_x_at, 224675_at, 224679_at, 235679_at, 239746_at	NP_055969.1, EAW99110.1, EAW99109.1
GeneID:647020	LOC647020	15	81,372,889	81,410,492	37,603	-	1	2_A375_pNL97_plus_lncRNA::1::2984	25660	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC647020		hypothetical protein LOC647020	XM_001714683, XM_001719614, XM_001714711		XP_001714735.3, XP_001719666.3, XP_001714763.3
GeneID:3603	IL16	15	81,489,219	81,605,104	115,885	+	1	2_A375_pNL97_plus_lncRNA::1::2986	39309	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene IL16	IL16, FLJ44234, prIL-16, FLJ16806, LCF, PRIL16, FLJ42735, NIL16	interleukin 16 (lymphocyte chemoattractant factor)	NM_004513, NM_001172128, NM_172217, hCT2344293.0, hCT2344294.0, hCT2344295.0, hCT2358291.0	1555016_at, 209827_s_at, 209828_s_at	NP_004504.3, NP_001165599.1, NP_757366.2, EAW99098.1, EAW99099.1, EAW99101.1, EAW99100.1
GeneID:84206	MEX3B	15	82,334,128	82,338,361	4,233	-	1	2_A375_pNL97_plus_lncRNA::1::2987	537	in gene	0	1	10	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MEX3B	RKHD3, DKFZp434J0617, MEX3B, RNF195, MEX-3B, MGC117199	mex-3 homolog B (C. elegans)	NM_032246, hCT2291035.0	223627_at	NP_115622.2, EAW99090.1
GeneID:6218	RPS17	15	82,821,161	82,824,865	3,704	-	2	1_A375_pNL7_minus_lncRNA::1::2115, 2_A375_pNL97_plus_lncRNA::1::2988	-111, -127	upstream, upstream	1	1	27	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene RPS17	DBA4, RPS17L2, MGC72007, S17, RPS17L1, RPS17	ribosomal protein S17	NM_001021, hCT2290903.0, hCT2290904.0, hCT2290905.0	201665_x_at, 211487_x_at, 212578_x_at	NP_001012.1, EAW62454.1, EAW62453.1, EAW62455.1
GeneID:64506	CPEB1	15	83,211,951	83,316,728	104,777	-	1	1_A375_pNL7_minus_lncRNA::1::2116	360	in gene	1	0	20	15	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CPEB1	FLJ13203, CPE-BP1, MGC34136, CEBP, CPEB, MGC60106, CPEB1	cytoplasmic polyadenylation element binding protein 1	NM_001079533, NM_001079534, NM_001079535, NM_030594, hCT18081.3, hCT1953029.1, hCT2290898.0, hCT2290899.0, hCT2290902.0	219578_s_at, 222903_s_at	NP_001073001.1, NP_001073002.1, NP_001073003.1, NP_085097.3, EAW62449.1, EAW62450.1, EAW62448.1, EAW62451.1, EAW62452.1
GeneID:8120	AP3B2	15	83,328,033	83,378,635	50,602	-	4	1_A375_pNL7_minus_lncRNA::1::2117, 1_A375_pNL7_minus_lncRNA::1::2118, 2_A375_pNL97_plus_lncRNA::1::2989, 2_A375_pNL97_plus_lncRNA::1::2990	46603, -53, 46603, -85	in gene, upstream, in gene, upstream	1	1	23.5	31	2	2_A375_pNL97_plus_lncRNA::1	36	Gene AP3B2	DKFZp686D17136, NAPTB, AP3B2	adaptor-related protein complex 3, beta 2 subunit	NM_004644, hCT17693.3	1570032_at, 205676_at	NP_004635.2, EAW62447.1
GeneID:338963	LOC338963	15	83,379,224	83,382,745	3,521	-	2	1_A375_pNL7_minus_lncRNA::1::2118, 2_A375_pNL97_plus_lncRNA::1::2990	4057, 4025	downstream, downstream	1	1	17	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC338963		epididymal protein pseudogene	NR_034139	1563678_a_at	
GeneID:123720	WHAMM	15	83,477,973	83,503,613	25,640	+	1	1_A375_pNL7_minus_lncRNA::1::2119	24171	in gene	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene WHAMM	WHDC1, WHAMM, KIAA1971	WAS protein homolog associated with actin, golgi membranes and microtubules	NM_001080435	228953_at	NP_001073904.1
GeneID:100505647	LOC100505647	15	83,509,834	83,512,196	2,362	-	1	1_A375_pNL7_minus_lncRNA::1::2119	10052	downstream	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100505647		hypothetical LOC100505647	XR_111540, XR_110598, XR_114679		
GeneID:123207	C15orf40	15	83,657,715	83,680,393	22,678	-	2	1_A375_pNL7_minus_lncRNA::1::2120, 2_A375_pNL97_plus_lncRNA::1::2991	-55, -23	upstream, upstream	1	1	99	102	1	2_A375_pNL97_plus_lncRNA::1	102	Gene C15orf40	C15orf40, FLJ33606, MGC29937	chromosome 15 open reading frame 40	NM_144597, NM_001160113, NM_001160114, NM_001160115, NM_001160116, NR_027649, NR_027650, hCT2353799.0, hCT9910.3	1552310_at, 235840_at	NP_653198.2, NP_001153585.1, NP_001153586.1, NP_001153587.1, NP_001153588.1, EAW62432.1, EAW62431.1
GeneID:53339	BTBD1	15	83,685,175	83,736,106	50,931	-	4	1_A375_pNL7_minus_lncRNA::1::2120, 1_A375_pNL7_minus_lncRNA::1::2121, 2_A375_pNL97_plus_lncRNA::1::2991, 2_A375_pNL97_plus_lncRNA::1::2992	55658, 447, 55690, 330	downstream, in gene, downstream, in gene	1	1	56.5	61	2	2_A375_pNL97_plus_lncRNA::1	102	Gene BTBD1	C15orf1, BTBD1, NS5ATP8	BTB (POZ) domain containing 1	NM_025238, NM_001011885, hCT2290882.0, hCT9913.2	217945_at	NP_079514.1, NP_001011885.1, EAW62429.1, EAW62430.1
GeneID:100506874	LOC100506874	15	85,115,423	85,123,412	7,989	+	1	2_A375_pNL97_plus_lncRNA::1::2993	-1247	upstream	0	1	12	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100506874		hypothetical LOC100506874	XR_111542, XR_109211, XR_114682		
GeneID:54993	ZSCAN2	15	85,144,249	85,166,947	22,698	+	1	2_A375_pNL97_plus_lncRNA::1::2994	71	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZSCAN2	ZNF854, ZSCAN2, ZFP29, FLJ20595	zinc finger and SCAN domain containing 2	NM_001007072, NM_181877, NM_017894, hCT1813294.2, hCT2268935.0, hCT2268936.0	220516_at, 231188_at	NP_001007073.1, NP_870992.2, NP_060364.4, EAX01934.1, EAX01935.1, EAX01936.1
GeneID:23478	SEC11A	15	85,212,775	85,259,674	46,899	-	2	1_A375_pNL7_minus_lncRNA::1::2122, 2_A375_pNL97_plus_lncRNA::1::2995	314, 330	in gene, in gene	1	1	24	15	1	1_A375_pNL7_minus_lncRNA::1	24	Gene SEC11A	SPC18, sid2895, 1810012E07Rik, SPCS4A, SEC11A, SEC11L1	SEC11 homolog A (S. cerevisiae)	NM_014300, hCT1961545.1, hCT1965538.1, hCT1965539.1, hCT2358620.0, hCT2358621.0	201290_at, 216274_s_at	NP_055115.1, EAX01953.1, EAX01952.1, EAX01954.1, EAX01955.1, EAX01956.1
GeneID:9640	ZNF592	15	85,291,818	85,349,663	57,845	+	1	2_A375_pNL97_plus_lncRNA::1::2996	-789	upstream	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene ZNF592	SCAR5, KIAA0211, CAMOS, ZNF592, MGC138437, MGC138439	zinc finger protein 592	NM_014630, hCT2268945.0, hCT2268946.0, hCT2268947.0	204473_s_at, 213389_at, 227507_at	NP_055445.2, EAX01959.1, EAX01957.1, EAX01958.1
GeneID:5151	PDE8A	15	85,525,205	85,682,373	157,168	+	3	1_A375_pNL7_minus_lncRNA::1::2123, 2_A375_pNL97_plus_lncRNA::1::2997, 2_A375_pNL97_plus_lncRNA::1::2998	-629, -597, 142283	upstream, upstream, in gene	1	1	19	26.5	2	2_A375_pNL97_plus_lncRNA::1	41	Gene PDE8A	HsT19550, PDE8A, FLJ16150	phosphodiesterase 8A	NM_002605, NM_173454, hCT2268955.0, hCT2268958.0, hCT2268959.0, hCT2358631.0, hCT2358632.0, hCT2358633.0	1552931_a_at, 212521_s_at, 212522_at, 239874_at	NP_002596.1, NP_775656.1, EAX01966.1, EAX01967.1, EAX01969.1, EAX01970.1, EAX01965.1, EAX01968.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Intersecting Features	Intersection Start	Intersection End	[A]	[B]	[C]	[D]	Active Regulatory Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:4916	NTRK2	15	88,419,865	88,799,861	379,973	+	1	2_A375_sh537_dox_lncRNA:1:3000	88622	si gene	0	1	16	20	1	2_A375_sh537_dox_lncRNA:1	20	Gene: NTRK2	NTRK2, gp145(trkC), TRKC	neurotrophic tyrosine kinase, receptor, type 2	NM_001007097.1, NM_002529.2, NM_001012338.1, ACT17758.3, ACT19849791.1, ACT22657118.0, ACT22657119.0, ACT22657120.0, ACT22657121.0	1307795_s_at, 206462_s_at, 215029_at, 215115_s_at, 215333_s_at, 215977_x_at, 216496_at	NP_001007097.1, NP_002521.2, NP_001012338.1, EAX01488.1, EAX01990.1, EAX01993.1, EAX01991.1, EAX01992.1
Gene:ID:2 6558	MRPL46	15	89,002,709	89,010,633	7,924	-	1	2_A375_sh537_dox_lncRNA:1:3000	71	si gene	0	1	17	22	1	2_A375_sh537_dox_lncRNA:1	22	Gene: MRPL46	L8CG22, P23CSL, MRPL46, MGC22762, C15orf41	mitochondrial ribosomal protein L46	NM_022163, ACT19014.2, ACT19859922.1, ACT19859923.1	1557795_s_at, 1557796_at	NP_071496.2, EAX01985.1, EAX01986.1, EAX01987.1, EAX01988.1
Gene:ID:4 4963	MRPS11	15	89,010,664	89,021,495	10,831	+	1	2_A375_sh537_dox_lncRNA:1:3000	-124	upstream	0	1	17	22	1	2_A375_sh537_dox_lncRNA:1	22	Gene: MRPS11	PL23496, PL23512, HCC-2	mitochondrial ribosomal protein S11	NM_022839, NM_176053, ACT19853.3, ACT19855551.1, ACT23586650.0, ACT23586651.0	211693_s_at, 211695_x_at, 211696_s_at	NP_073742.2, NP_788775.1, EAX01989.1, EAX02000.1, EAX02001.1, EAX02002.1
Gene:ID:5 5070	DET1	15	89,033,714	89,059,812	34,186	-	2	1_A375_sh537_dhrun_lncRNA:1:2123, 2_A375_sh537_dox_lncRNA:1:2000	-16, -6	upstream, upstream	1	1	42	39	1	1_A375_sh537_dhrun_lnc RNA:1	42	Gene: DET1	DET1, MGC126197, MGC126197, FLJ31103	de-etiolated homolog 1 (Arabidopsis)	NM_001136074, NR_026643, NM_017996, ACT19901.2, ACT19859160.1, ACT23587106.0, ACT23587107.0	219621_at	NP_001129546.1, NP_060466.2, EAX02003.1, EAX02004.1, EAX02005.1, EAX02006.1
Gene:ID:1 9013223	MIR1179	15	89,151,338	89,151,428	90	+	2	2_A375_sh537_dhrun_lncRNA:1:2127, 2_A375_sh537_dox_lncRNA:1:2000	-2250, -2346	upstream, upstream	1	1	33	39	1	2_A375_sh537_dox_lncRNA:1	39	Gene: MIR1179	MIRN179, hsa-mir-179, MIR1179	microRNA 1179	NR_031593		
Gene:ID:8 07044	MIR7-2	15	89,153,056	89,153,165	109	+	3	2_A375_sh537_dhrun_lncRNA:1:2127, 2_A375_sh537_dox_lncRNA:1:3003, 2_A375_sh537_dox_lncRNA:1:3004	-5965, -6064, 6382	upstream, downstream, downstream	1	1	23.5	26	2	2_A375_sh537_dox_lncRNA:1	34	Gene: MIR7-2	MIR7-2, mir-7-2, hsa-mir-7-2, MIRN7-2	microRNA 7-2	NR_029505		
Gene:ID:9 4762	AEN	15	89,164,327	89,173,512	10,985	+	3	2_A375_sh537_dhrun_lncRNA:1:2126, 2_A375_sh537_dox_lncRNA:1:3006, 2_A375_sh537_dox_lncRNA:1:3005	17409, -79, 17537	downstream, upstream, upstream	1	1	19	23	2	2_A375_sh537_dox_lncRNA:1	28	Gene: AEN	AEN, SI:20:I3.1, FLJ12484, dpf2744, FLJ12562	apoptosis enhancing nuclease	NM_022767, ACT22656817.0, ACT22656818.0, ACT22656960.0	218361_s_at	NP_073604.2, EAX02011.1, EAX02009.1, EAX02010.1
Gene:ID:3 999	ISG20	15	89,182,039	89,198,879	16,840	+	3	2_A375_sh537_dhrun_lncRNA:1:2126, 2_A375_sh537_dox_lncRNA:1:3005, 2_A375_sh537_dox_lncRNA:1:3004	-23, 23, 16573	upstream, si gene, si gene	1	1	19	24.5	2	2_A375_sh537_dox_lncRNA:1	28	Gene: ISG20	ISG20, ISG20, HEM45	interferon stimulated exonuclease gene 20kDa	NM_002201, ACT18143.6, ACT22660210.0, ACT22660222.0, ACT22660223.0	204698_s_at, 33304_at	NP_002192.2, EAX02014.1, EAX02013.1, EAX02015.1, EAX02016.1
Gene:ID:4 240	MPGES	15	89,441,814	89,456,663	14,749	-	1	1_A375_sh537_dhrun_lncRNA:1:2130	67	si gene	1	0	16	10	1	1_A375_sh537_dhrun_lnc RNA:1	16	Gene: MPGES	MVAT, MPGES, SPAG10, BAM, EGLL1, MPG-ES, HLY10655, SED1, CHAC/GDS	elvis tail globule-EGF factor 6 protein	NM_004825, NM_001114614, ACT17756.2, ACT22663650.0, ACT22663710.0, ACT23586230.0, ACT23586231.0	210605_s_at	NP_039219.2, NP_001108056.1, EAX02025.1, EAX02026.1, EAX02028.1, EAX02029.1, EAX02027.1, EAX02030.1
Gene:ID:1 1037	ABHD2	15	89,631,351	89,749,891	114,210	+	4	1_A375_sh537_dhrun_lncRNA:1:2131, 1_A375_sh537_dhrun_lncRNA:1:2132, 2_A375_sh537_dox_lncRNA:1:3007, 2_A375_sh537_dox_lncRNA:1:3006	122, 78551, -149, 78787	si gene, si gene, upstream, si gene	1	1	16	15.5	2	1_A375_sh537_dhrun_lnc RNA:1	20	Gene: ABHD2	ABHD2, PHPS1-2, HSI-2, MGC111112, LABH2, MGC26249	abhydrolase domain containing 2	NM_152924, NM_007011, ACT18922.3, ACT23603420, ACT23603510	209366_at, 221615_at, 226327_at, 226490_at, 60825_at, 67100_at	NP_689739.1, NP_009042.2, EAX02032.1, EAX02034.1, EAX02033.1
Gene:ID:6 217	RLIBP1	15	89,753,098	89,764,922	11,824	-	1	2_A375_sh537_dox_lncRNA:1:3009	-5206	upstream	0	1	12	17	1	2_A375_sh537_dox_lncRNA:1	17	Gene: RLIBP1	CRALBP, RLBP1, MGC3563	retinaldehyde binding protein 1	NM_000326, ACT19763.2	206154_at	NP_000317.1, EAX02038.1
Gene:ID:5 428	POLQ	15	89,859,536	89,876,626	16,480	+	2	1_A375_sh537_dhrun_lncRNA:1:2133, 2_A375_sh537_dox_lncRNA:1:3010	-166, -134	upstream, upstream	1	1	35	36	1	2_A375_sh537_dox_lncRNA:1	36	Gene: POLQ	MTDPSR1, MTDPS8, MDP1, SCAE, POLQ1, MRAS, PEO, POLQ, FLJ27114, SANDO, POLQA	polymerase (DNA directed), gamma	NM_002602, NM_001126131, ACT19802.2, ACT23603270, ACT23603280	202366_at, 207535_s_at, 207536_x_at	NP_002583.1, NP_001116603.1, EAX02045.1, EAX02046.1, EAX02047.1
Gene:ID:1 0350698 3	LOC100396983	15	89,876,902	89,879,284	692	+	2	1_A375_sh537_dhrun_lncRNA:1:2133, 2_A375_sh537_dox_lncRNA:1:3010	-210, -362	upstream, upstream	1	1	35	36	1	2_A375_sh537_dox_lncRNA:1	36	Gene: LOC100396983		hypothetical LOC100396983	XR_109216, XR_109217		
Gene:ID:4 07081	MIR9-2	15	89,911,248	89,911,337	89	+	4	1_A375_sh537_dhrun_lncRNA:1:2134, 1_A375_sh537_dhrun_lncRNA:1:2135, 2_A375_sh537_dox_lncRNA:1:3011, 2_A375_sh537_dox_lncRNA:1:3012	46160, -3419, -6224, -3872	upstream, upstream, upstream, upstream	1	1	22.5	23	2	2_A375_sh537_dox_lncRNA:1	28	Gene: MIR9-2	mir9-2, MIRN9-2, MIR9-2, hsa-mir-9-2	microRNA 9-2	NR_029692		
Gene:ID:9 3351	C15orf62	15	90,116,615	90,171,254	52,426	+	2	1_A375_sh537_dhrun_lncRNA:1:2136, 2_A375_sh537_dox_lncRNA:1:3013	585, -141	si gene, upstream	1	1	23	16	1	1_A375_sh537_dhrun_lnc RNA:1	23	Gene: C15orf62	Tmeta, PL49616, TYCRF, C15orf62, MGC45866	chromosome 15 open reading frame 62	NM_152259, ACT19903.2	235021_at, 232475_at	NP_689772.3, EAX02056.1
Gene:ID:1 0238	AP3S2	15	90,372,631	90,427,817	62,786	-	2	1_A375_sh537_dhrun_lncRNA:1:2137, 2_A375_sh537_dox_lncRNA:1:3014	432, 272	si gene, si gene	1	1	34	30	1	1_A375_sh537_dhrun_lnc RNA:1	34	Gene: AP3S2	AP3S2, sigma3b, AP3S2, PL-03855	adaptor-related protein complex 3, sigma 2 subunit	NM_005829, NR_023391, ACT19384.2, ACT19849923.1, ACT19849924.1, ACT22964310.0, ACT23586144.0	202396_at, 202393_s_at	NP_005820.1, EAX02071.1, EAX02072.1, EAX02073.1, EAX02074.1, EAX02075.1
Gene:ID:1 0350701 0	LOC100370101	15	90,439,764	90,442,755	2,991	-	2	1_A375_sh537_dhrun_lncRNA:1:2137, 2_A375_sh537_dox_lncRNA:1:3016	6371, 5411	downstream, downstream	1	1	34	30	1	1_A375_sh537_dhrun_lnc RNA:1	34	Gene: LOC100370101		hypothetical LOC100370101	XR_109216		
Gene:ID:3 85110	C15orf55	15	90,443,833	90,456,222	12,390	-	2	1_A375_sh537_dhrun_lncRNA:1:2137, 2_A375_sh537_dox_lncRNA:1:3016	16038, 16576	downstream, downstream	1	1	34	30	1	1_A375_sh537_dhrun_lnc RNA:1	34	Gene: C15orf55	MGC61550	chromosome 15 open reading frame 55	NM_182516, ACT19396.2, ACT23586500.0	217588_at, 226666_at, 228709_at	NP_872622.1, EAX02077.1, EAX02076.1
Gene:ID:3 5909	SEMA4B	15	90,736,152	90,772,882	36,730	+	1	2_A375_sh537_dox_lncRNA:1:3017	40516	downstream	0	1	11	16	1	2_A375_sh537_dox_lncRNA:1	16	Gene: SEMA4B	SEMA4B, SEMAC, MGC131531, KIAA1745, SemC	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	NM_020210, NM_198925, ACT19896.4, ACT22665511.1, ACT22665541.1	238725_s_at	NP_064615.2, NP_945119.1, EAX02058.1, EAX02059.1, EAX02060.1
Gene:ID:1 0318	CIB1	15	90,773,477	90,777,279	3,802	-	1	2_A375_sh537_dox_lncRNA:1:3017	511	si gene	0	1	11	16	1	2_A375_sh537_dox_lncRNA:1	16	Gene: CIB1	KIP1, CIBI, SIP2-26, KIP, CIB	calcium and integrin binding 1 (calmyrin)	NM_006384, ACT19459.2, ACT19851551.2, ACT23511176.0, ACT23511179.0	201653_at	NP_006375.2, EAX02065.1, EAX02067.1, EAX02069.1, EAX02090.1
Gene:ID:3 93837	C15orf58	15	90,777,487	90,783,212	5,726	+	1	2_A375_sh537_dox_lncRNA:1:3017	19104	upstream	0	1	11	16	1	2_A375_sh537_dox_lncRNA:1	16	Gene: C15orf58	C15orf58	chromosome 15 open reading frame 58	NM_001013657		NP_001013679.2
Gene:ID:4 79370	TTLL13	15	90,782,764	90,802,212	8,548	+	1	2_A375_sh537_dox_lncRNA:1:3018	16004	downstream	0	1	17	25	1	2_A375_sh537_dox_lncRNA:1	25	Gene: TTLL13	MGC33417, TTLL13, PL45079	tubulin tyrosine ligase-like family, member 13	NM_001029964, ACT22665551.1, ACT23511180.0	1565643_at	NP_001025135.2, EAX02093.1, EAX02094.1
Gene:ID:5 1338	NR3N	15	90,803,693	90,813,643	9,948	+	1	2_A375_sh537_dox_lncRNA:1:3018	-127	upstream	0	1	17	25	1	2_A375_sh537_dox_lncRNA:1	25	Gene: NR3N	DBC62, NGRN	neuron, sends outgrowth associated	NM_001013358, NR_026052, ACT19895.5, ACT19849956.2, ACT19849957.2, ACT22665564.1	207722_s_at, 224281_s_at	NP_001013340.1, EAX02097.1, EAX02098.1
Gene:ID:1 0350702 0	LOC100351 07029	15	90,816,186	90,821,105	4,919	+	1	2_A375_sh537_dox_lncRNA:1:3015	-7418	upstream	0	1	17	25	1	2_A375_sh537_dox_lncRNA:1	25	Gene: LOC100507029		hypothetical LOC100507029	XR_111587, XR_109219, XR_114557		
Gene:ID:2 242	FES	15	91,427,665	91,439,006	11,341	+	1	1_A375_sh537_dhrun_lncRNA:1:2155	16031	downstream	1	0	22	10	1	1_A375_sh537_dhrun_lnc RNA:1	22	Gene: FES	FES, FPS	feline sarcoma oncogene	NM_002005, NM_001143763, NM_001142764, NM_001142765, ACT19847.6, ACT22722.0, ACT22722.1, ACT22722.2, ACT22722.3	205416_at	NP_001998.1, NP_001137255.1, NP_001129236.1, NP_001137237.1, EAX02112.1, EAX02115.1, EAX02114.1, EAX02116.1
Gene:ID:4 122	MANZA2	15	91,447,420	91,463,615	16,195	+	3	1_A375_sh537_dhrun_lncRNA:1:2158, 1_A375_sh537_dhrun_lncRNA:1:2159, 2_A375_sh537_dox_lncRNA:1:3019	-1724, 2639, 26340	upstream, downstream, downstream	1	1	41.5	43	2	2_A375_sh537_dox_lncRNA:1	76	Gene: MANZA2	MANAZX, MANZA2	chromosome, alpha, class 2A, member 2	NM_198122, ACT19344.5, ACT22703280.0, ACT22702440.0, ACT22702460.0, ACT23586160.0, ACT23587.3	230933_s_at, 218699_at	NP_598113.2, EAX02119.1, EAX02120.1, EAX02121.1, EAX02122.1, EAX02123.1, EAX02118.1
Gene:ID:5 5005	UNC45A	15	91,873,410	91,897,323	23,913	+	2	1_A375_sh537_dhrun_lncRNA:1:2159, 2_A375_sh537_dox_lncRNA:1:3019	2366, 2380	si gene, si gene	1	1	31	36	1	1_A375_sh537_dhrun_lnc RNA:1	36	Gene: UNC45A	SNM1-1, IRO03/8700, FLJ10043, GCUNC45, GC-UNC45, UNC45A, SNM1, GCUNC-45	unc-45 homolog A (C. elegans)	NM_001039878, NM_018971, ACT22702600.0, ACT23586150.0, ACT23587.2	207499_s_at, 221705_s_at	NP_001034968.1, NP_061141.2, EAX02127.1, EAX02126.1, EAX02128.1
Gene:ID:3 74659	HDDC3	15	91,974,155	91,979,774	1,619	-	2	1_A375_sh537_dhrun_lncRNA:1:2159, 2_A375_sh537_dox_lncRNA:1:3019	-2, 14	upstream, si gene	1	1	31	36	1	1_A375_sh537_dhrun_lnc RNA:1	36	Gene: HDDC3	MGC45356, MESH1, HDDC3	HD domain containing 3	NM_198527, ACT22703650.0, ACT23722.3	227005_at	NP_940929.1, EAX02125.1, EAX02126.1
Gene:ID:9 555	PRC1	15	91,909,266	91,937,604	28,339	+	2	2_A375_sh537_dox_lncRNA:1:3020, 2_A375_sh537_dox_lncRNA:1:3020	-146, -146	upstream, upstream	1	1	11	16	1	2_A375_sh537_dox_lncRNA:1	20	Gene: PRC1	ASE1, PRC1, MGC3998, MGC1671	protein regulator of cytokinesis 1	NM_003981, NM_199413, NM_199414, ACT19947.5, ACT22703960.0, ACT22703630.0, ACT23586230.0, ACT23586.2	218009_s_at	NP_003972.1, NP_955448.1, NP_955449.1, EAX02133.1, EAX02136.1, EAX02137.1, EAX02138.1, EAX02135.1, EAX02139.1
Gene:ID:1 0350711 5	LOC100351 07118	15	91,939,603	91,951,217	21,614	+	2	1_A375_sh537_dhrun_lncRNA:1:2160, 2_A375_sh537_dox_lncRNA:1:3021	28349, 28349	downstream, downstream	1	1	16	20	1	2_A375_sh537_dox_lncRNA:1	20	Gene: LOC100507115		hypothetical LOC100507115	XR_109221		
Gene:ID:2 5276	VPS33B	15	91,941,774	91,965,833	24,059	-	2	1_A375_sh537_dhrun_lncRNA:1:2160, 2_A375_sh537_dox_lncRNA:1:3021	27551, 27551	downstream, downstream	1	1	16	20	1	2_A375_sh537_dox_lncRNA:1	20	Gene: VPS33B	VPS33B, PL-VPS45	vacuolar protein sorting 33 homolog B (yeast)	NM_018668, ACT23586160.0, ACT23711.2	218415_at, 64611_at	NP_061138.3, EAX02140.1, EAX02139.1
Gene:ID:2 5232	SLCO3A1	15	92,399,035	92,715,665	316,727	+	2	2_A375_sh537_dox_lncRNA:1:3022, 2_A375_sh537_dox_lncRNA:1:3022	-762, 160290	upstream, si gene	0	1	12	14	2	2_A375_sh537_dox_lncRNA:1	14	Gene: SLCO3A1	SLC21A11, OATP3A1, OATPD, SLCO3A1, OATP-D, PL-AM416	solute carrier organic anion transporter family, member 3A1	NM_001145046, NM_013272, ACT19827.2, ACT22659220.0, ACT23429860.0	216562_s_at, 216563_at	NP_001135518.1, NP_037483.2, EAX02166.1, EAX02167.1, EAX02146.1
Gene:ID:1 109	CHD2	15	93,443,551	93,571,237	127,686	+	1	1_A375_sh537_dhrun_lncRNA:1:2143	61155	si gene	1	0	16	11	1	1_A375_sh537_dhrun_lnc RNA:1	16	Gene: CHD2	CHD2, DKFZp434I1315, DKFZp686D01280, FLJ35914, DKFZp761D1727	chromodomain helicase DNA binding protein 2	NM_001042572, NM_001271, ACT22694780.0, ACT22694800.0, ACT22694802.0, ACT22694853.0, ACT22694855.0, ACT22694856.0	1554014_at, 1554015_s_at, 1554061_at, 225077_at, 225551_s_at, 226830_s_at, 226899_at, 230196_s_at, 231334_at, 244544_at	NP_001033037.1, NP_001262.2, EAX02160.1, EAX02161.1, EAX02162.1, EAX02163.1, EAX02164.1
Gene:ID:1 0350675 2	LOC100350675	15	93,512,001	93,570,590	58,589	-	1	2_A375_sh537_dox_lncRNA:1:3029	53470	si gene	0	1	19	24	1	2_A375_sh537_dox_lncRNA:1	24	Gene: LOC100350675		hypothetical protein LOC100350675	NM_001318977	223978_at, 242099_at, 244555_at	NP_001315906.1
Gene:ID:1 9440	LOC100349	15	93,526,846	93,617,659	131,813	+	2	1_A375_sh537_dhrun_lncRNA:1:2165, 2_A375_sh537_dox_lncRNA:1:3030	-1203, 1141	upstream, downstream	1	1	30	29	1	1_A375_sh537_dhrun_lnc RNA:1	30	Gene: LOC91948	MGC125556, MGC125558, MGC125557, MGC125555	hypothetical LOC91948	NR_026172, NR_026173	235017_at	
Gene:ID:1 1947	ARRDC4	15	95,503,833	95,517,066	13,233	+	2	2_A375_sh537_dox_lncRNA:1:3032, 2_A375_sh537_dox_lncRNA:1:3032	-157, -169	upstream, upstream	1	1	25	30	1	2_A375_sh537_dox_lncRNA:1	30	Gene: ARRDC4	ARRDC4, PL-DB045	arrestin domain containing 4	NM_183376, ACT12393.3, ACT22682320.0	225263_at	NP_898222.2, EAX02213.1, EAX02214.1
Gene:ID:3 480	IGF1R	15	99,192,761	99,307,799	314,998	+	2	1_A375_sh537_dhrun_lncRNA:1:2180, 2_A375_sh537_dox_lncRNA:1:3038	249951, 202798	si gene, si gene	1	1	16.5	15.5	2	2_A375_sh537_dox_lncRNA:1	19	Gene: IGF1R	IGFIR, CD221, IGFR_JTK12, MGC16216, MGC142172, IGF1R, MGC142170	insulin-like growth factor 1 receptor	NM_000875, ACT19483.2, ACT22862360.0, ACT22862430.0	203627_at, 203628_s_at, 205681_at, 225331_at, 241556_at	NP_000866.1, EAX02220.1, EAX02221.1, EAX02222.1
Gene:ID:2 5336	SYNM	15	99,645,286	99,673,800	28,514	-	2	1_A375_sh537_dhrun_lncRNA:1:2181, 2_A375_sh537_dox_lncRNA:1:3039	16746, 730	si gene, si gene	1	1	17	15	2	1_A375_sh537_dhrun_lnc RNA:1	21	Gene: SYNM	KIAA0353, DWIN, SYNM, SYN	synemin, intermediate filament protein	NM_145728, NM_015286, ACT18810.2, ACT22720770.0, ACT22720780.0	212730_at, 214304_s_at	NP_663782.2, NP_056101.5, EAX02230.1, EAX02231.1, EAX02232.1
Gene:ID:9 4927	TTC23	15	99,676,526	99,769,615	113,287	+	1	2_A375_sh537_dox_lncRNA:1:3038	-73	upstream	0	1	17	23	1	2_A375_sh537_dox_lncRNA:1	23	Gene: TTC23	FLJ12939, FLJ12572, HCC-5, TTC23	tetratricopeptide repeat domain 23	NM_001040655, NM_023605, NM_001040656, NM_001040657, NM_001040658, NM_001040659, NM_001040660, ACT19411.2, ACT22722220.0, ACT22722221.0, ACT22722228.0, ACT22722229.0, ACT23586210.0	1565521_at, 218656_at, 221734_at, 240716_at	NP_001035745.1, NP_076056.2, NP_001035746.1, NP_001035747.1, NP_001035748.1, NP_001035749.1, NP_001035750.1, EAX02234.1, EAX02235.1, EAX02236.1, EAX02237.1, EAX02238.1, EAX02239.1
Gene:ID:1 03355	LRRC26	15	99,791,652	99,826,498	134,846	+	1	2_A375_sh537_dox_lncRNA:1:3038	-1764	upstream	0	1	17	23	1	2_A375_sh537_dox_lncRNA:1	23	Gene: LRRC26	MGC24976, FLJ45242, LRRC26, FLJ36269	leucine rich repeat containing 26	NM_144986, ACT19405.3, ACT19849883.1, ACT23586220.0, ACT23586240.0, ACT23586.2	1553940_at, 1553941_s_at, 227423_at, 235697_at, 236671_at	NP_653189.2, EAX02241.1, EAX02240.1, EAX02242.1, EAX02243.1, EAX02244.1
Gene:ID:1 79984	ADAMTS1 5	15	100,511,643	100,552,153	370,540	+	1	2_A375_sh537_dox_lncRNA:1:3037	-7929	upstream	0	1	16	15	1	2_A375_sh537_dox_lncRNA:1	16	Gene: ADAMTS15	ADAMTS15, FLJ32766, PL-H1563	ADAM metallopeptidase with thrombospondin type 1 motif, 15	NM_139057, ACT27220.2, ACT22722530.0, ACT22722540.0, ACT22722550.0	1552725_s_at, 1552726_at, 1552727_s_at	NP_620565.2, EAX02264.1, EAX02261.1, EAX02262.1, EAX02263.1
Gene:ID:4 45152	PLA2G6	15	100,564,662	100,690,823	126,161	-	1	2_A375_sh537_dox_lncRNA:1:3037	611	si gene	0	1	16	15	1	2_A375_sh537_dox_lncRNA:1	16	Gene: PLA2G6	PLA2G7, HSD07	phospholipase A2, group VI	NM_003719, NR_026145, NM_001143678, NM_001143679, ACT19859.2, ACT22722560.0, ACT22722570.0	1553624_s_at	NP_003552.1, EAX02266.1, EAX02265.1
Gene:ID:2 20	ALDH1A3	15	101,420,009	101,456,631	36,622	+	2	1_A375_sh537_dhrun_lncRNA:1:3040, 2_A375_sh537_dox_lncRNA:1:3040	11871, 35639	si gene, downstream	1	1	15	20	2	1_A375_sh537_dhrun_lnc RNA:1	21	Gene: ALDH1A3	RALDH3, ALDH6, ALDH1A3, ALDH6	aldehyde dehydrogenase 1 family, member A3	NM_000693, ACT19161.2, ACT19859610.1, ACT23586.2	203180_at	NP_000684.2, EAX02262.1, EAX02261.1, EAX02263.1
Gene:ID:1 0350748 2	LOC100351 07452	15	101,433,926	101,499,468	65,543	-	2	1_A375_sh537_dhrun_lncRNA:1:3040, 2_A375_sh537_dox_lncRNA:1:3040	27555, 640	downstream, si gene	1	1	15	20	2	2_A375_sh537_dox_lncRNA:1	21	Gene: LOC100507452		hypothetical LOC100507452	XR_111593, XR_111596, XR_109233, XR_109232, XR_114800, XR_114998		
Gene:ID:5 7503	UXS1	15	101,498,460	101,610,217	150,837	+	1	2_A375_sh537_dox_lncRNA:1:3040	-612	upstream	0	1	14	19	1	2_A375_sh537_dox_lncRNA:1	19	Gene: UXS1	Rs101, PL27463, PL23119, KIAA1795	kiaa1795 protein	NM_033642, ACT18514.5, ACT22661210.0, ACT22661220.0	219841_s_at	NP_378662.2, EAX02267.1, EAX02268.1, EAX02269.1
Gene:ID:2 3536	CHEY1	15	101,715,926	101,742,137	26,209	-	2	1_A375_sh537_dhrun_lncRNA:1:2182, 2_A375_sh537_dox_lncRNA:1:3041	8, -263	si gene, upstream	1	1	20	19	1	1_A375_sh537_dhrun_lnc RNA:1	20	Gene: CHEY1	CEI31, KIAA0800, CHSY-1, DKFZp434M032, CHSY, FLJ35851, CHSY1	chondroitin sulfate synthase 1	NM_014918, ACT17730.2	203068_at	NP_055733.2, EAX02282.1
Gene:ID:6 627	SNRPA1	15	101,821,715	101,835,660	13,945	-	2	1_A375_sh537_dhrun_lncRNA:1:2184, 2_A375_sh537_dox_lncRNA:1:3042	-4, -26	si gene, upstream	1	1	42	43	1	2_A375_sh537_dox_lncRNA:1	43	Gene: SNRPA1	SNRPA1, Lsm1	small nuclear ribonucleoprotein polypeptide A'	NM_003090, ACT27033.0, ACT22703310.0, ACT22703322.0, ACT22703330.0, ACT23585600.0	206053_s_at, 215722_s_at, 216977_s_at, 241186_at	NP_003081.2, EAX02296.1, EAX02297.1, EAX02298.1, EAX02299.1, EAX02300.1
Gene:ID:5 946	PCSK6	15	101,844,133	102,030,167	186,034	+	2	1_A375_sh537_dhrun_lncRNA:1:2184, 2_A375_sh537_dox_lncRNA:1:3042	18472I, 146999	downstream, downstream	1	1	42	43	1	2_A375_sh537_dox_lncRNA:1	43	Gene: PCSK6	PCSK6, SPC4, PACE4	proprotein convertase subtilisin/kexin type 6	NM_138320, NM_138321, NM_138322, NM_138324, NM_138325, NM_138319, NM_002570, NM_138322, ACT16480.3, ACT19859661.1, ACT19859663.1, ACT22703160.0, ACT22703192.0, ACT22703210.0, ACT22703220.0, ACT22703224.0, ACT22703250.0, ACT22703326.0	1553531_at, 1553541_s_at, 1553542_at, 210563_s_at, 211262_x_at, 242662_at	NP_612183.1, NP_612184.1, NP_612185.1, NP_612186.2, NP_612187.1, NP_612188.2, NP_612189.1, NP_002561.1, EAX02286.1, EAX02287.1, EAX02288.1, EAX02289.1, EAX02290.1, EAX02291.1
Gene:ID:3 0212	TMD02	15	102,162,088	102,192,394	10,345	+	1	2_A375_sh537_dox_lncRNA:1:3044	118	si gene	0	1	15	17	1	2_A375_sh537_dox_lncRNA:1	17	Gene: TMD02	BLP2, TMD02	TMD domain containing 3	NM_015474, NM_025141, ACT17751.3, ACT19859441.1, ACT23586120.0	1552626_a_at, 221702_s_at	NP_056289.2, EAX02310.1, EAX02311.1
Gene:ID:1 0212353	TARSL2	15	102,183,955	102,264,649	70,880	-	1	2_A375_sh537_dox_lncRNA:1:3044	72163	downstream	0	1	15	17	1	2_A375_sh537_dox_lncRNA:1	17	Gene: TARSL2	FLJ35855, TARSL2	threonyl-tRNA synthetase-like 2	NM_152334, ACT15399.4	227911_at, 234618_s_at	NP_689417.2, EAX02316.1
Gene:ID:5 29484	OKAP6	15	102,349,323	102,349,861	538	+	1	2_A375_sh537_dox_lncRNA:1:3046	6373	downstream	0	1	10	17	1	2_A375_sh537_dox_lncRNA:1	17	Gene: OKAP6	OKAP6, OKAP2, ORF5-13	ofd1/cxor1 regulator, family 4, subfamily P, member 6	NM_001005326, ACT15380.1		NP_001005326.1, EAX02318.1
Gene:ID:3 29484	OKAP6	15	102,356,390	102,359,228	838	+	1	2_A375_sh537_dox_lncRNA:1:3046	7094	upstream	0	1	10	17	1	2_A375_sh537_dox_lncRNA:1	17	Gene: OKAP15	OKAP15		NM_001001674, ACT23587.0.1		NP_001001674.1, EAX02320.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:51728	POLR3K	16	96,979	103,632	6,653	-	1	2_A375_pNL97_plus_lncRNA::1::3046	80	in gene	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene POLR3K	hRPC11, RPC11, C11-RNP3, RPC12.5, POLR3K, RPC10, My010, C11	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa	NM_016310, hCT1826347.2	218566_s_at, 222766_at	NP_057394.2, EAW85879.1
GeneID:79622	SNRNP25	16	103,829	107,669	3,840	+	1	2_A375_pNL97_plus_lncRNA::1::3046	-277	upstream	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SNRNP25	FLJ22940, SNRNP25, C16orf33	small nuclear ribonucleoprotein 25kDa (U11/U12)	NM_024571, hCT1783566.2, hCT1956665.1	218493_at	NP_078847.1, EAW85876.1, EAW85877.1
GeneID:64285	RHBDF1	16	108,058	122,629	14,571	-	3	1_A375_pNL7_minus_lncRNA::1::2155, 2_A375_pNL97_plus_lncRNA::1::3046, 2_A375_pNL97_plus_lncRNA::1::3047	4101, 19077, -187	in gene, downstream, upstream	1	1	15.33	20	3	2_A375_pNL97_plus_lncRNA::1	19	Gene RHBDF1	gene-89, RHBDF1, Dist1, hDist1, FLJ22357, C16orf8, gene-90, EGFR-RS, FLJ2235	rhomboid 5 homolog 1 (Drosophila)	NM_022450, hCT1783567.2, hCT1953824.1, hCT2258266.0, hCT2356763.0	218686_s_at, 222711_s_at	NP_071895.3, EAW85876.1, EAW85873.1, EAW85874.1, EAW85875.1
GeneID:4350	MPG	16	127,018	135,845	8,827	+	2	1_A375_pNL7_minus_lncRNA::1::2155, 2_A375_pNL97_plus_lncRNA::1::3047	-8490, -4202	upstream, upstream	1	1	15	20.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene MPG	AAG, Mid1, MDG, anpg, ADPG, PIG16, APNG, CRA36.1, PIG11, MPG	N-methylpurine-DNA glycosylase	NM_001015052, NM_002434, NM_001015054, hCT1953839.2, hCT1966700.1, hCT1966701.1	203686_at	NP_001015052.1, NP_002425.2, NP_001015054.1, EAW85870.1, EAW85871.1, EAW85872.1
GeneID:55692	LUC7L	16	238,970	279,449	40,479	-	2	1_A375_pNL7_minus_lncRNA::1::2156, 2_A375_pNL97_plus_lncRNA::1::3048	57, 73	in gene, in gene	1	1	19	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LUC7L	LUC7L, Luc7, LUC7B1, FLJ10231, LUC7-LIKE, SR+89, hLuc7B1	LUC7-like (S. cerevisiae)	NM_201412, NM_018032, hCT1966703.1, hCT1966706.2, hCT2349137.0, hCT2349138.0, hCT2349139.0, hCT2349140.0, hCT2349141.0, hCT2349142.0, hCT2356655.0, hCT2356656.0, hCT2356657.0	1557066_at, 1557067_s_at, 220143_x_at, 223295_s_at, 223546_x_at	NP_958815.1, NP_060502.1, EAW85853.1, EAW85854.1, EAW85859.1, EAW85860.1, EAW85850.1, EAW85851.1, EAW85852.1, EAW85855.1, EAW85856.1, EAW85857.1, EAW85858.1
GeneID:100129478	LOC100129478	16	280,529	281,471	942	+	2	1_A375_pNL7_minus_lncRNA::1::2156, 2_A375_pNL97_plus_lncRNA::1::3048	-1137, -1153	upstream, upstream	1	1	19	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100129478		hypothetical LOC100129478	XM_001719774, XM_001721251, XM_001723250		XP_001719826.1, XP_001721303.1, XP_001723302.1
GeneID:83986	ITFG3	16	284,801	316,119	31,318	+	2	1_A375_pNL7_minus_lncRNA::1::2156, 2_A375_pNL97_plus_lncRNA::1::3048	-5409, -5425	upstream, upstream	1	1	19	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ITFG3	C16orf9, gs19, ITFG3, FLJ32603, DKFZp761D0211	integrin alpha FG-GAP repeat containing 3	NM_032039, hCT2260382.0, hCT2260384.0, hCT2260385.0, hCT2260387.0, hCT2260388.0, hCT2260389.0	224749_at	NP_114428.1, EAW85844.1, EAW85845.1, EAW85847.1, EAW85848.1, EAW85849.1, EAW85846.1
GeneID:8312	AXIN1	16	337,440	402,464	65,024	-	1	2_A375_pNL97_plus_lncRNA::1::3049	25024	in gene	0	1	15	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene AXIN1	AXIN, AXIN1, MGC52315	axin 1	NM_181050, NM_003502, hCT2258222.0, hCT2258225.1	212849_at	NP_851393.1, NP_003493.1, EAW85835.1, EAW85836.1
GeneID:9727	RAB11FIP3	16	475,668	572,481	96,813	+	4	1_A375_pNL7_minus_lncRNA::1::2157, 1_A375_pNL7_minus_lncRNA::1::2158, 2_A375_pNL97_plus_lncRNA::1::3050, 2_A375_pNL97_plus_lncRNA::1::3051	-420, 101568, 101612, 102972	upstream, downstream, downstream, downstream	1	1	18.67	18.33	3	2_A375_pNL97_plus_lncRNA::1	24	Gene RAB11FIP3	KIAA0665, RAB11FIP3, Rab11-FIP3	RAB11 family interacting protein 3 (class II)	NM_014700, NM_001142272, hCT2260403.0, hCT2260404.0, hCT2260405.0, hCT2260406.0, hCT2260407.0, hCT2260408.0	203933_at, 214999_s_at, 228613_at	NP_055515.1, NP_001135744.1, EAW85805.1, EAW85807.1, EAW85809.1, EAW85810.1, EAW85806.1, EAW85808.1
GeneID:64493	C16orf10	16	576,847	577,407	560	-	3	1_A375_pNL7_minus_lncRNA::1::2158, 2_A375_pNL97_plus_lncRNA::1::3050, 2_A375_pNL97_plus_lncRNA::1::3051	-129, 127, -1233	upstream, in gene, upstream	1	1	17	19.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene C16orf10	NCRNA00235, C16orf10	non-protein coding RNA 235	NR_024121		
GeneID:6650	SOLH	16	577,856	604,636	26,780	+	3	1_A375_pNL7_minus_lncRNA::1::2158, 2_A375_pNL97_plus_lncRNA::1::3050, 2_A375_pNL97_plus_lncRNA::1::3051	-320, -576, 784	upstream, upstream, in gene	1	1	17	19.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene SOLH	CAPN15, SOLH, MGC131491	small optic lobes homolog (Drosophila)	NM_005632, hCT13508.3	204275_at, 230295_at	NP_005623.1, EAW85803.1
GeneID:100507047	LOC100507047	16	588,950	589,861	911	+	1	2_A375_pNL97_plus_lncRNA::1::3051	-10310	upstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100507047		hypothetical LOC100507047	XR_109234		
GeneID:57799	RAB40C	16	639,357	679,273	39,916	+	2	1_A375_pNL7_minus_lncRNA::1::2159, 2_A375_pNL97_plus_lncRNA::1::3052	47075, 47075	downstream, downstream	1	1	43	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene RAB40C	RARL, RASL8C, RAB40C	RAB40C, member RAS oncogene family	NM_021168, NM_001172663, NM_001172664, NM_001172665, NM_001172666, hCT13524.3, hCT1964032.1, hCT1964033.1, hCT1964034.1	1569396_at, 213466_at, 227269_s_at, 227698_s_at	NP_066991.3, NP_001166134.1, NP_001166135.1, NP_001166136.1, NP_001166137.1, EAW85791.1, EAW85792.1, EAW85793.1, EAW85794.1
GeneID:117166	WFIKKN1	16	681,012	684,116	3,104	+	2	1_A375_pNL7_minus_lncRNA::1::2159, 2_A375_pNL97_plus_lncRNA::1::3052	5420, 5420	downstream, downstream	1	1	43	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene WFIKKN1	C16orf12, RJD2, WFIKKN1, WFIKKN, MGC126651, MGC126655	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1	NM_053284, hCT1658065.1	1552811_at	NP_444514.1, EAW85790.1
GeneID:84326	C16orf13	16	684,429	686,347	1,918	-	2	1_A375_pNL7_minus_lncRNA::1::2159, 2_A375_pNL97_plus_lncRNA::1::3052	-65, -65	upstream, upstream	1	1	43	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene C16orf13	C16orf13, JFP2, MGC13114	chromosome 16 open reading frame 13	NM_032366, NM_001040160, NM_001040161, NM_001040162, NM_001040165, hCT13538.3, hCT1956057.1, hCT1956060.1, hCT1966476.1, hCT2356727.0, hCT2356728.0	1554466_a_at, 227378_x_at, 227380_x_at, 228114_x_at, 228118_x_at, 230651_x_at	NP_115742.3, NP_001035250.1, NP_001035251.1, NP_001035252.1, NP_001035255.1, EAW85785.1, EAW85784.1, EAW85786.1, EAW85787.1, EAW85788.1, EAW85789.1
GeneID:100287175	LOC100287175	16	686,817	688,620	1,803	+	2	1_A375_pNL7_minus_lncRNA::1::2159, 2_A375_pNL97_plus_lncRNA::1::3052	-355, -355	upstream, upstream	1	1	43	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene LOC100287175		hypothetical LOC100287175	XR_111626, XR_109236, XR_114925		
GeneID:100130285	LOC100130285	16	691,039	691,735	696	-	2	1_A375_pNL7_minus_lncRNA::1::2159, 2_A375_pNL97_plus_lncRNA::1::3052	5303, 5303	downstream, downstream	1	1	43	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene LOC100130285	FLJ40285	hypothetical LOC100130285	XR_109235, XR_114924		
GeneID:84331	FAM195A	16	691,849	698,474	6,625	+	2	1_A375_pNL7_minus_lncRNA::1::2159, 2_A375_pNL97_plus_lncRNA::1::3052	-5417, -5417	upstream, upstream	1	1	43	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene FAM195A	C16orf14, MGC104301, FAM195A, c349E10.1, MGC15416	family with sequence similarity 195, member A	NM_138418, hCT13534.3, hCT1964039.1, hCT1966470.1, hCT2345138.0	1553715_s_at, 225861_at, 231516_at	NP_612427.2, EAW85781.1, EAW85779.1, EAW85780.1, EAW85782.1
GeneID:197335	WDR90	16	699,363	717,829	18,466	+	1	2_A375_pNL97_plus_lncRNA::1::3053	18621	downstream	0	1	12	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene WDR90	FLJ36483, C16orf16, KIAA1924, C16orf19, WDR90, C16orf15, C16orf18, FLJ44660, C16orf17	WD repeat domain 90	NM_145294	227894_at, 236049_at, 242211_x_at	NP_660337.3
GeneID:100507167	LOC100507167	16	713,960	715,607	1,647	+	1	2_A375_pNL97_plus_lncRNA::1::3053	4024	downstream	0	1	12	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100507167		hypothetical LOC100507167	XR_109238		
GeneID:89941	RHOT2	16	718,133	724,171	6,038	+	2	2_A375_pNL97_plus_lncRNA::1::3053, 2_A375_pNL97_plus_lncRNA::1::3054	-149, 15651	upstream, downstream	0	1	14.5	23	2	2_A375_pNL97_plus_lncRNA::1	24	Gene RHOT2	RHOT2, C16orf39, MIRO-2, RASL, ARHT2	ras homolog gene family, member T2	NM_138769, hCT13533.3, hCT1964036.1, hCT1964037.1, hCT2260451.0, hCT2260454.0, hCT2260457.0	221789_x_at, 222131_x_at, 65770_at	NP_620124.1, EAW85767.1, EAW85763.1, EAW85764.1, EAW85766.1, EAW85768.1, EAW85765.1
GeneID:9028	RHBDL1	16	726,075	728,267	2,192	+	2	2_A375_pNL97_plus_lncRNA::1::3053, 2_A375_pNL97_plus_lncRNA::1::3054	-8091, 7909	upstream, downstream	0	1	14.5	23	2	2_A375_pNL97_plus_lncRNA::1	24	Gene RHBDL1	RRP, RHBDL, RHBDL1	rhomboid, veinlet-like 1 (Drosophila)	NM_003961, hCT13512.2, hCT1964025.1, hCT2260460.0	207383_s_at	NP_003952.1, EAW85762.1, EAW85760.1, EAW85761.1
GeneID:10273	STUB1	16	730,115	732,768	2,653	+	2	2_A375_pNL97_plus_lncRNA::1::3054, 2_A375_pNL97_plus_lncRNA::1::3055	3669, 10237	downstream, downstream	0	1	17	22	2	2_A375_pNL97_plus_lncRNA::1	22	Gene STUB1	UBOX1, SDCCAG7, HSPABP2, STUB1, NY-CO-7, CHIP	STIP1 homology and U-box containing protein 1	NM_005861, hCT13513.2, hCT1966469.1, hCT2356747.0	217934_x_at, 227625_s_at, 233049_x_at	NP_005852.2, EAW85758.1, EAW85756.1, EAW85757.1
GeneID:339123	JMJD8	16	731,667	734,439	2,772	-	2	2_A375_pNL97_plus_lncRNA::1::3054, 2_A375_pNL97_plus_lncRNA::1::3055	455, -5913	in gene, upstream	0	1	17	22	2	2_A375_pNL97_plus_lncRNA::1	22	Gene JMJD8	PP14397, JMJD8, C16orf20	jumonji domain containing 8	NM_001005920, hCT13519.3, hCT1964028.1	224686_at	NP_001005920.2, EAW85755.1, EAW85754.1
GeneID:84219	WDR24	16	734,702	740,400	5,698	-	2	2_A375_pNL97_plus_lncRNA::1::3054, 2_A375_pNL97_plus_lncRNA::1::3055	6416, 46	downstream, in gene	0	1	17	22	2	2_A375_pNL97_plus_lncRNA::1	22	Gene WDR24	WDR24, JFP7, DKFZp434F054, C16orf21	WD repeat domain 24	NM_032259, hCT13529.3, hCT2258300.0, hCT2258301.0	223293_at	NP_115635.1, EAW85753.1, EAW85751.1, EAW85752.1
GeneID:146330	FBXL16	16	742,500	755,825	13,325	-	2	2_A375_pNL97_plus_lncRNA::1::3054, 2_A375_pNL97_plus_lncRNA::1::3055	21841, 15473	downstream, downstream	0	1	17	22	2	2_A375_pNL97_plus_lncRNA::1	22	Gene FBXL16	FLJ33735, c380A1.1, MGC33974, Fbl16, C16orf22, FBXL16	F-box and leucine-rich repeat protein 16	NM_153350, hCT1818672.2, hCT2258297.1	227641_at, 232409_x_at	NP_699181.2, EAW85749.1, EAW85750.1
GeneID:79006	METRN	16	765,173	767,480	2,307	+	1	2_A375_pNL97_plus_lncRNA::1::3056	6016	downstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene METRN	MGC2601, METRN, c380A1.2, C16orf23	meteorin, glial cell differentiation regulator	NM_024042, hCT13522.2, hCT1955263.1	219051_x_at, 232269_x_at	NP_076947.1, EAW85747.1, EAW85748.1
GeneID:65990	FAM173A	16	771,158	772,590	1,432	+	1	2_A375_pNL97_plus_lncRNA::1::3056	31	in gene	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene FAM173A	FAM173A, C16orf24, MGC2494	family with sequence similarity 173, member A	NM_023933, hCT13537.3	219709_x_at	NP_076422.1, EAW85746.1
GeneID:124093	CCDC78	16	772,582	776,473	3,891	-	1	2_A375_pNL97_plus_lncRNA::1::3056	5264	downstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CCDC78	CCDC78, FLJ34512, C16orf25, JFP10	coiled-coil domain containing 78	NM_001031737, hCT1818690.4, hCT1955248.3, hCT1955249.3, hCT2349065.1, hCT2349066.1, hCT2349067.0, hCT2356702.0, hCT2356703.0, hCT2356704.0, hCT2356705.0, hCT2356706.0, hCT2356707.0	236745_at	NP_001026907.2, EAW85741.1, EAW85734.1, EAW85735.1, EAW85739.1, EAW85740.1, EAW85736.1, EAW85737.1, EAW85738.1, EAW85742.1, EAW85743.1, EAW85744.1, EAW85745.1
GeneID:84264	HAGHL	16	776,958	779,715	2,757	+	1	2_A375_pNL97_plus_lncRNA::1::3056	-5769	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene HAGHL	MGC2605, HAGHL	hydroxyacylglutathione hydrolase-like	NM_032304, NM_207112, hCT13518.3, hCT1955259.1, hCT1955260.1, hCT2260466.0, hCT2260472.0, hCT2260473.0, hCT2356652.0, hCT2356653.0, hCT2356654.0	223485_at	NP_115680.1, NP_996995.1, EAW85727.1, EAW85728.1, EAW85731.1, EAW85733.1, EAW85725.1, EAW85726.1, EAW85729.1, EAW85730.1, EAW85732.1
GeneID:64428	NARFL	16	779,767	790,997	11,230	-	2	2_A375_pNL97_plus_lncRNA::1::3056, 2_A375_pNL97_plus_lncRNA::1::3057	19808, -107	downstream, upstream	0	1	18	20.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene NARFL	IOP1, HPRN, NARFL, LET1L, FLJ21988, PRN	nuclear prelamin A recognition factor-like	NM_022493, hCT13526.2, hCT1955271.1, hCT2356681.0	218742_at	NP_071938.1, EAW85722.1, EAW85723.1, EAW85724.1
GeneID:401827	MSLNL	16	819,428	832,926	13,498	-	1	2_A375_pNL97_plus_lncRNA::1::3058	-5794	upstream	0	1	13	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene MSLNL	C16orf37, MPFL, MSLNL	mesothelin-like	NM_001025190, hCT1644917.1, hCT2258286.0, hCT2258287.0		NP_001020361.1, EAW85718.1, EAW85716.1, EAW85717.1
GeneID:113000	RPUSD1	16	834,974	838,383	3,409	-	1	2_A375_pNL97_plus_lncRNA::1::3058	-337	upstream	0	1	13	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene RPUSD1	C16orf40, MGC19600, RLUCL, RPUSD1	RNA pseudouridylate synthase domain containing 1	NM_058192, hCT2258282.0, hCT2258283.0, hCT2258284.0, hCT2258285.0	226078_at	NP_478072.1, EAW85715.1, EAW85712.1, EAW85713.1, EAW85714.1
GeneID:63922	CHTF18	16	838,622	848,074	9,452	+	1	2_A375_pNL97_plus_lncRNA::1::3058	98	in gene	0	1	13	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene CHTF18	C321D2.2, CHTF18, CHL12, RUVBL, C321D2.4, Ctf18, C321D2.3, C16orf41	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	NM_022092, hCT2260482.0, hCT2260484.0, hCT2260485.0, hCT2260487.0, hCT2260488.0, hCT2260489.0, hCT2356731.0, hCT2356732.0	226569_s_at	NP_071375.1, EAW85705.1, EAW85704.1, EAW85706.1, EAW85707.1, EAW85711.1, EAW85708.1, EAW85709.1, EAW85710.1
GeneID:51764	GNG13	16	848,041	850,733	2,692	-	1	2_A375_pNL97_plus_lncRNA::1::3058	12013	downstream	0	1	13	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene GNG13	GNG13, h2-35, G(gamma)13	guanine nucleotide binding protein (G protein), gamma 13	NM_016541, hCT13541.2, hCT2258280.0	220806_x_at	NP_057625.1, EAW85702.1, EAW85703.1
GeneID:64788	LMF1	16	903,634	1,031,318	127,684	-	1	2_A375_pNL97_plus_lncRNA::1::3059	10582	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LMF1	TMEM112A, TMEM112, LMF1, C16orf26, FLJ22302, FLJ12681, HMFN1876, JFP11	lipase maturation factor 1	NM_022773, NR_033645, NR_033646, NR_036442, hCT13527.3, hCT2257824.0, hCT2257825.0, hCT2257827.0, hCT2356684.0	1569048_s_at, 219135_s_at, 219136_s_at, 242533_at, 46142_at	NP_073610.2, EAW85697.1, EAW85696.1, EAW85698.1, EAW85699.1, EAW85700.1
GeneID:7329	UBE2I	16	1,359,180	1,375,390	16,210	+	2	1_A375_pNL7_minus_lncRNA::1::2160, 2_A375_pNL97_plus_lncRNA::1::3060	84, -12	in gene, upstream	1	1	40	33	1	1_A375_pNL7_minus_lncRNA::1	40	Gene UBE2I	UBE2I, UBC9, C358B7.1, P18	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	NM_003345, NM_194259, NM_194260, NM_194261, hCT1955289.1, hCT1955290.1, hCT1967628.1, hCT1967629.1, hCT2265057.0, hCT2356682.0, hCT33970.3	1556086_a_at, 208760_at, 211008_s_at, 213535_s_at, 213536_s_at, 233360_at	NP_003336.1, NP_919235.1, NP_919236.1, NP_919237.1, EAW85673.1, EAW85679.1, EAW85674.1, EAW85675.1, EAW85676.1, EAW85677.1, EAW85678.1
GeneID:8938	BAIAP3	16	1,384,663	1,399,442	14,779	+	1	2_A375_pNL97_plus_lncRNA::1::3061	17145	downstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene BAIAP3	MGC138334, BAP3, BAIAP3, KIAA0734	BAI1-associated protein 3	NM_003933, hCT2264974.0, hCT2356668.0, hCT33972.1	204874_x_at, 216356_x_at	NP_003924.2, EAW85670.1, EAW85671.1, EAW85672.1
GeneID:115939	C16orf42	16	1,399,241	1,401,873	2,632	-	1	2_A375_pNL97_plus_lncRNA::1::3061	65	in gene	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene C16orf42	C16orf42, MGC24381	chromosome 16 open reading frame 42	NM_001001410, hCT33981.3	213104_at, 213105_s_at, 214067_at, 221993_s_at	NP_001001410.1, EAW85669.1
GeneID:84572	GNPTG	16	1,401,900	1,413,352	11,452	+	1	2_A375_pNL97_plus_lncRNA::1::3061	-92	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene GNPTG	RJD9, GNPTG, GNPTAG, C16orf27, LP2537	N-acetylglucosamine-1-phosphate transferase, gamma subunit	NM_032520, hCT1967636.1, hCT2356675.0, hCT33998.2	224887_at	NP_115909.1, EAW85668.1, EAW85666.1, EAW85667.1
GeneID:64718	UNKL	16	1,413,206	1,464,705	51,499	-	2	1_A375_pNL7_minus_lncRNA::1::2161, 2_A375_pNL97_plus_lncRNA::1::3062	-6095, -6031	upstream, upstream	1	1	27	25	1	1_A375_pNL7_minus_lncRNA::1	27	Gene UNKL	ZC3H5L, UNKL, FLJ23360, MGC5179, C16orf28, ZC3HDC5L, FLJ12623, KIAA0734	unkempt homolog (Drosophila)-like	NM_001037125, NM_023076, NM_001193388, NM_001193389, hCT2257871.1, hCT2257872.1, hCT2257875.1	235087_at	NP_001032202.1, NP_075564.3, NP_001180317.1, NP_001180318.1, EAW85659.1, EAW85660.1, EAW85661.1
GeneID:283951	C16orf91	16	1,469,944	1,479,345	9,401	-	2	1_A375_pNL7_minus_lncRNA::1::2161, 2_A375_pNL97_plus_lncRNA::1::3062	8545, 8609	in gene, in gene	1	1	27	25	1	1_A375_pNL7_minus_lncRNA::1	27	Gene C16orf91	gs103, MGC104723, CCSMST1, C16orf91	chromosome 16 open reading frame 91	NM_001010878, hCT1818687.1, hCT1955247.1	225749_at	NP_001010878.1, EAW85657.1, EAW85658.1
GeneID:1186	CLCN7	16	1,494,935	1,525,085	30,150	-	1	2_A375_pNL97_plus_lncRNA::1::3063	77	in gene	0	1	19	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene CLCN7	CLCN7, CLC-7, FLJ39644, OPTA2, FLJ26686, CLC7, OPTB4, FLJ46423	chloride channel 7	NM_001287, NM_001114331, hCT2257862.0, hCT2356676.0, hCT33999.3	209235_at, 221961_at, 38069_at	NP_001278.1, NP_001107803.1, EAW85653.1, EAW85654.1, EAW85655.1
GeneID:57585	CRAMP1L	16	1,664,641	1,727,909	63,268	+	2	1_A375_pNL7_minus_lncRNA::1::2162, 2_A375_pNL97_plus_lncRNA::1::3064	31455, 31519	in gene, in gene	1	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CRAMP1L	HN1L, MGC176736, CRAMP1L, TCE4	Crm, cramped-like (Drosophila)	NM_020825, hCT1955307.1, hCT1955308.1	225172_at, 240930_at, 242355_at	NP_065876.3, EAW85641.1, EAW85640.1
GeneID:90861	HN1L	16	1,728,278	1,752,073	23,795	+	2	1_A375_pNL7_minus_lncRNA::1::2163, 2_A375_pNL97_plus_lncRNA::1::3065	27946, 27706	downstream, downstream	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene HN1L	HN1L, L11, C16orf34, FLJ13092, KIAA1426	hematological and neurological expressed 1-like	NM_144570, hCT2265005.0, hCT2265006.0, hCT2265007.0, hCT2265008.0, hCT2265009.0	212109_at, 212115_at, 216031_x_at	NP_653171.1, EAW85636.1, EAW85634.1, EAW85635.1, EAW85637.1, EAW85638.1
GeneID:23162	MAPK8IP3	16	1,756,221	1,820,318	64,097	+	4	1_A375_pNL7_minus_lncRNA::1::2163, 2_A375_pNL97_plus_lncRNA::1::3065, 2_A375_pNL97_plus_lncRNA::1::3066, 2_A375_pNL97_plus_lncRNA::1::3067	3, -237, 65907, 66851	in gene, upstream, downstream, downstream	1	1	15.67	23	3	2_A375_pNL97_plus_lncRNA::1	30	Gene MAPK8IP3	KIAA1066, MAPK8IP3, SYD2, JIP3, FLJ00027, syd, JSAP1, DKFZp762N1113	mitogen-activated protein kinase 8 interacting protein 3	NM_001040439, NM_015133, hCT2265011.2, hCT2265012.2, hCT2356674.0, hCT33994.3	213177_at, 213178_s_at, 216137_s_at, 216139_s_at, 230162_s_at, 232085_at	NP_001035529.1, NP_055948.2, EAW85630.1, EAW85631.1, EAW85632.1, EAW85633.1
GeneID:4832	NME3	16	1,820,321	1,821,710	1,389	-	2	2_A375_pNL97_plus_lncRNA::1::3066, 2_A375_pNL97_plus_lncRNA::1::3067	-418, -1362	upstream, upstream	0	1	13	25	2	2_A375_pNL97_plus_lncRNA::1	30	Gene NME3	KIAA0516, NME3, NDPK-C, NM23H3, DR-nm23, c371H6.2, NDPKC, NM23-H3	non-metastatic cells 3, protein expressed in	NM_002513, hCT33975.3	204862_s_at	NP_002504.2, EAW85629.1
GeneID:65993	MRPS34	16	1,821,896	1,823,140	1,244	-	3	2_A375_pNL97_plus_lncRNA::1::3066, 2_A375_pNL97_plus_lncRNA::1::3067, 2_A375_pNL97_plus_lncRNA::1::3068	1012, 68, -9788	in gene, in gene, upstream	0	1	13	25.33	3	2_A375_pNL97_plus_lncRNA::1	30	Gene MRPS34	MRP-S12, MRP-S34, MRPS34, MGC2616, MRPS12	mitochondrial ribosomal protein S34	NM_023936, hCT1955306.1, hCT33993.2	218112_at	NP_076425.1, EAW85627.1, EAW85628.1
GeneID:197342	EME2	16	1,823,229	1,826,239	3,010	+	3	2_A375_pNL97_plus_lncRNA::1::3066, 2_A375_pNL97_plus_lncRNA::1::3067, 2_A375_pNL97_plus_lncRNA::1::3068	-1101, -157, 9699	upstream, upstream, downstream	0	1	13	25.33	3	2_A375_pNL97_plus_lncRNA::1	30	Gene EME2	FLJ00151, EME2, gs125, SLX2B	essential meiotic endonuclease 1 homolog 2 (S. pombe)	NM_001010865, hCT34006.3	1556024_at, 1569867_at, 1569868_s_at	NP_001010865.1, EAW85626.1
GeneID:90864	SPSB3	16	1,826,713	1,832,561	5,868	-	3	2_A375_pNL97_plus_lncRNA::1::3066, 2_A375_pNL97_plus_lncRNA::1::3067, 2_A375_pNL97_plus_lncRNA::1::3068	10453, 9509, -347	downstream, downstream, upstream	0	1	13	25.33	3	2_A375_pNL97_plus_lncRNA::1	30	Gene SPSB3	SSB3, C16orf31, SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	NM_080861, hCT1955312.1, hCT1955313.1, hCT1955314.1, hCT1955315.1, hCT2257841.0, hCT2356678.0, hCT34001.2	221769_at, 46256_at	NP_543137.2, EAW85623.1, EAW85618.1, EAW85619.1, EAW85621.1, EAW85624.1, EAW85620.1, EAW85622.1
GeneID:10101	NUBP2	16	1,832,933	1,839,192	6,259	+	2	2_A375_pNL97_plus_lncRNA::1::3067, 2_A375_pNL97_plus_lncRNA::1::3068	-9861, -5	upstream, upstream	0	1	13	26	2	2_A375_pNL97_plus_lncRNA::1	30	Gene NUBP2	NUBP2, CFD1, NUBP1	nucleotide binding protein 2 (MinD homolog, E. coli)	NM_012225, hCT1955291.1, hCT1962610.1, hCT2356719.0, hCT2356720.0, hCT33974.3	218227_at	NP_036357.1, EAW85616.1, EAW85613.1, EAW85614.1, EAW85615.1, EAW85617.1
GeneID:3483	IGFALS	16	1,840,414	1,844,909	4,495	-	1	2_A375_pNL97_plus_lncRNA::1::3068	11981	downstream	0	1	13	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene IGFALS	IGFALS, ALS	insulin-like growth factor binding protein, acid labile subunit	NM_004970, NM_001146006, NR_027389, hCT33973.2	215712_s_at	NP_004961.1, NP_001139478.1, EAW85612.1
GeneID:3029	HAGH	16	1,859,104	1,877,195	18,091	-	2	1_A375_pNL7_minus_lncRNA::1::2164, 2_A375_pNL97_plus_lncRNA::1::3069	-61, -55	upstream, upstream	1	1	18	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene HAGH	GLO2, GLX2, HAGH, HAGH1, GLXII	hydroxyacylglutathione hydrolase	NM_001040427, NM_005326, hCT1955294.0, hCT1955295.0, hCT33976.2	205012_s_at	NP_001035517.1, NP_005317.2, EAW85609.1, EAW85610.1, EAW85611.1
GeneID:81889	FAHD1	16	1,877,225	1,890,208	12,983	+	2	1_A375_pNL7_minus_lncRNA::1::2164, 2_A375_pNL97_plus_lncRNA::1::3069	31, 55	in gene, in gene	1	1	18	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene FAHD1	MGC74876, FAHD1, C16orf36, DKFZp566J2046, YISKL	fumarylacetoacetate hydrolase domain containing 1	NM_001018104, NM_031208, NM_001142398, hCT1641161.2	226767_s_at, 227960_s_at	NP_001018114.1, NP_112485.1, NP_001135870.1, EAW85608.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Internal Transcripts	Internal Dists to Start	Internal Pos.	[A]	[R]	[C]	[G]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:2345826	C16orf72	16	1,853,864	1,922,179	68,165	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2164,2_A275_dN37_dIvs_lncRNA:1:-2699	44823, 44899	downstream, downstream	1	1	16	45	1	2_A275_dN37_dIvs1_lncRNA:1	45	Gene C16orf72	cp129, C16orf72, MGC35212	Chromosome 16 open reading frame 72	NM_152764, NM_001116:3860, NCT16811524, NCT16552:86:1, NCT22285252.1, NCT22672:56.1	237263_at	NP_689777.2, NP_001191022.1, EAW65994.1, EAW65993.1, EAW65906.1, EAW65907.1	
Gene:ID:6123	RPL3L	16	1,994,500	2,004,679	10,180	-	2	1_A275_dN37_dIvs1_lncRNA:1:-2165,2_A275_dN37_dIvs_lncRNA:1:-3679	4825, 4837	upstream, upstream	1	1	26	34	1	2_A275_dN37_dIvs1_lncRNA:1	34	Gene RPL3L	RPL3L	ribosomal protein L3-like	NM_005061, NCT23955.2	206765_at	NP_005053.1, EAW53999.1	
Gene:ID:4716	NDUFB10	16	2,009,517	2,011,976	2,459	+	4	1_A275_dN37_dIvs1_lncRNA:1:-2165,1_A275_dN37_dIvs1_lncRNA:1:-2166,2_A275_dN37_dIvs_lncRNA:1:-3670,2_A275_dN37_dIvs_lncRNA:1:-3671	-13, 12455, 18, 12482	upstream, downstream, 4 gene, downstream	1	1	27	33	2	2_A275_dN37_dIvs_lncRNA:1	34	Gene NDUFB10	PDSW, NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	NM_004546, NCT19676:33.1, NCT33952.2	222112_s_at, 235301_s_at	NP_004529.1, EAW55987.1, EAW55988.1	
Gene:ID:6157	RPS2	16	2,012,262	2,014,827	2,766	+	4	1_A275_dN37_dIvs1_lncRNA:1:-2165,1_A275_dN37_dIvs1_lncRNA:1:-2166,2_A275_dN37_dIvs_lncRNA:1:-3670,2_A275_dN37_dIvs_lncRNA:1:-3671	5322, -7125, 5291, -7172	downstream, downstream, downstream, upstream	1	1	27	33	2	2_A275_dN37_dIvs_lncRNA:1	34	Gene RPS2	MGC117334, MGC117345, MGC102651, S2, RPS2, LLREP3	ribosomal protein S2	NM_002952, NCT23672.0, NCT22823.0, NCT23566:5.0, NCT23566:6.0, NCT23566:7.0	202107_s_at, 212453_s_at, 221798_s_at	NP_002943.2, EAW55985.1, EAW55992.1, EAW55993.1, EAW55994.1, EAW55996.1	
Gene:ID:6974842	SNORA10	16	2,012,335	2,012,467	132	-	4	1_A275_dN37_dIvs1_lncRNA:1:-2165,1_A275_dN37_dIvs1_lncRNA:1:-2166,2_A275_dN37_dIvs_lncRNA:1:-3670,2_A275_dN37_dIvs_lncRNA:1:-3671	2963, -6455, 2831, -6533	downstream, upstream, downstream, upstream	1	1	27	33	2	2_A275_dN37_dIvs_lncRNA:1	34	Gene SNORA10	ACA10, SNORA10	small nucleolar RNA, H/ACA box 10	NR_002327			
Gene:ID:26758	SNORA64	16	2,012,974	2,013,107	133	+	4	1_A275_dN37_dIvs1_lncRNA:1:-2165,1_A275_dN37_dIvs1_lncRNA:1:-2166,2_A275_dN37_dIvs_lncRNA:1:-3670,2_A275_dN37_dIvs_lncRNA:1:-3671	3603, -5545, 3371, -5693	downstream, upstream, downstream, upstream	1	1	27	33	2	2_A275_dN37_dIvs_lncRNA:1	34	Gene SNORA64	SNORA64, U64, RNU64	small nucleolar RNA, H/ACA box 64	NR_002326			
Gene:ID:7353201	SNHG9	16	2,014,997	2,015,505	508	+	4	1_A275_dN37_dIvs1_lncRNA:1:-2165,1_A275_dN37_dIvs1_lncRNA:1:-2166,2_A275_dN37_dIvs_lncRNA:1:-3670,2_A275_dN37_dIvs_lncRNA:1:-3671	4093, 6035, 3861, 7003	upstream, downstream, upstream, downstream	1	1	27	33	2	2_A275_dN37_dIvs_lncRNA:1	34	Gene SNHG9	SNHG9, NCRNA00052, DKFZp686N06141	small nucleolar RNA host gene 9 (non-protein coding)	NR_003142	226565_at		
Gene:ID:677644	SNORA78	16	2,015,165	2,015,311	126	+	4	1_A275_dN37_dIvs1_lncRNA:1:-2165,1_A275_dN37_dIvs1_lncRNA:1:-2166,2_A275_dN37_dIvs_lncRNA:1:-3670,2_A275_dN37_dIvs_lncRNA:1:-3671	4661, 6767, 5629, 6815	upstream, downstream, upstream, downstream	1	1	27	33	2	2_A275_dN37_dIvs_lncRNA:1	34	Gene SNORA78	ACA64, SNORA78	small nucleolar RNA, H/ACA box 78	NR_003020	1555934_at		
Gene:ID:49310	RAPSN	16	2,016,875	2,018,976	2,101	+	4	1_A275_dN37_dIvs1_lncRNA:1:-2165,1_A275_dN37_dIvs1_lncRNA:1:-2166,2_A275_dN37_dIvs_lncRNA:1:-3670,2_A275_dN37_dIvs_lncRNA:1:-3671	5371, 8077, 7339, 8125	upstream, downstream, upstream, downstream	1	1	27	33	2	2_A275_dN37_dIvs_lncRNA:1	34	Gene RAPSN	RAPSN1, MGC129021	ralg triple r protein 151	NM_174903	236569_at	NP_777563.2	
Gene:ID:10907	TBL3	16	2,022,064	2,026,751	6,687	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2166,2_A275_dN37_dIvs_lncRNA:1:-3671,2_A275_dN37_dIvs_lncRNA:1:-3672	-112, -4611696	upstream, downstream, upstream, downstream	1	1	23	27	2	2_A275_dN37_dIvs_lncRNA:1	32	Gene TBL3	GAZD, TBL3	transducin (beta)-like 3	NM_005453, NCT22710152, NCT22710160, NCT22710230, NCT23967:29.0, NCT22852.2	208620_s_at	NP_005444.2, EAW53598.1, EAW55555.1, EAW55557.1, EAW55558.1, EAW55559.1	
Gene:ID:24056	MOXD1	16	2,026,916	2,031,440	2,522	-	3	1_A275_dN37_dIvs1_lncRNA:1:-2166,2_A275_dN37_dIvs_lncRNA:1:-3671,2_A275_dN37_dIvs_lncRNA:1:-3672	6455, 6440, 2320	downstream, downstream, upstream	1	1	23	27	2	2_A275_dN37_dIvs_lncRNA:1	32	Gene MOXD1	MGC20256, PRO1MOXA, EHDP1D5, SNC25, PRO1MOXC, P41NOX, MOXD1, P41NOX-B	NADPH oxidase organizer 1	NM_149663, NM_172167, NM_172165, NCT23966:00.0, NCT23567:00.2, NCT23967:01.0, NCT38555.3	235329_at	NP_833547.1, NP_751927.1, NP_751955.1, EAW55551.1, EAW55552.1, EAW55553.1, EAW55554.1	
Gene:ID:973	GFER	16	2,034,190	2,037,749	3,558	+	1	1_A275_dN37_dIvs1_lncRNA:1:-3672	-280	upstream	0	1	18	22	1	2_A275_dN37_dIvs_lncRNA:1	22	Gene GFER	HEB, GYER, HPO1, HPO2, ALR, HERV1,	growth factor, augmenter of liver regeneration	NM_005262, NCT16552:96.1, NCT22710160.0, NCT22677.2	204439_s_at, 204440_at	NP_005253.2, EAW55576.1, EAW55578.1, EAW55580.1	
Gene:ID:143	SYNGR3	16	2,039,866	2,040,276	4,306	+	1	1_A275_dN37_dIvs1_lncRNA:1:-3672	-6206	upstream	0	1	18	22	1	2_A275_dN37_dIvs_lncRNA:1	22	Gene SYNGR3	MGC20002, SYNGR3, MGC20003	synaptogyrin 3	NM_004209, NCT22710:21.0	203691_at	NP_004200.2, EAW55577.1	
Gene:ID:9350	ZNF598	16	2,037,766	2,039,763	11,998	-	1	1_A275_dN37_dIvs1_lncRNA:1:-3672	-237	upstream	0	1	19	27	1	2_A275_dN37_dIvs_lncRNA:1	27	Gene ZNF598	DKFZp762F135, ZNF598, FLJ00086	zinc finger protein 598	NM_178167, NCT22672:40.0, NCT23672:19.0, NCT22672:19.0, NCT22672:20.0, NCT23567:90.0, NCT23567:30.0	225104_at, 232267_x_at	NP_835461.1, EAW55572.1, EAW55569.1, EAW55570.1, EAW55571.1, EAW55575.1	
Gene:ID:53556	NPW	16	2,069,321	2,070,756	1,435	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2167,2_A275_dN37_dIvs_lncRNA:1:-3673	3567, -8521	downstream, downstream	1	1	19	21	2	2_A275_dN37_dIvs_lncRNA:1	27	Gene NPW	LE, LEC, PPNPW, NPW, PPLE	neuropeptide W	NM_001099356	243110_s_at	NP_001092826.2	
Gene:ID:55351	SLC9A3R2	16	2,079,655	2,089,027	12,139	+	4	1_A275_dN37_dIvs1_lncRNA:1:-2167,1_A275_dN37_dIvs1_lncRNA:1:-2168,2_A275_dN37_dIvs_lncRNA:1:-3674,2_A275_dN37_dIvs_lncRNA:1:-3675	-2460, 29984, 9776, 29556	downstream, downstream, 4 gene, downstream	1	1	17	15.67	3	2_A275_dN37_dIvs1_lncRNA:1	19	Gene SLC9A3R2	NHERF2, SIP-1, TKA-1, NHE3RP2, SLC9A3R2, EBANP, OCT82, SIP1, NHERF-2, MGC104639	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	NM_004765, NM_001130012, NCT19676:21.1, NCT22710:29.0, NCT23967:24.0, NCT32850.2	208630_s_at	NP_004756.2, NP_001124564.1, EAW55562.1, EAW55563.1, EAW55564.1, EAW55565.1, EAW55566.1	
Gene:ID:4312	NTHL1	16	2,089,816	2,097,957	8,091	-	3	1_A275_dN37_dIvs1_lncRNA:1:-2166,2_A275_dN37_dIvs_lncRNA:1:-3674,2_A275_dN37_dIvs_lncRNA:1:-3675	-5, 14293, 123	upstream, downstream, 4 gene	1	1	16	19	2	2_A275_dN37_dIvs_lncRNA:1	17	Gene NTHL1	OCT83, NTHI, NTHL1	eth endonuclease III-like 1 (E. coli)	NM_002528, NCT22672:11.0	209731_at	NP_002519.1, EAW55562.1	
Gene:ID:24912	TSC2	16	2,097,990	2,138,713	40,723	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2168,2_A275_dN37_dIvs_lncRNA:1:-3674,2_A275_dN37_dIvs_lncRNA:1:-3675	-116, -366	upstream, upstream	1	1	17	15	1	1_A275_dN37_dIvs_lncRNA:1	17	Gene TSC2	TSC4, TSC2, PLJ43106, LAM	tuberous sclerosis 2	NM_001077183, NM_000548, NM_001114382, NCT22710:30.0, NCT22710:29.0, NCT22710:31.0, NCT22710:32.0, NCT22710:33.0	210644_at, 213735_s_at	NP_001070651.1, NP_000539.2, NP_001070584.1, EAW55557.1, EAW55558.1, EAW55559.1, EAW55560.1, EAW55561.1	
Gene:ID:5870	RAB26	16	2,190,651	2,204,141	5,490	+	1	1_A275_dN37_dIvs1_lncRNA:1:-3676	4165	at gene	0	1	18	21	1	2_A275_dN37_dIvs_lncRNA:1	31	Gene RAB26	VAR33, RAB26	RAB26, member RAS oncogene family	NM_014353, NCT19552:76.1, NCT19552:80.0, NCT22710:28.0	218552_at, 224660_at	NP_055152.2, EAW55550.1, EAW55551.1, EAW55552.1	
Gene:ID:100507436	LOC100507436	16	2,204,693	2,205,259	566	-	1	1_A275_dN37_dIvs1_lncRNA:1:-3676	2563	downstream	0	1	18	21	1	2_A275_dN37_dIvs_lncRNA:1	31	Gene LOC100507436	hypothetical LOC100507436	hypothetical LOC100507436	XR_111621, XR_109262, XR_114935			
Gene:ID:677857	SNORD60	16	2,205,024	2,205,106	82	-	1	2_A275_dN37_dIvs1_lncRNA:1:-3676	2290	downstream	0	1	16	21	1	2_A275_dN37_dIvs_lncRNA:1	31	Gene SNORD60	U60, RNU60, SNORD60	small nucleolar RNA, C/D box 60	NR_002736			
Gene:ID:9747	TRAIP	16	2,205,799	2,226,130	22,331	+	1	2_A275_dN37_dIvs1_lncRNA:1:-3676	2963	downstream	0	1	16	21	1	2_A275_dN37_dIvs_lncRNA:1	31	Gene TRAIP	RNF119, R-RING, DKFZp586l0621, TRAIP1, MGC7837	TNF receptor-associated factor 7	NM_032271, NCT22710:40.0, NCT22710:50.0, NCT22710:51.0, NCT23:00.2, NCT22710:52.0	223029_s_at, 223030_at, 223031_s_at	NP_115647.2, EAW55586.1, EAW55547.1, EAW55548.1, EAW55549.1	
Gene:ID:7524	CASKIN1	16	2,227,164	2,246,663	19,261	-	2	1_A275_dN37_dIvs1_lncRNA:1:-2169,2_A275_dN37_dIvs_lncRNA:1:-3677	4055, 8071	upstream, upstream	1	1	23	35	1	2_A275_dN37_dIvs_lncRNA:1	43	Gene CASKIN1	CASKIN1, KIAA0534	CASK interacting protein 1	NM_020764, NCT22671:87.0, NCT22671:88.0, NCT22:85.0	1553694_at, 1559727_at_at, 229109_at	NP_065815.1, EAW55565.1, EAW55563.1, EAW55564.1	
Gene:ID:4223	MLST8	16	2,255,650	2,259,416	3,966	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2169,2_A275_dN37_dIvs_lncRNA:1:-3677,2_A275_dN37_dIvs_lncRNA:1:-3678	70, 66, 8942	downstream, ut gene, downstream	1	1	27	28.5	2	2_A275_dN37_dIvs_lncRNA:1	43	Gene MLST8	GBL, Gbl44L, MGC111011, POP3, LST8, WAT1, MLST8	MTOR associated protein, LST8 homolog (S. cerevisiae)	NM_022372, NCT19552:87.1, NCT19552:91.1, NCT19552:92.1, NCT19552:93.1, NCT22:01.2	225507_s_at	NP_071767.2, EAW55537.1, EAW55538.1, EAW55539.1, EAW55540.1, EAW55541.1, EAW55542.1	
Gene:ID:53570	C16orf59	16	2,259,254	2,261,011	1,757	-	3	1_A275_dN37_dIvs1_lncRNA:1:-2169,2_A275_dN37_dIvs_lncRNA:1:-3677,2_A275_dN37_dIvs_lncRNA:1:-3678	5491, 9475, 4281	downstream, downstream, downstream	1	1	27	34.3	2	2_A275_dN37_dIvs_lncRNA:1	43	Gene C16orf59	C16orf59, MGC21630	chromosome 16 open reading frame 59	NM_152363, NCT16598:16.1, NCT22671:82.0	1553990_at	NP_872399.1, EAW55538.1, EAW55539.1	
Gene:ID:5371	PGP	16	2,261,603	2,264,822	3,219	-	3	1_A275_dN37_dIvs1_lncRNA:1:-2169,2_A275_dN37_dIvs_lncRNA:1:-3677,2_A275_dN37_dIvs_lncRNA:1:-3678	6302, 9286, 470	downstream, downstream, upstream	1	1	27	28.5	2	2_A275_dN37_dIvs_lncRNA:1	43	Gene PGP	PGP, MGC4882	phosphoglycolate phosphatase	NM_001042271	218410_s_at, 222622_at	NP_001035530.1	
Gene:ID:977	BAP1	16	2,270,567	2,285,743	12,176	+	1	1_A275_dN37_dIvs1_lncRNA:1:-3679	4175	upstream	0	1	11	14	1	2_A275_dN37_dIvs_lncRNA:1	14	Gene BAP1	BAP, BAP1, MGC99614	BAP1 transcription factor 1	NM_004324, NCT22710:95.1, NCT22710:96.1, NCT22710:97.1	210524_at	NP_004315.2, EAW55531.1, EAW55532.1, EAW55533.1	
Gene:ID:9921	RAPSN	16	2,303,121	2,318,314	15,193	-	2	1_A275_dN37_dIvs1_lncRNA:1:-2170,2_A275_dN37_dIvs_lncRNA:1:-3679	-1160, -46	upstream, downstream	1	1	43	41	1	2_A275_dN37_dIvs_lncRNA:1	43	Gene RAPSN	RNPS1, MGC117332, E5.1	RNA binding protein S1, serine-rich domain	NM_003469, NM_006711, NCT22671:72.0, NCT22671:73.0, NCT22671:74.0, NCT22671:75.0, NCT22671:77.0, NCT22671:78.0, NCT22671:80.0, NCT22671:81.0	200993_s_at, 200994_at, 200995_at, 201629_s_at	NP_003451.1, NP_006702.1, EAW55515.1, EAW55516.1, EAW55517.1, EAW55520.1, EAW55522.1, EAW55518.1, EAW55519.1, EAW55521.1	
Gene:ID:100126328	MIR940	16	2,321,748	2,321,841	93	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2170,2_A275_dN37_dIvs_lncRNA:1:-3679	-3444, 3540	upstream, upstream	1	1	43	41	1	2_A275_dN37_dIvs_lncRNA:1	43	Gene MIR940	hsa-mir-940, MIR940, MIR940	microRNA 940	NR_030639			
Gene:ID:1	ABCA3	16	2,335,879	2,390,747	54,868	-	3	1_A275_dN37_dIvs1_lncRNA:1:-2170,2_A275_dN37_dIvs_lncRNA:1:-3679,2_A275_dN37_dIvs_lncRNA:1:-3680	12443, 12539, 283	downstream, downstream, downstream	1	1	30	26	2	2_A275_dN37_dIvs_lncRNA:1	43	Gene ABCA3	ABC-C, MGC12201, ABCA3, ABC3, EST11683, MGC166976, EMDP3, LBM180	ATP-binding cassette, sub-family A (ABC1), member 3	NM_001089, NCT22291.3	204343_at	NP_001080.2, EAW55515.1	
Gene:ID:9170	CCNF	16	2,479,295	2,506,859	29,564	+	1	1_A275_dN37_dIvs1_lncRNA:1:-3681	28553	downstream	0	1	11	17	1	2_A275_dN37_dIvs_lncRNA:1	17	Gene CCNF	CCNF, FBXO1, FBX1	cyclin F	NM_001761, NCT19552:90.2	204626_at, 208527_s_at	NP_001752.2, EAW55510.1	
Gene:ID:51178	C16orf59	16	2,310,115	2,314,964	4,849	+	2	1_A275_dN37_dIvs1_lncRNA:1:-3681,2_A275_dN37_dIvs_lncRNA:1:-3682	7655, 16109	downstream, downstream	0	1	11.5	19	2	2_A275_dN37_dIvs_lncRNA:1	21	Gene C16orf59	FLJ13009, C16orf59	chromosome 16 open reading frame 59	NM_025105, NCT19552:76.1, NCT19552:77.1, NCT22710:99.0, NCT22:99.0, NCT24217.2	219596_at	NP_079354.2, EAW55505.1, EAW55506.1, EAW55507.1, EAW55508.1, EAW55509.1	
Gene:ID:4917	NTN3	16	2,321,300	2,324,748	3,448	+	2	1_A275_dN37_dIvs1_lncRNA:1:-3681,2_A275_dN37_dIvs_lncRNA:1:-3682	3452, 2724	upstream, downstream	0	1	11.5	19	2	2_A275_dN37_dIvs_lncRNA:1	21	Gene NTN3	NTN3, NTN2L	netrin 3	NM_006181, NCT22:159.2	207640_x_at, 211633_s_at, 211640_x_at	NP_006172.1, EAW55504.1	
Gene:ID:7465	TBC1D24	16	2,325,147	2,353,488	28,342	-	2	1_A275_dN37_dIvs1_lncRNA:1:-3681,2_A275_dN37_dIvs_lncRNA:1:-3682	7699, 423	upstream, upstream	0	1	11.5	19	2	2_A275_dN37_dIvs_lncRNA:1	21	Gene TBC1D24	MGC102685, FIME, TBC1D24, KIAA1117	TBC1 domain family, member 24	NM_020705	227632_at, 227906_at	NP_065756.1	
Gene:ID:5170	PDPX1	16	2,387,970	2,653,168	65,218	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2171,2_A275_dN37_dIvs_lncRNA:1:-3684	65936, 65554	downstream, downstream	1	1	17	24	2	2_A275_dN37_dIvs_lncRNA:1	24	Gene PDPX1	MGC33250, PDPX1, MGC20307, PRO3461, PDK1	3-phosphoinositide dependent protein kinase-1	NM_033260, NM_002612, NCT6568.4	204324_at, 226695_s_at, 53129_at	NP_112558.2, NP_002602.1, EAW55493.1	
Gene:ID:51276	PRO0461	16	2,650,265	2,650,495	231	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2171,2_A275_dN37_dIvs_lncRNA:1:-3684	46, 119	upstream, ut gene	1	1	17	24	1	2_A275_dN37_dIvs_lncRNA:1	24	Gene PRO0461	FLJ39075, MGC24492, MGC121033, MGC126197, LOC51276	hypothetical LOC51276	NR_015441			
Gene:ID:100507327	LOC100507327	16	2,711,150	2,723,440	12,290	-	2	1_A275_dN37_dIvs1_lncRNA:1:-2172,2_A275_dN37_dIvs_lncRNA:1:-3684	46666, 8008	upstream, upstream	1	1	23	30	1	1_A275_dN37_dIvs_lncRNA:1	23	Gene LOC100507327	hypothetical LOC100507327	hypothetical LOC100507327	XR_111633, XR_109243, XR_114936			
Gene:ID:8402	KCTD5	16	2,733,685	2,759,031	26,326	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2172,2_A275_dN37_dIvs_lncRNA:1:-3684	-47, -47	upstream, upstream	1	1	23	30	1	1_A275_dN37_dIvs_lncRNA:1	23	Gene KCTD5	KCTD5, PLD0340	potassium channel tetramerisation domain containing 5	NM_018992, NCT16558:8.1, NCT16558:9.1, NCT22709:60.0	218474_s_at, 222685_s_at, 226827_s_at	NP_061863.1, EAW53490.1, EAW55488.1, EAW55489.1, EAW55491.1	
Gene:ID:100126576	LOC100126576	16	2,767,077	2,852,601	15,524	-	2	1_A275_dN37_dIvs1_lncRNA:1:-2172,2_A275_dN37_dIvs_lncRNA:1:-3685	233, 201	at gene, ut gene	1	1	22	21	1	1_A275_dN37_dIvs_lncRNA:1	22	Gene LOC100126576	FLJ25760, FLJ31501	hypothetical LOC100126576	NM_027274, NR_027275			
Gene:ID:3324	SIRPA2	16	2,802,230	2,821,812	19,583	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2172,2_A275_dN37_dIvs_lncRNA:1:-3685	58, 70	at gene, ut gene	1	1	22	21	1	1_A275_dN37_dIvs_lncRNA:1	22	Gene SIRPA2	DKFZp686O13166, CNP21, DKFZp686Y2421, SIRL200, MGC40286, Owz1, SIRn300_300-KD, KAA0324, SIRPA2, FLJ22350, FLJ11926	transmembrane protein mature 2	NM_018333, NCT19552:00.1, NCT22709:61.0, NCT22709:62.0, NCT22709:63.0, NCT22709:67.0, NCT19641.1	1554671_a_at, 207433_s_at, 208610_s_at, 216629_at	NP_055417.3, EAW54809.1, EAW55477.1, EAW54979.1, EAW54981.1, EAW54978.1, EAW54982.1	
Gene:ID:4063	PRSS22	16	2,902,726	2,908,771	5,442	-	4	1_A275_dN37_dIvs1_lncRNA:1:-2172,1_A275_dN37_dIvs1_lncRNA:1:-2173,1_A275_dN37_dIvs1_lncRNA:1:-3686,2_A275_dN37_dIvs_lncRNA:1:-3687	-3029, 10149, 2125, 10092	upstream, downstream, upstream, downstream	1	1	17	26	2	2_A275_dN37_dIvs_lncRNA:1	26	Gene PRSS22	PRSS22, BSSP-4, MESSP-4, MGC8099, BP001LA	protease, serine, 22	NM_022119, NCT16276:94.2	203627_at	NP_071402.1, EAW54496.1	
Gene:ID:4298	FLYWCH1	16	2,961,980	3,001,209	39,229	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2176,2_A275_dN37_dIvs_lncRNA:1:-3688	-156, -124	upstream, upstream	1	1	22	22	1	2_A275_dN37_dIvs_lncRNA:1	22	Gene FLYWCH1	FLYWCH1	FLYWCH-type zinc finger 1	NM_032356, NM_020312, NCT22955:17.0, NCT22956:20.0, NCT22956:21.0, NCT22956:22.0, NCT16:90.1	223550_s_at, 225932_at, 234106_s_at	NP_115732.2, NP_065980.1, EAW54550.1, EAW54552.1, EAW54553.1, EAW54554.1, EAW54551.1	
Gene:ID:3412	KREMEN1	16	2,014,217	3,016,351	4,164	+	2	1_A275_dN37_dIvs1_lncRNA:1:-2177,2_A275_dN37_dIvs_lncRNA:1:-3688	4662, 4685	downstream, downstream	1	1	26	26	2	2_A275_dN37_dIvs_lncRNA:1	26	Gene KREMEN1	KRM2, MGC16709, MGC10791,	freizle containing transmembrane protein 2	NM_024507, NM_172229, NCT22955:23.0, NCT22956:24.0, NCT23967:30.0, NCT23967:29.0, NCT32:90.2	219952_at	NP_078783.1, NP_757356.1, EAW54483.1, EAW54484.1, EAW54485.1, EAW54486.1, EAW54487.1, EAW54488.1, EAW54489.1, EAW54490.1	
Gene:ID:24222	PAQR4	16	3,019,262	3,023,865	4,143	+	3	1_A275_dN37_dIvs1_lncRNA:1:-2177,2_A275_dN37_dIvs_lncRNA:1:-3688,2_A275_dN37_dIvs_lncRNA:1:-3689	-462, -270, 11298	upstream, upstream, downstream	1	1	17.5	23	2	2_A275_dN37_dIvs_lncRNA:1	26	Gene PAQR4	FLJ30002, PAQR4	progestin and adipoQ receptor family member IV	NM_152381, NCT16177:49.2, NCT22956:29.0, NCT22956:30.0, NCT23967:00.0	212558_at	NP_689594.2, EAW55491.1, EAW55492.1, EAW55493.1, EAW55494.1	
Gene:ID:555	PKMYT1	16	3,022,792	3,030,674	7,882	-	3	1_A275_dN37_dIvs1_lncRNA:1:-2177,2_A275_dN37_dIvs_lncRNA:1:-3688,2_A275_dN37_dIvs_lncRNA:1:-3689	11594, 11462, 166	downstream, downstream, upstream	1	1	17.5	23	2	2_A275_dN37_dIvs_lncRNA:1	26	Gene PKMYT1	PKMYT1, DKFZp547K161Q, MYT1, FLJ20393	protein kinase, membrane associated tyrosine/threonine 1	NM_182687, NM_004203, NCT22955:40.0, NCT16:39.2	206267_s_at	NP_872629.1, NP_004194.2, EAW54839.1, EAW54840.1	
Gene:ID:153576	LOC353576	16	3,039,055	3,044,510	5,456	+	1	2_A275_dN37_dIvs1_lncRNA:1:-3690	5415	upstream	0	1	9	16	1	2_A275_dN37_dIvs_lncRNA:1	16	Gene LOC353576	FLJ46402	hypothetical LOC353576	NR_033991	1564122_at		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9080	CLDN9	16	3,062,457	3,064,506	2,049	+	5	1_A375_pNL7_minus_lncRNA::1::2178, 1_A375_pNL7_minus_lncRNA::1::2179, 1_A375_pNL7_minus_lncRNA::1::2180, 2_A375_pNL97_plus_lncRNA::1::3091, 2_A375_pNL97_plus_lncRNA::1::3092	8455, 9607, 11783, 8903, 11815	downstream, downstream, downstream, downstream, downstream	1	1	21	20	2	1_A375_pNL7_minus_lncRNA::1	21	Gene CLDN9	CLDN9	claudin 9	NM_020982	214635_at	NP_066192.1
GeneID:9074	CLDN6	16	3,064,713	3,068,188	3,475	-	5	1_A375_pNL7_minus_lncRNA::1::2178, 1_A375_pNL7_minus_lncRNA::1::2179, 1_A375_pNL7_minus_lncRNA::1::2180, 2_A375_pNL97_plus_lncRNA::1::3091, 2_A375_pNL97_plus_lncRNA::1::3092	-2724, -3876, -6052, -3172, -6084	upstream, upstream, upstream, upstream, upstream	1	1	21	20	2	1_A375_pNL7_minus_lncRNA::1	21	Gene CLDN6	CLDN6		NM_021195, hCT1640118.2, hCT2257532.0	206474_at, 237810_at	NP_067018.2, EAW85431.1, EAW85432.1
GeneID:51330	TNFRSF12A	16	3,070,313	3,072,384	2,071	+	5	1_A375_pNL7_minus_lncRNA::1::2178, 1_A375_pNL7_minus_lncRNA::1::2179, 1_A375_pNL7_minus_lncRNA::1::2180, 2_A375_pNL97_plus_lncRNA::1::3091, 2_A375_pNL97_plus_lncRNA::1::3092	599, 1751, 3927, 1047, 3959	in gene, in gene, downstream, in gene, downstream	1	1	21	20	2	1_A375_pNL7_minus_lncRNA::1	21	Gene TNFRSF12A	TWEAKR, CD266, TNFRSF12A, FN14	tumor necrosis factor receptor superfamily, member 12A	NM_016639, hCT1955801.1, hCT2258636.0, hCT6652.2	218368_s_at	NP_057723.1, EAW85429.1, EAW85428.1, EAW85430.1
GeneID:54985	HCFC1R1	16	3,072,626	3,074,287	1,661	-	5	1_A375_pNL7_minus_lncRNA::1::2178, 1_A375_pNL7_minus_lncRNA::1::2179, 1_A375_pNL7_minus_lncRNA::1::2180, 2_A375_pNL97_plus_lncRNA::1::3091, 2_A375_pNL97_plus_lncRNA::1::3092	3375, 2223, 47, 2927, 15	downstream, downstream, in gene, downstream, in gene	1	1	21	20	2	1_A375_pNL7_minus_lncRNA::1	21	Gene HCFC1R1	HPIP, MGC70711, HCFC1R1, FLJ20568, MGC99622	host cell factor C1 regulator 1 (XPO1 dependent)	NM_001002017, NM_001002018, NM_017885, hCT1955802.1, hCT2356740.0, hCT2356741.0, hCT6654.3	218537_at, 45714_at	NP_001002017.1, NP_001002018.1, NP_060355.1, EAW85424.1, EAW85426.1, EAW85427.1, EAW85425.1
GeneID:79228	THOC6	16	3,074,032	3,077,756	3,724	+	5	1_A375_pNL7_minus_lncRNA::1::2178, 1_A375_pNL7_minus_lncRNA::1::2179, 1_A375_pNL7_minus_lncRNA::1::2180, 2_A375_pNL97_plus_lncRNA::1::3091, 2_A375_pNL97_plus_lncRNA::1::3092	-3120, -1968, 208, -2672, 240	upstream, upstream, in gene, upstream, in gene	1	1	21	20	2	1_A375_pNL7_minus_lncRNA::1	21	Gene THOC6	MGC2655, THOC6, WDR58, fSAP35	THO complex 6 homolog (Drosophila)	NM_024339, NM_001142350, hCT1958544.1, hCT2356752.0, hCT6655.3	218848_at	NP_077315.2, NP_001135822.1, EAW85421.1, EAW85422.1, EAW85423.1
GeneID:146439	CCDC64B	16	3,077,868	3,085,542	7,674	-	5	1_A375_pNL7_minus_lncRNA::1::2178, 1_A375_pNL7_minus_lncRNA::1::2179, 1_A375_pNL7_minus_lncRNA::1::2180, 2_A375_pNL97_plus_lncRNA::1::3091, 2_A375_pNL97_plus_lncRNA::1::3092	14630, 13478, 11302, 14182, 11270	downstream, downstream, downstream, downstream, downstream	1	1	21	20	2	1_A375_pNL7_minus_lncRNA::1	21	Gene CCDC64B	CCDC64B, BICDR-2, MGC158069	coiled-coil domain containing 64B	NM_001103175	235095_at	NP_001096645.1
GeneID:100128770	LOC100128770	16	3,082,482	3,089,134	6,652	+	2	1_A375_pNL7_minus_lncRNA::1::2180, 2_A375_pNL97_plus_lncRNA::1::3092	-8242, -8210	upstream, upstream	1	1	21	21	1	1_A375_pNL7_minus_lncRNA::1	21	Gene LOC100128770		hypothetical LOC100128770	XR_111634, XR_109245, XR_114908		
GeneID:81854	MGC3771	16	3,160,461	3,165,599	5,138	-	3	1_A375_pNL7_minus_lncRNA::1::2181, 2_A375_pNL97_plus_lncRNA::1::3093, 2_A375_pNL97_plus_lncRNA::1::3094	-9153, 9183, -9137	upstream, downstream, upstream	1	1	18	18	2	1_A375_pNL7_minus_lncRNA::1	23	Gene MGC3771	MGC1912	hypothetical LOC81854	NR_024166, NR_024167	208136_s_at	
GeneID:7755	ZNF205	16	3,162,563	3,170,518	7,955	+	3	1_A375_pNL7_minus_lncRNA::1::2181, 2_A375_pNL97_plus_lncRNA::1::3093, 2_A375_pNL97_plus_lncRNA::1::3094	12189, -6147, 12173	downstream, upstream, downstream	1	1	18	18	2	1_A375_pNL7_minus_lncRNA::1	23	Gene ZNF205	Zfp13, ZNF205, ZNF210	zinc finger protein 205	NM_003456, NM_001042428, hCT2258656.1, hCT2258657.1, hCT2258659.1, hCT2258664.1, hCT2343789.0, hCT2356683.0	206416_at	NP_003447.2, NP_001035893.1, EAW85396.1, EAW85397.1, EAW85399.1, EAW85400.1, EAW85398.1, EAW85401.1
GeneID:100507458	LOC100507458	16	3,181,669	3,184,878	3,209	-	2	1_A375_pNL7_minus_lncRNA::1::2181, 2_A375_pNL97_plus_lncRNA::1::3094	10126, 10142	downstream, downstream	1	1	23	21	1	1_A375_pNL7_minus_lncRNA::1	23	Gene LOC100507458		hypothetical LOC100507458	XR_111636, XR_111637, XR_109246, XR_109247, XR_114909, XR_114910		
GeneID:7760	ZNF213	16	3,185,057	3,192,805	7,748	+	5	1_A375_pNL7_minus_lncRNA::1::2181, 1_A375_pNL7_minus_lncRNA::1::2182, 2_A375_pNL97_plus_lncRNA::1::3094, 2_A375_pNL97_plus_lncRNA::1::3095, 2_A375_pNL97_plus_lncRNA::1::3096	-10305, 15626, -10321, 15903, 17791	upstream, downstream, upstream, downstream, downstream	1	1	20.33	18	3	1_A375_pNL7_minus_lncRNA::1	26	Gene ZNF213	ZKSCAN21, CR53, ZNF213	zinc finger protein 213	NM_004220, NM_001134555, hCT2258662.1, hCT2258663.1	227207_x_at	NP_004211.1, NP_001128127.1, EAW85393.1, EAW85394.1
GeneID:91151	TIGD7	16	3,348,832	3,351,400	2,568	-	2	1_A375_pNL7_minus_lncRNA::1::2184, 2_A375_pNL97_plus_lncRNA::1::3097	-4024, -4168	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene TIGD7	TIGD7, Sancho, FLJ99447, FLJ98002	tigger transposable element derived 7	NM_033208	224365_s_at, 232089_at, 238793_at	NP_149985.2
GeneID:7627	ZNF75A	16	3,355,433	3,368,576	13,143	+	2	1_A375_pNL7_minus_lncRNA::1::2184, 2_A375_pNL97_plus_lncRNA::1::3097	-9, 135	upstream, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ZNF75A	FLJ31529, ZNF75A, MGC59959	zinc finger protein 75a	NM_153028, hCT1964160.1, hCT1964161.1, hCT2356671.0, hCT2356672.0	227670_at, 239204_at, 242633_x_at	NP_694573.1, EAW85377.1, EAW85374.1, EAW85375.1, EAW85376.1
GeneID:4993	OR2C1	16	3,405,889	3,406,924	1,035	+	1	2_A375_pNL97_plus_lncRNA::1::3098	9247	downstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene OR2C1	OLFmf3, MGC163200, OR2C1, OR2C2P, MGC95444	olfactory receptor, family 2, subfamily C, member 1	NM_012368, hCT1647366.1	221460_at	NP_036500.2, EAW85373.1
GeneID:100463285	MTRNR2L4	16	3,421,053	3,422,283	1,230	-	1	2_A375_pNL97_plus_lncRNA::1::3098	7147	downstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MTRNR2L4	HN4, MTRNR2L4	MT-RNR2-like 4	NM_001190476		NP_001177405.1
GeneID:54925	ZNF434	16	3,432,085	3,451,025	18,940	-	2	1_A375_pNL7_minus_lncRNA::1::2185, 2_A375_pNL97_plus_lncRNA::1::3099	-111, -207	upstream, upstream	1	1	27	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene ZNF434	FLJ31901, MGC4179, ZNF434, FLJ20417	zinc finger protein 434	NM_017810, hCT2257554.0, hCT2257557.0, hCT2257558.0, hCT7668.3	218937_at, 220292_at	NP_060280.2, EAW85369.1, EAW85370.1, EAW85371.1, EAW85372.1
GeneID:7727	ZNF174	16	3,451,190	3,459,364	8,174	+	2	1_A375_pNL7_minus_lncRNA::1::2185, 2_A375_pNL97_plus_lncRNA::1::3099	-54, 42	upstream, in gene	1	1	27	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene ZNF174	ZNF174, ZSCAN8	zinc finger protein 174	NM_003450, NM_001032292, hCT7676.2	205252_at, 210290_at, 210291_s_at	NP_003441.1, NP_001027463.1, EAW85368.1
GeneID:79903	NAT15	16	3,493,668	3,536,963	43,295	+	2	1_A375_pNL7_minus_lncRNA::1::2186, 2_A375_pNL97_plus_lncRNA::1::3100	14172, 14220	in gene, in gene	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene NAT15	FLJ14154, NAT15, FLJ11693	N-acetyltransferase 15 (GCN5-related, putative)	NM_001083600, NM_001083601, NM_024845	218661_at, 45526_g_at	NP_001077069.1, NP_001077070.1, NP_079121.1
GeneID:646174	C16orf90	16	3,543,484	3,545,421	1,937	-	2	1_A375_pNL7_minus_lncRNA::1::2187, 2_A375_pNL97_plus_lncRNA::1::3101	-5459, -5395	upstream, upstream	1	1	24	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene C16orf90	C16orf90	chromosome 16 open reading frame 90	NM_001080524		NP_001073993.1
GeneID:23059	CLUAP1	16	3,550,963	3,587,669	36,706	+	2	1_A375_pNL7_minus_lncRNA::1::2187, 2_A375_pNL97_plus_lncRNA::1::3101	-83, -147	upstream, upstream	1	1	24	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CLUAP1	KIAA0643, FAP22, FLJ13297, CLUAP1	clusterin associated protein 1	NM_024793, NM_015041, hCT1957525.1, hCT2258681.0, hCT7681.1	204576_s_at, 204577_s_at	NP_079069.1, NP_055856.1, EAW85352.1, EAW85353.1, EAW85354.1
GeneID:84464	BTBD12	16	3,631,182	3,661,585	30,403	-	1	1_A375_pNL7_minus_lncRNA::1::2188	177	in gene	1	0	17	8	1	1_A375_pNL7_minus_lncRNA::1	17	Gene BTBD12	FANCP, MUS312, KIAA1987, SLX4, BTBD12, KIAA1784	BTB (POZ) domain containing 12	NM_032444, hCT2257548.1, hCT2257549.1, hCT2257550.1	232147_at, 239687_at	NP_115820.2, EAW85345.1, EAW85346.1, EAW85347.1
GeneID:10131	TRAP1	16	3,708,038	3,767,598	59,560	-	1	2_A375_pNL97_plus_lncRNA::1::3102	-82	upstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TRAP1	HSP75, TRAP1, HSP90L	TNF receptor-associated protein 1	NM_016292, hCT2257545.1, hCT2343698.0, hCT2343699.0, hCT2356711.0, hCT7672.4	201391_at, 239622_at	NP_057376.2, EAW85338.1, EAW85339.1, EAW85340.1, EAW85341.1, EAW85342.1
GeneID:1387	CREBBP	16	3,775,055	3,930,121	155,066	-	2	1_A375_pNL7_minus_lncRNA::1::2189, 2_A375_pNL97_plus_lncRNA::1::3102	569, 162441	in gene, downstream	1	1	15	17	2	2_A375_pNL97_plus_lncRNA::1	20	Gene CREBBP	CBP, CREBBP, RSTS, KAT3A	CREB binding protein	NM_001079846, NM_004380, hCT2257541.0, hCT2257543.0, hCT2356708.0, hCT5653.2	202160_at, 211808_s_at, 228177_at, 235858_at	NP_001073315.1, NP_004371.2, EAW85334.1, EAW85335.1, EAW85336.1, EAW85337.1
GeneID:6345	SRL	16	4,239,375	4,292,081	52,706	-	2	1_A375_pNL7_minus_lncRNA::1::2190, 2_A375_pNL97_plus_lncRNA::1::3103	56214, 58353	downstream, downstream	1	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SRL	SRL	sarcalumenin	NM_001098814	235718_at	NP_001092284.1
GeneID:100507501	LOC100507501	16	4,295,826	4,303,790	7,964	-	1	2_A375_pNL97_plus_lncRNA::1::3104	-274	upstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100507501		hypothetical LOC100507501	XR_111629, XR_109248, XR_114911		
GeneID:7023	TFAP4	16	4,307,187	4,323,001	15,814	-	2	2_A375_pNL97_plus_lncRNA::1::3104, 2_A375_pNL97_plus_lncRNA::1::3105	18937, 1129	downstream, in gene	0	1	15.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene TFAP4	AP-4, TFAP4, bHLHc41	transcription factor AP-4 (activating enhancer binding protein 4)	NM_003223, hCT2259305.0, hCT2259306.0, hCT2259307.0	205685_at	NP_003214.1, EAW85320.1, EAW85321.1, EAW85322.1
GeneID:79585	CORO7	16	4,404,543	4,466,639	62,096	-	2	1_A375_pNL7_minus_lncRNA::1::2191, 2_A375_pNL97_plus_lncRNA::1::3106	-9281, -9009	upstream, upstream	1	1	26	23	1	1_A375_pNL7_minus_lncRNA::1	26	Gene CORO7	CORO7, FLJ22021, POD1, FLJ44168, CRN7, 0610011B16Rik	coronin 7	NM_024535	219040_at	NP_078811.3
GeneID:9093	DNAJA3	16	4,475,858	4,506,776	30,918	+	2	1_A375_pNL7_minus_lncRNA::1::2191, 2_A375_pNL97_plus_lncRNA::1::3106	62, -210	in gene, upstream	1	1	26	23	1	1_A375_pNL7_minus_lncRNA::1	26	Gene DNAJA3	FLJ45758, DNAJA3, TID1, hTid-1	DnaJ (Hsp40) homolog, subfamily A, member 3	NM_005147, NM_001135110, hCT2260972.0, hCT2260973.0, hCT6186.2	1554078_s_at, 205963_s_at	NP_005138.3, NP_001128582.1, EAW85303.1, EAW85304.1, EAW85305.1
GeneID:57407	NMRAL1	16	4,511,695	4,524,896	13,201	-	1	1_A375_pNL7_minus_lncRNA::1::2192	-1040	upstream	1	0	14	15	1	1_A375_pNL7_minus_lncRNA::1	14	Gene NMRAL1	FLJ25918, NMRAL1, HSCARG, SDR48A1	NmrA-like family domain containing 1	NM_020677, hCT2259293.0, hCT2259294.0	223206_s_at, 231271_x_at	NP_065728.1, EAW85301.1, EAW85302.1
GeneID:3163	HMOX2	16	4,524,719	4,560,348	35,629	+	1	1_A375_pNL7_minus_lncRNA::1::2192	1217	in gene	1	0	14	15	1	1_A375_pNL7_minus_lncRNA::1	14	Gene HMOX2	HO-2, HMOX2	heme oxygenase (decycling) 2	NM_002134, NM_001127204, NM_001127205, NM_001127206, hCT2260976.0, hCT2260979.0	218120_s_at, 218121_at	NP_002125.3, NP_001120676.1, NP_001120677.1, NP_001120678.1, EAW85299.1, EAW85300.1
GeneID:29965	C16orf5	16	4,560,676	4,588,816	28,140	-	1	2_A375_pNL97_plus_lncRNA::1::3107	48	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene C16orf5	I1, C16orf5, CDIP	chromosome 16 open reading frame 5	NM_013399, hCT1958264.1, hCT1958265.1, hCT2356659.0, hCT2356660.0, hCT2356661.0, hCT2356662.0, hCT2356663.0, hCT6194.3	218183_at, 223960_s_at	NP_037531.2, EAW85294.1, EAW85291.1, EAW85292.1, EAW85296.1, EAW85298.1, EAW85293.1, EAW85295.1, EAW85297.1
GeneID:124402	FAM100A	16	4,658,883	4,664,927	6,044	-	5	1_A375_pNL7_minus_lncRNA::1::2193, 1_A375_pNL7_minus_lncRNA::1::2194, 1_A375_pNL7_minus_lncRNA::1::2195, 2_A375_pNL97_plus_lncRNA::1::3108, 2_A375_pNL97_plus_lncRNA::1::3109	143, -1121, -9697, -65, -9681	in gene, upstream, upstream, upstream, upstream	1	1	18.67	19.33	3	2_A375_pNL97_plus_lncRNA::1	23	Gene FAM100A	PP11303, FAM100A, FLJ31223, FLJ32185	family with sequence similarity 100, member A	NM_145253, hCT2343671.0, hCT2343672.0, hCT2343673.0, hCT2343674.0, hCT6206.3	1556975_at, 1556976_x_at, 225874_at	NP_660296.1, EAW85287.1, EAW85284.1, EAW85285.1, EAW85286.1, EAW85288.1
GeneID:23295	MGRN1	16	4,674,826	4,740,975	66,149	+	5	1_A375_pNL7_minus_lncRNA::1::2193, 1_A375_pNL7_minus_lncRNA::1::2194, 1_A375_pNL7_minus_lncRNA::1::2195, 2_A375_pNL97_plus_lncRNA::1::3108, 2_A375_pNL97_plus_lncRNA::1::3109	-10042, -8778, -202, -9834, -218	upstream, upstream, upstream, upstream, upstream	1	1	18.67	19.33	3	2_A375_pNL97_plus_lncRNA::1	23	Gene MGRN1	KIAA0544, MGRN1, RNF156	mahogunin, ring finger 1	NM_015246, NM_001142289, NM_001142290, NM_001142291, hCT2260984.0, hCT2260985.0, hCT2356666.0, hCT6198.2	212576_at	NP_056061.1, NP_001135761.1, NP_001135762.1, NP_001135763.1, EAW85279.1, EAW85280.1, EAW85281.1, EAW85282.1
GeneID:100507570	LOC100507570	16	4,684,326	4,690,624	6,298	-	2	1_A375_pNL7_minus_lncRNA::1::2195, 2_A375_pNL97_plus_lncRNA::1::3109	16000, 16016	downstream, downstream	1	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100507570		hypothetical LOC100507570	XR_111630, XR_109249, XR_114912		
GeneID:124401	ANKS3	16	4,746,513	4,784,163	37,650	-	1	2_A375_pNL97_plus_lncRNA::1::3110	3	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ANKS3	KIAA1977, FLJ32767, FLJ32345, ANKS3	ankyrin repeat and sterile alpha motif domain containing 3	NM_133450, hCT2259279.1, hCT2259280.1, hCT2343669.0, hCT2343670.0, hCT2356692.0, hCT2356693.0, hCT6204.3	227303_at	NP_597707.1, EAW85275.1, EAW85269.1, EAW85270.1, EAW85273.1, EAW85274.1, EAW85271.1, EAW85272.1
GeneID:146562	C16orf71	16	4,784,289	4,799,397	15,108	+	1	2_A375_pNL97_plus_lncRNA::1::3110	-129	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C16orf71	DKFZp686H2240, FLJ43261, C16orf71	chromosome 16 open reading frame 71	NM_139170, hCT2356694.0, hCT6205.2	222089_s_at	NP_631909.2, EAW85268.1, EAW85267.1
GeneID:26048	ZNF500	16	4,800,815	4,817,166	16,351	-	2	1_A375_pNL7_minus_lncRNA::1::2196, 2_A375_pNL97_plus_lncRNA::1::3111	14, -114	in gene, upstream	1	1	26	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ZNF500	ZKSCAN18, ZNF500	zinc finger protein 500	NM_021646, hCT6191.3	213639_s_at, 213641_at, 41113_at	NP_067678.1, EAW85266.1
GeneID:124404	12-Sep	16	4,827,670	4,838,399	10,729	-	1	2_A375_pNL97_plus_lncRNA::1::3111	21119	downstream	0	1	26	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene SEPT12	SEPT12, FLJ25410	septin 12	NM_144605, NM_001154458, hCT2356658.0, hCT6192.2	230947_at	NP_653206.2, NP_001147930.1, EAW85264.1, EAW85265.1
GeneID:29855	UBN1	16	4,897,912	4,932,363	34,451	+	2	1_A375_pNL7_minus_lncRNA::1::2197, 2_A375_pNL97_plus_lncRNA::1::3112	12104, 12136	in gene, in gene	1	1	18	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene UBN1	VT4, VT, UBN1	ubinuclein 1	NM_016936, NM_001079514, hCT2356751.0, hCT6189.3	207253_s_at, 209088_s_at	NP_058632.2, NP_001072982.1, EAW85249.1, EAW85250.1
GeneID:5493	PPL	16	4,932,508	4,987,136	54,628	-	3	1_A375_pNL7_minus_lncRNA::1::2198, 2_A375_pNL97_plus_lncRNA::1::3113, 2_A375_pNL97_plus_lncRNA::1::3114	-8704, -6208, -7776	upstream, upstream, upstream	1	1	17.67	13.33	3	1_A375_pNL7_minus_lncRNA::1	21	Gene PPL	KIAA0568, PPL, MGC134872	periplakin	NM_002705, hCT6199.3	203407_at	NP_002696.3, EAW85248.1
GeneID:25880	TMEM186	16	8,889,037	8,891,505	2,468	-	1	2_A375_pNL97_plus_lncRNA::1::3118	-79	upstream	0	1	18	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene TMEM186	C16orf51, TMEM186, DKFZp564K2062	transmembrane protein 186	NM_015421, hCT2256054.0, hCT5661.3	204676_at	NP_056236.2, EAW85205.1, EAW85206.1
GeneID:5373	PMM2	16	8,891,670	8,943,194	51,524	+	1	2_A375_pNL97_plus_lncRNA::1::3118	-86	upstream	0	1	18	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene PMM2	PMM2, CDG1a, PMM 2, CDG1, CDGS	phosphomannomutase 2	NM_000303, hCT1955058.2, hCT2356722.0, hCT2356723.0, hCT6423.3	203201_at	NP_000294.1, EAW85203.1, EAW85200.1, EAW85201.1, EAW85202.1
GeneID:7874	USP7	16	8,985,951	9,057,341	71,390	-	2	1_A375_pNL7_minus_lncRNA::1::2202, 2_A375_pNL97_plus_lncRNA::1::3119	31453, 31533	in gene, in gene	1	1	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene USP7	TEF1, USP7, HAUSP	ubiquitin specific peptidase 7 (herpes virus-associated)	NM_003470, hCT1955061.1, hCT2356746.0	201498_at, 201499_s_at, 222032_s_at, 230967_s_at	NP_003461.2, EAW85194.1, EAW85195.1
GeneID:4682	NUBP1	16	10,837,698	10,863,208	25,510	+	1	2_A375_pNL97_plus_lncRNA::1::3120	46	in gene	0	1	16	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene NUBP1	MGC130052, MGC130053, NBP, NBP1, NUBP1, MGC117406	nucleotide binding protein 1 (MinD homolog, E. coli)	NM_002484, hCT2257488.0	203978_at	NP_002475.2, EAW85178.1
GeneID:4261	CIITA	16	10,971,055	11,018,840	47,785	+	3	1_A375_pNL7_minus_lncRNA::1::2203, 1_A375_pNL7_minus_lncRNA::1::2204, 2_A375_pNL97_plus_lncRNA::1::3121	1420, 18129, 1937	in gene, in gene, in gene	1	1	16	17	2	2_A375_pNL97_plus_lncRNA::1	20	Gene CIITA	C2TA, CIITAIV, CIITA, MHC2TA, NLRA	class II, major histocompatibility complex, transactivator	NM_000246, hCT1954361.1, hCT2257491.0, hCT2257492.0, hCT2257494.0, hCT2257495.0, hCT2257497.0, hCT6089.3	205101_at, 210925_at, 211884_s_at	NP_000237.2, EAW85168.1, EAW85169.1, EAW85170.1, EAW85173.1, EAW85174.1, EAW85171.1, EAW85172.1
GeneID:28955	DEXI	16	11,022,748	11,036,257	13,509	-	2	1_A375_pNL7_minus_lncRNA::1::2205, 2_A375_pNL97_plus_lncRNA::1::3122	-2079, -2047	upstream, upstream	1	1	26	22	1	1_A375_pNL7_minus_lncRNA::1	26	Gene DEXI	MYLE, DEXI	Dexi homolog (mouse)	NM_014015, hCT1826701.1, hCT2356689.0	203733_at	NP_054734.2, EAW85167.1, EAW85166.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100505564	LOC100505564	16	11,034,576	11,036,878	2,302	+	2	1_A375_pNL7_minus_lncRNA::1::2205, 2_A375_pNL97_plus_lncRNA::1::3122	3760, 3728	downstream, downstream	1	1	26	22	1	1_A375_pNL7_minus_lncRNA::1	26	Gene LOC100505564		hypothetical protein LOC100505564	XM_003119652, XM_003118688, XM_003120834		XP_003119700.1, XP_003118736.1, XP_003120882.1
GeneID:23274	CLEC16A	16	11,038,345	11,276,046	237,701	+	2	1_A375_pNL7_minus_lncRNA::1::2205, 2_A375_pNL97_plus_lncRNA::1::3122	-9, -41	upstream, upstream	1	1	26	22	1	1_A375_pNL7_minus_lncRNA::1	26	Gene CLEC16A	MGC111457, KIAA0350, CLEC16A, Gop-1	C-type lectin domain family 16, member A	NM_015226, hCT1826707.3, hCT2356730.0	212786_at, 231221_at	NP_056041.1, EAW85165.1, EAW85164.1
GeneID:2935	GSPT1	16	11,961,985	12,010,519	48,534	-	2	1_A375_pNL7_minus_lncRNA::1::2207, 2_A375_pNL97_plus_lncRNA::1::3124	615, 503	in gene, in gene	1	1	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene GSPT1	GSPT1, eRF3a, FLJ39067, ETF3A, 551G9.2, FLJ38048, GST1	G1 to S phase transition 1	NM_002094, NM_001130007, NM_001130006, hCT2257905.0, hCT2356758.0, hCT5929.2	201912_s_at, 215438_x_at, 240452_at	NP_002085.2, NP_001123479.1, NP_001123478.1, EAW85130.1, EAW85131.1, EAW85132.1
GeneID:608	TNFRSF17	16	12,058,964	12,061,925	2,961	+	1	2_A375_pNL97_plus_lncRNA::1::3125	11372	downstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TNFRSF17	TNFRSF17, BCM, BCMA, CD269	tumor necrosis factor receptor superfamily, member 17	NM_001192, hCT5644.2	206641_at	NP_001183.2, EAW85129.1
GeneID:84127	RUNDC2A	16	12,070,602	12,147,141	76,539	+	1	2_A375_pNL97_plus_lncRNA::1::3125	-266	upstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene RUNDC2A	FLJ12363, RUNDC2A	RUN domain containing 2A	NM_032167	232485_at	NP_115543.2
GeneID:55313	CPPED1	16	12,753,656	12,897,744	144,088	-	3	1_A375_pNL7_minus_lncRNA::1::2208, 2_A375_pNL97_plus_lncRNA::1::3126, 2_A375_pNL97_plus_lncRNA::1::3127	368, 141904, -64	in gene, in gene, upstream	1	1	22.5	27.5	2	2_A375_pNL97_plus_lncRNA::1	33	Gene CPPED1	CPPED1, CSTP1, FLJ11151	calcineurin-like phosphoesterase domain containing 1	NM_018340, NM_001099455, hCT2255192.0, hCT28470.2	218610_s_at, 222686_s_at	NP_060810.2, NP_001092925.1, EAW85121.1, EAW85122.1
GeneID:729993	SHISA9	16	12,995,477	13,334,273	338,796	+	2	1_A375_pNL7_minus_lncRNA::1::2209, 2_A375_pNL97_plus_lncRNA::1::3128	135211, 208939	in gene, in gene	1	1	15	16	2	2_A375_pNL97_plus_lncRNA::1	21	Gene SHISA9	CKAMP44, FLJ10015, FLJ58277, DKFZp686E24206, SHISA9, FLJ37653, DKFZp686D24206, FLJ99079, FLJ99234	shisa homolog 9 (Xenopus laevis)	NM_001145205, NM_001145204		NP_001138677.2, NP_001138676.2
GeneID:2072	ERCC4	16	14,014,014	14,046,205	32,191	+	2	1_A375_pNL7_minus_lncRNA::1::2211, 2_A375_pNL97_plus_lncRNA::1::3130	37762, 37581	downstream, downstream	1	1	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ERCC4	ERCC11, ERCC4, RAD1, XPF	excision repair cross-complementing rodent repair deficiency, complementation group 4	NM_005236, hCT2256018.0, hCT28471.3	210158_at	NP_005227.1, EAW85118.1, EAW85117.1
GeneID:57496	MKL2	16	14,165,196	14,360,630	195,434	+	1	2_A375_pNL97_plus_lncRNA::1::3131	-156	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MKL2	NPD001, DKFZp686J1745, FLJ31823, MRTF-B, FLJ45623, MKL2	MKL/myocardin-like 2	NM_014048, hCT2256020.1, hCT2256021.1, hCT2256023.1, hCT2256024.1	1558777_at, 1558778_s_at, 1570202_a_at, 218259_at	NP_054767.3, EAW85112.1, EAW85113.1, EAW85114.1, EAW85115.1
GeneID:5073	PARN	16	14,529,558	14,724,124	194,566	-	3	1_A375_pNL7_minus_lncRNA::1::2214, 1_A375_pNL7_minus_lncRNA::1::2215, 2_A375_pNL97_plus_lncRNA::1::3133	118956, -2564, 128508	in gene, upstream, in gene	1	1	15	18	3	2_A375_pNL97_plus_lncRNA::1	27	Gene PARN	DAN, PARN	poly(A)-specific ribonuclease (deadenylation nuclease)	NM_002582, NM_001134477, hCT1954378.1, hCT2255250.0	203905_at	NP_002573.1, NP_001127949.1, EAW85110.1, EAW85111.1
GeneID:51283	BFAR	16	14,726,668	14,763,093	36,425	+	1	1_A375_pNL7_minus_lncRNA::1::2215	20	in gene	1	0	18	16	1	1_A375_pNL7_minus_lncRNA::1	18	Gene BFAR	BFAR, RNF47, BAR	bifunctional apoptosis regulator	NM_016561, hCT1962249.1, hCT1967264.1, hCT1967265.1, hCT2256033.0, hCT28551.3	218056_at	NP_057645.1, EAW85106.1, EAW85105.1, EAW85107.1, EAW85108.1, EAW85109.1
GeneID:9284	NPIP	16	15,031,300	15,045,931	14,631	+	2	1_A375_pNL7_minus_lncRNA::1::2216, 2_A375_pNL97_plus_lncRNA::1::3134	21596, 21708	downstream, downstream	1	1	24	16	1	1_A375_pNL7_minus_lncRNA::1	24	Gene NPIP	FLJ44848, NPIP, FLJ42525	nuclear pore complex interacting protein	NM_006985, hCT2356312.0, hCT23796.3	240377_at	NP_008916.2, EAW63296.1, EAW63295.1
GeneID:255027	MPV17L	16	15,489,611	15,503,543	13,932	+	2	1_A375_pNL7_minus_lncRNA::1::2217, 2_A375_pNL97_plus_lncRNA::1::3135	245, 245	in gene, in gene	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MPV17L	MLPH1, MGC70356, MLPH2, MPV17L1, FLJ39599, MPV17L	MPV17 mitochondrial membrane protein-like	NM_001128423, NM_173803, hCT1825714.3, hCT2352789.0	1559167_x_at	NP_001121895.1, NP_776164.2, EAW53914.1, EAW53915.1
GeneID:89927	C16orf45	16	15,528,325	15,682,116	153,791	+	3	1_A375_pNL7_minus_lncRNA::1::2218, 2_A375_pNL97_plus_lncRNA::1::3136, 2_A375_pNL97_plus_lncRNA::1::3137	156635, 27, 156603	downstream, in gene, downstream	1	1	17	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene C16orf45	FLJ32618, C16orf45	chromosome 16 open reading frame 45	NM_033201, NM_001142469, hCT1825712.1, hCT1957363.1, hCT2290431.0	1565641_at, 212736_at	NP_149978.1, NP_001135941.1, EAW53916.1, EAW53917.1, EAW53918.1
GeneID:9665	KIAA0430	16	15,688,226	15,737,023	48,797	-	3	1_A375_pNL7_minus_lncRNA::1::2218, 1_A375_pNL7_minus_lncRNA::1::2219, 2_A375_pNL97_plus_lncRNA::1::3137	52063, 43263, 52095	downstream, in gene, downstream	1	1	17.5	17	2	2_A375_pNL97_plus_lncRNA::1	21	Gene KIAA0430	A-362G6.1, LKAP, KIAA0430	KIAA0430	NM_001184998, NM_001184999, NM_014647, hCT2293075.0, hCT2293077.0, hCT2293079.0, hCT2293084.0	1556697_a_at, 202386_s_at	NP_001171927.1, NP_001171928.1, NP_055462.2, EAW53920.1, EAW53921.1, EAW53923.1, EAW53922.1
GeneID:54820	NDE1	16	15,737,124	15,820,210	83,086	+	1	2_A375_pNL97_plus_lncRNA::1::3138	29580	in gene	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene NDE1	FLJ20101, NDE1, HOM-TES-87, NUDE, NUDE1	nudE nuclear distribution gene E homolog 1 (A. nidulans)	NM_017668, NM_001143979, hCT1955642.1, hCT2290438.0, hCT30141.3	218414_s_at, 222625_s_at, 227249_at, 227843_at, 230219_at	NP_060138.1, NP_001137451.1, EAW53931.1, EAW53932.1, EAW53933.1
GeneID:123811	C16orf63	16	15,959,577	15,982,447	22,870	-	1	1_A375_pNL7_minus_lncRNA::1::2220	79	in gene	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene C16orf63	FOR20, DKFZp686N1651, C16orf63, PHSECRG2, FOPNL, FLJ31153	FGFR1OP N-terminal like	NM_144600, hCT1967452.1, hCT30142.3	225087_at, 225088_at	NP_653201.1, EAW53935.1, EAW53934.1
GeneID:368	ABCC6	16	16,243,422	16,317,328	73,906	-	1	2_A375_pNL97_plus_lncRNA::1::3139	-9040	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ABCC6	ARA, MLP1, ABCC6, EST349056, MOATE, URG7, MRP6, PXE, ABC34, PXE1	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	NM_001079528, NM_001171, hCT1971674.1, hCT2293052.0, hCT30137.3	208480_s_at, 214033_at, 215559_at	NP_001072996.1, NP_001162.4, EAW53950.1, EAW53951.1, EAW53952.1
GeneID:408050	NOMO3	16	16,326,389	16,388,667	62,278	+	1	2_A375_pNL97_plus_lncRNA::1::3139	-21	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene NOMO3	Nomo, NOMO3	NODAL modulator 3	NM_001004067		NP_001004067.1
GeneID:64131	XYLT1	16	17,196,181	17,564,738	368,557	-	9	1_A375_pNL7_minus_lncRNA::1::2223, 1_A375_pNL7_minus_lncRNA::1::2224, 1_A375_pNL7_minus_lncRNA::1::2225, 1_A375_pNL7_minus_lncRNA::1::2226, 2_A375_pNL97_plus_lncRNA::1::3141, 2_A375_pNL97_plus_lncRNA::1::3142, 2_A375_pNL97_plus_lncRNA::1::3143, 2_A375_pNL97_plus_lncRNA::1::3144, 2_A375_pNL97_plus_lncRNA::1::3145	331922, 320754, 292514, 65378, 331810, 320770, 304578, 292482, 73234	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	24.5	28.83	6	2_A375_pNL97_plus_lncRNA::1	57	Gene XYLT1	XYLTI, XT-I, XT1, PXYLT1, XYLT1, XTI	xylosyltransferase I	NM_022166, hCT10623.4	213725_x_at, 232574_at	NP_071449.1, EAW50949.1
GeneID:100506171	LOC100506171	16	17,228,361	17,232,589	4,228	+	2	1_A375_pNL7_minus_lncRNA::1::2223, 2_A375_pNL97_plus_lncRNA::1::3141	4455, 4567	downstream, downstream	1	1	25	22	1	1_A375_pNL7_minus_lncRNA::1	25	Gene LOC100506171		hypothetical LOC100506171	XR_109263		
GeneID:6210	RPS15A	16	18,794,277	18,801,656	7,379	-	2	1_A375_pNL7_minus_lncRNA::1::2228, 2_A375_pNL97_plus_lncRNA::1::3146	-104, -88	upstream, upstream	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene RPS15A	S15a, FLJ27457, MGC111208, RPS15A	ribosomal protein S15a	NM_001019, NM_001030009	200781_s_at, 229882_at	NP_001010.2, NP_001025180.1
GeneID:23204	ARL6IP1	16	18,802,991	18,812,857	9,866	-	4	1_A375_pNL7_minus_lncRNA::1::2228, 1_A375_pNL7_minus_lncRNA::1::2229, 2_A375_pNL97_plus_lncRNA::1::3148, 2_A375_pNL97_plus_lncRNA::1::3149	11097, -279, 11113, -279	downstream, upstream, downstream, upstream	1	1	46.5	53.5	2	2_A375_pNL97_plus_lncRNA::1	65	Gene ARL6IP1	ARMER, AIP1, KIAA0069, ARL6IP, ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	NM_015161	211935_at	NP_055976.1
GeneID:23049	SMG1	16	18,816,175	18,937,726	121,551	-	2	1_A375_pNL7_minus_lncRNA::1::2229, 2_A375_pNL97_plus_lncRNA::1::3149	124590, 124590	downstream, downstream	1	1	70	65	1	2_A375_pNL97_plus_lncRNA::1	65	Gene SMG1	KIAA0421, ATX, LIP, SMG1, 61E3.4	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	NM_015092	214984_at, 244766_at	NP_055907.3
GeneID:79905	TMC7	16	18,995,256	19,075,264	80,008	+	2	1_A375_pNL7_minus_lncRNA::1::2230, 2_A375_pNL97_plus_lncRNA::1::3150	83668, 83668	downstream, downstream	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TMC7	TMC7, DKFZp761O2274, FLJ21240	transmembrane channel-like 7	NM_024847, NM_001160364, hCT2272652.0, hCT2272654.0	220021_at	NP_079123.3, NP_001153836.1, EAW50266.1, EAW50267.1
GeneID:10229	COQ7	16	19,078,917	19,091,417	12,500	+	2	1_A375_pNL7_minus_lncRNA::1::2230, 2_A375_pNL97_plus_lncRNA::1::3150	27, 27	in gene, in gene	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene COQ7	COQ7, CLK1, CAT5, CLK-1	coenzyme Q7 homolog, ubiquinone (yeast)	NM_001190983, NM_016138, hCT1781213.3, hCT1962862.1, hCT2352379.0, hCT2352380.0	209745_at, 209746_s_at, 210820_x_at	NP_001177912.1, NP_057222.2, EAW50268.1, EAW50269.1, EAW50270.1, EAW50271.1
GeneID:162073	ITPRIPL2	16	19,125,254	19,132,952	7,698	+	2	2_A375_pNL97_plus_lncRNA::1::3151, 2_A375_pNL97_plus_lncRNA::1::3152	-6, 890	upstream, in gene	0	1	12.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene ITPRIPL2	MGC126800, MGC126798, FLJ22994, ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	NM_001034841, NR_028028, hCT1841995.2	1568619_s_at, 227792_at, 227954_at, 227956_at, 228074_at	NP_001030013.1, EAW50272.1
GeneID:51760	SYT17	16	19,179,638	19,278,554	98,916	+	1	2_A375_pNL97_plus_lncRNA::1::3153	-438	upstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SYT17	SYT17		NM_016524, hCT2272665.0, hCT29262.3	205613_at, 229053_at	NP_057608.2, EAW50273.1, EAW50274.1
GeneID:728276	LOC728276	16	19,297,105	19,315,716	18,611	+	2	1_A375_pNL7_minus_lncRNA::1::2231, 2_A375_pNL97_plus_lncRNA::1::3154	21999, 21999	downstream, downstream	1	1	43	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene LOC728276		hypothetical LOC728276	NR_024436		
GeneID:51573	GDE1	16	19,513,015	19,533,450	20,435	-	1	2_A375_pNL97_plus_lncRNA::1::3155	-1734	upstream	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene GDE1	GDE1, MIR16, 363E6.2	glycerophosphodiester phosphodiesterase 1	NM_016641, hCT1950869.2, hCT1969306.1, hCT2352378.0, hCT29258.3	202593_s_at, 226214_at	NP_057725.1, EAW50286.1, EAW50283.1, EAW50284.1, EAW50285.1
GeneID:9738	CP110	16	19,535,179	19,564,730	29,551	+	2	2_A375_pNL97_plus_lncRNA::1::3155, 2_A375_pNL97_plus_lncRNA::1::3156	5, 31637	in gene, downstream	0	1	13	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene CP110	Cep110, KIAA0419, DKFZp781G1416	CP110 protein	NM_014711, hCT1950868.1, hCT28467.2	1569353_at, 204662_at	NP_055526.3, EAW50287.1, EAW50288.1
GeneID:57020	C16orf62	16	19,567,040	19,712,444	145,404	+	1	2_A375_pNL97_plus_lncRNA::1::3156	-224	upstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C16orf62	DKFZp434B0212, MGC16824, DKFZp313M0539, FLJ21040, C16orf62	chromosome 16 open reading frame 62	NM_020314, hCT2272694.0, hCT2352376.0, hCT2352377.0	1556557_at, 203173_s_at	NP_064710.3, EAW50290.1, EAW50289.1, EAW50291.1
GeneID:400506	C16orf88	16	19,717,674	19,729,492	11,818	-	1	2_A375_pNL97_plus_lncRNA::1::3157	20	in gene	0	1	10	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene C16orf88	FAM191A, C16orf88, 101F10.1	chromosome 16 open reading frame 88	NM_001012991	213235_at, 213237_at	NP_001013009.2
GeneID:124152	IQCK	16	19,727,778	19,868,861	141,083	+	1	2_A375_pNL97_plus_lncRNA::1::3157	1694	in gene	0	1	10	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene IQCK	FLJ36575, IQCK, MGC35048, FLJ20115	IQ motif containing K	NM_153208, hCT1781215.2, hCT1950851.1, hCT1950852.1, hCT1950853.1, hCT1962863.1, hCT2272704.0, hCT2352375.0	213392_at, 215130_s_at, 215131_at, 216135_at	NP_694940.1, EAW50300.1, EAW50295.1, EAW50296.1, EAW50298.1, EAW50301.1, EAW50297.1, EAW50299.1
GeneID:55623	THUMPD1	16	20,744,986	20,753,199	8,213	-	1	2_A375_pNL97_plus_lncRNA::1::3158	111	in gene	0	1	20	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene THUMPD1	DKFZp686C1054, THUMPD1	THUMP domain containing 1	NM_017736, hCT1950985.1, hCT2270495.0, hCT29489.3	206555_s_at, 213025_at	NP_060206.2, EAW66830.1, EAW66831.1, EAW66832.1
GeneID:6296	ACSM3	16	20,775,312	20,808,479	33,167	+	2	1_A375_pNL7_minus_lncRNA::1::2232, 2_A375_pNL97_plus_lncRNA::1::3159	42384, 43168	downstream, downstream	1	1	28	18	1	1_A375_pNL7_minus_lncRNA::1	28	Gene ACSM3	ACSM3, SA, SAH	acyl-CoA synthetase medium-chain family member 3	NM_005622, NM_202000, hCT1950981.1, hCT28474.3	205942_s_at, 210377_at	NP_005613.2, NP_973729.1, EAW66834.1, EAW66835.1
GeneID:112479	ERI2	16	20,791,515	20,817,795	26,280	-	2	1_A375_pNL7_minus_lncRNA::1::2232, 2_A375_pNL97_plus_lncRNA::1::3159	99, -685	in gene, upstream	1	1	28	18	1	1_A375_pNL7_minus_lncRNA::1	28	Gene ERI2	EXOD1, KIAA1504, MGC16943, ERI2	ERI1 exoribonuclease family member 2	NM_080663, NM_001142725, hCT1963963.1, hCT29486.3	213365_at, 240603_s_at, 240604_at	NP_542394.2, NP_001136197.1, EAW66836.1, EAW66837.1
GeneID:81691	LOC81691	16	20,817,767	20,860,990	43,223	+	2	1_A375_pNL7_minus_lncRNA::1::2232, 2_A375_pNL97_plus_lncRNA::1::3159	-71, 713	upstream, in gene	1	1	28	18	1	1_A375_pNL7_minus_lncRNA::1	28	Gene LOC81691	DKFZp434J0315	exonuclease NEF-sp	NM_030941, NM_001144924, hCT2270309.0, hCT2354343.0, hCT2354344.0, hCT29491.3	208107_s_at, 215215_s_at	NP_112203.2, NP_001138396.1, EAW66838.1, EAW66839.1, EAW66840.1, EAW66841.1
GeneID:123879	DCUN1D3	16	20,869,396	20,911,561	42,165	-	1	2_A375_pNL97_plus_lncRNA::1::3160	-743	upstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene DCUN1D3	FLJ41725, DKFZp686G23203, DKFZp686O0290, MGC48972, DCUN1D3, 44M2.4	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)	NM_173475, hCT29484.4	239646_at	NP_775746.1, EAW66842.1
GeneID:100506372	LOC100506372	16	20,898,840	20,908,249	9,409	+	1	2_A375_pNL97_plus_lncRNA::1::3160	13464	downstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100506372		hypothetical LOC100506372	XR_111647, XR_109264, XR_114980		
GeneID:57149	LYRM1	16	20,911,557	20,936,328	24,771	+	1	2_A375_pNL97_plus_lncRNA::1::3160	747	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LYRM1	A211C6.1, LYRM1	LYR motif containing 1	NM_020424, NM_001128301, NM_001128302, hCT1950986.1, hCT1950987.1, hCT1950988.1, hCT2270312.0, hCT2270314.0, hCT2270316.0, hCT29490.3	203697_at	NP_065157.1, NP_001121773.1, NP_001121774.1, EAW66843.1, EAW66844.1, EAW66846.1, EAW66845.1, EAW66847.1, EAW66848.1, EAW66849.1
GeneID:51108	METTL9	16	21,610,856	21,668,792	57,936	+	2	1_A375_pNL7_minus_lncRNA::1::2234, 2_A375_pNL97_plus_lncRNA::1::3162	-88, -8	upstream, upstream	1	1	18	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene METTL9	METTL9, DREV, PAP1, FLJ21912, DREV1, CGI-81	methyltransferase like 9	NM_001077180, NM_016025, hCT12722.2, hCT1963588.1, hCT1963589.1, hCT1963590.1, hCT1963591.1, hCT2256823.0	217868_s_at, 222447_at, 226220_at, 230395_at	NP_001070648.1, NP_057109.3, EAW50517.1, EAW50520.1, EAW50521.1, EAW50522.1, EAW50518.1, EAW50519.1
GeneID:146183	OTOA	16	21,689,835	21,772,050	82,215	+	1	2_A375_pNL97_plus_lncRNA::1::3163	6613	in gene	0	1	8	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene OTOA	FLJ32773, CT108, MGC39813, MGC157747, OTOA, DFNB22	otoancorin	NM_144672, NM_170664, NM_001161683, hCT2349217.0, hCT2349323.0	1553432_s_at	NP_653273.3, NP_733764.1, NP_001155155.1, EAW50524.1, EAW50525.1
GeneID:7385	UQCRC2	16	21,964,609	21,994,668	30,059	+	2	1_A375_pNL7_minus_lncRNA::1::2235, 2_A375_pNL97_plus_lncRNA::1::3164	-145, 31	upstream, in gene	1	1	21	21	1	1_A375_pNL7_minus_lncRNA::1	21	Gene UQCRC2	QCR2, UQCRC2, UQCR2	ubiquinol-cytochrome c reductase core protein II	NM_003366, hCT2343383.0, hCT2343384.0, hCT9687.3	200883_at, 212600_s_at, 241755_at	NP_003357.2, EAW50590.1, EAW50591.1, EAW50592.1
GeneID:255762	C16orf65	16	21,995,186	22,012,431	17,245	-	2	1_A375_pNL7_minus_lncRNA::1::2236, 2_A375_pNL97_plus_lncRNA::1::3165	-6481, -6433	upstream, upstream	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C16orf65	PDZD9, C16orf65, MGC50721	PDZ domain containing 9	NM_173806, NR_033694, hCT1644251.3	241572_at	NP_776167.2, EAW50593.1
GeneID:730094	C16orf52	16	22,019,456	22,095,975	76,519	+	2	1_A375_pNL7_minus_lncRNA::1::2236, 2_A375_pNL97_plus_lncRNA::1::3165	-544, -592	upstream, upstream	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C16orf52	MGC26782, C16orf52	chromosome 16 open reading frame 52	NM_001164579		NP_001158051.1
GeneID:100288072	LOC100288072	16	22,176,904	22,201,714	24,810	+	1	2_A375_pNL97_plus_lncRNA::1::3166	24568	in gene	0	1	12	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100288072		short chain dehydrogenase/reductase family 42E, member 1-like	XM_002343452, XM_003119658, XM_003120848		XP_002343493.1, XP_003119706.1, XP_003120896.1
GeneID:29904	EEF2K	16	22,217,592	22,300,066	82,474	+	4	1_A375_pNL7_minus_lncRNA::1::2237, 1_A375_pNL7_minus_lncRNA::1::2238, 2_A375_pNL97_plus_lncRNA::1::3167, 2_A375_pNL97_plus_lncRNA::1::3168	787, 91192, 872, 91050	in gene, downstream, in gene, downstream	1	1	19	26.5	2	2_A375_pNL97_plus_lncRNA::1	31	Gene EEF2K	EEF2K, HSU93850, MGC45041, eEF-2K	eukaryotic elongation factor-2 kinase	NM_013302, hCT2272800.0	225545_at, 225546_at	NP_037434.1, EAW50604.1
GeneID:55718	POLR3E	16	22,308,741	22,345,346	36,605	+	2	1_A375_pNL7_minus_lncRNA::1::2238, 2_A375_pNL97_plus_lncRNA::1::3168	43, -69	in gene, upstream	1	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene POLR3E	POLR3E, SIN, RPC5	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	NM_018119, hCT2272803.0, hCT2272804.0, hCT2272806.0, hCT9690.2	218016_s_at, 222490_at, 233458_at, 233459_at	NP_060589.1, EAW50606.1, EAW50605.1, EAW50607.1, EAW50608.1
GeneID:9956	HS3ST2	16	22,825,860	22,927,659	101,799	+	1	2_A375_pNL97_plus_lncRNA::1::3171	74396	in gene	0	1	7	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene HS3ST2	30ST2, HS3ST2, 3OST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	NM_006043, hCT13052.3	219697_at	NP_006034.1, EAW55840.1
GeneID:6340	SCNN1G	16	23,194,040	23,228,200	34,160	+	1	2_A375_pNL97_plus_lncRNA::1::3174	-7960	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SCNN1G	BESC3, ENaCg, ENaCgamma, PHA1, SCNN1G, SCNEG	sodium channel, nonvoltage-gated 1, gamma	NM_001039, hCT1686430.3, hCT2265379.0	207295_at, 241436_at	NP_001030.2, EAW55837.1, EAW55838.1
GeneID:124454	EARS2	16	23,533,334	23,568,696	35,362	-	2	1_A375_pNL7_minus_lncRNA::1::2242, 2_A375_pNL97_plus_lncRNA::1::3175	-40, -104	upstream, upstream	1	1	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene EARS2	MSE1, EARS2, KIAA1970	glutamyl-tRNA synthetase 2, mitochondrial (putative)	NM_001083614, NR_003501, hCT14970.3, hCT2262565.0, hCT2262567.0, hCT2352971.0, hCT2352972.0	1555437_at, 1563796_s_at, 225993_at, 227374_at	NP_001077083.1, EAW55825.1, EAW55821.1, EAW55822.1, EAW55823.1, EAW55824.1
GeneID:56061	UBFD1	16	23,568,862	23,585,710	16,848	+	2	1_A375_pNL7_minus_lncRNA::1::2242, 2_A375_pNL97_plus_lncRNA::1::3175	-126, -62	upstream, upstream	1	1	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene UBFD1	UBFD1, FLJ42145, FLJ38870, UBPH	ubiquitin family domain containing 1	NM_019116, hCT14972.4, hCT2265389.0, hCT2265391.0	205687_at, 224878_at	NP_061989.2, EAW55818.1, EAW55817.1, EAW55819.1
GeneID:4706	NDUFAB1	16	23,592,335	23,607,639	15,304	-	2	1_A375_pNL7_minus_lncRNA::1::2243, 2_A375_pNL97_plus_lncRNA::1::3176	-57, -73	upstream, upstream	1	1	122	114	1	1_A375_pNL7_minus_lncRNA::1	122	Gene NDUFAB1	MGC65095, ACP, NDUFAB1, FASN2A, SDAP	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	NM_005003, hCT14968.4, hCT1969271.1	202077_at	NP_004994.1, EAW55816.1, EAW55815.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:79728	PALB2	16	23,614,483	23,652,678	38,195	-	4	1_A375_pNL7_minus_lncRNA::1::2243, 1_A375_pNL7_minus_lncRNA::1::2244, 2_A375_pNL97_plus_lncRNA::1::3176, 2_A375_pNL97_plus_lncRNA::1::3177	44982, 6, 44966, -26	downstream, in gene, downstream, upstream	1	1	81	81	2	1_A375_pNL7_minus_lncRNA::1	122	Gene PALB2	DKFZp667I166, FANCN, DKFZp686E1054, PALB2, FLJ21816, PNCA3	partner and localizer of BRCA2	NM_024675, hCT2262551.1, hCT2262552.1, hCT2352964.0	219530_at	NP_078951.2, EAW55813.1, EAW55811.1, EAW55812.1
GeneID:84516	DCTN5	16	23,652,807	23,681,182	28,375	+	4	1_A375_pNL7_minus_lncRNA::1::2244, 1_A375_pNL7_minus_lncRNA::1::2245, 2_A375_pNL97_plus_lncRNA::1::3177, 2_A375_pNL97_plus_lncRNA::1::3178	-135, 37337, -103, 37305	upstream, downstream, upstream, downstream	1	1	36	53.5	2	2_A375_pNL97_plus_lncRNA::1	59	Gene DCTN5	MGC3248, p25, DCTN5	dynactin 5 (p25)	NM_032486, hCT1950276.2, hCT2265394.1, hCT2265396.1	209231_s_at, 209232_s_at	NP_115875.1, EAW55809.1, EAW55808.1, EAW55810.1
GeneID:100506587	LOC100506587	16	23,681,332	23,684,448	3,116	+	2	1_A375_pNL7_minus_lncRNA::1::2245, 2_A375_pNL97_plus_lncRNA::1::3178	8812, 8780	downstream, downstream	1	1	32	59	1	2_A375_pNL97_plus_lncRNA::1	59	Gene LOC100506587		hypothetical LOC100506587	XR_109270		
GeneID:5347	PLK1	16	23,690,201	23,701,688	11,487	+	2	1_A375_pNL7_minus_lncRNA::1::2245, 2_A375_pNL97_plus_lncRNA::1::3178	-57, -89	upstream, upstream	1	1	32	59	1	2_A375_pNL97_plus_lncRNA::1	59	Gene PLK1	PLK1, STPK13, PLK	polo-like kinase 1 (Drosophila)	NM_005030, hCT14966.4, hCT1813165.2, hCT2350543.0, hCT2350544.0	202240_at	NP_005021.2, EAW55803.1, EAW55804.1, EAW55805.1, EAW55806.1
GeneID:5579	PRKCB	16	23,847,300	24,231,932	384,632	+	2	2_A375_pNL97_plus_lncRNA::1::3179, 2_A375_pNL97_plus_lncRNA::1::3180	138508, 342732	in gene, in gene	0	1	14.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene PRKCB	PRKCB1, PRKCB2, PKC-beta, MGC41878, PKCB, PRKCB	protein kinase C, beta	NM_002738, NM_212535, hCT1950274.1, hCT2261593.0, hCT2261594.0, hCT2352970.0	207957_s_at, 209685_s_at, 227817_at, 227824_at, 228795_at, 230437_s_at	NP_002729.2, NP_997700.1, EAW55796.1, EAW55797.1, EAW55798.1, EAW55799.1
GeneID:10368	CACNG3	16	24,266,876	24,373,737	106,861	+	2	1_A375_pNL7_minus_lncRNA::1::2246, 2_A375_pNL97_plus_lncRNA::1::3181	500, 420	in gene, in gene	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene CACNG3	Cacng2, CACNG3	calcium channel, voltage-dependent, gamma subunit 3	NM_006539, hCT14227.3, hCT2261596.0	206384_at	NP_006530.1, EAW55794.1, EAW55793.1
GeneID:5930	RBBP6	16	24,550,908	24,584,184	33,276	+	1	2_A375_pNL97_plus_lncRNA::1::3182	-252	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RBBP6	P2P-R, DKFZp686P0638, SNAMA, RBBP6, PACT, RBQ-1, DKFZp761B2423, MY038	retinoblastoma binding protein 6	NM_006910, NM_018703, NM_032626, hCT2261601.1, hCT2349864.0, hCT2349865.0, hCT2352963.0	1552329_at, 205178_s_at, 212781_at, 212783_at, 223602_s_at, 228614_at, 232044_at	NP_008841.2, NP_061173.1, NP_116015.2, EAW55789.1, EAW55791.1, EAW55792.1, EAW55790.1
GeneID:400511	FLJ45256	16	24,672,743	24,682,383	9,640	-	2	1_A375_pNL7_minus_lncRNA::1::2247, 2_A375_pNL97_plus_lncRNA::1::3183	1519, 1455	in gene, in gene	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene FLJ45256		hypothetical LOC400511	XR_111652, XR_109271, XR_114983		
GeneID:27327	TNRC6A	16	24,741,049	24,837,548	96,499	+	1	2_A375_pNL97_plus_lncRNA::1::3184	-265	upstream	0	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TNRC6A	KIAA1460, CAGH26, FLJ22043, TNRC6, GW1, TNRC6A, MGC75384, DKFZp666E117, GW182	trinucleotide repeat containing 6A	NM_014494, hCT2344469.0, hCT2344470.0, hCT2344471.0, hCT2344472.0, hCT2344473.0, hCT2344474.0	1553346_a_at, 224704_at, 224705_s_at, 233836_at, 234734_s_at, 243634_at	NP_055309.2, EAW55785.1, EAW55782.1, EAW55783.1, EAW55784.1, EAW55786.1, EAW55787.1
GeneID:115584	SLC5A11	16	24,857,552	24,922,944	65,392	+	2	1_A375_pNL7_minus_lncRNA::1::2248, 2_A375_pNL97_plus_lncRNA::1::3185	12304, 12336	in gene, in gene	1	1	25	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene SLC5A11	SMIT2, SGLT6, RKST1, KST1, SLC5A11	solute carrier family 5 (sodium/glucose cotransporter), member 11	NM_052944, hCT14141.3	237254_at	NP_443176.2, EAW55781.1
GeneID:342357	ZKSCAN2	16	25,247,322	25,268,855	21,533	-	1	1_A375_pNL7_minus_lncRNA::1::2250	-137	upstream	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ZKSCAN2	ZNF694, FLJ23199, ZKSCAN2, ZSCAN31	zinc finger with KRAB and SCAN domains 2	NM_001012981, hCT1814961.1	232019_at	NP_001012999.3, EAW55768.1
GeneID:79831	JMJD5	16	27,214,807	27,233,089	18,282	+	2	1_A375_pNL7_minus_lncRNA::1::2251, 2_A375_pNL97_plus_lncRNA::1::3187	57, 9	in gene, in gene	1	1	46	63	1	2_A375_pNL97_plus_lncRNA::1	63	Gene JMJD5	JMJD5, FLJ13798	jumonji domain containing 5	NM_024773, NM_001145348, hCT13742.2	220070_at, 237229_at	NP_079049.2, NP_001138820.1, EAW55759.1
GeneID:197370	NSMCE1	16	27,236,315	27,280,113	43,798	-	1	2_A375_pNL97_plus_lncRNA::1::3188	-271	upstream	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene NSMCE1	NSE1, NSMCE1	non-SMC element 1 homolog (S. cerevisiae)	NM_145080, hCT13744.3, hCT1950800.1, hCT2352960.0, hCT2352961.0, hCT2352962.0	224666_at	NP_659547.2, EAW55757.1, EAW55754.1, EAW55755.1, EAW55756.1, EAW55758.1
GeneID:400512	FLJ21408	16	27,280,167	27,295,975	15,808	+	1	2_A375_pNL97_plus_lncRNA::1::3188	217	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene FLJ21408		hypothetical LOC400512	XR_111654, XR_109274, XR_114985	234216_at, 234627_at	
GeneID:23247	KIAA0556	16	27,561,468	27,791,692	230,224	+	1	1_A375_pNL7_minus_lncRNA::1::2252	176996	in gene	1	0	25	18	1	1_A375_pNL7_minus_lncRNA::1	25	Gene KIAA0556	KIAA0556		NM_015202, hCT1958654.1	213185_at	NP_056017.2, EAW55743.1
GeneID:146395	GSG1L	16	27,798,850	28,074,830	275,980	-	2	1_A375_pNL7_minus_lncRNA::1::2253, 2_A375_pNL97_plus_lncRNA::1::3189	267358, 267342	in gene, in gene	1	1	30	55	1	2_A375_pNL97_plus_lncRNA::1	55	Gene GSG1L	PRO19651, GSG1L, MGC16079	GSG1-like	NM_001109763, NM_144675, hCT2259037.0, hCT2352969.0, hCT8411.3	236701_at	NP_001103233.1, NP_653276.1, EAW55740.1, EAW55741.1, EAW55742.1
GeneID:388228	SBK1	16	28,303,840	28,335,170	31,330	+	2	1_A375_pNL7_minus_lncRNA::1::2254, 2_A375_pNL97_plus_lncRNA::1::3190	11728, 11765	in gene, in gene	1	1	23	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene SBK1	SBK1, Sbk	SH3-binding domain kinase 1	NM_001024401, hCT6694.4	226548_at, 226549_at	NP_001019572.1, EAW55733.1
GeneID:1201	CLN3	16	28,488,600	28,503,623	15,023	-	1	2_A375_pNL97_plus_lncRNA::1::3191	151	in gene	0	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene CLN3	BTS, JNCL, CLN3, MGC102840	ceroid-lipofuscinosis, neuronal 3	NM_001042432, NM_000086, hCT1783483.2, hCT1957741.1, hCT1957742.1, hCT1957743.1, hCT1957744.1, hCT1957745.1, hCT1957746.1, hCT1957747.1, hCT2273233.0, hCT2273236.0, hCT2273237.0, hCT2273240.0, hCT2273242.0, hCT2273243.0, hCT2273247.0, hCT2273248.0, hCT227	209275_s_at, 210859_x_at	NP_001035897.1, NP_000077.1, EAW52281.1, EAW52283.1, EAW52298.1, EAW52299.1, EAW52282.1, EAW52284.1, EAW52285.1, EAW52286.1, EAW52287.1, EAW52288.1, EAW52289.1, EAW52296.1, EAW52290.1, EAW52291.1, EAW52292.1, EAW52293.1, EAW52294.1, EAW52295.1, EAW52297.1
GeneID:55911	APOB48R	16	28,505,993	28,510,282	4,289	+	1	2_A375_pNL97_plus_lncRNA::1::3191	-2521	upstream	0	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene APOB48R	APOB100R, APOBR, APOB48R	apolipoprotein B receptor	NM_018690, hCT1783484.1, hCT2273309.0, hCT2273310.0	220023_at	NP_061160.2, EAW52278.1, EAW52279.1, EAW52280.1
GeneID:246778	IL27	16	28,510,683	28,518,155	7,472	-	1	2_A375_pNL97_plus_lncRNA::1::3191	14683	downstream	0	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene IL27	IL27, IL30, IL-27, IL27p28, IL-27A, p28, MGC71873	interleukin 27	NM_145659, hCT1646619.3	1552995_at	NP_663634.2, EAW52277.1
GeneID:11273	ATXN2L	16	28,834,414	28,848,558	14,144	+	4	1_A375_pNL7_minus_lncRNA::1::2255, 2_A375_pNL97_plus_lncRNA::1::3192, 2_A375_pNL97_plus_lncRNA::1::3193, 2_A375_pNL97_plus_lncRNA::1::3194	23282, -430, 1058, 23346	downstream, upstream, in gene, downstream	1	1	17.33	23	3	2_A375_pNL97_plus_lncRNA::1	30	Gene ATXN2L	A2LP, A2D, ATXN2L, A2LG, A2RP	ataxin 2-like	NM_145714, NM_007245, NM_148414, NM_148415, NM_148416, hCT1785515.2, hCT1955506.1, hCT1955507.1, hCT2287188.0, hCT2287191.0, hCT2287193.0, hCT2287196.0, hCT2287199.0, hCT2287200.0, hCT2352511.0, hCT2352512.0	201806_s_at, 207798_s_at	NP_663760.1, NP_009176.2, NP_680780.1, NP_680781.1, NP_680782.1, EAW51994.1, EAW51986.1, EAW51987.1, EAW51988.1, EAW51989.1, EAW51990.1, EAW51991.1, EAW51992.1, EAW51993.1, EAW51995.1, EAW51996.1
GeneID:7284	TUFM	16	28,853,732	28,857,729	3,997	-	2	1_A375_pNL7_minus_lncRNA::1::2255, 2_A375_pNL97_plus_lncRNA::1::3194	33, -31	in gene, upstream	1	1	24	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene TUFM	COXPD4, EFTU, EF-TuMT, P43, TUFM	Tu translation elongation factor, mitochondrial	NM_003321, hCT1785516.1, hCT1957071.1	201113_at, 236190_at	NP_003312.3, EAW51997.1, EAW51998.1
GeneID:25970	SH2B1	16	28,875,078	28,885,534	10,456	+	1	2_A375_pNL97_plus_lncRNA::1::3195	-166	upstream	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SH2B1	SH2B, PSM, DKFZp547G1110, FLJ30542, SH2B1, KIAA1299	SH2B adaptor protein 1	NM_001145812, NM_015503, NM_001145795, NM_001145796, NM_001145797, hCT1955509.1, hCT1955510.1, hCT1955511.0, hCT2287202.0, hCT2287206.0, hCT2287209.0, hCT9701.3	209322_s_at, 40149_at	NP_001139284.1, NP_056318.2, NP_001139267.1, NP_001139268.1, NP_001139269.1, EAW51999.1, EAW52000.1, EAW52001.1, EAW52002.1, EAW52003.1, EAW52004.1, EAW52005.1
GeneID:84901	NFATC2IP	16	28,962,318	28,977,786	15,468	+	1	2_A375_pNL97_plus_lncRNA::1::3196	23794	downstream	0	1	22	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene NFATC2IP	FLJ14639, MGC126790, MGC138387, NIP45, ESC2, RAD60, NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	NM_032815, hCT2287163.0, hCT2287165.0	212808_at, 212809_at, 217526_at, 217527_s_at, 229235_at, 238130_at	NP_116204.3, EAW52014.1, EAW52015.1
GeneID:83985	SPNS1	16	28,986,096	28,995,869	9,773	+	1	2_A375_pNL97_plus_lncRNA::1::3196	16	in gene	0	1	22	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene SPNS1	SPINL, SPIN1, LAT, PP2030, SPNS1, HSpin1, nrs, FLJ36356	spinster homolog 1 (Drosophila)	NM_032038, NM_001142448, NM_001142449, NM_001142450, NM_001142451, hCT2287169.1, hCT2287170.1, hCT2287172.1, hCT2287175.1, hCT2287177.1, hCT2287179.1, hCT2352513.0, hCT2352514.0	223173_at	NP_114427.1, NP_001135920.1, NP_001135921.1, NP_001135922.1, NP_001135923.1, EAW52021.1, EAW52016.1, EAW52017.1, EAW52018.1, EAW52019.1, EAW52020.1, EAW52022.1, EAW52023.1
GeneID:27040	LAT	16	28,996,147	29,002,104	5,957	+	1	2_A375_pNL97_plus_lncRNA::1::3196	-10035	upstream	0	1	22	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene LAT	LAT, pp36, LAT1	linker for activation of T cells	NM_014387, NM_001014987, NM_001014988, NM_001014989, hCT2287173.0, hCT2287176.1, hCT2287180.1, hCT2287181.1, hCT2287183.0, hCT2344367.0, hCT2344368.0, hCT2352515.0	209881_s_at, 211005_at	NP_055202.1, NP_001014987.1, NP_001014989.2, NP_001014988.1, EAW52024.1, EAW52027.1, EAW52025.1, EAW52026.1, EAW52028.1, EAW52029.1, EAW52030.1, EAW52031.1
GeneID:653808	ZG16	16	29,789,561	29,791,840	2,279	+	2	1_A375_pNL7_minus_lncRNA::1::2257, 2_A375_pNL97_plus_lncRNA::1::3199	12359, 12039	downstream, downstream	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ZG16	JCLN1, ZG16A, MGC34820, FLJ92276, JCLN, ZG16, FLJ43571, MGC183567, hZG16	zymogen granule protein 16 homolog (rat)	NM_152338		NP_689551.1
GeneID:3835	KIF22	16	29,802,058	29,816,706	14,648	+	6	1_A375_pNL7_minus_lncRNA::1::2257, 1_A375_pNL7_minus_lncRNA::1::2258, 2_A375_pNL97_plus_lncRNA::1::3199, 2_A375_pNL97_plus_lncRNA::1::3200, 2_A375_pNL97_plus_lncRNA::1::3201, 2_A375_pNL97_plus_lncRNA::1::3202	-138, 19718, -458, 14710, 17142, 21142	upstream, downstream, upstream, downstream, downstream, downstream	1	1	17	18.2	5	2_A375_pNL97_plus_lncRNA::1	21	Gene KIF22	KID, A-328A3.2, OBP-1, KIF22, OBP, OBP-2, KNSL4	kinesin family member 22	NM_007317, hCT2344673.0, hCT2344674.0, hCT2344676.0, hCT2344677.0, hCT2344679.0, hCT2344680.0, hCT2344682.0	202183_s_at, 216969_s_at	NP_015556.1, EAW80008.1, EAW80004.1, EAW80007.1, EAW80009.1, EAW80010.1, EAW80005.1, EAW80006.1
GeneID:4150	MAZ	16	29,817,855	29,822,504	4,649	+	5	1_A375_pNL7_minus_lncRNA::1::2258, 2_A375_pNL97_plus_lncRNA::1::3200, 2_A375_pNL97_plus_lncRNA::1::3201, 2_A375_pNL97_plus_lncRNA::1::3202, 2_A375_pNL97_plus_lncRNA::1::3203	3921, -1087, 1345, 5345, 9569	in gene, upstream, in gene, downstream, downstream	1	1	17.2	18.2	5	2_A375_pNL97_plus_lncRNA::1	21	Gene MAZ	SAF-1, PUR1, ZNF801, ZF87, MAZ, SAF-3, Pur-1, SAF-2, Zif87	MYC-associated zinc finger protein (purine-binding transcription factor)	NM_001042539, NM_002383, hCT2260631.0, hCT2344672.0, hCT2344675.0, hCT2344678.0, hCT2344681.0, hCT2344683.0, hCT2344684.0, hCT2344685.0, hCT2344686.0, hCT2344687.0	207824_s_at, 212064_x_at, 226795_x_at, 229807_s_at	NP_001036004.1, NP_002374.2, EAW79995.1, EAW79996.1, EAW80001.1, EAW80003.1, EAW79994.1, EAW79997.1, EAW79998.1, EAW79999.1, EAW80000.1, EAW80002.1
GeneID:112476	PRRT2	16	29,823,409	29,827,202	3,793	+	5	1_A375_pNL7_minus_lncRNA::1::2258, 2_A375_pNL97_plus_lncRNA::1::3200, 2_A375_pNL97_plus_lncRNA::1::3201, 2_A375_pNL97_plus_lncRNA::1::3202, 2_A375_pNL97_plus_lncRNA::1::3203	-1633, -6641, -4209, -209, 4015	upstream, upstream, upstream, upstream, downstream	1	1	17.2	18.2	5	2_A375_pNL97_plus_lncRNA::1	21	Gene PRRT2	PRRT2, DKFZp547J199, FLJ25513, IFITMD1	proline-rich transmembrane protein 2	NM_145239, hCT2260642.1, hCT2260644.1, hCT2260657.1, hCT2355972.0	227192_at	NP_660282.2, EAW79993.1, EAW79990.1, EAW79991.1, EAW79992.1
GeneID:79447	C16orf53	16	29,827,528	29,833,816	6,288	+	4	1_A375_pNL7_minus_lncRNA::1::2258, 2_A375_pNL97_plus_lncRNA::1::3201, 2_A375_pNL97_plus_lncRNA::1::3202, 2_A375_pNL97_plus_lncRNA::1::3203	-5752, -8328, -4328, -104	upstream, upstream, upstream, upstream	1	1	17	17.5	4	2_A375_pNL97_plus_lncRNA::1	20	Gene C16orf53	C16orf53, PA1, GAS, MGC4606, FLJ22459	chromosome 16 open reading frame 53	NM_024516, hCT2260650.0	218300_at	NP_078792.1, EAW79989.1
GeneID:9961	MVP	16	29,831,767	29,859,341	27,554	+	3	1_A375_pNL7_minus_lncRNA::1::2258, 2_A375_pNL97_plus_lncRNA::1::3202, 2_A375_pNL97_plus_lncRNA::1::3203	-10011, -8587, -4363	upstream, upstream, upstream	1	1	17.67	16.67	3	2_A375_pNL97_plus_lncRNA::1	19	Gene MVP	MVP, LRP, VAULT1	major vault protein	NM_017458, NM_005115, hCT2260639.1, hCT2260640.1, hCT2260645.1, hCT2260646.1, hCT2260652.1, hCT2260655.1, hCT2344032.0, hCT2344033.0, hCT2355981.0	202180_s_at, 231878_at	NP_059447.2, NP_005106.2, EAW79979.1, EAW79980.1, EAW79982.1, EAW79984.1, EAW79981.1, EAW79983.1, EAW79985.1, EAW79986.1, EAW79987.1
GeneID:10423	CDIPT	16	29,869,678	29,874,578	4,900	-	2	1_A375_pNL7_minus_lncRNA::1::2259, 2_A375_pNL97_plus_lncRNA::1::3204	-142, -238	upstream, upstream	1	1	61	76	1	2_A375_pNL97_plus_lncRNA::1	76	Gene CDIPT	PIS, CDIPT, MGC1328, PIS1	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	NM_006319, hCT12719.4, hCT1961692.1, hCT2355974.0	201253_s_at	NP_006310.1, EAW79976.1, EAW79977.1, EAW79978.1
GeneID:440356	LOC440356	16	29,875,004	29,879,374	4,370	+	2	1_A375_pNL7_minus_lncRNA::1::2259, 2_A375_pNL97_plus_lncRNA::1::3204	-264, -168	upstream, upstream	1	1	61	76	1	2_A375_pNL97_plus_lncRNA::1	76	Gene LOC440356	FLJ27521	hypothetical LOC440356	NR_015396, NR_024370	240537_s_at	
GeneID:26470	SEZ6L2	16	29,882,480	29,910,580	28,100	-	3	1_A375_pNL7_minus_lncRNA::1::2259, 2_A375_pNL97_plus_lncRNA::1::3204, 2_A375_pNL97_plus_lncRNA::1::3205	35860, 35764, -844	downstream, downstream, upstream	1	1	37.5	48.5	2	2_A375_pNL97_plus_lncRNA::1	76	Gene SEZ6L2	SEZ6L2, FLJ90517, PSK-1	seizure related 6 homolog (mouse)-like 2	NM_012410, NM_201575, NM_001114099, NM_001114100, hCT1809246.3	218720_x_at, 223458_at, 233337_s_at, 235404_x_at, 235406_x_at	NP_036542.1, NP_963869.2, NP_001107571.1, NP_001107572.1, EAW79973.1
GeneID:253982	ASPHD1	16	29,912,147	29,917,377	5,230	+	1	2_A375_pNL97_plus_lncRNA::1::3205	-723	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ASPHD1	ASPHD1	aspartate beta-hydroxylase domain containing 1	NM_181718, hCT1830508.3, hCT2355962.0	1553997_a_at, 214993_at	NP_859069.2, EAW79972.1, EAW79971.1
GeneID:253980	KCTD13	16	29,917,660	29,937,545	19,885	-	2	2_A375_pNL97_plus_lncRNA::1::3205, 2_A375_pNL97_plus_lncRNA::1::3206	26121, -215	downstream, upstream	0	1	12	19.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene KCTD13	hBACURD1, POLDIP1, PDIP1, FKSG86, KCTD13	potassium channel tetramerisation domain containing 13	NM_178863, hCT1809247.1, hCT2355969.0	221889_at, 45653_at	NP_849194.1, EAW79969.1, EAW79970.1
GeneID:9344	TAOK2	16	29,985,222	30,003,581	18,359	+	2	1_A375_pNL7_minus_lncRNA::1::2260, 2_A375_pNL97_plus_lncRNA::1::3207	22202, 22426	downstream, downstream	1	1	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene TAOK2	PSK, KIAA0881, PSK1-BETA, TAO1, MAP3K17, TAOK2, PSK1, TAO2	TAO kinase 2	NM_004783, NM_016151, hCT1956039.1, hCT2260670.0, hCT9408.2	204877_s_at, 204878_s_at, 204986_s_at	NP_004774.1, NP_057235.2, EAW79963.1, EAW79964.1, EAW79965.1
GeneID:8479	HIRIP3	16	30,004,311	30,007,412	3,101	-	2	1_A375_pNL7_minus_lncRNA::1::2260, 2_A375_pNL97_plus_lncRNA::1::3207	-12, -236	upstream, upstream	1	1	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene HIRIP3	HIRIP3	HIRA interacting protein 3	NM_003609, hCT2257697.0, hCT9289.3	204504_s_at, 229697_at	NP_003600.2, EAW79960.1, EAW79961.1
GeneID:283899	INO80E	16	30,007,531	30,017,112	9,581	+	2	1_A375_pNL7_minus_lncRNA::1::2260, 2_A375_pNL97_plus_lncRNA::1::3207	-107, 117	upstream, in gene	1	1	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene INO80E	FLJ00079, CCDC95, INO80E, FLJ90652	INO80 complex subunit E	NM_173618, hCT1809255.3, hCT2260674.1, hCT2341216.0, hCT2355976.0, hCT2355977.0, hCT2355978.0, hCT2355979.0	227286_at	NP_775889.1, EAW79953.1, EAW79954.1, EAW79955.1, EAW79956.1, EAW79959.1, EAW79957.1, EAW79958.1
GeneID:8448	DOC2A	16	30,016,835	30,022,401	5,566	-	2	1_A375_pNL7_minus_lncRNA::1::2260, 2_A375_pNL97_plus_lncRNA::1::3207	14977, 14753	downstream, downstream	1	1	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene DOC2A	Doc2, DOC2A		NM_003586, hCT1809243.4, hCT1966550.2, hCT1966551.2, hCT1966552.2, hCT2257689.1, hCT2257690.1, hCT2257694.1, hCT2257696.1, hCT2341213.0, hCT2341214.0, hCT2341215.0	205744_at	NP_003577.2, EAW79948.1, EAW79942.1, EAW79947.1, EAW79951.1, EAW79952.1, EAW79943.1, EAW79944.1, EAW79945.1, EAW79946.1, EAW79949.1, EAW79950.1
GeneID:226	ALDOA	16	30,064,491	30,081,735	17,244	+	2	1_A375_pNL7_minus_lncRNA::1::2261, 2_A375_pNL97_plus_lncRNA::1::3208	12149, 12117	in gene, in gene	1	1	24	18	1	1_A375_pNL7_minus_lncRNA::1	24	Gene ALDOA	ALDA, MGC17767, ALDOA, MGC17716, MGC10942, GSD12	aldolase A, fructose-bisphosphate	NM_000034, NM_184041, NM_184043, NM_001127617, hCT1951970.2, hCT1966591.1, hCT2260662.0, hCT2260666.0	200966_x_at, 214687_x_at, 236996_x_at	NP_000025.1, NP_908930.1, NP_001121089.1, NP_908932.1, EAW79933.1, EAW79936.1, EAW79934.1, EAW79935.1
GeneID:5531	PPP4C	16	30,087,385	30,096,695	9,310	+	2	1_A375_pNL7_minus_lncRNA::1::2262, 2_A375_pNL97_plus_lncRNA::1::3209	15943, 15975	downstream, downstream	1	1	23	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene PPP4C	PP4C, PPX, PPH3, PPP4C, PP4, PPP4	protein phosphatase 4 (formerly X), catalytic subunit	NM_002720, hCT1809226.3, hCT1957456.2, hCT1966545.0, hCT1966547.1	208932_at	NP_002711.1, EAW79928.1, EAW79929.1, EAW79930.1, EAW79931.1
GeneID:6911	TBX6	16	30,097,114	30,103,205	6,091	-	2	1_A375_pNL7_minus_lncRNA::1::2262, 2_A375_pNL97_plus_lncRNA::1::3209	-123, -155	upstream, upstream	1	1	23	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene TBX6	DFNB67, TBX6	T-box 6	NM_004608, hCT1809227.1, hCT2257684.0	207684_at, 215122_at	NP_004599.2, EAW79926.1, EAW79927.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:83719	YPEL3	16	30,103,635	30,107,537	3,902	-	2	1_A375_pNL7_minus_lncRNA::1::2262, 2_A375_pNL97_plus_lncRNA::1::3209	4209, 4177	downstream, downstream	1	1	23	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene YPEL3	MGC10500, YPEL3	yippee-like 3 (Drosophila)	NM_031477, NM_001145524, hCT1809240.3, hCT1957458.2, hCT1965549.1, hCT2355971.0	223179_at, 232077_s_at	NP_113665.3, NP_001138996.1, EAW79922.1, EAW79923.1, EAW79924.1, EAW79925.1
GeneID:100271831	LOC100271831	16	30,105,065	30,125,826	20,761	+	2	1_A375_pNL7_minus_lncRNA::1::2262, 2_A375_pNL97_plus_lncRNA::1::3209	-1737, -1705	upstream, upstream	1	1	23	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene LOC100271831		hypothetical LOC100271831	NR_027081		
GeneID:100506914	LOC100506914	16	30,107,751	30,116,841	9,090	+	2	1_A375_pNL7_minus_lncRNA::1::2262, 2_A375_pNL97_plus_lncRNA::1::3209	-4423, -4391	upstream, upstream	1	1	23	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene LOC100506914		hypothetical LOC100506914	XR_109261		
GeneID:10421	CD2BP2	16	30,362,087	30,366,682	4,595	-	2	1_A375_pNL7_minus_lncRNA::1::2263, 2_A375_pNL97_plus_lncRNA::1::3210	-422, -262	upstream, upstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CD2BP2	FWP010, LIN1, CD2BP2, U5-52K, Snu40	CD2 (cytoplasmic tail) binding protein 2	NM_006110, NR_024465, hCT2280286.1, hCT87744.4	202256_at, 202257_s_at	NP_006101.1, EAW52260.1, EAW52261.1
GeneID:26000	TBC1D10B	16	30,368,422	30,381,522	13,100	-	3	1_A375_pNL7_minus_lncRNA::1::2263, 2_A375_pNL97_plus_lncRNA::1::3210, 2_A375_pNL97_plus_lncRNA::1::3211	14418, 14578, -8302	downstream, downstream, upstream	1	1	13.5	22	2	2_A375_pNL97_plus_lncRNA::1	25	Gene TBC1D10B	TBC1D10B, FP2461, DKFZp434P1750	TBC1 domain family, member 10B	NM_015527, hCT2280281.1, hCT2280282.1, hCT2352522.0	220947_s_at	NP_056342.3, EAW52258.1, EAW52256.1, EAW52257.1
GeneID:29895	MYLPF	16	30,386,123	30,389,310	3,187	+	1	2_A375_pNL97_plus_lncRNA::1::3211	3701	downstream	0	1	7	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MYLPF	DKFZp779C0757, MYL11, MRLC2, MYLPF, HUMMLC2B, MGC13450	myosin light chain, phosphorylatable, fast skeletal muscle	NM_013292, hCT1785993.1, hCT2282580.0	205163_at	NP_037424.2, EAW52254.1, EAW52255.1
GeneID:1731	1-Sep	16	30,389,456	30,394,171	4,715	-	1	2_A375_pNL97_plus_lncRNA::1::3211	4347	in gene	0	1	7	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene SEPT1	MGC20394, SEPT1, LARP, SEP1, DIFF6, PNUTL3	septin 1	NM_052838, hCT1785999.0, hCT2280279.0	227552_at	NP_443070.1, EAW52252.1, EAW52253.1
GeneID:79077	DCTPP1	16	30,435,019	30,441,373	6,354	-	1	2_A375_pNL97_plus_lncRNA::1::3212	109	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DCTPP1	DCTPP1, RS21C6, XTP3TPA, MGC5627, CDA03	dCTP pyrophosphatase 1	NM_024096, hCT1786000.2	218069_at	NP_077001.1, EAW52247.1
GeneID:22928	SEPHS2	16	30,454,952	30,457,224	2,272	-	1	2_A375_pNL97_plus_lncRNA::1::3213	392	in gene	0	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SEPHS2	SPS2, SEPHS2	selenophosphate synthetase 2	NM_012248, hCT1786001.2	200961_at	NP_036380.2, EAW52246.1
GeneID:79724	ZNF768	16	30,535,322	30,537,910	2,588	-	1	2_A375_pNL97_plus_lncRNA::1::3214	-8714	upstream	0	1	7	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ZNF768	ZNF768, FLJ23436	zinc finger protein 768	NM_024671, hCT1827660.3, hCT2280274.0	218916_at	NP_078947.3, EAW52241.1, EAW52242.1
GeneID:100506960	LOC100506960	16	30,538,147	30,541,977	3,830	+	1	2_A375_pNL97_plus_lncRNA::1::3214	8477	downstream	0	1	7	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100506960		hypothetical LOC100506960	XR_109262		
GeneID:65988	ZNF747	16	30,542,779	30,546,194	3,415	-	1	2_A375_pNL97_plus_lncRNA::1::3214	-430	upstream	0	1	7	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ZNF747	MGC2474, ZNF747	zinc finger protein 747	NM_023931, hCT1827661.3, hCT2280271.0	206180_x_at, 238606_at	NP_076420.1, EAW52239.1, EAW52240.1
GeneID:100506973	LOC100506973	16	30,546,391	30,548,470	2,079	+	1	2_A375_pNL97_plus_lncRNA::1::3214	233	in gene	0	1	7	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100506973		hypothetical LOC100506973	XR_111565, XR_109263, XR_114996		
GeneID:92595	ZNF764	16	30,565,085	30,569,642	4,557	-	1	2_A375_pNL97_plus_lncRNA::1::3215	10	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ZNF764	MGC13138, ZNF764	zinc finger protein 764	NM_033410, NM_001172679, hCT10385.3, hCT2280268.0	222120_at, 57516_at	NP_219363.2, NP_001166150.1, EAW52237.1, EAW52238.1
GeneID:115509	ZNF689	16	30,614,686	30,621,682	6,996	-	2	1_A375_pNL7_minus_lncRNA::1::2264, 2_A375_pNL97_plus_lncRNA::1::3216	-110, -142	upstream, upstream	1	1	22	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene ZNF689	TIPUH1, FLJ90415, DKFZp762C173, ZNF689	zinc finger protein 689	NM_138447, hCT1785995.1	227294_at, 227445_at	NP_612456.1, EAW52228.1
GeneID:78994	PRR14	16	30,662,241	30,667,734	5,493	+	4	1_A375_pNL7_minus_lncRNA::1::2265, 1_A375_pNL7_minus_lncRNA::1::2266, 2_A375_pNL97_plus_lncRNA::1::3217, 2_A375_pNL97_plus_lncRNA::1::3218	-321, 7867, -289, 7919	upstream, downstream, upstream, downstream	1	1	30.5	30	2	1_A375_pNL7_minus_lncRNA::1	37	Gene PRR14	DKFZp781A13196, PRR14, MGC3121	proline rich 14	NM_024031, hCT12250.3, hCT2282590.1, hCT2282591.0, hCT2344964.0, hCT2352541.0, hCT2352542.0, hCT2352543.0	1559397_s_at, 218714_at, 45687_at	NP_076936.1, EAW52222.1, EAW52221.1, EAW52223.1, EAW52225.1, EAW52227.1, EAW52224.1, EAW52226.1
GeneID:100506988	LOC100506988	16	30,670,987	30,674,147	3,160	+	4	1_A375_pNL7_minus_lncRNA::1::2265, 1_A375_pNL7_minus_lncRNA::1::2266, 2_A375_pNL97_plus_lncRNA::1::3217, 2_A375_pNL97_plus_lncRNA::1::3218	-9067, -859, -9035, -827	upstream, upstream, upstream, upstream	1	1	30.5	30	2	1_A375_pNL7_minus_lncRNA::1	37	Gene LOC100506988		hypothetical protein LOC100506988	XM_003118714, XM_003120850		XP_003118762.1, XP_003120898.1
GeneID:64319	FBRS	16	30,675,778	30,682,131	6,353	+	2	1_A375_pNL7_minus_lncRNA::1::2266, 2_A375_pNL97_plus_lncRNA::1::3218	-5650, -5618	upstream, upstream	1	1	37	35	1	1_A375_pNL7_minus_lncRNA::1	37	Gene FBRS	FLJ11618, Fibrosin-1, FBS, FBS1, FBRS	fibrosin	NM_001105079, hCT12249.3, hCT2282593.0, hCT2282594.0, hCT2344963.0	218255_s_at, 238771_at, 242217_s_at	NP_001098549.1, EAW52216.1, EAW52215.1, EAW52217.1, EAW52218.1
GeneID:730183	LOC730183	16	30,709,028	30,709,810	782	-	1	2_A375_pNL97_plus_lncRNA::1::3219	274	in gene	0	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC730183		hypothetical LOC730183	XR_111566, XR_109264, XR_114994		
GeneID:10847	SRCAP	16	30,710,462	30,751,450	40,988	+	1	2_A375_pNL97_plus_lncRNA::1::3219	-926	upstream	0	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SRCAP	KIAA0309, FLJ44499, EAF1, SRCAP, DOMO1, SWR1	Snf2-related CREBBP activator protein	NM_006662, hCT2282595.0, hCT2282596.0, hCT2282600.0	1552630_a_at, 1569138_a_at, 212275_s_at, 213667_at, 215053_at, 38766_at	NP_006653.2, EAW52212.1, EAW52213.1, EAW52214.1
GeneID:9810	RNF40	16	30,773,630	30,786,539	12,909	+	2	1_A375_pNL7_minus_lncRNA::1::2267, 2_A375_pNL97_plus_lncRNA::1::3220	13410, 13634	downstream, downstream	1	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RNF40	STARING, RBP95, RNF40, MGC13051, DKFZp686K191, KIAA0661, BRE1B	ring finger protein 40	NM_014771, hCT2282615.0, hCT2282617.0, hCT2282618.0, hCT2282620.0	206845_s_at, 217642_at	NP_055586.1, EAW52198.1, EAW52197.1, EAW52199.1, EAW52200.1
GeneID:23361	ZNF629	16	30,789,770	30,798,523	8,753	-	3	1_A375_pNL7_minus_lncRNA::1::2267, 2_A375_pNL97_plus_lncRNA::1::3220, 2_A375_pNL97_plus_lncRNA::1::3221	11483, 11259, -69	downstream, downstream, upstream	1	1	14	21	2	2_A375_pNL97_plus_lncRNA::1	23	Gene ZNF629	ZNF, ZNF629, KIAA0326, ZNF65	zinc finger protein 629	NM_001080417	213196_at	NP_001073886.1
GeneID:9274	BCL7C	16	30,899,116	30,905,399	6,283	-	2	1_A375_pNL7_minus_lncRNA::1::2269, 2_A375_pNL97_plus_lncRNA::1::3223	-313, -329	upstream, upstream	1	1	22	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene BCL7C	BCL7C	B-cell CLL/lymphoma 7C	NM_004765, hCT12236.3	219072_at	NP_004756.2, EAW52193.1
GeneID:100313837	MIR762	16	30,905,224	30,905,306	82	+	2	1_A375_pNL7_minus_lncRNA::1::2269, 2_A375_pNL97_plus_lncRNA::1::3223	488, 504	downstream, downstream	1	1	22	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene MIR762	hsa-mir-762, MIR762	microRNA 762	NR_031576		
GeneID:1489	CTF1	16	30,907,928	30,914,881	6,953	+	2	1_A375_pNL7_minus_lncRNA::1::2269, 2_A375_pNL97_plus_lncRNA::1::3223	-2216, -2200	upstream, upstream	1	1	22	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene CTF1	CT1, CT-1, CTF1	cardiotrophin 1	NM_001330, NM_001142544, hCT1967898.1	205813_at	NP_001321.1, NP_001136016.1, EAW52192.1
GeneID:283932	NCRNA00095	16	30,930,640	30,934,590	3,950	-	2	1_A375_pNL7_minus_lncRNA::1::2270, 2_A375_pNL97_plus_lncRNA::1::3224	190, 638	in gene, in gene	1	1	30	27	1	1_A375_pNL7_minus_lncRNA::1	30	Gene NCRNA00095	MGC125469, NCRNA00095, MGC125470, MGC125472, FBXL19-AS1	FBXL19 antisense RNA 1 (non-protein coding)	NR_024346, hCT2280251.1	1553586_at	EAW52191.1
GeneID:54620	FBXL19	16	30,935,896	30,960,104	24,208	+	4	1_A375_pNL7_minus_lncRNA::1::2270, 1_A375_pNL7_minus_lncRNA::1::2271, 2_A375_pNL97_plus_lncRNA::1::3224, 2_A375_pNL97_plus_lncRNA::1::3225	-1496, 33224, -1944, 33224	upstream, downstream, upstream, downstream	1	1	33	36	2	2_A375_pNL97_plus_lncRNA::1	45	Gene FBXL19	Fbl19, MGC50505, FBXL19, JHDM1C, DKFZp434K0410	F-box and leucine-rich repeat protein 19	NM_001099784, hCT2348111.0, hCT2348112.0, hCT2352527.0, hCT2352528.0	226277_at	NP_001093254.2, EAW52188.1, EAW52187.1, EAW52189.1, EAW52190.1
GeneID:93129	ORAI3	16	30,960,405	30,966,259	5,854	+	2	1_A375_pNL7_minus_lncRNA::1::2271, 2_A375_pNL97_plus_lncRNA::1::3225	8715, 8715	downstream, downstream	1	1	36	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene ORAI3	MGC13024, TMEM142C, ORAI3	ORAI calcium release-activated calcium modulator 3	NM_152288, hCT12248.3, hCT1967899.1	221864_at	NP_689501.1, EAW52185.1, EAW52186.1
GeneID:9739	SETD1A	16	30,968,615	30,995,981	27,366	+	2	1_A375_pNL7_minus_lncRNA::1::2271, 2_A375_pNL97_plus_lncRNA::1::3225	505, 505	in gene, in gene	1	1	36	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene SETD1A	KIAA0339, Set1, Set1A, SETD1A, KMT2F	SET domain containing 1A	NM_014712	213202_at	NP_055527.1
GeneID:6810	STX4	16	31,044,903	31,051,485	6,582	+	1	1_A375_pNL7_minus_lncRNA::1::2272	-263	upstream	1	0	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene STX4	STX4, STX4A, p35-2	syntaxin 4	NM_004604, hCT12235.3, hCT2352520.0, hCT2352521.0	203530_s_at, 236232_at	NP_004595.2, EAW52176.1, EAW52175.1, EAW52177.1
GeneID:79759	ZNF668	16	31,072,164	31,085,641	13,477	-	2	1_A375_pNL7_minus_lncRNA::1::2273, 2_A375_pNL97_plus_lncRNA::1::3226	665, 793	in gene, in gene	1	1	41	53	1	2_A375_pNL97_plus_lncRNA::1	53	Gene ZNF668	FLJ14492, ZNF668, FLJ13479	zinc finger protein 668	NM_024706, NM_001172668, NM_001172669, NM_001172670, hCT12243.4, hCT2279741.0, hCT2349634.0	219047_s_at, 222813_at	NP_078982.3, NP_001166139.1, NP_001166140.1, NP_001166141.1, EAW52173.1, EAW52174.1, EAW52172.1
GeneID:9726	ZNF646	16	31,085,743	31,094,833	9,090	+	2	1_A375_pNL7_minus_lncRNA::1::2273, 2_A375_pNL97_plus_lncRNA::1::3226	-767, -895	upstream, upstream	1	1	41	53	1	2_A375_pNL97_plus_lncRNA::1	53	Gene ZNF646	ZNF646, KIAA0296	zinc finger protein 646	NM_014699, hCT2340424.0, hCT9443.3	204676_at	NP_055514.3, EAW52170.1, EAW52171.1
GeneID:339105	POL3S	16	31,094,745	31,100,130	5,385	-	2	1_A375_pNL7_minus_lncRNA::1::2273, 2_A375_pNL97_plus_lncRNA::1::3226	15154, 15282	downstream, downstream	1	1	41	53	1	2_A375_pNL97_plus_lncRNA::1	53	Gene POL3S	POL3S, FLJ00289, UNQ308, PRSS53	polyserase 3	NM_001039503	214226_at	NP_001034592.1
GeneID:10295	BCKDK	16	31,119,662	31,124,112	4,450	+	1	2_A375_pNL97_plus_lncRNA::1::3227	18	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene BCKDK	BCKDK		NM_005881, NM_001122957, hCT12231.3, hCT2280981.0, hCT2280983.0, hCT2352534.0, hCT2352535.0	202030_at	NP_005872.2, NP_001116429.1, EAW52161.1, EAW52162.1, EAW52163.1, EAW52164.1, EAW52160.1
GeneID:84148	MYST1	16	31,128,985	31,142,714	13,729	+	1	2_A375_pNL97_plus_lncRNA::1::3227	-9305	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MYST1	hMOF, FLJ14040, MOF, KAT8, MYST1	MYST histone acetyltransferase 1	NM_032188, NM_182958, hCT12240.3, hCT2352536.0	214665_at, 221620_s_at	NP_115564.2, NP_892003.2, EAW52157.1, EAW52158.1
GeneID:100507092	LOC100507092	16	31,129,281	31,130,068	787	+	1	2_A375_pNL97_plus_lncRNA::1::3227	-9601	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100507092		hypothetical LOC100507092	XR_111567, XR_109265, XR_114993		
GeneID:2521	FUS	16	31,191,431	31,206,192	14,761	+	2	1_A375_pNL7_minus_lncRNA::1::2274, 2_A375_pNL97_plus_lncRNA::1::3228	-119, -103	upstream, upstream	1	1	20	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene FUS	HNRNPP2, POMP75, FUS, FUS1, ALS6, TLS	fused in sarcoma	NM_004960, NR_028388, NM_001170937, NM_001170634, hCT12233.3, hCT2280991.0, hCT2352537.0	1565715_at, 1565716_at, 1565717_s_at, 200959_at, 215744_at, 217370_x_at, 231108_at	NP_004951.1, NP_001164408.1, NP_001164105.1, EAW52150.1, EAW52151.1, EAW52152.1
GeneID:100507110	LOC100507110	16	31,442,796	31,465,400	22,604	-	3	1_A375_pNL7_minus_lncRNA::1::2275, 2_A375_pNL97_plus_lncRNA::1::3229, 2_A375_pNL97_plus_lncRNA::1::3230	-5480, 10952, -5304	upstream, in gene, upstream	1	1	17.5	23	2	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100507110		hypothetical LOC100507110	XR_111568, XR_109266, XR_114992		
GeneID:283933	ZNF843	16	31,446,885	31,454,348	7,463	-	1	2_A375_pNL97_plus_lncRNA::1::3229	-100	upstream	0	1	17	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ZNF843	ZNF843, MGC46336	zinc finger protein 843	NM_001136509	1555078_at, 1564362_x_at	NP_001129981.1
GeneID:79798	ARMC5	16	31,470,317	31,478,488	8,171	+	2	1_A375_pNL7_minus_lncRNA::1::2275, 2_A375_pNL97_plus_lncRNA::1::3230	563, 387	in gene, in gene	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene ARMC5	ARMC5, FLJ00019, FLJ13063	armadillo repeat containing 5	NM_024742, NM_001105247, hCT1810594.2, hCT2280942.1, hCT2352533.0	227738_s_at	NP_079018.1, NP_001098717.1, EAW52131.1, EAW52132.1, EAW52133.1
GeneID:64755	C16orf58	16	31,500,810	31,519,706	18,896	-	1	2_A375_pNL97_plus_lncRNA::1::3231	58	in gene	0	1	14	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene C16orf58	C16orf58, FLJ13868	chromosome 16 open reading frame 58	NM_022744, hCT12758.2, hCT1951458.1, hCT2352539.0, hCT2352540.0	217891_at, 222190_s_at	NP_073581.2, EAW52121.1, EAW52119.1, EAW52120.1, EAW52122.1
GeneID:55737	VPS35	16	46,693,589	46,723,144	29,555	-	1	2_A375_pNL97_plus_lncRNA::1::3233	-440	upstream	0	1	11	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene VPS35	FLJ20388, DKFZp434E1211, FLJ13588, FLJ10752, VPS35, DKFZp434P1672, MEM3	vacuolar protein sorting 35 homolog (S. cerevisiae)	NM_018206, hCT2356366.0, hCT23684.2	1561146_at, 217727_x_at, 222387_s_at, 222388_s_at, 233864_s_at	NP_060676.2, EAW82684.1, EAW82683.1
GeneID:23594	ORC6L	16	46,723,558	46,732,306	8,748	+	1	2_A375_pNL97_plus_lncRNA::1::3233	26	in gene	0	1	11	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ORC6L	ORC6, ORC6L	origin recognition complex, subunit 6	NM_014321, hCT2323677.0, hCT23557.2	219105_x_at	NP_055136.1, EAW82686.1, EAW82685.1
GeneID:84706	GPT2	16	46,918,308	46,965,201	46,893	+	2	1_A375_pNL7_minus_lncRNA::1::2277, 2_A375_pNL97_plus_lncRNA::1::3235	-356, -212	upstream, upstream	1	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene GPT2	ALT2, GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	NM_133443, NM_001142466, hCT14429.2, hCT1954784.1, hCT2356338.0	224839_s_at	NP_597700.1, NP_001135938.1, EAW82690.1, EAW82691.1, EAW82692.1
GeneID:81533	ITFG1	16	47,189,297	47,495,018	305,721	-	1	2_A375_pNL97_plus_lncRNA::1::3236	-86	upstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ITFG1	CDA08, TIP, ITFG1	integrin alpha FG-GAP repeat containing 1	NM_030790, hCT1953950.1, hCT2323638.0	1556151_at, 221449_s_at, 239044_at	NP_110417.2, EAW82698.1, EAW82699.1
GeneID:5257	PHKB	16	47,495,210	47,735,434	240,224	+	1	2_A375_pNL97_plus_lncRNA::1::3236	-106	upstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PHKB	DKFZp781E15103, FLJ41698, PHKB	phosphorylase kinase, beta	NM_000293, NM_001031835, hCT14783.2, hCT2323683.0	202738_s_at, 202739_s_at, 242248_at	NP_000284.1, NP_001027005.1, EAW82700.1, EAW82701.1
GeneID:94160	ABCC12	16	48,116,884	48,180,681	63,797	-	3	1_A375_pNL7_minus_lncRNA::1::2280, 2_A375_pNL97_plus_lncRNA::1::3239, 2_A375_pNL97_plus_lncRNA::1::3240	19625, 64969, 23465	in gene, downstream, in gene	1	1	18	21.33	3	2_A375_pNL97_plus_lncRNA::1	29	Gene ABCC12	MRP9, MGC27071, ABCC12	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	NM_033226, hCT1954816.1, hCT1971679.0, hCT1971680.1, hCT2323933.0, hCT2356367.0, hCT2356368.0, hCT2356369.0, hCT2356370.0, hCT2356371.0, hCT2356372.0	1552590_a_at, 1553410_a_at	NP_150229.2, EAW82710.1, EAW82705.1, EAW82711.1, EAW82712.1, EAW82714.1, EAW82706.1, EAW82707.1, EAW82708.1, EAW82709.1, EAW82713.1
GeneID:85320	ABCC11	16	48,200,822	48,269,088	68,266	-	2	1_A375_pNL7_minus_lncRNA::1::2281, 2_A375_pNL97_plus_lncRNA::1::3241	-9184, -9184	upstream, upstream	1	1	23	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene ABCC11	MRP8, WW, EWWD, ABCC11	ATP-binding cassette, sub-family C (CFTR/MRP), member 11	NM_033151, NM_032583, NM_145186, hCT1954776.1, hCT1954777.0, hCT2323924.0, hCT2323925.0, hCT2323926.0, hCT2323927.0, hCT2356359.0, hCT2356360.0	1554911_at, 224146_s_at	NP_149163.2, NP_115972.2, NP_660187.1, EAW82716.1, EAW82720.1, EAW82721.1, EAW82715.1, EAW82717.1, EAW82718.1, EAW82719.1, EAW82722.1
GeneID:83752	LONP2	16	48,278,211	48,387,407	109,196	+	2	1_A375_pNL7_minus_lncRNA::1::2281, 2_A375_pNL97_plus_lncRNA::1::3241	61, 61	in gene, in gene	1	1	23	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene LONP2	LONP2, MGC4840, LONPL, LONP	lon peptidase 2, peroxisomal	NM_031490, hCT14786.3, hCT2323566.1, hCT2356382.0	221833_at, 221834_at, 223098_s_at, 223099_s_at, 229663_at	NP_113678.2, EAW82724.1, EAW82723.1, EAW82725.1
GeneID:255919	TMEM188	16	50,059,189	50,070,999	11,810	+	2	1_A375_pNL7_minus_lncRNA::1::2284, 2_A375_pNL97_plus_lncRNA::1::3246	-213, -181	upstream, upstream	1	1	69	66	1	1_A375_pNL7_minus_lncRNA::1	69	Gene TMEM188	TMEM188, FLJ38101, DKFZp313D2416, TMP125, C16orf69	transmembrane protein 188	NM_153261, hCT1953966.2, hCT2344801.0, hCT2344802.0, hCT2356310.0	235812_at	NP_694993.2, EAW82739.1, EAW82738.1, EAW82740.1, EAW82741.1
GeneID:100505488	LOC100505488	16	50,134,250	50,186,967	52,717	-	2	1_A375_pNL7_minus_lncRNA::1::2285, 2_A375_pNL97_plus_lncRNA::1::3247	87, 119	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100505488		hypothetical LOC100505488	XR_109296, XR_109295		
GeneID:64282	PAPD5	16	50,186,829	50,269,221	82,392	+	2	1_A375_pNL7_minus_lncRNA::1::2285, 2_A375_pNL97_plus_lncRNA::1::3247	51, 19	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene PAPD5	FLJ40270, TRF4-2, PAPD5	PAP associated domain containing 5	NM_001040284, NM_001040285, hCT16012.3, hCT2323958.0, hCT2323960.0, hCT2323962.0	226843_s_at, 229043_at	NP_001035374.2, NP_001035375.2, EAW82747.1, EAW82748.1, EAW82749.1, EAW82750.1
GeneID:1540	CYLD	16	50,775,961	50,835,846	59,885	+	1	2_A375_pNL97_plus_lncRNA::1::3248	64467	downstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CYLD	FLJ31664, KIAA0849, TEM, MFT1, CDMT, USPL2, MFT, FLJ78684, EAC, FLJ20180, CYLD, CYLD1, SBS, HSPC057, CYLDI	cylindromatosis (turban tumor syndrome)	NM_015247, NM_001042355, NM_001042412, hCT1953955.1, hCT2323945.0, hCT2323946.0, hCT2323948.0, hCT2356304.0, hCT2356305.0	213295_at, 214272_at, 221903_s_at, 221905_at, 222142_at, 39582_at, 60084_at	NP_056062.1, NP_001035814.1, NP_001035877.1, EAW82768.1, EAW82769.1, EAW82773.1, EAW82770.1, EAW82771.1, EAW82772.1
GeneID:80205	CHD9	16	53,088,945	53,361,414	272,469	+	4	1_A375_pNL7_minus_lncRNA::1::2288, 2_A375_pNL97_plus_lncRNA::1::3252, 2_A375_pNL97_plus_lncRNA::1::3253, 2_A375_pNL97_plus_lncRNA::1::3254	44047, -177, 75807, 76847	in gene, upstream, in gene, in gene	1	1	13.5	17.25	4	2_A375_pNL97_plus_lncRNA::1	19	Gene CHD9	KISH2, CHD9, AD013, PRIC320, CReMM	chromodomain helicase DNA binding protein 9	NM_025134, hCT2324359.0, hCT2324360.0, hCT2324361.1, hCT2324363.0, hCT2324364.0, hCT2324367.1	212615_at, 212616_at, 220586_at, 229586_at, 235388_at, 239654_at, 240367_at, 243660_at	NP_079410.4, EAW82793.1, EAW82794.1, EAW82795.1, EAW82796.1, EAW82797.1, EAW82798.1
GeneID:5934	RBL2	16	53,468,351	53,525,560	57,209	+	2	1_A375_pNL7_minus_lncRNA::1::2289, 2_A375_pNL97_plus_lncRNA::1::3255	33, 321	in gene, in gene	1	1	22	18	1	1_A375_pNL7_minus_lncRNA::1	22	Gene RBL2	RBL2, FLJ26459, Rb2, P130	retinoblastoma-like 2 (p130)	NM_005611, hCT2324373.0, hCT2324374.0	212331_at, 212332_at	NP_005602.3, EAW82801.1, EAW82802.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:64400	AKTIP	16	53,525,192	53,537,170	11,978	-	1	1_A375_pNL7_minus_lncRNA::1::2290	-382	upstream	1	0	16	18	1	1_A375_pNL7_minus_lncRNA::1	16	Gene AKTIP	FTS, FT1, AKTIP	AKT interacting protein	NM_022476, NM_001012398, hCT2324415.0, hCT2324416.0, hCT2324417.0, hCT2324418.0, hCT2324419.0, hCT2324420.0, hCT2356360.0	218373_at, 223894_s_at	NP_071921.1, NP_001012398.1, EAW82805.1, EAW82807.1, EAW82808.1, EAW82809.1, EAW82803.1, EAW82804.1, EAW82806.1
GeneID:23322	RPGRIP1L	16	53,633,818	53,737,771	103,953	-	1	2_A375_pNL97_plus_lncRNA::1::3256	-37	upstream	0	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RPGRIP1L	JBTS7, CORS3, MKS5, NPHP8, KIAA1005, RPGRIP1L, FTM, DKFZp686C0668	RPGRIP1-like	NM_015272, NM_001127897, hCT14561.2	213959_s_at	NP_056087.2, NP_001121369.1, EAW82810.1
GeneID:79068	FTO	16	53,737,875	54,148,379	410,504	+	3	2_A375_pNL97_plus_lncRNA::1::3256, 1_A375_pNL7_minus_lncRNA::1::2291, 2_A375_pNL97_plus_lncRNA::1::3257	-67, 376665, 376685	upstream, in gene, in gene	1	1	17	20.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene FTO	FTO, KIAA1752, MGC5149	fat mass and obesity associated	NM_001080432	209702_at	NP_001073901.1
GeneID:79191	IRX3	16	54,317,212	54,320,378	3,166	-	2	1_A375_pNL7_minus_lncRNA::1::2292, 2_A375_pNL97_plus_lncRNA::1::3258	-726, 826	upstream, in gene	1	1	12.5	13	2	2_A375_pNL97_plus_lncRNA::1	19	Gene IRX3	IRX3, IRX-1, FLJ99187, IRXB1	iroquois homeobox 3	NM_024336, hCT14563.4, hCT2346082.0	229638_at	NP_077312.2, EAW82815.1, EAW82814.1
GeneID:54947	LPCAT2	16	55,542,913	55,620,582	77,669	+	1	1_A375_pNL7_minus_lncRNA::1::2293	30111	in gene	1	0	18	5	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LPCAT2	DKFZp686H22112, LysoPAFAT, AYTL1, LPCAT2, FLJ20481	lysophosphatidylcholine acyltransferase 2	NM_017839, hCT1780935.2	222633_at, 227889_at, 229791_at, 239598_s_at	NP_060309.2, EAW82829.1
GeneID:11051	NUDT21	16	56,463,048	56,485,261	22,213	-	1	2_A375_pNL97_plus_lncRNA::1::3262	85	in gene	0	1	14	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene NUDT21	CPSF5, DKFZp686H1588, CFIM25, NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	NM_007006, hCT15025.3, hCT2324618.0	202697_at, 213461_at, 224630_at	NP_008937.1, EAW82859.1, EAW82860.1
GeneID:55239	OGFOD1	16	56,485,424	56,511,407	25,983	+	1	2_A375_pNL97_plus_lncRNA::1::3262	-248	upstream	0	1	14	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene OGFOD1	TPA1, OGFOD1, FLJ10826, KIAA1612	2-oxoglutarate and iron-dependent oxygenase domain containing 1	NM_018233, hCT15023.3, hCT2324045.0	221090_s_at, 225106_s_at, 225110_at, 241739_at	NP_060703.3, EAW82861.1, EAW82862.1
GeneID:4502	MT2A	16	56,642,478	56,643,409	931	+	2	2_A375_pNL97_plus_lncRNA::1::3263, 2_A375_pNL97_plus_lncRNA::1::3264	-1198, -14	upstream, upstream	0	1	13.5	20.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene MT2A	MT2, MT2A	metallothionein 2A	NM_005953, hCT2324056.0, hCT2345305.1	212185_x_at	NP_005944.1, EAW82869.1, EAW82870.1
GeneID:100505742	LOC100505742	16	56,743,137	56,763,980	20,843	-	1	1_A375_pNL7_minus_lncRNA::1::2295	-244	upstream	1	0	18	14	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100505742		hypothetical LOC100505742	XR_109305		
GeneID:9688	NUP93	16	56,764,017	56,878,677	114,660	+	1	1_A375_pNL7_minus_lncRNA::1::2295	207	in gene	1	0	18	14	1	1_A375_pNL7_minus_lncRNA::1	18	Gene NUP93	NUP93, MGC21106, KIAA0095	nucleoporin 93kDa	NM_014669, hCT15014.3	202188_at	NP_055484.3, EAW82887.1
GeneID:84166	NLRC5	16	57,023,410	57,117,436	94,026	+	1	1_A375_pNL7_minus_lncRNA::1::2296	11134	in gene	1	0	21	11	1	1_A375_pNL7_minus_lncRNA::1	21	Gene NLRC5	CLR16.1, NLRC5, NOD4, NOD27, FLJ21709, FLJ39711	NLR family, CARD domain containing 5	NM_032206, hCT15019.3, hCT2324079.0, hCT2324082.0, hCT2324083.0, hCT2324084.0	226474_at	NP_115582.3, EAW82902.1, EAW82898.1, EAW82899.1, EAW82900.1, EAW82901.1
GeneID:89970	RSPRY1	16	57,220,241	57,272,950	52,709	+	2	1_A375_pNL7_minus_lncRNA::1::2297, 2_A375_pNL97_plus_lncRNA::1::3265	58575, 58607	downstream, downstream	1	1	29	25	1	1_A375_pNL7_minus_lncRNA::1	29	Gene RSPRY1	RSPRY1, KIAA1972	ring finger and SPRY domain containing 1	NM_133368, hCT15020.3, hCT2356361.0, hCT2356362.0	225770_at, 225773_at, 225774_at	NP_588609.1, EAW82911.1, EAW82909.1, EAW82910.1
GeneID:23568	ARL2BP	16	57,279,038	57,287,545	8,507	+	2	1_A375_pNL7_minus_lncRNA::1::2297, 2_A375_pNL97_plus_lncRNA::1::3265	-222, -190	upstream, upstream	1	1	29	25	1	1_A375_pNL7_minus_lncRNA::1	29	Gene ARL2BP	BART1, ARL2BP, BART	ADP-ribosylation factor-like 2 binding protein	NM_012106, hCT15011.2, hCT1961615.1	202091_at, 202092_s_at	NP_036238.1, EAW82913.1, EAW82914.1
GeneID:57019	CIAPIN1	16	57,462,086	57,481,369	19,283	-	2	1_A375_pNL7_minus_lncRNA::1::2298, 2_A375_pNL97_plus_lncRNA::1::3267	-39, -215	upstream, upstream	1	1	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CIAPIN1	PRO0915, Anamorsin, 2810413N20Rik, DRE2, CIAPIN1	cytokine induced apoptosis inhibitor 1	NM_020313, hCT1960342.1, hCT1960343.1, hCT7536.2	208424_s_at, 208968_s_at	NP_064709.2, EAW82922.1, EAW82923.1, EAW82924.1
GeneID:57017	COQ9	16	57,481,349	57,495,187	13,838	+	4	1_A375_pNL7_minus_lncRNA::1::2298, 1_A375_pNL7_minus_lncRNA::1::2299, 2_A375_pNL97_plus_lncRNA::1::3267, 2_A375_pNL97_plus_lncRNA::1::3268	59, 15163, 235, 15211	in gene, downstream, in gene, downstream	1	1	46	46.5	2	2_A375_pNL97_plus_lncRNA::1	60	Gene COQ9	COQ9, DKFZp434K046, C16orf49	coenzyme Q9 homolog (S. cerevisiae)	NM_020312	212228_s_at, 235622_at	NP_064708.1
GeneID:5432	POLR2C	16	57,496,551	57,505,921	9,370	+	2	1_A375_pNL7_minus_lncRNA::1::2299, 2_A375_pNL97_plus_lncRNA::1::3268	-39, 9	upstream, in gene	1	1	72	80	1	2_A375_pNL97_plus_lncRNA::1	80	Gene POLR2C	RPB31, hsRPB3, hRPB33, RPB3, POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	NM_032940	208996_s_at, 214263_x_at, 216282_x_at	NP_116558.1
GeneID:55715	DOK4	16	57,505,870	57,520,385	14,515	-	2	1_A375_pNL7_minus_lncRNA::1::2299, 2_A375_pNL97_plus_lncRNA::1::3268	23873, 23825	downstream, downstream	1	1	72	80	1	2_A375_pNL97_plus_lncRNA::1	80	Gene DOK4	FLJ10488, DOK4	docking protein 4	NM_018110, hCT1960339.1, hCT1960340.1, hCT7527.2	207747_s_at, 209690_s_at, 209691_s_at	NP_060580.2, EAW82933.1, EAW82932.1, EAW82934.1
GeneID:9289	GPR56	16	57,653,910	57,698,944	45,034	+	2	1_A375_pNL7_minus_lncRNA::1::2300, 2_A375_pNL97_plus_lncRNA::1::3269	14186, 3738	in gene, in gene	1	1	16.5	22	2	2_A375_pNL97_plus_lncRNA::1	26	Gene GPR56	BFPP, GPR56, TM7XN1, TM7LN4, DKFZp781L1398	G protein-coupled receptor 56	NM_005682, NM_201524, NM_201525, NM_001145770, NM_001145771, NM_001145772, NM_001145773, NM_001145774, hCT1953763.2, hCT1960337.2, hCT2324578.1, hCT2351963.0, hCT2351964.0, hCT2351965.0, hCT7520.3	206582_s_at, 212070_at	NP_005673.3, NP_958932.1, NP_001139242.1, NP_001139243.1, NP_001139244.1, NP_958933.1, NP_001139245.1, NP_001139246.1, EAW82939.1, EAW82940.1, EAW82941.1, EAW82942.1, EAW82943.1, EAW82944.1, EAW82945.1
GeneID:3801	KIFC3	16	57,792,129	57,836,439	44,310	-	1	2_A375_pNL97_plus_lncRNA::1::3270	-297	upstream	0	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene KIFC3	KIFC3, FLJ34694, DKFZp686D23201	kinesin family member C3	NM_005550, NM_001130099, NM_001130100, hCT1953760.1, hCT1953776.1, hCT2356298.0, hCT7528.3	209661_at	NP_005541.3, NP_001123571.1, NP_001123572.1, EAW82953.1, EAW82954.1, EAW82955.1, EAW82956.1
GeneID:388282	LOC388282	16	57,844,549	57,850,831	6,282	+	1	2_A375_pNL97_plus_lncRNA::1::3270	-7813	upstream	0	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC388282		hypothetical LOC388282	XR_111582, XR_109306, XR_115276		
GeneID:29105	C16orf80	16	58,147,496	58,163,296	15,800	-	1	2_A375_pNL97_plus_lncRNA::1::3271	-85	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene C16orf80	GTL3, EVORF, fSAP23, C16orf80	chromosome 16 open reading frame 80	NM_013242, hCT7523.1	217957_at	NP_037374.1, EAW82967.1
GeneID:1459	CSNK2A2	16	58,191,811	58,231,782	39,971	-	2	1_A375_pNL7_minus_lncRNA::1::2301, 2_A375_pNL97_plus_lncRNA::1::3272	-250, -234	upstream, upstream	1	1	26	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene CSNK2A2	CSNK2A2, CK2A2, FLJ43934, CSNK2A1	casein kinase 2, alpha prime polypeptide	NM_001896, hCT7524.2	203575_at, 224922_at	NP_001887.1, EAW82969.1
GeneID:64785	GINS3	16	58,426,298	58,440,048	13,750	+	2	1_A375_pNL7_minus_lncRNA::1::2302, 2_A375_pNL97_plus_lncRNA::1::3273	70, 70	in gene, in gene	1	1	51	74	1	2_A375_pNL97_plus_lncRNA::1	74	Gene GINS3	FLJ13912, PSF3, GINS3	GINS complex subunit 3 (Psf3 homolog)	NM_022770, NM_001126129, NM_001126130, hCT1953764.1, hCT1953765.1, hCT2323890.0, hCT6127.3	218719_s_at, 45633_at	NP_073607.2, NP_001119601.1, NP_001119602.1, EAW82973.1, EAW82975.1, EAW82976.1, EAW82974.1
GeneID:65009	NDRG4	16	58,497,549	58,547,523	49,974	+	1	2_A375_pNL97_plus_lncRNA::1::3274	51923	downstream	0	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene NDRG4	SMAP-8, KIAA1180, DKFZp686I1615, NDRG4, FLJ30586, FLJ42011, MGC19632	NDRG family member 4	NM_020465, NM_001130487, NM_022910, hCT1953766.1, hCT1953767.1, hCT6989.3	209159_s_at	NP_065198.1, NP_001123959.1, NP_075061.1, EAW82977.1, EAW82978.1, EAW82979.1
GeneID:79918	SETD6	16	58,549,383	58,554,431	5,048	+	1	2_A375_pNL97_plus_lncRNA::1::3274	89	in gene	0	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SETD6	FLJ21148, SETD6	SET domain containing 6	NM_024860, NM_001160305, hCT1971593.1, hCT1971594.0	1554555_a_at, 219751_at	NP_079136.2, NP_001153777.1, EAW82980.1, EAW82981.1
GeneID:23019	CNOT1	16	58,553,855	58,663,750	109,895	-	1	2_A375_pNL97_plus_lncRNA::1::3274	114278	downstream	0	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene CNOT1	CNOT1, NOT1H, KIAA1007, FLJ36492, CDC39, NOT1, AD-005, FLJ90644, DKFZp686E0722, DKFZp686O168	CCR4-NOT transcription complex, subunit 1	NM_016284, NM_206999	1554052_at, 200860_s_at, 200861_at	NP_057368.3, NP_996882.1
GeneID:55238	SLC38A7	16	58,700,298	58,718,674	18,376	-	1	1_A375_pNL7_minus_lncRNA::1::2303	82	in gene	1	0	18	19	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SLC38A7	SLC38A7, FLJ10815, FLJ12724	solute carrier family 38, member 7	NM_018231, hCT1952985.1, hCT1952986.1, hCT6988.2	218727_at, 222215_at, 56821_at	NP_060701.1, EAW82986.1, EAW82985.1, EAW82987.1
GeneID:2806	GOT2	16	58,741,035	58,768,246	27,211	-	2	1_A375_pNL7_minus_lncRNA::1::2304, 2_A375_pNL97_plus_lncRNA::1::3275	86, -10	in gene, upstream	1	1	53	56	1	2_A375_pNL97_plus_lncRNA::1	56	Gene GOT2	FLJ40994, KATIV, GOT2, mitAAT, KAT4	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	NM_002080, hCT2324016.0, hCT6113.2	200708_at	NP_002071.2, EAW82989.1, EAW82988.1
GeneID:283867	LOC283867	16	65,318,402	65,610,203	291,801	-	1	2_A375_pNL97_plus_lncRNA::1::3278	182939	in gene	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC283867		hypothetical LOC283867	NR_027755	231518_at	
GeneID:7084	TK2	16	66,541,906	66,584,315	42,409	-	2	1_A375_pNL7_minus_lncRNA::1::2309, 2_A375_pNL97_plus_lncRNA::1::3281	-2245, 379	upstream, in gene	1	1	18.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene TK2	TK2, MTDPS2, MTTK		NM_004614, NM_001172643, NM_001172644, NM_001172645, hCT1640853.2, hCT2324178.0, hCT2324179.1, hCT2324181.0, hCT2356320.0	204227_s_at, 204276_at, 204277_s_at, 230313_at, 240300_at	NP_004605.4, NP_001166114.1, NP_001166115.1, NP_001166116.1, EAW83014.1, EAW83016.1, EAW83013.1, EAW83015.1, EAW83017.1
GeneID:51192	CKLF	16	66,586,466	66,600,154	13,688	+	2	1_A375_pNL7_minus_lncRNA::1::2309, 2_A375_pNL97_plus_lncRNA::1::3281	94, -2530	in gene, upstream	1	1	18.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene CKLF	CKLF3, CKLF4, CKLF1, C32, CKLF2, UCK-1, CKLF, HSPC224	chemokine-like factor	NM_016951, NM_016326, NM_181640, NM_181641, NM_001040138, hCT1954049.1, hCT19980.2, hCT2324167.0, hCT2324169.0	219161_s_at, 221058_s_at, 223451_s_at	NP_058647.1, NP_057410.1, NP_857591.1, NP_857592.1, NP_001035228.1, EAW83019.1, EAW83020.1, EAW83021.1, EAW83022.1
GeneID:8883	NAE1	16	66,836,781	66,864,879	28,098	-	1	1_A375_pNL7_minus_lncRNA::1::2310	127	in gene	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene NAE1	A-116A10.1, HPP1, ula-1, APPBP1, NAE1	NEDD8 activating enzyme E1 subunit 1	NM_003905, NM_001018159, NM_001018160, hCT1813484.1, hCT2325347.0	202265_s_at	NP_003896.1, NP_001018169.1, NP_001018170.1, EAW83042.1, EAW83043.1
GeneID:57546	PDP2	16	66,914,436	66,921,855	7,419	+	2	1_A375_pNL7_minus_lncRNA::1::2311, 2_A375_pNL97_plus_lncRNA::1::3282	-7225, 124	upstream, in gene	1	1	18.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	26	Gene PDP2	PPM2C2, KIAA1348, PDP2	pyruvate dehydrogenase phosphatase catalytic subunit 2	NM_020786	232661_at	NP_065837.1
GeneID:100505926	LOC100505926	16	66,922,667	66,924,184	1,517	+	1	2_A375_pNL97_plus_lncRNA::1::3282	-8107	upstream	0	1	18	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100505926		hypothetical LOC100505926	XR_109312		
GeneID:6236	RRAD	16	66,955,582	66,959,439	3,857	-	1	2_A375_pNL97_plus_lncRNA::1::3283	-9169	upstream	0	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RRAD	RAD1, RAD, REM3, RRAD	Ras-related associated with diabetes	NM_004165, NM_001128850, hCT19975.2, hCT2325343.0, hCT2356306.0	204802_at, 204803_s_at, 231100_at	NP_004156.1, NP_001122322.1, EAW83053.1, EAW83054.1, EAW83055.1
GeneID:51647	FAM96B	16	66,965,958	66,968,320	2,362	-	1	2_A375_pNL97_plus_lncRNA::1::3283	-268	upstream	0	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene FAM96B	FAM96B, CGI-128	family with sequence similarity 96, member B	NM_016062, NR_024525, hCT19979.3	218074_at	NP_057146.1, EAW83056.1
GeneID:8824	CES2	16	66,968,347	66,978,999	10,652	+	1	2_A375_pNL97_plus_lncRNA::1::3283	261	in gene	0	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CES2	CES2A1, iCE, CES2, CE-2, PCE-2	carboxylesterase 2 (intestine, liver)	NM_003869, NM_198061, hCT19977.2, hCT2324460.0, hCT2324462.0	209667_at, 209668_x_at, 213509_x_at	NP_003860.2, NP_932327.1, EAW83057.1, EAW83058.1, EAW83059.1
GeneID:55336	FBXL8	16	67,193,891	67,198,077	4,186	+	1	2_A375_pNL97_plus_lncRNA::1::3284	14269	downstream	0	1	17	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene FBXL8	MGC19959, FBL8, FLJ11278, FBXL8	F-box and leucine-rich repeat protein 8	NM_018378	220080_at	NP_060848.2
GeneID:3299	HSF4	16	67,197,288	67,203,848	6,560	+	1	2_A375_pNL97_plus_lncRNA::1::3284	10872	downstream	0	1	17	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene HSF4	HSF4, CTM	heat shock transcription factor 4	NM_001538, NM_001040667	210977_s_at	NP_001529.2, NP_001035757.1
GeneID:8996	NOL3	16	67,204,405	67,209,643	5,238	+	2	2_A375_pNL97_plus_lncRNA::1::3284, 2_A375_pNL97_plus_lncRNA::1::3285	3755, 15051	in gene, downstream	0	1	18	25.5	2	2_A375_pNL97_plus_lncRNA::1	26	Gene NOL3	CARD2, NOL3, MYP, NOP, ARC, FLJ35304, MYC, NOP30	nucleolar protein 3 (apoptosis repressor with CARD domain)	NM_001185057, NM_001185058, NM_003946, hCT1966495.2, hCT2324486.1, hCT2345279.0	1558738_at, 221566_s_at, 221567_at, 59625_at	NP_001171986.1, NP_001171987.1, NP_003937.1, EAW83087.1, EAW83088.1, EAW83089.1
GeneID:653319	KIAA0895L	16	67,209,505	67,217,883	8,378	-	3	2_A375_pNL97_plus_lncRNA::1::3284, 2_A375_pNL97_plus_lncRNA::1::3285, 2_A375_pNL97_plus_lncRNA::1::3286	9723, -1573, -8005	downstream, upstream, upstream	0	1	17	25	3	2_A375_pNL97_plus_lncRNA::1	26	Gene KIAA0895L	KIAA0895L	KIAA0895-like	NM_001040715	1558041_a_at	NP_001035805.1
GeneID:283849	EXOC3L	16	67,218,282	67,224,107	5,825	-	3	2_A375_pNL97_plus_lncRNA::1::3284, 2_A375_pNL97_plus_lncRNA::1::3285, 2_A375_pNL97_plus_lncRNA::1::3286	15947, 4651, -1781	downstream, in gene, upstream	0	1	17	25	3	2_A375_pNL97_plus_lncRNA::1	26	Gene EXOC3L	EXOC3L1, FLJ35587, FLJ35539, MGC88052, EXOC3L	exocyst complex component 3-like	NM_178516	1554937_x_at, 1559272_at	NP_848611.2
GeneID:1874	E2F4	16	67,226,068	67,232,821	6,753	+	2	2_A375_pNL97_plus_lncRNA::1::3285, 2_A375_pNL97_plus_lncRNA::1::3286	-6612, -180	upstream, upstream	0	1	17	24.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene E2F4	E2F-4, E2F4	E2F transcription factor 4, p107/p130-binding	NM_001950, hCT2324482.1, hCT2324484.1, hCT2356345.0	202248_at, 38707_r_at	NP_001941.2, EAW83094.1, EAW83095.1, EAW83096.1
GeneID:79767	ELMO3	16	67,233,028	67,237,927	4,899	+	1	2_A375_pNL97_plus_lncRNA::1::3286	-7140	upstream	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ELMO3	CED-12, ELMO-3, ELMO3, FLJ13824, CED12	engulfment and cell motility 3	NM_024712, hCT2324483.0, hCT2324485.1	219411_at	NP_078988.2, EAW83097.1, EAW83098.1
GeneID:442901	MIR328	16	67,236,224	67,236,298	74	-	1	2_A375_pNL97_plus_lncRNA::1::3286	10410	downstream	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene MIR328	MIRN328, hsa-mir-328, MIR328	microRNA 328	NR_029887		
GeneID:26231	LRRC29	16	67,241,042	67,260,901	19,859	-	1	2_A375_pNL97_plus_lncRNA::1::3287	-155	upstream	0	1	16	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene LRRC29	FBL9, LRRC29, FBXL9	leucine rich repeat containing 29	NM_012163, NM_001004055, hCT19981.3, hCT2325332.0, hCT2325333.0, hCT2356307.0, hCT2356308.0, hCT2356309.0	232545_at	NP_036295.1, NP_001004055.1, EAW83099.1, EAW83100.1, EAW83102.1, EAW83104.1, EAW83101.1, EAW83103.1
GeneID:29100	TMEM208	16	67,261,016	67,263,182	2,166	+	1	2_A375_pNL97_plus_lncRNA::1::3287	40	in gene	0	1	16	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene TMEM208	HSPC171, TMEM208	transmembrane protein 208	NM_014187, hCT19989.3, hCT2324428.0, hCT2356301.0, hCT2356302.0	221597_s_at	NP_054906.2, EAW83108.1, EAW83105.1, EAW83106.1, EAW83107.1
GeneID:29109	FHOD1	16	67,263,292	67,281,425	18,133	-	1	2_A375_pNL97_plus_lncRNA::1::3287	20369	downstream	0	1	16	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene FHOD1	FHOD1, FHOS	formin homology 2 domain containing 1	NM_013241, hCT19972.2, hCT2345052.0, hCT2345053.0, hCT2345054.0, hCT2345055.0	218530_at	NP_037373.2, EAW83112.1, EAW83109.1, EAW83110.1, EAW83111.1, EAW83113.1
GeneID:6553	SLC9A5	16	67,282,855	67,306,094	23,239	+	3	1_A375_pNL7_minus_lncRNA::1::2312, 1_A375_pNL7_minus_lncRNA::1::2313, 2_A375_pNL97_plus_lncRNA::1::3288	19417, 30553, 30521	in gene, downstream, downstream	1	1	29	27	2	2_A375_pNL97_plus_lncRNA::1	43	Gene SLC9A5	SLC9A5, NHE5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	NM_004594, hCT19971.2, hCT2324429.0, hCT2324430.0	1559092_at, 220650_s_at, 232564_at	NP_004585.1, EAW83114.1, EAW83115.1, EAW83116.1
GeneID:25894	PLEKHG4	16	67,311,413	67,323,403	11,990	+	3	1_A375_pNL7_minus_lncRNA::1::2312, 1_A375_pNL7_minus_lncRNA::1::2313, 2_A375_pNL97_plus_lncRNA::1::3288	-9141, 1995, 1963	upstream, in gene, in gene	1	1	29	27	2	2_A375_pNL97_plus_lncRNA::1	43	Gene PLEKHG4	ARHGEF44, SCA4, DKFZp434I216, PRTPHN1, PLEKHG4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	NM_015432, NM_001129727, NM_001129728, NM_001129729, NM_001129731, hCT1954050.2, hCT2324433.1, hCT2356331.0, hCT2356332.0, hCT2356333.0	228171_s_at	NP_056247.1, NP_001123199.1, NP_001123200.1, NP_001123201.1, NP_001123203.1, EAW83121.1, EAW83117.1, EAW83118.1, EAW83119.1, EAW83120.1
GeneID:146212	KCTD19	16	67,323,393	67,360,661	37,268	-	3	1_A375_pNL7_minus_lncRNA::1::2313, 2_A375_pNL97_plus_lncRNA::1::3288, 2_A375_pNL97_plus_lncRNA::1::3289	47253, 47285, 14533	downstream, downstream, in gene	1	1	28.5	29	2	2_A375_pNL97_plus_lncRNA::1	43	Gene KCTD19	FLJ40162, KCTD19	potassium channel tetramerisation domain containing 19	NM_001100915	244538_at	NP_001094385.1
GeneID:9114	ATP6V0D1	16	67,471,917	67,515,089	43,172	-	2	2_A375_pNL97_plus_lncRNA::1::3290, 2_A375_pNL97_plus_lncRNA::1::3291	15329, -655	in gene, upstream	0	1	15	20.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene ATP6V0D1	ATP6V0D1, P39, VATX, ATP6DV, FLJ43534, VPATPD, ATP6D, VMA6	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	NM_004691, hCT1814064.1, hCT2356346.0	212041_at	NP_004682.2, EAW83135.1, EAW83136.1
GeneID:181	AGRP	16	67,516,474	67,517,716	1,242	-	1	2_A375_pNL97_plus_lncRNA::1::3291	1972	downstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene AGRP	AGRP, ASIP2, ART, MGC118963, AGRT	agouti related protein homolog (mouse)	NM_001138, hCT19970.2	207193_at	NP_001129.1, EAW83137.1
GeneID:100505942	LOC100505942	16	67,551,609	67,562,551	10,942	-	2	1_A375_pNL7_minus_lncRNA::1::2314, 2_A375_pNL97_plus_lncRNA::1::3292	7287, 6999	in gene, in gene	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100505942		hypothetical LOC100505942	XR_109313, XR_109314		
GeneID:79567	FAM65A	16	67,562,717	67,580,691	17,974	+	2	1_A375_pNL7_minus_lncRNA::1::2314, 2_A375_pNL97_plus_lncRNA::1::3292	-7453, -7165	upstream, upstream	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene FAM65A	FLJ13725, KIAA1930, FAM65A	family with sequence similarity 65, member A	NM_001193522, NM_024519, NM_001193523, NM_001193524, hCT1814045.2, hCT2324439.0, hCT2324440.0, hCT2324442.0	218029_at, 230806_s_at, 45749_at	NP_001180451.1, NP_078795.2, NP_001180452.1, NP_001180453.1, EAW83138.1, EAW83141.1, EAW83139.1, EAW83140.1
GeneID:10664	CTCF	16	67,596,310	67,673,088	76,778	+	3	1_A375_pNL7_minus_lncRNA::1::2315, 2_A375_pNL97_plus_lncRNA::1::3293, 2_A375_pNL97_plus_lncRNA::1::3294	-150, -70, 874	upstream, upstream, in gene	1	1	20	19	2	1_A375_pNL7_minus_lncRNA::1	26	Gene CTCF	CTCF		NM_001191022, NM_006565, hCT18269.3, hCT2351072.0, hCT2351073.0, hCT2351074.0, hCT2351075.0	202521_at	NP_001177951.1, NP_006556.1, EAW83142.1, EAW83143.1, EAW83145.1, EAW83146.1, EAW83144.1
GeneID:146206	RLTPR	16	67,679,030	67,691,472	12,442	+	2	2_A375_pNL97_plus_lncRNA::1::3295, 2_A375_pNL97_plus_lncRNA::1::3296	7306, 21989	in gene, downstream	0	1	11.5	16	2	2_A375_pNL97_plus_lncRNA::1	16	Gene RLTPR	CARMIL2b, CARMIL2, RLTPR, LRRC16C	RGD motif, leucine rich repeats, tropomodulin domain and proline-rich containing	NM_001013838	227216_at, 227218_at	NP_001013860.1
GeneID:65057	ACD	16	67,691,415	67,694,718	3,303	-	2	2_A375_pNL97_plus_lncRNA::1::3295, 2_A375_pNL97_plus_lncRNA::1::3296	8382, -6301	downstream, upstream	0	1	11.5	16	2	2_A375_pNL97_plus_lncRNA::1	16	Gene ACD	PIP1, PTOP, ACD, TINT1, TPP1	adrenocortical dysplasia homolog (mouse)	NM_001082486, NM_022914, NM_001082487, hCT18274.1, hCT2325356.0	204617_s_at	NP_001075955.1, NP_075065.2, NP_001075956.1, EAW83154.1, EAW83155.1
GeneID:50855	PARD6A	16	67,694,851	67,696,681	1,830	+	2	2_A375_pNL97_plus_lncRNA::1::3295, 2_A375_pNL97_plus_lncRNA::1::3296	-8515, 6168	upstream, downstream	0	1	11.5	16	2	2_A375_pNL97_plus_lncRNA::1	16	Gene PARD6A	TAX40, PAR6alpha, PARD6A, PAR6C, PAR-6A, TIP-40, PAR6	par-6 partitioning defective 6 homolog alpha (C. elegans)	NM_016948, NM_001037281	205245_at	NP_058644.1, NP_001032358.1
GeneID:84080	C16orf48	16	67,696,850	67,700,628	3,778	-	1	2_A375_pNL97_plus_lncRNA::1::3296	-391	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C16orf48	C16orf48, DKFZp434A1319, DAKV6410	chromosome 16 open reading frame 48	NM_032140	223407_at	NP_115516.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:388284	C16orf86	16	67,700,717	67,702,661	1,944	+	1	2_A375_pNL97_plus_lncRNA::1::3296	302	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C16orf86	C16orf86	chromosome 16 open reading frame 86	NM_001012984, hCT1642908.3, hCT2324450.0, hCT2356337.0	231153_at	NP_001013002.2, EAW83162.1, EAW83163.1, EAW83164.1
GeneID:81577	GFOD2	16	67,708,436	67,753,273	44,837	-	1	2_A375_pNL97_plus_lncRNA::1::3296	52254	downstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene GFOD2	FLJ23802, MGC11335, GFOD2	glucose-fructose oxidoreductase domain containing 2	NM_030819, NR_027398, NR_027399	221028_s_at	NP_110446.3
GeneID:57610	RANBP10	16	67,757,005	67,840,555	83,550	-	2	1_A375_pNL7_minus_lncRNA::1::2316, 2_A375_pNL97_plus_lncRNA::1::3297	-21, -117	upstream, upstream	1	1	30	25	1	1_A375_pNL7_minus_lncRNA::1	30	Gene RANBP10	KIAA1464, RANBP10, FLJ31165	RAN binding protein 10	NM_020850, hCT1814066.2, hCT2356324.0	1556773_s_at, 221809_at, 232329_at, 53987_at	NP_065901.1, EAW83167.1, EAW83168.1
GeneID:55815	TSNAXIP1	16	67,841,010	67,861,971	20,961	+	3	1_A375_pNL7_minus_lncRNA::1::2316, 2_A375_pNL97_plus_lncRNA::1::3297, 2_A375_pNL97_plus_lncRNA::1::3298	-434, -338, 26670	upstream, upstream, downstream	1	1	24.5	21.5	2	1_A375_pNL7_minus_lncRNA::1	30	Gene TSNAXIP1	TSNAXIP1, TXI1, MGC111443	translin-associated factor X interacting protein 1	NM_018430, hCT19262.3, hCT2324732.0, hCT2324733.0, hCT2324734.0, hCT2324735.0, hCT2324736.0, hCT2356321.0, hCT2356322.0, hCT2356323.0	222220_s_at	NP_060900.2, EAW83174.1, EAW83169.1, EAW83170.1, EAW83171.1, EAW83175.1, EAW83172.1, EAW83173.1, EAW83176.1, EAW83177.1
GeneID:80152	CENPT	16	67,862,060	67,881,361	19,301	-	4	1_A375_pNL7_minus_lncRNA::1::2317, 1_A375_pNL7_minus_lncRNA::1::2318, 2_A375_pNL97_plus_lncRNA::1::3298, 2_A375_pNL97_plus_lncRNA::1::3299	4785, 529, -13661, 673	in gene, in gene, in gene, in gene	1	1	20	21	3	2_A375_pNL97_plus_lncRNA::1	29	Gene CENPT	FLJ43376, C16orf56, FLJ13111, CENP-T, CENPT	centromere protein T	NM_025082, hCT2325094.0, hCT2344027.1	218148_at	NP_079358.3, EAW83178.1, EAW83179.1
GeneID:57215	THAP11	16	67,876,213	67,878,098	1,885	+	4	1_A375_pNL7_minus_lncRNA::1::2317, 1_A375_pNL7_minus_lncRNA::1::2318, 2_A375_pNL97_plus_lncRNA::1::3298, 2_A375_pNL97_plus_lncRNA::1::3299	363, 4619, -8533, 4475	in gene, downstream, upstream, downstream	1	1	20	21	3	2_A375_pNL97_plus_lncRNA::1	29	Gene THAP11	HRIHFB2206, CTG-B43a, THAP11, CTG-B45d, RONIN	THAP domain containing 11	NM_020457, hCT2347501.0	212910_at, 226788_at	NP_065190.2, EAW83180.1
GeneID:10204	NUTF2	16	67,880,819	67,905,219	24,400	+	4	1_A375_pNL7_minus_lncRNA::1::2317, 1_A375_pNL7_minus_lncRNA::1::2318, 2_A375_pNL97_plus_lncRNA::1::3299, 2_A375_pNL97_plus_lncRNA::1::3300	-4243, 13, -131, 26189	upstream, in gene, upstream, downstream	1	1	18	22	3	2_A375_pNL97_plus_lncRNA::1	29	Gene NUTF2	NUTF2, PP15, NTF2	nuclear transport factor 2	NM_005796, hCT19254.1, hCT2324738.0	202397_at, 228379_at	NP_005787.1, EAW83181.1, EAW83182.1
GeneID:23644	EDC4	16	67,906,999	67,918,406	11,407	+	1	2_A375_pNL97_plus_lncRNA::1::3300	9	in gene	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene EDC4	RCD-8, HEDLS, Ge-1, EDC4	enhancer of mRNA decapping 4	NM_014329, hCT19251.3	202496_at	NP_055144.3, EAW83183.1
GeneID:5681	PSKH1	16	67,927,175	67,963,581	36,406	+	1	2_A375_pNL97_plus_lncRNA::1::3301	42713	downstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PSKH1	PSKH1		NM_006742, hCT19257.3	213141_at	NP_006733.1, EAW83185.1
GeneID:1506	CTRL	16	67,963,473	67,965,765	2,292	-	1	2_A375_pNL97_plus_lncRNA::1::3301	-4123	upstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CTRL	CTRL1, CTRL, MGC70821	chymotrypsin-like	NM_001907	214377_s_at	NP_001898.1
GeneID:5699	PSMB10	16	67,968,407	67,970,753	2,346	-	1	2_A375_pNL97_plus_lncRNA::1::3301	865	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PSMB10	MGC1665, beta2i, LMP10, PSMB10, FLJ00366, MECL1	proteasome (prosome, macropain) subunit, beta type, 10	NM_002801	202659_at	NP_002792.1
GeneID:3931	LCAT	16	67,973,787	67,978,015	4,228	-	1	2_A375_pNL97_plus_lncRNA::1::3301	8127	downstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LCAT	LCAT		NM_000229, hCT2325082.0	204428_s_at, 216390_at	NP_000220.1, EAW83190.1
GeneID:6560	SLC12A4	16	67,977,377	68,002,597	25,220	-	1	2_A375_pNL97_plus_lncRNA::1::3301	32709	downstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SLC12A4	FLJ40489, SLC12A4, KCC1, FLJ17069	solute carrier family 12 (potassium/chloride transporters), member 4	NM_005072, NM_001145961, NM_001145962, NM_001145963, NM_001145964, hCT2344773.0, hCT2344774.0, hCT2344775.0, hCT2344776.0, hCT2356363.0, hCT2356364.0	209400_at, 209401_s_at, 209402_s_at, 211112_at, 228644_s_at	NP_005063.1, NP_001139433.1, NP_001139434.1, NP_001139435.1, NP_001139436.1, EAW83194.1, EAW83191.1, EAW83192.1, EAW83193.1, EAW83195.1, EAW83196.1
GeneID:55794	DDX28	16	68,055,177	68,057,770	2,593	-	1	2_A375_pNL97_plus_lncRNA::1::3302	618	in gene	0	1	25	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene DDX28	FLJ11282, DDX28, MDDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	NM_018380, hCT1643475.2	203784_s_at, 203785_s_at, 214025_at, 40255_at	NP_060850.2, EAW83206.1
GeneID:54920	DUS2L	16	68,057,204	68,113,184	55,980	+	3	1_A375_pNL7_minus_lncRNA::1::2319, 2_A375_pNL97_plus_lncRNA::1::3302, 2_A375_pNL97_plus_lncRNA::1::3303	62380, -52, 61676	downstream, upstream, downstream	1	1	17.67	16.67	3	2_A375_pNL97_plus_lncRNA::1	19	Gene DUS2L	DUS2L, URLC8, DUS2, FLJ20399, SMM1	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	NM_017803, hCT19261.2, hCT2324745.0, hCT2324746.0	219486_at, 47105_at	NP_060273.1, EAW83209.1, EAW83207.1, EAW83208.1
GeneID:4775	NFATC3	16	68,119,375	68,260,837	141,462	+	2	1_A375_pNL7_minus_lncRNA::1::2319, 2_A375_pNL97_plus_lncRNA::1::3303	209, -495	in gene, upstream	1	1	14	15.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene NFATC3	NFATC3, NFATX, NFAT4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	NM_004555, NM_173163, NM_173164, NM_173165, hCT19249.2, hCT2324748.0, hCT2324749.0, hCT2324751.0	207416_s_at, 210555_s_at, 210556_at	NP_004546.1, NP_775186.1, NP_775187.1, NP_775188.1, EAW83211.1, EAW83212.1, EAW83210.1, EAW83213.1
GeneID:80004	ESRP2	16	68,262,450	68,270,136	7,686	-	2	1_A375_pNL7_minus_lncRNA::1::2320, 2_A375_pNL97_plus_lncRNA::1::3304	-9048, -9032	upstream, upstream	1	1	25	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ESRP2	FLJ22248, RBM35B, FLJ21918, ESRP2	epithelial splicing regulatory protein 2	NM_024939, hCT19265.2, hCT2356329.0, hCT2356330.0	219395_at, 225137_at, 225139_at, 225141_at	NP_079215.2, EAW83214.1, EAW83215.1, EAW83216.1
GeneID:23659	PLA2G15	16	68,279,247	68,294,961	15,714	+	3	1_A375_pNL7_minus_lncRNA::1::2320, 2_A375_pNL97_plus_lncRNA::1::3304, 2_A375_pNL97_plus_lncRNA::1::3305	-63, -79, 19537	upstream, upstream, downstream	1	1	19	27	2	2_A375_pNL97_plus_lncRNA::1	28	Gene PLA2G15	LLPL, LPLA2, GXVPLA2, PLA2G15, LYPLA3, ACS, DKFZp564A0122	phospholipase A2, group XV	NM_012320, hCT19248.1, hCT2356349.0	204458_at	NP_036452.1, EAW83217.1, EAW83218.1
GeneID:9057	SLC7A6	16	68,298,423	68,335,722	37,299	+	3	1_A375_pNL7_minus_lncRNA::1::2321, 2_A375_pNL97_plus_lncRNA::1::3305, 2_A375_pNL97_plus_lncRNA::1::3306	46313, 361, 46345	downstream, in gene, downstream	1	1	15.5	23	2	2_A375_pNL97_plus_lncRNA::1	26	Gene SLC7A6	LAT3, SLC7A6, y+LAT-2, LAT-2, DKFZp686K15246, KIAA0245	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	NM_003983, NM_001076785, hCT19247.2, hCT2324754.0	203578_s_at, 203579_s_at, 203580_s_at, 229153_at	NP_003974.3, NP_001070253.1, EAW83219.1, EAW83220.1
GeneID:84138	SLC7A6OS	16	68,334,518	68,344,868	10,350	-	2	1_A375_pNL7_minus_lncRNA::1::2321, 2_A375_pNL97_plus_lncRNA::1::3306	132, 100	in gene, in gene	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC7A6OS	FLJ13291, SLC7A6OS	solute carrier family 7, member 6 opposite strand	NM_032178, hCT19264.2, hCT2356325.0	232057_at	NP_115554.2, EAW83223.1, EAW83222.1
GeneID:54496	PRMT7	16	68,344,877	68,391,169	46,292	+	2	1_A375_pNL7_minus_lncRNA::1::2321, 2_A375_pNL97_plus_lncRNA::1::3306	-141, -109	upstream, upstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PRMT7	KIAA1933, FLJ10640, PRMT7	protein arginine methyltransferase 7	NM_001184824, NM_019023, hCT19260.3, hCT1964124.1, hCT1964125.1, hCT1964126.1, hCT1964127.1, hCT1964128.1, hCT1964129.1, hCT2356314.0, hCT2356315.0	219408_at	NP_001171753.1, NP_061896.1, EAW83225.1, EAW83226.1, EAW83229.1, EAW83231.1, EAW83224.1, EAW83227.1, EAW83228.1, EAW83230.1, EAW83232.1
GeneID:55512	SMPD3	16	68,392,230	68,482,409	90,179	-	4	1_A375_pNL7_minus_lncRNA::1::2322, 1_A375_pNL7_minus_lncRNA::1::2323, 2_A375_pNL97_plus_lncRNA::1::3307, 2_A375_pNL97_plus_lncRNA::1::3308	4233, -87, 4265, -183	in gene, upstream, in gene, upstream	1	1	22	30	2	2_A375_pNL97_plus_lncRNA::1	32	Gene SMPD3	FLJ22593, SMPD3, NSMASE2, MGC138443	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	NM_018667, hCT2325105.0	219695_at, 231732_at	NP_061137.1, EAW83233.1
GeneID:1001	CDH3	16	68,678,151	68,732,957	54,806	+	2	1_A375_pNL7_minus_lncRNA::1::2324, 2_A375_pNL97_plus_lncRNA::1::3309	24121, 24249	in gene, in gene	1	1	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene CDH3	CDH3, HJMD, PCAD, CDHP	cadherin 3, type 1, P-cadherin (placental)	NM_001793, hCT17787.3, hCT2324729.0, hCT2356297.0	203256_at	NP_001784.2, EAW83239.1, EAW83237.1, EAW83238.1
GeneID:79613	TMCO7	16	68,877,509	69,119,085	241,576	+	1	2_A375_pNL97_plus_lncRNA::1::3310	229931	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene TMCO7	FLJ12688, TMCO7, KIAA1746	transmembrane and coiled-coil domains 7	NM_024562	226467_at	NP_078838.1
GeneID:84916	CIRH1A	16	69,166,499	69,202,937	36,438	+	1	1_A375_pNL7_minus_lncRNA::1::2325	33837	in gene	1	0	16	9	1	1_A375_pNL7_minus_lncRNA::1	16	Gene CIRH1A	NAIC, FLJ17146, FLJ14728, KIAA1988, CIRHIN, CIRH1A, TEX292	cirrhosis, autosomal recessive 1A (cirhin)	NM_032830, hCT19356.3, hCT2326195.0, hCT2326196.0, hCT2326197.0, hCT2326198.0, hCT2356327.0, hCT2356328.0	224903_at, 230656_s_at	NP_116219.2, EAW83251.1, EAW83252.1, EAW83253.1, EAW83254.1, EAW83256.1, EAW83255.1, EAW83257.1
GeneID:6645	SNTB2	16	69,221,050	69,342,955	121,905	+	2	1_A375_pNL7_minus_lncRNA::1::2326, 2_A375_pNL97_plus_lncRNA::1::3311	38, 6	in gene, in gene	1	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SNTB2	SNTB2, D16S2531E, EST25263, SNTL, SNT2B2, SNT3	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	NM_006750, hCT19348.2, hCT2326200.0, hCT2326201.0	205314_x_at, 205315_s_at, 213814_s_at, 214350_at, 226685_at, 227312_at, 238925_at	NP_006741.1, EAW83258.1, EAW83259.1, EAW83260.1
GeneID:27183	VPS4A	16	69,345,287	69,358,946	13,659	+	1	2_A375_pNL97_plus_lncRNA::1::3312	19257	downstream	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene VPS4A	VPS4A, FLJ22197, VPS4-1, SKD2, SKD1, VPS4, SKD1A	vacuolar protein sorting 4 homolog A (S. cerevisiae)	NM_013245, hCT19347.2, hCT2326203.0, hCT2326205.0, hCT2356346.0	217913_at	NP_037377.1, EAW83263.1, EAW83261.1, EAW83262.1, EAW83264.1
GeneID:100506031	LOC100506031	16	69,359,469	69,376,357	16,888	-	3	1_A375_pNL7_minus_lncRNA::1::2327, 2_A375_pNL97_plus_lncRNA::1::3312, 2_A375_pNL97_plus_lncRNA::1::3313	2821, 11813, 2885	in gene, in gene, in gene	1	1	30	32.5	2	2_A375_pNL97_plus_lncRNA::1	44	Gene LOC100506031	FLJ35053	hypothetical LOC100506031	XR_111589, XR_111590, XR_109315, XR_109316, XR_115016, XR_115017		
GeneID:64146	PDF	16	69,362,524	69,364,498	1,974	-	3	1_A375_pNL7_minus_lncRNA::1::2327, 2_A375_pNL97_plus_lncRNA::1::3312, 2_A375_pNL97_plus_lncRNA::1::3313	-9038, -46, -8974	upstream, upstream, upstream	1	1	30	32.5	2	2_A375_pNL97_plus_lncRNA::1	44	Gene PDF	PDF		NM_022341	219575_s_at	NP_071736.1
GeneID:84342	COG8	16	69,362,524	69,373,526	11,002	-	3	1_A375_pNL7_minus_lncRNA::1::2327, 2_A375_pNL97_plus_lncRNA::1::3312, 2_A375_pNL97_plus_lncRNA::1::3313	-10, 8982, 54	upstream, in gene, in gene	1	1	30	32.5	2	2_A375_pNL97_plus_lncRNA::1	44	Gene COG8	FLJ22315, DOR1, CDG2H, COG8	component of oligomeric golgi complex 8	NM_032382		NP_115758.3
GeneID:51388	NIP7	16	69,373,546	69,377,009	3,463	+	3	1_A375_pNL7_minus_lncRNA::1::2327, 2_A375_pNL97_plus_lncRNA::1::3312, 2_A375_pNL97_plus_lncRNA::1::3313	-10, -9002, -74	upstream, upstream, upstream	1	1	30	32.5	2	2_A375_pNL97_plus_lncRNA::1	44	Gene NIP7	KD93, NIP7, FLJ10296, HSPC031, CGI-37	nuclear import 7 homolog (S. cerevisiae)	NM_016101, hCT19346.2, hCT2326208.0	219031_s_at, 223397_s_at	NP_057185.1, EAW83271.1, EAW83270.1
GeneID:146456	TMED6	16	69,377,149	69,385,712	8,563	-	2	1_A375_pNL7_minus_lncRNA::1::2327, 2_A375_pNL97_plus_lncRNA::1::3313	12176, 12240	downstream, downstream	1	1	42	44	1	2_A375_pNL97_plus_lncRNA::1	44	Gene TMED6	PRO34237, TMED6, SPLL9146, MGC23911	transmembrane emp24 protein transport domain containing 6	NM_144676, hCT19357.2	236430_at	NP_653277.2, EAW83272.1
GeneID:80777	CYB5B	16	69,458,498	69,500,167	41,669	+	1	2_A375_pNL97_plus_lncRNA::1::3314	62	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene CYB5B	CYB5-M, DKFZp686M0619, CYPB5M, CYB5B, OMB5	cytochrome b5 type B (outer mitochondrial membrane)	NM_030579, hCT19353.2, hCT2326210.0	201633_s_at, 201634_s_at, 227382_at, 238554_at	NP_085056.2, EAW83275.1, EAW83276.1
GeneID:10725	NFAT5	16	69,598,997	69,738,553	139,556	+	1	2_A375_pNL97_plus_lncRNA::1::3316	747	in gene	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene NFAT5	NFAT5, NF-AT5, KIAA0827, OREBP, NFATL1, NFATZ, TONEBP	nuclear factor of activated T-cells 5, tonicity-responsive	NM_138714, NM_006599, NM_138713, NM_173214, NM_001113178, hCT17785.4, hCT2344109.0, hCT2344110.0, hCT2344111.0, hCT2344112.0	208003_s_at, 215092_s_at, 224984_at	NP_619728.2, NP_006590.1, NP_775321.1, NP_619727.2, NP_001106649.1, EAW83281.1, EAW83277.1, EAW83278.1, EAW83279.1, EAW83280.1
GeneID:100302119	MIR1538	16	69,599,711	69,599,771	60	-	1	2_A375_pNL97_plus_lncRNA::1::3316	27	in gene	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene MIR1538	hsa-mir-1538, MIR1538, MIRN1538	microRNA 1538	NR_031719		
GeneID:1728	NQO1	16	69,743,304	69,760,533	17,229	-	1	2_A375_pNL97_plus_lncRNA::1::3317	149	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NQO1	DIA4, NMOR1, QR1, NMORI, NQO1, DHQU, DTD	NAD(P)H dehydrogenase, quinone 1	NM_000903, NM_001025433, NM_001025434, hCT19352.3, hCT2326321.0, hCT2356316.0	201467_s_at, 201468_s_at, 210519_s_at	NP_000894.1, NP_001020604.1, NP_001020605.1, EAW83282.1, EAW83283.1, EAW83284.1
GeneID:28987	NOB1	16	69,775,774	69,788,829	13,055	-	1	2_A375_pNL97_plus_lncRNA::1::3318	61	in gene	0	1	11	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene NOB1	ART-4, NOB1, MST158, MSTP158, NOB1P, PSMD8BP1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	NM_014062, hCT1813234.1, hCT2324997.0	223018_at	NP_054781.1, EAW83285.1, EAW83286.1
GeneID:11060	WWP2	16	69,796,274	69,975,643	179,369	+	1	2_A375_pNL97_plus_lncRNA::1::3318	-7506	upstream	0	1	11	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene WWP2	WWP2, AIP2, WWp2-like	WW domain containing E3 ubiquitin protein ligase 2	NM_007014, NM_199423, NM_199424, hCT2324278.0, hCT2324279.0, hCT2324281.0	1552737_s_at, 1554580_a_at, 204022_at, 210200_at	NP_008945.2, NP_955455.1, NP_955456.1, EAW83287.1, EAW83288.1, EAW83289.1
GeneID:118460	EXOSC6	16	70,284,134	70,285,833	1,699	-	2	1_A375_pNL7_minus_lncRNA::1::2328, 2_A375_pNL97_plus_lncRNA::1::3319	9, -23	in gene, upstream	1	1	79	82	1	2_A375_pNL97_plus_lncRNA::1	82	Gene EXOSC6	hMtr3p, Mtr3p, EAP4, EXOSC6, p11, MTR3	exosome component 6	NM_058219, hCT1646330.3	1553947_at, 1556044_s_at, 227696_at, 231916_at	NP_478126.1, EAW51841.1
GeneID:16	AARS	16	70,286,297	70,323,412	37,115	-	4	1_A375_pNL7_minus_lncRNA::1::2328, 1_A375_pNL7_minus_lncRNA::1::2329, 2_A375_pNL97_plus_lncRNA::1::3319, 2_A375_pNL97_plus_lncRNA::1::3320	37568, -9708, 37556, -9820	downstream, upstream, downstream, upstream	1	1	47.5	49.5	2	2_A375_pNL97_plus_lncRNA::1	82	Gene AARS	CMT2N, AARS		NM_001605, hCT1962415.1, hCT1962416.1, hCT23802.2	201000_at	NP_001596.2, EAW51838.1, EAW51839.1, EAW51840.1
GeneID:11269	DDX19B	16	70,333,072	70,367,731	34,659	+	2	1_A375_pNL7_minus_lncRNA::1::2329, 2_A375_pNL97_plus_lncRNA::1::3320	48, 160	in gene, in gene	1	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene DDX19B	DBP5, RNAh, DDX19, DDX19B	DEAD (Asp-Glu-Ala-As) box polypeptide 19B	NM_007242, NM_001014449, NM_001014451	230974_at	NP_009173.1, NP_001014449.1, NP_001014451.1
GeneID:100506083	LOC100506083	16	70,349,543	70,380,678	31,135	-	2	1_A375_pNL7_minus_lncRNA::1::2330, 2_A375_pNL97_plus_lncRNA::1::3321	-122, -90	upstream, upstream	1	1	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene LOC100506083		hypothetical LOC100506083	XR_111591, XR_109317, XR_115018		
GeneID:55308	DDX19A	16	70,380,824	70,407,284	26,460	+	2	1_A375_pNL7_minus_lncRNA::1::2330, 2_A375_pNL97_plus_lncRNA::1::3321	-24, -56	upstream, upstream	1	1	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene DDX19A	DDX19L, DDX19-DDX19L, DKFZp686C21137, DDX19A, FLJ11126	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	NM_018332	1570128_at, 202577_s_at, 202578_s_at	NP_060802.1
GeneID:6483	ST3GAL2	16	70,413,338	70,472,991	59,653	-	2	1_A375_pNL7_minus_lncRNA::1::2331, 2_A375_pNL97_plus_lncRNA::1::3322	-257, -289	upstream, upstream	1	1	34	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene ST3GAL2	ST3GAL2, ST3GALII, SIAT4B, ST3GalA.2, Gal-NAc6S	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	NM_006927, hCT2280377.0, hCT2280379.0, hCT2280380.0, hCT23556.3	217650_x_at, 229336_at	NP_008858.1, EAW51820.1, EAW51818.1, EAW51819.1, EAW51821.1
GeneID:197258	FUK	16	70,488,498	70,514,177	25,679	+	3	1_A375_pNL7_minus_lncRNA::1::2332, 1_A375_pNL7_minus_lncRNA::1::2333, 2_A375_pNL97_plus_lncRNA::1::3323	-130, 3070, -146	upstream, in gene, upstream	1	1	34	42	2	2_A375_pNL97_plus_lncRNA::1	71	Gene FUK	1110046B12Rik, FLJ39408, FUK	fucokinase	NM_145059, hCT1812709.2, hCT2352496.0, hCT2352497.0, hCT2352498.0	226072_at	NP_659496.2, EAW51814.1, EAW51815.1, EAW51816.1, EAW51817.1
GeneID:25839	COG4	16	70,514,472	70,557,457	42,985	-	1	2_A375_pNL97_plus_lncRNA::1::3324	-431	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene COG4	COD1, DKFZp586E1519, CDG2J, COG4	component of oligomeric golgi complex 4	NM_015386, hCT2280370.0, hCT2280371.0, hCT2280373.0, hCT2280374.0, hCT2352493.0, hCT2352494.0, hCT2352495.0, hCT23804.2	212189_s_at	NP_056201.2, EAW51810.1, EAW51807.1, EAW51808.1, EAW51809.1, EAW51813.1, EAW51806.1, EAW51811.1, EAW51812.1
GeneID:23450	SF3B3	16	70,557,691	70,611,571	53,880	+	1	2_A375_pNL97_plus_lncRNA::1::3324	197	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SF3B3	SF3B3, KIAA0017, RSE1, STAF130, SF3b130, SAP130	splicing factor 3b, subunit 3, 130kDa	NM_012426, hCT2280811.0, hCT2280812.0, hCT2280813.0	200687_s_at, 200688_at	NP_036558.3, EAW51803.1, EAW51804.1, EAW51805.1
GeneID:100113402	SNORD111B	16	70,563,405	70,563,498	93	+	1	2_A375_pNL97_plus_lncRNA::1::3324	-5517	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORD111B	SNORD111B	small nucleolar RNA, C/D box 111B	NR_003696		
GeneID:55697	VAC14	16	70,721,342	70,835,061	113,719	-	1	2_A375_pNL97_plus_lncRNA::1::3325	53	in gene	0	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene VAC14	FLJ46582, MGC149816, ArPIKfyve, VAC14, TRX, TAX1BP2, FLJ10305, FLJ36622, MGC149815	Vac14 homolog (S. cerevisiae)	NM_018052, hCT2280359.0, hCT2280360.0, hCT2280361.0, hCT2280363.0, hCT2280364.0	216407_at, 216501_at, 218169_at	NP_060522.3, EAW51793.1, EAW51791.1, EAW51792.1, EAW51794.1, EAW51795.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervention Count	Interventions	Interval Dist to gene	Interval Pos.	(A)	(B)	(C)	(D)	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
Gene:ID:34764168	HYDIN	16	70,641,269	71,264,969	623,200	-	9	1_A275_shN37_shrna_loc#NA:1:-2334,1_A275_shN37_shrna_loc#NA:1:-2335,2_A275_shN37_shrna_loc#NA:1:-3326,2_A275_shN37_shrna_loc#NA:1:-3326,2_A275_shN37_shrna_loc#NA:1:-3327,2_A275_shN37_shrna_loc#NA:1:-3328	342237,211401,425951,365809,342193,211417	st gene, ut gene, downstream, st gene, ut gene, ut gene	27	30.5	4	2_A275_shN37_shrna_loc#NA:1	59	Gene HYDIN	DKFZp434G0350, HYDIN1, FLJ12571, HYDIN, HYDIN2, DKFZp434G0613, KIAA1064, FLJ14865	Hydrocephalus-inducing homolog (mouse)	NM_017555, NM_032521, XM_011523740.1	1864900_at, 2260996_at, 2323654_at	NP_060026.2, NP_116218.2, EAW80249.1
Gene:ID:5763	PTSJDI	16	71,316,203	71,323,809	7,606	-	2	1_A275_shN37_shrna_loc#NA:1:-2336,2_A275_shN37_shrna_loc#NA:1:-3329	389, 421	st gene, ut gene	1	1	21	17	1	1_A275_shN37_shrna_loc#NA:1	21	Gene PTSJDI	PTSJDI, APT, FLJ11371	PNJ methyltransferase domain containing 1	NM_018346, NM_001039842, NCT22987869.0, NCT22988000.0	222611_at	NP_060815.4, NP_001093112.1, EAW59246.1, EAW59247.1
Gene:ID:57827	ZNF23	16	71,451,800	71,466,117	14,317	-	4	1_A275_shN37_shrna_loc#NA:1:-2337,1_A275_shN37_shrna_loc#NA:1:-2335,2_A275_shN37_shrna_loc#NA:1:-3330,2_A275_shN37_shrna_loc#NA:1:-3331	-21, -9975, 66, -5107	upstream, upstream, st gene, upstream	1	1	34.5	42	2	2_A275_shN37_shrna_loc#NA:1	52	Gene ZNF23	MGC97383, KOX16, ZNF612, ZNF23, Zfp612, ZNF239	Zinc finger protein 23 (KOX 16)	NM_148911		NP_996016.1
Gene:ID:103509515	LOC100510615	16	71,499,198	71,497,970	1,772	+	4	1_A275_shN37_shrna_loc#NA:1:-2337,1_A275_shN37_shrna_loc#NA:1:-2335,2_A275_shN37_shrna_loc#NA:1:-3331,2_A275_shN37_shrna_loc#NA:1:-3332	-54, 5996, 190, 3628	upstream, downstream, upstream, downstream	1	1	34.5	42	2	2_A275_shN37_shrna_loc#NA:1	52	Gene LOC100509515		hypothetical LOC100509103	XR_111592, XR_109216, XR_115018		
Gene:ID:57827	ZNF19	16	71,307,976	71,323,254	15,278	-	4	1_A275_shN37_shrna_loc#NA:1:-2335,2_A275_shN37_shrna_loc#NA:1:-3332,2_A275_shN37_shrna_loc#NA:1:-3333,2_A275_shN37_shrna_loc#NA:1:-3334	21462, 21432, 14326, 4606	downstream, downstream, st gene, ut gene	1	1	24.33	29	3	2_A275_shN37_shrna_loc#NA:1	52	Gene ZNF19	KOX12, MGC31021, ZNF19	Zinc finger protein 19	NM_006961	210834_s_at	NP_008992.2
Gene:ID:64	AP1G1	16	71,762,903	71,842,976	80,073	-	2	1_A275_shN37_shrna_loc#NA:1:-2339,2_A275_shN37_shrna_loc#NA:1:-3335	98, 176	st gene, ut gene	1	1	21	36	1	2_A275_shN37_shrna_loc#NA:1	26	Gene AP1G1	ADTG, AP1G1, MGC16255, CLAPG1	adaptor-related protein complex 1, gamma 1 subunit	NM_001128, NM_001030007, NCT19637930.7, NCT22987869.0, NCT24283.4	203290_at, 203794_at, 203771_at	NP_001119.5, NP_001028175.1, EAW59222.1, EAW59223.1, EAW59224.1
Gene:ID:42371	ATXN1L	16	71,879,899	71,919,174	39,275	+	2	1_A275_shN37_shrna_loc#NA:1:-2339,2_A275_shN37_shrna_loc#NA:1:-3336	-122, 46351	upstream, downstream	0	1	14	23	2	2_A275_shN37_shrna_loc#NA:1	27	Gene ATXN1L	BOAT, DKFZp566D0513, DKFZp997M0214, DKFZp686I01189, ATXN1L, FLJ21696, FLJ21960	Ataxin 1-like	NR_026612, NM_001127675	226053_s_at, 227172_at	NP_001131147.1
Gene:ID:7165	GAA	17	71,929,436	71,962,806	33,460	+	1	1_A275_shN37_shrna_loc#NA:1:-2340,2_A275_shN37_shrna_loc#NA:1:-3337	-166	upstream	0	1	14	27	1	2_A275_shN37_shrna_loc#NA:1	27	Gene KIAA0174	BTT, MGC117220, KIAA0174	KIAA0174	NM_014761, NCT23015330.0, NCT23015260.0, NCT23023946.0, NCT23023960.0, NCT24284.2	200851_s_at, 215553_at	NP_055576.2, EAW59209.1, EAW59205.1, EAW59206.1, EAW59207.1, EAW59208.1
Gene:ID:43272	PKD1L2	16	71,963,841	72,033,877	70,036	-	2	1_A275_shN37_shrna_loc#NA:1:-2340,2_A275_shN37_shrna_loc#NA:1:-3338	-5545, 5843	upstream, downstream	1	1	25	21	1	1_A275_shN37_shrna_loc#NA:1	25	Gene PKD1L2	PKD1L2		NM_183535, NCT23046840.0, NCT23055550.0, NCT24285.0	1553514_s_at	NP_853514.1, EAW59204.1, EAW59202.1, EAW59203.1
Gene:ID:723	DHODH	16	72,042,643	72,056,855	16,212	+	2	1_A275_shN37_shrna_loc#NA:1:-2340,2_A275_shN37_shrna_loc#NA:1:-3339	77, 77	st gene, ut gene	1	1	25	21	1	2_A275_shN37_shrna_loc#NA:1	25	Gene DHODH	URA1, POADS, DHODH, OHDobrlike	dihydroorotate dehydrogenase	NM_001361, NCT19376481, NCT23015440.0, NCT24286.4	213632_at	NP_001352.2, EAW59196.1, EAW59199.1, EAW59200.1, EAW59201.1
Gene:ID:4927	TXNL4B	16	72,118,799	72,126,215	8,456	-	2	1_A275_shN37_shrna_loc#NA:1:-2341,2_A275_shN37_shrna_loc#NA:1:-3339	963, 4398	st gene, ut gene	1	1	18	22	1	2_A275_shN37_shrna_loc#NA:1	22	Gene TXNL4B	DLP, FLJ20511, DxIZ, TXNL4B	thioredoxin-like 4B	NM_017852, NM_001142317, NM_001162316, NCT19457321.1, NCT19376540	218794_s_at, 227748_s_at	NP_060322.1, NP_001128769.1, NP_001135790.1, EAW59191.1, EAW59192.1
Gene:ID:7165	DHX38	16	72,127,615	72,146,611	19,196	+	2	1_A275_shN37_shrna_loc#NA:1:-2341,2_A275_shN37_shrna_loc#NA:1:-3339	463, 161	upstream, ut gene	1	1	18	22	1	2_A275_shN37_shrna_loc#NA:1	22	Gene DHX38	FRP16, DDX38, PRPF16, KIAA0224, DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	NM_014003, NCT23015597.0, NCT23015580.1, NCT23023972.0, NCT23024720.0, NCT23024740.0, NCT23024719.0, NCT23024770.0, NCT23024760.0, NCT23024752.0, NCT24286.3	209178_at	NP_054732.2, EAW59180.1, EAW59182.1, EAW59183.1, EAW59185.1, EAW59186.1, EAW59187.1, EAW59188.1, EAW59189.1, EAW59190.1
Gene:ID:6603	ZFHX3	16	72,616,764	73,092,554	275,790	-	2	1_A275_shN37_shrna_loc#NA:1:-2342,2_A275_shN37_shrna_loc#NA:1:-3340,2_A275_shN37_shrna_loc#NA:1:-3341	28099, 130742, 28099	st gene, ut gene, ut gene	1	1	19	22.5	2	1_A275_shN37_shrna_loc#NA:1	25	Gene ZFHX3	ZFHX3, ATBF, ATBP1, ZNF927	Zinc finger homeobox 3	NM_006885, NM_001164766, NCT22987290.0, NCT22987279.0, NCT23023.2	208033_s_at, 239127_at, 233701_at, 233752_s_at, 240136_s_at, 243333_s_at	NP_006786.1, NP_001182235.1, EAW59166.1, EAW59169.1, EAW59170.1
Gene:ID:51335	LOC100510152	16	73,045,973	73,046,276	703	+	2	1_A275_shN37_shrna_loc#NA:1:-2342,2_A275_shN37_shrna_loc#NA:1:-3340	-6290, 8170	upstream, upstream	1	1	28	24	1	1_A275_shN37_shrna_loc#NA:1	26	Gene LOC100509152		hypothetical LOC100509152	XR_111994, XR_109320, XR_110021		
Gene:ID:62239	ZFP1	16	73,182,821	73,206,132	23,711	+	1	1_A275_shN37_shrna_loc#NA:1:-2343	-133	upstream	0	1	16	25	1	2_A275_shN37_shrna_loc#NA:1	25	Gene ZFP1	ZFP1, ZNF473, FLJ22243	zinc finger protein 1 homolog (mouse)	NM_133698, NCT12638.2, NCT22989060.0	226007_at, 234653_at, 234810_at	NP_710153.2, EAW59563.1, EAW59562.1
Gene:ID:24481	TMEM170A	16	73,660,917	73,668,584	17,667	-	2	1_A275_shN37_shrna_loc#NA:1:-2343,2_A275_shN37_shrna_loc#NA:1:-3340	24, 56	st gene, ut gene	1	1	16	23	1	2_A275_shN37_shrna_loc#NA:1	23	Gene TMEM170A	TMEM170, FLJ37611, TMEM170A	transmembrane protein 170A	NM_145258, NCT01145871.1, NCT19352143, NCT19445651.1	227566_at, 235503_s_at, 235414_s_at	NP_660297.1, EAW59564.1, EAW59542.1, EAW59543.1
Gene:ID:7869	CHST6	16	73,507,022	73,526,826	21,804	-	2	1_A275_shN37_shrna_loc#NA:1:-2343,2_A275_shN37_shrna_loc#NA:1:-3340	33396, 30430	downstream, downstream	1	1	16	23	1	2_A275_shN37_shrna_loc#NA:1	23	Gene CHST6	MCDC1, CHST6	carbohydrate (N-acetylgalactosamine 6-O) sulfotransferase 6	NM_021615, NCT01641692.2, NCT23021000.0	223799_at	NP_067626.1, EAW59541.1, EAW59540.1
Gene:ID:8653	TMEM231	16	73,572,013	73,590,170	18,158	-	2	1_A275_shN37_shrna_loc#NA:1:-2344,2_A275_shN37_shrna_loc#NA:1:-3340	160, 156	st gene, ut gene	1	1	21	24	1	2_A275_shN37_shrna_loc#NA:1	24	Gene TMEM231	ALY5670, FKO1699, FLJ22167, TMEM231	tetratricopeptide protein 231	NM_001077416, NM_001077418, NM_001077419	218162_at, 48900_at	NP_001070884.1, NP_001070885.1, NP_001070887.1
Gene:ID:1345	GABARAPL2	16	73,600,249	73,611,779	11,530	+	2	1_A275_shN37_shrna_loc#NA:1:-2344,2_A275_shN37_shrna_loc#NA:1:-3340	-10169, 15263	upstream, upstream	1	1	21	24	1	2_A275_shN37_shrna_loc#NA:1	24	Gene GABARAPL2	GEF2, GATE16, ATG8, ATG8C, GATE-16, GABARAPL2	GABA(A) receptor-associated protein-like 2	NM_007285, NCT12589.2, NCT19804779.1	209309_s_at	NP_009216.1, EAW59630.1, EAW59629.1
Gene:ID:3735	KARS	16	73,661,622	73,681,565	19,963	-	1	1_A275_shN37_shrna_loc#NA:1:-2345	-291	upstream	0	1	14	20	1	2_A275_shN37_shrna_loc#NA:1	20	Gene KARS	KARS2, IUAN0750, KARS, KRS, CMTR	lysyl-tRNA synthetase	NM_005546, NM_001130859, NCT19852.2, NCT19852.3, NCT19852.1, NCT19512241.1, NCT19512251.1, NCT23023980.0	200972_s_at, 200973_s_at	NP_005539.1, NP_001122561.1, EAW59619.1, EAW59620.1, EAW59621.1, EAW59622.1, EAW59624.1
Gene:ID:6386	TERF2IP	16	73,681,633	73,691,340	9,708	+	1	1_A275_shN37_shrna_loc#NA:1:-2346	541	st gene	0	1	14	20	1	2_A275_shN37_shrna_loc#NA:1	20	Gene TERF2IP	DRIP5, RAP1, TERF2IP	telomeric repeat binding factor 2, interacting protein	NM_018975, NCT23023972.0, NCT23023972.0, NCT23023.0	201174_s_at	NP_061845.2, EAW59617.1, EAW59616.1, EAW59618.1
Gene:ID:7921	SYCE1L	16	73,233,549	77,249,876	13,827	+	1	1_A275_shN37_shrna_loc#NA:1:-3348	14771	downstream	0	1	13	23	1	2_A275_shN37_shrna_loc#NA:1	23	Gene SYCE1L	SYCE1L, MYP2	synaptonemal complex central element protein 1-like	NM_001129978	1561233_at	NP_001123451.1
Gene:ID:7457	VAT1L	16	77,822,483	78,014,891	191,916	+	1	1_A275_shN37_shrna_loc#NA:1:-3338	-222	upstream	0	1	14	16	1	2_A275_shN37_shrna_loc#NA:1	16	Gene VAT1L	VAT1L, KIAA1376	vesicle amine transport protein 1 homolog (T. californicus)-like	NM_032627, NCT16444402.3	226413_at	NP_060976.1, EAW59594.1
Gene:ID:1741	WWOX	16	78,133,551	79,246,264	1,112,013	+	3	1_A275_shN37_shrna_loc#NA:1:-2347,2_A275_shN37_shrna_loc#NA:1:-3350	-111, -76	upstream, upstream	1	1	28	42	1	2_A275_shN37_shrna_loc#NA:1	42	Gene WWOX	SDR41C1, WWOX, WOX1, FRA16D, WHCR4656, DKFZp313E212, FOR, FRO1/2B	WW domain containing oxidoreductase	NM_016373, NM_130791, NM_130848	210553_s_at, 210977_s_at, 221147_s_at, 221734_s_at, 221956_s_at	NP_057417, NP_570607.1, NP_570859.1
Gene:ID:994	MAD	18	76,627,745	76,638,822	6,877	-	1	2_A275_shN37_shrna_loc#NA:1:-3350	-130	upstream	0	1	12	21	1	2_A275_shN37_shrna_loc#NA:1	21	Gene MAD	c-MAF, MGC71655, MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	NM_005360, NM_001031804	205353_s_at, 1566224_at, 205352_at, 205347_s_at, 205348_s_at	NP_005351.2, NP_001028974.1
Gene:ID:2837	DYNLRB2	16	80,514,654	80,564,841	9,957	+	1	1_A275_shN37_shrna_loc#NA:1:-3356	-102	upstream	0	1	20	25	1	2_A275_shN37_shrna_loc#NA:1	25	Gene DYNLRB2	DYNLRB2, MGC62033, DNCL2B, ROBLD2, DNLC2B	dynein, light chain, roadblock-type 2	NM_130597, NCT7756.2	226116_at	NP_570857.1, EAW59566.1
Gene:ID:9842	C16orf61	16	81,009,699	81,040,802	30,803	-	2	1_A275_shN37_shrna_loc#NA:1:-3358,2_A275_shN37_shrna_loc#NA:1:-3359	-135, -170	upstream, upstream	1	1	23	16	1	1_A275_shN37_shrna_loc#NA:1	23	Gene C16orf61	C16orf61, DC13, 2310061C15Rik	chromosome 16 open reading frame 61	NM_030160, NCT16413.2, NCT19352.1, NCT19512041, NCT19352.2, NCT22521.0	218447_at	NP_064573.1, EAW59390.1, EAW59397.1, EAW59398.1, EAW59399.1
Gene:ID:5538	CENPN	16	81,040,103	81,066,712	26,609	+	2	1_A275_shN37_shrna_loc#NA:1:-2352,2_A275_shN37_shrna_loc#NA:1:-3358	537, 998	st gene, ut gene	1	1	23	16	1	1_A275_shN37_shrna_loc#NA:1	23	Gene CENPN	CENP-N, 8146.0g, CENPN, FLJ22690, C16orf60, FLJ13607	centromere protein N	NM_018455, NM_001100624, NM_001100625, NCT19512111, NCT23021980.0, NCT23023980.0	218553_s_at, 222116_at, 234611_at	NP_060925.1, NP_001094094.1, NP_001094095.1, EAW59554.1, EAW59555.1, EAW59553.1
Gene:ID:139	GAN	16	81,346,571	81,413,853	63,282	+	1	2_A275_shN37_shrna_loc#NA:1:-2353,2_A275_shN37_shrna_loc#NA:1:-3360	63, -123	st gene, upstream	1	1	14	24	1	2_A275_shN37_shrna_loc#NA:1	24	Gene GAN	GAN2, GAN, KLHL16, FLJ38559	gigaxonin	NM_022041, NCT13209.2	226124_at	NP_071324.1, EAW59538.1
Gene:ID:3200	MPHOSPH6	16	82,151,767	82,203,629	22,082	-	2	1_A275_shN37_shrna_loc#NA:1:-2356,2_A275_shN37_shrna_loc#NA:1:-3360	277, 213	st gene, ut gene	1	1	16	21	1	2_A275_shN37_shrna_loc#NA:1	21	Gene MPHOSPH6	MPHOSPH6, MPP6, MPP-6, MPP	M-phase phosphoprotein 6	NM_005792, NCT23.5463760.0, NCT23.5463790.0, NCT2716.3	1554900_a_at, 203740_at	NP_005783.2, EAW59516.1, EAW59516.1, EAW59517.1
Gene:ID:1012	CDH13	16	82,660,378	83,830,291	1,169,823	+	8	1_A275_shN37_shrna_loc#NA:1:-2357,2_A275_shN37_shrna_loc#NA:1:-3355,2_A275_shN37_shrna_loc#NA:1:-3359,2_A275_shN37_shrna_loc#NA:1:-3360,2_A275_shN37_shrna_loc#NA:1:-3360,2_A275_shN37_shrna_loc#NA:1:-3364,2_A275_shN37_shrna_loc#NA:1:-3365,2_A275_shN37_shrna_loc#NA:1:-3366	7262, 606238, 829085, 1074752, 1022, 510430, 829035, 1091102	st gene, ut gene, downstream, st gene, ut gene, st gene, ut gene, st gene, ut gene	1	1	17	16.14	7	2_A275_shN37_shrna_loc#NA:1	34	Gene CDH13	CDH13, CDHH	cadherin 13, H-cadherin (heart)	NM_001257, NCT2971.7	204726_at	NP_001248.1, EAW59515.1
Gene:ID:4158	UPRC80	16	84,176,093	84,211,324	32,859	+	1	1_A275_shN37_shrna_loc#NA:1:-3368	41967	downstream	0	1	12	19	1	2_A275_shN37_shrna_loc#NA:1	19	Gene UPRC80	CLD13, DKFZp434A319, UPRC80, ORAD, FLJ25339	tetratricopeptide repeat domain 39C	NM_173552, NCT22534.0, NCT22534.1	219172_at	NP_775823.2, EAW59303.1, EAW59301.1
Gene:ID:8513	TAF1C	16	84,211,461	84,220,662	9,201	+	1	1_A275_shN37_shrna_loc#NA:1:-3369	230	st gene	0	1	12	19	1	2_A275_shN37_shrna_loc#NA:1	19	Gene TAF1C	MGC10979, TAF1B5, TAF1C, SL1, TAF5-10	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110 kDa	NM_138352, NM_005679, NCT22529470.0, NCT23023980.0, NCT23576740.0, NCT24313.3	203637_s_at, 203638_s_at	NP_619737.1, NP_005669.2, EAW59293.1, EAW59294.1, EAW59297.1, EAW59298.1, EAW59299.1
Gene:ID:3188	ADAD2	16	84,224,723	84,230,772	6,049	+	1	2_A275_shN37_shrna_loc#NA:1:-3374	4291	upstream	0	1	12	19	1	2_A275_shN37_shrna_loc#NA:1	19	Gene ADAD2	TENR/L, ADAD2, FLJ00337	testicular tissue zinc finger domain containing 2	NM_139170, NM_001145650, NCT19852312.2, NCT19852312.1, NCT23023982.0, NCT23023.2	236463_at	NP_619113.2, NP_001138772.1, EAW59491.1, EAW59492.1, EAW59493.1, EAW59494.1
Gene:ID:3328	LOC654756	16	84,236,164	84,250,659	14,495	-	1	2_A275_shN37_shrna_loc#NA:1:-3375	10227	downstream	0	1	12	19	1	2_A275_shN37_shrna_loc#NA:1	19	Gene LOC654756	FLJ38555, FLJ38512	SPPG	NM_001142.2, NR_109126, XR_110030	1552424_at	
Gene:ID:3197	SCN5A	16	84,255,823	84,273,356	17,533	+	1	1_A275_shN37_shrna_loc#NA:1:-3376	10934	st gene	0	1	10	20	1	2_A275_shN37_shrna_loc#NA:1	20	Gene SCN5A	MGC129699, IUVS-9, MGC8856, IUVS-3, SCN5A1	sodium voltage-gated channel, subfamily S, member 5	NM_198056, NCT23023982.0, NCT23024.2	1552768_at	NP_000326.2, EAW59089.1
Gene:ID:3406	CCTL1	16	84,399,202	84,681,669	82,467	-	1	1_A275_shN37_shrna_loc#NA:1:-3362	14709	st gene	1	1	23	16	1	2_A275_shN37_shrna_loc#NA:1	23	Gene CCTL1	CLF, MGC129733, CCTL1, FLJ43657	cholinesterase-like 1 (butyrylcholine)	NM_031116, NCT22533.0, NCT22533.2, NCT23023982.0, NCT23024.2	221039_s_at, 224557_at	NP_056077.1, EAW59775.1, EAW59776.1
Gene:ID:3716	CRISPLD2	16	84,653,567	84,683,116	69,329	+	1	1_A275_shN37_shrna_loc#NA:1:-3372	48877	st gene	0	1	14	17	1	2_A275_shN37_shrna_loc#NA:1	17	Gene CRISPLD2	MGC74668, DKFZp434B0428, CDRSP2, CRISPLD2, CRISP21	cysteine-rich secretory protein LCCL domain containing 2	NM_031476, NCT17994492.2, NCT23023.2	1555024_at, 221561_at	NP_113664.1, EAW59465.1, EAW59469.1
Gene:ID:3188	SAAS9SE2	16	84,845,029	85,709,812	64,783	+	1	1_A275_shN37_shrna_loc#NA:1:-3374	-869	upstream	0	1	10	16	1	2_A275_shN37_shrna_loc#NA:1	16	Gene KIAA0162	CEE1, KIAA0162	KIAA0162	NM_014615, NM_001134872, NCT19801693.1, NCT23023901.0, NCT23576776.0, NCT23576.2	212006_at, 212007_at, 212665_at	NP_055430.2, NP_001128473.1, EAW59449.1, EAW59447.1, EAW59446.1, EAW59448.1, EAW59450.1
Gene:ID:3328	CCK4NB	16	85,512,230	85,533,145	20,916	+	1	1_A275_shN37_shrna_loc#NA:1:-3375	-386	upstream	0	1	26	20	1	2_A275_shN37_shrna_loc#NA:1	20	Gene CCK4NB	C16orf2, C16orf8, PAM1568, CCK4NB, NOC4	CCK4 regulator	NM_198057, NM_001142266, NCT19584041.1, NCT8092.3	210037_s_at, 222504_s_at, 227262_s_at	NP_938061.1, NP_001128760.1, EAW59439.1, EAW59440.1
Gene:ID:100506832	LOC100506832	16	85,626,021	85,626,939	918	+	1	2_A275_shN37_shrna_loc#NA:1:-3375	7425	downstream	0	1	26	20	1	2_A275_shN37_shrna_loc#NA:1	20	Gene LOC100506832		hypothetical LOC100506521	XR_111607, XR_109331, XR_110033		
Gene:ID:1227	COX4I1	16	85,833,196	85,840,668	7,472	+	1	2_A275_shN37_shrna_loc#NA:1:-3375	260	st gene	0	1	26	20	1	2_A275_shN37_shrna_loc#NA:1	20	Gene COX4I1	COX4, COX4I1, COX4-1, FLJ23483, COX4V, MGC102016	cytochrome c oxidase subunit IV isoform 1	NM_001861, NCT19613961.1, NCT23058790, NCT8096.2	200099_s_at, 202695_s_at, 213756_at	NP_001853.1, EAW54338.1, EAW54339.1, EAW54337.1
Gene:ID:93550	FLJ45515	16	86,505,151	86,542,866	38,035	-	2	1_A275_shN37_shrna_loc#NA:1:-2360,2_A275_shN37_shrna_loc#NA:1:-3377	17310, 17554	st gene, ut gene	1	1	16	16	1	2_A275_shN37_shrna_loc#NA:1	16	Gene FLJ45515	FLJ45515, DKFZp566B0546, FLJ45415, DKFZp566B02196, PLU29993	hypothetical LOC93550	NR_032025, NM_030644		
Gene:ID:100506961	LOC100506961	16	87,336,620	87,350,885	14,376	+	2	1_A275_shN37_shrna_loc#NA:1:-2369,2_A275_shN37_shrna_loc#NA:1:-3380	230, 264	st gene, ut gene	1	1	14	15	1	2_A275_shN37_shrna_loc#NA:1	15	Gene LOC100506961	DKFZp434J1015, FLJ22477	hypothetical LOC100506561	XM_003119835, XM_003119836, XM_003119725, XM_003119726, XM_003120356, XM_003120357, XM_003120358		XP_003119883.1, XP_003119884.1, XP_003119885.1, XP_003119774.1, XP_003119775.1, XP_003120404.1, XP_003120405.1
Gene:ID:9761	FBXO31	16	87,362,842	87,423,768	62,766	-	3	1_A275_shN37_shrna_loc#NA:1:-2370,2_A275_shN37_shrna_loc#NA:1:-3382,2_A275_shN37_shrna_loc#NA:1:-3383	-52, 6012, 106	upstream, ut gene, upstream	1	1	18	22	2	2_A275_shN37_shrna_loc#NA:1	23	Gene FBXO31	pp2386, DKFZp434B027, FBXO14, Fbx31, MGC9027, MGC15419, FBXO31, DKFZp434J1015, FBX14, FLJ22477	F-box protein 31	NM_033177, NM_174356, NCT23023982.0, NCT23023982.0, NCT23023982.0, NCT23023982.0, NCT23023982.0, NCT23023982.0	219764_at, 219765_s_at, 220162_s_at	NP_778211.2, EAW59403.1, EAW59401.1, EAW59402.1, EAW59404.1
Gene:ID:1631	MAP1LC3B	16	87,835,801	87,838,388	12,379	+	3	1_A275_shN37_shrna_loc#NA:1:-2370,2_A275_shN37_shrna_loc#NA:1:-3382,2_A275_shN37_shrna_loc#NA:1:-3383	-41, -5165, 103	upstream, upstream, st gene	1	1	19	22	2	2_A275_shN37_shrna_loc#NA:1	23	Gene MAP1LC3B	LC3B, ATG8F, MAP1LC3B, MAP1A/1B LC3	microtubule-associated protein 1 light chain 3 beta	NM_022818, NCT19614391.1, NCT19614321.1, NCT19864931.1, NCT19864931.2, NCT23023982.0, NCT23023972.0, NCT23576790.0	208765_s_at, 208766_s_at	NP_073729.1, EAW59397.1, EAW59392.1, EAW59393.1, EAW59394.1, EAW59395.1, EAW59396.1, EAW59398.1
Gene:ID:3174	ZCCHC14	16	87,439,652	87,529,460	89,809	-	1	1_A275_shN37_shrna_loc#NA:1:-2371	-1305	upstream	1	0	19	8	1	1_A275_shN37_shrna_loc#NA:1	19	Gene ZCCHC14	ZCCHC14, MGC126527, MGC14139, BDG28, BDG-28	Zinc finger, CCHC domain containing 14	NM_015144, NCT22529379.1, NCT23023980.1, NCT23489664.0, NCT23580.3	212653_at, 215426_at, 215427_s_at	NP_055959.2, EAW59393.1, EAW59395.1, EAW59396.1
Gene:ID:7130	JPH3	16	87,639,499	87,731,762	93,262	+	4	1_A275_shN37_shrna_loc#NA:1:-2372,2_A275_shN37_shrna_loc#NA:1:-3383,2_A275_shN37_shrna_loc#NA:1:-3384,2_A275_shN37_shrna_loc#NA:1:-3385,2_A275_shN37_shrna_loc#NA:1:-3386	5737, 58823, 5741, 58529	st gene, ut gene, st gene, ut gene	1	1	33.5	36	2	2_A275_shN37_shrna_loc#NA:1	41	Gene JPH3	JP3, JP-3, TMFC22, JPH3, HDL2, FLJ40707, CAG/L227	junctophilin 3	NM_020655, NCT16501851.1, NCT23023970.0	220168_at, 226294_at, 234736_at, 240879_at	NP_065706.2, EAW59386.1, EAW59387.1
Gene:ID:63	CASA	17	37,921,623	37,970,112	48,487	-	1	2_A275_shN37_shrna_loc#NA:1:-3386	4320	st gene	0	1	19	17	1	2_A275_shN37_shrna_loc#NA:1	17	Gene CASA	CAS, CAV, CAVA, CASA	calponin antiprotease VA, vinculin-like	NM_007129, NCT17927.2, NCT23023980.0	207421_at	NP_007730.1, EAW53271.1, EAW53272.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:54971	BANP	16	87,985,036	88,110,924	125,886	+	2	1_A375_pNL7_minus_lncRNA::1::2374, 2_A375_pNL97_plus_lncRNA::1::3389	-366, -430	upstream, upstream	1	1	25	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene BANP	FLJ10177, DKFZp761H172, SMARBP1, SMAR1, FLJ20538, BANP, BEND1	BTG3 associated nuclear protein	NM_017869, NM_079837, NM_001173539, NM_001173540, NM_001173541, NM_001173542, NM_001173543, hCT2253589.1, hCT2253590.1, hCT2253591.1, hCT2253592.1, hCT2253593.1, hCT2253594.1, hCT2343768.0	228926_x_at	NP_060339.2, NP_524576.2, NP_001167010.1, NP_001167011.1, NP_001167012.1, NP_001167013.1, NP_001167014.1, EAW95364.1, EAW95365.1, EAW95366.1, EAW95367.1, EAW95368.1, EAW95369.1, EAW95370.1
GeneID:84627	ZNF469	16	88,493,879	88,507,165	13,286	+	1	2_A375_pNL97_plus_lncRNA::1::3391	15881	downstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ZNF469	KIAA1858, BCS, ZNF469	zinc finger protein 469	NM_001127464	230440_at	NP_001120936.1
GeneID:161882	ZFPM1	16	88,520,014	88,601,574	81,560	+	1	2_A375_pNL97_plus_lncRNA::1::3391	-10254	upstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ZFPM1	ZFPM1, ZNF408, FOG1, ZNF89A, FOG	zinc finger protein, multitype 1	NM_153813, hCT1953804.2, hCT2344502.0, hCT2344503.0	242282_at	NP_722520.2, EAW66806.1, EAW66807.1, EAW66808.1
GeneID:124245	ZC3H18	16	88,636,789	88,698,372	61,583	+	2	1_A375_pNL7_minus_lncRNA::1::2376, 2_A375_pNL97_plus_lncRNA::1::3392	-9493, -9365	upstream, upstream	1	1	37	34	1	1_A375_pNL7_minus_lncRNA::1	37	Gene ZC3H18	FLJ36075, FLJ22664, ZC3H18, NHN1, FLJ34530	zinc finger CCCH-type containing 18	NM_144604, hCT2257198.1, hCT2257200.0, hCT2257201.1, hCT2346543.0, hCT2346544.0, hCT2346545.0, hCT2346546.0	226108_at, 238416_x_at	NP_653205.3, EAW66804.1, EAW66799.1, EAW66801.1, EAW66802.1, EAW66805.1, EAW66800.1, EAW66803.1
GeneID:9780	FAM38A	16	88,781,746	88,851,372	69,626	-	2	1_A375_pNL7_minus_lncRNA::1::2377, 2_A375_pNL97_plus_lncRNA::1::3393	-564, -740	upstream, upstream	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FAM38A	FAM38A, PIEZO1, Mib, KIAA0233	family with sequence similarity 38, member A	NM_001142864	202771_at	NP_001136336.2
GeneID:81620	CDT1	16	88,870,186	88,875,666	5,480	+	4	1_A375_pNL7_minus_lncRNA::1::2378, 1_A375_pNL7_minus_lncRNA::1::2379, 2_A375_pNL97_plus_lncRNA::1::3394, 2_A375_pNL97_plus_lncRNA::1::3395	-266, 8438, -266, 8310	upstream, downstream, upstream, downstream	1	1	28	27.5	2	1_A375_pNL7_minus_lncRNA::1	31	Gene CDT1	RIS2, CDT1, DUP	chromatin licensing and DNA replication factor 1	NM_030928, hCT2257218.0, hCT2257219.0, hCT2257221.0	209832_s_at, 228868_x_at	NP_112190.2, EAW66763.1, EAW66762.1, EAW66764.1
GeneID:353	APRT	16	88,875,877	88,878,342	2,465	-	4	1_A375_pNL7_minus_lncRNA::1::2378, 1_A375_pNL7_minus_lncRNA::1::2379, 2_A375_pNL97_plus_lncRNA::1::3394, 2_A375_pNL97_plus_lncRNA::1::3395	8422, -282, 8422, -154	downstream, upstream, downstream, upstream	1	1	28	27.5	2	1_A375_pNL7_minus_lncRNA::1	31	Gene APRT	AMP, MGC125856, APRT, DKFZp686D13177, MGC125857, MGC129961	adenine phosphoribosyltransferase	NM_000485, NM_001030018, hCT10174.3, hCT2354320.0	203219_s_at, 213892_s_at	NP_000476.1, NP_001025189.1, EAW66760.1, EAW66761.1
GeneID:2588	GALNS	16	88,880,142	88,923,374	43,232	-	5	1_A375_pNL7_minus_lncRNA::1::2378, 1_A375_pNL7_minus_lncRNA::1::2379, 2_A375_pNL97_plus_lncRNA::1::3394, 2_A375_pNL97_plus_lncRNA::1::3395, 2_A375_pNL97_plus_lncRNA::1::3396	53454, 44750, 53454, 44878, -146	downstream, downstream, downstream, downstream, upstream	1	1	23	26	3	1_A375_pNL7_minus_lncRNA::1	31	Gene GALNS	GALNAC6S, FLJ42844, MPS4A, GALNS, FLJ98217, FLJ17434, GAS	galactosamine (N-acetyl)-6-sulfate sulfatase	NM_000512, hCT10175.2, hCT2346539.0, hCT2354321.0	206335_at, 236866_at	NP_000503.1, EAW66759.1, EAW66757.1, EAW66758.1
GeneID:51693	TRAPPC2L	16	88,923,506	88,927,520	4,014	+	1	2_A375_pNL97_plus_lncRNA::1::3396	14	in gene	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene TRAPPC2L	HSPC176, TRAPPC2L, FLJ44827, MGC111156	trafficking protein particle complex 2-like	NM_016209, hCT10168.2	218354_at, 238627_at, 238628_s_at	NP_057293.1, EAW66756.1
GeneID:390748	PABPN1L	16	88,928,034	88,933,014	4,980	-	1	2_A375_pNL97_plus_lncRNA::1::3396	9494	downstream	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene PABPN1L	ePABP2, PABPNL1, PABPN1L	poly(A) binding protein, nuclear 1-like (cytoplasmic)	NM_001080487		NP_001073956.1
GeneID:100506183	LOC100506183	16	89,112,580	89,119,373	6,793	-	1	2_A375_pNL97_plus_lncRNA::1::3399	15181	downstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100506183		hypothetical LOC100506183	XR_111619, XR_109341, XR_115040		
GeneID:197320	ZNF778	16	89,284,111	89,295,363	11,252	+	1	2_A375_pNL97_plus_lncRNA::1::3400	193	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZNF778	MGC150573, ZNF778, FLJ31875	zinc finger protein 778	NM_182531	1556581_at	NP_872337.2
GeneID:29123	ANKRD11	16	89,334,035	89,556,969	222,934	-	1	2_A375_pNL97_plus_lncRNA::1::3402	170281	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ANKRD11	ANCO-1, ANCO1, ANKRD11, LZ16, T13	ankyrin repeat domain 11	NM_013275, hCT2253337.0, hCT2253338.0, hCT2253341.0, hCT2253342.0	219437_s_at, 226012_at, 228356_at, 231999_at, 234701_at, 238538_at	NP_037407.4, EAW66732.1, EAW66731.1, EAW66733.1, EAW66734.1
GeneID:100287036	LOC100287036	16	89,387,541	89,391,518	3,977	+	1	2_A375_pNL97_plus_lncRNA::1::3402	-853	upstream	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100287036		hypothetical LOC100287036	XR_111616, XR_109342, XR_115041		
GeneID:100506268	LOC100506268	16	89,557,733	89,565,693	7,960	+	1	2_A375_pNL97_plus_lncRNA::1::3403	17547	downstream	0	1	8	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100506268		hypothetical LOC100506268	XR_109344		
GeneID:6687	SPG7	16	89,574,805	89,624,174	49,369	+	3	2_A375_pNL97_plus_lncRNA::1::3403, 2_A375_pNL97_plus_lncRNA::1::3404, 2_A375_pNL97_plus_lncRNA::1::3405	475, 52331, 57067	in gene, downstream, downstream	0	1	14.33	17.33	3	2_A375_pNL97_plus_lncRNA::1	19	Gene SPG7	SPG7, CAR, CMAR, FLJ37308, PGN, MGC126332, MGC126331, SPG5C	spastic paraplegia 7 (pure and complicated autosomal recessive)	NM_003119, NM_199367, hCT1953800.1, hCT2257273.0, hCT2257274.0, hCT6628.3	202104_s_at, 214494_s_at, 230884_s_at, 235325_at, 238286_at	NP_003110.1, NP_955399.1, EAW66726.1, EAW66727.1, EAW66728.1, EAW66729.1
GeneID:6137	RPL13	16	89,627,090	89,629,848	2,758	+	2	2_A375_pNL97_plus_lncRNA::1::3404, 2_A375_pNL97_plus_lncRNA::1::3405	46, 4782	in gene, downstream	0	1	17.5	17.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene RPL13	FLJ27454, BBC1, FLJ27453, L13, RPL13, MGC117342, MGC71373, D16S444E	ribosomal protein L13	NM_033251, NM_000977, hCT1964145.1, hCT1964146.1	1565758_at, 1565759_at, 208929_x_at, 212191_x_at, 212734_x_at, 212933_x_at, 229590_at	NP_150254.1, NP_000968.2, EAW66724.1, EAW66725.1
GeneID:606500	SNORD68	16	89,627,838	89,627,909	71	+	2	2_A375_pNL97_plus_lncRNA::1::3404, 2_A375_pNL97_plus_lncRNA::1::3405	-702, 4034	upstream, downstream	0	1	17.5	17.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene SNORD68	HBII-202, SNORD68	small nucleolar RNA, C/D box 68	NR_002450		
GeneID:27132	CPNE7	16	89,642,176	89,663,654	21,478	+	1	2_A375_pNL97_plus_lncRNA::1::3405	-10304	upstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CPNE7	CPNE7, MGC34192	copine VII	NM_014427, NM_153636, hCT2344205.0, hCT6734.4	219707_at	NP_055242.1, NP_705900.1, EAW66721.1, EAW66722.1
GeneID:9605	C16orf7	16	89,773,541	89,787,394	13,853	-	2	1_A375_pNL7_minus_lncRNA::1::2382, 2_A375_pNL97_plus_lncRNA::1::3406	-110, -62	upstream, upstream	1	1	36	23	1	1_A375_pNL7_minus_lncRNA::1	36	Gene C16orf7	ATP-BL, C16orf7	chromosome 16 open reading frame 7	NM_004913, hCT2253311.0, hCT2253312.0, hCT6627.3	205781_at	NP_004904.2, EAW66695.1, EAW66694.1, EAW66696.1
GeneID:100128881	LOC100128881	16	89,778,264	89,784,573	6,309	+	2	1_A375_pNL7_minus_lncRNA::1::2382, 2_A375_pNL97_plus_lncRNA::1::3406	9240, 9192	downstream, downstream	1	1	36	23	1	1_A375_pNL7_minus_lncRNA::1	36	Gene LOC100128881	FLJ38967	hypothetical LOC100128881	NR_036480		
GeneID:92822	ZNF276	16	89,787,393	89,807,333	19,940	+	2	1_A375_pNL7_minus_lncRNA::1::2382, 2_A375_pNL97_plus_lncRNA::1::3406	111, 63	in gene, in gene	1	1	36	23	1	1_A375_pNL7_minus_lncRNA::1	36	Gene ZNF276	MGC45417, FLJ77609, MGC111410, MGC126480, ZNF477, ZFP276, ZNF276, FLJ38685	zinc finger protein 276	NM_152287, NM_001113525, hCT1965845.2, hCT2257285.1, hCT2257287.1, hCT2344206.0, hCT2354322.0, hCT2354323.0, hCT7391.4	213776_x_at, 231922_at	NP_689500.2, NP_001106997.1, EAW66687.1, EAW66688.1, EAW66690.1, EAW66692.1, EAW66689.1, EAW66691.1, EAW66693.1
GeneID:2175	FANCA	16	89,803,959	89,883,065	79,106	-	1	1_A375_pNL7_minus_lncRNA::1::2383	-39	upstream	1	0	16	16	1	1_A375_pNL7_minus_lncRNA::1	16	Gene FANCA	MGC75158, FANCH, FAH, FACA, FAA, FA1, FANCA, FA-H, FA	Fanconi anemia, complementation group A	NM_001018112, NM_000135, hCT2253307.0, hCT6693.3	203805_s_at, 203806_s_at, 215530_at, 236976_at	NP_001018122.1, NP_000126.2, EAW66685.1, EAW66686.1
GeneID:84501	SPIRE2	16	89,894,907	89,937,727	42,820	+	1	2_A375_pNL97_plus_lncRNA::1::3407	149	in gene	0	1	6	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SPIRE2	MGC117166, SPIRE2, Spir-2	spire homolog 2 (Drosophila)	NM_032451, hCT2257295.0, hCT2354331.0, hCT7394.3	1568916_at, 1569723_a_at, 227706_at, 243594_x_at	NP_115827.1, EAW66680.1, EAW66681.1, EAW66682.1
GeneID:4157	MC1R	16	89,984,287	89,987,385	3,098	+	1	2_A375_pNL97_plus_lncRNA::1::3408	4225	downstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MC1R	MGC14337, CMM5, MSH-R, MC1R, SHEP2	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	NM_002386, hCT2257303.1	205458_at	NP_002377.4, EAW66676.1
GeneID:10381	TUBB3	16	89,989,745	90,002,505	12,760	+	1	2_A375_pNL97_plus_lncRNA::1::3408	-1233	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TUBB3	TUBB4, beta-4, TUBB3, MC1R, CFEOM3A	tubulin, beta 3	NM_006086	202154_x_at, 213476_x_at	NP_006077.2
GeneID:54849	DEF8	16	90,015,151	90,034,467	19,316	+	2	1_A375_pNL7_minus_lncRNA::1::2384, 2_A375_pNL97_plus_lncRNA::1::3409	-79, -79	upstream, upstream	1	1	38	56	1	2_A375_pNL97_plus_lncRNA::1	56	Gene DEF8	MGC104349, DEF8, FLJ20186	differentially expressed in FDCP 8 homolog (mouse)	NM_207514, NM_017702, hCT1953829.1, hCT2257310.0	219646_at, 225637_at	NP_997397.1, NP_060172.1, EAW66667.1, EAW66668.1
GeneID:79007	DBNDD1	16	90,071,279	90,085,937	14,658	-	2	1_A375_pNL7_minus_lncRNA::1::2385, 2_A375_pNL97_plus_lncRNA::1::3410	-1519, -1674	upstream, upstream	1	1	21	15	1	1_A375_pNL7_minus_lncRNA::1	21	Gene DBNDD1	FLJ12582, MGC3101, DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1	NM_024043, NM_001042610, hCT1953808.1, hCT1953809.1, hCT2354328.0, hCT7393.2	222234_s_at	NP_076948.2, NP_001036075.1, EAW66663.1, EAW66664.1, EAW66665.1, EAW66666.1
GeneID:2622	GAS8	16	90,089,008	90,111,379	22,371	+	2	1_A375_pNL7_minus_lncRNA::1::2385, 2_A375_pNL97_plus_lncRNA::1::3410	-1552, -1397	upstream, upstream	1	1	21	15	1	1_A375_pNL7_minus_lncRNA::1	21	Gene GAS8	GAS8, MGC138326, GAS11	growth arrest-specific 8	NR_023348, NM_001481, hCT1958882.1, hCT1958883.1, hCT2354317.0, hCT7389.3	204921_at	NP_001472.1, EAW66658.1, EAW66659.1, EAW66660.1, EAW66661.1
GeneID:750	C16orf3	16	90,095,316	90,096,309	993	-	2	1_A375_pNL7_minus_lncRNA::1::2385, 2_A375_pNL97_plus_lncRNA::1::3410	8853, 8698	downstream, downstream	1	1	21	15	1	1_A375_pNL7_minus_lncRNA::1	21	Gene C16orf3	MGC132509, C16orf3	chromosome 16 open reading frame 3	NM_001214, hCT1850151.2	207615_s_at	NP_001205.3, EAW66662.1
GeneID:55275	VPS53	17	411,908	618,096	206,188	-	2	1_A375_pNL7_minus_lncRNA::1::2386, 2_A375_pNL97_plus_lncRNA::1::3411	48, 48	in gene, in gene	1	1	36	28	1	1_A375_pNL7_minus_lncRNA::1	36	Gene VPS53	FLJ10979, VPS53, FLJ61757, MGC39512, FLJ41112, HCCS1, hVps53L, pp13624	vacuolar protein sorting 53 homolog (S. cerevisiae)	NM_018289, NM_001128159, hCT18993.3, hCT2264569.0, hCT2264570.0, hCT2357274.0, hCT2357275.0	219794_at, 221707_s_at, 235710_at	NP_060759.2, NP_001121631.1, EAW90658.1, EAW90659.1, EAW90661.1, EAW90662.1, EAW90660.1
GeneID:51031	GLOD4	17	662,549	685,571	23,022	-	2	1_A375_pNL7_minus_lncRNA::1::2387, 2_A375_pNL97_plus_lncRNA::1::3412	3, -29	in gene, upstream	1	1	19	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene GLOD4	GLOD4, C17orf25, CGI-150, HC71	glyoxalase domain containing 4	NM_016080, hCT2264547.0, hCT2264548.0, hCT2264550.0, hCT2264551.0, hCT2264553.0, hCT2357344.0, hCT2357345.0, hCT23687.4	209092_s_at	NP_057164.3, EAW90643.1, EAW90644.1, EAW90646.1, EAW90647.1, EAW90650.1, EAW90645.1, EAW90648.1, EAW90649.1
GeneID:55178	RNMTL1	17	685,513	695,741	10,228	+	2	1_A375_pNL7_minus_lncRNA::1::2387, 2_A375_pNL97_plus_lncRNA::1::3412	55, 87	in gene, in gene	1	1	19	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene RNMTL1	FLJ10581, HC90, RNMTL1	RNA methyltransferase like 1	NM_018146, hCT23689.2	218993_at	NP_060616.1, EAW90642.1
GeneID:29928	TIMM22	17	900,357	905,407	5,050	+	1	2_A375_pNL97_plus_lncRNA::1::3413	-469	upstream	0	1	18	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene TIMM22	TEX4, TIM22, TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	NM_013337, hCT2264846.0, hCT2264847.0	219164_x_at, 222841_s_at, 229100_s_at, 231400_s_at	NP_037469.2, EAW90636.1, EAW90637.1
GeneID:100506636	LOC100506636	17	905,807	909,265	3,458	+	1	2_A375_pNL97_plus_lncRNA::1::3413	-5919	upstream	0	1	18	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100506636		hypothetical LOC100506636	XR_109362		
GeneID:29	ABR	17	906,759	1,090,616	183,857	-	4	1_A375_pNL7_minus_lncRNA::1::2388, 1_A375_pNL7_minus_lncRNA::1::2389, 2_A375_pNL97_plus_lncRNA::1::3413, 2_A375_pNL97_plus_lncRNA::1::3414	36056, 56, 190728, 76280	in gene, in gene, downstream, in gene	1	1	21.75	17	4	1_A375_pNL7_minus_lncRNA::1	30	Gene ABR	ABR, FLJ45954, MDB	active BCR-related gene	NM_001092, NM_021962, NM_001159746, hCT1971514.1, hCT2264503.0, hCT2264508.0, hCT2264511.0, hCT2264512.0	212895_s_at, 214671_s_at	NP_001083.2, NP_068781.2, NP_001153218.1, EAW90631.1, EAW90632.1, EAW90634.1, EAW90633.1, EAW90635.1
GeneID:7531	YWHAE	17	1,247,834	1,303,556	55,722	-	1	2_A375_pNL97_plus_lncRNA::1::3417	340	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene YWHAE	YWHAE, MDS, FLJ53559, 14-3-3E, KCIP-1, MDCR, FLJ45465	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	NM_006761, NR_024058, hCT2264471.0, hCT2264473.0, hCT2357331.0	210317_s_at, 210996_s_at, 213655_at	NP_006752.1, EAW90628.1, EAW90627.1, EAW90629.1
GeneID:4641	MYO1C	17	1,367,480	1,396,001	28,521	-	2	1_A375_pNL7_minus_lncRNA::1::2390, 2_A375_pNL97_plus_lncRNA::1::3418	6561, 6593	in gene, in gene	1	1	28	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene MYO1C	FLJ23903, NMI, MYO1C, MMIb, myr2, MMI-beta	myosin IC	NM_001080779, NM_033375, NM_001080950, hCT19877.3, hCT2264459.0	214656_x_at, 225080_at, 32811_at	NP_001074248.1, NP_203693.3, NP_001074419.1, EAW90619.1, EAW90620.1
GeneID:51763	INPP5K	17	1,397,871	1,420,182	22,311	-	2	1_A375_pNL7_minus_lncRNA::1::2390, 2_A375_pNL97_plus_lncRNA::1::3418	30742, 30774	downstream, downstream	1	1	28	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene INPP5K	SKIP, PPS, INPP5K	inositol polyphosphate-5-phosphatase K	NM_016532, NM_130766, NM_001135642, hCT1814645.2, hCT2264454.0, hCT2264455.0, hCT2264456.0, hCT2264458.1	202781_s_at, 202782_s_at	NP_057616.2, NP_570122.1, NP_001129114.1, EAW90614.1, EAW90615.1, EAW90617.1, EAW90616.1, EAW90618.1
GeneID:5306	PITPNA	17	1,421,283	1,466,110	44,827	-	2	1_A375_pNL7_minus_lncRNA::1::2391, 2_A375_pNL97_plus_lncRNA::1::3419	-98, -50	upstream, upstream	1	1	36	30	1	1_A375_pNL7_minus_lncRNA::1	36	Gene PITPNA	PITPN, VIB1A, MGC99649, PI-TPalpha, PITPNA	phosphatidylinositol transfer protein, alpha	NM_006224, hCT1815693.2, hCT2264453.0, hCT2357330.0	201190_s_at, 201191_at, 201192_s_at	NP_006215.1, EAW90610.1, EAW90611.1, EAW90612.1
GeneID:100507036	LOC100507036	17	1,452,559	1,473,094	20,535	+	2	1_A375_pNL7_minus_lncRNA::1::2391, 2_A375_pNL97_plus_lncRNA::1::3419	13649, 13601	in gene, in gene	1	1	36	30	1	1_A375_pNL7_minus_lncRNA::1	36	Gene LOC100507036		hypothetical LOC100507036	XR_111664, XR_111665, XR_109368, XR_109369, XR_115047, XR_115048		
GeneID:10594	PRPF8	17	1,553,923	1,588,176	34,253	-	1	2_A375_pNL97_plus_lncRNA::1::3420	-48	upstream	0	1	9	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PRPF8	HPRP8, PRPC8, RP13, PRP8, PRPF8	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	NM_006445, hCT19870.3, hCT2261329.0, hCT2350281.0, hCT2350282.0, hCT2350283.0, hCT2350284.0, hCT2350285.0	200000_s_at	NP_006436.3, EAW90593.1, EAW90588.1, EAW90589.1, EAW90591.1, EAW90594.1, EAW90590.1, EAW90592.1
GeneID:727910	TLCD2	17	1,606,084	1,613,662	7,578	-	2	1_A375_pNL7_minus_lncRNA::1::2392, 2_A375_pNL97_plus_lncRNA::1::3421	-6946, -6898	upstream, upstream	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene TLCD2	TLCD2	TLC domain containing 2	NM_001164407		NP_001157879.1
GeneID:84981	C17orf91	17	1,614,798	1,619,566	4,768	-	2	1_A375_pNL7_minus_lncRNA::1::2392, 2_A375_pNL97_plus_lncRNA::1::3421	-1042, -994	upstream, upstream	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene C17orf91	MGC14376, C17orf91, MGC149751, DKFZp686O06159	chromosome 17 open reading frame 91	NR_028502, NR_028503, NR_028504, NR_028505, hCT1970576.1, hCT2261315.0	214696_at	EAW90586.1, EAW90585.1
GeneID:407004	MIR22	17	1,617,197	1,617,281	84	-	2	1_A375_pNL7_minus_lncRNA::1::2392, 2_A375_pNL97_plus_lncRNA::1::3421	-3327, -3279	upstream, upstream	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene MIR22	miR-22, hsa-mir-22, MIRN22, MIR22	microRNA 22	NR_029494		
GeneID:124997	WDR81	17	1,619,817	1,641,893	22,076	+	2	1_A375_pNL7_minus_lncRNA::1::2392, 2_A375_pNL97_plus_lncRNA::1::3421	791, 743	in gene, in gene	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene WDR81	WDR81, FLJ23776, FLJ33817	WD repeat domain 81	NM_001163673, NM_001163809, NM_152348, NM_001163811, hCT2289074.1, hCT2289075.1, hCT2349376.0	226738_at	NP_001157145.1, NP_001157281.1, NP_689561.2, NP_001157283.1, EAW90583.1, EAW90584.1, EAW90582.1
GeneID:146760	RTN4RL1	17	1,837,971	1,928,178	90,207	-	2	1_A375_pNL7_minus_lncRNA::1::2393, 2_A375_pNL97_plus_lncRNA::1::3422	-5230, -5230	upstream, upstream	1	1	61	77	1	2_A375_pNL97_plus_lncRNA::1	77	Gene RTN4RL1	RTN4RL1, NGRH2, NgR3, DKFZp547J144	reticulon 4 receptor-like 1	NM_178568, hCT1815706.1, hCT2261378.0	230700_at	NP_848663.1, EAW90570.1, EAW90571.1
GeneID:1801	DPH1	17	1,933,431	1,946,725	13,294	+	4	1_A375_pNL7_minus_lncRNA::1::2393, 1_A375_pNL7_minus_lncRNA::1::2394, 2_A375_pNL97_plus_lncRNA::1::3422, 2_A375_pNL97_plus_lncRNA::1::3423	-23, 11945, -23, 11945	upstream, in gene, upstream, in gene	1	1	41	50.5	2	2_A375_pNL97_plus_lncRNA::1	77	Gene DPH1	DPH1, FLJ33211, DPH2L1, DPH2L, OVCA1	DPH1 homolog (S. cerevisiae)	NM_001383	202632_at	NP_001374.3
GeneID:124641	OVCA2	17	1,945,277	1,946,725	1,448	+	2	1_A375_pNL7_minus_lncRNA::1::2394, 2_A375_pNL97_plus_lncRNA::1::3423	99, 99	in gene, in gene	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene OVCA2	OVCA2		NM_080822	222041_at	NP_543012.1
GeneID:406921	MIR132	17	1,953,202	1,953,302	100	-	2	1_A375_pNL7_minus_lncRNA::1::2394, 2_A375_pNL97_plus_lncRNA::1::3423	7926, 7926	downstream, downstream	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene MIR132	miRNA132, MIR132, MIRN132	microRNA 132	NR_029674		
GeneID:406994	MIR212	17	1,953,565	1,953,674	109	-	2	1_A375_pNL7_minus_lncRNA::1::2394, 2_A375_pNL97_plus_lncRNA::1::3423	8298, 8298	downstream, downstream	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene MIR212	MIR212, mir-212, MIRN212	microRNA 212	NR_029625		
GeneID:9905	SGSM2	17	2,240,806	2,284,348	43,542	+	1	1_A375_pNL7_minus_lncRNA::1::2395	21946	in gene	1	0	22	16	1	1_A375_pNL7_minus_lncRNA::1	22	Gene SGSM2	RUTBC1, KIAA0397, SGSM2	small G protein signaling modulator 2	NM_014853, NM_001098509, hCT2289065.0, hCT2357254.0, hCT24173.3	212319_at, 217538_at, 36129_at	NP_055668.2, NP_001091979.1, EAW90545.1, EAW90546.1, EAW90547.1
GeneID:4335	MNT	17	2,287,354	2,304,258	16,904	-	3	1_A375_pNL7_minus_lncRNA::1::2396, 2_A375_pNL97_plus_lncRNA::1::3424, 2_A375_pNL97_plus_lncRNA::1::3425	-734, 7426, -734	upstream, in gene, upstream	1	1	49	68.5	2	2_A375_pNL97_plus_lncRNA::1	116	Gene MNT	bHLHd3, ROX, MAD6, MXD6, MNT	MAX binding protein	NM_020310, hCT2261359.0, hCT2261360.0, hCT24175.3	204206_at, 236749_at	NP_064706.1, EAW90541.1, EAW90542.1, EAW90543.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:284009	LOC284009	17	2,310,275	2,318,730	8,455	-	2	1_A375_pNL7_minus_lncRNA::1::2396, 2_A375_pNL97_plus_lncRNA::1::3425	13736, 13738	downstream, downstream	1	1	83	116	1	2_A375_pNL97_plus_lncRNA::1	116	Gene LOC284009	MGC138239	hypothetical LOC284009	NR_026335, hCT2342777.0		EAW90540.1
GeneID:5048	PAFAH1B1	17	2,496,923	2,588,909	91,986	+	1	2_A375_pNL97_plus_lncRNA::1::3426	-283	upstream	0	1	13	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene PAFAH1B1	PAFAH1B1, MDS, LIS1, LIS2, PAFAH, MDCR	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	NM_000430, hCT24167.2	200813_s_at, 200815_s_at, 200816_s_at, 211547_s_at	NP_000421.1, EAW90536.1
GeneID:23277	KIAA0664	17	2,592,680	2,614,927	22,247	-	2	1_A375_pNL7_minus_lncRNA::1::2397, 2_A375_pNL97_plus_lncRNA::1::3427	-209, -225	upstream, upstream	1	1	23	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene KIAA0664	DKFZp686M09233, KIAA0664, FLJ23672, DKFZp686L05242, CLU1	KIAA0664	NM_015229, hCT2261346.0, hCT2357312.0, hCT24168.3	212456_at, 243258_at	NP_056044.3, EAW90534.1, EAW90532.1, EAW90533.1
GeneID:100302208	MIR1253	17	2,651,372	2,651,476	104	-	1	2_A375_pNL97_plus_lncRNA::1::3428	-1804	upstream	0	1	18	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MIR1253	MIRN1253, MIR1253, hsa-mir-1253	microRNA 1253	NR_031654		
GeneID:23108	RAP1GAP2	17	2,699,732	2,941,035	241,303	+	5	1_A375_pNL7_minus_lncRNA::1::2398, 1_A375_pNL7_minus_lncRNA::1::2399, 2_A375_pNL97_plus_lncRNA::1::3429, 2_A375_pNL97_plus_lncRNA::1::3430, 2_A375_pNL97_plus_lncRNA::1::3431	158924, 179116, 158812, 163946, 179148	in gene, in gene, in gene, in gene, in gene	1	1	18	21.67	3	2_A375_pNL97_plus_lncRNA::1	27	Gene RAP1GAP2	KIAA1039, DKFZp686O236, GARNL4, RAP1GAP2, RAP1GA3	RAP1 GTPase activating protein 2	NM_015085, NM_001100398, hCT1814367.2, hCT2336411.1, hCT2340621.0, hCT2340622.0	213280_at	NP_055900.4, NP_001093868.1, EAW90526.1, EAW90527.1, EAW90528.1, EAW90529.1
GeneID:8387	OR1E1	17	3,300,760	3,301,704	944	-	1	2_A375_pNL97_plus_lncRNA::1::3433	392	in gene	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene OR1E1	OST547, OR1E1, HGM071, OR1E6P, OR1E5, OR1E9P, OR17-2, OR17-32, OR13-66, OR1E6	olfactory receptor, family 1, subfamily E, member 1	NM_003553, hCT23823.3	208587_s_at, 214515_at	NP_003544.2, EAW90515.1
GeneID:8388	OR1E2	17	3,336,164	3,337,135	971	-	1	2_A375_pNL97_plus_lncRNA::1::3434	431	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene OR1E2	OR1E4, OR17-93, OST529, OR1E2, OR17-135, OR1E7	olfactory receptor, family 1, subfamily E, member 2	NM_003554, hCT1814346.0		NP_003545.1, EAW90513.1
GeneID:84690	SPATA22	17	3,343,305	3,375,142	31,837	-	1	2_A375_pNL97_plus_lncRNA::1::3434	38436	downstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SPATA22	SPATA22, NYD-SP20, NYDSP20	spermatogenesis associated 22	NM_001170696, NM_001170695, NM_001170697, NM_001170698, NM_032598, NM_001170699, hCT1644962.3, hCT2336335.0, hCT2357317.0, hCT2357318.0, hCT2357319.0	1558667_at, 1558668_s_at, 231114_at	NP_001164167.1, NP_001164166.1, NP_001164168.1, NP_001164169.1, NP_115987.2, NP_001164170.1, EAW90508.1, EAW90509.1, EAW90510.1, EAW90511.1, EAW90512.1
GeneID:162514	TRPV3	17	3,416,486	3,461,289	44,803	-	1	1_A375_pNL7_minus_lncRNA::1::2400	26153	in gene	1	0	18	14	1	1_A375_pNL7_minus_lncRNA::1	18	Gene TRPV3	VRL3, TRPV3	transient receptor potential cation channel, subfamily V, member 3	NM_145068, hCT1815450.2, hCT2336333.1, hCT2343262.1, hCT2357266.0	1552586_at, 1555291_at	NP_659505.1, EAW90503.1, EAW90502.1, EAW90504.1, EAW90505.1
GeneID:1497	CTNS	17	3,539,762	3,566,397	26,635	+	1	2_A375_pNL97_plus_lncRNA::1::3435	32366	downstream	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CTNS	CTNS-LSB, PQLC4, CTNS	cystinosis, nephropathic	NM_004937, NM_001031681, hCT2336430.0, hCT2357349.0, hCT24393.3	204925_at, 215459_at, 36566_at	NP_004928.2, NP_001026851.2, EAW90494.1, EAW90495.1, EAW90496.1
GeneID:30851	TAX1BP3	17	3,566,189	3,571,973	5,784	-	1	2_A375_pNL97_plus_lncRNA::1::3435	-155	upstream	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TAX1BP3	TAX1BP3, TIP-1	Tax1 (human T-cell leukemia virus type I) binding protein 3	NM_014604, hCT2336320.0, hCT2357315.0, hCT24409.2	209154_at, 215464_s_at	NP_055419.1, EAW90492.1, EAW90491.1, EAW90493.1
GeneID:83460	TMEM93	17	3,572,090	3,572,962	872	+	1	2_A375_pNL97_plus_lncRNA::1::3435	38	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TMEM93	MGC2963, TMEM93	transmembrane protein 93	NM_031298, NM_001014764, hCT24408.2	221255_s_at	NP_112588.1, NP_001014764.1, EAW90490.1
GeneID:5026	P2RX5	17	3,576,521	3,599,583	23,062	-	1	2_A375_pNL97_plus_lncRNA::1::3435	27455	downstream	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene P2RX5	P2X5R, P2X5, P2RX5, LRH-1, MGC47755	purinergic receptor P2X, ligand-gated ion channel, 5	NM_002561, NM_175080, NM_175081, hCT2336314.0, hCT2336315.0, hCT2336317.0, hCT2336318.0, hCT2357250.0, hCT2357251.0, hCT24394.2	210448_s_at	NP_002552.2, NP_778255.1, NP_778256.1, EAW90482.1, EAW90485.1, EAW90486.1, EAW90483.1, EAW90484.1, EAW90487.1, EAW90488.1
GeneID:100506618	LOC100506618	17	3,580,976	3,582,570	1,594	-	1	2_A375_pNL97_plus_lncRNA::1::3435	10442	downstream	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100506618		hypothetical protein LOC100506618	XM_003118730, XM_003120861		XP_003118778.1, XP_003120909.1
GeneID:3682	ITGAE	17	3,617,919	3,704,537	86,618	-	2	1_A375_pNL7_minus_lncRNA::1::2401, 2_A375_pNL97_plus_lncRNA::1::3436	77449, 77401	in gene, in gene	1	1	47	52	1	2_A375_pNL97_plus_lncRNA::1	52	Gene ITGAE	ITGAE, CD103, HUMINAE, MGC141996	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	NM_002208, hCT24396.3	205055_at	NP_002199.3, EAW90480.1
GeneID:83903	GSG2	17	3,627,197	3,629,993	2,796	+	2	1_A375_pNL7_minus_lncRNA::1::2401, 2_A375_pNL97_plus_lncRNA::1::3436	-109, -61	upstream, upstream	1	1	47	52	1	2_A375_pNL97_plus_lncRNA::1	52	Gene GSG2	GSG2, HASPIN	germ cell associated 2 (haspin)	NM_031965, hCT1640001.3	223759_s_at	NP_114171.2, EAW90481.1
GeneID:55421	C17orf85	17	3,714,460	3,749,540	35,080	-	1	2_A375_pNL97_plus_lncRNA::1::3437	-28	upstream	0	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene C17orf85	ELG, HSA277841, C17orf85	chromosome 17 open reading frame 85	NM_001114118, NM_018553, hCT2336309.0, hCT2336310.0, hCT2336312.0	218896_s_at, 222779_s_at	NP_001107590.1, NP_061023.1, EAW90477.1, EAW90478.1, EAW90479.1
GeneID:23140	ZZEF1	17	3,907,739	4,046,253	138,514	-	1	2_A375_pNL97_plus_lncRNA::1::3438	-755	upstream	0	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ZZEF1	FLJ10821, MGC166929, FLJ45574, ZZZ4, KIAA0399, FLJ23789, ZZEF1	zinc finger, ZZ-type with EF-hand domain 1	NM_015113	207189_s_at, 207190_at, 212601_at	NP_055928.3
GeneID:124936	CYB5D2	17	4,046,462	4,060,991	14,529	+	1	2_A375_pNL97_plus_lncRNA::1::3438	546	in gene	0	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CYB5D2	MGC32124, CYB5D2	cytochrome b5 domain containing 2	NM_144611, NR_023346, NR_023347, hCT2357271.0, hCT2357272.0, hCT24400.2	225804_at	NP_653212.1, EAW90454.1, EAW90452.1, EAW90453.1
GeneID:201305	SPNS3	17	4,337,219	4,391,499	54,280	+	2	1_A375_pNL7_minus_lncRNA::1::2402, 2_A375_pNL97_plus_lncRNA::1::3439	59549, 59453	downstream, downstream	1	1	30	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene SPNS3	SPNS3, MGC29671	spinster homolog 3 (Drosophila)	NM_182538, hCT1951844.1, hCT2357270.0	235900_at	NP_872344.3, EAW90439.1, EAW90440.1
GeneID:124976	SPNS2	17	4,402,129	4,443,228	41,099	+	2	1_A375_pNL7_minus_lncRNA::1::2402, 2_A375_pNL97_plus_lncRNA::1::3439	-5361, -5457	upstream, upstream	1	1	30	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene SPNS2	SPNS2	spinster homolog 2 (Drosophila)	NM_001124758	225671_at	NP_001118230.1
GeneID:27043	PELP1	17	4,574,679	4,607,632	32,953	-	1	2_A375_pNL97_plus_lncRNA::1::3440	432	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PELP1	P160, MNAR, HMX3, PELP1	proline, glutamate and leucine rich protein 1	NM_014389, hCT2261206.0, hCT2261207.0, hCT23890.3	215354_s_at	NP_055204.2, EAW90424.1, EAW90425.1, EAW90426.1
GeneID:409	ARRB2	17	4,613,789	4,624,795	11,006	+	3	1_A375_pNL7_minus_lncRNA::1::2403, 2_A375_pNL97_plus_lncRNA::1::3440, 2_A375_pNL97_plus_lncRNA::1::3441	20867, -6589, 21091	downstream, upstream, downstream	1	1	17.5	20	2	2_A375_pNL97_plus_lncRNA::1	21	Gene ARRB2	ARB2, DKFZp686L0365, ARRB2, BARR2, ARR2	arrestin, beta 2	NM_004313, NM_199004, hCT2262235.0, hCT2357332.0, hCT2357333.0, hCT23895.3	203388_at	NP_004304.1, NP_945355.1, EAW90419.1, EAW90420.1, EAW90421.1, EAW90422.1
GeneID:400569	MED11	17	4,634,723	4,636,902	2,179	+	2	1_A375_pNL7_minus_lncRNA::1::2403, 2_A375_pNL97_plus_lncRNA::1::3441	-67, 157	upstream, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene MED11	MGC88387, MED11, HSPC296	mediator complex subunit 11	NM_001001683, hCT2357328.0, hCT23893.2	226958_s_at	NP_001001683.1, EAW90418.1, EAW90417.1
GeneID:58191	CXCL16	17	4,636,828	4,643,223	6,395	-	2	1_A375_pNL7_minus_lncRNA::1::2403, 2_A375_pNL97_plus_lncRNA::1::3441	8567, 8343	downstream, downstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CXCL16	CXCLG16, SRPSOX, SR-PSOX, CXCL16	chemokine (C-X-C motif) ligand 16	NM_022059, NM_001100812, hCT23897.3	223454_at	NP_071342.2, NP_001094282.1, EAW90416.1
GeneID:84225	ZMYND15	17	4,643,319	4,649,410	6,091	+	2	1_A375_pNL7_minus_lncRNA::1::2403, 2_A375_pNL97_plus_lncRNA::1::3441	-8663, -8439	upstream, upstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ZMYND15	ZMYND15, DKFZp434N127	zinc finger, MYND-type containing 15	NM_032265, NM_001136046, hCT2357329.0, hCT23894.2	223683_at	NP_115641.1, NP_001129518.1, EAW90414.1, EAW90415.1
GeneID:9032	TM4SF5	17	4,675,187	4,686,506	11,319	+	1	2_A375_pNL97_plus_lncRNA::1::3442	18093	downstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TM4SF5	TM4SF5		NM_003963, hCT2357350.0, hCT23886.2	206242_at	NP_003954.2, EAW90412.1, EAW90413.1
GeneID:284013	VMO1	17	4,688,580	4,689,729	1,149	-	1	2_A375_pNL97_plus_lncRNA::1::3442	-3551	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene VMO1	ERGA6350, PRO21055, MGC125880, VMO1, MGC125881	vitelline membrane outer layer 1 homolog (chicken)	NM_182566, NM_001144939, NM_001144940, NM_001144941, hCT2261199.0, hCT23887.1	235751_s_at, 241894_at	NP_872372.1, NP_001138411.1, NP_001138412.1, NP_001138413.1, EAW90410.1, EAW90411.1
GeneID:388323	GLTPD2	17	4,692,254	4,693,685	1,431	+	1	2_A375_pNL97_plus_lncRNA::1::3442	1026	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene GLTPD2	GLTPD2	glycolipid transfer protein domain containing 2	NM_001014985, hCT23889.2	230971_x_at	NP_001014985.1, EAW90408.1
GeneID:100288822	LOC100288822	17	4,692,884	4,693,875	991	-	1	2_A375_pNL97_plus_lncRNA::1::3442	595	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100288822		hypothetical LOC100288822	XR_109351		
GeneID:5694	PSMB6	17	4,699,457	4,701,790	2,333	+	1	2_A375_pNL97_plus_lncRNA::1::3442	-6177	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PSMB6	Y, PSMB6, MGC5169, DELTA, LMPY	proteasome (prosome, macropain) subunit, beta type, 6	NM_002798, hCT23885.2	208827_at	NP_002789.1, EAW90407.1
GeneID:8402	SLC25A11	17	4,840,425	4,843,462	3,037	-	1	2_A375_pNL97_plus_lncRNA::1::3443	-8186	upstream	0	1	20	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SLC25A11	SLC25A11, OGC, SLC20A4	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	NM_003562, NM_001165417, NM_001165418, hCT1686726.1, hCT2261191.0, hCT2261192.0, hCT2357347.0	207088_s_at, 209003_at	NP_003553.2, NP_001158889.1, NP_001158890.1, EAW90389.1, EAW90390.1, EAW90392.1, EAW90391.1
GeneID:26001	RNF167	17	4,843,630	4,848,517	4,887	+	1	2_A375_pNL97_plus_lncRNA::1::3443	8018	downstream	0	1	20	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene RNF167	5730408C10Rik, LP2254, RING105, DKFZp566H073, RNF167	ring finger protein 167	NM_015528, hCT2262251.0, hCT2262253.0, hCT2357327.0, hCT23881.3	212047_s_at	NP_056343.1, EAW90387.1, EAW90385.1, EAW90386.1, EAW90388.1
GeneID:5216	PFN1	17	4,848,947	4,851,825	2,878	-	1	2_A375_pNL97_plus_lncRNA::1::3443	177	in gene	0	1	20	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PFN1	PFN1		NM_005022, hCT2261189.0, hCT2261190.0, hCT2357340.0, hCT23881.3	200634_at	NP_005013.1, EAW90382.1, EAW90381.1, EAW90383.1, EAW90384.1
GeneID:2027	ENO3	17	4,854,384	4,860,426	6,042	+	1	2_A375_pNL97_plus_lncRNA::1::3443	-2736	upstream	0	1	20	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ENO3	GSD13, ENO3, MSE	enolase 3 (beta, muscle)	NM_001976, NM_053013, NM_001193503, hCT2262254.0, hCT2262256.0, hCT2262257.0, hCT2262258.0, hCT2262259.0, hCT23883.3	204483_at, 237691_x_at	NP_001967.3, NP_443739.3, NP_001180432.1, EAW90375.1, EAW90378.1, EAW90380.1, EAW90376.1, EAW90377.1, EAW90379.1
GeneID:9552	SPAG7	17	4,862,521	4,871,132	8,611	-	2	1_A375_pNL7_minus_lncRNA::1::2404, 2_A375_pNL97_plus_lncRNA::1::3444	-1188, -1668	upstream, upstream	1	1	18	16	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SPAG7	FSA-1, SPAG7, MGC20134, ACRP	sperm associated antigen 7	NM_004890	200053_at	NP_004881.2
GeneID:23125	CAMTA2	17	4,871,287	4,890,960	19,673	-	6	1_A375_pNL7_minus_lncRNA::1::2404, 1_A375_pNL7_minus_lncRNA::1::2405, 1_A375_pNL7_minus_lncRNA::1::2406, 2_A375_pNL97_plus_lncRNA::1::3444, 2_A375_pNL97_plus_lncRNA::1::3445, 2_A375_pNL97_plus_lncRNA::1::3446	18640, 176, -10064, 18160, 208, -10064	in gene, in gene, upstream, in gene, in gene, upstream	1	1	45.33	41	3	1_A375_pNL7_minus_lncRNA::1	70	Gene CAMTA2	CAMTA2, KIAA0909	calmodulin binding transcription activator 2	NM_015099, NM_001171166, NM_001171167, NM_001171168	212948_at	NP_055914.2, NP_001164637.1, NP_001164638.1, NP_001164639.1
GeneID:388324	INCA1	17	4,891,425	4,900,905	9,480	-	4	1_A375_pNL7_minus_lncRNA::1::2405, 1_A375_pNL7_minus_lncRNA::1::2406, 2_A375_pNL97_plus_lncRNA::1::3445, 2_A375_pNL97_plus_lncRNA::1::3446	10121, -119, 10153, -119	downstream, upstream, downstream, upstream	1	1	59	53.5	2	1_A375_pNL7_minus_lncRNA::1	70	Gene INCA1	HSD45, INCA1, MGC148151, MGC148150	inhibitor of CDK, cyclin A1 interacting protein 1	NM_213726, NM_001167985, NM_001167986, NM_001167987		NP_998891.2, NP_001161457.1, NP_001161458.1, NP_001161459.1
GeneID:10749	KIF1C	17	4,901,243	4,931,694	30,451	+	3	1_A375_pNL7_minus_lncRNA::1::2405, 1_A375_pNL7_minus_lncRNA::1::2406, 2_A375_pNL97_plus_lncRNA::1::3446	-10459, -219, -219	upstream, upstream, upstream	1	1	59	53.5	2	1_A375_pNL7_minus_lncRNA::1	70	Gene KIF1C	LTXS1, KIF1C, KIAA0706	kinesin family member 1C	NM_006612, hCT2262262.0, hCT2262263.0, hCT2262264.0, hCT2262266.0	209244_s_at, 209245_s_at	NP_006603.2, EAW90369.1, EAW90366.1, EAW90367.1, EAW90368.1
GeneID:7775	ZNF232	17	5,009,031	5,026,397	17,366	-	2	1_A375_pNL7_minus_lncRNA::1::2407, 2_A375_pNL97_plus_lncRNA::1::3447	11389, 11325	in gene, in gene	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF232	ZNF232, ZSCAN11	zinc finger protein 232	NM_014519, hCT2260744.0	219123_at	NP_055334.2, EAW90358.1
GeneID:100506676	LOC100506676	17	5,014,763	5,017,677	2,914	+	2	1_A375_pNL7_minus_lncRNA::1::2407, 2_A375_pNL97_plus_lncRNA::1::3447	245, 309	in gene, in gene	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506676		hypothetical LOC100506676	XR_111661, XR_111660, XR_111659, XR_109354, XR_109353, XR_109352, XR_115053, XR_115052, XR_115051		
GeneID:84622	ZNF594	17	5,082,831	5,095,178	12,347	-	2	1_A375_pNL7_minus_lncRNA::1::2408, 2_A375_pNL97_plus_lncRNA::1::3448	-118, -118	upstream, upstream	1	1	129	145	1	2_A375_pNL97_plus_lncRNA::1	145	Gene ZNF594	DKFZp667J055, ZNF594	zinc finger protein 594	NM_032530	235690_at	NP_115919.1
GeneID:100130950	LOC100130950	17	5,095,379	5,138,931	43,552	+	2	1_A375_pNL7_minus_lncRNA::1::2408, 2_A375_pNL97_plus_lncRNA::1::3448	-83, -83	upstream, upstream	1	1	129	145	1	2_A375_pNL97_plus_lncRNA::1	145	Gene LOC100130950	FLJ11616	hypothetical LOC100130950	NR_034082		
GeneID:84268	RPAIN	17	5,322,961	5,336,340	13,379	+	2	1_A375_pNL7_minus_lncRNA::1::2409, 2_A375_pNL97_plus_lncRNA::1::3449	19503, 19471	downstream, downstream	1	1	26	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene RPAIN	FLJ25625, RIP, HRIP, RPAIN, FLJ30490, FLJ42429, MGC4189	RPA interacting protein	NM_001033002, NM_001160243, NM_001160244, NM_001160246, NR_027678, NR_027679, NR_027680, NR_027681, NR_027682, NR_027683, NR_027684, NR_027685, NM_001160266, NM_001160267, hCT2269493.0, hCT24107.3	1564301_a_at, 228183_s_at, 228288_at	NP_001028174.2, NP_001153715.1, NP_001153716.1, NP_001153718.1, NP_001153738.1, NP_001153739.1, EAW90338.1, EAW90339.1
GeneID:708	C1QBP	17	5,336,099	5,342,471	6,372	-	2	1_A375_pNL7_minus_lncRNA::1::2409, 2_A375_pNL97_plus_lncRNA::1::3449	7, 39	in gene, in gene	1	1	26	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene C1QBP	C1QBP, GC1QBP, gC1qR, gC1Q-R, p32, SF2p32, HABP1	complement component 1, q subcomponent binding protein	NM_001212, hCT2260732.1, hCT2260733.1, hCT2260736.1	208910_s_at, 214214_s_at	NP_001203.1, EAW90337.1, EAW90335.1, EAW90336.1
GeneID:56919	DHX33	17	5,345,575	5,372,181	26,606	-	4	1_A375_pNL7_minus_lncRNA::1::2409, 1_A375_pNL7_minus_lncRNA::1::2410, 2_A375_pNL97_plus_lncRNA::1::3449, 2_A375_pNL97_plus_lncRNA::1::3450	29717, -139, 29749, -235	downstream, upstream, downstream, upstream	1	1	25	27	2	2_A375_pNL97_plus_lncRNA::1	30	Gene DHX33	DHX33, DDX33, FLJ21972, DKFZp762F2011	DEAH (Asp-Glu-Ala-His) box polypeptide 33	NM_020162, hCT2260730.0, hCT2260735.1, hCT2350251.0, hCT2350252.0	222675_at	NP_064547.2, EAW90334.1, EAW90331.1, EAW90332.1, EAW90333.1
GeneID:51009	DERL2	17	5,377,613	5,389,497	11,884	-	4	1_A375_pNL7_minus_lncRNA::1::2410, 2_A375_pNL97_plus_lncRNA::1::3450, 2_A375_pNL97_plus_lncRNA::1::3451, 2_A375_pNL97_plus_lncRNA::1::3452	17177, 17081, 377, -487	downstream, downstream, in gene, upstream	1	1	16	19	3	2_A375_pNL97_plus_lncRNA::1	24	Gene DERL2	F-LANs, CGI-101, DERL2, FLANs, F-LAN1	Der1-like domain family, member 2	NM_016041, hCT1962149.1	218333_at	NP_057125.2, EAW90329.1
GeneID:79003	MIS12	17	5,390,247	5,394,131	3,884	+	2	2_A375_pNL97_plus_lncRNA::1::3451, 2_A375_pNL97_plus_lncRNA::1::3452	-1127, -263	upstream, upstream	0	1	12	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene MIS12	MGC2488, MTW1, 2510025F08Rik, KNTC2AP, hMis12, MIS12	MIS12, MIND kinetochore complex component, homolog (S. pombe)	NM_024039, hCT1644809.2	221559_s_at	NP_076944.1, EAW90328.1
GeneID:22861	NLRP1	17	5,404,719	5,487,832	83,113	-	2	2_A375_pNL97_plus_lncRNA::1::3453, 2_A375_pNL97_plus_lncRNA::1::3454	57496, -8192	in gene, upstream	0	1	17.5	23	2	2_A375_pNL97_plus_lncRNA::1	26	Gene NLRP1	NLRP1, KIAA0926, DEFCAP, DKFZp586O1822, VAMAS1, PP1044, NALP1, CARD7, NAC, SLEV1, CLR17.1, DEFCAP-L/S	NLR family, pyrin domain containing 1	NM_033006, NM_033004, NM_001033053, NM_033007, NM_014922, hCT2260711.0, hCT2260714.0, hCT2260715.0, hCT2260716.0, hCT2260717.0, hCT2260718.0, hCT2260720.0	1562256_at, 1562257_x_at, 210113_s_at, 211822_s_at, 211824_x_at, 218380_at	NP_127499.1, NP_127497.1, NP_127500.1, NP_055737.1, NP_001028225.1, EAW90323.1, EAW90321.1, EAW90322.1, EAW90324.1, EAW90325.1, EAW90326.1, EAW90327.1
GeneID:23302	WSCD1	17	5,973,934	6,027,747	53,813	+	1	2_A375_pNL97_plus_lncRNA::1::3455	-4158	upstream	0	1	12	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene WSCD1	WSCD1, KIAA0523	WSC domain containing 1	NM_015253, hCT2269502.0, hCT2269503.0, hCT2357287.0, hCT24106.3	213155_at, 213157_s_at	NP_056068.1, EAW90319.1, EAW90316.1, EAW90317.1, EAW90318.1
GeneID:83394	PITPNM3	17	6,354,583	6,459,877	105,294	-	1	1_A375_pNL7_minus_lncRNA::1::2413	29989	in gene	1	0	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene PITPNM3	MGC157741, NIR1, RDGBA3, CORD5, MGC157740, PITPNM3	PITPNM family member 3	NM_031220, NM_001165966, hCT2260079.1, hCT2260080.1	221254_s_at	NP_112497.2, NP_001159438.1, EAW90304.1, EAW90305.1
GeneID:9851	KIAA0753	17	6,481,645	6,544,247	62,602	-	2	1_A375_pNL7_minus_lncRNA::1::2414, 2_A375_pNL97_plus_lncRNA::1::3459	23, -41	in gene, upstream	1	1	33	22	1	1_A375_pNL7_minus_lncRNA::1	33	Gene KIAA0753	MGC130040, MGC130041, KIAA0753	KIAA0753	NM_014804, hCT2260081.1	204711_at	NP_055619.2, EAW90303.1
GeneID:84817	TXNDC17	17	6,544,222	6,547,861	3,639	+	3	1_A375_pNL7_minus_lncRNA::1::2414, 2_A375_pNL97_plus_lncRNA::1::3459, 2_A375_pNL97_plus_lncRNA::1::3460	2, 66, 11058	in gene, in gene, downstream	1	1	23.5	18	2	1_A375_pNL7_minus_lncRNA::1	33	Gene TXNDC17	TXNL5, TXNDC17, TRP14, MGC14353	thioredoxin domain containing 17	NM_032731, hCT24018.2	224511_s_at, 228743_at	NP_116120.1, EAW90302.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervening Count	Intervening	Intervening Dist to start	Intervening Pos.	[A]	[R]	[C]	[D]	Act Reg Count	Feat Simple	Feat Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:31661053	MED31	17	6,549,853	6,554,954	5,101	+	3	1_A7S_shL7_dhrot_lncRNA:1:-2414,1_A7S_shL7_dhrot_lncRNA:1:-2413,2_A7S_shL97_plus_lncRNA:1:-3459,2_A7S_shL97_plus_lncRNA:1:-3460,	18720, 10999, 5226	downstream, downstream, upstream	1	1	23.5	16	2	2_A7S_shL7_dhrot_lncRNA:1	33	Gene MED31	MED31, 311003441t3Rxt, Bt31,	Mediator complex subunit 31	NM_019060, XM_017240052.2	218316_s_at, 222667_s_at, 238241_at, 240319_at	NP_057144.1, EAW93201.1
Gene:ID:32441227	C17orf100	17	6,555,039	6,556,617	1,578	+	1	2_A7S_shL97_plus_lncRNA:1:-3460,	221	ut gene	0	1	14	14	1	2_A7S_shL97_plus_lncRNA:1	14	Gene C17orf100	C17orf100		NM_001105530	239071_at	NP_001092890.1
Gene:ID:100506713	LOC100506713	17	6,668,428	6,815,868	27,260	+	4	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3460,2_A7S_shL97_plus_lncRNA:1:-3461,	-76, -2484, -76, -2460	upstream, upstream, upstream, upstream	1	1	27.5	29.5	2	2_A7S_shL97_plus_lncRNA:1	32	Gene LOC100506713	hypothetical LOC100506713	XR_109355, XR_109356, XR_109355, XR_109357		
Gene:ID:239	ALOX12	17	6,699,264	6,814,655	14,601	+	4	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3460,2_A7S_shL97_plus_lncRNA:1:-3461,	16390, 16726, 16390, 16744	downstream, downstream, downstream, downstream	1	1	27.5	29.5	2	2_A7S_shL97_plus_lncRNA:1	32	Gene ALOX12	ALOX12, LOC12, 12S-LOX, 12-LOX	arachidonate 12-lipoxygenase	NM_000697, NCT02960308.0	207209_s_at	NP_000688.2, EAW80281.1
Gene:ID:40493	RNASEK	17	6,813,798	6,817,851	2,053	+	4	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3460,2_A7S_shL97_plus_lncRNA:1:-3461,	-54, 2316, -54, 2335	upstream, downstream, upstream, downstream	1	1	27.5	29.5	2	2_A7S_shL97_plus_lncRNA:1	32	Gene RNASEK	MGC71993, MGC65691, RNASEK	ribonuclease, RNase K	NM_001004333	224573_at	NP_001004333.1
Gene:ID:28846	C17orf49	17	6,816,873	6,820,838	3,966	+	4	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3460,2_A7S_shL97_plus_lncRNA:1:-3461,	-2329, 39, -2329, 58	upstream, ut gene, downstream, ut gene	1	1	27.5	29.5	2	2_A7S_shL97_plus_lncRNA:1	32	Gene C17orf49	C17orf49, BAP18, MGC40942	chromosome 17 open reading frame 49	NM_174892, NM_001142798, NM_001142798	226574_at	NP_777553.1, NP_001136270.1, NP_001136271.1
Gene:ID:100506678	LOC100506678	17	6,819,107	6,822,972	3,836	-	4	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3460,2_A7S_shL97_plus_lncRNA:1:-3461,	7229, 4661, 7229, 4585	downstream, downstream, downstream, downstream	1	1	27.5	29.5	2	2_A7S_shL97_plus_lncRNA:1	32	Gene LOC100506678	MIR497HG	hypothetical LOC100506755	XR_111962, XR_109359, XR_115056		
Gene:ID:99971	MIR195	17	6,820,834	6,821,020	66	+	4	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3460,2_A7S_shL97_plus_lncRNA:1:-3461,	5276, 2668, 5276, 2682	downstream, downstream, downstream, downstream	1	1	27.5	29.5	2	2_A7S_shL97_plus_lncRNA:1	32	Gene MIR195	miRNA195, MIR195, MIRN195	microRNA 195	NR_029712		
Gene:ID:74456	MIR497	17	6,821,230	6,821,341	111	+	4	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3460,2_A7S_shL97_plus_lncRNA:1:-3461,	5597, 3229, 5597, 3253	downstream, downstream, downstream, downstream	1	1	27.5	29.5	2	2_A7S_shL97_plus_lncRNA:1	32	Gene MIR497	MIRN497, hsa-mir-497, MIR497	microRNA 497	NR_030114		
Gene:ID:55677	BCL6B	17	6,826,269	6,832,981	6,592	+	2	2_A7S_shL97_plus_lncRNA:1:-3461,2_A7S_shL97_plus_lncRNA:1:-3462,	-8297, 8281	upstream, upstream	1	1	20	32	1	2_A7S_shL97_plus_lncRNA:1	32	Gene BCL6B	ZNF62, BCL6B, BAZF, ZBTB28	B-cell CLL/lymphoma 6, member B	NM_181844, NCT02372760.0, NCT24820.2	1564629_at, 228311_at, 240168_at	NP_863271.1, EAW93273.1, EAW93274.1
Gene:ID:742	DLG4	17	7,092,209	7,123,368	30,160	-	2	2_A7S_shL97_plus_lncRNA:1:-3462,2_A7S_shL97_plus_lncRNA:1:-3463,	8833, -216	ut gene, upstream	0	1	19	23	2	2_A7S_shL97_plus_lncRNA:1	26	Gene DLG4	PLIN7S2, SAP-90, DLG4, SAP90, PSD95, PLIN6574	discs, large homolog 4 (Drosophila)	NM_001128applied, NM_001365, NCT19821611.1, NCT 19821621., NCT23621400.0, NCT23621400.0, NCT23621400.0	203582_at, 210564_s_at	NP_001112269.1, NP_001356.1, EAW93231.1, EAW93253.1, EAW93254.1, EAW93255.1, EAW93252.1, EAW93253.1
Gene:ID:7	ACADVL	17	7,123,183	7,126,868	3,432	+	4	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3462,2_A7S_shL97_plus_lncRNA:1:-3463,	14655, 4617, 435, 14711	downstream, upstream, ut gene, downstream	1	1	19	22	3	2_A7S_shL97_plus_lncRNA:1	26	Gene ACADVL	ACADR, LCACD, VLCAD, ACADVL	acyl-CoA dehydrogenase, very long chain	NM_000018, NM_001033859, NCT22820000.0, NCT23572550.0, NCT23572560.0, NCT23572370.0, NCT31282.2	208710_at	NP_000009.1, NP_001033031.1, EAW93234.1, EAW93246.1, EAW93248.1, EAW93250.1, EAW93247.1
Gene:ID:42585	MIR324	17	7,126,616	7,126,698	82	-	2	2_A7S_shL97_plus_lncRNA:1:-3462,2_A7S_shL97_plus_lncRNA:1:-3463,	8362, 3114	downstream, downstream	0	1	19	23	2	2_A7S_shL97_plus_lncRNA:1	26	Gene MIR324	MIRN324, hsa-mir-324, MIR324	microRNA 324	NR_029896		
Gene:ID:1739	DVL2	17	7,126,661	7,137,863	9,202	-	3	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3462,2_A7S_shL97_plus_lncRNA:1:-3463,	55, 19527, 14279, -1, 8113	ut gene, downstream, downstream, upstream, upstream	1	1	16.25	21.5	4	2_A7S_shL97_plus_lncRNA:1	26	Gene DVL2	DVL2		NM_004422, NCT22613290.0, NCT13255.2	218799_at, 57532_at	NP_004413.1, EAW93245.1, EAW93244.1
Gene:ID:9167	PHF23	17	7,136,247	7,142,825	6,578	-	3	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3462,2_A7S_shL97_plus_lncRNA:1:-3463,	6017, 4981, -151	downstream, downstream, downstream, upstream	1	1	17.5	20	2	2_A7S_shL97_plus_lncRNA:1	20	Gene PHF23	FLJ16353, bJUNE19, FLJ22664, PHF23, MGC2981	PHD finger protein 23	NM_024297, NCT22613230.0, NCT23572550.0, NCT23572601.0, NCT13299.3	1565709_s_at, 220681_at	NP_077373.2, EAW93242.1, EAW93240.1, EAW93241.1, EAW93243.1
Gene:ID:1337	GABARAP	17	7,143,705	7,145,753	2,015	-	3	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2417,2_A7S_shL97_plus_lncRNA:1:-3463,2_A7S_shL97_plus_lncRNA:1:-3464,2_A7S_shL97_plus_lncRNA:1:-3465,	7645, -8699, 7689, 2777, -10151	downstream, upstream, downstream, downstream, upstream	1	1	17.67	20	3	2_A7S_shL97_plus_lncRNA:1	20	Gene GABARAP	FLJ25765, MM46, ATG8A, GABARAP, MGC120159, MGC120194	GABA(A) receptor-associated protein	NM_007278	209565_at	NP_009209.1
Gene:ID:3299	DULLARD	17	7,166,806	7,183,258	6,332	-	3	1_A7S_shL7_dhrot_lncRNA:1:-2416,1_A7S_shL7_dhrot_lncRNA:1:-2420,2_A7S_shL97_plus_lncRNA:1:-3465,2_A7S_shL97_plus_lncRNA:1:-3466,	17451, -452, 17089, 12251, 6448	downstream, upstream, downstream, downstream, upstream	1	1	17.67	20	3	2_A7S_shL97_plus_lncRNA:1	20	Gene DULLARD	HSA011916, CTDNEP1, DULLARD, NET56	CTD nuclear envelope phosphatase 1	NM_015353, NM_001143770	209035_at	NP_056138.2, NP_001137247.1
Gene:ID:3567	C17orf61	17	7,193,272	7,193,259	7,687	-	2	2_A7S_shL97_plus_lncRNA:1:-3463,2_A7S_shL97_plus_lncRNA:1:-3464,	540, 532	ut gene, ut gene	1	1	16	20	1	2_A7S_shL97_plus_lncRNA:1	20	Gene C17orf61	C17orf61, MSTP071, MSTO71, HSPC062, DERP6	chromosome 17 open reading frame 61	NM_202414, NM_202415, NM_016362, NM_202413, NCT19651390.1, NCT19651352.1, NCT13282.2	219260_s_at, 222206_at	NP_981959.1, NP_981960.1, NP_056177.3, NP_981958.1, EAW92230.1, EAW92232.1, EAW92231.1
Gene:ID:9396	CLDN7	17	7,167,222	7,168,512	2,290	-	2	2_A7S_shL97_plus_lncRNA:1:-3463,2_A7S_shL97_plus_lncRNA:1:-3464,	10500, 10508	downstream, downstream	1	1	16	20	1	2_A7S_shL97_plus_lncRNA:1	20	Gene CLDN7	claudin-7, HLS4359, CLDN7, CPETRL2, CPETRL2	claudin 7	NM_001185022, NM_001185023, NM_001307, NCT16414664.3, NCT23633910	202790_at	NP_001171931.1, NP_001171932.1, NP_001129.3, EAW92226.1, EAW92229.1
Gene:ID:1965	EIF5A	17	7,210,316	7,215,762	5,494	+	2	2_A7S_shL97_plus_lncRNA:1:-3466,2_A7S_shL97_plus_lncRNA:1:-3467,	130, 7922	ut gene, downstream	0	1	11	22.5	2	2_A7S_shL97_plus_lncRNA:1	26	Gene EIF5A	EIF5A2, eIF5A, eIF5A1, MGC196255	eukaryotic translation initiation factor 5A	NM_001142760, NM_001970, NM_001142761, NM_001142762, NCT23621210.0, NCT23621210.0, NCT23621210.0, NCT23621210.0	201122_s_at, 201123_s_at, 213752_x_at, 213757_at	NP_001137232.1, NP_001961.1, NP_001137233.1, NP_001137234.1, EAW92219.1, EAW92222.1, EAW92220.1, EAW92221.1
Gene:ID:574	GPS2	17	7,218,978	7,226,898	2,880	-	2	2_A7S_shL97_plus_lncRNA:1:-3466,2_A7S_shL97_plus_lncRNA:1:-3467,	8210, 418	downstream, ut gene	0	1	11	22.5	2	2_A7S_shL97_plus_lncRNA:1	26	Gene GPS2	MGC119287, MGC119288, MGC119289, G protein pathway suppressor 2	G protein pathway suppressor 2	NM_004489	209360_s_at	NP_004480.1
Gene:ID:84951	NEURL4	17	7,218,851	7,232,838	13,987	-	3	2_A7S_shL97_plus_lncRNA:1:-3466,2_A7S_shL97_plus_lncRNA:1:-3467,2_A7S_shL97_plus_lncRNA:1:-3468,	2190, 14398, 416	downstream, downstream, upstream	0	1	13.33	23.67	3	2_A7S_shL97_plus_lncRNA:1	26	Gene NEURL4	KIAA1787, FLJ33980, NEURL4	mind bomb homolog 4 (Drosophila)	NM_001005495, NM_032442	226703_at	NP_001005495.1, NP_115815.2
Gene:ID:92755	LOC92755	17	7,233,771	7,236,662	4,891	+	1	2_A7S_shL97_plus_lncRNA:1:-3470,	715	upstream	0	1	16	26	1	2_A7S_shL97_plus_lncRNA:1	26	Gene LOC92755		protein phosphatase inhibitor 2-like	XM_001719760, XM_001717472, XM_001719803		XP_001719812.1, XP_001719524.1, XP_001719803.1
Gene:ID:744	ACAP1	17	7,239,886	7,254,793	14,908	+	3	1_A7S_shL7_dhrot_lncRNA:1:-2421,2_A7S_shL97_plus_lncRNA:1:-3470,	15464, 8782, 15576	downstream, upstream, downstream	1	1	17.5	25.5	2	2_A7S_shL97_plus_lncRNA:1	26	Gene ACAP1	KIAA0050, ACAP1, CENTB1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	NM_014716, NCT22662117.0, NCT13289.3	208212_s_at, 208213_at, 242081_at	NP_055511.1, EAW92094.1, EAW92110.1
Gene:ID:47040	ICTD11	17	7,253,205	7,256,263	3,058	+	2	1_A7S_shL7_dhrot_lncRNA:1:-2421,2_A7S_shL97_plus_lncRNA:1:-3471,	104, 216	ut gene, ut gene	1	1	17	25	1	2_A7S_shL97_plus_lncRNA:1	25	Gene ICTD11	MGC129844, RENICTD11, REN, ICTD11, C17orf36	potassium channel tetramerisation domain containing 11	NM_001002914, NCT19480466.1	235697_at	NP_001002914.1, EAW92208.1
Gene:ID:79166	TMEM93	17	7,256,467	7,260,538	2,041	+	2	1_A7S_shL7_dhrot_lncRNA:1:-2421,2_A7S_shL97_plus_lncRNA:1:-3471,	3165, 3973	upstream, upstream	1	1	17	25	1	2_A7S_shL97_plus_lncRNA:1	25	Gene TMEM93	MGC129783, UNQ9396, TMEM93	transmembrane protein 93	NM_198154, NCT16554112.3, NCT23572532.0, NCT23572530.0	1560261_s_at	NP_937797.1, EAW92206.1, EAW92205.1, EAW92207.1
Gene:ID:7659	ZBTB4	17	7,262,665	7,267,566	20,902	-	3	1_A7S_shL7_dhrot_lncRNA:1:-2422,2_A7S_shL97_plus_lncRNA:1:-3472,2_A7S_shL97_plus_lncRNA:1:-3473,	336, 6416, 336	ut gene, ut gene, ut gene	1	1	16.5	26	2	1_A7S_shL7_dhrot_lncRNA:1	26	Gene ZBTB4	ZBTB4, ZNF803, KIAA0-L1, KIAA1538	zinc finger and BTB domain containing 4	NM_020899, NM_001128633, NCT24041410.0	235629_s_at, 227067_s_at	NP_065932.2, NP_001122305.1, EAW93163.1
Gene:ID:43964	AMACR1L2	17	7,264,721	7,266,353	1,662	+	2	1_A7S_shL7_dhrot_lncRNA:1:-2422,2_A7S_shL97_plus_lncRNA:1:-3472,2_A7S_shL97_plus_lncRNA:1:-3473,	2511, -1069, 2511	downstream, downstream, downstream	1	1	100	96	2	1_A7S_shL7_dhrot_lncRNA:1	201	Gene AMACR1L2	AMACR1L2, THEM21B	alpha-methylacyl-CoA racemase 1-like 2	NM_001102614		NP_001096084.1
Gene:ID:430	POLR2A	17	7,287,890	7,417,933	30,053	+	3	1_A7S_shL7_dhrot_lncRNA:1:-2422,2_A7S_shL97_plus_lncRNA:1:-3472,2_A7S_shL97_plus_lncRNA:1:-3473,	416, -8668, 416	upstream, upstream, upstream	1	1	100	96	2	1_A7S_shL7_dhrot_lncRNA:1	200	Gene POLR2A	POLR2, RPB1, POLRA, POLR2K, RPO2, RpIL5, RPOL2, RPB61, hRPB220, hsRPB1, MGC19453	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	NM_000937, NCT22991340, NCT22991370, NCT13269.3	202725_at, 217415_at, 217420_x_at	NP_000928.1, EAW93181.1, EAW93182.1, EAW93183.1
Gene:ID:6188	SENP3	17	7,365,319	7,475,267	9,968	+	2	2_A7S_shL97_plus_lncRNA:1:-3474,2_A7S_shL97_plus_lncRNA:1:-3475,	11031, 17465	downstream, downstream	0	1	15.5	20	2	2_A7S_shL97_plus_lncRNA:1	22	Gene SENP3	DKFZp586l0918, SSP3, SMT3IP1, SENP3, DKFZp762k152	SUMO1/sentrin/SMT3 specific peptidase 3	NM_015670, NCT01962985.1, NCT22661480.0, NCT07664.2	202871_at, 219113_s_at, 219114_at	NP_056655.2, EAW93170.1, EAW93171.1, EAW93172.1
Gene:ID:973	EIF4A3	17	7,476,037	7,482,324	6,287	+	2	2_A7S_shL97_plus_lncRNA:1:-3474,2_A7S_shL97_plus_lncRNA:1:-3475,	288, 6727, 10951	ut gene, downstream, downstream	0	1	16	20.67	3	2_A7S_shL97_plus_lncRNA:1	22	Gene EIF4A3	EIF4A, EIF4AIII, EIF-4A, DDX2A	eukaryotic translation initiation factor 4A, isoform 1	NM_001416, NCT22991480.0, NCT22991510.0, NCT22991520.0, NCT13032.1	201530_s_at, 211797_s_at, 214553_at	NP_001407.1, EAW93167.1, EAW93166.1, EAW93168.1, EAW93169.1
Gene:ID:52865	SNORA48	17	7,476,031	7,476,165	134	+	3	2_A7S_shL97_plus_lncRNA:1:-3474,2_A7S_shL97_plus_lncRNA:1:-3475,2_A7S_shL97_plus_lncRNA:1:-3476,	1879, 4753, 6877	upstream, downstream, downstream	0	1	16	20.67	3	2_A7S_shL97_plus_lncRNA:1	22	Gene SNORA48	ACA48, SNORA48	small nucleolar RNA, H/ACA box 48	NR_002918		
Gene:ID:52866	SNORD10	17	7,480,124	7,480,276	147	+	3	2_A7S_shL97_plus_lncRNA:1:-3474,2_A7S_shL97_plus_lncRNA:1:-3475,2_A7S_shL97_plus_lncRNA:1:-3476,	2777, 2655, 6579	upstream, downstream, downstream	0	1	16	20.67	3	2_A7S_shL97_plus_lncRNA:1	22	Gene SNORD10	SNORD10, mgU6-77	small nucleolar RNA, C/D box 10	NR_002924		
Gene:ID:6761	SNORA67	17	7,481,273	7,481,409	136	+	3	2_A7S_shL97_plus_lncRNA:1:-3474,2_A7S_shL97_plus_lncRNA:1:-3475,2_A7S_shL97_plus_lncRNA:1:-3476,	4521, 1811, 9733	upstream, downstream, downstream	0	1	16	20.67	3	2_A7S_shL97_plus_lncRNA:1	22	Gene SNORA67	U67, RNU67, SNORA67	small nucleolar RNA, H/ACA box 67	NR_002912		
Gene:ID:925	CD68	17	7,482,005	7,488,429	2,624	+	3	2_A7S_shL97_plus_lncRNA:1:-3474,2_A7S_shL97_plus_lncRNA:1:-3475,2_A7S_shL97_plus_lncRNA:1:-3476,	4483, -21, 4253	upstream, upstream, downstream	0	1	16	20.67	3	2_A7S_shL97_plus_lncRNA:1	22	Gene CD68	SCARD1, CD68, DKFZp686M18236, GP11	CD68 molecule	NM_001251, NM_001040059, NCT16454853.2	203507_at	NP_001242.2, NP_001030148.1, EAW93165.1
Gene:ID:528	MPDU1	17	7,490,965	7,491,830	4,565	+	2	2_A7S_shL97_plus_lncRNA:1:-3475,2_A7S_shL97_plus_lncRNA:1:-3476,	4101, 41	upstream, ut gene	0	1	17	20	2	2_A7S_shL97_plus_lncRNA:1	22	Gene MPDU1	MPDU1, CDGF, FLJ16836, PQLC5, Lec35, Hb556, HBEBP2BPA, SLI15, PP3856	mannose-P-dolichol utilization defect 1	NM_004870, NR_024602, NCT19821551.1, NCT19821561., NCT22661550.0, NCT22661560.0, NCT23621600.0, NCT31258.2	1557569_at, 203256_at	NP_004861.2, EAW93162.1, EAW93163.1, EAW93159.1, EAW93160.1, EAW93161.1
Gene:ID:993	SOX15	17	7,491,995	7,493,668	1,908	-	2	2_A7S_shL97_plus_lncRNA:1:-3475,2_A7S_shL97_plus_lncRNA:1:-3476,	10704, 6450	downstream, downstream	0	1	17	20	2	2_A7S_shL97_plus_lncRNA:1	22	Gene SOX15	SOX15, SOX20, SOX35, SOX37	SRY (sex determining region Y)-box 15	NM_006942, NCT22653430.0, NCT31287.2	206122_at, 207080_s_at	NP_008873.1, EAW93156.1, EAW93157.1
Gene:ID:513	FXR2	17	7,494,848	7,616,215	23,867	-	1	2_A7S_shL97_plus_lncRNA:1:-3476,	31207	downstream	0	1	17	22	1	2_A7S_shL97_plus_lncRNA:1	22	Gene FXR2	FXR2, FXR2P, FMR1L2	fragile X mental retardation, autosomal homolog 2	NM_004860, NCT16854521.1, NCT13291.3	203172_at, 223090_at, 223091_at	NP_004851.2, EAW93154.1, EAW93155.1
Gene:ID:52	ATP1B2	17	7,554,254	7,561,089	6,835	+	1	2_A7S_shL97_plus_lncRNA:1:-3477,	174	upstream	0	1	11	20	1	2_A7S_shL97_plus_lncRNA:1	20	Gene ATP1B2	ATP1B2, AMOG	ATPase, Na+/K+ transporting, beta 2 polypeptide	NM_001678, NCT22691640.0, NCT13290.2	204311_at	NP_001669.2, EAW93148.1, EAW93147.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervening Count	Intervening	Intervening Distance	Intervening Position	[A]	[B]	[C]	[D]	Active Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:7157	TP53	17	7,571,720	7,590,863	19,143	-	2	1_A375_shN7_rhrus_hicRNA:1:2423, 2_A375_shN7_glus_hicRNA:1:3478	11535, 1029	up gene, ust gene	1	1	16	17	1	2_A375_shN7_glus_hicRNA:1	17	Gene TP53	FLJ92943, LFS1, TP53, P53, TRP53;	further protein p53	NM_000546, NM_001126112, NM_001126113, NM_001126114, NM_001126115, NM_001126116, NM_001276117, NCT22634261, NCT22634311, NCT22637972, NCT22637980, NCT22637989, NCT23178154	201746_at, 211300_s_at	NP_000537.2, NP_001119584.1, NP_001119585.1, NP_001119586.1, NP_001119587.1, NP_001119588.1, NP_001119589.1, EAW80140.1, EAW80141.1, EAW80142.1, EAW80143.1, EAW80144.1, EAW80145.1
Gene:ID:100506609	LOC100506609	17	7,566,576	7,569,622	3,046	-	2	1_A375_shN7_rhrus_hicRNA:1:2423, 2_A375_shN7_glus_hicRNA:1:3478	-106, -262	upstream, upstream	1	1	16	17	1	2_A375_shN7_glus_hicRNA:1	17	Gene LOC100506609		hypothetical protein LOC100506609	XM_003114731		NP_003114779.1
Gene:ID:5133	WRAP53	17	7,569,089	7,606,520	17,431	+	2	1_A375_shN7_rhrus_hicRNA:1:2423, 1_A375_shN7_rhrus_hicRNA:1:2424, 2_A375_shN7_glus_hicRNA:1:3478	539, 18995, 425	up gene, downstream, up gene	1	1	20.5	16	2	1_A375_shN7_rhrus_hic RNA:1	25	Gene WRAP53	TCAB1, WRAP53, WDR79, FLJ10355	WD repeat containing, antisense to TP53	NM_018081, NM_001143800, NM_001143991, NM_001143992, NCT22981650, NCT22981670, NCT23027310, NCT23305.2	228256_s_at, 44863_at	NP_059511.2, NP_001137462.1, NP_001137463.1, NP_001137464.1, EAW80126.1, EAW80127.1, EAW80129.1
Gene:ID:9948	EPN82	17	7,606,520	7,614,863	8,172	+	3	1_A375_shN7_rhrus_hicRNA:1:2424, 1_A375_shN7_rhrus_hicRNA:1:2425, 2_A375_shN7_glus_hicRNA:1:3479	-136, 12585, 12120	upstream, downstream, downstream	1	1	27	31	2	2_A375_shN7_glus_hicRNA:1	43	Gene EPN82	EPN83, LERK2, EPLG6, EPL6	epsin-83	NM_001486, NCT18555221, NCT22981660, NCT23297	208031_at, 210863_s_at	NP_001159771, EAW80133.1, EAW80134.1, EAW80135.1
Gene:ID:1960754	DNAH2	17	7,623,039	7,737,856	114,818	+	7	1_A375_shN7_rhrus_hicRNA:1:2423, 1_A375_shN7_rhrus_hicRNA:1:2426, 1_A375_shN7_rhrus_hicRNA:1:2427, 1_A375_shN7_rhrus_hicRNA:1:2428, 1_A375_shN7_glus_hicRNA:1:3479, 2_A375_shN7_glus_hicRNA:1:3480, 2_A375_shN7_glus_hicRNA:1:3481, 2_A375_shN7_glus_hicRNA:1:3482	-2831, 117297, 122799, -2399, 117217, 122768, 128161	upstream, downstream, downstream, upstream, downstream, downstream, downstream	1	1	28.15	31.75	4	1_A375_shN7_rhrus_hic RNA:1	52	Gene DNAH2	DNAHC2, FLJ95675, DNAH2, DNHD2, KIAA1503	dynein, axonemal, heavy chain 2	NM_020877, NCT18155502.2, NCT22981710, NCT23406220	215580_at, 238499_at	NP_059282.2, EAW80131.1, EAW80129.1, EAW80130.1
Gene:ID:23135	IDMB	17	7,742,233	7,758,118	14,883	+	6	1_A375_shN7_rhrus_hicRNA:1:2426, 1_A375_shN7_rhrus_hicRNA:1:2427, 1_A375_shN7_rhrus_hicRNA:1:2428, 1_A375_shN7_glus_hicRNA:1:3480, 2_A375_shN7_glus_hicRNA:1:3481, 2_A375_shN7_glus_hicRNA:1:3482, 2_A375_shN7_glus_hicRNA:1:3483, 2_A375_shN7_glus_hicRNA:1:3484	-1599, 2573, 17181, 2979, 2973, 2985, 17213, 18203	upstream, ust gene, downstream, upstream, ust gene, ust gene, downstream, downstream	1	1	27.78	27.25	4	1_A375_shN7_rhrus_hic RNA:1	52	Gene IDMB	IDMB, KIAA0346, JAUD2	lysine (K)-specific demethylase 6B	NM_001080424	1559092_at, 1559097_a_at, 221396_at, 41366_x_at, 41367_r_at	NP_001073553.1
Gene:ID:2162	TMEM65	17	7,758,264	7,759,417	1,033	+	3	1_A375_shN7_rhrus_hicRNA:1:2426, 2_A375_shN7_glus_hicRNA:1:3482, 2_A375_shN7_glus_hicRNA:1:3484	2832, 2664, 3286	downstream, downstream, downstream	1	1	21	25	1	2_A375_shN7_glus_hicRNA:1	25	Gene TMEM65	FLJ20025, MGC17164, TMEM65	transmembrane protein 65	NM_203411, NCT22691760, NCT23205.2	236452_at	NP_981956.1, EAW80124.1, EAW80125.1
Gene:ID:4316	LSMD1	17	7,760,003	7,761,372	1,168	-	3	1_A375_shN7_rhrus_hicRNA:1:2426, 1_A375_shN7_glus_hicRNA:1:3482, 2_A375_shN7_glus_hicRNA:1:3484	786, 724, 266	up gene, ust gene, upstream	1	1	21	25	1	2_A375_shN7_glus_hicRNA:1	25	Gene LSMD1	MGC74637, PFAAP2, LSMD1, MGC14151	LSM domain containing 1	NM_032356, NCT23311.2	224512_s_at, 228441_x_at	NP_115722.2, EAW80123.1
Gene:ID:54631	CYBSD1	17	7,761,264	7,765,800	4,536	+	3	1_A375_shN7_rhrus_hicRNA:1:2426, 1_A375_shN7_glus_hicRNA:1:3482, 2_A375_shN7_glus_hicRNA:1:3484	648, -616, 376	upstream, upstream, ust gene	1	1	21	25	1	2_A375_shN7_glus_hicRNA:1	25	Gene CYBSD1	FLJ32489, CYBSD1	cytochrome b5 domain containing 1	NM_148607, NCT22494401.0, NCT22684420, NCT23372809.0, NCT23303.3	1552711_s_at, 236633_at	NP_683208.2, EAW80121.1, EAW80119.1, EAW80120.1, EAW80122.1
Gene:ID:107	CHD3	17	7,795,123	7,816,075	27,952	+	2	1_A375_shN7_rhrus_hicRNA:1:2429, 2_A375_shN7_glus_hicRNA:1:3486	1181, 901	up gene, ust gene	1	1	18	22	1	2_A375_shN7_glus_hicRNA:1	22	Gene CHD3	Mi-2a, CHD3.2, PPH, MJ-ALPHA	chromodomain helicase DNA binding protein 3	NM_001005271, NM_005852, NM_001005273, NCT22981652.0, NCT22981653.0, NCT23306.2	208026_at, 208027_s_at	NP_001005271.2, NP_005843.2, NP_001005273.1, EAW80114.1, EAW80115.1, EAW80116.1
Gene:ID:84148	ALOX12B	17	7,870,854	7,891,021	15,067	-	1	1_A375_shN7_glus_hicRNA:1:3486	7661	ust gene	0	1	10	15	1	2_A375_shN7_glus_hicRNA:1	15	Gene ALOX12B	12R-LOX, ALOX12B	arachidonate 12-lipoxygenase, 12R type	NM_001139, NCT18513271	207351_at	NP_001130.3, EAW80098.1
Gene:ID:100422982	MRM314	17	7,891,374	7,891,465	91	+	1	1_A375_shN7_rhrus_hicRNA:1:3486	-6014	upstream	0	1	10	15	1	2_A375_shN7_glus_hicRNA:1	15	Gene MRM314		rRNA adenine N(6)-methyltransferase-like 4	NR_026201		
Gene:ID:8344	ALOX15	17	7,899,218	8,022,234	23,016	-	4	1_A375_shN7_rhrus_hicRNA:1:2430, 1_A375_shN7_rhrus_hicRNA:1:2431, 1_A375_shN7_glus_hicRNA:1:3487, 2_A375_shN7_glus_hicRNA:1:3488	-606, -6684, 1695, 3716	upstream, downstream, upstream, upstream	1	1	19	17	3	1_A375_shN7_rhrus_hic RNA:1	25	Gene ALOX15	MGC119695, MGC119696, eLOX3, E-LOX, MGC119694, ALOX15	arachidonate lipoxygenase 3	NM_001140, NM_001165960, NCT22985.2, NCT23633860	207705_at, 222383_s_at	NP_067641.2, NP_001153432.1, EAW80092.1, EAW80093.1
Gene:ID:1967	HES7	17	8,023,005	8,027,410	3,502	-	4	1_A375_shN7_rhrus_hicRNA:1:2430, 1_A375_shN7_rhrus_hicRNA:1:2431, 1_A375_shN7_glus_hicRNA:1:3487, 2_A375_shN7_glus_hicRNA:1:3488	4270, -1916, 3490, 1466	downstream, upstream, ust gene, ust gene	1	1	19	17	3	1_A375_shN7_rhrus_hic RNA:1	25	Gene HES7	bHLH37, HES7, SCDOH	hairy and enhancer of split 7 (Drosophila)	NM_032580, NM_001163867, NCT18153513	226545_at	NP_116099.2, NP_001153432.1, EAW80092.1
Gene:ID:4314	TMEM107	17	8,079,295	8,079,714	2,416	-	2	1_A375_shN7_rhrus_hicRNA:1:2431, 2_A375_shN7_glus_hicRNA:1:3490, 2_A375_shN7_glus_hicRNA:1:3491	2594, 2690, 10430	ust gene, upstream, upstream	1	1	24	29.5	2	2_A375_shN7_glus_hicRNA:1	32	Gene TMEM107	PRO1268, TMEM107, CRVS535, MGC10744	transmembrane protein 107	NM_032354, NM_153359, NCT22985.2, NCT23637410, NCT23672000	224693_at, 224696_s_at, 238490_at, 238580_x_at, 238624_s_at	NP_115735.2, NP_705585.1, EAW80063.1, EAW80064.1, EAW80065.1
Gene:ID:27976	SNORD111	17	8,079,771	8,079,906	135	-	2	1_A375_shN7_rhrus_hicRNA:1:2431, 2_A375_shN7_glus_hicRNA:1:3490	-214, -116	upstream, upstream	1	1	22	32	1	2_A375_shN7_glus_hicRNA:1	32	Gene SNORD116	U8, SNORD116	small nucleolar RNA, C/D box 116	NR_033294		
Gene:ID:4785	C17orf59	17	8,091,651	8,093,964	1,913	-	5	1_A375_shN7_rhrus_hicRNA:1:2431, 1_A375_shN7_rhrus_hicRNA:1:2432, 1_A375_shN7_rhrus_hicRNA:1:2433, 2_A375_shN7_glus_hicRNA:1:3489, 2_A375_shN7_glus_hicRNA:1:3490, 2_A375_shN7_glus_hicRNA:1:3492	5292, -36, 3430, -62, 9077	downstream, upstream, downstream, upstream, upstream	1	1	18.67	25	2	2_A375_shN7_glus_hicRNA:1	32	Gene C17orf59	C17orf59, PRO2472, FLJ20014	chromosome 17 open reading frame 59	NM_017622	218417_s_at, 222662_s_at	NP_060092.2
Gene:ID:212	AURKB	17	8,108,049	8,113,883	5,834	-	1	1_A375_shN7_glus_hicRNA:1:3490	10342	upstream	0	1	10	16	1	2_A375_shN7_glus_hicRNA:1	16	Gene AURKB	AIRK2, aurk3-v2, AurB, STK12, IPL1-like1, AIM-1, AIK2, STK5, AURKB, AIM1, dor59-vrl1	aurora kinase B	NM_004217, NCT18621341.1, NCT22486.3, NCT22633960, NCT22633964.0, NCT23372760.0, NCT23372770.0, NCT23372784.0	209464_at, 209219_at	NP_004208.2, EAW80074.1, EAW80072.1, EAW80073.1, EAW80077.1, EAW80078.1, EAW80079.1, EAW80076.1
Gene:ID:54829	C17orf84	17	8,123,848	8,127,361	3,513	-	4	1_A375_shN7_rhrus_hicRNA:1:2436, 1_A375_shN7_rhrus_hicRNA:1:2437, 2_A375_shN7_glus_hicRNA:1:3496, 2_A375_shN7_glus_hicRNA:1:3497	2316, 1121, 2381, 1859	up gene, ust gene, ust gene, up gene	1	1	20.5	25	2	2_A375_shN7_glus_hicRNA:1	32	Gene C17orf84	FLJ32780, C17orf84, MGC102621	chromosome 17 open reading frame 84	NR_026931	233012_at	
Gene:ID:6169	C17orf66	17	8,128,129	8,151,413	23,284	-	4	1_A375_shN7_rhrus_hicRNA:1:2439, 1_A375_shN7_rhrus_hicRNA:1:2440, 1_A375_shN7_rhrus_hicRNA:1:2441, 2_A375_shN7_glus_hicRNA:1:3498, 2_A375_shN7_glus_hicRNA:1:3499	26570, 28173, 26612, 28141	downstream, downstream, downstream, downstream	1	1	20.5	25	2	2_A375_shN7_glus_hicRNA:1	32	Gene C17orf66	AAH132, MGC133331, CTC1, C17orf66, NA1-132, FLJ22170	CTS telomere maintenance complex component 1	NM_025099, NCT22633840.0, NCT22603810	218435_at, 240879_at	NP_079375.2, EAW80070.1, EAW80071.1
Gene:ID:23435	SLC25A33	17	8,191,082	8,198,170	7,088	+	1	1_A375_shN7_glus_hicRNA:1:3498	5696	up gene	0	1	10	16	1	2_A375_shN7_glus_hicRNA:1	16	Gene SLC25A33	SLC25A33, FLJ40217, MGC120849, MGC120488	solute carrier family 25, member 33	NM_201120, NCT22624612, NCT23372760	228630_at, 229053_at	NP_659208.1, EAW80062.1, EAW80063.1
Gene:ID:9246	RANGRF	17	8,191,969	8,193,809	1,840	+	1	1_A375_shN7_glus_hicRNA:1:3498	235	up gene	0	1	10	16	1	2_A375_shN7_glus_hicRNA:1	16	Gene RANGRF	RANGRF, DUTZ, bA556M21.2, MOS1, HSPC236, RANGRFP, MGC110373, HSPC165	RAN guanine nucleotide release factor	NM_001177801, NM_001177802, NM_016462, NCT18621361.1, NCT18621371.1, NCT22459.2	208236_s_at, 221554_s_at	NP_001170272.1, NP_001170273.1, NP_057976.2, EAW80065.1, EAW80066.1, EAW80065.1, EAW80066.1
Gene:ID:154	RPL26	17	8,200,834	8,206,565	5,731	-	2	1_A375_shN7_rhrus_hicRNA:1:2455, 1_A375_shN7_glus_hicRNA:1:3480	-59, -59	upstream, upstream	1	1	155	171	1	2_A375_shN7_glus_hicRNA:1	171	Gene RPL26	L26, RPL26	ribosomal protein L26	NM_000987		NP_000978.1
Gene:ID:43804	RNF222	17	8,294,822	8,301,144	7,122	-	2	1_A375_shN7_rhrus_hicRNA:1:2455, 2_A375_shN7_glus_hicRNA:1:3497	14532, 14520	downstream, downstream	1	1	155	171	1	2_A375_shN7_glus_hicRNA:1	171	Gene RNF222	RNF222		NM_001146554		NP_001140156.1
Gene:ID:96550	PIK3R6	17	8,709,855	8,710,894	64,939	-	2	1_A375_shN7_rhrus_hicRNA:1:2459, 2_A375_shN7_glus_hicRNA:1:3496	8355, 5342	up gene, ust gene	1	1	28	29	1	2_A375_shN7_glus_hicRNA:1	29	Gene PIK3R6	PIK3R6, p87PIKAP), PLI34500, p84, p87PIKAP, DKFZp666P156, HsT41026, C17orf65	phosphoinositide-3-kinase, regulatory subunit 6	NM_001010855, NCT22901491.1, NCT23406311.0, NCT23406320.0, NCT23351100.0	1555770_a_at	NP_001010855.1, EAW80039.1, EAW80038.1, EAW80040.1, EAW80041.1
Gene:ID:3523	PIK3R5	17	8,762,233	8,869,024	66,791	-	2	1_A375_shN7_rhrus_hicRNA:1:2460, 2_A375_shN7_glus_hicRNA:1:3498	48655, 48555	up gene, ust gene	1	1	17	19	1	2_A375_shN7_glus_hicRNA:1	19	Gene PIK3R5	p101, P101-PI3K, PCAP-2, PI3K005115Rk, PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_014308, NM_001143833, NCT18513.2, NCT22601403.0, NCT22601490.0	220366_at, 227665_at	NP_055123.2, NP_001136105.1, EAW80030.1, EAW80031.1, EAW80037.1
Gene:ID:462	STX6	17	8,153,766	8,479,215	325,450	-	2	1_A375_shN7_rhrus_hicRNA:1:2461, 1_A375_shN7_glus_hicRNA:1:3500	267, 123	up gene, ust gene	1	1	16	15	1	2_A375_shN7_glus_hicRNA:1	15	Gene STX6	GARS, STX6	syntaxin 6	NM_006652, NM_033556, NCT22987621.1, NCT22987632.0, NCT23407310.0, NCT23407321.0	1570357_at, 204690_at	NP_006643.1, EAW80029.1, EAW80026.1, EAW80030.1, EAW80031.1
Gene:ID:9948	WDR16	17	8,479,844	8,546,776	66,932	+	2	1_A375_shN7_rhrus_hicRNA:1:2461, 2_A375_shN7_glus_hicRNA:1:3500	4035, -782	upstream, upstream	1	1	16	15	1	2_A375_shN7_glus_hicRNA:1	15	Gene WDR16	WDRPLH, FLJ37525, WDR16	WD repeat domain 16	NM_001005339, NM_139154, NCT20366.2, NCT22984600.0, NCT23372840.0, NCT23372940.0	227753_s_at, 239816_at	NP_001005339.1, NP_620401.4, EAW80034.1, EAW80035.1, EAW80036.1, EAW80037.1
Gene:ID:54738	UBP42	17	8,846,890	8,853,864	64,864	+	1	1_A375_shN7_glus_hicRNA:1:2464	31338	up gene	0	1	16	20	1	2_A375_shN7_glus_hicRNA:1	16	Gene UBP42	UBP42, FLJ20626	ubiquitin specific peptidase 43	NM_152310	227439_at	NP_689442.2
Gene:ID:8227	QK37	17	9,811,926	10,101,868	287,942	-	3	1_A375_shN7_rhrus_hicRNA:1:2483, 2_A375_shN7_glus_hicRNA:1:3507, 2_A375_shN7_glus_hicRNA:1:3508	221164, 83068	up gene, ust gene	1	1	17.5	13.5	2	2_A375_shN7_glus_hicRNA:1	20	Gene QK37	KIAA0342, MLLQK37, MGC1346, QK37	growth arrest-specific 7	NM_002648, NM_201432, NM_201433, NM_001130531, NCT22987640.0, NCT22987670.0, NCT23406.2	202191_s_at, 202192_s_at, 202193_s_at, 215972_x_at, 215997_s_at	NP_002639.2, NP_958838.1, NP_001124332.1, NP_958839.1, EAW80031.1, EAW80032.1
Gene:ID:341	SCO1	17	10,583,689	10,600,885	17,206	-	1	1_A375_shN7_glus_hicRNA:1:3509	65	up gene	0	1	14	26	1	2_A375_shN7_glus_hicRNA:1	26	Gene SCO1	SCO1L, SCO1	SCO cytochrome oxidase deficient homolog 1 (yeast)	NM_004589, NCT18612.3	203221_at	NP_004580.1, EAW80087.1
Gene:ID:9965	C17orf66	17	10,600,927	10,618,875	13,948	+	1	1_A375_shN7_glus_hicRNA:1:3509	-127	upstream	0	1	14	26	1	2_A375_shN7_glus_hicRNA:1	26	Gene C17orf66	C17orf66, NBLA03831, MDS006	chromosome 17 open reading frame 66	NM_020233, NCT22239.3, NCT22621958	220606_s_at, 223001_at	NP_064618.2, EAW80085.1, EAW80086.1
Gene:ID:770	DNAH9	17	11,901,746	11,973,065	371,317	+	1	1_A375_shN7_glus_hicRNA:1:3558	259990	up gene	0	1	10	19	1	2_A375_shN7_glus_hicRNA:1	19	Gene DNAH9	DNEL1, DNAH17L, HL20, DNHL9, DYH9, DNAH9, KIAA0357, HL20	dynein, axonemal, heavy chain 9	NM_001372, NM_004662, NCT18603161.1, NCT18603562.1, NCT18603563.1, NCT22985600.0, NCT22985640.0, NCT23406530.0	207829_s_at, 210345_s_at, 240697_at	NP_001353.2, NP_004653.2, EAW80075.1, EAW80079.1, EAW80081.1, EAW80082.1, EAW80080.1, EAW80083.1
Gene:ID:9996	ZNF18	17	11,950,762	11,960,689	10,927	-	2	1_A375_shN7_rhrus_hicRNA:1:2483, 2_A375_shN7_glus_hicRNA:1:3506	61, 177	up gene, ust gene	1	1	16	17	1	2_A375_shN7_glus_hicRNA:1	17	Gene ZNF18	KOX11, ZSG38, ZNF18, HOSG1, ZKSCAN6, ZNF538	zinc finger protein 18	NM_134450, NCT22007.2	226707_at	NP_653251.2, EAW80077.1
Gene:ID:3526	ELAC2	17	12,894,829	12,921,281	26,452	-	2	1_A375_shN7_rhrus_hicRNA:1:2486, 2_A375_shN7_glus_hicRNA:1:3508	1, 281	up gene, ust gene	1	1	18	22	1	2_A375_shN7_glus_hicRNA:1	22	Gene ELAC2	ELAC2, FLJ98663, HPC2, FLJ10530, ELC2, FLJ42646	elaC homolog 2 (E. coli)	NM_018127, NM_001160982, NM_173717, NCT22993.3, NCT18512240.0, NCT23372320.0, NCT23372760.0	201799_at, 201767_s_at	NP_060597.4, NP_001138434.1, NP_776090.1, EAW80060.1, EAW80062.1, EAW80063.1, EAW80064.1
Gene:ID:9555	HS3ST3A1	17	12,399,006	13,005,240	106,235	+	2	1_A375_shN7_glus_hicRNA:1:3507, 2_A375_shN7_glus_hicRNA:1:3508	60090, 1276	up gene, ust gene	0	1	12.5	19	2	2_A375_shN7_glus_hicRNA:1	21	Gene HS3ST3A1	HS3ST3A1, 3OST3A1, 3OST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	NM_006042, NCT18513.2	210883_at	NP_006033.1, EAW80058.1
Gene:ID:100506698	LOC100506698	17	13,922,609	13,972,775	50,166	-	1	1_A375_shN7_glus_hicRNA:1:3509	-67	upstream	0	1	17	19	1	2_A375_shN7_glus_hicRNA:1	19	Gene LOC100506698		hypothetical LOC100506698	XR_109396, XR_110063		
Gene:ID:332	COX10	17	13,972,719	14,111,996	139,277	+	1	1_A375_shN7_glus_hicRNA:1:3509	113	up gene	0	1	17	19	1	2_A375_shN7_glus_hicRNA:1	19	Gene COX10	COX10		NM_001303, NCT22989861.1, NCT22989862.1	203555_s_at	NP_001294.2, EAW80087.1, EAW80086.1
Gene:ID:376	PNPT2	17	15,133,099	15,168,644	35,546	-	1	1_A375_shN7_glus_hicRNA:1:3511	2020	up gene	0	1	10	16	1	2_A375_shN7_glus_hicRNA:1	16	Gene PNPT2	CMT1A, CMT1E, HMPP, MGC20798, Spl10, DSS, PAP22, QKI-3, HMENA	phosphotidyl choline protein 2	NM_203354, NM_153325, NM_153322, NCT19276.2, NCT19303011.1, NCT23372320.0, NCT23372362.0	1561739_s_at	NP_989581.1, NP_989599.1, NP_989597.1, EAW80945.1, EAW80946.1, EAW80947.1, EAW80948.1, EAW80949.1
Gene:ID:7135	ZNF286A	17	15,602,691	15,624,101	21,410	+	1	1_A375_shN7_rhrus_hicRNA:1:2492	-27	upstream	1	0	13	12	1	1_A375_shN7_rhrus_hic RNA:1	13	Gene ZNF286A	MGC149827, MGC150551, ZNF286A, KIAA1674, ZNF286	zinc finger protein 286A	NM_032652, NM_001130542	1557684_at, 220250_at, 227077_at, 228566_s_at	NP_115913.1, NP_001123014.1
Gene:ID:25150	ZSWIM7	17	15,879,874	15,903,006	23,132	-	1	1_A375_shN7_glus_hicRNA:1:3534	30	up gene	0	1	21	22	1	2_A375_shN7_glus_hicRNA:1	22	Gene ZSWIM7	SWS1, ZSWIM7	zinc finger, SWIM-type containing 7	NM_001042698, NM_001042697	225719_at, 225113_s_at	NP_001035163.1, NP_001035162.1
Gene:ID:4922	TTC19	17	15,902,762	15,932,598	29,314	+	1	1_A375_shN7_glus_hicRNA:1:3534	184	up gene	0	1	21	22	1	2_A375_shN7_glus_hicRNA:1	22	Gene TTC19	MGC19520, 2010236O13Rik, PLOC042, MGC132512, TTC19	tetratricopeptide repeat domain 19	NM_017775, NCT20245.3, NCT22654653	219964_at	NP_060245.2, EAW80490.1, EAW80491
Gene:ID:314	UBB	17	16,284,567	16,286,654	1,687	+	1	1_A375_shN7_glus_hicRNA:1:3515	273	up gene	0	1	12	16	1	2_A375_shN7_glus_hicRNA:1	16	Gene UBB	RPS27A, UBC, UBB, MGC8385, FLJ39987, UBA52	ubiquitin B	NM_018955, NCT22614640.0, NCT22614470.0, NCT22614480.0, NCT22614490.0, NCT22614500.0, NCT22614510.0	200633_at	NP_061326.1, EAW80503.1, EAW80911.1, EAW80494.1, EAW80495.1, EAW80496.1, EAW80502.1
Gene:ID:1382	TRPV2	17	16,318,696	16,340,217	21,481	+	1	1_A375_shN7_glus_hicRNA:1:3519	23564	downstream	0	1	14	19	1	2_A375_shN7_glus_hicRNA:1	19	Gene TRPV2	TRPV2, VRL1, VRL-1, MGC12586, VRL	transient receptor potential cation channel, subfamily V, member 2	NM_016113, NCT18128317.1, NCT18568710.1, NCT23356507.0	218282_s_at, 222653_s_at	NP_057197.2, EAW80505.1, EAW80507.1, EAW80509.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:125144	NCRNA00188	17	16,342,301	16,373,962	31,661	+	1	2_A375_pNL97_plus_lncRNA::1::3516	-61	upstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene NCRNA00188	NCRNA00188, MGC40157, TSAP19, FLJ25777, C17orf45	non-protein coding RNA 188	NR_027158, NR_027159, NR_027160, NR_027161, NR_027162, NR_027163, NR_027164, NR_027165, NR_027166, NR_027167, NR_027168, NR_027169, NR_027170, NR_027171, NR_027172, NR_027173, NR_027174, NR_027175, NR_027176, NR_027177, NR_027178, NR_027179, NR_027667, hC	225065_x_at	EAX04511.1, EAX04510.1, EAX04512.1, EAX04513.1, EAX04514.1, EAX04515.1
GeneID:692087	SNORD49B	17	16,342,823	16,342,870	47	+	1	2_A375_pNL97_plus_lncRNA::1::3516	-583	upstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SNORD49B	U49B, SNORD49B	small nucleolar RNA, C/D box 49B	NR_003043		
GeneID:26800	SNORD49A	17	16,343,350	16,343,420	70	+	1	2_A375_pNL97_plus_lncRNA::1::3516	-1110	upstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SNORD49A	U49A, RNU49, SNORD49A, U49	small nucleolar RNA, C/D box 49A	NR_002744		
GeneID:692106	SNORD65	17	16,344,540	16,344,612	72	+	1	2_A375_pNL97_plus_lncRNA::1::3516	-2300	upstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SNORD65	HBII-135, SNORD65	small nucleolar RNA, C/D box 65	NR_003054		
GeneID:388341	C17orf76	17	16,345,328	16,395,480	50,152	-	1	2_A375_pNL97_plus_lncRNA::1::3516	53240	downstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C17orf76	C17orf76, FLJ35696	chromosome 17 open reading frame 76	NM_207387, NM_001113567, hCT20099.2, hCT2356886.0	229889_at	NP_997270.2, NP_001107039.1, EAX04516.1, EAX04517.1
GeneID:57336	ZNF287	17	16,453,631	16,472,520	18,889	-	1	2_A375_pNL97_plus_lncRNA::1::3517	232	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene ZNF287	MGC126536, MGC141923, ZKSCAN13, ZNF287	zinc finger protein 287	NM_020653, hCT1770372.1	216453_at, 216710_x_at, 220055_at	NP_065704.2, EAX04518.1
GeneID:57547	ZNF624	17	16,524,048	16,557,167	33,119	-	1	2_A375_pNL97_plus_lncRNA::1::3518	79	in gene	0	1	19	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF624	MGC119605, MGC119603, KIAA1349, MGC119602, ZNF624	zinc finger protein 624	NM_020787, hCT2282069.0	232272_at	NP_065838.2, EAX04519.1
GeneID:23164	MPRIP	17	16,946,107	17,088,874	142,767	+	1	2_A375_pNL97_plus_lncRNA::1::3519	533	in gene	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene MPRIP	p116Rip, MRIP, KIAA0864, RIP3, RHOIP3, M-RIP, MPRIP	myosin phosphatase Rho interacting protein	NM_201274, NM_015134, hCT2257592.0, hCT2257593.0, hCT2257594.0, hCT2257595.0	212197_x_at, 214771_x_at, 233278_at, 233414_at, 238328_at, 238329_at, 238330_s_at	NP_958431.2, NP_055949.2, EAW55721.1, EAW55722.1, EAW55723.1, EAW55724.1
GeneID:201164	PLD6	17	17,104,309	17,109,646	5,337	-	1	2_A375_pNL97_plus_lncRNA::1::3520	-178	upstream	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene PLD6	PLD6		NM_178836, hCT2347534.0	227037_at, 244430_at	NP_849158.2, EAW55718.1
GeneID:201163	FLCN	17	17,115,526	17,140,502	24,976	-	3	1_A375_pNL7_minus_lncRNA::1::2450, 2_A375_pNL97_plus_lncRNA::1::3520, 2_A375_pNL97_plus_lncRNA::1::3521	-74, 30678, -106	upstream, downstream, upstream	1	1	47.5	55	2	2_A375_pNL97_plus_lncRNA::1	66	Gene FLCN	FLJ45004, FLCL, MGC17998, FLCN, DKFZp547A118, MGC23445, BHD, FLJ99377	folliculin	NM_144997, NM_144606, hCT1814090.4, hCT1958009.2	1552664_at, 215645_at, 235250_at, 243062_at	NP_659434.2, NP_653207.1, EAW55715.1, EAW55716.1
GeneID:8533	COPS3	17	17,150,139	17,184,591	34,452	-	2	1_A375_pNL7_minus_lncRNA::1::2450, 2_A375_pNL97_plus_lncRNA::1::3521	44015, 43983	downstream, downstream	1	1	78	86	1	2_A375_pNL97_plus_lncRNA::1	86	Gene COPS3	CSN3, COPS3, SGN3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	NM_003653, hCT1958019.1, hCT1958020.2, hCT22618.2	202078_at	NP_003644.2, EAW55713.1, EAW55711.1, EAW55712.1
GeneID:55090	MED9	17	17,380,300	17,396,534	16,234	+	2	1_A375_pNL7_minus_lncRNA::1::2451, 2_A375_pNL97_plus_lncRNA::1::3522	116, 116	in gene, in gene	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MED9	MGC138234, MED9, MED25, FLJ10193	mediator complex subunit 9	NM_018019, hCT1641265.2, hCT1966053.1	218372_at	NP_060489.1, EAW55706.1, EAW55707.1
GeneID:10400	PEMT	17	17,408,877	17,494,994	86,117	-	2	1_A375_pNL7_minus_lncRNA::1::2452, 2_A375_pNL97_plus_lncRNA::1::3523	-30, -110	upstream, upstream	1	1	37	36	1	1_A375_pNL7_minus_lncRNA::1	37	Gene PEMT	PEMT, MGC2483, PEMT2, PNMT, PEAMT, PEMPT	phosphatidylethanolamine N-methyltransferase	NM_148172, NM_148173, NM_007169, hCT1958021.1, hCT22620.2, hCT2352949.0	207621_s_at	NP_680477.1, NP_680478.1, NP_009100.2, EAW55700.1, EAW55701.1, EAW55702.1
GeneID:10743	RAI1	17	17,584,787	17,714,767	129,980	+	1	2_A375_pNL97_plus_lncRNA::1::3524	12077	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene RAI1	KIAA1820, RAI1, SMS, MGC12824, DKFZp434A139, SMCR	retinoic acid induced 1	NM_030665, hCT1958026.2, hCT2261247.0, hCT2261252.0, hCT2261255.0, hCT22623.4	1552558_a_at, 219830_at, 226143_at	NP_109590.3, EAW55692.1, EAW55693.1, EAW55694.1, EAW55695.1, EAW55696.1
GeneID:6720	SREBF1	17	17,714,663	17,740,325	25,662	-	1	1_A375_pNL7_minus_lncRNA::1::2453	261	in gene	1	0	15	16	1	1_A375_pNL7_minus_lncRNA::1	15	Gene SREBF1	bHLHd1, SREBF1, SREBP1, SREBP-1c	sterol regulatory element binding transcription factor 1	NM_001005291, NM_004176, hCT1815966.1, hCT1958024.1, hCT22621.3, hCT2352950.0	1558875_at, 202308_at	NP_001005291.1, NP_004167.3, EAW55688.1, EAW55689.1, EAW55690.1, EAW55691.1
GeneID:146691	TOM1L2	17	17,746,822	17,875,784	128,962	-	3	1_A375_pNL7_minus_lncRNA::1::2453, 1_A375_pNL7_minus_lncRNA::1::2454, 2_A375_pNL97_plus_lncRNA::1::3525	135720, -280, -232	downstream, upstream, upstream	1	1	21.5	19.5	2	1_A375_pNL7_minus_lncRNA::1	28	Gene TOM1L2	TOM1L2, FLJ21501, FLJ32746	target of myb1-like 2 (chicken)	NM_001082968, NM_001033551, hCT1815678.3, hCT22625.4, hCT2352956.0, hCT2352957.0	214840_at, 226198_at, 237109_at	NP_001076437.1, NP_001028723.1, EAW55684.1, EAW55685.1, EAW55686.1, EAW55687.1
GeneID:83450	LRRC48	17	17,876,127	17,920,203	44,076	+	4	1_A375_pNL7_minus_lncRNA::1::2454, 1_A375_pNL7_minus_lncRNA::1::2455, 2_A375_pNL97_plus_lncRNA::1::3525, 2_A375_pNL97_plus_lncRNA::1::3526	-63, 53665, -111, 53601	upstream, downstream, upstream, downstream	1	1	26.5	25.5	2	1_A375_pNL7_minus_lncRNA::1	28	Gene LRRC48	DKFZp586M1120, LRRC48	leucine rich repeat containing 48	NM_001130090, NM_031294, NM_001130091, NM_001130092, hCT1815675.4, hCT1958012.2, hCT2350529.0	1554584_at, 208140_s_at	NP_001123562.1, NP_112584.3, NP_001123563.1, NP_001123564.1, EAW55681.1, EAW55683.1, EAW55682.1
GeneID:91647	ATPAF2	17	17,921,334	17,942,480	21,146	-	5	1_A375_pNL7_minus_lncRNA::1::2455, 1_A375_pNL7_minus_lncRNA::1::2456, 1_A375_pNL7_minus_lncRNA::1::2457, 2_A375_pNL97_plus_lncRNA::1::3526, 2_A375_pNL97_plus_lncRNA::1::3527	12688, 5552, -96, 12752, -32	in gene, in gene, upstream, in gene, upstream	1	1	23	21.67	3	2_A375_pNL97_plus_lncRNA::1	28	Gene ATPAF2	ATP12p, LP3663, ATPAF2, MGC29736, ATP12	ATP synthase mitochondrial F1 complex assembly factor 2	NM_145691, hCT1958034.1, hCT1958035.1, hCT2352952.0, hCT2352953.0, hCT32666.3	213057_at, 214330_at	NP_663729.1, EAW55677.1, EAW55676.1, EAW55678.1, EAW55679.1, EAW55680.1
GeneID:79018	C17orf39	17	17,942,611	17,971,718	29,107	+	3	1_A375_pNL7_minus_lncRNA::1::2456, 1_A375_pNL7_minus_lncRNA::1::2457, 2_A375_pNL97_plus_lncRNA::1::3527	-5683, -35, -99	upstream, upstream, upstream	1	1	22	18.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene C17orf39	MGC3048, C17orf39	chromosome 17 open reading frame 39	NM_024052, hCT1970929.1, hCT2261292.0	220058_at, 226452_at, 241465_at	NP_076957.3, EAW55674.1, EAW55673.1
GeneID:1819	DRG2	17	17,991,283	18,011,292	20,009	+	2	1_A375_pNL7_minus_lncRNA::1::2458, 2_A375_pNL97_plus_lncRNA::1::3528	-99, -51	upstream, upstream	1	1	18	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene DRG2	DRG2		NM_001388, hCT2261301.0, hCT2352954.0, hCT2352955.0	203267_s_at, 203268_s_at	NP_001379.1, EAW55669.1, EAW55670.1, EAW55671.1
GeneID:51168	MYO15A	17	18,012,020	18,083,116	71,096	+	2	1_A375_pNL7_minus_lncRNA::1::2459, 2_A375_pNL97_plus_lncRNA::1::3529	74988, 74124	downstream, downstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene MYO15A	DKFZp686N18198, MYO15, FLJ17274, FLJ31311, DFNB3, MYO15A	myosin XVA	NM_016239, hCT1815667.1, hCT2261305.0, hCT2261309.0, hCT2261311.0, hCT2352958.0	220288_at	NP_057323.3, EAW55663.1, EAW55664.1, EAW55665.1, EAW55666.1, EAW55667.1
GeneID:54890	ALKBH5	17	18,086,867	18,113,268	26,401	+	2	1_A375_pNL7_minus_lncRNA::1::2459, 2_A375_pNL97_plus_lncRNA::1::3529	141, -723	in gene, upstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ALKBH5	OFOXD1, FLJ20308, ABH5, OFOXD, ALKBH5	alkB, alkylation repair homolog 5 (E. coli)	NM_017758, hCT2261316.0, hCT29506.3	1553101_a_at, 228034_x_at, 234302_s_at	NP_060228.3, EAW55661.1, EAW55662.1
GeneID:2314	FLII	17	18,148,150	18,162,055	13,905	-	4	1_A375_pNL7_minus_lncRNA::1::2460, 1_A375_pNL7_minus_lncRNA::1::2461, 2_A375_pNL97_plus_lncRNA::1::3530, 2_A375_pNL97_plus_lncRNA::1::3531	487, -1753, 199, -1721	in gene, upstream, in gene, upstream	1	1	27.5	28.5	2	2_A375_pNL97_plus_lncRNA::1	36	Gene FLII	FLIL, FLII, MGC39265, FLI, Fli1	flightless I homolog (Drosophila)	NM_002018, hCT1958032.1, hCT2259971.0, hCT2352948.0, hCT32660.2	212024_x_at, 212025_s_at, 222065_s_at	NP_002009.1, EAW55655.1, EAW55653.1, EAW55654.1, EAW55656.1
GeneID:125170	SMCR7	17	18,163,848	18,169,095	5,247	+	4	1_A375_pNL7_minus_lncRNA::1::2460, 1_A375_pNL7_minus_lncRNA::1::2461, 2_A375_pNL97_plus_lncRNA::1::3530, 2_A375_pNL97_plus_lncRNA::1::3531	-2280, -40, -1992, -72	upstream, upstream, upstream, upstream	1	1	27.5	28.5	2	2_A375_pNL97_plus_lncRNA::1	36	Gene SMCR7	SMCR7, MGC23130	Smith-Magenis syndrome chromosome region, candidate 7	NM_148886, NM_001144900, NM_139162, hCT1958036.1, hCT2352947.0	235896_s_at	NP_683684.2, NP_001138372.1, NP_631901.2, EAW55651.1, EAW55652.1
GeneID:7156	TOP3A	17	18,177,235	18,218,321	41,086	-	1	2_A375_pNL97_plus_lncRNA::1::3532	81	in gene	0	1	12	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene TOP3A	TOP3, TOP3A	topoisomerase (DNA) III alpha	NM_004618, hCT1958033.1, hCT2259966.0, hCT2259967.0, hCT32665.2	204946_s_at, 214299_at, 214300_s_at	NP_004609.1, EAW55646.1, EAW55647.1, EAW55648.1, EAW55649.1
GeneID:140775	SMCR8	17	18,218,594	18,231,370	12,776	+	1	2_A375_pNL97_plus_lncRNA::1::3532	-354	upstream	0	1	12	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SMCR8	SMCR8, FLJ60657, FLJ34716	Smith-Magenis syndrome chromosome region, candidate 8	NM_144775, hCT2261349.1, hCT2352959.0	1552484_at, 1557986_s_at, 227304_at, 227305_s_at, 238434_at	NP_658988.2, EAW55644.1, EAW55645.1
GeneID:22905	EPN2	17	19,140,690	19,240,028	99,338	+	2	1_A375_pNL7_minus_lncRNA::1::2462, 2_A375_pNL97_plus_lncRNA::1::3533	80158, 80174	in gene, in gene	1	1	49	61	1	2_A375_pNL97_plus_lncRNA::1	61	Gene EPN2	EHB21, EPN2, KIAA1065	epsin 2	NM_014964, NM_148921, NM_001102664, hCT1955473.1, hCT2253722.0, hCT2253724.0	203463_s_at, 203464_s_at	NP_055779.2, NP_683723.2, NP_001096134.1, EAW50875.1, EAW50876.1, EAW50877.1
GeneID:224	ALDH3A2	17	19,552,064	19,580,908	28,844	+	1	2_A375_pNL97_plus_lncRNA::1::3534	256	in gene	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene ALDH3A2	ALDH3A2, FLJ20851, DKFZp686E23276, FALDH, SLS, ALDH10	aldehyde dehydrogenase 3 family, member A2	NM_000382, NM_001031806, hCT1971159.1, hCT21854.3, hCT2352425.0	202053_s_at, 202054_s_at, 210544_s_at	NP_000373.1, NP_001026976.1, EAW50898.1, EAW50899.1, EAW50900.1
GeneID:218	ALDH3A1	17	19,641,297	19,651,746	10,449	-	1	2_A375_pNL97_plus_lncRNA::1::3535	-4606	upstream	0	1	24	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ALDH3A1	ALDH3, MGC10406, ALDH3A1, ALDHIII	aldehyde dehydrogenase 3 family, member A1	NM_000691, NM_001135167, NM_001135168, hCT21856.3, hCT2352417.0	205623_at	NP_000682.3, NP_001128639.1, NP_001128640.1, EAW50908.1, EAW50909.1
GeneID:100507263	LOC100507263	17	20,795,662	20,833,354	37,692	+	1	2_A375_pNL97_plus_lncRNA::1::3537	30146	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100507263		hypothetical LOC100507263	XR_111675, XR_111674, XR_111676, XR_109375, XR_109374, XR_109376, XR_115069, XR_115068, XR_115070		
GeneID:23326	USP22	17	20,902,906	20,946,352	43,446	-	1	1_A375_pNL7_minus_lncRNA::1::2464	-528	upstream	1	0	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene USP22	USP3L, USP22, KIAA1063	ubiquitin specific peptidase 22	NM_015276	200083_at, 216957_at, 220862_s_at	NP_056091.1
GeneID:25979	DHRS7B	17	21,030,258	21,094,836	64,578	+	1	1_A375_pNL7_minus_lncRNA::1::2465	-18	upstream	1	0	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene DHRS7B	CGI-93, DKFZp566O084, SDR32C1, DHRS7B, MGC8916	dehydrogenase/reductase (SDR family) member 7B	NM_015510, hCT1965660.1, hCT19809.3	220690_s_at	NP_056325.2, EAX02597.1, EAX02596.1
GeneID:8834	TMEM11	17	21,101,263	21,117,908	16,645	-	2	1_A375_pNL7_minus_lncRNA::1::2466, 2_A375_pNL97_plus_lncRNA::1::3539	308, 308	in gene, in gene	1	1	31	29	1	1_A375_pNL7_minus_lncRNA::1	31	Gene TMEM11	TMEM11, C17orf35, PMI, PM1	transmembrane protein 11	NM_003876, NR_024547, hCT19372.3, hCT1955658.1	203437_at	NP_003867.1, EAX02598.1, EAX02599.1
GeneID:5606	MAP2K3	17	21,187,968	21,218,552	30,584	+	3	1_A375_pNL7_minus_lncRNA::1::2467, 1_A375_pNL7_minus_lncRNA::1::2468, 2_A375_pNL97_plus_lncRNA::1::3540	3504, 38400, 3280	in gene, downstream, in gene	1	1	24.5	19.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene MAP2K3	MKK3, PRKMK3, MAPKK3, MAP2K3, MEK3	mitogen-activated protein kinase kinase 3	NM_145109, NM_002756, hCT2252684.1	207667_s_at, 215498_s_at, 215499_at	NP_659731.1, NP_002747.2, EAW50386.1
GeneID:339263	C17orf51	17	21,431,571	21,454,941	23,370	-	1	2_A375_pNL97_plus_lncRNA::1::3541	381	in gene	0	1	7	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C17orf51	FLJ41148, FLJ12977, FLJ31874, FLJ38937, C17orf51, FLJ33618	chromosome 17 open reading frame 51	NM_001113434	228146_at, 238166_s_at, 238167_at	NP_001106905.1
GeneID:26118	WSB1	17	25,621,106	25,640,645	19,539	+	2	1_A375_pNL7_minus_lncRNA::1::2469, 2_A375_pNL97_plus_lncRNA::1::3542	462, 46	in gene, in gene	1	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene WSB1	WSB-1, SWIP1, WSB1	WD repeat and SOCS box containing 1	NM_134265, NM_015626, hCT19362.3, hCT1961867.1, hCT1961868.1, hCT2264868.0, hCT2264871.0, hCT2264873.0	201294_s_at, 201296_s_at, 210561_s_at, 213406_at	NP_599027.1, NP_056441.6, EAW51026.1, EAW51028.1, EAW51030.1, EAW51031.1, EAW51027.1, EAW51029.1
GeneID:8844	KSR1	17	25,799,036	25,950,718	151,682	+	2	1_A375_pNL7_minus_lncRNA::1::2470, 2_A375_pNL97_plus_lncRNA::1::3544	-199, -60	upstream, upstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene KSR1	KSR, RSU2, KSR1	kinase suppressor of ras 1	NM_014238, hCT1951466.1, hCT2264878.0	213767_at, 213769_at, 213770_at, 235252_at	NP_055053.1, EAW51035.1, EAW51034.1
GeneID:4843	NOS2	17	26,083,792	26,127,555	43,763	-	4	1_A375_pNL7_minus_lncRNA::1::2471, 1_A375_pNL7_minus_lncRNA::1::2472, 2_A375_pNL97_plus_lncRNA::1::3545, 2_A375_pNL97_plus_lncRNA::1::3546	37443, 23091, 37475, 23043	in gene, in gene, in gene, in gene	1	1	19	30.5	2	2_A375_pNL97_plus_lncRNA::1	40	Gene NOS2	NOS, INOS, HEP-NOS, NOS2, NOS2A	nitric oxide synthase 2, inducible	NM_000625, hCT19434.3, hCT2265131.0, hCT2265133.0	1560703_at, 210037_s_at	NP_000616.3, EAW51048.1, EAW51049.1, EAW51050.1
GeneID:51701	NLK	17	26,369,688	26,523,407	153,719	+	2	1_A375_pNL7_minus_lncRNA::1::2474, 2_A375_pNL97_plus_lncRNA::1::3549	-1112, -1080	upstream, upstream	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene NLK	DKFZp761G1211, FLJ21033, NLK	nemo-like kinase	NM_016231, hCT2264896.0, hCT2264898.0, hCT22985.2, hCT2352446.0	218318_s_at, 222589_at, 222590_s_at	NP_057315.3, EAW51063.1, EAW51060.1, EAW51061.1, EAW51062.1
GeneID:27346	TMEM97	17	26,646,121	26,655,711	9,590	+	4	1_A375_pNL7_minus_lncRNA::1::2475, 1_A375_pNL7_minus_lncRNA::1::2476, 2_A375_pNL97_plus_lncRNA::1::3550, 2_A375_pNL97_plus_lncRNA::1::3551	55, 16423, 119, 16279	in gene, downstream, in gene, downstream	1	1	18	22	2	2_A375_pNL97_plus_lncRNA::1	22	Gene TMEM97	TMEM97, MAC30	transmembrane protein 97	NM_014573, hCT1968027.0, hCT2265071.1, hCT22992.1	212279_at, 212281_s_at, 212282_at, 214283_at	NP_055388.2, EAW51068.1, EAW51067.1, EAW51069.1
GeneID:90410	IFT20	17	26,655,353	26,662,495	7,142	-	4	1_A375_pNL7_minus_lncRNA::1::2475, 1_A375_pNL7_minus_lncRNA::1::2476, 2_A375_pNL97_plus_lncRNA::1::3550, 2_A375_pNL97_plus_lncRNA::1::3551	16319, -49, 16255, 95	downstream, upstream, downstream, in gene	1	1	18	22	2	2_A375_pNL97_plus_lncRNA::1	22	Gene IFT20	IFT20		NM_174887, hCT1968032.1, hCT1968033.1, hCT1968034.1, hCT2281339.0, hCT23004.3, hCT2349966.0, hCT2349967.0	210312_s_at	NP_777547.1, EAW51074.1, EAW51070.1, EAW51071.1, EAW51075.1, EAW51076.1, EAW51072.1, EAW51073.1
GeneID:7126	TNFAIP1	17	26,662,548	26,674,035	11,487	+	2	1_A375_pNL7_minus_lncRNA::1::2476, 2_A375_pNL97_plus_lncRNA::1::3551	-4, -148	upstream, upstream	1	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene TNFAIP1	EDP1, hBACURD2, B61, TNFAIP1, MGC2317, B12	tumor necrosis factor, alpha-induced protein 1 (endothelial)	NM_021137, hCT22999.3	201207_at, 201208_s_at	NP_066960.1, EAW51077.1
GeneID:26073	POLDIP2	17	26,673,659	26,684,603	10,944	-	2	1_A375_pNL7_minus_lncRNA::1::2477, 2_A375_pNL97_plus_lncRNA::1::3552	59, 59	in gene, in gene	1	1	50	54	1	2_A375_pNL97_plus_lncRNA::1	54	Gene POLDIP2	POLDIP2, DKFZp586F1524, POLD4, PDIP38	polymerase (DNA-directed), delta interacting protein 2	NM_015584, hCT22984.4	217806_s_at, 222425_s_at	NP_056399.1, EAW51078.1
GeneID:147007	TMEM199	17	26,684,687	26,689,089	4,402	+	2	1_A375_pNL7_minus_lncRNA::1::2477, 2_A375_pNL97_plus_lncRNA::1::3552	-143, -143	upstream, upstream	1	1	50	54	1	2_A375_pNL97_plus_lncRNA::1	54	Gene TMEM199	TMEM199, C17orf32, MGC45714	transmembrane protein 199	NM_152464, hCT2265076.1, hCT23000.3	225374_at, 225375_at	NP_689677.1, EAW51080.1, EAW51079.1
GeneID:645832	SEBOX	17	26,691,290	26,692,265	975	-	3	1_A375_pNL7_minus_lncRNA::1::2477, 2_A375_pNL97_plus_lncRNA::1::3552, 2_A375_pNL97_plus_lncRNA::1::3553	7721, 7721, -8599	downstream, downstream, upstream	1	1	31.5	39	2	2_A375_pNL97_plus_lncRNA::1	54	Gene SEBOX	OG9X, SEBOX, OG9, OG-9	SEBOX homeobox	NM_001080837	234256_at	NP_001074306.2
GeneID:7448	VTN	17	26,694,298	26,697,373	3,075	-	3	1_A375_pNL7_minus_lncRNA::1::2477, 2_A375_pNL97_plus_lncRNA::1::3552, 2_A375_pNL97_plus_lncRNA::1::3553	12829, 12829, -3491	downstream, downstream, upstream	1	1	31.5	39	2	2_A375_pNL97_plus_lncRNA::1	54	Gene VTN	V75, VNT, VN, VTN	vitronectin	NM_000638, hCT22991.3	204534_at	NP_000629.3, EAW51082.1
GeneID:23098	SARM1	17	26,698,987	26,728,065	29,078	+	2	1_A375_pNL7_minus_lncRNA::1::2478, 2_A375_pNL97_plus_lncRNA::1::3553	34645, 1877	downstream, in gene	1	1	14	18	2	2_A375_pNL97_plus_lncRNA::1	24	Gene SARM1	SAMD2, KIAA0524, FLJ36296, SARM1, SARM	sterile alpha and TIR motif containing 1	NM_015077, hCT2265078.0, hCT22990.3	213257_at, 213259_s_at	NP_055892.2, EAW51083.1, EAW51084.1
GeneID:113235	SLC46A1	17	26,721,661	26,733,228	11,567	-	1	1_A375_pNL7_minus_lncRNA::1::2478	-404	upstream	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene SLC46A1	MGC9564, FLJ39875, HCP1, PCFT, SLC46A1	solute carrier family 46 (folate transporter), member 1	NM_080669, hCT1968028.1, hCT2281326.0, hCT2281327.0, hCT2281329.0, hCT22993.2	1552278_a_at, 1552279_a_at, 1558703_at, 233531_at	NP_542400.2, EAW51088.1, EAW51085.1, EAW51086.1, EAW51087.1, EAW51089.1
GeneID:10615	SPAG5	17	26,904,583	26,926,056	21,473	-	1	1_A375_pNL7_minus_lncRNA::1::2479	-424	upstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SPAG5	MAP126, hMAP126, DEEPEST, SPAG5	sperm associated antigen 5	NM_006461, hCT22977.3	203145_at	NP_006452.3, EAW51106.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Intervals Count	Internal Intervals	Internal Outside Start	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:103906408	LOC103906408	17	26,923,655	26,944,879	16,671	+	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2479	672	ui gene	1	0	20	14	1	2_A375_shL7_chr:rol_loc:RNA:1	20	Gene LOC103906408		Hypothetical LOC103906408	XR_111652, XR_111661, XR_109448, XR_109448, XR_110073, XR_110072		
Gene:ID:24621	FLJ20306	17	26,934,982	26,941,211	6,230	-	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2479	14731	downstream	1	0	20	14	1	1_A375_shL7_chr:rol_loc:RNA:1	20	Gene FLJ20306	SGSM4, MGC39833, FLJ20306	enchondromatosis with multiple other types of non-epithelial cancers	NM_001174103, ECT2201315.1, ECT2201316.1, ECT22455.4, ECT2455119.1	1863292_s_at	NP_001167574.1, ENSR01106.1, ENSR01108.1, ENSR01110.1, ENSR01111.1
Gene:ID:555	SDF2	17	26,973,607	26,988,833	13,326	+	1	2_A375_shL97_plus_loc:RNA:1 :-1554	-247	upstream	0	1	15	21	1	2_A375_shL97_plus_loc:RNA:1	21	Gene SDF2	SDF2	stromal cell-derived factor 2	NM_006923, ECT2344356.1, ECT2344359.1, ECT2344364.0, ECT2345900.0	202090_at	NP_006934.2, ENSR01122.1, ENSR01121.1, ENSR01123.1, ENSR01124.1
Gene:ID:530	SUPT6H	17	26,959,202	27,029,249	69,947	+	1	2_A375_shL97_plus_loc:RNA:1 :-1554	-22	upstream	0	1	15	21	1	2_A375_shL97_plus_loc:RNA:1	21	Gene SUPT6H	KIAA0162, wits-3, SPT6H, MGC87843, SPT6, SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	NM_003170, ECT1655386.1, ECT2369550.0, ECT2369806.0, ECT22967.3, ECT2455119.1	1854511_a_at, 1854520_s_at, 208630_s_at, 208631_at	NP_003161.2, ENSR01119.1, ENSR01116.1, ENSR01117.1, ENSR01118.1
Gene:ID:47011	PRDCA1	17	27,030,534	27,035,872	5,338	-	2	1_A375_shL7_chr:rol_loc:RNA:1 :-2460, 2_A375_shL97_plus_loc:RNA:1 :-1538	-8200, -5992	upstream, upstream	1	1	17.5	16	2	1_A375_shL7_chr:rol_loc:RNA:1	16	Gene PRDCA1	MGC39650, PRDCA1	proline-rich domain containing with cyclin A1	NM_182463, ECT2346116.1, ECT2369834.0	223607_at, 239289_at	NP_689761.1, ENSR01125.1, ENSR01126.1
Gene:ID:3871	RAB3A	17	27,041,299	27,045,286	3,987	-	5	1_A375_shL7_chr:rol_loc:RNA:1 :-2460, 2_A375_shL97_plus_loc:RNA:1 :-1538, 2_A375_shL97_plus_loc:RNA:1 :-1536, 2_A375_shL97_plus_loc:RNA:1 :-1537, 2_A375_shL97_plus_loc:RNA:1 :-1554	-1766, -622, -6330, -5772, -5442	upstream, ui gene, upstream, upstream, upstream	1	1	14.6	16.4	5	2_A375_shL97_plus_loc:RNA:1	21	Gene RAB3A	RAN, RAB3A, RAB3A	RAB3A, member RAS oncogene family	NR_026575, NR_024578, NM_033438, NM_001142630, NM_001142625, NM_001166942, NM_001166943, ECT2201280.0, ECT2201300.0, ECT2353532.0, ECT2369.2	1555630_s_at, 230710_at	NP_001149942.1, NP_001136099.2, NP_001136097.2, NP_001135414.1, NP_001135415.1, ENSR01127.1, ENSR01128.1, ENSR01129.1, ENSR01130.1
Gene:ID:147	RPL23A	17	27,047,000	27,051,374	4,374	+	5	1_A375_shL7_chr:rol_loc:RNA:1 :-2460, 2_A375_shL97_plus_loc:RNA:1 :-1555, 2_A375_shL97_plus_loc:RNA:1 :-1536, 2_A375_shL97_plus_loc:RNA:1 :-1537, 2_A375_shL97_plus_loc:RNA:1 :-1554	72, -2536, 4616, 6696, 6725	ui gene, upstream, downstream, downstream, downstream	1	1	14.6	16.4	5	2_A375_shL97_plus_loc:RNA:1	21	Gene RPL23A	FLJ27455, MDA20, RPL23A, L23A	ribosomal protein L23a	NM_000984, ECT2269090.1, ECT2269091.1	200012_x_at, 208625_s_at, 208634_s_at, 210054_s_at	NP_000975.2, ENSR01131.1, ENSR01132.1
Gene:ID:6666	SNORD42B	17	27,047,566	27,047,634	69	+	5	1_A375_shL7_chr:rol_loc:RNA:1 :-2460, 2_A375_shL97_plus_loc:RNA:1 :-1538, 2_A375_shL97_plus_loc:RNA:1 :-1536, 2_A375_shL97_plus_loc:RNA:1 :-1537, 2_A375_shL97_plus_loc:RNA:1 :-1554	-486, -3104, 4668, 6666, 6693	upstream, upstream, downstream, downstream, downstream	1	1	14.6	16.4	5	2_A375_shL97_plus_loc:RNA:1	21	Gene SNORD42B	RNU42B, U42B, SNORD42B	small nucleolar RNA, C/D box 42B	NR_003012		
Gene:ID:6773	SNORD42A	17	27,049,600	27,049,671	71	+	5	1_A375_shL7_chr:rol_loc:RNA:1 :-2460, 2_A375_shL97_plus_loc:RNA:1 :-1538, 2_A375_shL97_plus_loc:RNA:1 :-1536, 2_A375_shL97_plus_loc:RNA:1 :-1537, 2_A375_shL97_plus_loc:RNA:1 :-1554	-2526, -5136, 2016, 3496, 4125	upstream, upstream, downstream, downstream, downstream	1	1	14.6	16.4	5	2_A375_shL97_plus_loc:RNA:1	21	Gene SNORD42A	E17A, rig:6105-121, SNORD42A, RNU101A	small nucleolar RNA, C/D box 42A	NR_003010		
Gene:ID:6659	SNORD42A	17	27,050,846	27,050,909	61	+	5	1_A375_shL7_chr:rol_loc:RNA:1 :-2460, 2_A375_shL97_plus_loc:RNA:1 :-1538, 2_A375_shL97_plus_loc:RNA:1 :-1536, 2_A375_shL97_plus_loc:RNA:1 :-1537, 2_A375_shL97_plus_loc:RNA:1 :-1554	-3276, -1654, 1166, 2606, 3255	upstream, upstream, downstream, downstream, downstream	1	1	14.6	16.4	5	2_A375_shL97_plus_loc:RNA:1	21	Gene SNORD42A	RNU42A, SNORD42A, U42, U42A	small nucleolar RNA, C/D box 42A	NR_003014		
Gene:ID:6772	SNORD48	17	27,080,699	27,080,772	73	+	5	1_A375_shL7_chr:rol_loc:RNA:1 :-2460, 2_A375_shL97_plus_loc:RNA:1 :-1538, 2_A375_shL97_plus_loc:RNA:1 :-1536, 2_A375_shL97_plus_loc:RNA:1 :-1537, 2_A375_shL97_plus_loc:RNA:1 :-1554	-3627, -6233, 917, 2387, 3029	upstream, upstream, downstream, downstream, downstream	1	1	14.6	16.4	5	2_A375_shL97_plus_loc:RNA:1	21	Gene SNORD48	RNU101B, E17B, SNORD48	small nucleolar RNA, C/D box 48	NR_003009		
Gene:ID:16236	TLCD1	17	27,081,398	27,083,949	2,553	-	5	1_A375_shL7_chr:rol_loc:RNA:1 :-2460, 2_A375_shL97_plus_loc:RNA:1 :-1538, 2_A375_shL97_plus_loc:RNA:1 :-1536, 2_A375_shL97_plus_loc:RNA:1 :-1537, 2_A375_shL97_plus_loc:RNA:1 :-1554	6877, 6455, 2333, 692, 221	downstream, downstream, downstream, ui gene, ui gene	1	1	14.6	16.4	5	2_A375_shL97_plus_loc:RNA:1	21	Gene TLCD1	TLCD1	TLC domain containing 1	NM__135463, NM_001190407, ECT1660228.1, ECT22894.2	229564_at	NP_619721.1, NP_001183979.1, ENSR01132.1, ENSR01134.1
Gene:ID:54806	NEK6	17	27,053,632	27,069,764	13,982	+	4	1_A375_shL7_chr:rol_loc:RNA:1 :-2460, 2_A375_shL97_plus_loc:RNA:1 :-1538, 2_A375_shL97_plus_loc:RNA:1 :-1536, 2_A375_shL97_plus_loc:RNA:1 :-1537, 2_A375_shL97_plus_loc:RNA:1 :-1554	47561, -4215, 2776, 2104	upstream, upstream, upstream, upstream	1	1	14.25	17.25	4	2_A375_shL97_plus_loc:RNA:1	21	Gene NEK6	JCL, NEK6, MGC135445, NEK12A, NPHP8	NIMA (never in mitosis gene a)-related kinase 6	NM__170170, ECT2269092.1, ECT2324550.0, ECT2552451.0	1857172_at, 1857172_s_at	NP_619643.1, ENSR01135.1, ENSR01136.1, ENSR01137.1
Gene:ID:6264	ERAL1	17	27,161,043	27,168,972	8,029	+	2	1_A375_shL7_chr:rol_loc:RNA:1 :-2461, 2_A375_shL97_plus_loc:RNA:1 :-1539	693, 8	ui gene, ui gene	1	1	16	27	1	2_A375_shL97_plus_loc:RNA:1	27	Gene ERAL1	HERA-A, ERA, ERAL1, HERA-B, HERA, ERALTA	Era G-protein-like 1 (E. coli)	NM_003782, ECT1810258.2, ECT2265102.0, ECT2552102.0, ECT2322466.0	212087_s_at	NP_003963.1, ENSR01146.1, ENSR01147.1, ENSR01148.1, ENSR01149.1
Gene:ID:74411	MRM51	17	27,166,267	27,166,656	71	-	2	1_A375_shL7_chr:rol_loc:RNA:1 :-2461, 2_A375_shL97_plus_loc:RNA:1 :-1539	6330, 6460	downstream, downstream	1	1	16	27	1	2_A375_shL97_plus_loc:RNA:1	27	Gene MRM51	true-mv-451, MIRN451, MIR451	mycoRNA 451	NR_029970		
Gene:ID:99026	MIR148	17	27,166,551	27,166,636	85	-	2	1_A375_shL7_chr:rol_loc:RNA:1 :-2461, 2_A375_shL97_plus_loc:RNA:1 :-1539	6505, 6555	downstream, downstream	1	1	16	27	1	2_A375_shL97_plus_loc:RNA:1	27	Gene MIR148	MIR148, MIRN148	mycoRNA 148	NR_029655		
Gene:ID:7849	PHF12	17	27,232,271	27,278,906	46,227	-	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2462	-648	upstream	1	0	16	20	1	1_A375_shL7_chr:rol_loc:RNA:1	16	Gene PHF12	PHF12, PF1, FLJ38122, KIAA1323, MGC131918	PHD finger protein 12	NM_030939, NM_001033861, ECT1619262.0, ECT2261278.0, ECT2324469.0, ECT2552469.0	231613_at, 234639_s_at	NP_569481.1, NP_001027733.1, ENSR01162.1, ENSR01163.1, ENSR01165.1, ENSR01167.1
Gene:ID:24925	SEZ6	17	27,261,923	27,333,681	51,158	-	6	1_A375_shL7_chr:rol_loc:RNA:1 :-2462, 2_A375_shL97_plus_loc:RNA:1 :-1538, 2_A375_shL97_plus_loc:RNA:1 :-1536, 2_A375_shL97_plus_loc:RNA:1 :-1537, 2_A375_shL97_plus_loc:RNA:1 :-1554	53623, -71, -1991, 1099, -71, 1827	downstream, downstream, downstream, ui gene, upstream, upstream	1	1	26.5	22.3	4	1_A375_shL7_chr:rol_loc:RNA:1	32	Gene SEZ6	SEZ6		NM_178860, NM_001098635, ECT2324613.2, ECT2261272.0, ECT2552740, ECT2261275.0, ECT2324441.0	226651_at, 240430_at	NP_849191.2, NP_001092105.1, ENSR01171.1, ENSR01172.1, ENSR01173.1, ENSR01174.1, ENSR01170.1
Gene:ID:99657	MYO19A	17	27,400,326	27,507,497	109,279	-	3	1_A375_shL7_chr:rol_loc:RNA:1 :-2463, 2_A375_shL97_plus_loc:RNA:1 :-1540, 2_A375_shL97_plus_loc:RNA:1 :-1552	47247, 28719, 25327	ui gene, ui gene, ui gene	1	1	17	19	3	2_A375_shL97_plus_loc:RNA:1	23	Gene MYO19A	KIAA0216, MYO19A, MYSPDZ, DKFZp686J0243, SPR210	Myosin XVIIIA	NM_078471, NM_203316	202039_at	NP_510880.2, NP_976063.1
Gene:ID:262	CRYBA1	17	27,572,873	27,581,512	7,637	+	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2464	4555	upstream	0	1	11	20	1	2_A375_shL97_plus_loc:RNA:1	20	Gene CRYBA1	CRYB1, CRYBA1	crystallin, beta A1	NM_005208, ECT2302413.2	206662_at	NP_005191.2, ENSR0188.1
Gene:ID:7322	NUFIP2	17	27,582,854	27,621,166	38,312	+	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2467	-146	upstream	0	1	16	26	1	2_A375_shL97_plus_loc:RNA:1	26	Gene NUFIP2	FKD, MGC11292, 182-FIP, FIP-62, E2-induced gene 1, nuclear fragile X mental retardation protein interacting protein 2	nuclear fragile X mental retardation protein interacting protein 2	NM_030772, ECT2302417.2, ECT2365120.0	224556_at, 224558_at	NP_085223.1, ENSR01166.1, ENSR01167.1
Gene:ID:19228	ABHD15	17	27,657,879	27,694,842	36,963	-	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2468	-314	upstream	0	1	7	17	1	2_A375_shL97_plus_loc:RNA:1	17	Gene ABHD15	ABHD15	ethylbenzene dioxygenase containing 15	NM__198147, ECT1752265.2	226795_at	NP_937760.2, ENSR01191.1
Gene:ID:6310	TP53I13	17	27,695,739	27,900,175	4,436	+	1	2_A375_shL97_plus_loc:RNA:1 :-1556	-2011	upstream	0	1	7	17	1	2_A375_shL97_plus_loc:RNA:1	17	Gene TP53I13	TP53I13, OSCP1	tumor protein p53 inducible protein 13	NM_138349, ECT2771784.1, ECT2771785.1, ECT2771786.1, ECT2312009.0	229603_at, 229606_at	NP_612358.3, ENSR01182.1, ENSR01184.1, ENSR01183.1
Gene:ID:6964	QTT1	17	27,900,467	27,916,810	16,123	-	3	2_A375_shL97_plus_loc:RNA:1 :-1556, 2_A375_shL97_plus_loc:RNA:1 :-1549, 2_A375_shL97_plus_loc:RNA:1 :-1537	22552, 286, -4734	downstream, upstream, upstream	0	1	13.33	19.33	3	2_A375_shL97_plus_loc:RNA:1	23	Gene QTT1	QTT1		NM_014030, NM_001080454, ECT2324433.1, ECT2324433.0	218030_at	NP_054748.2, NP_001078923.1, ENSR01196.1, ENSR01197.1
Gene:ID:24930	ANKRD13B	17	27,920,227	27,941,779	21,252	+	2	2_A375_shL97_plus_loc:RNA:1 :-1559, 2_A375_shL97_plus_loc:RNA:1 :-1539	3631, 817	upstream, ui gene	0	1	16.5	20.5	2	2_A375_shL97_plus_loc:RNA:1	23	Gene ANKRD13B	FLJ25555, FLJ39318, ANKRD13B	Ankyrin repeat domain 13B	NM__152345, ECT2302463.2, ECT2371780.0, ECT2371790.0, ECT2324399.0, ECT2324400.0	227720_at	NP_689554.2, ENSR01203.1, ENSR01199.1, ENSR01200.1, ENSR01201.1, ENSR01202.1
Gene:ID:5464	SSH2	17	27,952,965	28,257,016	304,053	-	2	2_A375_shL97_plus_loc:RNA:1 :-1537, 2_A375_shL97_plus_loc:RNA:1 :-1539	168794, -264	ui gene, upstream	0	1	15	17	2	2_A375_shL97_plus_loc:RNA:1	19	Gene SSH2	SSH2, MGC75555, KIAA1725, SSH-2	slingshot homolog 2 (Drosophila)	NM_033389, ECT2556917.1, ECT2556916.0, ECT2556512.0, ECT2556523.1	1854114_s_at, 1855423_at, 1855429_s_at, 236660_at	NP_203747.2, ENSR01210.1, ENSR01209.1, ENSR01211.1, ENSR01212.1, ENSR01213.1
Gene:ID:74756	EFCAB5	17	28,256,674	28,435,470	178,896	+	1	2_A375_shL97_plus_loc:RNA:1 :-1572	438	ui gene	0	1	14	15	1	2_A375_shL97_plus_loc:RNA:1	15	Gene EFCAB5	FLJ46247, DKFZp686B0535, EFCAB5, DKFZp434G2420	EF-hand calcium binding domain 5	NM_198329, NM_001146053, NR_026748	1555293_at, 1555301_s_at	NP_940212.1, NP_001139525.1
Gene:ID:362	CFD	17	28,703,564	28,705,699	69,715	+	5	1_A375_shL7_chr:rol_loc:RNA:1 :-2469, 2_A375_shL97_plus_loc:RNA:1 :-1567, 2_A375_shL97_plus_loc:RNA:1 :-1572, 2_A375_shL97_plus_loc:RNA:1 :-1570, 2_A375_shL97_plus_loc:RNA:1 :-1573	-160, 66395, 2595, -123, 66536	upstream, downstream, downstream, downstream	1	1	43.33	47	2	2_A375_shL97_plus_loc:RNA:1	102	Gene CFD	CFD, GP150	carbonyperidase D	NM_001928, ECT1810052.2, ECT2370597.0	205168_at, 205641_at, 205642_s_at, 205643_s_at, 226603_s_at	NP_001919.2, ENSR01225.1, ENSR01227.1
Gene:ID:627	GOSR1	17	28,834,426	28,853,832	49,406	+	2	1_A375_shL7_chr:rol_loc:RNA:1 :-2467, 2_A375_shL97_plus_loc:RNA:1 :-1573	-74, -106	upstream, upstream	1	1	102	100	1	1_A375_shL7_chr:rol_loc:RNA:1	102	Gene GOSR1	GOS28/26, GOS-28, GOS28, GOSR1, GS28	golgi SNAP receptor complex member 1	NM_001007024, NM_001007025, GS28, P28, GOLM2	1555192_at, 208520_s_at, 210520_at, 211021_s_at	NP_001007025.1, NP_001007026.1, NP_004862.1, ENSR01229.1, ENSR01230.1, ENSR01231.1
Gene:ID:9683	TBC1D29	17	28,899,564	28,990,811	3,927	+	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2468	-5440	upstream	1	0	15	14	1	1_A375_shL7_chr:rol_loc:RNA:1	15	Gene TBC1D29	TBC1D29, DKFZp434G0047	TBC1 domain family, member 29	NM_015584, ECT1810084, ECT2370588.0	208005_at	NP_056569.1, ENSR01235.1, ENSR01237.1
Gene:ID:1379	CRLF3	17	28,109,702	29,151,776	42,076	-	3	1_A375_shL7_chr:rol_loc:RNA:1 :-2461, 2_A375_shL97_plus_loc:RNA:1 :-1562, 2_A375_shL97_plus_loc:RNA:1 :-1572	178, -7196	ui gene, upstream, upstream	1	1	23	24	2	2_A375_shL97_plus_loc:RNA:1	33	Gene CRLF3	CRIM1KIS, CYTOR4, p85.2, CRLF3, RIVAS, MGC20981	Cytokine receptor-like factor 3	NM_015986, ECT1614796.1	203474_at	NP_057070.3, ENSR0297.1
Gene:ID:9918	ATAD5	17	28,159,020	29,222,285	63,265	+	3	1_A375_shL7_chr:rol_loc:RNA:1 :-2461, 1_A375_shL97_plus_loc:RNA:1 :-2462, 2_A375_shL97_plus_loc:RNA:1 :-1572	-7420, -76, 44	upstream, upstream, upstream	1	1	23	24	2	1_A375_shL97_plus_loc:RNA:1	33	Gene ATAD5	FRAG1, EUS1, C17orf61, FLJ12735, ATAD5	ATPase family, AAA domain containing 5	NM_024857	220223_at	NP_079133.3
Gene:ID:8726	C17orf62	17	28,236,001	29,233,286	7,286	-	2	1_A375_shL7_chr:rol_loc:RNA:1 :-2462, 2_A375_shL97_plus_loc:RNA:1 :-1572	58, -122	ui gene, upstream	1	1	16	19	1	2_A375_shL97_plus_loc:RNA:1	19	Gene C17orf62	MGC24674, TEFM, C17orf62, FLJ22729	chromosome 17 open reading frame 62	NM_024663, ECT1612231.2, ECT1667341.1, ECT1667342.1	219186_at, 235353_at	NP_078959.3, ENSR02291.1, ENSR02292.1, ENSR02293.1
Gene:ID:4440	RAB11FIP4	17	28,716,642	29,065,232	149,590	+	2	1_A375_shL7_chr:rol_loc:RNA:1 :-2469, 1_A375_shL97_plus_loc:RNA:1 :-1568	22415, 89654, 109586	ui gene, ui gene, ui gene	1	1	17	14.67	2	1_A375_shL7_chr:rol_loc:RNA:1	20	Gene RAB11FIP4	RAB11-FIP4, MGC11218, FLJ00131, MGC126999, KIAA1621, RAB11FIP4	RAB11 family interacting protein 4 (class II)	NM_032932, ECT199992.2	224462_s_at, 226709_at, 235796_at	NP_116221.2, ENSR01265.1
Gene:ID:99966	MIR193A	17	28,857,013	28,857,102	87	+	2	1_A375_shL7_chr:rol_loc:RNA:1 :-2467, 2_A375_shL97_plus_loc:RNA:1 :-1556	4863, 6813	upstream, upstream	1	1	22	34	1	2_A375_shL97_plus_loc:RNA:1	34	Gene MIR193A	MIRN193, MIRN193A, MIR193A	mycoRNA 193a	NR_029710		
Gene:ID:100126235	MIR365-2	17	28,902,830	29,902,940	110	+	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2468	6378	downstream	1	0	20	14	1	1_A375_shL7_chr:rol_loc:RNA:1	20	Gene MIR365-2	MIRN365-2, MIR365-2	mycoRNA 365-2	NR_029599		
Gene:ID:8255	RHOT1	17	30,969,873	30,992,746	83,273	+	2	1_A375_shL7_chr:rol_loc:RNA:1 :-2500, 2_A375_shL97_plus_loc:RNA:1 :-1568	-161, -161	upstream, upstream	1	1	20	23	1	2_A375_shL97_plus_loc:RNA:1	23	Gene RHOT1	FLJ11040, FLJ12633, MIRO-1, RHOT1, Miro1	ras homolog gene family, member T1	NM_018307, NM_001032366, NM_001033858, ECT2564111.0, ECT2564112.0, ECT2564113.0, ECT2564115.0, ECT2564116.0, ECT2564117.0, ECT2564118.0, ECT2564119.0, ECT2565205.0	218322_at, 221345_s_at, 224504_at	NP_060773.2, NP_001028738.1, NP_001032535.1, NP_001032858.1, ENSR02780.1, ENSR02781.1, ENSR02782.1, ENSR02783.1, ENSR02784.1, ENSR02785.1, ENSR02786.1, ENSR02787.1, ENSR02788.1, ENSR02789.1, ENSR02790.1, ENSR02791.1
Gene:ID:6284	RHBDL2	17	30,993,193	30,651,680	50,488	+	2	1_A375_shL7_chr:rol_loc:RNA:1 :-2501, 2_A375_shL97_plus_loc:RNA:1 :-1598	6812, 8141	ui gene, ui gene	1	1	22	30	1	1_A375_shL7_chr:rol_loc:RNA:1	32	Gene RHBDL2	RHBDL2, MGC19301, RHBDL2, MGC119300, FLJ45582, VRHO	rhomboid, veinlet-like 2 (Drosophila)	NM__138328, ECT2269420.0, ECT2269421.0, ECT2359994.0	1553260_at, 230753_at, 231232_at, 232509_at	NP_612201.1, ENSR02401.1, ENSR02239.1, ENSR02240.1
Gene:ID:91317	C17orf75	17	30,658,381	30,669,169	10,788	-	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2467	-18	upstream	1	0	12	19	1	1_A375_shL7_chr:rol_loc:RNA:1	19	Gene C17orf75	NJMLHR1, C17orf75	chromosome 17 open reading frame 75	NM_022349, ECT1612564.2	203630_at	NP_071738.2, ENSR02238.1
Gene:ID:4233	MRS32	17	30,677,128	30,677,221	93	+	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2467	-7823	upstream	0	1	12	19	1	2_A375_shL97_plus_loc:RNA:1	19	Gene MRS32	MRS32, true-mv-432, MIR632	mycoRNA 632	NR_030352		
Gene:ID:756	ZNF207	17	30,677,157	30,697,666	20,311	+	1	1_A375_shL7_chr:rol_loc:RNA:1 :-2467	-7852	upstream	0	1	12	19	1	2_A375_shL97_plus_loc:RNA:1	19	Gene ZNF207	ZNF207, DKFZp761N202	zinc finger protein 207	NM_001005937, NM_003457, NM_001032293, ECT1675.2, ECT1697129.1, ECT1697127.1, ECT2564248.0, ECT2564249.0, ECT2564250.0, ECT2564268.0	1555533_s_at, 200625_s_at, 200626_s_at, 226157_at, 231568_s_at, 235772_at, 235773_s_at	NP_001027877.1, NP_003448.1, NP_001027456.1, ENSR02232.1, ENSR02236.1, ENSR02239.1, ENSR02311.1, ENSR02313.1, ENSR02335.1, ENSR02237.1
Gene:ID:217	PSMD11	17	30,771,902	30,808,042	36,340	+	1	1_A375_shL97_plus_loc:RNA:1 :-1598	106	ui gene	0	1	14	16	1	2_A375_shL97_plus_loc:RNA:1	16	Gene PSMD11	PSMD11, p44.5, MGC3544, S9, Rpn6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	NM_002815, ECT1612553.2, ECT2564310.0	200776_at, 200777_s_at	NP_002806.2, ENSR02239.1, ENSR02230.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:40	ACCN1	17	31,340,105	32,483,825	1,143,720	-	7	1_A375_pNL7_minus_lncRNA::1::2502, 1_A375_pNL7_minus_lncRNA::1::2503, 1_A375_pNL7_minus_lncRNA::1::2504, 2_A375_pNL97_plus_lncRNA::1::3589, 2_A375_pNL97_plus_lncRNA::1::3590, 2_A375_pNL97_plus_lncRNA::1::3591, 2_A375_pNL97_plus_lncRNA::1::3592	1013869, 889473, 828497, 1083761, 1013905, 889505, 828465	in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	23	26.5	4	1_A375_pNL7_minus_lncRNA::1	38	Gene ACCN1	BNC1, ASIC2, BNaC1, hBNaC1, ACCN1, ACCN, ASIC2a, MDEG	amiloride-sensitive cation channel 1, neuronal	NM_183377, NM_001094, hCT19260.3	206690_at	NP_899233.1, NP_001085.2, EAW80216.1
GeneID:10693	CCT6B	17	33,254,876	33,288,526	33,650	-	2	1_A375_pNL7_minus_lncRNA::1::2506, 2_A375_pNL97_plus_lncRNA::1::3595	64, 60	in gene, in gene	1	1	19	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene CCT6B	CCTZ-2, TCP-1-zeta-2, TSA303, CCT6B, CCT-zeta-2, Cctz2	chaperonin containing TCP1, subunit 6B (zeta 2)	NM_006584, NM_001193529, NM_001193530, hCT20459.2	206587_at	NP_006575.2, NP_001180458.1, NP_001180459.1, EAW80201.1
GeneID:91603	ZNF830	17	33,288,549	33,290,205	1,656	+	2	1_A375_pNL7_minus_lncRNA::1::2506, 2_A375_pNL97_plus_lncRNA::1::3595	-85, -101	upstream, upstream	1	1	19	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene ZNF830	CCDC16, SEL13, MGC20398, OMCG1, ZNF830	zinc finger protein 830	NM_052857, hCT20469.2	226315_at, 226323_at	NP_443089.3, EAW80200.1
GeneID:117584	RFFL	17	33,336,131	33,416,294	80,163	-	1	1_A375_pNL7_minus_lncRNA::1::2507	25542	in gene	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene RFFL	RNF34L, FRING, RNF189, RIFIFYLIN, CARP2, RFFL	ring finger and FYVE-like domain containing 1	NM_057178, NM_001017368	1552649_a_at, 1552651_a_at, 1562603_at, 1566171_at, 228980_at, 237919_at	NP_476519.1, NP_001017368.1
GeneID:5892	RAD51L3	17	33,426,811	33,446,888	20,077	-	1	1_A375_pNL7_minus_lncRNA::1::2508	200	in gene	1	0	14	13	1	1_A375_pNL7_minus_lncRNA::1	14	Gene RAD51L3	RAD51D, Trad, R51H3, RAD51L3, HsTRAD, TRAD	RAD51-like 3 (S. cerevisiae)	NM_001142571, NM_002878, NM_133629	209965_s_at, 37793_r_at	NP_001136043.1, NP_002869.3, NP_598332.1
GeneID:54752	FNDC8	17	33,448,631	33,457,751	9,120	+	1	1_A375_pNL7_minus_lncRNA::1::2508	-1943	upstream	1	0	14	13	1	1_A375_pNL7_minus_lncRNA::1	14	Gene FNDC8	FNDC8, DKFZp434H2215	fibronectin type III domain containing 8	NM_017559, hCT20458.2	220499_at	NP_060029.1, EAW80168.1
GeneID:54475	NLE1	17	33,458,368	33,469,322	10,954	-	2	1_A375_pNL7_minus_lncRNA::1::2509, 2_A375_pNL97_plus_lncRNA::1::3596	-22, 42	upstream, in gene	1	1	39	35	1	1_A375_pNL7_minus_lncRNA::1	39	Gene NLE1	NLE1, Nle, FLJ10458	notchless homolog 1 (Drosophila)	NM_001014445, NM_018096, hCT20465.3, hCT2266131.0, hCT2266132.0	203866_at, 203867_s_at	NP_001014445.1, NP_060566.2, EAW80165.1, EAW80166.1, EAW80167.1
GeneID:146862	UNC45B	17	33,474,836	33,516,364	41,528	+	2	1_A375_pNL7_minus_lncRNA::1::2509, 2_A375_pNL97_plus_lncRNA::1::3596	-5492, -5556	upstream, upstream	1	1	39	35	1	1_A375_pNL7_minus_lncRNA::1	39	Gene UNC45B	MGC119541, FLJ38610, SMUNC45, UNC45, MGC119540, UNC45B, CMYA4	unc-45 homolog B (C. elegans)	NM_173167, NM_001033576, hCT2270554.1, hCT2356010.0, hCT2356011.0	235261_at	NP_775259.1, NP_001028748.1, EAW80162.1, EAW80163.1, EAW80164.1
GeneID:162394	SLFN5	17	33,570,086	33,594,768	24,682	+	3	1_A375_pNL7_minus_lncRNA::1::2510, 2_A375_pNL97_plus_lncRNA::1::3597, 2_A375_pNL97_plus_lncRNA::1::3598	-838, -6, 634	upstream, upstream, in gene	1	1	11.67	16	3	2_A375_pNL97_plus_lncRNA::1	21	Gene SLFN5	MGC150611, MGC150612, SLFN5, MGC19764	schlafen family member 5	NM_144975, hCT1644323.3	1553055_a_at, 1557078_at, 238430_x_at, 243999_at	NP_659412.3, EAW80159.1
GeneID:91607	SLFN11	17	33,677,324	33,700,720	23,396	-	1	1_A375_pNL7_minus_lncRNA::1::2511	-112	upstream	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene SLFN11	SLFN8/9, FLJ34922, SLFN11	schlafen family member 11	NM_001104587, NM_001104588, NM_001104589, NM_001104590, NM_152270, hCT2266172.2, hCT2351564.0, hCT2356001.0	226743_at	NP_001098057.1, NP_001098058.1, NP_001098059.1, NP_001098060.1, NP_689483.3, EAW80157.1, EAW80156.1, EAW80158.1
GeneID:91608	RASL10B	17	34,058,679	34,070,540	11,861	+	2	1_A375_pNL7_minus_lncRNA::1::2512, 2_A375_pNL97_plus_lncRNA::1::3599	12265, 12297	downstream, downstream	1	1	40	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene RASL10B	RASL10B, VTS58635, RRP17, MGC47540	RAS-like, family 10, member B	NM_033315, hCT2270574.0	235486_at, 244656_at	NP_201572.1, EAW80132.1
GeneID:246176	GAS2L2	17	34,071,537	34,079,897	8,360	-	2	1_A375_pNL7_minus_lncRNA::1::2512, 2_A375_pNL97_plus_lncRNA::1::3599	8953, 8921	downstream, downstream	1	1	40	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene GAS2L2	GAR17, GAS2L2	growth arrest-specific 2 like 2	NM_139285, hCT1787618.1	1552596_at	NP_644814.1, EAW80131.1
GeneID:8148	TAF15	17	34,136,488	34,174,238	37,750	+	2	1_A375_pNL7_minus_lncRNA::1::2513, 2_A375_pNL97_plus_lncRNA::1::3600	-232, -168	upstream, upstream	1	1	27	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene TAF15	Npl3, TAF2N, TAFII68, RBP56, hTAFII68, TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	NM_003487, NM_139215, hCT2270576.0, hCT2270577.0, hCT2270578.0, hCT2356009.0	202840_at, 227684_at, 227891_s_at, 234168_at	NP_003478.1, NP_631961.1, EAW80124.1, EAW80125.1, EAW80126.1, EAW80127.1
GeneID:9326	ZNHIT3	17	34,842,473	34,851,662	9,189	+	3	1_A375_pNL7_minus_lncRNA::1::2515, 2_A375_pNL97_plus_lncRNA::1::3602, 2_A375_pNL97_plus_lncRNA::1::3603	-73, -3401, -73	upstream, upstream, upstream	1	1	29	32.5	2	2_A375_pNL97_plus_lncRNA::1	48	Gene ZNHIT3	TRIP3, ZNHIT3	zinc finger, HIT type 3	NM_004773, hCT1965544.1, hCT21369.3, hCT2353223.0, hCT2353224.0	212544_at	NP_004764.1, EAW57554.1, EAW57552.1, EAW57553.1, EAW57555.1
GeneID:80179	MYO19	17	34,851,599	34,891,305	39,706	-	5	1_A375_pNL7_minus_lncRNA::1::2515, 1_A375_pNL7_minus_lncRNA::1::2516, 2_A375_pNL97_plus_lncRNA::1::3603, 2_A375_pNL97_plus_lncRNA::1::3604, 2_A375_pNL97_plus_lncRNA::1::3605	48905, -10135, 48905, -7, -10311	downstream, upstream, downstream, upstream, upstream	1	1	30	27	3	2_A375_pNL97_plus_lncRNA::1	48	Gene MYO19	MYOHD1, FLJ22865, MYO19	myosin XIX	NM_001033580, NM_001163735, NM_025109, hCT1786615.2, hCT1950106.1, hCT1950107.1, hCT2291150.0, hCT2291151.0, hCT2291152.0	219320_at, 225947_at, 236022_at	NP_001028752.1, NP_001157207.1, NP_079385.2, EAW57556.1, EAW57558.1, EAW57560.1, EAW57557.1, EAW57559.1, EAW57561.1
GeneID:284098	PIGW	17	34,891,403	34,895,150	3,747	+	3	1_A375_pNL7_minus_lncRNA::1::2516, 2_A375_pNL97_plus_lncRNA::1::3604, 2_A375_pNL97_plus_lncRNA::1::3605	10037, -91, 10213	downstream, upstream, downstream	1	1	22	16.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene PIGW	Gwt1, PIGW, FLJ37433	phosphatidylinositol glycan anchor biosynthesis, class W	NM_178517, hCT2290691.1, hCT2349847.0	1558292_s_at	NP_848612.2, EAW57564.1, EAW57563.1
GeneID:79893	GGNBP2	17	34,900,737	34,946,278	45,541	+	3	1_A375_pNL7_minus_lncRNA::1::2516, 2_A375_pNL97_plus_lncRNA::1::3604, 2_A375_pNL97_plus_lncRNA::1::3605	703, -9425, 879	in gene, upstream, in gene	1	1	22	16.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene GGNBP2	DIF-3, ZFP403, GGNBP2, LCRG1, FLJ22561, DIF3, LZK1, ZNF403, FLJ42090, FLJ21230	gametogenetin binding protein 2	NM_024835, hCT2290694.0, hCT2290696.0	1554419_x_at, 218079_s_at, 233936_s_at, 233937_at	NP_079111.1, EAW57567.1, EAW57566.1
GeneID:3975	LHX1	17	35,294,499	35,300,494	5,995	+	1	2_A375_pNL97_plus_lncRNA::1::3611	11549	downstream	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LHX1	MGC126723, MGC138141, LIM-1, LIM1, LHX1	LIM homeobox 1	NM_005568, hCT18824.3	206230_at	NP_005559.2, EAW57574.1
GeneID:26574	AATF	17	35,306,175	35,414,171	107,996	+	1	2_A375_pNL97_plus_lncRNA::1::3611	-127	upstream	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene AATF	DED, CHE1, CHE-1, AATF	apoptosis antagonizing transcription factor	NM_012138, hCT21367.4	209165_at	NP_036270.1, EAW57575.1
GeneID:6871	TADA2A	17	35,766,977	35,837,226	70,249	+	1	1_A375_pNL7_minus_lncRNA::1::2519	76815	downstream	1	0	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TADA2A	TADA2A, ADA2, TADA2L, FLJ12705, KL04P, hADA2, ADA2A	transcriptional adaptor 2A	NM_133439, NM_001488, NM_001166105, hCT19335.3, hCT1950125.1, hCT2290729.0, hCT2290730.0, hCT2353221.0	209938_at, 210537_s_at	NP_597683.2, NP_001479.3, NP_001159577.1, EAW57587.1, EAW57588.1, EAW57589.1, EAW57590.1, EAW57591.1
GeneID:11072	DUSP14	17	35,849,951	35,873,588	23,637	+	1	1_A375_pNL7_minus_lncRNA::1::2519	-6159	upstream	1	0	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene DUSP14	MKP6, DUSP14, MKP-L	dual specificity phosphatase 14	NM_007026, hCT18825.3, hCT1950123.1	203367_at	NP_008957.1, EAW57593.1, EAW57592.1
GeneID:11276	SYNRG	17	35,874,900	35,969,486	94,586	-	1	2_A375_pNL97_plus_lncRNA::1::3612	30	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SYNRG	MGC104959, SYNG, AP1GBP1, SYNRG, FLJ34482	synergin, gamma	NM_007247, NM_080550, NM_198882, NM_001163544, NM_001163545, NM_001163546, NM_001163547, hCT19334.3, hCT1950124.1, hCT2290532.0, hCT2290535.0, hCT2290536.0	1553165_at, 222715_s_at, 232387_at, 232981_s_at	NP_009178.3, NP_542117.3, NP_942583.1, NP_001157016.1, NP_001157017.1, NP_001157018.1, NP_001157019.1, EAW57594.1, EAW57595.1, EAW57596.1, EAW57597.1, EAW57598.1
GeneID:11056	DDX52	17	35,972,413	36,003,487	31,074	-	2	2_A375_pNL97_plus_lncRNA::1::3612, 2_A375_pNL97_plus_lncRNA::1::3613	34031, 63	downstream, in gene	0	1	10	17.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene DDX52	ROK1, HUSSY19, DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	NM_152300, NM_007010, hCT19336.3, hCT2290530.0, hCT2353222.0	1570415_at, 210320_s_at, 212834_at	NP_689513.2, NP_008941.2, EAW57599.1, EAW57600.1, EAW57601.1
GeneID:440435	GPR179	17	36,481,493	36,499,693	18,200	-	1	2_A375_pNL97_plus_lncRNA::1::3615	-7907	upstream	0	1	10	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene GPR179	GPR158L1, GPR179	G protein-coupled receptor 179	NM_001004334		NP_001004334.2
GeneID:30837	SOCS7	17	36,508,005	36,556,019	48,014	+	1	2_A375_pNL97_plus_lncRNA::1::3615	-405	upstream	0	1	10	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SOCS7	NCKAP4, SOCS7, NAP4	suppressor of cytokine signaling 7	NM_014598, hCT30337.3	214015_at, 226572_at	NP_055413.1, EAW60512.1
GeneID:100170841	C17orf96	17	36,827,956	36,831,187	3,231	-	1	2_A375_pNL97_plus_lncRNA::1::3616	387	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C17orf96	C17orf96		NM_001130677		NP_001124149.1
GeneID:7703	PCGF2	17	36,890,150	36,904,558	14,408	-	2	1_A375_pNL7_minus_lncRNA::1::2520, 2_A375_pNL97_plus_lncRNA::1::3617	-4258, -4306	upstream, upstream	1	1	53	49	1	1_A375_pNL7_minus_lncRNA::1	53	Gene PCGF2	RNF110, MEL-18, MGC10545, PCGF2, ZNF144	polycomb group ring finger 2	NM_007144, hCT1956005.1, hCT22576.2, hCT2326895.0, hCT2353595.0	203792_x_at, 203793_x_at, 213551_x_at, 214239_x_at, 240752_at	NP_009075.1, EAW60527.1, EAW60528.1, EAW60529.1, EAW60530.1
GeneID:5691	PSMB3	17	36,909,002	36,920,478	11,476	+	2	1_A375_pNL7_minus_lncRNA::1::2520, 2_A375_pNL97_plus_lncRNA::1::3617	-186, -138	upstream, upstream	1	1	53	49	1	1_A375_pNL7_minus_lncRNA::1	53	Gene PSMB3	MGC4147, PSMB3, HC10-II	proteasome (prosome, macropain) subunit, beta type, 3	NM_002795, hCT22577.3	201400_at	NP_002786.2, EAW60531.1
GeneID:8396	PIP4K2B	17	36,921,944	36,956,158	34,214	-	3	1_A375_pNL7_minus_lncRNA::1::2521, 1_A375_pNL7_minus_lncRNA::1::2522, 2_A375_pNL97_plus_lncRNA::1::3618	862, -162, 830	in gene, upstream, in gene	1	1	20	20.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene PIP4K2B	PIP5KIIbeta, PI5P4KB, PIP4K2B, PIP5K2B, PIP5KIIB	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	NM_003559, hCT19340.2, hCT2345444.0, hCT2345445.0, hCT2345446.0, hCT2345447.0	1553047_at, 1553048_a_at, 201080_at, 201081_s_at	NP_003550.1, EAW60535.1, EAW60532.1, EAW60533.1, EAW60534.1, EAW60536.1
GeneID:54883	CWC25	17	36,957,446	36,981,589	24,143	-	5	1_A375_pNL7_minus_lncRNA::1::2521, 1_A375_pNL7_minus_lncRNA::1::2522, 1_A375_pNL7_minus_lncRNA::1::2523, 2_A375_pNL97_plus_lncRNA::1::3618, 2_A375_pNL97_plus_lncRNA::1::3619	26293, 25269, 21, 26261, 21	downstream, downstream, in gene, downstream, in gene	1	1	22.33	23	3	2_A375_pNL97_plus_lncRNA::1	28	Gene CWC25	CWC25, CCDC49, FLJ20291, DKFZp779M0968	CWC25 spliceosome-associated protein homolog (S. cerevisiae)	NM_017748, hCT22588.2	218655_s_at, 222706_at	NP_060218.1, EAW60537.1
GeneID:388381	C17orf98	17	36,991,341	36,997,642	6,301	-	2	1_A375_pNL7_minus_lncRNA::1::2523, 2_A375_pNL97_plus_lncRNA::1::3619	16074, 16074	downstream, downstream	1	1	27	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene C17orf98	C17orf98		NM_001080465	244316_at	NP_001073934.1
GeneID:9349	RPL23	17	37,006,321	37,010,053	3,732	-	1	2_A375_pNL97_plus_lncRNA::1::3620	-59	upstream	0	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene RPL23	MGC72008, RPL23, MGC111167, MGC117346, L23, rpL17	ribosomal protein L23	NM_000978, hCT2326888.0, hCT2326889.0, hCT2326890.0, hCT2326891.0	200888_s_at, 215224_at	NP_000969.1, EAW60539.1, EAW60540.1, EAW60541.1, EAW60542.1
GeneID:619505	SNORA21	17	37,009,116	37,009,248	132	-	1	2_A375_pNL97_plus_lncRNA::1::3620	-864	upstream	0	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SNORA21	SNORA21, ACA21	small nucleolar RNA, H/ACA box 21	NR_002576		
GeneID:3927	LASP1	17	37,026,112	37,078,023	51,911	+	1	2_A375_pNL97_plus_lncRNA::1::3621	192	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LASP1	Lasp-1, MLN50, LASP1	LIM and SH3 protein 1	NM_006148, hCT22579.1, hCT2294966.0, hCT2294969.0	200618_at	NP_006139.1, EAW60544.1, EAW60543.1, EAW60545.1
GeneID:57125	PLXDC1	17	37,219,556	37,307,902	88,346	-	2	1_A375_pNL7_minus_lncRNA::1::2525, 2_A375_pNL97_plus_lncRNA::1::3622	-2914, -2786	upstream, upstream	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PLXDC1	FLJ36270, TEM7, DKFZp686F0937, FLJ45632, TEM3, PLXDC1	plexin domain containing 1	NM_020405, hCT22583.2, hCT2326881.0, hCT2326882.0	214081_at, 219700_at, 240963_x_at	NP_065138.2, EAW60553.1, EAW60551.1, EAW60552.1
GeneID:390790	ARL5C	17	37,313,147	37,322,414	9,267	-	2	1_A375_pNL7_minus_lncRNA::1::2525, 2_A375_pNL97_plus_lncRNA::1::3622	11598, 11726	downstream, downstream	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ARL5C	FLJ17748, ARL12, ARL5C	ADP-ribosylation factor-like 5C	NM_001143968		NP_001137440.1
GeneID:84961	FBXL20	17	37,408,897	37,557,909	149,012	-	1	1_A375_pNL7_minus_lncRNA::1::2526	578	in gene	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene FBXL20	FLJ21037, SCRAPPER, Fbl2, MGC15482, SCR, DKFZp564O2364, FBXL20, Fbl20	F-box and leucine-rich repeat protein 20	NM_001184906, NM_032875, hCT1813441.1, hCT2348950.0	235089_at, 239223_s_at, 239224_at	NP_001171835.1, NP_116264.2, EAW60573.1, EAW60574.1
GeneID:5469	MED1	17	37,560,538	37,607,527	46,989	-	1	1_A375_pNL7_minus_lncRNA::1::2526	50196	downstream	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene MED1	DRIP230, TRIP2, PPARBP, PBP, DRIP205, PPARGBP, MGC71488, TRAP220, RB18A, MED1, CRSP200, CRSP1	mediator complex subunit 1	NM_004774, hCT1963875.1	203496_s_at, 203497_at, 225452_at, 225456_at	NP_004765.2, EAW60575.1
GeneID:84152	PPP1R1B	17	37,783,179	37,792,878	9,699	+	1	2_A375_pNL97_plus_lncRNA::1::3624	-8467	upstream	0	1	14	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PPP1R1B	DARPP-32, DARPP32, PPP1R1B, FLJ20940	protein phosphatase 1, regulatory (inhibitor) subunit 1B	NM_032192, NM_181505, hCT1953732.1, hCT1953733.1, hCT21183.3, hCT2353597.0	225165_at	NP_115568.2, NP_852606.1, EAW60580.1, EAW60581.1, EAW60582.1, EAW60583.1
GeneID:2064	ERBB2	17	37,844,393	37,884,915	40,522	+	1	2_A375_pNL97_plus_lncRNA::1::3625	42295	downstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ERBB2	HER-2, ERBB2, NGL, MLN19, NEU, TKR1, HER-2/neu, CD340, HER2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	NM_004448, NM_001005862, hCT19324.2, hCT2294817.0, hCT2294818.0	210930_s_at, 216836_s_at, 234354_x_at	NP_004439.2, NP_001005862.1, EAW60595.1, EAW60596.1, EAW60597.1
GeneID:84299	C17orf37	17	37,885,409	37,886,788	1,379	-	1	2_A375_pNL97_plus_lncRNA::1::3625	100	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C17orf37	C17orf37, C35, XTP4, ORB3, MGC14832, RDX12	chromosome 17 open reading frame 37	NM_032339, hCT1953735.1, hCT21186.2	224447_s_at	NP_115715.3, EAW60599.1, EAW60598.1
GeneID:2886	GRB7	17	37,894,187	37,903,538	9,351	+	3	1_A375_pNL7_minus_lncRNA::1::2528, 2_A375_pNL97_plus_lncRNA::1::3625, 2_A375_pNL97_plus_lncRNA::1::3626	16181, -7499, 16341	downstream, upstream, downstream	1	1	17.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene GRB7	GRB7		NM_005310, NM_001030002, hCT21176.2, hCT2294822.0	210761_s_at	NP_005301.2, NP_001025173.1, EAW60600.1, EAW60601.1
GeneID:55876	GSDMB	17	38,060,848	38,074,903	14,055	-	1	2_A375_pNL97_plus_lncRNA::1::3627	-8921	upstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GSDMB	GSDMB, GSDML, PP4052, PRO2521	gasdermin B	NM_001042471, NM_018530, NM_001165958, NM_001165959, hCT1953739.1, hCT21189.2, hCT2295469.0, hCT2353621.0	215659_at, 219233_s_at	NP_001035936.1, NP_061000.2, NP_001159430.1, NP_001159431.1, EAW60612.1, EAW60613.1, EAW60614.1, EAW60615.1
GeneID:94103	ORMDL3	17	38,077,296	38,083,854	6,558	-	1	2_A375_pNL97_plus_lncRNA::1::3627	30	in gene	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene ORMDL3	ORMDL3		NM_139280, hCT21188.2, hCT2295461.0, hCT2295463.0, hCT2353619.0, hCT2353620.0	223259_at, 235136_at, 240701_at	NP_644809.1, EAW60619.1, EAW60616.1, EAW60617.1, EAW60618.1, EAW60620.1
GeneID:284110	GSDMA	17	38,119,226	38,134,019	14,793	+	2	1_A375_pNL7_minus_lncRNA::1::2529, 2_A375_pNL97_plus_lncRNA::1::3628	17782, 17766	downstream, downstream	1	1	83	85	1	2_A375_pNL97_plus_lncRNA::1	85	Gene GSDMA	GSDMA, FLJ39120, GSDM1, FKSG9, GSDM, MGC129596	gasdermin A	NM_178171, hCT1827649.4		NP_835465.2, EAW60624.1
GeneID:5709	PSMD3	17	38,137,060	38,154,212	17,152	+	2	1_A375_pNL7_minus_lncRNA::1::2529, 2_A375_pNL97_plus_lncRNA::1::3628	-52, -68	upstream, upstream	1	1	83	85	1	2_A375_pNL97_plus_lncRNA::1	85	Gene PSMD3	S3, P58, TSTA2, PSMD3, RPN3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	NM_002809, hCT21179.2	201388_at	NP_002800.2, EAW60625.1
GeneID:9862	MED24	17	38,175,350	38,210,889	35,539	-	2	1_A375_pNL7_minus_lncRNA::1::2530, 2_A375_pNL97_plus_lncRNA::1::3629	-8599, -8631	upstream, upstream	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MED24	THRAP4, DRIP100, MED24, CRSP100, hTRAP100, KIAA0130, ARC100, MGC8748, TRAP100, CRSP4	mediator complex subunit 24	NM_001079518, NM_014815, hCT1953734.1, hCT21184.2, hCT2295454.0	213043_s_at, 215337_at	NP_001072986.1, NP_055630.2, EAW60629.1, EAW60630.1, EAW60631.1
GeneID:7067	THRA	17	38,218,446	38,250,120	31,674	+	3	1_A375_pNL7_minus_lncRNA::1::2530, 1_A375_pNL7_minus_lncRNA::1::2531, 2_A375_pNL97_plus_lncRNA::1::3629	1042, 38290, 1074	in gene, downstream, in gene	1	1	21	19.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene THRA	AR7, THRA1, THRA, c-ERBA-1, ERB-T-1, ERBA, EAR7, MGC43240, MGC000261, ERBA1, THRA2, NR1A1	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	NM_001190918, NM_001190919, NM_003250, NM_199334, hCT1787977.1, hCT2294831.0, hCT2294832.0	1316_at, 204100_at, 214883_at, 35846_at	NP_001177847.1, NP_001177848.1, NP_003241.2, NP_955366.1, EAW60632.1, EAW60633.1, EAW60634.1
GeneID:9572	NR1D1	17	38,249,037	38,256,973	7,936	-	1	1_A375_pNL7_minus_lncRNA::1::2531	237	in gene	1	0	21	14	1	1_A375_pNL7_minus_lncRNA::1	21	Gene NR1D1	THRA1, EAR1, THRAL, hRev, ear-1, NR1D1	nuclear receptor subfamily 1, group D, member 1	NM_021724, hCT85161.2		NP_068370.1, EAW60636.1
GeneID:339287	MSL1	17	38,278,790	38,293,042	14,252	+	1	2_A375_pNL97_plus_lncRNA::1::3630	1082	in gene	0	1	15	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MSL1	MSL1, MGC141861, hMSL1, MSL-1, DKFZp686J17211	male-specific lethal 1 homolog (Drosophila)	NM_001012241	212708_at, 224765_at, 230155_x_at	NP_001012241.1
GeneID:5914	RARA	17	38,465,423	38,513,895	48,472	+	2	1_A375_pNL7_minus_lncRNA::1::2532, 2_A375_pNL97_plus_lncRNA::1::3631	5651, 5617	in gene, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RARA	NR1B1, RAR, RARA	retinoic acid receptor, alpha	NM_000964, NM_001024809, NM_001145301, NM_001145302, hCT2294849.1, hCT2294850.1, hCT2294852.1, hCT2294853.1, hCT2294854.1, hCT2294855.1, hCT2348794.0	1565358_at, 203749_s_at, 203750_s_at, 211605_s_at, 216300_x_at	NP_000955.1, NP_001019980.1, NP_001138773.1, NP_001138774.1, EAW60652.1, EAW60658.1, EAW60653.1, EAW60654.1, EAW60655.1, EAW60656.1, EAW60657.1
GeneID:7153	TOP2A	17	38,544,773	38,574,202	29,429	-	2	1_A375_pNL7_minus_lncRNA::1::2533, 2_A375_pNL97_plus_lncRNA::1::3632	-70, 58	upstream, in gene	1	1	20	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene TOP2A	TOP2, TOP2A, TP2A	topoisomerase (DNA) II alpha 170kDa	NM_001067, hCT1958867.1, hCT2295437.0, hCT2295439.0	201291_s_at, 201292_at, 237469_at	NP_001058.2, EAW60663.1, EAW60661.1, EAW60662.1
GeneID:6605	SMARCE1	17	38,783,972	38,804,103	20,131	-	1	2_A375_pNL97_plus_lncRNA::1::3633	-313	upstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SMARCE1	BAF57, SMARCE1, FLJ35648	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	NM_003079, hCT2292319.0, hCT2292320.0	211988_at, 211989_at, 229511_at	NP_003070.3, EAW60670.1, EAW60671.1
GeneID:125113	KRT222	17	38,811,872	38,821,416	9,544	-	1	2_A375_pNL97_plus_lncRNA::1::3633	17000	downstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene KRT222	KA21, KRT222P, MGC45562, KRT222	keratin 222	NM_152349, hCT1788347.3, hCT2350136.0	243998_at, 244111_at	NP_689562.1, EAW60672.1, EAW60673.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Count	Internal Infometrics	Internal Dist to start	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:7462224	KRTAP4-6	17	39,253,233	39,254,375	1,142	+	1	2_A375_shLI7_shrus_lncRNA:1:-:3634	637	upstream	0	1	9	13	13	2_A375_shLI7_plus_lncRNA:1	13	Gene: KRTAP4-6	KRTAP4-6, KAP4.6, KRTAP4-6	keratin associated protein 4-6	NM_031960		NP_114199.1
Gene:ID:10112383	KRTAP4-6	17	39,261,641	39,262,740	1,099	+	1	2_A375_shLI7_shrus_lncRNA:1:-:3634	4729	upstream	0	1	9	13	13	2_A375_shLI7_plus_lncRNA:1	13	Gene: KRTAP4-6	KRTAP4-6, KAP4.6	keratin associated protein 4-6	NM_001146941		NP_001139813.1
Gene:ID:551	KRT31	17	39,549,976	39,553,648	3,666	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2534, 2_A375_shLI7_shrus_lncRNA:1:-:3638	4580, -1676	upstream, upstream	1	1	16	24	1	2_A375_shLI7_plus_lncRNA:1	24	Gene: KRT31	KRT31, KRTHA1, MGC139530, HA1, Hair1, Ha-1	keratin 31	NM_002277, NM_001322641.1	206677_at	NP_002266.2, EAW69730.1
Gene:ID:93060578	LOC100287182	17	39,555,955	39,565,640	10,172	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2534, 2_A375_shLI7_shrus_lncRNA:1:-:3638	1716, 1652	ia gene, us gene	1	1	16	24	1	2_A375_shLI7_plus_lncRNA:1	24	Gene: LOC100287182		hypothetical LOC100287582	XR_111692, XR_109283, XR_115101, XR_109272		
Gene:ID:3209	EIF1	17	39,645,127	39,647,898	2,771	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2539, 2_A375_shLI7_shrus_lncRNA:1:-:3637	4799, 6703	upstream, upstream	1	1	24	29	1	1_A375_shLI7_shrus_lnc:1	34	Gene: EIF1	EIF1, AT21, IEO1, EIF1A, EIF-1, SUI1	eukaryotic translation initiation factor 1	NM_005801, ENST00000376, 2, ENST00002	202021_s_at, 211936_s_at, 213136_s_at, 212225_at, 212227_x_at, 226607_at	NP_005792.1, EAW69734.1, EAW69735.1
Gene:ID:9908	SCG5	17	39,955,203	39,965,631	10,429	-	2	1_A375_shLI7_shrus_lncRNA:1:-:2537, 2_A375_shLI7_shrus_lncRNA:1:-:3639	-283, 33	upstream, us gene	1	1	19	36	1	2_A375_shLI7_plus_lncRNA:1	36	Gene: SCG5	LEPRELA, NCL55, SCG5, N155	secretogranin 5	NM_006453, ENST00001	204578_at	NP_006445.1, EAW69786.1
Gene:ID:50661	PKBP10	17	39,965,962	39,979,669	10,827	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2537, 2_A375_shLI7_shrus_lncRNA:1:-:3639	-226, -566	upstream, upstream	1	1	19	36	1	2_A375_shLI7_plus_lncRNA:1	36	Gene: PKBP10	FLJ23581, FLJ30553, OI6, FPHSE, FKBP10, FLJ23533, hFKBP65, FKBP65	FK506 binding protein 10, 65 kDa	NM_021939, ENST00001, ENST00021, ENST00021, ENST00021	219249_s_at	NP_068758.2, EAW69790.1, EAW69787.1, EAW69788.1, EAW69789.1
Gene:ID:4175	KLHL11	17	40,009,799	40,021,629	11,830	-	1	2_A375_shLI7_shrus_lncRNA:1:-:3639	62	ia gene	0	1	12	15	1	2_A375_shLI7_plus_lncRNA:1	16	Gene: KLHL11	KLHL11, PLI/1972	kelch-like 11 (Drosophila)	NM_081453, ENST00021, ENST00021	226837_at	NP_065613.1, EAW69779.1, EAW69778.1
Gene:ID:117	ACLY	17	40,023,179	40,075,272	52,093	-	1	2_A375_shLI7_shrus_lncRNA:1:-:3639	53736	downstream	0	1	12	15	1	2_A375_shLI7_plus_lncRNA:1	16	Gene: ACLY	CLATP, ACL, ACLY, ATPCL	ATP citrate lyase	NM_001096, NM_135530, ENST00021, ENST00021, ENST00021	201127_s_at, 201126_s_at, 202327_s_at	NP_001087.2, NP_942127.1, EAW69777.1, EAW69779.1, EAW69780.1, EAW69781.1, EAW69778.1
Gene:ID:51161	TTC28	17	40,088,668	40,117,669	30,781	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2535, 2_A375_shLI7_shrus_lncRNA:1:-:3640	-72, -390	upstream, upstream	1	1	14	15	1	2_A375_shLI7_plus_lncRNA:1	15	Gene: TTC28	KIAA1348, FLJ21153, TTC23	tetratricopeptide repeat domain 28	NM_031421, ENST00018, ENST00021, ENST00021	223624_at	NP_113609.1, EAW69784.1, EAW69782.1, EAW69783.1
Gene:ID:266	DNAJC7	17	40,128,439	40,169,715	41,276	+	4	1_A375_shLI7_shrus_lncRNA:1:-:2532, 2_A375_shLI7_shrus_lncRNA:1:-:2540, 2_A375_shLI7_shrus_lncRNA:1:-:3640, 2_A375_shLI7_shrus_lncRNA:1:-:3640	118, -2329, 275, -2217	ia gene, upstream, us gene, upstream	1	1	66.5	70	2	2_A375_shLI7_plus_lncRNA:1	108	Gene: DNAJC7	TTC2, DJC7, TPR2, DJI1, DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	NR_026831, NM_003315, NM_001164766, ENST00000527.0, ENST00000	1555053_at, 202416_at	NP_003306.3, NP_001138238.1, EAW69788.1, EAW69789.1
Gene:ID:5511	NKRAS2	17	40,169,294	40,177,699	8,406	+	4	1_A375_shLI7_shrus_lncRNA:1:-:2539, 1_A375_shLI7_shrus_lncRNA:1:-:2540, 2_A375_shLI7_shrus_lncRNA:1:-:3640, 2_A375_shLI7_shrus_lncRNA:1:-:3640	6, -2470, 184, 2438	ia gene, us gene, upstream, us gene	1	1	64.5	70	2	2_A375_shLI7_plus_lncRNA:1	105	Gene: NKRAS2	MGC074742, IDR1KB2, DKFZp434N1526,	NFKB inhibitor interacting Ras-like 2	NM_001001349, NM_017693, NM_001149927, NM_001149928, NM_001166929, ENST00000, ENST00002, ENST00002	214240_at, 222103_s_at	NP_001001349.1, NP_060053.2, NP_001136399.1, NP_001158400.1, NP_001135401.1, EAW69780.1, EAW69781.1, EAW69782.1, EAW69783.1
Gene:ID:51151	ZNF385C	17	40,177,994	40,180,707	3,113	+	4	1_A375_shLI7_shrus_lncRNA:1:-:2539, 1_A375_shLI7_shrus_lncRNA:1:-:2540, 2_A375_shLI7_shrus_lncRNA:1:-:3640, 2_A375_shLI7_shrus_lncRNA:1:-:3640	11107, 6841, 11267, 6975	downstream, downstream, downstream, downstream	1	1	66.5	70	2	2_A375_shLI7_plus_lncRNA:1	105	Gene: ZNF385C	ZNF385C	zinc finger protein 385C	XM_002348529, XM_002345556, XM_002347763	241363_at	XP_002348570.2, XP_002343599.2, XP_002347809.2
Gene:ID:93057628	LOC100287628	17	40,178,913	40,190,044	11,129	+	4	1_A375_shLI7_shrus_lncRNA:1:-:2539, 1_A375_shLI7_shrus_lncRNA:1:-:2540, 2_A375_shLI7_shrus_lncRNA:1:-:3640, 2_A375_shLI7_shrus_lncRNA:1:-:3640	20444, 19980, 20654, 19812	downstream, downstream, downstream, downstream	1	1	64.5	70	2	2_A375_shLI7_plus_lncRNA:1	105	Gene: LOC100287628		zinc finger protein 385C-like	XM_003119976, XM_003118752, XM_003120681		XP_003119824.1, XP_003116600.1, XP_003120829.1
Gene:ID:616	RASSC	17	40,276,997	40,307,822	30,825	-	1	2_A375_shLI7_shrus_lncRNA:1:-:3640	-114	upstream	0	1	13	15	1	2_A375_shLI7_plus_lncRNA:1	15	Gene: RASSC	RASSCL, MGC117217, RABL, RASSC, MGC135687	RASSC, member RAS oncogene family	NM_058583, NM_201439, ENST00000, ENST00002, ENST00002	241160_s_at, 231190_s_at	NP_058547.2, NP_958842.1, EAW69805.1, EAW69806.1, EAW69807.1, EAW69808.1
Gene:ID:3418	KCNH4	17	40,308,810	40,333,296	24,486	-	3	1_A375_shLI7_shrus_lncRNA:1:-:2541, 1_A375_shLI7_shrus_lncRNA:1:-:2542, 2_A375_shLI7_shrus_lncRNA:1:-:3640	19005, 26160, 984	ia gene, downstream, us gene	1	1	19.5	29	2	2_A375_shLI7_plus_lncRNA:1	40	Gene: KCNH4	KCNH4, BEC2, Kv12.3, ELK1	potassium voltage-gated channel, subfamily H (eag-related), member 4	NM_012285, ENST00011	209802_at	NP_036417.1, EAW69808.1
Gene:ID:993	HCRT	17	40,339,078	40,337,470	1,392	+	4	1_A375_shLI7_shrus_lncRNA:1:-:2541, 1_A375_shLI7_shrus_lncRNA:1:-:2542, 2_A375_shLI7_shrus_lncRNA:1:-:3640, 2_A375_shLI7_shrus_lncRNA:1:-:3640	9162, -9055, 5115, -9055	downstream, upstream, downstream, upstream	1	1	47.5	64.5	2	2_A375_shLI7_plus_lncRNA:1	69	Gene: HCRT	OX, NRCLP1, PPCR, HCRT	hypocretin (orexin) neuropeptide precursor	NM_001524, ENST00013	207642_at	NP_001518.1, EAW69810.1
Gene:ID:4514	GHDC	17	40,341,103	40,346,550	5,448	+	4	1_A375_shLI7_shrus_lncRNA:1:-:2541, 1_A375_shLI7_shrus_lncRNA:1:-:2542, 2_A375_shLI7_shrus_lncRNA:1:-:3640, 2_A375_shLI7_shrus_lncRNA:1:-:3640	14262, 22, 14185, 22	downstream, ia gene, downstream, ia gene	1	1	47.5	64.5	2	2_A375_shLI7_plus_lncRNA:1	69	Gene: GHDC	GHDC, LGP1, DI11GP1	GH3 domain containing	NR_026972, NM_001146822, NM_001142823, NM_032464, ENST00002, ENST00002, ENST00002, ENST00002, ENST00002	227192_at	NP_001139994.1, NP_001139995.1, NP_115813.2, EAW69812.1, EAW69813.1, EAW69814.1, EAW69815.1, EAW69816.1, EAW69817.1
Gene:ID:777	STAT5B	17	40,351,193	40,426,624	77,228	+	3	1_A375_shLI7_shrus_lncRNA:1:-:2542, 1_A375_shLI7_shrus_lncRNA:1:-:2543, 2_A375_shLI7_shrus_lncRNA:1:-:3640	81699, 6520, 81696	downstream, ia gene, downstream	1	1	42.5	52	2	2_A375_shLI7_plus_lncRNA:1	69	Gene: STAT5B	STAT5B, STAT5	signal transducer and activator of transcription 5B	NM_012448, ENST00016	1555096_at, 1555095_s_at, 208029_at, 212589_at, 212590_at	NP_036580.2, EAW69817.1
Gene:ID:774	STAT5A	17	40,439,063	40,461,261	24,386	+	1	2_A375_shLI7_shrus_lncRNA:1:-:3640	-109	upstream	0	1	16	25	1	2_A375_shLI7_plus_lncRNA:1	25	Gene: STAT5A	STAT5, MGF, STAT5A	signal transducer and activator of transcription 5A	NM_003152, ENST00020	203010_at	NP_003143.2, EAW69818.1
Gene:ID:774	STAT3	17	40,465,343	40,500,513	35,170	+	3	1_A375_shLI7_shrus_lncRNA:1:-:2544, 1_A375_shLI7_shrus_lncRNA:1:-:2544, 2_A375_shLI7_shrus_lncRNA:1:-:3640	-21, -79	upstream, upstream	1	1	65	84	1	2_A375_shLI7_plus_lncRNA:1	84	Gene: STAT3	APRF, STAT3, MGC19063, FLJ20552, HIES	signal transducer and activator of transcription 3 (acute-phase response factor)	NM_139276, NM_003150, NM_213662, ENST00000, ENST00002, ENST00002, ENST00002, ENST00002, ENST00002	1555991_at, 1555992_s_at, 225209_at, 243213_at	NP_644805.1, NP_003140.2, NP_998827.1, EAW69820.1, EAW69821.1, EAW69822.1, EAW69823.1, EAW69824.1, EAW69825.1, EAW69826.1, EAW69827.1
Gene:ID:339	ATP6V0A1	17	40,610,952	40,674,697	63,745	+	1	2_A375_shLI7_shrus_lncRNA:1:-:3646	92	ia gene	0	1	16	16	1	2_A375_shLI7_plus_lncRNA:1	16	Gene: ATP6V0A1	VPP1, DKFZp761H051, ATP6N1A, Vph1, ATP6N1, 0tv1, 81, ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	NM_005177, NM_001130020, NM_001130021, NC_123539980, ENST00000	205953_s_at, 212063_at	NP_005168.2, NP_001123492.1, NP_001123493.1, EAW69830.1, EAW69831.1
Gene:ID:9669	NAGLU	17	40,667,851	40,696,867	8,516	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2543, 2_A375_shLI7_shrus_lncRNA:1:-:3646	18637, 17321	downstream, downstream	1	1	11	17	2	2_A375_shLI7_plus_lncRNA:1	21	Gene: NAGLU	NAG, LYH5D, MPS3B, MPS-IIIB, NAGLU	N-acetylglucosaminidase, alpha	NM_000263, NC_123621236.0, ENST00	204360_s_at, 216080_at	NP_000252.2, EAW69832.1, EAW69833.1
Gene:ID:292	HSD17B1	17	40,703,854	40,707,232	3,248	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2545, 2_A375_shLI7_shrus_lncRNA:1:-:3646	2624, 1465	ia gene, us gene	1	1	11	17	2	2_A375_shLI7_plus_lncRNA:1	21	Gene: HSD17B1	HSD17, EDH17B2, MGC126180, HSD17B1, SDR3C1, EDH8T7	hydroxysteroid (17-beta) dehydrogenase 1	NM_000413, ENST00027	205529_at, 205593_at	NP_000404.2, EAW69836.1
Gene:ID:100290886	LOC100287886	17	40,704,454	40,706,766	2,312	-	2	1_A375_shLI7_shrus_lncRNA:1:-:2545, 2_A375_shLI7_shrus_lncRNA:1:-:3646	155, 1298	ia gene, us gene	1	1	11	17	2	2_A375_shLI7_plus_lncRNA:1	21	Gene: LOC100287886		hypothetical LOC100287886	XR_111701, XR_109284, XR_115104		
Gene:ID:5347	COASY	17	40,714,092	40,716,293	4,202	+	3	1_A375_shLI7_shrus_lncRNA:1:-:2545, 1_A375_shLI7_shrus_lncRNA:1:-:3646, 2_A375_shLI7_shrus_lncRNA:1:-:3646	7464, -, 6620, 496	downstream, downstream, downstream	1	1	12.67	19.67	3	2_A375_shLI7_plus_lncRNA:1	21	Gene: COASY	COASY, FLJ33179, UKR1, NBP, PPAT, pDYJ, DPCK	CoA synthase	NM_001042528, NM_023233, NM_001042530, NM_001042531, NM_001042532, ENST00021, ENST00021, ENST00021	201813_s_at	NP_001035994.1, NP_076009.2, NP_001035995.1, NP_001035996.1, NP_001035997.2, EAW69838.1, EAW69839.1, EAW69840.1
Gene:ID:845	MLX	17	40,719,078	40,725,221	6,143	+	1	2_A375_shLI7_shrus_lncRNA:1:-:3650	-70	upstream	0	1	16	16	1	2_A375_shLI7_plus_lncRNA:1	16	Gene: MLX	MLX, MXD7, MAD7, TCFL6, bHLHb13	MAX-like protein X	NM_170607, NM_198204, NM_198205, ENST00000, ENST00002, ENST00002, ENST00002, ENST00002, ENST00002	1570387_at, 210732_s_at, 213705_s_at, 213939_s_at, 227881_at	NP_733731.1, NP_937847.1, NP_937848.1, EAW69841.1, EAW69842.1, EAW69843.1, EAW69844.1
Gene:ID:9563	PSMC3IP	17	40,734,329	40,739,747	5,418	-	1	2_A375_shLI7_shrus_lncRNA:1:-:3650	10739	downstream	0	1	16	16	1	2_A375_shLI7_plus_lncRNA:1	16	Gene: PSMC3IP	HSPC, TBPIP, CT100, HUMGTI66A, PSMC3IP	PSMC3 interacting protein	NM_012390, NM_016396, ENST00000, ENST00002, ENST00002, ENST00002	203422_at, NP_037540.1, EAW69845.1, EAW69846.1, EAW69847.1, EAW69848.1	NP_037472.2, NP_037540.1, EAW69845.1, EAW69846.1, EAW69847.1
Gene:ID:9868	PLEKHH3	17	40,819,832	40,829,948	9,116	-	3	1_A375_shLI7_shrus_lncRNA:1:-:2549, 1_A375_shLI7_shrus_lncRNA:1:-:3651, 2_A375_shLI7_shrus_lncRNA:1:-:3651	2555, 645, -2999	ia gene, upstream, upstream	1	1	22	23	2	1_A375_shLI7_shrus_lnc:1	26	Gene: PLEKHH3	PLEKHH3	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	NM_024612, ENST00042, ENST00042, ENST00042, ENST00042	235239_at, 227246_at	NP_078888.2, EAW69853.1, EAW69854.1, EAW69855.1, EAW69856.1
Gene:ID:826	CCR10	17	40,831,820	40,833,845	2,026	-	3	1_A375_shLI7_shrus_lncRNA:1:-:2549, 2_A375_shLI7_shrus_lncRNA:1:-:3651, 2_A375_shLI7_shrus_lncRNA:1:-:3651	1909, 6149, 293	ia gene, downstream, ia gene	1	1	22	23	2	1_A375_shLI7_shrus_lnc:1	26	Gene: CCR10	GPR2, CCR10	chemokine (C-C motif) receptor 10	NM_016602, ENST00036	220563_at	NP_057686.2, EAW69866.1
Gene:ID:506	CNTNAP1	17	40,834,632	40,852,011	17,379	+	3	1_A375_shLI7_shrus_lncRNA:1:-:2549, 2_A375_shLI7_shrus_lncRNA:1:-:3651, 2_A375_shLI7_shrus_lncRNA:1:-:3651	-2696, -6635, 2655	upstream, upstream, upstream	1	1	22	23	2	1_A375_shLI7_shrus_lnc:1	26	Gene: CNTNAP1	CNTNAP, NRXN4, CNTNAP1, P190, CASPR	contactin associated protein 1	NM_003632, ENST00021, ENST00021	218400_at	NP_003623.1, EAW69868.1, EAW69867.1, EAW69865.1
Gene:ID:4298	WNK4	17	40,912,649	40,949,854	16,425	+	1	2_A375_shLI7_shrus_lncRNA:1:-:3651	16103	downstream	0	1	17	21	1	2_A375_shLI7_plus_lncRNA:1	21	Gene: WNK4	WNK4, PRKWNK4, PHA2B	WNK lysine deficient protein kinase 4	NM_032387, ENST00029, ENST00029	226155_at, 226154_at	NP_115793.2, EAW69861.1, EAW69862.1
Gene:ID:9930	CCDC96	17	40,949,652	40,950,704	1,052	+	1	2_A375_shLI7_shrus_lncRNA:1:-:3651	-48	upstream	0	1	17	21	1	2_A375_shLI7_plus_lncRNA:1	21	Gene: CCDC96	CCDC96, HSPC099, PLI50764	coiled-coil domain containing 96	NM_001040431	219526_at, 236995_at	NP_001035521.1
Gene:ID:24613	CNTD1	17	40,950,654	40,953,805	12,751	+	1	2_A375_shLI7_shrus_lncRNA:1:-:3652	-102	upstream	0	1	17	21	1	2_A375_shLI7_plus_lncRNA:1	21	Gene: CNTD1	CNTD, CNTD1, PLI40137	cyclin N-terminal (Huntington) domain containing 1	NM_173479, ENST00025, ENST00025	1554763_at, 227612_at	NP_775750.2, EAW69871.1, EAW69872.1
Gene:ID:610	BECN1	17	40,992,150	40,979,310	14,160	-	3	1_A375_shLI7_shrus_lncRNA:1:-:2547, 1_A375_shLI7_shrus_lncRNA:1:-:2548, 2_A375_shLI7_shrus_lncRNA:1:-:3650, 2_A375_shLI7_shrus_lncRNA:1:-:3650	84, -9905, 9130	ia gene, upstream, upstream	1	1	20.5	35.5	2	1_A375_shLI7_shrus_lnc:1	21	Gene: BECN1	ATG6, VPS30, beclin1, BECN1	beclin 1, autophagy related	NM_003766, ENST00025, ENST00025, ENST00025, ENST00025	1561652_at, 209183_s_at, 209184_s_at	NP_003757.1, EAW69865.1, EAW69866.1, EAW69867.1
Gene:ID:5187	PSME3	17	40,985,623	40,993,777	10,154	+	3	1_A375_shLI7_shrus_lncRNA:1:-:2547, 1_A375_shLI7_shrus_lncRNA:1:-:2548, 2_A375_shLI7_shrus_lncRNA:1:-:3650, 2_A375_shLI7_shrus_lncRNA:1:-:3650	4167, -307, 17	upstream, upstream, us gene	1	1	20.5	35.5	2	1_A375_shLI7_shrus_lnc:1	21	Gene: PSME3	REG-GAMMA, IG, PA28-gamma, PSME3, PA28G	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	NM_005789, NM_176093, ENST00000, ENST00002, ENST00002	208067_s_at, 208068_s_at, 208552_x_at, 208553_s_at	NP_005780.2, NP_788539.1, EAW69891.1, EAW69892.1, EAW69893.1, EAW69894.1
Gene:ID:49855	RUNDC1	17	41,132,552	41,145,707	13,125	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2549, 1_A375_shLI7_shrus_lncRNA:1:-:3650	17756, 17627	downstream, downstream	1	1	24	30	1	1_A375_shLI7_shrus_lnc:1	24	Gene: RUNDC1	RUND1, DKFZp761H0321	RUN domain containing 1	NM_173379, ENST00029, ENST00029	236298_at, 239040_at	NP_775102.2, EAW69905.1, EAW69907.1
Gene:ID:153	RPL27	17	41,150,486	41,154,876	4,530	+	3	1_A375_shLI7_shrus_lncRNA:1:-:2549, 1_A375_shLI7_shrus_lncRNA:1:-:3650, 2_A375_shLI7_shrus_lncRNA:1:-:3650	-28, -227, 12914	upstream, downstream, upstream	1	1	17.5	17	2	1_A375_shLI7_shrus_lnc:1	24	Gene: RPL27	RPL27, L27	ribosomal protein L27	NM_000988, ENST00025, ENST00025, ENST00025, ENST00025	200025_s_at	NP_000979.1, EAW69908.1, EAW69910.1, EAW69911.1, EAW69912.1, EAW69913.1
Gene:ID:430	IFI35	17	41,156,769	41,166,476	9,707	+	5	1_A375_shLI7_shrus_lncRNA:1:-:2549, 1_A375_shLI7_shrus_lncRNA:1:-:2550, 1_A375_shLI7_shrus_lncRNA:1:-:3650, 2_A375_shLI7_shrus_lncRNA:1:-:3650, 2_A375_shLI7_shrus_lncRNA:1:-:3650	6401, 15163, 6550, 4591, 15999	upstream, downstream, upstream, upstream, us gene, downstream	1	1	16.67	16	3	1_A375_shLI7_shrus_lnc:1	24	Gene: IFI35	IFI35, FLJ21753, IFP35	interferon-induced protein 35	NM_005533, ENST00018, ENST00021, ENST00021	208417_s_at	NP_005524.1, EAW69915.1, EAW69916.1
Gene:ID:9492	VAT1	17	41,169,622	41,174,659	7,837	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2550, 1_A375_shLI7_shrus_lncRNA:1:-:3650, 2_A375_shLI7_shrus_lncRNA:1:-:3650, 2_A375_shLI7_shrus_lncRNA:1:-:3650	607, 11099, 81	ia gene, downstream, us gene	1	1	17.5	17	2	1_A375_shLI7_shrus_lnc:1	24	Gene: VAT1	FLJ32120, VAT1, VAT1	vesicle amine transport protein 1 homolog (T. californica)	NM_006373, ENST00029, ENST00029	208826_s_at	NP_006364.2, EAW69917.1, EAW69918.1
Gene:ID:152	RND2	17	41,177,258	41,184,858	8,600	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2550, 2_A375_shLI7_shrus_lncRNA:1:-:3650, 2_A375_shLI7_shrus_lncRNA:1:-:3650	13396, 2690	downstream, us gene	1	1	24	20	1	1_A375_shLI7_shrus_lnc:1	24	Gene: RND2	RHO7, RhoN, RND2, ARHN	Rho family GTPase 2	NM_005440, ENST00029, ENST00029	212407_at, 214393_at	NP_005431.1, EAW69919.1, EAW69920.1
Gene:ID:100308811	LOC100308811	17	41,447,213	41,466,266	19,053	+	4	1_A375_shLI7_shrus_lncRNA:1:-:2552, 1_A375_shLI7_shrus_lncRNA:1:-:2553, 2_A375_shLI7_shrus_lncRNA:1:-:3656, 2_A375_shLI7_shrus_lncRNA:1:-:3656	27462, 26784, 27466, 26762	downstream, downstream, downstream, downstream	1	1	29	32.5	2	2_A375_shLI7_plus_lncRNA:1	36	Gene: LOC100308811	DKFZp686H1618, FLJ41591, FLJ10727	hypothetical LOC100130551	NR_023612, NR_027413		
Gene:ID:6599	MIR2117	17	41,522,174	41,522,253	79	+	1	2_A375_shLI7_shrus_lncRNA:1:-:3662	-1654	upstream	0	1	15	19	1	2_A375_shLI7_plus_lncRNA:1	19	Gene: MIR2117	MIR2117	microRNA 2117	NR_031751		
Gene:ID:659	DHX8	17	41,561,334	41,601,660	40,326	+	2	1_A375_shLI7_shrus_lncRNA:1:-:2554, 2_A375_shLI7_shrus_lncRNA:1:-:3662	-150, -116	upstream, upstream	1	1	45	27	1	1_A375_shLI7_shrus_lnc:1	45	Gene: DHX8	PRP22, DEAH, HRH1, PRP22, DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	NM_004941, ENST00152, ENST00158, ENST00158, ENST00158	202334_at, 227079_at	NP_004932.2, EAW69976.1, EAW69978.1, EAW69979.1, EAW69980.1
Gene:ID:54435	NARG5	17	42,062,032	42,099,436	8,404	+	1	2_A375_shLI7_shrus_lncRNA:1:-:2554	10304	downstream	0	1	20	30	1	2_A375_shLI7_plus_lncRNA:1	30	Gene: NARG5	NARG5, ARGA, ASA5, MGC133025	N-acetylglutamate synthase	NM_139099, ENST00147	1554832_at	NP_665511.1, EAW69982.1
Gene:ID:4136	TMEM101	17	42,095,556	42,092,345	3,788	-	1	2_A375_shLI7_shrus_lncRNA:1:-:2554	6	ia gene	0	1	20	30	1	2_A375_shLI7_plus_lncRNA:1	30	Gene: TMEM101	MGC4251, FLJ23927, TMEM101	transmembrane protein 101	NM_032376, ENST00280, ENST00280, ENST00280, ENST00280	225004_at	NP_115732.1, EAW69982.1, EAW69981.1
Gene:ID:9314	HDAC5	17	42,158,121	42,201,014	46,893	-	2	1_A375_shLI7_shrus_lncRNA:1:-:2555, 2_A375_shLI7_shrus_lncRNA:1:-:3663	-266, -350	upstream, upstream	1	1	26	15	1	1_A375_shLI7_shrus_lnc:1	26	Gene: HDAC5	HD5, HDAC5, FLJ00018, NY-CO-9	histone deacetylase 5	NM_005474, NM_001015053, NM_001015054, ENST00280, ENST00280, ENST00280	202553_at, 224405_at	NP_005465.2, NP_001015053.1, EAW69833.1, EAW69834.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Internal Transcripts	Internal Dists to start	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ENSG00000166913	C17orf53	17	42,219,274	42,239,844	20,570	+	4	1_A270_uN17_chr17_:40RN:1-:2556,1_A270_uN17_chr17_:40RN:1-:2557,2_A270_uN17_chr17_:1-:3696,2_A270_uN17_chr17_:1-:3697	-3629, 22, -3376, 6	upstream, utr gene, upstream, utr gene	1	1	16	16	2	2_A270_uN17_chr17_:40RN:1-	26	Gene C17orf53	MGC33130, C17orf53, FLJ11594	Chromosome 17 open reading frame 53	NM_001171251, NM_024032, NCT19326991, NCT19327001, NCT21478121, NCT23524620	216879_s_at	NP_001164722.1, NP_076927.2, EAW51629.1, EAW51630.1, EAW51631.1, EAW51632.1
Gene:ENSG00000005421	UBTF	17	42,262,401	42,296,250	33,849	-	2	1_A270_uN17_chr17_:40RN:1-:2555,2_A270_uN17_chr17_:1-:3695	-550, 12234	upstream, utr gene	1	1	17.5	14.5	2	1_A270_uN17_chr17_:40RN:1-	20	Gene UBTF	UBTF, UBF, NOR-90	nucleolar binding transcription factor, RNA polymerase I	NM_001076554, NM_001076553, NM_014233, NCT19326791, NCT19326801, NCT21478912, NCT23528002, NCT23528012	1555215_s_at, 202622_s_at, 214551_s_at	NP_001070152.1, NP_001070151.1, NP_055845.1, EAW51617.1, EAW51618.1, EAW51619.1, EAW51620.1, EAW51621.1
Gene:ENSG00000109930	RUNDC3A	17	42,365,827	42,399,938	10,111	+	9	1_A270_uN17_chr17_:40RN:1-:2559,1_A270_uN17_chr17_:1-:2560,1_A270_uN17_chr17_:1-:2561,1_A270_uN17_chr17_:1-:3698,2_A270_uN17_chr17_:1-:3699,2_A270_uN17_chr17_:1-:3700	171, 10,399, 16837, 163, 16345, 16487	upstream, downstream, upstream, downstream, downstream	1	1	32.33	25	3	1_A270_uN17_chr17_:40RN:1-	43	Gene RUNDC3A	RUNDC3A, KIF1F-5, KIF1F5, KAP2IP	RUN domain containing 3A	NM_020930, NM_001134635, NM_001144826, NCT19326821, NCT19326831, NCT21467121, NCT23674410, NCT23524016	209789_s_at, 213438_x_at	NP_065981.1, NP_001123251.1, NP_001130780.1, EAW51608.1, EAW51609.1, EAW51612.1, EAW51610.1, EAW51611.1
Gene:ENSG00000161928	SLC25A20	17	42,399,993	42,402,217	2,224	-	4	1_A270_uN17_chr17_:40RN:1-:2560,1_A270_uN17_chr17_:1-:2561,1_A270_uN17_chr17_:1-:3676,1_A270_uN17_chr17_:1-:3677	-76, -2187, -55, -2187	upstream, downstream, upstream, upstream	1	1	27.5	33.5	2	1_A270_uN17_chr17_:40RN:1-	43	Gene SLC25A20	CG169, CGI69, SLC25A39, FLJ22497	solute carrier family 25, member 20	NM_001143760, NM_018616, NCT19944526, NCT19944536, NCT19944601, NCT19944612, NCT20629273	223649_s_at	NP_001137252.1, NP_061100.1, EAW51602.1, EAW51603.1, EAW51605.1, EAW51607.1, EAW51604.1, EAW51605.1
Gene:ENSG00000141252	GPATCH8	17	42,472,645	42,580,857	108,212	+	1	2_A270_uN17_chr17_:1-:3672	253	at gene	0	1	11	19	1	2_A270_uN17_chr17_:1-	19	Gene GPATCH8	GPATCH8, KIAA0553, GPATC8	G patch domain containing 8	NM_001029909, NR_039074, NCT21481	212683_at, 212687_at	NP_001082809.1, EAW51593.1
Gene:ENSG00000141179	PZD2	17	42,634,923	42,636,897	1,982	+	2	1_A270_uN17_chr17_:40RN:1-:2562,1_A270_uN17_chr17_:1-:2673	-525, -787	upstream, upstream	1	1	16	16	1	2_A270_uN17_chr17_:40RN:1-	16	Gene PZD2	PZD2, Pd2		NM_001466, NCT19766851	219220_at	NP_001443.1, EAW51591.1
Gene:ENSG00000154665	CCDC43	17	42,754,603	42,767,165	12,380	-	2	1_A270_uN17_chr17_:40RN:1-:2563,2_A270_uN17_chr17_:1-:3674	-142, -25	upstream, upstream	1	1	14	20	1	2_A270_uN17_chr17_:40RN:1-	20	Gene CCDC43	FLJ31795, CCDC43	coiled-coil domain containing 43	NM_001099225, NM_144859, NCT19899125, NCT21716512	228407_at	NP_001092695.1, NP_653210.2, EAW51588.1, EAW51589.1
Gene:ENSG00000141179	DBF4B	17	42,765,976	42,829,832	63,856	+	2	1_A270_uN17_chr17_:40RN:1-:2564,1_A270_uN17_chr17_:1-:3675	8, 40	at gene, utr gene	1	1	18	31	1	2_A270_uN17_chr17_:40RN:1-	31	Gene DBF4B	MGC15009, chiffi, ASKL1, DRF1, ZDBF1B, DBF4B, CHIFB, FLJ13087	DBF4 homolog B (S. cerevisiae)	NM_025104, NM_145899, NCT23445131, NCT23445521, NCT23445531, NCT23445541, NCT23465320, NCT23524722, NCT23524732	1555215_at, 209861_at, 209862_s_at, 235157_at	NP_079583.1, NP_663599.1, EAW51551.1, EAW51552.1, EAW51553.1, EAW51554.1, EAW51571.1, EAW51582.1, EAW51583.1, EAW51584.1, EAW51585.1
Gene:ENSG00000141179	EFTUD2	17	42,827,655	42,976,893	149,238	-	1	2_A270_uN17_chr17_:40RN:1-:3676	113	at gene	0	1	23	20	1	2_A270_uN17_chr17_:40RN:1-	20	Gene EFTUD2	Snrp116, EFTUD2, U5-116KD, FLJ46855, Snrp116, KIAA0031, DKFZp686E24196	elongation factor Tu GTP binding domain containing 2	NM_004247, NM_001134605, NCT19326, NCT19326, NCT23524770	223397_at, 223398_s_at	NP_004238.2, NP_001130077.1, EAW51570.1, EAW51574.1
Gene:ENSG00000141252	CCDC103	17	42,977,154	42,980,629	3,476	+	1	2_A270_uN17_chr17_:40RN:1-:3679	-274	upstream	0	1	23	20	1	2_A270_uN17_chr17_:40RN:1-	20	Gene CCDC103	FLJ36311, FLJ10364, CCDC103	coiled-coil domain containing 103	NM_213607, NCT19153522	227977_at	NP_998772.1, EAW51572.1
Gene:ENSG00000141179	GPAP	17	42,982,093	42,992,614	9,521	-	1	2_A270_uN17_chr17_:40RN:1-:3676	16034	downstream	0	1	23	20	1	2_A270_uN17_chr17_:40RN:1-	20	Gene GPAP	GPAP, PLMS472	glial maturation factor beta	NM_002555, NM_001123010, NCT19326, NCT19326521, NCT19326541, NCT21478752, NCT23524752	203580_at, 226239_at	NP_002546.1, NP_001124691.1, EAW51567.1, EAW51568.1, EAW51570.1, EAW51571.1, EAW51599.1
Gene:ENSG00000141179	KIF15B	17	43,003,446	43,025,682	21,824	-	1	2_A270_uN17_chr17_:40RN:1-:3677	-166	upstream	0	1	13	25	1	2_A270_uN17_chr17_:40RN:1-	25	Gene KIF15B	KIF15B	kinesin family member 15B	NM_020535.3, NCT19326, NCT19326, NCT23524, NCT23524	220029_at	NP_065584.2, NP_001073312.1
Gene:ENSG00000141179	DCAKD	17	43,100,706	43,158,473	57,767	-	1	2_A270_uN17_chr17_:40RN:1-:3678	-247	upstream	0	1	20	23	1	2_A270_uN17_chr17_:40RN:1-	23	Gene DCAKD	FLJ22655, DCAKD	dephospho-CoA kinase domain containing	NM_024819, NM_001128831, NCT19326971, NCT19944221, NCT21716853, NCT21716872, NCT23524703	221224_s_at, 221225_at, 224522_s_at	NP_079095.2, NP_001121633.1, EAW51590.1, EAW51591.1, EAW51592.1, EAW51593.1
Gene:ENSG00000141179	NMT1	17	43,130,660	43,169,284	47,764	+	1	2_A270_uN17_chr17_:40RN:1-:3678	40	at gene	0	1	20	23	1	2_A270_uN17_chr17_:40RN:1-	23	Gene NMT1	NMT1, NMT1	N-myristoyltransferase 1	NM_021079, NCT19218.2, NCT19326551, NCT19326561, NCT19326571, NCT23524712	201197_s_at, 201198_s_at, 201199_s_at	NP_066953.1, EAW51554.1, EAW51555.1, EAW51556.1, EAW51557.1
Gene:ENSG00000141179	ACSL6	17	43,209,997	43,221,843	11,876	+	1	2_A270_uN17_chr17_:40RN:1-:3679	13251	downstream	0	1	28	36	1	2_A270_uN17_chr17_:40RN:1-	36	Gene ACSL6	HRSP70700, FLJ13222, FLJ60623, ACSL6	acyl-CoA synthetase family member 6	NM_001130704, NM_024722, NM_001130705, NM_001130706, NM_001130707, NCT19326, NCT19326, NCT19326911, NCT19326921, NCT23529811, NCT23529821	219813_at	NP_001123176.1, NP_079095.1, NP_001123177.1, NP_001123178.1, NP_001123179.1, EAW51552.1, EAW51545.1, EAW51546.1, EAW51550.1, EAW51551.1
Gene:ENSG00000141179	HEXIM1	17	43,224,664	43,229,466	4,764	-	2	1_A270_uN17_chr17_:40RN:1-:2563,1_A270_uN17_chr17_:1-:2564,2_A270_uN17_chr17_:1-:3680,2_A270_uN17_chr17_:1-:3681	14164, 864	downstream, at gene	1	1	34.5	24.5	2	2_A270_uN17_chr17_:40RN:1-	26	Gene HEXIM1	PRIP, HEXIM1, MAQI1, HIS1, CLP1, HEXIM1	thioredoxin like double domain containing 1	NM_006460	202414_s_at, 202415_s_at, 214156_at, 214157_at	NP_006451.1
Gene:ENSG00000141179	HEXIM2	17	43,235,264	43,247,406	9,142	+	4	1_A270_uN17_chr17_:40RN:1-:2563,1_A270_uN17_chr17_:1-:2564,1_A270_uN17_chr17_:1-:2565,2_A270_uN17_chr17_:1-:3680,2_A270_uN17_chr17_:1-:3681	1558, 11784, 10036, 11003	at gene, downstream, downstream, downstream	1	1	20	23.33	3	2_A270_uN17_chr17_:40RN:1-	34	Gene HEXIM2	PIP3-E, HEXIM2, L3	thioredoxin like double domain containing 2	NM_148958, NCT19218.2, NCT19326581	219387_at, 240798_at	NP_653209.1, EAW51542.1, EAW51541.1
Gene:ENSG00000205932	LOC100505672	17	43,246,167	43,248,852	2,685	-	4	1_A270_uN17_chr17_:40RN:1-:2563,1_A270_uN17_chr17_:1-:2566,1_A270_uN17_chr17_:1-:3680,2_A270_uN17_chr17_:1-:3681	10004, -1195, 1212	downstream, upstream, at gene, upstream	1	1	20	23.33	3	2_A270_uN17_chr17_:40RN:1-	34	Gene LOC100505672		hypothetical LOC100505672	XR_109387		
Gene:ENSG00000161926	MAP3K14	17	43,340,455	43,394,414	53,960	+	1	2_A270_uN17_chr17_:40RN:1-:2567	-242	upstream	1	0	17	16	1	1_A270_uN17_chr17_:40RN:1-	17	Gene MAP3K14	MAP3K14, HSNIK, PTDCR1B, HS_NIK	mitogen-activated protein kinase kinase kinase 14	NM_003954, NCT19745.1, NCT19326.1	203192_at	NP_003945.2, EAW51528.1, EAW51530.1
Gene:ENSG00000261897	LOC100128677	17	43,920,722	43,972,879	52,157	+	4	1_A270_uN17_chr17_:40RN:1-:2568,1_A270_uN17_chr17_:1-:2569,1_A270_uN17_chr17_:1-:3682,2_A270_uN17_chr17_:1-:3683	37,598, 1167, 27199, 1166	at gene, utr gene, at gene, at gene	1	1	20.5	21.5	2	1_A270_uN17_chr17_:40RN:1-	24	Gene LOC100128677		hypothetical LOC100128677	NR_026559		
Gene:ENSG00000141179	MAPT	17	43,971,745	44,105,700	133,852	+	2	1_A270_uN17_chr17_:40RN:1-:2569,2_A270_uN17_chr17_:1-:3684	-26, -15	upstream, upstream	1	1	17	20	1	2_A270_uN17_chr17_:40RN:1-	20	Gene MAPT	MSTD, DDPAC, MAPT, MTBT2, FLJ31424, TAU, MAPTL, MGC135549, MTBT1, PPND, PTDP17	microtubule-associated protein tau	NM_001123066, NM_001123067, NM_005910, NM_016834, NM_016835, NM_016841, NCT19509.2, NCT19746.2, NCT19746.3, NCT19746.4, NCT20120.2, NCT20120.3, NCT20120.4, NCT20120.5, NCT20120.6	203929_s_at, 203930_s_at, 203931_s_at, 205401_s_at, 205378_at	NP_001116535.2, NP_001116539.1, NP_005901.2, NP_058519.1, EAW53565.1, EAW53566.1, EAW53567.1, EAW53568.1, EAW53569.1, EAW53570.1, EAW53571.1, EAW53572.1, EAW53573.1, EAW53574.1
Gene:ENSG00000130164	LDLR	19	11,089,500	11,131,615	42,116	-	1	2_A270_uN17_chr19_:40RN:1-:2570	1	at gene	0	1	11	17	1	2_A270_uN17_chr19_:40RN:1-	17	Gene LDLR	LDLR, FHC	low density lipoprotein receptor	NM_000527, NCT19745.1, NCT19326.1	202352_s_at	NP_000518.1, EAW57652.1, EAW57653.1, EAW57654.1, EAW57655.1, EAW57656.1, EAW57657.1, EAW57658.1, EAW57659.1, EAW57660.1, EAW57661.1, EAW57662.1, EAW57663.1, EAW57664.1, EAW57665.1, EAW57666.1, EAW57667.1, EAW57668.1, EAW57669.1, EAW57670.1, EAW57671.1, EAW57672.1, EAW57673.1, EAW57674.1, EAW57675.1, EAW57676.1, EAW57677.1, EAW57678.1, EAW57679.1, EAW57680.1, EAW57681.1, EAW57682.1, EAW57683.1, EAW57684.1, EAW57685.1, EAW57686.1, EAW57687.1, EAW57688.1, EAW57689.1, EAW57690.1, EAW57691.1, EAW57692.1, EAW57693.1, EAW57694.1, EAW57695.1, EAW57696.1, EAW57697.1, EAW57698.1, EAW57699.1, EAW57700.1
Gene:ENSG00000141179	KIF1C	17	44,000,499	44,018,733	18,267	+	2	1_A270_uN17_chr17_:40RN:1-:2570,2_A270_uN17_chr17_:1-:3685	-61, -166	upstream, upstream	1	1	22	34	1	2_A270_uN17_chr17_:40RN:1-	34	Gene GOSR2	GS27, Bos1, GOSR2	golgi SNAP receptor complex member 2	NM_004287, NM_004287, NM_001012511, NCT23727310, NCT23727320, NCT23727340, NCT23727410, NCT23727420, NCT23532310, NCT23532330	210899_s_at, 212168_at, 212169_s_at, 212206_at, 212207_s_at, 235081_at, 235108_at	NP_073627.1, NP_004278.2, NP_001012529.1, EAW57694.1, EAW57695.1, EAW57699.1, EAW57697.1, EAW57698.1, EAW57700.1
Gene:ENSG00000141179	LOC100130148	17	45,133,972	45,144,654	11,261	-	2	1_A270_uN17_chr17_:40RN:1-:2572,2_A270_uN17_chr17_:1-:3687	54, 56	at gene, utr gene	1	1	26	24	1	2_A270_uN17_chr17_:40RN:1-	26	Gene LOC100506214		hypothetical LOC100506214	XR_111706, XR_109281, XR_115110		
Gene:ENSG00000161926	ITGB3	17	45,331,206	45,360,077	56,869	+	3	1_A270_uN17_chr17_:40RN:1-:2573,1_A270_uN17_chr17_:1-:3688,2_A270_uN17_chr17_:1-:3689	172, 26744, 41496	at gene, utr gene, at gene	1	1	13	15.67	3	2_A270_uN17_chr17_:40RN:1-	19	Gene ITGB3	CD61, ITGB3, GP3A, GPIIIa	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	NM_000212, NCT19745.2, NCT23727350, NCT23727351, NCT23727520	204627_s_at, 204626_s_at, 204628_s_at, 211979_at, 213240_at, 213241_at	NP_000203.2, EAW57682.1, EAW57676.1, EAW57680.1, EAW57681.1
Gene:ENSG00000205932	LOC100506252	17	45,360,626	45,363,051	2,425	+	1	2_A270_uN17_chr17_:40RN:1-:3689	10547	downstream	0	1	11	17	1	2_A270_uN17_chr17_:40RN:1-	17	Gene LOC100506252		hypothetical LOC100506252	XR_109392		
Gene:ENSG00000205932	LOC100506252	17	45,360,626	45,363,051	2,425	-	1	2_A270_uN17_chr17_:40RN:1-:3689	-220, -220	upstream, upstream	1	1	44	56	1	2_A270_uN17_chr17_:40RN:1-	56	Gene LOC100506252		hypothetical LOC100506252	XR_111706, XR_111709, XR_109392, XR_109393, XR_115112, XR_115113		
Gene:ENSG00000161926	SP2	17	45,373,516	46,006,223	32,807	+	2	1_A270_uN17_chr17_:40RN:1-:2577,2_A270_uN17_chr17_:1-:3692	-100, -100	upstream, upstream	1	1	44	56	1	2_A270_uN17_chr17_:40RN:1-	56	Gene SP2	SP2	Sp2 transcription factor	NM_003110, NCT19112.2, NCT19326971, NCT23585071, NCT23586440, NCT23586460, NCT23672440	204367_at, 211706_s_at, 207783_s_at	NP_003101.3, EAW57653.1, EAW57652.1, EAW57654.1, EAW57655.1, EAW57656.1, EAW57657.1, EAW57658.1
Gene:ENSG00000205932	LOC100506323	17	45,376,151	46,016,725	42,574	-	2	1_A270_uN17_chr17_:40RN:1-:2577,2_A270_uN17_chr17_:1-:3692	45317, 45317	downstream, downstream	1	1	44	56	1	2_A270_uN17_chr17_:40RN:1-	56	Gene LOC100506323		hypothetical LOC100506323	XR_111710, XR_109396, XR_115114		
Gene:ENSG00000205932	LOC100506299	17	45,382,479	45,384,629	2,150	+	1	2_A270_uN17_chr17_:40RN:1-:3693	167	at gene	0	1	17	20	1	2_A270_uN17_chr17_:40RN:1-	20	Gene CDK5RAP2	CNJ5/mrd_114, CDK5RAP2, KIS3, HEP27, CS3, LZAP, MSTO16	CDK5 regulatory subunit associated protein 2	NM_178096, NCT19909.1, NCT19909.2, NCT19909.3, NCT19909.4, NCT19909.5, NCT23529.2, NCT23672.2, NCT23672.3, NCT23672.4	218703_s_at	NP_785776.1, EAW54774.1, EAW54772.1, EAW54773.1, EAW54776.1, EAW54778.1, EAW54777.1
Gene:ENSG00000205932	COPZ2	17	45,103,533	45,115,152	11,619	-	2	1_A270_uN17_chr17_:40RN:1-:2575,2_A270_uN17_chr17_:1-:3694	-9936, 10096	upstream, upstream	1	1	19	15	1	2_A270_uN17_chr17_:40RN:1-	19	Gene COPZ2	COPZ2, MGC23006	coatomer protein complex, subunit zeta 2	NM_016429, NCT23551.2	214561_at, 235927_at	NP_057513.1, EAW57669.1
Gene:ENSG00000161926	NPEZL1	17	46,133,696	46,155,807	12,221	+	2	1_A270_uN17_chr17_:40RN:1-:2576,2_A270_uN17_chr17_:1-:3695	-590, -455	upstream, upstream	1	1	19	15	1	2_A270_uN17_chr17_:40RN:1-	19	Gene NPEZL1	LCRI-P1, NRPI, TCP11, FLJ00350, NPEZL1	nuclear factor (erythroid-derived 2)-like 1	NM_032308, NCT19653.1, NCT19653.2, NCT20510.2, NCT23586510, NCT23586520, NCT23672710	203755_s_at, 203799_s_at, 214179_s_at	NP_001241.1, EAW57662.1, EAW57664.1, EAW57665.1, EAW57667.1, EAW57663.1
Gene:ENSG00000161926	CBX1	17	46,147,414	46,176,663	31,469	+	2	1_A270_uN17_chr17_:40RN:1-:2578,2_A270_uN17_chr17_:1-:3695	-28, -8266	upstream, upstream	1	1	12.5	14.5	2	1_A270_uN17_chr17_:40RN:1-	16	Gene CBX1	CBX1, CBX, MOD1, HP1-BETA, HP1Hs-beta, p25beta, MOD1	chromobox homolog 1	NM_001127228, NM_006807, NCT23842240, NCT23842250, NCT23842270, NCT23573230	201516_at	NP_001120700.1, NP_006798.1, EAW54795.1, EAW54796.1, EAW54797.1, EAW54798.1
Gene:ENSG00000205932	SNX11	17	46,164,620	46,200,165	10,183	+	2	1_A270_uN17_chr17_:40RN:1-:2578,2_A270_uN17_chr17_:1-:3695	-8008, 221	upstream, at gene	1	1	12.5	14.5	2	1_A270_uN17_chr17_:40RN:1-	16	Gene SNX11	MGC11019, SNX11	sorting nexin 11	NM_013323, NM_152248, NCT19653.1, NCT19653668.1, NCT20509.2, NCT23573010, NCT23573220	220140_s_at, 220141_at	NP_037455.2, NP_689438.1, EAW54752.1, EAW54753.1, EAW54754.1, EAW54757.1, EAW54755.1
Gene:ENSG00000242265	SCG_2042066	17	46,667,823	46,683,776	15,953	+	2	1_A270_uN17_chr17_:40RN:1-:2580,2_A270_uN17_chr17_:1-:3696	20017, 20209	downstream, downstream	1	1	19	15	1	2_A270_uN17_chr17_:40RN:1-	16	Gene SCG_2042066	LOC650366	hypothetical LOC650366	NM_032201, NR_033252, NR_033202, NR_033203, NR_033204, NR_033205	230743_at, 239791_at	
Gene:ENSG00000205932	HOXB6	17	46,673,099	46,682,334	9,235	+	2	1_A270_uN17_chr17_:40RN:1-:2580,2_A270_uN17_chr17_:1-:3696	-9395, 9695	upstream, upstream	1	1	16	16	1	2_A270_uN17_chr17_:40RN:1-	16	Gene HOXB6	Hox-2.2, HOX2, HU-2, HOXB6, HOX2B	homeobox B6	NM_018952	203365_at, 203366_s_at	NP_061529.2
Gene:ENSG00000205932	HOXB7	17	46,684,094	46,695,263	3,769	+	2	1_A270_uN17_chr17_:40RN:1-:2580,2_A270_uN17_chr17_:1-:3696	643, 351	at gene, at gene	1	1	16	16	1	2_A270_uN17_chr17_:40RN:1-	16	Gene HOXB7	HOXB7, HOX2, HHO.C1, Hox-2.3, HOXJC	homeobox B7	NM_004502, NCT20519.1, NCT22982.1	204713_s_at, 204779_s_at, 216972_s_at	NP_004493.2, EAW54725.1, EAW54726.1
Gene:ENSG00000205932	HOXB8	17	46,689,705	46,692,201	2,592	+	2	1_A270_uN17_chr17_:40RN:1-:2580,2_A270_uN17_chr17_:1-:3696	4061, 4261	downstream, downstream	1	1	16	16	1	2_A270_uN17_chr17_:40RN:1-	16	Gene HOXB8	HOX2, HOX8B, Hox-2.4, HOX2D	homeobox B8	NM_024016, NCT19653.1, NCT19653.2, NCT19653.3	221276_at, 224967_s_at, 230114_at	NP_076921.1, EAW54723.1, EAW54724.1
Gene:ENSG00000205932	PRAC	17	46,799,051	46,799,652	601	-	1	2_A270_uN17_chr17_:40RN:1-:2581	-1334	upstream	1	0	20	19	1	1_A270_uN17_chr17_:40RN:1-	20	Gene PRAC	C17orf62, PRAC, MGC32520	prostate cancer susceptibility candidate	NM_032391, NCT19103040.0	230764_at	NP_115767.1, EAW54717.1
Gene:ENSG00000205932	C17orf62	17	46,800,542	46,802,119	1,577	+	1	2_A270_uN17_chr17_:40RN:1-:2581	874	at gene	0	1	20	19	1	2_A270_uN17_chr17_:40RN:1-	20	Gene C17orf62	PRAC2, C17orf62, NCRNA00252	chromosome 17 open reading frame 62	NR_026103	230565_at	
Gene:ENSG00000264290	MIR3165	17	46,801,770	46,801,837	67	+	1	2_A270_uN17_chr17_:40RN:1-:2581	621	downstream	1	0	20	19	1	2_A270_uN17_chr17_:40RN:1-	20	Gene MIR3165	MIR3165	microRNA 3165	NR_036150		
Gene:ENSG00000205932	HOXB13	17	46,802,125	46,806,111	3,986	+	1	2_A270_uN17_chr17_:40RN:1-:2581	4693	downstream	1	0	20	19	1	2_A270_uN17_chr17_:40RN:1-	20	Gene HOXB13	PSGD, HOXB13	homeobox B13	NM_006361, NCT19103597.2	209564_at, 209565_at	NP_006352.2, EAW54714.1
Gene:ENSG00000205932	SNRE	17	47,007,455	47,022,154	14,699	+	1	2_A270_uN17_chr17_:40RN:1-:2587	-150	upstream	0	1	16	20	1	2_A270_uN17_chr17_:40RN:1-	20	Gene SNRE	DX1, VPS22, SNRE, EAP30	SNRE, ESCRT-II complex subunit, homolog (S. cerevisiae)	NM_007241, NCT19848.2, NCT19953.1, NCT23737.2	218391_at, 242790_at	NP_009172.2, EAW54699.1, EAW54698.1, EAW54700.1
Gene:ENSG00000205932	QIP	17	47,033,918	47,043,855	10,027	-	1	2_A270_uN17_chr17_:40RN:1-:2588	-3901	upstream	0	1	11	21	1	2_A270_uN17_chr17_:40RN:1-	21	Gene QIP	QIP	glutamine-rich protein	NM_024122, NCT19944.2	227699_at	NP_076411.1, EAW54687.1
Gene:ENSG00000254877	PLA2G16	17	47,329,603	47,339,627	10,422	+	1	2_A270_uN17_chr17_:40RN:1-:2130	12267	downstream	0	1	10	15	1	2_A270_uN17_chr17_:40RN:1-	15	Gene PLA2G16	PLA2G16	hypothetical PLA2G16	NR_026161, NCT23585.2		EAW56553.1
Gene:ENSG00000205932	SLC35B1	17	47,778,690	47,783,282	6,592	-	2	1_A270_uN17_chr17_:40RN:1-:2583,2_A270_uN17_chr17_:1-:3702	-286, -286	upstream, upstream	1	1	46	56	1	2_A270_uN17_chr17_:40RN:1-	56	Gene SLC35B1	SLC35B1, UGTREL1	solute carrier family 35, member B1	NM_005827, NCT19610.2, NCT19610612, NCT19610622, NCT19610632, NCT23577552	202433_at	NP_005816.1, EAW54668.1, EAW54666.1, EAW54667.1, EAW54669.1, EAW54670.1
Gene:ENSG00000205932	FAM117A	17	47,787,687	47,841,516	53,831	-	2	1_A270_uN17_chr17_:40RN:1-:2583,2_A270_uN17_chr17_:1-:3702	55592, 55592	downstream, downstream	1	1	46	56	1	2_A270_uN17_chr17_:40RN:1-	56	Gene FAM117A	FAM117A		NM_032822, NCT19610.2, NCT19610612, NCT19610622, NCT19610632	221229_s_at	NP_116234.1, EAW54662.1, EAW54663.1, EAW54664.1
Gene:ENSG00000141179	MYST2	17	47,866,071	47,906,455	40,387	+	1	2_A270_uN17_chr17_:40RN:1-:2702	57	at gene	0	1	10	21	1	2_A270_uN17_chr17_:40RN:1-	21	Gene MYST2	HBOA, HAT7, HBO1, MYST2	MYST histone acetyltransferase 2	NM_007067, NCT22982.3, NCT22982650, NCT23577440, NCT23577460	203099_at	NP_008997.1, EAW54658.1, EAW54659.1, EAW54660.1, EAW54661.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:284060	LOC284060	17	48,127,713	48,133,103	5,390	-	1	2_A375_pNL97_plus_lncRNA::1::3705	8991	downstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC284060		hypothetical LOC284060	XR_111715, XR_109401, XR_115119	1557607_at, 1557608_a_at	
GeneID:3675	ITGA3	17	48,133,340	48,167,849	34,509	+	3	1_A375_pNL7_minus_lncRNA::1::2585, 2_A375_pNL97_plus_lncRNA::1::3705, 2_A375_pNL97_plus_lncRNA::1::3706	39236, -9228, 39204	downstream, upstream, downstream	1	1	17	22.5	2	2_A375_pNL97_plus_lncRNA::1	30	Gene ITGA3	VL3A, VLA3a, VCA-2, ITGA3, MSK18, GAP-B3, FLJ34631, FLJ34704, GAPB3, CD49C	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	NM_005501, NM_002204, hCT1960621.1, hCT1960622.1, hCT20771.3, hCT2286289.0	201474_s_at	NP_005492.1, NP_002195.1, EAW94645.1, EAW94646.1, EAW94647.1, EAW94648.1
GeneID:5164	PDK2	17	48,172,696	48,188,423	15,727	+	2	1_A375_pNL7_minus_lncRNA::1::2585, 2_A375_pNL97_plus_lncRNA::1::3706	-120, -152	upstream, upstream	1	1	24	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene PDK2	PDK2, PDHK2	pyruvate dehydrogenase kinase, isozyme 2	NM_002611, hCT1960660.1, hCT20774.3, hCT2357769.0	202590_s_at, 213724_s_at	NP_002602.2, EAW94643.1, EAW94642.1, EAW94644.1
GeneID:84687	PPP1R9B	17	48,211,101	48,227,877	16,776	-	2	1_A375_pNL7_minus_lncRNA::1::2586, 2_A375_pNL97_plus_lncRNA::1::3707	-1563, -1563	upstream, upstream	1	1	30	27	1	1_A375_pNL7_minus_lncRNA::1	30	Gene PPP1R9B	PPP1R9B, FLJ30345, Spn, PPP1R6, SPINO, PPP1R9	protein phosphatase 1, regulatory (inhibitor) subunit 9B	NM_032595, hCT1965674.1, hCT20777.3, hCT2285191.0	225124_at, 230455_at	NP_115984.3, EAW94638.1, EAW94636.1, EAW94637.1
GeneID:55379	LRRC59	17	48,458,594	48,474,914	16,320	-	2	1_A375_pNL7_minus_lncRNA::1::2587, 2_A375_pNL97_plus_lncRNA::1::3708	66, 34	in gene, in gene	1	1	29	24	1	1_A375_pNL7_minus_lncRNA::1	29	Gene LRRC59	PRO1855, FLJ21675, LRRC59	leucine rich repeat containing 59	NM_018509, hCT18556.3, hCT1961413.1	1569371_at, 222231_s_at, 234812_at	NP_060979.2, EAW94616.1, EAW94615.1
GeneID:80221	ACSF2	17	48,503,519	48,552,200	48,681	+	4	1_A375_pNL7_minus_lncRNA::1::2588, 1_A375_pNL7_minus_lncRNA::1::2589, 2_A375_pNL97_plus_lncRNA::1::3709, 2_A375_pNL97_plus_lncRNA::1::3710	52609, 56481, 52625, 56449	downstream, downstream, downstream, downstream	1	1	42	39.5	2	1_A375_pNL7_minus_lncRNA::1	55	Gene ACSF2	FLJ20920, ACSMW, AVYV493, ACSF2	acyl-CoA synthetase family member 2	NM_025149, hCT20806.3	218844_at	NP_079425.3, EAW94612.1
GeneID:1101	CHAD	17	48,541,853	48,546,227	4,374	-	2	1_A375_pNL7_minus_lncRNA::1::2588, 2_A375_pNL97_plus_lncRNA::1::3709	-9901, -9917	upstream, upstream	1	1	55	53	1	1_A375_pNL7_minus_lncRNA::1	55	Gene CHAD	SLRR4A, CHAD	chondroadherin	NM_001267, hCT20807.3, hCT2357768.0	206869_at	NP_001258.2, EAW94614.1, EAW94613.1
GeneID:55316	RSAD1	17	48,556,190	48,563,336	7,146	+	4	1_A375_pNL7_minus_lncRNA::1::2588, 1_A375_pNL7_minus_lncRNA::1::2589, 2_A375_pNL97_plus_lncRNA::1::3709, 2_A375_pNL97_plus_lncRNA::1::3710	-62, 3810, -46, 3778	upstream, in gene, upstream, in gene	1	1	42	39.5	2	1_A375_pNL7_minus_lncRNA::1	55	Gene RSAD1	FLJ11164, FLJ20975, RSAD1	radical S-adenosyl methionine domain containing 1	NM_018346, hCT20809.3	218307_at	NP_060816.1, EAW94610.1
GeneID:8714	ABCC3	17	48,712,218	48,769,063	56,845	+	1	2_A375_pNL97_plus_lncRNA::1::3711	4406	in gene	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ABCC3	ABC31, cMOAT2, DKFZp686E22157, MLP2, EST90757, MRP3, ABCC3, MOAT-D	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	NM_003786, NM_001144070, hCT1960215.1, hCT1961416.1, hCT1971661.1, hCT1971662.1, hCT20800.3	208161_s_at, 209641_s_at, 214979_at, 230682_x_at, 239217_x_at, 242553_at	NP_003777.2, NP_001137542.1, EAW94590.1, EAW94591.1, EAW94593.1, EAW94594.1, EAW94592.1
GeneID:51747	LUC7L3	17	48,796,926	48,830,072	33,146	+	1	2_A375_pNL97_plus_lncRNA::1::3712	210	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LUC7L3	CREAP-1, CRA, LUC7A, CROP, OA48-18, LUC7L3, hLuc7A	LUC7-like 3 (S. cerevisiae)	NM_016424, NM_006107, hCT1960623.1, hCT1960624.1, hCT1960625.1, hCT20801.2, hCT2286212.0	203804_s_at, 208835_s_at, 220044_x_at	NP_057508.2, NP_006098.2, EAW94583.1, EAW94584.1, EAW94585.1, EAW94587.1, EAW94586.1
GeneID:10140	TOB1	17	48,939,584	48,941,413	1,829	-	1	2_A375_pNL97_plus_lncRNA::1::3713	-2187	upstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TOB1	MGC34446, PIG49, TROB1, MGC104792, APRO6, TOB, TOB1, TROB	transducer of ERBB2, 1	NM_005749, hCT1639885.3, hCT2284901.0	202704_at, 228834_at	NP_005740.1, EAW94577.1, EAW94578.1
GeneID:400604	LOC400604	17	48,943,897	48,945,745	1,848	+	1	2_A375_pNL97_plus_lncRNA::1::3713	-297	upstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC400604		hypothetical LOC400604	XR_111718, XR_109405, XR_115123	241405_at	
GeneID:100506609	LOC100506609	17	49,012,350	49,022,074	9,724	-	1	1_A375_pNL7_minus_lncRNA::1::2590	11050	downstream	1	0	20	13	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100506609		hypothetical LOC100506609	XR_109406		
GeneID:654364	NME1-NME2	17	49,230,920	49,249,105	18,185	+	2	2_A375_pNL97_plus_lncRNA::1::3715, 2_A375_pNL97_plus_lncRNA::1::3716	24, 13304	in gene, in gene	0	1	18	25.5	2	2_A375_pNL97_plus_lncRNA::1	31	Gene NME1-NME2	NMELV, NME2, FLJ83990, NME1-NME2	NME1-NME2 readthrough	NM_001018136		NP_001018146.1
GeneID:4830	NME1	17	49,230,920	49,239,450	8,530	+	2	2_A375_pNL97_plus_lncRNA::1::3715, 2_A375_pNL97_plus_lncRNA::1::3716	24, 13304	in gene, downstream	0	1	18	25.5	2	2_A375_pNL97_plus_lncRNA::1	31	Gene NME1	NME1, NM23-H1, NB, NBS, NDKA, AWD, NDPKA, NM23, NDPK-A, GAAD	non-metastatic cells 1, protein (NM23A) expressed in	NM_000269, NM_198175	201577_at, 222038_s_at	NP_000260.1, NP_937818.1
GeneID:4831	NME2	17	49,242,891	49,249,105	6,214	+	1	2_A375_pNL97_plus_lncRNA::1::3716	1333	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene NME2	NDKB, NM23-H2, puf, NME2, NDPK-B, NM23B, PUF, MGC2212, NDPKB, MGC111212	non-metastatic cells 2, protein (NM23B) expressed in	NM_001018137, NM_002512, NM_001018138, NM_001018139	201268_at	NP_001018147.1, NP_002503.1, NP_001018148.1, NP_001018149.1
GeneID:54799	MBTD1	17	49,254,786	49,337,427	82,641	-	3	1_A375_pNL7_minus_lncRNA::1::2591, 2_A375_pNL97_plus_lncRNA::1::3716, 2_A375_pNL97_plus_lncRNA::1::3717	-173, 83203, -141	upstream, downstream, upstream	1	1	29.5	30	2	1_A375_pNL7_minus_lncRNA::1	46	Gene MBTD1	FLJ42067, SA49P01, FLJ20055, MBTD1, MGC126785	mbt domain containing 1	NM_017643, hCT1815785.1, hCT20813.3, hCT2284886.0	207115_x_at	NP_060113.2, EAW94560.1, EAW94561.1, EAW94562.1
GeneID:51096	UTP18	17	49,337,897	49,375,284	37,387	+	2	1_A375_pNL7_minus_lncRNA::1::2591, 2_A375_pNL97_plus_lncRNA::1::3717	-297, -329	upstream, upstream	1	1	46	40	1	1_A375_pNL7_minus_lncRNA::1	46	Gene UTP18	CGI-48, UTP18, WDR50	UTP18, small subunit (SSU) processome component, homolog (yeast)	NM_016001, hCT20805.3	203721_s_at	NP_057085.2, EAW94559.1
GeneID:56934	CA10	17	49,707,674	50,237,377	529,703	-	1	2_A375_pNL97_plus_lncRNA::1::3719	-959	upstream	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CA10	HUCEP-15, CARPX, CA-RPX, CA10	carbonic anhydrase X	NM_020178, NM_001082533, NM_001082534, hCT18555.3	220889_s_at, 223550_s_at	NP_064563.1, NP_001076002.1, NP_001076003.1, EAW94558.1
GeneID:252983	STXBP4	17	53,046,126	53,241,449	195,323	+	2	1_A375_pNL7_minus_lncRNA::1::2592, 2_A375_pNL97_plus_lncRNA::1::3720	193602, 193570	in gene, in gene	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene STXBP4	MGC50337, Synip, MGC149829, FLJ16496, STXBP4	syntaxin binding protein 4	NM_178509, hCT1813660.2, hCT2284582.1	1554328_at, 1554329_x_at, 237706_at, 244404_at	NP_848604.3, EAW94545.1, EAW94546.1
GeneID:162282	ANKFN1	17	54,230,836	54,560,007	329,171	+	1	2_A375_pNL97_plus_lncRNA::1::3722	167228	in gene	0	1	4	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ANKFN1	FLJ38335, ANKFN1	ankyrin-repeat and fibronectin type III domain containing 1	NM_153228, hCT2283423.1, hCT2348941.0, hCT2357737.0	1553211_at, 1559640_at	NP_694960.2, EAW94530.1, EAW94531.1, EAW94532.1
GeneID:7706	TRIM25	17	54,965,270	54,991,409	26,139	-	1	2_A375_pNL97_plus_lncRNA::1::3723	609	in gene	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TRIM25	RNF147, Z147, TRIM25, EFP, ZNF147	tripartite motif containing 25	NM_005082, hCT1961032.2, hCT2283528.1, hCT24575.3	206911_at, 224806_at	NP_005073.2, EAW94524.1, EAW94523.1, EAW94525.1
GeneID:8165	AKAP1	17	55,162,553	55,198,710	36,157	+	1	2_A375_pNL97_plus_lncRNA::1::3724	-345	upstream	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene AKAP1	D-AKAP1, AKAP1, MGC1807, AKAP121, AKAP84, AKAP149, PRKA1, AKAP, SAKAP84	A kinase (PRKA) anchor protein 1	NM_003488, hCT1952719.1, hCT1952720.1, hCT2284104.0, hCT24573.2	201674_s_at, 201675_at, 210625_s_at, 210626_at	NP_003479.1, EAW94515.1, EAW94516.1, EAW94517.1, EAW94518.1
GeneID:124540	MSI2	17	55,333,931	55,757,299	423,368	+	1	2_A375_pNL97_plus_lncRNA::1::3726	224341	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MSI2	MGC3245, MSI2, FLJ36569, MSI2H	musashi homolog 2 (Drosophila)	NM_138962, NM_170721, hCT2284107.1, hCT2284108.1, hCT2284109.1, hCT2344971.1, hCT2346173.0, hCT2346174.0, hCT2357731.0	1552364_s_at, 225233_at, 225237_s_at, 225238_at, 225240_s_at, 239232_at, 243010_at, 243579_at	NP_620412.1, NP_733839.1, EAW94506.1, EAW94508.1, EAW94511.1, EAW94512.1, EAW94507.1, EAW94509.1, EAW94510.1
GeneID:51649	MRPS23	17	55,916,842	55,927,399	10,557	-	2	1_A375_pNL7_minus_lncRNA::1::2594, 2_A375_pNL97_plus_lncRNA::1::3727	-89, -105	upstream, upstream	1	1	92	88	1	1_A375_pNL7_minus_lncRNA::1	92	Gene MRPS23	CGI-138, MRP-S23, HSPC329, MRPS23	mitochondrial ribosomal protein S23	NM_016070, hCT23419.3	223156_at	NP_057154.2, EAW94503.1
GeneID:6426	SFRS1	17	56,078,280	56,084,707	6,427	-	3	1_A375_pNL7_minus_lncRNA::1::2596, 2_A375_pNL97_plus_lncRNA::1::3728, 2_A375_pNL97_plus_lncRNA::1::3729	259, 619, -13	in gene, in gene, upstream	1	1	20	20	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SFRS1	ASF, SRp30a, MGC5228, SF2p33, SFRS1, FLJ53078, SRSF1, SF2	serine/arginine-rich splicing factor 1	NM_006924, NM_001078166, NR_034041, hCT1813050.2, hCT1952646.2, hCT1952647.2, hCT2287883.0, hCT2348044.0, hCT2348045.0, hCT2348046.0, hCT2348047.0	201741_x_at, 201742_x_at, 208863_s_at, 211784_s_at, 227164_at	NP_008855.1, NP_001071634.1, EAW94485.1, EAW94486.1, EAW94488.1, EAW94489.1, EAW94487.1, EAW94490.1, EAW94491.1, EAW94492.1
GeneID:124538	OR4D2	17	56,247,017	56,247,940	923	+	1	2_A375_pNL97_plus_lncRNA::1::3731	2807	downstream	0	1	10	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene OR4D2	BC2009, OR17-24, OR4D2	olfactory receptor, family 4, subfamily D, member 2	NM_001004707, hCT1686856.1	1555377_at	NP_001004707.1, EAW94481.1
GeneID:54903	MKS1	17	56,282,797	56,296,966	14,169	-	2	1_A375_pNL7_minus_lncRNA::1::2599, 2_A375_pNL97_plus_lncRNA::1::3732	366, 230	in gene, in gene	1	1	17	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene MKS1	POC12, FLJ20345, BBS13, MKS, MES, MKS1	Meckel syndrome, type 1	NM_017777, NM_001165927, hCT1952715.1, hCT21876.2, hCT2287870.0	1555820_a_at, 218630_at	NP_060247.2, NP_001159399.1, EAW94476.1, EAW94477.1, EAW94478.1
GeneID:100506779	LOC100506779	17	56,402,811	56,431,088	28,277	+	2	1_A375_pNL7_minus_lncRNA::1::2600, 2_A375_pNL97_plus_lncRNA::1::3733	26725, 26981	in gene, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506779		hypothetical LOC100506779	XR_111728, XR_111727, XR_109416, XR_109413, XR_109415, XR_109414, XR_115134, XR_115131, XR_115133, XR_115132		
GeneID:6827	SUPT4H1	17	56,422,539	56,429,563	7,024	-	2	1_A375_pNL7_minus_lncRNA::1::2600, 2_A375_pNL97_plus_lncRNA::1::3733	27, -229	in gene, upstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SUPT4H1	SUPT4H, SPT4H, SUPT4H1, SPT4	suppressor of Ty 4 homolog 1 (S. cerevisiae)	NM_003168, hCT2287844.0, hCT2287847.0, hCT2357777.0, hCT2357778.0	201483_s_at, 201484_at	NP_003159.1, EAW94464.1, EAW94465.1, EAW94466.1, EAW94467.1
GeneID:54894	RNF43	17	56,431,037	56,494,931	63,894	-	2	1_A375_pNL7_minus_lncRNA::1::2600, 2_A375_pNL97_plus_lncRNA::1::3733	65395, 65139	downstream, downstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RNF43	URCC, DKFZp781H02126, RNF43, MGC125630, FLJ20315, RNF124, DKFZp781H0392, FLJ99335, FLJ77466	ring finger protein 43	NM_017763, hCT21874.3, hCT2287940.0	218704_at	NP_060233.3, EAW94458.1, EAW94459.1
GeneID:56155	TEX14	17	56,634,039	56,769,416	135,377	-	7	1_A375_pNL7_minus_lncRNA::1::2601, 1_A375_pNL7_minus_lncRNA::1::2602, 1_A375_pNL7_minus_lncRNA::1::2603, 2_A375_pNL97_plus_lncRNA::1::3734, 2_A375_pNL97_plus_lncRNA::1::3735, 2_A375_pNL97_plus_lncRNA::1::3736, 2_A375_pNL97_plus_lncRNA::1::3737	60168, 32632, 12392, 60200, 32632, 25117, 12328	in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	21	20.25	4	1_A375_pNL7_minus_lncRNA::1	23	Gene TEX14	TEX14, CT113		NM_031272, NM_198393, hCT2287918.0, hCT2287920.0	221035_s_at	NP_112562.3, NP_938207.2, EAW94437.1, EAW94438.1
GeneID:22843	PPM1E	17	56,833,232	57,062,537	229,305	+	2	1_A375_pNL7_minus_lncRNA::1::2604, 2_A375_pNL97_plus_lncRNA::1::3738	-240, -240	upstream, upstream	1	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PPM1E	KIAA1072, PPM1E, DKFZp781F1422, CaMKP-N, PP2CH, POPX1	protein phosphatase 1E (PP2C domain containing)	NM_014906, hCT10351.2	205938_at, 236302_at	NP_055721.3, EAW94429.1
GeneID:4591	TRIM37	17	57,059,999	57,184,266	124,267	-	1	1_A375_pNL7_minus_lncRNA::1::2605	746	in gene	1	0	16	8	1	1_A375_pNL7_minus_lncRNA::1	16	Gene TRIM37	TEF3, MUL, KIAA0898, POB1, TRIM37	tripartite motif containing 37	NM_015294, NM_001005207, hCT1965926.1, hCT2283449.0, hCT2283450.0, hCT2357738.0	1554001_at, 213009_s_at	NP_056109.1, NP_001005207.1, EAW94424.1, EAW94425.1, EAW94426.1, EAW94427.1
GeneID:100506847	LOC100506847	17	57,183,851	57,195,514	11,663	+	1	1_A375_pNL7_minus_lncRNA::1::2605	-331	upstream	1	0	16	8	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100506847		hypothetical LOC100506847	XR_111729, XR_109417, XR_115135		
GeneID:348235	SKA2	17	57,187,308	57,232,800	45,492	-	2	1_A375_pNL7_minus_lncRNA::1::2605, 2_A375_pNL97_plus_lncRNA::1::3739	49280, -1184	downstream, upstream	1	1	11.5	10.5	2	1_A375_pNL7_minus_lncRNA::1	16	Gene SKA2	MGC110975, FLJ12758, FAM33A, SKA2	spindle and kinetochore associated complex subunit 2	NM_182620, NM_001100595, hCT2283447.2, hCT2351160.0, hCT2351161.0, hCT2351162.0	225684_at, 225686_at	NP_872426.1, NP_001094065.1, EAW94420.1, EAW94421.1, EAW94422.1, EAW94423.1
GeneID:407027	MIR301A	17	57,228,497	57,228,582	85	-	1	2_A375_pNL97_plus_lncRNA::1::3739	-5402	upstream	0	1	7	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene MIR301A	MIR301A, MIRN301, MIRN301A	microRNA 301a	NR_029842		
GeneID:55771	PRR11	17	57,232,860	57,284,070	51,210	+	1	2_A375_pNL97_plus_lncRNA::1::3739	1124	in gene	0	1	7	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene PRR11	PRR11, FLJ11029	proline rich 11	NM_018304, hCT1813876.1, hCT1964232.1, hCT2284727.0	219392_x_at, 232215_x_at	NP_060774.2, EAW94416.1, EAW94417.1, EAW94418.1
GeneID:55181	C17orf71	17	57,287,371	57,292,611	5,240	+	1	2_A375_pNL97_plus_lncRNA::1::3740	10549	downstream	0	1	9	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene C17orf71	C17orf71, SMG8, FLJ10587	chromosome 17 open reading frame 71	NM_018149, hCT18623.2, hCT2284739.0, hCT2284742.0	218514_at	NP_060619.4, EAW94414.1, EAW94413.1, EAW94415.1
GeneID:284161	GDPD1	17	57,297,828	57,353,331	55,503	+	1	2_A375_pNL97_plus_lncRNA::1::3740	92	in gene	0	1	9	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene GDPD1	GDE4, MGC35046, GDPD1, FLJ27503, FLJ37451	glycerophosphodiester phosphodiesterase domain containing 1	NM_182569, NM_001165993, NM_001165994, hCT1970459.1, hCT2357775.0	1555606_a_at, 1560227_at, 238681_at	NP_872375.2, NP_001159465.1, NP_001159466.1, EAW94411.1, EAW94412.1
GeneID:388403	YPEL2	17	57,409,053	57,479,095	70,042	+	1	2_A375_pNL97_plus_lncRNA::1::3741	23587	in gene	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene YPEL2	FKSG4, YPEL2, DKFZp761C2021	yippee-like 2 (Drosophila)	NM_001005404, hCT2284750.0, hCT2284753.0, hCT2284754.0, hCT2284757.0	1556420_s_at, 227020_at, 229060_at	NP_001005404.1, EAW94408.1, EAW94407.1, EAW94409.1, EAW94410.1
GeneID:79665	DHX40	17	57,642,886	57,685,713	42,827	+	2	1_A375_pNL7_minus_lncRNA::1::2606, 2_A375_pNL97_plus_lncRNA::1::3742	-102, 58	upstream, in gene	1	1	19	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene DHX40	DHX40, FLJ22060, DDX40, ARG147, FLJ34015, PAD	DEAH (Asp-Glu-Ala-His) box polypeptide 40	NM_024612, NM_001166301, hCT1813875.1, hCT1964230.1, hCT2284768.0, hCT2284771.0, hCT2284775.0	218277_s_at, 222574_s_at	NP_078888.4, NP_001159773.1, EAW94403.1, EAW94404.1, EAW94405.1, EAW94406.1, EAW94402.1
GeneID:1213	CLTC	17	57,697,050	57,774,317	77,267	+	2	1_A375_pNL7_minus_lncRNA::1::2607, 2_A375_pNL97_plus_lncRNA::1::3743	-250, -298	upstream, upstream	1	1	24	16	1	1_A375_pNL7_minus_lncRNA::1	24	Gene CLTC	KIAA0034, Hc, CLTCL2, CHC17, CHC, CLTC, CLH-17	clathrin, heavy chain (Hc)	NM_004859, hCT1964255.1, hCT2284783.0, hCT2284784.0, hCT2357762.0, hCT2357763.0	200614_at, 210498_at, 239671_at	NP_004850.1, EAW94399.1, EAW94395.1, EAW94396.1, EAW94397.1, EAW94398.1
GeneID:81671	TMEM49	17	57,784,863	57,917,954	133,091	+	2	1_A375_pNL7_minus_lncRNA::1::2608, 1_A375_pNL7_minus_lncRNA::1::2609	136225, 138273	downstream, downstream	1	0	17	10.5	2	1_A375_pNL7_minus_lncRNA::1	17	Gene TMEM49	EPG3, DKFZp566I133, VMP1, TMEM49	transmembrane protein 49	NM_030938, hCT1964247.1, hCT1964248.1, hCT2284644.0, hCT23920.2	1569003_at, 231697_s_at	NP_112200.2, EAW94392.1, EAW94390.1, EAW94391.1, EAW94393.1
GeneID:406991	MIR21	17	57,918,627	57,918,698	71	+	2	1_A375_pNL7_minus_lncRNA::1::2608, 1_A375_pNL7_minus_lncRNA::1::2609	2461, 4509	downstream, downstream	1	0	17	10.5	2	1_A375_pNL7_minus_lncRNA::1	17	Gene MIR21	miRNA21, miR-21, MIR21, hsa-mir-21, MIRN21	microRNA 21	NR_029493	224917_at	
GeneID:51174	TUBD1	17	57,936,840	57,970,306	33,466	-	2	2_A375_pNL97_plus_lncRNA::1::3744, 2_A375_pNL97_plus_lncRNA::1::3745	39522, -158	downstream, upstream	0	1	16.5	19.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene TUBD1	TUBD1, FLJ12709, TUBD	tubulin, delta 1	NM_016261, NM_001193609, NM_001193610, NM_001193611, NM_001193612, NM_001193613, hCT1968921.1, hCT1968922.1, hCT1968923.1, hCT2283975.0, hCT2283980.0	210389_x_at, 221326_s_at, 231853_at	NP_057345.2, NP_001180538.1, NP_001180539.1, NP_001180540.1, NP_001180541.1, NP_001180542.1, EAW94385.1, EAW94386.1, EAW94387.1, EAW94388.1, EAW94389.1
GeneID:6198	RPS6KB1	17	57,970,443	58,027,787	57,344	+	1	2_A375_pNL97_plus_lncRNA::1::3745	21	in gene	0	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene RPS6KB1	RPS6KB1, p70(S6K)-alpha, S6K, S6K1, p70-S6K, p70-alpha, STK14A, PS6K	ribosomal protein S6 kinase, 70kDa, polypeptide 1	NM_003161, hCT1815776.1, hCT2357739.0, hCT2357740.0	204171_at	NP_003152.1, EAW94382.1, EAW94383.1, EAW94384.1
GeneID:762	CA4	17	58,227,302	58,236,907	9,605	+	3	1_A375_pNL7_minus_lncRNA::1::2610, 2_A375_pNL97_plus_lncRNA::1::3746, 2_A375_pNL97_plus_lncRNA::1::3747	-10022, -9894, -8390	upstream, upstream, upstream	1	1	21.5	26	2	2_A375_pNL97_plus_lncRNA::1	33	Gene CA4	CA4, Car4, CAIV, RP17	carbonic anhydrase IV	NM_000717, hCT1786434.1, hCT1955340.1, hCT2357776.0	206208_at, 206209_s_at	NP_000708.1, EAW94362.1, EAW94361.1, EAW94363.1
GeneID:84669	USP32	17	58,254,691	58,469,586	214,895	-	1	2_A375_pNL97_plus_lncRNA::1::3748	658	in gene	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene USP32	USP10, NY-REN-60, USP32	ubiquitin specific peptidase 32	NM_032582, hCT2283956.0, hCT2283957.0, hCT2283958.0	211702_s_at, 226505_x_at, 244871_s_at	NP_115971.2, EAW94358.1, EAW94356.1, EAW94357.1
GeneID:10513	APPBP2	17	58,520,520	58,603,580	83,060	-	2	1_A375_pNL7_minus_lncRNA::1::2611, 2_A375_pNL97_plus_lncRNA::1::3749	92, 60	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene APPBP2	APPBP2, KIAA0228, HS.84084, PAT1	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	NM_006380, hCT2285106.0, hCT23367.2	202629_at, 202630_at, 202631_s_at, 215402_at	NP_006371.2, EAW51406.1, EAW51407.1
GeneID:8493	PPM1D	17	58,677,554	58,742,036	64,482	+	1	2_A375_pNL97_plus_lncRNA::1::3750	302	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PPM1D	WIP1, PP2C-DELTA, PPM1D	protein phosphatase 1D magnesium-dependent, delta isoform	NM_003620, hCT1640357.3, hCT2352464.0	204566_at	NP_003611.1, EAW51408.1, EAW51409.1
GeneID:54828	BCAS3	17	58,755,172	59,470,199	715,027	+	4	1_A375_pNL7_minus_lncRNA::1::2612, 2_A375_pNL97_plus_lncRNA::1::3751, 2_A375_pNL97_plus_lncRNA::1::3752, 2_A375_pNL97_plus_lncRNA::1::3753	643660, 573484, 634620, 643628	in gene, in gene, in gene, in gene	1	1	14.67	17.67	3	1_A375_pNL7_minus_lncRNA::1	22	Gene BCAS3	DKFZp686O1527, FLJ20128, BCAS3, MGC4973, GAOB1, MAAB	breast carcinoma amplified sequence 3	NM_017679, NM_001099432, hCT1955377.2, hCT2284743.1, hCT2284745.1, hCT2284747.1, hCT2284749.1, hCT2284751.1, hCT2352465.0	220488_s_at, 233128_at	NP_060149.3, NP_001092902.1, EAW51410.1, EAW51412.1, EAW51415.1, EAW51416.1, EAW51411.1, EAW51413.1, EAW51414.1
GeneID:645722	LOC645722	17	59,470,818	59,488,916	18,098	-	1	2_A375_pNL97_plus_lncRNA::1::3754	-780	upstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC645722		hypothetical LOC645722	XR_111731, XR_109419, XM_944447	1555216_a_at, 228978_at	XP_949540.3
GeneID:6909	TBX2	17	59,477,257	59,486,827	9,570	+	1	2_A375_pNL97_plus_lncRNA::1::3754	12439	downstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TBX2	TBX2, FLJ10169	T-box 2	NM_005994, hCT2284781.0, hCT23404.3, hCT2352466.0	205993_s_at, 213417_at, 40560_at	NP_005985.3, EAW51424.1, EAW51425.1, EAW51426.1
GeneID:388407	C17orf82	17	59,489,112	59,490,641	1,529	+	1	2_A375_pNL97_plus_lncRNA::1::3754	584	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C17orf82	C17orf82	chromosome 17 open reading frame 82	NM_203425, hCT2351251.0	1555478_at	NP_982249.1, EAW51427.1
GeneID:83990	BRIP1	17	59,756,547	59,940,920	184,373	-	1	2_A375_pNL97_plus_lncRNA::1::3755	53464	in gene	0	1	8	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene BRIP1	OF, FANCJ, MGC126521, BRIP1, BACH1, MGC126523, FLJ90232	BRCA1 interacting protein C-terminal helicase 1	NM_032043, hCT1643996.4, hCT2285633.0, hCT2285634.0, hCT2285636.0	221703_at	NP_114432.2, EAW51430.1, EAW51431.1, EAW51432.1, EAW51433.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:57508	INTS2	17	59,942,728	60,005,377	62,649	-	2	1_A375_pNL7_minus_lncRNA::1::2613, 2_A375_pNL97_plus_lncRNA::1::3756	97, 161	in gene, in gene	1	1	23	16	1	1_A375_pNL7_minus_lncRNA::1	23	Gene INTS2	INT2, KIAA1287, INTS2	integrator complex subunit 2	NR_026641, NM_020748, hCT1955375.1, hCT2352467.0, hCT2352468.0	224308_s_at	NP_065799.1, EAW51436.1, EAW51434.1, EAW51435.1
GeneID:9969	MED13	17	60,019,966	60,142,643	122,677	-	2	1_A375_pNL7_minus_lncRNA::1::2614, 2_A375_pNL97_plus_lncRNA::1::3757	-559, -525	upstream, upstream	1	1	20	20	1	1_A375_pNL7_minus_lncRNA::1	20	Gene MED13	THRAP1, HSPC221, MED13, TRAP240, DRIP250, ARC250, KIAA0593	mediator complex subunit 13	NM_005121, hCT2285829.0, hCT2285830.0, hCT23762.3	201986_at, 201987_at, 223780_s_at, 244611_at	NP_005112.2, EAW51437.1, EAW51438.1, EAW51439.1
GeneID:146779	EFCAB3	17	60,447,579	60,493,840	46,261	+	1	2_A375_pNL97_plus_lncRNA::1::3758	53765	downstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene EFCAB3	MGC126827, EFCAB3, MGC126801, FLJ25818	EF-hand calcium binding domain 3	NM_173503, NM_001144933, hCT2343830.0	1553392_at	NP_775774.1, NP_001138405.1, EAW94354.1
GeneID:339175	METTL2A	17	60,501,246	60,527,454	26,208	+	1	2_A375_pNL97_plus_lncRNA::1::3758	98	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene METTL2A	METTL2A, FLJ12760, METTL2	methyltransferase like 2A	NM_181725	221079_s_at, 225253_s_at	NP_859076.3
GeneID:9902	MRC2	17	60,704,762	60,770,953	66,191	+	3	1_A375_pNL7_minus_lncRNA::1::2615, 1_A375_pNL7_minus_lncRNA::1::2616, 2_A375_pNL97_plus_lncRNA::1::3759	326, 67302, 67382	in gene, downstream, downstream	1	1	16.5	17	2	2_A375_pNL97_plus_lncRNA::1	21	Gene MRC2	FLJ35911, CD280, CLEC13E, UPARAP, MRC2, ENDO180, KIAA0709	mannose receptor, C type 2	NM_006039, hCT1950235.1, hCT23401.2	209280_at, 37408_at	NP_006030.2, EAW94341.1, EAW94342.1
GeneID:162333	10-Mar	17	60,778,675	60,885,705	107,030	-	4	1_A375_pNL7_minus_lncRNA::1::2616, 2_A375_pNL97_plus_lncRNA::1::3759, 2_A375_pNL97_plus_lncRNA::1::3760, 2_A375_pNL97_plus_lncRNA::1::3761	113641, 113561, 46201, 16009	downstream, downstream, in gene, in gene	1	1	13.67	22	3	2_A375_pNL97_plus_lncRNA::1	26	Gene MARCH10	RNF190, FLJ35757, MARCH-X, MARCH10	membrane-associated ring finger (C3HC4) 10	NM_152598, NM_001100875, hCT2344492.0, hCT2357741.0, hCT2357742.0, hCT2357743.0	230624_at	NP_689811.2, NP_001094345.1, EAW94337.1, EAW94338.1, EAW94339.1, EAW94340.1
GeneID:26115	TANC2	17	61,086,898	61,505,067	418,169	+	3	1_A375_pNL7_minus_lncRNA::1::2617, 1_A375_pNL7_minus_lncRNA::1::2618, 2_A375_pNL97_plus_lncRNA::1::3762	266030, 346926, 265934	in gene, in gene, in gene	1	1	20.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene TANC2	FLJ11824, DKFZp564D166, rols, FLJ10215, KIAA1148, KIAA1636, TANC2, ROLSA	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	NM_025185	208425_s_at, 224952_at, 231799_at	NP_079461.2
GeneID:81033	KCNH6	17	61,600,695	61,626,338	25,643	+	2	1_A375_pNL7_minus_lncRNA::1::2619, 2_A375_pNL97_plus_lncRNA::1::3764	27433, 27011	downstream, downstream	1	1	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene KCNH6	KCNH6, ERG2, HERG2, Kv11.2	potassium voltage-gated channel, subfamily H (eag-related), member 6	NM_030779, NM_173092, hCT2295823.0, hCT2357760.0, hCT33102.2	211045_s_at, 211046_at, 221023_s_at	NP_110406.1, NP_775115.1, EAW94308.1, EAW94309.1, EAW94310.1
GeneID:10238	DCAF7	17	61,627,822	61,671,641	43,819	+	4	1_A375_pNL7_minus_lncRNA::1::2619, 1_A375_pNL7_minus_lncRNA::1::2620, 2_A375_pNL97_plus_lncRNA::1::3764, 2_A375_pNL97_plus_lncRNA::1::3765	306, 50322, -116, 50450	in gene, downstream, upstream, downstream	1	1	20	17.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene DCAF7	HAN11, WDR68, AN11, SWAN-1, DCAF7	DDB1 and CUL4 associated factor 7	NM_005828, hCT2295827.0, hCT33092.3	208592_s_at, 221744_at, 221745_at, 224730_at, 224748_at, 233782_at, 236134_at	NP_005819.3, EAW94306.1, EAW94305.1
GeneID:51204	TACO1	17	61,678,231	61,685,725	7,494	+	2	1_A375_pNL7_minus_lncRNA::1::2620, 2_A375_pNL97_plus_lncRNA::1::3765	-87, 41	upstream, in gene	1	1	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene TACO1	CCDC44, TACO1	translational activator of mitochondrially encoded cytochrome c oxidase I	NM_016360, hCT1786593.2, hCT1950229.1, hCT2357767.0	221069_s_at	NP_057444.2, EAW94304.1, EAW94302.1, EAW94303.1
GeneID:57003	CCDC47	17	61,822,610	61,851,088	28,478	-	2	1_A375_pNL7_minus_lncRNA::1::2621, 1_A375_pNL7_minus_lncRNA::1::2622	240, -446	in gene, upstream	1	0	18	16	2	1_A375_pNL7_minus_lncRNA::1	20	Gene CCDC47	GK001, CCDC47, MSTP041	coiled-coil domain containing 47	NM_020198, hCT2285296.0, hCT2285297.0, hCT2357780.0, hCT33104.3	217814_at, 222432_s_at	NP_064583.2, EAW94281.1, EAW94279.1, EAW94280.1, EAW94282.1
GeneID:11325	DDX42	17	61,851,567	61,896,677	45,110	+	3	1_A375_pNL7_minus_lncRNA::1::2621, 1_A375_pNL7_minus_lncRNA::1::2622, 2_A375_pNL97_plus_lncRNA::1::3766	-719, -31, 53489	upstream, upstream, downstream	1	1	17.33	18	3	2_A375_pNL97_plus_lncRNA::1	22	Gene DDX42	RHELP, FLJ43179, RNAHP, DDX42, SF3b125	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	NM_007372, NM_203499, hCT1950255.1, hCT2295843.0, hCT2295845.0	1559953_at, 1559954_s_at, 201786_at	NP_031398.2, NP_987095.1, EAW94276.1, EAW94277.1, EAW94278.1
GeneID:117246	FTSJ3	17	61,896,793	61,905,031	8,238	-	1	2_A375_pNL97_plus_lncRNA::1::3766	-25	upstream	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene FTSJ3	FLJ20062, EPCS3, FTSJ3	FtsJ homolog 3 (E. coli)	NM_017647, hCT2285290.0, hCT2285292.0, hCT33096.4	218103_at	NP_060117.3, EAW94274.1, EAW94273.1, EAW94275.1
GeneID:5705	PSMC5	17	61,904,810	61,909,387	4,577	+	1	2_A375_pNL97_plus_lncRNA::1::3766	246	in gene	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PSMC5	SUG1, p45, TBP10, SUG-1, p45/SUG, S8, TRIP1, PSMC5	proteasome (prosome, macropain) 26S subunit, ATPase, 5	NM_002805, hCT1812378.2, hCT1813989.2, hCT2295852.1, hCT33091.2	209503_s_at	NP_002796.4, EAW94269.1, EAW94270.1, EAW94271.1, EAW94272.1
GeneID:6603	SMARCD2	17	61,909,441	61,920,351	10,910	-	3	1_A375_pNL7_minus_lncRNA::1::2623, 2_A375_pNL97_plus_lncRNA::1::3766, 2_A375_pNL97_plus_lncRNA::1::3767	180, 15295, 207	in gene, downstream, in gene	1	1	19.5	27.5	2	2_A375_pNL97_plus_lncRNA::1	33	Gene SMARCD2	CRACD2, SMARCD2, PRO2451, BAF60B, Rsc6p	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	NM_001098426, hCT1950249.1, hCT2285284.0, hCT33089.3	201827_at	NP_001091896.1, EAW94266.1, EAW94267.1, EAW94268.1
GeneID:6329	SCN4A	17	62,015,914	62,050,278	34,364	-	2	1_A375_pNL7_minus_lncRNA::1::2624, 2_A375_pNL97_plus_lncRNA::1::3768	-1786, -1487	upstream, upstream	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SCN4A	HYPP, SkM1, Na(V)1.4, HOKPP2, NAC1A, HYKPP, Nav1.4, SCN4A	sodium channel, voltage-gated, type IV, alpha subunit	NM_000334, hCT2286741.0, hCT33088.2	206981_at	NP_000325.4, EAW94226.1, EAW94225.1
GeneID:692227	SNORD104	17	62,223,438	62,223,517	79	+	2	1_A375_pNL7_minus_lncRNA::1::2625, 2_A375_pNL97_plus_lncRNA::1::3769	-350, -110	upstream, upstream	1	1	23	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SNORD104	U104, SNORD104	small nucleolar RNA, C/D box 104	NR_004380		
GeneID:677842	SNORA76	17	62,223,699	62,223,831	132	+	2	1_A375_pNL7_minus_lncRNA::1::2625, 2_A375_pNL97_plus_lncRNA::1::3769	-611, -371	upstream, upstream	1	1	23	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SNORA76	SNORA76, ACA62	small nucleolar RNA, H/ACA box 76	NR_002995	226679_at	
GeneID:55852	TEX2	17	62,224,795	62,340,653	115,858	-	4	1_A375_pNL7_minus_lncRNA::1::2625, 1_A375_pNL7_minus_lncRNA::1::2626, 2_A375_pNL97_plus_lncRNA::1::3769, 2_A375_pNL97_plus_lncRNA::1::3770	117565, -179, 117325, -179	downstream, upstream, downstream, upstream	1	1	40	49	2	2_A375_pNL97_plus_lncRNA::1	71	Gene TEX2	TMEM96, TEX2, HT008, DKFZp781G0721, KIAA1738	testis expressed 2	NM_018469, hCT2357746.0, hCT33085.3	218099_at	NP_060939.3, EAW94210.1, EAW94211.1
GeneID:100506961	LOC100506961	17	62,396,775	62,398,041	1,266	-	1	2_A375_pNL97_plus_lncRNA::1::3771	-6087	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506961		hypothetical LOC100506961	XR_109420		
GeneID:5175	PECAM1	17	62,399,863	62,401,205	1,342	-	1	2_A375_pNL97_plus_lncRNA::1::3771	-2923	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PECAM1	FLJ58394, CD31, PECAM-1, PECAM1, FLJ34100	platelet/endothelial cell adhesion molecule	NM_000442, hCT2286685.0, hCT2286687.0	1559921_at, 208981_at, 208982_at, 208983_s_at	NP_000433.3, EAW94207.1, EAW94208.1
GeneID:11232	POLG2	17	62,473,902	62,493,184	19,282	-	2	2_A375_pNL97_plus_lncRNA::1::3772, 2_A375_pNL97_plus_lncRNA::1::3773	-64, -10046	upstream, upstream	0	1	11.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene POLG2	POLG2, HP55, MTPOLB, PEOA4, POLB, POLG-BETA, POLGB	polymerase (DNA directed), gamma 2, accessory subunit	NM_007215, hCT19316.2	205811_at	NP_009146.2, EAW94204.1
GeneID:1655	DDX5	17	62,494,374	62,502,484	8,110	-	2	2_A375_pNL97_plus_lncRNA::1::3772, 2_A375_pNL97_plus_lncRNA::1::3773	9236, -746	downstream, upstream	0	1	11.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene DDX5	DDX5, HLR1, p68, HUMP68, DKFZp686J01190, G17P1, DKFZp434E109	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	NM_004396, hCT18784.3, hCT1971014.1	200033_at	NP_004387.1, EAW94203.1, EAW94202.1
GeneID:90799	CCDC45	17	62,503,158	62,534,064	30,906	+	2	2_A375_pNL97_plus_lncRNA::1::3772, 2_A375_pNL97_plus_lncRNA::1::3773	-9910, 74	upstream, in gene	0	1	11.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene CCDC45	CCDC45, DKFZp667E1824	coiled-coil domain containing 45	NM_138363, hCT2287128.0, hCT2287129.0, hCT2287130.0, hCT2287131.0, hCT2357764.0	223815_at, 225705_at	NP_612372.1, EAW94196.1, EAW94197.1, EAW94198.1, EAW94199.1, EAW94200.1
GeneID:5578	PRKCA	17	64,298,926	64,806,862	507,936	+	4	1_A375_pNL7_minus_lncRNA::1::2632, 1_A375_pNL7_minus_lncRNA::1::2633, 2_A375_pNL97_plus_lncRNA::1::3781, 2_A375_pNL97_plus_lncRNA::1::3782	190754, 237570, 206738, 237650	in gene, in gene, in gene, in gene	1	1	16	19	3	2_A375_pNL97_plus_lncRNA::1	26	Gene PRKCA	AAG6, MGC129900, PRKACA, PKC-alpha, PKCA, PRKCA, MGC129901	protein kinase C, alpha	NM_002737, hCT20429.3	1560074_at, 206923_at, 213093_at, 215194_at, 215195_at	NP_002728.1, EAW89014.1
GeneID:5718	PSMD12	17	65,336,619	65,362,721	26,102	-	1	2_A375_pNL97_plus_lncRNA::1::3784	129	in gene	0	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene PSMD12	MGC75406, p55, Rpn5, PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	NM_002816, NM_174871, hCT1787664.3, hCT2264157.1, hCT2357209.0, hCT2357210.0	202352_s_at, 202353_s_at	NP_002807.1, NP_777360.1, EAW89026.1, EAW89027.1, EAW89028.1, EAW89029.1
GeneID:100507049	LOC100507049	17	65,671,272	65,713,744	42,472	-	1	2_A375_pNL97_plus_lncRNA::1::3785	-336	upstream	0	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100507049		hypothetical LOC100507049	XR_111744, XR_109422, XR_115138		
GeneID:25926	NOL11	17	65,714,061	65,740,266	26,205	+	1	2_A375_pNL97_plus_lncRNA::1::3785	19	in gene	0	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene NOL11	NOL11, DKFZp586L0724	nucleolar protein 11	NM_015462, hCT2263087.0, hCT2263088.0, hCT2263091.0, hCT2263093.0, hCT2263094.0	221970_s_at	NP_056277.2, EAW89036.1, EAW89033.1, EAW89034.1, EAW89035.1, EAW89037.1
GeneID:2186	BPTF	17	65,821,780	65,980,494	158,714	+	1	1_A375_pNL7_minus_lncRNA::1::2634	-212	upstream	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene BPTF	NURF301, FALZ, BPTF, FAC1	bromodomain PHD finger transcription factor	NM_182641, NM_004459, hCT2263098.1, hCT2263104.1	207186_s_at, 209271_at, 230056_at, 231953_at, 232909_s_at	NP_872579.2, NP_004450.3, EAW89038.1, EAW89039.1
GeneID:3838	KPNA2	17	66,031,848	66,042,970	11,122	+	1	2_A375_pNL97_plus_lncRNA::1::3787	280	in gene	0	1	14	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene KPNA2	RCH1, IPOA1, SRP1alpha, QIP2, KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	NM_002266, hCT2263099.1, hCT2348634.0	201088_at, 211762_s_at	NP_002257.1, EAW89041.1, EAW89040.1
GeneID:22901	ARSG	17	66,255,323	66,417,000	161,677	+	4	1_A375_pNL7_minus_lncRNA::1::2636, 1_A375_pNL7_minus_lncRNA::1::2637, 2_A375_pNL97_plus_lncRNA::1::3788, 2_A375_pNL97_plus_lncRNA::1::3789	122053, 140965, 122005, 141269	in gene, in gene, in gene, in gene	1	1	17	17.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene ARSG	ARSG, KIAA1001	arylsulfatase G	NM_014960, hCT1954101.1, hCT19613.3	1552632_a_at	NP_055775.2, EAW89056.1, EAW89055.1
GeneID:55062	WIPI1	17	66,417,422	66,453,653	36,231	-	1	1_A375_pNL7_minus_lncRNA::1::2638	21685	in gene	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene WIPI1	ATG18A, WIPI1, FLJ10055, ATG18, WIPI49	WD repeat domain, phosphoinositide interacting 1	NM_017983, hCT1954131.1, hCT1954132.1, hCT19620.3	203827_at, 213636_s_at	NP_060453.3, EAW89059.1, EAW89057.1, EAW89058.1
GeneID:5573	PRKAR1A	17	66,508,110	66,528,911	20,801	+	2	1_A375_pNL7_minus_lncRNA::1::2639, 2_A375_pNL97_plus_lncRNA::1::3790	530, 306	in gene, in gene	1	1	21	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene PRKAR1A	TSE1, CAR, PRKAR1, CNC1, PRKAR1A, DKFZp779L0468, MGC17251, CNC, PKR1, PPNAD1	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	NM_002734, NM_212471, NM_212472, hCT1954118.1, hCT1954120.1, hCT19614.3, hCT2357168.0, hCT2357169.0, hCT2357170.0	200603_at, 200604_s_at, 200605_s_at, 242462_at	NP_002725.1, NP_997636.1, NP_997637.1, EAW89060.1, EAW89063.1, EAW89065.1, EAW89061.1, EAW89062.1, EAW89064.1
GeneID:10351	ABCA8	17	66,863,430	66,951,533	88,103	-	1	2_A375_pNL97_plus_lncRNA::1::3792	46189	in gene	0	1	14	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene ABCA8	KIAA0822, MGC163152, ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	NM_007168, hCT1954125.1, hCT19616.3	1565778_at, 1565780_at, 204719_at	NP_009099.1, EAW89068.1, EAW89069.1
GeneID:5608	MAP2K6	17	67,410,838	67,538,470	127,632	+	1	2_A375_pNL97_plus_lncRNA::1::3793	125194	in gene	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MAP2K6	MAP2K6, MEK6, MKK6, MAPKK6, PRKMK6, SAPKK3	mitogen-activated protein kinase kinase 6	NM_002758, hCT1954133.1, hCT1954134.1, hCT19627.3	205698_s_at, 205699_at	NP_002749.2, EAW89084.1, EAW89085.1, EAW89086.1
GeneID:400617	FLJ36644	17	68,163,102	68,165,543	2,441	-	1	2_A375_pNL97_plus_lncRNA::1::3796	359	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FLJ36644		hypothetical LOC400617	NR_036534	1558234_at	
GeneID:3759	KCNJ2	17	68,165,676	68,176,185	10,509	+	1	2_A375_pNL97_plus_lncRNA::1::3796	-492	upstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene KCNJ2	SQT3, LQT7, KCNJ2, HHBIRK1, KIR2.1, IRK1, HHIRK1	potassium inwardly-rectifying channel, subfamily J, member 2	NM_000891, hCT18441.3	206765_at	NP_000882.1, EAW89092.1
GeneID:100499467	LOC100499467	17	70,399,463	70,588,943	189,480	-	2	1_A375_pNL7_minus_lncRNA::1::2645, 2_A375_pNL97_plus_lncRNA::1::3802	127119, 20735	in gene, in gene	1	1	16.5	13.5	2	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100499467	FLJ20470, FLJ26252	hypothetical LOC100499467	NR_036488		
GeneID:400619	FLJ26484	17	70,594,180	70,636,611	42,431	-	3	2_A375_pNL97_plus_lncRNA::1::3803, 2_A375_pNL97_plus_lncRNA::1::3804, 2_A375_pNL97_plus_lncRNA::1::3805	24675, 21955, 8035	in gene, in gene, in gene	0	1	18	23.33	3	2_A375_pNL97_plus_lncRNA::1	25	Gene FLJ26484		hypothetical LOC400619	NR_033876		
GeneID:201266	SLC39A11	17	70,642,085	71,088,853	446,768	-	7	1_A375_pNL7_minus_lncRNA::1::2646, 1_A375_pNL7_minus_lncRNA::1::2647, 1_A375_pNL7_minus_lncRNA::1::2648, 2_A375_pNL97_plus_lncRNA::1::3806, 2_A375_pNL97_plus_lncRNA::1::3807, 2_A375_pNL97_plus_lncRNA::1::3808, 2_A375_pNL97_plus_lncRNA::1::3809	436261, 430997, 408389, 436261, 430933, 408501, 368117	in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	17.25	18	4	2_A375_pNL97_plus_lncRNA::1	21	Gene SLC39A11	ZIP11, SLC39A11, C17orf26	solute carrier family 39 (metal ion transporter), member 11	NM_139177, NM_001159770, hCT2261740.1, hCT2261741.1, hCT2344419.0	227046_at	NP_631916.2, NP_001153242.1, EAW89107.1, EAW89108.1, EAW89109.1
GeneID:9382	COG1	17	71,189,173	71,204,646	15,473	+	1	2_A375_pNL97_plus_lncRNA::1::3810	123	in gene	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene COG1	KIAA1381, COG1, LDLB, CDG2G, DKFZp762L1710	component of oligomeric golgi complex 1	NM_018714, hCT1953331.1, hCT20152.3	227784_s_at, 230878_s_at, 231813_s_at	NP_061184.1, EAW89114.1, EAW89113.1
GeneID:23580	CDC42EP4	17	71,279,763	71,308,143	28,380	-	1	2_A375_pNL97_plus_lncRNA::1::3811	19855	in gene	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CDC42EP4	CDC42EP4, BORG4, MGC17125, MGC3740, CEP4, KAIA1777	CDC42 effector protein (Rho GTPase binding) 4	NM_012121, hCT18977.3, hCT2261732.0	214721_x_at, 218062_x_at, 218063_s_at	NP_036253.2, EAW89123.1, EAW89124.1
GeneID:6169	RPL38	17	72,199,795	72,206,019	6,224	+	2	1_A375_pNL7_minus_lncRNA::1::2649, 2_A375_pNL97_plus_lncRNA::1::3812	-51, -83	upstream, upstream	1	1	53	71	1	2_A375_pNL97_plus_lncRNA::1	71	Gene RPL38	RPL38, L38	ribosomal protein L38	NM_000999, NM_001035258, hCT2261218.1, hCT2261220.1, hCT2261223.1, hCT2344418.0	202028_s_at, 202029_x_at, 221943_x_at	NP_000990.1, NP_001030335.1, EAW89137.1, EAW89138.1, EAW89139.1, EAW89140.1
GeneID:85001	MGC16275	17	72,206,119	72,209,460	3,341	-	2	1_A375_pNL7_minus_lncRNA::1::2649, 2_A375_pNL97_plus_lncRNA::1::3812	9716, 9748	downstream, downstream	1	1	53	71	1	2_A375_pNL97_plus_lncRNA::1	71	Gene MGC16275		hypothetical protein MGC16275	NR_026914	1558166_at, 1558167_a_at	
GeneID:94015	TTYH2	17	72,209,696	72,256,159	46,463	+	2	1_A375_pNL7_minus_lncRNA::1::2649, 2_A375_pNL97_plus_lncRNA::1::3812	-9952, -9984	upstream, upstream	1	1	53	71	1	2_A375_pNL97_plus_lncRNA::1	71	Gene TTYH2	C17orf29, MGC126172, MGC4837, TTYH2	tweety homolog 2 (Drosophila)	NM_032646, NM_052869, hCT2261225.1, hCT2261227.0	223741_s_at, 232042_at	NP_116035.5, NP_443101.1, EAW89142.1, EAW89143.1
GeneID:342510	CD300E	17	72,608,712	72,619,801	11,089	-	1	2_A375_pNL97_plus_lncRNA::1::3813	13465	downstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CD300E	CD300E, IREM2, CLM2, CD300LE	CD300e molecule	NM_181449, hCT1813932.2, hCT2357208.0		NP_852114.1, EAW89175.1, EAW89176.1
GeneID:326624	RAB37	17	72,667,256	72,743,474	76,218	+	2	1_A375_pNL7_minus_lncRNA::1::2650, 2_A375_pNL97_plus_lncRNA::1::3814	264, 296	in gene, in gene	1	1	79	79	1	2_A375_pNL97_plus_lncRNA::1	79	Gene RAB37	FLJ30284, RAB37, FLJ32507	RAB37, member RAS oncogene family	NM_175738, NM_001006638, NM_001163989, NM_001163990, hCT2261866.1, hCT2348610.0, hCT2349091.0, hCT2349092.0, hCT2349093.0, hCT2357186.0	228113_at, 244124_at	NP_783865.1, NP_001006639.1, NP_001157461.1, NP_001157462.1, EAW89178.1, EAW89181.1, EAW89177.1, EAW89179.1, EAW89180.1, EAW89182.1
GeneID:9368	SLC9A3R1	17	72,744,763	72,765,499	20,736	+	1	2_A375_pNL97_plus_lncRNA::1::3815	27685	downstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SLC9A3R1	NHERF1, NPHLOP2, SLC9A3R1, NHERF, EBP50	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	NM_004252, hCT1954141.1, hCT1954142.1, hCT21000.2	201349_at	NP_004243.1, EAW89191.1, EAW89189.1, EAW89190.1
GeneID:26151	NAT9	17	72,766,686	72,772,470	5,784	-	1	2_A375_pNL97_plus_lncRNA::1::3815	22	in gene	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene NAT9	DKFZp564C103, EBSP, EBSP, hNATL, NAT9	N-acetyltransferase 9 (GCN5-related, putative)	NM_015654, hCT2262802.0, hCT2262803.0, hCT2357204.0, hCT2357205.0, hCT2357206.0	204382_at	NP_056469.2, EAW89193.1, EAW89194.1, EAW89195.1, EAW89196.1, EAW89197.1
GeneID:54866	TMEM104	17	72,772,622	72,835,922	63,300	+	1	2_A375_pNL97_plus_lncRNA::1::3815	-174	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene TMEM104	TMEM104, FLJ00021, FLJ20255	transmembrane protein 104	NM_017728, hCT1954149.1, hCT21003.3, hCT2357156.0, hCT2357157.0	220097_s_at	NP_060198.3, EAW89198.1, EAW89199.1, EAW89200.1, EAW89201.1
GeneID:283987	C17orf28	17	72,946,839	72,968,900	22,061	-	1	2_A375_pNL97_plus_lncRNA::1::3816	-9468	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C17orf28	FLJ43526, DMC1, C17orf28	chromosome 17 open reading frame 28	NM_030630, hCT2262856.0, hCT2262857.0, hCT2262858.0, hCT2348611.0, hCT2357167.0	225981_at, 244593_at	NP_085133.1, EAW89218.1, EAW89217.1, EAW89219.1, EAW89220.1, EAW89221.1
GeneID:30850	CDR2L	17	72,983,727	73,001,895	18,168	+	3	1_A375_pNL7_minus_lncRNA::1::2651, 2_A375_pNL97_plus_lncRNA::1::3816, 2_A375_pNL97_plus_lncRNA::1::3817	25121, -5359, 25153	downstream, upstream, downstream	1	1	16	19.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene CDR2L	HUMPPA, CDR2L	cerebellar degeneration-related protein 2-like	NM_014603, hCT21007.2, hCT2261880.0, hCT2261882.0, hCT2357181.0	213230_at	NP_055418.2, EAW89226.1, EAW89223.1, EAW89224.1, EAW89225.1
GeneID:3396	ICT1	17	73,008,780	73,017,356	8,576	+	2	1_A375_pNL7_minus_lncRNA::1::2651, 2_A375_pNL97_plus_lncRNA::1::3817	68, 100	in gene, in gene	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ICT1	DS-1, ICT1	immature colon carcinoma transcript 1	NM_001545, hCT21011.3	204868_at	NP_001536.1, EAW89227.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:10476	ATP5H	17	73,034,955	73,043,074	8,119	-	3	1_A375_pNL7_minus_lncRNA::1::2652, 2_A375_pNL97_plus_lncRNA::1::3818, 2_A375_pNL97_plus_lncRNA::1::3819	11890, 12562, 2	downstream, downstream, in gene	1	1	23	19.5	2	1_A375_pNL7_minus_lncRNA::1	31	Gene ATP5H	ATP5H, ATPQ, ATP5JD	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	NM_006356, NM_001003785, hCT1954147.1, hCT21002.2	1555998_at, 210149_s_at	NP_006347.1, NP_001003785.1, EAW89228.1, EAW89229.1
GeneID:23510	KCTD2	17	73,043,279	73,061,981	18,702	+	1	2_A375_pNL97_plus_lncRNA::1::3819	-207	upstream	0	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene KCTD2	KCTD2, KIAA0176	potassium channel tetramerisation domain containing 2	NM_015353, hCT1643661.3	212564_at, 34858_at	NP_056168.1, EAW89230.1
GeneID:79637	ARMC7	17	73,106,082	73,126,360	20,278	+	2	2_A375_pNL97_plus_lncRNA::1::3820, 2_A375_pNL97_plus_lncRNA::1::3821	14526, 21550	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene ARMC7	ARMC7, FLJ22160	armadillo repeat containing 7	NM_024585, hCT2261886.0, hCT2345066.0, hCT2345067.0, hCT2345068.0	219096_at, 229906_at	NP_078861.1, EAW89236.1, EAW89237.1, EAW89238.1, EAW89239.1
GeneID:30833	NT5C	17	73,126,323	73,127,877	1,554	-	2	2_A375_pNL97_plus_lncRNA::1::3820, 2_A375_pNL97_plus_lncRNA::1::3821	7269, 245	downstream, in gene	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene NT5C	UMPH2, PN-II, NT5C, dNT-1, P5N2, DNT, PN-I, cdN, DNT1	5', 3'-nucleotidase, cytosolic	NM_014595, hCT18606.2, hCT1954115.2, hCT1954117.2	1557303_at, 219214_s_at	NP_055410.1, EAW89243.1, EAW89241.1, EAW89242.1
GeneID:51155	HN1	17	73,131,343	73,150,775	19,432	-	1	2_A375_pNL97_plus_lncRNA::1::3821	23143	downstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene HN1	ARM2, HN1A, HN1	hematological and neurological expressed 1	NM_016185, NM_001002033, NM_001002032, hCT2262844.0, hCT2262845.0, hCT2357164.0, hCT2357165.0	217755_at, 222396_at	NP_057269.1, NP_001002033.1, NP_001002032.1, EAW89244.1, EAW89246.1, EAW89247.1, EAW89245.1
GeneID:79902	NUP85	17	73,201,597	73,231,854	30,257	+	2	1_A375_pNL7_minus_lncRNA::1::2653, 2_A375_pNL97_plus_lncRNA::1::3822	3, 35	in gene, in gene	1	1	53	55	1	2_A375_pNL97_plus_lncRNA::1	55	Gene NUP85	FLJ12549, Nup75, NUP85	nucleoporin 85kDa	NM_024844, hCT18605.3	218014_at	NP_079120.1, EAW89251.1
GeneID:23163	GGA3	17	73,232,694	73,258,444	25,750	-	2	1_A375_pNL7_minus_lncRNA::1::2654, 2_A375_pNL97_plus_lncRNA::1::3823	492, 812	in gene, in gene	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene GGA3	KIAA0154, GGA3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	NM_138619, NM_014001, NM_001172703, NM_001172704, NR_033345, hCT18603.2, hCT1954107.1, hCT1954108.1, hCT1954109.1, hCT2262838.0, hCT2262841.0, hCT2357215.0, hCT2357216.0, hCT2357217.0	209411_s_at, 211815_s_at	NP_619525.1, NP_054720.1, NP_001166174.1, NP_001166175.1, EAW89252.1, EAW89260.1, EAW89253.1, EAW89254.1, EAW89255.1, EAW89256.1, EAW89257.1, EAW89258.1, EAW89259.1
GeneID:51081	MRPS7	17	73,257,749	73,262,457	4,708	+	2	1_A375_pNL7_minus_lncRNA::1::2654, 2_A375_pNL97_plus_lncRNA::1::3823	203, -117	in gene, upstream	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MRPS7	bMRP27a, MRPS7, MRP-S, S7mt, RP-S7, RPMS7, MRP-S7	mitochondrial ribosomal protein S7	NM_015971, hCT18598.3, hCT1954096.1	217932_at	NP_057055.2, EAW89261.1, EAW89262.1
GeneID:57409	MIF4GD	17	73,262,309	73,267,303	4,994	-	2	1_A375_pNL7_minus_lncRNA::1::2654, 2_A375_pNL97_plus_lncRNA::1::3823	9351, 9671	downstream, downstream	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIF4GD	AD023, MGC45027, MIFD, MIF4GD, SLIP1	MIF4G domain containing	NM_020679, hCT18604.2, hCT1954111.1, hCT1954112.1, hCT1954113.1	223411_at, 231727_s_at	NP_065730.2, EAW89263.1, EAW89264.1, EAW89265.1, EAW89266.1
GeneID:100287042	LOC100287042	17	73,267,380	73,269,976	2,596	+	2	1_A375_pNL7_minus_lncRNA::1::2654, 2_A375_pNL97_plus_lncRNA::1::3823	-9428, -9748	upstream, upstream	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100287042		hypothetical LOC100287042	NR_036520		
GeneID:60386	SLC25A19	17	73,269,061	73,285,530	16,469	-	2	1_A375_pNL7_minus_lncRNA::1::2655, 2_A375_pNL97_plus_lncRNA::1::3824	-262, 154	upstream, in gene	1	1	23	14	1	1_A375_pNL7_minus_lncRNA::1	23	Gene SLC25A19	DNC, TPC, SLC25A19, MUP1, MCPHA	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	NM_021734, NM_001126121, NM_001126122, hCT18601.3, hCT1961008.1, hCT1961010.1	223222_at	NP_068380.3, NP_001119593.1, NP_001119594.1, EAW89267.1, EAW89268.1, EAW89269.1
GeneID:57513	CASKIN2	17	73,496,342	73,511,627	15,285	-	2	1_A375_pNL7_minus_lncRNA::1::2656, 2_A375_pNL97_plus_lncRNA::1::3825	-597, -769	upstream, upstream	1	1	28	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene CASKIN2	ANKS5B, CASKIN2, KIAA1139, FLJ21609	CASK interacting protein 2	NM_020753, NM_001142643, hCT2266318.0	221846_s_at, 61297_at	NP_065804.2, NP_001136115.1, EAW89278.1
GeneID:283989	TSEN54	17	73,512,609	73,520,820	8,211	+	2	1_A375_pNL7_minus_lncRNA::1::2656, 2_A375_pNL97_plus_lncRNA::1::3825	-385, -193	upstream, upstream	1	1	28	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene TSEN54	PCH2A, sen54, SEN54L, TSEN54, PCH4, FLJ37147	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	NM_207346	1556304_s_at, 225879_at, 241402_at	NP_997229.2
GeneID:3993	LLGL2	17	73,521,783	73,571,290	49,507	+	2	1_A375_pNL7_minus_lncRNA::1::2656, 2_A375_pNL97_plus_lncRNA::1::3825	-9559, -9367	upstream, upstream	1	1	28	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene LLGL2	HGL, LGL2, LLGL2	lethal giant larvae homolog 2 (Drosophila)	NM_004524, NM_001015002, NM_001031803, hCT18678.3, hCT2262872.0, hCT2357221.0, hCT2357222.0	1554006_a_at, 203713_s_at	NP_004515.2, NP_001015002.1, NP_001026973.1, EAW89281.1, EAW89282.1, EAW89283.1, EAW89280.1
GeneID:9400	RECQL5	17	73,622,950	73,663,269	40,319	-	1	2_A375_pNL97_plus_lncRNA::1::3826	-27	upstream	0	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene RECQL5	FLJ90603, RECQL5, RECQ5	RecQ protein-like 5	NM_001003715, NM_004259, NM_001003716, hCT2266306.0, hCT2266308.0, hCT2266309.0, hCT2266311.0, hCT2266312.0, hCT2266314.0, hCT2357182.0	1561720_at, 210309_at, 211468_s_at, 221686_s_at, 34063_at	NP_001003715.1, NP_004250.4, NP_001003716.1, EAW89289.1, EAW89290.1, EAW89294.1, EAW89291.1, EAW89292.1, EAW89293.1, EAW89295.1
GeneID:29115	SAP30BP	17	73,663,399	73,704,139	40,740	+	2	2_A375_pNL97_plus_lncRNA::1::3826, 2_A375_pNL97_plus_lncRNA::1::3827	-103, 24249	upstream, in gene	0	1	14.5	20.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene SAP30BP	HTRP, HTRG, DKFZp586L2022, HCNGP, SAP30BP	SAP30 binding protein	NM_013260, hCT18681.3, hCT2357236.0, hCT2357237.0, hCT2357238.0, hCT2357239.0, hCT2357240.0, hCT2357241.0	217965_s_at, 222475_at	NP_037392.1, EAW89298.1, EAW89299.1, EAW89300.1, EAW89302.1, EAW89304.1, EAW89301.1, EAW89303.1
GeneID:3021	H3F3B	17	73,772,515	73,775,860	3,345	-	4	1_A375_pNL7_minus_lncRNA::1::2657, 1_A375_pNL7_minus_lncRNA::1::2658, 2_A375_pNL97_plus_lncRNA::1::3828, 2_A375_pNL97_plus_lncRNA::1::3829	-76, -5356, 52, -5292	upstream, upstream, in gene, upstream	1	1	21.5	21.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene H3F3B	H3.3B, H3F3A, H3F3B	H3 histone, family 3B (H3.3B)	NM_005324, hCT2266299.1, hCT2266301.1, hCT2266303.1	209069_s_at, 211997_x_at, 211998_at, 211999_at	NP_005315.1, EAW89317.1, EAW89318.1, EAW89319.1
GeneID:85451	UNK	17	73,780,681	73,821,886	41,205	+	4	1_A375_pNL7_minus_lncRNA::1::2657, 1_A375_pNL7_minus_lncRNA::1::2658, 2_A375_pNL97_plus_lncRNA::1::3828, 2_A375_pNL97_plus_lncRNA::1::3829	-4745, 535, -4673, 471	upstream, in gene, upstream, in gene	1	1	21.5	21.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene UNK	ZC3HDC5, KIAA1753, UNK, ZC3H5	unkempt homolog (Drosophila)	NM_001080419	1562434_at, 226376_at, 226357_at	NP_001073888.1
GeneID:23558	WBP2	17	73,841,780	73,851,501	9,721	-	1	1_A375_pNL7_minus_lncRNA::1::2659	-275	upstream	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene WBP2	WBP-2, WBP2, MGC18269	WW domain binding protein 2	NM_012478, hCT1814785.1, hCT1960515.1, hCT2266291.0, hCT2357161.0, hCT2357162.0	209117_at	NP_036610.2, EAW89326.1, EAW89325.1, EAW89327.1, EAW89328.1, EAW89329.1
GeneID:91107	TRIM47	17	73,870,245	73,874,656	4,411	-	2	2_A375_pNL97_plus_lncRNA::1::3830, 2_A375_pNL97_plus_lncRNA::1::3831	2048, 128	in gene, in gene	0	1	15	19	2	2_A375_pNL97_plus_lncRNA::1	20	Gene TRIM47	TRIM47, GOA, RNF100	tripartite motif containing 47	NM_033452, hCT1814784.1, hCT2266288.0, hCT2357160.0	225868_at	NP_258411.2, EAW89330.1, EAW89331.1, EAW89332.1
GeneID:85302	FBF1	17	73,906,618	73,937,119	30,501	-	1	2_A375_pNL97_plus_lncRNA::1::3832	-33	upstream	0	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FBF1	KIAA1863, FBF-1, FLJ00103, FLJ13986, Alb, FBF1	Fas (TNFRSF6) binding factor 1	NM_001080542	1554468_s_at, 1555288_s_at, 1556131_s_at	NP_001074011.1
GeneID:51	ACOX1	17	73,937,588	73,975,515	37,927	-	2	2_A375_pNL97_plus_lncRNA::1::3832, 2_A375_pNL97_plus_lncRNA::1::3833	38363, 635	downstream, in gene	0	1	13.5	15.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene ACOX1	PALMCOX, SCOX, ACOX, ACOX1, MGC1198	acyl-CoA oxidase 1, palmitoyl	NM_001185039, NM_004035, NM_007292, hCT1814777.2, hCT1964295.1, hCT2266274.0, hCT2266276.0	207656_s_at, 209600_s_at, 209601_at, 213501_at, 227962_at	NP_001171968.1, NP_004026.2, NP_009223.2, EAW89350.1, EAW89351.1, EAW89352.1, EAW89349.1
GeneID:100134934	C17orf106	17	73,975,301	73,996,667	21,366	+	1	2_A375_pNL97_plus_lncRNA::1::3833	-421	upstream	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene C17orf106	TEN1, MGC54300, DKFZp686C0493, FLJ39785, C17orf106, DKFZp686G1463	chromosome 17 open reading frame 106	NM_001113324		NP_001106795.1
GeneID:6730	SRP68	17	74,035,191	74,068,607	33,416	-	2	1_A375_pNL7_minus_lncRNA::1::2660, 2_A375_pNL97_plus_lncRNA::1::3834	31, 31	in gene, in gene	1	1	29	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene SRP68	SRP68	signal recognition particle 68kDa	NM_014230, hCT2266260.1, hCT2266261.1, hCT2266262.1, hCT2266263.1, hCT2266266.1, hCT2357228.0	224607_s_at	NP_055045.2, EAW89358.1, EAW89359.1, EAW89360.1, EAW89361.1, EAW89363.1, EAW89362.1
GeneID:8811	GALR2	17	74,070,892	74,073,573	2,681	+	2	1_A375_pNL7_minus_lncRNA::1::2660, 2_A375_pNL97_plus_lncRNA::1::3834	-2316, -2316	upstream, upstream	1	1	29	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene GALR2	GALNR2, MGC125983, GALR2, MGC125984	galanin receptor 2	NM_003857, hCT32150.1	211226_at	NP_003848.1, EAW89364.1
GeneID:353174	ZACN	17	74,075,263	74,078,885	3,622	+	2	1_A375_pNL7_minus_lncRNA::1::2660, 2_A375_pNL97_plus_lncRNA::1::3834	-6687, -6687	upstream, upstream	1	1	29	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene ZACN	LGICZ, ZAC, MGC129841, LGICZ1, L2, ZACN, ZAC1	zinc activated ligand-gated ion channel	NM_180990, hCT1649968.3, hCT2357163.0	1555550_at	NP_851321.2, EAW89365.1, EAW89366.1
GeneID:23265	EXOC7	17	74,077,086	74,099,868	22,782	-	2	1_A375_pNL7_minus_lncRNA::1::2660, 2_A375_pNL97_plus_lncRNA::1::3834	31292, 31292	downstream, downstream	1	1	29	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene EXOC7	FLJ40965, DKFZp686J04253, Exo70p, EXO70, 2-5-3p, FLJ46415, EXO70, EXOC7, YJL085W, EXOC1	exocyst complex component 7	NM_001013839, NM_001145297, NM_001145298, NM_001145299, NM_015219, NR_028133, hCT2266267.1, hCT2266268.1, hCT2266269.1, hCT2351235.0, hCT2351236.0, hCT2351237.0, hCT2357219.0, hCT32154.3	212026_s_at, 212034_s_at, 212035_s_at, 214802_at, 215413_at	NP_001013861.1, NP_001138769.1, NP_001138770.1, NP_001138771.1, NP_056034.2, EAW89372.1, EAW89367.1, EAW89368.1, EAW89369.1, EAW89370.1, EAW89371.1, EAW89373.1, EAW89374.1
GeneID:114804	RNF157	17	74,138,534	74,236,390	97,856	-	2	1_A375_pNL7_minus_lncRNA::1::2661, 2_A375_pNL97_plus_lncRNA::1::3835	-794, -602	upstream, upstream	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene RNF157	RNF157	ring finger protein 157	NM_052916, hCT1960711.1, hCT2266256.0, hCT2266258.0, hCT2357211.0, hCT2357212.0	1569775_at, 226433_at	NP_443148.1, EAW89378.1, EAW89379.1, EAW89380.1, EAW89381.1, EAW89382.1
GeneID:100507230	LOC100507230	17	74,541,700	74,549,660	7,960	+	2	1_A375_pNL7_minus_lncRNA::1::2663, 2_A375_pNL97_plus_lncRNA::1::3837	11932, 12092	downstream, downstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100507230		hypothetical LOC100507230	XR_111739, XR_109428, XR_115143		
GeneID:100507246	LOC100507246	17	74,553,846	74,561,430	7,584	+	2	1_A375_pNL7_minus_lncRNA::1::2663, 2_A375_pNL97_plus_lncRNA::1::3837	-214, -54	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100507246		hypothetical LOC100507246	XR_111734, XR_111735, XR_111737, XR_111736, XR_111738, XR_109429, XR_109430, XR_109432, XR_109431, XR_109433, XR_115144, XR_115145, XR_115147, XR_115146, XR_115148		
GeneID:677850	SNORD1C	17	74,554,874	74,554,951	77	+	2	1_A375_pNL7_minus_lncRNA::1::2663, 2_A375_pNL97_plus_lncRNA::1::3837	-1242, -1082	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SNORD1C	SNORD1C, R38C, snR38C	small nucleolar RNA, C/D box 1C	NR_004397		
GeneID:677849	SNORD1B	17	74,557,190	74,557,275	85	+	2	1_A375_pNL7_minus_lncRNA::1::2663, 2_A375_pNL97_plus_lncRNA::1::3837	-3558, -3398	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SNORD1B	snR38B, SNORD1B, R38B	small nucleolar RNA, C/D box 1B	NR_004396		
GeneID:677848	SNORD1A	17	74,557,715	74,557,788	73	+	2	1_A375_pNL7_minus_lncRNA::1::2663, 2_A375_pNL97_plus_lncRNA::1::3837	-4083, -3923	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SNORD1A	SNORD1A, R38A, snR38A	small nucleolar RNA, C/D box 1A	NR_004395		
GeneID:10610	ST6GALNAC2	17	74,561,461	74,582,145	20,684	-	3	1_A375_pNL7_minus_lncRNA::1::2663, 2_A375_pNL97_plus_lncRNA::1::3837, 2_A375_pNL97_plus_lncRNA::1::3838	28513, 28353, 129	downstream, downstream, in gene	1	1	16	16.5	2	1_A375_pNL7_minus_lncRNA::1	18	Gene ST6GALNAC2	SIAT7, ST6GalNAII, SAITL1, SIAT7B, FLJ45660, ST6GALNAC2, SIATL1, STHM	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	NM_006456, hCT1962331.1, hCT22064.3, hCT2357190.0	204542_at	NP_006447.2, EAW89416.1, EAW89417.1, EAW89418.1
GeneID:23210	JMJD6	17	74,708,914	74,722,881	13,967	-	1	2_A375_pNL97_plus_lncRNA::1::3839	641	in gene	0	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene JMJD6	PTDSR, PTDSR1, PSR, JMJD6, KIAA0585	jumonji domain containing 6	NM_015167, NM_001081461, hCT22074.2, hCT2262629.1, hCT2349170.0, hCT2349171.0, hCT2349172.0, hCT2349173.0	1552629_a_at, 212722_s_at, 212723_at, 215233_at	NP_055982.2, NP_001074930.1, EAW89430.1, EAW89431.1, EAW89433.1, EAW89434.1, EAW89429.1, EAW89432.1
GeneID:124512	C17orf95	17	74,722,950	74,729,962	7,012	+	1	2_A375_pNL97_plus_lncRNA::1::3839	-710	upstream	0	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene C17orf95	C17orf95, METTL23	chromosome 17 open reading frame 95	NM_001080510	225808_at	NP_001073979.2
GeneID:6427	SFRS2	17	74,730,197	74,733,412	3,215	-	1	2_A375_pNL97_plus_lncRNA::1::3839	11172	downstream	0	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SFRS2	SFRS2A, SC35, PR264, SC-35, SRp30b, SFRS2, SRSF2	serine/arginine-rich splicing factor 2	NM_003016, hCT18984.3, hCT1955632.1, hCT2348059.0, hCT2348060.0, hCT2348061.0, hCT2348062.0, hCT2348063.0, hCT2348064.0, hCT2348065.0, hCT2357172.0	200753_x_at, 200754_x_at, 214882_s_at	NP_003007.2, EAW89439.1, EAW89440.1, EAW89441.1, EAW89443.1, EAW89445.1, EAW89442.1, EAW89444.1, EAW89446.1, EAW89447.1, EAW89448.1
GeneID:693221	MIR636	17	74,732,532	74,732,630	98	-	1	2_A375_pNL97_plus_lncRNA::1::3839	10390	downstream	0	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene MIR636	MIRN636, hsa-mir-636, MIR636	microRNA 636	NR_030366		
GeneID:146664	MGAT5B	17	74,864,798	74,946,471	81,673	+	3	1_A375_pNL7_minus_lncRNA::1::2664, 2_A375_pNL97_plus_lncRNA::1::3841, 2_A375_pNL97_plus_lncRNA::1::3842	4034, 3986, 41378	in gene, in gene, in gene	1	1	21	25	2	2_A375_pNL97_plus_lncRNA::1	25	Gene MGAT5B	FLJ25132, GnT-IX, GnT-VB, KIAA2008, MGAT5B	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	NM_144677, NM_198955, hCT22067.3, hCT2262120.0, hCT2262122.0, hCT2357191.0	1563137_at, 238445_x_at	NP_653278.2, NP_945193.1, EAW89457.1, EAW89458.1, EAW89459.1, EAW89460.1
GeneID:654434	C17orf86	17	75,084,725	75,091,068	6,343	+	2	1_A375_pNL7_minus_lncRNA::1::2665, 2_A375_pNL97_plus_lncRNA::1::3843	27, 75	in gene, in gene	1	1	38	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene C17orf86	PRO0872, FLJ25582, C17orf86, DKFZp686L05235	chromosome 17 open reading frame 86	NR_027058	221621_at	
GeneID:677781	SCARNA16	17	75,085,389	75,085,575	186	+	2	1_A375_pNL7_minus_lncRNA::1::2665, 2_A375_pNL97_plus_lncRNA::1::3843	-637, -589	upstream, upstream	1	1	38	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene SCARNA16	ACA47, SCARNA16	small Cajal body-specific RNA 16	NR_003013		
GeneID:10801	9-Sep	17	75,277,492	75,496,678	219,186	+	8	1_A375_pNL7_minus_lncRNA::1::2668, 1_A375_pNL7_minus_lncRNA::1::2669, 1_A375_pNL7_minus_lncRNA::1::2670, 2_A375_pNL97_plus_lncRNA::1::3845, 2_A375_pNL97_plus_lncRNA::1::3846, 2_A375_pNL97_plus_lncRNA::1::3847, 2_A375_pNL97_plus_lncRNA::1::3848, 2_A375_pNL97_plus_lncRNA::1::3849	41148, 84428, 144524, 4396, 5660, 6892, 41420, 174380	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	16.57	16.57	7	2_A375_pNL97_plus_lncRNA::1	24	Gene SEPT9	SINT1, FLJ75490, NAPB, MSF1, PNUTL4, SEPT9, MSF, KIAA0991, AF17q25, SeptD1	septin 9	NM_006640, NM_001113491, NM_001113492, NM_001113493, NM_001113494, NM_001113495, NM_001113496, hCT2262128.1, hCT2262129.1, hCT2262130.1, hCT2262131.1, hCT2262133.1, hCT2262134.1, hCT2345069.0, hCT2349049.0	1559025_at, 207425_s_at, 208657_s_at, 41220_at	NP_006631.2, NP_001106963.1, NP_001106964.1, NP_001106965.1, NP_001106966.1, NP_001106967.1, NP_001106968.1, EAW89461.1, EAW89462.1, EAW89463.1, EAW89464.1, EAW89465.1, EAW89466.1, EAW89467.1, EAW89468.1
GeneID:100507304	LOC100507304	17	75,440,786	75,444,581	3,795	+	1	2_A375_pNL97_plus_lncRNA::1::3849	11086	downstream	0	1	19	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100507304	FLJ40589	hypothetical protein LOC100507304	XM_003119687, XM_003118747, XM_003120897		XP_003119735.1, XP_003118795.1, XP_003120945.1
GeneID:400624	FLJ45079	17	75,875,083	75,880,169	5,086	-	1	2_A375_pNL97_plus_lncRNA::1::3850	-3943	upstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FLJ45079	FLJ46474	FLJ45079 protein	NR_026337, hCT2360334.0		EAW89479.1
GeneID:7083	TK1	17	76,170,160	76,183,285	13,125	-	1	2_A375_pNL97_plus_lncRNA::1::3851	149	in gene	0	1	23	44	1	2_A375_pNL97_plus_lncRNA::1	44	Gene TK1	TK2, TK1	thymidine kinase 1, soluble	NM_003258, hCT1962330.1, hCT1967444.1, hCT20555.2, hCT2336886.0	1554408_a_at, 202338_at, 243103_at	NP_003249.3, EAW89506.1, EAW89505.1, EAW89507.1, EAW89508.1
GeneID:125061	AFMID	17	76,183,398	76,203,782	20,384	+	3	1_A375_pNL7_minus_lncRNA::1::2671, 2_A375_pNL97_plus_lncRNA::1::3851, 2_A375_pNL97_plus_lncRNA::1::3852	26922, -262, 27002	downstream, upstream, downstream	1	1	23	36	2	2_A375_pNL97_plus_lncRNA::1	44	Gene AFMID	MGC167063, DKFZp686F03259, KF, AFMID	arylformamidase	NM_001010982, NR_027083, NM_001145526, hCT20560.4, hCT2351965.0	240318_at	NP_001010982.2, NP_001138998.1, EAW89509.1, EAW89510.1
GeneID:332	BIRC5	17	76,210,277	76,221,716	11,439	+	2	1_A375_pNL7_minus_lncRNA::1::2671, 2_A375_pNL97_plus_lncRNA::1::3852	43, 123	in gene, in gene	1	1	23	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene BIRC5	EPR-1, BIRC5, API4	baculoviral IAP repeat containing 5	NM_001168, NM_001012270, NM_001012271, hCT18953.2, hCT1955629.1, hCT1962326.1, hCT1962327.2	202094_at, 202095_s_at, 210334_x_at	NP_001159.2, NP_001012270.1, NP_001012271.1, EAW89511.1, EAW89513.1, EAW89514.1, EAW89512.1
GeneID:8475	EPR1	17	76,210,321	76,220,783	10,462	-	2	1_A375_pNL7_minus_lncRNA::1::2671, 2_A375_pNL97_plus_lncRNA::1::3852	10463, 10383	downstream, in gene	1	1	23	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene EPR1	BIRC5AS, NCRNA00007, EPR-1, EPR1, BIRC5OS, BIRC5-AS1	effector cell peptidase receptor 1 (non-protein coding)	NR_002219	1555826_at	
GeneID:9021	SOCS3	17	76,352,859	76,356,158	3,299	-	2	2_A375_pNL97_plus_lncRNA::1::3855, 2_A375_pNL97_plus_lncRNA::1::3856	-770, -5026	upstream, upstream	0	1	15.5	20	2	2_A375_pNL97_plus_lncRNA::1	21	Gene SOCS3	CIS3, SSI3, Cish3, MGC71791, SOCS3, SOCS-3, ATOD4, SSI-3	suppressor of cytokine signaling 3	NM_003955, hCT1815063.2, hCT2336905.0	206359_at, 206360_s_at, 214105_at, 227697_at	NP_003946.3, EAW89522.1, EAW89521.1
GeneID:8632	DNAH17	17	76,419,778	76,573,476	153,698	-	1	2_A375_pNL97_plus_lncRNA::1::3857	110692	in gene	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene DNAH17	MGC138489, DNAHL1, DNEL2, DNAH17, FLJ40457, MGC132767	dynein, axonemal, heavy chain 17	NM_173628	214229_at	NP_775899.3

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:57602	USP36	17	76,792,965	76,836,969	44,004	-	2	1_A375_pNL7_minus_lncRNA::1::2673, 2_A375_pNL97_plus_lncRNA::1::3858	9, -7	in gene, upstream	1	1	98	101	1	2_A375_pNL97_plus_lncRNA::1	101	Gene USP36	USP36, DUB1	ubiquitin specific peptidase 36	NM_025090, hCT2263688.0, hCT2263690.0, hCT2357166.0, hCT66865.3	1554636_at, 220370_s_at, 224976_s_at, 224979_s_at, 227093_at	NP_079366.3, EAW89534.1, EAW89533.1, EAW89535.1, EAW89536.1
GeneID:7077	TIMP2	17	76,849,059	76,921,472	72,413	-	2	2_A375_pNL97_plus_lncRNA::1::3859, 2_A375_pNL97_plus_lncRNA::1::3860	41861, -8272	in gene, upstream	0	1	13.5	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene TIMP2	TIMP2, CSC-21K	TIMP metallopeptidase inhibitor 2	NM_003255, hCT1958640.1, hCT1958641.1, hCT2357197.0, hCT66872.3	203167_at, 224560_at, 231579_s_at	NP_003246.1, EAW89540.1, EAW89538.1, EAW89539.1, EAW89541.1
GeneID:146713	hCG_1776007	17	77,085,427	77,478,563	393,136	-	3	1_A375_pNL7_minus_lncRNA::1::2674, 2_A375_pNL97_plus_lncRNA::1::3861, 2_A375_pNL97_plus_lncRNA::1::3862	187843, 289795, 187779	in gene, in gene, in gene	1	1	18.5	28.5	2	2_A375_pNL97_plus_lncRNA::1	31	Gene hCG_1776007	HRNBP3, FOX-3, RBFOX3, FOX3, NEUN, FLJ58356, FLJ56884	RNA binding protein, fox-1 homolog (C. elegans) 3	NM_001082575	229406_at, 235466_at, 240975_x_at	NP_001076044.1
GeneID:100507425	LOC100507425	17	77,774,397	77,776,328	1,931	+	1	2_A375_pNL97_plus_lncRNA::1::3863	11075	downstream	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100507425		hypothetical LOC100507425	XR_111748, XR_109436, XR_115152		
GeneID:55036	CCDC40	17	78,010,435	78,074,412	63,977	+	2	1_A375_pNL7_minus_lncRNA::1::2675, 2_A375_pNL97_plus_lncRNA::1::3864	27773, 27837	in gene, in gene	1	1	24	19	1	1_A375_pNL7_minus_lncRNA::1	24	Gene CCDC40	FLJ32021, FLJ20753, CCDC40, KIAA1640	coiled-coil domain containing 40	NM_017950	1563563_at, 220592_at, 220593_s_at, 229918_at, 239254_at	NP_060420.2
GeneID:6448	SGSH	17	78,183,079	78,194,199	11,120	-	1	2_A375_pNL97_plus_lncRNA::1::3865	151	in gene	0	1	11	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SGSH	HSS, SGSH, MPS3A, SFMD	N-sulfoglucosamine sulfohydrolase	NM_000199, hCT19722.3, hCT2357146.0	204293_at, 35626_at	NP_000190.1, EAW89591.1, EAW89590.1
GeneID:284129	SLC26A11	17	78,194,200	78,227,308	33,108	+	2	2_A375_pNL97_plus_lncRNA::1::3865, 2_A375_pNL97_plus_lncRNA::1::3866	-152, 41064	upstream, downstream	0	1	10	16.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene SLC26A11	MGC46523, SLC26A11	solute carrier family 26, member 11	NM_001166347, NM_001166348, NM_001166349, NM_173626, hCT1814680.2	226679_at	NP_001159819.1, NP_001159820.1, NP_001159821.1, NP_775897.3, EAW89592.1
GeneID:57674	RNF213	17	78,234,667	78,370,086	135,419	+	1	2_A375_pNL97_plus_lncRNA::1::3866	597	in gene	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene RNF213	KIAA1618, MGC9929, FLJ13051, C17orf27, KIAA1554, DKFZp762N1115, RNF213, NET57, MGC46622	ring finger protein 213	NM_020954, NM_020914, hCT2343543.1, hCT2347539.0, hCT2350173.0, hCT2350174.0, hCT2350175.0, hCT2350176.0	1569078_at, 225929_s_at, 225931_s_at, 230000_at, 233880_at, 241480_at	NP_066005.2, NP_065965.4, EAW89595.1, EAW89596.1, EAW89597.1, EAW89599.1, EAW89598.1, EAW89600.1
GeneID:100294362	LOC100294362	17	78,325,630	78,388,968	63,338	-	2	1_A375_pNL7_minus_lncRNA::1::2676, 2_A375_pNL97_plus_lncRNA::1::3867	-728, -13	upstream, upstream	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100294362		hypothetical LOC100294362	NR_029376		
GeneID:284131	FLJ35220	17	78,388,967	78,411,886	22,919	+	3	1_A375_pNL7_minus_lncRNA::1::2676, 2_A375_pNL97_plus_lncRNA::1::3867, 2_A375_pNL97_plus_lncRNA::1::3868	729, 14, 26073	in gene, in gene, downstream	1	1	15.5	23.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene FLJ35220	MGC74455	hypothetical protein FLJ35220	NM_173627, NM_001164637, NM_001164638, hCT2341046.1, hCT2341047.0, hCT2341048.0, hCT2341049.0, hCT2341050.1, hCT2341051.1, hCT2349108.0, hCT2349109.0, hCT2349110.0, hCT2349111.0, hCT2349112.0, hCT2357225.0, hCT2357226.0, hCT2357227.0	238400_at, 238401_at, 238402_s_at	NP_775898.2, NP_001158109.1, NP_001158110.1, EAW89602.1, EAW89612.1, EAW89615.1, EAW89603.1, EAW89604.1, EAW89605.1, EAW89606.1, EAW89607.1, EAW89608.1, EAW89609.1, EAW89610.1, EAW89611.1, EAW89613.1, EAW89614.1
GeneID:100507440	LOC100507440	17	78,391,217	78,392,679	1,462	+	2	1_A375_pNL7_minus_lncRNA::1::2676, 2_A375_pNL97_plus_lncRNA::1::3867	-1521, -2236	upstream, upstream	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100507440		hypothetical LOC100507440	XR_111750, XR_109437, XR_115153		
GeneID:57521	RPTOR	17	78,518,625	78,940,173	421,548	+	6	1_A375_pNL7_minus_lncRNA::1::2677, 2_A375_pNL97_plus_lncRNA::1::3870, 2_A375_pNL97_plus_lncRNA::1::3871, 2_A375_pNL97_plus_lncRNA::1::3872, 2_A375_pNL97_plus_lncRNA::1::3873, 2_A375_pNL97_plus_lncRNA::1::3874	85, 191, 105119, 288367, 328943, 347663	in gene, in gene, in gene, in gene, in gene, in gene	1	1	15.6	21.4	5	2_A375_pNL97_plus_lncRNA::1	26	Gene RPTOR	KIAA1303, KOG1, Mip1, RPTOR	regulatory associated protein of MTOR, complex 1	NM_020761, NM_001163034, hCT18416.4, hCT2263678.1	225715_at	NP_065812.1, NP_001156506.1, EAW89618.1, EAW89619.1
GeneID:100507520	LOC100507520	17	79,361,922	79,364,687	2,765	-	4	1_A375_pNL7_minus_lncRNA::1::2678, 1_A375_pNL7_minus_lncRNA::1::2679, 2_A375_pNL97_plus_lncRNA::1::3875, 2_A375_pNL97_plus_lncRNA::1::3876	-3153, -4129, -3345, -5745	upstream, upstream, upstream, upstream	1	1	17.67	15	3	1_A375_pNL7_minus_lncRNA::1	21	Gene LOC100507520		hypothetical LOC100507520	XR_109439, XR_109440		
GeneID:57597	BAHCC1	17	79,373,540	79,433,358	59,818	+	4	1_A375_pNL7_minus_lncRNA::1::2678, 1_A375_pNL7_minus_lncRNA::1::2679, 2_A375_pNL97_plus_lncRNA::1::3875, 2_A375_pNL97_plus_lncRNA::1::3876	-5700, -4724, -5508, -3108	upstream, upstream, upstream, upstream	1	1	17.67	15	3	1_A375_pNL7_minus_lncRNA::1	21	Gene BAHCC1	BAHCC1, BAHD2, FLJ23058, KIAA1447	BAH domain and coiled-coil containing 1	NM_001080519	1559048_at, 1559049_a_at, 1559075_s_at, 219218_at, 236604_at	NP_001073988.2
GeneID:100507545	LOC100507545	17	79,454,310	79,493,204	38,894	+	2	2_A375_pNL97_plus_lncRNA::1::3877, 2_A375_pNL97_plus_lncRNA::1::3878	25018, 26170	in gene, in gene	0	1	14.5	18	2	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100507545		hypothetical LOC100507545	XR_109444, XR_109445, XR_109441, XR_109442, XR_109443, XR_109446		
GeneID:71	ACTG1	17	79,476,999	79,479,827	2,828	-	2	2_A375_pNL97_plus_lncRNA::1::3877, 2_A375_pNL97_plus_lncRNA::1::3878	499, -653	in gene, upstream	0	1	14.5	18	2	2_A375_pNL97_plus_lncRNA::1	19	Gene ACTG1	DFNA20, ACT, ACTG1, ACTG, DFNA26	actin, gamma 1	NM_001614	201550_x_at, 211970_x_at, 211983_x_at, 211995_x_at, 212363_x_at, 212988_x_at, 213214_x_at, 221607_x_at, 224585_x_at	NP_001605.1
GeneID:5148	PDE6G	17	79,617,489	79,623,607	6,118	-	1	2_A375_pNL97_plus_lncRNA::1::3879	-10121	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PDE6G	DKFZp686C0587, PDE6G, RP57, PDEG, MGC125749	phosphodiesterase 6G, cGMP-specific, rod, gamma	NM_002602, NR_026872, hCT29293.3	210060_at	NP_002593.1, EAW89666.1
GeneID:339229	C17orf90	17	79,632,066	79,633,618	1,552	-	1	2_A375_pNL97_plus_lncRNA::1::3879	-110	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene C17orf90	MGC104712, C17orf90	chromosome 17 open reading frame 90	NM_001039842	221797_at, 50374_at	NP_001034931.1
GeneID:339230	CCDC137	17	79,633,761	79,640,937	7,176	+	3	1_A375_pNL7_minus_lncRNA::1::2680, 2_A375_pNL97_plus_lncRNA::1::3879, 2_A375_pNL97_plus_lncRNA::1::3880	17151, -33, 17327	downstream, upstream, downstream	1	1	17.5	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene CCDC137	MGC16597, CCDC137	coiled-coil domain containing 137	NM_199287	225933_at	NP_954981.1
GeneID:339231	ARL16	17	79,646,224	79,650,954	2,730	-	2	1_A375_pNL7_minus_lncRNA::1::2680, 2_A375_pNL97_plus_lncRNA::1::3880	42, -134	in gene, upstream	1	1	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ARL16	ARL16	ADP-ribosylation factor-like 16	NM_001040025	234972_at	NP_001035114.1
GeneID:9146	HGS	17	79,651,020	79,669,148	18,128	+	4	1_A375_pNL7_minus_lncRNA::1::2680, 1_A375_pNL7_minus_lncRNA::1::2681, 2_A375_pNL97_plus_lncRNA::1::3880, 2_A375_pNL97_plus_lncRNA::1::3881	-108, 19476, 68, 19380	upstream, downstream, in gene, downstream	1	1	20.5	19	2	1_A375_pNL7_minus_lncRNA::1	21	Gene HGS	Vps27, FLJ11421, FLJ39876, HRS, ZFYVE8, HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	NM_004712, hCT2263545.1, hCT2263546.1, hCT2263548.1, hCT2263549.1, hCT2263550.1	210428_s_at	NP_004703.1, EAW89678.1, EAW89675.1, EAW89676.1, EAW89677.1, EAW89679.1
GeneID:6182	MRPL12	17	79,670,407	79,674,548	4,141	+	2	1_A375_pNL7_minus_lncRNA::1::2681, 2_A375_pNL97_plus_lncRNA::1::3881	89, -7	in gene, upstream	1	1	21	21	1	1_A375_pNL7_minus_lncRNA::1	21	Gene MRPL12	RPML12, 5c5-2, MRPL12, L12mt, MGC8610, MRP-L31/34, MRPL7/L12, FLJ60124, MRPL7	mitochondrial ribosomal protein L12	NM_002949, hCT2263543.1	203931_s_at, 229165_at	NP_002940.2, EAW89680.1
GeneID:1468	SLC25A10	17	79,679,371	79,688,042	8,671	+	2	1_A375_pNL7_minus_lncRNA::1::2681, 2_A375_pNL97_plus_lncRNA::1::3881	-8875, -8971	upstream, upstream	1	1	21	21	1	1_A375_pNL7_minus_lncRNA::1	21	Gene SLC25A10	SLC25A10, DIC	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	NM_012140, hCT2263558.0, hCT29163.3	218275_at	NP_036272.2, EAW89681.1, EAW89682.1
GeneID:5034	P4HB	17	79,801,034	79,818,544	17,510	-	2	2_A375_pNL97_plus_lncRNA::1::3882, 2_A375_pNL97_plus_lncRNA::1::3883	-432, -6624	upstream, upstream	0	1	10.5	21	2	2_A375_pNL97_plus_lncRNA::1	24	Gene P4HB	P4HB, PO4DB, PDI, GIT, PDIA1, DSI, PROHB, PHDB, P4Hbeta, PO4HB, ERBA2L	prolyl 4-hydroxylase, beta polypeptide	NM_000918, hCT2269585.0, hCT2269587.0, hCT2269591.0, hCT2269593.0, hCT2269595.0, hCT2357183.0, hCT87194.3	1564494_s_at, 200654_at, 200656_s_at	NP_000909.2, EAW89691.1, EAW89690.1, EAW89693.1, EAW89695.1, EAW89696.1, EAW89692.1, EAW89694.1
GeneID:396	ARHGDIA	17	79,825,597	79,829,282	3,685	-	4	1_A375_pNL7_minus_lncRNA::1::2682, 2_A375_pNL97_plus_lncRNA::1::3882, 2_A375_pNL97_plus_lncRNA::1::3883, 2_A375_pNL97_plus_lncRNA::1::3884	-94, 10306, 4114, -158	upstream, downstream, downstream, upstream	1	1	20.67	27.33	3	1_A375_pNL7_minus_lncRNA::1	41	Gene ARHGDIA	RHOGDI-1, MGC117248, ARHGDIA, RHOGDI, GDIA1	Rho GDP dissociation inhibitor (GDI) alpha	NM_001185077, NM_001185078, NM_004309, hCT1968278.1, hCT1968279.1	201167_x_at, 211716_x_at, 213606_s_at	NP_001172006.1, NP_001172007.1, NP_004300.1, EAW89697.1, EAW89698.1
GeneID:51547	SIRT7	17	79,869,815	79,876,058	6,243	-	2	1_A375_pNL7_minus_lncRNA::1::2683, 2_A375_pNL97_plus_lncRNA::1::3885	-9638, -9590	upstream, upstream	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene SIRT7	SIRT7, MGC126840, MGC126842, SIR2L7	sirtuin (silent mating type information regulation 2 homolog) 7 (S. cerevisiae)	NM_016538	218797_s_at	NP_057622.1
GeneID:4097	MAFG	17	79,876,146	79,885,588	9,442	-	2	1_A375_pNL7_minus_lncRNA::1::2683, 2_A375_pNL97_plus_lncRNA::1::3885	-108, -60	upstream, upstream	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MAFG	MAFG, MGC20149, MGC13090	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	NM_032711, NM_002359	204970_s_at, 224466_s_at	NP_116100.2, NP_002350.1
GeneID:92659	LOC92659	17	79,885,705	79,888,629	2,924	+	2	1_A375_pNL7_minus_lncRNA::1::2683, 2_A375_pNL97_plus_lncRNA::1::3885	-9, -57	upstream, upstream	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC92659		hypothetical LOC92659	NR_015454	1559352_a_at	
GeneID:5831	PYCR1	17	79,890,267	79,894,968	4,701	-	2	1_A375_pNL7_minus_lncRNA::1::2683, 2_A375_pNL97_plus_lncRNA::1::3885	9272, 9320	downstream, downstream	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene PYCR1	P5C, PYCR1, PIG45, PP222, ARCL2B, PYCR, P5CR, PRO3	pyrroline-5-carboxylate reductase 1	NM_153824, NM_006907, hCT1963925.2, hCT1963926.2, hCT1963927.2, hCT2269558.1, hCT2269560.1, hCT2269562.1, hCT2269563.1, hCT2349174.0, hCT2349175.0, hCT30049.3	202148_s_at	NP_722546.1, NP_008838.2, EAW89717.1, EAW89718.1, EAW89719.1, EAW89720.1, EAW89721.1, EAW89722.1, EAW89723.1, EAW89724.1, EAW89725.1, EAW89726.1
GeneID:79058	ASPSCR1	17	79,935,426	79,975,282	39,856	+	2	1_A375_pNL7_minus_lncRNA::1::2684, 2_A375_pNL97_plus_lncRNA::1::3886	26270, 26366	in gene, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ASPSCR1	ASPS, TUG, UBXN9, ASPL, UBXD9, RCC17, ASPSCR1, ASPCR1, FLJ45380	alveolar soft part sarcoma chromosome region, candidate 1	NM_024083, hCT87197.3	218908_at	NP_076988.1, EAW89731.1
GeneID:201254	STRA13	17	79,976,579	79,980,773	4,194	-	1	2_A375_pNL97_plus_lncRNA::1::3887	-7835	upstream	0	1	22	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene STRA13	STRA13, MHF2, CENP-X, MGC14480	stimulated by retinoic acid 13 homolog (mouse)	NM_144998		NP_659435.2
GeneID:201255	LRRC45	17	79,981,280	79,989,027	7,747	+	3	1_A375_pNL7_minus_lncRNA::1::2685, 2_A375_pNL97_plus_lncRNA::1::3887, 2_A375_pNL97_plus_lncRNA::1::3888	14112, 7328, 13840	downstream, in gene, downstream	1	1	21.5	20	2	2_A375_pNL97_plus_lncRNA::1	24	Gene LRRC45	MGC20806, LRRC45	leucine rich repeat containing 45	NM_144999	226253_at	NP_659436.1
GeneID:5881	RAC3	17	79,989,532	79,992,080	2,548	+	3	1_A375_pNL7_minus_lncRNA::1::2685, 2_A375_pNL97_plus_lncRNA::1::3887, 2_A375_pNL97_plus_lncRNA::1::3888	5860, -924, 5588	downstream, upstream, downstream	1	1	21.5	20	2	2_A375_pNL97_plus_lncRNA::1	24	Gene RAC3	RAC3		NM_005052	206103_at	NP_005043.1
GeneID:51181	DCXR	17	79,993,757	79,995,573	1,816	-	3	1_A375_pNL7_minus_lncRNA::1::2685, 2_A375_pNL97_plus_lncRNA::1::3887, 2_A375_pNL97_plus_lncRNA::1::3888	181, 6965, 453	in gene, downstream, in gene	1	1	21.5	20	2	2_A375_pNL97_plus_lncRNA::1	24	Gene DCXR	KIDCR, P34H, HCR2, DCXR, SDR20C1, HCRII, DCR	dicarbonyl/L-xylulose reductase	NM_016286, hCT1957261.0, hCT31858.3	217973_at	NP_057370.1, EAW89732.1, EAW89733.1
GeneID:5986	RFNG	17	80,005,778	80,009,650	3,872	-	1	1_A375_pNL7_minus_lncRNA::1::2685	14258	downstream	1	0	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene RFNG	RFNG		NM_002917, hCT1970473.0, hCT2269547.0, hCT2269548.0, hCT2269549.0, hCT2269550.0, hCT2357207.0	212968_at	NP_002908.1, EAW89735.1, EAW89736.1, EAW89737.1, EAW89738.1, EAW89739.1, EAW89740.1
GeneID:2194	FASN	17	80,036,214	80,056,106	19,892	-	1	1_A375_pNL7_minus_lncRNA::1::2686	826	in gene	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene FASN	MGC14367, FAS, FASN, MGC15706, OA-519, SDR27X1	fatty acid synthase	NM_004104, hCT31647.3	212218_s_at	NP_004095.4, EAW89745.1
GeneID:284001	CCDC57	17	80,059,346	80,170,689	111,343	-	3	1_A375_pNL7_minus_lncRNA::1::2686, 2_A375_pNL97_plus_lncRNA::1::3889, 2_A375_pNL97_plus_lncRNA::1::3890	115409, 17, -4511	downstream, in gene, upstream	1	1	14	18	3	2_A375_pNL97_plus_lncRNA::1	21	Gene CCDC57	FLJ23754, CCDC57, FLJ00130, MGC102869, FLJ43953	coiled-coil domain containing 57	NM_198082	1553248_at, 1554554_at, 214818_at, 234661_at	NP_932348.2
GeneID:79701	C17orf101	17	80,347,086	80,376,513	29,427	-	2	1_A375_pNL7_minus_lncRNA::1::2688, 2_A375_pNL97_plus_lncRNA::1::3892	97, 97	in gene, in gene	1	1	25	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene C17orf101	C17orf101, FLJ22222	chromosome 17 open reading frame 101	NM_175902, NM_024648, NR_033265, hCT1950963.1, hCT2269518.0	219254_at, 53071_s_at, 64438_at	NP_787096.3, NP_078924.1, EAW89769.1, EAW89770.1
GeneID:284004	HEXDC	17	80,376,252	80,400,516	24,264	+	2	1_A375_pNL7_minus_lncRNA::1::2688, 2_A375_pNL97_plus_lncRNA::1::3892	164, 164	in gene, in gene	1	1	25	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene HEXDC	FLJ23825, HEXDC	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	NM_173620, hCT1642303.3, hCT1966860.1, hCT1966862.1, hCT2357229.0, hCT2357230.0	1555866_a_at, 238033_at, 238591_at	NP_775891.2, EAW89771.1, EAW89772.1, EAW89773.1, EAW89774.1, EAW89775.1
GeneID:100505970	LOC100505970	17	80,383,374	80,385,186	1,812	+	2	1_A375_pNL7_minus_lncRNA::1::2688, 2_A375_pNL97_plus_lncRNA::1::3892	-6958, -6958	upstream, upstream	1	1	25	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene LOC100505970		hypothetical protein LOC100505970	XM_003118729		XP_003118777.1
GeneID:79415	C17orf62	17	80,400,462	80,406,707	6,245	-	2	1_A375_pNL7_minus_lncRNA::1::2689, 2_A375_pNL97_plus_lncRNA::1::3893	-7693, -7421	upstream, upstream	1	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C17orf62	MGC4368, FLJ00406, FLJ90469, C17orf62	chromosome 17 open reading frame 62	NM_001100407, NM_001100408, NM_001033046, NM_001193653, NM_001193654, NM_001193655, NM_001193657, NR_036514, NR_036516, NR_036517, NR_036518, NR_036519, hCT1970609.2, hCT1970611.2, hCT21555.4, hCT2349398.0, hCT2349399.0, hCT2349400.0, hCT2349401.0, hCT234	218130_at	NP_001093877.1, NP_001093878.1, NP_001028218.1, NP_001180582.1, NP_001180583.1, NP_001180584.1, NP_001180586.1, EAW89776.1, EAW89777.1, EAW89778.1, EAW89779.1, EAW89780.1, EAW89782.1, EAW89783.1, EAW89781.1, EAW89784.1, EAW89785.1, EAW89786.1, EAW89787.1,
GeneID:26502	NARF	17	80,416,060	80,446,143	30,083	+	2	1_A375_pNL7_minus_lncRNA::1::2689, 2_A375_pNL97_plus_lncRNA::1::3893	340, 68	in gene, in gene	1	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene NARF	IOP2, DKFZp434G0420, NARF, FLJ10067	nuclear prelamin A recognition factor	NM_031968, NM_012336, NM_001038618, NM_001083608	219862_s_at	NP_114174.1, NP_036468.1, NP_001077077.1, NP_001033707.1
GeneID:3607	FOXK2	17	80,477,594	80,562,483	84,889	+	1	2_A375_pNL97_plus_lncRNA::1::3894	-186	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene FOXK2	ILF1, FOXK2, ILF, ILF-1	forkhead box K2	NM_004514, hCT1964900.2, hCT1965800.2, hCT21552.3	203064_s_at, 226224_at, 242938_s_at	NP_004505.2, EAW89802.1, EAW89800.1, EAW89801.1
GeneID:56270	WDR45L	17	80,572,438	80,606,411	33,973	-	1	2_A375_pNL97_plus_lncRNA::1::3895	155	in gene	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene WDR45L	WDR45L, WIPI-3, WIPI3	WDR45-like	NM_019613, hCT1959591.2, hCT1970601.1, hCT1970602.1, hCT21550.3, hCT2262724.0, hCT2357147.0, hCT2357148.0	209076_s_at	NP_062559.2, EAW89808.1, EAW89809.1, EAW89810.1, EAW89812.1, EAW89814.1, EAW89811.1, EAW89813.1
GeneID:100506019	LOC100506019	17	80,612,843	80,614,757	1,914	-	1	2_A375_pNL97_plus_lncRNA::1::3895	8501	downstream	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100506019		hypothetical LOC100506019	XR_109349		
GeneID:10966	RAB40B	17	80,614,943	80,656,598	41,655	-	1	2_A375_pNL97_plus_lncRNA::1::3895	50342	downstream	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene RAB40B	FLJ42385, RAB40B, RAR, SEC4L	RAB40B, member RAS oncogene family	NM_006822, hCT2262719.0	204547_at, 217597_x_at	NP_006813.1, EAW89815.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:64122	FN3K	17	80,693,452	80,709,073	15,621	+	2	1_A375_pNL7_minus_lncRNA::1::2690, 2_A375_pNL97_plus_lncRNA::1::3896	16452, 16404	downstream, downstream	1	1	25	25	1	1_A375_pNL7_minus_lncRNA::1	25	Gene FN3K	FN3K	fructosamine 3 kinase	NM_022158, hCT2262455.0, hCT2262457.0	219744_at	NP_071441.1, EAW89620.1, EAW89619.1
GeneID:6904	TBCD	17	80,709,940	80,901,062	191,122	+	2	1_A375_pNL7_minus_lncRNA::1::2690, 2_A375_pNL97_plus_lncRNA::1::3896	-36, -54	upstream, upstream	1	1	25	25	1	1_A375_pNL7_minus_lncRNA::1	25	Gene TBCD	TBCD, KIAA0988	tubulin folding cofactor D	NM_005993, hCT21554.4, hCT2262460.1, hCT2262462.1	201759_at, 211052_s_at, 216128_at, 228191_at, 228192_s_at, 229767_at	NP_005984.3, EAW89623.1, EAW89621.1, EAW89622.1
GeneID:146712	B3GNTL1	17	80,901,667	81,009,686	108,019	-	2	2_A375_pNL97_plus_lncRNA::1::3897, 2_A375_pNL97_plus_lncRNA::1::3898	65558, 556	in gene, in gene	0	1	11	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene B3GNTL1	B3GNTL1, B3GNT8, MGC126256, MGC126253	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	NM_001009905	213589_s_at, 215055_at	NP_001009905.1
GeneID:9984	THOC1	18	214,520	268,059	53,539	-	1	2_A375_pNL97_plus_lncRNA::1::3899	91	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene THOC1	THOC1, HPR1, P84, P84N5	THO complex 1	NM_005131, hCT1967813.1, hCT2274464.0, hCT2274466.0, hCT29266.3	204064_at	NP_005122.2, EAX01732.1, EAX01731.1, EAX01733.1, EAX01734.1
GeneID:27098	CLUL1	18	596,998	650,298	53,300	+	1	2_A375_pNL97_plus_lncRNA::1::3900	61114	downstream	0	1	10	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CLUL1	CLUL1, RA337M	clusterin-like 1 (retinal)	NM_199167, NM_014410, hCT2274779.0, hCT2274781.0, hCT29263.3	206556_at	NP_954636.1, NP_055225.1, EAX01724.1, EAX01725.1, EAX01726.1
GeneID:494514	C18orf56	18	649,620	658,340	8,720	-	1	2_A375_pNL97_plus_lncRNA::1::3900	228	in gene	0	1	10	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C18orf56	C18orf56	chromosome 18 open reading frame 56	NM_001012716, hCT2274455.0	228989_at	NP_001012734.2, EAX01723.1
GeneID:7298	TYMS	18	657,604	673,499	15,895	+	1	2_A375_pNL97_plus_lncRNA::1::3900	508	in gene	0	1	10	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TYMS	HST422, MGC88736, TYMS, TS, TMS	thymidylate synthetase	NM_001071, hCT2274763.0, hCT2274764.0, hCT2274765.0, hCT2343415.0, hCT2343416.0, hCT2343417.0, hCT2343418.0	1554696_s_at, 202589_at, 217684_at	NP_001062.1, EAX01721.1, EAX01716.1, EAX01717.1, EAX01720.1, EAX01722.1, EAX01718.1, EAX01719.1
GeneID:116	ADCYAP1	18	904,944	912,173	7,229	+	2	1_A375_pNL7_minus_lncRNA::1::2691, 2_A375_pNL97_plus_lncRNA::1::3901	-1120, -1104	upstream, upstream	1	1	39	39	1	1_A375_pNL7_minus_lncRNA::1	39	Gene ADCYAP1	ADCYAP1, PACAP, MGC126852	adenylate cyclase activating polypeptide 1 (pituitary)	NM_001099733, NM_001117, hCT28458.2	206281_at	NP_001093203.1, NP_001108.2, EAX01706.1
GeneID:64863	METTL4	18	2,537,524	2,571,489	33,965	-	1	2_A375_pNL97_plus_lncRNA::1::3903	-31	upstream	0	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene METTL4	FLJ23017, HsT661, MGC117235, METTL4	methyltransferase like 4	NM_022840, hCT29653.3	219698_s_at, 232194_at	NP_073751.3, EAX01698.1
GeneID:10403	NDC80	18	2,571,510	2,616,634	45,124	+	1	2_A375_pNL97_plus_lncRNA::1::3903	10	in gene	0	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene NDC80	HEC, KNTC2, TID3, hsNDC80, NDC80, HEC1	NDC80 homolog, kinetochore complex component (S. cerevisiae)	NM_006101, hCT1967816.1, hCT29652.2	204162_at	NP_006092.1, EAX01697.1, EAX01696.1
GeneID:645158	LOC645158	18	2,652,722	2,653,231	509	-	1	2_A375_pNL97_plus_lncRNA::1::3905	-3025	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC645158		chromobox homolog 3 pseudogene	NR_033754	1557458_at	
GeneID:23347	SMCHD1	18	2,655,886	2,805,015	149,129	+	1	2_A375_pNL97_plus_lncRNA::1::3905	370	in gene	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SMCHD1	SMCHD1, KIAA0650, DKFZp686O0631	structural maintenance of chromosomes flexible hinge domain containing 1	NM_015295	1558747_at, 212569_at, 212577_at, 212579_at, 241620_at, 241621_at	NP_056110.2
GeneID:84034	EMILIN2	18	2,847,028	2,914,090	67,062	+	1	2_A375_pNL97_plus_lncRNA::1::3906	59052	in gene	0	1	6	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene EMILIN2	FOAP-10, FLJ33200, EMILIN-2, EMILIN2	elastin microfibril interfacer 2	NM_032048, hCT1646254.3	221980_at, 224374_s_at, 242268_s_at	NP_114437.2, EAX01690.1
GeneID:10627	MYL12A	18	3,247,528	3,256,234	8,706	+	4	1_A375_pNL7_minus_lncRNA::1::2693, 1_A375_pNL7_minus_lncRNA::1::2694, 2_A375_pNL97_plus_lncRNA::1::3907, 2_A375_pNL97_plus_lncRNA::1::3908	120, 14424, 88, 14440	in gene, downstream, in gene, downstream	1	1	23	25	2	2_A375_pNL97_plus_lncRNA::1	32	Gene MYL12A	MYL12A, MYL2B, MRCL3, MLCB, MRLC3	myosin, light chain 12A, regulatory, non-sarcomeric	NM_006471, hCT2275383.1, hCT2275384.1, hCT2360791.0, hCT2360792.0	201319_at	NP_006462.1, EAX01678.1, EAX01679.1, EAX01680.1, EAX01681.1
GeneID:100505577	LOC100505577	18	3,255,434	3,261,845	6,411	-	4	1_A375_pNL7_minus_lncRNA::1::2693, 1_A375_pNL7_minus_lncRNA::1::2694, 2_A375_pNL97_plus_lncRNA::1::3907, 2_A375_pNL97_plus_lncRNA::1::3908	14197, -107, 14229, -123	downstream, upstream, downstream, upstream	1	1	23	25	2	2_A375_pNL97_plus_lncRNA::1	32	Gene LOC100505577		hypothetical LOC100505577	XR_111760, XR_109462, XR_115161		
GeneID:103910	MYL12B	18	3,262,111	3,278,282	16,171	+	2	1_A375_pNL7_minus_lncRNA::1::2694, 2_A375_pNL97_plus_lncRNA::1::3908	-159, -143	upstream, upstream	1	1	26	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene MYL12B	MLC-B, MRLC2, MYL12B	myosin, light chain 12B, regulatory	NM_033546, NM_001144944, NM_001144945, hCT2275385.1, hCT2275386.1, hCT2360793.0	221474_at	NP_291024.1, NP_001138416.1, NP_001138417.1, EAX01675.1, EAX01676.1, EAX01677.1
GeneID:7050	TGIF1	18	3,412,072	3,458,409	46,337	+	1	1_A375_pNL7_minus_lncRNA::1::2696	36296	in gene	1	0	18	7	1	1_A375_pNL7_minus_lncRNA::1	18	Gene TGIF1	TGIF1, TGIF, MGC5066, MGC39747, HPE4	TGFB-induced factor homeobox 1	NM_003244, NM_170695, NM_173207, NM_173208, NM_173209, NM_173210, NM_173211, NM_174886, hCT2274166.0, hCT2274167.0, hCT2274168.0	203313_s_at, 244858_at	NP_003235.1, NP_733796.2, NP_775299.1, NP_775300.1, NP_775301.1, NP_775302.1, NP_775303.1, NP_777480.1, EAX01670.1, EAX01671.1, EAX01672.1
GeneID:147525	C18orf18	18	5,236,723	5,238,028	1,305	-	1	1_A375_pNL7_minus_lncRNA::1::2697	-132	upstream	1	0	14	11	1	1_A375_pNL7_minus_lncRNA::1	14	Gene C18orf18	HsT959, MGC17515, C18orf18	chromosome 18 open reading frame 18	NR_026849	229829_at	
GeneID:339290	LOC339290	18	5,238,099	5,246,507	8,408	+	1	1_A375_pNL7_minus_lncRNA::1::2697	61	in gene	1	0	14	11	1	1_A375_pNL7_minus_lncRNA::1	14	Gene LOC339290	FLJ32367, DKFZp686I1198	hypothetical LOC339290	NR_015389	226235_at, 243426_at	
GeneID:201475	RAB12	18	8,609,443	8,639,380	29,937	+	2	1_A375_pNL7_minus_lncRNA::1::2698, 2_A375_pNL97_plus_lncRNA::1::3910	-67, -51	upstream, upstream	1	1	17	11	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RAB12	MGC104724, RAB12, FLJ45927	RAB12, member RAS oncogene family	NM_001025300	235059_at, 236019_at, 239891_x_at	NP_001020471.2
GeneID:4729	NDUFV2	18	9,102,628	9,134,343	31,715	+	2	1_A375_pNL7_minus_lncRNA::1::2699, 2_A375_pNL97_plus_lncRNA::1::3913	33900, 33868	downstream, downstream	1	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene NDUFV2	NDUFV2, CI-24k		NM_021074, hCT2273758.0	202941_at	NP_066552.2, EAX01612.1
GeneID:23253	ANKRD12	18	9,136,758	9,285,206	148,448	+	2	1_A375_pNL7_minus_lncRNA::1::2699, 2_A375_pNL97_plus_lncRNA::1::3913	-230, -262	upstream, upstream	1	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ANKRD12	ANCO-2, ANKRD12, Nbla00144, ANCO1, KIAA0874, GAC-1, FLJ20053	ankyrin repeat domain 12	NM_015208, NM_001083625, hCT1820043.2, hCT2358569.0	212286_at, 212289_at, 216550_x_at, 216563_at	NP_056023.3, NP_001077094.1, EAX01609.1, EAX01610.1
GeneID:9218	VAPA	18	9,913,955	9,960,018	46,063	+	1	1_A375_pNL7_minus_lncRNA::1::2700	125	in gene	1	0	15	13	1	1_A375_pNL7_minus_lncRNA::1	15	Gene VAPA	hVAP-33, VAP-A, VAPA, VAP33, MGC3745, VAP-33	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	NM_003574, NM_194434, hCT2274984.0, hCT2274986.0, hCT29929.2	208780_x_at, 225198_at, 226480_at, 238750_x_at, 242760_at	NP_003565.4, NP_919415.2, EAX01590.1, EAX01591.1, EAX01592.1
GeneID:2774	GNAL	18	11,689,136	11,883,144	194,008	+	2	1_A375_pNL7_minus_lncRNA::1::2701, 2_A375_pNL97_plus_lncRNA::1::3914	162144, 46	in gene, in gene	1	1	13.5	14	2	1_A375_pNL7_minus_lncRNA::1	17	Gene GNAL	GNAL		NM_001142339, NM_002071, NM_182978, hCT1819704.2, hCT2343979.1	206355_at, 206356_s_at	NP_001135811.1, NP_002062.1, NP_892023.1, EAX01573.1, EAX01574.1
GeneID:57132	CHMP1B	18	11,851,389	11,854,448	3,059	+	1	1_A375_pNL7_minus_lncRNA::1::2701	-109	upstream	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene CHMP1B	C10orf2, C18-ORF2, Vps46-2, CHMP1.5, Vps46B, C18orf2, CHMP1B	chromatin modifying protein 1B	NM_020412, hCT1819705.1	218177_at, 218178_s_at	NP_065145.2, EAX01575.1
GeneID:65258	MPPE1	18	11,883,470	11,908,641	25,171	-	1	2_A375_pNL97_plus_lncRNA::1::3915	-52	upstream	0	1	12	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene MPPE1	MPPE1, PGAP5	metallophosphoesterase 1	NM_023075, hCT1953857.1, hCT1966402.1, hCT1966403.1, hCT2273437.0, hCT2273438.0, hCT2273439.0, hCT2273442.0, hCT2273444.0, hCT2273445.0, hCT2358566.0, hCT2358567.0, hCT2358568.0	206764_x_at, 209858_x_at, 213727_x_at, 213924_at, 214071_at	NP_075563.3, EAX01571.1, EAX01561.1, EAX01562.1, EAX01569.1, EAX01572.1, EAX01563.1, EAX01564.1, EAX01565.1, EAX01566.1, EAX01567.1, EAX01568.1, EAX01570.1
GeneID:84617	TUBB6	18	12,308,257	12,326,568	18,311	+	1	2_A375_pNL97_plus_lncRNA::1::3916	-673	upstream	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TUBB6	HsT1601, MGC4083, TUBB6, TUBB-5, MGC132410	tubulin, beta 6	NM_032525, hCT1641731.3, hCT1965935.1	209191_at	NP_115914.1, EAX01554.1, EAX01553.1
GeneID:10650	SLMO1	18	12,407,895	12,432,237	24,342	+	1	2_A375_pNL97_plus_lncRNA::1::3917	12297	in gene	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene SLMO1	HFL-EDDG1, PRELID3A, C18orf43, FLJ31484, MGC120170, DKFZp547K106, SLMO1	slowmo homolog 1 (Drosophila)	NM_006553, NM_001142405, hCT2263351.0, hCT2263353.0, hCT2263354.0, hCT2358575.0	206273_at	NP_006544.2, NP_001135877.1, EAX01547.1, EAX01548.1, EAX01549.1, EAX01550.1
GeneID:79959	CEP76	18	12,672,631	12,702,703	30,072	-	2	1_A375_pNL7_minus_lncRNA::1::2702, 2_A375_pNL97_plus_lncRNA::1::3918	-177, -129	upstream, upstream	1	1	24	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene CEP76	FLJ12542, CEP76, HsT1705, C18orf9	centrosomal protein 76kDa	NM_024899, hCT28438.2	219311_at, 52285_f_at	NP_079175.2, EAX01543.1
GeneID:56984	PSMG2	18	12,703,064	12,725,739	22,675	+	2	1_A375_pNL7_minus_lncRNA::1::2702, 2_A375_pNL97_plus_lncRNA::1::3918	-184, -232	upstream, upstream	1	1	24	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene PSMG2	TNFSF5IP1, MDS003, HsT1707, CLAST3, HCCA3, PAC2, PSMG2, MGC15092	proteasome (prosome, macropain) assembly chaperone 2	NM_020232, hCT1639967.2, hCT1953849.1, hCT2263357.0	218467_at	NP_064617.2, EAX01540.1, EAX01541.1, EAX01542.1
GeneID:81929	SEH1L	18	12,947,983	12,987,535	39,552	+	1	2_A375_pNL97_plus_lncRNA::1::3919	43441	downstream	0	1	13	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene SEH1L	Seh1, SEH1A, SEH1B, SEC13L, SEH1L	SEH1-like (S. cerevisiae)	NM_031216, NM_001013437, hCT1953860.1, hCT29511.2	221931_s_at, 223225_s_at	NP_112493.2, NP_001013455.1, EAX01530.1, EAX01531.1
GeneID:55125	CEP192	18	12,991,361	13,125,052	133,691	+	1	2_A375_pNL97_plus_lncRNA::1::3919	63	in gene	0	1	13	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene CEP192	CEP192	centrosomal protein 192kDa	NM_032142	218827_s_at	NP_115518.3
GeneID:125228	C18orf19	18	13,663,346	13,726,591	63,245	-	1	2_A375_pNL97_plus_lncRNA::1::3920	63	in gene	0	1	15	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene C18orf19	C18orf19, HsT2329, MGC24180	chromosome 18 open reading frame 19	NM_152352, NM_001098801, hCT2348915.0, hCT29758.3	235022_at	NP_689565.2, NP_001092271.1, EAX01508.1, EAX01509.1
GeneID:8731	RNMT	18	13,726,704	13,764,554	37,850	+	1	2_A375_pNL97_plus_lncRNA::1::3920	-176	upstream	0	1	15	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene RNMT	KIAA0398, hCMT1c, MET, RG7MT1, RNMT, DKFZp686H1252	RNA (guanine-7-) methyltransferase	NM_003799, hCT2278103.0, hCT2278104.0, hCT29757.2	202683_s_at, 202684_s_at	NP_003790.1, EAX01506.1, EAX01505.1, EAX01507.1
GeneID:114799	ESCO1	18	19,109,262	19,180,693	71,431	-	1	2_A375_pNL97_plus_lncRNA::1::3921	117	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ESCO1	ESO1, CTF, EFO1, KIAA1911, ECO1, A930014I12Rik, ESCO1, MGC105022	establishment of cohesion 1 homolog 1 (S. cerevisiae)	NM_052911, hCT2351063.0, hCT2358556.0, hCT28635.4	226866_at, 235216_at, 235645_at	NP_443143.2, EAX01127.1, EAX01128.1, EAX01129.1
GeneID:6632	SNRPD1	18	19,192,260	19,210,206	17,946	+	2	1_A375_pNL7_minus_lncRNA::1::2703, 2_A375_pNL97_plus_lncRNA::1::3922	-4, -36	upstream, upstream	1	1	75	75	1	2_A375_pNL97_plus_lncRNA::1	75	Gene SNRPD1	SNRPD, SMD1, Sm-D1, SNRPD1, HsT2456	small nuclear ribonucleoprotein D1 polypeptide 16kDa	NM_006938, hCT2316776.0	202690_s_at, 202691_at	NP_008869.1, EAX01130.1
GeneID:85019	C18orf45	18	20,875,977	21,017,925	141,948	-	1	2_A375_pNL97_plus_lncRNA::1::3926	85	in gene	0	1	6	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C18orf45	C18orf45, MGC11386, MGC138577, FLJ44259	chromosome 18 open reading frame 45	NM_032933, hCT2317956.0	224493_x_at, 244495_x_at	NP_116322.3, EAX01150.1
GeneID:29919	C18orf8	18	21,083,462	21,111,746	28,284	+	2	1_A375_pNL7_minus_lncRNA::1::2706, 2_A375_pNL97_plus_lncRNA::1::3927	-134, -102	upstream, upstream	1	1	27	41	1	2_A375_pNL97_plus_lncRNA::1	41	Gene C18orf8	C18orf8, FLJ23453, HsT2591, MIC1	chromosome 18 open reading frame 8	NM_013326, hCT2317844.0, hCT2317845.0, hCT28990.3	221190_s_at, 232345_at, 232348_at	NP_037458.3, EAX01156.1, EAX01155.1, EAX01157.1
GeneID:3909	LAMA3	18	21,269,562	21,535,030	265,468	+	2	1_A375_pNL7_minus_lncRNA::1::2707, 2_A375_pNL97_plus_lncRNA::1::3928	27078, 27110	in gene, in gene	1	1	47	36	1	1_A375_pNL7_minus_lncRNA::1	47	Gene LAMA3	LAMA3, lama3a, LOCS, LAMNA, BM600, E170	laminin, alpha 3	NM_198129, NM_000227, NM_001127717, NM_001127718	1560078_at, 1563772_a_at, 1568879_a_at, 203726_s_at, 234608_at, 234719_at	NP_937762.1, NP_000218.2, NP_001121189.1, NP_001121190.1
GeneID:125488	TTC39C	18	21,572,737	21,715,574	142,837	+	1	2_A375_pNL97_plus_lncRNA::1::3929	83615	in gene	0	1	6	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TTC39C	FLJ33761, FLJ90394, C18orf17, TTC39C, HsT2697	tetratricopeptide repeat domain 39C	NM_153211, NM_001135993, NR_024232, hCT2317855.1, hCT2317857.1, hCT29561.4	1552307_a_at, 230747_s_at	NP_694943.2, NP_001129465.1, EAX01169.1, EAX01170.1, EAX01171.1
GeneID:114876	OSBPL1A	18	21,742,009	21,977,790	235,781	-	1	2_A375_pNL97_plus_lncRNA::1::3930	46	in gene	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene OSBPL1A	ORP1, ORP-1, OSBPL1A, FLJ10217, OSBPL1B	oxysterol binding protein-like 1A	NM_080597, NM_018030, hCT2315784.0, hCT2315785.0, hCT2315786.0, hCT2315787.0	1554646_at, 208158_s_at, 209485_s_at	NP_542164.2, NP_060500.3, EAX01180.1, EAX01181.1, EAX01182.1, EAX01183.1
GeneID:55364	IMPACT	18	22,006,609	22,033,495	26,886	+	1	1_A375_pNL7_minus_lncRNA::1::2708	-198	upstream	1	0	16	10	1	1_A375_pNL7_minus_lncRNA::1	16	Gene IMPACT	MGC33718, IMPACT	Impact homolog (mouse)	NM_018439, hCT1813052.1, hCT1951962.1, hCT2315723.0, hCT2358537.0, hCT29559.3	218637_at, 222698_s_at	NP_060909.1, EAX01188.1, EAX01184.1, EAX01185.1, EAX01186.1, EAX01187.1
GeneID:6760	SS18	18	23,596,217	23,670,611	74,394	-	2	1_A375_pNL7_minus_lncRNA::1::2709, 2_A375_pNL97_plus_lncRNA::1::3932	-77, -361	upstream, upstream	1	1	30	25	1	1_A375_pNL7_minus_lncRNA::1	30	Gene SS18	MGC116875, SSXT, SYT, SS18	synovial sarcoma translocation, chromosome 18	NM_005637, NM_001007559, hCT1951955.1, hCT2315894.0, hCT2315896.0, hCT2315897.0, hCT28405.3	202816_s_at, 202817_s_at, 209954_x_at, 216684_s_at, 217051_s_at	NP_005628.2, NP_001007560.1, EAX01209.1, EAX01210.1, EAX01211.1, EAX01212.1, EAX01213.1
GeneID:6875	TAF4B	18	23,806,409	23,971,649	165,240	+	1	2_A375_pNL97_plus_lncRNA::1::3933	471	in gene	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene TAF4B	TAF4B, TAF2C2, TAFII105	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	NM_005640	216226_at, 235020_at	NP_005631.1
GeneID:1825	DSC3	18	28,570,052	28,622,781	52,729	-	1	1_A375_pNL7_minus_lncRNA::1::2711	31261	in gene	1	0	16	9	1	1_A375_pNL7_minus_lncRNA::1	16	Gene DSC3	DSC3, CDHF3, DSC4, DSC1, HT-CP, DSC2, DSC	desmocollin 3	NM_001941, NM_024423, hCT2319338.0, hCT2319339.0, hCT2319340.0	206032_at, 206033_s_at	NP_001932.2, NP_077741.2, EAX01247.1, EAX01248.1, EAX01249.1
GeneID:9331	B4GALT6	18	29,202,209	29,264,686	62,477	-	1	2_A375_pNL97_plus_lncRNA::1::3934	5246	in gene	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene B4GALT6	B4GALT6, beta4Gal-T6, B4Gal-T6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	NM_004775, hCT16600.3, hCT2316355.0, hCT2358562.0	206232_s_at, 206233_at, 235333_at	NP_004766.2, EAX01267.1, EAX01268.1, EAX01269.1
GeneID:100507120	LOC100507120	18	29,265,049	29,266,701	1,652	+	1	2_A375_pNL97_plus_lncRNA::1::3934	-5609	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100507120		hypothetical protein LOC100507120	XM_003118759, XM_003120905		XP_003118807.1, XP_003120953.1
GeneID:22878	KIAA1012	18	29,409,136	29,523,091	113,955	-	1	2_A375_pNL97_plus_lncRNA::1::3935	19	in gene	0	1	6	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene KIAA1012	TRS85, HsT2706, KIAA1012, TRAPPC8, MGC71660, GSG1	KIAA1012	NM_014939, hCT1951966.1, hCT2316347.0, hCT2316348.0, hCT2316349.0, hCT2316350.0, hCT2358541.0	207305_s_at	NP_055754.2, EAX01273.1, EAX01271.1, EAX01272.1, EAX01274.1, EAX01276.1, EAX01275.1
GeneID:64762	FAM59A	18	29,847,463	30,050,447	202,984	-	1	1_A375_pNL7_minus_lncRNA::1::2712	97823	in gene	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene FAM59A	Gm944, GAREM, C18orf11, FAM59A	family with sequence similarity 59, member A	NM_022751, hCT16205.3, hCT2358552.0	219377_at	NP_073588.1, EAX01286.1, EAX01287.1
GeneID:10982	MAPRE2	18	32,556,892	32,722,378	165,486	+	2	1_A375_pNL7_minus_lncRNA::1::2713, 2_A375_pNL97_plus_lncRNA::1::3936	2244, 64644	in gene, in gene	1	1	13	12	2	1_A375_pNL7_minus_lncRNA::1	17	Gene MAPRE2	RP1, EB2, EB1, MAPRE2	microtubule-associated protein, RP/EB family, member 2	NM_014268, NM_001143826, NM_001143827, NR_026570, hCT15400.3, hCT1951939.1, hCT2316441.0, hCT2316443.0, hCT2316444.0	202501_at, 211556_at, 213489_at	NP_055083.1, NP_001137298.1, NP_001137299.1, EAX01336.1, EAX01337.1, EAX01339.1, EAX01338.1, EAX01340.1
GeneID:100101467	ZNF397OS	18	32,831,023	32,870,196	39,173	-	2	1_A375_pNL7_minus_lncRNA::1::2714, 2_A375_pNL97_plus_lncRNA::1::3937	-124, -140	upstream, upstream	1	1	34	34	1	1_A375_pNL7_minus_lncRNA::1	34	Gene ZNF397OS	ZSCAN30, ZNF917, ZNF397OS, FLJ45864, FLJ16245	zinc finger and SCAN domain containing 30	NM_001112734, NM_001166012		NP_001106205.1, NP_001159484.1
GeneID:7572	ZNF24	18	32,912,178	32,924,426	12,248	-	1	1_A375_pNL7_minus_lncRNA::1::2715	266	in gene	1	0	14	5	1	1_A375_pNL7_minus_lncRNA::1	14	Gene ZNF24	ZSCAN3, RSG-A, ZNF24, ZNF191, Zfp191, KOX17	zinc finger protein 24	NM_006965, hCT13607.2, hCT1951936.0, hCT2316553.0	1554045_at, 203247_s_at, 203248_at, 242210_at	NP_008896.2, EAX01350.1, EAX01348.1, EAX01349.1
GeneID:125476	INO80C	18	33,048,291	33,077,955	29,664	-	2	1_A375_pNL7_minus_lncRNA::1::2716, 2_A375_pNL97_plus_lncRNA::1::3938	275, 259	in gene, in gene	1	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene INO80C	IES6, C18orf37, FLJ38183, hIes6, INO80C	INO80 complex subunit C	NM_001098817, NM_194281, hCT2316542.0, hCT2358558.0	1559716_at, 229582_at	NP_001092287.1, NP_919257.2, EAX01357.1, EAX01358.1
GeneID:55197	RPRD1A	18	33,569,791	33,647,373	77,582	-	1	1_A375_pNL7_minus_lncRNA::1::2718	173	in gene	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RPRD1A	FLJ10656, HsT3101, P15RS, MGC19513, RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	NM_018170, hCT15963.3, hCT1951947.1, hCT1951948.1, hCT2316178.0, hCT2316179.0, hCT2358561.0	1555202_a_at, 218209_s_at, 222558_at, 222559_s_at, 225953_at, 228566_at	NP_060640.2, EAX01368.1, EAX01365.1, EAX01366.1, EAX01369.1, EAX01370.1, EAX01367.1
GeneID:25800	SLC39A6	18	33,688,494	33,709,357	20,863	-	2	1_A375_pNL7_minus_lncRNA::1::2719, 2_A375_pNL97_plus_lncRNA::1::3939	-403, -403	upstream, upstream	1	1	20	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene SLC39A6	LIV-1, SLC39A6	solute carrier family 39 (zinc transporter), member 6	NM_012319, NM_001099406, hCT14916.3, hCT2358553.0	1555460_a_at, 1556551_s_at, 202088_at, 202089_s_at	NP_036451.3, NP_001092876.1, EAX01371.1, EAX01372.1
GeneID:55250	ELP2	18	33,709,887	33,754,607	44,720	+	3	1_A375_pNL7_minus_lncRNA::1::2719, 2_A375_pNL97_plus_lncRNA::1::3939, 2_A375_pNL97_plus_lncRNA::1::3940	-127, -127, 47009	upstream, upstream, downstream	1	1	13.5	22	2	2_A375_pNL97_plus_lncRNA::1	29	Gene ELP2	SHINC-2, FLJ10879, ELP2, StIP, STATIP1	elongation protein 2 homolog (S. cerevisiae)	NM_018255, hCT14917.3, hCT2316062.0, hCT2316063.0, hCT2358554.0	231713_s_at, 235623_at	NP_060725.1, EAX01373.1, EAX01374.1, EAX01375.1, EAX01376.1
GeneID:56853	BRUNOL4	18	34,823,003	35,146,000	322,997	-	5	1_A375_pNL7_minus_lncRNA::1::2720, 1_A375_pNL7_minus_lncRNA::1::2721, 2_A375_pNL97_plus_lncRNA::1::3941, 2_A375_pNL97_plus_lncRNA::1::3942, 2_A375_pNL97_plus_lncRNA::1::3943	295760, 82352, 295792, 82256, 1088	in gene, in gene, in gene, in gene, in gene	1	1	27.67	36.67	3	2_A375_pNL97_plus_lncRNA::1	74	Gene BRUNOL4	CELF4, BRUNOL4, BRUNOL-4	CUGBP, Elav-like family member 4	NM_020180, NM_001025087, NM_001025088, NM_001025089, hCT13544.3, hCT2316027.0, hCT2316030.0, hCT2316031.0	223653_x_at, 223654_s_at, 231220_at, 232719_at, 238966_at	NP_064565.1, NP_001020258.1, NP_001020259.1, NP_001020260.1, EAX01395.1, EAX01397.1, EAX01394.1, EAX01396.1
GeneID:57724	KIAA1632	18	43,427,574	43,547,305	119,731	-	1	1_A375_pNL7_minus_lncRNA::1::2727	41	in gene	1	0	22	16	1	1_A375_pNL7_minus_lncRNA::1	22	Gene KIAA1632	hEPG5, DKFZp667P2311, KIAA1632, HEEW1, EPG5	KIAA1632	NM_020964, hCT2346836.0	1563471_at, 227638_at, 228453_at, 232030_at, 232031_s_at, 234048_s_at, 236108_at	NP_066015.2, EAX01465.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:498	ATP5A1	18	43,664,110	43,684,199	20,089	-	1	2_A375_pNL97_plus_lncRNA::1::3948	-121	upstream	0	1	6	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ATP5A1	ATP5A1, MOM2, ATPM, ATP5A, ATP5AL2, OMR, hATP1, ORM	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	NM_004046, NM_001001937	1569891_at, 213738_s_at	NP_004037.1, NP_001001937.1
GeneID:115106	HAUS1	18	43,684,298	43,708,299	24,001	+	1	2_A375_pNL97_plus_lncRNA::1::3948	22	in gene	0	1	6	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene HAUS1	HAUS1, FLJ21094, HEIC, HEI-C, FLJ40084, CCDC5, HsT1461	HAUS augmin-like complex, subunit 1	NR_026978, NM_138443, hCT1816418.1	225297_at	NP_612452.1, EAX01469.1
GeneID:147339	C18orf25	18	43,753,988	43,846,955	92,967	+	2	1_A375_pNL7_minus_lncRNA::1::2728, 2_A375_pNL97_plus_lncRNA::1::3949	-68, -68	upstream, upstream	1	1	64	63	1	1_A375_pNL7_minus_lncRNA::1	64	Gene C18orf25	C18orf25, MGC87799, ARKL1, MGC12909	chromosome 18 open reading frame 25	NM_001008239, NM_145055, hCT2316570.0, hCT2316572.0	1553686_at, 217508_s_at, 217539_at, 226406_at	NP_001008240.1, NP_659492.1, EAX01472.1, EAX01473.1
GeneID:125336	LOXHD1	18	44,056,935	44,236,996	180,061	-	6	1_A375_pNL7_minus_lncRNA::1::2729, 1_A375_pNL7_minus_lncRNA::1::2730, 1_A375_pNL7_minus_lncRNA::1::2731, 2_A375_pNL97_plus_lncRNA::1::3950, 2_A375_pNL97_plus_lncRNA::1::3951, 2_A375_pNL97_plus_lncRNA::1::3952	159748, 120324, 24068, 159716, 154436, 24068	in gene, in gene, in gene, in gene, in gene, in gene	1	1	17.75	17.25	4	1_A375_pNL7_minus_lncRNA::1	23	Gene LOXHD1	FLJ32670, LOXHD1, LH2D1, DFNB77	lipoxygenase homology domains 1	NM_144612, NM_001173129, NM_001145472, NM_001145473, hCT2341094.1, hCT2341095.1, hCT2348909.0, hCT2356555.0	241117_at	NP_653213.6, NP_001166600.1, NP_001138944.1, NP_001138945.1, EAX01477.1, EAX01480.1, EAX01478.1, EAX01479.1
GeneID:29906	ST8SIA5	18	44,259,081	44,337,039	77,958	-	1	2_A375_pNL97_plus_lncRNA::1::3953	-529	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ST8SIA5	SIAT8E, MGC119671, ST8SiaV, ST8SIA5, MGC119670	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	NM_013305, hCT1950755.1, hCT2316288.0	206258_at	NP_037437.2, EAX01482.1, EAX01483.1
GeneID:83473	KATNAL2	18	44,526,787	44,628,614	101,827	+	1	2_A375_pNL97_plus_lncRNA::1::3954	-7043	upstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene KATNAL2	KATNAL2, DKFZp667C165, MGC33211	katanin p60 subunit A-like 2	NM_031303, hCT14934.4, hCT2348442.0, hCT2348443.0, hCT2353876.0	1554234_at, 233644_at, 233649_at	NP_112593.2, EAW62903.1, EAW62901.1, EAW62902.1, EAW62904.1
GeneID:9811	KIAA0427	18	46,065,427	46,389,588	324,161	+	1	2_A375_pNL97_plus_lncRNA::1::3956	2157	in gene	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene KIAA0427	Gm672, CTIF, KIAA0427	KIAA0427	NM_014772, NM_001142397, hCT15756.3, hCT2250284.0, hCT2250286.0, hCT2353882.0	204302_s_at, 204303_s_at	NP_055587.1, NP_001135869.1, EAW62925.1, EAW62926.1, EAW62927.1, EAW62928.1
GeneID:9388	LIPG	18	47,088,427	47,119,278	30,851	+	1	2_A375_pNL97_plus_lncRNA::1::3957	24005	in gene	0	1	8	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LIPG	EL, LIPG, PRO719, EDL	lipase, endothelial	NM_006033, hCT15605.3, hCT2250318.0, hCT2250319.0	219181_at	NP_006024.1, EAW62949.1, EAW62947.1, EAW62948.1
GeneID:4645	MYO5B	18	47,349,156	47,721,451	372,295	-	2	1_A375_pNL7_minus_lncRNA::1::2732, 2_A375_pNL97_plus_lncRNA::1::3958	296491, 296459	in gene, in gene	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene MYO5B	KIAA1119, MYO5B	myosin VB	NM_001080467	1570141_at, 225299_at, 225301_s_at	NP_001073936.1
GeneID:55520	ELAC1	18	48,494,387	48,514,490	20,103	+	1	1_A375_pNL7_minus_lncRNA::1::2733	77	in gene	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ELAC1	D29, FLJ59261, ELAC1	elaC homolog 1 (E. coli)	NM_018696, hCT14801.1, hCT2353881.0	219325_s_at, 222869_s_at	NP_061166.1, EAW62984.1, EAW62983.1
GeneID:51320	MEX3C	18	48,700,920	48,724,051	23,131	-	1	2_A375_pNL97_plus_lncRNA::1::3959	-557	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MEX3C	MEX-3C, FLJ38871, BM-013, MEX3C, RKHD2, RNF194	mex-3 homolog C (C. elegans)	NM_016626, hCT1640425.3	1556873_at, 1556874_a_at, 218247_s_at, 222567_s_at, 227275_at	NP_057710.3, EAW62989.1
GeneID:11201	POLI	18	51,795,849	51,824,604	28,755	+	1	2_A375_pNL97_plus_lncRNA::1::3962	71	in gene	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene POLI	RAD30B, POLI, RAD3OB	polymerase (DNA directed) iota	NM_007195, hCT13763.2, hCT2250226.0	219317_at, 238992_at	NP_009126.2, EAW63000.1, EAW63001.1
GeneID:147323	STARD6	18	51,851,062	51,880,943	29,881	-	1	2_A375_pNL97_plus_lncRNA::1::3963	-3217	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene STARD6	STARD6		NM_139171, hCT2250244.1, hCT2250245.1, hCT2340510.0, hCT2340511.0	1553084_at	NP_631910.1, EAW63002.1, EAW63003.1, EAW63004.1, EAW63005.1
GeneID:162681	C18orf54	18	51,885,171	51,908,404	23,233	+	1	2_A375_pNL97_plus_lncRNA::1::3963	-1011	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene C18orf54	MGC33382, C18orf54, LAS2	chromosome 18 open reading frame 54	NM_173529, hCT14350.3	1553651_at, 1553652_a_at, 229442_at, 241733_at, 244324_at	NP_775800.3, EAW63006.1
GeneID:6925	TCF4	18	52,889,562	53,255,860	366,298	-	1	2_A375_pNL97_plus_lncRNA::1::3964	312927	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TCF4	SEF2-1B, SEF2-1A, SEF2-1, MGC149723, E2-2, TCF4, PTHS, MGC149724, ITF2, bHLHb19, SEF2	transcription factor 4	NM_001083962, NM_003199, hCT1954695.1, hCT2259991.0, hCT2259993.0, hCT2259997.0, hCT2259998.0, hCT2260000.0, hCT2260001.0, hCT2260003.0	203753_at, 212382_at, 212385_at, 212387_at, 222146_s_at	NP_001077431.1, NP_003190.1, EAW63020.1, EAW63021.1, EAW63023.1, EAW63024.1, EAW63017.1, EAW63018.1, EAW63019.1, EAW63022.1
GeneID:100505499	LOC100505499	18	54,305,962	54,318,505	12,543	-	1	1_A375_pNL7_minus_lncRNA::1::2736	89	in gene	1	0	16	17	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100505499		hypothetical protein LOC100505499	XM_003118894		XP_003118942.1
GeneID:23335	WDR7	18	54,318,616	54,697,036	378,420	+	1	1_A375_pNL7_minus_lncRNA::1::2736	-200	upstream	1	0	16	17	1	1_A375_pNL7_minus_lncRNA::1	16	Gene WDR7	WDR7, KIAA0541, TRAG	WD repeat domain 7	NM_015285, NM_052834, hCT2250549.0, hCT2250550.0, hCT2250552.0, hCT2250553.0	212880_at	NP_056100.2, NP_443066.2, EAW63037.1, EAW63038.1, EAW63039.1, EAW63040.1
GeneID:9480	ONECUT2	18	55,102,917	55,158,530	55,613	+	2	1_A375_pNL7_minus_lncRNA::1::2737, 2_A375_pNL97_plus_lncRNA::1::3965	11595, 11579	in gene, in gene	1	1	21	20	1	1_A375_pNL7_minus_lncRNA::1	21	Gene ONECUT2	MGC120376, MGC120377, OC-2, OC2, ONECUT2	one cut homeobox 2	NM_004852, hCT14358.1	207676_at, 230271_at, 233441_at, 233446_at, 239911_at	NP_004843.2, EAW63045.1
GeneID:4677	NARS	18	55,267,891	55,289,177	21,286	-	1	1_A375_pNL7_minus_lncRNA::1::2738	-103	upstream	1	0	18	10	1	1_A375_pNL7_minus_lncRNA::1	18	Gene NARS	NARS, ASNRS, NARS1	asparaginyl-tRNA synthetase	NM_004539, hCT14357.2, hCT1966713.0	200027_at	NP_004530.1, EAW63048.1, EAW63049.1
GeneID:100505549	LOC100505549	18	55,297,582	55,336,586	39,004	+	1	1_A375_pNL7_minus_lncRNA::1::2738	-8302	upstream	1	0	18	10	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100505549		hypothetical LOC100505549	XR_110145, XR_110144		
GeneID:23327	NEDD4L	18	55,711,619	56,068,772	357,153	+	1	2_A375_pNL97_plus_lncRNA::1::3966	140669	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene NEDD4L	NEDD4L, FLJ33870, KIAA0439, hNedd4-2, RSP5, NEDD4-2	neural precursor cell expressed, developmentally down-regulated 4-like	NM_001144965, NM_001144966, NM_001144967, NM_001144968, NM_001144969, NM_001144970, NM_001144971, NM_015277, NM_001144964, hCT14190.2, hCT1954707.2, hCT1954708.1, hCT1954709.1, hCT2250481.0, hCT2250484.0, hCT2250486.0, hCT2250487.0, hCT2250488.0, hCT22504	212445_s_at, 212448_at	NP_001138437.1, NP_001138438.1, NP_001138439.1, NP_001138440.1, NP_001138441.1, NP_001138442.1, NP_056092.2, NP_001138443.1, NP_001138436.1, EAW63064.1, EAW63065.1, EAW63066.1, EAW63067.1, EAW63068.1, EAW63069.1, EAW63070.1, EAW63071.1, EAW63072.1, EAW630
GeneID:115701	ALPK2	18	56,148,479	56,296,189	147,710	-	2	1_A375_pNL7_minus_lncRNA::1::2739, 2_A375_pNL97_plus_lncRNA::1::3967	49629, 23197	in gene, in gene	1	1	11.5	13	2	1_A375_pNL7_minus_lncRNA::1	16	Gene ALPK2	FLJ43253, ALPK2, FLJ34875, HAK	alpha-kinase 2	NM_052947, hCT7577.4	228367_at	NP_443179.3, EAW63077.1
GeneID:90701	SEC11C	18	56,807,125	56,826,064	18,939	+	1	2_A375_pNL97_plus_lncRNA::1::3968	-53	upstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SEC11C	SEC11C, SPCS4C, SPC21, SEC11L3	SEC11 homolog C (S. cerevisiae)	NM_033280, hCT2353886.0, hCT24927.3	223299_at	NP_150596.1, EAW63089.1, EAW63090.1
GeneID:54877	ZCCHC2	18	60,190,658	60,245,818	55,160	+	2	1_A375_pNL7_minus_lncRNA::1::2740, 2_A375_pNL97_plus_lncRNA::1::3970	-626, -610	upstream, upstream	1	1	18	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ZCCHC2	MGC13269, DKFZp451A185, KIAA1744, FLJ20281, ZCCHC2	zinc finger, CCHC domain containing 2	NM_017742, hCT2250454.0, hCT2250455.1, hCT2250456.1	219062_s_at, 222816_s_at, 224503_s_at, 233425_at, 244034_at	NP_060212.4, EAW63128.1, EAW63126.1, EAW63127.1
GeneID:23239	PHLPP1	18	60,382,672	60,647,666	264,994	+	2	1_A375_pNL7_minus_lncRNA::1::2741, 2_A375_pNL97_plus_lncRNA::1::3971	-384, -368	upstream, upstream	1	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PHLPP1	PLEKHE1, SCOP, MGC161555, PHLPP, PHLPP1	PH domain and leucine rich repeat protein phosphatase 1	NM_194449, hCT1954744.1	212719_at	NP_919431.2, EAW63135.1
GeneID:2531	KDSR	18	60,994,971	61,034,506	39,535	-	2	1_A375_pNL7_minus_lncRNA::1::2742, 2_A375_pNL97_plus_lncRNA::1::3972	-406, -438	upstream, upstream	1	1	30	22	1	1_A375_pNL7_minus_lncRNA::1	30	Gene KDSR	FLJ92680, FLJ36555, SDR35C1, DHSR, KDSR, FVT1	3-ketodihydrosphingosine reductase	NM_002035, hCT2250745.0, hCT25291.3	202419_at	NP_002026.1, EAW63140.1, EAW63141.1
GeneID:284293	HMSD	18	61,616,588	61,627,646	11,058	+	1	1_A375_pNL7_minus_lncRNA::1::2743	20772	downstream	1	0	15	10	1	1_A375_pNL7_minus_lncRNA::1	15	Gene HMSD	C18orf53, HSMD-v, ACC-6, HMSD	histocompatibility (minor) serpin domain containing	NM_001123366		NP_001116838.1
GeneID:5271	SERPINB8	18	61,637,263	61,656,608	19,345	+	1	1_A375_pNL7_minus_lncRNA::1::2743	97	in gene	1	0	15	10	1	1_A375_pNL7_minus_lncRNA::1	15	Gene SERPINB8	CAP2, PI8, SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	NM_198833, NM_002640, NM_001031848, hCT2250379.0, hCT2250380.0, hCT2250381.0	1554616_at, 206034_at	NP_942130.1, NP_002631.3, NP_001027018.1, EAW63163.1, EAW63164.1, EAW63165.1
GeneID:25914	RTTN	18	67,671,040	67,872,962	201,922	-	3	1_A375_pNL7_minus_lncRNA::1::2744, 2_A375_pNL97_plus_lncRNA::1::3973, 2_A375_pNL97_plus_lncRNA::1::3974	-62, 160882, -222	upstream, in gene, upstream	1	1	13	22.5	2	2_A375_pNL97_plus_lncRNA::1	29	Gene RTTN	DKFZp434G145, RTTN, FLJ39085, FLJ26356	rotatin	NM_173630, hCT1950650.2, hCT2276906.0, hCT2348518.0, hCT2348519.0, hCT2348520.0, hCT2354307.0	1553277_at, 1557388_at, 227072_at	NP_775901.3, EAW66519.1, EAW66516.1, EAW66517.1, EAW66518.1, EAW66520.1, EAW66521.1
GeneID:81832	NETO1	18	70,414,787	70,534,810	120,023	-	2	1_A375_pNL7_minus_lncRNA::1::2745, 2_A375_pNL97_plus_lncRNA::1::3975	37306, 37242	in gene, in gene	1	1	25	21	1	1_A375_pNL7_minus_lncRNA::1	25	Gene NETO1	FLJ41325, BTCL1, BCTL1, NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	NM_138999, NM_138966, NM_153181, hCT1640941.4, hCT2277045.1, hCT2277047.1, hCT2354308.0	1552736_a_at, 1552904_at, 1562713_a_at	NP_620552.1, NP_620416.1, NP_694821.2, EAW66530.1, EAW66531.1, EAW66532.1, EAW66533.1
GeneID:55748	CNDP2	18	72,163,500	72,190,689	27,189	+	1	1_A375_pNL7_minus_lncRNA::1::2747	212	in gene	1	0	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene CNDP2	PEPA, CN2, CPGL, FLJ10830, FLJ35544, HsT2298, CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)	NM_018235, NM_001168499, hCT1950649.1, hCT2277548.0, hCT2277549.0, hCT2277552.0, hCT2277554.0, hCT2277557.0, hCT2354309.0, hCT2354310.0, hCT7080.2	1562460_at, 217752_s_at	NP_060705.2, NP_001161971.1, EAW66550.1, EAW66555.1, EAW66556.1, EAW66558.1, EAW66551.1, EAW66552.1, EAW66553.1, EAW66554.1, EAW66557.1
GeneID:400657	LOC400657	18	72,259,010	72,265,071	6,061	-	1	2_A375_pNL97_plus_lncRNA::1::3977	-6	upstream	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC400657	FLJ10991	hypothetical LOC400657	NR_024484	226924_at	
GeneID:284273	ZADH2	18	72,909,278	72,921,281	12,003	-	1	1_A375_pNL7_minus_lncRNA::1::2748	1089	in gene	1	0	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene ZADH2	MGC45594, ZADH2	zinc binding alcohol dehydrogenase domain containing 2	NM_175907, hCT5954.2	1554239_s_at, 227049_at, 227977_at, 227978_s_at, 234977_at, 237776_at, 244067_x_at	NP_787103.1, EAW66569.1
GeneID:10194	TSHZ1	18	72,922,731	73,001,901	79,170	+	1	1_A375_pNL7_minus_lncRNA::1::2748	-2539	upstream	1	0	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TSHZ1	TSH1, TSHZ1, NY-CO-33, SDCCAG33	teashirt zinc finger homeobox 1	NM_005786	213905_x_at	NP_005777.3
GeneID:284274	C18orf62	18	73,121,827	73,139,589	17,762	-	2	1_A375_pNL7_minus_lncRNA::1::2749, 2_A375_pNL97_plus_lncRNA::1::3978	18597, 18437	downstream, downstream	1	1	21	14	1	1_A375_pNL7_minus_lncRNA::1	21	Gene C18orf62	C18orf62, MGC126049	chromosome 18 open reading frame 62	NM_001037331, hCT2278253.0	1556288_at, 1564400_at	NP_001032408.1, EAW66572.1
GeneID:7776	ZNF236	18	74,536,116	74,682,683	146,567	+	1	2_A375_pNL97_plus_lncRNA::1::3979	-2116	upstream	0	1	5	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZNF236	ZNF236B, ZNF236, ZNF236A	zinc finger protein 236	NM_007345	219171_s_at, 222227_at, 47571_at	NP_031371.3
GeneID:9150	CTDP1	18	77,439,801	77,514,507	74,706	+	2	1_A375_pNL7_minus_lncRNA::1::2750, 2_A375_pNL97_plus_lncRNA::1::3980	-473, -281	upstream, upstream	1	1	25	25	1	1_A375_pNL7_minus_lncRNA::1	25	Gene CTDP1	CTDP1, FCP1, CCFDN	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	NM_004715, NM_048368, hCT1967282.1, hCT1967283.1, hCT2277904.0, hCT2354314.0, hCT7203.3	205035_at	NP_004706.3, NP_430255.2, EAW66628.1, EAW66629.1, EAW66631.1, EAW66632.1, EAW66630.1
GeneID:54531	MIER2	19	305,575	344,791	39,216	-	2	1_A375_pNL7_minus_lncRNA::1::2752, 2_A375_pNL97_plus_lncRNA::1::3982	1431, 1975	in gene, in gene	1	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MIER2	MIER2, KIAA1193	mesoderm induction early response 1, family member 2	NM_017550	221862_at, 221863_at, 44822_s_at	NP_060020.1
GeneID:25759	SHC2	19	416,583	460,996	44,413	-	1	2_A375_pNL97_plus_lncRNA::1::3983	964	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SHC2	SHC2, SHCB, SCK, SLI	SHC (Src homology 2 domain containing) transforming protein 2	NM_012435	213464_at	NP_036567.2
GeneID:284451	ODF3L2	19	463,346	474,983	11,637	-	1	2_A375_pNL97_plus_lncRNA::1::3983	14951	downstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ODF3L2	MGC129962, ODF3L2, FLJ40059, MGC129963, C19orf19	outer dense fiber of sperm tails 3-like 2	NM_182577, hCT2251003.1	237620_at	NP_872383.1, EAW61196.1
GeneID:8174	MADCAM1	19	496,490	505,343	8,853	+	5	1_A375_pNL7_minus_lncRNA::1::2753, 1_A375_pNL7_minus_lncRNA::1::2754, 2_A375_pNL97_plus_lncRNA::1::3984, 2_A375_pNL97_plus_lncRNA::1::3985, 2_A375_pNL97_plus_lncRNA::1::3986	-7466, 11158, -7434, 10406, 11196	upstream, downstream, upstream, downstream, downstream	1	1	20	24	3	1_A375_pNL7_minus_lncRNA::1	26	Gene MADCAM1	MACAM1, MADCAM1	mucosal vascular addressin cell adhesion molecule 1	NM_130762, NM_130760, hCT11648.2, hCT2251595.0	208037_s_at	NP_570118.1, NP_570116.2, EAW61194.1, EAW61195.1
GeneID:91978	C19orf20	19	507,497	519,654	12,157	+	3	1_A375_pNL7_minus_lncRNA::1::2754, 2_A375_pNL97_plus_lncRNA::1::3985, 2_A375_pNL97_plus_lncRNA::1::3986	151, -601, 189	in gene, upstream, in gene	1	1	17	24	2	2_A375_pNL97_plus_lncRNA::1	25	Gene C19orf20	PGs1, GTRGEO22, C19orf20	chromosome 19 open reading frame 20	NM_033513, hCT11650.4, hCT2348297.0	227903_x_at, 243600_at	NP_277048.2, EAW61193.1, EAW61192.1
GeneID:5725	PTBP1	19	797,392	812,327	14,935	+	2	1_A375_pNL7_minus_lncRNA::1::2755, 2_A375_pNL97_plus_lncRNA::1::3987	-432, -448	upstream, upstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene PTBP1	HNRNP-I, PTB4, PTB3, pPTB, PTB, HNRPI, PTB-1, MGC10830, HNRNPI, PTB-T, MGC8461, PTB2, PTBP1	polypyrimidine tract binding protein 1	NM_002819, NM_031990, NM_031991, NM_175847, hCT11639.2, hCT1955356.1, hCT1955357.1, hCT2251619.0, hCT2251620.0, hCT2251622.0, hCT2353658.0	202189_x_at, 211270_x_at, 211271_x_at, 212015_x_at, 212016_s_at, 216306_x_at, 226491_x_at, 231158_x_at, 236819_at	NP_002810.1, NP_114367.1, NP_114368.1, NP_787041.1, EAW61154.1, EAW61155.1, EAW61152.1, EAW61153.1, EAW61156.1, EAW61157.1, EAW61158.1
GeneID:10025	MED16	19	867,962	893,218	25,256	-	2	1_A375_pNL7_minus_lncRNA::1::2756, 2_A375_pNL97_plus_lncRNA::1::3988	-126, -142	upstream, upstream	1	1	24	18	1	1_A375_pNL7_minus_lncRNA::1	24	Gene MED16	TRAP95, DRIP92, THRAP5, MED16	mediator complex subunit 16	NM_005481, hCT2288791.0, hCT2288792.0	221418_s_at, 221544_s_at, 221545_x_at, 221938_x_at, 43544_at	NP_005472.2, EAW69586.1, EAW69587.1
GeneID:91300	C19orf22	19	896,503	913,225	16,722	-	2	1_A375_pNL7_minus_lncRNA::1::2756, 2_A375_pNL97_plus_lncRNA::1::3988	19881, 19865	downstream, downstream	1	1	24	18	1	1_A375_pNL7_minus_lncRNA::1	24	Gene C19orf22	MGC16353, C19orf22	chromosome 19 open reading frame 22	NM_138774, hCT2288789.0	221764_at, 55705_at	NP_620129.2, EAW69584.1
GeneID:84634	KISS1R	19	917,342	921,015	3,673	+	2	1_A375_pNL7_minus_lncRNA::1::2757, 2_A375_pNL97_plus_lncRNA::1::3989	8274, 8226	downstream, downstream	1	1	20	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene KISS1R	HOT7T175, KISS1R, GPR54, AXOR12	KISS1 receptor	NM_032551, hCT12693.3	242517_at	NP_115940.2, EAW69583.1
GeneID:1820	ARID3A	19	926,037	972,816	46,779	+	2	1_A375_pNL7_minus_lncRNA::1::2757, 2_A375_pNL97_plus_lncRNA::1::3989	-421, -469	upstream, upstream	1	1	20	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene ARID3A	E2FBP1, DRIL3, BRIGHT, DRIL1, ARID3A	AT rich interactive domain 3A (BRIGHT-like)	NM_005224, hCT12670.2	205865_at	NP_005215.1, EAW69580.1
GeneID:91304	C19orf6	19	1,009,650	1,021,141	11,491	-	2	1_A375_pNL7_minus_lncRNA::1::2758, 2_A375_pNL97_plus_lncRNA::1::3990	-443, -107	upstream, upstream	1	1	21	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene C19orf6	C19orf6, R32184_3, ASBABP1, MGC4022, MEMBRALIN, MBRL	chromosome 19 open reading frame 6	NM_033420, NM_001033026, hCT12686.3, hCT1952854.1, hCT1952855.1, hCT2288782.0, hCT2354624.0	212574_x_at, 212575_at, 213985_s_at, 213986_s_at, 225247_at, 230089_s_at	NP_219488.1, NP_001028198.1, EAW69571.1, EAW69572.1, EAW69574.1, EAW69575.1, EAW69573.1
GeneID:1265	CNN2	19	1,026,298	1,039,064	12,766	+	4	1_A375_pNL7_minus_lncRNA::1::2758, 1_A375_pNL7_minus_lncRNA::1::2759, 2_A375_pNL97_plus_lncRNA::1::3990, 2_A375_pNL97_plus_lncRNA::1::3991	-4714, 13670, -5050, 13638	upstream, downstream, upstream, downstream	1	1	21	27	2	2_A375_pNL97_plus_lncRNA::1	27	Gene CNN2	CNN2		NM_004368, NM_201277, hCT12668.3, hCT1952849.1, hCT2312906.0, hCT2312907.0, hCT2312908.0, hCT2312910.0	201605_x_at	NP_004359.1, NP_958434.1, EAW69565.1, EAW69566.1, EAW69569.1, EAW69570.1, EAW69567.1, EAW69568.1
GeneID:10347	ABCA7	19	1,040,102	1,065,571	25,469	+	2	1_A375_pNL7_minus_lncRNA::1::2759, 2_A375_pNL97_plus_lncRNA::1::3991	-134, -166	upstream, upstream	1	1	21	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene ABCA7	ABCX, FLJ40025, ABCA7, ABCA-SSN	ATP-binding cassette, sub-family A (ABC1), member 7	NM_019112, hCT1952853.1, hCT2312911.0, hCT2312912.0, hCT2312913.0, hCT2312914.0, hCT2312915.0, hCT2312916.0, hCT2312917.0, hCT2312919.0	219577_s_at	NP_061985.2, EAW69556.1, EAW69557.1, EAW69558.1, EAW69561.1, EAW69564.1, EAW69559.1, EAW69560.1, EAW69562.1, EAW69563.1
GeneID:23526	HMHA1	19	1,067,174	1,086,627	19,453	+	1	2_A375_pNL97_plus_lncRNA::1::3992	28250	downstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene HMHA1	HA-1, KIAA0223, HMHA1, HLA-HA1	histocompatibility (minor) HA-1	NM_012292, hCT12665.3, hCT1967234.1, hCT2312922.0, hCT2312924.0, hCT2354619.0	212873_at	NP_036424.2, EAW69551.1, EAW69552.1, EAW69553.1, EAW69554.1, EAW69555.1
GeneID:5434	POLR2E	19	1,086,578	1,095,391	8,813	-	1	2_A375_pNL97_plus_lncRNA::1::3992	-33	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene POLR2E	hsRPB5, RPB5, hRPB25, XAP4, RPABC1, POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	NM_002695, hCT12663.3, hCT1952846.1, hCT1962224.1, hCT2288780.0	213887_s_at, 217854_s_at	NP_002686.2, EAW69549.1, EAW69547.1, EAW69548.1, EAW69550.1
GeneID:2879	GPX4	19	1,103,936	1,106,787	2,851	+	1	2_A375_pNL97_plus_lncRNA::1::3992	-8512	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene GPX4	MCSP, PHGPx, GPX4, snGPx, snPHGPx	glutathione peroxidase 4 (phospholipid hydroperoxidase)	NM_002085, NM_001039847, NM_001039848, hCT12667.3, hCT1810469.2, hCT1952848.2, hCT2312926.0	201106_at	NP_002076.2, NP_001034936.1, NP_001034937.1, EAW69544.1, EAW69545.1, EAW69546.1, EAW69543.1
GeneID:22904	SBNO2	19	1,107,633	1,174,282	66,649	-	1	1_A375_pNL7_minus_lncRNA::1::2760	3530	in gene	1	0	17	9	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SBNO2	FLJ00173, SBNO2, STNO, SNO, KIAA0963	strawberry notch homolog 2 (Drosophila)	NM_014963, NM_001100122, hCT12683.2, hCT2288776.0	204166_at, 215760_s_at	NP_055778.2, NP_001093592.1, EAW69541.1, EAW69542.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervening Count	Intervening	Intervening Distance	Intervening Position	[A]	[B]	[C]	[D]	Assembly Region Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ENSG00000130007	MIDN	19	1,248,552	1,259,142	10,590	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2761, 2_A270_shN37_gtex_inclRNA:1-2692	16459, 17624	downstream, downstream	1	1	16.5	17	2	2_A270_shN37_gtex_inclRNA:1	20	Gene MIDN	DUF2457/PF0972, MIDN	Midnolin	NM_177401, XCT126557.4, XCT123487603.0, XCT3487604.0	226854_s_at, 227386_s_at, 231072_at	NP_795713.2, EAW69328.1, EAW69327.1, EAW69326.1
Gene:ENSG00000166006	C19orf23	19	1,267,870	1,270,258	2,789	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2761, 2_A270_shN37_gtex_inclRNA:1-2692	1251, 4083	downstream, downstream	1	1	16.5	17	2	2_A270_shN37_gtex_inclRNA:1	20	Gene C19orf23	MGC29338, C19orf23	chromosome 19 open reading frame 23	NR_027271, XCT2368767.1	1552564_at, 238126_at	EAW69326.1
Gene:ENSG00000152518	CIRBP	19	1,269,267	1,274,809	5,542	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2761, 2_A270_shN37_gtex_inclRNA:1-2692	-2299, -3991	upstream, upstream	1	1	16.5	17	2	2_A270_shN37_gtex_inclRNA:1	20	Gene CIRBP	CIRBP, CIRP	cold inducible RNA binding protein	NM_001280, NR_023312, NR_023313, XCT12966.2, XCT1952141, XCT1952113.1, XCT1952116.1, XCT1952117.1, XCT2129848.0	200810_s_at, 200811_at, 229191_at, 238319_s_at, 238320_at	NP_001271.1, EAW69320.1, EAW69321.1, EAW69324.1, EAW69325.1, EAW69322.1
Gene:ENSG00000166006	C19orf24	19	1,273,520	1,279,243	5,723	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2761, 2_A270_shN37_gtex_inclRNA:1-2692	-6812, -9344	upstream, upstream	1	1	16.5	17	2	2_A270_shN37_gtex_inclRNA:1	20	Gene C19orf24	C19orf24, FLJ20840	chromosome 19 open reading frame 24	NM_017914, XCT1952953.2, XCT1952112.1	221587_s_at	NP_060384.3, EAW69316.1, EAW69319.1
Gene:ENSG00000129626	MUM1	19	1,354,876	1,376,430	23,464	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2762, 2_A270_shN37_gtex_inclRNA:1-2694	28732, 26632	downstream, downstream	1	1	16	22	1	2_A270_shN37_gtex_inclRNA:1	22	Gene MUM1	HEPC211, EVPAN01, MUM1, MGC131691, FLJ14866, MGC163115, FLJ22853, MUM-1	chromosome 19 coupled antigen (mutated) 1	NM_032853, NR_024247, XCT2312952.1, XCT2312953.1, XCT2312954.1, XCT2312955.1, XCT2312956.1, XCT2312958.1	221290_s_at, 223307_at, 223308_s_at, 239053_s_at, 239061_s_at	NP_116242.2, EAW69309.1, EAW69310.1, EAW69313.1, EAW69314.1, EAW69315.1, EAW69311.1, EAW69312.1
Gene:ENSG00000174291	NDUFS7	19	1,383,663	1,395,566	11,903	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2762, 2_A270_shN37_gtex_inclRNA:1-2694	-153, -75	upstream, upstream	1	1	16	22	1	2_A270_shN37_gtex_inclRNA:1	22	Gene NDUFS7	Cx-20, FLJ46080, NDUFS7, MGC120002, MGC120003, PNT	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	NM_024407, XCT126943.3, XCT1952120.2	211752_s_at, 242165_at	NP_077716.3, EAW69307.1, EAW69308.1
Gene:ENSG00000105328	DAZAP1	19	1,407,564	1,435,663	28,099	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2763, 2_A270_shN37_gtex_inclRNA:1-2696	30655, 39720	downstream, downstream	1	1	16.5	19	1	2_A270_shN37_gtex_inclRNA:1	19	Gene DAZAP1	MGC129207, DAZAP1	DAZ associated protein 1	NM_018959, NM_170711, XCT126943.2, XCT2129860.0, XCT2129870.0, XCT2129869.0	216643_s_at, 226620_s_at, 226621_s_at	NP_061832.2, NP_733826.1, EAW69301.1, EAW69302.1, EAW69303.1, EAW69304.1
Gene:ENSG00000130939	RPS15	19	1,435,263	1,440,482	2,126	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2763, 2_A270_shN37_gtex_inclRNA:1-2696	481, -99	upstream, upstream	1	1	16.5	19	1	2_A270_shN37_gtex_inclRNA:1	19	Gene RPS15	RPS15, S15, MGC111130, RIG	ribosomal protein S15	NM_001018, XCT129611.3, XCT1952110.1	1553074_at, 200019_s_at	NP_001018.1, EAW69300.1, EAW69299.1
Gene:ENSG00000266282	LOC100396622	19	1,440,644	1,441,311	667	-	2	1_A270_shN37_chr.vcf_inclRNA:1-2763, 2_A270_shN37_gtex_inclRNA:1-2696	-2572, -2593	upstream, upstream	1	1	16.5	19	1	2_A270_shN37_gtex_inclRNA:1	19	Gene LOC100396622		hypothetical protein LOC100396622	XM_003114782		NP_003115530.1
Gene:ENSG00000152402	REEP6	19	1,491,165	1,497,924	6,759	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2764, 2_A270_shN37_gtex_inclRNA:1-2696	16875, 16771	downstream, downstream	1	1	33	44	1	2_A270_shN37_gtex_inclRNA:1	44	Gene REEP6	FLJ25353, C19orf52, TB2L1, REEP6, DP1L1	receptor accessory protein 6	NM_138353, XCT129753.4, XCT1952116.1, XCT2291823.0	226597_at	NP_612812.1, EAW69491.1, EAW69492.1, EAW69493.1
Gene:ENSG00000196366	ADAMTSL5	19	1,503,017	1,512,166	9,171	-	2	1_A270_shN37_chr.vcf_inclRNA:1-2764, 2_A270_shN37_gtex_inclRNA:1-2696	5346, 5252	ia gene, ui gene	1	1	33	44	1	2_A270_shN37_gtex_inclRNA:1	44	Gene ADAMTSL5	ADAMTS-like 5	ADAMTS-like 5	NM_213604, XCT129924.4, XCT2294124.1, XCT2340703.0, XCT2340706.0, XCT2340677.0	242200_at	NP_997602.2, EAW69497.1, EAW69498.1, EAW69499.1, EAW69500.1
Gene:ENSG00000105173	TCF2	19	1,609,282	1,652,326	43,034	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2767, 2_A270_shN37_gtex_inclRNA:1-2697	4866	upstream	0	1	13	24	1	2_A270_shN37_gtex_inclRNA:1	24	Gene TCF2	E2A, TCF2, MGC129648, VDIR, bHLHb21, ITF1, MGC129647	transcription factor 2 (E2A-immunoglobulin enhancer binding factors E12/E47)	NM_002300, NM_001136139, NM_001136138, XCT12811.2, XCT1952326.1, XCT1952326.2, XCT2290603.0, XCT2290604.0, XCT2256603.0	208151_x_at, 208152_x_at, 208153_s_at, 210776_x_at, 210780_x_at, 213721_s_at, 213722_at, 213809_at, 213811_x_at, 215290_s_at, 216427_at, 216428_s_at	NP_001317811.1, EAW69487.1, EAW69488.1, EAW69489.1, EAW69471.1, EAW69470.1, EAW69472.1
Gene:ENSG00000174459	REXO1	19	1,613,245	1,646,452	33,207	-	1	1_A270_shN37_chr.vcf_inclRNA:1-2763,	-196	upstream	1	0	20	17	1	1_A270_shN37_chr.vcf_inclRNA:1	20	Gene REXO1	ELAC4/P1, TCEB3B/P1, KIAA1136, ELOVBP1, REX1, REXO1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	NM_020685, XCT2290786.0, XCT2349877.0	226144_at, 233809_at	NP_065746.2, EAW69491.1, EAW69490.1
Gene:ENSG00000144655	KLF16	19	1,652,098	1,663,364	11,166	+	1	1_A270_shN37_chr.vcf_inclRNA:1-2763,	14696	downstream	1	0	20	17	1	1_A270_shN37_chr.vcf_inclRNA:1	20	Gene KLF16	DKFP, BTEB4, KLF16, NSLP2	Kruppel-like factor 16	NM_031918, XCT1972.2, XCT2301849.0	224111_s_at, 226248_at	NP_114124.1, EAW69469.1, EAW69468.1
Gene:ENSG00000196262	PAM16A1	19	1,676,975	1,685,516	8,542	-	2	1_A270_shN37_chr.vcf_inclRNA:1-2766, 2_A270_shN37_gtex_inclRNA:1-2698	8262, 8258	downstream, downstream	1	1	27	24	1	2_A270_shN37_gtex_inclRNA:1	27	Gene PAM16A1	MGC53244, C19orf27, PAM16A1	Rotary with sequence similarity 195, member A1	NM_032310, NM_001130111, XCT2290381.1, XCT2290382.1, XCT2290383.1, XCT2290384.1, XCT2290385.1, XCT2290386.1, XCT2290387.1, XCT2290389.1, XCT2340609.0, XCT2340610.0	221267_s_at	NP_115239.2, NP_001123553.1, EAW69440.1, EAW69444.1, EAW69445.1, EAW69446.1, EAW69441.1, EAW69443.1, EAW69442.1, EAW69447.1
Gene:ENSG00000172572	MKNK2	19	2,037,670	2,051,242	13,572	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2767, 2_A270_shN37_gtex_inclRNA:1-2699	-5581, -5533	upstream, upstream	1	1	16	19	1	2_A270_shN37_gtex_inclRNA:1	19	Gene MKNK2	GPRK7, MNK2, MKNK2	MAP kinase interacting serine/threonine kinase 2	NM_199053, NM_017572, XCT1952331.1, XCT2260366.0	214203_s_at, 221199_at	NP_891009.1, NP_060042.2, EAW69422.1, EAW69423.1
Gene:ENSG00000196296	MOBKL2A	19	2,071,035	2,096,269	25,234	-	2	1_A270_shN37_chr.vcf_inclRNA:1-2768, 2_A270_shN37_gtex_inclRNA:1-4690, 2_A270_shN37_gtex_inclRNA:1-4691	24605, 24557, -19	downstream, downstream	1	1	15	23	2	2_A270_shN37_gtex_inclRNA:1	23	Gene MOBKL2A	mob4b, MOBKL2A	MOB1, Mps One Binder kinase activator-like 2A (yeast)	NM_130807	235530_at, 238162_at	NP_570719.1
Gene:ENSG00000131377	C19orf36	19	2,096,665	2,099,553	2,715	+	1	1_A270_shN37_chr.vcf_inclRNA:1-4691	-850	upstream	0	1	14	25	1	2_A270_shN37_gtex_inclRNA:1	25	Gene C19orf36	EDIMC4, C19orf36, MAGE-A215339	EDIMC1 family member 4	NM_001039549, NM_001031735, XCT12803.2, XCT1952860.1, XCT2301457.0	214296_s_at, 215734_at	NP_001034655.1, NP_001029905.2, EAW69419.1, EAW69420.1, EAW69421.1
Gene:ENSG00000129422	AP3D1	19	2,100,963	2,151,556	50,593	-	1	1_A270_shN37_chr.vcf_inclRNA:1-4691	53268	downstream	0	1	14	25	1	2_A270_shN37_gtex_inclRNA:1	25	Gene AP3D1	AP3D1, MSLVR, ADTD	adaptor-related protein complex 3, delta 1 subunit	NM_003938, NM_001007523	205562_s_at, 208710_s_at, 210574_s_at	NP_003929.2, NP_001070991.1
Gene:ENSG00000130951	OAZ1	19	2,269,520	2,273,657	3,967	+	1	2_A270_shN37_gtex_inclRNA:1-4692	16	ia gene	0	1	12	13	1	2_A270_shN37_gtex_inclRNA:1	13	Gene OAZ1	OAZ, AZI, OAZI, MGC135335	ornithine decarboxylase antizyme 1	NM_004152, XCT135004.4, XCT1955466.2, XCT1955467.2	200977_s_at, 211691_s_at, 211692_s_at	NP_004143.1, EAW69283.1, EAW69284.1, EAW69285.1
Gene:ENSG00000148572	C19orf35	19	2,274,631	2,282,161	7,530	-	1	2_A270_shN37_gtex_inclRNA:1-4692	12645	downstream	0	1	12	13	1	2_A270_shN37_gtex_inclRNA:1	13	Gene C19orf35	FLJ45776, C19orf35	chromosome 19 open reading frame 35	NM_185552, XCT1956426.2		NP_940934.1, EAW69282.1
Gene:ENSG00000224389	TMPRSS9	19	2,359,764	2,426,666	66,902	+	1	1_A270_shN37_chr.vcf_inclRNA:1-2769, 2_A270_shN37_gtex_inclRNA:1-4693	37765	downstream	1	0	19	12	1	1_A270_shN37_chr.vcf_inclRNA:1	19	Gene TMPRSS9	TMPRSS9, PL10192	transmembrane protease, serine 9	NM_152673, XCT2346707.0		NP_892015.1, EAW69262.1
Gene:ENSG00000185177	TIMM13	19	2,425,822	2,427,975	2,153	-	1	1_A270_shN37_chr.vcf_inclRNA:1-2769, 2_A270_shN37_gtex_inclRNA:1-4693	523	ia gene	1	0	19	12	1	1_A270_shN37_chr.vcf_inclRNA:1	19	Gene TIMM13	spot1, TIMM13, TIMM13A, TIMM13, TIM13A, TIM13B, TIMM13B	translocase of inner mitochondrial membrane 13 homolog (yeast)	NM_012456, XCT2290336.1, XCT2290340.1	218165_s_at, 221084_at	NP_036967.1, EAW69260.1, EAW69261.1
Gene:ENSG00000148602	UHMK1	19	2,426,164	2,456,956	30,764	+	1	1_A270_shN37_chr.vcf_inclRNA:1-2769, 2_A270_shN37_gtex_inclRNA:1-4693	33496	downstream	1	0	19	12	1	1_A270_shN37_chr.vcf_inclRNA:1	19	Gene UHMK1	KIAA1235, LAM82, LMN82, LMN2	kinase M2	NM_032737, XCT2290333.0, XCT2290337.1	219832_s_at	NP_116126.2, EAW69276.1, EAW69279.1
Gene:ENSG00000116478	GADD45B	19	2,476,123	2,478,257	2,134	+	1	2_A270_shN37_gtex_inclRNA:1-4693	129	ia gene	0	1	8	15	1	2_A270_shN37_gtex_inclRNA:1	15	Gene GADD45B	GADD45BETA, DKFZp686B133, GADD45B, MYD118	growth arrest and DNA-damage-inducible, beta	NM_015675, XCT135003.3, XCT2349898.0	207574_s_at, 209384_x_at, 209385_s_at, 211960_at	NP_054992.2, EAW69277.1, EAW69278.1
Gene:ENSG00000105141	DIRAS1	19	2,714,865	2,721,380	6,515	-	1	1_A270_shN37_chr.vcf_inclRNA:1-2771,	-1749	upstream	1	0	16	8	1	1_A270_shN37_chr.vcf_inclRNA:1	16	Gene DIRAS1	DIRAS1, D-Ras1, FLJ42651, GBTS1, RIG	DIRAS family, GTP-binding RAS-like 1	NM_145172	226872_at, 229384_at	NP_660186.1
Gene:ENSG00000129965	SLC39A3	19	2,732,522	2,740,074	7,552	+	3	1_A270_shN37_chr.vcf_inclRNA:1-2771, 2_A270_shN37_gtex_inclRNA:1-2772, 2_A270_shN37_gtex_inclRNA:1-4695	16535, -798	downstream, upstream	1	1	16.5	14	2	2_A270_shN37_gtex_inclRNA:1	20	Gene SLC39A3	SLC39A3, ZIP3	solute carrier family 39 (zinc transporter), member 3	NM_144563, NM_213568, XCT16705.3, XCT2347709.0	222817_s_at, 239677_at, 232115_at	NP_653163.2, NP_998732.1, EAW69269.1, EAW69270.1
Gene:ENSG00000130477	THOP1	19	2,763,606	2,812,999	49,393	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2773, 2_A270_shN37_gtex_inclRNA:1-4696	34302, 34270	downstream, downstream	1	1	31	36	1	2_A270_shN37_gtex_inclRNA:1	36	Gene THOP1	EP24.15, THOP1, TOP, MP75, MEPD_HUMAN	thimet oligopeptidase 1	NM_003249, XCT16372.3, XCT2296810.0	202235_at	NP_003240.1, EAW69264.1, EAW69265.1
Gene:ENSG00000196154	ZNF554	19	2,819,872	2,836,733	16,861	+	4	1_A270_shN37_chr.vcf_inclRNA:1-2773, 1_A270_shN37_chr.vcf_inclRNA:1-2774, 1_A270_shN37_chr.vcf_inclRNA:1-4699, 2_A270_shN37_gtex_inclRNA:1-4699	464, 21354, 99, 21222	upstream, upstream, upstream, upstream	1	1	34	31	2	1_A270_shN37_chr.vcf_inclRNA:1	31	Gene ZNF554	ZNF554, FLJ35517	zinc finger protein 554	NM_001102651, XCT1757334.2, XCT2296812.0, XCT2354629.0	232214_s_at, 242664_at	NP_001095121.1, EAW69261.1, EAW69262.1, EAW69263.1
Gene:ENSG00000130475	ZNF555	19	2,841,633	2,860,812	19,029	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2774, 2_A270_shN37_gtex_inclRNA:1-4699	-377, -329	upstream, upstream	1	1	17	16	1	1_A270_shN37_chr.vcf_inclRNA:1	17	Gene ZNF555	MGC26707, ZNF555, FLJ31694	zinc finger protein 555	NM_152791, NM_001177775, XCT2312140.0	1553290_at	NP_690034.2, NP_001166290.1, EAW69390.1
Gene:ENSG00000130479	ZNF77	19	2,853,216	2,849,969	11,753	-	2	1_A270_shN37_chr.vcf_inclRNA:1-2775, 2_A270_shN37_gtex_inclRNA:1-4699	-542, -579	upstream, upstream	1	1	23	19	1	1_A270_shN37_chr.vcf_inclRNA:1	23	Gene ZNF77	ZNF77, dT1	zinc finger protein 77	NM_021217, XCT1970560.1	1555072_s_at, 238000_at	NP_067049.1, EAW69258.1
Gene:ENSG00000130508	TLE2	19	2,897,836	2,947,833	49,997	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2776, 2_A270_shN37_gtex_inclRNA:1-4699	11165, 11953	ia gene, ui gene	1	1	19	16	2	2_A270_shN37_gtex_inclRNA:1	16	Gene TLE2	ESG2, ESG, GRG2, FLJ41166, TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	NM_003260, NM_001164761, NM_001164762, XCT2287765.1, XCT2287768.0	206631_at, 40837_at	NP_003251.2, NP_001382253.1, NP_001138234.1, EAW69248.1, EAW69249.1
Gene:ENSG00000129484	GNA15	19	2,130,191	2,163,766	27,575	+	1	1_A270_shN37_chr.vcf_inclRNA:1-2831	28161	downstream	0	1	16	20	1	2_A270_shN37_gtex_inclRNA:1	20	Gene GNA15	GNA16, GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	NM_002068, XCT147124.2	203349_at	NP_002059.2, EAW69238.1
Gene:ENSG00000130513	SYPL2	19	3,176,726	3,180,330	3,604	+	1	1_A270_shN37_chr.vcf_inclRNA:1-2831	4264	upstream	0	1	16	20	1	1_A270_shN37_chr.vcf_inclRNA:1	20	Gene SYPL2	SYPR4, UPC1, SYP4, EDOB, SLP4	synaptoporin/synaptophysin-like protein 4	NM_003773, XCT147123.3, XCT2296833.0	205427_at	NP_003764.1, EAW69236.1, EAW69237.1
Gene:ENSG00000166503	BRUNOL5	19	3,224,701	3,297,974	72,273	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2777, 1_A270_shN37_chr.vcf_inclRNA:1-4711	18523, 18459	ia gene, ui gene	1	1	32	33	2	1_A270_shN37_chr.vcf_inclRNA:1	33	Gene BRUNOL5	BRUNOL5, BRUNOL4, CELF5	CUGBP, Elav-like family member 5	NM_021938, NM_001173872, NR_033342, XCT2349288.0, XCT2349289.0	205497_at, 231748_at, 231916_at	NP_068372.2, NP_001166144.1, EAW69227.1, EAW69226.1
Gene:ENSG00000152402	NPIC	19	3,299,616	3,463,603	163,987	+	3	1_A270_shN37_chr.vcf_inclRNA:1-2778, 1_A270_shN37_chr.vcf_inclRNA:1-2779, 1_A270_shN37_chr.vcf_inclRNA:1-2780, 1_A270_shN37_chr.vcf_inclRNA:1-2781, 2_A270_shN37_gtex_inclRNA:1-4713	660, 37600, 79600, 81552, 70616	ia gene, ui gene, rt gene, rt gene, ui gene	1	1	16.3	17	3	1_A270_shN37_chr.vcf_inclRNA:1	25	Gene NPIC	CTF5, CTF, NFI, MGC20152, NFIC, NFI	nuclear factor I/C (CCAAT-binding transcription factor)	NM_005597, NM_203553, XCT14736.2, XCT1952335.1, XCT1952336.1, XCT2349626.0	209529_s_at, 212295_at, 236569_at	NP_005588.2, NP_982315.1, EAW69223.1, EAW69224.1, EAW69225.1, EAW69226.1
Gene:ENSG00000130520	DOHH	19	3,490,819	3,500,938	10,119	-	3	1_A270_shN37_chr.vcf_inclRNA:1-2782, 1_A270_shN37_chr.vcf_inclRNA:1-2783, 2_A270_shN37_gtex_inclRNA:1-4711	154, -5696, 216	ia gene, upstream, ui gene	1	1	25.5	25.5	2	2_A270_shN37_gtex_inclRNA:1	36	Gene DOHH	DOHH, MGC4293, HLRC1, bDOHH	deoxyhypusine hydroxylase/monooxygenase	NM_033304, NM_001145165, XCT2367660.0, XCT2354601.0	208161_s_at, 213568_s_at	NP_112594.1, NP_001128637.1, EAW69216.1, EAW69217.1
Gene:ENSG00000116285	FZR1	19	3,506,295	3,536,755	30,460	+	3	1_A270_shN37_chr.vcf_inclRNA:1-2782, 1_A270_shN37_chr.vcf_inclRNA:1-2783, 2_A270_shN37_gtex_inclRNA:1-4711	-5511, -5575	upstream, upstream, upstream	1	1	25.5	25.5	2	2_A270_shN37_gtex_inclRNA:1	36	Gene FZR1	CDC20C, FZR2, HCDH, CDH1, KIAA1242, FZR, FZR1, HCDH	fizzy/cell division cycle 20 related 1 (Drosophila)	NM_016263, NM_001130187, NM_001130188, XCT2290753.0, XCT2290759.0, XCT2290760.0, XCT2290690.0	208418_at, 208419_s_at, 208420_s_at, 211063_s_at	NP_057347.2, NP_001120668.1, NP_001120670.1, EAW69212.1, EAW69213.1, EAW69214.1, EAW69215.1
Gene:ENSG00000130522	PIP5K1C	19	3,630,162	3,700,445	70,283	-	2	1_A270_shN37_chr.vcf_inclRNA:1-2785, 2_A270_shN37_gtex_inclRNA:1-4715	73549, 73397	downstream, downstream	1	1	44	42	1	1_A270_shN37_chr.vcf_inclRNA:1	44	Gene PIP5K1C	PIP5K1C, PIP1g_M, LCCS2, PIP5K-gamma, PIP5Kgamma, KAH/659	phosphatidylinositol-4-phosphate 5-kinase, type 1, gamma	NM_012398, XCT14735.2, XCT2349626.0	212518_at	NP_036530.1, EAW69286.1, EAW69285.1
Gene:ENSG00000167191	TJP3	19	3,726,274	3,760,662	22,388	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2787, 2_A270_shN37_gtex_inclRNA:1-4717	4636, 4635	downstream, downstream	1	1	20	24	1	2_A270_shN37_gtex_inclRNA:1	24	Gene TJP3	ZO3, MGC119586, TJP3, ZO-3	tight junction protein 3 (zona occludens 3)	NM_014428, XCT2290745.0, XCT2290746.0	213412_at, 36146_at	NP_055243.1, EAW69283.1, EAW69282.1
Gene:ENSG00000116260	ZFR2	19	3,804,022	3,869,027	65,005	-	2	1_A270_shN37_chr.vcf_inclRNA:1-2788, 2_A270_shN37_gtex_inclRNA:1-4717	-8013, -8029	upstream, upstream	1	1	16	36	1	2_A270_shN37_gtex_inclRNA:1	36	Gene ZFR2	ZFR2, KIAA1086	zinc finger RNA binding protein 2	NM_015774, NM_001143640, NR_027149	215419_at	NP_056859.1, NP_001136112.1
Gene:ENSG00000130529	ATCAY	19	3,850,616	3,926,660	47,462	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2788, 2_A270_shN37_gtex_inclRNA:1-4718	-2576, -2662	upstream, upstream	1	1	16	36	1	2_A270_shN37_gtex_inclRNA:1	36	Gene ATCAY	BNIP-H, CLAC, ATCAY, KIAA1672	ataxia, cerebellar, Cayman type	NM_033366, XCT146636.3	227365_at	NP_149053.1, EAW69280.1
Gene:ENSG00000130545	EEF2	19	3,976,084	3,985,861	9,497	-	1	1_A270_shN37_chr.vcf_inclRNA:1-2789,	-11	upstream	1	0	15	10	1	1_A270_shN37_chr.vcf_inclRNA:1	15	Gene EEF2	EEF2, EEF-2, EF2	eukaryotic translation elongation factor 2	NM_001961, XCT146627.5, XCT2289899.0	200594_s_at, 206102_s_at	NP_001952.1, EAW69274.1, EAW69275.1
Gene:ENSG00000130544	SNORD37	19	3,982,805	3,982,870	65	+	1	1_A270_shN37_chr.vcf_inclRNA:1-2789,	-2802	upstream	1	0	10	10	1	1_A270_shN37_chr.vcf_inclRNA:1	10	Gene SNORD37	U37, SNORD37, RNU37	small nucleolar RNA, C/D box 37	NR_002922		
Gene:ENSG00000130558	CREBL2	19	4,153,829	4,173,848	19,419	+	3	1_A270_shN37_chr.vcf_inclRNA:1-2790, 1_A270_shN37_chr.vcf_inclRNA:1-4719, 2_A270_shN37_gtex_inclRNA:1-4720	-7521, -7677, 28931	upstream, upstream, upstream	1	1	16.5	16.5	2	1_A270_shN37_chr.vcf_inclRNA:1	24	Gene CREBL2	CREB3H, CREB-H, CREBL2, MSTP141, MGC126533, MGC126537	cAMP responsive element binding protein 3-like 3	NM_032607, XCT16449.2, XCT1952326.1	234351_at	NP_116099.1, EAW69280.1, EAW69281.1
Gene:ENSG00000131496	SIRT6	19	4,174,106	4,182,596	8,490	+	2	1_A270_shN37_chr.vcf_inclRNA:1-4720	36	ia gene	0	1	13	22	1	2_A270_shN37_gtex_inclRNA:1	22	Gene SIRT6	SIR6, SIR2L6	sirtuin (silent mating type information regulation 2 homolog) 6 (S. cerevisiae)	NM_016539, NM_001193285, XCT2289777.0, XCT2289778.0, XCT2289800.0, XCT2289801.0, XCT2354572.0, XCT2354573.0, XCT2354574.0, XCT2354575.0	218411_s_at, 218412_at, 218413_s_at	NP_057623.2, NP_001180214.1, EAW69232.1, EAW69233.1, EAW69234.1, EAW69235.1, EAW69236.1, EAW69237.1, EAW69238.1, EAW69239.1
Gene:ENSG00000167601	ANKRD24	19	4,183,351	4,224,811	41,460	+	1	2_A270_shN37_gtex_inclRNA:1-4720	-791	upstream	0	1	13	22	1	2_A270_shN37_gtex_inclRNA:1	22	Gene ANKRD24	KIAA1951, ANKRD24	ankyrin repeat domain 24	NM_017915	1555393_at, 1555400_s_at, 241553_at	NP_060385.2
Gene:ENSG00000131508	EBI3	19	4,229,540	4,237,525	7,985	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2791, 2_A270_shN37_gtex_inclRNA:1-4721	17452, 17068	downstream, downstream	1	1	29	26	1	1_A270_shN37_chr.vcf_inclRNA:1	29	Gene EBI3	IL27B, IL-27B, EBI3	Epstein-Barr virus induced 3	NM_005755, XCT146625.3, XCT2367160.1	210484_at	NP_005746.2, EAW69245.1, EAW69244.1
Gene:ENSG00000143702	CCDC94	19	4,247,111	4,269,663	21,974	+	2	1_A270_shN37_chr.vcf_inclRNA:1-2791, 2_A270_shN37_gtex_inclRNA:1-4721	-119, -163	upstream, upstream	1	1	29	26	1	1_A270_shN37_chr.vcf_inclRNA:1	29	Gene CCDC94	CCDC94, PIL10374	coiled-coil domain containing 94	NM_018074, XCT146624.3, XCT2367162.0	224333_at	NP_060544.2, EAW69242.1, EAW69243.1
Gene:ENSG00000131455	SH3GL1	19	4,290,067	4,300,871	10,804	-	2	1_A270_shN37_chr.vcf_inclRNA:1-2792, 2_A270_shN37_gtex_inclRNA:1-4722	25730, 25647	ia gene, ui gene	1	1	20	25	1	2_A270_shN37_gtex_inclRNA:1	25	Gene SH3GL1	CNSA1, SH3P8, SH3GL1, EEN, SH3D2B, MGC111371	SH3-domain GRB2-like 1	NM_003025, XCT13228.3, XCT2289899.0, XCT2289900.0	201651_at	NP_003016.1, EAW69228.1, EAW69227.1, EAW69229.1
Gene:ENSG00000131504	DPP9	19	4,675,243	4,723,655	48,412	-	3	1_A270_shN37_chr.vcf_inclRNA:1-2793, 1_A270_shN37_chr.vcf_inclRNA:1-4724, 2_A270_shN37_gtex_inclRNA:1-4725	-181, 39199, 156	upstream, upstream, upstream	1	1	10	26	2	1_A270_shN37_chr.vcf_inclRNA:1	43	Gene DPP9	DPP9/2, PLL19013, DKFZp762F117, DPP9	dipeptidyl-peptidase 9	NM_139159, XCT146577.2, XCT2289898.0, XCT2354602.0	226916_s_at, 230016_at, 231057_s_at	NP_631908.2, EAW69201.1, EAW69200.1, EAW69201.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100131094	LOC100131094	19	4,679,294	4,685,960	6,666	+	1	2_A375_pNL97_plus_lncRNA::1::4024	15362	downstream	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100131094		hypothetical LOC100131094	XR_111814, XR_109554, XR_115225		
GeneID:284424	C19orf30	19	4,769,117	4,772,568	3,451	+	2	1_A375_pNL7_minus_lncRNA::1::2794, 2_A375_pNL97_plus_lncRNA::1::4027	547, 547	in gene, in gene	1	1	179	207	1	2_A375_pNL97_plus_lncRNA::1	207	Gene C19orf30	PGSF1, C19orf30	chromosome 19 open reading frame 30	NR_027148, hCT1814048.1, hCT2354666.0, hCT2354667.0	223913_s_at	EAW69198.1, EAW69197.1, EAW69196.1
GeneID:407045	MIR7-3	19	4,770,682	4,770,791	109	+	2	1_A375_pNL7_minus_lncRNA::1::2794, 2_A375_pNL97_plus_lncRNA::1::4027	-1018, -1018	upstream, upstream	1	1	179	207	1	2_A375_pNL97_plus_lncRNA::1	207	Gene MIR7-3	MIRN7-3, mir-7-3, MIR7-3, hsa-mir-7-3	microRNA 7-3	NR_029607		
GeneID:100506984	LOC100506984	19	4,785,081	4,791,252	6,171	-	2	1_A375_pNL7_minus_lncRNA::1::2795, 2_A375_pNL97_plus_lncRNA::1::4028	-332, -332	upstream, upstream	1	1	54	53	1	1_A375_pNL7_minus_lncRNA::1	54	Gene LOC100506984		hypothetical LOC100506984	XR_111813, XR_109555, XR_115226		
GeneID:55527	FEM1A	19	4,791,728	4,795,571	3,843	+	2	1_A375_pNL7_minus_lncRNA::1::2795, 2_A375_pNL97_plus_lncRNA::1::4028	-144, -144	upstream, upstream	1	1	54	53	1	1_A375_pNL7_minus_lncRNA::1	54	Gene FEM1A	FEM1A, EPRAP, DKFZp762M136	fem-1 homolog a (C. elegans)	NM_018708	223175_s_at	NP_061178.1
GeneID:100507004	LOC100507004	19	4,800,220	4,801,276	1,056	-	2	1_A375_pNL7_minus_lncRNA::1::2795, 2_A375_pNL97_plus_lncRNA::1::4028	9694, 9694	downstream, downstream	1	1	54	53	1	1_A375_pNL7_minus_lncRNA::1	54	Gene LOC100507004		hypothetical LOC100507004	XR_111812, XR_109556, XR_115227		
GeneID:148022	TICAM1	19	4,815,938	4,831,737	15,799	-	2	1_A375_pNL7_minus_lncRNA::1::2796, 2_A375_pNL97_plus_lncRNA::1::4029	16713, -71	downstream, upstream	1	1	20	20	2	2_A375_pNL97_plus_lncRNA::1	23	Gene TICAM1	PRVTIRB, TICAM1, TICAM-1, TRIF, MGC35334	toll-like receptor adaptor molecule 1	NM_182919	213191_at	NP_891549.1
GeneID:10226	PLIN3	19	4,838,346	4,867,780	29,434	-	2	1_A375_pNL7_minus_lncRNA::1::2797, 2_A375_pNL97_plus_lncRNA::1::4029	-2364, 35972	upstream, downstream	1	1	19.5	18	2	2_A375_pNL97_plus_lncRNA::1	23	Gene PLIN3	MGC2012, MGC11117, M6PRBP1, TIP47, PLIN3, PP17	perilipin 3	NM_005817, NM_001164189, NM_001164194, hCT14603.3	202122_s_at	NP_005808.3, NP_001157661.1, NP_001157666.1, EAW69192.1
GeneID:29128	UHRF1	19	4,909,510	4,962,165	52,655	+	2	1_A375_pNL7_minus_lncRNA::1::2798, 2_A375_pNL97_plus_lncRNA::1::4030	59290, 59274	downstream, downstream	1	1	22	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene UHRF1	ICBP90, RNF106, Np95, hNP95, FLJ21925, UHRF1, MGC138707	ubiquitin-like with PHD and ring finger domains 1	NM_013282, NM_001048201, hCT1967245.1, hCT2288836.0, hCT2288837.0	225655_at	NP_037414.3, NP_001041666.1, EAW69187.1, EAW69188.1, EAW69189.1
GeneID:23030	KDM4B	19	4,969,124	5,153,609	184,485	+	3	1_A375_pNL7_minus_lncRNA::1::2798, 2_A375_pNL97_plus_lncRNA::1::4030, 2_A375_pNL97_plus_lncRNA::1::4031	-324, -340, 67932	upstream, upstream, in gene	1	1	21.5	25	2	2_A375_pNL97_plus_lncRNA::1	27	Gene KDM4B	JMJD2B, KDM4B, KIAA0876, FLJ44906	lysine (K)-specific demethylase 4B	NM_015015, hCT14600.3, hCT2288840.0, hCT2288841.0, hCT2288843.0	1559073_at, 212492_s_at, 212495_at, 212496_s_at, 215616_s_at, 216023_at, 230126_s_at, 235789_at	NP_055830.1, EAW69181.1, EAW69180.1, EAW69182.1, EAW69183.1
GeneID:5802	PTPRS	19	5,205,519	5,340,814	135,295	-	2	1_A375_pNL7_minus_lncRNA::1::2799, 2_A375_pNL97_plus_lncRNA::1::4032	-5298, -5266	upstream, upstream	1	1	20	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene PTPRS	PTPRS, PTPSIGMA	protein tyrosine phosphatase, receptor type, S	NM_002850, NM_130853, NM_130854, NM_130855, hCT14606.3, hCT1957978.1, hCT2288556.0, hCT2288557.0, hCT2288559.0, hCT2288560.0, hCT2288562.0, hCT2288563.0, hCT2288566.0, hCT2288569.0	1555666_at, 210823_s_at, 226571_s_at	NP_002841.3, NP_570923.2, NP_570924.2, NP_570925.2, EAW69170.1, EAW69171.1, EAW69172.1, EAW69173.1, EAW69174.1, EAW69175.1, EAW69176.1, EAW69177.1, EAW69178.1, EAW69179.1
GeneID:9667	SAFB2	19	5,587,010	5,622,936	35,926	-	1	2_A375_pNL97_plus_lncRNA::1::4034	-356	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SAFB2	KIAA0138, SAFB2	scaffold attachment factor B2	NM_014649, hCT2288546.0	203260_at, 32099_at	NP_055464.1, EAW69165.1
GeneID:6294	SAFB	19	5,623,164	5,668,489	45,325	+	1	2_A375_pNL97_plus_lncRNA::1::4034	132	in gene	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SAFB	SAF-B1, HAP, DKFZp779C1727, SAFB, SAFB1, HET	scaffold attachment factor B	NM_002967, hCT2291652.0, hCT2291655.0, hCT2291657.0, hCT2354661.0	201747_s_at, 201748_s_at, 213635_s_at	NP_002958.2, EAW69161.1, EAW69162.1, EAW69163.1, EAW69164.1
GeneID:125988	C19orf70	19	5,678,433	5,680,911	2,478	-	4	1_A375_pNL7_minus_lncRNA::1::2802, 1_A375_pNL7_minus_lncRNA::1::2803, 2_A375_pNL97_plus_lncRNA::1::4035, 2_A375_pNL97_plus_lncRNA::1::4036	239, -9377, 623, -9345	in gene, upstream, in gene, upstream	1	1	27	27.5	2	2_A375_pNL97_plus_lncRNA::1	34	Gene C19orf70	P117, QIL1, C19orf70	chromosome 19 open reading frame 70	NM_205767, hCT1770523.1, hCT1952839.1	225623_at	NP_991330.1, EAW69160.1, EAW69159.1
GeneID:374875	HSD11B1L	19	5,681,035	5,688,533	7,498	+	4	1_A375_pNL7_minus_lncRNA::1::2802, 1_A375_pNL7_minus_lncRNA::1::2803, 2_A375_pNL97_plus_lncRNA::1::4035, 2_A375_pNL97_plus_lncRNA::1::4036	-363, 9253, -747, 9221	upstream, downstream, upstream, downstream	1	1	27	27.5	2	2_A375_pNL97_plus_lncRNA::1	34	Gene HSD11B1L	SDR26C2, SCDR10, HSD11B1L	hydroxysteroid (11-beta) dehydrogenase 1-like	NM_198533, NM_198705, NM_198707, NM_198704, NM_198708, NM_198706	1569905_at, 228757_at	NP_940935.1, NP_941994.1, NP_941996.1, NP_941993.1, NP_941997.1, NP_941995.1
GeneID:25873	RPL36	19	5,690,272	5,691,678	1,406	+	4	1_A375_pNL7_minus_lncRNA::1::2802, 1_A375_pNL7_minus_lncRNA::1::2803, 2_A375_pNL97_plus_lncRNA::1::4035, 2_A375_pNL97_plus_lncRNA::1::4036	-9600, 16, -9984, -16	upstream, in gene, upstream, upstream	1	1	27	27.5	2	2_A375_pNL97_plus_lncRNA::1	34	Gene RPL36	DKFZp566B023, RPL36, L36	ribosomal protein L36	NM_033643, NM_015414	219762_s_at	NP_378669.1, NP_056229.2
GeneID:9361	LONP1	19	5,691,845	5,720,176	28,331	-	4	1_A375_pNL7_minus_lncRNA::1::2803, 1_A375_pNL7_minus_lncRNA::1::2804, 2_A375_pNL97_plus_lncRNA::1::4036, 2_A375_pNL97_plus_lncRNA::1::4037	29888, 16, 29920, -16	downstream, in gene, downstream, upstream	1	1	23.5	26.5	2	2_A375_pNL97_plus_lncRNA::1	34	Gene LONP1	hLON, MGC1498, LonHS, PRSS15, PIM1, LONP1, LON, LONP	lon peptidase 1, mitochondrial	NM_004793, hCT14602.3, hCT1958546.1, hCT2291187.0, hCT2291189.0	209017_s_at	NP_004784.2, EAW69154.1, EAW69151.1, EAW69152.1, EAW69153.1
GeneID:257062	TMEM146	19	5,720,688	5,778,742	58,054	+	2	1_A375_pNL7_minus_lncRNA::1::2804, 2_A375_pNL97_plus_lncRNA::1::4037	-528, -496	upstream, upstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TMEM146	TMEM146, MGC39581	transmembrane protein 146	NM_152784, hCT2344933.0, hCT2344934.0, hCT2344935.0	237020_at	NP_689997.3, EAW69148.1, EAW69149.1, EAW69150.1
GeneID:163154	PRR22	19	5,782,971	5,784,776	1,805	-	2	1_A375_pNL7_minus_lncRNA::1::2805, 2_A375_pNL97_plus_lncRNA::1::4038	-6008, -5992	upstream, upstream	1	1	26	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene PRR22	MGC24975, PRR22	proline rich 22	NM_001134316, hCT1646531.2	1552271_at, 1552272_a_at	NP_001127788.1, EAW69147.1
GeneID:56931	DUS3L	19	5,785,151	5,791,249	6,098	-	2	1_A375_pNL7_minus_lncRNA::1::2805, 2_A375_pNL97_plus_lncRNA::1::4038	465, 481	in gene, in gene	1	1	26	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene DUS3L	DUS3L, FLJ13896, DUS3	dihydrouridine synthase 3-like (S. cerevisiae)	NM_020175, NM_001161619, hCT201510.3, hCT2291292.0, hCT2291294.0, hCT2291295.0, hCT2291296.0, hCT2354633.0	224966_s_at, 230145_at	NP_064560.2, NP_001155091.1, EAW69141.1, EAW69142.1, EAW69143.1, EAW69144.1, EAW69145.1, EAW69146.1
GeneID:4902	NRTN	19	5,823,818	5,828,335	4,517	+	2	1_A375_pNL7_minus_lncRNA::1::2806, 2_A375_pNL97_plus_lncRNA::1::4039	4726, 4406	downstream, in gene	1	1	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene NRTN	NTN, NRTN	neurturin	NM_004558, hCT12876.2	210683_at	NP_004549.1, EAW69140.1
GeneID:2528	FUT6	19	5,830,637	5,839,742	9,105	-	2	1_A375_pNL7_minus_lncRNA::1::2806, 2_A375_pNL97_plus_lncRNA::1::4039	11198, 11518	downstream, downstream	1	1	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene FUT6	FLJ40754, Fuc-TVI, FT1A, FucT-VI, FUT6, FCT3A	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	NM_001040701, NM_000150	1565659_at, 1565660_at, 1565661_x_at, 210398_x_at, 210399_x_at, 211465_x_at, 211882_x_at, 211885_x_at	NP_001035791.1, NP_000141.1
GeneID:126328	NDUFA11	19	5,891,287	5,904,024	12,737	-	1	2_A375_pNL97_plus_lncRNA::1::4040	-10056	upstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene NDUFA11	B14.7, NDUFA11, FLJ76501	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	NM_175614, NM_001193375, NR_034166, hCT2291273.0, hCT2354635.0, hCT2354636.0	225304_s_at, 228689_at, 228690_s_at	NP_783313.1, NP_001180304.1, EAW69131.1, EAW69132.1, EAW69133.1
GeneID:400673	VMAC	19	5,904,852	5,910,263	5,411	+	1	2_A375_pNL97_plus_lncRNA::1::4040	9228	downstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene VMAC	MGC131656, VMAC	vimentin-type intermediate filament associated coiled-coil protein	NM_001017921, hCT1771270.2, hCT2340501.0		NP_001017921.1, EAW69130.1, EAW69129.1
GeneID:828	CAPS	19	5,914,193	5,916,222	2,029	+	1	2_A375_pNL97_plus_lncRNA::1::4040	-113	upstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CAPS	CAPS, CAPS1, MGC126562	calcyphosine	NM_004058, NM_080590, hCT14155.2, hCT1951849.2, hCT1951851.2, hCT2291699.0	226424_at, 231710_at, 231726_at, 231729_s_at	NP_004049.1, NP_542157.1, EAW69125.1, EAW69126.1, EAW69127.1, EAW69128.1
GeneID:8498	RANBP3	19	5,916,150	5,978,320	62,170	-	1	2_A375_pNL97_plus_lncRNA::1::4040	64240	downstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene RANBP3	DKFZp586I1520, RANBP3	RAN binding protein 3	NM_007322, NM_003624, NM_007320, hCT14152.2, hCT1771251.2, hCT2291255.0, hCT2291263.0, hCT2291268.0	202639_s_at, 202640_s_at, 208272_at, 210120_s_at	NP_015561.1, NP_003615.2, NP_015559.2, EAW69120.1, EAW69123.1, EAW69124.1, EAW69121.1, EAW69122.1
GeneID:5990	RFX2	19	5,993,175	6,110,664	117,489	-	1	1_A375_pNL7_minus_lncRNA::1::2807	22536	in gene	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RFX2	RFX2, FLJ14226	regulatory factor X, 2 (influences HLA class II expression)	NM_000635, NM_134433, hCT14159.3, hCT2291245.0, hCT2291247.0, hCT2291249.0, hCT2291250.0, hCT2291251.0	206031_s_at, 226872_at	NP_000626.2, NP_602309.1, EAW69112.1, EAW69113.1, EAW69114.1, EAW69117.1, EAW69115.1, EAW69116.1
GeneID:81616	ACSBG2	19	6,135,710	6,193,112	57,402	+	1	2_A375_pNL97_plus_lncRNA::1::4041	63778	downstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ACSBG2	BRGL, PRTD-NY3, MGC111089, ACSBG2, PRTDNY3, BGR, DKFZp434K1635	acyl-CoA synthetase bubblegum family member 2	NM_030924, hCT2291710.0	221716_s_at	NP_112186.3, EAW69111.1
GeneID:100507094	LOC100507094	19	6,189,739	6,199,540	9,801	-	1	2_A375_pNL97_plus_lncRNA::1::4041	52	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100507094		hypothetical LOC100507094	XR_111817, XR_109558, XR_115229		
GeneID:8570	KHSRP	19	6,413,115	6,424,822	11,707	-	1	2_A375_pNL97_plus_lncRNA::1::4042	-456	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene KHSRP	MGC99676, FBP2, KHSRP, KSRP, FUBP2	KH-type splicing regulatory protein	NM_003685, hCT14150.3, hCT2291220.0, hCT2291221.0	204371_s_at, 204372_s_at, 227555_s_at	NP_003676.2, EAW69097.1, EAW69095.1, EAW69096.1
GeneID:284427	SLC25A41	19	6,426,048	6,433,790	7,742	-	1	2_A375_pNL97_plus_lncRNA::1::4042	8510	downstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SLC25A41	MGC34725, FLJ40442, SLC25A41	solute carrier family 25, member 41	NM_173637, hCT1952861.2, hCT2291217.1, hCT2354627.0	1555509_a_at	NP_775908.2, EAW69094.1, EAW69092.1, EAW69093.1
GeneID:79085	SLC25A23	19	6,440,075	6,459,781	19,706	-	2	1_A375_pNL7_minus_lncRNA::1::2808, 2_A375_pNL97_plus_lncRNA::1::4043	-539, -699	upstream, upstream	1	1	25	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene SLC25A23	MGC2615, MCSC2, SCaMC-3, APC2, SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	NM_024103, hCT14161.3, hCT2291213.0, hCT2354647.0	220162_at, 226010_at	NP_077008.2, EAW69087.1, EAW69088.1, EAW69089.1
GeneID:92359	CRB3	19	6,464,260	6,467,232	2,972	+	2	1_A375_pNL7_minus_lncRNA::1::2808, 2_A375_pNL97_plus_lncRNA::1::4043	-3940, -3760	upstream, upstream	1	1	25	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene CRB3	CRB3		NM_139161, NM_174881	232609_at	NP_631900.1, NP_777377.1
GeneID:79958	DENND1C	19	6,467,218	6,481,798	14,580	-	2	1_A375_pNL7_minus_lncRNA::1::2808, 2_A375_pNL97_plus_lncRNA::1::4043	21478, 21318	downstream, downstream	1	1	25	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene DENND1C	FAM31C, DENND1C, FLJ22757	DENN/MADD domain containing 1C	NM_024898, hCT14168.3, hCT2291210.0, hCT2354596.0	221080_s_at	NP_079174.2, EAW69082.1, EAW69080.1, EAW69081.1
GeneID:10382	TUBB4	19	6,494,330	6,502,330	8,000	-	1	2_A375_pNL97_plus_lncRNA::1::4044	-2598	upstream	0	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene TUBB4	TUBB4, TUBB5, beta-5	tubulin, beta 4	NM_006087, hCT1641408.4, hCT2291204.0	212664_at	NP_006078.2, EAW69078.1, EAW69079.1
GeneID:100126300	MIR220B	19	6,495,959	6,496,045	86	+	1	2_A375_pNL97_plus_lncRNA::1::4044	8969	downstream	0	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MIR220B	MIRN220B, MIR220B	microRNA 220b	NR_030585		
GeneID:8744	TNFSF9	19	6,531,010	6,535,939	4,929	+	1	1_A375_pNL7_minus_lncRNA::1::2809	94	in gene	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TNFSF9	TNFSF9, CD137L, 4-1BB-L	tumor necrosis factor (ligand) superfamily, member 9	NM_003811, hCT12994.2, hCT2291637.0	206907_at	NP_003802.1, EAW69076.1, EAW69077.1
GeneID:970	CD70	19	6,585,850	6,591,163	5,313	-	1	1_A375_pNL7_minus_lncRNA::1::2811	123	in gene	1	0	19	10	1	1_A375_pNL7_minus_lncRNA::1	19	Gene CD70	CD27LG, CD70, TNFSF7, CD27L	CD70 molecule	NM_001252, hCT14146.3, hCT2291197.1	206508_at	NP_001243.1, EAW69074.1, EAW69075.1
GeneID:56927	GPR108	19	6,729,925	6,737,633	7,708	-	2	1_A375_pNL7_minus_lncRNA::1::2812, 2_A375_pNL97_plus_lncRNA::1::4046	257, 161	in gene, in gene	1	1	26	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene GPR108	LUSTR2, MGC14393, GPR108	G protein-coupled receptor 108	NM_001080452, NM_020171	225058_at	NP_001073921.1, NP_064556.1
GeneID:9322	TRIP10	19	6,739,707	6,751,529	11,822	+	2	1_A375_pNL7_minus_lncRNA::1::2812, 2_A375_pNL97_plus_lncRNA::1::4046	-2331, -2235	upstream, upstream	1	1	26	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene TRIP10	STP, TRIP10, STOT, HSTP, CIP4	thyroid hormone receptor interactor 10	NM_004240, hCT14160.3, hCT2289623.0, hCT2289625.0, hCT2354643.0, hCT2354644.0, hCT2354645.0	202734_at	NP_004231.1, EAW69065.1, EAW69060.1, EAW69061.1, EAW69062.1, EAW69064.1, EAW69063.1
GeneID:2015	EMR1	19	6,887,582	6,940,464	52,882	+	1	1_A375_pNL7_minus_lncRNA::1::2813	60354	downstream	1	0	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene EMR1	TM7LN3, EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	NM_001974, hCT12951.3, hCT2289628.0	207111_at	NP_001965.3, EAW69056.1, EAW69055.1
GeneID:3643	INSR	19	7,112,266	7,294,011	181,745	-	2	1_A375_pNL7_minus_lncRNA::1::2814, 2_A375_pNL97_plus_lncRNA::1::4047	96667, 96667	in gene, in gene	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene INSR	INSR, CD220, HHF5	insulin receptor	NM_000208, NM_001079817, hCT12886.3, hCT1951742.1, hCT2288727.0, hCT2288730.0, hCT2288732.0, hCT2354632.0	207851_s_at, 213792_s_at, 226212_s_at, 226216_at, 226450_at	NP_000199.2, NP_001073285.1, EAW69042.1, EAW69043.1, EAW69044.1, EAW69046.1, EAW69045.1, EAW69047.1
GeneID:374877	C19orf45	19	7,562,445	7,573,336	10,891	+	2	1_A375_pNL7_minus_lncRNA::1::2815, 2_A375_pNL97_plus_lncRNA::1::4048	12275, 12243	downstream, downstream	1	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene C19orf45	FLJ56642, C19orf45, FLJ35784	chromosome 19 open reading frame 45	NM_198534	241842_x_at, 241862_x_at	NP_940936.2
GeneID:140467	ZNF358	19	7,581,004	7,585,911	4,907	+	4	1_A375_pNL7_minus_lncRNA::1::2815, 1_A375_pNL7_minus_lncRNA::1::2816, 2_A375_pNL97_plus_lncRNA::1::4048, 2_A375_pNL97_plus_lncRNA::1::4049	-6284, 6356, -6316, 6356	upstream, downstream, upstream, downstream	1	1	26.5	33.5	2	2_A375_pNL97_plus_lncRNA::1	40	Gene ZNF358	FLJ10390, ZFEND, ZNF358	zinc finger protein 358	NM_018083	219379_x_at, 226260_x_at	NP_060553.4
GeneID:57192	MCOLN1	19	7,587,496	7,598,895	11,399	+	6	1_A375_pNL7_minus_lncRNA::1::2816, 1_A375_pNL7_minus_lncRNA::1::2817, 1_A375_pNL7_minus_lncRNA::1::2818, 2_A375_pNL97_plus_lncRNA::1::4049, 2_A375_pNL97_plus_lncRNA::1::4050, 2_A375_pNL97_plus_lncRNA::1::4051	-136, 11512, 13144, -136, 11480, 13112	upstream, downstream, downstream, upstream, downstream, downstream	1	1	29	34	3	2_A375_pNL97_plus_lncRNA::1	40	Gene MCOLN1	MSTP080, MST080, TRPM-L1, TRPML1, MCOLN1, TRP-ML1, ML4, MLIV	mucolipin 1	NM_020533, hCT13347.3, hCT1952321.1, hCT2289642.0, hCT2354642.0	219952_s_at	NP_065394.1, EAW69032.1, EAW69031.1, EAW69033.1, EAW69034.1
GeneID:10908	PNPLA6	19	7,599,038	7,626,653	27,615	+	6	1_A375_pNL7_minus_lncRNA::1::2817, 1_A375_pNL7_minus_lncRNA::1::2818, 1_A375_pNL7_minus_lncRNA::1::2819, 2_A375_pNL97_plus_lncRNA::1::4050, 2_A375_pNL97_plus_lncRNA::1::4051, 2_A375_pNL97_plus_lncRNA::1::4052	-30, 1602, 28898, -62, 1570, 28866	upstream, in gene, downstream, upstream, in gene, downstream	1	1	24.33	32.67	3	2_A375_pNL97_plus_lncRNA::1	36	Gene PNPLA6	PNPLA6, SPG39, NTEMND, sws, NTE	patatin-like phospholipase domain containing 6	NM_006702, NM_001166111, NM_001166112, NM_001166113, NM_001166114, hCT12887.3, hCT2289645.0	203718_at	NP_006693.3, NP_001159583.1, NP_001159584.1, NP_001159585.1, NP_001159586.1, EAW69029.1, EAW69030.1
GeneID:115704	EVI5L	19	7,895,161	7,929,862	34,701	+	2	1_A375_pNL7_minus_lncRNA::1::2820, 2_A375_pNL97_plus_lncRNA::1::4053	-249, -249	upstream, upstream	1	1	23	18	1	1_A375_pNL7_minus_lncRNA::1	23	Gene EVI5L	EVI5L		NM_145245, NM_001159944, hCT13657.3, hCT2290654.0, hCT2290655.0	226411_at, 242534_at, 244500_s_at, 244501_at	NP_660288.1, NP_001153416.1, EAW68973.1, EAW68974.1, EAW68975.1
GeneID:80131	LRRC8E	19	7,953,390	7,966,908	13,518	+	1	2_A375_pNL97_plus_lncRNA::1::4054	15250	downstream	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LRRC8E	FLJ23420, LRRC8E	leucine rich repeat containing 8 family, member E	NM_025061, hCT1646986.3	220174_at, 239433_at	NP_079337.2, EAW68969.1
GeneID:5609	MAP2K7	19	7,968,765	7,979,363	10,598	+	1	2_A375_pNL97_plus_lncRNA::1::4054	-125	upstream	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MAP2K7	MAP2K7, MKK7, PRKMK7, Jnkk2, MAPKK7	mitogen-activated protein kinase kinase 7	NM_145185, hCT13651.3, hCT1951272.1, hCT2290659.0, hCT2290660.0, hCT2290661.0, hCT2290663.0, hCT2354608.0	209951_s_at, 209952_s_at, 216206_x_at, 226023_at, 226053_at	NP_660186.1, EAW68968.1, EAW68963.1, EAW68964.1, EAW68965.1, EAW68967.1, EAW68962.1, EAW68966.1
GeneID:51293	CD320	19	8,367,011	8,373,240	6,229	-	2	1_A375_pNL7_minus_lncRNA::1::2821, 2_A375_pNL97_plus_lncRNA::1::4055	-232, -104	upstream, upstream	1	1	26	23	1	1_A375_pNL7_minus_lncRNA::1	26	Gene CD320	8D6, TCBLR, CD320, 8D6A	CD320 molecule	NM_016579, NM_001165895	218529_at	NP_057663.1, NP_001159367.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:4701	NDUFA7	19	8,376,234	8,386,280	10,046	-	3	1_A375_pNL7_minus_lncRNA::1::2821, 2_A375_pNL97_plus_lncRNA::1::4055, 2_A375_pNL97_plus_lncRNA::1::4056	12808, 12936, 104	downstream, downstream, in gene	1	1	20	21.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene NDUFA7	B14.5a, NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	NM_005001	1557532_at, 202785_at	NP_004992.2
GeneID:6234	RPS28	19	8,386,384	8,387,280	896	+	1	2_A375_pNL97_plus_lncRNA::1::4056	-208	upstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RPS28	RPS28, S28	ribosomal protein S28	NM_001031, hCT15075.3, hCT2290680.0	208903_at	NP_001022.1, EAW68933.1, EAW68934.1
GeneID:256949	KANK3	19	8,387,468	8,408,146	20,678	-	1	2_A375_pNL97_plus_lncRNA::1::4056	21970	downstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene KANK3	KANK3, ANKRD47, FLJ46061	KN motif and ankyrin repeat domains 3	NM_198471, hCT15079.3	213715_s_at	NP_940873.2, EAW68932.1
GeneID:51129	ANGPTL4	19	8,429,011	8,439,257	10,246	+	1	2_A375_pNL97_plus_lncRNA::1::4057	365	in gene	0	1	14	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ANGPTL4	NL2, ANGPTL4, FIAF, HFARP, ANGPTL2, ARP4, PGAR, pp1158	angiopoietin-like 4	NM_139314, NM_001039667, hCT15072.2, hCT2354640.0	221009_s_at, 223333_s_at	NP_647475.1, NP_001034756.1, EAW68930.1, EAW68931.1
GeneID:100507567	LOC100507567	19	8,439,260	8,455,569	16,309	-	1	2_A375_pNL97_plus_lncRNA::1::4057	26193	downstream	0	1	14	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100507567		hypothetical LOC100507567	XR_110600		
GeneID:284383	OR2Z1	19	8,841,391	8,842,335	944	+	1	2_A375_pNL97_plus_lncRNA::1::4058	561	in gene	0	1	10	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene OR2Z1	OR2Z2, OR19-4, OR2Z1	olfactory receptor, family 2, subfamily Z, member 1	NM_001004699, hCT1643180.3		NP_001004699.1, EAW68902.1
GeneID:146156	ZNF558	19	8,920,382	8,933,565	13,183	-	2	1_A375_pNL7_minus_lncRNA::1::2822, 2_A375_pNL97_plus_lncRNA::1::4059	-9315, -9347	upstream, upstream	1	1	18	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene ZNF558	FLJ30932, ZNF558	zinc finger protein 558	NM_144693, hCT2284714.0, hCT2284715.0	227810_at	NP_653294.1, EAW63995.1, EAW63994.1
GeneID:85509	MBD3L1	19	8,953,269	8,954,016	747	+	2	1_A375_pNL7_minus_lncRNA::1::2822, 2_A375_pNL97_plus_lncRNA::1::4059	-10389, -10357	upstream, upstream	1	1	18	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene MBD3L1	MBD3L, MBD3L1, MGC138269, MGC138263	methyl-CpG binding domain protein 3-like 1	NM_145208, hCT1645911.3	1552458_at, 1552459_a_at	NP_660209.2, EAW63996.1
GeneID:94025	MUC16	19	8,959,520	9,092,018	132,498	-	1	1_A375_pNL7_minus_lncRNA::1::2823	7666	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene MUC16	FLJ14303, CA125, MUC16	mucin 16, cell surface associated	NM_024690	220196_at	NP_078966.2
GeneID:57693	ZNF317	19	9,251,056	9,274,091	23,035	+	1	2_A375_pNL97_plus_lncRNA::1::4061	-48	upstream	0	1	8	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ZNF317	KIAA1588, ZNF317	zinc finger protein 317	NM_001190791, NM_020933, hCT2283497.0, hCT2283499.0, hCT23306.3, hCT2356479.0, hCT2356480.0, hCT2356481.0	1555337_a_at, 225296_at	NP_001177720.1, NP_065984.3, EAW84010.1, EAW84011.1, EAW84012.1, EAW84014.1, EAW84013.1, EAW84015.1
GeneID:374879	ZNF699	19	9,405,986	9,415,795	9,809	-	1	2_A375_pNL97_plus_lncRNA::1::4062	-4717	upstream	0	1	6	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ZNF699	MGC129880, hang, FLJ38144, ZNF699, MGC129881	zinc finger protein 699	NM_198535		NP_940937.1
GeneID:10781	ZNF266	19	9,523,271	9,546,234	22,963	-	2	1_A375_pNL7_minus_lncRNA::1::2825, 1_A375_pNL7_minus_lncRNA::1::2826	28442, 90	downstream, in gene	1	0	15	10	2	1_A375_pNL7_minus_lncRNA::1	15	Gene ZNF266	HZF1, ZNF266	zinc finger protein 266	NM_198058, NM_006631, hCT23309.2, hCT2356529.0, hCT2356530.0, hCT2356531.0	214686_at	NP_932175.1, NP_006622.2, EAW84033.1, EAW84034.1, EAW84035.1, EAW84036.1
GeneID:54811	ZNF562	19	9,759,330	9,785,776	26,446	-	2	1_A375_pNL7_minus_lncRNA::1::2827, 2_A375_pNL97_plus_lncRNA::1::4063	-16, 144	upstream, in gene	1	1	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene ZNF562	FLJ20079, ZNF562, MGC126160	zinc finger protein 562	NM_001130031, NM_001130032, NM_017656, hCT1963269.3, hCT201474.5, hCT2351841.0, hCT2356526.0	219163_at	NP_001123503.1, NP_001123504.1, NP_060126.2, EAW84044.1, EAW84045.1, EAW84047.1, EAW84046.1
GeneID:162993	ZNF846	19	9,868,151	9,879,410	11,259	-	2	1_A375_pNL7_minus_lncRNA::1::2828, 2_A375_pNL97_plus_lncRNA::1::4064	-78, -46	upstream, upstream	1	1	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ZNF846	ZNF846	zinc finger protein 846	NM_001077624	1564331_at, 1569156_at, 1569157_s_at	NP_001071092.1
GeneID:54850	FBXL12	19	9,920,943	9,929,731	8,788	-	2	1_A375_pNL7_minus_lncRNA::1::2829, 2_A375_pNL97_plus_lncRNA::1::4065	355, 291	in gene, in gene	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene FBXL12	Fbl12, FBXL12, FLJ20188	F-box and leucine-rich repeat protein 12	NM_017703, hCT1968999.1, hCT2356493.0, hCT2356494.0	220127_s_at, 237256_at	NP_060173.1, EAW84053.1, EAW84051.1, EAW84052.1
GeneID:59286	UBL5	19	9,938,568	9,940,797	2,229	+	2	1_A375_pNL7_minus_lncRNA::1::2829, 2_A375_pNL97_plus_lncRNA::1::4065	-9192, -9128	upstream, upstream	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene UBL5	FLJ46917, UBL5, MGC131795, HUB1	ubiquitin-like 5	NM_024292, NM_001048241, hCT2336715.0, hCT2336716.0, hCT2356597.0	218011_at	NP_077268.1, NP_001041706.1, EAW84054.1, EAW84055.1, EAW84056.1
GeneID:93145	OLFM2	19	9,964,394	10,047,070	82,676	-	2	1_A375_pNL7_minus_lncRNA::1::2830, 2_A375_pNL97_plus_lncRNA::1::4066	-2957, -3074	upstream, upstream	1	1	16	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene OLFM2	OLFM2, NOELIN2, NOELIN2_V1, OlfC, NOE2	olfactomedin 2	NM_058164, hCT19649.2	223601_at	NP_477512.1, EAW84060.1
GeneID:56342	PPAN	19	10,216,965	10,221,975	5,010	+	3	1_A375_pNL7_minus_lncRNA::1::2832, 2_A375_pNL97_plus_lncRNA::1::4068, 2_A375_pNL97_plus_lncRNA::1::4069	8283, 7851, 13563	downstream, downstream, downstream	1	1	19	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene PPAN	MGC14226, SSF, BXDC3, SSF-1, PPAN, SSF1, MGC45852, SSF2	peter pan homolog (Drosophila)	NM_020230	221649_s_at	NP_064615.3
GeneID:692312	PPAN-P2RY11	19	10,217,071	10,225,414	8,343	+	3	1_A375_pNL7_minus_lncRNA::1::2832, 2_A375_pNL97_plus_lncRNA::1::4068, 2_A375_pNL97_plus_lncRNA::1::4069	8177, 7745, 13457	in gene, in gene, downstream	1	1	19	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene PPAN-P2RY11	PPAN-P2RY11		NM_001040664		NP_001035754.1
GeneID:692229	SNORD105	19	10,218,327	10,218,411	84	+	2	1_A375_pNL7_minus_lncRNA::1::2832, 2_A375_pNL97_plus_lncRNA::1::4068	6921, 6489	downstream, downstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SNORD105	SNORD105, U105	small nucleolar RNA, C/D box 105	NR_004381		
GeneID:100113382	SNORD105B	19	10,220,425	10,220,516	91	+	3	1_A375_pNL7_minus_lncRNA::1::2832, 2_A375_pNL97_plus_lncRNA::1::4068, 2_A375_pNL97_plus_lncRNA::1::4069	4823, 4391, 10103	downstream, downstream, downstream	1	1	19	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene SNORD105B	SNORD105B	small nucleolar RNA, C/D box 105B	NR_003688		
GeneID:5032	P2RY11	19	10,222,197	10,226,065	3,868	+	3	1_A375_pNL7_minus_lncRNA::1::2832, 2_A375_pNL97_plus_lncRNA::1::4068, 2_A375_pNL97_plus_lncRNA::1::4069	3051, 2619, 8331	in gene, in gene, downstream	1	1	19	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene P2RY11	P2Y11, P2RY11	purinergic receptor P2Y, G-protein coupled, 11	NM_002566, hCT2336730.0	214546_s_at	NP_002557.2, EAW84077.1
GeneID:8666	EIF3G	19	10,225,690	10,230,599	4,909	-	3	1_A375_pNL7_minus_lncRNA::1::2832, 2_A375_pNL97_plus_lncRNA::1::4068, 2_A375_pNL97_plus_lncRNA::1::4069	5351, 5783, 71	downstream, downstream, in gene	1	1	19	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene EIF3G	EIF3G, eIF3-p44, eIF3-delta, EIF3-P42, EIF3S4	eukaryotic translation initiation factor 3, subunit G	NM_003755, hCT19626.3	208887_at	NP_003746.2, EAW84076.1
GeneID:1786	DNMT1	19	10,244,022	10,305,755	61,733	-	1	2_A375_pNL97_plus_lncRNA::1::4070	-5	upstream	0	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene DNMT1	DNMT1, FLJ16293, DNMT, CXXC9, MGC104992, MCMT, AIM	DNA (cytosine-5-)-methyltransferase 1	NM_001379, NM_001130823, hCT19625.2, hCT1967930.1	201697_s_at	NP_001370.1, NP_001124295.1, EAW84079.1, EAW84080.1
GeneID:9294	S1PR2	19	10,332,109	10,341,948	9,839	-	3	1_A375_pNL7_minus_lncRNA::1::2833, 2_A375_pNL97_plus_lncRNA::1::4071, 2_A375_pNL97_plus_lncRNA::1::4072	826, 3604, 668	in gene, in gene, in gene	1	1	18.5	23	2	1_A375_pNL7_minus_lncRNA::1	26	Gene S1PR2	S1PR2, EDG5, S1P2, H218, EDG-5, AGR16, LPB2, Gpcr13	sphingosine-1-phosphate receptor 2	NM_004230, hCT19628.2, hCT2336794.0	208537_at	NP_004221.3, EAW84081.1, EAW84082.1
GeneID:100422925	MIR4322	19	10,341,089	10,341,161	72	+	3	1_A375_pNL7_minus_lncRNA::1::2833, 2_A375_pNL97_plus_lncRNA::1::4071, 2_A375_pNL97_plus_lncRNA::1::4072	31, -2945, 191	in gene, upstream, downstream	1	1	18.5	23	2	1_A375_pNL7_minus_lncRNA::1	26	Gene MIR4322	MIR4322	microRNA 4322	NR_036206		
GeneID:51073	MRPL4	19	10,362,640	10,370,736	8,096	+	2	2_A375_pNL97_plus_lncRNA::1::4073, 2_A375_pNL97_plus_lncRNA::1::4074	208, 18432	in gene, downstream	0	1	13	21	2	2_A375_pNL97_plus_lncRNA::1	25	Gene MRPL4	MGC2681, MGC16367, MRPL4, L4mt, CGI-28	mitochondrial ribosomal protein L4	NM_015956, NM_146387, NM_146388, hCT19630.2, hCT1967931.1, hCT2356560.0	218105_s_at, 223742_at, 223743_s_at	NP_057040.2, NP_666499.1, NP_666500.1, EAW84083.1, EAW84084.1, EAW84085.1
GeneID:3383	ICAM1	19	10,381,517	10,397,291	15,774	+	2	2_A375_pNL97_plus_lncRNA::1::4074, 2_A375_pNL97_plus_lncRNA::1::4075	-445, 20371	upstream, downstream	0	1	17.5	22	2	2_A375_pNL97_plus_lncRNA::1	27	Gene ICAM1	P3.58, CD54, ICAM1, BB2	intercellular adhesion molecule 1	NM_000201, hCT19627.1, hCT2336738.0	202637_s_at, 202638_s_at, 215485_s_at	NP_000192.2, EAW84086.1, EAW84087.1
GeneID:3386	ICAM4	19	10,397,650	10,399,198	1,548	+	1	2_A375_pNL97_plus_lncRNA::1::4075	4236	downstream	0	1	21	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene ICAM4	CD242, ICAM4, LW	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	NM_001544, NM_022377, NM_001039132, hCT19631.2, hCT1967932.1, hCT2336741.0	207194_s_at	NP_001535.1, NP_071772.1, NP_001034221.1, EAW84088.1, EAW84089.1, EAW84090.1
GeneID:7087	ICAM5	19	10,400,655	10,407,454	6,799	+	1	2_A375_pNL97_plus_lncRNA::1::4075	1233	in gene	0	1	21	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene ICAM5	ICAM5, TLCN, TLN	intercellular adhesion molecule 5, telencephalin	NM_003259, hCT19632.2	206906_at	NP_003250.3, EAW84091.1
GeneID:125950	RAVER1	19	10,426,888	10,444,314	17,426	-	2	1_A375_pNL7_minus_lncRNA::1::2834, 2_A375_pNL97_plus_lncRNA::1::4076	698, 618	in gene, in gene	1	1	20	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene RAVER1	RAVER1, KIAA1978	ribonucleoprotein, PTB-binding 1	NM_133452	223425_at	NP_597709.2
GeneID:3385	ICAM3	19	10,444,452	10,450,345	5,893	-	2	1_A375_pNL7_minus_lncRNA::1::2834, 2_A375_pNL97_plus_lncRNA::1::4076	6729, 6649	downstream, downstream	1	1	20	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene ICAM3	ICAM3, CD50, ICAM-R, CDW50	intercellular adhesion molecule 3	NM_002162	204949_at	NP_002153.2
GeneID:7297	TYK2	19	10,461,204	10,491,248	30,044	-	1	2_A375_pNL97_plus_lncRNA::1::4077	-320	upstream	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TYK2	JTK1, TYK2	tyrosine kinase 2	NM_003331, hCT1959865.1, hCT19648.3	205546_s_at	NP_003322.3, EAW84099.1, EAW84100.1
GeneID:11140	CDC37	19	10,501,809	10,514,271	12,462	-	3	1_A375_pNL7_minus_lncRNA::1::2835, 2_A375_pNL97_plus_lncRNA::1::4077, 2_A375_pNL97_plus_lncRNA::1::4078	63, 22703, -17	in gene, downstream, upstream	1	1	21	24.5	2	2_A375_pNL97_plus_lncRNA::1	30	Gene CDC37	CDC37, P50CDC37	cell division cycle 37 homolog (S. cerevisiae)	NM_007065, hCT19629.3, hCT2336829.0, hCT2336831.0	209953_s_at	NP_008996.1, EAW84103.1, EAW84101.1, EAW84102.1
GeneID:100302213	MIR1181	19	10,514,134	10,514,214	80	-	2	1_A375_pNL7_minus_lncRNA::1::2835, 2_A375_pNL97_plus_lncRNA::1::4078	6, -74	in gene, upstream	1	1	26	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene MIR1181	hsa-mir-1181, MIR1181, MIRN1181	microRNA 1181	NR_031592		
GeneID:5141	PDE4A	19	10,531,333	10,580,307	48,974	+	4	1_A375_pNL7_minus_lncRNA::1::2836, 1_A375_pNL7_minus_lncRNA::1::2837, 2_A375_pNL97_plus_lncRNA::1::4079, 2_A375_pNL97_plus_lncRNA::1::4080	-3813, -549, -3877, -485	upstream, upstream, upstream, upstream	1	1	25.5	33.5	2	2_A375_pNL97_plus_lncRNA::1	38	Gene PDE4A	DPDE2, PDE4A, PDE4, PDE46	phosphodiesterase 4A, cAMP-specific	NM_006202, NM_001111307, NM_001111308, NM_001111309, hCT1686450.3, hCT19653.3, hCT2336748.0, hCT2336751.0, hCT2336753.0, hCT2336754.0	204735_at, 211447_s_at, 211591_s_at, 211901_s_at, 242435_at	NP_006193.1, NP_001104777.1, NP_001104778.1, NP_001104779.1, EAW84104.1, EAW84106.1, EAW84105.1, EAW84107.1, EAW84108.1, EAW84109.1
GeneID:9817	KEAP1	19	10,596,796	10,614,054	17,258	-	2	1_A375_pNL7_minus_lncRNA::1::2838, 2_A375_pNL97_plus_lncRNA::1::4081	566, 518	in gene, in gene	1	1	24	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene KEAP1	MGC4407, MGC10630, KIAA0132, MGC9454, INrf2, MGC20887, KEAP1, MGC1114, KLHL19	kelch-like ECH-associated protein 1	NM_012289, NM_203500, hCT19635.2, hCT1963738.0, hCT1963739.1	202417_at	NP_036421.2, NP_987096.1, EAW84110.1, EAW84111.1, EAW84112.1
GeneID:53637	S1PR5	19	10,623,418	10,628,668	5,250	-	2	1_A375_pNL7_minus_lncRNA::1::2838, 2_A375_pNL97_plus_lncRNA::1::4081	15180, 15132	downstream, downstream	1	1	24	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene S1PR5	EDG8, S1P5, S1PR5, Edg-8, SPPR-2, SPPR-1	sphingosine-1-phosphate receptor 5	NM_030760, NM_001166215, hCT1644280.2, hCT1963718.1, hCT2336821.0	221417_x_at, 230464_at, 233743_x_at	NP_110387.1, NP_001159687.1, EAW84113.1, EAW84114.1, EAW84115.1
GeneID:65095	KRI1	19	10,663,761	10,676,702	12,941	-	3	1_A375_pNL7_minus_lncRNA::1::2839, 2_A375_pNL97_plus_lncRNA::1::4082, 2_A375_pNL97_plus_lncRNA::1::4083	-3170, 206, -3202	upstream, in gene, upstream	1	1	26	25	2	1_A375_pNL7_minus_lncRNA::1	32	Gene KRI1	FLJ12949, KRI1	KRI1 homolog (S. cerevisiae)	NM_023008, hCT19651.3, hCT1967934.1	218798_at, 227587_at	NP_075384.3, EAW84121.1, EAW84120.1
GeneID:1032	CDKN2D	19	10,677,138	10,679,655	2,517	-	3	1_A375_pNL7_minus_lncRNA::1::2839, 2_A375_pNL97_plus_lncRNA::1::4082, 2_A375_pNL97_plus_lncRNA::1::4083	-217, 3159, -249	upstream, downstream, upstream	1	1	26	25	2	1_A375_pNL7_minus_lncRNA::1	32	Gene CDKN2D	CDKN2D, p19, INK4D, p19-INK4D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	NM_079421, NM_001800, hCT19634.3, hCT2336814.0	210240_s_at, 213586_at	NP_524145.1, NP_001791.1, EAW84122.1, EAW84123.1
GeneID:10053	AP1M2	19	10,683,347	10,697,991	14,644	-	3	1_A375_pNL7_minus_lncRNA::1::2839, 2_A375_pNL97_plus_lncRNA::1::4082, 2_A375_pNL97_plus_lncRNA::1::4083	18119, 21495, 18087	downstream, downstream, downstream	1	1	26	25	2	1_A375_pNL7_minus_lncRNA::1	32	Gene AP1M2	AP1M2, MU-1B, HSMU1B, MU1B, mu2, AP1-mu2	adaptor-related protein complex 1, mu 2 subunit	NM_005498, hCT19636.3, hCT2356602.0	218261_at, 65517_at	NP_005489.2, EAW84124.1, EAW84125.1
GeneID:57153	SLC44A2	19	10,713,121	10,755,235	42,114	+	3	1_A375_pNL7_minus_lncRNA::1::2840, 1_A375_pNL7_minus_lncRNA::1::2841, 2_A375_pNL97_plus_lncRNA::1::4084	191, 51583, 51711	in gene, downstream, downstream	1	1	31.5	24	2	1_A375_pNL7_minus_lncRNA::1	44	Gene SLC44A2	FLJ44586, SLC44A2, CTL2, DKFZp666A071, PP1292	solute carrier family 44, member 2	NM_001145056, NM_020428, hCT1959884.1, hCT19647.3, hCT2336761.0, hCT2336762.0	224609_at, 225175_s_at	NP_001138528.1, NP_065161.3, EAW84126.1, EAW84127.1, EAW84128.1, EAW84129.1
GeneID:147727	LOC147727	19	10,762,538	10,764,548	2,010	-	2	1_A375_pNL7_minus_lncRNA::1::2841, 2_A375_pNL97_plus_lncRNA::1::4084	-156, -284	upstream, upstream	1	1	44	36	1	1_A375_pNL7_minus_lncRNA::1	44	Gene LOC147727		hypothetical LOC147727	NR_024333		
GeneID:3609	ILF3	19	10,764,937	10,803,093	38,156	+	6	1_A375_pNL7_minus_lncRNA::1::2841, 1_A375_pNL7_minus_lncRNA::1::2842, 1_A375_pNL7_minus_lncRNA::1::2843, 2_A375_pNL97_plus_lncRNA::1::4084, 2_A375_pNL97_plus_lncRNA::1::4085, 2_A375_pNL97_plus_lncRNA::1::4086	-233, 41527, 47143, -105, 41607, 47415	upstream, downstream, downstream, upstream, downstream, downstream	1	1	29.33	26.33	3	1_A375_pNL7_minus_lncRNA::1	44	Gene ILF3	DRBP76, NFAR2, NFAR-1, NF110, ILF3, NF90, NF-AT-90, TCP80, CBTF, TCP110, MPP4, MMP4, MPHOSPH4, DRBF, NFAR	interleukin enhancer binding factor 3, 90kDa	NM_012218, NM_004516, NM_153464, NM_017620, NM_001137673, hCT2336765.0, hCT2336766.0, hCT2336768.0, hCT2336769.0, hCT2336770.0, hCT2336771.0, hCT2336772.0	208930_s_at, 208931_s_at, 211375_s_at, 217804_s_at, 217805_at	NP_036350.2, NP_004507.2, NP_703194.1, NP_060090.2, NP_001131145.1, EAW84133.1, EAW84131.1, EAW84132.1, EAW84134.1, EAW84135.1, EAW84136.1, EAW84137.1
GeneID:81890	QTRT1	19	10,812,112	10,824,043	11,931	+	5	1_A375_pNL7_minus_lncRNA::1::2842, 1_A375_pNL7_minus_lncRNA::1::2843, 2_A375_pNL97_plus_lncRNA::1::4085, 2_A375_pNL97_plus_lncRNA::1::4086, 2_A375_pNL97_plus_lncRNA::1::4087	-5648, -32, -5568, 240, 16384	upstream, upstream, upstream, in gene, downstream	1	1	23	24.33	3	2_A375_pNL97_plus_lncRNA::1	30	Gene QTRT1	QTRT1, FP3235, TGT	queuine tRNA-ribosyltransferase 1	NM_031209, hCT2336773.0, hCT2356582.0, hCT2356583.0, hCT2356584.0, hCT2356585.0, hCT2356586.0	221270_s_at	NP_112486.1, EAW84138.1, EAW84139.1, EAW84141.1, EAW84142.1, EAW84143.1, EAW84140.1
GeneID:1785	DNM2	19	10,828,729	10,942,586	113,857	+	5	1_A375_pNL7_minus_lncRNA::1::2844, 1_A375_pNL7_minus_lncRNA::1::2845, 2_A375_pNL97_plus_lncRNA::1::4087, 2_A375_pNL97_plus_lncRNA::1::4088, 2_A375_pNL97_plus_lncRNA::1::4089	91239, 118311, -233, 90951, 118087	in gene, downstream, upstream, in gene, downstream	1	1	24.67	28	3	2_A375_pNL97_plus_lncRNA::1	31	Gene DNM2	CMT2M, CMTDI1, CMTDIB, DYNII, DYN2, DNM2, DI-CMTB	dynamin 2	NM_001005360, NM_001005361, NM_001005362, NM_001190716, NM_004945, hCT2336774.0, hCT2336775.0, hCT2336776.0, hCT2336777.0, hCT2336778.0, hCT2336779.0, hCT2336780.0, hCT2356588.0	1555895_at, 202253_s_at, 216024_at	NP_001005360.1, NP_001005361.1, NP_004936.2, NP_001005362.1, NP_001177645.1, EAW84144.1, EAW84145.1, EAW84146.1, EAW84147.1, EAW84148.1, EAW84149.1, EAW84150.1, EAW84151.1
GeneID:693223	MIR638	19	10,829,080	10,829,179	99	+	1	2_A375_pNL97_plus_lncRNA::1::4087	-584	upstream	0	1	25	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene MIR638	MIR638, MIRN638, hsa-mir-638	microRNA 638	NR_030368		
GeneID:100507081	LOC100507081	19	10,921,015	10,922,472	1,457	+	2	1_A375_pNL7_minus_lncRNA::1::2844, 2_A375_pNL97_plus_lncRNA::1::4088	-1047, -1335	upstream, upstream	1	1	23	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100507081		hypothetical LOC100507081	XR_111833, XR_109560, XR_115261		
GeneID:406976	MIR199A1	19	10,928,102	10,928,172	70	-	2	1_A375_pNL7_minus_lncRNA::1::2844, 2_A375_pNL97_plus_lncRNA::1::4088	8204, 8492	downstream, downstream	1	1	23	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene MIR199A1	MIR199A1, MIRN199A1, MIR-199-s	microRNA 199a-1	NR_029586		
GeneID:11018	TMED1	19	10,943,114	10,946,983	3,869	-	2	1_A375_pNL7_minus_lncRNA::1::2845, 2_A375_pNL97_plus_lncRNA::1::4089	-57, 167	upstream, in gene	1	1	26	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene TMED1	Il1rl1l, IL1RL1LG, TMED1, MGC1270, ST2L	transmembrane emp24 protein transport domain containing 1	NM_006858, hCT17835.2	203679_at	NP_006849.1, EAW84152.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Count	Internal Intervals	Internal Gaps to Next	Internal Pos.	[A]	[R]	[C]	[G]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:3346	RTBDN	19	12,939,298	12,949,230	9,934	+	3	1_A27S_shL7_dhrus_isoRNA:1:2870,2_A27S_shL27_dhrs_isoRNA:1:4123,2_A27S_shL27_dhrs_isoRNA:1:4134	2870, 2756, -1066	vs gene, vs gene, upstream	33	48.5	2	2_A27S_shL27_dhrs_isoRNA:1	63	Gene:RTBDN	FLJ38353, RTBDN	rdhbdnd	NM_031429, NM_001080997, XM_017300311, XM_017306579.0, XM_017306580.0	NM_031429.1, NM_001080997.1, XM_017300311.1, XM_017306579.1, XM_017306580.1	ENM63414.1, ENM63415.1, ENM63416.1	223719_s_at	NP_113617.1, NP_001074469.1, ENP63414.1, ENP63415.1, ENP63416.1
Gene:ID:100507305	LOC100507305	19	12,939,523	12,943,840	7,418	+	2	1_A27S_shL7_dhrus_isoRNA:1:2870,2_A27S_shL27_dhrs_isoRNA:1:4123,2_A27S_shL27_dhrs_isoRNA:1:4134	6835, 6987, 10771	vs gene, vs gene, downstream	33	48.5	2	2_A27S_shL27_dhrs_isoRNA:1	63	Gene:LOC100507305		hypothetical LOC100507305	XR_111626, XR_111625, XR_109566, XR_109567, XR_115239, XR_115235	XR_111626.1, XR_111625.1, XR_109566.1, XR_109567.1, XR_115239.1, XR_115235.1		
Gene:ID:2953	MAST1	19	12,949,259	12,983,766	36,507	+	5	1_A27S_shL7_dhrus_isoRNA:1:2870,2_A27S_shL7_dhrus_isoRNA:1:2871,2_A27S_shL27_dhrs_isoRNA:1:4123,2_A27S_shL27_dhrs_isoRNA:1:4124,2_A27S_shL27_dhrs_isoRNA:1:4125	6899, 8301, -5707, -1863, 42633	upstream, vs gene, upstream, upstream, downstream	33.3	33.78	4	2_A27S_shL27_dhrs_isoRNA:1	63	Gene:MAST1	KIAA0972, SAST170, SAST, MAST1	microtubule associated serine/threonine kinase 1	NM_014975, XM_017130013.3, XM_017182653.1, XM_017264851.0	NM_014975.1, XM_017130013.1, XM_017182653.1, XM_017264851.0	ENM64317.1, ENM64318.1, ENM64319.1	217231_s_at	NP_055740.1, ENP64317.1, ENP64318.1, ENP64319.1
Gene:ID:1777	DNASE2	19	12,966,023	12,992,335	6,310	-	3	1_A27S_shL7_dhrus_isoRNA:1:2872,2_A27S_shL27_dhrs_isoRNA:1:4126,2_A27S_shL27_dhrs_isoRNA:1:4128	4521, 163, 4484	upstream, vs gene, upstream	46.5	51.5	2	1_A27S_shL7_dhrus_isoRNA:1	63	Gene:DNASE2	DNL2, DNL, DNASE2, DNASE2A	deoxyribonuclease II, lysosomal	NM_001370, XM_017123653.2, XM_017269110.0, XM_017269522.0	NM_001370.1, XM_017123653.1, XM_017269110.1, XM_017269522.1	ENM64320.1, ENM64321.1, ENM64322.1	208631_s_at, 214662_s_at	NP_001360.1, ENP64320.1, ENP64321.1, ENP64322.1
Gene:ID:9981	KLF1	19	12,995,236	12,999,017	3,781	-	3	1_A27S_shL7_dhrus_isoRNA:1:2872,2_A27S_shL27_dhrs_isoRNA:1:4128,2_A27S_shL27_dhrs_isoRNA:1:4129	-2639, 3625, -1807	upstream, downstream, upstream	46.5	51.5	2	1_A27S_shL7_dhrus_isoRNA:1	63	Gene:KLF1	INLU, HBPGTL6, KLF1, EKLF	Kruppel-like factor 1 (erythroid)	NM_006563, XM_017122922.1	NM_006563.4, XM_017122922.1	ENM64322.1	210504_at	NP_006554.1, ENP64322.1
Gene:ID:639	GCDH	19	13,001,974	13,010,763	8,808	+	3	1_A27S_shL7_dhrus_isoRNA:1:2872,2_A27S_shL27_dhrs_isoRNA:1:4128,2_A27S_shL27_dhrs_isoRNA:1:4129	-116, 3782, -50	upstream, upstream, upstream	46.5	51.5	2	1_A27S_shL7_dhrus_isoRNA:1	63	Gene:GCDH	AGADS, GCDH, GCD	glutaryl-CoA dehydrogenase	NM_000159, NM_013976, XM_017129782.2, XM_017268516.0, XM_017268516.0	NM_000159.3, NM_013976.4, XM_017129782.1, XM_017268516.1, XM_017268516.1	ENM64324.1, ENM64326.1	200390_s_at, 200399_s_at	NP_000150.2, NP_039860.1, ENP64324.1, ENP64326.1
Gene:ID:56126	SYCE2	19	13,009,694	13,030,666	20,192	+	2	1_A27S_shL7_dhrus_isoRNA:1:2872,2_A27S_shL27_dhrs_isoRNA:1:4128	28230, 25262	downstream, downstream	8.2	61	1	1_A27S_shL7_dhrus_isoRNA:1	63	Gene:SYCE2	CESC1, SYCE2	synaptonemal complex central element protein 2	NM_001155376	NM_001155376.1	ENM64325.1	237304_at	NP_001148848.1
Gene:ID:193	PARSA	19	13,033,264	13,044,898	11,274	-	2	1_A27S_shL7_dhrus_isoRNA:1:2872,2_A27S_shL27_dhrs_isoRNA:1:4130	4975, 4530	upstream, upstream	34	33	1	1_A27S_shL7_dhrus_isoRNA:1	34	Gene:PARSA	PRSA, PARSLA, PRoNA, CMLS3, PARSA	phenylalanyl-tRNA synthetase, alpha subunit	NM_004561, XM_017129852.2, XM_017269910.0	NM_004561.4, XM_017129852.1, XM_017269910.1	ENM64329.1, ENM64326.1	202159_at, 216852_s_at	NP_004552.1, ENP64329.1, ENP64326.1
Gene:ID:11	CALK	19	13,049,414	13,053,204	3,790	+	2	1_A27S_shL7_dhrus_isoRNA:1:2872,2_A27S_shL27_dhrs_isoRNA:1:4127	122, -336	vs gene, upstream	34	33	1	1_A27S_shL7_dhrus_isoRNA:1	34	Gene:CALK	FLJ39660, BSK, CRT, cCSK, RO, CALK	calicheckin	NM_004343, XM_017129854.2, XM_017269731.0, XM_017269469.0	NM_004343.3, XM_017129854.1, XM_017269731.1, XM_017269469.1	ENM64333.1, ENM64331.1, ENM64332.1	209033_at, 212652_at, 212653_x_at, 214315_x_at, 214316_x_at	NP_004334.1, ENP64333.1, ENP64331.1, ENP64332.1
Gene:ID:100507325	LOC100507325	19	13,054,904	13,076,265	23,361	-	4	1_A27S_shL7_dhrus_isoRNA:1:2872,1_A27S_shL7_dhrus_isoRNA:1:2874,1_A27S_shL27_dhrs_isoRNA:1:4127,2_A27S_shL27_dhrs_isoRNA:1:4128	29669, 10173, 29117, 10203	downstream, vs gene, downstream, vs gene	26	26.5	2	1_A27S_shL7_dhrus_isoRNA:1	34	Gene:LOC100507325		hypothetical LOC100507325	XR_109369, XR_109370	XR_109369.1, XR_109370.1		
Gene:ID:558	RAD23A	19	13,099,654	13,064,455	7,601	+	4	1_A27S_shL7_dhrus_isoRNA:1:2872,1_A27S_shL7_dhrus_isoRNA:1:2874,1_A27S_shL27_dhrs_isoRNA:1:4127,2_A27S_shL27_dhrs_isoRNA:1:4128	-7116, 7366, 11586	upstream, downstream, upstream, downstream	26	26.5	2	1_A27S_shL7_dhrus_isoRNA:1	34	Gene:RAD23A	RAD23A, HHR23A, MGC111065	RAD23 homolog A (S. cerevisiae)	NM_005053, XM_017129851.3, XM_017269729.0	NM_005053.3, XM_017129851.1, XM_017269729.0	ENM64334.1, ENM64332.1	200039_s_at, 200596_s_at	NP_005044.1, ENP64334.1, ENP64332.1
Gene:ID:3488	GADD45GIP1	19	13,064,972	13,066,650	3,078	+	2	1_A27S_shL7_dhrus_isoRNA:1:2874,2_A27S_shL27_dhrs_isoRNA:1:4128	18, 50	vs gene, vs gene	16	30	1	2_A27S_shL27_dhrs_isoRNA:1	20	Gene:GADD45GIP1	MDC4957, FLINP-1, PRG6, CRIF1, Pro32, MDC4795, GADD45GIP1, CKBBP2	growth arrest and DNA-damage-inducible, gamma-interacting protein 1	NM_032850, XM_017129868.2	NM_032850.2, XM_017129868.1	ENM64335.1	219891_s_at	NP_443082.2, ENP64335.1
Gene:ID:89999	DAND5	19	13,080,632	13,083,567	5,136	+	2	1_A27S_shL7_dhrus_isoRNA:1:2874,2_A27S_shL27_dhrs_isoRNA:1:4128	15555, 15504	downstream, downstream	18	21	1	2_A27S_shL27_dhrs_isoRNA:1	21	Gene:DAND5	CER2, GREM3, MGC126569, DAND5, CATCH18, SP1, CCN2, COCO, DANTE, CRL2	DAN domain family, member 5	NM_152554, XM_017264740.1, XM_017244982.0	NM_152554.3, XM_017264740.1, XM_017244982.1	ENM64337.1, ENM64336.1	1562772_a_at	NP_689957.1, ENP64337.1, ENP64336.1
Gene:ID:164	NPIX	19	13,109,564	13,209,810	103,026	+	4	1_A27S_shL7_dhrus_isoRNA:1:2873,1_A27S_shL7_dhrus_isoRNA:1:2876,2_A27S_shL27_dhrs_isoRNA:1:4129,2_A27S_shL27_dhrs_isoRNA:1:4130	-10264, 966, -10648, 362	upstream, upstream, upstream, vs gene	18.67	22.33	3	2_A27S_shL27_dhrs_isoRNA:1	24	Gene:NPIX	NPIX, NPTA	nuclear factor IX (CCAAT-binding transcription factor)	NM_002501, XM_017129922.2, XM_017264761.0, XM_017264762.0, XM_017264763.0, XM_017264767.0	NM_002501.3, XM_017129922.1, XM_017264761.0, XM_017264762.0, XM_017264763.0, XM_017264767.0	ENM64339.1, ENM64340.1, ENM64341.1, ENM64342.1	206077_s_at, 227400_at, 228278_at, 236634_at	NP_002492.2, ENP64339.1, ENP64340.1, ENP64341.1, ENP64342.1
Gene:ID:5621	TRMT1	19	13,215,714	13,227,063	11,349	-	2	1_A27S_shL7_dhrus_isoRNA:1:2877,2_A27S_shL27_dhrs_isoRNA:1:4131	-55, 92	upstream, vs gene	21	33	1	2_A27S_shL27_dhrs_isoRNA:1	33	Gene:TRMT1	FLJ22240, TRM1, TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	NM_001162554, NM_001136035, NM_017722, XM_017269072.2, XM_017269912.2, XM_017269913.2, XM_017269914.0, XM_017269915.0, XM_017269916.0	NM_001162554.1, NM_001136035.1, NM_017722.3, XM_017269072.2, XM_017269912.1, XM_017269913.1, XM_017269914.1, XM_017269915.1, XM_017269916.1	ENM64345.1, ENM64346.1, ENM64343.1, ENM64344.1	203701_s_at, 215853_x_at, 216454_at	NP_001136026.1, NP_001129507.1, NP_060182.1, ENP64345.1, ENP64346.1, ENP64343.1, ENP64344.1
Gene:ID:12039	NACC1	19	13,229,109	13,251,939	22,830	+	4	1_A27S_shL7_dhrus_isoRNA:1:2877,1_A27S_shL7_dhrus_isoRNA:1:2878,2_A27S_shL27_dhrs_isoRNA:1:4131,2_A27S_shL27_dhrs_isoRNA:1:4132	-1461, 32107, 1605, 31979	upstream, downstream, upstream, downstream	41	41	2	1_A27S_shL7_dhrus_isoRNA:1	51	Gene:NACC1	BTBD14B, NAC-1, NACC1, NAC1, FLJ23583, BEN/DE	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing	NM_052876, XM_017263512.1, XM_017267765.0, XM_017267766.0	NM_052876.3, XM_017263512.1, XM_017267765.1, XM_017267766.1	ENM64352.1, ENM64353.1, ENM64354.1	227651_at, 228047_s_at	NP_443108.1, ENP64352.1, ENP64353.1, ENP64354.1
Gene:ID:677	STX10	19	13,255,224	13,260,887	5,763	+	4	1_A27S_shL7_dhrus_isoRNA:1:2878,1_A27S_shL7_dhrus_isoRNA:1:2879,2_A27S_shL27_dhrs_isoRNA:1:4132,2_A27S_shL27_dhrs_isoRNA:1:4133	-229, 1613, -101, -1797	upstream, downstream, upstream, upstream	51	51	1	1_A27S_shL7_dhrus_isoRNA:1	51	Gene:STX10	STX10, SYN10, hsyn10	syntaxin 10	NM_003763, XM_017269013.3, XM_017270124.0	NM_003763.3, XM_017269013.1, XM_017270124.1	ENM64356.1, ENM64357.1	212625_at	NP_003752.1, ENP64356.1, ENP64357.1
Gene:ID:992	IER2	19	13,261,252	13,265,722	4,470	+	7	1_A27S_shL7_dhrus_isoRNA:1:2878,1_A27S_shL7_dhrus_isoRNA:1:2879,1_A27S_shL7_dhrus_isoRNA:1:2880,2_A27S_shL27_dhrs_isoRNA:1:4132,2_A27S_shL27_dhrs_isoRNA:1:4133,2_A27S_shL27_dhrs_isoRNA:1:4134,2_A27S_shL27_dhrs_isoRNA:1:4135	486, 1516, 1410, -1, 184, 1692, 13274, 14098	upstream, vs gene, downstream, upstream, vs gene, downstream, downstream	28	29.33	3	1_A27S_shL7_dhrus_isoRNA:1	51	Gene:IER2	MGC15265, ETR101, IER2, MGC111472	immediate early response 2	NM_004907, XM_017119033.2, XM_017264766.1, XM_017264140.0	NM_004907.3, XM_017119033.1, XM_017264766.1, XM_017264140.1	ENM64360.1	202081_at	NP_004498.2, ENP64360.1, ENP64358.1, ENP64359.1
Gene:ID:1376	CCDC130	19	13,556,753	13,574,106	16,353	+	2	1_A27S_shL7_dhrus_isoRNA:1:2880,2_A27S_shL27_dhrs_isoRNA:1:4135,2_A27S_shL27_dhrs_isoRNA:1:4136	161, 16319	upstream, downstream	0	1	17	21.3	2	2_A27S_shL27_dhrs_isoRNA:1	22	Gene:CCDC130	CCDC130, MGC10471	coiled-coil domain containing 130	NM_020510, XM_017126774.2, XM_017269237.0	NM_020510.2, XM_017126774.1, XM_017269237.1	ENM64367.1, ENM64366.1	208094_s_at	NP_115045.1, ENP64367.1, ENP64366.1
Gene:ID:4245	MRI1	19	13,618,337	13,653,896	8,786	+	3	1_A27S_shL7_dhrus_isoRNA:1:2884,2_A27S_shL27_dhrs_isoRNA:1:4140,2_A27S_shL27_dhrs_isoRNA:1:4142	8818, -263, 8647	downstream, upstream, downstream	27.5	39	2	2_A27S_shL27_dhrs_isoRNA:1	57	Gene:MRI1	Yjr118w, MGC3287, MTNA, MRI1	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae)	NM_001031727, NM_022565, XM_017269362.1, XM_017269363.0, XM_017269364.0	NM_001031727.1, NM_022565.3, XM_017269362.1, XM_017269363.1, XM_017269364.1	ENM64369.1, ENM64370.1, ENM64371.1	223770_x_at, 226077_at	NP_001026897.1, NP_071990.1, ENP64369.1, ENP64370.1, ENP64371.1
Gene:ID:9974	C19orf53	19	13,655,297	13,659,587	4,330	+	3	1_A27S_shL7_dhrus_isoRNA:1:2884,2_A27S_shL27_dhrs_isoRNA:1:4142,2_A27S_shL27_dhrs_isoRNA:1:4143	-103, 10163, -72	upstream, upstream, upstream	27.5	39	2	2_A27S_shL27_dhrs_isoRNA:1	57	Gene:C19orf53	C19orf53, LYDG10, HSPC023	chromosome 19 open reading frame 53	NM_014047, XM_017126662.2	NM_014047.3, XM_017126662.1	ENM64372.1	217626_at	NP_054766.1, ENP64372.1
Gene:ID:5249	ZSWIM4	19	13,906,274	13,943,044	36,770	+	4	1_A27S_shL7_dhrus_isoRNA:1:2885,1_A27S_shL7_dhrus_isoRNA:1:2886,2_A27S_shL27_dhrs_isoRNA:1:4144,2_A27S_shL27_dhrs_isoRNA:1:4145	41516, 45214, 164, 44777	downstream, downstream, upstream, downstream	20.33	22.33	3	1_A27S_shL7_dhrus_isoRNA:1	25	Gene:ZSWIM4	ZSWIM4		NM_023072, XM_017126662.2	NM_023072.3, XM_017126662.1		221915_at	NP_075560.2, ENP64370.1
Gene:ID:644454	LOC644454	19	13,945,330	13,947,103	1,773	+	4	1_A27S_shL7_dhrus_isoRNA:1:2885,1_A27S_shL7_dhrus_isoRNA:1:2886,1_A27S_shL7_dhrus_isoRNA:1:2887,2_A27S_shL27_dhrs_isoRNA:1:4145,2_A27S_shL27_dhrs_isoRNA:1:4146	-609, 4083, -15599, 3848	upstream, upstream, upstream, upstream	24.33	22	3	1_A27S_shL7_dhrus_isoRNA:1	29	Gene:LOC644454		hypothetical LOC644454	NR_036515	NR_036515.1	1555547_a_at, 228317_at	
Gene:ID:87012	MIR24-2	19	13,947,101	13,947,173	72	+	5	1_A27S_shL7_dhrus_isoRNA:1:2885,1_A27S_shL7_dhrus_isoRNA:1:2886,1_A27S_shL7_dhrus_isoRNA:1:2887,2_A27S_shL27_dhrs_isoRNA:1:4145,2_A27S_shL27_dhrs_isoRNA:1:4146	4118, 4315, 10774, 3676, 10557	upstream, upstream, upstream, upstream, upstream	24.33	22	3	1_A27S_shL7_dhrus_isoRNA:1	29	Gene:MIR24-2	miR24A2, MIR24-2, miR-24-2, MIRN24-2	microRNA 24-2	NR_029497				
Gene:ID:407016	MIR27A	19	13,947,254	13,947,331	77	+	5	1_A27S_shL7_dhrus_isoRNA:1:2885,1_A27S_shL7_dhrus_isoRNA:1:2886,1_A27S_shL7_dhrus_isoRNA:1:2887,2_A27S_shL27_dhrs_isoRNA:1:4145,2_A27S_shL27_dhrs_isoRNA:1:4146	4261, 4157, 10621, 3720, 10624	upstream, upstream, upstream, upstream, upstream	24.33	22	3	1_A27S_shL7_dhrus_isoRNA:1	29	Gene:MIR27A	MIRN27A, MIR27A, MIR27	microRNA 27a	NR_029501				
Gene:ID:407010	MIR23A	19	13,947,601	13,947,673	72	+	5	1_A27S_shL7_dhrus_isoRNA:1:2885,1_A27S_shL7_dhrus_isoRNA:1:2886,1_A27S_shL7_dhrus_isoRNA:1:2887,2_A27S_shL27_dhrs_isoRNA:1:4145,2_A27S_shL27_dhrs_isoRNA:1:4146	4116, 4515, 10474, 3976, 10287	upstream, upstream, upstream, upstream, upstream	24.33	22	3	1_A27S_shL7_dhrus_isoRNA:1	29	Gene:MIR23A	MIRN23A, hsa-mir-23a, MIR23A, miRNA23A	microRNA 23a	NR_029493				
Gene:ID:406913	MIR181C	19	13,953,513	13,953,622	109	+	1	1_A27S_shL7_dhrus_isoRNA:1:2886,1_A27S_shL7_dhrus_isoRNA:1:2887,2_A27S_shL27_dhrs_isoRNA:1:4146	5767	downstream	0	1	21	19	1	2_A27S_shL27_dhrs_isoRNA:1	19	Gene:MIR181C	MIRN181C, MIRN181C, mir-181c	microRNA 181c	NR_029613				
Gene:ID:406915	MIR181D	19	13,953,659	13,953,825	166	+	1	1_A27S_shL7_dhrus_isoRNA:1:2886,1_A27S_shL7_dhrus_isoRNA:1:2887,2_A27S_shL27_dhrs_isoRNA:1:4146	5591	downstream	0	1	21	19	1	2_A27S_shL27_dhrs_isoRNA:1	19	Gene:MIR181D	MIRN181D, MIR181D	microRNA 181d	NR_030179				
Gene:ID:92977	NANOS3	19	13,967,850	13,967,971	1,621	+	1	1_A27S_shL7_dhrus_isoRNA:1:2886,1_A27S_shL7_dhrus_isoRNA:1:2887,2_A27S_shL27_dhrs_isoRNA:1:4146	3330	vs gene	0	1	21	19	1	2_A27S_shL27_dhrs_isoRNA:1	19	Gene:NANOS3	MGC120118, NOS3, NANOS3, NANOS1L	nanos homolog 3 (Drosophila)	NM_001099622			238311_at	NP_001092092.1
Gene:ID:3173	C19orf57	19	13,992,168	13,996,809	23,741	-	4	1_A27S_shL7_dhrus_isoRNA:1:2889,2_A27S_shL27_dhrs_isoRNA:1:4146,2_A27S_shL27_dhrs_isoRNA:1:4147,2_A27S_shL27_dhrs_isoRNA:1:4148	2669, 23629, 2733, -35	vs gene, downstream, vs gene, upstream	1	1	23.33	21.33	3	2_A27S_shL27_dhrs_isoRNA:1	31	Gene:C19orf57	MGC112731, C19orf57, MGC142720	chromosome 19 open reading frame 57	NM_018323, XM_017101938.2, XM_017269392.2, XM_017245343.0, XM_017396405.0	NM_018323.3, XM_017101938.1, XM_017269392.1, XM_017245343.0, XM_017396405.0	ENM64376.1, ENM64378.1, ENM64379.1	208601_at	NP_060793.3, ENP64376.1, ENP64378.1, ENP64379.1
Gene:ID:4892	CC2D1A	19	14,016,696	14,041,693	24,737	+	3	1_A27S_shL7_dhrus_isoRNA:1:2889,2_A27S_shL27_dhrs_isoRNA:1:4149,2_A27S_shL27_dhrs_isoRNA:1:4150	-2716, 2780, -12	upstream, upstream, upstream	1	1	24.5	22.5	2	1_A27S_shL27_dhrs_isoRNA:1	31	Gene:CC2D1A	MRT3, FREUD-1, FLJ41160, FLJ20241, Freud-1/Aki1, CC2D1A	coiled-coil and C2 domain containing 1A	NM_017721, XM_017126668.4	NM_017721.3, XM_017126668.1	ENM64380.1	207083_s_at, 221686_at, 222127_at, 56004_at	NP_060191.3, ENP64380.1
Gene:ID:5889	RPX1	19	14,072,342	14,117,134	44,792	-	2	1_A27S_shL7_dhrs_isoRNA:1:2890,1_A27S_shL27_dhrs_isoRNA:1:4150	-852, -566	upstream, upstream	1	1	26	36	1	2_A27S_shL27_dhrs_isoRNA:1	36	Gene:RPX1	ERC, RPX, RPX1	regulatory factor X, 1 (influences HLA class II expression)	NM_002918, XM_017126653.4	NM_002918.3, XM_017126653.1	ENM64387.1	209271_at, 226706_at	NP_002909.2, ENP64387.1
Gene:ID:113230	LOC113230	19	14,163,821	14,165,874	2,053	+	1	1_A27S_shL7_dhrs_isoRNA:1:4152,1_A27S_shL27_dhrs_isoRNA:1:4153	6739	downstream	0	1	23	23	1	2_A27S_shL27_dhrs_isoRNA:1	23	Gene:LOC113230		hypothetical LOC113230	NR_033262			1558612_at	
Gene:ID:95637	C19orf57	19	14,191,852	14,196,629	4,457	-	1	1_A27S_shL7_dhrs_isoRNA:1:4152	3879	vs gene	0	1	23	23	1	2_A27S_shL27_dhrs_isoRNA:1	23	Gene:C19orf57	C19orf57	chromosome 19 open reading frame 57	XM_024352	XM_024352.1		1554475.1	
Gene:ID:6318	SIAH3	19	14,199,229	14,201,232	2,003	-	1	1_A27S_shL27_dhrs_isoRNA:1:4152	6872	downstream	0	1	23	23	1	2_A27S_shL27_dhrs_isoRNA:1	23	Gene:SIAH3	SIAH3		NM_138357, XM_017126672.2	NM_138357.1, XM_017126672.1	ENM64396.1	235650_at	NP_612391.1, ENP64396.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervals Count	Intervals	Intervals Dist to gene	Intervals Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:3996	PRKACA	19	14,202,900	14,226,559	26,659	-	2	2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA	35992, 1681	downstream, upstream	0	1	16.5	20	2	2_A375_shLS7_dtct_IncRNA:1	23	Gene PRKACA	PRKACA, MGC102831, PRKACA, MGC36593	protein kinase, cAMP-dependent, catalytic, alpha	NM_002730, NM_207518, ICT:10962.3, NCT02684605.0, NCT02684648.0, NCT02685440.0	2162254_s_at	NP_002721.1, NP_997491.1, EAW64397.1, EAW64398.1, EAW64399.1, EAW64400.1
Gene:ID:5723	ASF1B	19	14,230,221	14,247,440	17,119	+	3	1_A375_shLS7_dtct_IncRNA:1:-2691,2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA:1:-4152	166, 17840, 360	up gene, downstream, upstream	1	1	17.5	19.5	2	2_A375_shLS7_dtct_IncRNA:1	22	Gene ASF1B	ASF1B, FLJ10604, CIA-II	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	NM_018154, ICT:10971.2, NCT02685403.0	218119_at	NP_060624.1, EAW64405.1, EAW64402.1
Gene:ID:1003707373	LOC100373	19	14,247,680	14,279,814	31,934	+	2	1_A375_shLS7_dtct_IncRNA:1:-2691,2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA	4336, 20	upstream, up gene	1	1	21	22	1	2_A375_shLS7_dtct_IncRNA:1	22	Gene LOC100373732		hypothetical LOC100373732	XR_109374, XR_109373		
Gene:ID:2638	UPNH1	19	14,255,549	14,316,997	56,446	-	3	1_A375_shLS7_dtct_IncRNA:1:-2892,2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA:1:-4152	12775, 46997, 1275	upstream, downstream, upstream	1	1	30.5	35.5	2	2_A375_shLS7_dtct_IncRNA:1	55	Gene UPNH1	LEC2, UPNH1, CL1, CIRL1	lilrs4plus 1	NM_014921, NM_001082701, ICT:10961.2, NCT02684535.0, NCT02685360.0, NCT02685438.0, NCT02685503.0	202455_at, 219143_at, 47560_at	NP_055736.2, NP_001082701.1, EAW64404.1, EAW64406.1, EAW64408.1, EAW64409.1, EAW64403.1, EAW64407.1
Gene:ID:760	CD97	19	14,392,213	14,419,333	27,122	+	1	2_A375_shLS7_dtct_IncRNA:1:-4139	823	up gene	0	1	14	16	1	2_A375_shLS7_dtct_IncRNA:1	16	Gene CD97	TM7LN1, CD97	CD97 molecule	NM_078481, NM_001784, NM_001025183, NCT02685564.1, NCT02685607.0	202910_s_at	NP_519999.1, NP_001775.2, NP_001102331.1, EAW64410.1, EAW64412.1
Gene:ID:3655538	LOC1003 87395	19	14,493,031	14,493,672	641	+	1	2_A375_shLS7_dtct_IncRNA:1:-4139	2265	up gene	0	1	16	16	1	2_A375_shLS7_dtct_IncRNA:1	16	Gene LOC100387395		hypothetical protein LOC100387395	XM_003116768		NP_003115836.1
Gene:ID:555	PKN1	19	14,544,166	14,662,879	56,513	+	1	1_A375_shLS7_dtct_IncRNA:1:-2893	826	up gene	1	0	22	16	1	1_A375_shLS7_dtct_IncRNA:1	22	Gene PKN1	PKN1, PKN-ALPHA, PAK-1, MGC48204, PRKCL1, PRK1, DBK, PKN, PAK1	protein kinase N1	NM_002741, NM_213560, ICT:10957.3, NCT10629989.1, NCT02366227.0	202161_at	NP_002732.2, NP_998726.1, EAW64419.1, EAW64420.1, EAW64421.1
Gene:ID:3277	DNAJB1	19	14,629,562	14,629,201	1,618	-	2	1_A375_shLS7_dtct_IncRNA:1:-2894,2_A375_shLS7_dtct_IncRNA:1:-4152	1743, 1775	upstream, upstream	1	1	23	24	1	2_A375_shLS7_dtct_IncRNA:1	24	Gene DNAJB1	HSPF1, HLJ4, DNAJB1, HSPH1B, Sis1, Hdj1	DnaJ (Hsp40) homolog, subfamily B, member 1	NM_006145, ICT:10159.2, NCT02685222.0	200664_s_at, 200665_s_at	NP_006136.1, EAW64422.1, EAW64423.1
Gene:ID:8224	MRK38	19	14,640,253	14,640,252	97	+	2	1_A375_shLS7_dtct_IncRNA:1:-2894,2_A375_shLS7_dtct_IncRNA:1:-4152	6411, 6379	upstream, upstream	1	1	23	24	1	2_A375_shLS7_dtct_IncRNA:1	24	Gene MRK38	MRK38, fch-mrk-439, MRK38	mocRNA 439	NR_003399		
Gene:ID:524	TECR	19	14,640,352	14,676,782	36,430	+	4	1_A375_shLS7_dtct_IncRNA:1:-2894,2_A375_shLS7_dtct_IncRNA:1:-2893,2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA:1:-4152	6438, 42495, 6409, 42962	upstream, downstream, upstream, downstream	1	1	53	61.5	2	2_A375_shLS7_dtct_IncRNA:1	99	Gene TECR	TER, TECR, SC2, GPSN2	trans-2,3-enoyl-CoA reductase	NM_138501, ICT:10939.3, NCT10870826.1	1560392_at, 206395_s_at, 231896_at	NP_612510.1, EAW64434.1, EAW64435.1
Gene:ID:7713	NDUFB7	19	14,676,890	14,682,886	5,996	-	2	1_A375_shLS7_dtct_IncRNA:1:-2893,2_A375_shLS7_dtct_IncRNA:1:-4152	16, -58	up gene, upstream	1	1	63	69	1	2_A375_shLS7_dtct_IncRNA:1	98	Gene NDUFB7	NDUFB7, CI-B18, MGC2480, B18	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	NM_004146, ICT:10992.2	203039_s_at, 214407_at	NP_004137.2, EAW64436.1
Gene:ID:26270	CCDC103	19	15,121,539	15,134,083	12,544	+	1	2_A375_shLS7_dtct_IncRNA:1:-4139	6373	up gene	0	1	23	27	1	2_A375_shLS7_dtct_IncRNA:1	27	Gene CCDC103	CCDC103, FLJ40365	coiled-coil domain containing 103	NM_173462, ICT:10969.2	1553093_at	NP_775732.2, EAW64458.1
Gene:ID:26270	OR11H	19	15,197,077	15,198,044	1,067	+	1	2_A375_shLS7_dtct_IncRNA:1:-4139	269	up gene	0	1	16	26	1	2_A375_shLS7_dtct_IncRNA:1	26	Gene OR11H	OR11H, OR19-20, OR11P, OR11G	olfactory receptor, family 11, subfamily L, member 1	NM_001004713, ICT:03316.0	234403_at	NP_001004713.1, EAW64460.1
Gene:ID:9964	ILVBL	19	15,225,765	15,236,577	10,792	-	1	2_A375_shLS7_dtct_IncRNA:1:-4151	161	up gene	0	1	21	25	1	2_A375_shLS7_dtct_IncRNA:1	25	Gene ILVBL	MGC1269, ILVBL, ILVDH, 2B5LS, AHAS, MGC19133	ilvB (bacterial acetolactate synthase)-like	NM_006844, ICT:09530.3	202993_at, 219624_s_at	NP_006835.2, EAW64464.1
Gene:ID:9270	AKAP6	19	15,864,535	15,900,693	36,158	-	2	1_A375_shLS7_dtct_IncRNA:1:-2896,2_A375_shLS7_dtct_IncRNA:1:-4152	11, 43	up gene, up gene	1	1	27	27	1	2_A375_shLS7_dtct_IncRNA:1	27	Gene AKAP6	DKFZp586B1222, AKAP6, AKAP85	A kinase (PRKA) anchor protein 6	NM_004555, ICT:09539.3	203047_s_at, 203048_s_at	NP_004546.1, EAW64474.1
Gene:ID:9982	AKAP6L	19	15,900,859	15,929,833	30,974	+	4	1_A375_shLS7_dtct_IncRNA:1:-2896,2_A375_shLS7_dtct_IncRNA:1:-2897,2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA:1:-4152	18241, 232, 28272, 8	downstream, up gene, downstream, up gene	1	1	26	29.5	2	1_A375_shLS7_dtct_IncRNA:1	29	Gene AKAP6L	AKAP6L, DKFZp434U2630, NAXAP93, NAXAP, HH93, HAP85	A kinase (PRKA) anchor protein 6-like	NM_014371, ICT:02649.5, NCT02686261.1, NCT02684627.1, NCT2800.1.2	219741_s_at, 219064_s_at, 222160_at, 227691_at	NP_055186.2, EAW64476.1, EAW64478.1, EAW64477.1, EAW64479.1
Gene:ID:5525	WIZ	19	15,932,316	15,960,762	28,446	+	4	1_A375_shLS7_dtct_IncRNA:1:-2897,2_A375_shLS7_dtct_IncRNA:1:-2898,2_A375_shLS7_dtct_IncRNA:1:-4152,2_A375_shLS7_dtct_IncRNA:1:-4152	21162, 17092, 21015, 17114	downstream, up gene, downstream, up gene	1	1	30.5	39.5	2	2_A375_shLS7_dtct_IncRNA:1	55	Gene WIZ	WIZ, ZNF803	widely-interspaced zinc finger motifs	NM_021241	221763_at, 221764_at, 221765_at, 52805_at	NP_067064.2
Gene:ID:26119	CYP4F22	19	15,919,339	15,963,126	43,762	+	1	2_A375_shLS7_dtct_IncRNA:1:-4139	48248	downstream	0	1	20	21	1	2_A375_shLS7_dtct_IncRNA:1	21	Gene CYP4F22	FLJ39501, LTB, CYP4F22	cytochrome P450, family 4, subfamily F, polypeptide 22	NM_173483, ICT:03448.1	244692_at	NP_775754.2, EAW64484.1
Gene:ID:1283	CYP4F8	19	15,726,029	15,740,446	14,418	+	2	1_A375_shLS7_dtct_IncRNA:1:-2899,2_A375_shLS7_dtct_IncRNA:1:-4152	6691, 6669	up gene, up gene	1	1	28	41	1	2_A375_shLS7_dtct_IncRNA:1	41	Gene CYP4F8	CYP4F8, CYP4R5, CYP4	cytochrome P450, family 4, subfamily F, polypeptide 8	NM_007253, ICT:01640.1.2, NCT12365.3.0	210576_at	NP_009184.1, EAW64487.1, EAW64486.1
Gene:ID:55514	LOC5551 14	19	15,870,144	15,890,768	20,664	-	1	2_A375_shLS7_dtct_IncRNA:1:-4139	16206	up gene	0	1	17	30	1	2_A375_shLS7_dtct_IncRNA:1	30	Gene LOC55514		cytochrome P450, family 4, subfamily F, polypeptide 29 pseudogene	NR_033864		
Gene:ID:52935	UCA1	19	15,939,757	15,946,230	6,473	+	1	2_A375_shLS7_dtct_IncRNA:1:-4139	7823	downstream	0	1	19	27	1	2_A375_shLS7_dtct_IncRNA:1	27	Gene UCA1	NCRNA00178, CUDR, UCA1	urothelial cancer associated 1 (non-protein coding)	NR_015379	227919_at	
Gene:ID:45231	FLJ23328	19	16,147,266	16,152,921	5,635	+	2	1_A375_shLS7_dtct_IncRNA:1:-2900,2_A375_shLS7_dtct_IncRNA:1:-4151	18062, 18098	downstream, downstream	1	1	22	19	1	1_A375_shLS7_dtct_IncRNA:1	22	Gene FLJ23328	MGC126002	hypothetical LOC145231	NR_026333, NR_024336, ICT:02649.1, NCT02686402.0	1562914_at_at	EAW64520.1, EAW64519.1
Gene:ID:171	TPMI	19	16,116,317	16,213,513	35,486	+	2	1_A375_shLS7_dtct_IncRNA:1:-2901,2_A375_shLS7_dtct_IncRNA:1:-4152	43527, 42851	downstream, downstream	1	1	16	23	1	2_A375_shLS7_dtct_IncRNA:1	23	Gene TPMI	TPMI		NM_002290, NM_001145160, ICT:02640.0, NCT02684618.0, NCT02684660.0	1559959_at, 1557107_s_at, 200334_at, 200335_s_at	NP_002281.1, NP_001128632.1, EAW64521.1, EAW64522.1, EAW64523.1, EAW64524.1
Gene:ID:218	RABSA	19	16,222,490	16,244,445	21,955	+	2	1_A375_shLS7_dtct_IncRNA:1:-2901,2_A375_shLS7_dtct_IncRNA:1:-4152	-246, -362	upstream, upstream	1	1	16	23	1	2_A375_shLS7_dtct_IncRNA:1	23	Gene RABSA	RABSA, MEL, RABE	RABSA, member RAS oncogene family	NM_005370, ICT:02624497.0, ICT:2618.3	205519_at	NP_005361.2, EAW64526.1, EAW64527.1
Gene:ID:9901	HSH2D	19	16,248,638	16,269,261	20,623	+	2	1_A375_shLS7_dtct_IncRNA:1:-2902,2_A375_shLS7_dtct_IncRNA:1:-4153	27090, 27082	downstream, downstream	1	1	22	22	1	1_A375_shLS7_dtct_IncRNA:1	22	Gene HSH2D	ALX, FLJ14686, HSH2, HSH2D	hematopoietic SH2 domain containing	NM_032655, ICT:01967.07.1, ICT:02685960.0, NCT02686020.0, NCT02686102.0, NCT2618.2	1552622_at	NP_116248.1, EAW64528.1, EAW64529.1, EAW64530.1, EAW64531.1, EAW64532.1
Gene:ID:1326	CIB3	19	16,272,179	16,295,286	12,107	-	2	1_A375_shLS7_dtct_IncRNA:1:-2902,2_A375_shLS7_dtct_IncRNA:1:-4153	12352, 12396	downstream, downstream	1	1	22	22	1	1_A375_shLS7_dtct_IncRNA:1	22	Gene CIB3	MGC99822, MGC135405, IUP2, CIB3, MGC142151	calcium and integrin binding family member 3	NM_054113, ICT:01658.1, ICT:02686.2.0, NCT02686204.0	1552792_at, 1552791_s_at	NP_473654.1, EAW64533.1, EAW64534.1, EAW64535.1
Gene:ID:6317	PAM32A	19	16,298,233	16,302,697	6,622	+	1	2_A375_shLS7_dtct_IncRNA:1:-4153	12309	downstream	1	0	21	12	1	1_A375_shLS7_dtct_IncRNA:1	21	Gene PAM32A	PAM32A	family with sequence similarity 32, member A	NM_014577, ICT:02624711.0, NCT02685124.0, NCT02685164.0	201563_at	NP_054596.1, EAW64537.1, EAW64536.1, EAW64538.1
Gene:ID:907	AP1M1	19	16,300,665	16,346,156	27,491	+	1	2_A375_shLS7_dtct_IncRNA:1:-2903,2_A375_shLS7_dtct_IncRNA:1:-4153	4121	downstream	1	0	21	12	1	1_A375_shLS7_dtct_IncRNA:1	21	Gene AP1M1	MU1A, AP1M1, CLTNM, AP47, CLAP1M1	adaptor-related protein complex 1, mu 1 subunit	NM_032493, NM_001130524, ICT:02624740, NCT2618.2	223024_at, 223025_s_at	NP_115869.1, NP_001123996.1, EAW64539.1, EAW64540.1
Gene:ID:23672	CALR3	19	16,359,673	16,607,003	17,126	+	1	2_A375_shLS7_dtct_IncRNA:1:-4139	488	upstream	0	1	24	35	1	2_A375_shLS7_dtct_IncRNA:1	35	Gene CALR3	FLJ25355, MGC26577, CRT2, CALR2, CT-2	calreticulin 3	NM_145046, ICT:03518.2	1552421_at	NP_659431.2, EAW64545.1
Gene:ID:4167	C19orf44	19	16,607,203	16,632,163	24,956	+	1	2_A375_shLS7_dtct_IncRNA:1:-4139	133	downstream	0	1	24	35	1	2_A375_shLS7_dtct_IncRNA:1	35	Gene C19orf44	C19orf44, FLJ21742, PLC22492	chromosome 19 open reading frame 44	NM_022307, ICT:02624496.0, NCT2618.2	225154_at, 232130_at	NP_071883.1, EAW64547.1, EAW64548.1
Gene:ID:8323	CHERP	19	16,638,700	16,653,263	24,563	-	2	1_A375_shLS7_dtct_IncRNA:1:-2903,2_A375_shLS7_dtct_IncRNA:1:-4139	175, -177	up gene, upstream	1	1	19	25	1	2_A375_shLS7_dtct_IncRNA:1	25	Gene CHERP	SCAR6, DAH16, CHERP, SRA1	calcium homeostasis endoplasmic reticulum protein	NM_006387, ICT:02633.09.0	1560734_at_at, 202229_s_at, 202230_s_at	NP_006378.3, EAW64549.1
Gene:ID:9939	SLC35E1	19	16,660,648	16,683,163	22,515	-	2	1_A375_shLS7_dtct_IncRNA:1:-2903,2_A375_shLS7_dtct_IncRNA:1:-4139	32103, 29753	downstream, downstream	1	1	19	25	1	2_A375_shLS7_dtct_IncRNA:1	25	Gene SLC35E1	FLJ36699, DKFZp564G0862, FLJ14251, SLC35E1, MGC43464	solute carrier family 35, member E1	NM_030661, ICT:02633.09.0, NCT02631650.0, NCT02633060.0, NCT02633072.0	220796_at, 222263_at, 227916_at, 235033_at, 240035_at	NP_079187.2, EAW64553.1, EAW64550.1, EAW64551.1, EAW64552.1
Gene:ID:4401	MED26	19	16,665,718	16,730,015	53,297	-	1	2_A375_shLS7_dtct_IncRNA:1:-4177	417	upstream	0	1	16	21	1	2_A375_shLS7_dtct_IncRNA:1	21	Gene MED26	MED26, CRSP70, CRSP7	mediator complex subunit 26	NM_004811, ICT:27994.3	1559352_at, 1559091_at, 221666_at, 221938_at, 241224_at	NP_004622.2, EAW64554.1
Gene:ID:3878	LOC1003 87922	19	16,744,668	16,756,852	12,184	+	1	2_A375_shLS7_dtct_IncRNA:1:-4177	17170	downstream	0	1	16	21	1	2_A375_shLS7_dtct_IncRNA:1	21	Gene LOC100387922		hypothetical LOC100387922	XR_109376		
Gene:ID:9086	C19orf62	19	16,756,659	16,770,868	14,009	+	2	1_A375_shLS7_dtct_IncRNA:1:-2906,2_A375_shLS7_dtct_IncRNA:1:-4178	488, -96	upstream, upstream	1	1	27	31	1	1_A375_shLS7_dtct_IncRNA:1	27	Gene C19orf62	C19orf62, MGC2747	chromosome 19 open reading frame 62	NM_024150, ICT:10979.09.1, NCT02633770.0, NCT02686061.0, NCT26192.3	219097_s_at, 224712_s_at, 224717_s_at, 235830_s_at	NP_077009.2, EAW64555.1, EAW64556.1, EAW64557.1, EAW64558.1
Gene:ID:9041	TMEM38A	19	16,771,635	16,799,530	27,896	+	2	1_A375_shLS7_dtct_IncRNA:1:-2906,2_A375_shLS7_dtct_IncRNA:1:-4178	462, -414	upstream, upstream	1	1	27	31	1	1_A375_shLS7_dtct_IncRNA:1	27	Gene TMEM38A	TMEM38A, TRICA, TRIC-A, MGC3169	transmembrane protein 38A	NM_025074, ICT:02192.3	222696_at	NP_079274.1, EAW64559.1
Gene:ID:6444	NHD1	19	16,830,757	16,925,774	97,987	+	2	1_A375_shLS7_dtct_IncRNA:1:-4179,2_A375_shLS7_dtct_IncRNA:1:-4180	18741, 38228	up gene, up gene	0	1	13.5	31	2	2_A375_shLS7_dtct_IncRNA:1	33	Gene NHD1	MGC134680, NHD1	NACHT and WD repeat domain containing 1	NM_001007525		NP_001007526.2
Gene:ID:3323	HAUS8	19	17,160,971	17,169,243	25,772	-	3	1_A375_shLS7_dtct_IncRNA:1:-2907,2_A375_shLS7_dtct_IncRNA:1:-4180,2_A375_shLS7_dtct_IncRNA:1:-4180	7, 09, -4261	up gene, up gene, upstream	1	1	27	31.5	2	2_A375_shLS7_dtct_IncRNA:1	60	Gene HAUS8	DGT4, HICE1, MGC20533, HAUS8, NY-BAR-48	HAUS augmin-like complex, subunit 8	NM_024477, NM_001011669, ICT:03966.0.0, NCT03896.0	226355_at	NP_078953.1, NP_001011669.1, EAW64570.1, EAW64571.1
Gene:ID:4600	MYO9B	19	17,186,291	17,224,104	137,813	+	7	1_A375_shLS7_dtct_IncRNA:1:-2907,2_A375_shLS7_dtct_IncRNA:1:-2908,2_A375_shLS7_dtct_IncRNA:1:-2909,2_A375_shLS7_dtct_IncRNA:1:-4180,2_A375_shLS7_dtct_IncRNA:1:-4180,2_A375_shLS7_dtct_IncRNA:1:-4180,2_A375_shLS7_dtct_IncRNA:1:-4180	-255, 32163, 59561, 287, 4932, 32353, 139569	upstream, up gene, up gene, upstream, up gene, up gene, downstream	1	1	26.6	33	3	2_A375_shLS7_dtct_IncRNA:1	60	Gene MYO9B	CELPC4, MYO9B, MYR5	myosin IXB	NM_004145, NM_001130065, ICT:02640.3.0, NCT26898.3	206532_s_at, 214760_s_at, 217297_s_at	NP_004136.2, NP_001123537.1, EAW64572.1, EAW64573.1
Gene:ID:5550	USE1	19	17,326,155	17,330,638	4,483	+	3	1_A375_shLS7_dtct_IncRNA:1:-2910,2_A375_shLS7_dtct_IncRNA:1:-4181,2_A375_shLS7_dtct_IncRNA:1:-4181	11024, 8, 11125	downstream, up gene, downstream	1	1	27.5	33.5	2	2_A375_shLS7_dtct_IncRNA:1	56	Gene USE1	FI31, MGC6032, USE1, SLT1	exocyst-related SNARE of the ER 1 homolog (S. cerevisiae)	NM_016407, ICT:02684.0.0, NCT02686050.0, NCT26947.3	218268_at, 221706_s_at	NP_057627.1, EAW64575.1, EAW64574.1, EAW64576.1
Gene:ID:9628	OCEL1	19	17,337,055	17,340,026	2,972	+	4	1_A375_shLS7_dtct_IncRNA:1:-2910,2_A375_shLS7_dtct_IncRNA:1:-2911,2_A375_shLS7_dtct_IncRNA:1:-4182,2_A375_shLS7_dtct_IncRNA:1:-4182,2_A375_shLS7_dtct_IncRNA:1:-4182	129, 9508, 225, 9988	up gene, downstream, up gene, downstream	1	1	30	33	2	2_A375_shLS7_dtct_IncRNA:1	56	Gene OCEL1	FKI9098, FLJ22709, OCEL1, 556.04	occludin/ELL domain containing 1	NM_024578, ICT:02686.07.0, NCT26969.0	228441_at	NP_078854.1, EAW64577.1, EAW64578.1, EAW64579.1
Gene:ID:963	NR2F6	19	17,342,694	17,356,151	13,457	-	5	1_A375_shLS7_dtct_IncRNA:1:-2910,2_A375_shLS7_dtct_IncRNA:1:-2911,2_A375_shLS7_dtct_IncRNA:1:-4182,2_A375_shLS7_dtct_IncRNA:1:-4182,2_A375_shLS7_dtct_IncRNA:1:-4182,2_A375_shLS7_dtct_IncRNA:1:-4182	10997, 9091, 10571, 9511, -2196	downstream, up gene, downstream, up gene, upstream	1	1	23.67	28.33	3	2_A375_shLS7_dtct_IncRNA:1	36	Gene NR2F6	EAR-2, ERBAL2, NR2F6, EAR2	nuclear receptor subfamily 2, group F, member 6	NM_005234, ICT:26969.4	209261_s_at, 209262_s_at, 213354_s_at	NP_003289.2, EAW64580.1
Gene:ID:8518	USHBP1	19	17,360,649	17,373,844	14,488	+	1	2_A375_shLS7_dtct_IncRNA:1:-4182	16193	downstream	0	1	11	19	1	2_A375_shLS7_dtct_IncRNA:1	19	Gene USHBP1	USHBP1, FLJ90651, FLJ35708, AIEBP, MGC2	Usher syndrome 1C binding protein 1	NM_031941, ICT:02686.46.1, NCT02686469.1, NCT26903.3	235510_at	NP_114147.2, EAW64581.1, EAW64582.1, EAW64583.1
Gene:ID:55698	ANKLE1	19	17,392,454	17,398,454	6,000	+	1	2_A375_shLS7_dtct_IncRNA:1:-4182	16294	downstream	0	1	14	17	1	2_A375_shLS7_dtct_IncRNA:1	17	Gene ANKLE1	ANKDRD41, LEM06, LEM6, ANKLE1, FLJ39255	ankyrin repeat and LEM domain containing 1	NM_152383, ICT:02684.94.0, NCT02685558.0, NCT26892.0	1553135_at, 1553136_at	NP_689796.4, EAW64586.1, EAW64587.1, EAW64585.1
Gene:ID:9370	ABHD6	19	17,402,940	17,414,282	11,342	-	5	1_A375_shLS7_dtct_IncRNA:1:-2912,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183	14, 11434, 31, -3036, 8195	up gene, downstream, up gene, upstream, upstream	1	1	18.25	22.5	4	1_A375_shLS7_dtct_IncRNA:1	33	Gene ABHD6	FLJ11743, MGC2512, ABHD6, MGC14269	abhydrolase domain containing 6	NM_024527, ICT:26998.2	218101_s_at	NP_078803.4, EAW64589.1
Gene:ID:4981	MRPL34	19	17,416,477	17,417,652	1,176	+	4	1_A375_shLS7_dtct_IncRNA:1:-2912,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183	-2269, -2226, -169, 4803	upstream, upstream, upstream, downstream	1	1	21	24.33	3	1_A375_shLS7_dtct_IncRNA:1	33	Gene MRPL34	MGC2633, L34mt, MRPL34, MGC24974	mitochondrial ribosomal protein L34	NM_023037, ICT:02640.96.1, NCT02640597.0, NCT26940.99.1	221692_s_at	NP_078426.1, EAW64590.1, EAW64591.1, EAW64592.1
Gene:ID:9016	DDA1	19	17,420,337	17,434,107	13,770	+	4	1_A375_shLS7_dtct_IncRNA:1:-2912,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183	4129, -8095, -4049, 143	downstream, upstream, upstream, up gene	1	1	21	28.33	3	1_A375_shLS7_dtct_IncRNA:1	33	Gene DDA1	MGC2398, FCA1, C19orf55, DDA1	DET1 and DDB1 associated 1	NM_030930, ICT:26945.9.1, NCT02686060.1	218260_at, 227457_at, 227472_at	NP_078855.1, EAW64593.1, EAW64594.1
Gene:ID:7718	ANO8	19	17,434,032	17,449,838	11,806	-	4	1_A375_shLS7_dtct_IncRNA:1:-2912,2_A375_shLS7_dtct_IncRNA:1:-2914,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183,2_A375_shLS7_dtct_IncRNA:1:-4183	-26, -2462, 66, -2264	upstream, upstream, upstream, upstream	1	1	29	34	2	2_A375_shLS7_dtct_IncRNA:1	37	Gene ANO8	TMEM16H, NAA1623, ANO8	anoctamin 8	NM_020959, ICT:02699.42.1, NCT02686403.1	1563549_at_at	NP_066180.1, EAW64596.1, EAW64595.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:84705	GTPBP3	19	17,448,356	17,453,540	5,184	+	4	1_A375_pNL7_minus_lncRNA::1::2913, 1_A375_pNL7_minus_lncRNA::1::2914, 2_A375_pNL97_plus_lncRNA::1::4192, 2_A375_pNL97_plus_lncRNA::1::4193	-2692, -276, -2660, -164	upstream, upstream, upstream, upstream	1	1	29	34	2	2_A375_pNL97_plus_lncRNA::1	37	Gene GTPBP3	GTPBG3, THDF1, FLJ14700, MSS1, FLJ17636, MTGP1, GTPBP3	GTP binding protein 3 (mitochondrial)	NM_133644, NM_032620, NM_001128855, hCT1951459.1, hCT2284063.0, hCT28666.3	1555062_s_at, 213835_x_at	NP_598399.2, NP_116009.2, NP_001122327.1, EAW84597.1, EAW84598.1, EAW84599.1
GeneID:100507535	LOC100507535	19	17,516,550	17,536,142	19,592	+	2	1_A375_pNL7_minus_lncRNA::1::2915, 2_A375_pNL97_plus_lncRNA::1::4194	14157, 13994	in gene, in gene	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100507535		hypothetical LOC100507535	XR_111639, XR_109577, XR_115249		
GeneID:93343	FAM125A	19	17,530,912	17,536,140	5,228	+	2	1_A375_pNL7_minus_lncRNA::1::2915, 2_A375_pNL97_plus_lncRNA::1::4194	-205, -368	upstream, upstream	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene FAM125A	CFBP, FAM125A, FLJ32495	family with sequence similarity 125, member A	NM_138401, hCT1951460.1, hCT28900.3	1556643_at, 227864_s_at	NP_612410.1, EAW84605.1, EAW84604.1
GeneID:376497	SLC27A1	19	17,581,300	17,616,977	35,677	+	5	1_A375_pNL7_minus_lncRNA::1::2916, 1_A375_pNL7_minus_lncRNA::1::2917, 2_A375_pNL97_plus_lncRNA::1::4195, 2_A375_pNL97_plus_lncRNA::1::4196, 2_A375_pNL97_plus_lncRNA::1::4197	5324, 41548, 5420, 37636, 41548	in gene, downstream, in gene, downstream, downstream	1	1	22	25.33	3	2_A375_pNL97_plus_lncRNA::1	35	Gene SLC27A1	MGC71751, ACSVL5, SLC27A1, FATP1, FLJ00336, FATP	solute carrier family 27 (fatty acid transporter), member 1	NM_198580, hCT2284070.0, hCT2284071.0, hCT2356628.0	226728_at	NP_940982.1, EAW84609.1, EAW84610.1, EAW84611.1
GeneID:100507551	LOC100507551	19	17,611,431	17,613,273	1,842	-	3	1_A375_pNL7_minus_lncRNA::1::2917, 2_A375_pNL97_plus_lncRNA::1::4196, 2_A375_pNL97_plus_lncRNA::1::4197	-9575, -5863, -9575	upstream, upstream, upstream	1	1	24.5	28.5	2	2_A375_pNL97_plus_lncRNA::1	35	Gene LOC100507551		hypothetical protein LOC100507551	XM_003118791		XP_003118839.1
GeneID:25796	PGLS	19	17,622,432	17,632,097	9,665	+	3	1_A375_pNL7_minus_lncRNA::1::2917, 2_A375_pNL97_plus_lncRNA::1::4196, 2_A375_pNL97_plus_lncRNA::1::4197	416, -3296, 416	in gene, upstream, in gene	1	1	24.5	28.5	2	2_A375_pNL97_plus_lncRNA::1	35	Gene PGLS	6PGL, PGLS	6-phosphogluconolactonase	NM_012088, hCT1816931.2, hCT2284073.0	1554316_at, 218387_s_at, 218388_at, 230699_at	NP_036220.1, EAW84614.1, EAW84613.1
GeneID:199786	FAM129C	19	17,634,110	17,664,648	30,538	+	4	1_A375_pNL7_minus_lncRNA::1::2918, 1_A375_pNL7_minus_lncRNA::1::2919, 2_A375_pNL97_plus_lncRNA::1::4198, 2_A375_pNL97_plus_lncRNA::1::4199	16258, 32194, 16066, 32178	in gene, downstream, in gene, downstream	1	1	28.5	27.5	2	1_A375_pNL7_minus_lncRNA::1	37	Gene FAM129C	BCNP1, FLJ39802, FAM129C	family with sequence similarity 129, member C	NM_173544, NM_001098524, hCT1966826.2, hCT2356496.0, hCT2356497.0, hCT2356498.0, hCT2356499.0, hCT2356500.0	1553369_at, 1569422_at, 230983_at	NP_775815.2, NP_001091994.1, EAW84615.1, EAW84617.1, EAW84618.1, EAW84620.1, EAW84616.1, EAW84619.1
GeneID:79709	GLT25D1	19	17,666,511	17,693,965	27,454	+	2	1_A375_pNL7_minus_lncRNA::1::2919, 2_A375_pNL97_plus_lncRNA::1::4199	-207, -223	upstream, upstream	1	1	37	36	1	1_A375_pNL7_minus_lncRNA::1	37	Gene GLT25D1	MGC117270, FLJ22329, GLT25D1	glycosyltransferase 25 domain containing 1	NM_024656, hCT2284076.0, hCT2284077.0, hCT2284079.0, hCT2284080.0	218473_s_at, 222644_s_at	NP_078932.2, EAW84624.1, EAW84621.1, EAW84622.1, EAW84623.1
GeneID:23025	UNC13A	19	17,712,137	17,799,008	86,871	-	7	1_A375_pNL7_minus_lncRNA::1::2920, 1_A375_pNL7_minus_lncRNA::1::2921, 1_A375_pNL7_minus_lncRNA::1::2922, 2_A375_pNL97_plus_lncRNA::1::4200, 2_A375_pNL97_plus_lncRNA::1::4201, 2_A375_pNL97_plus_lncRNA::1::4202, 2_A375_pNL97_plus_lncRNA::1::4203	7616, 6528, -224, 81952, 7688, 6448, -224	in gene, in gene, upstream, in gene, in gene, in gene, upstream	1	1	27.75	29.25	4	2_A375_pNL97_plus_lncRNA::1	44	Gene UNC13A	Munc13-1, UNC13A, KIAA1032	unc-13 homolog A (C. elegans)	NM_001080421	214817_at, 227453_at	NP_001073890.2
GeneID:55201	MAP1S	19	17,830,303	17,845,324	15,021	+	1	2_A375_pNL97_plus_lncRNA::1::4204	-199	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MAP1S	VCY2IP1, MAP8, C19orf5, MAP1S, BPY2IP1, MGC133087, VCY2IP-1, FLJ10669	microtubule-associated protein 1S	NM_018174, hCT2284083.0	218522_s_at	NP_060644.4, EAW84626.1
GeneID:6142	RPL18A	19	17,970,731	17,974,124	3,393	+	2	1_A375_pNL7_minus_lncRNA::1::2923, 2_A375_pNL97_plus_lncRNA::1::4205	-203, -203	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene RPL18A	RPL18A, L18A		NM_000980, hCT2284458.0, hCT28103.3		NP_000971.1, EAW84642.1, EAW84641.1
GeneID:26780	SNORA68	19	17,973,397	17,973,529	132	+	2	1_A375_pNL7_minus_lncRNA::1::2923, 2_A375_pNL97_plus_lncRNA::1::4205	-2869, -2869	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SNORA68	U68, RNU68, SNORA68	small nucleolar RNA, H/ACA box 68	NR_000012	1566402_at, 1566403_at	
GeneID:6528	SLC5A5	19	17,982,762	18,005,963	23,201	+	2	2_A375_pNL97_plus_lncRNA::1::4206, 1_A375_pNL7_minus_lncRNA::1::2924	17762, 17762	in gene, in gene	1	1	60	72	1	2_A375_pNL97_plus_lncRNA::1	72	Gene SLC5A5	SLC5A5, NIS, TDH1	solute carrier family 5 (sodium iodide symporter), member 5	NM_000453, hCT28100.1	211123_at	NP_000444.1, EAW84643.1
GeneID:115098	CCDC124	19	18,043,824	18,054,794	10,970	+	2	1_A375_pNL7_minus_lncRNA::1::2925, 2_A375_pNL97_plus_lncRNA::1::4207	-272, 16	upstream, in gene	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CCDC124	CCDC124	coiled-coil domain containing 124	NM_138442, NM_001136203, hCT2284466.0, hCT2284467.0	225453_x_at, 225454_at	NP_612451.1, NP_001129675.1, EAW84644.1, EAW84645.1
GeneID:5143	PDE4C	19	18,318,771	18,359,010	40,239	-	2	1_A375_pNL7_minus_lncRNA::1::2926, 2_A375_pNL97_plus_lncRNA::1::4208	14562, 14530	in gene, in gene	1	1	72	81	1	2_A375_pNL97_plus_lncRNA::1	81	Gene PDE4C	PDE4C, MGC126222, DPDE1	phosphodiesterase 4C, cAMP-specific	NM_001098818, NM_001098819, NM_000923, hCT1967948.0, hCT2285506.0, hCT2285509.0, hCT2356505.0, hCT77995.3	206791_s_at, 206792_x_at, 211818_s_at	NP_001092288.1, NP_001092289.1, NP_000914.2, EAW84675.1, EAW84676.1, EAW84678.1, EAW84677.1, EAW84679.1
GeneID:80726	KIAA1683	19	18,367,906	18,385,319	17,413	-	3	1_A375_pNL7_minus_lncRNA::1::2927, 2_A375_pNL97_plus_lncRNA::1::4209, 2_A375_pNL97_plus_lncRNA::1::4210	-7257, -553, -6041	upstream, upstream, upstream	1	1	19	17.67	3	1_A375_pNL7_minus_lncRNA::1	24	Gene KIAA1683	MGC131731, KIAA1683	KIAA1683	NM_025249, NM_001145304, NM_001145305, hCT1643826.2	223600_s_at, 232433_at	NP_079525.1, NP_001138776.1, NP_001138777.1, EAW84681.1
GeneID:3727	JUND	19	18,390,563	18,392,432	1,869	-	4	1_A375_pNL7_minus_lncRNA::1::2927, 2_A375_pNL97_plus_lncRNA::1::4209, 2_A375_pNL97_plus_lncRNA::1::4210, 2_A375_pNL97_plus_lncRNA::1::4211	-144, 6560, 1072, -10576	upstream, downstream, in gene, upstream	1	1	21.25	22.5	4	2_A375_pNL97_plus_lncRNA::1	37	Gene JUND	JUND, AP-1	jun D proto-oncogene	NM_005354	203751_x_at, 203752_s_at, 214326_x_at, 229117_s_at	NP_005345.3
GeneID:100422833	MIR3188	19	18,392,887	18,392,971	84	+	5	1_A375_pNL7_minus_lncRNA::1::2927, 1_A375_pNL7_minus_lncRNA::1::2928, 2_A375_pNL97_plus_lncRNA::1::4209, 2_A375_pNL97_plus_lncRNA::1::4210, 2_A375_pNL97_plus_lncRNA::1::4211	-311, 10057, -7015, -1527, 10121	upstream, downstream, upstream, upstream, downstream	1	1	21.25	22.5	4	2_A375_pNL97_plus_lncRNA::1	37	Gene MIR3188	MIR3188	microRNA 3188	NR_036155		
GeneID:25804	LSM4	19	18,417,717	18,434,001	16,284	-	3	1_A375_pNL7_minus_lncRNA::1::2929, 2_A375_pNL97_plus_lncRNA::1::4212, 2_A375_pNL97_plus_lncRNA::1::4213	-175, 21905, -5519	upstream, downstream, upstream	1	1	19.33	21.67	3	2_A375_pNL97_plus_lncRNA::1	24	Gene LSM4	YER112W, LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_012321, hCT2285487.1, hCT2348030.0, hCT2348031.0, hCT28083.2	202736_s_at, 202737_s_at, 212924_s_at	NP_036453.1, EAW84688.1, EAW84686.1, EAW84687.1, EAW84689.1
GeneID:54858	PGPEP1	19	18,451,408	18,480,763	29,355	+	1	1_A375_pNL7_minus_lncRNA::1::2930	33872	downstream	1	0	25	21	1	1_A375_pNL7_minus_lncRNA::1	25	Gene PGPEP1	PGP, FLJ20208, PGPEP1, MGC10812, Pcp, PGP-I, PGPI	pyroglutamyl-peptidase I	NM_017712, hCT2356613.0, hCT2356614.0, hCT28281.3	1555165_a_at, 219591_at, 223469_at, 237202_at	NP_060182.1, EAW84692.1, EAW84690.1, EAW84691.1
GeneID:170463	SSBP4	19	18,530,221	18,545,372	15,151	+	2	1_A375_pNL7_minus_lncRNA::1::2931, 2_A375_pNL97_plus_lncRNA::1::4214	-317, -1773	upstream, upstream	1	1	21	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SSBP4	MGC3181, SSBP4	single stranded DNA binding protein 4	NM_001009998, NM_032627, hCT2284518.0, hCT2284519.0, hCT2284520.0, hCT2284521.0, hCT2356501.0, hCT2356502.0	223226_x_at	NP_001009998.1, NP_116016.1, EAW84698.1, EAW84700.1, EAW84701.1, EAW84702.1, EAW84697.1, EAW84699.1
GeneID:8178	ELL	19	18,553,473	18,632,937	79,464	-	4	1_A375_pNL7_minus_lncRNA::1::2932, 1_A375_pNL7_minus_lncRNA::1::2933, 2_A375_pNL97_plus_lncRNA::1::4215, 2_A375_pNL97_plus_lncRNA::1::4216	1705, -119, 1673, -151	in gene, upstream, in gene, upstream	1	1	75.5	74	2	1_A375_pNL7_minus_lncRNA::1	125	Gene ELL	C19orf17, ELL1, DKFZp434I1916, MEN, ELL	elongation factor RNA polymerase II	NM_006532, hCT1642741.3, hCT2285465.0	1565254_s_at, 204095_s_at, 204096_s_at	NP_006523.1, EAW84708.1, EAW84707.1
GeneID:23770	FKBP8	19	18,642,568	18,654,383	11,815	-	2	1_A375_pNL7_minus_lncRNA::1::2933, 2_A375_pNL97_plus_lncRNA::1::4216	21327, 21295	downstream, downstream	1	1	125	120	1	1_A375_pNL7_minus_lncRNA::1	125	Gene FKBP8	FKBP8, FKBPr38, FKBP38	FK506 binding protein 8, 38kDa	NM_012181, hCT1815626.2, hCT2285458.0, hCT2285462.0	208255_s_at, 222007_s_at, 40850_at	NP_036313.3, EAW84710.1, EAW84709.1, EAW84711.1
GeneID:79036	C19orf50	19	18,668,572	18,680,197	11,625	+	1	2_A375_pNL97_plus_lncRNA::1::4217	13968	downstream	0	1	23	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene C19orf50	C19orf50, DKFZp686B1036, MSTP096, FLJ25480, MGC2749, MST096, FLJ43375	chromosome 19 open reading frame 50	NM_001171948, NM_001171949, NM_024069, hCT2284526.0, hCT2356612.0, hCT28280.2	200076_s_at	NP_001165419.1, NP_001165420.1, NP_076974.2, EAW84712.1, EAW84713.1, EAW84714.1
GeneID:7311	UBA52	19	18,682,614	18,688,270	5,656	+	1	2_A375_pNL97_plus_lncRNA::1::4217	-54	upstream	0	1	23	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene UBA52	CEP52, MGC126881, L40, HUBCEP52, MGC126879, MGC57125, RPL40, UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	NM_001033930, NM_003333, hCT1686626.3, hCT1815617.2, hCT1967961.1, hCT1967962.1	221700_s_at	NP_001029102.1, NP_003324.1, EAW84715.1, EAW84716.1, EAW84717.1, EAW84718.1
GeneID:55049	C19orf60	19	18,699,495	18,703,147	3,652	+	2	1_A375_pNL7_minus_lncRNA::1::2934, 2_A375_pNL97_plus_lncRNA::1::4218	89, 121	in gene, in gene	1	1	69	76	1	2_A375_pNL97_plus_lncRNA::1	76	Gene C19orf60	FLJ34606, FLJ20850, C19orf60, FLJ37391, FLJ30108	chromosome 19 open reading frame 60	NM_001100419, NM_001100418, hCT1967964.1, hCT1967965.1, hCT2284534.0, hCT2356620.0, hCT28284.3	218958_at, 51200_at	NP_001093889.1, NP_001093888.1, EAW84719.1, EAW84720.1, EAW84721.1, EAW84722.1, EAW84723.1
GeneID:9244	CRLF1	19	18,704,035	18,717,660	13,625	-	2	1_A375_pNL7_minus_lncRNA::1::2934, 2_A375_pNL97_plus_lncRNA::1::4218	18076, 18044	downstream, downstream	1	1	69	76	1	2_A375_pNL97_plus_lncRNA::1	76	Gene CRLF1	CLF-1, CISS, NR6, CRLF1, zcytor5, CLF, CISS1	cytokine receptor-like factor 1	NM_004750, hCT2285451.0, hCT28277.2	206315_at	NP_004741.1, EAW84724.1, EAW84725.1
GeneID:55295	KLHL26	19	18,747,838	18,781,302	33,464	+	1	2_A375_pNL97_plus_lncRNA::1::4219	23506	in gene	0	1	31	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene KLHL26	KLHL26, FLJ11078	kelch-like 26 (Drosophila)	NM_018316, hCT2284539.0, hCT28279.2	219354_at	NP_060786.1, EAW84728.1, EAW84729.1
GeneID:5976	UPF1	19	18,942,744	18,979,039	36,295	+	2	1_A375_pNL7_minus_lncRNA::1::2935, 2_A375_pNL97_plus_lncRNA::1::4220	168, 72	in gene, in gene	1	1	27	15	1	1_A375_pNL7_minus_lncRNA::1	27	Gene UPF1	RENT1, UPF1, KIAA0221, HUPF1, FLJ46894, pNORF1, NORF1, FLJ43809	UPF1 regulator of nonsense transcripts homolog (yeast)	NM_002911, hCT2284544.0, hCT2284545.0, hCT2284546.0, hCT2356572.0, hCT28272.3	208947_s_at, 211168_s_at	NP_002902.2, EAW84740.1, EAW84738.1, EAW84739.1, EAW84741.1, EAW84742.1
GeneID:11316	COPE	19	19,010,323	19,030,199	19,876	-	2	1_A375_pNL7_minus_lncRNA::1::2936, 2_A375_pNL97_plus_lncRNA::1::4221	-273, -89	upstream, upstream	1	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene COPE	FLJ13241, COPE, epsilon-COP	coatomer protein complex, subunit epsilon	NM_007263, NM_199442, NM_199444, hCT2285430.0, hCT2285431.1, hCT2285432.1, hCT2285433.1, hCT2348351.0, hCT2356474.0, hCT2356475.0, hCT2356476.0, hCT2356477.0, hCT2356478.0	201264_at, 220469_at	NP_009194.2, NP_955474.1, NP_955476.1, EAW84748.1, EAW84750.1, EAW84757.1, EAW84749.1, EAW84751.1, EAW84752.1, EAW84753.1, EAW84754.1, EAW84755.1, EAW84756.1
GeneID:54555	DDX49	19	19,030,484	19,039,442	8,958	+	2	1_A375_pNL7_minus_lncRNA::1::2936, 2_A375_pNL97_plus_lncRNA::1::4221	-12, -196	upstream, upstream	1	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene DDX49	DDX49, FLJ10432, R27090_2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	NM_019070, NR_033677, hCT2284551.0, hCT2356607.0, hCT2356608.0, hCT29819.3	210811_s_at, 232915_at, 31807_at	NP_061943.2, EAW84760.1, EAW84758.1, EAW84759.1, EAW84761.1
GeneID:9454	HOMER3	19	19,040,010	19,052,041	12,031	-	2	1_A375_pNL7_minus_lncRNA::1::2936, 2_A375_pNL97_plus_lncRNA::1::4221	21569, 21753	downstream, downstream	1	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene HOMER3	VESL3, HOMER-3, HOMER3	homer homolog 3 (Drosophila)	NM_004838, NM_001145721, NM_001145722, NM_001145724, NR_027297, hCT1967950.1, hCT2285425.0, hCT2285426.0, hCT2285427.0	204647_at, 215489_x_at, 222222_s_at	NP_004829.3, NP_001139193.1, NP_001139194.1, NP_001139196.1, EAW84762.1, EAW84765.1, EAW84763.1, EAW84764.1
GeneID:10147	SFRS14	19	19,101,697	19,144,380	42,683	-	2	1_A375_pNL7_minus_lncRNA::1::2937, 2_A375_pNL97_plus_lncRNA::1::4222	-132, -116	upstream, upstream	1	1	26	24	1	1_A375_pNL7_minus_lncRNA::1	26	Gene SFRS14	SFRS14, FLJ21855, SUGP2, DKFZp686M2322, DKFZp779L2418	SURP and G patch domain containing 2	NM_014884, NM_001017392, hCT1967974.1, hCT2285373.0, hCT2285375.0, hCT2356507.0, hCT2356508.0, hCT2356509.0, hCT2356510.0, hCT29823.3	212000_at, 212001_at, 213505_s_at, 214092_x_at, 64371_at	NP_055699.2, NP_001017392.2, EAW84766.1, EAW84767.1, EAW84769.1, EAW84773.1, EAW84768.1, EAW84770.1, EAW84771.1, EAW84772.1
GeneID:93436	ARMC6	19	19,144,471	19,168,980	24,509	+	3	1_A375_pNL7_minus_lncRNA::1::2937, 2_A375_pNL97_plus_lncRNA::1::4222, 2_A375_pNL97_plus_lncRNA::1::4223	41, 25, 30185	in gene, in gene, downstream	1	1	21.5	23	2	1_A375_pNL7_minus_lncRNA::1	26	Gene ARMC6	ARMC6, R30923_1, MGC19595	armadillo repeat containing 6	NM_033415, hCT2284180.0, hCT29824.2	221758_at	NP_219483.1, EAW84776.1, EAW84775.1
GeneID:284439	SLC25A42	19	19,174,803	19,223,704	48,901	+	1	2_A375_pNL97_plus_lncRNA::1::4223	-147	upstream	0	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SLC25A42	SLC25A42, MGC26694	solute carrier family 25, member 42	NM_178526, hCT2284182.0, hCT2356559.0, hCT29807.2	214029_at, 226737_at, 228921_at, 242274_x_at	NP_848621.2, EAW84779.1, EAW84777.1, EAW84778.1
GeneID:4207	LOC729991-MEF2B	19	19,256,376	19,303,400	47,024	-	2	1_A375_pNL7_minus_lncRNA::1::2938, 2_A375_pNL97_plus_lncRNA::1::4224	392, 360	in gene, in gene	1	1	54	49	1	1_A375_pNL7_minus_lncRNA::1	54	Gene LOC729991-MEF2B	LOC729991-MEF2B, MEF2B, MEF2BNB-MEF2B	LOC729991-MEF2B readthrough	NM_005919, NR_027307, NR_027308, hCT2285362.0, hCT2285363.0, hCT2285364.0, hCT2285365.0, hCT2356537.0, hCT29802.3	1553978_at, 205124_at, 209926_at	NP_005910.1, EAW84792.1, EAW84788.1, EAW84789.1, EAW84790.1, EAW84793.1, EAW84791.1
GeneID:729991	LOC729991	19	19,287,713	19,303,400	15,687	-	2	1_A375_pNL7_minus_lncRNA::1::2938, 2_A375_pNL97_plus_lncRNA::1::4224	392, 360	in gene, in gene	1	1	54	49	1	1_A375_pNL7_minus_lncRNA::1	54	Gene LOC729991	MGC189732, MEF2BNB, AK128256, MGC189763, FLJ32599, FLJ46391	MEF2B neighbor	NM_001145783, NM_001145784		NP_001139255.1, NP_001139256.1
GeneID:8625	RFXANK	19	19,303,008	19,312,678	9,670	+	4	1_A375_pNL7_minus_lncRNA::1::2938, 1_A375_pNL7_minus_lncRNA::1::2939, 2_A375_pNL97_plus_lncRNA::1::4224, 2_A375_pNL97_plus_lncRNA::1::4225	0, 11296, 32, 11296	in gene, downstream, in gene, downstream	1	1	39	38	2	1_A375_pNL7_minus_lncRNA::1	54	Gene RFXANK	MGC138628, RFX-B, RFXANK, ANKRA1, BLS, F14150_1	regulatory factor X-associated ankyrin-containing protein	NM_003721, NM_134440, hCT1967973.1, hCT2284184.0, hCT2284185.0, hCT2284187.0, hCT29803.2	202758_s_at	NP_003712.1, NP_604389.1, EAW84795.1, EAW84796.1, EAW84798.1, EAW84799.1, EAW84797.1
GeneID:126382	NR2C2AP	19	19,312,224	19,314,238	2,014	-	4	1_A375_pNL7_minus_lncRNA::1::2938, 1_A375_pNL7_minus_lncRNA::1::2939, 2_A375_pNL97_plus_lncRNA::1::4224, 2_A375_pNL97_plus_lncRNA::1::4225	11230, -66, 11198, -66	downstream, upstream, downstream, upstream	1	1	39	38	2	1_A375_pNL7_minus_lncRNA::1	54	Gene NR2C2AP	NR2C2AP, TRA16	nuclear receptor 2C2-associated protein	NM_176880	226839_at	NP_795361.1
GeneID:1463	NCAN	19	19,322,782	19,363,061	40,279	+	3	1_A375_pNL7_minus_lncRNA::1::2939, 1_A375_pNL7_minus_lncRNA::1::2940, 2_A375_pNL97_plus_lncRNA::1::4225	-8478, 3074, -8478	upstream, in gene, upstream	1	1	25.5	25	2	2_A375_pNL97_plus_lncRNA::1	27	Gene NCAN	FLJ44681, CSPG3, NCAN	neurocan	NM_004386, hCT2284189.0, hCT29801.2	205143_at	NP_004377.2, EAW84802.1, EAW84801.1
GeneID:57794	SF4	19	19,387,322	19,431,307	43,985	-	2	1_A375_pNL7_minus_lncRNA::1::2941, 2_A375_pNL97_plus_lncRNA::1::4226	-85, -85	upstream, upstream	1	1	15	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SF4	DKFZp434E2216, SUGP1, RBP, F23858, SF4	SURP and G patch domain containing 1	NM_172231, hCT2285346.1, hCT2285348.1, hCT2285349.1, hCT2356611.0, hCT29821.3	209547_s_at, 215004_s_at	NP_757386.2, EAW84810.1, EAW84808.1, EAW84809.1, EAW84811.1, EAW84812.1
GeneID:23383	KIAA0892	19	19,431,630	19,469,563	37,933	+	2	1_A375_pNL7_minus_lncRNA::1::2941, 2_A375_pNL97_plus_lncRNA::1::4226	-238, -238	upstream, upstream	1	1	15	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene KIAA0892	MAU2L, MGC75361, SCC4, KIAA0892, MAU2, mau-2	KIAA0892	NM_015329, hCT1964195.1, hCT2284192.0, hCT2284193.0, hCT2284195.0	212505_s_at, 216926_s_at, 217652_at, 227465_at	NP_056144.3, EAW84817.1, EAW84814.1, EAW84815.1, EAW84816.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:54815	GATAD2A	19	19,496,642	19,619,741	123,099	+	3	1_A375_pNL7_minus_lncRNA::1::2942, 2_A375_pNL97_plus_lncRNA::1::4227, 2_A375_pNL97_plus_lncRNA::1::4228	19630, 19630, 130430	in gene, in gene, downstream	1	1	26.5	30.5	2	1_A375_pNL7_minus_lncRNA::1	33	Gene GATAD2A	FLJ21017, GATAD2A, p66alpha, FLJ20085	GATA zinc finger domain containing 2A	NM_017660, hCT2284195.0, hCT2284198.0, hCT2284199.0, hCT2284200.0, hCT2284202.0	218131_s_at, 222526_at, 228166_s_at, 234294_x_at, 236932_s_at, 236324_at	NP_060130.3, EAW84623.1, EAW84619.1, EAW84620.1, EAW84621.1, EAW84622.1
GeneID:83983	TSSK6	19	19,625,026	19,626,469	1,441	-	1	2_A375_pNL97_plus_lncRNA::1::4228	-603	upstream	0	1	20	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene TSSK6	FKSG82, TSSK6, SSTK, FLJ24002, CT72, TSSK4	testis-specific serine kinase 6	NM_032037, hCT1640514.2, hCT2285333.0	224409_s_at, 230989_s_at	NP_114426.1, EAW84624.1, EAW84625.1
GeneID:51079	NDUFA13	19	19,627,019	19,639,013	11,994	+	1	2_A375_pNL97_plus_lncRNA::1::4228	53	in gene	0	1	20	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene NDUFA13	CGI-39, GRIM-19, FLJ56045, GRIM19, CDA016, B16.6, FLJ59191, NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	NM_015965, hCT29604.2	220864_s_at	NP_057049.5, EAW84626.1
GeneID:80714	PBX4	19	19,672,522	19,729,439	56,917	-	2	1_A375_pNL7_minus_lncRNA::1::2943, 2_A375_pNL97_plus_lncRNA::1::4229	27007, 27231	in gene, in gene	1	1	23	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene PBX4	PBX4		NM_025245, hCT2356605.0, hCT29815.2	230536_at	NP_079521.1, EAW84634.1, EAW84635.1
GeneID:284440	LOC284440	19	19,867,180	19,887,222	20,042	-	2	1_A375_pNL7_minus_lncRNA::1::2944, 2_A375_pNL97_plus_lncRNA::1::4230	-42, -234	upstream, upstream	1	1	32	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene LOC284440	MGC39821, FLJ12356	hypothetical LOC284440	NR_026956	1555363_s_at, 1569318_at	
GeneID:91120	ZNF682	19	20,115,227	20,150,277	35,050	-	1	2_A375_pNL97_plus_lncRNA::1::4231	5	in gene	0	1	18	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ZNF682	BC39498_3, FLJ90362, ZNF682	zinc finger protein 682	NM_033196, NM_001077349, hCT1959888.1, hCT2283180.0, hCT27970.3	216468_s_at, 242915_at	NP_149973.1, NP_001070817.1, EAW84868.1, EAW84869.1, EAW84870.1
GeneID:80264	ZNF430	19	21,203,426	21,242,852	39,426	+	1	2_A375_pNL97_plus_lncRNA::1::4234	222	in gene	0	1	11	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ZNF430	FLJ13659, ZNF430, DKFZp762K012, MGC133232	zinc finger protein 430	NM_025189, NM_001172671, hCT28492.3	206829_x_at, 238614_x_at	NP_079465.3, NP_001166142.1, EAW84884.1
GeneID:7562	ZNF708	19	21,473,963	21,512,212	38,249	-	1	1_A375_pNL7_minus_lncRNA::1::2946	180	in gene	1	0	21	14	1	1_A375_pNL7_minus_lncRNA::1	21	Gene ZNF708	FLJ16755, ZNF15, ZNF708, FLJ46310, ZNF15L1, KOX8, DKFZp686L10267	zinc finger protein 708	NM_021269, hCT2283892.0, hCT2356625.0	239482_x_at	NP_067092.2, EAW84892.1, EAW84891.1
GeneID:163227	ZNF100	19	21,906,843	21,950,430	43,587	-	2	1_A375_pNL7_minus_lncRNA::1::2947, 2_A375_pNL97_plus_lncRNA::1::4235	126, 446	in gene, in gene	1	1	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ZNF100	FLJ44587, ZNF100	zinc finger protein 100	NM_173531, hCT1815314.2, hCT2283885.1	1569637_at, 236791_at	NP_775802.2, EAW84905.1, EAW84906.1
GeneID:148198	ZNF98	19	22,573,899	22,605,148	31,249	-	1	2_A375_pNL97_plus_lncRNA::1::4236	-100	upstream	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ZNF98	ZNF98, F7175, MGC129634, ZNF739	zinc finger protein 98 (F7175)	NM_001098626	215532_x_at	NP_001092096.1
GeneID:100132815	LOC100132815	19	23,437,855	23,457,032	19,177	-	1	2_A375_pNL97_plus_lncRNA::1::4237	23736	downstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100132815	FLJ12978	hypothetical LOC100132815	XR_111844, XR_109587, XR_115256		
GeneID:148213	ZNF681	19	23,921,997	23,941,693	19,696	-	2	1_A375_pNL7_minus_lncRNA::1::2948, 2_A375_pNL97_plus_lncRNA::1::4238	-4115, -4387	upstream, upstream	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZNF681	ZNF681, FLJ31526	zinc finger protein 681	NM_138286, hCT1838364.2, hCT2284018.0, hCT2356532.0		NP_612143.2, EAW84946.1, EAW84947.1, EAW84949.1
GeneID:730087	ZNF726	19	24,097,684	24,106,517	8,833	+	1	2_A375_pNL97_plus_lncRNA::1::4240	268	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF726	ZNF726	zinc finger protein 726	NM_001190829		NP_001177758.1
GeneID:148189	LOC148189	19	28,281,401	28,284,848	3,447	-	1	2_A375_pNL97_plus_lncRNA::1::4242	-528	upstream	0	1	17	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC148189		hypothetical LOC148189	NR_027301	1558256_at, 232281_at, 242663_at	
GeneID:100506694	LOC100506694	19	28,284,375	28,296,680	12,305	+	1	2_A375_pNL97_plus_lncRNA::1::4242	1001	in gene	0	1	17	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC100506694		hypothetical LOC100506694	XR_109507		
GeneID:10775	POP4	19	30,097,170	30,108,162	10,992	+	1	2_A375_pNL97_plus_lncRNA::1::4244	-194	upstream	0	1	10	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene POP4	POP4, RPP29	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)	NM_006627, NR_027368	202868_s_at, 227583_at	NP_006618.1
GeneID:22847	ZNF507	19	32,836,514	32,878,573	42,059	+	1	2_A375_pNL97_plus_lncRNA::1::4246	201	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ZNF507	ZNF507	zinc finger protein 507	NM_014910, NM_001136156	206225_at, 226327_at, 235618_at	NP_055725.2, NP_001129628.1
GeneID:9141	PDCD5	19	33,072,104	33,078,331	6,227	+	2	1_A375_pNL7_minus_lncRNA::1::2952, 2_A375_pNL97_plus_lncRNA::1::4247	344, -72	in gene, upstream	1	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PDCD5	MGC9294, PDCD5, FLJ42784, TFAR19	programmed cell death 5	NM_004708	219275_at, 227751_at	NP_004699.1
GeneID:390916	NUDT19	19	33,182,867	33,204,702	21,835	+	1	1_A375_pNL7_minus_lncRNA::1::2953	-115	upstream	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene NUDT19	RP2, NUDT19	nudix (nucleoside diphosphate linked moiety X)-type motif 19	NM_001105570		NP_001099040.1
GeneID:84902	CCDC123	19	33,369,904	33,462,869	92,965	-	2	1_A375_pNL7_minus_lncRNA::1::2954, 2_A375_pNL97_plus_lncRNA::1::4248	-123, -139	upstream, upstream	1	1	33	56	1	2_A375_pNL97_plus_lncRNA::1	56	Gene CCDC123	FLJ14640, CCDC123	coiled-coil domain containing 123	NM_032816	1553732_s_at, 1554512_a_at, 1554513_s_at, 1560599_a_at, 1563919_a_at, 232106_s_at	NP_116205.3
GeneID:91442	C19orf40	19	33,463,148	33,467,974	4,826	+	2	1_A375_pNL7_minus_lncRNA::1::2954, 2_A375_pNL97_plus_lncRNA::1::4248	-156, -140	upstream, upstream	1	1	33	56	1	2_A375_pNL97_plus_lncRNA::1	56	Gene C19orf40	FLJ45828, MGC32020, FAAP24, C19orf40	chromosome 19 open reading frame 40	NM_152266	214816_x_at	NP_689479.1
GeneID:85415	RHPN2	19	33,469,498	33,555,824	86,326	-	2	1_A375_pNL7_minus_lncRNA::1::2954, 2_A375_pNL97_plus_lncRNA::1::4248	92832, 92816	downstream, downstream	1	1	33	56	1	2_A375_pNL97_plus_lncRNA::1	56	Gene RHPN2	P76RBE, RHPN2, RHOBP	rhophilin, Rho GTPase binding protein 2	NM_033103	227196_at	NP_149094.3
GeneID:126248	WDR88	19	33,622,998	33,666,705	43,707	+	2	1_A375_pNL7_minus_lncRNA::1::2955, 2_A375_pNL97_plus_lncRNA::1::4249	45322, 45354	downstream, downstream	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene WDR88	WDR88, PQWD	WD repeat domain 88	NM_173479	1552452_at, 1552453_a_at	NP_775750.3
GeneID:56301	SLC7A10	19	33,699,570	33,716,756	17,186	-	1	2_A375_pNL97_plus_lncRNA::1::4250	6324	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SLC7A10	asc-1, FLJ20839, HASC-1, SLC7A10	solute carrier family 7, (neutral amino acid transporter, y+ system) member 10	NM_019849	220868_s_at	NP_062823.1
GeneID:64377	CHST8	19	34,112,861	34,264,414	151,553	+	4	1_A375_pNL7_minus_lncRNA::1::2956, 2_A375_pNL97_plus_lncRNA::1::4251, 2_A375_pNL97_plus_lncRNA::1::4252, 2_A375_pNL97_plus_lncRNA::1::4253	146019, 62387, 119043, 145966	in gene, in gene, in gene, in gene	1	1	18.33	21.33	3	1_A375_pNL7_minus_lncRNA::1	24	Gene CHST8	CHST8, GALNAC4ST1, GalNAc4ST	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	NM_022467, NM_001127895, NM_001127896	221065_s_at	NP_071912.2, NP_001121367.1, NP_001121368.1
GeneID:79047	KCTD15	19	34,287,751	34,306,666	18,915	+	1	2_A375_pNL97_plus_lncRNA::1::4254	23737	downstream	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene KCTD15	MGC25497, MGC2628, KCTD15	potassium channel tetramerisation domain containing 15	NM_024076, NM_001129994, NM_001129995	218553_s_at, 222664_at, 222665_at, 226683_s_at, 229683_s_at	NP_076981.2, NP_001123466.1, NP_001123467.1
GeneID:26065	LSM14A	19	34,663,352	34,720,420	57,068	+	2	1_A375_pNL7_minus_lncRNA::1::2958, 2_A375_pNL97_plus_lncRNA::1::4255	60776, -248	downstream, upstream	1	1	16	16	2	2_A375_pNL97_plus_lncRNA::1	19	Gene LSM14A	FAM61A, C19orf13, DKFZp434D1335, RAP55A, LSM14A, RAP55	LSM14A, SCD6 homolog A (S. cerevisiae)	NM_015578, NM_001114093	212131_at, 212132_at, 222099_s_at	NP_056393.2, NP_001107565.1
GeneID:9710	KIAA0355	19	34,745,456	34,846,471	101,015	+	1	2_A375_pNL97_plus_lncRNA::1::4256	104764	downstream	0	1	19	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene KIAA0355	KIAA0355		NM_014686	203288_at	NP_055501.2
GeneID:2821	GPI	19	34,855,645	34,893,318	37,673	+	2	2_A375_pNL97_plus_lncRNA::1::4256, 2_A375_pNL97_plus_lncRNA::1::4257	-5405, 39715	upstream, downstream	0	1	16.5	19	2	2_A375_pNL97_plus_lncRNA::1	19	Gene GPI	SA36, GNPI, DKFZp686C13233, AMF, GPI, PGI, PHI, NLK	glucose phosphate isomerase	NM_000175, NM_001184722	208308_s_at	NP_000166.2, NP_001171651.1
GeneID:84306	PDCD2L	19	34,895,303	34,917,073	21,770	+	1	2_A375_pNL97_plus_lncRNA::1::4257	57	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PDCD2L	MGC13096, PDCD2L	programmed cell death 2-like	NM_032346	224467_s_at	NP_115722.1
GeneID:55900	ZNF302	19	35,168,567	35,177,302	8,735	+	2	1_A375_pNL7_minus_lncRNA::1::2959, 2_A375_pNL97_plus_lncRNA::1::4258	-599, -167	upstream, upstream	1	1	20	20	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ZNF302	MST154, HSD16, ZNF140L, MSTP154, ZNF327, ZNF135L, ZNF302	zinc finger protein 302	NM_018443, NM_001012320	218490_s_at, 228392_at, 228393_s_at	NP_060913.2, NP_001012320.1
GeneID:148103	ZNF599	19	35,248,979	35,264,134	15,155	-	1	2_A375_pNL97_plus_lncRNA::1::4259	-26	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF599	ZNF599, FLJ50920	zinc finger protein 599	NM_001007248	1558390_at, 1558391_s_at, 228093_at, 243747_at	NP_001007249.1
GeneID:100128675	LOC100128675	19	35,549,963	35,597,208	47,245	-	3	1_A375_pNL7_minus_lncRNA::1::2960, 2_A375_pNL97_plus_lncRNA::1::4260, 2_A375_pNL97_plus_lncRNA::1::4261	466, 376, -5558	in gene, in gene, upstream	1	1	13.5	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100128675	FLJ42709	hypothetical LOC100128675	NR_024561, NR_024562		
GeneID:5349	FXYD3	19	35,606,732	35,615,228	8,496	+	3	1_A375_pNL7_minus_lncRNA::1::2960, 2_A375_pNL97_plus_lncRNA::1::4260, 2_A375_pNL97_plus_lncRNA::1::4261	-10012, -9900, -636	upstream, upstream, upstream	1	1	13.5	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene FXYD3	MAT8, FXYD3, PLML, MAT-8, MGC111076	FXYD domain containing ion transport regulator 3	NM_005971, NM_021910, NM_001136007, NM_001136008, NM_001136009, NM_001136010, NM_001136011, NM_001136012	202488_s_at, 202489_s_at	NP_005962.1, NP_068710.1, NP_001129479.1, NP_001129480.1, NP_001129481.1, NP_001129482.1, NP_001129483.1, NP_001129484.1
GeneID:163175	LGI4	19	35,615,417	35,626,178	10,761	+	1	2_A375_pNL97_plus_lncRNA::1::4261	20062	downstream	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LGI4	LGIL3, LGI4	leucine-rich repeat LGI family, member 4	NM_139284	227821_at, 242670_at	NP_644813.1
GeneID:4099	MAG	19	35,783,038	35,804,707	21,669	+	1	1_A375_pNL7_minus_lncRNA::1::2961	26994	downstream	1	0	25	16	1	1_A375_pNL7_minus_lncRNA::1	25	Gene MAG	SIGLEC4A, GMA, MAG, SIGLEC-4A, S-MAG	myelin associated glycoprotein	NM_002361, NM_080600	204581_at, 217422_s_at, 35521_at	NP_002352.1, NP_542167.1
GeneID:933	CD22	19	35,820,072	35,838,264	18,192	+	1	1_A375_pNL7_minus_lncRNA::1::2961	-10040	upstream	1	0	25	16	1	1_A375_pNL7_minus_lncRNA::1	25	Gene CD22	MGC130020, SIGLEC2, CD22, SIGLEC-2, FLJ22814	CD22 molecule	NM_001185099, NM_001185100, NM_001185101, NM_001771		NP_001172028.1, NP_001172029.1, NP_001762.2, NP_001172030.1
GeneID:23354	HAUS5	19	36,103,646	36,116,251	12,605	+	4	1_A375_pNL7_minus_lncRNA::1::2962, 1_A375_pNL7_minus_lncRNA::1::2963, 2_A375_pNL97_plus_lncRNA::1::4263, 2_A375_pNL97_plus_lncRNA::1::4264	34, 16290, 2, 16290	in gene, downstream, in gene, downstream	1	1	22.5	27	2	2_A375_pNL97_plus_lncRNA::1	29	Gene HAUS5	HAUS5, dgt5, KIAA0841	HAUS augmin-like complex, subunit 5	NM_015302	213053_at	NP_056117.1
GeneID:79171	RBM42	19	36,119,980	36,128,587	8,607	+	2	1_A375_pNL7_minus_lncRNA::1::2963, 2_A375_pNL97_plus_lncRNA::1::4264	-44, -44	upstream, upstream	1	1	26	25	1	1_A375_pNL7_minus_lncRNA::1	26	Gene RBM42	RBM42, MGC10433	RNA binding motif protein 42	NM_024321	205740_s_at	NP_077297.2
GeneID:27033	ZBTB32	19	36,203,830	36,207,940	4,110	+	3	1_A375_pNL7_minus_lncRNA::1::2965, 2_A375_pNL97_plus_lncRNA::1::4265, 2_A375_pNL97_plus_lncRNA::1::4266	4586, -10486, 4543	downstream, upstream, downstream	1	1	21	21.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene ZBTB32	FAZF, ZBTB32, ZNF538, TZFP, FAXF, Rog	zinc finger and BTB domain containing 32	NM_014383	220118_at	NP_055198.1
GeneID:9757	MLL4	19	36,208,921	36,229,779	20,858	+	2	1_A375_pNL7_minus_lncRNA::1::2965, 2_A375_pNL97_plus_lncRNA::1::4266	-505, -548	upstream, upstream	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MLL4	TRX2, WBP7, KIAA0304, MLL2, HRX2	myeloid/lymphoid or mixed-lineage leukemia 4	NM_014727	203419_at, 217069_at	NP_055542.1
GeneID:4868	NPHS1	19	36,316,274	36,342,895	26,621	-	2	1_A375_pNL7_minus_lncRNA::1::2966, 2_A375_pNL97_plus_lncRNA::1::4267	23119, 23087	in gene, in gene	1	1	30	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene NPHS1	NPHS1, CNF, NPHN	nephrosis 1, congenital, Finnish type (nephrin)	NM_004646	207673_at	NP_004637.1
GeneID:333	APLP1	19	36,359,401	36,370,699	11,298	+	2	1_A375_pNL7_minus_lncRNA::1::2967, 2_A375_pNL97_plus_lncRNA::1::4268	11479, 11479	downstream, downstream	1	1	35	41	1	2_A375_pNL97_plus_lncRNA::1	41	Gene APLP1	APLP, APLP1	amyloid beta (A4) precursor-like protein 1	NM_001024807, NM_005166	209462_at	NP_001019978.1, NP_005157.1
GeneID:84807	NFKBID	19	36,379,143	36,391,552	12,409	-	2	1_A375_pNL7_minus_lncRNA::1::2967, 2_A375_pNL97_plus_lncRNA::1::4268	20672, 20672	downstream, downstream	1	1	35	41	1	2_A375_pNL97_plus_lncRNA::1	41	Gene NFKBID	TA-NFKBH, MGC11314, IkappaBNS, MGC149503, NFKBID	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	NM_139239	1553042_a_at, 230052_s_at, 241889_at	NP_640332.1
GeneID:644096	SDHAF1	19	36,486,090	36,487,220	1,130	+	1	2_A375_pNL97_plus_lncRNA::1::4271	-10	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SDHAF1	SDHAF1		NM_001042631	221855_at, 44669_at	NP_001036096.1
GeneID:163183	C19orf46	19	36,494,002	36,499,672	5,670	-	2	1_A375_pNL7_minus_lncRNA::1::2969, 2_A375_pNL97_plus_lncRNA::1::4271	-659, 13592	upstream, downstream	1	1	15	16.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene C19orf46	FLJ36445, C19orf46	chromosome 19 open reading frame 46	NM_001039876	235515_at	NP_001034965.1
GeneID:84964	ALKBH6	19	36,500,022	36,505,141	5,119	-	1	1_A375_pNL7_minus_lncRNA::1::2969	4810	in gene	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene ALKBH6	ALKBH6, MGC15677, ABH6	alkB, alkylation repair homolog 6 (E. coli)	NM_198867, NM_032878	225969_at	NP_942567.1, NP_116267.3
GeneID:25999	CLIP3	19	36,505,563	36,523,775	18,212	-	1	1_A375_pNL7_minus_lncRNA::1::2969	23444	downstream	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene CLIP3	CLIP3, FLJ33413, DKFZp586N1922, CLIPR-59, RSNL1, CLIPR59	CAP-GLY domain containing linker protein 3	NM_015526	212358_at, 235243_at	NP_056341.1
GeneID:199745	THAP8	19	36,525,887	36,545,664	19,777	-	1	2_A375_pNL97_plus_lncRNA::1::4272	464	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene THAP8	THAP8, FLJ32891	THAP domain containing 8	NM_152658	226500_at	NP_689871.1
GeneID:284403	WDR62	19	36,545,783	36,596,012	50,229	+	2	1_A375_pNL7_minus_lncRNA::1::2970, 2_A375_pNL97_plus_lncRNA::1::4272	59945, -583	downstream, upstream	1	1	19	16.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene WDR62	C19orf14, DKFZp434J046, MGC166976, DKFZp686G1024, FLJ33298, WDR62, MCPH2	WD repeat domain 62	NM_001083961, NM_173636	1553123_at, 1553125_x_at, 215218_s_at	NP_001077430.1, NP_775907.4
GeneID:728361	LOC728361	19	36,602,105	36,604,563	2,458	+	1	1_A375_pNL7_minus_lncRNA::1::2970	3623	downstream	1	0	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene LOC728361		ovo-like 3 (Drosophila)	XM_001717165, XM_001715091		XP_001717217.2, XP_001715143.3
GeneID:5438	POLR2I	19	36,604,611	36,606,206	1,595	-	1	1_A375_pNL7_minus_lncRNA::1::2970	478	in gene	1	0	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene POLR2I	POLR2I, hRPB14.5, RPB9	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa	NM_006233		NP_006224.1
GeneID:1155	TBCB	19	36,605,888	36,616,849	10,961	+	1	1_A375_pNL7_minus_lncRNA::1::2970	-160	upstream	1	0	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene TBCB	CKAP1, CG22, TBCB, MGC14625, CKAPI	tubulin folding cofactor B	NM_001281	201804_x_at, 211759_x_at, 216194_s_at	NP_001272.2
GeneID:826	CAPNS1	19	36,630,918	36,641,255	10,337	+	2	1_A375_pNL7_minus_lncRNA::1::2971, 2_A375_pNL97_plus_lncRNA::1::4273	-38, -70	upstream, upstream	1	1	38	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene CAPNS1	CANPS, CSS1, CAPN4, CAPNS1, CALPAIN4, CANP, 30K, CDPS	calpain, small subunit 1	NM_001003962, NM_001749	200001_at	NP_001003962.1, NP_001740.1
GeneID:147929	ZNF565	19	36,673,187	36,705,986	32,799	-	1	2_A375_pNL97_plus_lncRNA::1::4274	546	in gene	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ZNF565	FLJ36991, ZNF565	zinc finger protein 565	NM_152477, NM_001042474	228305_at	NP_689690.3, NP_001035939.1
GeneID:7705	ZNF146	19	36,705,504	36,729,676	24,172	+	1	2_A375_pNL97_plus_lncRNA::1::4274	-64	upstream	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ZNF146	OZF, MGC125660, MGC125661, ZNF146	zinc finger protein 146	NM_001099639, NM_001099638, NM_007145	1554433_a_at, 200050_at	NP_001093109.1, NP_001093108.1, NP_009076.2
GeneID:57677	ZFP14	19	36,827,162	36,870,078	42,916	-	2	1_A375_pNL7_minus_lncRNA::1::2972, 2_A375_pNL97_plus_lncRNA::1::4275	110, 78	in gene, in gene	1	1	25	16	1	1_A375_pNL7_minus_lncRNA::1	25	Gene ZFP14	ZFP14, ZNF531, KIAA1559	zinc finger protein 14 homolog (mouse)	NM_020917	232911_at	NP_065968.1
GeneID:84924	ZNF566	19	36,936,021	36,980,463	44,442	-	1	2_A375_pNL97_plus_lncRNA::1::4276	-17	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZNF566	MGC12515, FLJ14779, ZNF566	zinc finger protein 566	NM_001145343, NM_001145344, NM_032838, NM_001145345	240239_at	NP_001138815.1, NP_001138816.1, NP_116227.1, NP_001138817.1
GeneID:728752	LOC728752	19	36,980,529	36,981,942	1,413	+	1	2_A375_pNL97_plus_lncRNA::1::4276	-49	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC728752		hypothetical LOC728752	NR_036504		
GeneID:57711	ZNF529	19	37,034,517	37,096,178	61,661	-	1	1_A375_pNL7_minus_lncRNA::1::2973	32114	in gene	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ZNF529	KIAA1615, ZNF529	zinc finger protein 529	NM_020951, NM_001145649, NM_001145650, NR_027239	215307_at, 231940_at, 237453_at	NP_066002.3, NP_001139121.1, NP_001139122.1
GeneID:284408	LOC284408	19	37,288,087	37,319,011	30,924	+	1	1_A375_pNL7_minus_lncRNA::1::2974	40889	downstream	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC284408		hypothetical LOC284408	XR_111857, XR_109513, XR_115275	1558809_s_at, 235779_at	
GeneID:388536	ZNF790	19	37,308,330	37,329,284	20,954	-	1	1_A375_pNL7_minus_lncRNA::1::2974	308	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ZNF790	ZNF790, MGC62100, FLJ20350	zinc finger protein 790	NM_206894		NP_996777.2
GeneID:374899	ZNF829	19	37,379,026	37,407,193	28,167	-	1	1_A375_pNL7_minus_lncRNA::1::2975	-199	upstream	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ZNF829	MGC129866, ZNF829, DKFZp686K21248, DKFZp779O175, MGC129867, FLJ27459	zinc finger protein 829	NM_001037232, NM_001171979	237306_at, 238952_x_at	NP_001032309.2, NP_001165450.1
GeneID:374900	ZNF568	19	37,407,234	37,442,450	35,216	+	1	1_A375_pNL7_minus_lncRNA::1::2975	158	in gene	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ZNF568	ZNF568, DKFZp686B0797, FLJ35804, DKFZp667O0524, FLJ34820	zinc finger protein 568	NM_198539	1561425_a_at, 1562282_at, 1564356_at, 1568900_a_at	NP_940941.2
GeneID:92285	ZNF585B	19	37,672,481	37,701,451	28,970	-	1	2_A375_pNL97_plus_lncRNA::1::4277	-7733	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZNF585B	FLJ33255, ZNF585B, SZFP41, FLJ14928	zinc finger protein 585B	NM_152279	235262_at	NP_689492.3
GeneID:163087	ZNF383	19	37,717,366	37,734,574	17,208	+	1	2_A375_pNL97_plus_lncRNA::1::4277	-8182	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZNF383	HSD17, ZNF383, FLJ35863	zinc finger protein 383	NM_152604	235414_at	NP_689817.1
GeneID:100507342	LOC100507342	19	37,808,802	37,815,826	7,024	+	1	2_A375_pNL97_plus_lncRNA::1::4278	16590	downstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100507342		hypothetical LOC100507342	XR_109514		
GeneID:284459	HKR1	19	37,825,580	37,855,357	29,777	+	2	2_A375_pNL97_plus_lncRNA::1::4278, 2_A375_pNL97_plus_lncRNA::1::4279	-188, 36436	upstream, downstream	0	1	12	21	2	2_A375_pNL97_plus_lncRNA::1	26	Gene HKR1	HKR1, ZNF875		NM_181786, hCT2353145.0, hCT2353146.0, hCT2353147.0, hCT2353148.0, hCT2353149.0, hCT33661.3	1569979_at, 1569980_x_at, 231836_at	NP_861451.1, EAW56724.1, EAW56721.1, EAW56722.1, EAW56723.1, EAW56726.1, EAW56725.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:84503	ZNF527	19	37,862,059	37,883,966	21,907	+	1	2_A375_pNL97_plus_lncRNA::1::4279	-43	upstream	0	1	15	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ZNF527	ZNF527, KIAA1829	zinc finger protein 527	NM_032453	1570238_at, 244661_at	NP_115829.1
GeneID:126231	ZNF573	19	38,229,203	38,270,230	41,027	-	1	1_A375_pNL7_minus_lncRNA::1::2976	86	in gene	1	0	21	14	1	1_A375_pNL7_minus_lncRNA::1	21	Gene ZNF573	ZNF573, FLJ30921	zinc finger protein 573	NM_152360, NM_001172689, NM_001172690, NM_001172691, NM_001172692, hCT2275610.1, hCT2351041.0, hCT2351042.0	1556513_at, 217627_at	NP_689573.3, NP_001166160.1, NP_001166161.1, NP_001166162.1, NP_001166163.1, EAW56751.1, EAW56752.1, EAW56753.1
GeneID:83889	WDR87	19	38,375,472	38,397,317	21,845	-	1	2_A375_pNL97_plus_lncRNA::1::4280	-347	upstream	0	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene WDR87	FLJ52608, WDR87, NYD-SP11	WD repeat domain 87	NM_031951	224135_at	NP_114157.3
GeneID:23094	SIPA1L3	19	38,397,868	38,699,009	301,141	+	1	2_A375_pNL97_plus_lncRNA::1::4280	-204	upstream	0	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SIPA1L3	SPAL3, SIPA1L3	signal-induced proliferation-associated 1 like 3	NM_015073, hCT34142.2	213600_at, 230564_at, 236096_at, 37831_at	NP_055888.1, EAW56756.1
GeneID:57828	CATSPERG	19	38,826,443	38,861,589	35,146	+	2	1_A375_pNL7_minus_lncRNA::1::2977, 2_A375_pNL97_plus_lncRNA::1::4281	38613, 39029	downstream, downstream	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene CATSPERG	FLJ46353, C19orf15, CATSPERG, DKFZp434A1022, FLJ38899, MGC125664	cation channel, sperm-associated, gamma	NM_021185, hCT1642286.2, hCT1965855.0, hCT1965856.1, hCT2277281.0, hCT2277287.0, hCT2277292.0, hCT34149.4	221316_at, 231261_at, 234353_at	NP_067008.3, EAW56777.1, EAW56778.1, EAW56780.1, EAW56781.1, EAW56783.1, EAW56779.1, EAW56782.1
GeneID:5714	PSMD8	19	38,865,190	38,874,464	9,274	+	2	1_A375_pNL7_minus_lncRNA::1::2977, 2_A375_pNL97_plus_lncRNA::1::4281	-134, 282	upstream, in gene	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene PSMD8	p31, HIP6, MGC1660, S14, Nin1p, PSMD8, HYPF, Rpn12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	NM_002812, hCT34137.4	200820_at	NP_002803.2, EAW56785.1
GeneID:199720	GGN	19	38,874,992	38,878,668	3,676	-	2	1_A375_pNL7_minus_lncRNA::1::2977, 2_A375_pNL97_plus_lncRNA::1::4281	13612, 13196	downstream, downstream	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene GGN	MGC33369, FLJ35713, GGN	gametogenetin	NM_152657, hCT1951985.1, hCT2353113.0, hCT34153.2	231420_at, 244305_at	NP_689870.3, EAW56786.1, EAW56787.1, EAW56788.1
GeneID:399473	SPRED3	19	38,880,939	38,886,871	5,932	+	1	2_A375_pNL97_plus_lncRNA::1::4282	12821	downstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SPRED3	SPRED3, Eve-3	sprouty-related, EVH1 domain containing 3	NM_001039616, NM_001042522		NP_001034705.1, NP_001035987.1
GeneID:147965	FAM98C	19	38,893,775	38,899,728	5,953	+	1	2_A375_pNL97_plus_lncRNA::1::4282	-15	upstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene FAM98C	FLJ44669, FAM98C	family with sequence similarity 98, member C	NM_174905, hCT2353100.0, hCT2353101.0, hCT2353102.0, hCT34145.2	227951_s_at	NP_777565.3, EAW56790.1, EAW56791.1, EAW56792.1, EAW56793.1
GeneID:115727	RASGRP4	19	38,899,698	38,916,945	17,247	-	1	2_A375_pNL97_plus_lncRNA::1::4282	23185	downstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene RASGRP4	RASGRP4		NM_170604, NM_001146202, NM_001146203, NM_001146204, NM_001146205, NM_001146206, NM_001146207, hCT1649456.4	231328_s_at, 240862_at	NP_733749.1, NP_001139674.1, NP_001139675.1, NP_001139676.1, NP_001139677.1, NP_001139678.1, NP_001139679.1, EAW56794.1
GeneID:6261	RYR1	19	38,924,340	39,078,204	153,864	+	2	1_A375_pNL7_minus_lncRNA::1::2978, 2_A375_pNL97_plus_lncRNA::1::4283	21484, 21484	in gene, in gene	1	1	21	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene RYR1	SKRR, CCO, RYDR, MHS, MHS1, RYR1, RYR	ryanodine receptor 1 (skeletal)	NM_000540, NM_001042723, hCT1967691.1, hCT2277302.0, hCT2277304.0, hCT2353106.0	205485_at	NP_000531.2, NP_001036188.1, EAW56795.1, EAW56796.1, EAW56797.1, EAW56798.1
GeneID:11184	MAP4K1	19	39,076,281	39,106,643	30,362	-	1	2_A375_pNL97_plus_lncRNA::1::4284	-1229	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MAP4K1	MAP4K1, HPK1	mitogen-activated protein kinase kinase kinase kinase 1	NM_007181, NM_001042600, hCT1967683.1, hCT1967684.1, hCT2278743.0, hCT34135.3	206296_x_at, 214219_x_at, 214339_s_at	NP_009112.1, NP_001036065.1, EAW56799.1, EAW56800.1, EAW56801.1, EAW56802.1
GeneID:27335	EIF3K	19	39,109,722	39,127,595	17,873	+	1	2_A375_pNL97_plus_lncRNA::1::4284	150	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene EIF3K	EIF3S12, EIF3K, MSTP001, M9, PLAC24, PRO1474, PTD001, PLAC-24, HSPC029, EIF3-p28, ARG134	eukaryotic translation initiation factor 3, subunit K	NM_013234, hCT2277311.0, hCT2277314.0, hCT2277316.0, hCT2345152.0, hCT2345153.0, hCT2353080.0	210501_x_at, 212716_s_at, 221494_x_at, 236605_at	NP_037366.1, EAW56805.1, EAW56803.1, EAW56804.1, EAW56807.1, EAW56808.1, EAW56806.1
GeneID:81	ACTN4	19	39,138,327	39,221,170	82,843	+	6	1_A375_pNL7_minus_lncRNA::1::2979, 1_A375_pNL7_minus_lncRNA::1::2980, 2_A375_pNL97_plus_lncRNA::1::4285, 2_A375_pNL97_plus_lncRNA::1::4286, 2_A375_pNL97_plus_lncRNA::1::4287, 2_A375_pNL97_plus_lncRNA::1::4288	36073, 44585, -151, 10313, 35817, 44169	in gene, in gene, upstream, in gene, in gene, in gene	1	1	16.25	16.5	4	2_A375_pNL97_plus_lncRNA::1	21	Gene ACTN4	DKFZp686K23158, ACTN4, FSGS, FSGS1, ACTININ-4	actinin, alpha 4	NM_004924, hCT2277310.1, hCT2277312.1, hCT2277319.0	200601_at	NP_004915.2, EAW56809.1, EAW56810.1, EAW56811.1
GeneID:3191	HNRNPL	19	39,327,026	39,342,979	15,951	-	1	2_A375_pNL97_plus_lncRNA::1::4289	-189	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene HNRNPL	HNRNPL, FLJ35509, HNRPL, P/OKcl.14, hnRNP-L	heterogeneous nuclear ribonucleoprotein L	NM_001533, NM_001005335, hCT2278728.0, hCT2278729.0, hCT2278730.0	202072_at, 221860_at, 35201_at	NP_001524.2, NP_001005335.1, EAW56826.1, EAW56827.1, EAW56828.1
GeneID:126432	RINL	19	39,358,470	39,368,894	10,424	-	2	1_A375_pNL7_minus_lncRNA::1::2981, 2_A375_pNL97_plus_lncRNA::1::4290	8286, 8254	in gene, in gene	1	1	35	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene RINL	FLJ45909, RINL, FLJ44131	Ras and Rab interactor-like	NM_198445		NP_940847.1
GeneID:22933	SIRT2	19	39,369,195	39,390,502	21,307	-	4	1_A375_pNL7_minus_lncRNA::1::2981, 1_A375_pNL7_minus_lncRNA::1::2982, 2_A375_pNL97_plus_lncRNA::1::4290, 2_A375_pNL97_plus_lncRNA::1::4291	29894, 91, 29862, 294	downstream, in gene, downstream, in gene	1	1	26	29.5	2	2_A375_pNL97_plus_lncRNA::1	37	Gene SIRT2	SIR2L2, SIRT2, FLJ35621, SIR2, FLJ37491, SIR2L	sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	NM_012237, NM_030593, NM_001193286, NR_034146, hCT2278720.0, hCT2278721.0, hCT2278722.0, hCT2278723.0, hCT2278724.0, hCT2353091.0	1558331_at, 220605_s_at	NP_036369.2, NP_085096.1, NP_001180215.1, EAW56834.1, EAW56837.1, EAW56838.1, EAW56833.1, EAW56835.1, EAW56836.1
GeneID:4793	NFKBIB	19	39,390,615	39,399,534	8,919	+	2	1_A375_pNL7_minus_lncRNA::1::2982, 2_A375_pNL97_plus_lncRNA::1::4291	-204, -407	upstream, upstream	1	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene NFKBIB	IKBB, NFKBIB, TRIP9	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	NM_002503, NM_001001716, hCT11606.5, hCT1966665.2, hCT1966666.2, hCT1966667.2, hCT2353189.0	214062_x_at, 214448_x_at, 226388_at	NP_002494.2, NP_001001716.1, EAW56839.1, EAW56840.1, EAW56841.1, EAW56842.1, EAW56843.1
GeneID:643669	LOC643669	19	39,399,623	39,402,798	3,175	-	2	1_A375_pNL7_minus_lncRNA::1::2982, 2_A375_pNL97_plus_lncRNA::1::4291	12367, 12590	downstream, downstream	1	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC643669		hypothetical protein LOC643669	XM_001717465, XM_933621, XM_946053		XP_001717517.1, XP_938714.3, XP_951146.3
GeneID:9535	GMFG	19	39,818,999	39,826,726	7,727	-	2	1_A375_pNL7_minus_lncRNA::1::2986, 2_A375_pNL97_plus_lncRNA::1::4295	-5898, -5882	upstream, upstream	1	1	106	116	1	2_A375_pNL97_plus_lncRNA::1	116	Gene GMFG	GMFG, MGC126867, GMF-GAMMA	glia maturation factor, gamma	NM_004877, hCT34639.4	204220_at	NP_004868.1, EAW56874.1
GeneID:55095	SAMD4B	19	39,833,108	39,875,542	42,434	+	4	1_A375_pNL7_minus_lncRNA::1::2986, 1_A375_pNL7_minus_lncRNA::1::2987, 2_A375_pNL97_plus_lncRNA::1::4295, 2_A375_pNL97_plus_lncRNA::1::4296	-484, 49100, -500, 49004	upstream, downstream, upstream, downstream	1	1	62	69	2	2_A375_pNL97_plus_lncRNA::1	116	Gene SAMD4B	SMGB, FLJ10211, MGC99832, SAMD4B, hSmaug2	sterile alpha motif domain containing 4B	NM_018028, hCT1960832.1, hCT1960833.1, hCT2277374.0, hCT2353209.0, hCT34646.3	220457_at, 226714_at, 227511_at, 229871_at	NP_060498.2, EAW56875.1, EAW56876.1, EAW56877.1, EAW56878.1, EAW56879.1
GeneID:54623	PAF1	19	39,876,269	39,881,679	5,410	-	2	1_A375_pNL7_minus_lncRNA::1::2987, 2_A375_pNL97_plus_lncRNA::1::4296	-529, -433	upstream, upstream	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PAF1	FLJ11123, PAF1, PD2, F23149_1	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	NM_019088, hCT2278699.0, hCT2278701.0, hCT2278702.0, hCT34641.3	202093_s_at	NP_061961.2, EAW56883.1, EAW56880.1, EAW56881.1, EAW56882.1
GeneID:55588	MED29	19	39,881,963	39,891,203	9,240	+	2	1_A375_pNL7_minus_lncRNA::1::2987, 2_A375_pNL97_plus_lncRNA::1::4296	245, 149	in gene, in gene	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MED29	IXL, DKFZp434H247, MED29	mediator complex subunit 29	NM_017592, hCT34650.2	225708_at	NP_060062.1, EAW56884.1
GeneID:7538	ZFP36	19	39,897,487	39,900,045	2,558	+	2	1_A375_pNL7_minus_lncRNA::1::2988, 2_A375_pNL97_plus_lncRNA::1::4297	5606, 5553	downstream, downstream	1	1	23	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene ZFP36	NUP475, GOS24, G0S24, TTP, RNF162A, TIS11, ZFP36	zinc finger protein 36, C3H type, homolog (mouse)	NM_003407, hCT2277378.0, hCT34637.3	201531_at	NP_003398.1, EAW56886.1, EAW56885.1
GeneID:64857	PLEKHG2	19	39,903,750	39,919,055	15,305	+	3	1_A375_pNL7_minus_lncRNA::1::2988, 2_A375_pNL97_plus_lncRNA::1::4297, 2_A375_pNL97_plus_lncRNA::1::4298	-657, -710, 22810	upstream, upstream, downstream	1	1	18	24	2	2_A375_pNL97_plus_lncRNA::1	27	Gene PLEKHG2	FLJ36638, DKFZp667J2325, FLJ22458, CLG, PLEKHG2, FLJ00018, ARHGEF42	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	NM_022835, hCT2277380.0, hCT2277382.0, hCT2277383.0, hCT2277384.0, hCT34647.3	225979_at, 233966_s_at	NP_073746.2, EAW56888.1, EAW56887.1, EAW56889.1, EAW56890.1, EAW56891.1
GeneID:6217	RPS16	19	39,923,847	39,926,618	2,771	-	1	2_A375_pNL97_plus_lncRNA::1::4298	58	in gene	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene RPS16	RPS16, S16	ribosomal protein S16	NM_001020, hCT1967697.1, hCT2353169.0, hCT2353170.0, hCT2353171.0	201258_at, 213890_x_at, 226131_s_at	NP_001011.1, EAW56894.1, EAW56892.1, EAW56893.1, EAW56895.1
GeneID:6829	SUPT5H	19	39,936,186	39,967,310	31,124	+	2	1_A375_pNL7_minus_lncRNA::1::2989, 2_A375_pNL97_plus_lncRNA::1::4298	35270, -9626	downstream, upstream	1	1	14.5	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene SUPT5H	SUPT5H, SPT5, Tat-CT1, SPT5H, FLJ34157	suppressor of Ty 5 homolog (S. cerevisiae)	NM_003169, NM_001111020, NM_001130824, NM_001130825, hCT1962793.1, hCT1962794.1, hCT2353151.0, hCT2353152.0, hCT34635.3	201480_s_at	NP_003160.2, NP_001104490.1, NP_001124296.1, NP_001124297.1, EAW56897.1, EAW56900.1, EAW56896.1, EAW56898.1, EAW56899.1
GeneID:92609	TIMM50	19	39,971,052	39,981,528	10,476	+	1	1_A375_pNL7_minus_lncRNA::1::2989	404	in gene	1	0	16	17	1	1_A375_pNL7_minus_lncRNA::1	16	Gene TIMM50	TIMM50, MGC102733, TIM50, TIM50L	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	NM_001001563, hCT2277395.0, hCT2277396.0, hCT2277398.0	217612_at, 229913_s_at	NP_001001563.1, EAW56902.1, EAW56901.1, EAW56903.1
GeneID:126272	EID2B	19	40,021,630	40,023,494	1,864	-	1	1_A375_pNL7_minus_lncRNA::1::2990	-7290	upstream	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene EID2B	EID-3, FLJ38944, EID2B	EP300 interacting inhibitor of differentiation 2B	NM_152361, hCT1657237.3	242470_at	NP_689574.1, EAW56908.1
GeneID:163126	EID2	19	40,029,446	40,030,838	1,392	-	1	1_A375_pNL7_minus_lncRNA::1::2990	54	in gene	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene EID2	EID2, MGC20452, CRI2, EID-2	EP300 interacting inhibitor of differentiation 2	NM_153232, hCT1970660.1	225936_at	NP_694964.3, EAW56909.1
GeneID:29124	LGALS13	19	40,093,169	40,098,114	4,945	-	2	1_A375_pNL7_minus_lncRNA::1::2991, 2_A375_pNL97_plus_lncRNA::1::4299	-3233, -3169	upstream, upstream	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LGALS13	PLAC8, LGALS13, GAL13, PP13	lectin, galactoside-binding, soluble, 13	NM_013268, hCT34636.3	220440_at	NP_037400.1, EAW56910.1
GeneID:148003	LGALS16	19	40,146,558	40,151,287	4,729	+	2	1_A375_pNL7_minus_lncRNA::1::2992, 2_A375_pNL97_plus_lncRNA::1::4300	-10014, -9966	upstream, upstream	1	1	27	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene LGALS16		beta-galactoside-binding lectin	NM_001190441		NP_001177370.1
GeneID:5704	PSMC4	19	40,477,073	40,487,353	10,280	+	1	2_A375_pNL97_plus_lncRNA::1::4301	-193	upstream	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene PSMC4	TBP7, MIP224, MGC23214, S6, MGC8570, PSMC4, MGC13687	proteasome (prosome, macropain) 26S subunit, ATPase, 4	NM_153001, NM_006503, hCT2275865.0, hCT34631.3	201252_at	NP_694546.1, NP_006494.1, EAW56928.1, EAW56929.1
GeneID:284323	ZNF780A	19	40,575,059	40,596,845	21,786	-	1	2_A375_pNL97_plus_lncRNA::1::4302	221	in gene	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ZNF780A	ZNF780A, ZNF780	zinc finger protein 780A	NM_001142577, NM_001010880, NM_001142578, NM_001142579, hCT2276861.1		NP_001136049.1, NP_001010880.2, NP_001136050.1, NP_001136051.1, EAW56936.1
GeneID:4294	MAP3K10	19	40,697,651	40,721,482	23,831	+	1	2_A375_pNL97_plus_lncRNA::1::4304	28125	downstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene MAP3K10	MST, MLK2, MAP3K10, MEKK10	mitogen-activated protein kinase kinase kinase 10	NM_002446, hCT11318.3	206362_x_at	NP_002437.2, EAW56937.1
GeneID:146014	TTC9B	19	40,721,965	40,724,306	2,341	-	1	2_A375_pNL97_plus_lncRNA::1::4304	-1470	upstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene TTC9B	FLJ30373, MGC33962, TTC9B	tetratricopeptide repeat domain 9B	NM_152479, hCT11879.3	235375_x_at, 242464_at	NP_689692.2, EAW56938.1
GeneID:78935	CNTD2	19	40,728,115	40,732,597	4,482	-	1	2_A375_pNL97_plus_lncRNA::1::4304	6821	downstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CNTD2	CNTD2, FLJ13265	cyclin N-terminal domain containing 2	NM_024877, hCT1816466.2, hCT2276858.0	220323_at	NP_079153.2, EAW56939.1, EAW56940.1
GeneID:208	AKT2	19	40,736,224	40,791,265	55,041	-	1	2_A375_pNL97_plus_lncRNA::1::4304	65489	downstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene AKT2	RAC-BETA, PRKBB, AKT2, PKBBETA, PKBB	v-akt murine thymoma viral oncogene homolog 2	NM_001626, hCT11881.3, hCT2276852.0, hCT2276854.0	1560689_s_at, 203809_s_at, 211453_s_at, 225471_s_at, 226156_at, 236664_at	NP_001617.1, EAW56941.1, EAW56942.1, EAW56943.1
GeneID:126526	C19orf47	19	40,826,970	40,854,293	27,323	-	1	2_A375_pNL97_plus_lncRNA::1::4305	-75	upstream	0	1	20	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene C19orf47	DKFZp686P05129, FLJ36888, C19orf47	chromosome 19 open reading frame 47	NM_178830, hCT2276845.0, hCT2276847.0, hCT2353122.0, hCT2353123.0, hCT2353124.0	1554475_a_at, 234999_at	NP_849152.1, EAW56946.1, EAW56945.1, EAW56947.1, EAW56948.1, EAW56949.1
GeneID:23646	PLD3	19	40,854,332	40,884,390	30,058	+	1	2_A375_pNL97_plus_lncRNA::1::4305	36	in gene	0	1	20	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene PLD3	HU-K4, PLD3, HUK4	phospholipase D family, member 3	NM_001031696, NM_012268, hCT2275873.0, hCT2275874.0, hCT2275875.0, hCT2275876.0, hCT2275877.0, hCT2275878.0, hCT2275879.0, hCT2275880.0, hCT2275881.0, hCT2275882.0	201050_at	NP_001026866.1, NP_036400.2, EAW56950.1, EAW56952.1, EAW56958.1, EAW56959.1, EAW56951.1, EAW56953.1, EAW56954.1, EAW56955.1, EAW56956.1, EAW56957.1
GeneID:645	BLVRB	19	40,953,691	40,971,725	18,034	-	1	2_A375_pNL97_plus_lncRNA::1::4306	-510	upstream	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene BLVRB	FLR, SDR43U1, MGC117413, BLVRB, BVRB	biliverdin reductase B (flavin reductase (NADPH))	NM_000713, hCT1966652.1, hCT201417.2, hCT2353161.0, hCT2353162.0	202201_at	NP_000704.1, EAW56972.1, EAW56969.1, EAW56970.1, EAW56971.1
GeneID:57731	SPTBN4	19	40,973,126	41,082,365	109,239	+	3	1_A375_pNL7_minus_lncRNA::1::2994, 2_A375_pNL97_plus_lncRNA::1::4306, 2_A375_pNL97_plus_lncRNA::1::4307	109626, -891, 109626	downstream, upstream, downstream	1	1	19	27.5	2	2_A375_pNL97_plus_lncRNA::1	34	Gene SPTBN4	SPNB4, SPTBN3, KIAA1642, SPTBN4, QV	spectrin, beta, non-erythrocytic 4	NM_020971, NM_025213, hCT2275886.0, hCT2353164.0, hCT2353165.0, hCT2353166.0, hCT2353167.0, hCT2353168.0	220185_at, 224144_at, 224145_s_at, 224297_s_at, 224551_s_at	NP_066022.2, NP_079489.2, EAW56973.1, EAW56974.1, EAW56976.1, EAW56978.1, EAW56975.1, EAW56977.1
GeneID:92799	SHKBP1	19	41,082,757	41,097,305	14,548	+	2	1_A375_pNL7_minus_lncRNA::1::2994, 2_A375_pNL97_plus_lncRNA::1::4307	-5, -5	upstream, upstream	1	1	21	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene SHKBP1	PP203, Sb1, SHKBP1	SH3KBP1 binding protein 1	NM_138392, hCT2275889.0, hCT2353205.0, hCT2353206.0	224846_at	NP_612401.2, EAW56979.1, EAW56980.1, EAW56981.1
GeneID:8425	LTBP4	19	41,099,072	41,135,725	36,653	+	4	1_A375_pNL7_minus_lncRNA::1::2995, 1_A375_pNL7_minus_lncRNA::1::2996, 2_A375_pNL97_plus_lncRNA::1::4308, 2_A375_pNL97_plus_lncRNA::1::4309	12496, 17954, 18080, 21280	in gene, in gene, in gene, in gene	1	1	15.67	17	3	1_A375_pNL7_minus_lncRNA::1	21	Gene LTBP4	LTBP-4L, FLJ90018, LTBP4S, FLJ46318, LTBP-4, LTBP4, LTBP4L	latent transforming growth factor beta binding protein 4	NM_003573, NM_001042544, NM_001042545, hCT11329.3, hCT1951974.2, hCT2275890.0, hCT2275891.0	204442_x_at, 210628_x_at, 213176_s_at, 227989_at	NP_003564.2, NP_001036009.1, NP_001036010.1, EAW56982.1, EAW56983.1, EAW56985.1, EAW56984.1
GeneID:79934	ADCK4	19	41,197,434	41,222,790	25,356	-	3	1_A375_pNL7_minus_lncRNA::1::2997, 1_A375_pNL7_minus_lncRNA::1::2998, 2_A375_pNL97_plus_lncRNA::1::4310	1046, 6, 806	in gene, in gene, in gene	1	1	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene ADCK4	FLJ12229, ADCK4	aarF domain containing kinase 4	NM_024876, NM_001142555, hCT2276436.1, hCT2276437.0, hCT2276438.0, hCT2345216.0, hCT2353163.0	220434_at, 227324_at	NP_079152.3, NP_001136027.1, EAW56987.1, EAW56988.1, EAW56990.1, EAW56991.1, EAW56989.1
GeneID:80271	ITPKC	19	41,223,008	41,246,765	23,757	+	3	1_A375_pNL7_minus_lncRNA::1::2997, 1_A375_pNL7_minus_lncRNA::1::2998, 2_A375_pNL97_plus_lncRNA::1::4310	-1264, -224, -1024	upstream, upstream, upstream	1	1	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene ITPKC	IP3KC, ITPKC, IP3-3KC	inositol 1,4,5-trisphosphate 3-kinase C	NM_025194, hCT11875.3, hCT2275947.0	213076_at	NP_079470.1, EAW56992.1, EAW56993.1
GeneID:100507668	LOC100507668	19	41,223,549	41,239,209	15,660	-	3	1_A375_pNL7_minus_lncRNA::1::2997, 1_A375_pNL7_minus_lncRNA::1::2998, 2_A375_pNL97_plus_lncRNA::1::4310	17465, 16425, 17225	downstream, downstream, downstream	1	1	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene LOC100507668		hypothetical LOC100507668	XR_111892, XR_109530, XR_115290		
GeneID:558	AXL	19	41,725,108	41,767,671	42,563	+	1	2_A375_pNL97_plus_lncRNA::1::4311	45196	downstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene AXL	JTK11, UFO, AXL	AXL receptor tyrosine kinase	NM_021913, NM_001699, hCT2275923.2, hCT2275926.2	202685_s_at, 202686_s_at	NP_068713.2, NP_001690.2, EAW57022.1, EAW57023.1
GeneID:11100	HNRNPUL1	19	41,768,391	41,813,811	45,420	+	3	1_A375_pNL7_minus_lncRNA::1::2999, 2_A375_pNL97_plus_lncRNA::1::4311, 2_A375_pNL97_plus_lncRNA::1::4312	47769, 1913, 47865	downstream, in gene, downstream	1	1	19.5	21.5	2	1_A375_pNL7_minus_lncRNA::1	24	Gene HNRNPUL1	HNRNPUL1, E1BAP5, HNRPUL1, FLJ12944, E1B-AP5	heterogeneous nuclear ribonucleoprotein U-like 1	NM_007040, NM_144732, hCT2275927.0, hCT2353131.0, hCT2353132.0, hCT2353133.0, hCT2353134.0, hCT2353135.0	208713_at, 209675_s_at	NP_008971.2, NP_653333.1, EAW57024.1, EAW57025.1, EAW57026.1, EAW57029.1, EAW57027.1, EAW57028.1
GeneID:90324	CCDC97	19	41,816,094	41,830,788	14,694	+	4	1_A375_pNL7_minus_lncRNA::1::2999, 2_A375_pNL97_plus_lncRNA::1::4312, 2_A375_pNL97_plus_lncRNA::1::4313, 2_A375_pNL97_plus_lncRNA::1::4314	66, 162, 11682, 13570	in gene, in gene, in gene, in gene	1	1	16.33	18.33	3	1_A375_pNL7_minus_lncRNA::1	24	Gene CCDC97	MGC20255, FLJ40267, CCDC97	coiled-coil domain containing 97	NM_052848, hCT13415.2, hCT2275932.0	225254_at, 225257_at, 235495_at	NP_443080.1, EAW57031.1, EAW57030.1
GeneID:7040	TGFB1	19	41,836,812	41,859,831	23,019	-	3	2_A375_pNL97_plus_lncRNA::1::4313, 2_A375_pNL97_plus_lncRNA::1::4314, 2_A375_pNL97_plus_lncRNA::1::4315	32055, 30167, -10153	downstream, downstream, upstream	0	1	13	16.33	3	2_A375_pNL97_plus_lncRNA::1	16	Gene TGFB1	TGFbeta, TGFB, LAP, DPD1, TGFB1, CED	transforming growth factor, beta 1	NM_000660, hCT13414.3, hCT2276464.0	203084_at, 203085_s_at	NP_000651.3, EAW57032.1, EAW57033.1
GeneID:80776	B9D2	19	41,860,322	41,870,078	9,756	-	1	2_A375_pNL97_plus_lncRNA::1::4315	94	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene B9D2	B9D2, MKSR2, MGC4093, ICIS-1	B9 protein domain 2	NM_030578, hCT13417.3	219766_at	NP_085055.2, EAW57034.1
GeneID:641649	TMEM91	19	41,869,871	41,889,988	20,117	+	1	2_A375_pNL97_plus_lncRNA::1::4315	113	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TMEM91	IFITMD6, FLJ45695, TMEM91, FLJ27310	transmembrane protein 91	NM_001098824, NM_001098822, NM_001098825, NM_001042595, NM_001098823, NM_001098821	229957_at	NP_001092294.1, NP_001092292.1, NP_001036060.1, NP_001092295.1, NP_001092293.1, NP_001092291.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Exon Count	Intervening Sequences	Intervening Gap Size	Intervening Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
Gene ID:3155101	ATP5SL	19	41,937,223	41,949,843	6,620	+	2	1_A275_shL7_shrna_1kcRNA:1-3000, 2_A275_shL87_gkm_1kcRNA:1-4316	169, -49	upstream, upstream	1	1	65	61	1	1_A275_shL7_shrna_1kc RNA:1	65	Gene ATP5SL	ATP5SL, FLJ10241	ATP5S-like	NM_001167997, NM_001167995, NM_001167999, NR_037693, NM_018533, NM_001167971, NM_001167970, XCT:13812.4, XCT:1867116.1, XCT:1867179.1, XCT:1867224.1	1557799_at, 210036_at, 68526_at	NP_001161339.1, XP_001611340.1, NP_001161341.1, NP_066935.2, NP_001161343.1, NP_001161342.1, EAW57642.1, EAW57643.1, EAW57644.1, EAW57645.1
Gene ID:1100178 3	C19orf69	19	41,949,063	41,950,670	1,607	+	2	1_A275_shL7_shrna_1kcRNA:1-3000, 2_A275_shL87_gkm_1kcRNA:1-4316	-2111, -2175	upstream, upstream	1	1	65	61	1	1_A275_shL7_shrna_1kc RNA:1	65	Gene C19orf69	C19orf69	chromosome 19 open reading frame 69	NM_001123514		NP_001123506.1
Gene ID:1100054853	LOC100354853	19	41,955,425	42,006,554	51,129	-	2	1_A275_shL7_shrna_1kcRNA:1-3000, 2_A275_shL87_gkm_1kcRNA:1-4316	60602, 60666	downstream, downstream	1	1	65	61	1	1_A275_shL7_shrna_1kc RNA:1	65	Gene LOC100354853	hypothetical LOC100353853	XR_111962.XR_111960.XR_111961, XR_109534.XR_109532.XR_109533, XR_110293.XR_110291.XR_115292		
Gene ID:1100058	CEACAM20	19	42,125,344	42,133,442	8,098	-	2	1_A275_shL7_shrna_1kcRNA:1-3001, 2_A275_shL87_gkm_1kcRNA:1-4317	9542, 9922	downstream, downstream	1	1	16	19	1	2_A275_shN97_gkm_1kcR NA:1	19	Gene CEACAM8	NCA, CEACAM4, CGM7, CGM7_HUMAN	carcinoembryonic antigen-related cell adhesion molecule 4	NM_001817, XCT:1340.1, XCT:2331185.0, XCT:2331186.0	207205_at	NP_001803.2, EAW57038.1, EAW57054.1, EAW57055.1, EAW57696.1
Gene ID:1100058	CEACAM21	19	42,300,534	42,313,991	13,457	+	2	1_A275_shL7_shrna_1kcRNA:1-3002, 2_A275_shL87_gkm_1kcRNA:1-4318	17176, 17146	downstream, downstream	1	1	21	23	1	2_A275_shN97_gkm_1kcR NA:1	23	Gene CEACAM3	MGC119875,W282, CGM1, CEA, W282, CEACAM2, CGM20	carcinoembryonic antigen-related cell adhesion molecule 3	NM_001815, XCT:1340.2, XCT:1982607.1, XCT:2332112.0	208552_x_at, 210799_x_at	NP_001806.2, EAW57062.1, EAW57063.1, EAW57065.1
Gene ID:6096	DMRTC2	19	42,349,666	42,356,266	7,312	+	2	1_A275_shL7_shrna_1kcRNA:1-3003, 2_A275_shL87_gkm_1kcRNA:1-4319	14690, 14756	downstream, downstream	1	1	17	17	1	2_A275_shN97_gkm_1kcR NA:1	17	Gene DMRTC2	DMRTC2	DMRT-like family C2	NM_001080263, XCT:1618387.2, XCT:2790310.0, XCT:2331340.0	236611_at	NP_001035373.1, EAW57070.1, EAW57066.1, EAW57069.1
Gene ID:6223	RPS19	19	42,360,855	42,373,454	11,486	+	2	1_A275_shL7_shrna_1kcRNA:1-3003, 2_A275_shL87_gkm_1kcRNA:1-4319	-212, -116	upstream, upstream	1	1	17	17	1	2_A275_shN97_gkm_1kcR NA:1	17	Gene RPS19	DBA1, S19, DBA, RPS19	ribosomal protein S19	NM_001022, XCT:2790305.0, XCT:2790306.0, XCT:2790307.0, XCT:2790308.0	202649_x_at, 213474_s_at, 242451_x_at	NP_001012.1, EAW57074.1, EAW57071.1, EAW57072.1, EAW57073.1
Gene ID:1100058	LOC100358664	19	42,365,217	42,373,281	8,064	-	2	1_A275_shL7_shrna_1kcRNA:1-3003, 2_A275_shL87_gkm_1kcRNA:1-4319	9303, 9409	downstream, downstream	1	1	17	17	1	2_A275_shN97_gkm_1kcR NA:1	17	Gene LOC100358664	hypothetical LOC100358664	XR_111963, XR_109537, XR_115298		
Gene ID:1173	CD79A	19	42,381,190	42,383,439	4,248	+	2	1_A275_shL7_shrna_1kcRNA:1-4320, 2_A275_shL87_gkm_1kcRNA:1-4432	1162, 10874	downstream, downstream	0	1	13.8	21	2	2_A275_shN97_gkm_1kcR NA:1	21	Gene CD79A	CD79A, MB-1, IGA	CD79A molecule, immunoglobulin-associated alpha	NM_001783, NM_021601, XCT:13482.3, XCT:1983666.1	1555779_a_at, 205569_s_at	NP_001774.1, NP_067612.1, EAW57075.1, EAW57076.1
Gene ID:1365	ARHGEF1	19	42,387,267	42,411,804	24,537	+	2	1_A275_shL7_shrna_1kcRNA:1-4320, 2_A275_shL87_gkm_1kcRNA:1-4321	1855, 4797	u gene, u gene	0	1	13.8	21	2	2_A275_shN97_gkm_1kcR NA:1	21	Gene ARHGEF1	GEF1, ARHGEF1, P115-PKOSEF, SUB1.5, LBCL2, LBC	Rho guanine nucleotide exchange factor (GEF) 1	NM_004706, NM_180577, NM_180602, XCT:1482.2, XCT:1983676.1, XCT:1983677.0, XCT:1983678.1, XCT:1983679.0, XCT:2790312.0, XCT:2331111.0, XCT:2331111.0	1560945_s_at, 203053_s_at	NP_004697.2, NP_945326.1, NP_945553.1, EAW57077.1, EAW57081.1, EAW57082.1, EAW57083.1, EAW57078.1, EAW57079.1, EAW57080.1, EAW57084.1
Gene ID:4171	ATP1A3	19	42,470,734	42,495,352	27,946	-	1	2_A275_shN97_gkm_1kcRNA:1-4322	2894	upstream	0	1	14	21	1	2_A275_shN97_gkm_1kcR NA:1	21	Gene ATP1A3	ATP1A3, RDP, DYT12, MGC15276	ATPase, Na+/K+ transporting, alpha 3 polypeptide	NM_152296, XCT:12965.2	214432_at	NP_689509.1, EAW57089.1
Gene ID:2801	QPRL5	19	42,502,473	42,569,697	67,464	+	1	1_A275_shL7_shrna_1kcRNA:1-4322	68551	downstream	0	1	14	21	1	2_A275_shN97_gkm_1kcR NA:1	21	Gene QPRL5	QPRL5, EAA2, KA2, QRRK2	glutaminyl-peptide cyclotransferase-like 5	NM_032555, XCT:12965.3, XCT:2790311.0	1553165_at, 214899_at, 221809_s_at	NP_002797.3, EAW57091.1, EAW57090.1
Gene ID:452	POU2F2	19	42,592,850	42,639,830	46,980	-	2	1_A275_shL7_shrna_1kcRNA:1-3004, 2_A275_shL87_gkm_1kcRNA:1-4322	7830, -1052	upstream, downstream	1	1	39	41	1	2_A275_shN97_gkm_1kcR NA:1	41	Gene POU2F2	OCT2, OTF2, POU2F2, Oct-2	POU class 2 homeobox 2	NM_002698, XCT:12964.3, XCT:1982669.1, XCT:1984000.1, XCT:1984001.1, XCT:1984002.1, XCT:2790320.0, XCT:2790322.0, XCT:2790324.0, XCT:2790326.0, XCT:2790327.0	211660_at, 211731_s_at, 226563_at, 229750_at	NP_002689.2, EAW57100.1, EAW57102.1, EAW57103.1, EAW57105.1, EAW57106.1, EAW57099.1, EAW57101.1, EAW57104.1, EAW57107.1
Gene ID:1100058	LOC100358622	19	42,636,707	42,641,291	4,584	+	4	1_A275_shL7_shrna_1kcRNA:1-3004, 1_A275_shL7_shrna_1kcRN A:1-3005, 2_A275_shL87_gkm_1kcRNA:1-4322, 2_A275_shL87_gkm_1kcRNA:1-4324	7773, 11053, 7805, 10873	downstream, downstream, downstream, downstream	1	1	46.5	53	2	2_A275_shN97_gkm_1kcR NA:1	65	Gene LOC100358622	hypothetical LOC100358622	XR_111966, XR_109538, XR_115297		
Gene ID:1100244980	MIR4323	19	42,637,997	42,637,865	66	-	4	1_A275_shL7_shrna_1kcRNA:1-3004, 1_A275_shL7_shrna_1kcRN A:1-3005, 2_A275_shL87_gkm_1kcRNA:1-4322, 2_A275_shL87_gkm_1kcRNA:1-4324	4815, -10047, 5547, -10015	upstream, downstream, upstream, downstream	1	1	46.5	53	2	2_A275_shN97_gkm_1kcR NA:1	65	Gene MIR4323	MIR4323	microRNA 4323	NR_036358		
Gene ID:1100058	LOC100358639	19	42,656,721	42,661,675	4,954	+	2	1_A275_shL7_shrna_1kcRNA:1-3005, 2_A275_shL87_gkm_1kcRNA:1-4325	4009, -6041	upstream, upstream	1	1	52	65	1	2_A275_shN97_gkm_1kcR NA:1	65	Gene LOC100358639	hypothetical LOC100358639	XR_109539		
Gene ID:62889	DEDD2	19	42,702,752	42,721,813	19,061	-	2	1_A275_shL7_shrna_1kcRNA:1-3006, 2_A275_shL87_gkm_1kcRNA:1-4326	1019, 961	upstream, u gene	1	1	13.8	17	2	2_A275_shN97_gkm_1kcR NA:1	21	Gene DEDD2	FLAME-2, DEDD2	death effector domain containing 2	NM_132325, XCT:12961.2, XCT:1982655.1, XCT:1986983.1	225454_at	NP_079754.1, EAW57112.1, EAW57110.1, EAW57111.1
Gene ID:16115	ZNF526	19	42,724,492	42,732,253	7,761	+	2	1_A275_shL7_shrna_1kcRNA:1-3006, 2_A275_shL87_gkm_1kcRNA:1-4326	1660, -3300	upstream, downstream	1	1	13.8	17	2	2_A275_shN97_gkm_1kcR NA:1	21	Gene ZNF526	KIAA1931, ZNF526, DKFZp762C039, MGC42267	zinc finger protein 526	NM_132444, XCT:12979.3	228229_at	NP_597701.1, EAW57113.1
Gene ID:931	GSK3A	19	42,734,335	42,746,736	12,388	+	4	1_A275_shL7_shrna_1kcRNA:1-3007, 1_A275_shL7_shrna_1kcRN A:1-3008, 2_A275_shL87_gkm_1kcRNA:1-4326, 2_A275_shL87_gkm_1kcRNA:1-4327	-160, -2448, -525, 2144	upstream, downstream, upstream, upstream	1	1	16.5	21	2	2_A275_shN97_gkm_1kcR NA:1	25	Gene GSK3A	GSK3A, DKFZp686B08636	glycogen synthase kinase 3 alpha	NM_019884, XCT:12985.3, XCT:2790311.0	202310_s_at, 632_at	NP_063937.2, EAW57114.1, EAW57115.1
Gene ID:1100132272	LOC100132272	19	42,749,827	42,749,125	2,196	+	5	1_A275_shL7_shrna_1kcRNA:1-3007, 1_A275_shL7_shrna_1kcRN A:1-3008, 2_A275_shL87_gkm_1kcRNA:1-4326, 2_A275_shL87_gkm_1kcRNA:1-4327, 2_A275_shL87_gkm_1kcRNA:1-4328	-31, 2287, 337, 1652, 11393	upstream, downstream, u gene, u gene, downstream	1	1	17.33	21	3	2_A275_shN97_gkm_1kcR NA:1	25	Gene LOC100132272	hypothetical LOC100132272	XR_111969, XR_109540, XR_115299		
Gene ID:2077	ERF	19	42,751,717	42,759,309	7,592	-	5	1_A275_shL7_shrna_1kcRNA:1-3007, 1_A275_shL7_shrna_1kcRN A:1-3008, 2_A275_shL87_gkm_1kcRNA:1-4326, 2_A275_shL87_gkm_1kcRNA:1-4327, 2_A275_shL87_gkm_1kcRNA:1-4328	12813, 10125, 12033, 10424, 869	downstream, downstream, downstream, downstream, u gene	1	1	17.33	21	3	2_A275_shN97_gkm_1kcR NA:1	25	Gene ERF	PE-2, PE2, ERF	Ets2 repressor factor	NM_006494, XCT:11431.2, XCT:1983610.0, XCT:2790310.0	202643_at, 230366_at	NP_006483.2, EAW57116.1, EAW57117.1, EAW57118.1
Gene ID:5132	CIC	19	42,766,817	42,799,949	11,132	+	5	1_A275_shL7_shrna_1kcRNA:1-3010, 1_A275_shL7_shrna_1kcRN A:1-3011, 2_A275_shL87_gkm_1kcRNA:1-4330, 2_A275_shL87_gkm_1kcRNA:1-4331, 2_A275_shL87_gkm_1kcRNA:1-4332	-4129, 4196, 1009, 17807	upstream, downstream, upstream, upstream, downstream	1	1	21	22.67	3	2_A275_shN97_gkm_1kcR NA:1	31	Gene CIC	KIAA0306, CIC	capicua homolog (Drosophila)	NM_015125, XCT:12983.2, XCT:1982651.1, XCT:2790309.0	212764_at	NP_055940.2, EAW57121.1, EAW57119.1, EAW57120.1
Gene ID:9331	LOC100330668	19	42,799,686	42,808,282	8,796	-	3	1_A275_shL7_shrna_1kcRNA:1-3011, 2_A275_shL87_gkm_1kcRNA:1-4332, 2_A275_shL87_gkm_1kcRNA:1-4333	1656, 1656, 8555	u gene, u gene, u gene	1	1	16.5	17	2	1_A275_shL7_shrna_1kc RNA:1	22	Gene LOC100330668	hypothetical LOC100330668	XR_111969, XR_109541, XR_115300		
Gene ID:550	PAFAH1B3	19	42,801,163	42,806,852	5,767	+	2	1_A275_shL7_shrna_1kcRNA:1-3011, 2_A275_shL87_gkm_1kcRNA:1-4332	328, 326	u gene, u gene	1	1	22	17	1	1_A275_shL7_shrna_1kc RNA:1	22	Gene PAFAH1B3	PAFAH2, PLA8/9/0, PAFAH1B2	platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (29 kDa)	NM_002573, NM_001146299, NM_001146940, XCT:2662.2, XCT:1982657.0, XCT:1983658.0, XCT:1983659.0, XCT:2790309.0	203226_at	NP_002564.1, NP_001138411.1, NP_001138412.1, EAW57122.1, EAW57123.1, EAW57124.1, EAW57125.1, EAW57122.1, EAW57126.1
Gene ID:64332	PRR18	19	42,809,264	42,814,873	5,609	+	3	1_A275_shL7_shrna_1kcRNA:1-3011, 2_A275_shL87_gkm_1kcRNA:1-4332, 2_A275_shL87_gkm_1kcRNA:1-4331	340, 340, 11596	u gene, u gene, downstream	1	1	13.8	17	2	2_A275_shN97_gkm_1kcR NA:1	22	Gene PRR18	MGC70824, PRR18	proline rich 18	NM_199283, XCT:1616396.2	231176_at	NP_954876.2, EAW57127.1
Gene ID:84329	TMEM145	19	42,817,477	42,829,214	11,737	+	1	1_A275_shL7_shrna_1kcRNA:1-4330	363	u gene	0	1	9	17	1	2_A275_shN97_gkm_1kcR NA:1	17	Gene TMEM145	FLJ96555, TMEM145	transmembrane protein 145	NM_173633, XCT:12992.2, XCT:1982661.1, XCT:2331129.0	1553479_at	NP_775904.2, EAW57130.1, EAW57126.1, EAW57129.1
Gene ID:4516	CNPY	19	42,891,171	42,894,444	3,273	-	1	1_A275_shL7_shrna_1kcRNA:1-4330	4636	upstream	0	1	10	22	1	2_A275_shN97_gkm_1kcR NA:1	22	Gene CNPY	PLAC-B,2, CNPIV	Canopy	NM_032466, XCT:12987.2	224329_s_at	NP_115877.2, EAW57134.1
Gene ID:9201	LIPE	19	42,903,668	42,931,378	25,912	-	2	1_A275_shL7_shrna_1kcRNA:1-4330, 2_A275_shL87_gkm_1kcRNA:1-4429	32595, 3562	u gene, u gene	0	1	8.9	20	2	2_A275_shN97_gkm_1kcR NA:1	22	Gene LIPE	LIPE, HSL, LHS	lipase, hormone-sensitive	NM_005357, XCT:12972.3	205195_x_at, 213553_s_at	NP_005348.2, EAW57135.1
Gene ID:64340	CXCL17	19	42,932,695	42,947,136	14,441	-	1	1_A275_shL7_shrna_1kcRNA:1-4329	16120	downstream	0	1	9	16	1	2_A275_shN97_gkm_1kcR NA:1	16	Gene CXCL17	VCC-1, MGC136300, VCC1, Dcpl, CXCL17, UNQ473, DMC	chemokine (C-X-C motif) ligand 17	NM_198477	236960_at	NP_940979.1
Gene ID:666	CEACAM8	19	43,054,293	43,059,952	10,667	-	1	1_A275_shL7_shrna_1kcRNA:1-4329	7094	upstream	0	1	16	26	1	2_A275_shN97_gkm_1kcR NA:1	26	Gene CEACAM8	CD66b, CGM1, NCA-95, CGM6, CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 8	NM_001816, XCT:12973.3	206676_at	NP_001807.2, EAW57148.1
Gene ID:5550	PSG11	19	43,069,240	43,530,631	124,291	+	1	1_A275_shL7_shrna_1kcRNA:1-3012	60935	u gene	1	0	12	9	1	1_A275_shL7_shrna_1kc RNA:1	10	Gene PSG11	PSG16, PSG11, MGC22464, PSG13	pregnancy specific beta-1-glycoprotein 11	NM_002785, NM_203287, NM_001113410, XCT:2790196.0, XCT:2790197.0, XCT:2790198.0	206176_at	NP_002776.2, NP_976032.2, NP_001106681.1, EAW57166.1, EAW57167.1, EAW57168.1
Gene ID:3474	ETHE1	19	44,010,671	44,031,298	20,628	+	4	1_A275_shL7_shrna_1kcRNA:1-3015, 2_A275_shL87_gkm_1kcRNA:1-4336, 2_A275_shL87_gkm_1kcRNA:1-4338, 2_A275_shL87_gkm_1kcRNA:1-4340	58, 1324, 4, -6522	u gene, u gene, u gene, u gene	1	1	16	21.67	3	1_A275_shL7_shrna_1kc RNA:1	30	Gene ETHE1	ETHE1, FYH3H2, HSCO	ethylmalonic encephalopathy 1	NM_014297, XCT:2790195.0, XCT:2790193.0, XCT:2790172.0	204034_at	NP_055112.2, EAW57183.1, EAW57186.1, EAW57187.1
Gene ID:64856	ZNF575	19	44,037,340	44,040,290	2,950	+	4	1_A275_shL7_shrna_1kcRNA:1-3015, 2_A275_shL87_gkm_1kcRNA:1-4336, 2_A275_shL87_gkm_1kcRNA:1-4339, 2_A275_shL87_gkm_1kcRNA:1-4340	-5950, -7855, 8946, -412	upstream, downstream, upstream, upstream	1	1	16	21.67	3	1_A275_shL7_shrna_1kc RNA:1	30	Gene ZNF575	FLJ32167, ZNF575	zinc finger protein 575	NM_178465, XCT:1650220.2, XCT:2753556.0, XCT:2753555.0	1567119_a_at	NP_776903.1, EAW57196.1, EAW57190.1
Gene ID:9177	CNOT6	19	44,103,344	44,143,387	40,043	+	2	1_A275_shL7_shrna_1kcRNA:1-3016, 2_A275_shL87_gkm_1kcRNA:1-4340	-256, -256	upstream, upstream	1	1	17	26	1	2_A275_shN97_gkm_1kcR NA:1	26	Gene ZNF576	FLJ22700, MGC23508, ZNF576, FLJ36397	zinc finger protein 576	NM_024327, NM_001145347, XCT:1985734.1, XCT:2753560.0, XCT:2790612.2	219555_s_at, 219009_s_at	NP_077303.1, NP_001138819.1, EAW57206.1, EAW57207.1, EAW57208.1
Gene ID:26269	ZNF426	19	44,111,276	44,123,814	12,539	-	2	1_A275_shL7_shrna_1kcRNA:1-3017, 2_A275_shL87_gkm_1kcRNA:1-4342	182, 14	u gene, u gene	1	1	20	24	1	2_A275_shN97_gkm_1kcR NA:1	24	Gene ZNF426	CHP-247, ZNF426, MGC35052, Zfp038	zinc finger protein 426	NM_152460, XCT:1641327.4, XCT:2790186.1	1555548_at, 215429_s_at	NP_872304.2, EAW57209.1, EAW57210.1
Gene ID:1100170229	SRRM5	19	44,119,253	44,119,830	2,397	+	2	1_A275_shL7_shrna_1kcRNA:1-3017, 2_A275_shL87_gkm_1kcRNA:1-4342	7819, 7747	downstream, downstream	1	1	20	24	1	2_A275_shN97_gkm_1kcR NA:1	24	Gene SRRM5	ERRMS, ZNF576, FLJ33727	serine/arginine repetitive matrix 5	NM_001145641		NP_001138113.1
Gene ID:99731	CADM4	19	44,126,522	44,143,891	17,369	-	2	1_A275_shL7_shrna_1kcRNA:1-3017, 2_A275_shL87_gkm_1kcRNA:1-4342	28119, 16991	downstream, downstream	1	1	20	24	1	2_A275_shN97_gkm_1kcR NA:1	24	Gene CADM4	Necl-4, synCAM4, CADM4, TSLL2, NECL4, IGSF4C	cell adhesion molecule 4	NM_148290, XCT:2790191.1, XCT:2790192.1, XCT:2790194.1	224207_s_at, 219256_at, 219259_s_at, 222293_at, 228339_at	NP_660339.1, EAW57214.1, EAW57212.1, EAW57213.1
Gene ID:9886	C19orf61	19	44,235,301	44,259,142	23,841	+	1	2_A275_shL87_gkm_1kcRNA:1-4342	16298	upstream	0	1	14	25	1	2_A275_shN97_gkm_1kcR NA:1	25	Gene C19orf61	C19orf61, FITT21_1, FLJ12656, DKFZp564H122, EMG8	chromosome 19 open reading frame 61	NM_018105, XCT:1650222.1, XCT:2790197.0, XCT:2790199.0, XCT:2790140.0, XCT:2331114.0, XCT:2790613.1	221333_s_at, 221166_at, 223160_at	NP_060661.2, EAW57223.1, EAW57224.1, EAW57225.1, EAW57226.1, EAW57227.1, EAW57228.1
Gene ID:163	SCN4A	19	44,270,655	44,293,409	14,754	+	4	1_A275_shL7_shrna_1kcRNA:1-3017, 1_A275_shL7_shrna_1kcRN A:1-3018, 2_A275_shL87_gkm_1kcRNA:1-4342, 2_A275_shL87_gkm_1kcRNA:1-4344, 2_A275_shL87_gkm_1kcRNA:1-4345	-7967, 19989, 237, -7851	upstream, downstream, u gene, downstream	1	1	20.67	27.67	3	2_A275_shN97_gkm_1kcR NA:1	40	Gene SCN4A	NSA, NISCat, NCNM, SCa3.1, Ik1, SkM, NCM, HCA1, HyCa4	potassium inwardly-rectifying channel, subfamily N, member 4	NM_000334, XCT:2331156.0, XCT:24967.2	206001_at	NP_000325.1, EAW57230.1, EAW57231.1
Gene ID:5733	LYPD5	19	44,300,079	44,324,898	24,729	-	2	1_A275_shL7_shrna_1kcRNA:1-3018, 2_A275_shL87_gkm_1kcRNA:1-4345	31432, 31446	downstream, downstream	1	1	24	40	1	2_A275_shN97_gkm_1kcR NA:1	40	Gene LYPD5	FRO3356, FLJ30969, LYPD5	LY6/PLAUR domain containing 5	NM_182573, NM_001031748, XCT:1650660.1	238039_at	NP_872379.2, NP_001030819.2, EAW57232.1
Gene ID:1100058	LOC100358715	19	44,393,656	44,403,857	10,001	-	1	1_A275_shL7_shrna_1kcRNA:1-3019	-299	upstream	1	0	16	16	1	1_A275_shL7_shrna_1kc RNA:1	16	Gene LOC100358715	hypothetical LOC100358715	XR_111972, XR_111971, XR_109544, XR_109543, XR_115303, XR_115302		
Gene ID:7711	ZNF155	19	44,466,353	44,502,477	14,122	+	1	2_A275_shL87_gkm_1kcRNA:1-4346	10665	downstream	0	1	14	21	1	2_A275_shN97_gkm_1kcR NA:1	21	Gene ZNF155	dHS-46, MGC161655, ZNF155	zinc finger protein 155	NM_002449, NM_198559, XCT:2330559.0, XCT:2330560.0, XCT:2330561.0	221201_s_at	NP_003439.2, NP_932335.1, EAW57235.1, EAW57239.1, EAW57240.1
Gene ID:1100358574	LOC100358574	19	44,501,048	44,509,895	8,848	-	1	1_A275_shL7_shrna_1kcRNA:1-4346	-52	upstream	0	1	14	21	1	2_A275_shN97_gkm_1kcR NA:1	21	Gene LOC100358574	hypothetical LOC100358743	XR_111974, XR_109545, XR_115305		
Gene ID:7712	ZNF230	19	44,507,077	44,518,072	10,995	+	1	2_A275_shL87_gkm_1kcRNA:1-4346	-37	upstream	0	1	14	21	1	2_A275_shN97_gkm_1kcR NA:1	21	Gene ZNF230	FDZP2, ZNF230	zinc finger protein 230	NM_003200, XCT:1039002.2	1557122_at, 1570135_at, 208791_s_at	NP_003191.2, EAW57241.1
Gene ID:42809	ZNF284	19	44,576,297	44,591,623	15,326	+	1	2_A275_shL87_gkm_1kcRNA:1-4347	22162	downstream	0	1	11	15	1	2_A275_shN97_gkm_1kcR NA:1	15	Gene ZNF284	ZNF284L, ZNF284, DKFZp761F1713	zinc finger protein 284	NM_020739.2	219462_at	NP_065792.2
Gene ID:767	ZNF224	19	44,590,462	44,612,479	13,997	+	2	1_A275_shL7_shrna_1kcRNA:1-3020, 2_A275_shL87_gkm_1kcRNA:1-4347	16530, -2	downstream, upstream	1	1	16	16.5	2	1_A275_shL7_shrna_1kc RNA:1	19	Gene ZNF224	BMZP-2, ZMP27, BMZP2, ZNP255, ZNF224, KIAA22	zinc finger protein 224	NM_013368, XCT:1647699.3, XCT:2770260.0, XCT:2770729.0, XCT:2770703.0	1555355, XCT:1647699.3, XCT:2770260.0, XCT:2770729.0, XCT:2770703.0	NP_037530.2, EAW57253.1, EAW57250.1, EAW57251.1, EAW57252.1, EAW57254.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100379224	LOC100379224	19	44,609,492	44,617,336	7,844	-	1	1_A375_pNL7_minus_lncRNA::1::3020	24	in gene	1	0	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene LOC100379224		hypothetical LOC100379224	NR_033341		
GeneID:7768	ZNF225	19	44,617,548	44,637,255	19,707	+	1	1_A375_pNL7_minus_lncRNA::1::3020	-236	upstream	1	0	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ZNF225	ZNF225, MGC119735	zinc finger protein 225	NM_013362, hCT30601.3	207125_at, 229123_at, 235702_at	NP_037494.2, EAW57255.1
GeneID:353355	ZNF233	19	44,764,076	44,779,468	15,392	+	2	1_A375_pNL7_minus_lncRNA::1::3021, 2_A375_pNL97_plus_lncRNA::1::4348	-76, -12	upstream, upstream	1	1	37	30	1	1_A375_pNL7_minus_lncRNA::1	37	Gene ZNF233	FLJ38032, ZNF233	zinc finger protein 233	NM_181756, hCT1646990.4, hCT2349620.0, hCT2349621.0, hCT2349622.0	230919_at, 232986_at	NP_861421.1, EAW57265.1, EAW57263.1, EAW57264.1, EAW57266.1
GeneID:9310	ZNF235	19	44,790,501	44,809,178	18,677	-	1	2_A375_pNL97_plus_lncRNA::1::4349	186	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZNF235	HZF6, ANF270, ZNF235, ZNF270, ZFP93	zinc finger protein 235	NM_004234, hCT1641537.2	210595_at, 220350_at	NP_004225.3, EAW57267.1
GeneID:7733	ZNF180	19	44,979,856	45,004,574	24,718	-	2	1_A375_pNL7_minus_lncRNA::1::3022, 2_A375_pNL97_plus_lncRNA::1::4350	17, 94	in gene, in gene	1	1	14	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ZNF180	HHZ168, ZNF180	zinc finger protein 180	NM_013256, hCT11419.3, hCT2353181.0, hCT2353182.0, hCT2353183.0, hCT2353184.0, hCT2353185.0	219495_s_at	NP_037388.2, EAW57279.1, EAW57274.1, EAW57275.1, EAW57276.1, EAW57277.1, EAW57278.1
GeneID:125931	CEACAM20	19	45,010,211	45,033,548	23,337	-	3	1_A375_pNL7_minus_lncRNA::1::3022, 2_A375_pNL97_plus_lncRNA::1::4350, 2_A375_pNL97_plus_lncRNA::1::4351	28991, 29068, 16428	downstream, downstream, in gene	1	1	11	20.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene CEACAM20	CEACAM20, UNQ9366	carcinoembryonic antigen-related cell adhesion molecule 20	NM_001102597, NM_001102598, NM_001102599, NM_001102600, hCT13236.3		NP_001096067.1, NP_001096068.1, NP_001096069.1, NP_001096070.1, EAW57280.1
GeneID:602	BCL3	19	45,251,978	45,263,301	11,323	+	1	1_A375_pNL7_minus_lncRNA::1::3023	-6666	upstream	1	0	24	13	1	1_A375_pNL7_minus_lncRNA::1	24	Gene BCL3	D19S37, BCL3, BCL4	B-cell CLL/lymphoma 3	NM_005178, hCT13225.2	204907_s_at, 204908_s_at	NP_005169.2, EAW57291.1
GeneID:346	APOC4	19	45,445,495	45,448,751	3,256	+	2	1_A375_pNL7_minus_lncRNA::1::3024, 2_A375_pNL97_plus_lncRNA::1::4352	12649, 12777	downstream, downstream	1	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene APOC4	APOC-IV, APO-CIV, APOC4		NM_001646, hCT2277012.0	206738_at	NP_001637.1, EAW57310.1
GeneID:344	APOC2	19	45,449,243	45,452,818	3,575	+	2	1_A375_pNL7_minus_lncRNA::1::3024, 2_A375_pNL97_plus_lncRNA::1::4352	8901, 9029	downstream, downstream	1	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene APOC2	APOC2, MGC75082, APO-CII, APOC-II	apolipoprotein C-II	NM_000483, hCT11410.3, hCT1950656.1, hCT2277015.0	204561_x_at, 231561_s_at, 231562_at	NP_000474.2, EAW57312.1, EAW57311.1, EAW57313.1
GeneID:1209	CLPTM1	19	45,458,636	45,496,599	37,961	+	2	1_A375_pNL7_minus_lncRNA::1::3024, 2_A375_pNL97_plus_lncRNA::1::4352	-494, -366	upstream, upstream	1	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CLPTM1	CLPTM1	cleft lip and palate associated transmembrane protein 1	NM_001294, hCT11295.3, hCT2277018.0	201640_x_at, 211136_s_at	NP_001285.1, EAW57315.1, EAW57314.1
GeneID:11129	SFRS16	19	45,542,298	45,574,214	31,916	+	1	2_A375_pNL97_plus_lncRNA::1::4353	40230	downstream	0	1	22	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SFRS16	FLJ90109, CLASRP, CLASP, SFRS16, SWAP2	CLK4-associating serine/arginine rich protein	NM_007056, hCT13231.2, hCT2353077.0, hCT2353078.0	204978_at	NP_008987.2, EAW57317.1, EAW57318.1, EAW57319.1
GeneID:162979	ZNF296	19	45,574,758	45,579,688	4,930	-	1	2_A375_pNL97_plus_lncRNA::1::4353	-2840	upstream	0	1	22	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ZNF296	ZFP296, ZNF296, ZNF342	zinc finger protein 296	NM_145288, hCT1644650.3	236607_at	NP_660331.1, EAW57320.1
GeneID:79760	GEMIN7	19	45,582,518	45,594,782	12,264	+	2	2_A375_pNL97_plus_lncRNA::1::4353, 2_A375_pNL97_plus_lncRNA::1::4354	10, 13770	in gene, downstream	0	1	21	25	2	2_A375_pNL97_plus_lncRNA::1	26	Gene GEMIN7	SIP3, GEMIN7	gem (nuclear organelle) associated protein 7	NM_024707, NM_001007269, NM_001007270, hCT13243.3	1555751_a_at, 219085_s_at, 222821_s_at	NP_078983.1, NP_001007270.1, NP_001007271.1, EAW57321.1
GeneID:284352	LRRC68	19	45,596,216	45,650,549	54,333	+	1	2_A375_pNL97_plus_lncRNA::1::4354	72	in gene	0	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LRRC68	LRRC68, KIAA1986	leucine rich repeat containing 68	XM_001722969, XM_001723010, XM_001724714, XM_003119730, XM_003119732, XM_003119734, XM_003119733, XM_003119731, XM_003118775, XM_003118777, XM_003118779, XM_003118778, XM_003118776, XM_003120946, XM_003120948, XM_003120950, XM_003120949, XM_003120947	213751_at, 213781_at, 229262_at	XP_001723021.1, XP_001723062.1, XP_001724766.1, XP_003119778.1, XP_003119780.1, XP_003119782.1, XP_003119781.1, XP_003119779.1, XP_003118823.1, XP_003118825.1, XP_003118827.1, XP_003118826.1, XP_003118824.1, XP_003120994.1, XP_003120996.1, XP_003120998.1,
GeneID:1158	CKM	19	45,809,671	45,826,233	16,562	-	1	2_A375_pNL97_plus_lncRNA::1::4355	-3335	upstream	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CKM	CKMM, CKM, M-CK	creatine kinase, muscle	NM_001824, hCT13233.3	204810_s_at	NP_001815.2, EAW57337.1
GeneID:2068	ERCC2	19	45,854,649	45,873,845	19,196	-	2	1_A375_pNL7_minus_lncRNA::1::3025, 2_A375_pNL97_plus_lncRNA::1::4356	-43, -43	upstream, upstream	1	1	47	47	1	2_A375_pNL97_plus_lncRNA::1	47	Gene ERCC2	MGC126218, COFS2, XPD, ERCC2, TTD, MGC126219, MGC102762, EM9	excision repair cross-complementing rodent repair deficiency, complementation group 2	NM_000400, NM_001130867, hCT11812.3, hCT2277766.0	213468_at	NP_000391.1, NP_001124339.1, EAW57341.1, EAW57342.1
GeneID:10848	PPP1R13L	19	45,882,892	45,909,607	26,715	-	5	1_A375_pNL7_minus_lncRNA::1::3025, 1_A375_pNL7_minus_lncRNA::1::3026, 1_A375_pNL7_minus_lncRNA::1::3027, 2_A375_pNL97_plus_lncRNA::1::4356, 2_A375_pNL97_plus_lncRNA::1::4357	35719, 8135, -153, 35719, -121	downstream, in gene, upstream, downstream, upstream	1	1	66.67	66.67	3	2_A375_pNL97_plus_lncRNA::1	146	Gene PPP1R13L	RAI, RAI4, NKIP1, IASPP, PPP1R13L	protein phosphatase 1, regulatory (inhibitor) subunit 13 like	NM_006663, NM_001142502, hCT1815489.2, hCT2277763.0, hCT2353089.0	218849_s_at	NP_006654.2, NP_001135974.1, EAW57343.1, EAW57344.1, EAW57345.1
GeneID:10849	CD3EAP	19	45,909,467	45,914,024	4,557	+	3	1_A375_pNL7_minus_lncRNA::1::3026, 1_A375_pNL7_minus_lncRNA::1::3027, 2_A375_pNL97_plus_lncRNA::1::4357	-7995, 293, 261	upstream, in gene, in gene	1	1	76.5	79.5	2	2_A375_pNL97_plus_lncRNA::1	146	Gene CD3EAP	CAST, ASE-1, MGC118851, PAF49, CD3EAP	CD3e molecule, epsilon associated protein	NM_012099, hCT11804.2, hCT2276116.1	205264_at	NP_036231.1, EAW57347.1, EAW57346.1
GeneID:2067	ERCC1	19	45,910,591	45,927,177	16,586	-	4	1_A375_pNL7_minus_lncRNA::1::3026, 1_A375_pNL7_minus_lncRNA::1::3027, 2_A375_pNL97_plus_lncRNA::1::4357, 2_A375_pNL97_plus_lncRNA::1::4358	25705, 17417, 17449, 153	downstream, downstream, downstream, in gene	1	1	55.67	60	3	2_A375_pNL97_plus_lncRNA::1	146	Gene ERCC1	UV20, ERCC1, RAD10, COFS4	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	NM_001983, NM_202001, NM_001166049, hCT11808.3, hCT1950214.1, hCT1950215.1	203719_at, 203720_s_at, 228131_at	NP_001974.1, NP_973730.1, NP_001159521.1, EAW57348.1, EAW57349.1, EAW57350.1
GeneID:2354	FOSB	19	45,971,253	45,978,437	7,184	+	3	1_A375_pNL7_minus_lncRNA::1::3030, 2_A375_pNL97_plus_lncRNA::1::4361, 2_A375_pNL97_plus_lncRNA::1::4362	10763, 10731, 17451	downstream, downstream, downstream	1	1	27.5	29.5	2	2_A375_pNL97_plus_lncRNA::1	32	Gene FOSB	FOSB, GOSB, AP-1, MGC42291, G0S3, DKFZp686C0818, GOS3	FBJ murine osteosarcoma viral oncogene homolog B	NM_006732, NM_001114171, hCT11805.2, hCT2276121.0	202768_at	NP_006723.2, NP_001107643.1, EAW57351.1, EAW57352.1
GeneID:6253	RTN2	19	45,988,550	46,000,313	11,763	-	8	1_A375_pNL7_minus_lncRNA::1::3030, 1_A375_pNL7_minus_lncRNA::1::3031, 1_A375_pNL7_minus_lncRNA::1::3032, 1_A375_pNL7_minus_lncRNA::1::3033, 2_A375_pNL97_plus_lncRNA::1::4361, 2_A375_pNL97_plus_lncRNA::1::4362, 2_A375_pNL97_plus_lncRNA::1::4363, 2_A375_pNL97_plus_lncRNA::1::4364	18297, 537, -9353, -10311, 18329, 11609, 569, -10311	downstream, in gene, upstream, upstream, downstream, in gene, in gene, upstream	1	1	25.8	29.2	5	2_A375_pNL97_plus_lncRNA::1	50	Gene RTN2	RTN2, NSPL1, NSP2	reticulon 2	NM_206900, NM_206901, NM_005619, hCT2277751.0, hCT2277754.0, hCT2353157.0, hCT2353158.0, hCT2353159.0, hCT2353160.0	204217_s_at, 34408_at	NP_996783.1, NP_996784.1, NP_005610.1, EAW57354.1, EAW57358.1, EAW57359.1, EAW57355.1, EAW57356.1, EAW57357.1
GeneID:147699	FLJ40125	19	46,001,731	46,005,768	4,037	+	5	1_A375_pNL7_minus_lncRNA::1::3031, 1_A375_pNL7_minus_lncRNA::1::3032, 1_A375_pNL7_minus_lncRNA::1::3033, 2_A375_pNL97_plus_lncRNA::1::4363, 2_A375_pNL97_plus_lncRNA::1::4364	-1955, 7965, 8893, -1987, 8893	upstream, downstream, downstream, upstream, downstream	1	1	24.67	29	3	2_A375_pNL97_plus_lncRNA::1	50	Gene FLJ40125	FLJ40125, PPM1N	protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative)	NM_001080401, hCT1969106.1	229559_at, 238930_at	NP_001073870.1, EAW57360.1
GeneID:7408	VASP	19	46,010,688	46,030,241	19,553	+	3	1_A375_pNL7_minus_lncRNA::1::3032, 1_A375_pNL7_minus_lncRNA::1::3033, 2_A375_pNL97_plus_lncRNA::1::4364	-992, -64, -64	upstream, upstream, upstream	1	1	27	31	2	2_A375_pNL97_plus_lncRNA::1	50	Gene VASP	VASP	vasodilator-stimulated phosphoprotein	NM_003370, hCT11807.3, hCT1967148.1, hCT2276130.0, hCT2276133.0	202205_at	NP_003361.1, EAW57362.1, EAW57363.1, EAW57364.1, EAW57365.1
GeneID:80207	OPA3	19	46,031,025	46,088,122	57,097	-	5	1_A375_pNL7_minus_lncRNA::1::3034, 1_A375_pNL7_minus_lncRNA::1::3035, 1_A375_pNL7_minus_lncRNA::1::3036, 2_A375_pNL97_plus_lncRNA::1::4365, 2_A375_pNL97_plus_lncRNA::1::4366	40538, 3186, -70, 42298, -70	in gene, in gene, upstream, in gene, upstream	1	1	23	23.5	4	2_A375_pNL97_plus_lncRNA::1	46	Gene OPA3	FLJ22187, OPA3, MGC75494, FLJ25932, MGA3	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	NM_001017989, NM_025136, hCT2277755.0	206357_at, 238630_at	NP_001017989.2, NP_079412.1, EAW57367.1
GeneID:2828	GPR4	19	46,093,022	46,105,466	12,444	-	3	1_A375_pNL7_minus_lncRNA::1::3035, 1_A375_pNL7_minus_lncRNA::1::3036, 2_A375_pNL97_plus_lncRNA::1::4366	20530, 17274, 17274	downstream, downstream, downstream	1	1	26.5	30	2	2_A375_pNL97_plus_lncRNA::1	46	Gene GPR4	GPR4		NM_005282	206236_at, 211266_s_at	NP_005273.1
GeneID:24139	EML2	19	46,112,658	46,148,775	36,117	-	1	2_A375_pNL97_plus_lncRNA::1::4367	3191	in gene	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene EML2	EMAP-2, EMAP2, EML2, ELP70	echinoderm microtubule associated protein like 2	NM_012155, NM_001193268, NM_001193269, NR_034098, hCT11810.3, hCT1950216.1	204397_at, 204398_s_at, 204399_s_at, 234021_at, 234026_at	NP_036287.1, NP_001180197.1, NP_001180198.1, EAW57369.1, EAW57370.1
GeneID:442902	MIR330	19	46,142,252	46,142,345	93	-	1	2_A375_pNL97_plus_lncRNA::1::4367	-3239	upstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MIR330	hsa-mir-330, MIR330, MIRN330	microRNA 330	NR_029886		
GeneID:100287177	LOC100287177	19	46,144,948	46,146,098	1,150	+	1	2_A375_pNL97_plus_lncRNA::1::4367	636	in gene	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100287177		hypothetical LOC100287177	XR_111875, XR_109547, XR_115306		
GeneID:2696	GIPR	19	46,171,502	46,185,717	14,215	+	1	2_A375_pNL97_plus_lncRNA::1::4368	24524	downstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene GIPR	GIPR, PGQTL2, MGC126722	gastric inhibitory polypeptide receptor	NM_000164, hCT11803.2, hCT2276145.0	208105_at	NP_000155.1, EAW57371.1, EAW57372.1
GeneID:6633	SNRPD2	19	46,190,712	46,195,443	4,731	-	1	2_A375_pNL97_plus_lncRNA::1::4368	-583	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SNRPD2	SNRPD2, Sm-D2, SNRPD1, SMD2	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	NM_004597, NM_177542, hCT11802.3, hCT1967146.2	200826_at	NP_004588.1, NP_808210.2, EAW57373.1, EAW57374.1
GeneID:54814	QPCTL	19	46,195,741	46,207,248	11,507	+	1	2_A375_pNL97_plus_lncRNA::1::4368	285	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene QPCTL	FLJ20084, QPCTL	glutaminyl-peptide cyclotransferase-like	NM_017659, NM_001163377, hCT11814.3, hCT2276148.0	220438_at	NP_060129.2, NP_001156849.1, EAW57375.1, EAW57376.1
GeneID:23403	FBXO46	19	46,213,887	46,234,151	20,264	-	2	1_A375_pNL7_minus_lncRNA::1::3037, 2_A375_pNL97_plus_lncRNA::1::4369	13319, 13319	in gene, in gene	1	1	38	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene FBXO46	Fbx46, 20D7-FC4, FBXO46, FBXO34L	F-box protein 46	NM_001080469	205310_at, 237380_at	NP_001073938.1
GeneID:8189	SYMPK	19	46,318,700	46,366,548	47,848	-	1	2_A375_pNL97_plus_lncRNA::1::4370	-92	upstream	0	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SYMPK	FLJ27092, SYM, SYMPK, SPK	symplekin	NM_004819, hCT11892.2, hCT2277710.0, hCT2277712.0, hCT2353200.0, hCT2353201.0	1554595_at, 1559567_at, 202339_at, 32402_s_at	NP_004810.2, EAW57391.1, EAW57389.1, EAW57390.1, EAW57392.1, EAW57393.1
GeneID:3171	FOXA3	19	46,367,518	46,377,055	9,537	+	1	2_A375_pNL97_plus_lncRNA::1::4370	-878	upstream	0	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene FOXA3	MGC10179, FKHH3, FOXA3, TCF3G, HNF3G	forkhead box A3	NM_004497, hCT11361.3, hCT2276167.0	228463_at	NP_004488.2, EAW57395.1, EAW57394.1
GeneID:26145	IRF2BP1	19	46,386,866	46,389,376	2,510	-	3	1_A375_pNL7_minus_lncRNA::1::3038, 2_A375_pNL97_plus_lncRNA::1::4371, 2_A375_pNL97_plus_lncRNA::1::4372	-672, 448, -640	upstream, in gene, upstream	1	1	17.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene IRF2BP1	IRF2BP1, DKFZp434M154	interferon regulatory factor 2 binding protein 1	NM_015649, hCT1639928.2	213771_at	NP_056464.1, EAW57396.1
GeneID:339344	MYPOP	19	46,393,281	46,405,862	12,581	-	4	1_A375_pNL7_minus_lncRNA::1::3038, 2_A375_pNL97_plus_lncRNA::1::4371, 2_A375_pNL97_plus_lncRNA::1::4372, 2_A375_pNL97_plus_lncRNA::1::4373	15814, 16934, 15846, -330	downstream, downstream, downstream, upstream	1	1	15.33	19.33	3	2_A375_pNL97_plus_lncRNA::1	27	Gene MYPOP	P42pop, MYPOP	Myb-related transcription factor, partner of profilin	NM_001012643	227937_at	NP_001012661.1
GeneID:4858	NOVA2	19	46,442,771	46,476,657	33,886	-	1	2_A375_pNL97_plus_lncRNA::1::4375	20721	in gene	0	1	17	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene NOVA2	ANOVA, NOVA2, NOVA3	neuro-oncological ventral antigen 2	NM_002516, hCT11890.3	206476_s_at, 206477_s_at	NP_002507.1, EAW57397.1
GeneID:93429	DKFZp434J0226	19	46,713,499	46,718,095	4,596	+	2	1_A375_pNL7_minus_lncRNA::1::3040, 2_A375_pNL97_plus_lncRNA::1::4377	8101, 8133	downstream, downstream	1	1	29	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene DKFZp434J0226		hypothetical LOC93429	NR_027003	232832_at	
GeneID:100506012	LOC100506012	19	46,984,045	47,104,457	120,412	-	2	1_A375_pNL7_minus_lncRNA::1::3041, 2_A375_pNL97_plus_lncRNA::1::4378	201, 361	in gene, in gene	1	1	28	27	1	1_A375_pNL7_minus_lncRNA::1	28	Gene LOC100506012		serine/threonine-protein phosphatase 5-like	XM_003119735, XM_003119736, XM_003118780, XM_003118781, XM_003120951, XM_003120952		XP_003119783.1, XP_003119784.1, XP_003118828.1, XP_003118829.1, XP_003120999.1, XP_003121000.1
GeneID:808	CALM3	19	47,104,512	47,114,039	9,527	+	2	1_A375_pNL7_minus_lncRNA::1::3041, 2_A375_pNL97_plus_lncRNA::1::4378	-256, -416	upstream, upstream	1	1	28	27	1	1_A375_pNL7_minus_lncRNA::1	28	Gene CALM3	CALM2, CALM1, CALM3, PHKD, PHKD3	calmodulin 3 (phosphorylase kinase, delta)	NM_005184, hCT11390.3, hCT2276069.0, hCT2276071.0, hCT2276072.0, hCT2353210.0	1563431_x_at, 200622_x_at, 200623_s_at	NP_005175.2, EAW57426.1, EAW57425.1, EAW57427.1, EAW57428.1, EAW57429.1
GeneID:25865	PRKD2	19	47,177,573	47,220,384	42,811	-	1	2_A375_pNL97_plus_lncRNA::1::4379	-256	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PRKD2	HSPC187, PKD2, PRKD2	protein kinase D2	NM_001079880, NM_016457, NM_001079881, NM_001079882, hCT2276658.0	209282_at, 241669_x_at, 38269_at	NP_001073349.1, NP_057541.2, NP_001073350.1, NP_001073351.1, EAW57441.1
GeneID:100422913	MIR320E	19	47,212,550	47,212,602	52	-	1	2_A375_pNL97_plus_lncRNA::1::4379	-8038	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MIR320E	MIR320E	microRNA 320e	NR_036157		
GeneID:29888	STRN4	19	47,222,768	47,249,720	26,952	-	1	2_A375_pNL97_plus_lncRNA::1::4379	29080	downstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene STRN4	STRN4, ZIN, FLJ35594	striatin, calmodulin binding protein 4	NM_013403, NM_001039877, hCT2276656.0, hCT2276657.0	217903_at	NP_037535.2, NP_001034966.1, EAW57442.1, EAW57443.1
GeneID:6510	SLC1A5	19	47,278,140	47,291,842	13,702	-	4	1_A375_pNL7_minus_lncRNA::1::3042, 1_A375_pNL7_minus_lncRNA::1::3043, 1_A375_pNL7_minus_lncRNA::1::3044, 2_A375_pNL97_plus_lncRNA::1::4380	3554, -30, -4862, 3556	in gene, upstream, upstream, in gene	1	1	19.67	14.67	3	1_A375_pNL7_minus_lncRNA::1	25	Gene SLC1A5	ASCT2, M7VS1, SLC1A5, R16, M7V1, FLJ31068, ATBO, AAAT, RDRC	solute carrier family 1 (neutral amino acid transporter), member 5	NM_005628, NM_001145144, NM_001145145, hCT1967152.2	208916_at	NP_005619.1, NP_001138616.1, NP_001138617.1, EAW57446.1
GeneID:1175	AP2S1	19	47,341,423	47,354,203	12,780	-	2	1_A375_pNL7_minus_lncRNA::1::3045, 2_A375_pNL97_plus_lncRNA::1::4381	-5957, -55	upstream, upstream	1	1	18	18	2	2_A375_pNL97_plus_lncRNA::1	22	Gene AP2S1	AP17, AP2S1, AP17-DELTA, CLAPS2	adaptor-related protein complex 2, sigma 1 subunit	NM_004069, NM_021575, hCT1955532.1, hCT1965774.1	202120_x_at, 208074_s_at, 211047_x_at	NP_004060.2, NP_067586.1, EAW57448.1, EAW57449.1
GeneID:4861	NPAS1	19	47,524,143	47,549,017	24,874	+	1	2_A375_pNL97_plus_lncRNA::1::4382	27825	downstream	0	1	21	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene NPAS1	PASD5, bHLHe11, NPAS1, MOP5	neuronal PAS domain protein 1	NM_002517, hCT2276045.0	206699_x_at, 216975_x_at	NP_002508.2, EAW57454.1
GeneID:54958	TMEM160	19	47,549,167	47,551,882	2,715	-	1	2_A375_pNL97_plus_lncRNA::1::4382	-56	upstream	0	1	21	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene TMEM160	TMEM160, FLJ20512	transmembrane protein 160	NM_017854, hCT1641696.2	219219_at	NP_060324.1, EAW57455.1
GeneID:23211	ZC3H4	19	47,567,444	47,617,009	49,565	-	1	2_A375_pNL97_plus_lncRNA::1::4383	1457	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZC3H4	ZC3H4, KIAA1064, C19orf7	zinc finger CCCH-type containing 4	NM_015168	213390_at, 240022_at	NP_055983.1
GeneID:10055	SAE1	19	47,634,080	47,713,893	79,813	+	1	1_A375_pNL7_minus_lncRNA::1::3046	8	in gene	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SAE1	SAE1, UBLE1A, HSPC140, AOS1, FLJ3091, SUA1	SUMO1 activating enzyme subunit 1	NM_005500, NM_001145713, NM_001145714, NR_027280, hCT1965769.1, hCT1965770.1, hCT2353141.0, hCT2353142.0, hCT2353143.0	1555618_s_at, 217946_s_at, 241185_at	NP_005491.1, NP_001139185.1, NP_001139186.1, EAW57460.1, EAW57461.1, EAW57462.1, EAW57463.1, EAW57464.1
GeneID:26093	CCDC9	19	47,759,731	47,775,210	15,479	+	2	2_A375_pNL97_plus_lncRNA::1::4384, 2_A375_pNL97_plus_lncRNA::1::4385	13, 16973	in gene, downstream	0	1	16	24	2	2_A375_pNL97_plus_lncRNA::1	30	Gene CCDC9	CCDC9, DKFZp586M1019	coiled-coil domain containing 9	NM_015603, hCT11284.3	206257_at	NP_056418.1, EAW57465.1
GeneID:255783	PRR24	19	47,776,142	47,776,980	838	+	1	2_A375_pNL97_plus_lncRNA::1::4385	-1438	upstream	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PRR24	PRR24	proline rich 24	NM_178511	227325_at	NP_848606.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:728	C5AR1	19	47,813,104	47,825,327	12,223	+	1	1_A375_pNL7_minus_lncRNA::1::3048	5664	in gene	1	0	16	16	1	1_A375_pNL7_minus_lncRNA::1	16	Gene C5AR1	CD88, C5AR1, C5A, C5R1, C5AR	complement component 5a receptor 1	NM_001736, hCT1814442.2, hCT2276304.0	220088_at	NP_001727.1, EAW57470.1, EAW57471.1
GeneID:6543	SLC8A2	19	47,931,279	47,975,307	44,028	-	4	1_A375_pNL7_minus_lncRNA::1::3049, 1_A375_pNL7_minus_lncRNA::1::3050, 2_A375_pNL97_plus_lncRNA::1::4386, 2_A375_pNL97_plus_lncRNA::1::4387	34539, 27595, 34331, 27595	in gene, in gene, in gene, in gene	1	1	24.5	25	2	2_A375_pNL97_plus_lncRNA::1	29	Gene SLC8A2	SLC8A2, NCX2	solute carrier family 8 (sodium/calcium exchanger), member 2	NM_015063, hCT11627.3, hCT2277476.0, hCT2277477.0	215267_s_at	NP_055878.1, EAW57466.1, EAW57464.1, EAW57465.1
GeneID:11133	KPTN	19	47,978,400	47,987,521	9,121	-	1	2_A375_pNL97_plus_lncRNA::1::4388	81	in gene	0	1	23	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene KPTN	2E4, KPTN	kaptin (actin binding protein)	NM_007059, hCT11629.2	220160_s_at	NP_008990.2, EAW57487.1
GeneID:100505661	LOC100505661	19	47,987,470	47,999,639	12,169	+	1	2_A375_pNL97_plus_lncRNA::1::4388	-30	upstream	0	1	23	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene LOC100505661		hypothetical LOC100505661	XR_111878, XR_109481, XR_115308		
GeneID:8775	NAPA	19	47,990,891	48,018,497	27,606	-	2	2_A375_pNL97_plus_lncRNA::1::4388, 2_A375_pNL97_plus_lncRNA::1::4389	31057, 193	downstream, in gene	0	1	19.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene NAPA	NAPA, SNAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha	NM_003827, hCT11628.3, hCT1967142.1, hCT2277460.0, hCT2353115.0, hCT2353116.0, hCT2353117.0, hCT2353118.0, hCT2353119.0, hCT2353120.0, hCT2353121.0	206491_s_at, 208751_at	NP_003818.2, EAW57495.1, EAW57489.1, EAW57491.1, EAW57492.1, EAW57496.1, EAW57490.1, EAW57493.1, EAW57494.1, EAW57497.1, EAW57498.1
GeneID:84215	ZNF541	19	48,023,947	48,059,113	35,166	-	1	2_A375_pNL97_plus_lncRNA::1::4389	40609	downstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF541	MGC119519, ZNF541, MGC119518, MGC119521, DKFZp434I1930	zinc finger protein 541	NM_001101419, hCT1814453.1, hCT2277456.0, hCT2353144.0	232604_at	NP_001094889.1, EAW57499.1, EAW57500.1, EAW57501.1
GeneID:29998	GLTSCR1	19	48,111,453	48,206,534	95,081	+	1	2_A375_pNL97_plus_lncRNA::1::4390	259	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene GLTSCR1	GLTSCR1	glioma tumor suppressor candidate region gene 1	NM_015711, hCT1814448.2, hCT2276278.0	219445_at	NP_056526.3, EAW57504.1, EAW57503.1
GeneID:30846	EHD2	19	48,216,601	48,246,391	29,790	+	3	1_A375_pNL7_minus_lncRNA::1::3051, 2_A375_pNL97_plus_lncRNA::1::4391, 2_A375_pNL97_plus_lncRNA::1::4392	30311, 9703, 30258	downstream, in gene, downstream	1	1	15.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene EHD2	PAST2, EHD2, FLJ96617	EH-domain containing 2	NM_014601, hCT11626.2, hCT1965777.1	205341_at, 221870_at, 45297_at	NP_055416.2, EAW57506.1, EAW57505.1
GeneID:29997	GLTSCR2	19	48,248,793	48,260,323	11,530	+	2	1_A375_pNL7_minus_lncRNA::1::3051, 2_A375_pNL97_plus_lncRNA::1::4392	-1661, -1934	upstream, upstream	1	1	23	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene GLTSCR2	GLTSCR2, PICT1, PICT-1	glioma tumor suppressor candidate region gene 2	NM_015710, hCT11625.2, hCT1958533.1, hCT2276284.0, hCT2276285.0	217807_s_at, 234339_s_at, 234918_at	NP_056525.2, EAW57509.1, EAW57507.1, EAW57508.1, EAW57510.1
GeneID:729626	LOC729626	19	48,260,293	48,272,097	11,804	-	3	1_A375_pNL7_minus_lncRNA::1::3052, 1_A375_pNL7_minus_lncRNA::1::3053, 2_A375_pNL97_plus_lncRNA::1::4393	-5247, -9695, -9759	upstream, upstream, upstream	1	1	20.5	24.5	2	2_A375_pNL97_plus_lncRNA::1	35	Gene LOC729626		hypothetical LOC729626	XM_001133811, XM_001134333, XM_001725164		XP_001133811.1, XP_001134333.1, XP_001725216.1
GeneID:6415	SEPW1	19	48,281,842	48,287,939	6,097	+	3	1_A375_pNL7_minus_lncRNA::1::3052, 1_A375_pNL7_minus_lncRNA::1::3053, 2_A375_pNL97_plus_lncRNA::1::4393	-4498, -50, 14	upstream, upstream, in gene	1	1	20.5	24.5	2	2_A375_pNL97_plus_lncRNA::1	35	Gene SEPW1	selW, SEPW1	selenoprotein W, 1	NM_003009, hCT11299.2, hCT2276287.0, hCT2353136.0	1555851_s_at, 201194_at	NP_003000.1, EAW57512.1, EAW57511.1, EAW57513.1
GeneID:8605	PLA2G4C	19	48,551,100	48,614,109	63,009	-	1	2_A375_pNL97_plus_lncRNA::1::4394	221	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PLA2G4C	DKFZp586C0423, FLJ42247, FLJ44164, PLA2G4C, CPLA2-gamma	phospholipase A2, group IVC (cytosolic, calcium-independent)	NM_003706, NM_001159322, NM_001159323, hCT1967175.1, hCT1967176.1, hCT2283777.0, hCT2352567.0, hCT6277.4	1554610_at, 209785_s_at	NP_003697.2, NP_001152794.1, NP_001152795.1, EAW52311.1, EAW52312.1, EAW52314.1, EAW52313.1, EAW52315.1
GeneID:3978	LIG1	19	48,618,703	48,673,560	54,857	-	3	1_A375_pNL7_minus_lncRNA::1::3054, 2_A375_pNL97_plus_lncRNA::1::4394, 2_A375_pNL97_plus_lncRNA::1::4395	-200, 59672, -200	upstream, downstream, upstream	1	1	15.5	22	2	2_A375_pNL97_plus_lncRNA::1	24	Gene LIG1	MGC130025, LIG1, MGC117397	ligase I, DNA, ATP-dependent	NM_000234, hCT1953509.1, hCT6050.3	202726_at	NP_000225.1, EAW52317.1, EAW52316.1
GeneID:374920	C19orf68	19	48,675,210	48,700,516	25,306	+	2	1_A375_pNL7_minus_lncRNA::1::3054, 2_A375_pNL97_plus_lncRNA::1::4395	-1450, -1450	upstream, upstream	1	1	18	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene C19orf68	C19orf68, MGC50339	chromosome 19 open reading frame 68	XM_001713770, XM_001713771, XM_001713772, hCT1640152.4	238666_at	XP_001713822.2, XP_001713823.2, XP_001713824.2, EAW52318.1
GeneID:93233	CCDC114	19	48,799,709	48,823,332	23,623	-	1	2_A375_pNL97_plus_lncRNA::1::4396	-1884	upstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CCDC114	CCDC114, FLJ32926	coiled-coil domain containing 114	NM_144577, hCT2283760.1, hCT2283761.1, hCT2283765.1, hCT2283766.1, hCT2283768.1, hCT2352557.0	233157_x_at	NP_653178.3, EAW52332.1, EAW52327.1, EAW52328.1, EAW52329.1, EAW52330.1, EAW52331.1
GeneID:2014	EMP3	19	48,828,629	48,833,810	5,181	+	1	2_A375_pNL97_plus_lncRNA::1::4396	-3413	upstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene EMP3	YMP, EMP3	epithelial membrane protein 3	NM_001425, hCT1953510.1, hCT6276.2	203729_at	NP_001416.1, EAW52334.1, EAW52333.1
GeneID:55260	TMEM143	19	48,835,616	48,867,186	31,570	-	2	1_A375_pNL7_minus_lncRNA::1::3055, 2_A375_pNL97_plus_lncRNA::1::4397	722, 754	in gene, in gene	1	1	27	25	1	1_A375_pNL7_minus_lncRNA::1	27	Gene TMEM143	TMEM143, FLJ10922	transmembrane protein 143	NM_018273, hCT1953511.3, hCT2349456.0, hCT2352579.0, hCT6280.2	219589_s_at, 222905_s_at	NP_060743.2, EAW52336.1, EAW52335.1, EAW52337.1, EAW52338.1
GeneID:23546	SYNGR4	19	48,867,657	48,879,634	11,977	+	2	1_A375_pNL7_minus_lncRNA::1::3055, 2_A375_pNL97_plus_lncRNA::1::4397	-1193, -1225	upstream, upstream	1	1	27	25	1	1_A375_pNL7_minus_lncRNA::1	27	Gene SYNGR4	SYNGR4, MGC125805	synaptogyrin 4	NM_012451, hCT2279903.0	206719_at	NP_036583.2, EAW52339.1
GeneID:2906	GRIN2D	19	48,898,132	48,948,188	50,056	+	1	2_A375_pNL97_plus_lncRNA::1::4398	51020	downstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene GRIN2D	GRIN2D, EB11, NMDAR2D, NR2D	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	NM_000836, hCT6283.3	207036_x_at, 229683_at	NP_000827.2, EAW52346.1
GeneID:83743	GRWD1	19	48,949,030	48,957,164	8,134	+	1	2_A375_pNL97_plus_lncRNA::1::4398	122	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene GRWD1	CDW4, GRWD1, GRWD, KIAA1942, WDR28, RRB1	glutamate-rich WD repeat containing 1	NM_031485, hCT6294.3	221549_at	NP_113673.3, EAW52347.1
GeneID:3770	KCNJ14	19	48,958,766	48,969,367	10,601	+	1	2_A375_pNL97_plus_lncRNA::1::4398	-9614	upstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene KCNJ14	KCNJ14, KIAA1942, IRK4, MGC46111, KIR2.4	potassium inwardly-rectifying channel, subfamily J, member 14	NM_013348, NM_170720, hCT2279906.0	220776_at	NP_037480.1, NP_733838.1, EAW52348.1
GeneID:54554	FAM83E	19	49,103,857	49,116,694	12,837	-	1	2_A375_pNL97_plus_lncRNA::1::4399	-5578	upstream	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene FAM83E	MGC138177, FAM83E, MGC138175, FLJ20200	family with sequence similarity 83, member E	NM_017708, hCT6290.2	220312_at	NP_060178.2, EAW52356.1
GeneID:6141	RPL18	19	49,118,588	49,122,433	3,845	-	1	2_A375_pNL97_plus_lncRNA::1::4399	161	in gene	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene RPL18	L18, RPL18	ribosomal protein L18	NM_000979, hCT2283744.1, hCT2283745.1, hCT2283746.1, hCT2283748.1, hCT2283749.1, hCT2283751.1, hCT2283752.1	200022_at, 214335_at	NP_000970.1, EAW52362.1, EAW52358.1, EAW52359.1, EAW52360.1, EAW52364.1, EAW52361.1, EAW52363.1
GeneID:56848	SPHK2	19	49,122,548	49,133,662	11,114	+	3	1_A375_pNL7_minus_lncRNA::1::3056, 2_A375_pNL97_plus_lncRNA::1::4399, 2_A375_pNL97_plus_lncRNA::1::4400	18604, -276, 18558	downstream, upstream, downstream	1	1	26.5	27	2	1_A375_pNL7_minus_lncRNA::1	35	Gene SPHK2	SPHK2		NM_020126, hCT1953521.1, hCT1953522.1, hCT1953523.1, hCT2279923.0, hCT2352577.0, hCT2352578.0, hCT6295.3	208857_s_at, 40273_at	NP_064511.2, EAW52365.1, EAW52366.1, EAW52367.1, EAW52369.1, EAW52370.1, EAW52368.1, EAW52371.1
GeneID:1628	DBP	19	49,133,817	49,140,639	6,822	-	5	1_A375_pNL7_minus_lncRNA::1::3056, 1_A375_pNL7_minus_lncRNA::1::3057, 1_A375_pNL7_minus_lncRNA::1::3058, 2_A375_pNL97_plus_lncRNA::1::4400, 2_A375_pNL97_plus_lncRNA::1::4401	-513, -7633, -9217, -487, -9057	upstream, upstream, upstream, upstream, upstream	1	1	28	24.67	3	1_A375_pNL7_minus_lncRNA::1	35	Gene DBP	DABP, DBP	D site of albumin promoter (albumin D-box) binding protein	NM_001352, hCT2283747.1, hCT2283750.1, hCT2343387.0, hCT2343388.0	209782_s_at, 209783_at	NP_001343.2, EAW52372.1, EAW52373.1, EAW52374.1, EAW52375.1
GeneID:770	CA11	19	49,141,272	49,149,451	8,179	-	5	1_A375_pNL7_minus_lncRNA::1::3056, 1_A375_pNL7_minus_lncRNA::1::3057, 1_A375_pNL7_minus_lncRNA::1::3058, 2_A375_pNL97_plus_lncRNA::1::4400, 2_A375_pNL97_plus_lncRNA::1::4401	8299, 1179, -405, 8315, -245	downstream, in gene, upstream, downstream, upstream	1	1	28	24.67	3	1_A375_pNL7_minus_lncRNA::1	35	Gene CA11	CA11, CARPX1	carbonic anhydrase XI	NM_001217, hCT1967178.1, hCT2283753.0, hCT6289.3	209726_at	NP_001208.2, EAW52378.1, EAW52376.1, EAW52377.1
GeneID:284358	MAMSTR	19	49,216,255	49,222,976	6,721	-	2	1_A375_pNL7_minus_lncRNA::1::3059, 2_A375_pNL97_plus_lncRNA::1::4402	-1056, -960	upstream, upstream	1	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MAMSTR	FLJ36070, MGC117259, MAMSTR, MASTR	MEF2 activating motif and SAP domain containing transcriptional regulator	NM_182574, NM_001130915, hCT1644137.3, hCT2349459.0, hCT2352552.0	1557091_at	NP_872380.1, NP_001124387.1, EAW52390.1, EAW52391.1, EAW52392.1
GeneID:54922	RASIP1	19	49,223,842	49,243,970	20,128	-	2	1_A375_pNL7_minus_lncRNA::1::3059, 2_A375_pNL97_plus_lncRNA::1::4402	19938, 20034	in gene, in gene	1	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene RASIP1	RAIN, FLJ20401, RASIP1	Ras interacting protein 1	NM_017805, hCT2283737.0, hCT7264.3	220027_s_at, 244830_at	NP_060275.2, EAW52393.1, EAW52394.1
GeneID:587	BCAT2	19	49,298,319	49,314,320	16,001	-	2	1_A375_pNL7_minus_lncRNA::1::3060, 2_A375_pNL97_plus_lncRNA::1::4403	15600, 15552	in gene, in gene	1	1	46	35	1	1_A375_pNL7_minus_lncRNA::1	46	Gene BCAT2	BCAM, BCATM, BCAT2, BCT2, PP18	branched chain amino-acid transaminase 2, mitochondrial	NM_001190, NM_001164773, NR_028450, NR_028451, hCT7248.2	203576_at, 215654_at	NP_001181.2, NP_001158245.1, EAW52403.1
GeneID:581	BAX	19	49,458,117	49,465,055	6,938	+	2	1_A375_pNL7_minus_lncRNA::1::3061, 2_A375_pNL97_plus_lncRNA::1::4404	11051, 11099	downstream, downstream	1	1	21	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene BAX	BAX, BCL2L4	BCL2-associated X protein	NM_004324, NM_138761, NM_138763, NM_138764, NR_027882, hCT1953542.1, hCT1953543.1, hCT1953544.1, hCT2279941.0, hCT2279943.0, hCT2352570.0, hCT2352571.0	208478_s_at, 211833_s_at	NP_004315.1, NP_620116.1, NP_620118.1, NP_620119.2, EAW52419.1, EAW52420.1, EAW52415.1, EAW52416.1, EAW52417.1, EAW52418.1, EAW52421.1
GeneID:2512	FTL	19	49,468,566	49,470,136	1,570	+	2	1_A375_pNL7_minus_lncRNA::1::3061, 2_A375_pNL97_plus_lncRNA::1::4404	602, 650	in gene, in gene	1	1	21	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene FTL	MGC71996, NBIA3, FTL	ferritin, light polypeptide	NM_000146, hCT1953553.1, hCT30656.3	212788_x_at, 213187_x_at	NP_000137.2, EAW52423.1, EAW52422.1
GeneID:2997	GYS1	19	49,471,382	49,496,610	25,228	-	4	1_A375_pNL7_minus_lncRNA::1::3061, 1_A375_pNL7_minus_lncRNA::1::3062, 2_A375_pNL97_plus_lncRNA::1::4404, 2_A375_pNL97_plus_lncRNA::1::4405	27442, -430, 27394, -494	downstream, upstream, downstream, upstream	1	1	24.5	21	2	1_A375_pNL7_minus_lncRNA::1	28	Gene GYS1	GSY, GYS, GYS1	glycogen synthase 1 (muscle)	NM_002103, NM_001161587, NR_027763, hCT1787823.3, hCT1787824.3	201673_s_at	NP_002094.2, NP_001155059.1, EAW52424.1, EAW52425.1
GeneID:10856	RUVBL2	19	49,497,156	49,519,182	22,026	+	2	1_A375_pNL7_minus_lncRNA::1::3062, 2_A375_pNL97_plus_lncRNA::1::4405	-116, -52	upstream, upstream	1	1	28	21	1	1_A375_pNL7_minus_lncRNA::1	28	Gene RUVBL2	RUVBL2, TIP48, CGI-46, REPTIN, TIP49B, INO80J, ECP51, TIH2, RVB2	RuvB-like 2 (E. coli)	NM_006666, hCT1953530.2, hCT1953531.2, hCT1953532.2, hCT2352553.0, hCT2352554.0, hCT7246.4	1559945_at, 1559946_s_at, 201459_at	NP_006657.1, EAW52426.1, EAW52427.1, EAW52428.1, EAW52429.1, EAW52430.1, EAW52431.1
GeneID:6625	SNRNP70	19	49,588,465	49,611,870	23,405	+	4	1_A375_pNL7_minus_lncRNA::1::3063, 1_A375_pNL7_minus_lncRNA::1::3064, 2_A375_pNL97_plus_lncRNA::1::4406, 2_A375_pNL97_plus_lncRNA::1::4407	399, 33759, 239, 33711	in gene, downstream, in gene, downstream	1	1	27.5	28.5	2	1_A375_pNL7_minus_lncRNA::1	37	Gene SNRNP70	SNRP70, U170K, U1RNP, RPU1, SNRNP70, U1AP, Snp1, RNPU1Z, U1-70K	small nuclear ribonucleoprotein 70kDa (U1)	NM_003089, hCT1962210.1, hCT2279957.0, hCT2279958.0, hCT2279959.0, hCT2279960.0, hCT2279962.0, hCT2352550.0, hCT2352551.0, hCT7245.3	201221_s_at, 213121_at	NP_003080.2, EAW52450.1, EAW52445.1, EAW52446.1, EAW52451.1, EAW52452.1, EAW52447.1, EAW52448.1, EAW52449.1, EAW52453.1
GeneID:64130	LIN7B	19	49,617,618	49,621,717	4,099	+	2	1_A375_pNL7_minus_lncRNA::1::3064, 2_A375_pNL97_plus_lncRNA::1::4407	4606, 4558	downstream, downstream	1	1	37	34	1	1_A375_pNL7_minus_lncRNA::1	37	Gene LIN7B	MALS-2, MALS2, LIN7B, LIN-7B, VELI2	lin-7 homolog B (C. elegans)	NM_022165, hCT2352555.0, hCT7255.4	219760_at, 241957_x_at	NP_071448.1, EAW52454.1, EAW52455.1
GeneID:55150	C19orf73	19	49,621,654	49,622,397	743	-	2	1_A375_pNL7_minus_lncRNA::1::3064, 2_A375_pNL97_plus_lncRNA::1::4407	173, 221	in gene, in gene	1	1	37	34	1	1_A375_pNL7_minus_lncRNA::1	37	Gene C19orf73	C19orf73, FLJ10490	chromosome 19 open reading frame 73	NM_018111, hCT1787850.1	220151_at	NP_060581.2, EAW52456.1
GeneID:8541	PPFIA3	19	49,622,663	49,654,283	31,620	+	4	1_A375_pNL7_minus_lncRNA::1::3064, 1_A375_pNL7_minus_lncRNA::1::3065, 2_A375_pNL97_plus_lncRNA::1::4407, 2_A375_pNL97_plus_lncRNA::1::4408	-439, 31001, -487, 31033	upstream, in gene, upstream, in gene	1	1	32	30	2	1_A375_pNL7_minus_lncRNA::1	37	Gene PPFIA3	KIAA0654, MGC126569, LPNA3, MGC126567, PPFIA3	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	NM_003660, hCT1640228.2	213368_x_at, 215280_s_at	NP_003651.1, EAW52457.1
GeneID:3270	HRC	19	49,654,455	49,658,681	4,226	-	2	1_A375_pNL7_minus_lncRNA::1::3065, 2_A375_pNL97_plus_lncRNA::1::4408	5017, 4985	downstream, downstream	1	1	27	26	1	1_A375_pNL7_minus_lncRNA::1	27	Gene HRC	HRC, MGC133236	histidine rich calcium binding protein	NM_002152, hCT2352549.0, hCT7244.3	207066_at	NP_002143.1, EAW52458.1, EAW52459.1
GeneID:54795	TRPM4	19	49,661,052	49,715,093	54,041	+	2	1_A375_pNL7_minus_lncRNA::1::3065, 2_A375_pNL97_plus_lncRNA::1::4408	-7388, -7356	upstream, upstream	1	1	27	26	1	1_A375_pNL7_minus_lncRNA::1	27	Gene TRPM4	FLJ20041, TRPM4, PFHB1B, TRPM4B	transient receptor potential cation channel, subfamily M, member 4	NM_017636, hCT2343207.0, hCT2349457.0, hCT2352561.0, hCT7257.3	219360_s_at	NP_060106.2, EAW52463.1, EAW52460.1, EAW52461.1, EAW52462.1
GeneID:57030	SLC17A7	19	49,932,655	49,944,808	12,153	-	2	1_A375_pNL7_minus_lncRNA::1::3066, 2_A375_pNL97_plus_lncRNA::1::4409	-2296, -2248	upstream, upstream	1	1	25	21	1	1_A375_pNL7_minus_lncRNA::1	25	Gene SLC17A7	SLC17A7, VGLUT1, BNPI	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	NM_020309, hCT7254.3	204229_at, 204230_s_at	NP_064705.1, EAW52465.1
GeneID:55011	PIH1D1	19	49,949,550	49,955,115	5,565	-	3	1_A375_pNL7_minus_lncRNA::1::3066, 1_A375_pNL7_minus_lncRNA::1::3067, 2_A375_pNL97_plus_lncRNA::1::4409	8011, -1781, 8059	downstream, upstream, downstream	1	1	24.5	17.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene PIH1D1	PIH1D1, FLJ20643	PIH1 domain containing 1	NM_017916, hCT1953541.2, hCT1965232.1	217872_at	NP_060386.1, EAW52466.1, EAW52467.1
GeneID:126133	ALDH16A1	19	49,956,473	49,974,305	17,832	+	5	1_A375_pNL7_minus_lncRNA::1::3066, 1_A375_pNL7_minus_lncRNA::1::3067, 1_A375_pNL7_minus_lncRNA::1::3068, 2_A375_pNL97_plus_lncRNA::1::4409, 2_A375_pNL97_plus_lncRNA::1::4410	-9369, 423, 25767, -9417, 25767	upstream, in gene, downstream, upstream, downstream	1	1	30.33	29.33	3	2_A375_pNL97_plus_lncRNA::1	53	Gene ALDH16A1	MGC10204, ALDH16A1	aldehyde dehydrogenase 16 family, member A1	NM_153329, NM_001145396, hCT2279977.0, hCT2279978.0, hCT7265.3	227592_at	NP_699160.2, NP_001138868.1, EAW52482.1, EAW52483.1, EAW52484.1
GeneID:2323	FLT3LG	19	49,977,466	49,989,468	12,002	+	2	1_A375_pNL7_minus_lncRNA::1::3068, 2_A375_pNL97_plus_lncRNA::1::4410	4754, 4754	in gene, in gene	1	1	42	53	1	2_A375_pNL97_plus_lncRNA::1	53	Gene FLT3LG	FL, FLT3L, FLT3LG	fms-related tyrosine kinase 3 ligand	NM_001459, hCT1953525.1, hCT1953526.2, hCT1967183.1, hCT2352546.0, hCT2352547.0, hCT2352548.0, hCT7242.3	206980_s_at, 210607_at	NP_001450.2, EAW52493.1, EAW52489.1, EAW52490.1, EAW52491.1, EAW52492.1, EAW52488.1, EAW52494.1
GeneID:23521	RPL13A	19	49,990,865	49,995,565	4,700	+	2	1_A375_pNL7_minus_lncRNA::1::3068, 2_A375_pNL97_plus_lncRNA::1::4410	-8625, -8625	upstream, upstream	1	1	42	53	1	2_A375_pNL97_plus_lncRNA::1	53	Gene RPL13A	L13A, RPL13A, TSTA1		NM_012423, hCT2279986.0, hCT2352580.0	211942_x_at	NP_036555.1, EAW52495.1, EAW52496.1
GeneID:57479	PRR12	19	50,094,912	50,129,696	34,784	+	1	2_A375_pNL97_plus_lncRNA::1::4411	22704	in gene	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PRR12	KIAA1205, PRR12	proline rich 12	NM_020719	226716_at	NP_065770.1
GeneID:6237	RRAS	19	50,138,552	50,143,400	4,848	-	4	1_A375_pNL7_minus_lncRNA::1::3069, 1_A375_pNL7_minus_lncRNA::1::3070, 2_A375_pNL97_plus_lncRNA::1::4412, 2_A375_pNL97_plus_lncRNA::1::4413	-104, -1816, -88, -1848	upstream, upstream, upstream, upstream	1	1	31	22.5	2	1_A375_pNL7_minus_lncRNA::1	32	Gene RRAS	RRAS		NM_006270, hCT12210.3, hCT2283805.0	212647_at	NP_006261.1, EAW52507.1, EAW52506.1
GeneID:58506	SCAF1	19	50,145,382	50,161,906	16,524	+	4	1_A375_pNL7_minus_lncRNA::1::3069, 1_A375_pNL7_minus_lncRNA::1::3070, 2_A375_pNL97_plus_lncRNA::1::4412, 2_A375_pNL97_plus_lncRNA::1::4413	-1878, -166, -1894, -134	upstream, upstream, upstream, upstream	1	1	31	22.5	2	1_A375_pNL7_minus_lncRNA::1	32	Gene SCAF1	SCAF1, SRA1, FLJ00034	SR-related CTD-associated factor 1	NM_021228, hCT1954374.1, hCT2280001.0	225500_x_at	NP_067051.2, EAW52509.1, EAW52508.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:126129	CPT1C	19	50,194,401	50,216,988	22,587	+	2	1_A375_pNL7_minus_lncRNA::1::3071, 2_A375_pNL97_plus_lncRNA::1::4414	26527, 26463	downstream, downstream	1	1	28	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene CPT1C	CPT1P, CATL1, FLJ23809, CPTIC, CPT1C	carnitine palmitoyltransferase 1C	NM_152359, NM_001136052, hCT2344636.0, hCT2344639.0, hCT2344641.0, hCT2344642.0, hCT2344643.0, hCT2344644.0, hCT2344645.0, hCT2344646.0, hCT2344650.0, hCT2352592.0, hCT2352593.0	227466_at	NP_689572.1, NP_001129524.1, EAW52523.1, EAW52525.1, EAW52526.1, EAW52533.1, EAW52524.1, EAW52527.1, EAW52528.1, EAW52529.1, EAW52530.1, EAW52531.1, EAW52532.1
GeneID:160	AP2A1	19	50,270,180	50,310,369	40,189	+	2	1_A375_pNL7_minus_lncRNA::1::3072, 2_A375_pNL97_plus_lncRNA::1::4415	46556, 46716	downstream, downstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene AP2A1	AP2A1, CLAPA1, ADTAA, AP2-ALPHA	adaptor-related protein complex 2, alpha 1 subunit	NM_014203, NM_130787, hCT12209.3, hCT2280013.0, hCT2280015.0	1558792_x_at, 223237_x_at, 229617_x_at, 234068_s_at	NP_055018.2, NP_570603.2, EAW52535.1, EAW52536.1, EAW52537.1
GeneID:80199	FUZ	19	50,310,123	50,316,567	6,444	-	2	1_A375_pNL7_minus_lncRNA::1::3072, 2_A375_pNL97_plus_lncRNA::1::4415	-169, -329	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene FUZ	FUZ, FLJ22688, FY	fuzzy homolog (Drosophila)	NM_001171937, NM_025129, NR_033269, hCT12207.3, hCT1954375.1, hCT1954376.1, hCT2283792.0, hCT2352583.0, hCT2352584.0	221187_s_at	NP_001165408.1, NP_079405.2, EAW52538.1, EAW52540.1, EAW52542.1, EAW52543.1, EAW52539.1, EAW52541.1
GeneID:81857	MED25	19	50,321,536	50,340,237	18,701	+	2	1_A375_pNL7_minus_lncRNA::1::3072, 2_A375_pNL97_plus_lncRNA::1::4415	-4800, -4640	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene MED25	ACID1, TCBAP0758, MED25, MGC70671, ARC92, DKFZp434K0512, PTOV2, CMT2B2, P78	mediator complex subunit 25	NM_030973, hCT2344649.0, hCT2344651.0, hCT2344652.0, hCT2344653.0, hCT2344654.0, hCT2344655.0, hCT2352594.0, hCT2352595.0	1553993_s_at, 208110_x_at, 215897_at	NP_112235.2, EAW52544.1, EAW52545.1, EAW52547.1, EAW52550.1, EAW52551.1, EAW52546.1, EAW52548.1, EAW52549.1
GeneID:100506033	LOC100506033	19	50,341,902	50,354,933	13,031	-	1	2_A375_pNL97_plus_lncRNA::1::4416	565	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506033		hypothetical LOC100506033	XR_111894, XR_111893, XR_109492, XR_109491, XR_115316, XR_115315		
GeneID:53635	PTOV1	19	50,354,416	50,363,999	9,583	+	1	2_A375_pNL97_plus_lncRNA::1::4416	-48	upstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PTOV1	MGC71475, DKFZp586I111, ACID2, PTOV1	prostate tumor overexpressed 1	NM_017432, hCT2344635.0, hCT2344637.0, hCT2344638.0, hCT2344640.1, hCT2344647.0, hCT2344648.0, hCT2349490.0, hCT2349491.0, hCT2352587.0, hCT2352588.0, hCT2352589.0	212032_s_at, 235665_at	NP_059128.2, EAW52553.1, EAW52552.1, EAW52556.1, EAW52557.1, EAW52558.1, EAW52554.1, EAW52555.1, EAW52559.1, EAW52560.1, EAW52561.1, EAW52562.1
GeneID:100506002	LOC100506002	19	50,360,984	50,362,544	1,560	-	1	2_A375_pNL97_plus_lncRNA::1::4416	8176	downstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506002		hypothetical protein LOC100506002	XM_003119739, XM_003118761, XM_003120954		XP_003119787.1, XP_003118809.1, XP_003121002.1
GeneID:11284	PNKP	19	50,364,461	50,370,818	6,357	-	3	1_A375_pNL7_minus_lncRNA::1::3073, 2_A375_pNL97_plus_lncRNA::1::4416, 2_A375_pNL97_plus_lncRNA::1::4417	-9022, 16450, -9758	upstream, downstream, upstream	1	1	17.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	21	Gene PNKP	EIEE10, MCSZ, PNKP, PNK	polynucleotide kinase 3'-phosphatase	NM_007254, hCT12191.4, hCT2283784.0, hCT2283788.0	218961_s_at	NP_009185.2, EAW52567.1, EAW52565.1, EAW52566.1
GeneID:84335	AKT1S1	19	50,372,296	50,380,644	8,348	-	2	1_A375_pNL7_minus_lncRNA::1::3073, 2_A375_pNL97_plus_lncRNA::1::4417	804, 68	in gene, in gene	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene AKT1S1	AKT1S1, Lobe, MGC2865, PRAS40	AKT1 substrate 1 (proline-rich)	NM_001098633, NM_032375, NM_001098632, hCT12202.3, hCT1967224.1, hCT2273994.0, hCT2352590.0	1555821_a_at, 224982_at	NP_001092103.1, NP_115751.2, NP_001092102.1, EAW52568.1, EAW52569.1, EAW52570.1, EAW52571.1
GeneID:79735	TBC1D17	19	50,380,682	50,392,007	11,325	+	2	1_A375_pNL7_minus_lncRNA::1::3073, 2_A375_pNL97_plus_lncRNA::1::4417	-842, -106	upstream, upstream	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene TBC1D17	TBC1D17, FLJ12168	TBC1 domain family, member 17	NM_024682, NM_001168222, hCT12203.3	218466_at	NP_078958.2, NP_001161694.1, EAW52572.1
GeneID:259307	IL4I1	19	50,392,911	50,432,762	39,851	-	2	1_A375_pNL7_minus_lncRNA::1::3074, 2_A375_pNL97_plus_lncRNA::1::4418	330, 154	in gene, in gene	1	1	16	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene IL4I1	IL4I1, FIG1	interleukin 4 induced 1	NM_152899, NM_172374	230966_at	NP_690863.1, NP_758962.1
GeneID:23636	NUP62	19	50,410,082	50,432,988	22,906	-	2	1_A375_pNL7_minus_lncRNA::1::3074, 2_A375_pNL97_plus_lncRNA::1::4418	556, 380	in gene, in gene	1	1	16	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene NUP62	FLJ20822, FLJ43869, MGC841, SNDI, IBSN, p62, DKFZp547L134, NUP62	nucleoporin 62kDa	NM_016553, NM_153719, NM_153718, NM_012346, NM_001193357	214935_at	NP_057637.2, NP_714941.1, NP_036478.2, NP_714940.1, NP_001180286.1
GeneID:22809	ATF5	19	50,431,959	50,437,193	5,234	+	2	1_A375_pNL7_minus_lncRNA::1::3074, 2_A375_pNL97_plus_lncRNA::1::4418	473, 649	in gene, in gene	1	1	16	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ATF5	ATFX, HMFN0395, FLJ34666, ATF5	activating transcription factor 5	NM_012068, NM_001193646, hCT12190.3, hCT1954368.1, hCT2273658.0	204998_s_at, 204999_s_at, 217389_s_at, 230936_x_at	NP_036200.2, NP_001180575.1, EAW52581.1, EAW52582.1, EAW52583.1
GeneID:51231	VRK3	19	50,479,724	50,528,805	49,081	-	2	1_A375_pNL7_minus_lncRNA::1::3075, 2_A375_pNL97_plus_lncRNA::1::4419	38213, 38213	in gene, in gene	1	1	257	320	1	2_A375_pNL97_plus_lncRNA::1	320	Gene VRK3	VRK3		NM_016440, NM_001025778, hCT12192.2, hCT2273991.0, hCT2273993.0, hCT2352585.0, hCT2352586.0	1566700_at, 1566701_at, 218022_at, 221998_s_at, 221999_at, 239190_at	NP_057524.3, NP_001020949.1, EAW52589.1, EAW52590.1, EAW52591.1, EAW52592.1, EAW52588.1
GeneID:3748	KCNC3	19	50,818,765	50,832,634	13,869	-	1	1_A375_pNL7_minus_lncRNA::1::3076	-4198	upstream	1	0	22	15	1	1_A375_pNL7_minus_lncRNA::1	22	Gene KCNC3	KSHIIID, KV3.3, SCA13, KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3	NM_004977, hCT10755.2	207600_at, 230531_at, 243593_at	NP_004968.2, EAW71844.1
GeneID:126119	JOSD2	19	51,009,259	51,014,345	5,086	-	2	1_A375_pNL7_minus_lncRNA::1::3077, 2_A375_pNL97_plus_lncRNA::1::4420	-279, -386	upstream, upstream	1	1	24	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene JOSD2	JOSD2, FLJ29018, SBBI54	Josephin domain containing 2	NM_138334, hCT1771482.3, hCT1966758.2, hCT2355049.0, hCT2355050.0	227096_at	NP_612207.1, EAW71874.1, EAW71875.1, EAW71876.1, EAW71877.1
GeneID:554235	ASPDH	19	51,014,857	51,017,947	3,090	-	2	1_A375_pNL7_minus_lncRNA::1::3077, 2_A375_pNL97_plus_lncRNA::1::4420	3323, 3216	downstream, downstream	1	1	24	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ASPDH	ASPDH		NM_001024656, NM_001114598, hCT14042.3, hCT2355002.0, hCT2355003.0, hCT2355004.0, hCT2355005.0, hCT2355006.0	230912_at	NP_001019827.2, NP_001108070.1, EAW71878.1, EAW71880.1, EAW71881.1, EAW71883.1, EAW71879.1, EAW71882.1
GeneID:94030	LRRC4B	19	51,020,149	51,071,302	51,153	-	2	1_A375_pNL7_minus_lncRNA::1::3077, 2_A375_pNL97_plus_lncRNA::1::4420	56678, 56571	downstream, downstream	1	1	24	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LRRC4B	DKFZp761A179, LRRC4B, HSM, LRIG4	leucine rich repeat containing 4B	NM_001080457	239320_at	NP_001073926.1
GeneID:342918	LOC342918	19	51,152,702	51,162,567	9,865	+	1	2_A375_pNL97_plus_lncRNA::1::4421	9218	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC342918		hypothetical protein LOC342918	NM_001195076	230614_at	NP_001182005.1
GeneID:50944	SHANK1	19	51,165,084	51,220,195	55,111	-	1	2_A375_pNL97_plus_lncRNA::1::4421	56275	downstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SHANK1	SSTRIP, SHANK1, synamon, SPANK-1	SH3 and multiple ankyrin repeat domains 1	NM_016148, hCT1952523.2, hCT2296953.1	220563_s_at	NP_057232.2, EAW71893.1, EAW71894.1
GeneID:93650	ACPT	19	51,293,672	51,298,481	4,809	+	2	1_A375_pNL7_minus_lncRNA::1::3078, 2_A375_pNL97_plus_lncRNA::1::4422	14312, 14264	downstream, downstream	1	1	43	62	1	2_A375_pNL97_plus_lncRNA::1	62	Gene ACPT	ACPT	acid phosphatase, testicular	NM_033068, hCT1770427.1, hCT2296235.0, hCT2296236.0, hCT2296237.0, hCT2296239.0	241715_x_at	NP_149059.1, EAW71902.1, EAW71900.1, EAW71901.1, EAW71903.1, EAW71904.1
GeneID:84798	C19orf48	19	51,300,961	51,307,974	7,013	-	2	1_A375_pNL7_minus_lncRNA::1::3078, 2_A375_pNL97_plus_lncRNA::1::4422	-10, 38	upstream, in gene	1	1	43	62	1	2_A375_pNL97_plus_lncRNA::1	62	Gene C19orf48	MGC13170, C19orf48	chromosome 19 open reading frame 48	NM_199249, NM_199250, hCT2296946.1, hCT2296947.1, hCT2296948.1, hCT2296949.1, hCT2354990.0	224468_s_at	NP_954857.1, NP_954858.1, EAW71905.1, EAW71906.1, EAW71907.1, EAW71909.1, EAW71908.1
GeneID:692203	SNORD88B	19	51,302,286	51,302,382	96	-	2	1_A375_pNL7_minus_lncRNA::1::3078, 2_A375_pNL97_plus_lncRNA::1::4422	-5602, -5554	upstream, upstream	1	1	43	62	1	2_A375_pNL97_plus_lncRNA::1	62	Gene SNORD88B	HBII-180B, SNORD88B	small nucleolar RNA, C/D box 88B	NR_003066		
GeneID:692202	SNORD88A	19	51,302,696	51,302,792	96	-	2	1_A375_pNL7_minus_lncRNA::1::3078, 2_A375_pNL97_plus_lncRNA::1::4422	-5192, -5144	upstream, upstream	1	1	43	62	1	2_A375_pNL97_plus_lncRNA::1	62	Gene SNORD88A	HBII-180A, SNORD88A	small nucleolar RNA, C/D box 88A	NR_003067		
GeneID:692204	SNORD88C	19	51,305,582	51,305,678	96	-	2	1_A375_pNL7_minus_lncRNA::1::3078, 2_A375_pNL97_plus_lncRNA::1::4422	-2306, -2258	upstream, upstream	1	1	43	62	1	2_A375_pNL97_plus_lncRNA::1	62	Gene SNORD88C	SNORD88C, HBII-180C	small nucleolar RNA, C/D box 88C	NR_003069		
GeneID:354	KLK3	19	51,358,171	51,364,020	5,849	+	2	1_A375_pNL7_minus_lncRNA::1::3079, 2_A375_pNL97_plus_lncRNA::1::4423	15701, 15589	downstream, downstream	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene KLK3	KLK3, KLK2A1, PSA, hK3, APS	kallikrein-related peptidase 3	NM_001648, NM_001030047, NM_001030048, NM_001030050, hCT14028.4, hCT1952527.2, hCT1967887.2, hCT2296243.1, hCT2296244.1, hCT2296245.1, hCT2296246.1, hCT2349989.0, hCT2349990.0, hCT2349991.0, hCT2349992.0, hCT2349994.0, hCT2349995.0, hCT2349996.0, hCT23499	204582_s_at, 204583_x_at, 231629_x_at	NP_001639.1, NP_001025218.1, NP_001025219.1, NP_001025221.1, EAW71925.1, EAW71935.1, EAW71922.1, EAW71923.1, EAW71924.1, EAW71926.1, EAW71927.1, EAW71928.1, EAW71929.1, EAW71933.1, EAW71930.1, EAW71931.1, EAW71932.1, EAW71934.1, EAW71936.1
GeneID:3817	KLK2	19	51,376,689	51,383,823	7,134	+	2	1_A375_pNL7_minus_lncRNA::1::3079, 2_A375_pNL97_plus_lncRNA::1::4423	-2817, -2929	upstream, upstream	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene KLK2	KLK2A2, MGC12201, hK2, KLK2	kallikrein-related peptidase 2	NM_005551, NM_001002231, hCT14031.2, hCT1961849.1, hCT1961850.1, hCT2296251.0, hCT2296252.0, hCT2354977.0	1555545_at, 209854_s_at, 209855_s_at, 210339_s_at	NP_005542.1, NP_001002231.1, EAW71937.1, EAW71938.1, EAW71939.1, EAW71941.1, EAW71940.1, EAW71942.1
GeneID:2109	ETFB	19	51,848,409	51,869,672	21,263	-	1	2_A375_pNL97_plus_lncRNA::1::4424	1926	in gene	0	1	11	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ETFB	FP585, MADD, ETFB	electron-transfer-flavoprotein, beta polypeptide	NM_001014763, NM_001985, hCT63247.2	202942_at	NP_001014763.1, NP_001976.1, EAW72004.1
GeneID:125875	CLDND2	19	51,870,352	51,872,257	1,905	-	1	2_A375_pNL97_plus_lncRNA::1::4424	4513	downstream	0	1	11	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CLDND2	CLDND2, MGC33839	claudin domain containing 2	NM_152353, hCT63265.3	231162_at	NP_689566.1, EAW72005.1
GeneID:4818	NKG7	19	51,874,874	51,875,960	1,086	-	1	2_A375_pNL97_plus_lncRNA::1::4424	8216	downstream	0	1	11	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene NKG7	GIG1, p15-TIA-1, GMP-17, NKG7	natural killer cell group 7 sequence	NM_005601, hCT1953908.1, hCT1953909.0, hCT63248.2	213915_at	NP_005592.1, EAW72007.1, EAW72006.1, EAW72008.1
GeneID:89790	SIGLEC10	19	51,913,275	51,921,057	7,782	-	2	1_A375_pNL7_minus_lncRNA::1::3080, 2_A375_pNL97_plus_lncRNA::1::4425	-4351, -4319	upstream, upstream	1	1	23	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene SIGLEC10	SIGLEC10, PRO940, SIGLEC-10, MGC126774, SLG2	sialic acid binding Ig-like lectin 10	NM_033130, NM_001171156, NM_001171157, NM_001171158, NM_001171159, NM_001171160, NM_001171161, hCT1641412.4, hCT2296385.0, hCT2296386.0, hCT2355000.0, hCT2355001.0	1552806_a_at, 1552807_a_at	NP_149121.2, NP_001164627.1, NP_001164628.1, NP_001164629.1, NP_001164630.1, NP_001164631.1, NP_001164632.1, EAW72012.1, EAW72013.1, EAW72014.1, EAW72015.1, EAW72016.1
GeneID:100129083	LOC100129083	19	51,919,160	51,920,679	1,519	+	2	1_A375_pNL7_minus_lncRNA::1::3080, 2_A375_pNL97_plus_lncRNA::1::4425	6248, 6216	downstream, downstream	1	1	23	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene LOC100129083		similar to hCG2045285	NR_033235		
GeneID:729767	CEACAM18	19	51,979,838	51,986,611	6,773	+	1	2_A375_pNL97_plus_lncRNA::1::4426	4130	in gene	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene CEACAM18	CEACAM18	carcinoembryonic antigen-related cell adhesion molecule 18	NM_001080405		NP_001073874.1
GeneID:7728	ZNF175	19	52,074,531	52,092,991	18,460	+	2	1_A375_pNL7_minus_lncRNA::1::3082, 2_A375_pNL97_plus_lncRNA::1::4426	-163, 23293	upstream, downstream	1	1	18.5	19	2	2_A375_pNL97_plus_lncRNA::1	24	Gene ZNF175	ZNF175, OTK18	zinc finger protein 175	NM_007147, hCT1953910.0, hCT63249.2	205497_at, 243128_at	NP_009078.1, EAW72029.1, EAW72030.1
GeneID:729975	FLJ30403	19	52,095,036	52,097,633	2,597	-	1	2_A375_pNL97_plus_lncRNA::1::4426	-191	upstream	0	1	18	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene FLJ30403		hypothetical LOC729975	NR_034159	1559093_at	
GeneID:8778	SIGLEC5	19	52,114,781	52,133,727	18,946	-	2	1_A375_pNL7_minus_lncRNA::1::3083, 2_A375_pNL97_plus_lncRNA::1::4429	22319, 22303	downstream, downstream	1	1	33	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene SIGLEC5	SIGLEC-5, OB-BP2, SIGLEC5, CD33L2, CD170, OBBP2	sialic acid binding Ig-like lectin 5	NM_003830, hCT63250.2	220000_at	NP_003821.1, EAW72033.1
GeneID:80110	ZNF614	19	52,516,577	52,531,680	15,103	-	1	2_A375_pNL97_plus_lncRNA::1::4430	0	in gene	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ZNF614	MGC120638, FLJ21941, ZNF614	zinc finger protein 614	NM_025040	210599_at, 220721_at, 227045_at	NP_079316.2
GeneID:9668	ZNF432	19	52,536,677	52,552,073	15,396	-	1	2_A375_pNL97_plus_lncRNA::1::4430	20393	downstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ZNF432	ZNF432	zinc finger protein 432	NM_014650	219848_s_at	NP_055465.1
GeneID:90321	ZNF766	19	52,772,824	52,795,976	23,152	+	1	2_A375_pNL97_plus_lncRNA::1::4431	27912	downstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF766	ZNF766	zinc finger protein 766	NM_001010851, hCT1955431.1, hCT2354970.0, hCT2354971.0	227284_at	NP_001010851.1, EAW72068.1, EAW72067.1, EAW72069.1
GeneID:147657	ZNF480	19	52,800,426	52,829,175	28,749	+	1	2_A375_pNL97_plus_lncRNA::1::4431	310	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF480	ZNF480, MGC32104	zinc finger protein 480	NM_144684, hCT1955430.1	222283_at	NP_653285.2, EAW72071.1
GeneID:55422	ZNF331	19	54,024,177	54,083,523	59,346	+	1	1_A375_pNL7_minus_lncRNA::1::3084	-1	upstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ZNF331	ZNF331, RITA, DKFZp686L0787, ZNF463, ZNF361	zinc finger protein 331	NM_001079906, NM_001079907, NM_018555, hCT2297616.0, hCT2297617.0, hCT2297618.0, hCT2297619.0, hCT2355008.0	219228_at, 227613_at	NP_001073375.1, NP_001073376.1, NP_061025.5, EAW72144.1, EAW72145.1, EAW72147.1, EAW72146.1, EAW72148.1
GeneID:5582	PRKCG	19	54,385,467	54,410,901	25,434	+	2	1_A375_pNL7_minus_lncRNA::1::3085, 2_A375_pNL97_plus_lncRNA::1::4432	21029, 20965	in gene, in gene	1	1	21	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene PRKCG	PKC-gamma, SCA14, PRKCG, MGC57564, PKCG, PKCC	protein kinase C, gamma	NM_002739, hCT12033.3	206270_at, 236195_x_at	NP_002730.1, EAW72161.1
GeneID:59284	CACNG7	19	54,416,071	54,446,268	30,197	+	4	1_A375_pNL7_minus_lncRNA::1::3085, 1_A375_pNL7_minus_lncRNA::1::3086, 2_A375_pNL97_plus_lncRNA::1::4432, 2_A375_pNL97_plus_lncRNA::1::4433	-9575, 15129, -9639, 15097	upstream, in gene, upstream, in gene	1	1	23	33.5	2	2_A375_pNL97_plus_lncRNA::1	37	Gene CACNG7	CACNG7		NM_031896, hCT12031.3, hCT1961836.1, hCT1967879.1, hCT2297828.0, hCT2297831.0	224137_at	NP_114102.2, EAW72166.1, EAW72162.1, EAW72163.1, EAW72164.1, EAW72165.1
GeneID:59283	CACNG8	19	54,466,294	54,486,139	19,845	+	1	2_A375_pNL97_plus_lncRNA::1::4434	16970	in gene	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CACNG8	FLJ30598, CACNG8, FLJ16240		NM_031895, hCT12032.4	234750_at, 234756_at	NP_114101.4, EAW72168.1
GeneID:100126325	MIR935	19	54,485,561	54,485,651	90	+	1	2_A375_pNL97_plus_lncRNA::1::4434	-2297	upstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MIR935	MIR935, MIRN935, hsa-mir-935	microRNA 935	NR_030632		
GeneID:126014	OSCAR	19	54,597,933	54,604,148	6,215	-	1	2_A375_pNL97_plus_lncRNA::1::4435	-1964	upstream	0	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene OSCAR	MGC33613, OSCAR, PIGR3	osteoclast associated, immunoglobulin-like receptor	NM_206818, NM_130771, NM_133168, NM_133169, hCT12038.3, hCT1956265.1, hCT2298266.0, hCT2298267.0, hCT2355040.0	1554503_a_at	NP_996554.1, NP_570127.2, NP_573398.1, NP_573399.1, EAW72174.1, EAW72175.1, EAW72176.1, EAW72177.1, EAW72178.1
GeneID:4696	NDUFA3	19	54,606,160	54,610,281	4,121	+	3	1_A375_pNL7_minus_lncRNA::1::3087, 2_A375_pNL97_plus_lncRNA::1::4435, 2_A375_pNL97_plus_lncRNA::1::4436	12720, -48, 12848	downstream, upstream, downstream	1	1	22	27	2	2_A375_pNL97_plus_lncRNA::1	30	Gene NDUFA3	NDUFA3, B9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	NM_004542, hCT12030.3, hCT1956256.1, hCT1956257.0, hCT1956258.1, hCT1956259.1, hCT2297852.0	218563_at	NP_004533.1, EAW72184.1, EAW72180.1, EAW72181.1, EAW72182.1, EAW72183.1, EAW72179.1
GeneID:29844	TFPT	19	54,610,320	54,619,055	8,735	-	3	1_A375_pNL7_minus_lncRNA::1::3087, 2_A375_pNL97_plus_lncRNA::1::4435, 2_A375_pNL97_plus_lncRNA::1::4436	175, 12943, 47	in gene, downstream, in gene	1	1	22	27	2	2_A375_pNL97_plus_lncRNA::1	30	Gene TFPT	amida, TFPT, FB1, INO80F	TCF3 (E2A) fusion partner (in childhood Leukemia)	NM_013342, hCT12029.3, hCT1956254.0, hCT1956255.1, hCT2298260.0, hCT2354999.0	218996_at	NP_037474.1, EAW72187.1, EAW72185.1, EAW72186.1, EAW72188.1, EAW72189.1
GeneID:26121	PRPF31	19	54,618,790	54,635,150	16,360	+	2	1_A375_pNL7_minus_lncRNA::1::3087, 2_A375_pNL97_plus_lncRNA::1::4436	90, 218	in gene, in gene	1	1	24	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene PRPF31	NY-BR-99, PRP31, DKFZp566J153, RP11, PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	NM_015629, hCT12028.3, hCT2354997.0	202407_s_at, 202408_s_at, 214380_at	NP_056444.3, EAW72190.1, EAW72191.1
GeneID:4849	CNOT3	19	54,641,436	54,659,446	18,010	+	1	2_A375_pNL97_plus_lncRNA::1::4437	21684	downstream	0	1	9	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CNOT3	CNOT3, LENG2, NOT3H, NOT3, KIAA0691	CCR4-NOT transcription complex, subunit 3	NM_014516, hCT1956235.1, hCT1956236.1, hCT2297866.0	203239_s_at, 211141_s_at, 229143_at	NP_055331.1, EAW72192.1, EAW72193.1, EAW72194.1
GeneID:79165	LENG1	19	54,659,377	54,663,446	4,069	-	1	2_A375_pNL97_plus_lncRNA::1::4437	326	in gene	0	1	9	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LENG1	LENG1	leukocyte receptor cluster (LRC) member 1	NM_024316, hCT12036.3	232018_at	NP_077292.1, EAW72195.1
GeneID:147798	TMC4	19	54,663,833	54,676,944	13,111	-	1	2_A375_pNL97_plus_lncRNA::1::4437	13824	downstream	0	1	9	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TMC4	MGC39329, TMC4	transmembrane channel-like 4	NM_001145303, NM_144686, hCT12037.3, hCT2355036.0, hCT2355037.0	226403_at	NP_001138775.1, NP_653287.1, EAW72196.1, EAW72197.1, EAW72198.1
GeneID:353514	LILRA5	19	54,818,353	54,824,409	6,056	-	2	1_A375_pNL7_minus_lncRNA::1::3088, 2_A375_pNL97_plus_lncRNA::1::4438	8505, 8537	downstream, downstream	1	1	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LILRA5	LILRB7, ILT11, CD85, LIR9, CD85F, LILRA5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	NM_181879, NM_181985, NM_181986, NM_021250	1555634_a_at, 1555643_s_at, 215838_at, 215839_at	NP_870994.1, NP_871714.1, NP_067073.1, NP_871715.1
GeneID:114823	LENG8	19	54,960,065	54,973,196	13,131	+	4	1_A375_pNL7_minus_lncRNA::1::3089, 1_A375_pNL7_minus_lncRNA::1::3090, 2_A375_pNL97_plus_lncRNA::1::4439, 2_A375_pNL97_plus_lncRNA::1::4440	255, 15391, 351, 15727	in gene, downstream, in gene, downstream	1	1	18	22.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene LENG8	KIAA1932, MGC40108, LENG8, pp13842	leukocyte receptor cluster (LRC) member 8	NM_052925, hCT2297892.2, hCT2350686.0, hCT2350687.0	224673_at	NP_443157.1, EAW72250.1, EAW72248.1, EAW72249.1
GeneID:94059	LENG9	19	54,972,976	54,974,894	1,918	-	2	1_A375_pNL7_minus_lncRNA::1::3090, 2_A375_pNL97_plus_lncRNA::1::4440	-562, -898	upstream, upstream	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LENG9	LENG9	leukocyte receptor cluster (LRC) member 9	NM_198988, hCT1956223.2	1554589_at	NP_945339.2, EAW72251.1
GeneID:148170	CDC42EP5	19	54,976,210	54,984,422	8,212	-	2	1_A375_pNL7_minus_lncRNA::1::3090, 2_A375_pNL97_plus_lncRNA::1::4440	8966, 8630	downstream, downstream	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CDC42EP5	Borg3, MGC21945, MGC71153, CDC42EP5, CEP5	CDC42 effector protein (Rho GTPase binding) 5	NM_145057, hCT1642964.3	227850_x_at	NP_659494.2, EAW72252.1

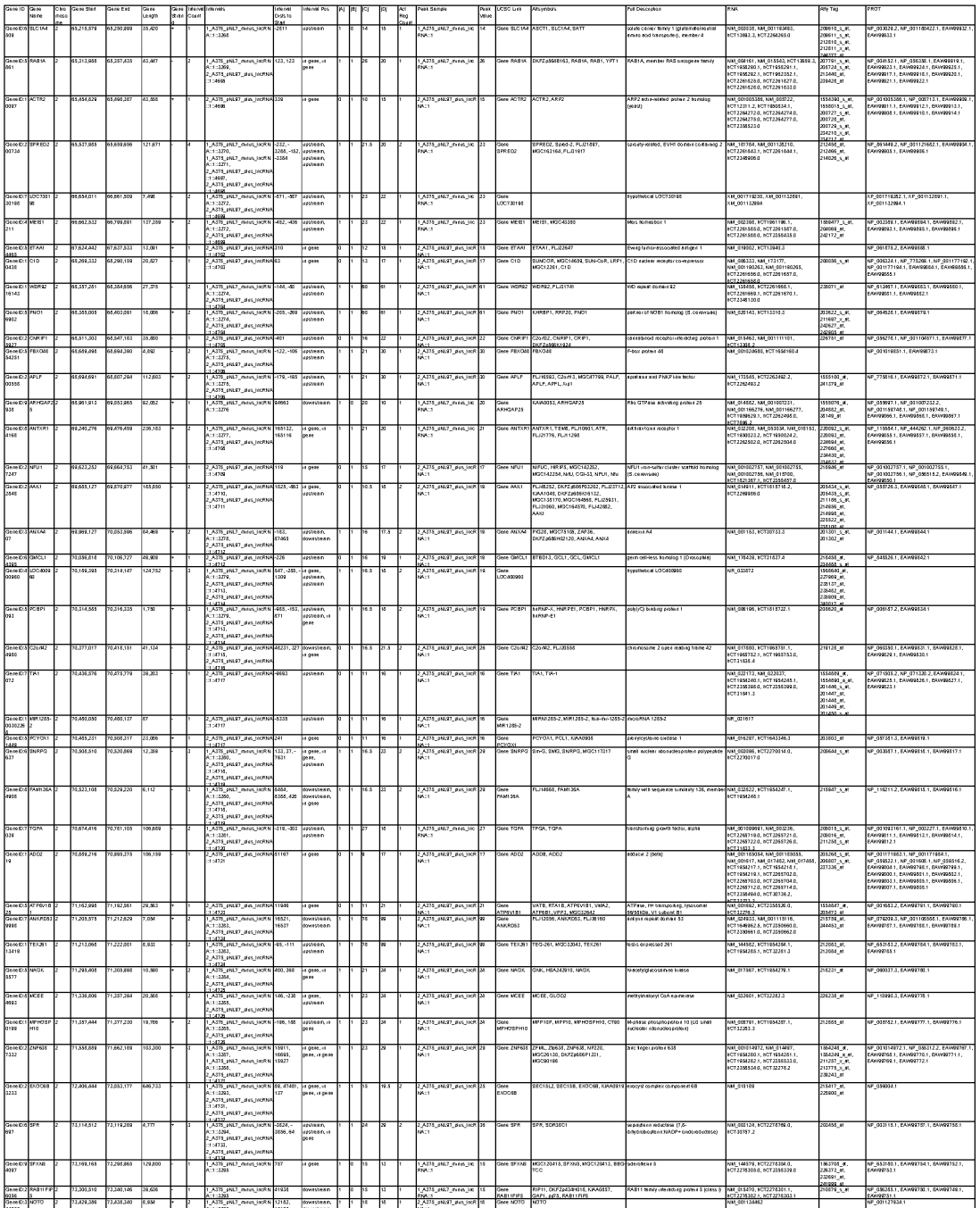
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Internal Transcripts	Internal Distance to Start	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:3	UAR2	19	53,014,013	53,021,697	7,684	+	2	1_A275_shL37_dhrot_isoRNA:1-3391, 1_A275_shL37_dhrot_isoRNA:1-4440	14997, 14755	downstream, downstream	1	1	19	29	1	2_A275_shL37_dhrot_isoRNA:1	29	Gene UAR2	CD309, UAR2, MGC71834	leukocyte-associated immunoglobulin-like receptor 2	NM_002295, NM_021270, ncT:1700066.2, ncT:1700067.2	207609_s_at	NP_002279.2, NP_067134.1, EAW72253.1, EAW72254.1
Gene:ID:6	SYT5	19	53,664,469	53,681,720	17,251	-	4	1_A275_shL37_dhrot_isoRNA:1-3392, 1_A275_shL37_dhrot_isoRNA:1-3394, 1_A275_shL37_dhrot_isoRNA:1-4442, 2_A275_shL37_dhrot_isoRNA:1-4442, 2_A275_shL37_dhrot_isoRNA:1-4442	1168, -4176, 452, -9125	at gene, upstream, at gene, upstream	1	1	23.5	22	2	1_A275_shL37_dhrot_isoRNA:1	25	Gene SYT5	SYT5		NM_003180, ncT:1700062, ncT:1952461.0, ncT:2550507.0	206161_x_at, 206162_x_at	NP_003171.2, EAW72243.1, EAW72246.1, EAW72247.1
Gene:ID:3	PTPRH	19	53,692,813	53,720,874	28,259	-	8	1_A275_shL37_dhrot_isoRNA:1-3392, 1_A275_shL37_dhrot_isoRNA:1-3394, 1_A275_shL37_dhrot_isoRNA:1-3395, 1_A275_shL37_dhrot_isoRNA:1-4442, 2_A275_shL37_dhrot_isoRNA:1-4442, 2_A275_shL37_dhrot_isoRNA:1-4442	28322, 19976, 7094, 28357, 20026, 7076	downstream, at gene, upstream, downstream, at gene, upstream	1	1	28.33	30.67	3	2_A275_shL37_dhrot_isoRNA:1	46	Gene PTPRH	MGC133056, PTPRH, MGC133056, SAP1, FLJ39638	protein tyrosine phosphatase, receptor-type, H	NM_002842, NM_001161440, ncT:1952.2	208300_at	NP_002833.2, NP_001148812.1, EAW72246.1
Gene:ID:2	TMEM868	19	53,736,002	53,740,632	2,630	-	2	1_A275_shL37_dhrot_isoRNA:1-3393, 1_A275_shL37_dhrot_isoRNA:1-3394, 1_A275_shL37_dhrot_isoRNA:1-3395, 1_A275_shL37_dhrot_isoRNA:1-4440	12664, 12164	downstream, downstream	1	1	41	46	1	2_A275_shL37_dhrot_isoRNA:1	46	Gene TMEM868	MGC30200, TMEM868	transmembrane protein 868	NM_173804, ncT:2350934.0, ncT:2350935.0	230796_at	NP_776165.2, EAW72351.1, EAW72350.1
Gene:ID:2	SAPS1	19	53,741,147	53,770,038	28,891	-	2	1_A275_shL37_dhrot_isoRNA:1-3393, 1_A275_shL37_dhrot_isoRNA:1-4440	4666, -480	upstream, upstream	1	1	25	31	1	2_A275_shL37_dhrot_isoRNA:1	31	Gene SAPS1	SAPS90, MGC135159, MGC142003, FPRP1, SAPS1, NAA1115, FPRP1	SAPS domain family, member 1	NM_014931, ncT:1105533, ncT:1952460.2, ncT:2350922.0	208229_s_at	NP_055746.3, EAW72354.1, EAW72352.1, EAW72353.1
Gene:ID:2	HSPBP1	19	53,773,991	53,791,751	16,760	-	2	1_A275_shL37_dhrot_isoRNA:1-3390, 1_A275_shL37_dhrot_isoRNA:1-4436	21047, 21223	downstream, downstream	1	1	28	31	1	2_A275_shL37_dhrot_isoRNA:1	31	Gene HSPBP1	FES1, HSPBP1	HSPA (heat shock 70 kDa) binding protein, cytoplasmic cochaperone 1	NM_001130196, NM_012267, ncT:2267171.1, ncT:2267172.1, ncT:2267173.1, ncT:2267174.1	202415_s_at	NP_001123578.1, NP_036299.2, EAW72358.1, EAW72359.1, EAW72357.1, EAW72356.1
Gene:ID:2	UBE2E	19	53,812,650	53,819,325	6,675	-	2	1_A275_shL37_dhrot_isoRNA:1-3397, 1_A275_shL37_dhrot_isoRNA:1-4447	125, -221	at gene, upstream	1	1	17	21	1	2_A275_shL37_dhrot_isoRNA:1	21	Gene UBE2E	E2EPF, E2-EPF, UBE2S, EPF1	ubiquitin-conjugating enzyme E2E	NM_014501, ncT:1960779.1	202779_s_at	NP_055316.2, EAW72377.1
Gene:ID:7	SHISA7	19	53,940,103	53,954,230	14,125	+	2	1_A275_shL37_dhrot_isoRNA:1-3398, 1_A275_shL37_dhrot_isoRNA:1-4451	5350, 5324	at gene, at gene	1	1	48	52	1	2_A275_shL37_dhrot_isoRNA:1	52	Gene SHISA7	FLJ35290, FLJ37680, MGC129235, FLJ39341, MGC135402, SHISA7, DKFZp547H214	shisa homolog 7 (Xenopus laevis)	NM_001145176		NP_001138648.1
Gene:ID:6	ZNF626	19	53,967,699	53,993,834	6,136	+	3	1_A275_shL37_dhrot_isoRNA:1-3399, 1_A275_shL37_dhrot_isoRNA:1-4449, 2_A275_shL37_dhrot_isoRNA:1-4449	733, 366, 677	at gene, at gene, at gene	1	1	23	30.3	2	2_A275_shL37_dhrot_isoRNA:1	30	Gene ZNF626	MGC105139, ZNF626, Zfp626, ZEC	zinc finger protein 626	NM_033113	236269_at	NP_149104.2
Gene:ID:3	NAT14	19	53,999,594	53,998,035	2,341	+	3	1_A275_shL37_dhrot_isoRNA:1-3399, 1_A275_shL37_dhrot_isoRNA:1-4449, 2_A275_shL37_dhrot_isoRNA:1-4449	-6162, -8626, -8015	upstream, upstream, upstream	1	1	23	30.3	2	2_A275_shL37_dhrot_isoRNA:1	30	Gene NAT14	KLP1, NAT14	N-acetyltransferase 14 (GCN5-related, putative)	NM_030776, ncT:1952113.1, ncT:2268.2	232264_at	NP_0651111, EAW72358.1, EAW72356.1
Gene:ID:2	SSC5D	19	53,999,670	56,030,466	30,796	+	2	1_A275_shL37_dhrot_isoRNA:1-3399, 1_A275_shL37_dhrot_isoRNA:1-4449	31295, 31295	downstream, downstream	1	1	16	35	1	2_A275_shL37_dhrot_isoRNA:1	35	Gene SSC5D	SSC5D	scavenger receptor cysteine-rich glycoprotein	NM_001144950	235226_at	NP_001135622.1
Gene:ID:9	SBK2	19	54,041,100	54,048,439	7,339	+	2	1_A275_shL37_dhrot_isoRNA:1-3390, 1_A275_shL37_dhrot_isoRNA:1-4440	17299, 17299	downstream, downstream	1	1	16	35	1	2_A275_shL37_dhrot_isoRNA:1	35	Gene SBK2	SBK2, BC030089	SH3-binding domain kinase family, member 2	NM_001101451		NP_001094871.2
Gene:ID:1	ZNF579	19	54,055,891	56,097,211	2,130	-	1	1_A275_shL37_dhrot_isoRNA:1-4452	-733	upstream	0	1	12	20	1	2_A275_shL37_dhrot_isoRNA:1	20	Gene ZNF579	FLJ38453, ZNF579	zinc finger protein 579	NM_152600, ncT:2341153.0	226140_at, 236703_at	NP_689513.2, EAW72360.1
Gene:ID:8	PIZ1	19	56,102,727	56,110,693	8,186	-	2	1_A275_shL37_dhrot_isoRNA:1-3391, 1_A275_shL37_dhrot_isoRNA:1-4452, 2_A275_shL37_dhrot_isoRNA:1-4452	-563, 17592, 499	downstream, downstream, upstream	1	1	22	22	2	1_A275_shL37_dhrot_isoRNA:1	22	Gene PIZ1	ZNF748, FLH14768, PIZ1, FLJ30416	PLT3-interacting zinc finger 1	NM_032636, ncT:2297147.0, ncT:29063.2	236967_at, 236663_x_at	NP_116233.2, EAW72362.1, EAW72361.1
Gene:ID:1	ZNF324	19	56,111,730	56,114,504	2,774	+	2	1_A275_shL37_dhrot_isoRNA:1-3391, 1_A275_shL37_dhrot_isoRNA:1-4452	-274, -258	upstream, upstream	1	1	32	38	1	1_A275_shL37_dhrot_isoRNA:1	32	Gene ZNF324	ZNF324, MGC23143	zinc finger protein 324	NM_152319	236663_at	NP_689511.1
Gene:ID:5	ZNF980	19	56,152,092	56,154,836	2,744	+	4	1_A275_shL37_dhrot_isoRNA:1-3392, 1_A275_shL37_dhrot_isoRNA:1-3393, 1_A275_shL37_dhrot_isoRNA:1-4456, 2_A275_shL37_dhrot_isoRNA:1-4456	-1765, -7000, 2584, 7096	upstream, downstream, downstream, downstream	1	1	24.67	26.67	3	2_A275_shL37_dhrot_isoRNA:1	44	Gene ZNF980	ZNF550		NM_207115, NM_016352, NM_001163423, ncT:2296564.0	235746_s_at	NP_996993.1, NP_057286.1, NP_001156558.1, EAW72399.1
Gene:ID:5	ZNF561	19	56,154,666	56,156,669	2,003	+	4	1_A275_shL37_dhrot_isoRNA:1-3392, 1_A275_shL37_dhrot_isoRNA:1-3393, 1_A275_shL37_dhrot_isoRNA:1-4456, 2_A275_shL37_dhrot_isoRNA:1-4456	-4362, -6606, -92, 4502	upstream, downstream, upstream, downstream	1	1	24.67	26.67	3	2_A275_shL37_dhrot_isoRNA:1	44	Gene ZNF561	ZNF551, FLJ22530, HSPC109	zinc finger protein 561	NM_018535, ncT:2296556.0	223309_s_at	NP_057619.1, EAW72400.1
Gene:ID:2	CCDC106	19	56,156,654	56,164,827	8,173	+	4	1_A275_shL37_dhrot_isoRNA:1-3392, 1_A275_shL37_dhrot_isoRNA:1-3393, 1_A275_shL37_dhrot_isoRNA:1-4456, 2_A275_shL37_dhrot_isoRNA:1-4456	-4330, 455, -9978, 534	upstream, at gene, upstream, at gene	1	1	24.67	26.67	3	2_A275_shL37_dhrot_isoRNA:1	44	Gene CCDC106	ZNF551, CCDC106, HSUT6303	coiled-coil domain containing 106	NM_018301, ncT:1957623.1	207009_s_at	NP_037433.2, EAW72401.1
Gene:ID:1	UZAP2	19	56,165,416	56,166,652	20,866	+	4	1_A275_shL37_dhrot_isoRNA:1-3393, 1_A275_shL37_dhrot_isoRNA:1-3394, 1_A275_shL37_dhrot_isoRNA:1-4458, 2_A275_shL37_dhrot_isoRNA:1-4458	-6024, 21112, 5926, 20964	upstream, downstream, upstream, downstream	1	1	30	31.5	2	2_A275_shL37_dhrot_isoRNA:1	44	Gene UZAP2	UZAP65, UZAP2	UZ UHM nuclear RNA auxiliary factor 2	NM_057279, NM_001012675, ncT:1952125.1, ncT:2295502.0, ncT:63676.2	214171_x_at, 215351_s_at, 216352_s_at, 226508_at	NP_002010.1, NP_001012095.1, EAW72452.1, EAW72453.1, EAW72456.1
Gene:ID:2	EPN1	19	56,189,961	56,207,133	20,972	-	2	1_A275_shL37_dhrot_isoRNA:1-3393, 1_A275_shL37_dhrot_isoRNA:1-4458	-33, -161	upstream, upstream	1	1	21	19	1	1_A275_shL37_dhrot_isoRNA:1	21	Gene EPN1	EPN1		NM_001130072, NM_013332, NM_001130071, ncT:1952123.1, ncT:1952124.1, ncT:2354998.0, ncT:63675.1	221141_x_at, 236667_s_at	NP_001123544.1, NP_037463.2, NP_001123543.1, EAW72405.1, EAW72406.1, EAW72408.1, EAW72407.1
Gene:ID:1	NLRP11	19	56,299,763	56,308,128	51,365	-	1	1_A275_shL37_dhrot_isoRNA:1-3393	27392	at gene	1	0	20	17	1	1_A275_shL37_dhrot_isoRNA:1	20	Gene NLRP11	FLJ36273, PYPAF7, PYPAF9, NALP11, PAN10, NLRP11, NOD17, CLR19.6	NLR family, pyrin domain containing 11	NM_145007, ncT:2341190.0, ncT:2341187.0	1552531_at, 1557433_at	NP_659447.2, EAW72416.1, EAW72415.1
Gene:ID:1	NLRP5	19	56,511,092	56,573,176	62,084	+	1	2_A275_shL37_dhrot_isoRNA:1-4457	16292	at gene	0	1	8	17	1	2_A275_shL37_dhrot_isoRNA:1	17	Gene NLRP5	NLRP5, PYPAF5, CLR19.2, NALP5, MATER, PAN11	NLR family, pyrin domain containing 5	NM_153447	1552003_at	NP_703148.4
Gene:ID:5	ZNF444	19	56,652,596	56,672,262	19,706	+	1	2_A275_shL37_dhrot_isoRNA:1-4458	-105	upstream	0	1	15	25	1	2_A275_shL37_dhrot_isoRNA:1	25	Gene ZNF444	ZSCAN17, FLJ11137, EZF-2, ZNF444, EZF.2	zinc finger protein 444	NM_015137, NCT:1952126.1, NCT:1985557.1, NCT:1985555.1, NCT:1985559.1, NCT:1985560.1, NCT:2296552.0, NCT:2296553.0	210707_at, 90376_at	NP_056007.2, EAW72427.1, EAW72424.1, EAW72429.1, EAW72426.1, EAW72430.1, EAW72431.1, EAW72426.1, EAW72428.1
Gene:ID:6	ZSCAN30	19	56,751,773	56,755,866	7,093	+	1	1_A275_shL37_dhrot_isoRNA:1-3399	12515	downstream	1	0	16	15	1	1_A275_shL37_dhrot_isoRNA:1	16	Gene ZSCAN30	ZNF495D, ZSCAN30	zinc finger and SCAN domain containing 30	NM_031729.2		XP_001729620.1
Gene:ID:1	LOC1003 96374	19	56,812,303	56,821,819	8,514	+	1	2_A275_shL37_dhrot_isoRNA:1-3400	12639	downstream	0	1	14	16	1	2_A275_shL37_dhrot_isoRNA:1	16	Gene LOC100396374	hypothetical LOC100396374	XR_109498		
Gene:ID:3	ZNF471	19	57,019,212	57,040,270	21,058	+	1	2_A275_shL37_dhrot_isoRNA:1-3400	28724	downstream	0	1	15	20	1	2_A275_shL37_dhrot_isoRNA:1	20	Gene ZNF471	ERP1, MGC139598, ZNF471, ZIR71, KIAA1295, MGC130587	zinc finger protein 471	NM_032813, ncT:1942389.2, ncT:2296572.0, ncT:2354999.0	211623_s_at, 232117_at	NP_116064.2, EAW72459.1, EAW72460.1, EAW72461.1
Gene:ID:2	ZFP28	19	57,030,217	57,068,170	17,953	+	1	2_A275_shL37_dhrot_isoRNA:1-3400	-281	upstream	0	1	15	20	1	2_A275_shL37_dhrot_isoRNA:1	20	Gene ZFP28	KIAA1431, mKIAA1431, DKFZp686I02203, MGC104580, ZFP28	zinc finger protein 28 homolog (mouse)	NM_020928, ncT:1952358.2, ncT:2296570.0, ncT:2295672.0	221643_at, 234300_s_at, 234927_s_at, 240865_at	NP_065781.1, EAW72463.1, EAW72464.1, EAW72465.1
Gene:ID:1	LOC1003 96419	19	57,036,633	57,076,762	21,567	-	2	2_A275_shL37_dhrot_isoRNA:1-3400, 2_A275_shL37_dhrot_isoRNA:1-4460	28546, 193	downstream, at gene	0	1	13	19	2	2_A275_shL37_dhrot_isoRNA:1	20	Gene LOC100396419	hypothetical LOC100396419	XR_111902, XR_109500, XR_115326		
Gene:ID:2	ZNF470	19	57,076,890	57,094,262	15,372	+	1	2_A275_shL37_dhrot_isoRNA:1-3400	-268	upstream	0	1	11	15	1	2_A275_shL37_dhrot_isoRNA:1	16	Gene ZNF470	ZNF470, FLJ26546, CZF-1, FLJ26178	zinc finger protein 470	NM_001001665, NCT:1633578.3	234621_at	NP_001001665.3, EAW72466.1
Gene:ID:5	ZNF71	19	57,109,664	57,133,550	23,886	+	1	2_A275_shL37_dhrot_isoRNA:1-4462	56	at gene	0	1	9	15	1	2_A275_shL37_dhrot_isoRNA:1	15	Gene ZNF71	ZNF71, EZF17	zinc finger protein 71	NM_021716, NCT:1952126.1, NCT:63276.2	206514_at, 233734_x_at, 234570_at, 241078_at	NP_067039.1, EAW72467.1, EAW72468.1
Gene:ID:1	LOC1076 70	19	57,154,527	57,165,614	14,087	-	2	1_A275_shL37_dhrot_isoRNA:1-3401, 1_A275_shL37_dhrot_isoRNA:1-4462	-4991, -4839	upstream, upstream	1	1	134	144	1	2_A275_shL37_dhrot_isoRNA:1	144	Gene LOC107670	hypothetical protein LOC107670	NM_001163628		1557430_at	NP_001155157.1
Gene:ID:9	ZNF264	19	57,702,665	57,734,214	31,549	+	1	2_A275_shL37_dhrot_isoRNA:1-4464	-116	upstream	0	1	8	15	1	2_A275_shL37_dhrot_isoRNA:1	15	Gene ZNF264	ZNF264	zinc finger protein 264	NM_003417, NCT:1793300.2, NCT:2295433.0	1556695_at, 203017_at, 220052_at	NP_003408.1, EAW72483.1, EAW72482.1
Gene:ID:9	AURKC	19	57,742,277	57,749,816	8,539	+	2	1_A275_shL37_dhrot_isoRNA:1-3395, 1_A275_shL37_dhrot_isoRNA:1-4465	6607, 6763	downstream, downstream	1	1	16	23	1	2_A275_shL37_dhrot_isoRNA:1	23	Gene AURKC	aurora-C, AIK2, STK13, AIK3, ARK3, AurC, AURKC	aurora kinase C	NM_003160, NCT:1950035.0, NCT:63275.1	211107_s_at	NP_001158576.1, NP_001015878.1, NP_003151.2, EAW72485.1, EAW72486.1
Gene:ID:2	ZNF805	19	57,752,052	57,774,106	22,053	+	2	1_A275_shL37_dhrot_isoRNA:1-3395, 1_A275_shL37_dhrot_isoRNA:1-4465	169, 27	upstream, at gene	1	1	16	23	1	2_A275_shL37_dhrot_isoRNA:1	23	Gene ZNF805	DKFZp686P06106, ZNF805	zinc finger protein 805	NM_001033963, NM_001145076	235395_at, 238436_s_at, 238437_at	NP_001029135.2, NP_001135580.1
Gene:ID:1	ZNF460	19	57,791,553	57,803,436	13,883	+	1	2_A275_shL37_dhrot_isoRNA:1-4466	-49	upstream	0	1	17	26	1	2_A275_shL37_dhrot_isoRNA:1	26	Gene ZNF460	ZNF460, HZF6, ZNF272	zinc finger protein 460	NM__006635	216273_at, 216279_at, 231173_at	NP_009626.3
Gene:ID:5	ZNF324	19	57,862,643	57,871,266	8,621	+	3	1_A275_shL37_dhrot_isoRNA:1-3396, 1_A275_shL37_dhrot_isoRNA:1-3710, 1_A275_shL37_dhrot_isoRNA:1-4466, 2_A275_shL37_dhrot_isoRNA:1-4466	-27, 12391, 12235	upstream, downstream, downstream	1	1	16	16.5	2	2_A275_shL37_dhrot_isoRNA:1	23	Gene ZNF324	MGC129703, MGC129704, ZNF324	zinc finger protein 324	NM_030637, NCT:1811635.1, NCT:2291400.0	207753_at	NP_057016.2, EAW72498.1, EAW72492.1
Gene:ID:2	ZNF547	19	57,874,691	57,890,827	16,026	+	2	1_A275_shL37_dhrot_isoRNA:1-3710, 1_A275_shL37_dhrot_isoRNA:1-4466, 2_A275_shL37_dhrot_isoRNA:1-4466	-150, -11, 26165	upstream, upstream, downstream	1	1	16.5	19.5	2	2_A275_shL37_dhrot_isoRNA:1	23	Gene ZNF547	FLJ31100, ZNF547	zinc finger protein 547	NM__173631, NCT:1952114.1, NCT:2295402.0, NCT:2354999.0, NCT:64286.2	1562764_a_at, 1565993_at	NP_775802.2, EAW72497.1, EAW72495.1, EAW72496.1, EAW72498.1
Gene:ID:1	ZNF546	19	57,901,218	57,913,819	12,781	+	3	1_A275_shL37_dhrot_isoRNA:1-3396, 1_A275_shL37_dhrot_isoRNA:1-3711, 1_A275_shL37_dhrot_isoRNA:1-4466, 2_A275_shL37_dhrot_isoRNA:1-4466	126, -162, 21496	at gene, upstream, downstream	1	1	17.5	18.5	2	2_A275_shL37_dhrot_isoRNA:1	18	Gene ZNF546	ZNF546, FLJ32932	zinc finger protein 546	NM_152609, NM_001177573, NCT:1811629.2	1563716_at, 1563719_s_at, 1563622_s_at	NP_689573.2, NP_001166244.1, EAW72499.1
Gene:ID:7	ZNF17	19	57,922,529	57,933,207	10,778	+	1	2_A275_shL37_dhrot_isoRNA:1-4469	148	at gene	0	1	20	15	1	2_A275_shL37_dhrot_isoRNA:1	15	Gene ZNF17	KOX10, FLJ98615, KIAA1987, FLJ98055	zinc finger protein 17	NM_006959, NCT:1953381.1	1555163_at, 1555164_s_at	NP_008890.2, EAW72500.1
Gene:ID:3	ZNF749	19	57,949,693	57,957,191	10,498	+	1	2_A275_shL37_dhrot_isoRNA:1-4470	27	at gene	0	1	16	21	1	2_A275_shL37_dhrot_isoRNA:1	21	Gene ZNF749	ZNF749, FLJ16263, FLJ16360	zinc finger protein 749	NM_020923.3561	215299_at	NP_001018553.2
Gene:ID:3	ZNF416	19	58,052,934	58,060,243	7,309	-	2	1_A275_shL37_dhrot_isoRNA:1-4471, 2_A275_shL37_dhrot_isoRNA:1-4472	-125, -5099	upstream, upstream	1	1	12	16.5	2	2_A275_shL37_dhrot_isoRNA:1	16	Gene ZNF416	FLJ33537, ZNF416	zinc finger protein 416	NM_017679, NCT:1627636.3, NCT:2276566.0	223509_at, 234902_s_at	NP_0053416.1, EAW72515.1, EAW72514.1
Gene:ID:2	ZIK1	19	58,093,825	58,103,755	8,130	+	2	1_A275_shL37_dhrot_isoRNA:1-4471, 2_A275_shL37_dhrot_isoRNA:1-4472	-3260, -316	upstream, upstream	1	1	12	16.5	2	2_A275_shL37_dhrot_isoRNA:1	16	Gene ZIK1	ZNF762, ZIK1, MGC119701, MGC119700, MGC119699	zinc finger protein interacting with K protein 1 homolog (mouse)	NM_001010978, NCT:1942140.2	232774_x_at, 233773_at	NP_001010978.2, EAW72516.1
Gene:ID:2	ZSCAN4	19	58,169,303	58,180,820	10,217	+	1	2_A275_shL37_dhrot_isoRNA:1-4473	13103	downstream	0	1	16	19	1	2_A275_shL37_dhrot_isoRNA:1	19	Gene ZSCAN4	ZSCAN4, FLJ35109, MGC126769, MGC126767, ZNF800	zinc finger and SCAN domain containing 4	NM_152677, NCT:2341152.0	1552551_at, 1552552_s_at	NP_689901.1, EAW72523.1
Gene:ID:9	ZNF551	19	58,193,297	58,201,179	7,822	+	1	2_A275_shL37_dhrot_isoRNA:1-4473	31	at gene	0	1	16	19	1	2_A275_shL37_dhrot_isoRNA:1	19	Gene ZNF551	DKFZp686H1035, MGC52307, ZNF551	zinc finger protein 551	NM_1.82347, NCT:1811632.2	231721_s_at, 242992_at, 243193_s_at	NP_612356.1, EAW72524.1
Gene:ID:1	ZNF286	19	58,452,201	58,459,077	6,876	+	2	1_A275_shL37_dhrot_isoRNA:1-3412, 2_A275_shL37_dhrot_isoRNA:1-4478	-122, -183	upstream, upstream	1	1	21	22	1	2_A275_shL37_dhrot_isoRNA:1	22	Gene ZNF286	BM273, BM27-1, ZNF286	zinc finger protein 286	NM_003772, NCT:2013642.3	223714_at	NP_0037642.2, EAW72548.1
Gene:ID:6	ZNF805	19	58,555,680	58,814,714	26,274	+	2	1_A275_shL37_dhrot_isoRNA:1-3413, 2_A275_shL37_dhrot_isoRNA:1-4479	586, -6302	at gene, upstream	1	1	15	15	2	2_A275_shL37_dhrot_isoRNA:1	16	Gene ZNF805	KIAA1452, FLJ14260, ZNF806, ZNF526	zinc finger protein 806	NM_025227, NCT:1633414.2, NCT:1953164.2, NCT:2350071.0	219655_at, 224707_at	NP_079503.2, EAW72547.1, EAW72546.1, EAW72545.1
Gene:ID:1	LOC1001 26266	19	58,814,262	58,816,974	4,312	+	2	1_A275_shL37_dhrot_isoRNA:1-3413, 2_A275_shL37_dhrot_isoRNA:1-4479	-134, -9954	upstream, downstream	1	1	15	15	2	2_A275_shL37_dhrot_isoRNA:1	16	Gene LOC100126266	hypothetical LOC100126266	XR_039365		
Gene:ID:7	ZNF329	19	58,837,998	58,862,148	24,483	+	1	2_A275_shL37_dhrot_isoRNA:1-4479	4196	upstream	0	1	17	16	1	2_A275_shL37_dhrot_isoRNA:1	16	Gene ZNF329	FLJ12586, ZNF329	zinc finger protein 329	NM_024620, NCT:1636120.3, NCT:2297325.1, NCT:2341169.0, NCT:2350540.0	218765_at	NP_078996.3, EAW72561.1, EAW72560.1, EAW72562.1
Gene:ID:2	ZNF544	19	58,740,070	58,775,610	34,540	+	1	1_A275_shL37_dhrot_isoRNA:1-3414	216	at gene	0	1	23	14	1	1_A275_shL37_dhrot_isoRNA:1	23	Gene ZNF544	ZNF544	zinc finger protein 544	NM_014600, NCT:1653265.1, NCT:2352327.1	218733_s_at, 240896_at	NP_055743.2, EAW72569.1, EAW72568.1
Gene:ID:1	LOC1003 96561	19	58,770,394	58,790,157	19,763	-	1	1_A275_shL37_dhrot_isoRNA:1-4477	-360	upstream	0	1	13	16	1	1_A275_shL37_dhrot_isoRNA:1	16	Gene LOC100396561	hypothetical LOC100396561	XR_109503		
Gene:ID:7	ZNF6	19	58,790,318	58,807,254	16,936	+	2	1_A275_shL37_dhrot_isoRNA:1-3415, 1_A275_shL37_dhrot_isoRNA:1-4477, 2_A275_shL37_dhrot_isoRNA:1-4478	28416, 199, 26389	downstream, at gene, downstream	1	1	16	19.5	2	2_A275_shL37_dhrot_isoRNA:1	23	Gene ZNF6	HF.16, ZNF6_ZK126	zinc finger protein 6	NM_021999, NCT:2297018.1	214601_at	NP_0695713.2, EAW72570.1
Gene:ID:1	LOC1003 96564	19	58,816,743	58,827,823	10,280	-	2	1_A275_shL37_dhrot_isoRNA:1-3415, 1_A275_shL37_dhrot_isoRNA:1-4478	17, -39	upstream, upstream	1	1	23	23	1	1_A275_shL37_dhrot_isoRNA:1	23	Gene LOC100396564	FLJ30309, DKFZp313G2310, MGC16727	hypothetical protein LOC100396564	XM_002117456		XP_002115814.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:342945	ZSCAN22	19	58,838,385	58,853,712	15,327	+	2	1_A375_pNL7_minus_lncRNA::1::3116, 2_A375_pNL97_plus_lncRNA::1::4479	175, 271	in gene, in gene	1	1	34	34	1	1_A375_pNL7_minus_lncRNA::1	34	Gene ZSCAN22	MGC138482, HKR2, ZSCAN22, MGC126679, ZNF50	zinc finger and SCAN domain containing 22	NM_181846, hCT2350522.0	228769_at	NP_862829.1, EAW72574.1
GeneID:1	A1BG	19	58,858,172	58,864,865	6,693	-	2	1_A375_pNL7_minus_lncRNA::1::3117, 2_A375_pNL97_plus_lncRNA::1::4480	-8959, -9039	upstream, upstream	1	1	22	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene A1BG	A1B, A1BG, GAB, ABG, DKFZp686F0970, HYST2477	alpha-1-B glycoprotein	NM_130786, hCT1953212.1	229819_at	NP_570602.2, EAW72575.1
GeneID:503538	NCRNA00181	19	58,863,336	58,866,549	3,213	+	2	1_A375_pNL7_minus_lncRNA::1::3117, 2_A375_pNL97_plus_lncRNA::1::4480	10488, 10568	downstream, downstream	1	1	22	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene NCRNA00181	A1BG-AS, A1BGAS, NCRNA00181, FLJ23569, A1BG-AS1	A1BG antisense RNA (non-protein coding)	NR_015380	232462_s_at	
GeneID:162968	ZNF497	19	58,865,725	58,874,120	8,395	-	2	1_A375_pNL7_minus_lncRNA::1::3117, 2_A375_pNL97_plus_lncRNA::1::4480	296, 216	in gene, in gene	1	1	22	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ZNF497	FLJ44773, ZNF497, FLJ42722	zinc finger protein 497	NM_198458, hCT201367.4, hCT2355032.0	230857_s_at	NP_940860.1, EAW72577.1, EAW72578.1
GeneID:116412	ZNF837	19	58,878,990	58,892,389	13,399	-	5	1_A375_pNL7_minus_lncRNA::1::3117, 1_A375_pNL7_minus_lncRNA::1::3118, 2_A375_pNL97_plus_lncRNA::1::4480, 2_A375_pNL97_plus_lncRNA::1::4481, 2_A375_pNL97_plus_lncRNA::1::4482	18565, 165, 18485, 197, -6155	downstream, in gene, downstream, in gene, upstream	1	1	20	22.33	3	2_A375_pNL97_plus_lncRNA::1	25	Gene ZNF837	ZNF837	zinc finger protein 837	NM_138466, NM_001128730	1556822_s_at, 241277_x_at	NP_612475.1, NP_001123202.1
GeneID:6193	RPS5	19	58,898,636	58,906,171	7,535	+	4	1_A375_pNL7_minus_lncRNA::1::3118, 2_A375_pNL97_plus_lncRNA::1::4481, 2_A375_pNL97_plus_lncRNA::1::4482, 2_A375_pNL97_plus_lncRNA::1::4483	-6412, -6444, -92, 14356	upstream, upstream, upstream, downstream	1	1	17	21	3	2_A375_pNL97_plus_lncRNA::1	25	Gene RPS5	S5, RPS5	ribosomal protein S5	NM_001009, hCT1962048.1, hCT1962050.1, hCT2355075.0	200024_at	NP_001000.2, EAW72582.1, EAW72581.1, EAW72583.1
GeneID:100506612	LOC100506612	19	58,907,457	58,908,446	989	+	2	2_A375_pNL97_plus_lncRNA::1::4482, 2_A375_pNL97_plus_lncRNA::1::4483	-8913, 5535	upstream, downstream	0	1	15	19	2	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100506612		hypothetical protein LOC100506612	XM_003118767		XP_003118815.1
GeneID:100506657	LOC100506657	19	58,911,409	58,913,269	1,860	-	3	1_A375_pNL7_minus_lncRNA::1::3119, 2_A375_pNL97_plus_lncRNA::1::4483, 2_A375_pNL97_plus_lncRNA::1::4484	-6843, 277, -7011	upstream, in gene, upstream	1	1	18	18	2	1_A375_pNL7_minus_lncRNA::1	23	Gene LOC100506657		hypothetical LOC100506657	XR_111904, XR_109506, XR_115331		
GeneID:100506634	LOC100506634	19	58,915,605	58,918,663	3,058	-	3	1_A375_pNL7_minus_lncRNA::1::3119, 2_A375_pNL97_plus_lncRNA::1::4483, 2_A375_pNL97_plus_lncRNA::1::4484	-1449, 5671, -1617	upstream, downstream, upstream	1	1	18	18	2	1_A375_pNL7_minus_lncRNA::1	23	Gene LOC100506634		hepatocellular carcinoma-associated antigen HCA25a	XM_003118768, XM_003120972		XP_003118816.1, XP_003121020.1
GeneID:201514	ZNF584	19	58,920,063	58,929,694	9,631	+	3	1_A375_pNL7_minus_lncRNA::1::3119, 2_A375_pNL97_plus_lncRNA::1::4483, 2_A375_pNL97_plus_lncRNA::1::4484	49, -7071, 217	in gene, upstream, in gene	1	1	18	18	2	1_A375_pNL7_minus_lncRNA::1	23	Gene ZNF584	ZNF584, FLJ39899	zinc finger protein 584	NM_173548, hCT1953170.1, hCT1953171.1, hCT2355012.0	226146_at	NP_775819.1, EAW72587.1, EAW72588.1, EAW72589.1
GeneID:388569	ZNF324B	19	58,962,971	58,969,199	6,228	+	1	2_A375_pNL97_plus_lncRNA::1::4485	261	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ZNF324B	FLJ45850, ZNF324B	zinc finger protein 324B	NM_207395, hCT2346513.0	222318_at, 236406_at	NP_997278.2, EAW72593.1
GeneID:10998	SLC27A5	19	59,009,700	59,023,432	13,732	-	3	1_A375_pNL7_minus_lncRNA::1::3120, 2_A375_pNL97_plus_lncRNA::1::4486, 2_A375_pNL97_plus_lncRNA::1::4487	-7960, -2104, -7992	upstream, upstream, upstream	1	1	19	24.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene SLC27A5	SLC27A5, FATP5, ACSVL6, ACSB, VLCSH2, VLCSH2, FACVL3, FLJ22987, VLACSR	solute carrier family 27 (fatty acid transporter), member 5	NM_012254, hCT201372.2	219733_s_at, 234948_at	NP_036386.1, EAW72601.1
GeneID:84878	ZBTB45	19	59,024,897	59,030,921	6,024	-	3	1_A375_pNL7_minus_lncRNA::1::3120, 2_A375_pNL97_plus_lncRNA::1::4486, 2_A375_pNL97_plus_lncRNA::1::4487	-471, 5385, -503	upstream, in gene, upstream	1	1	19	24.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene ZBTB45	ZBTB45, DKFZp547H249, FLJ14486, ZNF499	zinc finger and BTB domain containing 45	NM_032792, hCT1647692.3, hCT1953164.1, hCT1967084.1	229862_x_at, 240551_at	NP_116181.1, EAW72602.1, EAW72603.1, EAW72604.1
GeneID:10155	TRIM28	19	59,055,836	59,062,082	6,246	+	2	1_A375_pNL7_minus_lncRNA::1::3121, 2_A375_pNL97_plus_lncRNA::1::4488	14596, 10660	downstream, downstream	1	1	18	15	2	1_A375_pNL7_minus_lncRNA::1	20	Gene TRIM28	RNF96, TRIM28, KAP1, FLJ29029, TF1B, TIF1B	tripartite motif containing 28	NM_005762, hCT1953193.2, hCT1953194.2, hCT201356.3	200990_at	NP_005753.1, EAW72605.1, EAW72606.1, EAW72607.1
GeneID:27243	CHMP2A	19	59,062,933	59,066,486	3,553	-	2	1_A375_pNL7_minus_lncRNA::1::3121, 2_A375_pNL97_plus_lncRNA::1::4488	-3946, -10	upstream, upstream	1	1	18	15	2	1_A375_pNL7_minus_lncRNA::1	20	Gene CHMP2A	CHMP2A, BC2, CHMP2, VPS2, VPS2A, BC-2	chromatin modifying protein 2A	NM_198426, NM_014453, hCT1953197.1, hCT201358.2, hCT2355073.0, hCT2355074.0	202121_s_at	NP_940818.1, NP_055268.1, EAW72608.1, EAW72609.1, EAW72610.1, EAW72611.1
GeneID:9040	UBE2M	19	59,067,079	59,070,343	3,264	-	2	1_A375_pNL7_minus_lncRNA::1::3121, 2_A375_pNL97_plus_lncRNA::1::4488	-89, 3847	upstream, downstream	1	1	18	15	2	1_A375_pNL7_minus_lncRNA::1	20	Gene UBE2M	UBC-RS2, UBC12, UBE2M, hUbc12	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	NM_003969, hCT2297306.1, hCT2297309.1	203109_at	NP_003960.1, EAW72612.1, EAW72613.1
GeneID:100131691	LOC100131691	19	59,070,592	59,086,164	15,572	+	2	1_A375_pNL7_minus_lncRNA::1::3121, 2_A375_pNL97_plus_lncRNA::1::4488	-160, -4096	upstream, upstream	1	1	18	15	2	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100131691		hypothetical LOC100131691	NR_027334		
GeneID:7593	MZF1	19	59,073,284	59,084,942	11,658	-	2	1_A375_pNL7_minus_lncRNA::1::3121, 2_A375_pNL97_plus_lncRNA::1::4488	14510, 18446	downstream, downstream	1	1	18	15	2	1_A375_pNL7_minus_lncRNA::1	20	Gene MZF1	MZF1, MZF-1, MZF1B, ZNF42, ZSCAN6, Zfp98	myeloid zinc finger 1	NM_198055, NM_003422, hCT2297303.1, hCT2297304.1, hCT2297307.1, hCT2297308.1, hCT2297310.1	204138_s_at, 204139_x_at, 210336_x_at, 40569_at	NP_932172.1, NP_003413.2, EAW72614.1, EAW72615.1, EAW72616.1, EAW72618.1, EAW72617.1
GeneID:26751	SH3YL1	2	218,136	264,068	45,932	-	1	1_A375_pNL7_minus_lncRNA::1::3122	-796	upstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SH3YL1	FLJ39121, RAY, SH3YL1, DKFZp586F1318	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	NM_015677, NM_001159597	1554198_at, 204019_s_at	NP_056492.2, NP_001153069.1
GeneID:52	ACP1	2	264,869	278,283	13,414	+	1	1_A375_pNL7_minus_lncRNA::1::3122	-5	upstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ACP1	HAAP, MGC111030, ACP1, MGC3499	acid phosphatase 1, soluble	NM_001040649, NM_004300, NM_007099, NR_024080, hCT1823781.2, hCT1962197.1, hCT1962198.1, hCT1962199.1, hCT2267768.0, hCT2358351.0	1554808_at, 201629_s_at, 201630_s_at, 215227_x_at	NP_001035739.1, NP_004291.1, NP_009030.1, EAX01111.1, EAX01114.1, EAX01115.1, EAX01112.1, EAX01113.1, EAX01116.1
GeneID:23040	MYT1L	2	1,792,885	2,335,045	542,160	-	1	2_A375_pNL97_plus_lncRNA::1::4489	2245	in gene	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MYT1L	MYT1L, NZF1	myelin transcription factor 1-like	NM_015025	1554633_a_at, 210016_at, 216672_s_at, 241485_at	NP_055840.2
GeneID:730811	LOC730811	2	2,323,004	2,330,880	7,876	+	1	2_A375_pNL97_plus_lncRNA::1::4489	8796	downstream	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC730811	FLJ44020, FLJ32836	hypothetical LOC730811	NR_024468		
GeneID:7260	TSSC1	2	3,192,741	3,381,653	188,912	-	3	1_A375_pNL7_minus_lncRNA::1::3123, 2_A375_pNL97_plus_lncRNA::1::4491, 2_A375_pNL97_plus_lncRNA::1::4492	-267, 213, -1931	upstream, in gene, upstream	1	1	17.5	20	2	2_A375_pNL97_plus_lncRNA::1	20	Gene TSSC1	TSSC1		NM_003310, hCT1963938.1, hCT1963939.1	217968_at	NP_003301.1, EAX01071.1, EAX01070.1
GeneID:51112	TTC15	2	3,383,446	3,483,342	99,896	+	3	1_A375_pNL7_minus_lncRNA::1::3123, 2_A375_pNL97_plus_lncRNA::1::4491, 2_A375_pNL97_plus_lncRNA::1::4492	-1526, -2006, 138	upstream, upstream, in gene	1	1	17.5	20	2	2_A375_pNL97_plus_lncRNA::1	20	Gene TTC15	FLJ36862, CGI-87, TTC15, FLJ44560	tetratricopeptide repeat domain 15	NM_016030, hCT2267690.0, hCT2358467.0, hCT9597.3	203122_at, 229556_at	NP_057114.5, EAX01069.1, EAX01067.1, EAX01068.1
GeneID:55256	ADI1	2	3,501,690	3,523,350	21,660	-	1	2_A375_pNL97_plus_lncRNA::1::4493	374	in gene	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene ADI1	HMFT1638, SIPL, FLJ10913, ARD, MTCBP1, APL1, SIP-L, Ni-ARD, MTCBP-1, ADI1	acireductone dioxygenase 1	NM_018269, hCT1971493.1, hCT9595.2	217761_at, 222400_s_at	NP_060739.2, EAX01064.1, EAX01065.1
GeneID:100506014	LOC100506014	2	3,579,403	3,581,797	2,394	-	1	1_A375_pNL7_minus_lncRNA::1::3124	-2587	upstream	1	0	27	20	1	1_A375_pNL7_minus_lncRNA::1	27	Gene LOC100506014		hypothetical LOC100506014	XR_112283, XR_112282, XR_112281, XR_109909, XR_109908, XR_109907, XR_115568, XR_115567, XR_115566		
GeneID:246243	RNASEH1	2	3,592,678	3,605,940	13,262	-	1	1_A375_pNL7_minus_lncRNA::1::3124	21556	downstream	1	0	27	20	1	1_A375_pNL7_minus_lncRNA::1	27	Gene RNASEH1	H1RNA, RNASEH1, RNH1	ribonuclease H1	NM_002936, hCT2267225.0	218496_at, 218497_s_at, 241343_at	NP_002927.2, EAX01061.1
GeneID:6201	RPS7	2	3,622,853	3,628,509	5,656	+	2	1_A375_pNL7_minus_lncRNA::1::3125, 2_A375_pNL97_plus_lncRNA::1::4494	-69, 59	upstream, in gene	1	1	34	24	1	1_A375_pNL7_minus_lncRNA::1	34	Gene RPS7	RPS7, DBA8, S7	ribosomal protein S7	NM_001011, hCT1823234.2, hCT1963940.1, hCT1963941.1, hCT1963942.1	200082_s_at, 213941_x_at	NP_001002.1, EAX01059.1, EAX01056.1, EAX01057.1, EAX01058.1
GeneID:8853	ASAP2	2	9,346,894	9,545,812	198,918	+	6	1_A375_pNL7_minus_lncRNA::1::3133, 2_A375_pNL97_plus_lncRNA::1::4507, 2_A375_pNL97_plus_lncRNA::1::4508, 2_A375_pNL97_plus_lncRNA::1::4509, 2_A375_pNL97_plus_lncRNA::1::4510, 2_A375_pNL97_plus_lncRNA::1::4511	81074, 27922, 28994, 81106, 81746, 171938	in gene, in gene, in gene, in gene, in gene, in gene	1	1	13.75	20.5	4	2_A375_pNL97_plus_lncRNA::1	27	Gene ASAP2	PAG3, CENTB3, KIAA0400, PAP, ASAP2, DDEF2, SHAG1, Pap-alpha, AMAP2, FLJ42910	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	NM_003887, NM_001135191, hCT1964190.1, hCT1967490.1, hCT2276915.0, hCT2276917.0, hCT2358456.0	206414_s_at	NP_003878.1, NP_001128663.1, EAX01003.1, EAX01004.1, EAX01005.1, EAX01006.1, EAX01002.1
GeneID:9270	ITGB1BP1	2	9,545,813	9,563,643	17,830	-	1	2_A375_pNL97_plus_lncRNA::1::4512	59	in gene	0	1	21	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene ITGB1BP1	ICAP1B, ICAP1A, ICAP1, ICAP-1B, ICAP-1alpha, ITGB1BP1, ICAP-1A, DKFZp686K08158	integrin beta 1 binding protein 1	NM_004763, NM_022334, hCT1690257.3, hCT1964080.2, hCT1964081.2, hCT2276418.1, hCT2343704.0, hCT2343705.0, hCT2343706.0, hCT2358508.0, hCT2358509.0, hCT2358510.0, hCT2358511.0	203336_s_at, 203337_x_at, 226227_at	NP_004754.1, NP_071729.1, EAX00991.1, EAX00992.1, EAX00997.1, EAX01000.1, EAX00993.1, EAX00994.1, EAX00995.1, EAX00996.1, EAX00998.1, EAX00999.1, EAX01001.1
GeneID:51692	CPSF3	2	9,563,868	9,613,227	49,359	+	1	2_A375_pNL97_plus_lncRNA::1::4512	-264	upstream	0	1	21	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene CPSF3	CPSF, CPSF73, CPSF3, CPSF-73, YSH1	cleavage and polyadenylation specific factor 3, 73kDa	NM_016207, hCT1823269.2, hCT2358381.0	225082_at	NP_057291.1, EAX00989.1, EAX00990.1
GeneID:6868	ADAM17	2	9,629,392	9,695,917	66,525	-	2	1_A375_pNL7_minus_lncRNA::1::3134, 2_A375_pNL97_plus_lncRNA::1::4513	-259, -179	upstream, upstream	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ADAM17	ADAM17, MGC71942, CSVP, TACE, CD156B, ADAM18	ADAM metallopeptidase domain 17	NM_003183, hCT2276409.0, hCT2276412.0	205745_x_at, 205746_s_at, 213532_at, 237897_at	NP_003174.3, EAX00982.1, EAX00981.1
GeneID:10971	YWHAQ	2	9,724,106	9,771,106	47,000	-	3	1_A375_pNL7_minus_lncRNA::1::3135, 2_A375_pNL97_plus_lncRNA::1::4514, 2_A375_pNL97_plus_lncRNA::1::4515	-286, -275, -7518	upstream, upstream, upstream	1	1	14.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene YWHAQ	HS1, 1C5, YWHAQ, 14-3-3	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	NM_006826, hCT2276405.0, hCT2276406.0, hCT2276407.0	200693_at, 212426_s_at, 213699_s_at	NP_006817.1, EAX00978.1, EAX00977.1, EAX00979.1
GeneID:100506386	LOC100506386	2	9,897,625	9,910,470	12,845	-	2	1_A375_pNL7_minus_lncRNA::1::3136, 2_A375_pNL97_plus_lncRNA::1::4516	17734, 17318	downstream, downstream	1	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100506386		hypothetical LOC100506386	XR_112292, XR_108392, XR_115580		
GeneID:9014	TAF1B	2	9,983,571	10,074,545	90,974	+	1	2_A375_pNL97_plus_lncRNA::1::4517	109	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene TAF1B	TAFI63, RAFI63, RAF1B, MGC:9349, TAF1B, SL1	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	NM_005680, hCT14944.3, hCT2358500.0, hCT2358501.0	214690_at, 216941_s_at, 235878_at	NP_005671.2, EAX00976.1, EAX00974.1, EAX00975.1
GeneID:6241	RRM2	2	10,262,695	10,271,546	8,851	+	4	1_A375_pNL7_minus_lncRNA::1::3137, 1_A375_pNL7_minus_lncRNA::1::3138, 2_A375_pNL97_plus_lncRNA::1::4518, 2_A375_pNL97_plus_lncRNA::1::4519	137, 13273, 121, 13401	in gene, downstream, in gene, downstream	1	1	30.5	38.5	2	2_A375_pNL97_plus_lncRNA::1	53	Gene RRM2	RR2, RRM2, RR2M, R2	ribonucleotide reductase M2	NM_001034, NM_001165931	201890_at, 209773_s_at	NP_001025.1, NP_001159403.1
GeneID:348738	C2orf48	2	10,281,509	10,351,856	70,347	+	2	1_A375_pNL7_minus_lncRNA::1::3138, 2_A375_pNL97_plus_lncRNA::1::4519	-5541, -5413	upstream, upstream	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene C2orf48	FLJ25102, C2orf48	chromosome 2 open reading frame 48	NM_182626		NP_872432.1
GeneID:3241	HPCAL1	2	10,443,040	10,567,743	124,703	+	3	2_A375_pNL97_plus_lncRNA::1::4521, 2_A375_pNL97_plus_lncRNA::1::4522, 2_A375_pNL97_plus_lncRNA::1::4523	1248, 9456, 102688	in gene, in gene, in gene	0	1	13	20	3	2_A375_pNL97_plus_lncRNA::1	24	Gene HPCAL1	HLP2, BDR1, VILIP-3, HPCAL1	hippocalcin-like 1	NM_002149, NM_134421, hCT14940.3, hCT1964978.1, hCT2267465.0, hCT2267467.0, hCT2267468.1, hCT2267470.0, hCT2267471.0	205462_s_at, 212552_at	NP_002140.2, NP_602293.1, EAX00960.1, EAX00961.1, EAX00962.1, EAX00965.1, EAX00963.1, EAX00964.1, EAX00966.1
GeneID:79954	NOL10	2	10,710,894	10,830,112	119,218	-	1	2_A375_pNL97_plus_lncRNA::1::4525	32	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene NOL10	NOL10, PQBP5, FLJ14075, FLJ13938	nucleolar protein 10	NM_024894, hCT14943.2, hCT1964192.0, hCT2266831.0	218591_s_at, 222684_s_at	NP_079170.2, EAX00953.1, EAX00954.1, EAX00955.1
GeneID:130813	C2orf50	2	11,273,179	11,286,916	13,737	+	1	2_A375_pNL97_plus_lncRNA::1::4529	22501	downstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C2orf50	MGC149401, FLJ25143, C2orf50	chromosome 2 open reading frame 50	NM_182500, hCT1645253.3, hCT2267929.1	1563814_at	NP_872306.1, EAX00944.1, EAX00943.1
GeneID:130814	PQLC3	2	11,295,540	11,319,000	23,460	+	1	2_A375_pNL97_plus_lncRNA::1::4529	140	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PQLC3	MGC33602, PQLC3, C2orf22	PQ loop repeat containing 3	NM_152391, hCT2267930.0, hCT2267931.0, hCT2345150.0, hCT2345151.0	216458_at, 225579_at	NP_689604.1, EAX00939.1, EAX00940.1, EAX00941.1, EAX00942.1
GeneID:9475	ROCK2	2	11,321,778	11,484,711	162,933	-	1	2_A375_pNL97_plus_lncRNA::1::4530	711	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ROCK2	KIAA0619, ROCK2	Rho-associated, coiled-coil containing protein kinase 2	NM_004850, hCT12724.3, hCT2265549.0	202762_at, 211504_x_at	NP_004841.2, EAX00938.1, EAX00937.1
GeneID:650157	LOC650157	2	11,491,753	11,512,199	20,446	+	3	1_A375_pNL7_minus_lncRNA::1::3141, 2_A375_pNL97_plus_lncRNA::1::4530, 2_A375_pNL97_plus_lncRNA::1::4531	23247, -7753, 23191	downstream, upstream, downstream	1	1	14	18	2	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC650157		peptidyl-prolyl cis-trans isomerase A-like	XM_001129774, XM_001726994, XM_001727011		XP_001129774.2, XP_001727046.1, XP_001727063.1
GeneID:1876	E2F6	2	11,584,501	11,606,297	21,796	-	2	1_A375_pNL7_minus_lncRNA::1::3142, 2_A375_pNL97_plus_lncRNA::1::4532	-103, -23	upstream, upstream	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene E2F6	E2F6, MGC111545, E2F-6	E2F transcription factor 6	NM_198256, NR_003093, NR_003095, NR_003092, NR_003094, hCT2265545.1, hCT2265546.1, hCT2265547.1, hCT2350530.0, hCT2350531.0, hCT2358532.0	203957_at	NP_937987.2, EAX00933.1, EAX00931.1, EAX00932.1, EAX00934.1, EAX00935.1, EAX00936.1
GeneID:23620	NTSR2	2	11,798,304	11,810,329	12,025	-	2	1_A375_pNL7_minus_lncRNA::1::3143, 2_A375_pNL97_plus_lncRNA::1::4533	249, 217	in gene, in gene	1	1	34	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene NTSR2	NTR2, NTSR2	neurotensin receptor 2	NM_012344, hCT12721.3, hCT1967764.2, hCT2266539.1	206899_at	NP_036476.1, EAX00924.1, EAX00922.1, EAX00923.1
GeneID:23175	LPIN1	2	11,886,740	11,967,535	80,795	+	3	1_A375_pNL7_minus_lncRNA::1::3144, 2_A375_pNL97_plus_lncRNA::1::4534, 2_A375_pNL97_plus_lncRNA::1::4535	-2324, -2260, 83660	upstream, upstream, downstream	1	1	22.5	20.5	2	1_A375_pNL7_minus_lncRNA::1	32	Gene LPIN1	LPIN1, PAP1, DKFZp781P1796, KIAA0188	lipin 1	NM_145693, hCT14053.3, hCT1964189.1, hCT2267940.0	212272_at, 212274_at, 212276_at	NP_663731.1, EAX00919.1, EAX00918.1, EAX00920.1
GeneID:100422996	MIR4262	2	11,977,059	11,977,112	53	-	1	2_A375_pNL97_plus_lncRNA::1::4535	6712	downstream	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene MIR4262	MIR4262	microRNA 4262	NR_036226		
GeneID:100506457	LOC100506457	2	12,246,750	12,271,711	24,961	+	1	2_A375_pNL97_plus_lncRNA::1::4536	13970	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100506457		hypothetical LOC100506457	XR_112297, XR_108396, XR_115585		
GeneID:51594	NBAS	2	15,307,032	15,701,454	394,422	-	2	1_A375_pNL7_minus_lncRNA::1::3147, 2_A375_pNL97_plus_lncRNA::1::4539	14, 46	in gene, in gene	1	1	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene NBAS	NBAS, FLJ40407, NAG, DKFZp586G1219	neuroblastoma amplified sequence	NM_015909, hCT2265842.1, hCT2265843.0, hCT2265845.1, hCT2265847.1	202926_at, 240579_at, 242049_s_at	NP_056993.2, EAX00900.1, EAX00901.1, EAX00902.1, EAX00903.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:1653	DDX1	2	15,731,770	15,771,225	39,455	+	1	2_A375_pNL97_plus_lncRNA::1::4540	38	in gene	0	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene DDX1	UKVH5d, DDX1, DBP-RB	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	NM_004939, hCT2266081.1, hCT2266083.1, hCT2350462.0, hCT2350463.0, hCT6944.3	201241_at	NP_004930.1, EAX00894.1, EAX00895.1, EAX00896.1, EAX00897.1, EAX00898.1
GeneID:81553	FAM49A	2	16,730,727	16,805,287	74,560	-	2	1_A375_pNL7_minus_lncRNA::1::3148, 2_A375_pNL97_plus_lncRNA::1::4541	77751, 77767	downstream, downstream	1	1	19	16	1	1_A375_pNL7_minus_lnc RNA::1	19	Gene FAM49A	FLJ33961, FAM49A, DKFZp566A1524, FLJ11080	family with sequence similarity 49, member A	NM_030797, hCT1965010.1, hCT2265707.0	208092_s_at, 209683_at, 230276_at	NP_110424.1, EAX00878.1, EAX00879.1
GeneID:729475	RAD51AP2	2	17,691,986	17,699,706	7,720	-	1	1_A375_pNL7_minus_lncRNA::1::3149	106	in gene	1	0	16	15	1	1_A375_pNL7_minus_lnc RNA::1	16	Gene RAD51AP2	RAD51AP2	RAD51 associated protein 2	NM_001099218		NP_001092688.1
GeneID:7447	VSNL1	2	17,721,807	17,837,706	115,899	+	2	1_A375_pNL7_minus_lncRNA::1::3150, 1_A375_pNL7_minus_lncRNA::1::3151	-1467, -399	upstream, upstream	1	0	22	17	2	1_A375_pNL7_minus_lnc RNA::1	26	Gene VSNL1	VSNL1, HLP3, VILIP, HPCAL3, VILIP-1, HUVISL1	visinin-like 1	NM_003385, hCT1965018.1, hCT1965019.1, hCT2265956.0, hCT23242.2, hCT2358383.0, hCT2358384.0	203797_at, 203798_s_at	NP_003376.2, EAX00872.1, EAX00871.1, EAX00873.1, EAX00874.1, EAX00875.1, EAX00870.1
GeneID:57665	RDH14	2	18,735,989	18,741,959	5,970	-	2	1_A375_pNL7_minus_lncRNA::1::3152, 2_A375_pNL97_plus_lncRNA::1::4542	55, 7	in gene, in gene	1	1	23	23	1	1_A375_pNL7_minus_lnc RNA::1	23	Gene RDH14	PAN2, RDH14, SDR7C4	retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	NM_020905, hCT1641564.1, hCT2265445.0, hCT2265446.0, hCT2265448.0	222203_s_at	NP_065956.1, EAX00857.1, EAX00855.1, EAX00856.1, EAX00858.1
GeneID:93034	NT5C1B	2	18,744,137	18,770,838	26,701	-	2	1_A375_pNL7_minus_lncRNA::1::3152, 2_A375_pNL97_plus_lncRNA::1::4542	26934, 26886	downstream, downstream	1	1	23	23	1	1_A375_pNL7_minus_lnc RNA::1	23	Gene NT5C1B	NT5C1B, AIRP, CN1B, CN-IB, MGC26640	5'-nucleotidase, cytosolic IB	NM_033253, NM_001002006, hCT2265442.0, hCT2265443.0, hCT23206.2	1554368_at, 243100_at	NP_150278.2, NP_001002006.1, EAX00852.1, EAX00853.1, EAX00854.1
GeneID:130497	OSR1	2	19,551,246	19,558,372	7,126	-	2	1_A375_pNL7_minus_lncRNA::1::3155, 2_A375_pNL97_plus_lncRNA::1::4546	10612, 10521	downstream, downstream	1	1	19	15	1	1_A375_pNL7_minus_lnc RNA::1	19	Gene OSR1	ODD, OSR1	odd-skipped related 1 (Drosophila)	NM_145260, hCT2265426.0, hCT2265428.0, hCT22919.2	228399_at	NP_660303.1, EAX00846.1, EAX00847.1, EAX00848.1
GeneID:130502	TTC32	2	20,096,514	20,101,747	5,233	-	2	1_A375_pNL7_minus_lncRNA::1::3156, 2_A375_pNL97_plus_lncRNA::1::4548	19, -29	in gene, upstream	1	1	27	24	1	1_A375_pNL7_minus_lnc RNA::1	27	Gene TTC32	TTC32		NM_001008237, hCT1966394.1, hCT23256.2	226838_at	NP_001008238.1, EAX00843.1, EAX00842.1
GeneID:57539	WDR35	2	20,110,024	20,189,884	79,860	-	4	1_A375_pNL7_minus_lncRNA::1::3158, 1_A375_pNL7_minus_lncRNA::1::3159, 2_A375_pNL97_plus_lncRNA::1::4548, 2_A375_pNL97_plus_lncRNA::1::4549	88156, -100, 88108, 60	downstream, upstream, downstream, in gene	1	1	24	21.5	2	1_A375_pNL7_minus_lnc RNA::1	27	Gene WDR35	KIAA1336, WDR35, MGC33196, CED2	WD repeat domain 35	NM_001006657, NM_020779, hCT2265421.0, hCT23255.3, hCT2358429.0, hCT2358430.0	226889_at, 226890_at	NP_001006658.1, NP_065830.2, EAX00838.1, EAX00839.1, EAX00840.1, EAX00841.1
GeneID:4148	MATN3	2	20,191,813	20,212,455	20,642	-	2	1_A375_pNL7_minus_lncRNA::1::3159, 2_A375_pNL97_plus_lncRNA::1::4549	22471, 22631	downstream, downstream	1	1	21	19	1	1_A375_pNL7_minus_lnc RNA::1	21	Gene MATN3	HOA, OADIP, DIPOA, MATN3, EDM5, OS2	matrilin 3	NM_002381, hCT23276.1	206091_at	NP_002372.1, EAX00837.1
GeneID:388	RHOB	2	20,646,835	20,649,201	2,366	+	1	2_A375_pNL97_plus_lncRNA::1::4551	925	in gene	0	1	17	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene RHOB	ARHB, RHOB, RHOH6, ARH6, MST081, MSTP081	ras homolog gene family, member B	NM_004040, hCT2266410.0, hCT22918.3	1553962_s_at, 1553963_at, 1553965_x_at, 212099_at, 226417_at	NP_004031.1, EAX00820.1, EAX00819.1
GeneID:64342	HS1BP3	2	20,817,564	20,850,864	33,300	-	1	2_A375_pNL97_plus_lncRNA::1::4553	-80	upstream	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene HS1BP3	HS1BP3, FLJ14249, ETM2, HS1-BP3	HCLS1 binding protein 3	NM_022460, hCT1823643.1, hCT1964360.1, hCT1967726.1, hCT1967727.1, hCT2266201.0, hCT2358413.0	1568734_a_at, 219020_at, 236530_at, 237407_at	NP_071905.3, EAX00812.1, EAX00813.1, EAX00814.1, EAX00815.1, EAX00816.1, EAX00817.1
GeneID:60526	C2orf43	2	20,884,818	21,022,827	138,009	-	2	1_A375_pNL7_minus_lncRNA::1::3162, 2_A375_pNL97_plus_lncRNA::1::4554	75, 11	in gene, in gene	1	1	23	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene C2orf43	C2orf43, FLJ21820	chromosome 2 open reading frame 43	NM_021925, hCT1966396.1, hCT1966397.1, hCT1966398.1, hCT2266232.0, hCT23279.3	219008_at, 222192_s_at, 222193_at	NP_068744.1, EAX00807.1, EAX00806.1, EAX00808.1, EAX00809.1, EAX00810.1
GeneID:114818	KLHL29	2	23,608,298	23,931,483	323,185	+	2	1_A375_pNL7_minus_lncRNA::1::3164, 2_A375_pNL97_plus_lncRNA::1::4556	139062, 138998	in gene, in gene	1	1	19	18	1	1_A375_pNL7_minus_lnc RNA::1	19	Gene KLHL29	KLHL29, KIAA1921, KBTBD9	kelch-like 29 (Drosophila)	NM_052920	1554261_at, 1554262_s_at, 220348_at, 229310_at	NP_443152.1
GeneID:54454	ATAD2B	2	23,971,534	24,149,934	178,400	-	1	2_A375_pNL97_plus_lncRNA::1::4557	-114	upstream	0	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ATAD2B	ATAD2B, MGC88424, KIAA1240	ATPase family, AAA domain containing 2B	NM_017552	1558807_at, 213387_at, 232908_at	NP_060022.1
GeneID:51639	SF3B14	2	24,290,454	24,299,314	8,860	-	4	1_A375_pNL7_minus_lncRNA::1::3165, 1_A375_pNL7_minus_lncRNA::1::3166, 2_A375_pNL97_plus_lncRNA::1::4558, 2_A375_pNL97_plus_lncRNA::1::4559	50, -7982, 34, -8206	in gene, upstream, in gene, upstream	1	1	38	33.5	2	1_A375_pNL7_minus_lnc RNA::1	52	Gene SF3B14	HSPC175, CGI-110, Ht006, SF3B14a, SAP14, P14	splicing factor 3B, 14 kDa subunit	NM_016047, hCT13480.2	1561923_a_at, 223416_at	NP_057131.1, EAX00767.1
GeneID:9540	TP53I3	2	24,300,305	24,307,728	7,423	-	4	1_A375_pNL7_minus_lncRNA::1::3165, 1_A375_pNL7_minus_lncRNA::1::3166, 2_A375_pNL97_plus_lncRNA::1::4558, 2_A375_pNL97_plus_lncRNA::1::4559	8464, 432, 8448, 208	downstream, in gene, downstream, in gene	1	1	38	33.5	2	1_A375_pNL7_minus_lnc RNA::1	52	Gene TP53I3	PIG3, TP53I3	tumor protein p53 inducible protein 3	NM_004881, NM_147184, hCT13479.2, hCT1967779.1, hCT1967780.1, hCT2265672.0, hCT2358486.0	210609_s_at	NP_004872.2, NP_671713.1, EAX00762.1, EAX00763.1, EAX00765.1, EAX00766.1, EAX00764.1
GeneID:375189	PFN4	2	24,338,244	24,346,151	7,907	-	2	1_A375_pNL7_minus_lncRNA::1::3167, 2_A375_pNL97_plus_lncRNA::1::4560	39, -249	in gene, upstream	1	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PFN4	PFN4		NM_199346, hCT1822872.1, hCT2358380.0	1557476_at, 235627_at	NP_955378.1, EAX00760.1, EAX00761.1
GeneID:375190	LOC375190	2	24,346,350	24,392,507	46,157	+	2	1_A375_pNL7_minus_lncRNA::1::3167, 2_A375_pNL97_plus_lncRNA::1::4560	-238, 50	upstream, in gene	1	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC375190	FLJ30851	hypothetical protein LOC375190	NM_001145710	230435_at	NP_001139182.1
GeneID:50618	ITSN2	2	24,425,735	24,583,397	157,662	-	2	1_A375_pNL7_minus_lncRNA::1::3168, 2_A375_pNL97_plus_lncRNA::1::4561	128981, -123	in gene, upstream	1	1	17.5	12.5	2	1_A375_pNL7_minus_lnc RNA::1	19	Gene ITSN2	SWAP, ITSN2, SWA, PRO2015, SH3P18, SH3D1B, KIAA1256	intersectin 2	NM_006277, NM_019595, NM_147152, hCT2265659.1, hCT2265660.1, hCT2265661.1, hCT2265662.1	209896_x_at, 209907_s_at, 210545_at, 240941_at	NP_006268.2, NP_062541.3, NP_671494.2, EAX00750.1, EAX00751.1, EAX00752.1, EAX00753.1
GeneID:100507630	LOC100507630	2	24,447,506	24,449,402	1,896	-	1	1_A375_pNL7_minus_lncRNA::1::3168	-5014	upstream	1	0	19	12	1	1_A375_pNL7_minus_lnc RNA::1	19	Gene LOC100507630		hypothetical protein LOC100507630	XM_003119858, XM_003118863, XM_003121039		XP_003119906.1, XP_003118911.1, XP_003121087.1
GeneID:8648	NCOA1	2	24,807,346	24,993,571	186,225	+	1	1_A375_pNL7_minus_lncRNA::1::3169	124302	in gene	1	0	19	8	1	1_A375_pNL7_minus_lnc RNA::1	19	Gene NCOA1	bHLHe74, bHLHe42, SRC1, RIP160, KAT13A, MGC129720, NCOA1, F-SRC-1, MGC129719	nuclear receptor coactivator 1	NM_003743, NM_147233, NM_147223, hCT12467.3, hCT2266053.0, hCT2266054.0	209105_at, 209106_at, 209107_x_at, 210249_s_at, 231289_at	NP_003734.3, NP_671766.1, NP_671756.1, EAX00746.1, EAX00747.1, EAX00748.1
GeneID:391356	C2orf79	2	25,013,136	25,016,251	3,115	-	2	1_A375_pNL7_minus_lncRNA::1::3170, 2_A375_pNL97_plus_lncRNA::1::4562	-69, -325	upstream, upstream	1	1	19	18	1	1_A375_pNL7_minus_lnc RNA::1	19	Gene C2orf79	C2orf79	chromosome 2 open reading frame 79	NM_001013663, hCT13884.3	226243_at	NP_001013685.1, EAX00745.1
GeneID:79172	CENPO	2	25,016,333	25,042,784	26,451	+	2	1_A375_pNL7_minus_lncRNA::1::3170, 2_A375_pNL97_plus_lncRNA::1::4562	-13, 243	upstream, in gene	1	1	19	18	1	1_A375_pNL7_minus_lnc RNA::1	19	Gene CENPO	MCM21R, CENP-O, ICEN-36, CENPO, MGC11266	centromere protein O	NM_024322, hCT1815707.1, hCT1823320.3, hCT2266056.0	219472_at, 226118_at	NP_077298.1, EAX00742.1, EAX00743.1, EAX00744.1
GeneID:22979	EFR3B	2	25,264,973	25,382,004	117,031	+	1	2_A375_pNL97_plus_lncRNA::1::4563	61263	in gene	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene EFR3B	EFR3B, KIAA0953	EFR3 homolog B (S. cerevisiae)	NM_014971	215328_at, 215334_at	NP_055786.1
GeneID:1788	DNMT3A	2	25,455,845	25,565,459	109,614	-	2	1_A375_pNL7_minus_lncRNA::1::3171, 2_A375_pNL97_plus_lncRNA::1::4564	19, -13	in gene, upstream	1	1	23	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene DNMT3A	DNMT3A, DNMT3A2, M.HsaIIIA	DNA (cytosine-5-)-methyltransferase 3 alpha	NM_022552, NM_153759, NM_175629, NM_175630, hCT13885.2, hCT2265463.0	218457_s_at, 222640_at, 244428_at	NP_072046.2, NP_715640.2, NP_783328.1, NP_783329.1, EAX00727.1, EAX00728.1
GeneID:1838	DTNB	2	25,600,112	25,896,503	296,391	-	1	2_A375_pNL97_plus_lncRNA::1::4565	-489	upstream	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene DTNB	MGC57126, MGC17163, DTNB	dystrobrevin, beta	NM_183360, NM_183361, NM_033147, NM_033148, NM_021907, hCT14241.3, hCT2265455.0, hCT2265456.0, hCT2265457.0, hCT2265458.0, hCT2265460.0, hCT2358418.0	214253_s_at, 215295_at, 215565_at	NP_899204.1, NP_899205.1, NP_068707.1, NP_149160.1, NP_149159.2, EAX00724.1, EAX00719.1, EAX00720.1, EAX00721.1, EAX00722.1, EAX00723.1, EAX00725.1
GeneID:729769	LOC729769	2	26,217,604	26,218,140	536	+	1	2_A375_pNL97_plus_lncRNA::1::4566	3076	downstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC729769	UQCRHP2	ubiquinol-cytochrome c reductase hinge protein pseudogene 2			
GeneID:391358	LOC391358	2	26,251,074	26,251,481	407	-	1	2_A375_pNL97_plus_lncRNA::1::4567	-5511	upstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC391358		tRNA methyltransferase 11-2 homolog (S. cerevisiae) pseudogene			
GeneID:10890	RAB10	2	26,256,729	26,360,323	103,594	+	1	2_A375_pNL97_plus_lncRNA::1::4567	263	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RAB10	RAB10		NM_016131, hCT14236.3, hCT2267373.0	222980_at, 222981_s_at	NP_057215.3, EAX00710.1, EAX00711.1
GeneID:3030	HADHA	2	26,413,504	26,467,594	54,090	-	2	1_A375_pNL7_minus_lncRNA::1::3172, 2_A375_pNL97_plus_lncRNA::1::4568	10, -54	in gene, upstream	1	1	20	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene HADHA	LCEH, HADH, LCHAD, HADHA, MTPA, ECHA, TP-ALPHA, MGC1728, GBP	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	NM_000182, hCT14237.3, hCT2280302.0	208629_s_at, 208630_at, 208631_s_at	NP_000173.2, EAX00703.1, EAX00704.1
GeneID:3032	HADHB	2	26,467,616	26,513,333	45,717	+	2	1_A375_pNL7_minus_lncRNA::1::3172, 2_A375_pNL97_plus_lncRNA::1::4568	-32, 32	upstream, in gene	1	1	20	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene HADHB	MGC87480, ECHB, HADHB, MTPB, TP-BETA, MSTP029	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	NM_000183, hCT14242.3, hCT1957722.1, hCT2358420.0	201007_at	NP_000174.1, EAX00701.1, EAX00700.1, EAX00702.1
GeneID:165082	GPR113	2	26,531,041	26,569,685	38,644	-	2	1_A375_pNL7_minus_lncRNA::1::3173, 2_A375_pNL97_plus_lncRNA::1::4569	629, 717	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lnc RNA::1	18	Gene GPR113	FLJ16767, GPR113, hGPCR37, PGR23	G protein-coupled receptor 113	NM_153835, NM_001145168, NM_001145169, hCT1642838.3, hCT2280299.1, hCT2343784.1, hCT2358502.0, hCT2358503.0, hCT2358504.0	1553016_at, 236608_at	NP_722577.2, NP_001138640.1, NP_001138641.1, EAX00694.1, EAX00696.1, EAX00697.1, EAX00695.1, EAX00698.1, EAX00699.1
GeneID:85465	SELI	2	26,568,954	26,618,759	49,805	+	2	1_A375_pNL7_minus_lncRNA::1::3173, 2_A375_pNL97_plus_lncRNA::1::4569	102, 14	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lnc RNA::1	18	Gene SELI	SELI, SEPI, EPT1, KIAA1724	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)	NM_033505, hCT1651443.3, hCT2267407.0, hCT2267411.0, hCT2358490.0	1555274_a_at, 1570371_a_at, 224688_at	NP_277040.1, EAX00690.1, EAX00691.1, EAX00692.1, EAX00693.1
GeneID:3777	KCNK3	2	26,915,581	26,954,066	38,485	+	1	1_A375_pNL7_minus_lncRNA::1::3174	3939	in gene	1	0	18	17	1	1_A375_pNL7_minus_lnc RNA::1	18	Gene KCNK3	KCNK3, TBAK1, TASK, K2p3.1, TASK-1, OAT1	potassium channel, subfamily K, member 3	NM_002246, hCT12485.2, hCT2267433.0	205952_at	NP_002237.1, EAX00678.1, EAX00679.1
GeneID:54976	C2orf18	2	26,987,142	27,004,099	16,957	+	3	2_A375_pNL97_plus_lncRNA::1::4570, 1_A375_pNL7_minus_lncRNA::1::3175, 2_A375_pNL97_plus_lncRNA::1::4571	-6230, 21658, 21669	upstream, downstream, downstream	1	1	19.5	17.5	2	1_A375_pNL7_minus_lnc RNA::1	24	Gene C2orf18	FLJ20555, C2orf18, ANT2BP	chromosome 2 open reading frame 18	NM_017877, hCT2267312.0, hCT2344588.0, hCT2358373.0, hCT2358374.0	1554444_s_at, 219763_at, 225695_at	NP_060347.2, EAX00676.1, EAX00673.1, EAX00674.1, EAX00675.1
GeneID:1058	CENPA	2	27,008,882	27,017,457	8,575	+	2	1_A375_pNL7_minus_lncRNA::1::3175, 2_A375_pNL97_plus_lncRNA::1::4571	-82, -71	upstream, upstream	1	1	24	19	1	1_A375_pNL7_minus_lnc RNA::1	24	Gene CENPA	CENP-A, CENPA	centromere protein A	NM_001042426, NM_001809, hCT2267308.0, hCT2267310.1, hCT2267315.1, hCT2267316.0	204962_s_at, 210821_x_at	NP_001035891.1, NP_001800.1, EAX00669.1, EAX00670.1, EAX00671.1, EAX00672.1
GeneID:56896	DPYSL5	2	27,070,969	27,173,219	102,250	+	2	1_A375_pNL7_minus_lncRNA::1::3176, 2_A375_pNL97_plus_lncRNA::1::4572	-9433, -9353	upstream, upstream	1	1	29	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene DPYSL5	DPYSL5, Ulip6, CRMP5, FLJ45383, CRMP-5, CRAM	dihydropyrimidinase-like 5	NM_020134, hCT2267318.0, hCT2267319.0	222797_at, 224100_s_at	NP_064519.2, EAX00668.1, EAX00667.1
GeneID:22924	MAPRE3	2	27,193,525	27,250,087	56,562	+	4	1_A375_pNL7_minus_lncRNA::1::3177, 2_A375_pNL97_plus_lncRNA::1::4573, 2_A375_pNL97_plus_lncRNA::1::4574, 2_A375_pNL97_plus_lncRNA::1::4575	23254, -85, 23179, 62347	in gene, upstream, in gene, downstream	1	1	19	31.33	3	2_A375_pNL97_plus_lncRNA::1	53	Gene MAPRE3	EBF3-S, EBF3, MAPRE3, EB3, RP3	microtubule-associated protein, RP/EB family, member 3	NM_012326, hCT14820.1, hCT2267320.0, hCT2267321.0, hCT2267323.0, hCT2267324.0, hCT2358396.0, hCT2358397.0	203841_x_at, 203842_s_at, 214270_s_at, 229682_at	NP_036458.2, EAX00662.1, EAX00660.1, EAX00663.1, EAX00664.1, EAX00666.1, EAX00661.1, EAX00665.1
GeneID:54867	TMEM214	2	27,255,774	27,264,565	8,791	+	3	1_A375_pNL7_minus_lncRNA::1::3178, 2_A375_pNL97_plus_lncRNA::1::4575, 2_A375_pNL97_plus_lncRNA::1::4576	18338, 98, 18402	downstream, in gene, downstream	1	1	18	22	2	1_A375_pNL7_minus_lnc RNA::1	23	Gene TMEM214	FLJ39682, FLJ20254, TMEM214	transmembrane protein 214	NM_001083590, NM_017727, hCT14833.3, hCT1963760.1, hCT2267327.0, hCT2267328.0, hCT2358487.0, hCT2358488.0	217899_at	NP_001077059.1, NP_060197.4, EAX00654.1, EAX00655.1, EAX00656.1, EAX00658.1, EAX00657.1, EAX00659.1
GeneID:60509	AGBL5	2	27,274,491	27,293,490	18,999	+	3	1_A375_pNL7_minus_lncRNA::1::3178, 2_A375_pNL97_plus_lncRNA::1::4576, 2_A375_pNL97_plus_lncRNA::1::4577	-379, -315, 20037	upstream, upstream, downstream	1	1	18.5	20.5	2	1_A375_pNL7_minus_lnc RNA::1	23	Gene AGBL5	FLJ21839, AGBL5	ATP/GTP binding protein-like 5	NM_001035507, NM_021831, hCT2267329.0, hCT2267330.0, hCT2267331.0, hCT2267332.0, hCT2358454.0	218480_at, 231857_s_at, 238889_at	NP_001030584.1, NP_068603.4, EAX00649.1, EAX00650.1, EAX00651.1, EAX00653.1, EAX00652.1
GeneID:100128731	LOC100128731	2	27,293,340	27,294,567	1,227	-	1	2_A375_pNL97_plus_lncRNA::1::4577	39	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100128731	OST4, DKFZp566A0722	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4	NM_001134693		NP_001128165.1
GeneID:11117	EMILIN1	2	27,301,435	27,309,271	7,836	+	3	1_A375_pNL7_minus_lncRNA::1::3179, 2_A375_pNL97_plus_lncRNA::1::4577, 2_A375_pNL97_plus_lncRNA::1::4578	7269, -6907, 7429	in gene, upstream, in gene	1	1	19	19.5	2	1_A375_pNL7_minus_lnc RNA::1	24	Gene EMILIN1	gp115, EMILIN1, DKFZp586M121, EMI, EMILIN	elastin microfibril interfacer 1	NM_007046, hCT14817.3, hCT1957724.1, hCT2267333.0, hCT2358395.0	204163_at	NP_008977.1, EAX00644.1, EAX00645.1, EAX00646.1, EAX00647.1
GeneID:3795	KHK	2	27,309,611	27,323,619	14,008	+	2	1_A375_pNL7_minus_lncRNA::1::3179, 2_A375_pNL97_plus_lncRNA::1::4578	-907, -747	upstream, upstream	1	1	24	20	1	1_A375_pNL7_minus_lnc RNA::1	24	Gene KHK	KHK		NM_000221, NM_006488, hCT14818.3, hCT14819.3, hCT2358437.0, hCT2358438.0	205175_s_at, 211026_s_at	NP_000212.1, NP_006479.1, EAX00640.1, EAX00641.1, EAX00642.1, EAX00643.1
GeneID:84696	ABHD1	2	27,346,657	27,353,680	7,023	+	2	1_A375_pNL7_minus_lncRNA::1::3180, 2_A375_pNL97_plus_lncRNA::1::4579	10799, 10879	downstream, downstream	1	1	24	21	1	1_A375_pNL7_minus_lnc RNA::1	24	Gene ABHD1	LABH1, FLJ36126, ABHD1	abhydrolase domain containing 1	NM_032604, hCT14838.3, hCT2358497.0, hCT2358498.0, hCT2358499.0	1560117_at, 232550_at, 236461_at	NP_115993.3, EAX00632.1, EAX00631.1, EAX00633.1, EAX00634.1
GeneID:10113	PREB	2	27,353,624	27,357,542	3,918	-	2	1_A375_pNL7_minus_lncRNA::1::3180, 2_A375_pNL97_plus_lncRNA::1::4579	86, 6	in gene, in gene	1	1	24	21	1	1_A375_pNL7_minus_lnc RNA::1	24	Gene PREB	PREB, MGC3467, SEC12	prolactin regulatory element binding	NM_013388, hCT14821.3, hCT2265812.0, hCT2265814.0, hCT2358400.0, hCT2358401.0	217861_s_at	NP_037520.1, EAX00627.1, EAX00626.1, EAX00628.1, EAX00629.1, EAX00630.1
GeneID:339779	C2orf53	2	27,359,715	27,362,332	2,617	-	2	1_A375_pNL7_minus_lncRNA::1::3180, 2_A375_pNL97_plus_lncRNA::1::4579	4876, 4796	downstream, downstream	1	1	24	21	1	1_A375_pNL7_minus_lnc RNA::1	24	Gene C2orf53	C2orf53, MGC44505	chromosome 2 open reading frame 53	NM_178553, hCT1960496.3	237319_at	NP_848648.2, EAX00625.1
GeneID:8884	SLC5A6	2	27,422,455	27,435,175	12,720	-	2	1_A375_pNL7_minus_lncRNA::1::3181, 2_A375_pNL97_plus_lncRNA::1::4580	-121, 71	upstream, in gene	1	1	16	16	1	1_A375_pNL7_minus_lnc RNA::1	16	Gene SLC5A6	SMVT, SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	NM_021095, NR_028323, hCT14835.3, hCT1955577.1, hCT2265810.0, hCT2358491.0	204087_s_at	NP_066918.2, EAX00622.1, EAX00620.1, EAX00621.1, EAX00623.1
GeneID:51374	C2orf28	2	27,434,899	27,440,046	5,147	+	2	1_A375_pNL7_minus_lncRNA::1::3181, 2_A375_pNL97_plus_lncRNA::1::4580	397, 205	in gene, in gene	1	1	16	16	1	1_A375_pNL7_minus_lnc RNA::1	16	Gene C2orf28	p18, PRO240, C2orf28, APR--3, APR3, HSPC013, APR-3	chromosome 2 open reading frame 28	NM_016085, NM_080592, NM_001170795, hCT14824.4, hCT1955576.1, hCT1970700.1, hCT2267343.0, hCT2267344.0	219329_s_at	NP_057169.2, NP_542159.3, NP_001164266.1, EAX00615.1, EAX00616.1, EAX00617.1, EAX00618.1, EAX00619.1
GeneID:790	CAD	2	27,440,258	27,466,654	26,396	+	2	1_A375_pNL7_minus_lncRNA::1::3181, 2_A375_pNL97_plus_lncRNA::1::4580	-4962, -5154	upstream, upstream	1	1	16	16	1	1_A375_pNL7_minus_lnc RNA::1	16	Gene CAD	CAD		NM_004341, hCT14822.3, hCT2267345.0, hCT2267346.0	1564084_at, 202715_at	NP_004332.2, EAX00612.1, EAX00613.1, EAX00614.1
GeneID:4358	MPV17	2	27,532,360	27,545,969	13,609	-	1	1_A375_pNL7_minus_lncRNA::1::3182	-79	upstream	1	0	21	20	1	1_A375_pNL7_minus_lnc RNA::1	21	Gene MPV17	SYM1, MTDPS6, MPV17	MpV17 mitochondrial inner membrane protein	NM_002437, hCT14825.3, hCT1964967.1, hCT1964968.1, hCT1964969.1, hCT1964970.1, hCT1964971.1, hCT1964972.1, hCT2265797.0	203466_at	NP_002428.1, EAX00600.1, EAX00597.1, EAX00598.1, EAX00601.1, EAX00603.1, EAX00599.1, EAX00602.1, EAX00604.1
GeneID:2976	GTF3C2	2	27,548,721	27,579,868	31,147	-	2	1_A375_pNL7_minus_lncRNA::1::3182, 2_A375_pNL97_plus_lncRNA::1::4581	33820, 460	downstream, in gene	1	1	19	18	2	1_A375_pNL7_minus_lnc RNA::1	21	Gene GTF3C2	KIAA0011, GTF3C2, TFIIIC-BETA, TFIIIC110	general transcription factor IIIC, polypeptide 2, beta 110kDa	NM_001521, NM_001035521, hCT14831.3, hCT2265791.0, hCT2265794.0	204366_s_at, 210620_s_at, 212429_s_at	NP_001512.1, NP_001030598.1, EAX00594.1, EAX00595.1, EAX00596.1
GeneID:100505605	LOC100505605	2	27,579,113	27,583,123	4,010	+	3	1_A375_pNL7_minus_lncRNA::1::3183, 2_A375_pNL97_plus_lncRNA::1::4581, 2_A375_pNL97_plus_lncRNA::1::4582	14103, 295, 14135	downstream, in gene, downstream	1	1	41.5	45	2	2_A375_pNL97_plus_lncRNA::1	74	Gene LOC100505605		hypothetical LOC100505605	XR_112299, XR_109962, XR_115595		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:8890	EIF2B4	2	27,587,219	27,593,324	6,105	-	3	1_A375_pNL7_minus_lncRNA::1::3183, 2_A375_pNL97_plus_lncRNA::1::4581, 2_A375_pNL97_plus_lncRNA::1::4582	108, 13916, 76	in gene, downstream, in gene	1	1	41.5	45	2	2_A375_pNL97_plus_lncRNA::1	74	Gene EIF2B4	EIF-2B, EIF2Bdelta, EIF2B4, DKFZp586J0119, EIF2B	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa	NM_015636, NM_001034116, NM_172195, hCT1823410.1, hCT1964358.1, hCT1964359.1, hCT2358369.0, hCT2358370.0, hCT2358371.0	209429_x_at, 215482_s_at	NP_056451.3, NP_001029288.1, NP_751945.2, EAX00587.1, EAX00588.1, EAX00592.1, EAX00589.1, EAX00590.1, EAX00591.1
GeneID:9784	SNX17	2	27,593,389	27,599,994	6,605	+	2	1_A375_pNL7_minus_lncRNA::1::3183, 2_A375_pNL97_plus_lncRNA::1::4582	-173, -141	upstream, upstream	1	1	66	74	1	2_A375_pNL97_plus_lncRNA::1	74	Gene SNX17	KIAA0064, SNX17	sorting nexin 17	NM_014748, hCT1823407.1, hCT2358358.0, hCT2358359.0	200991_s_at	NP_055563.1, EAX00585.1, EAX00584.1, EAX00586.1
GeneID:130557	ZNF513	2	27,600,102	27,603,593	3,491	-	2	1_A375_pNL7_minus_lncRNA::1::3183, 2_A375_pNL97_plus_lncRNA::1::4582	10377, 10345	downstream, downstream	1	1	66	74	1	2_A375_pNL97_plus_lncRNA::1	74	Gene ZNF513	RP58, HMFT0656, ZNF513, FLJ32203	zinc finger protein 513	NM_144631, hCT1823416.2	225753_at	NP_653232.3, EAX00583.1
GeneID:84450	ZNF512	2	27,805,893	27,845,963	40,070	+	1	2_A375_pNL97_plus_lncRNA::1::4583	45947	downstream	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZNF512	MGC111046, KIAA1805, ZNF512, FLJ51176	zinc finger protein 512	NM_032434, hCT1823417.2, hCT2267299.0, hCT2358404.0, hCT2358405.0	1553218_a_at, 225050_at	NP_115810.2, EAX00562.1, EAX00563.1, EAX00564.1, EAX00565.1
GeneID:79635	CCDC121	2	27,848,506	27,851,898	3,392	-	1	2_A375_pNL97_plus_lncRNA::1::4583	58	in gene	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CCDC121	FLJ13646, FLJ43364, CCDC121	coiled-coil domain containing 121	NM_024584, NM_001142683	220321_s_at	NP_078860.2, NP_001136155.1
GeneID:11321	GPN1	2	27,851,515	27,873,713	22,198	+	1	2_A375_pNL97_plus_lncRNA::1::4583	325	in gene	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene GPN1	NTPBP, MBDIN, XAB1, GPN1, FLJ51176, ATPBD1A	GPN-loop GTPase 1	NM_007266, NM_001145047, NM_001145048, NM_001145049, NR_026735, hCT12317.3, hCT1964366.1	209313_at	NP_009197.2, NP_001138519.1, NP_001138520.1, NP_001138521.1, EAX00557.1, EAX00558.1
GeneID:9553	MRPL33	2	27,994,584	28,002,608	8,024	+	2	1_A375_pNL7_minus_lncRNA::1::3185, 2_A375_pNL97_plus_lncRNA::1::4585	168, 40	in gene, in gene	1	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MRPL33	MGC13694, C2orf1, L33mt, MGC111093, RPL33L, MRP-L33, MGC23922, MRPL33	mitochondrial ribosomal protein L33	NM_145330, NM_004891, hCT1971564.1, hCT2358468.0	203781_at	NP_663303.1, NP_004882.1, EAX00552.1, EAX00553.1
GeneID:64080	RBKS	2	28,004,266	28,113,223	108,957	-	4	1_A375_pNL7_minus_lncRNA::1::3185, 1_A375_pNL7_minus_lncRNA::1::3186, 2_A375_pNL97_plus_lncRNA::1::4585, 2_A375_pNL97_plus_lncRNA::1::4586	118471, 19431, 118599, 19399	downstream, in gene, downstream, in gene	1	1	21	22.5	2	1_A375_pNL7_minus_lncRNA::1	27	Gene RBKS	RBSK, RBKS, DKFZp686G13268	ribokinase	NM_022128, hCT2358474.0, hCT8062.2	219222_at, 57540_at	NP_071411.1, EAX00551.1, EAX00550.1
GeneID:9577	BRE	2	28,113,482	28,561,768	448,286	+	2	1_A375_pNL7_minus_lncRNA::1::3187, 2_A375_pNL97_plus_lncRNA::1::4587	123190, 123158	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene BRE	BRE, BRCC45, BRCC4	brain and reproductive organ-expressed (TNFRSF1A modulator)	NM_199193, NM_199194, NM_199192, NM_199191, NM_004899, hCT1951009.2, hCT2267967.0, hCT2267968.0, hCT2358360.0, hCT2358361.0, hCT2358362.0, hCT6849.2	1568768_s_at, 205550_s_at, 211566_x_at, 212645_x_at	NP_954663.1, NP_954664.1, NP_004890.2, NP_954662.1, NP_954661.1, EAX00548.1, EAX00542.1, EAX00543.1, EAX00544.1, EAX00545.1, EAX00546.1, EAX00547.1
GeneID:403150	FLJ31356	2	28,607,276	28,617,539	10,263	-	3	1_A375_pNL7_minus_lncRNA::1::3188, 2_A375_pNL97_plus_lncRNA::1::4588, 2_A375_pNL97_plus_lncRNA::1::4589	2099, 3651, 2115	in gene, in gene, in gene	1	1	20.5	20.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene FLJ31356		hypothetical protein FLJ31356	XR_112303, XR_109966, XR_115599	1560932_at	
GeneID:2355	FOSL2	2	28,615,779	28,637,516	21,737	+	3	1_A375_pNL7_minus_lncRNA::1::3188, 2_A375_pNL97_plus_lncRNA::1::4588, 2_A375_pNL97_plus_lncRNA::1::4589	-339, -1891, -355	upstream, upstream, upstream	1	1	20.5	20.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene FOSL2	FOSL2, FRA2, FLJ23306	FOS-like antigen 2	NM_005253, hCT2267971.0, hCT2267972.0, hCT2267973.0, hCT2358524.0	205409_at, 218880_at, 218881_s_at, 225262_at	NP_005244.1, EAX00537.1, EAX00538.1, EAX00539.1, EAX00540.1
GeneID:151056	PLB1	2	28,718,938	28,866,654	147,716	+	2	1_A375_pNL7_minus_lncRNA::1::3189, 2_A375_pNL97_plus_lncRNA::1::4590	88118, 114630	in gene, in gene	1	1	19.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene PLB1	PLB, PLB1, PLB/LIP, hPLB	phospholipase B1	NM_153021, NM_001170585, hCT2267975.3, hCT2342678.1, hCT2351204.0, hCT2351205.0, hCT2351206.0	235703_at	NP_694566.4, NP_001164056.1, EAX00532.1, EAX00533.1, EAX00535.1, EAX00536.1, EAX00534.1
GeneID:100505774	LOC100505774	2	28,931,916	28,959,030	27,114	-	2	1_A375_pNL7_minus_lncRNA::1::3190, 2_A375_pNL97_plus_lncRNA::1::4591	18534, 18518	in gene, in gene	1	1	27	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene LOC100505774		hypothetical LOC100505774	XR_112304, XR_109967, XR_115600		
GeneID:5500	PPP1CB	2	28,974,614	29,025,806	51,192	+	2	1_A375_pNL7_minus_lncRNA::1::3191, 2_A375_pNL97_plus_lncRNA::1::4592	-86, -150	upstream, upstream	1	1	22	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene PPP1CB	PP1beta, PPP1CD, MGC3672, PP-1B, PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	NM_002709, NM_206876, hCT1639990.2, hCT2267976.0, hCT2358378.0, hCT2358379.0	201407_s_at, 201408_at, 201409_s_at, 228222_at	NP_002700.1, NP_996759.1, EAX00527.1, EAX00528.1, EAX00529.1, EAX00530.1
GeneID:55006	TRMT61B	2	29,072,687	29,093,175	20,488	-	2	1_A375_pNL7_minus_lncRNA::1::3192, 2_A375_pNL97_plus_lncRNA::1::4593	87, -73	in gene, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene TRMT61B	DKFZp564I2178, FLJ20628, TRMT61B	tRNA methyltransferase 61 homolog B (S. cerevisiae)	NM_017910, hCT1822715.2, hCT2264902.0	221229_s_at	NP_060380.3, EAX00525.1, EAX00524.1
GeneID:23160	WDR43	2	29,117,533	29,171,080	53,547	+	2	1_A375_pNL7_minus_lncRNA::1::3193, 2_A375_pNL97_plus_lncRNA::1::4594	-157, -157	upstream, upstream	1	1	38	47	1	2_A375_pNL97_plus_lncRNA::1	47	Gene WDR43	NET12, WDR43	WD repeat domain 43	NM_015131	214662_at	NP_055946.1
GeneID:79745	CLIP4	2	29,338,308	29,406,679	68,371	+	2	2_A375_pNL97_plus_lncRNA::1::4595, 2_A375_pNL97_plus_lncRNA::1::4596	-788, 764	upstream, in gene	0	1	11.5	14.5	2	2_A375_pNL97_plus_lncRNA::1	15	Gene CLIP4	RSNL2, FLJ32705, FLJ21069, CLIP4	CAP-GLY domain containing linker protein family, member 4	NM_024692, hCT1822711.2, hCT2267986.0, hCT2267987.0, hCT2267988.0, hCT2267989.0, hCT2267990.0, hCT2267991.0	219944_at, 226425_at	NP_078968.3, EAX00509.1, EAX00510.1, EAX00511.1, EAX00512.1, EAX00514.1, EAX00513.1, EAX00515.1
GeneID:238	ALK	2	29,415,640	30,144,432	728,792	-	5	1_A375_pNL7_minus_lncRNA::1::3194, 1_A375_pNL7_minus_lncRNA::1::3195, 2_A375_pNL97_plus_lncRNA::1::4597, 1_A375_pNL7_minus_lncRNA::1::3196, 2_A375_pNL97_plus_lncRNA::1::4598	627468, 173296, 173264, 1264, 1216	in gene, in gene, in gene, in gene, in gene	1	1	30.67	31	3	2_A375_pNL97_plus_lncRNA::1	41	Gene ALK	NBLST3, ALK, TFG/ALK, CD246	anaplastic lymphoma receptor tyrosine kinase	NM_004304, hCT1656334.3, hCT2264312.0, hCT2264313.0	208211_s_at, 208212_s_at	NP_004295.2, EAX00506.1, EAX00507.1, EAX00508.1
GeneID:51646	YPEL5	2	30,369,750	30,383,399	13,649	+	1	2_A375_pNL97_plus_lncRNA::1::4600	-310	upstream	0	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene YPEL5	YPEL5, CGI-127	yippee-like 5 (Drosophila)	NM_016061, NM_001127399, NM_001127400, NM_001127401, hCT1964309.1, hCT1964310.0, hCT1964311.1, hCT1964312.1, hCT1966037.1, hCT2358522.0, hCT6847.1	217783_s_at, 222406_s_at	NP_057145.1, NP_001120871.1, NP_001120872.1, NP_001120873.1, EAX00499.1, EAX00500.1, EAX00501.1, EAX00502.1, EAX00503.1, EAX00504.1, EAX00505.1
GeneID:253558	LCLAT1	2	30,670,123	30,867,091	196,968	+	1	2_A375_pNL97_plus_lncRNA::1::4602	37	in gene	0	1	9	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LCLAT1	LCLAT1, ALCAT1, AGPAT8, HSRG1849, FLJ37965, LYCAT, 1AGPAT8, UNQ1849	lysocardiolipin acyltransferase 1	NM_001002257, NM_182551, hCT1641103.4	226996_at	NP_001002257.1, NP_872357.2, EAX00495.1
GeneID:79623	GALNT14	2	31,133,333	31,361,571	228,238	-	5	1_A375_pNL7_minus_lncRNA::1::3199, 1_A375_pNL7_minus_lncRNA::1::3200, 2_A375_pNL97_plus_lncRNA::1::4603, 2_A375_pNL97_plus_lncRNA::1::4604, 2_A375_pNL97_plus_lncRNA::1::4605	30947, 163, 30915, 29699, -29	in gene, in gene, in gene, in gene, upstream	1	1	21.33	23.67	3	2_A375_pNL97_plus_lncRNA::1	36	Gene GALNT14	FLJ12691, FLJ13977, GALNT14, GalNac-T14, GalNac-T10, GALNT15	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	NM_024572, hCT1822791.2, hCT2264429.0, hCT2264432.0, hCT2358536.0	1560180_at, 219271_at	NP_078848.2, EAX00487.1, EAX00486.1, EAX00488.1, EAX00489.1
GeneID:30845	EHD3	2	31,456,880	31,491,260	34,380	+	2	1_A375_pNL7_minus_lncRNA::1::3201, 2_A375_pNL97_plus_lncRNA::1::4606	0, 16	in gene, in gene	1	1	25	20	1	1_A375_pNL7_minus_lncRNA::1	25	Gene EHD3	EHD3, PAST3	EH-domain containing 3	NM_014600, hCT12598.3, hCT2264965.0	218935_at, 241267_at	NP_055415.1, EAX00460.1, EAX00461.1
GeneID:51072	MEMO1	2	32,092,892	32,235,698	142,806	-	2	1_A375_pNL7_minus_lncRNA::1::3202, 2_A375_pNL97_plus_lncRNA::1::4607	-366, -334	upstream, upstream	1	1	27	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene MEMO1	MEMO1, C2orf4, FLJ25031, DKFZp434I0135, NS5ATP7, MEMO, CGI-27	mediator of cell motility 1	NM_015955, NM_001137602, hCT2264777.0, hCT2264778.0, hCT2264779.0, hCT2264781.1, hCT2264782.0, hCT2358439.0, hCT2358440.0, hCT2358441.0	219065_s_at	NP_057039.1, NP_001131074.1, EAX00468.1, EAX00469.1, EAX00471.1, EAX00472.1, EAX00467.1, EAX00470.1, EAX00473.1, EAX00474.1
GeneID:84661	DPY30	2	32,248,972	32,264,844	15,872	-	2	1_A375_pNL7_minus_lncRNA::1::3203, 2_A375_pNL97_plus_lncRNA::1::4608	-116, -180	upstream, upstream	1	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene DPY30	Saf19, DPY30, HDPY-30	dpy-30 homolog (C. elegans)	NM_032574, hCT2264776.0, hCT2344586.0, hCT2344587.0, hCT2358372.0	224129_s_at	NP_115963.1, EAX00463.1, EAX00464.1, EAX00465.1, EAX00466.1
GeneID:6683	SPAST	2	32,288,680	32,382,706	94,026	+	2	1_A375_pNL7_minus_lncRNA::1::3204, 2_A375_pNL97_plus_lncRNA::1::4609	102136, 102104	downstream, downstream	1	1	25	24	1	1_A375_pNL7_minus_lncRNA::1	25	Gene SPAST	ADPSP, KIAA1083, SPG4, FSP2, SPAST	spastin	NM_014946, NM_199436, hCT14164.2, hCT1957721.1	207724_s_at, 209748_at	NP_055761.2, NP_955468.1, EAX00461.1, EAX00462.1
GeneID:55676	SLC30A6	2	32,390,910	32,449,181	58,271	+	2	1_A375_pNL7_minus_lncRNA::1::3204, 2_A375_pNL97_plus_lncRNA::1::4609	-94, -126	upstream, upstream	1	1	25	24	1	1_A375_pNL7_minus_lncRNA::1	25	Gene SLC30A6	MST103, MGC45055, MSTP103, SLC30A6, FLJ31101, ZNT6	solute carrier family 30 (zinc transporter), member 6	NM_017964, NM_001193513, NM_001193514, NM_001193515, hCT14186.3, hCT2358340.0, hCT2358341.0, hCT2358342.0, hCT2358343.0	226161_at, 226162_at, 243643_x_at	NP_060434.2, NP_001180442.1, NP_001180443.1, NP_001180444.1, EAX00456.1, EAX00459.1, EAX00457.1, EAX00458.1, EAX00460.1
GeneID:57448	BIRC6	2	32,582,096	32,843,966	261,870	+	2	1_A375_pNL7_minus_lncRNA::1::3205, 2_A375_pNL97_plus_lncRNA::1::4610	-219, -48	upstream, upstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene BIRC6	FLJ13726, KIAA1289, FLJ13786, BRUCE, BIRC6, APOLLON	baculoviral IAP repeat containing 6	NM_016252, hCT14641.3, hCT2265371.0, hCT2265372.0, hCT2265373.0, hCT2358515.0	224635_s_at, 233093_s_at	NP_057336.3, EAX00443.1, EAX00444.1, EAX00445.1, EAX00446.1, EAX00447.1
GeneID:4052	LTBP1	2	33,172,369	33,624,576	452,207	+	5	1_A375_pNL7_minus_lncRNA::1::3206, 2_A375_pNL97_plus_lncRNA::1::4611, 2_A375_pNL97_plus_lncRNA::1::4612, 2_A375_pNL97_plus_lncRNA::1::4613, 2_A375_pNL97_plus_lncRNA::1::4614	122671, 123183, 187023, 328543, 428207	in gene, in gene, in gene, in gene, in gene	1	1	16.25	17.5	4	2_A375_pNL97_plus_lncRNA::1	20	Gene LTBP1	MGC163161, LTBP1	latent transforming growth factor beta binding protein 1	NM_206943, NM_000627, NM_001166264, NM_001166265, NM_001166266, hCT2264591.0, hCT2264592.0, hCT2264593.0, hCT2264594.0, hCT2358465.0	202728_s_at, 202729_s_at	NP_996826.2, NP_000618.3, NP_001159736.1, NP_001159737.1, NP_001159738.1, EAX00435.1, EAX00436.1, EAX00437.1, EAX00438.1, EAX00439.1
GeneID:25780	RASGRP3	2	33,661,416	33,789,798	128,382	+	1	1_A375_pNL7_minus_lncRNA::1::3207	39576	in gene	1	0	18	8	1	1_A375_pNL7_minus_lncRNA::1	18	Gene RASGRP3	RASGRP3, GRP3, KIAA0846	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	NM_170672, NM_001139488, NM_015376, hCT1963457.1, hCT1963458.1, hCT2264596.0	205801_s_at, 244526_at	NP_733772.1, NP_001132960.1, NP_056191.1, EAX00432.1, EAX00433.1, EAX00434.1
GeneID:25940	FAM98A	2	33,808,729	33,824,362	15,633	-	2	1_A375_pNL7_minus_lncRNA::1::3208, 2_A375_pNL97_plus_lncRNA::1::4615	-374, -163	upstream, upstream	1	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FAM98A	FAM98A, DKFZp686O03192, DKFZp564F0522	family with sequence similarity 98, member A	NM_015475, hCT1641750.3	212333_at, 239487_at, 241832_at	NP_056290.3, EAX00431.1
GeneID:100288911	LOC100288911	2	36,565,035	36,582,713	17,678	-	1	1_A375_pNL7_minus_lncRNA::1::3213	-2311	upstream	1	0	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100288911		hypothetical LOC100288911	XR_109968, XR_115525, XR_108260		
GeneID:51232	CRIM1	2	36,583,397	36,778,278	194,881	+	2	1_A375_pNL7_minus_lncRNA::1::3213, 2_A375_pNL97_plus_lncRNA::1::4618	1627, 71659	in gene, in gene	1	1	15	18.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene CRIM1	MGC138194, CRIM1, S52	cysteine rich transmembrane BMP regulator 1 (chordin-like)	NM_016441, hCT8309.2	202551_s_at, 202552_s_at, 228496_s_at	NP_057525.1, EAX00426.1
GeneID:10153	CEBPZ	2	37,428,772	37,458,740	29,968	-	1	2_A375_pNL97_plus_lncRNA::1::4619	-124	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CEBPZ	CBF2, CEBPZ, HSP-CBF, CBF, NOC1	CCAAT/enhancer binding protein (C/EBP), zeta	NM_005760, hCT7940.3	203341_at	NP_005751.2, EAX00403.1
GeneID:55471	C2orf56	2	37,458,774	37,476,303	17,529	+	1	2_A375_pNL97_plus_lncRNA::1::4619	90	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C2orf56	C2orf56, PRO1853, MidA	chromosome 2 open reading frame 56	NM_144736, NM_001083946, hCT2264499.0, hCT2264502.0, hCT7945.3	220943_s_at, 223560_s_at, 230379_x_at	NP_653337.1, NP_001077415.1, EAX00400.1, EAX00401.1, EAX00402.1
GeneID:23683	PRKD3	2	37,477,645	37,544,222	66,577	-	1	1_A375_pNL7_minus_lncRNA::1::3214	-8034	upstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene PRKD3	PRKD3, EPK2, PKC-NU, PRKCN, PKD3, nPKC-NU	protein kinase D3	NM_005813, hCT2264246.0, hCT7941.3	1554910_at, 211084_x_at, 218236_s_at, 222565_s_at, 242549_at	NP_005804.1, EAX00398.1, EAX00399.1
GeneID:25797	QPCT	2	37,571,753	37,600,465	28,712	+	3	1_A375_pNL7_minus_lncRNA::1::3215, 2_A375_pNL97_plus_lncRNA::1::4620, 2_A375_pNL97_plus_lncRNA::1::4621	32279, 32263, 35383	downstream, downstream, downstream	1	1	15.5	17	2	1_A375_pNL7_minus_lncRNA::1	19	Gene QPCT	QC, GCT, QPCT	glutaminyl-peptide cyclotransferase	NM_012413, hCT1963449.1, hCT1963450.1, hCT1963451.1, hCT1963452.1, hCT2264514.0, hCT7943.2	205174_s_at	NP_036545.1, EAX00392.1, EAX00393.1, EAX00395.1, EAX00396.1, EAX00397.1, EAX00394.1
GeneID:10602	CDC42EP3	2	37,870,743	37,899,326	28,583	-	2	1_A375_pNL7_minus_lncRNA::1::3217, 2_A375_pNL97_plus_lncRNA::1::4622	158, -386	in gene, upstream	1	1	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene CDC42EP3	CDC42EP3, BORG2, UB1, CEP3, FLJ46903	CDC42 effector protein (Rho GTPase binding) 3	NM_006449, hCT5638.5	209286_at, 209287_s_at, 209288_s_at	NP_006440.2, EAX00390.1
GeneID:151393	FAM82A1	2	38,152,462	38,294,285	141,823	+	2	2_A375_pNL97_plus_lncRNA::1::4624, 2_A375_pNL97_plus_lncRNA::1::4625	266, 151826	in gene, downstream	0	1	15	19	2	2_A375_pNL97_plus_lncRNA::1	19	Gene FAM82A1	RMD2, BLOCK18, FLJ38143, FAM82A, PYST9371, FLJ32954, RMD4, FAM82A1, MGC33318, PRO34163	family with sequence similarity 82, member A1	NM_001170791, NM_001170792, NM_001170793, NM_144713, hCT1642929.4, hCT1963447.2, hCT2264800.1, hCT2348890.0	1553232_at, 1560042_at, 235349_at	NP_001164262.1, NP_001164263.1, NP_001164264.1, NP_653314.2, EAX00385.1, EAX00386.1, EAX00384.1, EAX00387.1
GeneID:1545	CYP1B1	2	38,294,746	38,303,323	8,577	-	1	2_A375_pNL97_plus_lncRNA::1::4625	-965	upstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CYP1B1	CYP1B1, P4501B1, CP1B, GLC3A	cytochrome P450, family 1, subfamily B, polypeptide 1	NM_000104, hCT2264290.0, hCT5840.2	202434_s_at, 202435_s_at, 202436_s_at, 202437_s_at	NP_000095.2, EAX00382.1, EAX00383.1
GeneID:285154	C2orf58	2	38,356,247	38,406,997	50,750	+	1	2_A375_pNL97_plus_lncRNA::1::4626	15737	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene C2orf58	C2orf58, MGC34824	chromosome 2 open reading frame 58	NR_027252, hCT2344308.1, hCT2346636.1, hCT2350928.0	1553629_at, 233285_at, 233410_at	EAX00380.1, EAX00379.1, EAX00378.1
GeneID:64225	ATL2	2	38,522,027	38,604,432	82,405	-	2	1_A375_pNL7_minus_lncRNA::1::3219, 2_A375_pNL97_plus_lncRNA::1::4628	16, 48	in gene, in gene	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ATL2	atlastin2, FLJ23293, ARL6IP2, ARL3IP2, ATL2	atlastin GTPase 2	NM_022374, NM_001135673, NR_024191, hCT1963440.1, hCT2358422.0, hCT6909.3	1553603_s_at, 222700_at, 237968_at	NP_071769.2, NP_001129145.1, EAX00375.1, EAX00376.1, EAX00377.1
GeneID:130589	GALM	2	38,893,052	38,961,909	68,857	+	1	1_A375_pNL7_minus_lncRNA::1::3220	24708	in gene	1	0	16	7	1	1_A375_pNL7_minus_lncRNA::1	16	Gene GALM	IBD1, BLOCK25, GALM	galactose mutarotase (aldose 1-epimerase)	NM_138801, hCT1963435.1	234974_at, 235256_s_at	NP_620156.1, EAX00367.1
GeneID:90957	DHX57	2	39,024,871	39,103,021	78,150	-	2	1_A375_pNL7_minus_lncRNA::1::3221, 2_A375_pNL97_plus_lncRNA::1::4630	77, 157	in gene, in gene	1	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene DHX57	DHX57, FLJ32861, DDX57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	NM_198963	213420_at, 244784_at	NP_945314.1
GeneID:729967	MORN2	2	39,103,103	39,109,850	6,747	+	2	1_A375_pNL7_minus_lncRNA::1::3221, 2_A375_pNL97_plus_lncRNA::1::4630	-159, -239	upstream, upstream	1	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene MORN2	MORN2, MOPT, MGC126131, BLOCK27, MGC126132, MGC111382, MGC126130	MORN repeat containing 2	NM_001145450	1556881_at	NP_001138922.1
GeneID:6654	SOS1	2	39,208,690	39,347,604	138,914	-	3	1_A375_pNL7_minus_lncRNA::1::3222, 2_A375_pNL97_plus_lncRNA::1::4631, 2_A375_pNL97_plus_lncRNA::1::4632	-3980, -524, -3948	upstream, upstream, upstream	1	1	34.5	31.5	2	1_A375_pNL7_minus_lncRNA::1	49	Gene SOS1	GGF1, GINGF, SOS1, GF1, NS4, HGF	son of sevenless homolog 1 (Drosophila)	NM_005633, hCT1641178.3, hCT1963445.1, hCT2264435.0, hCT2264438.0	1557354_at, 212777_at, 212780_at, 230337_at	NP_005624.2, EAX00350.1, EAX00351.1, EAX00352.1, EAX00353.1
GeneID:8491	MAP4K3	2	39,476,422	39,664,219	187,797	-	1	1_A375_pNL7_minus_lncRNA::1::3223	66843	in gene	1	0	18	12	1	1_A375_pNL7_minus_lncRNA::1	18	Gene MAP4K3	GLK, MEKKK3, RAB8IPL1, MAP4K3, MAPKKKK3	mitogen-activated protein kinase kinase kinase kinase 3	NM_003618, hCT1950486.2, hCT2264428.0	218311_at	NP_003609.2, EAX00347.1, EAX00348.1
GeneID:27436	EML4	2	42,396,490	42,559,688	163,198	+	3	1_A375_pNL7_minus_lncRNA::1::3227, 1_A375_pNL7_minus_lncRNA::1::3228, 2_A375_pNL97_plus_lncRNA::1::4637	172022, 172790, 173254	downstream, downstream, downstream	1	1	21	17	2	1_A375_pNL7_minus_lncRNA::1	22	Gene EML4	DKFZp686P18118, ROPP120, FLJ10942, FLJ32318, EMAPL4, EML4, ELP120, C2orf2, EMAP-4	echinoderm microtubule associated protein like 4	NM_019063, NM_001145076, hCT6992.3	1556732_at, 220386_s_at, 223068_at, 223069_s_at, 226673_s_at, 226674_s_at, 232587_at	NP_061936.2, NP_001138548.1, EAX00324.1
GeneID:9167	COX7A2L	2	42,577,642	42,588,356	10,714	-	4	1_A375_pNL7_minus_lncRNA::1::3227, 1_A375_pNL7_minus_lncRNA::1::3228, 2_A375_pNL97_plus_lncRNA::1::4637, 2_A375_pNL97_plus_lncRNA::1::4638	18844, 19076, 18612, 116	downstream, downstream, downstream, in gene	1	1	19.67	17.33	3	1_A375_pNL7_minus_lncRNA::1	22	Gene COX7A2L	COX7RP, COX7A2L, SIG81, EB1, COX7AR	cytochrome c oxidase subunit VIIa polypeptide 2 like	NM_004718, hCT1822853.2, hCT1963453.1, hCT1963454.1, hCT2263599.0	201256_at	NP_004709.2, EAX00320.1, EAX00321.1, EAX00322.1, EAX00323.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:678	ZFP36L2	2	43,449,541	43,453,745	4,204	-	3	1_A375_pNL7_minus_lncRNA::1::3230, 2_A375_pNL97_plus_lncRNA::1::4641, 2_A375_pNL97_plus_lncRNA::1::4642	-831, 6577, 1361	upstream, downstream, in gene	1	1	15.33	16.67	3	2_A375_pNL97_plus_lncRNA::1	24	Gene ZFP36L2	ERF-2, RNF162C, ERF2, ZFP36L2, BRF2, TIS11D	zinc finger protein 36, C3H type-like 2	NM_006887, hCT2263541.0, hCT6815.3	201367_s_at, 201368_at, 201369_s_at, 227681_at	NP_008818.3, EAX00305.1, EAX00306.1
GeneID:100129726	LOC100129726	2	43,454,350	43,455,994	1,644	+	3	1_A375_pNL7_minus_lncRNA::1::3230, 2_A375_pNL97_plus_lncRNA::1::4641, 2_A375_pNL97_plus_lncRNA::1::4642	226, -7182, -1966	in gene, upstream, upstream	1	1	15.33	16.67	3	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100129726	MGC40574	hypothetical LOC100129726	NR_027251		
GeneID:63892	THADA	2	43,457,975	43,823,185	365,210	-	6	1_A375_pNL7_minus_lncRNA::1::3230, 1_A375_pNL7_minus_lncRNA::1::3231, 1_A375_pNL7_minus_lncRNA::1::3232, 2_A375_pNL97_plus_lncRNA::1::4642, 2_A375_pNL97_plus_lncRNA::1::4643, 2_A375_pNL97_plus_lncRNA::1::4644	365609, 302033, 81, 370501, 302097, -47	downstream, in gene, in gene, downstream, in gene, upstream	1	1	22	19.5	4	1_A375_pNL7_minus_lncRNA::1	41	Gene THADA	GITA, FLJ21877, FLJ77530, KIAA1767, FLJ44876, THADA, FLJ44016	thyroid adenoma associated	NM_022065, NM_001083953	1554492_at, 1554493_s_at, 1558306_at, 1566888_at, 1566889_at, 220212_s_at, 54632_at	NP_071348.3, NP_001077422.1
GeneID:10128	LRPPRC	2	44,113,363	44,223,144	109,781	-	2	1_A375_pNL7_minus_lncRNA::1::3233, 2_A375_pNL97_plus_lncRNA::1::4645	-120, -68	upstream, upstream	1	1	44	32	1	1_A375_pNL7_minus_lncRNA::1	44	Gene LRPPRC	LRPPRC, GP130, LSFC, CLONE-23970, LRP130	leucine-rich PPR-motif containing	NM_133259, hCT2263467.0	1557360_at, 211615_s_at, 211971_s_at	NP_573566.2, EAX00284.1
GeneID:5495	PPM1B	2	44,396,000	44,461,742	65,742	+	1	2_A375_pNL97_plus_lncRNA::1::4646	-63	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PPM1B	PP2CB, PPM1B, PP2CBETA, MGC21657, PP2C-beta-X, PPC2BETAX	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	NM_002706, NM_177968, NM_177969, NM_001033556, NM_001033557, hCT1813715.1, hCT1962943.1, hCT2263929.0, hCT2263934.0	209296_at, 213225_at	NP_002697.1, NP_808907.1, NP_808908.1, NP_001028728.1, NP_001028729.1, EAX00282.1, EAX00280.1, EAX00281.1, EAX00283.1
GeneID:9581	PREPL	2	44,544,746	44,589,001	44,255	-	1	1_A375_pNL7_minus_lncRNA::1::3235	-119	upstream	1	0	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene PREPL	PREPL, KIAA0436, FLJ16627	prolyl endopeptidase-like	NM_006036, NM_001042385, NM_001042386, NM_001171603, NM_001171606, NM_001171613, NM_001171617, hCT1686313.3, hCT2358407.0, hCT2358408.0	212215_at, 212216_at, 212217_at, 243542_at	NP_006027.2, NP_001035844.1, NP_001035845.1, NP_001165074.1, NP_001165077.1, NP_001165084.1, NP_001165088.1, EAX00275.1, EAX00276.1, EAX00277.1
GeneID:79823	C2orf34	2	44,589,043	44,999,729	410,686	+	1	1_A375_pNL7_minus_lncRNA::1::3235	77	in gene	1	0	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene C2orf34	CLNMT, FLJ23451, Cam, CaM KMT, C2orf34, CAMKMT, KMT	chromosome 2 open reading frame 34	NM_024766, hCT1962944.1, hCT2263220.0, hCT2263221.0	1554875_at, 219617_at	NP_079042.1, EAX00273.1, EAX00272.1, EAX00274.1
GeneID:5581	PRKCE	2	45,879,043	46,415,129	536,086	+	6	1_A375_pNL7_minus_lncRNA::1::3236, 1_A375_pNL7_minus_lncRNA::1::3237, 1_A375_pNL7_minus_lncRNA::1::3238, 2_A375_pNL97_plus_lncRNA::1::4651, 2_A375_pNL97_plus_lncRNA::1::4652, 2_A375_pNL97_plus_lncRNA::1::4653	200077, 287293, 447021, 200013, 446893, 519549	in gene, in gene, in gene, in gene, in gene, in gene	1	1	14.5	15.75	4	2_A375_pNL97_plus_lncRNA::1	16	Gene PRKCE	PKCE, MGC125657, MGC125656, PRKCE, nPKC-epsilon	protein kinase C, epsilon	NM_005400, hCT1960473.1, hCT2276459.0, hCT6798.2	206248_at, 226101_at, 236459_at, 239011_at	NP_005391.1, EAX00257.1, EAX00258.1, EAX00259.1
GeneID:388946	LOC388946	2	46,706,704	46,711,565	4,861	+	1	2_A375_pNL97_plus_lncRNA::1::4655	2128	in gene	0	1	9	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC388946		transmembrane protein ENSP00000343375	NM_001145051	1556489_at, 1556490_a_at	NP_001138523.1
GeneID:100506177	LOC100506177	2	47,126,414	47,135,963	9,549	+	1	2_A375_pNL97_plus_lncRNA::1::4657	10610	downstream	0	1	21	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100506177		hypothetical LOC100506177	XR_112320, XR_109984, XR_115540		
GeneID:90411	MCFD2	2	47,129,009	47,168,994	39,985	-	1	2_A375_pNL97_plus_lncRNA::1::4657	31970	in gene	0	1	21	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MCFD2	DKFZp686G21263, LMAN1IP, F5F8D2, SDNSF, F5F8D, MCFD2	multiple coagulation factor deficiency 2	NM_001171506, NM_001171507, NM_001171508, NM_001171509, NM_001171510, NM_001171511, NM_139279, hCT1964082.2, hCT1971286.2, hCT2348893.0, hCT6082.3	212245_at, 212246_at	NP_001164977.1, NP_001164978.1, NP_001164979.1, NP_001164980.1, NP_001164981.1, NP_001164982.1, NP_644808.1, EAX00230.1, EAX00231.1, EAX00232.1, EAX00233.1
GeneID:57217	TTC7A	2	47,168,313	47,303,275	134,962	+	1	1_A375_pNL7_minus_lncRNA::1::3239	144607	downstream	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TTC7A	TTC7, MGC134630, MGC131720, TTC7A	tetratricopeptide repeat domain 7A	NM_020458, hCT2263790.1, hCT2263791.1, hCT2263792.1, hCT6081.4	224912_at, 224923_at, 224924_at, 240369_at	NP_065191.2, EAX00228.1, EAX00226.1, EAX00227.1, EAX00229.1
GeneID:285051	C2orf61	2	47,314,130	47,382,517	68,387	-	1	1_A375_pNL7_minus_lncRNA::1::3239	69397	downstream	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene C2orf61	C2orf61, FLJ40172	chromosome 2 open reading frame 61	NM_173649, NM_001163561, hCT2263137.1, hCT2351039.0	1553460_at	NP_775920.1, NP_001157033.1, EAX00224.1, EAX00225.1
GeneID:805	CALM2	2	47,387,221	47,403,740	16,519	-	2	1_A375_pNL7_minus_lncRNA::1::3240, 2_A375_pNL97_plus_lncRNA::1::4658	-132, -132	upstream, upstream	1	1	20	20	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CALM2	CALM2, PHKD2, FLJ99410, CALM1, CALM3, PHKD, CAMII	calmodulin 2 (phosphorylase kinase, delta)	NM_001743, hCT1962954.2, hCT1969340.2, hCT2348839.0, hCT2348840.0	207243_s_at	NP_001734.1, EAX00220.1, EAX00221.1, EAX00222.1, EAX00223.1
GeneID:4436	MSH2	2	47,630,263	47,710,360	80,097	+	2	1_A375_pNL7_minus_lncRNA::1::3242, 2_A375_pNL97_plus_lncRNA::1::4660	233, -23	in gene, upstream	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MSH2	MSH2, LCFS2, HNPCC, HNPCC1, COCA1, FCC1	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	NM_000251, hCT1962957.1, hCT2263797.0, hCT6890.3	209421_at	NP_000242.1, EAX00213.1, EAX00214.1, EAX00215.1
GeneID:56660	KCNK12	2	47,747,914	47,797,470	49,556	-	2	1_A375_pNL7_minus_lncRNA::1::3243, 2_A375_pNL97_plus_lncRNA::1::4661	-1170, -1090	upstream, upstream	1	1	32	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene KCNK12	THIK2, KCNK12, THIK-2	potassium channel, subfamily K, member 12	NM_022055, hCT1640308.3	220448_at	NP_071338.1, EAX00212.1
GeneID:2956	MSH6	2	48,010,221	48,034,092	23,871	+	1	2_A375_pNL97_plus_lncRNA::1::4662	179	in gene	0	1	11	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MSH6	HSAP, HNPCC5, MSH6, GTBP	mutS homolog 6 (E. coli)	NM_000179, hCT2263614.0, hCT6743.3	202911_at, 211449_at, 211450_s_at, 240145_at	NP_000170.1, EAX00208.1, EAX00209.1
GeneID:129285	KLRAQ1	2	48,667,908	48,742,531	74,623	+	1	2_A375_pNL97_plus_lncRNA::1::4663	-164	upstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene KLRAQ1	CCDC128, FLJ16566, MGC111761, KLRAQ1	KLRAQ motif containing 1	NM_001135629, NM_152994, NR_024186, NM_001193475, hCT2263625.0, hCT2263626.0, hCT2358368.0, hCT2358369.0, hCT2358390.0	1553955_at, 1554145_a_at	NP_001129101.1, NP_694539.1, NP_001180404.1, EAX00197.1, EAX00199.1, EAX00200.1, EAX00198.1, EAX00201.1
GeneID:286749	STON1-GTF2A1L	2	48,796,159	48,906,742	110,583	+	1	2_A375_pNL97_plus_lncRNA::1::4664	-2399	upstream	0	1	6	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene STON1-GTF2A1L	SALF, STON1-GTF2A1L, MGC126823, MGC126821	STON1-GTF2A1L readthrough	NM_172311		NP_758515.1
GeneID:9378	NRXN1	2	50,145,643	51,259,674	1,114,031	-	3	1_A375_pNL7_minus_lncRNA::1::3244, 1_A375_pNL7_minus_lncRNA::1::3245, 2_A375_pNL97_plus_lncRNA::1::4665	79354, 218, 250	in gene, in gene, in gene	1	1	24	31	2	2_A375_pNL97_plus_lncRNA::1	53	Gene NRXN1	KIAA0578, DKFZp313P2036, PTHSL2, NRXN1, Hs.22998, FLJ35941	neurexin 1	NM_001135659, NM_004801, NM_138735, hCT1960121.1, hCT2262608.0, hCT2262611.0, hCT2262613.0, hCT2262616.0	1558708_at, 209914_s_at, 209915_s_at, 216096_s_at, 228547_at, 237535_x_at	NP_001129131.1, NP_004792.1, NP_620072.1, EAX00182.1, EAX00184.1, EAX00185.1, EAX00183.1, EAX00186.1
GeneID:51130	ASB3	2	53,897,118	54,014,079	116,961	-	1	2_A375_pNL97_plus_lncRNA::1::4667	-241	upstream	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ASB3	FLJ10421, ASB-3, MGC132002, MGC996, FLJ10123, ASB3, MGC12531	ankyrin repeat and SOCS box containing 3	NM_145863, NM_016115, hCT2262553.1, hCT2262558.1, hCT2262560.0, hCT2358402.0, hCT2358403.0	1560219_at, 224524_s_at	NP_665862.1, NP_057199.1, EAX00167.1, EAX00169.1, EAX00170.1, EAX00171.1, EAX00168.1
GeneID:100302652	LOC100302652	2	53,897,430	54,087,170	189,740	-	1	2_A375_pNL97_plus_lncRNA::1::4667	72650	in gene	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100302652	MGC132002	GPR75-ASB3	NM_001164165		NP_001157637.1
GeneID:27248	ERLEC1	2	54,014,068	54,046,495	32,427	+	1	2_A375_pNL97_plus_lncRNA::1::4667	252	in gene	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ERLEC1	CL25084, XTP3TPB, CL24936, XTP3-B, ERLEC1, C2orf30	endoplasmic reticulum lectin 1	NM_015701, NM_001127397, NM_001127398, hCT1964084.1, hCT2262695.0, hCT2358495.0, hCT6392.2	224626_at, 224630_at	NP_056516.2, NP_001120869.1, NP_001120870.1, EAX00163.1, EAX00164.1, EAX00166.1, EAX00165.1
GeneID:98	ACYP2	2	54,342,410	54,532,437	190,027	+	1	2_A375_pNL97_plus_lncRNA::1::4669	246	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ACYP2	ACYP, ACYM, ACYP2	acylphosphatase 2, muscle type	NM_138448, hCT2264115.1, hCT2264116.1, hCT2264117.1, hCT2345322.0, hCT2345323.0, hCT2345324.0	206833_s_at	NP_612457.1, EAX00154.1, EAX00152.1, EAX00155.1, EAX00156.1, EAX00157.1, EAX00153.1
GeneID:6711	SPTBN1	2	54,683,454	54,898,583	215,129	+	1	1_A375_pNL7_minus_lncRNA::1::3248	26498	in gene	1	0	18	10	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SPTBN1	SPTBN1, ELF, betaSpII, SPTB2	spectrin, beta, non-erythrocytic 1	NM_003128, NM_178313, hCT1961251.2, hCT1961252.2, hCT1962938.2, hCT2264077.1, hCT2264082.1, hCT2264084.1, hCT2264088.1, hCT2264090.1, hCT2264093.1, hCT2264094.1, hCT6420.4	200671_s_at, 200672_x_at, 212071_s_at, 213914_s_at, 214856_at, 215918_s_at, 226342_at, 226765_at, 228246_s_at, 242220_at	NP_003119.2, NP_842565.2, EAX00137.1, EAX00138.1, EAX00139.1, EAX00145.1, EAX00140.1, EAX00141.1, EAX00142.1, EAX00143.1, EAX00144.1, EAX00146.1, EAX00147.1
GeneID:400954	EML6	2	54,952,149	55,199,157	247,008	+	2	1_A375_pNL7_minus_lncRNA::1::3249, 2_A375_pNL97_plus_lncRNA::1::4670	-1557, 179211	upstream, in gene	1	1	17.5	19	2	2_A375_pNL97_plus_lncRNA::1	23	Gene EML6	FLJ16635, FLJ42562, EML6, DKFZp686G14111	echinoderm microtubule associated protein like 6	NM_001039753	229656_s_at, 242785_at	NP_001034842.2
GeneID:57142	RTN4	2	55,199,325	55,277,734	78,409	-	2	1_A375_pNL7_minus_lncRNA::1::3250, 2_A375_pNL97_plus_lncRNA::1::4671	1499, 1446	in gene, in gene	1	1	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene RTN4	RTN4-C, RTN4, RTN4-A, RTN4-B2, NSP, RTN4-B1, RTN-X, NI220/250, NOGO-A, NOGOC, Nogo-B, ASY, Nogo-C, Nbla10545, NSP-CL, NOGO, Nbla00271	reticulon 4	NM_020532, NM_207520, NM_153828, NM_007008, NM_207521, hCT1823278.2, hCT1960132.1, hCT1960133.1, hCT1962960.1, hCT2263023.0, hCT2263025.0, hCT2263029.0, hCT2263033.0, hCT2358442.0, hCT2358443.0, hCT2358444.0, hCT2358445.0, hCT2358446.0, hCT2358447.0, hCT2	1556049_at, 210968_s_at, 211509_s_at, 214629_x_at	NP_065393.1, NP_997403.1, NP_722550.1, NP_008939.1, NP_997404.1, EAX00115.1, EAX00116.1, EAX00117.1, EAX00118.1, EAX00119.1, EAX00120.1, EAX00121.1, EAX00122.1, EAX00128.1, EAX00123.1, EAX00124.1, EAX00125.1, EAX00126.1, EAX00127.1, EAX00129.1, EAX00130.1
GeneID:4528	MTIF2	2	55,463,756	55,496,384	32,628	-	1	1_A375_pNL7_minus_lncRNA::1::3251	-80	upstream	1	0	18	22	1	1_A375_pNL7_minus_lncRNA::1	18	Gene MTIF2	MTIF2		NM_002453, NM_001005369, hCT1960125.1, hCT2274118.0, hCT6019.3	203095_at	NP_002444.2, NP_001005369.1, EAX00103.1, EAX00104.1, EAX00105.1
GeneID:55704	CCDC88A	2	55,514,978	55,647,057	132,079	-	1	1_A375_pNL7_minus_lncRNA::1::3252	-15	upstream	1	0	21	17	1	1_A375_pNL7_minus_lncRNA::1	21	Gene CCDC88A	DKFZp686D0630, KIAA1212, GRDN, GIV, HkRP1, GIRDIN, APE, CCDC88A	coiled-coil domain containing 88A	NM_001135597, NM_018084, hCT1960119.1, hCT2274114.0, hCT2274115.0	1562648_at, 219387_at, 221078_s_at, 225045_at, 238759_at, 239233_at	NP_001129069.1, NP_060554.3, EAX00099.1, EAX00100.1, EAX00101.1
GeneID:57223	SMEK2	2	55,775,514	55,844,796	69,282	-	2	1_A375_pNL7_minus_lncRNA::1::3253, 2_A375_pNL97_plus_lncRNA::1::4672	76, -36	in gene, upstream	1	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SMEK2	KIAA1387, SMEK2, smk1, FLJ31474, PSY2, FLFL2, PP4R3B	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	NM_001122964, NM_020463, hCT1969339.1, hCT2274103.0, hCT2274106.0, hCT2358477.0, hCT2358478.0, hCT2358479.0, hCT8023.3	1568627_at, 222270_at, 224474_x_at, 226230_at, 233759_s_at, 241103_at	NP_001116436.1, NP_065196.1, EAX00090.1, EAX00092.1, EAX00093.1, EAX00094.1, EAX00091.1, EAX00095.1, EAX00096.1
GeneID:7444	VRK2	2	58,273,777	58,387,055	113,278	+	1	1_A375_pNL7_minus_lncRNA::1::3254	-113	upstream	1	0	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene VRK2	VRK2		NM_001130480, NM_001130481, NM_001130482, NM_001130483, NR_036441, NM_006296, hCT2262514.0, hCT2358527.0, hCT2358528.0, hCT2358529.0, hCT2358530.0, hCT2358531.0, hCT6222.3	205126_at	NP_001123952.1, NP_001123953.1, NP_001123954.1, NP_001123955.1, NP_006287.2, EAX00068.1, EAX00062.1, EAX00063.1, EAX00064.1, EAX00065.1, EAX00066.1, EAX00067.1
GeneID:55120	FANCL	2	58,386,378	58,468,515	82,137	-	1	1_A375_pNL7_minus_lncRNA::1::3255	-93	upstream	1	0	15	10	1	1_A375_pNL7_minus_lncRNA::1	15	Gene FANCL	FAAP43, FLJ10335, PHF9, FANCL, POG	Fanconi anemia, complementation group L	NM_018062, NM_001114636, hCT1950370.1, hCT1958280.1, hCT1958281.1, hCT1970737.1, hCT2358535.0, hCT6223.2	218397_at	NP_060532.2, NP_001108108.1, EAX00056.1, EAX00057.1, EAX00059.1, EAX00060.1, EAX00058.1, EAX00061.1
GeneID:400955	FLJ30838	2	58,747,888	59,290,901	543,013	+	2	1_A375_pNL7_minus_lncRNA::1::3256, 2_A375_pNL97_plus_lncRNA::1::4674	40176, 60400	in gene, in gene	1	1	13.5	11.5	2	2_A375_pNL97_plus_lncRNA::1	16	Gene FLJ30838	DKFZp547K0718	hypothetical LOC400955	NR_033873	1557472_a_at, 1562326_at	
GeneID:400957	FLJ16341	2	61,074,895	61,108,449	33,554	-	1	2_A375_pNL97_plus_lncRNA::1::4675	-255	upstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene FLJ16341		hypothetical LOC400957	NR_033960		
GeneID:5966	REL	2	61,108,752	61,150,178	41,426	+	1	2_A375_pNL97_plus_lncRNA::1::4675	-48	upstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene REL	REL, C-Rel	v-rel reticuloendotheliosis viral oncogene homolog (avian)	NM_002908, hCT6175.2	206035_at, 206036_s_at	NP_002899.1, EAX00028.1
GeneID:150962	PUS10	2	61,167,548	61,245,365	77,817	-	2	1_A375_pNL7_minus_lncRNA::1::3257, 2_A375_pNL97_plus_lncRNA::1::4676	629, 661	in gene, in gene	1	1	78	65	1	1_A375_pNL7_minus_lncRNA::1	78	Gene PUS10	PUS10, CCDC139, MGC126729, DOBI, FLJ32312, MGC126755	pseudouridylate synthase 10	NM_144709, hCT2262479.0, hCT2262480.0, hCT2262481.0, hCT2262482.0, hCT2262483.0, hCT2358464.0	1553280_at, 229362_at, 232945_at	NP_653310.2, EAX00022.1, EAX00023.1, EAX00024.1, EAX00025.1, EAX00026.1, EAX00027.1
GeneID:5194	PEX13	2	61,244,812	61,279,125	34,313	+	2	1_A375_pNL7_minus_lncRNA::1::3257, 2_A375_pNL97_plus_lncRNA::1::4676	-76, -108	upstream, upstream	1	1	78	65	1	1_A375_pNL7_minus_lncRNA::1	78	Gene PEX13	NALD, PEX13, ZWS	peroxisomal biogenesis factor 13	NM_002618, hCT2340836.0, hCT2340837.0, hCT2340838.0, hCT2340839.0, hCT6174.3	1556009_at, 1558163_at, 1558164_s_at, 205246_at	NP_002609.1, EAX00020.1, EAX00017.1, EAX00018.1, EAX00019.1, EAX00021.1
GeneID:130872	AHSA2	2	61,404,555	61,414,686	10,131	+	2	1_A375_pNL7_minus_lncRNA::1::3258, 2_A375_pNL97_plus_lncRNA::1::4677	-331, -331	upstream, upstream	1	1	17	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene AHSA2	FLJ34679, Hch1, AHSA2, DKFZp564C236, FLJ41715	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	NM_152392, hCT1950366.1, hCT1950367.1, hCT1958276.1, hCT2262796.0, hCT2262797.0, hCT2262801.0, hCT2358432.0, hCT2358433.0	226334_s_at, 226665_at, 230148_at	NP_689605.1, EAX00004.1, EAX00002.1, EAX00005.1, EAX00007.1, EAX00009.1, EAX00003.1, EAX00006.1, EAX00008.1
GeneID:7514	XPO1	2	61,705,069	61,765,418	60,349	-	1	2_A375_pNL97_plus_lncRNA::1::4678	-22	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene XPO1	emb, XPO1, DKFZp686B1823, CRM1	exportin 1 (CRM1 homolog, yeast)	NM_003400, hCT2262467.0, hCT2262469.0, hCT2262471.0	208775_at	NP_003391.1, EAW99995.1, EAW99993.1, EAW99994.1
GeneID:84140	FAM161A	2	62,051,983	62,081,278	29,295	-	1	2_A375_pNL97_plus_lncRNA::1::4680	-738	upstream	0	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FAM161A	MGC129962, FAM161A, RP28, FLJ13305, MGC129963	family with sequence similarity 161, member A	NM_032180, hCT1647500.3, hCT2262112.0, hCT2358348.0, hCT2358349.0	1557385_at, 1564467_at, 239090_at, 242584_at	NP_115556.2, EAW99991.1, EAW99988.1, EAW99989.1, EAW99990.1
GeneID:10575	CCT4	2	62,095,262	62,115,791	20,529	-	2	1_A375_pNL7_minus_lncRNA::1::3259, 2_A375_pNL97_plus_lncRNA::1::4681	15, -49	in gene, upstream	1	1	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene CCT4	MGC126165, CCT4, MGC126164, CCT-DELTA, SRB, Cctd	chaperonin containing TCP1, subunit 4 (delta)	NM_006430, hCT1950380.1, hCT1950381.1, hCT2262109.0, hCT87698.3	200877_at	NP_006421.2, EAW99984.1, EAW99985.1, EAW99986.1, EAW99987.1
GeneID:150684	COMMD1	2	62,132,803	62,363,205	230,402	+	5	1_A375_pNL7_minus_lncRNA::1::3260, 1_A375_pNL7_minus_lncRNA::1::3261, 2_A375_pNL97_plus_lncRNA::1::4682, 2_A375_pNL97_plus_lncRNA::1::4683, 2_A375_pNL97_plus_lncRNA::1::4684	-3, 133853, -35, 133757, 150109	upstream, in gene, upstream, in gene, in gene	1	1	19.33	19.33	3	1_A375_pNL7_minus_lncRNA::1	21	Gene COMMD1	C2orf5, COMMD1, MGC27155	copper metabolism (Murr1) domain containing 1	NM_152516, hCT1821351.3	226024_at	NP_689729.1, EAW99981.1
GeneID:23301	EHBP1	2	62,900,986	63,273,622	372,636	+	1	1_A375_pNL7_minus_lncRNA::1::3262	31494	in gene	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene EHBP1	EHBP1, KIAA0903, HPC12, NACSIN	EH domain binding protein 1	NM_015252, NM_001142614, NM_001142616, NM_001142615, hCT2344318.0, hCT2358355.0, hCT2358356.0	212650_at, 212653_s_at	NP_056067.2, NP_001136086.1, NP_001136087.1, NP_001136088.1, EAW99970.1, EAW99971.1, EAW99969.1
GeneID:51057	C2orf86	2	63,348,518	63,815,851	467,333	-	2	1_A375_pNL7_minus_lncRNA::1::3263, 2_A375_pNL97_plus_lncRNA::1::4685	-53, -85	upstream, upstream	1	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene C2orf86	fritz, DKFZp686C12204, hFritz, BBS15, FRITZ, FRTZ, WDPCP, C2orf86	WD repeat containing planar cell polarity effector	NM_015910, NM_001042692, hCT2261726.0, hCT2261729.0	224180_x_at, 231770_x_at	NP_056994.3, NP_001036157.1, EAW99964.1, EAW99965.1
GeneID:4190	MDH1	2	63,816,122	63,834,328	18,206	+	2	1_A375_pNL7_minus_lncRNA::1::3263, 2_A375_pNL97_plus_lncRNA::1::4685	-218, -186	upstream, upstream	1	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MDH1	MGC:1375, MDH1, MDHA, MOR2, MDH-s	malate dehydrogenase 1, NAD (soluble)	NM_005917, hCT13472.1, hCT1950287.1, hCT1950289.1, hCT1950290.1, hCT2262203.0	200978_at, 235374_at	NP_005908.1, EAW99959.1, EAW99960.1, EAW99961.1, EAW99962.1, EAW99963.1
GeneID:7360	UGP2	2	64,068,098	64,118,696	50,598	+	2	1_A375_pNL7_minus_lncRNA::1::3264, 2_A375_pNL97_plus_lncRNA::1::4686	574, -2	in gene, upstream	1	1	22	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene UGP2	UDPG, UGPP2, UDPGP2, pHC379, UGP2	UDP-glucose pyrophosphorylase 2	NM_006759, NM_001001521, hCT13476.4, hCT1950379.1, hCT1958289.1, hCT2262218.0, hCT2262219.0	205480_s_at	NP_006750.3, NP_001001521.1, EAW99953.1, EAW99954.1, EAW99955.1, EAW99957.1, EAW99956.1
GeneID:100507006	LOC100507006	2	64,455,588	64,479,960	24,372	+	2	1_A375_pNL7_minus_lncRNA::1::3265, 2_A375_pNL97_plus_lncRNA::1::4687	-116, -68	upstream, upstream	1	1	65	47	1	1_A375_pNL7_minus_lncRNA::1	65	Gene LOC100507006		hypothetical LOC100507006	XR_109941		
GeneID:54812	AFTPH	2	64,751,439	64,820,139	68,700	+	1	2_A375_pNL97_plus_lncRNA::1::4691	369	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene AFTPH	Nbla10388, FLJ23793, AFTPH, MGC33965, FLJ20080	aftiphilin	NM_001002243, NM_017657, NM_203437, hCT13692.3, hCT1950838.1, hCT2262373.0, hCT2262375.0, hCT2358459.0	217939_s_at, 222472_at	NP_001002243.1, NP_060127.3, NP_982261.2, EAW99938.1, EAW99939.1, EAW99941.1, EAW99937.1, EAW99940.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Intervals Count	Internal Intervals	Internal Gaps to next	Internal Pos.	[A]	[B]	[C]	[D]	Acc Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene ID:9348	SLC16A4	2	65,213,978	65,250,899	36,920	+	1	1_A2S_sNL97_dhrsd_blcRNA:1:-3365	3311	upstream	1	0	14	15	1	1_A2S_sNL97_dhrsd_blc RNA:1	14	Gene SLC16A4	ASCT1, SLC16A4, SATT	lipate cotrer family 1 (glutamate/neutral amino acid transporter), member 4	NM_003535, NM_001163983, NCT13883.3, NCT22662693.0	208610_s_at, 208611_s_at, 212016_s_at, 212051_s_at, 244022_at	NP_003526.2, NP_001155422.1, EAW99832.1, EAW99833.1
Gene ID:5 861	RAB1A	2	65,312,665	65,357,635	43,467	+	2	1_A2S_sNL97_dhrsd_blcRNA:1:-3366, 2_A2S_sNL97_glcs_blcRNA:1:-4498	123, 123	at gene, ut gene	1	1	26	20	1	1_A2S_sNL97_dhrsd_blc RNA:1	26	Gene RAB1A	DKFZp564B163, RAB1A, RAB1, YPT1	RAB1A, member RAS oncogene family	NM_004161, NM_015543, NCT13883.3, NCT16853901, NCT16853911, NCT19852762.1, NCT19852752.1, NCT22662629, NCT22661627.0, NCT22662620, NCT22661633.0	207781_s_at, 208724_s_at, 213480_at, 228426_at	NP_004152.1, NP_056356.1, EAW99819.1, EAW99820.1, EAW99824.1, EAW99825.1, EAW99817.1, EAW99815.1, EAW99820.1, EAW99821.1, EAW99822.1
Gene ID:1 0097	ACTR2	2	65,454,629	65,495,267	40,566	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4498	339	at gene	0	1	10	15	1	2_A2S_sNL97_glcs_blcR NA:1	15	Gene ACTR2	ACTR2, ARP2	ARP2 actin-related protein 2 homolog (yeast)	NM_005722.3, NM_020036, NCT13211.2, NCT19855434.1, NCT22642772.0, NCT22642764.0, NCT22642770.0, NCT22642777.0, NCT22662322.0	1554392_s_at, 1555019_s_at, 203727_s_at, 203728_at, 203729_s_at, 224210_s_at, 224211_at	NP_005703.3, EAW99999.1, EAW99911.1, EAW99912.1, EAW99913.1, EAW99915.1, EAW99914.1
Gene ID:1 00188	LOC1003 96	2	66,654,011	66,661,509	7,498	-	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3372, 2_A2S_sNL97_glcs_blcRNA:1:-4499	-371, -367	upstream, upstream	1	1	23	22	1	1_A2S_sNL97_dhrsd_blc RNA:1	23	Gene LOC730196		hypothetical LOC730196	XM_001719230, NM_001132691, XM_001132894		XP_001719282.1, XP_001132691.1, XP_001132894.1
Gene ID:4 211	MEIS1	2	66,662,532	66,799,691	137,159	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3372, 2_A2S_sNL97_glcs_blcRNA:1:-4499	-452, -439	upstream, upstream	1	1	23	22	1	1_A2S_sNL97_dhrsd_blc RNA:1	23	Gene MEIS1	MEIS1, MGC45360	Meis homeobox 1	NM_002398, NCT19611981.1, NCT22658550.0, NCT22661087.0, NCT22658580.0, NCT23584430.0	1555477_s_at, 206099_at, 242172_at	NP_002389.1, EAW99894.1, EAW99892.1, EAW99893.1, EAW99895.1, EAW99896.1
Gene ID:5 3438	ETAA1	2	67,624,642	67,637,833	13,191	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4782	310	at gene	0	1	12	15	1	2_A2S_sNL97_glcs_blcR NA:1	15	Gene ETAA1	ETAA1, FLJ22647	Ewing tumor-associated antigen 1	NM_018092, NCT13940.3		NP_060162.2, EAW99898.1
Gene ID:1 0428	C1D	2	68,269,332	68,290,159	20,827	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4782	62	at gene	0	1	12	17	1	2_A2S_sNL97_glcs_blcR NA:1	17	Gene C1D	SUNCR5, MGC10659, SUN-CR, LRP1, MGC12261, C1D	C1D nuclear receptor co-repressor	NM_006333, NM_173177, NM_001160262, NM_001160263, NCT22661656.0, NCT22661657.0, NCT23584580.0	208096_s_at	NP_006324.1, NP_775298.1, NP_001177192.1, NP_001177193.1, EAW99884.1, EAW99885.1, EAW99886.1, EAW99885.1
Gene ID:1 16143	WDR62	2	68,357,261	68,384,636	27,376	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3374, 2_A2S_sNL97_glcs_blcRNA:1:-4500	-140, -60	upstream, upstream	1	1	60	61	1	2_A2S_sNL97_glcs_blcR NA:1	61	Gene WDR62	WDR62, FLJ31081	WD repeat domain 62	NM_126458, NCT22658665.1, NCT22658693.1, NCT22661670.1, NCT23461100.0	238071_at	NP_612967.1, EAW99853.1, EAW99850.1, EAW99851.1, EAW99852.1
Gene ID:5 6902	PNO1	2	68,383,003	68,401,091	18,088	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3374, 2_A2S_sNL97_glcs_blcRNA:1:-4500	-265, -260	upstream, upstream	1	1	60	61	1	2_A2S_sNL97_glcs_blcR NA:1	61	Gene PNO1	DKFZp761P1210, PNO1	partner of MOB1 homolog (S. cerevisiae)	NM_020143, NCT13310.2	203622_s_at, 211697_x_at, 242672_at, 242903_at	NP_064528.1, EAW99879.1
Gene ID:2 4427	CNKP1	2	68,511,203	68,547,163	35,960	-	1	2_A2S_sNL97_glcs_blcRNA:1:-4708	-601	upstream	0	1	16	22	1	2_A2S_sNL97_glcs_blcR NA:1	22	Gene CNKP1	C2orf32, CNRP1, CKIP1, DKFZp566G1924	Connexin-type receptor-interacting protein 1	NM_015463, NM_001111101, NCT13308.2	228791_at	NP_056278.1, NP_001104571.1, EAW99877.1
Gene ID:5 54251	FBXO48	2	68,689,298	68,694,390	5,092	-	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3375, 2_A2S_sNL97_glcs_blcRNA:1:-4709	-1122, -106	upstream, upstream	1	1	21	30	1	2_A2S_sNL97_glcs_blcR NA:1	30	Gene FBXO48	FBXO48	F-box protein 48	NM_080428.2, NCT16340160.4		NP_001074851.1, EAW99873.1
Gene ID:2 00556	APLF	2	68,694,691	68,807,298	112,608	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3375, 2_A2S_sNL97_glcs_blcRNA:1:-4709	-179, -165	upstream, upstream	1	1	21	30	1	2_A2S_sNL97_glcs_blcR NA:1	30	Gene APLF	FLJ10303, C2orf13, MGC47799, PALF, APLF, APF_hum	apaxiliana and PNKP-like factor	NM_173345, NCT22624682.2, NCT22624692.2	1555100_at, 241379_at	NP_775616.1, EAW99872.1, EAW99871.1
Gene ID:9 936	ARHGAP2 5	2	68,961,913	69,053,985	92,052	+	1	2_A2S_sNL97_glcs_blcRNA:1:-3376	84951	downstream	1	0	20	10	1	2_A2S_sNL97_glcs_blcR NA:1	20	Gene ARHGAP25	KIAA0053, ARHGAP25	Rho GTPase activating protein 25	NM_014662, NM_001007231, NM_001166276, NM_001166277, NCT16896210.1, NCT22624968.0, NCT16896.2	1555076_at, 204662_at, 204663_at	NP_039017, NP_001007222.2, NP_001166748.1, NP_001166749.1, EAW99896.1, EAW99897.1
Gene ID:3 4168	ANTXR1	2	69,240,276	69,476,459	236,183	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3377, 2_A2S_sNL97_glcs_blcRNA:1:-4709	185132, 163116	ut gene, ut gene	1	1	21	20	1	1_A2S_sNL97_dhrsd_blc RNA:1	21	Gene ANTXR1	ANTXR1, TEM8, PLI10901, ATR, FLJ21776, FLJ11286	tellhalin/core receptor 1	NM_032208, NM_058179, NM_018153, NCT19800223.2, NCT19800242.2, NCT22625002.0, NCT22625043.0	1555092_s_at, 220082_s_at, 220083_at, 224568_at, 227660_at, 228430_at, 244632_at	NP_115554.1, NP_444262.1, NP_060522.2, EAW99855.1, EAW99857.1, EAW99856.1, EAW99858.1
Gene ID:2 7247	NPU1	2	69,623,252	69,664,753	41,501	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4709	119	at gene	0	1	15	17	1	2_A2S_sNL97_glcs_blcR NA:1	17	Gene NPU1	NIFUC, HIRIP5, MGC142252, MGC142254, NAU, CGI-33, NPU1, Nfu	NPU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	NM_001002757, NM_001002755, NM_001002756, NM_015700, NCT14521857.1, NCT23584607.0	1555079_at, 204663_at, 204664_at	NP_001002757.1, NP_001002755.1, NP_001002756.1, NP_056515.2, EAW99849.1, EAW99850.1
Gene ID:2 3546	AAK1	2	69,665,127	69,870,877	165,850	+	2	2_A2S_sNL97_glcs_blcRNA:1:-4710, 2_A2S_sNL97_glcs_blcRNA:1:-4711	1625, -953	ut gene, upstream, upstream	0	1	16.5	15	2	2_A2S_sNL97_glcs_blcR NA:1	19	Gene AAK1	FLJ20252, DKFZp666R02022, FLJ23712, KIAA1048, DKFZp686H02122, MGC135170, MGC164995, FLJ25231, FLJ31660, MGC164939, FLJ42982, AAK1	AP2 associated kinase 1	NM_014911, NCT10157.2, NCT22699806.0	1555434_s_at, 203425_s_at, 211166_s_at, 214696_at, 214698_at, 225522_at, 225523_at, 232100_at	NP_055726.2, EAW99865.1, EAW99867.1
Gene ID:3 977	ANXA6	2	69,999,127	70,053,896	54,769	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3378, 2_A2S_sNL97_glcs_blcRNA:1:-4712	1163, 87963	upstream, downstream	1	1	16	17.5	2	2_A2S_sNL97_glcs_blcR NA:1	19	Gene ANXA6	FKSG6, MGC31106, ZAP36, DKFZp686H02120, ANX6, ANX6	annexin A6	NM_001155, NCT20703.3	201201_s_at, 201202_at	NP_001144.1, EAW99844.1
Gene ID:6 4335	GMCL1	2	70,099,818	70,106,727	49,909	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4712	-226	upstream	0	1	16	19	1	2_A2S_sNL97_glcs_blcR NA:1	19	Gene GMCL1	BTBD13, GCL1, GCL, GMCL1	germ cell-less, homolog 1 (Drosophila)	NM_178439, NCT21837.4	218555_at, 224555_s_at	NP_848526.1, EAW99842.1
Gene ID:4 09360	LOC4092 60	2	70,169,393	70,214,147	124,752	-	3	1_A2S_sNL97_dhrsd_blcRN A:1:-3379, 2_A2S_sNL97_glcs_blcRNA:1:-4713, 2_A2S_sNL97_glcs_blcRNA:1:-4714	587, -285, 1309	at gene, upstream, upstream	1	1	16.5	15	2	2_A2S_sNL97_glcs_blcR NA:1	19	Gene LOC409360		hypothetical LOC409360	NR_033872	1555540_at, 227969_at, 228127_at, 228402_at, 228909_at, 229013_at	
Gene ID:5 092	PCBP1	2	70,314,553	70,316,235	1,730	+	3	1_A2S_sNL97_dhrsd_blcRN A:1:-3379, 2_A2S_sNL97_glcs_blcRNA:1:-4713, 2_A2S_sNL97_glcs_blcRNA:1:-4714	-655, -153, 671	upstream, upstream, upstream	1	1	16.5	15	2	2_A2S_sNL97_glcs_blcR NA:1	19	Gene PCBP1	hnRNP-K, HNRPEP1, PCBP1, HNRPK, hnRNP-E1	poly(rC) binding protein 1	NM_006196, NCT10157.2	200620_at	NP_006187.2, EAW99834.1
Gene ID:5 9900	C2orf42	2	70,377,017	70,418,151	41,134	-	2	2_A2S_sNL97_glcs_blcRNA:1:-4715, 2_A2S_sNL97_glcs_blcRNA:1:-4714	48231, 327	downstream, ut gene	0	1	16.5	21.5	2	2_A2S_sNL97_glcs_blcR NA:1	26	Gene C2orf42	C2orf42, FLJ35556	chromosome 2 open reading frame 42	NM_017660, NCT19857791.1, NCT19857802.1, NCT23614534.0	218128_at	NP_060180.2, EAW99830.1, EAW99828.1, EAW99829.1, EAW99830.1
Gene ID:7 072	TK1	2	70,435,376	70,473,779	38,403	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4717	4663	upstream	0	1	11	16	1	2_A2S_sNL97_glcs_blcR NA:1	16	Gene TK1	TK1, TK-1		NM_003173, NM_022037, NCT19843401.1, NCT19843405.1, NCT23583960.0, NCT23583999.0, NCT21841.3	1554559_at, 1554560_at, 201445_s_at, 201446_at, 201447_at, 201448_at, 201449_s_at, 201450_s_at	NP_071553.2, NP_071330.2, EAW99824.1, EAW99825.1, EAW99826.1, EAW99827.1, EAW99823.1
Gene ID:1 0030238	MIR1285-2	2	70,460,050	70,460,137	87	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4717	5335	upstream	0	1	11	16	1	2_A2S_sNL97_glcs_blcR NA:1	16	Gene MIR1285-2	MIRN1285-2, MIR1285-2, hsa-mir-1285-2	microRNA 1285-2	NR_031617		
Gene ID:5 1448	PCYOX1	2	70,483,231	70,508,317	23,086	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4717	241	at gene	0	1	11	16	1	2_A2S_sNL97_glcs_blcR NA:1	16	Gene PCYOX1	PCYOX1, PCL1, KIAA0905	prenylcysteine oxidase 1	NM_016297, NCT21843348.3	203503_at	NP_057511.2, EAW99819.1
Gene ID:6 637	SNRPG	2	70,508,510	70,520,869	12,359	+	3	1_A2S_sNL97_dhrsd_blcRN A:1:-3380, 2_A2S_sNL97_glcs_blcRNA:1:-4716, 2_A2S_sNL97_glcs_blcRNA:1:-4718	133, 37, 7631	at gene, upstream, upstream	1	1	16.5	23	2	2_A2S_sNL97_glcs_blcR NA:1	29	Gene SNRPG	Sm-G, SMG, SNRPG, MGC117317	small nuclear ribonucleoprotein polypeptide G	NM_003096, NCT22700140.0, NCT22700117.0	208643_s_at	NP_003077.1, EAW99816.1, EAW99817.1
Gene ID:9 4905	FAM136A	2	70,523,108	70,529,220	6,112	+	3	1_A2S_sNL97_dhrsd_blcRN A:1:-3380, 2_A2S_sNL97_glcs_blcRNA:1:-4716, 2_A2S_sNL97_glcs_blcRNA:1:-4718	6868, 6355, 420	downstream, downstream, ut gene	1	1	16.5	23	2	2_A2S_sNL97_glcs_blcR NA:1	29	Gene FAM136A	FLJ14668, FAM136A	family with sequence similarity 136, member A	NM_032622, NCT16842471.1, NCT19842461.1	218647_s_at	NP_116211.2, EAW99815.1, EAW99816.1
Gene ID:7 038	TGFA	2	70,674,418	70,761,105	106,689	+	3	1_A2S_sNL97_dhrsd_blcRN A:1:-3381, 2_A2S_sNL97_glcs_blcRNA:1:-4720	219, -353	upstream, upstream	1	1	11	27	1	1_A2S_sNL97_dhrsd_blc RNA:1	27	Gene TGFA	TFGA, TGFA	fibroblast-derived growth factor, alpha	NM_001099691, NM_003236, NCT22687190.0, NCT22687221.0, NCT22687222.0, NCT22687236.0, NCT21853.2	208013_s_at, 208016_at, 211250_s_at	NP_001091161.1, NP_003227.1, EAW99810.1, EAW99811.1, EAW99813.1, EAW99814.1, EAW99812.1
Gene ID:1 19	ADD2	2	70,859,216	70,893,275	109,159	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4721	51167	ut gene	0	1	9	17	1	2_A2S_sNL97_glcs_blcR NA:1	17	Gene ADD2	ADDB, ADD2	adducin 2 (beta)	NM_001166934, NM_001166935, NM_001617, NM_017455, NCT16842171, NCT16842181, NCT19842191, NCT22657002.0, NCT22657004.0, NCT22657024.0, NCT22657122.0, NCT22657142.0, NCT23584640, NCT.87362	203265_s_at, 206807_s_at, 227236_at	NP_001171853.1, NP_001171854.1, NP_058522.1, NP_001606.1, NP_058516.2, EAW99801.1, EAW99802.1, EAW99785.1, EAW99786.1, EAW99800.1, EAW99803.1, EAW99804.1, EAW99805.1, EAW99806.1, EAW99807.1, EAW99808.1
Gene ID:5 3222	ATP6V1B 2	2	71,162,998	71,182,561	29,563	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4722	11946	ut gene	0	1	11	21	1	2_A2S_sNL97_glcs_blcR NA:1	21	Gene ATP6V1B2	VATB, RTA1B, ATP6V1B1, VMA2, ATP6B1, VPP3, MGC32562	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1	NM_001692, NCT23583836.0, NCT22702.2	1554547_at, 205672_at	NP_001684.2, EAW99781.1, EAW99780.1
Gene ID:9 9966	ANKRD63	2	71,203,573	71,212,629	7,056	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3383, 2_A2S_sNL97_glcs_blcRNA:1:-4724	16521, 16537	downstream, downstream	1	1	16	69	1	2_A2S_sNL97_glcs_blcR NA:1	69	Gene ANKRD63	FLJ12056, ANKRD63, FLJ30160	Ankyrin repeat domain 63	NM_024672, NM_001119116, NCT19849923.0, NCT23599600.0, NCT23599601.0, NCT23599602.0	213759_at, 244452_at	NP_078932.3, NP_001106655.1, EAW99786.1, EAW99787.1, EAW99788.1, EAW99789.1
Gene ID:1 13419	TEX261	2	71,210,066	71,222,201	8,833	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3383, 2_A2S_sNL97_glcs_blcRNA:1:-4724	485, -111	upstream, upstream	1	1	16	69	1	2_A2S_sNL97_glcs_blcR NA:1	69	Gene TEX261	TEG-261, MGC33043, TEX261	testis-expressed 261	NM_144582, NCT19842561.1, NCT19842551.1, NCT22261.2	212662_at, 212664_at	NP_653162.2, EAW99784.1, EAW99783.1, EAW99785.1
Gene ID:3 5377	NAGK	2	71,295,468	71,303,868	10,380	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3384, 2_A2S_sNL97_glcs_blcRNA:1:-4724	400, 366	at gene, ut gene	1	1	21	34	1	2_A2S_sNL97_glcs_blcR NA:1	34	Gene NAGK	GNK, HSA242910, NAGK	N-acetylglucosamine kinase	NM_017567, NCT19842479.1	218231_at	NP_060037.3, EAW99780.1
Gene ID:4 8692	MCEE	2	71,339,806	71,357,284	20,368	-	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3385, 2_A2S_sNL97_glcs_blcRNA:1:-4726	146, -238	ut gene, upstream, ut gene	1	1	23	34	1	2_A2S_sNL97_glcs_blcR NA:1	34	Gene MCEE	MCEE, GLOD2	methylmalonyl CoA epimerase	NM_032601, NCT22262.3	226238_at	NP_116090.3, EAW99776.1
Gene ID:1 0198	MPHOSPH 10	2	71,357,444	71,377,220	19,776	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3385, 2_A2S_sNL97_glcs_blcRNA:1:-4726	-186, 165	upstream, ut gene	1	1	23	24	1	2_A2S_sNL97_glcs_blcR NA:1	24	Gene MPHOSPH10	MPP10P, MPP10, MPHOSPH10, CTI30	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	NM_005791, NCT19842457.1, NCT22262.2	212665_at	NP_005782.1, EAW99777.1, EAW99776.1
Gene ID:2 7332	ZNF638	2	71,555,559	71,662,169	103,200	+	3	1_A2S_sNL97_dhrsd_blcRN A:1:-3387, 2_A2S_sNL97_glcs_blcRNA:1:-4727, 2_A2S_sNL97_glcs_blcRNA:1:-4728	15911, 16593, 15927	at gene, ut gene, ut gene	1	1	23	29	1	2_A2S_sNL97_glcs_blcR NA:1	29	Gene ZNF638	ZFI6L, ZI638, ZNF638, NP220, MGC26105, DKFZp686F1231, MGC90196	zinc finger protein 638	NM_001014972, NM_014497, NCT19842003.1, NCT19842051.1, NCT19842021.1, NCT23585533.0, NCT23585549, NCT.82216.2	1554343_at, 1554344_at, 201257_s_at, 201773_s_at, 238243_at	NP_001014972.1, NP_055312.2, EAW99767.1, EAW99768.1, EAW99769.1, EAW99771.1, EAW99769.1, EAW99772.1
Gene ID:2 3202	EXOC6B	2	72,405,644	72,653,177	249,533	+	3	1_A2S_sNL97_dhrsd_blcRN A:1:-3393, 2_A2S_sNL97_glcs_blcRNA:1:-4735, 2_A2S_sNL97_glcs_blcRNA:1:-4736	69, 47480, 127	at gene, ut gene, ut gene	1	1	15	19.3	2	2_A2S_sNL97_glcs_blcR NA:1	23	Gene EXOC6B	SEC15L2, SEC15B, EXOC6B, KIAA0619	exocyst complex component 6B	NM_015189	213417_at, 228900_at	NP_056004.1
Gene ID:6 697	SPR	2	73,114,512	73,119,289	4,777	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3394, 2_A2S_sNL97_glcs_blcRNA:1:-4737, 2_A2S_sNL97_glcs_blcRNA:1:-4738	-2624, -3696, 64	upstream, upstream, ut gene	1	1	24	29	2	2_A2S_sNL97_glcs_blcR NA:1	35	Gene SPR	SPR, SDR2EC1	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	NM_003124, NCT22767692.0, NCT20797.2	200858_at	NP_003115.1, EAW99757.1, EAW99758.1
Gene ID:9 4097	SFXN5	2	73,199,163	73,295,865	129,800	+	1	2_A2S_sNL97_glcs_blcRNA:1:-3395	797	at gene	1	0	10	13	1	1_A2S_sNL97_dhrsd_blc RNA:1	13	Gene SFXN5	MGC12415, SFXN3, MGC12412, BIBG1	sideroflexin 5	NM_144579, NCT22763390.0, NCT22763500.0, NCT23583239.0	1563705_at, 226372_at, 232681_at	NP_653180.2, EAW99753.1, EAW99752.1, EAW99753.1
Gene ID:2 9036	RAB11FIP 5	2	73,300,510	73,340,146	39,636	+	1	2_A2S_sNL97_glcs_blcRNA:1:-3395	41938	downstream	1	0	10	13	1	1_A2S_sNL97_dhrsd_blc RNA:1	13	Gene RAB11FIP5	RIP11, DKFZp434H016, KIAA0857, GAP1, pp75, RAB11FIP5	RAB11 family interacting protein 5 (class I)	NM_015470, NCT22763301.1, NCT22763302.1, NCT22763303.1	1568795_s_at, 216974_s_at	NP_056285.1, EAW99730.1, EAW99749.1, EAW99731.1
Gene ID:3 4622	NOTO	2	73,479,389	73,480,340	8,934	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3396, 2_A2S_sNL97_glcs_blcRNA:1:-4739	12182, 12102	downstream, downstream	1	1	16	16	1	2_A2S_sNL97_glcs_blcR NA:1	16	Gene NOTO	NOTO		NM_030753.2, NCT19843.3		NP_001170734.1
Gene ID:1 0322	SMYD5	2	73,641,366	73,654,355	12,989	+	4	1_A2S_sNL97_dhrsd_blcRN A:1:-3396, 2_A2S_sNL97_glcs_blcRNA:1:-4739, 2_A2S_sNL97_glcs_blcRNA:1:-4740, 2_A2S_sNL97_glcs_blcRNA:1:-4741	252, 18914, 122, 20176	at gene, downstream, at gene, downstream	1	1	16.5	16.5	2	2_A2S_sNL97_glcs_blcR NA:1	19	Gene SMYD5	MNB/MAQ, ZMYND23, ERG1, RAI15, SMYD5	SMYD family member 5	NM_020882, NCT22767492.0, NCT22767504.0	208316_at	NP_065813.2, EAW99748.1, EAW99749.1
Gene ID:5 4278	C2orf8	2	73,455,134	73,460,356	5,222	-	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3397, 2_A2S_sNL97_glcs_blcRNA:1:-4739	-624, -168	upstream, upstream	1	1	19	19	1	2_A2S_sNL97_glcs_blcR NA:1	19	Gene C2orf8	C2orf8, FRADC1, FAP21, MGC13004	chromosome 2 open reading frame 7	NM_032319, NCT16842381.1, NCT.31620.3	223312_at	NP_115693.1, EAW99742.1, EAW99742.1
Gene ID:1 0574	CCT7	2	73,461,264	73,480,150	18,886	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3397, 2_A2S_sNL97_glcs_blcRNA:1:-4739	-62, 180	upstream, ut gene	1	1	19	19	1	2_A2S_sNL97_glcs_blcR NA:1	19	Gene CCT7	NIP7-1, CCT7, CCTH, CCTETA, TCP1ETA, MGC110555	chaperonin containing TCP1, subunit 7 (eta)	NM_006429, NM_001009570, NM_001166264, NM_001166265, NM_030932, NM_132931, NCT22767972.0, NCT22767985.0, NCT23584643.0	200312_at	NP_006410.1, NP_001009570.1, NP_001159736.1, NP_001159737.1, EAW99736.1, EAW99740.1, EAW99738.1
Gene ID:1 0030713	LOC1003 07133	2	73,511,653	73,518,113	6,460	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3398, 2_A2S_sNL97_glcs_blcRNA:1:-4740	6651, 6863	downstream, downstream	1	1	22	26	1	2_A2S_sNL97_glcs_blcR NA:1	26	Gene LOC100307133		hypothetical LOC100307133	XR_109343		
Gene ID:1 961	EGR4	2	73,516,097	73,520,829	2,772	+	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3398, 2_A2S_sNL97_glcs_blcRNA:1:-4740	2525, 2483	at gene, ut gene	1	1	22	26	1	2_A2S_sNL97_glcs_blcR NA:1	26	Gene EGR4	FAT133, NGFIC, EGR4, NGFIC	early growth response 4	NM_001965, NCT21811.3	207767_s_at, 207768_at, 231579_at	NP_001956.3, EAW99734.1
Gene ID:7 840	ALMS1	2	73,612,886	73,637,046	224,160	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4738	352	at gene	0	1	10	19	1	2_A2S_sNL97_glcs_blcR NA:1	19	Gene ALMS1	DKFZp686A118, DKFZp686D18235, ALMS1, ALSS, KIAA0328	Alstrom syndrome 1	NM_015120, NCT22767761.0, NCT22767762.0, NCT22767763.0, NCT22655572.0	214220_s_at, 214221_at, 214707_s_at	NP_056935.2, EAW99729.1, EAW99728.1, EAW99730.1, EAW99731.1
Gene ID:5 1022	TPRKB	2	73,956,957	73,964,517	7,560	-	2	1_A2S_sNL97_dhrsd_blcRN A:1:-3399, 2_A2S_sNL97_glcs_blcRNA:1:-4739	-123, -176	upstream, upstream	1	1	23	23	1	2_A2S_sNL97_glcs_blc RNA:1	23	Gene TPRKB	TPRKB, CGI-121	TP53RK binding protein	NM_016058, NCT10157.5, NCT19845041.1, NCT19851277.1, NCT23583813.0	219030_at	NP_057122.1, EAW99720.1, EAW99721.1, EAW99722.1, EAW99723.1
Gene ID:5 448	DUSP11	2	73,959,523	74,007,264	17,989	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4740	-12	upstream	0	1	16	26	1	2_A2S_sNL97_glcs_blcR NA:1	26	Gene DUSP11	DUSP11, PIR1	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	NM_003584, NCT16842591.1, NCT19842581.1	202703_at	NP_003575.2, EAW99716.1, EAW99716.2
Gene ID:5 55860	C2orf56	2	74,011,316	74,044,274	32,958	+	1	2_A2S_sNL97_glcs_blcRNA:1:-4740	4520	upstream	0	1	16	26	1	2_A2S_sNL97_glcs_blcR NA:1	26	Gene C2orf56	FLJ43697, C2orf56, CGI-53373, MGC102958	chromosome 2 open reading frame 56	NM_001080474		NP_001073943.1
Gene ID:1 0917	STAMBP	2	74,059,099	74,090,011	33,928	+	3	1_A2S_sNL97_dhrsd_blcRN A:1:-3400, 2_A2S_sNL97_glcs_blcRNA:1:-4741, 2_A2S_sNL97_glcs_blcRNA:1:-4742	2529, 23222, 10	at gene, ut gene, ut gene	1	1	15.33	12.33	3	2_A2S_sNL97_glcs_blcR NA:1	16	Gene STAMBP	AMSH, MGC126515, MGC126516, STAMBP	STAM binding protein	NM_006463, NM_001047, NM_213622, NM_030932, NM_132931, NCT22767972.0, NCT22767985.0, NCT22655572.0	202811_at, 225115_at	NP_006454.1, NP_954010.1, NP_598757.1, EAW99714.1, EAW99715.1, EAW99716.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:72	ACTG2	2	74,120,093	74,146,780	26,687	+	1	2_A375_pNL97_plus_lncRNA::1::4742	34051	downstream	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ACTG2	ACTG2, ACTSG, ACT, ACTL3, ACTA3, ACTE	actin, gamma 2, smooth muscle, enteric	NM_001615, hCT2356493.0, hCT32003.3	202274_at, 241146_at	NP_001606.1, EAW99712.1, EAW99713.1
GeneID:1716	DGUOK	2	74,153,953	74,186,088	32,135	+	1	2_A375_pNL97_plus_lncRNA::1::4742	191	in gene	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DGUOK	MTDPS3, dGK, DGUOK	deoxyguanosine kinase	NM_080916, NM_080918	203816_at, 209549_s_at	NP_550438.1, NP_550440.1
GeneID:388962	BOLA3	2	74,362,526	74,375,039	12,511	-	2	1_A375_pNL7_minus_lncRNA::1::3303, 2_A375_pNL97_plus_lncRNA::1::4744	-1, -1	upstream, upstream	1	1	103	136	1	2_A375_pNL97_plus_lncRNA::1	136	Gene BOLA3	BOLA3		NM_001035505, NM_212552, hCT2264704.0, hCT2264706.0	227291_s_at	NP_001030582.1, NP_997717.2, EAW99699.1, EAW99700.1
GeneID:100507171	LOC100507171	2	74,375,166	74,377,188	2,022	+	2	1_A375_pNL7_minus_lncRNA::1::3303, 2_A375_pNL97_plus_lncRNA::1::4744	-126, -126	upstream, upstream	1	1	103	136	1	2_A375_pNL97_plus_lncRNA::1	136	Gene LOC100507171		hypothetical LOC100507171	XR_112337, XR_112338, XR_109947, XR_109948, XR_115557, XR_115558		
GeneID:55233	MOBKL1B	2	74,383,211	74,405,995	22,784	-	2	1_A375_pNL7_minus_lncRNA::1::3303, 2_A375_pNL97_plus_lncRNA::1::4744	30955, 30955	downstream, downstream	1	1	103	136	1	2_A375_pNL97_plus_lncRNA::1	136	Gene MOBKL1B	C2orf6, MOB1, MOBK1B, MATS1, FLJ10788, MOBKL1B, Mob4B, FLJ11595	MOB1, Mps One Binder kinase activator-like 1B (yeast)	NM_018221, hCT1963553.1, hCT31999.3	201297_s_at, 201298_s_at, 201299_s_at, 214812_s_at	NP_060691.2, EAW99696.1, EAW99695.1
GeneID:10797	MTHFD2	2	74,425,690	74,442,425	16,735	+	1	2_A375_pNL97_plus_lncRNA::1::4745	54	in gene	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MTHFD2	MTHFD2, NMDMC	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	NM_006636, NR_027405, hCT1685604.3, hCT1816943.1, hCT2266668.0, hCT31994.3	201761_at	NP_006627.2, EAW99671.1, EAW99670.1, EAW99672.1, EAW99673.1
GeneID:1639	DCTN1	2	74,588,281	74,619,214	30,933	-	1	1_A375_pNL7_minus_lncRNA::1::3304	14	in gene	1	0	16	16	1	1_A375_pNL7_minus_lncRNA::1	16	Gene DCTN1	HMN7B, DAP-150, DCTN1, P135, DP-150	dynactin 1 (p150, glued homolog, Drosophila)	NM_001135040, NM_001135041, NM_001190836, NM_001190837, NM_004082, NM_023019, NR_033935, hCT2264671.0, hCT2264673.0, hCT2264674.0, hCT2264676.0	201082_s_at, 204296_at, 211780_x_at	NP_001128512.1, NP_001128513.1, NP_075408.1, NP_004073.2, NP_001177765.1, NP_001177766.1, EAW99684.1, EAW99685.1, EAW99686.1, EAW99687.1
GeneID:100189589	LOC100189589	2	74,612,845	74,621,008	8,163	+	1	1_A375_pNL7_minus_lncRNA::1::3304	6355	in gene	1	0	16	16	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100189589		hypothetical LOC100189589	NR_024463		
GeneID:388963	C2orf81	2	74,641,303	74,644,844	3,541	-	1	2_A375_pNL97_plus_lncRNA::1::4746	-3860	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C2orf81	hCG40743, C2orf81	chromosome 2 open reading frame 81	NM_001145054	236070_at	NP_001138526.1
GeneID:100130009	LOC100130009	2	74,645,222	74,645,569	347	-	1	2_A375_pNL97_plus_lncRNA::1::4746	-3135	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100130009		hypothetical LOC100130009	XM_001719388, XM_001718914, XM_001720338		XP_001719440.3, XP_001718966.3, XP_001720390.3
GeneID:84058	WDR54	2	74,648,885	74,652,882	3,997	+	1	2_A375_pNL97_plus_lncRNA::1::4746	-161	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene WDR54	WDR54, FLJ12953	WD repeat domain 54	NM_032118, hCT1954265.1, hCT1954266.1, hCT2356505.0, hCT2356506.0, hCT32006.2	225698_at	NP_115494.1, EAW99680.1, EAW99677.1, EAW99678.1, EAW99679.1, EAW99681.1
GeneID:6242	RTKN	2	74,652,988	74,669,060	16,072	-	3	1_A375_pNL7_minus_lncRNA::1::3305, 2_A375_pNL97_plus_lncRNA::1::4746, 2_A375_pNL97_plus_lncRNA::1::4747	1264, 20356, 1252	in gene, downstream, in gene	1	1	20.5	29	2	2_A375_pNL97_plus_lncRNA::1	40	Gene RTKN	RTKN	rhotekin	NM_033046, NM_001015055, NM_001015056, hCT1954263.1, hCT1954264.1, hCT32005.3	225150_s_at, 225151_at, 239226_at	NP_149035.1, NP_001015055.1, NP_001015056.1, EAW99674.1, EAW99675.1, EAW99676.1
GeneID:83444	INO80B	2	74,682,199	74,685,087	2,888	+	1	2_A375_pNL97_plus_lncRNA::1::4748	169	in gene	0	1	23	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene INO80B	INO80B, PAP-1BP, ZNHIT4, IES2, HMGA1L4, hIes2, PAPA-1, HMGIYL4	INO80 complex subunit B	NM_031288	221251_x_at, 222093_s_at, 65133_i_at	NP_112578.2
GeneID:23559	WBP1	2	74,685,577	74,688,010	2,433	+	1	2_A375_pNL97_plus_lncRNA::1::4748	-3209	upstream	0	1	23	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene WBP1	WBP1, MGC15305, WBP-1	WW domain binding protein 1	NM_012477	223072_s_at	NP_036609.1
GeneID:7841	MOGS	2	74,688,184	74,692,537	4,353	-	3	1_A375_pNL7_minus_lncRNA::1::3306, 2_A375_pNL97_plus_lncRNA::1::4748, 2_A375_pNL97_plus_lncRNA::1::4749	-7223, 10169, -7207	upstream, downstream, upstream	1	1	21.5	21	2	2_A375_pNL97_plus_lncRNA::1	22	Gene MOGS	MOGS, CDG2B, GCS1	mannosyl-oligosaccharide glucosidase	NM_006302, NM_001146158, hCT1954255.1, hCT31995.3	210627_s_at	NP_006293.2, NP_001139630.1, EAW99652.1, EAW99653.1
GeneID:116540	MRPL53	2	74,699,109	74,699,927	818	-	4	1_A375_pNL7_minus_lncRNA::1::3306, 1_A375_pNL7_minus_lncRNA::1::3307, 2_A375_pNL97_plus_lncRNA::1::4749, 2_A375_pNL97_plus_lncRNA::1::4750	167, -10329, 183, -10057	in gene, upstream, in gene, upstream	1	1	19.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene MRPL53	MRPL53, L53MT, FLJ90726, MGC20402	mitochondrial ribosomal protein L53	NM_053050, hCT2264643.1	225523_at	NP_444278.1, EAW99651.1
GeneID:84865	CCDC142	2	74,699,959	74,710,357	10,398	-	4	1_A375_pNL7_minus_lncRNA::1::3306, 1_A375_pNL7_minus_lncRNA::1::3307, 2_A375_pNL97_plus_lncRNA::1::4749, 2_A375_pNL97_plus_lncRNA::1::4750	10597, 101, 10613, 373	downstream, in gene, downstream, in gene	1	1	19.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene CCDC142	FLJ14397, CCDC142, FLJ90726	coiled-coil domain containing 142	NM_032779, hCT2264650.1	239922_at	NP_116168.3, EAW99650.1
GeneID:64427	TTC31	2	74,710,200	74,721,691	11,491	+	3	1_A375_pNL7_minus_lncRNA::1::3306, 1_A375_pNL7_minus_lncRNA::1::3307, 2_A375_pNL97_plus_lncRNA::1::4750	-10440, 56, -216	upstream, in gene, upstream	1	1	19.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene TTC31	MGC120200, FLJ12788, TTC31, FLJ33201	tetratricopeptide repeat domain 31	NM_022492, NR_027749, hCT1954220.2, hCT1954222.2, hCT2341450.0, hCT2341451.0, hCT2341452.0, hCT2356424.0, hCT2356425.0, hCT2356426.0, hCT2356427.0, hCT2356428.0, hCT32012.4	218838_s_at	NP_071937.4, EAW99638.1, EAW99639.1, EAW99642.1, EAW99646.1, EAW99648.1, EAW99640.1, EAW99641.1, EAW99643.1, EAW99644.1, EAW99645.1, EAW99647.1
GeneID:85474	LBX2	2	74,724,644	74,730,443	5,799	-	2	1_A375_pNL7_minus_lncRNA::1::3308, 2_A375_pNL97_plus_lncRNA::1::4751	-4005, -4021	upstream, upstream	1	1	28	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene LBX2	LBX2, LP3727	ladybird homeobox 2	NM_001009812		NP_001009812.1
GeneID:151534	hCG_1811732	2	74,729,744	74,732,192	2,448	+	2	1_A375_pNL7_minus_lncRNA::1::3308, 2_A375_pNL97_plus_lncRNA::1::4751	4704, 4720	downstream, downstream	1	1	28	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene hCG_1811732	LOC151534, MGC120166	hypothetical LOC151534	NR_024606	238422_at	
GeneID:84759	PCGF1	2	74,732,170	74,734,821	2,651	-	2	1_A375_pNL7_minus_lncRNA::1::3308, 2_A375_pNL97_plus_lncRNA::1::4751	373, 357	in gene, in gene	1	1	28	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene PCGF1	MGC10882, 2010002K04Rik, PCGF1, NSPC1, RNF68, FLJ43754, RNF3A-2	polycomb group ring finger 1	NM_032673, hCT1954309.2, hCT2356470.0	210022_at, 210023_s_at	NP_116062.2, EAW99632.1, EAW99633.1
GeneID:3196	TLX2	2	74,741,596	74,744,275	2,679	+	2	1_A375_pNL7_minus_lncRNA::1::3308, 2_A375_pNL97_plus_lncRNA::1::4751	-7148, -7132	upstream, upstream	1	1	28	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene TLX2	TLX2, NCX, Enx, HOX11L1	T-cell leukemia homeobox 2	NM_016170	207410_s_at, 211049_at	NP_057254.1
GeneID:165545	DQX1	2	74,745,258	74,753,408	8,150	-	1	2_A375_pNL97_plus_lncRNA::1::4752	-3200	upstream	0	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene DQX1	DQX1, FLJ23757	DEAQ box RNA-dependent ATPase 1	NM_133637, hCT1954301.1, hCT2356423.0, hCT32335.3	236055_at	NP_598376.2, EAW99627.1, EAW99626.1, EAW99628.1
GeneID:550	AUP1	2	74,753,775	74,756,974	3,199	-	1	2_A375_pNL97_plus_lncRNA::1::4752	366	in gene	0	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene AUP1	AUP1	ancient ubiquitous protein 1	NM_181575, hCT1686578.2, hCT1954298.1, hCT1954299.1, hCT32333.3	220525_s_at	NP_853553.1, EAW99622.1, EAW99623.1, EAW99624.1, EAW99625.1
GeneID:27429	HTRA2	2	74,756,532	74,760,683	4,151	+	1	2_A375_pNL97_plus_lncRNA::1::4752	76	in gene	0	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene HTRA2	PARK13, HTRA2, OMI, PRSS25	HtrA serine peptidase 2	NM_013247, NM_145074, hCT1954291.2, hCT1954292.2, hCT1954293.2, hCT2356417.0, hCT32331.4	203089_s_at, 211152_s_at	NP_037379.1, NP_659540.1, EAW99617.1, EAW99618.1, EAW99619.1, EAW99620.1, EAW99621.1
GeneID:84695	LOXL3	2	74,759,946	74,781,062	21,116	-	1	2_A375_pNL97_plus_lncRNA::1::4752	24454	downstream	0	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene LOXL3	LOXL3, LOXL	lysyl oxidase-like 3	NM_032603, hCT1954302.1, hCT32337.2	226253_at	NP_115992.1, EAW99615.1, EAW99616.1
GeneID:3099	HK2	2	75,059,782	75,120,481	60,699	+	1	2_A375_pNL97_plus_lncRNA::1::4753	2330	in gene	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene HK2	DKFZp686M1669, HXK2, HKII, HK2	hexokinase 2	NM_000189, hCT2261454.0, hCT2261455.0, hCT32336.3	202934_at, 222305_at	NP_000180.2, EAW99603.1, EAW99601.1, EAW99602.1
GeneID:6869	TACR1	2	75,273,590	75,426,645	153,055	-	1	1_A375_pNL7_minus_lncRNA::1::3310	151413	in gene	1	0	22	16	1	1_A375_pNL7_minus_lncRNA::1	22	Gene TACR1	SPR, NK1R, NKIR, TAC1R, TACR1	tachykinin receptor 1	NM_001058, NM_015727, hCT1965757.1, hCT32334.2	208048_at, 208049_s_at, 210637_at	NP_001049.1, NP_056542.1, EAW99595.1, EAW99596.1
GeneID:9801	MRPL19	2	75,873,909	75,889,334	15,425	+	2	1_A375_pNL7_minus_lncRNA::1::3312, 2_A375_pNL97_plus_lncRNA::1::4756	-21, 11	upstream, in gene	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MRPL19	MGC20675, MRP-L19, KIAA0104, L19mt, MRP-L15, MRPL19, MRPL15, RPML15, RLX1	mitochondrial ribosomal protein L19	NM_014763, hCT30767.3	203465_at, 232071_at, 235446_at	NP_055578.2, EAW99590.1
GeneID:6936	C2orf3	2	75,889,831	75,936,111	46,280	-	1	2_A375_pNL97_plus_lncRNA::1::4757	143	in gene	0	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene C2orf3	TCF9, DNABF, C2orf3, GCF	chromosome 2 open reading frame 3	NM_003203, hCT1961443.1, hCT1961446.1, hCT2260910.0, hCT31614.4	210175_at, 216305_s_at, 237531_at	NP_003194.3, EAW99586.1, EAW99587.1, EAW99588.1, EAW99589.1
GeneID:80059	LRRTM4	2	76,974,849	77,749,502	774,653	-	2	1_A375_pNL7_minus_lncRNA::1::3314, 2_A375_pNL97_plus_lncRNA::1::4759	563454, 563438	in gene, in gene	1	1	20	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LRRTM4	LRRTM4, FLJ12568, MGC120633, MGC120636	leucine rich repeat transmembrane neuronal 4	NM_024993, NM_001134745, hCT1645355.3	220345_at	NP_079269.4, NP_001128217.1, EAW99585.1
GeneID:8802	SUCLG1	2	84,650,647	84,686,586	35,939	-	2	1_A375_pNL7_minus_lncRNA::1::3319, 2_A375_pNL97_plus_lncRNA::1::4762	26, -6	in gene, upstream	1	1	40	37	1	1_A375_pNL7_minus_lncRNA::1	40	Gene SUCLG1	GALPHA, MTDPS9, SUCLA1, FLJ21114, FLJ43513, SUCLG1, G-ALPHA	succinate-CoA ligase, alpha subunit	NM_003849, hCT1815055.2	217874_at	NP_003840.2, EAW99556.1
GeneID:1768	DNAH6	2	84,743,579	85,046,713	303,134	+	1	2_A375_pNL97_plus_lncRNA::1::4763	225093	in gene	0	1	10	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene DNAH6	KIAA1697, HL2, MGC132544, FLJ37357, HL-2, MGC141984, Dnahc6, FLJ23529, DNAH6, MGC177197, DNHL1, DKFZp667K087	dynein, axonemal, heavy chain 6	NM_001370	1561616_a_at, 1561617_at, 1565337_at, 1565338_x_at	NP_001361.1
GeneID:9168	TMSB10	2	85,132,763	85,133,799	1,036	+	1	2_A375_pNL97_plus_lncRNA::1::4764	229	in gene	0	1	10	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TMSB10	TB10, MIG12, TMSB10	thymosin beta 10	NM_021103, hCT1815300.1, hCT2268411.0	217733_s_at	NP_066926.1, EAW99547.1, EAW99548.1
GeneID:10618	TGOLN2	2	85,545,146	85,555,374	10,228	-	2	1_A375_pNL7_minus_lncRNA::1::3322, 2_A375_pNL97_plus_lncRNA::1::4766	14, 142	in gene, in gene	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TGOLN2	TGN38, TGN46, MGC14722, TTGN2, TGOLN2, TGN51, TGN48	trans-golgi network protein 2	NM_006464, hCT1954185.1, hCT1954186.1, hCT2266998.0, hCT2267001.0, hCT2356458.0, hCT25814.2	1554608_at, 203833_s_at, 203834_s_at, 212040_at, 212043_at	NP_006455.2, EAW99535.1, EAW99536.1, EAW99537.1, EAW99538.1, EAW99540.1, EAW99539.1
GeneID:54884	RETSAT	2	85,569,078	85,581,821	12,743	-	1	2_A375_pNL97_plus_lncRNA::1::4767	-35	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene RETSAT	FLJ20296, RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	NM_017750, hCT1954211.1, hCT1954212.1, hCT1954214.1, hCT25829.3	1566472_s_at, 218124_at	NP_060220.3, EAW99531.1, EAW99530.1, EAW99532.1, EAW99533.1
GeneID:84173	ELMOD3	2	85,581,843	85,618,875	37,032	+	1	2_A375_pNL97_plus_lncRNA::1::4767	13	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ELMOD3	LST3, FLJ35601, RBM29, RBED1, FLJ21977, MGC111036, ELMOD3	ELMO/CED-12 domain containing 3	NM_032213, NM_001135021, NM_001135022, NM_001135023, hCT1954195.2, hCT1954197.2, hCT1969079.2, hCT1969080.2, hCT1969082.2, hCT2356516.0, hCT2356517.0, hCT2356518.0, hCT25824.3	226286_at	NP_115589.2, NP_001128493.1, NP_001128494.1, NP_001128495.1, EAW99521.1, EAW99528.1, EAW99522.1, EAW99523.1, EAW99524.1, EAW99525.1, EAW99526.1, EAW99527.1, EAW99529.1
GeneID:822	CAPG	2	85,621,871	85,637,676	15,805	-	1	2_A375_pNL97_plus_lncRNA::1::4768	-10196	upstream	0	1	11	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CAPG	MCP, AFCP, CAPG	capping protein (actin filament), gelsolin-like	NM_001747, hCT1954179.1, hCT1954180.1, hCT1954182.1, hCT25812.2	201850_at	NP_001738.2, EAW99519.1, EAW99517.1, EAW99518.1, EAW99520.1
GeneID:284948	SH2D6	2	85,661,918	85,664,152	2,234	+	1	2_A375_pNL97_plus_lncRNA::1::4769	2946	downstream	0	1	11	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SH2D6	SH2D6, FLJ35993	SH2 domain containing 6	NM_198482	242543_at	NP_940884.1
GeneID:4144	MAT2A	2	85,766,288	85,772,403	6,115	+	2	1_A375_pNL7_minus_lncRNA::1::3323, 2_A375_pNL97_plus_lncRNA::1::4770	112, 656	in gene, in gene	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene MAT2A	MATII, SAMS2, MAT2A, MATA2	methionine adenosyltransferase II, alpha	NM_005911, hCT1954175.1, hCT1954176.1, hCT1954177.1, hCT25811.3	200768_s_at, 200769_s_at	NP_005902.1, EAW99511.1, EAW99512.1, EAW99513.1, EAW99514.1
GeneID:100507238	LOC100507238	2	85,770,915	85,773,392	2,477	-	2	1_A375_pNL7_minus_lncRNA::1::3323, 2_A375_pNL97_plus_lncRNA::1::4770	6992, 6448	downstream, downstream	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene LOC100507238		hypothetical LOC100507238	XR_109950		
GeneID:2677	GGCX	2	85,776,193	85,788,657	12,464	-	2	1_A375_pNL7_minus_lncRNA::1::3323, 2_A375_pNL97_plus_lncRNA::1::4770	22257, 21713	downstream, downstream	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene GGCX	VKCFD1, GGCX, FLJ26629	gamma-glutamyl carboxylase	NM_000821, NM_001142269, hCT1954172.1, hCT25810.3	205351_at, 214005_at, 214006_s_at, 235413_at	NP_000812.2, NP_001135741.1, EAW99509.1, EAW99510.1
GeneID:10791	VAMP5	2	85,811,531	85,820,511	8,980	+	2	2_A375_pNL97_plus_lncRNA::1::4771, 2_A375_pNL97_plus_lncRNA::1::4772	10965, 18389	downstream, downstream	0	1	14	20	2	2_A375_pNL97_plus_lncRNA::1	23	Gene VAMP5	VAMP5		NM_006634	204929_s_at, 214115_at	NP_006625.1
GeneID:51255	RNF181	2	85,822,837	85,824,831	1,994	+	2	2_A375_pNL97_plus_lncRNA::1::4771, 2_A375_pNL97_plus_lncRNA::1::4772	-341, 7063	upstream, downstream	0	1	14	20	2	2_A375_pNL97_plus_lncRNA::1	23	Gene RNF181	RNF181, HSPC238	ring finger protein 181	NM_016494, hCT1954204.1, hCT25828.2	223064_at, 229932_at	NP_057578.1, EAW99505.1, EAW99504.1
GeneID:129303	TMEM150A	2	85,825,670	85,829,822	4,152	-	3	2_A375_pNL97_plus_lncRNA::1::4771, 2_A375_pNL97_plus_lncRNA::1::4772, 2_A375_pNL97_plus_lncRNA::1::4773	7326, -98, -9282	downstream, upstream, upstream	0	1	14.67	20.33	3	2_A375_pNL97_plus_lncRNA::1	23	Gene TMEM150A	FLJ90024, TM6P1, TMEM150A, TMEM150	transmembrane protein 150A	NM_001031738, NR_033179, hCT1954198.1, hCT1954199.1, hCT1954201.1, hCT1954202.1, hCT2266980.0, hCT2356519.0, hCT2356520.0, hCT25825.2	226239_at	NP_001026908.1, EAW99498.1, EAW99496.1, EAW99497.1, EAW99500.1, EAW99502.1, EAW99499.1, EAW99501.1, EAW99503.1
GeneID:388969	C2orf68	2	85,832,376	85,839,179	6,803	-	3	2_A375_pNL97_plus_lncRNA::1::4771, 2_A375_pNL97_plus_lncRNA::1::4772, 2_A375_pNL97_plus_lncRNA::1::4773	16663, 9259, 75	downstream, downstream, in gene	0	1	14.67	20.33	3	2_A375_pNL97_plus_lncRNA::1	23	Gene C2orf68	C2orf68, FLJ35653, FLJ14112, MGC131675	chromosome 2 open reading frame 68	NM_001013649, hCT25827.4	221876_at, 232145_at, 238768_at	NP_001013671.2, EAW99495.1
GeneID:10713	USP39	2	85,843,283	85,876,406	33,123	+	1	2_A375_pNL97_plus_lncRNA::1::4773	-4179	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene USP39	MGC75069, SNRNP65, HSPC332, CGI-21, SAD1, USP39	ubiquitin specific peptidase 39	NM_006590, hCT1954191.1, hCT2356512.0, hCT2356513.0, hCT2356514.0, hCT25823.2	217829_s_at	NP_006581.2, EAW99490.1, EAW99491.1, EAW99492.1, EAW99493.1, EAW99494.1
GeneID:6439	SFTPB	2	85,884,440	85,895,864	11,424	-	1	2_A375_pNL97_plus_lncRNA::1::4774	5688	in gene	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SFTPB	SFTPB, SMDP1, SFTB3, SP-B, PSP-B, SFTP3	surfactant protein B	NM_198843, NM_000542, hCT1954168.1, hCT2266971.0, hCT25808.3	209810_at, 213936_x_at, 214354_x_at, 37004_at	NP_942140.2, NP_000533.3, EAW99487.1, EAW99488.1, EAW99489.1
GeneID:84913	ATOH8	2	85,980,909	86,018,506	37,597	+	2	1_A375_pNL7_minus_lncRNA::1::3324, 2_A375_pNL97_plus_lncRNA::1::4775	18835, 18739	in gene, in gene	1	1	23	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ATOH8	HATH6, FLJ38730, FLJ14708, bHLHa21, ATOH8	atonal homolog 8 (Drosophila)	NM_032827, hCT1954190.1, hCT25822.3	1558705_at, 1558706_a_at, 228890_at	NP_116216.2, EAW99482.1, EAW99481.1
GeneID:8869	ST3GAL5	2	86,066,271	86,116,157	49,886	-	1	2_A375_pNL97_plus_lncRNA::1::4776	-4691	upstream	0	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ST3GAL5	SATI, ST3GalV, ST3GAL5, SIATGM3S, SIAT9	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	NM_003896, NM_001042437, hCT1954188.1, hCT1965728.1, hCT1965731.1, hCT1965733.1, hCT1965734.1, hCT2356492.0, hCT25819.3	203217_s_at, 239755_at	NP_003887.3, NP_001035902.1, EAW99474.1, EAW99475.1, EAW99476.1, EAW99480.1, EAW99477.1, EAW99478.1, EAW99479.1
GeneID:25885	POLR1A	2	86,253,451	86,333,278	79,827	-	2	1_A375_pNL7_minus_lncRNA::1::3325, 2_A375_pNL97_plus_lncRNA::1::4778	78, 510	in gene, in gene	1	1	25	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene POLR1A	A190, RPA194, MGC87965, FLJ21915, RPO14, RPO1-4, POLR1A, DKFZp586M0122, RPA1	polymerase (RNA) I polypeptide A, 194kDa	NM_015425, hCT2261119.0, hCT2261120.0, hCT25395.3	222704_at	NP_056240.2, EAW99468.1, EAW99467.1, EAW99469.1
GeneID:55037	PTCD3	2	86,333,305	86,369,280	35,975	+	2	1_A375_pNL7_minus_lncRNA::1::3325, 2_A375_pNL97_plus_lncRNA::1::4778	-105, -537	upstream, upstream	1	1	25	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene PTCD3	FLJ20758, DKFZp666K071, PTCD3	Pentatricopeptide repeat domain 3	NM_017952, hCT1954991.1, hCT1954994.1, hCT25399.3	217895_at, 228020_at, 228512_at, 228590_at	NP_060422.4, EAW99464.1, EAW99465.1, EAW99466.1
GeneID:65055	REEP1	2	86,441,116	86,565,206	124,090	-	2	1_A375_pNL7_minus_lncRNA::1::3326, 2_A375_pNL97_plus_lncRNA::1::4779	37190, 37014	in gene, in gene	1	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene REEP1	REEP1, FLJ13110, SPG31, C2orf23	receptor accessory protein 1	NM_022912, NM_001164731, NM_001164730, NM_001164732, hCT1954988.0, hCT25396.1	204364_s_at, 204365_s_at	NP_075063.1, NP_001158203.1, NP_001158202.1, NP_001158204.1, EAW99457.1, EAW99458.1
GeneID:55818	KDM3A	2	86,668,271	86,719,839	51,568	+	2	1_A375_pNL7_minus_lncRNA::1::3327, 2_A375_pNL97_plus_lncRNA::1::4780	-271, 1057	upstream, in gene	1	1	13	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene KDM3A	DKFZp686P07111, TSGA, KIAA0742, JHDM2A, KDM3A, JMJD1A, JMJD1, DKFZp686A24246, JHMD2A	lysine (K)-specific demethylase 3A	NM_018433, NM_001146688, hCT1818953.2, hCT2356409.0, hCT2356410.0, hCT2356411.0	212689_s_at	NP_060903.2, NP_001140160.1, EAW99453.1, EAW99454.1, EAW99455.1, EAW99456.1
GeneID:51652	VPS24	2	86,730,553	86,790,620	60,067	-	2	1_A375_pNL7_minus_lncRNA::1::3328, 2_A375_pNL97_plus_lncRNA::1::4781	412, 444	in gene, in gene	1	1	29	24	1	1_A375_pNL7_minus_lncRNA::1	29	Gene VPS24	FLJ36114, CHMP3, VPS24, CGI-149, NEDF	vacuolar protein sorting 24 homolog (S. cerevisiae)	NM_001005753, NM_016079, NM_001193517, NR_036454, hCT1954986.1, hCT2356365.0, hCT2356366.0, hCT2356367.0, hCT25393.2	217837_s_at, 222436_s_at, 222437_s_at	NP_001005753.1, NP_057163.1, NP_001180446.1, EAW99449.1, EAW99451.1, EAW99452.1, EAW99448.1, EAW99450.1
GeneID:150572	SMYD1	2	88,367,382	88,412,903	45,521	+	1	2_A375_pNL97_plus_lncRNA::1::4782	50314	downstream	0	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SMYD1	KMT3D, SMYD1, ZMYND22, ZMYND18, BOP	SET and MYND domain containing 1	NM_198274, hCT1952979.1, hCT2355667.0, hCT2355668.0, hCT24466.2	228406_at, 243045_at	NP_938015.1, EAW77077.1, EAW77078.1, EAW77079.1, EAW77080.1
GeneID:2168	FABP1	2	88,422,510	88,427,576	5,066	-	1	2_A375_pNL97_plus_lncRNA::1::4782	9882	downstream	0	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FABP1	L-FABP, FABP1, FABPL	fatty acid binding protein 1, liver	NM_001443, hCT2252922.0, hCT24139.1	205892_s_at, 231693_at	NP_001434.1, EAW77075.1, EAW77076.1
GeneID:9451	EIF2AK3	2	88,856,259	88,927,094	70,835	-	1	1_A375_pNL7_minus_lncRNA::1::3329	-330	upstream	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene EIF2AK3	WRS, DKFZp781H1925, EIF2AK3, HRI, PERK, PEK	eukaryotic translation initiation factor 2-alpha kinase 3	NM_004836, hCT1786243.1, hCT2252915.0	218696_at	NP_004827.4, EAW77068.1, EAW77069.1
GeneID:100507360	LOC100507360	2	88,927,039	88,931,343	4,304	+	1	1_A375_pNL7_minus_lncRNA::1::3329	385	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100507360		hypothetical LOC100507360	XR_112345, XR_109953, XR_115626		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:22934	RPIA	2	88,991,176	89,050,452	59,276	+	2	1_A375_pNL7_minus_lncRNA::1::3330, 2_A375_pNL97_plus_lncRNA::1::4784	-40, -136	upstream, upstream	1	1	24	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene RPIA	RPIA, RPI	ribose 5-phosphate isomerase A	NM_144563, hCT2253010.0, hCT2253012.0	212973_at	NP_653164.2, EAW77067.1, EAW77066.1
GeneID:64969	MRPS5	2	95,752,952	95,787,754	34,802	-	1	2_A375_pNL97_plus_lncRNA::1::4787	136	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MRPS5	S5mt, MRPS5, MRP-S5	mitochondrial ribosomal protein S5	NM_031902, hCT2286427.0, hCT31039.3	224333_s_at, 224877_s_at, 236779_at, 237560_at	NP_114108.1, EAX10713.1, EAX10712.1
GeneID:84874	ZNF514	2	95,813,400	95,825,263	11,863	-	1	2_A375_pNL97_plus_lncRNA::1::4788	-6289	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ZNF514	ZNF514, MGC126230, MGC126229	zinc finger protein 514	NM_032788, hCT1784492.2	235729_at	NP_116177.1, EAX10714.1
GeneID:7549	ZNF2	2	95,831,183	95,850,065	18,882	+	1	2_A375_pNL97_plus_lncRNA::1::4788	369	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ZNF2	ZNF2, Zfp661, A1-5, ZNF661	zinc finger protein 2	NM_021088, NM_001017396, hCT1784488.2, hCT1953712.1	223792_at	NP_066574.2, NP_001017396.1, EAX10715.1, EAX10716.1
GeneID:30818	KCNIP3	2	95,963,072	96,051,825	88,753	+	1	1_A375_pNL7_minus_lncRNA::1::3332	36576	in gene	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene KCNIP3	CSEN, DREAM, MGC18289, KCNIP3, KCHIP3	Kv channel interacting protein 3, calsenilin	NM_013434, NM_001034914, hCT1963194.1, hCT1963195.1, hCT2287997.0, hCT2287998.0, hCT28121.4	1555694_a_at, 1569355_at, 226269_x_at, 231774_at, 233665_at, 234198_at, 234647_at	NP_038462.1, NP_001030086.1, EAX10723.1, EAX10724.1, EAX10725.1, EAX10727.1, EAX10726.1
GeneID:51011	FAHD2A	2	96,068,448	96,078,879	10,431	+	1	2_A375_pNL97_plus_lncRNA::1::4789	32	in gene	0	1	6	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene FAHD2A	CGI-105, FAHD2A, MGC131995	fumarylacetoacetate hydrolase domain containing 2A	NM_016044, hCT2288000.0, hCT2288001.0, hCT2288002.0, hCT2288003.0, hCT2288004.0	218504_at, 222056_s_at	NP_057128.2, EAX10732.1, EAX10729.1, EAX10730.1, EAX10731.1, EAX10733.1
GeneID:285033	LOC285033	2	96,905,977	96,907,701	1,724	+	1	2_A375_pNL97_plus_lncRNA::1::4790	11655	downstream	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC285033	MGC126779, MGC126781	hypothetical protein LOC285033	NM_001037228, hCT2289920.0, hCT2354908.0	235584_at	NP_001032305.1, EAW71380.1, EAW71381.1
GeneID:55654	TMEM127	2	96,916,312	96,931,751	15,439	-	1	2_A375_pNL97_plus_lncRNA::1::4790	14119	in gene	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TMEM127	FLJ22257, TMEM127, FLJ20507	transmembrane protein 127	NM_017849, NM_001193304, hCT1967805.1, hCT2289249.0, hCT2289251.0, hCT28534.3	219460_s_at, 222887_s_at	NP_060319.1, NP_001180233.1, EAW71376.1, EAW71377.1, EAW71378.1, EAW71379.1
GeneID:150771	ITPRIPL1	2	96,991,062	96,994,091	3,029	+	2	1_A375_pNL7_minus_lncRNA::1::3333, 2_A375_pNL97_plus_lncRNA::1::4791	10527, 10522	downstream, downstream	1	1	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene ITPRIPL1	ITPRIPL1, KIAA1754L	inositol 1,4,5-triphosphate receptor interacting protein-like 1	NM_178495, NM_001008949, NM_001163523, NM_001163524	240037_at	NP_848590.3, NP_001008949.1, NP_001156995.1, NP_001156996.1
GeneID:23397	NCAPH	2	97,001,484	97,041,274	39,790	+	2	1_A375_pNL7_minus_lncRNA::1::3333, 2_A375_pNL97_plus_lncRNA::1::4791	105, 100	in gene, in gene	1	1	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene NCAPH	HCAP-H, CAP-H, NCAPH, BRRN1	non-SMC condensin I complex, subunit H	NM_015341, hCT28532.3	212949_at	NP_056156.2, EAW71370.1
GeneID:10865	ARID5A	2	97,202,464	97,218,371	15,907	+	2	1_A375_pNL7_minus_lncRNA::1::3334, 2_A375_pNL97_plus_lncRNA::1::4793	20320, 20368	downstream, downstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ARID5A	RP11-363D14, MRF-1, ARID5A, MRF1	AT rich interactive domain 5A (MRF1-like)	NM_212481, hCT2289879.0, hCT2354918.0, hCT2354919.0, hCT2354920.0, hCT2354921.0, hCT2354922.0, hCT2354923.0, hCT28530.3	213138_at	NP_997646.1, EAW71360.1, EAW71359.1, EAW71361.1, EAW71365.1, EAW71366.1, EAW71362.1, EAW71363.1, EAW71364.1
GeneID:55683	KIAA1310	2	97,258,907	97,304,115	45,208	-	2	1_A375_pNL7_minus_lncRNA::1::3335, 2_A375_pNL97_plus_lncRNA::1::4794	67, -61	in gene, upstream	1	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene KIAA1310	KIAA1310, FLJ10081, Rcd1, FLJ23799	KIAA1310	NM_017991, NM_001115016, hCT1950358.1, hCT1950359.1, hCT2289237.0, hCT2289238.0, hCT2289241.0, hCT2354899.0, hCT2354900.0, hCT2354901.0, hCT2354902.0, hCT2354903.0, hCT2354904.0, hCT9706.3	1558652_at, 220950_s_at, 223756_at, 224318_s_at	NP_060461.3, NP_001108488.1, EAW71347.1, EAW71354.1, EAW71357.1, EAW71358.1, EAW71348.1, EAW71349.1, EAW71350.1, EAW71351.1, EAW71352.1, EAW71353.1, EAW71355.1, EAW71356.1
GeneID:90342	FER1L5	2	97,308,574	97,370,624	62,050	+	2	1_A375_pNL7_minus_lncRNA::1::3335, 2_A375_pNL97_plus_lncRNA::1::4794	-4526, -4398	upstream, upstream	1	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene FER1L5	FER1L5	fer-1-like 5 (C. elegans)	NM_001113382	233353_at	NP_001106853.1
GeneID:26504	CNNM4	2	97,426,639	97,477,628	50,989	+	1	1_A375_pNL7_minus_lncRNA::1::3336	55377	downstream	1	0	20	10	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CNNM4	KIAA1592, FLJ42791, CNNM4, FLJ37746, ACDP4	cyclin M4	NM_020184, hCT9245.3	218900_at	NP_064569.3, EAW71340.1
GeneID:100506036	LOC100506036	2	97,477,976	97,480,170	2,194	-	1	1_A375_pNL7_minus_lncRNA::1::3336	-1846	upstream	1	0	20	10	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100506036		hypothetical LOC100506036	XR_109916		
GeneID:26505	CNNM3	2	97,481,991	97,501,121	19,130	+	1	1_A375_pNL7_minus_lncRNA::1::3336	25	in gene	1	0	20	10	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CNNM3	ACDP3, FLJ20018, DKFZp434I1016, CNNM3	cyclin M3	NM_017623, NM_199078, hCT1771436.2, hCT1966165.1, hCT2289897.0, hCT2289900.0	220739_s_at	NP_060093.3, NP_951060.1, EAW71334.1, EAW71335.1, EAW71336.1, EAW71337.1
GeneID:10120	ACTR1B	2	98,272,402	98,280,561	8,159	-	1	1_A375_pNL7_minus_lncRNA::1::3337	-111	upstream	1	0	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene ACTR1B	ACTR1B, CTRN2, ARP1B, PC3	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	NM_005735, hCT2262763.0, hCT2262764.0, hCT2262765.0, hCT2262766.0, hCT2262767.0, hCT2262768.0	202135_s_at	NP_005726.1, EAX01923.1, EAX01925.1, EAX01926.1, EAX01927.1, EAX01928.1, EAX01924.1
GeneID:493753	C2orf64	2	99,215,865	99,224,955	9,090	-	1	2_A375_pNL97_plus_lncRNA::1::4795	187	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C2orf64	6330578E17Rik, C2orf64, MGC52110	chromosome 2 open reading frame 64	NM_001008215, hCT1955213.2	225409_at, 225410_at	NP_001008216.1, EAX01903.1
GeneID:25972	UNC50	2	99,225,042	99,234,978	9,936	+	1	2_A375_pNL97_plus_lncRNA::1::4795	-274	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene UNC50	UNCL, HSD23, URP, GMH1, UNC50, DKFZp564G0222	unc-50 homolog (C. elegans)	NM_014044, hCT1963233.2, hCT2348913.0, hCT29661.2	203583_at	NP_054763.2, EAX01900.1, EAX01901.1, EAX01902.1
GeneID:129531	MITD1	2	99,785,726	99,797,492	11,766	-	1	2_A375_pNL97_plus_lncRNA::1::4796	-76	upstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MITD1	MITD1	MIT, microtubule interacting and transport, domain containing 1	NM_138798, hCT2358577.0, hCT2358578.0, hCT2358579.0, hCT29667.3	226329_s_at	NP_620153.1, EAX01885.1, EAX01884.1, EAX01886.1, EAX01887.1
GeneID:51263	MRPL30	2	99,797,578	99,814,089	16,511	+	1	2_A375_pNL97_plus_lncRNA::1::4796	-10	upstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MRPL30	MGC3314, MRPL28, RPML28, MRP-L28, MRPL28M, L28MT, MRPL30, MGC24095, L30MT, FLJ44436	mitochondrial ribosomal protein L30	NM_145212	223996_s_at, 224173_s_at, 224971_at	NP_660213.1
GeneID:10190	TXNDC9	2	99,935,487	99,952,860	17,373	-	1	1_A375_pNL7_minus_lncRNA::1::3338	-900	upstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TXNDC9	TXNDC9, APACD, PHLP3	thioredoxin domain containing 9	NM_005783, hCT1771591.1, hCT2262996.0, hCT2262997.0, hCT2358586.0	1554047_at, 203008_x_at, 211756_x_at	NP_005774.2, EAX01870.1, EAX01868.1, EAX01869.1, EAX01871.1
GeneID:9669	EIF5B	2	99,953,834	100,016,728	62,894	+	1	1_A375_pNL7_minus_lncRNA::1::3338	-74	upstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene EIF5B	FLJ10524, EIF5B, DKFZp434I036, IF2, KIAA0741	eukaryotic translation initiation factor 5B	NM_015904, hCT2263253.0, hCT2263255.0, hCT2263256.0, hCT29664.3	201024_x_at, 201025_at, 201026_at, 201027_s_at, 214313_s_at, 214314_s_at	NP_056988.3, EAX01864.1, EAX01865.1, EAX01866.1, EAX01867.1
GeneID:3899	AFF3	2	100,163,715	100,759,037	595,322	-	1	1_A375_pNL7_minus_lncRNA::1::3339	260573	in gene	1	0	14	5	1	1_A375_pNL7_minus_lncRNA::1	14	Gene AFF3	AFF3, LAF4, MLLT2-like	AF4/FMR2 family, member 3	NM_002285, NM_001025108, hCT1958878.2, hCT2263035.1, hCT2263037.1, hCT2263039.1, hCT2263040.1, hCT2263046.1	205734_s_at, 205735_s_at, 227198_at, 243967_at	NP_002276.2, NP_001020279.1, EAX01854.1, EAX01855.1, EAX01857.1, EAX01859.1, EAX01856.1, EAX01858.1
GeneID:129521	NMS	2	101,086,944	101,099,742	12,798	+	2	1_A375_pNL7_minus_lncRNA::1::3340, 2_A375_pNL97_plus_lncRNA::1::4797	544, 576	in gene, in gene	1	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene NMS	NMS	neuromedin S	NM_001011717		NP_001011717.1
GeneID:11138	TBC1D8	2	101,623,690	101,767,846	144,156	-	2	1_A375_pNL7_minus_lncRNA::1::3341, 2_A375_pNL97_plus_lncRNA::1::4798	30678, 30534	in gene, in gene	1	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TBC1D8	TBC1D8, HBLP1, VRP, TBC1D8A, AD3	TBC1 domain family, member 8 (with GRAM domain)	NM_001102426, hCT18754.2, hCT2262771.0, hCT2262774.0	204526_s_at, 221592_at, 241017_at	NP_001095896.1, EAX01825.1, EAX01823.1, EAX01824.1
GeneID:731220	RFX8	2	102,013,823	102,091,165	77,342	-	2	1_A375_pNL7_minus_lncRNA::1::3342, 2_A375_pNL97_plus_lncRNA::1::4799	27645, 27581	in gene, in gene	1	1	23	18	1	1_A375_pNL7_minus_lncRNA::1	23	Gene RFX8	FLJ16242, RFX8, FLJ42986, FLJ52890	regulatory factor X, 8	NM_001145664		NP_001139136.1
GeneID:9392	TGFBRAP1	2	105,883,529	105,946,148	62,619	-	1	2_A375_pNL97_plus_lncRNA::1::4800	-7740	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TGFBRAP1	TGFBRAP1, TRAP1, TRAP-1	transforming growth factor, beta receptor associated protein 1	NM_004257, NM_001142621, hCT2262441.0, hCT2262442.0	205210_at	NP_004248.2, NP_001136093.1, EAX01764.1, EAX01765.1
GeneID:100506473	LOC100506473	2	105,950,491	105,952,005	1,514	-	1	2_A375_pNL97_plus_lncRNA::1::4800	-1883	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506473		hypothetical LOC100506473	XR_109933		
GeneID:79074	C2orf49	2	105,954,013	105,961,984	7,971	+	1	2_A375_pNL97_plus_lncRNA::1::4800	-125	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C2orf49	C2orf49, MGC5508, FLJ45759, ashwin	chromosome 2 open reading frame 49	NM_024093, hCT1642206.2	219662_at, 226951_at, 243093_at	NP_076998.1, EAX01763.1
GeneID:80146	UXS1	2	106,709,759	106,810,795	101,036	-	2	1_A375_pNL7_minus_lncRNA::1::3345, 2_A375_pNL97_plus_lncRNA::1::4801	76923, 76843	in gene, in gene	1	1	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene UXS1	FLJ23591, UGD, UXS1, SDR6E1	UDP-glucuronate decarboxylase 1	NM_025076, hCT1955977.1, hCT2265425.0, hCT2358580.0, hCT2358581.0	219675_s_at, 225583_at	NP_079352.2, EAX01750.1, EAX01747.1, EAX01748.1, EAX01749.1
GeneID:5903	RANBP2	2	109,335,937	109,402,267	66,330	+	1	2_A375_pNL97_plus_lncRNA::1::4802	-17	upstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RANBP2	NUP358, TRP1, RANBP2, TRP2, ANE1	RAN binding protein 2	NM_006267	201711_x_at, 201712_s_at, 201713_s_at, 226922_at	NP_006258.3
GeneID:100287216	LOC100287216	2	109,743,783	109,746,575	2,792	-	1	2_A375_pNL97_plus_lncRNA::1::4803	1163	in gene	0	1	7	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100287216	FLJ53560	hypothetical LOC100287216	NR_029193		
GeneID:344558	SH3RF3	2	109,745,997	110,107,395	361,398	+	3	2_A375_pNL97_plus_lncRNA::1::4803, 2_A375_pNL97_plus_lncRNA::1::4804, 2_A375_pNL97_plus_lncRNA::1::4805	-605, 84627, 113619	upstream, in gene, in gene	0	1	8	17.67	3	2_A375_pNL97_plus_lncRNA::1	19	Gene SH3RF3	SH3MD4, POSH2, FLJ00204, SH3RF3	SH3 domain containing ring finger 3	NM_001099289	226461_at	NP_001092759.1
GeneID:100506574	LOC100506574	2	109,867,878	109,868,105	227	+	1	2_A375_pNL97_plus_lncRNA::1::4805	-8262	upstream	0	1	8	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100506574	SNRPGP9	small nuclear ribonucleoprotein G-like	XM_003119869, XM_003118859, XM_003120363		XP_003119917.1, XP_003118907.1, XP_003120411.1
GeneID:699	BUB1	2	111,395,409	111,435,684	40,275	-	1	2_A375_pNL97_plus_lncRNA::1::4806	-92	upstream	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene BUB1	BUB1L, BUB1A, BUB1, hBUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	NM_004336, hCT2255329.0	209642_at, 215508_at, 215509_s_at, 216275_at, 216277_at	NP_004327.1, EAW50355.1
GeneID:55289	ACOXL	2	111,490,150	111,875,799	385,649	+	2	1_A375_pNL7_minus_lncRNA::1::3346, 2_A375_pNL97_plus_lncRNA::1::4807	368442, 368378	in gene, in gene	1	1	26	24	1	1_A375_pNL7_minus_lncRNA::1	26	Gene ACOXL	FLJ11042, ACOXL	acyl-CoA oxidase-like	NM_001142807, hCT2255305.0, hCT2255307.0, hCT2255309.0, hCT7860.3	220845_at	NP_001136279.1, EAW50360.1, EAW50357.1, EAW50358.1, EAW50359.1
GeneID:400997	FLJ44006	2	111,855,918	111,871,762	15,844	-	2	1_A375_pNL7_minus_lncRNA::1::3346, 2_A375_pNL97_plus_lncRNA::1::4807	13170, 13234	in gene, in gene	1	1	26	24	1	1_A375_pNL7_minus_lncRNA::1	26	Gene FLJ44006		hypothetical FLJ44006	XR_112372, XR_109903, XR_113363		
GeneID:64682	ANAPC1	2	112,526,638	112,641,741	115,103	-	1	2_A375_pNL97_plus_lncRNA::1::4808	-115	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ANAPC1	MCPR, TSG24, APC1, ANAPC1	anaphase promoting complex subunit 1	NM_022662, hCT1644042.3	218575_at, 231973_s_at	NP_073153.1, EAW52095.1
GeneID:376940	ZC3H6	2	113,033,178	113,097,640	64,462	+	1	2_A375_pNL97_plus_lncRNA::1::4809	-218	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ZC3H6	FLJ41410, ZC3H6, FLJ16526, ZC3HDC6, FLJ45877, KIAA2035	zinc finger CCCH-type containing 6	NM_198581	227609_at, 241372_at	NP_940983.2
GeneID:150465	TTL	2	113,239,743	113,290,223	50,480	+	1	2_A375_pNL97_plus_lncRNA::1::4810	59673	downstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TTL	TTL, MGC46235	tubulin tyrosine ligase	NM_153712, hCT7290.3	1559680_at, 224896_s_at, 224905_s_at	NP_714923.1, EAW73589.1
GeneID:84172	POLR1B	2	113,299,492	113,334,727	35,235	+	1	2_A375_pNL97_plus_lncRNA::1::4810	124	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene POLR1B	FLJ10816, RPA2, MGC131780, POLR1B, Rpo1-2, RPA135, FLJ21921	polymerase (RNA) I polypeptide B, 128kDa	NM_019014, NM_001137604, hCT1952953.1, hCT2273820.0, hCT2273822.0, hCT7291.2	1557331_at, 220113_x_at, 223403_s_at, 233341_s_at	NP_061887.2, NP_001131076.1, EAW73590.1, EAW73591.1, EAW73592.1, EAW73593.1
GeneID:400999	FLJ42351	2	113,399,407	113,401,757	2,350	-	2	2_A375_pNL97_plus_lncRNA::1::4811, 2_A375_pNL97_plus_lncRNA::1::4812	3229, -2003	downstream, upstream	0	1	12.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene FLJ42351		hypothetical LOC400999	NR_033871	230452_at	
GeneID:6574	SLC20A1	2	113,403,527	113,421,402	17,875	+	2	2_A375_pNL97_plus_lncRNA::1::4811, 2_A375_pNL97_plus_lncRNA::1::4812	-4999, 233	upstream, in gene	0	1	12.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene SLC20A1	Glvr-1, PIT1, DKFZp686J2397, FLJ41426, SLC20A1, GLVR1, PiT-1	solute carrier family 20 (phosphate transporter), member 1	NM_005415, hCT2273828.1, hCT2273829.1, hCT6777.3	201920_at	NP_005406.3, EAW73599.1, EAW73597.1, EAW73598.1
GeneID:150468	CKAP2L	2	113,495,444	113,522,254	26,810	-	2	1_A375_pNL7_minus_lncRNA::1::3347, 2_A375_pNL97_plus_lncRNA::1::4813	-66, 78	upstream, in gene	1	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CKAP2L	MGC39683, FLJ40629, CKAP2L	cytoskeleton associated protein 2-like	NM_152515, hCT2343355.0, hCT7293.3	229610_at	NP_689728.3, EAW73603.1, EAW73602.1
GeneID:3552	IL1A	2	113,531,492	113,542,971	11,479	-	2	1_A375_pNL7_minus_lncRNA::1::3347, 2_A375_pNL97_plus_lncRNA::1::4813	20651, 20795	downstream, downstream	1	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene IL1A	IL1, IL1-ALPHA, IL1F1, IL-1A, IL1A	interleukin 1, alpha	NM_000575, hCT7292.3	208200_at, 210118_s_at	NP_000566.3, EAW73604.1
GeneID:27178	IL1F7	2	113,670,548	113,676,459	5,911	+	1	2_A375_pNL97_plus_lncRNA::1::4815	8172	downstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene IL1F7	IL1RP1, IL-1F7, IL-1H4, FIL1, FIL1Z, FIL1(ZETA), IL-1RP1, IL1F7, IL1H4	interleukin 1 family, member 7 (zeta)	NM_014439, NM_173202, NM_173203, NM_173204, NM_173205, hCT18382.3, hCT2273787.0, hCT2273789.0, hCT2273790.0, hCT2273791.0	221470_s_at, 224555_x_at	NP_055254.2, NP_775294.1, NP_775295.1, NP_775296.1, NP_775297.1, EAW73611.1, EAW73608.1, EAW73609.1, EAW73610.1, EAW73612.1
GeneID:7849	PAX8	2	113,973,574	114,036,498	62,924	-	2	1_A375_pNL7_minus_lncRNA::1::3349, 2_A375_pNL97_plus_lncRNA::1::4816	37842, 37970	in gene, in gene	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PAX8	PAX8		NM_003466, NM_013952, NM_013953, NM_013992, hCT18378.3, hCT18379.3, hCT18380.3, hCT1970998.1, hCT1970999.1, hCT1971000.1, hCT2274188.0, hCT2274191.0, hCT2274192.0, hCT2274193.0, hCT2274194.0	121_at, 207921_x_at, 207923_x_at, 207924_x_at, 209552_at, 213917_at, 214528_s_at, 221990_at	NP_003457.1, NP_039246.1, NP_039247.1, NP_054698.1, EAW73629.1, EAW73637.1, EAW73630.1, EAW73631.1, EAW73632.1, EAW73633.1, EAW73634.1, EAW73635.1, EAW73636.1, EAW73638.1, EAW73639.1
GeneID:654433	LOC654433	2	113,993,846	114,024,580	30,734	+	2	1_A375_pNL7_minus_lncRNA::1::3349, 2_A375_pNL97_plus_lncRNA::1::4816	4610, 4682	in gene, in gene	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC654433	FLJ44467, DKFZp686E10196, FLJ31793, DKFZp547P134, FLJ17200	hypothetical LOC654433	NR_015377	227474_at, 228425_at	
GeneID:100506707	LOC100506707	2	113,995,646	113,998,419	2,773	+	2	1_A375_pNL7_minus_lncRNA::1::3349, 2_A375_pNL97_plus_lncRNA::1::4816	3010, 2882	downstream, downstream	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100506707		hypothetical LOC100506707	XR_109877, XR_113366		
GeneID:654412	FAM138B	2	114,334,959	114,336,429	1,470	+	2	1_A375_pNL7_minus_lncRNA::1::3350, 2_A375_pNL97_plus_lncRNA::1::4817	6385, 6321	downstream, downstream	1	1	30	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene FAM138B	FAM138B, F379, bA395L14.6	family with sequence similarity 138, member B	NR_026821	1555822_at	
GeneID:100302128	MIR1302-3	2	114,340,536	114,340,673	137	-	2	1_A375_pNL7_minus_lncRNA::1::3350, 2_A375_pNL97_plus_lncRNA::1::4817	-671, -607	upstream, upstream	1	1	30	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene MIR1302-3	hsa-mir-1302-3, MIRN1302-3, MIR1302-3	microRNA 1302-3	NR_031632		
GeneID:57628	DPP10	2	115,199,899	116,602,326	1,402,427	+	1	1_A375_pNL7_minus_lncRNA::1::3351	501	in gene	1	0	14	13	1	1_A375_pNL7_minus_lncRNA::1	14	Gene DPP10	DPP10, DPPY, DPL2, DPRP3	dipeptidyl-peptidase 10	NM_001004360, NM_001178034, NM_001178036, NM_001178037, NM_020868, hCT2349636.0, hCT2349637.0, hCT7222.4	228598_at	NP_001004360.2, NP_001171505.1, NP_065919.2, NP_001171507.1, NP_001171508.1, EAW95186.1, EAW95187.1, EAW95188.1
GeneID:8886	DDX18	2	118,572,255	118,589,953	17,698	+	2	1_A375_pNL7_minus_lncRNA::1::3352, 2_A375_pNL97_plus_lncRNA::1::4818	-127, -95	upstream, upstream	1	1	69	73	1	2_A375_pNL97_plus_lncRNA::1	73	Gene DDX18	DDX18, FLJ33908, MrDb	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	NM_006773, hCT2292691.1, hCT2292692.0, hCT2350256.0	205763_s_at, 208895_s_at, 208896_at, 208897_s_at	NP_006764.3, EAW95192.1, EAW95193.1, EAW95194.1
GeneID:165257	C1QL2	2	119,913,819	119,916,471	2,652	-	1	1_A375_pNL7_minus_lncRNA::1::3353	-8297	upstream	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene C1QL2	C1QTNF10, CTRP10, C1QL2	complement component 1, q subcomponent-like 2	NM_182528, hCT9332.3		NP_872334.2, EAW95208.1
GeneID:57669	EPB41L5	2	120,770,604	120,936,697	166,093	+	3	1_A375_pNL7_minus_lncRNA::1::3354, 2_A375_pNL97_plus_lncRNA::1::4820, 2_A375_pNL97_plus_lncRNA::1::4821	-108, -12, 121364	upstream, upstream, in gene	1	1	24.5	34	2	2_A375_pNL97_plus_lncRNA::1	53	Gene EPB41L5	FLJ12957, KIAA1548, BE37, YMO1, EPB41L5	erythrocyte membrane protein band 4.1 like 5	NM_001184937, NM_001184938, NM_001184939, NM_020909, hCT1957127.2, hCT2350791.0, hCT2357650.0, hCT8373.3	220977_x_at, 225855_at, 229292_at	NP_001171866.1, NP_001171867.1, NP_065960.2, NP_001171868.1, EAW95233.1, EAW95234.1, EAW95235.1, EAW95236.1
GeneID:23332	CLASP1	2	122,095,352	122,407,052	311,700	-	2	1_A375_pNL7_minus_lncRNA::1::3355, 2_A375_pNL97_plus_lncRNA::1::4822	118700, 118748	in gene, in gene	1	1	23	23	1	1_A375_pNL7_minus_lncRNA::1	23	Gene CLASP1	FLJ41222, DKFZp686D1968, DKFZp686H2039, MGC131895, CLASP1, KIAA0622, MAST1, FLJ33821	cytoplasmic linker associated protein 1	NM_015282, NM_001142273, NM_001142274, hCT1957123.2, hCT2293635.0, hCT2357847.0, hCT7275.3	212752_at, 240757_at	NP_056097.1, NP_001135745.1, NP_001135746.1, EAW95252.1, EAW95253.1, EAW95254.1, EAW95255.1
GeneID:100151683	RNU4ATAC	2	122,288,456	122,288,585	129	+	2	1_A375_pNL7_minus_lncRNA::1::3355, 2_A375_pNL97_plus_lncRNA::1::4822	-104, -152	upstream, upstream	1	1	23	23	1	1_A375_pNL7_minus_lncRNA::1	23	Gene RNU4ATAC	U4ATAC, RNU4ATAC, RNU4ATAC1	RNA, U4atac small nuclear (U12-dependent splicing)	NR_023343		
GeneID:100506849	LOC100506849	2	122,288,535	122,304,029	15,494	-	2	1_A375_pNL7_minus_lncRNA::1::3355, 2_A375_pNL97_plus_lncRNA::1::4822	15677, 15725	downstream, downstream	1	1	23	23	1	1_A375_pNL7_minus_lncRNA::1	23	Gene LOC100506849		hypothetical LOC100506849	XR_109884		
GeneID:7247	TSN	2	122,513,121	122,525,429	12,308	+	2	1_A375_pNL7_minus_lncRNA::1::3356, 2_A375_pNL97_plus_lncRNA::1::4823	31, 63	in gene, in gene	1	1	37	28	1	1_A375_pNL7_minus_lncRNA::1	37	Gene TSN	REHF-1, TSN, TRSLN, TBRBP, RCHF1, BCLF-1	translin	NM_004622, hCT2357834.0, hCT28875.2	201504_s_at, 201513_at, 201515_s_at	NP_004613.1, EAW95263.1, EAW95262.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:2995	GYPC	2	127,413,684	127,454,246	40,562	+	1	2_A375_pNL97_plus_lncRNA::1::4824	556	in gene	0	1	5	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene GYPC	CD236R, MGC126191, GPC, GE, MGC117309, GYPD, MGC126192, CD236, PAS-2, GYPC	glycophorin C (Gerbich blood group)	NM_002101, NM_016815, hCT2293465.0, hCT31699.3	202947_s_at	NP_002092.1, NP_058131.1, EAW95275.1, EAW95276.1
GeneID:56886	UGGT1	2	128,848,754	128,953,251	104,497	+	2	1_A375_pNL7_minus_lncRNA::1::3357, 2_A375_pNL97_plus_lncRNA::1::4826	-18, -82	upstream, upstream	1	1	23	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene UGGT1	FLJ23671, UGT1, HUGT1, UGCGL1, UGGT1, FLJ21763, FLJ23796	UDP-glucose glycoprotein glucosyltransferase 1	NM_020120, NR_027671, hCT1960138.2	218257_s_at, 222568_at, 222569_at	NP_064505.1, EAW95356.1
GeneID:55627	SMPD4	2	130,908,965	130,940,323	31,358	-	2	1_A375_pNL7_minus_lncRNA::1::3358, 2_A375_pNL97_plus_lncRNA::1::4827	1219, 1187	in gene, in gene	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SMPD4	SMPD4, NSMASE-3, FLJ20756, nSMase-3, NSMASE3, FLJ20297, NET13, KIAA1418	sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase-3)	NM_001171083, NM_017751, NM_017951, NR_033230, NR_033231, NR_033232, hCT2270969.0, hCT2270971.0, hCT2270972.0, hCT2270974.0, hCT2270976.0		NP_001164554.1, NP_060221.2, NP_060421.2, EAW55597.1, EAW55598.1, EAW55601.1, EAW55599.1, EAW55600.1
GeneID:80097	FAM128B	2	130,939,501	130,948,300	8,799	+	2	1_A375_pNL7_minus_lncRNA::1::3358, 2_A375_pNL97_plus_lncRNA::1::4827	-397, -365	upstream, upstream	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene FAM128B	MOZART2B, FAM128B, FLJ14346, MGC87017, MZT2B	family with sequence similarity 128, member B	NM_025029, hCT2270545.0, hCT2270546.0, hCT2270547.0, hCT2270548.0	212995_x_at, 220720_x_at	NP_079305.2, EAW55604.1, EAW55602.1, EAW55603.1, EAW55605.1
GeneID:112714	TUBA3E	2	130,949,318	130,956,034	6,716	-	2	1_A375_pNL7_minus_lncRNA::1::3358, 2_A375_pNL97_plus_lncRNA::1::4827	16930, 16898	downstream, downstream	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TUBA3E	TUBA3E		NM_207312		NP_997195.1
GeneID:84317	CCDC115	2	131,095,816	131,099,922	4,106	-	1	2_A375_pNL97_plus_lncRNA::1::4828	-590	upstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CCDC115	MGC12981, FLJ30131, CCDC115, ccp1	coiled-coil domain containing 115	NM_032357, hCT1964520.1, hCT1964521.1, hCT1964522.1	224946_s_at	NP_115733.2, EAW55612.1, EAW55610.1, EAW55611.1
GeneID:92856	IMP4	2	131,100,489	131,104,197	3,708	+	1	2_A375_pNL97_plus_lncRNA::1::4828	23	in gene	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene IMP4	BXDC4, MGC19606, IMP4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	NM_033416, hCT2270535.0, hCT2270538.0, hCT2270540.0, hCT30326.3	212411_at	NP_219484.1, EAW55615.1, EAW55613.1, EAW55614.1, EAW55616.1
GeneID:113457	TUBA3D	2	132,233,666	132,240,507	6,841	+	1	2_A375_pNL97_plus_lncRNA::1::4829	16670	downstream	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene TUBA3D	H2-ALPHA, TUBA3D, TUBA3C	tubulin, alpha 3d	NM_080386	216323_x_at	NP_525125.2
GeneID:653784	FAM128A	2	132,241,533	132,250,064	8,531	-	1	2_A375_pNL97_plus_lncRNA::1::4829	-472	upstream	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene FAM128A	MOZART2A, FAM128A, MZT2A	mitotic spindle organizing protein 2A	NM_001085365	213166_x_at	NP_001078834.1
GeneID:646915	ZNF806	2	133,074,675	133,076,309	1,634	+	2	1_A375_pNL7_minus_lncRNA::1::3359, 2_A375_pNL97_plus_lncRNA::1::4830	1597, 1561	in gene, in gene	1	1	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene ZNF806	ZNF806	zinc finger protein 806	XM_002345581, XM_001724242		XP_002345622.2, XP_001724294.3
GeneID:339742	LOC339742	2	133,106,790	133,110,894	4,104	+	2	1_A375_pNL7_minus_lncRNA::1::3360, 2_A375_pNL97_plus_lncRNA::1::4831	-1606, -1894	upstream, upstream	1	1	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene LOC339742	FAM201B		XM_929883, XM_003120760	1569008_at	XP_934976.4, XP_003120808.1
GeneID:2863	GPR39	2	133,174,147	133,404,169	230,022	+	2	1_A375_pNL7_minus_lncRNA::1::3361, 2_A375_pNL97_plus_lncRNA::1::4832	72669, 72797	in gene, in gene	1	1	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene GPR39	MGC149541, GPR39	G protein-coupled receptor 39	NM_001508, hCT2295974.1, hCT2295975.1, hCT2295976.1	208600_s_at, 229104_s_at, 229105_at	NP_001499.1, EAX11678.1, EAX11679.1, EAX11680.1
GeneID:344148	NCKAP5	2	133,429,372	134,326,031	896,659	-	3	1_A375_pNL7_minus_lncRNA::1::3362, 2_A375_pNL97_plus_lncRNA::1::4833, 2_A375_pNL97_plus_lncRNA::1::4834	504527, 541487, 504479	in gene, in gene, in gene	1	1	16	16.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene NCKAP5	NCKAP5, ERIH1, FLJ34870, NAP5, ERIH2	NCK-associated protein 5	NM_207363, NM_207481	239650_at	NP_997246.2, NP_997364.3
GeneID:80122	YSK4	2	135,722,273	135,782,248	59,975	-	2	1_A375_pNL7_minus_lncRNA::1::3363, 2_A375_pNL97_plus_lncRNA::1::4836	-6456, -6424	upstream, upstream	1	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene YSK4	YSK4, FLJ23074, RCK	YSK4 Sps1/Ste20-related kinase homolog (S. cerevisiae)	NM_001018046, NM_025052, hCT16784.3, hCT2294413.0	1555604_a_at, 221180_at	NP_001018056.1, NP_079328.3, EAX11642.1, EAX11643.1
GeneID:53353	LRP1B	2	140,988,996	142,889,270	1,900,274	-	1	1_A375_pNL7_minus_lncRNA::1::3367	574150	in gene	1	0	15	7	1	1_A375_pNL7_minus_lncRNA::1	15	Gene LRP1B	LRP-DIT, LRPDIT, LRP1B	low density lipoprotein receptor-related protein 1B	NM_018557, hCT2344117.0	219643_at	NP_061027.2, EAX11602.1
GeneID:8942	KYNU	2	143,635,195	143,799,885	164,690	+	1	1_A375_pNL7_minus_lncRNA::1::3368	2757	in gene	1	0	16	7	1	1_A375_pNL7_minus_lncRNA::1	16	Gene KYNU	KYNU		NM_003937, NM_001032998, hCT10777.1, hCT2293696.0, hCT2293698.0	204385_at, 210662_at, 210663_s_at, 217388_s_at, 241305_at	NP_003928.1, NP_001028170.1, EAX11599.1, EAX11600.1, EAX11601.1
GeneID:27249	MMADHC	2	150,426,147	150,444,330	18,183	-	1	2_A375_pNL97_plus_lncRNA::1::4840	106	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MMADHC	cblD, CL25022, MMADHC, C2orf25	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	NM_015702, hCT2293491.0, hCT2293492.0, hCT2293493.0, hCT2293495.0, hCT2293496.0	217883_at	NP_056517.1, EAX11533.1, EAX11534.1, EAX11535.1, EAX11536.1, EAX11537.1
GeneID:642340	LOC642340	2	150,443,872	150,704,748	260,876	+	1	2_A375_pNL97_plus_lncRNA::1::4840	352	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC642340		hypothetical LOC642340	XR_112399, XR_108438, XR_113417		
GeneID:390	RND3	2	151,324,709	151,344,180	19,471	-	1	2_A375_pNL97_plus_lncRNA::1::4842	1348	in gene	0	1	9	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene RND3	ARHE, memB, Rho8, RhoE, RND3	Rho family GTPase 3	NM_005168, hCT1964476.1, hCT2293323.0, hCT2293324.0, hCT2359638.0, hCT6821.3	212724_at	NP_005159.1, EAX11528.1, EAX11524.1, EAX11525.1, EAX11526.1, EAX11527.1
GeneID:55183	RIF1	2	152,266,397	152,333,860	67,463	+	2	1_A375_pNL7_minus_lncRNA::1::3369, 2_A375_pNL97_plus_lncRNA::1::4843	3, -45	in gene, upstream	1	1	26	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene RIF1	RIF1, DKFZp434D1026, DKFZp781N1478, FLJ12870	RAP1 interacting factor homolog (yeast)	NM_001177663, NM_001177664, NM_001177665, NM_018151, hCT2294870.0, hCT2294872.0, hCT2294873.0, hCT33240.3	214700_x_at, 214872_at, 226503_at, 233760_at, 233781_s_at, 236620_at, 240098_at, 241820_at	NP_001171134.1, NP_001171135.1, NP_060621.3, NP_001171136.1, EAX11507.1, EAX11508.1, EAX11509.1, EAX11510.1
GeneID:10254	STAM2	2	152,973,315	153,032,506	59,191	-	1	2_A375_pNL97_plus_lncRNA::1::4844	-38	upstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene STAM2	DKFZp564C047, STAM2A, STAM2B, STAM2, Hbp	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	NM_005843, hCT1822252.1, hCT1954349.1, hCT2294713.0	209194_s_at, 209649_at, 215044_s_at, 242569_at	NP_005834.4, EAX11491.1, EAX11490.1, EAX11492.1
GeneID:114793	FMNL2	2	153,191,751	153,506,348	314,597	+	1	2_A375_pNL97_plus_lncRNA::1::4845	121241	in gene	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene FMNL2	FLJ37546, FHOD2, FMNL2	formin-like 2	NM_052905, hCT1954347.1, hCT2359617.0	226184_at, 235881_at, 242665_at	NP_443137.2, EAX11486.1, EAX11485.1
GeneID:55660	PRPF40A	2	153,508,107	153,573,975	65,868	-	2	1_A375_pNL7_minus_lncRNA::1::3371, 2_A375_pNL97_plus_lncRNA::1::4846	-805, -761	upstream, upstream	1	1	41	44	1	2_A375_pNL97_plus_lncRNA::1	44	Gene PRPF40A	FLAF1, FBP11, HYPA, NY-REN-6, FLJ20585, HIP-10, HIP10, PRPF40A, Prp40, FNBP3, FBP-11	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	NM_017892	213729_at, 214941_s_at, 218053_at, 226687_at, 233080_s_at, 236477_at	NP_060362.3
GeneID:151188	ARL6IP6	2	153,574,423	153,617,767	43,344	+	2	1_A375_pNL7_minus_lncRNA::1::3371, 2_A375_pNL97_plus_lncRNA::1::4846	457, 313	in gene, in gene	1	1	41	44	1	2_A375_pNL97_plus_lncRNA::1	44	Gene ARL6IP6	PFAAP1, ARL6IP6, MGC33864	ADP-ribosylation-like factor 6 interacting protein 6	NM_152522, NR_024526, hCT2295061.0, hCT2295062.0, hCT2295063.0, hCT2295064.0	225707_at, 225709_at, 225711_at	NP_689735.1, EAX11477.1, EAX11475.1, EAX11476.1, EAX11478.1
GeneID:4929	NR4A2	2	157,180,944	157,189,287	8,343	-	1	1_A375_pNL7_minus_lncRNA::1::3372	23	in gene	1	0	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene NR4A2	NURR1, HZF-3, TINUR, NR4A2, NOT, RNR1	nuclear receptor subfamily 4, group A, member 2	NM_006186, hCT2292851.0, hCT29898.2	204621_s_at, 204622_x_at, 216248_s_at	NP_006177.1, EAX11454.1, EAX11455.1
GeneID:10010	TANK	2	161,993,466	162,092,682	99,216	+	1	1_A375_pNL7_minus_lncRNA::1::3373	23574	in gene	1	0	18	11	1	1_A375_pNL7_minus_lncRNA::1	18	Gene TANK	I-TRAF, TANK, TRAF2	TRAF family member-associated NFKB activator	NM_004180, NM_133484, hCT1953494.1, hCT2293335.0, hCT2293336.0, hCT30252.3	207616_s_at, 209451_at, 210458_s_at, 243376_at	NP_004171.2, NP_597841.1, EAX11374.1, EAX11375.1, EAX11376.1, EAX11377.1
GeneID:10213	PSMD14	2	162,164,786	162,268,226	103,440	+	1	2_A375_pNL97_plus_lncRNA::1::4849	270	in gene	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PSMD14	PSMD14, POH1, RPN11, PAD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	NM_005805, hCT31670.3	212296_at	NP_005796.1, EAX11370.1
GeneID:90134	KCNH7	2	163,227,917	163,695,240	467,323	-	2	1_A375_pNL7_minus_lncRNA::1::3374, 2_A375_pNL97_plus_lncRNA::1::4850	-2104, -2072	upstream, upstream	1	1	43	48	1	2_A375_pNL97_plus_lncRNA::1	48	Gene KCNH7	KCNH7, HERG3, Kv11.3, MGC45986, ERG3	potassium voltage-gated channel, subfamily H (eag-related), member 7	NM_033272, NM_173162, hCT1953501.1	1555316_a_at, 224099_at	NP_150375.2, NP_775185.1, EAX11346.1
GeneID:79809	TTC21B	2	166,730,453	166,810,348	79,895	-	2	1_A375_pNL7_minus_lncRNA::1::3375, 2_A375_pNL97_plus_lncRNA::1::4851	-52, -31	upstream, upstream	1	1	27	16	1	1_A375_pNL7_minus_lncRNA::1	27	Gene TTC21B	THM1, TTC21B, FLJ11457, Nbla10696	tetratricopeptide repeat domain 21B	NM_024753, hCT2291756.0, hCT2291757.0	220064_at	NP_079029.3, EAX11321.1, EAX11322.1
GeneID:100506134	LOC100506134	2	166,790,367	166,804,831	14,464	+	2	1_A375_pNL7_minus_lncRNA::1::3375, 2_A375_pNL97_plus_lncRNA::1::4851	20033, 20012	downstream, downstream	1	1	27	16	1	1_A375_pNL7_minus_lncRNA::1	27	Gene LOC100506134		hypothetical LOC100506134	XR_108448, XR_113390		
GeneID:29081	METTL5	2	170,668,267	170,681,353	13,086	-	1	2_A375_pNL97_plus_lncRNA::1::4852	-23	upstream	0	1	10	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene METTL5	FLJ10459, HSPC133, METTL5	methyltransferase like 5	NM_014168, hCT2291646.0, hCT2291649.0, hCT2291650.0, hCT2291654.0	220639_at, 221570_s_at	NP_054887.2, EAX11252.1, EAX11253.1, EAX11254.1, EAX11255.1
GeneID:130507	UBR3	2	170,684,018	170,940,641	256,623	+	1	2_A375_pNL97_plus_lncRNA::1::4852	-2642	upstream	0	1	10	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene UBR3	KIAA2024, ZNF650, FLJ37422, DKFZp434P117, MGC126489, UBR3, DKFZp686N10165	ubiquitin protein ligase E3 component n-recognin 3 (putative)	NM_172070, hCT2349581.0, hCT2359610.0, hCT2359611.0	230029_x_at, 234982_at, 235265_at, 244121_at	NP_742067.3, EAX11248.1, EAX11249.1, EAX11250.1
GeneID:26003	GORASP2	2	171,785,711	171,823,640	37,929	+	2	1_A375_pNL7_minus_lncRNA::1::3376, 2_A375_pNL97_plus_lncRNA::1::4853	-111, -47	upstream, upstream	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene GORASP2	GRASP55, FLJ13139, GRS2, p59, GORASP2, GOLPH6, DKFZp434D156	golgi reassembly stacking protein 2, 55kDa	NM_015530, hCT1953466.1, hCT2359668.0, hCT6862.3	207812_s_at, 208842_s_at, 208843_s_at	NP_056345.3, EAX11227.1, EAX11225.1, EAX11226.1
GeneID:254042	MAP1D	2	172,864,804	172,945,587	80,783	+	1	1_A375_pNL7_minus_lncRNA::1::3377	84828	downstream	1	0	13	12	1	1_A375_pNL7_minus_lncRNA::1	13	Gene MAP1D	MAP1D, METAP1D, Metapll	methionyl aminopeptidase type 1D (mitochondrial)	NM_199227, hCT2294672.1, hCT2294673.1, hCT2294674.1, hCT7830.4	1565755_at, 1565756_a_at	NP_954697.1, EAX11191.1, EAX11188.1, EAX11189.1, EAX11190.1
GeneID:1745	DLX1	2	172,950,208	172,954,402	4,194	+	2	1_A375_pNL7_minus_lncRNA::1::3377, 2_A375_pNL97_plus_lncRNA::1::4854	-576, 9952	upstream, downstream	1	1	13.5	13.5	2	2_A375_pNL97_plus_lncRNA::1	15	Gene DLX1	DLX1		NM_001038493, NM_178120, hCT1953477.1, hCT1953478.1, hCT1953479.1, hCT2294676.0, hCT2294677.0, hCT2294678.0, hCT7832.1	1560100_at, 242138_at	NP_001033582.1, NP_835221.2, EAX11181.1, EAX11182.1, EAX11183.1, EAX11186.1, EAX11184.1, EAX11185.1, EAX11187.1
GeneID:1746	DLX2	2	172,964,166	172,967,478	3,312	-	1	2_A375_pNL97_plus_lncRNA::1::4854	7318	downstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene DLX2	TES1, TES-1, DLX2	distal-less homeobox 2	NM_004405, hCT7829.3	207147_at, 215685_s_at	NP_004396.1, EAX11180.1
GeneID:51776	ZAK	2	173,940,565	174,132,737	192,172	+	2	1_A375_pNL7_minus_lncRNA::1::3379, 2_A375_pNL97_plus_lncRNA::1::4855	76027, 75979	in gene, in gene	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ZAK	MLK7, MLTK, pk, mltkk, MLT, MRK, AZK	sterile alpha motif and leucine zipper containing kinase AZK	NM_016653, NM_133646, hCT1952808.1, hCT2359622.0, hCT7645.2	1555259_at, 218833_at, 222757_s_at, 223519_at, 225662_at, 225665_at, 238613_at	NP_057737.2, NP_598407.1, EAX11164.1, EAX11165.1, EAX11166.1
GeneID:83879	CDCA7	2	174,219,561	174,233,718	14,157	+	2	1_A375_pNL7_minus_lncRNA::1::3380, 2_A375_pNL97_plus_lncRNA::1::4856	-73, -137	upstream, upstream	1	1	19	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene CDCA7	MGC34109, JPO1, FLJ14736, FLJ14722, CDCA7	cell division cycle associated 7	NM_145810, NM_031942, hCT2292987.0, hCT2359620.0, hCT2359621.0, hCT7844.2	224428_s_at, 230060_at	NP_665809.1, NP_114148.3, EAX11158.1, EAX11159.1, EAX11160.1, EAX11161.1
GeneID:344191	EVX2	2	176,944,835	176,948,690	3,855	-	3	1_A375_pNL7_minus_lncRNA::1::3381, 2_A375_pNL97_plus_lncRNA::1::4857, 2_A375_pNL97_plus_lncRNA::1::4858	-4446, -4430, -8262	upstream, upstream, upstream	1	1	15	18.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene EVX2	EVX2, EVX-2		NM_001080458		NP_001073927.1
GeneID:3239	HOXD13	2	176,957,532	176,960,666	3,134	+	3	1_A375_pNL7_minus_lncRNA::1::3381, 2_A375_pNL97_plus_lncRNA::1::4857, 2_A375_pNL97_plus_lncRNA::1::4858	-4396, -4412, 420	upstream, upstream, in gene	1	1	15	18.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene HOXD13	BDE, HOXD13, BDSD, HOX4I, SPD	homeobox D13	NM_000523, hCT8491.3	207397_s_at, 207398_at, 236681_at	NP_000514.2, EAX11095.1
GeneID:3238	HOXD12	2	176,964,530	176,965,488	958	+	1	2_A375_pNL97_plus_lncRNA::1::4858	-6578	upstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene HOXD12	HOX4H, HOXD12	homeobox D12	NM_021193, hCT1817235.2, hCT2291362.1	221411_at	NP_067016.3, EAX11094.1, EAX11093.1
GeneID:4780	NFE2L2	2	178,095,033	178,129,859	34,826	-	1	1_A375_pNL7_minus_lncRNA::1::3382	1539	in gene	1	0	19	13	1	1_A375_pNL7_minus_lncRNA::1	19	Gene NFE2L2	NRF2, NFE2L2	nuclear factor (erythroid-derived 2)-like 2	NM_006164, NM_001145412, NM_001145413, hCT12360.3, hCT1952818.1	1567013_at, 1567014_s_at, 1567015_at, 201146_at	NP_006155.2, NP_001138884.1, NP_001138885.1, EAX11061.1, EAX11062.1
GeneID:100422824	MIR3128	2	178,120,673	178,120,738	65	-	1	1_A375_pNL7_minus_lncRNA::1::3382	-7582	upstream	1	0	19	13	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MIR3128	MIR3128	microRNA 3128	NR_036075		
GeneID:92104	TTC30A	2	178,479,026	178,483,694	4,668	-	1	2_A375_pNL97_plus_lncRNA::1::4860	-18	upstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TTC30A	FLJ13946, FLJ77601, TTC30A	tetratricopeptide repeat domain 30A	NM_152275, hCT1834771.2	213679_at	NP_689488.3, EAX11053.1
GeneID:50940	PDE11A	2	178,487,977	178,973,066	485,089	-	3	1_A375_pNL7_minus_lncRNA::1::3383, 2_A375_pNL97_plus_lncRNA::1::4860, 2_A375_pNL97_plus_lncRNA::1::4861	-4054, 489354, -4054	upstream, downstream, upstream	1	1	23	27	2	2_A375_pNL97_plus_lncRNA::1	35	Gene PDE11A	FLJ23693, PDE11A, MGC133356, MGC133355, PPNAD2	phosphodiesterase 11A	NM_001077196, NM_016953, NM_001077197, NM_001077358, hCT2345076.0, hCT2345077.0, hCT2345078.0, hCT2345079.0, hCT2359589.0	221110_x_at, 224223_s_at, 224224_s_at, 237248_at	NP_001070664.1, NP_058649.3, NP_001070665.1, NP_001070826.1, EAX11049.1, EAX11051.1, EAX11047.1, EAX11048.1, EAX11050.1
GeneID:129831	RBM45	2	178,977,182	178,994,383	17,201	+	2	1_A375_pNL7_minus_lncRNA::1::3383, 2_A375_pNL97_plus_lncRNA::1::4861	-62, -62	upstream, upstream	1	1	34	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene RBM45	RBM45, DRB1, FLJ44612, MGC42237	RNA binding motif protein 45	NM_152945, hCT2294452.0, hCT2294453.0, hCT34520.3	228578_at, 237702_at	NP_694453.2, EAX11044.1, EAX11045.1, EAX11046.1
GeneID:114880	OSBPL6	2	179,059,374	179,260,877	201,503	+	1	2_A375_pNL97_plus_lncRNA::1::4862	209938	downstream	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene OSBPL6	OSBPL6, DKFZp686M06110, FLJ41254, MGC59642, ORP6, FLJ36583	oxysterol binding protein-like 6	NM_032523, NM_145739, hCT1966007.1, hCT2294438.0, hCT2294440.0, hCT2294441.0, hCT34518.3	223805_at, 235575_at	NP_115912.1, NP_665682.1, EAX11039.1, EAX11040.1, EAX11042.1, EAX11043.1, EAX11041.1
GeneID:100506831	LOC100506831	2	179,278,652	179,298,818	20,166	+	2	2_A375_pNL97_plus_lncRNA::1::4862, 2_A375_pNL97_plus_lncRNA::1::4863	-9340, -188	upstream, upstream	0	1	12.5	18	2	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100506831		hypothetical LOC100506831	XR_112412, XR_108401, XR_113396		
GeneID:57703	CWC22	2	180,809,604	180,871,780	62,176	-	1	1_A375_pNL7_minus_lncRNA::1::3384	-236	upstream	1	0	16	10	1	1_A375_pNL7_minus_lncRNA::1	16	Gene CWC22	NCM, CWC22, KIAA1604, EIF4GL, fSAPb	CWC22 spliceosome-associated protein homolog (S. cerevisiae)	NM_020943, hCT12351.3, hCT2359591.0, hCT2359592.0	226588_at	NP_065994.1, EAX10996.1, EAX10997.1, EAX10998.1
GeneID:3676	ITGA4	2	182,321,619	182,402,474	80,855	+	1	1_A375_pNL7_minus_lncRNA::1::3386	333	in gene	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ITGA4	ITGA4, IA4, CD49D, MGC90518	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	NM_000885, hCT1955222.1, hCT2290987.0, hCT2290988.0	205884_at, 205885_s_at, 213416_at	NP_000876.3, EAX10986.1, EAX10985.1, EAX10987.1
GeneID:4760	NEUROD1	2	182,541,194	182,545,381	4,187	-	3	1_A375_pNL7_minus_lncRNA::1::3387, 1_A375_pNL7_minus_lncRNA::1::3388, 2_A375_pNL97_plus_lncRNA::1::4864	2565, -4763, 2533	in gene, upstream, in gene	1	1	22.5	25.5	2	2_A375_pNL97_plus_lncRNA::1	38	Gene NEUROD1	BETA2, MODY6, NEUROD, BHF-1, bHLHa3, NEUROD1	neurogenic differentiation 1	NM_002500, hCT1815600.2	1556057_s_at, 206282_at	NP_002491.2, EAX10983.1
GeneID:54431	DNAJC10	2	183,580,999	183,643,255	62,256	+	1	1_A375_pNL7_minus_lncRNA::1::3389	9	in gene	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene DNAJC10	ERdj5, DKFZp434J1813, JPDI, DNAJC10, MGC104194	DnaJ (Hsp40) homolog, subfamily C, member 10	NM_018981, hCT13328.3, hCT2291041.0, hCT2291042.0, hCT2359639.0, hCT2359640.0, hCT2359641.0	221781_s_at, 221782_at, 225174_at, 229588_at	NP_061854.1, EAX10964.1, EAX10959.1, EAX10960.1, EAX10962.1, EAX10963.1, EAX10961.1
GeneID:55854	ZC3H15	2	187,350,885	187,374,088	23,203	+	2	1_A375_pNL7_minus_lncRNA::1::3390, 2_A375_pNL97_plus_lncRNA::1::4865	-197, -149	upstream, upstream	1	1	21	15	1	1_A375_pNL7_minus_lncRNA::1	21	Gene ZC3H15	HT010, ZC3H15, MSTP012, LEREPO4	zinc finger CCCH-type containing 15	NM_018471, hCT13167.2, hCT2290977.0	201593_s_at, 201595_s_at	NP_060941.2, EAX10936.1, EAX10935.1
GeneID:3685	ITGAV	2	187,454,790	187,545,628	90,838	+	1	2_A375_pNL97_plus_lncRNA::1::4866	26	in gene	0	1	6	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ITGAV	CD51, MSK8, ITGAV, VNRA, DKFZp686A08142	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	NM_002210, NM_001144999, NM_001145000, hCT12330.2, hCT2290960.0	202351_at	NP_002201.1, NP_001138471.1, NP_001138472.1, EAX10933.1, EAX10934.1
GeneID:51454	GULP1	2	189,157,390	189,460,653	303,263	+	1	1_A375_pNL7_minus_lncRNA::1::3391	-995	upstream	1	0	13	10	1	1_A375_pNL7_minus_lncRNA::1	13	Gene GULP1	CED6, GULP1, CED-6, FLJ31156, GULP	GULP, engulfment adaptor PTB domain containing 1	NM_016315, hCT1955223.1, hCT2290500.0, hCT2290501.0, hCT2359632.0, hCT2359633.0	204235_s_at, 204237_at, 215913_s_at, 215915_at, 223837_at	NP_057399.1, EAX10913.1, EAX10914.1, EAX10915.1, EAX10916.1, EAX10917.1
GeneID:693146	MIR561	2	189,162,219	189,162,315	96	+	1	1_A375_pNL7_minus_lncRNA::1::3391	-5824	upstream	1	0	13	10	1	1_A375_pNL7_minus_lncRNA::1	13	Gene MIR561	MIR561, MIRN561, hsa-mir-561	microRNA 561	NR_030287		
GeneID:64172	OSGEPL1	2	190,611,386	190,627,924	16,538	-	1	1_A375_pNL7_minus_lncRNA::1::3392	628	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene OSGEPL1	OSGEPL1		NM_022353, hCT2290864.0, hCT2290866.0	220631_at, 230032_at	NP_071748.2, EAX10890.1, EAX10891.1
GeneID:94101	ORMDL1	2	190,634,993	190,649,097	14,104	-	1	1_A375_pNL7_minus_lncRNA::1::3392	21801	downstream	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ORMDL1	DKFZp686G141, FLJ44364, ORMDL1	ORM1-like 1 (S. cerevisiae)	NM_016467, NM_001128150, hCT15913.3, hCT1963893.1, hCT1963895.1	223187_s_at, 227548_at, 228801_at	NP_057551.1, NP_001121622.1, EAX10887.1, EAX10888.1, EAX10889.1
GeneID:26275	HIBCH	2	191,069,360	191,184,771	115,411	-	2	1_A375_pNL7_minus_lncRNA::1::3393, 2_A375_pNL97_plus_lncRNA::1::4867	35, 19	in gene, in gene	1	1	22	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene HIBCH	HIBYL-COA-H, HIBCH, HIBYLCOAH	3-hydroxyisobutyryl-CoA hydrolase	NM_014362, NM_198047, hCT15915.3, hCT1958135.1, hCT1958136.1, hCT2290321.0, hCT2290323.0	203711_s_at, 213374_x_at	NP_055177.2, NP_932164.1, EAX10873.1, EAX10874.1, EAX10876.1, EAX10877.1, EAX10875.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:6772	STAT1	2	191,833,762	191,878,976	45,214	-	1	1_A375_pNL7_minus_lncRNA::1::3394	-6304	upstream	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene STAT1	STAT91, ISGF-3, DKFZp686B04100, STAT1	signal transducer and activator of transcription 1, 91kDa	NM_139266, NM_007315, hCT16921.3, hCT1971092.1, hCT1971093.1, hCT2290309.0, hCT2290311.0, hCT2290312.0	200887_s_at, 209969_s_at, AFFX-HUMISGF3A/M97935_3_at, AFFX-HUMISGF3A/M97935_5_at, AFFX-HUMISGF3A/M97935_MA_at, AFFX-HUMISGF3A/M97935_MB_at	NP_644671.1, NP_009330.1, EAX10850.1, EAX10851.1, EAX10852.1, EAX10855.1, EAX10853.1, EAX10854.1
GeneID:6775	STAT4	2	191,894,306	192,015,925	121,619	-	1	1_A375_pNL7_minus_lncRNA::1::3394	130645	downstream	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene STAT4	SLEB11, STAT4	signal transducer and activator of transcription 4	NM_003151, hCT1641682.3, hCT2290306.0, hCT2290307.0, hCT2359664.0	206118_at	NP_003142.1, EAX10848.1, EAX10846.1, EAX10847.1, EAX10849.1
GeneID:284992	CCDC150	2	197,504,356	197,597,530	93,174	+	2	1_A375_pNL7_minus_lncRNA::1::3396, 2_A375_pNL97_plus_lncRNA::1::4869	-52, 188	upstream, in gene	1	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CCDC150	CCDC150, DKFZp434P055, MGC72171, FLJ10202, FLJ39660, FLJ36811	coiled-coil domain containing 150	NM_001080539	1553459_at, 232398_at, 243565_at	NP_001074008.1
GeneID:3329	HSPD1	2	198,351,308	198,364,998	13,690	-	2	1_A375_pNL7_minus_lncRNA::1::3397, 2_A375_pNL97_plus_lncRNA::1::4870	326, 454	in gene, in gene	1	1	25	17	1	1_A375_pNL7_minus_lncRNA::1	25	Gene HSPD1	HuCHA60, GROEL, SPG13, HLD4, CPN60, HSP60, HSPD1, HSP65	heat shock 60kDa protein 1 (chaperonin)	NM_002156, NM_199440, hCT2302720.1, hCT2302721.0, hCT2302722.1, hCT2354851.0, hCT2354852.0, hCT2354853.0	200806_s_at, 200807_s_at, 241716_at	NP_002147.2, NP_955472.1, EAW70148.1, EAW70150.1, EAW70152.1, EAW70153.1, EAW70149.1, EAW70151.1
GeneID:3336	HSPE1	2	198,364,721	198,368,187	3,466	+	2	1_A375_pNL7_minus_lncRNA::1::3397, 2_A375_pNL97_plus_lncRNA::1::4870	-49, -177	upstream, upstream	1	1	25	17	1	1_A375_pNL7_minus_lncRNA::1	25	Gene HSPE1	HSP10, CPN10, GROES, HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	NM_002157, hCT2343424.0, hCT2343425.0, hCT2343426.0, hCT2343427.0, hCT2343428.1, hCT2343429.0, hCT2348053.0, hCT2348054.0, hCT2348055.0, hCT2348056.0	205133_s_at	NP_002148.1, EAW70155.1, EAW70156.1, EAW70157.1, EAW70161.1, EAW70162.1, EAW70154.1, EAW70158.1, EAW70159.1, EAW70160.1, EAW70163.1
GeneID:25843	MOBKL3	2	198,380,320	198,417,515	37,195	+	1	2_A375_pNL97_plus_lncRNA::1::4871	288	in gene	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene MOBKL3	MOB1, MOBKL3, MGC12264, MOB3, PREI3, CGI-95, 2C4D	MOB1, Mps One Binder kinase activator-like 3 (yeast)	NM_015387, NM_199482, NM_001100819, hCT11164.1, hCT1964655.1, hCT1964656.1, hCT2354848.0, hCT2354849.0	202918_s_at, 202919_at	NP_056202.2, NP_955776.1, NP_001094289.1, EAW70164.1, EAW70166.1, EAW70168.1, EAW70165.1, EAW70167.1
GeneID:23314	SATB2	2	200,134,223	200,335,989	201,766	-	3	1_A375_pNL7_minus_lncRNA::1::3398, 2_A375_pNL97_plus_lncRNA::1::4872, 2_A375_pNL97_plus_lncRNA::1::4873	11685, 155653, 11861	in gene, in gene, in gene	1	1	18	23.5	2	2_A375_pNL97_plus_lncRNA::1	32	Gene SATB2	FLJ32076, MGC119477, KIAA1034, MGC119474, SATB2, FLJ21474	SATB homeobox 2	NM_015265, NM_001172509, NM_001172517, hCT11165.3, hCT1952884.1	213435_at, 215591_at	NP_056080.1, NP_001165980.1, NP_001165988.1, EAW70180.1, EAW70181.1
GeneID:100288092	LOC100288092	2	200,322,423	200,325,977	3,554	+	2	1_A375_pNL7_minus_lncRNA::1::3398, 2_A375_pNL97_plus_lncRNA::1::4873	1881, 1705	in gene, in gene	1	1	27	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene LOC100288092		hypothetical LOC100288092	XR_108415		
GeneID:150538	FLJ32063	2	200,332,821	200,337,481	4,660	+	2	1_A375_pNL7_minus_lncRNA::1::3398, 2_A375_pNL97_plus_lncRNA::1::4873	-8517, -8693	upstream, upstream	1	1	27	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene FLJ32063	MGC126831	hypothetical LOC150538	NR_026830, hCT2302364.2, hCT2351046.0	1553420_at, 1560010_a_at	EAW70183.1, EAW70182.1
GeneID:129450	C2orf60	2	200,793,634	200,820,459	26,825	-	2	1_A375_pNL7_minus_lncRNA::1::3399, 2_A375_pNL97_plus_lncRNA::1::4874	75, 107	in gene, in gene	1	1	32	20	1	1_A375_pNL7_minus_lncRNA::1	32	Gene C2orf60	FLJ37953, C2orf60, hTYW5, MGC70509, TYW5	chromosome 2 open reading frame 60	NM_001039693, NR_004862, hCT12049.3, hCT2349279.0, hCT2349280.0, hCT2349281.0	235181_at, 235686_at, 241825_at	NP_001034782.1, EAW70191.1, EAW70192.1, EAW70193.1, EAW70194.1
GeneID:79568	C2orf47	2	200,820,040	200,828,848	8,808	+	2	1_A375_pNL7_minus_lncRNA::1::3399, 2_A375_pNL97_plus_lncRNA::1::4874	344, 312	in gene, in gene	1	1	32	20	1	1_A375_pNL7_minus_lncRNA::1	32	Gene C2orf47	C2orf47, FLJ22555, DKFZp566A212	chromosome 2 open reading frame 47	NM_024520, hCT12048.3, hCT2354879.0	219176_at	NP_078796.2, EAW70196.1, EAW70195.1
GeneID:130535	KCTD18	2	201,353,681	201,374,792	21,111	-	1	1_A375_pNL7_minus_lncRNA::1::3400	-56	upstream	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene KCTD18	6530404F10Rik, FLJ31322, FLJ37818, KCTD18	potassium channel tetramerisation domain containing 18	NM_152387, hCT2343755.0, hCT2343756.0, hCT2343757.0, hCT7602.3	1553136_at, 226493_at	NP_689600.2, EAW70204.1, EAW70203.1, EAW70205.1, EAW70206.1
GeneID:316	AOX1	2	201,450,731	201,536,218	85,487	+	1	2_A375_pNL97_plus_lncRNA::1::4875	76853	in gene	0	1	8	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene AOX1	AOH1, AO, AOX1	aldehyde oxidase 1	NM_001159, hCT2302561.0, hCT7596.3	205082_s_at, 205083_at	NP_001150.3, EAW70208.1, EAW70209.1
GeneID:9689	BZW1	2	201,676,647	201,688,560	11,913	+	2	1_A375_pNL7_minus_lncRNA::1::3401, 2_A375_pNL97_plus_lncRNA::1::4876	-231, -167	upstream, upstream	1	1	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene BZW1	Nbla10236, KIAA0005, BZW1, BZAP45	basic leucine zipper and W2 domains 1	NM_014670, hCT2302566.0, hCT2302567.0		NP_055485.2, EAW70213.1, EAW70212.1
GeneID:285172	FAM126B	2	201,838,441	201,936,392	97,951	-	1	1_A375_pNL7_minus_lncRNA::1::3402	-136	upstream	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene FAM126B	HYCC2, FAM126B, FLJ42947, FLJ37917, MGC39518, FLJ10981	family with sequence similarity 126, member B	NM_173822, hCT1953570.2, hCT2354840.0, hCT2354841.0	1554178_a_at, 231874_at	NP_776183.1, EAW70232.1, EAW70230.1, EAW70231.1
GeneID:4709	NDUFB3	2	201,936,462	201,950,473	14,011	+	1	1_A375_pNL7_minus_lncRNA::1::3402	66	in gene	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene NDUFB3	NDUFB3, B12	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	NM_002491, hCT1815346.1, hCT1967335.1	203371_s_at	NP_002482.1, EAW70234.1, EAW70233.1
GeneID:8837	CFLAR	2	201,980,816	202,029,016	48,200	+	1	2_A375_pNL97_plus_lncRNA::1::4877	368	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CFLAR	c-FLIPS, c-FLIP, MRIT, I-FLICE, c-FLIPR, FLAME-1, FLIP, FLAME, c-FLIPL, CASH, FLAME1, CFLAR, Casper, CLARP, CASP8AP1	CASP8 and FADD-like apoptosis regulator	NM_003879, NM_001127183, NM_001127184, hCT1967289.1, hCT1967290.1, hCT2303159.0, hCT2303162.0, hCT2303164.0, hCT2303166.0, hCT2303167.0, hCT2303168.0, hCT2303171.0, hCT2354776.0, hCT7591.3	208485_x_at, 209508_x_at, 209939_x_at, 210563_x_at, 210564_x_at, 211316_x_at, 211317_s_at, 211862_x_at, 214486_x_at, 214618_at, 237367_x_at, 239629_at	NP_003870.4, NP_001120655.1, NP_001120656.1, EAW70235.1, EAW70236.1, EAW70242.1, EAW70237.1, EAW70238.1, EAW70239.1, EAW70240.1, EAW70241.1, EAW70243.1, EAW70244.1, EAW70245.1
GeneID:66008	TRAK2	2	202,241,930	202,316,319	74,389	-	1	1_A375_pNL7_minus_lncRNA::1::3403	47	in gene	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TRAK2	GRIF1, CALS-C, KIAA0549, GRIF-1, ALS2CR3, TRAK2, OIP98	trafficking protein, kinesin binding 2	NM_015049, hCT2303293.0, hCT6039.2	202124_s_at, 202125_s_at	NP_055864.2, EAW70272.1, EAW70271.1
GeneID:55437	STRADB	2	202,316,392	202,345,574	29,182	+	1	1_A375_pNL7_minus_lncRNA::1::3403	-120	upstream	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene STRADB	ILPIPA, CALS-21, PRO1038, ALS2CR2, STRADB, MGC102916, ILPIP, PAPK	STE20-related kinase adaptor beta	NM_018571, hCT2303199.1, hCT2303201.1, hCT2303202.1, hCT2303204.1	223266_at	NP_061041.2, EAW70273.1, EAW70274.1, EAW70275.1, EAW70276.1
GeneID:57679	ALS2	2	202,564,986	202,645,895	80,909	-	1	1_A375_pNL7_minus_lncRNA::1::3404	7	in gene	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ALS2	KIAA1563, ALS2CR6, MGC87187, IAHSP, ALSJ, FLJ31851, ALS2, PLSJ	amyotrophic lateral sclerosis 2 (juvenile)	NM_020919, NM_001135745, hCT2303279.0, hCT2303280.0, hCT6035.2	1555264_at, 226291_at, 232184_at	NP_065970.2, NP_001129217.1, EAW70291.1, EAW70292.1, EAW70293.1
GeneID:8324	FZD7	2	202,899,310	202,903,160	3,850	+	1	2_A375_pNL97_plus_lncRNA::1::4878	850	in gene	0	1	8	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FZD7	FzE3, FZD7	frizzled homolog 7 (Drosophila)	NM_003507, hCT6116.2	203705_s_at, 203706_s_at	NP_003498.1, EAW70298.1
GeneID:51602	NOP58	2	203,130,515	203,168,384	37,869	+	2	1_A375_pNL7_minus_lncRNA::1::3405, 2_A375_pNL97_plus_lncRNA::1::4879	-19, 141	upstream, in gene	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene NOP58	HSPC120, NOP58, NOP5, NOP5/NOP58	NOP58 ribonucleoprotein homolog (yeast)	NM_015934, hCT23667.3	223096_at	NP_057018.1, EAW70308.1
GeneID:55759	WDR12	2	203,745,323	203,776,949	31,626	-	2	1_A375_pNL7_minus_lncRNA::1::3406, 2_A375_pNL97_plus_lncRNA::1::4880	661, 597	in gene, in gene	1	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene WDR12	WDR12, FLJ12720, FLJ10881, YTM1, FLJ12719	WD repeat domain 12	NM_018256, hCT1818766.2, hCT2348676.0	218512_at	NP_060726.3, EAW70318.1, EAW70319.1
GeneID:79800	ALS2CR8	2	203,776,978	203,851,060	74,082	+	2	1_A375_pNL7_minus_lncRNA::1::3406, 2_A375_pNL97_plus_lncRNA::1::4880	-690, -626	upstream, upstream	1	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ALS2CR8	ALS2CR8, DKFZp667N246, FLJ12675, NYD-SP24, FLJ21579, CARF	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8	NM_024744, NM_001104586, hCT1818767.2, hCT2304423.0, hCT2304424.0, hCT2304428.0, hCT2304430.0	1555391_a_at, 219834_at	NP_079020.13, NP_001098056.1, EAW70320.1, EAW70322.1, EAW70323.1, EAW70324.1, EAW70321.1
GeneID:100507265	LOC100507265	2	204,098,609	204,102,676	4,067	-	2	1_A375_pNL7_minus_lncRNA::1::3407, 2_A375_pNL97_plus_lncRNA::1::4881	-1004, -876	upstream, upstream	1	1	27	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene LOC100507265		hypothetical LOC100507265	XR_112429, XR_108421, XR_113424		
GeneID:57404	CYP20A1	2	204,103,164	204,170,563	67,399	+	2	1_A375_pNL7_minus_lncRNA::1::3407, 2_A375_pNL97_plus_lncRNA::1::4881	516, 388	in gene, in gene	1	1	27	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene CYP20A1	CYP20A1, CYP-M, MGC22229	cytochrome P450, family 20, subfamily A, polypeptide 1	NM_177538, hCT10461.5, hCT1953576.3, hCT2354787.0	219565_at	NP_803882.1, EAW70334.1, EAW70332.1, EAW70333.1
GeneID:8828	NRP2	2	206,547,224	206,662,857	115,633	+	1	1_A375_pNL7_minus_lncRNA::1::3410	-2264	upstream	1	0	21	12	1	1_A375_pNL7_minus_lncRNA::1	21	Gene NRP2	NP2, MGC126574, VEGF165R2, NRP2, PRO2714, NPN2	neuropilin 2	NM_003872, NM_018534, NM_201264, NM_201266, NM_201267, NM_201279, hCT1967277.2, hCT1967278.2, hCT2303051.1, hCT2303052.1, hCT2303055.1, hCT2303056.1, hCT2354748.0, hCT2354749.0, hCT2354750.0, hCT2354751.0, hCT2354752.0, hCT6225.4	1555468_at, 210841_s_at, 210842_at, 211844_s_at, 214632_at, 223510_at, 225566_at, 228102_at, 228103_s_at, 228699_at, 229225_at, 230410_at	NP_003863.2, NP_061004.3, NP_957716.1, NP_957718.1, NP_957719.1, NP_958436.1, EAW70362.1, EAW70363.1, EAW70364.1, EAW70365.1, EAW70366.1, EAW70367.1, EAW70368.1, EAW70369.1, EAW70370.1, EAW70371.1, EAW70372.1, EAW70373.1
GeneID:54891	INO80D	2	206,858,445	206,950,906	92,461	-	1	2_A375_pNL97_plus_lncRNA::1::4882	218	in gene	0	1	9	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene INO80D	INO80D, FLJ20309	INO80 complex subunit D	NM_017759, hCT2303368.0, hCT2303369.0	220165_at, 243070_at	NP_060229.3, EAW70374.1, EAW70375.1
GeneID:729570	LOC729570	2	206,949,320	206,951,584	2,264	+	1	2_A375_pNL97_plus_lncRNA::1::4882	1368	in gene	0	1	9	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene LOC729570		hypothetical LOC729570	XR_112430, XR_112431, XR_108422, XR_108423, XR_113425, XR_113426	227637_at	
GeneID:151194	FAM119A	2	208,473,839	208,489,973	16,134	-	2	1_A375_pNL7_minus_lncRNA::1::3413, 2_A375_pNL97_plus_lncRNA::1::4884	-11, -11	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene FAM119A	MGC45373, METTL21A, FAM119A, HCA557b	family with sequence similarity 119, member A	NM_145280, NM_001127395, hCT1953564.1, hCT2344884.0, hCT2344885.0, hCT2344886.0, hCT2344887.0, hCT2354770.0, hCT6486.3	1553743_at, 235177_at	NP_660323.3, NP_001120867.1, EAW70411.1, EAW70412.1, EAW70416.1, EAW70417.1, EAW70413.1, EAW70414.1, EAW70415.1
GeneID:100507475	LOC100507475	2	209,119,957	209,120,893	936	+	2	1_A375_pNL7_minus_lncRNA::1::3414, 2_A375_pNL97_plus_lncRNA::1::4885	10795, 10891	downstream, downstream	1	1	47	43	1	1_A375_pNL7_minus_lncRNA::1	47	Gene LOC100507475		hypothetical LOC100507475	XR_112434, XR_108426, XR_113429		
GeneID:200576	PIKFYVE	2	209,130,981	209,223,475	92,494	+	2	1_A375_pNL7_minus_lncRNA::1::3414, 2_A375_pNL97_plus_lncRNA::1::4885	-239, -143	upstream, upstream	1	1	47	43	1	1_A375_pNL7_minus_lncRNA::1	47	Gene PIKFYVE	MGC40423, KIAA0981, FLJ37746, CFD, FAB1, PIP5K3, PIP5K, PIKFYVE	phosphoinositide kinase, FYVE finger containing	NM_015040, NM_152671, NM_001178000, hCT2340612.0, hCT2340613.0, hCT2340614.0, hCT2340615.0, hCT2340616.0, hCT2354825.0	1553917_at, 1557719_at, 213111_at	NP_055855.2, NP_689884.1, NP_001171471.1, EAW70444.1, EAW70445.1, EAW70446.1, EAW70447.1, EAW70448.1, EAW70449.1
GeneID:285175	UNC80	2	210,636,717	210,864,024	227,307	+	1	2_A375_pNL97_plus_lncRNA::1::4886	-173	upstream	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene UNC80	UNC-80, FLJ33496, KIAA1843, FLJ14677, FLJ53903, UNC80, C2orf21	unc-80 homolog (C. elegans)	NM_032504, NM_182587, hCT1971839.2, hCT2302626.2, hCT2302627.2, hCT2302851.1, hCT2345139.2, hCT2348699.1		NP_115893.1, NP_872393.3, EAW70465.1, EAW70467.1, EAW70469.1, EAW70470.1, EAW70466.1, EAW70468.1
GeneID:79582	SPAG16	2	214,149,116	215,275,225	1,126,109	+	1	2_A375_pNL97_plus_lncRNA::1::4887	1126756	downstream	0	1	12	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene SPAG16	SPAG16, WDR29, FLJ22724, MGC87036, FLJ37717, DKFZp666P1710, PF20	sperm associated antigen 16	NM_001025436, NM_024532, hCT2349309.0	1560174_at, 219109_at, 240586_at	NP_001020607.1, NP_078808.3, EAW70515.1
GeneID:402117	VWC2L	2	215,276,461	215,440,653	164,192	+	1	2_A375_pNL97_plus_lncRNA::1::4887	-589	upstream	0	1	12	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene VWC2L	VWC2L	von Willebrand factor C domain-containing protein 2-like	NM_001080500		NP_001073969.1
GeneID:55686	MREG	2	216,807,314	216,878,346	71,032	-	1	2_A375_pNL97_plus_lncRNA::1::4888	7178	in gene	0	1	6	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene MREG	WDT2, DSU, MGC90296, FLJ10116, MREG	melanoregulin	NM_018000, hCT2302966.0, hCT2302968.0, hCT7734.2	219648_at, 232682_at	NP_060470.2, EAW70555.1, EAW70554.1, EAW70556.1
GeneID:57574	4-Mar	2	217,122,585	217,236,750	114,165	-	4	1_A375_pNL7_minus_lncRNA::1::3415, 1_A375_pNL7_minus_lncRNA::1::3416, 2_A375_pNL97_plus_lncRNA::1::4889, 2_A375_pNL97_plus_lncRNA::1::4890	-338, -1698, -338, -1666	upstream, upstream, upstream, upstream	1	1	21.5	30.5	2	2_A375_pNL97_plus_lncRNA::1	41	Gene MARCH4	MARCH4, MARCH-IV, MGC104908, RNF174	membrane-associated ring finger (C3HC4) 4	NM_020814, hCT7419.2	230112_at	NP_065865.1, EAW70566.1
GeneID:50485	SMARCAL1	2	217,277,137	217,347,776	70,639	+	2	1_A375_pNL7_minus_lncRNA::1::3417, 2_A375_pNL97_plus_lncRNA::1::4891	143, -68	in gene, upstream	1	1	16	16	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SMARCAL1	SMARCAL1, HARP, HHARP	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	NM_014140, NM_001127207, hCT2302926.0	218452_at	NP_054859.2, NP_001120679.1, EAW70567.1
GeneID:100507554	LOC100507554	2	217,351,335	217,363,469	12,134	-	1	1_A375_pNL7_minus_lncRNA::1::3418	-115	upstream	1	0	24	12	1	1_A375_pNL7_minus_lncRNA::1	24	Gene LOC100507554		hypothetical LOC100507554	XR_112436, XR_108428, XR_113433		
GeneID:6168	RPL37A	2	217,363,520	217,366,190	2,670	+	1	1_A375_pNL7_minus_lncRNA::1::3418	64	in gene	1	0	24	12	1	1_A375_pNL7_minus_lncRNA::1	24	Gene RPL37A	L37A, RPL37A, MGC74786, FLJ13357	ribosomal protein L37a	NM_000998, hCT1686475.4, hCT1815270.3, hCT2302892.1	213459_at, 214041_x_at	NP_000989.1, EAW70569.1, EAW70570.1, EAW70571.1
GeneID:729582	DIRC3	2	218,148,746	218,621,316	472,570	-	1	2_A375_pNL97_plus_lncRNA::1::4892	478644	downstream	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene DIRC3	DIRC3, FLJ14199	disrupted in renal carcinoma 3	NR_026597		
GeneID:6556	SLC11A1	2	219,246,752	219,261,617	14,865	+	4	1_A375_pNL7_minus_lncRNA::1::3419, 1_A375_pNL7_minus_lncRNA::1::3420, 2_A375_pNL97_plus_lncRNA::1::4893, 2_A375_pNL97_plus_lncRNA::1::4894	14240, 17776, 14272, 17744	in gene, downstream, in gene, downstream	1	1	25.5	37.5	2	2_A375_pNL97_plus_lncRNA::1	38	Gene SLC11A1	LSH, NRAMP1, NRAMP, SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	NM_000578, hCT2303101.0, hCT2303102.0, hCT2303104.0, hCT7337.3	1555116_s_at, 210422_x_at, 210423_s_at, 217473_x_at, 217507_at, 230382_at	NP_000569.3, EAW70611.1, EAW70612.1, EAW70613.1, EAW70614.1
GeneID:58190	CTDSP1	2	219,264,478	219,270,664	6,186	+	4	1_A375_pNL7_minus_lncRNA::1::3419, 1_A375_pNL7_minus_lncRNA::1::3420, 2_A375_pNL97_plus_lncRNA::1::4893, 2_A375_pNL97_plus_lncRNA::1::4894	-3486, 50, -3454, 18	upstream, in gene, upstream, in gene	1	1	25.5	37.5	2	2_A375_pNL97_plus_lncRNA::1	38	Gene CTDSP1	CTDSP1, NLIIF, SCP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	NM_021198, NM_182642, hCT1955108.1, hCT2303107.0, hCT2303108.0, hCT7331.2	217844_at	NP_067021.1, NP_872580.1, EAW70615.1, EAW70616.1, EAW70617.1, EAW70618.1
GeneID:407017	MIR26B	2	219,267,369	219,267,445	76	+	4	1_A375_pNL7_minus_lncRNA::1::3419, 1_A375_pNL7_minus_lncRNA::1::3420, 2_A375_pNL97_plus_lncRNA::1::4893, 2_A375_pNL97_plus_lncRNA::1::4894	-6377, -2841, -6345, -2873	upstream, upstream, upstream, upstream	1	1	25.5	37.5	2	2_A375_pNL97_plus_lncRNA::1	38	Gene MIR26B	MIR26B, hsa-mir-26b, MIRN26B, miR-26b	microRNA 26b	NR_029500		
GeneID:8941	CDK5R2	2	219,824,398	219,826,877	2,479	+	2	1_A375_pNL7_minus_lncRNA::1::3422, 2_A375_pNL97_plus_lncRNA::1::4895	3410, 3330	downstream, downstream	1	1	22	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene CDK5R2	NCK5AI, P39, CDK5R2, p39nck5ai	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	NM_003936, hCT6592.2	205852_at	NP_003927.1, EAW70662.1
GeneID:54738	FEV	2	219,845,809	219,850,379	4,570	-	1	1_A375_pNL7_minus_lncRNA::1::3423	-6229	upstream	1	0	17	7	1	1_A375_pNL7_minus_lncRNA::1	17	Gene FEV	PET-1, FEV, HSRNAFEV	FEV (ETS oncogene family)	NM_017521, hCT6593.2	207260_at	NP_059991.1, EAW70664.1
GeneID:1412	CRYBA2	2	219,854,912	219,858,127	3,215	-	1	1_A375_pNL7_minus_lncRNA::1::3423	1519	in gene	1	0	17	7	1	1_A375_pNL7_minus_lncRNA::1	17	Gene CRYBA2	CRYBA2		NM_005209, NM_057093, NM_057094, hCT1955095.2, hCT1967464.0, hCT2304361.0	220136_s_at	NP_005200.1, NP_476434.1, NP_476435.1, EAW70665.1, EAW70666.1, EAW70667.1
GeneID:494324	MIR375	2	219,866,367	219,866,430	63	-	1	1_A375_pNL7_minus_lncRNA::1::3423	9822	downstream	1	0	17	7	1	1_A375_pNL7_minus_lncRNA::1	17	Gene MIR375	MIRN375, MIR375, miRNA375, hsa-mir-375	microRNA 375	NR_029867		
GeneID:255101	CCDC108	2	219,867,576	219,906,245	38,669	-	2	1_A375_pNL7_minus_lncRNA::1::3424, 2_A375_pNL97_plus_lncRNA::1::4896	-4603, -4571	upstream, upstream	1	1	26	24	1	1_A375_pNL7_minus_lncRNA::1	26	Gene CCDC108	CCDC108, DKFZp434O0527, MGC35338	coiled-coil domain containing 108	NM_194302, NM_152389	1553686_at, 1556969_at, 1557879_at, 239508_x_at	NP_919278.2, NP_689602.2
GeneID:3549	IHH	2	219,919,142	219,925,238	6,096	-	2	1_A375_pNL7_minus_lncRNA::1::3424, 2_A375_pNL97_plus_lncRNA::1::4896	14390, 14422	downstream, downstream	1	1	26	24	1	1_A375_pNL7_minus_lncRNA::1	26	Gene IHH	IHH, BDA1, HHG2	Indian hedgehog	NM_002181, hCT2304456.0	215420_at, 229358_at	NP_002172.2, EAW70675.1
GeneID:79840	NHEJ1	2	219,940,046	220,025,587	85,541	-	2	1_A375_pNL7_minus_lncRNA::1::3425, 2_A375_pNL97_plus_lncRNA::1::4897	35491, 35411	in gene, in gene	1	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene NHEJ1	NHEJ1, FLJ12610, XLF	nonhomologous end-joining factor 1	NM_024782	219418_at	NP_079058.1
GeneID:130617	ZFAND2B	2	220,071,538	220,074,370	2,832	+	1	2_A375_pNL97_plus_lncRNA::1::4898	12046	downstream	0	1	14	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene ZFAND2B	ZFAND2B, AIRAPL		NM_138802, hCT1819607.1, hCT1966296.1, hCT2354774.0, hCT2354775.0	226168_at	NP_620157.1, EAW70690.1, EAW70691.1, EAW70692.1, EAW70693.1
GeneID:10058	ABCB6	2	220,074,494	220,083,672	9,178	-	1	2_A375_pNL97_plus_lncRNA::1::4898	88	in gene	0	1	14	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene ABCB6	ABCB6, ABC, ABC14, MTABC3, EST45597, umat, PRP, FLJ22414	ATP-binding cassette, sub-family B (MDR/TAP), member 6	NM_005689, hCT1966025.1, hCT2343394.0, hCT2343395.0, hCT2343396.0, hCT2343397.0, hCT2343398.0, hCT2343399.0, hCT2343400.0, hCT2343401.0, hCT2343402.0, hCT2343403.0, hCT6602.2	203191_at, 203192_at	NP_005680.1, EAW70694.1, EAW70695.1, EAW70696.1, EAW70698.1, EAW70699.1, EAW70697.1, EAW70700.1, EAW70701.1, EAW70702.1, EAW70703.1, EAW70704.1, EAW70705.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:79065	ATG9A	2	220,084,102	220,094,361	10,259	-	2	1_A375_pNL7_minus_lncRNA::1::3426, 2_A375_pNL97_plus_lncRNA::1::4898	132, 10777	in gene, downstream	1	1	15.5	14.5	2	1_A375_pNL7_minus_lncRNA::1	17	Gene ATG9A	APG9L1, mATG9, MGD3208, ATG9A	ATG9 autophagy related 9 homolog A (S. cerevisiae)	NM_001077198, NM_024085, hCT2304441.0, hCT6608.3	202492_at	NP_001070666.1, NP_076990.4, EAW70706.1, EAW70707.1
GeneID:55139	ANKZF1	2	220,094,479	220,101,391	6,912	+	2	1_A375_pNL7_minus_lncRNA::1::3426, 2_A375_pNL97_plus_lncRNA::1::4899	-250, 15657	upstream, downstream	1	1	13	15	2	1_A375_pNL7_minus_lncRNA::1	17	Gene ANKZF1	ZNF744, FLJ13144, FLJ10415, ANKZF1	ankyrin repeat and zinc finger domain containing 1	NM_018089, NM_001042410, hCT1955104.1, hCT1955105.1, hCT6607.3	218274_s_at	NP_060559.2, NP_001035869.1, EAW70708.1, EAW70709.1, EAW70710.1
GeneID:79411	GLB1L	2	220,101,493	220,110,131	8,638	-	2	1_A375_pNL7_minus_lncRNA::1::3426, 2_A375_pNL97_plus_lncRNA::1::4899	15902, -205	downstream, upstream	1	1	13	15	2	1_A375_pNL7_minus_lncRNA::1	17	Gene GLB1L	MGC10771, GLB1L	galactosidase, beta 1-like	NM_024506, hCT1955097.1, hCT2304437.0, hCT6599.3	205540_at	NP_078782.3, EAW70713.1, EAW70711.1, EAW70712.1
GeneID:8576	STK16	2	220,110,192	220,115,059	4,867	+	1	2_A375_pNL97_plus_lncRNA::1::4899	144	in gene	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene STK16	MPSK, FLJ39635, KRCT, TSF1, MGC16211, PKL12, STK16	serine/threonine kinase 16	NM_001008910, NR_026909, hCT1955092.1, hCT1955093.1, hCT2354890.0, hCT6591.2	209622_at	NP_001008910.1, EAW70714.1, EAW70715.1, EAW70716.1, EAW70717.1
GeneID:7277	TUBA4A	2	220,115,001	220,118,638	3,637	-	1	2_A375_pNL97_plus_lncRNA::1::4899	8302	downstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TUBA4A	H2-ALPHA, FLJ30169, TUBA1, TUBA4A	tubulin, alpha 4a	NM_006000, hCT2304429.0, hCT2304431.1	212242_at	NP_005991.1, EAW70718.1, EAW70719.1
GeneID:5798	PTPRN	2	220,154,345	220,174,143	19,798	-	2	1_A375_pNL7_minus_lncRNA::1::3427, 2_A375_pNL97_plus_lncRNA::1::4900	927, 1007	in gene, in gene	1	1	24	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene PTPRN	IA2, ICA512, R-PTP-N, IA-2, IA-2/PTP, PTPRN, FLJ16131	protein tyrosine phosphatase, receptor type, N	NM_002846, hCT1955091.1, hCT2354886.0, hCT6590.3	204945_at	NP_002837.1, EAW70725.1, EAW70724.1, EAW70726.1
GeneID:389075	RESP18	2	220,192,131	220,197,899	5,768	-	1	2_A375_pNL97_plus_lncRNA::1::4901	1440	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RESP18	RESP18	regulated endocrine-specific protein 18 homolog (rat)	NM_001007089, hCT1645737.3		NP_001007090.3, EAW70727.1
GeneID:23549	DNPEP	2	220,238,180	220,252,662	14,482	-	1	1_A375_pNL7_minus_lncRNA::1::3428	-682	upstream	1	0	20	15	1	1_A375_pNL7_minus_lncRNA::1	20	Gene DNPEP	DNPEP, ASPEP, DAP	aspartyl aminopeptidase	NM_012100, hCT1955103.1, hCT2304416.1, hCT2304418.1, hCT2340840.0, hCT2340841.0, hCT2340842.0, hCT2340843.0, hCT2340844.0, hCT2348654.0, hCT2348655.0, hCT6606.3	201937_s_at, 215135_at, 38703_at	NP_036232.2, EAW70730.1, EAW70728.1, EAW70731.1, EAW70736.1, EAW70738.1, EAW70729.1, EAW70732.1, EAW70733.1, EAW70734.1, EAW70735.1, EAW70737.1
GeneID:10056	FARSB	2	223,436,162	223,520,827	84,665	-	1	2_A375_pNL97_plus_lncRNA::1::4904	155	in gene	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene FARSB	PheHB, HSPC173, PheRS, FARSB, FARSLB, FRSB	phenylalanyl-tRNA synthetase, beta subunit	NM_005687, hCT2303002.0, hCT2348700.0, hCT2354829.0	223035_s_at, 223036_at, 232063_x_at	NP_005678.3, EAW70802.1, EAW70803.1, EAW70804.1
GeneID:116255	MOGAT1	2	223,536,457	223,574,649	38,192	+	1	2_A375_pNL97_plus_lncRNA::1::4905	37719	in gene	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene MOGAT1	DGAT2L, MGAT1, DGAT2L1, MOGAT1	monoacylglycerol O-acyltransferase 1	NM_058165, hCT12102.3, hCT2302989.0	1553062_at	NP_477513.2, EAW70805.1, EAW70806.1
GeneID:2181	ACSL3	2	223,725,732	223,808,119	82,387	+	1	1_A375_pNL7_minus_lncRNA::1::3430	28	in gene	1	0	20	10	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ACSL3	ACSL3, ACS3, PRO2194, FACL3	acyl-CoA synthetase long-chain family member 3	NM_004457, NM_203372, hCT1955136.1, hCT2303712.0, hCT2303714.0	201661_s_at, 201662_s_at	NP_004448.2, NP_976251.1, EAW70807.1, EAW70808.1, EAW70809.1
GeneID:57590	WDFY1	2	224,740,065	224,810,052	69,987	-	3	1_A375_pNL7_minus_lncRNA::1::3432, 2_A375_pNL97_plus_lncRNA::1::4906, 2_A375_pNL97_plus_lncRNA::1::4907	4, 49540, -44	in gene, in gene, upstream	1	1	13	21	2	2_A375_pNL97_plus_lncRNA::1	21	Gene WDFY1	ZFYVE17, FENS-1, WDF1, WDFY1	WD repeat and FYVE domain containing 1	NM_020830, hCT2303142.0, hCT2303143.0	224800_at, 233559_s_at	NP_065881.1, EAW70817.1, EAW70818.1
GeneID:65080	MRPL44	2	224,822,121	224,832,431	10,310	+	1	2_A375_pNL97_plus_lncRNA::1::4908	87	in gene	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MRPL44	FLJ37688, L44MT, MRPL44, FLJ12701, MRP-L44, FLJ13990	mitochondrial ribosomal protein L44	NM_022915, hCT11133.2, hCT2303013.0	218202_x_at, 222555_s_at	NP_075066.1, EAW70820.1, EAW70819.1
GeneID:5270	SERPINE2	2	224,839,765	224,904,036	64,271	-	1	1_A375_pNL7_minus_lncRNA::1::3433	-3196	upstream	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SERPINE2	DKFZp686A13110, PNI, GDN, SERPINE2, PI7, PI-7, PN-1, PN1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	NM_006216, NM_001136528, NM_001136530, hCT12527.2, hCT2303138.0, hCT2303139.0, hCT2354862.0	212190_at, 227487_s_at	NP_006207.1, NP_001130000.1, NP_001130002.1, EAW70822.1, EAW70823.1, EAW70824.1, EAW70821.1
GeneID:3267	AGFG1	2	228,336,888	228,425,938	89,050	+	2	1_A375_pNL7_minus_lncRNA::1::3436, 2_A375_pNL97_plus_lncRNA::1::4913	-88, -72	upstream, upstream	1	1	89	90	1	2_A375_pNL97_plus_lncRNA::1	90	Gene AGFG1	MGC116940, RIP, HRB, AGFG1, MGC116938, RAB, DKFZp686I15205	ArfGAP with FG repeats 1	NM_004504, NM_001135187, NM_001135188, NM_001135189, hCT2304299.0, hCT2304300.0	213926_s_at, 213928_s_at, 218091_at, 218092_s_at	NP_004495.2, NP_001128659.1, NP_001128660.1, NP_001128661.1, EAW70871.1, EAW70872.1
GeneID:164781	WDR69	2	228,736,327	228,789,026	52,699	+	1	2_A375_pNL97_plus_lncRNA::1::4914	-8695	upstream	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene WDR69	FLJ25955, WDR69	WD repeat domain 69	NM_178821, hCT1815011.3, hCT2348672.0, hCT2348673.0, hCT2348674.0, hCT2354798.0	242162_at	NP_849143.1, EAW70884.1, EAW70880.1, EAW70881.1, EAW70882.1, EAW70883.1
GeneID:92737	DNER	2	230,222,345	230,579,286	356,941	-	2	1_A375_pNL7_minus_lncRNA::1::3437, 2_A375_pNL97_plus_lncRNA::1::4915	-586, -458	upstream, upstream	1	1	19	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene DNER	UNQ26, bet, DNER	delta/notch-like EGF repeat containing	NM_139072, hCT2303273.0, hCT2303274.0, hCT2354884.0, hCT25012.3	226281_at	NP_620711.3, EAW70895.1, EAW70892.1, EAW70893.1, EAW70894.1
GeneID:51719	CAB39	2	231,577,557	231,685,790	108,233	+	2	1_A375_pNL7_minus_lncRNA::1::3438, 2_A375_pNL97_plus_lncRNA::1::4916	-85, -53	upstream, upstream	1	1	37	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene CAB39	CGI-66, FLJ22682, CAB39, MO25	calcium binding protein 39	NM_016289, NM_001130849, NM_001130850, hCT2303766.0, hCT25537.3	217873_at, 224311_s_at	NP_057373.1, NP_001124321.1, NP_001124322.1, EAW70932.1, EAW70933.1
GeneID:9290	GPR55	2	231,772,043	231,789,941	17,898	-	1	2_A375_pNL97_plus_lncRNA::1::4917	16325	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene GPR55	GPR55		NM_005683, hCT1645302.2, hCT2303873.1	231745_at, 237559_at	NP_005674.2, EAW70939.1, EAW70940.1
GeneID:257407	C2orf72	2	231,902,281	231,914,429	12,148	+	3	1_A375_pNL7_minus_lncRNA::1::3439, 2_A375_pNL97_plus_lncRNA::1::4918, 2_A375_pNL97_plus_lncRNA::1::4919	19063, 15431, 19031	downstream, downstream, downstream	1	1	61.5	59.5	2	1_A375_pNL7_minus_lncRNA::1	113	Gene C2orf72	C2orf72	chromosome 2 open reading frame 72	NM_001144994	1556464_a_at, 213143_at, 213148_at	NP_001138466.1
GeneID:5707	PSMD1	2	231,921,578	232,037,541	115,963	+	3	1_A375_pNL7_minus_lncRNA::1::3439, 2_A375_pNL97_plus_lncRNA::1::4918, 2_A375_pNL97_plus_lncRNA::1::4919	-234, -3866, -266	upstream, upstream, upstream	1	1	61.5	59.5	2	1_A375_pNL7_minus_lncRNA::1	113	Gene PSMD1	MGC133041, S1, P112, MGC133040, Rpn2, PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	NM_001191037, NM_002807, NR_034059, hCT2354765.0, hCT25536.2	201198_s_at, 201199_s_at	NP_001177966.1, NP_002798.2, EAW70947.1, EAW70948.1
GeneID:93010	B3GNT7	2	232,260,335	232,265,875	5,540	+	2	1_A375_pNL7_minus_lncRNA::1::3441, 2_A375_pNL97_plus_lncRNA::1::4921	-7039, -7007	upstream, upstream	1	1	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene B3GNT7	B3GNT7, beta3GnT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	NM_145236, hCT2341139.0, hCT2341140.0	1552965_a_at, 1555962_at, 1555963_x_at, 232337_at	NP_660279.1, EAW70959.1, EAW70958.1
GeneID:5757	PTMA	2	232,573,235	232,578,251	5,016	+	4	1_A375_pNL7_minus_lncRNA::1::3442, 1_A375_pNL7_minus_lncRNA::1::3443, 2_A375_pNL97_plus_lncRNA::1::4924, 2_A375_pNL97_plus_lncRNA::1::4925	-1523, -19, -1459, -195	upstream, upstream, upstream, upstream	1	1	20.5	25.5	2	2_A375_pNL97_plus_lncRNA::1	34	Gene PTMA	PTMA, TMSA, MGC104802	prothymosin, alpha	NM_002823, NM_001099285, hCT2303930.0, hCT2303931.0, hCT2303933.0, hCT2303934.0, hCT2303935.0, hCT2303937.0, hCT2303938.0	200772_x_at, 211921_x_at	NP_002814.3, NP_001092755.1, EAW70969.1, EAW70970.1, EAW70974.1, EAW70975.1, EAW70971.1, EAW70972.1, EAW70973.1
GeneID:5147	PDE6D	2	232,597,147	232,645,974	48,827	-	3	1_A375_pNL7_minus_lncRNA::1::3444, 2_A375_pNL97_plus_lncRNA::1::4926, 2_A375_pNL97_plus_lncRNA::1::4927	-5130, 22, -5194	upstream, in gene, upstream	1	1	15.5	20.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene PDE6D	PDED, PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta	NM_002601, hCT1961980.1, hCT24143.3	204091_at, 216683_x_at, 231065_at	NP_002592.1, EAW70977.1, EAW70976.1
GeneID:64708	COPS7B	2	232,651,162	232,673,434	22,272	+	3	1_A375_pNL7_minus_lncRNA::1::3444, 2_A375_pNL97_plus_lncRNA::1::4926, 2_A375_pNL97_plus_lncRNA::1::4927	-58, -5210, 6	upstream, upstream, in gene	1	1	15.5	20.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene COPS7B	COPS7B, CSN7B, MGC111077, FLJ12612	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	NM_022730, hCT1961985.2, hCT2348719.0, hCT2348720.0, hCT25181.4	219997_s_at, 225696_at, 243628_at	NP_073567.1, EAW70982.1, EAW70979.1, EAW70980.1, EAW70981.1
GeneID:129563	DIS3L2	2	232,826,293	233,201,908	375,615	+	2	1_A375_pNL7_minus_lncRNA::1::3445, 2_A375_pNL97_plus_lncRNA::1::4928	353899, 354139	in gene, in gene	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DIS3L2	DIS3L2, FAM6A, FLJ36974, MGC42174	DIS3 mitotic control homolog (S. cerevisiae)-like 2	NM_152383	227597_at, 235602_at	NP_689596.4
GeneID:79054	TRPM8	2	234,826,043	234,928,166	102,123	+	2	1_A375_pNL7_minus_lncRNA::1::3446, 2_A375_pNL97_plus_lncRNA::1::4929	-4443, -4475	upstream, upstream	1	1	23	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene TRPM8	LTRPC6, TRPM8, TRPP8, MGC2849	transient receptor potential cation channel, subfamily M, member 8	NM_024080, hCT2303397.0, hCT2303398.0	220226_at, 243483_at	NP_076985.4, EAW71068.1, EAW71067.1
GeneID:10920	COPS8	2	237,994,084	238,007,489	13,405	+	2	1_A375_pNL7_minus_lncRNA::1::3448, 2_A375_pNL97_plus_lncRNA::1::4933	284, 444	in gene, in gene	1	1	18	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene COPS8	MGC43256, COP9, CSN8, COPS8, MGC1297, SGN8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	NM_006710, NM_198189, hCT1815594.2, hCT1961954.1, hCT2354866.0, hCT2354867.0	202141_s_at, 202142_at, 202143_s_at, 214260_at, 243152_at	NP_006701.1, NP_937832.1, EAW71097.1, EAW71098.1, EAW71099.1, EAW71100.1
GeneID:79083	MLPH	2	238,395,878	238,463,961	68,083	+	1	2_A375_pNL97_plus_lncRNA::1::4937	76698	downstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MLPH	MGC2771, MGC59733, MLPH, SLAC2-A	melanophilin	NM_001042467, NM_024101, hCT14132.2, hCT2303728.0, hCT2303729.0, hCT2354846.0, hCT2354847.0	218211_s_at	NP_001035932.1, NP_077006.1, EAW71113.1, EAW71114.1, EAW71115.1, EAW71116.1, EAW71112.1
GeneID:51052	PRLH	2	238,475,217	238,475,818	601	+	1	2_A375_pNL97_plus_lncRNA::1::4937	-2641	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PRLH	PRH, PRLH, PRRP	prolactin releasing hormone	NM_015893, hCT14122.0	221443_x_at	NP_056977.1, EAW71117.1
GeneID:10267	RAMP1	2	238,768,187	238,820,756	52,569	+	2	1_A375_pNL7_minus_lncRNA::1::3450, 2_A375_pNL97_plus_lncRNA::1::4938	39173, 39301	in gene, in gene	1	1	20	20	1	1_A375_pNL7_minus_lncRNA::1	20	Gene RAMP1	RAMP1		NM_005855, hCT14123.4	204916_at	NP_005846.1, EAW71127.1
GeneID:140739	UBE2F	2	238,875,700	238,950,684	74,984	+	1	1_A375_pNL7_minus_lncRNA::1::3451	-180	upstream	1	0	16	10	1	1_A375_pNL7_minus_lncRNA::1	16	Gene UBE2F	MGC18120, UBE2F, NCE2	ubiquitin-conjugating enzyme E2F (putative)	NM_080678, hCT2344156.0, hCT2344158.0, hCT2344159.0, hCT2354766.0, hCT2354767.0, hCT2354768.0, hCT2354769.0	225783_at, 225787_at, 231948_s_at	NP_542409.1, EAW71130.1, EAW71128.1, EAW71132.1, EAW71133.1, EAW71134.1, EAW71129.1, EAW71131.1
GeneID:51540	SCLY	2	238,969,632	239,008,054	38,422	+	1	2_A375_pNL97_plus_lncRNA::1::4939	-256	upstream	0	1	7	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SCLY	SCL, SCLY	selenocysteine lyase	NM_016510, hCT2344157.1, hCT2344160.1, hCT2344161.1, hCT2344162.1, hCT2354764.1	219608_at, 221575_at, 59705_at	NP_057594.3, EAW71135.1, EAW71136.1, EAW71137.1, EAW71138.1, EAW71139.1
GeneID:8864	PER2	2	239,152,679	239,197,207	44,528	-	4	1_A375_pNL7_minus_lncRNA::1::3452, 1_A375_pNL7_minus_lncRNA::1::3453, 2_A375_pNL97_plus_lncRNA::1::4940, 2_A375_pNL97_plus_lncRNA::1::4941	31831, -297, 31831, -329	in gene, upstream, in gene, upstream	1	1	23.5	24	2	2_A375_pNL97_plus_lncRNA::1	32	Gene PER2	KIAA0347, PER2, FASPS	period homolog 2 (Drosophila)	NM_022817, hCT2304251.0, hCT2304252.0, hCT2304254.0	205251_at, 205518_s_at	NP_073728.1, EAW71153.1, EAW71154.1, EAW71155.1
GeneID:9759	HDAC4	2	239,969,864	240,322,643	352,779	-	3	1_A375_pNL7_minus_lncRNA::1::3457, 2_A375_pNL97_plus_lncRNA::1::4943, 2_A375_pNL97_plus_lncRNA::1::4944	-749, 125619, -653	upstream, in gene, upstream	1	1	12	16.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene HDAC4	HA6116, BDMR, HD4, AHO3, HDAC4, HDAC-A, KIAA0288, HDACA	histone deacetylase 4	NM_006037, hCT13281.3, hCT2354796.0	1554322_a_at, 204225_at, 228813_at	NP_006028.2, EAW71166.1, EAW71165.1
GeneID:4705	NDUFA10	2	240,896,789	240,964,819	68,030	-	1	2_A375_pNL97_plus_lncRNA::1::4945	-45	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene NDUFA10	NDUFA10, CI-42k, FLJ21923, CI-42KD, MGC5103	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	NM_004544, hCT11609.3, hCT2303673.0, hCT2303674.0, hCT2303675.0	1554719_at, 1555548_at	NP_004535.1, EAW71173.1, EAW71172.1, EAW71174.1, EAW71175.1
GeneID:389090	OR6B2	2	240,968,908	240,969,846	938	-	1	2_A375_pNL97_plus_lncRNA::1::4945	4982	downstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene OR6B2	OR6B2P, OR6B2, OR2-1	olfactory receptor, family 6, subfamily B, member 2	NM_001005853, hCT2345564.0		NP_001005853.1, EAW71176.1
GeneID:25992	SNED1	2	241,938,255	242,033,643	95,388	+	1	1_A375_pNL7_minus_lncRNA::1::3458	103537	downstream	1	0	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SNED1	FLJ00133, SST3, Snep, SNED1, DKFZp586B2420	sushi, nidogen and EGF-like domains 1	NM_001080437	1554798_at, 213488_at, 213493_at	NP_001073906.1
GeneID:130916	MTERFD2	2	242,026,509	242,041,747	15,238	-	1	1_A375_pNL7_minus_lncRNA::1::3458	-45	upstream	1	0	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene MTERFD2	MTERFD2, FLJ16261, MGC61716	MTERF domain containing 2	NM_182501, NR_026049, NR_026050, NR_026051, hCT2354863.0, hCT24247.4	1557965_at, 1557966_x_at, 214364_at, 226486_at	NP_872307.2, EAW71234.1, EAW71235.1
GeneID:23178	PASK	2	242,045,515	242,088,878	43,363	-	1	1_A375_pNL7_minus_lncRNA::1::3458	47086	downstream	1	0	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene PASK	DKFZp434O051, DKFZp686P2031, PASK, PASKIN, STK37, KIAA0135	PAS domain containing serine/threonine kinase	NM_015148, hCT1950053.1, hCT1958412.1, hCT2304907.0, hCT2304909.0, hCT2354827.0, hCT2354828.0, hCT24240.1	206594_at, 213534_s_at, 216945_x_at	NP_055963.2, EAW71236.1, EAW71237.1, EAW71240.1, EAW71241.1, EAW71242.1, EAW71238.1, EAW71239.1
GeneID:3069	HDLBP	2	242,166,679	242,255,254	88,575	-	4	1_A375_pNL7_minus_lncRNA::1::3459, 1_A375_pNL7_minus_lncRNA::1::3460, 2_A375_pNL97_plus_lncRNA::1::4946, 2_A375_pNL97_plus_lncRNA::1::4947	43862, 502, 43798, 502	in gene, in gene, in gene, in gene	1	1	25	21.5	2	1_A375_pNL7_minus_lncRNA::1	34	Gene HDLBP	PRO2900, HDLBP, FLJ16432, VGL, HBP	high density lipoprotein binding protein	NM_005336, NM_203346, hCT1966929.1, hCT2304954.0, hCT24241.3	200643_at, 219674_s_at, 221767_x_at, 222916_s_at, 225012_at, 235624_at, 240152_at	NP_005327.1, NP_976221.1, EAW71253.1, EAW71254.1, EAW71255.1
GeneID:4735	2-Sep	2	242,254,723	242,293,442	38,719	+	2	1_A375_pNL7_minus_lncRNA::1::3460, 2_A375_pNL97_plus_lncRNA::1::4947	29, 29	in gene, in gene	1	1	34	27	1	1_A375_pNL7_minus_lncRNA::1	34	Gene SEPT2	Pnutl3, SEPT2, NEDD5, DIFF6, KIAA0158, hNedd5	septin 2	NM_001008491, NM_001008492, NM_006155, NM_004404, hCT2304481.1, hCT2304482.1, hCT2304483.1, hCT2304484.1	1554747_a_at, 1559038_at, 200015_s_at, 200778_s_at, 232637_at	NP_001008491.1, NP_001008492.1, NP_004395.1, NP_006146.1, EAW71258.1, EAW71261.1, EAW71259.1, EAW71260.1
GeneID:10494	STK25	2	242,434,432	242,448,034	13,602	-	1	2_A375_pNL97_plus_lncRNA::1::4948	-94	upstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene STK25	SOK1, DKFZp686J1430, STK25, YSK1	serine/threonine kinase 25 (STE20 homolog, yeast)	NM_006374, hCT2304944.0, hCT2304945.0	201314_at	NP_006365.2, EAW71265.1, EAW71266.1
GeneID:100507459	LOC100507459	20	300,971	305,896	4,925	-	1	2_A375_pNL97_plus_lncRNA::1::4949	552	in gene	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100507459		hypothetical LOC100507459	XR_112112, XR_109638, XR_115335		
GeneID:6666	SOX12	20	306,239	310,868	4,629	+	1	2_A375_pNL97_plus_lncRNA::1::4949	-895	upstream	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SOX12	SOX12, SOX22	SRY (sex determining region Y)-box 12	NM_006943, hCT2314747.0	204432_at, 226356_at	NP_008874.2, EAX10683.1
GeneID:57761	TRIB3	20	361,308	378,203	16,895	+	1	2_A375_pNL97_plus_lncRNA::1::4950	27076	downstream	0	1	22	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TRIB3	SKIP3, NIPK, TRIB3, SINK, TRB3, C20orf97	tribbles homolog 3 (Drosophila)	NM_021158, hCT2314750.2	1555788_a_at, 218145_at	NP_066981.2, EAX10678.1
GeneID:10616	RBCK1	20	388,709	411,610	22,901	+	2	1_A375_pNL7_minus_lncRNA::1::3461, 2_A375_pNL97_plus_lncRNA::1::4950	23483, -325	downstream, upstream	1	1	19	13	2	2_A375_pNL97_plus_lncRNA::1	18	Gene RBCK1	XAP3, RBCK2, HOIL-1, HOIL1, XAP4, C20orf18, UBCE7IP3, RNF54, ZRANB4, RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	NM_031229, NM_006462	207713_s_at, 221827_at	NP_112506.2, NP_006453.1
GeneID:128637	TBC1D20	20	416,124	443,187	27,063	-	1	1_A375_pNL7_minus_lncRNA::1::3461	30995	downstream	1	0	16	8	1	1_A375_pNL7_minus_lncRNA::1	16	Gene TBC1D20	FLJ45119, TBC1D20, C20orf140	TBC1 domain family, member 20	NM_144628, hCT2359534.0, hCT2359535.0, hCT31128.3	226409_at, 226664_at	NP_653229.1, EAX10672.1, EAX10670.1, EAX10671.1
GeneID:1457	CSNK2A1	20	463,338	524,482	61,144	-	2	1_A375_pNL7_minus_lncRNA::1::3462, 2_A375_pNL97_plus_lncRNA::1::4951	226, -46	in gene, upstream	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene CSNK2A1	CK2A1, CKII, CSNK2A1	casein kinase 2, alpha 1 polypeptide	NM_177559, NM_001895, NM_177560, hCT1963004.1, hCT1963005.1, hCT1963006.1, hCT1963007.1, hCT2359579.0	206075_s_at, 212072_s_at, 212075_s_at, 229212_at, 229216_s_at	NP_808227.1, NP_001886.1, NP_808228.1, EAX10665.1, EAX10668.1, EAX10669.1, EAX10666.1, EAX10667.1
GeneID:85508	SCRT2	20	642,240	656,823	14,583	-	1	2_A375_pNL97_plus_lncRNA::1::4952	727	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SCRT2	SCRT2, ZNF898B, FLJ43353		NM_033129, hCT2314449.0, hCT31125.3		NP_149120.1, EAX10660.1, EAX10661.1
GeneID:83541	FAM110A	20	814,356	826,922	12,566	+	2	1_A375_pNL7_minus_lncRNA::1::3463, 2_A375_pNL97_plus_lncRNA::1::4953	-52, 108	upstream, in gene	1	1	29	18	1	1_A375_pNL7_minus_lncRNA::1	29	Gene FAM110A	C20orf55, MGC2450, F10, bA371L19.3, FAM110A, MGC4675	family with sequence similarity 110, member A	NM_031424, NM_001042353, NM_207121	226564_s_at	NP_113612.1, NP_001035812.1, NP_997004.1
GeneID:51378	ANGPT4	20	853,296	896,960	43,664	-	1	2_A375_pNL97_plus_lncRNA::1::4954	37376	in gene	0	1	12	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ANGPT4	ANG4, MGC138183, AGP4, ANGPT4, MGC138181, ANG-3	angiopoietin 4	NM_015985, hCT31122.1	221134_at	NP_057069.1, EAX10654.1
GeneID:9491	PSMF1	20	1,093,906	1,148,426	54,520	+	2	1_A375_pNL7_minus_lncRNA::1::3464, 2_A375_pNL97_plus_lncRNA::1::4955	5262, 5230	in gene, in gene	1	1	23	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene PSMF1	PSMF1, PI31	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	NM_006814, NM_178578, hCT1967637.1, hCT2359498.0, hCT30666.2	201052_s_at, 201053_s_at	NP_006805.2, NP_848693.2, EAX10649.1, EAX10650.1, EAX10651.1
GeneID:27111	SDCBP2	20	1,290,619	1,309,838	19,219	-	1	2_A375_pNL97_plus_lncRNA::1::4956	3918	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SDCBP2	SDCBP2, ST-2, FLJ12256, SITAC18	syndecan binding protein (syntenin) 2	NM_080489, NM_015685, hCT2314394.1, hCT2314395.1	233565_s_at	NP_536737.3, NP_056500.2, EAX10639.1, EAX10640.1
GeneID:100507495	LOC100507495	20	1,306,054	1,359,379	53,325	+	1	2_A375_pNL97_plus_lncRNA::1::4956	-134	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100507495		hypothetical LOC100507495	XR_112113, XR_112114, XR_109639, XR_109640, XR_115336, XR_115337		
GeneID:100288764	LOC100288764	20	1,316,211	1,317,555	1,344	-	1	2_A375_pNL97_plus_lncRNA::1::4956	11635	downstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100288764		similar to hCG2043693	XM_002344166, XM_003120973		XP_002344207.1, XP_003121021.1
GeneID:55968	NSFL1C	20	1,422,811	1,448,417	25,606	-	2	1_A375_pNL7_minus_lncRNA::1::3465, 2_A375_pNL97_plus_lncRNA::1::4958	833, 865	in gene, in gene	1	1	25	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene NSFL1C	MGC3347, p47, UBX1, dJ776F14.1, NSFL1C, FLJ46689, UBXN2C, P47, UBXD10	NSFL1 (p97) cofactor (p47)	NM_016839, NM_016143, NM_182483, hCT2314383.0, hCT2314384.0, hCT2314385.0, hCT2314386.0, hCT2314387.0, hCT2314388.0, hCT2314389.0	217830_s_at, 217831_s_at, 220248_x_at, 232519_at, 232520_s_at, 236951_at	NP_061327.2, NP_057227.2, NP_872289.1, EAX10626.1, EAX10629.1, EAX10630.1, EAX10627.1, EAX10628.1, EAX10631.1, EAX10632.1
GeneID:284759	SIRPB2	20	1,455,236	1,472,233	16,997	-	3	1_A375_pNL7_minus_lncRNA::1::3465, 2_A375_pNL97_plus_lncRNA::1::4958, 2_A375_pNL97_plus_lncRNA::1::4959	24649, 24681, 7065	downstream, downstream, in gene	1	1	17.5	21	2	2_A375_pNL97_plus_lncRNA::1	25	Gene SIRPB2	SIRPB2, PTPNS1L3, PTPN1L, dJ776F14.2	signal-regulatory protein beta 2	NM_001122962, NM_001134836	1559034_at	NP_001116434.1, NP_001128308.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervening Count	Intervening	Intervening Distance	Intervening Position	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Attributes	Full Description	RNA	Ally Tag	PROT
Gene:ID:10268478473	LOC10026478473	20	1,979,609	1,782,837	67,021	-	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4690	46027, 4821	up gene, us gene	1	1	80	55	1	2_A270_shL97_shcs_IncRNA:1	55	Gene LOC100269478473	cytoskeleton associated protein 2-like pseudogene				
Gene:ID:100901	STX3B	20	2,082,328	2,129,201	46,873	+	2	1_A270_shL7_shcs_IncRNA:1-3464, 2_A270_shL97_shcs_IncRNA:1-4690	668, 640	up gene, us gene	1	1	97	82	1	1_A270_shL7_shcs_IncRNA:1	97	Gene STX3B	STX3, STX3B1, CLR3	syntaxin 3	NM_006939, NCT22149277.0	1853073_at, 226645_at, 229649_s_at, 229696_at	NP_543026.2, EAX10603.1
Gene:ID:55755	LOC55755	20	2,187,896	2,183,797	5,631	-	1	2_A270_shL97_shcs_IncRNA:1-4694	462	up gene	0	1	64	16	1	2_A270_shL97_shcs_IncRNA:1	16	Gene LOC55755	hypothetical LOC55755		XR_112116, XR_109642, XR_115338	235674_at	
Gene:ID:43641	TGM5	20	2,391,554	2,413,399	91,845	+	1	2_A270_shL97_shcs_IncRNA:1-4695	2310	up gene	0	1	16	16	1	2_A270_shL97_shcs_IncRNA:1	16	Gene TGM5	SCA35, TG7, TGM51, dJ173M14.3, TGM5	transglutaminase 5	NM_139064, NCT03005153	2319563_at	NP_945343.2, EAX10600.1
Gene:ID:626	SNRPB	20	2,642,281	2,651,499	9,218	+	2	2_A270_shL97_shcs_IncRNA:1-4692, 2_A270_shL97_shcs_IncRNA:1-4690	91, 299	up gene, us gene	1	1	22	25	1	2_A270_shL97_shcs_IncRNA:1	25	Gene SNRPB	SNRPB, SmB/SmB', SNRPB1, Sm-B/B', snRNP-B, COD, SmB/B'	small nuclear ribonucleoprotein polypeptides B and B1	NM_003091, NM_198216, NCT23145700.0, NCT23145973.1, NCT23145740.0, NCT23985133.0	206021_at, 210175_s_at	NP_003072.1, NP_937838.1, EAX10386.1, EAX10597.1, EAX10595.1, EAX10599.1
Gene:ID:10011337	SNORD111	20	2,443,998	2,443,893	93	+	2	1_A270_shL7_shcs_IncRNA:1-3460, 2_A270_shL97_shcs_IncRNA:1-4690	17715, -7907	upstream, downstream	1	1	22	25	1	2_A270_shL97_shcs_IncRNA:1	25	Gene SNORD111B	SNORD111B	small nucleolar RNA, C/D box 111B	NR_003664		
Gene:ID:9775	ZNF343	20	2,462,463	2,489,776	27,313	-	2	1_A270_shL7_shcs_IncRNA:1-3470, 2_A270_shL97_shcs_IncRNA:1-4697	306, 176	up gene, us gene	1	1	10	13	1	1_A270_shL7_shcs_IncRNA:1	13	Gene ZNF343	dJ736F18.3, MGC33590, ZNF343, MGC103715, PLZF362	zinc finger protein 343	NM_024329, NCT22145876.1, NCT22155750.0	207296_at, 227686_at	NP_077031.4, EAX10594.1, EAX10595.1
Gene:ID:5326	NOP56	20	2,633,254	2,639,030	5,785	+	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4696	166, 11516	up gene, downstream	0	1	15	23.5	2	2_A270_shL97_shcs_IncRNA:1	24	Gene NOP56	NOL5A, NOP56	NOP56 ribonucleoprotein homolog (yeast)	NM_006392, NP_027700, NCT19850535.1, NCT23146306.0, NCT23149270.0, NCT23955203.0, NCT23981249.0, NCT23985...	200874_s_at, 200875_s_at	NP_006383.2, EAX10596.1, EAX10564.1, EAX10565.1, EAX10567.1, EAX10565.1, EAX10569.1
Gene:ID:9730213	MIR1292	20	2,633,423	2,633,488	65	+	1	2_A270_shL97_shcs_IncRNA:1-4696	17	up gene	0	1	14	24	1	2_A270_shL97_shcs_IncRNA:1	24	Gene MIR1292	MIRN1292, hsa-mir-1292, MIR1292	microRNA 1292	NR_031692		
Gene:ID:92213	SNORD110	20	2,634,856	2,634,912	74	+	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4696	1416, 8974	upstream, downstream	0	1	19	23.5	2	2_A270_shL97_shcs_IncRNA:1	24	Gene SNORD110	SNORD110, HBII-85	small nucleolar RNA, C/D box 110	NR_003076		
Gene:ID:77621	SNORA51	20	2,639,713	2,639,844	131	+	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4696	2273, 8119	upstream, downstream	0	1	15	23.5	2	2_A270_shL97_shcs_IncRNA:1	24	Gene SNORA51	SNORA51, ACA51	small nucleolar RNA, H/ACA box 51	NR_002981		
Gene:ID:22201	SNORD66	20	2,636,743	2,636,828	85	+	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4696	4303, 6589	upstream, downstream	0	1	15	23.5	2	2_A270_shL97_shcs_IncRNA:1	24	Gene SNORD66	U66, SNORD66	small nucleolar RNA, C/D box 66	NR_003292		
Gene:ID:6763	SNORD96	20	2,637,270	2,637,340	70	+	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4696	4830, 7362	upstream, downstream	0	1	15	23.5	2	2_A270_shL97_shcs_IncRNA:1	24	Gene SNORD96	RNU96, U96, SNO96 D96	small nucleolar RNA, C/D box 96	NR_027739		
Gene:ID:6742	SNORD97	20	2,637,583	2,637,696	71	+	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4696	4145, 7247	upstream, downstream	0	1	15	23.5	2	2_A270_shL97_shcs_IncRNA:1	24	Gene SNORD97	RNU97, SNORD97, U97	small nucleolar RNA, C/D box 97	NR_027738		
Gene:ID:420	IDH3B	20	2,639,041	2,648,843	9,802	-	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4699	1403, 11	downstream, up gene	0	1	15	23.5	2	2_A270_shL97_shcs_IncRNA:1	24	Gene IDH3B	IDH3B, IHDHB, FLJ11043, MGC9493, RP46	isocitrate dehydrogenase 3 (NAD+) beta	NM_174855, NM_174856, NM_006899, NCT19850483.1, NCT19975948.1, NCT19975949.1, NCT23985133.0, NCT23985212.0, NCT23985...	201500_at, 210014_s_at, 210015_s_at	NP_777280.1, NP_777281.1, NP_006890.2, EAX10578.1, EAX10579.1, EAX10581.1, EAX10583.1, EAX10582.1, EAX10583.1
Gene:ID:4601	VPS16	20	2,631,373	2,647,376	26,003	+	1	1_A270_shL7_shcs_IncRNA:1-3471	30147	downstream	1	0	20	12	1	1_A270_shL7_shcs_IncRNA:1	20	Gene VPS16	VPS16, hVPS16	vacuolar protein sorting 16 homolog (S. cerevisiae)	NM_022575, NM_080413	203459_s_at, 219216_at, 240316_at	NP_072097.2, NP_536338.1
Gene:ID:7586	PTPRA	20	2,644,641	3,019,318	174,674	+	1	1_A270_shL7_shcs_IncRNA:1-3471	4679	up gene	1	0	20	12	1	1_A270_shL7_shcs_IncRNA:1	20	Gene PTPRA	KPTPA, PTPRL2, HLPK, PTPRA, HEPTP, HPTPA, R-PTP-alpha, LKP, HPTPalpha, PTPA	protein tyrosine phosphatase, receptor type, A	NM_080840, NM_002836, NM_080841	213793_s_at, 213795_s_at, 233776_at, 236018_at	NP_3430031, NP_002827.1, NP_543031.1
Gene:ID:520	OXT	20	3,052,266	3,053,162	896	+	2	1_A270_shL7_shcs_IncRNA:1-3472, 2_A270_shL97_shcs_IncRNA:1-4697	-2376, -2376	upstream, downstream	1	1	22	24	1	2_A270_shL97_shcs_IncRNA:1	24	Gene OXT	MGC126592, OT-NPI, OXT, MGC126590, OT	oxytocin, prepropeptide	NM_000915, NCT03057133	207570_s_at	NP_000909.1, EAX10553.1
Gene:ID:5555	UBOX5	20	3,055,219	3,140,540	52,321	-	1	1_A270_shL7_shcs_IncRNA:1-3473	60	up gene	1	0	23	21	1	1_A270_shL7_shcs_IncRNA:1	25	Gene UBOX5	RNF37, UBOX5, UBCETIPS, UIPS, KIAA0061	U-box domain containing 5	NM_014668, NM_199415	204599_at, 231594_s_at	NP_0015631, NP_955347.1
Gene:ID:6452	FASTKD5	20	3,127,165	3,140,532	13,367	-	1	1_A270_shL7_shcs_IncRNA:1-3473	52	up gene	1	0	23	21	1	1_A270_shL7_shcs_IncRNA:1	25	Gene FASTKD5	FLJ39293, FLJ13199, FASTKD5, LOC151307	FAST kinase domains 5	NM_025126	219016_at	NP_0665961
Gene:ID:782	PoSA/P1	20	3,140,272	3,149,207	8,936	-	3	2_A270_shL97_shcs_IncRNA:1-4697, 2_A270_shL97_shcs_IncRNA:1-4697, 2_A270_shL97_shcs_IncRNA:1-4697	6727, -5239, 5492	downstream, up gene, upstream	1	1	27.5	21.5	2	1_A270_shL7_shcs_IncRNA:1	30	Gene PoSA/P1	KIAA0552	PoSA/P1 protein	NM_014731, NCT22145857.0, NCT23985453.0, NCT26166.0	206457_at	NP_055565.1, EAX10565.1, EAX10566.1, EAX10567.1
Gene:ID:3998	SLC4A11	20	3,206,663	3,219,857	11,824	-	2	2_A270_shL97_shcs_IncRNA:1-4697, 2_A270_shL97_shcs_IncRNA:1-4697	15, -241	up gene, upstream	1	1	21	23	1	2_A270_shL97_shcs_IncRNA:1	23	Gene SLC4A11	SLC4A11, FECD4, CDPD1, NABC1, BTR1, MGC126419, CHED2, CDPD, EIEN46.2, MGC126418	solute carrier family 4, sodium borate transporter, member 11	NM_001174089, NM_001174090, NM_032034, NCT19591810.1, NCT23146849.0, NCT23146591.0, NCT23985072.0, NCT26162.0	223765_at, 233593_s_at	NP_001167560.1, NP_001167561.1, NP_114622.1, EAX10535.1, EAX10537.1, EAX10539.1, EAX10536.1, EAX10538.1
Gene:ID:9443	C20orf194	20	3,229,848	3,368,255	138,307	-	2	2_A270_shL97_shcs_IncRNA:1-4697, 2_A270_shL97_shcs_IncRNA:1-4697	166353, 168127	downstream, downstream	1	1	21	23	1	2_A270_shL97_shcs_IncRNA:1	23	Gene C20orf194	C20orf194, MGC117489, MGC141663, DKFZp434N061	chromosome 20 open reading frame 194	NM_001009954	235825_at, 236607_at	NP_001009954.1
Gene:ID:455	ATRN	20	3,451,665	3,631,769	180,104	+	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4693	-65, 47	upstream, us gene	1	1	17	25	1	2_A270_shL97_shcs_IncRNA:1	25	Gene ATRN	MGC126756, KIAA0585, ATRN, MGC4, DPPT-L	attractin	NM_139321, NM_139322, NCT22155540.0, NCT22155596.0, NCT23946.2	215552_s_at, 215717_at	NP_6475371, NP_6475381, EAX10530.1, EAX10531.1, EAX10532.1
Gene:ID:100391791	LOC10039179107610	20	3,490,642	3,464,337	3,695	+	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4693	4642, 6930	upstream, upstream	1	1	17	25	1	2_A270_shL97_shcs_IncRNA:1	25	Gene LOC100391761	hypothetical protein LOC100391761	hypothetical protein LOC100391761	NM_001319813, NM_002115894, XM_003112874		XP_003119861.1, XP_003115832.1, XP_003119322.1
Gene:ID:9478	CENPB	20	3,764,695	3,767,337	2,638	-	1	2_A270_shL97_shcs_IncRNA:1-4694	4239	upstream	0	1	12	16	1	2_A270_shL97_shcs_IncRNA:1	16	Gene CENPB	CENPB		NM_001810, NCT03005.3	212427_at	NP_001801.1, EAX10502.1
Gene:ID:9484	CDC20B	20	3,776,601	3,766,762	10,361	-	2	2_A270_shL97_shcs_IncRNA:1-4697, 2_A270_shL97_shcs_IncRNA:1-4694	18100, 175	downstream, up gene	1	1	16.5	21	2	2_A270_shL97_shcs_IncRNA:1	26	Gene CDC20B	CDC20B		NM_054358, NM_021872, NM_021873	201653_s_at	NP_0043491, NP_066568.1, NP_066569.1
Gene:ID:5317	C20orf29	20	3,801,203	3,805,934	4,731	+	3	2_A270_shL97_shcs_IncRNA:1-4697, 2_A270_shL97_shcs_IncRN A:1-4697, 2_A270_shL97_shcs_IncRNA:1-4694	4702, 181, 173	upstream, us gene, nt gene	1	1	23.5	23	2	2_A270_shL97_shcs_IncRNA:1	26	Gene C20orf29	FLJ11160, C20orf29	chromosome 20 open reading frame 29	NM_018347, NCT22155231.1, NCT22155234.1, NCT22155276.1, NCT22155277.1	1559252_a_at, 219706_at	NP_0608171, EAX10556.1, EAX10453.1, EAX10456.1, EAX10455.1
Gene:ID:7506	MAVS	20	3,827,689	3,836,762	29,213	+	2	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4677	481, 119	upstream, us gene	0	1	12	16	2	2_A270_shL97_shcs_IncRNA:1	16	Gene MAVS	FLJ21862, FLJ35031, FLJ35306, KIAA1271, DKFZp686M0515, IPS-1, MGC32260, CARDIF, VISA, MAVS, DKFZp547C224, FLJ21908, FLJ27462, IPS1	mitochondrial antiviral signaling protein	NM_020746, NCT22142298.0, NCT30982.1	1554493_at, 231629_at	NP_0629472, EAX10551.1, EAX10452.1
Gene:ID:9025	PAIP2	20	3,899,499	3,904,902	33,016	+	1	2_A270_shL97_shcs_IncRNA:1-4678	336	up gene	0	1	10	21	1	2_A270_shL97_shcs_IncRNA:1	21	Gene PAIP2	HEB, PAIAI, C20orf45, PAIAB2, HNRP, MGC19053, FLJ17232, NIBA1	polyadenylate binding protein 2	NM_138928, NM_024990, NM_138940	218509_at, 226735_s_at, 226965_s_at, 226966_at, 231192_at, 235576_at	NP_7099022, NP_079238.2, NP_709934.1
Gene:ID:621	PRNP	20	4,696,797	4,682,234	15,437	-	1	2_A270_shL97_shcs_IncRNA:1-4693	-2665	upstream	0	1	10	19	1	2_A270_shL97_shcs_IncRNA:1	19	Gene PRNP	PrPC, PrP27-30C, CJD, PRNP, CD230, PrP, MGC26979, PrP27-30, GSS, PRIP, PRNI	prion protein	NM_000311, NM_183079, NM_001080121, NM_001080122, NM_001080123, NCT19842852.1, NCT22983719.0	1558199_s_at, 201303_s_at, 201304_at	NP_0003021, NP_898902.1, NP_001073590.1, NP_001073591.1, NP_001073592.1, EAX10451.1, EAX10450.1, EAX10449.1
Gene:ID:9056	C20orf30	20	5,090,464	5,093,733	13,249	-	3	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4694, 2_A270_shL97_shcs_IncRNA:1-4691	-59, 21, -6747	upstream, us gene, upstream	1	1	16.5	27	2	2_A270_shL97_shcs_IncRNA:1	32	Gene C20orf30	HSPC274, dJ1116H23.2.1, C20orf30	chromosome 20 open reading frame 30	NM_014165, NM_001009823, NM_001009824, NM_001009825, NCT22154509.0, NCT22154509.0, NCT22154110.0, NCT22154111.0, NCT23985749.0, NCT23985750.0, NCT23985750.0	225477_s_at, 224564_at	NP_0548642, NP_001009823.1, NP_001009824.1, NP_001009825.1, EAX10426.1, EAX10427.1, EAX10431.1, EAX10432.1, EAX10433.1, EAX10434.1, EAX10435.1
Gene:ID:111	PCNA	20	5,095,599	5,107,266	11,668	-	3	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4695	15476, 13596, 8766	downstream, downstream, us gene	1	1	16.5	27	2	2_A270_shL97_shcs_IncRNA:1	32	Gene PCNA	MGC8367, PCNA	proliferating cell nuclear antigen	NM_002592, NM_182649, NCT19812850.1, NCT23154004.0, NCT30982.1	201202_at	NP_0025831, NP_8722961, EAX10435.1, EAX10429.1, EAX10430.1
Gene:ID:9302733	PCNAAS	20	5,100,232	5,100,615	383	+	3	2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4695	4640, 9520, 248	upstream, upstream, us gene	1	1	16.5	27	2	2_A270_shL97_shcs_IncRNA:1	32	Gene PCNAAS	PCNA-AS, PCNA-AS1, PCNAAS	PCNA antisense RNA (non-protein coding)	NR_028370		
Gene:ID:760	CDS2	20	5,107,662	5,171,969	64,307	+	1	2_A270_shL97_shcs_IncRNA:1-4695	-7002	upstream	0	1	10	22	1	2_A270_shL97_shcs_IncRNA:1	22	Gene CDS2	CDS2, FLJ38111	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	NM_003818, NCT22155509.0, NCT23985190.0, NCT23985200.0	212662_at, 212664_at, 212665_at	NP_0038091, EAX10424.1, EAX10425.1, EAX10426.1
Gene:ID:49940	C20orf196	20	5,731,043	5,844,358	113,315	+	1	2_A270_shL97_shcs_IncRNA:1-4697	64102	up gene	0	1	16	24	1	2_A270_shL97_shcs_IncRNA:1	24	Gene C20orf196	RP4-764N16.1, C20orf196, FLJ23097	chromosome 20 open reading frame 196	NM_152585, NCT19513361.1, NCT23155003.0	228063_at, 228064_s_at, 240397_s_at, 240398_at	NP_6897172, EAX10411.1, EAX10412.1
Gene:ID:114	CHGB	20	5,891,874	5,906,007	14,033	+	2	1_A270_shL7_shcs_IncRNA:1-3464, 2_A270_shL97_shcs_IncRNA:1-4699	314, 282	up gene, us gene	1	1	33	66	1	2_A270_shL97_shcs_IncRNA:1	66	Gene CHGB	SCG1, CHGB	chromogranin B (secretogranin 1)	NM_001819, NCT26364.3	204390_at	NP_001810.2, EAX10410.1
Gene:ID:1655	TRMT6	20	5,916,696	5,931,173	12,667	-	1	1_A270_shL7_shcs_IncRNA:1-3463	133	up gene	1	0	14	14	1	1_A270_shL7_shcs_IncRNA:1	14	Gene TRMT6	CGI-69, Gcd10p, MGC5629, GCD10, TRMT6	tRNA methyltransferase 6 homolog (S. cerevisiae)	NM_019339, NCT19616931.1, NCT30772.2	223765_s_at, 231870_s_at	NP_0703212, EAX10407.1, EAX10408.1
Gene:ID:4515	MCM6	20	5,931,298	5,979,833	48,535	+	1	1_A270_shL7_shcs_IncRNA:1-3465	-256	upstream	0	1	14	14	1	1_A270_shL7_shcs_IncRNA:1	14	Gene MCM6	KIF5, MGC116322, MCM6, MGC116323	mini-chromosome maintenance complex component 6	NM_182932, NM_032485, NCT22141661.0, NCT23955212.0, NCT30772.2	224320_s_at, 233560_s_at	NP_079541, NP_115870.2, EAX10403.1, EAX10404.1, EAX10405.1
Gene:ID:9612	PERMT1	20	6,055,662	6,104,161	48,499	-	1	2_A270_shL97_shcs_IncRNA:1-4699	843	up gene	0	1	15	16	1	2_A270_shL97_shcs_IncRNA:1	16	Gene PERMT1	UNC112A, C20orf82, FLJ23323, FLJ25116, URP1, KIND1, PERMT1, DTGCL2	keratinocyte terminally differentiation-associated protein 1 (Drosophila)	NM_017671, NCT19513355.1, NCT22141022.0, NCT23985359.0, NCT23985377.0	1557334_at, 219796_at, 229549_at, 231479_at, 244236_at	NP_0600141, EAX10262.1, EAX10263.1, EAX10264.1, EAX10265.1
Gene:ID:332	PLCB4	20	6,549,701	6,961,463	411,762	+	1	1_A270_shL7_shcs_IncRNA:1-3463	167	up gene	1	0	16	14	1	1_A270_shL7_shcs_IncRNA:1	14	Gene PLCB4	PLCB4, PI-PLC, PLC4	phospholipase C, beta 4	NM_000933, NM_182797, NM_001172648, NCT19513361.1, NCT22141260.0, NCT22141320.0, NCT22141322.0, NCT22141324.0, NCT23941...	203563_at, 203564_s_at, 240128_at	NP_0009242, NP_5770482, NP_001166117.1, EAX10363.1, EAX10364.1, EAX10370.1, EAX10364.1, EAX10366.1, EAX10367.1, EAX10369.1
Gene:ID:9301200126	LOC10013012685	20	10,004,490	10,200,151	193,691	+	7	1_A270_shL7_shcs_IncRNA:1-3464, 1_A270_shL7_shcs_IncRN A:1-3464, 1_A270_shL7_shcs_IncRNA:1-3464, 1_A270_shL7_shcs_IncRNA:1-3466, 2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4699, 2_A270_shL97_shcs_IncRNA:1-4690, 2_A270_shL97_shcs_IncRNA:1-4697	19993, 126231, 105, 179255, 159591, 1335, -105	up gene, us gene, upstream, us gene, nt gene, upstream	1	1	23.5	24.5	3	2_A270_shL97_shcs_IncRNA:1	27	Gene LOC100131206			SK_112133, XR_109646, XR_115343		
Gene:ID:9826	ANKRD6	20	10,018,697	10,037,407	21,710	+	3	1_A270_shL7_shcs_IncRNA:1-3464, 1_A270_shL7_shcs_IncRNA:1-3464, 2_A270_shL97_shcs_IncRNA:1-4695, 2_A270_shL97_shcs_IncRNA:1-4695	23291, 5199, 23503	downstream, us gene, downstream	1	1	20.5	17.5	2	1_A270_shL7_shcs_IncRNA:1	20	Gene ANKRD6	FLJ21669, ANKRD6, dJ839H4.6	ankyrin repeat domain 6	NM_022068, NM_198766, NCT19851357.1	220133_s_at, 222931_s_at	NP_0713763, NP_942092.1, EAX10335.1
Gene:ID:616	SNAP23	20	10,199,077	10,268,663	68,586	+	3	1_A270_shL7_shcs_IncRNA:1-3466, 2_A270_shL97_shcs_IncRNA:1-4696, 2_A270_shL97_shcs_IncRNA:1-4696	779, -691, 779	up gene, upstream, us gene	1	1	30	38.5	2	2_A270_shL97_shcs_IncRNA:1	57	Gene SNAP23	FLJ23079, SNAP-23, RVC-4, dJ1065P16.2, RVC6, SNAP, bA416M4.2, SNAP23, SEC9	synaptosomal-associated protein, 23kDa	NM_003581, NM_130811, NCT19850851.1, NCT19916929.1, NCT19916953.1, NCT23958520.0, NCT23963193.0, NCT23985940.0, NCT23985410.0, NCT24660.3	1569629_at, 202507_s_at, 202508_s_at	NP_0035722, NP_570838.1, EAX10346.1, EAX10347.1, EAX10350.1, EAX10352.1, EAX10348.1, EAX10348.1, EAX10351.1, EAX10353.1
Gene:ID:4193	MKKS	20	10,355,832	10,414,866	59,034	-	2	2_A270_shL97_shcs_IncRNA:1-4697, 2_A270_shL97_shcs_IncRNA:1-4692	-174, 80	upstream, us gene	1	1	28	27	1	2_A270_shL97_shcs_IncRNA:1	27	Gene MKKS	KMS, MKS, HMCS, MKKS, BBS6	McKusick-Kaufman syndrome	NM_018646, NM_170754, NCT19851358.1, NCT23958402.0, NCT31461.3	218126_at, 222530_s_at	NP_0611396, NP_7407941, EAX10345.1, EAX10344.1, EAX10343.1
Gene:ID:26710	C20orf64	20	10,415,851	10,604,027	188,076	+	3	1_A270_shL7_shcs_IncRNA:1-3467, 1_A270_shL7_shcs_IncRNA:1-3467, 1_A270_shL7_shcs_IncRNA:1-3466, 2_A270_shL97_shcs_IncRNA:1-4692	411, 16213.1, 1135	upstream, us gene, upstream	1	1	16.5	19.5	2	2_A270_shL97_shcs_IncRNA:1	27	Gene C20orf64	BA354M13.1, BA204H22.1, dJ1098E15.2	chromosome 20 open reading frame 64	NM_001009906, NCT21482.2	236390_at	NP_1009896.1, EAX10342.1
Gene:ID:182	JAG1	20	10,616,332	10,654,694	38,362	-	1	2_A270_shL97_shcs_IncRNA:1-4692	-262	upstream	0	1	15	16	1	2_A270_shL97_shcs_IncRNA:1	16	Gene JAG1	MGC102546, CD339, HJ1, JAGL1, AHS, AGS, JAG1, AHD	jagged 1 (Alagille syndrome)	NM_000214, NCT26399.3	209097_s_at, 209098_s_at, 209099_s_at, 216266_s_at, 239624_s_at, 241183_s_at	NP_0002051, EAX10341.1
Gene:ID:1378	ESF1	20	10,694,969	10,765,832	70,863	-	1	2_A270_shL97_shcs_IncRNA:1-4696	-100	upstream	0	1	15	20	1	2_A270_shL97_shcs_IncRNA:1	20	Gene ESF1	C20orf6, ESF1, bA526K24.1, ABTAP, HSCARG, FLJ20366	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	NM_016949, NCT23155652.0	218559_s_at, 221783_s_at	NP_0577332, EAX10313.1
Gene:ID:9133	C20orf7	20	10,769,972	10,769,267	33,295	+	1	2_A270_shL97_shcs_IncRNA:1-4696	-48	upstream	0	1	15	20	1	2_A270_shL97_shcs_IncRNA:1	20	Gene C20orf7	MGC90272, FLJ23324, bA526K24.2, dJ1042G8.1, C20orf7	chromosome 20 open reading frame 7	NM_024120, NM_001039375, NR_026277	222694_s_at, 227186_s_at	NP_0772252, NP_001034964.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:140733	MACROD2	20	13,976,146	16,033,842	2,057,696	+	3	1_A375_pNL7_minus_lncRNA::1::3504, 2_A375_pNL97_plus_lncRNA::1::5009, 1_A375_pNL7_minus_lncRNA::1::3505	293614, 869742, 1704142	in gene, in gene, in gene	1	1	18	18.67	3	1_A375_pNL7_minus_lncRNA::1	28	Gene MACROD2	dJ631M13.5, MACROD2, C20orf133	MACRO domain containing 2	NM_001033087, NM_080676	1553564_at, 1561677_at, 1563209_a_at, 235278_at	NP_001028259.1, NP_542407.2
GeneID:55614	KIF16B	20	16,252,749	16,554,078	301,329	-	2	1_A375_pNL7_minus_lncRNA::1::3506, 2_A375_pNL97_plus_lncRNA::1::5011	-1442, 14	upstream, in gene	1	1	18.5	17	2	2_A375_pNL97_plus_lncRNA::1	22	Gene KIF16B	KIF16B, C20orf23, KISC20ORF, SNX23	kinesin family member 16B	NM_024704, hCT1951347.1, hCT2313765.0, hCT2313766.0, hCT2313769.0	219570_at, 232083_at	NP_078980.3, EAX10287.1, EAX10288.1, EAX10289.1, EAX10290.1
GeneID:6629	SNRPB2	20	16,710,609	16,722,417	11,808	+	2	1_A375_pNL7_minus_lncRNA::1::3507, 2_A375_pNL97_plus_lncRNA::1::5012	-17, 15	upstream, in gene	1	1	60	76	1	2_A375_pNL97_plus_lncRNA::1	76	Gene SNRPB2	MGC24807, MGC45309, Msl1, SNRPB2	small nuclear ribonucleoprotein polypeptide B	NM_198220, NM_003092, hCT1961785.1, hCT2313836.0, hCT29395.2	1561965_at, 202505_at	NP_937863.1, NP_003083.1, EAX10284.1, EAX10285.1, EAX10286.1
GeneID:5126	PCSK2	20	17,207,631	17,465,223	257,592	+	5	1_A375_pNL7_minus_lncRNA::1::3508, 1_A375_pNL7_minus_lncRNA::1::3509, 2_A375_pNL97_plus_lncRNA::1::5016, 2_A375_pNL97_plus_lncRNA::1::5017, 2_A375_pNL97_plus_lncRNA::1::5018	753, 190417, -335, 669, 190417	in gene, in gene, upstream, in gene, in gene	1	1	20.33	25.67	3	2_A375_pNL97_plus_lncRNA::1	31	Gene PCSK2	PC2, NEC2, NEC-2, PCSK2, SPC2	proprotein convertase subtilisin/kexin type 2	NM_002594, hCT2313869.0, hCT2359566.0, hCT30932.3	204869_at, 204870_s_at	NP_002585.2, EAX10279.1, EAX10280.1, EAX10281.1
GeneID:27131	SNX5	20	17,922,244	17,949,490	27,246	-	2	1_A375_pNL7_minus_lncRNA::1::3511, 2_A375_pNL97_plus_lncRNA::1::5021	210, 162	in gene, in gene	1	1	23	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene SNX5	SNX5, FLJ10931	sorting nexin 5	NM_014426, NM_152227, hCT2313915.0, hCT2313917.0, hCT2313918.0, hCT2313920.0, hCT2313922.0, hCT2359494.0	217792_at, 222417_s_at, 223666_at, 229960_s_at, 229961_at, 238433_at	NP_055241.1, NP_689413.1, EAX10263.1, EAX10264.1, EAX10265.1, EAX10268.1, EAX10266.1, EAX10267.1
GeneID:692086	SNORD17	20	17,943,353	17,943,589	236	-	2	1_A375_pNL7_minus_lncRNA::1::3511, 2_A375_pNL97_plus_lncRNA::1::5021	-5691, -5739	upstream, upstream	1	1	23	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene SNORD17	SNORD17, HBI-43	small nucleolar RNA, C/D box 17	NR_003045		
GeneID:92667	C20orf72	20	17,949,762	17,971,761	21,999	+	2	1_A375_pNL7_minus_lncRNA::1::3511, 2_A375_pNL97_plus_lncRNA::1::5021	-482, -434	upstream, upstream	1	1	23	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene C20orf72	C20orf72, FLJ14597, bA504H3.4	chromosome 20 open reading frame 72	NM_052865, hCT1967818.1, hCT2314015.0, hCT29768.3	225690_at	NP_443097.1, EAX10262.1, EAX10260.1, EAX10261.1
GeneID:100303755	PET117	20	18,118,499	18,123,813	5,314	+	2	1_A375_pNL7_minus_lncRNA::1::3512, 2_A375_pNL97_plus_lncRNA::1::5022	-3, -3	upstream, upstream	1	1	44	44	1	1_A375_pNL7_minus_lncRNA::1	44	Gene PET117		cytochrome c oxidase assembly factor-like	NM_001164811		NP_001158283.1
GeneID:57325	CSRP2BP	20	18,122,868	18,169,031	46,163	+	2	1_A375_pNL7_minus_lncRNA::1::3512, 2_A375_pNL97_plus_lncRNA::1::5022	-4372, -4372	upstream, upstream	1	1	44	44	1	1_A375_pNL7_minus_lncRNA::1	44	Gene CSRP2BP	CSRP2BP, PRO1194, CRP2BP, KAT14, dJ717M23.1, MGC15388	CSRP2 binding protein	NR_028402, NM_020536, hCT1823052.1, hCT1827847.3, hCT2359543.0	225432_s_at, 227316_at, 228543_at, 228544_s_at, 233396_s_at	NP_065397.3, EAX10255.1, EAX10254.1, EAX10256.1
GeneID:7692	ZNF133	20	18,269,121	18,297,640	28,519	+	1	2_A375_pNL97_plus_lncRNA::1::5023	-193	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZNF133	pHZ-66, ZNF150, ZNF133, pHZ-13	zinc finger protein 133	NM_003434, NM_001083330, hCT2349558.0, hCT2349559.0, hCT2349560.0, hCT2349561.0, hCT2349562.0	216960_s_at, 37254_at	NP_003425.2, NP_001076799.1, EAX10249.1, EAX10250.1, EAX10251.1, EAX10252.1, EAX10253.1
GeneID:55184	C20orf12	20	18,364,011	18,447,829	83,818	-	3	1_A375_pNL7_minus_lncRNA::1::3513, 1_A375_pNL7_minus_lncRNA::1::3514, 2_A375_pNL97_plus_lncRNA::1::5024	53893, -91, -43	in gene, upstream, upstream	1	1	21	17	2	1_A375_pNL7_minus_lncRNA::1	24	Gene C20orf12	FLJ10600, bA189K21.1, FLJ30692, dJ568F9.2, bA189K21.8, DKFZp781J2425, C20orf12, C20orf64	chromosome 20 open reading frame 12	NM_001099407, hCT12770.3, hCT2313905.0, hCT2313906.0, hCT2313907.0, hCT2359565.0	1554618_s_at, 219951_s_at	NP_001092877.1, EAX10244.1, EAX10242.1, EAX10243.1, EAX10245.1, EAX10246.1
GeneID:10621	POLR3F	20	18,448,033	18,465,287	17,254	+	2	1_A375_pNL7_minus_lncRNA::1::3514, 2_A375_pNL97_plus_lncRNA::1::5024	-113, -161	upstream, upstream	1	1	24	24	1	1_A375_pNL7_minus_lncRNA::1	24	Gene POLR3F	RPC39, POLR3F, RPC6, MGC13517	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	NM_006466, hCT12216.2, hCT2359567.0, hCT2359568.0	205218_at	NP_006457.2, EAX10240.1, EAX10239.1, EAX10241.1
GeneID:100422875	MIR3192	20	18,451,259	18,451,335	76	+	2	1_A375_pNL7_minus_lncRNA::1::3514, 2_A375_pNL97_plus_lncRNA::1::5024	-3339, -3387	upstream, upstream	1	1	24	24	1	1_A375_pNL7_minus_lncRNA::1	24	Gene MIR3192	MIR3192	microRNA 3192	NR_036160		
GeneID:10741	RBBP9	20	18,467,184	18,477,887	10,703	-	1	2_A375_pNL97_plus_lncRNA::1::5025	47	in gene	0	1	8	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RBBP9	RBBP10, RBBP9, BOG, MGC9236	retinoblastoma binding protein 9	NM_006606, hCT12768.3, hCT2313903.0, hCT2359564.0	221439_at, 221440_s_at, 226696_at, 232751_at	NP_006597.2, EAX10236.1, EAX10237.1, EAX10238.1
GeneID:10483	SEC23B	20	18,488,188	18,542,059	53,871	+	2	1_A375_pNL7_minus_lncRNA::1::3515, 2_A375_pNL97_plus_lncRNA::1::5026	196, 228	in gene, in gene	1	1	21	13	1	1_A375_pNL7_minus_lncRNA::1	21	Gene SEC23B	CDAN2, CDA-II, HEMPAS, CDAII, SEC23B	Sec23 homolog B (S. cerevisiae)	NM_006363, NM_032986, NM_032985, NM_001172745, NM_001172746, hCT12766.3, hCT1967765.1, hCT1967766.1, hCT2314030.0, hCT2359563.0	201582_at, 201583_s_at, 210293_s_at	NP_006354.2, NP_116781.1, NP_116780.1, NP_001166216.1, NP_001166217.1, EAX10232.1, EAX10231.1, EAX10233.1, EAX10234.1, EAX10235.1
GeneID:92675	DTD1	20	18,568,556	18,744,561	176,005	+	1	2_A375_pNL97_plus_lncRNA::1::5027	-28	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DTD1	DUEB, MGC41905, DTD1, bA379J5.3, bA555E18.1, C20orf88, MGC119131, pqn-68, HARS2	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	NM_080820, hCT2349563.0, hCT2359553.0	1552718_at, 234107_s_at	NP_543010.3, EAX10227.1, EAX10228.1
GeneID:51126	NAA20	20	19,997,937	20,014,269	16,332	+	2	1_A375_pNL7_minus_lncRNA::1::3517, 2_A375_pNL97_plus_lncRNA::1::5028	15, 15	in gene, in gene	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene NAA20	dJ1002M8.1, NAT3, NAT5, NAA20	N(alpha)-acetyltransferase 20, NatB catalytic subunit	NM_181528, NM_181527, NM_016100, hCT12189.3, hCT1957535.2, hCT2349557.0	223040_at	NP_852669.1, NP_852668.1, NP_057184.1, EAX10213.1, EAX10214.1, EAX10215.1
GeneID:57186	RALGAPA2	20	20,373,411	20,693,266	319,855	-	2	1_A375_pNL7_minus_lncRNA::1::3518, 2_A375_pNL97_plus_lncRNA::1::5030	17138, 17138	in gene, in gene	1	1	25	25	1	1_A375_pNL7_minus_lncRNA::1	25	Gene RALGAPA2	FLJ12619, dJ1049G11, C20orf74, KIAA1272, RALGAPA2, bA287B20.1, AS250, dJ1049G11.4	Ral GTPase activating protein, alpha subunit 2 (catalytic)	NM_020343	1559699_at, 231626_at, 232500_at, 234314_at, 234934_at, 239660_at	NP_065076.2
GeneID:22803	XRN2	20	21,283,942	21,370,463	86,521	+	2	1_A375_pNL7_minus_lncRNA::1::3519, 2_A375_pNL97_plus_lncRNA::1::5031	394, -230	in gene, upstream	1	1	25	15	1	1_A375_pNL7_minus_lncRNA::1	25	Gene XRN2	XRN2		NM_012255, hCT12188.3, hCT2313642.0	223002_s_at, 233878_s_at	NP_036387.2, EAX10187.1, EAX10186.1
GeneID:29107	NXT1	20	23,331,373	23,335,408	4,035	+	3	1_A375_pNL7_minus_lncRNA::1::3521, 2_A375_pNL97_plus_lncRNA::1::5035, 2_A375_pNL97_plus_lncRNA::1::5036	11167, -461, 10995	downstream, upstream, downstream	1	1	20.5	21.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene NXT1	NXT1, MTR2, P15	NTF2-like export factor 1	NM_013248, hCT13460.2	218708_at	NP_037380.1, EAX10163.1
GeneID:100505663	LOC100505663	20	23,337,231	23,338,642	1,411	-	3	1_A375_pNL7_minus_lncRNA::1::3521, 2_A375_pNL97_plus_lncRNA::1::5035, 2_A375_pNL97_plus_lncRNA::1::5036	-3918, 7730, -3726	upstream, downstream, upstream	1	1	20.5	21.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene LOC100505663		hypothetical LOC100505663	XR_109654, XR_115351		
GeneID:64412	GZF1	20	23,345,021	23,353,683	8,662	+	2	1_A375_pNL7_minus_lncRNA::1::3521, 2_A375_pNL97_plus_lncRNA::1::5036	-2461, -2653	upstream, upstream	1	1	25	23	1	1_A375_pNL7_minus_lncRNA::1	25	Gene GZF1	ZNF336, GZF1, ZBTB23	GDNF-inducible zinc finger protein 1	NM_022482, hCT13462.4, hCT2313400.1, hCT2313401.1	225584_s_at, 234055_s_at	NP_071927.1, EAX10160.1, EAX10159.1, EAX10161.1
GeneID:79953	TMEM90B	20	24,449,835	24,647,167	197,332	+	1	2_A375_pNL97_plus_lncRNA::1::5037	165909	in gene	0	1	8	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TMEM90B	C20orf39, TMEM90B, IFITMD5, FLJ14220	transmembrane protein 90B	NM_024893, hCT8749.2	219310_at	NP_079169.1, EAX10117.1
GeneID:57136	C20orf3	20	24,943,580	24,973,425	29,845	-	2	1_A375_pNL7_minus_lncRNA::1::3522, 2_A375_pNL97_plus_lncRNA::1::5038	113, 209	in gene, in gene	1	1	24	16	1	1_A375_pNL7_minus_lncRNA::1	24	Gene C20orf3	C20orf3, BSCv, APMAP	chromosome 20 open reading frame 3	NM_020531, hCT2359577.0, hCT8687.3	206656_s_at	NP_065392.1, EAX10114.1, EAX10113.1
GeneID:84532	ACSS1	20	24,986,873	25,039,616	52,743	-	2	1_A375_pNL7_minus_lncRNA::1::3523, 2_A375_pNL97_plus_lncRNA::1::5039	3606, 3792	in gene, in gene	1	1	35	32	1	1_A375_pNL7_minus_lncRNA::1	35	Gene ACSS1	AceCS2L, MGC33843, ACSS1, ACAS2L, FLJ45659	acyl-CoA synthetase short-chain family member 1	NM_032501, hCT2313252.0, hCT2313254.0, hCT2359531.0, hCT2359532.0, hCT2359533.0, hCT8681.2	224882_at, 234463_at, 234464_s_at, 234801_s_at, 235724_at	NP_115890.2, EAX10106.1, EAX10108.1, EAX10109.1, EAX10110.1, EAX10111.1, EAX10107.1
GeneID:955	ENTPD6	20	25,176,339	25,207,360	31,021	+	3	1_A375_pNL7_minus_lncRNA::1::3525, 2_A375_pNL97_plus_lncRNA::1::5041, 2_A375_pNL97_plus_lncRNA::1::5042	27597, -211, 27597	in gene, upstream, in gene	1	1	16	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene ENTPD6	FLJ36711, ENTPD6, NTPDase-6, DKFZp781G2277, DKFZp781K21102, CD39L2, IL6ST2, dJ738P15.3, IL-6SAG	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	NM_001247, NM_001114089, hCT1966537.1, hCT2313367.0, hCT2359529.0, hCT2359530.0, hCT8679.3	201704_at, 234946_at	NP_001238.2, NP_001107561.1, EAX10095.1, EAX10096.1, EAX10097.1, EAX10098.1, EAX10099.1
GeneID:5834	PYGB	20	25,228,706	25,278,648	49,942	+	1	2_A375_pNL97_plus_lncRNA::1::5043	-10146	upstream	0	1	17	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene PYGB	MGC9213, PYGB	phosphorylase, glycogen; brain	NM_002862, hCT1961632.1, hCT1965536.1, hCT8676.3	201481_s_at, 243238_at	NP_002853.2, EAX10092.1, EAX10091.1, EAX10093.1
GeneID:26090	ABHD12	20	25,275,379	25,371,477	96,098	-	1	2_A375_pNL97_plus_lncRNA::1::5044	60951	in gene	0	1	10	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ABHD12	PHARC, ABHD12, C20orf22, dJ965G21.2, BEM46L2, ABHD12A, DKFZp434P106	abhydrolase domain containing 12	NM_001042472, NM_015600, hCT1965538.1, hCT1965539.1, hCT8665.4	224742_at, 228123_s_at, 228124_at	NP_001035937.1, NP_056415.1, EAX10088.1, EAX10089.1, EAX10090.1
GeneID:9837	GINS1	20	25,388,323	25,429,191	40,868	+	1	2_A375_pNL97_plus_lncRNA::1::5045	29	in gene	0	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene GINS1	PSF1, KIAA0186, GINS1	GINS complex subunit 1 (Psf1 homolog)	NM_021067, hCT8686.3	206102_at	NP_066545.3, EAX10087.1
GeneID:22981	NINL	20	25,433,337	25,566,153	132,816	-	1	1_A375_pNL7_minus_lncRNA::1::3526	68249	in gene	1	0	26	24	1	1_A375_pNL7_minus_lncRNA::1	26	Gene NINL	NINL, KIAA0980, dJ691N24.1, FLJ11792, NLP	ninein-like	NM_025176, hCT1958886.1, hCT1958887.1, hCT2313340.0, hCT2359572.0, hCT8663.3	207705_s_at	NP_079452.3, EAX10085.1, EAX10082.1, EAX10083.1, EAX10084.1, EAX10086.1
GeneID:140838	NANP	20	25,593,571	25,604,648	11,077	-	2	1_A375_pNL7_minus_lncRNA::1::3527, 2_A375_pNL97_plus_lncRNA::1::5046	-184, 232	upstream, in gene	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene NANP	MGC26833, C20orf147, NANP, HDHD4, dJ694B14.3	N-acetylneuraminic acid phosphatase	NM_152667, hCT8664.3	228073_at	NP_689880.1, EAX10081.1
GeneID:26152	ZNF337	20	25,654,851	25,677,469	22,618	-	2	1_A375_pNL7_minus_lncRNA::1::3528, 2_A375_pNL97_plus_lncRNA::1::5047	-35, 253	upstream, in gene	1	1	27	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ZNF337	ZNF337	zinc finger protein 337	NM_015655, hCT2313334.0, hCT8680.3	214760_at, 37860_at	NP_056470.1, EAX10077.1, EAX10078.1
GeneID:81502	HM13	20	30,102,241	30,157,370	55,129	+	3	1_A375_pNL7_minus_lncRNA::1::3529, 1_A375_pNL7_minus_lncRNA::1::3530, 2_A375_pNL97_plus_lncRNA::1::5048	95, 58367, 223	in gene, downstream, in gene	1	1	22.5	15	2	1_A375_pNL7_minus_lncRNA::1	24	Gene HM13	IMPAS, PSENL3, IMP1, HM13, PSL3, MSTP086, SPP, IMPAS-1, dJ324O17.1, H13	histocompatibility (minor) 13	NM_178580, NM_178581, NM_178582, NM_030789, hCT1964352.1, hCT2314096.0, hCT2355485.0, hCT28625.3	1557148_at, 1558561_at, 224615_x_at, 232209_x_at	NP_848695.1, NP_848696.1, NP_110416.1, NP_848697.1, EAW76435.1, EAW76436.1, EAW76437.1, EAW76438.1
GeneID:598	BCL2L1	20	30,252,261	30,310,656	58,395	-	2	1_A375_pNL7_minus_lncRNA::1::3531, 2_A375_pNL97_plus_lncRNA::1::5050	-640, -864	upstream, upstream	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene BCL2L1	bcl-xL, BCL2L, BCLXL, BCL2L1, BCLX, Bcl-X, BCL-XL/S, DKFZp781P2092, BCLXS, bcl-xS	BCL2-like 1	NM_001191, NM_138578, hCT2313721.0, hCT2313722.0, hCT2313723.0, hCT2313724.0, hCT2313725.0, hCT30057.3	206665_s_at, 212312_at, 215037_s_at, 231228_at	NP_001182.1, NP_612815.1, EAW76424.1, EAW76425.1, EAW76426.1, EAW76427.1, EAW76428.1, EAW76429.1
GeneID:22974	TPX2	20	30,326,904	30,389,603	62,699	+	2	1_A375_pNL7_minus_lncRNA::1::3532, 2_A375_pNL97_plus_lncRNA::1::5051	264, 136	in gene, in gene	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene TPX2	REPP86, C20orf2, GD:C20orf1, HCTP4, TPX2, DIL2, DIL-2, FLS353, HCA519, p100, C20orf1	TPX2, microtubule-associated, homolog (Xenopus laevis)	NM_012112, hCT1951803.1, hCT2314059.0, hCT2314060.0, hCT2355570.0, hCT30067.3	210052_s_at	NP_036244.2, EAW76419.1, EAW76418.1, EAW76420.1, EAW76421.1, EAW76422.1
GeneID:128853	DUSP15	20	30,448,870	30,458,479	9,609	-	1	2_A375_pNL97_plus_lncRNA::1::5052	207	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene DUSP15	DUSP15, FLJ40111, VHY	dual specificity phosphatase 15	NM_080611, NM_177991, NM_001012644, hCT2313705.0, hCT30064.2	230402_at	NP_542178.2, NP_817130.1, NP_001012662.1, EAW76409.1, EAW76410.1
GeneID:164395	TTLL9	20	30,458,505	30,530,858	72,353	+	1	2_A375_pNL97_plus_lncRNA::1::5052	-233	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TTLL9	C20orf125, TTLL9, MGC120486, dJ310O13.1, MGC120487	tubulin tyrosine ligase-like family, member 9	NM_001008409, hCT2314067.0, hCT2314068.0, hCT2314069.0, hCT2314070.0, hCT2355537.0, hCT2355538.0, hCT2355539.0, hCT30059.3	232357_at, 234336_s_at, 234337_at	NP_001008409.1, EAW76405.1, EAW76402.1, EAW76404.1, EAW76407.1, EAW76408.1, EAW76401.1, EAW76403.1, EAW76406.1
GeneID:343702	XKR7	20	30,555,805	30,586,256	30,451	+	2	1_A375_pNL7_minus_lncRNA::1::3533, 2_A375_pNL97_plus_lncRNA::1::5053	611, 579	in gene, in gene	1	1	56	71	1	2_A375_pNL97_plus_lncRNA::1	71	Gene XKR7	XKR7, C20orf159, dJ310O13.4	XK, Kell blood group complex subunit-related family, member 7	NM_001011718, hCT30063.3		NP_001011718.1, EAW76398.1
GeneID:3055	HCK	20	30,639,991	30,689,659	49,668	+	1	1_A375_pNL7_minus_lncRNA::1::3534	57449	downstream	1	0	22	11	1	1_A375_pNL7_minus_lncRNA::1	22	Gene HCK	JTK9, HCK	hemopoietic cell kinase	NM_002110, NM_001172129, NM_001172130, NM_001172131, NM_001172132, NM_001172133, hCT2314079.0, hCT2314080.0, hCT30056.3	208018_s_at	NP_002101.2, NP_001165600.1, NP_001165601.1, NP_001165602.1, NP_001165603.1, NP_001165604.1, EAW76392.1, EAW76393.1, EAW76394.1
GeneID:9777	TM9SF4	20	30,697,309	30,755,061	57,752	+	1	1_A375_pNL7_minus_lncRNA::1::3534	131	in gene	1	0	22	11	1	1_A375_pNL7_minus_lncRNA::1	22	Gene TM9SF4	KIAA0255, TM9SF4, dJ836N17.2	transmembrane 9 superfamily protein member 4	NM_014742, hCT2314082.0, hCT2355490.0, hCT30055.3	212194_s_at, 212196_s_at	NP_055557.2, EAW76391.1, EAW76389.1, EAW76390.1
GeneID:5326	PLAGL2	20	30,780,307	30,795,546	15,239	-	1	1_A375_pNL7_minus_lncRNA::1::3535	-134	upstream	1	0	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene PLAGL2	ZNF900, FLJ23283, PLAGL2	pleiomorphic adenoma gene-like 2	NM_002657, hCT2313686.0, hCT30054.3	202924_s_at, 202925_s_at	NP_002648.1, EAW76386.1, EAW76387.1
GeneID:23509	POFUT1	20	30,795,696	30,826,467	30,771	+	1	1_A375_pNL7_minus_lncRNA::1::3535	-16	upstream	1	0	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene POFUT1	O-FUT, FUT12, O-Fuc-T, O-FucT-1, MGC2482, POFUT1, KIAA0180	protein O-fucosyltransferase 1	NM_015352, NM_172236, hCT2314084.0, hCT2314086.0, hCT30065.2	210433_at, 212349_at	NP_056167.1, NP_758436.1, EAW76383.1, EAW76384.1, EAW76385.1
GeneID:100506402	LOC100506402	20	30,922,055	30,939,859	17,804	-	2	1_A375_pNL7_minus_lncRNA::1::3536, 2_A375_pNL97_plus_lncRNA::1::5054	-6029, -6253	upstream, upstream	1	1	23	21	1	1_A375_pNL7_minus_lncRNA::1	23	Gene LOC100506402		hypothetical LOC100506402	XR_112137, XR_109631, XR_115354		
GeneID:171023	ASXL1	20	30,946,147	31,027,122	80,975	+	2	1_A375_pNL7_minus_lncRNA::1::3536, 2_A375_pNL97_plus_lncRNA::1::5054	-259, -35	upstream, upstream	1	1	23	21	1	1_A375_pNL7_minus_lncRNA::1	23	Gene ASXL1	MGC71111, KIAA0978, ASXL1, MGC117280	additional sex combs like 1 (Drosophila)	NM_015338, NM_001164603, hCT2314198.0, hCT2355545.0, hCT2355546.0, hCT30062.3	212234_at, 212237_at, 212238_at, 244519_at	NP_056153.2, NP_001158075.1, EAW76377.1, EAW76378.1, EAW76379.1, EAW76380.1
GeneID:140688	C20orf112	20	31,030,862	31,071,288	40,426	-	3	1_A375_pNL7_minus_lncRNA::1::3537, 2_A375_pNL97_plus_lncRNA::1::5055, 2_A375_pNL97_plus_lncRNA::1::5056	19632, 19640, 744	in gene, in gene, in gene	1	1	12	21.5	2	2_A375_pNL97_plus_lncRNA::1	26	Gene C20orf112	DKFZp566G1424, dJ1184F4.4, C20orf113, dJ1184F4.2, C20orf112	chromosome 20 open reading frame 112	NM_080616, hCT2313940.0, hCT2313941.0, hCT2313942.0, hCT2313943.0, hCT2313944.0, hCT2313946.0, hCT2313947.0	225224_at, 230954_at, 230955_s_at, 234031_at, 241830_at	NP_542183.2, EAW76373.1, EAW76367.1, EAW76369.1, EAW76370.1, EAW76372.1, EAW76368.1, EAW76371.1
GeneID:100506597	LOC100506597	20	31,073,767	31,124,451	50,684	-	1	2_A375_pNL97_plus_lncRNA::1::5056	53907	downstream	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100506597		hypothetical protein LOC100506597	XM_003118802, XM_003120989		XP_003118850.1, XP_003121037.1
GeneID:128861	C20orf71	20	31,805,135	31,815,559	10,424	+	1	2_A375_pNL97_plus_lncRNA::1::5058	-7407	upstream	0	1	17	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene C20orf71	SPLUNC3, C20orf71, MGC44525	chromosome 20 open reading frame 71	NM_178466, NM_001042439, hCT2355565.0, hCT2355566.0, hCT2355567.0, hCT29146.2	240359_at	NP_848561.2, NP_001035904.1, EAW76330.1, EAW76331.1, EAW76332.1, EAW76333.1
GeneID:51654	CDK5RAP1	20	31,946,645	31,989,337	42,692	-	2	1_A375_pNL7_minus_lncRNA::1::3539, 2_A375_pNL97_plus_lncRNA::1::5059	-55, -39	upstream, upstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CDK5RAP1	CGI-05, CDK5RAP1.3, HSPC167, CDK5RAP1, C20orf34, C42, CDK5RAP1.4	CDK5 regulatory subunit associated protein 1	NM_016408, NM_016082, hCT1951309.1, hCT1963211.1, hCT1963212.1, hCT1963213.1, hCT2313954.0, hCT2313964.0, hCT2355529.0, hCT29138.2	218315_s_at	NP_057492.2, NP_057166.3, EAW76318.1, EAW76321.1, EAW76323.1, EAW76324.1, EAW76319.1, EAW76320.1, EAW76322.1, EAW76325.1
GeneID:6640	SNTA1	20	31,995,763	32,031,698	35,935	-	2	1_A375_pNL7_minus_lncRNA::1::3539, 2_A375_pNL97_plus_lncRNA::1::5059	42306, 42322	downstream, downstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNTA1	SNTA1, dJ1187J4.5, TACIP1, SNT1, LQT12	syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)	NM_003098, hCT2313950.0, hCT2355523.0, hCT2355524.0, hCT29137.3	203516_at	NP_003089.1, EAW76317.1, EAW76314.1, EAW76315.1, EAW76316.1
GeneID:63941	NECAB3	20	32,244,893	32,262,264	17,371	-	2	1_A375_pNL7_minus_lncRNA::1::3540, 2_A375_pNL97_plus_lncRNA::1::5060	6840, 6776	in gene, in gene	1	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene NECAB3	APBA2BP, NECAB3, NIP1, XB51, EFCBP3, SYTIP2, dJ63M2.5, dJ63M2.4, STIP3	N-terminal EF-hand calcium binding protein 3	NM_031232, NM_031231, hCT1951310.1, hCT2313233.0, hCT2313234.0, hCT2313236.0, hCT2313237.0, hCT2313238.0, hCT2313239.0, hCT29140.2	210720_s_at, 223954_x_at	NP_112509.3, NP_112508.3, EAW76301.1, EAW76303.1, EAW76307.1, EAW76308.1, EAW76302.1, EAW76304.1, EAW76305.1, EAW76306.1
GeneID:128864	C20orf144	20	32,250,120	32,251,720	1,600	+	2	1_A375_pNL7_minus_lncRNA::1::3540, 2_A375_pNL97_plus_lncRNA::1::5060	5304, 5368	downstream, downstream	1	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C20orf144	dJ63M2.6, C20orf144	chromosome 20 open reading frame 144	NM_080825, hCT29148.3	231522_at	NP_543015.1, EAW76310.1
GeneID:170487	C20orf134	20	32,254,304	32,256,331	2,027	+	2	1_A375_pNL7_minus_lncRNA::1::3540, 2_A375_pNL97_plus_lncRNA::1::5060	1120, 1184	in gene, in gene	1	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C20orf134	dJ63M2.2, C20orf134	chromosome 20 open reading frame 134	NM_001024675, hCT1971309.1	232619_at	NP_001019846.1, EAW76309.1
GeneID:1869	E2F1	20	32,263,292	32,274,210	10,918	-	2	1_A375_pNL7_minus_lncRNA::1::3540, 2_A375_pNL97_plus_lncRNA::1::5060	18786, 18722	downstream, downstream	1	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene E2F1	E2F-1, RBAP1, RBBP3, RBP3, E2F1	E2F transcription factor 1	NM_005225, hCT2313231.0, hCT29147.3	2028_s_at, 204947_at	NP_005216.1, EAW76299.1, EAW76300.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:11264	PXMP4	20	32,290,550	32,308,136	17,586	-	1	2_A375_pNL97_plus_lncRNA::1::5061	104	in gene	0	1	12	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene PXMP4	PXMP4, PMP24	peroxisomal membrane protein 4, 24kDa	NM_183397, NM_007238, hCT2313228.0	219428_s_at, 224210_s_at, 236746_at	NP_899634.1, NP_009169.3, EAW76298.1
GeneID:128866	CHMP4B	20	32,399,110	32,442,173	43,063	+	1	2_A375_pNL97_plus_lncRNA::1::5062	-134	upstream	0	1	27	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene CHMP4B	Shax1, dJ553F4.4, C20orf178, SNF7-2, CHMP4A, Vps32-2, SNF7, CHMP4B, CTPP3, VPS32B	chromatin modifying protein 4B	NM_176812, hCT2313657.0, hCT29145.2	225119_at, 225498_at	NP_789782.1, EAW76294.1, EAW76293.1
GeneID:100505490	LOC100505490	20	32,580,294	32,582,162	1,868	-	1	2_A375_pNL97_plus_lncRNA::1::5064	530	in gene	0	1	20	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100505490		hypothetical LOC100505490	XR_112135, XR_112136, XR_109594, XR_109595, XR_115355, XR_115356		
GeneID:22913	RALY	20	32,581,732	32,668,067	86,335	+	1	2_A375_pNL97_plus_lncRNA::1::5064	-100	upstream	0	1	20	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene RALY	P542, RALY, MGC117312, HNRPCL2	RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse))	NM_016732, NM_007367, hCT1951308.1, hCT1963197.1, hCT2313660.0, hCT2313666.0, hCT29134.3	201271_s_at	NP_057951.1, NP_031393.2, EAW76287.1, EAW76288.1, EAW76289.1, EAW76291.1, EAW76290.1
GeneID:8894	EIF2S2	20	32,676,115	32,700,085	23,970	-	1	2_A375_pNL97_plus_lncRNA::1::5065	229	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene EIF2S2	DKFZp686L18198, MGC8508, EIF2S2, EIF2beta, EIF2B, EIF2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	NM_003908, hCT2313218.0, hCT2313219.0, hCT2313220.0	208725_at, 208726_s_at	NP_003899.2, EAW76286.1, EAW76284.1, EAW76285.1
GeneID:191	AHCY	20	32,868,071	32,899,608	31,537	-	3	1_A375_pNL7_minus_lncRNA::1::3542, 2_A375_pNL97_plus_lncRNA::1::5066, 2_A375_pNL97_plus_lncRNA::1::5067	8408, 8440, -2904	in gene, in gene, upstream	1	1	44.5	55.5	2	2_A375_pNL97_plus_lncRNA::1	88	Gene AHCY	SAHH, AHCY	adenosylhomocysteinase	NM_001161766, NM_000687, hCT2313210.0, hCT2355416.0, hCT29752.3	200903_s_at	NP_001155238.1, NP_000678.1, EAW76279.1, EAW76280.1, EAW76281.1
GeneID:83737	ITCH	20	32,951,062	33,099,197	148,135	+	2	2_A375_pNL97_plus_lncRNA::1::5068, 2_A375_pNL97_plus_lncRNA::1::5069	42, 152490	in gene, downstream	0	1	20	21	2	2_A375_pNL97_plus_lncRNA::1	21	Gene ITCH	ITCH, NAPP1, AIP4, dJ468O1.1, AIF4	itchy E3 ubiquitin protein ligase homolog (mouse)	NM_031483, hCT2313674.0, hCT2313675.0, hCT2313676.0, hCT2313677.0, hCT2313678.0, hCT2313679.0, hCT2355520.0	208743_s_at, 208744_x_at, 217094_s_at, 235057_at, 236235_at, 239101_at	NP_113671.3, EAW76277.1, EAW76272.1, EAW76273.1, EAW76275.1, EAW76278.1, EAW76274.1, EAW76276.1
GeneID:83658	DYNLRB1	20	33,104,204	33,128,762	24,558	+	3	1_A375_pNL7_minus_lncRNA::1::3543, 2_A375_pNL97_plus_lncRNA::1::5069, 2_A375_pNL97_plus_lncRNA::1::5070	9716, -652, 9652	in gene, upstream, in gene	1	1	22.5	26	2	2_A375_pNL97_plus_lncRNA::1	31	Gene DYNLRB1	DNLC2A, BITH, ROBLD1, DYNLRB1, DNCL2A, BLP	dynein, light chain, roadblock-type 1	NM_014183	1554568_at, 1555611_at, 1555612_at, 217917_s_at, 217918_at	NP_054902.1
GeneID:84557	MAP1LC3A	20	33,134,692	33,148,149	13,457	+	1	2_A375_pNL97_plus_lncRNA::1::5071	11628	in gene	0	1	21	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene MAP1LC3A	LC3A, MAP1ALC3, MAP1LC3A, LC3, ATG8E, MAP1BLC3	microtubule-associated protein 1 light chain 3 alpha	NM_181509, NM_032514, hCT1957436.1, hCT2315919.0, hCT2315921.0, hCT29754.3	224378_x_at, 227219_x_at, 232011_s_at	NP_852610.1, NP_115903.1, EAW76263.1, EAW76264.1, EAW76265.1, EAW76266.1
GeneID:128869	PIGU	20	33,148,346	33,265,089	116,743	-	2	2_A375_pNL97_plus_lncRNA::1::5071, 2_A375_pNL97_plus_lncRNA::1::5072	116769, 193	downstream, in gene	0	1	19.5	29	2	2_A375_pNL97_plus_lncRNA::1	31	Gene PIGU	CDC91L1, PIGU, GAB1, MGC40420	phosphatidylinositol glycan anchor biosynthesis, class U	NM_080476, hCT2313822.0, hCT2313823.0, hCT2355591.0, hCT29744.2	225903_at	NP_536724.1, EAW76259.1, EAW76260.1, EAW76261.1, EAW76262.1
GeneID:2686	GGT7	20	33,432,523	33,460,661	28,138	-	1	2_A375_pNL97_plus_lncRNA::1::5073	-107	upstream	0	1	12	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene GGT7	GGTL5, D20S101, dJ18C9.2, GGT4, GGTL3, GGT7	gamma-glutamyltransferase 7	NM_178026, hCT2313812.0, hCT2313813.1, hCT2313815.0, hCT29747.3	226469_s_at, 226470_at, 226471_at	NP_821158.2, EAW76249.1, EAW76250.1, EAW76251.1, EAW76252.1
GeneID:55902	ACSS2	20	33,462,766	33,515,769	53,003	+	3	1_A375_pNL7_minus_lncRNA::1::3544, 2_A375_pNL97_plus_lncRNA::1::5073, 2_A375_pNL97_plus_lncRNA::1::5074	33031, -1998, 32754	in gene, upstream, in gene	1	1	14.5	20.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene ACSS2	ACECS, ACSA, dJ1161H23.1, ACSS2, ACS, DKFZp762G026, ACAS2	acyl-CoA synthetase short-chain family member 2	NM_018677, NM_001076552, NR_028046, hCT1957435.1, hCT2315928.0, hCT2315929.0, hCT2315930.0, hCT2315932.0, hCT2355413.0, hCT29750.3	234312_s_at	NP_061147.1, NP_001070020.2, EAW76242.1, EAW76243.1, EAW76245.1, EAW76246.1, EAW76244.1, EAW76247.1, EAW76248.1
GeneID:2937	GSS	20	33,516,236	33,543,601	27,365	-	2	1_A375_pNL7_minus_lncRNA::1::3545, 2_A375_pNL97_plus_lncRNA::1::5075	257, 230	in gene, in gene	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene GSS	GSS, GSHS, MGC14098	glutathione synthetase	NM_000178, hCT1963235.1, hCT2355556.0, hCT29740.3	201415_at, 211630_s_at	NP_000169.1, EAW76239.1, EAW76240.1, EAW76241.1
GeneID:57644	MYH7B	20	33,543,704	33,590,240	46,536	+	2	1_A375_pNL7_minus_lncRNA::1::3545, 2_A375_pNL97_plus_lncRNA::1::5075	-360, -333	upstream, upstream	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene MYH7B	MGC96940, MGC96928, MHC14, MYH7B, MYH14	myosin, heavy chain 7B, cardiac muscle, beta	NM_020884, hCT1640780.2, hCT2315934.0, hCT2315935.0	215795_at, 233949_s_at	NP_065935.2, EAW76236.1, EAW76237.1, EAW76238.1
GeneID:26133	TRPC4AP	20	33,590,207	33,680,618	90,411	-	2	1_A375_pNL7_minus_lncRNA::1::3546, 2_A375_pNL97_plus_lncRNA::1::5076	178, 10	in gene, in gene	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TRPC4AP	TRUSS, C20orf188, TRPC4AP, TRRP4AP	transient receptor potential cation channel, subfamily C, member 4 associated protein	NM_015638, NM_199368, hCT2313804.0, hCT2313805.0, hCT2313806.0, hCT2313807.0, hCT2355409.0, hCT2355410.0, hCT29748.3	212059_s_at	NP_056453.1, NP_955400.1, EAW76229.1, EAW76230.1, EAW76234.1, EAW76235.1, EAW76231.1, EAW76232.1, EAW76233.1
GeneID:10893	MMP24	20	33,814,539	33,864,804	50,265	+	3	1_A375_pNL7_minus_lncRNA::1::3547, 2_A375_pNL97_plus_lncRNA::1::5078, 2_A375_pNL97_plus_lncRNA::1::5079	501, 597, 58149	in gene, in gene, downstream	1	1	23.5	27	2	2_A375_pNL97_plus_lncRNA::1	33	Gene MMP24	MT5-MMP, MMP24, MMP25, MT-MMP5	matrix metallopeptidase 24 (membrane-inserted)	NM_006690, hCT29449.3	208387_s_at, 213171_s_at, 221953_s_at, 49679_s_at	NP_006681.1, EAW76222.1
GeneID:3692	EIF6	20	33,866,725	33,872,594	5,869	-	1	2_A375_pNL97_plus_lncRNA::1::5079	-94	upstream	0	1	23	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene EIF6	CAB, EIF3A, EIF6, ITGB4BP, gcn, b(2)gcn, 2, b, p27BBP	eukaryotic translation initiation factor 6	NM_181466, NM_181468, NM_002212, hCT1963218.1, hCT1963223.1, hCT29451.3	210213_s_at	NP_852131.1, NP_852133.1, NP_002203.1, EAW76219.1, EAW76220.1, EAW76221.1
GeneID:128876	FAM83C	20	33,873,534	33,880,225	6,691	-	1	2_A375_pNL97_plus_lncRNA::1::5079	7537	downstream	0	1	23	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene FAM83C	C20orf128, dJ614O4.7, FAM83C, MGC142043	family with sequence similarity 83, member C	NM_178468, hCT1644893.1	1556793_a_at, 1563805_a_at	NP_848563.1, EAW76218.1
GeneID:55245	UQCC	20	33,890,369	33,999,945	109,576	-	3	1_A375_pNL7_minus_lncRNA::1::3548, 2_A375_pNL97_plus_lncRNA::1::5080, 2_A375_pNL97_plus_lncRNA::1::5081	106217, 106313, 103753	in gene, in gene, in gene	1	1	19.5	22.5	2	1_A375_pNL7_minus_lncRNA::1	29	Gene UQCC	UQCC, CBP3, MGC104353, MGC141902, C20orf44, BFZB	ubiquinol-cytochrome c reductase complex chaperone	NM_001184977, NM_018244, NM_199487, hCT1963224.1, hCT1963226.1, hCT1965803.1, hCT2355593.0, hCT2355594.0, hCT2355595.0, hCT2355596.0, hCT29456.3	217935_s_at, 222470_s_at, 229672_at, 244795_at	NP_001171906.1, NP_060714.3, NP_955781.2, EAW76210.1, EAW76211.1, EAW76217.1, EAW76212.1, EAW76213.1, EAW76214.1, EAW76215.1, EAW76216.1
GeneID:100302125	MIR1289-1	20	34,041,776	34,041,919	143	-	1	1_A375_pNL7_minus_lncRNA::1::3549	-1516	upstream	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene MIR1289-1	hsa-mir-1289-1, MIRN1289-1, MIR1289-1	microRNA 1289-1	NR_031620		
GeneID:11190	CEP250	20	34,043,223	34,099,803	56,580	+	1	1_A375_pNL7_minus_lncRNA::1::3549	212	in gene	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene CEP250	CNAP1, C-NAP1, MGC88542, CEP250, CEP2	centrosomal protein 250kDa	NM_007186, hCT2315944.0, hCT2315945.0, hCT2315946.0, hCT2315947.0	209495_at, 210894_s_at	NP_009117.2, EAW76204.1, EAW76205.1, EAW76206.1, EAW76207.1
GeneID:6676	SPAG4	20	34,203,809	34,208,965	5,156	+	2	1_A375_pNL7_minus_lncRNA::1::3550, 2_A375_pNL97_plus_lncRNA::1::5082	79, -49	in gene, upstream	1	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SPAG4	SPAG4, CT127, SUN4	sperm associated antigen 4	NM_003116, hCT29462.3	219888_at	NP_003107.1, EAW76191.1
GeneID:8904	CPNE1	20	34,213,966	34,252,848	38,882	-	2	1_A375_pNL7_minus_lncRNA::1::3550, 2_A375_pNL97_plus_lncRNA::1::5082	48960, 49088	downstream, downstream	1	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CPNE1	MGC1142, COPN1, CPN1, CPNE1	copine I	NM_152925, NM_152926, NM_152927, NM_152928, NM_152929, NM_152930, NM_152931, NM_003915	206918_s_at	NP_690902.1, NP_690903.1, NP_690904.1, NP_690905.1, NP_690906.1, NP_690907.1, NP_690908.1, NP_003906.2
GeneID:9054	NFS1	20	34,256,611	34,287,274	30,663	-	1	2_A375_pNL97_plus_lncRNA::1::5083	-86	upstream	0	1	22	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene NFS1	NFS1, NIFS, IscS, HUSSY-08	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	NM_021100, hCT2313487.0, hCT2355448.0, hCT29459.3	1554321_a_at, 218455_at	NP_066923.3, EAW76170.1, EAW76171.1, EAW76172.1
GeneID:140823	ROMO1	20	34,287,232	34,288,902	1,670	+	1	2_A375_pNL97_plus_lncRNA::1::5083	128	in gene	0	1	22	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ROMO1	MTGMP, ROMO1, MGC111180, bA353C18.2, C20orf52	reactive oxygen species modulator 1	NM_080748, hCT1824728.1, hCT1969213.1	224972_at	NP_542786.1, EAW76168.1, EAW76169.1
GeneID:9584	RBM39	20	34,291,531	34,330,193	38,662	-	2	2_A375_pNL97_plus_lncRNA::1::5083, 2_A375_pNL97_plus_lncRNA::1::5084	42833, -79	downstream, upstream	0	1	21.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene RBM39	DKFZp781C0423, RBM39, CAPERalpha, FLJ44170, CAPER, CC1.3, HCC1, fSAP59, RNPC2	RNA binding motif protein 39	NM_184234, NM_004902, hCT2313483.0, hCT2313485.0, hCT2313486.0, hCT2355452.0, hCT2355453.0, hCT2355454.0, hCT2355455.0, hCT2355456.0, hCT29460.3	207941_s_at, 208720_s_at, 236355_at, 236357_at	NP_909122.1, NP_004893.1, EAW76159.1, EAW76160.1, EAW76163.1, EAW76166.1, EAW76161.1, EAW76162.1, EAW76164.1, EAW76165.1, EAW76167.1
GeneID:51230	PHF20	20	34,359,923	34,538,288	178,365	+	3	1_A375_pNL7_minus_lncRNA::1::3551, 2_A375_pNL97_plus_lncRNA::1::5085, 2_A375_pNL97_plus_lncRNA::1::5086	182541, -2675, 182701	downstream, upstream, downstream	1	1	26.5	26	2	1_A375_pNL7_minus_lncRNA::1	31	Gene PHF20	NZF, PHF20, GLEA2, FLJ33479, HCA58, TZP, C20orf104	PHD finger protein 20	NM_016436, hCT1951313.1, hCT2315106.0, hCT2315107.0, hCT2315108.0, hCT2315109.0, hCT2315113.0	1569906_s_at, 209567_s_at, 209422_at, 209423_s_at	NP_057520.2, EAW76153.1, EAW76154.1, EAW76155.1, EAW76156.1, EAW76158.1, EAW76157.1
GeneID:51282	SCAND1	20	34,541,546	34,542,428	882	-	2	1_A375_pNL7_minus_lncRNA::1::3551, 2_A375_pNL97_plus_lncRNA::1::5086	-36, -196	upstream, upstream	1	1	31	27	1	1_A375_pNL7_minus_lncRNA::1	31	Gene SCAND1	SCAND1, RAZ1, SDP1	SCAN domain containing 1	NM_016558, NM_033630, hCT2313460.0, hCT2313461.0, hCT29461.3	218206_x_at, 231059_x_at, 232652_x_at	NP_057642.1, NP_361012.1, EAW76150.1, EAW76151.1, EAW76152.1
GeneID:647979	LOC647979	20	34,633,540	34,638,882	5,342	-	2	1_A375_pNL7_minus_lncRNA::1::3552, 2_A375_pNL97_plus_lncRNA::1::5087	130, 98	in gene, in gene	1	1	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC647979		hypothetical LOC647979	NR_027451	1558028_x_at, 224597_at	
GeneID:2036	EPB41L1	20	34,700,348	34,820,721	120,373	+	2	1_A375_pNL7_minus_lncRNA::1::3553, 2_A375_pNL97_plus_lncRNA::1::5090	123716, 123988	downstream, downstream	1	1	19	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene EPB41L1	DKFZp686H17242, MGC11072, EPB41L1, 4.1N, KIAA0338	erythrocyte membrane protein band 4.1-like 1	NM_012156, NM_177996, hCT1824725.2, hCT2315116.0, hCT2315118.0	212336_at, 212339_at, 222066_at, 230269_at	NP_036288.2, NP_818932.1, EAW76144.1, EAW76145.1, EAW76146.1
GeneID:25980	C20orf4	20	34,824,447	34,844,853	20,406	+	2	1_A375_pNL7_minus_lncRNA::1::3553, 2_A375_pNL97_plus_lncRNA::1::5090	-383, -111	upstream, upstream	1	1	19	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene C20orf4	CGI-23, C20orf4, bA234K24.2, DKFZp564N1363	chromosome 20 open reading frame 4	NM_015511, hCT2315119.0, hCT2315121.0, hCT28359.3	218089_at	NP_056326.2, EAW76143.1, EAW76141.1, EAW76142.1
GeneID:22839	DLGAP4	20	34,995,444	35,157,040	161,596	+	2	1_A375_pNL7_minus_lncRNA::1::3555, 2_A375_pNL97_plus_lncRNA::1::5092	17164, 17132	in gene, in gene	1	1	44	60	1	2_A375_pNL97_plus_lncRNA::1	60	Gene DLGAP4	KIAA0964, DLGAP4, DLP4, DAP4, RP5-977B1.6, MGC131862, SAPAP4, FLJ20588	discs, large (Drosophila) homolog-associated protein 4	NM_183006, NM_014902, NM_001042486, hCT2315123.0, hCT2315124.0, hCT2315125.0, hCT2315126.0, hCT2315127.0, hCT2315128.0	1556701_at, 1557394_at, 202570_s_at, 202571_s_at, 202572_s_at, 233056_x_at	NP_892118.1, NP_055717.2, NP_001035951.1, EAW76135.1, EAW76139.1, EAW76140.1, EAW76136.1, EAW76137.1, EAW76138.1
GeneID:55969	C20orf24	20	35,234,167	35,240,960	6,793	+	2	1_A375_pNL7_minus_lncRNA::1::3556, 2_A375_pNL97_plus_lncRNA::1::5093	-215, -103	upstream, upstream	1	1	26	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene C20orf24	RIP5, PNAS-11, C20orf24	chromosome 20 open reading frame 24	NM_018840, NM_199483, NR_026562, hCT1962412.1, hCT1962413.1, hCT22971.3, hCT2315141.0, hCT2355450.0, hCT2355451.0	217835_x_at, 223880_x_at, 224376_s_at	NP_061328.1, NP_955777.1, EAW76120.1, EAW76121.1, EAW76122.1, EAW76125.1, EAW76123.1, EAW76124.1
GeneID:84174	SLA2	20	35,240,922	35,274,558	33,636	-	2	1_A375_pNL7_minus_lncRNA::1::3556, 2_A375_pNL97_plus_lncRNA::1::5093	40606, 40494	downstream, downstream	1	1	26	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene SLA2	SLA2, MGC49845, SLAP2, FLJ21992, C20orf156, SLAP-2	Src-like-adaptor 2	NM_032214, NM_175077, hCT22972.2, hCT2313469.1, hCT2313470.1, hCT2313471.1	1555688_s_at, 232234_at	NP_115590.1, NP_778252.1, EAW76116.1, EAW76117.1, EAW76118.1, EAW76119.1
GeneID:5933	RBL1	20	35,626,178	35,724,410	98,232	-	2	1_A375_pNL7_minus_lncRNA::1::3557, 2_A375_pNL97_plus_lncRNA::1::5094	-6, 122	upstream, in gene	1	1	18	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene RBL1	RBL1, PRB1, MGC40006, p107, CP107	retinoblastoma-like 1 (p107)	NM_183404, NM_002895, hCT1824110.2, hCT2355575.0	1555003_at, 1555004_a_at, 1559307_s_at, 205296_at	NP_899662.1, NP_002886.2, EAW76088.1, EAW76089.1
GeneID:140699	C20orf132	20	35,729,629	35,807,974	78,345	-	4	1_A375_pNL7_minus_lncRNA::1::3557, 1_A375_pNL7_minus_lncRNA::1::3558, 2_A375_pNL97_plus_lncRNA::1::5094, 2_A375_pNL97_plus_lncRNA::1::5095	83558, 486, 83686, 486	downstream, in gene, downstream, in gene	1	1	56.5	60	2	2_A375_pNL97_plus_lncRNA::1	96	Gene C20orf132	DKFZp434N0426, FLJ36113, C20orf131, dJ621N11.4, C20orf132, dJ621N11.3	chromosome 20 open reading frame 132	NM_213631, NM_213632, NM_152503	232185_at, 236618_at	NP_998796.1, NP_998797.1, NP_689716.4
GeneID:6185	RPN2	20	35,807,456	35,870,026	62,570	+	2	1_A375_pNL7_minus_lncRNA::1::3558, 2_A375_pNL97_plus_lncRNA::1::5095	32, 32	in gene, in gene	1	1	95	96	1	2_A375_pNL97_plus_lncRNA::1	96	Gene RPN2	RPN2, SWP1, RPN-II, RIBIIR, RPNII	ribophorin II	NM_002951, NM_001135771, hCT2313839.0, hCT2313840.0, hCT2313841.0, hCT2355505.0, hCT28372.2	208689_s_at, 213399_x_at, 213491_x_at	NP_002942.2, NP_001129243.1, EAW76073.1, EAW76074.1, EAW76076.1, EAW76077.1, EAW76075.1
GeneID:63905	MANBAL	20	35,918,051	35,945,663	27,612	+	1	2_A375_pNL97_plus_lncRNA::1::5096	45	in gene	0	1	21	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene MANBAL	MANBAL		NM_022077, NM_001003897, hCT1963216.1, hCT2313843.0, hCT2313844.0, hCT29286.2	224689_at	NP_071360.1, NP_001003897.1, EAW76068.1, EAW76069.1, EAW76070.1, EAW76071.1
GeneID:6714	SRC	20	35,973,088	36,033,821	60,733	+	1	2_A375_pNL97_plus_lncRNA::1::5097	-1024	upstream	0	1	24	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene SRC	SRC1, p60-Src, SRC, c-SRC, ASV	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	NM_005417, NM_198291, hCT2313846.0, hCT2313847.0, hCT2313848.0, hCT2313849.0, hCT2355463.0, hCT29285.3	1558210_at, 1558211_s_at, 1565080_at, 1565082_x_at, 213324_at, 221281_at, 221284_s_at	NP_005408.1, NP_938033.1, EAW76062.1, EAW76063.1, EAW76065.1, EAW76067.1, EAW76064.1, EAW76066.1
GeneID:10904	BLCAP	20	36,145,619	36,156,333	10,514	-	2	1_A375_pNL7_minus_lncRNA::1::3559, 2_A375_pNL97_plus_lncRNA::1::5098	-179, -147	upstream, upstream	1	1	82	88	1	2_A375_pNL97_plus_lncRNA::1	88	Gene BLCAP	BLCAP, BC10	bladder cancer associated protein	NM_006698, NM_001167820, NM_001167821, NM_001167822, NM_001167823, hCT29278.3	201032_at	NP_006689.1, NP_001161292.1, NP_001161293.1, NP_001161294.1, NP_001161295.1, EAW76056.1
GeneID:4826	NNAT	20	36,149,607	36,152,092	2,485	+	2	1_A375_pNL7_minus_lncRNA::1::3559, 2_A375_pNL97_plus_lncRNA::1::5098	6905, 6873	downstream, downstream	1	1	82	88	1	2_A375_pNL97_plus_lncRNA::1	88	Gene NNAT	Peg5, MGC1439, NNAT	neuronatin	NM_005386, NM_181689, hCT1963215.1, hCT2313857.0, hCT2313860.0, hCT2355447.0, hCT29279.2	204239_s_at	NP_005377.1, NP_859017.1, EAW76057.1, EAW76058.1, EAW76059.1, EAW76061.1, EAW76060.1
GeneID:128434	VSTM2L	20	36,531,499	36,573,752	42,253	+	4	1_A375_pNL7_minus_lncRNA::1::3562, 1_A375_pNL7_minus_lncRNA::1::3563, 2_A375_pNL97_plus_lncRNA::1::5101, 2_A375_pNL97_plus_lncRNA::1::5102	-1547, -923, -1515, -1003	upstream, upstream, upstream, upstream	1	1	26.5	22.5	2	1_A375_pNL7_minus_lncRNA::1	31	Gene VSTM2L	VSTM2L, C20orf102, dJ1118M15.2	V-set and transmembrane domain containing 2 like	NM_080607, hCT2314796.0, hCT2314797.0, hCT29269.3	226973_at	NP_542174.1, EAW76053.1, EAW76051.1, EAW76052.1
GeneID:9675	KIAA0406	20	36,611,423	36,661,833	50,410	-	1	2_A375_pNL97_plus_lncRNA::1::5103	41	in gene	0	1	15	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene KIAA0406	KIAA0406, TTI1	Tel2 interacting protein 1 homolog (S. pombe)	NM_014657, hCT2313027.0, hCT2313029.0, hCT2355461.0, hCT29283.2	212698_at	NP_055472.1, EAW76047.1, EAW76048.1, EAW76049.1, EAW76050.1
GeneID:58490	RPRD1B	20	36,661,948	36,720,766	58,818	+	1	2_A375_pNL97_plus_lncRNA::1::5103	-156	upstream	0	1	15	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene RPRD1B	NET60, CREPT, FLJ44520, dJ1057B20.2, C20orf77, RPRD1B, DKFZp434P0735	regulation of nuclear pre-mRNA domain containing 1B	NM_021215, hCT2314799.0, hCT29284.3	225024_at, 230801_at	NP_067038.1, EAW76046.1, EAW76045.1
GeneID:7052	TGM2	20	36,756,863	36,793,700	36,837	-	1	2_A375_pNL97_plus_lncRNA::1::5104	12580	in gene	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TGM2	GNAH, G-ALPHA-h, TG2, TGM2, TGC	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	NM_004613, NM_198951, hCT2313021.0, hCT2313022.0, hCT2313024.0, hCT2313025.0, hCT2313026.0	201042_at, 211003_x_at, 211573_x_at, 216183_at	NP_004604.2, NP_945189.1, EAW76040.1, EAW76041.1, EAW76043.1, EAW76044.1, EAW76042.1
GeneID:388796	LOC388796	20	37,049,239	37,064,018	14,779	-	2	1_A375_pNL7_minus_lncRNA::1::3566, 2_A375_pNL97_plus_lncRNA::1::5105	50, 50	in gene, in gene	1	1	44	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene LOC388796		hypothetical LOC388796	NR_015366, NR_027241	225857_s_at, 65588_at	
GeneID:26776	SNORA71B	20	37,053,843	37,053,978	135	-	2	1_A375_pNL7_minus_lncRNA::1::3566, 2_A375_pNL97_plus_lncRNA::1::5105	-9990, -9990	upstream, upstream	1	1	44	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene SNORA71B	RNU71B, SNORA71B, U71b	small nucleolar RNA, H/ACA box 71B	NR_002910	1568248_x_at, 1568249_at	
GeneID:26777	SNORA71A	20	37,055,949	37,056,086	137	-	2	1_A375_pNL7_minus_lncRNA::1::3566, 2_A375_pNL97_plus_lncRNA::1::5105	-7682, -7682	upstream, upstream	1	1	44	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene SNORA71A	U71a, RNU71A, SNORA71A	small nucleolar RNA, H/ACA box 71A	NR_002911	1565658_at, 1565659_at	
GeneID:677839	SNORA71C	20	37,058,310	37,058,447	137	-	2	1_A375_pNL7_minus_lncRNA::1::3566, 2_A375_pNL97_plus_lncRNA::1::5105	-5521, -5521	upstream, upstream	1	1	44	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene SNORA71C	U71c, SNORA71C	small nucleolar RNA, H/ACA box 71C	NR_003017		
GeneID:677840	SNORA71D	20	37,062,505	37,062,642	137	-	2	1_A375_pNL7_minus_lncRNA::1::3566, 2_A375_pNL97_plus_lncRNA::1::5105	-1326, -1326	upstream, upstream	1	1	44	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene SNORA71D	SNORA71D, U71d	small nucleolar RNA, H/ACA box 71D	NR_003018		
GeneID:128439	SNHG11	20	37,075,297	37,079,564	4,267	+	2	1_A375_pNL7_minus_lncRNA::1::3567, 2_A375_pNL97_plus_lncRNA::1::5106	-33, -33	upstream, upstream	1	1	69	84	1	2_A375_pNL97_plus_lncRNA::1	84	Gene SNHG11	SNHG11, C20orf198, NCRNA00101	small nucleolar RNA host gene 11 (non-protein coding)	NR_003239, hCT2314807.0, hCT2314808.0, hCT2349453.0, hCT2355495.0, hCT2355496.0, hCT2355497.0	226149_at	EAW76027.1, EAW76029.1, EAW76025.1, EAW76026.1, EAW76028.1, EAW76030.1
GeneID:677821	SNORA39	20	37,076,726	37,076,861	135	+	2	1_A375_pNL7_minus_lncRNA::1::3567, 2_A375_pNL97_plus_lncRNA::1::5106	-1462, -1462	upstream, upstream	1	1	69	84	1	2_A375_pNL97_plus_lncRNA::1	84	Gene SNORA39	SNORA39, ACA39	small nucleolar RNA, H/ACA box 39	NR_002972		
GeneID:677837	SNORA60	20	37,078,012	37,078,147	135	+	2	1_A375_pNL7_minus_lncRNA::1::3567, 2_A375_pNL97_plus_lncRNA::1::5106	-2748, -2748	upstream, upstream	1	1	69	84	1	2_A375_pNL97_plus_lncRNA::1	84	Gene SNORA60	ACA60, SNORA60	small nucleolar RNA, H/ACA box 60	NR_002986		
GeneID:343578	C20orf95	20	37,230,577	37,279,295	48,718	+	1	2_A375_pNL97_plus_lncRNA::1::5107	44303	in gene	0	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene C20orf95	dJ1100H13.4, ARHGAP40, C20orf95	Rho GTPase activating protein 40	NM_001164431		NP_001157903.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Internal Transcripts	Internal Dist to 3'-end	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ENSG00000009413	ACTR5	20	37,377,097	37,401,689	23,982	+	2	2_A7S_sNL97_plus_lncRNA:1:3111, 2_A7S_sNL97_plus_lncRNA:1:3112	23,183,169	at gene, ut gene	0	1	16	19.5	2	2_A7S_sNL97_plus_lncRNA:1	20	Gene ACTR5	FLJ12765, ACTR5, hCG1641, Arp5	ARP5 actin-related protein 5 homolog (yeast)	NM_024533, NCT02146612, NCT26302.3	298623_at, 222147_s_at	NP_078531.2; EAW76011.1; EAW76010.1
Gene:ENSG00000166351	PPP1R16B	20	37,434,348	37,531,867	117,519	+	3	1_A7S_sNL97_plus_lncRNA:1:3371, 1_A7S_sNL97_plus_lncRNA:1:3372, 1_A7S_sNL97_plus_lncRNA:1:3113, 2_A7S_sNL97_plus_lncRNA:1:3114, 2_A7S_sNL97_plus_lncRNA:1:3115	64816, 120756, 64816, 91606, 120532	at gene, downstream, at gene, ut gene, downstream	1	1	21.33	22.33	3	2_A7S_sNL97_plus_lncRNA:1	30	Gene PPP1R16B	PPP1R16B, TIMAP, ANKRD4, KIAA0823	protein phosphatase 1, regulatory (inhibitor) subunit 16B	NM_015568, NM_001177235, NCT26300.2	212790_at, 233513_at, 41577_at	NP_056553.1, NP_001166206.1; EAW76039.1
Gene:ENSG00000161610	FAM83D	20	37,544,833	37,581,763	36,748	+	3	1_A7S_sNL97_plus_lncRNA:1:3372, 2_A7S_sNL97_plus_lncRNA:1:3115, 2_A7S_sNL97_plus_lncRNA:1:3116	148,-70, 36993	at gene, upstream, downstream	1	1	20	22	2	2_A7S_sNL97_plus_lncRNA:1	23	Gene FAM83D	C20orf29, FAM83D, dJ616I8B.2, FLJ38341, CHICA	family with sequence similarity 83, member D	NM_030919, NCT26299.3	235607_at	NP_112161.2; EAW76006.1
Gene:ENSG00000009625	DHX35	20	37,590,661	37,668,266	77,385	+	2	2_A7S_sNL97_plus_lncRNA:1:3116, 2_A7S_sNL97_plus_lncRNA:1:3117	132, 77563	upstream, downstream	0	1	17.5	22.5	2	2_A7S_sNL97_plus_lncRNA:1	23	Gene DHX35	DDX35, KIAA0378, C20orf15, DHX35, FLJ22759	DEAH (Asp-Glu-Ala-His) box polypeptide 35	NM_001166509, NM_029231, NR_033905, NCT21263635.0, NCT21126400.0, NCT26301.3	1361132_at, 216579_s_at, 234725_s_at	NP_001777.2; NP_080750.2; EAW76005.1, EAW76006.1, EAW76007.1
Gene:ENSG00000125685	LOC100128585	20	38,609,429	39,654,036	44,610	+	4	1_A7S_sNL97_plus_lncRNA:1:3374, 1_A7S_sNL97_plus_lncRNA:1:3375, 2_A7S_sNL97_plus_lncRNA:1:3120, 2_A7S_sNL97_plus_lncRNA:1:3121	22790, 48046, 24974, 48046	at gene, downstream, at gene, downstream	1	1	16.67	19.67	3	2_A7S_sNL97_plus_lncRNA:1	27	Gene LOC100128585	FLJ13552	hypothetical LOC100128585	XR_112141, XR_109801, XR_115362		
Gene:ENSG00000167513	TOP1	20	39,657,462	39,753,127	95,665	+	3	1_A7S_sNL97_plus_lncRNA:1:3373, 2_A7S_sNL97_plus_lncRNA:1:3120, 2_A7S_sNL97_plus_lncRNA:1:3117	10, 10, 42594	at gene, ut gene, at gene	1	1	17.5	23.5	2	2_A7S_sNL97_plus_lncRNA:1	27	Gene TOP1	TOP1, TOPI	topoisomerase (DNA) I	NM_003286, NCT21126503.0, NCT21126540.0, NCT21126560.0, NCT30946.3	208900_s_at, 208901_s_at	NP_003277.1, EAW76997.1, EAW76984.1, EAW76983.1, EAW76985.1
Gene:ENSG00000095752	ICC 1003 95752	20	39,726,959	39,766,640	39,681	-	1	2_A7S_sNL97_plus_lncRNA:1:3123	-3535	upstream	0	1	20	26	1	2_A7S_sNL97_plus_lncRNA:1	26	Gene LOC100505732		hypothetical LOC100505732	XR_112142, XR_109802, XR_115363		
Gene:ENSG00000133105	PLCG1	20	39,799,161	39,904,287	58,186	+	1	2_A7S_sNL97_plus_lncRNA:1:3122	4015	at gene	0	1	20	26	1	2_A7S_sNL97_plus_lncRNA:1	26	Gene PLCG1	PLCG1, PLC148, NCKAP3, PLC1, PLC-II, PLCgamma1	phospholipase C, gamma 1	NM_182511, NM_002660, NCT23126900.0, NCT21270102.0, NCT23127502.0, NCT21270103.0, NCT23126510.0	202709_at, 216551_x_at	NP_877962.1, NP_002651.2; EAW76993.1, EAW76992.1, EAW76992.1, EAW76990.1
Gene:ENSG00000144431	SFRS6	20	42,086,504	42,092,245	5,741	+	2	1_A7S_sNL97_plus_lncRNA:1:3360, 2_A7S_sNL97_plus_lncRNA:1:3127	56, 40	at gene, ut gene	1	1	20	28	1	2_A7S_sNL97_plus_lncRNA:1	28	Gene SFRS6	SRP96, MSC53485, SFRS6, FLJ30861, SRP55, IBI2	serine/arginine-rich splicing factor 6	NM_006275, NM_033088, NCT15424242, NCT19620997.1, NCT19630701.1, NCT21263503.0	208108_s_at, 208584_s_at	NP_006266.2; EAW76964.1, EAW76965.1, EAW76966.1, EAW76967.1
Gene:ENSG00000101110	SGK2	20	42,167,686	42,214,273	46,587	+	2	1_A7S_sNL97_plus_lncRNA:1:3361, 2_A7S_sNL97_plus_lncRNA:1:3128	21770, 31602	downstream, downstream	1	1	21	30	1	2_A7S_sNL97_plus_lncRNA:1	31	Gene SGK2	SGK2, H-SGK2, dJ1338T.2	serum/glucocorticoid regulated kinase 2	NM_016276, NM_170693, NCT23126522.0, NCT26301.2	230357_s_at, 230373_at	NP_057360.2, 722748.1, EAW76955.1, EAW76956.1
Gene:ENSG00000101096	IPT52	20	42,219,379	42,275,662	56,283	+	3	1_A7S_sNL97_plus_lncRNA:1:3361, 2_A7S_sNL97_plus_lncRNA:1:3128, 2_A7S_sNL97_plus_lncRNA:1:3129	-122, -91, 56963	upstream, upstream, downstream	1	1	25	30	2	1_A7S_sNL97_plus_lncRNA:1	31	Gene IPT52	CGI-63, MGC6, C20orf8, dJ1026D15.1, IPT52, MC02	chorioallantoic transport 52 homolog (Chlamydomonas)	NM_016004, NCT21126560.0, NCT26714.2	218709_s_at, 233562_s_at	NP_057656.2; EAW76954.1, EAW76953.1
Gene:ENSG00000093009	MYBL2	20	42,293,709	42,345,122	49,413	+	1	2_A7S_sNL97_plus_lncRNA:1:3129	4965	upstream	0	1	16	30	1	2_A7S_sNL97_plus_lncRNA:1	30	Gene MYBL2	B-MYB, B-MYB, MYBL2, MGC15600	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	NM_002466, NCT20713.3	207110_at	NP_002457.1, EAW76931.1
Gene:ENSG00000124888	TOX2	20	42,343,492	42,696,256	154,764	+	2	2_A7S_sNL97_plus_lncRNA:1:3130, 2_A7S_sNL97_plus_lncRNA:1:3131	10620, 50620	at gene, ut gene	0	1	17	26.5	2	2_A7S_sNL97_plus_lncRNA:1	29	Gene TOX2	dJ1105D11.2, TOX2, QC9-1, MGC15886, C20orf180, dJ485G2.1	TOX high mobility group box family member 2	NM_001080798, NM_032853, NM_001080797, NM_001080798, NCT19874261, NCT23131162.0, NCT23131163.0, NCT26455.1	226737_at	NP_001072266.1, NP_116272.1, NP_001072267.1, NP_001082368.1, EAW76944.1, EAW76945.1, EAW76946.1, EAW76947.1
Gene:ENSG00000125826	C20orf111	20	42,833,139	42,839,631	14,288	+	1	2_A7S_sNL97_plus_lncRNA:1:3132	71	at gene	0	1	20	21	1	2_A7S_sNL97_plus_lncRNA:1	21	Gene C20orf111	dJ1163J21.1, C20orf111, HEPC207, Pard	chromosome 20 open reading frame 111	NM_018470, NCT23130870.0, NCT26455.2	209820_at	NP_060940.2; EAW76939.1, EAW76938.1
Gene:ENSG00000283783	LOC100505783	20	42,839,513	42,858,664	19,151	+	1	2_A7S_sNL97_plus_lncRNA:1:3132	-153	upstream	0	1	20	21	1	2_A7S_sNL97_plus_lncRNA:1	21	Gene LOC100505783		hypothetical LOC100505783	XR_109607, XR_109608, XR_109609, XR_109610, XR_109609		
Gene:ENSG00000125977	GDAP1L1	20	42,875,935	42,909,013	33,105	+	4	1_A7S_sNL97_plus_lncRNA:1:3362, 1_A7S_sNL97_plus_lncRNA:1:3363, 2_A7S_sNL97_plus_lncRNA:1:3132, 2_A7S_sNL97_plus_lncRNA:1:3133	1064, 17264, 1052, 17116	at gene, ut gene, at gene, ut gene	1	1	24	25	2	2_A7S_sNL97_plus_lncRNA:1	29	Gene GDAP1L1	dJ651L22.1, GDAP1L1, dJ693J12.1.1, DKFZp761E226	ganglioside-induced differentiation-associated protein 1-like 1	NM_030534, NCT23131195.0, NCT23131200.0, NCT23131201.0, NCT23554200.0, NCT26366.3	219666_at	NP_078939.2; EAW76938.1, EAW76930.1, EAW76931.1, EAW76933.1, EAW76932.1
Gene:ENSG00000125172	HNF4A	20	42,984,841	43,060,030	75,189	+	3	1_A7S_sNL97_plus_lncRNA:1:3365, 2_A7S_sNL97_plus_lncRNA:1:3134	72903, 72919	at gene, ut gene	1	1	20	46	1	2_A7S_sNL97_plus_lncRNA:1	46	Gene HNF4A	HNF4A, HNF4A7, MODY1, NR2A21, FLJ38854, HNF4alf, HNF4alfa, HNF4alpha, HNF4, NR2A1, TCF, TCF-14, MODY	hepatocyte nuclear factor 4, alpha	NM_000457, NM_175884, NM_178850, NM_001030003, NM_178849, NM_001030004, NM_178810, NM_001030002, NCT23131693.1, NCT23131710.1, NCT23131712.1, NCT23437660.0, NCT26343.2	206379_x_at, 214832_at, 214551_at, 216556_s_at, 230814_at	NP_000448.2, NP_848180.1, NP_848181.1, NP_001030004.1, NP_001030003.1, NP_001030174.1, EAW76821.1, EAW76922.1, EAW76923.1, EAW76924.1, EAW76925.1
Gene:ENSG00000125648	TTPAL	20	43,104,547	43,123,244	18,697	+	2	2_A7S_sNL97_plus_lncRNA:1:3137, 2_A7S_sNL97_plus_lncRNA:1:3138	-3, 19995	upstream, downstream	0	1	16.5	20.5	2	2_A7S_sNL97_plus_lncRNA:1	23	Gene TTPAL	TTPAL, DKFZp686E0370, MGC2470, C20orf121	tocopherol (alpha) transfer protein-like	NM_001039102, NM_024231, NCT23131750.0, NCT26350.3	218653_at, 226031_at	NP_001034255.1, NP_077307.2; EAW75916.1, EAW75919.1
Gene:ENSG00000119655	SERINC3	20	43,124,664	43,160,726	35,862	-	2	2_A7S_sNL97_plus_lncRNA:1:3138, 2_A7S_sNL97_plus_lncRNA:1:3139	36214, 230	upstream, downstream	0	1	16.5	20	2	2_A7S_sNL97_plus_lncRNA:1	22	Gene SERINC3	TMS1, SSB999, DIP33, TDE, SERINC3, ASER1, TDE1	serine incorporator 3	NM_006811, NM_199041, NCT23129883.0, NCT26338.2	211799_x_at, 221471_at, 221472_at, 224572_s_at	NP_009052.1, NP_945178.1; EAW75913.1, EAW75916.1
Gene:ENSG00000101142	PKIG	20	43,160,439	43,247,878	87,342	+	2	2_A7S_sNL97_plus_lncRNA:1:3366, 2_A7S_sNL97_plus_lncRNA:1:3139	41212, 6900	at gene, upstream	1	1	19.5	17	2	2_A7S_sNL97_plus_lncRNA:1	22	Gene PKIG	PKIG, MGC126499, MGC126455	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	NM_181864, NM_181865, NM_007066, NCT19831212.1, NCT23131705.0, NCT23131760.0, NCT23131761.0, NCT23555705.0, NCT26365.2	202732_at	NP_061203.1, NP_891521.1, NP_008997.1; EAW75914.1, EAW75915.1, EAW75912.1, EAW75905.1, EAW75911.1, EAW75912.1, EAW75914.1
Gene:ENSG00000125629	WISP2	20	43,243,553	43,256,452	12,387	+	1	2_A7S_sNL97_plus_lncRNA:1:3367	12747	downstream	1	0	24	31	1	2_A7S_sNL97_plus_lncRNA:1	24	Gene WISP2	CCN5, CTGF-L, WISP2, CTGF-L	WNT inducible signaling pathway protein 2	NM_003881, NCT19874721.1, NCT23131569.0	208792_at	NP_003872.2; EAW75903.1, EAW75902.1
Gene:ENSG00000140730	RWTM	20	43,350,489	43,436,912	86,463	+	4	1_A7S_sNL97_plus_lncRNA:1:3365, 1_A7S_sNL97_plus_lncRNA:1:3366, 1_A7S_sNL97_plus_lncRNA:1:3140, 2_A7S_sNL97_plus_lncRNA:1:3141, 2_A7S_sNL97_plus_lncRNA:1:3142	33245, 29965, 33055, 29932	at gene, ut gene, at gene, ut gene, at gene	1	1	33	44.5	2	2_A7S_sNL97_plus_lncRNA:1	49	Gene RWTM	RWtm4, C20orf180, dJ781B1.3, RWM3, RWtm4, RWtm4gamma	regulating synaptic membrane exocytosis 4	NM_152970, NCT23129980.0, NCT23554760.0, NCT26346.2	225684_at, 233299_at	NP_690015.1, EAW75897.1, EAW75898.1, EAW75899.1
Gene:ENSG00000166329	YWHAB	20	43,514,344	43,537,161	22,817	+	2	1_A7S_sNL97_plus_lncRNA:1:3142, 2_A7S_sNL97_plus_lncRNA:1:3143	-248, 20536	upstream, downstream	0	1	12.5	20.5	2	2_A7S_sNL97_plus_lncRNA:1	21	Gene YWHAB	YWHAA, HS1, GW128, YWHAB, KCIP-1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	NM_003404, NM_139323, NCT23132760.0, NCT23126527.0, NCT23554650.0, NCT26619.3	200783_s_at, 217717_s_at, 217718_s_at	NP_003397.1, NP_647538.1; EAW75893.1, EAW75894.1, EAW75895.1, EAW75896.1
Gene:ENSG00000125630	PABPC1L	20	43,535,703	43,567,962	29,259	+	1	2_A7S_sNL97_plus_lncRNA:1:3143	177	at gene	0	1	11	20	1	2_A7S_sNL97_plus_lncRNA:1	20	Gene PABPC1L	PABPC1L2, dJ1060F2.2, C20orf119, FLJ38550, eIF4E, FLJ10681, FLJ40313, PABPC1L	poly(A) binding protein, cytoplasmic 1-like	NM_001129756	236670_s_at, 201638_at, 231104_at	NP_001116228.1
Gene:ENSG00000125651	TOMM34	20	43,570,771	43,589,114	18,343	-	2	1_A7S_sNL97_plus_lncRNA:1:3360, 1_A7S_sNL97_plus_lncRNA:1:3140, 1_A7S_sNL97_plus_lncRNA:1:3141	-5870, 154, -5530	upstream, at gene, upstream	1	1	17	21	2	2_A7S_sNL97_plus_lncRNA:1	24	Gene TOMM34	TOMM34, TOM34, UKCC3, HTOM34P	translocase of outer mitochondrial membrane 34	NM_006809, NCT23555565.0, NCT26592.2	201070_at	NP_006800.2; EAW75888.1, EAW75889.1
Gene:ENSG00000283652	LOC100505652	20	43,592,435	43,593,099	2,664	-	2	1_A7S_sNL97_plus_lncRNA:1:3360, 1_A7S_sNL97_plus_lncRNA:1:3140, 1_A7S_sNL97_plus_lncRNA:1:3141	318, 6139, 155	at gene, downstream, at gene	1	1	17	21	2	2_A7S_sNL97_plus_lncRNA:1	24	Gene LOC100505652		hypothetical LOC100505626	XR_109610		
Gene:ENSG00000167601	STX4	20	43,593,120	43,708,593	113,474	+	4	1_A7S_sNL97_plus_lncRNA:1:3360, 1_A7S_sNL97_plus_lncRNA:1:3361, 1_A7S_sNL97_plus_lncRNA:1:3140, 2_A7S_sNL97_plus_lncRNA:1:3141, 2_A7S_sNL97_plus_lncRNA:1:3142, 2_A7S_sNL97_plus_lncRNA:1:3143	-236, 121555, -9160, -76	upstream, downstream, upstream, upstream	1	1	16.67	20.67	3	2_A7S_sNL97_plus_lncRNA:1	24	Gene STX4	STX4, DKFZp686A2068, MST1, YSK3, KRS2	taxin enhancer kinase 4	NM_006262, NCT23554743.0, NCT26601.2	1860791_at, 208411_at, 211055_s_at, 223799_at, 226364_at, 236299_at, 242601_at	NP_003773.1; EAW75883.1, EAW75882.1
Gene:ENSG00000101851	NCMS1	20	43,720,650	43,729,753	8,602	-	1	2_A7S_sNL97_plus_lncRNA:1:3361	12745	downstream	1	0	22	20	1	1_A7S_sNL97_plus_lncRNA:1	22	Gene NCMS1	NCMS1, XV81	aldehyde oxidase/xanthine dehydrogenase, molybdopterin binding 1	NM_152351, NCT23127505.0, NCT26492.2	207366_at	NP_002242.2; EAW75879.1, EAW75880.1
Gene:ENSG00000167193	MATN4	20	43,822,087	43,836,987	14,900	+	1	2_A7S_sNL97_plus_lncRNA:1:3146	14663	at gene	0	1	18	21	1	2_A7S_sNL97_plus_lncRNA:1	21	Gene MATN4	MATN4, HEMWCRS4, FLJ14417	matrilin 4	NM_003833, NM_030590, NM_030992, NCT23127190.0, NCT23127760.0, NCT26602.4	207122_s_at	NP_003824.2, NP_085080.1, NP_085093.1; EAW75866.1, EAW75867.1, EAW75868.1
Gene:ENSG00000125657	SDC4	20	43,853,628	43,877,264	23,136	+	1	2_A7S_sNL97_plus_lncRNA:1:3362	786	at gene	1	0	17	17	1	1_A7S_sNL97_plus_lncRNA:1	17	Gene SDC4	SDC4, MGC22217, SYND4	syndecan 4	NM_002999, NCT19874726.0, NCT23127540.0, NCT26604.2	202071_at	NP_002990.2; EAW75890.1, EAW75891.1, EAW75892.1
Gene:ENSG00000101196	SYS1	20	43,991,701	43,997,849	6,148	+	2	1_A7S_sNL97_plus_lncRNA:1:3363, 1_A7S_sNL97_plus_lncRNA:1:3145	283, 139	at gene, ut gene	1	1	24	31	1	2_A7S_sNL97_plus_lncRNA:1	31	Gene SYS1	SYS1, C20orf169, dJ853C12.2, dJ853C12.4.1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	NM_152542	224665_at, 224669_at, 224670_at	NP_741031.1
Gene:ENSG00000167587	SYS1-DBNDD2	20	43,991,880	44,039,247	47,367	+	2	1_A7S_sNL97_plus_lncRNA:1:3363, 2_A7S_sNL97_plus_lncRNA:1:3146	64, 0	at gene, ut gene	1	1	24	31	1	2_A7S_sNL97_plus_lncRNA:1	31	Gene SYS1-DBNDD2	C20orf169-DBNDD2	SYS1-DBNDD2 read-through transcript	NR_003159		
Gene:ENSG00000167291	TPST2TG5	20	44,002,520	44,006,857	4,437	+	2	1_A7S_sNL97_plus_lncRNA:1:3363, 2_A7S_sNL97_plus_lncRNA:1:3146	15051, 10117	downstream, downstream	1	1	24	31	1	2_A7S_sNL97_plus_lncRNA:1	31	Gene TPST2TG5	C20orf169, TPST2TG5, CLG9	TPST2 target 5	NM_014377, NCT19874830.1, NCT26605.1	207662_at	NP_055242.1, EAW75859.1, EAW75858.1
Gene:ENSG00000049618	WIPDC1	20	44,402,647	44,420,547	17,900	+	2	1_A7S_sNL97_plus_lncRNA:1:3364, 2_A7S_sNL97_plus_lncRNA:1:3146	16390, 61	at gene, upstream	1	1	16	21.5	2	2_A7S_sNL97_plus_lncRNA:1	26	Gene WIPDC1	WIPDC3, dJ447F2.3, WAIP14	WAIP four-transmembrane cover domain 3	NM_018034, NCT23127529.0, NCT23127270.0, NCT23559490.0, NCT23559491.0, NCT26625.3	223602_at	NP_542161.1; EAW75816.1, EAW75812.1, EAW75814.1, EAW75815.1, EAW75817.1
Gene:ENSG00000166922	DNTTIP1	20	44,420,376	44,440,666	19,480	+	3	1_A7S_sNL97_plus_lncRNA:1:3365, 1_A7S_sNL97_plus_lncRNA:1:3146, 2_A7S_sNL97_plus_lncRNA:1:3147	20072, 32, 20576	downstream, at gene, downstream	1	1	21.5	28	2	2_A7S_sNL97_plus_lncRNA:1	28	Gene DNTTIP1	C20orf167, TdIT, dJ447F2.2, DNTTIP1	deoxynucleotidyltransferase, terminal, interacting protein 1	NM_032921, NCT23130570.0, NCT23135760.0, NCT26624.2	224629_at, 234542_s_at	NP_443163.1, EAW75810.1, EAW75811.1, EAW75812.1
Gene:ENSG00000101265	UBE2C	20	44,841,255	44,863,596	6,341	+	2	1_A7S_sNL97_plus_lncRNA:1:3369, 2_A7S_sNL97_plus_lncRNA:1:3148	-7, -103	upstream, upstream	1	1	20	22	1	2_A7S_sNL97_plus_lncRNA:1	25	Gene UBE2C	dJ447F3.2, UBE2C, UBCH10	ubiquitin-conjugating enzyme E2C	NM_181799, NM_181800, NM_181802, NM_181803, NM_007019, NM_181801, NCT19874322.0, NCT19874333.1, NCT23564622.0, NCT23564623.0, NCT23564640.0, NCT26613.2	202954_at	NP_001161.1, NP_861518.1, NP_861519.1, NP_861520.1, NP_861521.1, NP_861522.1, EAW75804.1, EAW75805.1, EAW75806.1, EAW75807.1, EAW75808.1, EAW75809.1
Gene:ENSG00000167772	TNNC2	20	44,851,853	44,855,953	4,100	-	2	1_A7S_sNL97_plus_lncRNA:1:3366, 2_A7S_sNL97_plus_lncRNA:1:3149	4899, -7119	upstream, upstream	1	1	16	26	1	2_A7S_sNL97_plus_lncRNA:1	26	Gene TNNC2	TNNC2		NM_003279, NCT23127720.0, NCT26654.2	209368_at	NP_003270.1; EAW75802.1, EAW75803.1
Gene:ENSG00000101294	SNX21	20	44,962,470	44,977,914	9,444	+	2	1_A7S_sNL97_plus_lncRNA:1:3366, 2_A7S_sNL97_plus_lncRNA:1:3149	442, 602	at gene, ut gene	1	1	16	26	1	2_A7S_sNL97_plus_lncRNA:1	26	Gene SNX21	dJ337O16.2, SNX21, C20orf61, SNX-L, FLJ20383, MGC20493	sorting nexin family member 21	NM_031431, NM_153597, NM_001042632, NM_001042633, NCT23135503.0, NCT23135564.1, NCT26662.2	1860960_at, 1853961_s_at, 235593_at	NP_114699.1, NP_699057.1, NP_001036097.1, NP_001036098.1, EAW75768.1, EAW75800.1, EAW75801.1
Gene:ENSG00000125676	ACOT8	20	44,970,361	44,986,035	15,674	+	4	1_A7S_sNL97_plus_lncRNA:1:3366, 1_A7S_sNL97_plus_lncRNA:1:3367, 2_A7S_sNL97_plus_lncRNA:1:3149, 2_A7S_sNL97_plus_lncRNA:1:3150, 2_A7S_sNL97_plus_lncRNA:1:3151	23123, -24, 22961, 66	downstream, downstream, upstream, downstream	1	1	20	25	2	2_A7S_sNL97_plus_lncRNA:1	26	Gene ACOT8	PTE-2, ACOT8, ATE, hACTE-II, PTE1, hNACTE, PTE2	acyl-CoA thioesterase 8	NM_005469, NCT19632291.1, NCT19832100.1, NCT23554600.0, NCT23564610.0, NCT26612.2	206212_at, 206213_at	NP_005460.2; EAW75785.1, EAW75784.1, EAW75785.1, EAW75786.1, EAW75787.1
Gene:ENSG00000049321	ZSWIM3	20	44,989,262	44,997,370	21,808	+	2	1_A7S_sNL97_plus_lncRNA:1:3367, 2_A7S_sNL97_plus_lncRNA:1:3150	-283, -161	upstream, upstream	1	1	21	22	1	2_A7S_sNL97_plus_lncRNA:1	22	Gene ZSWIM3	ZSWIM3, C20orf164	zinc finger, SWIM-type containing 3	NM_080752, NCT2786222.2	226223_at	NP_542790.2; EAW80407.1
Gene:ENSG00000125304	ZSWIM1	20	44,999,648	45,012,803	4,037	+	2	1_A7S_sNL97_plus_lncRNA:1:3368, 2_A7S_sNL97_plus_lncRNA:1:3152	10120, 10036	downstream, downstream	1	1	24	25	1	2_A7S_sNL97_plus_lncRNA:1	25	Gene ZSWIM1	ZSWIM1, C20orf162	zinc finger, SWIM-type containing 1	NM_020863, NCT23135586.0, NCT23135873.0	217092_at, 222607_s_at	NP_542753.3; EAW75783.1, EAW75782.1
Gene:ENSG00000125497	C20orf163	20	44,515,130	44,516,238	1,108	-	2	1_A7S_sNL97_plus_lncRNA:1:3368, 2_A7S_sNL97_plus_lncRNA:1:3152	-2730, -3666	upstream, upstream	1	1	24	25	1	2_A7S_sNL97_plus_lncRNA:1	25	Gene C20orf163	dJ337O16.6, C20orf163, TP322	chromosome 20 open reading frame 163	NM_030600, NCT21624790.1	1553732_at	NP_542751.1; EAW75781.1
Gene:ENSG00000140626	NEURL2	20	44,517,267	44,519,901	2,634	-	2	1_A7S_sNL97_plus_lncRNA:1:3368, 2_A7S_sNL97_plus_lncRNA:1:3152	467, -2	upstream, upstream	1	1	24	25	1	2_A7S_sNL97_plus_lncRNA:1	25	Gene NEURL2	C20orf163, MGC129930, MGC129934, Ozz-E3, OZZ, NEURL2	deubiquitinase homolog 2 (Drosophila)	NM_030749, NCT2786172	230263_at	NP_542767.1; EAW75780.1
Gene:ENSG00000101335	CTSA	20	44,519,991	44,527,699	7,708	+	2	1_A7S_sNL97_plus_lncRNA:1:3368, 2_A7S_sNL97_plus_lncRNA:1:3152	377, 313	at gene, ut gene	1	1	24	25	1	2_A7S_sNL97_plus_lncRNA:1	25	Gene CTSA	PPGB, GLB2, CTSA, NGBE, GSL, PPCA	cathepsin A	NM_000308, NM_001127685, NM_001167594, NCT19863661.3, NCT23126600.0	200661_at	NP_000299.2, NP_001121167.1, NP_001161066.1; EAW75768.1, EAW75769.1
Gene:ENSG00000125730	PLTP	20	44,527,397	44,560,706	33,309	+	3	1_A7S_sNL97_plus_lncRNA:1:3368, 1_A7S_sNL97_plus_lncRNA:1:3152, 2_A7S_sNL97_plus_lncRNA:1:3153	20516, 20552, 159	downstream, downstream, at gene	1	1	20	23.5	2	2_A7S_sNL97_plus_lncRNA:1	25	Gene PLTP	PLTP, HDLCQ8	phospholipid transfer protein	NM_182676, NM_006227, NCT23125880.0, NCT23125900.0, NCT23125902.0, NCT23125903.0, NCT23555140.0, NCT23555153.0, NCT26650.3	202073_s_at	NP_872617.1, NP_006218.1; EAW75761.1, EAW75762.1, EAW75763.1, EAW75765.1, EAW75764.1, EAW75766.1, EAW75767.1
Gene:ENSG00000125735	PCIP1	20	44,563,217	44,576,662	13,345	+	2	1_A7S_sNL97_plus_lncRNA:1:3369, 2_A7S_sNL97_plus_lncRNA:1:3154	107, 91	at gene, ut gene	1	1	20	26	1	2_A7S_sNL97_plus_lncRNA:1	26	Gene PCIP1	C20orf87, PCIP1	PDX1 C-terminal inhibitory factor 1	NM_022104, NCT23126562.1, NCT23559650.0, NCT26262.4	221762_s_at, 220643_s_at, 69640_at	NP_071357.1; EAW75776.1, EAW75779.1, EAW75780.1
Gene:ENSG00000125820	ZNF335	20	44,577,292	44,600,833	23,541	+	2	1_A7S_sNL97_plus_lncRNA:1:3360, 2_A7S_sNL97_plus_lncRNA:1:3155	283, 229	at gene, ut gene	1	1	33	40	1	2_A7S_sNL97_plus_lncRNA:1	40	Gene ZNF335	NIF1, ZNF335, NIF2, NIF-1	zinc finger protein 335	NM_022095, NCT23126560.0	221690_at, 222059_at, 78120_at	NP_071376.1; EAW75777.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100128028	LOC100128028	20	44,642,139	44,650,712	8,573	-	3	1_A375_pNL7_minus_lncRNA::1::3601, 1_A375_pNL7_minus_lncRNA::1::3602, 2_A375_pNL97_plus_lncRNA::1::5156	-5416, -7400, -5352	upstream, upstream, upstream	1	1	30	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene LOC100128028		hypothetical LOC100128028	XR_112154, XR_109614, XR_115375		
GeneID:57468	SLC12A5	20	44,650,329	44,688,789	38,460	+	5	1_A375_pNL7_minus_lncRNA::1::3601, 1_A375_pNL7_minus_lncRNA::1::3602, 1_A375_pNL7_minus_lncRNA::1::3603, 2_A375_pNL97_plus_lncRNA::1::5156, 2_A375_pNL97_plus_lncRNA::1::5157	5799, 7783, 19303, 5735, 18791	in gene, in gene, in gene, in gene, in gene	1	1	34.5	34	2	1_A375_pNL7_minus_lncRNA::1	39	Gene SLC12A5	KCC2, KIAA1176, SLC12A5	solute carrier family 12 (potassium-chloride transporter), member 5	NM_020708, NM_001134771, hCT2312886.0, hCT2312887.0, hCT31280.2	210040_at	NP_065759.1, NP_001128243.1, EAW75771.1, EAW75772.1, EAW75773.1
GeneID:57727	NCOA5	20	44,689,624	44,718,580	28,956	-	2	1_A375_pNL7_minus_lncRNA::1::3604, 2_A375_pNL97_plus_lncRNA::1::5158	20, 52	in gene, in gene	1	1	20	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene NCOA5	bA465L10.6, CIA, NCOA5	nuclear receptor coactivator 5	NM_020967, hCT1951316.1, hCT2312580.0, hCT2312582.0, hCT2312583.0, hCT2355589.0, hCT2355590.0, hCT31276.3	225145_at, 234471_s_at	NP_066018.1, EAW75764.1, EAW75765.1, EAW75766.1, EAW75767.1, EAW75770.1, EAW75768.1, EAW75769.1
GeneID:64405	CDH22	20	44,802,376	44,880,334	77,958	-	2	1_A375_pNL7_minus_lncRNA::1::3605, 2_A375_pNL97_plus_lncRNA::1::5159	20654, 20654	in gene, in gene	1	1	61	64	1	2_A375_pNL97_plus_lncRNA::1	64	Gene CDH22	dJ998H6.1, CDH22, C20orf25, MGC39564	cadherin 22, type 2	NM_021248, hCT2312573.0, hCT31271.2	1569679_at, 215181_at	NP_067071.1, EAW75755.1, EAW75754.1
GeneID:51006	SLC35C2	20	44,978,177	44,993,064	14,887	-	1	2_A375_pNL97_plus_lncRNA::1::5161	456	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SLC35C2	C20orf5, OVCOV1, CGI-15, FLJ37039, MGC32079, BA394O2.1, MGC39183, MGC20633, FLJ46434, SLC35C2	solute carrier family 35, member C2	NM_173073, NM_015945, NM_173179, hCT1953380.1, hCT1953381.1, hCT1953382.1, hCT1953383.1, hCT1953384.1, hCT1953385.1, hCT31270.3	219447_s_at, 225037_at	NP_775096.1, NP_057029.6, NP_775271.1, EAW75747.1, EAW75751.1, EAW75753.1, EAW75748.1, EAW75749.1, EAW75750.1, EAW75752.1
GeneID:63916	ELMO2	20	44,994,689	45,035,271	40,582	-	3	2_A375_pNL97_plus_lncRNA::1::5161, 1_A375_pNL7_minus_lncRNA::1::3607, 2_A375_pNL97_plus_lncRNA::1::5162	42663, -137, -137	downstream, upstream, upstream	1	1	18.5	20.5	2	1_A375_pNL7_minus_lncRNA::1	24	Gene ELMO2	KIAA1834, ELMO2, CED-12, FLJ11656, ELMO-2, CED12	engulfment and cell motility 2	NM_182764, NM_133171	1554857_at, 220363_s_at, 221526_s_at, 55692_at	NP_877496.1, NP_573403.1
GeneID:55713	ZNF334	20	45,129,707	45,142,194	12,487	-	1	2_A375_pNL97_plus_lncRNA::1::5163	50	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZNF334	ZNF334	zinc finger protein 334	NM_018102, NM_199441, hCT2349186.0, hCT2355582.0, hCT2355583.0, hCT31273.4	220022_at	NP_060572.3, NP_955473.1, EAW75732.1, EAW75733.1, EAW75734.1, EAW75735.1
GeneID:64849	SLC13A3	20	45,186,462	45,313,124	126,662	-	1	2_A375_pNL97_plus_lncRNA::1::5165	53060	in gene	0	1	17	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene SLC13A3	SDCT2, NADC3, SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	NM_001011554, NM_022829, NM_001193339, NM_001193340, NM_001193342	205243_at, 205244_s_at, 230686_s_at, 230687_at	NP_001011554.1, NP_073740.2, NP_001180268.1, NP_001180269.1, NP_001180271.1
GeneID:23613	ZMYND8	20	45,838,381	45,985,474	147,093	-	1	2_A375_pNL97_plus_lncRNA::1::5166	25154	in gene	0	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ZMYND8	PRKCBP1, MGC31836, PRO2893, RACK7, ZMYND8	zinc finger, MYND-type containing 8	NM_183047, NM_183048, NM_012408, hCT1951303.1, hCT1951304.2, hCT1951305.1, hCT1953283.2, hCT1953284.2, hCT1953285.2, hCT1953286.2, hCT1953287.2, hCT2341399.0, hCT2341400.0, hCT2341401.0, hCT2355459.0, hCT2355460.0	1556571_at, 207130_at, 209048_s_at, 209049_s_at, 214795_at, 230533_at, 243814_at	NP_898868.1, NP_898869.1, NP_036540.3, EAW75703.1, EAW75704.1, EAW75714.1, EAW75705.1, EAW75706.1, EAW75707.1, EAW75708.1, EAW75709.1, EAW75710.1, EAW75711.1, EAW75712.1, EAW75713.1, EAW75715.1
GeneID:100505983	LOC100505983	20	46,579,543	46,580,799	1,256	+	1	2_A375_pNL97_plus_lncRNA::1::5169	609	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100505983		hypothetical LOC100505983	XR_109617		
GeneID:57580	PREX1	20	47,240,793	47,444,420	203,627	-	1	2_A375_pNL97_plus_lncRNA::1::5172	189092	in gene	0	1	14	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene PREX1	P-REX1, PREX1, KIAA1415	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	NM_020820, hCT1953370.1, hCT1953371.1, hCT29578.3	224909_s_at, 224925_at	NP_065871.2, EAW75684.1, EAW75685.1, EAW75686.1
GeneID:6780	STAU1	20	47,729,876	47,804,904	75,028	-	3	1_A375_pNL7_minus_lncRNA::1::3610, 2_A375_pNL97_plus_lncRNA::1::5174, 2_A375_pNL97_plus_lncRNA::1::5175	-216, 920, -216	upstream, in gene, upstream	1	1	19.5	21	2	2_A375_pNL97_plus_lncRNA::1	26	Gene STAU1	FLJ25010, STAU, STAU1	staufen, RNA binding protein, homolog 1 (Drosophila)	NM_004602, NM_017452, NM_017453, NM_017454, NM_001037328, hCT1953342.1, hCT1953343.2, hCT1953344.1, hCT1967122.1, hCT28389.3, hCT29572.3	207320_x_at, 208948_s_at, 211505_s_at, 213037_x_at	NP_004593.2, NP_059346.2, NP_059347.2, NP_059348.2, NP_001032405.1, EAW75670.1, EAW75669.1, EAW75671.1, EAW75672.1, EAW75673.1, EAW75674.1
GeneID:57169	ZNFX1	20	47,862,437	47,894,756	32,319	-	2	1_A375_pNL7_minus_lncRNA::1::3611, 2_A375_pNL97_plus_lncRNA::1::5176	-380, -412	upstream, upstream	1	1	23	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene ZNFX1	ZNFX1, MGC131926, FLJ39275	zinc finger, NFX1-type containing 1	NM_021035, hCT1953368.1, hCT1953369.1, hCT2355471.0, hCT29576.2	225076_s_at	NP_066363.1, EAW75661.1, EAW75662.1, EAW75663.1, EAW75664.1
GeneID:441951	C20orf199	20	47,894,715	47,905,797	11,082	+	2	1_A375_pNL7_minus_lncRNA::1::3611, 2_A375_pNL97_plus_lncRNA::1::5176	421, 453	in gene, in gene	1	1	23	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene C20orf199	C20orf199, HSUP1, NCRNA00275, HSUP2	chromosome 20 open reading frame 199	NR_003606, NR_003604, NR_003605	229699_s_at	
GeneID:26765	SNORD12C	20	47,895,482	47,895,560	78	+	2	1_A375_pNL7_minus_lncRNA::1::3611, 2_A375_pNL97_plus_lncRNA::1::5176	-346, -314	upstream, upstream	1	1	23	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene SNORD12C	E3, E2, SNORD106, U106, SNORD12C, RNU106, E2-1	small nucleolar RNA, C/D box 12C	NR_002433		
GeneID:100113383	SNORD12B	20	47,896,850	47,896,952	102	+	2	1_A375_pNL7_minus_lncRNA::1::3611, 2_A375_pNL97_plus_lncRNA::1::5176	-1714, -1682	upstream, upstream	1	1	23	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene SNORD12B	SNORD12B	small nucleolar RNA, C/D box 12B	NR_003695		
GeneID:692057	SNORD12	20	47,897,220	47,897,309	89	+	2	1_A375_pNL7_minus_lncRNA::1::3611, 2_A375_pNL97_plus_lncRNA::1::5176	-2084, -2052	upstream, upstream	1	1	23	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene SNORD12	HBII-99, SNORD12, MIRN1259, MIR1259	small nucleolar RNA, C/D box 12	NR_003030		
GeneID:3745	KCNB1	20	47,988,505	48,099,181	110,676	-	5	1_A375_pNL7_minus_lncRNA::1::3612, 1_A375_pNL7_minus_lncRNA::1::3613, 2_A375_pNL97_plus_lncRNA::1::5177, 2_A375_pNL97_plus_lncRNA::1::5178, 2_A375_pNL97_plus_lncRNA::1::5179	-222, -1763, 82301, -179, -1747	upstream, upstream, in gene, upstream, upstream	1	1	19	23.67	3	2_A375_pNL97_plus_lncRNA::1	32	Gene KCNB1	DRK1, KCNB1, h-DRK1, KV2.1	potassium voltage-gated channel, Shab-related subfamily, member 1	NM_004975, hCT29123.3	211006_s_at	NP_004966.1, EAW75656.1
GeneID:728671	LOC728671	20	48,232,412	48,237,694	5,282	+	2	1_A375_pNL7_minus_lncRNA::1::3614, 2_A375_pNL97_plus_lncRNA::1::5180	-4860, -4796	upstream, upstream	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC728671		hypothetical LOC728671	XM_001716479, XM_001128100, XM_001129176		XP_001716531.2, XP_001128100.2, XP_001129176.2
GeneID:9334	B4GALT5	20	48,249,482	48,330,421	80,939	-	2	2_A375_pNL97_plus_lncRNA::1::5181, 2_A375_pNL97_plus_lncRNA::1::5182	51941, -3915	in gene, upstream	0	1	15	17	2	2_A375_pNL97_plus_lncRNA::1	19	Gene B4GALT5	MGC138470, B4Gal-T5, beta4GalT-V, B4GALT5, beta4Gal-T5, BETA4-GALT-IV, gt-V	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	NM_004776, hCT2312294.0, hCT29122.3	221484_at, 221485_at	NP_004767.1, EAW75654.1, EAW75653.1
GeneID:23315	SLC9A8	20	48,429,250	48,508,772	79,522	+	3	1_A375_pNL7_minus_lncRNA::1::3616, 2_A375_pNL97_plus_lncRNA::1::5183, 2_A375_pNL97_plus_lncRNA::1::5184	75022, -466, 75054	in gene, upstream, in gene	1	1	18	20	2	1_A375_pNL7_minus_lncRNA::1	22	Gene SLC9A8	FLJ42500, MGC138418, KIAA0939, NHE8, SLC9A8, DKFZp686C03237	solute carrier family 9 (sodium/hydrogen exchanger), member 8	NM_015266, hCT2318423.0, hCT2318424.0, hCT2318425.0, hCT2318426.0, hCT2355429.0, hCT29125.3	212947_at	NP_056081.1, EAW75650.1, EAW75647.1, EAW75648.1, EAW75649.1, EAW75651.1, EAW75652.1
GeneID:9825	SPATA2	20	48,519,928	48,532,080	12,152	-	2	1_A375_pNL7_minus_lncRNA::1::3617, 2_A375_pNL97_plus_lncRNA::1::5185	-112, -112	upstream, upstream	1	1	34	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene SPATA2	FLJ13167, tamo, PD1, KIAA0757, SPATA2	spermatogenesis associated 2	NM_001135773, NM_006038, hCT2312291.0, hCT28388.3	204433_s_at, 204434_at	NP_001129245.1, NP_006029.1, EAW75645.1, EAW75646.1
GeneID:55905	RNF114	20	48,552,914	48,570,422	17,508	+	2	1_A375_pNL7_minus_lncRNA::1::3618, 2_A375_pNL97_plus_lncRNA::1::5186	-114, 382	upstream, in gene	1	1	23	19	1	1_A375_pNL7_minus_lncRNA::1	23	Gene RNF114	PSORS12, RNF114, ZNF313	ring finger protein 114	NM_018683, hCT1953355.1, hCT2355433.0, hCT2355434.0, hCT29126.3	200867_at, 200868_s_at, 211678_s_at	NP_061153.1, EAW75641.1, EAW75642.1, EAW75643.1, EAW75644.1
GeneID:6615	SNAI1	20	48,599,513	48,605,423	5,910	+	1	2_A375_pNL97_plus_lncRNA::1::5187	6919	downstream	0	1	14	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SNAI1	SNAH, SLUGH2, dJ710H13.1, SNAI1, SNA	snail homolog 1 (Drosophila)	NM_005985, hCT29121.2	219480_at	NP_005976.2, EAW75640.1
GeneID:7335	UBE2V1	20	48,697,661	48,732,494	34,833	-	1	2_A375_pNL97_plus_lncRNA::1::5189	-2	upstream	0	1	16	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene UBE2V1	UEV1A, CROC-1, UEV1, CROC1, UBE2V1, UBE2V, CIR1, UEV-1	ubiquitin-conjugating enzyme E2 variant 1	NM_199144, NM_001032288, NM_021988, NM_022442		NP_954595.1, NP_001027459.1, NP_071887.1, NP_068823.2
GeneID:387522	TMEM189-UBE2V1	20	48,697,661	48,770,335	72,674	-	3	1_A375_pNL7_minus_lncRNA::1::3619, 2_A375_pNL97_plus_lncRNA::1::5189, 2_A375_pNL97_plus_lncRNA::1::5190	15039, 37839, 14863	in gene, in gene, in gene	1	1	19.5	25	2	2_A375_pNL97_plus_lncRNA::1	25	Gene TMEM189-UBE2V1	CROC1B, TMEM189-UBE2V1, KUA-UEV, CROC-1B, UBE2V1	TMEM189-UBE2V1 readthrough	NM_199203	201001_s_at, 201002_s_at, 216315_x_at	NP_954673.1
GeneID:387521	TMEM189	20	48,740,274	48,770,335	30,061	-	3	1_A375_pNL7_minus_lncRNA::1::3619, 2_A375_pNL97_plus_lncRNA::1::5189, 2_A375_pNL97_plus_lncRNA::1::5190	15039, 37839, 14863	in gene, downstream, in gene	1	1	19.5	25	2	2_A375_pNL97_plus_lncRNA::1	25	Gene TMEM189	KUA, TMEM189, UBE2V1	transmembrane protein 189	NM_199129, NM_001162505, NR_027889	223166_at	NP_954580.1, NP_001155977.1
GeneID:100506115	LOC100506115	20	48,884,035	48,896,332	12,297	+	2	1_A375_pNL7_minus_lncRNA::1::3621, 2_A375_pNL97_plus_lncRNA::1::5192	-211, -163	upstream, upstream	1	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506115		hypothetical LOC100506115	XR_109621, XR_109622		
GeneID:5770	PTPN1	20	49,126,891	49,201,088	74,197	+	2	1_A375_pNL7_minus_lncRNA::1::3623, 2_A375_pNL97_plus_lncRNA::1::5195	-299, 51477	upstream, in gene	1	1	16.5	20	2	2_A375_pNL97_plus_lncRNA::1	24	Gene PTPN1	PTP1B, PTPN1	protein tyrosine phosphatase, non-receptor type 1	NM_002827, hCT2314155.0, hCT2314156.0, hCT28364.2	202716_at, 217686_at, 217689_at, 239526_x_at	NP_002818.1, EAW75624.1, EAW75625.1, EAW75626.1
GeneID:100506153	LOC100506153	20	49,187,512	49,194,578	7,066	-	1	2_A375_pNL97_plus_lncRNA::1::5195	16210	downstream	0	1	14	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100506153		hypothetical LOC100506153	XR_112163, XR_109624, XR_115384		
GeneID:140876	FAM65C	20	49,202,645	49,253,426	50,781	-	2	1_A375_pNL7_minus_lncRNA::1::3624, 2_A375_pNL97_plus_lncRNA::1::5196	-8734, -8582	upstream, upstream	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene FAM65C	FLJ32230, FAM65C, FLJ00360, dJ530I15.2, C20orf175	family with sequence similarity 65, member C	NM_080829, hCT1953349.2, hCT1953350.2, hCT2314055.0, hCT2314056.1, hCT28773.4	227654_at, 243976_at	NP_543019.2, EAW75618.1, EAW75619.1, EAW75620.1, EAW75621.1, EAW75622.1
GeneID:100506175	LOC100506175	20	49,262,008	49,276,828	14,820	+	2	1_A375_pNL7_minus_lncRNA::1::3624, 2_A375_pNL97_plus_lncRNA::1::5196	152, 0	in gene, in gene	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100506175		hypothetical LOC100506175	XR_109625		
GeneID:84612	PARD6B	20	49,348,081	49,370,278	22,197	+	1	1_A375_pNL7_minus_lncRNA::1::3625	15	in gene	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene PARD6B	PAR6B, PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	NM_032521, hCT1950760.1, hCT2314142.0, hCT28340.3	211907_s_at, 214827_at, 235165_at	NP_115910.1, EAW75617.1, EAW75615.1, EAW75616.1
GeneID:23394	ADNP	20	49,506,883	49,547,527	40,644	-	2	1_A375_pNL7_minus_lncRNA::1::3626, 2_A375_pNL97_plus_lncRNA::1::5197	-745, -825	upstream, upstream	1	1	20	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ADNP	KIAA0784, ADNP, ADNP1	activity-dependent neuroprotector homeobox	NM_181442, NM_015339, hCT1950768.1, hCT29337.2	201773_at	NP_852107.1, NP_056154.1, EAW75611.1, EAW75612.1
GeneID:8813	DPM1	20	49,551,405	49,575,060	23,655	-	4	1_A375_pNL7_minus_lncRNA::1::3626, 1_A375_pNL7_minus_lncRNA::1::3627, 2_A375_pNL97_plus_lncRNA::1::5197, 2_A375_pNL97_plus_lncRNA::1::5198	26788, 122, 26708, -380	downstream, in gene, downstream, upstream	1	1	20	30	2	2_A375_pNL97_plus_lncRNA::1	32	Gene DPM1	DPM1, CDGIE, MPDS	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	NM_003859, hCT2314047.0, hCT2355553.0, hCT2355554.0	202673_at	NP_003850.1, EAW75608.1, EAW75607.1, EAW75609.1
GeneID:27304	MOCS3	20	49,575,363	49,577,820	2,457	+	2	1_A375_pNL7_minus_lncRNA::1::3627, 2_A375_pNL97_plus_lncRNA::1::5198	-425, 77	upstream, in gene	1	1	20	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene MOCS3	MOCS3, UBA4, dJ914P20.3, MGC9252	molybdenum cofactor synthesis 3	NM_014484, hCT28363.2	206141_at	NP_055299.1, EAW75606.1
GeneID:3755	KCNG1	20	49,620,193	49,639,675	19,482	-	1	2_A375_pNL97_plus_lncRNA::1::5200	251	in gene	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene KCNG1	K13, kH2, KCNG1, KV6.1, MGC12878, KCNG	potassium voltage-gated channel, subfamily G, member 1	NM_002237, hCT29333.1	211053_at, 214595_at	NP_002228.2, EAW75605.1
GeneID:4773	NFATC2	20	50,007,765	50,179,168	171,403	-	9	1_A375_pNL7_minus_lncRNA::1::3631, 1_A375_pNL7_minus_lncRNA::1::3632, 1_A375_pNL7_minus_lncRNA::1::3633, 1_A375_pNL7_minus_lncRNA::1::3634, 2_A375_pNL97_plus_lncRNA::1::5207, 2_A375_pNL97_plus_lncRNA::1::5208, 2_A375_pNL97_plus_lncRNA::1::5209, 2_A375_pNL97_plus_lncRNA::1::5210, 2_A375_pNL97_plus_lncRNA	137040, 124688, 64608, -1392, 137056, 124632, 65024, 8208, -1216	in gene, in gene, in gene, upstream, in gene, in gene, in gene, in gene, upstream	1	1	22.8	26.2	5	2_A375_pNL97_plus_lncRNA::1	47	Gene NFATC2	NFATC2, NFATP, NFAT1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	NM_173091, NM_012340, NM_001136021, hCT2312681.0, hCT2312683.0	224542_s_at, 226991_at, 231801_at	NP_775114.1, NP_036472.2, NP_001129493.1, EAW75602.1, EAW75603.1
GeneID:57167	SALL4	20	50,400,581	50,419,048	18,467	-	1	2_A375_pNL97_plus_lncRNA::1::5212	2232	in gene	0	1	10	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SALL4	MGC133050, dJ1112F19.1, DRRS, HSAL4, ZNF797, SALL4	sal-like 4 (Drosophila)	NM_020436, hCT2355576.0, hCT29336.2	229661_at, 236501_at	NP_065169.1, EAW75595.1, EAW75596.1
GeneID:55734	ZFP64	20	50,700,550	50,808,524	107,974	-	2	1_A375_pNL7_minus_lncRNA::1::3636, 2_A375_pNL97_plus_lncRNA::1::5214	428, 492	in gene, in gene	1	1	25	23	1	1_A375_pNL7_minus_lncRNA::1	25	Gene ZFP64	MGC940, ZFP64, ZNF338	zinc finger protein 64 homolog (mouse)	NM_018197, NM_022088, NM_199426, NM_199427, hCT2312671.0, hCT2312672.0, hCT2312673.0, hCT2312674.0	218968_s_at, 219536_s_at, 222697_s_at, 229186_s_at	NP_060667.2, NP_071371.3, NP_955459.2, NP_955458.1, EAW75591.1, EAW75592.1, EAW75590.1, EAW75593.1
GeneID:7764	ZNF217	20	52,183,610	52,199,636	16,026	-	1	2_A375_pNL97_plus_lncRNA::1::5215	4	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ZNF217	ZNF217, ZABC1	zinc finger protein 217	NM_006526, hCT1950762.1, hCT2311964.0, hCT2311965.0, hCT28357.2	203739_at	NP_006517.1, EAW75579.1, EAW75578.1, EAW75580.1, EAW75581.1
GeneID:5203	PFDN4	20	52,824,502	52,836,492	11,990	+	2	1_A375_pNL7_minus_lncRNA::1::3642, 2_A375_pNL97_plus_lncRNA::1::5221	58, 10	in gene, in gene	1	1	29	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene PFDN4	C1, PFD4, PFDN4	prefoldin subunit 4	NM_002623, hCT28592.2	205361_s_at, 205362_s_at	NP_002614.2, EAW75572.1
GeneID:116151	C20orf108	20	54,933,983	54,943,719	9,736	+	1	2_A375_pNL97_plus_lncRNA::1::5226	1121	in gene	0	1	14	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene C20orf108	5A3, DKFZp434A1114, dJ1167H4.1, C20orf108	chromosome 20 open reading frame 108	NM_080821, hCT2312006.0, hCT2312007.0, hCT30347.2	224690_at, 224693_at	NP_543011.2, EAW75563.1, EAW75564.1, EAW75565.1
GeneID:6790	AURKA	20	54,944,445	54,967,351	22,906	-	3	1_A375_pNL7_minus_lncRNA::1::3646, 2_A375_pNL97_plus_lncRNA::1::5226, 2_A375_pNL97_plus_lncRNA::1::5227	-265, 32247, -281	upstream, downstream, upstream	1	1	35	42	2	2_A375_pNL97_plus_lncRNA::1	59	Gene AURKA	MGC34538, ARK1, AURA, AURKA, AURORA2, STK7, BTAK, AIK, STK15, STK6	aurora kinase A	NM_003600, NM_198433, NM_198434, NM_198435, NM_198436, NM_198437, hCT1950770.0, hCT1953374.1, hCT1953375.1, hCT1953376.2, hCT1965747.1, hCT2311845.0, hCT2311850.0, hCT2355418.0, hCT2355419.0, hCT2355420.0, hCT2355421.0, hCT2355423.0, hCT30342.3	204092_s_at, 208079_s_at, 208080_at	NP_003591.2, NP_940835.1, NP_940836.1, NP_940837.1, NP_940838.1, NP_940839.1, EAW75550.1, EAW75551.1, EAW75552.1, EAW75553.1, EAW75554.1, EAW75555.1, EAW75556.1, EAW75557.1, EAW75558.1, EAW75559.1, EAW75560.1, EAW75561.1, EAW75562.1
GeneID:1477	CSTF1	20	54,967,427	54,979,582	12,155	+	2	1_A375_pNL7_minus_lncRNA::1::3646, 2_A375_pNL97_plus_lncRNA::1::5227	189, 205	in gene, in gene	1	1	56	59	1	2_A375_pNL97_plus_lncRNA::1	59	Gene CSTF1	CstFp50, CSTF1, CstF-50	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa	NM_001033521, NM_001324, NM_001033522, hCT2312009.0, hCT30344.3	202190_at, 32723_at	NP_001028693.1, NP_001315.1, NP_001028694.1, EAW75548.1, EAW75549.1
GeneID:57091	CASS4	20	54,987,168	55,034,396	47,228	+	2	1_A375_pNL7_minus_lncRNA::1::3647, 2_A375_pNL97_plus_lncRNA::1::5228	56416, 56384	downstream, downstream	1	1	34	26	1	1_A375_pNL7_minus_lncRNA::1	34	Gene CASS4	HEPL, CASS4, C20orf32, HEFL, CAS4	Cas scaffolding protein family member 4	NM_020356, NM_001164114, NM_001164115, NM_001164116, hCT1950772.1, hCT1953379.1, hCT2312012.0, hCT2355498.0, hCT2355499.0, hCT2355500.0, hCT30348.2	1554786_at, 220686_s_at	NP_065089.2, NP_001157586.1, NP_001157587.1, NP_001157588.1, EAW75546.1, EAW75547.1, EAW75541.1, EAW75542.1, EAW75543.1, EAW75544.1, EAW75545.1
GeneID:51507	C20orf43	20	55,043,647	55,093,942	50,295	+	2	1_A375_pNL7_minus_lncRNA::1::3647, 2_A375_pNL97_plus_lncRNA::1::5228	-63, -95	upstream, upstream	1	1	34	26	1	1_A375_pNL7_minus_lncRNA::1	34	Gene C20orf43	SHUJUN-3, C20orf43, CDAO5, HSPC164	chromosome 20 open reading frame 43	NM_016407	217737_x_at, 224128_at, 233842_x_at, 234926_s_at, 236702_at	NP_057491.2

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:7022	TFAP2C	20	55,204,358	55,214,339	9,981	+	1	2_A375_pNL97_plus_lncRNA::1::5229	1146	in gene	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene TFAP2C	ERF1, AP2-GAMMA, TFAP2G, TFAP2C, hAP-2g	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	NM_003222, hCT29104.2	205286_at, 205287_s_at	NP_003213.1, EAW75532.1
GeneID:655	BMP7	20	55,743,809	55,841,707	97,898	-	3	1_A375_pNL7_minus_lncRNA::1::3650, 2_A375_pNL97_plus_lncRNA::1::5237, 2_A375_pNL97_plus_lncRNA::1::5238	60875, 75979, 70987	in gene, in gene, in gene	1	1	19.67	24.33	3	2_A375_pNL97_plus_lncRNA::1	33	Gene BMP7	BMP7, OP-1	bone morphogenetic protein 7	NM_001719, hCT1953393.1, hCT1953394.1, hCT31354.3	209590_at, 209591_s_at, 211259_s_at, 211260_at	NP_001710.1, EAW75529.1, EAW75530.1, EAW75531.1
GeneID:23626	SPO11	20	55,904,831	55,919,049	14,218	+	1	2_A375_pNL97_plus_lncRNA::1::5239	21633	downstream	0	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene SPO11	MGC39953, CT35, SPO11	SPO11 meiotic protein covalently bound to DSB homolog (S. cerevisiae)	NM_012444, NM_198265, hCT1953392.1, hCT31353.2	222259_s_at	NP_036576.1, NP_937998.1, EAW75526.1, EAW75527.1
GeneID:8480	RAE1	20	55,926,145	55,953,519	27,374	+	1	2_A375_pNL97_plus_lncRNA::1::5239	319	in gene	0	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene RAE1	RAE1, MGC126077, MRNP41, Mnrp41, MIG14, FLJ30608, MGC117333, MGC126076, dJ800J21.1, dJ481F12.3	RAE1 RNA export 1 homolog (S. pombe)	NM_001015885, NM_003610, hCT2312071.0, hCT2312072.0, hCT2355436.0	201558_at, 211318_s_at	NP_001015885.1, NP_003601.1, EAW75523.1, EAW75524.1, EAW75525.1
GeneID:100462983	MTRNR2L3	20	55,933,496	55,934,878	1,382	-	1	2_A375_pNL97_plus_lncRNA::1::5239	8414	downstream	0	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MTRNR2L3	HN3, MTRNR2L3	MT-RNR2-like 3	NM_001190472		NP_001177401.1
GeneID:81030	ZBP1	20	56,178,902	56,195,632	16,730	-	1	2_A375_pNL97_plus_lncRNA::1::5241	19248	downstream	0	1	22	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ZBP1	ZBP1, DLM-1, DAI, DLM1, C20orf183	Z-DNA binding protein 1	NM_030776, NM_001160417, NM_001160418, NM_001160419, hCT1950773.1, hCT1953397.1, hCT1953398.1, hCT2355449.0, hCT31357.1	208087_s_at, 242020_s_at	NP_110403.2, NP_001153889.1, NP_001153890.1, NP_001153891.1, EAW75511.1, EAW75512.1, EAW75509.1, EAW75510.1, EAW75513.1
GeneID:56937	PMEPA1	20	56,223,452	56,286,541	63,089	-	6	1_A375_pNL7_minus_lncRNA::1::3652, 1_A375_pNL7_minus_lncRNA::1::3653, 1_A375_pNL7_minus_lncRNA::1::3654, 2_A375_pNL97_plus_lncRNA::1::5242, 2_A375_pNL97_plus_lncRNA::1::5243, 2_A375_pNL97_plus_lncRNA::1::5244	13101, 1325, -7187, 13005, 1277, -7155	in gene, in gene, upstream, in gene, in gene, upstream	1	1	33.33	33.33	3	2_A375_pNL97_plus_lncRNA::1	46	Gene PMEPA1	PMEPA1, TMEPAI, STAG1	prostate transmembrane protein, androgen induced 1	NM_020182, NM_199169, NM_199170, NM_199171, hCT1953395.1, hCT1953396.1, hCT2355442.0, hCT2355443.0, hCT31355.2	217875_s_at, 222449_at, 222450_at, 237166_at	NP_064567.2, NP_954638.1, NP_954639.1, NP_954640.1, EAW75504.1, EAW75507.1, EAW75505.1, EAW75506.1, EAW75508.1
GeneID:9217	VAPB	20	56,964,245	57,021,963	57,718	+	1	2_A375_pNL97_plus_lncRNA::1::5254	50987	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene VAPB	ALS8, VAMP-C, VAPB, VAP-C, VAP-B, VAMP-B	VAMP (vesicle-associated membrane protein)-associated protein B and C	NM_004738, hCT17825.3, hCT1953298.1, hCT2314478.0	202549_at, 202550_s_at	NP_004729.1, EAW75494.1, EAW75493.1, EAW75495.1
GeneID:149773	LOC149773	20	57,090,435	57,194,948	104,513	+	1	1_A375_pNL7_minus_lncRNA::1::3659	108621	downstream	1	0	29	25	1	1_A375_pNL7_minus_lncRNA::1	29	Gene LOC149773	FLJ33293, FLJ34385	hypothetical LOC149773	NR_034147	1556900_at, 1556901_s_at, 1559433_at	
GeneID:79160	MGC4294	20	57,209,827	57,210,794	967	+	1	2_A375_pNL97_plus_lncRNA::1::5255	10845	downstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MGC4294		hypothetical MGC4294	XR_112170, XR_109628, XR_115388	220698_at	
GeneID:8675	STX16	20	57,226,328	57,254,582	28,254	+	3	1_A375_pNL7_minus_lncRNA::1::3660, 2_A375_pNL97_plus_lncRNA::1::5255, 2_A375_pNL97_plus_lncRNA::1::5256	8, -5656, -56	in gene, upstream, upstream	1	1	21	29.5	2	2_A375_pNL97_plus_lncRNA::1	42	Gene STX16	SYN16, STX16, hsyn16, MGC90328	syntaxin 16	NM_001001433, NM_003763, NM_001134772, NM_001134773, hCT1953321.1, hCT1953323.1, hCT1953324.1, hCT19703.3, hCT2345028.0, hCT2345029.0, hCT2355531.0	1558249_s_at, 221499_s_at, 221500_s_at, 221638_s_at	NP_001001433.1, NP_003754.2, NP_001128244.1, NP_001128245.1, EAW75481.1, EAW75485.1, EAW75482.1, EAW75483.1, EAW75484.1, EAW75486.1, EAW75487.1
GeneID:1522	CTSZ	20	57,570,242	57,582,309	12,067	-	1	2_A375_pNL97_plus_lncRNA::1::5258	165	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CTSZ	CTSZ, CTSX, FLJ17088	cathepsin Z	NM_001336, hCT1953309.1, hCT19700.2, hCT2355522.0	210042_s_at, 212562_s_at	NP_001327.2, EAW75448.1, EAW75449.1, EAW75450.1
GeneID:81027	TUBB1	20	57,594,309	57,601,709	7,400	+	2	1_A375_pNL7_minus_lncRNA::1::3661, 2_A375_pNL97_plus_lncRNA::1::5259	12859, 12827	downstream, downstream	1	1	25	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene TUBB1	TUBB1, dJ543J19.4	tubulin, beta 1	NM_030773, hCT19704.4	208601_s_at, 230690_at	NP_110400.1, EAW75447.1
GeneID:514	ATP5E	20	57,603,733	57,607,422	3,689	-	4	1_A375_pNL7_minus_lncRNA::1::3661, 1_A375_pNL7_minus_lncRNA::1::3662, 2_A375_pNL97_plus_lncRNA::1::5259, 2_A375_pNL97_plus_lncRNA::1::5260	254, -10562, 286, -10498	in gene, upstream, in gene, upstream	1	1	24.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene ATP5E	MGC104243, ATP5E, ATPE	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	NM_006886, NM_001001977, hCT1953318.1, hCT1953319.1, hCT19702.3	217801_at	NP_008817.1, NP_001001977.1, EAW75444.1, EAW75445.1, EAW75446.1
GeneID:51012	SLMO2	20	57,608,200	57,617,901	9,701	-	4	1_A375_pNL7_minus_lncRNA::1::3661, 1_A375_pNL7_minus_lncRNA::1::3662, 2_A375_pNL97_plus_lncRNA::1::5259, 2_A375_pNL97_plus_lncRNA::1::5260	10733, -83, 10765, -19	downstream, upstream, downstream, upstream	1	1	24.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene SLMO2	dJ543J19.5, C20orf45, SLMO2, PRELID3B	slowmo homolog 2 (Drosophila)	NM_016045, hCT1953307.1, hCT19699.3	217851_s_at, 222441_x_at	NP_057129.2, EAW75443.1, EAW75442.1
GeneID:100287547	LOC100287547	20	57,707,998	57,729,904	21,906	-	4	1_A375_pNL7_minus_lncRNA::1::3664, 1_A375_pNL7_minus_lncRNA::1::3665, 2_A375_pNL97_plus_lncRNA::1::5261, 2_A375_pNL97_plus_lncRNA::1::5262	20464, 12528, 20496, 12464	in gene, in gene, in gene, in gene	1	1	34.5	42	2	2_A375_pNL97_plus_lncRNA::1	49	Gene LOC100287547		hypothetical protein LOC100287547	XM_002343714, XM_002346049, XM_003119823		XP_002343755.1, XP_002346090.1, XP_003119871.1
GeneID:128611	ZNF831	20	57,766,075	57,834,168	68,093	+	3	1_A375_pNL7_minus_lncRNA::1::3666, 1_A375_pNL7_minus_lncRNA::1::3667, 2_A375_pNL97_plus_lncRNA::1::5263	30037, 57189, 51813	in gene, in gene, in gene	1	1	14	17	3	2_A375_pNL97_plus_lncRNA::1	22	Gene ZNF831	dJ492J12.1, ZNF831, C20orf174	zinc finger protein 831	NM_178457	1556826_at, 1556827_a_at	NP_848552.1
GeneID:116154	PHACTR3	20	58,179,603	58,422,766	243,163	+	2	1_A375_pNL7_minus_lncRNA::1::3669, 2_A375_pNL97_plus_lncRNA::1::5265	161229, 161325	in gene, in gene	1	1	32	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene PHACTR3	C20orf101, PHACTR3, SCAPININ, MGC117178, H17739, SCAPIN1	phosphatase and actin regulator 3	NM_183244, NM_183246, NM_080672, hCT18808.2, hCT1950759.0, hCT1953304.1	227949_at	NP_899067.1, NP_899069.1, NP_542403.1, EAW75428.1, EAW75429.1, EAW75430.1
GeneID:10388	SYCP2	20	58,438,618	58,507,209	68,591	-	3	1_A375_pNL7_minus_lncRNA::1::3670, 2_A375_pNL97_plus_lncRNA::1::5266, 2_A375_pNL97_plus_lncRNA::1::5267	-8439, -7207, -8568	upstream, upstream, upstream	1	1	16	17.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene SYCP2	SYCP2, SCP2	synaptonemal complex protein 2	NM_014258, hCT1953303.1, hCT2312240.0	206546_at, 237920_at	NP_055073.2, EAW75426.1, EAW75427.1
GeneID:63939	C20orf177	20	58,508,819	58,523,702	14,883	+	3	1_A375_pNL7_minus_lncRNA::1::3670, 2_A375_pNL97_plus_lncRNA::1::5266, 2_A375_pNL97_plus_lncRNA::1::5267	6629, 5597, 6978	in gene, in gene, in gene	1	1	16	17.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene C20orf177	C20orf177, dJ551D2.5	chromosome 20 open reading frame 177	NM_001190826, NM_001190827, NM_022106, hCT1644430.2	225313_at	NP_001177755.1, NP_001177756.1, NP_071389.1, EAW75424.1
GeneID:5509	PPP1R3D	20	58,511,887	58,515,352	3,465	-	3	1_A375_pNL7_minus_lncRNA::1::3670, 2_A375_pNL97_plus_lncRNA::1::5266, 2_A375_pNL97_plus_lncRNA::1::5267	-296, 936, -445	upstream, in gene, upstream	1	1	16	17.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene PPP1R3D	PPP1R3D, PPP1R6, DKFZp781L2441	protein phosphatase 1, regulatory (inhibitor) subunit 3D	NM_006242, hCT17852.3	204554_at, 204555_s_at	NP_006233.1, EAW75425.1
GeneID:1002	CDH4	20	59,827,559	60,512,299	684,740	+	2	2_A375_pNL97_plus_lncRNA::1::5271, 2_A375_pNL97_plus_lncRNA::1::5272	278361, 356025	in gene, in gene	0	1	16.5	27.5	2	2_A375_pNL97_plus_lncRNA::1	29	Gene CDH4	MGC138355, RCAD, CAD4, FLJ22202, FLJ40547, MGC126700, CDH4	cadherin 4, type 1, R-cadherin (retinal)	NM_001794, hCT2312091.0, hCT33046.2	1563587_at, 206866_at, 220227_at, 239485_at	NP_001785.2, EAW75410.1, EAW75409.1
GeneID:6874	TAF4	20	60,549,854	60,640,866	91,012	-	1	1_A375_pNL7_minus_lncRNA::1::3674	95341	downstream	1	0	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene TAF4	TAF2C, TAF4A, TAF4, FLJ41943, TAFII135, TAF2C1, TAFII130	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	NM_003185, hCT2311878.0, hCT33044.3	208545_x_at, 213090_s_at	NP_003176.2, EAW75406.1, EAW75407.1
GeneID:149986	LSM14B	20	60,697,517	60,710,434	12,917	+	1	2_A375_pNL97_plus_lncRNA::1::5273	21939	downstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LSM14B	FLJ25473, bA11M20.3, C20orf40, LSM14B, RAP55B, LSM13, MGC61931, FAM61B	LSM14B, SCD6 homolog B (S. cerevisiae)	NM_144703, hCT2312099.1, hCT2312101.1, hCT2312102.1, hCT2312103.1, hCT2312104.1	1553304_at, 219653_at, 224171_at, 231200_at, 244455_at	NP_653304.2, EAW75403.1, EAW75401.1, EAW75402.1, EAW75404.1, EAW75405.1
GeneID:5688	PSMA7	20	60,711,791	60,718,474	6,683	-	1	2_A375_pNL97_plus_lncRNA::1::5273	-982	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PSMA7	XAPC7, PSMA7, C6, MGC3755, RC6-1, HSPC	proteasome (prosome, macropain) subunit, alpha type, 7	NM_002792	201114_x_at, 216088_s_at	NP_002783.1
GeneID:26039	SS18L1	20	60,718,822	60,757,566	38,744	+	3	1_A375_pNL7_minus_lncRNA::1::3675, 2_A375_pNL97_plus_lncRNA::1::5273, 2_A375_pNL97_plus_lncRNA::1::5274	39002, 634, 39375	downstream, in gene, downstream	1	1	21.5	25.5	2	2_A375_pNL97_plus_lncRNA::1	30	Gene SS18L1	MGC78386, MGC26711, CREST, KIAA0693, SS18L1, LP2261	synovial sarcoma translocation gene on chromosome 18-like 1	NM_198935, hCT2312106.0, hCT2312107.0, hCT2312109.0, hCT2355466.0, hCT2355467.0, hCT2355468.0, hCT2355469.0, hCT33050.2	213140_s_at	NP_945173.1, EAW75394.1, EAW75392.1, EAW75393.1, EAW75395.1, EAW75396.1, EAW75389.1, EAW75390.1, EAW75391.1
GeneID:26164	GTPBP5	20	60,758,081	60,777,823	19,742	+	2	1_A375_pNL7_minus_lncRNA::1::3675, 2_A375_pNL97_plus_lncRNA::1::5274	-257, 116	upstream, in gene	1	1	27	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene GTPBP5	GTPBP5, FLJ10741, ObgH1, MGC29512, dJ1005F21.2	GTP binding protein 5 (putative)	NM_015666, hCT2312111.0, hCT2312113.0, hCT33049.3	1558822_at, 226598_s_at, 226606_s_at, 235690_at	NP_056481.1, EAW75386.1, EAW75387.1, EAW75388.1
GeneID:9885	OSBPL2	20	60,813,580	60,871,269	57,689	+	3	1_A375_pNL7_minus_lncRNA::1::3676, 2_A375_pNL97_plus_lncRNA::1::5275, 2_A375_pNL97_plus_lncRNA::1::5276	64308, 64212, 66324	downstream, downstream, downstream	1	1	20	28.5	2	2_A375_pNL97_plus_lncRNA::1	39	Gene OSBPL2	KIAA0772, OSBPL2, ORP-2, MGC8342, FLJ20223, MGC4307, ORP2	oxysterol binding protein-like 2	NM_014835, NM_144498, hCT2312814.0, hCT2312815.0, hCT2312816.0	209221_s_at, 209222_s_at	NP_055650.1, NP_653081.1, EAW75377.1, EAW75378.1, EAW75379.1
GeneID:11047	ADRM1	20	60,878,027	60,883,918	5,891	+	3	1_A375_pNL7_minus_lncRNA::1::3676, 2_A375_pNL97_plus_lncRNA::1::5275, 2_A375_pNL97_plus_lncRNA::1::5276	-139, -235, 1877	upstream, upstream, in gene	1	1	20	28.5	2	2_A375_pNL97_plus_lncRNA::1	39	Gene ADRM1	MGC29536, ARM1, ADRM1, GP110, Rpn13	adhesion regulating molecule 1	NM_007002, NM_175573, hCT33040.3	201281_at	NP_008933.2, NP_783163.1, EAW75375.1
GeneID:3911	LAMA5	20	60,884,121	60,942,368	58,247	-	3	1_A375_pNL7_minus_lncRNA::1::3676, 2_A375_pNL97_plus_lncRNA::1::5275, 2_A375_pNL97_plus_lncRNA::1::5276	64480, 64576, 62464	downstream, downstream, downstream	1	1	20	28.5	2	2_A375_pNL97_plus_lncRNA::1	39	Gene LAMA5	LAMA5, KIAA1907	laminin, alpha 5	NM_005560, hCT2312184.0, hCT2355464.0, hCT33047.3	210150_s_at, 229570_at	NP_005551.3, EAW75374.1, EAW75372.1, EAW75373.1
GeneID:6227	RPS21	20	60,962,121	60,963,576	1,455	+	1	2_A375_pNL97_plus_lncRNA::1::5277	-297	upstream	0	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RPS21	S21, RPS21		NM_001024, hCT1950775.1, hCT2312821.0, hCT2312822.0, hCT2312823.0, hCT33041.3	200834_s_at, 214097_at	NP_001015.1, EAW75367.1, EAW75368.1, EAW75369.1, EAW75370.1, EAW75371.1
GeneID:81928	CABLES2	20	60,963,686	60,982,339	18,653	-	3	1_A375_pNL7_minus_lncRNA::1::3677, 2_A375_pNL97_plus_lncRNA::1::5277, 2_A375_pNL97_plus_lncRNA::1::5278	-157, 20515, -189	upstream, downstream, upstream	1	1	28.5	31	2	2_A375_pNL97_plus_lncRNA::1	42	Gene CABLES2	C20orf150, CABLES2, ik3-2, dJ908M14.2	Cdk5 and Abl enzyme substrate 2	NM_031215, hCT2312180.0, hCT2312182.0, hCT33052.2	226004_at	NP_112492.2, EAW75364.1, EAW75365.1, EAW75366.1
GeneID:140893	C20orf151	20	60,985,293	61,002,629	17,336	-	2	1_A375_pNL7_minus_lncRNA::1::3677, 2_A375_pNL97_plus_lncRNA::1::5278	20133, 20101	downstream, downstream	1	1	38	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene C20orf151	C20orf151	chromosome 20 open reading frame 151	NM_080833, hCT2312179.1, hCT2344845.0	236258_at	NP_543023.2, EAW75362.1, EAW75363.1
GeneID:128826	C20orf166	20	61,147,660	61,167,971	20,311	+	2	1_A375_pNL7_minus_lncRNA::1::3678, 2_A375_pNL97_plus_lncRNA::1::5280	26580, 26164	downstream, downstream	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene C20orf166	C20orf166, MGC129808, dJ353C17.1, FLJ32423	chromosome 20 open reading frame 166	NM_178463, hCT9735.3	232892_at	NP_848558.1, EAW75355.1
GeneID:100131174	LOC100131174	20	61,172,797	61,174,714	1,917	+	2	1_A375_pNL7_minus_lncRNA::1::3678, 2_A375_pNL97_plus_lncRNA::1::5280	1443, 1027	in gene, in gene	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene LOC100131174		hypothetical LOC100131174	XR_112174, XR_109637, XR_115397		
GeneID:28231	SLCO4A1	20	61,273,797	61,303,647	29,850	+	2	1_A375_pNL7_minus_lncRNA::1::3679, 2_A375_pNL97_plus_lncRNA::1::5282	24539, 26299	in gene, in gene	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene SLCO4A1	OATPRP1, SLC21A12, OATPE, SLCO4A1, OATP-E, POAT, OATP4A1, OATP1	solute carrier organic anion transporter family, member 4A1	NM_016354, hCT2312841.0, hCT2312842.0, hCT2312843.0, hCT2312844.0	219911_s_at, 229239_x_at	NP_057438.3, EAW75351.1, EAW75348.1, EAW75349.1, EAW75350.1
GeneID:100127888	hCG_2018279	20	61,294,379	61,297,973	3,594	-	2	1_A375_pNL7_minus_lncRNA::1::3679, 2_A375_pNL97_plus_lncRNA::1::5282	-363, -2123	upstream, upstream	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene hCG_2018279	LOC100127888, MGC39393	hypothetical LOC100127888	NR_024470		
GeneID:4923	NTSR1	20	61,340,189	61,394,123	53,934	+	3	1_A375_pNL7_minus_lncRNA::1::3680, 2_A375_pNL97_plus_lncRNA::1::5283, 2_A375_pNL97_plus_lncRNA::1::5284	32227, -4589, 31651	in gene, upstream, in gene	1	1	22.5	28.5	2	2_A375_pNL97_plus_lncRNA::1	31	Gene NTSR1	NTR, NTSR1	neurotensin receptor 1 (high affinity)	NM_002531, hCT1786414.2	207360_s_at	NP_002522.2, EAW75345.1
GeneID:55257	C20orf20	20	61,427,805	61,431,945	4,140	+	1	2_A375_pNL97_plus_lncRNA::1::5285	-845	upstream	0	1	18	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene C20orf20	C20orf20, MRGBP, MRG15BP, FLJ10914, Eaf7, URCC4	chromosome 20 open reading frame 20	NM_018270, hCT14524.3, hCT2312853.0	218586_at	NP_060740.1, EAW75342.1, EAW75343.1
GeneID:11054	OGFR	20	61,436,177	61,445,352	9,175	+	2	2_A375_pNL97_plus_lncRNA::1::5285, 2_A375_pNL97_plus_lncRNA::1::5286	-9217, 13295	upstream, downstream	0	1	17.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene OGFR	OGFR		NM_007346, hCT12108.2, hCT1950754.2, hCT2312859.0, hCT2312860.0, hCT2312861.0, hCT2312862.0, hCT2355492.0	202841_x_at, 210443_x_at, 211512_s_at, 211513_s_at	NP_031372.2, EAW75337.1, EAW75336.1, EAW75338.1, EAW75340.1, EAW75341.1, EAW75335.1, EAW75339.1
GeneID:1299	COL9A3	20	61,448,414	61,472,511	24,097	+	1	2_A375_pNL97_plus_lncRNA::1::5286	1058	in gene	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene COL9A3	MED, DJ885L7.4.1, FLJ90759, EDM3, IDD, COL9A3	collagen, type IX, alpha 3	NM_001853, hCT1962387.1, hCT1962388.1	204724_s_at	NP_001844.3, EAW75334.1, EAW75333.1
GeneID:11083	DIDO1	20	61,509,090	61,569,304	60,214	-	4	1_A375_pNL7_minus_lncRNA::1::3681, 2_A375_pNL97_plus_lncRNA::1::5287, 2_A375_pNL97_plus_lncRNA::1::5288, 2_A375_pNL97_plus_lncRNA::1::5289	312, 11976, 152, -520	in gene, in gene, in gene, upstream	1	1	14.33	17	3	1_A375_pNL7_minus_lncRNA::1	20	Gene DIDO1	DIO-1, DIDO1, DATF1, DIDO2, BYE1, MGC16140, DIDO3, C20orf158, DKFZp434P1115, FLJ11265, dJ885L7.8, DIO1, KIAA0333	death inducer-obliterator 1	NM_033081, NM_080797, NM_080796, NM_022105, NM_001193369, NM_001193370, hCT2312150.2, hCT2344531.1, hCT2344532.1, hCT2344534.0, hCT2344535.1, hCT2346135.0	213213_at, 218325_s_at, 222595_s_at, 227335_at	NP_149072.2, NP_542987.2, NP_071388.2, NP_542986.1, NP_001180298.1, NP_001180299.1, EAW75321.1, EAW75322.1, EAW75323.1, EAW75324.1, EAW75325.1, EAW75326.1
GeneID:54994	C20orf11	20	61,569,441	61,579,827	10,386	+	3	1_A375_pNL7_minus_lncRNA::1::3681, 2_A375_pNL97_plus_lncRNA::1::5288, 2_A375_pNL97_plus_lncRNA::1::5289	-449, -289, 383	upstream, upstream, in gene	1	1	16	17.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene C20orf11	C20orf11, TWA1	chromosome 20 open reading frame 11	NM_017896, hCT14530.3, hCT2312857.1	218448_at, 225376_at	NP_060366.1, EAW75318.1, EAW75319.1
GeneID:63930	LOC63930	20	61,640,735	61,716,423	75,688	+	4	1_A375_pNL7_minus_lncRNA::1::3682, 1_A375_pNL7_minus_lncRNA::1::3683, 2_A375_pNL97_plus_lncRNA::1::5290, 2_A375_pNL97_plus_lncRNA::1::5291	60577, 73057, 60641, 73121	in gene, in gene, in gene, in gene	1	1	32	41	2	2_A375_pNL97_plus_lncRNA::1	47	Gene LOC63930	FLJ46471, FLJ17648	hypothetical LOC63930	NR_033370, hCT1963188.1, hCT2355530.0	231760_at	EAW75309.1, EAW75310.1
GeneID:3785	KCNQ2	20	62,037,542	62,103,993	66,451	-	1	1_A375_pNL7_minus_lncRNA::1::3684	-2823	upstream	1	0	21	15	1	1_A375_pNL7_minus_lncRNA::1	21	Gene KCNQ2	KVEBN1, KCNA11, EBN1, KV7.2, ENB1, EIEE7, BFNC, EBN, KCNQ2, BFNS1, HNSPC	potassium voltage-gated channel, KQT-like subfamily, member 2	NM_172106, NM_172109, NM_172107, NM_172108, NM_004518, hCT14533.2, hCT1950304.0, hCT1962391.1, hCT1962392.1, hCT2312456.0, hCT2312460.0, hCT2312461.0, hCT2312462.0, hCT2312463.0, hCT2355542.0, hCT2355543.0, hCT2355544.0	205737_at, 210508_s_at, 211486_s_at	NP_742104.1, NP_742107.1, NP_004509.2, NP_742105.1, NP_742106.1, EAW75281.1, EAW75271.1, EAW75272.1, EAW75273.1, EAW75274.1, EAW75275.1, EAW75276.1, EAW75277.1, EAW75278.1, EAW75279.1, EAW75280.1, EAW75282.1
GeneID:1917	EEF1A2	20	62,119,366	62,130,505	11,139	-	1	2_A375_pNL97_plus_lncRNA::1::5293	809	in gene	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene EEF1A2	FLJ41696, EEF1A2, STNL, HS1, EF1A, STN, EF-1-alpha-2, EEF1AL	eukaryotic translation elongation factor 1 alpha 2	NM_001958, hCT14522.3, hCT2312440.0	204540_at	NP_001949.1, EAW75260.1, EAW75259.1
GeneID:26205	GMEB2	20	62,218,955	62,258,381	39,426	-	1	2_A375_pNL97_plus_lncRNA::1::5294	-435	upstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GMEB2	KIAA1269, P79PIF, GMEB2, PIF79	glucocorticoid modulatory element binding protein 2	NM_012384, hCT14521.3, hCT2312435.0, hCT2312436.0	222251_s_at, 44146_at	NP_036516.1, EAW75253.1, EAW75252.1, EAW75254.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100505771	LOC100505771	20	62,258,587	62,260,061	1,474	+	1	2_A375_pNL97_plus_lncRNA::1::5294	229	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100505771		hypothetical LOC100505771	XR_109591, XR_109592, XR_115400, XR_115401		
GeneID:50861	STMN3	20	62,271,061	62,284,780	13,719	-	3	2_A375_pNL97_plus_lncRNA::1::5295, 2_A375_pNL97_plus_lncRNA::1::5296, 2_A375_pNL97_plus_lncRNA::1::5297	7980, 140, -5044	in gene, in gene, upstream	0	1	16.33	26.33	3	2_A375_pNL97_plus_lncRNA::1	27	Gene STMN3	SCLIP, STMN3	stathmin-like 3	NM_015894, hCT2312416.1, hCT2312420.1	218207_s_at, 222557_at	NP_056978.2, EAW75250.1, EAW75249.1
GeneID:51750	RTEL1	20	62,289,647	62,327,601	37,954	+	3	1_A375_pNL7_minus_lncRNA::1::3685, 2_A375_pNL97_plus_lncRNA::1::5296, 2_A375_pNL97_plus_lncRNA::1::5297	40913, -5007, 177	downstream, upstream, in gene	1	1	17.67	22.67	3	2_A375_pNL97_plus_lncRNA::1	27	Gene RTEL1	RTEL, DKFZp434C013, KIAA1088, bK3184A7.3, RTEL1, C20orf41, NHL	regulator of telomere elongation helicase 1	NM_016434, NM_032957	208467_x_at	NP_057518.1, NP_116575.2
GeneID:8771	TNFRSF6B	20	62,326,288	62,330,037	3,749	+	3	1_A375_pNL7_minus_lncRNA::1::3685, 1_A375_pNL7_minus_lncRNA::1::3686, 2_A375_pNL97_plus_lncRNA::1::5298	4272, 12944, 12944	downstream, downstream, downstream	1	1	26	26	2	2_A375_pNL97_plus_lncRNA::1	37	Gene TNFRSF6B	DCR3, DJ583P15.1.1, M68, TR6, TNFRSF6B	tumor necrosis factor receptor superfamily, member 6b, decoy	NM_003823, NM_032945		NP_003814.1, NP_116563.1
GeneID:10139	ARFRP1	20	62,329,995	62,339,355	9,360	-	3	1_A375_pNL7_minus_lncRNA::1::3685, 1_A375_pNL7_minus_lncRNA::1::3686, 2_A375_pNL97_plus_lncRNA::1::5298	8795, 123, 123	in gene, in gene, in gene	1	1	26	26	2	2_A375_pNL97_plus_lncRNA::1	37	Gene ARFRP1	ARP, ARFRP1, ARL18, Arp1	ADP-ribosylation factor related protein 1	NM_003224, NM_001134758, hCT12109.4, hCT1970952.1, hCT1970953.1, hCT1970955.1, hCT2312422.0, hCT2312423.0, hCT2312427.0, hCT2312429.0	203174_s_at, 215984_s_at	NP_003215.1, NP_001128230.1, EAW75230.1, EAW75232.1, EAW75235.1, EAW75236.1, EAW75231.1, EAW75233.1, EAW75234.1, EAW75237.1
GeneID:84619	ZGPAT	20	62,338,794	62,367,494	28,700	+	3	1_A375_pNL7_minus_lncRNA::1::3685, 1_A375_pNL7_minus_lncRNA::1::3686, 2_A375_pNL97_plus_lncRNA::1::5298	-8234, 436, 436	upstream, in gene, in gene	1	1	26	26	2	2_A375_pNL97_plus_lncRNA::1	37	Gene ZGPAT	GPATC6, GPATCH6, ZC3H9, KIAA1847, ZC3HDC9, ZIP, MGC44880, ZGPAT	zinc finger, CCCH-type with G patch domain	NM_181485, NM_032527, NM_001083113, hCT2344173.0, hCT2344174.0, hCT2344175.0, hCT2344177.0, hCT2344185.0, hCT2344187.0, hCT2355501.0, hCT2355502.0, hCT2355503.0, hCT2355504.0	221848_at, 235398_s_at, 235399_x_at, 57539_at	NP_852150.2, NP_115916.3, NP_001076582.1, EAW75220.1, EAW75222.1, EAW75228.1, EAW75221.1, EAW75223.1, EAW75224.1, EAW75225.1, EAW75226.1, EAW75227.1, EAW75229.1
GeneID:140701	C20orf135	20	62,492,566	62,494,341	1,775	+	2	1_A375_pNL7_minus_lncRNA::1::3687, 2_A375_pNL97_plus_lncRNA::1::5299	3882, 3322	downstream, downstream	1	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C20orf135	dJ591C20.1, ABHD16B, MGC42974, C20orf135	abhydrolase domain containing 16B	NM_080622, hCT2312411.0	234002_at	NP_542189.1, EAW75203.1
GeneID:7165	TPD52L2	20	62,496,590	62,522,891	26,301	+	3	1_A375_pNL7_minus_lncRNA::1::3687, 1_A375_pNL7_minus_lncRNA::1::3688, 2_A375_pNL97_plus_lncRNA::1::5299	-142, 29778, -702	upstream, downstream, upstream	1	1	20.5	17	2	1_A375_pNL7_minus_lncRNA::1	24	Gene TPD52L2	D54, DKFZp686A1765, hD54, TPD52L2	tumor protein D52-like 2	NM_003288, NM_199359, NM_199360, NM_199361, NM_199362, NM_199363, hCT13853.3, hCT1962381.1, hCT1962382.1, hCT1962383.1, hCT2317439.0, hCT2317442.0, hCT2355431.0, hCT2355432.0	201379_s_at	NP_003279.2, NP_955391.1, NP_955392.1, NP_955393.1, NP_955394.1, NP_955395.1, EAW75194.1, EAW75195.1, EAW75196.1, EAW75197.1, EAW75198.1, EAW75199.1, EAW75200.1, EAW75201.1
GeneID:80331	DNAJC5	20	62,526,518	62,565,395	38,877	+	2	1_A375_pNL7_minus_lncRNA::1::3688, 2_A375_pNL97_plus_lncRNA::1::5300	-150, 45130	upstream, downstream	1	1	16.5	18	2	1_A375_pNL7_minus_lncRNA::1	24	Gene DNAJC5	CSP, DNAJC5A, DKFZp761N1221, FLJ13070, DKFZp434N1429, FLJ00118, DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5	NM_025219, hCT2317443.0, hCT2317444.0, hCT2355521.0	224611_s_at, 224612_s_at, 224613_s_at, 244601_at	NP_079495.1, EAW75193.1, EAW75191.1, EAW75192.1
GeneID:54963	UCKL1	20	62,571,182	62,587,800	16,618	-	3	1_A375_pNL7_minus_lncRNA::1::3689, 2_A375_pNL97_plus_lncRNA::1::5300, 2_A375_pNL97_plus_lncRNA::1::5301	24, 16152, -168	in gene, in gene, upstream	1	1	19	26.5	2	2_A375_pNL97_plus_lncRNA::1	31	Gene UCKL1	URKL1, UCK1L, UCK1-LIKE, UCKL1	uridine-cytidine kinase 1-like 1	NM_017859, NM_001193379, hCT13861.3, hCT1970961.1, hCT2312407.0, hCT2355493.0, hCT2355494.0	218533_s_at, 232675_s_at, 232727_at	NP_060329.2, NP_001180308.1, EAW75185.1, EAW75186.1, EAW75188.1, EAW75189.1, EAW75187.1
GeneID:100302137	MIR1914	20	62,572,818	62,572,897	79	-	1	2_A375_pNL97_plus_lncRNA::1::5300	1249	downstream	0	1	9	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MIR1914	MIRN1914, hsa-mir-1914, MIR1914	microRNA 1914	NR_031735		
GeneID:693232	MIR647	20	62,573,984	62,574,079	95	-	1	2_A375_pNL97_plus_lncRNA::1::5300	2431	downstream	0	1	9	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MIR647	MIR647, hsa-mir-647, MIRN647	microRNA 647	NR_030377		
GeneID:100113386	UCKL1AS	20	62,584,737	62,588,338	3,601	+	2	1_A375_pNL7_minus_lncRNA::1::3689, 2_A375_pNL97_plus_lncRNA::1::5301	3039, 3231	in gene, in gene	1	1	29	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene UCKL1AS	UCKL1OS, UCKL1-AS, UCKL1-AS1, FLJ46647, UCKL1AS	UCKL1 antisense RNA (non-protein coding)	NR_027287		
GeneID:57473	ZNF512B	20	62,588,055	62,601,218	13,163	-	2	1_A375_pNL7_minus_lncRNA::1::3689, 2_A375_pNL97_plus_lncRNA::1::5301	13442, 13250	downstream, downstream	1	1	29	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene ZNF512B	KIAA1196, MGC149846, GM632, ZNF512B, MGC149845	zinc finger protein 512B	NM_020713	221869_at, 55872_at	NP_065764.1
GeneID:140700	SAMD10	20	62,605,466	62,610,995	5,529	-	2	1_A375_pNL7_minus_lncRNA::1::3690, 2_A375_pNL97_plus_lncRNA::1::5302	-1357, -1357	upstream, upstream	1	1	29	47	1	2_A375_pNL97_plus_lncRNA::1	47	Gene SAMD10	C20orf136, SAMD10, dJ591C20.7, dJ591C20	sterile alpha motif domain containing 10	NM_080621, hCT13863.2, hCT1950301.1	227773_at, 233001_at	NP_542188.1, EAW75180.1, EAW75181.1
GeneID:24148	PRPF6	20	62,612,431	62,664,453	52,022	+	3	1_A375_pNL7_minus_lncRNA::1::3690, 2_A375_pNL97_plus_lncRNA::1::5302, 2_A375_pNL97_plus_lncRNA::1::5303	-79, -79, 57649	upstream, upstream, downstream	1	1	21	32	2	2_A375_pNL97_plus_lncRNA::1	47	Gene PRPF6	C20orf14, ANT-1, TOM, Prp6, PRPF6, hPrp6, U5-102K	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	NM_012469, hCT13855.2, hCT1957410.2, hCT2317328.1, hCT2317330.1, hCT2350264.0, hCT2355444.0	208879_x_at, 208880_s_at	NP_036601.2, EAW75174.1, EAW75175.1, EAW75176.1, EAW75177.1, EAW75179.1, EAW75178.1
GeneID:284739	NCRNA00176	20	62,665,697	62,671,315	5,618	+	1	2_A375_pNL97_plus_lncRNA::1::5303	4383	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NCRNA00176	DKFZp434G015, PRR17, NCRNA00176, FLJ27267, FLJ17673	non-protein coding RNA 176	NR_027686, NR_027687	233355_at	
GeneID:54345	SOX18	20	62,679,079	62,680,979	1,900	-	1	2_A375_pNL97_plus_lncRNA::1::5303	10699	downstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SOX18	HLTS, SOX18	SRY (sex determining region Y)-box 18	NM_018419	219568_x_at	NP_060889.1
GeneID:6919	TCEA2	20	62,688,439	62,703,700	15,261	+	2	1_A375_pNL7_minus_lncRNA::1::3691, 2_A375_pNL97_plus_lncRNA::1::5304	5961, 5961	in gene, in gene	1	1	33	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene TCEA2	TFIIS, TCEA2	transcription elongation factor A (SII), 2	NM_003195, NM_198723, hCT2317338.0, hCT2317339.0, hCT2355574.0	203919_at, 238173_at, 241428_x_at	NP_003186.1, NP_942016.1, EAW75168.1, EAW75169.1, EAW75170.1
GeneID:10287	RGS19	20	62,704,534	62,711,324	6,790	-	2	1_A375_pNL7_minus_lncRNA::1::3691, 2_A375_pNL97_plus_lncRNA::1::5304	16924, 16924	downstream, downstream	1	1	33	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene RGS19	RGS19, GAIP, RGSGAIP	regulator of G-protein signaling 19	NM_005873, NM_001039467, hCT2312397.0, hCT2312399.0	204336_s_at	NP_005864.1, NP_001034556.1, EAW75166.1, EAW75167.1
GeneID:4661	MYT1	20	62,795,827	62,873,606	77,779	+	5	1_A375_pNL7_minus_lncRNA::1::3692, 2_A375_pNL97_plus_lncRNA::1::5305, 2_A375_pNL97_plus_lncRNA::1::5306, 2_A375_pNL97_plus_lncRNA::1::5307, 2_A375_pNL97_plus_lncRNA::1::5308	-2403, -2419, 2477, 28068, 41229	upstream, upstream, in gene, in gene, in gene	1	1	18.5	26.25	4	2_A375_pNL97_plus_lncRNA::1	38	Gene MYT1	MYT1, C20orf36, MYTI, PLPB1, MTF1	myelin transcription factor 1	NM_004535	1556269_at, 210341_at, 215622_x_at	NP_004526.1
GeneID:55251	PCMTD2	20	62,887,048	62,907,579	20,531	+	2	1_A375_pNL7_minus_lncRNA::1::3693, 2_A375_pNL97_plus_lncRNA::1::5309	-40, -72	upstream, upstream	1	1	29	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene PCMTD2	FLJ10883, C20orf36, KIAA0835, KIAA1050, PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	NM_018257, NM_001104925	212406_s_at	NP_060727.2, NP_001098395.1
GeneID:8204	NRIP1	21	16,333,556	16,437,126	103,570	-	1	2_A375_pNL97_plus_lncRNA::1::5311	-1002	upstream	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene NRIP1	RIP140, NRIP1, FLJ77253	nuclear receptor interacting protein 1	NM_003489	202599_s_at, 202600_s_at	NP_003480.2
GeneID:54149	C21orf91	21	19,161,284	19,191,703	30,419	-	2	1_A375_pNL7_minus_lncRNA::1::3695, 2_A375_pNL97_plus_lncRNA::1::5314	-105, -105	upstream, upstream	1	1	48	42	1	1_A375_pNL7_minus_lncRNA::1	48	Gene C21orf91	DKFZp781D1223, EURL, C21orf38, YG81, C21orf14, C21orf91	chromosome 21 open reading frame 91	NM_001100421, NM_017447, NM_001100420, hCT2296264.0, hCT2296265.0, hCT2359465.0	220941_s_at, 226109_at	NP_001093891.1, NP_059143.3, NP_001093890.1, EAX10020.1, EAX10021.1, EAX10022.1
GeneID:54148	MRPL39	21	26,957,968	26,979,801	21,833	-	1	2_A375_pNL97_plus_lncRNA::1::5315	-7	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MRPL39	FLJ20451, MGC104174, PRED22, PRED66, MRPL5, C21orf92, MRPL39, MSTP003, RPML5, MGC3400, L39mt, MRP-L5	mitochondrial ribosomal protein L39	NM_080794, NM_017446, hCT1958517.1, hCT1958518.1, hCT2295879.0, hCT401157.3	218558_s_at, 236910_at	NP_542984.2, NP_059142.2, EAX09979.1, EAX09980.1, EAX09981.1, EAX09982.1
GeneID:351	APP	21	27,252,861	27,543,138	290,277	-	1	1_A375_pNL7_minus_lncRNA::1::3696	30434	in gene	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene APP	ABETA, AD1, AAA, CVAP, APP, APPI, PN2, ABPP, CTFgamma	amyloid beta (A4) precursor protein	NM_001136130, NM_001136129, NM_000484, NM_201413, NM_201414, hCT1950206.1, hCT2296412.0, hCT2296413.0, hCT2296415.0, hCT2296416.0, hCT2296417.0, hCT2296419.0, hCT2359476.0, hCT2359477.0, hCT2359478.0	200602_at, 211277_x_at, 214953_s_at	NP_001129602.1, NP_001129601.1, NP_000475.1, NP_958816.1, NP_958817.1, EAX09965.1, EAX09957.1, EAX09958.1, EAX09959.1, EAX09960.1, EAX09961.1, EAX09962.1, EAX09963.1, EAX09964.1, EAX09966.1
GeneID:26046	RNF160	21	30,300,466	30,365,277	64,811	-	1	2_A375_pNL97_plus_lncRNA::1::5317	-3	upstream	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RNF160	FLJ11053, LTN1, KIAA0714, RNF160, C21orf98, ZNF294, C21orf10	listerin E3 ubiquitin protein ligase 1	NM_015565, hCT1818919.3, hCT2359400.0, hCT2359401.0	215596_s_at, 233818_at, 233819_s_at	NP_056380.2, EAX09937.1, EAX09935.1, EAX09936.1
GeneID:10694	CCT8	21	30,428,647	30,446,010	17,363	-	1	2_A375_pNL97_plus_lncRNA::1::5318	-70	upstream	0	1	17	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene CCT8	KIAA0002, PRED71, Cctq, C21orf112, D21S246, CCT8	chaperonin containing TCP1, subunit 8 (theta)	NM_006585, hCT1950308.1, hCT2295274.0, hCT2359479.0	200873_s_at, 210436_at	NP_006576.2, EAX09924.1, EAX09925.1, EAX09926.1
GeneID:56911	C21orf7	21	30,452,873	30,548,204	95,331	+	1	2_A375_pNL97_plus_lncRNA::1::5318	-6793	upstream	0	1	17	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene C21orf7	HC21ORF7, C21orf7, TAK1L, TAKL-1, TAKL, TAKL-2, TAKL-4	chromosome 21 open reading frame 7	NM_020152, hCT1950309.1, hCT2295487.0, hCT2295490.0, hCT2359464.0, hCT2359465.0, hCT401171.2	221211_s_at	NP_064537.1, EAX09918.1, EAX09919.1, EAX09920.1, EAX09921.1, EAX09922.1, EAX09923.1
GeneID:571	BACH1	21	30,671,220	30,734,217	62,997	+	1	2_A375_pNL97_plus_lncRNA::1::5319	1420	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene BACH1	BACH-1, BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	NM_001186, NM_206866, NR_027655, hCT1963242.1, hCT401170.3	204194_at, 210818_s_at, 234315_at, 234935_at	NP_001177.1, NP_996749.1, EAX09913.1, EAX09914.1
GeneID:2897	GRIK1	21	30,909,254	31,312,282	403,028	-	1	1_A375_pNL7_minus_lncRNA::1::3697	283130	in gene	1	0	14	7	1	1_A375_pNL7_minus_lncRNA::1	14	Gene GRIK1	GLR5, EEA3, GLUR5, EAA3, GRIK1	glutamate receptor, ionotropic, kainate 1	NM_000830, NM_175611, hCT2295266.0, hCT2295267.0, hCT2295268.0, hCT2359469.0, hCT401172.3	207242_s_at, 214611_at	NP_000821.1, NP_783300.1, EAX09906.1, EAX09907.1, EAX09908.1, EAX09909.1, EAX09910.1
GeneID:54069	C21orf45	21	33,640,530	33,651,376	10,846	-	1	2_A375_pNL97_plus_lncRNA::1::5320	96	in gene	0	1	20	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene C21orf45	C21orf46, MIS18alpha, B28, FASP1, hMis18alpha, MIS18A, C21orf45	MIS18 kinetochore protein homolog A (S. pombe)	NM_018944, hCT401208.3	219004_s_at, 226597_at, 229671_s_at	NP_061817.1, EAX09881.1
GeneID:140290	TCP10L	21	33,947,151	33,957,845	10,694	-	1	2_A375_pNL97_plus_lncRNA::1::5321	16117	downstream	0	1	11	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene TCP10L	MGC34297, TCP10L, C21orf77, PRED77, TCP10A-2, FLJ10932	t-complex 10 (mouse)-like	NM_144659	230394_at	NP_653260.1
GeneID:56683	C21orf59	21	33,973,984	33,984,918	10,934	-	3	1_A375_pNL7_minus_lncRNA::1::3698, 2_A375_pNL97_plus_lncRNA::1::5322, 2_A375_pNL97_plus_lncRNA::1::5323	15286, 15286, -10	downstream, downstream, upstream	1	1	33	28.5	2	1_A375_pNL7_minus_lncRNA::1	53	Gene C21orf59	C21orf59, FLJ20467, C21orf48, FLJ37137, FLJ40247	chromosome 21 open reading frame 59	NM_021254, NR_036552, hCT1787519.2, hCT1955664.1, hCT2295907.0, hCT401205.3	218123_at	NP_067077.1, EAX09868.1, EAX09865.1, EAX09866.1, EAX09867.1
GeneID:8867	SYNJ1	21	34,001,069	34,100,351	99,282	-	1	2_A375_pNL97_plus_lncRNA::1::5324	-481	upstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SYNJ1	SYNJ1, INPP5G	synaptojanin 1	NM_203446, NM_003895, NM_001160302, NM_001160306, hCT1955682.1, hCT401201.2	207594_s_at, 212990_at, 232993_at	NP_982271.2, NP_003886.3, NP_001153774.1, NP_001153778.1, EAX09863.1, EAX09864.1
GeneID:100506215	LOC100506215	21	34,100,425	34,115,433	15,008	+	1	2_A375_pNL97_plus_lncRNA::1::5324	407	in gene	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100506215	GCFC1-AS1	hypothetical LOC100506215	XR_112180, XR_112179, XR_109663, XR_109662, XR_115411, XR_115410		
GeneID:94104	C21orf66	21	34,106,210	34,144,169	37,959	-	3	1_A375_pNL7_minus_lncRNA::1::3699, 2_A375_pNL97_plus_lncRNA::1::5324, 2_A375_pNL97_plus_lncRNA::1::5325	-119, 43337, -151	upstream, downstream, upstream	1	1	24.5	33.5	2	2_A375_pNL97_plus_lncRNA::1	46	Gene C21orf66	GCFC1, C21orf66, FLJ90561, PSAP105, BM020, GCFC	GC-rich sequence DNA-binding factor 1	NM_016631, NM_013329, NR_027873, hCT1816937.1, hCT1816938.1, hCT1816939.1, hCT1816941.1, hCT1829195.2	1555125_at, 218515_at, 221158_at, 240105_at	NP_057715.2, NP_037461.2, EAX09857.1, EAX09858.1, EAX09859.1, EAX09861.1, EAX09860.1
GeneID:54067	C21orf49	21	34,144,411	34,170,017	25,606	+	2	1_A375_pNL7_minus_lncRNA::1::3699, 2_A375_pNL97_plus_lncRNA::1::5325	-123, -91	upstream, upstream	1	1	36	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene C21orf49	C21orf49	chromosome 21 open reading frame 49	NR_024622, NR_024623, hCT2296142.0	1557782_s_at, 1559755_at	EAX09855.1
GeneID:3454	IFNAR1	21	34,697,214	34,732,129	34,915	+	1	2_A375_pNL97_plus_lncRNA::1::5326	-190	upstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene IFNAR1	IFNAR, AVP, IFNAR1, IFNBR, IFRC, IFN-alpha-REC	interferon (alpha, beta and omega) receptor 1	NM_000629, hCT2297060.0, hCT2297061.0, hCT2297062.0	204191_at, 225661_at, 225669_at	NP_000620.2, EAX09837.1, EAX09838.1, EAX09839.1
GeneID:3460	IFNGR2	21	34,775,202	34,809,828	34,626	+	1	2_A375_pNL97_plus_lncRNA::1::5327	1438	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene IFNGR2	IFNGR2, AF-1, IFNGT1, IFGR2	interferon gamma receptor 2 (interferon gamma transducer 1)	NM_005534, hCT1962492.1, hCT401181.3	201642_at	NP_005525.2, EAX09835.1, EAX09834.1
GeneID:757	TMEM50B	21	34,821,448	34,852,281	30,833	-	1	1_A375_pNL7_minus_lncRNA::1::3701	-391	upstream	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene TMEM50B	FLJ26146, DKFZp586C2482, TMEM50B, HCVP7TP3, C21orf4	transmembrane protein 50B	NM_006134, hCT1971239.1, hCT1971240.1	219600_s_at, 222907_x_at, 225182_at	NP_006125.2, EAX09833.1, EAX09832.1
GeneID:54943	DNAJC28	21	34,860,238	34,864,023	3,785	-	1	1_A375_pNL7_minus_lncRNA::1::3701	11351	downstream	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene DNAJC28	DNAJC28, C21orf55, C21orf78	DnaJ (Hsp40) homolog, subfamily C, member 28	NM_017833, NM_001040192, hCT1642617.3, hCT2295787.0	220372_at	NP_060303.2, NP_001035282.1, EAX09830.1, EAX09831.1
GeneID:1827	RCAN1	21	35,888,782	35,987,382	98,600	-	2	1_A375_pNL7_minus_lncRNA::1::3702, 2_A375_pNL97_plus_lncRNA::1::5329	-234, -202	upstream, upstream	1	1	33	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene RCAN1	RCN1, CSP1, ADAPT78, DSC1, DSCR1, RCAN1, MCIP1	regulator of calcineurin 1	NM_203417, NM_203418, NM_004414, hCT1957582.1, hCT1957583.1, hCT1957584.1, hCT2295708.0, hCT2295711.0, hCT401174.3	208370_s_at, 215253_s_at, 215254_at	NP_981962.1, NP_981963.1, NP_004405.3, EAX09777.1, EAX09778.1, EAX09782.1, EAX09779.1, EAX09780.1, EAX09781.1
GeneID:54093	SETD4	21	37,406,839	37,432,816	25,977	-	1	1_A375_pNL7_minus_lncRNA::1::3703	48	in gene	1	0	16	8	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SETD4	SETD4, C21orf18, C21orf27	SET domain containing 4	NM_001007259, NM_017438, hCT2336150.0, hCT2336151.0, hCT2359402.0, hCT2359403.0, hCT2359404.0, hCT2359405.0, hCT401085.2	213989_x_at, 219482_at, 230899_at	NP_001007260.1, NP_059134.1, EAX09756.1, EAX09757.1, EAX09759.1, EAX09761.1, EAX09758.1, EAX09760.1, EAX09762.1
GeneID:873	CBR1	21	37,442,285	37,445,462	3,177	+	1	1_A375_pNL7_minus_lncRNA::1::3703	-9517	upstream	1	0	16	8	1	1_A375_pNL7_minus_lncRNA::1	16	Gene CBR1	SDR21C1, hCBR1, CBR, CBR1	carbonyl reductase 1	NM_001757, hCT1957579.1, hCT1957580.1, hCT2336474.0, hCT401084.3	209213_at	NP_001748.1, EAX09754.1, EAX09752.1, EAX09753.1, EAX09755.1
GeneID:51227	PIGP	21	38,437,664	38,445,458	7,794	-	2	1_A375_pNL7_minus_lncRNA::1::3704, 2_A375_pNL97_plus_lncRNA::1::5330	-526, -596	upstream, upstream	1	1	22	17	1	1_A375_pNL7_minus_lncRNA::1	22	Gene PIGP	PIGP, DSCR5, DCRC, DSRC, DCRC-S	phosphatidylinositol glycan anchor biosynthesis, class P	NM_153681, NM_153682, NR_026352, hCT1962905.1, hCT1962906.1, hCT2359425.0, hCT2359426.0, hCT401237.2	221689_s_at	NP_710148.1, NP_710149.1, EAX09724.1, EAX09725.1, EAX09726.1, EAX09728.1, EAX09727.1
GeneID:7267	TTC3	21	38,445,571	38,575,408	129,837	+	2	1_A375_pNL7_minus_lncRNA::1::3704, 2_A375_pNL97_plus_lncRNA::1::5330	413, 483	in gene, in gene	1	1	22	17	1	1_A375_pNL7_minus_lncRNA::1	22	Gene TTC3	TTC3, DKFZp686M0150, DCRR1, TPRDIII, RNF105	tetratricopeptide repeat domain 3	NM_003316, NM_001001894, hCT1957581.1, hCT1960361.0, hCT1960362.0, hCT2296200.0, hCT2296204.0, hCT2359432.0, hCT2359433.0, hCT401239.3	1569472_s_at, 208073_x_at, 208661_s_at, 208662_s_at, 208663_s_at, 208664_s_at, 210645_s_at	NP_003307.3, NP_001001894.1, EAX09717.1, EAX09721.1, EAX09722.1, EAX09723.1, EAX09716.1, EAX09718.1, EAX09719.1, EAX09720.1
GeneID:3772	KCNJ15	21	39,628,664	39,673,748	45,084	+	1	1_A375_pNL7_minus_lncRNA::1::3705	20904	in gene	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene KCNJ15	KIR4.2, KCNJ15, MGC13584, IRKK, KIR1.3	potassium inwardly-rectifying channel, subfamily J, member 15	NM_002243, NM_170736, NM_170737, hCT1957931.1, hCT1964864.1, hCT2295211.0	210119_at, 211806_s_at, 238428_at	NP_002234.2, NP_733932.1, NP_733933.1, EAX09683.1, EAX09684.1, EAX09685.1
GeneID:150082	LCA5L	21	40,777,770	40,816,128	38,358	-	1	1_A375_pNL7_minus_lncRNA::1::3706	-1824	upstream	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LCA5L	LCA5L, C21orf13, MGC33295	Leber congenital amaurosis 5-like	NM_152505, hCT2294786.0, hCT2294787.0, hCT2359396.0, hCT401233.3	232196_at	NP_689718.1, EAX09643.1, EAX09641.1, EAX09642.1, EAX09644.1
GeneID:6450	SH3BGR	21	40,817,797	40,887,433	69,636	+	1	1_A375_pNL7_minus_lncRNA::1::3706	155	in gene	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SH3BGR	SH3BGR, 21-GARP	SH3 domain binding glutamic acid-rich protein	NM_007341, NM_001001713, hCT1961502.1, hCT2294699.0, hCT2359484.0, hCT401228.2	204979_s_at	NP_031367.1, NP_001001713.1, EAX09637.1, EAX09638.1, EAX09639.1, EAX09640.1
GeneID:63977	PRDM15	21	43,218,385	43,299,591	81,206	-	1	2_A375_pNL97_plus_lncRNA::1::5332	-9657	upstream	0	1	8	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene PRDM15	C21orf83, ZNF298, PFM15, PRDM15	PR domain containing 15	NM_022115, NM_001040424, hCT2295245.0, hCT2295246.0, hCT2295247.0, hCT2295248.0	231931_at, 234524_at, 236061_at	NP_071398.3, NP_001035514.1, EAX09584.1, EAX09585.1, EAX09586.1, EAX09587.1
GeneID:25966	C2CD2	21	43,305,219	43,373,999	68,780	-	1	2_A375_pNL97_plus_lncRNA::1::5332	64751	in gene	0	1	8	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene C2CD2	DKFZp686O198, MGC71445, C21orf25, C21orf258, DKFZp686F0422, C2CD2, TMEM24L	C2 calcium-dependent domain containing 2	NM_015500, NM_199050, hCT2295240.0, hCT401251.3	212875_s_at	NP_056315.1, NP_950251.1, EAX09582.1, EAX09583.1
GeneID:53347	UBASH3A	21	43,824,019	43,867,774	43,755	+	1	2_A375_pNL97_plus_lncRNA::1::5333	33997	in gene	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene UBASH3A	TULA, UBASH3A, CLIP4, STS-2	ubiquitin associated and SH3 domain containing A	NM_018961, NM_001001895, hCT2295416.0, hCT2359408.0, hCT2359409.0, hCT401273.3	220418_at	NP_061834.1, NP_001001895.1, EAX09560.1, EAX09561.1, EAX09562.1, EAX09563.1
GeneID:10785	WDR4	21	44,263,204	44,299,678	36,474	-	2	1_A375_pNL7_minus_lncRNA::1::3707, 2_A375_pNL97_plus_lncRNA::1::5334	94, 158	in gene, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene WDR4	WDR4, TRM82	WD repeat domain 4	NM_018669, NM_033661, hCT1950241.1, hCT2294771.0, hCT401275.2	221632_s_at, 226882_x_at, 235551_at, 241937_s_at	NP_061139.2, NP_387510.1, EAX09527.1, EAX09528.1, EAX09529.1

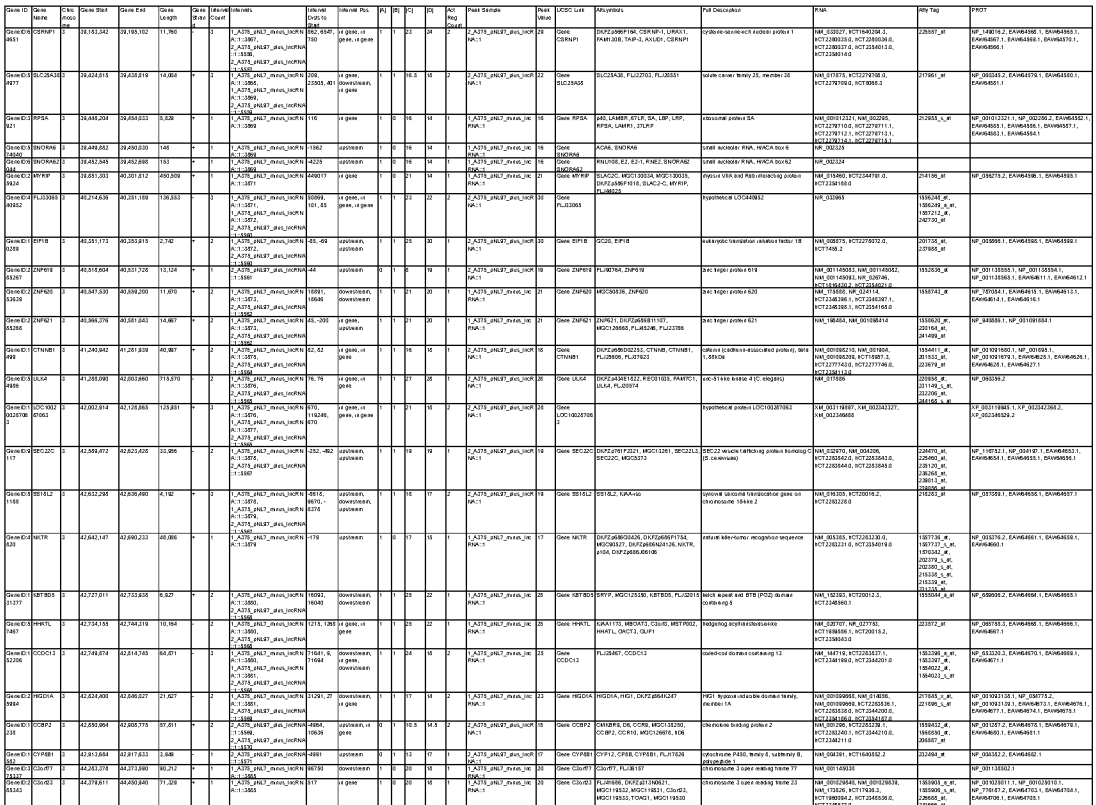
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:5316	PKNOX1	21	44,394,643	44,453,688	59,045	+	2	1_A375_pNL7_minus_lncRNA::1::3708, 2_A375_pNL97_plus_lncRNA::1::5335	77, 77	in gene, in gene	1	1	37	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene PKNOX1	PKNOX1, pknox1c, PREP1	PBX/knotted 1 homeobox 1	NM_004571, hCT2349574.0, hCT2349575.0	204195_s_at, 204196_x_at, 216004_s_at, 221883_at, 54051_at	NP_004562.2, EAX09516.1, EAX09517.1
GeneID:875	CBS	21	44,473,301	44,496,472	23,171	-	1	1_A375_pNL7_minus_lncRNA::1::3709	1112	in gene	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene CBS	CBS, HIP4	cystathionine-beta-synthase	NM_000071, NM_001178008, NM_001178009, hCT1961506.0, hCT1961507.0, hCT2295140.0, hCT2295142.0, hCT2295145.0, hCT2295146.0, hCT2359411.0, hCT2359412.0, hCT401291.2	1553972_a_at, 212816_s_at, 240517_at	NP_000062.1, NP_001171479.1, NP_001171480.1, EAX09511.1, EAX09512.1, EAX09514.1, EAX09507.1, EAX09508.1, EAX09509.1, EAX09510.1, EAX09513.1, EAX09515.1
GeneID:8568	RRP1	21	45,209,418	45,223,983	14,565	+	1	2_A375_pNL97_plus_lncRNA::1::5337	-10	upstream	0	1	6	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RRP1	NOP52, D21S2056E, RRP1A, NNP-1, RRP1	ribosomal RNA processing 1 homolog (S. cerevisiae)	NM_003683, hCT1957965.1, hCT2298947.0, hCT401295.2	218758_s_at, 222733_x_at	NP_003674.1, EAX09471.1, EAX09470.1, EAX09472.1
GeneID:755	C21orf2	21	45,748,827	45,759,285	10,458	-	1	1_A375_pNL7_minus_lncRNA::1::3711	-91	upstream	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene C21orf2	C21orf2, YF5, A2	chromosome 21 open reading frame 2	NM_004928, hCT1961509.1, hCT2295527.0, hCT2359438.0, hCT2359439.0, hCT401315.3	203993_x_at, 203994_s_at, 203995_at, 203996_s_at, 214309_s_at, 221975_s_at, 235582_at, 238965_at	NP_004919.1, EAX09431.1, EAX09432.1, EAX09433.1, EAX09434.1, EAX09435.1
GeneID:100505684	LOC100505684	21	45,755,735	45,756,327	592	+	1	1_A375_pNL7_minus_lncRNA::1::3711	3641	downstream	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100505684		hypothetical LOC100505684	XR_109679		
GeneID:7327	UBE2G2	21	46,188,955	46,221,738	32,783	-	1	2_A375_pNL97_plus_lncRNA::1::5338	74	in gene	0	1	11	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene UBE2G2	UBC7, UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	NM_003343, NM_182688, hCT1641551.3, hCT1961465.1, hCT1961466.1, hCT2295505.0, hCT2295506.0, hCT2359475.0	1557053_s_at, 209041_s_at, 209042_s_at, 232755_at	NP_003334.2, NP_872630.1, EAX09395.1, EAX09396.1, EAX09397.1, EAX09400.1, EAX09398.1, EAX09399.1
GeneID:6612	SUMO3	21	46,225,532	46,238,044	12,512	-	1	2_A375_pNL97_plus_lncRNA::1::5338	16380	downstream	0	1	11	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SUMO3	SMT3H1, SUMO-3, Smt3B, SMT3A, SUMO3	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	NM_006936, hCT1961508.1, hCT1966270.1, hCT2359421.0, hCT401310.3	200739_s_at, 200740_s_at	NP_008867.2, EAX09390.1, EAX09391.1, EAX09392.1, EAX09393.1
GeneID:754	PTTG1IP	21	46,269,513	46,293,741	24,228	-	2	1_A375_pNL7_minus_lncRNA::1::3712, 2_A375_pNL97_plus_lncRNA::1::5339	-275, -147	upstream, upstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PTTG1IP	C21orf1, PTTG1IP, C21orf3, PBF	pituitary tumor-transforming 1 interacting protein	NM_004339, hCT2295556.0, hCT2359480.0, hCT401316.3	200677_at	NP_004330.1, EAX09388.1, EAX09386.1, EAX09387.1
GeneID:100505746	LOC100505746	21	46,340,966	46,349,595	8,629	+	1	2_A375_pNL97_plus_lncRNA::1::5340	18626	downstream	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100505746		hypothetical LOC100505746	XR_109682		
GeneID:84536	C21orf67	21	46,353,199	46,359,828	6,629	-	1	2_A375_pNL97_plus_lncRNA::1::5340	36	in gene	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C21orf67	C21orf67, MGC120189, MGC120188, C21orf69, MGC149386, MGC120186, PRED54, MGC149387, MGC120187	chromosome 21 open reading frame 67	NR_027128, NR_027129	1555627_s_at	
GeneID:85395	C21orf70	21	46,359,955	46,396,888	36,933	+	1	2_A375_pNL97_plus_lncRNA::1::5340	-163	upstream	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C21orf70	C21orf70, PRED56	chromosome 21 open reading frame 70	NM_058190, hCT1966271.1, hCT1966272.1, hCT2296831.1, hCT2296834.1, hCT2296836.1, hCT401312.4	243750_x_at	NP_478070.1, EAX09367.1, EAX09368.1, EAX09369.1, EAX09370.1, EAX09371.1, EAX09372.1
GeneID:8888	MCM3AP	21	47,655,048	47,705,236	50,188	-	1	2_A375_pNL97_plus_lncRNA::1::5343	-652	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MCM3AP	MCM3AP, GANP, FLJ45306, MAP80, FLJ44336, KIAA0572	minichromosome maintenance complex component 3 associated protein	NM_003906, hCT1950237.1	212269_s_at, 214514_at, 215580_at, 215581_s_at, 215582_x_at	NP_003897.2, EAX09296.1
GeneID:54059	C21orf57	21	47,706,267	47,717,665	11,398	+	1	2_A375_pNL97_plus_lncRNA::1::5343	-379	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C21orf57	YBEY, FLJ46907, C21orf57	chromosome 21 open reading frame 57	NM_058181, NM_001006114, hCT1950239.1, hCT1966263.1, hCT1966264.1, hCT2297971.0, hCT2297972.0, hCT2359462.0, hCT2359463.0, hCT401262.2	227421_at, 239208_s_at, 242565_x_at	NP_478061.1, NP_001006114.1, EAX09288.1, EAX09289.1, EAX09291.1, EAX09292.1, EAX09290.1, EAX09293.1, EAX09294.1, EAX09295.1
GeneID:3275	PRMT2	21	48,055,527	48,084,863	29,336	+	2	1_A375_pNL7_minus_lncRNA::1::3715, 2_A375_pNL97_plus_lncRNA::1::5344	185, 185	in gene, in gene	1	1	21	20	1	1_A375_pNL7_minus_lncRNA::1	21	Gene PRMT2	HRMT1L1, PRMT2, MGC111373	protein arginine methyltransferase 2	NM_001535, NM_206962, hCT1963093.1, hCT1963094.1, hCT2297988.0, hCT2297990.0, hCT2297991.0, hCT2297993.0, hCT2359436.0, hCT401256.3	202098_s_at, 210384_at, 221564_at, 228722_at, 228725_x_at	NP_001526.2, NP_996845.1, EAX09258.1, EAX09259.1, EAX09260.1, EAX09264.1, EAX09261.1, EAX09262.1, EAX09263.1, EAX09265.1
GeneID:27440	CECR5	22	17,618,410	17,646,177	27,767	-	2	1_A375_pNL7_minus_lncRNA::1::3716, 2_A375_pNL97_plus_lncRNA::1::5345	-6671, -6623	upstream, upstream	1	1	21	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene CECR5	CECR5	cat eye syndrome chromosome region, candidate 5	NM_017829, NM_033070, hCT12126.2, hCT1959952.1	218592_s_at	NP_060299.4, NP_149061.1, EAW57747.1, EAW57748.1
GeneID:100130717	CECR4	22	17,640,279	17,646,335	6,056	+	2	1_A375_pNL7_minus_lncRNA::1::3716, 2_A375_pNL97_plus_lncRNA::1::5345	12569, 12521	downstream, downstream	1	1	21	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene CECR4	CECR4, NCRNA00017	cat eye syndrome chromosome region, candidate 4 (non-protein coding)	NR_024482, NR_024483		
GeneID:51816	CECR1	22	17,660,192	17,690,779	30,587	-	2	1_A375_pNL7_minus_lncRNA::1::3716, 2_A375_pNL97_plus_lncRNA::1::5345	37931, 37979	downstream, downstream	1	1	21	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene CECR1	IDGFL, ADA2, ADGF, CECR1	cat eye syndrome chromosome region, candidate 1	NM_017424, NM_177405, hCT12121.1, hCT2279182.0	219505_at	NP_059120.2, NP_803124.1, EAW57750.1, EAW57751.1
GeneID:57553	MICAL3	22	18,270,415	18,507,325	236,910	-	3	1_A375_pNL7_minus_lncRNA::1::3717, 2_A375_pNL97_plus_lncRNA::1::5346, 2_A375_pNL97_plus_lncRNA::1::5347	22845, 51645, 22845	in gene, in gene, in gene	1	1	47.5	47	2	1_A375_pNL7_minus_lncRNA::1	86	Gene MICAL3	KIAA0819, MGC189703, MICAL3	microtubule associated monoxygenase, calponin and LIM domain containing 3	NM_001122731, NM_015241, NM_001136004	229474_at, 231553_s_at, 231985_at	NP_001116203.1, NP_056056.2, NP_001129476.1
GeneID:693233	MIR648	22	18,463,634	18,463,727	93	-	1	2_A375_pNL97_plus_lncRNA::1::5346	8047	downstream	0	1	9	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MIR648	MIRN648, hsa-mir-648, MIR648	microRNA 648	NR_030378		
GeneID:55670	PEX26	22	18,560,686	18,572,207	11,521	+	1	2_A375_pNL97_plus_lncRNA::1::5348	18	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PEX26	PEX26, Pex26pM1T, FLJ20695, PEX26M1T	peroxisomal biogenesis factor 26	NM_017929, NM_001127649, hCT1959957.1, hCT1959958.0, hCT2353234.0	219180_s_at, 235098_at	NP_060399.1, NP_001121121.1, EAW57762.1, EAW57763.1, EAW57764.1
GeneID:9993	DGCR2	22	19,023,795	19,109,967	86,172	-	1	2_A375_pNL97_plus_lncRNA::1::5349	815	in gene	0	1	6	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene DGCR2	SEZ-12, LAN, KIAA0163, DGS-C, IDD, DKFZp686I1730, DGCR2	DiGeorge syndrome critical region gene 2	NM_005137, NM_001173533, NM_001173534, NM_001184781, NR_033674, hCT1955594.1, hCT2287069.0, hCT8293.3	202099_s_at, 214198_s_at, 227028_s_at	NP_005128.1, NP_001167004.1, NP_001167005.1, NP_001171710.1, EAX03062.1, EAX03063.1, EAX03061.1
GeneID:8220	DGCR14	22	19,117,792	19,132,190	14,398	-	1	2_A375_pNL97_plus_lncRNA::1::5349	23038	downstream	0	1	6	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene DGCR14	DGS-H, DGCR14, DGCR13, DGSH, DGSI, DGS-I, ES2, Es2el	DiGeorge syndrome critical region gene 14	NM_022719, hCT1955595.1, hCT1964782.1, hCT1964783.1, hCT8294.3	204383_at, 216285_at, 217285_at, 239730_at, 241748_x_at, 32032_at	NP_073210.1, EAX03053.1, EAX03054.1, EAX03055.1, EAX03056.1
GeneID:23617	TSSK2	22	19,118,321	19,120,136	1,815	+	1	2_A375_pNL97_plus_lncRNA::1::5349	-9169	upstream	0	1	6	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TSSK2	STK22B, DGS-G, SPOGA2, FLJ38613, TSSK2	testis-specific serine kinase 2	NM_053006	214371_at, 217275_at	NP_443732.3
GeneID:6576	SLC25A1	22	19,163,094	19,166,301	3,207	-	1	1_A375_pNL7_minus_lncRNA::1::3718	7261	downstream	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SLC25A1	CTP, SLC25A1, SEA, SLC20A3	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	NM_005984, NR_033687, hCT1955598.1, hCT1955599.1, hCT2358705.0, hCT8296.1	210010_s_at	NP_005975.1, EAX03048.1, EAX03049.1, EAX03050.1, EAX03051.1
GeneID:8218	CLTCL1	22	19,166,986	19,279,239	112,253	-	3	1_A375_pNL7_minus_lncRNA::1::3718, 1_A375_pNL7_minus_lncRNA::1::3719, 2_A375_pNL97_plus_lncRNA::1::5350	120199, 69559, 69543	downstream, in gene, in gene	1	1	16	18.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene CLTCL1	CLTCL1, CLH22, CLTD, CHC22, FLJ36032, CLTCL	clathrin, heavy chain-like 1	NM_007098, NM_001835, hCT1955579.1, hCT8286.2	205944_s_at	NP_009029.3, NP_001826.3, EAX03046.1, EAX03047.1
GeneID:7290	HIRA	22	19,318,224	19,419,219	100,995	-	2	1_A375_pNL7_minus_lncRNA::1::3720, 2_A375_pNL97_plus_lncRNA::1::5351	-765, -781	upstream, upstream	1	1	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene HIRA	TUPLE1, HIRA, TUP1, DGCR1	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	NM_003325, hCT1686385.2, hCT2287052.0	1569560_at, 217427_s_at	NP_003316.3, EAX03044.1, EAX03043.1
GeneID:64976	MRPL40	22	19,420,036	19,423,598	3,562	+	2	1_A375_pNL7_minus_lncRNA::1::3720, 2_A375_pNL97_plus_lncRNA::1::5351	-52, -36	upstream, upstream	1	1	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene MRPL40	MRP-L22, MGC9400, MRPL40, NLVCF, FLJ41774, URIM	mitochondrial ribosomal protein L40	NM_003776, hCT8946.3	203152_at	NP_003767.2, EAX03042.1
GeneID:128977	C22orf39	22	19,428,409	19,435,755	7,346	-	3	1_A375_pNL7_minus_lncRNA::1::3720, 1_A375_pNL7_minus_lncRNA::1::3721, 2_A375_pNL97_plus_lncRNA::1::5351	15771, 1179, 15755	downstream, in gene, downstream	1	1	14.5	10	2	1_A375_pNL7_minus_lncRNA::1	15	Gene C22orf39	MGC74441, DKFZp686I08210, C22orf39	chromosome 22 open reading frame 39	NM_173793, NM_001166242, hCT2287050.1, hCT2349253.0, hCT8956.3	1553974_at, 227086_at	NP_776154.3, NP_001159714.1, EAX03039.1, EAX03040.1, EAX03041.1
GeneID:100506503	LOC100506503	22	19,435,416	19,437,628	2,212	+	1	1_A375_pNL7_minus_lncRNA::1::3721	-840	upstream	1	0	14	5	1	1_A375_pNL7_minus_lncRNA::1	14	Gene LOC100506503		hypothetical LOC100506503	XR_112220, XR_109701, XR_115442		
GeneID:7353	UFD1L	22	19,437,464	19,466,738	29,274	-	3	1_A375_pNL7_minus_lncRNA::1::3721, 1_A375_pNL7_minus_lncRNA::1::3722, 2_A375_pNL97_plus_lncRNA::1::5352	32162, -350, -94	downstream, upstream, upstream	1	1	15.5	11.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene UFD1L	UFD1L, UFD1	ubiquitin fusion degradation 1 like (yeast)	NM_005659, NM_001035247, hCT1955653.1, hCT8955.3	209103_s_at	NP_005650.2, NP_001030324.2, EAX03037.1, EAX03038.1
GeneID:8318	CDC45L	22	19,467,414	19,508,135	40,721	+	2	1_A375_pNL7_minus_lncRNA::1::3722, 2_A375_pNL97_plus_lncRNA::1::5352	-326, -582	upstream, upstream	1	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CDC45L	CDC45L2, CDC45L, PORC-PI-1, CDC45	CDC45 cell division cycle 45 homolog (S. cerevisiae)	NM_003504, NM_001178010, NM_001178011, hCT8950.3	204126_s_at	NP_003495.1, NP_001171481.1, NP_001171482.1, EAX03036.1
GeneID:54584	GNB1L	22	19,775,934	19,842,462	66,528	-	1	2_A375_pNL97_plus_lncRNA::1::5353	-162	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene GNB1L	FKSG1, DGCRK3, KIAA1645, GNB1L, WDR14, WDVCF, GY2	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	NM_053004	220762_s_at, 223563_at, 223564_s_at	NP_443730.1
GeneID:79680	C22orf29	22	19,833,661	19,842,371	8,710	-	1	2_A375_pNL97_plus_lncRNA::1::5353	-253	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C22orf29	C22orf29, FLJ21125	chromosome 22 open reading frame 29	NM_024627	219560_at, 226204_at	NP_078903.3
GeneID:54487	DGCR8	22	20,067,755	20,099,400	31,645	+	2	1_A375_pNL7_minus_lncRNA::1::3723, 2_A375_pNL97_plus_lncRNA::1::5354	36917, 36949	downstream, downstream	1	1	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene DGCR8	C22orf12, Gy1, pasha, DGCR8, DGCRK6	DiGeorge syndrome critical region gene 8	NM_001190326, NM_022720, hCT2286392.0, hCT2286393.0, hCT2286395.0	218650_at, 219811_at, 64474_g_at, 91617_at	NP_001177255.1, NP_073557.3, EAX02998.1, EAX02999.1, EAX03000.1
GeneID:27037	TRMT2A	22	20,099,398	20,104,768	5,370	-	2	1_A375_pNL7_minus_lncRNA::1::3723, 2_A375_pNL97_plus_lncRNA::1::5354	96, 64	in gene, in gene	1	1	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene TRMT2A	MGC102728, TRMT2A, HTF9C	TRM2 tRNA methyltransferase 2 homolog A (S. cerevisiae)	NM_022727, NM_182984, hCT1783543.2, hCT1813407.1, hCT1813408.1	218475_at	NP_073564.3, NP_892029.2, EAX02995.1, EAX02996.1, EAX02997.1
GeneID:5902	RANBP1	22	20,105,024	20,114,704	9,680	+	3	1_A375_pNL7_minus_lncRNA::1::3723, 2_A375_pNL97_plus_lncRNA::1::5354, 2_A375_pNL97_plus_lncRNA::1::5355	-352, -320, 13632	upstream, upstream, downstream	1	1	18.5	24.5	2	2_A375_pNL97_plus_lncRNA::1	29	Gene RANBP1	RANBP1, HTF9A, MGC88701	RAN binding protein 1	NM_002882, hCT1955627.2, hCT1955628.1, hCT1955629.1, hCT1955630.2, hCT2340553.0, hCT2340554.0, hCT2340555.0, hCT2358713.0, hCT8940.4	202482_x_at, 202483_s_at, 221915_s_at	NP_002873.1, EAX02988.1, EAX02986.1, EAX02989.1, EAX02992.1, EAX02994.1, EAX02987.1, EAX02990.1, EAX02991.1, EAX02993.1
GeneID:29801	ZDHHC8	22	20,119,364	20,135,530	16,166	+	1	2_A375_pNL97_plus_lncRNA::1::5355	-708	upstream	0	1	13	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene ZDHHC8	ZDHHC8, ZDHHCL1, DHHC8, ZNF378	zinc finger, DHHC-type containing 8	NM_001185024, NM_013373, hCT1783546.2, hCT2286404.0, hCT2286406.0	225744_at	NP_001171953.1, NP_037505.1, EAX02982.1, EAX02983.1, EAX02984.1
GeneID:51586	MED15	22	20,861,886	20,941,919	80,033	+	2	1_A375_pNL7_minus_lncRNA::1::3724, 2_A375_pNL97_plus_lncRNA::1::5356	2, 10	in gene, in gene	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MED15	CAG7A, CTG7A, ARC105, TIG1, DKFZp686A2214, TNRC7, TIG-1, MED15, PCQAP, DKFZp762B1216, FLJ42935, FLJ42282	mediator complex subunit 15	NM_015889, NM_001003891, hCT2286422.0, hCT2286423.0, hCT2286425.0, hCT2286426.0, hCT2358700.0, hCT2358701.0, hCT2358702.0, hCT2358703.0, hCT32547.3	222175_s_at	NP_056973.2, NP_001003891.1, EAX02950.1, EAX02952.1, EAX02955.1, EAX02956.1, EAX02948.1, EAX02949.1, EAX02951.1, EAX02953.1, EAX02954.1
GeneID:5297	PI4KA	22	21,061,979	21,213,070	151,091	-	2	1_A375_pNL7_minus_lncRNA::1::3725, 2_A375_pNL97_plus_lncRNA::1::5357	-114, -82	upstream, upstream	1	1	25	21	1	1_A375_pNL7_minus_lncRNA::1	25	Gene PI4KA	FLJ16556, PI4KA, pi4K230, PIK4CA, PI4K-ALPHA	phosphatidylinositol 4-kinase, catalytic, alpha	NM_058004, NM_002650	207081_s_at	NP_477352.2, NP_002641.1
GeneID:9342	SNAP29	22	21,213,292	21,245,502	32,210	+	2	1_A375_pNL7_minus_lncRNA::1::3725, 2_A375_pNL97_plus_lncRNA::1::5357	-108, -140	upstream, upstream	1	1	25	21	1	1_A375_pNL7_minus_lncRNA::1	25	Gene SNAP29	SNAP29, FLJ21051, CEDNIK, SNAP-29	synaptosomal-associated protein, 29kDa	NM_004782, hCT32543.3	218327_s_at, 222597_at	NP_004773.1, EAX02935.1
GeneID:150209	AIFM3	22	21,319,418	21,335,649	16,231	+	1	2_A375_pNL97_plus_lncRNA::1::5358	17190	downstream	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene AIFM3	FLJ45137, AIFM3, FLJ30473, AIFL	apoptosis-inducing factor, mitochondrion-associated, 3	NM_144704, NM_001018060, NM_001146288, NR_027464, hCT1970625.1, hCT1970632.1, hCT1970633.1, hCT1970635.1, hCT1970636.1, hCT2286438.0, hCT2358711.0, hCT32550.3	244084_at	NP_653305.1, NP_001018070.1, NP_001139760.1, EAX02924.1, EAX02925.1, EAX02929.1, EAX02926.1, EAX02927.1, EAX02928.1, EAX02930.1, EAX02931.1
GeneID:8216	LZTR1	22	21,336,558	21,353,326	16,768	+	3	1_A375_pNL7_minus_lncRNA::1::3726, 2_A375_pNL97_plus_lncRNA::1::5358, 2_A375_pNL97_plus_lncRNA::1::5359	19426, 50, 19698	downstream, in gene, downstream	1	1	16.5	19.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene LZTR1	MGC21205, LZTR1, LZTR-1	leucine-zipper-like transcription regulator 1	NM_006767, hCT32540.3	203412_at	NP_006758.2, EAX02923.1
GeneID:80764	THAP7	22	21,354,061	21,356,404	2,343	-	3	1_A375_pNL7_minus_lncRNA::1::3726, 2_A375_pNL97_plus_lncRNA::1::5359, 2_A375_pNL97_plus_lncRNA::1::5360	420, 148, -7596	in gene, in gene, upstream	1	1	16	21	2	2_A375_pNL97_plus_lncRNA::1	21	Gene THAP7	THAP7, MGC10963	THAP domain containing 7	NM_030573, NM_001008695, hCT2282952.1, hCT2282954.1, hCT2282963.1, hCT2282965.1	218492_s_at	NP_085050.2, NP_001008695.1, EAX02918.1, EAX02919.1, EAX02920.1, EAX02921.1
GeneID:439931	FLJ39582	22	21,356,211	21,364,663	8,452	+	3	1_A375_pNL7_minus_lncRNA::1::3726, 2_A375_pNL97_plus_lncRNA::1::5359, 2_A375_pNL97_plus_lncRNA::1::5360	-227, 45, 7789	upstream, in gene, in gene	1	1	16	21	2	2_A375_pNL97_plus_lncRNA::1	21	Gene FLJ39582	FLJ40420	hypothetical LOC439931	NR_027051, NR_027052	236403_at, 239015_at	
GeneID:9127	P2RX6	22	21,369,442	21,382,302	12,860	+	1	2_A375_pNL97_plus_lncRNA::1::5360	-5442	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene P2RX6	P2X6, P2XM, MGC129625, P2RXL1, P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6	NM_005446, NM_001159554, hCT1970624.1, hCT2358714.0, hCT2358715.0, hCT2358716.0, hCT32544.1	206880_at, 211147_s_at	NP_005437.2, NP_001153026.1, EAX02910.1, EAX02911.1, EAX02912.1, EAX02913.1, EAX02914.1
GeneID:7332	UBE2L3	22	21,921,957	21,978,323	56,366	+	2	1_A375_pNL7_minus_lncRNA::1::3727, 2_A375_pNL97_plus_lncRNA::1::5361	61691, 61787	downstream, downstream	1	1	42	38	1	1_A375_pNL7_minus_lncRNA::1	42	Gene UBE2L3	E2-F1, UbcM4, UBE2L3, UBCH7, L-UBC	ubiquitin-conjugating enzyme E2L 3	NM_003347, NR_028436, NR_028437, hCT1962722.1, hCT1967644.1	200676_s_at, 200682_s_at, 200683_s_at, 200684_s_at	NP_003338.1, EAW59459.1, EAW59460.1
GeneID:150223	YDJC	22	21,982,378	21,984,340	1,962	-	2	1_A375_pNL7_minus_lncRNA::1::3727, 2_A375_pNL97_plus_lncRNA::1::5361	692, 596	in gene, in gene	1	1	42	38	1	1_A375_pNL7_minus_lncRNA::1	42	Gene YDJC	YDJC, MGC133160	YdjC homolog (bacterial)	NM_001017964, hCT1953847.1, hCT2353491.0, hCT2353492.0, hCT23752.2	227042_at	NP_001017964.1, EAW59461.1, EAW59462.1, EAW59463.1, EAW59464.1
GeneID:164592	CCDC116	22	21,987,086	21,991,616	4,530	+	2	1_A375_pNL7_minus_lncRNA::1::3727, 2_A375_pNL97_plus_lncRNA::1::5361	-3438, -3342	upstream, upstream	1	1	42	38	1	1_A375_pNL7_minus_lncRNA::1	42	Gene CCDC116	FLJ36046, CCDC116	coiled-coil domain containing 116	NM_152612, hCT1649121.3, hCT2300037.1	1555792_a_at	NP_689825.2, EAW59466.1, EAW59465.1
GeneID:23759	PPIL2	22	22,020,273	22,052,202	31,929	+	1	1_A375_pNL7_minus_lncRNA::1::3728	79	in gene	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene PPIL2	hCyP-60, MGC787, PPIL2, FLJ39930, CYP60, Cyp-60, MGC33174, CYC4	peptidylprolyl isomerase (cyclophilin)-like 2	NM_014337, NM_148175, NM_148176, hCT1963280.1, hCT1963282.1, hCT1963283.1, hCT2353449.0, hCT2353450.0, hCT2353451.0, hCT2353452.0, hCT23748.3	206063_x_at, 206064_s_at, 209299_x_at, 214986_x_at, 217407_x_at, 223999_at, 243414_at	NP_055152.1, NP_680480.1, NP_680481.1, EAW59469.1, EAW59474.1, EAW59475.1, EAW59470.1, EAW59471.1, EAW59472.1, EAW59473.1, EAW59476.1
GeneID:729832	LOC729832	22	24,350,106	24,352,079	1,973	-	1	2_A375_pNL97_plus_lncRNA::1::5362	-7665	upstream	0	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC729832		glutathione S-transferase theta-1-like			
GeneID:83606	C22orf13	22	24,936,406	24,951,275	14,869	-	1	2_A375_pNL97_plus_lncRNA::1::5363	-613	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C22orf13	C22orf13, LLN4, MGC1842	chromosome 22 open reading frame 13	NM_031444, hCT1951848.2, hCT2353506.0, hCT2353507.0, hCT2353508.0, hCT32472.4	223039_at	NP_113632.2, EAW59665.1, EAW59666.1, EAW59667.1, EAW59668.1, EAW59669.1
GeneID:6634	SNRPD3	22	24,951,618	24,968,509	16,891	+	1	2_A375_pNL97_plus_lncRNA::1::5363	270	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNRPD3	SNRPD3, Sm-D3, SMD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	NM_004175, hCT2300316.1	202567_at	NP_004166.1, EAW59670.1
GeneID:129049	SGSM1	22	25,202,136	25,322,813	120,677	+	1	2_A375_pNL97_plus_lncRNA::1::5364	69976	in gene	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SGSM1	MGC133296, KIAA1941, SGSM1, RUTBC2	small G protein signaling modulator 1	NM_133454, NM_001098497, NM_001039948, NM_001098498	1562239_at, 230287_at, 242921_at	NP_597711.1, NP_001091967.1, NP_001091968.1, NP_001035037.1
GeneID:84700	MYO18B	22	26,138,120	26,427,007	288,887	+	1	1_A375_pNL7_minus_lncRNA::1::3729	5304	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene MYO18B	FLJ41942, DKFZp779C1668, MYO18B, DKFZp434C2422	myosin XVIIIB	NM_032608, hCT2301174.0, hCT2301175.0, hCT2301176.0, hCT2301177.0, hCT2353423.0, hCT2353424.0, hCT2353425.0	1554579_a_at	NP_115997.5, EAW59707.1, EAW59702.1, EAW59703.1, EAW59705.1, EAW59706.1, EAW59704.1, EAW59708.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:24144	TFIP11	22	26,887,893	26,908,437	20,544	-	1	2_A375_pNL97_plus_lncRNA::1::5365	5	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TFIP11	hNtr1, NTR1, TIP39, TFIP11, FLJ22086, Spp382, bK445C9.6	tuftelin interacting protein 11	NM_012143, NM_001008697, hCT2301316.0, hCT2353515.0, hCT31342.3	202750_s_at, 202751_at	NP_036275.1, NP_001008697.1, EAW59722.1, EAW59723.1, EAW59724.1
GeneID:100507599	LOC100507599	22	26,908,476	26,910,531	2,055	+	1	2_A375_pNL97_plus_lncRNA::1::5365	-44	upstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100507599		hypothetical LOC100507599	XR_112230, XR_109753, XR_115478		
GeneID:129080	EMID1	22	29,601,953	29,655,586	53,633	+	2	1_A375_pNL7_minus_lncRNA::1::3733, 2_A375_pNL97_plus_lncRNA::1::5369	62175, 62143	downstream, downstream	1	1	32	41	1	2_A375_pNL97_plus_lncRNA::1	41	Gene EMID1	EMI5, MGC50557, EMU1, hEmu1, EMID1	EMI domain containing 1	NM_133455, hCT1644223.3, hCT2300848.0	1564251_at, 213779_at	NP_597712.2, EAW59776.1, EAW59777.1
GeneID:25807	RHBDD3	22	29,655,844	29,663,914	8,070	-	2	1_A375_pNL7_minus_lncRNA::1::3733, 2_A375_pNL97_plus_lncRNA::1::5369	-214, -182	upstream, upstream	1	1	32	41	1	2_A375_pNL97_plus_lncRNA::1	41	Gene RHBDD3	RHBDD3, PTAG, C22orf3, HS984G1A	rhomboid domain containing 3	NM_012265, hCT1967611.1, hCT32910.3	204402_at, 217622_at	NP_036397.1, EAW59778.1, EAW59779.1
GeneID:2130	EWSR1	22	29,663,998	29,696,515	32,517	+	4	1_A375_pNL7_minus_lncRNA::1::3733, 1_A375_pNL7_minus_lncRNA::1::3734, 2_A375_pNL97_plus_lncRNA::1::5369, 2_A375_pNL97_plus_lncRNA::1::5370	130, 38306, 98, 38818	in gene, downstream, in gene, downstream	1	1	24	30	2	2_A375_pNL97_plus_lncRNA::1	41	Gene EWSR1	bK984G1.4, EWSR1, EWS	Ewing sarcoma breakpoint region 1	NM_005243, NM_013986, NM_001163285, NM_001163286, NM_001163287, hCT2300850.0, hCT2300851.0, hCT2300852.0, hCT2300853.0, hCT2300854.0, hCT2353499.0, hCT2353500.0, hCT2353501.0	209214_s_at, 210011_s_at, 210012_s_at, 229966_at	NP_005234.1, NP_053733.2, NP_001156757.1, NP_001156758.1, NP_001156759.1, EAW59780.1, EAW59781.1, EAW59782.1, EAW59783.1, EAW59784.1, EAW59785.1, EAW59786.1, EAW59787.1
GeneID:10634	GAS2L1	22	29,702,997	29,708,774	5,777	+	2	1_A375_pNL7_minus_lncRNA::1::3734, 2_A375_pNL97_plus_lncRNA::1::5370	-693, -161	upstream, upstream	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene GAS2L1	GAS2L1, MGC17243, GAR22	growth arrest-specific 2 like 1	NM_006478, NM_152236, NM_152237, hCT1951342.1, hCT1967610.1, hCT2300855.0, hCT2300856.0, hCT2353484.0, hCT2353485.0, hCT2353486.0, hCT32905.2	208255_s_at, 209729_at, 31874_at	NP_006469.2, NP_689422.1, NP_689423.1, EAW59789.1, EAW59793.1, EAW59795.1, EAW59788.1, EAW59790.1, EAW59791.1, EAW59792.1, EAW59794.1
GeneID:10633	RASL10A	22	29,708,922	29,711,748	2,826	-	2	1_A375_pNL7_minus_lncRNA::1::3734, 2_A375_pNL97_plus_lncRNA::1::5370	9444, 8932	downstream, downstream	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RASL10A	RASL10A, RRP22	RAS-like, family 10, member A	NM_006477, NM_001007279, hCT2301165.0, hCT32906.3	206850_at	NP_006468.1, NP_001007280.1, EAW59796.1, EAW59797.1
GeneID:8563	THOC5	22	29,904,156	29,949,736	45,580	-	2	1_A375_pNL7_minus_lncRNA::1::3735, 2_A375_pNL97_plus_lncRNA::1::5371	-40, -72	upstream, upstream	1	1	24	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene THOC5	PK1.3, C22orf19, THOC5, Fmip, fSAP79	THO complex 5	NM_003678, NM_001002877, NM_001002878, NM_001002879	209418_s_at, 209419_at	NP_003669.4, NP_001002877.1, NP_001002878.1, NP_001002879.1
GeneID:8508	NIPSNAP1	22	29,950,797	29,977,144	26,347	-	2	1_A375_pNL7_minus_lncRNA::1::3735, 2_A375_pNL97_plus_lncRNA::1::5371	27368, 27336	downstream, downstream	1	1	24	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene NIPSNAP1	NIPSNAP1		NM_003634	201708_s_at, 201709_s_at	NP_003625.2
GeneID:164633	CABP7	22	30,116,344	30,127,822	11,478	+	2	1_A375_pNL7_minus_lncRNA::1::3736, 2_A375_pNL97_plus_lncRNA::1::5372	-3480, -3512	upstream, upstream	1	1	52	55	1	2_A375_pNL97_plus_lncRNA::1	55	Gene CABP7	CALN2, MGC57793, CABP7	calcium binding protein 7	NM_182527, hCT2300885.0, hCT2300887.0	234796_at, 243173_at	NP_872333.1, EAW59835.1, EAW59834.1
GeneID:55954	ZMAT5	22	30,126,945	30,162,969	36,024	-	1	2_A375_pNL97_plus_lncRNA::1::5373	-455	upstream	0	1	14	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ZMAT5	ZMAT5		NM_019103, NM_001003692, hCT2301148.0, hCT2301149.0	218752_at	NP_061976.1, NP_001003692.1, EAW59837.1, EAW59838.1
GeneID:29796	UQCR10	22	30,163,358	30,166,402	3,044	+	1	2_A375_pNL97_plus_lncRNA::1::5373	66	in gene	0	1	14	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene UQCR10	HSPC151, UCCR7.2, UCRC, HSPC119, QCR9, HSPC051, UQCR10	ubiquinol-cytochrome c reductase, complex III subunit X	NM_013387, NM_001003684, hCT1641645.2, hCT2300889.0, hCT2300891.0	218190_s_at, 228142_at	NP_037519.2, NP_001003684.1, EAW59839.1, EAW59840.1, EAW59841.1
GeneID:84164	ASCC2	22	30,184,600	30,234,254	49,654	-	1	1_A375_pNL7_minus_lncRNA::1::3737	38990	in gene	1	0	15	10	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ASCC2	ASCC2, ASC1p100	activating signal cointegrator 1 complex subunit 2	NM_032204, hCT1951343.1, hCT1967612.1, hCT1967613.1, hCT1967614.1, hCT2301146.0, hCT2353525.0, hCT32912.3	215684_s_at	NP_115580.2, EAW59846.1, EAW59842.1, EAW59843.1, EAW59844.1, EAW59848.1, EAW59845.1, EAW59847.1
GeneID:10291	SF3A1	22	30,727,977	30,752,913	24,936	-	1	2_A375_pNL97_plus_lncRNA::1::5375	145	in gene	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SF3A1	SF3A120, SF3A1, PRPF21, SAP114, PRP21	splicing factor 3a, subunit 1, 120kDa	NM_005877, NM_001005409, hCT2300790.0, hCT32568.3	1568796_at, 201356_at, 201357_s_at, 216457_s_at, 227516_at, 232920_at, 242949_x_at	NP_005868.1, NP_001005409.1, EAW59878.1, EAW59879.1
GeneID:550631	CCDC157	22	30,752,627	30,772,818	20,191	+	1	2_A375_pNL97_plus_lncRNA::1::5375	141	in gene	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CCDC157	CCDC157	coiled-coil domain containing 157	NM_001017437		NP_001017437.2
GeneID:23541	SEC14L2	22	30,792,933	30,821,278	28,345	+	1	1_A375_pNL7_minus_lncRNA::1::3738	27291	in gene	1	0	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene SEC14L2	C22orf6, MGC65053, KIAA1186, TAP1, SEC14L2, SPF, KIAA1658, TAP	SEC14-like 2 (S. cerevisiae)	NM_012429, NM_033382, hCT2300543.0, hCT2353566.0, hCT2353567.0, hCT32567.3	204541_at, 230316_at, 232400_at, 232894_at, 232895_s_at, 240024_at	NP_036561.1, NP_203740.1, EAW59865.1, EAW59866.1, EAW59867.1, EAW59868.1
GeneID:51537	MTP18	22	30,821,720	30,825,041	3,321	+	1	1_A375_pNL7_minus_lncRNA::1::3738	-1496	upstream	1	0	21	18	1	1_A375_pNL7_minus_lncRNA::1	21	Gene MTP18	MTFP1, MTP18, HSPC242	mitochondrial fission process 1	NM_016498, NM_001003704, hCT1967593.1, hCT2300504.0, hCT32580.4	223172_s_at	NP_057582.2, NP_001003704.1, EAW59889.1, EAW59890.1, EAW59891.1
GeneID:266629	SEC14L3	22	30,855,216	30,868,034	12,818	-	2	1_A375_pNL7_minus_lncRNA::1::3739, 2_A375_pNL97_plus_lncRNA::1::5376	12578, 12610	in gene, in gene	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SEC14L3	SEC14L3, MGC119367, MGC119366, TAP2, MGC119368	SEC14-like 3 (S. cerevisiae)	NM_174975, hCT1816305.1, hCT2300782.0	216346_at, 240699_at, 241221_at	NP_777635.1, EAW59894.1, EAW59893.1
GeneID:23762	OSBP2	22	31,090,793	31,303,811	213,018	+	4	1_A375_pNL7_minus_lncRNA::1::3740, 1_A375_pNL7_minus_lncRNA::1::3741, 2_A375_pNL97_plus_lncRNA::1::5377, 2_A375_pNL97_plus_lncRNA::1::5378	108119, 111751, 108119, 111735	in gene, in gene, in gene, in gene	1	1	26.5	30.5	2	2_A375_pNL97_plus_lncRNA::1	33	Gene OSBP2	OSBPL4, ORP-4, OSBPL1, ORP4, OSBP2	oxysterol binding protein 2	NM_030758, hCT2300515.0, hCT2300516.0, hCT2353465.0, hCT32573.3	1569617_at, 221237_s_at, 223432_at	NP_110385.1, EAW59919.1, EAW59916.1, EAW59917.1, EAW59918.1
GeneID:22880	MORC2	22	31,322,600	31,364,187	41,587	-	2	1_A375_pNL7_minus_lncRNA::1::3742, 2_A375_pNL97_plus_lncRNA::1::5379	-1125, -1093	upstream, upstream	1	1	33	20	1	1_A375_pNL7_minus_lncRNA::1	33	Gene MORC2	ZCWG, MORC2, ZCWCC1	MORC family CW-type zinc finger 2	NM_014941, hCT2300760.0, hCT31329.3	203956_at, 216863_s_at	NP_055756.1, EAW59922.1, EAW59921.1
GeneID:55000	TUG1	22	31,365,634	31,375,381	9,747	+	2	1_A375_pNL7_minus_lncRNA::1::3742, 2_A375_pNL97_plus_lncRNA::1::5379	-322, -354	upstream, upstream	1	1	33	20	1	1_A375_pNL7_minus_lncRNA::1	33	Gene TUG1	FLJ20618, TI-227H, TUG1, MGC46067, NCRNA00080	taurine upregulated 1 (non-protein coding)	NR_002323	222244_s_at, 226397_at, 230635_at	
GeneID:56478	EIF4ENIF1	22	31,835,345	31,885,874	50,529	-	1	2_A375_pNL97_plus_lncRNA::1::5380	-174	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene EIF4ENIF1	FLJ26551, EIF4ENIF1, Clast4, FLJ21601, 4E-T	eukaryotic translation initiation factor 4E nuclear import factor 1	NM_019843, NM_001164501, NM_001164502, hCT1951335.1, hCT2300200.0, hCT32790.3	218626_at, 242291_at	NP_062817.2, NP_001157973.1, NP_001157974.1, EAW59977.1, EAW59978.1, EAW59979.1
GeneID:9814	SFI1	22	31,892,261	32,014,534	122,273	+	1	2_A375_pNL97_plus_lncRNA::1::5380	-6213	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SFI1	MGC57874, hSfi1p, RP5-858B16.1, MGC131712, MGC150663, SFI1, PISD, MGC156283	Sfi1 homolog, spindle assembly associated (yeast)	NM_014775, NM_001007467, hCT2300078.0, hCT2300079.0, hCT2300081.0, hCT2353552.0	213431_x_at, 214402_s_at, 215699_x_at, 36545_s_at	NP_055590.2, NP_001007468.1, EAW59980.1, EAW59981.1, EAW59982.1, EAW59983.1
GeneID:23761	PISD	22	32,014,477	32,026,810	12,333	-	2	1_A375_pNL7_minus_lncRNA::1::3743, 2_A375_pNL97_plus_lncRNA::1::5381	-230, -198	upstream, upstream	1	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PISD	PSSC, DKFZp566G2246, DJ858B16, PSDC, dJ858B16.2, PISD, PSD	phosphatidylserine decarboxylase	NM_014338, hCT2300193.0, hCT2300194.0, hCT2300195.0, hCT2300196.0, hCT2300197.0, hCT2300198.0, hCT2300199.0, hCT2353545.0	202392_s_at	NP_055153.1, EAW59984.1, EAW59985.1, EAW59989.1, EAW59990.1, EAW59991.1, EAW59986.1, EAW59987.1, EAW59988.1
GeneID:253143	C22orf30	22	32,077,333	32,146,120	68,787	-	2	1_A375_pNL7_minus_lncRNA::1::3744, 2_A375_pNL97_plus_lncRNA::1::5382	-152, -88	upstream, upstream	1	1	17	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene C22orf30	MGC50372, DKFZp761P2326, PRR14L, FLJ33247, FLJ23059, FLJ31368, C22orf30	chromosome 22 open reading frame 30	NM_173566, hCT1815995.4, hCT2300189.2, hCT2300190.2, hCT2300192.1	1553761_at, 1558097_at, 216555_at, 236941_at	NP_775837.2, EAW59995.1, EAW59992.1, EAW59993.1, EAW59994.1
GeneID:9681	DEPDC5	22	32,150,069	32,303,001	152,932	+	2	1_A375_pNL7_minus_lncRNA::1::3744, 2_A375_pNL97_plus_lncRNA::1::5382	-3797, -3861	upstream, upstream	1	1	17	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene DEPDC5	DEP.5, DKFZp779P2027, DEPDC5	DEP domain containing 5	NM_014662, NM_001007188, NM_001136029, hCT1967602.0, hCT2300084.0, hCT2300085.0, hCT2300086.0	205223_at	NP_055477.1, NP_001007189.1, NP_001129501.1, EAW59996.1, EAW59997.1, EAW59999.1, EAW59998.1
GeneID:6523	SLC5A1	22	32,439,019	32,509,016	69,997	+	2	2_A375_pNL97_plus_lncRNA::1::5383, 2_A375_pNL97_plus_lncRNA::1::5384	61173, 64085	in gene, in gene	0	1	12.5	20.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene SLC5A1	NAGT, D22S675, SLC5A1, SGLT1	solute carrier family 5 (sodium/glucose cotransporter), member 1	NM_000343, NR_033411, hCT32782.2	206628_at	NP_000334.1, EAW60006.1
GeneID:25793	FBXO7	22	32,870,707	32,894,818	24,111	+	2	1_A375_pNL7_minus_lncRNA::1::3745, 2_A375_pNL97_plus_lncRNA::1::5385	125, -35	in gene, upstream	1	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene FBXO7	FBX, DKFZp686B08113, FBX07, PKPS, FBXO7, FBX7, PARK15	F-box protein 7	NM_012179, NM_001033024, hCT1962587.1, hCT1962588.1, hCT2353469.0, hCT32663.3	1554423_a_at, 201178_at, 243649_at	NP_036311.3, NP_001028196.1, EAW60023.1, EAW60024.1, EAW60025.1, EAW60026.1
GeneID:8224	SYN3	22	32,908,539	33,454,377	545,838	-	2	2_A375_pNL97_plus_lncRNA::1::5386, 1_A375_pNL7_minus_lncRNA::1::3746	526057, 261385	in gene, in gene	1	1	18	13.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene SYN3	SYN3		NM_003490, NM_133633, NM_001135774, hCT1955486.2, hCT2300906.1, hCT2300907.1, hCT2300908.1, hCT2300910.0, hCT2300911.1, hCT2300912.1, hCT2300913.0, hCT2300914.1	206322_at	NP_003481.3, NP_598344.2, NP_001129246.1, EAW60034.1, EAW60035.1, EAW60036.1, EAW60029.1, EAW60030.1, EAW60031.1, EAW60032.1, EAW60033.1, EAW60037.1
GeneID:7078	TIMP3	22	33,196,802	33,259,028	62,226	+	1	1_A375_pNL7_minus_lncRNA::1::3746	-3810	upstream	1	0	20	10	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TIMP3	SFD, K222TA2, K222, HSMRK222, TIMP3	TIMP metallopeptidase inhibitor 3	NM_000362, hCT32665.2	201147_s_at, 201148_s_at, 201149_s_at, 201150_s_at	NP_000353.1, EAW60038.1
GeneID:10042	HMGXB4	22	35,653,445	35,691,800	38,355	+	4	1_A375_pNL7_minus_lncRNA::1::3747, 1_A375_pNL7_minus_lncRNA::1::3748, 2_A375_pNL97_plus_lncRNA::1::5387, 2_A375_pNL97_plus_lncRNA::1::5388	-69, 42603, 11, 42635	upstream, downstream, in gene, downstream	1	1	15	25.5	2	2_A375_pNL97_plus_lncRNA::1	31	Gene HMGXB4	HMG2L1, HMGBCG, HMGXB4, THC211630	HMG box domain containing 4	NM_001003681, NR_027780, hCT2300114.0, hCT2300116.0, hCT2353522.0, hCT32805.3	212596_s_at, 212597_s_at	NP_001003681.1, EAW60048.1, EAW60049.1, EAW60050.1, EAW60051.1
GeneID:10043	TOM1	22	35,695,268	35,743,987	48,719	+	2	1_A375_pNL7_minus_lncRNA::1::3748, 2_A375_pNL97_plus_lncRNA::1::5388	780, 812	in gene, in gene	1	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TOM1	TOM1, FLJ33404	target of myb1 (chicken)	NM_005488, NM_001135729, NM_001135730, NR_024194, NR_024195, NM_001135732, hCT1950809.1, hCT2300117.0, hCT2300120.0, hCT2353479.0, hCT2353480.0, hCT32796.3	202807_s_at	NP_005479.1, NP_001129201.1, NP_001129202.1, NP_001129204.1, EAW60056.1, EAW60058.1, EAW60053.1, EAW60054.1, EAW60055.1, EAW60057.1
GeneID:3162	HMOX1	22	35,777,060	35,790,207	13,147	+	1	1_A375_pNL7_minus_lncRNA::1::3749	-4020	upstream	1	0	17	9	1	1_A375_pNL7_minus_lncRNA::1	17	Gene HMOX1	bK286B10, HO-1, HSP32, HMOX1	heme oxygenase (decycling) 1	NM_002133, hCT2300122.0	203665_at	NP_002124.1, EAW60059.1
GeneID:25828	TXN2	22	36,863,093	36,877,687	14,594	-	1	2_A375_pNL97_plus_lncRNA::1::5389	151	in gene	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TXN2	TRX2, MT-TRX, MTRX, TXN2	thioredoxin 2	NM_012473, hCT2301099.0, hCT2301105.0	209077_at, 209078_s_at	NP_036605.2, EAW60104.1, EAW60103.1
GeneID:80020	FOXRED2	22	36,883,233	36,903,148	19,915	-	1	2_A375_pNL97_plus_lncRNA::1::5389	25612	downstream	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FOXRED2	ERFAD, FLJ23322, FLJ33734, FOXRED2	FAD-dependent oxidoreductase domain containing 2	NM_024955, NM_001102371, hCT2301103.0, hCT2301104.1, hCT2353446.0, hCT2353447.0	220707_s_at, 231846_at, 233250_x_at	NP_079231.4, NP_001095841.1, EAW60105.1, EAW60106.1, EAW60107.1, EAW60108.1
GeneID:8664	EIF3D	22	36,906,897	36,925,277	18,380	-	1	1_A375_pNL7_minus_lncRNA::1::3750	125	in gene	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene EIF3D	eIF3-p66, MGC126526, EIF3S7, MGC17258, EIF3D, eIF3-zeta	eukaryotic translation initiation factor 3, subunit D	NM_003753, hCT1815324.2, hCT2301098.0	200005_at	NP_003744.1, EAW60109.1, EAW60110.1
GeneID:10369	CACNG2	22	36,960,104	37,098,903	138,799	-	5	1_A375_pNL7_minus_lncRNA::1::3751, 1_A375_pNL7_minus_lncRNA::1::3752, 2_A375_pNL97_plus_lncRNA::1::5391, 2_A375_pNL97_plus_lncRNA::1::5392, 2_A375_pNL97_plus_lncRNA::1::5393	58423, -649, 58455, 42727, -601	in gene, upstream, in gene, in gene, upstream	1	1	20.33	23.67	3	2_A375_pNL97_plus_lncRNA::1	36	Gene CACNG2	MGC138502, FLJ41437, MGC138504, CACNG2	calcium channel, voltage-dependent, gamma subunit 2	NM_006078, hCT1827810.3	214495_at	NP_006069.1, EAW60113.1
GeneID:26088	GGA1	22	38,004,481	38,029,571	25,090	+	2	1_A375_pNL7_minus_lncRNA::1::3753, 2_A375_pNL97_plus_lncRNA::1::5394	127, 191	in gene, in gene	1	1	32	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene GGA1	GGA1		NM_013365, NM_001001560, NM_001001561, NM_001172687, NM_001172688, hCT2300998.0, hCT2301002.0, hCT33108.3	1554670_at, 217560_at, 218114_at, 45572_s_at, 50277_at	NP_037497.1, NP_001001560.1, NP_001001561.1, NP_001166158.1, NP_001166159.1, EAW60168.1, EAW60169.1, EAW60170.1
GeneID:3956	LGALS1	22	38,071,613	38,075,809	4,196	+	2	1_A375_pNL7_minus_lncRNA::1::3754, 2_A375_pNL97_plus_lncRNA::1::5395	10643, 10787	downstream, downstream	1	1	23	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LGALS1	GAL1, DKFZp686E23103, LGALS1, GBP	lectin, galactoside-binding, soluble, 1	NM_002305, hCT33111.2	201105_at, 216405_at	NP_002296.1, EAW60178.1
GeneID:79159	NOL12	22	38,082,344	38,089,485	7,141	+	2	1_A375_pNL7_minus_lncRNA::1::3754, 2_A375_pNL97_plus_lncRNA::1::5395	-88, 56	upstream, in gene	1	1	23	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene NOL12	MGC3731, Nop25, NOL12, dJ37E16.7, FLJ34609	nucleolar protein 12	NM_024313, hCT2353462.0, hCT33122.3	222057_at	NP_077289.1, EAW60180.1, EAW60179.1
GeneID:129138	ANKRD54	22	38,226,862	38,240,353	13,491	-	2	2_A375_pNL97_plus_lncRNA::1::5396, 2_A375_pNL97_plus_lncRNA::1::5397	17, -5119	in gene, upstream	0	1	13.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene ANKRD54	LIAR, ANKRD54		NM_138797, NR_036556, hCT2353503.0, hCT2353504.0, hCT33127.4	231847_at	NP_620152.1, EAW60194.1, EAW60192.1, EAW60193.1
GeneID:724028	MIR658	22	38,240,279	38,240,378	99	-	2	2_A375_pNL97_plus_lncRNA::1::5396, 2_A375_pNL97_plus_lncRNA::1::5397	42, -5094	in gene, upstream	0	1	13.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene MIR658	MIRN658, hsa-mir-658, MIR658	microRNA 658	NR_030395		
GeneID:724029	MIR659	22	38,243,665	38,243,761	96	-	2	2_A375_pNL97_plus_lncRNA::1::5396, 2_A375_pNL97_plus_lncRNA::1::5397	3445, -1691	downstream, upstream	0	1	13.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene MIR659	MIRN659, MIR659, hsa-mir-659	microRNA 659	NR_030396		
GeneID:51386	EIF3L	22	38,245,370	38,284,638	39,268	+	2	2_A375_pNL97_plus_lncRNA::1::5396, 2_A375_pNL97_plus_lncRNA::1::5397	-5034, 102	upstream, in gene	0	1	13.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene EIF3L	EIF3L, EIF3S6IP, HSPC025, EIF3EIP, EIF3S11, HSPC021, MSTP005	eukaryotic translation initiation factor 3, subunit L	NM_016091, hCT2300963.0, hCT2300964.0, hCT2353448.0, hCT33113.3	217719_at	NP_057175.1, EAW60195.1, EAW60196.1, EAW60197.1, EAW60198.1
GeneID:85377	MICALL1	22	38,302,346	38,338,026	35,680	+	1	1_A375_pNL7_minus_lncRNA::1::3755	-1194	upstream	1	0	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene MICALL1	KIAA1668, FLJ45921, MICAL-L1, MICALL1, DKFZp686M2226, MIRAB13	MICAL-like 1	NM_033386, hCT2349011.0	221779_at, 55081_at	NP_203744.1, EAW60199.1
GeneID:5435	POLR2F	22	38,349,674	38,365,319	15,645	+	1	1_A375_pNL7_minus_lncRNA::1::3756	14526	in gene	1	0	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene POLR2F	RPB6, RPB14.4, POLR2F, POLRF, HRBP14.4, RPABC2	polymerase (RNA) II (DNA directed) polypeptide F	NM_021974, hCT1962608.1, hCT33131.2	209511_at, 232643_at	NP_068809.1, EAW60202.1, EAW60203.1
GeneID:6663	SOX10	22	38,368,319	38,380,539	12,220	-	2	1_A375_pNL7_minus_lncRNA::1::3756, 2_A375_pNL97_plus_lncRNA::1::5398	16339, 1051	downstream, in gene	1	1	14.5	15.5	2	1_A375_pNL7_minus_lncRNA::1	16	Gene SOX10	WS4, WS2E, WS4C, DOM, MGC15649, PCWH, SOX10	SRY (sex determining region Y)-box 10	NM_006941, hCT1962606.1, hCT33116.3	209842_at, 209843_s_at	NP_008872.1, EAW60205.1, EAW60204.1
GeneID:100131530	LOC100131530	22	38,382,170	38,384,341	2,171	+	1	2_A375_pNL97_plus_lncRNA::1::5398	-2682	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100131530	FLJ36715	hypothetical LOC100131530	XR_112241, XR_109712, XR_115457		
GeneID:25776	CBY1	22	39,052,658	39,069,855	17,197	+	2	1_A375_pNL7_minus_lncRNA::1::3757, 2_A375_pNL97_plus_lncRNA::1::5401	25230, 25262	downstream, downstream	1	1	112	130	1	2_A375_pNL97_plus_lncRNA::1	130	Gene CBY1	HS508I15A, PGEA1, CBY1, PIGEA14, C22orf2, CBY, PIGEA-14, arb1	chibby homolog 1 (Drosophila)	NM_015373, NM_001002880	1560220_a_at, 203450_at	NP_056188.1, NP_001002880.1
GeneID:100506326	LOC100506326	22	39,063,590	39,077,775	14,185	-	2	1_A375_pNL7_minus_lncRNA::1::3757, 2_A375_pNL97_plus_lncRNA::1::5401	-113, -145	upstream, upstream	1	1	112	130	1	2_A375_pNL97_plus_lncRNA::1	130	Gene LOC100506326		hypothetical LOC100506326	XR_112242, XR_112243, XR_109713, XR_109714, XR_115458, XR_115459		
GeneID:56993	TOMM22	22	39,077,954	39,080,765	2,811	+	2	1_A375_pNL7_minus_lncRNA::1::3757, 2_A375_pNL97_plus_lncRNA::1::5401	-66, -34	upstream, upstream	1	1	112	130	1	2_A375_pNL97_plus_lncRNA::1	130	Gene TOMM22	MSTP065, MST065, 1C9-2, TOMM22, TOM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	NM_020243	217960_s_at, 222474_s_at, 229076_s_at	NP_064628.1
GeneID:100506349	LOC100506349	22	39,080,356	39,099,041	18,685	-	5	1_A375_pNL7_minus_lncRNA::1::3757, 1_A375_pNL7_minus_lncRNA::1::3758, 2_A375_pNL97_plus_lncRNA::1::5401, 2_A375_pNL97_plus_lncRNA::1::5402, 2_A375_pNL97_plus_lncRNA::1::5403	21153, -2815, 21121, 1953, -2783	downstream, upstream, downstream, in gene, upstream	1	1	50.33	55.67	3	2_A375_pNL97_plus_lncRNA::1	130	Gene LOC100506349		hypothetical LOC100506349	XR_112244, XR_109715, XR_115460		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9929	JOSD1	22	39,081,548	39,096,459	14,911	-	5	1_A375_pNL7_minus_lncRNA::1::3757, 1_A375_pNL7_minus_lncRNA::1::3758, 2_A375_pNL97_plus_lncRNA::1::5401, 2_A375_pNL97_plus_lncRNA::1::5402, 2_A375_pNL97_plus_lncRNA::1::5403	18571, -5397, 18539, -629, -5365	downstream, upstream, downstream, upstream, upstream	1	1	50.33	55.67	3	2_A375_pNL97_plus_lncRNA::1	130	Gene JOSD1	dJ508I15.2, KIAA0063, JOSD1	Josephin domain containing 1	NM_014876, hCT2305436.0, hCT2305441.0	201751_at	NP_055691.1, EAW60259.1, EAW60260.1
GeneID:9567	GTPBP1	22	39,101,807	39,129,592	27,785	+	3	1_A375_pNL7_minus_lncRNA::1::3758, 2_A375_pNL97_plus_lncRNA::1::5402, 2_A375_pNL97_plus_lncRNA::1::5403	49, -4719, 17	in gene, upstream, in gene	1	1	19.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	20	Gene GTPBP1	GTPBP1, GP-1, MGC20069, GP1, HSPC018	GTP binding protein 1	NM_004286, hCT2300567.0, hCT2300568.0, hCT2300569.0, hCT2300570.0	205274_at, 205275_at, 205276_s_at, 219357_at, 226359_at	NP_004277.2, EAW60261.1, EAW60262.1, EAW60263.1, EAW60264.1
GeneID:25777	SUN2	22	39,130,735	39,151,947	21,212	-	3	1_A375_pNL7_minus_lncRNA::1::3759, 1_A375_pNL7_minus_lncRNA::1::3760, 2_A375_pNL97_plus_lncRNA::1::5404	331, -357, -213	in gene, upstream, upstream	1	1	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene SUN2	KIAA0668, MGC133055, UNC84B, SUN2, MGC133056	Sad1 and UNC84 domain containing 2	NM_015374, hCT1951599.1, hCT1951600.1, hCT2305432.0, hCT2305433.0, hCT2353489.0, hCT2353490.0, hCT32979.3	212144_at	NP_056189.1, EAW60269.1, EAW60265.1, EAW60266.1, EAW60268.1, EAW60271.1, EAW60267.1, EAW60270.1
GeneID:10126	DNAL4	22	39,174,513	39,190,161	15,648	-	1	1_A375_pNL7_minus_lncRNA::1::3761	-143	upstream	1	0	15	8	1	1_A375_pNL7_minus_lncRNA::1	15	Gene DNAL4	PIG27, DNAL4	dynein, axonemal, light chain 4	NM_005740, hCT32973.1	204008_at	NP_005731.1, EAW60272.1
GeneID:23467	NPTXR	22	39,214,457	39,240,017	25,560	-	3	1_A375_pNL7_minus_lncRNA::1::3762, 2_A375_pNL97_plus_lncRNA::1::5405, 2_A375_pNL97_plus_lncRNA::1::5406	19249, 19345, 12497	in gene, in gene, in gene	1	1	16.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene NPTXR	NPTXR, NPR	neuronal pentraxin receptor	NM_014293, hCT1962089.1, hCT2305429.0, hCT32961.3	213040_s_at, 217041_at	NP_055108.2, EAW60275.1, EAW60273.1, EAW60274.1
GeneID:100506361	LOC100506361	22	39,247,189	39,262,334	15,145	+	1	2_A375_pNL97_plus_lncRNA::1::5407	21291	downstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506361		hypothetical LOC100506361	XR_112245, XR_109716, XR_115461		
GeneID:23466	CBX6	22	39,260,243	39,268,258	8,015	-	1	2_A375_pNL97_plus_lncRNA::1::5407	-222	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CBX6	CBX6	chromobox homolog 6	NM_014292, hCT32978.3	202047_s_at, 202048_s_at	NP_055107.3, EAW60276.1
GeneID:6122	RPL3	22	39,708,887	39,715,670	6,783	-	1	2_A375_pNL97_plus_lncRNA::1::5409	214	in gene	0	1	10	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RPL3	RPL3, TARBP-B, L3, MGC104284	ribosomal protein L3	NM_000967, NM_001033853, hCT2307359.1, hCT2307360.0, hCT2307361.1, hCT2307362.0, hCT2307363.0, hCT2307364.1, hCT2307365.1, hCT2307366.1, hCT2307367.1, hCT2307368.1, hCT2307369.1	201217_x_at, 211073_x_at, 211666_x_at, 212039_x_at	NP_000958.1, NP_001029025.1, EAW60312.1, EAW60316.1, EAW60319.1, EAW60320.1, EAW60310.1, EAW60311.1, EAW60313.1, EAW60314.1, EAW60315.1, EAW60317.1, EAW60318.1
GeneID:116938	SNORD83B	22	39,709,824	39,709,916	92	-	1	2_A375_pNL97_plus_lncRNA::1::5409	-5540	upstream	0	1	10	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SNORD83B	RNU83B, U83B, SNORD83B	small nucleolar RNA, C/D box 83B	NR_000028		
GeneID:116937	SNORD83A	22	39,711,218	39,711,312	94	-	1	2_A375_pNL97_plus_lncRNA::1::5409	-4144	upstream	0	1	10	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SNORD83A	RNU83A, SNORD83A, U83A	small nucleolar RNA, C/D box 83A	NR_000027		
GeneID:116936	RNU86	22	39,712,847	39,712,901	54	-	1	2_A375_pNL97_plus_lncRNA::1::5409	-2555	upstream	0	1	10	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RNU86	U62, U86	RNA, U86 small nucleolar	NR_000026		
GeneID:26807	SNORD43	22	39,715,057	39,715,118	61	-	1	2_A375_pNL97_plus_lncRNA::1::5409	-338	upstream	0	1	10	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SNORD43	SNORD43, RNU43, U43	small nucleolar RNA, C/D box 43	NR_002439		
GeneID:10454	MAP3K7IP1	22	39,795,759	39,833,132	37,373	+	2	1_A375_pNL7_minus_lncRNA::1::3763, 2_A375_pNL97_plus_lncRNA::1::5410	-47, -111	upstream, upstream	1	1	32	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene MAP3K7IP1	3'-Tab1, TAB1, MGC57664, MAP3K7IP1	TGF-beta activated kinase 1/MAP3K7 binding protein 1	NM_153497, NM_006116, hCT1649757.3, hCT2306648.0, hCT2306692.1, hCT2340545.0, hCT2340546.0, hCT2340547.0, hCT32980.4	203901_at, 233679_at, 235480_at, 235627_at	NP_705717.1, NP_006107.1, EAW60325.1, EAW60326.1, EAW60327.1, EAW60331.1, EAW60328.1, EAW60329.1, EAW60330.1
GeneID:4248	MGAT3	22	39,853,325	39,888,199	34,874	+	2	1_A375_pNL7_minus_lncRNA::1::3764, 2_A375_pNL97_plus_lncRNA::1::5411	21235, 21267	in gene, in gene	1	1	20	15	1	1_A375_pNL7_minus_lncRNA::1	20	Gene MGAT3	MGAT3, GNT-III, MGC142278, FLJ43371, MGC141943, GNT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	NM_002409, NM_001098270, hCT2306650.0	208058_s_at, 209764_at, 244104_at	NP_002400.3, NP_001091740.1, EAW60332.1
GeneID:100506493	LOC100506493	22	39,871,446	39,873,556	2,110	+	2	1_A375_pNL7_minus_lncRNA::1::3764, 2_A375_pNL97_plus_lncRNA::1::5411	3114, 3146	downstream, downstream	1	1	20	15	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100506493		hypothetical protein LOC100506493	XM_003119851, XM_003118817, XM_003121012		XP_003119899.1, XP_003118865.1, XP_003121060.1
GeneID:468	ATF4	22	39,916,569	39,918,691	2,122	+	1	1_A375_pNL7_minus_lncRNA::1::3765	8743	downstream	1	0	17	11	1	1_A375_pNL7_minus_lncRNA::1	17	Gene ATF4	TAXREB67, ATF4, CREB-2, TXREB, CREB2	activating transcription factor 4 (tax-responsive enhancer element B67)	NM_182810, NM_001675, hCT1951603.1, hCT32994.2	200779_at	NP_877962.1, NP_001666.2, EAW60341.1, EAW60342.1
GeneID:91582	RPS19BP1	22	39,925,098	39,928,860	3,762	-	1	1_A375_pNL7_minus_lncRNA::1::3765	3548	in gene	1	0	17	11	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RPS19BP1	MGC52010, RPS19BP1, dJ1104E15.4, AROS, FLJ21770, S19BP	ribosomal protein S19 binding protein 1	NM_194326, hCT2353565.0, hCT33002.3	225148_at	NP_919307.1, EAW60343.1, EAW60344.1
GeneID:158	ADSL	22	40,742,504	40,762,577	20,073	+	1	1_A375_pNL7_minus_lncRNA::1::3767	11	in gene	1	0	12	14	1	1_A375_pNL7_minus_lncRNA::1	12	Gene ADSL	ASASE, AMPS, ADSL, ASL	adenylosuccinate lyase	NM_000026, NM_001123378, hCT1951571.1, hCT2300646.0, hCT31313.3	202144_s_at, 210250_x_at	NP_000017.1, NP_001116850.1, EAW60375.1, EAW60376.1, EAW60377.1
GeneID:57591	MKL1	22	40,806,292	41,032,690	226,398	-	2	1_A375_pNL7_minus_lncRNA::1::3768, 2_A375_pNL97_plus_lncRNA::1::5413	-190, -350	upstream, upstream	1	1	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene MKL1	MKL1, MAL, MRTF-A, BSAC	megakaryoblastic leukemia (translocation) 1	NM_020831, hCT1951576.1, hCT2300952.0, hCT32369.3	1555763_x_at, 1559902_at, 212748_at, 215291_at, 215292_s_at	NP_065882.1, EAW60382.1, EAW60383.1, EAW60384.1
GeneID:5905	RANGAP1	22	41,641,615	41,682,216	40,601	-	1	2_A375_pNL97_plus_lncRNA::1::5414	-120	upstream	0	1	15	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene RANGAP1	MGC20266, RANGAP1, KIAA1835, SD, Fug1	Ran GTPase activating protein 1	NM_002883, hCT1951580.1, hCT2300930.0, hCT2300931.0, hCT2300933.0, hCT32609.3	1553535_a_at, 212125_at, 212127_at	NP_002874.1, EAW60420.1, EAW60421.1, EAW60422.1, EAW60423.1, EAW60424.1
GeneID:10766	TOB2	22	41,829,492	41,843,027	13,535	-	2	1_A375_pNL7_minus_lncRNA::1::3769, 2_A375_pNL97_plus_lncRNA::1::5415	156, 72	in gene, in gene	1	1	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TOB2	TOB2, TOBL, TOB4, TROB2	transducer of ERBB2, 2	NM_016272	221496_s_at, 222243_s_at, 234720_s_at	NP_057356.1
GeneID:84844	PHF5A	22	41,855,721	41,864,708	8,987	-	2	1_A375_pNL7_minus_lncRNA::1::3770, 2_A375_pNL97_plus_lncRNA::1::5416	-264, -316	upstream, upstream	1	1	16	16	1	1_A375_pNL7_minus_lncRNA::1	16	Gene PHF5A	bK223H9.2, SAP14b, MGC1346, SF3b14b, Rds3, PHF5A, INI	PHD finger protein 5A	NM_032758, hCT1951592.1, hCT32829.3	225309_at	NP_116147.1, EAW60434.1, EAW60433.1
GeneID:50	ACO2	22	41,865,129	41,924,993	59,864	+	2	1_A375_pNL7_minus_lncRNA::1::3770, 2_A375_pNL97_plus_lncRNA::1::5416	-137, -105	upstream, upstream	1	1	16	16	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ACO2	ACONM, MGC20605, ACO2, MGC33908	aconitase 2, mitochondrial	NM_001098, hCT2304019.0, hCT32812.3	200793_s_at	NP_001089.1, EAW60436.1, EAW60435.1
GeneID:171568	POLR3H	22	41,921,803	41,940,479	18,676	-	1	1_A375_pNL7_minus_lncRNA::1::3771	351	in gene	1	0	20	15	1	1_A375_pNL7_minus_lncRNA::1	20	Gene POLR3H	RPC8, POLR3H, RPC22.9, MGC29654, KIAA1665, MGC111097	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	NM_001018050, NM_001018052, NM_138338, hCT1951589.1, hCT2304727.0, hCT2353444.0, hCT2353445.0, hCT32827.3	225678_at, 225682_s_at, 232857_at	NP_001018060.1, NP_001018062.1, NP_612211.1, EAW60437.1, EAW60439.1, EAW60441.1, EAW60438.1, EAW60440.1
GeneID:2547	XRCC6	22	42,017,295	42,060,052	42,757	+	1	2_A375_pNL97_plus_lncRNA::1::5417	45601	downstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene XRCC6	CTCBF, KU70, TLAA, XRCC6, G22P1, ML8, CTC75	X-ray repair complementing defective repair in Chinese hamster cells 6	NM_001469, hCT2304022.0, hCT2304023.0, hCT2353550.0	200792_at, 215308_at	NP_001460.1, EAW60447.1, EAW60446.1, EAW60448.1
GeneID:4809	NHP2L1	22	42,069,937	42,084,913	14,976	-	1	2_A375_pNL97_plus_lncRNA::1::5417	22017	downstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NHP2L1	NHP2L1, OTK27, FA-1, SPAG12, FA1, NHPX, SSFA1, SNRNP15-5, SNU13, 15.5K	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	NM_005008, NM_001003796, hCT1962077.1, hCT1962078.1, hCT2304709.0, hCT32810.2	201076_at, 201077_s_at, 230443_at	NP_004999.1, NP_001003796.1, EAW60450.1, EAW60451.1, EAW60452.1, EAW60453.1
GeneID:100506562	LOC100506562	22	42,072,746	42,073,252	506	-	1	2_A375_pNL97_plus_lncRNA::1::5417	10356	downstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100506562		protein LLP homolog	XM_003119852, XM_003118818, XM_003121013		XP_003119900.1, XP_003118866.1, XP_003121061.1
GeneID:79879	CCDC134	22	42,196,678	42,222,306	25,628	+	2	1_A375_pNL7_minus_lncRNA::1::3772, 2_A375_pNL97_plus_lncRNA::1::5418	32218, 32218	downstream, downstream	1	1	39	30	1	1_A375_pNL7_minus_lncRNA::1	39	Gene CCDC134	dJ821D11.3, FLJ22349, MGC21013, CCDC134	coiled-coil domain containing 134	NM_024821, hCT32830.2	220077_at	NP_079097.1, EAW60468.1
GeneID:6721	SREBF2	22	42,229,106	42,302,375	73,269	+	2	1_A375_pNL7_minus_lncRNA::1::3772, 2_A375_pNL97_plus_lncRNA::1::5418	-210, -210	upstream, upstream	1	1	39	30	1	1_A375_pNL7_minus_lncRNA::1	39	Gene SREBF2	bHLHd2, SREBF2, SREBP2	sterol regulatory element binding transcription factor 2	NM_004599, hCT2303983.0, hCT2353558.0, hCT32813.3	201248_s_at, 242748_at	NP_004590.2, EAW60471.1, EAW60469.1, EAW60470.1
GeneID:79019	CENPM	22	42,334,741	42,343,148	8,407	-	2	1_A375_pNL7_minus_lncRNA::1::3773, 2_A375_pNL97_plus_lncRNA::1::5419	60, 76	in gene, in gene	1	1	32	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene CENPM	C22orf18, MGC861, PANE1, CENP-M, CENPM, bK250D10.2	centromere protein M	NM_024053, NM_001002876, NM_001110215, hCT1951588.1, hCT2353438.0, hCT32822.3	218741_at	NP_076958.1, NP_001002876.1, NP_001103685.1, EAW60474.1, EAW60475.1, EAW60476.1
GeneID:339674	LOC339674	22	42,348,191	42,354,946	6,755	+	2	1_A375_pNL7_minus_lncRNA::1::3773, 2_A375_pNL97_plus_lncRNA::1::5419	-5103, -5119	upstream, upstream	1	1	32	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene LOC339674	bK250D10.8	hypothetical LOC339674	NR_024355		
GeneID:6942	TCF20	22	42,556,019	42,611,445	55,426	-	2	1_A375_pNL7_minus_lncRNA::1::3774, 2_A375_pNL97_plus_lncRNA::1::5420	43285, 43301	in gene, in gene	1	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TCF20	AR1, TCF20, SPBP, KIAA0292	transcription factor 20 (AR1)	NM_181492, NM_005650, hCT1951105.1, hCT1965569.1, hCT2353442.0, hCT32825.2	212931_at, 215511_at, 238667_at	NP_852469.1, NP_005641.1, EAW60495.1, EAW60496.1, EAW60497.1, EAW60498.1
GeneID:84271	POLDIP3	22	42,979,727	43,010,962	31,235	-	2	1_A375_pNL7_minus_lncRNA::1::3775, 2_A375_pNL97_plus_lncRNA::1::5421	-206, -142	upstream, upstream	1	1	24	22	1	1_A375_pNL7_minus_lncRNA::1	24	Gene POLDIP3	KIAA1649, PDIP46, POLDIP3, SKAR	polymerase (DNA-directed), delta interacting protein 3	NM_032311, NM_178136, hCT2264698.1, hCT2264701.1, hCT2264705.1, hCT2264707.1	210583_at, 212100_s_at, 215357_s_at, 243411_at	NP_115687.2, NP_835237.1, EAW73264.1, EAW73265.1, EAW73266.1, EAW73267.1
GeneID:267010	RNU12	22	43,011,251	43,011,399	148	+	2	1_A375_pNL7_minus_lncRNA::1::3775, 2_A375_pNL97_plus_lncRNA::1::5421	-83, -147	upstream, upstream	1	1	24	22	1	1_A375_pNL7_minus_lncRNA::1	24	Gene RNU12	RNU12P, RNU12L, RNU12, RNU12-1, dJ222E13.7	RNA, U12 small nuclear	NR_029422		
GeneID:1727	CYB5R3	22	43,013,846	43,045,405	31,559	-	2	1_A375_pNL7_minus_lncRNA::1::3775, 2_A375_pNL97_plus_lncRNA::1::5421	34237, 34301	downstream, downstream	1	1	24	22	1	1_A375_pNL7_minus_lncRNA::1	24	Gene CYB5R3	CYB5R3, B5R, DIA1	cytochrome b5 reductase 3	NM_001129819, NM_007326, NM_000398, NM_001171660, NM_001171661, hCT1951108.1, hCT1951109.1, hCT2264690.0, hCT2264691.0, hCT2264693.0, hCT31319.2	1554574_a_at, 201885_s_at	NP_001123291.1, NP_015565.1, NP_000389.1, NP_001165131.1, NP_001165132.1, EAW73268.1, EAW73269.1, EAW73270.1, EAW73271.1, EAW73272.1, EAW73273.1
GeneID:25809	TTLL1	22	43,435,522	43,485,434	49,912	-	2	1_A375_pNL7_minus_lncRNA::1::3776, 2_A375_pNL97_plus_lncRNA::1::5423	234, 282	in gene, in gene	1	1	33	53	1	2_A375_pNL97_plus_lncRNA::1	53	Gene TTLL1	TTLL1, HS323M22B, C22orf7	tubulin tyrosine ligase-like family, member 1	NM_012263, NR_027779, hCT1772361.2, hCT1951037.1, hCT2264664.0	1570085_at, 205652_s_at	NP_036395.1, EAW73280.1, EAW73279.1, EAW73281.1
GeneID:64800	EFCAB6	22	43,924,624	44,208,217	283,593	-	1	2_A375_pNL97_plus_lncRNA::1::5424	-135	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene EFCAB6	dJ185D5.1, EFCAB6, HSCBCIP1, KIAA1672, DJBP, FLJ23588	EF-hand calcium binding domain 6	NM_022785, NM_198856	1562815_at, 220271_x_at, 233345_at, 233600_at, 233639_at, 234732_s_at, 234853_s_at	NP_073622.2, NP_942153.1
GeneID:25830	SULT4A1	22	44,220,387	44,258,378	37,991	-	2	1_A375_pNL7_minus_lncRNA::1::3777, 2_A375_pNL97_plus_lncRNA::1::5425	-5478, -5494	upstream, upstream	1	1	20	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene SULT4A1	hBR-STL-1, DJ388M5.3, BR-STL-1, SULTX3, NST, BRSTL1, MGC40032, SULT4A1	sulfotransferase family 4A, member 1	NM_014351, hCT1951026.1, hCT1957728.1, hCT2355190.0, hCT6615.2	219425_at	NP_055166.1, EAW73317.1, EAW73318.1, EAW73319.1, EAW73320.1
GeneID:80339	PNPLA3	22	44,319,619	44,343,448	23,829	+	2	1_A375_pNL7_minus_lncRNA::1::3778, 2_A375_pNL97_plus_lncRNA::1::5426	31549, 31725	downstream, downstream	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene PNPLA3	C22orf20, PNPLA3, ADPN, iPLA(2)epsilon	patatin-like phospholipase domain containing 3	NM_025225, hCT1950036.2, hCT1967567.0, hCT2355196.0	220675_s_at, 233030_at	NP_079501.2, EAW73324.1, EAW73323.1, EAW73325.1
GeneID:25813	SAMM50	22	44,351,261	44,392,412	41,151	+	2	1_A375_pNL7_minus_lncRNA::1::3778, 2_A375_pNL97_plus_lncRNA::1::5426	-93, 83	upstream, in gene	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SAMM50	FLJ99036, TRG-3, OMP85, CGI-51, TOB55, FLJ42905, FLJ35825, YNL026W, SAMM50, SAM50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	NM_015380, hCT8344.3	201569_s_at, 201570_at, 230396_at, 243239_at	NP_056195.3, EAW73326.1
GeneID:112885	PHF21B	22	45,277,042	45,405,809	128,767	-	2	1_A375_pNL7_minus_lncRNA::1::3779, 2_A375_pNL97_plus_lncRNA::1::5427	34300, 34241	in gene, in gene	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene PHF21B	PHF4, PHF21B, FLJ34161, BHC80L	PHD finger protein 21B	NM_138415, NM_001135862, hCT2266666.0, hCT2266669.0, hCT2266670.0	1560091_a_at, 1562309_s_at	NP_612424.1, NP_001129334.1, EAW73365.1, EAW73366.1, EAW73367.1
GeneID:100506695	LOC100506695	22	45,364,867	45,368,165	3,298	-	2	1_A375_pNL7_minus_lncRNA::1::3779, 2_A375_pNL97_plus_lncRNA::1::5427	-3344, -3403	upstream, upstream	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100506695		hypothetical LOC100506695	XR_112257, XR_109729, XR_115484		
GeneID:25814	ATXN10	22	46,067,678	46,241,187	173,509	+	1	2_A375_pNL97_plus_lncRNA::1::5429	786	in gene	0	1	6	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ATXN10	ATXN10, HUMEEP, SCA10, E46L, FLJ37990	ataxin 10	NM_013236, NM_001167621, hCT1951027.1, hCT2355187.0	208832_at, 208833_s_at	NP_037368.1, NP_001161093.1, EAW73392.1, EAW73393.1
GeneID:7477	WNT7B	22	46,316,246	46,373,008	56,762	-	1	2_A375_pNL97_plus_lncRNA::1::5430	7952	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene WNT7B	WNT7B	wingless-type MMTV integration site family, member 7B	NM_058238, hCT7322.2		NP_478679.1, EAW73394.1
GeneID:100506756	LOC100506756	22	46,345,836	46,373,008	27,172	+	1	2_A375_pNL97_plus_lncRNA::1::5430	19220	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100506756		hypothetical LOC100506756	XR_109733, XR_109735, XR_109734		
GeneID:400931	LOC400931	22	46,481,877	46,509,808	27,931	+	1	1_A375_pNL7_minus_lncRNA::1::3780	-21	upstream	1	0	17	11	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC400931	FLJ27365	hypothetical LOC400931	NR_027033, hCT1951036.1, hCT2351319.0	232480_at	EAW73398.1, EAW73399.1
GeneID:55020	TTC38	22	46,663,861	46,689,905	26,044	+	2	1_A375_pNL7_minus_lncRNA::1::3781, 2_A375_pNL97_plus_lncRNA::1::5431	28907, 28923	downstream, downstream	1	1	22	20	1	1_A375_pNL7_minus_lncRNA::1	22	Gene TTC38	TTC38, FLJ20699	tetratricopeptide repeat domain 38	NM_017931, hCT1965576.1, hCT2271408.0, hCT2271410.0, hCT33071.2	216434_at, 216768_x_at, 218272_at	NP_060401.2, EAW73412.1, EAW73413.1, EAW73414.1, EAW73415.1
GeneID:150384	CN5H6.4	22	46,691,040	46,692,557	1,517	-	2	1_A375_pNL7_minus_lncRNA::1::3781, 2_A375_pNL97_plus_lncRNA::1::5431	-211, -227	upstream, upstream	1	1	22	20	1	1_A375_pNL7_minus_lncRNA::1	22	Gene CN5H6.4		hypothetical LOC150384	NR_024009	1556661_at	
GeneID:51512	GTSE1	22	46,692,638	46,726,707	34,069	+	3	1_A375_pNL7_minus_lncRNA::1::3781, 2_A375_pNL97_plus_lncRNA::1::5431, 2_A375_pNL97_plus_lncRNA::1::5432	130, 146, 38978	in gene, in gene, downstream	1	1	18	24.5	2	2_A375_pNL97_plus_lncRNA::1	29	Gene GTSE1	B99, GTSE1	G-2 and S-phase expressed 1	NM_016426, hCT2271415.0, hCT2271416.0, hCT2271418.0, hCT2271419.0	204315_s_at, 204317_at, 204318_s_at, 211040_x_at, 215942_s_at, 229343_at	NP_057510.4, EAW73419.1, EAW73418.1, EAW73420.1, EAW73421.1
GeneID:55687	TRMU	22	46,731,298	46,753,237	21,939	+	1	2_A375_pNL97_plus_lncRNA::1::5432	318	in gene	0	1	14	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene TRMU	TRMU, TRNT1, MTU1, TRMT, MGC99627, TRMT1, MTO2	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	NM_018006, hCT2271421.0, hCT2271422.0, hCT2355181.0, hCT2355182.0, hCT2355183.0	213634_s_at	NP_060476.2, EAW73425.1, EAW73422.1, EAW73423.1, EAW73424.1, EAW73426.1
GeneID:9620	CELSR1	22	46,756,731	46,933,067	176,336	-	1	2_A375_pNL97_plus_lncRNA::1::5433	82827	in gene	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene CELSR1	FMI2, ME2, CDHF9, CELSR1, DKFZp434P0729, HFMI2	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	NM_014246, hCT2272632.0, hCT33068.4	204539_s_at, 217262_s_at, 41660_at	NP_055061.1, EAW73429.1, EAW73428.1
GeneID:25771	TBC1D22A	22	47,158,518	47,571,342	412,824	+	2	1_A375_pNL7_minus_lncRNA::1::3782, 2_A375_pNL97_plus_lncRNA::1::5434	-86, -54	upstream, upstream	1	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TBC1D22A	C22orf4, HSC79E021, TBC1D22A	TBC1 domain family, member 22A	NM_014346, hCT1772962.2, hCT2271436.0, hCT2271439.0	209650_s_at, 210144_at, 33778_at	NP_055161.1, EAW73443.1, EAW73444.1, EAW73445.1
GeneID:400932	RP11-191L9.1	22	48,016,792	48,027,318	10,526	-	1	2_A375_pNL97_plus_lncRNA::1::5435	-266	upstream	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RP11-191L9.1	FLJ46257	hypothetical LOC400932	NR_033377, hCT2343900.1		EAW73451.1
GeneID:25817	FAM19A5	22	48,885,288	49,147,744	262,456	+	2	1_A375_pNL7_minus_lncRNA::1::3783, 2_A375_pNL97_plus_lncRNA::1::5436	213240, 154936	in gene, in gene	1	1	13.5	15	2	2_A375_pNL97_plus_lncRNA::1	18	Gene FAM19A5	UNQ5208, QLLK5208, TAFA-5, TAFA5, FAM19A5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	NM_001082967, NM_015381, hCT1951012.1, hCT5875.2	229459_at, 229655_at, 237094_at	NP_001076436.1, NP_056196.2, EAW73462.1, EAW73463.1
GeneID:164714	TTLL8	22	50,453,552	50,493,055	39,503	-	1	2_A375_pNL97_plus_lncRNA::1::5438	26847	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TTLL8	TTLL8		NM_001080447		NP_001073916.1
GeneID:85378	TUBGCP6	22	50,656,118	50,683,400	27,282	-	1	2_A375_pNL97_plus_lncRNA::1::5439	-88	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TUBGCP6	TUBGCP6, GCP6	tubulin, gamma complex associated protein 6	NM_020461, hCT1965012.1, hCT2264513.0, hCT23032.2, hCT2355184.0	225758_s_at, 234308_at	NP_065194.2, EAW73508.1, EAW73507.1, EAW73509.1, EAW73510.1
GeneID:83933	HDAC10	22	50,683,612	50,689,834	6,222	-	1	2_A375_pNL97_plus_lncRNA::1::5439	6346	downstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene HDAC10	HD10, DKFZp761B039, HDAC10, MGC149722	histone deacetylase 10	NM_032019, NM_001159286, hCT1965013.1, hCT1965014.1, hCT1965015.1, hCT1965016.1, hCT1965017.1, hCT2264496.0, hCT2264497.0, hCT2264507.0, hCT23038.3, hCT2355197.0	226672_s_at, 232870_at	NP_114408.3, NP_001152758.1, EAW73511.1, EAW73516.1, EAW73517.1, EAW73519.1, EAW73512.1, EAW73513.1, EAW73514.1, EAW73515.1, EAW73518.1, EAW73520.1
GeneID:6300	MAPK12	22	50,691,331	50,700,089	8,758	-	1	2_A375_pNL97_plus_lncRNA::1::5439	16601	downstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MAPK12	ERK3, SAPK-3, ERK6, MAPK12, SAPK3, P38GAMMA, PRKM12	mitogen-activated protein kinase 12	NM_002969, hCT2264478.0, hCT2355180.0	1556340_at, 1556341_s_at, 206106_at	NP_002960.2, EAW73522.1, EAW73521.1
GeneID:414918	FAM116B	22	50,750,392	50,765,489	15,097	-	2	1_A375_pNL7_minus_lncRNA::1::3784, 2_A375_pNL97_plus_lncRNA::1::5440	-207, -527	upstream, upstream	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene FAM116B	FAM116B, MGC33692	family with sequence similarity 116, member B	NM_001001794, hCT1813351.1, hCT2355192.0	228678_at, 229739_s_at	NP_001001794.3, EAW73529.1, EAW73528.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:29781	NCAPH2	22	50,946,645	50,963,209	16,564	+	1	2_A375_pNL97_plus_lncRNA::1::5441	18187	downstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene NCAPH2	384D8_6, CAP-H2, MGC2455, hCAP-H2, 384D8-2, MGC4133, MGC8640, MGC16000, NCAPH2, MGC5305, CAPH2, MGC15856	non-SMC condensin II complex, subunit H2	NM_014551, NM_001185011, NM_152299, hCT2263998.0, hCT2263999.0, hCT2264000.0, hCT2264002.0, hCT2264003.0, hCT2355159.0, hCT2355160.0, hCT7925.2	205086_s_at, 209718_at, 221633_at, 40640_at	NP_055366.3, NP_001171940.1, NP_689512.2, EAW73552.1, EAW73555.1, EAW73559.1, EAW73553.1, EAW73554.1, EAW73556.1, EAW73557.1, EAW73558.1
GeneID:9997	SCO2	22	50,961,997	50,964,868	2,871	-	1	2_A375_pNL97_plus_lncRNA::1::5441	36	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SCO2	MGC125825, MGC125823, SCO1L, SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	NM_005138, NM_001169109, NM_001169110, NM_001169111	205241_at	NP_005129.2, NP_001162580.1, NP_001162581.1, NP_001162582.1
GeneID:1890	TYMP	22	50,964,181	50,968,514	4,333	-	1	2_A375_pNL97_plus_lncRNA::1::5441	3682	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TYMP	MEDPS1, MTDPS1, ECGF, MNGIE, TP, hPD-ECGF, PDECGF, ECGF1, TYMP	thymidine phosphorylase	NM_001113755, NM_001953, NM_001113756	204858_s_at, 217497_at	NP_001107227.1, NP_001944.1, NP_001107228.1
GeneID:440836	ODF3B	22	50,968,838	50,971,008	2,170	-	1	2_A375_pNL97_plus_lncRNA::1::5441	6176	downstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ODF3B	ODF3L3, ODF3B	outer dense fiber of sperm tails 3B	NM_001014440	235257_at, 238325_s_at, 238326_at, 238327_at	NP_001014440.2
GeneID:23542	MAPK8IP2	22	51,039,131	51,049,979	10,848	+	2	1_A375_pNL7_minus_lncRNA::1::3785, 2_A375_pNL97_plus_lncRNA::1::5442	-507, -523	upstream, upstream	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene MAPK8IP2	JIP2, MAPK8IP2, PRKM8IPL, IB2	mitogen-activated protein kinase 8 interacting protein 2	NM_016431, NM_012324, hCT2264008.0, hCT2264009.0, hCT2264010.0, hCT7914.3	205050_s_at, 208603_s_at	NP_057515.1, NP_036456.1, EAW73577.1, EAW73578.1, EAW73579.1, EAW73580.1
GeneID:27255	CNTN6	3	1,134,629	1,445,278	310,649	+	1	1_A375_pNL7_minus_lncRNA::1::3788	86139	in gene	1	0	18	12	1	1_A375_pNL7_minus_lncRNA::1	18	Gene CNTN6	CNTN6, MGC133256, NB3	contactin 6	NM_014461, hCT2354138.0, hCT31378.2	207195_at	NP_055276.1, EAW63872.1, EAW63871.1
GeneID:51095	TRNT1	3	3,168,600	3,190,707	22,107	+	1	2_A375_pNL97_plus_lncRNA::1::5444	72	in gene	0	1	18	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene TRNT1	CGI-47, TRNT1, CCA1, MtCCA	tRNA nucleotidyl transferase, CCA-adding, 1	NM_182916, hCT2274314.1, hCT2274315.1, hCT2274317.0, hCT2274318.0, hCT2354092.0	1552625_a_at, 222754_at, 223614_at	NP_886552.2, EAW63885.1, EAW63886.1, EAW63887.1, EAW63888.1, EAW63889.1
GeneID:51185	CRBN	3	3,191,317	3,221,401	30,084	-	2	1_A375_pNL7_minus_lncRNA::1::3789, 2_A375_pNL97_plus_lncRNA::1::5445	25, 25	in gene, in gene	1	1	102	127	1	2_A375_pNL97_plus_lncRNA::1	127	Gene CRBN	MRT2A, CRBN, DKFZp781K0715, MGC27358	cereblon	NM_001173482, NM_016302, hCT2274405.0, hCT2274406.0, hCT2274408.0, hCT2274409.0, hCT2274411.0, hCT2274412.0, hCT2354025.0, hCT2354026.0	218142_s_at, 222533_at	NP_001166953.1, NP_057386.2, EAW63890.1, EAW63894.1, EAW63895.1, EAW63896.1, EAW63891.1, EAW63892.1, EAW63893.1, EAW63897.1
GeneID:6419	SETMAR	3	4,344,988	4,358,949	13,961	+	1	1_A375_pNL7_minus_lncRNA::1::3790	36	in gene	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SETMAR	SETMAR, METNASE	SET domain and mariner transposase fusion gene	NM_006515, NR_024022, hCT1958780.0, hCT2277789.0, hCT5743.2	1554059_at, 1554060_s_at, 206554_x_at	NP_006506.3, EAW63904.1, EAW63903.1, EAW63905.1
GeneID:285362	SUMF1	3	4,402,829	4,508,966	106,137	-	2	1_A375_pNL7_minus_lncRNA::1::3791, 2_A375_pNL97_plus_lncRNA::1::5446	70, 102	in gene, in gene	1	1	34	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene SUMF1	MGC150436, AAPA3037, SUMF1, FGE, MGC131853	sulfatase modifying factor 1	NM_182760, NM_001164674, NM_001164675, hCT1958781.1, hCT6228.3	226850_at	NP_877437.2, NP_001158146.1, NP_001158147.1, EAW63906.1, EAW63907.1
GeneID:3708	ITPR1	3	4,535,032	4,889,524	354,492	+	2	1_A375_pNL7_minus_lncRNA::1::3792, 2_A375_pNL97_plus_lncRNA::1::5447	-168, -77	upstream, upstream	1	1	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ITPR1	SCA15, INSP3R1, DKFZp313E1334, ITPR1, SCA16, IP3R1, DKFZp313N1434, IP3R	inositol 1,4,5-triphosphate receptor, type 1	NM_001099952, NM_002222, NM_001168272, hCT12824.3, hCT1958801.1, hCT2277792.0, hCT2277793.0, hCT2277795.0, hCT2277796.0, hCT2277797.0, hCT2277799.0	203710_at, 211323_s_at, 216944_s_at, 240052_at	NP_001093422.2, NP_002213.5, NP_001161744.1, EAW63910.1, EAW63913.1, EAW63915.1, EAW63908.1, EAW63909.1, EAW63911.1, EAW63912.1, EAW63914.1
GeneID:8553	BHLHE40	3	5,021,097	5,026,866	5,769	+	1	2_A375_pNL97_plus_lncRNA::1::5449	-1177	upstream	0	1	11	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene BHLHE40	STRA13, FLJ99214, BHLHE40, Stra14, SHARP-2, BHLHB2, DEC1, HLHB2	basic helix-loop-helix family, member e40	NM_003670, hCT11435.2, hCT2277802.0	201169_s_at, 201170_s_at	NP_003661.1, EAW63916.1, EAW63917.1
GeneID:55207	ARL8B	3	5,163,930	5,222,601	58,671	+	2	1_A375_pNL7_minus_lncRNA::1::3794, 2_A375_pNL97_plus_lncRNA::1::5450	-58, -26	upstream, upstream	1	1	189	203	1	2_A375_pNL97_plus_lncRNA::1	203	Gene ARL8B	ARL8B, FLJ10702, ARL10C, Gie1	ADP-ribosylation factor-like 8B	NM_018184, hCT12825.2, hCT1965391.1, hCT1965392.1, hCT2354015.0	217852_s_at, 222442_s_at	NP_060654.1, EAW63920.1, EAW63919.1, EAW63921.1, EAW63922.1
GeneID:2917	GRM7	3	6,902,802	7,783,218	880,416	+	4	1_A375_pNL7_minus_lncRNA::1::3795, 1_A375_pNL7_minus_lncRNA::1::3796, 2_A375_pNL97_plus_lncRNA::1::5451, 2_A375_pNL97_plus_lncRNA::1::5452	49502, 128638, 49598, 644270	in gene, in gene, in gene, in gene	1	1	15	15	3	1_A375_pNL7_minus_lncRNA::1	17	Gene GRM7	MGLUR7, GPRC1G, FLJ40498, GRM7, GLUR7, MGLU7	glutamate receptor, metabotropic 7	NM_000844, NM_181874, hCT1643937.3, hCT2354051.0, hCT2354052.0	207548_at, 217008_s_at, 241049_at	NP_000835.1, NP_870989.1, EAW63933.1, EAW63934.1, EAW63935.1
GeneID:100288428	LOC100288428	3	8,262,834	8,543,344	280,510	-	1	2_A375_pNL97_plus_lncRNA::1::5454	-80	upstream	0	1	11	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100288428	FLJ42094	hypothetical LOC100288428	NR_033378		
GeneID:29995	LMCD1	3	8,543,511	8,609,806	66,295	+	1	2_A375_pNL97_plus_lncRNA::1::5454	-87	upstream	0	1	11	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LMCD1	LMCD1		NM_014583, hCT12835.2, hCT1966377.1	218574_s_at, 227317_at, 242767_at	NP_055398.1, EAW63938.1, EAW63937.1
GeneID:51066	C3orf32	3	8,661,317	8,693,737	32,420	-	2	1_A375_pNL7_minus_lncRNA::1::3797, 2_A375_pNL97_plus_lncRNA::1::5455	22457, 22361	in gene, in gene	1	1	23	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene C3orf32	fls485, C3orf32	chromosome 3 open reading frame 32	NM_015931, hCT12833.2, hCT2274756.0, hCT2354061.0	206741_at	NP_057015.1, EAW63941.1, EAW63942.1, EAW63943.1
GeneID:56852	RAD18	3	8,918,880	9,005,159	86,279	-	1	1_A375_pNL7_minus_lncRNA::1::3798	87	in gene	1	0	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene RAD18	RNF73, RAD18	RAD18 homolog (S. cerevisiae)	NM_020165, hCT12648.2, hCT2274749.0	223417_at, 224200_s_at	NP_064550.3, EAW63949.1, EAW63948.1
GeneID:25917	THUMPD3	3	9,404,717	9,428,475	23,758	+	1	2_A375_pNL97_plus_lncRNA::1::5457	34099	downstream	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene THUMPD3	DKFZp434F091, THUMPD3	THUMP domain containing 3	NM_015453, NM_001114092, hCT1797614.1, hCT1958785.1, hCT1958786.1, hCT2276212.0, hCT2276214.0, hCT2276215.0	223804_s_at, 225730_s_at, 225741_at, 242377_x_at	NP_056268.2, NP_001107564.1, EAW63954.1, EAW63955.1, EAW63956.1, EAW63958.1, EAW63957.1, EAW63959.1
GeneID:440944	LOC440944	3	9,430,537	9,439,174	8,637	-	1	2_A375_pNL97_plus_lncRNA::1::5457	358	in gene	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC440944		hypothetical LOC440944	NR_027007	1557357_at, 232052_at	
GeneID:100507618	LOC100507618	3	9,435,634	9,438,752	3,118	-	1	2_A375_pNL97_plus_lncRNA::1::5457	-64	upstream	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100507618		putative uncharacterized protein FLJ46541-like	XM_003118871		XP_003118919.1
GeneID:55209	SETD5	3	9,439,403	9,519,838	80,435	+	2	1_A375_pNL7_minus_lncRNA::1::3799, 2_A375_pNL97_plus_lncRNA::1::5457	25205, -587	in gene, upstream	1	1	17	17	2	2_A375_pNL97_plus_lncRNA::1	21	Gene SETD5	SETD5, FLJ10707, KIAA1757, DKFZp686J16276	SET domain containing 5	NM_001080517	1569105_at, 1569106_s_at, 221806_s_at, 222575_at, 244691_at	NP_001073986.1
GeneID:375323	LHFPL4	3	9,540,045	9,595,486	55,441	-	1	2_A375_pNL97_plus_lncRNA::1::5458	1390	in gene	0	1	13	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene LHFPL4	LHFPL4, MGC133162	lipoma HMGIC fusion partner-like 4	NM_198560, hCT12651.2	228422_at	NP_940962.1, EAW63964.1
GeneID:151835	CPNE9	3	9,745,510	9,771,592	26,082	+	1	2_A375_pNL97_plus_lncRNA::1::5459	27770	downstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CPNE9	KIAA4217, CPNE9	copine family member IX	NM_153635	239139_at	NP_705899.2
GeneID:7862	BRPF1	3	9,773,434	9,789,699	16,265	+	1	2_A375_pNL97_plus_lncRNA::1::5459	-154	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene BRPF1	BR140, BRPF1	bromodomain and PHD finger containing, 1	NM_001003694, NM_004634, hCT12637.4, hCT2276236.0, hCT2276237.0, hCT2276238.0, hCT2276239.0	204461_at	NP_001003694.1, NP_004625.2, EAW63972.1, EAW63973.1, EAW63975.1, EAW63976.1, EAW63974.1
GeneID:10474	TADA3	3	9,821,651	9,834,420	12,769	-	1	2_A375_pNL97_plus_lncRNA::1::5460	-204	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TADA3	NGG1, ADA3, FLJ20221, FLJ21329, TADA3L, hADA3, TADA3	transcriptional adaptor 3	NM_006354, NM_133480, hCT12641.3, hCT2277616.0, hCT2277617.0, hCT2277618.0	211221_at, 215273_s_at	NP_006345.1, NP_597814.1, EAW63994.1, EAW63995.1, EAW63996.1, EAW63997.1
GeneID:10093	ARPC4	3	9,834,227	9,848,789	14,562	+	1	2_A375_pNL97_plus_lncRNA::1::5460	397	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ARPC4	P20-ARC, ARC20, MGC13544, ARPC4, p20-Arc	actin related protein 2/3 complex, subunit 4, 20kDa	NM_005718, NM_001024959, NM_001024960	211672_s_at, 217817_at, 217818_s_at	NP_005709.1, NP_001020130.1, NP_001020131.1
GeneID:84522	JAGN1	3	9,932,271	9,936,033	3,762	+	2	1_A375_pNL7_minus_lncRNA::1::3800, 2_A375_pNL97_plus_lncRNA::1::5461	81, 81	in gene, in gene	1	1	23	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene JAGN1	FLJ14602, GL009, JAGN1	jagunal homolog 1 (Drosophila)	NM_032492, hCT11665.1	223104_at	NP_115881.3, EAW64015.1
GeneID:84818	IL17RC	3	9,958,764	9,975,314	16,550	+	2	1_A375_pNL7_minus_lncRNA::1::3801, 2_A375_pNL97_plus_lncRNA::1::5462	16692, 16692	downstream, downstream	1	1	19	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene IL17RC	MGC10763, FLJ96005, FLJ95963, IL17RC, IL17RL, IL17-RL	interleukin 17 receptor C	NM_153460, NM_032732, NM_153461, hCT2276270.1, hCT2276271.0, hCT2348419.0, hCT2348420.0, hCT2348421.0, hCT2348422.0, hCT2348423.0, hCT2348424.0, hCT2348425.0, hCT2348426.0, hCT2354088.0, hCT2354089.0	221926_s_at, 224514_x_at, 64440_at	NP_703190.1, NP_116121.2, NP_703191.1, EAW64022.1, EAW64023.1, EAW64024.1, EAW64021.1, EAW64025.1, EAW64026.1, EAW64027.1, EAW64028.1, EAW64029.1, EAW64030.1, EAW64032.1, EAW64031.1
GeneID:78987	CRELD1	3	9,975,524	9,987,097	11,573	+	4	1_A375_pNL7_minus_lncRNA::1::3801, 1_A375_pNL7_minus_lncRNA::1::3802, 2_A375_pNL97_plus_lncRNA::1::5462, 2_A375_pNL97_plus_lncRNA::1::5463	-68, 12796, -68, 12780	upstream, downstream, upstream, downstream	1	1	39	60	2	2_A375_pNL97_plus_lncRNA::1	64	Gene CRELD1	AVSD2, CRELD1, CIRRIN, DKFZp566D213	cysteine-rich with EGF-like domains 1	NM_001031717, NM_001077415, NM_015513, hCT2276251.1, hCT2276262.1, hCT2276263.0, hCT2348430.0, hCT2348431.0, hCT2348432.0, hCT2348433.0, hCT2348434.0, hCT2348435.0, hCT2354123.0	203368_at	NP_001026887.1, NP_001070883.1, NP_056328.2, EAW64034.1, EAW64036.1, EAW64043.1, EAW64035.1, EAW64037.1, EAW64038.1, EAW64039.1, EAW64040.1, EAW64041.1, EAW64042.1
GeneID:285368	PRRT3	3	9,987,226	9,994,078	6,852	-	2	1_A375_pNL7_minus_lncRNA::1::3802, 2_A375_pNL97_plus_lncRNA::1::5463	5758, 5774	in gene, in gene	1	1	59	64	1	2_A375_pNL97_plus_lncRNA::1	64	Gene PRRT3	FLJ33674, PRRT3, MGC105134, MGC33990	proline-rich transmembrane protein 3	NM_207351, hCT1642998.3, hCT2277607.0	1556308_at	NP_997234.3, EAW64044.1, EAW64045.1
GeneID:55831	TMEM111	3	10,005,636	10,028,522	22,886	-	2	1_A375_pNL7_minus_lncRNA::1::3803, 2_A375_pNL97_plus_lncRNA::1::5464	10, -11	in gene, upstream	1	1	26	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene TMEM111	POB, TMEM111	transmembrane protein 111	NM_018447	215250_at, 217882_at	NP_060917.1
GeneID:442075	LOC442075	3	10,028,595	10,046,944	18,349	+	2	1_A375_pNL7_minus_lncRNA::1::3803, 2_A375_pNL97_plus_lncRNA::1::5464	-83, -62	upstream, upstream	1	1	26	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene LOC442075	FLJ43570	hypothetical LOC442075	XR_112457, XR_110030, XR_113459	237005_at	
GeneID:2177	FANCD2	3	10,068,113	10,143,614	75,501	+	2	1_A375_pNL7_minus_lncRNA::1::3804, 2_A375_pNL97_plus_lncRNA::1::5465	-65, -33	upstream, upstream	1	1	33	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene FANCD2	FACD, FLJ23826, FANCD2, FA4, FAD, FAD2, DKFZp762A223, FANCD, FA-D2	Fanconi anemia, complementation group D2	NM_033084, NM_001018115, hCT1952810.1, hCT2274945.0, hCT2274946.0, hCT2354166.0	1568869_at, 1568891_x_at, 223545_at, 242560_at	NP_149075.2, NP_001018125.1, EAW64055.1, EAW64056.1, EAW64057.1, EAW64058.1
GeneID:3656	IRAK2	3	10,206,563	10,285,427	78,864	+	1	2_A375_pNL97_plus_lncRNA::1::5466	41469	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene IRAK2	IRAK2, MGC150550, IRAK-2	interleukin-1 receptor-associated kinase 2	NM_001570, hCT2274962.0	1553739_at, 1553740_a_at, 231779_at	NP_001561.3, EAW64069.1
GeneID:6396	SEC13	3	10,342,615	10,362,858	20,243	-	1	2_A375_pNL97_plus_lncRNA::1::5467	42	in gene	0	1	18	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene SEC13	npp-20, SEC13R, D3S1231E, SEC13L1, SEC13	SEC13 homolog (S. cerevisiae)	NM_183352, NM_001136232, NR_024272, NR_024273, hCT1962202.1, hCT1962203.1	207707_s_at	NP_899195.1, NP_001129704.1, EAW64077.1, EAW64078.1
GeneID:491	ATP2B2	3	10,365,707	10,547,268	181,561	-	3	1_A375_pNL7_minus_lncRNA::1::3805, 2_A375_pNL97_plus_lncRNA::1::5467, 2_A375_pNL97_plus_lncRNA::1::5468	45220, 184452, 45204	in gene, downstream, in gene	1	1	67.5	74	2	2_A375_pNL97_plus_lncRNA::1	119	Gene ATP2B2	PMCA2, PMCA2i, ATP2B2, PMCA2a	ATPase, Ca++ transporting, plasma membrane 2	NM_001001331, NM_001683, hCT1952827.1, hCT1964891.1, hCT2277646.0, hCT2277647.0, hCT2277648.0, hCT2277650.0	204685_s_at, 211586_s_at, 216120_s_at, 234714_x_at, 234741_at	NP_001001331.1, NP_001674.2, EAW64079.1, EAW64080.1, EAW64082.1, EAW64083.1, EAW64081.1, EAW64084.1
GeneID:100422933	MIR378B	3	10,371,913	10,371,969	56	+	1	2_A375_pNL97_plus_lncRNA::1::5467	-9097	upstream	0	1	18	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene MIR378B	MIR378B	microRNA 378b	NR_036084		
GeneID:285370	LOC285370	3	10,801,169	10,805,877	4,708	-	2	1_A375_pNL7_minus_lncRNA::1::3809, 2_A375_pNL97_plus_lncRNA::1::5473	10037, 10037	downstream, downstream	1	1	25	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene LOC285370		hypothetical LOC285370	NR_027102	1556447_at, 1556448_a_at	
GeneID:9686	VGLL4	3	11,597,544	11,762,220	164,676	-	3	1_A375_pNL7_minus_lncRNA::1::3811, 2_A375_pNL97_plus_lncRNA::1::5476, 2_A375_pNL97_plus_lncRNA::1::5477	152380, 152460, 110700	in gene, in gene, in gene	1	1	21	24.5	2	2_A375_pNL97_plus_lncRNA::1	26	Gene VGLL4	KIAA0121, VGL-4, VGLL4	vestigial like 4 (Drosophila)	NM_014667, NM_001128219, NM_001128220, NM_001128221, hCT1816009.3, hCT1952811.2, hCT2287349.1, hCT2287350.1, hCT2287351.0, hCT2287352.1, hCT2287353.0, hCT2287354.1, hCT2354151.0	212399_s_at, 214004_s_at	NP_055482.2, NP_001121691.1, NP_001121692.1, NP_001121693.1, EAW64099.1, EAW64100.1, EAW64098.1, EAW64101.1, EAW64102.1, EAW64103.1, EAW64104.1, EAW64105.1, EAW64106.1
GeneID:100133039	LOC100133039	3	11,602,886	11,605,949	3,063	-	2	1_A375_pNL7_minus_lncRNA::1::3811, 2_A375_pNL97_plus_lncRNA::1::5476	-3891, -3811	upstream, upstream	1	1	26	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100133039		hypothetical LOC100133039	XR_112484, XR_110031, XR_113469		
GeneID:132001	C3orf31	3	11,831,919	11,888,352	56,433	-	2	1_A375_pNL7_minus_lncRNA::1::3812, 2_A375_pNL97_plus_lncRNA::1::5478	-64, -64	upstream, upstream	1	1	193	174	1	1_A375_pNL7_minus_lncRNA::1	193	Gene C3orf31	MGC16471, C3orf31, DKFZp434E0519	chromosome 3 open reading frame 31	NM_138807, hCT19191.1, hCT2287346.0, hCT2344411.0, hCT2344412.0, hCT2344413.0, hCT2344414.0, hCT2344415.0	226815_at, 231958_at, 234697_x_at	NP_620162.1, EAW64113.1, EAW64108.1, EAW64109.1, EAW64110.1, EAW64111.1, EAW64112.1, EAW64114.1
GeneID:6854	SYN2	3	12,045,862	12,233,532	187,670	+	2	1_A375_pNL7_minus_lncRNA::1::3813, 2_A375_pNL97_plus_lncRNA::1::5479	151642, 151642	in gene, in gene	1	1	20	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene SYN2	SYNIIb, SYNII, SYNIIa, SYN2	synapsin II	NM_133625, NM_003178, hCT19467.2, hCT2274906.0, hCT2274907.0, hCT2274908.0, hCT2354053.0	1553037_a_at, 210247_at, 210315_at, 229039_at, 240197_at	NP_598328.1, NP_003169.2, EAW64118.1, EAW64119.1, EAW64120.1, EAW64121.1, EAW64117.1
GeneID:7079	TIMP4	3	12,194,568	12,200,647	6,079	-	2	1_A375_pNL7_minus_lncRNA::1::3813, 2_A375_pNL97_plus_lncRNA::1::5479	3143, 3143	in gene, in gene	1	1	20	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene TIMP4	TIMP4		NM_003256, hCT19466.3	206243_at	NP_003247.1, EAW64122.1
GeneID:5468	PPARG	3	12,329,349	12,475,855	146,506	+	2	1_A375_pNL7_minus_lncRNA::1::3814, 2_A375_pNL97_plus_lncRNA::1::5480	107963, 118043	in gene, in gene	1	1	10.5	12	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PPARG	PPARG2, PPARG1, CIMT1, NR1C3, PPARG, PPARgamma, GLM1	peroxisome proliferator-activated receptor gamma	NM_005037, NM_138712, NM_015869, NM_138711, hCT19464.2, hCT1951704.1, hCT2275109.0	208510_s_at	NP_005028.4, NP_619726.2, NP_056953.2, NP_619725.2, EAW64124.1, EAW64125.1, EAW64123.1
GeneID:80746	TSEN2	3	12,525,931	12,574,820	48,889	+	2	1_A375_pNL7_minus_lncRNA::1::3815, 2_A375_pNL97_plus_lncRNA::1::5481	165, 133	in gene, in gene	1	1	19	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TSEN2	SEN2L, TSEN2, MGC4440, MGC2776, SEN2, PCH2B	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	NM_025265, NM_001145392, NM_001145393, NM_001145394, NM_001145395, hCT19470.3, hCT2275119.0, hCT2275120.0, hCT2354093.0	219581_at, 244391_at	NP_079541.1, NP_001138864.1, NP_001138865.1, NP_001138866.1, NP_001138867.1, EAW64130.1, EAW64127.1, EAW64128.1, EAW64129.1
GeneID:23609	MKRN2	3	12,598,594	12,625,212	26,618	+	2	1_A375_pNL7_minus_lncRNA::1::3816, 2_A375_pNL97_plus_lncRNA::1::5482	158, -66	in gene, upstream	1	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene MKRN2	RNF62, MKRN2, HSPC070	makorin ring finger protein 2	NM_014160, hCT19469.3, hCT2275122.0	216995_x_at, 218071_s_at, 222510_s_at	NP_054879.3, EAW64132.1, EAW64133.1
GeneID:5894	RAF1	3	12,625,100	12,705,700	80,600	-	2	1_A375_pNL7_minus_lncRNA::1::3817, 2_A375_pNL97_plus_lncRNA::1::5483	-12, 4	upstream, in gene	1	1	35	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene RAF1	Raf-1, RAF1, c-Raf, NS5, CRAF	v-raf-1 murine leukemia viral oncogene homolog 1	NM_002880, hCT19462.3, hCT2300428.0	1557675_at, 201244_s_at	NP_002871.1, EAW64134.1, EAW64135.1
GeneID:23066	CAND2	3	12,838,171	12,876,313	38,142	+	1	2_A375_pNL97_plus_lncRNA::1::5484	45013	downstream	0	1	13	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene CAND2	KIAA0667, TIP120B, CAND2, Tp120b	cullin-associated and neddylation-dissociated 2 (putative)	NM_012298, NM_001162499	213547_at	NP_036430.1, NP_001155971.1
GeneID:6161	RPL32	3	12,876,444	12,883,081	6,637	-	1	2_A375_pNL97_plus_lncRNA::1::5484	-103	upstream	0	1	13	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene RPL32	PP9932, RPL32, L32	ribosomal protein L32	NM_001007073, NM_001007074, NM_000994, hCT19461.3, hCT1951717.1	200674_s_at	NP_001007074.1, NP_001007075.1, NP_000985.1, EAW64144.1, EAW64145.1
GeneID:619563	SNORA7A	3	12,881,811	12,881,949	138	-	1	2_A375_pNL97_plus_lncRNA::1::5484	-1235	upstream	0	1	13	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene SNORA7A	ACA7, SNORA7A	small nucleolar RNA, H/ACA box 7A	NR_002582		
GeneID:9922	IQSEC1	3	12,938,719	13,114,617	175,898	-	4	1_A375_pNL7_minus_lncRNA::1::3818, 2_A375_pNL97_plus_lncRNA::1::5485, 2_A375_pNL97_plus_lncRNA::1::5486, 2_A375_pNL97_plus_lncRNA::1::5487	78009, 124505, 78009, 18073	in gene, in gene, in gene, in gene	1	1	25.67	36	3	2_A375_pNL97_plus_lncRNA::1	71	Gene IQSEC1	ARFGEP100, IQSEC1, KIAA0763	IQ motif and Sec7 domain 1	NM_014869, NM_001134382, hCT17904.2, hCT1951716.1	203906_at, 203907_s_at, 243523_at	NP_055684.3, NP_001127854.1, EAW64147.1, EAW64148.1
GeneID:131474	CHCHD4	3	14,153,577	14,166,371	12,794	-	1	2_A375_pNL97_plus_lncRNA::1::5489	-829	upstream	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CHCHD4	MIA40, CHCHD4, TIMM40, FLJ31709	coiled-coil-helix-coiled-coil-helix domain containing 4	NM_001098502, NM_144636, hCT1640280.3, hCT1951690.1, hCT1964863.1, hCT2275226.0	229595_at	NP_001091972.1, NP_653237.1, EAW64180.1, EAW64181.1, EAW64182.1, EAW64183.1
GeneID:79188	TMEM43	3	14,166,440	14,185,180	18,740	+	1	2_A375_pNL97_plus_lncRNA::1::5489	760	in gene	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene TMEM43	LUMA, ARVD5, TMEM43, DKFZp586G1919, MGC3222, ARVC5	transmembrane protein 43	NM_024334, hCT18374.3, hCT2275076.0, hCT2275077.0, hCT2354094.0	217795_s_at, 222418_s_at, 233480_at, 233489_at	NP_077310.1, EAW64184.1, EAW64185.1, EAW64186.1, EAW64187.1
GeneID:7508	XPC	3	14,186,647	14,220,172	33,525	-	2	1_A375_pNL7_minus_lncRNA::1::3820, 2_A375_pNL97_plus_lncRNA::1::5490	204, 204	in gene, in gene	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene XPC	XPC, RAD4, XP3, XPCC	xeroderma pigmentosum, complementation group C	NM_004628, NM_001145769, NR_027299, hCT18373.3, hCT2275219.0	209375_at	NP_004619.3, NP_001139241.1, EAW64188.1, EAW64189.1
GeneID:27258	LSM3	3	14,220,228	14,239,869	19,641	+	2	1_A375_pNL7_minus_lncRNA::1::3820, 2_A375_pNL97_plus_lncRNA::1::5490	-260, -260	upstream, upstream	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LSM3	USS2, SMX4, YLR438C, LSM3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_014463, hCT17863.3	202209_at	NP_055278.1, EAW64190.1
GeneID:6533	SLC6A6	3	14,444,106	14,530,857	86,751	+	3	1_A375_pNL7_minus_lncRNA::1::3821, 2_A375_pNL97_plus_lncRNA::1::5492, 2_A375_pNL97_plus_lncRNA::1::5493	29814, 29814, 50356	in gene, in gene, in gene	1	1	18.5	16.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene SLC6A6	MGC131729, SLC6A6, TAUT, MGC10619	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	NM_003043, NM_001134367, NM_001134368, hCT2275545.0, hCT2275547.0, hCT2275548.0, hCT2275549.0	205920_at, 205921_s_at, 211030_s_at, 226754_at, 226756_at	NP_003034.2, NP_001127839.1, NP_001127840.1, EAW64192.1, EAW64194.1, EAW64195.1, EAW64193.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100505673	LOC100505673	3	14,961,857	14,989,931	28,074	-	1	2_A375_pNL97_plus_lncRNA::1::5496	1227	in gene	0	1	8	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100505673		hypothetical LOC100505673	XR_112481, XR_110037, XR_113476		
GeneID:100505641	LOC100505641	3	14,984,287	14,989,400	5,113	-	1	2_A375_pNL97_plus_lncRNA::1::5496	696	in gene	0	1	8	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100505641		hypothetical LOC100505641	XR_110036, XR_110034, XR_110035		
GeneID:7182	NR2C2	3	14,989,236	15,090,780	101,544	+	1	2_A375_pNL97_plus_lncRNA::1::5496	-532	upstream	0	1	8	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene NR2C2	TAK1, hTAK1, NR2C2, TR4, TR2R1	nuclear receptor subfamily 2, group C, member 2	NM_003298, hCT1951707.1, hCT2275559.0, hCT2275560.0	206038_s_at, 225477_s_at	NP_003289.2, EAW64215.1, EAW64213.1, EAW64214.1
GeneID:64145	ZFYVE20	3	15,111,580	15,140,655	29,075	-	2	1_A375_pNL7_minus_lncRNA::1::3823, 2_A375_pNL97_plus_lncRNA::1::5497	-1, -49	upstream, upstream	1	1	46	43	1	1_A375_pNL7_minus_lncRNA::1	46	Gene ZFYVE20	Rabenosyn-5, MGC126210, FLJ34993, ZFYVE20	zinc finger, FYVE domain containing 20	NM_022340, hCT18974.3, hCT2276756.0	1569714_at, 226581_at, 231765_at	NP_071735.2, EAW64221.1, EAW64220.1
GeneID:23473	CAPN7	3	15,247,733	15,294,423	46,690	+	1	2_A375_pNL97_plus_lncRNA::1::5498	235	in gene	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CAPN7	FLJ36423, PALBH, CALPAIN7, CAPN7	calpain 7	NM_014296, hCT18962.3, hCT1965791.1	203356_at, 203357_s_at	NP_055111.1, EAW64223.1, EAW64224.1
GeneID:100505696	LOC100505696	3	15,295,159	15,305,995	10,836	+	1	1_A375_pNL7_minus_lncRNA::1::3824	15945	downstream	1	0	24	19	1	1_A375_pNL7_minus_lncRNA::1	24	Gene LOC100505696		hypothetical LOC100505696	XR_112477, XR_110038, XR_113477		
GeneID:9467	SH3BP5	3	15,296,357	15,382,901	86,544	-	6	1_A375_pNL7_minus_lncRNA::1::3824, 1_A375_pNL7_minus_lncRNA::1::3825, 1_A375_pNL7_minus_lncRNA::1::3826, 2_A375_pNL97_plus_lncRNA::1::5499, 2_A375_pNL97_plus_lncRNA::1::5500, 2_A375_pNL97_plus_lncRNA::1::5501	71797, 40437, 9173, 40485, 30517, 9365	in gene, in gene, in gene, in gene, in gene, in gene	1	1	22.5	23	4	1_A375_pNL7_minus_lncRNA::1	33	Gene SH3BP5	SAB, SH3BP5	SH3-domain binding protein 5 (BTK-associated)	NM_004844, NM_001018009, hCT17896.3, hCT1951702.1, hCT2276739.0, hCT2354115.0	201810_s_at, 201811_x_at, 227591_at	NP_004835.2, NP_001018009.2, EAW64225.1, EAW64226.1, EAW64227.1, EAW64228.1
GeneID:131965	METTL6	3	15,451,377	15,469,042	17,665	-	1	2_A375_pNL97_plus_lncRNA::1::5502	434	in gene	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene METTL6	METTL6, MGC24132	methyltransferase like 6	NM_152396, hCT1640276.4, hCT1964861.1	1553688_at, 1553689_s_at, 1557991_at, 232102_at	NP_689609.2, EAW64232.1, EAW64233.1
GeneID:85403	EAF1	3	15,469,064	15,484,120	15,056	+	1	2_A375_pNL97_plus_lncRNA::1::5502	-456	upstream	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene EAF1	EAF1		NM_033083, hCT18969.4	226952_at	NP_149074.3, EAW64234.1
GeneID:23243	ANKRD28	3	15,708,743	15,901,053	192,310	-	2	2_A375_pNL97_plus_lncRNA::1::5503, 2_A375_pNL97_plus_lncRNA::1::5504	413, -707	in gene, upstream	0	1	14.5	18	2	2_A375_pNL97_plus_lncRNA::1	18	Gene ANKRD28	PITK, KIAA0379, ANKRD28	ankyrin repeat domain 28	NM_015199, NM_001195098, NM_001195099, hCT1951695.1, hCT2346854.0, hCT2346855.0, hCT2346856.0, hCT2346857.0, hCT2346858.0, hCT2346859.0, hCT2346860.0, hCT2346861.0	1561079_at, 213035_at, 226025_at, 229307_at	NP_056014.2, NP_001182027.1, NP_001182028.1, EAW64258.1, EAW64259.1, EAW64262.1, EAW64257.1, EAW64260.1, EAW64261.1, EAW64263.1, EAW64264.1, EAW64265.1
GeneID:285381	DPH3	3	16,298,568	16,306,496	7,928	-	1	1_A375_pNL7_minus_lncRNA::1::3828	128	in gene	1	0	24	19	1	1_A375_pNL7_minus_lncRNA::1	24	Gene DPH3	DELGIP, DESR1, MGC20197, DPH3A, DELGIP1, ZCSL2, DPH3, KTI11	DPH3, KTI11 homolog (S. cerevisiae)	NM_001047434, NM_206831, hCT18791.3, hCT2275390.0	225195_at, 225200_at	NP_001040899.1, NP_996662.1, EAW64268.1, EAW64269.1
GeneID:92106	OXNAD1	3	16,306,667	16,347,594	40,927	+	1	1_A375_pNL7_minus_lncRNA::1::3828	-299	upstream	1	0	24	19	1	1_A375_pNL7_minus_lncRNA::1	24	Gene OXNAD1	MGC15763, OXNAD1	oxidoreductase NAD-binding domain containing 1	NM_138381, hCT1643550.3, hCT2275138.0, hCT2275139.0	227686_at	NP_612390.1, EAW64272.1, EAW64270.1, EAW64271.1
GeneID:23180	RFTN1	3	16,357,352	16,555,222	197,870	-	1	1_A375_pNL7_minus_lncRNA::1::3829	86262	in gene	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene RFTN1	MGC141678, RAFTLIN, MIG2, MGC44480, RFTN1, PIB10, PIG9, FLJ23866, KIAA0084	raftlin, lipid raft linker 1	NM_015150, hCT1965790.1, hCT2354007.0, hCT2354008.0	212646_at	NP_055965.1, EAW64273.1, EAW64274.1, EAW64275.1
GeneID:1618	DAZL	3	16,628,299	16,647,006	18,707	-	1	1_A375_pNL7_minus_lncRNA::1::3830	21806	downstream	1	0	20	10	1	1_A375_pNL7_minus_lncRNA::1	20	Gene DAZL	SPGYLA, MGC26406, DAZL, DAZLA, DAZL1, DAZH	deleted in azoospermia-like	NM_001190811, NM_001351, hCT17895.3, hCT2354114.0	206588_at	NP_001177740.1, NP_001342.2, EAW64278.1, EAW64279.1
GeneID:23228	PLCL2	3	16,926,452	17,132,098	205,646	+	1	1_A375_pNL7_minus_lncRNA::1::3831	4412	in gene	1	0	16	9	1	1_A375_pNL7_minus_lncRNA::1	16	Gene PLCL2	PLCL2, KIAA1092, PLCE2, FLJ13484	phospholipase C-like 2	NM_015184, NM_001144382, hCT18615.2, hCT2275158.0	213309_at, 216217_at, 216218_s_at	NP_055999.2, NP_001137854.1, EAW64282.1, EAW64283.1
GeneID:131096	KCNH8	3	19,190,017	19,577,135	387,118	+	5	1_A375_pNL7_minus_lncRNA::1::3832, 1_A375_pNL7_minus_lncRNA::1::3833, 2_A375_pNL97_plus_lncRNA::1::5506, 2_A375_pNL97_plus_lncRNA::1::5507, 2_A375_pNL97_plus_lncRNA::1::5508	479, 1087, -428, 287, 1151	in gene, in gene, upstream, in gene, in gene	1	1	19.33	22	3	2_A375_pNL97_plus_lncRNA::1	32	Gene KCNH8	elk3, ELK, Kv12.1, KCNH8, ELK1	potassium voltage-gated channel, subfamily H (eag-related), member 8	NM_144633, hCT17911.4, hCT2275133.0	1552742_at	NP_653234.2, EAW64296.1, EAW64297.1
GeneID:5868	RAB5A	3	19,988,572	20,026,667	38,095	+	1	2_A375_pNL97_plus_lncRNA::1::5509	36	in gene	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RAB5A	RAB5, RAB5A	RAB5A, member RAS oncogene family	NM_004162, hCT1814967.2, hCT1964882.1, hCT1964883.1	206113_s_at, 209089_at, 240990_at	NP_004153.2, EAW64303.1, EAW64301.1, EAW64302.1
GeneID:151648	SGOL1	3	20,202,085	20,227,683	25,598	-	1	2_A375_pNL97_plus_lncRNA::1::5510	-13	upstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SGOL1	Sgo1, NY-BR-85, SGO, FLJ14230, SGOL1	shugoshin-like 1 (S. pombe)	NM_001012409, NM_001012411, NM_001012413, NM_001012410, NM_001012412, NM_138484, hCT1645686.3, hCT2275339.0, hCT2275340.1, hCT2354126.0	1553690_at, 231936_at	NP_001012409.1, NP_001012411.1, NP_612493.1, NP_001012410.1, NP_001012412.1, NP_001012413.1, EAW64307.1, EAW64308.1, EAW64309.1, EAW64310.1
GeneID:100505877	LOC100505877	3	23,236,561	23,244,069	7,508	-	1	2_A375_pNL97_plus_lncRNA::1::5512	-795	upstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100505877		hypothetical LOC100505877	XR_112471, XR_112472, XR_110043, XR_110044, XR_113482, XR_113483		
GeneID:7325	UBE2E2	3	23,244,784	23,632,296	387,512	+	1	2_A375_pNL97_plus_lncRNA::1::5512	80	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene UBE2E2	FLJ25157, UBE2E2, UBCH8	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	NM_152653, hCT2275577.0, hCT2275578.0, hCT2275579.0, hCT2275580.0, hCT2354071.0	225651_at	NP_689866.1, EAW64325.1, EAW64321.1, EAW64322.1, EAW64323.1, EAW64324.1
GeneID:28512	NKIRAS1	3	23,933,572	23,958,537	24,965	-	1	2_A375_pNL97_plus_lncRNA::1::5513	169	in gene	0	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene NKIRAS1	NKIRAS1, kappaB-Ras1, KBRAS1	NFKB inhibitor interacting Ras-like 1	NM_020345, hCT2277964.0, hCT2277966.0	225930_at	NP_065078.1, EAW64336.1, EAW64335.1
GeneID:6138	RPL15	3	23,958,639	23,962,334	3,695	+	1	2_A375_pNL97_plus_lncRNA::1::5513	-271	upstream	0	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene RPL15	RPLY10, L15, MGC88603, RPYL10, RPL10, RPL15, FLJ26304, EC45	ribosomal protein L15	NM_002948, hCT2277499.0, hCT2277500.0, hCT2277501.0	221475_s_at, 221476_s_at, 240806_at	NP_002939.2, EAW64339.1, EAW64337.1, EAW64338.1
GeneID:100505901	LOC100505901	3	23,961,600	23,982,515	20,915	-	2	2_A375_pNL97_plus_lncRNA::1::5513, 2_A375_pNL97_plus_lncRNA::1::5514	24147, -5277	downstream, upstream	0	1	15	21	2	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100505901		hypothetical LOC100505901	XR_110045, XR_113484		
GeneID:9975	NR1D2	3	23,986,751	24,022,109	35,358	+	1	2_A375_pNL97_plus_lncRNA::1::5514	1041	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene NR1D2	BD73, EAR-1R, NR1D2, RVR	nuclear receptor subfamily 1, group D, member 2	NM_005126, NM_001145425, hCT1816541.2, hCT2354197.0	209750_at, 225768_at	NP_005117.3, NP_001138897.1, EAW64340.1, EAW64341.1
GeneID:7068	THRB	3	24,158,644	24,536,313	377,669	-	6	1_A375_pNL7_minus_lncRNA::1::3836, 1_A375_pNL7_minus_lncRNA::1::3837, 2_A375_pNL97_plus_lncRNA::1::5515, 2_A375_pNL97_plus_lncRNA::1::5516, 2_A375_pNL97_plus_lncRNA::1::5517, 2_A375_pNL97_plus_lncRNA::1::5518	338201, 185, 273369, 129497, 22329, 553	in gene, in gene, in gene, in gene, in gene, in gene	1	1	14.2	18.8	5	1_A375_pNL7_minus_lncRNA::1	23	Gene THRB	THRB2, THRB1, MGC126109, GRTH, THR1, NR1A2, ERBA2, PRTH, MGC126110, ERBA-BETA, THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	NM_000461, NM_001128176, NM_001128177, hCT1957928.1, hCT2277950.0, hCT2277953.0, hCT2277954.0, hCT2354171.0, hCT6550.3	207044_at, 226716_at, 229657_at	NP_000452.2, NP_001121648.1, NP_001121649.1, EAW64345.1, EAW64348.1, EAW64350.1, EAW64346.1, EAW64347.1, EAW64349.1
GeneID:7155	TOP2B	3	25,639,475	25,705,788	66,313	-	1	2_A375_pNL97_plus_lncRNA::1::5520	28	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TOP2B	TOP2B, top2beta, TOPIIB	topoisomerase (DNA) II beta 180kDa	NM_001068, hCT19508.3, hCT2276094.0, hCT2276095.0	211987_at	NP_001059.2, EAW64357.1, EAW64358.1, EAW64359.1
GeneID:55768	NGLY1	3	25,760,435	25,831,530	71,095	-	1	1_A375_pNL7_minus_lncRNA::1::3839	-22	upstream	1	0	16	9	1	1_A375_pNL7_minus_lncRNA::1	16	Gene NGLY1	FLJ11005, PNGase, FLJ12409, PNG1, NGLY1	N-glycanase 1	NM_018297, NM_001145293, NM_001145294, NM_001145295, hCT19506.3, hCT1965794.1, hCT1965795.1, hCT2276088.0, hCT2276091.0	207492_at, 220742_s_at	NP_060767.2, NP_001138765.1, NP_001138766.1, NP_001138767.1, EAW64364.1, EAW64365.1, EAW64362.1, EAW64363.1, EAW64366.1
GeneID:54995	OXSM	3	25,831,563	25,836,025	4,462	+	1	1_A375_pNL7_minus_lncRNA::1::3839	-11	upstream	1	0	16	9	1	1_A375_pNL7_minus_lncRNA::1	16	Gene OXSM	KASI, FLJ20604, KS, FASN2D, OXSM	3-oxoacyl-ACP synthase, mitochondrial	NM_017897, NM_001145391, NR_026937, hCT19504.2, hCT1951233.1, hCT2275806.0	219133_at	NP_060367.1, NP_001138863.1, EAW64367.1, EAW64368.1, EAW64369.1
GeneID:8320	EOMES	3	27,757,868	27,763,785	5,917	-	2	1_A375_pNL7_minus_lncRNA::1::3843, 2_A375_pNL97_plus_lncRNA::1::5523	57, -71	in gene, upstream	1	1	18	16	1	1_A375_pNL7_minus_lncRNA::1	18	Gene EOMES	TBR2, EOMES	eomesodermin homolog (Xenopus laevis)	NM_005442, hCT19343.3, hCT2354152.0	231776_at	NP_005433.2, EAW64387.1, EAW64388.1
GeneID:7048	TGFBR2	3	30,647,994	30,735,634	87,640	+	1	2_A375_pNL97_plus_lncRNA::1::5527	49030	in gene	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TGFBR2	TAAD2, RIIC, FAA3, TGFBR2, TGFR-2, TGFbeta-RII, AAT3, LDS1B, LDS2B, MFS2	transforming growth factor, beta receptor II (70/80kDa)	NM_001024847, NM_003242, hCT2279541.0, hCT2279543.0, hCT2279545.0	207334_s_at, 208944_at	NP_001020018.1, NP_003233.4, EAW64410.1, EAW64411.1, EAW64412.1
GeneID:201595	STT3B	3	31,574,491	31,677,556	103,065	+	2	1_A375_pNL7_minus_lncRNA::1::3847, 2_A375_pNL97_plus_lncRNA::1::5531	-1115, -747	upstream, upstream	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene STT3B	STT3B, FLJ90106, STT3-B, SIMP	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	NM_178862, hCT19161.3, hCT2354170.0	224700_at, 231294_at, 236303_at	NP_849193.1, EAW64416.1, EAW64415.1
GeneID:114884	OSBPL10	3	31,702,317	32,023,342	321,025	-	4	1_A375_pNL7_minus_lncRNA::1::3848, 1_A375_pNL7_minus_lncRNA::1::3849, 2_A375_pNL97_plus_lncRNA::1::5532, 2_A375_pNL97_plus_lncRNA::1::5533	44398, 206, 44398, 94	in gene, in gene, in gene, in gene	1	1	18	19	2	2_A375_pNL97_plus_lncRNA::1	20	Gene OSBPL10	ORP10, OSBP9, OSBPL10, FLJ20363	oxysterol binding protein-like 10	NM_001174060, NM_017784, hCT2276519.0, hCT2276521.0	216755_at, 217017_at, 219073_s_at, 222818_at, 231656_x_at	NP_001167531.1, NP_060254.2, EAW64417.1, EAW64418.1
GeneID:344787	ZNF860	3	32,023,266	32,033,120	9,854	+	2	1_A375_pNL7_minus_lncRNA::1::3849, 2_A375_pNL97_plus_lncRNA::1::5533	-130, -18	upstream, upstream	1	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF860	ZNF860, FLJ60236	zinc finger protein 860	NM_001137674		NP_001131146.1
GeneID:23171	GPD1L	3	32,148,003	32,210,207	62,204	+	1	1_A375_pNL7_minus_lncRNA::1::3850	-163	upstream	1	0	21	15	1	1_A375_pNL7_minus_lncRNA::1	21	Gene GPD1L	KIAA0089, GPD1-L, GPD1L	glycerol-3-phosphate dehydrogenase 1-like	NM_015141, hCT19160.3, hCT1965792.1	212510_at	NP_055956.1, EAW64422.1, EAW64421.1
GeneID:51143	DYNC1LI1	3	32,567,463	32,612,366	44,903	-	1	2_A375_pNL97_plus_lncRNA::1::5534	-114	upstream	0	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene DYNC1LI1	LIC1, DNCLI1, FLJ10219, DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1	NM_016141, hCT10298.2, hCT1957947.1, hCT2354176.0	217976_s_at, 222479_s_at	NP_057225.2, EAW64433.1, EAW64431.1, EAW64432.1
GeneID:25904	CNOT10	3	32,726,698	32,815,354	88,656	+	2	1_A375_pNL7_minus_lncRNA::1::3852, 2_A375_pNL97_plus_lncRNA::1::5535	-170, -202	upstream, upstream	1	1	17	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene CNOT10	FLJ12890, DKFZp434K115, CNOT10, FLJ13165	CCR4-NOT transcription complex, subunit 10	NM_015442, hCT2277170.0, hCT2277171.0, hCT2354091.0	223219_s_at, 237959_at	NP_056257.1, EAW64436.1, EAW64434.1, EAW64435.1
GeneID:2720	GLB1	3	33,038,100	33,138,694	100,594	-	1	2_A375_pNL97_plus_lncRNA::1::5536	14	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene GLB1	MPS4B, ELNR1, EBP, GLB1	galactosidase, beta 1	NM_000404, NM_001079811, NM_001135602, hCT2277509.0, hCT2277510.0, hCT22936.3, hCT2354045.0	201576_s_at	NP_000395.2, NP_001073279.1, NP_001129074.1, EAW64442.1, EAW64443.1, EAW64445.1, EAW64444.1
GeneID:643853	TMPPE	3	33,131,908	33,138,293	6,385	-	1	2_A375_pNL97_plus_lncRNA::1::5536	-387	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TMPPE	FLJ46376, TMPPE, FLJ45032	transmembrane protein with metallophosphoesterase domain	NM_001039770, NM_001136238		NP_001034859.2, NP_001129710.1
GeneID:10491	CRTAP	3	33,155,450	33,189,265	33,815	+	1	2_A375_pNL97_plus_lncRNA::1::5537	390	in gene	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CRTAP	LEPREL3, CRTAP, CASP	cartilage associated protein	NM_006371, hCT2277091.0, hCT2277093.0, hCT2277095.0	1554464_a_at, 1555889_a_at, 201380_at, 226656_at, 227138_at	NP_006362.1, EAW64449.1, EAW64448.1, EAW64450.1
GeneID:7342	UBP1	3	33,429,828	33,481,897	52,069	-	1	2_A375_pNL97_plus_lncRNA::1::5538	-471	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene UBP1	DKFZp686L1745, LBP-1a, LBP1B, LBP1A, UBP1, LBP-1B	upstream binding protein 1 (LBP-1a)	NM_014517, NM_001128160, NM_001128161, hCT11147.4, hCT2278925.0, hCT2278926.0, hCT2354050.0	218082_s_at	NP_055332.3, NP_001121632.1, NP_001121633.1, EAW64454.1, EAW64455.1, EAW64457.1, EAW64456.1
GeneID:23122	CLASP2	3	33,537,737	33,759,848	222,111	-	4	1_A375_pNL7_minus_lncRNA::1::3853, 1_A375_pNL7_minus_lncRNA::1::3854, 2_A375_pNL97_plus_lncRNA::1::5539, 2_A375_pNL97_plus_lncRNA::1::5540	59208, 40, 59128, 40	in gene, in gene, in gene, in gene	1	1	20.5	17.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene CLASP2	CLASP2		NM_015097, hCT2278921.2, hCT2278922.2, hCT2278923.2, hCT2348862.1, hCT2348863.0, hCT2348864.1, hCT2348865.1, hCT2348866.1, hCT2348867.1	1555469_a_at, 1556759_s_at, 212306_at, 212308_at, 212309_at, 238046_at	NP_055912.1, EAW64466.1, EAW64459.1, EAW64462.1, EAW64463.1, EAW64464.1, EAW64460.1, EAW64461.1, EAW64465.1, EAW64467.1
GeneID:10015	PDCD6IP	3	33,840,066	33,911,195	71,129	+	1	2_A375_pNL97_plus_lncRNA::1::5541	94	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PDCD6IP	PDCD6IP, AIP1, Alix, DRIP4, HP95, MGC17003	programmed cell death 6 interacting protein	NM_013374, NM_001162429, NR_027867, NR_027868, hCT2277109.0, hCT29770.4	217746_s_at, 222394_at	NP_037506.2, NP_001155901.1, EAW64468.1, EAW64469.1
GeneID:6769	STAC	3	36,422,097	36,589,496	167,399	+	2	1_A375_pNL7_minus_lncRNA::1::3855, 2_A375_pNL97_plus_lncRNA::1::5542	-81, -81	upstream, upstream	1	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene STAC	STAC, STAC1, FLJ32331	SH3 and cysteine rich domain	NM_003149, hCT6690.2	205743_at	NP_003140.1, EAW64474.1
GeneID:9852	EPM2AIP1	3	37,027,357	37,034,795	7,438	-	2	1_A375_pNL7_minus_lncRNA::1::3857, 2_A375_pNL97_plus_lncRNA::1::5543	299, 267	in gene, in gene	1	1	22	20	1	1_A375_pNL7_minus_lncRNA::1	22	Gene EPM2AIP1	EPM2AIP1, KIAA0766, FLJ11207	EPM2A (laforin) interacting protein 1	NM_014805, hCT8187.2	202909_at, 227847_at	NP_055620.1, EAW64482.1
GeneID:4292	MLH1	3	37,034,841	37,092,337	57,496	+	2	1_A375_pNL7_minus_lncRNA::1::3857, 2_A375_pNL97_plus_lncRNA::1::5543	-345, -313	upstream, upstream	1	1	22	20	1	1_A375_pNL7_minus_lncRNA::1	22	Gene MLH1	MLH1, hMLH1, HNPCC, HNPCC2, MGC5172, COCA2, FCC2	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	NM_000249, NM_001167617, NM_001167618, NM_001167619, hCT2279372.0, hCT2354086.0, hCT8190.2	202520_s_at	NP_000240.1, NP_001161089.1, NP_001161090.1, NP_001161091.1, EAW64483.1, EAW64484.1, EAW64485.1
GeneID:9209	LRRFIP2	3	37,094,117	37,217,851	123,734	-	3	1_A375_pNL7_minus_lncRNA::1::3858, 2_A375_pNL97_plus_lncRNA::1::5544, 2_A375_pNL97_plus_lncRNA::1::5545	-165, 12987, -122	upstream, in gene, upstream	1	1	17.5	19.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene LRRFIP2	FLJ56304, FLJ20248, HUFI-2, DKFZp434H2035, LRRFIP2, FLJ22683	leucine rich repeat (in FLII) interacting protein 2	NM_017724, NM_006309, NM_001134369, hCT2280904.0, hCT2280906.0, hCT2280907.0, hCT2280908.0, hCT2280909.0, hCT2280910.0	218364_at, 220610_s_at, 232673_at, 232704_s_at, 232705_at	NP_060194.1, NP_006300.1, NP_001127841.1, EAW64487.1, EAW64489.1, EAW64491.1, EAW64486.1, EAW64488.1, EAW64490.1
GeneID:2803	GOLGA4	3	37,284,682	37,408,370	123,688	+	2	1_A375_pNL7_minus_lncRNA::1::3859, 2_A375_pNL97_plus_lncRNA::1::5546	-42, -90	upstream, upstream	1	1	23	19	1	1_A375_pNL7_minus_lncRNA::1	23	Gene GOLGA4	GOLGA4, MU-RMS-40.18, GOLG, GCP2, p230	golgi autoantigen, golgin subfamily a, 4	NM_002078, NM_001172713, hCT1960099.2, hCT2279375.1, hCT8192.4	201567_s_at, 215203_at	NP_002069.2, NP_001166184.1, EAW64494.1, EAW64495.1, EAW64496.1
GeneID:3680	ITGA9	3	37,493,813	37,861,281	367,468	+	3	1_A375_pNL7_minus_lncRNA::1::3860, 2_A375_pNL97_plus_lncRNA::1::5547, 2_A375_pNL97_plus_lncRNA::1::5548	168091, 168043, 241451	in gene, in gene, in gene	1	1	13	23	2	2_A375_pNL97_plus_lncRNA::1	30	Gene ITGA9	ITGA4L, ALPHA-RLC, RLC, ITGA9	integrin, alpha 9	NM_002207, hCT8191.2	1555335_at, 1555336_a_at, 206009_at, 227297_at	NP_002198.2, EAW64501.1
GeneID:10217	CTDSPL	3	37,903,669	38,025,960	122,291	+	4	1_A375_pNL7_minus_lncRNA::1::3861, 2_A375_pNL97_plus_lncRNA::1::5549, 2_A375_pNL97_plus_lncRNA::1::5550, 2_A375_pNL97_plus_lncRNA::1::5551	363, 267, 47227, 74283	in gene, in gene, in gene, in gene	1	1	14	19	3	2_A375_pNL97_plus_lncRNA::1	23	Gene CTDSPL	PSR1, HYA22, C3orf8, CTDSPL, SCP3, RBSP3	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	NM_005808, NM_001008392, hCT2278342.0, hCT2278343.0, hCT2354028.0, hCT33701.3	201904_s_at, 201905_s_at, 201906_s_at, 213597_s_at, 214187_x_at	NP_005799.2, NP_001008393.1, EAW64502.1, EAW64503.1, EAW64504.1, EAW64505.1
GeneID:30	ACAA1	3	38,164,201	38,178,733	14,532	-	2	1_A375_pNL7_minus_lncRNA::1::3862, 1_A375_pNL7_minus_lncRNA::1::3863	-259, -1427	upstream, upstream	1	0	17	16.5	2	1_A375_pNL7_minus_lncRNA::1	17	Gene ACAA1	THIO, ACAA, ACAA1, PTHIO	acetyl-CoA acyltransferase 1	NM_001607, NM_001130410, NR_024024, hCT1967980.1, hCT2278964.0, hCT2278965.0, hCT2278966.0, hCT2278968.0, hCT33702.3	202025_x_at, 214274_s_at	NP_001598.1, NP_001123882.1, EAW64513.1, EAW64515.1, EAW64516.1, EAW64517.1, EAW64514.1, EAW64518.1
GeneID:4615	MYD88	3	38,179,969	38,184,513	4,544	+	2	1_A375_pNL7_minus_lncRNA::1::3862, 1_A375_pNL7_minus_lncRNA::1::3863	-977, 191	upstream, in gene	1	0	17	16.5	2	1_A375_pNL7_minus_lncRNA::1	17	Gene MYD88	MYD88D, MYD88	myeloid differentiation primary response gene (88)	NM_002468, NM_001172566, NM_001172567, NM_001172568, NM_001172569, hCT2354031.0, hCT33703.2	209124_at	NP_002459.2, NP_001166037.1, NP_001166038.1, NP_001166039.1, NP_001166040.1, EAW64520.1, EAW64521.1
GeneID:9942	XYLB	3	38,388,251	38,456,467	68,216	+	2	1_A375_pNL7_minus_lncRNA::1::3864, 2_A375_pNL97_plus_lncRNA::1::5552	37, 101	in gene, in gene	1	1	22	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene XYLB	XYLB, FLJ12539, FLJ22075, FLJ10343	xylulokinase homolog (H. influenzae)	NM_005108, hCT2278368.0, hCT2278370.0, hCT2354024.0, hCT33700.1	1569683_at, 208317_at, 208318_s_at, 214776_x_at	NP_005099.2, EAW64531.1, EAW64532.1, EAW64533.1, EAW64534.1
GeneID:64689	GORASP1	3	39,138,091	39,149,130	11,039	-	2	1_A375_pNL7_minus_lncRNA::1::3866, 2_A375_pNL97_plus_lncRNA::1::5555	10, 74	in gene, in gene	1	1	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene GORASP1	P65, GORASP1, MGC118894, GOLPH5, GRASP65, FLJ23443, MGC118897	golgi reassembly stacking protein 1, 65kDa	NM_031899, hCT10093.3, hCT1967892.1, hCT2280039.0, hCT2280040.0, hCT2280043.0, hCT2354039.0, hCT2354040.0, hCT2354041.0, hCT2354042.0	215749_s_at, 243677_at	NP_114105.1, EAW64559.1, EAW64552.1, EAW64553.1, EAW64554.1, EAW64558.1, EAW64555.1, EAW64556.1, EAW64557.1, EAW64560.1
GeneID:199223	TTC21A	3	39,149,152	39,180,394	31,242	+	3	1_A375_pNL7_minus_lncRNA::1::3866, 2_A375_pNL97_plus_lncRNA::1::5555, 2_A375_pNL97_plus_lncRNA::1::5556	-32, -96, 39403	upstream, upstream, downstream	1	1	23.5	20	2	1_A375_pNL7_minus_lncRNA::1	24	Gene TTC21A	TTC21A, STI2, MGC70523, DKFZp686P18239, MGC156293	tetratricopeptide repeat domain 21A	NM_145755, NM_001105513, hCT10095.3, hCT2344910.0, hCT2344911.0, hCT2344912.0	230997_at, 232305_at	NP_665698.2, NP_001098983.2, EAW64561.1, EAW64562.1, EAW64563.1, EAW64564.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervals Count	Intervals	Intervals Distance	Intervals Position	[A]	[B]	[C]	[D]	Assigned Region Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:9745651	CSNK1E	3	39,153,342	39,193,102	11,760	+	3	1_A375_shL7_shrna1_blockRNA:1:3967, 2_A375_shL87_gfp_blockRNA:1:5536, 3_A375_shL87_gfp_blockRNA:1:5538	1562, 6547, 760	up gene, up gene, up gene	1	1	23	24	2	2_A375_shL87_gfp_blockRNA:1	28	Gene CSNK1E	DKFZp686P194, CSNK1E, CKIepsilon, CKIE, HAN37.3B, TAP-3, AXUD1, CSNK1E	Cytosine-serine-rich nuclear protein 1	NM_033237, ICT164029R.3; NCT2800335.0, NCT2800036.0, NCT2800327.0, NCT2354013.0, NCT2356014.0	235537_at	NP_149016.2, EAW64998.1, EAW64999.1, EAW64997.1, EAW64998.1, EAW65370.1, EAW65999.1
Gene:ID:3336774	SLC25A32	3	39,324,815	39,338,819	14,004	+	3	1_A375_shL7_shrna1_blockRNA:1:3966, 2_A375_shL87_gfp_blockRNA:1:5969, 3_A375_shL87_gfp_blockRNA:1:5970	209, 23505, 451	up gene, downstream, up gene	1	1	16.5	16	2	2_A375_shL87_gfp_blockRNA:1	22	Gene SLC25A32	SLC25A32, FLJ22703, FLJ30551	solute carrier family 25, member 32	NM_017573, ICT2297638.0, ICT2297690.0, ICT8066.0	217991_at	NP_060345.2, EAW64579.1, EAW64580.1, EAW64581.1
Gene:ID:3357221	RPSA	3	39,446,204	39,454,033	5,829	+	1	1_A375_shL7_shrna1_blockRNA:1:3969	116	up gene	1	0	16	14	1	1_A375_shL7_shrna1_blockRNA:1	16	Gene RPSA	p40, LAMBR, 67LR, SA, LBP, LRP, RPSA, LAMR1, 37LRP	ribosomal protein SA	NM_001012321.1, NM_002295, ICT2297110.0, ICT2297111.1, ICT2297112.0, ICT2297113.1, ICT2297114.1, ICT2297115.1	212855_s_at	NP_001012321.1, NP_002286.2, EAW64552.1, EAW64555.1, EAW64556.1, EAW64557.1, EAW64553.1, EAW64554.1
Gene:ID:3357222	SNORA62	3	39,449,662	39,450,030	148	+	1	1_A375_shL7_shrna1_blockRNA:1:3969	-1562	upstream	1	0	16	14	1	1_A375_shL7_shrna1_blockRNA:1	16	Gene SNORA62	ACA6, SNORA6	Small nucleolar RNA, H/ACA box 62	NR_002323		
Gene:ID:6767844	SNORA62	3	39,452,545	39,452,696	153	+	1	1_A375_shL7_shrna1_blockRNA:1:3964	-4225	upstream	1	0	16	14	1	1_A375_shL7_shrna1_blockRNA:1	16	Gene SNORA62	RNU108, E2, E2-1, KNE2, SNORA62	Small nucleolar RNA, H/ACA box 62	NR_002324		
Gene:ID:9924	MYRIP	3	39,651,303	40,001,812	490,509	+	1	1_A375_shL7_shrna1_blockRNA:1:3971	4490117	up gene	1	0	21	14	1	1_A375_shL7_shrna1_blockRNA:1	21	Gene MYRIP	SLAC2-C, MGC130034, MGC130035, DKFZp686F1615, SLAC2-C, MYRIP, FLJ46825	myosin VIIA and Rab interacting protein	NM_015460, ICT2344781.0, ICT2344810.0	214196_at	NP_056275.2, EAW64596.1, EAW64598.1
Gene:ID:4809052	FLJ33983	3	40,214,639	40,351,189	136,550	-	3	1_A375_shL7_shrna1_blockRNA:1:3971, 2_A375_shL87_gfp_blockRNA:1:5972, 3_A375_shL87_gfp_blockRNA:1:5980	50999, 101, 55	up gene, up gene, up gene	1	1	23	22	2	2_A375_shL87_gfp_blockRNA:1	30	Gene FLJ33983		hypothetical LOC440832	NR_033983	1556248_at, 1556294_a_at, 1557212_at, 242730_at	
Gene:ID:3386	EIF1B	3	40,351,173	40,353,915	2,742	+	2	1_A375_shL7_shrna1_blockRNA:1:3972, 2_A375_shL87_gfp_blockRNA:1:5980	-55, -59	upstream, upstream	1	1	25	30	1	2_A375_shL87_gfp_blockRNA:1	30	Gene EIF1B	GC20, EIF1B	eukaryotic translation initiation factor 1B	NM_005879, ICT2276972.0, ICT7466.2	201756_at, 237866_at	NP_005869.1, EAW64595.1, EAW64599.1
Gene:ID:9745652	ZNF918	3	40,516,664	40,531,726	15,124	+	1	1_A375_shL7_shrna1_blockRNA:1:3961	-44	upstream	0	1	8	19	1	2_A375_shL87_gfp_blockRNA:1	19	Gene ZNF918	FLJ90764, ZNF919	zinc finger protein 918	NM_001145953, NM_001145952, NM_001145951, NM_020746, NCT1616492.2, NCT2345021.0	1552539_at	NP_001138553.1, NP_001138554.1, NP_001138555.1, EAW64611.1, EAW64612.1
Gene:ID:5362820	ZNF620	3	40,547,530	40,559,290	11,760	+	2	1_A375_shL7_shrna1_blockRNA:1:3972, 2_A375_shL87_gfp_blockRNA:1:5982	16891, 16040	downstream, downstream	1	1	21	20	1	1_A375_shL7_shrna1_blockRNA:1	21	Gene ZNF620	MGC936536, ZNF620	zinc finger protein 620	NM_175668, NR_024114, ICT2345396.1, ICT2345397.1, ICT2345398.1, ICT2345166.0	1558743_at	NP_787063.1, EAW64618.1, EAW64619.1, EAW64614.1, EAW64616.1
Gene:ID:5362821	ZNF621	3	40,566,376	40,581,843	15,467	+	2	1_A375_shL7_shrna1_blockRNA:1:3972, 2_A375_shL87_gfp_blockRNA:1:5982	43, -300	up gene, upstream	1	1	21	30	1	1_A375_shL7_shrna1_blockRNA:1	21	Gene ZNF621	ZNF621, DKFZp686B11167, MGC126666, FLJ45246, FLJ23766	zinc finger protein 621	NM_198464, NM_001098414	1558532_at, 220164_at, 241499_at	NP_940859.1, NP_001091554.1
Gene:ID:1499	CTNNB1	3	41,240,942	41,261,839	40,897	+	2	1_A375_shL7_shrna1_blockRNA:1:3975, 2_A375_shL87_gfp_blockRNA:1:5988	62, 62	up gene, up gene	1	1	16	15	1	2_A375_shL87_gfp_blockRNA:1	16	Gene CTNNB1	DKFZp686D02253, CTNNB, CTNNB1, FLJ25606, FLJ37623	catenin (cadherin-associated protein), beta 1, 88kDa	NM_001098210, NM_001904, NM_001098209, NCT16887.3, ICT2277140.0, NCT2277146.0, NCT2280113.0	1554411_at, 201533_at, 201534_s_at	NP_001091680.1, NP_001893.1, NP_001091679.1, EAW64625.1, EAW64626.1, EAW64627.1
Gene:ID:4926	ULK4	3	41,255,090	42,003,960	715,870	+	2	1_A375_shL7_shrna1_blockRNA:1:3976, 2_A375_shL87_gfp_blockRNA:1:5990	76, 76	up gene, up gene	1	1	27	28	1	2_A375_shL87_gfp_blockRNA:1	28	Gene ULK4	DKFZp434E1622, RED01025, PANK1L, ULK4, FLJ20974	unc-51-like kinase 4 (C. elegans)	NM_017566	226955_at, 231149_s_at, 222299_at, 241165_s_at	NP_060036.2
Gene:ID:102870063	LOC100270063	3	42,003,914	42,126,685	123,891	+	3	1_A375_shL7_shrna1_blockRNA:1:3976, 2_A375_shL87_gfp_blockRNA:1:5977, 3_A375_shL87_gfp_blockRNA:1:5980	670, 119246, 670	up gene, up gene, up gene	1	1	21	16	2	2_A375_shL87_gfp_blockRNA:1	28	Gene LOC100270063		hypothetical protein LOC100387063	XM_003119897, XM_003343237, XM_002346666		XP_003119945.1, XP_003343286.2, XP_002346924.2
Gene:ID:1177	SEC22C	3	42,569,472	42,623,426	53,955	-	2	1_A375_shL7_shrna1_blockRNA:1:3976, 2_A375_shL87_gfp_blockRNA:1:5987	-252, -462	upstream, upstream	1	1	19	19	1	2_A375_shL87_gfp_blockRNA:1	19	Gene SEC22C	DKFZp761F2221, MGC13261, SEC22L3, SEC22C, MGC33213	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	NM_032970, NM_004206, ICT2283542.0, ICT2283543.0, ICT2283544.0, ICT2283545.0	226470_at, 225460_at, 228120_at, 238268_at, 238012_at, 238056_at	NP_116152.1, NP_004197.1, EAW64653.1, EAW64654.1, EAW64655.1, EAW64656.1
Gene:ID:1168	SS18L2	3	42,632,298	42,639,490	4,192	+	3	1_A375_shL7_shrna1_blockRNA:1:3976, 2_A375_shL87_gfp_blockRNA:1:5979, 3_A375_shL87_gfp_blockRNA:1:5981	-6816, 6670, -6316	upstream, downstream, upstream	1	1	16	17	2	2_A375_shL87_gfp_blockRNA:1	19	Gene SS18L2	SS18L2, KIAA-sb	synovial sarcoma translocation gene on chromosome 18-like 2	NM_018305, ICT2280182.2, ICT2283228.0	219282_at	NP_037389.1, EAW64655.1, EAW64657.1
Gene:ID:5208	NKTR	3	42,642,147	42,690,233	48,086	+	1	1_A375_shL7_shrna1_blockRNA:1:3974	-179	upstream	1	0	17	15	1	1_A375_shL7_shrna1_blockRNA:1	17	Gene NKTR	DKFZp686G0626, DKFZp686P1754, MGC99327, DKFZp686N24126, NKTR, p108, DKFZp686L06106	natural killer-tumor recognition sequence	NM_005385, ICT2283230.0, ICT2283231.0, ICT2354019.0	1557736_at, 1557737_s_at, 1570342_at, 202379_s_at, 202380_s_at, 215336_s_at, 215329_at, 215330_s_at	NP_005376.2, EAW64661.1, EAW64659.1, EAW64660.1
Gene:ID:7497	HHATL	3	42,734,155	42,744,219	10,164	-	2	1_A375_shL7_shrna1_blockRNA:1:3980, 2_A375_shL87_gfp_blockRNA:1:5992	1215, 1265	up gene, up gene	1	1	28	22	1	1_A375_shL7_shrna1_blockRNA:1	28	Gene HHATL	KIAA1170, MBOAT2, C3orf3, MSTP002, HHATL, OACT1, GLP1	Hedgehog acyltransferase-like	NM_020707, NR_027732, ICT1698556.1, NCT2703.2, ICT2356053.0	223572_at	NP_065785.2, EAW64666.1, EAW64666.1, EAW64667.1
Gene:ID:62396	CCDC13	3	42,749,874	42,814,745	64,871	-	3	1_A375_shL7_shrna1_blockRNA:1:3980, 2_A375_shL87_gfp_blockRNA:1:5991, 3_A375_shL87_gfp_blockRNA:1:5992	71641, 6, 71694	downstream, up gene, downstream	1	1	24	16	2	1_A375_shL7_shrna1_blockRNA:1	25	Gene CCDC13	FLJ25467, CCDC13	coiled-coil domain containing 13	NM_144719, ICT2283537.1, ICT2341993.0, ICT2342201.0	1553396_a_at, 1553397_at, 1554022_at, 1554023_s_at	NP_653293.2, EAW64670.1, EAW64669.1, EAW64671.1
Gene:ID:9994	HIGD1A	3	42,824,600	42,846,627	21,827	-	2	1_A375_shL7_shrna1_blockRNA:1:3981, 2_A375_shL87_gfp_blockRNA:1:5993	31291, 27	downstream, up gene	1	1	17	14	2	1_A375_shL7_shrna1_blockRNA:1	23	Gene HIGD1A	HIGD1A, HIG1, DKFZp564K247	HIG1 hypoxia-inducible domain family, member 1A	NM_001098966, NM_014056, NM_001098968, ICT2355356.1, ICT2355357.0, ICT2344200.0, ICT2345180.0, ICT2345187.0	217645_s_at, 221696_s_at	NP_001092136.1, NP_054773.2, NP_001092139.1, EAW64672.1, EAW64676.1, EAW64677.1, EAW64674.1, EAW64675.1
Gene:ID:1538	CCBP2	3	42,850,964	42,866,775	57,811	+	2	2_A375_shL87_gfp_blockRNA:1:5996, 3_A375_shL87_gfp_blockRNA:1:5997	-4964, 19636	upstream, up gene	1	1	16.5	14.5	2	2_A375_shL87_gfp_blockRNA:1	16	Gene CCBP2	CMKBR8, D6, CCR8, MGC136250, CCBP2, CCR10, MGC129976, ID6	chemokine binding protein 2	NM_001296, ICT2283238.1, ICT2283240.1, ICT2342210.0, ICT2342211.0	1555452_at, 1565830_at, 206687_at	NP_001287.2, EAW64678.1, EAW64679.1, EAW64680.1, EAW64681.1
Gene:ID:1552	CYP5B1	3	42,912,664	42,917,853	3,848	+	1	1_A375_shL7_shrna1_blockRNA:1:3971	-4891	upstream	0	1	12	17	1	2_A375_shL87_gfp_blockRNA:1	17	Gene CYP5B1	CYP12, CP5B, CYP5B1, FLJ17626	cytochrome P450, family 5, subfamily B, polypeptide 1	NM_004381, ICT1630452.2	222494_at	NP_004362.2, EAW64682.1
Gene:ID:2152274	C3orf17	3	44,263,378	44,273,890	60,212	+	1	1_A375_shL7_shrna1_blockRNA:1:3983	66793	downstream	1	0	20	15	1	1_A375_shL7_shrna1_blockRNA:1	20	Gene C3orf17	C3orf17, FLJ36137	chromosome 3 open reading frame 17	NM_001145030		NP_001138502.1
Gene:ID:5534366	C3orf23	3	44,279,611	44,293,840	71,329	+	1	1_A375_shL7_shrna1_blockRNA:1:3983	517	up gene	1	0	20	15	1	1_A375_shL7_shrna1_blockRNA:1	20	Gene C3orf23	FLJ41699, DKFZp311N0921, MGC119532, MGC119531, C3orf23, MGC119533, TOAG1, MGC119530	chromosome 3 open reading frame 23	NM_001278545, NM_001278539, NM_152626, ICT1793833.2, ICT1990094.2, ICT2345539.0, ICT2345540.0	1553693_at, 1553696_s_at, 235656_at, 241696_at	NP_001103011.1, NP_001229510.1, NP_001265467.1, NP_689839.2, EAW64703.1, EAW64704.1, EAW64705.1, EAW64706.1
Gene:ID:5227	ZNF485	3	44,451,252	44,519,182	27,980	-	1	2_A375_shL87_gfp_blockRNA:1:5979	-162	upstream	0	1	7	15	1	2_A375_shL87_gfp_blockRNA:1	15	Gene ZNF485	ZNS5CAN15, MGC126535, ZNF165, ZNF515	zinc finger protein 485	NM_153489, ICT2345210.0	234705_at, 235952_s_at	NP_703995.1, EAW64708.1
Gene:ID:6531406	ZNF852	3	44,540,862	44,552,132	11,270	-	1	2_A375_shL87_gfp_blockRNA:1:5980	100	up gene	0	1	9	19	1	2_A375_shL87_gfp_blockRNA:1	19	Gene ZNF852	ZNF852	zinc finger protein 852	XM_001717560, XM_001725370	1569552_at	XP_001717592.2, XP_001725122.2
Gene:ID:6166	ZNF197	3	44,666,511	44,682,963	23,452	+	2	2_A375_shL87_gfp_blockRNA:1:5987, 3_A375_shL87_gfp_blockRNA:1:5992	-76, -47	upstream, up gene	1	1	16	20	1	2_A375_shL87_gfp_blockRNA:1	20	Gene ZNF197	VIK4A, ZNF197, ZNF166, ZXDC4A6, ZNF20, DKFZp686I0516, P16	zinc finger protein 197	NM_006991, NM_001032655, ICT2279277.0	205553_at, 213070_at	NP_008922.1, NP_001028026.1, EAW64714.1
Gene:ID:1282	ZNF802	3	44,754,135	44,763,323	11,188	+	1	1_A375_shL7_shrna1_blockRNA:1:3983	-67	upstream	0	1	13	20	1	1_A375_shL7_shrna1_blockRNA:1	20	Gene ZNF802	FLJ14555, FLJ12515, ZNF502	zinc finger protein 502	NM_032210, NM_001134460, NM_001134461, NM_001134442, ICT2342009.0, ICT2342201.0	226532_at, 232247_at	NP_149857.2, NP_001127612.1, NP_001127613.1, NP_001127614.1, EAW64716.1, EAW64717.1, EAW64718.1
Gene:ID:4866	CDCP1	3	45,123,769	45,167,814	64,145	+	4	1_A375_shL7_shrna1_blockRNA:1:3985, 2_A375_shL87_gfp_blockRNA:1:5999, 3_A375_shL87_gfp_blockRNA:1:6004, 4_A375_shL87_gfp_blockRNA:1:6005	40456, 22410, 40810, 6109	up gene, up gene, up gene, upstream	1	1	16.33	16	3	2_A375_shL87_gfp_blockRNA:1	22	Gene CDCP1	TRASK, SIMA135, CDCP1, CD318	CUB domain containing protein 1	NM_178181, NM_022842, ICT2365403.0, ICT6498.3	1564110_at, 219581_at, 236632_s_at	NP_835457.1, NP_073732.2, EAW64727.1, EAW64728.1
Gene:ID:3389	LARS2	3	45,430,075	45,590,326	160,253	+	2	1_A375_shL7_shrna1_blockRNA:1:3991, 2_A375_shL87_gfp_blockRNA:1:6007	120757, 59477	up gene, up gene	1	1	15	14	2	1_A375_shL7_shrna1_blockRNA:1	20	Gene LARS2	LEURS, LARS2, KIAA0626, MGC26121	leucyl-tRNA synthetase 2, mitochondrial	NM_015340, ICT6961.2	204016_at, 57164_at	NP_056155.1, EAW64740.1
Gene:ID:9944	UMD1	3	45,636,223	45,722,755	86,432	+	3	1_A375_shL7_shrna1_blockRNA:1:3992, 2_A375_shL87_gfp_blockRNA:1:6006, 3_A375_shL87_gfp_blockRNA:1:6008	64205, 61949, 64237	downstream, up gene, downstream	1	1	16	26	2	2_A375_shL87_gfp_blockRNA:1	33	Gene UMD1	UMD1	UMI-domains containing 1	NM_014240, ICT5634.2	2165901_s_at, 222332_at, 227762_s_at, 238927_s_at, 234743_at	NP_055155.1, EAW64742.1
Gene:ID:84714	LOC84714	3	45,719,657	45,730,374	10,717	-	2	1_A375_shL7_shrna1_blockRNA:1:3992, 2_A375_shL87_gfp_blockRNA:1:6008	-156, -166	upstream, upstream	1	1	24	33	1	2_A375_shL87_gfp_blockRNA:1	33	Gene LOC84714		hypothetical LOC84714	NR_033947	231561_at	
Gene:ID:2908	SACM1L	3	45,730,754	45,766,900	56,146	+	2	1_A375_shL7_shrna1_blockRNA:1:3992, 2_A375_shL87_gfp_blockRNA:1:6008	-226, -164	upstream, upstream	1	1	24	33	1	2_A375_shL87_gfp_blockRNA:1	33	Gene SACM1L	KIAA0351, SACM1L, DKFZp686A0231, SAC1	SAC1 suppressor of actin mutations 1-like (yeast)	NM_014216, ICT2279930.0, ICT2279931.0, NCT4960.0	202727_at	NP_055133.2, EAW64746.1, EAW64748.1, EAW64749.1
Gene:ID:4585	LZTFL1	3	45,893,446	45,953,821	16,175	+	4	1_A375_shL7_shrna1_blockRNA:1:3993, 2_A375_shL87_gfp_blockRNA:1:6004, 3_A375_shL87_gfp_blockRNA:1:6008, 4_A375_shL87_gfp_blockRNA:1:6009	23621, 50, 23693, 229	downstream, up gene, downstream, up gene	1	1	17	16	2	2_A375_shL87_gfp_blockRNA:1	21	Gene LZTFL1	FLJ36356, LZTFL1	leucine zipper transducation factor-like 1	NM_020347, ICT2279937.0, ICT6334.2	218437_s_at, 228632_s_at, 232416_at	NP_065093.1, EAW64750.1, EAW64749.1
Gene:ID:4443	PYCO1	3	45,959,295	46,037,207	77,912	-	1	1_A375_shL7_shrna1_blockRNA:1:3995	61	up gene	1	0	17	16	1	1_A375_shL7_shrna1_blockRNA:1	17	Gene PYCO1	MGC126519, PYCO1, ZFVVT7, MGC126517, FLJ13335, DKFZp779D1142, PLPP2	PYVE and coiled-coil domain containing 1	NM_024513, ICT1627775.2	1555522_a_at, 218204_s_at	NP_078789.2, EAW64753.1
Gene:ID:9744653	CCDC12	3	46,063,220	47,016,270	55,050	+	2	1_A375_shL7_shrna1_blockRNA:1:3992, 2_A375_shL87_gfp_blockRNA:1:6002	-260, -80	upstream, upstream	1	1	25	25	1	2_A375_shL87_gfp_blockRNA:1	25	Gene CCDC12	MGC126515, PYCO1_ZFVVT7, MGC126517, FLJ13335, DKFZp779D1142, PLPP2	coiled-coil domain containing 12	NM_144716, ICT2279337.0, ICT2279338.0, ICT2279339.0, ICT2279340.0, ICT2279341.0, ICT6455.2	226011_at	NP_653317.2, EAW64758.1, EAW64759.1, EAW64760.1, EAW64761.1, EAW64762.1
Gene:ID:1210	NBEAL2	3	47,021,173	47,051,160	30,020	+	2	1_A375_shL7_shrna1_blockRNA:1:3999, 2_A375_shL87_gfp_blockRNA:1:6002	-2613, 2645	upstream, upstream	1	1	23	25	1	2_A375_shL87_gfp_blockRNA:1	25	Gene NBEAL2	KIAA0340, NBEAL2	neurobeachin-like 2	NM_015175	1556017_at, 212463_at	NP_055990.1
Gene:ID:9272	SETD2	3	47,037,998	47,203,467	147,469	+	2	1_A375_shL7_shrna1_blockRNA:1:3997, 2_A375_shL87_gfp_blockRNA:1:6002	-277, -361	upstream, upstream	1	1	23	25	1	2_A375_shL87_gfp_blockRNA:1	25	Gene SETD2	FLJ22184, FLJ36420, HIF-1, SETD2, HIF3A, SET2, HIF231, HSPC069, KIAA1732, FLJ22472, p231HBF, FLJ46850, FLJ48217, HYPB	SET domain containing 2	NM_014159, ICT1616599.2, ICT1616622.2, NCT2343497.0, ICT2343766.0, NCT2345853.0, ICT2345854.0, NCT4933.4	212491_s_at, 212492_at, 2209845_s_at	NP_054878.5, EAW64806.1, EAW64803.1, EAW64805.1, EAW64810.1, EAW64811.1, EAW64807.1, EAW64809.1
Gene:ID:55352	FLJ39334	3	47,203,660	47,263,606	59,746	+	2	1_A375_shL7_shrna1_blockRNA:1:3997, 2_A375_shL87_gfp_blockRNA:1:6002	-116, -152	upstream, upstream	1	1	25	25	1	2_A375_shL87_gfp_blockRNA:1	25	Gene FLJ39334	FLJ39334	hypothetical FLJ39334	NR_033373	1557613_at	
Gene:ID:4147	NIPA	3	47,269,516	47,323,237	54,521	+	1	1_A375_shL7_shrna1_blockRNA:1:3994	-18	upstream	0	1	16	25	1	2_A375_shL87_gfp_blockRNA:1	25	Gene NIPA	MGC104166, NIPB	tubulin family member 9	NM_182342, NM_152902, NM_001134516, NCT1693023.1, NCT1693024.1, NCT1693028.1, ICT2279340.0, NCT4954.2	223776_at, 226429_s_at, 230701_s_at, 231319_s_at	NP_071737.1, NP_076908.2, NP_001125390.1, EAW64812.1, EAW64814.1, EAW64815.1, EAW64816.1, EAW64817.1
Gene:ID:3276	KLHL18	3	47,334,330	47,366,306	63,976	+	1	2_A375_shL87_gfp_blockRNA:1:5994	22	up gene	0	1	16	25	1	2_A375_shL87_gfp_blockRNA:1	25	Gene KLHL18	FLJ13703, FLJ61263, KIAA0769, KLHL18	kelch-like 18 (Drosophila)	NM_020803, ICT1693018.1, ICT2345760.0, ICT2345977.0, NCT4957.2	1557168_s_at, 207679_at, 227640_s_at	NP_065854.2, EAW64820.1, EAW64816.1, EAW64819.1, EAW64821.1
Gene:ID:9930	PTPN23	3	47,422,991	47,554,931	32,460	+	2	1_A375_shL7_shrna1_blockRNA:1:3998, 2_A375_shL87_gfp_blockRNA:1:6009	-176, 27	upstream, up gene	1	1	16	19	1	2_A375_shL87_gfp_blockRNA:1	19	Gene PTPN23	DKFZp566F0623, HDPTP, PTPN23, PTP-TD14, KIAA1471, HD-PTP	protein tyrosine phosphatase, non-receptor type 23	NM_015466, ICT2279958.0, ICT2280200.0, NCT6451.3	221193_s_at, 221192_s_at	NP_056281.1, EAW64823.1, EAW64822.1, EAW64824.1
Gene:ID:2837	SCAP	3	47,555,164	47,617,465	62,301	+	1	2_A375_shL87_gfp_blockRNA:1:6009	325	up gene	0	1	12	17	1	2_A375_shL87_gfp_blockRNA:1	17	Gene SCAP	SCAP, KIAA0182	SREBP chaperone	NM_012235, ICT2279346.0, ICT6456.2	212329_at	NP_036367.2, EAW64825.1, EAW64826.1
Gene:ID:4659	C3orf15	3	47,577,130	47,593,199	16,069	-	1	1_A375_shL7_shrna1_blockRNA:1:3999	-6641	upstream	1	0	16	14	1	1_A375_shL7_shrna1_blockRNA:1	16	Gene C3orf15	C3orf15, TMEM102, FLJ22211	chromosome 3 open reading frame 75	NM_001031703, ICT1693020.1, ICT1697126.1	226600_at, 222277_at, 226663_s_at, 231554_at	NP_001026872.2, EAW64827.1, EAW64828.1
Gene:ID:9907	DHX30	3	47,644,299	47,691,866	47,267	+	4	1_A375_shL7_shrna1_blockRNA:1:3999, 2_A375_shL87_gfp_blockRNA:1:6001, 3_A375_shL87_gfp_blockRNA:1:6007, 4_A375_shL87_gfp_blockRNA:1:6008	465, 32994, 673, 32989	up gene, up gene, up gene, up gene	1	1	85	87.5	2	2_A375_shL87_gfp_blockRNA:1	117	Gene DHX30	DDX30, FLJ11214, DHX30, RETCOR, KIAA0990	DEAH (Asp-Glu-Ala-His) box polypeptide 30	NM_138615, NM_014589, ICT6910110.1, ICT2279621.0, ICT2279622.0, NCT6617.3	1555144_at, 1555145_s_at, 204339_at, 212674_s_at, 236071_at, 236548_at, 236772_x_at	NP_619520.1, NP_055701.2, EAW64833.1, EAW64834.1, EAW64835.1, EAW64836.1
Gene:ID:134	MAP4	3	47,692,150	48,130,769	235,589	-	2	1_A375_shL7_shrna1_blockRNA:1:3998, 2_A375_shL87_gfp_blockRNA:1:6009	178321, 113	up gene, up gene	1	1	20.5	17	2	2_A375_shL87_gfp_blockRNA:1	25	Gene MAP4	DKFZp779A1753, MAP4, MGC9617	microtubule-associated protein 4	NM_002375, NM_030665, NM_001039851, NCT1693111.0, ICT1996948.0, NCT1996949.0, ICT1996986.1, NCT1996987.1, ICT2023961.0, NCT2023963.0, ICT2023967.0, ICT2023722.0, NCT2023723.0, NCT4961.2	200035_s_at, 200036_s_at, 212666_at, 212667_at, 212671_s_at, 241_g_at, 33690_at	NP_002366.2, NP_112187.2, NP_001127838.1, EAW64837.1, EAW64842.1, EAW64843.1, EAW64838.1, EAW64839.1, EAW64840.1, EAW64844.1, EAW64845.1, EAW64846.1, EAW64847.1, EAW64841.1
Gene:ID:93	CDC25A	3	48,190,665	48,229,801	31,133	-	2	1_A375_shL7_shrna1_blockRNA:1:3993, 2_A375_shL87_gfp_blockRNA:1:6000	-133, -39	upstream, upstream	1	1	19	16	1	1_A375_shL7_shrna1_blockRNA:1	19	Gene CDC25A	CDC25A2, CDC25A	cell division cycle 25 homolog A (S. pombe)	NM_001789, NM_201567, ICT2283555.0, ICT2283556.0, ICT2283560.0, NCT6342.2	1555772_a_at, 204695_at, 204696_s_at	NP_001780.2, NP_963991.1, EAW64849.1, EAW64850.1, EAW64851.1, EAW64852.1
Gene:ID:1365	ZNF988	3	48,262,598	48,312,460	29,864	+	1	1_A375_shL7_shrna1_blockRNA:1:3991	-132	upstream	0	1	16	22	1	2_A375_shL87_gfp_blockRNA:1	23	Gene ZNF988	ZNF988, SZF1	zinc finger protein 988	NM_018089, ICT1693081.2, ICT1696726.1, ICT2354129.0, ICT2354130.0, ICT2354131.0, ICT6126.2	1569105_at, 210061_at, 210062_s_at, 210063_at	NP_059773.2, EAW64853.1, EAW64856.1, EAW64859.1, EAW64860.1, EAW64857.1
Gene:ID:54209	NMB5	3	48,333,576	48,342,646	7,272	-	1	2_A375_shL87_gfp_blockRNA:1:5992	160	up gene	0	1	10	22	1	2_A375_shL87_gfp_blockRNA:1	22	Gene NMB5	IPVALA, IPVA, NA22-HI, NDK-5, NMB5	sialo-metabolic cells 5, protein expressed in (nucleoside-diphosphate kinase)	NM_030762, ICT1615256.2	203533_at	NP_085135.1, EAW64866.1
Gene:ID:96424	SPANX	3	48,348,336	48,369,631	21,295	+	1	2_A375_shL87_gfp_blockRNA:1:5992	27163	downstream	0	1	10	22	1	2_A375_shL87_gfp_blockRNA:1	22	Gene SPANX2	SPANX	sarcoma antigen, family, family type 5 (putative)	NM_020555		NP_001073894.1
Gene:ID:9714	CCDC51	3	48,373,560	48,461,829	7,948	-	2	1_A375_shL7_shrna1_blockRNA:1:3994, 2_A375_shL87_gfp_blockRNA:1:6002	4519, 9439	upstream, downstream	1	1	21	20	1	1_A375_shL7_shrna1_blockRNA:1	21	Gene CCDC51	FLJ12436, CCDC51	coiled-coil domain containing 51	NM_024661, ICT2282540.1, ICT2282542.0, ICT2282543.0, ICT2282549.0, ICT2341332.0	219722_s_at	NP_079017.2, EAW64867.1, EAW64868.1, EAW64869.1, EAW64870.1, EAW64871.1, EAW64872.1
Gene:ID:1372	CCDC72	3	48,461,686	48,483,537	3,691	+	2	1_A375_shL7_shrna1_blockRNA:1:3994, 2_A375_shL87_gfp_blockRNA:1:6002	8282, 8282	downstream, downstream	1	1	21	20	1	1_A375_shL7_shrna1_blockRNA:1	21	Gene CCDC72	HSPC016, CCDC72	coiled-coil domain containing 72	NM_018332, ICT2279849.0, ICT2345466.0	221791_s_at	NP_060802.1, EAW64874.1, EAW64872.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Identical Transcripts	Identical Outside Exon	Identical Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:34126	ATRIP	3	48,465,218	48,507,654	42,436	+	2	1_A375_sh17_shrna_bioRNA:1:23904,2_A375_sh187_shrna_bioRNA:1:5592	-170, -250	upstream, upstream	1	1	21	20	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	ATR interacting protein	ATR-interacting protein	NM_032166, NM_130384	1552937_s_at	NP_115942.2, NP_998053.1
Gene:ID:3210	PFKFB4	3	48,333,117	48,384,227	39,110	-	3	1_A375_sh17_shrna_bioRNA:1:23903,1_A375_sh17_shrna_bioRNA:1:23905,2_A375_sh187_shrna_bioRNA:1:5592	-4621, -6625, -7533	upstream, upstream, upstream	1	1	20	21	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	NM_004567, NCT01851083.1	205240_at, 205499_at	NP_004558.1, EAW64590.1
Gene:ID:80226	UCN2	3	48,599,151	48,601,201	2,050	-	3	1_A375_sh17_shrna_bioRNA:1:23903,1_A375_sh17_shrna_bioRNA:1:23905,2_A375_sh187_shrna_bioRNA:1:5592	2353, 49, 599	downstream, in gene, upstream	1	1	20	21	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Urocortin 2	Urocortin 2	NM_033199, NCT01851092.1	232674_at	NP_149078.1, EAW64591.1
Gene:ID:1294	COL3A1	3	48,601,809	48,632,893	31,087	-	3	1_A375_sh17_shrna_bioRNA:1:23903,1_A375_sh17_shrna_bioRNA:1:23905,2_A375_sh187_shrna_bioRNA:1:5592	33748, 37441, 30633	downstream, downstream, in gene	1	1	20	21	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Collagen, type VIII, alpha 1	COLLAGEN, TYPE VIII, ALPHA 1	NM_000094, NCT02826828.2, NCT02826311.1, NCT02826533.2, NCT02340817.1, NCT02437.5	204136_at, 213312_s_at	NP_000083.1, EAW64584.1, EAW64592.1, EAW64593.1, EAW64596.1, EAW64597.1
Gene:ID:5010	SLC26A6	3	48,663,196	48,672,926	9,770	-	2	1_A375_sh17_shrna_bioRNA:1:23907,2_A375_sh187_shrna_bioRNA:1:5609	-66, -236	upstream, upstream	1	1	23	21	1	1_A375_sh17_shrna_bioRNA:1	RNA:1	Solute carrier family 26, member 6	DIDP2,ASSB6E1422, SLC26A6	solute carrier family 26, member 6	NM_022911, NM_134263, NM_134426, NM_005630454, NCT02826533.1, NCT02826555.1, NCT02826311.1, NCT02826516.1, NCT02826200.0, NCT02826320.0, NCT02826290.1, NCT02340168.0, NCT02340169.0, NCT02340170, NCT02340168.0, NCT02340170	221572_s_at, 222551_at	NP_079062.2, NP_598026.2, NP_932292.2, NP_001335561.1, EAW64602.1, EAW64611.1, EAW64600.1, EAW64601.1, EAW64603.1, EAW64604.1, EAW64605.1, EAW64606.1, EAW64607.1, EAW64608.1, EAW64609.1, EAW64610.1, EAW64612.1, EAW64613.1
Gene:ID:1317	NCKIPSD	3	48,711,277	48,723,334	12,057	-	3	1_A375_sh17_shrna_bioRNA:1:23907,2_A375_sh187_shrna_bioRNA:1:5607	22693	downstream	0	1	17	30	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	NCK interacting protein with SH3 domain	DIP, WISH, DIP1, WASLBP, AP2P21, NCKIPSD	NCK interacting protein with SH3 domain	NM_138231, NM_016452, NCT02826906.0, NCT02826905.0, NCT02826311.0, NCT02826529.0	219114_at, 219116_at, 219697_at, 230153_at	NP_938191.1, NP_057537.1, EAW64615.1, EAW64616.1, EAW64617.1, EAW64618.1
Gene:ID:84080	CSorf71	3	48,955,221	48,956,816	1,597	-	1	2_A375_sh187_shrna_bioRNA:1:5598	894	in gene	0	1	13	20	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Chromosome 3 open reading frame 71	Chromosome 3 open reading frame 71	NM_001123040	1559532_at	NP_001116512.1
Gene:ID:5426	ARIH2	3	48,999,281	49,022,974	66,693	+	1	2_A375_sh187_shrna_bioRNA:1:5608	-67	upstream	0	1	13	20	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Ariadne homolog 2 (Drosophila)	Ariadne homolog 2 (Drosophila)	NM_006321, NCT01851071.1, NCT02851851.0, NCT02851852.0, NCT02851853.0	1568121_s_at, 201206_s_at, 201229_s_at, 201230_s_at, 218055_s_at, 1559564_at	NP_006312.1, EAW64630.1, EAW64631.1, EAW64632.1, EAW64633.1
Gene:ID:4551	RHTM1	3	49,027,341	49,044,882	17,541	+	1	2_A375_sh187_shrna_bioRNA:1:5609	17459	downstream	0	1	22	22	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Rhotekin	FSHTM, FSHTM1, HFPH4, PHD4, ECSA4, PHL PHH4	prolyl-4-hydroxylase, transmembrane (endoplasmic reticulum)	NM_177839, NM_177838, NCT01851083.1, NCT02851555.1, NCT02851556.1, NCT02851591.1, NCT02852	223123_s_at	NP_808097.1, NP_808007.2, EAW64634.1, EAW64635.1, EAW64640.1, EAW64637.1, EAW64638.1, EAW64639.1
Gene:ID:1150	WDR6	3	49,044,637	49,053,395	8,746	+	4	1_A375_sh17_shrna_bioRNA:1:23909,2_A375_sh187_shrna_bioRNA:1:5609,2_A375_sh187_shrna_bioRNA:1:5610,2_A375_sh187_shrna_bioRNA:1:5611	14551, 163, 10627, 14551	downstream, in gene, downstream, downstream	1	1	45	61	3	2_A375_sh187_shrna_bioRNA:1	RNA:1	WD repeat domain 6	WDR6, MGC142327, PLI16214, PLI36107, PLI52552, MGC126756	WD repeat domain 6	NM_018031	217754_s_at, 233972_s_at	NP_060501.3
Gene:ID:5152	DALRD3	3	49,052,833	49,058,867	6,032	+	4	1_A375_sh17_shrna_bioRNA:1:23909,2_A375_sh187_shrna_bioRNA:1:5609,2_A375_sh187_shrna_bioRNA:1:5610,2_A375_sh187_shrna_bioRNA:1:5611	-1621, -10667, -12203, -1521	upstream, downstream, in gene, upstream	1	1	45	61	3	2_A375_sh187_shrna_bioRNA:1	RNA:1	DALR anticodon binding domain containing 3	DALR anticodon binding domain containing 3	NM_001009998, NM_018114	218808_at, 221634_s_at	NP_001009998.1, NP_060564.2
Gene:ID:9915	NDUFAF3	3	49,057,808	49,060,826	3,020	+	3	1_A375_sh17_shrna_bioRNA:1:23909,1_A375_sh187_shrna_bioRNA:1:5610,2_A375_sh187_shrna_bioRNA:1:5612	1560, -4644, -1560	in gene, downstream, in gene	1	1	56.5	60.5	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	Cbl/Nbl E3-2 DKFZp564K0123, NDUFAF3, ZP1, MGC16527	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 3	NM_198569, NM_199070, NM_198073, NM_198074, NCT01851138.1, NCT02341717.0, NCT02341718.0, NCT07322.3	208177_at	NP_951022.1, NP_951032.1, NP_951047.1, NP_951061.1, EAW64642.1, EAW64643.1, EAW64643.1, EAW64644.1
Gene:ID:99666	MIR191	3	49,058,051	49,058,142	91	-	3	1_A375_sh17_shrna_bioRNA:1:23909,2_A375_sh187_shrna_bioRNA:1:5610,2_A375_sh187_shrna_bioRNA:1:5611	-1396, -2078, -1396	upstream, downstream, upstream	1	1	56.5	60.5	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	miR-191, MIR191, MIRN191	microRNA 191	NR_029690		
Gene:ID:5013	IMPDH2	3	49,061,758	49,066,875	5,117	-	3	1_A375_sh17_shrna_bioRNA:1:23909,2_A375_sh187_shrna_bioRNA:1:5610,2_A375_sh187_shrna_bioRNA:1:5611	7267, 11611, 7267	downstream, downstream, downstream	1	1	56.5	60.5	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	IMP (inosine 5'-monophosphate) dehydrogenase 2	IMPDH-II, IMPD2, IMPDH2	IMP (inosine 5'-monophosphate) dehydrogenase 2	NM_000884	201892_s_at, 201272_at	NP_000875.2
Gene:ID:4570	QRICH1	3	49,097,142	49,131,804	64,362	+	4	1_A375_sh17_shrna_bioRNA:1:23909,1_A375_sh187_shrna_bioRNA:1:5610,2_A375_sh187_shrna_bioRNA:1:5611,2_A375_sh187_shrna_bioRNA:1:5612	72016, -464, 72016, -668	in gene, upstream, downstream, downstream	1	1	84.9	100.5	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	Glutamine-rich 1	MGC131636, PLI20236, QRICH1	glutamine-rich 1	NM_017730, NM_195650	209174_s_at, 236896_at	NP_060200.2, NP_942585.1
Gene:ID:559	QARS	3	49,133,365	49,142,171	8,806	-	3	1_A375_sh17_shrna_bioRNA:1:23910,1_A375_sh187_shrna_bioRNA:1:5612,1_A375_sh187_shrna_bioRNA:1:5613	16203, 16203, 59	downstream, downstream, in gene	1	1	51.5	66	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	glutaminyl-tRNA synthetase	PRO2163, GLNRS, QARS	glutaminyl-tRNA synthetase	NM_005051, NCT01851181.0, NCT02340844.0, NCT05329.3	217696_at	NP_005042.1, EAW64652.1, EAW64653.1, EAW64654.1
Gene:ID:6969	USP19	3	49,146,105	49,158,213	12,109	-	2	1_A375_sh17_shrna_bioRNA:1:23913,2_A375_sh187_shrna_bioRNA:1:5614	16101, 5	downstream, in gene	0	1	13.5	20	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	Ubiquitin specific peptidase 19	DMYN09, USP19	ubiquitin specific peptidase 19	NM_006677, NCT01852266.3, NCT01910742.0, NCT02455517.1	214674_at, 226357_at	NP_006668.1, EAW64655.1, EAW64656.1, EAW64657.1
Gene:ID:913	UAMB2	3	49,158,047	49,170,599	12,552	-	2	1_A375_sh17_shrna_bioRNA:1:23913,2_A375_sh187_shrna_bioRNA:1:5614	-441, -12391	upstream, downstream	1	1	17	23	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	Ubiquitin associated domain containing 2	UAMB2, UAMB	ubiquitin associated domain containing 2	NM_022362, NCT01852166.1, NCT05823.3	219264_s_at	NP_072053.3, EAW64658.1, EAW64659.1
Gene:ID:9625	CCDC71	3	49,169,968	49,203,765	33,817	-	1	2_A375_sh187_shrna_bioRNA:1:5615	-39	upstream	0	1	16	23	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Coiled-coil domain containing 71	CCDC71	coiled-coil domain containing 71	NM_032803, NCT02865533.0	219863_at	NP_076054.2, EAW64660.1
Gene:ID:93442	SLHOC68	3	49,209,018	49,213,819	4,801	+	1	2_A375_sh187_shrna_bioRNA:1:5615	-5164	upstream	0	1	16	23	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Solute carrier family 68 (choline transporter-like), member 1	SLHOC68	solute carrier family 68 (choline transporter-like), member 1	NM_173546, NCT01120.2, NCT02865520.0, NCT02865526.0	235753_at	NP_775817.1, EAW64662.1, EAW64663.1, EAW64664.1
Gene:ID:74341	C3orf62	3	49,309,030	49,314,808	5,816	+	1	2_A375_sh187_shrna_bioRNA:1:5639	-386	in gene	0	1	12	16	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Chromosome 3 open reading frame 62	C3orf62, MGC23381, MGC61662, PLI43654, MGC42078, C3orf62	chromosome 3 open reading frame 62	NM_198562, NCT01233598.1	1569274_at, 241017_at	NP_940964.1, EAW64667.1
Gene:ID:100422952	MIR4271	3	49,311,553	49,311,619	66	+	1	2_A375_sh187_shrna_bioRNA:1:5616	-2559	downstream	0	1	12	16	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	microRNA 4271	MIR4271	microRNA 4271	NR_036233		
Gene:ID:375	USP4	3	49,314,977	49,377,536	62,559	-	3	1_A375_sh17_shrna_bioRNA:1:23912,1_A375_sh187_shrna_bioRNA:1:5616,2_A375_sh187_shrna_bioRNA:1:5616	68, 63404, 160	-in gene, downstream, upstream	1	1	19	19.5	2	1_A375_sh17_shrna_bioRNA:1	RNA:1	Ubiquitin specific peptidase 4 (proto-oncogene)	USP4, MGC149546, MGC149549, Unph, UNP	ubiquitin specific peptidase 4 (proto-oncogene)	NM_198483, NM_003363, NCT11265.3, NCT01851851.1, NCT02865218.0, NCT02865216.0, NCT02865220.0, NCT03417.2.0	202681_at, 202682_s_at, 211600_s_at	NP_953475.1, NP_003338.2, EAW64665.1, EAW64670.1, EAW64672.1, EAW64673.1, EAW64869.1, EAW64871.1
Gene:ID:100289130	LOC100289130	3	49,355,251	49,367,760	12,509	+	2	1_A375_sh17_shrna_bioRNA:1:23912,2_A375_sh187_shrna_bioRNA:1:5617	-7811, -7653	upstream, upstream	1	1	26	33	1	1_A375_sh17_shrna_bioRNA:1	RNA:1	Uncharacterized LOC100289130	Clorf32	hypothetical LOC100289130	XR_112936, XR_112935, XR_110935, XR_110004, XR_113497		
Gene:ID:387	RHOA	3	49,395,576	49,409,526	52,948	-	1	1_A375_sh17_shrna_bioRNA:1:23913	-220	upstream	1	0	20	11	1	1_A375_sh17_shrna_bioRNA:1	RNA:1	ras homolog gene family, member A	RHOH12, ARHA, RHOA, RHO12, ARH12	ras homolog gene family, member A	NM_001664, NCT11211.3, NCT02865190.0, NCT02865200.0	1555814_a_at, 200059_s_at, 200060_at	NP_001655.1, EAW64676.1, EAW64676.1, EAW64680.1
Gene:ID:7474	TCTA	3	49,409,639	49,453,909	44,270	+	1	1_A375_sh17_shrna_bioRNA:1:23913	217	upstream	1	0	20	11	1	1_A375_sh17_shrna_bioRNA:1	RNA:1	T-cell leukemia translocation altered gene	TCTA	T-cell leukemia translocation altered gene	NM_032171, NCT11208.1, NCT05329.3, NCT01851842.0	203554_s_at	NP_071353.1, EAW64682.1, EAW64683.1
Gene:ID:175	AMT	3	49,454,211	49,460,111	5,900	+	1	1_A375_sh17_shrna_bioRNA:1:23913	10255	downstream	1	0	20	11	1	1_A375_sh17_shrna_bioRNA:1	RNA:1	Aminomethyltransferase	GCE, AMT, GCST, NKH, GCVT	aminomethyltransferase	NM_000481, NM_001164710, NM_001164711, NM_001164712, NR_026443	202439_at	NP_000472.2, NP_001157631.1, NP_001157632.1, NP_001157633.1, NP_001158163.1, NP_001158164.1
Gene:ID:4376	NICN1	3	49,492,766	49,496,757	6,991	-	1	1_A375_sh17_shrna_bioRNA:1:23913	19901	downstream	1	0	20	11	1	1_A375_sh17_shrna_bioRNA:1	RNA:1	Nucleolar cysteine-rich protein 1	NICN1	nucleolar cysteine-rich protein 1	NM_032116	223462_at	NP_115992.1
Gene:ID:27	APEH	3	49,711,439	49,720,834	9,496	+	1	2_A375_sh187_shrna_bioRNA:1:5615	15373	downstream	0	1	21	26	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Acylaminoacyl-peptide hydrolase	DKFP15B2, DKFP15B2, DKFP15B2, MSTI1, HSPL, MSP	N-acylaminoacyl-peptide hydrolase	NM_006480, NCT01853571.1, NCT01853580.1, NCT02077.2, NCT02077.2, NCT02340.2, NCT02340.2	201264_s_at, 242015_s_at	NP_001631.2, EAW64685.1, EAW64694.1, EAW64695.1, EAW64696.1, EAW64697.1
Gene:ID:455	MSTI1	3	49,721,380	49,726,196	4,816	+	1	2_A375_sh187_shrna_bioRNA:1:5616	-612	upstream	0	1	21	26	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Macrophage stimulating 1 (hepatocyte growth factor-like)	MST1, DKFZp564K0123	macrophage stimulating 1 (hepatocyte growth factor-like)	NM_020998, NCT02864.0, NCT02865502.0, NCT02865849, NCT02865501.0	203614_s_at, 216329_s_at	NP_066278.3, EAW65002.1, EAW64999.1, EAW65000.1, EAW65003.1
Gene:ID:5661	RNF123	3	49,729,990	49,755,982	31,972	+	2	1_A375_sh17_shrna_bioRNA:1:23915,1_A375_sh187_shrna_bioRNA:1:5616,2_A375_sh187_shrna_bioRNA:1:5617	16, 34394	in gene, upstream	1	1	20	28	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	FP1477, DKFZp686C02222, KPC1, MGC16304, PLI12995, RNF123	ring finger protein 123	NM_022064	221063_s_at, 224195_s_at	NP_071347.2
Gene:ID:93210	AMIGO3	3	49,754,267	49,757,235	2,971	+	1	2_A375_sh187_shrna_bioRNA:1:5618	-4105	upstream	0	1	19	22	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Adhesion molecule with Ig-like domain 3	AMIGO3, MGC131552, AMIGO-3	adhesion molecule with Ig-like domain 3	NM_198722	229717_at	NP_942015.1
Gene:ID:2918	GMPPB	3	49,758,932	49,761,264	2,452	+	1	2_A375_sh187_shrna_bioRNA:1:5618	48	up gene	0	1	19	22	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	GDP-mannose pyrophosphorylase B	GMPPB, KIAA1551, GMPPB	GDP-mannose pyrophosphorylase B	NM_013358, NM_021971, NCT11167.3, NCT11697.1, NCT13796.1, NCT02864512	219820_s_at, 222710_at	NP_037966.2, NP_068598.1, EAW65012.1, EAW65013.1, EAW65014.1, EAW65015.1
Gene:ID:937	IP6K1	3	49,761,728	49,823,870	62,248	+	1	2_A375_sh187_shrna_bioRNA:1:5618	82629	downstream	0	1	19	22	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Inositol hexakisphosphate kinase 1	PLIS, MGC20925, IP6K1, IHPK1	inositol hexakisphosphate kinase 1	NM_153273, NM_001005915, NCT11.210.3, NCT02826300.0, NCT02826340.0, NCT02826341.0, NCT02841620.0	212429_at	NP_699033.1, NP_001006115.1, EAW65016.1, EAW65018.1, EAW65020.1, EAW65017.1
Gene:ID:59118	CDH16	3	49,826,165	49,837,254	9,089	-	1	2_A375_sh187_shrna_bioRNA:1:5620	-3002	upstream	0	1	12	24	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Cadherin-related family member 6	CDH16, PRO34306, MGC150952, CDH22, CDH6	cadherin-related family member 6	NM_005070.5		NP_001007.5
Gene:ID:26119	C3orf64	3	49,840,667	49,842,463	1,776	+	1	2_A375_sh187_shrna_bioRNA:1:5620	-421	upstream	0	1	12	24	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Chromosome 3 open reading frame 64	C3orf64, MAX1, MGC20416	chromosome 3 open reading frame 64	NM_202170, NCT01233591.1	229307_at	NP_976248.1, EAW65032.1
Gene:ID:218	UBA7	3	49,842,638	49,851,391	8,753	+	1	2_A375_sh187_shrna_bioRNA:1:5620	11135	downstream	0	1	12	24	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Ubiquitin-like modifier activating enzyme 7	DB, UBE2, UBA7, UBE1, UBA1B, MGC27211	ubiquitin-like modifier activating enzyme 7	NM_003133, NCT01233585.2, NCT02340227.0	1564_at, 201231_s_at	NP_003124.2, EAW65023.1, EAW65024.1
Gene:ID:9230	TRAIP	3	49,866,024	49,893,992	27,968	-	1	2_A375_sh187_shrna_bioRNA:1:5621	187	up gene	0	1	20	17	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	TRAF interacting protein	RNF206, TRIP, TRAIP	TRAF interacting protein	NM_025879, NCT01852105.2, NCT02340.4	203554_s_at	NP_055752.2, EAW65036.1, EAW65525.1
Gene:ID:9012	CAMKV	3	49,893,622	49,907,369	11,987	-	3	1_A375_sh17_shrna_bioRNA:1:23914,2_A375_sh187_shrna_bioRNA:1:5621,2_A375_sh187_shrna_bioRNA:1:5622	2557, 13554, 1855	up gene, downstream, in gene	1	1	22.5	22.5	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	CaM kinase-like vesicle-associated	VACAMKL, MGC50497, YQS, CAMKV	CaM kinase-like vesicle-associated	NM_032385, NCT01852195.1, NCT01921107.1, NCT02341610.0, NCT02341624.0, NCT02341625.0, NCT02341626.0, NCT02341627.0, NCT07380.3	219263_s_at	NP_078851.2, EAW65035.1, EAW65037.1, EAW65039.1, EAW65040.1, EAW65041.1, EAW65042.1, EAW65030.1, EAW65031.1, EAW65033.1
Gene:ID:4315	MON1A	3	49,949,302	49,967,445	21,143	-	1	2_A375_sh187_shrna_bioRNA:1:5623	-10123	upstream	0	1	16	25	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	MON1 homolog A (yeast)	FLJ39555, SAND1, MGC13272, MON1A	MON1 homolog A (yeast)	NM_022355, NM_001142501, NCT01853565.1, NCT05454.2	224500_s_at	NP_071731.2, NP_001128073.1, EAW65070.1, EAW65071.1
Gene:ID:5180	RBM6	3	49,977,477	50,114,665	137,205	+	1	2_A375_sh187_shrna_bioRNA:1:5623	61	up gene	0	1	16	25	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	RNA binding motif protein 6	DJ735J5.3, FLJ35577, DJ735J5.2, RBM6, FLJ36517, g19, NY-LU-12, DEF2, DEF-2, HLC-11, FLJ35589, PLI40339	RNA binding motif protein 6	NM_001161532, NM_005777, NCT05329.4	1559572_a_at, 201867_at, 201868_s_at	NP_001155001.1, NP_005766.1, EAW65038.1
Gene:ID:6771	SLC35A3	3	50,242,692	50,256,406	13,714	+	2	1_A375_sh17_shrna_bioRNA:1:23915,1_A375_sh187_shrna_bioRNA:1:5624	22364, 22364	downstream, downstream	1	1	27	34	1	1_A375_sh17_shrna_bioRNA:1	RNA:1	Solute carrier family 35, member 3	NATT, SNT, GT7, SLC35A3	solute carrier family 35, member 3	NM_006541, NCT02779585.0, NCT05144.2	203872_at	NP_006532.1, EAW65048.1, EAW65050.1
Gene:ID:2771	GNAI2	3	50,273,647	50,296,786	23,139	+	2	1_A375_sh17_shrna_bioRNA:1:23915,1_A375_sh187_shrna_bioRNA:1:5624	4591, -5591	upstream, upstream	1	1	27	34	1	1_A375_sh17_shrna_bioRNA:1	RNA:1	G protein subunit alpha i2	H_LUCA13.1, GNAI2B, H_LUCA16.1, GIP, GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	NM_002070, NM_001166425, NCT02780970.0, NCT02780981.0, NCT02446290.0, NCT02446300.0, NCT02841272, NCT02841240.0	201030_x_at	NP_002061.1, NP_001153897.1, EAW65031.1, EAW65032.1, EAW65033.1, EAW65035.1, EAW65053.1, EAW65054.1
Gene:ID:12226	C3orf65	3	50,316,516	50,329,845	8,027	+	2	1_A375_sh187_shrna_bioRNA:1:5625,2_A375_sh187_shrna_bioRNA:1:5626	13434, 10995	downstream, downstream	1	1	55	55	1	2_A375_sh187_shrna_bioRNA:1	RNA:1	Chromosome 3 open reading frame 65	C3orf65, PLI58505	chromosome 3 open reading frame 65	NM_152215, NCT05329.4	237024_at	NP_689447.1, EAW65056.1
Gene:ID:996	IFIH2	3	50,323,163	50,330,826	6,663	+	4	1_A375_sh17_shrna_bioRNA:1:23916,1_A375_sh187_shrna_bioRNA:1:5625,1_A375_sh187_shrna_bioRNA:1:5626,2_A375_sh187_shrna_bioRNA:1:5627	74, -6676, 42, -6676	in gene, upstream, in gene, downstream	1	1	49.5	47.5	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	Interferon induced with helicase C domain 2	IFIH2, SNAI15, PLI40446, IFIHP, SNI15	interferon-induced, double-stranded RNA-activated, helicase-like protein	NM_022168, NCT02344546.1, NCT02344550.1	208102_at	NP_073554.4, EAW65066.1, EAW65070.1
Gene:ID:372	HYAL3	3	50,330,262	50,336,899	6,637	+	4	1_A375_sh17_shrna_bioRNA:1:23916,1_A375_sh187_shrna_bioRNA:1:5625,1_A375_sh187_shrna_bioRNA:1:5626,2_A375_sh187_shrna_bioRNA:1:5627	6647, 195, 6915, 195	downstream, in gene, downstream, in gene	1	1	49.5	47.5	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	Hyaluronoglucosaminidase 3	Mosa-14, LUCA2, LUCA-3, LUCA14, HYAL3, HYAL-3	hyaluronoglucosaminidase 3	NM_033049, NCT02344587.1, NCT02344549.1, NCT02344551.1, NCT02345636.0, NCT02345637.0, NCT02346436.0	217728_s_at	NP_033492.2, EAW65073.1, EAW65072.1, EAW65073.1, EAW65074.1, EAW65076.1, EAW65077.1
Gene:ID:4142	NAT6	3	50,333,833	50,336,712	2,879	+	4	1_A375_sh17_shrna_bioRNA:1:23916,1_A375_sh187_shrna_bioRNA:1:5625,1_A375_sh187_shrna_bioRNA:1:5626,2_A375_sh187_shrna_bioRNA:1:5627	6760, -6726, -	downstream, in gene, downstream, in gene	1	1	49.5	47.5	2	2_A375_sh187_shrna_bioRNA:1	RNA:1	N-acetyltransferase 6 (GCN5-related)	NAT6, FLI52, FLI8-2	N-acetyltransferase 6 (GCN5-related)	NM_012191, NCT02344537.1, NCT02345381.1, NCT02345384.1, NCT02345385.1, NCT02345643.1, NCT02360640.0	218574_s_at	NP_036323.2, EAW65077.1, EAW65078.1, EAW65080.1, EAW65082.1, EAW65083.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:3373	HYAL1	3	50,337,320	50,349,812	12,492	-	6	1_A375_pNL7_minus_lncRNA::1::3916, 1_A375_pNL7_minus_lncRNA::1::3917, 1_A375_pNL7_minus_lncRNA::1::3918, 2_A375_pNL97_plus_lncRNA::1::5625, 2_A375_pNL97_plus_lncRNA::1::5626, 2_A375_pNL97_plus_lncRNA::1::5627	19860, 13108, -9228, 19828, 13108, -9228	downstream, downstream, upstream, downstream, downstream, upstream	1	1	80	86	3	2_A375_pNL97_plus_lncRNA::1	163	Gene HYAL1	NAT6, HYAL-1, MGC45987, LUCA1, HYAL1	hyaluronoglucosaminidase 1	NM_007312, NM_033159, NM_153281, NM_153282, NM_153283, NM_153285, hCT1951042.2, hCT1951043.2, hCT2350328.0, hCT2350329.0, hCT2350330.0, hCT2350331.0, hCT2350332.0, hCT2350333.0, hCT8509.3	210619_s_at	NP_009296.1, NP_149349.2, NP_695013.1, NP_695014.1, NP_695015.1, NP_695017.1, EAW65083.1, EAW65084.1, EAW65085.1, EAW65086.1, EAW65087.1, EAW65088.1, EAW65089.1, EAW65091.1, EAW65090.1
GeneID:8692	HYAL2	3	50,355,221	50,360,281	5,060	-	2	1_A375_pNL7_minus_lncRNA::1::3918, 2_A375_pNL97_plus_lncRNA::1::5627	1241, 1241	in gene, in gene	1	1	149	163	1	2_A375_pNL97_plus_lncRNA::1	163	Gene HYAL2	HYAL2, LUCA2, LuCa-2	hyaluronoglucosaminidase 2	NM_003773, NM_033158, hCT2282771.0, hCT2282772.1, hCT2282773.0	206855_s_at	NP_003764.3, NP_149348.2, EAW65092.1, EAW65093.1, EAW65094.1
GeneID:11334	TUSC2	3	50,362,341	50,365,668	3,327	-	3	1_A375_pNL7_minus_lncRNA::1::3918, 2_A375_pNL97_plus_lncRNA::1::5627, 2_A375_pNL97_plus_lncRNA::1::5628	6628, 6628, -9004	downstream, downstream, upstream	1	1	85.5	93	2	2_A375_pNL97_plus_lncRNA::1	163	Gene TUSC2	PAP, PDAP2, C3orf11, TUSC2, FUS1	tumor suppressor candidate 2	NM_007275, hCT2282769.1, hCT2282774.0, hCT2344197.0	203272_s_at, 203273_s_at	NP_009206.1, EAW65096.1, EAW65095.1, EAW65097.1
GeneID:11186	RASSF1	3	50,367,217	50,378,367	11,150	-	5	1_A375_pNL7_minus_lncRNA::1::3918, 1_A375_pNL7_minus_lncRNA::1::3919, 2_A375_pNL97_plus_lncRNA::1::5627, 2_A375_pNL97_plus_lncRNA::1::5628, 2_A375_pNL97_plus_lncRNA::1::5629	19327, -10113, 19327, 3695, -10097	downstream, upstream, downstream, in gene, upstream	1	1	67.33	71.67	3	2_A375_pNL97_plus_lncRNA::1	163	Gene RASSF1	RASSF1, 123F2, RDA32, NORE2A, RASSF1A, REH3P21	Ras association (RalGDS/AF-6) domain family member 1	NM_007182, NM_170714, NM_170713, NM_170712, hCT1951045.1, hCT1951046.1, hCT1957764.1, hCT1957765.1, hCT1957766.1	204346_s_at, 240278_at	NP_009113.3, NP_733832.1, NP_733830.1, NP_733831.1, EAW65100.1, EAW65101.1, EAW65098.1, EAW65099.1, EAW65102.1
GeneID:51364	ZMYND10	3	50,378,537	50,383,156	4,619	-	3	1_A375_pNL7_minus_lncRNA::1::3919, 2_A375_pNL97_plus_lncRNA::1::5628, 2_A375_pNL97_plus_lncRNA::1::5629	-5324, 8484, -5308	upstream, downstream, upstream	1	1	26.5	26	2	1_A375_pNL7_minus_lncRNA::1	31	Gene ZMYND10	ZMYND10, BLU, FLU	zinc finger, MYND-type containing 10	NM_015896, hCT1961317.1, hCT1961318.1, hCT8519.3	205714_s_at, 216663_s_at	NP_056980.2, EAW65103.1, EAW65104.1, EAW65105.1
GeneID:10641	TUSC4	3	50,384,919	50,388,486	3,567	-	5	1_A375_pNL7_minus_lncRNA::1::3919, 1_A375_pNL7_minus_lncRNA::1::3920, 2_A375_pNL97_plus_lncRNA::1::5628, 2_A375_pNL97_plus_lncRNA::1::5629, 2_A375_pNL97_plus_lncRNA::1::5630	6, -8602, 13814, 22, -8698	in gene, upstream, downstream, in gene, upstream	1	1	25.33	25.33	3	1_A375_pNL7_minus_lncRNA::1	31	Gene TUSC4	NPR2, NPR2L, NPRL2, TUSC4	nitrogen permease regulator-like 2 (S. cerevisiae)	NM_006545, hCT1951055.1, hCT2354103.0, hCT2354104.0, hCT2354105.0, hCT2354106.0, hCT2354107.0, hCT8523.3	203246_s_at, 210373_at	NP_006536.3, EAW65108.1, EAW65106.1, EAW65109.1, EAW65110.1, EAW65112.1, EAW65107.1, EAW65111.1
GeneID:11068	CYB561D2	3	50,388,297	50,391,500	3,203	+	4	1_A375_pNL7_minus_lncRNA::1::3919, 1_A375_pNL7_minus_lncRNA::1::3920, 2_A375_pNL97_plus_lncRNA::1::5629, 2_A375_pNL97_plus_lncRNA::1::5630	183, 8791, 167, 8887	in gene, downstream, in gene, downstream	1	1	27	26.5	2	1_A375_pNL7_minus_lncRNA::1	31	Gene CYB561D2	101F6, TSP10, CYB561D2	cytochrome b-561 domain containing 2	NM_007022, hCT1951053.1, hCT1951054.1	209665_at	NP_008953.1, EAW65113.1, EAW65114.1
GeneID:11070	TMEM115	3	50,392,180	50,396,939	4,759	-	4	1_A375_pNL7_minus_lncRNA::1::3919, 1_A375_pNL7_minus_lncRNA::1::3920, 2_A375_pNL97_plus_lncRNA::1::5629, 2_A375_pNL97_plus_lncRNA::1::5630	8459, -149, 8475, -245	downstream, upstream, downstream, upstream	1	1	27	26.5	2	1_A375_pNL7_minus_lncRNA::1	31	Gene TMEM115	PL6, TMEM115	transmembrane protein 115	NM_007024, hCT2282748.0, hCT2282751.0, hCT8515.3	216267_s_at	NP_008955.1, EAW65115.1, EAW65116.1, EAW65117.1
GeneID:9254	CACNA2D2	3	50,400,230	50,540,892	140,662	-	2	1_A375_pNL7_minus_lncRNA::1::3920, 2_A375_pNL97_plus_lncRNA::1::5630	143804, 143708	downstream, downstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CACNA2D2	KIAA0558, CACNA2D, LUAC11.1, CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	NM_001005505, NM_006030, NM_001174051, hCT2282744.0, hCT2282746.0, hCT2354111.0, hCT8527.3	204811_s_at	NP_001005505.1, NP_006021.2, NP_001167522.1, EAW65118.1, EAW65120.1, EAW65121.1, EAW65119.1
GeneID:100506825	LOC100506825	3	50,402,761	50,404,894	2,133	+	2	1_A375_pNL7_minus_lncRNA::1::3920, 2_A375_pNL97_plus_lncRNA::1::5630	-5673, -5577	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100506825		hypothetical LOC100506825	XR_110010		
GeneID:100506802	LOC100506802	3	50,404,933	50,405,628	695	+	2	1_A375_pNL7_minus_lncRNA::1::3920, 2_A375_pNL97_plus_lncRNA::1::5630	-7845, -7749	upstream, upstream	1	1	23	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100506802		hypothetical LOC100506802	XR_110009, XR_113500		
GeneID:51161	C3orf18	3	50,595,456	50,608,458	13,002	-	2	1_A375_pNL7_minus_lncRNA::1::3922, 2_A375_pNL97_plus_lncRNA::1::5632	1642, 1578	in gene, in gene	1	1	24	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene C3orf18	G20, C3orf18	chromosome 3 open reading frame 18	NM_001171740, NM_001171741, NM_001171743, NM_016210, hCT1951038.1, hCT1951039.1, hCT8506.1	219114_at	NP_001165211.1, NP_001165212.1, NP_057294.2, NP_001165214.2, EAW65122.1, EAW65124.1, EAW65123.1
GeneID:51409	HEMK1	3	50,606,909	50,622,422	15,513	+	2	1_A375_pNL7_minus_lncRNA::1::3922, 2_A375_pNL97_plus_lncRNA::1::5632	-93, -29	upstream, upstream	1	1	24	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene HEMK1	MTQ1, FLJ22320, HEMK1, HEMK	HemK methyltransferase family member 1	NM_016173, hCT1951015.1, hCT2279613.0	1556092_s_at, 218620_s_at, 218621_at, 52159_at	NP_057257.1, EAW65126.1, EAW65125.1
GeneID:7867	MAPKAPK3	3	50,654,601	50,686,719	32,118	+	1	2_A375_pNL97_plus_lncRNA::1::5633	10295	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MAPKAPK3	MAPKAP3, MAPKAPK3, 3PK	mitogen-activated protein kinase-activated protein kinase 3	NM_004635, hCT1951041.1, hCT2279618.0, hCT8508.3	202787_s_at, 202788_at	NP_004626.1, EAW65132.1, EAW65131.1, EAW65133.1
GeneID:9730	VPRBP	3	51,433,298	51,534,018	100,720	-	1	2_A375_pNL97_plus_lncRNA::1::5634	418	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene VPRBP	VPRBP, MGC102804, KIAA0800, DCAF1	Vpr (HIV-1) binding protein	NM_014703, NM_001171904, hCT1951016.1, hCT2279214.0, hCT2279215.0, hCT6360.3	204376_at, 204377_s_at, 226476_s_at, 226477_at, 226481_at	NP_055518.1, NP_001165375.1, EAW65140.1, EAW65141.1, EAW65142.1, EAW65143.1
GeneID:23132	RAD54L2	3	51,575,596	51,697,634	122,038	+	2	1_A375_pNL7_minus_lncRNA::1::3923, 2_A375_pNL97_plus_lncRNA::1::5635	-2988, -2956	upstream, upstream	1	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene RAD54L2	KIAA0809, ARIP4, FLJ22400, HSPC325, FLJ21396, SRISNF2L, RAD54L2	RAD54-like 2 (S. cerevisiae)	NM_015106	213205_s_at	NP_055921.2
GeneID:100506840	LOC100506840	3	51,851,620	51,864,874	13,254	+	1	2_A375_pNL97_plus_lncRNA::1::5636	19292	downstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100506840		hypothetical LOC100506840	XR_112498, XR_110011, XR_113451		
GeneID:401067	IQCF3	3	51,862,569	51,864,876	2,307	+	1	2_A375_pNL97_plus_lncRNA::1::5636	8343	downstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene IQCF3	IQCF3	IQ motif containing F3	NM_001085479	1555235_s_at, 236871_s_at	NP_001078948.1
GeneID:9136	RRP9	3	51,967,446	51,975,922	8,476	-	3	1_A375_pNL7_minus_lncRNA::1::3924, 1_A375_pNL7_minus_lncRNA::1::3925, 2_A375_pNL97_plus_lncRNA::1::5637	12274, -430, 12210	downstream, upstream, downstream	1	1	24.5	26.5	2	2_A375_pNL97_plus_lncRNA::1	39	Gene RRP9	RRP9, U3-55K, RNU3IP2	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)	NM_004704, hCT33861.2	204133_at	NP_004695.1, EAW65159.1
GeneID:10039	PARP3	3	51,976,361	51,982,883	6,522	+	1	1_A375_pNL7_minus_lncRNA::1::3925	-9	upstream	1	0	23	14	1	1_A375_pNL7_minus_lncRNA::1	23	Gene PARP3	PADPRT-3, ADPRT3, ADPRTL3, IRT1, PARP3, ADPRTL2	poly (ADP-ribose) polymerase family, member 3	NM_001003931, NM_005485, hCT1951118.1, hCT2348571.0, hCT2354056.0, hCT33859.3	209940_at	NP_001003931.2, NP_005476.3, EAW65160.1, EAW65161.1, EAW65162.1, EAW65163.1
GeneID:84836	ABHD14B	3	52,002,526	52,008,646	6,120	-	2	1_A375_pNL7_minus_lncRNA::1::3926, 2_A375_pNL97_plus_lncRNA::1::5638	-8090, -8666	upstream, upstream	1	1	25	19	1	1_A375_pNL7_minus_lncRNA::1	25	Gene ABHD14B	ABHD14B, MGC15429, CIB	abhydrolase domain containing 14B	NR_027476, NM_032750, NM_001146314, hCT2283542.0, hCT33875.3	224821_at	NP_116139.1, NP_001139786.1, EAW65178.1, EAW65179.1
GeneID:25864	ABHD14A	3	52,009,042	52,015,216	6,174	+	2	1_A375_pNL7_minus_lncRNA::1::3926, 2_A375_pNL97_plus_lncRNA::1::5638	7694, 8270	downstream, downstream	1	1	25	19	1	1_A375_pNL7_minus_lncRNA::1	25	Gene ABHD14A	FLJ60467, DORZ1, ABHD14A, DKFZp564O243, FLJ60317	abhydrolase domain containing 14A	NM_015407, hCT33870.1	210006_at	NP_056222.2, EAW65180.1
GeneID:95	ACY1	3	52,017,563	52,023,218	5,655	+	4	1_A375_pNL7_minus_lncRNA::1::3926, 1_A375_pNL7_minus_lncRNA::1::3927, 2_A375_pNL97_plus_lncRNA::1::5638, 2_A375_pNL97_plus_lncRNA::1::5639	-827, 12357, -251, 12309	upstream, downstream, upstream, downstream	1	1	22.5	20.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene ACY1	ACY1D, ACYLASE, ACY1	aminoacylase 1	NM_000666, hCT33858.3	202740_at, 235649_at	NP_000657.1, EAW65181.1
GeneID:6159	RPL29	3	52,027,644	52,029,958	2,314	-	3	1_A375_pNL7_minus_lncRNA::1::3926, 1_A375_pNL7_minus_lncRNA::1::3927, 2_A375_pNL97_plus_lncRNA::1::5639	13222, 38, 86	downstream, in gene, in gene	1	1	22.5	20.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene RPL29	HUMRPL29, HIP, RPL29, MGC88589, L29	ribosomal protein L29	NM_000992, hCT2283669.0, hCT2283670.0	200823_x_at, 213969_x_at	NP_000983.1, EAW65182.1, EAW65183.1
GeneID:1849	DUSP7	3	52,082,935	52,090,461	7,526	-	2	1_A375_pNL7_minus_lncRNA::1::3928, 2_A375_pNL97_plus_lncRNA::1::5640	-787, -643	upstream, upstream	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene DUSP7	DKFZp586F2224, PYST2, MKPX, DUSP7	dual specificity phosphatase 7	NM_001947, hCT33868.3	214793_at	NP_001938.2, EAW65184.1
GeneID:100128378	C3orf74	3	52,096,110	52,099,128	3,018	-	2	1_A375_pNL7_minus_lncRNA::1::3928, 2_A375_pNL97_plus_lncRNA::1::5640	7880, 8024	downstream, downstream	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene C3orf74	C3orf74	chromosome 3 open reading frame 74	NR_027331		
GeneID:25886	WDR51A	3	52,109,249	52,188,706	79,457	-	2	1_A375_pNL7_minus_lncRNA::1::3929, 2_A375_pNL97_plus_lncRNA::1::5641	205, 226	in gene, in gene	1	1	52	76	1	2_A375_pNL97_plus_lncRNA::1	76	Gene WDR51A	PIX2, WDR51A, POC1A, MGC131902, DKFZp434C245	POC1 centriolar protein homolog A (Chlamydomonas)	NM_015426, NM_001161580, NM_001161581, hCT1965585.1, hCT33873.2	226355_at, 234749_s_at	NP_056241.3, NP_001155052.1, NP_001155053.1, EAW65185.1, EAW65186.1
GeneID:211	ALAS1	3	52,232,116	52,248,343	16,227	+	1	2_A375_pNL97_plus_lncRNA::1::5642	60	in gene	0	1	24	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ALAS1	MIG4, ALASH, ALAS1, ALAS, ALAS3	aminolevulinate, delta-, synthase 1	NM_199166, NM_000688, hCT1951115.1, hCT1965584.1, hCT33857.3	205633_s_at	NP_954635.1, NP_000679.1, EAW65188.1, EAW65189.1, EAW65190.1
GeneID:80335	WDR82	3	52,288,438	52,312,659	24,221	-	4	1_A375_pNL7_minus_lncRNA::1::3930, 1_A375_pNL7_minus_lncRNA::1::3931, 2_A375_pNL97_plus_lncRNA::1::5643, 2_A375_pNL97_plus_lncRNA::1::5644	-205, -9261, 467, -9283	upstream, upstream, in gene, upstream	1	1	19.5	20	2	1_A375_pNL7_minus_lncRNA::1	22	Gene WDR82	MST107, PRO34047, SWD2, TMEM113, MSTP107, WDR82, WDR82A, PRO2730	WD repeat domain 82	NM_025222, hCT2283643.0, hCT2283647.0	201934_at	NP_079498.2, EAW65202.1, EAW65203.1
GeneID:406890	MIRLET7G	3	52,302,294	52,302,377	83	-	1	2_A375_pNL97_plus_lncRNA::1::5643	-9815	upstream	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIRLET7G	MIRLET7G, MIRNLET7G, LET7G, hsa-let-7g	microRNA let-7g	NR_029660		
GeneID:132158	GLYCTK	3	52,321,836	52,329,272	7,436	+	4	1_A375_pNL7_minus_lncRNA::1::3930, 1_A375_pNL7_minus_lncRNA::1::3931, 2_A375_pNL97_plus_lncRNA::1::5643, 2_A375_pNL97_plus_lncRNA::1::5644	-8972, 84, -9644, 116	upstream, in gene, upstream, in gene	1	1	19.5	20	2	1_A375_pNL7_minus_lncRNA::1	22	Gene GLYCTK	HBEBP4, HBEBP2, GLYCTK, HBeAgBP4A	glycerate kinase	NM_145262, NM_001144951, NR_026699, NR_026700, NR_026701, NR_026702, hCT1951123.1, hCT1951124.1, hCT1951125.1, hCT2354099.0, hCT2354100.0, hCT2354101.0, hCT2354102.0, hCT33864.3	238518_x_at, 242341_x_at	NP_660305.2, NP_001138423.1, EAW65205.1, EAW65206.1, EAW65207.1, EAW65208.1, EAW65209.1, EAW65210.1, EAW65211.1, EAW65212.1
GeneID:406925	MIR135A1	3	52,328,235	52,328,324	89	-	2	1_A375_pNL7_minus_lncRNA::1::3931, 2_A375_pNL97_plus_lncRNA::1::5644	6404, 6372	downstream, downstream	1	1	22	22	1	1_A375_pNL7_minus_lncRNA::1	22	Gene MIR135A1	MIRN135A1, MIR135A1, MIRN135-1	microRNA 135a-1	NR_029677		
GeneID:23166	STAB1	3	52,529,356	52,558,511	29,155	+	1	2_A375_pNL97_plus_lncRNA::1::5645	39044	downstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene STAB1	KIAA0246, CLEVER-1, FEEL-1, FEX1, STAB1, STAB-1, FELE-1	stabilin 1	NM_015136, hCT2280453.0, hCT2280456.0, hCT8611.4	1555319_at, 1555320_a_at, 204150_at, 38487_at	NP_055951.2, EAW65232.1, EAW65233.1, EAW65234.1
GeneID:64943	NT5DC2	3	52,558,385	52,569,093	10,708	-	2	2_A375_pNL97_plus_lncRNA::1::5645, 2_A375_pNL97_plus_lncRNA::1::5646	693, -1595	in gene, upstream	0	1	12	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene NT5DC2	NT5DC2, FLJ12442	5'-nucleotidase domain containing 2	NM_022908, NM_001134231, hCT1951067.1, hCT2283609.0	218051_s_at	NP_075059.1, NP_001127703.1, EAW65236.1, EAW65237.1
GeneID:440957	LOC440957	3	52,570,621	52,574,586	3,965	+	2	2_A375_pNL97_plus_lncRNA::1::5645, 2_A375_pNL97_plus_lncRNA::1::5646	-2221, 67	upstream, in gene	0	1	12	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC440957	C3orf78		NM_001124767	1556894_at, 1556895_a_at, 225220_at, 229826_at	NP_001118239.1
GeneID:55193	PBRM1	3	52,579,368	52,719,866	140,498	-	4	2_A375_pNL97_plus_lncRNA::1::5646, 2_A375_pNL97_plus_lncRNA::1::5647, 2_A375_pNL97_plus_lncRNA::1::5648, 2_A375_pNL97_plus_lncRNA::1::5649	149178, 76250, 14906, -198	downstream, in gene, in gene, upstream	0	1	13.5	18	4	2_A375_pNL97_plus_lncRNA::1	21	Gene PBRM1	PBRM1, MGC156155, MGC156156, BAF180, PB1	polybromo 1	NM_181042, NM_018313, NM_018165, hCT1951062.1, hCT2283591.0, hCT2283595.1, hCT2283600.0, hCT2354189.0, hCT2354190.0, hCT2354191.0, hCT2354192.0, hCT2354193.0, hCT8612.3	220355_s_at, 221212_x_at, 223238_s_at, 223399_x_at, 223400_s_at, 223899_at, 223900_s_at, 224152_s_at, 232613_at	NP_851385.1, NP_060783.3, NP_060635.2, EAW65241.1, EAW65243.1, EAW65244.1, EAW65239.1, EAW65240.1, EAW65242.1, EAW65245.1, EAW65246.1, EAW65247.1, EAW65248.1
GeneID:26354	GNL3	3	52,719,936	52,728,513	8,577	+	1	2_A375_pNL97_plus_lncRNA::1::5649	128	in gene	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene GNL3	MGC800, C77032, GNL3, NS, E2IG3	guanine nucleotide binding protein-like 3 (nucleolar)	NM_014366, NM_206825, NM_206826, hCT1951058.1, hCT2354136.0, hCT2354137.0, hCT8606.2	217850_at	NP_055181.3, NP_996561.1, NP_996562.1, EAW65249.1, EAW65250.1, EAW65252.1, EAW65251.1
GeneID:692089	SNORD19	3	52,723,256	52,723,331	75	+	1	2_A375_pNL97_plus_lncRNA::1::5649	-3192	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD19	SNORD19, HBII-108	small nucleolar RNA, C/D box 19	NR_003047		
GeneID:100113381	SNORD19B	3	52,724,754	52,724,846	92	+	1	2_A375_pNL97_plus_lncRNA::1::5649	-4690	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD19B	SNORD19B	small nucleolar RNA, C/D box 19B	NR_003687		
GeneID:692109	SNORD69	3	52,726,752	52,726,828	76	+	1	2_A375_pNL97_plus_lncRNA::1::5649	-6688	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD69	HBII-210, SNORD69	small nucleolar RNA, C/D box 69	NR_003057		
GeneID:55830	GLT8D1	3	52,728,504	52,740,048	11,544	-	3	1_A375_pNL7_minus_lncRNA::1::3932, 2_A375_pNL97_plus_lncRNA::1::5649, 2_A375_pNL97_plus_lncRNA::1::5650	-112, 19864, -208	upstream, downstream, upstream	1	1	19.5	23	2	2_A375_pNL97_plus_lncRNA::1	25	Gene GLT8D1	AD-017, FLJ14611, MSTP139, GLT8D1, DKFZp781O20198	glycosyltransferase 8 domain containing 1	NM_152932, NM_018446, NM_001010983, hCT1951065.1, hCT2354195.0, hCT2354196.0, hCT8614.3	218146_at, 218147_s_at	NP_690909.1, NP_060916.1, NP_001010983.1, EAW65253.1, EAW65254.1, EAW65255.1, EAW65256.1
GeneID:28972	SPCS1	3	52,739,857	52,742,198	2,341	+	2	1_A375_pNL7_minus_lncRNA::1::3932, 2_A375_pNL97_plus_lncRNA::1::5650	303, 399	in gene, in gene	1	1	23	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene SPCS1	HSPC033, SPCS1, YJR010C-A, SPC1, SPC12	signal peptidase complex subunit 1 homolog (S. cerevisiae)	NM_014041, hCT8605.2	217927_at	NP_054760.3, EAW65257.1
GeneID:6787	NEK4	3	52,744,796	52,804,965	60,169	-	4	1_A375_pNL7_minus_lncRNA::1::3932, 1_A375_pNL7_minus_lncRNA::1::3933, 2_A375_pNL97_plus_lncRNA::1::5650, 2_A375_pNL97_plus_lncRNA::1::5651	64805, 165, 64709, 5	downstream, in gene, downstream, in gene	1	1	20	22	2	2_A375_pNL97_plus_lncRNA::1	25	Gene NEK4	STK2, NRK2, MGC33171, pp12301, NEK4	NIMA (never in mitosis gene a)-related kinase 4	NM_001193533, NM_003157, hCT8603.3	1554659_at, 204634_at	NP_001180462.1, NP_003148.2, EAW65258.1
GeneID:3697	ITIH1	3	52,811,608	52,826,077	14,469	+	2	1_A375_pNL7_minus_lncRNA::1::3933, 2_A375_pNL97_plus_lncRNA::1::5651	-6808, -6648	upstream, upstream	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ITIH1	MGC126415, IATIH, IGHEP1, ITIH, H1P, SHAP, ITIH1	inter-alpha (globulin) inhibitor H1	NM_002215, NM_001166434, NM_001166435, NM_001166436, hCT2280467.0, hCT2280468.0, hCT8602.3	210868_s_at	NP_002206.2, NP_001159906.1, NP_001159907.1, NP_001159908.1, EAW65259.1, EAW65260.1, EAW65261.1
GeneID:5580	PRKCD	3	53,195,223	53,226,733	31,510	+	1	2_A375_pNL97_plus_lncRNA::1::5652	9225	in gene	0	1	16	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene PRKCD	MAY1, PKCD, MGC49908, nPKC-delta, PRKCD	protein kinase C, delta	NM_006254, NM_212539, hCT1950509.1, hCT8601.3	202545_at	NP_006245.2, NP_997704.1, EAW65279.1, EAW65280.1
GeneID:7086	TKT	3	53,256,723	53,290,068	31,345	-	1	2_A375_pNL97_plus_lncRNA::1::5653	17524	in gene	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TKT	TKT, TKT1, FLJ34765	transketolase	NM_001064, NM_001135055, hCT1950490.1, hCT7053.3	208699_x_at, 208700_s_at, 228205_at	NP_001055.1, NP_001128527.1, EAW65281.1, EAW65282.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervening Count	Intervening	Intervening Distance	Intervening Pos.	[A]	[B]	[C]	[D]	Acc Reg Count	Peak Sample	Peak Value	UCSC Loci	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:35662	DCP1A	3	53,317,442	53,381,654	64,211	+	2	1_A375_shN7_dhrus_lncRNA:1:-3934, 2_A375_shN97_dhrs_lncRNA:1:-5934	160,-10	upstream, upstream	1	1	33	42	1	2_A375_shN97_dhrs_lncRNA:1	42	Gene DCP1A	DCP1A, SMADIP1, FLJ21691, NM60390, SMIP, HSA279986	DCP1 decapping enzyme homolog A (S. cerevisiae)	NM_018403, NCT20341902, NCT6868.2	218555_at	NP_060073.4, EAW63263.1, EAW63264.1
Gene:ID:37776	CACNA1D	3	53,529,031	53,849,492	317,461	+	2	1_A375_shN7_dhrus_lncRNA:1:-2433, 2_A375_shN97_dhrs_lncRNA:1:-5935	59873, 75961	st gene, ut gene	1	1	14	19	1	2_A375_shN97_dhrs_lncRNA:1	19	Gene CACNA1D	CACN1A2, CACNA1D, CACH1, Cav1.2	calcium channel, voltage-dependent, L type, alpha 1D subunit	NM_000720, NM_001128839, NM_001128840, NCT01986466.2, NCT27851202, NCT27851103, NCT27851402, NCT27851103, NCT27851602, NCT27851917.0, NCT27851602, NCT27851910, NCT27851902	207669_s_at	NP_000711, NP_001122311.1, NP_001122312.1, EAW63269.1, EAW63292.1, EAW63293.1, EAW63356.1, EAW63371.1, EAW63565.1, EAW63290.1, EAW63291.1, EAW63292.1, EAW63294.1
Gene:ID:39870	ACTR6	3	53,901,093	53,916,229	15,136	-	4	1_A375_shN7_dhrus_lncRNA:1:-3929, 1_A375_shN7_dhrus_lncRNA:1:-3927, 2_A375_shN97_dhrs_lncRNA:1:-5936, 2_A375_shN97_dhrs_lncRNA:1:-5937	160, -9819, 229, -9787	st gene, upstream, ut gene, upstream	1	1	24.8	22.3	2	1_A375_shN7_dhrus_lnc RNA:1	27	Gene ACTR6	MrujB, FLJ22879, ACTR6_ARP6, bK360N, FLJ12434	ARP6 actin-related protein 6 homolog (yeast)	NM_022899, NCT6152.3	218666_s_at, 222707_s_at	NP_076030.3, EAW63300.1
Gene:ID:35515	SELK	3	53,919,226	53,923,989	4,763	+	4	1_A375_shN7_dhrus_lncRNA:1:-3926, 1_A375_shN7_dhrus_lncRNA:1:-3927, 2_A375_shN97_dhrs_lncRNA:1:-5936, 2_A375_shN97_dhrs_lncRNA:1:-5937	9825, -99, 9004, -27	downstream, upstream, downstream, upstream	1	1	24.5	22.3	2	1_A375_shN7_dhrus_lnc RNA:1	27	Gene SELK	HSPC297, MGC17657, HSPC035	selenoprotein K	NM_521237, NCT16431236.4	223570_at	NP_067093.2, EAW63291.1
Gene:ID:37788	CACNA2D3	3	54,159,693	55,108,564	951,891	+	4	1_A375_shN7_dhrus_lncRNA:1:-3928, 2_A375_shN97_dhrs_lncRNA:1:-5939, 2_A375_shN97_dhrs_lncRNA:1:-5940, 2_A375_shN97_dhrs_lncRNA:1:-5941	69723, 69738, 433531, 466663	st gene, ut gene, st gene, st gene	1	1	24.67	21.67	3	2_A375_shN97_dhrs_lncRNA:1	97	Gene CACNA2D3	CACNA2D3, HSA272265	calcium channel, voltage-dependent, alpha 2/delta subunit 3	NM_018398, NCT16169982.2, NCT22790750	219714_s_at	NP_060964.2, EAW63302.1, EAW63304.1
Gene:ID:43474	WNT5A	3	55,099,743	55,221,231	21,368	+	1	2_A375_shN97_dhrs_lncRNA:1:-5994	679	st gene	0	1	14	26	1	2_A375_shN97_dhrs_lncRNA:1	26	Gene WNT5A	WNT5A, WNT5A	wingless-type MMTV integration site family, member 5A	NM_003392, NCT16693.2, NCT16693.1	205990_s_at, 213425_at, 231227_at	NP_003383.2, EAW63310.1, EAW63311.1
Gene:ID:43272	C3orf63	3	56,654,160	56,717,135	62,975	-	1	2_A375_shN97_dhrs_lncRNA:1:-5998	473	upstream	0	1	12	21	1	2_A375_shN97_dhrs_lncRNA:1	21	Gene C3orf63	C3orf63, RAP140, KIAA1105, DKFZp686C2496, sb59-1	chromosome 3 open reading frame 63	NM_015224, NM_001112735, NCT14812.2, NCT16693.2, NCT22985910, NCT22985902.2, NCT22985902.0, NCT22985902.2	209264_s_at, 209265_s_at, 227460_at	NP_056039.2, NP_001106207.1, EAW65320.1, EAW65321.1, EAW65322.1, EAW65324.1, EAW65319.1, EAW65322.1
Gene:ID:39690	ARHGEF3	3	56,761,446	57,113,236	351,890	+	2	1_A375_shN7_dhrus_lncRNA:1:-3942, 1_A375_shN7_dhrus_lncRNA:1:-3940, 2_A375_shN97_dhrs_lncRNA:1:-5946	65499, 66390, 81963	st gene, ut gene, ut gene	1	1	18	21	2	2_A375_shN97_dhrs_lncRNA:1	28	Gene ARHGEF3	GEF3, FLJ95126, DKFZp434P0429, MGC118903, ARHGEF3, XPLN, STA3	Rho guanine nucleotide exchange factor (GEF) 3	NM_019555, NM_001128615, NM_001128616, NCT13883.3, NCT16693.2	218501_at	NP_063953.1, NP_001120057.1, NP_001120058.1, EAW63328.1, EAW63329.1
Gene:ID:21626	PDE12	3	57,541,951	57,547,768	5,787	+	2	1_A375_shN7_dhrus_lncRNA:1:-3943, 2_A375_shN97_dhrs_lncRNA:1:-5949	-205, -381	upstream, upstream	1	1	23	16	1	1_A375_shN7_dhrus_lnc RNA:1	23	Gene PDE12	2'-PDE, PDE12	phosphodiesterase 12	NM_177966, NCT16529231.2, NCT23541200	1555915_s_at, 214626_at, 231629_at, 236081_at	NP_808813.3, EAW63362.1, EAW63363.1
Gene:ID:716	ARPP4	3	57,557,090	57,583,215	26,125	+	2	1_A375_shN7_dhrus_lncRNA:1:-3944, 2_A375_shN97_dhrs_lncRNA:1:-5950	47, 47	st gene, ut gene	1	1	22	22	1	2_A375_shN97_dhrs_lncRNA:1	22	Gene ARPP4	ARP2, ARPP4	cAMP-dependent tether 4	NM_001660, NCT16161.3	201096_s_at, 201097_s_at	NP_001651.1, EAW63344.1
Gene:ID:10028778	LOC100287709	3	57,742,034	57,742,642	608	-	1	2_A375_shN97_dhrs_lncRNA:1:-5971	626	downstream	0	1	16	20	1	2_A375_shN97_dhrs_lncRNA:1	20	Gene LOC100287709		hypothetical protein LOC100287709	XM_002342340		XP_002342381.1
Gene:ID:871	SLMAP	3	57,743,174	57,914,894	171,720	+	5	1_A375_shN7_dhrus_lncRNA:1:-3945, 1_A375_shN7_dhrus_lncRNA:1:-3946, 2_A375_shN97_dhrs_lncRNA:1:-5971, 2_A375_shN97_dhrs_lncRNA:1:-5972, 2_A375_shN97_dhrs_lncRNA:1:-5973	46330, 46376, 1156, 46330, 45426	st gene, ut gene, st gene, upstream, ut gene, st gene	1	1	23	24.33	3	1_A375_shN7_dhrus_lnc RNA:1	33	Gene SLMAP	KIAA1601, MGC138761, FLJ42209, SLAP, SLMAP, MGC138760	sarcolemma associated protein	NM_007159, NCT16694471, NCT17813.3, NCT23807700, NCT22807733.0	222624_at, 222625_at, 225243_s_at	NP_009090.2, EAW63360.1, EAW63347.1, EAW63348.1, EAW63349.1
Gene:ID:7406	ABHD6	3	58,222,259	58,260,491	67,352	+	1	2_A375_shN97_dhrs_lncRNA:1:-3934	653	st gene	0	1	11	16	1	2_A375_shN97_dhrs_lncRNA:1	16	Gene ABHD6	ABHD6		NM_020676, NCT16576.4, NCT16693.2, NCT16693.1, NCT22985501.2, NCT16693501.1, NCT16693501.2	221552_at, 221678_s_at, 224576_s_at, 224580_at	NP_057274.4, EAW63360.1, EAW63361.1, EAW63362.1, EAW63363.1, EAW63364.1
Gene:ID:1102	RPF1I	3	58,291,972	58,293,820	12,848	+	2	1_A375_shN7_dhrus_lncRNA:1:-3947, 2_A375_shN97_dhrs_lncRNA:1:-5975	-26, -65	upstream, upstream	1	1	110	127	1	2_A375_shN97_dhrs_lncRNA:1	127	Gene RPF1I	FLJ31508, RPF1I4, P14	ribonuclease P/MRP 14kDa subunit	NM_025162, NM_001098763, NCT16811.2, NCT16693451.1	224243_s_at, 224244_s_at, 227003_at	NP_079713, NP_001092253.1, EAW63396.1, EAW63397.1
Gene:ID:4599	PXK	3	58,316,617	58,410,876	62,261	+	2	1_A375_shN7_dhrus_lncRNA:1:-3948, 2_A375_shN97_dhrs_lncRNA:1:-5976	-73, -69	upstream, upstream	1	1	28	30	1	2_A375_shN97_dhrs_lncRNA:1	30	Gene PXK	MDNetKA, PXK, FLJ20235	PX domain containing serine/threonine kinase	NM_017771, NCT16573.3, NCT23496800.0, NCT23540061.0	1552274_at, 1552275_s_at, 225795_at	NP_060241.2, EAW63369.1, EAW63368.1, EAW65370.1
Gene:ID:30845	NCTC6	3	58,677,823	58,695,887	18,064	+	3	1_A375_shN7_dhrus_lncRNA:1:-3949, 1_A375_shN7_dhrus_lncRNA:1:-3950, 2_A375_shN97_dhrs_lncRNA:1:-5977	-4792, -101, -239	upstream, upstream, upstream	1	1	22	17.5	2	1_A375_shN7_dhrus_lnc RNA:1	27	Gene NCTC6	MGC27355, NCTC6	palmitoylation cluster-containing protein 6	NM_153331, NM_001128214, NCT13820.2	235001_at, 235077_at	NP_699162.2, NP_001121656.1, EAW65376.1
Gene:ID:308	ACOX2	3	58,990,953	58,922,829	32,096	-	2	1_A375_shN7_dhrus_lncRNA:1:-3951, 2_A375_shN97_dhrs_lncRNA:1:-5978	16209, 16321	st gene, ut gene	1	1	21	24	1	2_A375_shN97_dhrs_lncRNA:1	24	Gene ACOX2	BCOX, BRCOX, BRCACOX, THCGu, ACOX2	acyl-CoA oxidase 2, branched chain	NM_003500, NCT13821.2, NCT16693271.1, NCT22813384.0	208364_at	NP_003491.1, EAW63375.1, EAW63376.1, EAW63377.1
Gene:ID:1170	FAM107A	3	58,349,844	58,363,891	13,847	-	2	1_A375_shN7_dhrus_lncRNA:1:-3952, 2_A375_shN97_dhrs_lncRNA:1:-5979	-15982, 15297	upstream, upstream	1	1	21	27	1	2_A375_shN97_dhrs_lncRNA:1	27	Gene FAM107A	DRR1, TUSA, FLJ20158, FLJ45472, FAM107A	family with sequence similarity 107, member A	NM_007176736, NM_007177, NCT13112.1, NCT16693526.1, NCT16693501.1, NCT23541120.0	207047_s_at, 208076_s_at	NP_007176246.1, NP_008105.1, EAW63378.1, EAW63379.1, EAW65360.1, EAW65361.1
Gene:ID:272	FHIT	3	59,733,036	61,237,133	1,502,097	-	1	2_A375_shN97_dhrs_lncRNA:1:-5980	47129013	st gene	0	1	9	17	1	2_A375_shN97_dhrs_lncRNA:1	17	Gene FHIT	FRAXB, AP3Aase, FHIT	fragile histidine triad gene	NM_002012, NM_001166243, NCT22795611.1, NCT27795643.2	205492_at	NP_002003.1, NP_001178715.1, EAW65382.1, EAW65384.1
Gene:ID:793	PTPRG	3	61,547,243	62,260,573	713,330	+	1	2_A375_shN97_dhrs_lncRNA:1:-5981	-587	upstream	1	0	16	13	1	2_A375_shN97_dhrs_lncRNA:1	16	Gene PTPRG	protein tyrosine phosphatase, receptor type, G	protein tyrosine phosphatase, receptor type, G	NM_002841, NCT15849.3	1555321_at, 204944_at	NP_002832.2, EAW63397.1
Gene:ID:100506988	LOC100506988	3	62,246,540	62,204,622	56,082	-	2	1_A375_shN7_dhrus_lncRNA:1:-3953, 2_A375_shN97_dhrs_lncRNA:1:-5982	-176, -162	upstream, upstream	1	1	22	22	1	2_A375_shN97_dhrs_lncRNA:1	22	Gene LOC100506988		hypothetical LOC100506988	XR_112492, XR_112493, XR_112491, XR_110017, XR_110018, XR_110016, XR_113497, XR_113498, XR_113496		
Gene:ID:7418	C3orf14	3	62,303,299	62,219,321	13,979	-	2	1_A375_shN7_dhrus_lncRNA:1:-3953, 2_A375_shN97_dhrs_lncRNA:1:-5983	-998, -912	upstream, upstream	1	1	22	22	1	2_A375_shN97_dhrs_lncRNA:1	22	Gene C3orf14	HTG21, C3orf14	chromosome 3 open reading frame 14	NM_020653, NCT16693542.1, NCT22802160, NCT23541653.0	219255_at	NP_065706.1, EAW63400.1, EAW63402.1, EAW63402.1
Gene:ID:618	CADPS	3	62,364,021	62,861,864	477,043	+	9	1_A375_shN7_dhrus_lncRNA:1:-3955, 1_A375_shN7_dhrus_lncRNA:1:-3957, 1_A375_shN7_dhrus_lncRNA:1:-3958, 2_A375_shN97_dhrs_lncRNA:1:-5985, 2_A375_shN97_dhrs_lncRNA:1:-5986, 2_A375_shN97_dhrs_lncRNA:1:-5987	270762, 1416, -656, 349944, 357624, -824	st gene, ut gene, upstream, ut gene, st gene, upstream	1	1	17.8	21.2	5	2_A375_shN97_dhrs_lncRNA:1	31	Gene CADPS	CAPS, CAPS1, KIAA1121, CADPS1, CADPS	Ca++-dependent secretion activator	NM_183393, NM_003716, NM_183394, NCT16693.2, NCT16693451.1, NCT22802220.0, NCT22802240.0, NCT22802260.0, NCT23541790.0, NCT23541800.0	1569603_at, 1569604_at, 206514_at, 233950_x_at, 234220_at	NP_859031.1, NP_003707.2, NP_859031.1, EAW63403.1, EAW63405.1, EAW63406.1, EAW63409.1, EAW65407.1, EAW65408.1, EAW65410.1, EAW65411.1
Gene:ID:100133538	LOC100133538	3	63,136,271	63,190,811	60,540	+	2	1_A375_shN7_dhrus_lncRNA:1:-3960, 1_A375_shN7_dhrus_lncRNA:1:-3959	1299, 59355	st gene, upstream	1	1	20	14	2	1_A375_shN7_dhrus_lnc RNA:1	26	Gene LOC100133538		cadherin-related family member 3-like	XM_001719464, XM_001718216, XM_001718696		XP_001719516.1, XP_001718266.1, XP_001718638.1
Gene:ID:122020	C3orf49	3	63,803,041	63,834,312	29,271	+	1	2_A375_shN97_dhrs_lncRNA:1:-5991	-4469	upstream	1	0	26	11	1	2_A375_shN97_dhrs_lncRNA:1	26	Gene C3orf49	MGC17310, C3orf49	chromosome 3 open reading frame 49	NR_026999	1553933_at	
Gene:ID:314	ATXN7	3	63,850,233	63,869,138	136,905	+	3	1_A375_shN7_dhrus_lncRNA:1:-3962, 2_A375_shN97_dhrs_lncRNA:1:-5992, 2_A375_shN97_dhrs_lncRNA:1:-5993	67623, 67691, 89922	st gene, ut gene, st gene	1	1	14.5	15.5	2	1_A375_shN7_dhrus_lnc RNA:1	16	Gene ATXN7	ASCA11, FLJ17757, OPCA3, SCA7, ATXN7	ataxin 7	NM_000333, NM_001126149, NM_001177351, NCT13330.3, NCT22805220.0	206516_at, 206964_s_at	NP_000324.1, NP_001120621.2, NP_001170550.1, EAW63421.1, EAW65422.1
Gene:ID:591	PSMD6	3	63,999,231	64,009,120	12,889	-	2	1_A375_shN7_dhrus_lncRNA:1:-3963, 2_A375_shN97_dhrs_lncRNA:1:-5994	-22, -52	upstream, upstream	1	1	120	133	1	2_A375_shN97_dhrs_lncRNA:1	133	Gene PSMD6	KIAA0107, S10, Rpn7, p48/S10, PSMD6, SGA-11.04	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	NM_014814, NCT16693531.1, NCT23541602.0, NCT23541990.0, NCT23541600.0	1555554_at, 202753_at, 202754_at	NP_055629.1, EAW65424.1, EAW65425.1, EAW65426.1, EAW65427.1
Gene:ID:66336	PRICKLE2	3	64,079,826	64,211,131	131,805	+	3	1_A375_shN7_dhrus_lncRNA:1:-3964, 1_A375_shN7_dhrus_lncRNA:1:-3965, 2_A375_shN97_dhrs_lncRNA:1:-5995	120999, 120971, 7621	st gene, ut gene, upstream	1	1	18.8	20	2	2_A375_shN97_dhrs_lncRNA:1	22	Gene PRICKLE2	DKFZp686D143, DKFZp686M031, DKFZp686H1748, PRICKLE2	prickle homolog 2 (Drosophila)	NM_198599, NCT22810982.1, NCT23465900.0	228965_at	NP_942599.1, EAW65428.1, EAW65429.1
Gene:ID:6999	ADAMTS9	3	64,901,330	64,973,365	172,035	-	3	1_A375_shN7_dhrus_lncRNA:1:-3965, 1_A375_shN7_dhrus_lncRNA:1:-3966, 2_A375_shN97_dhrs_lncRNA:1:-5996	3229, -653, -610	st gene, upstream, upstream	1	1	16.5	14.5	2	2_A375_shN97_dhrs_lncRNA:1	16	Gene ADAMTS9	FLJ42655, ADAMTS9, KIAA1312	ADAM metallopeptidase with thrombospondin type 1 motif, 9	NM_182920, NCT23459817.0, NCT23560756.0	1554697_at, 230207_at, 236014_at, 237703_at	NP_619537.1, EAW63434.1, EAW63435.1
Gene:ID:100507036	LOC100507036	3	64,670,546	64,961,216	290,670	+	2	1_A375_shN7_dhrus_lncRNA:1:-3965, 1_A375_shN7_dhrus_lncRNA:1:-3966, 2_A375_shN97_dhrs_lncRNA:1:-5996	580, 3374, 3455	st gene, ut gene, st gene	1	1	16.5	14.5	2	2_A375_shN97_dhrs_lncRNA:1	16	Gene LOC100507036		hypothetical LOC100507036	XR_112455, XR_112456, XR_110021, XR_110022, XR_113462, XR_113463		
Gene:ID:223	MAGI1	3	65,329,906	66,024,909	695,003	+	4	1_A375_shN7_dhrus_lncRNA:1:-3701, 1_A375_shN7_dhrus_lncRNA:1:-3702, 1_A375_shN7_dhrus_lncRNA:1:-3969, 2_A375_shN97_dhrs_lncRNA:1:-5998	78653, 46961, 3027, -483	st gene, ut gene, upstream, upstream	1	1	19	20.33	3	2_A375_shN97_dhrs_lncRNA:1	22	Gene MAGI1	MAGI1, BAP1, WWP2, MAGI-1, BAIAP1, TNRC16, AIP3	membrane associated guanylate kinase, WW and PDZ domain containing 1	NM_004742, NM_015370, NM_001033057, NCT15163112.2, NCT16693511.1, NCT16693512.1, NCT22806410.0, NCT22806402.0, NCT22806490.0, NCT22806490.2	1553262_s_at, 1553296_at, 1559237_at, 206144_at, 228465_at, 228474_at, 232659_s_at	NP_004732.2, NP_056538.1, NP_001028229.1, EAW63439.1, EAW63440.1, EAW65441.1, EAW65442.1, EAW65443.1, EAW65444.1, EAW65445.1
Gene:ID:61677	LOC151677	3	65,856,409	65,940,233	81,764	+	1	2_A375_shN97_dhrs_lncRNA:1:-5781	4823	upstream	0	1	12	17	1	2_A375_shN97_dhrs_lncRNA:1	17	Gene LOC151677		hypothetical LOC151677	XR_112466, XR_110023, XR_113464	1561201_at	
Gene:ID:6616	LRIG1	3	66,429,221	66,550,845	121,624	+	1	2_A375_shN97_dhrs_lncRNA:1:-5784	488	upstream	0	1	16	27	1	2_A375_shN97_dhrs_lncRNA:1	27	Gene LRIG1	DKFZp586D1624, LIG-1, LIG1, LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	NM_015541, NCT22806490.0, NCT22804911.0	211599_x_at, 239172_x_at, 239324_x_at	NP_056356.2, EAW65452.1, EAW65453.1
Gene:ID:43451	KBTBD8	3	67,045,727	67,061,834	12,107	+	2	1_A375_shN7_dhrus_lncRNA:1:-3970, 2_A375_shN97_dhrs_lncRNA:1:-5788	29393, 29702	downstream, downstream	1	1	16	17	1	2_A375_shN97_dhrs_lncRNA:1	17	Gene KBTBD8	KIAA1542, KBTBD8, FLJ35932, TA-KRP	kelch repeat and BTB (POZ) domain containing 8	NM_032505, NCT7352.4	229653_at	NP_115924.2, EAW65456.1
Gene:ID:991	SUCLG2	3	67,410,884	67,705,038	294,154	-	1	2_A375_shN97_dhrs_lncRNA:1:-5787	16	st gene	1	0	17	14	1	2_A375_shN97_dhrs_lncRNA:1	17	Gene SUCLG2	G-BETA, GBETA, SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	NM_003849, NM_001177599, NM_002606, NCT22805910.0, NCT7342.3	212059_x_at, 214535_s_at, 218722_s_at	NP_003839.1, NP_001171070.1, NP_002597.2, EAW65467.1
Gene:ID:97338	FAM160A1	3	68,053,854	68,093,772	581,218	+	1	2_A375_shN97_dhrs_lncRNA:1:-5972	332458	st gene	1	0	16	11	1	2_A375_shN97_dhrs_lncRNA:1	16	Gene FAM160A1	TAPA-1, PRAM1A1, TAPA1	family with sequence similarity 160, member A1	NM_213609, NCT16582415.1	1555023_at	NP_998774.2, EAW65480.1
Gene:ID:43253	C3orf58	3	69,024,368	69,062,774	38,406	+	1	2_A375_shN97_dhrs_lncRNA:1:-5797	78	upstream	0	1	12	14	1	2_A375_shN97_dhrs_lncRNA:1	14	Gene C3orf58	DJ966N18.2, FLJ35219, FLJ35976, AER61, MGC34132, C3orf58, FLJ33770	chromosome 3 open reading frame 58	NM_173554	221635_s_at	NP_775925.1
Gene:ID:110	TNFF1	3	69,065,978	69,101,884	32,306	+	1	2_A375_shN97_dhrs_lncRNA:1:-5797	33636	upstream	0	1	12	14	1	2_A375_shN97_dhrs_lncRNA:1	14	Gene TNFF1	ARA160, TNFF1, TNFF	TATA element modulatory factor 1	NM_007114, NCT22805830.0, NCT6360.2	213024_at, 214945_s_at, 216835_s_at, 227663_at, 233996_at, 236629_at, 241283_at	NP_009045.2, EAW65465.1, EAW65466.1
Gene:ID:3150	FRMD4B	3	69,219,146	69,433,430	214,284	+	3	1_A375_shN7_dhrus_lncRNA:1:-3974, 2_A375_shN97_dhrs_lncRNA:1:-5798, 2_A375_shN97_dhrs_lncRNA:1:-5799	204198, 204336, 76590	st gene, ut gene, ut gene	1	1	17	23	2	2_A375_shN97_dhrs_lncRNA:1	24	Gene FRMD4B	GRSP1, FRMD4B, 9030049035Rik, KIAA1013	FERM domain containing 4B	NM_018123	213096_at, 219131_at, 219134_at	NP_059816.1
Gene:ID:386	MITF	3	69,765,566	70,017,468	228,902	+	1	2_A375_shN97_dhrs_lncRNA:1:-5792	10	upstream	0	1	17	16	1	2_A375_shN97_dhrs_lncRNA:1	16	Gene MITF	WS2, bHLHe32, MI, MITF, WS2A	microphthalmia-associated transcription factor	NM_000248, NM_001114847, NM_001184967, NM_001184968, NM_006722, NM_198155, NM_198158, NM_198177, NM_198178, NCT16583481.1, NCT22807101.0, NCT22807102.0, NCT22807603.0, NCT22807604.0, NCT13886.2	1554074_at, 1554075_a_at, 207233_s_at, 207234_x_at, 236096_at	NP_000239.1, NP_001171095.1, NP_937801.1, NP_937802.1, NP_000707.1, NP_001171097.1, NP_001171098.1, NP_001171099.1, NP_937803.2, EAW65481.1, EAW65482.1, EAW65483.1, EAW65484.1
Gene:ID:100506866	LOC100506866	3	72,712,433	72,713,490	965	-	1	2_A375_shN7_dhrus_lncRNA:1:-3976	2901	downstream	1	0	16	8	1	1_A375_shN7_dhrus_lnc RNA:1	16	Gene LOC100506866		hypothetical LOC100506866	XR_112511, XR_110097, XR_113468		
Gene:ID:9164	SHQ1	3	72,798,426	72,897,396	98,170	+	2	1_A375_shN7_dhrus_lncRNA:1:-3715	64	st gene	0	1	13	22	1	2_A375_shN97_dhrs_lncRNA:1	22	Gene SHQ1	SHQ1, Shq1p, FLJ10338, DKFZp686H07226	SHQ1 homolog (S. cerevisiae)	NM_018130, NCT16479301.2, NCT22812460.0, NCT23540220.0	218053_at, 62009_at	NP_060600.2, EAW63521.1, EAW63522.1, EAW65523.1
Gene:ID:27836	GXYLT2	3	72,937,383	73,024,525	87,140	+	2	1_A375_shN7_dhrus_lncRNA:1:-3979, 2_A375_shN97_dhrs_lncRNA:1:-5539	50423, -313	st gene, upstream	1	1	16	14.5	2	2_A375_shN97_dhrs_lncRNA:1	20	Gene GXYLT2	GXYLT2, OLTD4	glucoside xylosyltransferase 2	NM_001083363	223371_at	NP_001073382.1
Gene:ID:3024	PDZRN3	3	73,251,652	73,670,872	243,220	-	2	1_A375_shN7_dhrus_lncRNA:1:-3979, 2_A375_shN97_dhrs_lncRNA:1:-5120	48344, 264	st gene, upstream	0	1	12	22.5	2	2_A375_shN97_dhrs_lncRNA:1	26	Gene PDZRN3	SEMCAP2, PDZRN3, LNX3	PDZ domain containing ring finger 3	NM_015009, NCT16693691.1, NCT6948.2	1555557_at, 212915_at, 231165_at	NP_055824.1, EAW65532.1, EAW65531.1
Gene:ID:100285981	PRG2C	3	73,713,667	73,716,366	2,681	+	2	1_A375_shN7_dhrus_lncRNA:1:-3980, 2_A375_shN97_dhrs_lncRNA:1:-5124	5359, 5359	upstream, upstream	1	1	51	43	1	1_A375_shN7_dhrus_lnc RNA:1	51	Gene PRG2C	PRG2C		NM_001124758		NP_001118231.1
Gene:ID:100506876	LOC100506876	3	73,717,279	73,719,165	1,886	+	2	1_A375_shN7_dhrus_lncRNA:1:-3980, 2_A375_shN97_dhrs_lncRNA:1:-5124	8251, 8251	upstream, upstream	1	1	51	43	1	1_A375_shN7_dhrus_lnc RNA:1	51	Gene LOC100506876		Sialidase 1 (membrane sialidase)	XM_002116564		XP_002116612.1
Gene:ID:691	ROBO1	3	78,646,388	79,017,059	1,170,671	+	2	1_A375_shN7_dhrus_lncRNA:1:-3982, 2_A375_shN97_dhrs_lncRNA:1:-5126	146322, 146276	st gene, ut gene	1	1	55	47	1	1_A375_shN7_dhrus_lnc RNA:1	55	Gene ROBO1	SAX3, FLJ21662, MGC131599, MGC132277, ROBO1, DUTT1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	NM_002941, NM_001145845, NM_133631, NCT22814280.0, NCT22814427.0, NCT22814290.0, NCT22815420.0	212158_at	NP_002932.1, NP_001136317.1, NP_598334.2, EAW65564.1, EAW65565.1, EAW65567.1, EAW65569.1, EAW65566.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:2632	GBE1	3	81,538,850	81,810,950	272,100	-	2	1_A375_pNL7_minus_lncRNA::1::3984, 2_A375_pNL97_plus_lncRNA::1::5728	166, 166	in gene, in gene	1	1	19	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene GBE1	GBE1, GBE	glucan (1,4-alpha-), branching enzyme 1	NM_000158, hCT17930.2, hCT1957149.1	203282_at	NP_000149.3, EAW68680.1, EAW68679.1
GeneID:253559	CADM2	3	85,008,133	86,123,579	1,115,446	+	1	2_A375_pNL97_plus_lncRNA::1::5731	601563	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CADM2	Necl-3, MGC138341, IGSF4D, NECL3, MGC138343, CADM2, synCAM2, MGC104534	cell adhesion molecule 2	NM_153184, NM_001167674, NM_001167675, hCT1641365.3, hCT2344788.0	1552752_a_at, 1552754_a_at, 1555544_a_at	NP_694854.2, NP_001161146.1, NP_001161147.1, EAW68874.1, EAW68875.1
GeneID:8545	CGGBP1	3	88,101,100	88,108,146	7,046	-	1	2_A375_pNL97_plus_lncRNA::1::5735	-334	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CGGBP1	CGGBP1, CGGBP, p20-CGGBP	CGG triplet repeat binding protein 1	NM_003663, NM_001008390, hCT1641716.3, hCT1957124.1	206861_s_at, 224600_at	NP_003654.3, NP_001008391.1, EAW68863.1, EAW68864.1
GeneID:55279	ZNF654	3	88,188,262	88,193,814	5,552	+	2	1_A375_pNL7_minus_lncRNA::1::3987, 2_A375_pNL97_plus_lncRNA::1::5736	10682, 10714	downstream, downstream	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene ZNF654	ZNF654, FLJ10997, FLJ21142	zinc finger protein 654	NM_018293, hCT2283209.1, hCT2283210.1	1556743_at, 1556744_a_at, 219239_s_at, 222851_at, 241348_at, 242017_at	NP_060763.2, EAW68861.1, EAW68862.1
GeneID:285237	C3orf38	3	88,198,893	88,207,115	8,222	+	2	1_A375_pNL7_minus_lncRNA::1::3987, 2_A375_pNL97_plus_lncRNA::1::5736	51, 83	in gene, in gene	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene C3orf38	FLJ54270, MGC26717, C3orf38	chromosome 3 open reading frame 38	NM_173824, hCT1965715.1, hCT2283213.0, hCT23686.2	226524_at	NP_776185.2, EAW68860.1, EAW68858.1, EAW68859.1
GeneID:2042	EPHA3	3	89,156,674	89,531,284	374,610	+	3	2_A375_pNL97_plus_lncRNA::1::5737, 2_A375_pNL97_plus_lncRNA::1::5738, 2_A375_pNL97_plus_lncRNA::1::5739	30, 7118, 64350	in gene, in gene, in gene	0	1	11.67	20.33	3	2_A375_pNL97_plus_lncRNA::1	24	Gene EPHA3	TYRO4, HEK, ETK, EPHA3, ETK1, HEK4, EK4	EPH receptor A3	NM_005233, NM_182644, hCT1957158.1	206070_s_at, 206071_s_at, 211164_at	NP_005224.2, NP_872585.1, EAW68857.1
GeneID:285220	EPHA6	3	96,533,425	97,467,786	934,361	+	3	1_A375_pNL7_minus_lncRNA::1::3988, 2_A375_pNL97_plus_lncRNA::1::5744, 2_A375_pNL97_plus_lncRNA::1::5745	-353, -1009, -401	upstream, upstream, upstream	1	1	17	17	1	1_A375_pNL7_minus_lncRNA::1	17	Gene EPHA6	EPA6, PRO57066, EPHA6, DKFZp434C1418, FLJ35246	EPH receptor A6	NM_001080448, NM_173655	1561396_at, 233184_at	NP_001073917.2, NP_775926.1
GeneID:131544	CRYBG3	3	97,540,569	97,663,826	123,257	+	1	2_A375_pNL97_plus_lncRNA::1::5746	903	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CRYBG3	DKFZp667G2110, CRYBG3, FLJ60082, DKFZp686L13211	beta-gamma crystallin domain containing 3	XM_003119805, XM_003118522, XM_003120421	214030_at	XP_003119853.1, XP_003118570.1, XP_003120469.1
GeneID:84864	MINA	3	97,660,661	97,691,295	30,634	-	1	2_A375_pNL97_plus_lncRNA::1::5747	31	in gene	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene MINA	FLJ14393, DKFZp762O1912, MINA, MINA53, MDIG, NO52	MYC induced nuclear antigen	NM_001042533, NM_153182, NM_032778, hCT1952464.1, hCT2319834.0, hCT2355807.0, hCT2355808.0	1554774_at, 213188_s_at, 213189_at, 229132_at, 229675_at	NP_001035998.1, NP_694822.2, NP_116167.3, EAW79872.1, EAW79874.1, EAW79875.1, EAW79873.1
GeneID:56650	CLDND1	3	98,234,317	98,241,910	7,593	-	1	1_A375_pNL7_minus_lncRNA::1::3989	86	in gene	1	0	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene CLDND1	MGC111162, GENX-3745, C3orf4, MGC3316, MGC9861, CLDND1	claudin domain containing 1	NM_001040181, NM_001040182, NM_001040183, NM_019895, NM_001040199, NM_001040200, hCT11215.3, hCT1957467.1, hCT2355797.0, hCT2355798.0, hCT2355799.0	1554149_at, 208925_at, 239146_at	NP_001035271.1, NP_001035272.1, NP_063948.1, NP_001035273.1, NP_001035289.1, NP_001035290.1, EAW79856.1, EAW79857.1, EAW79858.1, EAW79859.1, EAW79860.1
GeneID:2838	GPR15	3	98,250,878	98,251,960	1,082	+	1	1_A375_pNL7_minus_lncRNA::1::3989	-9054	upstream	1	0	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene GPR15	MGC126828, GPR15, MGC126830	G protein-coupled receptor 15	NM_005290, hCT1647821.2	208524_at	NP_005281.1, EAW79855.1
GeneID:10402	ST3GAL6	3	98,451,572	98,513,237	61,665	+	1	1_A375_pNL7_minus_lncRNA::1::3990	37660	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ST3GAL6	SIAT10, ST3GALVI, ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	NM_006100, hCT1966622.1, hCT1966623.1, hCT1966624.1, hCT2320237.0, hCT9858.4	210942_s_at, 213335_s_at, 213355_at	NP_006091.1, EAW79849.1, EAW79850.1, EAW79851.1, EAW79852.1, EAW79853.1
GeneID:131566	DCBLD2	3	98,514,814	98,620,533	105,719	-	1	2_A375_pNL97_plus_lncRNA::1::5748	133	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DCBLD2	DCBLD2, CLCP1, ESDN	discoidin, CUB and LCCL domain containing 2	NM_080927, hCT11214.3, hCT2320036.0, hCT2355962.0	213865_at, 224911_s_at, 239446_x_at	NP_563615.3, EAW79847.1, EAW79845.1, EAW79846.1
GeneID:100506377	LOC100506377	3	98,699,902	98,701,940	2,038	+	1	2_A375_pNL97_plus_lncRNA::1::5749	-3230	upstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100506377		hypothetical LOC100506377	XR_112526, XR_108458, XR_113568		
GeneID:84319	C3orf26	3	99,536,678	99,897,476	360,798	+	4	1_A375_pNL7_minus_lncRNA::1::3991, 1_A375_pNL7_minus_lncRNA::1::3992, 2_A375_pNL97_plus_lncRNA::1::5752, 2_A375_pNL97_plus_lncRNA::1::5753	-147, 357914, -102, 358026	upstream, in gene, upstream, in gene	1	1	16	25.5	2	2_A375_pNL97_plus_lncRNA::1	33	Gene C3orf26	C3orf26, MGC4308	chromosome 3 open reading frame 26	NM_032359, NM_001167924	224523_s_at	NP_115735.2, NP_001161396.1
GeneID:55773	TBC1D23	3	99,979,686	100,044,082	64,396	+	2	1_A375_pNL7_minus_lncRNA::1::3993, 2_A375_pNL97_plus_lncRNA::1::5754	154, 218	in gene, in gene	1	1	24	16	1	1_A375_pNL7_minus_lncRNA::1	24	Gene TBC1D23	TBC1D23, NS4ATP1, FLJ11046, DKFZp667G062	TBC1 domain family, member 23	NM_018309, hCT19390.3, hCT2320725.0	225121_at	NP_060779.2, EAW79826.1, EAW79827.1
GeneID:55076	TMEM45A	3	100,211,463	100,296,285	84,822	+	1	1_A375_pNL7_minus_lncRNA::1::3994	33577	in gene	1	0	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TMEM45A	TMEM45A, FLJ10134, DERP7	transmembrane protein 45A	NM_018004, hCT1952486.1, hCT1955349.1	219410_at	NP_060474.1, EAW79819.1, EAW79820.1
GeneID:54931	RG9MTD1	3	101,280,712	101,285,089	4,377	+	2	1_A375_pNL7_minus_lncRNA::1::3995, 2_A375_pNL97_plus_lncRNA::1::5755	12152, 11926	downstream, downstream	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene RG9MTD1	MRPP1, RG9MTD1, FLJ20432	RNA (guanine-9-) methyltransferase domain containing 1	NM_017819, hCT30525.3	223267_at	NP_060289.2, EAW79795.1
GeneID:57092	PCNP	3	101,293,042	101,313,281	20,239	+	2	1_A375_pNL7_minus_lncRNA::1::3995, 2_A375_pNL97_plus_lncRNA::1::5755	-178, -402	upstream, upstream	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene PCNP	PCNP, DKFZp781I24156	PEST proteolytic signal containing nuclear protein	NM_020357, hCT2319957.0, hCT2319958.0, hCT2319959.0, hCT2355932.0, hCT2355933.0	237577_at	NP_065090.1, EAW79791.1, EAW79790.1, EAW79792.1, EAW79793.1, EAW79794.1
GeneID:27107	ZBTB11	3	101,368,283	101,395,988	27,705	-	1	2_A375_pNL97_plus_lncRNA::1::5756	1264	in gene	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZBTB11	ZBTB11, MGC133303, ZNF913, FLJ13426, ZNF-U69274	zinc finger and BTB domain containing 11	NM_014415, hCT28910.3	204847_at, 242433_at	NP_055230.2, EAW79786.1
GeneID:100009676	LOC100009676	3	101,395,274	101,398,061	2,787	+	1	2_A375_pNL97_plus_lncRNA::1::5756	-570	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100009676		hypothetical LOC100009676	NR_024407	232259_s_at, 232260_at	
GeneID:6152	RPL24	3	101,399,934	101,405,563	5,629	-	1	2_A375_pNL97_plus_lncRNA::1::5756	10659	downstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene RPL24	RPL24, L24		NM_000986, hCT2319865.1, hCT2319866.1, hCT2319867.1, hCT2340321.0, hCT2340322.0	200013_at	NP_000977.1, EAW79781.1, EAW79780.1, EAW79782.1, EAW79783.1, EAW79784.1
GeneID:91775	FAM55C	3	101,498,029	101,547,075	49,046	+	1	2_A375_pNL97_plus_lncRNA::1::5757	19	in gene	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene FAM55C	MST115, FLJ30102, MGC15606, MSTP115, FAM55C	family with sequence similarity 55, member C	NM_001134456, NM_145037, hCT1815071.1, hCT2355900.0	235030_at, 243011_at	NP_001127928.1, NP_659474.1, EAW79774.1, EAW79775.1
GeneID:64332	NFKBIZ	3	101,546,834	101,579,869	33,035	+	1	2_A375_pNL97_plus_lncRNA::1::5758	21582	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene NFKBIZ	MAIL, INAP, FLJ34463, IKBZ, FLJ30225, NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	NM_001005474, NM_031419, hCT1815073.1, hCT2355880.0, hCT29945.3	1556153_s_at, 223217_s_at, 223218_s_at	NP_001005474.1, NP_113607.1, EAW79771.1, EAW79772.1, EAW79773.1
GeneID:214	ALCAM	3	105,085,713	105,295,744	210,031	+	2	2_A375_pNL97_plus_lncRNA::1::5760, 2_A375_pNL97_plus_lncRNA::1::5761	751, 2799	in gene, in gene	0	1	13.5	17.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene ALCAM	CD166, FLJ38514, ALCAM, MGC71733, MEMD	activated leukocyte cell adhesion molecule	NM_001627, hCT19103.3, hCT2319816.0, hCT2319818.0	1569362_at, 201951_at, 201952_at	NP_001618.2, EAW79755.1, EAW79756.1, EAW79757.1
GeneID:868	CBLB	3	105,377,109	105,587,887	210,778	-	1	1_A375_pNL7_minus_lncRNA::1::3999	-625	upstream	1	0	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene CBLB	RNF56, Nbla00127, DKFZp779F1443, DKFZp686J10223, CBLB, DKFZp779A0729, FLJ41152, FLJ36865	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	NM_170662, hCT1953753.1, hCT2319696.0, hCT2319697.0, hCT2355953.0	208348_s_at, 209682_at, 227900_at	NP_733762.2, EAW79753.1, EAW79751.1, EAW79752.1, EAW79754.1
GeneID:961	CD47	3	107,761,941	107,809,935	47,994	-	2	1_A375_pNL7_minus_lncRNA::1::4003, 2_A375_pNL97_plus_lncRNA::1::5767	-113, 239	upstream, in gene	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CD47	CD47, IAP, MER6, OA3	CD47 molecule	NM_001777, NM_198793, hCT19528.3, hCT1971139.1, hCT1971144.1	211075_s_at, 213055_at, 213856_at, 213857_s_at, 226016_at, 227259_at, 242974_at	NP_001768.1, NP_942088.1, EAW79732.1, EAW79733.1, EAW79734.1
GeneID:22989	MYH15	3	108,099,216	108,248,169	148,953	-	2	1_A375_pNL7_minus_lncRNA::1::4004, 2_A375_pNL97_plus_lncRNA::1::5768	108297, 108201	in gene, in gene	1	1	25	25	1	1_A375_pNL7_minus_lncRNA::1	25	Gene MYH15	MYH15		NM_014981	215331_at	NP_055796.1
GeneID:57650	KIAA1524	3	108,268,716	108,308,491	39,775	-	1	1_A375_pNL7_minus_lncRNA::1::4005	-65	upstream	1	0	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene KIAA1524	CIP2A, MGC163436, KIAA1524, p90, FLJ12850	KIAA1524	NM_020890, hCT19531.2, hCT2319851.0	1553810_a_at, 231855_at	NP_065941.2, EAW79724.1, EAW79723.1
GeneID:9666	DZIP3	3	108,308,337	108,413,693	105,356	+	1	1_A375_pNL7_minus_lncRNA::1::4005	239	in gene	1	0	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene DZIP3	DZIP3, KIAA0675, FLJ58022, FLJ57977, FLJ58223, hRUL138, FLJ13327, UURF2	DAZ interacting protein 3, zinc finger	NM_014648, hCT19530.3, hCT1971373.1	207231_at, 207232_s_at, 213186_at	NP_055463.1, EAW79721.1, EAW79722.1
GeneID:100506555	LOC100506555	3	110,764,162	110,788,242	24,080	-	1	2_A375_pNL97_plus_lncRNA::1::5769	-2126	upstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506555		hypothetical LOC100506555	XR_112522, XR_108462, XR_113572		
GeneID:25945	PVRL3	3	110,790,865	110,853,062	62,197	+	1	2_A375_pNL97_plus_lncRNA::1::5769	-497	upstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PVRL3	PPR3, CDw113, PVRR3, PRR3, FLJ90624, nectin-3, PVRL3, DKFZp566B0846, CD113	poliovirus receptor-related 3	NM_015480, hCT1818696.2	213325_at	NP_056295.1, EAW79703.1
GeneID:257068	PLCXD2	3	111,393,523	111,565,294	171,771	+	1	2_A375_pNL97_plus_lncRNA::1::5771	39757	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PLCXD2	FLJ31579, PLCXD2	phosphatidylinositol-specific phospholipase C, X domain containing 2	NM_001185106, NM_153268, hCT18704.3	1553281_at	NP_001172035.1, NP_695000.1, EAW79695.1
GeneID:90102	PHLDB2	3	111,451,327	111,695,364	244,037	+	2	1_A375_pNL7_minus_lncRNA::1::4007, 2_A375_pNL97_plus_lncRNA::1::5772	127009, 127105	in gene, in gene	1	1	27	25	1	1_A375_pNL7_minus_lncRNA::1	27	Gene PHLDB2	PHLDB2, DKFZp686J05113, DKFZp434G227, DKFZp313O2433, LL5b, FLJ21791, LL5beta	pleckstrin homology-like domain, family B, member 2	NM_145753, NM_001134437, NM_001134438, NM_001134439, hCT2341162.0, hCT2341163.0, hCT2341164.0	1554778_at, 1554779_s_at, 1557578_at, 225688_s_at, 238419_at	NP_665696.1, NP_001127909.1, NP_001127910.1, NP_001127911.1, EAW79691.1, EAW79692.1, EAW79690.1
GeneID:285335	SLC9A10	3	111,859,752	112,013,074	153,322	-	1	1_A375_pNL7_minus_lncRNA::1::4008	94402	in gene	1	0	24	11	1	1_A375_pNL7_minus_lncRNA::1	24	Gene SLC9A10	SLC9A10		NM_183061, hCT2319687.1		NP_898884.1, EAW79679.1
GeneID:64422	ATG3	3	112,251,359	112,280,485	29,126	-	2	1_A375_pNL7_minus_lncRNA::1::4009, 2_A375_pNL97_plus_lncRNA::1::5773	-208, -358	upstream, upstream	1	1	25	21	1	1_A375_pNL7_minus_lncRNA::1	25	Gene ATG3	ATG3, PC3-96, FLJ22125, APG3-LIKE, MGC15201, APG3L, DKFZp564M1178, APG3	ATG3 autophagy related 3 homolog (S. cerevisiae)	NM_022488, hCT2319675.0, hCT2319676.0, hCT2355835.0, hCT6843.3	220237_at, 221492_s_at	NP_071933.2, EAW79668.1, EAW79669.1, EAW79670.1, EAW79671.1
GeneID:55032	SLC35A5	3	112,280,895	112,303,003	22,108	+	2	1_A375_pNL7_minus_lncRNA::1::4009, 2_A375_pNL97_plus_lncRNA::1::5773	-202, -52	upstream, upstream	1	1	25	21	1	1_A375_pNL7_minus_lncRNA::1	25	Gene SLC35A5	DKFZp434E102, FLJ25973, SLC35A5, FLJ20730, FLJ11130	solute carrier family 35, member A5	NM_017945, hCT1962431.1, hCT6841.2	218519_at	NP_060415.1, EAW79666.1, EAW79667.1
GeneID:151887	CCDC80	3	112,323,407	112,359,977	36,570	-	1	2_A375_pNL97_plus_lncRNA::1::5774	-263	upstream	0	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CCDC80	CCDC80, MGC134851, MGC131605, URB, okuribin, SSG1, DRO1	coiled-coil domain containing 80	NM_199511, NM_199512, hCT1968260.3, hCT2348565.1, hCT2349449.1	225241_at, 225242_s_at, 243864_at	NP_955805.1, NP_955806.1, EAW79663.1, EAW79664.1, EAW79665.1
GeneID:205717	KIAA2018	3	113,367,232	113,415,493	48,261	-	1	1_A375_pNL7_minus_lncRNA::1::4011	-347	upstream	1	0	25	23	1	1_A375_pNL7_minus_lncRNA::1	25	Gene KIAA2018	KIAA2018, DKFZp781O0144	KIAA2018	NM_001009899	1559601_at, 227433_at, 227435_at, 242508_at, 242513_x_at	NP_001009899.2
GeneID:100506638	LOC100506638	3	113,425,926	113,436,570	10,644	-	1	1_A375_pNL7_minus_lncRNA::1::4011	20730	downstream	1	0	25	23	1	1_A375_pNL7_minus_lncRNA::1	25	Gene LOC100506638		hypothetical LOC100506638	XR_112516, XR_108467, XR_113578		
GeneID:80218	NAA50	3	113,437,841	113,465,096	27,255	-	1	1_A375_pNL7_minus_lncRNA::1::4012	-952	upstream	1	0	20	11	1	1_A375_pNL7_minus_lncRNA::1	20	Gene NAA50	hSAN, hNAT5, NAA50, FLJ13194, NAT5, SAN, NAT13, MAK3	N(alpha)-acetyltransferase 50, NatE catalytic subunit	NM_025146, hCT1640399.2, hCT1966422.1, hCT2355887.0	217745_s_at, 222393_s_at	NP_079422.1, EAW79630.1, EAW79629.1, EAW79631.1
GeneID:523	ATP6V1A	3	113,465,908	113,530,903	64,995	+	1	1_A375_pNL7_minus_lncRNA::1::4012	140	in gene	1	0	20	11	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ATP6V1A	Vma1, VA68, ATP6V1A, HO68, ATP6V1A1, ATP6A1, VPP2	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	NM_001690, hCT2320551.0, hCT2320552.0, hCT2320553.0, hCT9937.3	201971_s_at, 201972_at	NP_001681.2, EAW79626.1, EAW79625.1, EAW79627.1, EAW79628.1
GeneID:57577	KIAA1407	3	113,682,984	113,775,460	92,476	-	2	1_A375_pNL7_minus_lncRNA::1::4013, 2_A375_pNL97_plus_lncRNA::1::5775	-28, -12	upstream, upstream	1	1	25	22	1	1_A375_pNL7_minus_lncRNA::1	25	Gene KIAA1407	KIAA1407, FLJ43314	KIAA1407	NM_020817, hCT9939.3	228476_at	NP_065868.1, EAW79615.1
GeneID:79691	QTRTD1	3	113,775,611	113,807,269	31,658	+	2	1_A375_pNL7_minus_lncRNA::1::4013, 2_A375_pNL97_plus_lncRNA::1::5775	-123, -139	upstream, upstream	1	1	25	22	1	1_A375_pNL7_minus_lncRNA::1	25	Gene QTRTD1	QTRTD1, FLJ12960	queuine tRNA-ribosyltransferase domain containing 1	NM_024638, hCT2320559.0, hCT9938.3	1560695_at, 1560696_x_at, 219178_at	NP_078914.1, EAW79613.1, EAW79614.1
GeneID:1814	DRD3	3	113,847,557	113,897,899	50,342	-	2	1_A375_pNL7_minus_lncRNA::1::4014, 2_A375_pNL97_plus_lncRNA::1::5776	139, 139	in gene, in gene	1	1	27	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene DRD3	FET1, MGC149204, ETM1, DRD3, MGC149205, D3DR	dopamine receptor D3	NM_000796, NM_033663, hCT1962444.1, hCT2319746.0, hCT2319748.0, hCT2319750.0, hCT2319752.0, hCT2319756.0, hCT2319758.0, hCT9934.3	211625_s_at, 214559_at	NP_000787.2, NP_387512.3, EAW79606.1, EAW79607.1, EAW79609.1, EAW79612.1, EAW79605.1, EAW79608.1, EAW79610.1, EAW79611.1
GeneID:26137	ZBTB20	3	114,056,941	114,866,127	809,186	-	1	1_A375_pNL7_minus_lncRNA::1::4015	734767	in gene	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene ZBTB20	HOF, FLJ26458, DPZF, DKFZp566F123, ZBTB20, ODA-8S, ZNF288	zinc finger and BTB domain containing 20	NM_001164342, NM_001164343, NM_015642, NM_001164344, NM_001164345, NM_001164346, NM_001164347, hCT2319609.0	205383_s_at, 222357_at, 235308_at	NP_001157814.1, NP_001157815.1, NP_056457.3, NP_001157816.1, NP_001157817.1, NP_001157818.1, NP_001157819.1, EAW79598.1
GeneID:4045	LSAMP	3	115,521,210	116,164,385	643,175	-	4	1_A375_pNL7_minus_lncRNA::1::4020, 1_A375_pNL7_minus_lncRNA::1::4021, 1_A375_pNL7_minus_lncRNA::1::4022, 2_A375_pNL97_plus_lncRNA::1::5781	559777, 445057, 296385, 559713	in gene, in gene, in gene, in gene	1	1	18.67	16.33	3	1_A375_pNL7_minus_lncRNA::1	24	Gene LSAMP	FLJ34254, FLJ35396, LSAMP, FLJ54658, FLJ37216, LAMP, IGLON3	limbic system-associated membrane protein	NM_002338, hCT2319616.1, hCT2344077.0, hCT2344078.0, hCT2344079.0	1570190_at, 214460_at	NP_002329.2, EAW79590.1, EAW79588.1, EAW79589.1, EAW79591.1
GeneID:57514	CDGAP	3	119,013,220	119,138,323	125,103	+	1	2_A375_pNL97_plus_lncRNA::1::5785	28764	in gene	0	1	9	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CDGAP	MGC138370, CDGAP, KIAA1204, MGC138368, ARHGAP31	Cdc42 GTPase-activating protein	NM_020754, hCT13668.2, hCT1971072.1	226056_at, 226057_at	NP_065805.2, EAW79573.1, EAW79574.1
GeneID:55254	TMEM39A	3	119,149,701	119,182,471	32,770	-	1	2_A375_pNL97_plus_lncRNA::1::5786	-25	upstream	0	1	15	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene TMEM39A	TMEM39A, FLJ10902	transmembrane protein 39A	NM_018266, hCT13664.3, hCT2319379.0	218615_s_at, 222690_s_at, 241392_at	NP_060736.1, EAW79571.1, EAW79572.1
GeneID:56983	KTELC1	3	119,187,785	119,213,555	25,770	+	1	2_A375_pNL97_plus_lncRNA::1::5786	-5289	upstream	0	1	15	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene KTELC1	CLP46, Rumi, hCLP46, MGC32995, KTELC1, MDSRP, MDS010, C3orf9, KDELCL1, POGLUT1	KTEL (Lys-Tyr-Glu-Leu) containing 1	NM_152305, NR_024265, hCT1818963.2	218587_s_at, 222681_at	NP_689518.1, EAW79570.1
GeneID:141	ADPRH	3	119,298,523	119,308,792	10,269	+	1	2_A375_pNL97_plus_lncRNA::1::5787	-27	upstream	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ADPRH	ARH1, ADPRH	ADP-ribosylarginine hydrolase	NM_001125, hCT11854.3, hCT2319573.0, hCT2319574.0	207863_at, 228042_at, 238505_at	NP_001116.1, EAW79563.1, EAW79561.1, EAW79562.1
GeneID:2932	GSK3B	3	119,540,800	119,813,264	272,464	-	1	1_A375_pNL7_minus_lncRNA::1::4025	-784	upstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene GSK3B	GSK3B		NM_002093, NM_001146156, hCT1960900.1, hCT2319591.0, hCT2319593.0, hCT2319594.0	209945_s_at	NP_002084.2, NP_001139628.1, EAW79533.1, EAW79534.1, EAW79535.1, EAW79536.1
GeneID:100506784	LOC100506784	3	119,814,477	119,817,871	3,394	+	1	1_A375_pNL7_minus_lncRNA::1::4025	-429	upstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LOC100506784		hypothetical LOC100506784	XR_112527, XR_108473, XR_113584		
GeneID:116064	LRRC58	3	120,043,576	120,068,186	24,610	-	1	2_A375_pNL97_plus_lncRNA::1::5788	250	in gene	0	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LRRC58	LRRC58	leucine rich repeat containing 58	NM_001099678	225479_at, 238506_at	NP_001093148.1
GeneID:100130701	LOC100130701	3	120,076,665	120,106,964	30,299	+	1	2_A375_pNL97_plus_lncRNA::1::5788	-8729	upstream	0	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100130701		hypothetical protein LOC100130701	XM_001715398, XM_001717180, XM_001717549		XP_001715450.2, XP_001717232.2, XP_001717601.2
GeneID:2960	GTF2E1	3	120,461,558	120,501,916	40,358	+	1	1_A375_pNL7_minus_lncRNA::1::4026	36474	in gene	1	0	25	13	1	1_A375_pNL7_minus_lncRNA::1	25	Gene GTF2E1	GTF2E1, TF2E1, TFIIE-A, FE	general transcription factor IIE, polypeptide 1, alpha 56kDa	NM_005513, hCT11858.3	205930_at	NP_005504.2, EAW79519.1
GeneID:9515	STXBP5L	3	120,627,050	121,143,608	516,558	+	1	2_A375_pNL97_plus_lncRNA::1::5789	86	in gene	0	1	16	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene STXBP5L	KIAA1006, LLGL4, STXBP5L	syntaxin binding protein 5-like	NM_014980	1568896_at, 215518_at	NP_055795.1
GeneID:10721	POLQ	3	121,150,273	121,264,853	114,580	-	1	1_A375_pNL7_minus_lncRNA::1::4027	149	in gene	1	0	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene POLQ	POLQ, DKFZp781A0112, POLH, PRO0327	polymerase (DNA directed), theta	NM_199420, hCT2319185.0, hCT2319186.0, hCT2319187.0, hCT2319188.0, hCT2355802.0	207746_at, 219510_at	NP_955452.3, EAW79510.1, EAW79511.1, EAW79512.1, EAW79513.1, EAW79514.1
GeneID:3836	KPNA1	3	122,140,748	122,233,786	93,038	-	2	1_A375_pNL7_minus_lncRNA::1::4028, 2_A375_pNL97_plus_lncRNA::1::5790	-230, 186	upstream, in gene	1	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene KPNA1	SRP1, NPI-1, KPNA1, RCH2, IPOA5	karyopherin alpha 1 (importin alpha 5)	NM_002264, NR_026698, hCT1644532.2, hCT2319232.0	202055_at, 202056_at, 202057_at, 202058_s_at, 202059_s_at, 213741_s_at	NP_002255.3, EAW79483.1, EAW79482.1
GeneID:10954	PDIA5	3	122,785,856	122,880,953	95,097	+	1	1_A375_pNL7_minus_lncRNA::1::4029	312	in gene	1	0	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene PDIA5	PDIR, FLJ30401, PDIA5	protein disulfide isomerase family A, member 5	NM_006810, NR_028444, hCT1968259.1, hCT2319550.0, hCT2319552.0, hCT2355842.0, hCT8258.4	203857_s_at	NP_006801.1, EAW79455.1, EAW79452.1, EAW79453.1, EAW79454.1, EAW79456.1
GeneID:26984	SEC22A	3	122,920,774	122,992,983	72,209	+	1	2_A375_pNL97_plus_lncRNA::1::5791	71462	in gene	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SEC22A	SEC22L2, SEC22A	SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	NM_012430, hCT1827079.2	218703_at	NP_036562.2, EAW79451.1
GeneID:111	ADCY5	3	123,003,399	123,167,392	163,993	-	2	1_A375_pNL7_minus_lncRNA::1::4030, 2_A375_pNL97_plus_lncRNA::1::5792	162032, 162016	in gene, in gene	1	1	34	41	1	2_A375_pNL97_plus_lncRNA::1	41	Gene ADCY5	AC5, ADCY5	adenylate cyclase 5	NM_183357, hCT9060.3	228182_at, 242891_at	NP_899200.1, EAW79450.1
GeneID:201562	PTPLB	3	123,213,363	123,303,924	90,561	-	1	2_A375_pNL97_plus_lncRNA::1::5793	-124	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene PTPLB	PTPLB, HACD2	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	NM_198402	212640_at, 227741_at	NP_940684.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100506826	LOC100506826	3	123,304,403	123,349,667	45,264	+	1	2_A375_pNL97_plus_lncRNA::1::5793	-355	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100506826		hypothetical LOC100506826	XR_112538, XR_108474, XR_113565		
GeneID:8997	KALRN	3	123,813,558	124,440,036	626,478	+	7	1_A375_pNL7_minus_lncRNA::1::4031, 1_A375_pNL7_minus_lncRNA::1::4032, 1_A375_pNL7_minus_lncRNA::1::4033, 1_A375_pNL7_minus_lncRNA::1::4034, 2_A375_pNL97_plus_lncRNA::1::5794, 2_A375_pNL97_plus_lncRNA::1::5795, 2_A375_pNL97_plus_lncRNA::1::5796	122970, 334410, 436330, 635669, 123018, 435754, 635770	in gene, in gene, in gene, downstream, in gene, in gene, downstream	1	1	22	22.6	5	2_A375_pNL97_plus_lncRNA::1	52	Gene KALRN	KALRN, FLJ12332, DUET, ARHGEF24, FLJ16196, FLJ16623, DUO, TRAD, FLJ16443, HAPIP	kalirin, RhoGEF kinase	NM_001024660, NM_003947, NR_028136, NM_007064	205635_at, 206078_at, 227750_at, 232717_at, 232756_at, 236651_at	NP_001019831.2, NP_003938.1, NP_008995.2
GeneID:100506841	LOC100506841	3	124,443,943	124,445,172	1,229	+	2	1_A375_pNL7_minus_lncRNA::1::4034, 2_A375_pNL97_plus_lncRNA::1::5796	5284, 5385	downstream, downstream	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100506841		hypothetical LOC100506841	XR_112537, XR_108475, XR_113566		
GeneID:7372	UMPS	3	124,449,213	124,468,120	18,907	+	2	1_A375_pNL7_minus_lncRNA::1::4034, 2_A375_pNL97_plus_lncRNA::1::5796	14, 115	in gene, in gene	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene UMPS	OPRT, UMPS	uridine monophosphate synthetase	NM_000373, NR_033434, NR_033437, hCT1819635.1, hCT2355960.0	202706_s_at, 202707_at, 215165_x_at	NP_000364.1, EAW79408.1, EAW79407.1
GeneID:100422864	MIR544B	3	124,451,286	124,451,363	77	+	2	1_A375_pNL7_minus_lncRNA::1::4034, 2_A375_pNL97_plus_lncRNA::1::5796	-2059, -1958	upstream, upstream	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MIR544B	MIR544B	microRNA 544b	NR_036088		
GeneID:3693	ITGB5	3	124,481,795	124,606,144	124,349	-	1	2_A375_pNL97_plus_lncRNA::1::5797	74352	in gene	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ITGB5	FLJ26658, ITGB5	integrin, beta 5	NM_002213, hCT2319106.0, hCT6657.3	201124_at, 201125_s_at, 214020_x_at, 214021_x_at	NP_002204.2, EAW79405.1, EAW79406.1
GeneID:57493	HEG1	3	124,684,554	124,774,802	90,248	-	1	2_A375_pNL97_plus_lncRNA::1::5798	69522	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene HEG1	HEG, MGC72175, HEG1, MSTP112, MST112, KIAA1237	HEG homolog 1 (zebrafish)	NM_020733	212822_at, 213069_at	NP_065784.1
GeneID:84561	SLC12A8	3	124,801,480	124,931,609	130,129	-	1	2_A375_pNL97_plus_lncRNA::1::5799	128729	in gene	0	1	6	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SLC12A8	FLJ23188, SLC12A8, CCC9, DKFZp686L18248	solute carrier family 12 (potassium/chloride transporters), member 8	NM_024628, hCT2319372.1, hCT2344021.1	219874_at	NP_078904.3, EAW79400.1, EAW79399.1
GeneID:7707	ZNF148	3	124,944,513	125,094,198	149,685	-	2	1_A375_pNL7_minus_lncRNA::1::4035, 2_A375_pNL97_plus_lncRNA::1::5800	-42, 22	upstream, in gene	1	1	27	23	1	1_A375_pNL7_minus_lncRNA::1	27	Gene ZNF148	ZBP-89, BERF-1, BFCOL1, ZNF148, HT-BETA, DKFZp686L18248, pHZ-52, ZFP148	zinc finger protein 148	NM_021964, hCT2355906.0, hCT2355907.0, hCT2355908.0, hCT2355909.0, hCT7502.3	203318_s_at, 203319_s_at	NP_068799.2, EAW79397.1, EAW79394.1, EAW79395.1, EAW79396.1, EAW79398.1
GeneID:8723	SNX4	3	125,165,494	125,239,058	73,564	-	1	1_A375_pNL7_minus_lncRNA::1::4036	66	in gene	1	0	14	13	1	1_A375_pNL7_minus_lncRNA::1	14	Gene SNX4	ATG24B, SNX4	sorting nexin 4	NM_003794, hCT1955477.2, hCT2319363.0, hCT2319364.0, hCT2319365.0	205329_s_at, 212652_s_at	NP_003785.1, EAW79390.1, EAW79391.1, EAW79392.1, EAW79393.1
GeneID:114885	OSBPL11	3	125,247,702	125,314,381	66,679	-	1	1_A375_pNL7_minus_lncRNA::1::4036	75389	downstream	1	0	14	13	1	1_A375_pNL7_minus_lncRNA::1	14	Gene OSBPL11	ORP11, TCCCIA00292, FLJ13164, FLJ13012, OSBP12, OSBPL11, ORP-11	oxysterol binding protein-like 11	NM_022776, hCT30330.4	218304_s_at, 222586_s_at, 229527_s_at	NP_073613.2, EAW79389.1
GeneID:152015	ROPN1B	3	125,688,028	125,702,297	14,269	+	1	2_A375_pNL97_plus_lncRNA::1::5801	6788	in gene	0	1	5	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ROPN1B	ROPN1B		NM_001012337	220425_x_at	NP_001012337.1
GeneID:28999	KLF15	3	126,061,478	126,076,236	14,758	-	1	2_A375_pNL97_plus_lncRNA::1::5803	1015	in gene	0	1	20	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene KLF15	KKLF, DKFZp779M1320, KLF15	Kruppel-like factor 15	NM_014079, hCT2319109.0	221302_at, 231015_at	NP_054798.1, EAW79367.1
GeneID:100506907	LOC100506907	3	126,082,705	126,112,485	29,780	-	1	2_A375_pNL97_plus_lncRNA::1::5803	37264	downstream	0	1	20	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506907		hypothetical LOC100506907	XR_112534, XR_108478, XR_113568		
GeneID:84303	CHCHD6	3	126,423,118	126,679,244	256,126	+	3	1_A375_pNL7_minus_lncRNA::1::4037, 2_A375_pNL97_plus_lncRNA::1::5804, 2_A375_pNL97_plus_lncRNA::1::5805	206951, -174, 207210	in gene, upstream, in gene	1	1	15	20.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene CHCHD6	CHCHD6, MGC13016	coiled-coil-helix-coiled-coil-helix domain containing 6	NM_032343, hCT1960345.1	224462_s_at	NP_115719.1, EAW79352.1
GeneID:100132461	LOC100132461	3	126,426,195	126,427,493	1,298	+	1	2_A375_pNL97_plus_lncRNA::1::5804	-3251	upstream	0	1	11	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100132461		hypothetical LOC100132461	XR_112533, XR_108479, XR_113569		
GeneID:5361	PLXNA1	3	126,707,437	126,756,235	48,798	+	1	1_A375_pNL7_minus_lncRNA::1::4038	-5805	upstream	1	0	22	16	1	1_A375_pNL7_minus_lncRNA::1	22	Gene PLXNA1	PLXNA1, NOVP, DKFZp761P19121, PLEXIN-A1, PLXN1, NOV	plexin A1	NM_032242, hCT1961630.0, hCT2321666.0, hCT32106.2	1556140_at, 221537_at, 221538_s_at	NP_115618.3, EAW79349.1, EAW79350.1, EAW79351.1
GeneID:131601	TPRA1	3	127,291,908	127,309,568	17,660	-	4	1_A375_pNL7_minus_lncRNA::1::4041, 1_A375_pNL7_minus_lncRNA::1::4042, 2_A375_pNL97_plus_lncRNA::1::5810, 2_A375_pNL97_plus_lncRNA::1::5811	-160, -7552, 64, -7680	upstream, upstream, in gene, upstream	1	1	28.5	30.5	2	2_A375_pNL97_plus_lncRNA::1	45	Gene TPRA1	TPRA1, FLJ32197, TMEM227, GPR175, TPRA40	transmembrane protein, adipocyte asscociated 1	NM_001136053, NM_016372, NM_001142646, hCT1956203.1, hCT1960840.0, hCT2319972.0, hCT2319974.0, hCT32104.3	218555_at	NP_001129525.1, NP_057456.2, NP_001136118.1, EAW79340.1, EAW79341.1, EAW79344.1, EAW79342.1, EAW79343.1
GeneID:4171	MCM2	3	127,317,253	127,341,279	24,026	+	4	1_A375_pNL7_minus_lncRNA::1::4041, 1_A375_pNL7_minus_lncRNA::1::4042, 2_A375_pNL97_plus_lncRNA::1::5810, 2_A375_pNL97_plus_lncRNA::1::5811	-7525, -133, -7749, -5	upstream, upstream, upstream, upstream	1	1	28.5	30.5	2	2_A375_pNL97_plus_lncRNA::1	45	Gene MCM2	cdc19, CCNL1, MITOTIN, MCM2, MGC10606, BM28, CDCL1, KIAA0030, D3S3194	minichromosome maintenance complex component 2	NM_004526, hCT30519.2	202107_s_at	NP_004517.2, EAW79339.1
GeneID:11343	MGLL	3	127,407,909	127,542,051	134,142	-	3	1_A375_pNL7_minus_lncRNA::1::4043, 2_A375_pNL97_plus_lncRNA::1::5812, 2_A375_pNL97_plus_lncRNA::1::5813	72499, 72195, 47395	in gene, in gene, in gene	1	1	15	17	2	2_A375_pNL97_plus_lncRNA::1	17	Gene MGLL	MGLL, HU-K5, HUK5, MGL, MAGL	monoglyceride lipase	NM_007283, NM_001003794, hCT2319960.0, hCT2319963.0, hCT32107.3	211026_s_at, 225102_at	NP_009214.1, NP_001003794.1, EAW79329.1, EAW79330.1, EAW79331.1
GeneID:29927	SEC61A1	3	127,771,212	127,790,526	19,314	+	2	1_A375_pNL7_minus_lncRNA::1::4044, 2_A375_pNL97_plus_lncRNA::1::5814	-684, -266	upstream, upstream	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SEC61A1	SEC61, SEC61A, SEC61A1, HSEC61	Sec61 alpha 1 subunit (S. cerevisiae)	NM_013336, hCT2320149.0, hCT2355820.0, hCT2355821.0, hCT31362.2	217716_s_at, 222385_x_at	NP_037468.1, EAW79327.1, EAW79324.1, EAW79325.1, EAW79326.1
GeneID:8607	RUVBL1	3	127,799,800	127,842,671	42,871	-	1	2_A375_pNL97_plus_lncRNA::1::5815	63	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene RUVBL1	INO80H, PONTIN, TIH1, TIP49, ECP54, Pontin52, TIP49A, RUVBL1, RVB1, NMP238	RuvB-like 1 (E. coli)	NM_003707, hCT1956201.1	201614_s_at	NP_003698.1, EAW79323.1
GeneID:60678	EEFSEC	3	127,872,313	128,127,489	255,176	+	2	1_A375_pNL7_minus_lncRNA::1::4045, 2_A375_pNL97_plus_lncRNA::1::5816	-153, 167	upstream, in gene	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene EEFSEC	EEFSEC, SELB, EFSEC	eukaryotic elongation factor, selenocysteine-tRNA-specific	NM_021937, hCT31361.2	227540_at	NP_068756.2, EAW79322.1
GeneID:2624	GATA2	3	128,198,265	128,212,030	13,765	-	1	2_A375_pNL97_plus_lncRNA::1::5817	5374	in gene	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene GATA2	NFE1B, GATA2, FLJ45948, MGC2306	GATA binding protein 2	NM_032638, NM_001145661, NM_001145662, hCT1967834.1, hCT2319198.0, hCT2319199.0, hCT2319201.0, hCT30520.2	207954_at, 209710_at, 210358_x_at	NP_116027.2, NP_001139133.1, NP_001139134.1, EAW79313.1, EAW79316.1, EAW79317.1, EAW79314.1, EAW79315.1
GeneID:100506995	LOC100506995	3	128,207,952	128,222,050	14,098	+	1	2_A375_pNL97_plus_lncRNA::1::5817	-1296	upstream	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506995		hypothetical LOC100506995	XR_112541, XR_108482, XR_113591		
GeneID:6184	RPN1	3	128,338,813	128,369,719	30,906	-	4	1_A375_pNL7_minus_lncRNA::1::4046, 1_A375_pNL7_minus_lncRNA::1::4047, 2_A375_pNL97_plus_lncRNA::1::5818, 2_A375_pNL97_plus_lncRNA::1::5819	32983, 204, 33015, 55	downstream, in gene, downstream, in gene	1	1	63.5	67.5	2	2_A375_pNL97_plus_lncRNA::1	116	Gene RPN1	RPN1, RBPH1, OST1, DKFZp686B16177	ribophorin I	NM_002950, hCT2319191.0, hCT2319193.0, hCT2355817.0, hCT31360.3	201011_at, 230862_at	NP_002941.1, EAW79306.1, EAW79307.1, EAW79308.1, EAW79309.1
GeneID:653712	LOC653712	3	128,580,351	128,590,384	10,033	-	2	1_A375_pNL7_minus_lncRNA::1::4048, 2_A375_pNL97_plus_lncRNA::1::5821	-8016, -8080	upstream, upstream	1	1	25	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene LOC653712		intraflagellar transport 122 homolog (Chlamydomonas) pseudogene	NR_034179		
GeneID:28976	ACAD9	3	128,598,333	128,631,957	33,624	+	2	1_A375_pNL7_minus_lncRNA::1::4048, 2_A375_pNL97_plus_lncRNA::1::5821	67, 131	in gene, in gene	1	1	25	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene ACAD9	ACAD9, NPD002, MGC14452, ACAD-9, FLJ23533	acyl-CoA dehydrogenase family, member 9	NM_014049, NR_033426, hCT2319512.0, hCT2319513.0, hCT2319514.0, hCT2355961.0	224160_s_at, 238976_at	NP_054768.2, EAW79293.1, EAW79294.1, EAW79295.1, EAW79296.1
GeneID:79825	CCDC48	3	128,720,472	128,759,585	39,113	+	1	1_A375_pNL7_minus_lncRNA::1::4049	25464	in gene	1	0	22	12	1	1_A375_pNL7_minus_lncRNA::1	22	Gene CCDC48	CCDC48, C3orf73, FLJ12053, DKFZp686B0146, FLJ12057, MGC138400	coiled-coil domain containing 48	NM_024768, hCT1819723.0	220006_at, 233259_at	NP_079044.2, EAW79286.1
GeneID:2815	GP9	3	128,779,645	128,781,253	1,608	+	2	1_A375_pNL7_minus_lncRNA::1::4050, 2_A375_pNL97_plus_lncRNA::1::5822	-6677, -6645	upstream, upstream	1	1	30	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene GP9	CD42a, GP9, GPIX	glycoprotein IX (platelet)	NM_000174, hCT9720.1	208683_x_at	NP_000165.1, EAW79285.1
GeneID:57461	ISY1	3	128,848,235	128,880,029	31,794	-	2	1_A375_pNL7_minus_lncRNA::1::4051, 2_A375_pNL97_plus_lncRNA::1::5823	-275, -195	upstream, upstream	1	1	22	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ISY1	ISY1, fSAP33, KIAA1160, FSAP33	ISY1 splicing factor homolog (S. cerevisiae)	NM_020701	223425_s_at, 223429_x_at, 223831_x_at	NP_065752.1
GeneID:7555	CNBP	3	128,886,658	128,902,810	16,152	-	2	1_A375_pNL7_minus_lncRNA::1::4051, 2_A375_pNL97_plus_lncRNA::1::5823	22506, 22586	downstream, downstream	1	1	22	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CNBP	ZCCHC22, PROMM, RNF163, CNBP, CNBP1, DM2, FLJ11631, ZNF9	CCHC-type zinc finger, nucleic acid binding protein	NM_003418, NM_001127192, NM_001127193, NM_001127194, NM_001127195, NM_001127196, hCT11072.2, hCT1962611.1, hCT1967757.1, hCT1967758.1, hCT2355646.0, hCT2355647.0, hCT2355648.0	206158_s_at	NP_003409.1, NP_001120664.1, NP_001120665.1, NP_001120666.1, NP_001120667.1, NP_001120668.1, EAW79271.1, EAW79272.1, EAW79273.1, EAW79274.1, EAW79275.1, EAW79276.1, EAW79277.1
GeneID:22820	COPG	3	128,968,453	128,996,616	28,163	+	2	1_A375_pNL7_minus_lncRNA::1::4052, 2_A375_pNL97_plus_lncRNA::1::5825	91, -133	in gene, upstream	1	1	19	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene COPG	COPG, FLJ21068, COPG1	coatomer protein complex, subunit gamma	NM_016128, hCT1830522.2, hCT2319524.0, hCT2355653.0, hCT2355654.0	217749_at	NP_057212.1, EAW79267.1, EAW79268.1, EAW79269.1, EAW79270.1
GeneID:8971	H1FX	3	129,033,614	129,035,120	1,506	-	1	2_A375_pNL97_plus_lncRNA::1::5826	-528	upstream	0	1	19	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene H1FX	MGC8350, H1X, H1FX, MGC15959	H1 histone family, member X	NM_006026, hCT2319276.0	204805_s_at, 231004_s_at	NP_006017.1, EAW79264.1
GeneID:339942	C3orf47	3	129,035,114	129,043,412	8,298	+	1	2_A375_pNL97_plus_lncRNA::1::5826	534	in gene	0	1	19	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C3orf47	C3orf47, FLJ34151, MGC126788	chromosome 3 open reading frame 47	NR_026991, hCT1960110.1	1558168_at	EAW79263.1
GeneID:677797	SNORA7B	3	129,116,053	129,116,191	138	-	2	1_A375_pNL7_minus_lncRNA::1::4053, 2_A375_pNL97_plus_lncRNA::1::5827	-2305, -2225	upstream, upstream	1	1	38	34	1	1_A375_pNL7_minus_lncRNA::1	38	Gene SNORA7B	SNORA7B, ACA7B	small nucleolar RNA, H/ACA box 7B	NR_002992		
GeneID:90288	C3orf25	3	129,120,164	129,147,494	27,330	-	2	1_A375_pNL7_minus_lncRNA::1::4053, 2_A375_pNL97_plus_lncRNA::1::5827	28998, 29078	downstream, downstream	1	1	38	34	1	1_A375_pNL7_minus_lncRNA::1	38	Gene C3orf25	C3orf25	chromosome 3 open reading frame 25	NM_207307, hCT1819732.2, hCT2355872.0	232639_at	NP_997190.1, EAW79256.1, EAW79257.1
GeneID:27032	ATP2C1	3	130,613,434	130,735,556	122,122	+	2	1_A375_pNL7_minus_lncRNA::1::4054, 2_A375_pNL97_plus_lncRNA::1::5830	132102, 131974	downstream, downstream	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ATP2C1	KIAA1347, SPCA1, BCPM, PMR1, ATP2C1, ATP2C1A, hSPCA1, HHD	ATPase, Ca++ transporting, type 2C, member 1	NM_014382, NM_001001485, NM_001001486, NM_001001487, hCT2319056.0, hCT2319058.0, hCT2319059.0, hCT5631.3	209934_s_at, 209935_at, 211137_s_at, 212255_s_at	NP_055197.2, NP_001001485.1, NP_001001486.1, NP_001001487.1, EAW79217.1, EAW79220.1, EAW79218.1, EAW79219.1
GeneID:28990	ASTE1	3	130,732,721	130,745,646	12,925	-	2	1_A375_pNL7_minus_lncRNA::1::4054, 2_A375_pNL97_plus_lncRNA::1::5830	110, 238	in gene, in gene	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ASTE1	ASTE1, MGC129960, HT001	asteroid homolog 1 (Drosophila)	NM_014065, hCT2319006.0, hCT2355822.0, hCT6819.2	221135_s_at	NP_054784.2, EAW79214.1, EAW79215.1, EAW79216.1
GeneID:79858	NEK11	3	130,745,694	131,069,309	323,615	+	2	1_A375_pNL7_minus_lncRNA::1::4054, 2_A375_pNL97_plus_lncRNA::1::5830	-158, -286	upstream, upstream	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene NEK11	NEK11, FLJ23495	NIMA (never in mitosis gene a)- related kinase 11	NM_024800, NM_001146003, NM_145910, hCT1960408.1, hCT2319061.0	1554380_at, 1555082_a_at, 219542_at	NP_079076.3, NP_001139475.1, NP_665917.1, EAW79212.1, EAW79213.1
GeneID:11222	MRPL3	3	131,181,045	131,221,829	40,784	-	1	2_A375_pNL97_plus_lncRNA::1::5831	-123	upstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MRPL3	RPML3, MRPL3, MRL3	mitochondrial ribosomal protein L3	NM_007208, hCT5827.3	208787_at	NP_009139.1, EAW79209.1
GeneID:131034	CPNE4	3	131,253,572	131,753,844	500,272	-	2	1_A375_pNL7_minus_lncRNA::1::4055, 2_A375_pNL97_plus_lncRNA::1::5832	-140, -204	upstream, upstream	1	1	24	22	1	1_A375_pNL7_minus_lncRNA::1	24	Gene CPNE4	COPN4, CPNE4, CPN4, MGC15604	copine IV	NM_130808, hCT2318978.1, hCT7219.3	228796_at, 231336_at	NP_570720.1, EAW79207.1, EAW79206.1
GeneID:23317	DNAJC13	3	132,136,553	132,257,876	121,323	+	1	1_A375_pNL7_minus_lncRNA::1::4056	-89	upstream	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene DNAJC13	RME8, FLJ25863, DNAJC13, KIAA0678	DnaJ (Hsp40) homolog, subfamily C, member 13	NM_015268, hCT2319040.0, hCT2319041.0	1560020_at, 1564627_at, 212467_at	NP_056083.3, EAW79198.1, EAW79199.1
GeneID:84129	ACAD11	3	132,276,982	132,378,975	101,993	-	2	1_A375_pNL7_minus_lncRNA::1::4057, 2_A375_pNL97_plus_lncRNA::1::5833	-193, -257	upstream, upstream	1	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ACAD11	ACAD11, FLJ12592, MGC150619	acyl-CoA dehydrogenase family, member 11	NM_032169, hCT2318990.0, hCT2318992.0, hCT6826.3	225573_at	NP_115545.3, EAW79194.1, EAW79193.1, EAW79195.1
GeneID:79876	UBA5	3	132,373,290	132,396,944	23,654	+	2	1_A375_pNL7_minus_lncRNA::1::4057, 2_A375_pNL97_plus_lncRNA::1::5833	5878, 5942	in gene, in gene	1	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene UBA5	FLJ23251UBA5, UBA5, THIFP1, UBE1DC1, FLJ17261, FLJ23251	ubiquitin-like modifier activating enzyme 5	NM_198329, NM_024818, hCT2319044.0, hCT2355895.0, hCT2355896.0, hCT6829.3	218289_s_at, 222578_s_at, 222579_at	NP_938143.1, NP_079094.1, EAW79189.1, EAW79190.1, EAW79191.1, EAW79192.1
GeneID:58477	SRPRB	3	133,502,877	133,540,336	37,459	+	1	2_A375_pNL97_plus_lncRNA::1::5834	21859	in gene	0	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SRPRB	SRPRB, APMCF1	signal recognition particle receptor, B subunit	NM_021203, hCT2320702.0, hCT2320703.0, hCT2320704.0	218140_x_at, 222532_at, 227737_at	NP_067026.3, EAW79160.1, EAW79161.1, EAW79162.1
GeneID:6578	SLCO2A1	3	133,651,540	133,748,920	97,380	-	1	2_A375_pNL97_plus_lncRNA::1::5835	85096	in gene	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SLCO2A1	SLCO2A1, OATP2A1, SLC21A2, MATR1, PGT	solute carrier organic anion transporter family, member 2A1	NM_005630, hCT1785403.1	204368_at	NP_005621.2, EAW79156.1
GeneID:100507224	LOC100507224	3	134,151,299	134,183,454	32,155	+	1	1_A375_pNL7_minus_lncRNA::1::4059	-4931	upstream	1	0	27	21	1	1_A375_pNL7_minus_lncRNA::1	27	Gene LOC100507224		hypothetical LOC100507224	XR_112555, XR_108490, XR_113518		
GeneID:25847	ANAPC13	3	134,196,546	134,204,865	8,319	-	2	1_A375_pNL7_minus_lncRNA::1::4060, 2_A375_pNL97_plus_lncRNA::1::5836	-223, 161	upstream, in gene	1	1	22	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene ANAPC13	SWM1, APC13, DKFZp566D193, ANAPC13	anaphase promoting complex subunit 13	NM_015391, NR_024400, NR_024401, hCT1645953.3, hCT1951507.1, hCT1951508.1, hCT1951509.1, hCT1964572.1, hCT2320462.0, hCT2320463.0	209001_s_at, 215282_at	NP_056206.1, EAW79143.1, EAW79144.1, EAW79145.1, EAW79146.1, EAW79149.1, EAW79147.1, EAW79148.1
GeneID:80254	CEP63	3	134,204,575	134,293,855	89,280	+	2	1_A375_pNL7_minus_lncRNA::1::4060, 2_A375_pNL97_plus_lncRNA::1::5836	513, 129	in gene, in gene	1	1	22	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene CEP63	CEP63, MGC78416, FLJ13386	centrosomal protein 63kDa	NM_001042383, NM_001042384, NM_025180, NM_001042400, hCT1951502.1, hCT2320708.0, hCT2320710.1, hCT2355859.0, hCT2355860.0, hCT2355861.0, hCT7122.3	219242_at, 222151_s_at, 233650_at	NP_001035842.1, NP_001035843.1, NP_079456.2, NP_001035859.1, EAW79136.1, EAW79139.1, EAW79137.1, EAW79138.1, EAW79140.1, EAW79141.1, EAW79142.1
GeneID:2047	EPHB1	3	134,514,099	134,979,309	465,210	+	5	1_A375_pNL7_minus_lncRNA::1::4061, 1_A375_pNL7_minus_lncRNA::1::4062, 1_A375_pNL7_minus_lncRNA::1::4063, 2_A375_pNL97_plus_lncRNA::1::5837, 2_A375_pNL97_plus_lncRNA::1::5838	-187, 311405, 330093, 311421, 330125	upstream, in gene, in gene, in gene, in gene	1	1	27	23	3	1_A375_pNL7_minus_lncRNA::1	41	Gene EPHB1	NET, ELK, EPHT2, Hek6, FLJ37986, EPHB1	EPH receptor B1	NM_004441, hCT1642722.3, hCT2318923.0, hCT2318924.0	210753_s_at, 211898_s_at, 230425_at	NP_004432.1, EAW79127.1, EAW79128.1, EAW79129.1
GeneID:5523	PPP2R3A	3	135,684,515	135,866,752	182,237	+	4	1_A375_pNL7_minus_lncRNA::1::4065, 1_A375_pNL7_minus_lncRNA::1::4066, 2_A375_pNL97_plus_lncRNA::1::5840, 2_A375_pNL97_plus_lncRNA::1::5841	-259, 509, -195, 5213	upstream, in gene, upstream, in gene	1	1	17	18	2	1_A375_pNL7_minus_lncRNA::1	19	Gene PPP2R3A	PPP2R3, PR72, PR130, PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	NM_001190447, NM_002718, NM_181897, hCT2318964.0, hCT2318965.0, hCT2318966.0, hCT2318967.0, hCT2318968.0	207749_s_at, 209632_at, 209633_at	NP_001177376.1, NP_002709.2, NP_871626.1, EAW79124.1, EAW79125.1, EAW79126.1, EAW79122.1, EAW79123.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:55167	MSL2	3	135,867,760	135,914,688	46,928	-	3	1_A375_pNL7_minus_lncRNA::1::4067, 2_A375_pNL97_plus_lncRNA::1::5642, 2_A375_pNL97_plus_lncRNA::1::5643	-912, 224, -757	upstream, in gene, upstream	1	1	18.5	20	2	1_A375_pNL7_minus_lncRNA::1	22	Gene MSL2	MSL2L1, MSL-2, MSL2, FLJ10546, FLJ54913, RNF184, KIAA1585	male-specific lethal 2 homolog (Drosophila)	NM_018133, NM_001145417, hCT2318933.0, hCT6255.3	218733_at	NP_060603.2, NP_001138889.1, EAW79119.1, EAW79120.1
GeneID:5096	PCCB	3	135,969,167	136,049,013	79,846	+	1	1_A375_pNL7_minus_lncRNA::1::4068	145	in gene	1	0	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene PCCB	DKFZp451E113, PCCB	propionyl CoA carboxylase, beta polypeptide	NM_000532, NM_001178014, hCT2318973.1, hCT2355927.0, hCT6256.4	1557502_at, 212694_s_at	NP_000523.2, NP_001171485.1, EAW79116.1, EAW79117.1, EAW79118.1
GeneID:80723	TMEM22	3	136,537,861	136,574,734	36,873	+	3	1_A375_pNL7_minus_lncRNA::1::4069, 2_A375_pNL97_plus_lncRNA::1::5644, 2_A375_pNL97_plus_lncRNA::1::5645	1323, 1019, 43227	in gene, in gene, downstream	1	1	18.5	25	2	2_A375_pNL97_plus_lncRNA::1	31	Gene TMEM22	DKFZp564K2464, TMEM22, MGC3295	transmembrane protein 22	NM_001097600, NM_025246, NM_001097599, hCT1646469.3, hCT1951506.1, hCT1964570.1	219569_s_at	NP_001091069.1, NP_079522.2, NP_001091068.1, EAW79111.1, EAW79112.1, EAW79113.1
GeneID:100507239	LOC100507239	3	136,560,818	136,580,902	20,084	-	1	2_A375_pNL97_plus_lncRNA::1::5645	-186	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100507239		hypothetical LOC100507239	XR_112564, XR_112562, XR_112563, XR_108493, XR_108491, XR_108492, XR_113521, XR_113519, XR_113520		
GeneID:4690	NCK1	3	136,581,050	136,667,968	86,918	+	1	2_A375_pNL97_plus_lncRNA::1::5645	38	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene NCK1	NCKalpha, MGC12668, NCK, NCK1	NCK adaptor protein 1	NM_001190796, NM_006153, hCT2318878.0, hCT2344065.0, hCT2344066.0, hCT2344067.0, hCT2344068.0	204725_s_at, 211063_s_at, 229895_s_at	NP_001177725.1, NP_006144.1, EAW79105.1, EAW79106.1, EAW79107.1, EAW79108.1, EAW79109.1
GeneID:199221	DZIP1L	3	137,780,827	137,834,451	53,624	-	2	1_A375_pNL7_minus_lncRNA::1::4070, 2_A375_pNL97_plus_lncRNA::1::5646	99, 195	in gene, in gene	1	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene DZIP1L	DZIP1L, DZIP2, FLJ32844	DAZ interacting protein 1-like	NM_173543, NM_001170538, hCT2318830.1, hCT2318832.1, hCT2318834.2, hCT2344060.0, hCT2344061.1, hCT2351293.0	239785_at	NP_775814.2, NP_001164009.1, EAW79085.1, EAW79087.1, EAW79088.1, EAW79090.1, EAW79086.1, EAW79089.1
GeneID:51146	A4GNT	3	137,842,560	137,851,229	8,669	-	2	1_A375_pNL7_minus_lncRNA::1::4070, 2_A375_pNL97_plus_lncRNA::1::5646	16877, 16973	downstream, downstream	1	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene A4GNT	MGC149493, alpha4GnT, A4GNT	alpha-1,4-N-acetylglucosaminyltransferase	NM_016161, hCT7083.3	221131_at	NP_057245.1, EAW79084.1
GeneID:25852	ARMC8	3	137,906,148	138,016,219	110,071	+	1	2_A375_pNL97_plus_lncRNA::1::5647	135	in gene	0	1	14	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ARMC8	ARMC8, HSPC056, MGC10058, MGC4880, S863-2	armadillo repeat containing 8	NM_213654, NM_014154, NM_015396, hCT1951512.1, hCT1961935.1, hCT1961936.1, hCT2319292.0, hCT2319294.0, hCT2319297.0, hCT2319298.0, hCT2355855.0	1555279_at, 1555281_x_at, 203486_s_at, 203487_s_at, 219094_at, 236966_at, 244528_at	NP_998819.1, NP_054873.2, NP_056211.2, EAW79076.1, EAW79077.1, EAW79081.1, EAW79075.1, EAW79078.1, EAW79079.1, EAW79080.1, EAW79082.1
GeneID:22808	MRAS	3	138,066,625	138,124,377	57,752	+	2	1_A375_pNL7_minus_lncRNA::1::4071, 2_A375_pNL97_plus_lncRNA::1::5648	575, 383	in gene, in gene	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MRAS	M-RAs, FLJ42964, MRAS, RRAS3, R-RAS3	muscle RAS oncogene homolog	NM_001085049, NM_012219, hCT1951513.1, hCT1951514.1, hCT2319301.0, hCT8152.3	206538_at, 225185_at	NP_001078518.1, NP_036351.3, EAW79068.1, EAW79069.1, EAW79070.1, EAW79071.1
GeneID:80321	CEP70	3	138,213,186	138,313,129	99,943	-	1	2_A375_pNL97_plus_lncRNA::1::5649	-247	upstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene CEP70	CEP70, FLJ13036, BITE	centrosomal protein 70kDa	NM_024491, hCT1951516.1, hCT2318815.0, hCT2355866.0, hCT8269.3	1554468_at, 1554469_a_at, 219036_at, 224150_s_at, 238154_at	NP_077817.2, EAW79060.1, EAW79061.1, EAW79062.1, EAW79063.1
GeneID:55179	FAIM	3	138,327,542	138,352,218	24,676	+	1	2_A375_pNL97_plus_lncRNA::1::5650	-22	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene FAIM	FAIM1, FAIM	Fas apoptotic inhibitory molecule	NM_018147, NM_001033032, NM_001033030, NM_001033031, hCT1951517.1, hCT2319307.0, hCT8270.3	220643_s_at	NP_060617.1, NP_001028204.1, NP_001028202.1, NP_001028203.1, EAW79058.1, EAW79059.1, EAW79057.1
GeneID:64084	CLSTN2	3	139,654,027	140,286,919	632,892	+	2	1_A375_pNL7_minus_lncRNA::1::4075, 2_A375_pNL97_plus_lncRNA::1::5655	271701, 358149	in gene, in gene	1	1	18.5	15	2	1_A375_pNL7_minus_lncRNA::1	23	Gene CLSTN2	FLJ39113, CSTN2, CDHR13, ALC-GAMMA, CS2, MGC119560, CLSTN2, alcagamma, FLJ39499	calsyntenin 2	NM_022131, hCT2319018.0, hCT2355885.0, hCT7091.3	219414_at	NP_071414.2, EAW79016.1, EAW79017.1, EAW79018.1
GeneID:55186	SLC25A36	3	140,660,662	140,698,785	38,123	+	1	1_A375_pNL7_minus_lncRNA::1::4077	106	in gene	1	0	13	11	1	1_A375_pNL7_minus_lncRNA::1	13	Gene SLC25A36	SLC25A36, DKFZp564C053, FLJ10618	solute carrier family 25, member 36	NM_001104647, NM_018155, hCT2319015.0, hCT2355801.0, hCT8654.3	201917_s_at, 201918_at, 201919_at, 223698_at, 237741_at	NP_001098117.1, NP_060625.2, EAW79011.1, EAW79012.1, EAW79013.1
GeneID:92370	ACPL2	3	140,950,682	141,013,486	62,804	+	3	2_A375_pNL97_plus_lncRNA::1::5657, 1_A375_pNL7_minus_lncRNA::1::4078, 2_A375_pNL97_plus_lncRNA::1::5658	8566, 70758, 70918	in gene, downstream, downstream	1	1	13	19	2	2_A375_pNL97_plus_lncRNA::1	22	Gene ACPL2	ACPL2, FLJ23751	acid phosphatase-like 2	NM_001037172, NM_152282, hCT2318937.0, hCT2355795.0, hCT8652.3	226925_at, 239475_at	NP_001032249.1, NP_689495.1, EAW79007.1, EAW79008.1, EAW79009.1
GeneID:253461	ZBTB38	3	141,043,055	141,168,634	125,579	+	5	1_A375_pNL7_minus_lncRNA::1::4079, 1_A375_pNL7_minus_lncRNA::1::4080, 2_A375_pNL97_plus_lncRNA::1::5660, 2_A375_pNL97_plus_lncRNA::1::5661, 2_A375_pNL97_plus_lncRNA::1::5662	43185, 43873, 11409, 43281, 44177	in gene, in gene, in gene, in gene, in gene	1	1	13	18	2	2_A375_pNL97_plus_lncRNA::1	18	Gene ZBTB38	FLJ22332, FLJ31131, ZNF921, CIBZ, FLJ35036, ZBTB38	zinc finger and BTB domain containing 38	NM_001080412	1558733_at, 219221_at, 225512_at, 230754_at, 236557_at	NP_001073881.2
GeneID:5922	RASA2	3	141,205,926	141,331,197	125,271	+	1	2_A375_pNL97_plus_lncRNA::1::5663	602	in gene	0	1	12	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene RASA2	GAP1M, RASA2	RAS p21 protein activator 2	NM_006506, hCT1961930.1, hCT7092.4	206636_at, 230669_at	NP_006497.2, EAW78998.1, EAW78999.1
GeneID:9616	RNF7	3	141,457,051	141,465,243	8,192	+	2	1_A375_pNL7_minus_lncRNA::1::4081, 2_A375_pNL97_plus_lncRNA::1::5664	5, -11	in gene, upstream	1	1	23	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene RNF7	ROC2, RNF7, CKBBP1, SAG	ring finger protein 7	NM_183237, NM_014245, hCT1951510.1, hCT1951511.1, hCT2318947.0, hCT2318949.0, hCT2355942.0, hCT7578.3	218286_s_at, 224394_at, 224395_s_at, 224439_x_at, 239620_at	NP_899060.1, NP_055060.1, EAW78991.1, EAW78992.1, EAW78993.1, EAW78994.1, EAW78995.1, EAW78996.1
GeneID:7029	TFDP2	3	141,663,270	141,868,386	205,116	-	3	1_A375_pNL7_minus_lncRNA::1::4082, 2_A375_pNL97_plus_lncRNA::1::5665, 2_A375_pNL97_plus_lncRNA::1::5666	209186, 209170, 98	downstream, downstream, in gene	1	1	16	15	2	1_A375_pNL7_minus_lncRNA::1	21	Gene TFDP2	DP2, FLJ39131, Dp-2, DKFZp313O196, TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	NM_001178138, NM_001178139, NM_001178140, NM_001178141, NM_001178142, NM_006286, hCT1951526.1, hCT1951527.1, hCT2318695.0, hCT2318696.0, hCT2355963.0	203588_s_at, 203589_s_at, 226157_at	NP_001171609.1, NP_001171610.1, NP_006277.1, NP_001171611.1, NP_001171612.1, NP_001171613.1, EAW78977.1, EAW78978.1, EAW78979.1, EAW78980.1, EAW78981.1
GeneID:256356	GK5	3	141,876,369	141,944,449	68,080	-	1	2_A375_pNL97_plus_lncRNA::1::5666	76161	downstream	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene GK5	FLJ45739, FLJ33582, MGC40579, GK5	glycerol kinase 5 (putative)	NM_001039547, NR_033289, hCT1826043.3, hCT2355910.0, hCT2355911.0	1553772_at, 238121_at, 241364_x_at	NP_001034636.1, EAW78976.1, EAW78974.1, EAW78975.1
GeneID:545	ATR	3	142,168,077	142,297,668	129,591	-	2	1_A375_pNL7_minus_lncRNA::1::4083, 2_A375_pNL97_plus_lncRNA::1::5667	-12, -28	upstream, upstream	1	1	49	53	1	2_A375_pNL97_plus_lncRNA::1	53	Gene ATR	SCKL, SCKL1, ATR, FRP1, MEC1	ataxia telangiectasia and Rad3 related	NM_001184, hCT1951523.1, hCT2318691.0	209902_at	NP_001175.2, EAW78970.1, EAW78969.1
GeneID:5357	PLS1	3	142,315,229	142,432,506	117,277	+	1	2_A375_pNL97_plus_lncRNA::1::5668	51	in gene	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PLS1	Plastin-1, FIMBRIN, PLS1	plastin 1 (I isoform)	NM_002670, NM_001145319, NM_001172312, hCT13076.2, hCT1952058.0, hCT2319535.0	205190_at	NP_002661.2, NP_001138791.1, NP_001165783.1, EAW78965.1, EAW78966.1, EAW78967.1
GeneID:26577	PCOLCE2	3	142,536,702	142,608,045	71,343	-	2	2_A375_pNL97_plus_lncRNA::1::5669, 2_A375_pNL97_plus_lncRNA::1::5670	1037, -7134	in gene, upstream	0	1	12.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene PCOLCE2	PCPE2, PCOLCE2	procollagen C-endopeptidase enhancer 2	NM_013363, hCT12595.2, hCT2318687.0	219295_s_at	NP_037495.1, EAW78961.1, EAW78962.1
GeneID:100289361	LOC100289361	3	142,719,687	142,720,309	622	-	2	1_A375_pNL7_minus_lncRNA::1::4085, 2_A375_pNL97_plus_lncRNA::1::5671	-75, 5	upstream, in gene	1	1	38	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene LOC100289361		hypothetical LOC100289361	NR_034032		
GeneID:23350	SR140	3	142,720,372	142,779,567	59,195	+	2	1_A375_pNL7_minus_lncRNA::1::4085, 2_A375_pNL97_plus_lncRNA::1::5671	12, -68	in gene, upstream	1	1	38	42	1	2_A375_pNL97_plus_lncRNA::1	42	Gene SR140	SR140, KIAA0332, MGC133197, fSAPa, U2SURP	U2 snRNP-associated SURP domain containing	NM_001080415	212058_at, 212060_at, 212061_at, 236431_at, 236696_at	NP_001073884.1
GeneID:285195	SLC9A9	3	142,984,064	143,567,373	583,309	-	3	1_A375_pNL7_minus_lncRNA::1::4086, 2_A375_pNL97_plus_lncRNA::1::5672, 2_A375_pNL97_plus_lncRNA::1::5673	161645, 405773, 161741	in gene, in gene, in gene	1	1	16	17.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene SLC9A9	Nbla00118, FLJ35613, NHE9, AUTS16, SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	NM_173653, hCT2343785.0, hCT2343786.0	227791_at, 242587_at	NP_775924.1, EAW78950.1, EAW78951.1
GeneID:205428	C3orf58	3	143,690,640	143,711,210	20,570	+	6	1_A375_pNL7_minus_lncRNA::1::4087, 1_A375_pNL7_minus_lncRNA::1::4088, 1_A375_pNL7_minus_lncRNA::1::4089, 2_A375_pNL97_plus_lncRNA::1::5674, 2_A375_pNL97_plus_lncRNA::1::5675, 2_A375_pNL97_plus_lncRNA::1::5676	-688, 160, 1072, -785, 672, 1520	upstream, in gene, in gene, upstream, in gene, in gene	1	1	15.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene C3orf58	MGC33365, DIA1, C3orf58	chromosome 3 open reading frame 58	NM_173552, NM_001134470, hCT1964553.2, hCT1964554.1, hCT5806.3	226464_at, 228079_at, 235653_at	NP_775823.1, NP_001127942.1, EAW78946.1, EAW78947.1, EAW78948.1
GeneID:5352	PLOD2	3	145,787,227	145,879,282	92,055	-	1	2_A375_pNL97_plus_lncRNA::1::5677	29378	in gene	0	1	7	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene PLOD2	LH2, PLOD2, TLH	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	NM_182943, NM_000935, hCT2318729.0, hCT2355805.0, hCT7119.3	202619_s_at, 202620_s_at	NP_891988.1, NP_000926.2, EAW78939.1, EAW78940.1, EAW78941.1
GeneID:57088	PLSCR4	3	145,910,122	145,968,966	58,844	-	1	2_A375_pNL97_plus_lncRNA::1::5678	390	in gene	0	1	10	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PLSCR4	PLSCR4, TRA1	phospholipid scramblase 4	NM_020353, NM_001128306, NM_001177304, NR_033438, NR_033439, hCT1961934.1, hCT2355928.0, hCT2355929.0, hCT7840.3	218901_at	NP_065086.2, NP_001121778.1, NP_001170775.1, EAW78935.1, EAW78937.1, EAW78938.1, EAW78936.1
GeneID:57047	PLSCR2	3	146,151,082	146,213,722	62,640	-	1	1_A375_pNL7_minus_lncRNA::1::4090	-8038	upstream	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene PLSCR2	PLSCR2		NM_020359, hCT1640638.2, hCT2318561.0	207374_at	NP_065092.1, EAW78932.1, EAW78931.1
GeneID:2992	GYG1	3	148,709,195	148,745,456	36,261	+	1	1_A375_pNL7_minus_lncRNA::1::4091	19361	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene GYG1	GYG, GYG1, GSD15	glycogenin 1	NM_001184720, NM_001184721, NM_004130, hCT12297.2, hCT1952050.0, hCT1963020.1, hCT1963021.1, hCT1963022.1, hCT2318603.0, hCT2318607.0, hCT2318610.0	201554_x_at, 211275_s_at	NP_001171649.1, NP_001171650.1, NP_004121.2, EAW78895.1, EAW78896.1, EAW78898.1, EAW78894.1, EAW78897.1, EAW78899.1, EAW78900.1, EAW78901.1
GeneID:6596	HLTF	3	148,747,904	148,804,341	56,437	-	1	2_A375_pNL97_plus_lncRNA::1::5680	-171	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene HLTF	SMARCA3, HLTF1, HLTF, SNF2L3, HIP116, ZBU1, RNF80, HIP116A	helicase-like transcription factor	NM_139048, NM_003071, hCT12299.3, hCT1952051.1, hCT2318582.0, hCT2318584.0, hCT2355905.0	202983_at	NP_620636.1, NP_003062.2, EAW78889.1, EAW78890.1, EAW78892.1, EAW78893.1, EAW78891.1
GeneID:84343	HPS3	3	148,847,371	148,891,305	43,934	+	2	2_A375_pNL97_plus_lncRNA::1::5681, 2_A375_pNL97_plus_lncRNA::1::5682	149, 50837	in gene, downstream	0	1	15	21	2	2_A375_pNL97_plus_lncRNA::1	23	Gene HPS3	DKFZp686F0413, SUTAL, FLJ22704, HPS3	Hermansky-Pudlak syndrome 3	NM_032383, hCT1826064.2, hCT2318612.0, hCT2318614.0, hCT2318615.0	227139_s_at, 231121_at, 235539_at	NP_115759.2, EAW78886.1, EAW78885.1, EAW78887.1, EAW78888.1
GeneID:1356	CP	3	148,890,286	148,939,832	49,546	-	1	2_A375_pNL97_plus_lncRNA::1::5682	41624	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CP	CP-2, CP	ceruloplasmin (ferroxidase)	NM_000096, hCT1820064.2, hCT2318579.0, hCT2355814.0	1558034_s_at, 204846_at, 227253_at	NP_000087.1, EAW78882.1, EAW78883.1, EAW78884.1
GeneID:4071	TM4SF1	3	149,086,805	149,095,568	8,763	-	1	1_A375_pNL7_minus_lncRNA::1::4092	-9120	upstream	1	0	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene TM4SF1	H-L6, L6, TM4SF1, TAAL6, M3S1	transmembrane 4 L six family member 1	NM_014220, hCT12304.3, hCT1965325.1, hCT2318572.0	209386_at, 209387_s_at, 215033_at, 215034_s_at, 238168_at	NP_055035.1, EAW78875.1, EAW78874.1, EAW78876.1
GeneID:25937	WWTR1	3	149,235,022	149,421,060	186,038	-	3	1_A375_pNL7_minus_lncRNA::1::4093, 1_A375_pNL7_minus_lncRNA::1::4094, 2_A375_pNL97_plus_lncRNA::1::5683	45316, 24740, 24788	in gene, in gene, in gene	1	1	16.5	19	2	2_A375_pNL97_plus_lncRNA::1	23	Gene WWTR1	FLJ27004, FLJ45718, DKFZp586I1419, TAZ, WWTR1	WW domain containing transcription regulator 1	NM_015472, NM_001168278, NM_001168280, hCT12303.3, hCT2319086.0	202132_at, 202133_at, 202134_s_at	NP_056287.1, NP_001161750.1, NP_001161752.1, EAW78868.1, EAW78869.1
GeneID:51122	COMMD2	3	149,456,257	149,470,286	14,029	-	2	1_A375_pNL7_minus_lncRNA::1::4095, 2_A375_pNL97_plus_lncRNA::1::5684	78, 14	in gene, in gene	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene COMMD2	MGC57611, COMMD2, HSPC042	COMM domain containing 2	NM_016094, hCT10727.3, hCT1952616.1	223491_at	NP_057178.2, EAW78867.1, EAW78866.1
GeneID:389161	C3orf16	3	149,478,887	149,510,610	31,723	-	2	1_A375_pNL7_minus_lncRNA::1::4095, 2_A375_pNL97_plus_lncRNA::1::5684	40402, 40338	downstream, downstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene C3orf16	FLJ40759, C3orf16	chromosome 3 open reading frame 16	NM_001144960	1561927_at, 1561928_s_at	NP_001138432.1
GeneID:11342	RNF13	3	149,530,475	149,679,926	149,451	+	4	1_A375_pNL7_minus_lncRNA::1::4096, 1_A375_pNL7_minus_lncRNA::1::4097, 2_A375_pNL97_plus_lncRNA::1::5685, 2_A375_pNL97_plus_lncRNA::1::5686	1413, 158677, 373, 158693	in gene, downstream, in gene, downstream	1	1	16	19.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene RNF13	FLJ93817, RNF13, MGC13689, RZF	ring finger protein 13	NM_183381, NM_007282, hCT12430.3, hCT1952052.1, hCT2319138.0, hCT2319140.0, hCT2355823.0, hCT2355824.0	201779_s_at, 201780_s_at	NP_899237.1, NP_009213.1, EAW78859.1, EAW78860.1, EAW78861.1, EAW78863.1, EAW78858.1, EAW78862.1
GeneID:5217	PFN2	3	149,682,691	149,688,741	6,050	-	2	1_A375_pNL7_minus_lncRNA::1::4097, 2_A375_pNL97_plus_lncRNA::1::5686	-411, -427	upstream, upstream	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PFN2	D3S1319E, PFL, PFN2	profilin 2	NM_002628, NM_053024, hCT12431.3, hCT1952053.1, hCT1963023.1, hCT1965326.1, hCT2319075.0, hCT2319076.0, hCT2319080.0	204992_s_at	NP_002619.1, NP_444252.1, EAW78852.1, EAW78853.1, EAW78854.1, EAW78855.1, EAW78850.1, EAW78851.1, EAW78856.1
GeneID:646903	LOC646903	3	149,689,066	149,691,029	1,963	+	2	1_A375_pNL7_minus_lncRNA::1::4097, 2_A375_pNL97_plus_lncRNA::1::5686	86, 102	in gene, in gene	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC646903		hypothetical LOC646903	NR_036536	237116_at	
GeneID:653659	TMEM183B	3	149,699,448	149,701,153	1,705	-	1	2_A375_pNL97_plus_lncRNA::1::5686	11985	downstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TMEM183B	C1orf37-DUP, TMEM183B	transmembrane protein 183B	NM_001079809	212165_at	NP_001073277.1
GeneID:9819	TSC22D2	3	150,126,788	150,177,631	50,843	+	2	1_A375_pNL7_minus_lncRNA::1::4098, 2_A375_pNL97_plus_lncRNA::1::5689	-132, -612	upstream, upstream	1	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TSC22D2	TILZ4a, TILZ4c, KIAA0669, TILZ4b, TSC22D2	TSC22 domain family, member 2	NM_014779, hCT12432.2, hCT1952054.1, hCT1952055.1, hCT2319152.0, hCT2319153.0	204094_s_at, 210953_at, 210954_s_at, 215547_at	NP_055594.1, EAW78839.1, EAW78837.1, EAW78838.1, EAW78840.1, EAW78841.1
GeneID:27230	SERP1	3	150,259,780	150,264,428	4,648	-	2	1_A375_pNL7_minus_lncRNA::1::4099, 2_A375_pNL97_plus_lncRNA::1::5690	76, 12	in gene, in gene	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SERP1	MGC133321, RAMP4, MGC133322, MGC117327, SERP1	stress-associated endoplasmic reticulum protein 1	NM_014445, hCT12434.3, hCT1952056.1, hCT1952057.1, hCT2319067.0	200969_at, 200970_s_at, 200971_s_at, 235475_at	NP_055260.1, EAW78836.1, EAW78833.1, EAW78834.1, EAW78835.1
GeneID:83939	EIF2A	3	150,264,574	150,303,803	39,229	+	2	1_A375_pNL7_minus_lncRNA::1::4099, 2_A375_pNL97_plus_lncRNA::1::5690	-222, -158	upstream, upstream	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene EIF2A	MSTP089, EIF-2A, EIF2A, MST089, CDA02, MSTP004	eukaryotic translation initiation factor 2A, 65kDa	NM_032025, hCT1825728.2, hCT2319156.0, hCT2355785.0	223015_at	NP_114414.2, EAW78831.1, EAW78830.1, EAW78832.1
GeneID:51714	SELT	3	150,321,066	150,348,234	27,168	+	2	1_A375_pNL7_minus_lncRNA::1::4100, 2_A375_pNL97_plus_lncRNA::1::5691	246, 206	in gene, in gene	1	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene SELT		selenoprotein T	NM_016275, hCT11995.3, hCT1952047.1, hCT2319158.0	217811_at, 225561_at	NP_057359.2, EAW78827.1, EAW78828.1, EAW78829.1
GeneID:6478	SIAH2	3	150,458,910	150,481,263	22,353	-	1	2_A375_pNL97_plus_lncRNA::1::5692	-337	upstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SIAH2	hSiah2, SIAH2	seven in absentia homolog 2 (Drosophila)	NM_005067, hCT10728.3	209339_at	NP_005058.3, EAW78821.1
GeneID:116931	MED12L	3	150,804,676	151,154,465	349,789	+	3	1_A375_pNL7_minus_lncRNA::1::4101, 2_A375_pNL97_plus_lncRNA::1::5693, 2_A375_pNL97_plus_lncRNA::1::5694	309100, 309068, 358524	in gene, in gene, downstream	1	1	17.5	20.5	2	1_A375_pNL7_minus_lncRNA::1	24	Gene MED12L	TRALP, NOPAR, MED12L, TNRC11L, TRALPUSH, FLJ46288, KIAA1635	mediator complex subunit 12-like	NM_053002, hCT1952049.2, hCT2318513.1, hCT2355903.0	1555300_a_at, 232114_at	NP_443728.3, EAW78800.1, EAW78801.1, EAW78802.1
GeneID:285313	IGSF10	3	151,153,778	151,176,497	22,719	-	1	2_A375_pNL97_plus_lncRNA::1::5694	13297	in gene	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene IGSF10	CMF608, IGSF10, FLJ25972	immunoglobulin superfamily, member 10	NM_001178145, NM_001178146, NM_178822, hCT11998.2, hCT2355889.0	1556579_s_at, 230670_at	NP_001171616.1, NP_001171617.1, NP_849144.2, EAW78798.1, EAW78799.1
GeneID:401093	hCG_1806964	3	151,980,405	151,987,415	7,010	-	3	1_A375_pNL7_minus_lncRNA::1::4103, 2_A375_pNL97_plus_lncRNA::1::5696, 2_A375_pNL97_plus_lncRNA::1::5697	11031, 2903, 311	downstream, in gene, in gene	1	1	14.67	16	3	1_A375_pNL7_minus_lncRNA::1	23	Gene hCG_1806964	LOC401093, FLJ79414	hypothetical LOC401093	NR_027037, NR_027038	232298_at, 235173_at	



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Counts	Intervals	Intervals Details	Intervals Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alts/probs	Full Description	RNA	Alts Tag	PROT
Gene:ID:4154	MBNL1	3	151,955,829	152,153,899	197,740	+	3	1_A7S_sNL97_dtvs/s_lncRNA:1-1:4163, 2_A7S_sNL97_dtvs_lncRNA:1:5596, 2_A7S_sNL97_dtvs_lncRNA:1:5697	5443, - 1317, 1275	upstream, upstream, ut gene		1	1	14.67	16	3	1_A7S_sNL7_dtvs/s_blC RNA:1	23	Gene MBNL1	DKFZp686F09174, EXP40, EXP, MBNL1, MBNL, EXP42, KIAA0428, EXP38	Alu/click-like-like (Drosophila)	NM_021038, NM_207292, NM_207293, NM_207294, NM_207295, NM_207297, XCT19174.3, XCT23192117.0, XCT23193119.0, XCT23193200.0, XCT23193221.0, XCT23193222.0, XCT23193223.0, XCT23986030.0, XCT23986040.0	NM_021038_at, NM_207292_at, NM_207293_at, NM_207294_at, NM_207295_at, NM_207297_at, XCT19174.3_at, XCT23192117.0_at, XCT23193119.0_at, XCT23193200.0_at, XCT23193221.0_at, XCT23193222.0_at, XCT23193223.0_at, XCT23986030.0_at, XCT23986040.0_at	1869594_at, 1869111_at, 2201551_s_at, 2201552_s_at, 2201553_s_at, 2196663_at, 2220315_at, 2220316_at	NP_066956.2, NP_997179.1, NP_997178.1, NP_997177.1, NP_997176.1, NP_997175.1, EAW67783.1, EAW67778.1, EAW67777.1, EAW67776.1, EAW67782.1, EAW67780.1, EAW67781.1, EAW67782.1, EAW67783.1
Gene:ID:5328	P2RY1	3	152,552,736	152,555,845	3,109	+	1	1_A7S_sNL97_dtvs_lncRNA:1-5596	220	ut gene	0	1	0.2	17	1	2_A7S_sNL97_dtvs_lncRNA:1	17	Gene P2RY1	P2Y1, P2RY1	G-protein-coupled receptor P2Y, G-protein coupled	NM_002563, XCT19354.2	2074555_at	NP_002554.1, EAW67772.1
Gene:ID:5912	RAP2B	3	152,550,029	152,556,265	6,236	+	2	1_A7S_sNL97_dtvs_lncRNA:1-4199, 2_A7S_sNL97_dtvs_lncRNA:1:5912	-225, 2	upstream, ut gene	1	1	1	27	29	1	2_A7S_sNL97_dtvs_lncRNA:1	29	Gene RAP2B	RAP2B, MGC20464	RAP2B, member of RAS oncogene family	NM_002886, XCT19369.3	213623_at, 2144695_at, 2219597_at, 2183122_at	NP_002877.2, EAW67771.1
Gene:ID:4476	GPR149	3	154,035,461	154,147,934	92,043	-	2	1_A7S_sNL97_dtvs_lncRNA:1-5165, 2_A7S_sNL97_dtvs_lncRNA:1:5665	5464, 5464	ut gene, ut gene	1	1	1	28	30	1	2_A7S_sNL97_dtvs_lncRNA:1	30	Gene GPR149	PGR16, IEDA, GPR149	G protein-coupled receptor 149	NM_020367705		NP_001033784.1
Gene:ID:3630798	LOC100506	3	155,490,931	155,491,515	1,584	+	1	1_A7S_sNL97_dtvs_lncRNA:1:5992	1333	upstream	0	1	1	16	16	1	2_A7S_sNL97_dtvs_lncRNA:1	16	Gene LOC100507586	putative uncharacterized protein hCINAP(3)284-like	XM_003119812, XM_003116521, NM_001312417		XP_003119860.1, NP_003120569.1, NP_001312346.1
Gene:ID:633	GMPS	3	155,566,325	155,653,521	87,196	+	1	2_A7S_sNL97_dtvs_lncRNA:1:5992	898	ut gene	0	1	1.2	14	1	2_A7S_sNL97_dtvs_lncRNA:1	14	Gene GMPS	GMPS		NM_003875, XCT19539.1, XCT23437.0	214631_at	NP_003866.1, EAW67481.1, EAW67480.1
Gene:ID:551	SCN4B1	3	155,636,337	156,299,927	663,590	+	1	1_A7S_sNL97_dtvs_lncRNA:1:5994	416457	ut gene	0	1	1.2	16	1	2_A7S_sNL97_dtvs_lncRNA:1	16	Gene SCN4B1	HBuNa1, HBuNa2, hBH 3, AF05A2, KCNA1B, HVB3, HVB3, IGI-BETA-1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	NM_170160, NM_003471, NM_172199, XCT19381.3, XCT23167.0, XCT23167.1, XCT23485.0, XCT23485.1, XCT23485.2, XCT23485.3	208212_s_at, 210976_s_at, 210976_s_at, 208212_s_at	NP_731927.1, NP_003462.2, NP_731951.1, EAW67312.1, EAW67334.1, EAW67315.1, EAW67313.1, EAW67316.1
Gene:ID:747	SSR3	3	156,257,929	156,272,873	15,044	-	1	2_A7S_sNL97_dtvs_lncRNA:1:5994	19794	downstream	0	1	1.2	15	1	2_A7S_sNL97_dtvs_lncRNA:1	16	Gene SSR3	TRAP3, SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	NM_007107, XCT19557.2, XCT23185.0	217790_s_at, 222411_s_at, 222412_s_at, 221617_at	NP_009038.1, EAW67331.1, EAW67330.1
Gene:ID:3026722	LOC1002	3	156,290,995	156,293,302	2,342	-	2	1_A7S_sNL97_dtvs_lncRNA:1:5996, 2_A7S_sNL97_dtvs_lncRNA:1:5996	1355, 1422	ut gene, ut gene	1	1	1	27	29	1	2_A7S_sNL97_dtvs_lncRNA:1	29	Gene LOC100287227	hypothetical LOC100287227		NR_027954		
Gene:ID:9976	TIPARP	3	156,292,203	156,424,559	32,356	+	2	1_A7S_sNL97_dtvs_lncRNA:1:5996, 2_A7S_sNL97_dtvs_lncRNA:1:5996	41, -128	upstream, upstream	1	1	1	27	29	1	2_A7S_sNL97_dtvs_lncRNA:1	29	Gene TIPARP	TIPARP, PAR7, DKFZp686P19136, DKFZp434J216, PARP7, PARP-7, DKFZp686N0251, PARP-7, FLJ40695, PRO1, ARET14	TCCD-inducible poly(ADP-ribose) polymerase	NM_001174091, NM_001184718, NM_015508, XCT19655.1, XCT23187.0, XCT23599119.0, XCT23986030.0	212665_at	NP_001171566.1, NP_001171647.1, NP_056223.2, EAW67725.1, EAW67726.1, EAW67727.1
Gene:ID:3009191	LOC1330	3	156,465,137	156,534,623	69,686	+	4	1_A7S_sNL97_dtvs_lncRNA:1:5910, 1_A7S_sNL97_dtvs_lncRNA:1:5911, 2_A7S_sNL97_dtvs_lncRNA:1:5996, 2_A7S_sNL97_dtvs_lncRNA:1:5997	25741, - 121, 28631, 38	ut gene, upstream, ut gene, ut gene	1	1	1	21.5	24	2	2_A7S_sNL97_dtvs_lncRNA:1	24	Gene LOC730091	hypothetical LOC730091		XR_112566, XR_116507, XR_113534	2307000_at	
Gene:ID:89176	LEKR1	3	156,544,096	156,763,818	219,722	+	2	1_A7S_sNL97_dtvs_lncRNA:1:5911, 2_A7S_sNL97_dtvs_lncRNA:1:5997	48182, - 5212	upstream, upstream	1	1	1	23	26	1	2_A7S_sNL97_dtvs_lncRNA:1	26	Gene LEKR1	LEKR1, FLJ16641, FLJ27161	leucine, glutamate and lysine rich 1	NM_001004316, NM_001181263, XCT23183402.0, XCT23183403.0, XCT23183440.0, XCT23183481.0, XCT23183500.0		NP_001004316.2, NP_001180212.1, EAW67815.1, EAW67816.1, EAW67820.1, EAW67822.1, EAW67821.1
Gene:ID:79084	LOC3388	3	156,799,856	156,840,791	41,335	-	3	1_A7S_sNL97_dtvs_lncRNA:1:5996, 2_A7S_sNL97_dtvs_lncRNA:1:5996, 2_A7S_sNL97_dtvs_lncRNA:1:5997	41207, 33815, 8355	ut gene, ut gene, upstream	0	1	1.4	22	3	2_A7S_sNL97_dtvs_lncRNA:1	25	Gene LOC338094	hypothetical LOC338094		NR_038007	1561802_at, 1561722_at	
Gene:ID:100466869	LOC1004	3	156,667,670	156,818,924	11,254	+	2	1_A7S_sNL97_dtvs_lncRNA:1:5996, 2_A7S_sNL97_dtvs_lncRNA:1:5997	-6066, -694	upstream, upstream	0	1	1	12.5	20.5	2	2_A7S_sNL97_dtvs_lncRNA:1	24	Gene LOC100466569	hypothetical LOC100466569		NR_034068		
Gene:ID:7010	CCNL1	3	156,865,555	156,878,462	12,907	-	2	1_A7S_sNL97_dtvs_lncRNA:1:5912, 2_A7S_sNL97_dtvs_lncRNA:1:5911	466, 466	ut gene, ut gene	1	1	1	35	35	1	1_A7S_sNL7_dtvs/s_blC RNA:1	35	Gene CCNL1	FRO1973, CCNL1, BH4-001, AHA84A, cyclin L	cyclin L1	NM_020307, XCT19620.3, XCT19620.2, XCT23589802.0	1555411_s_at, 1555827_at, 2200496_s_at, 1810681_at	NP_064703.1, EAW67312.1, EAW67314.1
Gene:ID:474	SHOX2	3	157,613,800	157,623,852	10,152	-	2	1_A7S_sNL97_dtvs_lncRNA:1:5913, 2_A7S_sNL97_dtvs_lncRNA:1:5914	-3864, 3864	upstream, downstream	1	1	1	40	49	1	2_A7S_sNL97_dtvs_lncRNA:1	49	Gene SHOX2	OG12, OG12X, SHOX2, SHOT	short stature homeobox 2	NM_006884, NM_003030, NM_001163678	206643_s_at, 2161134_s_at, 2161135_s_at	NP_009715.2, NP_003021.3, NP_001157190.1
Gene:ID:1318	RSRC1	3	157,627,592	157,762,562	434,690	+	2	1_A7S_sNL97_dtvs_lncRNA:1:5913, 2_A7S_sNL97_dtvs_lncRNA:1:5914, 2_A7S_sNL97_dtvs_lncRNA:1:5997	44, 44, 17554	ut gene, ut gene	1	1	1	27	33	2	2_A7S_sNL97_dtvs_lncRNA:1	49	Gene RSRC1	BAG11, SFRS21, MGC12197, RSRC1, Srrsp53	arginine/serine-rich coiled-coil 1	NM_016525, XCT19535.2, XCT23183381.0, XCT23183382.0	1555501_s_at, 1555507_at, 2205084_s_at	NP_057709.2, EAW67694.1, EAW67692.1, EAW67693.1
Gene:ID:291	MLP1	3	158,255,953	158,324,252	23,299	+	1	1_A7S_sNL97_dtvs_lncRNA:1:5919	7	ut gene	0	1	9	19	1	2_A7S_sNL97_dtvs_lncRNA:1	19	Gene MLP1	MLP1		NM_032443, NM_001130156, NM_001130157, XCT19529693.1, XCT23865030.0, XCT23865040.0, XCT23865041.0, XCT23865...	2047631_at, 2047634_s_at	NP_071555.1, NP_001122625.1, NP_001122626.1, EAW78665.1, EAW78667.1, EAW78669.1, EAW78665.1, EAW78665.1, EAW78666.1
Gene:ID:5476	GFM1	3	158,362,217	158,410,361	48,044	+	2	1_A7S_sNL97_dtvs_lncRNA:1:5919, 2_A7S_sNL97_dtvs_lncRNA:1:5919	-77, -45	upstream, upstream	1	1	1	100	177	1	1_A7S_sNL7_dtvs/s_blC RNA:1	180	Gene GFM1	EFGM, EFG, HEPD1, FLJ13662, COXPD11, FLJ13622, EFG1, GFM1, EGP1, FLJ20773, GFM	G elongation factor, mitochondrial 1	NM_024996, XCT19258590.2, XCT19258591.0, XCT23163060.0, XCT23163061.0, XCT23970540.0	2059602_at, 2215153_at, 2215156_at, 2215161_at, 2222293_at, 2212961_s_at	NP_079272.2, EAW67670.1, EAW67677.1, EAW67679.1, EAW78663.1, EAW78661.1, EAW78662.1
Gene:ID:54502	IQCJ	3	158,787,117	158,953,892	166,775	+	4	1_A7S_sNL97_dtvs_lncRNA:1:4117, 2_A7S_sNL97_dtvs_lncRNA:1:5916, 2_A7S_sNL97_dtvs_lncRNA:1:5916, 2_A7S_sNL97_dtvs_lncRNA:1:5917, 2_A7S_sNL97_dtvs_lncRNA:1:5918, 2_A7S_sNL97_dtvs_lncRNA:1:5919	204992, 13962, 59279, 204851	downstream, ut gene, ut gene, downstream	1	1	1	17.67	17.67	3	1_A7S_sNL7_dtvs/s_blC RNA:1	25	Gene IQCJ	IQCJ		NM_001042706, NM_001042705		NP_001036171.1, NP_001036170.1
Gene:ID:7966	SCHIP1	3	158,991,544	159,015,139	623,595	+	4	1_A7S_sNL97_dtvs_lncRNA:1:4117, 2_A7S_sNL97_dtvs_lncRNA:1:5920, 2_A7S_sNL97_dtvs_lncRNA:1:5919, 2_A7S_sNL97_dtvs_lncRNA:1:5918, 2_A7S_sNL97_dtvs_lncRNA:1:5924	72, 24, 491304, 481460	ut gene, ut gene, ut gene, ut gene	1	1	1	22.5	30.5	2	1_A7S_sNL7_dtvs/s_blC RNA:1	25	Gene SCHIP1	SCHIP1, FLJ39190, SCHIP-1	schwannomin interacting protein 1	NM_014575, XCT23152341.1, XCT23152350.0, XCT23440357.0, XCT23440358.0	2040030_s_at	NP_055390.1, EAW67660.1, EAW67659.1, EAW67660.1, EAW67662.1
Gene:ID:7996	IFT52	3	159,074,734	160,117,320	162,586	+	2	1_A7S_sNL97_dtvs_lncRNA:1:5922, 1_A7S_sNL97_dtvs_lncRNA:1:5924	18182, - 166	upstream, ut gene	0	1	1	13.5	21	2	2_A7S_sNL97_dtvs_lncRNA:1	23	Gene IFT52	IFT52, ATD2, WDR56, bA61374, MGC12643	intraflagellar transport 52 homolog (Chlamydomonas)	NM_001190241, NM_001190242, NM_020800, XCT23154490.2, XCT23154491.0, XCT23589970.0, XCT23589980.0, XCT23589...	1555558_s_at, 1554231_at, 2060996_at, 2052251_at	NP_001177170.1, NP_001177171.1, NP_065931.1, EAW78643.1, EAW78646.1, EAW78645.1, EAW78644.1, EAW78645.1, EAW78647.1
Gene:ID:9351	SMC4	3	160,117,430	160,152,741	35,311	+	1	1_A7S_sNL97_dtvs_lncRNA:1:5924	55	ut gene	0	1	1.6	23	1	2_A7S_sNL97_dtvs_lncRNA:1	23	Gene SMC4	SCAP-C, SMC4L1, SMC4, CAPC	structural maintenance of chromosomes 4	NM_005496, XCT19683.3, XCT19683.2, XCT23188110.1, XCT23188210.0, XCT23188220.0, XCT23188...	201663_s_at, 201664_at, 214623_x_at	NP_001002800.1, NP_005487.2, EAW78630.1, EAW78640.1, EAW78641.1, EAW78642.1
Gene:ID:3169	MIR155	3	160,122,376	160,122,473	97	+	1	2_A7S_sNL97_dtvs_lncRNA:1:5924	4855	upstream	0	1	1.6	23	1	2_A7S_sNL97_dtvs_lncRNA:1	23	Gene MIR155	MIRN155, hsa-mir-155, mir-155, MIR155	microRNA 155	NR_030784		
Gene:ID:99931	MIR16-2	3	160,122,533	160,122,613	80	+	1	2_A7S_sNL97_dtvs_lncRNA:1:5924	5045	upstream	0	1	1.6	23	1	2_A7S_sNL97_dtvs_lncRNA:1	23	Gene MIR16-2	MIRN16-2, mir-16-3	microRNA 16-2	NR_029523		
Gene:ID:3509764	LOC1005	3	160,213,705	160,213,712	2,007	-	1	1_A7S_sNL97_dtvs_lncRNA:1:5925	1600	ut gene	0	1	4	17	1	1_A7S_sNL7_dtvs/s_blC RNA:1	17	Gene LOC100507647	hypothetical LOC100507647		XR_112567, XR_116508, XR_113535		
Gene:ID:5143	KPNA4	3	160,217,962	160,263,376	65,414	+	2	1_A7S_sNL97_dtvs_lncRNA:1:5925, 2_A7S_sNL97_dtvs_lncRNA:1:5926	66344	downstream	0	1	4	17	1	2_A7S_sNL97_dtvs_lncRNA:1	17	Gene KPNA4	SRP3, KPNA4, MGC26703, QIP1, IPOA2, hSrp1gamma	karyopherin alpha 4 (importin alpha 3)	NM_002268, XCT23184491.0, XCT23184492.0, XCT23184...	2036653_at, 2212901_at, 2212902_at	NP_002259.1, EAW78632.1, EAW78631.1, EAW78633.1
Gene:ID:51742	PPM1L	3	160,473,998	160,758,817	314,821	+	2	1_A7S_sNL97_dtvs_lncRNA:1:4119, 2_A7S_sNL97_dtvs_lncRNA:1:5926	440, -972	upstream, upstream	1	1	1	62	53	1	2_A7S_sNL97_dtvs_lncRNA:1	53	Gene PPM1L	EPM1-LIKE, MGC12565, PP2CE_, PPM1L, PP2C-delta-, MGC12247	protein phosphatase 1 (formerly 2C)-like	NM_139245, XCT19581.4	2139353_at	NP_640338.2, EAW78626.1
Gene:ID:7333	GOLIM4	3	167,727,654	167,813,417	85,763	+	1	1_A7S_sNL97_dtvs_lncRNA:1:5928	47	upstream	0	1	1.6	10	21	1	2_A7S_sNL97_dtvs_lncRNA:1	21	Gene GOLIM4	GOLIM4, GPP130, GMPC, GOLPH4, P138	golgi integral membrane protein 4	NM_004486, XCT19521.1, XCT23175630.0, XCT23175663.0	2043222_at, 2043224_s_at, 2205092_at	NP_055313.1, EAW65964.1, EAW65965.1, EAW78666.1
Gene:ID:3536	C3orf62	3	167,997,310	168,046,387	661,077	+	2	1_A7S_sNL97_dtvs_lncRNA:1:4120, 2_A7S_sNL97_dtvs_lncRNA:1:5928	23136, 468	ut gene, ut gene	1	1	1.3	15.3	2	2_A7S_sNL97_dtvs_lncRNA:1	19	Gene C3orf62	C3orf62, EGFEMTP, NCRNA00259	EGF-like and EMI domain containing 1; pseudogene	NR_021455	1556811_at	
Gene:ID:5584	PRKCI	3	169,649,230	170,023,770	63,360	+	2	1_A7S_sNL97_dtvs_lncRNA:1:4121, 2_A7S_sNL97_dtvs_lncRNA:1:5928	-220, -220	upstream, upstream	1	1	1.2	36	1	2_A7S_sNL97_dtvs_lncRNA:1	36	Gene PRKCI	aPKC-iota, PKCI, DXS1179E, PRKCI, MGC26534	protein kinase C, iota	NM_002740, XCT23166731.0, XCT23166739.0, XCT6298.3	2049777_at, 2049778_s_at, 2139156_at	NP_002731.4, EAW65514.1, EAW65512.1, EAW78618.1
Gene:ID:7709	SLC7A14	3	170,177,342	170,303,663	126,321	+	3	1_A7S_sNL97_dtvs_lncRNA:1:4122, 1_A7S_sNL97_dtvs_lncRNA:1:5929, 2_A7S_sNL97_dtvs_lncRNA:1:5927	1303, 1351, - 6823	ut gene, upstream, upstream	1	1	1	16.5	17.5	2	1_A7S_sNL7_dtvs/s_blC RNA:1	21	Gene SLC7A14	FLJ37225, KIAA1613, SLC7A14	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14	NM_020849, XCT6301.2	2229004_at	NP_065930.2, EAW65510.1
Gene:ID:693	GHSR	3	172,161,051	172,166,246	5,195	+	2	1_A7S_sNL97_dtvs_lncRNA:1:4122, 2_A7S_sNL97_dtvs_lncRNA:1:5929	-1434, 1402	upstream, upstream	1	1	1	25	30	1	2_A7S_sNL97_dtvs_lncRNA:1	30	Gene GHSR	GHSR		NM_004122, NM_198407, XCT10198.2, XCT19321.0	2213901_s_at, 2206554_at	NP_004113.1, NP_940798.1, EAW65466.1, EAW65469.1
Gene:ID:7552	NCEH1	3	172,346,435	172,429,005	82,570	+	2	1_A7S_sNL97_dtvs_lncRNA:1:4124, 2_A7S_sNL97_dtvs_lncRNA:1:5930	16, 64	ut gene, ut gene	1	1	1	20	22	1	1_A7S_sNL7_dtvs/s_blC RNA:1	24	Gene NCEH1	NCEH, AADACL1, hCEH1	neutral cholesterol ester hydrolase 1	NM_001146276, NM_020792, NM_001146277, NM_001146278, XCT11026.2	226567_at	NP_001139748.1, NP_065843.2, NP_001139749.1, NP_001139750.1, EAW78634.1
Gene:ID:3105116	LOC1005	3	172,427,787	172,443,853	16,166	+	2	1_A7S_sNL97_dtvs_lncRNA:1:4124, 2_A7S_sNL97_dtvs_lncRNA:1:5930	1205, 1157	ut gene, ut gene	1	1	1	20	23	1	2_A7S_sNL97_dtvs_lncRNA:1	26	Gene LOC100505532	hypothetical LOC100505532		XR_112563, XR_116513, XR_113540		
Gene:ID:694	BCT2	3	172,472,299	172,539,263	66,964	+	1	1_A7S_sNL97_dtvs_lncRNA:1:4125	-3931	upstream	1	0	16	8	1	1_A7S_sNL7_dtvs/s_blC RNA:1	16	Gene BCT2	FLJ10461, ECT2, MGC138291, ARHGEF31	epithelial cell transforming sequence 2 oncogene	NM_018098, XCT19531.1, XCT23309640	2107973_s_at, 2349962_x_at, 2212481_at	NP_060568.2, EAW65460.1, EAW78461.1
Gene:ID:5338	NUSN1	3	173,116,244	174,001,116	884,872	+	1	1_A7S_sNL97_dtvs_lncRNA:1:4126	-984	upstream	1	0	17	16	1	1_A7S_sNL7_dtvs/s_blC RNA:1	17	Gene NUSN1	NUSN1, KIAA1070, MGC48115, NL1	nucleusin 1	NM_054032, XCT23177010, XCT23177040.1, XCT23405330.0, XCT23605560.0	2080693_at, 2213612_at	NP_063941.2, EAW78455.1, EAW78453.1, EAW78455.1
Gene:ID:6242	KCNAB2	3	176,254,224	176,562,217	307,993	+	2	1_A7S_sNL97_dtvs_lncRNA:1:4126, 2_A7S_sNL97_dtvs_lncRNA:1:5936, 2_A7S_sNL97_dtvs_lncRNA:1:5937	426624, 1465645, 154256	ut gene, ut gene	1	1	1	19	19.5	2	2_A7S_sNL97_dtvs_lncRNA:1	25	Gene KCNAB2	KCNAB2, MGC23021	potassium voltage-gated channel, shaker-related subfamily, beta member 2	NM_003636, NM_181361, XCT23190310.0, XCT6520.2	221097_s_at, 225523_at	NP_003618.2, NP_852098.1, EAW78428.1, EAW78429.1
Gene:ID:7116	SNAPC4	3	178,532,227	178,582,717	50,491	+	1	1_A7S_sNL97_dtvs_lncRNA:1:4127	1	ut gene	0	1	1	21	13	1	1_A7S_sNL7_dtvs/s_blC RNA:1	21	Gene SNAPC4	SNAP190, SNAP1, SNAP190, SNAP1	small nuclear RNA activating complex, polypeptide 4, 190kDa	NM_003082, XCT19655.2, XCT23187.0, XCT23187.1, XCT23485.0, XCT23485.1, XCT23485.2, XCT23485.3	203445_s_at, 203446_s_at, 219375_s_at, 220102_at	NP_003073.2, EAW78427.1, EAW78426.1
Gene:ID:6655	SOX5	3	183,564,993	184,060,023	215,033	+	3	1_A7S_sNL97_dtvs_lncRNA:1:5940, 1_A7S_sNL97_dtvs_lncRNA:1:5941, 1_A7S_sNL97_dtvs_lncRNA:1:5936, 2_A7S_sNL97_dtvs_lncRNA:1:5940	141735, 54871, 54855	ut gene, ut gene, ut gene	1	1	1	16.5	16	2	1_A7S_sNL7_dtvs/s_blC RNA:1	26	Gene SOX5	SOX5, MGC133330, MGC104993, DGKb	diacylglycerol kinase, gamma 80kDa	NM_001007144, NM_006940, NM_001005749	206393_at, 226843_at, 242319_at	NP_997042.1, NP_001307.2, NP_997042.1
Gene:ID:5171	TBCCD1	3	186,263,556	186,295,332	31,776	-	1	1_A7S_sNL97_dtvs_lncRNA:1:4127	2404	ut gene	1	0	16	12	1	1_A7S_sNL7_dtvs/s_blC RNA:1	16	Gene TBCCD1	TBCCD1, FLJ10560	TBCC domain containing 1	NM_018135, NM_001136419, XCT23166000.0, XCT23570700.0, XCT1109.3	2086451_at	NP_060605.1, NP_001129587.1, EAW78190.1, EAW78192.1, EAW78193.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:51726	DNAJB11	3	186,288,467	186,303,589	15,122	+	1	1_A375_pNL7_minus_lncRNA::1::4137	-3539	upstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene DNAJB11	DNAJB11, ABBP-2, EDJ, UNQ537, hDj9, HEDJ, Dj9, ERdj3, ABBP2, PRO1080, ERj3	DnaJ (Hsp40) homolog, subfamily B, member 11	NM_016306, hCT2317216.0	223054_at	NP_057390.1, EAW78190.1
GeneID:1974	EIF4A2	3	186,501,361	186,507,686	6,325	+	1	2_A375_pNL97_plus_lncRNA::1::5949	-81	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene EIF4A2	BM-010, EIF4A, eIF-4A-II, EIF4F, EIF4A2, DDX2B, eIF4A-II	eukaryotic translation initiation factor 4A, isoform 2	NM_001967, hCT1823010.2, hCT1823011.2, hCT1954856.1, hCT1965307.1, hCT2317229.0, hCT2317230.0, hCT2317231.0	1555996_s_at, 1556350_a_at, 200912_s_at	NP_001958.2, EAW78173.1, EAW78172.1, EAW78174.1, EAW78176.1, EAW78178.1, EAW78175.1, EAW78177.1
GeneID:619567	SNORD2	3	186,502,585	186,502,654	69	+	1	2_A375_pNL97_plus_lncRNA::1::5949	-1305	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SNORD2	SNR39B, SNORD2, R39B	small nucleolar RNA, C/D box 2	NR_002567		
GeneID:677847	SNORA81	3	186,504,464	186,504,641	177	+	1	2_A375_pNL97_plus_lncRNA::1::5949	-3184	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SNORA81	HBI-61, SNORA81	small nucleolar RNA, H/ACA box 81	NR_002989		
GeneID:6043	SNORA63	3	186,505,088	186,505,222	134	+	1	2_A375_pNL97_plus_lncRNA::1::5949	-3808	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SNORA63	E3, RNU107, SNORA63, RNE3, E3-2	small nucleolar RNA, H/ACA box 63	NR_002586		
GeneID:619566	SNORA4	3	186,505,402	186,505,538	136	+	1	2_A375_pNL97_plus_lncRNA::1::5949	-4122	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SNORA4	SNORA4, ACA4	small nucleolar RNA, H/ACA box 4	NR_002588		
GeneID:5984	RFC4	3	186,507,681	186,524,484	16,803	-	2	2_A375_pNL97_plus_lncRNA::1::5949, 2_A375_pNL97_plus_lncRNA::1::5950	23204, 84	downstream, in gene	0	1	13	18	2	2_A375_pNL97_plus_lncRNA::1	21	Gene RFC4	A1, MGC27291, RFC37, RFC4	replication factor C (activator 1) 4, 37kDa	NM_002916, NM_181573, hCT2316671.0, hCT2316672.0, hCT2316673.0	204023_at	NP_002907.1, NP_853551.1, EAW78169.1, EAW78170.1, EAW78171.1
GeneID:6750	SST	3	187,386,694	187,388,201	1,507	-	2	1_A375_pNL7_minus_lncRNA::1::4138, 2_A375_pNL97_plus_lncRNA::1::5951	585, 585	in gene, in gene	1	1	21	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene SST	SST, SMST	somatostatin	NM_001048, hCT2316610.0, hCT6261.2	213921_at	NP_001039.1, EAW78146.1, EAW78145.1
GeneID:604	BCL6	3	187,439,165	187,463,513	24,348	-	2	1_A375_pNL7_minus_lncRNA::1::4139, 2_A375_pNL97_plus_lncRNA::1::5952	89, 41	in gene, in gene	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene BCL6	BCL5, BCL6, LAZ3, ZNF51, BCL6A, ZBTB27	B-cell CLL/lymphoma 6	NM_001130845, NM_001134738, NM_001706, hCT1954830.1, hCT7052.3	203140_at, 215990_s_at, 228758_at, 239249_at	NP_001124317.1, NP_001128210.1, NP_001697.2, EAW78140.1, EAW78141.1
GeneID:3556	IL1RAP	3	190,231,840	190,374,986	143,146	+	2	1_A375_pNL7_minus_lncRNA::1::4141, 2_A375_pNL97_plus_lncRNA::1::5954	71966, -363	in gene, upstream	1	1	13.5	11.5	2	1_A375_pNL7_minus_lncRNA::1	16	Gene IL1RAP	C3orf13, IL-1RAcP, IL1RAP, FLJ37788, IL1R3	interleukin 1 receptor accessory protein	NM_002182, NM_134470, NM_001167928, NM_001167929, NM_001167930, NM_001167931, hCT1954834.1, hCT2316592.0, hCT2316593.0, hCT7061.1	205227_at, 210233_at	NP_002173.1, NP_608273.1, NP_001161400.1, NP_001161401.1, NP_001161402.1, NP_001161403.1, EAW78100.1, EAW78101.1, EAW78102.1, EAW78103.1
GeneID:2257	FGF12	3	191,859,684	192,445,388	585,704	-	1	2_A375_pNL97_plus_lncRNA::1::5956	539788	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FGF12	FHF1, FGF12B, FGF12	fibroblast growth factor 12	NM_021032, NM_004113, hCT2316392.0, hCT2344053.0, hCT2344054.0	207501_s_at, 214589_at	NP_066360.1, NP_004104.3, EAW78084.1, EAW78085.1, EAW78086.1
GeneID:4976	OPA1	3	193,310,933	193,415,600	104,667	+	2	1_A375_pNL7_minus_lncRNA::1::4142, 2_A375_pNL97_plus_lncRNA::1::5958	-21, -53	upstream, upstream	1	1	25	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene OPA1	KIAA0567, MGM1, NPG, largeG, FLJ12460, OPA1, NTG	optic atrophy 1 (autosomal dominant)	NM_015560, NM_130831, NM_130832, NM_130833, NM_130834, NM_130835, NM_130836, NM_130837, hCT1954850.1, hCT2317766.0, hCT2317769.0, hCT2355944.0, hCT2355945.0, hCT2355946.0, hCT2355947.0, hCT2355948.0, hCT6320.2	212213_x_at, 212214_at, 214306_at, 241027_at	NP_056375.2, NP_570844.1, NP_570845.1, NP_570846.1, NP_570848.1, NP_570847.2, NP_570849.2, NP_570850.2, EAW78064.1, EAW78065.1, EAW78066.1, EAW78067.1, EAW78068.1, EAW78069.1, EAW78070.1, EAW78071.1, EAW78072.1
GeneID:647323	LOC647323	3	193,675,161	193,721,448	46,287	-	2	1_A375_pNL7_minus_lncRNA::1::4145, 2_A375_pNL97_plus_lncRNA::1::5959	136, -152	in gene, upstream	1	1	20	20	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC647323		hypothetical LOC647323	NR_033944	1564539_at	
GeneID:100505902	LOC100505902	3	193,727,752	193,788,741	60,989	-	2	1_A375_pNL7_minus_lncRNA::1::4145, 2_A375_pNL97_plus_lncRNA::1::5959	67429, 67141	downstream, downstream	1	1	20	20	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100505902		hypothetical LOC100505902	XR_112543, XR_108533, XR_113560		
GeneID:3280	HES1	3	193,853,934	193,856,396	2,462	+	1	1_A375_pNL7_minus_lncRNA::1::4146	-1022	upstream	1	0	19	11	1	1_A375_pNL7_minus_lncRNA::1	19	Gene HES1	FLJ20408, HHL, HES-1, bHLHb39, HRY, HES1	hairy and enhancer of split 1, (Drosophila)	NM_005524, hCT7353.2	203393_at, 203394_s_at, 203395_s_at	NP_005515.1, EAW78058.1
GeneID:55341	LSG1	3	194,361,517	194,393,206	31,689	-	2	1_A375_pNL7_minus_lncRNA::1::4147, 2_A375_pNL97_plus_lncRNA::1::5960	54, 22	in gene, in gene	1	1	28	20	1	1_A375_pNL7_minus_lncRNA::1	28	Gene LSG1	FLJ27294, LSG1, FLJ11301	large subunit GTPase 1 homolog (S. cerevisiae)	NM_018385, hCT13478.3, hCT1961003.1, hCT1961004.1, hCT1967081.1, hCT2316477.0, hCT2316479.0	221535_at, 221536_s_at, 223200_s_at	NP_060855.2, EAW78036.1, EAW78035.1, EAW78037.1, EAW78038.1, EAW78039.1, EAW78034.1
GeneID:100507391	LOC100507391	3	194,429,150	194,502,897	73,747	+	1	2_A375_pNL97_plus_lncRNA::1::5961	32498	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100507391		hypothetical LOC100507391	XR_112592, XR_112593, XR_110393, XR_110392, XR_113565, XR_113566		
GeneID:152002	C3orf21	3	194,789,013	194,991,895	202,882	-	2	1_A375_pNL7_minus_lncRNA::1::4149, 2_A375_pNL97_plus_lncRNA::1::5962	-169, -105	upstream, upstream	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene C3orf21	C3orf21, FLJ35155	chromosome 3 open reading frame 21	NM_152531, hCT13831.2, hCT1950189.1, hCT2316490.0	226891_at	NP_689744.3, EAW78028.1, EAW78029.1, EAW78030.1
GeneID:23527	ACAP2	3	194,995,465	195,163,817	168,352	-	2	1_A375_pNL7_minus_lncRNA::1::4149, 2_A375_pNL97_plus_lncRNA::1::5962	171753, 171817	downstream, downstream	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ACAP2	ACAP2, CENTB2, CNT-B2, KIAA0041	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	NM_012287, hCT13930.3, hCT2316487.0	1552472_a_at, 212476_at, 212477_at	NP_036419.3, EAW78027.1, EAW78026.1
GeneID:5130	PCYT1A	3	195,965,253	196,014,584	49,331	-	1	1_A375_pNL7_minus_lncRNA::1::4150	8152	in gene	1	0	18	8	1	1_A375_pNL7_minus_lncRNA::1	18	Gene PCYT1A	CTA, CCTA, PCYT1, PCYT1A, CT, CTPCT	phosphate cytidylyltransferase 1, choline, alpha	NM_005017	204209_at, 204210_s_at, 225069_at	NP_005008.2
GeneID:205564	SENP5	3	196,594,727	196,661,585	66,858	+	1	2_A375_pNL97_plus_lncRNA::1::5963	74585	downstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SENP5	DKFZp564O1016, FLJ42398, MGC27076, SENP5	SUMO1/sentrin specific peptidase 5	NM_152699, hCT1950996.1, hCT1966902.1, hCT1966903.1, hCT2269808.0, hCT32463.3	222110_at, 57703_at	NP_689912.2, EAW53625.1, EAW53626.1, EAW53627.1, EAW53628.1, EAW53629.1
GeneID:22916	NCBP2	3	196,662,273	196,669,464	7,191	-	1	2_A375_pNL97_plus_lncRNA::1::5963	152	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NCBP2	NCBP2, NIP1, CBP20, CBC2, PIG55	nuclear cap binding protein subunit 2, 20kDa	NM_001042540, NM_007362, hCT1950989.1, hCT1966900.1, hCT2352758.0, hCT2352759.0, hCT31551.2	201517_at, 201521_s_at	NP_001036005.1, NP_031388.2, EAW53620.1, EAW53621.1, EAW53622.1, EAW53623.1, EAW53624.1
GeneID:152217	LOC152217	3	196,669,494	196,670,884	1,390	+	1	2_A375_pNL97_plus_lncRNA::1::5963	-182	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC152217	FLJ41024, MGC71256, DKFZp762I1415	hypothetical LOC152217	NR_024388	225657_at	
GeneID:80235	PIGZ	3	196,673,214	196,695,704	22,490	-	1	2_A375_pNL97_plus_lncRNA::1::5963	26392	downstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PIGZ	SMP3, MGC52163, PIGZ, FLJ12768, GPI-MT-IV	phosphatidylinositol glycan anchor biosynthesis, class Z	NM_025163, hCT32461.3	220041_at	NP_079439.2, EAW53618.1
GeneID:4241	MFI2	3	196,728,611	196,756,687	28,076	-	2	1_A375_pNL7_minus_lncRNA::1::4151, 2_A375_pNL97_plus_lncRNA::1::5964	-1809, 1103	upstream, in gene	1	1	15	17	2	1_A375_pNL7_minus_lncRNA::1	21	Gene MFI2	MAP97, FLJ38863, MGC4856, MFI2, CD228, MTF1	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	NM_033316, NM_005929, hCT2287853.0, hCT32460.2	1556538_at, 220043_s_at, 223723_at	NP_201573.1, NP_005920.2, EAW53616.1, EAW53617.1
GeneID:622	BDH1	3	197,236,654	197,300,194	63,540	-	1	2_A375_pNL97_plus_lncRNA::1::5965	18482	in gene	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene BDH1	BDH, SDR9C1, BDH1, MGC2723, MGC4347, MGC9788	3-hydroxybutyrate dehydrogenase, type 1	NM_004051, NM_203315, NM_203314, hCT13166.2, hCT1950978.1, hCT2287934.0, hCT2287936.0	1570336_at, 211715_s_at	NP_004042.1, NP_976060.1, NP_976059.1, EAW53607.1, EAW53608.1, EAW53609.1, EAW53606.1
GeneID:152687	ZNF595	4	53,227	88,099	34,872	+	2	1_A375_pNL7_minus_lncRNA::1::4152, 2_A375_pNL97_plus_lncRNA::1::5966	-96, -171	upstream, upstream	1	1	34	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene ZNF595	FLJ31740, ZNF595	zinc finger protein 595	NM_182524, hCT23529.5		NP_872330.1, EAW82675.1
GeneID:170960	ZNF721	4	433,777	493,442	59,665	-	3	1_A375_pNL7_minus_lncRNA::1::4154, 2_A375_pNL97_plus_lncRNA::1::5967, 2_A375_pNL97_plus_lncRNA::1::5968	514, 25730, 450	in gene, in gene, in gene	1	1	20.5	19	2	1_A375_pNL7_minus_lncRNA::1	25	Gene ZNF721	ZNF721, FLJ11452, KIAA1982	zinc finger protein 721	NM_133474	226029_at	NP_597731.2
GeneID:54872	PIGG	4	492,989	533,320	40,331	+	2	1_A375_pNL7_minus_lncRNA::1::4154, 2_A375_pNL97_plus_lncRNA::1::5968	-61, 3	upstream, in gene	1	1	25	19	1	1_A375_pNL7_minus_lncRNA::1	25	Gene PIGG	PIGG, DKFZp434M1131, FLJ20265, LAS21, RLGS1930, DKFZp434C1712, MGC131903, DKFZp434A1810, FLJ39925, PRO4405, GPI7	phosphatidylinositol glycan anchor biosynthesis, class G	NM_017733, NM_001127178, hCT2255687.0, hCT2256689.0, hCT25659.3	1563842_at, 218652_s_at, 231692_at, 233654_at	NP_060203.3, NP_001120650.1, EAW82663.1, EAW82664.1, EAW82665.1
GeneID:5158	PDE6B	4	619,363	664,681	45,318	+	1	2_A375_pNL97_plus_lncRNA::1::5970	48797	downstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene PDE6B	CSNB3, CSNBAD2, PDE6B, PDEB, rd1, RP40	phosphodiesterase 6B, cGMP-specific, rod, beta	NM_001145292, NM_000283, NM_001145291, hCT2256691.0, hCT25657.3	1557777_at, 210304_at, 236085_at, 236153_at	NP_001138764.1, NP_000274.2, NP_001138763.1, EAW82661.1, EAW82662.1
GeneID:521	ATP5I	4	666,225	668,127	1,902	-	1	2_A375_pNL97_plus_lncRNA::1::5970	-33	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ATP5I	MGC12532, ATP5I, ATP5K	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	NM_007100, NR_033743, hCT1642746.4	207335_x_at	NP_009031.1, EAW82660.1
GeneID:4636	MYL5	4	671,711	675,817	4,106	+	1	2_A375_pNL97_plus_lncRNA::1::5970	-3551	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MYL5	MYL5		NM_002477	205145_s_at	NP_002468.1
GeneID:84179	MFSD7	4	675,618	682,973	7,355	-	1	2_A375_pNL97_plus_lncRNA::1::5970	14813	downstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MFSD7	LP2561, MFSD7, FLJ22269	major facilitator superfamily domain containing 7	NM_032219, hCT1969045.1, hCT1969049.1	205144_at, 214269_at	NP_115595.2, EAW82658.1, EAW82659.1
GeneID:100129917	LOC100129917	4	773,937	775,636	1,699	-	1	2_A375_pNL97_plus_lncRNA::1::5971	212	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100129917		hypothetical LOC100129917	NR_036511, NR_036512		
GeneID:10815	CPLX1	4	778,745	819,945	41,200	-	1	2_A375_pNL97_plus_lncRNA::1::5971	44521	downstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CPLX1	CPX1, CPLX1, CPX-I	complexin 1	NM_006651, hCT1966930.1, hCT2356258.0, hCT25650.3	223500_at	NP_006642.1, EAW82648.1, EAW82647.1, EAW82649.1
GeneID:2580	GAK	4	843,065	926,174	83,109	-	1	2_A375_pNL97_plus_lncRNA::1::5972	270	in gene	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene GAK	GAK, FLJ40395, FLJ16629, MGC99654	cyclin G associated kinase	NM_005255, hCT2255093.1, hCT2255095.1, hCT2255097.1	202281_at, 40225_at	NP_005246.2, EAW82645.1, EAW82644.1, EAW82646.1
GeneID:84286	TMEM175	4	926,262	952,444	26,182	+	1	2_A375_pNL97_plus_lncRNA::1::5972	-358	upstream	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TMEM175	MGC4618, TMEM175	transmembrane protein 175	NM_032326, hCT1966932.1, hCT1966933.1, hCT1966934.1, hCT1966935.1, hCT1966938.1, hCT1966939.1, hCT2356286.0, hCT2356287.0, hCT2356288.0, hCT2356289.0, hCT2356290.0	223462_at	NP_115702.1, EAW82633.1, EAW82636.1, EAW82638.1, EAW82639.1, EAW82640.1, EAW82634.1, EAW82635.1, EAW82637.1, EAW82641.1, EAW82642.1, EAW82643.1
GeneID:10861	SLC26A1	4	972,861	987,224	14,363	-	1	2_A375_pNL97_plus_lncRNA::1::5973	6312	in gene	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SLC26A1	SLC26A1, SAT1, EDM4, SAT-1	solute carrier family 26 (sulfate transporter), member 1	NM_022042, NM_134425, NM_213613, hCT2255081.0, hCT25655.2	1552843_at, 205058_at, 220733_at, 228195_s_at, 228199_at	NP_071325.2, NP_602297.1, NP_998778.1, EAW82628.1, EAW82629.1
GeneID:3425	IDUA	4	980,785	998,317	17,532	+	1	2_A375_pNL97_plus_lncRNA::1::5973	127	in gene	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene IDUA	IDA, MPS1, IDUA	iduronidase, alpha-L-	NM_000203, hCT1972689.1, hCT1972690.1, hCT1972691.1, hCT1972692.1, hCT1972693.1, hCT1972694.1, hCT2256718.0, hCT2256721.0, hCT2256723.0, hCT2256725.0, hCT2356284.0, hCT25656.3	205057_s_at, 205059_s_at	NP_000194.2, EAW82616.1, EAW82618.1, EAW82624.1, EAW82625.1, EAW82627.1, EAW82617.1, EAW82619.1, EAW82620.1, EAW82621.1, EAW82622.1, EAW82623.1, EAW82626.1
GeneID:285498	RNF212	4	1,065,266	1,107,582	42,316	-	1	1_A375_pNL7_minus_lncRNA::1::4156	31356	in gene	1	0	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene RNF212	MGC120227, RNF212, ZHP3, FLJ42587, MGC120228, FLJ38841	ring finger protein 212	NM_001131034, NM_194439, NM_001193318, hCT1646976.4, hCT2341104.0, hCT2341105.0, hCT2341106.0, hCT2356257.0	1557031_at, 236454_at	NP_001124506.1, NP_919420.1, NP_001180247.1, EAW82611.1, EAW82613.1, EAW82614.1, EAW82610.1, EAW82612.1
GeneID:10296	MAEA	4	1,283,672	1,333,925	50,253	+	2	1_A375_pNL7_minus_lncRNA::1::4157, 2_A375_pNL97_plus_lncRNA::1::5975	56936, 56984	downstream, downstream	1	1	16	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene MAEA	PIG5, EMLP, HLC-10, EMP, MAEA	macrophage erythroblast attacher	NM_005882, NM_001017405, hCT1646978.3, hCT1969026.1, hCT1969027.1, hCT2256752.0, hCT2256758.0, hCT2256760.0, hCT2256765.0, hCT2356274.0, hCT2356275.0, hCT2356276.0, hCT2356277.0	207922_s_at	NP_005873.2, NP_001017405.1, EAW82586.1, EAW82588.1, EAW82594.1, EAW82596.1, EAW82587.1, EAW82589.1, EAW82590.1, EAW82591.1, EAW82592.1, EAW82593.1, EAW82595.1
GeneID:57654	KIAA1530	4	1,341,104	1,381,837	40,733	+	2	1_A375_pNL7_minus_lncRNA::1::4157, 2_A375_pNL97_plus_lncRNA::1::5975	-496, -448	upstream, upstream	1	1	16	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene KIAA1530	KIAA1530, MGC117169	KIAA1530	NM_020894, hCT1655221.3	1555107_a_at, 233893_s_at, 241201_at	NP_065945.2, EAW82584.1
GeneID:54729	NKX1-1	4	1,396,720	1,400,119	3,399	-	2	1_A375_pNL7_minus_lncRNA::1::4158, 2_A375_pNL97_plus_lncRNA::1::5976	-4265, -4233	upstream, upstream	1	1	81	119	1	2_A375_pNL97_plus_lncRNA::1	119	Gene NKX1-1	NKX1-1, SAX2, HSPX153	NK1 homeobox 1	XM_926341, XM_937659	1565537_at	XP_931434.4, XP_942752.5
GeneID:7884	SLBP	4	1,694,527	1,714,030	19,503	-	4	1_A375_pNL7_minus_lncRNA::1::4159, 1_A375_pNL7_minus_lncRNA::1::4160, 2_A375_pNL97_plus_lncRNA::1::5977, 2_A375_pNL97_plus_lncRNA::1::5978	-274, -2482, -274, -2498	upstream, upstream, upstream, upstream	1	1	35	29	2	1_A375_pNL7_minus_lncRNA::1	50	Gene SLBP	SLBP, HBP	stem-loop binding protein	NM_006527, hCT10743.3, hCT1970752.1, hCT2356247.0, hCT2356248.0, hCT2356249.0	206052_s_at	NP_006518.1, EAW82577.1, EAW82576.1, EAW82578.1, EAW82579.1, EAW82580.1
GeneID:92305	TMEM129	4	1,717,679	1,723,084	5,405	-	4	1_A375_pNL7_minus_lncRNA::1::4159, 1_A375_pNL7_minus_lncRNA::1::4160, 2_A375_pNL97_plus_lncRNA::1::5977, 2_A375_pNL97_plus_lncRNA::1::5978	8780, 6572, 8780, 6556	downstream, downstream, downstream, downstream	1	1	35	29	2	1_A375_pNL7_minus_lncRNA::1	50	Gene TMEM129	TMEM129, FLJ25600, D4S2561E	transmembrane protein 129	NM_138385, NM_001127266, hCT2254352.0, hCT2254354.0, hCT2254355.0, hCT2254357.0, hCT2254358.0	225567_at, 225568_s_at	NP_612394.1, NP_001120738.1, EAW82569.1, EAW82571.1, EAW82572.1, EAW82573.1, EAW82570.1
GeneID:10460	TACC3	4	1,723,266	1,746,898	23,632	+	4	1_A375_pNL7_minus_lncRNA::1::4159, 1_A375_pNL7_minus_lncRNA::1::4160, 2_A375_pNL97_plus_lncRNA::1::5977, 2_A375_pNL97_plus_lncRNA::1::5978	-8962, -6754, -8962, -6738	upstream, upstream, upstream, upstream	1	1	35	29	2	1_A375_pNL7_minus_lncRNA::1	50	Gene TACC3	MGC133242, ERIC1, MGC117382, TACC3	transforming, acidic coiled-coil containing protein 3	NM_006342, hCT10020.3, hCT2356273.0	1569487_at, 218308_at	NP_006333.1, EAW82574.1, EAW82575.1
GeneID:3954	LETM1	4	1,813,206	1,857,974	44,768	-	2	1_A375_pNL7_minus_lncRNA::1::4161, 2_A375_pNL97_plus_lncRNA::1::5979	-186, -74	upstream, upstream	1	1	24	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene LETM1	LETM1		NM_012318, hCT1962194.1, hCT2254342.0	218939_at, 222006_at, 233439_at	NP_036450.1, EAW82561.1, EAW82560.1
GeneID:7469	WHSC2	4	1,984,443	2,010,959	26,516	-	1	2_A375_pNL97_plus_lncRNA::1::5980	431	in gene	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene WHSC2	WHSC2, NELF-A, FLJ10442, FLJ25112, NELFA, P/OKcl.15	Wolf-Hirschhorn syndrome candidate 2	NM_005663, hCT1970748.1, hCT2356264.0, hCT9143.4	203112_s_at, 34225_at	NP_005654.3, EAW82545.1, EAW82546.1, EAW82547.1
GeneID:79441	HAUS3	4	2,230,096	2,243,860	13,764	-	1	2_A375_pNL97_plus_lncRNA::1::5981	100	in gene	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene HAUS3	DKFZp686I1858, MGC4701, IT1, HAUS3, C4orf15, dgt3	HAUS augmin-like complex, subunit 3	NM_024511, hCT9148.3	210054_at, 242804_at	NP_078787.2, EAW82537.1
GeneID:10608	MXD4	4	2,249,160	2,263,739	14,579	-	1	2_A375_pNL97_plus_lncRNA::1::5981	19979	downstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MXD4	bHLHc12, MST149, MXD4, MSTP149	MAX dimerization protein 4	NM_006454, hCT1960873.1, hCT1960874.1, hCT1960875.1, hCT1960876.1, hCT2254311.0, hCT2254318.0, hCT9141.2	210778_s_at, 212346_s_at, 212347_x_at	NP_006445.1, EAW82530.1, EAW82531.1, EAW82533.1, EAW82534.1, EAW82536.1, EAW82532.1, EAW82535.1
GeneID:57732	ZFYVE28	4	2,271,324	2,420,370	149,046	-	1	2_A375_pNL97_plus_lncRNA::1::5982	5106	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ZFYVE28	MGC43699, LYST2, ZFYVE28, MGC61592	zinc finger, FYVE domain containing 28	NM_020972, NM_001172656, NM_001172657, NM_001172658, NM_001172659, NM_001172660, hCT2254302.0, hCT9144.2	1569369_at, 1569383_s_at, 232408_at	NP_066023.2, NP_001166127.1, NP_001166128.1, NP_001166129.1, NP_001166130.1, NP_001166131.1, EAW82528.1, EAW82529.1
GeneID:402160	LOC402160	4	2,420,701	2,464,690	43,989	+	1	2_A375_pNL97_plus_lncRNA::1::5982	-5437	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC402160		hypothetical protein LOC402160	NM_001193282		NP_001180211.1
GeneID:6452	SH3BP2	4	2,794,750	2,842,823	48,073	+	1	1_A375_pNL7_minus_lncRNA::1::4162	50578	downstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SH3BP2	RES4-23, CRBM, SH3BP2, 3BP2, FLJ42079, CRPM, FLJ54978	SH3-domain binding protein 2	NM_003023, NM_001122681, NM_001145855, NM_001145856, hCT11709.2, hCT1656341.3, hCT2259386.0, hCT2259388.0, hCT2259389.0, hCT2259390.0, hCT2259391.0, hCT2356266.0	209370_s_at, 209371_s_at, 211250_s_at	NP_003014.3, NP_001116153.1, NP_001139327.1, NP_001139328.1, EAW82506.1, EAW82512.1, EAW82507.1, EAW82508.1, EAW82509.1, EAW82510.1, EAW82511.1, EAW82513.1
GeneID:118	ADD1	4	2,845,584	2,931,789	86,205	+	2	1_A375_pNL7_minus_lncRNA::1::4162, 2_A375_pNL97_plus_lncRNA::1::5983	-256, 91120	upstream, downstream	1	1	17.5	17.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene ADD1	ADDA, ADD1, MGC44427, MGC3339	adducin 1 (alpha)	NM_001119, NM_014189, NM_014190, NM_176801, hCT2259393.0, hCT2259394.0, hCT2259395.0, hCT2259397.0, hCT2259398.0, hCT2259399.0, hCT2259400.0, hCT2259401.0	208030_s_at, 214726_x_at, 214736_s_at, 238939_at	NP_001110.2, NP_054908.2, NP_054909.2, NP_789771.1, EAW82498.1, EAW82500.1, EAW82499.1, EAW82501.1, EAW82502.1, EAW82503.1, EAW82504.1, EAW82505.1
GeneID:10227	MFSD10	4	2,932,288	2,936,586	4,298	-	1	2_A375_pNL97_plus_lncRNA::1::5983	-118	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MFSD10	TETRAN, TETTRAN, MFSD10	major facilitator superfamily domain containing 10	NM_001120, NM_001146069, hCT11710.4, hCT1970756.1	209215_at	NP_001111.3, NP_001139541.1, EAW82496.1, EAW82497.1
GeneID:317648	C4orf10	4	2,937,273	2,952,794	15,521	+	1	2_A375_pNL97_plus_lncRNA::1::5983	-569	upstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene C4orf10	C4orf10, RES4-24	chromosome 4 open reading frame 10	NR_015453	214123_s_at, 214685_at, 215141_at	
GeneID:8602	NOP14	4	2,939,663	2,965,118	25,455	-	2	2_A375_pNL97_plus_lncRNA::1::5983, 2_A375_pNL97_plus_lncRNA::1::5984	28414, -34	downstream, upstream	0	1	15	22	2	2_A375_pNL97_plus_lncRNA::1	23	Gene NOP14	NOL14, RES4-25, NOP14, C4orf9, RES425	NOP14 nucleolar protein homolog (yeast)	NM_003703, hCT11713.3, hCT2254501.0, hCT2254503.0, hCT2356270.0, hCT2356271.0	214661_s_at	NP_003694.1, EAW82492.1, EAW82489.1, EAW82490.1, EAW82491.1, EAW82493.1
GeneID:2868	GRK4	4	2,965,343	3,042,474	77,131	+	1	2_A375_pNL97_plus_lncRNA::1::5984	-191	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene GRK4	GRK4a, GRK4, GPRK2L, IT11, GPRK4	G protein-coupled receptor kinase 4	NM_182982, NM_001004056, NM_001004057, hCT11711.3, hCT1970766.1, hCT2259407.0, hCT2259408.0, hCT2259409.0, hCT2259410.0, hCT2259412.0	208365_s_at, 210600_s_at, 241989_at	NP_892027.2, NP_001004056.1, NP_001004057.1, EAW82480.1, EAW82482.1, EAW82483.1, EAW82479.1, EAW82481.1, EAW82484.1, EAW82485.1

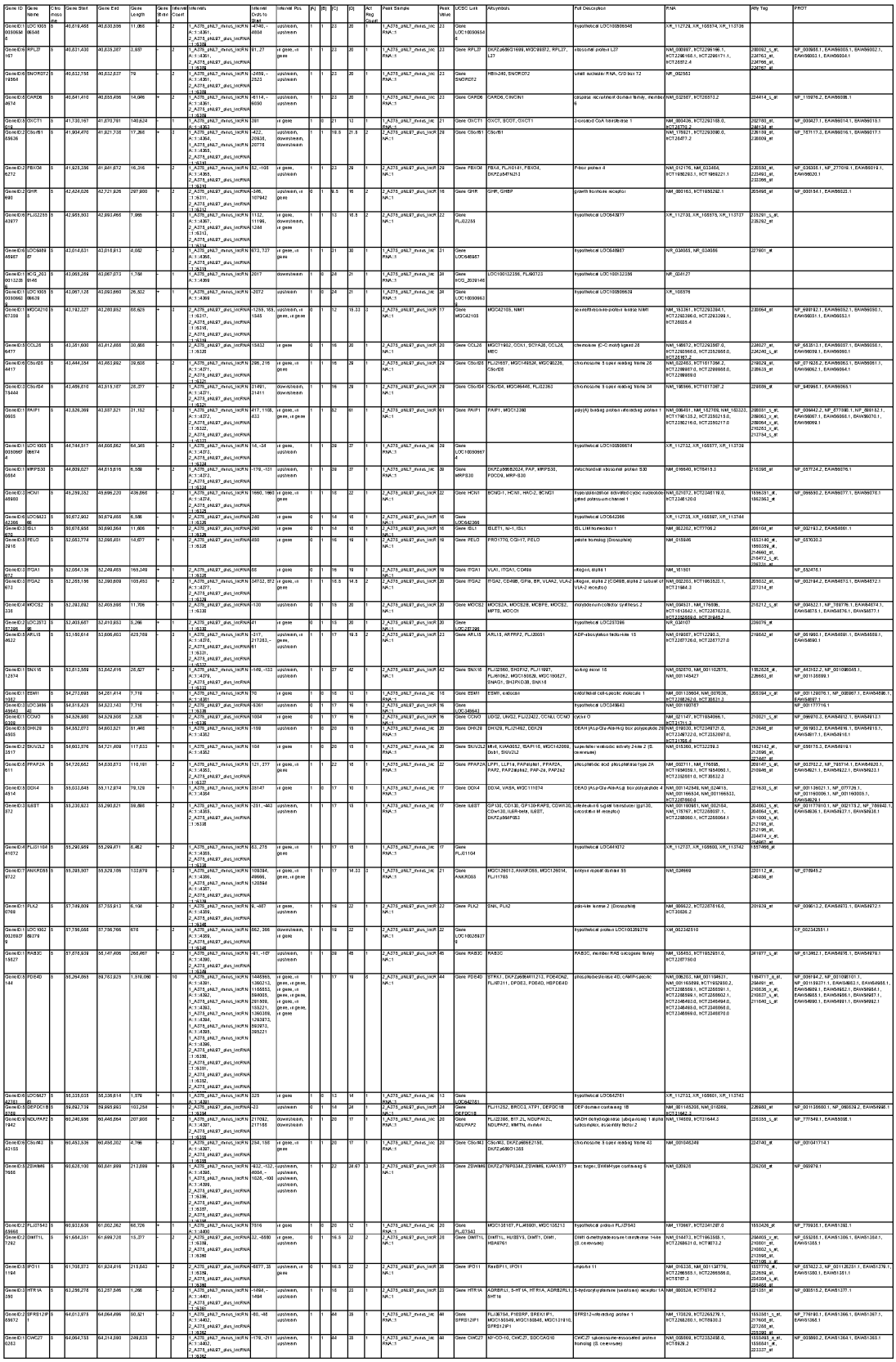
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:85013	TMEM128	4	4,237,269	4,249,934	12,665	-	2	1_A375_pNL7_minus_lncRNA::1::4164, 2_A375_pNL97_plus_lncRNA::1::5986	-114, -66	upstream, upstream	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TMEM128	MGC110944, TMEM128, MGC13159	transmembrane protein 128	NM_032927, hCT2254170.0, hCT2254171.0, hCT2356281.0, hCT2356282.0, hCT2356283.0	225462_at	NP_116316.1, EAW82444.1, EAW82440.1, EAW82441.1, EAW82442.1, EAW82443.1
GeneID:100507225	LOC100507225	4	4,250,028	4,252,255	2,227	-	2	1_A375_pNL7_minus_lncRNA::1::4164, 2_A375_pNL97_plus_lncRNA::1::5986	2207, 2255	in gene, downstream	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100507225		hypothetical LOC100507225	XR_112608, XR_108537, XR_113607		
GeneID:53407	STX18	4	4,420,695	4,543,775	123,080	-	2	1_A375_pNL7_minus_lncRNA::1::4165, 2_A375_pNL97_plus_lncRNA::1::5987	-1, -65	upstream, upstream	1	1	38	36	1	1_A375_pNL7_minus_lncRNA::1	38	Gene STX18	Ufe1, STX18, DKFZp686O15149	syntaxin 18	NM_016930, hCT1965500.1, hCT1965501.1, hCT30372.3	218763_at	NP_058626.1, EAW82427.1, EAW82428.1, EAW82429.1
GeneID:100507266	LOC100507266	4	4,543,858	4,712,665	168,807	+	2	1_A375_pNL7_minus_lncRNA::1::4165, 2_A375_pNL97_plus_lncRNA::1::5987	-82, -18	upstream, upstream	1	1	38	36	1	1_A375_pNL7_minus_lncRNA::1	38	Gene LOC100507266		hypothetical LOC100507266	XR_112609, XR_112610, XR_108538, XR_108539, XR_113608, XR_113609		
GeneID:55351	STK32B	4	5,053,527	5,502,725	449,198	+	5	1_A375_pNL7_minus_lncRNA::1::4168, 1_A375_pNL7_minus_lncRNA::1::4169, 2_A375_pNL97_plus_lncRNA::1::5989, 2_A375_pNL97_plus_lncRNA::1::5990, 2_A375_pNL97_plus_lncRNA::1::5991	154729, 286761, 168457, 286793, 314041	in gene, in gene, in gene, in gene, in gene	1	1	17.5	19	4	2_A375_pNL97_plus_lncRNA::1	25	Gene STK32B	YANK2, STK32B, HSA250839, STKG6, STK32	serine/threonine kinase 32B	NM_018401, hCT1953081.1, hCT2253875.0	219686_at	NP_060871.1, EAW82417.1, EAW82416.1
GeneID:132884	EVC2	4	5,564,146	5,711,275	147,129	-	1	2_A375_pNL97_plus_lncRNA::1::5992	-3141	upstream	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene EVC2	LBN, EVC2	Ellis van Creveld syndrome 2	NM_147127, NM_001166136, hCT2253762.1, hCT2254162.1, hCT2356255.0	1555256_at, 229974_at	NP_667338.3, NP_001159608.1, EAW82412.1, EAW82413.1, EAW82414.1
GeneID:2121	EVC	4	5,712,924	5,816,031	103,107	+	1	2_A375_pNL97_plus_lncRNA::1::5992	1492	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene EVC	EVCL, EVC, DWF-1, MGC105107, EVC1	Ellis van Creveld syndrome	NM_153717	210887_s_at, 234421_s_at	NP_714928.1
GeneID:1400	CRMP1	4	5,822,491	5,894,785	72,294	-	1	2_A375_pNL97_plus_lncRNA::1::5993	11553	in gene	0	1	13	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene CRMP1	DPYSL1, DRP-1, DRP1, CRMP1, ULIP-3, CRMP-1	collapsin response mediator protein 1	NM_001313, NM_001014809, hCT2254151.0, hCT2356267.0, hCT2356268.0, hCT2356269.0, hCT31146.2	202517_at	NP_001304.1, NP_001014809.1, EAW82403.1, EAW82404.1, EAW82406.1, EAW82407.1, EAW82405.1
GeneID:100507292	LOC100507292	4	5,869,059	5,891,958	22,899	-	1	2_A375_pNL97_plus_lncRNA::1::5993	8726	in gene	0	1	13	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene LOC100507292		hypothetical LOC100507292	XR_112612, XR_108540		
GeneID:285484	LOC285484	4	6,202,460	6,234,809	32,349	+	2	1_A375_pNL7_minus_lncRNA::1::4170, 2_A375_pNL97_plus_lncRNA::1::5994	24772, 24772	in gene, in gene	1	1	28	15	1	1_A375_pNL7_minus_lncRNA::1	28	Gene LOC285484		hypothetical LOC285484	XR_112613, XR_108542, XR_113611		
GeneID:5522	PPP2R2C	4	6,322,305	6,474,326	152,021	-	4	1_A375_pNL7_minus_lncRNA::1::4171, 1_A375_pNL7_minus_lncRNA::1::4172, 2_A375_pNL97_plus_lncRNA::1::5995, 2_A375_pNL97_plus_lncRNA::1::5996	128470, 109494, 109462, -5503	in gene, in gene, in gene, upstream	1	1	22.33	26.33	3	2_A375_pNL97_plus_lncRNA::1	48	Gene PPP2R2C	IMYPNO1, PR52, B55-GAMMA, IMYPNO, MGC33570, PR55G, PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	NM_020416, NM_181876, hCT1837937.1, hCT2254142.1, hCT30893.3	223573_s_at, 223574_x_at, 228010_at, 228025_s_at, 228137_s_at, 228140_s_at	NP_065149.2, NP_870991.1, EAW82393.1, EAW82394.1, EAW82395.1
GeneID:23324	MAN2B2	4	6,576,902	6,624,188	47,286	+	1	1_A375_pNL7_minus_lncRNA::1::4173	122	in gene	1	0	19	10	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MAN2B2	MAN2B2, KIAA0935	mannosidase, alpha, class 2B, member 2	NM_015274, hCT2254770.0, hCT2254772.0, hCT2254773.0, hCT2254776.0	214703_s_at	NP_056089.1, EAW82390.1, EAW82389.1, EAW82391.1, EAW82392.1
GeneID:114932	MRFAP1L1	4	6,709,428	6,711,606	2,178	-	3	1_A375_pNL7_minus_lncRNA::1::4174, 2_A375_pNL97_plus_lncRNA::1::5997, 2_A375_pNL97_plus_lncRNA::1::5998	-6250, 470, -6762	upstream, in gene, upstream	1	1	16	21.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene MRFAP1L1	MGC8651, PP784, MRFAP1L1	Morf4 family associated protein 1-like 1	NM_203462, hCT2350911.0	212199_at	NP_982287.1, EAW82383.1
GeneID:55330	CNO	4	6,717,842	6,719,387	1,545	+	4	1_A375_pNL7_minus_lncRNA::1::4174, 2_A375_pNL97_plus_lncRNA::1::5997, 2_A375_pNL97_plus_lncRNA::1::5998, 2_A375_pNL97_plus_lncRNA::1::5999	14, -6706, 526, 11310	in gene, upstream, in gene, downstream	1	1	12.67	20.33	3	2_A375_pNL97_plus_lncRNA::1	22	Gene CNO	FLJ11230, BCAS4L, CNO	cappuccino homolog (mouse)	NM_018366	223431_at	NP_060836.1
GeneID:57533	TBC1D14	4	6,911,171	7,034,845	123,674	+	6	1_A375_pNL7_minus_lncRNA::1::4175, 1_A375_pNL7_minus_lncRNA::1::4176, 1_A375_pNL7_minus_lncRNA::1::4177, 2_A375_pNL97_plus_lncRNA::1::6000, 2_A375_pNL97_plus_lncRNA::1::6001, 2_A375_pNL97_plus_lncRNA::1::6002	-83, 7309, 77741, -35, 7261, 77837	upstream, in gene, in gene, upstream, in gene, in gene	1	1	23	27	3	2_A375_pNL97_plus_lncRNA::1	33	Gene TBC1D14	KIAA1322, TBC1D14, FLJ32400	TBC1 domain family, member 14	NM_020773, NM_001113361, NM_001113363, hCT2254797.0, hCT2356254.0, hCT30890.3	224622_at	NP_065824.2, NP_001106832.1, NP_001106834.1, EAW82375.1, EAW82376.1, EAW82377.1
GeneID:93624	TADA2B	4	7,045,156	7,059,679	14,523	+	1	2_A375_pNL97_plus_lncRNA::1::6003	24540	downstream	0	1	21	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TADA2B	ADA2B, ADA2(beta), MGC21874, TADA2B	transcriptional adaptor 2B	NM_152293	226240_at, 236246_x_at	NP_689506.2
GeneID:80273	GRPEL1	4	7,061,780	7,069,800	8,020	-	1	2_A375_pNL97_plus_lncRNA::1::6003	104	in gene	0	1	21	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene GRPEL1	GRPEL1, HMGE, FLJ25609	GrpE-like 1, mitochondrial (E. coli)	NM_025196, hCT2349958.1, hCT30891.3	212432_at, 212434_at	NP_079472.1, EAW82370.1, EAW82371.1
GeneID:57537	SORCS2	4	7,194,374	7,744,564	550,190	+	6	1_A375_pNL7_minus_lncRNA::1::4178, 1_A375_pNL7_minus_lncRNA::1::4179, 1_A375_pNL7_minus_lncRNA::1::4180, 2_A375_pNL97_plus_lncRNA::1::6004, 2_A375_pNL97_plus_lncRNA::1::6005, 2_A375_pNL97_plus_lncRNA::1::6006	14042, 103066, 544442, 14378, 457162, 544376	in gene, in gene, in gene, in gene, in gene, in gene	1	1	24	26.75	4	2_A375_pNL97_plus_lncRNA::1	56	Gene SORCS2	SORCS2		NM_020777, hCT2254805.1, hCT2254807.0	226720_at	NP_065828.2, EAW82364.1, EAW82363.1
GeneID:60312	AFAP1	4	7,760,440	7,941,653	181,213	-	2	1_A375_pNL7_minus_lncRNA::1::4181, 2_A375_pNL97_plus_lncRNA::1::6007	362, 309	in gene, in gene	1	1	22	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene AFAP1	AFAP, FLJ56849, AFAP-110, AFAP1	actin filament associated protein 1	NM_198595, NM_001134647, hCT2254075.0	203563_at	NP_940997.1, NP_001128119.1, EAW82360.1
GeneID:84448	ABLIM2	4	7,967,037	8,160,559	193,522	-	2	1_A375_pNL7_minus_lncRNA::1::4182, 2_A375_pNL97_plus_lncRNA::1::6008	202415, 202351	downstream, downstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ABLIM2	MGC141918, FLJ39664, KIAA1808, DKFZp761F129, FLJ26534, ABLIM2	actin binding LIM protein family, member 2	NM_001130083, NM_001130084, NM_001130085, NM_001130086, NM_001130087, NM_032432, NM_001130088, hCT2254071.0, hCT2254072.0, hCT22761.3	1567622_at, 1567623_at, 226132_at, 236087_at, 242624_at	NP_001123555.1, NP_001123556.1, NP_115808.3, NP_001123557.1, NP_001123558.1, NP_001123559.1, NP_001123560.1, EAW82357.1, EAW82358.1, EAW82359.1
GeneID:8310	ACOX3	4	8,368,009	8,442,452	74,443	-	3	1_A375_pNL7_minus_lncRNA::1::4183, 1_A375_pNL7_minus_lncRNA::1::4184, 2_A375_pNL97_plus_lncRNA::1::6009	12308, -172, 116	in gene, upstream, in gene	1	1	18	16.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene ACOX3	ACOX3		NM_003501, NM_001101667, hCT1950283.1, hCT2254064.0, hCT2356245.0, hCT8436.3	204241_at, 204242_s_at	NP_003492.2, NP_001095137.1, EAW82339.1, EAW82340.1, EAW82341.1, EAW82342.1
GeneID:152992	C4orf23	4	8,442,532	8,478,282	35,750	+	2	1_A375_pNL7_minus_lncRNA::1::4184, 2_A375_pNL97_plus_lncRNA::1::6009	92, -196	in gene, upstream	1	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C4orf23	C4orf23, METTL19, FLJ35725, FLJ12891	chromosome 4 open reading frame 23	NM_152544	1554192_s_at, 220891_at, 235097_at	NP_689757.2
GeneID:693157	MIR572	4	11,370,451	11,370,545	94	+	2	1_A375_pNL7_minus_lncRNA::1::4186, 2_A375_pNL97_plus_lncRNA::1::6013	-1171, -1235	upstream, upstream	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MIR572	MIR572, MIRN572, hsa-mir-572	microRNA 572	NR_030298		
GeneID:643446	LOC643446	4	11,370,535	11,375,359	4,824	+	2	1_A375_pNL7_minus_lncRNA::1::4186, 2_A375_pNL97_plus_lncRNA::1::6013	-1255, -1319	upstream, upstream	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene LOC643446		RNA binding protein S1, serine-rich domain pseudogene			
GeneID:9364	RAB28	4	13,369,347	13,485,989	116,642	-	1	2_A375_pNL97_plus_lncRNA::1::6015	-155	upstream	0	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene RAB28	RAB28, MGC41862	RAB28, member RAS oncogene family	NM_004249, NM_001017979, NM_001159601, hCT1961602.1, hCT7412.2	207495_at, 209064_s_at, 227003_at	NP_004240.2, NP_001017979.1, NP_001153073.1, EAW92711.1, EAW92712.1
GeneID:259282	BOD1L	4	13,570,366	13,629,328	58,962	-	1	1_A375_pNL7_minus_lncRNA::1::4187	-96	upstream	1	0	22	13	1	1_A375_pNL7_minus_lncRNA::1	22	Gene BOD1L	BOD1L, FLJ33215, KIAA1327, FAM44A	biorientation of chromosomes in cell division 1-like	NM_148894, hCT2325865.0	225621_s_at, 235009_at, 242594_at	NP_683692.2, EAW92716.1
GeneID:441009	LOC441009	4	15,003,373	15,003,964	591	-	2	1_A375_pNL7_minus_lncRNA::1::4192, 2_A375_pNL97_plus_lncRNA::1::6023	-260, -132	upstream, upstream	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC441009		hypothetical LOC441009	XM_001723280, XM_498965, XM_944418	1561471_at	XP_001723332.1, XP_498965.3, XP_949511.2
GeneID:132864	CPEB2	4	15,004,298	15,071,777	67,479	+	2	1_A375_pNL7_minus_lncRNA::1::4192, 2_A375_pNL97_plus_lncRNA::1::6023	-74, -202	upstream, upstream	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CPEB2	CPEB-2, MGC119577, CPEB2, MGC119575, MGC119576	cytoplasmic polyadenylation element binding protein 2	NM_001177381, NM_001177382, NM_001177383, NM_001177384, NM_182485, NM_182646, hCT2346793.1, hCT2349392.0, hCT2349393.0, hCT2349394.0	226939_at, 235462_at, 235479_at	NP_001170852.1, NP_001170853.1, NP_001170854.1, NP_001170855.1, NP_872291.2, NP_872587.2, EAW92727.1, EAW92728.1, EAW92729.1, EAW92730.1
GeneID:57545	CC2D2A	4	15,471,489	15,603,180	131,691	+	1	2_A375_pNL97_plus_lncRNA::1::6024	92575	in gene	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CC2D2A	JBTS9, MKS6, CC2D2A, KIAA1345	coiled-coil and C2 domain containing 2A	NM_001080522, NM_001164720, NM_020785	1559409_a_at, 234933_at, 234936_s_at, 236473_at	NP_001073991.2, NP_001158192.1, NP_065836.2
GeneID:285550	LOC285550	4	15,683,352	15,692,070	8,718	+	3	1_A375_pNL7_minus_lncRNA::1::4193, 2_A375_pNL97_plus_lncRNA::1::6025, 2_A375_pNL97_plus_lncRNA::1::6026	13784, -24, 13688	downstream, upstream, downstream	1	1	16.5	19.5	2	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC285550	FAM200B	family with sequence similarity 200, member B	NM_001145191	227270_at, 227466_at, 236321_at	NP_001138663.1
GeneID:683	BST1	4	15,704,573	15,733,796	29,223	+	2	1_A375_pNL7_minus_lncRNA::1::4193, 2_A375_pNL97_plus_lncRNA::1::6026	-7437, -7533	upstream, upstream	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene BST1	BST1, CD157	bone marrow stromal cell antigen 1	NM_004334, hCT30856.2	205715_at	NP_004325.2, EAW92744.1
GeneID:9079	LDB2	4	16,503,164	16,900,424	397,260	-	1	1_A375_pNL7_minus_lncRNA::1::4195	325416	in gene	1	0	18	8	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LDB2	LDB2, LDB1, CLIM1	LIM domain binding 2	NM_001290, NM_001130834, hCT1953751.2, hCT1953752.2, hCT2325901.0	206481_s_at, 242360_at	NP_001281.1, NP_001124306.1, EAW92765.1, EAW92766.1, EAW92767.1
GeneID:5860	QDPR	4	17,488,016	17,513,857	25,841	-	2	1_A375_pNL7_minus_lncRNA::1::4196, 2_A375_pNL97_plus_lncRNA::1::6029	1, -31	in gene, upstream	1	1	24	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene QDPR	FLJ42391, PKU2, DHPR, QDPR, SDR33C1	quinoid dihydropteridine reductase	NM_000320, hCT1962487.2, hCT1971220.2, hCT2357574.0, hCT2357575.0, hCT2357576.0	209123_at, 238616_at	NP_000311.2, EAW92775.1, EAW92774.1, EAW92776.1, EAW92777.1, EAW92778.1
GeneID:645104	CLRN2	4	17,516,788	17,528,727	11,939	+	2	1_A375_pNL7_minus_lncRNA::1::4196, 2_A375_pNL97_plus_lncRNA::1::6029	-2932, -2900	upstream, upstream	1	1	24	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene CLRN2	CLRN2		NM_001079827		NP_001073296.1
GeneID:51056	LAP3	4	17,578,927	17,609,590	30,663	+	1	2_A375_pNL97_plus_lncRNA::1::6030	37361	downstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LAP3	LAPEP, LAP, LAP3, PEPS	leucine aminopeptidase 3	NM_015907, hCT32195.3	217933_s_at	NP_056991.2, EAW92780.1
GeneID:80306	MED28	4	17,616,273	17,626,160	9,887	+	1	2_A375_pNL97_plus_lncRNA::1::6030	15	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MED28	magicin, DKFZp434N185, MED28, 1500003D12Rik, EG1	mediator complex subunit 28	NM_025205, hCT2325923.0, hCT2325924.0	214831_at, 218438_s_at, 222635_s_at, 222636_at, 224416_s_at, 228992_at, 243668_at	NP_079481.2, EAW92782.1, EAW92781.1
GeneID:27146	FAM184B	4	17,633,696	17,783,135	149,439	-	4	1_A375_pNL7_minus_lncRNA::1::4197, 1_A375_pNL7_minus_lncRNA::1::4198, 2_A375_pNL97_plus_lncRNA::1::6031, 2_A375_pNL97_plus_lncRNA::1::6032	93770, 90527, 93791, 90463	in gene, in gene, in gene, in gene	1	1	22.5	28	2	2_A375_pNL97_plus_lncRNA::1	29	Gene FAM184B	FAM184B, KIAA1276	family with sequence similarity 184, member B	NM_015688	233623_at	NP_056503.1
GeneID:54876	DCAF16	4	17,802,278	17,812,381	10,103	-	2	1_A375_pNL7_minus_lncRNA::1::4199, 2_A375_pNL97_plus_lncRNA::1::6033	-163, 93	upstream, in gene	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DCAF16	MGC126767, C4orf30, DCAF16, MGC126765, FLJ20280	DDB1 and CUL4 associated factor 16	NM_017741, hCT2326004.0	219717_at, 228106_at, 239187_at	NP_060211.3, EAW92784.1
GeneID:64151	NCAPG	4	17,812,525	17,846,488	33,963	+	2	1_A375_pNL7_minus_lncRNA::1::4199, 2_A375_pNL97_plus_lncRNA::1::6033	19, -237	in gene, upstream	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene NCAPG	CHCG, HCAP-G, MGC126525, NY-MEL-3, CAPG, NCAPG, FLJ12450	non-SMC condensin I complex, subunit G	NM_022346, hCT32197.3	218662_s_at, 218663_at	NP_071741.2, EAW92785.1
GeneID:254251	LCORL	4	17,844,839	18,023,483	178,644	-	2	1_A375_pNL7_minus_lncRNA::1::4200, 2_A375_pNL97_plus_lncRNA::1::6034	-191, -325	upstream, upstream	1	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LCORL	MLR1, FLJ30696, LCORL	ligand dependent nuclear receptor corepressor-like	NM_153686, NM_001166139, hCT1660901.3, hCT2349345.0, hCT2349346.0, hCT2349347.0	232293_at, 235970_at, 240592_at	NP_710153.2, NP_001159611.1, EAW92786.1, EAW92787.1, EAW92788.1, EAW92789.1
GeneID:9353	SLIT2	4	20,255,235	20,620,788	365,553	+	3	1_A375_pNL7_minus_lncRNA::1::4201, 2_A375_pNL97_plus_lncRNA::1::6035, 2_A375_pNL97_plus_lncRNA::1::6036	220648, -1619, 220733	in gene, upstream, in gene	1	1	12.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene SLIT2	SLIL3, Slit-2, SLIT2, FLJ14420	slit homolog 2 (Drosophila)	NM_004787, hCT1954496.1, hCT2325983.0	209897_s_at, 230130_at	NP_004778.1, EAW92792.1, EAW92793.1
GeneID:80333	KCNIP4	4	20,730,239	21,950,374	1,220,135	-	5	1_A375_pNL7_minus_lncRNA::1::4202, 2_A375_pNL97_plus_lncRNA::1::6037, 1_A375_pNL7_minus_lncRNA::1::4203, 2_A375_pNL97_plus_lncRNA::1::6038, 2_A375_pNL97_plus_lncRNA::1::6039	1069702, 1069734, 48182, 935142, 60086	in gene, in gene, in gene, in gene, in gene	1	1	19.25	17.5	4	1_A375_pNL7_minus_lncRNA::1	38	Gene KCNIP4	CALP, MGC44947, KCNIP4, KCHIP4	Kv channel interacting protein 4	NM_025221, NM_147181, NM_147182, NM_147183, NM_001035003, NM_001035004, hCT1954497.1, hCT2326016.0	224530_s_at, 236783_at, 240591_at	NP_079497.2, NP_671710.1, NP_671711.1, NP_671712.1, NP_001030175.1, NP_001030176.1, EAW92797.1, EAW92798.1
GeneID:10891	PPARGC1A	4	23,793,644	23,891,700	98,056	-	1	1_A375_pNL7_minus_lncRNA::1::4207	33568	in gene	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene PPARGC1A	PGC1A, PGC-1v, PGC1, LEM6, PGC-1(alpha), PPARGC1A, PPARGC1	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	NM_013261, hCT1954499.1, hCT2326025.0	1569141_a_at, 219195_at	NP_037393.1, EAW92812.1, EAW92811.1
GeneID:729175	LOC729175	4	24,473,456	24,484,502	11,046	-	1	2_A375_pNL97_plus_lncRNA::1::6044	9494	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC729175		hypothetical LOC729175	XM_001129558, XM_001131204, XM_001717514		XP_001129558.1, XP_001131204.1, XP_001717566.1
GeneID:1665	DHX15	4	24,529,087	24,586,184	57,097	-	1	2_A375_pNL97_plus_lncRNA::1::6045	72	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DHX15	DBP1, PrPp43p, DHX15, PRP43, DDX15, PRPF43, HRH2	DEAH (Asp-Glu-Ala-His) box polypeptide 15	NM_001358, hCT2350293.0, hCT2350294.0, hCT2350295.0, hCT2350296.0, hCT2350482.0, hCT2350483.0, hCT2350484.0, hCT30900.2	201385_at, 201386_s_at	NP_001349.2, EAW92817.1, EAW92814.1, EAW92818.1, EAW92819.1, EAW92821.1, EAW92815.1, EAW92816.1, EAW92820.1
GeneID:51091	SEPSECS	4	25,121,627	25,162,204	40,577	-	1	2_A375_pNL97_plus_lncRNA::1::6047	60	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SEPSECS	LP, SLA/LP, SEPSECS, SLA, DKFZp434B1417, MGC161491	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	NM_016955, hCT1954502.1, hCT2326132.0, hCT2326133.0, hCT2326135.0, hCT9307.3	1553167_a_at, 1569634_at, 231730_at, 235516_at	NP_058651.3, EAW92832.1, EAW92831.1, EAW92833.1, EAW92834.1, EAW92835.1
GeneID:285540	LOC285540	4	25,162,294	25,200,128	37,834	+	2	2_A375_pNL97_plus_lncRNA::1::6047, 2_A375_pNL97_plus_lncRNA::1::6048	-150, 12906	upstream, in gene	0	1	16.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC285540		hypothetical LOC285540	XR_112624, XR_108552, XR_113627	1559479_at	
GeneID:55300	PI4K2B	4	25,235,653	25,280,831	45,178	+	1	2_A375_pNL97_plus_lncRNA::1::6049	347	in gene	0	1	8	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PI4K2B	PI4KIIB, PI4K2B, PIK42B, FLJ11105	phosphatidylinositol 4-kinase type 2 beta	NM_018323, hCT10686.2	222631_at	NP_060793.2, EAW92836.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:29063	ZCCHC4	4	25,314,396	25,372,005	57,609	+	3	1_A375_pNL7_minus_lncRNA::1::4209, 2_A375_pNL97_plus_lncRNA::1::6050, 2_A375_pNL97_plus_lncRNA::1::6051	-28, 4, 64692	upstream, in gene, downstream	1	1	42.5	52	2	2_A375_pNL97_plus_lncRNA::1	88	Gene ZCCHC4	MGC21108, HSPC052, ZCCHC4	zinc finger, CCHC domain containing 4	NM_024936	219917_at, 220472_at, 220473_s_at	NP_079212.2
GeneID:29945	ANAPC4	4	25,378,848	25,420,120	41,272	+	1	2_A375_pNL97_plus_lncRNA::1::6051	240	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ANAPC4	ANAPC4, APC4	anaphase promoting complex subunit 4	NM_013367, hCT10662.3, hCT2326112.0	226917_s_at, 232524_x_at	NP_037499.2, EAW92839.1, EAW92840.1
GeneID:100506024	LOC100506024	4	25,906,314	25,908,462	2,148	-	2	1_A375_pNL7_minus_lncRNA::1::4210, 2_A375_pNL97_plus_lncRNA::1::6052	-1778, -1938	upstream, upstream	1	1	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100506024		hypothetical LOC100506024	XR_112625, XR_108553, XR_113628		
GeneID:389203	C4orf52	4	25,915,814	25,931,501	15,687	+	2	1_A375_pNL7_minus_lncRNA::1::4210, 2_A375_pNL97_plus_lncRNA::1::6052	-5574, -5414	upstream, upstream	1	1	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene C4orf52	C4orf52	chromosome 4 open reading frame 52	NM_001145432	225014_at	NP_001138904.1
GeneID:3516	RBPJ	4	26,321,332	26,433,278	111,946	+	3	1_A375_pNL7_minus_lncRNA::1::4212, 1_A375_pNL7_minus_lncRNA::1::4213, 2_A375_pNL97_plus_lncRNA::1::6055	-420, 956, 1036	upstream, in gene, in gene	1	1	26	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene RBPJ	csl, RBPJ, RBPJK, CBF1, KBF2, IGKJRB, IGKJRB1, RBP-J, SUH, RBPSUH, MGC61669	recombination signal binding protein for immunoglobulin kappa J region	NM_203284, NM_203283, NM_005349, NM_015874, hCT1954500.1, hCT2326122.0, hCT2326123.0, hCT8168.3	207785_s_at, 211974_x_at	NP_976029.1, NP_976028.1, NP_005340.2, NP_056958.3, EAW92848.1, EAW92849.1, EAW92846.1, EAW92847.1
GeneID:55296	TBC1D19	4	26,585,546	26,756,917	171,371	+	2	1_A375_pNL7_minus_lncRNA::1::4214, 2_A375_pNL97_plus_lncRNA::1::6056	-10, 150	upstream, in gene	1	1	23	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene TBC1D19	TBC1D19, FLJ11082	TBC1 domain family, member 19	NM_018317, hCT1968258.0, hCT8167.2	220260_at	NP_060787.2, EAW92851.1, EAW92852.1
GeneID:100506048	LOC100506048	4	26,861,246	26,862,221	975	-	3	1_A375_pNL7_minus_lncRNA::1::4215, 1_A375_pNL7_minus_lncRNA::1::4216, 2_A375_pNL97_plus_lncRNA::1::6057	2701, 141, 3053	downstream, in gene, downstream	1	1	17	14.5	2	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100506048		hypothetical LOC100506048	XR_112627, XR_112626, XR_108555, XR_108554, XR_113630, XR_113629		
GeneID:57620	STIM2	4	26,862,313	27,027,003	164,690	+	3	1_A375_pNL7_minus_lncRNA::1::4215, 1_A375_pNL7_minus_lncRNA::1::4216, 2_A375_pNL97_plus_lncRNA::1::6057	-2793, -233, -3145	upstream, upstream, upstream	1	1	17	14.5	2	1_A375_pNL7_minus_lncRNA::1	18	Gene STIM2	FLJ39527, STIM2, KIAA1482	stromal interaction molecule 2	NM_020860, NM_001169117, NM_001169118, hCT2326049.0, hCT2357600.0, hCT7622.3	225246_at, 225250_at, 234140_s_at	NP_065911.3, NP_001162588.1, NP_001162589.1, EAW92853.1, EAW92854.1, EAW92855.1
GeneID:5099	PCDH7	4	30,722,037	31,148,423	426,386	+	1	2_A375_pNL97_plus_lncRNA::1::6063	-2805	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PCDH7	FLJ97161, BH-Pcdh, PCDH7, BHPCDH	protocadherin 7	NM_002589, NM_032456, NM_001173523, NM_032457, hCT2326070.0, hCT2326071.0, hCT2326072.0, hCT2326073.0, hCT2326074.0	205534_at, 205535_s_at, 210273_at, 210941_at, 228640_at	NP_002580.2, NP_115832.1, NP_001166994.1, NP_115833.2, EAW92863.1, EAW92864.1, EAW92861.1, EAW92862.1, EAW92865.1
GeneID:55286	C4orf19	4	37,455,552	37,595,132	139,580	+	1	1_A375_pNL7_minus_lncRNA::1::4225	23403	in gene	1	0	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene C4orf19	C4orf19, FLJ11017	chromosome 4 open reading frame 19	NM_001104629, NM_018302, hCT1640834.1, hCT1950224.1	219450_at	NP_001098099.1, NP_060772.2, EAW92882.1, EAW92883.1
GeneID:768211	RELL1	4	37,592,422	37,687,999	95,577	-	3	2_A375_pNL97_plus_lncRNA::1::6068, 2_A375_pNL97_plus_lncRNA::1::6069, 2_A375_pNL97_plus_lncRNA::1::6070	57279, 38079, 287	in gene, in gene, in gene	0	1	14.67	24.33	3	2_A375_pNL97_plus_lncRNA::1	27	Gene RELL1	FLJ21778, RELL1, MGC50583	RELT-like 1	NM_001085399, NM_001085400	1554714_at, 226430_at	NP_001078868.1, NP_001078869.1
GeneID:55276	PGM2	4	37,828,282	37,864,559	36,277	+	1	1_A375_pNL7_minus_lncRNA::1::4226	262	in gene	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene PGM2	MSTP006, PGM2, FLJ10983	phosphoglucomutase 2	NM_018290, hCT30128.3	223738_s_at, 225366_at, 225367_at	NP_060760.2, EAW92886.1
GeneID:79667	FLJ13197	4	38,614,322	38,666,249	51,927	-	1	2_A375_pNL97_plus_lncRNA::1::6072	43673	in gene	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FLJ13197		hypothetical FLJ13197	NR_026804, hCT2326621.0, hCT30270.3	1570414_x_at, 219871_at	EAW92894.1, EAW92893.1
GeneID:5981	RFC1	4	39,289,076	39,367,995	78,919	-	1	2_A375_pNL97_plus_lncRNA::1::6074	123	in gene	0	1	16	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene RFC1	MHCBFB, A1, RFC, RECC1, MGC51786, RFC140, RFC1, PO-GA	replication factor C (activator 1) 1, 145kDa	NM_002913, hCT2350365.0, hCT2357585.0, hCT29790.3	208021_s_at, 208133_at, 209085_x_at	NP_002904.3, EAW92922.1, EAW92923.1, EAW92924.1
GeneID:152831	KLB	4	39,408,473	39,453,153	44,680	+	2	1_A375_pNL7_minus_lncRNA::1::4228, 2_A375_pNL97_plus_lncRNA::1::6075	52103, 52039	downstream, downstream	1	1	31	28	1	1_A375_pNL7_minus_lncRNA::1	31	Gene KLB	KLB, BKL, MGC142213	klotho beta	NM_175737, hCT29793.4	235706_at, 244276_at	NP_783864.1, EAW92925.1
GeneID:6133	RPL9	4	39,455,744	39,460,568	4,824	-	2	1_A375_pNL7_minus_lncRNA::1::4228, 2_A375_pNL97_plus_lncRNA::1::6075	-8, 56	upstream, in gene	1	1	31	28	1	1_A375_pNL7_minus_lncRNA::1	31	Gene RPL9	RPL9P9, RPL9P7, RPL9P8, RPL9, MGC15545, FLJ27456, DKFZp313J1510, NPC-A-16, L9	ribosomal protein L9	NM_001024921, NM_000661, hCT1950690.1, hCT1961484.2, hCT1961485.2, hCT2326519.1, hCT2326522.1, hCT28694.3	200032_s_at	NP_001020092.1, NP_000652.2, EAW92926.1, EAW92927.1, EAW92929.1, EAW92930.1, EAW92928.1, EAW92931.1
GeneID:11019	LIAS	4	39,460,665	39,479,273	18,608	+	2	1_A375_pNL7_minus_lncRNA::1::4228, 2_A375_pNL97_plus_lncRNA::1::6075	-89, -153	upstream, upstream	1	1	31	28	1	1_A375_pNL7_minus_lncRNA::1	31	Gene LIAS	LS, LAS, MGC23245, HUSSY-01, LIP1, LIAS	lipoic acid synthetase	NM_194451, NM_006859, hCT2326294.0, hCT2357586.0, hCT29798.2	214045_at	NP_919433.1, NP_006850.2, EAW92932.1, EAW92933.1, EAW92934.1
GeneID:7358	UGDH	4	39,500,375	39,529,218	28,843	-	2	1_A375_pNL7_minus_lncRNA::1::4229, 2_A375_pNL97_plus_lncRNA::1::6076	-158, -222	upstream, upstream	1	1	20	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene UGDH	UDP-GlcDH, UGDH, UDPGDH, UGD, GDH	UDP-glucose dehydrogenase	NM_001184700, NM_001184701, NM_003359, hCT2326516.0, hCT2357583.0, hCT29797.3	203343_at	NP_001171629.1, NP_001171630.1, NP_003350.1, EAW92936.1, EAW92937.1, EAW92938.1
GeneID:201895	C4orf34	4	39,552,550	39,640,481	87,931	-	1	1_A375_pNL7_minus_lncRNA::1::4230	-810	upstream	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene C4orf34	FLJ13289, C4orf34	chromosome 4 open reading frame 34	NM_174921, hCT1965806.2, hCT2357577.0, hCT29796.4	222336_at, 224990_at	NP_777581.1, EAW92942.1, EAW92940.1, EAW92941.1
GeneID:23244	PDS5A	4	39,824,483	39,979,576	155,093	-	2	1_A375_pNL7_minus_lncRNA::1::4231, 2_A375_pNL97_plus_lncRNA::1::6077	8, -40	in gene, upstream	1	1	45	42	1	1_A375_pNL7_minus_lncRNA::1	45	Gene PDS5A	PDS5A, PIG54, MGC131948, DKFZp686B19246, FLJ41012, SCC-112, MGC161503, KIAA0648	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	NM_001100399, NM_001100400, hCT2326508.0, hCT2326509.0, hCT2357572.0, hCT29794.3	212136_at, 212140_at, 213983_s_at, 213984_at	NP_001093869.1, NP_001093870.1, EAW92952.1, EAW92953.1, EAW92954.1, EAW92955.1
GeneID:55728	N4BP2	4	40,058,524	40,157,028	98,504	+	2	1_A375_pNL7_minus_lncRNA::1::4232, 2_A375_pNL97_plus_lncRNA::1::6078	-892, -876	upstream, upstream	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene N4BP2	KIAA1413, B3BP, N4BP2, FLJ10680	NEDD4 binding protein 2	NM_018177, hCT2326304.0, hCT2326305.0, hCT28816.3	231996_at	NP_060647.2, EAW92959.1, EAW92957.1, EAW92958.1
GeneID:54502	RBM47	4	40,425,272	40,631,883	206,611	-	1	2_A375_pNL97_plus_lncRNA::1::6080	75	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene RBM47	RBM47, DKFZp686P02235, FLJ21643, NET18, FLJ21344, FLJ20273	RNA binding motif protein 47	NM_019027, NM_001098634, hCT1950686.1, hCT22910.2, hCT2326501.0, hCT2326504.0, hCT2326505.0, hCT2357596.0	218035_s_at, 222496_s_at, 229421_s_at, 229439_s_at, 229440_at	NP_061900.2, NP_001092104.1, EAW92965.1, EAW92967.1, EAW92968.1, EAW92969.1, EAW92964.1, EAW92966.1
GeneID:323	APBB2	4	40,812,044	41,216,635	404,591	-	4	1_A375_pNL7_minus_lncRNA::1::4234, 2_A375_pNL97_plus_lncRNA::1::6081, 2_A375_pNL97_plus_lncRNA::1::6082, 2_A375_pNL97_plus_lncRNA::1::6083	305227, 316923, 123, -2064	in gene, in gene, in gene, upstream	1	1	16.75	19.25	4	2_A375_pNL97_plus_lncRNA::1	27	Gene APBB2	FE65L1, APBB2, MGC35575, FE65L, DKFZp434E033	amyloid beta (A4) precursor protein-binding, family B, member 2	NM_173075, NM_004307, NM_001166050, NM_001166051, NM_001166052, NM_001166053, NM_001166054, hCT2357592.0, hCT2357593.0, hCT24282.3	213419_at, 216747_at, 216750_at, 40148_at	NP_775098.2, NP_004298.1, NP_001159522.1, NP_001159523.1, NP_001159524.1, NP_001159525.1, NP_001159526.1, EAW92975.1, EAW92976.1, EAW92977.1
GeneID:8929	PHOX2B	4	41,746,099	41,750,987	4,888	-	1	1_A375_pNL7_minus_lncRNA::1::4235	14411	downstream	1	0	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene PHOX2B	PMX2B, PHOX2B, NBPhox, NBLST2	paired-like homeobox 2b	NM_003924, hCT23489.1	207009_at	NP_003915.2, EAW92989.1
GeneID:285429	DCAF4L1	4	41,983,713	41,988,484	4,771	+	1	2_A375_pNL97_plus_lncRNA::1::6084	8831	downstream	0	1	21	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene DCAF4L1	MGC126021, WDR21B, DCAF4L1, MGC126022	DDB1 and CUL4 associated factor 4-like 1	NM_001029955, hCT1643188.3	1562209_at, 233491_at	NP_001025126.2, EAW92995.1
GeneID:10463	SLC30A9	4	41,992,523	42,089,551	97,028	+	1	2_A375_pNL97_plus_lncRNA::1::6084	21	in gene	0	1	21	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC30A9	GAC63, HUEL, ZNT9, C4orf1, SLC30A9	solute carrier family 30 (zinc transporter), member 9	NM_006345, hCT1640889.3, hCT2326233.0, hCT2326235.0, hCT2357597.0	202614_at	NP_006336.3, EAW92999.1, EAW92996.1, EAW92997.1, EAW92998.1
GeneID:10396	ATP8A1	4	42,410,390	42,659,122	248,732	-	2	1_A375_pNL7_minus_lncRNA::1::4236, 2_A375_pNL97_plus_lncRNA::1::6085	-238, -302	upstream, upstream	1	1	37	27	1	1_A375_pNL7_minus_lncRNA::1	37	Gene ATP8A1	ATPP2, MGC26327, ATPIA, MGC130042, MGC130043, ATP8A1, ATPASEII	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	NM_006095, NM_001105529, hCT1950326.1, hCT2326283.0	1569773_at, 210192_at	NP_006086.1, NP_001098999.1, EAW93003.1, EAW93004.1
GeneID:60558	GUF1	4	44,680,433	44,702,697	22,264	+	1	2_A375_pNL97_plus_lncRNA::1::6086	15	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GUF1	GUF1, FLJ13220, EF-4	GUF1 GTPase homolog (S. cerevisiae)	NM_021927, hCT2326193.0, hCT24099.3	218884_s_at, 222770_s_at	NP_068746.2, EAW93016.1, EAW93017.1
GeneID:54951	COMMD8	4	47,452,815	47,465,676	12,861	-	1	2_A375_pNL97_plus_lncRNA::1::6087	140	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene COMMD8	FLJ20502, COMMD8	COMM domain containing 8	NM_017845, hCT1950966.1, hCT2326388.0	218351_at	NP_060315.1, EAW93033.1, EAW93034.1
GeneID:285527	FRYL	4	48,499,380	48,782,316	282,936	-	2	1_A375_pNL7_minus_lncRNA::1::4238, 2_A375_pNL97_plus_lncRNA::1::6088	268, 204	in gene, in gene	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FRYL	FRYL, KIAA0826, FLJ16177, DKFZp686E205	FRY-like	NM_015030	1554260_a_at, 1562625_at, 1562650_at, 1563687_a_at, 212546_s_at, 212548_s_at	NP_055845.1
GeneID:54940	OCIAD1	4	48,833,060	48,863,834	30,774	+	2	1_A375_pNL7_minus_lncRNA::1::4239, 2_A375_pNL97_plus_lncRNA::1::6089	-196, 92	upstream, in gene	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene OCIAD1	OCIA, MGC111072, FLJ20455, ASRIJ, TPA018, OCIAD1	OCIA domain containing 1	NM_017830, NM_001079839, NM_001079840, NM_001079841, NM_001168254, NM_001079842, hCT1641699.3, hCT1957674.1, hCT1957676.1, hCT1957677.1	223010_s_at, 223011_s_at, 232644_x_at, 235537_at, 238748_x_at	NP_060300.1, NP_001073308.1, NP_001073309.1, NP_001073310.1, NP_001161726.1, NP_001073311.2, EAW93070.1, EAW93071.1, EAW93072.1, EAW93073.1
GeneID:23142	DCUN1D4	4	52,709,276	52,783,003	73,727	+	1	2_A375_pNL97_plus_lncRNA::1::6090	80036	downstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene DCUN1D4	KIAA0276, FLJ42355, DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	NM_001040402, NM_015115, hCT12509.3, hCT1967380.1, hCT2359050.0, hCT2359051.0, hCT2359052.0	212851_at, 212853_at, 212855_at	NP_001035492.1, NP_055930.2, EAX05425.1, EAX05426.1, EAX05427.1, EAX05428.1, EAX05424.1
GeneID:57291	KIAA0114	4	53,578,621	53,580,305	1,684	+	1	2_A375_pNL97_plus_lncRNA::1::6091	67	in gene	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene KIAA0114	KIAA00167, KIAA0114	KIAA0114	NR_024031	224870_at	
GeneID:677810	SNORA26	4	53,579,416	53,579,537	121	+	1	2_A375_pNL97_plus_lncRNA::1::6091	-728	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SNORA26	HBI-6, SNORA26	small nucleolar RNA, H/ACA box 26	NR_003016		
GeneID:152579	SCFD2	4	53,739,149	54,232,242	493,093	-	2	1_A375_pNL7_minus_lncRNA::1::4241, 2_A375_pNL97_plus_lncRNA::1::6092	-46, -14	upstream, upstream	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SCFD2	FLJ39514, SCFD2, FLJ21060, STXBP1L1	sec1 family domain containing 2	NM_152540, hCT12606.3, hCT2358988.0	226923_at, 236634_at	NP_689753.2, EAX05442.1, EAX05443.1
GeneID:81608	FIP1L1	4	54,243,820	54,326,103	82,283	+	2	1_A375_pNL7_minus_lncRNA::1::4242, 2_A375_pNL97_plus_lncRNA::1::6093	426, 100	in gene, in gene	1	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FIP1L1	Rhe, DKFZp586K0717, FLJ33619, FIP1L1, hFip1	FIP1 like 1 (S. cerevisiae)	NM_030917, NM_001134937, NM_001134938, hCT1957989.1, hCT2326360.0, hCT2326361.0, hCT2326363.0, hCT2326364.0	1554424_at, 221007_s_at	NP_112179.2, NP_001128409.1, NP_001128410.1, EAX05445.1, EAX05446.1, EAX05449.1, EAX05447.1, EAX05448.1
GeneID:84708	LNX1	4	54,326,437	54,457,724	131,287	-	1	2_A375_pNL97_plus_lncRNA::1::6094	83516	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LNX1	PDZRN2, MPDZ, LNX1, LNX	ligand of numb-protein X 1	NM_032622, NM_001126328, hCT12609.3, hCT2326387.0	223611_s_at, 223612_s_at	NP_116011.2, NP_001119800.1, EAX05450.1, EAX05451.1
GeneID:100506444	LOC100506444	4	54,562,068	54,600,681	38,613	+	2	1_A375_pNL7_minus_lncRNA::1::4243, 2_A375_pNL97_plus_lncRNA::1::6095	7276, 7052	in gene, in gene	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506444		hypothetical LOC100506444	XR_112639, XR_110059, XR_113663		
GeneID:100506462	LOC100506462	4	56,232,768	56,251,747	18,979	-	2	1_A375_pNL7_minus_lncRNA::1::4246, 2_A375_pNL97_plus_lncRNA::1::6097	-10125, -10397	upstream, upstream	1	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100506462		hypothetical LOC100506462	XR_112633, XR_110060, XR_113666		
GeneID:55858	TMEM165	4	56,262,090	56,292,342	30,252	+	2	1_A375_pNL7_minus_lncRNA::1::4246, 2_A375_pNL97_plus_lncRNA::1::6097	-218, 54	upstream, in gene	1	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene TMEM165	TMEM165, TPARL, TMPT27	transmembrane protein 165	NM_018475, hCT1967377.1	218095_s_at, 222515_x_at, 226825_s_at, 226827_at, 230512_x_at	NP_060945.2, EAX05467.1
GeneID:132954	PDCL2	4	56,422,692	56,458,379	35,687	-	1	2_A375_pNL97_plus_lncRNA::1::6098	43	in gene	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene PDCL2	PDCL2, GCPHLP	phosducin-like 2	NM_152401, hCT2326444.0	237477_at	NP_689614.2, EAX05469.1
GeneID:10874	NMU	4	56,461,398	56,502,465	41,067	-	1	2_A375_pNL97_plus_lncRNA::1::6098	44129	downstream	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene NMU	NMU	neuromedin U	NM_006681, hCT11678.2, hCT1962295.1	206023_at	NP_006672.1, EAX05471.1, EAX05470.1
GeneID:55763	EXOC1	4	56,719,816	56,771,244	51,428	+	1	2_A375_pNL97_plus_lncRNA::1::6099	56	in gene	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene EXOC1	SEC3L1, SEC3, BM-102, FLJ10893, SEC3P, EXOC1	exocyst complex component 1	NM_018261, NM_178237, NM_001024924, hCT11650.3, hCT2326350.0, hCT2326352.0, hCT2359047.0	222127_s_at	NP_060731.2, NP_839955.1, NP_001020095.1, EAX05473.1, EAX05474.1, EAX05475.1, EAX05476.1
GeneID:9662	CEP135	4	56,815,037	56,899,527	84,490	+	1	2_A375_pNL97_plus_lncRNA::1::6100	3	in gene	0	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CEP135	KIAA0635, CEP4, CEP135	centrosomal protein 135kDa	NM_025009	206003_at, 207286_at	NP_079285.2
GeneID:5471	PPAT	4	57,259,528	57,301,845	42,317	-	1	2_A375_pNL97_plus_lncRNA::1::6102	-171	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PPAT	PPAT, ATASE, GPAT, PRAT	phosphoribosyl pyrophosphate amidotransferase	NM_002703, hCT2326605.0, hCT2326606.0	209433_s_at, 209434_s_at, 235833_at	NP_002694.3, EAX05488.1, EAX05487.1
GeneID:10606	PAICS	4	57,301,915	57,327,534	25,619	+	1	2_A375_pNL97_plus_lncRNA::1::6102	101	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PAICS	ADE2H1, MGC5024, PAIS, MGC1343, ADE2, PAICS, AIRC, DKFZp781N1372	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	NM_006452, NM_001079524, NM_001079525, hCT2326464.0, hCT2326465.0, hCT2326466.0, hCT2326467.0, hCT2326468.0, hCT2359014.0	201013_s_at, 201014_s_at, 214664_at	NP_006443.1, NP_001072992.1, NP_001072993.1, EAX05489.1, EAX05490.1, EAX05494.1, EAX05491.1, EAX05492.1, EAX05493.1
GeneID:132946	ARL9	4	57,371,375	57,390,058	18,683	+	1	2_A375_pNL97_plus_lncRNA::1::6103	26673	downstream	0	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ARL9	ARL9	ADP-ribosylation factor-like 9	NM_206919, hCT1785161.1, hCT2359044.0	229062_at	NP_996802.1, EAX05500.1, EAX05499.1
GeneID:100506564	LOC100506564	4	57,396,843	57,469,489	72,646	+	1	2_A375_pNL97_plus_lncRNA::1::6103	1205	in gene	0	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100506564		hypothetical LOC100506564	XM_003118877, XM_003120434		XP_003118925.1, XP_003120482.1
GeneID:5978	REST	4	57,774,042	57,802,010	27,968	+	3	1_A375_pNL7_minus_lncRNA::1::4247, 1_A375_pNL7_minus_lncRNA::1::4248, 2_A375_pNL97_plus_lncRNA::1::6104	262, 1382, 566	in gene, in gene, in gene	1	1	16.5	17	2	2_A375_pNL97_plus_lncRNA::1	18	Gene REST	XBR, REST, NRSF	RE1-silencing transcription factor	NM_005612, NM_001193508, hCT1785153.2, hCT2326478.0	204535_s_at	NP_005603.3, NP_001180437.1, EAX05516.1, EAX05517.1
GeneID:5431	POLR2B	4	57,845,109	57,897,334	52,225	+	1	2_A375_pNL97_plus_lncRNA::1::6105	42027	in gene	0	1	17	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene POLR2B	POL2RB, RPB2, hRPB140, POLR2B, hsRPB2	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	NM_000938, hCT2326480.0	1555836_at, 1555837_s_at, 201803_at	NP_000929.1, EAX05519.1
GeneID:3490	IGFBP7	4	57,897,244	57,976,539	79,295	-	1	2_A375_pNL97_plus_lncRNA::1::6105	89403	downstream	0	1	17	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene IGFBP7	IGFBP-7, MAC25, IGFBP7, IGFBPRP1, IGFBP-7v, FSTL2, AGM, PSF	insulin-like growth factor binding protein 7	NM_001553, hCT1785304.1, hCT2326597.0	201162_at, 201163_s_at, 213910_at	NP_001544.1, EAX05521.1, EAX05520.1
GeneID:255130	LOC255130	4	57,975,928	58,071,465	95,537	+	1	1_A375_pNL7_minus_lncRNA::1::4249	54552	in gene	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC255130		hypothetical LOC255130	NR_034081	1557395_at	
GeneID:57050	UTP3	4	71,554,196	71,556,268	2,072	+	1	1_A375_pNL7_minus_lncRNA::1::4250	-180	upstream	1	0	20	10	1	1_A375_pNL7_minus_lncRNA::1	20	Gene UTP3	SAS10, CRLZ1, FLJ23256, CRL1, UTP3	UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae)	NM_020368, hCT8049.2	209486_at	NP_065101.1, EAX05627.1
GeneID:8671	SLC4A4	4	72,053,003	72,437,804	384,801	+	1	1_A375_pNL7_minus_lncRNA::1::4251	269733	in gene	1	0	16	5	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SLC4A4	NBC2, KNBC, DKFZp781H1314, hhNMC, HNBC1, SLC4A5, NBC1, pNBC, SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	NM_001098484, NM_003759, NM_001134742, hCT1954854.1, hCT1954855.1, hCT2326991.0, hCT2326992.0, hCT2326993.0, hCT2359046.0	1554027_a_at, 203908_at, 210738_s_at, 210739_x_at, 211494_s_at	NP_001091954.1, NP_003750.1, NP_001128214.1, EAX05639.1, EAX05642.1, EAX05644.1, EAX05640.1, EAX05641.1, EAX05643.1
GeneID:10886	NPFFR2	4	72,897,521	73,013,918	116,397	+	2	1_A375_pNL7_minus_lncRNA::1::4252, 2_A375_pNL97_plus_lncRNA::1::6108	80847, 80911	in gene, in gene	1	1	15	15	1	1_A375_pNL7_minus_lncRNA::1	15	Gene NPFFR2	NPGPR, GPR74, HLWAR77, NPFF2, NPFFR2	neuropeptide FF receptor 2	NM_001144756, NM_004885, NM_053036, hCT1961268.1, hCT1961269.1, hCT2326981.0, hCT6047.1	224169_at	NP_001138228.1, NP_004876.2, NP_444264.1, EAX05647.1, EAX05648.1, EAX05650.1, EAX05649.1
GeneID:285521	COX18	4	73,920,416	73,935,472	15,056	-	1	2_A375_pNL97_plus_lncRNA::1::6109	-96	upstream	0	1	11	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene COX18	FLJ38991, COX18HS, COX18, MGC126733	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	NM_173827, hCT1647445.4	227442_at, 230909_at	NP_776188.1, EAX05653.1
GeneID:26057	ANKRD17	4	73,940,502	74,124,502	184,000	-	1	2_A375_pNL97_plus_lncRNA::1::6109	168934	downstream	0	1	11	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ANKRD17	GTAR, KIAA0697, ANKRD17, FLJ22206, NY-BR-16	ankyrin repeat domain 17	NM_032217, NM_198889, hCT1954827.2, hCT1970736.1, hCT2358986.0, hCT2358987.0, hCT6049.3	212211_at, 225852_at	NP_115593.3, NP_942592.1, EAX05654.1, EAX05655.1, EAX05657.1, EAX05658.1, EAX05656.1
GeneID:2920	CXCL2	4	74,962,752	74,964,997	2,245	-	1	2_A375_pNL97_plus_lncRNA::1::6111	-10395	upstream	0	1	11	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CXCL2	MIP2, CINC-2a, GROb, CXCL2, GRO2, MGSA-b, SCYB2, MIP2A, MIP-2a	chemokine (C-X-C motif) ligand 2	NM_002089, hCT2327076.0, hCT7397.3	1569203_at, 209774_x_at, 230101_at	NP_002080.1, EAX05700.1, EAX05701.1
GeneID:441024	MTHFD2L	4	75,023,829	75,168,816	144,987	+	2	1_A375_pNL7_minus_lncRNA::1::4253, 2_A375_pNL97_plus_lncRNA::1::6112	-133, -165	upstream, upstream	1	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MTHFD2L	MGC72244, MTHFD2L, FLJ13105, MGC45532	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	NM_001144978, hCT1959730.2, hCT1959731.2, hCT1959732.2, hCT2327046.1, hCT2351731.0, hCT7405.2	1554841_at, 1562644_at, 220346_at, 233083_at, 238762_at, 239562_at, 242370_at	NP_001138450.1, EAX05702.1, EAX05703.1, EAX05705.1, EAX05706.1, EAX05707.1, EAX05704.1
GeneID:25898	RCHY1	4	76,404,347	76,439,628	35,281	-	2	1_A375_pNL7_minus_lncRNA::1::4254, 2_A375_pNL97_plus_lncRNA::1::6114	-148, -52	upstream, upstream	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RCHY1	RCHY1, RNF199, DKFZp586C1620, PRO1996, hARNIP, ZNF363, PIRH2, CHIMP, ARNIP	ring finger and CHY zinc finger domain containing 1	NM_015436, NM_001008925, NM_001009922, hCT2327573.0, hCT2327574.0, hCT2327575.0, hCT2327576.0, hCT2359003.0	212743_at, 212749_s_at, 214281_s_at, 235300_x_at	NP_056251.2, NP_001008925.1, NP_001009922.1, EAX05724.1, EAX05725.1, EAX05728.1, EAX05726.1, EAX05727.1
GeneID:152815	THAP6	4	76,439,654	76,455,236	15,582	+	2	1_A375_pNL7_minus_lncRNA::1::4254, 2_A375_pNL97_plus_lncRNA::1::6114	122, 26	in gene, in gene	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene THAP6	THAP6, MGC30052	THAP domain containing 6	NM_144721, hCT15502.3, hCT1955559.0, hCT1955560.1, hCT2327118.0, hCT2359041.0, hCT2359042.0, hCT2359043.0	227813_at, 230169_at, 235218_x_at, 235653_s_at	NP_653322.1, EAX05731.1, EAX05730.1, EAX05732.1, EAX05735.1, EAX05736.1, EAX05733.1, EAX05734.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:166785	MMAA	4	146,540,540	146,581,187	40,647	+	1	2_A375_pNL97_plus_lncRNA::1::6164	-124	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MMAA	MGC120010, MGC120013, MGC120012, MMAA, cblA, MGC120011	methylmalonic aciduria (cobalamin deficiency) cblA type	NM_172250, hCT2341295.0	236347_at, 237831_x_at, 239852_at, 242750_at	NP_758454.1, EAX05036.1
GeneID:646603	C4orf51	4	146,601,356	146,653,949	52,593	+	1	2_A375_pNL97_plus_lncRNA::1::6165	54740	downstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C4orf51	C4orf51	chromosome 4 open reading frame 51	NM_001080531		NP_001074000.1
GeneID:84068	SLC10A7	4	147,175,137	147,443,123	267,986	-	2	1_A375_pNL7_minus_lncRNA::1::4285, 2_A375_pNL97_plus_lncRNA::1::6166	-29, -29	upstream, upstream	1	1	21	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene SLC10A7	DKFZp779O2438, C4orf13, MGC25043, SLC10A7, DKFZp566M114, DKFZp313H0531, P7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7	NM_001029998, NM_032128	1555108_at, 224126_at, 235143_at	NP_001025169.1, NP_115504.1
GeneID:5458	POU4F2	4	147,560,045	147,563,623	3,578	+	3	1_A375_pNL7_minus_lncRNA::1::4286, 1_A375_pNL7_minus_lncRNA::1::4287, 2_A375_pNL97_plus_lncRNA::1::6167	-1773, 5139, -1805	upstream, downstream, upstream	1	1	17.5	20	2	2_A375_pNL97_plus_lncRNA::1	27	Gene POU4F2	BRN3.2, BRN3B, Brn-3b, POU4F2	POU class 4 homeobox 2	NM_004575, hCT30290.3	207725_at	NP_004566.2, EAX05025.1
GeneID:987	LRBA	4	151,185,594	151,936,879	751,285	-	1	2_A375_pNL97_plus_lncRNA::1::6169	514527	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LRBA	FLJ16600, DKFZp686A09128, LAB300, DKFZp686P2258, CDC4L, FLJ25686, BGL, LRBA, DKFZp686K03100, LBA, MGC72086	LPS-responsive vesicle trafficking, beach and anchor containing	NM_006726, hCT1959776.1	212692_s_at, 214109_at	NP_006717.2, EAX04996.1
GeneID:6189	RPS3A	4	152,020,754	152,025,804	5,050	+	1	2_A375_pNL97_plus_lncRNA::1::6170	14	in gene	0	1	15	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene RPS3A	FTE1, S3A, MGC23240, RPS3A, MFTL	ribosomal protein S3A	NM_001006, hCT2325156.0, hCT2325157.0, hCT2325158.0, hCT2325159.0, hCT2325160.0, hCT2325161.0, hCT2325162.0, hCT2325163.0	201257_x_at, 212391_x_at	NP_000997.1, EAX04988.1, EAX04989.1, EAX04990.1, EAX04991.1, EAX04995.1, EAX04992.1, EAX04993.1, EAX04994.1
GeneID:8944	SNORD73A	4	152,024,979	152,025,043	64	+	1	2_A375_pNL97_plus_lncRNA::1::6170	-4211	upstream	0	1	15	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SNORD73A	RNU73, U73, U73a, RNU73A, SNORD73A	small nucleolar RNA, C/D box 73A	NR_000007		
GeneID:729830	FAM160A1	4	152,330,398	152,584,784	254,386	+	1	1_A375_pNL7_minus_lncRNA::1::4289	-478	upstream	1	0	14	10	1	1_A375_pNL7_minus_lncRNA::1	14	Gene FAM160A1	FAM160A1, FLJ43373	family with sequence similarity 160, member A1	NM_001109977	1569465_at, 242687_at	NP_001103447.1
GeneID:5188	PET112L	4	152,591,808	152,682,175	90,367	-	1	1_A375_pNL7_minus_lncRNA::1::4290	-1	upstream	1	0	21	11	1	1_A375_pNL7_minus_lncRNA::1	21	Gene PET112L	PET112, HSPC199, PET112L	PET112-like (yeast)	NM_004564, hCT18117.3, hCT1959579.1, hCT1959580.1	204300_at	NP_004555.1, EAX04961.1, EAX04962.1, EAX04963.1
GeneID:201798	TIGD4	4	153,690,506	153,700,877	10,371	-	1	1_A375_pNL7_minus_lncRNA::1::4292	-227	upstream	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TIGD4	MGC43837, TIGD4	tigger transposable element derived 4	NM_145720, hCT1648440.3	1552522_at, 1552523_a_at	NP_663772.1, EAX04973.1
GeneID:27236	ARFIP1	4	153,701,112	153,833,064	131,952	+	1	1_A375_pNL7_minus_lncRNA::1::4292	-8	upstream	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ARFIP1	MGC117369, ARFIP1, HSU52521	ADP-ribosylation factor interacting protein 1	NM_014447, NM_001025593, NM_001025595, hCT1772643.2, hCT18114.3, hCT1959578.1, hCT2325064.0, hCT2325066.0	214483_s_at, 218230_at	NP_055262.1, NP_001020764.1, NP_001020766.1, EAX04968.1, EAX04970.1, EAX04971.1, EAX04969.1, EAX04972.1
GeneID:85462	FHDC1	4	153,864,135	153,900,848	36,713	+	2	1_A375_pNL7_minus_lncRNA::1::4293, 2_A375_pNL97_plus_lncRNA::1::6171	40537, 40601	downstream, downstream	1	1	22	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene FHDC1	KIAA1727, FHDC1	FH2 domain containing 1	NM_033393, hCT19231.3	226599_at	NP_203751.2, EAX04967.1
GeneID:54798	DCHS2	4	155,155,527	155,412,930	257,403	-	1	2_A375_pNL97_plus_lncRNA::1::6172	156706	in gene	0	1	3	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene DCHS2	PCDHJ, CDHR7, CDH27, CDHJ, DCHS2, FLJ20047, PCDH23	dachsous 2 (Drosophila)	NM_017639, NM_001142552, NM_001142553, hCT1782315.2, hCT2325378.1, hCT2325379.1, hCT2325380.1, hCT2325381.1, hCT2325382.1	220373_at, 242764_at	NP_060109.2, NP_001136024.1, NP_001136025.1, EAX04942.1, EAX04943.1, EAX04945.1, EAX04944.1, EAX04946.1, EAX04947.1
GeneID:2891	GRIA2	4	158,141,736	158,287,227	145,491	+	1	2_A375_pNL97_plus_lncRNA::1::6173	-200	upstream	0	1	22	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene GRIA2	GluA2, GRIA2, HBGR2, GluR-K2, GLUR2, GLURB	glutamate receptor, ionotropic, AMPA 2	NM_001083619, NM_000826, NM_001083620, hCT18060.3, hCT1955228.1, hCT2325192.0, hCT2325194.0, hCT2325196.0, hCT2325197.0, hCT2325198.0	205358_at, 236538_at, 241172_at	NP_001077088.1, NP_000817.2, NP_001077089.1, EAX04866.1, EAX04867.1, EAX04870.1, EAX04865.1, EAX04868.1, EAX04869.1, EAX04871.1
GeneID:201725	C4orf46	4	159,587,631	159,593,202	5,371	-	2	1_A375_pNL7_minus_lncRNA::1::4294, 2_A375_pNL97_plus_lncRNA::1::6175	-238, -254	upstream, upstream	1	1	119	124	1	2_A375_pNL97_plus_lncRNA::1	124	Gene C4orf46	C4orf46	chromosome 4 open reading frame 46	NM_001008393	235088_at, 236015_at	NP_001008394.1
GeneID:2110	ETFDH	4	159,593,277	159,629,842	36,565	+	2	1_A375_pNL7_minus_lncRNA::1::4294, 2_A375_pNL97_plus_lncRNA::1::6175	163, 179	in gene, in gene	1	1	119	124	1	2_A375_pNL97_plus_lncRNA::1	124	Gene ETFDH	ETFQO, ETFDH, MADD	electron-transferring-flavoprotein dehydrogenase	NM_004453, hCT1955220.1	205530_at, 33494_at	NP_004444.2, EAX04854.1
GeneID:5481	PPID	4	159,630,279	159,644,552	14,273	-	1	2_A375_pNL97_plus_lncRNA::1::6176	104	in gene	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene PPID	CYP-40, CYPD, MGC33096, PPID	peptidylprolyl isomerase D	NM_005038, hCT7442.2	204185_x_at, 204186_s_at, 228469_at	NP_005029.1, EAX04853.1
GeneID:56884	FSTL5	4	162,305,049	163,085,186	780,137	-	2	1_A375_pNL7_minus_lncRNA::1::4296, 2_A375_pNL97_plus_lncRNA::1::6177	34, 66	in gene, in gene	1	1	22	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene FSTL5	KIAA1263, DKFZp566D234, FSTL5	follistatin-like 5	NM_020116, NM_001128427, NM_001128428, hCT1961918.2	232010_at	NP_064501.2, NP_001121899.1, NP_001121900.1, EAX04846.1
GeneID:55319	C4orf43	4	164,415,673	164,441,691	26,018	+	2	1_A375_pNL7_minus_lncRNA::1::4297, 2_A375_pNL97_plus_lncRNA::1::6178	135, 7	in gene, in gene	1	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C4orf43	FLJ52950, C4orf43, FLJ11184	chromosome 4 open reading frame 43	NM_018352, hCT18753.4, hCT1971109.1	218513_at	NP_060822.2, EAX04836.1, EAX04837.1
GeneID:55601	DDX60	4	169,137,442	169,239,958	102,516	-	1	2_A375_pNL97_plus_lncRNA::1::6179	44774	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DDX60	FLJ10787, DDX60, FLJ20035	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	NM_017631, hCT1782733.3, hCT1952480.1, hCT2324715.0, hCT2324716.0	218986_s_at	NP_060101.3, EAX04806.1, EAX04807.1, EAX04808.1, EAX04809.1
GeneID:9848	MFAP3L	4	170,907,748	170,947,429	39,681	-	2	1_A375_pNL7_minus_lncRNA::1::4300, 2_A375_pNL97_plus_lncRNA::1::6181	-1163, -1147	upstream, upstream	1	1	20	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene MFAP3L	NYD-sp9, MFAP3L	microfibrillar-associated protein 3-like	NM_021647, NM_001009554, hCT2324823.0, hCT2324824.0, hCT8360.3	205442_at, 210492_at, 210493_s_at, 210843_s_at	NP_067679.6, NP_001009554.1, EAX04773.1, EAX04774.1, EAX04775.1
GeneID:51809	GALNT7	4	174,089,904	174,245,118	155,214	+	2	1_A375_pNL7_minus_lncRNA::1::4302, 2_A375_pNL97_plus_lncRNA::1::6183	83726, 83744	in gene, in gene	1	1	18	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene GALNT7	GALNAC-T7, GalNAcT7, GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	NM_017423, hCT1609927.1	218313_s_at, 222587_s_at	NP_059119.2, EAX04761.1
GeneID:3148	HMGB2	4	174,252,527	174,255,595	3,068	-	1	2_A375_pNL97_plus_lncRNA::1::6184	-277	upstream	0	1	15	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene HMGB2	HMGB2, HMG2	high mobility group box 2	NM_002129, NM_001130688, NM_001130689, hCT2324675.0, hCT31773.3	208808_s_at, 236091_at, 243365_at	NP_002120.1, NP_001124160.1, NP_001124161.1, EAX04758.1, EAX04759.1
GeneID:26269	FBXO8	4	175,157,809	175,205,402	47,593	-	1	2_A375_pNL97_plus_lncRNA::1::6186	346	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FBXO8	DC10, FBX8, FBS, FBXO8	F-box protein 8	NM_012180, hCT2324636.0, hCT2324637.0, hCT2324638.0, hCT2358959.0, hCT31259.2	1554806_a_at, 223240_at	NP_036312.2, EAX04741.1, EAX04742.1, EAX04743.1, EAX04744.1, EAX04745.1
GeneID:80817	KIAA1712	4	175,204,828	175,254,531	49,703	+	1	2_A375_pNL97_plus_lncRNA::1::6186	228	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene KIAA1712	PS1TP3, KIAA1712	KIAA1712	NM_001040157, NM_001145314, hCT2349267.0, hCT2349268.0, hCT31260.3	228334_x_at, 231850_x_at, 241426_at	NP_001035247.1, NP_001138786.1, EAX04738.1, EAX04739.1, EAX04740.1
GeneID:8001	GLRA3	4	175,563,198	175,750,465	187,267	-	3	1_A375_pNL7_minus_lncRNA::1::4304, 1_A375_pNL7_minus_lncRNA::1::4305, 2_A375_pNL97_plus_lncRNA::1::6187	365, -303, 365	in gene, upstream, in gene	1	1	19	17.5	2	2_A375_pNL97_plus_lncRNA::1	29	Gene GLRA3	GLRA3		NM_001042543, NM_006529, hCT1825781.2, hCT2324628.0, hCT2324630.0, hCT31258.3	207926_s_at, 210661_at, 216021_s_at	NP_001036008.1, NP_006520.2, EAX04730.1, EAX04731.1, EAX04732.1, EAX04733.1
GeneID:140458	ASB5	4	177,134,824	177,190,373	55,549	-	1	2_A375_pNL97_plus_lncRNA::1::6188	-1579	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ASB5	ASB5	ankyrin repeat and SOCS box containing 5	NM_080874, hCT31782.3	235503_at	NP_543150.1, EAX04720.1
GeneID:175	AGA	4	178,351,928	178,363,657	11,729	-	2	1_A375_pNL7_minus_lncRNA::1::4306, 2_A375_pNL97_plus_lncRNA::1::6191	-2503, 469	upstream, in gene	1	1	14	17.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene AGA	AGU, GA, AGA, ASRG	aspartylglucosaminidase	NM_000027, NM_001171988, NR_033655, hCT2324530.0, hCT2324532.0, hCT2324533.0, hCT30294.2	204332_s_at, 204333_s_at, 216064_s_at	NP_000018.2, NP_001165459.1, EAX04712.1, EAX04713.1, EAX04714.1, EAX04715.1
GeneID:55714	ODZ3	4	183,245,137	183,724,177	479,040	+	2	2_A375_pNL97_plus_lncRNA::1::6201, 2_A375_pNL97_plus_lncRNA::1::6202	43535, 124655	in gene, in gene	0	1	12.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene ODZ3	TNM3, FLJ10886, FLJ10474, Ten-m3, ODZ3, KIAA1455	odz, odd Oz/ten-m homolog 3 (Drosophila)	NM_001080477	1559661_at, 219523_s_at, 227050_at	NP_001073946.1
GeneID:152641	C4orf38	4	184,018,174	184,020,352	2,178	-	2	1_A375_pNL7_minus_lncRNA::1::4315, 2_A375_pNL97_plus_lncRNA::1::6203	160, 668	in gene, in gene	1	1	32	17	1	1_A375_pNL7_minus_lncRNA::1	32	Gene C4orf38	C4orf38, FLJ30277, MGC161755, FLJ30278, MGC161757	chromosome 4 open reading frame 38	NR_024008, hCT2324303.1	1557685_at, 230572_at	EAX04695.1
GeneID:80014	WWC2	4	184,020,463	184,241,930	221,467	+	2	1_A375_pNL7_minus_lncRNA::1::4315, 2_A375_pNL97_plus_lncRNA::1::6203	-271, -799	upstream, upstream	1	1	32	17	1	1_A375_pNL7_minus_lncRNA::1	32	Gene WWC2	FLJ34082, WWC2, FLJ22029, BOMB	WW and C2 domain containing 2	NM_024949, hCT2324355.0	1554762_a_at, 218775_s_at, 222738_at, 237656_at	NP_079225.5, EAX04694.1
GeneID:55602	CDKN2AIP	4	184,365,789	184,369,049	3,260	+	2	1_A375_pNL7_minus_lncRNA::1::4316, 2_A375_pNL97_plus_lncRNA::1::6204	-285, 179	upstream, in gene	1	1	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene CDKN2AIP	FLJ20036, CDKN2AIP, CARF	CDKN2A interacting protein	NM_017632, hCT87122.3	218929_at	NP_060102.1, EAX04691.1
GeneID:389247	LOC389247	4	184,415,890	184,425,668	9,778	-	3	1_A375_pNL7_minus_lncRNA::1::4317, 2_A375_pNL97_plus_lncRNA::1::6205, 2_A375_pNL97_plus_lncRNA::1::6206	-28, -60, -1628	upstream, upstream, upstream	1	1	25	28.5	2	2_A375_pNL97_plus_lncRNA::1	40	Gene LOC389247		hypothetical LOC389247	NR_033995	1560841_at	
GeneID:3622	ING2	4	184,426,220	184,432,249	6,029	+	3	1_A375_pNL7_minus_lncRNA::1::4317, 2_A375_pNL97_plus_lncRNA::1::6205, 2_A375_pNL97_plus_lncRNA::1::6206	-524, -492, 1076	upstream, upstream, in gene	1	1	25	28.5	2	2_A375_pNL97_plus_lncRNA::1	40	Gene ING2	ING1L, p33ING2, ING2	inhibitor of growth family, member 2	NM_001564, hCT2324397.0, hCT7486.3	205981_s_at, 213544_at	NP_001555.1, EAX04689.1, EAX04690.1
GeneID:201965	RWDD4A	4	184,560,789	184,580,331	19,542	-	1	2_A375_pNL97_plus_lncRNA::1::6207	-85	upstream	0	1	11	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene RWDD4A	MGC10198, RWDD4A, RWDD4, FAM28A	RWD domain containing 4	NM_152682, hCT1826304.1	225574_at	NP_689895.2, EAX04688.1
GeneID:60684	C4orf41	4	184,580,446	184,634,745	54,299	+	1	2_A375_pNL97_plus_lncRNA::1::6207	-30	upstream	0	1	11	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene C4orf41	gry, fzgr, C4orf41, FLJ12716	chromosome 4 open reading frame 41	NM_021942, NM_199053, hCT2324398.0, hCT2324400.0	218179_s_at, 233558_s_at, 234747_at	NP_068761.4, NP_951008.1, EAX04686.1, EAX04687.1
GeneID:3660	IRF2	4	185,308,876	185,395,726	86,850	-	2	2_A375_pNL97_plus_lncRNA::1::6208, 2_A375_pNL97_plus_lncRNA::1::6209	56510, -722	in gene, upstream	0	1	14	21.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene IRF2	IRF-2, IRF2, DKFZp686F0244	interferon regulatory factor 2	NM_002199, hCT2324317.0, hCT2358908.0, hCT2358909.0, hCT7276.2	203275_at	NP_002190.2, EAX04678.1, EAX04677.1, EAX04679.1, EAX04680.1
GeneID:79682	MLF1IP	4	185,615,219	185,655,286	40,067	-	2	1_A375_pNL7_minus_lncRNA::1::4318, 2_A375_pNL97_plus_lncRNA::1::6210	-106, -74	upstream, upstream	1	1	49	59	1	2_A375_pNL97_plus_lncRNA::1	59	Gene MLF1IP	CENPU50, CENPU, MLF1IP, KLIP1, PBIP1, CENP50, FLJ23468	MLF1 interacting protein	NM_024629, hCT2324333.0	218883_s_at, 229304_s_at, 229305_at	NP_078905.2, EAX04666.1
GeneID:2180	ACSL1	4	185,676,749	185,747,215	70,466	-	3	1_A375_pNL7_minus_lncRNA::1::4319, 2_A375_pNL97_plus_lncRNA::1::6211, 2_A375_pNL97_plus_lncRNA::1::6212	12543, 12623, 655	in gene, in gene, in gene	1	1	16.5	20	2	1_A375_pNL7_minus_lncRNA::1	24	Gene ACSL1	FACL2, ACSL1, LACS2, FACL1, LACS, LACS1, ACS1	acyl-CoA synthetase long-chain family member 1	NM_001995, hCT2324327.1, hCT2324328.1, hCT2324329.1, hCT8051.4	201963_at, 207275_s_at	NP_001986.2, EAX04665.1, EAX04662.1, EAX04663.1, EAX04664.1
GeneID:291	SLC25A4	4	186,064,417	186,071,538	7,121	+	1	2_A375_pNL97_plus_lncRNA::1::6214	63	in gene	0	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC25A4	ANT1, AAC1, ANT, PEO3, SLC25A4, T1, PEO2	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	NM_001151, hCT2324365.0, hCT7175.2	1557631_at, 202825_at	NP_001142.2, EAX04655.1, EAX04656.1
GeneID:83891	SNX25	4	186,131,284	186,285,120	153,836	+	1	1_A375_pNL7_minus_lncRNA::1::4320	96204	in gene	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SNX25	MSTP043, FLJ23161, SNX25, SBBI31	sorting nexin 25	NM_031953, hCT2324368.0, hCT7669.2	1555368_s_at, 227311_at, 227408_s_at, 230066_at, 232425_at	NP_114159.2, EAX04651.1, EAX04652.1
GeneID:353322	ANKRD37	4	186,317,840	186,321,390	3,550	+	1	2_A375_pNL97_plus_lncRNA::1::6215	-496	upstream	0	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ANKRD37	MGC111507, Lrp2bp, ANKRD37	ankyrin repeat domain 37	NM_181726, hCT2324390.0, hCT7671.2	227337_at, 242546_x_at	NP_859077.1, EAX04648.1, EAX04647.1
GeneID:55325	UFSP2	4	186,320,694	186,347,139	26,445	-	3	1_A375_pNL7_minus_lncRNA::1::4321, 2_A375_pNL97_plus_lncRNA::1::6215, 2_A375_pNL97_plus_lncRNA::1::6216	-29, 29795, -29	upstream, downstream, upstream	1	1	23.5	28	2	2_A375_pNL97_plus_lncRNA::1	33	Gene UFSP2	C4orf20, FLJ11200, UFSP2	UFM1-specific peptidase 2	NM_018359, NR_028085, hCT2358926.0, hCT7668.2	218449_at	NP_060829.2, EAX04646.1, EAX04645.1
GeneID:441054	C4orf47	4	186,350,545	186,370,821	20,276	+	2	1_A375_pNL7_minus_lncRNA::1::4321, 2_A375_pNL97_plus_lncRNA::1::6216	-3377, -3377	upstream, upstream	1	1	27	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene C4orf47	C4orf47		NM_001114357	236915_at, 237585_at	NP_001107829.1
GeneID:27295	PDLIM3	4	186,421,814	186,456,712	34,898	-	1	1_A375_pNL7_minus_lncRNA::1::4322	232	in gene	1	0	17	11	1	1_A375_pNL7_minus_lncRNA::1	17	Gene PDLIM3	ALP, PDLIM3, FLJ26096, DKFZp686L0362	PDZ and LIM domain 3	NM_001114107, NM_014476, hCT1966774.1, hCT1966775.1, hCT2358904.0, hCT7350.2	209621_s_at, 210170_at, 238592_at	NP_001107579.1, NP_055291.2, EAX04638.1, EAX04639.1, EAX04640.1, EAX04641.1
GeneID:8470	SORBS2	4	186,506,598	186,877,870	371,272	-	4	1_A375_pNL7_minus_lncRNA::1::4323, 1_A375_pNL7_minus_lncRNA::1::4324, 2_A375_pNL97_plus_lncRNA::1::6218, 2_A375_pNL97_plus_lncRNA::1::6219	117422, 109134, 117358, 23534	in gene, in gene, in gene, in gene	1	1	19.67	20	3	1_A375_pNL7_minus_lncRNA::1	27	Gene SORBS2	SORBS2, KIAA0777, ARGBP2, PRO0618, FLJ93447	sorbin and SH3 domain containing 2	NM_003603, NM_021069, NM_001145670, NM_001145671, NM_001145672, NM_001145673, NM_001145674, NM_001145675, hCT1826400.1, hCT1826401.1, hCT2324660.0, hCT2324661.0, hCT2324663.0, hCT2324665.0, hCT2324669.0	1555472_at, 1558815_at, 204288_s_at, 220858_at, 225728_at, 233720_at, 237285_at	NP_003594.3, NP_066547.1, NP_001139142.1, NP_001139143.1, NP_001139144.1, NP_001139145.1, NP_001139146.1, NP_001139147.1, EAX04630.1, EAX04631.1, EAX04632.1, EAX04633.1, EAX04634.1, EAX04635.1, EAX04636.1
GeneID:285440	CYP4V2	4	187,112,674	187,134,617	21,943	+	2	1_A375_pNL7_minus_lncRNA::1::4325, 2_A375_pNL97_plus_lncRNA::1::6220	-66, 30	upstream, in gene	1	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene CYP4V2	MGC43534, BCD, CYP4V2, FLJ18432, CYP4AH1	cytochrome P450, family 4, subfamily V, polypeptide 2	NM_207352, hCT1826884.2	226745_at, 228391_at, 229959_at, 235719_at	NP_997235.3, EAX04624.1
GeneID:2195	FAT1	4	187,508,937	187,644,987	136,050	-	2	2_A375_pNL97_plus_lncRNA::1::6221, 2_A375_pNL97_plus_lncRNA::1::6222	539, -2901	in gene, upstream	0	1	11.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene FAT1	CDHF7, ME5, CDHR8, FAT, hFat1, FAT1	FAT tumor suppressor homolog 1 (Drosophila)	NM_005245, hCT2324646.0, hCT2324647.0, hCT7282.2	201579_at	NP_005236.2, EAX04616.1, EAX04614.1, EAX04615.1
GeneID:2483	FRG1	4	190,861,974	190,884,359	22,385	+	2	1_A375_pNL7_minus_lncRNA::1::4327, 2_A375_pNL97_plus_lncRNA::1::6228	-11, -54	upstream, upstream	1	1	23	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene FRG1	FRG1, FRG1A, FSG1	FSHD region gene 1	NM_004477, hCT2324273.0	235535_x_at	NP_004468.1, EAX04600.1
GeneID:133957	CCDC127	5	204,875	218,297	13,422	-	1	2_A375_pNL97_plus_lncRNA::1::6231	-887	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CCDC127	CCDC127, FLJ25701	coiled-coil domain containing 127	NM_145265, hCT1796292.1	1560354_at, 226515_at	NP_660308.1, EAW50981.1
GeneID:6389	SDHA	5	218,356	256,815	38,459	+	1	2_A375_pNL97_plus_lncRNA::1::6231	828	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SDHA	SDHF, CMD1GG, FP, SDH1, SDH2, SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	NM_004168, hCT1639941.3, hCT1961094.1, hCT2352428.0	201093_x_at	NP_004159.2, EAW50983.1, EAW50982.1, EAW50984.1
GeneID:100507671	LOC100507671	5	270,019	271,611	1,592	-	1	2_A375_pNL97_plus_lncRNA::1::6232	59	in gene	0	1	13	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100507671		hypothetical LOC100507671	XR_108556		
GeneID:10016	PDCD6	5	271,736	315,089	43,353	+	1	2_A375_pNL97_plus_lncRNA::1::6232	-184	upstream	0	1	13	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene PDCD6	PEF1B, MGC9123, FLJ46208, ALG-2, MGC111017, MGC119050, PDCD6	programmed cell death 6	NM_013232	1568762_at, 1568763_s_at, 1568764_x_at, 229283_at, 234297_at	NP_037364.1
GeneID:57491	AHRR	5	304,291	438,406	134,115	+	2	1_A375_pNL7_minus_lncRNA::1::4330, 2_A375_pNL97_plus_lncRNA::1::6233	94429, 69021	in gene, in gene	1	1	13.5	13	2	2_A375_pNL97_plus_lncRNA::1	16	Gene AHRR	AHRR, AHHR, MGC167813, MGC176630, AHH, bHLHe77, KIAA1234	aryl-hydrocarbon receptor repressor	NM_020731	229354_at	NP_065782.2
GeneID:9319	TRIP13	5	892,969	918,164	25,195	+	2	1_A375_pNL7_minus_lncRNA::1::4331, 2_A375_pNL97_plus_lncRNA::1::6234	19735, 19735	in gene, in gene	1	1	36	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene TRIP13	TRIP13, 16E1BP	thyroid hormone receptor interactor 13	NM_004237, NM_001166260, hCT2267036.0, hCT7953.2	204033_at	NP_004228.1, NP_001159732.1, EAX08185.1, EAX08186.1
GeneID:348932	SLC6A18	5	1,225,470	1,246,304	20,834	+	2	1_A375_pNL7_minus_lncRNA::1::4332, 2_A375_pNL97_plus_lncRNA::1::6235	21778, 21698	downstream, downstream	1	1	20	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SLC6A18	Xtrp2, FLJ31236, SLC6A18	solute carrier family 6, member 18	NM_182632, hCT2266832.0, hCT2266833.0	238215_at	NP_872438.2, EAX08172.1, EAX08173.1
GeneID:7015	TERT	5	1,253,262	1,295,162	41,880	-	2	1_A375_pNL7_minus_lncRNA::1::4332, 2_A375_pNL97_plus_lncRNA::1::6235	47914, 47994	downstream, downstream	1	1	20	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene TERT	EST2, TP2, TCS1, TRT, TERT, hEST2	telomerase reverse transcriptase	NM_198253, NM_001193376, hCT2268566.0, hCT2268567.0, hCT2268568.0, hCT2359282.0, hCT2359283.0, hCT2359284.0, hCT2359285.0	1555271_a_at, 207199_at	NP_937983.2, NP_001180305.1, EAX08165.1, EAX08166.1, EAX08168.1, EAX08170.1, EAX08167.1, EAX08169.1, EAX08171.1
GeneID:170690	ADAMTS16	5	5,140,443	5,320,412	179,969	+	1	2_A375_pNL97_plus_lncRNA::1::6241	131141	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ADAMTS16	FLJ16731, ADAMTS16s, ADAMTS16	ADAM metallopeptidase with thrombospondin type 1 motif, 16	NM_139056, hCT1953083.1, hCT2266928.0, hCT2266929.0, hCT2359271.0	238125_at	NP_620687.2, EAX08120.1, EAX08117.1, EAX08118.1, EAX08119.1
GeneID:23379	KIAA0947	5	5,422,807	5,490,338	67,531	+	2	1_A375_pNL7_minus_lncRNA::1::4334, 2_A375_pNL97_plus_lncRNA::1::6242	-295, -279	upstream, upstream	1	1	22	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene KIAA0947	KIAA0947, DKFZp781J2344	KIAA0947	NM_015325	209654_at	NP_056140.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:401172	FLJ33360	5	6,310,554	6,337,405	26,851	-	2	2_A375_pNL97_plus_lncRNA::1::6243, 2_A375_pNL97_plus_lncRNA::1::6244	34525, 8957	downstream, in gene	0	1	13.5	21	2	2_A375_pNL97_plus_lncRNA::1	25	Gene FLJ33360		FLJ33360 protein	NR_026351, hCT2342593.0	1563969_at	EAX08111.1
GeneID:84246	MED10	5	6,372,039	6,378,639	6,600	-	2	2_A375_pNL97_plus_lncRNA::1::6245, 2_A375_pNL97_plus_lncRNA::1::6246	12679, 399	downstream, in gene	0	1	12	16	2	2_A375_pNL97_plus_lncRNA::1	18	Gene MED10	L6, MGC5309, NUT2, MED10, TRG20	mediator complex subunit 10	NM_032286, hCT9426.2	223247_at	NP_115662.2, EAX08110.1
GeneID:54888	NSUN2	5	6,599,352	6,633,473	34,121	-	1	2_A375_pNL97_plus_lncRNA::1::6247	-367	upstream	0	1	17	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene NSUN2	MISU, FLJ20303, SAKI, NSUN2, TRM4	NOP2/Sun domain family, member 2	NM_017755, NM_001193455, hCT1956662.1, hCT1956663.1, hCT9427.2	223076_s_at	NP_060225.4, NP_001180384.1, EAX08105.1, EAX08106.1, EAX08107.1
GeneID:6715	SRD5A1	5	6,633,500	6,669,675	36,175	+	1	2_A375_pNL97_plus_lncRNA::1::6247	340	in gene	0	1	17	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SRD5A1	S5AR 1, SRD5A1		NM_001047, hCT1961521.1, hCT7567.3	204675_at, 210959_s_at, 211056_s_at	NP_001038.1, EAX08103.1, EAX08104.1
GeneID:100505625	LOC100505625	5	6,686,438	6,707,824	21,386	-	1	2_A375_pNL97_plus_lncRNA::1::6248	-4656	upstream	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100505625		hypothetical LOC100505625	XR_112713, XR_108557, XR_113720		
GeneID:11044	PAPD7	5	6,714,718	6,757,161	42,443	+	1	2_A375_pNL97_plus_lncRNA::1::6248	-2236	upstream	0	1	14	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene PAPD7	TRF4-1, POLK, POLS, TUTASE5, LAK-1, TRF4, LAK1, PAPD7, TRF41	PAP associated domain containing 7	NM_006999, NM_001171805, NM_001171806, hCT9425.2	202466_at	NP_008930.1, NP_001165276.1, NP_001165277.1, EAX08101.1
GeneID:100288963	LOC100288963	5	7,850,919	7,862,131	11,212	+	2	1_A375_pNL7_minus_lncRNA::1::4335, 2_A375_pNL97_plus_lncRNA::1::6249	18281, 18233	downstream, downstream	1	1	18	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100288963		hypothetical LOC100288963	XR_108558, XR_108559		
GeneID:79072	FASTKD3	5	7,859,272	7,869,150	9,878	-	2	1_A375_pNL7_minus_lncRNA::1::4335, 2_A375_pNL97_plus_lncRNA::1::6249	-50, -2	upstream, upstream	1	1	18	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene FASTKD3	MGC5297, FLJ23274, FASTKD3, MGC142123	FAST kinase domains 3	NM_024091, NR_036553, hCT1956200.1, hCT28853.2	219200_at	NP_076996.2, EAX08095.1, EAX08094.1
GeneID:4552	MTRR	5	7,869,217	7,901,237	32,020	+	2	1_A375_pNL7_minus_lncRNA::1::4335, 2_A375_pNL97_plus_lncRNA::1::6249	-17, -65	upstream, upstream	1	1	18	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MTRR	MGC129643, MSR, cblE, MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	NM_024010, NM_002454, hCT1956198.1, hCT2359274.0, hCT2359275.0, hCT28090.2	203199_s_at, 203200_s_at	NP_076915.2, NP_002445.2, EAX08090.1, EAX08091.1, EAX08092.1, EAX08093.1
GeneID:9037	SEMA5A	5	9,035,138	9,546,233	511,095	-	1	2_A375_pNL97_plus_lncRNA::1::6251	301529	in gene	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene SEMA5A	semF, FLJ12815, SEMAF, SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	NM_003966, hCT1641022.3, hCT2266574.0	205405_at, 213169_at, 229427_at	NP_003957.2, EAX08079.1, EAX08078.1
GeneID:134145	FAM173B	5	10,226,438	10,250,014	23,576	-	2	1_A375_pNL7_minus_lncRNA::1::4337, 2_A375_pNL97_plus_lncRNA::1::6252	222, -770	in gene, upstream	1	1	15.5	14	2	1_A375_pNL7_minus_lncRNA::1	17	Gene FAM173B	FLJ20667, FAM173B	family with sequence similarity 173, member B	NM_199133, hCT2359272.0, hCT28088.2	225668_at, 225670_at	NP_954584.2, EAX08073.1, EAX08074.1
GeneID:22948	CCT5	5	10,250,282	10,266,501	16,219	+	2	1_A375_pNL7_minus_lncRNA::1::4337, 2_A375_pNL97_plus_lncRNA::1::6252	-490, 502	upstream, in gene	1	1	15.5	14	2	1_A375_pNL7_minus_lncRNA::1	17	Gene CCT5	CCT-epsilon, CCTE, KIAA0098, TCP-1-epsilon, CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	NM_012073, hCT28661.3	208696_at, 229068_at	NP_036205.1, EAX08072.1
GeneID:10299	6-Mar	5	10,353,828	10,435,491	81,663	+	1	2_A375_pNL97_plus_lncRNA::1::6253	-164	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene MARCH6	TEB4, MARCH6, MARCH-VI, RNF176, KIAA0597, DOA10	membrane-associated ring finger (C3HC4) 6	NM_005885, hCT2267408.0, hCT2267411.0, hCT28242.3	201736_s_at, 201737_s_at, 215512_at	NP_005876.2, EAX08065.1, EAX08066.1, EAX08067.1
GeneID:1611	DAP	5	10,679,342	10,761,387	82,045	-	2	2_A375_pNL97_plus_lncRNA::1::6254, 2_A375_pNL97_plus_lncRNA::1::6255	36267, -325	in gene, upstream	0	1	11	18	2	2_A375_pNL97_plus_lncRNA::1	19	Gene DAP	DAP, MGC99796	death-associated protein	NM_004394, hCT2266873.0, hCT2266875.0, hCT29090.2	201095_at	NP_004385.1, EAX08056.1, EAX08057.1, EAX08058.1
GeneID:1767	DNAH5	5	13,690,437	13,944,589	254,152	-	1	2_A375_pNL97_plus_lncRNA::1::6258	77421	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DNAH5	KIAA1603, CILD3, DNAH5, KTGNR, HL1, DNAHC5, PCD, FLJ46759	dynein, axonemal, heavy chain 5	NM_001369, hCT1805376.2	232381_s_at, 243938_x_at	NP_001360.1, EAX08050.1
GeneID:7204	TRIO	5	14,143,829	14,509,458	365,629	+	2	2_A375_pNL97_plus_lncRNA::1::6259, 2_A375_pNL97_plus_lncRNA::1::6260	34944, 124699	in gene, in gene	0	1	14	19	2	2_A375_pNL97_plus_lncRNA::1	19	Gene TRIO	ARHGEF23, TRIO, tgat, FLJ42780	triple functional domain (PTPRF interacting)	NM_007118, hCT1962736.1, hCT2278654.0, hCT2278656.0, hCT2278657.0, hCT28221.3	208178_x_at, 209010_s_at, 209011_at, 209012_at, 209013_x_at, 216697_at, 216700_at, 231403_at, 244527_at	NP_009049.2, EAX08044.1, EAX08045.1, EAX08046.1, EAX08047.1, EAX08048.1
GeneID:90268	FAM105B	5	14,664,783	14,699,842	35,059	+	2	1_A375_pNL7_minus_lncRNA::1::4340, 2_A375_pNL97_plus_lncRNA::1::6262	-335, -245	upstream, upstream	1	1	18	14	1	1_A375_pNL7_minus_lncRNA::1	18	Gene FAM105B	FAM105B, FLJ34884	family with sequence similarity 105, member B	NM_138348, hCT1955382.2, hCT1955383.2, hCT29070.4	228382_at, 229268_at, 229470_at, 240834_at	NP_612357.4, EAX08037.1, EAX08038.1, EAX08039.1
GeneID:56172	ANKH	5	14,704,909	14,871,887	166,978	-	3	1_A375_pNL7_minus_lncRNA::1::4341, 2_A375_pNL97_plus_lncRNA::1::6263, 2_A375_pNL97_plus_lncRNA::1::6264	-9073, 95903, -9137	upstream, in gene, upstream	1	1	14	19.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene ANKH	CCAL2, FLJ27166, CPPDD, ANK, HANK, ANKH, CMDJ, MANK	ankylosis, progressive homolog (mouse)	NM_054027, hCT2278371.0, hCT2359276.0	1560369_at, 1560370_x_at, 220076_at, 223092_at, 223093_at, 223094_s_at, 229176_at	NP_473368.1, EAX08035.1, EAX08034.1
GeneID:100128508	LOC100128508	5	14,775,189	14,777,141	1,952	-	1	2_A375_pNL97_plus_lncRNA::1::6263	1157	in gene	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100128508		PP12100	XM_003118526, XM_003120456		XP_003118574.1, XP_003120504.1
GeneID:441061	11-Mar	5	16,067,474	16,179,897	112,423	-	1	2_A375_pNL97_plus_lncRNA::1::6266	793	in gene	0	1	10	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MARCH11	MARCH-XI, MARCH11	membrane-associated ring finger (C3HC4) 11	NM_001102562	239359_at	NP_001096032.1
GeneID:401176	LOC401176	5	16,180,347	16,185,694	5,347	+	1	2_A375_pNL97_plus_lncRNA::1::6266	-1243	upstream	0	1	10	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC401176		hypothetical LOC401176	XR_112715, XR_108565, XR_113728	1562645_at	
GeneID:90441	ZNF622	5	16,451,628	16,465,894	14,266	-	2	1_A375_pNL7_minus_lncRNA::1::4343, 2_A375_pNL97_plus_lncRNA::1::6267	134, 6	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ZNF622	MGC2485, ZPR9, ZNF622, MGC17552	zinc finger protein 622	NM_033414, hCT28605.2	1560075_at, 225152_at	NP_219482.1, EAX08025.1
GeneID:54463	FAM134B	5	16,473,147	16,617,118	143,971	-	3	1_A375_pNL7_minus_lncRNA::1::4343, 2_A375_pNL97_plus_lncRNA::1::6267, 2_A375_pNL97_plus_lncRNA::1::6268	151358, 151230, 113993	downstream, downstream, in gene	1	1	13	17	2	1_A375_pNL7_minus_lncRNA::1	18	Gene FAM134B	FLJ20152, FLJ22179, HSAN2B, FAM134B, FLJ22155, JK1	family with sequence similarity 134, member B	NM_019000, NM_001034850, hCT1815068.1, hCT1815069.1	218510_x_at, 218532_s_at	NP_061873.2, NP_001030022.1, EAX08022.1, EAX08023.1
GeneID:1010	CDH12	5	21,750,973	22,853,731	1,102,758	-	2	1_A375_pNL7_minus_lncRNA::1::4345, 2_A375_pNL97_plus_lncRNA::1::6273	461235, 461123	in gene, in gene	1	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CDH12	CDHB, FLJ34857, CDH12	cadherin 12, type 2 (N-cadherin 2)	NM_004061, hCT1964290.2, hCT2348496.0, hCT28626.5	207149_at	NP_004052.2, EAX10734.1, EAX10735.1, EAX10736.1
GeneID:29102	RNASEN	5	31,400,601	31,532,282	131,681	-	1	2_A375_pNL97_plus_lncRNA::1::6278	-6	upstream	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RNASEN	RNASE3L, HSA242976, DROSHA, RN3, ETOHI2, RNASEN, RANSE3L	ribonuclease type III, nuclear	NM_013235, NM_001100412, hCT2289486.1, hCT2289487.1, hCT2289488.1, hCT2289490.1	218269_at	NP_037367.3, NP_001093882.1, EAX10767.1, EAX10768.1, EAX10769.1, EAX10770.1
GeneID:55322	C5orf22	5	31,532,373	31,555,165	22,792	+	1	2_A375_pNL97_plus_lncRNA::1::6278	-85	upstream	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C5orf22	FLJ11193, C5orf22, MGC33010, DKFZp667N066, FLJ23805	chromosome 5 open reading frame 22	NM_018356, hCT13922.3, hCT1954758.1, hCT2289362.0, hCT2359587.0	1552660_a_at, 1565939_at, 203736_at	NP_060826.2, EAX10772.1, EAX10771.1, EAX10773.1, EAX10774.1
GeneID:64083	GOLPH3	5	32,124,824	32,174,425	49,601	-	1	2_A375_pNL97_plus_lncRNA::1::6279	-39	upstream	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene GOLPH3	FLJ90675, MIDAS, GOPP1, GPP34, GOLPH3	golgi phosphoprotein 3 (coat-protein)	NM_022130, hCT13923.2, hCT1952506.1, hCT1958295.1	217803_at	NP_071413.1, EAX10760.1, EAX10761.1, EAX10762.1
GeneID:51663	ZFR	5	32,354,456	32,444,844	90,388	-	1	2_A375_pNL97_plus_lncRNA::1::6280	53676	in gene	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene ZFR	FLJ41312, ZFR1, ZFR	zinc finger RNA binding protein	NM_016107, hCT2289945.0, hCT2289947.0, hCT2289948.0	201856_s_at, 201857_at, 213286_at, 33148_at	NP_057191.2, EAX10790.1, EAX10789.1, EAX10791.1
GeneID:693164	MIR579	5	32,394,484	32,394,581	97	-	1	2_A375_pNL97_plus_lncRNA::1::6280	3413	downstream	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene MIR579	MIR579, MIRN579, hsa-mir-579	microRNA 579	NR_030305		
GeneID:6897	TARS	5	33,440,898	33,468,196	27,298	+	1	2_A375_pNL97_plus_lncRNA::1::6282	-226	upstream	0	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TARS	ThrRS, MGC9344, TARS	threonyl-tRNA synthetase	NM_152295, hCT2289499.0, hCT28056.3	201263_at, 240206_at	NP_689508.3, EAX10803.1, EAX10804.1
GeneID:81792	ADAMTS12	5	33,527,286	33,892,124	364,838	-	1	2_A375_pNL97_plus_lncRNA::1::6283	200988	in gene	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ADAMTS12	ADAMTS12, PRO4389	ADAM metallopeptidase with thrombospondin type 1 motif, 12	NM_030955, hCT1957567.2, hCT2289678.0	221421_s_at	NP_112217.2, EAX10808.1, EAX10809.1
GeneID:51289	RXFP3	5	33,936,491	33,939,023	2,532	+	2	1_A375_pNL7_minus_lncRNA::1::4348, 2_A375_pNL97_plus_lncRNA::1::6284	-267, -331	upstream, upstream	1	1	33	29	1	1_A375_pNL7_minus_lncRNA::1	33	Gene RXFP3	RLN3R1, MGC142000, SALPR, GPCR135, RXFP3, RXFPR3, MGC141998	relaxin/insulin-like family peptide receptor 3	NM_016568, hCT1645300.2	221066_at	NP_057652.1, EAX10810.1
GeneID:51151	SLC45A2	5	33,944,721	33,984,780	40,059	-	2	1_A375_pNL7_minus_lncRNA::1::4348, 2_A375_pNL97_plus_lncRNA::1::6284	48556, 48620	downstream, downstream	1	1	33	29	1	1_A375_pNL7_minus_lncRNA::1	33	Gene SLC45A2	1A1, SHEP5, SLC45A2, MATP, AIM1	solute carrier family 45, member 2	NM_016180, NM_001012509, hCT1952515.1, hCT2359585.0, hCT2359586.0, hCT28644.2	220245_at, 221644_s_at	NP_057264.3, NP_001012527.1, EAX10811.1, EAX10812.1, EAX10813.1, EAX10814.1
GeneID:23600	AMACR	5	33,987,091	34,008,220	21,129	-	2	2_A375_pNL97_plus_lncRNA::1::6285, 2_A375_pNL97_plus_lncRNA::1::6286	6732, 68	in gene, in gene	0	1	11	16	2	2_A375_pNL97_plus_lncRNA::1	17	Gene AMACR	RACE, RM, AMACR, CBAS4	alpha-methylacyl-CoA racemase	NM_014324, NM_203382, NM_001167595, NM_001167596, NM_001167597, NM_001167598, hCT1952511.1, hCT1958301.1, hCT2289659.0, hCT28298.2	209424_s_at, 209425_at, 209426_s_at, 217111_at, 217113_at, 236365_at	NP_055139.4, NP_976316.1, NP_001161067.1, NP_001161068.1, NP_001161069.1, NP_001161070.1, EAX10815.1, EAX10816.1, EAX10817.1, EAX10818.1
GeneID:114899	C1QTNF3	5	34,017,963	34,043,317	25,354	-	3	1_A375_pNL7_minus_lncRNA::1::4349, 1_A375_pNL7_minus_lncRNA::1::4350, 2_A375_pNL97_plus_lncRNA::1::6286	-4123, -10219, 35165	upstream, upstream, downstream	1	1	16	14	3	1_A375_pNL7_minus_lncRNA::1	19	Gene C1QTNF3	FLJ37576, CORS, CORS-26, C1QTNF3, Cors-26, CTRP3, C1ATNF3, Corcs, CORS26, Cors, CORCS	C1q and tumor necrosis factor related protein 3	NM_181435, NM_030945, hCT2289652.0, hCT2289654.0, hCT2289656.0	1561263_at, 220988_s_at	NP_852100.3, NP_112207.1, EAX10819.1, EAX10820.1, EAX10821.1
GeneID:26064	RAI14	5	34,656,433	34,832,717	176,284	+	1	2_A375_pNL97_plus_lncRNA::1::6287	182943	downstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RAI14	RAI13, RAI14, KIAA1334, DKFZp564G013, NORPEG	retinoic acid induced 14	NM_015577, NM_001145520, NM_001145521, NM_001145522, NM_001145523, NM_001145525, hCT2292780.0	202052_s_at	NP_056392.2, NP_001138992.1, NP_001138993.1, NP_001138994.1, NP_001138995.1, NP_001138997.1, EAW55898.1
GeneID:153657	TTC23L	5	34,839,269	34,899,567	60,298	+	1	2_A375_pNL97_plus_lncRNA::1::6287	107	in gene	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TTC23L	FLJ25439, TTC23L	tetratricopeptide repeat domain 23-like	NM_144725, hCT2344497.0, hCT2344501.0	1557003_at, 239620_at	NP_653326.3, EAW55900.1, EAW55901.1
GeneID:5810	RAD1	5	34,905,365	34,915,780	10,415	-	2	1_A375_pNL7_minus_lncRNA::1::4351, 2_A375_pNL97_plus_lncRNA::1::6288	4, -60	in gene, upstream	1	1	21	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene RAD1	HRAD1, RAD1, REC1	RAD1 homolog (S. pombe)	NM_002853, NR_026591	204460_s_at, 204461_x_at, 210216_x_at, 226535_at, 235253_at	NP_002844.1
GeneID:55299	BRIX1	5	34,915,820	34,925,787	9,967	+	2	1_A375_pNL7_minus_lncRNA::1::4351, 2_A375_pNL97_plus_lncRNA::1::6288	-44, 20	upstream, in gene	1	1	21	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene BRIX1	BRIX1, BXDC2, FLJ11100	BRX1, biogenesis of ribosomes, homolog (S.cerevisiae)	NM_018321, hCT2344499.0, hCT2344500.0	219177_at	NP_060791.3, EAW55909.1, EAW55910.1
GeneID:79925	SPEF2	5	35,617,989	35,814,713	196,724	+	2	1_A375_pNL7_minus_lncRNA::1::4352, 2_A375_pNL97_plus_lncRNA::1::6290	-101, -69	upstream, upstream	1	1	94	96	1	2_A375_pNL97_plus_lncRNA::1	96	Gene SPEF2	FLJ25395, KPL2, KIAA1770, CT122, MGC102842, FLJ23577, SPEF2, FLJ23164	sperm flagellar 2	NM_144722, NM_024867, hCT2292758.0, hCT2292760.0, hCT2292761.0, hCT2292762.0	1552716_at, 232745_x_at, 233429_at	NP_653323.1, NP_079143.3, EAW55920.1, EAW55921.1, EAW55922.1, EAW55923.1
GeneID:92255	LMBRD2	5	36,103,414	36,152,015	48,601	-	1	2_A375_pNL97_plus_lncRNA::1::6291	-81	upstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LMBRD2	MGC125692, MGC125693, DKFZp434H2226, DKFZp686G1057, LMBRD2	LMBR1 domain containing 2	NM_001007527, hCT2293043.0, hCT28813.3	232893_at	NP_001007528.1, EAW55933.1, EAW55932.1
GeneID:693165	MIR580	5	36,147,994	36,148,090	96	-	1	2_A375_pNL97_plus_lncRNA::1::6291	-4006	upstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MIR580	MIR580, hsa-mir-580, MIRN580	microRNA 580	NR_030306		
GeneID:6502	SKP2	5	36,152,189	36,184,147	31,958	+	1	2_A375_pNL97_plus_lncRNA::1::6291	-93	upstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SKP2	FLB1, FBL1, MGC1366, SKP2, FBXL1	S-phase kinase-associated protein 2 (p45)	NM_032637, NM_005983, hCT2292772.0, hCT2292774.0, hCT2292775.0, hCT2292776.0, hCT28123.3	203626_s_at, 210567_s_at	NP_116026.1, NP_005974.2, EAW55934.1, EAW55935.1, EAW55936.1, EAW55937.1, EAW55938.1
GeneID:133686	C5orf33	5	36,192,694	36,242,258	49,564	-	3	1_A375_pNL7_minus_lncRNA::1::4353, 2_A375_pNL97_plus_lncRNA::1::6292, 2_A375_pNL97_plus_lncRNA::1::6293	50, 925, -94	in gene, in gene, upstream	1	1	19.5	17.5	2	1_A375_pNL7_minus_lncRNA::1	29	Gene C5orf33	FLJ30596, C5orf33, MGC43298	chromosome 5 open reading frame 33	NM_001085411, NM_153013, hCT2352981.0, hCT2352982.0, hCT28815.3	226946_at, 228594_at, 229299_at	NP_001078880.1, NP_694558.1, EAW55939.1, EAW55940.1, EAW55941.1
GeneID:202151	RANBP3L	5	36,249,104	36,302,011	52,907	-	3	1_A375_pNL7_minus_lncRNA::1::4353, 2_A375_pNL97_plus_lncRNA::1::6292, 2_A375_pNL97_plus_lncRNA::1::6293	59803, 60678, 59659	downstream, downstream, downstream	1	1	19.5	17.5	2	1_A375_pNL7_minus_lncRNA::1	29	Gene RANBP3L	FLJ25422, RANBP3L	RAN binding protein 3-like	NM_145000, NM_001161429, hCT2293038.1, hCT2293039.1, hCT2352977.0	1553147_at	NP_659437.3, NP_001154901.1, EAW55942.1, EAW55943.1, EAW55944.1
GeneID:6507	SLC1A3	5	36,606,457	36,688,436	81,979	+	1	2_A375_pNL97_plus_lncRNA::1::6294	51367	in gene	0	1	12	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SLC1A3	FLJ25094, GLAST, GLAST1, SLC1A3, EA6, EAAT1	solute carrier family 1 (glial high affinity glutamate transporter), member 3	NM_004172, NM_001166695, NM_001166696, hCT2293438.0, hCT28065.3	1569054_at, 202800_at	NP_004163.3, NP_001160167.1, NP_001160168.1, EAW55945.1, EAW55946.1
GeneID:9631	NUP155	5	37,291,941	37,371,197	79,256	-	4	1_A375_pNL7_minus_lncRNA::1::4354, 1_A375_pNL7_minus_lncRNA::1::4355, 2_A375_pNL97_plus_lncRNA::1::6295, 2_A375_pNL97_plus_lncRNA::1::6296	-3, -8099, -3, -8099	upstream, upstream, upstream, upstream	1	1	91	96	2	2_A375_pNL97_plus_lncRNA::1	166	Gene NUP155	N155, NUP155, KIAA0791	nucleoporin 155kDa	NM_004298, NM_153485, hCT2293635.0, hCT2293637.0, hCT28791.4	206550_s_at	NP_004289.1, NP_705618.1, EAW55957.1, EAW55958.1, EAW55959.1
GeneID:55100	WDR70	5	37,379,412	37,752,774	373,362	+	5	1_A375_pNL7_minus_lncRNA::1::4354, 1_A375_pNL7_minus_lncRNA::1::4355, 1_A375_pNL7_minus_lncRNA::1::4356, 2_A375_pNL97_plus_lncRNA::1::6295, 2_A375_pNL97_plus_lncRNA::1::6296	-8212, -116, 343772, -8212, -116	upstream, upstream, in gene, upstream, upstream	1	1	67.33	67.33	3	2_A375_pNL97_plus_lncRNA::1	166	Gene WDR70	WDR70, FLJ10233	WD repeat domain 70	NM_018034, hCT2293453.0, hCT2352980.0	219193_at	NP_060504.1, EAW55961.1, EAW55960.1
GeneID:3977	LIFR	5	38,475,065	38,595,507	120,442	-	2	1_A375_pNL7_minus_lncRNA::1::4358, 2_A375_pNL97_plus_lncRNA::1::6299	-6589, -6557	upstream, upstream	1	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LIFR	LIFR, FLJ98923, SWS, LIF-R, STWS, FLJ98106, CD118, SJS2	leukemia inhibitory factor receptor alpha	NM_001127671, NM_002310, hCT28063.3	205876_at, 225571_at, 225575_at, 227771_at	NP_001121143.1, NP_002301.1, EAW55972.1
GeneID:100506495	LOC100506495	5	38,556,864	38,608,964	52,100	+	2	1_A375_pNL7_minus_lncRNA::1::4358, 2_A375_pNL97_plus_lncRNA::1::6299	45232, 45200	in gene, in gene	1	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100506495		hypothetical LOC100506495	XR_108573		
GeneID:9180	OSMR	5	38,845,960	38,935,743	89,783	+	1	2_A375_pNL97_plus_lncRNA::1::6302	75512	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene OSMR	MGC150626, MGC150627, OSMR, MGC75127, OSMRB	oncostatin M receptor	NM_001168355, NM_003999, hCT2292868.0, hCT28778.3	1554008_at, 205729_at	NP_001161827.1, NP_003990.1, EAW55976.1, EAW55977.1
GeneID:253260	RICTOR	5	38,938,022	39,074,501	136,479	-	1	1_A375_pNL7_minus_lncRNA::1::4359	-251	upstream	1	0	22	15	1	1_A375_pNL7_minus_lncRNA::1	22	Gene RICTOR	mAVO3, RICTOR, KIAA1999, DKFZp686B11164, PIA, MGC39830	RPTOR independent companion of MTOR, complex 2	NM_152756, hCT2293413.1, hCT2293416.1, hCT2352978.0	1552734_at, 226310_at, 226312_at, 228248_at	NP_689969.2, EAW55978.1, EAW55979.1, EAW55980.1
GeneID:2533	FYB	5	39,105,357	39,219,667	114,310	-	1	2_A375_pNL97_plus_lncRNA::1::6303	22603	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene FYB	PRO0823, ADAP, SLAP-130, FYB	FYN binding protein	NM_199335, NM_001465, hCT1956011.1, hCT2293406.0, hCT2293409.0, hCT2293412.0, hCT28779.3	205285_s_at, 211794_at, 211795_s_at, 227266_s_at	NP_955367.1, NP_001456.3, EAW55982.1, EAW55983.1, EAW55984.1, EAW55985.1, EAW55981.1
GeneID:1601	DAB2	5	39,371,780	39,425,335	53,555	-	2	2_A375_pNL97_plus_lncRNA::1::6304, 2_A375_pNL97_plus_lncRNA::1::6305	25527, 247	in gene, in gene	0	1	13.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene DAB2	DOC2, FLJ26626, DOC-2, DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	NM_001343, hCT1816997.3, hCT1963174.2, hCT2293389.1, hCT2293390.1, hCT2293393.1, hCT2293395.1	1559370_at, 201278_at, 201279_s_at, 201280_s_at, 210757_x_at, 232898_at, 240873_x_at	NP_001334.2, EAW55989.1, EAW55990.1, EAW55991.1, EAW55993.1, EAW55994.1, EAW55992.1
GeneID:23548	TTC33	5	40,711,678	40,756,072	44,394	-	2	1_A375_pNL7_minus_lncRNA::1::4360, 2_A375_pNL97_plus_lncRNA::1::6306	-58, 272	upstream, in gene	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TTC33	TTC33, OSRF	tetratricopeptide repeat domain 33	NM_012382, hCT2352979.0, hCT28059.3	219421_at, 231479_at	NP_036514.1, EAW55999.1, EAW55998.1
GeneID:5562	PRKAA1	5	40,759,481	40,798,297	38,816	-	2	1_A375_pNL7_minus_lncRNA::1::4360, 2_A375_pNL97_plus_lncRNA::1::6306	42137, 42497	downstream, downstream	1	1	20	18	1	1_A375_pNL7_minus_lncRNA::1	20	Gene PRKAA1	AMPK, MGC33776, MGC57364, PRKAA1, AMPKa1	protein kinase, AMP-activated, alpha 1 catalytic subunit	NM_206907, NM_006251, hCT2296181.0, hCT28571.3	1555177_at, 209799_at, 214917_at, 225984_at, 225985_at	NP_996790.3, NP_006242.5, EAW56000.1, EAW56001.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:11174	ADAMTS6	5	64,444,563	64,777,704	333,141	-	1	1_A375_pNL7_minus_lncRNA::1::4403	263144	in gene	1	0	15	9	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ADAMTS6	ADAM-TS 6, ADAMTS-6, ADAMTS6, ADAM-TS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	NM_197941	1570351_at, 220866_at, 237411_at	NP_922932.2
GeneID:64105	CENPK	5	64,813,593	64,858,995	45,402	-	1	2_A375_pNL97_plus_lncRNA::1::6363	-109	upstream	0	1	13	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CENPK	P33, AF5alpha, CENP-K, Solt, FKSG14, CENPK	centromere protein K	NM_022145, hCT1765461.3, hCT1966906.1	222848_at	NP_071428.2, EAW51353.1, EAW51354.1
GeneID:23398	PPWD1	5	64,859,131	64,883,373	24,242	+	1	2_A375_pNL97_plus_lncRNA::1::6363	-27	upstream	0	1	13	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene PPWD1	PPWD1, KIAA0073	peptidylprolyl isomerase domain and WD repeat containing 1	NM_015342, hCT8916.2	213483_at	NP_056157.1, EAW51352.1
GeneID:140890	SFRS12	5	65,440,085	65,476,716	36,631	+	2	1_A375_pNL7_minus_lncRNA::1::4404, 2_A375_pNL97_plus_lncRNA::1::6364	43, 43	in gene, in gene	1	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SFRS12	SREK1, DKFZp564B176, SRrp86, SFRS12, MGC133045, SRrp508	splicing factor, arginine/serine-rich 12	NM_139168, NM_001077199, hCT2266675.0, hCT2266678.0, hCT2352462.0, hCT8917.3	1568783_at, 212721_at, 243361_at, 244287_at	NP_631907.1, NP_001070667.1, EAW51328.1, EAW51329.1, EAW51330.1, EAW51331.1
GeneID:401191	FLJ46010	5	65,492,117	65,867,801	375,684	+	1	1_A375_pNL7_minus_lncRNA::1::4405	36555	in gene	1	0	23	18	1	1_A375_pNL7_minus_lncRNA::1	23	Gene FLJ46010		FLJ46010 protein	XR_112740, XR_108603, XR_113746		
GeneID:891	CCNB1	5	68,462,913	68,474,072	11,159	+	1	2_A375_pNL97_plus_lncRNA::1::6371	-65	upstream	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CCNB1	CCNB1, CCNB	cyclin B1	NM_031966, hCT18307.3	214710_s_at, 228729_at	NP_114172.1, EAW51306.1
GeneID:64946	CENPH	5	68,485,375	68,506,184	20,809	+	1	2_A375_pNL97_plus_lncRNA::1::6372	193	in gene	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CENPH	CENPH, PMF1, NNF1	centromere protein H	NM_022909, hCT18305.3, hCT2352463.0	231772_x_at	NP_075060.1, EAW51304.1, EAW51305.1
GeneID:6880	TAF9	5	68,647,553	68,665,840	18,287	-	2	1_A375_pNL7_minus_lncRNA::1::4406, 2_A375_pNL97_plus_lncRNA::1::6374	288, 272	in gene, in gene	1	1	21	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene TAF9	AD-004, TAF9, MGC:1603, CGI-137, MGC1603, MGC:5067, MGC5067, CINAP, TAFII32, TAF2G, TAFII31, MGC:3647, AK6, CIP, hCINAP, TAFII32 MGC3647	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	NM_001015891, NM_001015892, NM_016283, NM_003187, hCT2265305.0, hCT2265307.0, hCT2265309.0, hCT2265310.0, hCT2348066.0, hCT2348067.0, hCT2352461.0, hCT26432.2	202168_at, 203893_at	NP_001015891.1, NP_001015892.1, NP_003178.1, NP_057367.1, EAW51292.1, EAW51296.1, EAW51290.1, EAW51291.1, EAW51293.1, EAW51294.1, EAW51295.1, EAW51297.1
GeneID:5884	RAD17	5	68,665,124	68,710,628	45,504	+	2	1_A375_pNL7_minus_lncRNA::1::4406, 2_A375_pNL97_plus_lncRNA::1::6374	428, 444	in gene, in gene	1	1	21	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RAD17	RAD24, RAD17, FLJ41520, RAD17SP, R24L, HRAD17, CCYC	RAD17 homolog (S. pombe)	NM_002873, NM_133338, NM_133339, NM_133340, NM_133341, NM_133342, NM_133343, NM_133344, hCT1959762.1, hCT1961992.1, hCT1961993.1, hCT1966941.1, hCT2265538.0, hCT2265541.0, hCT2265544.0, hCT2265546.0, hCT2265547.0, hCT2265550.0, hCT26290.2	207405_s_at, 210826_x_at, 211228_s_at	NP_002864.1, NP_579916.1, NP_579917.1, NP_579918.1, NP_579919.1, NP_579920.1, NP_579921.1, NP_579922.1, EAW51279.1, EAW51280.1, EAW51281.1, EAW51282.1, EAW51283.1, EAW51284.1, EAW51285.1, EAW51286.1, EAW51287.1, EAW51288.1, EAW51289.1
GeneID:153562	MARVELD2	5	68,710,939	68,737,890	26,951	+	1	1_A375_pNL7_minus_lncRNA::1::4407	35237	downstream	1	0	19	10	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MARVELD2	MARVELD2, FLJ30532, MARVD2, DFNB49, MRVLDC2, Tric	MARVEL domain containing 2	NM_001038603, hCT1761389.3, hCT2349464.0	235141_at, 235955_at	NP_001033692.2, EAW51277.1, EAW51278.1
GeneID:100505674	LOC100505674	5	70,647,682	70,742,169	94,487	-	2	1_A375_pNL7_minus_lncRNA::1::4408, 2_A375_pNL97_plus_lncRNA::1::6375	-9287, -9351	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LOC100505674		hypothetical LOC100505674	XR_108584		
GeneID:55814	BDP1	5	70,751,442	70,863,649	112,207	+	2	1_A375_pNL7_minus_lncRNA::1::4408, 2_A375_pNL97_plus_lncRNA::1::6375	14, 78	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene BDP1	KIAA1241, BDP1, TFIIIB", TFC5, TFIIIB150, DKFZp686C01233, HSA238520, TFIIIB90, DKFZp686K0831, KIAA1689, TFNR, TAF3B1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	NM_018429, hCT2308214.1, hCT29087.3	224227_s_at, 226290_at, 231939_s_at	NP_060899.2, EAW95688.1, EAW95689.1
GeneID:9607	CARTPT	5	71,014,990	71,016,875	1,885	+	2	1_A375_pNL7_minus_lncRNA::1::4409, 2_A375_pNL97_plus_lncRNA::1::6376	402, 285	in gene, in gene	1	1	25	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene CARTPT	CARTPT, CART	CART prepropeptide	NM_004291, hCT28342.1	206339_at	NP_004282.1, EAW95694.1
GeneID:4131	MAP1B	5	71,403,118	71,505,397	102,279	+	1	1_A375_pNL7_minus_lncRNA::1::4412	413	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene MAP1B	FUTSCH, DKFZp686F1345, FLJ38954, DKFZp686E1099, MAP1B, MAP5	microtubule-associated protein 1B	NM_005909, hCT2308221.0, hCT2308223.0, hCT2357900.0, hCT2357901.0, hCT29063.3	214577_at, 226084_at	NP_005900.2, EAW95697.1, EAW95696.1, EAW95698.1, EAW95699.1, EAW95700.1
GeneID:23107	MRPS27	5	71,515,236	71,616,084	100,848	-	2	1_A375_pNL7_minus_lncRNA::1::4413, 2_A375_pNL97_plus_lncRNA::1::6379	11668, 11748	in gene, in gene	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MRPS27	MRPS27, FLJ23348, FLJ21764, KIAA0264, MRP-S27, S27mt	mitochondrial ribosomal protein S27	NM_015084, hCT2308240.0, hCT2357896.0, hCT29088.3	1563970_at, 212145_at	NP_055899.2, EAW95701.1, EAW95702.1, EAW95703.1
GeneID:100130998	LOC100130998	5	71,601,740	71,604,201	2,461	-	2	1_A375_pNL7_minus_lncRNA::1::4413, 2_A375_pNL97_plus_lncRNA::1::6379	-215, -135	upstream, upstream	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100130998		hypothetical protein LOC100130998	XM_003119951, XM_003118537, XM_003120464		XP_003119999.1, XP_003118585.1, XP_003120512.1
GeneID:167465	ZNF366	5	71,739,234	71,803,249	64,015	-	1	1_A375_pNL7_minus_lncRNA::1::4414	41425	in gene	1	0	17	17	1	1_A375_pNL7_minus_lncRNA::1	17	Gene ZNF366	DCSCRIPT, FLJ39796, ZNF366	zinc finger protein 366	NM_152625, hCT28939.4	236570_at	NP_689838.1, EAW95707.1
GeneID:3842	TNPO1	5	72,112,418	72,210,215	97,797	+	3	1_A375_pNL7_minus_lncRNA::1::4415, 2_A375_pNL97_plus_lncRNA::1::6380, 2_A375_pNL97_plus_lncRNA::1::6381	31566, -226, 31456	in gene, upstream, in gene	1	1	20	24	2	2_A375_pNL97_plus_lncRNA::1	34	Gene TNPO1	MIP, MIP1, TNPO1, IPO2, KPNB2, TRN	transportin 1	NM_153188, NM_002270, hCT2308251.0, hCT2308252.0, hCT2308253.0	1557278_s_at, 207657_x_at, 209225_x_at, 209226_s_at, 221829_s_at	NP_694858.1, NP_002261.3, EAW95713.1, EAW95714.1, EAW95715.1
GeneID:115548	FCHO2	5	72,251,808	72,386,349	134,541	+	1	2_A375_pNL97_plus_lncRNA::1::6382	-224	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FCHO2	FCHO2	FCH domain only 2	NM_138782, NM_001146032, hCT1797265.2	1555153_s_at, 226220_at	NP_620137.2, NP_001139504.1, EAW95716.1
GeneID:689	BTF3	5	72,794,250	72,801,448	7,198	+	2	1_A375_pNL7_minus_lncRNA::1::4417, 2_A375_pNL97_plus_lncRNA::1::6385	310, 310	in gene, in gene	1	1	20	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene BTF3	BTF3a, NACB, BETA-NAC, BTF3b, BTF3	basic transcription factor 3	NM_001207, NM_001037637, hCT1950011.1, hCT1950012.1, hCT2308325.0, hCT2308332.0, hCT2357895.0, hCT29079.3	208517_x_at, 211939_x_at, 214800_x_at, 217461_x_at, 243165_at	NP_001198.2, NP_001032726.1, EAW95723.1, EAW95726.1, EAW95727.1, EAW95728.1, EAW95724.1, EAW95725.1
GeneID:57763	ANKRA2	5	72,848,025	72,861,511	13,486	-	1	2_A375_pNL97_plus_lncRNA::1::6386	327	in gene	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ANKRA2	ANKRA2, ANKRA	ankyrin repeat, family A (RFXANK-like), 2	NM_023039, hCT2308369.0, hCT29082.3	218769_s_at	NP_075526.1, EAW95730.1, EAW95729.1
GeneID:84135	UTP15	5	72,861,598	72,877,794	16,196	+	1	2_A375_pNL97_plus_lncRNA::1::6386	-414	upstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene UTP15	FLJ12787, UTP15, NET21	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	NM_032175, hCT29081.3	226043_at, 226050_at	NP_115551.2, EAW95731.1
GeneID:84340	GFM2	5	74,017,031	74,063,042	46,011	-	2	1_A375_pNL7_minus_lncRNA::1::4419, 2_A375_pNL97_plus_lncRNA::1::6390	66, 34	in gene, in gene	1	1	51	49	1	1_A375_pNL7_minus_lncRNA::1	51	Gene GFM2	hEFG2, RRF2mt, GFM2, mEF-G 2, EF-G2mt, EFG2, MRRF2, MST027, RRF2	G elongation factor, mitochondrial 2	NM_032380, NM_170681, NM_170691, hCT1951658.1, hCT1969086.1, hCT2308719.0, hCT2308720.0, hCT2357904.0, hCT29439.3	225392_at, 231917_at, 231918_s_at	NP_115756.2, NP_733781.1, NP_733792.1, EAW95743.1, EAW95747.1, EAW95748.1, EAW95744.1, EAW95745.1, EAW95746.1
GeneID:10412	NSA2	5	74,063,103	74,072,734	9,631	+	2	1_A375_pNL7_minus_lncRNA::1::4419, 2_A375_pNL97_plus_lncRNA::1::6390	-127, -95	upstream, upstream	1	1	51	49	1	1_A375_pNL7_minus_lncRNA::1	51	Gene NSA2	TINP1, YR-29, NSA2, HUSSY-29, HCLG1, CDK105, HUSSY29, HCL-G1	NSA2 ribosome biogenesis homolog (S. cerevisiae)	NM_014886, hCT29438.3	201922_at	NP_055701.1, EAW95749.1
GeneID:26049	FAM169A	5	74,073,399	74,162,615	89,216	-	1	1_A375_pNL7_minus_lncRNA::1::4419	99639	downstream	1	0	51	49	1	1_A375_pNL7_minus_lncRNA::1	51	Gene FAM169A	KIAA0888, FAM169A	family with sequence similarity 169, member A	NM_015566	213954_at, 235048_at	NP_056381.1
GeneID:3156	HMGCR	5	74,632,993	74,657,926	24,933	+	1	2_A375_pNL97_plus_lncRNA::1::6391	-321	upstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene HMGCR	HMGCR, LDLCQ3	3-hydroxy-3-methylglutaryl-CoA reductase	NM_000859, NM_001130996, hCT1795806.2, hCT2308397.0, hCT2357902.0	202539_s_at, 202540_s_at	NP_000850.1, NP_001124468.1, EAW95754.1, EAW95755.1, EAW95756.1
GeneID:10087	COL4A3BP	5	74,666,928	74,807,806	140,878	-	2	1_A375_pNL7_minus_lncRNA::1::4420, 2_A375_pNL97_plus_lncRNA::1::6392	46, -18	in gene, upstream	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene COL4A3BP	CERTL, COL4A3BP, FLJ20597, STARD11, CERT, GPBP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	NM_001130105, NM_031361, NM_005713, hCT1967070.2, hCT2357887.0, hCT2357888.0, hCT2357889.0, hCT9879.4	219625_s_at, 223465_at, 223466_x_at	NP_001123577.1, NP_112729.1, NP_005704.1, EAW95757.1, EAW95758.1, EAW95760.1, EAW95759.1, EAW95761.1
GeneID:51426	POLK	5	74,807,657	74,895,646	87,989	+	2	1_A375_pNL7_minus_lncRNA::1::4420, 2_A375_pNL97_plus_lncRNA::1::6392	103, 167	in gene, in gene	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene POLK	DINP, POLQ, POLK, DINB1	polymerase (DNA directed) kappa	NM_016218, hCT1951642.1, hCT2308400.0, hCT2357906.0, hCT9412.3	1555317_at, 223260_s_at, 223261_at	NP_057302.1, EAW95763.1, EAW95762.1, EAW95764.1, EAW95765.1
GeneID:728780	ANKDD1B	5	74,907,460	74,965,449	57,989	+	1	1_A375_pNL7_minus_lncRNA::1::4421	52124	in gene	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene ANKDD1B	ANKDD1B	ankyrin repeat and death domain containing 1B	XM_001714483, XM_001128459, XM_001715633		XP_001714535.2, XP_001128459.3, XP_001715685.2
GeneID:134359	C5orf37	5	74,970,023	75,013,313	43,290	-	3	1_A375_pNL7_minus_lncRNA::1::4421, 1_A375_pNL7_minus_lncRNA::1::4422, 2_A375_pNL97_plus_lncRNA::1::6393	53729, 97, 145	downstream, in gene, in gene	1	1	17	17.5	2	2_A375_pNL97_plus_lncRNA::1	20	Gene C5orf37	C5orf37, MGC120443, MGC120442, POC5, FLJ35779, MGC120444	POC5 centriolar protein homolog (Chlamydomonas)	NM_152408, NM_001099271, hCT2350225.0, hCT2350226.0, hCT9880.4	227267_at	NP_689621.2, NP_001092741.1, EAW95767.1, EAW95768.1, EAW95769.1
GeneID:22987	SV2C	5	75,379,305	75,621,416	242,111	+	2	1_A375_pNL7_minus_lncRNA::1::4423, 2_A375_pNL97_plus_lncRNA::1::6396	20695, 20759	in gene, in gene	1	1	41	65	1	2_A375_pNL97_plus_lncRNA::1	65	Gene SV2C	MGC118875, MGC118877, SV2C, MGC118876, MGC118874	synaptic vesicle glycoprotein 2C	NM_014979, hCT10295.3, hCT2308383.0	1562372_at, 216086_at	NP_055794.1, EAW95772.1, EAW95771.1
GeneID:2150	F2RL1	5	76,114,833	76,131,140	16,307	+	1	2_A375_pNL97_plus_lncRNA::1::6396	20047	downstream	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene F2RL1	F2RL1, PAR2, GPR11	coagulation factor II (thrombin) receptor-like 1	NM_005242, hCT28289.3	206429_at, 213506_at	NP_005233.3, EAW95782.1
GeneID:170591	S100Z	5	76,145,826	76,217,056	71,230	+	1	1_A375_pNL7_minus_lncRNA::1::4424	24366	in gene	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene S100Z	Gm625, S100-zeta, S100Z	S100 calcium binding protein Z	NM_130772, hCT1797345.1, hCT2308559.0	1554876_a_at	NP_570128.2, EAW95783.1, EAW95784.1
GeneID:84327	ZBED3	5	76,372,532	76,383,030	10,498	-	2	1_A375_pNL7_minus_lncRNA::1::4425, 2_A375_pNL97_plus_lncRNA::1::6398	214, 374	in gene, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ZBED3	ZBED3, MGC15435	zinc finger, BED-type containing 3	NM_032367, hCT1646174.3, hCT2308684.0	226402_at	NP_115743.1, EAW95791.1, EAW95790.1
GeneID:677828	SNORA47	5	76,376,259	76,376,396	137		2	1_A375_pNL7_minus_lncRNA::1::4425, 2_A375_pNL97_plus_lncRNA::1::6398	-6420, -6260	upstream, upstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SNORA47	HBI-115, SNORA47	small nucleolar RNA, H/ACA box 47	NR_003014		
GeneID:728723	LOC728723	5	76,382,623	76,444,176	61,553		3	1_A375_pNL7_minus_lncRNA::1::4425, 1_A375_pNL7_minus_lncRNA::1::4426, 2_A375_pNL97_plus_lncRNA::1::6398	193, 46609, 33	in gene, in gene, in gene	1	1	16	16	2	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC728723		hypothetical LOC728723	NR_024398	241423_at	
GeneID:55255	WDR41	5	76,728,069	76,788,332	60,263	-	2	1_A375_pNL7_minus_lncRNA::1::4427, 2_A375_pNL97_plus_lncRNA::1::6401	204, 119	in gene, in gene	1	1	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene WDR41	MSTP048, WDR41, FLJ10904	WD repeat domain 41	NM_018268, hCT1951665.1, hCT2308678.0, hCT29327.3	218055_s_at, 222503_s_at, 240637_at	NP_060738.2, EAW95806.1, EAW95805.1, EAW95807.1
GeneID:8546	AP3B1	5	77,298,150	77,590,526	292,376	-	1	1_A375_pNL7_minus_lncRNA::1::4429	-192	upstream	1	0	16	17	1	1_A375_pNL7_minus_lncRNA::1	16	Gene AP3B1	HPS2, PE, HPS, ADTB3, AP3B1, ADTB3A	adaptor-related protein complex 3, beta 1 subunit	NM_003664, hCT1767035.2, hCT2308497.0, hCT2308499.0	203141_s_at, 203142_s_at	NP_003655.3, EAW95813.1, EAW95811.1, EAW95812.1
GeneID:728769	LOC728769	5	77,654,625	77,658,734	4,109	-	2	1_A375_pNL7_minus_lncRNA::1::4430, 2_A375_pNL97_plus_lncRNA::1::6403	2590, 2862	in gene, in gene	1	1	24	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene LOC728769		hypothetical LOC728769	XR_112743, XR_108586, XR_113750	238039_at	
GeneID:9522	SCAMP1	5	77,656,339	77,776,562	120,223	+	2	1_A375_pNL7_minus_lncRNA::1::4430, 2_A375_pNL97_plus_lncRNA::1::6403	-195, -467	upstream, upstream	1	1	24	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene SCAMP1	SCAMP1, SCAMP, SCAMP37	secretory carrier membrane protein 1	NM_004866, hCT1951679.1, hCT1951680.3, hCT1965737.2, hCT28976.3	1552978_a_at, 206667_s_at, 206668_s_at, 212416_at, 212417_at, 212425_at	NP_004857.4, EAW95817.1, EAW95814.1, EAW95815.1, EAW95816.1
GeneID:10184	LHFPL2	5	77,781,038	77,944,648	163,610	-	4	1_A375_pNL7_minus_lncRNA::1::4431, 1_A375_pNL7_minus_lncRNA::1::4432, 1_A375_pNL7_minus_lncRNA::1::4433, 2_A375_pNL97_plus_lncRNA::1::6404	62440, 51304, 1272, 62360	in gene, in gene, in gene, in gene	1	1	17.33	11.67	3	1_A375_pNL7_minus_lncRNA::1	18	Gene LHFPL2	LHFPL2, KIAA0206, DKFZp761E0375	lipoma HMGIC fusion partner-like 2	NM_005779, hCT1951681.1, hCT28978.3	212658_at	NP_005770.1, EAW95818.1, EAW95819.1
GeneID:9456	HOMER1	5	78,669,786	78,809,700	139,914	-	2	1_A375_pNL7_minus_lncRNA::1::4436, 2_A375_pNL97_plus_lncRNA::1::6406	-828, -476	upstream, upstream	1	1	25	20	1	1_A375_pNL7_minus_lncRNA::1	25	Gene HOMER1	HOMER1, HOMER1B, HOMER1A, HOMER, Ves-1, SYN47, HOMER1C	homer homolog 1 (Drosophila)	NM_004272, hCT1797494.2, hCT2308768.1	213793_s_at, 226651_at	NP_004263.1, EAW95836.1, EAW95835.1
GeneID:167153	PAPD4	5	78,908,243	78,982,471	74,228	+	1	1_A375_pNL7_minus_lncRNA::1::4437	173	in gene	1	0	18	12	1	1_A375_pNL7_minus_lncRNA::1	18	Gene PAPD4	FLJ38499, GLD2, PAPD4	PAP associated domain containing 4	NM_173797, NM_001114393, NM_001114394, hCT2308667.0, hCT29692.3	1556277_a_at, 225761_at, 238706_at	NP_776158.2, NP_001107865.1, NP_001107866.1, EAW95837.1, EAW95838.1
GeneID:256987	SERINC5	5	79,407,050	79,551,898	144,848	-	1	2_A375_pNL97_plus_lncRNA::1::6409	129903	in gene	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene SERINC5	TPO1, SERINC5, C5orf12	serine incorporator 5	NM_001174071, NM_001174072, NM_178276, hCT2349674.0, hCT2349675.0, hCT29693.4		NP_001167542.1, NP_001167543.1, NP_840060.1, EAW95843.1, EAW95844.1, EAW95845.1
GeneID:9765	ZFYVE16	5	79,703,838	79,775,498	71,660	+	1	1_A375_pNL7_minus_lncRNA::1::4439	-8430	upstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ZFYVE16	DKFZp686E13162, ENDOFIN, ZFYVE16, KIAA0305	zinc finger, FYVE domain containing 16	NM_014733, NM_001105251, hCT2357903.0, hCT29165.3	1554638_at, 1555011_at, 203651_at	NP_055548.3, NP_001098721.1, EAW95850.1, EAW95851.1
GeneID:100131067	LOC100131067	5	80,533,384	80,597,388	64,004	-	2	1_A375_pNL7_minus_lncRNA::1::4440, 2_A375_pNL97_plus_lncRNA::1::6410	44, 12	in gene, in gene	1	1	23	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene LOC100131067	FLJ39361, FLJ38695	hypothetical LOC100131067	NR_034121, NR_034122, NR_034123		
GeneID:84240	ZCCHC9	5	80,597,402	80,608,966	11,564	+	2	1_A375_pNL7_minus_lncRNA::1::4440, 2_A375_pNL97_plus_lncRNA::1::6410	-58, -26	upstream, upstream	1	1	23	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ZCCHC9	ZCCHC9, DKFZp761J139	zinc finger, CCHC domain containing 9	NM_032280, NM_001131035, NM_001131036, hCT1951193.2, hCT1951194.1, hCT2357894.0, hCT28972.4	225536_at	NP_115656.1, NP_001124507.1, NP_001124508.1, EAW95870.1, EAW95871.1, EAW95872.1, EAW95873.1
GeneID:23635	SSBP2	5	80,715,672	81,047,072	331,400	-	3	2_A375_pNL97_plus_lncRNA::1::6411, 1_A375_pNL7_minus_lncRNA::1::4441, 2_A375_pNL97_plus_lncRNA::1::6412	330992, 16, 288	in gene, in gene, in gene	1	1	13	21	2	2_A375_pNL97_plus_lncRNA::1	27	Gene SSBP2	SSBP2, SOSS-B2, HSPC116, DKFZp686F03273	single-stranded DNA binding protein 2	NM_012446, hCT1797461.2, hCT2308589.0, hCT2308590.0, hCT2308591.0	203787_at, 210829_s_at	NP_036578.2, EAW95879.1, EAW95877.1, EAW95878.1, EAW95880.1
GeneID:83734	ATG10	5	81,267,844	81,551,213	283,369	+	1	2_A375_pNL97_plus_lncRNA::1::6414	44	in gene	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene ATG10	ATG10, FLJ13954, APG10, APG10L, pp12616, DKFZp586I0418	ATG10 autophagy related 10 homolog (S. cerevisiae)	NM_031482, NM_001131028, hCT2308456.1, hCT2308458.1, hCT2308459.1, hCT2349652.0, hCT2349653.0, hCT2349654.0	1559820_at, 1570523_s_at, 207774_at, 223677_at, 243477_at	NP_113670.1, NP_001124500.1, EAW95882.1, EAW95883.1, EAW95884.1, EAW95886.1, EAW95881.1, EAW95885.1
GeneID:6228	RPS23	5	81,569,139	81,574,235	5,096	-	1	2_A375_pNL97_plus_lncRNA::1::6415	91	in gene	0	1	10	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene RPS23	S23, FLJ35016, RPS23	ribosomal protein S23	NM_001025, hCT2308585.0, hCT29428.2	200926_at, 227722_at	NP_001016.1, EAW95887.1, EAW95888.1
GeneID:7518	XRCC4	5	82,373,317	82,649,579	276,262	+	1	2_A375_pNL97_plus_lncRNA::1::6418	260016	in gene	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene XRCC4	XRCC4		NM_022406, NM_003401, NM_022550, hCT1951195.1, hCT2308414.0, hCT2308415.0, hCT2308416.0, hCT2357885.0, hCT29429.2	205071_x_at, 205072_s_at, 210812_at, 210813_s_at	NP_071801.1, NP_003392.1, NP_072044.1, EAW95897.1, EAW95900.1, EAW95902.1, EAW95898.1, EAW95899.1, EAW95901.1
GeneID:1462	VCAN	5	82,767,493	82,878,122	110,629	+	1	2_A375_pNL97_plus_lncRNA::1::6419	1979	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene VCAN	ERVR, DKFZp686K06110, GHAP, VCAN, PG-M, WGN1, CSPG2, WGN	versican	NM_004385, NM_001126336, NM_001164097, NM_001164098, hCT2308601.0, hCT2308602.0, hCT2308603.0, hCT2308604.0, hCT2308605.0, hCT2308606.0, hCT2308607.0, hCT2308608.0	204619_s_at, 204620_s_at, 211571_s_at, 215646_s_at, 221731_x_at	NP_004376.2, NP_001119808.1, NP_001157569.1, NP_001157570.1, EAW95906.1, EAW95911.1, EAW95904.1, EAW95905.1, EAW95907.1, EAW95908.1, EAW95909.1, EAW95910.1
GeneID:10085	EDIL3	5	83,238,126	83,680,611	442,485	-	1	1_A375_pNL7_minus_lncRNA::1::4444	412403	in gene	1	0	22	10	1	1_A375_pNL7_minus_lncRNA::1	22	Gene EDIL3	MGC26287, DEL1, EDIL3	EGF-like repeats and discoidin I-like domains 3	NM_005711, hCT1957909.1, hCT2357899.0, hCT28350.3	1558643_s_at, 207379_at, 225275_at	NP_005702.3, EAW95916.1, EAW95917.1, EAW95918.1
GeneID:5921	RASA1	5	86,564,151	86,687,733	123,582	+	3	1_A375_pNL7_minus_lncRNA::1::4446, 1_A375_pNL7_minus_lncRNA::1::4447, 2_A375_pNL97_plus_lncRNA::1::6422	-791, 32665, -663	upstream, in gene, upstream	1	1	20.5	16.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene RASA1	CM-AVM, RASA1, RASA, DKFZp434N071, PKWS, CMAVM, p120GAP, RASGAP, GAP, p120RASGAP	RAS p21 protein activator (GTPase activating protein) 1	NM_002890, NM_022650, hCT1951189.1, hCT2308705.0, hCT28074.3	202677_at, 210621_s_at	NP_002881.1, NP_072179.1, EAW95931.1, EAW95932.1, EAW95933.1
GeneID:902	CCNH	5	86,690,082	86,708,836	18,754	-	2	1_A375_pNL7_minus_lncRNA::1::4448, 2_A375_pNL97_plus_lncRNA::1::6423	68, 92	in gene, in gene	1	1	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene CCNH	CCNH, p34, CAK, p37	cyclin H	NM_001239, hCT2357897.0, hCT28236.2	204093_at	NP_001230.1, EAW95934.1, EAW95935.1
GeneID:645323	LOC645323	5	87,836,597	87,980,620	144,023	-	6	1_A375_pNL7_minus_lncRNA::1::4451, 1_A375_pNL7_minus_lncRNA::1::4452, 1_A375_pNL7_minus_lncRNA::1::4453, 2_A375_pNL97_plus_lncRNA::1::6426, 2_A375_pNL97_plus_lncRNA::1::6427, 2_A375_pNL97_plus_lncRNA::1::6428	9852, 8764, 4380, 23553, 9116, 3980	in gene, in gene, in gene, in gene, in gene, in gene	1	1	16	18.67	3	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC645323		hypothetical LOC645323	NR_015436, NR_024383, NR_024384	230272_at, 235850_at	

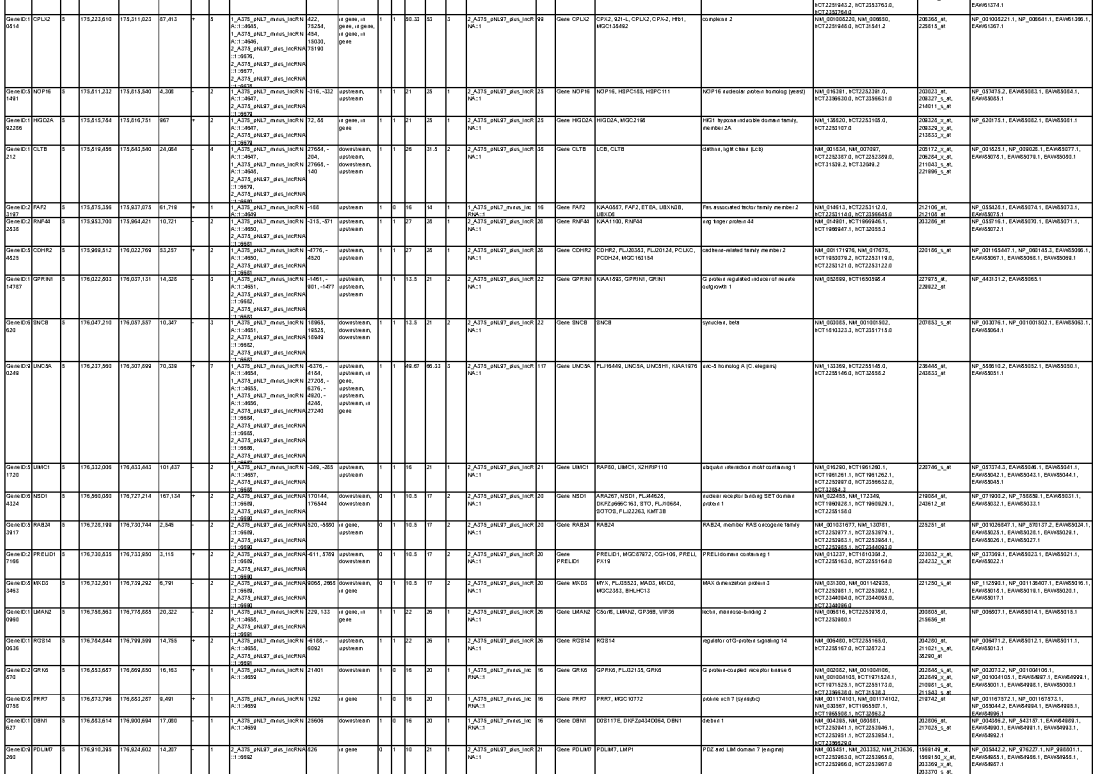
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:407047	MIR9-2	5	87,962,671	87,962,757	86	-	4	1_A375_pNL7_minus_lncRNA::1::4451, 1_A375_pNL7_minus_lncRNA::1::4452, 2_A375_pNL97_plus_lncRNA::1::6426, 2_A375_pNL97_plus_lncRNA::1::6427	-8011, -9099, 5690, -8747	upstream, upstream, downstream, upstream	1	1	17.5	20	2	2_A375_pNL97_plus_lncRNA::1	22	Gene MIR9-2	hsa-mir-9-2, MIRN9-2, MIR9-2, mirRNA9-2	microRNA 9-2	NR_030741		
GeneID:4208	MEF2C	5	88,014,058	88,199,922	185,864	-	2	1_A375_pNL7_minus_lncRNA::1::4454, 2_A375_pNL97_plus_lncRNA::1::6429	119026, 119154	in gene, in gene	1	1	21	17	1	1_A375_pNL7_minus_lncRNA::1	21	Gene MEF2C	MEF2C, C5DELq14.3; DEL5q14.3		NM_001131005, NM_002397, NM_001193347, NM_001193348, NM_001193349, NM_001193350, hCT1957907.1, hCT2309734.0, hCT2309735.0, hCT2309736.0, hCT2309737.0, hCT2309740.0, hCT2357693.0, hCT28068.2	207968_s_at, 209199_s_at, 209200_at	NP_001124477.1, NP_002388.2, NP_001180276.1, NP_001180277.1, NP_001180278.1, NP_001180279.1, EAW95961.1, EAW95962.1, EAW95963.1, EAW95964.1, EAW95965.1, EAW95966.1, EAW95967.1, EAW95968.1
GeneID:153364	MBLAC2	5	89,754,020	89,770,585	16,565	-	2	1_A375_pNL7_minus_lncRNA::1::4455, 2_A375_pNL97_plus_lncRNA::1::6430	345, 89	in gene, in gene	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene MBLAC2	MGC46734, DKFZp686P15118, MBLAC2	metallo-beta-lactamase domain containing 2	NM_203406, hCT28393.2	1554619_at, 230298_at	NP_981951.1, EAW95979.1
GeneID:10622	POLR3G	5	89,770,681	89,810,369	39,688	+	2	1_A375_pNL7_minus_lncRNA::1::4455, 2_A375_pNL97_plus_lncRNA::1::6430	-441, -185	upstream, upstream	1	1	21	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene POLR3G	RPC32, POLR3G, RPC7	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	NM_006467, hCT1951191.1, hCT2308808.0, hCT28395.3	206653_at, 206654_s_at, 231544_s_at	NP_006458.2, EAW95980.1, EAW95981.1, EAW95982.1
GeneID:84059	GPR98	5	89,854,617	90,460,033	605,416	+	2	1_A375_pNL7_minus_lncRNA::1::4457, 2_A375_pNL97_plus_lncRNA::1::6432	-153, -169	upstream, upstream	1	1	52	42	1	1_A375_pNL7_minus_lncRNA::1	52	Gene GPR98	GPR98, KIAA0686, USH2B, VLGR1b, VLGR1, FEB4, DKFZp761P0710, MASS1, USH2C	G protein-coupled receptor 98	NM_032119, NR_003149, hCT2308810.0, hCT2308811.0, hCT2308813.0, hCT2308814.0, hCT2308815.0, hCT2308816.0, hCT2308817.0, hCT2308818.1, hCT2308819.0	215396_at, 223582_at, 224275_at, 234871_at, 240631_at	NP_115495.3, EAW95992.1, EAW95986.1, EAW95987.1, EAW95991.1, EAW95993.1, EAW95988.1, EAW95989.1, EAW95990.1, EAW95994.1
GeneID:729040	LOC729040	5	90,575,914	90,576,959	1,045	-	1	2_A375_pNL97_plus_lncRNA::1::6433	655	in gene	0	1	17	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC729040		hypothetical LOC729040	XR_112752, XR_108595, XR_113759		
GeneID:57561	ARRDC3	5	90,664,541	90,679,149	14,608	-	1	1_A375_pNL7_minus_lncRNA::1::4458	-307	upstream	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene ARRDC3	TLIMP, ARRDC3, KIAA1376	arrestin domain containing 3	NM_020801, hCT28052.3	224797_at	NP_065852.1, EAW95997.1
GeneID:100129716	LOC100129716	5	90,676,164	90,716,532	40,368	+	1	1_A375_pNL7_minus_lncRNA::1::4458	3292	in gene	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC100129716		hypothetical LOC100129716	NR_027435		
GeneID:441094	FLJ42709	5	92,745,065	92,917,003	171,938	-	3	1_A375_pNL7_minus_lncRNA::1::4462, 2_A375_pNL97_plus_lncRNA::1::6437, 2_A375_pNL97_plus_lncRNA::1::6438	-229, 875, -245	upstream, in gene, upstream	1	1	22.5	25.5	2	1_A375_pNL7_minus_lncRNA::1	33	Gene FLJ42709	DKFZp686H18199	hypothetical LOC441094	NR_015369, NR_021490, NR_021491	1556695_a_at, 1556696_s_at, 229014_at	
GeneID:7025	NR2F1	5	92,919,043	92,929,788	10,745	+	3	1_A375_pNL7_minus_lncRNA::1::4462, 2_A375_pNL97_plus_lncRNA::1::6437, 2_A375_pNL97_plus_lncRNA::1::6438	-1811, -2915, -1795	upstream, upstream, upstream	1	1	22.5	25.5	2	1_A375_pNL7_minus_lncRNA::1	33	Gene NR2F1	COUP-TFI, NR2F2, NR2F1, TFCOUP1, TCFCOUP1, ERBAL3, EAR-3, SVP44, EAR3	nuclear receptor subfamily 2, group F, member 1	NM_005654, hCT1970618.1, hCT28075.3	209505_at, 209506_s_at	NP_005645.1, EAW96008.1, EAW96009.1
GeneID:83989	FAM172A	5	92,953,431	93,447,404	493,973	-	7	2_A375_pNL97_plus_lncRNA::1::6439, 2_A375_pNL97_plus_lncRNA::1::6440, 2_A375_pNL97_plus_lncRNA::1::6441, 2_A375_pNL97_plus_lncRNA::1::6442, 1_A375_pNL7_minus_lncRNA::1::4463, 2_A375_pNL97_plus_lncRNA::1::6443, 2_A375_pNL97_plus_lncRNA::1::6444	499308, 498924, 491004, 490156, 220, 90188, 236	downstream, downstream, in gene, in gene, in gene, in gene, in gene	1	1	13.67	19.5	6	2_A375_pNL97_plus_lncRNA::1	25	Gene FAM172A	DKFZp564D172, C5orf21, FAM172A	family with sequence similarity 172, member A	NM_032042, NM_001163417, NM_001163418, NR_028080, hCT2308996.2, hCT2308998.2, hCT2309000.1, hCT2350694.0	212936_at, 223882_at	NP_114431.2, NP_001156889.1, NP_001156890.1, EAW96011.1, EAW96013.1, EAW96014.1, EAW96012.1
GeneID:100313887	MIR2277	5	92,956,402	92,956,494	92	-	4	2_A375_pNL97_plus_lncRNA::1::6439, 2_A375_pNL97_plus_lncRNA::1::6440, 2_A375_pNL97_plus_lncRNA::1::6441, 2_A375_pNL97_plus_lncRNA::1::6442	8398, 8014, 94, -754	downstream, downstream, downstream, upstream	0	1	12	21	4	2_A375_pNL97_plus_lncRNA::1	25	Gene MIR2277	MIR2277	microRNA 2277	NR_031754		
GeneID:285600	C5orf36	5	93,486,556	93,954,309	467,753	-	2	1_A375_pNL7_minus_lncRNA::1::4464, 2_A375_pNL97_plus_lncRNA::1::6445	5, -283	in gene, upstream	1	1	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene C5orf36	DKFZp686F0372, MGC34713, KIAA0825, FLJ27431, C5orf36	chromosome 5 open reading frame 36	NM_173665, NM_001145678, hCT1646817.3	1553868_a_at	NP_775936.1, NP_001139150.1, EAW96025.1
GeneID:84250	ANKRD32	5	93,954,391	94,031,573	77,182	+	2	1_A375_pNL7_minus_lncRNA::1::4464, 2_A375_pNL97_plus_lncRNA::1::6445	-87, 201	upstream, in gene	1	1	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ANKRD32	DKFZp761C121, DKFZp564C0469, BRCTx, BRCTD1, ANKRD32	ankyrin repeat domain 32	NM_032290, hCT2308791.0, hCT2308793.0, hCT2308794.0, hCT2308795.0	1558076_at, 223542_at	NP_115666.2, EAW96027.1, EAW96026.1, EAW96028.1, EAW96029.1
GeneID:79772	MCTP1	5	94,042,284	94,620,279	577,995	-	1	1_A375_pNL7_minus_lncRNA::1::4465	491079	in gene	1	0	15	7	1	1_A375_pNL7_minus_lncRNA::1	15	Gene MCTP1	MCTP1, FLJ22344	multiple C2 domains, transmembrane 1	NM_024717, NM_001002796, hCT1951496.1, hCT2308828.0, hCT2308830.0	1554730_at, 220122_at	NP_078993.4, NP_001002796.1, EAW96031.1, EAW96032.1, EAW96033.1
GeneID:153643	FAM81B	5	94,727,048	94,786,144	59,096	+	1	1_A375_pNL7_minus_lncRNA::1::4466	26808	in gene	1	0	16	6	1	1_A375_pNL7_minus_lncRNA::1	16	Gene FAM81B	FAM81B, FLJ25333	family with sequence similarity 81, member B	NM_152548, hCT1817821.2, hCT1957690.1	240065_at	NP_689761.2, EAW96035.1, EAW96036.1
GeneID:9652	TTC37	5	94,799,599	94,890,709	91,110	-	2	1_A375_pNL7_minus_lncRNA::1::4467, 2_A375_pNL97_plus_lncRNA::1::6446	-11, -86	upstream, upstream	1	1	33	26	1	1_A375_pNL7_minus_lncRNA::1	33	Gene TTC37	TTC37, KIAA0372, MGC32587	tetratricopeptide repeat domain 37	NM_014639, hCT1951500.1, hCT2357907.0	1554029_a_at, 203048_s_at, 203049_s_at	NP_055454.1, EAW96037.1, EAW96038.1
GeneID:153642	ARSK	5	94,890,825	94,940,806	49,981	+	2	1_A375_pNL7_minus_lncRNA::1::4467, 2_A375_pNL97_plus_lncRNA::1::6446	-105, -30	upstream, upstream	1	1	33	26	1	1_A375_pNL7_minus_lncRNA::1	33	Gene ARSK	ARSK, DKFZp313G1735, TSULF	arylsulfatase family, member K	NM_198150, hCT2357890.0, hCT28705.3	1569132_s_at, 1569133_x_at, 239147_at	NP_937793.1, EAW96039.1, EAW96040.1
GeneID:22836	RHOBTB3	5	95,066,850	95,132,071	65,221	+	1	2_A375_pNL97_plus_lncRNA::1::6448	766	in gene	0	1	11	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RHOBTB3	KIAA0878, RHOBTB3	Rho-related BTB domain containing 3	NM_014899, hCT1951499.0, hCT2309445.0, hCT2309449.0, hCT28701.3	202975_s_at, 202976_s_at, 216048_s_at, 216049_at, 225202_at, 240111_at	NP_055714.3, EAW96049.1, EAW96050.1, EAW96051.1, EAW96052.1
GeneID:202299	C5orf27	5	95,187,936	95,195,837	7,901	+	1	2_A375_pNL97_plus_lncRNA::1::6449	6752	in gene	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C5orf27	MGC126626, FLJ38821, C5orf27, FIS	chromosome 5 open reading frame 27	NR_026936, hCT1646754.4, hCT2309455.1	239380_at	EAW96058.1, EAW96059.1
GeneID:5122	PCSK1	5	95,726,040	95,768,985	42,945	-	5	1_A375_pNL7_minus_lncRNA::1::4468, 1_A375_pNL7_minus_lncRNA::1::4469, 2_A375_pNL97_plus_lncRNA::1::6450, 2_A375_pNL97_plus_lncRNA::1::6451, 2_A375_pNL97_plus_lncRNA::1::6452	1561, -967, 48729, 1577, -1031	in gene, upstream, downstream, in gene, upstream	1	1	26.67	36	3	2_A375_pNL97_plus_lncRNA::1	62	Gene PCSK1	PC1, SPC3, BMIQ12, NEC1, PCSK1, PC3	proprotein convertase subtilisin/kexin type 1	NM_000439, NM_001177875, NM_001177876, hCT2309749.0, hCT7570.3	205825_at	NP_000430.3, NP_001171346.1, NP_001171347.1, EAW96062.1, EAW96063.1
GeneID:831	CAST	5	95,997,741	96,110,387	112,646	+	3	2_A375_pNL97_plus_lncRNA::1::6454, 2_A375_pNL97_plus_lncRNA::1::6455, 1_A375_pNL7_minus_lncRNA::1::4472	19, 1107, 40723	in gene, in gene, in gene	1	1	15.33	18	3	2_A375_pNL97_plus_lncRNA::1	20	Gene CAST	CAST, MGC9402, BS-17	calpastatin	NM_001042440, NM_001190442, NM_173060, NR_033798, hCT2309463.0, hCT2309464.0, hCT2309466.0, hCT2309468.0, hCT2309470.0, hCT2309472.0, hCT2309473.0, hCT2309476.0, hCT2309478.0, hCT2309479.0, hCT2309481.0, hCT2309482.0, hCT2309484.0	1564010_at, 207467_x_at, 208908_s_at, 212586_at	NP_001035905.1, NP_001177371.1, NP_775083.1, EAW96069.1, EAW96070.1, EAW96075.1, EAW96064.1, EAW96065.1, EAW96066.1, EAW96067.1, EAW96068.1, EAW96071.1, EAW96072.1, EAW96073.1, EAW96074.1, EAW96076.1
GeneID:51752	ERAP1	5	96,096,514	96,143,892	47,378	-	2	1_A375_pNL7_minus_lncRNA::1::4473, 2_A375_pNL97_plus_lncRNA::1::6456	692, 532	in gene, in gene	1	1	15	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ERAP1	APPILS, ERAAP, ALAP, ERAAP1, ARTS1, PILS-AP, KIAA0525, ARTS-1, A-LAP, PILSAP, ERAP1	endoplasmic reticulum aminopeptidase 1	NM_001040458, NM_016442, hCT1773554.1, hCT1773556.1, hCT2309745.0	209701_at, 209788_s_at, 210385_s_at, 212580_at, 214012_at, 214034_at	NP_001035548.1, NP_057526.3, EAW96077.1, EAW96078.1, EAW96079.1
GeneID:4012	LNPEP	5	96,271,346	96,365,115	93,769	+	2	1_A375_pNL7_minus_lncRNA::1::4474, 2_A375_pNL97_plus_lncRNA::1::6457	366, 270	in gene, in gene	1	1	38	30	1	1_A375_pNL7_minus_lncRNA::1	38	Gene LNPEP	PLAP, P-LAP, LNPEP, CAP, IRAP	leucyl/cystinyl aminopeptidase	NM_175920, NM_005575, hCT1773553.2	207904_s_at, 231866_at, 236728_at	NP_787116.2, NP_005566.2, EAW96084.1
GeneID:55781	RIOK2	5	96,496,571	96,519,005	22,434	-	2	1_A375_pNL7_minus_lncRNA::1::4475, 2_A375_pNL97_plus_lncRNA::1::6458	40, -51	in gene, upstream	1	1	17	17	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RIOK2	RIO2, RIOK2, FLJ11159	RIO kinase 2 (yeast)	NM_018343, NM_001159749, hCT28788.2	218535_s_at, 222663_at	NP_060813.2, NP_001153221.1, EAW96088.1
GeneID:285704	RGMB	5	98,104,999	98,132,198	27,199	+	1	2_A375_pNL97_plus_lncRNA::1::6459	4526	in gene	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene RGMB	DKFZp434P228, RGMB, DRAGON, FLJ90406, MGC86970	RGM domain family, member B	NM_001012761, hCT18626.4, hCT2348374.0, hCT2348375.0	226989_at, 227339_at, 227340_s_at, 242450_at	NP_001012779.2, EAW96095.1, EAW96093.1, EAW96094.1
GeneID:503569	FLJ35946	5	98,105,322	98,108,788	3,466	-	1	2_A375_pNL97_plus_lncRNA::1::6459	-737	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene FLJ35946		hypothetical protein FLJ35946	NR_033932	1558899_s_at	
GeneID:1105	CHD1	5	98,190,908	98,262,238	71,330	-	2	1_A375_pNL7_minus_lncRNA::1::4476, 2_A375_pNL97_plus_lncRNA::1::6460	-2242, -2754	upstream, upstream	1	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CHD1	DKFZp686E2337, CHD1	chromodomain helicase DNA binding protein 1	NM_001270, hCT18624.3	204258_at, 235791_x_at	NP_001261.2, EAW96098.1
GeneID:100289230	LOC100289230	5	98,264,838	98,266,713	1,875	+	2	1_A375_pNL7_minus_lncRNA::1::4476, 2_A375_pNL97_plus_lncRNA::1::6460	-358, 154	upstream, in gene	1	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100289230		hypothetical LOC100289230	NR_036530		
GeneID:7903	ST8SIA4	5	100,142,639	100,238,987	96,348	-	2	2_A375_pNL97_plus_lncRNA::1::6462, 2_A375_pNL97_plus_lncRNA::1::6463	62667, 2715	in gene, in gene	0	1	7.5	19	2	2_A375_pNL97_plus_lncRNA::1	22	Gene ST8SIA4	PST1, PST, ST8SIA-IV, MGC34450, MGC61459, SIAT8D, ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	NM_175052, NM_005668, hCT2327988.0, hCT30817.2	1554460_at, 206925_at, 230261_at, 230836_at, 242943_at	NP_778222.1, NP_005659.1, EAW49104.1, EAW49105.1
GeneID:353189	SLCO4C1	5	101,569,690	101,632,253	62,563	-	2	1_A375_pNL7_minus_lncRNA::1::4477, 2_A375_pNL97_plus_lncRNA::1::6464	157, 93	in gene, in gene	1	1	27	23	1	1_A375_pNL7_minus_lncRNA::1	27	Gene SLCO4C1	OATP-H, OATP4C1, PRO2176, OATP-M1, SLC21A20, OATPX, SLCO4C1	solute carrier organic anion transporter family, member 4C1	NM_180991, hCT1950262.3, hCT2352215.0	222071_s_at	NP_851322.3, EAW49099.1, EAW49100.1
GeneID:5066	PAM	5	102,201,527	102,366,809	165,282	+	1	1_A375_pNL7_minus_lncRNA::1::4478	361	in gene	1	0	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene PAM	PAM, PHM, PAL	peptidylglycine alpha-amidating monooxygenase	NM_000919, NM_001177306, NM_138766, NM_138821, NM_138822, NR_033440, hCT2344388.0, hCT2344389.0, hCT2344390.0, hCT2344391.0, hCT2344393.0, hCT2344395.0, hCT2344396.0, hCT2352217.0, hCT2352218.0	202336_s_at, 212958_x_at, 214620_x_at	NP_000910.2, NP_001170777.1, NP_620121.1, NP_620176.1, NP_620177.1, EAW49084.1, EAW49085.1, EAW49086.1, EAW49087.1, EAW49088.1, EAW49089.1, EAW49090.1, EAW49091.1, EAW49092.1
GeneID:54826	GIN1	5	102,421,704	102,455,842	34,138	-	2	1_A375_pNL7_minus_lncRNA::1::4479, 2_A375_pNL97_plus_lncRNA::1::6466	-30, 2	upstream, in gene	1	1	28	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene GIN1	GIN-1, FLJ20125, TGIN1, ZH2C2, GIN1	gypsy retrotransposon integrase 1	NM_017676, hCT2352213.0, hCT30860.2	1554345_a_at, 219467_at	NP_060146.2, EAW49081.1, EAW49080.1
GeneID:23262	PPIP5K2	5	102,465,257	102,538,910	73,653	+	2	1_A375_pNL7_minus_lncRNA::1::4479, 2_A375_pNL97_plus_lncRNA::1::6466	-9385, -9417	upstream, upstream	1	1	28	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene PPIP5K2	FLJ23463, FLJ21506, HISPPD1, KIAA0433, IP7K2, VIP2, PPIP5K2	diphosphoinositol pentakisphosphate kinase 2	NM_015216, hCT2328156.0, hCT2328157.0, hCT2352211.0, hCT29590.3	203253_s_at	NP_056031.2, EAW49079.1, EAW49076.1, EAW49077.1, EAW49078.1
GeneID:83594	NUDT12	5	102,884,556	102,898,490	13,934	-	1	2_A375_pNL97_plus_lncRNA::1::6467	170	in gene	0	1	10	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene NUDT12	DKFZp761I172, NUDT12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	NM_031438, hCT29584.3	1562775_at, 223535_at	NP_113626.1, EAW49073.1
GeneID:1946	EFNA5	5	106,712,590	107,006,596	294,006	-	5	1_A375_pNL7_minus_lncRNA::1::4481, 2_A375_pNL97_plus_lncRNA::1::6471, 2_A375_pNL97_plus_lncRNA::1::6472, 2_A375_pNL97_plus_lncRNA::1::6473, 2_A375_pNL97_plus_lncRNA::1::6474	-2012, 281572, 201348, -476, -1468	upstream, in gene, in gene, upstream, upstream	1	1	13.4	18.2	5	2_A375_pNL97_plus_lncRNA::1	23	Gene EFNA5	EFL5, EPLG7, LERK7, EFNA5, RAGS, GLC1M, AF1	ephrin-A5	NM_001962, hCT1774737.3, hCT2340228.0, hCT28146.4	207301_at	NP_001953.1, EAW49063.1, EAW49064.1, EAW49065.1
GeneID:64839	FBXL17	5	107,194,734	107,717,799	523,065	-	1	2_A375_pNL97_plus_lncRNA::1::6476	7	in gene	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene FBXL17	Fbl17, FBXO13, DKFZp434C1715, MGC161424, FBXL17, Fbx13, MGC161422	F-box and leucine-rich repeat protein 17	NM_001163315, hCT2327873.0, hCT28882.3	227203_at, 233087_at, 242034_at, 244360_at	NP_001156787.2, EAW49062.1, EAW49061.1
GeneID:91137	SLC25A46	5	110,074,754	110,098,484	23,730	+	1	2_A375_pNL97_plus_lncRNA::1::6478	-18	upstream	0	1	15	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SLC25A46	SLC25A46	solute carrier family 25, member 46	NM_138773, hCT1950144.1, hCT28677.3	212833_at, 226831_at	NP_620128.1, EAW49041.1, EAW49040.1
GeneID:134430	WDR36	5	110,427,870	110,466,200	38,330	+	2	1_A375_pNL7_minus_lncRNA::1::4484, 2_A375_pNL97_plus_lncRNA::1::6479	82, 66	in gene, in gene	1	1	21	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene WDR36	TAWDRP, TA-WDRP, DKFZp686I1650, GLC1G, UTP21, WDR36	WD repeat domain 36	NM_139281, hCT2344386.0, hCT2344387.0	226180_at, 238677_at	NP_644810.1, EAW49036.1, EAW49035.1
GeneID:814	CAMK4	5	110,560,082	110,820,749	260,667	+	6	1_A375_pNL7_minus_lncRNA::1::4485, 1_A375_pNL7_minus_lncRNA::1::4486, 2_A375_pNL97_plus_lncRNA::1::6480, 2_A375_pNL97_plus_lncRNA::1::6481, 2_A375_pNL97_plus_lncRNA::1::6482, 2_A375_pNL97_plus_lncRNA::1::6483	140846, 142862, -354, 140798, 142798, 159438	in gene, in gene, upstream, in gene, in gene, in gene	1	1	16.75	21.5	4	2_A375_pNL97_plus_lncRNA::1	42	Gene CAMK4	CaMK-GR, IV, CAMK4, CaMK IV, caMK, MGC36771	calcium/calmodulin-dependent protein kinase IV	NM_001744, hCT2328084.0, hCT2328085.0, hCT28678.3	210349_at, 241871_at	NP_001735.1, EAW49032.1, EAW49033.1, EAW49034.1
GeneID:134429	STARD4	5	110,834,022	110,848,157	14,135	-	1	1_A375_pNL7_minus_lncRNA::1::4487	541	in gene	1	0	17	11	1	1_A375_pNL7_minus_lncRNA::1	17	Gene STARD4	STARD4		NM_139164, hCT2349225.0, hCT2349226.0, hCT2349227.0, hCT2352204.0, hCT2352205.0, hCT28676.4	226390_at	NP_631903.1, EAW49030.1, EAW49026.1, EAW49027.1, EAW49028.1, EAW49029.1, EAW49031.1
GeneID:100505678	LOC100505678	5	110,847,924	111,075,423	227,499	+	1	1_A375_pNL7_minus_lncRNA::1::4487	-308	upstream	1	0	17	11	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC100505678		hypothetical LOC100505678	XR_112774, XR_110556, XR_113766		
GeneID:114915	NCRNA00219	5	111,496,223	111,498,198	1,975	+	2	1_A375_pNL7_minus_lncRNA::1::4488, 2_A375_pNL97_plus_lncRNA::1::6484	241, 257	in gene, in gene	1	1	113	126	1	2_A375_pNL97_plus_lncRNA::1	126	Gene NCRNA00219	MGC126893, NCRNA00219, TIGA1, C5orf26, MGC138282	non-protein coding RNA 219	NR_015370, hCT1950151.1	225698_at	EAW49016.1
GeneID:654322	SNORA13	5	111,497,182	111,497,314	132	+	2	1_A375_pNL7_minus_lncRNA::1::4488, 2_A375_pNL97_plus_lncRNA::1::6484	-718, -702	upstream, upstream	1	1	113	126	1	2_A375_pNL97_plus_lncRNA::1	126	Gene SNORA13	ACA13, SNORA13	small nucleolar RNA, H/ACA box 13	NR_002922		
GeneID:64097	EPB41L4A	5	111,498,315	111,755,010	256,695	-	2	1_A375_pNL7_minus_lncRNA::1::4488, 2_A375_pNL97_plus_lncRNA::1::6484	256546, 256530	downstream, downstream	1	1	113	126	1	2_A375_pNL97_plus_lncRNA::1	126	Gene EPB41L4A	NBL4, FLJ38738, EPB41L4, EPB41L4A, DKFZp566L203	erythrocyte membrane protein band 4.1 like 4A	NM_022140, hCT1950140.2, hCT1950141.2, hCT2328292.1, hCT28472.4	1555038_at, 220119_at, 220120_s_at, 228256_s_at, 228259_s_at	NP_071423.3, EAW49010.1, EAW49011.1, EAW49012.1, EAW49013.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:324	APC	5	112,043,218	112,181,936	138,718	+	1	2_A375_pNL97_plus_lncRNA::1::6485	-50	upstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene APC	DP2.5, DP3, APC, DP2, GS, BTPS2	adenomatous polyposis coli	NM_000038, NM_001127510, NM_001127511	203525_s_at, 203526_s_at, 203527_s_at, 215310_at, 216933_x_at	NP_000029.2, NP_001120982.1, NP_001120983.1
GeneID:7905	REEP5	5	112,212,081	112,258,031	45,950	-	1	2_A375_pNL97_plus_lncRNA::1::6486	271	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene REEP5	D5S346, C5orf18, REEP5, TB2, DP1, MGC70440, YOP1	receptor accessory protein 5	NM_005669, hCT1950148.1, hCT2328300.1, hCT2328303.0	208872_s_at, 208873_s_at	NP_005660.4, EAW48995.1, EAW48993.1, EAW48994.1
GeneID:100287967	LOC100287967	5	112,312,399	112,327,938	15,539	-	2	1_A375_pNL7_minus_lncRNA::1::4490, 2_A375_pNL97_plus_lncRNA::1::6487	15746, 15346	downstream, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100287967		hypothetical LOC100287967	XR_112773, XR_110558, XR_110557, XR_113767		
GeneID:167227	DCP2	5	112,312,433	112,356,667	44,234	+	2	1_A375_pNL7_minus_lncRNA::1::4490, 2_A375_pNL97_plus_lncRNA::1::6487	-241, 159	upstream, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene DCP2	NUDT20, FLJ33245, DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	NM_152624, hCT2348070.1, hCT2350517.0, hCT2350518.0, hCT2350519.0, hCT2352208.0	212919_at, 235258_at, 238779_at, 244777_at	NP_689837.2, EAW48988.1, EAW48989.1, EAW48990.1, EAW48991.1, EAW48992.1
GeneID:4163	MCC	5	112,357,796	112,824,527	466,731	-	3	1_A375_pNL7_minus_lncRNA::1::4491, 1_A375_pNL7_minus_lncRNA::1::4492, 2_A375_pNL97_plus_lncRNA::1::6488	285583, 399, 527	in gene, in gene, in gene	1	1	16.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene MCC	FLJ38893, MCC, MCC1, FLJ46755, DKFZp762O1615	mutated in colorectal cancers	NM_002387, NM_001085377, hCT1775722.2, hCT1950103.2, hCT2352220.0, hCT2352221.0	206132_at, 226225_at	NP_002378.1, NP_001078846.1, EAW48984.1, EAW48985.1, EAW48986.1, EAW48987.1
GeneID:64848	YTHDC2	5	112,849,391	112,930,984	81,593	+	1	1_A375_pNL7_minus_lncRNA::1::4493	113	in gene	1	0	20	11	1	1_A375_pNL7_minus_lncRNA::1	20	Gene YTHDC2	YTHDC2	YTH domain containing 2	NM_022828, hCT2327839.0, hCT2327841.0, hCT2327842.0	1568660_s_at, 205835_s_at, 205836_s_at, 213077_at	NP_073739.3, EAW48979.1, EAW48978.1, EAW48980.1
GeneID:5229	PGGT1B	5	114,546,527	114,598,569	52,042	-	1	2_A375_pNL97_plus_lncRNA::1::6489	73	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PGGT1B	GGTI, BGGI, PGGT1B	protein geranylgeranyltransferase type I, beta subunit	NM_005023, hCT2327874.0, hCT2327875.0	206288_at, 235615_at, 242844_at, 244684_at	NP_005014.2, EAW48968.1, EAW48969.1
GeneID:153733	CCDC112	5	114,602,885	114,632,458	29,573	-	1	2_A375_pNL97_plus_lncRNA::1::6489	33962	downstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CCDC112	CCDC112, MBC1, MGC39633	coiled-coil domain containing 112	NM_001040440, NM_152549, hCT2349228.0, hCT28798.4	235208_at	NP_001035530.1, NP_689762.2, EAW48966.1, EAW48967.1
GeneID:100302736	TMED7-TICAM2	5	114,914,339	114,961,876	47,537	-	1	2_A375_pNL97_plus_lncRNA::1::6491	228	in gene	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene TMED7-TICAM2	TMED7-TICAM2, TAG, FLJ90737	TMED7-TICAM2 readthrough	NM_001164468, NM_001164469		NP_001157940.1, NP_001157941.1
GeneID:100505719	LOC100505719	5	114,937,842	114,956,356	18,514	+	1	2_A375_pNL97_plus_lncRNA::1::6491	23606	downstream	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC100505719		hypothetical LOC100505719	XR_112771, XR_112770, XR_112772, XR_110561, XR_110560, XR_110559, XR_113770, XR_113769, XR_113768		
GeneID:51014	TMED7	5	114,948,905	114,961,876	12,971	-	1	2_A375_pNL97_plus_lncRNA::1::6491	228	in gene	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene TMED7	FLJ90461, FLJ57776, TMED7, CGI-109	transmembrane emp24 protein transport domain containing 7	NM_181836	209404_s_at, 214658_at	NP_861974.1
GeneID:9140	ATG12	5	115,163,893	115,177,548	13,655	-	2	1_A375_pNL7_minus_lncRNA::1::4495, 2_A375_pNL97_plus_lncRNA::1::6492	140, 236	in gene, in gene	1	1	28	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene ATG12	FBR93, ATG12, APG12L, HAPG12, APG12	ATG12 autophagy related 12 homolog (S. cerevisiae)	NM_004707, NR_033362, NR_033363, hCT1962062.1, hCT2328134.0, hCT28198.3	204833_at, 213026_at	NP_004698.3, EAW48956.1, EAW48954.1, EAW48955.1
GeneID:1176	AP3S1	5	115,177,619	115,249,778	72,159	+	2	1_A375_pNL7_minus_lncRNA::1::4495, 2_A375_pNL97_plus_lncRNA::1::6492	-211, -307	upstream, upstream	1	1	28	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene AP3S1	AP3S1, Sigma3A, CLAPS3	adaptor-related protein complex 3, sigma 1 subunit	NM_001284, hCT2328177.0, hCT2352209.0	202442_at	NP_001275.1, EAW48952.1, EAW48953.1
GeneID:57556	SEMA6A	5	115,779,251	115,910,551	131,300	-	1	2_A375_pNL97_plus_lncRNA::1::6493	-105	upstream	0	1	22	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene SEMA6A	SEMAQ, SEMA6A1, KIAA1368, SEMA6A, SEMA, HT018, VIA	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	NM_020796, hCT2328121.1, hCT2328122.1, hCT2328123.1, hCT2328124.1, hCT2328126.0	1558338_at, 215028_at, 220454_s_at, 223449_at, 225660_at	NP_065847.1, EAW48934.1, EAW48935.1, EAW48936.1, EAW48937.1, EAW48938.1
GeneID:285605	DTWD2	5	118,172,569	118,324,240	151,671	-	2	1_A375_pNL7_minus_lncRNA::1::4496, 2_A375_pNL97_plus_lncRNA::1::6494	240, 176	in gene, in gene	1	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene DTWD2	FLJ33977, MGC138580, MGC138579, DTWD2	DTW domain containing 2	NM_173666, hCT1646419.3, hCT2327836.0, hCT2327837.0, hCT2352210.0	231277_x_at	NP_775937.1, EAW48923.1, EAW48922.1, EAW48924.1, EAW48925.1
GeneID:25816	TNFAIP8	5	118,604,418	118,730,294	125,876	+	1	1_A375_pNL7_minus_lncRNA::1::4497	-322	upstream	1	0	19	11	1	1_A375_pNL7_minus_lncRNA::1	19	Gene TNFAIP8	SCC-S2, SCCS2, MDC-3.13, TNFAIP8, GG2-1	tumor necrosis factor, alpha-induced protein 8	NM_014350, NM_001077654, hCT1950131.0, hCT28066.2	208296_x_at, 210260_s_at	NP_055165.2, NP_001071122.1, EAW48913.1, EAW48914.1
GeneID:153443	SRFBP1	5	121,297,656	121,364,295	66,639	+	2	1_A375_pNL7_minus_lncRNA::1::4499, 2_A375_pNL97_plus_lncRNA::1::6495	-24, -56	upstream, upstream	1	1	26	18	1	1_A375_pNL7_minus_lncRNA::1	26	Gene SRFBP1	SRFBP1, Rlb1, STRAP, p49/STRAP, BUD22, FLJ25286, P49	serum response factor binding protein 1	NM_152546, hCT2327889.0, hCT28062.2	241734_at	NP_689759.2, EAW48899.1, EAW48900.1
GeneID:9627	SNCAIP	5	121,647,620	121,799,794	151,974	+	1	1_A375_pNL7_minus_lncRNA::1::4500	38644	in gene	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SNCAIP	Sph1, SYPH1, MGC39814, SNCAIP	synuclein, alpha interacting protein	NM_005460, hCT1962064.1, hCT1962065.1, hCT2352206.0, hCT2352207.0, hCT28595.3	219511_s_at, 237833_s_at, 237834_at	NP_005451.2, EAW48887.1, EAW48888.1, EAW48889.1, EAW48890.1, EAW48891.1
GeneID:5480	PPIC	5	122,359,078	122,372,425	13,347	-	1	1_A375_pNL7_minus_lncRNA::1::4501	-407	upstream	1	0	18	18	1	1_A375_pNL7_minus_lncRNA::1	18	Gene PPIC	CYPC, PPIC, MGC3673	peptidylprolyl isomerase C (cyclophilin C)	NM_000943, hCT2327946.0, hCT28594.3	204517_at, 204518_s_at	NP_000934.1, EAW48879.1, EAW48878.1
GeneID:153241	CEP120	5	122,680,579	122,759,286	78,707	-	2	1_A375_pNL7_minus_lncRNA::1::4503, 2_A375_pNL97_plus_lncRNA::1::6497	86, 118	in gene, in gene	1	1	78	74	1	1_A375_pNL7_minus_lncRNA::1	78	Gene CEP120	CEP120, CCDC100, DKFZp686I06246, FLJ38327, FLJ36090	centrosomal protein 120kDa	NM_153223, NM_001166226, hCT13088.4, hCT2327949.1, hCT2352222.0	1554606_at, 226449_at	NP_694955.2, NP_001159698.1, EAW48873.1, EAW48874.1, EAW48875.1
GeneID:1456	CSNK1G3	5	122,847,793	122,952,465	104,672	+	1	2_A375_pNL97_plus_lncRNA::1::6498	-55	upstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene CSNK1G3	CSNK1G3		NM_001031812, NM_001044722, NM_001044723, NM_004384, hCT12581.3, hCT1961333.1, hCT1961334.1, hCT2328054.0, hCT2328055.0, hCT2328057.0	220768_s_at, 227767_at, 229702_at	NP_001026982.1, NP_001038187.1, NP_001038188.1, NP_004375.2, EAW48867.1, EAW48868.1, EAW48869.1, EAW48870.1, EAW48871.1, EAW48872.1
GeneID:57507	ZNF608	5	123,972,610	124,080,805	108,195	-	2	1_A375_pNL7_minus_lncRNA::1::4507, 2_A375_pNL97_plus_lncRNA::1::6500	83349, 83221	in gene, in gene	1	1	13.5	17	2	2_A375_pNL97_plus_lncRNA::1	25	Gene ZNF608	MGC166851, NY-REN-36, ZNF608, DKFZp781C0723	zinc finger protein 608	NM_020747, hCT18135.4, hCT1833701.2, hCT1950119.2, hCT2350097.0	229817_at, 232303_at	NP_065798.2, EAW48859.1, EAW48858.1, EAW48860.1, EAW48861.1
GeneID:65983	GRAMD3	5	125,695,788	125,829,853	134,065	+	1	1_A375_pNL7_minus_lncRNA::1::4509	94132	in gene	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene GRAMD3	FLJ21313, GRAMD3, NS3TP2	GRAM domain containing 3	NM_023927, NM_001146319, NM_001146320, NM_001146321, NM_001146322, hCT18718.3, hCT1950120.1, hCT1950121.1, hCT2377808.0	218706_s_at, 238049_at	NP_076416.2, NP_001139791.1, NP_001139792.1, NP_001139793.1, NP_001139794.1, EAW48852.1, EAW48853.1, EAW48854.1, EAW48855.1
GeneID:501	ALDH7A1	5	125,878,918	125,931,082	52,164	-	4	1_A375_pNL7_minus_lncRNA::1::4510, 1_A375_pNL7_minus_lncRNA::1::4511, 2_A375_pNL97_plus_lncRNA::1::6504, 2_A375_pNL97_plus_lncRNA::1::6505	42, -5526, 250, -5558	in gene, upstream, in gene, upstream	1	1	56	56	2	2_A375_pNL97_plus_lncRNA::1	69	Gene ALDH7A1	FLJ92814, EPD, ALDH7A1, FLJ11738, PDE, ATQ1	aldehyde dehydrogenase 7 family, member A1	NM_001182, hCT2327745.1	208950_s_at, 208951_at, 213591_at	NP_001173.2, EAW48851.1
GeneID:51808	PHAX	5	125,936,607	125,962,944	26,337	+	4	1_A375_pNL7_minus_lncRNA::1::4510, 1_A375_pNL7_minus_lncRNA::1::4511, 2_A375_pNL97_plus_lncRNA::1::6504, 2_A375_pNL97_plus_lncRNA::1::6505	-5567, 1, -5775, 33	upstream, in gene, upstream, in gene	1	1	56	56	2	2_A375_pNL97_plus_lncRNA::1	69	Gene PHAX	RNUXA, PHAX, FLJ13193	phosphorylated adaptor for RNA export	NM_032177, hCT1639909.3	231812_x_at, 234405_s_at	NP_115553.2, EAW48850.1
GeneID:4001	LMNB1	5	126,112,833	126,172,709	59,876	+	3	1_A375_pNL7_minus_lncRNA::1::4512, 2_A375_pNL97_plus_lncRNA::1::6506, 2_A375_pNL97_plus_lncRNA::1::6507	-321, -355, 1567	upstream, upstream, in gene	1	1	16.5	18.5	2	1_A375_pNL7_minus_lncRNA::1	21	Gene LMNB1	MGC111419, ADLD, LMN2, LMNB, LMN, LMNB1	lamin B1	NM_005573, hCT18166.4, hCT2352214.0	203276_at	NP_005564.1, EAW48846.1, EAW48845.1
GeneID:115123	3-Mar	5	126,203,406	126,366,440	163,034	-	1	2_A375_pNL97_plus_lncRNA::1::6508	232	in gene	0	1	19	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MARCH3	MARCH3, MARCH-III, FLJ20096, MGC48332, RNF173	membrane-associated ring finger (C3HC4) 3	NM_178450, hCT19406.2	213256_at	NP_848545.1, EAW48844.1
GeneID:644873	FLJ33630	5	127,357,243	127,418,766	61,523	-	2	1_A375_pNL7_minus_lncRNA::1::4513, 2_A375_pNL97_plus_lncRNA::1::6510	-178, -194	upstream, upstream	1	1	20	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FLJ33630		hypothetical LOC644873	NR_015360	228686_at, 230665_at, 244769_at	
GeneID:6558	SLC12A2	5	127,419,483	127,525,380	105,897	+	2	1_A375_pNL7_minus_lncRNA::1::4513, 2_A375_pNL97_plus_lncRNA::1::6510	-539, -523	upstream, upstream	1	1	20	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC12A2	BSC, NKCC1, MGC104233, BSC2, SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	NM_001046, hCT18167.3, hCT2254454.0, hCT2353773.0	204404_at, 225635_at	NP_001037.1, EAW62393.1, EAW62392.1, EAW62394.1
GeneID:51735	RAPGEF6	5	130,759,614	130,970,929	211,315	-	1	2_A375_pNL97_plus_lncRNA::1::6511	113	in gene	0	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RAPGEF6	RAPGEF6, PDZ-GEF2, DKFZp667N084, PDZGEF2, RAGEF2, DKFZp686I15116, KIA001LB, RA-GEF-2	Rap guanine nucleotide exchange factor (GEF) 6	NM_016340, NM_001164386, NM_001164387, NM_001164388, NM_001164389, NM_001164390	1555247_a_at, 219112_at, 230078_at, 239436_at	NP_057424.3, NP_001157858.1, NP_001157859.1, NP_001157860.1, NP_001157861.1, NP_001157862.1
GeneID:96459	FNIP1	5	130,977,407	131,132,756	155,349	-	2	2_A375_pNL97_plus_lncRNA::1::6511, 2_A375_pNL97_plus_lncRNA::1::6512	161940, 116	downstream, in gene	0	1	16	20.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene FNIP1	DKFZp781P0215, DKFZp686E18167, MGC667, FNIP1, KIAA1961	folliculin interacting protein 1	NM_001008738, NM_133372	1559060_a_at, 223997_at, 226250_at, 226768_at	NP_001008738.2, NP_588613.2
GeneID:100505572	LOC100505572	5	131,142,796	131,192,621	49,825	-	1	2_A375_pNL97_plus_lncRNA::1::6512	59981	downstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100505572		hypothetical protein LOC100505572	XM_003119958, XM_003118996, XM_003120479		XP_003120006.1, XP_003119044.1, XP_003120527.1
GeneID:23305	ACSL6	5	131,289,152	131,347,349	58,197	-	2	1_A375_pNL7_minus_lncRNA::1::4515, 2_A375_pNL97_plus_lncRNA::1::6513	-971, -875	upstream, upstream	1	1	19	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene ACSL6	ACS2, LACS2, LACS 6, LACS5, ACSL6, KIAA0837, FLJ16173, FACL6	acyl-CoA synthetase long-chain family member 6	NM_015256, NM_001009185, hCT14585.2, hCT2253649.0, hCT2253650.0, hCT2253651.0, hCT2253654.0, hCT2253655.0	211207_s_at, 213683_at, 216409_at, 223918_at, 228725_at	NP_056071.2, NP_001009185.1, EAW62355.1, EAW62356.1, EAW62357.1, EAW62360.1, EAW62358.1, EAW62359.1
GeneID:6583	SLC22A4	5	131,630,145	131,679,899	49,754	+	1	1_A375_pNL7_minus_lncRNA::1::4516	-595	upstream	1	0	15	16	1	1_A375_pNL7_minus_lncRNA::1	15	Gene SLC22A4	SLC22A4, OCTN1, MGC34546, MGC40524	solute carrier family 22 (organic cation/ergothioneine transporter), member 4	NM_003059, hCT15231.2	205896_at	NP_003050.2, EAW62340.1
GeneID:6584	SLC22A5	5	131,705,401	131,731,306	25,905	+	2	1_A375_pNL7_minus_lncRNA::1::4517, 2_A375_pNL97_plus_lncRNA::1::6516	20284, 20039	in gene, in gene	1	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC22A5	OCTN2, SLC22A5, CDSP, FLJ46769, OCTN2VT	solute carrier family 22 (organic cation/carnitine transporter), member 5	NM_003060, hCT15228.2, hCT2254465.0, hCT2254466.0	205074_at	NP_003051.1, EAW62339.1, EAW62337.1, EAW62338.1
GeneID:3659	IRF1	5	131,817,301	131,826,465	9,164	-	3	1_A375_pNL7_minus_lncRNA::1::4518, 2_A375_pNL97_plus_lncRNA::1::6517, 2_A375_pNL97_plus_lncRNA::1::6518	113, 225, -5951	in gene, in gene, upstream	1	1	16	19	2	2_A375_pNL97_plus_lncRNA::1	20	Gene IRF1	MAR, IRF1, IRF-1	interferon regulatory factor 1	NM_002198, hCT1970765.1	202531_at	NP_002189.1, EAW62332.1
GeneID:10111	RAD50	5	131,892,616	131,980,313	87,697	+	1	2_A375_pNL97_plus_lncRNA::1::6519	24	in gene	0	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RAD50	RAD50-2, RAD502, NBSLD, hRad50, RAD50	RAD50 homolog (S. cerevisiae)	NM_005732, hCT15239.2, hCT2254472.0, hCT2254474.0	208393_s_at, 209349_at	NP_005723.2, EAW62329.1, EAW62328.1, EAW62330.1
GeneID:11127	KIF3A	5	132,028,323	132,073,265	44,942	-	1	2_A375_pNL97_plus_lncRNA::1::6520	113	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene KIF3A	KIF3A		NM_007054, hCT15226.2, hCT2253907.0, hCT2253909.0	213623_at, 228680_at	NP_008985.3, EAW62319.1, EAW62320.1, EAW62321.1
GeneID:645121	CCNI2	5	132,083,137	132,089,856	6,719	+	1	2_A375_pNL97_plus_lncRNA::1::6520	-9985	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CCNI2	CCNI2, FLJ16793	cyclin I family, member 2	NM_001039780		NP_001034869.1
GeneID:2661	GDF9	5	132,196,878	132,200,477	3,599	-	2	1_A375_pNL7_minus_lncRNA::1::4519, 2_A375_pNL97_plus_lncRNA::1::6521	-1779, -1779	upstream, upstream	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GDF9	GDF9		NM_005260, hCT15243.2	221314_at	NP_005251.1, EAW62309.1
GeneID:27089	UQCRQ	5	132,202,319	132,204,536	2,217	+	2	1_A375_pNL7_minus_lncRNA::1::4519, 2_A375_pNL97_plus_lncRNA::1::6521	-63, -63	upstream, upstream	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene UQCRQ	QPC, QP-C, QCR8, UQCRQ, UQCR7	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	NM_014402, hCT13564.2	201568_at	NP_055217.2, EAW62308.1
GeneID:116842	LEAP2	5	132,209,358	132,210,582	1,224	+	2	1_A375_pNL7_minus_lncRNA::1::4519, 2_A375_pNL97_plus_lncRNA::1::6521	-7102, -7102	upstream, upstream	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LEAP2	LEAP2, LEAP-2	liver expressed antimicrobial peptide 2	NM_052971, hCT1644469.4, hCT1969025.1	1552362_a_at	NP_443203.1, EAW62306.1, EAW62307.1
GeneID:27125	AFF4	5	132,211,071	132,299,354	88,283	-	4	1_A375_pNL7_minus_lncRNA::1::4519, 1_A375_pNL7_minus_lncRNA::1::4520, 2_A375_pNL97_plus_lncRNA::1::6521, 2_A375_pNL97_plus_lncRNA::1::6522	97098, 122, 97098, 122	downstream, in gene, downstream, in gene	1	1	19.5	19.5	2	2_A375_pNL97_plus_lncRNA::1	20	Gene AFF4	AF5Q31, MCEF, AFF4, MGC75036	AF4/FMR2 family, member 4	NM_014423, hCT15236.2, hCT2253893.0, hCT2253894.0, hCT2253895.0, hCT2253897.0	1555435_at, 1555436_a_at, 219199_at, 225229_at, 232864_s_at, 232865_at, 239439_at, 243487_at	NP_055238.1, EAW62305.1, EAW62301.1, EAW62302.1, EAW62303.1, EAW62304.1
GeneID:100506073	LOC100506073	5	132,294,837	132,297,278	2,441	-	2	1_A375_pNL7_minus_lncRNA::1::4520, 2_A375_pNL97_plus_lncRNA::1::6522	-1954, -1954	upstream, upstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100506073		hypothetical protein LOC100506073	XM_003119000, XM_003120481		XP_003119048.1, XP_003120529.1
GeneID:23105	FSTL4	5	132,532,152	132,948,223	416,071	-	8	1_A375_pNL7_minus_lncRNA::1::4521, 1_A375_pNL7_minus_lncRNA::1::4522, 1_A375_pNL7_minus_lncRNA::1::4523, 1_A375_pNL7_minus_lncRNA::1::4524, 2_A375_pNL97_plus_lncRNA::1::6523, 2_A375_pNL97_plus_lncRNA::1::6524, 2_A375_pNL97_plus_lncRNA::1::6525, 2_A375_pNL97_plus_lncRNA	366799, 364826, 316815, 46271, 371935, 366879, 316799, 46367	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	21.4	21.6	5	1_A375_pNL7_minus_lncRNA::1	30	Gene FSTL4	FSTL4		NM_015082, hCT2253549.0, hCT6765.2	1564511_a_at, 1565910_at, 214859_at	NP_055897.1, EAW62291.1, EAW62292.1
GeneID:7416	VDAC1	5	133,307,607	133,340,433	32,826	-	2	1_A375_pNL7_minus_lncRNA::1::4525, 2_A375_pNL97_plus_lncRNA::1::6528	-303, 417	upstream, in gene	1	1	15.5	17.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene VDAC1	PORIN, VDAC1, MGC111064, PORIN-31-HL	voltage-dependent anion channel 1	NM_003374, hCT2253502.0, hCT2253503.0, hCT2253505.0, hCT2253506.0, hCT2253508.0, hCT2353796.0	212038_s_at, 217139_at, 217140_s_at	NP_003365.1, EAW62281.1, EAW62282.1, EAW62283.1, EAW62284.1, EAW62286.1, EAW62285.1
GeneID:6500	SKP1	5	133,492,082	133,512,724	20,642	-	2	1_A375_pNL7_minus_lncRNA::1::4527, 2_A375_pNL97_plus_lncRNA::1::6529	212, 164	in gene, in gene	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene SKP1	SKP1A, TCEB1L, MGC34403, OCP2, OCP-II, p19A, SKP1, EMC19	S-phase kinase-associated protein 1	NM_006930, NM_170679, hCT2253493.0, hCT2253495.0, hCT2253497.0, hCT2253499.0, hCT2253500.0, hCT2353790.0, hCT2353791.0	200711_s_at, 200718_s_at, 200719_at, 207974_s_at	NP_008861.2, NP_733779.1, EAW62270.1, EAW62271.1, EAW62274.1, EAW62276.1, EAW62272.1, EAW62273.1, EAW62275.1
GeneID:5515	PPP2CA	5	133,532,148	133,561,950	29,802	-	2	1_A375_pNL7_minus_lncRNA::1::4528, 2_A375_pNL97_plus_lncRNA::1::6530	-210, 254	upstream, in gene	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PPP2CA	PPP2CA, RP-C, PP2CA, PP2Calpha, PP2Ac	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	NM_002715, hCT1963000.1, hCT7625.3	208652_at	NP_002706.1, EAW62268.1, EAW62269.1
GeneID:51265	CDKL3	5	133,634,115	133,702,765	68,650	-	2	1_A375_pNL7_minus_lncRNA::1::4529, 2_A375_pNL97_plus_lncRNA::1::6531	-4179, -4115	upstream, upstream	1	1	22	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene CDKL3	CDKL3, NKIAMRE	cyclin-dependent kinase-like 3	NM_016508, NM_001113575, hCT2253568.1, hCT2253571.1, hCT2253574.1, hCT2253576.1	1561190_at, 219831_at, 236017_at, 241911_at	NP_057592.2, NP_001107047.1, EAW62263.1, EAW62264.1, EAW62265.1, EAW62266.1
GeneID:7320	UBE2B	5	133,706,870	133,727,799	20,929	+	2	1_A375_pNL7_minus_lncRNA::1::4529, 2_A375_pNL97_plus_lncRNA::1::6531	74, 10	in gene, in gene	1	1	22	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene UBE2B	E2-17kDa, HHR6B, UBE2B, UBC2, HR6B, RAD6B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	NM_003337, hCT1641133.2, hCT1969023.1	202333_s_at, 202334_s_at, 202335_s_at, 211763_s_at, 224118_at, 228588_s_at, 239163_at	NP_003328.1, EAW62256.1, EAW62257.1
GeneID:100506132	LOC100506132	5	133,731,431	133,737,612	6,181	+	2	1_A375_pNL7_minus_lncRNA::1::4530, 2_A375_pNL97_plus_lncRNA::1::6532	16169, 16153	downstream, downstream	1	1	52	61	1	2_A375_pNL97_plus_lncRNA::1	61	Gene LOC100506132		hypothetical LOC100506132	XR_112760, XR_110571, XR_113774		
GeneID:91368	CDKN2AIPNL	5	133,737,756	133,747,598	9,842	-	2	1_A375_pNL7_minus_lncRNA::1::4530, 2_A375_pNL97_plus_lncRNA::1::6532	-2, 14	upstream, in gene	1	1	52	61	1	2_A375_pNL97_plus_lncRNA::1	61	Gene CDKN2AIPNL	CDKN2AIPNL, MGC13017	CDKN2A interacting protein N-terminal like	NM_080656, hCT2253579.1, hCT2253581.1, hCT7635.3	1554348_s_at, 235006_at	NP_542387.1, EAW62259.1, EAW62260.1, EAW62261.1
GeneID:23338	PHF15	5	133,861,798	133,918,918	57,120	+	1	2_A375_pNL97_plus_lncRNA::1::6533	15738	in gene	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PHF15	JADE2, KIAA0239, PHF15	PHD finger protein 15	NM_015288, hCT2254263.0, hCT2254264.0, hCT2254266.0, hCT2353709.0, hCT7629.3	208202_s_at, 212660_at, 232279_at	NP_056103.4, EAW62253.1, EAW62252.1, EAW62254.1, EAW62255.1, EAW62256.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:819	CAMLG	5	134,074,206	134,087,847	13,641	+	4	1_A375_pNL7_minus_lncRNA::1::4531, 1_A375_pNL7_minus_lncRNA::1::4532, 2_A375_pNL97_plus_lncRNA::1::6534, 2_A375_pNL97_plus_lncRNA::1::6535	2, 20194, -126, 20178	in gene, downstream, upstream, downstream	1	1	81.5	80.5	2	1_A375_pNL7_minus_lncRNA::1	139	Gene CAMLG	MGC163197, CAML, CAMLG	calcium modulating ligand	NM_001745, hCT2254277.0, hCT2254279.0	203538_at	NP_001736.1, EAW62244.1, EAW62243.1
GeneID:9879	DDX46	5	134,094,461	134,166,811	72,350	+	2	1_A375_pNL7_minus_lncRNA::1::4532, 2_A375_pNL97_plus_lncRNA::1::6535	-61, -77	upstream, upstream	1	1	139	132	1	1_A375_pNL7_minus_lncRNA::1	139	Gene DDX46	PRPF5, FLJ25329, MGC9936, KIAA0801, DDX46, Prp5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	NM_014829, hCT2254281.0, hCT2254285.0, hCT2353713.0, hCT2353714.0, hCT7634.2	202462_s_at, 228039_at	NP_055644.2, EAW62238.1, EAW62239.1, EAW62240.1, EAW62241.1, EAW62242.1
GeneID:134553	C5orf24	5	134,181,370	134,195,425	14,055	+	1	2_A375_pNL97_plus_lncRNA::1::6536	358	in gene	0	1	13	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene C5orf24	C5orf24, FLJ37562	chromosome 5 open reading frame 24	NM_152409, NM_001135586	1553106_at, 1553107_s_at, 1553108_at, 224875_at, 224876_at, 229098_s_at	NP_689622.2, NP_001129058.1
GeneID:79770	TXNDC15	5	134,209,460	134,237,323	27,863	+	3	1_A375_pNL7_minus_lncRNA::1::4533, 1_A375_pNL7_minus_lncRNA::1::4534, 2_A375_pNL97_plus_lncRNA::1::6537	1484, 31084, 31148	in gene, downstream, downstream	1	1	16.5	15.5	2	1_A375_pNL7_minus_lncRNA::1	18	Gene TXNDC15	FLJ22625, UNQ335, C5orf14, TXNDC15	thioredoxin domain containing 15	NM_024715, hCT1784313.2, hCT2353792.0, hCT2353793.0	220495_s_at, 227873_at	NP_078991.3, EAW62231.1, EAW62232.1, EAW62233.1
GeneID:84105	PCBD2	5	134,240,810	134,298,336	57,526	+	2	1_A375_pNL7_minus_lncRNA::1::4534, 2_A375_pNL97_plus_lncRNA::1::6537	-266, -202	upstream, upstream	1	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PCBD2	PCBD2, DCOH2, DCOHM, PHS2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	NM_032151, hCT2349005.0	1554894_a_at, 223712_at, 240846_at	NP_115527.3, EAW62229.1
GeneID:9555	H2AFY	5	134,670,071	134,735,577	65,506	-	1	2_A375_pNL97_plus_lncRNA::1::6539	665	in gene	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene H2AFY	mH2A1, H2A.y, MACROH2A1.1, H2AF12M, H2AFJ, H2A/y, H2AFY, macroH2A1.2	H2A histone family, member Y	NM_004893, NM_138609, NM_138610, NM_001040158, hCT1954327.2, hCT1970850.2, hCT1970853.2, hCT2253492.1, hCT29569.2	1558779_at, 1558780_a_at, 207168_s_at, 214500_at, 214501_s_at, 226840_at	NP_004884.1, NP_613075.1, NP_613258.2, NP_001035248.1, EAW62220.1, EAW62222.1, EAW62218.1, EAW62219.1, EAW62221.1
GeneID:7045	TGFBI	5	135,364,584	135,399,507	34,923	+	4	1_A375_pNL7_minus_lncRNA::1::4535, 1_A375_pNL7_minus_lncRNA::1::4536, 2_A375_pNL97_plus_lncRNA::1::6540, 2_A375_pNL97_plus_lncRNA::1::6541	-8312, 24888, -8296, 24888	upstream, in gene, upstream, in gene	1	1	18	20	2	2_A375_pNL97_plus_lncRNA::1	20	Gene TGFBI	CDB1, CSD, BIGH3, CSD3, CDGG1, EBMD, TGFBI, CSD1, LCD1, CSD2, CDG2	transforming growth factor, beta-induced, 68kDa	NM_000358, hCT2253103.0, hCT2353684.0, hCT32670.3	201506_at	NP_000349.1, EAW62199.1, EAW62198.1, EAW62200.1
GeneID:9597	SMAD5OS	5	135,465,202	135,470,579	5,377	-	2	1_A375_pNL7_minus_lncRNA::1::4537, 2_A375_pNL97_plus_lncRNA::1::6542	1971, 1843	in gene, in gene	1	1	24	17	1	1_A375_pNL7_minus_lncRNA::1	24	Gene SMAD5OS	SMAD5AS, SMAD5OS, DAMS	SMAD family member 5 opposite strand	NR_026763	220263_at	
GeneID:4090	SMAD5	5	135,468,536	135,518,422	49,886	+	2	1_A375_pNL7_minus_lncRNA::1::4537, 2_A375_pNL97_plus_lncRNA::1::6542	72, 200	in gene, in gene	1	1	24	17	1	1_A375_pNL7_minus_lncRNA::1	24	Gene SMAD5	SMAD5, DKFZp781O1323, Dwfc, MADH5, DKFZp781C1895, DWFC, JV5-1	SMAD family member 5	NM_005903, NM_001001419, NM_001001420, hCT2253108.0, hCT2253113.0, hCT32672.2	205187_at, 205188_s_at, 225219_at, 225223_at, 235451_at	NP_005894.3, NP_001001419.1, NP_001001420.1, EAW62194.1, EAW62195.1, EAW62196.1
GeneID:57113	TRPC7	5	135,548,999	135,701,164	152,165	-	2	1_A375_pNL7_minus_lncRNA::1::4538, 2_A375_pNL97_plus_lncRNA::1::6543	92, 108	in gene, in gene	1	1	35	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene TRPC7	TRP7, TRPC7	transient receptor potential cation channel, subfamily C, member 7	NM_020389, NM_001167576, NM_001167577, hCT2353685.0, hCT2353686.0, hCT2353687.0, hCT2353688.0, hCT2353689.0, hCT32674.3	208589_at, 234407_s_at	NP_065122.1, NP_001161048.1, NP_001161049.1, EAW62187.1, EAW62188.1, EAW62192.1, EAW62189.1, EAW62190.1, EAW62191.1
GeneID:6695	SPOCK1	5	136,310,987	136,835,018	524,031	-	5	1_A375_pNL7_minus_lncRNA::1::4539, 1_A375_pNL7_minus_lncRNA::1::4540, 1_A375_pNL7_minus_lncRNA::1::4541, 2_A375_pNL97_plus_lncRNA::1::6544, 2_A375_pNL97_plus_lncRNA::1::6545	356410, 45674, 28426, 45674, 28426	in gene, in gene, in gene, in gene, in gene	1	1	25.33	27.67	3	2_A375_pNL97_plus_lncRNA::1	37	Gene SPOCK1	TESTICAN, SPOCK1, SPOCK, FLJ37170, TIC1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	NM_004598, hCT2353752.0, hCT30730.3	202363_at	NP_004589.1, EAW62185.1, EAW62186.1
GeneID:10949	HNRNPA0	5	137,087,073	137,090,039	2,966	-	1	2_A375_pNL97_plus_lncRNA::1::6546	7	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene HNRNPA0	HNRPA0, HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	NM_006805, hCT1640078.4	201054_at, 201055_s_at	NP_006796.1, EAW62182.1
GeneID:51306	FAM13B	5	137,273,638	137,368,802	95,164	-	1	2_A375_pNL97_plus_lncRNA::1::6547	594	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FAM13B	N61, KHCHP, FAM13B1, MGC57159, DKFZp667F249, C5orf5, FLJ26735, FAM13B	family with sequence similarity 13, member B	NM_016603, NM_001101800, NM_001101801, hCT1821582.1, hCT2254838.0, hCT2353734.0, hCT2353735.0	218518_at	NP_057687.2, NP_001095270.1, NP_001095271.1, EAW62170.1, EAW62171.1, EAW62172.1, EAW62173.1
GeneID:100130172	LOC100130172	5	137,368,482	137,373,321	4,839	+	1	2_A375_pNL97_plus_lncRNA::1::6547	-274	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100130172		hypothetical LOC100130172	XR_112756, XR_110574, XR_113779		
GeneID:995	CDC25C	5	137,620,959	137,667,516	46,557	-	3	1_A375_pNL7_minus_lncRNA::1::4542, 1_A375_pNL7_minus_lncRNA::1::4543, 2_A375_pNL97_plus_lncRNA::1::6548	92, -6052, -6020	in gene, upstream, upstream	1	1	71	88.5	2	2_A375_pNL97_plus_lncRNA::1	164	Gene CDC25C	CDC25C, CDC25	cell division cycle 25 homolog C (S. pombe)	NM_022809, NM_001790, hCT1821584.2, hCT2254821.0, hCT2254822.0, hCT2254823.0, hCT2353753.0, hCT2353754.0	205167_s_at, 216914_at, 217010_s_at	NP_073720.1, NP_001781.2, EAW62146.1, EAW62147.1, EAW62149.1, EAW62150.1, EAW62145.1, EAW62148.1
GeneID:51307	FAM53C	5	137,673,224	137,685,418	12,194	+	6	1_A375_pNL7_minus_lncRNA::1::4542, 1_A375_pNL7_minus_lncRNA::1::4543, 1_A375_pNL7_minus_lncRNA::1::4544, 1_A375_pNL7_minus_lncRNA::1::4545, 2_A375_pNL97_plus_lncRNA::1::6548, 2_A375_pNL97_plus_lncRNA::1::6549	-5800, 344, 14952, 15896, 312, 14936	upstream, in gene, downstream, downstream, in gene, downstream	1	1	58	69.33	3	2_A375_pNL97_plus_lncRNA::1	164	Gene FAM53C	C5orf6, FAM53C	family with sequence similarity 53, member C	NM_001135647, NM_016605, hCT1954332.1, hCT9846.2	218023_s_at	NP_001129119.1, NP_057689.1, EAW62143.1, EAW62144.1
GeneID:51780	KDM3B	5	137,688,285	137,772,716	84,431	+	3	1_A375_pNL7_minus_lncRNA::1::4544, 1_A375_pNL7_minus_lncRNA::1::4545, 2_A375_pNL97_plus_lncRNA::1::6549	-109, 835, -125	upstream, in gene, upstream	1	1	32	31	1	1_A375_pNL7_minus_lncRNA::1	32	Gene KDM3B	KDM3B, KIAA1082, JMJD1B, NET22, 5qNCA, C5orf7	lysine (K)-specific demethylase 3B	NM_016604, hCT2256307.0, hCT9838.2	201643_x_at, 210878_s_at	NP_057688.2, EAW62141.1, EAW62142.1
GeneID:1958	EGR1	5	137,801,181	137,805,004	3,823	+	2	1_A375_pNL7_minus_lncRNA::1::4546, 2_A375_pNL97_plus_lncRNA::1::6550	-381, -125	upstream, upstream	1	1	36	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene EGR1	ZIF-268, ZNF225, KROX-24, TIS8, EGR1, NGFI-A, G0S30, AT225	early growth response 1	NM_001964, hCT2256315.1, hCT9839.1	201693_s_at, 201694_s_at, 227404_s_at	NP_001955.1, EAW62136.1, EAW62135.1
GeneID:2107	ETF1	5	137,841,784	137,878,932	37,148	-	2	1_A375_pNL7_minus_lncRNA::1::4548, 2_A375_pNL97_plus_lncRNA::1::6551	116, 148	in gene, in gene	1	1	18	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ETF1	MGC111066, ETF1, D5S1995, ERF1, TB3-1, SUP45L1, ERF, RF1	eukaryotic translation termination factor 1	NM_004730, hCT2254811.0, hCT2254812.0, hCT2254813.0, hCT2353728.0, hCT2353729.0	201573_s_at, 201574_at	NP_004721.1, EAW62134.1, EAW62130.1, EAW62131.1, EAW62132.1, EAW62133.1
GeneID:3313	HSPA9	5	137,890,571	137,911,318	20,747	-	2	1_A375_pNL7_minus_lncRNA::1::4549, 2_A375_pNL97_plus_lncRNA::1::6552	102, 182	in gene, in gene	1	1	24	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene HSPA9	HSPA9B, GRP75, MTHSP75, PBP74, CSA, HSPA9, MOT, mot-2, MGC4500, MOT2	heat shock 70kDa protein 9 (mortalin)	NM_004134, hCT1954329.2, hCT9841.3	200690_at, 200691_s_at, 200692_s_at, 232200_at	NP_004125.3, EAW62129.1, EAW62128.1
GeneID:724102	SNHG4	5	138,609,441	138,618,873	9,432	+	1	1_A375_pNL7_minus_lncRNA::1::4552	159	in gene	1	0	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SNHG4	U19H, NCRNA00059, SNHG4	small nucleolar RNA host gene 4 (non-protein coding)	NR_036536, NR_003141	1564906_at, 1564911_at, 1565325_at	
GeneID:9782	MATR3	5	138,609,441	138,667,366	57,925	+	2	1_A375_pNL7_minus_lncRNA::1::4552, 2_A375_pNL97_plus_lncRNA::1::6555	159, 68111	in gene, downstream	1	1	16	17.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene MATR3	MGC9105, KIAA0723, MPD2, DKFZp686K23100, VCPDM, DKFZp686K0542, MATR3	matrin 3	NM_018834, NM_199189, NM_001194954, NM_001194955, NM_001194956, NR_036535	1558093_s_at, 200624_s_at, 200626_s_at, 214363_s_at, 226012_at, 242260_at	NP_061322.2, NP_954659.1, NP_001181883.1, NP_001181884.1, NP_001181885.1
GeneID:26821	SNORA74A	5	138,614,469	138,614,668	199	+	1	1_A375_pNL7_minus_lncRNA::1::4552	-4869	upstream	1	0	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SNORA74A	SNORA74A, U19, RNU19	small nucleolar RNA, H/ACA box 74A	NR_002915	1567679_at, 1567681_at, 1567682_x_at	
GeneID:51247	PAIP2	5	138,677,519	138,705,409	27,890	+	1	2_A375_pNL97_plus_lncRNA::1::6555	33	in gene	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PAIP2	PAIP2A, MGC72018, PAIP2	poly(A) binding protein interacting protein 2	NM_016480, NM_001033112, hCT2253795.0, hCT2253796.0, hCT2353704.0, hCT2353705.0, hCT2353706.0, hCT7701.1	222983_s_at, 222984_at	NP_057564.3, NP_001028284.1, EAW62107.1, EAW62108.1, EAW62110.1, EAW62112.1, EAW62109.1, EAW62111.1
GeneID:389333	LOC389333	5	138,727,635	138,730,885	3,250	-	1	2_A375_pNL97_plus_lncRNA::1::6556	-8923	upstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC389333		hypothetical protein LOC389333	NM_001161546		NP_001155018.1
GeneID:202051	SPATA24	5	138,732,456	138,739,776	7,320	-	1	2_A375_pNL97_plus_lncRNA::1::6556	-32	upstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SPATA24	T6441, CCDC161, SPATA24	spermatogenesis associated 24	NM_194296	1556641_at, 238027_at	NP_919272.1
GeneID:202052	DNAJC18	5	138,745,892	138,775,214	29,322	-	2	1_A375_pNL7_minus_lncRNA::1::4553, 2_A375_pNL97_plus_lncRNA::1::6556	-18, 35406	upstream, downstream	1	1	17.5	17	2	2_A375_pNL97_plus_lncRNA::1	20	Gene DNAJC18	MGC29463, DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	NM_152686, hCT7699.3	227166_at, 227169_at	NP_689899.1, EAW62102.1
GeneID:641700	ECSCR	5	138,784,245	138,784,863	618	-	1	1_A375_pNL7_minus_lncRNA::1::4553	9631	downstream	1	0	18	14	1	1_A375_pNL7_minus_lncRNA::1	18	Gene ECSCR	ARIA, ECSCR, ECSM2	endothelial cell-specific chemotaxis regulator	NM_001077693	227780_s_at, 228339_at	NP_001071161.1
GeneID:7322	UBE2D2	5	138,940,751	139,008,019	67,268	+	1	2_A375_pNL97_plus_lncRNA::1::6557	76481	downstream	0	1	17	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene UBE2D2	UBC4/5, PUBC1, UBCH5B, UBC4, E2(17)KB2, UBE2D2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	NM_181838, NM_003339, hCT2253808.0, hCT2253809.0, hCT2253811.0	201343_at, 201344_at, 201345_s_at	NP_862821.1, NP_003330.1, EAW62095.1, EAW62096.1, EAW62097.1
GeneID:9542	NRG2	5	139,226,364	139,422,884	196,520	-	4	1_A375_pNL7_minus_lncRNA::1::4554, 1_A375_pNL7_minus_lncRNA::1::4555, 2_A375_pNL97_plus_lncRNA::1::6559, 2_A375_pNL97_plus_lncRNA::1::6560	57476, -300, 57508, -268	in gene, upstream, in gene, upstream	1	1	17.5	18	2	2_A375_pNL97_plus_lncRNA::1	19	Gene NRG2	Don-1, NRG2, DON1, NTAK, HRG2	neuregulin 2	NM_001184935, NM_004883, NM_013981, NM_013982, NM_013983, hCT2252851.0, hCT2252852.0, hCT2252853.0, hCT2252855.0, hCT2252856.0, hCT2252857.0, hCT2252859.0, hCT2252860.0, hCT2353746.0, hCT2353747.0	206679_s_at, 208062_s_at	NP_001171864.1, NP_004874.1, NP_053584.1, NP_053585.1, NP_053586.1, EAW62084.1, EAW62078.1, EAW62079.1, EAW62080.1, EAW62081.1, EAW62082.1, EAW62083.1, EAW62085.1, EAW62086.1, EAW62087.1
GeneID:100505636	LOC100505636	5	139,462,505	139,468,150	5,645	-	4	1_A375_pNL7_minus_lncRNA::1::4556, 1_A375_pNL7_minus_lncRNA::1::4557, 2_A375_pNL97_plus_lncRNA::1::6561, 2_A375_pNL97_plus_lncRNA::1::6562	822, -5946, -5082, -6042	in gene, upstream, upstream, upstream	1	1	13.67	16.67	3	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100505636		hypothetical LOC100505636	XR_112769, XR_112768, XR_110310, XR_110309, XR_113783, XR_113782		
GeneID:5813	PURA	5	139,493,708	139,496,321	2,613	+	4	1_A375_pNL7_minus_lncRNA::1::4556, 1_A375_pNL7_minus_lncRNA::1::4557, 2_A375_pNL97_plus_lncRNA::1::6561, 2_A375_pNL97_plus_lncRNA::1::6562	-6380, 388, -476, 484	upstream, in gene, upstream, in gene	1	1	13.67	16.67	3	2_A375_pNL97_plus_lncRNA::1	22	Gene PURA	PURALPHA, PUR1, PUR-ALPHA, PURA	purine-rich element binding protein A	NM_005859	204020_at, 204021_s_at, 213806_at	NP_005850.1
GeneID:84418	C5orf32	5	139,554,653	139,623,374	68,721	+	1	2_A375_pNL97_plus_lncRNA::1::6563	46979	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C5orf32	ORF1-FL49, C5orf32	chromosome 5 open reading frame 32	NM_032412, hCT1690270.1, hCT36601.2	224707_at	NP_115788.1, EAW62073.1, EAW62074.1
GeneID:404734	ANKHD1-EIF4EBP3	5	139,781,429	139,929,163	147,734	+	2	1_A375_pNL7_minus_lncRNA::1::4558, 2_A375_pNL97_plus_lncRNA::1::6564	-293, -1093	upstream, upstream	1	1	30	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene ANKHD1-EIF4EBP3	MASK-BP3ARF, MASK-BP3alt, MASK-BP3, ANKHD1-EIF4EBP3	ANKHD1-EIF4EBP3 readthrough	NM_020690	208772_at, 208773_s_at, 214919_s_at, 233292_s_at	NP_065741.3
GeneID:54882	ANKHD1	5	139,781,429	139,919,441	138,012	+	2	1_A375_pNL7_minus_lncRNA::1::4558, 2_A375_pNL97_plus_lncRNA::1::6564	-293, -1093	upstream, upstream	1	1	30	34	1	2_A375_pNL97_plus_lncRNA::1	34	Gene ANKHD1	ANKHD1, MASK, VBARP	ankyrin repeat and KH domain containing 1	NM_017747, NM_017978, NM_024668	219081_at, 229457_at	NP_060217.1, NP_060448.1, NP_078944.2
GeneID:10011	SRA1	5	139,929,653	139,937,678	8,025	-	2	1_A375_pNL7_minus_lncRNA::1::4559, 2_A375_pNL97_plus_lncRNA::1::6565	-6450, -6482	upstream, upstream	1	1	33	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene SRA1	MGC87674, STRAA1, SRAP, SRA, SRA1, pp7684	steroid receptor RNA activator 1	NM_001035235, hCT11375.2, hCT1953450.1, hCT2353720.0	224130_s_at, 224864_at	NP_001030312.2, EAW62052.1, EAW62051.1, EAW62053.1
GeneID:10307	APBB3	5	139,937,853	139,944,189	6,336	-	2	1_A375_pNL7_minus_lncRNA::1::4559, 2_A375_pNL97_plus_lncRNA::1::6565	61, 29	in gene, in gene	1	1	33	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene APBB3	MGC87674, SRA, FE65L2, APBB3, MGC150555	amyloid beta (A4) precursor protein-binding, family B, member 3	NM_133172, NM_006051, NM_133173, NM_133174, hCT2252827.0, hCT2252828.0, hCT2252829.0, hCT2252830.0, hCT2252832.0, hCT2252833.0, hCT2252835.0, hCT2252836.0, hCT2252837.0, hCT2353703.0	204650_s_at	NP_573418.2, NP_006042.3, NP_573419.2, NP_573420.2, EAW62046.1, EAW62050.1, EAW62041.1, EAW62042.1, EAW62043.1, EAW62044.1, EAW62045.1, EAW62047.1, EAW62048.1, EAW62049.1
GeneID:113829	SLC35A4	5	139,944,420	139,948,683	4,263	+	2	1_A375_pNL7_minus_lncRNA::1::4559, 2_A375_pNL97_plus_lncRNA::1::6565	-292, -260	upstream, upstream	1	1	33	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene SLC35A4	SLC35A4, MGC2541	solute carrier family 35, member A4	NM_080670, hCT1821828.0	224626_at	NP_542401.1, EAW62040.1
GeneID:100505798	LOC100505798	5	139,949,633	139,971,677	22,044	-	2	1_A375_pNL7_minus_lncRNA::1::4559, 2_A375_pNL97_plus_lncRNA::1::6565	27549, 27517	downstream, downstream	1	1	33	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene LOC100505798		hypothetical protein LOC100505798	XM_003118935		XP_003118983.1
GeneID:929	CD14	5	140,011,313	140,013,286	1,973	-	1	2_A375_pNL97_plus_lncRNA::1::6566	-6010	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CD14	CD14		NM_000591, NM_001040021, NM_001174104, NM_001174105, hCT2252825.0	201743_at	NP_000582.1, NP_001035110.1, NP_001167575.1, NP_001167576.1, EAW62037.1
GeneID:55374	TMCO6	5	140,019,012	140,024,989	5,977	+	2	1_A375_pNL7_minus_lncRNA::1::4560, 2_A375_pNL97_plus_lncRNA::1::6566	8012, 284	downstream, in gene	1	1	15.5	16	2	1_A375_pNL7_minus_lncRNA::1	16	Gene TMCO6	TMCO6, PRO1580, FLJ39769	transmembrane and coiled-coil domains 6	NM_018502, hCT11377.2, hCT1953451.1, hCT2255734.0, hCT2353750.0, hCT2353751.0	221096_s_at	NP_060972.3, EAW62033.1, EAW62032.1, EAW62034.1, EAW62035.1, EAW62036.1
GeneID:4695	NDUFA2	5	140,024,948	140,027,370	2,422	-	2	1_A375_pNL7_minus_lncRNA::1::4560, 2_A375_pNL97_plus_lncRNA::1::6566	346, 8074	in gene, downstream	1	1	15.5	16	2	1_A375_pNL7_minus_lncRNA::1	16	Gene NDUFA2	B8, CD14, CIB8, NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	NM_001185012, NM_002488, NR_033697, hCT1953449.1	209223_at, 209224_s_at, 222971_at	NP_001171941.1, NP_002479.1, EAW62031.1
GeneID:3550	IK	5	140,027,384	140,042,065	14,681	+	4	1_A375_pNL7_minus_lncRNA::1::4560, 1_A375_pNL7_minus_lncRNA::1::4561, 2_A375_pNL97_plus_lncRNA::1::6566, 2_A375_pNL97_plus_lncRNA::1::6567	-360, 16712, -8088, 16648	upstream, downstream, upstream, downstream	1	1	16	18.33	3	2_A375_pNL97_plus_lncRNA::1	23	Gene IK	IK, MGC59741, RED, CSA2	IK cytokine, down-regulator of HLA II	NM_006083, hCT1821814.1, hCT2255740.0, hCT2255742.0	200066_at	NP_006074.2, EAW62028.1, EAW62029.1, EAW62030.1
GeneID:54853	WDR55	5	140,044,384	140,050,553	6,169	+	2	1_A375_pNL7_minus_lncRNA::1::4561, 2_A375_pNL97_plus_lncRNA::1::6567	-288, -352	upstream, upstream	1	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene WDR55	FLJ20195, FLJ21702, WDR55	WD repeat domain 55	NM_017706, hCT1821813.2, hCT2255744.0, hCT2255752.0	219509_at, 222114_x_at, 223833_at	NP_060176.2, EAW62024.1, EAW62025.1, EAW62026.1
GeneID:373863	DND1	5	140,050,381	140,053,171	2,790	-	2	1_A375_pNL7_minus_lncRNA::1::4561, 2_A375_pNL97_plus_lncRNA::1::6567	8075, 8139	downstream, downstream	1	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene DND1	RBMS4, MGC34750, DND1	dead end homolog 1 (zebrafish)	NM_194249, hCT2351851.0	57739_at	NP_919225.1, EAW62027.1
GeneID:3035	HARS	5	140,053,490	140,070,971	17,481	-	3	1_A375_pNL7_minus_lncRNA::1::4561, 1_A375_pNL7_minus_lncRNA::1::4562, 2_A375_pNL97_plus_lncRNA::1::6567	26875, -101, 26939	downstream, upstream, downstream	1	1	19	19.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene HARS	HARS, FLJ20491, HRS	histidyl-tRNA synthetase	NM_002109, hCT1821805.3, hCT2252820.1, hCT2353741.0	202042_at	NP_002100.2, EAW62023.1, EAW62021.1, EAW62022.1
GeneID:23438	HARS2	5	140,071,018	140,078,890	7,872	+	1	1_A375_pNL7_minus_lncRNA::1::4562	54	in gene	1	0	21	16	1	1_A375_pNL7_minus_lncRNA::1	21	Gene HARS2	HARSR, HARSL, HO3, HARS2	histidyl-tRNA synthetase 2, mitochondrial (putative)	NM_012208, hCT2255764.0, hCT2353763.0	209252_at	NP_036340.1, EAW62020.1, EAW62019.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:153527	ZMAT2	5	140,080,032	140,086,239	6,207	+	3	1_A375_pNL7_minus_lncRNA::1::4562, 1_A375_pNL7_minus_lncRNA::1::4563, 2_A375_pNL97_plus_lncRNA::1::6568	-8960, 10656, 10720	upstream, downstream, downstream	1	1	25	21	2	1_A375_pNL7_minus_lncRNA::1	29	Gene ZMAT2	hSNU23, FLJ31121, Snu23, ZMAT2	zinc finger, matrin type 2	NM_144723, hCT2255766.1, hCT2344113.0, hCT2353717.0	224782_at	NP_653324.1, EAW62016.1, EAW62017.1, EAW62018.1
GeneID:56147	PCDHA1	5	140,165,876	140,391,929	226,053	+	1	2_A375_pNL97_plus_lncRNA::1::6571	140396	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA1	PCDH-ALPHA1, PCDHA1	protocadherin alpha 1	NM_018900, NM_031410, NM_031411		NP_061723.1, NP_113598.1, NP_113599.1
GeneID:56117	PCDHA@	5	140,165,876	140,391,929	226,053	+	1	2_A375_pNL97_plus_lncRNA::1::6571	140396	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA@	PCDHA@, CNR1, CNRS1	protocadherin alpha cluster			
GeneID:56146	PCDHA2	5	140,174,444	140,391,929	217,485	+	1	2_A375_pNL97_plus_lncRNA::1::6571	131828	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA2	PCDH-ALPHA2, PCDHA2	protocadherin alpha 2	NM_018905, NM_031495	210572_at, 211365_s_at	NP_061728.1, NP_113683.1
GeneID:56145	PCDHA3	5	140,180,783	140,391,929	211,146	+	1	2_A375_pNL97_plus_lncRNA::1::6571	125469	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA3	MGC141669, PCDH-ALPHA3, PCDHA3	protocadherin alpha 3	NM_018906, NM_031497	211870_s_at	NP_061729.1, NP_113685.1
GeneID:56144	PCDHA4	5	140,186,672	140,391,929	205,257	+	1	2_A375_pNL97_plus_lncRNA::1::6571	119600	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA4	CNR1, PCDH-ALPHA4, MGC138307, PCDHA4, MGC142169, CNRN1, CRNR1	protocadherin alpha 4	NM_018907, NM_031500		NP_061730.1, NP_113686.1
GeneID:56143	PCDHA5	5	140,201,361	140,391,929	190,568	+	1	2_A375_pNL97_plus_lncRNA::1::6571	104911	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA5	CRNR6, PCDHA5, CNRS6, CNR6, CNRN6, PCDH-ALPHA5	protocadherin alpha 5	NM_018908, NM_031501	211836_x_at	NP_061731.1, NP_113689.1
GeneID:56142	PCDHA6	5	140,207,650	140,391,929	184,279	+	1	2_A375_pNL97_plus_lncRNA::1::6571	98622	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA6	CNRN2, CRNR2, PCDH-ALPHA6, CNRS2, PCDHA6, CNR2	protocadherin alpha 6	NM_018909, NM_031848, NM_031849	211811_s_at	NP_061732.1, NP_114036.1, NP_114037.1
GeneID:56141	PCDHA7	5	140,213,969	140,391,929	177,960	+	1	2_A375_pNL97_plus_lncRNA::1::6571	92303	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA7	CRNR4, CNRN4, PCDHA7, CNRS4, PCDH-ALPHA7, CNR4	protocadherin alpha 7	NM_018910, NM_031852		NP_061733.1, NP_114040.1
GeneID:56140	PCDHA8	5	140,220,907	140,391,929	171,022	+	1	2_A375_pNL97_plus_lncRNA::1::6571	85365	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA8	PCDHA8, PCDH-ALPHA8	protocadherin alpha 8	NM_018911, NM_031856		NP_061734.1, NP_114062.1
GeneID:9752	PCDHA9	5	140,227,357	140,391,929	164,572	+	1	2_A375_pNL97_plus_lncRNA::1::6571	78915	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA9	PCDH-ALPHA9, KIAA0345, PCDHA9	protocadherin alpha 9	NM_031857, NM_014005	208205_at	NP_114063.1, NP_054724.1
GeneID:56139	PCDHA10	5	140,235,634	140,391,929	156,295	+	1	2_A375_pNL97_plus_lncRNA::1::6571	70638	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA10	PCDHA10, CNR8, CRNR8, CNRN8, CNRS8, PCDH-ALPHA10	protocadherin alpha 10	NM_018901, NM_031859, NM_031860	211867_s_at	NP_061724.1, NP_114065.1, na:2919
GeneID:56138	PCDHA11	5	140,247,831	140,391,929	144,098	+	1	2_A375_pNL97_plus_lncRNA::1::6571	58441	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA11	CRNR7, CNRS7, PCDH-ALPHA11, PCDHA11, CNRN7, CNR7	protocadherin alpha 11	NM_031861, NM_018902		NP_114067.1, NP_061725.1
GeneID:56137	PCDHA12	5	140,254,931	140,391,929	136,998	+	1	2_A375_pNL97_plus_lncRNA::1::6571	51341	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA12	PCDHA12, MGC138485, MGC141932, PCDH-ALPHA12	protocadherin alpha 12	NM_018903, NM_031864		NP_061726.1, NP_114070.1
GeneID:56136	PCDHA13	5	140,261,854	140,391,929	130,075	+	1	2_A375_pNL97_plus_lncRNA::1::6571	44418	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHA13	CNR5, PCDHA13, CNRN5, PCDH-ALPHA13, CRNR5, CNRS5	protocadherin alpha 13	NM_018904, NM_031865		NP_061727.1, NP_114071.1
GeneID:56135	PCDHAC1	5	140,306,302	140,391,929	85,627	+	1	2_A375_pNL97_plus_lncRNA::1::6571	-30	upstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PCDHAC1	PCDHAC1, PCDH-ALPHA-C1	protocadherin alpha subfamily C, 1	NM_018898, NM_031882	1553235_at, 1553237_x_at	NP_061721.2, NP_114088.2
GeneID:29930	PCDHB1	5	140,430,979	140,433,512	2,533	+	3	1_A375_pNL7_minus_lncRNA::1::4566, 2_A375_pNL97_plus_lncRNA::1::6572, 2_A375_pNL97_plus_lncRNA::1::6573	-10403, -10275, 189	upstream, upstream, in gene	1	1	17	21	2	1_A375_pNL7_minus_lncRNA::1	25	Gene PCDHB1	MGC138303, PCDHB1, MGC138301, PCDH-BETA1	protocadherin beta 1	NM_013340, hCT33793.3	221303_at	NP_037472.2, EAW61985.1
GeneID:56116	PCDHB@	5	140,430,979	140,627,802	196,823	+	4	1_A375_pNL7_minus_lncRNA::1::4566, 2_A375_pNL97_plus_lncRNA::1::6572, 2_A375_pNL97_plus_lncRNA::1::6573, 2_A375_pNL97_plus_lncRNA::1::6574	-10403, -10275, 189, 43245	upstream, upstream, in gene, in gene	1	1	16	20.33	3	1_A375_pNL7_minus_lncRNA::1	25	Gene PCDHB@	PCDHB@, PCDH3	protocadherin beta cluster			
GeneID:56133	PCDHB2	5	140,474,237	140,476,964	2,727	+	1	2_A375_pNL97_plus_lncRNA::1::6574	-13	upstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PCDHB2	MGC111392, PCDHB2, PCDH-BETA2	protocadherin beta 2	NM_018936, hCT1963271.1	231725_at	NP_061759.1, EAW61983.1
GeneID:56132	PCDHB3	5	140,480,234	140,483,406	3,172	+	1	2_A375_pNL97_plus_lncRNA::1::6574	-6010	upstream	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PCDHB3	PCDHB3, PCDH-BETA3	protocadherin beta 3	NM_018937, hCT33796.3	221410_x_at, 244163_x_at	NP_061760.1, EAW61981.1
GeneID:56114	PCDHGA1	5	140,710,252	140,892,546	182,294	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	145492, 183284	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA1	PCDHGA1, PCDH-GAMMA-A1, MGC138287, MGC138289	protocadherin gamma subfamily A, 1	NM_018912, NM_031993	211880_x_at	NP_061735.1, NP_114382.1
GeneID:56113	PCDHGA2	5	140,718,354	140,892,546	174,192	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	137390, 175182	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA2	PCDHGA2, PCDH-GAMMA-A2	protocadherin gamma subfamily A, 2	NM_018915, NM_032009		NP_061738.1, NP_114398.1
GeneID:56112	PCDHGA3	5	140,723,601	140,892,546	168,945	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	132143, 169935	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA3	PCDH-GAMMA-A3, PCDHGA3	protocadherin gamma subfamily A, 3	NM_032011, NM_018916	211879_x_at, 216343_at, 216352_x_at	NP_114400.1, NP_061739.2
GeneID:56104	PCDHGB1	5	140,729,828	140,892,546	162,718	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	125916, 163708	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGB1	MGC119469, PCDHGB1, MGC119467, PCDH-GAMMA-B1, MGC119466	protocadherin gamma subfamily B, 1	NM_018922, NM_032095		NP_061745.1, NP_115266.1
GeneID:56111	PCDHGA4	5	140,734,768	140,892,546	157,778	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	120976, 158768	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA4	PCDH-GAMMA-A4, PCDHGA4	protocadherin gamma subfamily A, 4	NM_018917, NM_032053	1552735_at	NP_061740.1, NP_114442.1
GeneID:56103	PCDHGB2	5	140,739,703	140,892,546	152,843	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	116041, 153833	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGB2	PCDHGB2, PCDH-GAMMA-B2, MGC126854	protocadherin gamma subfamily B, 2	NM_018923, NM_032096		NP_061746.1, NP_115267.1
GeneID:56110	PCDHGA5	5	140,743,898	140,892,546	148,648	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	111846, 149638	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA5	PCDH-GAMMA-A5, ME3, MGC142020, PCDHGA5, CDH-GAMMA-A5	protocadherin gamma subfamily A, 5	NM_018918, NM_032054		NP_061741.1, NP_114443.1
GeneID:56102	PCDHGB3	5	140,749,962	140,892,546	142,584	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	105782, 143574	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGB3	PCDH-GAMMA-B3, PCDHGB3	protocadherin gamma subfamily B, 3	NM_018924, NM_032097		NP_061747.1, NP_115268.1
GeneID:56109	PCDHGA6	5	140,753,651	140,892,546	138,895	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	102093, 139885	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA6	PCDH-GAMMA-A6, PCDHGA6	protocadherin gamma subfamily A, 6	NM_018919, NM_032086		NP_061742.1, NP_114475.1
GeneID:56108	PCDHGA7	5	140,762,467	140,892,546	130,079	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	93277, 131069	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA7	PCDH-GAMMA-A7, PCDHGA7	protocadherin gamma subfamily A, 7	NM_018920, NM_032087		NP_061743.1, NP_114476.1
GeneID:8641	PCDHGB4	5	140,767,452	140,892,546	125,094	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	88292, 126084	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGB4	CDH20, MGC142167, PCDH-GAMMA-B4, FIB2, PCDHGB4, MGC138293	protocadherin gamma subfamily B, 4	NM_003736, NM_032098	210366_at	NP_003727.1, NP_115269.1
GeneID:9708	PCDHGA8	5	140,771,483	140,892,546	121,063	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	84261, 122053	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA8	PCDHGA8, KIAA0327, PCDH-GAMMA-A8	protocadherin gamma subfamily A, 8	NM_014004, NM_032088		NP_054723.1, NP_114477.1
GeneID:56101	PCDHGB5	5	140,777,695	140,892,546	114,851	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	78049, 115841	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGB5	PCDHGB5, PCDH-GAMMA-B5	protocadherin gamma subfamily B, 5	NM_018925, NM_032099	211807_x_at	NP_061748.1, NP_115270.1
GeneID:56107	PCDHGA9	5	140,782,520	140,892,546	110,026	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	73224, 111016	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA9	PCDHGA9, PCDH-GAMMA-A9	protocadherin gamma subfamily A, 9	NM_018921, NM_032089	211873_s_at	NP_061744.1, NP_114478.1
GeneID:56100	PCDHGB6	5	140,787,770	140,892,546	104,776	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	67974, 105766	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGB6	PCDHGB6, PCDH-GAMMA-B6	protocadherin gamma subfamily B, 6	NM_018926, NM_032100	221682_s_at	NP_061749.1, NP_115271.1
GeneID:56106	PCDHGA10	5	140,792,743	140,892,546	99,803	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	63001, 100793	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA10	PCDH-GAMMA-A10, PCDHGA10	protocadherin gamma subfamily A, 10	NM_018913, NM_032090	211875_x_at	NP_061736.1, NP_114479.1
GeneID:56099	PCDHGB7	5	140,797,282	140,892,546	95,264	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	58462, 96254	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGB7	ME6, PCDHGB7, PCDH-GAMMA-B7	protocadherin gamma subfamily B, 7	NM_018927, NM_032101	1552661_at, 1552662_a_at	NP_061750.1, NP_115272.1
GeneID:56105	PCDHGA11	5	140,800,537	140,892,546	92,009	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	55207, 92999	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA11	PCDHGA11, PCDH-GAMMA-A11	protocadherin gamma subfamily A, 11	NM_018914, NM_032091, NM_032092	211877_s_at	NP_061737.1, NP_114480.1, NP_114481.1
GeneID:26025	PCDHGA12	5	140,810,158	140,892,546	82,388	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	45586, 83378	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGA12	FIB3, CDH21, PCDH-GAMMA-A12, PCDHGA12, KIAA0588	protocadherin gamma subfamily A, 12	NM_003735, NM_032094	205717_x_at, 209079_x_at, 211066_x_at, 211876_x_at, 215836_s_at	NP_003726.1, NP_115265.1
GeneID:5098	PCDHGC3	5	140,855,569	140,892,546	36,977	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	175, 37967	in gene, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGC3	PCDH2, PCDH-GAMMA-C3, PC43, PCDHGC3	protocadherin gamma subfamily C, 3	NM_002588, NM_032402, NM_032403	214563_at, 214564_s_at	NP_002579.2, NP_115778.1, NP_115779.1
GeneID:56098	PCDHGC4	5	140,864,741	140,892,546	27,805	+	2	2_A375_pNL97_plus_lncRNA::1::6575, 2_A375_pNL97_plus_lncRNA::1::6576	-8997, 28795	upstream, downstream	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PCDHGC4	MGC24976, PCDHGC4, PCDH-GAMMA-C4, MGC119489	protocadherin gamma subfamily C, 4	NM_018928, NM_032406	231753_s_at, 231754_at	NP_061751.1, NP_115782.1
GeneID:56097	PCDHGC5	5	140,868,808	140,892,546	23,738	+	1	2_A375_pNL97_plus_lncRNA::1::6576	24728	downstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene PCDHGC5	MGC138288, PCDHGC5, PCDH-GAMMA-C5, MGC138286	protocadherin gamma subfamily C, 5	NM_018929, NM_032407	224536_s_at, 224537_at	NP_061752.1, NP_115783.1
GeneID:1729	DIAPH1	5	140,894,588	140,998,622	104,034	-	8	1_A375_pNL7_minus_lncRNA::1::4567, 1_A375_pNL7_minus_lncRNA::1::4568, 1_A375_pNL7_minus_lncRNA::1::4569, 1_A375_pNL7_minus_lncRNA::1::4570, 2_A375_pNL97_plus_lncRNA::1::6576, 2_A375_pNL97_plus_lncRNA::1::6577, 2_A375_pNL97_plus_lncRNA::1::6578, 2_A375_pNL97_plus_lncRNA	94110, 61246, 54750, -82, 105086, 61278, 54782, -114	in gene, in gene, in gene, upstream, downstream, in gene, in gene, upstream	1	1	43.6	39.2	5	1_A375_pNL7_minus_lncRNA::1	111	Gene DIAPH1	DIAPH1, hDIA1, LFHL1, DRF1, DFNA1, FLJ25265, DIA1	diaphanous homolog 1 (Drosophila)	NM_005219, NM_001079812, hCT2253167.0, hCT33605.3	1560080_at, 209190_s_at, 213514_s_at, 215541_s_at	NP_005210.3, NP_001073280.1, EAW61919.1, EAW61920.1
GeneID:100505658	LOC100505658	5	140,937,878	140,944,827	6,949	+	4	1_A375_pNL7_minus_lncRNA::1::4568, 1_A375_pNL7_minus_lncRNA::1::4569, 2_A375_pNL97_plus_lncRNA::1::6577, 2_A375_pNL97_plus_lncRNA::1::6578	-502, 5984, -534, 5952	upstream, in gene, upstream, in gene	1	1	70.5	64	2	1_A375_pNL7_minus_lncRNA::1	111	Gene LOC100505658		hypothetical LOC100505658	XR_112787, XR_110311, XR_113784		
GeneID:8841	HDAC3	5	141,000,443	141,016,423	15,980	-	4	1_A375_pNL7_minus_lncRNA::1::4570, 2_A375_pNL97_plus_lncRNA::1::6579, 1_A375_pNL7_minus_lncRNA::1::4571, 2_A375_pNL97_plus_lncRNA::1::6580	17719, 17687, -1145, -1113	downstream, downstream, upstream, upstream	1	1	33.5	36	2	1_A375_pNL7_minus_lncRNA::1	47	Gene HDAC3	HD3, RPD3-2, HDAC3, RPD3	histone deacetylase 3	NM_003883, hCT1817569.1, hCT2253159.0, hCT2253162.0, hCT28566.2	216326_s_at	NP_003874.2, EAW61918.1, EAW61915.1, EAW61916.1, EAW61917.1
GeneID:285613	RELL2	5	141,016,517	141,020,631	4,114	+	2	1_A375_pNL7_minus_lncRNA::1::4571, 2_A375_pNL97_plus_lncRNA::1::6580	1051, 1019	in gene, in gene	1	1	20	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene RELL2	C5orf16, FLJ90583, RELL2	RELT-like 2	NM_173828, NM_001130029, hCT2255499.0, hCT2353777.0, hCT2353778.0, hCT33604.2	1564031_a_at	NP_776189.3, NP_001123501.1, EAW61911.1, EAW61912.1, EAW61913.1, EAW61914.1
GeneID:89848	FCHSD1	5	141,018,869	141,030,986	12,117	-	4	1_A375_pNL7_minus_lncRNA::1::4571, 1_A375_pNL7_minus_lncRNA::1::4572, 2_A375_pNL97_plus_lncRNA::1::6580, 2_A375_pNL97_plus_lncRNA::1::6581	13418, -6886, 13450, -6870	downstream, upstream, downstream, upstream	1	1	18.5	26	2	2_A375_pNL97_plus_lncRNA::1	29	Gene FCHSD1	NWK2, FLJ00007, FCHSD1	FCH and double SH3 domains 1	NM_033449, hCT2353771.0, hCT2353772.0, hCT33602.4	226698_at, 226699_at	NP_258260.1, EAW61908.1, EAW61909.1, EAW61910.1
GeneID:64411	ARAP3	5	141,032,968	141,061,800	28,832	-	5	1_A375_pNL7_minus_lncRNA::1::4572, 1_A375_pNL7_minus_lncRNA::1::4573, 2_A375_pNL97_plus_lncRNA::1::6581, 2_A375_pNL97_plus_lncRNA::1::6582, 2_A375_pNL97_plus_lncRNA::1::6583	23928, -10392, 23944, -312, -10408	in gene, upstream, in gene, upstream, upstream	1	1	24	28	3	2_A375_pNL97_plus_lncRNA::1	43	Gene ARAP3	ARAP3, CENTD3, FLJ21065, DRAG1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	NM_022481, hCT2253152.0, hCT2253154.0, hCT2253155.0, hCT2353698.0	218950_at, 235806_at	NP_071926.4, EAW61905.1, EAW61904.1, EAW61906.1, EAW61907.1
GeneID:5097	PCDH1	5	141,232,672	141,257,944	25,272	-	5	1_A375_pNL7_minus_lncRNA::1::4577, 1_A375_pNL7_minus_lncRNA::1::4578, 1_A375_pNL7_minus_lncRNA::1::4579, 2_A375_pNL97_plus_lncRNA::1::6589, 2_A375_pNL97_plus_lncRNA::1::6590	28120, 1528, -5144, -664, -5160	downstream, in gene, upstream, upstream, upstream	1	1	18.75	19	4	2_A375_pNL97_plus_lncRNA::1	32	Gene PCDH1	PCDH1, MGC45991, PCDH42, PC42, FLJ53887	protocadherin 1	NM_002587, NM_032420, hCT1641260.2, hCT1811578.1, hCT2252411.0, hCT2252413.0	203918_at, 215277_at	NP_002578.2, NP_115796.2, EAW61900.1, EAW61901.1, EAW61902.1, EAW61903.1
GeneID:80762	NDFIP1	5	141,488,324	141,534,008	45,684	+	1	2_A375_pNL97_plus_lncRNA::1::6592	-4	upstream	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene NDFIP1	N4WBP5, MGC10924, NDFIP1	Nedd4 family interacting protein 1	NM_030571, hCT2252666.0, hCT28223.2	217800_s_at, 222422_s_at, 222423_at	NP_085048.1, EAW61888.1, EAW61889.1
GeneID:81848	SPRY4	5	141,689,992	141,704,620	14,628	-	1	2_A375_pNL97_plus_lncRNA::1::6594	10780	in gene	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SPRY4	SPRY4		NM_030964, NM_001127496	220983_s_at, 221489_s_at	NP_112226.2, NP_001120968.1
GeneID:23092	ARHGAP26	5	142,150,292	142,608,572	458,280	+	4	1_A375_pNL7_minus_lncRNA::1::4582, 1_A375_pNL7_minus_lncRNA::1::4583, 2_A375_pNL97_plus_lncRNA::1::6597, 2_A375_pNL97_plus_lncRNA::1::6598	51436, 56556, 556, 51468	in gene, in gene, in gene, in gene	1	1	21	23	3	2_A375_pNL97_plus_lncRNA::1	33	Gene ARHGAP26	GRAF, OPHN1L, FLJ42530, KIAA0621, ARHGAP26, OPHN1L1	Rho GTPase activating protein 26	NM_001135608, NM_015071, hCT1821273.2, hCT2263474.0	205068_s_at, 205069_s_at, 215955_x_at, 226576_at	NP_001129080.1, NP_055886.1, EAW61876.1, EAW61877.1
GeneID:2908	NR3C1	5	142,657,496	142,815,077	157,581	-	3	2_A375_pNL97_plus_lncRNA::1::6600, 2_A375_pNL97_plus_lncRNA::1::6601, 2_A375_pNL97_plus_lncRNA::1::6602	32133, 31269, 29893	in gene, in gene, in gene	0	1	15	18.33	3	2_A375_pNL97_plus_lncRNA::1	21	Gene NR3C1	GR, GCCR, NR3C1, GRL, GCR	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NM_000176, NM_001018074, NM_001018075, NM_001018076, NM_001018077, NM_001020825, NM_001024094, hCT2263081.1, hCT2353707.0, hCT2353708.0, hCT28834.3	201865_x_at, 201866_s_at, 211671_s_at, 216321_s_at	NP_000167.1, NP_001018084.1, NP_001018085.1, NP_001018086.1, NP_001018087.1, NP_001018661.1, NP_001019265.1, EAW61870.1, EAW61871.1, EAW61872.1, EAW61873.1
GeneID:153769	SH3RF2	5	145,316,126	145,442,879	126,753	+	1	2_A375_pNL97_plus_lncRNA::1::6603	10018	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene SH3RF2	MGC90410, RNF158, MGC149789, FLJ23654, SH3RF2, HEPP1, MGC149788	SH3 domain containing ring finger 2	NM_152550, hCT2251972.0, hCT2353727.0, hCT29358.3	226892_at, 235766_at, 243582_at	NP_689763.3, EAW61853.1, EAW61852.1, EAW61854.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:51520	LARS	5	145,492,589	145,562,294	69,705	-	2	1_A375_pNL7_minus_lncRNA::1::4585, 2_A375_pNL97_plus_lncRNA::1::6604	-10, -74	upstream, upstream	1	1	26	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene LARS	LEUS, LEURS, FLJ21788, RNTLS, KIAA1352, PIG44, HSPC192, hr025Cl, FLJ10595, LARS1, LARS, LRS	leucyl-tRNA synthetase	NM_020117, hCT1821149.2, hCT2251913.0, hCT2251915.0	217810_x_at, 222427_s_at, 222428_s_at, 223888_s_at	NP_064502.9, EAW61849.1, EAW61848.1, EAW61850.1
GeneID:54439	RBM27	5	145,583,163	145,668,786	85,623	+	2	1_A375_pNL7_minus_lncRNA::1::4586, 2_A375_pNL97_plus_lncRNA::1::6605	-187, -139	upstream, upstream	1	1	32	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene RBM27	Psc1, KIAA1311, RBM27, ARRS1	RNA binding motif protein 27	NM_018989	225326_at, 243295_at	NP_061862.1
GeneID:10915	TCERG1	5	145,826,873	145,891,069	64,196	+	2	1_A375_pNL7_minus_lncRNA::1::4587, 2_A375_pNL97_plus_lncRNA::1::6606	-217, -185	upstream, upstream	1	1	58	50	1	1_A375_pNL7_minus_lncRNA::1	58	Gene TCERG1	TCERG1, Urn1, TAF2S, MGC133200, CA150	transcription elongation regulator 1	NM_006706, NM_001040006, hCT2252261.0, hCT2353700.0, hCT29354.2	202396_at, 229706_at, 238838_at	NP_006697.2, NP_001035095.1, EAW61840.1, EAW61841.1, EAW61842.1
GeneID:5521	PPP2R2B	5	145,969,067	146,461,033	491,966	-	2	1_A375_pNL7_minus_lncRNA::1::4588, 2_A375_pNL97_plus_lncRNA::1::6607	256265, 256265	in gene, in gene	1	1	33	59	1	2_A375_pNL97_plus_lncRNA::1	59	Gene PPP2R2B	PP2AB-BETA, PR2APR55BETA, PP2APR55BETA, SCA12, MGC24888, B55-BETA, PR2APR55-BETA, FLJ95686, PR2AB55BETA, PP2A-PR55B, PP2ABBETA, PP2A-B55BETA, PR2ABBETA, PR55-BETA, PR52B, PP2APR55-BETA, PP2APR55B, PPP2R2B, PR2AB55-BETA, PP2AB55BETA, PR2AB-BETA, B55BETA, PR	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	NM_004576, NM_181674, NM_181675, NM_181676, NM_181677, NM_181678, NM_001127381, hCT2252050.1, hCT2252051.1, hCT2252052.1, hCT2344918.0, hCT2344919.0, hCT2344920.0, hCT2353743.0	205643_s_at, 213849_s_at	NP_004567.1, NP_858060.1, NP_858061.1, NP_858062.1, NP_858063.1, NP_858064.1, NP_001120853.1, EAW61829.1, EAW61830.1, EAW61831.1, EAW61832.1, EAW61833.1, EAW61834.1, EAW61835.1
GeneID:79628	SH3TC2	5	148,361,713	148,442,737	81,024	-	4	1_A375_pNL7_minus_lncRNA::1::4589, 1_A375_pNL7_minus_lncRNA::1::4590, 2_A375_pNL97_plus_lncRNA::1::6609, 2_A375_pNL97_plus_lncRNA::1::6610	61265, 657, 61201, 657	in gene, in gene, in gene, in gene	1	1	22	19	2	1_A375_pNL7_minus_lncRNA::1	28	Gene SH3TC2	MNMN, SH3TC2, KIAA1985, FLJ13605, CMT4C	SH3 domain and tetratricopeptide repeats 2	NM_024577	219710_at, 233561_at, 240966_at	NP_078853.2
GeneID:693169	MIR584	5	148,441,876	148,441,972	96	-	2	1_A375_pNL7_minus_lncRNA::1::4590, 2_A375_pNL97_plus_lncRNA::1::6610	-108, -108	upstream, upstream	1	1	28	22	1	1_A375_pNL7_minus_lncRNA::1	28	Gene MIR584	MIR584, hsa-mir-584, MIRN584	microRNA 584	NR_030310		
GeneID:255187	hCG_1980447	5	148,443,066	148,446,548	3,482	+	2	1_A375_pNL7_minus_lncRNA::1::4590, 2_A375_pNL97_plus_lncRNA::1::6610	-986, -986	upstream, upstream	1	1	28	22	1	1_A375_pNL7_minus_lncRNA::1	28	Gene hCG_1980447	FLJ32216, LOC255187	hCG1980447	XR_112784, XR_110313, XR_113788		
GeneID:22885	ABLIM3	5	148,521,054	148,639,999	118,945	+	2	1_A375_pNL7_minus_lncRNA::1::4591, 2_A375_pNL97_plus_lncRNA::1::6611	-6878, 21570	upstream, in gene	1	1	18	15.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene ABLIM3	ABLIM3, HMFN1661	actin binding LIM protein family, member 3	NM_014945, hCT2252747.0, hCT2252748.0, hCT2353690.0, hCT2353691.0, hCT28725.3	205730_s_at	NP_055760.1, EAW61788.1, EAW61789.1, EAW61790.1, EAW61791.1, EAW61792.1
GeneID:134265	AFAP1L1	5	148,651,401	148,721,368	69,967	+	1	1_A375_pNL7_minus_lncRNA::1::4592	73527	downstream	1	0	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene AFAP1L1	FLJ36748, MGC149773, AFAP1L1	actin filament associated protein 1-like 1	NM_152406, NM_001146337, hCT1821379.2	1555542_at, 226955_at	NP_689619.1, NP_001139809.1, EAW61787.1
GeneID:134266	GRPEL2	5	148,724,977	148,734,146	9,169	+	1	1_A375_pNL7_minus_lncRNA::1::4592	-49	upstream	1	0	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene GRPEL2	Mt-GrpE#2, FLJ23713, FLJ33918, GRPEL2, DKFZp451C205	GrpE-like 2, mitochondrial (E. coli)	NM_152407, hCT28723.3	226881_at, 238427_at	NP_689620.2, EAW61786.1
GeneID:728264	LOC728264	5	148,786,440	148,812,399	25,959	+	1	1_A375_pNL7_minus_lncRNA::1::4593	-2056	upstream	1	0	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene LOC728264	DKFZp586C0721, FLJ36638, DKFZp781L018	hypothetical LOC728264	NR_027180	1558828_s_at, 231987_at	
GeneID:1452	CSNK1A1	5	148,874,845	148,931,007	56,162	-	3	1_A375_pNL7_minus_lncRNA::1::4597, 2_A375_pNL97_plus_lncRNA::1::6613, 2_A375_pNL97_plus_lncRNA::1::6614	-129, 65183, -209	upstream, downstream, upstream	1	1	18.5	17.5	2	1_A375_pNL7_minus_lncRNA::1	20	Gene CSNK1A1	CSNK1A1, HLCDGP1, PRO2975, CK1	casein kinase 1, alpha 1	NM_001892, NM_001025105, hCT1962993.1, hCT1962994.1, hCT1964753.1, hCT1964754.1, hCT1964755.1, hCT201515.3, hCT2260944.0, hCT2260947.0, hCT2260949.0, hCT2260950.0	1556006_s_at, 1556007_s_at, 206562_s_at, 208865_at, 208866_at, 208867_s_at, 213086_s_at, 213860_x_at, 226920_at, 235464_at, 240221_at, 243738_at	NP_001883.4, NP_001020276.1, EAW61768.1, EAW61771.1, EAW61772.1, EAW61775.1, EAW61767.1, EAW61769.1, EAW61770.1, EAW61773.1, EAW61774.1, EAW61776.1
GeneID:1836	SLC26A2	5	149,340,300	149,366,963	26,663	+	1	2_A375_pNL97_plus_lncRNA::1::6615	124	in gene	0	1	16	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SLC26A2	D5S1708, DTDST, MSTP157, SLC26A2, EDM4, MST153, DTD	solute carrier family 26 (sulfate transporter), member 2	NM_000112	205097_at, 224959_at, 224963_at	NP_000103.2
GeneID:81789	TIGD6	5	149,372,681	149,380,217	7,536	-	2	1_A375_pNL7_minus_lncRNA::1::4598, 2_A375_pNL97_plus_lncRNA::1::6616	-7, -71	upstream, upstream	1	1	24	24	1	1_A375_pNL7_minus_lncRNA::1	24	Gene TIGD6	DKFZp761E2110, TIGD6	tigger transposable element derived 6	NM_030953, hCT29858.2	220986_s_at	NP_112215.1, EAW61753.1
GeneID:22993	HMGXB3	5	149,380,169	149,432,706	52,537	+	3	1_A375_pNL7_minus_lncRNA::1::4598, 1_A375_pNL7_minus_lncRNA::1::4599, 2_A375_pNL97_plus_lncRNA::1::6616	55, 36215, 119	in gene, in gene, in gene	1	1	25	17	2	1_A375_pNL7_minus_lncRNA::1	26	Gene HMGXB3	HMGX3, KIAA0194, HMGXB3, SMF	HMG box domain containing 3	NM_014983	212431_at, 34221_at	NP_055798.2
GeneID:6949	TCOF1	5	149,737,202	149,779,871	42,669	+	1	2_A375_pNL97_plus_lncRNA::1::6618	446	in gene	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TCOF1	MFD1, TCS1, TCOF1, treacle	Treacher Collins-Franceschetti syndrome 1	NM_001008657, NM_000356, NM_001135243, NM_001135244, NM_001135245, hCT2261930.0, hCT2261931.0, hCT2261933.0, hCT2261934.0, hCT2353766.0, hCT2353767.0, hCT2353768.0, hCT29852.3	202384_s_at, 202385_s_at, 244686_at	NP_001008657.1, NP_000347.2, NP_001128715.1, NP_001128716.1, NP_001128717.1, EAW61734.1, EAW61732.1, EAW61733.1, EAW61735.1, EAW61736.1, EAW61737.1, EAW61738.1, EAW61739.1
GeneID:6208	RPS14	5	149,823,792	149,829,319	5,527	-	2	1_A375_pNL7_minus_lncRNA::1::4601, 2_A375_pNL97_plus_lncRNA::1::6619	-121, -249	upstream, upstream	1	1	31	51	1	2_A375_pNL97_plus_lncRNA::1	51	Gene RPS14	S14, RPS14, EMTB	ribosomal protein S14	NM_005617, NM_001025070, NM_001025071, hCT1952785.1, hCT2253202.0, hCT2253204.0, hCT29854.4	208645_s_at, 214245_at, 217298_at, 241241_at	NP_005608.1, NP_001020241.1, NP_001020242.1, EAW61723.1, EAW61725.1, EAW61726.1, EAW61724.1
GeneID:3340	NDST1	5	149,887,674	149,937,773	50,099	+	1	1_A375_pNL7_minus_lncRNA::1::4602	-7066	upstream	1	0	23	13	1	1_A375_pNL7_minus_lncRNA::1	23	Gene NDST1	HSST, NST1, NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	NM_001543, hCT2256227.0, hCT2256229.0, hCT29850.3	1554010_at, 202607_at, 202608_s_at	NP_001534.1, EAW61722.1, EAW61720.1, EAW61721.1
GeneID:11346	SYNPO	5	149,980,642	150,038,792	58,150	+	1	2_A375_pNL97_plus_lncRNA::1::6620	39486	in gene	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SYNPO	KIAA1029, SYNPO	synaptopodin	NM_007286, NM_001109974, NM_001166208, NM_001166209, hCT2256234.0, hCT2256235.0	202796_at, 235128_at, 235914_at	NP_009217.3, NP_001103444.1, NP_001159680.1, NP_001159681.1, EAW61715.1, EAW61716.1
GeneID:55696	RBM22	5	150,070,352	150,080,669	10,317	-	2	1_A375_pNL7_minus_lncRNA::1::4603, 2_A375_pNL97_plus_lncRNA::1::6621	-67, 477	upstream, in gene	1	1	21	20	1	1_A375_pNL7_minus_lncRNA::1	21	Gene RBM22	RBM22, Cwc2, FLJ10290, ZC3H16, fSAP47	RNA binding motif protein 22	NM_018047, hCT1829130.3, hCT2253193.0, hCT29863.4	218134_s_at, 222527_s_at, 224068_x_at, 236872_at	NP_060517.1, EAW61711.1, EAW61710.1, EAW61712.1
GeneID:51164	DCTN4	5	150,088,309	150,138,657	50,348	-	3	1_A375_pNL7_minus_lncRNA::1::4603, 1_A375_pNL7_minus_lncRNA::1::4604, 2_A375_pNL97_plus_lncRNA::1::6621	57921, 33, 58465	downstream, in gene, downstream	1	1	19	17.5	2	1_A375_pNL7_minus_lncRNA::1	21	Gene DCTN4	DCTN4		NM_016221, NM_001135643, NM_001135644, hCT2253189.0, hCT2253191.0, hCT2353692.0, hCT29862.3	218013_x_at, 222488_s_at, 233490_at	NP_057305.1, NP_001129115.1, NP_001129116.1, EAW61706.1, EAW61707.1, EAW61708.1, EAW61709.1
GeneID:85027	C5orf62	5	150,157,508	150,176,298	18,790	+	1	2_A375_pNL97_plus_lncRNA::1::6622	23356	downstream	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C5orf62	C5orf62, NID67, MGC117221, MST150, MGC126887, MGC126889	chromosome 5 open reading frame 62	NM_032947, hCT1642802.5	223276_at	NP_116565.3, EAW61705.1
GeneID:91975	ZNF300	5	150,273,954	150,284,545	10,591	-	2	1_A375_pNL7_minus_lncRNA::1::4605, 2_A375_pNL97_plus_lncRNA::1::6623	-127, -95	upstream, upstream	1	1	38	52	1	2_A375_pNL97_plus_lncRNA::1	52	Gene ZNF300	ZNF300, DKFZp686B24204	zinc finger protein 300	NM_052860, NM_001172831, NM_001172832, hCT2253185.0, hCT2253186.0, hCT2253187.0, hCT2253188.0, hCT2353757.0	228144_at	NP_443092.1, NP_001166302.1, NP_001166303.1, EAW61699.1, EAW61701.1, EAW61702.1, EAW61698.1, EAW61700.1
GeneID:2760	GM2A	5	150,632,613	150,649,955	17,342	+	1	2_A375_pNL97_plus_lncRNA::1::6625	59	in gene	0	1	19	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene GM2A	GM2A, SAP-3	GM2 ganglioside activator	NM_000405, NM_001167607, hCT1685597.3, hCT2256222.0	209727_at, 212737_at, 215890_at, 215891_s_at, 235678_at, 33646_g_at, 35820_at	NP_000396.2, NP_001161079.1, EAW61680.1, EAW61681.1
GeneID:206358	SLC36A1	5	150,827,163	150,871,940	44,777	+	1	2_A375_pNL97_plus_lncRNA::1::6626	69	in gene	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SLC36A1	LYAAT1, TRAMD3, Dct1, SLC36A1, PAT1	solute carrier family 36 (proton/amino acid symporter), member 1	NM_078483, hCT2253237.0, hCT2253238.0, hCT2253239.0, hCT2353760.0	1553272_at, 213119_at	NP_510968.2, EAW61676.1, EAW61674.1, EAW61675.1, EAW61677.1
GeneID:475	ATOX1	5	151,122,383	151,138,210	15,827	-	2	1_A375_pNL7_minus_lncRNA::1::4606, 1_A375_pNL7_minus_lncRNA::1::4607	15490, 13026	in gene, in gene	1	0	21.5	16.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene ATOX1	ATOX1, HAH1, MGC138455, ATX1, MGC138453	ATX1 antioxidant protein 1 homolog (yeast)	NM_004045, hCT1952790.1, hCT30394.1	203454_s_at	NP_004036.1, EAW61663.1, EAW61664.1
GeneID:10146	G3BP1	5	151,151,476	151,184,915	33,439	+	1	1_A375_pNL7_minus_lncRNA::1::4608	-52	upstream	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene G3BP1	MGC111040, HDH-VIII, G3BP, G3BP1	GTPase activating protein (SH3 domain) binding protein 1	NM_005754, NM_198395, hCT1821762.1, hCT2253219.0, hCT2253222.0, hCT2253226.0	1557350_at, 201503_at, 201514_s_at, 222187_x_at, 244396_at	NP_005745.1, NP_938405.1, EAW61659.1, EAW61660.1, EAW61661.1, EAW61662.1
GeneID:2741	GLRA1	5	151,202,074	151,304,397	102,323	-	2	1_A375_pNL7_minus_lncRNA::1::4609, 2_A375_pNL97_plus_lncRNA::1::6627	141, 125	in gene, in gene	1	1	48	67	1	2_A375_pNL97_plus_lncRNA::1	67	Gene GLRA1	STHE, GLRA1, MGC138878, MGC138879	glycine receptor, alpha 1	NM_000171, NM_001146040, hCT2252309.0, hCT30393.3	207972_at	NP_000162.2, NP_001139512.1, EAW61656.1, EAW61657.1
GeneID:10827	FAM114A2	5	153,371,263	153,418,497	47,234	-	1	2_A375_pNL97_plus_lncRNA::1::6628	-63	upstream	0	1	16	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene FAM114A2	FAM114A2, 133K02, C5orf3	family with sequence similarity 114, member A2	NM_018691, hCT1971880.1, hCT2251771.0, hCT2251772.0	218588_s_at, 222682_s_at	NP_061161.2, EAW61648.1, EAW61646.1, EAW61647.1
GeneID:4238	MFAP3	5	153,418,519	153,437,014	18,495	+	1	2_A375_pNL97_plus_lncRNA::1::6628	41	in gene	0	1	16	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MFAP3	DKFZp586F0219, MFAP3	microfibrillar-associated protein 3	NM_005927, NM_001135037, NR_024152, hCT1971098.1	1552312_a_at, 213123_at, 214588_s_at	NP_005918.1, NP_001128509.1, EAW61645.1
GeneID:55568	GALNT10	5	153,570,295	153,800,544	230,249	+	3	1_A375_pNL7_minus_lncRNA::1::4610, 2_A375_pNL97_plus_lncRNA::1::6629, 2_A375_pNL97_plus_lncRNA::1::6630	-311, 7529, 86505	upstream, in gene, in gene	1	1	16.33	17	3	2_A375_pNL97_plus_lncRNA::1	21	Gene GALNT10	GALNACT10, pp-GalNAc-T10, GalNAcT10, FLJ11715, DKFZp586H0623, PPGANTASE10, GALNT10, FLJ00205, PPGALNACT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	NM_198321, hCT1821190.3, hCT1828946.4, hCT2257016.2, hCT2257018.0, hCT2353718.0, hCT28036.5	207357_s_at, 212256_at, 220296_at, 230906_at	NP_938080.1, EAW61639.1, EAW61640.1, EAW61642.1, EAW61643.1, EAW61644.1, EAW61641.1
GeneID:23367	LARP1	5	154,092,462	154,197,165	104,703	+	2	1_A375_pNL7_minus_lncRNA::1::4611, 2_A375_pNL97_plus_lncRNA::1::6631	42098, 42098	in gene, in gene	1	1	21	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene LARP1	LARP1, MGC19556, LARP, KIAA0731	La ribonucleoprotein domain family, member 1	NM_015315, hCT2254109.1, hCT2344691.0, hCT28082.4	210966_x_at, 212137_at, 212193_s_at, 239663_x_at	NP_056130.2, EAW61634.1, EAW61632.1, EAW61633.1
GeneID:100505847	LOC100505847	5	154,135,135	154,166,244	31,109	-	2	1_A375_pNL7_minus_lncRNA::1::4611, 2_A375_pNL97_plus_lncRNA::1::6631	-575, -575	upstream, upstream	1	1	21	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene LOC100505847		la-related protein 1-like	XM_003118936		XP_003118984.1
GeneID:10826	C5orf4	5	154,198,052	154,230,213	32,161	-	2	1_A375_pNL7_minus_lncRNA::1::4612, 2_A375_pNL97_plus_lncRNA::1::6632	-7771, -7867	upstream, upstream	1	1	23	21	1	1_A375_pNL7_minus_lncRNA::1	23	Gene C5orf4	C5orf4, FLJ13758	chromosome 5 open reading frame 4	NM_032385, hCT2251697.0, hCT2251698.0, hCT2251699.0	220751_s_at, 48030_i_at, 48031_r_at	NP_115761.2, EAW61629.1, EAW61630.1, EAW61631.1
GeneID:9337	CNOT8	5	154,238,198	154,256,352	18,154	+	2	1_A375_pNL7_minus_lncRNA::1::4612, 2_A375_pNL97_plus_lncRNA::1::6632	-214, -118	upstream, upstream	1	1	23	21	1	1_A375_pNL7_minus_lncRNA::1	23	Gene CNOT8	POP2, hCAF1, CNOT8, CAF1, CALIF	CCR4-NOT transcription complex, subunit 8	NM_004779, hCT1952778.1, hCT1952779.1, hCT2254112.0, hCT28227.2	202162_s_at, 202163_s_at, 202164_s_at	NP_004770.4, EAW61625.1, EAW61626.1, EAW61627.1, EAW61628.1
GeneID:25929	GEMIN5	5	154,266,976	154,317,776	50,800	-	3	1_A375_pNL7_minus_lncRNA::1::4613, 2_A375_pNL97_plus_lncRNA::1::6633, 2_A375_pNL97_plus_lncRNA::1::6634	-16, -48, -2928	upstream, upstream, upstream	1	1	17	21.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene GEMIN5	GEMIN5, MGC142174, DKFZp586M1824	gem (nuclear organelle) associated protein 5	NM_015465, hCT2251694.0, hCT2251695.0	225712_at	NP_056280.2, EAW61623.1, EAW61624.1
GeneID:29093	MRPL22	5	154,320,633	154,348,971	28,338	+	3	1_A375_pNL7_minus_lncRNA::1::4613, 2_A375_pNL97_plus_lncRNA::1::6633, 2_A375_pNL97_plus_lncRNA::1::6634	-2841, -2809, 71	upstream, upstream, in gene	1	1	17	21.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene MRPL22	DKFZp781F1071, HSPC158, MRP-L22, L22mt, MRPL22, MRP-L25, RPML25	mitochondrial ribosomal protein L22	NM_014180, NM_001014990, hCT28226.2	218339_at	NP_054899.2, NP_001014990.1, EAW61622.1
GeneID:54974	THG1L	5	157,158,323	157,166,772	8,449	+	3	1_A375_pNL7_minus_lncRNA::1::4614, 2_A375_pNL97_plus_lncRNA::1::6636, 2_A375_pNL97_plus_lncRNA::1::6637	125, 77, 12413	in gene, in gene, downstream	1	1	27.5	29	2	1_A375_pNL7_minus_lncRNA::1	44	Gene THG1L	FLJ11601, FLJ20546, THG1L, ICF45	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	NM_017872, hCT1952293.1, hCT6874.3	219122_s_at	NP_060342.2, EAW61590.1, EAW61591.1
GeneID:134353	LSM11	5	157,170,755	157,183,746	12,991	+	1	2_A375_pNL97_plus_lncRNA::1::6637	-19	upstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LSM11	FLJ38273, LSM11	LSM11, U7 small nuclear RNA associated	NM_173491, hCT6875.3	241599_at, 242112_at	NP_775762.1, EAW61589.1
GeneID:1879	EBF1	5	158,122,923	158,526,788	403,865	-	4	1_A375_pNL7_minus_lncRNA::1::4616, 1_A375_pNL7_minus_lncRNA::1::4617, 1_A375_pNL7_minus_lncRNA::1::4618, 2_A375_pNL97_plus_lncRNA::1::6640	362948, 372628, -604, 372663	in gene, in gene, upstream, in gene	1	1	17.67	13	3	1_A375_pNL7_minus_lncRNA::1	19	Gene EBF1	FLJ39389, O/E-1, FLJ41763, OLF1, COE1, EBF, EBF1	early B-cell factor 1	NM_024007, hCT2349019.0, hCT2349020.0, hCT2353769.0	232204_at, 233261_at	NP_076870.1, EAW61582.1, EAW61580.1, EAW61581.1
GeneID:147	ADRA1B	5	159,343,740	159,400,017	56,277	+	1	2_A375_pNL97_plus_lncRNA::1::6644	11684	in gene	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ADRA1B	ADRA1B, ADRA1, ALPHA1BAR	adrenergic, alpha-1B-, receptor	NM_000679, hCT5771.2	207589_at	NP_000670.1, EAW61572.1
GeneID:7265	TTC1	5	159,436,180	159,492,550	56,370	+	1	2_A375_pNL97_plus_lncRNA::1::6645	-84	upstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TTC1	TPR1, FLJ46404, TTC1	tetratricopeptide repeat domain 1	NM_003314, hCT2251528.0, hCT2251529.0	201434_at	NP_003305.1, EAW61570.1, EAW61571.1
GeneID:114825	PWWP2A	5	159,502,889	159,546,452	43,563	-	1	2_A375_pNL97_plus_lncRNA::1::6646	180	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PWWP2A	MGC132770, MST101, PWWP2A, KIAA1935	PWWP domain containing 2A	NM_052927, NM_001130864	226720_at, 228336_at, 228337_at, 236544_at	NP_443159.1, NP_001124336.1
GeneID:10569	SLU7	5	159,828,648	159,846,168	17,520	-	1	2_A375_pNL97_plus_lncRNA::1::6648	-2824	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SLU7	9G8, hSlu7, MGC9280, SLU7	SLU7 splicing factor homolog (S. cerevisiae)	NM_006425, hCT1964842.1, hCT2251446.0, hCT7344.3	227990_at, 231718_at	NP_006416.3, EAW61554.1, EAW61555.1, EAW61556.1
GeneID:9232	PTTG1	5	159,848,865	159,855,746	6,881	+	1	2_A375_pNL97_plus_lncRNA::1::6648	127	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene PTTG1	EAP1, PTTG1, MGC138276, HPTTG, MGC126883, PTTG, TUTR1	pituitary tumor-transforming 1	NM_004219, hCT1952294.1, hCT1961458.1, hCT7343.3	203554_x_at	NP_004210.1, EAW61551.1, EAW61552.1, EAW61553.1
GeneID:100422938	MIR3142	5	159,901,451	159,901,532	81	+	1	2_A375_pNL97_plus_lncRNA::1::6650	-6347	upstream	0	1	17	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MIR3142	MIR3142	microRNA 3142	NR_036095		
GeneID:2566	GABRG2	5	161,494,648	161,582,545	87,897	+	2	1_A375_pNL7_minus_lncRNA::1::4621, 2_A375_pNL97_plus_lncRNA::1::6651	1000, 1000	in gene, in gene	1	1	51	64	1	2_A375_pNL97_plus_lncRNA::1	64	Gene GABRG2	CAE2, GEFSP3, GABRG2, ECA2	gamma-aminobutyric acid (GABA) A receptor, gamma 2	NM_198904, NM_000816, NM_198903, hCT2353774.0, hCT2353775.0, hCT2353776.0, hCT28201.3	1568612_at, 206849_at	NP_944494.1, NP_000807.2, NP_944493.2, EAW61532.1, EAW61534.1, EAW61535.1, EAW61533.1
GeneID:134492	NUDCD2	5	162,880,586	162,887,143	6,557	-	1	2_A375_pNL97_plus_lncRNA::1::6652	-57	upstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NUDCD2	DKFZp686E10109, NUDCD2	NudC domain containing 2	NM_145266, hCT2251151.0	1558124_at, 226642_s_at, 226643_s_at	NP_660309.1, EAW61527.1
GeneID:3161	HMMR	5	162,887,517	162,918,951	31,434	+	1	2_A375_pNL97_plus_lncRNA::1::6652	-317	upstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene HMMR	MGC119495, MGC119494, IHABP, HMMR, CD168, RHAMM	hyaluronan-mediated motility receptor (RHAMM)	NM_001142556, NM_001142557, NM_012484, NM_012485, hCT2251253.0, hCT2251254.0, hCT2251255.0, hCT2353764.0, hCT28206.3	207165_at, 209709_s_at	NP_001136028.1, NP_001136029.1, NP_036616.2, NP_036617.2, EAW61523.1, EAW61524.1, EAW61521.1, EAW61522.1, EAW61525.1
GeneID:27430	MAT2B	5	162,930,231	162,946,328	16,097	+	2	1_A375_pNL7_minus_lncRNA::1::4622, 2_A375_pNL97_plus_lncRNA::1::6653	2377, 2313	in gene, in gene	1	1	24	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene MAT2B	MATIIbeta, TGR, MAT2B, MGC12237, SDR23E1, MAT-II, Nbla02999	methionine adenosyltransferase II, beta	NM_182796, NM_013283, hCT2251245.0, hCT2251246.0, hCT2353715.0, hCT28945.2	217993_s_at, 229284_at	NP_877725.1, NP_037415.1, EAW61517.1, EAW61518.1, EAW61519.1, EAW61520.1
GeneID:100507193	LOC100507193	5	163,724,057	164,598,619	874,562	+	1	2_A375_pNL97_plus_lncRNA::1::6654	303591	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100507193		hypothetical LOC100507193	XR_112798, XR_110063, XR_113797		
GeneID:5917	RARS	5	167,913,463	167,946,311	32,848	+	3	1_A375_pNL7_minus_lncRNA::1::4625, 2_A375_pNL97_plus_lncRNA::1::6657, 2_A375_pNL97_plus_lncRNA::1::6658	-71, -23, 42217	upstream, upstream, downstream	1	1	54.5	47	2	1_A375_pNL7_minus_lncRNA::1	95	Gene RARS	MGC8641, ArgRS, RARS, DALRD1	arginyl-tRNA synthetase	NM_002887, hCT29644.3	201330_at	NP_002878.2, EAW61507.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:3187	HNRNPH1	5	179,041,179	179,050,722	9,543	-	1	2_A375_pNL97_plus_lncRNA::1::6700	178	in gene	0	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene HNRNPH1	HNRNPH1, hnRNPH, DKFZp686A15170, HNRPH, HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	NM_005520, hCT2257899.0, hCT2257903.0, hCT87455.1	201031_s_at, 213470_s_at, 213472_at, 213619_at	NP_005511.1, EAW53807.1, EAW53808.1, EAW53809.1
GeneID:646019	CBY3	5	179,105,559	179,107,975	2,416	-	1	1_A375_pNL7_minus_lncRNA::1::4664	2055	in gene	1	0	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene CBY3	CBY3		NM_001164444		NP_001157916.1
GeneID:11282	MGAT4B	5	179,224,597	179,233,952	9,355	-	1	2_A375_pNL97_plus_lncRNA::1::6701	-523	upstream	0	1	12	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene MGAT4B	GNT-IVB, GNT-IV, MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	NM_014275, NM_054013, hCT1960374.1, hCT1960375.1, hCT2257878.0, hCT2257879.0, hCT2257880.0, hCT2257882.0, hCT2257884.0, hCT2257887.0	220189_s_at, 224598_at	NP_055090.1, NP_463459.1, EAW53788.1, EAW53789.1, EAW53790.1, EAW53795.1, EAW53791.1, EAW53792.1, EAW53793.1, EAW53794.1
GeneID:100302156	MIR1229	5	179,225,278	179,225,346	68	-	1	2_A375_pNL97_plus_lncRNA::1::6701	-9129	upstream	0	1	12	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene MIR1229	hsa-mir-1229, MIRN1229, MIR1229	microRNA 1229	NR_031598		
GeneID:8878	SQSTM1	5	179,233,388	179,265,078	31,690	+	5	1_A375_pNL7_minus_lncRNA::1::4665, 1_A375_pNL7_minus_lncRNA::1::4666, 2_A375_pNL97_plus_lncRNA::1::6701, 2_A375_pNL97_plus_lncRNA::1::6702, 2_A375_pNL97_plus_lncRNA::1::6703	13332, 14420, 1087, 13268, 14516	in gene, in gene, in gene, in gene, in gene	1	1	21	17.67	3	1_A375_pNL7_minus_lncRNA::1	26	Gene SQSTM1	PDB3, OSIL, p60, SQSTM1, p62, A170, ZIP3, p62B	sequestosome 1	NM_003900, NM_001142298, NM_001142299, hCT1960371.1, hCT6300.3	201471_s_at, 213112_s_at, 217252_at, 217255_at, 239004_at, 244804_at	NP_003891.1, NP_001135770.1, NP_001135771.1, EAW53786.1, EAW53787.1
GeneID:55819	RNF130	5	179,382,474	179,499,109	116,635	-	1	2_A375_pNL97_plus_lncRNA::1::6704	645	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene RNF130	GP, RNF130, MGC99542, MGC117241, MGC138647, GOLIATH, G1RZFP	ring finger protein 130	NM_018434, hCT1960379.1, hCT1960380.1, hCT2258996.0, hCT6308.3	1563975_at, 217865_at, 236292_at	NP_060904.2, EAW53774.1, EAW53772.1, EAW53773.1, EAW53775.1
GeneID:9945	GFPT2	5	179,727,700	179,780,315	52,615	-	2	1_A375_pNL7_minus_lncRNA::1::4667, 2_A375_pNL97_plus_lncRNA::1::6705	107, 507	in gene, in gene	1	1	20	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GFPT2	FLJ10380, GFPT2, GFAT2	glutamine-fructose-6-phosphate transaminase 2	NM_005110, hCT2259060.0, hCT6298.3	205100_at, 237352_at	NP_005101.1, EAW53755.1, EAW53756.1
GeneID:57472	CNOT6	5	179,921,417	180,005,353	83,936	+	2	1_A375_pNL7_minus_lncRNA::1::4668, 2_A375_pNL97_plus_lncRNA::1::6706	-153, -137	upstream, upstream	1	1	25	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene CNOT6	CCR4, CNOT6, KIAA1194	CCR4-NOT transcription complex, subunit 6	NM_015455, hCT2259723.1, hCT2259725.1, hCT2349964.0	217970_s_at, 222476_at	NP_056270.2, EAW53753.1, EAW53752.1, EAW53754.1
GeneID:4245	MGAT1	5	180,217,541	180,237,137	19,596	-	2	1_A375_pNL7_minus_lncRNA::1::4669, 2_A375_pNL97_plus_lncRNA::1::6707	-175, -591	upstream, upstream	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MGAT1	GNT-1, GLYT1, MGAT1, GLCT1, GLCNAC-TI, MGAT, GNT-I	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	NM_002406, NM_001114617, NM_001114618, NM_001114619, NM_001114620, hCT1641758.2, hCT1960385.1, hCT1960386.1, hCT1960387.1, hCT1967984.1, hCT2259027.0, hCT2259028.0	201126_s_at	NP_002397.2, NP_001108089.1, NP_001108090.1, NP_001108091.1, NP_001108092.1, EAW53739.1, EAW53740.1, EAW53741.1, EAW53742.1, EAW53743.1, EAW53744.1, EAW53745.1
GeneID:643836	ZFP62	5	180,274,611	180,288,286	13,675	-	2	1_A375_pNL7_minus_lncRNA::1::4670, 2_A375_pNL97_plus_lncRNA::1::6708	94, -402	in gene, upstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ZFP62	MGC176438, ZET, FLJ58781, ZNF755, FLJ34231, ZFP62, FLJ34057, FLJ59694, FLJ11344, DKFZp667F2013	zinc finger protein 62 homolog (mouse)	NM_152283, NM_001172638	227796_at	NP_689496.4, NP_001166109.1
GeneID:81786	TRIM7	5	180,620,924	180,632,177	11,253	-	4	1_A375_pNL7_minus_lncRNA::1::4671, 2_A375_pNL97_plus_lncRNA::1::6711, 2_A375_pNL97_plus_lncRNA::1::6712, 2_A375_pNL97_plus_lncRNA::1::6713	13457, 17553, 13425, 17	downstream, downstream, downstream, in gene	1	1	15.33	21.33	3	1_A375_pNL7_minus_lncRNA::1	23	Gene TRIM7	GNIP, TRIM7, RNF90	tripartite motif containing 7	NM_033342, NM_203293, NM_203294, NM_203295, NM_203296, NM_203297, hCT1773618.3, hCT1960390.2, hCT1960391.0, hCT2259014.1, hCT2351992.0, hCT2351993.0	1554735_a_at, 223694_at, 239694_at	NP_203128.1, NP_976038.1, NP_976039.1, NP_976040.1, NP_976041.1, NP_976042.1, EAW53715.1, EAW53716.1, EAW53717.1, EAW53718.1, EAW53719.1, EAW53720.1
GeneID:100507546	LOC100507546	5	180,625,202	180,630,117	4,915	+	3	1_A375_pNL7_minus_lncRNA::1::4671, 2_A375_pNL97_plus_lncRNA::1::6712, 2_A375_pNL97_plus_lncRNA::1::6713	-6482, -6450, 6958	upstream, upstream, downstream	1	1	17	22.5	2	1_A375_pNL7_minus_lncRNA::1	23	Gene LOC100507546		hypothetical LOC100507546	XR_112804, XR_112802, XR_112803, XR_110079, XR_110077, XR_110078, XR_113812, XR_113813, XR_113811		
GeneID:90933	TRIM41	5	180,650,306	180,662,808	12,502	+	6	1_A375_pNL7_minus_lncRNA::1::4672, 1_A375_pNL7_minus_lncRNA::1::4673, 1_A375_pNL7_minus_lncRNA::1::4674, 1_A375_pNL7_minus_lncRNA::1::4675, 2_A375_pNL97_plus_lncRNA::1::6714, 2_A375_pNL97_plus_lncRNA::1::6715	-4962, -1058, 190, 20542, -962, 30	upstream, upstream, in gene, downstream, upstream, in gene	1	1	20.5	19.75	4	2_A375_pNL97_plus_lncRNA::1	29	Gene TRIM41	MGC31991, TRIM41, MGC1127, RINCK	tripartite motif containing 41	NM_033549, NM_201627, hCT11046.2, hCT1960402.1, hCT1960403.0, hCT2259742.0, hCT2259743.0, hCT2259744.0, hCT2259747.0, hCT2352769.0	226445_s_at	NP_291027.3, NP_963921.1, EAW53707.1, EAW53712.1, EAW53713.1, EAW53714.1, EAW53708.1, EAW53709.1, EAW53710.1, EAW53711.1
GeneID:10399	GNB2L1	5	180,663,928	180,670,906	6,978	-	1	1_A375_pNL7_minus_lncRNA::1::4675	58	in gene	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene GNB2L1	Gnb2-rs1, H12.3, PIG21, GNB2L1, RACK1, HLC-7	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	NM_006098, hCT10125.4, hCT1960398.3, hCT1960399.2, hCT1960400.3, hCT1960401.3, hCT2349976.1, hCT2349977.1, hCT2349978.1, hCT2349979.1, hCT2349980.1, hCT2349982.1	200651_at, 222034_at	NP_006089.1, EAW53694.1, EAW53692.1, EAW53695.1, EAW53700.1, EAW53702.1, EAW53693.1, EAW53696.1, EAW53697.1, EAW53698.1, EAW53699.1, EAW53701.1
GeneID:619571	SNORD96A	5	180,668,818	180,668,889	71	-	1	1_A375_pNL7_minus_lncRNA::1::4675	-1959	upstream	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SNORD96A	SNORD96A, U96A	small nucleolar RNA, C/D box 96A	NR_002592		
GeneID:100289627	LOC100289627	5	180,668,965	180,670,914	1,949	+	1	1_A375_pNL7_minus_lncRNA::1::4675	1883	in gene	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene LOC100289627		hypothetical LOC100289627	XR_112805, XR_110080, XR_113814		
GeneID:619570	SNORD95	5	180,670,314	180,670,376	62	-	1	1_A375_pNL7_minus_lncRNA::1::4675	-472	upstream	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SNORD95	U95, SNORD95	small nucleolar RNA, C/D box 95	NR_002591		
GeneID:100507619	LOC100507619	5	180,673,507	180,684,587	11,080	+	3	1_A375_pNL7_minus_lncRNA::1::4675, 1_A375_pNL7_minus_lncRNA::1::4676, 2_A375_pNL97_plus_lncRNA::1::6716	-2659, 14621, 14573	upstream, downstream, downstream	1	1	22.5	15	2	1_A375_pNL7_minus_lncRNA::1	26	Gene LOC100507619		hypothetical LOC100507619	XR_112807, XR_110082, XR_113816		
GeneID:84851	TRIM52	5	180,683,373	180,688,119	4,746	-	2	1_A375_pNL7_minus_lncRNA::1::4676, 2_A375_pNL97_plus_lncRNA::1::6716	-9, 39	upstream, in gene	1	1	26	18	1	1_A375_pNL7_minus_lncRNA::1	26	Gene TRIM52	RNF102, TRIM52, MGC16175	tripartite motif containing 52	NM_032765, hCT1832819.3, hCT1960397.0, hCT2259005.1	1568594_s_at, 221897_at	NP_116154.1, EAW53704.1, EAW53703.1, EAW53705.1
GeneID:100507602	LOC100507602	5	180,688,213	180,691,259	3,046	+	2	1_A375_pNL7_minus_lncRNA::1::4676, 2_A375_pNL97_plus_lncRNA::1::6716	-85, -133	upstream, upstream	1	1	26	18	1	1_A375_pNL7_minus_lncRNA::1	26	Gene LOC100507602		hypothetical LOC100507602	XR_112806, XR_110081, XR_113815		
GeneID:56940	DUSP22	6	292,101	351,355	59,254	+	1	2_A375_pNL97_plus_lncRNA::1::6717	187	in gene	0	1	15	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene DUSP22	VHX, LMWDSP2, JSP1, JKAP, MKPX, FLJ35864, DUSP22	dual specificity phosphatase 22	NM_020185, hCT2343655.0	218845_at, 226440_at	NP_064570.1, EAW53895.1
GeneID:55770	EXOC2	6	485,138	693,109	207,971	-	2	1_A375_pNL7_minus_lncRNA::1::4677, 2_A375_pNL97_plus_lncRNA::1::6718	10, -43	in gene, upstream	1	1	37	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene EXOC2	EXOC2, SEC5L1, Sec5p, SEC5, FLJ11026	exocyst complex component 2	NM_018303, hCT13746.4, hCT2251308.0	219349_s_at, 226270_at	NP_060773.3, EAW55062.1, EAW55061.1
GeneID:340156	MYLK4	6	2,663,863	2,751,154	87,291	-	1	2_A375_pNL97_plus_lncRNA::1::6721	91986	downstream	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MYLK4	SgK085, MYLK4	myosin light chain kinase family, member 4	NM_001012418, hCT13977.4, hCT2351864.0	1556136_at, 1561503_at, 1561504_s_at	NP_001012418.2, EAW55083.1, EAW55084.1
GeneID:56897	WRNIP1	6	2,765,666	2,785,979	20,313	+	2	1_A375_pNL7_minus_lncRNA::1::4678, 2_A375_pNL97_plus_lncRNA::1::6722	14, -50	in gene, upstream	1	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene WRNIP1	RP11-420G6.2, WHIP, WRNIP1, FLJ22526, bA420G6.2	Werner helicase interacting protein 1	NM_020135, NM_130395, hCT13979.2, hCT1962922.0, hCT1962923.1, hCT2250669.0	218015_s_at, 222489_s_at, 227619_at	NP_064520.2, NP_569079.1, EAW55085.1, EAW55086.1, EAW55087.1, EAW55088.1
GeneID:401232	DKFZP686I15217	6	2,988,201	2,991,405	3,204	+	1	2_A375_pNL97_plus_lncRNA::1::6723	1655	in gene	0	1	13	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene DKFZP686I15217		hypothetical LOC401232	NR_026855, NR_026856		
GeneID:4835	NQO2	6	3,000,067	3,019,994	19,927	+	1	2_A375_pNL97_plus_lncRNA::1::6723	-10211	upstream	0	1	13	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene NQO2	NQO2, QR2, DHQV, DIA6, NMOR2	NAD(P)H dehydrogenase, quinone 2	NM_000904, hCT13974.2, hCT1953936.1, hCT2250674.0, hCT2250675.0, hCT2250679.0	203814_s_at	NP_000895.2, EAW55109.1, EAW55107.1, EAW55108.1, EAW55110.1, EAW55111.1
GeneID:8737	RIPK1	6	3,077,058	3,115,421	38,363	+	1	2_A375_pNL97_plus_lncRNA::1::6724	-7767	upstream	0	1	11	12	1	2_A375_pNL97_plus_lncRNA::1	12	Gene RIPK1	RIP, RIP1, RIPK1, FLJ39204	receptor (TNFRSF)-interacting serine-threonine kinase 1	NM_003804, hCT13972.3, hCT1960109.0, hCT2250682.0, hCT2250665.0	209941_at, 226551_at	NP_003795.2, EAW55115.1, EAW55116.1, EAW55117.1, EAW55118.1
GeneID:100507294	LOC100507294	6	3,226,159	3,267,301	59,142	+	2	1_A375_pNL7_minus_lncRNA::1::4679, 2_A375_pNL97_plus_lncRNA::1::6725	31020, 31041	in gene, in gene	1	1	18	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene LOC100507294		hypothetical LOC100507294	XR_112809, XR_108698, XR_113819		
GeneID:389362	PSMG4	6	3,259,162	3,268,300	9,138	+	2	1_A375_pNL7_minus_lncRNA::1::4679, 2_A375_pNL97_plus_lncRNA::1::6725	17, 38	in gene, in gene	1	1	18	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene PSMG4	C6orf86, PAC4, PSMG4, bA506K6.2	proteasome (prosome, macropain) assembly chaperone 4	NM_001128591, NM_001128592, NM_001135750	1561304_a_at, 226217_s_at, 233443_at, 233447_at, 242055_at, 242623_x_at	NP_001122063.1, NP_001122064.1, NP_001129222.1
GeneID:63027	SLC22A23	6	3,269,207	3,456,793	187,586	-	3	1_A375_pNL7_minus_lncRNA::1::4679, 2_A375_pNL97_plus_lncRNA::1::6725, 2_A375_pNL97_plus_lncRNA::1::6726	187614, 187593, 131929	downstream, downstream, in gene	1	1	15	22	2	2_A375_pNL97_plus_lncRNA::1	27	Gene SLC22A23	C6orf85, SLC22A23, DKFZp434F011, FLJ22174	solute carrier family 22, member 23	NM_021945, NM_015482, hCT13976.2, hCT2255257.0, hCT2255258.0, hCT2255260.0	1566718_at, 1566719_s_at, 223194_s_at, 233206_at	NP_068764.3, NP_056297.1, EAW55132.1, EAW55133.1, EAW55134.1, EAW55135.1
GeneID:10799	RPP40	6	4,995,260	5,004,271	8,991	-	1	2_A375_pNL97_plus_lncRNA::1::6728	239	in gene	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene RPP40	RPP40, bA428J1.3, RNASEP1	ribonuclease P/MRP 40kDa subunit	NM_006638, hCT1956276.1, hCT1963393.1, hCT1963394.1, hCT2250904.0, hCT2250906.0	213427_at	NP_006629.2, EAW55170.1, EAW55171.1, EAW55172.1, EAW55173.1, EAW55174.1
GeneID:57128	LYRM4	6	5,108,653	5,261,172	152,519	-	1	2_A375_pNL97_plus_lncRNA::1::6729	-444	upstream	0	1	8	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LYRM4	LYRM4, ISD11, C6orf149, CGI-203	LYR motif containing 4	NM_020408, NM_001164840, NM_001164841, hCT1640219.3, hCT2250900.0, hCT2250901.0	218561_s_at, 222672_at	NP_065141.3, NP_001158312.1, NP_001158313.1, EAW55176.1, EAW55177.1, EAW55178.1
GeneID:10667	FARS2	6	5,261,584	5,771,816	510,232	+	1	2_A375_pNL97_plus_lncRNA::1::6729	32	in gene	0	1	8	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FARS2	HSPC320, PheRS, FARS1, dJ520B18.2, FARS2	phenylalanyl-tRNA synthetase 2, mitochondrial	NM_006567, hCT2250616.0	204282_s_at, 204283_at, 215414_at	NP_006558.1, EAW55179.1
GeneID:6745	SSR1	6	7,281,283	7,313,541	32,258	-	1	2_A375_pNL97_plus_lncRNA::1::6730	218	in gene	0	1	14	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene SSR1	SSR1, FLJ93042, DKFZp781N23103, FLJ22100, TRAPA, FLJ14232, FLJ78242, FLJ23034	signal sequence receptor, alpha	NM_003144, hCT2254020.0, hCT2254021.0, hCT2254022.0	200889_s_at, 200890_s_at, 200891_s_at, 201894_s_at, 225435_at	NP_003135.2, EAW55204.1, EAW55202.1, EAW55203.1
GeneID:347744	C6orf52	6	10,671,651	10,695,030	23,379	-	1	1_A375_pNL7_minus_lncRNA::1::4680	54	in gene	1	0	14	10	1	1_A375_pNL7_minus_lncRNA::1	14	Gene C6orf52	C6orf52	chromosome 6 open reading frame 52	NM_001145020, NR_026736, NR_026737	236504_x_at, 239417_x_at, 243943_x_at	NP_001138492.1
GeneID:55003	PAK1IP1	6	10,695,188	10,709,972	14,784	+	1	1_A375_pNL7_minus_lncRNA::1::4680	-212	upstream	1	0	14	10	1	1_A375_pNL7_minus_lncRNA::1	14	Gene PAK1IP1	PIP1, FLJ20624, RP11-421M1.5, WDR84, PAK1IP1, hPIP1, MAK11, bA421M1.5	PAK1 interacting protein 1	NM_017906, hCT1816839.1, hCT1954768.1, hCT1963392.1, hCT2352910.0	218886_at	NP_060376.2, EAW55267.1, EAW55268.1, EAW55269.1, EAW55270.1
GeneID:51522	TMEM14C	6	10,723,148	10,731,362	8,214	+	2	1_A375_pNL7_minus_lncRNA::1::4681, 2_A375_pNL97_plus_lncRNA::1::6731	20, -28	in gene, upstream	1	1	22	21	1	1_A375_pNL7_minus_lncRNA::1	22	Gene TMEM14C	HSPC194, bA421M1.6, C6orf53, MSTP073, NET26, TMEM14C	transmembrane protein 14C	NM_016462, NM_001165258, hCT1821900.2, hCT1954767.1, hCT1963391.1, hCT2251174.0, hCT2251177.0	223105_s_at	NP_057546.1, NP_001158730.1, EAW55271.1, EAW55272.1, EAW55274.1, EAW55275.1, EAW55273.1
GeneID:100506379	LOC100506379	6	10,743,557	10,747,896	4,339	-	2	1_A375_pNL7_minus_lncRNA::1::4682, 2_A375_pNL97_plus_lncRNA::1::6732	104, 88	in gene, in gene	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506379		hypothetical LOC100506379	XR_112817, XR_112816, XR_108672, XR_108671, XR_113838, XR_113837		
GeneID:81853	TMEM14B	6	10,747,995	10,757,214	9,219	+	2	1_A375_pNL7_minus_lncRNA::1::4682, 2_A375_pNL97_plus_lncRNA::1::6732	-203, -187	upstream, upstream	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TMEM14B	FLJ60466, TMEM14B, MGC1223	transmembrane protein 14B	NM_030969, NM_001127711, hCT1821899.2, hCT1963387.1, hCT1963388.1, hCT1963389.1, hCT1963390.1, hCT2251182.0	221452_s_at, 223133_at	NP_112231.3, NP_001121183.1, EAW55276.1, EAW55278.1, EAW55280.1, EAW55281.1, EAW55277.1, EAW55279.1
GeneID:9247	GCM2	6	10,873,456	10,882,098	8,642	-	2	1_A375_pNL7_minus_lncRNA::1::4683, 2_A375_pNL97_plus_lncRNA::1::6733	-5166, -5166	upstream, upstream	1	1	36	33	1	1_A375_pNL7_minus_lncRNA::1	36	Gene GCM2	GCM2, GCMB, hGCMb	glial cells missing homolog 2 (Drosophila)	NM_004752, hCT27986.3	220799_at	NP_004743.1, EAW55287.1
GeneID:221711	SYCP2L	6	10,887,064	10,974,542	87,478	+	2	1_A375_pNL7_minus_lncRNA::1::4683, 2_A375_pNL97_plus_lncRNA::1::6733	200, 200	in gene, in gene	1	1	36	33	1	1_A375_pNL7_minus_lncRNA::1	36	Gene SYCP2L	NO145, C6orf177, SYCP2L, dJ62D2.1	synaptonemal complex protein 2-like	NM_001040274, hCT1815433.1	236337_at	NP_001035364.2, EAW55288.1
GeneID:221710	LOC221710	6	11,094,266	11,138,971	44,705	+	4	1_A375_pNL7_minus_lncRNA::1::4684, 1_A375_pNL7_minus_lncRNA::1::4685, 2_A375_pNL97_plus_lncRNA::1::6734, 2_A375_pNL97_plus_lncRNA::1::6735	-250, 49894, -58, 49862	upstream, downstream, upstream, downstream	1	1	25	22	2	1_A375_pNL7_minus_lncRNA::1	32	Gene LOC221710		hypothetical protein LOC221710	NM_001135575	1564651_at, 227124_at, 235707_at	NP_001129047.1
GeneID:405754	HERV-FRD	6	11,102,722	11,112,071	9,349	-	2	1_A375_pNL7_minus_lncRNA::1::4684, 2_A375_pNL97_plus_lncRNA::1::6734	18055, 17863	downstream, downstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene HERV-FRD	FLJ41944, HERV-FRD, UNQ6191, GLLL6191, FLJ90611, MGC87555	HERV-FRD provirus ancestral Env polyprotein	NM_207582	1555580_at	NP_997465.1
GeneID:4739	NEDD9	6	11,183,531	11,382,581	199,050	-	1	1_A375_pNL7_minus_lncRNA::1::4686	175061	in gene	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene NEDD9	dJ761I2.1, dJ49G10.2, NEDD9, CASL, CASS2, CAS2, CAS-L, HEF1	neural precursor cell expressed, developmentally down-regulated 9	NM_182966, NM_006403, NM_001142393, hCT1956286.1, hCT1956288.1, hCT2251366.0, hCT2352914.0, hCT27987.1	1569020_at, 202149_at, 202150_s_at	NP_892011.2, NP_006394.1, NP_001135865.1, EAW55299.1, EAW55300.1, EAW55302.1, EAW55301.1, EAW55303.1
GeneID:100506431	LOC100506431	6	11,198,541	11,199,708	1,167	-	1	1_A375_pNL7_minus_lncRNA::1::4686	-7812	upstream	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC100506431		B2 RNA	XR_108674		
GeneID:100113407	TMEM170B	6	11,538,511	11,583,757	45,246	+	2	1_A375_pNL7_minus_lncRNA::1::4687, 2_A375_pNL97_plus_lncRNA::1::6736	-2383, -2415	upstream, upstream	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene TMEM170B	TMEM170B	transmembrane protein 170B	NM_001100829		NP_001094299.1
GeneID:51256	TBC1D7	6	13,305,183	13,328,787	23,604	-	1	2_A375_pNL97_plus_lncRNA::1::6738	19	in gene	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TBC1D7	TBC7, TBC1D7, FLJ32666, dJ257A7.3, PIG51, DKFZp686N2317	TBC1 domain family, member 7	NM_001143966, NM_001143964, NM_001143965, NM_016495, hCT1956296.1, hCT1968053.1, hCT1968054.1, hCT2251655.0, hCT28654.3	1563539_at, 223461_at	NP_001137438.1, NP_001137436.1, NP_001137437.1, NP_057579.1, EAW55323.1, EAW55326.1, EAW55324.1, EAW55325.1, EAW55327.1
GeneID:23408	SIRT5	6	13,574,792	13,614,790	39,998	+	3	1_A375_pNL7_minus_lncRNA::1::4688, 2_A375_pNL97_plus_lncRNA::1::6739, 2_A375_pNL97_plus_lncRNA::1::6740	40728, 568, 40744	downstream, in gene, downstream	1	1	44	44	2	1_A375_pNL7_minus_lncRNA::1	77	Gene SIRT5	SIR2L5, FLJ36950, SIRT5	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	NM_012241, NM_031244, NM_001193267, hCT1954773.2, hCT1968050.1, hCT1968051.1, hCT1968052.0, hCT2251419.0, hCT2251420.0, hCT28652.3	1569938_at, 219185_at, 221010_s_at	NP_036373.1, NP_112534.1, NP_001180196.1, EAW55333.1, EAW55335.1, EAW55338.1, EAW55332.1, EAW55334.1, EAW55336.1, EAW55337.1
GeneID:51406	NOL7	6	13,615,559	13,621,127	5,568	+	2	1_A375_pNL7_minus_lncRNA::1::4688, 2_A375_pNL97_plus_lncRNA::1::6740	-39, -23	upstream, upstream	1	1	77	76	1	1_A375_pNL7_minus_lncRNA::1	77	Gene NOL7	MGC71933, dJ223E5.2, C6orf90, NOL7, RARG-1, PQBP3	nucleolar protein 7, 27kDa	NM_016167, hCT2251427.0, hCT28650.2	202882_x_at, 210097_s_at, 213836_at	NP_057251.2, EAW55339.1, EAW55340.1
GeneID:10048	RANBP9	6	13,621,730	13,711,796	90,066	-	3	1_A375_pNL7_minus_lncRNA::1::4688, 1_A375_pNL7_minus_lncRNA::1::4689, 2_A375_pNL97_plus_lncRNA::1::6740	96276, -620, 96260	downstream, upstream, downstream	1	1	47	43.5	2	1_A375_pNL7_minus_lncRNA::1	77	Gene RANBP9	RANBPM, RANBP9, BPM90, BPM-L, RanBP7	RAN binding protein 9	NM_005493, hCT1961876.1, hCT1961877.1, hCT2251642.0, hCT2352912.0, hCT27985.4	202582_s_at, 202583_s_at, 216125_s_at	NP_005484.2, EAW55344.1, EAW55341.1, EAW55342.1, EAW55343.1, EAW55345.1
GeneID:3720	JARID2	6	15,246,527	15,522,253	275,726	+	2	1_A375_pNL7_minus_lncRNA::1::4691, 2_A375_pNL97_plus_lncRNA::1::6741	-511, -575	upstream, upstream	1	1	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene JARID2	JMJ, JARID2	jumonji, AT rich interactive domain 2	NM_004973, hCT1954770.1, hCT2251275.0	203297_s_at, 203298_s_at	NP_004964.2, EAW55357.1, EAW55358.1
GeneID:100506661	LOC100506661	6	15,246,048	15,246,887	839	-	2	1_A375_pNL7_minus_lncRNA::1::4691, 2_A375_pNL97_plus_lncRNA::1::6741	2871, 2935	downstream, downstream	1	1	24	21	1	1_A375_pNL7_minus_lncRNA::1	24	Gene LOC100506661		hypothetical LOC100506661	XR_108680, XR_113845		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:6310	ATXN1	6	16,299,343	16,761,721	462,378	-	5	1_A375_pNL7_minus_lncRNA::1::4693, 1_A375_pNL7_minus_lncRNA::1::4694, 1_A375_pNL7_minus_lncRNA::1::4695, 2_A375_pNL97_plus_lncRNA::1::6742, 2_A375_pNL97_plus_lncRNA::1::6743	426633, 79737, -4871, 426633, 79801	in gene, in gene, upstream, in gene, in gene	1	1	14.67	13.67	3	2_A375_pNL97_plus_lncRNA::1	18	Gene ATXN1	D6S504E, ATX1, SCA1, ATXN1	ataxin 1	NM_000332, NM_001128164, hCT1963398.1, hCT1963399.1, hCT2251554.0, hCT2352907.0, hCT27979.4	1559249_at, 203231_s_at, 203232_s_at, 230507_at, 242230_at	NP_000323.2, NP_001121636.1, EAW55370.1, EAW55371.1, EAW55372.1, EAW55373.1, EAW55374.1
GeneID:9972	NUP153	6	17,615,269	17,706,818	91,549	-	1	2_A375_pNL97_plus_lncRNA::1::6744	-302	upstream	0	1	16	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene NUP153	NUP153, HNUP153, N153	nucleoporin 153kDa	NM_005124, hCT2252377.0, hCT28538.2	1559064_at, 202097_at, 239948_at	NP_005115.2, EAW55385.1, EAW55384.1
GeneID:63971	KIF13A	6	17,760,585	17,987,799	227,214	-	1	2_A375_pNL97_plus_lncRNA::1::6745	79639	in gene	0	1	11	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene KIF13A	FLJ27232, bA500C11.2, KIF13A	kinesin family member 13A	NM_022113, NM_001105566, NM_001105567, NM_001105568, hCT2252370.0, hCT2252371.0, hCT2252372.0, hCT2252373.0, hCT2252374.0	220777_at, 223520_s_at, 230990_at, 232637_at	NP_071396.4, NP_001099036.1, NP_001099037.1, NP_001099038.1, EAW55389.1, EAW55391.1, EAW55387.1, EAW55388.1, EAW55390.1
GeneID:378884	NHLRC1	6	18,120,718	18,122,851	2,133	-	1	1_A375_pNL7_minus_lncRNA::1::4696	35	in gene	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene NHLRC1	EPM2A, MGC119262, MALIN, NHLRC1, MGC119265, bA204B7.2, EPM2B, MGC119264	NHL repeat containing 1	NM_198586, hCT2345217.0		NP_940988.2, EAW55392.1
GeneID:7172	TPMT	6	18,128,542	18,155,374	26,832	-	1	1_A375_pNL7_minus_lncRNA::1::4696	32558	downstream	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene TPMT	TPMT	thiopurine S-methyltransferase	NM_000367, hCT1826356.3, hCT2251477.1, hCT2251478.1, hCT2343408.0, hCT2343409.0, hCT2343410.0, hCT2343411.0	203671_at, 203672_x_at, 238272_at	NP_000358.1, EAW55396.1, EAW55393.1, EAW55395.1, EAW55397.1, EAW55398.1, EAW55394.1, EAW55399.1
GeneID:54901	CDKAL1	6	20,534,688	21,232,635	697,947	+	4	1_A375_pNL7_minus_lncRNA::1::4698, 1_A375_pNL7_minus_lncRNA::1::4699, 2_A375_pNL97_plus_lncRNA::1::6747, 1_A375_pNL7_minus_lncRNA::1::4700	-64, 343184, 343072, 488112	upstream, in gene, in gene, in gene	1	1	15.67	13	3	1_A375_pNL7_minus_lncRNA::1	17	Gene CDKAL1	FLJ20342, FLJ46705, MGC75469, CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	NM_017774, hCT1956010.1, hCT2251813.0, hCT2352922.0	214877_at, 220039_s_at	NP_060244.2, EAW55426.1, EAW55425.1, EAW55427.1
GeneID:140767	NRSN1	6	24,126,414	24,147,757	21,343	+	1	2_A375_pNL97_plus_lncRNA::1::6748	754	in gene	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NRSN1	NRSN1, VMP, p24	neurensin 1	NM_080723, hCT1656169.2, hCT1952424.1	239293_at	NP_542454.3, EAW55439.1, EAW55438.1
GeneID:57380	MRS2	6	24,403,153	24,425,816	22,663	+	2	1_A375_pNL7_minus_lncRNA::1::4701, 2_A375_pNL97_plus_lncRNA::1::6749	47, 47	in gene, in gene	1	1	16	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MRS2	HPT, MRS2L, MGC78523, MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	NM_020662, hCT2251850.0, hCT2352903.0, hCT28749.2	218536_at, 218538_s_at, 224101_x_at, 227789_at, 228542_at, 238752_at, 244844_at	NP_065713.1, EAW55447.1, EAW55445.1, EAW55446.1
GeneID:2822	GPLD1	6	24,428,405	24,489,850	61,445	-	1	1_A375_pNL7_minus_lncRNA::1::4702	-5286	upstream	1	0	22	11	1	1_A375_pNL7_minus_lncRNA::1	22	Gene GPLD1	GPLD1, GPIPLDM, PIGPLD1, PIGPLD, MGC22590, GPIPLD	glycosylphosphatidylinositol specific phospholipase D1	NM_001503, NM_177483, hCT2252179.1, hCT2252181.1, hCT2252182.1, hCT28748.4	206264_at, 206265_s_at, 206266_at, 215554_at, 217405_x_at	NP_001494.2, NP_803436.1, EAW55448.1, EAW55449.1, EAW55450.1, EAW55451.1
GeneID:7915	ALDH5A1	6	24,495,197	24,537,435	42,238	+	1	1_A375_pNL7_minus_lncRNA::1::4702	-61	upstream	1	0	22	11	1	1_A375_pNL7_minus_lncRNA::1	22	Gene ALDH5A1	SSADH, ALDH5A1, SSDH	aldehyde dehydrogenase 5 family, member A1	NM_001080, NM_170740, hCT2251851.0, hCT2352904.0, hCT28742.2	203608_at, 203609_s_at	NP_001071.1, NP_733936.1, EAW55452.1, EAW55453.1, EAW55454.1
GeneID:51567	TTRAP	6	24,650,205	24,667,115	16,910	-	1	2_A375_pNL97_plus_lncRNA::1::6750	11	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TTRAP	AD022, TTRAP, MGC9099, MGC111021, dJ30M3.3, EAP2, TDP2	TRAF and TNF receptor associated protein	NM_016614, hCT2352906.0, hCT28752.2	202266_at	NP_057698.2, EAW55459.1, EAW55458.1
GeneID:55856	ACOT13	6	24,667,263	24,705,297	38,034	+	1	2_A375_pNL97_plus_lncRNA::1::6750	-159	upstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ACOT13	HT012, MGC4961, ACOT13, THEM2, PNAS-27	acyl-CoA thioesterase 13	NM_018473, NM_001160094, hCT28750.2	204565_at	NP_060943.1, NP_001153566.1, EAW55460.1
GeneID:51053	GMNN	6	24,775,164	24,786,278	11,114	+	1	2_A375_pNL97_plus_lncRNA::1::6751	335	in gene	0	1	11	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene GMNN	RP3-369A17.3, Gem, GMNN	geminin, DNA replication inhibitor	NM_015895, hCT1963206.1, hCT28743.2	218350_s_at	NP_056979.1, EAW55465.1, EAW55466.1
GeneID:10590	SCGN	6	25,652,429	25,702,011	49,582	+	4	1_A375_pNL7_minus_lncRNA::1::4703, 1_A375_pNL7_minus_lncRNA::1::4704, 2_A375_pNL97_plus_lncRNA::1::6753, 2_A375_pNL97_plus_lncRNA::1::6754	131, 8563, 147, 8467	in gene, in gene, in gene, in gene	1	1	27	26.5	2	1_A375_pNL7_minus_lncRNA::1	37	Gene SCGN	SCGN, setagin, SECRET, DJ501N12.8, CALBL, SEGN	secretagogin, EF-hand calcium binding protein	NM_006998, hCT10190.2, hCT2252549.0	205697_at	NP_008929.2, EAW55487.1, EAW55488.1
GeneID:3024	HIST1H1A	6	26,017,260	26,018,040	780	-	1	1_A375_pNL7_minus_lncRNA::1::4705	-2856	upstream	1	0	15	9	1	1_A375_pNL7_minus_lncRNA::1	15	Gene HIST1H1A	H1A, HIST1H1A, MGC126642, MGC138345, HIST1, H1F1, H1.1	histone cluster 1, H1a	NM_005325, hCT1655757.2	208484_at	NP_005316.1, EAW55507.1
GeneID:8350	HIST1H3A	6	26,020,718	26,021,186	468	+	1	1_A375_pNL7_minus_lncRNA::1::4705	178	in gene	1	0	15	9	1	1_A375_pNL7_minus_lncRNA::1	15	Gene HIST1H3A	HIST1H3D, H3FA, H3/A, HIST1H3E, HIST1H3G, HIST1H3B, HIST1H3I, HIST1H3H, HIST1H3J, HIST1H3A, HIST1H3F, HIST1H3C	histone cluster 1, H3a	NM_003529, hCT1644026.2	208575_at	NP_003520.1, EAW55508.1
GeneID:8359	HIST1H4A	6	26,021,907	26,022,278	371	+	2	1_A375_pNL7_minus_lncRNA::1::4705, 2_A375_pNL97_plus_lncRNA::1::6755	-1011, 10157	upstream, downstream	1	1	13	11.5	2	1_A375_pNL7_minus_lncRNA::1	15	Gene HIST1H4A	HIST1H4D, HIST1H4H, HIST1H4E, HIST1H4B, H4/a, HIST2H4A, HIST2H4B, HIST1H4A, HIST1H4L, HIST1H4J, HIST1H4C, HIST4H4, H4FA, HIST1H4I, HIST1H4F, HIST1H4K	histone cluster 1, H4a	NM_003538, hCT1644025.1	208046_at	NP_003529.1, EAW55509.1
GeneID:8366	HIST1H4B	6	26,027,124	26,027,480	356	-	3	1_A375_pNL7_minus_lncRNA::1::4705, 2_A375_pNL97_plus_lncRNA::1::6755, 2_A375_pNL97_plus_lncRNA::1::6756	6584, -4584, -5992	downstream, upstream, upstream	1	1	10.67	12.33	3	1_A375_pNL7_minus_lncRNA::1	15	Gene HIST1H4B	HIST1H4D, HIST1H4H, HIST1H4E, HIST1H4B, H4/I, H4FI, HIST2H4A, HIST2H4B, HIST1H4A, HIST1H4L, HIST1H4J, HIST1H4C, HIST4H4, HIST1H4I, HIST1H4F, HIST1H4K	histone cluster 1, H4b	NM_003544, hCT1826437.1	214516_at	NP_003535.1, EAW55510.1
GeneID:8358	HIST1H3B	6	26,031,817	26,032,288	471	-	2	2_A375_pNL97_plus_lncRNA::1::6755, 2_A375_pNL97_plus_lncRNA::1::6756	224, -1184	in gene, upstream	0	1	8.5	14	2	2_A375_pNL97_plus_lncRNA::1	14	Gene HIST1H3B	HIST1H3D, H3FL, HIST1H3E, HIST1H3G, HIST1H3B, HIST1H3I, HIST1H3H, HIST1H3J, HIST1H3A, HIST1H3F, HIST1H3C, H3/l	histone cluster 1, H3b	NM_003537, hCT10191.2	208576_s_at	NP_003528.1, EAW55511.1
GeneID:8335	HIST1H2AB	6	26,033,320	26,033,796	476	-	2	2_A375_pNL97_plus_lncRNA::1::6755, 2_A375_pNL97_plus_lncRNA::1::6756	1732, 324	downstream, in gene	0	1	8.5	14	2	2_A375_pNL97_plus_lncRNA::1	14	Gene HIST1H2AB	HIST1H2AB, H2AFM, H2A/m, HIST1H2AE	histone cluster 1, H2ab	NM_003513, hCT1826441.1	208569_at	NP_003504.2, EAW55512.1
GeneID:3018	HIST1H2BB	6	26,043,455	26,043,885	430	-	1	2_A375_pNL97_plus_lncRNA::1::6756	10413	downstream	0	1	6	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene HIST1H2BB	MGC119804, H2BFF, HIST1H2BB, H2B.1, H2B/f	histone cluster 1, H2bb	NM_021062, hCT1826444.1	208547_at	NP_066406.1, EAW55513.1
GeneID:3006	HIST1H1C	6	26,055,915	26,056,699	784	-	1	2_A375_pNL97_plus_lncRNA::1::6757	59	in gene	0	1	4	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene HIST1H1C	H1F2, H1.2, HIST1H1C, MGC3992, H1C	histone cluster 1, H1c	NM_005319, hCT1640612.1	209398_at	NP_005310.1, EAW55515.1
GeneID:8339	HIST1H2BG	6	26,216,428	26,216,872	444	-	1	1_A375_pNL7_minus_lncRNA::1::4706	-3864	upstream	1	0	15	13	1	1_A375_pNL7_minus_lncRNA::1	15	Gene HIST1H2BG	dJ221C16.8, H2BFA, H2B/k, H2B/a, HIST1H2BE, H2B.1A, HIST1H2BI, HIST1H2BF, H2B/g, H2B/l, HIST1H2BC, HIST1H2BG, H2B/h	histone cluster 1, H2bg	NM_003518, hCT1641112.1	214455_at	NP_003509.1, EAW55545.1
GeneID:3012	HIST1H2AE	6	26,217,148	26,217,711	563	+	1	1_A375_pNL7_minus_lncRNA::1::4706	3568	downstream	1	0	15	13	1	1_A375_pNL7_minus_lncRNA::1	15	Gene HIST1H2AE	H2A.1, H2A.2, HIST1H2AB, H2AFA, H2A/a, HIST1H2AE	histone cluster 1, H2ae	NM_021052, hCT1641111.1	214469_at	NP_066390.1, EAW55546.1
GeneID:8353	HIST1H3E	6	26,225,383	26,225,844	461	+	1	1_A375_pNL7_minus_lncRNA::1::4706	-4647	upstream	1	0	15	13	1	1_A375_pNL7_minus_lncRNA::1	15	Gene HIST1H3E	HIST1H3D, H3FD, H3/d, HIST1H3E, H3.1, HIST1H3G, HIST1H3B, HIST1H3I, HIST1H3H, HIST1H3J, HIST1H3A, HIST1H3F, HIST1H3C	histone cluster 1, H3e	NM_003532	214616_at	NP_003523.1
GeneID:3007	HIST1H1D	6	26,234,440	26,235,216	776	-	1	2_A375_pNL97_plus_lncRNA::1::6758	-5488	upstream	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene HIST1H1D	H1F3, H1.3, HIST1H1D, MGC138176, H1D	histone cluster 1, H1d	NM_005320, hCT1647046.1	214537_at	NP_005311.1, EAW55548.1
GeneID:8361	HIST1H4F	6	26,240,654	26,241,021	367	+	1	2_A375_pNL97_plus_lncRNA::1::6758	50	in gene	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene HIST1H4F	HIST1H4D, HIST1H4H, H4, HIST1H4E, HIST1H4B, HIST2H4A, HIST2H4B, HIST1H4A, HIST1H4L, HIST1H4J, H4/c, HIST1H4C, HIST4H4, HIST1H4I, HIST1H4F, HIST1H4K, H4FC	histone cluster 1, H4f	NM_003540, hCT1641911.1	208026_at	NP_003531.1, EAW55549.1
GeneID:8369	HIST1H4G	6	26,246,839	26,247,205	366	-	1	2_A375_pNL97_plus_lncRNA::1::6758	6501	downstream	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene HIST1H4G	H4/l, HIST1H4G, H4FL	histone cluster 1, H4g	NM_003547, hCT1641910.1	208551_at	NP_003538.1, EAW55550.1
GeneID:8968	HIST1H3F	6	26,250,370	26,250,835	465	-	1	2_A375_pNL97_plus_lncRNA::1::6758	10131	downstream	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene HIST1H3F	HIST1H3D, H3/i, HIST1H3E, H3FI, HIST1H3G, HIST1H3B, HIST1H3I, HIST1H3H, HIST1H3J, HIST1H3A, HIST1H3F, HIST1H3C	histone cluster 1, H3f	NM_021018, hCT1641909.1	208506_at	NP_066298.1, EAW55551.1
GeneID:100507025	LOC100507025	6	26,281,278	26,285,763	4,485	-	1	2_A375_pNL97_plus_lncRNA::1::6759	243	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100507025		hypothetical LOC100507025	XR_112839, XR_108687, XR_113851		
GeneID:8365	HIST1H4H	6	26,285,354	26,285,727	373	-	1	2_A375_pNL97_plus_lncRNA::1::6759	207	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene HIST1H4H	HIST1H4D, HIST1H4H, HIST1H4E, HIST1H4B, HIST2H4A, HIST2H4B, HIST1H4A, HIST1H4L, HIST1H4J, H4/h, HIST1H4C, HIST4H4, HIST1H4I, H4FH, HIST1H4F, HIST1H4K	histone cluster 1, H4h	NM_003543, hCT1641108.3, hCT2252692.0	208180_s_at, 208181_at, 232035_at	NP_003534.1, EAW55556.1, EAW55555.1
GeneID:493812	HCG11	6	26,521,934	26,527,621	5,687	+	1	2_A375_pNL97_plus_lncRNA::1::6760	530	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene HCG11	HCG11, bK14H9.3, FLJ14049, FLJ30357	HLA complex group 11	NR_026790	1557167_at, 1557169_x_at	
GeneID:10473	HMGN4	6	26,538,572	26,547,165	8,593	+	2	2_A375_pNL97_plus_lncRNA::1::6761, 2_A375_pNL97_plus_lncRNA::1::6762	-140, 15844	upstream, downstream	0	1	9.5	16	2	2_A375_pNL97_plus_lncRNA::1	16	Gene HMGN4	HMGN4, MGC5145, NHC, HMG17L3	high mobility group nucleosomal binding domain 4	NM_006353, hCT1641107.4, hCT1963176.2, hCT2340850.0, hCT2340851.0, hCT2340852.0	202579_x_at, 209786_at, 209787_s_at	NP_006344.1, EAW55587.1, EAW55586.1, EAW55588.1, EAW55589.1, EAW55590.1
GeneID:8362	HIST1H4K	6	27,798,952	27,799,305	353	-	1	2_A375_pNL97_plus_lncRNA::1::6765	-5783	upstream	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene HIST1H4K	HIST1H4D, HIST1H4H, HIST1H4E, HIST1H4B, H4F2iii, dJ160A22.1, HIST2H4A, HIST2H4B, H4FD, HIST1H4A, HIST1H4L, HIST1H4J, H4/d, HIST1H4C, HIST4H4, HIST1H4I, HIST1H4F, HIST1H4K	histone cluster 1, H4k	NM_003541, hCT1781243.3	208580_x_at, 214463_x_at	NP_003532.1, EAX03112.1
GeneID:8330	HIST1H2AK	6	27,805,626	27,806,124	498	-	1	2_A375_pNL97_plus_lncRNA::1::6765	1036	downstream	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene HIST1H2AK	HIST1H2AJ, H2AFD, HIST1H2AM, HIST1H2AL, HIST1H2AK, H2A/d, HIST1H2AG	histone cluster 1, H2ak	NM_003510, hCT1643881.3	214644_at, 239041_at	NP_003501.1, EAX03113.1
GeneID:8341	HIST1H2BN	6	27,806,364	27,806,894	530	+	1	2_A375_pNL97_plus_lncRNA::1::6765	-1276	upstream	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene HIST1H2BN	H2B/d, MGC125414, H2BFD, MGC9386, MGC125415, HIST1H3I, MGC125416, HIST1H2BN	histone cluster 1, H2bn	NM_003520, hCT1781246.2, hCT1953815.2, hCT2281564.1, hCT2281566.1	207226_at	NP_003511.1, EAX03116.1, EAX03114.1, EAX03115.1, EAX03117.1
GeneID:8356	HIST1H3J	6	27,858,093	27,858,570	477	-	1	1_A375_pNL7_minus_lncRNA::1::4708	-2486	upstream	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene HIST1H3J	HIST1H3D, H3FJ, H3/j, HIST1H3E, HIST1H3G, HIST1H3B, HIST1H3I, HIST1H3H, HIST1H3J, HIST1H3A, HIST1H3F, HIST1H3C	histone cluster 1, H3j	NM_003535, hCT1643882.1	214646_at	NP_003526.1, EAX03122.1
GeneID:8336	HIST1H2AM	6	27,860,477	27,860,963	486	-	1	1_A375_pNL7_minus_lncRNA::1::4708	-93	upstream	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene HIST1H2AM	H2A/n, H2A.1, H2AFN, HIST1H2AM, HIST1H2AL, HIST1H2AK, HIST1H2AI, HIST1H2AG, dJ193B12.1	histone cluster 1, H2am	NM_003514, hCT1640594.3	214481_at	NP_003505.1, EAX03123.1
GeneID:8348	HIST1H2BO	6	27,861,203	27,861,669	466	+	1	1_A375_pNL7_minus_lncRNA::1::4708	-147	upstream	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene HIST1H2BO	MGC119806, HIST1H2BO, H2B/n, H2B.2, dJ193B12.2, H2BFN	histone cluster 1, H2bo	NM_003527, hCT2281570.1	214540_at	NP_003518.2, EAX03124.1
GeneID:100507241	LOC100507241	6	28,046,570	28,048,957	2,387	-	1	1_A375_pNL7_minus_lncRNA::1::4709	253	in gene	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene LOC100507241		hypothetical LOC100507241	XR_112845, XR_108695, XR_113861		
GeneID:7718	ZNF165	6	28,048,482	28,057,341	8,859	+	1	1_A375_pNL7_minus_lncRNA::1::4709	222	in gene	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ZNF165	CT53, ZNF165, ZSCAN7, LD65	zinc finger protein 165	NM_003447, hCT22607.3	206683_at	NP_003438.1, EAX03131.1
GeneID:100129195	LOC100129195	6	28,058,336	28,105,071	46,735	-	4	1_A375_pNL7_minus_lncRNA::1::4709, 1_A375_pNL7_minus_lncRNA::1::4710, 2_A375_pNL97_plus_lncRNA::1::6766, 2_A375_pNL97_plus_lncRNA::1::6767	56367, -4625, 12655, -4529	downstream, upstream, in gene, upstream	1	1	15	16	3	1_A375_pNL7_minus_lncRNA::1	19	Gene LOC100129195	FLJ99327	hypothetical LOC100129195	XR_112871, XR_108694, XR_113860		
GeneID:80345	ZSCAN16	6	28,092,367	28,097,857	5,470	+	1	2_A375_pNL97_plus_lncRNA::1::6766	29	in gene	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZSCAN16	ZSCAN16, ZNF392, ZNF435, FLJ22191, dJ265C24.3	zinc finger and SCAN domain containing 16	NM_025231, hCT1643884.2	219676_at	NP_079507.1, EAX03134.1
GeneID:7745	ZNF192	6	28,109,716	28,125,236	15,520	+	2	1_A375_pNL7_minus_lncRNA::1::4710, 2_A375_pNL97_plus_lncRNA::1::6767	-20, -116	upstream, upstream	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ZNF192	ZNF192, LD5-1, ZKSCAN8	zinc finger protein 192	NM_006298, hCT22606.3, hCT2281900.0	206579_at	NP_006289.2, EAX03135.1, EAX03136.1
GeneID:64288	ZNF323	6	28,292,514	28,324,048	31,534	-	1	2_A375_pNL97_plus_lncRNA::1::6768	272	in gene	0	1	6	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene ZNF323	dJ874C20.2, ZNF323, FLJ23407, ZNF310P, ZNF20-Lp	zinc finger protein 323	NM_145909, NM_001135215, NM_001135216, NM_030899, NR_024164, NR_024165, hCT1808764.3, hCT1808772.3, hCT1954682.1, hCT2350558.0, hCT2350559.0	222016_s_at	NP_665916.1, NP_001128687.1, NP_001128688.1, NP_112161.3, EAX03152.1, EAX03153.1, EAX03154.1, EAX03155.1, EAX03156.1
GeneID:80317	ZKSCAN3	6	28,317,691	28,334,524	16,833	+	1	2_A375_pNL97_plus_lncRNA::1::6768	6085	in gene	0	1	6	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene ZKSCAN3	FLJ33906, ZNF306, ZFP306, ZKSCAN3, ZF47, KIAA0426, ZSCAN13, ZNF309, Zfp47, dJ874C20.1	zinc finger with KRAB and SCAN domains 3	NM_024493, hCT22609.3, hCT2358727.0	1562303_at, 1562305_x_at, 211773_s_at	NP_077819.2, EAX03158.1, EAX03157.1
GeneID:114821	SCAND3	6	28,539,407	28,555,112	15,705	-	1	2_A375_pNL97_plus_lncRNA::1::6769	72	in gene	0	1	10	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SCAND3	ZNF452, MGC131782, ZNF305P2, FLJ31087, DKFZp434N092, MGC133311, SCAND3, ZFP38-L, KIAA1925, MGC133310, dJ1186N24.3	SCAN domain containing 3	NM_052923, hCT2282036.1	244758_at	NP_443155.1, EAX03170.1
GeneID:401242	LOC401242	6	28,827,402	28,831,454	4,052	-	1	2_A375_pNL97_plus_lncRNA::1::6771	-2894	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC401242		hypothetical LOC401242	NR_033379		
GeneID:414777	HCG18	6	30,255,174	30,294,927	39,753	-	1	2_A375_pNL97_plus_lncRNA::1::6772	-129	upstream	0	1	8	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene HCG18	FLJ31095, FLJ31598, FLJ25550, HCG18	HLA complex group 18	NR_024052, NR_024053	225577_at, 225584_at	
GeneID:56658	TRIM39	6	30,294,621	30,311,506	16,885	+	1	2_A375_pNL97_plus_lncRNA::1::6772	435	in gene	0	1	8	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TRIM39	RNF23, TFP, MGC32984, TRIM39, TRIM39B	tripartite motif containing 39	NM_021253, NM_172016, hCT14881.4, hCT2291559.1, hCT2291560.1, hCT2291561.1	222732_at	NP_067076.2, NP_742013.1, EAX03283.1, EAX03284.1, EAX03285.1, EAX03286.1
GeneID:2794	GNL1	6	30,509,154	30,525,371	16,217	-	1	2_A375_pNL97_plus_lncRNA::1::6774	1115	in gene	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene GNL1	HSR1, GNL1, DKFZp547E128, FLJ37752, DKFZp547E038	guanine nucleotide binding protein-like 1	NM_005275, hCT17139.3, hCT2294079.0	203307_at, 233544_at	NP_005266.2, EAX03295.1, EAX03294.1
GeneID:80742	PRR3	6	30,524,486	30,532,473	7,987	+	1	2_A375_pNL97_plus_lncRNA::1::6774	-230	upstream	0	1	13	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PRR3	PRR3, CAT56, MGC161735, MGC161733	proline rich 3	NM_025263, NM_001077497, hCT17143.3, hCT2291570.0	204795_at	NP_079539.2, NP_001070965.1, EAX03297.1, EAX03298.1
GeneID:8449	DHX16	6	30,620,896	30,640,830	19,934	-	2	1_A375_pNL7_minus_lncRNA::1::4713, 2_A375_pNL97_plus_lncRNA::1::6775	-98, -2	upstream, upstream	1	1	32	30	1	1_A375_pNL7_minus_lncRNA::1	32	Gene DHX16	Prp2, DBP2, PRPF2, DDX16, DHX16, PRP8, PRO2014	DEAH (Asp-Glu-Ala-His) box polypeptide 16	NM_003587, NM_001164239, hCT2294069.1, hCT2294072.1, hCT2350275.0, hCT2350276.0, hCT17136.4, hCT1808903.3	203694_s_at	NP_003578.2, NP_001157711.1, EAX03312.1, EAX03314.1, EAX03315.1, EAX03317.1, EAX03313.1, EAX03316.1
GeneID:170954	KIAA1949	6	30,644,166	30,655,672	11,506	-	2	1_A375_pNL7_minus_lncRNA::1::4713, 2_A375_pNL97_plus_lncRNA::1::6775	14744, 14840	downstream, downstream	1	1	32	30	1	1_A375_pNL7_minus_lncRNA::1	32	Gene KIAA1949	HKMT1098, KIAA1949	KIAA1949	NM_001134870, NM_133471	224927_at	NP_001128342.1, NP_597728.1
GeneID:780	DDR1	6	30,851,861	30,867,933	16,072	+	1	2_A375_pNL97_plus_lncRNA::1::6776	23947	downstream	0	1	17	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene DDR1	RTK6, NTRK4, PTK3, EDDR1, CD167, PTK3A, DDR1, CAK, NEP, DDR, TRKE, MCK10	discoidin domain receptor tyrosine kinase 1	NM_013993, NM_013994, NM_001954, hCT2291593.0, hCT2291595.0, hCT2291600.0, hCT2291601.0, hCT2291605.0, hCT2291606.0, hCT2291609.0, hCT2358802.0, hCT17131.3, hCT1954730.1, hCT1954731.1, hCT1962052.1	1007_s_at, 207169_x_at, 208779_x_at, 210749_x_at	NP_054699.2, NP_054700.2, NP_001945.3, EAX03335.1, EAX03337.1, EAX03340.1, EAX03336.1, EAX03338.1, EAX03339.1, EAX03341.1, EAX03342.1, EAX03343.1, EAX03344.1, EAX03346.1, EAX03345.1
GeneID:2968	GTF2H4	6	30,875,977	30,881,880	5,903	+	2	2_A375_pNL97_plus_lncRNA::1::6776, 2_A375_pNL97_plus_lncRNA::1::6777	-169, 6295	upstream, downstream	0	1	14	18.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene GTF2H4	GTF2H4, TFIIH, TFB2	general transcription factor IIH, polypeptide 4, 52kDa	NM_001517, hCT17133.3	203577_at	NP_001508.1, EAX03347.1
GeneID:57176	VARS2	6	30,881,982	30,894,236	12,254	+	2	2_A375_pNL97_plus_lncRNA::1::6776, 2_A375_pNL97_plus_lncRNA::1::6777	-6174, 290	upstream, in gene	0	1	14	18.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene VARS2	VARS2L, MGC142165, VARS2, VARSL, MGC138259	valyl-tRNA synthetase 2, mitochondrial (putative)	NM_020442, NM_001167733, NM_001167734, hCT2291616.0, hCT1827780.2	226200_at	NP_065175.4, NP_001161205.1, NP_001161206.1, EAX03348.1, EAX03349.1
GeneID:7919	BAT1	6	31,497,996	31,510,225	12,229	-	2	1_A375_pNL7_minus_lncRNA::1::4715, 2_A375_pNL97_plus_lncRNA::1::6779	497, 113	in gene, in gene	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene BAT1	DDX39B, D6S81E, BAT1, UAP56	HLA-B associated transcript 1	NM_080598, NM_004640	200041_s_at, 212384_at	NP_542165.1, NP_004631.1
GeneID:692233	SNORD117	6	31,504,151	31,504,226	75	-	2	1_A375_pNL7_minus_lncRNA::1::4715, 2_A375_pNL97_plus_lncRNA::1::6779	-5502, -5886	upstream, upstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SNORD117	SNORD117, U83	small nucleolar RNA, C/D box 117	NR_003140		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:692199	SNORD84	6	31,508,878	31,508,955	77	-	2	1_A375_pNL7_minus_lncRNA::1::4715, 2_A375_pNL97_plus_lncRNA::1::6779	-773, -1157	upstream, upstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SNORD84	SNORD84, U84	small nucleolar RNA, C/D box 84	NR_003065		
GeneID:534	ATP6V1G2	6	31,512,239	31,514,627	2,388	-	2	1_A375_pNL7_minus_lncRNA::1::4715, 2_A375_pNL97_plus_lncRNA::1::6779	4899, 4515	downstream, downstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene ATP6V1G2	VMA10, NG38, ATP6G, ATP6G2, ATP6V1G2	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2	NM_130463, NM_138282	214762_at	NP_569730.1, NP_612139.1
GeneID:4795	NFKBIL1	6	31,514,628	31,526,606	11,978	+	2	1_A375_pNL7_minus_lncRNA::1::4715, 2_A375_pNL97_plus_lncRNA::1::6779	-4900, -4516	upstream, upstream	1	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene NFKBIL1	NFKBIL1, LST1, IKBL, NFKBIL	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	NM_005007, NM_001144961, NM_001144962, NM_001144963, hCT2356644.0, hCT34967.2, hCT1952762.0, hCT1952764.0, hCT1952765.0	209973_at	NP_004998.3, NP_001138433.1, NP_001138434.1, NP_001138435.1, EAX03420.1, EAX03421.1, EAX03417.1, EAX03418.1, EAX03419.1
GeneID:55937	APOM	6	31,623,671	31,625,987	2,316	+	1	2_A375_pNL97_plus_lncRNA::1::6780	9945	downstream	0	1	8	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene APOM	NG20, APOM, G3a, MGC22400, HSPC336	apolipoprotein M	NM_019101, hCT34975.2, hCT1953419.0, hCT1953420.1, hCT1953421.1	205682_x_at, 214910_s_at	NP_061974.2, EAX03463.1, EAX03461.1, EAX03462.1, EAX03464.1
GeneID:57827	C6orf47	6	31,626,075	31,628,549	2,474	-	1	2_A375_pNL97_plus_lncRNA::1::6780	-5067	upstream	0	1	8	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene C6orf47	G4, D6S53E, C6orf47, NG34	chromosome 6 open reading frame 47	NM_021184, hCT2292508.1	204968_at	NP_067007.3, EAX03465.1
GeneID:7916	BAT4	6	31,629,862	31,633,163	3,301	-	1	2_A375_pNL97_plus_lncRNA::1::6780	-453	upstream	0	1	8	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene BAT4	GPANK1, GPATCH10, D6S54E, G5, ANKRD59, BAT4	HLA-B associated transcript 4	NM_033177, hCT2292507.0, hCT2356667.0, hCT35007.2, hCT1953438.1, hCT1953439.0	225472_at, 225476_at	NP_149417.1, EAX03470.1, EAX03467.1, EAX03468.1, EAX03469.1, EAX03471.1
GeneID:1460	CSNK2B	6	31,633,657	31,637,843	4,186	+	1	2_A375_pNL97_plus_lncRNA::1::6780	-41	upstream	0	1	8	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene CSNK2B	MGC138224, CSK2B, CSNK2B, CK2N, CK2B, MGC138222, G5A	casein kinase 2, beta polypeptide	NM_001320, hCT35010.2, hCT1953442.1, hCT1953443.0, hCT1953444.0	201390_s_at, 231777_at	NP_001311.3, EAX03473.1, EAX03472.1, EAX03474.1, EAX03475.1
GeneID:58496	LY6G5B	6	31,638,728	31,640,227	1,499	+	1	2_A375_pNL97_plus_lncRNA::1::6780	-5112	upstream	0	1	8	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LY6G5B	G5b, C6orf19, LY6G5B	lymphocyte antigen 6 complex, locus G5B	NM_021221, hCT35002.3, hCT1953437.1		NP_067044.2, EAX03477.1, EAX03476.1
GeneID:23564	DDAH2	6	31,694,817	31,698,039	3,222	-	1	2_A375_pNL97_plus_lncRNA::1::6781	-9545	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene DDAH2	G6a, DDAH, DDAHII, NG30, DDAH2	dimethylarginine dimethylaminohydrolase 2	NM_013974, hCT2344565.0, hCT2356739.0, hCT2356740.0	202262_x_at, 214909_s_at, 215537_x_at	NP_039268.1, EAX03500.1, EAX03501.1, EAX03502.1
GeneID:1192	CLIC1	6	31,698,358	31,704,341	5,983	-	1	2_A375_pNL97_plus_lncRNA::1::6781	-3243	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene CLIC1	CLIC1, G6, NCC27	chloride intracellular channel 1	NM_001288, hCT2292474.1, hCT2356729.0, hCT2356730.0	208659_at	NP_001279.2, EAX03504.1, EAX03503.1, EAX03505.1
GeneID:4439	MSH5	6	31,707,725	31,730,455	22,730	+	1	2_A375_pNL97_plus_lncRNA::1::6781	-141	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MSH5	MUTSH5, NG23, DKFZp434C1615, MSH5, G7, MGC2939	mutS homolog 5 (E. coli)	NM_002441, NM_172166, NM_025259, NM_172165, hCT2285764.0, hCT2285765.0, hCT2285767.0, hCT2285769.0, hCT2285771.0, hCT2285773.0, hCT2285774.0, hCT2285776.0, hCT2285778.0, hCT2285780.0, hCT2285782.0, hCT2356647.0, hCT2356648.0, hCT2356649.0, hCT2356650.0	210410_s_at	NP_002432.1, NP_751898.1, NP_751897.1, NP_079535.4, EAX03514.1, EAX03519.1, EAX03506.1, EAX03507.1, EAX03508.1, EAX03509.1, EAX03510.1, EAX03511.1, EAX03512.1, EAX03513.1, EAX03515.1, EAX03516.1, EAX03517.1, EAX03518.1, EAX03520.1
GeneID:4758	NEU1	6	31,826,829	31,830,709	3,880	-	1	2_A375_pNL97_plus_lncRNA::1::6782	-43	upstream	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene NEU1	SIAL1, NEU1, NANH, NEU, FLJ93471	sialidase 1 (lysosomal sialidase)	NM_000434, hCT34977.3, hCT1953422.1	208926_at	NP_000425.1, EAX03536.1, EAX03537.1
GeneID:80736	SLC44A4	6	31,830,969	31,846,823	15,854	-	1	2_A375_pNL97_plus_lncRNA::1::6782	16071	downstream	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene SLC44A4	SLC44A4, C6orf29, FLJ14491, CTL4, NG22	solute carrier family 44, member 4	NM_025257, NM_001178044, NM_001178045, hCT35012.3, hCT1953445.1	1555203_s_at, 205597_at	NP_079533.2, NP_001171515.1, NP_001171516.1, EAX03538.1, EAX03539.1
GeneID:6499	SKIV2L	6	31,926,581	31,937,532	10,951	+	2	1_A375_pNL7_minus_lncRNA::1::4716, 2_A375_pNL97_plus_lncRNA::1::6783	13483, 13285	downstream, downstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SKIV2L	SKI2, SKIV2, DDX13, SKI2W, 170A, HLP, SKIV2L	superkiller viralicidic activity 2-like (S. cerevisiae)	NM_006929, hCT2285818.0, hCT2285819.0, hCT34983.3, hCT1953428.1	203727_at	NP_008860.4, EAX03555.1, EAX03554.1, EAX03556.1, EAX03557.1
GeneID:1797	DOM3Z	6	31,937,588	31,940,032	2,444	-	2	1_A375_pNL7_minus_lncRNA::1::4716, 2_A375_pNL97_plus_lncRNA::1::6783	-32, 166	upstream, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene DOM3Z	DOM3Z, DOM3L, NG6, RAI1	dom-3 homolog Z (C. elegans)	NM_005510, hCT2292437.0, hCT2292438.0, hCT2356795.0, hCT2356796.0, hCT2356797.0, hCT34991.3, hCT1955524.1, hCT1955525.1	204522_at, 215982_s_at, 35157_at	NP_005501.2, EAX03559.1, EAX03560.1, EAX03561.1, EAX03562.1, EAX03563.1, EAX03558.1, EAX03564.1, EAX03565.1
GeneID:8859	STK19	6	31,938,952	31,949,223	10,271	+	2	1_A375_pNL7_minus_lncRNA::1::4716, 2_A375_pNL97_plus_lncRNA::1::6783	1112, 914	in gene, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene STK19	RP1, G11, STK19, D6S60E, HLA-RP1, MGC117388, D6S60	serine/threonine kinase 19	NM_004197, NM_032454, NR_026717, hCT1953432.1, hCT1953433.1, hCT1953434.1	204090_at, 36019_at	NP_004188.1, NP_115830.1, EAX03566.1, EAX03567.1, EAX03568.1
GeneID:720	C4A	6	31,949,834	31,970,457	20,623	+	2	1_A375_pNL7_minus_lncRNA::1::4716, 2_A375_pNL97_plus_lncRNA::1::6783	-9770, -9968	upstream, upstream	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C4A	C4S, C4A4, C4A, CPAMD2, C4A6, RG, C4A2, MGC164979, C4, C4A3, CO4	complement component 4A (Rodgers blood group)	NM_007293	208451_s_at, 214428_x_at	NP_009224.2
GeneID:7148	TNXB	6	32,008,932	32,077,153	68,221	-	1	2_A375_pNL97_plus_lncRNA::1::6784	3777	in gene	0	1	7	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TNXB	TNXB1, TNXBS, TNXB2, TENX, HXBL, XB, TNXB, TNX, XBS	tenascin XB	NM_019105, NM_032470, hCT2285740.0, hCT2285742.0, hCT2285744.0, hCT2285746.0, hCT2285748.0, hCT2285749.0, hCT2285751.0, hCT2285753.0	1565242_at, 206093_x_at, 213451_x_at, 216333_x_at, 216654_at, 217413_s_at	NP_061978.6, NP_115859.2, EAX03572.1, EAX03573.1, EAX03576.1, EAX03577.1, EAX03574.1, EAX03575.1, EAX03578.1, EAX03579.1
GeneID:1388	ATF6B	6	32,083,045	32,096,030	12,985	-	3	1_A375_pNL7_minus_lncRNA::1::4717, 2_A375_pNL97_plus_lncRNA::1::6784, 2_A375_pNL97_plus_lncRNA::1::6785	-2242, 22654, -2178	upstream, downstream, upstream	1	1	15.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	28	Gene ATF6B	CREB-RP, FLJ10066, G13, CREBL1, ATF6B	activating transcription factor 6 beta	NM_004381, NM_001136153, hCT2285729.0, hCT2285733.0, hCT2285735.0, hCT34989.2, hCT1953431.0	211611_s_at	NP_004372.3, NP_001129625.1, EAX03582.1, EAX03583.1, EAX03584.1, EAX03585.1, EAX03581.1
GeneID:63943	FKBPL	6	32,096,484	32,098,067	1,583	-	2	1_A375_pNL7_minus_lncRNA::1::4717, 2_A375_pNL97_plus_lncRNA::1::6785	-205, -141	upstream, upstream	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene FKBPL	FKBPL, DIR1, WISP39, NG7	FK506 binding protein like	NM_022110, hCT2285724.0, hCT1643244.3	219187_at	NP_071393.2, EAX03586.1, EAX03587.1
GeneID:3112	HLA-DOB	6	32,780,540	32,784,825	4,285	-	1	2_A375_pNL97_plus_lncRNA::1::6786	-2823	upstream	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene HLA-DOB	DOB, HLA-DOB, FLJ57033	major histocompatibility complex, class II, DO beta	NM_002120, hCT2285805.1, hCT2285808.1, hCT2285810.0, hCT2343625.0	1554954_a_at, 205671_s_at	NP_002111.1, EAX03640.1, EAX03638.1, EAX03639.1, EAX03641.1
GeneID:6891	TAP2	6	32,789,610	32,806,547	16,937	-	1	2_A375_pNL97_plus_lncRNA::1::6786	18899	downstream	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene TAP2	APT2, PSF2, RING11, ABC18, ABCB3, D6S217E, TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	NM_000544, NM_018833, hCT2285803.0, hCT2285806.0	204769_s_at, 204770_at, 208428_at, 225973_at	NP_000535.3, NP_061313.2, EAX03642.1, EAX03643.1
GeneID:6046	BRD2	6	32,936,437	32,949,282	12,845	+	1	1_A375_pNL7_minus_lncRNA::1::4718	1163	in gene	1	0	13	6	1	1_A375_pNL7_minus_lncRNA::1	13	Gene BRD2	RING3, FLJ31942, NAT, FSRG1, D6S113E, RNF3, FSH, BRD2, DKFZp686N0336, KIAA9001	bromodomain containing 2	NM_005104, NM_001113182, hCT2283115.0, hCT2283117.0, hCT2356784.0, hCT2356785.0, hCT5872.3	208685_x_at, 208686_s_at, 214911_s_at	NP_005095.1, NP_001106653.1, EAX03662.1, EAX03663.1, EAX03664.1, EAX03665.1, EAX03666.1
GeneID:6257	RXRB	6	33,161,365	33,168,432	7,067	-	1	1_A375_pNL7_minus_lncRNA::1::4719	-7664	upstream	1	0	25	14	1	1_A375_pNL7_minus_lncRNA::1	25	Gene RXRB	MGC1831, H-2RIIBP, RCoR-1, RXRB, NR2B2, DAUDI6	retinoid X receptor, beta	NM_021976, hCT2347458.1	209148_at, 215098_at, 215099_s_at	NP_068811.1, EAX03679.1
GeneID:7922	SLC39A7	6	33,168,603	33,172,214	3,611	+	1	1_A375_pNL7_minus_lncRNA::1::4719	7493	downstream	1	0	25	14	1	1_A375_pNL7_minus_lncRNA::1	25	Gene SLC39A7	ZIP7, D6S115E, KE4, D6S2244E, H2-KE4, RING5, HKE4, SLC39A7	solute carrier family 39 (zinc transporter), member 7	NM_006979, NM_001077516, hCT2347483.1, hCT2349265.0	202667_s_at	NP_008910.2, NP_001070984.1, EAX03680.1, EAX03681.1
GeneID:7923	HSD17B8	6	33,172,419	33,174,607	2,188	+	1	1_A375_pNL7_minus_lncRNA::1::4719	3677	downstream	1	0	25	14	1	1_A375_pNL7_minus_lncRNA::1	25	Gene HSD17B8	FABG, FABGL, dJ1033B10.9, RING2, SDR30C1, D6S2245E, HKE6, HSD17B8, KE6, H2-KE6	hydroxysteroid (17-beta) dehydrogenase 8	NM_014234, hCT2344275.0	213540_at	NP_055049.1, EAX03682.1
GeneID:407002	MIR219-1	6	33,175,612	33,175,721	109	+	1	1_A375_pNL7_minus_lncRNA::1::4719	484	downstream	1	0	25	14	1	1_A375_pNL7_minus_lncRNA::1	25	Gene MIR219-1	MIR219-1, MRI219-1, mir-219, MIRN219-1	microRNA 219-1	NR_029633		
GeneID:6015	RING1	6	33,176,286	33,180,499	4,213	+	1	1_A375_pNL7_minus_lncRNA::1::4719	-190	upstream	1	0	25	14	1	1_A375_pNL7_minus_lncRNA::1	25	Gene RING1	RNF1, RING1, RING1A	ring finger protein 1	NM_002931, hCT2264167.0, hCT6564.4	205371_s_at, 35665_at	NP_002922.2, EAX03683.1, EAX03684.1
GeneID:6293	VPS52	6	33,218,049	33,239,662	21,613	-	3	1_A375_pNL7_minus_lncRNA::1::4720, 1_A375_pNL7_minus_lncRNA::1::4721, 2_A375_pNL97_plus_lncRNA::1::6787	21038, -242, -210	in gene, upstream, upstream	1	1	16	12	2	1_A375_pNL7_minus_lncRNA::1	17	Gene VPS52	SAC2, DKFZp547I194, ARE1, VPS52, RP5-1033B10, SACM2L, dJ1033B10.5	vacuolar protein sorting 52 homolog (S. cerevisiae)	NM_022553, hCT2286068.0, hCT2286069.0, hCT2286071.0, hCT2286072.0, hCT2286073.0, hCT2286075.0, hCT2356779.0, hCT2356780.0	214585_s_at	NP_072047.4, EAX03687.1, EAX03686.1, EAX03688.1, EAX03691.1, EAX03692.1, EAX03689.1, EAX03690.1, EAX03693.1
GeneID:6222	RPS18	6	33,239,852	33,244,281	4,429	+	2	1_A375_pNL7_minus_lncRNA::1::4721, 2_A375_pNL97_plus_lncRNA::1::6787	52, 20	in gene, in gene	1	1	17	17	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RPS18	KE3, D6S218E, MGC126837, KE-3, HKE3, MGC126835, S18, MGC117351, RPS18	ribosomal protein S18	NM_022551, hCT1640294.3, hCT1963723.1, hCT1963724.0, hCT1963725.1, hCT1963726.0, hCT1963727.0	201049_s_at	NP_072045.1, EAX03695.1, EAX03694.1, EAX03696.1, EAX03698.1, EAX03699.1, EAX03697.1
GeneID:8705	B3GALT4	6	33,244,917	33,246,602	1,685	+	2	1_A375_pNL7_minus_lncRNA::1::4721, 2_A375_pNL97_plus_lncRNA::1::6787	-5013, -5045	upstream, upstream	1	1	17	17	1	1_A375_pNL7_minus_lncRNA::1	17	Gene B3GALT4	BETA3GALT4, GALT4, B3GALT4, GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	NM_003782, hCT6562.3	210205_at	NP_003773.1, EAX03700.1
GeneID:9277	WDR46	6	33,246,880	33,257,304	10,424	-	4	1_A375_pNL7_minus_lncRNA::1::4721, 1_A375_pNL7_minus_lncRNA::1::4722, 2_A375_pNL97_plus_lncRNA::1::6787, 2_A375_pNL97_plus_lncRNA::1::6788	17400, -9864, 17432, -9960	downstream, upstream, downstream, upstream	1	1	20	16	2	1_A375_pNL7_minus_lncRNA::1	23	Gene WDR46	WDR46, BING4, C6orf11, FP221	WD repeat domain 46	NM_005452, NM_001164267, hCT1966763.1, hCT2286135.0, hCT6575.3, hCT1962875.1	209196_at	NP_005443.3, NP_001157739.1, EAX03701.1, EAX03702.1, EAX03703.1, EAX03704.1
GeneID:10471	PFDN6	6	33,257,378	33,258,711	1,333	+	2	1_A375_pNL7_minus_lncRNA::1::4722, 2_A375_pNL97_plus_lncRNA::1::6788	9790, 9886	downstream, downstream	1	1	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene PFDN6	PFD6, H2-KE2, KE-2, MGC70744, HKE2, PFDN6	prefoldin subunit 6	NM_014260, NM_001185181, hCT2264130.0, hCT6578.3, hCT1962876.1	222019_at, 222029_x_at, 233588_x_at, 242046_at	NP_055075.1, NP_001172110.1, EAX03705.1, EAX03706.1, EAX03707.1
GeneID:5863	RGL2	6	33,259,431	33,267,176	7,745	-	2	1_A375_pNL7_minus_lncRNA::1::4722, 2_A375_pNL97_plus_lncRNA::1::6788	8, -88	in gene, upstream	1	1	23	15	1	1_A375_pNL7_minus_lncRNA::1	23	Gene RGL2	RAB2L, KE1.5, HKE1.5, RGL2	ral guanine nucleotide dissociation stimulator-like 2	NR_026387, NM_004761, hCT2286129.0, hCT2286130.0, hCT2286131.0, hCT2356862.0, hCT2356863.0, hCT2356864.0, hCT6571.3	209110_s_at	NP_004752.1, EAX03713.1, EAX03708.1, EAX03709.1, EAX03710.1, EAX03711.1, EAX03712.1, EAX03714.1
GeneID:6892	TAPBP	6	33,267,471	33,282,164	14,693	-	5	1_A375_pNL7_minus_lncRNA::1::4722, 1_A375_pNL7_minus_lncRNA::1::4723, 2_A375_pNL97_plus_lncRNA::1::6788, 2_A375_pNL97_plus_lncRNA::1::6789, 2_A375_pNL97_plus_lncRNA::1::6790	14996, -3468, 14900, -3420, -9100	downstream, upstream, downstream, upstream, upstream	1	1	20	20.33	3	1_A375_pNL7_minus_lncRNA::1	26	Gene TAPBP	TPSN, TPN, NGS17, TAPA, TAPBP	TAP binding protein (tapasin)	NM_003190, NM_172208, NM_172209, hCT2286123.0, hCT2286125.0, hCT2286126.0, hCT6570.4, hCT1962873.1, hCT1962874.1	1555565_s_at, 208829_at, 210294_at	NP_003181.3, NP_757345.2, NP_757346.2, EAX03715.1, EAX03716.1, EAX03719.1, EAX03717.1, EAX03718.1, EAX03720.1
GeneID:9278	ZBTB22	6	33,282,182	33,285,719	3,537	-	3	1_A375_pNL7_minus_lncRNA::1::4723, 2_A375_pNL97_plus_lncRNA::1::6789, 2_A375_pNL97_plus_lncRNA::1::6790	87, 135, -5545	in gene, in gene, upstream	1	1	18.5	23	2	1_A375_pNL7_minus_lncRNA::1	26	Gene ZBTB22	ZBTB22A, ZNF297, ZNF297A, BING1, ZBTB22, fruitless, fru	zinc finger and BTB domain containing 22	NM_005453, NM_001145338, hCT2286120.0	213081_at	NP_005444.4, NP_001138810.1, EAX03721.1
GeneID:1616	DAXX	6	33,286,335	33,290,793	4,458	-	3	1_A375_pNL7_minus_lncRNA::1::4723, 2_A375_pNL97_plus_lncRNA::1::6789, 2_A375_pNL97_plus_lncRNA::1::6790	5161, 5209, -471	downstream, downstream, upstream	1	1	18.5	23	2	1_A375_pNL7_minus_lncRNA::1	26	Gene DAXX	MGC126245, EAP1, BING2, DAP6, DAXX, MGC126246	death-domain associated protein	NR_024517, NM_001141970, NM_001141969, NM_001350, hCT1967013.1, hCT2356826.0, hCT6566.2	201763_s_at, 216038_x_at	NP_001135442.1, NP_001135441.1, NP_001341.1, EAX03722.1, EAX03723.1, EAX03724.1
GeneID:221496	LEMD2	6	33,738,990	33,756,906	17,916	-	1	1_A375_pNL7_minus_lncRNA::1::4724	-22	upstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene LEMD2	NET25, LEMD2, dJ482C21.1	LEM domain containing 2	NM_001143944, NM_181336, hCT2356858.0, hCT32527.3	224980_at	NP_001137416.1, NP_851853.1, EAX03750.1, EAX03751.1
GeneID:4295	MLN	6	33,762,449	33,771,793	9,344	-	3	1_A375_pNL7_minus_lncRNA::1::4724, 1_A375_pNL7_minus_lncRNA::1::4725, 2_A375_pNL97_plus_lncRNA::1::6791	14865, -8783, -8783	downstream, upstream, upstream	1	1	17.5	17.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene MLN	MGC138519, MLN	motilin	NM_001040109, NM_002418, NM_001184698, hCT32524.2, hCT1963737.0	207473_at	NP_001035198.1, NP_002409.1, NP_001171627.1, EAX03752.1, EAX03753.1
GeneID:2914	GRM4	6	33,989,628	34,101,443	111,815	-	3	1_A375_pNL7_minus_lncRNA::1::4726, 2_A375_pNL97_plus_lncRNA::1::6792, 2_A375_pNL97_plus_lncRNA::1::6793	915, 18163, 931	in gene, in gene, in gene	1	1	14.5	22.5	2	2_A375_pNL97_plus_lncRNA::1	31	Gene GRM4	GPRC1D, GRM4, MGLUR4, MGC177594, mGlu4	glutamate receptor, metabotropic 4	NM_000841, hCT2286086.0, hCT32525.3	210234_at	NP_000832.1, EAX03759.1, EAX03760.1
GeneID:6882	TAF11	6	34,845,555	34,855,819	10,264	-	1	2_A375_pNL97_plus_lncRNA::1::6794	11	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TAF11	PRO2134, TAFII28, TAF11, MGC:15243, TAF2I	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	NM_005643	1558135_at, 1558136_s_at, 209356_at	NP_005634.1
GeneID:23294	ANKS1A	6	34,857,038	35,059,190	202,152	+	1	2_A375_pNL97_plus_lncRNA::1::6794	-1230	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ANKS1A	KIAA0229, MGC42354, ANKS1A, ANKS1	ankyrin repeat and sterile alpha motif domain containing 1A	NM_015245, hCT2282657.0, hCT2282659.0, hCT2282660.0, hCT2356731.0, hCT7113.3	212747_at	NP_056060.2, EAX03801.1, EAX03800.1, EAX03802.1, EAX03803.1, EAX03804.1
GeneID:2178	FANCE	6	35,420,138	35,434,881	14,743	+	2	1_A375_pNL7_minus_lncRNA::1::4727, 2_A375_pNL97_plus_lncRNA::1::6795	15974, 16028	downstream, downstream	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene FANCE	FAE, FACE, FANCE	Fanconi anemia, complementation group E	NM_021922, hCT1643777.3	220255_at	NP_068741.1, EAX03830.1
GeneID:4736	RPL10A	6	35,436,178	35,438,558	2,380	+	2	1_A375_pNL7_minus_lncRNA::1::4727, 2_A375_pNL97_plus_lncRNA::1::6795	-66, -12	upstream, upstream	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene RPL10A	Csa-19, RPL10A, NEDD6, L10A	ribosomal protein L10a	NM_007104, hCT6712.5, hCT1963313.2, hCT1963314.1, hCT1963315.2	200036_s_at, 229563_s_at	NP_009035.3, EAX03831.1, EAX03832.1, EAX03833.1, EAX03834.1
GeneID:7005	TEAD3	6	35,441,374	35,464,861	23,487	-	2	1_A375_pNL7_minus_lncRNA::1::4727, 2_A375_pNL97_plus_lncRNA::1::6795	28749, 28695	downstream, downstream	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TEAD3	ETFR-1, TEAD3, TEAD5, TEF5, DTEF-1, TEF-5	TEA domain family member 3	NM_003214, hCT2285017.0, hCT2285018.0, hCT2356843.0, hCT6717.3	209454_s_at	NP_003205.2, EAX03835.1, EAX03836.1, EAX03837.1, EAX03838.1
GeneID:1208	CLPS	6	35,762,760	35,765,102	2,342	-	2	1_A375_pNL7_minus_lncRNA::1::4728, 2_A375_pNL97_plus_lncRNA::1::6796	-8050, -8082	upstream, upstream	1	1	22	17	1	1_A375_pNL7_minus_lncRNA::1	22	Gene CLPS	CLPS		NM_001832, hCT6805.3, hCT1962846.1	206131_at	NP_001823.1, EAX03850.1, EAX03851.1
GeneID:222662	LHFPL5	6	35,773,071	35,791,852	18,781	+	2	1_A375_pNL7_minus_lncRNA::1::4728, 2_A375_pNL97_plus_lncRNA::1::6796	81, 113	in gene, in gene	1	1	22	17	1	1_A375_pNL7_minus_lncRNA::1	22	Gene LHFPL5	LHFPL5, TMHS, DFNB67, MGC33835, dJ510O8.8	lipoma HMGIC fusion partner-like 5	NM_182548, hCT2283918.1	1555043_at	NP_872354.1, EAX03852.1
GeneID:116369	SLC26A8	6	35,911,291	35,992,413	81,122	-	2	1_A375_pNL7_minus_lncRNA::1::4729, 2_A375_pNL97_plus_lncRNA::1::6797	-2883, -2931	upstream, upstream	1	1	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SLC26A8	TAT1, FLJ32714, SLC26A8	solute carrier family 26, member 8	NM_001193476, NM_052961, NM_138718, hCT2284991.2, hCT2350355.0, hCT2350356.0, hCT2356877.0, hCT2356878.0	237340_at	NP_001180405.1, NP_443193.1, NP_619732.2, EAX03862.1, EAX03863.1, EAX03866.1, EAX03864.1, EAX03865.1
GeneID:1432	MAPK14	6	35,995,454	36,079,013	83,559	+	2	1_A375_pNL7_minus_lncRNA::1::4729, 2_A375_pNL97_plus_lncRNA::1::6797	-158, -110	upstream, upstream	1	1	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene MAPK14	EXIP, p38ALPHA, PRKM14, SAPK2A, CSBP1, p38, PRKM15, Mxi2, CSBP2, MAPK14, CSPB1, RK	mitogen-activated protein kinase 14	NM_139012, NM_139013, NM_139014, NM_001315, hCT2283924.0, hCT2283927.0, hCT2283928.0, hCT2283929.0, hCT2283931.0, hCT2356840.0, hCT1960854.1	202530_at, 210449_x_at, 211087_x_at, 211561_x_at	NP_620581.1, NP_620583.1, NP_620582.1, NP_001306.1, EAX03871.1, EAX03873.1, EAX03867.1, EAX03868.1, EAX03869.1, EAX03870.1, EAX03872.1
GeneID:1026	CDKN1A	6	36,646,459	36,655,109	8,650	+	2	1_A375_pNL7_minus_lncRNA::1::4730, 2_A375_pNL97_plus_lncRNA::1::6798	1909, 1941	in gene, in gene	1	1	22	17	1	1_A375_pNL7_minus_lncRNA::1	22	Gene CDKN1A	CDKN1A, MDA-6, P21, SDI1, CDKN1, WAF1, p21CIP1, CAP20, CIP1	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_078467, NM_000389, hCT6389.4, hCT1965598.1, hCT1965599.1, hCT1965600.1	1555186_at, 202284_s_at	NP_510867.1, NP_000380.1, EAX03904.1, EAX03905.1, EAX03906.1, EAX03907.1
GeneID:23787	MTCH1	6	36,935,917	36,953,949	18,032	-	1	2_A375_pNL97_plus_lncRNA::1::6799	29	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene MTCH1	MTCH1, CGI-64, MGC131998, PIG60, PSAP	mitochondrial carrier homolog 1 (C. elegans)	NM_014341, hCT2290205.0, hCT2290207.0, hCT2356782.0, hCT2356783.0, hCT6387.3, hCT1962844.1, hCT1962845.1	221619_s_at	NP_055156.1, EAX03928.1, EAX03926.1, EAX03927.1, EAX03930.1, EAX03931.1, EAX03925.1, EAX03929.1
GeneID:9025	RNF8	6	37,321,748	37,362,514	40,766	+	1	1_A375_pNL7_minus_lncRNA::1::4731	124	in gene	1	0	13	11	1	1_A375_pNL7_minus_lncRNA::1	13	Gene RNF8	KIAA0646, FLJ12013, RNF8	ring finger protein 8	NM_003958, NM_183078, hCT2289185.0, hCT23539.3, hCT2356807.0	203160_s_at, 203161_s_at	NP_003949.1, NP_898901.1, EAX03943.1, EAX03944.1, EAX03945.1
GeneID:266727	MDGA1	6	37,600,284	37,665,766	65,482	-	1	2_A375_pNL97_plus_lncRNA::1::6801	67462	downstream	0	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene MDGA1	DKFZp686K0262, MDGA1, MAMDC3, DKFZp686L0262, FLJ45018, GPIM	MAM domain containing glycosylphosphatidylinositol anchor 1	NM_153487, hCT2283271.1, hCT2283281.1, hCT1818036.3, hCT1818038.2, hCT1818039.1	232237_at, 236543_x_at, 242757_at	NP_705691.1, EAX03953.1, EAX03950.1, EAX03951.1, EAX03952.1, EAX03954.1
GeneID:60685	ZFAND3	6	37,787,307	38,122,400	335,093	+	2	1_A375_pNL7_minus_lncRNA::1::4733, 2_A375_pNL97_plus_lncRNA::1::6802	-139, -347	upstream, upstream	1	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ZFAND3	ZFAND3, FLJ17799, FLJ13222, TEX27	zinc finger, AN1-type domain 3	NM_021943, hCT2283021.0, hCT1951839.1	218020_s_at, 222493_s_at	NP_068762.1, EAX03955.1, EAX03956.1
GeneID:114781	BTBD9	6	38,136,227	38,607,924	471,697	-	2	2_A375_pNL97_plus_lncRNA::1::6803, 2_A375_pNL97_plus_lncRNA::1::6804	410226, 281972	in gene, in gene	0	1	11	23.5	2	2_A375_pNL97_plus_lncRNA::1	33	Gene BTBD9	MGC120520, MGC120519, BTBD9, MGC120517, FLJ32945, dJ322I12.1, KIAA1880	BTB (POZ) domain containing 9	NM_052893, NM_001099272, NM_152733, NM_001172418, hCT2344016.0, hCT2349263.0, hCT2349264.0	1553375_at, 229867_at, 234682_at, 235248_at	NP_443125.1, NP_001092742.1, NP_659946.2, NP_001165889.1, EAX03959.1, EAX03960.1, EAX03961.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:2739	GLO1	6	38,643,701	38,670,952	27,251	-	2	1_A375_pNL7_minus_lncRNA::1::4734, 2_A375_pNL97_plus_lncRNA::1::6805	8, -24	in gene, upstream	1	1	22	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene GLO1	GLYI, GLO1, GLOD1	glyoxalase I	NM_006708, hCT2282857.0, hCT23538.3	200681_at	NP_006699.2, EAX03964.1, EAX03965.1
GeneID:2740	GLP1R	6	39,016,557	39,055,520	38,963	+	1	2_A375_pNL97_plus_lncRNA::1::6806	39795	downstream	0	1	4	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene GLP1R	MGC138331, GLP1R	glucagon-like peptide 1 receptor	NM_002062, hCT2282514.0, hCT2282516.0, hCT2358871.0, hCT2358872.0, hCT2358873.0	208390_s_at, 208391_s_at, 208400_at, 208401_s_at, 211232_x_at	NP_002053.3, EAX03970.1, EAX03971.1, EAX03972.1, EAX03973.1, EAX03974.1
GeneID:8645	KCNK5	6	39,156,747	39,197,251	40,504	-	1	2_A375_pNL97_plus_lncRNA::1::6808	195	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene KCNK5	TASK-2, KCNK5, FLJ11035, TASK2, K2p5.1	potassium channel, subfamily K, member 5	NM_003740, hCT23540.3, hCT2358809.0	219615_s_at	NP_003731.1, EAX03979.1, EAX03980.1
GeneID:54209	TREM2	6	41,126,246	41,130,922	4,676	-	1	2_A375_pNL97_plus_lncRNA::1::6810	-3874	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TREM2	TREM-2, TREM2, Trem2a, Trem2b, Trem2c	triggering receptor expressed on myeloid cells 2	NM_018965, hCT1968189.1, hCT2358818.0, hCT24530.4	219725_at	NP_061838.1, EAX04033.1, EAX04032.1, EAX04034.1
GeneID:7942	TFEB	6	41,651,716	41,703,997	52,281	-	2	1_A375_pNL7_minus_lncRNA::1::4735, 2_A375_pNL97_plus_lncRNA::1::6811	557, 573	in gene, in gene	1	1	31	29	1	1_A375_pNL7_minus_lncRNA::1	31	Gene TFEB	TCFEB, BHLHE35, TFEB, ALPHATFEB	transcription factor EB	NM_007162, NM_001167827, hCT2283872.1, hCT2283873.1, hCT2283875.1, hCT24064.4	221866_at, 50221_at	NP_009093.1, NP_001161299.1, EAX04055.1, EAX04056.1, EAX04057.1, EAX04058.1
GeneID:5225	PGC	6	41,704,449	41,715,139	10,690	-	2	1_A375_pNL7_minus_lncRNA::1::4735, 2_A375_pNL97_plus_lncRNA::1::6811	11699, 11715	downstream, downstream	1	1	31	29	1	1_A375_pNL7_minus_lncRNA::1	31	Gene PGC	PEPC, PGII, FLJ99563, PGC	progastricsin (pepsinogen C)	NM_002630, NM_001166424, hCT24059.3	1555236_a_at, 205261_at	NP_002621.1, NP_001159896.1, EAX04059.1
GeneID:10817	FRS3	6	41,737,914	41,747,630	9,716	-	2	1_A375_pNL7_minus_lncRNA::1::4736, 2_A375_pNL97_plus_lncRNA::1::6812	-7618, -7602	upstream, upstream	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene FRS3	MGC17167, SNT-2, SNT2, FRS2beta, FRS3, FRS2B	fibroblast growth factor receptor substrate 3	NM_006653, hCT2284457.0	219907_at	NP_006644.1, EAX04060.1
GeneID:29964	PRICKLE4	6	41,748,500	41,755,110	6,610	+	2	1_A375_pNL7_minus_lncRNA::1::4736, 2_A375_pNL97_plus_lncRNA::1::6812	6748, 6732	downstream, downstream	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PRICKLE4	OEBT, MGC120396, OBTP, PRICKLE4, TOMM6, C6orf49	prickle homolog 4 (Drosophila)	NM_013397, hCT2283964.0, hCT2358841.0, hCT2358842.0, hCT24060.3	218233_s_at, 223516_s_at	NP_037529.3, EAX04064.1, EAX04061.1, EAX04062.1, EAX04063.1
GeneID:100188893	TOMM6	6	41,755,181	41,757,634	2,453	+	2	1_A375_pNL7_minus_lncRNA::1::4736, 2_A375_pNL97_plus_lncRNA::1::6812	67, 51	in gene, in gene	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene TOMM6	FLJ32622, OBTP, TOMM6, DKFZp761H221	translocase of outer mitochondrial membrane 6 homolog (yeast)	NM_001134493		NP_001127965.1
GeneID:25862	USP49	6	41,765,383	41,863,099	97,716	-	2	1_A375_pNL7_minus_lncRNA::1::4736, 2_A375_pNL97_plus_lncRNA::1::6812	107851, 107867	downstream, downstream	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene USP49	MGC20741, USP49	ubiquitin specific peptidase 49	NM_018561, hCT2344276.0	1564029_at, 243392_at	NP_061031.2, EAX04065.1
GeneID:9477	MED20	6	41,873,092	41,888,877	15,785	-	2	1_A375_pNL7_minus_lncRNA::1::4737, 2_A375_pNL97_plus_lncRNA::1::6813	-275, -211	upstream, upstream	1	1	39	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene MED20	MGC29869, TRFP, MED20, PRO0213, DKFZp586D2223	mediator complex subunit 20	NM_004275, hCT2284451.0, hCT2358717.0	206961_s_at, 212872_s_at	NP_004266.2, EAX04067.1, EAX04066.1
GeneID:705	BYSL	6	41,888,965	41,900,784	11,819	+	2	1_A375_pNL7_minus_lncRNA::1::4737, 2_A375_pNL97_plus_lncRNA::1::6813	167, 123	in gene, in gene	1	1	39	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene BYSL	BYSL, BYSTIN	bystin-like	NM_004053, hCT1951323.1	203612_at	NP_004044.3, EAX04069.1
GeneID:647024	C6orf132	6	42,068,857	42,110,715	41,858	-	1	2_A375_pNL97_plus_lncRNA::1::6814	43547	downstream	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C6orf132	C6orf132, bA7K24.2, FLJ90086	chromosome 6 open reading frame 132	NM_001164446		NP_001157918.1
GeneID:55809	TRERF1	6	42,192,669	42,419,783	227,114	-	1	1_A375_pNL7_minus_lncRNA::1::4738	199	in gene	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene TRERF1	BCAR2, FLJ21198, HSA277276, TReP-132, RAPA, RP1-139D8.5, dJ139D8.5, TRERF1	transcriptional regulating factor 1	NM_033502, hCT2284471.0, hCT2284475.0, hCT2284477.0, hCT1817939.2, hCT1964492.1, hCT1964493.1	228016_s_at, 233324_at, 236520_at	NP_277037.1, EAX04091.1, EAX04088.1, EAX04089.1, EAX04090.1, EAX04093.1, EAX04092.1
GeneID:6903	TBCC	6	42,712,234	42,713,884	1,650	-	1	2_A375_pNL97_plus_lncRNA::1::6815	124	in gene	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene TBCC	CFC, TBCC	tubulin folding cofactor C	NM_003192, hCT8641.3	202495_at	NP_003183.1, EAX04100.1
GeneID:285855	RPL7L1	6	42,847,671	42,854,731	7,060	+	2	2_A375_pNL97_plus_lncRNA::1::6816, 2_A375_pNL97_plus_lncRNA::1::6817	-183, 11113	upstream, downstream	0	1	15.5	17	2	2_A375_pNL97_plus_lncRNA::1	22	Gene RPL7L1	RPL7L1, MGC62004, dJ475N16.4	ribosomal protein L7-like 1	NM_198486, hCT2286312.1, hCT2286313.1, hCT1817938.3	224738_x_at	NP_940888.2, EAX04106.1, EAX04104.1, EAX04105.1
GeneID:441150	C6orf226	6	42,858,003	42,858,554	551	-	1	2_A375_pNL97_plus_lncRNA::1::6817	-230	upstream	0	1	12	12	1	2_A375_pNL97_plus_lncRNA::1	12	Gene C6orf226	C6orf226	chromosome 6 open reading frame 226	NM_001008739	228458_at	NP_001008739.1
GeneID:6722	SRF	6	43,138,920	43,149,244	10,324	+	1	2_A375_pNL97_plus_lncRNA::1::6818	10968	downstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SRF	SRF, MCM1	serum response factor (c-fos serum response element-binding transcription factor)	NM_003131, hCT2286355.0, hCT8690.3	202400_s_at, 202401_s_at	NP_003122.1, EAX04161.1, EAX04162.1
GeneID:23113	CUL9	6	43,149,922	43,192,325	42,403	+	1	2_A375_pNL97_plus_lncRNA::1::6818	-34	upstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CUL9	RP3-330M21.2, DKFZp686P2024, DKFZp686G1042, H7AP1, PARC, CUL9	cullin 9	NM_015089, hCT2286357.0, hCT1963320.1	213204_at, 236392_at	NP_055904.1, EAX04164.1, EAX04163.1
GeneID:89845	ABCC10	6	43,399,489	43,418,163	18,674	+	1	1_A375_pNL7_minus_lncRNA::1::4739	-4289	upstream	1	0	23	9	1	1_A375_pNL7_minus_lncRNA::1	23	Gene ABCC10	EST182763, MRP7, ABCC10, SIMRP7	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	NM_033450, hCT1967874.1, hCT1969068.1, hCT1969069.1, hCT2358821.0, hCT2358822.0, hCT10074.4	213485_s_at, 215873_x_at	NP_258261.2, EAX04180.1, EAX04181.1, EAX04183.1, EAX04184.1, EAX04185.1, EAX04182.1
GeneID:93643	TJAP1	6	43,445,261	43,474,294	29,033	+	1	1_A375_pNL7_minus_lncRNA::1::4740	31939	downstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene TJAP1	PILT, TJP4, DKFZp686F06131, TJAP1	tight junction associated protein 1 (peripheral)	NM_001146016, NM_001146017, NM_001146018, NM_080604, NM_001146019, NM_001146020, NR_027394, hCT1966974.1, hCT1966975.1, hCT2358719.0, hCT2358720.0, hCT2358721.0, hCT2358722.0, hCT2358723.0, hCT2358724.0, hCT2358725.0, hCT2358726.0	221857_s_at, 47608_at	NP_001139488.1, NP_001139489.1, NP_001139490.1, NP_542171.2, NP_001139491.1, NP_001139492.1, EAX04192.1, EAX04193.1, EAX04194.1, EAX04195.1, EAX04196.1, EAX04197.1, EAX04198.1, EAX04199.1, EAX04200.1, EAX04201.1
GeneID:221424	C6orf154	6	43,474,707	43,478,424	3,717	-	1	1_A375_pNL7_minus_lncRNA::1::4740	1224	in gene	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene C6orf154	C6orf154, FLJ44636, dJ337H4.2, MGC131686	chromosome 6 open reading frame 154	NM_001012974, hCT10081.2	235935_at	NP_001012992.1, EAX04202.1
GeneID:25844	YIPF3	6	43,479,565	43,484,728	5,163	-	1	1_A375_pNL7_minus_lncRNA::1::4740	7528	downstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene YIPF3	FinGER3, C6orf109, KLIP1, dJ337H4.3, YIPF3, DKFZp566C243	Yip1 domain family, member 3	NM_015388, hCT10072.3	216338_s_at	NP_056203.2, EAX04203.1
GeneID:9533	POLR1C	6	43,484,791	43,497,114	12,323	+	1	1_A375_pNL7_minus_lncRNA::1::4740	-7591	upstream	1	0	16	12	1	1_A375_pNL7_minus_lncRNA::1	16	Gene POLR1C	RPA39, TCS3, POLR1C, RPA5, RPA40, RPAC1	polymerase (RNA) I polypeptide C, 30kDa	NM_203290, NM_004875, hCT2286377.0, hCT2286378.0	207515_s_at, 209317_at	NP_976035.1, NP_004866.1, EAX04204.1, EAX04205.1
GeneID:54676	GTPBP2	6	43,588,218	43,596,936	8,718	-	1	2_A375_pNL97_plus_lncRNA::1::6819	-6728	upstream	0	1	6	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene GTPBP2	GTPBP2, MGC74725	GTP binding protein 2	NM_019096, hCT2286299.0, hCT2286300.0, hCT2286301.0, hCT2286302.0, hCT2286303.0, hCT10073.3	221050_s_at, 223789_s_at	NP_061969.3, EAX04218.1, EAX04213.1, EAX04214.1, EAX04216.1, EAX04217.1, EAX04215.1
GeneID:9587	MAD2L1BP	6	43,597,279	43,608,689	11,410	+	2	2_A375_pNL97_plus_lncRNA::1::6819, 2_A375_pNL97_plus_lncRNA::1::6820	6385, 10977	in gene, in gene	0	1	5.5	16	2	2_A375_pNL97_plus_lncRNA::1	18	Gene MAD2L1BP	CMT2, MGC11282, MAD2L1BP, KIAA0110, RP1-261G23.6	MAD2L1 binding protein	NM_014628, NM_001003690, hCT10062.3	203094_at	NP_055443.1, NP_001003690.1, EAX04219.1
GeneID:221421	RSPH9	6	43,612,767	43,638,748	25,981	+	2	2_A375_pNL97_plus_lncRNA::1::6819, 2_A375_pNL97_plus_lncRNA::1::6820	-9103, -4511	upstream, upstream	0	1	5.5	16	2	2_A375_pNL97_plus_lncRNA::1	18	Gene RSPH9	C6orf206, MRPS18AL1, FLJ30845, RSPH9, CILD12	radial spoke head 9 homolog (Chlamydomonas)	NM_152732, NM_001193341, hCT1968134.1, hCT1968135.1, hCT10079.2	230695_s_at	NP_689945.2, NP_001180270.1, EAX04220.1, EAX04221.1, EAX04222.1
GeneID:100505819	LOC100505819	6	44,209,727	44,221,620	11,893	-	3	1_A375_pNL7_minus_lncRNA::1::4741, 2_A375_pNL97_plus_lncRNA::1::6821, 2_A375_pNL97_plus_lncRNA::1::6822	6820, 6932, -3452	in gene, in gene, upstream	1	1	22	26	2	1_A375_pNL7_minus_lncRNA::1	31	Gene LOC100505819		hypothetical LOC100505819	XR_112882, XR_108652, XR_113895		
GeneID:3326	HSP90AB1	6	44,214,849	44,221,614	6,765	+	3	1_A375_pNL7_minus_lncRNA::1::4741, 2_A375_pNL97_plus_lncRNA::1::6821, 2_A375_pNL97_plus_lncRNA::1::6822	-49, -161, 10223	upstream, upstream, downstream	1	1	22	26	2	1_A375_pNL7_minus_lncRNA::1	31	Gene HSP90AB1	HSP90-BETA, D6S182, HSP90AB1, HSP90B, HSPC2, HSPCB, FLJ26984	heat shock protein 90kDa alpha (cytosolic), class B member 1	NM_007355, hCT2285894.1, hCT2285895.1, hCT2358806.0, hCT10066.3	1557910_at, 200064_at, 214359_s_at	NP_031381.2, EAX04257.1, EAX04258.1, EAX04259.1, EAX04260.1
GeneID:347734	SLC35B2	6	44,221,838	44,225,283	3,445	-	3	1_A375_pNL7_minus_lncRNA::1::4741, 2_A375_pNL97_plus_lncRNA::1::6821, 2_A375_pNL97_plus_lncRNA::1::6822	10483, 10595, 211	downstream, downstream, in gene	1	1	22	26	2	1_A375_pNL7_minus_lncRNA::1	31	Gene SLC35B2	PAPST1, UGTrel4, SLC35B2, SLL	solute carrier family 35, member B2	NM_178148, hCT10067.3	224716_at	NP_835361.1, EAX04261.1
GeneID:4794	NFKBIE	6	44,225,903	44,233,525	7,622	-	1	2_A375_pNL97_plus_lncRNA::1::6822	8453	downstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene NFKBIE	NFKBIE, IKBE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	NM_004556, hCT2286055.0, hCT10064.4, hCT1963327.1	203927_at	NP_004547.2, EAX04262.1, EAX04263.1, EAX04264.1
GeneID:441151	TMEM151B	6	44,238,460	44,247,162	8,702	+	2	1_A375_pNL7_minus_lncRNA::1::4742, 2_A375_pNL97_plus_lncRNA::1::6823	15048, 14992	downstream, downstream	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TMEM151B	TMEM151B, FLJ42511, FLJ44891, TMEM193, C6orf137, FLJ37046, bA444E17.5, FLJ44683	transmembrane protein 151B	NM_001137560	213676_at, 213678_at	NP_001131032.1
GeneID:202500	TCTE1	6	44,247,897	44,265,458	17,561	-	2	1_A375_pNL7_minus_lncRNA::1::4742, 2_A375_pNL97_plus_lncRNA::1::6823	11930, 11986	in gene, in gene	1	1	20	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TCTE1	FLJ50041, TCTE1, D6S46, MGC33600	t-complex-associated-testis-expressed 1	NM_182539, hCT2347546.0	237280_at	NP_872345.2, EAX04266.1
GeneID:57505	AARS2	6	44,266,463	44,281,063	14,600	-	2	1_A375_pNL7_minus_lncRNA::1::4743, 2_A375_pNL97_plus_lncRNA::1::6824	7, -25	in gene, upstream	1	1	62	68	1	2_A375_pNL97_plus_lncRNA::1	68	Gene AARS2	AARSL, KIAA1270, MTALARS, AARS2, bA444E17.1, MT-ALARS	alanyl-tRNA synthetase 2, mitochondrial (putative)	NM_020745, hCT9577.3	231645_at	NP_065796.1, EAX04268.1
GeneID:51302	CYP39A1	6	46,517,445	46,620,523	103,078	-	2	1_A375_pNL7_minus_lncRNA::1::4744, 2_A375_pNL97_plus_lncRNA::1::6825	-501, -469	upstream, upstream	1	1	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene CYP39A1	CYP39A1		NM_016593, hCT9824.3	1553977_a_at, 220432_s_at, 244407_at	NP_057677.2, EAX04297.1
GeneID:9481	SLC25A27	6	46,620,679	46,645,927	25,248	+	2	1_A375_pNL7_minus_lncRNA::1::4744, 2_A375_pNL97_plus_lncRNA::1::6825	345, 313	in gene, in gene	1	1	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene SLC25A27	UCP4, SLC25A27, FLJ33552	solute carrier family 25, member 27	NM_004277, hCT7934.4, hCT1962852.1	1552774_a_at, 1554161_at, 229361_at, 230624_at, 231767_at	NP_004268.3, EAX04299.1, EAX04298.1
GeneID:83741	TFAP2D	6	50,681,257	50,740,746	59,489	+	1	2_A375_pNL97_plus_lncRNA::1::6828	7191	in gene	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TFAP2D	TFAP2D, TFAP2BL1	transcription factor AP-2 delta (activating enhancer binding protein 2 delta)	NM_172238, hCT1817639.3	233987_at	NP_758438.2, EAX04354.1
GeneID:114327	EFHC1	6	52,284,994	52,360,583	75,589	+	1	2_A375_pNL97_plus_lncRNA::1::6829	3966	in gene	0	1	6	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene EFHC1	FLJ37290, EFHC1, EJM, EJM1, dJ304B14.2, FLJ10466, JAE, EJA1	EF-hand domain (C-terminal) containing 1	NM_018100, NR_033327, NM_001172420, hCT2288825.0, hCT12282.4, hCT1963344.1	219833_s_at, 225656_at, 231026_at	NP_060570.2, NP_001165891.1, EAX04370.1, EAX04371.1, EAX04372.1
GeneID:2941	GSTA4	6	52,842,746	52,860,178	17,432	-	1	2_A375_pNL97_plus_lncRNA::1::6830	162	in gene	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene GSTA4	GSTA4, DKFZp686D21185, GSTA4-4, GTA4	glutathione S-transferase alpha 4	NM_001512, hCT2287506.0, hCT2358859.0, hCT2358860.0, hCT13033.3, hCT1963352.1, hCT1963353.1, hCT1963354.1	202967_at, 235405_at	NP_001503.1, EAX04394.1, EAX04395.1, EAX04396.1, EAX04398.1, EAX04399.1, EAX04393.1, EAX04397.1
GeneID:125050	RN7SK	6	52,860,418	52,860,749	331	+	1	2_A375_pNL97_plus_lncRNA::1::6830	-402	upstream	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene RN7SK	RN7SK, 7SK	RNA, 7SK small nuclear	NR_001445		
GeneID:22858	ICK	6	52,866,098	52,926,600	60,502	-	3	1_A375_pNL7_minus_lncRNA::1::4750, 2_A375_pNL97_plus_lncRNA::1::6830, 2_A375_pNL97_plus_lncRNA::1::6831	-3048, 66584, -3064	upstream, downstream, upstream	1	1	14	17.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene ICK	LCK2, MGC46090, ICK, ECO, KIAA0936, MRK	intestinal cell (MAK-like) kinase	NM_014920, NM_016513, hCT2287502.1, hCT2287503.1, hCT11897.4, hCT1963340.2, hCT1963341.2	1552837_at, 204569_at	NP_055735.1, NP_057597.2, EAX04400.1, EAX04401.1, EAX04402.1, EAX04403.1, EAX04404.1
GeneID:26268	FBXO9	6	52,929,796	52,965,671	35,875	+	2	1_A375_pNL7_minus_lncRNA::1::4750, 2_A375_pNL97_plus_lncRNA::1::6831	-148, -132	upstream, upstream	1	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene FBXO9	NY-REN-57, FBXO9, DKFZp434C0118, FBX9, dJ341E18.2, KIAA0936, VCIA1	F-box protein 9	NM_012347, NM_033481, NM_033480, hCT2286839.0, hCT2286840.0, hCT2286842.0, hCT2286843.0, hCT2286844.0, hCT1950794.1	1559094_at, 1559096_x_at, 1566507_a_at, 1566509_s_at, 1566511_at, 210638_s_at, 212987_at, 212991_at, 238472_at	NP_036479.1, NP_258442.2, NP_258441.1, EAX04406.1, EAX04407.1, EAX04408.1, EAX04405.1, EAX04409.1, EAX04410.1
GeneID:60481	ELOVL5	6	53,132,196	53,213,942	81,746	-	3	1_A375_pNL7_minus_lncRNA::1::4751, 1_A375_pNL7_minus_lncRNA::1::4752, 2_A375_pNL97_plus_lncRNA::1::6832	454, -10506, -10618	in gene, upstream, upstream	1	1	18.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene ELOVL5	ELOVL5, dJ483K16.1, HELO1	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	NM_021814, hCT2285388.0, hCT2285390.0, hCT2285391.0, hCT2285393.0, hCT2285395.0, hCT2285397.0, hCT2285399.0, hCT2285401.0, hCT2285403.0, hCT2358633.0	1567222_x_at, 208788_at, 214153_at, 215082_at	NP_068586.1, EAX04419.1, EAX04413.1, EAX04417.1, EAX04421.1, EAX04422.1, EAX04414.1, EAX04415.1, EAX04416.1, EAX04418.1, EAX04420.1
GeneID:2729	GCLC	6	53,362,139	53,409,831	47,692	-	4	1_A375_pNL7_minus_lncRNA::1::4753, 1_A375_pNL7_minus_lncRNA::1::4754, 2_A375_pNL97_plus_lncRNA::1::6833, 2_A375_pNL97_plus_lncRNA::1::6834	-25, -3033, -57, -2969	upstream, upstream, upstream, upstream	1	1	34.5	29.5	2	1_A375_pNL7_minus_lncRNA::1	38	Gene GCLC	GCL, GLCLC, GCS, GCLC, GLCL	glutamate-cysteine ligase, catalytic subunit	NM_001498, hCT2285384.0, hCT13035.3	1555330_at, 202922_at, 202923_s_at	NP_001489.1, EAX04425.1, EAX04426.1
GeneID:55227	LRRC1	6	53,659,778	53,788,919	129,141	+	1	2_A375_pNL97_plus_lncRNA::1::6835	-130	upstream	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LRRC1	LRRC1, FLJ11834, LANO, FLJ10775, dJ523E19.1	leucine rich repeat containing 1	NM_018214, hCT2284977.0, hCT1817829.1	207790_at	NP_060684.4, EAX04430.1, EAX04429.1
GeneID:3062	HCRTR2	6	55,039,071	55,147,418	108,347	+	2	1_A375_pNL7_minus_lncRNA::1::4755, 2_A375_pNL97_plus_lncRNA::1::6837	2881, 2881	in gene, in gene	1	1	29	19	1	1_A375_pNL7_minus_lncRNA::1	29	Gene HCRTR2	OX2R, HCRTR2	hypocretin (orexin) receptor 2	NM_001526, hCT2284958.0	207393_at	NP_001517.2, EAX04440.1
GeneID:202559	KHDRBS2	6	62,389,865	62,996,100	606,235	-	2	1_A375_pNL7_minus_lncRNA::1::4757, 2_A375_pNL97_plus_lncRNA::1::6840	-76, -156	upstream, upstream	1	1	28	21	1	1_A375_pNL7_minus_lncRNA::1	28	Gene KHDRBS2	SLM-1, MGC26664, KHDRBS2, bA535F17.1, SLM1, FLJ38664	KH domain containing, RNA binding, signal transduction associated 2	NM_152688, hCT2280880.1, hCT2280881.1, hCT1953076.2	215527_at	NP_689901.2, EAW48490.1, EAW48489.1, EAW48491.1
GeneID:7803	PTP4A1	6	64,281,920	64,293,489	11,569	+	4	1_A375_pNL7_minus_lncRNA::1::4758, 1_A375_pNL7_minus_lncRNA::1::4759, 2_A375_pNL97_plus_lncRNA::1::6841, 2_A375_pNL97_plus_lncRNA::1::6842	-128, 2432, 1552, 2464	upstream, in gene, in gene, in gene	1	1	21.33	17.67	3	1_A375_pNL7_minus_lncRNA::1	28	Gene PTP4A1	PRL1, PTP4A1, DKFZp779M0721, PRL-1, PTPCAAX1, HH72, PTP(CAAX1)	protein tyrosine phosphatase type IVA, member 1	NM_003463, hCT2281169.0, hCT1797443.1	200730_s_at, 200731_s_at, 200732_s_at, 200733_s_at, 240329_at	NP_003454.1, EAW48495.1, EAW48494.1
GeneID:577	BAI3	6	69,345,632	70,099,403	753,771	+	2	1_A375_pNL7_minus_lncRNA::1::4765, 2_A375_pNL97_plus_lncRNA::1::6847	597296, 597248	in gene, in gene	1	1	27	35	1	2_A375_pNL97_plus_lncRNA::1	35	Gene BAI3	KIAA0550, BAI3, MGC133100	brain-specific angiogenesis inhibitor 3	NM_001704, hCT2332673.0, hCT1959644.1	205638_at, 211568_at	NP_001695.1, EAW48837.1, EAW48836.1
GeneID:1310	COL19A1	6	70,576,448	70,922,157	345,709	+	1	1_A375_pNL7_minus_lncRNA::1::4766	51456	in gene	1	0	16	10	1	1_A375_pNL7_minus_lncRNA::1	16	Gene COL19A1	COL19A1, COL9A1L, D6S228E	collagen, type XIX, alpha 1	NM_001858, hCT2332678.0, hCT2332680.0, hCT6078.3	211011_at	NP_001849.2, EAW48828.1, EAW48829.1, EAW48830.1
GeneID:56479	KCNQ5	6	73,331,571	73,908,574	577,003	+	2	1_A375_pNL7_minus_lncRNA::1::4767, 2_A375_pNL97_plus_lncRNA::1::6848	499949, 499885	in gene, in gene	1	1	21	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene KCNQ5	Kv7.5, KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5	NM_019842, NM_001160130, NM_001160132, NM_001160133, NM_001160134, hCT2344244.0, hCT2344246.0	223691_at	NP_062816.2, NP_001153602.1, NP_001153604.1, NP_001153605.1, NP_001153606.1, EAW48782.1, EAW48783.1
GeneID:1915	EEF1A1	6	74,225,473	74,230,755	5,282	-	2	1_A375_pNL7_minus_lncRNA::1::4768, 2_A375_pNL97_plus_lncRNA::1::6849	-141, -61	upstream, upstream	1	1	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene EEF1A1	EF-Tu, FLJ25721, MGC131894, EEF-1, GRAF-1EF, CCS-3, MGC102687, CCS3, eEF1A-1, LENG7, EF1A, HNGC:16303, EEF1A, EEF1A1, MGC16224, EE1A1, PTI1	eukaryotic translation elongation factor 1 alpha 1	NM_001402, hCT2336043.1	1557120_at, 204892_x_at, 206559_x_at, 213477_x_at, 213614_x_at, 227708_at	NP_001393.1, EAW48759.1
GeneID:100506740	LOC100506740	6	74,403,615	74,405,854	2,239	-	2	1_A375_pNL7_minus_lncRNA::1::4769, 2_A375_pNL97_plus_lncRNA::1::6850	318, 126	in gene, in gene	1	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC100506740		hypothetical LOC100506740	XR_108607		
GeneID:135228	CD109	6	74,405,508	74,538,041	132,533	+	2	1_A375_pNL7_minus_lncRNA::1::4769, 2_A375_pNL97_plus_lncRNA::1::6850	28, 220	in gene, in gene	1	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene CD109	RP11-525G3.1, DKFZp762L1111, CPAMD7, FLJ38569, CD109, FLJ41966	CD109 molecule	NM_133493, NM_001159587, NM_001159588, hCT2336059.0, hCT2336060.0, hCT2336061.0, hCT2352076.0	226545_at, 229900_at, 239719_at	NP_598000.2, NP_001153059.1, NP_001153060.1, EAW48752.1, EAW48753.1, EAW48755.1, EAW48754.1
GeneID:55603	FAM46A	6	82,455,447	82,462,428	6,981	-	1	1_A375_pNL7_minus_lncRNA::1::4770	-580	upstream	1	0	24	13	1	1_A375_pNL7_minus_lncRNA::1	24	Gene FAM46A	FLJ20037, C6orf37, FAM46A, FLJ31495, XTP11	family with sequence similarity 46, member A	NM_017633, hCT401094.3, hCT1959598.1	221766_s_at, 224973_at, 229737_at	NP_060103.2, EAW48692.1, EAW48691.1
GeneID:134701	RIPPLY2	6	84,562,985	84,567,234	4,249	+	2	1_A375_pNL7_minus_lncRNA::1::4771, 2_A375_pNL97_plus_lncRNA::1::6852	6231, 6247	downstream, downstream	1	1	45	62	1	2_A375_pNL97_plus_lncRNA::1	62	Gene RIPPLY2	RIPPLY2, C6orf159, dJ237I15.1	ripply2 homolog (zebrafish)	NM_001009994	236771_at	NP_001009994.1

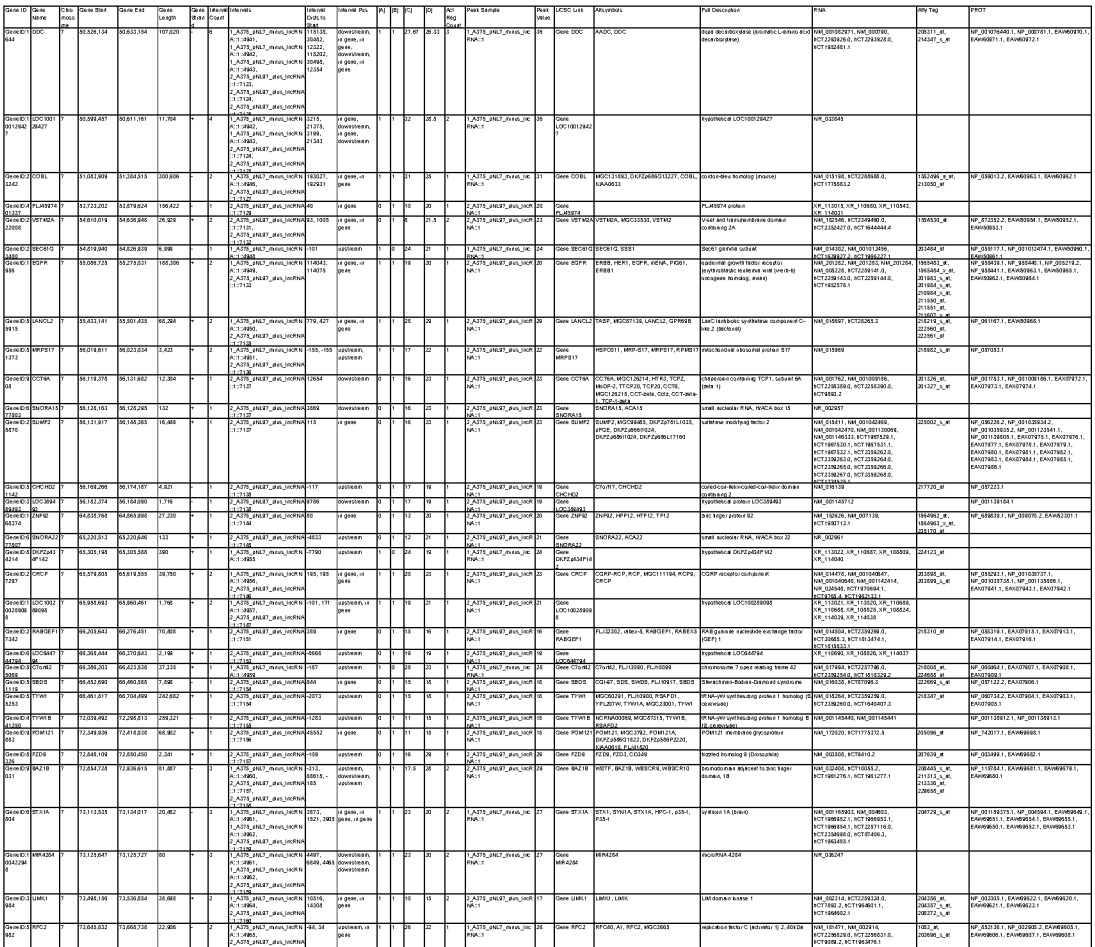
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:51167	CYB5R4	6	84,569,370	84,670,146	100,776	+	2	1_A375_pNL7_minus_lncRNA::1::4771, 2_A375_pNL97_plus_lncRNA::1::6852	-154, -138	upstream, upstream	1	1	45	62	1	2_A375_pNL97_plus_lncRNA::1	62	Gene CYB5R4	cb5/cb5R, dJ676J13.1, RP4-676J13.1, CYB5R4, NCB5OR	cytochrome b5 reductase 4	NM_016230	219079_at	NP_057314.2
GeneID:9096	TBX18	6	85,444,157	85,473,899	29,742	-	1	2_A375_pNL97_plus_lncRNA::1::6854	-533	upstream	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TBX18	TBX18		NM_001080508	1559639_at, 1559640_s_at, 233689_at	NP_001073977.1
GeneID:4907	NT5E	6	86,159,302	86,205,498	46,196	+	1	2_A375_pNL97_plus_lncRNA::1::6856	15274	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NT5E	NT, CD73, eNT, NT5E, eN, E5NT, NTE, NT5	5'-nucleotidase, ecto (CD73)	NM_002526, hCT2352169.0, hCT401111.1, hCT1959599.1	1553994_at, 1553995_a_at, 203939_at, 227486_at	NP_002517.1, EAW48635.1, EAW48634.1, EAW48636.1
GeneID:387066	SNHG5	6	86,386,725	86,388,451	1,726	-	2	1_A375_pNL7_minus_lncRNA::1::4772, 2_A375_pNL97_plus_lncRNA::1::6857	131, 35	in gene, in gene	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SNHG5	NCRNA00044, MGC16362, bA33E24.2, SNHG5, U50HG, C6orf160	small nucleolar RNA host gene 5 (non-protein coding)	NR_003038	225155_at	
GeneID:26799	SNORD50A	6	86,387,012	86,387,086	74	-	2	1_A375_pNL7_minus_lncRNA::1::4772, 2_A375_pNL97_plus_lncRNA::1::6857	-1234, -1330	upstream, upstream	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SNORD50A	SNORD50A, RNU50, U50	small nucleolar RNA, C/D box 50A	NR_002743	244669_at	
GeneID:692088	SNORD50B	6	86,387,307	86,387,377	70	-	2	1_A375_pNL7_minus_lncRNA::1::4772, 2_A375_pNL97_plus_lncRNA::1::6857	-943, -1039	upstream, upstream	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SNORD50B	U50', U50B, SNORD50B	small nucleolar RNA, C/D box 50B	NR_003044		
GeneID:375519	GJB7	6	87,992,697	88,038,996	46,299	-	2	1_A375_pNL7_minus_lncRNA::1::4773, 2_A375_pNL97_plus_lncRNA::1::6858	6772, 6740	in gene, in gene	1	1	64	82	1	2_A375_pNL97_plus_lncRNA::1	82	Gene GJB7	bA136M9.1, connexin25, CX25, GJB7, MGC71746	gap junction protein, beta 7, 25kDa	NM_198568		NP_940970.1
GeneID:57150	C6orf162	6	88,032,306	88,052,043	19,737	+	2	1_A375_pNL7_minus_lncRNA::1::4773, 2_A375_pNL97_plus_lncRNA::1::6858	-82, -50	upstream, upstream	1	1	64	82	1	2_A375_pNL97_plus_lncRNA::1	82	Gene C6orf162	DKFZp586E1923, dJ102H19.2, C6orf162	chromosome 6 open reading frame 162	NM_020425, NM_001042493, hCT2349211.0, hCT2349212.0, hCT2349213.0	213312_at, 213314_at, 236178_at	NP_065158.3, NP_001035958.1, EAW48601.1, EAW48602.1, EAW48603.1
GeneID:154313	C6orf165	6	88,117,690	88,174,191	56,501	+	4	1_A375_pNL7_minus_lncRNA::1::4774, 1_A375_pNL7_minus_lncRNA::1::4775, 2_A375_pNL97_plus_lncRNA::1::6859, 2_A375_pNL97_plus_lncRNA::1::6860	28646, 64902, 28614, 64790	in gene, downstream, in gene, downstream	1	1	30	37	2	2_A375_pNL97_plus_lncRNA::1	54	Gene C6orf165	dJ382I10.1, FLJ46091, FLJ25974, C6orf165	chromosome 6 open reading frame 165	NM_001031743	230273_at	NP_001026913.1
GeneID:10559	SLC35A1	6	88,182,643	88,222,057	39,414	+	2	1_A375_pNL7_minus_lncRNA::1::4775, 2_A375_pNL97_plus_lncRNA::1::6860	-51, -163	upstream, upstream	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC35A1	CMPST, SLC35A1, FLJ76955, CST, hCST, CDG2F	solute carrier family 35 (CMP-sialic acid transporter), member A1	NM_006416, NM_001168398	203306_s_at	NP_006407.1, NP_001161870.1
GeneID:51465	UBE2J1	6	90,036,344	90,062,619	26,275	-	1	2_A375_pNL97_plus_lncRNA::1::6862	187	in gene	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene UBE2J1	HSPC205, NCUBE1, HSU93243, CGI-76, NCUBE-1, HSPC153, UBE2J1, Ubc6p, MGC12555	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	NM_016021, hCT2333110.0, hCT24262.3	217823_s_at, 217824_at, 217825_s_at, 217826_s_at, 222435_s_at, 228924_s_at	NP_057105.2, EAW48556.1, EAW48555.1
GeneID:23195	MDN1	6	90,353,231	90,529,442	176,211	-	1	2_A375_pNL97_plus_lncRNA::1::6863	2	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MDN1	KIAA0301, FLJ23395, FLJ42031, FLJ25587, MDN1, FLJ43191, DKFZp686H16106	MDN1, midasin homolog (yeast)	NM_014611, hCT2340243.0, hCT2340244.1	1569484_s_at, 212693_at, 234854_at	NP_055426.1, EAW48545.1, EAW48546.1
GeneID:9994	CASP8AP2	6	90,539,619	90,584,155	44,536	+	1	2_A375_pNL97_plus_lncRNA::1::6863	-10179	upstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CASP8AP2	FLJ11208, CED-4, FLASH, CASP8AP2, RIP25, KIAA1315	caspase 8 associated protein 2	NM_001137668, NM_012115, NM_001137667, hCT2333142.1, hCT2348015.0, hCT2348016.0, hCT2352062.0, hCT23591.2	1570001_at, 222201_s_at	NP_001131140.1, NP_036247.1, NP_001131139.1, EAW48540.1, EAW48542.1, EAW48543.1, EAW48541.1, EAW48544.1
GeneID:84694	GJA10	6	90,604,188	90,605,819	1,631	+	2	1_A375_pNL7_minus_lncRNA::1::4777, 2_A375_pNL97_plus_lncRNA::1::6864	1028, 996	in gene, in gene	1	1	43	56	1	2_A375_pNL97_plus_lncRNA::1	56	Gene GJA10	CX62, GJA10, RP11-63K6.6	gap junction protein, alpha 10, 62kDa	NM_032602, hCT1646356.1	1553044_at	NP_115991.1, EAW48537.1
GeneID:60468	BACH2	6	90,636,247	91,006,627	370,380	-	1	2_A375_pNL97_plus_lncRNA::1::6865	74019	in gene	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene BACH2	BACH2		NM_021813, NM_001170794, hCT2333070.1, hCT2333074.1, hCT2340902.0, hCT2340903.0, hCT24266.2	221234_s_at, 227173_s_at, 236796_at	NP_068585.1, NP_001164265.1, EAW48530.1, EAW48531.1, EAW48533.1, EAW48534.1, EAW48532.1
GeneID:6885	MAP3K7	6	91,225,353	91,296,907	71,554	-	1	2_A375_pNL97_plus_lncRNA::1::6866	-181	upstream	0	1	15	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MAP3K7	TAK1, MAP3K7, MEKK7, TGF1a	mitogen-activated protein kinase kinase kinase 7	NM_003188, NM_145331, NM_145332, NM_145333, hCT2332196.0, hCT2352058.0, hCT2352059.0, hCT23590.3, hCT1956063.1	206853_s_at, 206854_s_at, 211536_x_at, 211537_x_at	NP_003179.1, NP_663304.1, NP_663305.1, NP_663306.1, EAW48526.1, EAW48528.1, EAW48525.1, EAW48527.1, EAW48529.1
GeneID:29078	NDUFAF4	6	97,337,187	97,345,767	8,580	-	2	1_A375_pNL7_minus_lncRNA::1::4778, 2_A375_pNL97_plus_lncRNA::1::6868	-9, -9	upstream, upstream	1	1	46	40	1	1_A375_pNL7_minus_lncRNA::1	46	Gene NDUFAF4	NDUFAF4, My013, bA22L21.1, HRPAP20, C6orf66, HSPC125	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	NM_014165, hCT7745.2	219006_at	NP_054884.1, EAW48501.1
GeneID:84553	C6orf168	6	99,720,793	99,797,531	76,738	-	2	1_A375_pNL7_minus_lncRNA::1::4780, 2_A375_pNL97_plus_lncRNA::1::6870	-3621, -3685	upstream, upstream	1	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C6orf168	C6orf168, dJ273F20, MGC2817, FLJ30539	chromosome 6 open reading frame 168	NM_032511, hCT2331975.0, hCT2352064.0, hCT2352065.0, hCT1660090.3, hCT1963906.1	232067_at	NP_115900.1, EAW48483.1, EAW48484.1, EAW48485.1, EAW48486.1, EAW48487.1
GeneID:85015	USP45	6	99,880,182	99,963,252	83,070	-	1	2_A375_pNL97_plus_lncRNA::1::6871	20	in gene	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene USP45	USP45, MGC14793	ubiquitin specific peptidase 45	NM_001080481	224441_s_at, 238057_at	NP_001073950.1
GeneID:2898	GRIK2	6	101,846,861	102,517,958	671,097	+	4	1_A375_pNL7_minus_lncRNA::1::4781, 2_A375_pNL97_plus_lncRNA::1::6872, 1_A375_pNL7_minus_lncRNA::1::4782, 2_A375_pNL97_plus_lncRNA::1::6873	-5421, -5469, 215939, 267411	upstream, upstream, in gene, in gene	1	1	14.67	16.67	3	2_A375_pNL97_plus_lncRNA::1	21	Gene GRIK2	MGC74427, GLR6, GLUR6, EAA4, GLUK6, GRIK2, MRT6	glutamate receptor, ionotropic, kainate 2	NM_021956, NM_175768, NM_001166247, hCT2331888.2, hCT2331889.2, hCT2341428.1	1555375_at, 1560142_at, 1560265_at, 1563754_at, 213845_at, 215655_at	NP_068775.1, NP_786944.1, NP_001159719.1, EAW48446.1, EAW48447.1, EAW48448.1
GeneID:57531	HACE1	6	105,175,968	105,307,794	131,826	-	1	2_A375_pNL97_plus_lncRNA::1::6874	274	in gene	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene HACE1	HACE1		NM_020771, hCT2349187.0, hCT2349188.0, hCT2349189.0	227471_at	NP_065822.2, EAW48438.1, EAW48437.1, EAW48439.1
GeneID:5550	PREP	6	105,725,442	105,850,999	125,557	-	2	1_A375_pNL7_minus_lncRNA::1::4783, 2_A375_pNL97_plus_lncRNA::1::6877	23, -355	in gene, upstream	1	1	22	14	1	1_A375_pNL7_minus_lncRNA::1	22	Gene PREP	MGC16060, PE, PEP, PREP	prolyl endopeptidase	NM_002726, hCT1955484.1	204117_at, 229644_at, 37950_at	NP_002717.3, EAW48426.1
GeneID:100506148	LOC100506148	6	105,825,260	105,851,000	25,740	+	2	1_A375_pNL7_minus_lncRNA::1::4783, 2_A375_pNL97_plus_lncRNA::1::6877	25716, 26094	in gene, downstream	1	1	22	14	1	1_A375_pNL7_minus_lncRNA::1	22	Gene LOC100506148		hypothetical LOC100506148	XR_112906, XR_110205, XR_113966		
GeneID:639	PRDM1	6	106,534,195	106,557,814	23,619	+	1	2_A375_pNL97_plus_lncRNA::1::6878	-3	upstream	0	1	10	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene PRDM1	MGC118922, PRDM1, MGC118923, MGC118924, PRDI-BF1, BLIMP1, MGC118925	PR domain containing 1, with ZNF domain	NM_182907, NM_001198, hCT2332066.1, hCT2332067.1, hCT2352163.0, hCT24713.4	217192_s_at, 228964_at, 235666_at	NP_878911.1, NP_001189.2, EAW48419.1, EAW48420.1, EAW48421.1, EAW48422.1
GeneID:9474	ATG5	6	106,632,352	106,773,695	141,343	-	1	2_A375_pNL97_plus_lncRNA::1::6879	116	in gene	0	1	13	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene ATG5	hAPG5, APG5-LIKE, ATG5, ASP, APG5L, APG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	NM_004849, hCT2331941.0, hCT2352093.0, hCT2352094.0, hCT24151.3, hCT1962562.1	202511_s_at, 202512_s_at, 210639_s_at	NP_004840.1, EAW48415.1, EAW48414.1, EAW48416.1, EAW48417.1, EAW48418.1
GeneID:202	AIM1	6	106,959,730	107,018,335	58,605	+	1	2_A375_pNL97_plus_lncRNA::1::6880	-1170	upstream	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene AIM1	CRYBG1, ST4, AIM1	absent in melanoma 1	NM_001624, hCT2332070.0, hCT24714.3	212543_at	NP_001615.1, EAW48412.1, EAW48413.1
GeneID:84816	RTN4IP1	6	107,018,903	107,077,373	58,470	-	1	2_A375_pNL97_plus_lncRNA::1::6881	-3	upstream	0	1	9	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RTN4IP1	MGC12934, NIMP, RTN4IP1	reticulon 4 interacting protein 1	NM_032730, hCT2331935.0, hCT2352057.0, hCT35127.3	1555679_a_at, 224509_s_at	NP_116119.2, EAW48409.1, EAW48410.1, EAW48411.1
GeneID:55278	QRSL1	6	107,077,441	107,116,292	38,851	+	1	2_A375_pNL97_plus_lncRNA::1::6881	-65	upstream	0	1	9	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene QRSL1	DKFZp564C1278, QRSL1, GatA, FLJ12189, FLJ13447, FLJ10989	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	NM_018292, hCT2332071.0, hCT35123.3	218948_at, 218949_s_at, 233089_at, 241933_at	NP_060762.3, EAW48408.1, EAW48407.1
GeneID:51250	C6orf203	6	107,349,407	107,372,546	23,139	+	2	1_A375_pNL7_minus_lncRNA::1::4784, 2_A375_pNL97_plus_lncRNA::1::6882	-95, -63	upstream, upstream	1	1	57	72	1	2_A375_pNL97_plus_lncRNA::1	72	Gene C6orf203	FLJ34245, C6orf203, PRED31, RP11-59I9.1	chromosome 6 open reading frame 203	NM_016487, NM_001142468, NM_001142470, hCT2331908.0	223576_at	NP_057571.1, NP_001135940.1, NP_001135942.1, EAW48402.1
GeneID:57673	BEND3	6	107,386,385	107,435,636	49,251	-	1	2_A375_pNL97_plus_lncRNA::1::6883	20	in gene	0	1	9	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene BEND3	KIAA1553, BEND3, RP11-59I9.2	BEN domain containing 3	NM_001080450	227920_at	NP_001073919.1
GeneID:55084	SOBP	6	107,811,317	107,982,513	171,196	+	1	2_A375_pNL97_plus_lncRNA::1::6884	-437	upstream	0	1	7	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SOBP	FLJ10159, SOBP, JXC1, MRAMS	sine oculis binding protein homolog (Drosophila)	NM_018013, hCT2331921.0, hCT2331923.0, hCT2331924.0	1563906_at, 1569351_at, 218974_at, 229034_at, 229646_at, 233766_at, 234098_at, 244279_at	NP_060483.3, EAW48399.1, EAW48397.1, EAW48398.1
GeneID:8763	CD164	6	109,687,717	109,703,762	16,045	-	1	2_A375_pNL97_plus_lncRNA::1::6885	-46	upstream	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CD164	MGC-24, MUC-24, CD164, endolyn	CD164 molecule, sialomucin	NM_006016, NM_001142401, NM_001142402, NM_001142403, NM_001142404, hCT2331843.0, hCT2331844.0, hCT2352095.0, hCT2352096.0, hCT2352097.0, hCT25321.3, hCT1962572.1, hCT1966512.1	208405_s_at, 208653_s_at, 208654_s_at	NP_006007.2, NP_001135873.1, NP_001135874.1, NP_001135875.1, NP_001135876.1, EAW48355.1, EAW48348.1, EAW48349.1, EAW48350.1, EAW48351.1, EAW48352.1, EAW48353.1, EAW48354.1
GeneID:285755	PPIL6	6	109,711,418	109,762,374	50,956	-	1	2_A375_pNL97_plus_lncRNA::1::6885	58566	downstream	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PPIL6	dJ919F19.1, RSPH12, MGC27054, MGC41939, bA425D10.6, PPIL6, MGC27056	peptidylprolyl isomerase (cyclophilin)-like 6	NM_173672, NM_001111298, hCT25327.3	1553684_at, 1560910_at, 236187_s_at	NP_775943.1, NP_001104768.2, EAW48347.1
GeneID:2830	GPR6	6	110,300,298	110,301,923	1,625	+	2	1_A375_pNL7_minus_lncRNA::1::4785, 2_A375_pNL97_plus_lncRNA::1::6886	-410, -394	upstream, upstream	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene GPR6	GPR6		NM_005284	1553507_a_at, 214655_at	NP_005275.1
GeneID:8936	WASF1	6	110,421,022	110,501,207	80,185	-	2	2_A375_pNL97_plus_lncRNA::1::6887, 2_A375_pNL97_plus_lncRNA::1::6888	6295, 183	in gene, in gene	0	1	9.5	17	2	2_A375_pNL97_plus_lncRNA::1	18	Gene WASF1	WAVE1, KIAA0269, SCAR1, FLJ31482, WASF1, WAVE	WAS protein family, member 1	NM_003931, NM_001024934, NM_001024935, NM_001024936, hCT2331807.0, hCT2331809.0, hCT33166.3, hCT1952470.1, hCT1952471.1, hCT1952472.1	204165_at	NP_003922.1, NP_001020105.1, NP_001020106.1, NP_001020107.1, EAW48325.1, EAW48329.1, EAW48326.1, EAW48327.1, EAW48328.1, EAW48330.1
GeneID:51362	CDC40	6	110,501,624	110,553,423	51,799	+	2	2_A375_pNL97_plus_lncRNA::1::6887, 2_A375_pNL97_plus_lncRNA::1::6888	-6712, -600	upstream, upstream	0	1	9.5	17	2	2_A375_pNL97_plus_lncRNA::1	18	Gene CDC40	MGC102802, EHB3, CDC40, PRPF17, FLJ10564, PRP17	cell division cycle 40 homolog (S. cerevisiae)	NM_015891, hCT2332039.2, hCT2332040.1, hCT2348022.0, hCT2348023.1, hCT2350507.0, hCT1960520.3	203376_at, 203377_s_at	NP_056975.1, EAW48324.1, EAW48319.1, EAW48320.1, EAW48322.1, EAW48323.1, EAW48321.1
GeneID:728464	C6orf186	6	110,567,149	110,679,475	112,326	-	2	1_A375_pNL7_minus_lncRNA::1::4786, 2_A375_pNL97_plus_lncRNA::1::6889	102771, 102771	in gene, in gene	1	1	20	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene C6orf186	C6orf186, dJ71D21.2, FLJ45203	chromosome 6 open reading frame 186	NM_001123364		NP_001116836.1
GeneID:23097	CDK19	6	110,931,181	111,136,412	205,231	-	2	2_A375_pNL97_plus_lncRNA::1::6891, 2_A375_pNL97_plus_lncRNA::1::6892	412, -196	in gene, upstream	0	1	12.5	14.5	2	2_A375_pNL97_plus_lncRNA::1	15	Gene CDK19	bA346C16.3, CDK19, CDC2L6, CDK11, KIAA1028	cyclin-dependent kinase 19	NM_015076, hCT25091.3	211706_s_at, 212897_at, 212899_at, 235226_at	NP_055891.1, EAW48312.1
GeneID:84154	RPF2	6	111,303,291	111,346,794	43,503	+	1	2_A375_pNL97_plus_lncRNA::1::6893	53	in gene	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene RPF2	RPF2, BXDC1, bA397G5.4, FLJ21087	ribosome production factor 2 homolog (S. cerevisiae)	NM_032194, hCT2348140.0, hCT2348141.0, hCT2352063.0, hCT25092.5	225866_at	NP_115570.1, EAW48302.1, EAW48301.1, EAW48303.1, EAW48304.1
GeneID:5980	REV3L	6	111,620,234	111,804,414	184,180	-	2	1_A375_pNL7_minus_lncRNA::1::4787, 2_A375_pNL97_plus_lncRNA::1::6894	-306, -194	upstream, upstream	1	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene REV3L	POLZ, REV3, REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	NM_002912, hCT2331963.0, hCT2331966.0, hCT1960519.1	208070_s_at, 238736_at	NP_002903.3, EAW48292.1, EAW48293.1, EAW48294.1
GeneID:643749	LOC643749	6	111,804,675	111,923,498	118,823	+	2	1_A375_pNL7_minus_lncRNA::1::4787, 2_A375_pNL97_plus_lncRNA::1::6894	45, -67	in gene, upstream	1	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC643749		hypothetical LOC643749	NR_034108, NR_034109, NR_034110, NR_034111	1562566_at, 236555_at	
GeneID:3910	LAMA4	6	112,429,134	112,575,828	146,694	-	1	2_A375_pNL97_plus_lncRNA::1::6896	-556	upstream	0	1	6	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LAMA4	LAMA3, LAMA4, LAMA4*-1, DKFZp686D23145	laminin, alpha 4	NM_002290, NM_001105206, NM_001105207, NM_001105208, NM_001105209, hCT2331765.0, hCT2331766.0, hCT2331767.0, hCT2352087.0, hCT24147.3	202202_s_at, 210089_s_at, 210989_at, 210990_s_at, 216081_at	NP_002281.2, NP_001098676.1, NP_001098677.1, NP_001098678.1, NP_001098679.1, EAW48266.1, EAW48267.1, EAW48268.1, EAW48269.1, EAW48270.1
GeneID:100506430	LOC100506430	6	112,557,797	112,627,885	70,088	+	1	2_A375_pNL97_plus_lncRNA::1::6896	18587	in gene	0	1	6	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100506430		hypothetical LOC100506430	XR_112921, XR_110211, XR_113909		
GeneID:3066	HDAC2	6	114,257,320	114,292,359	35,039	-	2	1_A375_pNL7_minus_lncRNA::1::4789, 2_A375_pNL97_plus_lncRNA::1::6898	-57, 231	upstream, in gene	1	1	21	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene HDAC2	YAF1, HDAC2, RPD3	histone deacetylase 2	NM_001527, NR_033441, hCT2331725.0, hCT2352103.0, hCT2352104.0, hCT12472.3	201833_at, 242141_at	NP_001518.3, EAW48255.1, EAW48252.1, EAW48253.1, EAW48254.1
GeneID:51389	RWDD1	6	116,892,583	116,914,438	21,855	+	4	1_A375_pNL7_minus_lncRNA::1::4790, 1_A375_pNL7_minus_lncRNA::1::4791, 2_A375_pNL97_plus_lncRNA::1::6899, 2_A375_pNL97_plus_lncRNA::1::6900	-103, 25593, -103, 25561	upstream, downstream, upstream, downstream	1	1	34	38	2	2_A375_pNL97_plus_lncRNA::1	63	Gene RWDD1	PTD013, CGI-24, RWDD1	RWD domain containing 1	NM_015952, NM_016104, NM_001007464, hCT2352070.0, hCT11949.2	219598_s_at	NP_057036.2, NP_057188.2, NP_001007465.1, EAW48221.1, EAW48222.1
GeneID:221302	ZUFSP	6	116,956,781	116,989,973	33,192	-	1	2_A375_pNL97_plus_lncRNA::1::6901	149	in gene	0	1	13	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene ZUFSP	dJ412I7.3, ZUFSP, C6orf113	zinc finger with UFM1-specific peptidase domain	NM_145062, hCT2332371.0, hCT12855.3	228330_at	NP_659499.2, EAW48217.1, EAW48218.1
GeneID:116150	NUS1	6	117,996,617	118,031,890	35,273	+	2	1_A375_pNL7_minus_lncRNA::1::4792, 2_A375_pNL97_plus_lncRNA::1::6902	-105, -105	upstream, upstream	1	1	116	137	1	2_A375_pNL97_plus_lncRNA::1	137	Gene NUS1	NgBR, MGC:7199, MGC117249, MGC7199, C6orf68, NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	NM_138459, hCT1640994.2	225070_at, 225071_at	NP_612468.1, EAW59309.1
GeneID:387119	C6orf204	6	118,781,935	119,031,238	249,303	-	3	1_A375_pNL7_minus_lncRNA::1::4793, 2_A375_pNL97_plus_lncRNA::1::6903, 2_A375_pNL97_plus_lncRNA::1::6904	-90, 214246, 59174	upstream, in gene, in gene	1	1	19	16.33	3	1_A375_pNL7_minus_lncRNA::1	30	Gene C6orf204	C6orf204, bA57K17.2, NY-BR-15, MGC131785	chromosome 6 open reading frame 204	NM_206921, NM_001042475, NM_001178035, hCT2331605.0, hCT12046.3	228007_at, 232444_at	NP_996804.2, NP_001035940.1, NP_001171506.1, EAW48196.1, EAW48197.1
GeneID:25842	ASF1A	6	119,215,241	119,230,336	15,095	+	2	1_A375_pNL7_minus_lncRNA::1::4794, 2_A375_pNL97_plus_lncRNA::1::6905	23, 23	in gene, in gene	1	1	81	80	1	1_A375_pNL7_minus_lncRNA::1	81	Gene ASF1A	CGI-98, HSPC146, ASF1A, CIA, DKFZp547E2110	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	NM_014034, hCT8593.2	203427_at, 203428_s_at, 213561_at	NP_054753.1, EAW48193.1
GeneID:221322	C6orf170	6	121,400,627	121,655,644	255,017	-	1	2_A375_pNL97_plus_lncRNA::1::6906	-36	upstream	0	1	10	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene C6orf170	C6orf170, dJ310J6.1, bA57L9.1, C6orf171, bA301B7.2, BROMI, FLJ30899, FLJ34235	chromosome 6 open reading frame 170	NM_152730, hCT2331483.1, hCT2331484.1, hCT10866.3	1553726_s_at, 232038_at	NP_689943.4, EAW48182.1, EAW48180.1, EAW48181.1
GeneID:7164	TPD52L1	6	125,474,879	125,584,644	109,765	+	1	1_A375_pNL7_minus_lncRNA::1::4795	1	in gene	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene TPD52L1	TPD52L2, TPD52L1, hD53, MGC8556, D53	tumor protein D52-like 1	NM_003287, NM_001003395, NM_001003396, NM_001003397, hCT1970951.1, hCT2352108.0, hCT2352109.0, hCT12023.2, hCT1951799.1, hCT1951800.1	203786_s_at, 210372_s_at	NP_003278.1, NP_001003395.1, NP_001003396.1, NP_001003397.1, EAW48144.1, EAW48147.1, EAW48142.1, EAW48143.1, EAW48145.1, EAW48146.1
GeneID:51020	HDDC2	6	125,596,496	125,623,282	26,786	-	1	2_A375_pNL97_plus_lncRNA::1::6907	162	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene HDDC2	NS5ATP2, HDDC2, dJ167O5.2, MGC87330, C6orf74, CGI-130	HD domain containing 2	NM_016063, hCT1969242.2, hCT1969243.2, hCT2340250.0, hCT2340251.0, hCT11060.3, hCT1951796.2	203259_s_at, 203260_at	NP_057147.2, EAW48141.1, EAW48136.1, EAW48137.1, EAW48139.1, EAW48140.1, EAW48138.1
GeneID:135112	NCOA7	6	126,112,001	126,252,266	140,265	+	2	1_A375_pNL7_minus_lncRNA::1::4796, 2_A375_pNL97_plus_lncRNA::1::6908	21951, 21983	in gene, in gene	1	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene NCOA7	NCOA7, MGC88425, dJ187J11.3, ESNA1, Nbla10993, ERAP140, Nbla00052, FLJ45605	nuclear receptor coactivator 7	NM_181782, NM_001122842, hCT2331523.0, hCT2331524.0, hCT2331525.0, hCT2352173.0, hCT2352174.0	1568805_at, 225344_at, 243807_at	NP_861447.3, NP_001116314.1, EAW48130.1, EAW48131.1, EAW48132.1, EAW48133.1, EAW48134.1
GeneID:135114	HINT3	6	126,277,861	126,301,390	23,529	+	2	1_A375_pNL7_minus_lncRNA::1::4797, 2_A375_pNL97_plus_lncRNA::1::6909	27, 27	in gene, in gene	1	1	28	27	1	1_A375_pNL7_minus_lncRNA::1	28	Gene HINT3	HINT3, FLJ33126, HINT4, FLJ99898, MGC22976	histidine triad nucleotide binding protein 3	NM_138571, hCT2331526.0, hCT12418.3	226533_at, 226537_at, 228697_at	NP_612638.3, EAW48129.1, EAW48128.1
GeneID:81847	RNF146	6	127,588,020	127,609,507	21,487	+	1	2_A375_pNL97_plus_lncRNA::1::6911	204	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene RNF146	dJ351K20.1, RP3-351K20.1, RNF146, DKFZp434O1427	ring finger protein 146	NM_030963, hCT2352186.0, hCT2352187.0, hCT1825330.2, hCT1951792.1, hCT1951793.1	221430_s_at, 223886_s_at	NP_112225.2, EAW48109.1, EAW48110.1, EAW48111.1, EAW48112.1, EAW48113.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:387104	C6orf174	6	127,759,551	127,840,500	80,949	-	2	1_A375_pNL7_minus_lncRNA::1::4800, 2_A375_pNL97_plus_lncRNA::1::6912	2996, 2932	in gene, in gene	1	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C6orf174	C6orf174, dJ403A15.3	chromosome 6 open reading frame 174	NM_001012279	1569146_s_at, 233050_at	NP_001012279.1
GeneID:9439	MED23	6	131,895,106	131,949,363	54,257	-	2	1_A375_pNL7_minus_lncRNA::1::4801, 2_A375_pNL97_plus_lncRNA::1::6913	-109, -45	upstream, upstream	1	1	29	47	1	2_A375_pNL97_plus_lncRNA::1	47	Gene MED23	MED23, CRSP3, SUR2, DRIP130, CRSP133, DKFZp434H0117, SUR-2, CRSP130	mediator complex subunit 23	NM_015979, NM_004830, hCT2331416.0, hCT2331417.0, hCT2352135.0, hCT12114.3	218846_at, 223946_at, 223947_s_at, 242706_s_at, 242707_at	NP_057063.2, NP_004821.2, EAW48049.1, EAW48050.1, EAW48051.1, EAW48052.1
GeneID:5169	ENPP3	6	131,958,442	132,068,550	110,108	+	2	1_A375_pNL7_minus_lncRNA::1::4801, 2_A375_pNL97_plus_lncRNA::1::6913	-8970, -9034	upstream, upstream	1	1	29	47	1	2_A375_pNL97_plus_lncRNA::1	47	Gene ENPP3	NPP3, B10, PDNP3, ENPP3, CD203c, PD-IBETA	ectonucleotide pyrophosphatase/phosphodiesterase 3	NM_005021, hCT2331597.0, hCT2331598.0, hCT2331599.0	222938_x_at, 232737_s_at	NP_005012.2, EAW48045.1, EAW48044.1, EAW48046.1
GeneID:100131774	LOC100131774	6	132,266,630	132,269,801	3,171	+	1	2_A375_pNL97_plus_lncRNA::1::6914	5066	downstream	0	1	17	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100131774		hypothetical LOC100131774	XR_112914, XR_110171, XR_113917		
GeneID:1490	CTGF	6	132,269,316	132,272,518	3,202	-	1	2_A375_pNL97_plus_lncRNA::1::6914	822	in gene	0	1	17	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CTGF	IGFBP8, CTGF, CCN2, HCS24, MGC102839, NOV2	connective tissue growth factor	NM_001901, hCT2331409.0, hCT13202.3	209101_at	NP_001892.1, EAW48038.1, EAW48039.1
GeneID:6206	RPS12	6	133,135,708	133,138,703	2,995	+	2	1_A375_pNL7_minus_lncRNA::1::4802, 2_A375_pNL97_plus_lncRNA::1::6915	-236, -220	upstream, upstream	1	1	37	32	1	1_A375_pNL7_minus_lncRNA::1	37	Gene RPS12	S12, RPS12		NM_001016, hCT2331681.0, hCT2331682.0, hCT2331683.0, hCT2331684.0	213377_x_at	NP_001007.2, EAW48008.1, EAW48009.1, EAW48010.1, EAW48011.1
GeneID:594837	SNORD101	6	133,136,446	133,136,518	72	+	2	1_A375_pNL7_minus_lncRNA::1::4802, 2_A375_pNL97_plus_lncRNA::1::6915	-974, -958	upstream, upstream	1	1	37	32	1	1_A375_pNL7_minus_lncRNA::1	37	Gene SNORD101	SNORD101, U101	small nucleolar RNA, C/D box 101	NR_002434		
GeneID:594838	SNORD100	6	133,137,941	133,138,016	75	+	2	1_A375_pNL7_minus_lncRNA::1::4802, 2_A375_pNL97_plus_lncRNA::1::6915	-2469, -2453	upstream, upstream	1	1	37	32	1	1_A375_pNL7_minus_lncRNA::1	37	Gene SNORD100	SNORD100, HBII-429	small nucleolar RNA, C/D box 100	NR_002435		
GeneID:594839	SNORA33	6	133,138,358	133,138,490	132	+	2	1_A375_pNL7_minus_lncRNA::1::4802, 2_A375_pNL97_plus_lncRNA::1::6915	-2886, -2870	upstream, upstream	1	1	37	32	1	1_A375_pNL7_minus_lncRNA::1	37	Gene SNORA33	ACA33, SNORA33	small nucleolar RNA, H/ACA box 33	NR_002436		
GeneID:9519	TBPL1	6	134,274,301	134,308,629	34,328	+	1	1_A375_pNL7_minus_lncRNA::1::4803	-957	upstream	1	0	20	12	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TBPL1	TLF, STUD, MGC:8389, MGC:9620, TRF2, TBPL1, TLP	TBP-like 1	NM_004865, hCT2331230.0, hCT2331231.0, hCT2331232.0, hCT2352066.0	208398_s_at	NP_004856.1, EAW47996.1, EAW47995.1, EAW47997.1, EAW47998.1
GeneID:54806	AHI1	6	135,605,110	135,818,903	213,793	-	2	1_A375_pNL7_minus_lncRNA::1::4806, 2_A375_pNL97_plus_lncRNA::1::6916	71, 87	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene AHI1	FLJ20069, JBTS3, dJ71N10.1, AHI1, ORF1, FLJ14023, AHI-1, DKFZp686J1653	Abelson helper integration site 1	NM_017651, NM_001134830, NM_001134831, NM_001134832, hCT2331254.0, hCT2331256.0, hCT2331257.0, hCT2331258.0, hCT2331259.0	220841_s_at, 220842_at, 221569_at, 232461_at, 244699_at	NP_060121.3, NP_001128302.1, NP_001128303.1, NP_001128304.1, EAW47962.1, EAW47966.1, EAW47963.1, EAW47964.1, EAW47965.1
GeneID:100131814	C6orf217	6	135,818,939	136,011,976	193,037	+	2	1_A375_pNL7_minus_lncRNA::1::4806, 2_A375_pNL97_plus_lncRNA::1::6916	-107, -123	upstream, upstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene C6orf217	C6orf217, NCRNA00271	chromosome 6 open reading frame 217	NR_026805		
GeneID:113115	FAM54A	6	136,552,168	136,571,449	19,281	-	1	2_A375_pNL97_plus_lncRNA::1::6918	-103	upstream	0	1	12	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene FAM54A	DUFD1, FAM54A	family with sequence similarity 54, member A	NM_138419, NM_001099286, hCT2331245.0, hCT2331246.0, hCT24553.2	228069_at, 234944_s_at, 234945_at	NP_612428.2, NP_001092756.1, EAW47953.1, EAW47954.1, EAW47955.1
GeneID:9774	BCLAF1	6	136,578,001	136,610,989	32,988	-	1	2_A375_pNL97_plus_lncRNA::1::6918	39437	downstream	0	1	12	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene BCLAF1	KIAA0164, BCLAF1, BTF, bK211L9.1	BCL2-associated transcription factor 1	NM_001077440, NM_014739, NM_001077441, hCT2331242.0, hCT2331244.0, hCT2352069.0, hCT24550.3	201083_s_at, 201084_s_at, 201101_s_at, 214499_s_at, 229454_at, 239697_at	NP_001070908.1, NP_055554.1, NP_001070909.1, EAW47949.1, EAW47951.1, EAW47952.1, EAW47950.1
GeneID:85021	REPS1	6	139,225,620	139,309,398	83,778	-	1	2_A375_pNL97_plus_lncRNA::1::6919	54	in gene	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene REPS1	RALBP1, REPS1	RALBP1 associated Eps domain containing 1	NM_031922, NM_001128617, hCT2331167.0, hCT2352180.0, hCT2352181.0, hCT9340.2, hCT1951797.1	215201_at, 215922_at, 224366_s_at	NP_114128.3, NP_001122089.1, EAW47904.1, EAW47905.1, EAW47906.1, EAW47907.1, EAW47903.1
GeneID:10370	CITED2	6	139,693,396	139,695,785	2,389	-	2	1_A375_pNL7_minus_lncRNA::1::4807, 2_A375_pNL97_plus_lncRNA::1::6920	-759, -151	upstream, upstream	1	1	25	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene CITED2	MRG1, P35SRJ, CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	NM_006079, NM_001168388, NM_001168389, hCT2331154.0, hCT2331156.0, hCT2331157.0, hCT2331158.0, hCT24122.3	207980_s_at, 209357_at, 227287_at	NP_006070.2, NP_001161860.1, NP_001161861.1, EAW47891.1, EAW47893.1, EAW47894.1, EAW47892.1, EAW47895.1
GeneID:51534	VTA1	6	142,468,410	142,542,085	73,675	+	2	1_A375_pNL7_minus_lncRNA::1::4808, 2_A375_pNL97_plus_lncRNA::1::6923	-154, -186	upstream, upstream	1	1	18	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene VTA1	DRG-1, C6orf55, My012, VTA1, DRG1, SBP1, HSPC228, LIP5, FLJ27228	Vps20-associated 1 homolog (S. cerevisiae)	NM_016485, hCT1969226.2, hCT9175.5, hCT1962368.2	223021_x_at, 223022_s_at, 224437_s_at	NP_057569.2, EAW47884.1, EAW47883.1, EAW47885.1
GeneID:57211	GPR126	6	142,623,056	142,767,403	144,347	+	1	1_A375_pNL7_minus_lncRNA::1::4809	16	in gene	1	0	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene GPR126	GPR126, APG1, PS1TP2, VIGR, DREG	G protein-coupled receptor 126	NM_001032395, NM_001032394, NM_020455, NM_198569, hCT2331298.0, hCT2331304.0, hCT2331309.1, hCT2352107.0, hCT9176.3, hCT1824736.3, hCT1824738.1	1553025_at, 213094_at, 233887_at	NP_001027567.1, NP_001027566.1, NP_940971.1, NP_065188.4, EAW47878.1, EAW47881.1, EAW47875.1, EAW47876.1, EAW47877.1, EAW47879.1, EAW47880.1
GeneID:134637	ADAT2	6	143,743,969	143,771,841	27,872	-	2	1_A375_pNL7_minus_lncRNA::1::4810, 2_A375_pNL97_plus_lncRNA::1::6924	-15, -15	upstream, upstream	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ADAT2	FLJ44213, dJ20N2, ADAT2, DKFZp686L1118, DEADC1, dJ20N2.1, TAD2	adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. cerevisiae)	NM_182503, hCT2349197.0, hCT9154.3	227213_at, 236817_at	NP_872309.2, EAW47868.1, EAW47867.1
GeneID:8504	PEX3	6	143,771,918	143,811,753	39,835	+	2	1_A375_pNL7_minus_lncRNA::1::4810, 2_A375_pNL97_plus_lncRNA::1::6924	-62, -62	upstream, upstream	1	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene PEX3	DKFZp686N14184, TRG18, FLJ13531, PEX3	peroxisomal biogenesis factor 3	NM_003630, hCT9157.4	203970_s_at, 203972_s_at	NP_003621.1, EAW47866.1
GeneID:7957	EPM2A	6	145,946,440	146,056,991	110,551	-	1	2_A375_pNL97_plus_lncRNA::1::6925	863	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene EPM2A	EPM2A, EPM2, MELF	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	NM_005670, NM_001018041, hCT2352164.0, hCT2352165.0, hCT9118.3	205231_s_at, 210870_s_at, 216079_at	NP_005661.1, NP_001018051.1, EAW47842.1, EAW47843.1, EAW47844.1
GeneID:100507557	LOC100507557	6	146,056,008	146,208,186	152,178	+	1	2_A375_pNL97_plus_lncRNA::1::6925	120	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100507557		hypothetical LOC100507557	XR_112933, XR_112934, XR_112935, XR_110184, XR_110183, XR_110185, XR_113930, XR_113929, XR_113931		
GeneID:2911	GRM1	6	146,348,782	146,758,731	409,949	+	2	1_A375_pNL7_minus_lncRNA::1::4811, 2_A375_pNL97_plus_lncRNA::1::6926	722, 818	in gene, in gene	1	1	15	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene GRM1	MGLUR1, GRM1A, GPRC1A, mGlu1, GRM1, MGLUR1A	glutamate receptor, metabotropic 1	NM_000838, NM_001114329, hCT2331330.0, hCT7607.3	207299_s_at, 210939_s_at, 210940_s_at	NP_000829.2, NP_001107801.1, EAW47834.1, EAW47835.1
GeneID:23328	SASH1	6	148,663,729	148,873,184	209,455	+	1	2_A375_pNL97_plus_lncRNA::1::6927	175	in gene	0	1	8	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SASH1	dJ323M4, KIAA0790, SH3D6A, SASH1, RP3-323M4.1, dJ323M4.1	SAM and SH3 domain containing 1	NM_015278, hCT2330910.0, hCT7809.3	213236_at, 226022_at, 41644_at	NP_056093.3, EAW47815.1, EAW47816.1
GeneID:10090	UST	6	149,068,271	149,398,126	329,855	+	3	1_A375_pNL7_minus_lncRNA::1::4812, 1_A375_pNL7_minus_lncRNA::1::4813, 2_A375_pNL97_plus_lncRNA::1::6928	188785, 265073, 265073	in gene, in gene, in gene	1	1	16	12.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene UST	2OST, UST	uronyl-2-sulfotransferase	NM_005715, hCT2330916.0	205138_s_at, 205139_s_at	NP_005706.1, EAW47812.1
GeneID:23118	MAP3K7IP2	6	149,639,436	149,732,747	93,311	+	1	2_A375_pNL97_plus_lncRNA::1::6929	-1068	upstream	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MAP3K7IP2	FLJ21885, MAP3K7IP2, TAB2, CHTD2, KIAA0733	TGF-beta activated kinase 1/MAP3K7 binding protein 2	NM_015093, hCT2330924.0, hCT2330926.0, hCT13625.3	210284_s_at, 212184_s_at	NP_055908.1, EAW47805.1, EAW47806.1, EAW47807.1
GeneID:85313	PPIL4	6	149,825,631	149,867,171	41,540	-	2	1_A375_pNL7_minus_lncRNA::1::4814, 2_A375_pNL97_plus_lncRNA::1::6930	-29, 3	upstream, in gene	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PPIL4	HDCME13P, PPIL4	peptidylprolyl isomerase (cyclophilin)-like 4	NM_139126, hCT2330712.1, hCT13623.4	226472_at	NP_624311.1, EAW47800.1, EAW47799.1
GeneID:348995	NUP43	6	150,045,457	150,067,688	22,231	-	1	2_A375_pNL97_plus_lncRNA::1::6931	-3320	upstream	0	1	9	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene NUP43	NUP43, bA350J20.1, p42, FLJ13287	nucleoporin 43kDa	NM_198887	219007_at, 235474_at	NP_942590.1
GeneID:5110	PCMT1	6	150,070,831	150,132,557	61,726	+	1	2_A375_pNL97_plus_lncRNA::1::6931	177	in gene	0	1	9	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene PCMT1	PCMT1		NM_005389, hCT2330960.0, hCT12094.2, hCT1953605.1	205202_at, 208857_s_at, 210156_s_at	NP_005380.2, EAW47788.1, EAW47786.1, EAW47787.1
GeneID:55005	RMND1	6	151,725,989	151,773,316	47,327	-	1	1_A375_pNL7_minus_lncRNA::1::4815	-60	upstream	1	0	21	14	1	1_A375_pNL7_minus_lncRNA::1	21	Gene RMND1	bA351K16.3, MGC88260, MGC117362, RMND1, FLJ20627, bA351K16, RMD1, MGC149570, C6orf96	required for meiotic nuclear division 1 homolog (S. cerevisiae)	NM_017909, hCT2330734.0, hCT2352200.0, hCT13079.3, hCT1953609.1	1555201_a_at, 220329_s_at	NP_060379.2, EAW47749.1, EAW47746.1, EAW47747.1, EAW47748.1
GeneID:79624	C6orf211	6	151,773,422	151,791,232	17,810	+	1	1_A375_pNL7_minus_lncRNA::1::4815	-46	upstream	1	0	21	14	1	1_A375_pNL7_minus_lncRNA::1	21	Gene C6orf211	C6orf211, DKFZp566I174, FLJ12910	chromosome 6 open reading frame 211	NM_024573, hCT2352203.0, hCT1953611.1	218195_at	NP_078849.1, EAW47744.1, EAW47745.1
GeneID:2099	ESR1	6	152,011,631	152,424,409	412,778	+	1	1_A375_pNL7_minus_lncRNA::1::4816	156669	in gene	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ESR1	ESRA, ESR, DKFZp686N23123, ER, NR3A1, Era, ESR1	estrogen receptor 1	NM_000125, NM_001122740, NM_001122741, NM_001122742, hCT2331066.0, hCT1953606.1	205225_at, 211233_x_at, 211234_x_at, 211235_s_at, 211627_x_at, 215552_s_at, 217163_at, 217190_x_at	NP_000116.2, NP_001116212.1, NP_001116213.1, NP_001116214.1, EAW47740.1, EAW47741.1
GeneID:7432	VIP	6	153,071,933	153,080,900	8,967	+	1	1_A375_pNL7_minus_lncRNA::1::4817	19	in gene	1	0	14	13	1	1_A375_pNL7_minus_lncRNA::1	14	Gene VIP	PHM27, VIP, MGC13587	vasoactive intestinal peptide	NM_003381, NM_194435, hCT2352148.0, hCT13142.2	206577_at	NP_003372.1, NP_919416.1, EAW47724.1, EAW47725.1
GeneID:4988	OPRM1	6	154,331,636	154,568,001	236,365	+	2	1_A375_pNL7_minus_lncRNA::1::4818, 2_A375_pNL97_plus_lncRNA::1::6932	29068, 29100	in gene, in gene	1	1	45	76	1	2_A375_pNL97_plus_lncRNA::1	76	Gene OPRM1	LMOR, MOR1, OPRM, OPRM1, KIAA0403, MOR	opioid receptor, mu 1	NM_001008503, NM_001008505, NM_001145285, NM_000914, NM_001008504, NM_001145279, NM_001145280, NM_001145281, NM_001145284, NM_001145287, NM_001145286, NM_001145282, NM_001145283, hCT2330621.0, hCT23523.1	207994_s_at, 211359_s_at	NP_001008503.2, NP_001008505.2, NP_001008504.2, NP_000905.3, NP_001138757.1, NP_001138751.1, NP_001138752.1, NP_001138753.1, NP_001138756.1, NP_001138759.1, NP_001138758.1, NP_001138754.1, NP_001138755.1, EAW47704.1, EAW47705.1
GeneID:22828	RBM16	6	155,054,512	155,155,194	100,682	+	1	2_A375_pNL97_plus_lncRNA::1::6933	64	in gene	0	1	17	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene RBM16	KIAA1116, RBM16, SCAF8	RNA binding motif protein 16	NM_014892, hCT2330614.0, hCT24177.3	203250_at	NP_055707.3, EAW47696.1, EAW47697.1
GeneID:26230	TIAM2	6	155,411,423	155,578,857	167,434	+	2	1_A375_pNL7_minus_lncRNA::1::4819, 2_A375_pNL97_plus_lncRNA::1::6934	36961, 81137	in gene, in gene	1	1	16.5	14.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene TIAM2	TIAM-2, STEF, FLJ41865, TIAM2	T-cell lymphoma invasion and metastasis 2	NM_012454, NM_001010927, hCT2330615.0, hCT1953626.2	219950_s_at, 222942_s_at	NP_036586.2, NP_001010927.1, EAW47692.1, EAW47693.1
GeneID:57492	ARID1B	6	157,099,064	157,531,913	432,849	+	2	1_A375_pNL7_minus_lncRNA::1::4820, 2_A375_pNL97_plus_lncRNA::1::6935	371016, 243656	in gene, in gene	1	1	12.5	13.5	2	2_A375_pNL97_plus_lncRNA::1	15	Gene ARID1B	OSA2, KIAA1235, ARID1B, ELD/OSA1, BRIGHT, 6A3-5, p250R, P250R, BAF250B, DAN15, BAF250b	AT rich interactive domain 1B (SWI1-like)	NM_017519, NM_020732, hCT2332458.1, hCT2332459.1, hCT2332460.1, hCT2332461.1, hCT2332462.1, hCT2332463.1, hCT2332467.1, hCT2352061.0	1566989_at, 1566990_x_at, 1566991_at, 233339_s_at	NP_059989.2, NP_065783.3, EAW47679.1, EAW47683.1, EAW47684.1, EAW47685.1, EAW47678.1, EAW47680.1, EAW47681.1, EAW47682.1
GeneID:729515	C6orf35	6	157,710,054	157,745,253	35,199	-	1	2_A375_pNL97_plus_lncRNA::1::6936	784	in gene	0	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene C6orf35	FLJ10029, BM033, MGC34308, C6orf35	chromosome 6 open reading frame 35	NM_018452	218453_s_at, 222638_s_at, 230457_at	NP_060922.2
GeneID:79683	ZDHHC14	6	157,802,557	158,094,977	292,420	+	2	1_A375_pNL7_minus_lncRNA::1::4821, 2_A375_pNL97_plus_lncRNA::1::6937	147939, 74563	in gene, in gene	1	1	14.5	13	2	2_A375_pNL97_plus_lncRNA::1	17	Gene ZDHHC14	FLJ20984, ZDHHC14, NEW1CP	zinc finger, DHHC-type containing 14	NM_024630, NM_153746, hCT2332472.0, hCT2332474.0, hCT2332475.0, hCT2352162.0, hCT6453.3, hCT1814540.1	1556967_at, 219247_s_at	NP_078906.2, NP_714968.1, EAW47670.1, EAW47671.1, EAW47672.1, EAW47675.1, EAW47673.1, EAW47674.1
GeneID:57583	TMEM181	6	158,957,468	159,056,467	98,999	+	3	1_A375_pNL7_minus_lncRNA::1::4823, 2_A375_pNL97_plus_lncRNA::1::6939, 1_A375_pNL7_minus_lncRNA::1::4824	-252, -156, 108132	upstream, upstream, downstream	1	1	20.5	18	2	2_A375_pNL97_plus_lncRNA::1	27	Gene TMEM181	GPR178, KIAA1423, TMEM181	transmembrane protein 181	NM_020823	225127_at	NP_065874.1
GeneID:6993	DYNLT1	6	159,057,506	159,065,804	8,298	-	1	1_A375_pNL7_minus_lncRNA::1::4824	204	in gene	1	0	17	9	1	1_A375_pNL7_minus_lncRNA::1	17	Gene DYNLT1	DYNLT1, MGC111571, tctex-1, CW-1, TCTEL1	dynein, light chain, Tctex-type 1	NM_006519, hCT2343703.0, hCT2352176.0, hCT7863.3, hCT1953582.2, hCT1963141.2	201999_s_at	NP_006510.1, EAW47656.1, EAW47655.1, EAW47657.1, EAW47658.1, EAW47659.1
GeneID:94120	SYTL3	6	159,071,046	159,185,901	114,855	+	1	1_A375_pNL7_minus_lncRNA::1::4824	-5446	upstream	1	0	17	9	1	1_A375_pNL7_minus_lncRNA::1	17	Gene SYTL3	MGC118883, MGC118885, SYTL3, MGC105130, MGC118884, SLP3	synaptotagmin-like 3	NM_001009991, hCT2330940.0, hCT2352078.0, hCT2352079.0, hCT2352080.0, hCT9214.4, hCT1966347.1, hCT1966348.1	1561882_at, 1562255_at, 236864_at, 238423_at, 242109_at	NP_001009991.2, EAW47650.1, EAW47648.1, EAW47651.1, EAW47652.1, EAW47654.1, EAW47649.1, EAW47653.1
GeneID:83861	RSPH3	6	159,398,266	159,421,198	22,932	-	1	2_A375_pNL97_plus_lncRNA::1::6940	225	in gene	0	1	11	11	1	2_A375_pNL97_plus_lncRNA::1	11	Gene RSPH3	dJ111C20.1, RSHL2, RSPH3, RSP3	radial spoke 3 homolog (Chlamydomonas)	NM_031924, hCT25232.3, hCT1953636.1, hCT1953637.1	1568613_at, 223713_at	NP_114130.3, EAW47643.1, EAW47641.1, EAW47642.1
GeneID:6648	SOD2	6	160,100,148	160,114,353	14,205	-	2	2_A375_pNL97_plus_lncRNA::1::6941, 2_A375_pNL97_plus_lncRNA::1::6942	417, -207	in gene, upstream	0	1	13	17.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene SOD2	MNSOD, MVCD6, Mn-SOD, IPOB, IPO-B, SOD2	superoxide dismutase 2, mitochondrial	NM_000636, NM_001024465, NM_001024466, hCT2330550.0, hCT25235.3, hCT1953639.1	1566342_at, 215078_at, 215223_s_at, 216841_s_at	NP_000627.2, NP_001019636.1, NP_001019637.1, EAW47629.1, EAW47630.1, EAW47631.1
GeneID:9589	WTAP	6	160,148,152	160,177,351	29,199	+	2	1_A375_pNL7_minus_lncRNA::1::4825, 2_A375_pNL97_plus_lncRNA::1::6943	-72, 35246	upstream, downstream	1	1	12	11	2	1_A375_pNL7_minus_lncRNA::1	13	Gene WTAP	WTAP, MGC3925, KIAA0105, DKFZp686F20131	Wilms tumor 1 associated protein	NM_004906, NM_152857, NM_152858, hCT2330634.1, hCT2330637.1, hCT2330638.1, hCT2350292.0, hCT2352159.0, hCT25228.3, hCT1953629.2	1560274_at, 203137_at, 210285_x_at, 214759_at, 229630_s_at, 241626_at	NP_004897.2, NP_690596.1, NP_690597.1, EAW47625.1, EAW47627.1, EAW47628.1, EAW47622.1, EAW47623.1, EAW47624.1, EAW47626.1
GeneID:100129518	LOC100129518	6	160,181,290	160,183,364	2,074	-	1	2_A375_pNL97_plus_lncRNA::1::6943	-34	upstream	0	1	11	10	1	2_A375_pNL97_plus_lncRNA::1	10	Gene LOC100129518	FLJ40076	hypothetical LOC100129518	XR_112942, XR_110194, XR_113939		
GeneID:39	ACAT2	6	160,182,989	160,200,087	17,098	+	1	2_A375_pNL97_plus_lncRNA::1::6943	409	in gene	0	1	11	10	1	2_A375_pNL97_plus_lncRNA::1	10	Gene ACAT2	ACAT2		NM_005891, hCT25231.1, hCT1953633.1	209608_s_at	NP_005882.2, EAW47620.1, EAW47619.1
GeneID:4216	MAP3K4	6	161,412,822	161,538,417	125,595	+	2	1_A375_pNL7_minus_lncRNA::1::4826, 2_A375_pNL97_plus_lncRNA::1::6944	-22, 46456	upstream, in gene	1	1	15.5	17	2	2_A375_pNL97_plus_lncRNA::1	19	Gene MAP3K4	MEKK4, PRO0412, MAP3K4, MTK1, MAPKKK4, KIAA0213, FLJ42439	mitogen-activated protein kinase kinase kinase 4	NM_006724, NM_005922, hCT24617.3, hCT1950009.1	204089_x_at, 216199_s_at	NP_006715.2, NP_005913.2, EAW47586.1, EAW47587.1
GeneID:9444	QKI	6	163,835,675	163,999,628	163,953	+	1	2_A375_pNL97_plus_lncRNA::1::6945	-1083	upstream	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene QKI	QK1, Hqk, QK3, QKI, DKFZp586I0923, QK	quaking homolog, KH domain RNA binding (mouse)	NM_006775, NM_206853, NM_206854, NM_206855, hCT2331178.0, hCT2331179.0, hCT2331180.0, hCT2331181.0, hCT2331182.0, hCT2331183.0, hCT1950075.1	1555154_a_at, 212262_at, 212263_at, 212265_at, 212636_at, 214541_s_at, 214543_x_at, 241938_at	NP_006766.1, NP_996735.1, NP_996736.1, NP_996737.1, EAW47554.1, EAW47556.1, EAW47555.1, EAW47557.1, EAW47558.1, EAW47559.1, EAW47560.1
GeneID:100505705	LOC100505705	6	166,307,330	166,309,725	2,395	-	2	1_A375_pNL7_minus_lncRNA::1::4827, 2_A375_pNL97_plus_lncRNA::1::6946	477, 653	in gene, in gene	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100505705	SDIM1	hypothetical protein LOC100505705	XM_003120019, XM_003118900, XM_003120538		XP_003120067.1, XP_003118948.1, XP_003120586.1
GeneID:90632	C6orf176	6	166,337,536	166,401,527	63,991	-	2	1_A375_pNL7_minus_lncRNA::1::4828, 2_A375_pNL97_plus_lncRNA::1::6949	-9, 7	upstream, in gene	1	1	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene C6orf176	bA142J11.1, C6orf176	chromosome 6 open reading frame 176	NR_026860, NR_026861	230251_at	
GeneID:441177	LOC441177	6	166,401,039	166,403,103	2,064	+	2	1_A375_pNL7_minus_lncRNA::1::4828, 2_A375_pNL97_plus_lncRNA::1::6949	497, 481	in gene, in gene	1	1	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene LOC441177	MGC131672	hypothetical LOC441177	NR_027284		
GeneID:51660	BRP44L	6	166,778,407	166,796,486	18,079	-	1	2_A375_pNL97_plus_lncRNA::1::6950	630	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene BRP44L	BRP44L, CGI-129, dJ68L15.3	brain protein 44-like	NM_016098, hCT1968330.2, hCT2330320.1, hCT6037.2, hCT1961265.2, hCT1961266.1	218024_at	NP_057182.1, EAW47527.1, EAW47528.1, EAW47529.1, EAW47530.1, EAW47531.1
GeneID:11116	FGFR1OP	6	167,412,816	167,454,066	41,250	+	1	2_A375_pNL97_plus_lncRNA::1::6951	112	in gene	0	1	11	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene FGFR1OP	FGFR1OP, FOP	FGFR1 oncogene partner	NM_007045, NM_194429	1565678_s_at, 205587_at, 205588_s_at	NP_008976.1, NP_919410.1
GeneID:401286	LOC401286	6	168,067,520	168,079,903	12,383	-	1	2_A375_pNL97_plus_lncRNA::1::6952	-4001	upstream	0	1	11	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC401286		hypothetical LOC401286	XR_112949, XR_110199, XR_113944, hCT2359785.0		EAW47492.1
GeneID:253769	WDR27	6	169,857,307	170,102,159	244,852	-	2	1_A375_pNL7_minus_lncRNA::1::4829, 2_A375_pNL97_plus_lncRNA::1::6955	-65, -81	upstream, upstream	1	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene WDR27	MGC43690, WDR27	WD repeat domain 27	NM_182552, hCT2330187.1, hCT2330189.1, hCT2330190.1, hCT2330192.1	228326_at, 235298_at, 235576_at, 238074_at, 238239_at	NP_872358.3, EAW47446.1, EAW47447.1, EAW47449.1, EAW47450.1
GeneID:387263	C6orf120	6	170,102,257	170,106,402	4,145	+	2	1_A375_pNL7_minus_lncRNA::1::4829, 2_A375_pNL97_plus_lncRNA::1::6955	-33, -17	upstream, upstream	1	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C6orf120	C6orf120, bA160E12.4	chromosome 6 open reading frame 120	NM_001029863	221786_at, 221787_at	NP_001025034.1

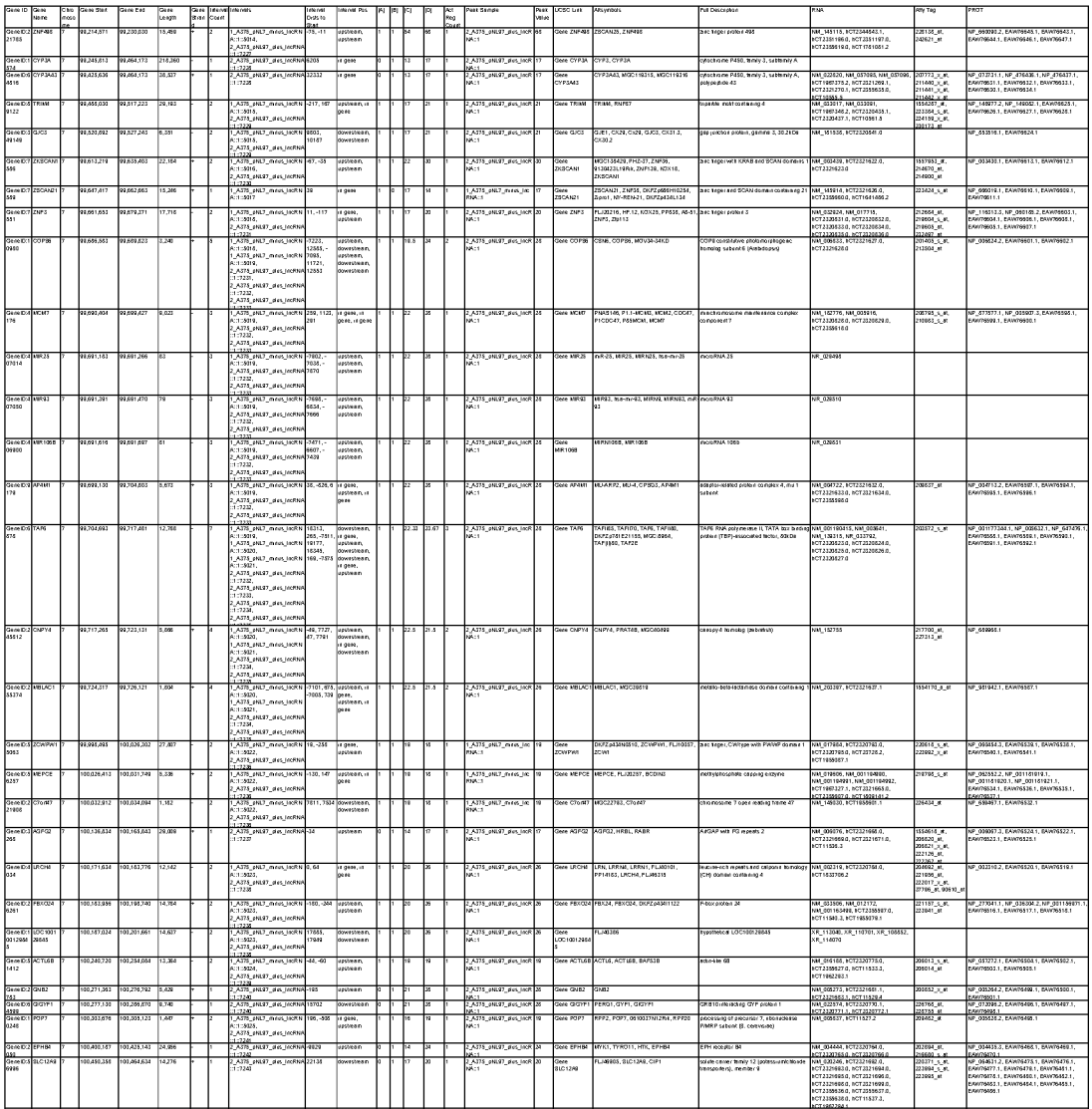
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:55274	PHF10	6	170,104,001	170,124,106	20,105	-	2	1_A375_pNL7_minus_lncRNA::1::4829, 2_A375_pNL97_plus_lncRNA::1::6955	21882, 21866	downstream, downstream	1	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PHF10	FLJ10975, PHF10, BAF45A, XAP135, MGC111009	PHD finger protein 10	NM_018288, NM_133325, hCT2330175.0, hCT2330176.0, hCT2330181.0	219126_at, 225048_at	NP_060758.2, NP_579866.2, EAW47442.1, EAW47443.1, EAW47444.1
GeneID:6991	TCTE3	6	170,140,215	170,151,638	11,423	-	1	2_A375_pNL97_plus_lncRNA::1::6956	-138	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TCTE3	TCTE3, TCTEX1D3, MGC142199	t-complex-associated-testis-expressed 3	NM_174910, hCT1640662.3	1554400_at, 1554401_a_at, 1557945_at, 232258_at	NP_777570.1, EAW47439.1
GeneID:55780	C6orf70	6	170,151,721	170,181,617	29,896	+	1	2_A375_pNL97_plus_lncRNA::1::6956	55	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene C6orf70	C6orf70, FLJ11152, dJ266L20.3	chromosome 6 open reading frame 70	NM_018341, hCT2352160.0, hCT6211.3, hCT1950066.1	227656_at	NP_060811.1, EAW47437.1, EAW47436.1, EAW47438.1
GeneID:5689	PSMB1	6	170,844,204	170,862,417	18,213	-	2	1_A375_pNL7_minus_lncRNA::1::4830, 2_A375_pNL97_plus_lncRNA::1::6958	-879, -1231	upstream, upstream	1	1	15	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene PSMB1	PSC5, PSMB1, FLJ25321, KIAA1838, HC5, PMSB1	proteasome (prosome, macropain) subunit, beta type, 1	NM_002793, hCT2330138.0, hCT2330139.0, hCT2330140.0, hCT2330142.0	200876_s_at, 214288_s_at, 214289_at	NP_002784.1, EAW47422.1, EAW47420.1, EAW47421.1, EAW47423.1
GeneID:6908	TBP	6	170,863,421	170,881,958	18,537	+	2	1_A375_pNL7_minus_lncRNA::1::4830, 2_A375_pNL97_plus_lncRNA::1::6958	-125, 227	upstream, in gene	1	1	15	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene TBP	GTF2D1, TBP, TFIID, MGC126055, GTF2D, HDL4, SCA17, MGC117320, MGC126054	TATA box binding protein	NM_003194, NM_001172085, hCT2330396.0, hCT2330398.0	203135_at	NP_003185.1, NP_001165556.1, EAW47418.1, EAW47419.1
GeneID:5154	PDGFA	7	536,895	559,481	22,586	-	1	2_A375_pNL97_plus_lncRNA::1::6960	889	in gene	0	1	7	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PDGFA	PDGF-A, PDGFA, PDGF1	platelet-derived growth factor alpha polypeptide	NM_002607, NM_033023, hCT2272389.0, hCT2272390.0, hCT1963886.1	1564472_at, 205463_s_at, 216867_s_at	NP_002598.4, NP_148983.1, EAW87160.1, EAW87161.1, EAW87162.1
GeneID:441307	FLJ44511	7	560,028	564,869	4,841	+	1	2_A375_pNL97_plus_lncRNA::1::6960	-1436	upstream	0	1	7	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FLJ44511		hypothetical LOC441307	NR_033963		
GeneID:23353	SUN1	7	855,194	914,557	59,363	+	2	1_A375_pNL7_minus_lncRNA::1::4831, 2_A375_pNL97_plus_lncRNA::1::6961	60902, 60758	downstream, downstream	1	1	24	23	1	1_A375_pNL7_minus_lncRNA::1	24	Gene SUN1	SUN1, KIAA0810, UNC84A, FLJ12407, MGC176649	Sad1 and UNC84 domain containing 1	NM_001130965, NM_025154, NM_001171944, NM_001171945, NM_001171946, hCT2271241.1, hCT2271242.1, hCT2271243.1, hCT2271244.1, hCT1955830.2	206487_at, 212074_at, 230210_at	NP_001124437.1, NP_079430.3, NP_001165415.1, NP_001165416.1, NP_001165417.1, EAW87174.1, EAW87175.1, EAW87176.1, EAW87177.1, EAW87178.1
GeneID:51608	C7orf20	7	916,191	936,071	19,880	+	2	1_A375_pNL7_minus_lncRNA::1::4831, 2_A375_pNL97_plus_lncRNA::1::6961	-95, -239	upstream, upstream	1	1	24	23	1	1_A375_pNL7_minus_lncRNA::1	24	Gene C7orf20	GET4, CEE, C7orf20, CGI-20, TRC35	chromosome 7 open reading frame 20	NM_015949, hCT1786064.1, hCT1955831.1	223511_s_at, 224808_s_at, 224816_at, 227588_s_at	NP_057033.2, EAW87180.1, EAW87179.1
GeneID:100505531	LOC100505531	7	919,586	921,830	2,244	+	2	1_A375_pNL7_minus_lncRNA::1::4831, 2_A375_pNL97_plus_lncRNA::1::6961	-3490, -3634	upstream, upstream	1	1	24	23	1	1_A375_pNL7_minus_lncRNA::1	24	Gene LOC100505531		hypothetical LOC100505531	XR_112963, XR_110623, XR_108724, XR_113974		
GeneID:90639	COX19	7	1,004,486	1,015,235	10,749	-	2	1_A375_pNL7_minus_lncRNA::1::4832, 2_A375_pNL97_plus_lncRNA::1::6962	67, 35	in gene, in gene	1	1	40	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene COX19	COX19, MGC104475	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	NM_001031617, hCT1645068.3	231831_at, 235533_at	NP_001026788.1, EAW87185.1
GeneID:54905	CYP2W1	7	1,022,835	1,029,276	6,441	+	2	1_A375_pNL7_minus_lncRNA::1::4832, 2_A375_pNL97_plus_lncRNA::1::6962	-7667, -7635	upstream, upstream	1	1	40	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene CYP2W1	MGC34287, CYP2W1	cytochrome P450, family 2, subfamily W, polypeptide 1	NM_017781, hCT2356923.0, hCT1786066.1	220562_at	NP_060251.2, EAW87187.1, EAW87186.1
GeneID:90637	ZFAND2A	7	1,192,543	1,199,855	7,312	-	1	1_A375_pNL7_minus_lncRNA::1::4833	175	in gene	1	0	15	16	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ZFAND2A	ZFAND2A, AIRAP	zinc finger, AN1-type domain 2A	NM_182491, hCT2356895.0, hCT1783095.2	226650_at	NP_872297.2, EAW87197.1, EAW87196.1
GeneID:79778	MICALL2	7	1,473,995	1,499,109	25,114	-	1	1_A375_pNL7_minus_lncRNA::1::4834	325	in gene	1	0	25	12	1	1_A375_pNL7_minus_lncRNA::1	25	Gene MICALL2	FLJ44858, MICAL-L2, MGC46023, FLJ23471, FLJ41996, MICALL2, FLJ45410, JRAB	MICAL-like 2	NM_182924, hCT2356924.0, hCT8762.3	1555862_s_at, 219332_at	NP_891554.1, EAW87201.1, EAW87200.1
GeneID:26173	INTS1	7	1,509,913	1,544,018	34,105	-	3	1_A375_pNL7_minus_lncRNA::1::4835, 2_A375_pNL97_plus_lncRNA::1::6963, 2_A375_pNL97_plus_lncRNA::1::6964	-78, -78, -9022	upstream, upstream, upstream	1	1	48.5	64.5	2	2_A375_pNL97_plus_lncRNA::1	107	Gene INTS1	FLJ46624, KIAA1440, INTS1, INT1, NET28, DKFZp586J0619	integrator complex subunit 1	NM_001080453	212210_at, 212212_s_at	NP_001073922.2
GeneID:7975	MAFK	7	1,570,368	1,582,679	12,311	+	1	2_A375_pNL97_plus_lncRNA::1::6965	1952	in gene	0	1	7	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene MAFK	NFE2U, FLJ32205, MAFK, MGC71717, P18	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	NM_002360, hCT2271316.1, hCT9963.3	206750_at, 226206_at	NP_002351.1, EAW87208.1, EAW87207.1
GeneID:100128653	LOC100128653	7	1,572,090	1,574,516	2,426	-	1	2_A375_pNL97_plus_lncRNA::1::6965	2196	in gene	0	1	7	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100128653		hypothetical LOC100128653	XR_112966, XR_110626, XR_108727, XR_113977		
GeneID:202915	TMEM184A	7	1,581,871	1,596,066	14,195	-	1	2_A375_pNL97_plus_lncRNA::1::6965	23746	downstream	0	1	7	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TMEM184A	FLJ24011, MGC9712, TMEM184A	transmembrane protein 184A	NM_001097620, hCT2272412.0, hCT2356894.0, hCT10533.2	1558281_a_at, 235817_at	NP_001091089.1, EAW87210.1, EAW87209.1, EAW87211.1
GeneID:84262	PSMG3	7	1,606,968	1,609,668	2,700	-	1	2_A375_pNL97_plus_lncRNA::1::6966	-92	upstream	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene PSMG3	MGC10911, PSMG3, PAC3, C7orf48	proteasome (prosome, macropain) assembly chaperone 3	NM_032302, NM_001134340, hCT10534.3, hCT1960836.1	223363_at	NP_115678.1, NP_001127812.1, EAW87212.1, EAW87213.1
GeneID:114796	KIAA1908	7	1,609,709	1,629,262	19,553	+	1	2_A375_pNL97_plus_lncRNA::1::6966	51	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene KIAA1908		hypothetical LOC114796	NR_027328, NR_027329, NR_021487	1561666_a_at	
GeneID:8379	MAD1L1	7	1,855,428	2,272,583	417,155	-	1	1_A375_pNL7_minus_lncRNA::1::4836	-89	upstream	1	0	28	18	1	1_A375_pNL7_minus_lncRNA::1	28	Gene MAD1L1	MAD1, TP53I9, TXBP181, PIG9, HsMAD1, MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	NM_003550, NM_001013836, NM_001013837, hCT2281848.0, hCT2281849.0	204857_at	NP_003541.2, NP_001013858.1, NP_001013859.1, EAW87219.1, EAW87220.1
GeneID:29960	FTSJ2	7	2,273,926	2,281,833	7,907	-	1	1_A375_pNL7_minus_lncRNA::1::4836	9161	downstream	1	0	28	18	1	1_A375_pNL7_minus_lncRNA::1	28	Gene FTSJ2	DKFZp686J14194, FJH1, FTSJ2	FtsJ homolog 2 (E. coli)	NM_013393	218356_at, 222130_s_at	NP_037525.1
GeneID:4521	NUDT1	7	2,281,857	2,290,780	8,923	+	1	1_A375_pNL7_minus_lncRNA::1::4836	-9185	upstream	1	0	28	18	1	1_A375_pNL7_minus_lncRNA::1	28	Gene NUDT1	MTH1, NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	NM_002452, NM_198948, NM_198949, NM_198950, NM_198952, NM_198953, NM_198954, hCT2356910.0, hCT2356911.0, hCT2356912.0, hCT2356913.0, hCT2356914.0, hCT2356915.0, hCT9490.2, hCT1962802.1	204766_s_at	NP_002443.3, NP_945186.1, NP_945187.1, NP_945188.1, NP_945190.1, NP_945191.1, NP_945192.1, EAW87225.1, EAW87226.1, EAW87227.1, EAW87228.1, EAW87229.1, EAW87230.1, EAW87231.1, EAW87232.1
GeneID:8662	EIF3B	7	2,394,474	2,420,380	25,906	+	2	1_A375_pNL7_minus_lncRNA::1::4837, 2_A375_pNL97_plus_lncRNA::1::6967	-136, -170	upstream, upstream	1	1	52	59	1	2_A375_pNL97_plus_lncRNA::1	59	Gene EIF3B	EIF3-P116, EIF3-ETA, MGC104664, EIF3 P110, PRT1, EIF3B, MGC131875, EIF3S9	eukaryotic translation initiation factor 3, subunit B	NM_001037283, NM_003751, hCT2281510.0, hCT2356898.0, hCT2356899.0, hCT2356900.0, hCT2356901.0	203462_x_at, 208688_x_at, 211501_s_at, 236274_at, 237457_at, 242550_at	NP_001032360.1, NP_003742.2, EAW87237.1, EAW87238.1, EAW87240.1, EAW87241.1, EAW87239.1
GeneID:221927	C7orf27	7	2,577,511	2,595,146	17,635	-	4	1_A375_pNL7_minus_lncRNA::1::4838, 1_A375_pNL7_minus_lncRNA::1::4839, 2_A375_pNL97_plus_lncRNA::1::6968, 2_A375_pNL97_plus_lncRNA::1::6969	106, -3462, -86, -3446	in gene, upstream, upstream, upstream	1	1	17.5	23	2	2_A375_pNL97_plus_lncRNA::1	26	Gene C7orf27	BRAT1, C7orf27, BAAT1, MGC22916	BRCA1-associated ATM activator 1	NM_152743, hCT1967739.1, hCT2281828.0, hCT2281831.0, hCT2281832.0, hCT2356918.0, hCT9492.2	225437_s_at	NP_689956.1, EAW87259.1, EAW87255.1, EAW87256.1, EAW87258.1, EAW87260.1, EAW87257.1
GeneID:23288	IQCE	7	2,598,632	2,654,368	55,736	+	4	1_A375_pNL7_minus_lncRNA::1::4838, 1_A375_pNL7_minus_lncRNA::1::4839, 2_A375_pNL97_plus_lncRNA::1::6968, 2_A375_pNL97_plus_lncRNA::1::6969	-3592, -24, -3400, -40	upstream, upstream, upstream, upstream	1	1	17.5	23	2	2_A375_pNL97_plus_lncRNA::1	26	Gene IQCE	MGC41907, KIAA1023, IQCE, 1700028P05Rik	IQ motif containing E	NM_152558, NM_001100390, hCT2281529.0, hCT2356916.0, hCT2356917.0, hCT1828117.2	204202_at, 217124_at	NP_689771.3, NP_001093860.1, EAW87261.1, EAW87262.1, EAW87263.1, EAW87264.1
GeneID:80727	TTYH3	7	2,671,603	2,704,436	32,833	+	1	2_A375_pNL97_plus_lncRNA::1::6970	1885	in gene	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TTYH3	KIAA1691, TTYH3	tweety homolog 3 (Drosophila)	NM_025250, hCT2281531.0, hCT2281533.0, hCT2356921.0, hCT9496.3	224674_at	NP_079526.1, EAW87265.1, EAW87266.1, EAW87267.1, EAW87268.1
GeneID:84433	CARD11	7	2,945,769	3,083,579	137,810	-	2	1_A375_pNL7_minus_lncRNA::1::4841, 2_A375_pNL97_plus_lncRNA::1::6972	15739, 15675	in gene, in gene	1	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CARD11	CARD11, CARMA1, MGC133069, BIMP3	caspase recruitment domain family, member 11	NM_032415, hCT1967740.1, hCT2270083.0, hCT9497.4, hCT1950355.2	223514_at	NP_115791.3, EAW87277.1, EAW87276.1, EAW87278.1, EAW87279.1
GeneID:221937	FOXK1	7	4,721,930	4,811,074	89,144	+	2	1_A375_pNL7_minus_lncRNA::1::4843, 2_A375_pNL97_plus_lncRNA::1::6977	93366, 93302	downstream, downstream	1	1	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene FOXK1	FOXK1L, FOXK1, FLJ14977	forkhead box K1	NM_001037165, hCT5982.3	226715_at, 230342_at, 235519_at	NP_001032242.1, EAW87291.1
GeneID:9907	KIAA0415	7	4,815,264	4,831,399	16,135	+	2	1_A375_pNL7_minus_lncRNA::1::4843, 2_A375_pNL97_plus_lncRNA::1::6977	32, -32	in gene, upstream	1	1	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene KIAA0415	KIAA0415, SPG48		NM_014855, hCT2270007.0, hCT2270009.0, hCT2270011.0, hCT2270012.0, hCT2270013.0, hCT2356919.0	209912_s_at	NP_055670.1, EAW87297.1, EAW87294.1, EAW87295.1, EAW87298.1, EAW87299.1, EAW87296.1
GeneID:221938	MMD2	7	4,945,620	4,998,844	53,224	-	2	1_A375_pNL7_minus_lncRNA::1::4844, 2_A375_pNL97_plus_lncRNA::1::6978	6748, 6844	in gene, in gene	1	1	23	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene MMD2	FLJ37205, PAQR10, MMD2	monocyte to macrophage differentiation-associated 2	NM_198403, NM_001100600, hCT2270269.0, hCT2270270.0, hCT2356896.0, hCT2356897.0	1569998_at, 230826_at	NP_940685.3, NP_001094070.1, EAW87305.1, EAW87306.1, EAW87307.1, EAW87308.1
GeneID:57786	RBAK	7	5,085,553	5,109,119	23,566	+	1	1_A375_pNL7_minus_lncRNA::1::4845	-161	upstream	1	0	22	22	1	1_A375_pNL7_minus_lncRNA::1	22	Gene RBAK	ZNF769, RBAK	RB-associated KRAB zinc finger	NM_021163	1553122_s_at, 228571_at, 241366_at	NP_066986.1
GeneID:80028	FBXL18	7	5,515,428	5,553,399	37,971	-	2	1_A375_pNL7_minus_lncRNA::1::4846, 2_A375_pNL97_plus_lncRNA::1::6979	-201, -137	upstream, upstream	1	1	25	21	1	1_A375_pNL7_minus_lncRNA::1	25	Gene FBXL18	Fbl18, FBXL18, FLJ38075, FLJ41541, FLJ11467, FLJ10776, FLJ26934	F-box and leucine-rich repeat protein 18	NM_024963, hCT2273122.0, hCT2273123.0, hCT2273125.0, hCT2273126.0	1553359_at, 1553361_x_at, 215068_s_at, 216395_at, 220896_at	NP_079239.3, EAW87337.1, EAW87338.1, EAW87339.1, EAW87340.1
GeneID:6624	FSCN1	7	5,632,454	5,646,286	13,832	+	1	2_A375_pNL97_plus_lncRNA::1::6983	474	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FSCN1	FSCN1, FLJ38511, p55, SNL	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	NM_003088, hCT2270940.0, hCT2270942.0, hCT2270943.0	201564_s_at, 210933_s_at	NP_003079.1, EAW87346.1, EAW87344.1, EAW87345.1
GeneID:54476	RNF216	7	5,659,678	5,821,292	161,614	-	1	2_A375_pNL97_plus_lncRNA::1::6984	12	in gene	0	1	15	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene RNF216	ZIN, RNF216, UBCE7IP1, TRIAD3, U7I1	ring finger protein 216	NM_207111, NM_207116, hCT2273101.0, hCT2273102.0, hCT2273104.0	1563361_at, 218425_at, 218426_s_at, 227065_at	NP_996994.1, NP_996999.1, EAW87347.1, EAW87348.1, EAW87349.1
GeneID:5395	PMS2	7	6,012,870	6,048,737	35,867	-	1	2_A375_pNL97_plus_lncRNA::1::6985	225	in gene	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene PMS2	PMS2CL, PMSL2, HNPCC4, PMS2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	NM_000535, NR_003085, hCT2297235.0	221206_at	NP_000526.1, EAW55055.1
GeneID:7965	AIMP2	7	6,048,882	6,063,465	14,583	+	1	2_A375_pNL97_plus_lncRNA::1::6985	-370	upstream	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene AIMP2	JTV-1, PRO0992, P38, AIMP2	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	NM_006303, hCT2297404.0, hCT2297405.0	202138_x_at, 209971_x_at	NP_006294.2, EAW55053.1, EAW55054.1
GeneID:84132	USP42	7	6,144,550	6,201,195	56,645	+	2	1_A375_pNL7_minus_lncRNA::1::4848, 2_A375_pNL97_plus_lncRNA::1::6987	-230, -345	upstream, upstream	1	1	23	17	1	1_A375_pNL7_minus_lncRNA::1	23	Gene USP42	USP42, FLJ12697	ubiquitin specific peptidase 42	NM_032172, hCT2297410.0, hCT1686319.3	226172_at, 226174_at, 226176_s_at, 226669_at, 226982_s_at	NP_115548.1, EAW55047.1, EAW55048.1
GeneID:221955	DAGLB	7	6,448,747	6,487,643	38,896	-	1	1_A375_pNL7_minus_lncRNA::1::4849	379	in gene	1	0	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene DAGLB	FLJ33909, FLJ45532, KCCR13L, FLJ33624, DAGLB, DAGLBETA	diacylglycerol lipase, beta	NM_139179, NM_001142936, hCT2349699.0, hCT2349700.0, hCT2349701.0, hCT2352899.0, hCT7010.4	225626_at, 225632_s_at, 225633_at, 226640_at	NP_631918.3, NP_001136408.1, EAW55033.1, EAW55034.1, EAW55036.1, EAW55037.1, EAW55035.1
GeneID:55146	ZDHHC4	7	6,617,065	6,628,610	11,545	+	2	1_A375_pNL7_minus_lncRNA::1::4850, 2_A375_pNL97_plus_lncRNA::1::6988	12903, 12871	downstream, downstream	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene ZDHHC4	ZNF374, FLJ10479, ZDHHC4	zinc finger, DHHC-type containing 4	NM_018106, NM_001134387, NM_001134388, NM_001134389, hCT2297397.1, hCT2297399.1, hCT2297400.1, hCT2297401.1, hCT2352898.0	220261_s_at, 223137_at, 230905_at	NP_060576.1, NP_001127859.1, NP_001127860.1, NP_001127861.1, EAW55024.1, EAW55025.1, EAW55023.1, EAW55026.1, EAW55027.1
GeneID:79034	C7orf26	7	6,629,915	6,648,355	18,440	+	2	1_A375_pNL7_minus_lncRNA::1::4850, 2_A375_pNL97_plus_lncRNA::1::6988	53, 21	in gene, in gene	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene C7orf26	MGC2718, C7orf26	chromosome 7 open reading frame 26	NM_024067, hCT2297395.1, hCT2344274.0	219261_at, 222002_at, 47083_at	NP_076972.2, EAW55021.1, EAW55022.1
GeneID:56913	C1GALT1	7	7,222,246	7,283,981	61,735	+	2	1_A375_pNL7_minus_lncRNA::1::4851, 2_A375_pNL97_plus_lncRNA::1::6989	39386, 458	in gene, in gene	1	1	15.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	18	Gene C1GALT1	C1GALT1, C1GALT, T-synthase	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	NM_020156, hCT2298949.0, hCT2298950.0, hCT10605.2	219439_at	NP_064541.1, EAW93589.1, EAW93588.1, EAW93590.1
GeneID:340267	COL28A1	7	7,398,244	7,575,460	177,216	-	2	1_A375_pNL7_minus_lncRNA::1::4852, 2_A375_pNL97_plus_lncRNA::1::6990	108420, 96740	in gene, in gene	1	1	13.5	14	2	2_A375_pNL97_plus_lncRNA::1	19	Gene COL28A1	COL28A1, COL28	collagen, type XXVIII, alpha 1	NM_001037763	239921_at, 242345_at	NP_001032852.2
GeneID:729852	tcag7.903	7	7,680,342	7,918,854	238,512	+	2	1_A375_pNL7_minus_lncRNA::1::4853, 2_A375_pNL97_plus_lncRNA::1::6991	155082, 121898	in gene, in gene	1	1	13	12.5	2	2_A375_pNL97_plus_lncRNA::1	16	Gene tcag7.903	LOC729852	hypothetical LOC729852	NR_034084	226596_x_at	
GeneID:100505921	LOC100505921	7	7,989,470	7,998,211	8,741	-	1	2_A375_pNL97_plus_lncRNA::1::6992	-10269	upstream	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100505921		hypothetical LOC100505921	XR_112975, XR_110641, XR_108739, XR_113991		
GeneID:113263	GLCCI1	7	8,008,423	8,128,710	120,287	+	1	2_A375_pNL97_plus_lncRNA::1::6992	57	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene GLCCI1	GLCCI1, GIG18, TSSN1, FAM117C	glucocorticoid induced transcript 1	NM_138426, hCT2357673.0, hCT8451.3	1560315_at, 1560316_s_at, 225700_at, 225706_at, 227525_at	NP_612435.1, EAW93607.1, EAW93608.1
GeneID:30010	NXPH1	7	8,473,585	8,792,593	319,008	+	3	1_A375_pNL7_minus_lncRNA::1::4854, 2_A375_pNL97_plus_lncRNA::1::6993, 2_A375_pNL97_plus_lncRNA::1::6994	-17, 111, 8943	upstream, in gene, in gene	1	1	16.5	20.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene NXPH1	NXPH1, NPH1, Nbla00697	neurexophilin 1	NM_152745	232377_at	NP_689958.1
GeneID:4697	NDUFA4	7	10,972,815	10,979,813	6,998	-	2	1_A375_pNL7_minus_lncRNA::1::4855, 2_A375_pNL97_plus_lncRNA::1::6996	-187, 69	upstream, in gene	1	1	24	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene NDUFA4	FLJ27440, NDUFA4, CI-9k, CI-MLRQ, MGC126843, MLRQ, MGC126845, MGC104422	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	NM_002489, hCT9483.3, hCT1963324.0, hCT1964216.1	217773_s_at	NP_002480.1, EAW93631.1, EAW93630.1, EAW93632.1
GeneID:54664	TMEM106B	7	12,250,848	12,276,890	26,042	+	2	1_A375_pNL7_minus_lncRNA::1::4856, 2_A375_pNL97_plus_lncRNA::1::6998	160, 432	in gene, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TMEM106B	MGC33727, TMEM106B, FLJ11273	transmembrane protein 106B	NM_018374, NM_001134232, hCT2298656.0, hCT2357713.0, hCT1640036.4, hCT1963721.1, hCT1963722.1	218930_s_at, 222787_s_at, 226529_at, 233666_at	NP_060844.2, NP_001127704.1, EAW93638.1, EAW93639.1, EAW93641.1, EAW93642.1, EAW93640.1
GeneID:10124	ARL4A	7	12,726,481	12,730,559	4,078	+	1	2_A375_pNL97_plus_lncRNA::1::6999	527	in gene	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ARL4A	ARL4, ARL4A	ADP-ribosylation factor-like 4A	NM_212460, NM_005738, NM_001037164, hCT2298669.0, hCT8435.3, hCT1962858.0	205020_s_at	NP_997625.1, NP_005729.1, NP_001032241.1, EAW93650.1, EAW93651.1, EAW93652.1
GeneID:1607	DGKB	7	14,184,674	14,881,075	696,401	-	1	1_A375_pNL7_minus_lncRNA::1::4858	608275	in gene	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene DGKB	DAGK2, DGKB, KIAA0718, DGK, DGK-BETA	diacylglycerol kinase, beta 90kDa	NM_004080, NM_145695, hCT2298699.1, hCT2350352.0	1553524_at, 216307_at	NP_004071.1, NP_663733.1, EAW93663.1, EAW93664.1
GeneID:392636	TMEM195	7	15,239,943	15,601,640	361,697	-	1	2_A375_pNL97_plus_lncRNA::1::7002	363208	downstream	0	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TMEM195	FLJ16237, TMEM195, MGC131748, AGMO	transmembrane protein 195	NM_001004320, hCT1782886.2		NP_001004320.1, EAW93665.1
GeneID:729920	ISPD	7	16,127,152	16,460,947	333,795	-	4	1_A375_pNL7_minus_lncRNA::1::4859, 1_A375_pNL7_minus_lncRNA::1::4860, 2_A375_pNL97_plus_lncRNA::1::7003, 2_A375_pNL97_plus_lncRNA::1::7004	102003, -141, 101971, 99	in gene, upstream, in gene, in gene	1	1	19.5	15	2	1_A375_pNL7_minus_lncRNA::1	22	Gene ISPD	FLJ42815, ISPD, Nip	isoprenoid synthase domain containing	NM_001101417, NM_001101426		NP_001094887.1, NP_001094896.1
GeneID:57037	ANKMY2	7	16,639,401	16,685,442	46,041	-	2	1_A375_pNL7_minus_lncRNA::1::4862, 2_A375_pNL97_plus_lncRNA::1::7005	-190, -94	upstream, upstream	1	1	56	46	1	1_A375_pNL7_minus_lncRNA::1	56	Gene ANKMY2	ANKMY2, DKFZp564O043, ZMYND20	ankyrin repeat and MYND domain containing 2	NM_020319, hCT2298907.0, hCT2357666.0, hCT2357667.0, hCT10362.3	212798_s_at	NP_064715.1, EAW93672.1, EAW93671.1, EAW93673.1, EAW93674.1
GeneID:28969	BZW2	7	16,685,759	16,746,148	60,389	+	3	1_A375_pNL7_minus_lncRNA::1::4862, 1_A375_pNL7_minus_lncRNA::1::4863, 2_A375_pNL97_plus_lncRNA::1::7005	-127, 22097, -223	upstream, in gene, upstream	1	1	36.5	29.5	2	1_A375_pNL7_minus_lncRNA::1	56	Gene BZW2	MSTP017, HSPC028, MST017, BZW2	basic leucine zipper and W2 domains 2	NM_001159767, NM_014038, NR_027624, hCT2298863.0, hCT2298864.0, hCT2298865.0, hCT2357665.0, hCT10361.3	217809_at	NP_001153239.1, NP_054757.1, EAW93676.1, EAW93677.1, EAW93678.1, EAW93679.1, EAW93675.1
GeneID:27075	TSPAN13	7	16,793,351	16,824,161	30,810	+	1	2_A375_pNL97_plus_lncRNA::1::7006	713	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TSPAN13	TM4SF13, FLJ22934, NET6, TSPAN13, NET-6	tetraspanin 13	NM_014399, hCT1966995.1, hCT8425.3	217979_at	NP_055214.1, EAW93681.1, EAW93680.1
GeneID:196	AHR	7	17,338,276	17,385,775	47,499	+	1	2_A375_pNL97_plus_lncRNA::1::7009	124	in gene	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene AHR	bHLHe76, AHR	aryl hydrocarbon receptor	NM_001621, hCT2357668.0, hCT8423.3	202820_at	NP_001612.1, EAW93686.1, EAW93687.1
GeneID:23161	SNX13	7	17,830,385	17,980,131	149,746	-	1	2_A375_pNL97_plus_lncRNA::1::7012	291	in gene	0	1	15	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SNX13	SNX13, RGS-PX1, KIAA0713	sorting nexin 13	NM_015132, hCT2298977.1, hCT2298978.1, hCT2298979.1, hCT2298980.1, hCT2349646.0, hCT2349647.0, hCT2349648.0, hCT2349649.0, hCT2349650.0, hCT2349651.0, hCT2357687.0	1553148_a_at, 213292_s_at, 215366_at, 215820_x_at	NP_055947.1, EAW93690.1, EAW93689.1, EAW93691.1, EAW93692.1, EAW93698.1, EAW93693.1, EAW93694.1, EAW93695.1, EAW93696.1, EAW93697.1, EAW93699.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9734	HDAC9	7	18,535,369	19,036,993	501,624	+	1	2_A375_pNL97_plus_lncRNA::1::7014	371063	in gene	0	1	9	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene HDAC9	HDAC9B, HDAC7B, HD7b, HDAC9, HDAC9FL, DKFZp779K1053, HDAC7, HDAC, MITR, HDRP, KIAA0744, HD9, HD7	histone deacetylase 9	NM_014707, NM_178423, NM_178425, NM_058176, hCT2295892.0, hCT2295893.0, hCT2295894.0, hCT2295895.0, hCT2295896.0, hCT2295897.0, hCT2295898.0, hCT2295899.0, hCT2295900.0, hCT2295901.0	1552758_at, 1552760_at, 205659_at, 234393_at	NP_055522.1, NP_848510.1, NP_478056.1, NP_848512.1, EAW93703.1, EAW93709.1, EAW93701.1, EAW93702.1, EAW93704.1, EAW93705.1, EAW93706.1, EAW93707.1, EAW93708.1, EAW93710.1
GeneID:221830	TWISTNB	7	19,735,085	19,748,660	13,575	-	1	2_A375_pNL97_plus_lncRNA::1::7015	132	in gene	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TWISTNB	TWISTNB		NM_001002926, hCT29154.2	214729_at, 226784_at	NP_001002926.1, EAW93714.1
GeneID:100422867	MIR3146	7	19,744,981	19,745,059	78	-	1	2_A375_pNL97_plus_lncRNA::1::7015	-3469	upstream	0	1	16	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene MIR3146	MIR3146	microRNA 3146	NR_036101		
GeneID:256130	TMEM196	7	19,758,938	19,812,404	53,466	-	3	1_A375_pNL7_minus_lncRNA::1::4869, 2_A375_pNL97_plus_lncRNA::1::7015, 2_A375_pNL97_plus_lncRNA::1::7016	-268, 63876, -364	upstream, downstream, upstream	1	1	19	20.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene TMEM196	TMEM196, DKFZp686K0753, DKFZp686H19205, MGC42090	transmembrane protein 196	NM_152774, hCT2295997.1, hCT2357697.0, hCT1657064.3	1552293_at, 236705_at	NP_689987.3, EAW93716.1, EAW93715.1, EAW93717.1
GeneID:346389	MACC1	7	20,174,278	20,257,013	82,735	-	3	1_A375_pNL7_minus_lncRNA::1::4871, 1_A375_pNL7_minus_lncRNA::1::4872, 2_A375_pNL97_plus_lncRNA::1::7018	57909, -2731, -2427	in gene, upstream, upstream	1	1	20.5	18.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene MACC1	SH3BP4L, MACC1, 7A5	metastasis associated in colon cancer 1	NM_182762, hCT30175.3		NP_877439.3, EAW93719.1
GeneID:100506098	LOC100506098	7	20,257,200	20,261,328	4,128	+	2	1_A375_pNL7_minus_lncRNA::1::4872, 2_A375_pNL97_plus_lncRNA::1::7018	2544, 2240	in gene, in gene	1	1	22	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOC100506098		hypothetical LOC100506098	XR_112981, XR_112980, XR_112982, XR_110647, XR_110646, XR_110648, XR_108745, XR_108744, XR_108746, XR_113997, XR_113996, XR_113998		
GeneID:100506130	LOC100506130	7	20,367,924	20,371,370	3,446	-	2	1_A375_pNL7_minus_lncRNA::1::4873, 2_A375_pNL97_plus_lncRNA::1::7019	1050, 1354	in gene, in gene	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506130		hypothetical LOC100506130	XR_112983, XR_112984, XR_110649, XR_110650, XR_108747, XR_108748, XR_113999, XR_114000		
GeneID:3696	ITGB8	7	20,370,725	20,455,382	84,657	+	3	1_A375_pNL7_minus_lncRNA::1::4873, 2_A375_pNL97_plus_lncRNA::1::7019, 2_A375_pNL97_plus_lncRNA::1::7020	-405, -709, 21985	upstream, upstream, in gene	1	1	16.5	16.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene ITGB8	ITGB8	integrin, beta 8	NM_002214, hCT2303791.0, hCT28543.3	205816_at, 211488_s_at, 226189_at, 242962_x_at	NP_002205.1, EAW93724.1, EAW93725.1
GeneID:221833	SP8	7	20,821,894	20,826,508	4,614	-	1	2_A375_pNL97_plus_lncRNA::1::7022	1836	in gene	0	1	10	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene SP8	BTD, SP8	Sp8 transcription factor	NM_198956, NM_182700, hCT2303801.1, hCT2349677.0, hCT2357685.0, hCT30173.3	237449_at, 239743_at	NP_945194.1, NP_874359.2, EAW93729.1, EAW93730.1, EAW93731.1, EAW93732.1
GeneID:8701	DNAH11	7	21,582,833	21,941,457	358,624	+	1	1_A375_pNL7_minus_lncRNA::1::4875	224175	in gene	1	0	15	7	1	1_A375_pNL7_minus_lncRNA::1	15	Gene DNAH11	CILD7, DPL11, FLJ37699, DNAH11, FLJ30095, DNAHC11, DNHBL, DNAHBL	dynein, axonemal, heavy chain 11	NM_003777, hCT2295990.0, hCT2295991.0, hCT2295992.0, hCT1961201.2	1553159_at, 1560416_at, 237604_at	NP_003768.2, EAW93737.1, EAW93736.1, EAW93738.1, EAW93739.1
GeneID:55536	CDCA7L	7	21,940,517	21,985,542	45,025	-	2	1_A375_pNL7_minus_lncRNA::1::4876, 2_A375_pNL97_plus_lncRNA::1::7023	-122, -74	upstream, upstream	1	1	45	58	1	2_A375_pNL97_plus_lncRNA::1	58	Gene CDCA7L	JPO2, CDCA7L, DKFZp762L0311, R1, RAM2	cell division cycle associated 7-like	NM_018719, NM_001127370, NM_001127371, hCT1966944.1, hCT2349681.0, hCT2349682.0, hCT2357710.0, hCT31255.5	225081_s_at	NP_061189.2, NP_001120842.1, NP_001120843.1, EAW93740.1, EAW93741.1, EAW93744.1, EAW93742.1, EAW93743.1
GeneID:256227	MGC87042	7	22,459,063	22,539,901	80,838	-	1	2_A375_pNL97_plus_lncRNA::1::7025	61	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MGC87042		STEAP family protein MGC87042	NM_207342, NM_001164460	217553_at	NP_997225.1, NP_001157932.1
GeneID:54543	TOMM7	7	22,852,251	22,862,421	10,170	-	1	2_A375_pNL97_plus_lncRNA::1::7026	-43	upstream	0	1	14	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TOMM7	TOM7, TOMM7	translocase of outer mitochondrial membrane 7 homolog (yeast)	NM_019059, hCT1659702.2, hCT1963307.0, hCT1963308.1, hCT1965963.0		NP_061932.1, EAW93761.1, EAW93760.1, EAW93762.1, EAW93763.1
GeneID:692210	SNORD93	7	22,896,232	22,896,305	73	+	2	1_A375_pNL7_minus_lncRNA::1::4877, 2_A375_pNL97_plus_lncRNA::1::7027	1960, 2104	downstream, downstream	1	1	19	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SNORD93	HBII-336, SNORD93	small nucleolar RNA, C/D box 93	NR_003075		
GeneID:84668	FAM126A	7	22,980,878	23,053,770	72,892	-	1	1_A375_pNL7_minus_lncRNA::1::4878	-7158	upstream	1	0	16	17	1	1_A375_pNL7_minus_lncRNA::1	16	Gene FAM126A	HCC, HYCC1, DRCTNNB1A, HLD5, FAM126A	family with sequence similarity 126, member A	NM_032581, hCT2322590.0, hCT29470.3	223625_at, 227239_at, 231396_s_at, 244115_at	NP_115970.2, EAW93767.1, EAW93768.1
GeneID:100506198	LOC100506198	7	23,126,671	23,140,052	13,381	+	2	1_A375_pNL7_minus_lncRNA::1::4879, 2_A375_pNL97_plus_lncRNA::1::7029	18673, 18737	downstream, downstream	1	1	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100506198		hypothetical LOC100506198	XR_112987, XR_110653, XR_108751, XR_114003		
GeneID:55975	KLHL7	7	23,145,353	23,215,040	69,687	+	4	1_A375_pNL7_minus_lncRNA::1::4879, 1_A375_pNL7_minus_lncRNA::1::4880, 2_A375_pNL97_plus_lncRNA::1::7029, 2_A375_pNL97_plus_lncRNA::1::7030	-9, 76183, 55, 76151	upstream, downstream, in gene, downstream	1	1	22	20.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene KLHL7	RP42, SBBI26, KLHL6, KLHL7	kelch-like 7 (Drosophila)	NM_001031710, NM_018846, NR_033328, NR_033329, NM_001172428, hCT2357676.0, hCT1827997.2, hCT1962890.0, hCT1962891.1, hCT1962892.1	220238_s_at, 220239_at, 223250_at	NP_001026880.2, NP_061334.4, NP_001165899.1, EAW93770.1, EAW93771.1, EAW93773.1, EAW93772.1, EAW93774.1
GeneID:11097	NUPL2	7	23,221,446	23,240,630	19,184	+	2	1_A375_pNL7_minus_lncRNA::1::4880, 2_A375_pNL97_plus_lncRNA::1::7030	90, 58	in gene, in gene	1	1	24	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene NUPL2	NLP-1, hCG1, NUPL2, CG1, NLP_1	nucleoporin like 2	NM_007342, hCT2299127.0, hCT2357689.0, hCT28547.4, hCT1963714.1, hCT1963715.1	204003_s_at	NP_031368.1, EAW93778.1, EAW93775.1, EAW93776.1, EAW93777.1, EAW93779.1
GeneID:10457	GPNMB	7	23,286,316	23,314,729	28,413	+	1	2_A375_pNL97_plus_lncRNA::1::7031	532	in gene	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene GPNMB	GPNMB, NMB, HGFIN	glycoprotein (transmembrane) nmb	NM_002510, NM_001005340, hCT2299130.0, hCT2299133.0, hCT2357714.0, hCT29213.3	1554018_at, 201141_at	NP_002501.1, NP_001005340.1, EAW93781.1, EAW93782.1, EAW93783.1, EAW93784.1
GeneID:115416	C7orf30	7	23,338,940	23,349,180	10,240	+	1	1_A375_pNL7_minus_lncRNA::1::4881	-28	upstream	1	0	19	19	1	1_A375_pNL7_minus_lncRNA::1	19	Gene C7orf30	C7orf30	chromosome 7 open reading frame 30	NM_138446, hCT29220.3	226385_s_at, 226386_at, 230516_at, 244641_at	NP_612455.1, EAW93785.1
GeneID:10643	IGF2BP3	7	23,349,828	23,509,995	160,167	-	2	1_A375_pNL7_minus_lncRNA::1::4882, 2_A375_pNL97_plus_lncRNA::1::7032	-949, -3561	upstream, upstream	1	1	16.5	14	2	2_A375_pNL97_plus_lncRNA::1	18	Gene IGF2BP3	VICKZ3, IMP-3, KOC1, DKFZp686F1078, IGF2BP3, IMP3, CT98	insulin-like growth factor 2 mRNA binding protein 3	NM_006547, hCT2299349.0, hCT2299350.0	1569033_at, 203819_s_at, 203820_s_at	NP_006538.2, EAW93787.1, EAW93786.1
GeneID:1687	DFNA5	7	24,737,974	24,797,639	59,665	-	2	1_A375_pNL7_minus_lncRNA::1::4883, 2_A375_pNL97_plus_lncRNA::1::7033	247, 103	in gene, in gene	1	1	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene DFNA5	ICERE-1, DFNA5	deafness, autosomal dominant 5	NM_004403, NM_001127453, NM_001127454, hCT30081.3, hCT1963734.1, hCT1963735.1	203695_s_at	NP_004394.1, NP_001120925.1, NP_001120926.1, EAW93812.1, EAW93813.1, EAW93814.1
GeneID:26031	OSBPL3	7	24,836,159	25,019,760	183,601	-	3	1_A375_pNL7_minus_lncRNA::1::4884, 1_A375_pNL7_minus_lncRNA::1::4885, 2_A375_pNL97_plus_lncRNA::1::7034	193008, 158432, -240	downstream, in gene, upstream	1	1	18	14	3	1_A375_pNL7_minus_lncRNA::1	22	Gene OSBPL3	MGC21526, DKFZp667P1518, OSBPL3, KIAA0704, ORP-3, ORP3, OSBP3	oxysterol binding protein-like 3	NM_015550, NM_145320, NM_145321, NM_145322	209626_s_at, 209627_s_at	NP_056365.1, NP_663160.1, NP_663161.1, NP_663162.1
GeneID:54205	CYCS	7	25,158,270	25,164,980	6,710	-	2	1_A375_pNL7_minus_lncRNA::1::4886, 2_A375_pNL97_plus_lncRNA::1::7035	-108, -12	upstream, upstream	1	1	28	25	1	1_A375_pNL7_minus_lncRNA::1	28	Gene CYCS	CYCS, HCS, CYC, THC4	cytochrome c, somatic	NM_018947, hCT2299206.1, hCT2299207.1, hCT2299209.1	208905_at, 229415_at, 244546_at	NP_061820.1, EAW93824.1, EAW93822.1, EAW93823.1
GeneID:136895	C7orf31	7	25,174,316	25,219,817	45,501	-	2	1_A375_pNL7_minus_lncRNA::1::4886, 2_A375_pNL97_plus_lncRNA::1::7035	54729, 54825	downstream, downstream	1	1	28	25	1	1_A375_pNL7_minus_lncRNA::1	28	Gene C7orf31	C7orf31		NM_138811, hCT2349678.0, hCT2349679.0, hCT2349680.0, hCT30275.3	228146_at	NP_620166.3, EAW93825.1, EAW93826.1, EAW93827.1, EAW93828.1
GeneID:3181	HNRNPA2B1	7	26,229,556	26,240,413	10,857	-	1	2_A375_pNL97_plus_lncRNA::1::7037	-1059	upstream	0	1	15	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene HNRNPA2B1	HNRPB1, HNRPA2B1, DKFZp779B0244, HNRNPA2B1, HNRNPB1, HNRPA2, SNRPB1, RNPA2, HNRNPA2, FLJ22720	heterogeneous nuclear ribonucleoprotein A2/B1	NM_002137, NM_031243, hCT2299295.0, hCT2299296.0, hCT2299297.0, hCT2299298.0, hCT2299299.0, hCT2357674.0, hCT2357675.0, hCT29630.3	205292_s_at, 225107_at, 225932_s_at, 235454_at, 244131_at	NP_002128.1, NP_112533.1, EAW93834.1, EAW93835.1, EAW93836.1, EAW93839.1, EAW93837.1, EAW93838.1, EAW93840.1, EAW93841.1
GeneID:11335	CBX3	7	26,241,099	26,252,976	11,877	+	1	2_A375_pNL97_plus_lncRNA::1::7037	373	in gene	0	1	15	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene CBX3	HECH, HP1-GAMMA, HP1Hs-gamma, CBX3	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	NM_016587, NM_007276, hCT1967003.2, hCT1967005.2, hCT2357670.0, hCT1783632.4, hCT1952443.2	1555920_at, 200037_s_at	NP_057671.2, NP_009207.2, EAW93843.1, EAW93844.1, EAW93845.1, EAW93846.1, EAW93842.1
GeneID:100133311	LOC100133311	7	27,179,983	27,195,547	15,564	+	1	2_A375_pNL97_plus_lncRNA::1::7038	10561	in gene	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100133311		hypothetical LOC100133311	XR_112992, XR_112993, XR_112994, XR_110658, XR_110659, XR_110660, XR_108756, XR_108757, XR_108758, XR_114008, XR_114009, XR_114010		
GeneID:3202	HOXA5	7	27,180,996	27,183,287	2,291	-	1	2_A375_pNL97_plus_lncRNA::1::7039	-7257	upstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene HOXA5	HOX1.3, HOX1, MGC9376, HOXA5, HOX1C	homeobox A5	NM_019102, hCT1640753.3	213844_at	NP_061975.2, EAW93873.1
GeneID:3203	HOXA6	7	27,185,116	27,187,368	2,252	-	1	2_A375_pNL97_plus_lncRNA::1::7039	-3176	upstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene HOXA6	HOX1B, HOXA6, HOX1, HOX1.2	homeobox A6	NM_024014, hCT2299374.1, hCT1640752.3	208557_at	NP_076919.1, EAW93875.1, EAW93874.1
GeneID:3204	HOXA7	7	27,193,335	27,196,296	2,961	-	1	2_A375_pNL97_plus_lncRNA::1::7039	5752	downstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene HOXA7	HOXA7, HOX1, HOX1A, HOX1.1, ANTP	homeobox A7	NM_006896, hCT1640455.3	206847_s_at, 206848_at, 235753_at	NP_008827.2, EAW93877.1
GeneID:11112	HIBADH	7	27,565,059	27,702,620	137,561	-	2	1_A375_pNL7_minus_lncRNA::1::4889, 2_A375_pNL97_plus_lncRNA::1::7040	28, 28	in gene, in gene	1	1	44	34	1	1_A375_pNL7_minus_lncRNA::1	44	Gene HIBADH	NS5ATP1, HIBADH, MGC40361	3-hydroxyisobutyrate dehydrogenase	NM_152740, hCT1969095.1, hCT1969096.1, hCT2357715.0, hCT30281.4	224812_at, 231955_s_at, 234452_at	NP_689953.1, EAW93898.1, EAW93897.1, EAW93899.1, EAW93900.1
GeneID:8887	TAX1BP1	7	27,779,738	27,869,386	89,648	+	1	2_A375_pNL97_plus_lncRNA::1::7041	22	in gene	0	1	11	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene TAX1BP1	CALCOCO3, TAX1BP1, T6BP, TXBP151	Tax1 (human T-cell leukemia virus type I) binding protein 1	NM_001079864, NM_006024, hCT2299137.0, hCT2299140.0, hCT30279.3, hCT1961211.1	200976_s_at, 200977_s_at, 213786_at	NP_001073333.1, NP_006015.4, EAW93901.1, EAW93902.1, EAW93903.1, EAW93904.1
GeneID:221895	JAZF1	7	27,870,192	28,220,437	350,245	-	2	1_A375_pNL7_minus_lncRNA::1::4890, 2_A375_pNL97_plus_lncRNA::1::7042	118437, 118293	in gene, in gene	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene JAZF1	TIP27, ZNF802, JAZF1, DKFZp761K2222	JAZF zinc finger 1	NM_175061, hCT30282.2	225798_at, 225800_at	NP_778231.2, EAW93905.1
GeneID:9586	CREB5	7	28,338,940	28,865,511	526,571	+	1	2_A375_pNL97_plus_lncRNA::1::7043	386852	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CREB5	CREB5, CRE-BPA	cAMP responsive element binding protein 5	NM_182898, NM_182899, NM_004904, NM_001011666, hCT2299254.1, hCT1783344.3, hCT1962864.1	205931_s_at, 229228_at	NP_878901.2, NP_878902.2, NP_004895.2, NP_001011666.1, EAW93908.1, EAW93910.1, EAW93909.1
GeneID:54504	CPVL	7	29,035,247	29,186,153	150,906	-	1	2_A375_pNL97_plus_lncRNA::1::7045	110857	in gene	0	1	14	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene CPVL	HVLP, CPVL, MGC10029	carboxypeptidase, vitellogenic-like	NM_031311, NM_019029, hCT1966998.1, hCT1966999.0, hCT1967000.1, hCT1967001.1, hCT1783341.2	1555710_at, 1555711_x_at, 208146_s_at, 211878_at	NP_112601.3, NP_061902.2, EAW93914.1, EAW93915.1, EAW93917.1, EAW93918.1, EAW93916.1
GeneID:9805	SCRN1	7	29,959,719	30,029,905	70,186	-	1	2_A375_pNL97_plus_lncRNA::1::7046	1009	in gene	0	1	9	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene SCRN1	KIAA0193, SES1, SCRN1	secernin 1	NM_014766, NM_001145514, NM_001145515, NM_001145513, hCT2301908.0, hCT2301910.0, hCT28557.3	201462_at	NP_055581.3, NP_001138986.1, NP_001138987.1, NP_001138985.1, EAW93926.1, EAW93927.1, EAW93928.1
GeneID:55033	FKBP14	7	30,052,884	30,066,268	13,384	-	4	1_A375_pNL7_minus_lncRNA::1::4892, 1_A375_pNL7_minus_lncRNA::1::4893, 2_A375_pNL97_plus_lncRNA::1::7047, 2_A375_pNL97_plus_lncRNA::1::7048	-68, -1668, -132, -1604	upstream, upstream, upstream, upstream	1	1	36	43	2	2_A375_pNL97_plus_lncRNA::1	43	Gene FKBP14	FLJ20731, FKBP22, FKBP14	FK506 binding protein 14, 22 kDa	NM_017946, hCT29554.3	219390_at, 235311_at	NP_060416.1, EAW93929.1
GeneID:84725	PLEKHA8	7	30,068,288	30,130,360	62,072	+	4	1_A375_pNL7_minus_lncRNA::1::4892, 1_A375_pNL7_minus_lncRNA::1::4893, 2_A375_pNL97_plus_lncRNA::1::7047, 2_A375_pNL97_plus_lncRNA::1::7048	-1952, -352, -1888, -416	upstream, upstream, upstream, upstream	1	1	36	43	2	2_A375_pNL97_plus_lncRNA::1	43	Gene PLEKHA8	DKFZp686J09164, MGC3358, FAPP2, DKFZp313M1034, PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	NM_032639, hCT2301819.0, hCT2301820.0, hCT28559.3, hCT1955378.1	1560556_a_at, 224208_at, 231543_at, 232212_at, 233943_x_at	NP_116028.1, EAW93930.1, EAW93931.1, EAW93932.1, EAW93933.1
GeneID:223082	ZNRF2	7	30,323,923	30,407,308	83,385	+	2	2_A375_pNL97_plus_lncRNA::1::7049, 2_A375_pNL97_plus_lncRNA::1::7050	445, 1693	in gene, in gene	0	1	12	14.5	2	2_A375_pNL97_plus_lncRNA::1	15	Gene ZNRF2	ZNRF2, RNF202	zinc and ring finger 2	NM_147128, hCT1640683.3, hCT1965581.2	226261_at	NP_667339.1, EAW93938.1, EAW93939.1
GeneID:693133	MIR550-1	7	30,329,410	30,329,506	96	+	2	2_A375_pNL97_plus_lncRNA::1::7049, 2_A375_pNL97_plus_lncRNA::1::7050	-5042, -3794	upstream, upstream	0	1	12	14.5	2	2_A375_pNL97_plus_lncRNA::1	15	Gene MIR550-1	MIR550-1, hsa-mir-550a-1, MIR550A1, MIRN550-1	microRNA 550-1	NR_030319		
GeneID:10392	NOD1	7	30,464,143	30,518,393	54,250	-	1	2_A375_pNL97_plus_lncRNA::1::7051	-151	upstream	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene NOD1	NOD1, CLR7.1, NLRC1, CARD4	nucleotide-binding oligomerization domain containing 1	NM_006092, hCT2301899.0, hCT2301901.0, hCT2301902.0, hCT2357702.0, hCT2357703.0, hCT30385.3	221073_s_at, 224190_x_at	NP_006083.1, EAW93946.1, EAW93944.1, EAW93945.1, EAW93947.1, EAW93948.1, EAW93949.1
GeneID:401320	LOC401320	7	30,587,974	30,617,375	29,401	-	1	2_A375_pNL97_plus_lncRNA::1::7052	26543	in gene	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC401320		hypothetical LOC401320	XR_113001, XR_110667, XR_108765, XR_114017	1558458_at, 1558459_s_at, 233732_at, 238540_at, 239313_at, 239640_at	
GeneID:2617	GARS	7	30,634,181	30,673,649	39,468	+	1	2_A375_pNL97_plus_lncRNA::1::7053	235	in gene	0	1	15	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene GARS	GlyRS, DSMAV, CMT2D, SMAD1, HMN5, GARS	glycyl-tRNA synthetase	NM_002047, hCT2301809.0, hCT30383.3	208693_s_at	NP_002038.2, EAW93960.1, EAW93961.1
GeneID:1395	CRHR2	7	30,692,863	30,722,140	29,277	-	2	1_A375_pNL7_minus_lncRNA::1::4894, 2_A375_pNL97_plus_lncRNA::1::7054	10476, 10428	in gene, in gene	1	1	110	139	1	2_A375_pNL97_plus_lncRNA::1	139	Gene CRHR2	CRHR2, CRF2, CRFR2	corticotropin releasing hormone receptor 2	NM_001883, hCT2299480.0, hCT2299481.0, hCT2299482.0, hCT1955337.1	207897_at, 211510_s_at	NP_001874.2, EAW93964.1, EAW93962.1, EAW93963.1, EAW93965.1
GeneID:84182	FAM188B	7	30,811,033	30,932,002	120,969	+	1	2_A375_pNL97_plus_lncRNA::1::7055	28423	in gene	0	1	14	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene FAM188B	FLJ51453, FAM188B, FLJ22374, MGC44277, C7orf67	family with sequence similarity 188, member B	NM_032222	1557141_at, 235559_at	NP_115598.2
GeneID:117	ADCYAP1R1	7	31,092,142	31,146,311	54,169	+	2	1_A375_pNL7_minus_lncRNA::1::4896, 2_A375_pNL97_plus_lncRNA::1::7056	62610, 62594	downstream, downstream	1	1	51	98	1	2_A375_pNL97_plus_lncRNA::1	98	Gene ADCYAP1R1	PACAPRI, PAC1, PACAPR, ADCYAP1R1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	NM_001118, hCT1641237.3	207151_at, 226690_at	NP_001109.2, EAW93976.1
GeneID:5137	PDE1C	7	31,792,632	32,338,383	545,751	-	2	1_A375_pNL7_minus_lncRNA::1::4897, 2_A375_pNL97_plus_lncRNA::1::7057	247567, 437679	in gene, in gene	1	1	13.5	20	2	2_A375_pNL97_plus_lncRNA::1	24	Gene PDE1C	PDE1C, Hcam3	phosphodiesterase 1C, calmodulin-dependent 70kDa	NM_005020, NM_001191056, NM_001191057, NM_001191058, NM_001191059, hCT2299406.0, hCT2299407.0, hCT2299408.0, hCT2299409.0	1554378_a_at, 207303_at, 216869_at	NP_005011.1, NP_001177985.1, NP_001177986.1, NP_001177987.1, NP_001177988.1, EAW93984.1, EAW93985.1, EAW93986.1, EAW93987.1
GeneID:23658	LSM5	7	32,524,945	32,534,870	9,925	-	2	1_A375_pNL7_minus_lncRNA::1::4899, 2_A375_pNL97_plus_lncRNA::1::7060	4918, 4838	in gene, in gene	1	1	42	49	1	2_A375_pNL97_plus_lncRNA::1	49	Gene LSM5	YER146W, FLJ12710, LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_001130710, NM_012322, NM_001139499, NR_024466, hCT28960.3, hCT1955379.0	202903_at, 202904_s_at, 211747_s_at	NP_001124182.1, NP_036454.1, NP_001132971.1, EAW93990.1, EAW93991.1
GeneID:23080	AVL9	7	32,535,176	32,623,779	88,603	+	2	1_A375_pNL7_minus_lncRNA::1::4899, 2_A375_pNL97_plus_lncRNA::1::7060	-5224, -5144	upstream, upstream	1	1	42	49	1	2_A375_pNL97_plus_lncRNA::1	49	Gene AVL9	AVL9, DKFZp686G0344, KIAA0241	AVL9 homolog (S. cerevisiase)	NM_015060, hCT2299340.0, hCT2299344.0, hCT2357664.0, hCT29002.3, hCT1955380.1, hCT1955381.1	1555055_at, 212471_at, 212474_at, 212475_at	NP_055875.1, EAW93992.1, EAW93993.1, EAW93995.1, EAW93996.1, EAW93997.1, EAW93994.1
GeneID:11328	FKBP9	7	32,997,005	33,046,543	49,538	+	2	1_A375_pNL7_minus_lncRNA::1::4900, 2_A375_pNL97_plus_lncRNA::1::7062	243, 243	in gene, in gene	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene FKBP9	PPIase, FKBP60, FKBP63, FKBP9, MGC126772, MGC138258, DKFZp586B1723	FK506 binding protein 9, 63 kDa	NM_007270	212169_at	NP_009201.2
GeneID:51251	NT5C3	7	33,053,742	33,102,409	48,667	-	1	2_A375_pNL97_plus_lncRNA::1::7063	73	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene NT5C3	PSN1, P5'N-1, cN-III, MGC27337, MGC87828, UMPH, NT5C3, PN-I, MGC87109, UMPH1	5'-nucleotidase, cytosolic III	NM_001002010, NM_016489, NR_029372, NM_001166118, hCT2299556.1, hCT2299557.1, hCT2357698.1, hCT2357699.1, hCT2357700.1	223298_s_at	NP_001002010.1, NP_057573.2, NP_001159590.1, EAW94007.1, EAW94008.1, EAW94009.1, EAW94010.1, EAW94011.1

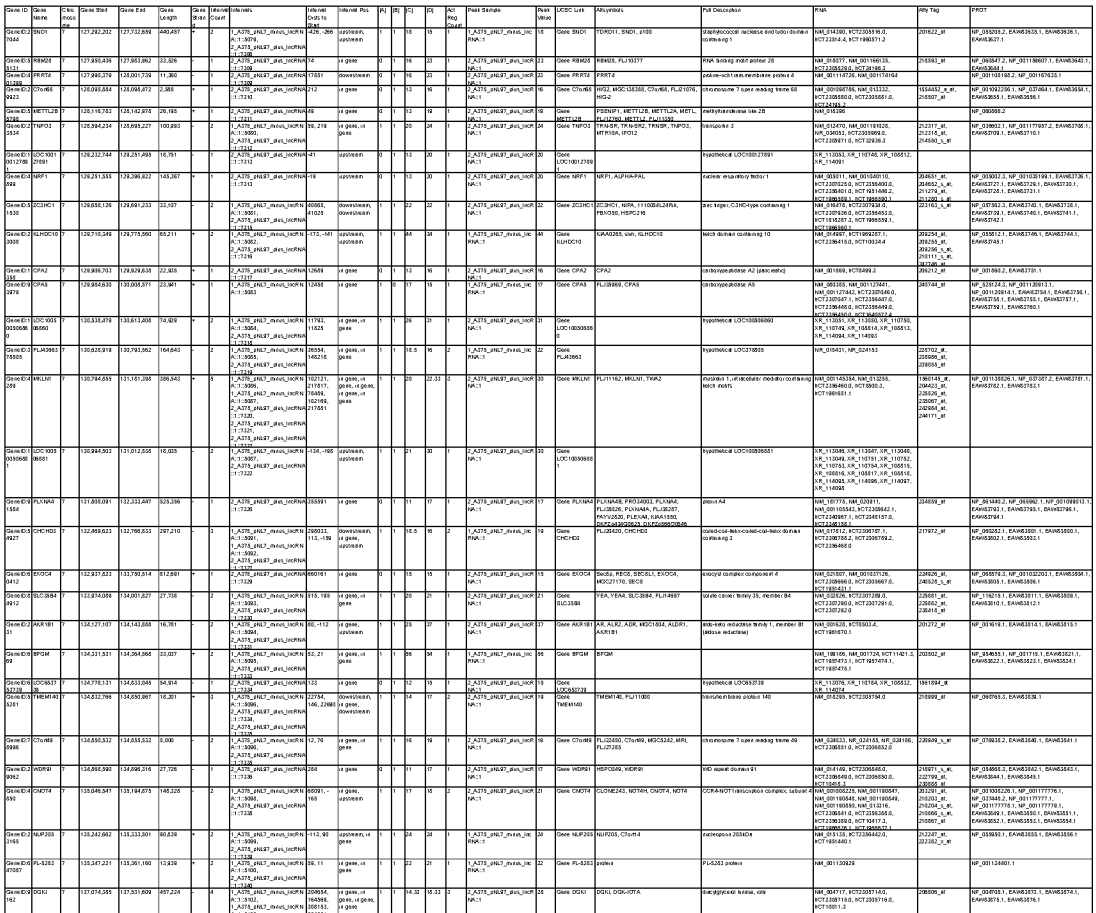
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Internal Transcripts	Internal Distance to start	Internal Position	[A]	[B]	[C]	[D]	Active Regulatory Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:9100	RPE	7	33,134,409	33,149,202	14,793	+	4	1_A375_shN7_dhrus_lncRNA:1:-9901,1_A375_shN7_dhrus_lncRNA:1:-9902,1_A375_shN7_dhrus_lncRNA:1:-9903,1_A375_shN7_dhrus_lncRNA:1:-9904	1462, 2,94, 100, -162	ut gene, ut gene, upstream, upstream	1	1	27.5	36	2	2_A375_shN7_dhrus_lncRNA:1	61	Gene: RPE	FAP1, RP9	ribulose-phosphate 3-epimerase [Source:HGNC Symbol;Acc:HGNC:10256]	NM_002255, XCT23453330, XCT23463280, XCT 167377.2	2276S9_at, 2276S2_at	NP_9780331, EAW84814.1, EAW84812.1, EAW84813.1
Gene:ID:7241	BBS9	7	33,169,152	33,845,680	676,528	+	1	2_A375_shN7_dhrus_lncRNA:1:-7055	148	ut gene	0	1	10	21	1	2_A375_shN7_dhrus_lncRNA:1	21	Gene: BBS9	PTHB1, BBS9, D1, MGC149917, C1orf, B1	Bardet-Biedl syndrome 9	NM_014451, NM_198428, NM_001033904, NM_001033905, XCT23842.0, XCT23843.0, XCT23844.0, XCT 1762599.2	1555555_at, 2080S5_s_at, 2162J9_at, 2154T_at, 2154T_x_at	NP_055298.2, NP_940528.1, NP_001025778.1, NP_001025777.1, EAW84817.1, EAW84816.1, EAW84813.1, EAW84816.1
Gene:ID:100861	BMPER	7	33,945,112	34,194,112	249,000	+	2	1_A375_shN7_dhrus_lncRNA:1:-9904,2_A375_shN7_dhrus_lncRNA:1:-7056	82055, 81928	ut gene, ut gene	1	1	20	27	1	2_A375_shN7_dhrus_lncRNA:1	27	Gene: BMPER	CV2, CRIM3, CV-2, BMPER	BMP binding endothelial regulator	NM_133468	2418S5_at	NP_997235.1
Gene:ID:3333	DPY19L1	7	34,966,493	35,077,653	109,160	-	1	2_A375_shN7_dhrus_lncRNA:1:-7057	33055	ut gene	0	1	15	19	1	2_A375_shN7_dhrus_lncRNA:1	19	Gene: DPY19L1	KIAA0377, DPY19L1	dpy-19-like 1 (C. elegans)	NM_015263	1560915_at, 1560916_s_at, 1570355_s_at, 212792_at, 212833_at	NP_056078.1
Gene:ID:4224	HERPUD2	7	35,072,269	35,734,792	62,363	-	2	1_A375_shN7_dhrus_lncRNA:1:-9905,2_A375_shN7_dhrus_lncRNA:1:-7058	132, -12	ut gene, upstream	1	1	26	25	1	1_A375_shN7_dhrus_lncRNA:1	26	Gene: HERPUD2	HERPUD2, FLJ22313, FLJ31032	HERPUD family member 2	NM_022373, XCT2292725.0, XCT23827260.0, XCT23576565.0, XCT23576660.0, XCT9225.2, XCT23812522.0	1552628_a_at, 1555094_at, 222791_at, 1561130_a_at	NP_071765.3, EAW84833.1, EAW84832.1, EAW84833.1, EAW84834.1, EAW84835.1, EAW84836.1
Gene:ID:69	TYSnp	7	35,640,627	35,644,617	104,290	+	1	2_A375_shN7_dhrus_lncRNA:1:-7059	841	ut gene	0	1	11	17	1	2_A375_shN7_dhrus_lncRNA:1	17	Gene: SEPT7	CDC10, NM402942, SEPT7, CDC3, SEPT7A	septin 7	NM_001011553, NM_001785, XCT23867170.0, XCT23868000.0, XCT23868010.0, XCT23868020.0	1555622_at, 213191_s_at, 244555_at	NP_001011553.2, NP_001779.3, EAW84090.1, EAW84091.1, EAW84092.1
Gene:ID:3366	KIAA0888	7	36,363,799	36,429,734	65,976	-	2	1_A375_shN7_dhrus_lncRNA:1:-9906,2_A375_shN7_dhrus_lncRNA:1:-7060	22774, 22693	ut gene, ut gene	0	1	16	23	1	2_A375_shN7_dhrus_lncRNA:1	23	Gene: KIAA0888	KIAA0888	NM_015314, NM_001159429, XCT23868010.0, XCT23868020.0, XCT6185.2	213424_at	NP_056129.2, NP_001092093.1, EAW84094.1, EAW84095.1, EAW84096.1
Gene:ID:644	ADAH	7	39,352,549	39,764,154	211,605	-	1	2_A375_shN7_dhrus_lncRNA:1:-9907	217376	downstream	1	0	17	15	1	1_A375_shN7_dhrus_lncRNA:1	17	Gene: ADAH	ADAH	alcoholic liver disease	NM_001177936, NM_001177937, NM_000627, XCT6777.2	203639_at	NP_001170877.1, NP_001170878.1, NP_000618.1, EAW84872.1
Gene:ID:644	ELMO1	7	39,892,961	37,660,511	594,550	-	6	1_A375_shN7_dhrus_lncRNA:1:-9908,1_A375_shN7_dhrus_lncRNA:1:-9909,1_A375_shN7_dhrus_lncRNA:1:-9910,2_A375_shN7_dhrus_lncRNA:1:-7076,2_A375_shN7_dhrus_lncRNA:1:-7077	2000321, 63557, 551, 416396, 389998, 61	ut gene, ut gene, ut gene, ut gene, upstream	1	1	15.2	16.2	3	2_A375_shN7_dhrus_lncRNA:1	23	Gene: ELMO1	ELMO1, MGC126499, ELMO-1, CED-12	engulfment and cell motility 1	NM_014550, NM_001163459, NM_130442, XCT2299360.0, XCT23859540.0, XCT23859550.0, XCT23877120.0, XCT 6236.3	209313_s_at	NP_001156.1, NP_001153454.1, NP_569706.1, EAW84870.1, EAW84870.1, EAW84870.1, EAW84877.1, EAW84876.1
Gene:ID:1281	POU6F2	7	39,017,609	39,504,280	486,761	+	4	1_A375_shN7_dhrus_lncRNA:1:-9911,1_A375_shN7_dhrus_lncRNA:1:-9912,2_A375_shN7_dhrus_lncRNA:1:-7077,2_A375_shN7_dhrus_lncRNA:1:-7078	270515, 438434, 27671, 435535	ut gene, ut gene, ut gene, ut gene	1	1	16.5	16.8	2	1_A375_shN7_dhrus_lncRNA:1	20	Gene: POU6F2	WFS6, RPF-1, WFS, POU6F2	POU class 6 homeobox 2	NM_007252, NM_001164618, XCT23861660.0, XCT 9552.24.1	207490_s_at	NP_008183.2, NP_001158490.1, EAW84816.1, EAW84817.1
Gene:ID:7052	CTCnf06	7	39,909,003	39,912,480	6,477	+	1	2_A375_shN7_dhrus_lncRNA:1:-7079	77	ut gene	0	1	12	24	1	2_A375_shN7_dhrus_lncRNA:1	24	Gene: CTnf06	CTnf06, GH083	chromosome 7 open reading frame 36	NM_020182, XCT6262.1	223632_at	NP_064577.1, EAW84120.1
Gene:ID:598	RALA	7	39,960,162	39,747,719	66,557	+	1	2_A375_shN7_dhrus_lncRNA:1:-7080	-56	upstream	1	0	17	16	1	1_A375_shN7_dhrus_lncRNA:1	17	Gene: RALA	RAL, MGC45499, RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	NM_005402, XCT6261.2, XCT 1883372.1	204633_s_at, 204633_at	NP_005372.2, EAW84123.1, EAW84122.1
Gene:ID:821	CDK12	7	39,959,959	40,136,733	146,774	+	1	1_A375_shN7_dhrus_lncRNA:1:-9913	-263	upstream	1	0	20	13	1	1_A375_shN7_dhrus_lncRNA:1	20	Gene: CDK12	CHED, FLJ53215, CDC2L, KIAA1791, CDC2L5, CDC12, HCDC12	cyclin-dependent kinase 12	NM_003718, NM_031267, XCT23866050.0, XCT23866110.0, XCT23866120.0, XCT23866130.0	207316_s_at, 207316_s_at, 210953_x_at, 210957_s_at, 210957_x_at, 214267_x_at, 231266_s_at	NP_003709.3, NP_112597.2, EAW84129.1, EAW84130.1, EAW84131.1, EAW84132.1, EAW84126.1, EAW84123.1
Gene:ID:38647	CTnrf11	7	40,172,342	40,174,251	1,909	-	2	1_A375_shN7_dhrus_lncRNA:1:-9916,2_A375_shN7_dhrus_lncRNA:1:-7081	-372, -83	upstream, upstream	1	1	13	19	1	2_A375_shN7_dhrus_lncRNA:1	19	Gene: CTnrf11	ASB18, TTDN1, ORF26, CTnrf11	chromosome 7 open reading frame 11	NM_138781, XCT1819417.1	225419_at	NP_619648.1, EAW84134.1
Gene:ID:9763	CTnrf10	7	40,174,373	40,800,266	725,791	+	4	1_A375_shN7_dhrus_lncRNA:1:-9916,1_A375_shN7_dhrus_lncRNA:1:-9917,1_A375_shN7_dhrus_lncRNA:1:-9918,2_A375_shN7_dhrus_lncRNA:1:-7082	-68, 416077, -239, 416668	ut gene, ut gene, upstream, ut gene	1	1	16.5	16.3	2	2_A375_shN7_dhrus_lncRNA:1	19	Gene: CTnrf10	DERP13, FLJ11606, ORF19, FLJ63872, CTnrf10	chromosome 7 open reading frame 10	NM_032128, NM_001163311, NM_001163312, NM_001163313, XCT2298200.0, XCT2298522.0, XCT2298524.0	216655_at	NP_079004.1, NP_001152001.1, NM_001163312, NM_001163313, EAW84136.1, EAW84137.1, EAW84135.1
Gene:ID:4633	PSMA2	7	42,936,860	42,971,855	15,345	-	1	2_A375_shN7_dhrus_lncRNA:1:-7083	-291	upstream	0	1	11	16	1	2_A375_shN7_dhrus_lncRNA:1	16	Gene: PSMA2	PSC2, PMSA2, HC2, PSMA2, MU	proteasome (prosome, macropain) subunit, alpha type, 2	NM_002787, XCT23877090.0, XCT23877100.0, XCT 1830129.1	201316_at, 201317_s_at	NP_002778.1, EAW84151.1, EAW84152.1, EAW84153.1
Gene:ID:9653	MRPL32	7	42,971,839	42,977,656	5,817	+	1	2_A375_shN7_dhrus_lncRNA:1:-7084	157	ut gene	0	1	11	16	1	2_A375_shN7_dhrus_lncRNA:1	16	Gene: MRPL32	L32-like, HEP2283, MRP-L32, bMRP-94b, MRPL32	mitochondrial ribosomal protein L32	NM_031903, XCT10355.2, XCT19833370.0, XCT19833380.0, XCT19833390.0	2252S3_s_at	NP_114109.1, EAW84157.1, EAW84158.1, EAW84155.1, EAW84156.1
Gene:ID:3072	HECW1	7	43,152,198	43,602,838	450,640	+	2	1_A375_shN7_dhrus_lncRNA:1:-9921,2_A375_shN7_dhrus_lncRNA:1:-7089	107634, 457052	ut gene, downstream	1	1	19	19	2	2_A375_shN7_dhrus_lncRNA:1	24	Gene: HECW1	HECW1, NEDL1, KIAA1522	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	NM_015052, XCT23496840.0, XCT23496850.0, XCT10462.2	2102J1_at, 215564_at	NP_055877.2, EAW84158.1, EAW84159.1, EAW84160.1
Gene:ID:263	STX17A	7	43,622,992	43,666,976	44,256	+	1	2_A375_shN7_dhrus_lncRNA:1:-7090	412	ut gene	0	1	11	22	1	2_A375_shN7_dhrus_lncRNA:1	22	Gene: STX17A	DRAK1, STX17A	serine/threonine kinase 17a	NM_004760, XCT2299580.0, XCT10469.3	202693_s_at, 202694_at, 202695_s_at	NP_004911.2, EAW84162.1, EAW84163.1
Gene:ID:5744	CTnrf44	7	43,676,659	43,769,083	90,224	-	4	1_A375_shN7_dhrus_lncRNA:1:-9922,1_A375_shN7_dhrus_lncRNA:1:-9923,1_A375_shN7_dhrus_lncRNA:1:-7091,2_A375_shN7_dhrus_lncRNA:1:-7092	514O3, 181, 54715, 49	ut gene, upstream, ut gene, upstream	1	1	16.67	21.67	3	2_A375_shN7_dhrus_lncRNA:1	33	Gene: CTnrf44	CTnrf44, FLJ10503	chromosome 7 open reading frame 44	NM_032224, XCT2297730.0, XCT23896810.0, XCT 10496.2, XCT19833301.1, XCT19833321.1	208497_s_at, 208498_s_at, 208499_s_at, 232326_at, 238490_at	NP_060904.2, EAW84167.1, EAW84165.1, EAW84166.1, EAW84168.1, EAW84170.1
Gene:ID:5744	CTnrf44	7	43,676,659	43,769,083	90,224	-	4	1_A375_shN7_dhrus_lncRNA:1:-9922,1_A375_shN7_dhrus_lncRNA:1:-9923,1_A375_shN7_dhrus_lncRNA:1:-7091,2_A375_shN7_dhrus_lncRNA:1:-7092	514O3, 181, 54715, 49	ut gene, upstream, ut gene, upstream	1	1	16.67	21.67	3	2_A375_shN7_dhrus_lncRNA:1	33	Gene: CTnrf44	CTnrf44, FLJ10503	chromosome 7 open reading frame 44	NM_032224, XCT2297730.0, XCT23896810.0, XCT 10496.2, XCT19833301.1, XCT19833321.1	208497_s_at, 208498_s_at, 208499_s_at, 232326_at, 238490_at	NP_060904.2, EAW84167.1, EAW84165.1, EAW84166.1, EAW84168.1, EAW84170.1
Gene:ID:9976	MPP524	7	43,905,157	43,909,145	2,988	-	1	2_A375_shN7_dhrus_lncRNA:1:-7093	-58	ut gene	0	1	15	20	1	2_A375_shN7_dhrus_lncRNA:1	20	Gene: MPP524	MPP524, HSPC335, MPP524	mitochondrial ribosomal protein S36	NM_032314, XCT19939871.1, XCT19939881.1	226955_at	NP_114603.1, EAW84172.1, EAW84173.1
Gene:ID:5965	URGCP	7	43,915,501	43,963,896	50,465	-	2	1_A375_shN7_dhrus_lncRNA:1:-9924,2_A375_shN7_dhrus_lncRNA:1:-7094	140, 50980	ut gene, downstream	1	1	15.5	17	2	2_A375_shN7_dhrus_lncRNA:1	20	Gene: URGCP	DKFZp686O0457, URGCP, URG4, DKFZp686G166	upregulator of cell proliferation	NM_005779953, NM_005779564, NM_017620, XCT23979190.0, XCT23979840.0, XCT 10492.3	218501_at, 240636_at	NP_2603912.2, EAW84174.1, EAW84175.1, EAW84176.1
Gene:ID:1618	UBE2D4	7	43,966,033	43,993,735	29,760	+	1	2_A375_shN7_dhrus_lncRNA:1:-9924	-179	upstream	1	0	16	14	1	1_A375_shN7_dhrus_lncRNA:1	16	Gene: UBE2D4	FLJ32004, UBE2D4, HBUCE1	ubiquitin-conjugating enzyme E2D 4 (putative)	NM_015983, XCT19967851, XCT19967861, XCT19967871, XCT19967881, XCT6222.2, XCT19825833.1, XCT19825841.1, XCT19825851.1, XCT19825861.1	216837_s_at, 65521_at	NP_057067.1, EAW84182.1, EAW84178.1, EAW84179.1, EAW84180.1, EAW84181.1, EAW84183.1
Gene:ID:53655	SPDYE1	7	44,040,459	44,049,723	9,234	+	2	1_A375_shN7_dhrus_lncRNA:1:-9925,2_A375_shN7_dhrus_lncRNA:1:-7096	16293, 16327	downstream, downstream	1	1	134	147	1	2_A375_shN7_dhrus_lncRNA:1	147	Gene: SPDYE1	Regc1, KIBBCR19, SPDYE, DKFZp434A1014, SPDYE1	Speedy homolog E1 (Xenopus laevis)	NM_178064	232964_at	NP_785334.2
Gene:ID:100287164	LOC100287164	7	44,039,662	44,063,852	5,970	-	2	1_A375_shN7_dhrus_lncRNA:1:-9925,2_A375_shN7_dhrus_lncRNA:1:-7096	7165, 7135	downstream, downstream	1	1	134	147	1	2_A375_shN7_dhrus_lncRNA:1	147	Gene: LOC100287164		hypothetical protein LOC100287164	XM_002342717		XP_002342758.2
Gene:ID:55031	FLJ35390	7	44,078,695	44,082,662	3,356	+	2	1_A375_shN7_dhrus_lncRNA:1:-9926,1_A375_shN7_dhrus_lncRNA:1:-9927	4922, 5486	downstream, downstream	1	0	16.5	15	2	1_A375_shN7_dhrus_lncRNA:1	16	Gene: FLJ35390		hypothetical LOC285031	NR_015401, NR_024416	1555123_at, 1564207_at, 1564208_s_at, 1569099_at, 1569099_x_at	
Gene:ID:9966	DBNL	7	44,084,239	44,101,315	17,076	+	2	1_A375_shN7_dhrus_lncRNA:1:-9926,1_A375_shN7_dhrus_lncRNA:1:-9927	-1919, -93	upstream, upstream	1	0	16.5	15	2	1_A375_shN7_dhrus_lncRNA:1	16	Gene: DBNL	ABP1, SH3P7, DBNL, HIP-55	drebrin-like	NM_014963, NM_001014436, NM_001122936, XCT23900470.0, XCT23900480.0, XCT23539290.0, XCT 10484.1	222429_at	NP_054782.2, NP_001014436.1, NP_001116620.1, EAW81126.1, EAW81130.1, EAW81132.1, EAW81131.1
Gene:ID:9514	YKT6	7	44,240,976	44,253,893	12,918	+	1	2_A375_shN7_dhrus_lncRNA:1:-9927,2_A375_shN7_dhrus_lncRNA:1:-7098	174	ut gene	0	1	22	13	1	2_A375_shN7_dhrus_lncRNA:1	22	Gene: YKT6	YKT6		NM_006555, XCT23900940.0, XCT23900950.0, XCT 6512.2	217764_at, 217763_s_at	NP_008845.1, EAW81113.1, EAW81111.1, EAW81112.1
Gene:ID:9606	DDX36	7	44,605,003	44,618,137	8,734	+	1	2_A375_shN7_dhrus_lncRNA:1:-9929,2_A375_shN7_dhrus_lncRNA:1:-7099	-2479, 689	upstream, ut gene	1	1	16.5	19.5	2	2_A375_shN7_dhrus_lncRNA:1	23	Gene: DDX36	DDX21, NOH61, DDX36, DDX36	DEAD (Asp-Glu-Ala-Asp) box polypeptide 36	NM_018980, XCT2306280.0, XCT23062810.0, XCT6338.2	217754_at	NP_061953.1, EAW81088.1, EAW81092.1, EAW81084.1
Gene:ID:22066	TMED4	7	44,616,762	44,621,827	2,066	-	2	1_A375_shN7_dhrus_lncRNA:1:-9929,2_A375_shN7_dhrus_lncRNA:1:-7099	211, 5339	ut gene, downstream	1	1	16.5	19.5	2	2_A375_shN7_dhrus_lncRNA:1	23	Gene: TMED4	ERS25, HNLF, TMED4	transmembrane emp24 protein transport domain containing 4	NM_182547, XCT23562291.1, XCT23482400.1, XCT10359.2	1555052_at, 1555053_s_at, 1555057_s_at, 224676_at, 224677_s_at	NP_872353.2, EAW81091.1, EAW81090.1, EAW81092.1
Gene:ID:997	OGDH	7	44,646,121	44,746,669	102,548	+	2	1_A375_shN7_dhrus_lncRNA:1:-7099,2_A375_shN7_dhrus_lncRNA:1:-7100	555, 32567	ut gene, ut gene	0	1	16	20.5	2	2_A375_shN7_dhrus_lncRNA:1	21	Gene: OGDH	AKGDH, OGDH, E1k, OGDC	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	NM_002541, NM_001030941, NM_001169036, XCT23984490.0, XCT23984611.0, XCT23984630.0, XCT 1430.1	1554531_at, 1554532_a_at, 201262_at	NP_002532.2, NP_001030941.1, NP_001159508.1, EAW81087.1, EAW81086.1, EAW81089.1, EAW81088.1
Gene:ID:9637	ZMIZ2	7	44,765,530	44,809,480	20,950	+	2	1_A375_shN7_dhrus_lncRNA:1:-9930,2_A375_shN7_dhrus_lncRNA:1:-7100	-242, -302	upstream, upstream	1	1	41	50	1	2_A375_shN7_dhrus_lncRNA:1	50	Gene: ZMIZ2	ZMIZ2, KIAA1656, ZIMP7, DKFZp761H1523, TRAIP2R, NET27	zinc finger, MIZ-type containing 2	NM_020449, NM_178829, XCT23864650.1, XCT23864661.1, XCT23864671.1	221625_at, 221624_s_at, 236309_x_at, 240370_at	NP_115373.2, NP_777582.2, EAW81083.1, EAW81084.1, EAW81085.1
Gene:ID:478	PPIA	7	44,836,241	44,842,716	6,475	+	1	2_A375_shN7_dhrus_lncRNA:1:-7099	143	ut gene	0	1	19	15	1	2_A375_shN7_dhrus_lncRNA:1	15	Gene: PPIA	MGC117158, CYPA, CYPH, MGC23297, PPIA, MGC13856	peptidylprolyl isomerase A (cyclophilin A)	NM_021130	201293_x_at, 211376_x_at, 211763_s_at, 211978_x_at, 212661_s_at, 215502_at, 226536_at, 227458_at	NP_066953.1
Gene:ID:514	PURB	7	44,918,692	44,924,890	6,098	-	2	2_A375_shN7_dhrus_lncRNA:1:-7100,2_A375_shN7_dhrus_lncRNA:1:-7100	104, -336	ut gene, upstream	0	1	16.5	17	2	2_A375_shN7_dhrus_lncRNA:1	22	Gene: PURB	PURBETA, MGC126766, MGC126764, PURB	purine-rich element binding protein B	NM_033224, XCT11640362.3	225170_at, 226762_at, 227716_at, 235467_at, 235513_at	NP_149013.2, EAW81073.1
Gene:ID:8003	MYCH2	7	45,002,260	45,018,764	16,504	-	1	2_A375_shN7_dhrus_lncRNA:1:-7102	-7664	upstream	0	1	17	21	1	2_A375_shN7_dhrus_lncRNA:1	21	Gene: MYCH2	MRAG, MYCH2, MGC142168, HA2	myosin IG	NM_033034, XCT23062630.0, XCT23062640.0, XCT23536370.0, XCT23536380.0, XCT 6218.2	227799_at, 246654_at	NP_149043.2, EAW81069.1, EAW81068.1, EAW81070.1, EAW81071.1, EAW81072.1
Gene:ID:53828	CTnrf60	7	45,022,827	45,026,259	3,432	+	1	2_A375_shN7_dhrus_lncRNA:1:-7102	-109	upstream	0	1	17	21	1	2_A375_shN7_dhrus_lncRNA:1	21	Gene: CTnrf60	CTnrf60, FLJ35560	chromosome 7 open reading frame 60	NM_020997	235692_at	
Gene:ID:677888	SNORA62	7	45,024,977	45,025,109	132	-	1	2_A375_shN7_dhrus_lncRNA:1:-7102	-1259	upstream	0	1	17	21	1	2_A375_shN7_dhrus_lncRNA:1	21	Gene: SNORA62	SNORA62, ACA9	small nucleolar RNA, H/ACA box 9	NR_002952		
Gene:ID:235	TBRG4	7	45,139,699	45,151,217	11,518	-	2	1_A375_shN7_dhrus_lncRNA:1:-9931,2_A375_shN7_dhrus_lncRNA:1:-7103	101, -107	ut gene, ut gene	1	1	16	24	1	2_A375_shN7_dhrus_lncRNA:1	24	Gene: TBRG4	FASTKD4, TBRG4, KIAA0846, CFP2	transforming growth factor beta regulator 4	NM_138122, NM_004749, NM_033000, XCT23872720.0, XCT23872730.0, XCT23872770.0, XCT23872780.0, XCT10312.2, XCT1782781.0	200792_s_at, 200801_x_at	NP_954573.1, NP_004740.2, NP_112162.1, EAW81053.1, EAW81054.1, EAW81055.1, EAW81052.1, EAW81053.1, EAW81054.1
Gene:ID:34319	SNORA5A	7	45,143,846	45,144,081	133	-	2	1_A375_shN7_dhrus_lncRNA:1:-9931,2_A375_shN7_dhrus_lncRNA:1:-7103	-7135, -7343	upstream, upstream	1	1	16	24	1	2_A375_shN7_dhrus_lncRNA:1	24	Gene: SNORA5A	SNORA5A, ACA5A/B/C, ACA5	small nucleolar RNA, H/ACA box 5A	NR_002919		
Gene:ID:77795	SNORA5C	7	45,144,503	45,144,641	139	-	2	1_A375_shN7_dhrus_lncRNA:1:-9931,2_A375_shN7_dhrus_lncRNA:1:-7103	-6575, -6783	upstream, upstream	1	1	16	24	1	2_A375_shN7_dhrus_lncRNA:1	24	Gene: SNORA5C	ACA5C, SNORA5C	small nucleolar RNA, H/ACA box 5C	NR_002991		
Gene:ID:77795	SNORA5B	7	45,145,367	45,145,666	131	-	2	1_A375_shN7_dhrus_lncRNA:1:-9931,2_A375_shN7_dhrus_lncRNA:1:-7103	-5516, -5726	upstream, upstream	1	1	16	24	1	2_A375_shN7_dhrus_lncRNA:1	24	Gene: SNORA5B	SNORA5B, ACA5b	small nucleolar RNA, H/ACA box 5B	NR_002990		
Gene:ID:486	IGFBP3	7	45,951,644	45,960,671	9,027	-	1	2_A375_shN7_dhrus_lncRNA:1:-7107	163	ut gene	0	1	12	16	1	2_A375_shN7_dhrus_lncRNA:1	16	Gene: IGFBP3	BP-53, IBP3, IGFBP3	insulin-like growth factor binding protein 3	NM_000598, NM_001013398, XCT23926340, XCT23926350, XCT1733211.0, XCT 9611110.1, XCT 9611111.0	210095_s_at, 212143_s_at	NP_000589.2, NP_001013416.1, EAW81029.1, EAW81026.1, EAW81027.1, EAW81028.1, EAW81026.1
Gene:ID:4700	TNS3	7	47,314,752	47,579,199	264,447	+	6	1_A375_shN7_dhrus_lncRNA:1:-9926,1_A375_shN7_dhrus_lncRNA:1:-9927,1_A375_shN7_dhrus_lncRNA:1:-7114,1_A375_shN7_dhrus_lncRNA:1:-7115,1_A375_shN7_dhrus_lncRNA:1:-7116,2_A375_shN7_dhrus_lncRNA:1:-7117	247998, 238515, 287902, 211551, 176798, 94239	ut gene, ut gene, ut gene, ut gene, ut gene, ut gene	1	1	16	20.5	3	2_A375_shN7_dhrus_lncRNA:1	28	Gene: TNS3	FLJ13732, DKFZp686M1045, TENS1, TENS, DKFZp686K12123, MGC26424, FLJ35545, TNS3, H_NH0392J2.2	tensin 3	NM_022748, XCT23942295.1, XCT23942305.0, XCT23942390.1, XCT23942401.1, XCT23942492.0	217553_at, 236297_at	NP_073585.6, EAW81011.1, EAW81012.1, EAW81013.1, EAW81014.1, EAW81015.1
Gene:ID:65007	PKD1L1	7	47,514,290	47,555,037	172,747	+	1	2_A375_shN7_dhrus_lncRNA:1:-7116	161999	ut gene	0	1	10	19	1	2_A375_shN7_dhrus_lncRNA:1	19	Gene: PKD1L1	PKD1L1, PRO19353	polycystic kidney disease 1 like 1	NM_138295, XCT23555112.0, XCT23555140.0, XCT23555150.0, XCT 9435.27.2	1553004_at, 1563463_at	NP_612152.1, EAW81006.1, EAW81003.1, EAW81008.1, EAW81006.1, EAW81007.1
Gene:ID:3364	CTnrf69	7	47,534,559	47,559,445	24,886	+	1	2_A375_shN7_dhrus_lncRNA:1:-7118	4521	upstream	0	1	10	19	1	2_A375_shN7_dhrus_lncRNA:1	19	Gene: CTnrf69	FLJ21075, CTnrf69	chromosome 7 open reading frame 69	NM_025031, XCT1782422.1	221172_at	NP_079307.2, EAW81006.1
Gene:ID:364	HUS1	7	48,003,783	48,019,246	15,463	-	2	1_A375_shN7_dhrus_lncRNA:1:-9940,2_A375_shN7_dhrus_lncRNA:1:-7119	142, 46	ut gene, ut gene	1	1	16	16	1	2_A375_shN7_dhrus_lncRNA:1	19	Gene: HUS1	HUS1		NM_004507, XCT180563.2, XCT1837.23.1	204853_s_at, 204854_s_at, 217616_s_at	NP_004498.1, EAW81002.1, EAW81001.1
Gene:ID:99379	SUN2	7	48,026,745	48,068,716	41,971	-	3	1_A375_shN7_dhrus_lncRNA:1:-9940,2_A375_shN7_dhrus_lncRNA:1:-7119,2_A375_shN7_dhrus_lncRNA:1:-7120	49612, 48516, 8547	downstream, downstream, upstream	1	1	16.5	16.3	2	2_A375_shN7_dhrus_lncRNA:1	19	Gene: SUN2	MGC33326, SUN2, SUNC1	Sad1 and UNC84 domain containing 2	NM_152782, NM_001130019, XCT23926360, XCT 1937.62.1	231616_s_at	NP_689033.3, NP_001025190.1, EAW80998.1, EAW81000.1
Gene:ID:26258	CTnrf57	7	48,078,117	48,100,684	25,777	+	1	2_A375_shN7_dhrus_lncRNA:1:-7120	486	upstream	0	1	10	15	1	2_A375_shN7_dhrus_lncRNA:1	15	Gene: CTnrf57	CTnrf57	chromosome 7 open reading frame 57	NM_015001158	1557636_a_at	NP_001029629.1
Gene:ID:215	UPF1	7	48,126,353	48,146,230	19,878	+	1	2_A375_shN7_dhrus_lncRNA:1:-7120	-2779	upstream	0	1	13	16	1	2_A375_shN7_dhrus_lncRNA:1	16	Gene: UPF1	UP, UPASE, UPRPASE, UPF1, UPF	eukaryotic translation termination factor 1	NM_002911, NM_1613097, XCT23961110.0, XCT23961120.0, XCT23961130.0	203252_at	NP_002902.1, NP_057626.2, EAW80993.1, EAW80994.1, EAW80995.1
Gene:ID:10349	ABCA13	7	48,211,097	48,687,091	476,034	+	1	2_A375_shN7_dhrus_lncRNA:1:-7122	73551	ut gene	0	1	14	25	1	2_A375_shN7_dhrus_lncRNA:1	25	Gene: ABCA13	FLJ32831, DKFZp312D2411, FLJ33576, ABCA13, FLJ16396	ATP-binding cassette, sub-family A (ABC1), member 13	NM_152701, XCT23991180.0, XCT23491260.1, XCT8364.4	1553293_at, 1553904_at, 1553905_at	NP_689914.2, EAW80981.1, EAW80980.1, EAW80982.1
Gene:ID:3978	FIGNL1	7	50,311,831	50,510,866	6,237	-	2	1_A375_shN7_dhrus_lncRNA:1:-9941,2_A375_shN7_dhrus_lncRNA:1:-7123	72, 136	ut gene, ut gene	1	1	16	22	1	2_A375_shN7_dhrus_lncRNA:1	22	Gene: FIGNL1	FIGNL1		NM_001042762, NM_022116, XCT23263330, XCT16451090.3	1552921_a_at, 1552921_at, 222643_at	NP_001036227.1, NP_071299.2, EAW80978.1, EAW80976.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9988	DMTF1	7	86,781,677	86,825,648	43,971	+	1	2_A375_pNL97_plus_lncRNA::1::7190	-109	upstream	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene DMTF1	FLJ41265, FLJ25186, DMTF1, FLJ76054, hDMP1, DMP1, DMTF	cyclin D binding myb-like transcription factor 1	NR_024549, NR_024550, NM_021145, NM_001142326, NM_001142327, hCT2320660.0, hCT2320661.0, hCT2320662.0, hCT8263.3	203301_s_at	NP_066968.3, NP_001135798.1, NP_001135799.1, EAW76962.1, EAW76964.1, EAW76965.1, EAW76963.1
GeneID:100505951	LOC100505951	7	86,788,836	86,790,759	1,923	+	1	2_A375_pNL97_plus_lncRNA::1::7190	-7268	upstream	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene LOC100505951		hypothetical LOC100505951	XR_113036, XR_110713, XR_108844, XR_114064		
GeneID:79161	C7orf23	7	86,825,476	86,849,031	23,553	-	2	1_A375_pNL7_minus_lncRNA::1::4954, 2_A375_pNL97_plus_lncRNA::1::7191	-633, -1001	upstream, upstream	1	1	16	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene C7orf23	MM-TRAG, C7orf23, MGC4175	chromosome 7 open reading frame 23	NM_024315, hCT2320610.0, hCT1781406.2	204215_at	NP_077291.1, EAW76960.1, EAW76961.1
GeneID:11257	TP53TG1	7	86,954,663	86,974,808	20,145	-	2	1_A375_pNL7_minus_lncRNA::1::4955, 2_A375_pNL97_plus_lncRNA::1::7192	160, 152	in gene, in gene	1	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene TP53TG1	TP53AP1, NCRNA00096, P53TG1, TP53TG1, P53TG1-D	TP53 target 1 (non-protein coding)	NR_015381, hCT2320605.1, hCT2320606.1, hCT2320607.0, hCT2352011.0, hCT1781405.3	209917_s_at, 210241_s_at, 210886_x_at	EAW76957.1, EAW76955.1, EAW76956.1, EAW76958.1, EAW76959.1
GeneID:54677	CROT	7	86,974,951	87,029,112	54,161	+	2	1_A375_pNL7_minus_lncRNA::1::4955, 2_A375_pNL97_plus_lncRNA::1::7192	-303, -295	upstream, upstream	1	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene CROT	CROT, COT	carnitine O-octanoyltransferase	NM_021151, NM_001143935, NR_026585, hCT2320665.0	204573_at, 231102_at	NP_066974.2, NP_001137407.1, EAW76954.1
GeneID:5243	ABCB1	7	87,132,948	87,342,564	209,616	-	2	1_A375_pNL7_minus_lncRNA::1::4956, 2_A375_pNL97_plus_lncRNA::1::7193	84932, 85252	in gene, in gene	1	1	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ABCB1	ABCB1, MGC163296, CLCS, CD243, PGY1, GP170, P-GP, MDR1, ABC20	ATP-binding cassette, sub-family B (MDR/TAP), member 1	NM_000927, hCT2320743.1, hCT2343419.0, hCT2343420.0, hCT8260.4	209993_at, 243951_at	NP_000918.2, EAW76940.1, EAW76941.1, EAW76942.1, EAW76943.1
GeneID:154661	RUNDC3B	7	87,257,729	87,461,613	203,884	+	2	1_A375_pNL7_minus_lncRNA::1::4956, 2_A375_pNL97_plus_lncRNA::1::7193	-97, -417	upstream, upstream	1	1	19	16	1	1_A375_pNL7_minus_lncRNA::1	19	Gene RUNDC3B	MGC26655, FLJ30671, RPIB9, RPIP9, RUNDC3B	RUN domain containing 3B	NM_138290, NM_001134405, NM_001134406, hCT2320913.0, hCT2320916.0, hCT1781409.2, hCT1954042.1	215321_at, 241703_at	NP_612147.1, NP_001127877.1, NP_001127878.1, EAW76937.1, EAW76938.1, EAW76939.1, EAW76936.1
GeneID:53616	ADAM22	7	87,563,702	87,826,454	262,752	+	2	2_A375_pNL97_plus_lncRNA::1::7194, 2_A375_pNL97_plus_lncRNA::1::7195	42, 250618	in gene, in gene	0	1	15	19	2	2_A375_pNL97_plus_lncRNA::1	22	Gene ADAM22	MGC149832, ADAM22, MDC2	ADAM metallopeptidase domain 22	NM_016351, NM_021721, NM_021723, NM_004194, NM_021722, hCT1966957.1, hCT2320920.0, hCT2320922.0, hCT2320929.0, hCT2320930.0, hCT2320932.0, hCT2355643.0, hCT2355644.0, hCT2355645.0, hCT2355646.0, hCT11898.2, hCT11899.3, hCT1954866.1, hCT1963956.1, hCT19639	1555024_at, 206615_s_at, 206616_s_at, 208226_x_at, 208227_x_at, 208237_x_at	NP_057435.2, NP_068367.1, NP_068369.1, NP_068368.2, NP_004185.1, EAW76922.1, EAW76913.1, EAW76914.1, EAW76915.1, EAW76916.1, EAW76917.1, EAW76918.1, EAW76919.1, EAW76920.1, EAW76921.1, EAW76923.1, EAW76924.1, EAW76925.1, EAW76926.1, EAW76927.1, EAW76928.1
GeneID:6717	SRI	7	87,834,432	87,856,308	21,876	-	2	1_A375_pNL7_minus_lncRNA::1::4957, 2_A375_pNL97_plus_lncRNA::1::7196	6852, 6836	in gene, in gene	1	1	20	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene SRI	SCN, FLJ26259, CP22, SRI	sorcin	NM_198901, NM_003130, hCT2355650.0, hCT11900.2, hCT1961287.1	208920_at, 208921_s_at	NP_944490.1, NP_003121.1, EAW76909.1, EAW76910.1, EAW76911.1
GeneID:79689	STEAP4	7	87,905,744	87,936,209	30,465	-	1	1_A375_pNL7_minus_lncRNA::1::4958	27809	in gene	1	0	17	7	1	1_A375_pNL7_minus_lncRNA::1	17	Gene STEAP4	TNFAIP9, DKFZp666D049, STAMP2, TIARP, STEAP4, FLJ23153	STEAP family member 4	NM_024636, hCT2320729.0, hCT11902.3	220187_at, 225987_at	NP_078912.2, EAW76906.1, EAW76907.1
GeneID:85865	GTPBP10	7	89,975,990	90,016,650	40,660	+	2	1_A375_pNL7_minus_lncRNA::1::4959, 2_A375_pNL97_plus_lncRNA::1::7197	42, 74	in gene, in gene	1	1	23	16	1	1_A375_pNL7_minus_lncRNA::1	23	Gene GTPBP10	FLJ38242, DKFZp686A10121, MGC104191, GTPBP10, UG0751c10, ObgH2	GTP-binding protein 10 (putative)	NM_001042717, NM_033107, hCT2320418.0, hCT2320420.0, hCT2355663.0, hCT10230.3, hCT1954043.1	216619_at, 234311_s_at	NP_001036182.1, NP_149098.2, EAW76878.1, EAW76879.1, EAW76880.1, EAW76882.1, EAW76881.1
GeneID:5218	CDK14	7	90,338,712	90,839,904	501,192	+	1	2_A375_pNL97_plus_lncRNA::1::7198	55640	in gene	0	1	8	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene CDK14	PFTAIRE1, KIAA0834, CDK14, PFTK1	cyclin-dependent kinase 14	NM_012395, hCT2320351.0, hCT2351154.0, hCT1960141.2	204604_at, 211502_s_at	NP_036527.1, EAW76874.1, EAW76872.1, EAW76873.1
GeneID:8321	FZD1	7	90,893,783	90,898,132	4,349	+	1	1_A375_pNL7_minus_lncRNA::1::4990	-119	upstream	1	0	30	14	1	1_A375_pNL7_minus_lncRNA::1	30	Gene FZD1	FZD1, DKFZp564G072, FLJ95923	frizzled homolog 1 (Drosophila)	NM_003505, hCT8283.3	204451_at, 204452_s_at	NP_003496.1, EAW76871.1
GeneID:7978	MTERF	7	91,502,021	91,510,016	7,995	-	2	1_A375_pNL7_minus_lncRNA::1::4991, 2_A375_pNL97_plus_lncRNA::1::7199	-96, 0	upstream, in gene	1	1	47	61	1	2_A375_pNL97_plus_lncRNA::1	61	Gene MTERF	MGC131634, MTERF	mitochondrial transcription termination factor	NM_006980, hCT1961275.1	204871_at	NP_008911.1, EAW76869.1
GeneID:10142	AKAP9	7	91,570,189	91,739,987	169,798	+	1	1_A375_pNL7_minus_lncRNA::1::4992	-61	upstream	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene AKAP9	AKAP450, YOTIAO, KIAA0803, AKAP350, PRKA9, MU-RMS-40.16A, HYPERION, AKAP9, CG-NAP	A kinase (PRKA) anchor protein (yotiao) 9	NM_147185, NM_005751, hCT2326688.1, hCT2326689.1, hCT2326692.1, hCT2326693.1, hCT2326694.1, hCT2326696.1, hCT1955572.2, hCT1955573.1, hCT1955574.1	207870_at, 210962_s_at, 215483_at	NP_671714.1, NP_005742.4, EAW76860.1, EAW76861.1, EAW76862.1, EAW76867.1, EAW76863.1, EAW76864.1, EAW76865.1, EAW76866.1, EAW76868.1
GeneID:1595	CYP51A1	7	91,741,463	91,764,059	22,596	-	2	1_A375_pNL7_minus_lncRNA::1::4993, 2_A375_pNL97_plus_lncRNA::1::7200	-5, 859	upstream, in gene	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CYP51A1	LDM, CYP51, CP51, P450-14DM, CYPL1, P450L1, CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	NM_000786, NM_001146152, hCT2326687.1, hCT9827.2	202314_at, 216607_s_at	NP_000777.1, NP_001139624.1, EAW76858.1, EAW76859.1
GeneID:613126	LOC613126	7	91,763,176	91,810,039	46,863	+	2	1_A375_pNL7_minus_lncRNA::1::4993, 2_A375_pNL97_plus_lncRNA::1::7200	888, 24	in gene, in gene	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC613126		hypothetical LOC613126	XR_113035, XR_110714, XR_108845, XR_114065	233942_at	
GeneID:401387	LOC401387	7	91,774,198	91,794,590	20,392	-	2	1_A375_pNL7_minus_lncRNA::1::4993, 2_A375_pNL97_plus_lncRNA::1::7200	30526, 31390	downstream, downstream	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC401387	FLJ34004, MGC178225, MGC178229	leucine-rich repeat and death domain-containing protein	NM_001161528	1569783_at	NP_001155000.1
GeneID:889	KRIT1	7	91,828,283	91,875,414	47,131	-	1	2_A375_pNL97_plus_lncRNA::1::7201	107	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene KRIT1	KRIT1, CCM1, CAM	KRIT1, ankyrin repeat containing	NM_194455, NM_194456, NM_004912, NM_194454, NM_001013406, hCT2326681.0, hCT2326682.1	204738_s_at, 216713_at, 229765_at, 34031_i_at	NP_919437.1, NP_919438.1, NP_004903.2, NP_919436.1, NP_001013424.1, EAW76854.1, EAW76855.1
GeneID:54467	ANKIB1	7	91,875,548	92,030,698	155,150	+	1	2_A375_pNL97_plus_lncRNA::1::7201	-241	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene ANKIB1	FLJ33123, KIAA1386, ANKIB1, DKFZp434A0225	ankyrin repeat and IBR domain containing 1	NM_019004	224682_at, 224687_at, 243181_at	NP_061877.1
GeneID:57798	GATAD1	7	92,076,765	92,088,742	11,977	+	1	2_A375_pNL97_plus_lncRNA::1::7202	67	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene GATAD1	ODAG, GATAD1, RG083M05.2, FLJ40695, FLJ22489	GATA zinc finger domain containing 1	NM_021167, hCT2326700.1, hCT2326701.1, hCT2326702.2, hCT2355623.0	208503_s_at, 213018_at, 214718_at, 242634_at	NP_066990.3, EAW76848.1, EAW76849.1, EAW76850.1, EAW76851.1
GeneID:5189	PEX1	7	92,116,337	92,157,845	41,508	-	2	1_A375_pNL7_minus_lncRNA::1::4994, 2_A375_pNL97_plus_lncRNA::1::7203	-171, -139	upstream, upstream	1	1	112	120	1	2_A375_pNL97_plus_lncRNA::1	120	Gene PEX1	ZWS1, PEX1, ZWS	peroxisomal biogenesis factor 1	NM_000466, hCT2326677.0, hCT2326679.0, hCT2355664.0, hCT10613.3, hCT1959428.1	204873_at, 215023_s_at	NP_000457.1, EAW76841.1, EAW76840.1, EAW76842.1, EAW76843.1, EAW76844.1
GeneID:84060	C7orf64	7	92,158,087	92,166,823	8,736	+	2	1_A375_pNL7_minus_lncRNA::1::4994, 2_A375_pNL97_plus_lncRNA::1::7203	-71, -103	upstream, upstream	1	1	112	120	1	2_A375_pNL97_plus_lncRNA::1	120	Gene C7orf64	DKFZP564O0523, HSPC304, C7orf64, DKFZp686D1651	chromosome 7 open reading frame 64	NM_032120, hCT10615.4, hCT1963797.1	221594_at, 221595_s_at, 232661_s_at	NP_115496.2, EAW76839.1, EAW76838.1
GeneID:84549	MGC16142	7	92,167,789	92,169,079	1,290	+	2	1_A375_pNL7_minus_lncRNA::1::4994, 2_A375_pNL97_plus_lncRNA::1::7203	-9773, -9805	upstream, upstream	1	1	112	120	1	2_A375_pNL97_plus_lncRNA::1	120	Gene MGC16142		hypothetical protein MGC16142	NR_026902	1553661_at	
GeneID:257415	FAM133B	7	92,190,072	92,219,706	29,634	-	2	1_A375_pNL7_minus_lncRNA::1::4995, 2_A375_pNL97_plus_lncRNA::1::7204	-6, -6	upstream, upstream	1	1	135	159	1	2_A375_pNL97_plus_lncRNA::1	159	Gene FAM133B	FAM133B, MGC40405	family with sequence similarity 133, member B	NM_001040057, NM_152789, hCT2326669.1, hCT2326673.1, hCT2326674.1, hCT2355605.0, hCT2355606.0, hCT10617.4	226332_at, 235469_at	NP_001035146.1, NP_690002.2, EAW76831.1, EAW76832.1, EAW76834.1, EAW76835.1, EAW76833.1, EAW76836.1
GeneID:1021	CDK6	7	92,234,235	92,465,941	231,706	-	3	1_A375_pNL7_minus_lncRNA::1::4996, 1_A375_pNL7_minus_lncRNA::1::4997, 2_A375_pNL97_plus_lncRNA::1::7205	3365, 885, 2677	in gene, in gene, in gene	1	1	14.33	13.67	3	1_A375_pNL7_minus_lncRNA::1	18	Gene CDK6	PLSTIRE, MGC59692, CDK6	cyclin-dependent kinase 6	NM_001259, NM_001145306, hCT2326667.0, hCT2326668.0	207143_at, 224847_at, 224848_at, 224851_at, 231198_at, 235287_at, 243000_at	NP_001250.1, NP_001138778.1, EAW76828.1, EAW76829.1
GeneID:253012	HEPACAM2	7	92,817,899	92,855,782	37,883	-	2	1_A375_pNL7_minus_lncRNA::1::4998, 2_A375_pNL97_plus_lncRNA::1::7206	-5786, -5850	upstream, upstream	1	1	23	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene HEPACAM2	HEPACAM2	HEPACAM family member 2	NM_198151, NM_001039372	242601_at	NP_937794.1, NP_001034461.1
GeneID:55610	CCDC132	7	92,861,653	92,988,338	126,685	+	2	1_A375_pNL7_minus_lncRNA::1::4998, 2_A375_pNL97_plus_lncRNA::1::7206	-85, -21	upstream, upstream	1	1	23	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene CCDC132	FLJ20097, FLJ23581, CCDC132, KIAA1861, MGC176659	coiled-coil domain containing 132	NM_024553, NM_017667, hCT2320317.0, hCT2320319.0, hCT2320320.0, hCT2320321.0, hCT2320323.0, hCT2320324.0, hCT1955570.1	1554216_at, 1554217_a_at, 207045_at, 226031_at	NP_078829.1, NP_060137.2, EAW76816.1, EAW76817.1, EAW76820.1, EAW76821.1, EAW76815.1, EAW76818.1, EAW76819.1
GeneID:7980	TFPI2	7	93,515,745	93,520,065	4,320	-	1	2_A375_pNL97_plus_lncRNA::1::7207	17	in gene	0	1	7	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TFPI2	TFPI2, REF1, PP5, TFPI-2, FLJ21164	tissue factor pathway inhibitor 2	NM_006528, hCT2345205.0, hCT10262.3, hCT1961278.1, hCT1961279.2	209277_at, 209278_s_at	NP_006519.1, EAW76810.1, EAW76808.1, EAW76809.1, EAW76811.1
GeneID:10282	BET1	7	93,621,000	93,633,690	12,690	-	1	2_A375_pNL97_plus_lncRNA::1::7208	-56	upstream	0	1	15	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene BET1	BET1, DKFZp781C0425, HBET1	blocked early in transport 1 homolog (S. cerevisiae)	NM_005868, hCT2320277.1, hCT2320279.1, hCT2355630.1, hCT10264.3	202710_at	NP_005859.1, EAW76800.1, EAW76801.1, EAW76802.1, EAW76803.1
GeneID:64921	CASD1	7	94,139,170	94,186,331	47,161	+	2	1_A375_pNL7_minus_lncRNA::1::4999, 2_A375_pNL97_plus_lncRNA::1::7209	766, 334	in gene, in gene	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene CASD1	FLJ21879, FLJ21213, CASD1, FLJ41901, C7orf12, NBLA04196	CAS1 domain containing 1	NM_022900, hCT2320996.0, hCT2320997.0, hCT2320998.0, hCT2320999.0, hCT2321000.0	219342_at, 231244_at, 242000_at, 243500_at	NP_075051.4, EAW76792.1, EAW76789.1, EAW76790.1, EAW76791.1, EAW76793.1
GeneID:8910	SGCE	7	94,214,536	94,285,521	70,985	-	1	1_A375_pNL7_minus_lncRNA::1::5000	35233	in gene	1	0	22	13	1	1_A375_pNL7_minus_lncRNA::1	22	Gene SGCE	DYT11, ESG, SGCE	sarcoglycan, epsilon	NM_001099401, NM_003919, NM_001099400, hCT2320216.0, hCT2320217.0, hCT2355626.0, hCT6966.2, hCT1961449.1	204688_at	NP_001092871.1, NP_003910.1, NP_001092870.1, EAW76784.1, EAW76786.1, EAW76788.1, EAW76785.1, EAW76787.1
GeneID:55607	PPP1R9A	7	94,536,949	94,925,727	388,778	+	3	1_A375_pNL7_minus_lncRNA::1::5001, 2_A375_pNL97_plus_lncRNA::1::7210, 2_A375_pNL97_plus_lncRNA::1::7211	-85, -85, 66263	upstream, upstream, in gene	1	1	15.5	21	2	2_A375_pNL97_plus_lncRNA::1	24	Gene PPP1R9A	Neurabin-I, FLJ20068, PPP1R9A, NRBI, NRB1, KIAA1222	protein phosphatase 1, regulatory (inhibitor) subunit 9A	NM_017650, NM_001166160, NM_001166161, NM_001166162, NM_001166163	221088_s_at, 228494_at, 231966_at, 233985_x_at	NP_060120.2, NP_001159632.1, NP_001159633.1, NP_001159634.1, NP_001159635.1
GeneID:5445	PON2	7	95,034,174	95,064,384	30,210	-	1	1_A375_pNL7_minus_lncRNA::1::5002	96	in gene	1	0	16	9	1	1_A375_pNL7_minus_lncRNA::1	16	Gene PON2	PON2		NM_000305, NM_001018161, hCT2320310.0, hCT2355655.0, hCT2355656.0, hCT2355657.0, hCT1640947.2	201876_at, 210830_s_at, 242700_at	NP_000296.2, NP_001018171.1, EAW76764.1, EAW76765.1, EAW76766.1, EAW76767.1, EAW76763.1
GeneID:51666	ASB4	7	95,115,284	95,167,071	51,787	+	1	1_A375_pNL7_minus_lncRNA::1::5003	15644	in gene	1	0	14	10	1	1_A375_pNL7_minus_lncRNA::1	14	Gene ASB4	ASB-4, MGC142041, MGC142039, ASB4	ankyrin repeat and SOCS box-containing 4	NM_016116, NM_145872, hCT2320341.0, hCT31800.3, hCT1962183.1	208481_at, 217228_s_at, 217229_at, 237720_at, 237721_s_at	NP_057200.1, NP_665879.1, EAW76760.1, EAW76761.1, EAW76762.1
GeneID:100506064	LOC100506064	7	95,171,457	95,173,854	2,397	+	1	2_A375_pNL97_plus_lncRNA::1::7212	8095	downstream	0	1	14	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC100506064		putative uncharacterized protein NCRNA00269-like	XM_003120046, XM_003119049, XM_003118586, XM_003120584		XP_003120094.1, XP_003119097.1, XP_003118634.1, XP_003120632.1
GeneID:10165	SLC25A13	7	95,749,532	95,951,459	201,927	-	2	1_A375_pNL7_minus_lncRNA::1::5004, 2_A375_pNL97_plus_lncRNA::1::7213	-29, -29	upstream, upstream	1	1	26	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SLC25A13	CTLN2, SLC25A13, ARALAR2, CITRIN	solute carrier family 25, member 13 (citrin)	NM_014251, NM_001160210, NR_027662, hCT2355651.0, hCT31894.1	203775_at, 229061_s_at, 229081_at	NP_055066.1, NP_001153682.1, EAW76748.1, EAW76749.1
GeneID:7979	SHFM1	7	96,318,079	96,339,203	21,124	-	1	2_A375_pNL97_plus_lncRNA::1::7214	163	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SHFM1	SHFM1, ECD, SEM1, SHFD1, Shfdg1, SHSF1, DSS1	split hand/foot malformation (ectrodactyly) type 1	NM_006304, hCT2320081.0, hCT2320082.0	202276_at	NP_006295.1, EAW76747.1, EAW76746.1
GeneID:57001	ACN9	7	96,745,905	96,811,075	65,170	+	2	1_A375_pNL7_minus_lncRNA::1::5006, 2_A375_pNL97_plus_lncRNA::1::7216	975, 1007	in gene, in gene	1	1	22	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene ACN9	ACN9, DC11	ACN9 homolog (S. cerevisiae)	NM_020186, hCT30262.3, hCT1962160.1	218981_at	NP_064571.1, EAW76740.1, EAW76739.1
GeneID:22853	LMTK2	7	97,736,197	97,838,945	102,748	+	2	1_A375_pNL7_minus_lncRNA::1::5007, 2_A375_pNL97_plus_lncRNA::1::7217	11, -21	in gene, upstream	1	1	16	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene LMTK2	KPI-2, BREK, KIAA1079, LMTK2, cprk, AATYK2, LMR2, FLJ46659, KPI2	lemur tyrosine kinase 2	NM_014916, hCT2320268.0, hCT2320269.0, hCT9310.3	206223_at, 235307_at	NP_055731.2, EAW76721.1, EAW76719.1, EAW76720.1
GeneID:25851	TECPR1	7	97,846,036	97,881,468	35,432	-	1	2_A375_pNL97_plus_lncRNA::1::7218	-180	upstream	0	1	21	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TECPR1	FLJ23419, FLJ90593, TECPR1, DKFZP434B0335	tectonin beta-propeller repeat containing 1	NM_015395, hCT2320186.0, hCT2355642.0, hCT32595.3	227580_s_at, 227581_at, 231912_s_at	NP_056210.1, EAW76718.1, EAW76716.1, EAW76717.1
GeneID:222865	TMEM130	7	98,444,111	98,467,673	23,562	-	2	1_A375_pNL7_minus_lncRNA::1::5009, 2_A375_pNL97_plus_lncRNA::1::7220	-8871, -8871	upstream, upstream	1	1	30	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene TMEM130	DKFZp761L1417, FLJ42643, TMEM130	transmembrane protein 130	NM_152913, NM_001134450, NM_001134451, hCT2320166.0, hCT2355647.0, hCT2355648.0, hCT32598.2	238426_at	NP_690877.1, NP_001127922.1, NP_001127923.1, EAW76701.1, EAW76703.1, EAW76704.1, EAW76702.1
GeneID:8295	TRRAP	7	98,476,113	98,610,864	134,751	+	2	1_A375_pNL7_minus_lncRNA::1::5009, 2_A375_pNL97_plus_lncRNA::1::7220	431, 431	in gene, in gene	1	1	30	39	1	2_A375_pNL97_plus_lncRNA::1	39	Gene TRRAP	PAF400, PAF350/400, Tra1, TRRAP, TR-AP, FLJ10671, STAF40	transformation/transcription domain-associated protein	NM_003496, hCT2321223.0, hCT2321226.0, hCT2321227.0, hCT2321228.0, hCT2355640.0, hCT2355641.0, hCT32594.2, hCT1955644.1	202642_s_at, 214908_s_at	NP_003487.1, EAW76695.1, EAW76693.1, EAW76696.1, EAW76698.1, EAW76699.1, EAW76694.1, EAW76697.1, EAW76700.1
GeneID:10552	ARPC1A	7	98,923,496	98,963,885	40,389	+	1	2_A375_pNL97_plus_lncRNA::1::7222	48576	downstream	0	1	15	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene ARPC1A	SOP2Hs, Arc40, SOP2L, ARPC1A	actin related protein 2/3 complex, subunit 1A, 41kDa	NM_001190996, NM_006409, hCT2321232.0, hCT2321234.0, hCT2321236.0	200950_at	NP_001177925.1, NP_006400.2, EAW76681.1, EAW76682.1, EAW76683.1
GeneID:10095	ARPC1B	7	98,972,329	98,992,424	20,095	+	1	2_A375_pNL97_plus_lncRNA::1::7222	-257	upstream	0	1	15	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene ARPC1B	ARC41, ARPC1B, p40-ARC, p41-ARC	actin related protein 2/3 complex, subunit 1B, 41kDa	NM_005720, hCT1967373.1, hCT1967374.1, hCT2321240.0, hCT8142.3	201954_at, 217217_at, 217260_x_at	NP_005711.1, EAW76677.1, EAW76678.1, EAW76679.1, EAW76680.1
GeneID:11333	PDAP1	7	98,992,589	99,006,292	13,703	-	2	1_A375_pNL7_minus_lncRNA::1::5010, 2_A375_pNL97_plus_lncRNA::1::7223	404, -108	in gene, upstream	1	1	19	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene PDAP1	HASPP28, PAP, PDAP1, PAP1	PDGFA associated protein 1	NM_014891, hCT2320454.0, hCT2320455.0, hCT2320456.0	202290_at, 217624_at	NP_055706.1, EAW76675.1, EAW76674.1, EAW76676.1
GeneID:8896	BUD31	7	99,006,601	99,017,239	10,638	+	2	1_A375_pNL7_minus_lncRNA::1::5010, 2_A375_pNL97_plus_lncRNA::1::7223	-713, -201	upstream, upstream	1	1	19	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene BUD31	fSAP17, MGC111202, G10, EDG-2, EDG2, BUD31, YCR063W	BUD31 homolog (S. cerevisiae)	NM_003910, hCT2321241.0, hCT2321242.0, hCT2355628.0, hCT2355629.0	205690_s_at, 215815_at	NP_003901.2, EAW76673.1, EAW76670.1, EAW76671.1, EAW76672.1
GeneID:26024	PTCD1	7	99,016,745	99,036,419	19,674	-	4	1_A375_pNL7_minus_lncRNA::1::5010, 1_A375_pNL7_minus_lncRNA::1::5011, 2_A375_pNL97_plus_lncRNA::1::7223, 2_A375_pNL97_plus_lncRNA::1::7224	30531, -61, 30019, -93	downstream, upstream, downstream, upstream	1	1	44	47.5	2	1_A375_pNL7_minus_lncRNA::1	69	Gene PTCD1	KIAA0632, PTCD1	pentatricopeptide repeat domain 1	NM_015545, hCT2320453.0	218956_s_at, 222796_at	NP_056360.2, EAW76669.1
GeneID:10898	CPSF4	7	99,036,563	99,054,996	18,433	+	2	1_A375_pNL7_minus_lncRNA::1::5011, 2_A375_pNL97_plus_lncRNA::1::7224	-83, -51	upstream, upstream	1	1	69	66	1	1_A375_pNL7_minus_lncRNA::1	69	Gene CPSF4	NAR, CPSF4, CPSF30, NEB1	cleavage and polyadenylation specific factor 4, 30kDa	NM_006693, NM_001081559, hCT2321246.0, hCT2321247.0, hCT2321250.0, hCT10563.3, hCT1962287.1, hCT1962288.1, hCT1962289.1	206688_s_at	NP_006684.1, NP_001075028.1, EAW76664.1, EAW76665.1, EAW76667.1, EAW76668.1, EAW76662.1, EAW76663.1, EAW76666.1
GeneID:84124	ZNF394	7	99,090,854	99,097,877	7,023	-	2	1_A375_pNL7_minus_lncRNA::1::5012, 2_A375_pNL97_plus_lncRNA::1::7225	-75, -43	upstream, upstream	1	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZNF394	ZKSCAN14, ZNF394, FLJ12298	zinc finger protein 394	NM_032164, hCT1781085.1	214714_at	NP_115540.2, EAW76659.1
GeneID:23660	ZKSCAN5	7	99,102,273	99,131,445	29,172	+	2	1_A375_pNL7_minus_lncRNA::1::5012, 2_A375_pNL97_plus_lncRNA::1::7225	-4321, -4353	upstream, upstream	1	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZKSCAN5	ZNF914, ZFP95, KIAA1015, ZKSCAN5, FLJ39233, MGC33710	zinc finger with KRAB and SCAN domains 5	NM_014569, NM_145102, hCT1967340.2, hCT2321253.1, hCT2355608.0, hCT2355609.0, hCT1877663.5	203730_s_at, 203731_s_at	NP_055384.1, NP_659570.1, EAW76654.1, EAW76655.1, EAW76656.1, EAW76658.1, EAW76657.1
GeneID:221786	C7orf38	7	99,143,923	99,149,757	5,834	-	2	1_A375_pNL7_minus_lncRNA::1::5013, 2_A375_pNL97_plus_lncRNA::1::7226	45, 61	in gene, in gene	1	1	29	25	1	1_A375_pNL7_minus_lncRNA::1	29	Gene C7orf38	C7orf38, DKFZp727G131, FAM200A, FLJ36794	chromosome 7 open reading frame 38	NM_145111, hCT2351194.0, hCT1645807.3	1566665_at, 229762_at, 238609_at	NP_659802.1, EAW76652.1, EAW76653.1
GeneID:79027	ZNF655	7	99,156,045	99,174,076	18,031	+	2	1_A375_pNL7_minus_lncRNA::1::5013, 2_A375_pNL97_plus_lncRNA::1::7226	-6333, -6349	upstream, upstream	1	1	29	25	1	1_A375_pNL7_minus_lncRNA::1	29	Gene ZNF655	DKFZp686M1631, ZNF655, FLJ23461, MGC16203, VIK-1, MGC10659, MGC5521, VIK	zinc finger protein 655	NM_024061, NM_138494, NM_001009958, NM_001009960, NM_001083956, NM_001085366, NM_001085367, NM_001085368, hCT2321256.1, hCT1781072.3, hCT1955824.2, hCT1955825.2	1554726_at, 223302_s_at, 225945_at	NP_076966.1, NP_612503.1, NP_001077425.1, NP_001078835.1, NP_001009958.1, NP_001009960.1, NP_001078836.1, NP_001078837.1, EAW76648.1, EAW76649.1, EAW76650.1, EAW76651.1
GeneID:100506199	LOC100506199	7	99,195,848	99,208,456	12,608	+	2	1_A375_pNL7_minus_lncRNA::1::5014, 2_A375_pNL97_plus_lncRNA::1::7227	18648, 18712	downstream, downstream	1	1	54	66	1	2_A375_pNL97_plus_lncRNA::1	66	Gene LOC100506199		hypothetical protein LOC100506199	XM_003120051, XM_003120050, XM_003120052, XM_003119041, XM_003119040, XM_003119042, XM_003118589, XM_003118588, XM_003118590, XM_003120587, XM_003120586, XM_003120588		XP_003120099.1, XP_003120098.1, XP_003120100.1, XP_003119089.1, XP_003119088.1, XP_003119090.1, XP_003118637.1, XP_003118636.1, XP_003118638.1, XP_003120635.1, XP_003120634.1, XP_003120636.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:79706	PRKRIP1	7	102,036,804	102,067,129	30,325	+	2	1_A375_pNL7_minus_lncRNA::1::5035, 2_A375_pNL97_plus_lncRNA::1::7256	-132, -196	upstream, upstream	1	1	25	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene PRKRIP1	C114, KRBOX3, FLJ13902, PRKRIP1, FLJ40957	PRKR interacting protein 1 (IL11 inducible)	NM_024653, hCT2265995.0, hCT2265996.0, hCT2352369.0	1564165_at, 1564166_s_at, 218378_s_at, 222615_s_at	NP_078929.1, EAW50243.1, EAW50241.1, EAW50242.1
GeneID:100313829	MIR548O	7	102,046,189	102,046,302	113	-	2	1_A375_pNL7_minus_lncRNA::1::5035, 2_A375_pNL97_plus_lncRNA::1::7256	9630, 9694	downstream, downstream	1	1	25	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene MIR548O	MIRN548O, MIR548O	microRNA 548o	NR_031669		
GeneID:222229	LRWD1	7	102,105,390	102,113,612	8,222	+	2	1_A375_pNL7_minus_lncRNA::1::5036, 2_A375_pNL97_plus_lncRNA::1::7257	13954, 13938	downstream, downstream	1	1	46	64	1	2_A375_pNL97_plus_lncRNA::1	64	Gene LRWD1	ORCA, LRWD1, DKFZp434K1815	leucine-rich repeats and WD repeat domain containing 1	NM_152892, hCT1774802.3	225680_at	NP_690852.1, EAW50250.1
GeneID:5439	POLR2J	7	102,113,547	102,119,381	5,834	-	2	1_A375_pNL7_minus_lncRNA::1::5036, 2_A375_pNL97_plus_lncRNA::1::7257	37, 53	in gene, in gene	1	1	46	64	1	2_A375_pNL97_plus_lncRNA::1	64	Gene POLR2J	POLR2J, RPB11, MGC71910, hRPB14, RPB11m, POLR2J1, RPB11A	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa	NM_006234	212782_x_at	NP_006225.1
GeneID:100506726	LOC100506726	7	102,122,205	102,123,513	1,308	-	2	1_A375_pNL7_minus_lncRNA::1::5036, 2_A375_pNL97_plus_lncRNA::1::7257	4169, 4185	downstream, downstream	1	1	46	64	1	2_A375_pNL97_plus_lncRNA::1	64	Gene LOC100506726		hypothetical LOC100506726	XR_110725, XR_108860		
GeneID:100271927	RASA4B	7	102,123,586	102,158,224	34,638	-	2	1_A375_pNL7_minus_lncRNA::1::5036, 2_A375_pNL97_plus_lncRNA::1::7257	38880, 38896	downstream, downstream	1	1	46	64	1	2_A375_pNL97_plus_lncRNA::1	64	Gene RASA4B	FLJ59902, RASA4B	RAS p21 protein activator 4B	XM_003119052, XM_003119055, XM_003119054, XM_003119053, XM_003119056, XM_003118597, XM_003118600, XM_003118596, XM_003118599, XM_003118598		XP_003119100.1, XP_003119103.1, XP_003119102.1, XP_003119101.1, XP_003119104.1, XP_003118645.1, XP_003118648.1, XP_003118644.1, XP_003118647.1, XP_003118646.1
GeneID:222235	FBXL13	7	102,453,308	102,715,288	261,980	-	3	1_A375_pNL7_minus_lncRNA::1::5037, 1_A375_pNL7_minus_lncRNA::1::5038, 2_A375_pNL97_plus_lncRNA::1::7258	198856, 82968, 198936	in gene, in gene, in gene	1	1	21	20	2	2_A375_pNL97_plus_lncRNA::1	26	Gene FBXL13	FBXL13, Fbl13, FLJ38068, MGC21636	F-box and leucine-rich repeat protein 13	NM_145032, NM_001111038, hCT2305303.0, hCT2305304.0, hCT2356430.0, hCT2356431.0, hCT2356432.0, hCT2356433.0, hCT2356434.0, hCT2356435.0, hCT1646378.2	1553798_a_at, 1556770_a_at	NP_659469.3, NP_001104508.1, EAW83298.1, EAW83301.1, EAW83302.1, EAW83306.1, EAW83299.1, EAW83300.1, EAW83303.1, EAW83304.1, EAW83305.1
GeneID:222236	NAPEPLD	7	102,740,023	102,789,569	49,546	-	2	1_A375_pNL7_minus_lncRNA::1::5039, 2_A375_pNL97_plus_lncRNA::1::7259	-47, -63	upstream, upstream	1	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NAPEPLD	FMP30, NAPEPLD, NAPE-PLD, DKFZp781D1098	N-acyl phosphatidylethanolamine phospholipase D	NM_198990, NM_001122838, hCT2305300.0, hCT9251.3	226041_at, 233539_at, 238722_x_at, 242229_at, 242635_s_at	NP_945341.3, NP_001116310.1, EAW83314.1, EAW83315.1
GeneID:27000	DNAJC2	7	102,952,921	102,985,320	32,399	-	2	1_A375_pNL7_minus_lncRNA::1::5040, 2_A375_pNL97_plus_lncRNA::1::7260	232, 232	in gene, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene DNAJC2	DNAJC2, MPP11, ZRF1, ZUO1, MPHOSPH11	DnaJ (Hsp40) homolog, subfamily C, member 2	NM_014377, NM_001129887	1568884_at, 213097_s_at	NP_055192.1, NP_001123359.1
GeneID:5701	PSMC2	7	102,988,089	103,008,656	20,567	+	2	1_A375_pNL7_minus_lncRNA::1::5040, 2_A375_pNL97_plus_lncRNA::1::7260	-3001, -3001	upstream, upstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene PSMC2	Nbla10058, MSS1, MGC3004, S7, PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	NM_002803, hCT2305051.0, hCT2305052.0, hCT2305053.0	201068_s_at, 238020_at	NP_002794.1, EAW83332.1, EAW83331.1, EAW83333.1
GeneID:375611	SLC26A5	7	102,993,177	103,086,624	93,447	-	2	1_A375_pNL7_minus_lncRNA::1::5040, 2_A375_pNL97_plus_lncRNA::1::7260	101536, 101536	downstream, downstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SLC26A5	DFNB61, MGC118887, SLC26A5, MGC118888, MGC118889, MGC118886, PRES	solute carrier family 26, member 5 (prestin)	NM_206883, NM_206884, NM_206885, NM_198999, NM_001167962, hCT2305291.0, hCT1952587.1		NP_996766.1, NP_996767.1, NP_001161434.1, NP_945350.1, NP_996768.1, EAW83334.1, EAW83335.1
GeneID:5649	RELN	7	103,112,231	103,629,963	517,732	-	2	1_A375_pNL7_minus_lncRNA::1::5041, 2_A375_pNL97_plus_lncRNA::1::7261	353163, 353163	in gene, in gene	1	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene RELN	PRO1598, RL, RELN	reelin	NM_005045, NM_173054, hCT2305275.0, hCT2305279.0, hCT9253.3	205923_at	NP_005036.2, NP_774959.1, EAW83336.1, EAW83337.1, EAW83338.1
GeneID:5001	ORC5L	7	103,766,788	103,848,463	81,675	-	2	1_A375_pNL7_minus_lncRNA::1::5042, 2_A375_pNL97_plus_lncRNA::1::7262	15, -1	in gene, upstream	1	1	23	22	1	1_A375_pNL7_minus_lncRNA::1	23	Gene ORC5L	ORC5P, ORC5T, ORC5, ORC5L	origin recognition complex, subunit 5	NM_002553, NM_181747, hCT2306225.1, hCT2341398.0, hCT8046.4	204957_at, 211212_s_at, 211213_at	NP_002544.1, NP_859531.1, EAW83341.1, EAW83342.1, EAW83343.1
GeneID:375612	LHFPL3	7	103,969,104	104,549,005	579,901	+	3	1_A375_pNL7_minus_lncRNA::1::5043, 2_A375_pNL97_plus_lncRNA::1::7263, 2_A375_pNL97_plus_lncRNA::1::7264	299008, 223600, 299024	in gene, in gene, in gene	1	1	18.5	26	2	2_A375_pNL97_plus_lncRNA::1	27	Gene LHFPL3	LHFPL4, LHFPL3	lipoma HMGIC fusion partner-like 3	NM_199000	236761_at	NP_945351.1
GeneID:100216545	LOC100216545	7	104,650,989	104,654,588	3,599	-	1	2_A375_pNL97_plus_lncRNA::1::7265	1212	in gene	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100216545	FLJ37053, FLJ42052, FLJ41482	hypothetical LOC100216545	NR_024586		
GeneID:55904	MLL5	7	104,654,637	104,754,532	99,895	+	1	2_A375_pNL97_plus_lncRNA::1::7265	-1261	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene MLL5	MLL5, FLJ10078, MGC70452, FLJ14026, KMT2E, HDCMC04P	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	NM_182931, NM_018682, hCT2306194.0, hCT2306195.0, hCT2306196.0, hCT2306199.0	223189_x_at, 223190_s_at, 226100_at	NP_891847.1, NP_061152.3, EAW83355.1, EAW83356.1, EAW83357.1, EAW83358.1
GeneID:6733	SRPK2	7	104,756,823	105,029,341	272,518	-	1	2_A375_pNL97_plus_lncRNA::1::7266	84429	in gene	0	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SRPK2	SRPK2, FLJ36101, SFRSK2	SFRS protein kinase 2	NM_182691, NM_182692, hCT2305118.0, hCT2305119.0, hCT2356429.0	1558254_s_at, 203181_x_at, 203182_s_at, 214931_s_at, 217517_x_at	NP_872633.1, NP_872634.1, EAW83359.1, EAW83360.1, EAW83361.1
GeneID:54517	PUS7	7	105,096,958	105,162,685	65,727	-	2	1_A375_pNL7_minus_lncRNA::1::5044, 2_A375_pNL97_plus_lncRNA::1::7267	-10035, -9907	upstream, upstream	1	1	23	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene PUS7	PUS7, KIAA1897, MGC17720, FLJ20485	pseudouridylate synthase 7 homolog (S. cerevisiae)	NM_019042, hCT2305113.0, hCT1953072.1	218984_at	NP_061915.2, EAW83364.1, EAW83363.1
GeneID:60561	RINT1	7	105,172,532	105,208,124	35,592	+	2	1_A375_pNL7_minus_lncRNA::1::5044, 2_A375_pNL97_plus_lncRNA::1::7267	188, 60	in gene, in gene	1	1	23	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene RINT1	DKFZp667H2324, RINT1, RINT-1	RAD50 interactor 1	NM_021930, hCT2304879.0, hCT1818538.2	218598_at	NP_068749.3, EAW83366.1, EAW83367.1
GeneID:222255	ATXN7L1	7	105,245,221	105,517,031	271,810	-	2	1_A375_pNL7_minus_lncRNA::1::5045, 2_A375_pNL97_plus_lncRNA::1::7268	100327, 100327	in gene, in gene	1	1	28	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene ATXN7L1	FLJ40255, MGC33190, FLJ56242, ATXN7L4, MGC10760, KIAA1218, ATXN7L1	ataxin 7-like 1	NM_152749, NM_020725, NM_138495, hCT2305092.1, hCT2305094.1, hCT2305096.1, hCT2305097.1, hCT2344936.0	214342_at, 214343_s_at	NP_689962.1, NP_065776.1, NP_612504.1, EAW83370.1, EAW83371.1, EAW83373.1, EAW83372.1, EAW83374.1
GeneID:6856	SYPL1	7	105,730,951	105,753,057	22,106	-	2	1_A375_pNL7_minus_lncRNA::1::5046, 2_A375_pNL97_plus_lncRNA::1::7270	-63, 185	upstream, in gene	1	1	18	15	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SYPL1	H-SP1, SYPL, SYPL1	synaptophysin-like 1	NM_006754, NM_182715, hCT2305085.0, hCT7975.3, hCT1961883.1	201259_s_at, 201260_s_at	NP_006745.1, NP_874384.1, EAW83379.1, EAW83380.1, EAW83381.1
GeneID:168455	FLJ36031	7	106,299,149	106,301,591	2,442	-	1	2_A375_pNL97_plus_lncRNA::1::7271	903	in gene	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FLJ36031	FLJ25556, MGC16181, FLJ11436	hypothetical protein FLJ36031	NM_175884	227883_at, 228668_x_at, 229521_at	NP_787080.2
GeneID:10466	COG5	7	106,842,189	107,204,959	362,770	-	3	1_A375_pNL7_minus_lncRNA::1::5048, 1_A375_pNL7_minus_lncRNA::1::5049, 2_A375_pNL97_plus_lncRNA::1::7273	236255, 767, 671	in gene, in gene, in gene	1	1	23.5	26	2	2_A375_pNL97_plus_lncRNA::1	41	Gene COG5	GTC90, COG5, FLJ41732, GOLTC1, FLJ44289, CDG2I	component of oligomeric golgi complex 5	NM_006348, NM_181733, NM_001161520, hCT2305494.0, hCT2356413.0, hCT1953971.1	203629_s_at, 203630_s_at	NP_006339.3, NP_859422.2, NP_001154992.1, EAW83395.1, EAW83396.1, EAW83397.1
GeneID:11062	DUS4L	7	107,204,432	107,218,968	14,536	+	2	1_A375_pNL7_minus_lncRNA::1::5049, 2_A375_pNL97_plus_lncRNA::1::7273	-240, -144	upstream, upstream	1	1	30	41	1	2_A375_pNL97_plus_lncRNA::1	41	Gene DUS4L	PP35, MGC133233, DUS4, DUS4L	dihydrouridine synthase 4-like (S. cerevisiae)	NM_181581, hCT1968321.1, hCT1968322.1, hCT7977.3, hCT1955453.1, hCT1961884.1, hCT1961885.1	205761_s_at, 205762_s_at	NP_853559.1, EAW83400.1, EAW83399.1, EAW83401.1, EAW83402.1, EAW83404.1, EAW83403.1
GeneID:100128737	LOC100128737	7	107,363,198	107,365,026	1,828	-	1	2_A375_pNL97_plus_lncRNA::1::7274	258	in gene	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100128737		hypothetical LOC100128737	XR_113067, XR_113066, XR_113068, XR_110731, XR_110730, XR_110732, XR_108796, XR_108795, XR_108797, XR_114078, XR_114077, XR_114079		
GeneID:79872	CBLL1	7	107,384,279	107,402,083	17,804	+	1	2_A375_pNL97_plus_lncRNA::1::7274	489	in gene	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CBLL1	MGC163401, FLJ23109, MGC163403, CBLL1, RNF188, HAKA	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	NM_024814, NR_024199, hCT8165.3, hCT1953974.1	220018_at	NP_079090.2, EAW83417.1, EAW83416.1
GeneID:4897	NRCAM	7	107,788,071	108,096,841	308,770	-	4	2_A375_pNL97_plus_lncRNA::1::7275, 1_A375_pNL7_minus_lncRNA::1::5050, 2_A375_pNL97_plus_lncRNA::1::7276, 2_A375_pNL97_plus_lncRNA::1::7277	108565, 14105, 25065, 1225	in gene, in gene, in gene, in gene	1	1	15.25	16.75	4	2_A375_pNL97_plus_lncRNA::1	26	Gene NRCAM	MGC138845, NRCAM, MGC138846, KIAA0343	neuronal cell adhesion molecule	NM_001037132, NM_005010, NM_001193582, NM_001193583, NM_001193584, hCT2305481.0, hCT2356392.0, hCT8159.3, hCT1953973.1	204105_s_at, 216959_x_at	NP_001032209.1, NP_005001.3, NP_001180511.1, NP_001180512.1, NP_001180513.1, EAW83430.1, EAW83427.1, EAW83428.1, EAW83429.1
GeneID:50640	PNPLA8	7	108,112,071	108,166,638	54,567	-	1	2_A375_pNL97_plus_lncRNA::1::7278	-210	upstream	0	1	15	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PNPLA8	PNPLA8, IPLA2-2, IPLA2(GAMMA), IPLA2G	patatin-like phospholipase domain containing 8	NM_015723, hCT2356402.0, hCT2356403.0, hCT2356404.0, hCT8164.3	223309_x_at, 223310_x_at, 223982_s_at	NP_056538.1, EAW83433.1, EAW83432.1, EAW83434.1, EAW83435.1
GeneID:168451	THAP5	7	108,202,671	108,210,167	7,496	-	2	1_A375_pNL7_minus_lncRNA::1::5051, 2_A375_pNL97_plus_lncRNA::1::7279	-169, -41	upstream, upstream	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene THAP5	DKFZp313O1132, THAP5	THAP domain containing 5	NM_001130475, NM_182529, hCT2304826.0, hCT2349816.0	227636_at, 244190_at	NP_001123947.1, NP_872335.2, EAW83436.1, EAW83437.1
GeneID:4189	DNAJB9	7	108,210,356	108,215,294	4,938	+	2	1_A375_pNL7_minus_lncRNA::1::5051, 2_A375_pNL97_plus_lncRNA::1::7279	-20, -146	upstream, upstream	1	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene DNAJB9	MST049, MSTP049, ERdj4, DNAJB9, DKFZp564F1862, MDG1, MDG-1	DnaJ (Hsp40) homolog, subfamily B, member 9	NM_012328, hCT2304807.0, hCT8161.2, hCT1961886.0, hCT1961887.0	1554462_a_at, 202842_s_at, 202843_at	NP_036460.1, EAW83439.1, EAW83438.1, EAW83440.1, EAW83441.1
GeneID:83943	IMMP2L	7	110,303,110	111,202,347	899,237	-	1	1_A375_pNL7_minus_lncRNA::1::5052	-357	upstream	1	0	16	11	1	1_A375_pNL7_minus_lncRNA::1	16	Gene IMMP2L	IMMP2L, IMP2-LIKE, IMP2	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	NM_032549, hCT2344102.0, hCT2344103.0, hCT2344104.0, hCT2344105.0	1555571_at, 227153_at	NP_115938.1, EAW83445.1, EAW83444.1, EAW83446.1, EAW83447.1
GeneID:9732	DOCK4	7	111,366,164	111,846,462	480,298	-	3	1_A375_pNL7_minus_lncRNA::1::5053, 2_A375_pNL97_plus_lncRNA::1::7280, 2_A375_pNL97_plus_lncRNA::1::7281	-66, 205198, -2	upstream, in gene, upstream	1	1	14.5	19	2	2_A375_pNL97_plus_lncRNA::1	23	Gene DOCK4	MGC134912, KIAA0716, FLJ34238, MGC134911, DOCK4	dedicator of cytokinesis 4	NM_014705, hCT2305066.0, hCT2305067.0, hCT2305068.0, hCT2305069.0, hCT2305070.0, hCT2305072.0	1556691_a_at, 205003_at, 241313_at, 244840_x_at	NP_055520.3, EAW83452.1, EAW83451.1, EAW83453.1, EAW83454.1, EAW83455.1, EAW83456.1
GeneID:11179	ZNF277	7	111,846,643	111,983,989	137,346	+	2	1_A375_pNL7_minus_lncRNA::1::5053, 2_A375_pNL97_plus_lncRNA::1::7281	-115, -179	upstream, upstream	1	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ZNF277	NRIF4, ZNF277, ZNF277P	zinc finger protein 277	NM_021994, hCT2304968.0, hCT2356416.0, hCT5774.3, hCT1961879.1, hCT1966253.1	1555192_at, 1555193_a_at, 215887_at, 218645_at	NP_068834.2, EAW83457.1, EAW83458.1, EAW83459.1, EAW83460.1, EAW83461.1
GeneID:3475	IFRD1	7	112,063,226	112,116,247	53,021	+	4	1_A375_pNL7_minus_lncRNA::1::5054, 1_A375_pNL7_minus_lncRNA::1::5055, 2_A375_pNL97_plus_lncRNA::1::7282, 2_A375_pNL97_plus_lncRNA::1::7283	27670, 58838, 27206, 61734	in gene, downstream, in gene, downstream	1	1	15.33	17	3	2_A375_pNL97_plus_lncRNA::1	25	Gene IFRD1	TIS7, PC4, IFRD1	interferon-related developmental regulator 1	NM_001550, NM_001007245, hCT2304958.0, hCT6796.3	202146_at, 202147_s_at	NP_001541.2, NP_001007246.1, EAW83462.1, EAW83463.1
GeneID:286006	C7orf53	7	112,120,908	112,130,943	10,035	+	2	1_A375_pNL7_minus_lncRNA::1::5055, 2_A375_pNL97_plus_lncRNA::1::7283	1156, 4052	in gene, in gene	1	1	12.5	13	2	2_A375_pNL97_plus_lncRNA::1	17	Gene C7orf53	MGC161427, C7orf53, MGC163440, FLJ39575, MGC42850	chromosome 7 open reading frame 53	NM_182597, NM_001134468, hCT2304960.0, hCT2349817.0	1569852_at, 239203_at	NP_872403.1, NP_001127940.1, EAW83464.1, EAW83465.1
GeneID:64418	TMEM168	7	112,405,787	112,430,478	24,691	-	1	1_A375_pNL7_minus_lncRNA::1::5056	462	in gene	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene TMEM168	TMEM168, DKFZp564O012, FLJ13576	transmembrane protein 168	NM_022484, hCT2356470.0, hCT6795.3, hCT1807969.1	218962_s_at, 234726_s_at	NP_071929.3, EAW83472.1, EAW83470.1, EAW83471.1
GeneID:401397	LOC401397	7	112,756,773	112,758,637	1,864	-	1	2_A375_pNL97_plus_lncRNA::1::7284	-179	upstream	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC401397	MGC104490	hypothetical LOC401397	NR_024412, NR_015442	224723_x_at	
GeneID:93986	FOXP2	7	113,726,365	114,333,827	607,462	+	1	2_A375_pNL97_plus_lncRNA::1::7286	299427	in gene	0	1	7	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene FOXP2	SPCH1, FOXP2, TNRC10, DKFZp686H1726, CAGH44	forkhead box P2	NM_001172766, NM_001172767, NM_014491, NM_148898, NM_148899, NM_148900, NR_033766, NR_033767, hCT2304975.0, hCT2304976.0, hCT2304977.0, hCT2356425.0, hCT2356426.0, hCT2356427.0, hCT2356428.0, hCT1813385.1	1552902_a_at, 1555352_at, 1555516_at, 1555647_a_at, 1555648_at, 1562139_a_at, 1564876_s_at	NP_001166237.1, NP_001166238.1, NP_055306.1, NP_683696.2, NP_683698.2, NP_683697.2, EAW83479.1, EAW83480.1, EAW83481.1, EAW83482.1, EAW83483.1, EAW83484.1, EAW83485.1, EAW83486.1
GeneID:857	CAV1	7	116,164,839	116,201,239	36,400	+	2	1_A375_pNL7_minus_lncRNA::1::5061, 2_A375_pNL97_plus_lncRNA::1::7289	1849, 1785	in gene, in gene	1	1	27	19	1	1_A375_pNL7_minus_lncRNA::1	27	Gene CAV1	CAV1, BSCL3, CGL3, CAV, MSTP085, VIP21	caveolin 1, caveolae protein, 22kDa	NM_001753, NM_001172895, NM_001172896, NM_001172897, hCT2305358.0, hCT30335.3, hCT1962974.1	203065_s_at, 212097_at	NP_001744.2, NP_001166366.1, NP_001166367.1, NP_001166368.1, EAW83503.1, EAW83504.1, EAW83505.1
GeneID:4233	MET	7	116,312,459	116,438,440	125,981	+	2	1_A375_pNL7_minus_lncRNA::1::5064, 1_A375_pNL7_minus_lncRNA::1::5065	44293, 104117	in gene, in gene	1	0	18	14.5	2	1_A375_pNL7_minus_lncRNA::1	24	Gene MET	RCCP2, HGFR, MET, c-Met, AUTS9	met proto-oncogene (hepatocyte growth factor receptor)	NM_000245, NM_001127500, hCT2305360.0, hCT2305362.0, hCT2305363.0, hCT2356396.0, hCT29949.3	203510_at, 211599_x_at, 213807_x_at, 213816_s_at	NP_000236.2, NP_001120972.1, EAW83508.1, EAW83509.1, EAW83510.1, EAW83511.1, EAW83507.1
GeneID:93653	ST7OT1	7	116,592,500	116,594,388	1,888	-	1	1_A375_pNL7_minus_lncRNA::1::5066	68	in gene	1	0	15	13	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ST7OT1	ST7AS1, ST7OT1	ST7 overlapping transcript 1 (non-protein coding)	NR_002330	1555912_at	
GeneID:7982	ST7	7	116,593,381	116,870,077	276,696	+	1	1_A375_pNL7_minus_lncRNA::1::5066	939	in gene	1	0	15	13	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ST7	DKFZp762O2113, HELG, FAM4A, ETS7q, FAM4A1, RAY1, ST7, TSG7, SEN4	suppression of tumorigenicity 7	NM_021908, NM_018412, hCT2305155.0, hCT2305157.0, hCT2305158.0, hCT2305160.0, hCT6985.3, hCT1952565.1	207524_at, 207871_s_at	NP_068708.1, NP_060882.2, EAW83518.1, EAW83519.1, EAW83520.1, EAW83521.1, EAW83516.1, EAW83517.1
GeneID:338069	ST7OT4	7	116,593,953	116,599,867	5,914	+	1	1_A375_pNL7_minus_lncRNA::1::5066	367	in gene	1	0	15	13	1	1_A375_pNL7_minus_lncRNA::1	15	Gene ST7OT4	NCRNA00042, ST7OT4	ST7 overlapping transcript 4 (non-protein coding)	NR_002329	1559208_at	
GeneID:7472	WNT2	7	116,916,685	116,963,343	46,658	-	2	1_A375_pNL7_minus_lncRNA::1::5067, 2_A375_pNL97_plus_lncRNA::1::7291	53711, 53711	downstream, downstream	1	1	28	23	1	1_A375_pNL7_minus_lncRNA::1	28	Gene WNT2	WNT2, INT1L1, IRP	wingless-type MMTV integration site family member 2	NM_003391, NR_024047, hCT5668.3	205648_at	NP_003382.1, EAW83525.1
GeneID:54556	ING3	7	120,590,817	120,615,711	24,894	+	2	1_A375_pNL7_minus_lncRNA::1::5068, 2_A375_pNL97_plus_lncRNA::1::7292	-97, -97	upstream, upstream	1	1	22	22	1	1_A375_pNL7_minus_lncRNA::1	22	Gene ING3	FLJ20089, ING3, p47ING3, MEAF4, Eaf4, ING2	inhibitor of growth family, member 3	NM_019071, NM_198267, hCT2305177.0, hCT2305179.0, hCT2305180.0, hCT24278.3	205070_at, 231863_at, 242293_at	NP_061944.2, NP_938008.1, EAW83546.1, EAW83547.1, EAW83548.1, EAW83549.1
GeneID:79974	C7orf58	7	120,628,751	120,937,498	308,747	+	1	1_A375_pNL7_minus_lncRNA::1::5069	216081	in gene	1	0	15	11	1	1_A375_pNL7_minus_lncRNA::1	15	Gene C7orf58	FLJ21986, FLJ26813, C7orf58	chromosome 7 open reading frame 58	NM_024913, NM_001105533, hCT2305181.0, hCT2305185.0, hCT2356471.0, hCT1958418.1, hCT1958419.1, hCT1958420.1	220032_at, 228728_at	NP_079189.4, NP_001099003.1, EAW83550.1, EAW83552.1, EAW83554.1, EAW83555.1, EAW83551.1, EAW83553.1
GeneID:10447	FAM3C	7	120,988,905	121,036,422	47,517	-	2	1_A375_pNL7_minus_lncRNA::1::5070, 2_A375_pNL97_plus_lncRNA::1::7293	-10, -58	upstream, upstream	1	1	28	41	1	2_A375_pNL97_plus_lncRNA::1	41	Gene FAM3C	GS3786, FAM3C, ILEI	family with sequence similarity 3, member C	NM_014888, NM_001040020, hCT23515.3	201889_at, 236316_at, 240062_at	NP_055703.1, NP_001035109.1, EAW83558.1
GeneID:10157	AASS	7	121,713,598	121,784,344	70,746	-	1	1_A375_pNL7_minus_lncRNA::1::5071	120	in gene	1	0	15	14	1	1_A375_pNL7_minus_lncRNA::1	15	Gene AASS	AASS, LKRSDH, LORSDH, LKR/SDH	aminoadipate-semialdehyde synthase	NM_005763, hCT2305311.0, hCT24606.3	210852_s_at, 214829_at	NP_005754.2, EAW83564.1, EAW83565.1
GeneID:4698	NDUFA5	7	123,181,083	123,197,958	16,875	-	2	1_A375_pNL7_minus_lncRNA::1::5072, 2_A375_pNL97_plus_lncRNA::1::7295	70, 70	in gene, in gene	1	1	29	24	1	1_A375_pNL7_minus_lncRNA::1	29	Gene NDUFA5	FLJ12147, NDUFA5, B13, UQOR13, DKFZp781K1356, CI-13kB, CI-13KD-B, NUFM	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	NM_005000, hCT1971475.1, hCT2305321.0, hCT2305323.0, hCT2305326.0, hCT1817741.2, hCT1962955.1, hCT1962956.2	201304_at, 215850_s_at	NP_004991.1, EAW83590.1, EAW83587.1, EAW83588.1, EAW83591.1, EAW83592.1, EAW83589.1, EAW83593.1
GeneID:8976	WASL	7	123,321,997	123,389,116	67,119	-	2	1_A375_pNL7_minus_lncRNA::1::5073, 2_A375_pNL97_plus_lncRNA::1::7296	60, 252	in gene, in gene	1	1	18	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene WASL	WASL, DKFZp779G0847, NWASP, MGC48327, N-WASP	Wiskott-Aldrich syndrome-like	NM_003941, hCT24112.4	205809_s_at, 205810_s_at, 224813_at, 230340_s_at	NP_003932.3, EAW83599.1
GeneID:730130	TMEM229A	7	123,670,970	123,673,523	2,553	-	1	2_A375_pNL97_plus_lncRNA::1::7297	723	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TMEM229A	MGC189723, TMEM229A	transmembrane protein 229A	NM_001136002		NP_001129474.1
GeneID:2861	GPR37	7	124,386,114	124,405,681	19,567	-	2	1_A375_pNL7_minus_lncRNA::1::5075, 2_A375_pNL97_plus_lncRNA::1::7299	-175, -239	upstream, upstream	1	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene GPR37	GPR37, EDNRBL, hET(B)R-LP, PAELR	G protein-coupled receptor 37 (endothelin receptor type B-like)	NM_005302, hCT23509.3	209631_s_at, 214586_at	NP_005293.1, EAW83613.1
GeneID:2918	GRM8	7	126,078,652	126,892,428	813,776	-	3	1_A375_pNL7_minus_lncRNA::1::5077, 1_A375_pNL7_minus_lncRNA::1::5078, 2_A375_pNL97_plus_lncRNA::1::7302	144556, -1524, 144524	in gene, upstream, in gene	1	1	28.5	33.5	2	2_A375_pNL97_plus_lncRNA::1	52	Gene GRM8	GLUR8, MGLUR8, GPRC1H, MGC126724, GRM8, mGlu8, FLJ41058	glutamate receptor, metabotropic 8	NM_000845, NM_001127323, NR_028041, hCT2305306.0, hCT2356454.0, hCT2356455.0, hCT1952026.1	216255_s_at, 216256_at, 216992_s_at	NP_000836.2, NP_001120795.1, EAW83621.1, EAW83622.1, EAW83623.1, EAW83624.1
GeneID:168850	ZNF800	7	127,010,353	127,032,767	22,414	-	2	2_A375_pNL97_plus_lncRNA::1::7303, 2_A375_pNL97_plus_lncRNA::1::7304	639, -289	in gene, upstream	0	1	14	15.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene ZNF800	MGC130032, ZNF800, MGC130033, FLJ43301	zinc finger protein 800	NM_176814, hCT2305845.0, hCT2305846.0, hCT2305847.0	227101_at, 227104_x_at	NP_789784.2, EAW83625.1, EAW83626.1, EAW83627.1
GeneID:100506682	LOC100506682	7	127,116,932	127,125,858	8,926	+	1	2_A375_pNL97_plus_lncRNA::1::7305	-2292	upstream	0	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100506682		hypothetical LOC100506682	XR_113058, XR_110741, XR_108805, XR_114086		



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervening Features Count	Intervening Features	Intervening Distance to gene	Intervening Position	[A]	[B]	[C]	[D]	Active Regulatory Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:27044	SNDI1	7	127,292,202	127,732,699	440,497	+	2	1_A270_shN37_dhrsx_blcRNA:1-13976, 2_A270_shN37_glcs_blcRNA:1-7236	4226, -366	upstream, upstream	1	1	16	15	1	2_A270_shN37_dhrsx_blcRNA:1	16	Gene SND1	TDRD11, SND1, p100	staphylococcal nuclease and tudor domain containing 1	NM_014390, XCT2035519.0, XCT2339142, XCT1960571.2	2016622_at	NP_055203.2, EAW63935.1, EAW63936.1, EAW63937.1
Gene:ID:84131	RBM28	7	127,930,436	127,963,862	33,426	+	1	2_A270_shN37_glcs_blcRNA:1-7236	14	st gene	0	1	16	23	1	2_A270_shN37_glcs_blcRNA:1	23	Gene RBM28	KIBRE28, FLJ10377	RNA binding motif protein 28	NM_018077, NM_001166135, XCT2035290.0, XCT2116962	2015593_at	NP_060547.2, NP_001186071.1, EAW63940.1, EAW63964.1
Gene:ID:21969	PRRT2	7	127,960,279	128,001,739	11,360	-	1	2_A270_shN37_glcs_blcRNA:1-7236	17551	downstream	0	1	16	23	1	2_A270_shN37_glcs_blcRNA:1	23	Gene PRRT2	PRRT2	proline-rich transmembrane protein 2	NM_001114128, NM_001170164		NP_001163182.2, NP_001161629.1
Gene:ID:29223	C7orf66	7	128,093,884	128,098,472	2,588	+	1	2_A270_shN37_glcs_blcRNA:1-7310	212	st gene	0	1	13	16	1	2_A270_shN37_glcs_blcRNA:1	16	Gene C7orf66	HIG2, MGC135358, C7orf66, FLJ21076, HIG-2	chromosome 7 open reading frame 66	NM_030968766, NM_013122, XCT2035550.0, XCT2035551.0, XCT2116162	1554832_s_at, 2165071_at	NP_001922356.1, NP_037464.1, EAW63934.1, EAW63955.1, EAW63956.1
Gene:ID:51538	METTL2B	7	128,116,763	128,142,976	26,195	+	1	2_A270_shN37_glcs_blcRNA:1-7311	1	st gene	0	1	13	19	1	2_A270_shN37_glcs_blcRNA:1	19	Gene METTL2B	PSSIP1, METTL2B, METTL2A, METL, FLJ12780, METTL2, FLJ11293,	methyltransferase like 2B	NM_013396		NP_060866.2
Gene:ID:53345	TNPO3	7	128,594,234	128,695,227	100,993	-	2	1_A270_shN37_dhrsx_blcRNA:1-7311, 2_A270_shN37_glcs_blcRNA:1-7237	58, 278	st gene, st gene	1	1	20	24	1	2_A270_shN37_glcs_blcRNA:1	24	Gene TNPO3	TRN-SR, TRN-SR2, TRN3R, TNPO3, MTR10A, IPO12	transportin 3	NM_012470, NM_001190326, NM_338052, XCT2035559.0, XCT2339577.0, XCT2339.3	212217_at, 212216_at, 214593_s_at	NP_036921.1, NP_001177957.2, EAW63758.1, EAW63759.1, EAW63760.1
Gene:ID:100127580	LOC100127580, 27691	7	128,232,744	128,251,693	18,751	-	1	2_A270_shN37_glcs_blcRNA:1-7313	41	upstream	0	1	13	20	1	2_A270_shN37_glcs_blcRNA:1	20	Gene LOC100127580		hypothetical LOC100127691	XR_113053, XR_110746, XR_106512, XR_114091		
Gene:ID:4882	NRF1	7	129,251,555	129,396,922	145,367	+	1	2_A270_shN37_glcs_blcRNA:1-7312	19	upstream	0	1	13	20	1	2_A270_shN37_glcs_blcRNA:1	20	Gene NRF1	NRF1, ALPHA-PAL	nuclear respiratory factor 1	NM_005011, NM_001540110, XCT2035252.0, XCT2356400.0, XCT2356401.0, XCT1951686.2, XCT2356153.0, XCT1958390.1	204653_at, 204652_s_at, 214279_at, EAW63721.1	NP_005002.2, NP_001530199.1, EAW63736.1, EAW63737.1, EAW63738.1, EAW63739.1, EAW63740.1, EAW63741.1
Gene:ID:1530	ZCSHC1	7	129,656,126	129,691,233	33,107	-	2	1_A270_shN37_dhrsx_blcRNA:1-7311, 2_A270_shN37_glcs_blcRNA:1-7315	40665, 41023	downstream, downstream	1	1	22	22	1	2_A270_shN37_glcs_blcRNA:1	22	Gene ZCSHC1	ZCSHC1, NIPA, 1110064L24Rik, FBXO50, HSPC216	zinc finger, C2HC-type containing 1	NM_016470, XCT2307938.0, XCT2307939.0, XCT2356453.0, XCT1951287.2, XCT1955599.1, XCT1961592.1	224163_s_at	NP_057562.2, EAW63740.1, EAW63738.1, EAW63739.1, EAW63745.1, EAW63741.1, EAW63742.1
Gene:ID:3998	KLHDC10	7	129,710,349	129,775,560	65,211	+	2	1_A270_shN37_dhrsx_blcRNA:1-7312, 2_A270_shN37_glcs_blcRNA:1-7316	-173, -161	upstream, upstream	1	1	44	34	1	1_A270_shN37_dhrsx_blcRNA:1	44	Gene KLHDC10	KIAA0255, Ush, KLHDC10	kelch domain containing 10	NM_014907, XCT1992267.1, XCT2356410.0, XCT1992.4	209254_at, 209255_s_at, 209256_s_at, 210111_s_at, 221744_at	NP_055512.1, EAW63745.1, EAW63744.1, EAW63749.1
Gene:ID:1316	CPA2	7	129,906,703	129,929,838	22,935	+	1	2_A270_shN37_glcs_blcRNA:1-7317	12609	st gene	0	1	13	16	1	2_A270_shN37_glcs_blcRNA:1	16	Gene CPA2	CPA2	carboxypeptidase A2 (pancreatic)	NM_001969, XCT5099.2	209312_at	NP_001960.2, EAW63791.1
Gene:ID:3476	CPA3	7	129,954,630	130,008,371	53,741	+	1	2_A270_shN37_dhrsx_blcRNA:1-7313	12458	st gene	1	0	17	15	1	1_A270_shN37_dhrsx_blcRNA:1	17	Gene CPA3	FLJ38999, CPA3	carboxypeptidase A3	NM_009263, NM_001127441, NM_001127442, XCT2370846.0, XCT2370847.1, XCT2356407.0, XCT2356460.0, XCT2356469.0, XCT2356470.0, XCT1965957.2	240748_at	NP_001121913.1, NP_001120814.1, EAW63754.1, EAW63756.1, EAW63758.1, EAW63755.1, EAW63757.1, EAW63759.1, EAW63760.1
Gene:ID:100506806	LOC100506806, 96660	7	130,536,479	130,613,466	76,988	+	2	1_A270_shN37_dhrsx_blcRNA:1-7314, 2_A270_shN37_glcs_blcRNA:1-7314	11793, 1623	st gene, st gene	1	1	26	31	1	2_A270_shN37_glcs_blcRNA:1	31	Gene LOC100506806		hypothetical LOC100506960	XR_113051, XR_110750, XR_110795, XR_110748, XR_106514, XR_106513, XR_114094, XR_114093		
Gene:ID:155065	PLA3G63	7	130,626,919	130,793,262	164,843	-	2	1_A270_shN37_dhrsx_blcRNA:1-7305, 2_A270_shN37_glcs_blcRNA:1-7299	36554, 146216	st gene, st gene	1	1	16.5	16	2	1_A270_shN37_dhrsx_blcRNA:1	22	Gene PLA3G63		hypothetical LOC155065	NR_038431, NR_024153	226702_at, 226703_at, 229236_at, 229237_at, 229238_at, 229239_at, 229240_at, 229241_at, 229242_at, 229243_at	NP_001138529.1, NP_037387.2, EAW63761.1, EAW63762.1, EAW63763.1
Gene:ID:4289	MKLN1	7	130,764,533	131,161,298	396,943	+	8	1_A270_shN37_dhrsx_blcRNA:1-7309, 2_A270_shN37_glcs_blcRNA:1-7315, 3_A270_shN37_dhrsx_blcRNA:1-7307, 4_A270_shN37_glcs_blcRNA:1-7320, 5_A270_shN37_glcs_blcRNA:1-7321, 6_A270_shN37_glcs_blcRNA:1-7322	182121, 217617, 76859, 182168, 217651	st gene, st gene, st gene, st gene, st gene, st gene	1	1	20	22.33	2	2_A270_shN37_glcs_blcRNA:1	33	Gene MKLN1	FLJ11162, MKLN1, TWAP2	muskelin 1, intracellular mediator containing kelch motifs	NM_001145334, NM_013255, XCT2364600.0, XCT5800.3, XCT1961651.1	1560143_at, 204422_at, 226326_at, 230067_at, 240305_at, 244171_at	NP_001138526.1, NP_037387.2, EAW63761.1, EAW63762.1, EAW63763.1
Gene:ID:100506866	LOC100506866, 96661	7	130,994,503	131,012,535	18,033	-	2	1_A270_shN37_dhrsx_blcRNA:1-7307, 2_A270_shN37_glcs_blcRNA:1-7322	-134, -195	upstream, upstream	1	1	21	30	1	2_A270_shN37_glcs_blcRNA:1	30	Gene LOC100506866 1		hypothetical LOC100506551	XR_113046, XR_113047, XR_113048, XR_113049, XR_110751, XR_110752, XR_110753, XR_110754, XR_106515, XR_106516, XR_106517, XR_106518, XR_114092, XR_114096, XR_110827, XR_114098		
Gene:ID:1564	PLXNA4	7	131,606,091	132,233,447	625,356	+	1	2_A270_shN37_glcs_blcRNA:1-7328	185991	st gene	0	1	11	17	1	2_A270_shN37_glcs_blcRNA:1	17	Gene PLXNA4	PLXNA4B, PRO34003, PLXNA4, FLJ38326, PLXNA4A, FLJ38327, FAYV2520, PLEXA4, KIAA1550, DKFZp434K0821, DKFZp686O20046	plexin A4	NM_181775, NM_020911, NM_001105543, XCT2356442.1, XCT2349677.1, XCT2345157.0, XCT2349158.1	224859_at	NP_861480.2, NP_065992.1, NP_001099013.1, EAW63782.1, EAW63785.1, EAW63786.1, EAW63794.1
Gene:ID:9827	CHCHD3	7	132,469,623	132,799,833	297,210	-	2	1_A270_shN37_dhrsx_blcRNA:1-7301, 2_A270_shN37_glcs_blcRNA:1-7302	280533, 113, -19	downstream, st gene, upstream	1	1	16.5	16	2	1_A270_shN37_dhrsx_blcRNA:1	19	Gene CHCHD3	FLJ20420, CHCHD2	coiled-coil-helix-coiled-coil-helix domain containing 3	NM_017812, XCT2356787.1, XCT2356788.2, XCT2356460.0	217972_at	NP_060262.1, EAW63800.1, EAW63802.1, EAW63803.1
Gene:ID:9412	EXOC4	7	132,937,823	133,790,814	612,991	+	1	2_A270_shN37_glcs_blcRNA:1-7329	860161	st gene	0	1	15	15	1	2_A270_shN37_glcs_blcRNA:1	15	Gene EXOC4	Sec8p, REC8, SEC8L1, EXOC4, MGC27170, SEC8	exocyst complex component 4	NM_021097, NM_001037126, NM_001178131, XCT2356666.0, XCT2356667.0, XCT1954211.1	236626_at, 240525_s_at	NP_066978.2, NP_001032203.1, EAW63808.1, EAW63809.1, EAW63806.1
Gene:ID:4912	SLC35B4	7	133,974,669	134,001,827	27,158	-	2	1_A270_shN37_dhrsx_blcRNA:1-7332, 2_A270_shN37_glcs_blcRNA:1-7330	515, 185	st gene, st gene	1	1	20	21	1	2_A270_shN37_glcs_blcRNA:1	21	Gene SLC35B4	YEA, YEA4, SLC35B4, FLJ14987	solute carrier family 35, member B4	NM_018226, XCT2307289.0, XCT2307290.0, XCT2307291.0, XCT2307292.0	226661_at, 226662_at, 238418_at	NP_116213.1, EAW63811.1, EAW63809.1, EAW63810.1, EAW63812.1
Gene:ID:2131	AKR1B1	7	134,127,107	134,143,888	16,781	-	2	1_A270_shN37_dhrsx_blcRNA:1-7340, 2_A270_shN37_glcs_blcRNA:1-7340	60, -112	downstream, upstream	1	1	25	27	1	2_A270_shN37_glcs_blcRNA:1	27	Gene AKR1B1	AR, ALR2, ADR, MGC1834, ALDR1, AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	NM_001628, XCT83603.2, XCT1955703.1	209772_at	NP_001619.1, EAW63814.1, EAW63815.1
Gene:ID:99	BPGM	7	134,331,531	134,364,566	33,037	+	2	1_A270_shN37_dhrsx_blcRNA:1-7335, 2_A270_shN37_glcs_blcRNA:1-7332	53, 21	st gene, st gene	1	1	56	54	1	1_A270_shN37_dhrsx_blcRNA:1	56	Gene BPGM	BPGM		NM_199109, NM_001724, XCT11421.3, XCT1955713.1, XCT1974074.1, XCT1955719.1	203502_at	NP_954633.1, NP_001715.1, EAW63821.1, EAW63822.1, EAW63823.1, EAW63824.1
Gene:ID:53739	LOC53739	7	134,736,131	134,833,045	96,914	+	1	2_A270_shN37_glcs_blcRNA:1-7334	133	st gene	0	1	12	15	1	2_A270_shN37_glcs_blcRNA:1	15	Gene LOC53739		hypothetical LOC53739	XR_113076, XR_110764, XR_106532, XR_114074	1561694_at	
Gene:ID:5281	TMEM140	7	134,832,798	134,850,997	18,201	+	3	1_A270_shN37_dhrsx_blcRNA:1-7339, 2_A270_shN37_glcs_blcRNA:1-7338, 3_A270_shN37_glcs_blcRNA:1-7338	22754, 146, 22983	downstream, st gene, downstream	1	1	14	17	2	2_A270_shN37_glcs_blcRNA:1	19	Gene TMEM140	TMEM140, FLJ11000	transmembrane protein 140	NM_014289, XCT2035794.0	218999_at	NP_055753.2, EAW63838.1
Gene:ID:29996	C7orf69	7	134,850,532	134,855,532	5,000	+	2	1_A270_shN37_dhrsx_blcRNA:1-7336, 2_A270_shN37_glcs_blcRNA:1-7339	12, 76	st gene, st gene	1	1	16	19	1	2_A270_shN37_glcs_blcRNA:1	19	Gene C7orf69	FLJ22450, C7orf69, MGC5242, MRL, FLJ37263	chromosome 7 open reading frame 69	NM_028533, NM_024165, NR_026166, XCT2356531.0, XCT2356532.0	226893_s_at	NP_079838.2, EAW63840.1, EAW63841.1
Gene:ID:9062	WDR91	7	134,866,590	134,899,316	27,726	+	1	2_A270_shN37_glcs_blcRNA:1-7338	258	st gene	0	1	11	17	1	2_A270_shN37_glcs_blcRNA:1	17	Gene WDR91	WDR91, MGC9269, WDR91	WD repeat domain 91	NM_014199, XCT2356566.0, XCT2356569.0, XCT2356570.0, XCT2116.2	218571_s_at, 218572_s_at, 222799_at, 222800_at	NP_056055.2, EAW63842.1, EAW63843.1, EAW63844.1, EAW63845.1
Gene:ID:550	CNOT4	7	135,046,547	135,194,673	148,126	+	1	2_A270_shN37_glcs_blcRNA:1-7338	80931, 165	st gene, upstream	1	1	17	16	2	2_A270_shN37_glcs_blcRNA:1	21	Gene CNOT4	CCR4-NOT transcription complex, subunit 4, NOT4	CCR4-NOT transcription complex, subunit 4	NM_001098225, NM_001190541, NM_001190546, NM_001190549, NM_001190550, NM_013316, XCT2356814.0, XCT2356815.0, XCT2356819.0, XCT1957.2, XCT2356820.1, XCT2356821.1	201505_at, 201503_at, 201504_s_at, 201506_s_at, 210957_at	NP_001035235.1, NP_001177776.1, NP_001774.2, NP_001177777.1, NP_001177778.1, NP_001177779.1, EAW63839.1, EAW63850.1, EAW63851.1, EAW63852.1, EAW63853.1, EAW63854.1
Gene:ID:3168	NUP205	7	135,247,662	135,333,501	90,839	+	2	1_A270_shN37_dhrsx_blcRNA:1-7309, 2_A270_shN37_glcs_blcRNA:1-7308	-113, 90	upstream, st gene	1	1	22	24	1	1_A270_shN37_dhrsx_blcRNA:1	24	Gene NUP205	NUP205, C7orf4	nucleoporin 205kDa	NM_015135, XCT2356842.0, XCT1960400.1	212207_at, 223362_s_at	NP_055937.1, EAW63853.1, EAW63856.1
Gene:ID:47007	PL-5263	7	135,347,221	135,351,160	13,939	+	2	1_A270_shN37_dhrsx_blcRNA:1-7310, 2_A270_shN37_glcs_blcRNA:1-7310	59, 11	st gene, st gene	1	1	22	21	1	1_A270_shN37_dhrsx_blcRNA:1	22	Gene PL-5263	protein	PL-5263 protein	NM_001126429		NP_001119601.1
Gene:ID:162	DGKI	7	137,074,555	137,531,609	457,224	-	4	1_A270_shN37_dhrsx_blcRNA:1-7302, 2_A270_shN37_glcs_blcRNA:1-7303, 3_A270_shN37_dhrsx_blcRNA:1-7304, 4_A270_shN37_glcs_blcRNA:1-7306, 5_A270_shN37_glcs_blcRNA:1-7306	204654, 154599, 358153, 204601	st gene, st gene, st gene, st gene	1	1	14.33	16.33	3	2_A270_shN37_glcs_blcRNA:1	26	Gene DGKI	DGKI, DGK-IOTA	diacylglycerol kinase, iota	NM_004717, XCT2035714.0, XCT2307193.0, XCT2357716.0, XCT1961.3	206509_at	NP_004705.1, EAW63870.1, EAW63874.1, EAW63875.1, EAW63876.1
Gene:ID:4764	CREB3L2	7	137,599,725	137,669,646	127,121	+	1	2_A270_shN37_glcs_blcRNA:1-7340	23290	st gene	0	1	13	15	1	2_A270_shN37_glcs_blcRNA:1	15	Gene CREB3L2	MGC131709, BBF2H7, MGC71086, BBF2H3.2	cAMP responsive element binding protein 3-like 2	NM_194071, XCT2369932.1, XCT2364566.0, XCT2356607.0	212343_s_at, 226739_at, 229219_at	NP_919047.2, EAW63878.1, EAW63879.1, EAW63880.1
Gene:ID:9517	ATP6AP1L	7	138,291,039	138,452,841	161,802	-	2	1_A270_shN37_dhrsx_blcRNA:1-7304, 2_A270_shN37_glcs_blcRNA:1-7303	45597, 42552	st gene, st gene	1	0	16.5	16.5	2	2_A270_shN37_glcs_blcRNA:1	22	Gene ATP6AP1L	ATP6AP2, RTADR, ATP6VOA4, MGC130016, RTA1C, RDRTA2, MGC133017, ST1, VPH1, AA, ATP6IN18, VPP2	ATPase, H+ transporting, lysosomal V0 subunit a4	NM_020632, NM_130849, NM_130851, XCT2356555.0, XCT2356559.0, XCT2356560.0, XCT2356561.0, XCT2356562.0, XCT1429.3	209437_s_at	NP_065683.2, NP_570838.2, NP_570839.2, EAW63894.1, EAW63895.1, EAW63897.1, EAW63898.1, EAW63899.1
Gene:ID:7870	KIAA1549	7	138,516,126	138,620,829	104,703	-	2	1_A270_shN37_dhrsx_blcRNA:1-7346, 2_A270_shN37_glcs_blcRNA:1-7346	70993, 44757	st gene, st gene	0	1	16.5	21.5	2	2_A270_shN37_glcs_blcRNA:1	23	Gene KIAA1549	FLJ11731, FLJ35703, FLJ40644,	KIAA1549	NM_020910, NM_001164865	223573_at	NP_065961.2, NP_001161317.1
Gene:ID:6629	ZC3HAV1	7	138,726,266	138,794,863	68,189	+	1	2_A270_shN37_glcs_blcRNA:1-7340	705	st gene	0	1	13	15	1	2_A270_shN37_glcs_blcRNA:1	15	Gene ZC3HAV1	FLJ12266, ZC3HZ, ZAP, FLJ36421, PARP13, DKFZp686H1969, MGC48898, ZC3HDC2, DKFZp686O19171, ZC3HAV1	zinc finger CCCH type, antiviral 1	NM_024625, NM_020119, XCT2356468.0, XCT2356469.0, XCT2356470.0, XCT2356552.0	210051_at, 220104_at, 220634_at	NP_078901.3, NP_064504.2, EAW63902.1, EAW63903.1, EAW63904.1, EAW63905.1
Gene:ID:54898	UBN2	7	138,916,231	138,992,882	76,751	+	3	1_A270_shN37_dhrsx_blcRNA:1-7306, 2_A270_shN37_glcs_blcRNA:1-7306, 3_A270_shN37_glcs_blcRNA:1-7306	-410, -151	upstream, upstream	1	1	16	21	1	2_A270_shN37_glcs_blcRNA:1	21	Gene UBN2	UBN2, FLJ22876	ubinuclein 2	NM_173569	235350_at, 235352_at	NP_775840.3
Gene:ID:54791	C7orf65	7	139,025,697	139,030,541	4,844	+	2	1_A270_shN37_dhrsx_blcRNA:1-7307, 2_A270_shN37_glcs_blcRNA:1-7310	-521, -316	upstream, upstream	1	1	20	19	1	1_A270_shN37_dhrsx_blcRNA:1	20	Gene C7orf65	C7orf65, FLJ38699, HSPC266, FMC1	chromosome 7 open reading frame 65	NM_197964, XCT2035812.1, XCT2461543, XCT2461555.0, XCT2461560	236793_s_at, 236791_at	NP_933968.2, EAW63915.1, EAW63912.1, EAW63913.1, EAW63914.1
Gene:ID:100506852	LOC100506852	7	139,413,130	139,477,693	64,563	-	3	1_A270_shN37_dhrsx_blcRNA:1-7305, 2_A270_shN37_glcs_blcRNA:1-7302, 3_A270_shN37_glcs_blcRNA:1-7304	8201, 6265, -451	st gene, st gene, st gene	1	1	16.5	17	2	1_A270_shN37_dhrsx_blcRNA:1	16	Gene LOC100506852		ribonucleoside-triphosphate reductase-like protein 2-like	XM_003118879		XP_003118927.1
Gene:ID:916	TBXAS1	7	139,476,047	139,720,125	242,078	+	3	1_A270_shN37_dhrsx_blcRNA:1-7306, 2_A270_shN37_glcs_blcRNA:1-7305, 3_A270_shN37_glcs_blcRNA:1-7305	4853, -5719, 87	upstream, upstream, st gene	1	1	13.5	17	2	1_A270_shN37_dhrsx_blcRNA:1	16	Gene TBXAS1	TXAS, FLJ23731, TXS, TBXAS1, CHRDSAL, TS, CYP5A1, CYP5, THAS	thromboxane A synthase 1 (platelet)	NM_030981, NM_030999, NM_001132866, NM_001166252, NM_001166254, NR_024094	208130_s_at	NP_031522.2, NP_112246.2, NP_001124438.1, NP_001166723.1, NP_001166726.1
Gene:ID:9819	PARP12	7	139,723,549	139,763,521	39,972	+	1	2_A270_shN37_glcs_blcRNA:1-7339	841	st gene	0	1	9	19	1	2_A270_shN37_glcs_blcRNA:1	19	Gene PARP12	PARP12, MSTP139, ZC3HDC1, ZC3HDC2, MSTP139_ZC3H1, DKFZp686O19171, ZC3HAV1	poly (ADP-ribose) polymerase family, member 12	NM_022750, XCT2356392.0, XCT2461432.0	218563_s_at	NP_073587.1, EAW63938.1, EAW63939.1
Gene:ID:3906	MKRN1	7	140,152,680	140,179,369	26,689	+	1	2_A270_shN37_glcs_blcRNA:1-7336	287	st gene	0	1	13	16	1	2_A270_shN37_glcs_blcRNA:1	16	Gene MKRN1	MKRN1, FLJ13334, MKRN1	makorin, ring finger protein 1	NM_013449, NM_001145125, NM_001145126, XCT2461456.0, XCT2461457.0, XCT2461458.0, XCT1951532.2, XCT1956.2	201265_at, 201563_at	NP_035874.2, NP_001128397.1, EAW63992.1, EAW63993.1, EAW63952.1, EAW63953.1, EAW63949.1
Gene:ID:7147	DENND2A	7	140,216,230	140,302,342	64,122	-	2	1_A270_shN37_dhrsx_blcRNA:1-7309, 2_A270_shN37_glcs_blcRNA:1-7310	13734, -5146	st gene, upstream	1	0	17	13	2	2_A270_shN37_glcs_blcRNA:1	18	Gene DENND2A	KIAA1277, DENND2A, FAM31D	DENN/MADD domain containing 2A	NM_014939, XCT1958.3	221653_at, 221609_at, 53691_at	NP_055754.2, EAW63954.1
Gene:ID:9986	ADCK2	7	140,372,983	140,394,808	21,825	+	2	1_A270_shN37_dhrsx_blcRNA:1-7311, 2_A270_shN37_glcs_blcRNA:1-7309	22599, 23719	downstream, downstream	1	1	15	26	1	2_A270_shN37_glcs_blcRNA:1	26	Gene ADCK2	MGC20727, ADCK2, AARF	aarF domain containing kinase 2	NM_052853, XCT2035777.0, XCT1389.3	221683_s_at, 221684_at, 221717_s_at, 240120_at	NP_443065.2, EAW63957.1, EAW63956.1
Gene:ID:7055	LOC100170401, 347 13	7	140,395,136	140,396,877	1,741	-	2	1_A270_shN37_dhrsx_blcRNA:1-7311, 2_A270_shN37_glcs_blcRNA:1-7309	365, 203	st gene, st gene	1	1	15	26	1	2_A270_shN37_glcs_blcRNA:1	26	Gene LOC100170401 3	FLJ36573	hypothetical LOC100134713	NR_038454		
Gene:ID:705	NDUFB2	7	140,396,951	140,408,496	9,965	+	2	1_A270_shN37_dhrsx_blcRNA:1-7311, 2_A270_shN37_glcs_blcRNA:1-7309	51, 191	st gene, st gene	1	1	15	26	1	2_A270_shN37_glcs_blcRNA:1	26	Gene NDUFB2	MGC370768, AGGG, NDUFB2, CI-AGGG	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, (SDB	NM_004546, XCT1967662.1, XCT2112.6, XCT1956246.1, XCT1956248.1, XCT1956250.1	218200_s_at, 218201_at, 240391_at	NP_004537.1, EAW63962.1, EAW63958.1, EAW63959.1, EAW63960.1, EAW63961.1
Gene:ID:673	BRAF	7	140,433,812	140,624,564	190,752	-	2	1_A270_shN37_dhrsx_blcRNA:1-7312, 2_A270_shN37_glcs_blcRNA:1-7310	532, -298	st gene, upstream	1	1	16.5	19	2	1_A270_shN37_dhrsx_blcRNA:1	20	Gene BRAF	NS7, FLJ35109, MGC126354, B-RAF1, MGC126606, BRAF, RAFB1, BRAF1	v-raf murine sarcoma viral oncogene homolog B1	NM_004333, XCT2356938.0, XCT2609.2	206044_s_at, 240629_at	NP_004324.2, EAW63964.1, EAW63965.1
Gene:ID:1650	MRPS33	7	140,765,961	140,774,761	8,830	+	2	1_A270_shN37_dhrsx_blcRNA:1-7312, 2_A270_shN37_glcs_blcRNA:1-7309	-3, -67	upstream, upstream	1	1	19	25	1	2_A270_shN37_glcs_blcRNA:1	25	Gene MRPS33	FLJ21123, MRP-S33, MRP-S33, PTD003, CGI-139	mitochondrial ribosomal protein S33	NM_018071, NM_033238, XCT13167.4, XCT1962764.1	218654_s_at	NP_037153.1, NP_644262.1, EAW63966.1, EAW63967.1
Gene:ID:100507421, 421	LOC100507421, 421	7	140,772,624	141,170,586	397,762	+	6	1_A270_shN37_dhrsx_blcRNA:1-7310, 2_A270_shN37_glcs_blcRNA:1-7313, 3_A270_shN37_dhrsx_blcRNA:1-7316, 4_A270_shN37_glcs_blcRNA:1-7316, 5_A270_shN37_glcs_blcRNA:1-7316, 6_A270_shN37_glcs_blcRNA:1-7316	-1200, 23552, 147164, 886, 23564, 53655, 211104, 147165	upstream, st gene, st gene, upstream, st gene, st gene, st gene, st gene	1	1	21.2	25.2	5	2_A270_shN37_glcs_blcRNA:1	41	Gene LOC100507421		transmembrane protein 176A-like	NM_003120359, NM_003119360, XM_003118875, XM_003120359		NP_003120307.1, NP_003119100.1, XP_003120407.1
Gene:ID:8730	AGK	7	141,251,076	141,354,209	103,133	+	2	1_A270_shN37_dhrsx_blcRNA:1-7317, 2_A270_shN37_glcs_blcRNA:1-7316	154, 95	st gene, st gene	1	1	17	13	1	1_A270_shN37_dhrsx_blcRNA:1	17	Gene AGK	FLJ10542, AGK, MULK	acylglycerol kinase	NM_018238, XCT30702.4, XCT1962781.1	1555610_at, 218356_at, 222132_s_at	NP_060708.1, EAW63972.1, EAW63973.1
Gene:ID:55952	FLJ40552	7	141,404,136	141,435,030	30,895	-	2	1_A270_shN37_dhrsx_blcRNA:1-7315, 2_A270_shN37_glcs_blcRNA:1-7307	-80, -16	upstream, upstream	1	1	16	16	2	2_A270_shN37_glcs_blcRNA:1	16	Gene FLJ40552		hypothetical LOC55952	NR_015392, XCT2035698.1	1553634_a_at	EAW63978.1
Gene:ID:94551	WEE2	7	141,466,153	141,481,071	22,918	+	1	2_A270_shN37_dhrsx_blcRNA:1-7315, 2_A270_shN37_glcs_blcRNA:1-7307	28927, 28093	downstream, downstream	1	1	16	16	2	2_A270_shN37_glcs_blcRNA:1	16	Gene WEE2	WEE2, WEE1B, FLJ16107	WEE1 homolog 2 (S. pombe)	NM_001105558		NP_001099028.1
Gene:ID:142	SSBP1	7	141,535,176	141,550,257	12,081	+	2	1_A270_shN37_dhrsx_blcRNA:1-7316, 2_A270_shN37_glcs_blcRNA:1-7307	-66, -126	upstream, upstream	1	1	16	16	2	2_A270_shN37_glcs_blcRNA:1	16	Gene SSBP1	mtSSB, SSBP1, SOSS-B1, SSBP, MT-SSB	single-stranded DNA binding protein 1	NM_003143, XCT2035780.0, XCT2035783.0, XCT2345047.0, XCT2349048.0	1562482_s_at, 202591_s_at, 214990_at	NP_003134.1, EAW63981.1, EAW63978.1, EAW63980.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Internal Transcripts	Internal Gc/Gs Pair	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:6957	TRBD	7	141,998,851	142,010,972	12,121	+	2	1_A275_shL7_dhrus_lncRNA:1:5119, 2_A275_shL87_dlrs_lncRNA:1:7266	276643, 27677	ss gene, us gene	1	1	16	34	1	2_A275_shL87_dlrs_lncR NA:1	24	Gene TRBD	TRB, TRBD, TCRB	T cell receptor beta locus			
Gene:ID:6964	TRBV6-1	7	142,020,694	142,021,263	569	+	2	1_A275_shL7_dhrus_lncRNA:1:5119, 2_A275_shL87_dlrs_lncRNA:1:7266	6602, 6624	downstream, downstream	1	1	16	34	1	2_A275_shL87_dlrs_lncR NA:1	24	Gene TRBV6-1	TCRBV6S1A17, TCRBV6S1, TRBV6-1, TRBV6S1	T cell receptor beta variable 6-1			
Gene:ID:6966	TRBV6-4	7	142,026,176	142,026,810	632	+	2	1_A275_shL7_dhrus_lncRNA:1:5119, 2_A275_shL87_dlrs_lncRNA:1:7266	-1652, -1650	upstream, upstream	1	1	16	34	1	2_A275_shL87_dlrs_lncR NA:1	24	Gene TRBV6-4	TCRBV6S1, TCRBV6S1S3, TCRBV6S1, TRBV6-4	T cell receptor beta variable 6-4			
Gene:ID:84268	TASR:HR3	7	142,918,172	142,920,143	971	+	1	1_A275_shL7_dhrus_lncRNA:1:7370,	-4796	upstream	0	1	9	19	1	2_A275_shL87_dlrs_lncR NA:1	19	Gene TAS2R40	TAS2R40, GPR60, MGC126648, MGC126649, TAS2R40, T2R40	taste receptor, type 2, member 40	NM_176882	1553399_at	NP_783863.1
Gene:ID:59822	TMEM139	7	142,962,063	142,965,141	3,078	+	2	1_A275_shL7_dhrus_lncRNA:1:7370, 2_A275_shL87_dlrs_lncRNA:1:7371	2629, 3537	ss gene, downstream	0	1	13.5	16	2	2_A275_shL87_dlrs_lncR NA:1	19	Gene TMEM139	TMEM139, PLP/B0366	transmembrane protein 139	NM_153348, XCT:2352298.2, XCT:2348467.1, XCT:2348468.1, XCT:2352302.0	2377752_at, 2398534_at	NP_694976.1, EAW51671.1, EAW51672.1, EAW51673.1, EAW51674.1, EAW51675.1
Gene:ID:6738	CASP2	7	142,985,402	143,004,765	19,363	+	2	1_A275_shL7_dhrus_lncRNA:1:7370, 2_A275_shL87_dlrs_lncRNA:1:7371	-410, 196	upstream, us gene	0	1	13.5	16	2	2_A275_shL87_dlrs_lncR NA:1	19	Gene CASP2	ICH1/ICH, CASP2, NEDD2, ICH-1L, ICH-1S, ICH1, CASP-2	caspase 2, apoptosis-related cysteine peptidase	NM_032982, NM_032983	203690_s_at, 203811_at, 203812_s_at, 211160_s_at, 226032_at, 226036_s_at, 34466_at	NP_116764.2, NP_116765.2
Gene:ID:100507937	LOC100507937	7	143,076,246	143,077,585	1,340	-	1	2_A275_shL87_dlrs_lncRNA:1:7372	-396	upstream	0	1	12	23	1	2_A275_shL87_dlrs_lncR NA:1	23	Gene LOC100507937		hypothetical LOC100507937	XR_108763		
Gene:ID:791	ZYX	7	143,076,260	143,086,204	9,944	+	1	2_A275_shL87_dlrs_lncRNA:1:7372	-376	upstream	0	1	12	23	1	2_A275_shL87_dlrs_lncR NA:1	23	Gene ZYX	ZYX, ESP-2, HED-2	zyxin	NM_003461, NM_001010972, XCT:2352370.0, XCT:2352538.0, XCT:2352809.0, XCT:2352839.2	200605_s_at, 213799_s_at	NP_003452.1, NP_001010972.1, EAW51646.1, EAW51649.1, EAW51650.1, EAW51651.1
Gene:ID:1041	EPHA1	7	143,086,205	143,103,853	17,760	-	1	2_A275_shL87_dlrs_lncRNA:1:7372	-20001	downstream	0	1	12	23	1	2_A275_shL87_dlrs_lncR NA:1	23	Gene EPHA1	EPH1, EPH, EPHA1, EPHT1, MGC163163	EPH receptor A1	NM_005232, XCT:2357177.0, XCT:2357210.0, XCT:1769.2	203977_s_at, 210004_at	NP_005223.2, EAW51647.1, EAW51648.1, EAW51649.1
Gene:ID:7010	TFL1	7	144,149,034	144,333,146	184,112	+	2	1_A275_shL7_dhrus_lncRNA:1:5120, 2_A275_shL87_dlrs_lncRNA:1:7373	-58, 26	ss gene, us gene	1	1	22	45	1	2_A275_shL87_dlrs_lncR NA:1	45	Gene TFL1	FFB2, TFL1, HFFL1	thalamic pyruvate phosphatase 1	NM_182483, NM_001042452, XCT:2266228.0, XCT:1774732.2	221215_s_at, 221216_x_at, 223695_at	NP_071995.2, NP_001038847.1, EAW50981.1, EAW50982.1
Gene:ID:6047	CNTNAP2	7	145,812,453	146,116,090	2,303,637	+	3	1_A275_shL7_dhrus_lncRNA:1:5122, 2_A275_shL87_dlrs_lncRNA:1:7377, 2_A275_shL87_dlrs_lncRNA:1:7378	-233, -387, 1717139	upstream, upstream, us gene	1	1	14.5	26.5	2	2_A275_shL87_dlrs_lncR NA:1	39	Gene CNTNAP2	DUIR2,DIB1,DISB, PTHSL1, AUTS15, CASPR2, CDFE, NRXN4, CNTNAP2	contactin associated protein-like 2	NM_014141, XCT:2264182.1, XCT:2266169.1, XCT:5523.4	210143_s_at, 219200_s_at, 219201_s_at, 219202_s_at	NP_014900.1, EAW50553.1, EAW50552.1, EAW50553.1
Gene:ID:6069	RNY3	7	146,635,580	146,635,663	83	+	2	1_A275_shL7_dhrus_lncRNA:1:5124, 2_A275_shL87_dlrs_lncRNA:1:7379	-356, -428	upstream, upstream	0	1	16	16	1	2_A275_shL87_dlrs_lncR NA:1	16	Gene RNY3	Y3, RNY3	RNA, Ro-associated Y3	NR_001371		
Gene:ID:6053	RNY2	7	146,680,647	146,680,848	101	+	3	1_A275_shL7_dhrus_lncRNA:1:5125, 1_A275_shL7_dhrus_lncRNA:1:5126, 2_A275_shL87_dlrs_lncRNA:1:7380	-1402, 3489, 3873	upstream, downstream, downstream	1	1	16	16	2	1_A275_shL7_dhrus_lnc RNA:1	19	Gene RNY2	Y2, HY2, RNY2	RNA, Ro-associated Y2	NR_004392		
Gene:ID:6054	RNY1	7	146,684,226	146,684,340	112	-	3	1_A275_shL7_dhrus_lncRNA:1:5125, 1_A275_shL7_dhrus_lncRNA:1:5126, 2_A275_shL87_dlrs_lncRNA:1:7380	3636, 4,20	downstream, us gene, us gene	1	1	16	16	2	1_A275_shL7_dhrus_lnc RNA:1	19	Gene RNY1	Y1, RNY1, HY1	RNA, Ro-associated Y1	NR_004391		
Gene:ID:59351	ZNF786	7	146,766,733	146,767,859	21,126	-	3	1_A275_shL7_dhrus_lncRNA:1:5127, 2_A275_shL87_dlrs_lncRNA:1:7381, 2_A275_shL87_dlrs_lncRNA:1:7382	24924, 24961, 157	downstream, downstream, us gene	1	1	27.5	35	2	2_A275_shL87_dlrs_lncR NA:1	47	Gene ZNF786	DKFZp762I127, MGC156120, ZNF786	zinc finger protein 786	NM_152411, XCT:2355563.0, XCT:7793802.2, XCT:1964797.2	2380653_at	NP_689624.2, EAW50065.1, EAW50062.1, EAW50064.1
Gene:ID:55658	ZNF425	7	146,799,876	146,823,436	23,562	-	2	1_A275_shL7_dhrus_lncRNA:1:5128, 2_A275_shL87_dlrs_lncRNA:1:7382	-18, 14	upstream, us gene	1	1	48	43	1	1_A275_shL7_dhrus_lnc RNA:1	46	Gene ZNF425	MGC150566,ZNF425	zinc finger protein 425	NM_001001661, XCT:7778081.1	2315563_at, 2323554_at	NP_001001661.1, EAW50061.1
Gene:ID:7541	ZNF398	7	146,823,508	146,890,134	66,626	+	3	1_A275_shL7_dhrus_lncRNA:1:5128, 2_A275_shL87_dlrs_lncRNA:1:7382, 2_A275_shL87_dlrs_lncRNA:1:7383	-52, -54, 21604	upstream, upstream, us gene	1	1	21	32	2	1_A275_shL7_dhrus_lnc RNA:1	46	Gene ZNF398	ZNF398, KIAA1339, PT, PS1, ZER6	zinc finger protein 398	NM_178566, NM_020781, XCT:2365132.1, XCT:2344399.0, XCT:2346460.0, XCT:3206.2	1553013_a_at, 1553013_at, 226202_at, 226145_s_at	NP_733871.1, NP_065832.1, EAW50057.1, EAW50058.1, EAW50059.1, EAW50060.1
Gene:ID:6582	ZNF252	7	146,892,577	146,923,329	30,752	+	2	1_A275_shL7_dhrus_lncRNA:1:5129, 2_A275_shL87_dlrs_lncRNA:1:7385	65, 63	ss gene, us gene	1	1	46	70	1	2_A275_shL87_dlrs_lncR NA:1	70	Gene ZNF252	ZNF252, HLI01	zinc finger protein 252	NM_003579, XCT:2265726.0, XCT:1640576.2		NP_003996.1, EAW50056.1, EAW50055.1
Gene:ID:9665	ZNF212	7	148,036,742	148,053,700	16,958	+	4	1_A275_shL7_dhrus_lncRNA:1:5130, 1_A275_shL7_dhrus_lncRN A:1:5131, 2_A275_shL87_dlrs_lncRNA:1:7386, 2_A275_shL87_dlrs_lncRNA:1:7387	-70, 22554, -64, 22558	upstream, downstream, upstream, downstream	1	1	61.5	68	2	2_A275_shL87_dlrs_lncR NA:1	100	Gene ZNF212	CZH2-100, MGC9707, ZNFC100, ZNF182, ZNF212	zinc finger protein 212	NM_012296, XCT:2265738.0, XCT:1930167.1	202955_at	NP_036558.2, EAW50034.1, EAW50032.1
Gene:ID:100507937	LOC100507937	7	148,959,262	148,994,803	35,141	+	2	1_A275_shL7_dhrus_lncRNA:1:5131, 2_A275_shL87_dlrs_lncRNA:1:7389	58, 14	ss gene, us gene	1	1	27	30	1	2_A275_shL87_dlrs_lncR NA:1	30	Gene LOC100507937		protein ZNF763-like	XM_003118877		XP_003118925.1
Gene:ID:7552	ZNF777	7	149,126,454	149,156,053	29,599	+	2	1_A275_shL7_dhrus_lncRNA:1:5132, 1_A275_shL7_dhrus_lncRNA:1:5133, 2_A275_shL87_dlrs_lncRNA:1:7390	209, 261	ss gene, us gene	1	1	65	61	1	1_A275_shL7_dhrus_lnc RNA:1	65	Gene ZNF777	ZNF777, KIAA1255	zinc finger protein 777	NM_015694, XCT:2265.3	1553172_at, 226963_at, 236667_at, 240343_at	NP_056809.2, EAW50064.1
Gene:ID:9883	REPIN1	7	150,065,878	150,071,133	5,254	+	1	1_A275_shL7_dhrus_lncRNA:1:7391	-377	ss gene	0	1	10	19	1	2_A275_shL87_dlrs_lncR NA:1	19	Gene REPIN1	REPIN1, RIP60, AP4, Zfp464, ZNF464	replication initiator 1	NM_013400, NM_014374, NM_001099695, NM_001099696	216641_s_at, 222001_s_at, 226618_s_at	NP_037512.2, NP_055188.2, NP_001093196.1, NP_001093163.1
Gene:ID:53871	ZNF775	7	150,076,806	150,095,719	19,312	+	3	1_A275_shL7_dhrus_lncRNA:1:5134, 2_A275_shL87_dlrs_lncRNA:1:7391, 2_A275_shL87_dlrs_lncRNA:1:7392, 2_A275_shL87_dlrs_lncRNA:1:7393	25898, 10180, 25595	downstream, upstream, downstream	1	1	22.5	27.5	2	2_A275_shL87_dlrs_lncR NA:1	36	Gene ZNF775	ZNF775, MGC33364	zinc finger protein 775	NM_173600	226226_s_at, 226284_s_at, 226831_at, 238499_at	NP_776851.2
Gene:ID:26743	fcag7.1196	7	150,102,580	150,109,255	6,716	+	2	1_A275_shL7_dhrus_lncRNA:1:5134, 2_A275_shL87_dlrs_lncRNA:1:7392	-636, -636	upstream, upstream	1	1	35	36	1	2_A275_shL87_dlrs_lncR NA:1	36	Gene fcag7.1196	FLJ12702, FLJ12709, LOC126743	similar to GLI-Kruppel family member HKR1	NR_027237	235077_at, 235929_at	
Gene:ID:787	KCNH2	7	150,642,049	150,675,914	32,865	-	2	1_A275_shL7_dhrus_lncRNA:1:5135, 2_A275_shL87_dlrs_lncRNA:1:7394	-6202, -6156	upstream, upstream	1	1	33	29	1	1_A275_shL7_dhrus_lnc RNA:1	33	Gene KCNH2	SQT1, HERG, KCNH2, ERG1, LQT2, Kv11.1, HERG1	potassium voltage-gated channel, subfamily H (eag-related), member 2	NM_000238, NM_172056, NM_172057, XCT:2366504.0, XCT:2366903.0, XCT:2366906.0, XCT:2366907.0, XCT:6700.3	209262_at, 210035_s_at	NP_000222.1, NP_742053.1, NP_742054.1, EAW54070.1, EAW54073.1, EAW54074.1, EAW54072.1, EAW54075.1
Gene:ID:646	NOS3	7	150,695,144	150,711,667	23,343	+	2	1_A275_shL7_dhrus_lncRNA:1:5135, 2_A275_shL87_dlrs_lncRNA:1:7394	-6835, 6992	upstream, upstream	1	1	30	29	1	1_A275_shL7_dhrus_lnc RNA:1	30	Gene NOS3	eNOS, ECNOS, NOS3	nitric oxide synthase 3 (endothelial cell)	NM_000603, NM_001160109, NM_001160110, NM_001160111, XCT:6700.3	206581_s_at, 236063_at	NP_000594.2, NP_001153551.1, NP_001153552.1, NP_001153553.1, EAW54099.1
Gene:ID:55972	ATG9B	7	150,709,297	150,721,566	12,269	-	2	1_A275_shL7_dhrus_lncRNA:1:5136, 2_A275_shL87_dlrs_lncRNA:1:7394	-4296, 4156	upstream, upstream	1	1	17	19	1	2_A275_shL87_dlrs_lncR NA:1	19	Gene ATG9B	ATG9B, APG9L2, SONE, MDS3AS	ATG9 autophagy related 9 homolog B (S. cerevisiae)	NM_173681	1553392_at, 236252_at	NP_776043.4
Gene:ID:1104	ABCB8	7	150,729,510	150,744,899	19,389	+	5	1_A275_shL7_dhrus_lncRNA:1:5136, 1_A275_shL7_dhrus_lncRNA:1:5137, 2_A275_shL87_dlrs_lncRNA:1:7394, 2_A275_shL87_dlrs_lncRNA:1:7395	-282, -28690, 236, 11002, 29656	ss gene, downstream, us gene, us gene, downstream	1	1	16.33	22	3	2_A275_shL87_dlrs_lncR NA:1	26	Gene ABCB8	ABCB8, EST32128, MABC1, mABC1	ATP-binding cassette, sub-family B (MDR/TAP), member 8	NM_007188, XCT:2343629.0, XCT:2343630.0, XCT:2343631.0, XCT:2343632.0, XCT:2343633.0, XCT:2343634.0, XCT:2343635.0, XCT:2343636.0, XCT:2343637.0, XCT:6746.3, XCT:1953011.1	206317_s_at	NP_009118.2, EAW54087.1, EAW54088.1, EAW54089.1, EAW54090.1, EAW54091.1, EAW54092.1, EAW54093.1, EAW54094.1, EAW54095.1
Gene:ID:311	ACCN3	7	150,745,603	150,749,643	4,230	+	4	1_A275_shL7_dhrus_lncRNA:1:5137, 2_A275_shL87_dlrs_lncRNA:1:7396, 2_A275_shL87_dlrs_lncRNA:1:7397, 2_A275_shL87_dlrs_lncRNA:1:7398	9593, 8093, 8563, 12539	downstream, upstream, downstream, downstream	1	1	16.33	20.67	3	2_A275_shL87_dlrs_lncR NA:1	26	Gene ACCN3	ACCN3, DRASIC, SLNAC1, TNC1, ASIC3	amiloride-sensitive cation channel 3	NM_020322, NM_020323, NM_064989, XCT:2352787.0, XCT:6211.3, XCT:1773846.2, XCT:1966228.1	207561_s_at	NP_064715.1, NP_064717.1, NP_064790.1, EAW54052.1, EAW54053.1, EAW54055.1, EAW54054.1
Gene:ID:5080	CDK5	7	150,760,898	150,763,052	2,153	-	3	1_A275_shL7_dhrus_lncRNA:1:5137, 2_A275_shL87_dlrs_lncRNA:1:7396, 2_A275_shL87_dlrs_lncRNA:1:7397	-148, -116, 2092	upstream, upstream, upstream	1	1	17.5	21.5	2	2_A275_shL87_dlrs_lncR NA:1	26	Gene CDK5	CDK5, PSSALRE	cyclin-dependent kinase 5	NM_001164410, NM_004935, XCT:2366569.0, XCT:6312.2, XCT:1966234.1	204247_s_at	NP_001157682.1, NP_004926.1, EAW54048.1, EAW54050.1, EAW54051.1
Gene:ID:6322	SLC4A2	7	150,766,637	150,773,614	16,957	+	4	1_A275_shL7_dhrus_lncRNA:1:5137, 2_A275_shL87_dlrs_lncRNA:1:7396, 2_A275_shL87_dlrs_lncRNA:1:7397, 2_A275_shL87_dlrs_lncRNA:1:7398	-1407, -1409, 1467, 21039	upstream, upstream, upstream, downstream	1	1	17	21.67	3	2_A275_shL87_dlrs_lncR NA:1	26	Gene SLC4A2	AE2, HKB3, BND3L, MBND2, FLJ39220, EPB3L1, SLCA2	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	NM_003040, XCT:2292745.0, XCT:2367440.0, XCT:2367790.0, XCT:6730.3, XCT:1953012.1	202111_at	NP_003031.2, EAW54046.1, EAW54044.1, EAW54045.1, EAW54046.1, EAW54047.1
Gene:ID:9322	PASTK	7	150,773,708	150,777,851	4,143	+	2	1_A275_shL7_dhrus_lncRNA:1:5138, 2_A275_shL87_dlrs_lncRNA:1:7398	-255, -6769	ss gene, upstream	0	1	13	21.5	2	2_A275_shL87_dlrs_lncR NA:1	22	Gene PASTK	PAST, PASTK	Pas-activated serine/threonine kinase	NM_015717, NM_033315, XCT:2366597.0, XCT:2366598.0, XCT:2352799.0, XCT:2352800.0, XCT:6747.2, XCT:1952010.0, XCT:1966231.1, XCT:1966232.1, XCT:1966233.1	202676_s_at, 210875_s_at, 214114_s_at	NP_056532.1, EAW54042.1, EAW54043.1, EAW54045.1, EAW54036.1, EAW54040.1, EAW54041.1
Gene:ID:3980	TMUB1	7	150,776,172	150,780,620	2,448	-	2	1_A275_shL7_dhrus_lncRNA:1:7396, 1_A275_shL7_dhrus_lncRNA:1:7397	2624, 6100	downstream, downstream	1	1	16	21.5	2	2_A275_shL87_dlrs_lncR NA:1	22	Gene TMUB1	SB144, C7orf21, TMUB1, MGC9442	transmembrane and ubiquitin-like domain containing 1	NM_001130044, NM_031452, XCT:2366564.1, XCT:2348710.0, XCT:6739.3	223153_s_at	NP_001123516.1, NP_113622.1, EAW54030.1, EAW54031.1, EAW54032.1
Gene:ID:19985	ASAP3	7	150,783,826	150,841,823	57,997	+	2	1_A275_shL7_dhrus_lncRNA:1:5138, 2_A275_shL87_dlrs_lncRNA:1:7398	4130, 2894	upstream, upstream	1	1	16	21.5	2	2_A275_shL87_dlrs_lncR NA:1	22	Gene ASAP3	MRP-1, ADAP3, FLJ16149, FLJ34852, CRAG, CENTG3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	NM_031946, NM_001042539, XCT:2366701.0, XCT:2367744.0, XCT:2367753.0, XCT:2352801.0, XCT:6736.3, XCT:1953013.1	223709_at, 231299_at, 236626_s_at	NP_114132.2, NP_001035003.1, EAW54034.1, EAW54035.1, EAW54036.1, EAW54037.1, EAW54038.1, EAW54039.1
Gene:ID:9961	ABCF2	7	150,904,923	150,924,317	19,394	-	2	1_A275_shL7_dhrus_lncRNA:1:5139, 2_A275_shL87_dlrs_lncRNA:1:7400	-63, -31	upstream, upstream	1	1	24	23	1	1_A275_shL7_dhrus_lnc RNA:1	24	Gene ABCF2	ABC26, EST13090, HUSSY-18, HU-ABC1, DKFZp686G1623, ABCP2, HUSSY18	ATP-binding cassette, sub-family F (GCN20), member 2	NM_005692, NM_007189, XCT:2366572.0, XCT:2366574.0, XCT:2366576.0, XCT:1951479.1, XCT:1951480.1	207622_s_at, 221763_at, 232295_at, 235240_at, 242247_s_at, 242322_at	NP_005683.2, NP_009120.1, EAW54012.1, EAW54014.1, EAW54015.1, EAW54016.1, EAW54017.1, EAW54015.1
Gene:ID:9650	CHPF2	7	150,929,585	150,935,903	6,330	+	2	1_A275_shL7_dhrus_lncRNA:1:5139, 2_A275_shL87_dlrs_lncRNA:1:7400	-5165, 5217	upstream, upstream	1	1	24	23	1	1_A275_shL7_dhrus_lnc RNA:1	24	Gene CHPF2	CHPF2, CSGLCA-T, Cs0p3, CSGlcAT, KIAA1402	chondroitin polymerizing factor 2	NM_018015, XCT:6735.3, XCT:1966001.1, XCT:1965002.1	221799_at, 55093_at	NP_060485.1, EAW54011.1, EAW54010.1, EAW54012.1
Gene:ID:928	RHEB	7	151,163,098	151,217,010	53,912	-	2	1_A275_shL7_dhrus_lncRNA:1:5139, 1_A275_shL7_dhrus_lncRN A:1:5140	51909, 47954	ss gene, us gene	1	1	19	16	2	1_A275_shL7_dhrus_lnc RNA:1	22	Gene RHEB	RHEB, RHEB2, MGC111559	Ras homolog enriched in brain	NM_005614, XCT:2365551.0, XCT:1966545.0, XCT:1966235.1, XCT:1966236.1	1555700_at, 201451_s_at, 201452_at, 201453_x_at, 213404_s_at, 213409_s_at, 241364_at, 241366_at	NP_005605.1, EAW53995.1, EAW53997.1, EAW53995.1, EAW53998.1
Gene:ID:1422	PRKAG2	7	151,253,200	151,374,216	121,116	+	4	1_A275_shL7_dhrus_lncRNA:1:5140, 1_A275_shL7_dhrus_lncRNA:1:5141, 1_A275_shL7_dhrus_lncRNA:1:5142, 2_A275_shL87_dlrs_lncRNA:1:7401, 2_A275_shL87_dlrs_lncRNA:1:7402	68060, 65955, 121452, 69636	ss gene, us gene, ss gene, us gene	1	1	16	17.33	3	1_A275_shL7_dhrus_lnc RNA:1	22	Gene PRKAG2	CMH6, AAG22, PRKAG2, H91620p, AAAG, WPWS	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	NM_016203, NM_001040632, XCT:2349855.0, XCT:2352600.0	1557231_at, 215292_s_at, 225562_at, 225724_s_at, 232765_s_at	NP_077737.1, NP_037287.2, NP_001032722.1, EAW53953.1, EAW53954.1
Gene:ID:56381	GALNTL5	7	151,657,464	151,717,019	60,555	+	1	1_A275_shL7_dhrus_lncRNA:1:7402	60965	downstream	0	1	16	16	1	2_A275_shL87_dlrs_lncR NA:1	16	Gene GALNTL5	GALNTL5, GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5	NM_145292, NR_033164, XCT:2266117.1, XCT:2266118.0, XCT:2348690.0, XCT:2348690.0, XCT:2352802.0	232150_at	NP_660335.2, EAW53976.1, EAW53977.1, EAW53979.1, EAW53980.1, EAW53981.1
Gene:ID:2917	GALNT11	7	151,722,776	151,819,427	96,649	+	1	2_A275_shL87_dlrs_lncRNA:1:7402	-346	upstream	0	1	16	16	1	2_A275_shL87_dlrs_lncR NA:1	16	Gene GALNT11	FLJ21638, MGC71630, GALNT11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-11)	NM_022087, XCT:2265120.0, XCT:2265121.0	219013_at	NP_071370.2, EAW53975.1, EAW53976.1
Gene:ID:5595	MLL3	7	151,832,016	152,133,090	301,060	-	3	1_A275_shL7_dhrus_lncRNA:1:5140, 2_A275_shL87_dlrs_lncRNA:1:7402, 2_A275_shL87_dlrs_lncRNA:1:7403	-646, -766	upstream, upstream	1	1	22	30	1	2_A275_shL87_dlrs_lncR NA:1	30	Gene MLL3	HALR, KIAA1506, MGC119253, FLJ12625, MGC116830, KMT2C, DKFZp686C06112, FLJ35309, MLL3, MGC116831	myeloid/lymphoid or mixed-lineage leukemia 3	NM_170606	1555404_a_at	NP_733751.2
Gene:ID:100126822	LOC100126822	7	152,161,209	152,162,630	1,421	+	2	1_A275_shL7_dhrus_lncRNA:1:5144, 2_A275_shL87_dlrs_lncRNA:1:7406	467, 359	ss gene, us gene	1	1	29	32	1	1_A275_shL7_dhrus_lnc RNA:1	30	Gene LOC100126822	LOC100126822	hypothetical LOC100126822	NR_027557		
Gene:ID:804	DPP6	7	153,564,418	154,264,033	679,616	+	1	1_A275_shL7_dhrus_lncRNA:1:5146	166317	ss gene	0	1	11	16	1	2_A275_shL87_dlrs_lncR NA:1	16	Gene DPP6	FLJ39660, MGC49605, DPP-X, VF2, DPP6	dipeptidyl-peptidase 6	NM_130797, NM_001936, NM_006203(3), XCT:2357116.0, XCT:1954126.1	1554799_at, 207799_s_at, 244546_at	NP_570620.2, NP_001927.3, NP_001034438.1, EAW54121.1, EAW54122.1
Gene:ID:2976	PAX3IP1	7	154,735,400	154,794,662	59,262	-	2	1_A275_shL7_dhrus_lncRNA:1:5147, 1_A275_shL7_dhrus_lncRNA:1:5148	-326, -364	upstream, upstream	1	1	24	27	1	2_A275_shL87_dlrs_lncR NA:1	27	Gene PAX3IP1	CAGH28, CAGH28, FLJ41348, PAX3IP1L, TNRC2, PAXIP1, PTIP, PAC1P1	PAX interacting (with transcription-activation domain) protein 1	NM_007349, XCT:2351610.0, XCT:10307.3	1553625_at, 213625_at	NP_031375.3, EAW53825.1, EAW53824.1
Gene:ID:92761	LOC202761	7	154,785,143	154,797,413	2,270	-	2	1_A275_shL7_dhrus_lncRNA:1:5147, 1_A275_shL7_dhrus_lncRNA:1:5148	-135, -163	upstream, upstream	1	1	24	27	1	2_A275_shL87_dlrs_lncR NA:1	27	Gene LOC202761		hypothetical LOC202761	NR_026090	235507_at	

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100128264	LOC100128264	7	154,858,777	154,863,267	4,490	-	4	1_A375_pNL7_minus_lncRNA::1::5149, 2_A375_pNL97_plus_lncRNA::1::7411, 2_A375_pNL97_plus_lncRNA::1::7412, 2_A375_pNL97_plus_lncRNA::1::7413	1443, 4947, 1443, 163	in gene, downstream, in gene, in gene	1	1	53.67	76	3	2_A375_pNL97_plus_lncRNA::1	194	Gene LOC100128264	FLJ50038	hypothetical LOC100128264	XR_113090, XR_110773, XR_108707, XR_114117		
GeneID:3361	HTR5A	7	154,862,546	154,877,459	14,913	+	4	1_A375_pNL7_minus_lncRNA::1::5149, 2_A375_pNL97_plus_lncRNA::1::7411, 2_A375_pNL97_plus_lncRNA::1::7412, 2_A375_pNL97_plus_lncRNA::1::7413	-722, -4226, -722, 558	upstream, upstream, upstream, in gene	1	1	53.67	76	3	2_A375_pNL97_plus_lncRNA::1	194	Gene HTR5A	MGC138226, HTR5A, 5-HT5A	5-hydroxytryptamine (serotonin) receptor 5A	NM_024012, hCT8200.2	221362_at	NP_076917.1, EAX04526.1
GeneID:3638	INSIG1	7	155,089,486	155,101,945	12,459	+	1	1_A375_pNL7_minus_lncRNA::1::5150	-622	upstream	1	0	17	16	1	1_A375_pNL7_minus_lncRNA::1	17	Gene INSIG1	MGC1405, CL6, CL-6, INSIG1	insulin induced gene 1	NM_005542, NM_198336, NM_198337, hCT2351193.0, hCT1642107.5, hCT1962635.2, hCT1962636.2	201625_s_at, 201626_at, 201627_s_at	NP_005533.2, NP_938150.2, NP_938151.1, EAX04529.1, EAX04531.1, EAX04532.1, EAX04530.1
GeneID:2020	EN2	7	155,250,824	155,257,526	6,702	+	2	1_A375_pNL7_minus_lncRNA::1::5151, 2_A375_pNL97_plus_lncRNA::1::7414	-744, -712	upstream, upstream	1	1	44	49	1	2_A375_pNL97_plus_lncRNA::1	49	Gene EN2	EN2		NM_001427, hCT11166.3	207060_at	NP_001418.2, EAX04535.1
GeneID:100506302	LOC100506302	7	155,434,610	155,437,074	2,464	-	3	1_A375_pNL7_minus_lncRNA::1::5152, 1_A375_pNL7_minus_lncRNA::1::5153, 2_A375_pNL97_plus_lncRNA::1::7415	178, -590, 178	in gene, upstream, in gene	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC100506302		hypothetical LOC100506302	XR_113096, XR_110774, XR_108708, XR_114118		
GeneID:155435	RBM33	7	155,437,203	155,574,179	136,976	+	4	1_A375_pNL7_minus_lncRNA::1::5152, 1_A375_pNL7_minus_lncRNA::1::5153, 1_A375_pNL7_minus_lncRNA::1::5154, 2_A375_pNL97_plus_lncRNA::1::7415	-307, 461, 16045, -307	upstream, in gene, in gene, upstream	1	1	20	16	2	1_A375_pNL7_minus_lncRNA::1	21	Gene RBM33	PRR8, DKFZp434D1319, RBM33, MGC20460	RNA binding motif protein 33	NM_053043, hCT1822159.1	225639_at, 226732_at, 235601_at	NP_444271.2, EAX04541.1
GeneID:389602	tcag7.1275	7	155,755,251	155,759,037	3,786	+	1	2_A375_pNL97_plus_lncRNA::1::7417	-787	upstream	0	1	16	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene tcag7.1275	FLJ42330, LOC389602	hypothetical LOC389602	XR_113095, XR_110775, XR_108709, XR_114119		
GeneID:129790	C7orf13	7	156,431,060	156,433,348	2,288	-	1	2_A375_pNL97_plus_lncRNA::1::7418	228	in gene	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C7orf13	MY040, C7orf13	chromosome 7 open reading frame 13	NR_026665, hCT1641604.3	223630_at	EAX04550.1
GeneID:140545	RNF32	7	156,433,401	156,469,824	36,423	+	1	2_A375_pNL97_plus_lncRNA::1::7418	-261	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene RNF32	RNF32, HSD15, FKSG33	ring finger protein 32	NM_030936, NM_001184996, NM_001184997, hCT2262008.0, hCT2262009.0, hCT2356891.0, hCT2356892.0, hCT9921.3, hCT1950336.0, hCT1950337.0, hCT1950338.0	1554642_at, 220991_s_at, 232830_at	NP_112198.1, NP_001171925.1, NP_001171926.1, EAX04551.1, EAX04553.1, EAX04557.1, EAX04552.1, EAX04554.1, EAX04555.1, EAX04556.1, EAX04558.1
GeneID:64434	NOM1	7	156,742,417	156,765,876	23,459	+	2	1_A375_pNL7_minus_lncRNA::1::5156, 2_A375_pNL97_plus_lncRNA::1::7419	15, -17	in gene, upstream	1	1	47	33	1	1_A375_pNL7_minus_lncRNA::1	47	Gene NOM1	FLJ16401, C7orf3, SGD1, NOM1	nucleolar protein with MIF4G domain 1	NM_138400, hCT9920.3	227161_at, 229220_x_at	NP_612409.1, EAX04563.1
GeneID:10049	DNAJB6	7	157,129,710	157,210,133	80,423	+	2	1_A375_pNL7_minus_lncRNA::1::5157, 2_A375_pNL97_plus_lncRNA::1::7420	68130, 68210	in gene, in gene	1	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene DNAJB6	HSJ-2, MSJ-1, HSJ2, DKFZp566D0824, MGC117297, DnaJ, DJ4, MRJ, MGC1152, HHDJ1, DNAJB6, FLJ42837	DnaJ (Hsp40) homolog, subfamily B, member 6	NM_005494, NM_058246, hCT2282244.0, hCT2282246.0	208811_s_at, 209015_s_at	NP_005485.1, NP_490647.1, EAX04570.1, EAX04571.1
GeneID:5799	PTPRN2	7	157,331,750	158,380,482	1,048,732	-	4	1_A375_pNL7_minus_lncRNA::1::5158, 1_A375_pNL7_minus_lncRNA::1::5159, 2_A375_pNL97_plus_lncRNA::1::7421, 2_A375_pNL97_plus_lncRNA::1::7422	1022818, 33490, 1022882, 33442	in gene, in gene, in gene, in gene	1	1	26.5	30.5	2	2_A375_pNL97_plus_lncRNA::1	33	Gene PTPRN2	PTPRP, IAR, PTPRN2, ICAAR, IA-2beta	protein tyrosine phosphatase, receptor type, N polypeptide 2	NM_130842, NM_002847, NM_130843, hCT2282964.0, hCT2282969.0	203029_s_at, 203030_s_at, 211534_x_at	NP_570857.2, NP_002838.2, NP_570858.2, EAX04577.1, EAX04578.1
GeneID:406945	MIR153-2	7	157,367,028	157,367,114	86	-	2	1_A375_pNL7_minus_lncRNA::1::5158, 2_A375_pNL97_plus_lncRNA::1::7421	9450, 9514	downstream, downstream	1	1	27	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene MIR153-2	MIR153-2, MIRN153-2	microRNA 153-2	NR_029689		
GeneID:57488	ESYT2	7	158,523,689	158,622,319	98,630	-	3	1_A375_pNL7_minus_lncRNA::1::5160, 1_A375_pNL7_minus_lncRNA::1::5161, 2_A375_pNL97_plus_lncRNA::1::7423	11023, -49, 10863	in gene, upstream, in gene	1	1	19	21	2	2_A375_pNL97_plus_lncRNA::1	23	Gene ESYT2	ESYT2, E-Syt2, KIAA1228, CHR2SYT, FAM62B	extended synaptotagmin-like protein 2	NM_020728, hCT2282315.0, hCT11253.4	1555829_at, 1555830_s_at, 1556511_s_at, 224698_at, 224699_s_at, 239334_at	NP_065779.1, EAX04590.1, EAX04591.1
GeneID:55112	WDR60	7	158,649,269	158,738,883	89,614	+	2	1_A375_pNL7_minus_lncRNA::1::5162, 2_A375_pNL97_plus_lncRNA::1::7424	-85, -117	upstream, upstream	1	1	46	55	1	2_A375_pNL97_plus_lncRNA::1	55	Gene WDR60	FLJ23575, FLJ10300, WDR60	WD repeat domain 60	NM_018051, hCT1959855.1	1562516_at, 219251_s_at, 229006_at	NP_060521.4, EAX04592.1
GeneID:100507448	LOC100507448	8	1,710,788	1,712,750	1,962	-	2	1_A375_pNL7_minus_lncRNA::1::5163, 2_A375_pNL97_plus_lncRNA::1::7425	1406, 8974	in gene, downstream	1	1	13	11.5	2	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100507448		hypothetical LOC100507448	XR_113103, XR_113104, XR_113102, XR_110091, XR_110092, XR_114132, XR_114133, XR_114134		
GeneID:2055	CLN8	8	1,711,870	1,734,736	22,866	+	2	1_A375_pNL7_minus_lncRNA::1::5163, 2_A375_pNL97_plus_lncRNA::1::7425	-526, -8094	upstream, upstream	1	1	13	11.5	2	2_A375_pNL97_plus_lncRNA::1	16	Gene CLN8	C8orf61, CLN8, FLJ39417, EPMR	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	NM_018941, hCT2291976.1, hCT2351272.0, hCT6131.3	219340_s_at, 219341_at, 222874_s_at, 223912_s_at, 229958_at	NP_061764.2, EAW51478.1, EAW51477.1, EAW51479.1
GeneID:64478	CSMD1	8	2,792,875	4,852,328	2,059,453	-	1	2_A375_pNL97_plus_lncRNA::1::7426	1811720	in gene	0	1	11	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CSMD1	CSMD1, KIAA1890	CUB and Sushi multiple domains 1	NM_033225, hCT2344401.2, hCT2350239.0	1553405_a_at, 1562329_at, 1562330_s_at, 231223_at, 241960_at	NP_150094.5, EAW80463.1, EAW80464.1
GeneID:157285	PRAGMIN	8	8,175,258	8,239,257	63,999	-	4	1_A375_pNL7_minus_lncRNA::1::5164, 1_A375_pNL7_minus_lncRNA::1::5165, 2_A375_pNL97_plus_lncRNA::1::7428, 2_A375_pNL97_plus_lncRNA::1::7429	70745, 29257, 70681, 29230	downstream, in gene, downstream, in gene	1	1	17	17.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene PRAGMIN	DKFZp761P0423, PRAGMIN	homolog of rat pragma of Rnd2	NM_001080826	235085_at	NP_001074295.1
GeneID:54984	PINX1	8	10,622,884	10,697,299	74,415	-	1	2_A375_pNL97_plus_lncRNA::1::7431	83	in gene	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene PINX1	LPTL, LPTS, MGC8850, FLJ20565, PINX1	PIN2-interacting protein 1	NM_017884, hCT10467.4, hCT1963960.1, hCT1964747.1	223907_s_at	NP_060354.4, EAW65596.1, EAW65595.1, EAW65597.1
GeneID:286046	XKR6	8	10,753,654	11,058,875	305,221	-	6	1_A375_pNL7_minus_lncRNA::1::5167, 1_A375_pNL7_minus_lncRNA::1::5168, 1_A375_pNL7_minus_lncRNA::1::5169, 2_A375_pNL97_plus_lncRNA::1::7432, 2_A375_pNL97_plus_lncRNA::1::7433, 2_A375_pNL97_plus_lncRNA::1::7434	211003, 108699, -325, 210971, 108683, -229	in gene, in gene, upstream, in gene, in gene, upstream	1	1	32	40	3	2_A375_pNL97_plus_lncRNA::1	55	Gene XKR6	FLJ31557, XRG6, C8orf7, C8orf21, XKR6, C8orf5	XK, Kell blood group complex subunit-related family, member 6	NM_173683, hCT1647103.4	1553640_at, 1557436_at	NP_775954.2, EAW65599.1
GeneID:66036	MTMR9	8	11,142,000	11,185,655	43,655	+	2	1_A375_pNL7_minus_lncRNA::1::5170, 2_A375_pNL97_plus_lncRNA::1::7435	-144, 48	upstream, in gene	1	1	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MTMR9	MTMR9, MTMR8, DKFZp434K171, MGC126672, C8orf9, LIP-STYX	myotubularin related protein 9	NM_015458, hCT2268686.0, hCT2354201.0, hCT10465.3	204837_at, 213278_at, 233101_at	NP_056273.2, EAW65608.1, EAW65607.1, EAW65609.1
GeneID:83648	FAM167A	8	11,278,973	11,324,276	45,303	-	1	2_A375_pNL97_plus_lncRNA::1::7436	-268	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene FAM167A	DKFZp761G151, MGC120650, D8S265, MGC120651, MGC120649, C8orf13, FAM167A	family with sequence similarity 167, member A	NM_053279, hCT2349278.0	226614_s_at, 233641_s_at	NP_444509.2, EAW65616.1
GeneID:100506990	LOC100506990	8	12,294,549	12,408,558	114,009	+	1	2_A375_pNL97_plus_lncRNA::1::7439	123195	downstream	0	1	6	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100506990		hypothetical LOC100506990	XR_110861		
GeneID:51201	ZDHHC2	8	17,013,836	17,080,241	66,405	+	1	1_A375_pNL7_minus_lncRNA::1::5172	-412	upstream	1	0	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ZDHHC2	ZDHHC2, ZNF372, DHHC2	zinc finger, DHHC-type containing 2	NM_016353, hCT2274220.0, hCT18284.3	1563502_at, 222730_s_at, 222731_at	NP_057437.1, EAW63824.1, EAW63825.1
GeneID:5157	PDGFRL	8	17,433,942	17,500,642	66,700	+	1	1_A375_pNL7_minus_lncRNA::1::5173	46986	in gene	1	0	15	9	1	1_A375_pNL7_minus_lncRNA::1	15	Gene PDGFRL	PDGRL, PRLTS, PDGFRL	platelet-derived growth factor receptor-like	NM_006207, hCT18894.3	205226_at	NP_006198.1, EAW63811.1
GeneID:5108	PCM1	8	17,780,366	17,887,457	107,091	+	2	1_A375_pNL7_minus_lncRNA::1::5174, 2_A375_pNL97_plus_lncRNA::1::7440	-174, -46	upstream, upstream	1	1	16	14	1	1_A375_pNL7_minus_lncRNA::1	16	Gene PCM1	PTC4, PCM1	pericentriolar material 1	NM_006197, hCT2274262.0, hCT2274265.0, hCT19402.3	202174_s_at, 208986_x_at, 208987_x_at, 214118_x_at, 214937_x_at, 226905_at	NP_006188.3, EAW63796.1, EAW63797.1, EAW63798.1
GeneID:427	ASAH1	8	17,913,925	17,942,507	28,582	-	1	2_A375_pNL97_plus_lncRNA::1::7441	768	in gene	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ASAH1	PHP32, FLJ21558, ACDase, ASAH, PHP, ASAH1, FLJ22079, AC	N-acylsphingosine amidohydrolase (acid ceramidase) 1	NM_004315, NM_177924, NM_001127505, hCT2273573.0, hCT2273578.0, hCT2273579.0, hCT19403.3, hCT1958859.1	1555419_a_at, 210979_at, 210980_s_at, 213702_x_at, 213902_at	NP_004306.3, NP_808592.2, NP_001120977.1, EAW63793.1, EAW63794.1, EAW63795.1, EAW63791.1, EAW63792.1
GeneID:55790	CSGALNACT1	8	19,261,672	19,540,261	278,589	-	1	2_A375_pNL97_plus_lncRNA::1::7443	177221	in gene	0	1	8	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene CSGALNACT1	beta4GalNAcT, CSGalNAcT-1, ChGn, CSGALNACT1, FLJ13760, FLJ11264	chondroitin sulfate N-acetylgalactosaminyltransferase 1	NM_018371, NM_001130518, NR_024040, hCT2273325.0, hCT2273326.0, hCT1824454.2	219049_at	NP_060841.5, NP_001123990.1, EAW63770.1, EAW63771.1, EAW63772.1
GeneID:55174	INTS10	8	19,674,918	19,709,589	34,671	+	2	1_A375_pNL7_minus_lncRNA::1::5175, 2_A375_pNL97_plus_lncRNA::1::7445	-102, -70	upstream, upstream	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene INTS10	C8orf35, INT10, INTS10, FLJ10569	integrator complex subunit 10	NM_018142, hCT2274273.0, hCT2274274.0, hCT2274276.0, hCT14667.3, hCT1958858.1	1560172_at, 229632_s_at, 229633_at, 237504_at	NP_060612.2, EAW63765.1, EAW63766.1, EAW63767.1, EAW63768.1, EAW63769.1
GeneID:526	ATP6V1B2	8	20,054,704	20,079,207	24,503	+	1	1_A375_pNL7_minus_lncRNA::1::5176	-48	upstream	1	0	20	16	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ATP6V1B2	ATP6B1B2, VATB, ATP6B2, Vma2, HO57, ATP6V1B2, VPP3	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	NM_001693, hCT2274287.0, hCT14665.3	201089_at	NP_001684.2, EAW63758.1, EAW63759.1
GeneID:80346	REEP4	8	21,995,533	21,999,448	3,915	-	2	1_A375_pNL7_minus_lncRNA::1::5177, 2_A375_pNL97_plus_lncRNA::1::7446	-40, -40	upstream, upstream	1	1	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene REEP4	PP432, FLJ22246, C8orf20, REEP4, FLJ22277	receptor accessory protein 4	NM_025232, hCT2274624.0, hCT2274629.0, hCT2353892.0, hCT14912.3, hCT1964976.1, hCT1964977.1	218777_at	NP_079508.2, EAW63712.1, EAW63710.1, EAW63713.1, EAW63714.1, EAW63715.1, EAW63711.1
GeneID:203190	LGI3	8	22,004,343	22,014,344	10,001	-	2	1_A375_pNL7_minus_lncRNA::1::5177, 2_A375_pNL97_plus_lncRNA::1::7446	14856, 14856	downstream, downstream	1	1	22	19	1	1_A375_pNL7_minus_lncRNA::1	22	Gene LGI3	LGIL4, LGI3	leucine-rich repeat LGI family, member 3	NM_139278, hCT2341193.0, hCT2353935.0	238061_at	NP_644807.1, EAW63708.1, EAW63709.1
GeneID:407037	MIR320A	8	22,102,475	22,102,556	81	-	1	2_A375_pNL97_plus_lncRNA::1::7447	-15	upstream	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene MIR320A	MIRN320A, MIRN320, hsa-mir-320a, MIR320A	microRNA 320a	NR_029714		
GeneID:661	POLR3D	8	22,102,619	22,108,680	6,061	+	1	2_A375_pNL97_plus_lncRNA::1::7447	-48	upstream	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene POLR3D	TSBN51, RPC53, BN51T, POLR3D, RPC4	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	NM_001722, hCT2275706.0, hCT2275707.0, hCT2353919.0, hCT1825218.3	208361_s_at	NP_001713.2, EAW63692.1, EAW63689.1, EAW63690.1, EAW63691.1
GeneID:100507071	LOC100507071	8	22,112,089	22,132,675	20,586	-	1	2_A375_pNL97_plus_lncRNA::1::7447	30104	downstream	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC100507071		hypothetical LOC100507071	XR_113112, XR_110863, XR_114151		
GeneID:23516	SLC39A14	8	22,224,762	22,291,642	66,880	+	1	2_A375_pNL97_plus_lncRNA::1::7448	26022	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SLC39A14	cig19, NET34, SLC39A14, LZT-Hs4, ZIP14, KIAA0062	solute carrier family 39 (zinc transporter), member 14	NM_015359, NM_001128431, NM_001135153, NM_001135154, hCT2275710.0, hCT2275712.0, hCT7028.2, hCT1964912.1	1555433_at, 1555434_a_at, 212110_at	NP_056174.2, NP_001121903.1, NP_001128625.1, NP_001128626.1, EAW63680.1, EAW63682.1, EAW63681.1, EAW63683.1
GeneID:55909	BIN3	8	22,477,931	22,526,661	48,730	-	1	2_A375_pNL97_plus_lncRNA::1::7449	101	in gene	0	1	12	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene BIN3	MGC14978, BIN3	bridging integrator 3	NM_018688, hCT2274144.0, hCT2274149.0, hCT1964905.1, hCT1964906.1, hCT1964907.0, hCT1964908.1, hCT1964909.1	1557582_at, 222199_s_at	NP_061156.1, EAW63655.1, EAW63650.1, EAW63651.1, EAW63652.1, EAW63654.1, EAW63653.1, EAW63656.1
GeneID:157310	PEBP4	8	22,570,765	22,785,421	214,656	-	2	2_A375_pNL97_plus_lncRNA::1::7450, 2_A375_pNL97_plus_lncRNA::1::7451	183293, 176813	in gene, in gene	0	1	9	15	2	2_A375_pNL97_plus_lncRNA::1	17	Gene PEBP4	PRO4408, MGC22776, CORK-1, hPEBP4, PEBP-4, GWTM1933, PEBP4, CORK1	phosphatidylethanolamine-binding protein 4	NM_144962, hCT7029.3	227848_at	NP_659399.2, EAW63647.1
GeneID:100507139	LOC100507139	8	22,612,323	22,615,705	3,382	+	2	2_A375_pNL97_plus_lncRNA::1::7450, 2_A375_pNL97_plus_lncRNA::1::7451	-10195, -3715	upstream, upstream	0	1	9	15	2	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100507139		hypothetical LOC100507139	XR_110867		
GeneID:203069	R3HCC1	8	23,145,612	23,153,792	8,180	+	2	1_A375_pNL7_minus_lncRNA::1::5178, 2_A375_pNL97_plus_lncRNA::1::7452	52, 20	in gene, in gene	1	1	22	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene R3HCC1	R3HCC1, DKFZp564N123	R3H domain and coiled-coil containing 1	NM_001136108	212866_at, 35156_at	NP_001129580.1
GeneID:4017	LOXL2	8	23,154,410	23,261,722	107,312	-	2	1_A375_pNL7_minus_lncRNA::1::5178, 2_A375_pNL97_plus_lncRNA::1::7452	116056, 116090	downstream, downstream	1	1	22	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene LOXL2	LOXL2, LOR2, WS9-14	lysyl oxidase-like 2	NM_002318, hCT2274128.0, hCT2274129.0, hCT7729.3	1562263_at, 202997_s_at, 202998_s_at, 202999_s_at, 228808_s_at	NP_002309.1, EAW63625.1, EAW63626.1, EAW63627.1
GeneID:51312	SLC25A37	8	23,386,363	23,430,063	43,700	+	1	1_A375_pNL7_minus_lncRNA::1::5179	12773	in gene	1	0	19	13	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SLC25A37	HT015, MSCP, MFRN, MFRN1, PRO1278, MSC, SLC25A37, PRO1584, PRO2217	solute carrier family 25, member 37	NM_016612	218136_s_at, 218978_s_at, 221920_s_at, 222528_s_at, 222529_at, 226179_at, 226928_x_at, 228527_s_at, 231274_s_at, 242335_at	NP_057696.2
GeneID:80005	DOCK5	8	25,042,287	25,270,619	228,332	+	1	2_A375_pNL97_plus_lncRNA::1::7454	3081	in gene	0	1	9	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DOCK5	DKFZp761J211, DKFZp779M164, DOCK5, DKFZp451J181	dedicator of cytokinesis 5	NM_024940, hCT2273023.0, hCT2273026.0, hCT6517.3	1561276_at, 1569590_at, 1570078_a_at, 219921_s_at, 222721_at, 230206_at, 230207_s_at, 230263_s_at	NP_079216.4, EAW63595.1, EAW63593.1, EAW63594.1
GeneID:54793	KCTD9	8	25,285,363	25,315,984	30,621	-	2	1_A375_pNL7_minus_lncRNA::1::5180, 2_A375_pNL97_plus_lncRNA::1::7455	-640, -624	upstream, upstream	1	1	33	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene KCTD9	FLJ20038, KCTD9	potassium channel tetramerisation domain containing 9	NM_017634, hCT2272952.0, hCT2272954.0, hCT2272955.0, hCT1814491.2	218823_s_at, 224316_at	NP_060104.2, EAW63589.1, EAW63587.1, EAW63588.1, EAW63590.1
GeneID:157313	CDCA2	8	25,316,513	25,365,425	48,912	+	2	1_A375_pNL7_minus_lncRNA::1::5180, 2_A375_pNL97_plus_lncRNA::1::7455	111, 95	in gene, in gene	1	1	33	38	1	2_A375_pNL97_plus_lncRNA::1	38	Gene CDCA2	MGC129907, Repo-Man, CDCA2, MGC129906, FLJ25804	cell division cycle associated 2	NM_152562	226661_at, 236957_at	NP_689775.2
GeneID:5520	PPP2R2A	8	26,149,007	26,230,196	81,189	+	1	1_A375_pNL7_minus_lncRNA::1::5181	91393	downstream	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene PPP2R2A	FLJ41727, PR55A, PR52A, B55A, MGC52248, B55-ALPHA, B55ALPHA, PPP2R2A, FLJ26613, DKFZp686N05117	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	NM_001177591, NM_002717, hCT2274996.0, hCT2274998.0, hCT8210.3, hCT1964921.1	202313_at, 236492_at, 237636_at	NP_001171062.1, NP_002708.1, EAW63577.1, EAW63578.1, EAW63579.1, EAW63580.1
GeneID:665	BNIP3L	8	26,240,523	26,270,644	30,121	+	1	1_A375_pNL7_minus_lncRNA::1::5181	-123	upstream	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene BNIP3L	NIX, BNIP3a, BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	NM_004331, hCT1690263.3	221478_at, 221479_s_at	NP_004322.1, EAW63576.1
GeneID:1808	DPYSL2	8	26,435,421	26,515,693	80,272	+	1	2_A375_pNL97_plus_lncRNA::1::7456	-957	upstream	0	1	5	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DPYSL2	CRMP2, DHPRP2, DRP-2, DPYSL2, DRP2	dihydropyrimidinase-like 2	NM_001386, hCT2275002.0, hCT8209.3	200762_at	NP_001377.1, EAW63573.1, EAW63574.1
GeneID:55872	PBK	8	27,667,138	27,695,349	28,211	-	2	1_A375_pNL7_minus_lncRNA::1::5182, 2_A375_pNL97_plus_lncRNA::1::7457	37, 53	in gene, in gene	1	1	23	20	1	1_A375_pNL7_minus_lncRNA::1	23	Gene PBK	CT84, Nori-3, TOPK, PBK, SPK, FLJ14385	PDZ binding kinase	NM_018492, hCT8336.4, hCT1961592.1	219148_at	NP_060962.2, EAW63535.1, EAW63537.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervals	Intervals	Intervals Count	Intervals Distance	Intervals Position	[A]	[B]	[C]	[D]	Accession Reg Count	Feature Sample	Feature Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene:ID:2	SCARA5	8	27,727,736	27,850,166	122,462	+	1	2_A375_shLS7_dtct_locRNA:1:7496		120162	st gene	0	1	10	16	1	2_A375_shLS7_dtct_locRNA:1		Gene SCARA5	SCARA5, Tcc, NET33, FLJ23907, MGC45780	Scavenger receptor class A, member 5 (putative)	NM_173553, NCT23509712.0, NCT23529269.0, NCT 1648131.3	1864703_at, 236639_at, 236639_at	NP_776194.2, EAW63534.1, EAW63532.1, EAW63533.1
Gene:ID:3	INTS9	8	28,625,175	28,747,898	122,523	-	2	1_A375_shLS7_dtct_locRNA:1:3165, 2_A375_shLS7_dtct_locRNA:1:7496		-121, -110	upstream, upstream	1	1	10	24	1	2_A375_shLS7_dtct_locRNA:1		Gene INTS9	CPSF2L, RC-74, INTS, FLJ10571, RC74,	Integrator complex subunit 9	NM_001172992, NM_015350, NM_001165156, NCT23529269.0, NCT23579210.0, NCT23539490.0, NCT23539.2	202841_at, 237266_at	NP_001159653.1, NP_056720.2, NP_001158531.1, EAW63506.1, EAW63505.1, EAW63506.1
Gene:ID:7	HMBOX1	8	28,747,911	28,910,242	162,331	+	2	1_A375_shLS7_dtct_locRNA:1:3165, 2_A375_shLS7_dtct_locRNA:1:7481		-62, -103	upstream, upstream	1	1	16	24	1	2_A375_shLS7_dtct_locRNA:1		Gene HMBOX1	HMBOX1, FBHNP, FLJ21616, HNFTLA	homeobox containing 1	NM_024567, NM_001135726, NCT23529453.1, NCT23529496.1, NCT23529477.1, NCT23529461.1, NCT23529483.0, NCT23529469.0, NCT23529.2	219269_at	NP_078843.2, NP_001129193.1, EAW63496.1, EAW63498.1, EAW63501.1, EAW63502.1, EAW63497.1, EAW63498.1, EAW63500.1
Gene:ID:1	DUSP4	8	28,192,811	28,208,165	14,874	-	1	2_A375_shLS7_dtct_locRNA:1:7482		1609	st gene	0	1	8	15	1	2_A375_shLS7_dtct_locRNA:1		Gene DUSP4	TYP, MKP2, HVH2, MKP-2, DUSP4	dual specificity phosphatase 4	NM_001394, NM_001135, NCT23742626.0, NCT 1639803.3, NCT 1661543.1, NCT 1664811.1	204014_at, 204015_s_at	NP_476997.1, NP_001128.1, EAW63481.1, EAW63482.1, EAW63483.1, EAW63484.1
Gene:ID:1	DCTN6	8	30,013,813	30,041,660	27,387	+	2	1_A375_shLS7_dtct_locRNA:1:3166, 2_A375_shLS7_dtct_locRNA:1:7496		78, 123	st gene, ut gene	1	1	22	16	1	1_A375_shLS7_dtct_locRNA:1		Gene DCTN6	p27, WB3, DCTN6, p27, WB-3	dynactin 6	NM_006570, NCT 1753124	203261_at	NP_006562.1, EAW63496.1
Gene:ID:3	PPP2CB	8	30,643,126	30,670,252	27,126	-	2	1_A375_shLS7_dtct_locRNA:1:3166, 2_A375_shLS7_dtct_locRNA:1:7496		16, -50	st gene, upstream	1	1	38	32	1	2_A375_shLS7_dtct_locRNA:1		Gene PPP2CB	PPP2CB, PP2CB, PP2Abeta	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	NM_001009552, NCT23625310.0, NCT23625560.0, NCT23625552.0, NCT23625562.0	201370_s_at, 201375_s_at	NP_001009552.1, EAW63436.1, EAW63433.1, EAW63434.1, EAW63435.1
Gene:ID:8	FUT10	8	33,235,582	33,330,664	102,322	+	2	1_A375_shLS7_dtct_locRNA:1:3191, 2_A375_shLS7_dtct_locRNA:1:7493		-24, -56	upstream, upstream	1	1	22	23	1	2_A375_shLS7_dtct_locRNA:1		Gene FUT10	MGC11161, FUT10	fucosyltransferase 10 (alpha (1,2) fucosyltransferase)	NM_032666, NCT22771730.0, NCT23509910.0, NCT 1624555.1, NCT 1664946.1	223879_at, 225472_at, 239520_at	NP_116053.2, EAW63453.1, EAW63451.1, EAW63452.1, EAW63454.1
Gene:ID:8	C8orf61	8	33,359,233	33,370,703	14,470	-	2	1_A375_shLS7_dtct_locRNA:1:3192, 2_A375_shLS7_dtct_locRNA:1:7496		-192, -145	upstream, upstream	1	1	51	40	1	1_A375_shLS7_dtct_locRNA:1		Gene C8orf61	C8orf61, FLJ23263	chromosome 8 open reading frame 61	NM_025119, NM_001163401, NCT 1624551.1, NCT 1664944.1, NCT 1664948.1	218124_at	NP_079391.2, NP_001158871.1, EAW63397.1, EAW63398.1, EAW63399.1
Gene:ID:8	RAB11FIP1	8	27,716,663	27,757,015	40,350	-	2	1_A375_shLS7_dtct_locRNA:1:3182, 2_A375_shLS7_dtct_locRNA:1:7496		49527, 49493	downstream, downstream	1	1	17	16	1	2_A375_shLS7_dtct_locRNA:1		Gene RAB11FIP1	MGC76466, eb11-FIP1, D4S234E/EZH2 f-t, FLJ22339, NOEL1A, RCP, FLJ22622, RAB11FIP1	RAB11 family interacting protein 1 (class I)	NM_001002814, NM_020181, NCT22716230.1, NCT22716231.1, NCT 1621.2	219661_s_at, 221177_at, 221630_s_at	NP_001002814.2, NP_064477.4, EAW63347.1, EAW63348.1, EAW63349.1
Gene:ID:9	ASH2L	8	27,963,011	27,997,228	34,217	+	2	1_A375_shLS7_dtct_locRNA:1:3190, 2_A375_shLS7_dtct_locRNA:1:7496		-38, -99	upstream, upstream	1	1	22	24	1	2_A375_shLS7_dtct_locRNA:1		Gene ASH2L	ASH2L1, ASH2L1, ASH2L, Bre2, ASH2	ash2 (absent, small, or homeotic)-like (Drosophila)	NM_004674, NM_001105214, NCT23525902.0, NCT 1624556.2, NCT19855122.1, NCT19855181.1	209517_s_at	NP_004665.2, NP_001098654.1, EAW63336.1, EAW63337.1, EAW63338.1, EAW63340.1, EAW63339.1
Gene:ID:2	DDHD2	8	38,099,009	38,120,287	31,278	+	2	1_A375_shLS7_dtct_locRNA:1:3197, 2_A375_shLS7_dtct_locRNA:1:7479		47, 175	st gene, ut gene	1	1	20	21	1	2_A375_shLS7_dtct_locRNA:1		Gene DDHD2	SAMWD1, DDHD2, KIAA0725	DDHD domain containing 2	NM_015214, NM_001164232, NM_001164234, NCT23727116.0, NCT 1629442.2	212690_at	NP_056029.2, NP_001157104.1, NP_001157106.1, EAW63224.1, EAW63224.2
Gene:ID:2	PGRP1	8	38,266,659	38,326,252	57,886	-	1	2_A375_shLS7_dtct_locRNA:1:7471		164	st gene	0	1	11	15	1	2_A375_shLS7_dtct_locRNA:1		Gene PGRP1	N-SAM, CE6, PGRP, FLJ46998, FLG, CD321, FLT2, FGFR1, OGD, KAJ2, HBGFR, BFGFR	fibroblast growth factor receptor 1	NM_015650, NM_023109, NM_023103, NM_022110, NM_001174853, NM_001174854, NM_001174855, NM_001174856, NM_001174857, NCT22718222.0, NCT22719226.0, NCT23529103.0, NCT23529811.0, NCT23529120.0, NCT23529813.0, NCT23529114.0, NCT 1629.2, NCT19851540.1, NCT 19851540.1	207622_at, 207627_s_at, 210973_s_at, 211526_s_at, 215404_s_at, 221164_at, 238703_at	NP_056844.2, NP_075994.1, NP_075993.1, NP_071859.2, NP_001157535.1, NP_001157536.1, NP_001157537.1, NP_001157538.1, EAW63303.1, EAW63304.1, EAW63305.1, EAW63306.1, EAW63307.1, EAW63308.1, EAW63309.1, EAW63310.1, EAW63311.1, EAW63312.1, EAW
Gene:ID:2	ANK1	8	41,510,744	41,754,280	243,536	-	1	2_A375_shLS7_dtct_locRNA:1:3201, 2_A375_shLS7_dtct_locRNA:1:5322, 2_A375_shLS7_dtct_locRNA:1:7474		176524, 660, 712	st gene, ut gene, ut gene	1	1	22	16.5	2	2_A375_shLS7_dtct_locRNA:1		Gene ANK1	SPH1, ANK, ANK1, SPH2	ankyrin 1, erythrocytic	NM_020478, NM_020477, NM_000037, NM_020479, NM_001142445, NM_001142446, NM_020478, NM_020480, NCT22730321.1, NCT22730322.1, NCT22730324.1, NCT22730326.1, NCT22730327.1, NCT22730328.1, NCT22730340.1, NCT22730341.1, NCT22730344.1, NCT22730345.2	203509_s_at, 203510_at, 203511_at, 203512_s_at, 203513_s_at, 203514_at, 203515_at, 203516_s_at, 203517_s_at, 203518_s_at	NP_065358.2, NP_065210.2, NP_001113917.1, NP_001113918.1, NP_000028.3, NP_065208.2, NP_065212.2, EAW63240.1, EAW63242.1, EAW63243.1, EAW63244.1, EAW63245.1, EAW63246.1, EAW63247.1, EAW63248.1, EAW63249.1, EAW63250.1
Gene:ID:3	IKBKB	8	42,126,620	42,190,171	61,351	+	1	1_A375_shLS7_dtct_locRNA:1:3203		6718	downstream	1	0	15	10	1	1_A375_shLS7_dtct_locRNA:1		Gene IKBKB	FLJ30509, IKK-beta, FLJ36216, MGC131051, FLJ23771, IKK2, NFKBIKB, FLJ35366, IKKB, KIAA0	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	NM_001190720, NM_001190721, NM_001190722, NM_001556, NM_023515, NM_033516, NR_033520, NCT22729200.0, NCT22729221.0, NCT23529810.0, NCT23529814.0, NCT23529.2	203351_s_at, 203352_s_at, 203353_s_at, 210727_x_at	NP_001177449.1, NP_001177450.1, NP_001547.1, NP_001177451.1, EAW63222.1, EAW63223.1, EAW63224.1, EAW63229.1
Gene:ID:5	POLB	8	42,199,030	42,229,213	30,183	+	1	1_A375_shLS7_dtct_locRNA:1:3203		-62	upstream	1	0	15	10	1	1_A375_shLS7_dtct_locRNA:1		Gene POLB	MGC129976, POLB	polymerase (DNA directed), beta	NM_002690, NCT5442.3	203619_at	NP_002681.1, EAW63221.1
Gene:ID:2	PNTA	8	42,911,842	42,940,831	29,489	+	2	1_A375_shLS7_dtct_locRNA:1:3204, 2_A375_shLS7_dtct_locRNA:1:7473		37562, 37562	downstream, downstream	1	1	21	23	1	2_A375_shLS7_dtct_locRNA:1		Gene PNTA	MGC99550, PNTA, PGGT1A, PPTA, PTAR2	hexokinase/ribokinase, CAAX box, alpha	NM_002627, NM_033968, NCT22710910.0, NCT22710921.0, NCT23539390.0, NCT23539372.0	200090_at, 208471_s_at, 208505_at	NP_002618.1, EAW63166.1, EAW63169.1, EAW63190.1, EAW63191.1, EAW63192.1
Gene:ID:6	SGK196	8	42,948,657	42,978,323	29,666	+	2	1_A375_shLS7_dtct_locRNA:1:3204, 2_A375_shLS7_dtct_locRNA:1:7473		367, 367	downstream, ut gene	1	1	21	23	1	2_A375_shLS7_dtct_locRNA:1		Gene SGK196	MGC126597, FLJ33396	protein kinase-like protein SgK196	NM_032237, NCT19419732.2	1553249_a_at	NP_115613.1, EAW63187.1
Gene:ID:2	KIAA0146	8	48,173,542	48,648,475	474,933	+	1	2_A375_shLS7_dtct_locRNA:1:7476		477962	downstream	0	1	9	16	1	2_A375_shLS7_dtct_locRNA:1		Gene KIAA0146	KIAA0146		NM_001080394	212633_s_at, 225123_at, 236246_at	NP_001073863.1
Gene:ID:1	CEBPD	8	48,649,476	48,650,726	1,250	-	1	2_A375_shLS7_dtct_locRNA:1:7476		-776	upstream	0	1	9	16	1	2_A375_shLS7_dtct_locRNA:1		Gene CEBPD	CRP3, CEBP-delta, NF-IL6-beta, CEBPD, CELP	CCAAT/enhancer binding protein (C/EBP), delta	NM_005195, NCT5382.3	201973_s_at, 215053_s_at, 215059_at	NP_005180.2, EAW65079.1
Gene:ID:3	PRKDC	8	48,665,669	48,872,743	167,074	-	1	2_A375_shLS7_dtct_locRNA:1:7477		401	upstream	0	1	23	35	1	2_A375_shLS7_dtct_locRNA:1		Gene PRKDC	XRCC7, HYRC, DNPK1, DNA-PKcs, DNAPK, p350, PRKDC, HYRC1	protein kinase, DNA-activated, catalytic polypeptide	NM_006904, NM_001081640, NCT22971291.1, NCT23371127.1, NCT23371128.1, NCT19419437.2	209644_at, 210343_s_at, 211394_s_at	NP_008835.3, NP_001079109.1, EAW66980.1, EAW66981.1, EAW66982.1, EAW66983.1
Gene:ID:4	MCM4	8	48,813,494	48,890,866	16,874	+	1	2_A375_shLS7_dtct_locRNA:1:7477		-150	upstream	0	1	23	38	1	2_A375_shLS7_dtct_locRNA:1		Gene MCM4	CDC54, MCM4, hCdc21, P1-CDC21, CDC21, MGC33130	minichromosome maintenance complex component 4	NM_182746, NM_005914, NCT23965910.0, NCT23965999.0, NCT19251.2	212141_at, 212142_at, 222036_s_at, 224327_at	NP_874372.1, NP_005900.2, EAW66864.1, EAW66865.1, EAW66866.1
Gene:ID:7	UBE2V2	8	48,930,993	48,974,454	53,459	+	1	1_A375_shLS7_dtct_locRNA:1:3203		29	st gene	1	0	21	12	1	1_A375_shLS7_dtct_locRNA:1		Gene UBE2V2	UBE2V2, LIEI/2, DDVI-1, EDAF-1, EDPF1, DDVIT1, LIEI-2, EDPF-1, HMS2	ubiquitin-conjugating enzyme E2 variant 2	NM_003350, NCT22965512.0, NCT23653402.0, NCT23653407.0, NCT19459.2.3	200096_at	NP_003331.1, EAW66982.1, EAW66987.1, EAW66988.1, EAW66989.1
Gene:ID:5	LOC5443 34	8	49,620,194	49,626,830	6,636	+	3	1_A375_shLS7_dtct_locRNA:1:3200, 2_A375_shLS7_dtct_locRNA:1:7480, 2_A375_shLS7_dtct_locRNA:1:7480		7556, 7556, 10962	upstream, upstream, downstream	1	1	16	12	2	1_A375_shLS7_dtct_locRNA:1		Gene LOC544334		basal cell-1-like protein 5-like	NM_001114697, NM_527697, XM_537001		NP_001114169.2, NP_922950.4, XP_542934.4
Gene:ID:9	SNAI2	8	49,630,236	49,633,898	3,752	+	1	1_A375_shLS7_dtct_locRNA:1:7481		132	st gene	0	1	11	15	1	2_A375_shLS7_dtct_locRNA:1		Gene SNAI2	SNAI2, SLUG, WS2D, MGC10102, SLUGH1	snail homolog 2 (Drosophila)	NM_003068, NCT23469.3	213139_at	NP_003059.1, EAW65700.1
Gene:ID:3	SNTG1	8	50,624,997	51,703,427	660,830	+	4	1_A375_shLS7_dtct_locRNA:1:3207, 2_A375_shLS7_dtct_locRNA:1:7482, 2_A375_shLS7_dtct_locRNA:1:7483, 2_A375_shLS7_dtct_locRNA:1:7484		-292, -309, 149635, 631371	upstream, upstream, upstream, ut gene, ut gene	1	1	12.67	23	3	2_A375_shLS7_dtct_locRNA:1		Gene SNTG1	SNTG1, SYN4I, G1SYN	syntrophin, gamma 1	NM_018967, NCT22964440.0, NCT22964470.0, NCT 1621.2	1562267_at, 235403_at, 236918_s_at	NP_061840.1, EAW65704.1, EAW65705.1, EAW65706.1
Gene:ID:1	PXDNL	8	52,232,137	52,722,005	489,868	+	2	1_A375_shLS7_dtct_locRNA:1:3205, 2_A375_shLS7_dtct_locRNA:1:7498		414821, 414557	ut gene, ut gene	1	1	24	23	1	1_A375_shLS7_dtct_locRNA:1		Gene PXDNL	PXDNL, VPO2, FLJ25451	peroxidasin homolog (Drosophila)-like	NM_144651, NCT23566590.0, NCT19505095.2	241642_at	NP_653253.2, EAW66708.1, EAW66707.1
Gene:ID:1	PCMTD1	8	52,730,140	52,811,725	81,585	+	1	2_A375_shLS7_dtct_locRNA:1:7498		-281	upstream	0	1	14	16	1	2_A375_shLS7_dtct_locRNA:1		Gene PCMTD1	PCMTD1, FLJ10553	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	NM_052837, NCT22565590.0, NCT22565603.0, NCT23566774.0, NCT 1623.2	235119_at, 235262_s_at, 235407_at, 236114_at, 240706_at	NP_443149.2, EAW65711.1, EAW65710.1, EAW65712.1, EAW65713.1
Gene:ID:1	LOC1002 37213	8	52,811,842	53,859,733	47,891	+	1	2_A375_shLS7_dtct_locRNA:1:7498		174	ut gene	0	1	14	16	1	2_A375_shLS7_dtct_locRNA:1		Gene LOC100237213		hypothetical protein LOC100237213	XM_002342651		NP_002342692.2
Gene:ID:2	FAM150A	8	53,446,597	53,478,621	31,824	-	1	2_A375_shLS7_dtct_locRNA:1:7497		29157	st gene	0	1	11	16	1	2_A375_shLS7_dtct_locRNA:1		Gene FAM150A	MGC163315, FAM150A, UNQ6403, MGC163313	family with sequence similarity 150, member A	NM_207413		NP_997296.1
Gene:ID:9	RB1CC1	8	53,535,018	53,627,026	92,008	-	2	1_A375_shLS7_dtct_locRNA:1:7498, 2_A375_shLS7_dtct_locRNA:1:7498		1110, -302	st gene, upstream	1	1	13	19.5	2	2_A375_shLS7_dtct_locRNA:1		Gene RB1CC1	FIP200, CC1, RB1CC1	RB1-inducible coiled-coil 1	NM_014781, NM_001083617, NCT23565503.0, NCT 1623.7	202033_s_at, 202034_s_at	NP_055992.3, NP_001077066.1, EAW66719.1, EAW66720.1, EAW66721.1
Gene:ID:5	RGS20	8	54,764,366	54,971,863	107,695	+	3	1_A375_shLS7_dtct_locRNA:1:3210, 2_A375_shLS7_dtct_locRNA:1:7495, 2_A375_shLS7_dtct_locRNA:1:7495		28580, 28720, 28376	st gene, ut gene, ut gene	1	1	13.5	16	2	1_A375_shLS7_dtct_locRNA:1		Gene RGS20	ZGAP1, RGS21, RGS20	regulator of G-protein signaling 20	NM_170587, NM_003702, NCT22965422.0, NCT23529267.2, NCT19829403.1, NCT19829561.1, NCT19829622.1	1569303_s_at, 210106_at	NP_733969.1, NP_003692.2, EAW66734.1, EAW66736.1, EAW66737.1, EAW66738.1, EAW66735.1
Gene:ID:6	TCEA1	8	54,879,116	54,933,008	53,892	+	2	1_A375_shLS7_dtct_locRNA:1:3211, 2_A375_shLS7_dtct_locRNA:1:7495		66, 64	st gene, ut gene	1	1	16.5	16	1	2_A375_shLS7_dtct_locRNA:1		Gene TCEA1	TCEA, GTF2S, S9, TFIIS, TF2S, TCEA1	transcription elongation factor A (SII), 1	NM_006756, NM_201437, NCT22953483.0, NCT23573346.0, NCT19914371.1	1866207_at, 1866208_at, 216241_s_at	NP_006747.1, NP_958846.1, EAW66729.1, EAW66740.1, EAW66741.1
Gene:ID:2	MRPL15	8	55,047,761	55,061,874	13,282	+	2	1_A375_shLS7_dtct_locRNA:1:3212, 2_A375_shLS7_dtct_locRNA:1:7496		16171, 16267	downstream, downstream	1	1	26	17	1	1_A375_shLS7_dtct_locRNA:1		Gene MRPL15	MRP-L15, MRPL15, RPML7, L15mt, MRP-L7, HSPC145	mitochondrial ribosomal protein L15	NM_014175, NCT23167.2	218027_at	NP_054894.1, EAW65747.1
Gene:ID:1	XKR4	8	55,615,017	56,438,714	823,697	+	2	1_A375_shLS7_dtct_locRNA:1:3214, 2_A375_shLS7_dtct_locRNA:1:7496		471, 535	ut gene, ut gene	1	1	22	46	1	2_A375_shLS7_dtct_locRNA:1		Gene XKR4	XKR4, KIAA1659, XRG4	XK, Kell blood group complex subunit-related family, member 4	NM_052898	227002_at	NP_443130.1
Gene:ID:1	TMEM66	8	56,651,320	56,663,885	24,566	-	2	1_A375_shLS7_dtct_locRNA:1:3215, 2_A375_shLS7_dtct_locRNA:1:7496		61, 13	st gene, ut gene	1	1	16	21	1	2_A375_shLS7_dtct_locRNA:1		Gene TMEM66	TMEM66, FLJ22276, MGC67776	transmembrane protein 66	NM_182417, NCT22972450.0, NCT23969767.0, NCT 1623.0	236463_at, 237636_at	NP_872313.2, EAW67960.1, EAW67956.1, EAW66739.1
Gene:ID:6	TGS1	8	56,663,791	56,730,005	52,214	+	2	1_A375_shLS7_dtct_locRNA:1:3215, 2_A375_shLS7_dtct_locRNA:1:7496		33, 61	st gene, ut gene	1	1	16	21	1	2_A375_shLS7_dtct_locRNA:1		Gene TGS1	FLJ22985, MCD4eIF, PIPMT, DKFZp762A163, PIMT, TGS1	trimethylguanosine synthase 1	NM_024831, NCT22970001.0, NCT23969540.0, NCT19316499.2	218231_at, 236371_s_at, 236396_s_at	NP_079107.6, EAW65763.1, EAW65761.1, EAW66762.1
Gene:ID:5	RPS30	8	56,980,739	56,987,140	6,401	-	2	1_A375_shLS7_dtct_locRNA:1:3216, 2_A375_shLS7_dtct_locRNA:1:7497		-28, -28	upstream, upstream	1	1	100	143	2	1_A375_shLS7_dtct_locRNA:1		Gene RPS30	MGC102630, RPS30, S30, FLJ27481	ribosomal protein S30	NM_001032, NM_001146227, NCT23565.3, NCT19852251.1, NCT19852353.1	200589_s_at, 214003_x_at	NP_001014.1, NP_001138699.1, EAW65770.1, EAW65771.1, EAW65772.1
Gene:ID:2	SNORD64	8	56,986,298	56,986,460	62	-	2	1_A375_shLS7_dtct_locRNA:1:3216, 2_A375_shLS7_dtct_locRNA:1:7496		-706, -706	upstream, upstream	1	1	100	143	2	1_A375_shLS7_dtct_locRNA:1		Gene SNORD64	U64, SNORD64, RNU64	small nucleolar RNA, C/D box 64	NR_002437		
Gene:ID:3	PLAG1	8	57,073,466	57,123,699	50,391	+	1	2_A375_shLS7_dtct_locRNA:1:7498		477	upstream	0	1	10	13	1	2_A375_shLS7_dtct_locRNA:1		Gene PLAG1	PLAG1, PSA, ZNF912, SGPA	pleiomorphic adenoma gene 1	NM_002655, NM_001114634, NM_001114635, NCT22982870.0, NCT 1623.2	205722_at	NP_002646.2, NP_001108108.1, NP_001108107.1, EAW66773.1, EAW66774.1
Gene:ID:5	CHCHD7	8	57,124,213	57,131,178	6,892	+	1	2_A375_shLS7_dtct_locRNA:1:7498		421	st gene	0	1	10	13	1	2_A375_shLS7_dtct_locRNA:1		Gene CHCHD7	CHCHD7, MGC2217, FLJ40866	coiled-coil-helix-coiled-coil-helix domain containing 7	NM_001031667, NM_001031666, NM_001031668, NM_001031670, NM_001031671, NM_024000, NCT23565602.0, NCT23565609.0, NCT23565710.0, NCT 2018.0	219542_s_at, 222701_s_at	NP_001031667.1, NP_001031666.1, NP_001031668.1, NP_001031670.1, NP_001031671.1, NP_077276.2, EAW66776.1, EAW66777.1, EAW66778.1, EAW66779.1
Gene:ID:3	PENK	8	57,353,513	57,359,282	5,769	+	1	2_A375_shLS7_dtct_locRNA:1:7499		1258	st gene	0	1	8	21	1	2_A375_shLS7_dtct_locRNA:1		Gene PENK	PENK	proenkephalin	NM_006211, NM_001135690, NCT22982102.0, NCT22982333.0, NCT 2006.3	211791_at	NP_006202.1, NP_001128162.1, EAW66782.1, EAW66783.1, EAW66784.1
Gene:ID:1	UBXN2B	8	58,223,623	59,064,060	40,437	+	1	2_A375_shLS7_dtct_locRNA:1:7501		61	st gene	0	1	8	16	1	2_A375_shLS7_dtct_locRNA:1		Gene UBXN2B	UBXN2B, p37	UBX domain protein 2B	NM_001079818	212634_at	NP_001073057.1
Gene:ID:5	NSMAF	8	58,995,053	59,072,604	76,541	+	1	2_A375_shLS7_dtct_locRNA:1:7501		564	st gene	0	1	16	16	1	2_A375_shLS7_dtct_locRNA:1		Gene NSMAF	FAN, NSMAF	neutral sphingomyelinase (N-SMase) activator associated factor	NM_003550, NM_001164572, NCT19914466.1	1555773_s_at, 1563269_at, 232106_at, 232109_s_at	NP_003571.2, NP_001138248.1, EAW66517.1
Gene:ID:7	TOX	8	59,717,977	60,031,767	313,790	+	1	1_A375_shLS7_dtct_locRNA:1:3213		317466	downstream	1	0	14	16	1	1_A375_shLS7_dtct_locRNA:1		Gene TOX	TOX, KIAA0808, TOX1	thymocyte selection-associated high mobility group box	NM_014729, NCT22737516.0, NCT 1699.2	1554554_a_at, 1554555_at	NP_055544.1, EAW66519.1, EAW66518.1
Gene:ID:1	LOC1003 38532	8	61,315,771	61,329,277	10,866	+	2	2_A375_shLS7_dtct_locRNA:1:3214, 2_A375_shLS7_dtct_locRNA:1:7502		201, -2581	st gene, upstream	1	1	14	16	2	2_A375_shLS7_dtct_locRNA:1		Gene LOC100038532		hypothetical LOC100038532	XR_112148, XR_110912, XR_114175	240429_x_at, 240430_s_at	
Gene:ID:1	CLVS1	8	62,200,523	62,414,200	213,678	+	4	1_A375_shLS7_dtct_locRNA:1:3222, 1_A375_shLS7_dtct_locRNA:1:3221, 2_A375_shLS7_dtct_locRNA:1:7506, 2_A375_shLS7_dtct_locRNA:1:7506		307, 208275, 265, 208371	st gene, ut gene, ut gene, ut gene	1	1	22	40.5	2	2_A375_shLS7_dtct_locRNA:1		Gene CLVS1	CRALBP1, FLJ37288, MGC33696, CLVS1, RLBP1L1	clavesin 1	NM_173519, NCT23567727.0, NCT 1627.2	230217_at	NP_775743.1, EAW66530.1, EAW66531.1
Gene:ID:4	ASPH	8	62,413,113	62,627,189	214,084	+	6	1_A375_shLS7_dtct_locRNA:1:3223, 1_A375_shLS7_dtct_locRNA:1:3224, 1_A375_shLS7_dtct_locRNA:1:3225, 2_A375_shLS7_dtct_locRNA:1:7507, 2_A375_shLS7_dtct_locRNA:1:7508, 2_A375_shLS7_dtct_locRNA:1:7508		216398, 129441, 6861, 215302, 122442, 207	downstream, ut gene, upstream, downstream, ut gene, ut gene	1	1	22.75	22.5	4	2_A375_shLS7_dtct_locRNA:1		Gene ASPH	HAAH, CASQ2BP1, JCTN, AAH, ASPH, BAH, junctin	aspartate beta-hydroxylase	NM_004318, NM_032466, NM_032464, NM_001164780, NM_020164, NM_001164781, NM_001164782, NM_032467, NM_001164783, NM_001164784, NM_001164785, NM_001164786, NCT22712620.0, NCT22712286.0, NCT22712288.0, NCT23712301.0, NCT22712610.0, NCT22712927.0, NCT2	208698_at, 208364_s_at, 208139_at, 210566_s_at	NP_004309.2, NP_115698.1, NP_115857.1, NP_001158522.1, NP_001158523.1, NP_004459.1, NP_115696.1, NP_001158228.1, NP_001158225.1, NP_001158226.1, NP_001158227.1, NP_001158229.1, NP_001158230.1, EAW66540.1, EAW66541.1, EAW66542.1, EAW66543.1, EAW66544.1, EAW66545.1, EAW666
Gene:ID:2	YTHDF3	8	64,051,121	64,123,346	68,225	+	2	2_A375_shLS7_dtct_locRNA:1:7511, 2_A375_shLS7_dtct_locRNA:1:7512		-140, 51931	upstream, downstream	0	1	14.5	19	2	2_A375_shLS7_dtct_locRNA:1		Gene YTHDF3	FLJ31657, YTHDF3	YTH domain family, member 3	NM_152755, NCT23566510.0, NCT23566532.0, NCT23566553.0, NCT22347.3	1564552_a_at, 227169_at	NP_689714.4, EAW66566.1, EAW66564.1, EAW66565.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100130155	LOC100130155	8	65,285,775	65,291,388	5,613	+	2	1_A375_pNL7_minus_lncRNA::1::5228, 2_A375_pNL97_plus_lncRNA::1::7513	6865, 6769	downstream, downstream	1	1	18	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100130155		hypothetical LOC100130155	NR_034102, NR_034103		
GeneID:406908	MIR124-2	8	65,291,706	65,291,814	108	+	2	1_A375_pNL7_minus_lncRNA::1::5228, 2_A375_pNL97_plus_lncRNA::1::7513	934, 838	downstream, downstream	1	1	18	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene MIR124-2	MIRN124A2, MIRN124-2, MIR124-2	microRNA 124-2	NR_029669		
GeneID:55156	ARMC1	8	66,514,691	66,546,452	31,761	-	2	1_A375_pNL7_minus_lncRNA::1::5230, 2_A375_pNL97_plus_lncRNA::1::7515	100, 116	in gene, in gene	1	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene ARMC1	FLJ10511, ARMC1, Arcp	armadillo repeat containing 1	NM_018120, hCT31765.3	218185_s_at, 222550_at	NP_060590.1, EAW86880.1
GeneID:5150	PDE7A	8	66,629,905	66,753,755	123,850	-	2	1_A375_pNL7_minus_lncRNA::1::5231, 2_A375_pNL97_plus_lncRNA::1::7516	-933, -851	upstream, upstream	1	1	19	18	1	1_A375_pNL7_minus_lncRNA::1	19	Gene PDE7A	PDE7, HCP1, PDE7A	phosphodiesterase 7A	NM_002603, NM_002604, hCT1967677.2, hCT2257727.1, hCT2257730.1, hCT31784.2	1552343_s_at, 223359_s_at, 224046_s_at	NP_002594.1, NP_002595.1, EAW86883.1, EAW86884.1, EAW86885.1, EAW86886.1
GeneID:85479	DNAJC5B	8	66,933,791	67,012,755	78,964	+	1	1_A375_pNL7_minus_lncRNA::1::5232	5057	in gene	1	0	22	12	1	1_A375_pNL7_minus_lncRNA::1	22	Gene DNAJC5B	DNAJC5B, CSP-beta, MGC26226	DnaJ (Hsp40) homolog, subfamily C, member 5 beta	NM_033105, hCT2258423.0, hCT2258425.0, hCT9447.3	1554258_a_at, 232798_at	NP_149096.2, EAW86889.1, EAW86887.1, EAW86888.1
GeneID:84675	TRIM55	8	67,039,278	67,087,720	48,442	+	3	1_A375_pNL7_minus_lncRNA::1::5234, 2_A375_pNL97_plus_lncRNA::1::7519, 2_A375_pNL97_plus_lncRNA::1::7520	50482, -2958, 50546	downstream, upstream, downstream	1	1	32.5	35.5	2	2_A375_pNL97_plus_lncRNA::1	53	Gene TRIM55	TRIM55, MURF-2, RNF29	tripartite motif containing 55	NM_033058, NM_184085, NM_184086, NM_184087, hCT2258432.0, hCT2356843.0, hCT9446.3	232721_at, 236175_at	NP_149047.2, NP_908973.1, NP_908974.1, NP_908975.1, EAW86893.1, EAW86895.1, EAW86894.1
GeneID:1392	CRH	8	67,088,612	67,090,846	2,234	-	2	1_A375_pNL7_minus_lncRNA::1::5234, 2_A375_pNL97_plus_lncRNA::1::7520	1086, 1022	in gene, in gene	1	1	53	53	1	2_A375_pNL97_plus_lncRNA::1	53	Gene CRH	CRH, CRF	corticotropin releasing hormone	NM_000756, hCT1639986.3	205629_s_at, 205630_at	NP_000747.1, EAW86897.1
GeneID:100505676	LOC100505676	8	67,331,822	67,341,212	9,390	-	2	1_A375_pNL7_minus_lncRNA::1::5235, 2_A375_pNL97_plus_lncRNA::1::7521	76, 92	in gene, in gene	1	1	19	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene LOC100505676		hypothetical LOC100505676	XR_113145, XR_108917, XR_114180		
GeneID:23212	RRS1	8	67,341,263	67,342,968	1,705	+	2	1_A375_pNL7_minus_lncRNA::1::5235, 2_A375_pNL97_plus_lncRNA::1::7521	-127, -143	upstream, upstream	1	1	19	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene RRS1	RRS1, KIAA0112	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	NM_015169, hCT1639985.2	209567_at	NP_055984.1, EAW86900.1
GeneID:137872	ADHFE1	8	67,344,718	67,381,044	36,326	+	2	1_A375_pNL7_minus_lncRNA::1::5235, 2_A375_pNL97_plus_lncRNA::1::7521	-3582, -3598	upstream, upstream	1	1	19	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene ADHFE1	HOT, ADH8, MGC48605, FLJ32430, ADHFE1, HMFT2263	alcohol dehydrogenase, iron containing, 1	NM_144650, hCT2258436.0, hCT2258438.0, hCT2258439.0, hCT2356682.0, hCT2356683.0, hCT2356684.0, hCT2356685.0	227113_at	NP_653251.2, EAW86905.1, EAW86901.1, EAW86902.1, EAW86904.1, EAW86906.1, EAW86903.1, EAW86907.1
GeneID:4603	MYBL1	8	67,474,410	67,525,480	51,070	-	2	1_A375_pNL7_minus_lncRNA::1::5236, 2_A375_pNL97_plus_lncRNA::1::7522	-40, -120	upstream, upstream	1	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene MYBL1	A-MYB, MGC120061, AMYB, MYBL1, MGC120059	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	NM_001080416, NM_001144755	213906_at	NP_001073885.1, NP_001138227.1
GeneID:80124	VCPIP1	8	67,542,488	67,579,452	36,964	-	2	1_A375_pNL7_minus_lncRNA::1::5237, 2_A375_pNL97_plus_lncRNA::1::7523	-52, -148	upstream, upstream	1	1	22	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene VCPIP1	DUBA3, FLJ60694, DKFZp586G038, FLJ23132, VCPIP1, VCIP135, KIAA1850	valosin containing protein (p97)/p47 complex interacting protein 1	NM_025054, hCT1644612.3	1556227_at, 1556228_a_at, 219810_at, 234988_at	NP_079330.2, EAW86916.1
GeneID:56260	C8orf44	8	67,588,454	67,593,235	4,781	+	2	1_A375_pNL7_minus_lncRNA::1::5237, 2_A375_pNL97_plus_lncRNA::1::7523	-8950, -8854	upstream, upstream	1	1	22	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene C8orf44	C8orf44, FLJ11267	chromosome 8 open reading frame 44	NM_019607, hCT1813235.1, hCT1826307.2	220216_at	NP_062553.1, EAW86917.1, EAW86918.1
GeneID:23678	SGK3	8	67,624,891	67,774,257	149,366	+	1	2_A375_pNL97_plus_lncRNA::1::7524	-91	upstream	0	1	12	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene SGK3	DKFZp781N0293, SGK2, SGK3, CISK, SGKL	serum/glucocorticoid regulated kinase family, member 3	NM_013257, NM_170709, NM_001033578, hCT2258446.0, hCT9448.3	220038_at, 227627_at	NP_037389.4, NP_733827.2, NP_001028750.1, EAW86919.1, EAW86920.1
GeneID:157777	C8orf45	8	67,782,984	67,834,283	51,299	+	1	1_A375_pNL7_minus_lncRNA::1::5238	54744	downstream	1	0	19	14	1	1_A375_pNL7_minus_lncRNA::1	19	Gene C8orf45	C8orf45, FLJ25692	chromosome 8 open reading frame 45	NM_173518, NM_001136160, NM_001136161, hCT2344086.0, hCT2348632.0, hCT2348633.0	1552359_at, 1569677_a_at	NP_775789.3, NP_001129632.1, NP_001129633.1, EAW86921.1, EAW86922.1, EAW86923.1
GeneID:641638	SNHG6	8	67,834,165	67,837,777	3,612	-	1	1_A375_pNL7_minus_lncRNA::1::5238	49	in gene	1	0	19	14	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SNHG6	NCRNA00058, U87HG, SNHG6, HBII-276HG	small nucleolar RNA host gene 6 (non-protein coding)	NR_002599	225547_at	
GeneID:641648	SNORD87	8	67,834,709	67,834,784	75	-	1	1_A375_pNL7_minus_lncRNA::1::5238	-2944	upstream	1	0	19	14	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SNORD87	U87, SNORD87, HBII-276	small nucleolar RNA, C/D box 87	NR_002598		
GeneID:286187	LRRC67	8	67,900,366	67,940,786	40,420	-	1	2_A375_pNL97_plus_lncRNA::1::7525	20962	in gene	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LRRC67	LRRC67, dtr	leucine rich repeat containing 67	NM_001013626, hCT1816681.2		NP_001013648.1, EAW86927.1
GeneID:10987	COPS5	8	67,955,314	67,974,562	19,248	-	4	1_A375_pNL7_minus_lncRNA::1::5239, 2_A375_pNL97_plus_lncRNA::1::7526, 2_A375_pNL97_plus_lncRNA::1::7527, 2_A375_pNL97_plus_lncRNA::1::7528	-1982, 194, -1950, -2686	upstream, in gene, upstream, upstream	1	1	33.33	43.33	3	2_A375_pNL97_plus_lncRNA::1	94	Gene COPS5	MOV-34, COPS5, JAB1, MGC3149, SGN5, CSN5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	NM_006837, hCT2257621.0, hCT2257622.0, hCT2257624.0, hCT18948.3	201652_at	NP_006828.2, EAW86931.1, EAW86928.1, EAW86929.1, EAW86930.1
GeneID:79848	CSPP1	8	67,976,603	68,108,849	132,246	+	4	1_A375_pNL7_minus_lncRNA::1::5239, 2_A375_pNL97_plus_lncRNA::1::7526, 2_A375_pNL97_plus_lncRNA::1::7527, 2_A375_pNL97_plus_lncRNA::1::7528	-59, -2235, -91, 645	upstream, upstream, upstream, in gene	1	1	33.33	43.33	3	2_A375_pNL97_plus_lncRNA::1	94	Gene CSPP1	CSPP, FLJ22490, FLJ38886, CSPP1	centrosome and spindle pole associated protein 1	NM_024790, hCT2257178.0, hCT2257180.0, hCT2257183.0	1554873_at, 220072_at, 221925_s_at, 227105_at, 242041_at	NP_079066.5, EAW86932.1, EAW86933.1, EAW86934.1
GeneID:10565	ARFGEF1	8	68,109,897	68,255,912	146,015	-	1	2_A375_pNL97_plus_lncRNA::1::7529	8	in gene	0	1	8	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ARFGEF1	ARFGEF1, D730028O16Rik, ARFGEP1, DKFZP434L057, BIG1, P200	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	NM_006421, hCT18946.4, hCT1962700.1	202955_s_at, 202956_at, 216266_s_at	NP_006412.2, EAW86935.1, EAW86936.1
GeneID:81796	SLCO5A1	8	70,584,568	70,747,299	162,731	-	1	2_A375_pNL97_plus_lncRNA::1::7530	53923	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene SLCO5A1	OATP-J, SLCO5A1, SLC21A15, OATP5A1, FLJ39560, OATPRP4	solute carrier organic anion transporter family, member 5A1	NM_030958, NM_001146009, NM_001146008, hCT2356872.0, hCT6424.2	220984_s_at	NP_112220.2, NP_001139481.1, NP_001139480.1, EAW86957.1, EAW86958.1
GeneID:10499	NCOA2	8	71,024,267	71,316,020	291,753	-	2	2_A375_pNL97_plus_lncRNA::1::7532, 2_A375_pNL97_plus_lncRNA::1::7533	276820, 1444	in gene, in gene	0	1	9	19	2	2_A375_pNL97_plus_lncRNA::1	19	Gene NCOA2	SRC2, MGC138808, GRIP1, TIF2, bHLHe75, NCOA2, NCoA-2, KAT13C	nuclear receptor coactivator 2	NM_006540, hCT9508.3	205731_s_at, 205732_s_at, 215605_at	NP_006531.1, EAW86963.1
GeneID:23471	TRAM1	8	71,485,453	71,520,694	35,241	-	2	1_A375_pNL7_minus_lncRNA::1::5240, 2_A375_pNL97_plus_lncRNA::1::7534	-10, 6	upstream, in gene	1	1	61	66	1	2_A375_pNL97_plus_lncRNA::1	66	Gene TRAM1	PNAS8, TRAMP, PRO1292, TRAM, TRAM1	translocation associated membrane protein 1	NM_014294, hCT2258949.0, hCT2356887.0, hCT9506.3	201398_s_at, 201399_s_at, 210733_at	NP_055109.1, EAW86967.1, EAW86966.1, EAW86968.1
GeneID:51110	LACTB2	8	71,549,501	71,581,447	31,946	-	2	1_A375_pNL7_minus_lncRNA::1::5241, 2_A375_pNL97_plus_lncRNA::1::7535	167, 87	in gene, in gene	1	1	18	16	1	1_A375_pNL7_minus_lncRNA::1	18	Gene LACTB2	LACTB2, CGI-83	lactamase, beta 2	NM_016027, hCT2258948.0, hCT1665680.2	218701_at, 222714_s_at	NP_057111.1, EAW86970.1, EAW86969.1
GeneID:389668	XKR9	8	71,581,600	71,648,177	66,577	+	2	1_A375_pNL7_minus_lncRNA::1::5241, 2_A375_pNL97_plus_lncRNA::1::7535	-320, -240	upstream, upstream	1	1	18	16	1	1_A375_pNL7_minus_lncRNA::1	18	Gene XKR9	XKR9, XRG9	XK, Kell blood group complex subunit-related family, member 9	NM_001011720, hCT1647482.2		NP_001011720.1, EAW86971.1
GeneID:2138	EYA1	8	72,109,668	72,274,467	164,799	-	2	1_A375_pNL7_minus_lncRNA::1::5242, 2_A375_pNL97_plus_lncRNA::1::7536	96131, 96131	in gene, in gene	1	1	29	25	1	1_A375_pNL7_minus_lncRNA::1	29	Gene EYA1	MGC141875, EYA1, BOR, BOP	eyes absent homolog 1 (Drosophila)	NM_172060, NM_172058, NM_000503, NM_172059, hCT2257478.0, hCT2356689.0, hCT2356690.0, hCT2356691.0, hCT2356692.0, hCT6429.2, hCT1961649.1, hCT1961650.1	214608_s_at	NP_742057.1, NP_742055.1, NP_000494.2, NP_742056.1, EAW86975.1, EAW86976.1, EAW86973.1, EAW86974.1, EAW86977.1, EAW86978.1, EAW86979.1, EAW86980.1
GeneID:9242	MSC	8	72,753,777	72,756,731	2,954	-	1	2_A375_pNL97_plus_lncRNA::1::7538	411	in gene	0	1	21	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene MSC	MYOR, ABF-1, MSC, bHLHa22, ABF1	musculin (activated B-cell factor-1)	NM_005098, hCT9713.3	209928_s_at	NP_005089.2, EAW86984.1
GeneID:100132891	LOC100132891	8	72,755,358	72,968,547	213,189	+	1	2_A375_pNL97_plus_lncRNA::1::7538	962	in gene	0	1	21	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100132891	FLJ53548	hypothetical LOC100132891	NR_033651, NR_033652		
GeneID:6129	RPL7	8	74,202,874	74,205,869	2,995	-	3	1_A375_pNL7_minus_lncRNA::1::5243, 2_A375_pNL97_plus_lncRNA::1::7539, 2_A375_pNL97_plus_lncRNA::1::7540	-467, -371, -1795	upstream, upstream, upstream	1	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene RPL7	L7, humL7-1, MGC117326, RPL7	ribosomal protein L7	NM_000971, hCT2258063.0, hCT2258064.0	200717_x_at, 212042_x_at	NP_000962.2, EAW87000.1, EAW86999.1
GeneID:157506	RDH10	8	74,207,265	74,237,516	30,251	+	3	1_A375_pNL7_minus_lncRNA::1::5243, 2_A375_pNL97_plus_lncRNA::1::7539, 2_A375_pNL97_plus_lncRNA::1::7540	-929, -1025, 399	upstream, upstream, in gene	1	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene RDH10	RDH10, SDR16C4	retinol dehydrogenase 10 (all-trans)	NM_172037, hCT10251.3, hCT1966635.1	1552378_s_at, 1552379_at, 226021_at, 227467_at	NP_742034.1, EAW87002.1, EAW87001.1
GeneID:27067	STAU2	8	74,332,604	74,659,943	327,339	-	2	2_A375_pNL97_plus_lncRNA::1::7541, 2_A375_pNL97_plus_lncRNA::1::7542	287783, 227015	in gene, in gene	0	1	13	16.5	2	2_A375_pNL97_plus_lncRNA::1	17	Gene STAU2	DKFZp781K0371, MGC119606, 39K2, 39K3, STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)	NM_014393, NM_001164380, NM_001164381, NM_001164382, NM_001164383, NM_001164384, NM_001164385, hCT2258059.0, hCT2258061.0, hCT1950888.1, hCT1950889.1, hCT1955348.1	1554686_at, 204226_at, 227179_at	NP_055208.2, NP_001157852.1, NP_001157853.1, NP_001157854.1, NP_001157855.1, NP_001157856.1, NP_001157857.1, EAW87003.1, EAW87004.1, EAW87005.1, EAW87006.1, EAW87007.1
GeneID:55284	UBE2W	8	74,702,840	74,791,110	88,270	-	1	1_A375_pNL7_minus_lncRNA::1::5244	134	in gene	1	0	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene UBE2W	FLJ11011, hUBC-16, UBE2W	ubiquitin-conjugating enzyme E2W (putative)	NM_001001481, NM_018299, hCT2258052.0, hCT2258053.0, hCT1641752.3, hCT1965853.1	1555217_at, 1562456_at, 218521_s_at, 222656_at, 222657_s_at	NP_001001481.1, NP_060769.3, EAW87009.1, EAW87010.1, EAW87011.1, EAW87012.1
GeneID:6921	TCEB1	8	74,858,634	74,884,346	25,712	-	2	1_A375_pNL7_minus_lncRNA::1::5245, 2_A375_pNL97_plus_lncRNA::1::7543	-358, -326	upstream, upstream	1	1	26	18	1	1_A375_pNL7_minus_lncRNA::1	26	Gene TCEB1	SIII, TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	NM_005648, hCT2343683.0, hCT2343684.0, hCT2343685.0, hCT2343686.0, hCT2356848.0, hCT2356849.0, hCT1641273.4	202823_at, 202824_s_at	NP_005639.1, EAW87015.1, EAW87016.1, EAW87017.1, EAW87018.1, EAW87021.1, EAW87019.1, EAW87020.1
GeneID:54968	TMEM70	8	74,888,377	74,895,018	6,641	+	2	1_A375_pNL7_minus_lncRNA::1::5245, 2_A375_pNL97_plus_lncRNA::1::7543	-3673, -3705	upstream, upstream	1	1	26	18	1	1_A375_pNL7_minus_lncRNA::1	26	Gene TMEM70	FLJ20533, TMEM70	transmembrane protein 70	NM_017866, NM_001040613, NR_033334, hCT1641272.2, hCT1962630.1	219448_at, 219449_s_at, 226083_at	NP_060336.3, NP_001035703.1, EAW87022.1, EAW87023.1
GeneID:56704	JPH1	8	75,146,939	75,233,562	86,623	-	1	1_A375_pNL7_minus_lncRNA::1::5246	570	in gene	1	0	18	12	1	1_A375_pNL7_minus_lncRNA::1	18	Gene JPH1	JP-1, DKFZp762L0313, JPH1, JP1	junctophilin 1	NM_020647, hCT2258612.0, hCT2258613.0, hCT2258614.0, hCT2356857.0, hCT2356858.0, hCT13928.3	1553533_at, 229139_at	NP_065698.1, EAW87026.1, EAW87027.1, EAW87028.1, EAW87030.1, EAW87031.1, EAW87029.1
GeneID:54332	GDAP1	8	75,262,618	75,279,345	16,727	+	2	1_A375_pNL7_minus_lncRNA::1::5247, 2_A375_pNL97_plus_lncRNA::1::7544	166, 134	in gene, in gene	1	1	34	62	1	2_A375_pNL97_plus_lncRNA::1	62	Gene GDAP1	CMTRIA, GDAP1, CMT4A, CMT4	ganglioside-induced differentiation-associated protein 1	NM_018972, NM_001040875, hCT2356859.0, hCT13925.3	221279_at, 226269_at, 226271_at	NP_061845.2, NP_001035808.1, EAW87032.1, EAW87033.1
GeneID:441355	FLJ39080	8	75,512,101	75,670,587	158,486	+	1	1_A375_pNL7_minus_lncRNA::1::5248	2299	in gene	1	0	17	7	1	1_A375_pNL7_minus_lncRNA::1	17	Gene FLJ39080		hypothetical LOC441355	NR_033830	1561371_at	
GeneID:51050	PI15	8	75,736,772	75,767,264	30,492	+	2	1_A375_pNL7_minus_lncRNA::1::5249, 2_A375_pNL97_plus_lncRNA::1::7545	-1764, 732	upstream, in gene	1	1	15.5	10.5	2	1_A375_pNL7_minus_lncRNA::1	21	Gene PI15	P25TI, P24TI, PI15, DKFZp586F0366, CRISP8	peptidase inhibitor 15	NM_015886, hCT13927.2	207938_at, 229947_at	NP_056970.1, EAW87037.1
GeneID:100192378	LOC100192378	8	77,523,114	77,595,510	72,396	-	2	1_A375_pNL7_minus_lncRNA::1::5251, 2_A375_pNL97_plus_lncRNA::1::7547	-4154, -4042	upstream, upstream	1	1	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene LOC100192378		hypothetical LOC100192378	NR_024360		
GeneID:79776	ZFHX4	8	77,593,515	77,779,521	186,006	+	2	1_A375_pNL7_minus_lncRNA::1::5251, 2_A375_pNL97_plus_lncRNA::1::7547	6149, 6037	in gene, in gene	1	1	24	20	1	1_A375_pNL7_minus_lncRNA::1	24	Gene ZFHX4	FLJ16514, FLJ20980, ZFH-4, ZFH4, ZFHX4, ZHF4	zinc finger homeobox 4	NM_024721, hCT2257644.1, hCT2257645.1, hCT1951444.2	1559270_at, 219779_at, 241700_at	NP_078997.4, EAW87049.1, EAW87050.1, EAW87051.1
GeneID:5569	PKIA	8	79,428,336	79,515,485	87,149	+	1	2_A375_pNL97_plus_lncRNA::1::7548	96	in gene	0	1	23	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene PKIA	PRKACN1, PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	NM_181839, NM_006823, hCT2257640.0, hCT2257643.0, hCT10998.2, hCT1950077.1	204612_at, 226864_at	NP_862822.1, NP_006814.1, EAW87055.1, EAW87056.1, EAW87057.1, EAW87058.1
GeneID:51101	FAM164A	8	79,578,282	79,632,000	53,718	+	1	2_A375_pNL97_plus_lncRNA::1::7549	86	in gene	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FAM164A	FAM164A, CGI-62, C8orf70	family with sequence similarity 164, member A	NM_016010, hCT12359.3	1560197_at, 205308_at	NP_057094.2, EAW87059.1
GeneID:11075	STMN2	8	80,523,380	80,577,237	53,857	+	4	1_A375_pNL7_minus_lncRNA::1::5253, 2_A375_pNL97_plus_lncRNA::1::7552, 2_A375_pNL97_plus_lncRNA::1::7553, 2_A375_pNL97_plus_lncRNA::1::7554	-1972, -1972, -777, 1644	upstream, upstream, upstream, in gene	1	1	13.33	19	3	1_A375_pNL7_minus_lncRNA::1	25	Gene STMN2	SCG10, SGC10, STMN2, SCGN10, FLJ50995, FLJ34866	stathmin-like 2	NM_007029, hCT2257941.1, hCT11921.4, hCT1965324.2	203000_at, 203001_s_at	NP_008960.2, EAW87064.1, EAW87063.1, EAW87065.1
GeneID:23462	HEY1	8	80,676,245	80,680,098	3,853	-	2	1_A375_pNL7_minus_lncRNA::1::5254, 2_A375_pNL97_plus_lncRNA::1::7555	2418, 2434	in gene, in gene	1	1	17	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene HEY1	HERP2, OAF1, BHLHb31, CHF2, HEY1, HRT-1, MGC1274, HESR1	hairy/enhancer-of-split related with YRPW motif 1	NM_001040708, NM_012258, hCT10999.3	218839_at, 44783_s_at	NP_001035798.1, NP_036390.3, EAW87066.1
GeneID:100507186	LOC100507186	8	80,680,377	80,715,077	34,700	+	2	1_A375_pNL7_minus_lncRNA::1::5254, 2_A375_pNL97_plus_lncRNA::1::7555	-2697, -2713	upstream, upstream	1	1	17	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene LOC100507186		hypothetical LOC100507186	XR_108901		
GeneID:28957	MRPS28	8	80,831,095	80,942,506	111,411	-	1	2_A375_pNL97_plus_lncRNA::1::7556	458	in gene	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MRPS28	HSPC007, MRPS35, MRPS28, MRP-S35, FLJ22853, MRP-S28	mitochondrial ribosomal protein S28	NM_014018, hCT2258096.0, hCT11918.2, hCT1963019.1, hCT1965323.1	219819_s_at	NP_054737.1, EAW87072.1, EAW87069.1, EAW87070.1, EAW87071.1
GeneID:7163	TPD52	8	80,947,103	81,083,836	136,733	-	2	2_A375_pNL97_plus_lncRNA::1::7556, 2_A375_pNL97_plus_lncRNA::1::7557	141788, 332	downstream, in gene	0	1	10	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene TPD52	PC-1, TPD52, D52, N8L, hD52, PrLZ	tumor protein D52	NM_001025252, NM_001025253, NM_005079, hCT2258092.0, hCT1640759.3	201688_s_at, 201689_s_at, 201690_s_at, 201691_s_at, 236655_at	NP_001020423.1, NP_001020424.1, NP_005070.1, EAW87073.1, EAW87074.1
GeneID:619279	ZNF704	8	81,540,686	81,787,016	246,330	-	3	1_A375_pNL7_minus_lncRNA::1::5255, 2_A375_pNL97_plus_lncRNA::1::7558, 2_A375_pNL97_plus_lncRNA::1::7559	183688, 183688, 1192	in gene, in gene, in gene	1	1	24	21.5	2	1_A375_pNL7_minus_lncRNA::1	36	Gene ZNF704	ZNF704, MGC10858, FLJ16218, Gig1	zinc finger protein 704	NM_001033723, hCT12657.2	1558941_at, 241963_at	NP_001028895.1, EAW87083.1
GeneID:55824	PAG1	8	81,880,045	82,024,303	144,258	-	1	2_A375_pNL97_plus_lncRNA::1::7560	85487	in gene	0	1	21	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene PAG1	CBP, PAG, PAG1, FLJ37858, MGC138364	phosphoprotein associated with glycosphingolipid microdomains 1	NM_018440, hCT2260827.0, hCT12658.3	225622_at, 225626_at, 227354_at	NP_060910.3, EAW87085.1, EAW87086.1
GeneID:2171	FABP5	8	82,192,785	82,197,008	4,223	+	1	2_A375_pNL97_plus_lncRNA::1::7561	495	in gene	0	1	15	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene FABP5	PA-FABP, E-FABP, FABP5, EFABP, PAFABP	fatty acid binding protein 5 (psoriasis-associated)	NM_001444	202345_s_at	NP_001435.1
GeneID:3612	IMPA1	8	82,569,151	82,598,589	29,438	-	1	2_A375_pNL97_plus_lncRNA::1::7562	157	in gene	0	1	8	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene IMPA1	IMP, IMPA1, IMPA	inositol(myo)-1(or 4)-monophosphatase 1	NM_005536, NM_001144878, NM_001144879, hCT2259495.0, hCT12389.2, hCT1950941.1, hCT1963426.1, hCT1966237.1, hCT1966238.1	203011_at	NP_005527.1, NP_001138350.1, NP_001138351.1, EAW87095.1, EAW87098.1, EAW87100.1, EAW87096.1, EAW87097.1, EAW87099.1
GeneID:347051	SLC10A5	8	82,605,891	82,607,207	1,316	-	1	2_A375_pNL97_plus_lncRNA::1::7562	8775	downstream	0	1	8	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC10A5	P5, SLC10A5	solute carrier family 10 (sodium/bile acid cotransporter family), member 5	NM_001010893, hCT2259490.0		NP_001010893.1, EAW87101.1
GeneID:79752	ZFAND1	8	82,613,566	82,633,539	19,973	-	1	2_A375_pNL97_plus_lncRNA::1::7563	-285	upstream	0	1	13	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene ZFAND1	FLJ14007, ZFAND1	zinc finger, AN1-type domain 1	NM_024699, NM_001170796, NM_001170797, NR_033193, NR_033194, NR_033195, NR_033196, hCT2356873.0, hCT12392.2, hCT1950942.1, hCT1950943.1	218919_at	NP_078975.2, NP_001164267.1, NP_001164268.1, EAW87103.1, EAW87104.1, EAW87105.1, EAW87106.1
GeneID:64089	SNX16	8	82,711,818	82,754,521	42,703	-	2	1_A375_pNL7_minus_lncRNA::1::5256, 2_A375_pNL97_plus_lncRNA::1::7564	-231, -199	upstream, upstream	1	1	34	29	1	1_A375_pNL7_minus_lncRNA::1	34	Gene SNX16	DKFZp666H147, SNX16	sorting nexin 16	NM_152837, NM_152836, NM_022133, hCT12393.3, hCT1950944.1	219793_at, 229618_at	NP_690050.1, NP_690049.1, NP_071416.2, EAW87108.1, EAW87109.1
GeneID:11059	WWP1	8	87,354,994	87,480,181	125,187	+	2	1_A375_pNL7_minus_lncRNA::1::5259, 2_A375_pNL97_plus_lncRNA::1::7566	-466, -402	upstream, upstream	1	1	27	21	1	1_A375_pNL7_minus_lncRNA::1	27	Gene WWP1	Tiul1, hSDRP1, WWP1, AIP5, DKFZp434D2111	WW domain containing E3 ubiquitin protein ligase 1	NM_007013, hCT2299356.0, hCT2299357.0, hCT2299358.0, hCT2299359.0	212637_s_at, 212638_s_at	NP_008944.1, EAW91635.1, EAW91634.1, EAW91636.1, EAW91637.1

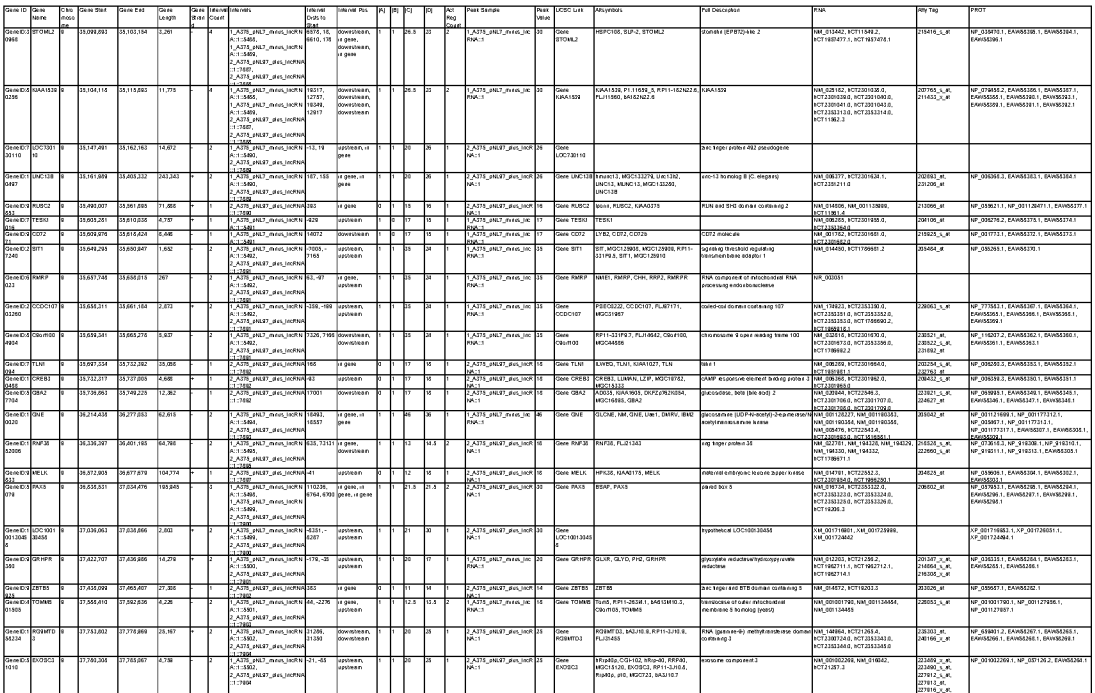
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:4325	MMP16	8	89,049,460	89,339,717	290,257	-	3	1_A375_pNL7_minus_lncRNA::1::5260, 2_A375_pNL97_plus_lncRNA::1::7569, 2_A375_pNL97_plus_lncRNA::1::7570	87365, 87461, 24496	in gene, in gene, in gene	1	1	18	17.5	2	1_A375_pNL7_minus_lncRNA::1	26	Gene MMP16	C8orf57, MMP16, DKFZp761D112, MT3-MMP, MT-MMP2, MMP-X2, MT-MMP3	matrix metallopeptidase 16 (membrane-inserted)	NM_022564, NM_005941, hCT2296475.0, hCT23495.3	207012_at, 207013_s_at, 208166_at, 208167_s_at	NP_072086.2, NP_005932.2, EAW91651.1, EAW91652.1
GeneID:8767	RIPK2	8	90,769,975	90,803,292	33,317	+	1	2_A375_pNL97_plus_lncRNA::1::7572	185	in gene	0	1	18	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RIPK2	RIPK2, CCK, CARDIAK, CARD3, RIP2, GIG30, RICK	receptor-interacting serine-threonine kinase 2	NM_003821, hCT23504.3, hCT2357460.0	209544_at, 209545_s_at	NP_003812.1, EAW91655.1, EAW91656.1
GeneID:4683	NBN	8	90,945,564	90,996,899	51,335	-	2	1_A375_pNL7_minus_lncRNA::1::5261, 2_A375_pNL97_plus_lncRNA::1::7573	323, 291	in gene, in gene	1	1	36	52	1	2_A375_pNL97_plus_lncRNA::1	52	Gene NBN	FLJ10155, NBS1, NBS, ATV, AT-V2, P95, AT-V1, NBN, MGC87362	nibrin	NM_002485, hCT2357459.0, hCT24254.2	202905_x_at, 202906_s_at, 202907_s_at, 217299_s_at, 240510_at	NP_002476.2, EAW91661.1, EAW91660.1
GeneID:793	CALB1	8	91,070,836	91,095,107	24,269	-	2	1_A375_pNL7_minus_lncRNA::1::5262, 2_A375_pNL97_plus_lncRNA::1::7574	35, 67	in gene, in gene	1	1	31	43	1	2_A375_pNL97_plus_lncRNA::1	43	Gene CALB1	CALB1, CALB	calbindin 1, 28kDa	NM_004929, hCT24252.3, hCT1964131.1	205625_s_at, 205626_s_at	NP_004920.1, EAW91666.1, EAW91665.1
GeneID:64168	NECAB1	8	91,803,921	91,971,630	167,709	+	1	2_A375_pNL97_plus_lncRNA::1::7576	69583	in gene	0	1	12	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene NECAB1	STIP-1, EFCBP1, NECAB1	N-terminal EF-hand calcium binding protein 1	NM_022351, hCT2297130.1, hCT1642829.3	233305_at	NP_071746.1, EAW91669.1, EAW91670.1
GeneID:286144	C8orf83	8	93,895,758	93,978,372	82,614	-	2	1_A375_pNL7_minus_lncRNA::1::5264, 1_A375_pNL7_minus_lncRNA::1::5265	42964, 180	in gene, in gene	1	0	17.5	13	2	1_A375_pNL7_minus_lncRNA::1	21	Gene C8orf83	DKFZp779L1068, TRIQK, FLJ40637, UPF0599, triqk, C8orf83	chromosome 8 open reading frame 83	NM_001171796, NM_001171799, NM_001171795, NM_001171797, NM_001171798, NM_001191035, NM_001191036	1562066_at	NP_001165267.1, NP_001165270.1, NP_001165266.1, NP_001165268.1, NP_001165269.1, NP_001177964.1, NP_001177965.1
GeneID:642924	LOC642924	8	94,358,695	94,712,661	353,966	-	1	2_A375_pNL97_plus_lncRNA::1::7578	112757	in gene	0	1	11	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene LOC642924		hypothetical LOC642924	NR_033858	1561423_at, 238244_at	
GeneID:91147	TMEM67	8	94,767,072	94,831,462	64,390	+	1	1_A375_pNL7_minus_lncRNA::1::5266	51136	in gene	1	0	13	8	1	1_A375_pNL7_minus_lncRNA::1	13	Gene TMEM67	MECKELIN, TMEM67, JBTS6, MGC26979, TNEM67, MKS3, NPHP11	transmembrane protein 67	NM_153704, NM_001142301, NR_024522, hCT2357473.0, hCT2357474.0, hCT1643362.3	1552763_at, 1552765_x_at, 1563646_a_at, 1569377_at, 1569411_at, 232023_at	NP_714915.3, NP_001135773.1, EAW91701.1, EAW91702.1, EAW91703.1
GeneID:2669	GEM	8	95,261,481	95,274,547	13,066	-	1	1_A375_pNL7_minus_lncRNA::1::5268	20211	downstream	1	0	22	18	1	1_A375_pNL7_minus_lncRNA::1	22	Gene GEM	KIR, MGC26294, GEM	GTP binding protein overexpressed in skeletal muscle	NM_005261, NM_181702, hCT2357467.0, hCT12745.3	204472_at	NP_005252.1, NP_859053.1, EAW91709.1, EAW91710.1
GeneID:25788	RAD54B	8	95,384,188	95,487,310	103,122	-	1	2_A375_pNL97_plus_lncRNA::1::7580	67	in gene	0	1	14	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene RAD54B	FSBP, RDH54, RAD54B	RAD54 homolog B (S. cerevisiae)	NM_012415	219494_at, 220549_at	NP_036547.1
GeneID:25962	KIAA1429	8	95,500,600	95,565,688	65,088	-	2	1_A375_pNL7_minus_lncRNA::1::5269, 2_A375_pNL97_plus_lncRNA::1::7581	-120, -104	upstream, upstream	1	1	24	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene KIAA1429	fSAP121, KIAA1429, MGC138493, MSTP054, MGC141940, DKFZp781B2117, DKFZp434I116	KIAA1429	NM_183009, NM_015496, hCT2298057.0, hCT12750.3, hCT1955575.1	223110_at, 238818_at, 243927_x_at	NP_892121.1, NP_056311.2, EAW91715.1, EAW91716.1, EAW91717.1
GeneID:286148	DPY19L4	8	95,732,103	95,806,076	73,973	+	2	1_A375_pNL7_minus_lncRNA::1::5270, 2_A375_pNL97_plus_lncRNA::1::7582	73, 25	in gene, in gene	1	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene DPY19L4	DPY19L4, MGC131885	dpy-19-like 4 (C. elegans)	NM_181787, hCT2296886.1, hCT2296887.1, hCT2348617.0, hCT2357503.0	213391_at, 226721_at	NP_861452.2, EAW91722.1, EAW91723.1, EAW91724.1, EAW91725.1
GeneID:55656	INTS8	8	95,835,534	95,892,721	57,187	+	1	2_A375_pNL97_plus_lncRNA::1::7583	-366	upstream	0	1	12	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene INTS8	INT8, INTS8, C8orf52, FLJ20530, MGC131633	integrator complex subunit 8	NM_017864, hCT2296889.0	218905_at	NP_060334.2, EAW91726.1
GeneID:137682	C8orf38	8	96,037,221	96,070,938	33,717	+	1	2_A375_pNL97_plus_lncRNA::1::7584	11	in gene	0	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C8orf38	C8orf38, MGC40214	chromosome 8 open reading frame 38	NM_152416, hCT2296892.1, hCT2349354.0, hCT2349355.0, hCT2349356.0, hCT2349357.0, hCT1820452.3	1556571_at, 230016_at, 235509_at, 236766_at	NP_689629.2, EAW91736.1, EAW91733.1, EAW91734.1, EAW91735.1, EAW91737.1, EAW91738.1
GeneID:157657	C8orf37	8	96,258,235	96,281,437	23,202	-	2	1_A375_pNL7_minus_lncRNA::1::5271, 2_A375_pNL97_plus_lncRNA::1::7585	-579, -451	upstream, upstream	1	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene C8orf37	FLJ30600, C8orf37	chromosome 8 open reading frame 37	NM_177965, hCT2349343.0, hCT1642561.4	244569_at	NP_808880.1, EAW91745.1, EAW91744.1
GeneID:51001	MTERFD1	8	97,251,645	97,273,796	22,151	-	2	1_A375_pNL7_minus_lncRNA::1::5272, 2_A375_pNL97_plus_lncRNA::1::7586	-156, -188	upstream, upstream	1	1	43	38	1	1_A375_pNL7_minus_lncRNA::1	43	Gene MTERFD1	FLJ10939, CGI-12, MTERFD1, mTERF3	MTERF domain containing 1	NM_015942, hCT2296911.0, hCT2357469.0, hCT1820232.2	219363_s_at	NP_057026.3, EAW91751.1, EAW91750.1, EAW91752.1
GeneID:9791	PTDSS1	8	97,274,167	97,346,774	72,607	+	2	1_A375_pNL7_minus_lncRNA::1::5272, 2_A375_pNL97_plus_lncRNA::1::7586	-215, -183	upstream, upstream	1	1	43	38	1	1_A375_pNL7_minus_lncRNA::1	43	Gene PTDSS1	KIAA0024, PTDSS1, PSS1, PSSA	phosphatidylserine synthase 1	NM_014754, hCT2296876.0, hCT6775.3	201433_s_at	NP_055569.1, EAW91753.1, EAW91754.1
GeneID:92140	MTDH	8	98,656,407	98,742,488	86,081	+	1	2_A375_pNL97_plus_lncRNA::1::7588	25	in gene	0	1	15	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene MTDH	3D3, LYRIC, AEG-1, MTDH, AEG1, LYRIC/3D3	metadherin	NM_178812, hCT2297059.0, hCT2357483.0, hCT6323.3	212250_at, 212251_at	NP_848927.2, EAW91760.1, EAW91761.1, EAW91762.1
GeneID:55353	LAPTM4B	8	98,787,609	98,864,630	77,021	+	1	2_A375_pNL97_plus_lncRNA::1::7589	-33	upstream	0	1	9	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LAPTM4B	LAPTM4beta, LAPTM4B, LC27	lysosomal protein transmembrane 4 beta	NM_018407, hCT2297063.1	1554679_a_at, 208029_s_at, 208767_s_at, 214039_s_at	NP_060877.3, EAW91763.1
GeneID:4147	MATN2	8	98,881,311	99,048,948	167,637	+	1	1_A375_pNL7_minus_lncRNA::1::5273	176705	downstream	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene MATN2	MATN2	matrilin 2	NM_002380, NM_030583, hCT2297069.0, hCT2297071.0, hCT2297075.0, hCT2357500.0, hCT6307.3	202350_s_at	NP_002371.3, NP_085072.2, EAW91764.1, EAW91765.1, EAW91766.1, EAW91767.1, EAW91768.1
GeneID:6156	RPL30	8	99,053,942	99,057,773	3,831	-	1	1_A375_pNL7_minus_lncRNA::1::5273	-243	upstream	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene RPL30	RPL30, L30	ribosomal protein L30	NM_000989, hCT2297242.0, hCT2357471.0, hCT9279.3	200062_s_at	NP_000980.1, EAW91771.1, EAW91769.1, EAW91770.1
GeneID:26775	SNORA72	8	99,054,314	99,054,445	131	-	1	1_A375_pNL7_minus_lncRNA::1::5273	-3571	upstream	1	0	19	12	1	1_A375_pNL7_minus_lncRNA::1	19	Gene SNORA72	RNU72, U72, SNORA72	small nucleolar RNA, H/ACA box 72	NR_002581	228047_at	
GeneID:79815	NIPAL2	8	99,204,387	99,306,621	102,234	-	1	2_A375_pNL97_plus_lncRNA::1::7590	45	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene NIPAL2	NPAL2, NIPAL2, FLJ13955	NIPA-like domain containing 2	NM_024759, hCT2297252.0, hCT2297253.0, hCT9282.3	220126_s_at, 222950_at, 227001_at	NP_079035.1, EAW91778.1, EAW91777.1, EAW91779.1
GeneID:116039	OSR2	8	99,956,631	99,964,328	7,697	+	2	1_A375_pNL7_minus_lncRNA::1::5274, 2_A375_pNL97_plus_lncRNA::1::7591	73, -23	in gene, upstream	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene OSR2	OSR2, FLJ90037	odd-skipped related 2 (Drosophila)	NM_053001, NM_001142462, hCT2296864.0, hCT9280.2	213568_at	NP_443727.2, NP_001135934.1, EAW91784.1, EAW91785.1
GeneID:157680	VPS13B	8	100,025,494	100,889,808	864,314	+	1	1_A375_pNL7_minus_lncRNA::1::5275	-102	upstream	1	0	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene VPS13B	CHS1, DKFZp313I0811, KIAA0532, COH1, VPS13B	vacuolar protein sorting 13 homolog B (yeast)	NM_152564, NM_017890, NM_015243, NM_181661, hCT2348474.0, hCT2348475.0, hCT2348476.0	1553852_at, 213243_at, 220400_at, 236254_at	NP_689777.3, NP_060360.3, NP_056047.2, NP_056058.2, EAW91787.1, EAW91788.1, EAW91786.1
GeneID:1345	COX6C	8	100,890,223	100,906,242	16,019	-	2	1_A375_pNL7_minus_lncRNA::1::5276, 2_A375_pNL97_plus_lncRNA::1::7592	418, 322	in gene, in gene	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene COX6C	COX6C		NM_004374, hCT2297277.0, hCT2297278.0, hCT1820372.2	201754_at	NP_004365.1, EAW91793.1, EAW91791.1, EAW91792.1
GeneID:5440	POLR2K	8	101,162,839	101,166,230	3,391	+	1	1_A375_pNL7_minus_lncRNA::1::5277	7461	downstream	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene POLR2K	RPB10alpha, RPB7.0, hsRPB10a, hRPB7.0, POLR2K, RPABC4, ABC10-alpha, RPB12	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	NM_005034, hCT2297041.0, hCT5900.3	202634_at, 202635_s_at	NP_005025.1, EAW91798.1, EAW91799.1
GeneID:6674	SPAG1	8	101,170,263	101,254,130	83,867	+	1	1_A375_pNL7_minus_lncRNA::1::5277	57	in gene	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene SPAG1	SP75, TPIS, FLJ32920, SPAG1, HSD-3.8	sperm associated antigen 1	NM_003114, NM_172218, hCT2297043.1, hCT2297045.1, hCT2349333.0, hCT2349334.0, hCT2357481.0, hCT2357482.0, hCT6714.4	210117_at	NP_003105.2, NP_757367.1, EAW91800.1, EAW91801.1, EAW91802.1, EAW91806.1, EAW91803.1, EAW91804.1, EAW91805.1
GeneID:25897	RNF19A	8	101,269,288	101,322,327	53,039	-	1	2_A375_pNL97_plus_lncRNA::1::7593	359	in gene	0	1	13	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene RNF19A	DORFIN, RNF19, RNF19A, DKFZp566B1346	ring finger protein 19A	NM_015435, NM_183419, hCT6715.4	220483_s_at, 223085_at	NP_056250.3, NP_904355.1, EAW91807.1
GeneID:157567	ANKRD46	8	101,533,000	101,572,012	39,012	-	2	1_A375_pNL7_minus_lncRNA::1::5279, 2_A375_pNL97_plus_lncRNA::1::7596	108, -20	in gene, upstream	1	1	28	23	1	1_A375_pNL7_minus_lncRNA::1	28	Gene ANKRD46	ANKRD46		NM_198401, hCT2344202.0, hCT2344203.0, hCT2344204.0, hCT6716.2	212731_at, 238807_at	NP_940683.1, EAW91808.1, EAW91809.1, EAW91810.1, EAW91811.1
GeneID:26986	PABPC1	8	101,715,144	101,734,315	19,171	-	1	2_A375_pNL97_plus_lncRNA::1::7597	-533	upstream	0	1	11	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene PABPC1	PABPC2, PAB1, PABP1, PABP, PABPC1, PABPL1	poly(A) binding protein, cytoplasmic 1	NM_002568, hCT2297933.0, hCT2297936.0, hCT2297938.0, hCT6708.3, hCT1964101.1, hCT1964102.1, hCT1964103.1, hCT1964104.1	215823_x_at	NP_002559.2, EAW91820.1, EAW91814.1, EAW91815.1, EAW91816.1, EAW91817.1, EAW91818.1, EAW91819.1, EAW91821.1
GeneID:7534	YWHAZ	8	101,930,804	101,965,623	34,819	-	3	1_A375_pNL7_minus_lncRNA::1::5280, 1_A375_pNL7_minus_lncRNA::1::5281, 2_A375_pNL97_plus_lncRNA::1::7598	2647, 1399, 1431	in gene, in gene, in gene	1	1	21	15	2	1_A375_pNL7_minus_lncRNA::1	22	Gene YWHAZ	YWHAZ, YWHAD, 14-3-3-zeta, KCIP-1, MGC111427, MGC138156, MGC126532	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	NM_003406, NM_145690, NM_001135699, NM_001135700, NM_001135701, NM_001135702, hCT2297926.0, hCT2297927.0, hCT2297928.0, hCT2297929.0, hCT2297930.0, hCT2297931.0, hCT2297932.0	200638_s_at, 200639_s_at, 200640_at, 200641_s_at	NP_003397.1, NP_663723.1, NP_001129171.1, NP_001129172.1, NP_001129173.1, NP_001129174.1, EAW91823.1, EAW91824.1, EAW91825.1, EAW91826.1, EAW91827.1, EAW91828.1, EAW91829.1
GeneID:441374	FLJ42969	8	102,064,282	102,088,479	24,197	+	1	2_A375_pNL97_plus_lncRNA::1::7600	11589	in gene	0	1	10	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene FLJ42969		hypothetical LOC441374	NR_033962		
GeneID:83988	NCALD	8	102,698,770	103,137,135	438,365	-	1	1_A375_pNL7_minus_lncRNA::1::5286	112271	in gene	1	0	20	11	1	1_A375_pNL7_minus_lncRNA::1	20	Gene NCALD	MGC33870, MGC74858, NCALD	neurocalcin delta	NM_032041, NM_001040624, NM_001040625, NM_001040626, NM_001040627, NM_001040628, NM_001040629, NM_001040630, hCT2297341.0, hCT2297343.0, hCT7273.2	1562790_at, 211685_s_at	NP_114430.2, NP_001035714.1, NP_001035715.1, NP_001035716.1, NP_001035717.1, NP_001035718.1, NP_001035719.1, NP_001035720.1, EAW91835.1, EAW91836.1, EAW91837.1
GeneID:4956	ODF1	8	103,563,848	103,573,245	9,397	+	1	2_A375_pNL97_plus_lncRNA::1::7606	16536	downstream	0	1	10	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ODF1	MGC129929, ODFPGB, RT7, ODF2, ODF27, ODF1, CT133, MGC129928, SODF, ODFP, HSPB10, ODF, ODFPG, ODFPGA	outer dense fiber of sperm tails 1	NM_024410, hCT2349336.0, hCT2349337.0, hCT1640266.4	214485_at	NP_077721.2, EAW91847.1, EAW91848.1, EAW91849.1
GeneID:401472	FLJ45248	8	103,819,050	103,819,818	768	+	1	1_A375_pNL7_minus_lncRNA::1::5288	710	in gene	1	0	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene FLJ45248		FLJ45248 protein	XR_113157, XR_108873, XR_114193		
GeneID:51582	AZIN1	8	103,838,536	103,876,397	37,861	-	1	2_A375_pNL97_plus_lncRNA::1::7608	-211	upstream	0	1	15	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene AZIN1	ODC1L, OAZIN, AZIN1, MGC3832, OAZI, MGC691	antizyme inhibitor 1	NM_015878, NM_148174, hCT1969300.1, hCT2298965.0, hCT2298966.0	201772_at, 212461_at	NP_056962.2, NP_680479.1, EAW91851.1, EAW91852.1, EAW91853.1
GeneID:100506753	LOC100506753	8	103,876,565	103,877,553	988	+	1	2_A375_pNL97_plus_lncRNA::1::7608	43	in gene	0	1	15	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC100506753		hypothetical LOC100506753	XR_113158, XR_108874, XR_114194		
GeneID:528	ATP6V1C1	8	104,033,248	104,085,285	52,037	+	1	2_A375_pNL97_plus_lncRNA::1::7609	80	in gene	0	1	15	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ATP6V1C1	ATP6V1C1, FLJ20057, Vma5, ATP6C, ATP6D, VATC	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	NM_001695, hCT2298631.0, hCT5623.2	202872_at, 202873_at, 202874_s_at, 226463_at	NP_001686.1, EAW91860.1, EAW91859.1
GeneID:8323	FZD6	8	104,310,661	104,345,094	34,433	+	1	2_A375_pNL97_plus_lncRNA::1::7611	635	in gene	0	1	14	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene FZD6	FZ6, HFZ6, FZD6	frizzled homolog 6 (Drosophila)	NM_003506, NM_001164615, NM_001164616, hCT2298639.0, hCT2298640.0, hCT2357449.0, hCT2357450.0, hCT2357451.0, hCT6062.2, hCT1966009.1	203987_at	NP_003497.2, NP_001158087.1, NP_001158088.1, EAW91867.1, EAW91868.1, EAW91871.1, EAW91869.1, EAW91870.1, EAW91872.1, EAW91873.1
GeneID:115908	CTHRC1	8	104,383,786	104,395,217	11,431	+	1	2_A375_pNL97_plus_lncRNA::1::7612	374	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CTHRC1	CTHRC1	collagen triple helix repeat containing 1	NM_138455, hCT2357452.0, hCT2357453.0, hCT6063.3	225681_at	NP_612464.1, EAW91874.1, EAW91875.1, EAW91876.1
GeneID:81034	SLC25A32	8	104,410,866	104,427,468	16,602	-	2	1_A375_pNL7_minus_lncRNA::1::5291, 2_A375_pNL97_plus_lncRNA::1::7613	332, -52	in gene, upstream	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SLC25A32	MFT, FLJ23872, SLC25A32, MFTC	solute carrier family 25, member 32	NM_030780, hCT2298955.0, hCT6060.3	221020_s_at	NP_110407.2, EAW91877.1, EAW91878.1
GeneID:25879	DCAF13	8	104,426,942	104,455,681	28,739	+	2	1_A375_pNL7_minus_lncRNA::1::5291, 2_A375_pNL97_plus_lncRNA::1::7613	194, 578	in gene, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene DCAF13	WDSOF1, GM83, HSPC064, DCAF13, DKFZp564O0463, MGC138247, MGC126859	DDB1 and CUL4 associated factor 13	NM_015420, hCT2298644.1, hCT2349327.0, hCT2349328.0, hCT6059.3, hCT1820720.2	1568840_at, 220643_s_at, 225676_s_at, 231764_s_at	NP_056235.4, EAW91880.1, EAW91879.1, EAW91881.1, EAW91882.1, EAW91883.1
GeneID:9699	RIMS2	8	104,512,976	105,265,451	752,475	+	4	1_A375_pNL7_minus_lncRNA::1::5293, 2_A375_pNL97_plus_lncRNA::1::7615, 2_A375_pNL97_plus_lncRNA::1::7616, 2_A375_pNL97_plus_lncRNA::1::7617	976, 848, 479856, 722560	in gene, in gene, in gene, in gene	1	1	14.67	23	3	2_A375_pNL97_plus_lncRNA::1	26	Gene RIMS2	KIAA0751, RIMS2, RAB3IP3, OBOE, RIM2, DKFZp781A0653	regulating synaptic membrane exocytosis 2	NM_014677, NM_001100117, hCT2344427.0, hCT2344428.0, hCT2357475.0, hCT2357476.0	206137_at, 215478_at	NP_055492.3, NP_001093587.1, EAW91888.1, EAW91889.1, EAW91890.1, EAW91891.1
GeneID:81501	TM7SF4	8	105,352,054	105,368,916	16,862	+	1	1_A375_pNL7_minus_lncRNA::1::5294	-2625	upstream	1	0	21	15	1	1_A375_pNL7_minus_lncRNA::1	21	Gene TM7SF4	TM7SF4, FIND, DCSTAMP, MGC138223, MGC138225	transmembrane 7 superfamily member 4	NM_030788, hCT1645205.1	221266_s_at	NP_110415.1, EAW91892.1
GeneID:29967	LRP12	8	105,501,459	105,601,252	99,793	-	2	1_A375_pNL7_minus_lncRNA::1::5295, 2_A375_pNL97_plus_lncRNA::1::7618	-252, -220	upstream, upstream	1	1	47	36	1	1_A375_pNL7_minus_lncRNA::1	47	Gene LRP12	DKFZp781F1053, FLJ12929, ST7, LRP12	low density lipoprotein receptor-related protein 12	NM_013437, NM_001135703, hCT2297264.0, hCT2297265.0, hCT2297266.0, hCT2357461.0	219631_at, 220253_s_at, 220254_at	NP_038465.1, NP_001129175.1, EAW91895.1, EAW91896.1, EAW91897.1, EAW91898.1
GeneID:55074	OXR1	8	107,282,473	107,764,922	482,449	+	3	1_A375_pNL7_minus_lncRNA::1::5297, 2_A375_pNL97_plus_lncRNA::1::7622, 2_A375_pNL97_plus_lncRNA::1::7623	387415, 567, 387415	in gene, in gene, in gene	1	1	29.5	33	2	2_A375_pNL97_plus_lncRNA::1	45	Gene OXR1	OXR1, FLJ42450, Nbla00307, FLJ45656, FLJ38829, FLJ10125, FLJ40849, FLJ41673	oxidation resistance 1	NM_018002, NM_181354, hCT2297261.0, hCT2297262.0, hCT6098.2	218197_s_at, 222553_x_at, 223879_s_at, 238409_x_at	NP_060472.2, NP_851999.2, EAW91903.1, EAW91904.1, EAW91905.1
GeneID:284	ANGPT1	8	108,261,710	108,510,254	248,544	-	1	2_A375_pNL97_plus_lncRNA::1::7624	-3442	upstream	0	1	15	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene ANGPT1	ANGPT1, AGPT, AGP1, ANG1	angiopoietin 1	NM_001146, hCT2297355.0, hCT2357456.0, hCT2357457.0, hCT5621.3	1552939_at, 205608_s_at, 205609_at	NP_001137.2, EAW91909.1, EAW91910.1, EAW91911.1, EAW91912.1
GeneID:3646	EIF3E	8	109,213,972	109,260,959	46,987	-	2	1_A375_pNL7_minus_lncRNA::1::5299, 2_A375_pNL97_plus_lncRNA::1::7626	85, -97	in gene, upstream	1	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene EIF3E	EIF3-P48, INT6, eIF3-p46, EIF3E, EIF3S6	eukaryotic translation initiation factor 3, subunit E	NM_001568, hCT2297426.0, hCT2357470.0	208697_s_at	NP_001559.1, EAW91918.1, EAW91919.1
GeneID:84955	NUDCD1	8	110,253,148	110,346,350	93,202	-	2	1_A375_pNL7_minus_lncRNA::1::5300, 2_A375_pNL97_plus_lncRNA::1::7627	-82, -82	upstream, upstream	1	1	26	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene NUDCD1	FLJ14991, CML66, NUDCD1, OVA66	NudC domain containing 1	NM_032869, NM_001128211, hCT2349329.0, hCT2349330.0, hCT6068.3	225438_at, 225439_at	NP_116258.2, NP_001121683.1, EAW91924.1, EAW91925.1, EAW91926.1
GeneID:56943	ENY2	8	110,346,552	110,358,189	11,637	+	2	1_A375_pNL7_minus_lncRNA::1::5300, 2_A375_pNL97_plus_lncRNA::1::7627	-120, -120	upstream, upstream	1	1	26	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene ENY2	ENY2, DC6, e(y)2, FLJ20480	enhancer of yellow 2 homolog (Drosophila)	NM_020189, NM_001193557, NR_036471, NR_036472, hCT2297362.0, hCT2357466.0, hCT2357467.0, hCT1820582.1	218482_at, 226775_at, 226776_at	NP_064574.1, NP_001180486.1, EAW91927.1, EAW91928.1, EAW91929.1, EAW91930.1
GeneID:55638	GOLSYN	8	110,586,405	110,704,020	117,615	-	2	1_A375_pNL7_minus_lncRNA::1::5301, 2_A375_pNL97_plus_lncRNA::1::7628	5556, 5588	in gene, in gene	1	1	19	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene GOLSYN	KIAA1472, OCSYN, GOLSYN, FLJ20366, SYBU, SNPHL	Golgi-localized protein	NM_001099743, NM_017786, NM_001099744, NM_001099745, NM_001099746, NM_001099747, NM_001099749, NM_001099748, NM_001099750, NM_001099752, NM_001099751, NM_001099753, NM_001099754, NM_001099756, NM_001099755, hCT2297469.0, hCT2297470.0, hCT6069.2	218692_at	NP_001093213.1, NP_060256.3, NP_001093214.1, NP_001093215.1, NP_001093216.1, NP_001093217.1, NP_001093219.1, NP_001093218.1, NP_001093220.1, NP_001093222.1, NP_001093221.1, NP_001093223.1, NP_001093224.1, NP_001093226.1, NP_001093225.1, EAW91935.1, EAW919
GeneID:114788	CSMD3	8	113,235,157	114,449,242	1,214,085	-	2	2_A375_pNL97_plus_lncRNA::1::7630, 1_A375_pNL7_minus_lncRNA::1::5303	820378, -1094	in gene, upstream	1	1	16	17.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene CSMD3	KIAA1894, CSMD3	CUB and Sushi multiple domains 3	NM_052900, NM_198123, NM_198124, hCT2348469.0, hCT2357490.0, hCT2357491.0, hCT2357492.0, hCT2357493.0	240228_at	NP_443132.3, NP_937756.1, NP_937757.1, EAW91945.1, EAW91946.1, EAW91948.1, EAW91944.1, EAW91947.1
GeneID:7227	TRPS1	8	116,420,724	116,681,228	260,504	-	1	2_A375_pNL97_plus_lncRNA::1::7631	20620	in gene	0	1	14	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene TRPS1	TRPS1, GC79, LGCR, MGC134928	trichorhinophalangeal syndrome I	NM_014112, hCT12219.1	218502_s_at, 222651_s_at, 224218_s_at, 234351_x_at	NP_054831.2, EAW91952.1
GeneID:84294	UTP23	8	117,778,742	117,786,923	8,181	+	1	1_A375_pNL7_minus_lncRNA::1::5306	-150	upstream	1	0	18	23	1	1_A375_pNL7_minus_lncRNA::1	18	Gene UTP23	C8orf53, UTP23, MGC14595	UTP23, small subunit (SSU) processome component, homolog (yeast)	NM_032334, hCT2297484.0, hCT2297485.0, hCT1640220.2	227402_s_at	NP_115710.2, EAW91961.1, EAW91960.1, EAW91962.1
GeneID:90390	MED30	8	118,532,965	118,552,501	19,536	+	2	1_A375_pNL7_minus_lncRNA::1::5307, 2_A375_pNL97_plus_lncRNA::1::7634	-5, 187	upstream, in gene	1	1	19	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene MED30	THRAP6, TRAP25, MED30S, MGC9890, MED30	mediator complex subunit 30	NM_080651, hCT2297517.0, hCT11633.1	227786_at, 227787_s_at, 230555_s_at	NP_542382.1, EAW91970.1, EAW91971.1
GeneID:401474	SAMD12	8	119,201,694	119,634,184	432,490	-	3	1_A375_pNL7_minus_lncRNA::1::5308, 1_A375_pNL7_minus_lncRNA::1::5309, 2_A375_pNL97_plus_lncRNA::1::7635	425896, 182008, 425896	in gene, in gene, in gene	1	1	19	17.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene SAMD12	SAMD12, FLJ39458, MGC148140, MGC148139	sterile alpha motif domain containing 12	NM_207506, NM_001101676	1562637_at	NP_997389.2, NP_001095146.1
GeneID:79075	DSCC1	8	120,846,181	120,868,170	21,989	-	1	1_A375_pNL7_minus_lncRNA::1::5311	298	in gene	1	0	20	21	1	1_A375_pNL7_minus_lncRNA::1	20	Gene DSCC1	MGC5528, DCC1, DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	NM_024094, hCT2298295.0, hCT12356.2	216646_at, 219000_s_at	NP_076999.2, EAW91994.1, EAW91995.1
GeneID:64798	DEPDC6	8	120,885,900	121,063,157	177,257	+	1	2_A375_pNL97_plus_lncRNA::1::7637	324	in gene	0	1	18	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene DEPDC6	DKFZp564B1778, FLJ12341, DEP.6, DEPTOR, FLJ13854, DEPDC6, FLJ12428	DEP domain containing 6	NM_022783, hCT1640617.3	218858_at	NP_073620.2, EAW91997.1
GeneID:7373	COL14A1	8	121,137,352	121,384,273	246,921	+	2	1_A375_pNL7_minus_lncRNA::1::5312, 2_A375_pNL97_plus_lncRNA::1::7638	133240, 133176	in gene, in gene	1	1	12	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene COL14A1	COL14A1, UND	collagen, type XIV, alpha 1	NM_021110, hCT2298028.0, hCT2298032.0, hCT8933.3, hCT1955624.1, hCT1955625.1	212865_s_at, 216865_at, 216866_s_at	NP_066933.1, EAW92002.1, EAW91998.1, EAW91999.1, EAW92000.1, EAW92001.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100507316	LOC100507316	8	144,362,331	144,363,860	1,529	-	4	1_A375_pNL7_minus_lncRNA::1::5372, 1_A375_pNL7_minus_lncRNA::1::5373, 2_A375_pNL97_plus_lncRNA::1::7743, 2_A375_pNL97_plus_lncRNA::1::7744	-60, -9644, -44, -9644	upstream, upstream, upstream, upstream	1	1	82.5	88.5	2	2_A375_pNL97_plus_lncRNA::1	150	Gene LOC100507316		hypothetical LOC100507316	XR_108896, XR_108897, XR_108898		
GeneID:79943	ZNF696	8	144,373,559	144,382,122	8,563	+	4	1_A375_pNL7_minus_lncRNA::1::5372, 1_A375_pNL7_minus_lncRNA::1::5373, 2_A375_pNL97_plus_lncRNA::1::7743, 2_A375_pNL97_plus_lncRNA::1::7744	-9639, -55, -9655, -55	upstream, upstream, upstream, upstream	1	1	82.5	88.5	2	2_A375_pNL97_plus_lncRNA::1	150	Gene ZNF696	ZNF696, FLJ14129	zinc finger protein 696	NM_030895	220967_s_at, 232162_at	NP_112157.2
GeneID:23144	ZC3H3	8	144,519,825	144,623,620	103,795	-	1	2_A375_pNL97_plus_lncRNA::1::7745	-172	upstream	0	1	14	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ZC3H3	ZC3H3, ZC3HDC3, KIAA0150	zinc finger CCCH-type containing 3	NM_015117, hCT23253.1	213445_at	NP_055932.2, EAW82249.1
GeneID:1936	EEF1D	8	144,661,898	144,679,845	17,947	-	3	1_A375_pNL7_minus_lncRNA::1::5374, 2_A375_pNL97_plus_lncRNA::1::7746, 2_A375_pNL97_plus_lncRNA::1::7747	133, 133, -603	in gene, in gene, upstream	1	1	30.5	40	2	2_A375_pNL97_plus_lncRNA::1	54	Gene EEF1D	EF1D, EF-1D, FP1047, FLJ20897, EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	NM_032378, NM_001960, NM_001130053, NM_001130055, NM_001130056, NM_001130057, hCT2274544.0, hCT2274545.0, hCT2274547.0, hCT2274548.0, hCT2274550.0, hCT2274552.0, hCT2274554.0, hCT2274556.0, hCT2356228.0	203113_s_at	NP_115754.2, NP_001951.2, NP_001123525.1, NP_001123527.1, NP_001123528.1, NP_001123529.1, EAW82227.1, EAW82228.1, EAW82229.1, EAW82230.1, EAW82231.1, EAW82232.1, EAW82233.1, EAW82234.1, EAW82235.1
GeneID:84948	TIGD5	8	144,680,074	144,682,485	2,411	+	3	1_A375_pNL7_minus_lncRNA::1::5374, 2_A375_pNL97_plus_lncRNA::1::7746, 2_A375_pNL97_plus_lncRNA::1::7747	-362, -362, 374	upstream, upstream, in gene	1	1	30.5	40	2	2_A375_pNL97_plus_lncRNA::1	54	Gene TIGD5	MGC44883, FLJ14926, TIGD5	tigger transposable element derived 5	NM_032862, hCT1971207.1	229756_at	NP_116251.4, EAW82226.1
GeneID:65263	PYCRL	8	144,686,063	144,691,764	5,701	-	4	1_A375_pNL7_minus_lncRNA::1::5374, 2_A375_pNL97_plus_lncRNA::1::7746, 2_A375_pNL97_plus_lncRNA::1::7747, 2_A375_pNL97_plus_lncRNA::1::7748	12072, 12072, 11336, -8568	downstream, downstream, downstream, upstream	1	1	24.67	32.67	3	2_A375_pNL97_plus_lncRNA::1	54	Gene PYCRL	PYCRL, FLJ13852	pyrroline-5-carboxylate reductase-like	NM_023078, hCT1966035.1, hCT2274541.0, hCT23245.3	218944_at	NP_075566.2, EAW82223.1, EAW82224.1, EAW82225.1
GeneID:7264	TSTA3	8	144,694,788	144,699,732	4,944	-	1	2_A375_pNL97_plus_lncRNA::1::7748	-620	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TSTA3	SDR4E1, P35B, TSTA3, FX	tissue specific transplantation antigen P35B	NM_003313, hCT2274532.0, hCT2274533.0, hCT2274537.0, hCT23243.3, hCT1952560.1, hCT1952561.1	201644_at, 36936_at	NP_003304.1, EAW82219.1, EAW82217.1, EAW82218.1, EAW82220.1, EAW82222.1, EAW82221.1
GeneID:9831	ZNF623	8	144,718,373	144,735,900	17,527	+	2	1_A375_pNL7_minus_lncRNA::1::5375, 2_A375_pNL97_plus_lncRNA::1::7749	-581, -517	upstream, upstream	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF623	MGC104128, MGC103965, ZNF623	zinc finger protein 623	NM_001082480, NM_014789, hCT2274531.0	206188_at	NP_001075949.1, NP_055604.3, EAW82215.1
GeneID:286075	ZNF707	8	144,766,622	144,777,555	10,933	+	2	1_A375_pNL7_minus_lncRNA::1::5376, 2_A375_pNL97_plus_lncRNA::1::7750	-110, 50	upstream, in gene	1	1	19	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ZNF707	ZNF707	zinc finger protein 707	NM_173831, NM_001100598, NM_001100599, hCT2349691.0, hCT2356236.0, hCT1808836.3, hCT1952551.1, hCT1952552.1	232076_at	NP_776192.2, NP_001094068.1, NP_001094069.1, EAW82210.1, EAW82211.1, EAW82212.1, EAW82213.1, EAW82214.1
GeneID:22827	PUF60	8	144,898,547	144,911,537	12,990	-	1	2_A375_pNL97_plus_lncRNA::1::7751	113	in gene	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene PUF60	FLJ31379, RoBPI, SIAHBP1, FIR, PUF60	poly-U binding splicing factor 60KDa	NM_014281, NM_078480, NM_001136033, hCT1966843.1, hCT1966844.1, hCT2274516.0, hCT2274517.0, hCT2274521.0, hCT2274522.0, hCT2356232.0, hCT2356233.0, hCT2356234.0, hCT31979.2, hCT1952566.1, hCT1952567.1	209899_s_at	NP_055096.2, NP_510965.1, NP_001129505.1, EAW82184.1, EAW82187.1, EAW82192.1, EAW82185.1, EAW82186.1, EAW82188.1, EAW82189.1, EAW82190.1, EAW82191.1, EAW82193.1, EAW82194.1, EAW82195.1
GeneID:340371	NRBP2	8	144,915,755	144,923,146	7,391	-	1	2_A375_pNL97_plus_lncRNA::1::7751	11722	downstream	0	1	16	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene NRBP2	pp9320, DKFZp434P086, TRG16, NRBP2, MGC138699	nuclear receptor binding protein 2	NM_178564, hCT2274512.0, hCT2274514.0, hCT2356230.0, hCT2356231.0, hCT31978.3, hCT1952565.1	225949_at	NP_848659.2, EAW82178.1, EAW82179.1, EAW82180.1, EAW82181.1, EAW82182.1, EAW82183.1
GeneID:5339	PLEC1	8	144,989,321	145,050,913	61,592	-	8	1_A375_pNL7_minus_lncRNA::1::5377, 1_A375_pNL7_minus_lncRNA::1::5378, 1_A375_pNL7_minus_lncRNA::1::5379, 1_A375_pNL7_minus_lncRNA::1::5380, 2_A375_pNL97_plus_lncRNA::1::7752, 2_A375_pNL97_plus_lncRNA::1::7753, 2_A375_pNL97_plus_lncRNA::1::7754, 2_A375_pNL97_plus_lncRNA::1::7755	40033, 32833, 28129, 1649, 33889, 28065, 27201, 1633	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	20.8	23.4	5	2_A375_pNL97_plus_lncRNA::1	26	Gene PLEC1	LGMD2Q, PLTN, EBSO, PLEC1b, PCN, PLEC1, PLEC, EBS1, HD1	plectin 1, intermediate filament binding protein 500kDa	NM_201379, NM_201381, NM_201383, NM_201384, NM_201380, NM_201382, NM_201378, NM_000445, hCT2274504.0, hCT2274505.0, hCT2274506.0, hCT2274507.0, hCT2356224.0	201373_at, 216971_s_at	NP_958781.1, NP_958783.1, NP_958785.1, NP_958782.1, NP_958784.1, NP_958786.1, NP_958780.1, NP_000436.2, EAW82170.1, EAW82171.1, EAW82172.1, EAW82173.1, EAW82174.1
GeneID:724031	MIR661	8	145,019,359	145,019,447	88	-	6	1_A375_pNL7_minus_lncRNA::1::5377, 1_A375_pNL7_minus_lncRNA::1::5378, 1_A375_pNL7_minus_lncRNA::1::5379, 2_A375_pNL97_plus_lncRNA::1::7752, 2_A375_pNL97_plus_lncRNA::1::7753, 2_A375_pNL97_plus_lncRNA::1::7754	8567, 1367, -3337, 2423, -3401, -4265	downstream, downstream, upstream, downstream, upstream, upstream	1	1	21.75	22.25	4	2_A375_pNL97_plus_lncRNA::1	26	Gene MIR661	hsa-mir-661, MIR661, MIRN661	microRNA 661	NR_030383		
GeneID:84875	PARP10	8	145,051,320	145,060,635	9,315	-	2	1_A375_pNL7_minus_lncRNA::1::5380, 2_A375_pNL97_plus_lncRNA::1::7755	11371, 11355	downstream, downstream	1	1	17	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene PARP10	FLJ14464, PARP10	poly (ADP-ribose) polymerase family, member 10	NM_032789, hCT2274501.1	226401_at, 226669_x_at, 229350_x_at, 238063_at	NP_116178.2, EAW82169.1
GeneID:54512	EXOSC4	8	145,133,522	145,135,551	2,029	+	2	1_A375_pNL7_minus_lncRNA::1::5381, 2_A375_pNL97_plus_lncRNA::1::7756	195, 462	in gene, in gene	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene EXOSC4	RRP41A, hRrp41p, Ski6p, p12A, SKI6, Rrp41p, FLJ20591, EXOSC4, RRP41	exosome component 4	NM_019037, hCT1786229.2	218695_at, 58696_at, 91684_g_at	NP_061910.1, EAW82166.1
GeneID:8733	GPAA1	8	145,137,524	145,141,119	3,595	+	2	1_A375_pNL7_minus_lncRNA::1::5381, 2_A375_pNL97_plus_lncRNA::1::7756	-3807, -3540	upstream, upstream	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene GPAA1	GAA1, GPAA1, hGAA1	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)	NM_003801, hCT2271671.0, hCT10587.2, hCT1958358.0, hCT1958359.0, hCT1958360.1	201618_x_at, 211060_x_at, 215690_x_at	NP_003792.1, EAW82162.1, EAW82161.1, EAW82163.1, EAW82164.1, EAW82165.1
GeneID:1537	CYC1	8	145,149,960	145,152,428	2,468	+	2	1_A375_pNL7_minus_lncRNA::1::5382, 2_A375_pNL97_plus_lncRNA::1::7757	9272, 9304	downstream, downstream	1	1	36	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene CYC1	UQCR4, CYC1	cytochrome c-1	NM_001916, hCT10630.3	201066_at	NP_001907.2, EAW82160.1
GeneID:100507362	LOC100507362	8	145,151,231	145,151,943	712	-	2	1_A375_pNL7_minus_lncRNA::1::5382, 2_A375_pNL97_plus_lncRNA::1::7757	-7289, -7321	upstream, upstream	1	1	36	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene LOC100507362		hypothetical LOC100507362	XR_108900		
GeneID:81858	SHARPIN	8	145,153,536	145,159,140	5,604	-	2	1_A375_pNL7_minus_lncRNA::1::5382, 2_A375_pNL97_plus_lncRNA::1::7757	-92, -124	upstream, upstream	1	1	36	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene SHARPIN	SHARPIN, SIPL1, DKFZp434N1923	SHANK-associated RH domain interactor	NM_030974, hCT2270671.0, hCT1958361.1, hCT1958362.1, hCT1958363.1, hCT1958364.1, hCT1958365.1, hCT1958366.1	220973_s_at	NP_112236.3, EAW82153.1, EAW82151.1, EAW82152.1, EAW82154.1, EAW82155.1, EAW82150.1, EAW82156.1
GeneID:84232	MAF1	8	145,159,305	145,162,515	3,210	+	2	1_A375_pNL7_minus_lncRNA::1::5382, 2_A375_pNL97_plus_lncRNA::1::7757	-73, -41	upstream, upstream	1	1	36	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene MAF1	MGC20332, MAF1, MGC31779, MGC39758	MAF1 homolog (S. cerevisiae)	NM_032272, hCT2271881.0, hCT10632.2	222998_at	NP_115648.2, EAW82158.1, EAW82159.1
GeneID:340390	KIAA1875	8	145,162,629	145,173,218	10,589	+	2	1_A375_pNL7_minus_lncRNA::1::5382, 2_A375_pNL97_plus_lncRNA::1::7757	-3397, -3365	upstream, upstream	1	1	36	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene KIAA1875	KIAA1875		NR_024207	233344_x_at	
GeneID:8694	DGAT1	8	145,538,247	145,550,567	12,320	-	3	1_A375_pNL7_minus_lncRNA::1::5383, 2_A375_pNL97_plus_lncRNA::1::7758, 2_A375_pNL97_plus_lncRNA::1::7759	39, -153, -8686	in gene, upstream, upstream	1	1	19.5	19	2	1_A375_pNL7_minus_lncRNA::1	23	Gene DGAT1	DGAT1, DGAT, ARGP1	diacylglycerol O-acyltransferase homolog 1 (mouse)	NM_012079, hCT2270665.0, hCT15120.3, hCT1961865.1, hCT1961866.1	203669_s_at	NP_036211.2, EAW82129.1, EAW82127.1, EAW82128.1, EAW82130.1
GeneID:83482	SCRT1	8	145,554,454	145,559,943	5,489	-	3	1_A375_pNL7_minus_lncRNA::1::5383, 2_A375_pNL97_plus_lncRNA::1::7758, 2_A375_pNL97_plus_lncRNA::1::7759	9415, 9223, 690	downstream, downstream, in gene	1	1	19.5	19	2	1_A375_pNL7_minus_lncRNA::1	23	Gene SCRT1	SCRT, ZNF898, SCRT1, DKFZp547F072	scratch homolog 1, zinc finger protein (Drosophila)	NM_031309, hCT1786231.3	221026_s_at, 226761_at	NP_112599.1, EAW82125.1
GeneID:340393	C8ORFK29	8	145,576,886	145,578,505	1,619	-	1	2_A375_pNL97_plus_lncRNA::1::7760	-3751	upstream	0	1	25	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C8ORFK29		hypothetical LOC340393	NR_015426		
GeneID:26233	FBXL6	8	145,579,091	145,582,132	3,041	-	1	2_A375_pNL97_plus_lncRNA::1::7760	-124	upstream	0	1	25	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene FBXL6	FBL6, PP14630, FBXL6, FBL6A	F-box and leucine-rich repeat protein 6	NM_012162, NM_024555, hCT2270656.0, hCT2356214.0, hCT15130.3, hCT1958351.1, hCT1958352.1, hCT1958353.1	219189_at, 239416_at	NP_036294.1, NP_078831.3, EAW82118.1, EAW82119.1, EAW82120.1, EAW82122.1, EAW82117.1, EAW82121.1
GeneID:79581	GPR172A	8	145,582,225	145,584,946	2,721	+	1	2_A375_pNL97_plus_lncRNA::1::7760	31	in gene	0	1	25	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene GPR172A	GPCR41, GPCR, PAR1, hRFT3, RFT3, D15Ertd747e, GPR172A	G protein-coupled receptor 172A	NM_024531, hCT2271898.0, hCT2271899.0	218151_x_at, 222155_s_at	NP_078807.1, EAW82116.1, EAW82115.1
GeneID:203054	ADCK5	8	145,597,731	145,618,457	20,726	+	1	2_A375_pNL97_plus_lncRNA::1::7761	-147	upstream	0	1	8	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene ADCK5	ADCK5, FLJ35454, MGC126708	aarF domain containing kinase 5	NM_174922, hCT2271907.0, hCT2356241.0, hCT2356242.0, hCT15128.3	226524_at	NP_777582.3, EAW82111.1, EAW82112.1, EAW82113.1, EAW82114.1
GeneID:51160	VPS28	8	145,649,000	145,653,927	4,927	-	2	1_A375_pNL7_minus_lncRNA::1::5384, 2_A375_pNL97_plus_lncRNA::1::7762	-57, -57	upstream, upstream	1	1	37	34	1	1_A375_pNL7_minus_lncRNA::1	37	Gene VPS28	MGC60323, VPS28	vacuolar protein sorting 28 homolog (S. cerevisiae)	NM_016208, NM_183057, hCT15119.3, hCT1958372.1, hCT1958373.1, hCT1958374.1, hCT1958375.1, hCT1958376.1, hCT1958380.1	218679_s_at	NP_057292.1, NP_898880.1, EAW82094.1, EAW82098.1, EAW82099.1, EAW82100.1, EAW82095.1, EAW82096.1, EAW82097.1
GeneID:4796	NFKBIL2	8	145,654,163	145,669,812	15,649	-	2	1_A375_pNL7_minus_lncRNA::1::5384, 2_A375_pNL97_plus_lncRNA::1::7762	15828, 15828	downstream, downstream	1	1	37	34	1	1_A375_pNL7_minus_lncRNA::1	37	Gene NFKBIL2	IKBR, FLJ40087, TONSL, NFKBIL2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	NM_013432, hCT2270636.0, hCT1952002.2	1558329_at, 1558330_x_at, 207137_at	NP_038460.4, EAW82093.1, EAW82092.1
GeneID:50626	CYHR1	8	145,675,315	145,691,031	15,716	-	1	2_A375_pNL97_plus_lncRNA::1::7763	279	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CYHR1	CHRP, CYHR1, KIAA0496, MGC13010	cysteine/histidine-rich 1	NM_138496, NM_032687, NM_001129888, hCT2270633.0, hCT2270634.0, hCT2356243.0, hCT15136.3	213072_at, 213681_at, 223421_at, 229945_at	NP_612505.1, NP_116076.1, NP_001123360.1, EAW82088.1, EAW82089.1, EAW82091.1, EAW82090.1
GeneID:90990	KIFC2	8	145,691,738	145,699,499	7,761	+	1	2_A375_pNL97_plus_lncRNA::1::7763	-986	upstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene KIFC2	KIFC2	kinesin family member C2	NM_145754, hCT2271914.0, hCT2356216.0, hCT15132.3	226791_at, 226792_s_at	NP_665697.1, EAW82086.1, EAW82085.1, EAW82087.1
GeneID:8928	FOXH1	8	145,699,115	145,701,718	2,603	-	1	2_A375_pNL97_plus_lncRNA::1::7763	10966	downstream	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene FOXH1	FAST-1, FOXH1, FAST1	forkhead box H1	NM_003923, hCT2270630.0, hCT15116.3	207644_at, 231407_s_at	NP_003914.1, EAW82084.1, EAW82083.1
GeneID:84988	PPP1R16A	8	145,722,109	145,727,504	5,395	+	1	2_A375_pNL97_plus_lncRNA::1::7764	13027	downstream	0	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene PPP1R16A	MYPT3, PPP1R16A, MGC14333	protein phosphatase 1, regulatory (inhibitor) subunit 16A	NM_032902, hCT2271921.0, hCT2271923.0, hCT15127.3	225203_at	NP_116291.1, EAW82080.1, EAW82081.1, EAW82082.1
GeneID:2875	GPT	8	145,729,465	145,732,555	3,090	+	1	2_A375_pNL97_plus_lncRNA::1::7764	5671	downstream	0	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene GPT	AAT1, ALT1, GPT1, GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	NM_005309, hCT1968008.0, hCT2271933.0, hCT15118.3	206709_x_at	NP_005300.1, EAW82079.1, EAW82077.1, EAW82078.1
GeneID:113655	MFSD3	8	145,734,552	145,736,589	2,037	+	1	2_A375_pNL97_plus_lncRNA::1::7764	584	in gene	0	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene MFSD3	MFSD3	major facilitator superfamily domain containing 3	NM_138431, hCT2271938.1, hCT2271941.1, hCT2271943.1, hCT2356226.0, hCT2356227.0	227296_at, 238947_at	NP_612440.1, EAW82075.1, EAW82072.1, EAW82073.1, EAW82074.1, EAW82076.1
GeneID:9401	RECQL4	8	145,736,667	145,743,210	6,543	-	1	2_A375_pNL97_plus_lncRNA::1::7764	8074	downstream	0	1	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RECQL4	RECQ4, RECQL4	RecQ protein-like 4	NM_004260, hCT2356239.0, hCT15117.3	1553015_a_at, 213520_at	NP_004251.3, EAW82070.1, EAW82071.1
GeneID:9684	LRRC14	8	145,743,391	145,750,557	7,166	+	2	1_A375_pNL7_minus_lncRNA::1::5385, 2_A375_pNL97_plus_lncRNA::1::7764	11105, -8255	downstream, upstream	1	1	19	18.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene LRRC14	LRRC14A, LRRC14, KIAA0014	leucine rich repeat containing 14	NM_014665, hCT2271940.1, hCT2271942.0, hCT2271944.0, hCT2271945.1	203495_at, 32062_at	NP_055480.1, EAW82069.1, EAW82066.1, EAW82067.1, EAW82068.1
GeneID:441381	LRRC24	8	145,747,761	145,752,416	4,655	-	1	1_A375_pNL7_minus_lncRNA::1::5385	-2080	upstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LRRC24	MGC111464, LRRC24, LRRC14OS	leucine rich repeat containing 24	NM_001024678, hCT1961240.1		NP_001019849.2, EAW82065.1
GeneID:414919	C8orf82	8	145,751,603	145,754,458	2,855	-	1	1_A375_pNL7_minus_lncRNA::1::5385	-38	upstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene C8orf82	C8orf82, MGC70857	chromosome 8 open reading frame 82	NM_001001795, hCT1966010.1, hCT15134.3	226710_at	NP_001001795.1, EAW82064.1, EAW82063.1
GeneID:80728	KIAA1688	8	145,754,563	145,838,891	84,328	-	1	1_A375_pNL7_minus_lncRNA::1::5385	84395	downstream	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene KIAA1688	ARHGAP39, KIAA1688, CrGAP, Vilse	Rho GTPase activating protein 39	NM_025251, hCT15124.3	227876_at	NP_079527.1, EAW82062.1
GeneID:90987	ZNF251	8	145,946,294	145,980,970	34,676	-	2	1_A375_pNL7_minus_lncRNA::1::5386, 2_A375_pNL97_plus_lncRNA::1::7765	10, -54	in gene, upstream	1	1	18	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene ZNF251	FLJ34319, ZNF251	zinc finger protein 251	NM_138367	226754_at	NP_612376.1
GeneID:80778	ZNF34	8	145,998,499	146,012,725	14,226	-	3	1_A375_pNL7_minus_lncRNA::1::5387, 2_A375_pNL97_plus_lncRNA::1::7766, 2_A375_pNL97_plus_lncRNA::1::7767	-5270, 85, -5099	upstream, in gene, upstream	1	1	15	19.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene ZNF34	MGC10520, KOX32, ZNF34	zinc finger protein 34	NM_030580, hCT2270609.0, hCT2349690.0, hCT1786226.2, hCT1958339.1	219801_at	NP_085057.3, EAW82055.1, EAW82056.1, EAW82057.1, EAW82058.1
GeneID:6132	RPL8	8	146,015,154	146,017,805	2,651	-	3	1_A375_pNL7_minus_lncRNA::1::5387, 2_A375_pNL97_plus_lncRNA::1::7766, 2_A375_pNL97_plus_lncRNA::1::7767	-190, 5165, -19	upstream, downstream, upstream	1	1	15	19.5	2	2_A375_pNL97_plus_lncRNA::1	22	Gene RPL8	L8, RPL8	ribosomal protein L8	NM_033301, NM_000973, hCT2270601.0, hCT15114.4, hCT1952000.2, hCT1961861.1, hCT1961862.1, hCT1961863.1, hCT1961864.1, hCT1964069.1	200936_at	NP_150644.1, NP_000964.1, EAW82048.1, EAW82052.1, EAW82053.1, EAW82054.1, EAW82047.1, EAW82049.1, EAW82050.1, EAW82051.1
GeneID:340385	ZNF517	8	146,024,261	146,034,529	10,268	+	2	1_A375_pNL7_minus_lncRNA::1::5387, 2_A375_pNL97_plus_lncRNA::1::7767	-6266, -6437	upstream, upstream	1	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ZNF517	ZNF517	zinc finger protein 517	NM_213605, hCT2271959.1, hCT2341267.0, hCT2341268.0, hCT2356244.0		NP_998770.2, EAW82044.1, EAW82043.1, EAW82045.1, EAW82046.1
GeneID:100130027	LOC100130027	8	146,032,252	146,052,425	20,173	-	2	1_A375_pNL7_minus_lncRNA::1::5388, 2_A375_pNL97_plus_lncRNA::1::7768	-535, -503	upstream, upstream	1	1	18	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene LOC100130027		hypothetical LOC100130027	XR_110587, XR_114228		
GeneID:100129596	LOC100129596	8	146,045,697	146,046,149	452	-	2	1_A375_pNL7_minus_lncRNA::1::5388, 2_A375_pNL97_plus_lncRNA::1::7768	-6811, -6779	upstream, upstream	1	1	18	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene LOC100129596		hypothetical LOC100129596	XR_113185, XR_110585, XR_114226		
GeneID:7553	ZNF7	8	146,052,903	146,068,606	15,703	+	4	1_A375_pNL7_minus_lncRNA::1::5388, 1_A375_pNL7_minus_lncRNA::1::5389, 2_A375_pNL97_plus_lncRNA::1::7768, 2_A375_pNL97_plus_lncRNA::1::7769	57, 25625, 25, 25305	in gene, downstream, in gene, downstream	1	1	17	22.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene ZNF7	FLJ36706, HF.16, ZNF7, KOX4, zf30	zinc finger protein 7	NM_003416, hCT2271962.0, hCT2271963.0, hCT2271965.0, hCT2356225.0, hCT8157.3	1559980_at, 205069_at, 234914_at, 234920_at	NP_003407.1, EAW82038.1, EAW82039.1, EAW82040.1, EAW82041.1, EAW82042.1
GeneID:28991	COMMD5	8	146,075,551	146,078,932	3,381	-	2	1_A375_pNL7_minus_lncRNA::1::5389, 2_A375_pNL97_plus_lncRNA::1::7769	404, 724	in gene, in gene	1	1	16	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene COMMD5	FLJ13008, HT002, COMMD5, HCARG, MGC72046	COMM domain containing 5	NM_014066, NM_001081004, NM_001081003, hCT2270593.0, hCT2270594.0, hCT2270595.0, hCT2270596.0, hCT15113.3	223198_x_at, 223819_x_at, 224387_at, 232640_at	NP_054785.2, NP_001074473.1, NP_001074472.1, EAW82033.1, EAW82034.1, EAW82035.1, EAW82036.1, EAW82037.1
GeneID:58500	ZNF250	8	146,102,336	146,126,846	24,510	-	2	1_A375_pNL7_minus_lncRNA::1::5390, 2_A375_pNL97_plus_lncRNA::1::7770	-610, 62	upstream, in gene	1	1	24	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ZNF250	MGC9718, MGC111123, ZNF250, ZFP647, FLJ57354, ZNF647	zinc finger protein 250	NM_021061, NM_001109689, hCT2356237.0, hCT2356238.0, hCT15125.3, hCT1952001.1	213858_at	NP_066405.1, NP_001103159.1, EAW82029.1, EAW82030.1, EAW82031.1, EAW82032.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:286103	C8orf77	8	146,228,197	146,231,432	3,235	+	1	2_A375_pNL97_plus_lncRNA::1::7771	11	in gene	0	1	14	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene C8orf77	C8orf77, MGC141859	chromosome 8 open reading frame 77	NR_026974	1556790_s_at	
GeneID:65265	C8orf33	8	146,277,824	146,281,416	3,592	+	1	2_A375_pNL97_plus_lncRNA::1::7772	96	in gene	0	1	15	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene C8orf33	FLJ20989, C8orf33	chromosome 8 open reading frame 33	NM_023080, hCT2271971.0, hCT2271972.0	218187_s_at, 222551_s_at	NP_075568.1, EAW82022.1, EAW82023.1
GeneID:23189	KANK1	9	504,703	746,103	241,400	+	6	1_A375_pNL7_minus_lncRNA::1::5391, 1_A375_pNL7_minus_lncRNA::1::5392, 2_A375_pNL97_plus_lncRNA::1::7773, 2_A375_pNL97_plus_lncRNA::1::7774, 2_A375_pNL97_plus_lncRNA::1::7775, 2_A375_pNL97_plus_lncRNA	246593, 251201, 190017, 208161, 234145, 251169	downstream, downstream, in gene, in gene, in gene, downstream	1	1	15.8	20.8	5	2_A375_pNL97_plus_lncRNA::1	25	Gene KANK1	KIAA0172, MGC43128, ANKRD15, DKFZp451G231, KANK, KANK1	KN motif and ankyrin repeat domains 1	NM_153186, NM_015158, hCT21570.3, hCT2353320.0	1555832_at, 213005_s_at, 216762_at, 216763_at, 237162_at, 238789_at	NP_694856.1, NP_055973.2, EAW58821.1, EAW58822.1
GeneID:6595	SMARCA2	9	2,015,342	2,193,624	178,282	+	2	2_A375_pNL97_plus_lncRNA::1::7777, 2_A375_pNL97_plus_lncRNA::1::7778	-366, 1842	upstream, in gene	0	1	15	18.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene SMARCA2	hSNF2a, SWI2, Sth1p, MGC74511, SNF2, SMARCA2, hBRM, SNF2LA, FLJ36757, SNF2L2, BAF190, BRM	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	NM_139045, NM_003070, hCT2301911.0, hCT2301913.0, hCT2301915.0, hCT2301918.0, hCT1950952.1	206542_s_at, 206543_at, 206544_x_at, 212257_s_at, 212258_s_at, 217707_x_at, 228826_s_at	NP_620614.2, NP_003061.3, EAW58812.1, EAW58813.1, EAW58814.1, EAW58815.1, EAW58811.1
GeneID:401491	FLJ35024	9	2,535,652	2,622,373	86,721	-	2	1_A375_pNL7_minus_lncRNA::1::5394, 2_A375_pNL97_plus_lncRNA::1::7781	47959, 62565	in gene, in gene	1	1	13.5	12.5	2	2_A375_pNL97_plus_lncRNA::1	16	Gene FLJ35024		hypothetical LOC401491	NR_015375	1558212_at	
GeneID:7436	VLDLR	9	2,621,793	2,654,485	32,692	+	1	2_A375_pNL97_plus_lncRNA::1::7782	33775	downstream	0	1	13	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene VLDLR	FLJ35024, VLDLRCH, CHRMQ1, VLDLR, CARMQ1	very low density lipoprotein receptor	NM_001018056, NM_003383, hCT2301922.0, hCT2301924.0, hCT2353317.0, hCT19070.3, hCT1958431.1	209822_s_at	NP_001018066.1, NP_003374.3, EAW58805.1, EAW58806.1, EAW58807.1, EAW58808.1, EAW58804.1
GeneID:9933	KIAA0020	9	2,804,152	2,844,130	39,978	-	2	1_A375_pNL7_minus_lncRNA::1::5395, 2_A375_pNL97_plus_lncRNA::1::7783	-30, -158	upstream, upstream	1	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene KIAA0020	MGC8749, PEN, KIAA0020, HLA-HA8, PUF6, XTP5	KIAA0020	NM_014878, hCT2301726.0	1570529_at, 203712_at	NP_055693.4, EAW58802.1
GeneID:5991	RFX3	9	3,224,645	3,525,983	301,338	-	2	1_A375_pNL7_minus_lncRNA::1::5396, 2_A375_pNL97_plus_lncRNA::1::7784	-769, -737	upstream, upstream	1	1	21	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene RFX3	RFX3, MGC87155, bA32F11.1	regulatory factor X, 3 (influences HLA class II expression)	NM_002919, NM_134428, hCT2301653.0, hCT2301654.0, hCT2301655.0, hCT2301657.0, hCT19084.3, hCT1950953.1	207234_at, 238610_at	NP_002910.1, NP_602304.1, EAW58794.1, EAW58796.1, EAW58797.1, EAW58799.1, EAW58795.1, EAW58798.1
GeneID:169792	GLIS3	9	3,824,128	4,300,035	475,907	-	15	1_A375_pNL7_minus_lncRNA::1::5397, 1_A375_pNL7_minus_lncRNA::1::5398, 1_A375_pNL7_minus_lncRNA::1::5399, 1_A375_pNL7_minus_lncRNA::1::5400, 1_A375_pNL7_minus_lncRNA::1::5401, 2_A375_pNL97_plus_lncRNA::1::7785, 2_A375_pNL97_plus_lncRNA::1::7786, 2_A375_pNL97_plus_lncRNA::1::7787, 2_A375_pNL97_plus_lncRNA::1::7788, 2_A375_pNL97_plus_lncRNA::1::7789, 2_A375_pNL97_plus_lncRNA::1::7790, 2_A375_pNL97_plus_lncRNA::1::7791, 2_A375_pNL97_plus_lncRNA::1::7792, 2_A375_pNL97_plus_lncRNA::1::7793, 2_A375_pNL97_plus_lncRNA	392963, 367459, 38339, 6179, 1347, 436624, 393411, 330979, 215491, 61251, 9315, 6275, 2339, 1571, 131	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	15.75	17.63	12	2_A375_pNL97_plus_lncRNA::1	26	Gene GLIS3	FLJ90578, ZNF515, GLIS3, MGC33662, FLJ38999	GLIS family zinc finger 3	NM_152629, NM_001042413	229435_at, 230258_at	NP_689842.3, NP_001035878.1
GeneID:84650	C9orf70	9	3,898,646	3,901,248	2,602	+	2	1_A375_pNL7_minus_lncRNA::1::5397, 2_A375_pNL97_plus_lncRNA::1::7786	8426, 7978	downstream, downstream	1	1	17	14	1	1_A375_pNL7_minus_lncRNA::1	17	Gene C9orf70	C9orf70, MGC16153	chromosome 9 open reading frame 70	NR_026663	1553756_at	
GeneID:100287493	LOC100287493	9	4,294,224	4,300,092	5,868	+	7	1_A375_pNL7_minus_lncRNA::1::5400, 1_A375_pNL7_minus_lncRNA::1::5401, 2_A375_pNL97_plus_lncRNA::1::7790, 2_A375_pNL97_plus_lncRNA::1::7791, 2_A375_pNL97_plus_lncRNA::1::7792, 2_A375_pNL97_plus_lncRNA::1::7793, 2_A375_pNL97_plus_lncRNA	-368, 4464, -3504, -464, 3472, 4240, 5650	upstream, in gene, upstream, upstream, in gene, in gene, in gene	1	1	15	20.6	5	2_A375_pNL97_plus_lncRNA::1	25	Gene LOC100287493		hypothetical protein LOC100287493	XM_002342902, XM_003120092, XM_003120630		XP_002342943.1, XP_003120140.1, XP_003120678.1
GeneID:6505	SLC1A1	9	4,490,427	4,587,469	97,042	+	3	1_A375_pNL7_minus_lncRNA::1::5403, 2_A375_pNL97_plus_lncRNA::1::7796, 2_A375_pNL97_plus_lncRNA::1::7797	37, 58, 40133	in gene, in gene, in gene	1	1	21	23.5	2	1_A375_pNL7_minus_lncRNA::1	29	Gene SLC1A1	SLC1A1, EAAC1, EAAT3	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	NM_004170, hCT19085.3	206396_at, 213664_at	NP_004161.4, EAW58786.1
GeneID:55064	C9orf68	9	4,598,316	4,666,674	68,358	-	3	1_A375_pNL7_minus_lncRNA::1::5404, 2_A375_pNL97_plus_lncRNA::1::7798, 2_A375_pNL97_plus_lncRNA::1::7799	4338, 4274, 146	in gene, in gene, in gene	1	1	15.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene C9orf68	bA6J24.2, FLJ10058, C9orf68	chromosome 9 open reading frame 68	NM_001039395	1554707_at, 1554708_s_at, 1555079_at, 220218_at, 237363_at	NP_001034484.3
GeneID:403313	PPAPDC2	9	4,662,298	4,665,258	2,960	+	3	1_A375_pNL7_minus_lncRNA::1::5404, 2_A375_pNL97_plus_lncRNA::1::7798, 2_A375_pNL97_plus_lncRNA::1::7799	38, 102, 4230	in gene, in gene, downstream	1	1	15.5	21.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene PPAPDC2	FLJ90191, PSDP, FLJ46512, bA6J24.6, MGC15483, PPAPDC2, PDP1	phosphatidic acid phosphatase type 2 domain containing 2	NM_203453, hCT1653199.3	227385_at	NP_982278.3, EAW58785.1
GeneID:55664	CDC37L1	9	4,679,566	4,706,594	27,028	+	2	1_A375_pNL7_minus_lncRNA::1::5405, 2_A375_pNL97_plus_lncRNA::1::7800	-14, -46	upstream, upstream	1	1	20	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene CDC37L1	FLJ20639, HARC, CDC37B, CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	NM_017913, hCT22486.3	219343_at, 226561_at	NP_060383.2, EAW58782.1
GeneID:50808	AK3	9	4,711,158	4,741,227	30,069	-	2	1_A375_pNL7_minus_lncRNA::1::5406, 2_A375_pNL97_plus_lncRNA::1::7801	11, 123	in gene, in gene	1	1	17	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene AK3	FIX, AKL3L1, AK3, AK6, AKL3L, AK3L1	adenylate kinase 3	NM_016282, hCT2301643.0, hCT2301644.0, hCT2301645.0	224151_s_at, 224655_at	NP_057366.2, EAW58781.1, EAW58779.1, EAW58780.1
GeneID:10171	RCL1	9	4,792,834	4,861,064	68,230	+	1	1_A375_pNL7_minus_lncRNA::1::5407	-258	upstream	1	0	24	17	1	1_A375_pNL7_minus_lncRNA::1	24	Gene RCL1	RCL1, RPCL1, RNAC	RNA terminal phosphate cyclase-like 1	NM_005772, hCT2301639.0, hCT1952023.1	218544_s_at, 222666_s_at	NP_005763.3, EAW58776.1, EAW58777.1
GeneID:3717	JAK2	9	4,985,245	5,128,183	142,938	+	2	1_A375_pNL7_minus_lncRNA::1::5408, 2_A375_pNL97_plus_lncRNA::1::7802	-285, -125	upstream, upstream	1	1	27	23	1	1_A375_pNL7_minus_lncRNA::1	27	Gene JAK2	JTK10, JAK2	Janus kinase 2	NM_004972, hCT22485.3	1562031_at, 205841_at, 205842_s_at	NP_004963.1, EAW58774.1
GeneID:55848	C9orf46	9	5,357,971	5,437,860	79,889	-	2	1_A375_pNL7_minus_lncRNA::1::5409, 2_A375_pNL97_plus_lncRNA::1::7803	-3324, 164	upstream, in gene	1	1	21.5	22	2	1_A375_pNL7_minus_lncRNA::1	28	Gene C9orf46	C9orf46, FLJ14688, FLJ39176, MDS030, AD025	chromosome 9 open reading frame 46	NM_018465, hCT1971473.1, hCT1971474.1, hCT1760495.3	218992_at	NP_060935.1, EAW58766.1, EAW58764.1, EAW58765.1
GeneID:29126	CD274	9	5,450,503	5,470,567	20,064	+	3	1_A375_pNL7_minus_lncRNA::1::5409, 1_A375_pNL7_minus_lncRNA::1::5410, 2_A375_pNL97_plus_lncRNA::1::7804	-9319, 137, 69	upstream, in gene, in gene	1	1	23	23.5	2	1_A375_pNL7_minus_lncRNA::1	28	Gene CD274	PDCD1LG1, PDL1, B7H1, CD274, PD-L1, MGC142296, B7-H, PDCD1L1, MGC142294	CD274 molecule	NM_014143, hCT19081.2	223834_at	NP_054862.1, EAW58763.1
GeneID:79956	ERMP1	9	5,784,572	5,833,081	48,509	-	1	1_A375_pNL7_minus_lncRNA::1::5411	69	in gene	1	0	23	18	1	1_A375_pNL7_minus_lncRNA::1	23	Gene ERMP1	ERMP1, KIAA1815, FXNA, bA207C16.3	endoplasmic reticulum metallopeptidase 1	NM_024896, hCT2301780.0, hCT2301781.0	218342_s_at, 222603_at	NP_079172.2, EAW58757.1, EAW58758.1
GeneID:158358	KIAA2026	9	5,919,008	6,008,003	88,995	-	1	2_A375_pNL97_plus_lncRNA::1::7805	-7581	upstream	0	1	17	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene KIAA2026	KIAA2026		NM_001017969, hCT1960122.2	228446_at, 238490_at	NP_001017969.2, EAW58754.1
GeneID:26953	RANBP6	9	6,011,019	6,015,640	4,621	-	1	2_A375_pNL97_plus_lncRNA::1::7805	56	in gene	0	1	17	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene RANBP6	RANBP6, FLJ54311	RAN binding protein 6	NM_012416, NR_024094, NR_024095, hCT2301775.0	213019_at	NP_036548.1, EAW58753.1
GeneID:115426	UHRF2	9	6,413,151	6,507,051	93,900	+	1	1_A375_pNL7_minus_lncRNA::1::5413	1	in gene	1	0	17	18	1	1_A375_pNL7_minus_lncRNA::1	17	Gene UHRF2	DKFZp686G0837, URF2, NIRF, UHRF2, MGC33463, DKFZp434B0920, RNF107	ubiquitin-like with PHD and ring finger domains 2	NM_152896	225610_at	NP_690856.1
GeneID:2731	GLDC	9	6,532,464	6,645,692	113,228	-	4	1_A375_pNL7_minus_lncRNA::1::5414, 1_A375_pNL7_minus_lncRNA::1::5415, 1_A375_pNL7_minus_lncRNA::1::5416, 2_A375_pNL97_plus_lncRNA::1::7807	107020, 78428, -132, 107148	in gene, in gene, upstream, in gene	1	1	22.33	15.67	3	1_A375_pNL7_minus_lncRNA::1	27	Gene GLDC	HYGN1, MGC138200, GCE, GLDC, GCSP, MGC138198	glycine dehydrogenase (decarboxylating)	NM_000170, hCT2301579.0, hCT2301580.0	204836_at	NP_000161.2, EAW58739.1, EAW58740.1
GeneID:23081	KDM4C	9	6,720,863	7,175,648	454,785	+	2	1_A375_pNL7_minus_lncRNA::1::5418, 2_A375_pNL97_plus_lncRNA::1::7809	36913, 37009	in gene, in gene	1	1	27	25	1	1_A375_pNL7_minus_lncRNA::1	27	Gene KDM4C	JMJD2C, bA146B14.1, KIAA0780, JHDM3C, KDM4C, GASC1, FLJ25949	lysine (K)-specific demethylase 4C	NM_015061, NM_001146694, NM_001146695, NM_001146696, hCT2301763.0, hCT2301765.0, hCT2353354.0, hCT2353355.0, hCT1952022.1	1556493_a_at, 209984_at, 214861_at, 244385_at	NP_055876.2, NP_001140166.1, NP_001140167.1, NP_001140168.1, EAW58730.1, EAW58734.1, EAW58731.1, EAW58732.1, EAW58733.1
GeneID:90871	C9orf123	9	7,796,490	7,799,799	3,309	-	1	2_A375_pNL97_plus_lncRNA::1::7812	55	in gene	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene C9orf123	C9orf123, MGC4730	chromosome 9 open reading frame 123	NM_033428, hCT1829961.2	224860_at, 224879_at	NP_219500.1, EAW58728.1
GeneID:7306	TYRP1	9	12,693,386	12,710,266	16,880	+	1	2_A375_pNL97_plus_lncRNA::1::7814	15334	in gene	0	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TYRP1	GP75, TRP, b-PROTEIN, TYRP1, CATB, TYRP, CAS2	tyrosinase-related protein 1	NM_000550, hCT1971504.1, hCT1971505.1, hCT2301521.0, hCT18394.4	205694_at	NP_000541.1, EAW58709.1, EAW58710.1, EAW58711.1, EAW58712.1
GeneID:100506267	LOC100506267	9	12,699,999	12,814,372	114,373	-	6	1_A375_pNL7_minus_lncRNA::1::5421, 1_A375_pNL7_minus_lncRNA::1::5422, 2_A375_pNL97_plus_lncRNA::1::7814, 2_A375_pNL97_plus_lncRNA::1::7815, 2_A375_pNL97_plus_lncRNA::1::7816, 2_A375_pNL97_plus_lncRNA::1::7817	38100, -3484, 105652, 38148, 29764, -3388	in gene, upstream, in gene, in gene, in gene, upstream	1	1	20.25	24.25	4	1_A375_pNL7_minus_lncRNA::1	31	Gene LOC100506267		hypothetical LOC100506267	XR_113203, XR_113204, XR_108929, XR_108930, XR_114245, XR_114246		
GeneID:286343	C9orf150	9	12,775,012	12,823,059	48,047	+	5	1_A375_pNL7_minus_lncRNA::1::5421, 1_A375_pNL7_minus_lncRNA::1::5422, 2_A375_pNL97_plus_lncRNA::1::7815, 2_A375_pNL97_plus_lncRNA::1::7816, 2_A375_pNL97_plus_lncRNA::1::7817	1260, 42844, 1212, 9596, 42748	in gene, in gene, in gene, in gene, in gene	1	1	22	26.67	3	1_A375_pNL7_minus_lncRNA::1	31	Gene C9orf150	bA3L8.2, C9orf150, FLJ38505, FLJ90271, MGC46502, HYST0841	chromosome 9 open reading frame 150	NM_203403	227443_at	NP_981948.1
GeneID:4781	NFIB	9	14,081,842	14,398,982	317,140	-	4	1_A375_pNL7_minus_lncRNA::1::5426, 2_A375_pNL97_plus_lncRNA::1::7820, 2_A375_pNL97_plus_lncRNA::1::7821, 2_A375_pNL97_plus_lncRNA::1::7822	76262, 160710, 120614, 76262	in gene, in gene, in gene, in gene	1	1	22.67	31.67	3	2_A375_pNL97_plus_lncRNA::1	52	Gene NFIB	NFI-RED, HMGIC/NFIB, NFIB2, NFIB3, NFIB	nuclear factor I/B	NM_001190737, NM_001190738, NM_005596, hCT2303120.0, hCT2303121.0, hCT2303122.0, hCT2303123.0, hCT2353321.0, hCT1780239.2	209289_at, 209290_s_at, 211466_at, 211467_s_at, 213029_at, 213032_at, 213033_s_at, 230291_s_at, 233304_at, 233394_at	NP_001177666.1, NP_001177667.1, NP_005587.2, EAW58695.1, EAW58697.1, EAW58698.1, EAW58694.1, EAW58696.1, EAW58699.1
GeneID:340481	ZDHHC21	9	14,611,069	14,693,480	82,411	-	2	1_A375_pNL7_minus_lncRNA::1::5427, 2_A375_pNL97_plus_lncRNA::1::7823	136, 104	in gene, in gene	1	1	17	31	1	2_A375_pNL97_plus_lncRNA::1	31	Gene ZDHHC21	DHHC-21, DNZ1, ZDHHC21		NM_178566, hCT2349819.0, hCT1642983.4	229240_at, 229923_at, 233215_s_at, 233216_at, 233247_x_at, 235068_at, 241946_at, 243550_at, 243835_at	NP_848661.1, EAW58693.1, EAW58692.1
GeneID:6619	SNAPC3	9	15,422,782	15,461,627	38,845	+	2	1_A375_pNL7_minus_lncRNA::1::5428, 2_A375_pNL97_plus_lncRNA::1::7824	-94, -62	upstream, upstream	1	1	28	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene SNAPC3	MGC132011, SNAPC3, MGC33124, SNAP50, PTFbeta	small nuclear RNA activating complex, polypeptide 3, 50kDa	NM_001039697, hCT2301501.0, hCT18887.3, hCT1951491.0	204001_at, 210465_s_at, 222286_at, 229712_at	NP_001034786.1, EAW58681.1, EAW58680.1, EAW58682.1
GeneID:11168	PSIP1	9	15,464,064	15,511,003	46,939	-	2	1_A375_pNL7_minus_lncRNA::1::5429, 2_A375_pNL97_plus_lncRNA::1::7825	-101, -53	upstream, upstream	1	1	25	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene PSIP1	LEDGF, PAIP, PSIP2, p52, MGC74712, PSIP1, p75, DFS70	PC4 and SFRS1 interacting protein 1	NM_033222, NM_021144, NM_001128217, hCT2301466.1, hCT2301467.1, hCT2301469.2, hCT2353367.0, hCT18392.4	1554933_at, 205961_s_at, 209337_at, 210758_at	NP_150091.2, NP_066967.3, NP_001121689.1, EAW58675.1, EAW58676.1, EAW58678.1, EAW58677.1, EAW58679.1
GeneID:203238	C9orf93	9	15,553,097	15,971,897	418,800	+	3	1_A375_pNL7_minus_lncRNA::1::5430, 2_A375_pNL97_plus_lncRNA::1::7826, 2_A375_pNL97_plus_lncRNA::1::7827	39, -329, 144759	in gene, upstream, in gene	1	1	19	19.5	2	1_A375_pNL7_minus_lncRNA::1	21	Gene C9orf93	MGC50805, bA536D16.1, C9orf93, DKFZp686P12113, bA776P13.1, FLJ46740, FLJ39267	chromosome 9 open reading frame 93	NM_173550	1553433_at, 1556516_at, 1558082_at, 1558160_at, 1559672_a_at, 236945_at, 239712_at, 242621_at	NP_775821.2
GeneID:54796	BNC2	9	16,409,501	16,870,786	461,285	-	3	1_A375_pNL7_minus_lncRNA::1::5433, 1_A375_pNL7_minus_lncRNA::1::5434, 2_A375_pNL97_plus_lncRNA::1::7831	243986, -14, 143842	in gene, upstream, in gene	1	1	18.33	19	3	1_A375_pNL7_minus_lncRNA::1	21	Gene BNC2	FLJ34928, BNC2, FLJ20043, BSN2, DKFZp686A01127	basonuclin 2	NM_017637	220272_at, 229942_at, 230722_at, 235723_at, 238478_at, 243445_at	NP_060107.3
GeneID:54875	CNTLN	9	17,135,038	17,503,917	368,879	+	2	1_A375_pNL7_minus_lncRNA::1::5437, 2_A375_pNL97_plus_lncRNA::1::7833	-510, 2	upstream, in gene	1	1	18	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene CNTLN	C9orf101, bA340N12.1, RP11-340N12.1, FLJ25636, CNTLN, FLJ20276, C9orf39	centlein, centrosomal protein	NM_017738, NM_001114395, hCT1815595.1	1559005_s_at, 220095_at, 241696_at	NP_060208.2, NP_001107867.1, EAW58664.1
GeneID:6456	SH3GL2	9	17,578,953	17,797,122	218,169	+	2	1_A375_pNL7_minus_lncRNA::1::5438, 2_A375_pNL97_plus_lncRNA::1::7834	165975, 166007	in gene, in gene	1	1	19	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene SH3GL2	EEN-B1, CNSA2, SH3P4, FLJ25015, SH3D2A, SH3GL2, FLJ20276	SH3-domain GRB2-like 2	NM_003026, hCT2301336.0, hCT19519.3	205751_at	NP_003017.1, EAW58662.1, EAW58661.1, EAW58663.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:10670	RRAGA	9	19,049,372	19,051,023	1,651	+	2	1_A375_pNL7_minus_lncRNA::1::5442, 2_A375_pNL97_plus_lncRNA::1::7636	-92, -26	upstream, upstream	1	1	21	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene RRAGA	RAGA, FIP1, FIP-1, RRAGA	Ras-related GTP binding A	NM_006570, hCT18490.3	201628_s_at	NP_006561.1, EAW58653.1
GeneID:54801	HAUS6	9	19,053,141	19,102,902	49,761	-	3	1_A375_pNL7_minus_lncRNA::1::5442, 2_A375_pNL97_plus_lncRNA::1::7636, 2_A375_pNL97_plus_lncRNA::1::7637	53622, 53558, -42	downstream, downstream, upstream	1	1	20.5	26.5	2	2_A375_pNL97_plus_lncRNA::1	30	Gene HAUS6	MGC138799, Dgt6, MGC102696, MGC138798, HAUS6, RP11-296P7.3, FAM29A	HAUS augmin-like complex, subunit 6	NM_017645, hCT1818219.2	218602_s_at, 222685_at, 233655_s_at	NP_060115.3, EAW58652.1
GeneID:123	PLIN2	9	19,115,759	19,127,573	11,814	-	1	2_A375_pNL97_plus_lncRNA::1::7638	117	in gene	0	1	17	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene PLIN2	MGC10598, ADRP, ADFP, PLIN2	perilipin 2	NM_001122, hCT1971506.1, hCT2302021.0, hCT19419.3, hCT1951493.1	209122_at, 215695_x_at	NP_001113.2, EAW58651.1, EAW58648.1, EAW58649.1, EAW58650.1
GeneID:55667	DENND4C	9	19,290,749	19,374,139	83,390	+	2	1_A375_pNL7_minus_lncRNA::1::5445, 2_A375_pNL97_plus_lncRNA::1::7640	89443, 89539	downstream, downstream	1	1	36	35	1	1_A375_pNL7_minus_lncRNA::1	36	Gene DENND4C	bA513M16.3, FLJ20686, C9orf55, DENND4C, DKFZp686I09113, C9orf55B	DENN/MADD domain containing 4C	NM_017925, hCT2302202.2, hCT2302203.2, hCT2302204.2, hCT19417.5	205684_s_at, 226867_at, 234968_at	NP_060395.4, EAW58644.1, EAW58645.1, EAW58646.1, EAW58647.1
GeneID:6194	RPS6	9	19,376,254	19,380,235	3,981	-	2	1_A375_pNL7_minus_lncRNA::1::5445, 2_A375_pNL97_plus_lncRNA::1::7640	43, -53	in gene, upstream	1	1	36	35	1	1_A375_pNL7_minus_lncRNA::1	36	Gene RPS6	RPS6, S6		NM_001010, hCT1971469.1, hCT1971470.1, hCT1971471.1, hCT1971472.1, hCT2302009.0, hCT2302010.0, hCT2302012.0, hCT2302019.0, hCT1779654.3	200081_s_at, 201254_x_at, 209134_s_at	NP_001001.2, EAW58643.1, EAW58636.1, EAW58637.1, EAW58639.1, EAW58640.1, EAW58635.1, EAW58638.1, EAW58641.1, EAW58642.1
GeneID:340485	ACER2	9	19,408,925	19,452,500	43,575	+	1	2_A375_pNL97_plus_lncRNA::1::7641	131	in gene	0	1	12	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene ACER2	ACER2, ASAH3L, FLJ41587, ALKCDase2	alkaline ceramidase 2	NM_001010887, hCT2302207.0		NP_001010887.2, EAW58634.1
GeneID:25769	SLC24A2	9	19,507,450	19,788,591	281,141	-	3	1_A375_pNL7_minus_lncRNA::1::5446, 2_A375_pNL97_plus_lncRNA::1::7642, 2_A375_pNL97_plus_lncRNA::1::7643	40111, 66111, 39855	in gene, in gene, in gene	1	1	18	20	2	2_A375_pNL97_plus_lncRNA::1	22	Gene SLC24A2	SLC24A2, FLJ45149, NCKX2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	NM_020344, NM_001193288, hCT1641931.3	220867_s_at	NP_065077.1, NP_001180217.1, EAW58633.1
GeneID:4300	MLLT3	9	20,344,968	20,622,514	277,546	-	3	1_A375_pNL7_minus_lncRNA::1::5449, 1_A375_pNL7_minus_lncRNA::1::5450, 2_A375_pNL97_plus_lncRNA::1::7644	63602, -291, -286	in gene, upstream, upstream	1	1	19	17.5	2	1_A375_pNL7_minus_lncRNA::1	22	Gene MLLT3	AF9, MLLT3, YEATS3, FLJ2035	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	NM_004529, hCT2301290.0, hCT2301293.0, hCT1951490.1	1569652_at, 204917_s_at, 204918_s_at	NP_004520.2, EAW58632.1, EAW58630.1, EAW58631.1
GeneID:54914	KIAA1797	9	20,658,309	20,995,954	337,645	+	2	1_A375_pNL7_minus_lncRNA::1::5451, 2_A375_pNL97_plus_lncRNA::1::7645	26171, 26331	in gene, in gene	1	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene KIAA1797	KIAA1797, FLJ20375	KIAA1797	NM_017794, hCT1971361.1, hCT2340911.0, hCT2351264.0	218503_at	NP_060264.3, EAW58627.1, EAW58628.1, EAW58629.1
GeneID:55958	KLHL9	9	21,331,018	21,335,429	4,411	-	1	2_A375_pNL97_plus_lncRNA::1::7646	293	in gene	0	1	21	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene KLHL9	KLHL9, FLJ21815	kelch-like 9 (Drosophila)	NM_018847, hCT1647803.4	213117_at, 213233_s_at, 233197_at, 237123_x_at	NP_061335.1, EAW58614.1
GeneID:554202	LOC554202	9	21,454,267	21,559,697	105,430	-	5	1_A375_pNL7_minus_lncRNA::1::5452, 2_A375_pNL97_plus_lncRNA::1::7647, 2_A375_pNL97_plus_lncRNA::1::7648, 2_A375_pNL97_plus_lncRNA::1::7649, 2_A375_pNL97_plus_lncRNA::1::7650	54097, 104257, 54065, 9969, 49	in gene, in gene, in gene, in gene, in gene	1	1	14.5	19.75	4	2_A375_pNL97_plus_lncRNA::1	27	Gene LOC554202		hypothetical LOC554202	NR_027054	1554097_a_at	
GeneID:407035	MIR31	9	21,512,114	21,512,184	70	-	2	1_A375_pNL7_minus_lncRNA::1::5452, 2_A375_pNL97_plus_lncRNA::1::7648	6584, 6552	downstream, downstream	1	1	25	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene MIR31	MIR31, hsa-mir-31, MIRN31, miR-31	microRNA 31	NR_029505		
GeneID:4507	MTAP	9	21,802,635	21,865,970	63,335	+	3	1_A375_pNL7_minus_lncRNA::1::5456, 1_A375_pNL7_minus_lncRNA::1::5457, 2_A375_pNL97_plus_lncRNA::1::7652	53, 34165, 101	in gene, in gene, in gene	1	1	25	26	2	2_A375_pNL97_plus_lncRNA::1	34	Gene MTAP	c86fus, MTAP, MSAP	methylthioadenosine phosphorylase	NM_002451, hCT2301440.0, hCT1950947.1	204956_at, 211363_s_at, 211364_at, 216665_s_at, 217134_at, 231984_at	NP_002442.2, EAW58605.1, EAW58606.1
GeneID:1993	ELAVL2	9	23,690,102	23,826,063	135,961	-	4	1_A375_pNL7_minus_lncRNA::1::5461, 1_A375_pNL7_minus_lncRNA::1::5462, 2_A375_pNL97_plus_lncRNA::1::7654, 2_A375_pNL97_plus_lncRNA::1::7655	-337, -3713, -305, -3729	upstream, upstream, upstream, upstream	1	1	39.5	41.5	2	2_A375_pNL97_plus_lncRNA::1	64	Gene ELAVL2	HELN1, HEL-N1, ELAVL2, HUB	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	NM_004432, NM_001171195, NM_001171197, hCT2301219.0, hCT2301221.0, hCT2301225.0, hCT2353330.0, hCT18513.3, hCT1950950.1	206427_s_at, 226260_at	NP_004423.2, NP_001164666.1, NP_001164668.1, EAW58583.1, EAW58584.1, EAW58586.1, EAW58581.1, EAW58582.1, EAW58585.1
GeneID:286319	TUSC1	9	25,676,387	25,678,856	2,469	-	2	1_A375_pNL7_minus_lncRNA::1::5463, 2_A375_pNL97_plus_lncRNA::1::7656	1336, 1117	in gene, in gene	1	1	16	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene TUSC1	TUSC1, TSG-9, MGC131751, TSG9	tumor suppressor candidate 1	NM_001004125, hCT2301172.0	227388_at	NP_001004125.1, EAW58580.1
GeneID:79886	C9orf82	9	26,840,683	26,892,826	52,143	-	2	1_A375_pNL7_minus_lncRNA::1::5465, 2_A375_pNL97_plus_lncRNA::1::7660	442, 58	in gene, in gene	1	1	25	36	1	2_A375_pNL97_plus_lncRNA::1	36	Gene C9orf82	FLJ13657, RP11-337A23.1, C9orf82	chromosome 9 open reading frame 82	NM_024828, NM_001167575, hCT2301130.0, hCT2353368.0, hCT1950948.0, hCT1950949.0	219276_x_at, 231995_at	NP_079104.3, NP_001161047.1, EAW58576.1, EAW58577.1, EAW58578.1, EAW58579.1
GeneID:9373	PLAA	9	26,903,368	26,947,468	44,100	-	4	1_A375_pNL7_minus_lncRNA::1::5466, 1_A375_pNL7_minus_lncRNA::1::5467, 2_A375_pNL97_plus_lncRNA::1::7661, 2_A375_pNL97_plus_lncRNA::1::7662	364, -8756, 204, -8564	in gene, upstream, in gene, upstream	1	1	22	26.5	2	2_A375_pNL97_plus_lncRNA::1	36	Gene PLAA	FLJ12699, FLJ11281, PLAP, PLAA, DOA1, PLA2P	phospholipase A2-activating protein	NM_001031689, hCT22007.3	209532_at, 209533_s_at	NP_001026859.1, EAW58575.1
GeneID:80173	IFT74	9	26,947,037	27,062,931	115,894	+	4	1_A375_pNL7_minus_lncRNA::1::5466, 1_A375_pNL7_minus_lncRNA::1::5467, 2_A375_pNL97_plus_lncRNA::1::7661, 2_A375_pNL97_plus_lncRNA::1::7662	67, 9187, 227, 8995	in gene, in gene, in gene, in gene	1	1	22	26.5	2	2_A375_pNL97_plus_lncRNA::1	36	Gene IFT74	CMG1, IFT74, CMG-1, MGC111562, CCDC2, FLJ22621	intraflagellar transport 74 homolog (Chlamydomonas)	NM_001099223, NM_001099224, NM_001099222, NM_025103, hCT1642329.3	219174_at, 61732_r_at	NP_001092693.1, NP_001092694.1, NP_001092692.1, NP_079379.2, EAW58573.1
GeneID:7010	TEK	9	27,109,147	27,230,172	121,025	+	5	1_A375_pNL7_minus_lncRNA::1::5468, 1_A375_pNL7_minus_lncRNA::1::5469, 2_A375_pNL97_plus_lncRNA::1::7664, 2_A375_pNL97_plus_lncRNA::1::7665, 2_A375_pNL97_plus_lncRNA::1::7666	16261, 118341, 16165, 45829, 85509	in gene, in gene, in gene, in gene, in gene	1	1	19	22	4	2_A375_pNL97_plus_lncRNA::1	33	Gene TEK	TIE2, TEK, VMCM, CD202B, TIE-2, VMCM1	TEK tyrosine kinase, endothelial	NM_000459, hCT2353331.0, hCT19235.3	206702_at, 217711_at	NP_000450.2, EAW58571.1, EAW58572.1
GeneID:203228	C9orf72	9	27,546,544	27,573,842	27,298	-	3	1_A375_pNL7_minus_lncRNA::1::5470, 2_A375_pNL97_plus_lncRNA::1::7667, 2_A375_pNL97_plus_lncRNA::1::7668	-78, 882, 50	upstream, in gene, in gene	1	1	15	17.5	2	2_A375_pNL97_plus_lncRNA::1	19	Gene C9orf72	RP11-27J8.2, C9orf72, MGC23980	chromosome 9 open reading frame 72	NM_018325, NM_145005, hCT2301205.0, hCT2349871.0, hCT19234.3, hCT1950954.2	1553133_at, 1553134_s_at, 225919_s_at	NP_060795.1, NP_659442.2, EAW58558.1, EAW58559.1, EAW58560.1, EAW58561.1
GeneID:48	ACO1	9	32,384,601	32,450,834	66,233	+	1	1_A375_pNL7_minus_lncRNA::1::5473	119	in gene	1	0	19	17	1	1_A375_pNL7_minus_lncRNA::1	19	Gene ACO1	IRP1, ACONS, ACO1, IREBP, IREBP1, IREB1	aconitase 1, soluble	NM_002197, hCT21332.3, hCT2353332.0, hCT2353333.0, hCT1954593.1	207071_s_at	NP_002188.1, EAW58550.1, EAW58549.1, EAW58551.1, EAW58552.1
GeneID:10210	TOPORS	9	32,540,542	32,552,622	12,080	-	2	1_A375_pNL7_minus_lncRNA::1::5474, 2_A375_pNL97_plus_lncRNA::1::7670	238, 206	in gene, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TOPORS	P53BP3, TP53BPL, LUN, RP31, TOPORS	topoisomerase I binding, arginine/serine-rich	NM_005802, hCT21442.3	1564403_at, 204071_s_at, 221979_at, 78383_at	NP_005793.2, EAW58546.1
GeneID:100129250	LOC100129250	9	32,551,142	32,553,015	1,873	+	2	1_A375_pNL7_minus_lncRNA::1::5474, 2_A375_pNL97_plus_lncRNA::1::7670	1242, 1274	in gene, in gene	1	1	20	19	1	1_A375_pNL7_minus_lncRNA::1	20	Gene LOC100129250		hypothetical LOC100129250	NR_033991, NR_033992		
GeneID:4712	NDUFB6	9	32,553,523	32,573,182	19,659	-	3	1_A375_pNL7_minus_lncRNA::1::5474, 1_A375_pNL7_minus_lncRNA::1::5475, 2_A375_pNL97_plus_lncRNA::1::7670	20798, -66, 20766	downstream, upstream, downstream	1	1	21	20	2	1_A375_pNL7_minus_lncRNA::1	22	Gene NDUFB6	CI, MGC13675, B17, NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	NM_182739, NM_002493, hCT21443.2, hCT2353336.0, hCT1954601.1	1559042_at, 203613_s_at	NP_877416.1, NP_002484.1, EAW58541.1, EAW58542.1, EAW58543.1
GeneID:54840	APTX	9	32,972,608	33,001,626	29,018	-	1	1_A375_pNL7_minus_lncRNA::1::5476	122	in gene	1	0	20	13	1	1_A375_pNL7_minus_lncRNA::1	20	Gene APTX	FHA-HIT, AXA1, FLJ20157, AOA1, MGC1072, EAOH, APTX, EOAHA, AOA	aprataxin	NM_175069, NM_175073, hCT21444.2, hCT2301395.0, hCT1644689.2, hCT1954603.1, hCT1954604.1, hCT1954605.1, hCT1954606.0, hCT1954607.1	218527_at, 222658_s_at	NP_778239.1, NP_778243.1, EAW58528.1, EAW58529.1, EAW58532.1, EAW58533.1, EAW58530.1, EAW58531.1, EAW58534.1, EAW58535.1
GeneID:3301	DNAJA1	9	33,025,209	33,039,062	13,853	+	2	1_A375_pNL7_minus_lncRNA::1::5477, 2_A375_pNL97_plus_lncRNA::1::7671	71, -121	in gene, upstream	1	1	21	19	1	1_A375_pNL7_minus_lncRNA::1	21	Gene DNAJA1	DjA1, DNAJA1, HSPF4, DJ-2, HSDJ, HSJ2, NEDD7, HDJ2, hDJ-2	DnaJ (Hsp40) homolog, subfamily A, member 1	NM_001539, hCT21440.3, hCT2343734.0, hCT2343735.0, hCT2353315.0	200880_at, 200881_s_at	NP_001530.1, EAW58526.1, EAW58524.1, EAW58525.1, EAW58527.1
GeneID:55234	SMU1	9	33,041,850	33,076,714	34,864	-	2	1_A375_pNL7_minus_lncRNA::1::5478, 2_A375_pNL97_plus_lncRNA::1::7672	122, 58	in gene, in gene	1	1	22	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene SMU1	DKFZp761L0916, FLJ10870, RP11-54K16.3, fSAP57, FLJ10805, SMU-1, FLJ11970, MGC117363, SMU1, BWD	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	NM_018225, hCT21449.3, hCT2301430.0	222618_at	NP_060695.2, EAW58522.1, EAW58523.1
GeneID:27290	SPINK4	9	33,240,196	33,248,565	8,369	+	2	1_A375_pNL7_minus_lncRNA::1::5479, 2_A375_pNL97_plus_lncRNA::1::7673	-6084, -6084	upstream, upstream	1	1	23	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene SPINK4	PEC-60, MGC133107, SPINK4	serine peptidase inhibitor, Kazal type 4	NM_014471, hCT21438.3	207214_at	NP_055286.1, EAW58518.1
GeneID:51510	CHMP5	9	33,264,877	33,281,516	16,639	+	2	1_A375_pNL7_minus_lncRNA::1::5480, 2_A375_pNL97_plus_lncRNA::1::7674	25523, 25587	downstream, downstream	1	1	36	34	1	1_A375_pNL7_minus_lncRNA::1	36	Gene CHMP5	PNAS-2, HSPC177, SNF7DC2, CGI-34, CHMP5, Vps60, C9orf83	chromatin modifying protein 5	NM_016410, hCT2301512.0, hCT2301513.0	218085_at, 219356_s_at	NP_057494.3, EAW58512.1, EAW58513.1
GeneID:4799	NFX1	9	33,290,418	33,371,155	80,737	+	2	1_A375_pNL7_minus_lncRNA::1::5480, 2_A375_pNL97_plus_lncRNA::1::7674	-18, 46	upstream, in gene	1	1	36	34	1	1_A375_pNL7_minus_lncRNA::1	36	Gene NFX1	DKFZp779G2416, NFX1, MGC20369, NFX2	nuclear transcription factor, X-box binding 1	NM_002504, NM_147133, NM_147134, hCT21447.3, hCT2301516.0, hCT2301517.0, hCT2353346.0, hCT2353347.0	1553103_at, 1553348_a_at, 202584_at, 202585_s_at, 210268_at	NP_002495.2, NP_667344.1, NP_667345.1, EAW58507.1, EAW58508.1, EAW58511.1, EAW58509.1, EAW58510.1
GeneID:441459	ANKRD18B	9	33,523,927	33,572,358	48,431	+	1	2_A375_pNL97_plus_lncRNA::1::7675	-359	upstream	0	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene ANKRD18B	bA255A11.5, bA255A11.3, ANKRD18B	ankyrin repeat domain 18B	XM_001718334, XM_001717197		XP_001718386.3, XP_001717249.3
GeneID:55833	UBAP2	9	33,921,691	34,048,947	127,256	-	2	1_A375_pNL7_minus_lncRNA::1::5481, 2_A375_pNL97_plus_lncRNA::1::7676	-541, -189	upstream, upstream	1	1	19	25	1	2_A375_pNL97_plus_lncRNA::1	25	Gene UBAP2	KIAA1491, UBAP2, bA176F3.5, FLJ22435, UBAP-2, FLJ46567, FLJ43947	ubiquitin associated protein 2	NM_018449	219192_at, 221839_s_at	NP_060919.2
GeneID:25853	DCAF12	9	34,086,381	34,126,771	40,390	-	1	2_A375_pNL97_plus_lncRNA::1::7677	171	in gene	0	1	12	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene DCAF12	DCAF12, CT102, MGC1058, WDR40A, TCC52, DKFZp434O125, KIAA1892	DDB1 and CUL4 associated factor 12	NM_015397, hCT20041.3, hCT2336538.0, hCT2336539.0	224789_at	NP_056212.1, EAW58472.1, EAW58473.1, EAW58474.1
GeneID:203259	C9orf25	9	34,398,182	34,458,568	60,386	-	6	1_A375_pNL7_minus_lncRNA::1::5482, 1_A375_pNL7_minus_lncRNA::1::5483, 1_A375_pNL7_minus_lncRNA::1::5484, 2_A375_pNL97_plus_lncRNA::1::7678, 2_A375_pNL97_plus_lncRNA::1::7679, 2_A375_pNL97_plus_lncRNA::1::7680	45096, 27816, -24, 45160, 27576, -56	in gene, in gene, upstream, in gene, in gene, upstream	1	1	26.67	23.67	3	1_A375_pNL7_minus_lncRNA::1	38	Gene C9orf25	C9orf25, FLJ39031, bA573M23.5	chromosome 9 open reading frame 25	NM_147202, NM_001184940, NM_001184941, NM_001184942, NM_001184943, NM_001184944, NM_001184945, hCT2336528.1, hCT2353369.0	225146_at	NP_671735.1, NP_001171869.1, NP_001171870.1, NP_001171871.1, NP_001171872.1, NP_001171873.1, NP_001171874.1, EAW58454.1, EAW58455.1
GeneID:27019	DNAI1	9	34,458,811	34,520,982	62,171	+	4	1_A375_pNL7_minus_lncRNA::1::5484, 1_A375_pNL7_minus_lncRNA::1::5485, 2_A375_pNL97_plus_lncRNA::1::7680, 2_A375_pNL97_plus_lncRNA::1::7681	-219, 35301, -187, 35365	upstream, in gene, upstream, in gene	1	1	35.5	28	2	1_A375_pNL7_minus_lncRNA::1	38	Gene DNAI1	DNAI1, CILD1, ICS1, MGC26204, PCD, ICS	dynein, axonemal, intermediate chain 1	NM_012144, hCT1951968.1	220125_at, 233195_at	NP_036276.1, EAW58453.1
GeneID:138715	ARID3C	9	34,621,455	34,628,011	6,556	-	1	2_A375_pNL97_plus_lncRNA::1::7682	-9717	upstream	0	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene ARID3C	ARID3C		NM_001017363, hCT11560.2		NP_001017363.1, EAW58438.1
GeneID:10280	SIGMAR1	9	34,634,719	34,637,768	3,049	-	2	2_A375_pNL97_plus_lncRNA::1::7682, 2_A375_pNL97_plus_lncRNA::1::7683	40, -5872	in gene, upstream	0	1	21	18.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene SIGMAR1	OPRS1, SIGMAR1, SR-BP1, SRBP, FLJ25585, MGC3851	sigma non-opioid intracellular receptor 1	NM_005866, NM_147157	201692_at, 214484_s_at	NP_005857.1, NP_671513.1
GeneID:2592	GALT	9	34,646,635	34,650,574	3,939	+	2	2_A375_pNL97_plus_lncRNA::1::7682, 2_A375_pNL97_plus_lncRNA::1::7683	-5907, 5	upstream, in gene	0	1	21	18.5	2	2_A375_pNL97_plus_lncRNA::1	23	Gene GALT	GALT		NM_000155	203179_at, 232708_at, 242734_x_at	NP_000146.2
GeneID:3590	IL11RA	9	34,652,182	34,661,884	9,702	+	1	2_A375_pNL97_plus_lncRNA::1::7683	-5542	upstream	0	1	22	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene IL11RA	IL11RA, MGC2146	interleukin 11 receptor, alpha	NM_004512, NM_147162, NM_001142784	1552646_at, 204773_at	NP_004503.1, NP_671518.1, NP_001136256.1
GeneID:23349	KIAA1045	9	34,958,192	34,982,541	24,349	+	2	1_A375_pNL7_minus_lncRNA::1::5486, 2_A375_pNL97_plus_lncRNA::1::7684	26064, 26048	downstream, downstream	1	1	25	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene KIAA1045	KIAA1045, RP11-392A14.4, DKFZp434I2112	KIAA1045	NM_015297	213636_at, 37566_at	NP_056112.1
GeneID:25822	DNAJB5	9	34,989,725	34,998,428	8,703	+	2	1_A375_pNL7_minus_lncRNA::1::5486, 2_A375_pNL97_plus_lncRNA::1::7684	-5469, -5485	upstream, upstream	1	1	25	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene DNAJB5	KIAA1045, DNAJB5, Hsc40	DnaJ (Hsp40) homolog, subfamily B, member 5	NM_012266, NM_001135004, NM_001135005, hCT11547.3	207453_s_at, 212817_at	NP_036398.3, NP_001128476.1, NP_001128477.1, EAW58407.1
GeneID:7415	VCP	9	35,056,065	35,072,739	16,674	-	3	1_A375_pNL7_minus_lncRNA::1::5487, 2_A375_pNL97_plus_lncRNA::1::7685, 2_A375_pNL97_plus_lncRNA::1::7686	259, 195, -7101	in gene, in gene, upstream	1	1	16	21	2	2_A375_pNL97_plus_lncRNA::1	24	Gene VCP	VCP, p97, MGC148092, MGC8560, MGC131997, IBMPFD, TERA	valosin containing protein	NM_007126, hCT2301054.0, hCT11566.3	208648_at, 208649_s_at	NP_009057.1, EAW58403.1, EAW58404.1
GeneID:2189	FANCG	9	35,073,835	35,080,013	6,178	-	3	1_A375_pNL7_minus_lncRNA::1::5487, 2_A375_pNL97_plus_lncRNA::1::7685, 2_A375_pNL97_plus_lncRNA::1::7686	7533, 7469, 173	downstream, downstream, in gene	1	1	16	21	2	2_A375_pNL97_plus_lncRNA::1	24	Gene FANCG	XRCC9, FAG, FANCG	Fanconi anemia, complementation group G	NM_004629, hCT11548.2, hCT1957476.1	203564_at	NP_004620.1, EAW58401.1, EAW58402.1
GeneID:84720	PIGO	9	35,088,688	35,096,579	7,891	-	5	1_A375_pNL7_minus_lncRNA::1::5488, 1_A375_pNL7_minus_lncRNA::1::5489, 2_A375_pNL97_plus_lncRNA::1::7686, 2_A375_pNL97_plus_lncRNA::1::7687, 2_A375_pNL97_plus_lncRNA::1::7688	3, -6557, 16739, 35, -6397	in gene, upstream, downstream, in gene, upstream	1	1	21.67	23.33	3	1_A375_pNL7_minus_lncRNA::1	30	Gene PIGO	DKFZp434M222, PIGO, FLJ00135, MGC3079, RP11-182N22.4, MGC20536	phosphatidylinositol glycan anchor biosynthesis, class O	NM_032634, NM_152850, hCT2301047.0, hCT2301049.0, hCT11559.3, hCT1951976.1	209998_at, 214991_s_at	NP_116023.2, NP_690577.2, EAW58397.1, EAW58398.1, EAW58399.1, EAW58400.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervening Sequences	Intervening Counts	Intervening Positions	[A]	[B]	[C]	[D]	Acceptor Register Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
GeneID:30966	STOML2	9	35,099,893	35,103,154	3,261	-	4	1_A270_shL7_dhrus_loc#N A:1-3460, 1_A270_shL7_dhrus_loc#N A:1-3459, 2_A270_shL87_glus_loc#RNA 1:7697, 2_A270_shL87_glus_loc#RNA 1:7698	9870, 10, 6610, 136	downstream, ut gene, downstream, ut gene	1	1	26.5	23	2	1_A270_shL7_dhrus_loc#NA:1	30	Gene STOML2	HSPC150, SLP-2, STOML2	Stomatin (EPB72)-like 2	NM_013442, XCT113492.2, XCT193747.1, XCT 193747.1	215416_s_at	NP_031467.1, XAH65398.1, XAH65384.1, EAH65396.1
GeneID:6256	IUAA1539	9	35,104,115	35,115,693	11,778	-	4	1_A270_shL7_dhrus_loc#N A:1-3465, 1_A270_shL7_dhrus_loc#N A:1-3469, 2_A270_shL87_glus_loc#RNA 1:7697, 2_A270_shL87_glus_loc#RNA 1:7698	18317, 12757, 19349, 12917	downstream, downstream, downstream, downstream	1	1	26.5	23	2	1_A270_shL7_dhrus_loc#NA:1	30	Gene KIAA1539	KIAA1539, P1.11692_3, RP11-162N22.6, KIAA1539	KIAA1539	NM_025162, XCT2301838.0, XCT2301840.0, XCT2301841.0, XCT2301842.0, XCT2332131.0, XCT2332314.0, XCT11362.2	207765_s_at, 215433_s_at	NP_079455.2, EAH65396.1, EAH65387.1, EAH65555.1, EAH65390.1, EAH65292.1, EAH65389.1, EAH65391.1, EAH65292.1
GeneID:3511	UXC1301	9	35,147,491	35,162,163	14,672	-	2	1_A270_shL7_dhrus_loc#N A:1-3480, 2_A270_shL87_glus_loc#RNA 1:7699	-13, 19	upstream, ut gene	1	1	20	26	1	2_A270_shL87_glus_loc#NA:1	26	Gene UXC1301		Zinc finger protein 492 pseudogene			
GeneID:6987	UNC13B	9	35,161,889	35,203,232	243,343	+	2	1_A270_shL7_dhrus_loc#N A:1-3480, 2_A270_shL87_glus_loc#RNA 1:7699	167, 153	ut gene, ut gene	1	1	20	26	1	2_A270_shL87_glus_loc#NA:1	26	Gene UNC13B	Munc13, MGC133274, Unc13b2, UNC13, MUNC13, MGC133280, UNC13B	unc-13 homolog B (C. elegans)	NM_006377, XCT2301834.1, XCT2335211.0	202693_at, 231206_at	NP_006368.2, EAH65383.1, EAH65384.1
GeneID:653	RUSC2	9	35,490,007	35,561,695	71,689	+	1	2_A270_shL87_glus_loc#RNA 1:7699	283	ut gene	0	1	15	16	1	2_A270_shL87_glus_loc#NA:1	16	Gene RUSC2	Iporin, RUSC2, KIAA0275	RUN and SH3 domain containing 2	NM_014939, NM_001132899, XCT11961.4	213099_at	NP_055821.1, NP_001128471.1, EAH65377.1
GeneID:9518	TESK2	9	35,603,251	35,610,038	6,787	+	1	1_A270_shL7_dhrus_loc#N A:1-3481	-629	upstream	1	0	17	15	1	1_A270_shL7_dhrus_loc#NA:1	17	Gene TESK2	TESK1		NM_006285, XCT2301855.0, XCT2335250.0	206109_at	NP_006276.2, EAH65375.1, EAH65374.1
GeneID:71	CCR2	9	35,609,976	35,616,624	6,648	-	1	1_A270_shL7_dhrus_loc#N A:1-3481	16072	downstream	1	0	17	15	1	1_A270_shL7_dhrus_loc#NA:1	17	Gene CCR2	LYBJ, CCR2, CCR2b	CCR2 molecule	NM_001795, XCT2301851.0, XCT2335249.0	210525_s_at	NP_001770.1, EAH65372.1, EAH65373.1
GeneID:7240	SIT1	9	35,649,293	35,650,847	1,552	-	2	1_A270_shL7_dhrus_loc#N A:1-3482, 2_A270_shL87_glus_loc#RNA 1:7699	-7003, -7163	upstream, upstream	1	1	35	24	1	1_A270_shL7_dhrus_loc#NA:1	35	Gene SIT1	SIT, MGC129908, MGC129909, RP11-231P9.3, SIT1, MGC129910	Signaling threshold regulating transmembrane adaptor 1	NM_014450, XCT1799851.2	203464_at	NP_055265.1, EAH65370.1
GeneID:5223	RMRP	9	35,653,748	35,655,015	267	-	2	1_A270_shL7_dhrus_loc#N A:1-3482, 2_A270_shL87_glus_loc#RNA 1:7699	63, -97	ut gene, upstream	1	1	35	24	1	1_A270_shL7_dhrus_loc#NA:1	35	Gene RMRP	NME1, RMRP, CHH, RRP2, RMRPR	RNA component of mitochondrial RNA processing endoribonuclease	NR_003051		
GeneID:31260	CCDC107	9	35,655,311	35,661,164	5,873	+	2	1_A270_shL7_dhrus_loc#N A:1-3482, 2_A270_shL87_glus_loc#RNA 1:7699	-259, -169	upstream, upstream	1	1	35	24	1	1_A270_shL7_dhrus_loc#NA:1	35	Gene CCDC107	FSEC0222, CCDC107, FLJ97171, MGC31987	coiled-coil domain containing 107	NM_178823, XCT2331290.0, XCT2335310.0, XCT2335352.0, XCT2335353.0, XCT1756690.2, XCT1986812.2	236063_s_at	NP_775813.1, EAH65387.1, EAH65366.1, EAH65366.1, EAH65366.1, EAH65392.1
GeneID:4904	C9orf100	9	35,659,341	35,663,276	3,937	-	2	1_A270_shL7_dhrus_loc#N A:1-3482, 2_A270_shL87_glus_loc#RNA 1:7699	7326, 1166	downstream, downstream	1	1	35	24	1	1_A270_shL7_dhrus_loc#NA:1	35	Gene C9orf100	RP11-331F9.7, FLJ14542, C9orf100, MGC45506	chromosome 9 open reading frame 100	NM_032516, XCT2301830.0, XCT2335972.0, XCT2333356.0, XCT1756662.2	235521_at, 235522_s_at, 235562_at	NP_116207.2, EAH65362.1, EAH65360.1, EAH65361.1, EAH65360.1
GeneID:694	TLN1	9	35,697,534	35,752,282	55,068	-	1	2_A270_shL87_glus_loc#RNA 1:7699	166	ut gene	0	1	17	15	1	2_A270_shL87_glus_loc#NA:1	16	Gene TLN1	ILWEQ, TLN1, IUAA1027, TLN	talin 1	NM_006289, XCT2301856.0, XCT1997881.1	200754_s_at, 232760_at	NP_006280.2, EAH65353.1, EAH65352.1
GeneID:5468	CREB3	9	35,732,317	35,737,005	4,688	+	1	1_A270_shL7_dhrus_loc#N A:1-3482	83	upstream	0	1	17	15	1	1_A270_shL7_dhrus_loc#NA:1	16	Gene CREB3	CREB3, LUMAN, LZIP, MGC10762, MGC31830	CAMP responsive element binding protein 3	NM_006368, XCT2301862.0, XCT2335963.0	209422_s_at	NP_006359.2, EAH65393.1, EAH65351.1
GeneID:7704	GBA2	9	35,739,953	35,749,225	12,362	-	1	1_A270_shL7_dhrus_loc#N A:1-3482, 2_A270_shL87_glus_loc#RNA 1:7699	17001	downstream	0	1	17	15	1	1_A270_shL7_dhrus_loc#NA:1	16	Gene GBA2	KIAA1015, KIAA1903, DKFZp762h354, MGC16899, GBA2	glucosidase, beta (bile acid) 2	NM_020944, XCT225489.2, XCT2301766.0, XCT2301767.0, XCT2301768.0, XCT2331709.0	223521_s_at, 224627_at	NP_065997.1, EAH65349.1, EAH65345.1, EAH65346.1, EAH65347.1, EAH65346.1
GeneID:9020	GNE	9	36,214,434	36,277,053	62,619	-	2	1_A270_shL7_dhrus_loc#N A:1-3484, 2_A270_shL87_glus_loc#RNA 1:7699	16491, 16357	ut gene, ut gene	1	1	46	36	1	1_A270_shL7_dhrus_loc#NA:1	36	Gene GNE	GLCNE, NM_GNE, Uae1, DMRV, IBM2	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	NM_001128227, NM_001160361, NM_001160364, NM_001160365, NM_005476, XCT225414, XCT2301853.0, XCT1985811.1	203502_at	NP_001119699.1, NP_001177212.1, NP_001159877.1, NP_001177213.1, NP_001177211.1, EAH65357.1, EAH65358.1, EAH65359.1
GeneID:52006	RNF38	9	36,336,397	36,401,195	64,799	-	2	1_A270_shL7_dhrus_loc#N A:1-3485, 2_A270_shL87_glus_loc#RNA 1:7699	633, 73121	ut gene, downstream	1	1	13	14.5	2	2_A270_shL87_glus_loc#NA:1	16	Gene RNF38	RNF38, FLJ21343	ring finger protein 38	NM_022781, NM_194328, NM_194329, NM_194330, NM_194332, XCT1786971.1	218526_s_at, 223660_s_at	NP_073618.3, NP_918306.1, NP_918310.1, NP_918311.1, NP_918313.1, EAH65355.1
GeneID:9194	MELK	9	36,372,803	36,377,879	104,774	+	1	1_A270_shL7_dhrus_loc#N A:1-3487	-41	upstream	0	1	12	16	1	1_A270_shL7_dhrus_loc#NA:1	16	Gene MELK	HPK38, KIAA1179, MELK	maternal embryonic leucine zipper kinase	NM_014791, XCT225522.2, XCT2301849.0, XCT1986290.1	204825_at	NP_059909.1, EAH65394.1, EAH65352.1, EAH65353.1
GeneID:678	PAX5	9	36,835,531	37,034,476	199,945	+	3	1_A270_shL7_dhrus_loc#N A:1-3488, 1_A270_shL7_dhrus_loc#N A:1-3489, 2_A270_shL87_glus_loc#RNA 1:7699	110238, 6764, 8793	ut gene, ut gene, ut gene	1	1	21.5	21.5	2	2_A270_shL87_glus_loc#NA:1	30	Gene PAX5	BSAP, PAX5	paired box 5	NM_016734, XCT2353322.0, XCT2353323.0, XCT2353324.0, XCT2353325.0, XCT2353326.0, XCT19206.2	208502_at	NP_057953.1, EAH65298.1, EAH65294.1, EAH65296.1, EAH65297.1, EAH65295.1, EAH65295.1
GeneID:100130485	LOC100130485	9	37,036,063	37,038,666	2,602	+	2	1_A270_shL7_dhrus_loc#N A:1-3489, 2_A270_shL87_glus_loc#RNA 1:7699	4331, -5287	upstream, upstream	1	1	21	30	1	2_A270_shL87_glus_loc#NA:1	30	Gene LOC100130485		hypothetical LOC100130485	XM_001716801, XM_001723998, XM_001723442		XP_001716853.1, XP_001726051.1, XP_001724484.1
GeneID:380	GRHPR	9	37,422,707	37,439,866	16,276	+	2	1_A270_shL7_dhrus_loc#N A:1-3500, 2_A270_shL87_glus_loc#RNA 1:7699	-179, -25	upstream, upstream	1	1	20	17	1	1_A270_shL7_dhrus_loc#NA:1	20	Gene GRHPR	GLUR, GLYO, PH2, GRHPR	glyoxylate reductase/hydroxypyruvate reductase	NM_012203, XCT21356.2, XCT1982711.1, XCT1982712.1, XCT1982714.1	220347_s_at, 214664_s_at, 216305_s_at	NP_036335.1, EAH65264.1, EAH65262.1, EAH65263.1, EAH65266.1
GeneID:916	ZBTB5	9	37,435,099	37,465,407	27,308	-	1	2_A270_shL87_glus_loc#RNA 1:7699	383	ut gene	0	1	11	14	1	2_A270_shL87_glus_loc#NA:1	14	Gene ZBTB5	ZBTB5	zinc finger and BTB domain containing 5	NM_014572, XCT2301823.1	205926_at	NP_055657.1, EAH65292.1
GeneID:51806	TOMM6	9	37,555,410	37,562,836	6,226	-	2	1_A270_shL7_dhrus_loc#N A:1-3501, 2_A270_shL87_glus_loc#RNA 1:7699	446, -2256	ut gene, upstream	1	1	12.5	12.5	2	2_A270_shL87_glus_loc#NA:1	16	Gene TOMM6	Tom6, RP11-283J6.1, bA421M10.2, C9orf105, TOMM6	translocase of outer mitochondrial membrane 6 homolog (yeast)	NM_020001792, NM_001134454, NM_001134455	218553_s_at	NP_001001790.1, NP_001127956.1, NP_001127957.1
GeneID:56234	RGMTD3	9	37,753,802	37,770,869	20,167	+	2	1_A270_shL7_dhrus_loc#N A:1-3502, 2_A270_shL87_glus_loc#RNA 1:7699	31286, 31393	downstream, downstream	1	1	20	25	1	2_A270_shL87_glus_loc#NA:1	25	Gene RGMTD3	RGMTD3, bA210.8, RP11-210.8, FLJ31455	RNA (guanine-N(7)-)-methyltransferase domain containing 3	NM_144864, XCT212634, XCT2307240.0, XCT2332340.0, XCT2332344.0, XCT2332345.0	235303_at, 240166_s_at	NP_659801.2, EAH65267.1, EAH65265.1, EAH65266.1, EAH65266.1
GeneID:1010	EXOSC3	9	37,760,308	37,765,087	4,780	+	2	1_A270_shL7_dhrus_loc#N A:1-3502, 2_A270_shL87_glus_loc#RNA 1:7699	-21, -65	upstream, upstream	1	1	20	25	1	2_A270_shL87_glus_loc#NA:1	25	Gene EXOSC3	hRrp42p, CGI-102, hRrp-40, RRP40, MGC15126, EXOSC3, RP11-3J10.6, Rrp42p, p10, MGC22, bA310.7	exosome component 3	NM_016042, NM_016236, NM_001282269, NM_016042, NCT21287.3	223389_s_at, 223490_s_at, 227912_s_at, 227916_s_at, 231683_at	NP_057126.2, EAH65268.1, EAH65269.1, EAH65270.1, EAH65268.1
GeneID:30423016	MIR3159	9	37,769,453	37,809,807	20,654	+	4	1_A270_shL7_dhrus_loc#N A:1-3502, 1_A270_shL7_dhrus_loc#N A:1-3503, 2_A270_shL87_glus_loc#RNA 1:7699, 2_A270_shL87_glus_loc#RNA 1:7698	-4365, 11155, -4301, 11219	upstream, ut gene, upstream, ut gene	1	1	21.5	25	2	2_A270_shL87_glus_loc#NA:1	31	Gene MIR3159	MIR3159	microRNA 3159	NR_036116		
GeneID:9269	DCAP10	9	37,800,790	37,807,666	66,876	+	2	1_A270_shL7_dhrus_loc#N A:1-3503, 2_A270_shL87_glus_loc#RNA 1:7699	-162, -116	upstream, upstream	1	1	23	31	1	2_A270_shL87_glus_loc#NA:1	31	Gene DCAP10	DCAP10, WDR32, MGC31761, FLJ23201, MGC10765	DDB1 and CUL4 associated factor 10	NM_024343, XCT2307033.0, XCT2307035.0, XCT2307036.0	219301_s_at, 220894_s_at, 220911_at, 220979_at	NP_077321.3, EAH65263.1, EAH65261.1, EAH65262.1
GeneID:4661	SH3	9	37,915,093	38,069,210	153,215	+	1	1_A270_shL7_dhrus_loc#N A:1-3505	-552	upstream	0	1	16	22	1	1_A270_shL7_dhrus_loc#NA:1	22	Gene SH3	SH3, RP11-321I.6, bA321I.2	SH3 homology 2 domain containing adaptor protein B	NM_003025, XCT1999295.1, XCT21259.2	1557458_s_at, 204696_at, 204697_s_at, 204698_s_at, 204699_at	NP_003018.2, EAH65254.1, EAH65255.1
GeneID:53650	ANKRD16	9	38,571,351	38,620,360	49,009	+	2	1_A270_shL7_dhrus_loc#N A:1-3504, 2_A270_shL87_glus_loc#RNA 1:7699	-276, -460	upstream, upstream	1	1	21	26	1	2_A270_shL87_glus_loc#NA:1	26	Gene ANKRD16A	KIAA2013, MGC176674, ANKRD16A, FLJ40632, PLJ33740	ankyrin repeat domain 16A	NM_145165	1555899_at, 242045_at, 244291_at	NP_077725.2
GeneID:56226	C9orf122	9	38,621,033	38,623,281	2,249	-	2	1_A270_shL7_dhrus_loc#N A:1-3504, 2_A270_shL87_glus_loc#RNA 1:7699	-249, -263	upstream, upstream	1	1	21	26	1	2_A270_shL87_glus_loc#NA:1	26	Gene C9orf122	C9orf122, FAM201A	chromosome 9 open reading frame 122	NM_027294	1557014_s_at, 1557541_at	NP_081570.2
GeneID:414	FAM27A	9	45,727,029	45,728,253	1,234	+	1	1_A270_shL7_dhrus_loc#N A:1-3509	2219	downstream	0	1	8	17	1	1_A270_shL7_dhrus_loc#NA:1	17	Gene FAM27A	MGC11241, FAM27A1, bA723.2.5, FAM27A	family with sequence similarity 27, member A	NR_030900	1555002_at	
GeneID:6020912	FAM27E2	9	45,733,568	45,733,877	309	+	1	1_A270_shL7_dhrus_loc#N A:1-3509	4340	upstream	0	1	8	17	1	1_A270_shL7_dhrus_loc#NA:1	17	Gene FAM27E2	MGC163337, FAM27E2	family with sequence similarity 27, member E2	XR_110603		
GeneID:100369586	LOC1003 69586	9	99,457,269	99,469,314	12,025	+	1	2_A270_shL87_glus_loc#RNA 1:7810	1111	ut gene	0	1	29	36	1	2_A270_shL87_glus_loc#NA:1	36	Gene LOC100369586	LOC100125775	hypothetical LOC100125775	XR_110555		
GeneID:4227286	LOC4227 86	9	99,457,763	99,464,375	26,562	+	1	2_A270_shL87_glus_loc#RNA 1:7811	-1273	upstream	0	1	18	25	1	2_A270_shL87_glus_loc#NA:1	25	Gene LOC4227 86	LOC100130989	hypothetical LOC100130989	XR_110554		
GeneID:393	PIP5K1B	9	71,320,616	71,624,091	303,475	+	2	1_A270_shL7_dhrus_loc#N A:1-3905, 2_A270_shL87_glus_loc#RNA 1:7912	74292, 74392	ut gene, ut gene	1	1	14	17	1	2_A270_shL87_glus_loc#NA:1	17	Gene PIP5K1B	STM7, PIP5K1B, MSS4	phosphatidylinositol-4-phosphate 5-kinase, type 1, beta	NM_003558, XCT20955.3, XCT2389877.0, XCT2332666.0	208632_s_at, 217477_at	NP_003549.1, EAH62467.1, EAH62465.1, EAH63666.1
GeneID:16224	FAM122A	9	71,394,964	71,395,609	3,646	+	2	1_A270_shL7_dhrus_loc#N A:1-3905, 2_A270_shL87_glus_loc#RNA 1:7913	44, 44	ut gene, ut gene	1	1	14	17	1	2_A270_shL87_glus_loc#NA:1	17	Gene FAM122A	C9orf62, FAM122A, MGC17307	family with sequence similarity 122A	NM_138333, XCT1929835.3	226453_at, 235053_at	NP_612356.2, EAH62466.1
GeneID:414	TJP2	9	71,736,224	71,870,124	133,900	+	1	2_A270_shL87_glus_loc#RNA 1:7913	59356	ut gene	0	1	10	22	1	2_A270_shL87_glus_loc#NA:1	22	Gene TJP2	MGC26306, ZO2, TJP2, X104	tight junction protein 2 (zona occludens 2)	NM_001170630, NM_004817, NM_207629, NM_001170414, NM_001170415, NM_001170416, XCT21709.3, XCT2307112.0, XCT2332710.0, XCT2332712.0, XCT1935619.1	202553_at, 202017_at, 227132_at, 242691_at	NP_001164101.1, NP_004805.2, NP_001163655.1, NP_001163656.1, NP_001163657.1, NP_001163658.1, EAH62476.1, EAH62478.1, EAH62479.1, EAH63600.1
GeneID:99681	MRMDC2	9	72,656,297	72,841,688	183,391	+	3	1_A270_shL7_dhrus_loc#N A:1-3907, 2_A270_shL87_glus_loc#RNA 1:7939	41727, 41623	ut gene, ut gene	1	1	31	27	1	1_A270_shL7_dhrus_loc#NA:1	31	Gene MRMDC2	MGC21681, MRMDC2	MRAM domain containing 2	NM_152387, XCT2356568.0, XCT2356710.0, XCT2356809.0, XCT2356907.0, XCT1656537.2	226883_at	NP_689999.2, EAH62468.1, EAH62483.1, EAH63694.1, EAH62466.1, EAH62467.1
GeneID:100369726	LOC1003 69726	9	72,805,914	72,873,762	64,868	-	1	2_A270_shL87_glus_loc#RNA 1:7917	-626	upstream	0	1	15	16	1	2_A270_shL87_glus_loc#NA:1	16	Gene LOC100369726	LOC100507299	hypothetical LOC100507299	XR_110979		
GeneID:3127	SMC5	9	72,873,878	72,899,799	65,911	+	1	2_A270_shL7_dhrus_loc#N A:1-3917	330	ut gene	0	1	15	16	1	2_A270_shL87_glus_loc#NA:1	16	Gene SMC5	SMC5L1, SMC5, KIAA0594	structural maintenance of chromosomes 5	NM_015110, XCT19732.3, XCT2335540.0	212626_at, 212627_at, 227723_s_at	NP_055925.2, EAH62501.1, EAH62502.1
GeneID:57	KLF9	9	72,999,513	73,029,573	30,060	-	5	1_A270_shL7_dhrus_loc#N A:1-3908, 1_A270_shL7_dhrus_loc#N A:1-3909, 1_A270_shL7_dhrus_loc#N A:1-3910, 2_A270_shL87_glus_loc#RNA 1:7915, 2_A270_shL87_glus_loc#RNA 1:7916, 2_A270_shL87_glus_loc#RNA 1:7917	469, -4279, 24769, 469, -497	ut gene, upstream, ut gene, ut gene, upstream	1	1	26.33	29.67	3	2_A270_shL87_glus_loc#NA:1	40	Gene KLF9	BTEB, BTEB1, KLF9	Kruppel-like factor 9	NM_001206, XCT22611302.0, XCT19209.4	203541_s_at, 203542_s_at, 203543_s_at, 235474_s_at, 239536_s_at	NP_001197.1, EAH62503.1, EAH62504.1
GeneID:9076	TRPM3	9	73,149,849	73,736,514	586,665	+	2	1_A270_shL7_dhrus_loc#N A:1-3910, 2_A270_shL87_glus_loc#RNA 1:7921	1020130, 215629	ut gene, ut gene	1	1	14.5	15	2	1_A270_shL7_dhrus_loc#NA:1	16	Gene TRPM3	GON-2, LTRPC3, MLSN2, TRPM3	transient receptor potential cation channel, subfamily M, member 3	NM_206945, NM_001007470, NM_206946, NM_206947, NM_024971, NM_001007471, NM_206948, NM_020952, XCT2349161.0, XCT2349162.0, XCT2349163.0, XCT2332519.0, XCT2352620.0, XCT1934910.2	1554722_at, 1555252_s_at, 1554422_at, 216402_at, 216609_at, 220462_at, 233022_at	NP_006572.3, NP_001007471.1, NP_996539.2, NP_996540.2, NP_001007472.2, NP_996535.2, NP_996527.2, NP_065933.2, EAH62518.1, EAH62519.1, EAH62520.1, EAH62521.1, EAH62522.1
GeneID:1104	FAM105B	9	74,677,368	74,826,168	48,760	+	1	2_A270_shL87_glus_loc#RNA 1:7926	212	ut gene	0	1	16	20	1	2_A270_shL87_glus_loc#NA:1	20	Gene FAM105B1	CGI-67, RP11-402H11.2, C9orf77	family with sequence similarity 105, member B1	NM_018061, NM_001127503, XCT2086.3, XCT2356369.0	225265_at, 227551_at, 244572_at	NP_076990.2, NP_001120851.1, EAH62521.1, EAH62522.1
GeneID:55241	C9orf85	9	74,826,423	74,866,373	61,950	+	1	2_A270_shL87_glus_loc#RNA 1:7926	-467	upstream	0	1	16	20	1	2_A270_shL87_glus_loc#NA:1	20	Gene C9orf85	MGC61599, C9orf85	chromosome 9 open reading frame 85	NM_152503, XCT20559.4, XCT2346307.0, XCT2346308.1, XCT1934913.0	235899_at, 235979_at, 236812_s_at	NP_872311.2, EAH62523.1, EAH62524.1, EAH62525.1, EAH62526.1
GeneID:919	CD2A	9	74,764,293	74,867,140	102,847	+	1	2_A270_shL87_glus_loc#RNA 1:7926	-37	upstream	0	1	16	17	1	2_A270_shL87_glus_loc#NA:1	17	Gene CD2A	KIAA1236, MGC9852, CYPIN, FLJ40826, CD2A, MEGHER	guanine deaminase	NM_004392, XCT2356391.0, XCT2356509.0, XCT1935845.1	1555533_at, 204209_s_at	NP_004382.1, EAH62530.1, EAH62529.1, EAH62528.1
GeneID:763	ZFAND5	9	74,999,341	74,999,163	12,822	-	2	1_A270_shL7_dhrus_loc#N A:1-3914, 2_A270_shL87_glus_loc#RNA 1:7929	147, -317	ut gene, upstream	1	1	22	19	1	2_A270_shL87_glus_loc#NA:1	22	Gene ZFAND5	ZA20D2, ZNF216, ZFAND5, ZFAND5A	zinc finger, AN1-type domain 5	NM_006037, NM_001102420, NM_001102421, XCT1452858.2, XCT1452859.2, XCT1982.4, XCT1985469.1, XCT1985470.1	210273_s_at, 217741_s_at, 225317_at	NP_001093891.1, NP_001093892.1, NP_001093893.1, EAH62534.1, EAH62536.1, EAH62537.1, EAH62533.1, EAH62535.1
GeneID:17521	TNIC1	9	76,136,717	76,231,267	314,550	+	2	1_A270_shL7_dhrus_loc#N A:1-3915, 1_A270_shL7_dhrus_loc#N A:1-3916	33923, 66515	ut gene, ut gene	1	1	8	17.5	12	2	1_A270_shL7_dhrus_loc#NA:1	16	Gene TNIC1	DFNA36, TNIC1, DFNB7, DFNB11	tetratricopeptide repeat domain 1	NM_138691, XCT2356394.0, XCT2356565.0, XCT6856.3	1554591_s_at	NP_619636.2, EAH62540.1, EAH62539.1, EAH62541.1
GeneID:5071	C9orf46	9	77,361,499	77,367,682	6,202	-	2	1_A270_shL7_dhrus_loc#N A:1-3916, 2_A270_shL87_glus_loc#RNA 1:7932	42, 474	ut gene, ut gene	1	1	15	16	1	2_A270_shL87_glus_loc#NA:1	16	Gene C9orf46	FLJ35765, FLJ10110, C9orf46	chromosome 9 open reading frame 46	NM_017668, XCT1979.2	218504_s_at, 222761_s_at	NP_060366.2, EAH62564.1
GeneID:5472	C9orf41	9	77,397,672	77,643,310	45,407	+	1	2_A270_shL87_glus_loc#RNA 1:7932	270	ut gene	0	1	15	17	1	2_A270_shL87_glus_loc#NA:1	17	Gene C9orf41	FLJ35765, C9orf41	chromosome 9 open reading frame 41	NM_152420, XCT2356553.0, XCT2356556.0, XCT1935.2	235324_at, 241761_at	NP_689633.1, EAH62567.1, EAH62568.1, EAH62569.1
GeneID:4661	C9orf85	9	77,676,116	77,703,133	27,017	-	1	1_A270_shL7_dhrus_loc#N A:1-3919	237	upstream	1	0	15	11	1	1_A270_shL7_dhrus_loc#NA:1	15	Gene C9orf85	FLJ35399, C9orf85, NRG1, RP11-230H4.2, bA230H4.2	chromosome 9 open reading frame 85	NM_017651, NM_001129682, NM_033352, XCT1761698.1, XCT1986259.1	1552781_at, 219147_s_at	NP_060121.1, NP_001120173.1, EAH62566.1, EAH62569.1
GeneID:6378	OSTF1	9	77,703,288	77,762,114	58,716	+	1	1_A270_shL7_dhrus_loc#N A:1-3919	-802	upstream	1	0	15	11	1	1_A270_shL7_dhrus_loc#NA:1	15	Gene OSTF1	bA230H4.1, FLJ35399, OSTF1, OSTF1L	osteoclast stimulating factor 1	NM_012183, XCT2356577.0, XCT2356716.0, XCT2352626.0, XCT1985.2	204479_at	NP_036514.4, EAH62570.1, EAH62570.1, EAH62571.1, EAH62572.1
GeneID:125	PCSK5	9	78,505,560	78,977,255	471,695	+	4	1_A270_shL7_dhrus_loc#N A:1-3920, 1_A270_shL7_dhrus_loc#N A:1-3921, 2_A270_shL87_glus_loc#RNA 1:7936, 2_A270_shL87_glus_loc#RNA 1:7937, 2_A270_shL87_glus_loc#RNA 1:7938, 2_A270_shL87_glus_loc#RNA 1:7939	323704, 181, 163016, 329649	ut gene, ut gene, ut gene, ut gene	1	1	17.67	21	3	2_A270_shL87_glus_loc#NA:1	28	Gene PCSK5	PCSK5, PC6, SPC6, FLJ11149, FLJ16213, PCSK5A, PC5	proprotein convertase subtilisin/kexin type 5	NM_006200, NM_001190882, XCT2356902.0, XCT2356903.0, XCT2356922.0	208539_s_at, 208540_at	NP_006191.2, NP_001170411.1, EAH62575.1, EAH62576.1, EAH62577.1
GeneID:5312	RPK	9	79,030,433	79,099,444	9,011	-	2	1_A270_shL7_dhrus_loc#N A:1-3921, 2_A270_shL87_glus_loc#RNA 1:7939	560, 612	ut gene, ut gene	1	1	17	21	1	2_A270_shL87_glus_loc#NA:1	21	Gene RPK	RPK, RPK, FLJ11149	citrullinated histone	NM_005329, XCT22674.0, XCT19856.2	200224_at, 200225_s_at	NP_005309.3, EAH62576.1, EAH62579.1
GeneID:58471	PRUNE2	9	78,226,292	79,521,053	294,711	-	5	1_A270_shL7_dhrus_loc#N A:1-3923, 1_A270_shL7_dhrus_loc#N A:1-3924, 2_A270_shL87_glus_loc#RNA 1:7940, 2_A270_shL87_glus_loc#RNA 1:7941, 2_A270_shL87_glus_loc#RNA 1:7942	87627, -341, 213503, 87819, -215	ut gene, upstream, ut gene, ut gene, upstream	1	1	22	25	3	2_A270_shL87_glus_loc#NA:1	27	Gene PRUNE2	PRUNE2, DKFZp762G137, BMCC1, FLJ90990, BNIP3L, RP11-96J1.2, FLJ35876, AZH.NI.3, KIAA0367, bA21N4.3, FLJ00115, C9orf85	prune homolog 2 (Drosophila)	NM_015225, XCT1761655.2	1552453_at	NP_059040.2, EAH62584.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Transcripts	Internal Exons	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
GeneID:10026690	RPS11-470P4.2	9	78,791,972	79,792,833	1,161	+	1	2_A375_sh37_dtct_lncRNA:1:7840	259	st gene	0	1	11	16	1	2_A375_sh37_dtct_lncRNA:1	16	Gene RPS11-470P4.2	LOC100269936	hypothetical LOC100269936	NR_038966		
GeneID:23330	VPS13A	9	78,792,361	80,022,269	240,035	+	1	2_A375_sh37_dtct_lncRNA:1:7840	163	st gene	0	1	11	16	1	2_A375_sh37_dtct_lncRNA:1	16	Gene VPS13A	KIAA0986, CHAC, PLA2G3D, VPS13A, CHOREIN	vacuolar protein sorting 13 homolog A (S. cerevisiae)	NM_001018037, NM_033305, NM_001018039, NM_015186, NCT22984440, NCT22984453, NCT22984460, NCT22984477, NCT13382224, NCT13382231	2147763_at, 2148352_x_at, 2219907_at, 2219906_s_at, 2219902_s_at	NP_001018047.1, NP_150648.2, NP_056091.1, NP_001018038.1, EAW62600.1, EAW62601.1, EAW62597.1, EAW62595.1, EAW62592.1, EAW62602.1
GeneID:9918	GNA14	9	80,037,995	80,263,232	225,237	-	2	1_A375_sh37_dtct_lncRNA:1:5525, 1_A375_sh37_dtct_lncRNA:1:7298	72352, 72352	st gene, ut gene	1	1	17	24	1	1_A375_sh37_dtct_lncRNA:1	24	Gene GNA14	GNA14		NM_004297, NCT16482.3	220106_at, 2453590_at	NP_004288.1, EAW62603.1
GeneID:9966	PSAT1	9	80,912,059	80,949,009	32,950	+	1	2_A375_sh37_dtct_lncRNA:1:7840	455	st gene	0	1	16	19	1	2_A375_sh37_dtct_lncRNA:1	19	Gene PSAT1	PSAT1, PSA, MGC1466, EPIP, PSAT	phosphoserine aminotransferase 1	NM_021154, NM_058179, NCT22987260, NCT22987272, NCT22987280, NCT22987300, NCT22987310, NCT13382247	223592_s_at, 223592_s_at	NP_066977.1, NP_478356.1, EAW62617.1, EAW62619.1, EAW62620.1, EAW62622.1, EAW62618.1, EAW62621.1, EAW62623.1
GeneID:7174	TLE4	9	82,199,878	83,241,896	1,041,019	+	1	1_A375_sh37_dtct_lncRNA:1:5526	262	upstream	1	0	19	19	1	1_A375_sh37_dtct_lncRNA:1	19	Gene TLE4	GRG4, ESG4, E(sp)1, ESG, BCE1, BCE-1, TLE4	transducin-like enhancer of split 4 (E(sp)1 homolog, Drosophila)	NM_007005, NCT22989232, NCT22989244, NCT22989260, NCT22989277, NCT22989295	204572_at, 214668_at, 216947_x_at, 233575_s_at, 233576_at	NP_009039.2, EAW62632.1, EAW62627.1, EAW62626.1, EAW62630.1, EAW62631.1, EAW62629.1
GeneID:57019	PRMD3	9	93,662,300	96,153,246	291,046	-	5	1_A375_sh37_dtct_lncRNA:1:5535, 1_A375_sh37_dtct_lncRNA:1:5529, 1_A375_sh37_dtct_lncRNA:1:7846, 1_A375_sh37_dtct_lncRNA:1:7856, 1_A375_sh37_dtct_lncRNA:1:7860	236660, 20, 220724, 16854, 346	ut gene, ut gene, ut gene, st gene, upstream	1	1	17.33	21.33	3	2_A375_sh37_dtct_lncRNA:1	24	Gene PRMD3	PRIS, 4.1O, EPB41L4O, MGC20551, EPB41LO, PRMD3	PERM domain containing 2	NM_178535, NCT22992230, NCT22992241, NCT22992253, NCT22992267, NCT13382241	230593_at, 230595_at, 242600_at	NP_777593.2, EAW62665.1, EAW62667.1, EAW62669.1, EAW62663.1, EAW62651.1
GeneID:4267	C9orf64	9	96,553,226	96,571,663	18,437	-	1	1_A375_sh37_dtct_lncRNA:1:5529	63	st gene	1	0	14	12	1	1_A375_sh37_dtct_lncRNA:1	14	Gene C9orf64	MGC10999, RP11-573L7.3, C9orf64	chromosome 9 open reading frame 64	NM_032307, NCT13349731.0, NCT22998722.0, NCT22998732.0	223697_s_at, 223697_at	NP_115683.2, EAW62674.1, EAW62672.1, EAW62673.1
GeneID:190	HNRNPK	9	96,582,998	96,593,569	12,571	+	1	2_A375_sh37_dtct_lncRNA:1:7851	661	st gene	0	1	14	20	1	2_A375_sh37_dtct_lncRNA:1	20	Gene HNRNPK	CSBP, TUNP, PLA1112, HNRPIL, HNRNPK	heterogeneous nuclear ribonucleoprotein K	NM_031263, NM_031262, NM_001142276, NCT22998440, NCT22998453, NCT22998465, NCT22998477, NCT13382258	200097_s_at, 200773_s_at	NP_112533.1, NP_112582.1, NP_002131.2, EAW62676.1, EAW62678.1, EAW62681.1, EAW62675.1, EAW62677.1, EAW62679.1, EAW62680.1
GeneID:27043	MRT-1	9	96,564,663	96,564,772	109	-	1	1_A375_sh37_dtct_lncRNA:1:7851	1	upstream	0	1	14	20	1	1_A375_sh37_dtct_lncRNA:1	20	Gene MRT-1	eu-7-1, MRT-1, hua-eu-7-1, MRT-1	eucuRNA 7-1	NR_029903		
GeneID:9410	RNH1	9	96,593,627	96,618,809	23,352	+	1	2_A375_sh37_dtct_lncRNA:1:7851	429	upstream	0	1	14	20	1	2_A375_sh37_dtct_lncRNA:1	20	Gene RNH1	C9orf16, RNH1, RP11-345E1.1, BLAP75, PLI12666	ribonuclease/angiogenin inhibitor 1, human HK cytosolic)	NM_002939, NCT19933.1, NCT13382258.0	216979_at	NP_002930.2, EAW62682.1, EAW62682.1
GeneID:1268	GCLM1	9	96,641,036	96,715,116	74,080	-	1	1_A375_sh37_dtct_lncRNA:1:5531	40665	upstream	1	0	23	14	1	1_A375_sh37_dtct_lncRNA:1	23	Gene GCLM1	GCOPH2, GCLM1, PLI02634, C9orf59, GP70, FLJ23905, PSEC0297, bA379P1.3	gglg- methionine protein 1	NM_182566, NM_177437, NCT22983324, NCT22983337, NCT22983344, NCT22983357, NCT13382265	1552245_at, 213771_at	NP_057632.2, NP_808080.1, EAW62705.1, EAW62706.1
GeneID:9670	ISCA1	9	96,679,961	96,697,690	16,629	-	1	2_A375_sh37_dtct_lncRNA:1:7852	454	st gene	0	1	17	19	1	2_A375_sh37_dtct_lncRNA:1	19	Gene ISCA1	BCA1, HBLD2, RP11-507D14.2, hlaCA, BA1, MGC4276	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	NM_030940, NCT22983214, NCT22983377	209272_s_at, 209274_s_at, 241624_s_at	NP_112202.2, EAW62713.1, EAW62712.1
GeneID:9070	ZCCHC6	9	95,902,646	95,969,402	66,754	-	3	1_A375_sh37_dtct_lncRNA:1:5533, 1_A375_sh37_dtct_lncRNA:1:7852, 1_A375_sh37_dtct_lncRNA:1:7860	80, 72346, 42	ut gene, downstream, st gene	1	1	24.5	20	2	1_A375_sh37_dtct_lncRNA:1	24	Gene ZCCHC6	DKFZp686F116, DKFZp686I1269, DKFZp686B1412, DKFZp686C11112, ZCCHC6, PAPD6	zinc finger, CCHC domain containing 6	NM_001159316, NM_001159074, NM_024617, NCT22998160, NCT22998172, NCT22998184, NCT22998197, NCT13382282	228563_s_at, 236185_at, 236203_at, 236500_s_at, 242776_at	NP_001177685.1, NP_001172093.1, NP_078942.2, EAW62714.1, EAW62715.1, EAW62716.1, EAW62717.1, EAW62718.1
GeneID:619	GAS1	9	96,559,277	96,562,164	2,827	-	1	2_A375_sh37_dtct_lncRNA:1:7859	1364	upstream	0	1	17	24	1	2_A375_sh37_dtct_lncRNA:1	24	Gene GAS1	GAS1		NM_002048	204656_s_at, 204657_s_at	NP_002039.2
GeneID:100506548	LOC100506548	9	96,562,801	96,566,451	3,650	+	1	2_A375_sh37_dtct_lncRNA:1:7859	687	ut gene	0	1	17	24	1	2_A375_sh37_dtct_lncRNA:1	24	Gene LOC100506548	LOC100506548	hypothetical LOC100506548	XR_108969		
GeneID:612	DAPK1	9	90,112,756	90,323,549	210,793	+	2	1_A375_sh37_dtct_lncRNA:1:5535, 1_A375_sh37_dtct_lncRNA:1:7859, 1_A375_sh37_dtct_lncRNA:1:7860	215552, 215765	downstream, downstream	1	1	22	22	1	2_A375_sh37_dtct_lncRNA:1	22	Gene DAPK1	DAPK1, DAPK, DKFZp781I035	death-associated protein kinase 1	NM_004938, NCT22998140, NCT22998160, NCT22998177, NCT13382224, NCT13382231	202199_at, 211214_s_at	NP_004929.2, EAW62727.1, EAW62728.1, EAW62729.1, EAW62726.1, EAW62725.1
GeneID:514	CTSL1	9	90,340,874	90,349,284	8,410	+	1	1_A375_sh37_dtct_lncRNA:1:7857	488	st gene	0	1	16	16	1	1_A375_sh37_dtct_lncRNA:1	16	Gene CTSL1	MEP, FLJ10377, CTSL, CATL, CTSL1	cathepsin L1	NM_145918, NM_001912, NCT19982762.2, NCT19982772.2, NCT13382282, NCT13382289	202087_s_at	NP_690023.1, NP_001903.1, EAW62733.1, EAW62732.1, EAW62734.1, EAW62735.1, EAW62736.1
GeneID:5552	COX20	9	90,381,396	90,389,685	8,338	+	1	2_A375_sh37_dtct_lncRNA:1:7858	127	st gene	0	1	20	17	1	2_A375_sh37_dtct_lncRNA:1	17	Gene COX20	FAM2, C20ORF, PNGAL/EE, COX20, CCRK	cytochrome c oxidase assembly protein 20	NM_001170536, NM_001170540, NM_020130933, NCT22983356, NCT22983369, NCT22983640, NCT22983660, NCT22983674, NCT13382304	203271_s_at	NP_945191.1, NP_036291.2, NP_001164110.1, NP_001164111.1, NP_001035852.1, EAW62746.1, EAW62743.1, EAW62744.1, EAW62745.1, EAW62747.1, EAW62748.1
GeneID:3556	SHC3	9	91,630,696	91,763,652	172,956	-	2	1_A375_sh37_dtct_lncRNA:1:5537, 2_A375_sh37_dtct_lncRNA:1:7860	-1263, -1433	upstream, upstream	1	1	17	16	1	1_A375_sh37_dtct_lncRNA:1	17	Gene SHC3	SHC3, RAI, SHCC, hSHC, PLI55325, DKFZp686H1544, N-Shc	SHC (Src homology 2 domain containing) transforming protein 3	NM_130466, NCT22983023, NCT22983235, NCT22983258	209330_s_at	NP_035443.2, EAW62780.1, EAW62759.1
GeneID:164	CK02	9	91,826,113	91,831,816	5,908	+	2	1_A375_sh37_dtct_lncRNA:1:5535, 1_A375_sh37_dtct_lncRNA:1:7860	7339, 7247	downstream, downstream	1	1	19	23	1	2_A375_sh37_dtct_lncRNA:1	23	Gene CK02	CK02H02, CK02	CDC28 protein kinase regulatory subunit 2	NM_001827, NCT21061.3	204170_s_at	NP_001818.1, EAW62762.1
GeneID:3552262	MIR3153	9	91,927,140	91,927,221	81	+	2	1_A375_sh37_dtct_lncRNA:1:5535, 1_A375_sh37_dtct_lncRNA:1:7860	6332, 6220	downstream, downstream	1	1	19	23	1	2_A375_sh37_dtct_lncRNA:1	23	Gene MIR3153	MIR3153	microRNA 3153	NR_036108		
GeneID:9046	SEC16BP2	9	91,933,812	91,974,561	41,749	+	2	1_A375_sh37_dtct_lncRNA:1:5535, 1_A375_sh37_dtct_lncRNA:1:7860	60, -52	st gene, upstream	1	1	19	23	1	2_A375_sh37_dtct_lncRNA:1	23	Gene SEC16BP2	SEC16BP2, SBP2, DKFZp686O09168	SEC16 binding protein 2	NM_024077, NCT21055.3, NCT22983772.0	214263_at, 224290_s_at	NP_076942.3, EAW62763.1, EAW62764.1
GeneID:101128983	LOC100128983	9	92,551,420	93,625,540	64,120	-	1	2_A375_sh37_dtct_lncRNA:1:7864	1660	upstream	0	1	14	20	1	2_A375_sh37_dtct_lncRNA:1	20	Gene LOC100128983		hypothetical LOC100128983	XR_112235, XR_108975, XR_114270		
GeneID:100507137	LOC100507137	9	92,995,457	93,072,569	4,112	-	1	2_A375_sh37_dtct_lncRNA:1:7865	12645	downstream	0	1	23	20	1	2_A375_sh37_dtct_lncRNA:1	20	Gene LOC100507137		hypothetical protein LOC100507137	XM_003119512		XP_003119560.1
GeneID:54414	AUH	9	93,976,097	94,124,206	148,109	+	1	2_A375_sh37_dtct_lncRNA:1:7866	270	ut gene	0	1	9	16	1	2_A375_sh37_dtct_lncRNA:1	16	Gene AUH	AUH		NM_001698, NCT22983430, NCT22983443	203052_at	NP_001679.1, EAW62788.1, EAW62784.1
GeneID:783	NPL3	9	94,171,227	94,186,148	14,917	-	3	1_A375_sh37_dtct_lncRNA:1:5539, 1_A375_sh37_dtct_lncRNA:1:7867, 1_A375_sh37_dtct_lncRNA:1:7868	4544, 4424, -320	ut gene, ut gene, upstream	1	1	15.5	19	2	2_A375_sh37_dtct_lncRNA:1	21	Gene NPL3	NPL3A, E4BP4, IL3BP1, NP-IL3A, NPL3	nuclear factor, interleukin 3 regulated	NM_005386, NCT21555.3, NCT19825594.1	203574_at	NP_005375.2, EAW62797.1, EAW62796.1
GeneID:6935	SPTLC1	9	94,793,627	94,877,690	84,063	-	2	1_A375_sh37_dtct_lncRNA:1:5540, 1_A375_sh37_dtct_lncRNA:1:7868	58, -6	ut gene, upstream	1	1	23	27	1	2_A375_sh37_dtct_lncRNA:1	27	Gene SPTLC1	MGC19645, HSN1, SPT1, HSAN1, SPT, HSAN, LBC1, LCB1, SPTLC1	serine palmitoyltransferase, long chain base subunit 1	NM_006415, NM_175324, NCT22983124.0, NCT22983129.0, NCT22983142.0	1554652_at, 202277_at, 202278_s_at	NP_006406.1, NP_787846.1, EAW62800.1, EAW62805.1, EAW62806.1
GeneID:100507816	LOC100507816	9	94,903,721	94,910,866	6,667	+	1	2_A375_sh37_dtct_lncRNA:1:5541	5831	ut gene	1	0	15	12	1	1_A375_sh37_dtct_lncRNA:1	15	Gene LOC100507816		hypothetical LOC100507197	XR_112236, XR_112237, XR_109976, XR_108977, XR_114271, XR_114272		
GeneID:55314	AIRE	9	94,972,823	95,006,038	63,413	-	2	1_A375_sh37_dtct_lncRNA:1:5542, 1_A375_sh37_dtct_lncRNA:1:7870	-10, -90	upstream, upstream	1	1	26	27	1	1_A375_sh37_dtct_lncRNA:1	27	Gene AIRE	PRO7053, IAR3, PLI20736, ILEIR3, IRR, EPS, IAR31	autoimmune regulator	NM_010477, NM_002161, NCT22012.2, NCT22981200.1, NCT22983004.0, NCT22983050.0, NCT19825601.1	206773_s_at	NP_032032.2, NP_002132.2, EAW62810.1, EAW62811.1, EAW62812.1, EAW62813.1, EAW62809.1
GeneID:26824	SNORA64	9	95,054,743	95,054,875	132	-	2	1_A375_sh37_dtct_lncRNA:1:5542, 1_A375_sh37_dtct_lncRNA:1:7870	-1173, -1253	upstream, upstream	1	1	26	27	1	1_A375_sh37_dtct_lncRNA:1	27	Gene SNORA64	SNORA64	small nucleolar RNA, H/ACA box 64	NR_003764		
GeneID:9533	NOL6	9	95,059,640	95,097,876	38,236	+	4	1_A375_sh37_dtct_lncRNA:1:5542, 1_A375_sh37_dtct_lncRNA:1:5543, 1_A375_sh37_dtct_lncRNA:1:7870, 1_A375_sh37_dtct_lncRNA:1:7878	21626, 220, 21746, 220	downstream, upstream, downstream, upstream	1	1	30	67	2	2_A375_sh37_dtct_lncRNA:1	107	Gene NOL6	Nop132, DKFZp686P12242, PLI20735, C9orf64, NOL6, bA62C5.2, bA62C5.4	nucleolar protein 6	NM_017649, NP_024520, NCT22981140, NCT22983117, NCT19825621	2162A4_at	NP_059818.4, EAW62814.1, EAW62815.1, EAW62816.1
GeneID:91541	CENPP	9	95,087,741	95,277,446	289,705	+	3	1_A375_sh37_dtct_lncRNA:1:5543, 1_A375_sh37_dtct_lncRNA:1:7878, 1_A375_sh37_dtct_lncRNA:1:7879	255, 19851, 255	st gene, ut gene, ut gene	1	1	44	60	2	2_A375_sh37_dtct_lncRNA:1	107	Gene CENPP	CENPP, CENP-P, PLI33928	centromere protein P	NM_001012267		NP_001012267.1
GeneID:642	BCM2	9	95,237,999	95,295,252	60,683	-	1	1_A375_sh37_dtct_lncRNA:1:5544	10700	ut gene	1	0	17	13	1	1_A375_sh37_dtct_lncRNA:1	17	Gene BCM2	BCM2, MGC126155, MGC126356	extracellular matrix protein 2, female organ and adipocyte specific	NM_001393, NCT22306.2	1555772_a_at, 1555101_at	NP_001384.1, EAW62826.1
GeneID:4766	IPPK	9	95,375,466	95,422,547	47,081	+	1	2_A375_sh37_dtct_lncRNA:1:7872	28	upstream	0	1	16	22	1	2_A375_sh37_dtct_lncRNA:1	22	Gene IPPK	KIAA0999, IPPX, INSP5K2, bM058513.1, PLI13163, IP5K, C9orf12, IPK1	inositol 1,2,3,5,6-pentakis/tetrakis/trisphosphate 2-kinase	NM_022755, NCT22313.3	219092_s_at, 222622_at	NP_073921.1, EAW62825.1
GeneID:3268	BICD2	9	95,412,645	95,527,093	53,408	-	2	1_A375_sh37_dtct_lncRNA:1:5545, 1_A375_sh37_dtct_lncRNA:1:7872	-661, -213	upstream, upstream	1	1	19	28	1	2_A375_sh37_dtct_lncRNA:1	28	Gene BICD2	KIAA0989, BICD2, bA539D6.1	bicaudal D homolog 2 (Drosophila)	NM_001003800, NM_015250, NCT22350.2	1553021_s_at, 1553021_s_at, 212702_s_at, 212158_s_at	NP_001003800.1, NP_056065.1, EAW62829.1
GeneID:4270	C9orf69	9	95,556,850	95,573,565	17,115	+	4	1_A375_sh37_dtct_lncRNA:1:5546, 1_A375_sh37_dtct_lncRNA:1:7874, 1_A375_sh37_dtct_lncRNA:1:7875, 1_A375_sh37_dtct_lncRNA:1:7878	2635, 396, 1486, 221	st gene, ut gene, upstream, st gene	1	1	14.33	15.67	3	1_A375_sh37_dtct_lncRNA:1	24	Gene C9orf69	MGC110898, BioCAR:D, C9orf69, MGC111118, bA270F5.1	chromosome 9 open reading frame 69	NM_032310, NCT22333589.0, NCT22350503.0, NCT22350513.0, NCT19130.3, NCT19836421, NCT19861001	1562559_at, 223366_at	NP_115698.3, EAW62833.1, EAW62850.1, EAW62852.1, EAW62853.1, EAW62854.1, EAW62851.1
GeneID:3196	PAM120A	9	96,241,172	96,326,297	114,224	+	1	2_A375_sh37_dtct_lncRNA:1:7877	114726	downstream	0	1	10	14	1	2_A375_sh37_dtct_lncRNA:1	14	Gene PAM120A	DNAPTP6, PAM120A, DNAPTP1, MGC111527, MGC132237, C9SPA, C9orf10	family with sequence similarity 129A	NM_014612, NCT22992242.0, NCT22992253.0, NCT22992264.0, NCT22992605.0	1555955_at, 1555944_at, 1555943_s_at, 1555947_at, 1555911_s_at, 206767_s_at, 206774_at, 206746_at	NP_055827.2, EAW62866.1, EAW62862.1, EAW62864.1, EAW62865.1
GeneID:4908	C9orf3	9	97,455,886	97,549,800	360,814	+	4	1_A375_sh37_dtct_lncRNA:1:5548, 1_A375_sh37_dtct_lncRNA:1:7880, 1_A375_sh37_dtct_lncRNA:1:7881, 1_A375_sh37_dtct_lncRNA:1:7882	56610, 106, 56610, 202968	ut gene, ut gene, st gene, st gene	1	1	22	30.33	3	2_A375_sh37_dtct_lncRNA:1	32	Gene C9orf3	C9ORF3, APO, FLJ14975, C9orf3, FLJ40323, APO, FLJ58532, CNPEF, AONEP	chromosome 9 open reading frame 3	NM_001163330, NM_052833, NM_001163331, NM_001163332, NCT22992612, NCT22992941, NCT22992953, NCT22992972, NCT22993000.0, NCT22975969.0	212565_s_at, 242370_at	NP_001152259.1, NP_777593.2, NP_001152260.1, NP_001152261.1, EAW62818.1, EAW62822.1, EAW62819.1, EAW62820.1, EAW62821.1, EAW62823.1
GeneID:727	PTCH1	9	98,205,264	98,279,247	73,983	-	3	1_A375_sh37_dtct_lncRNA:1:5549, 1_A375_sh37_dtct_lncRNA:1:7882, 1_A375_sh37_dtct_lncRNA:1:7884	6853, 6855	ut gene, ut gene, upstream	1	1	17.5	19	2	1_A375_sh37_dtct_lncRNA:1	25	Gene PTCH1	PTCH1, PTC, PLI26746, PLI43602, BCNS, PTCH1, PTCH, HPE7, PTC1, NBCCS	patched 1	NM_001083603, NM_001083606, NM_000264, NM_001083607, NM_001083604, NM_001083602, NM_001083605, NCT22985411.0, NCT19804691.1	1555520_at, 206523_s_at, 206513_at, 206516_at	NP_001077072.1, NP_001077073.1, NP_000255.2, NP_001077070.1, NP_001077071.1, NP_001077074.1, EAW62831.1, EAW62832.1
GeneID:100132782	C9orf30	9	98,566,370	98,636,259	69,889	+	2	1_A375_sh37_dtct_lncRNA:1:5550, 1_A375_sh37_dtct_lncRNA:1:7885	51, 115	st gene, ut gene	1	1	26	24	1	2_A375_sh37_dtct_lncRNA:1	26	Gene C9orf30	NAG11, PLI54618, PLI54629, C9orf30, bN312	chromosome 9 open reading frame 130	NM_023599, NR_023390		
GeneID:79746	C9orf152	9	98,637,900	98,701,122	63,222	+	2	1_A375_sh37_dtct_lncRNA:1:5550, 1_A375_sh37_dtct_lncRNA:1:7885	356, 244	ut gene, ut gene	1	1	26	24	1	2_A375_sh37_dtct_lncRNA:1	26	Gene C9orf152	SR216, PLI07709, MGC43264, RAD26L, MGC30162, C9orf152	chromosome 9 open reading frame 152	NM_001010859, NCT22979700.0, NCT19795542.0, NCT19836063.1	2328011_at	NP_001010859.1, EAW62836.1, EAW62838.1, EAW62837.1
GeneID:283716	HSD17B3	9	98,997,569	99,064,634	66,845	-	1	1_A375_sh37_dtct_lncRNA:1:5552	43202	ut gene	1	0	16	13	1	1_A375_sh37_dtct_lncRNA:1	16	Gene HSD17B3	EDH17B3, SDR12C2, HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	NM_000197, NCT16563.2	206663_at	NP_000181.1, EAW62848.1
GeneID:93626	ZNF367	9	99,148,223	99,160,669	12,446	-	3	1_A375_sh37_dtct_lncRNA:1:5553, 1_A375_sh37_dtct_lncRNA:1:7886, 1_A375_sh37_dtct_lncRNA:1:7887	1521, 172, 107	ut gene, ut gene, ut gene	1	1	16.5	14	2	1_A375_sh37_dtct_lncRNA:1	21	Gene ZNF367	ZFP29, PLI33470, ZNF367, CDC14B	zinc finger protein 367	NM_152693, NCT22975957.0, NCT22323.4	1565551_s_at	NP_710162.1, EAW62856.1, EAW62855.1
GeneID:93627	C9orf21	9	99,803,533	99,817,599	14,066	-	1	1_A375_sh37_dtct_lncRNA:1:7888	479	ut gene	0	1	12	16	1	2_A375_sh37_dtct_lncRNA:1	16	Gene C9orf21	C9orf21	chromosome 9 open reading frame 21	NM_152690, NCT19955556.1, NCT19955581.1, NCT22982004.4	227558_at	NP_710427.1, EAW62862.1, EAW62861.1, EAW62863.1
GeneID:7853	KIAA1529	9	100,000,705	100,139,877	138,899	+	1	2_A375_sh37_dtct_lncRNA:1:7889	145764	downstream	0	1	15	26	1	2_A375_sh37_dtct_lncRNA:1	26	Gene KIAA1529	DKFZp686G17125, DKFZp634D420, FLJ11233, KIAA1529, FLJ41397, C9orf114	KIAA1529	NM_020910, NM_030625, NM_030626, NCT22135400.0, NCT22135403.0	229627_at, 229625_s_at	NP_065963.2, EAW65540.1, EAW65541.1
GeneID:604984	C9orf174	9	100,000,910	100,139,877	69,867	+	1	2_A375_sh37_dtct_lncRNA:1:7889	76562	downstream	0	1	15	26	1	2_A375_sh37_dtct_lncRNA:1	26	Gene C9orf174	DKFZp686G17125, FLJ60036, DKFZp634D420, DKFZp686B20311, BDAG1, KIAA1529, FLJ41397, C9orf114	chromosome 9 open reading frame 174	NM_030893		NP_0009444.2
GeneID:89356	NCO_2049856	9	100,153,116	100,154,973	3,858	-	1	2_A375_sh37_dtct_lncRNA:1:7889	83001	downstream	0	1	15	26	1	2_A375_sh37_dtct_lncRNA:1	26	Gene NCO_2049856	LOC286359, FLJ17233, FLJ17217	hypothetical LOC286359	NR_026547	1563609_a_at, 1563607_s_at	
GeneID:3424	TDRD7	9	100,734,302	100,758,407	64,105	+	2	1_A375_sh37_dtct_lncRNA:1:5555, 1_A375_sh37_dtct_lncRNA:1:7890	-156, -156	upstream, upstream	1	1	24	30	1	2_A375_sh37_dtct_lncRNA:1	30	Gene TDRD7	TDRD7, RP11-350D10.1, PCTAIRE2BP, KIAA1528, TRAP	tudor domain containing 7	NM_014290, NCT22332398.0, NCT19235.3	213361_at	NP_055103.2, EAW65568.1, EAW65563.1
GeneID:111	TMOD1	9	100,263,462	100,364,825	100,963	+	1	2_A375_sh37_dtct_lncRNA:1:7890	28874	ut gene	0	1	12	13	1	2_A375_sh37_dtct_lncRNA:1	13	Gene TMOD1	TMOD1, TMOD, DKFZp686E, ETMOD	tropomodulin 1	NM_003275, NM_001166116, NCT22753531.0, NCT19956942.1	203661_s_at, 203662_s_at, 203663_s_at	NP_003266.1, NP_001150555.1, EAW65549.1, EAW65550.1
GeneID:55427	TSTD2	9	100,362,262	100,393,962	33,800	-	1	2_A375_sh37_dtct_lncRNA:1:7892	252	st gene	0	1	16	16	1	2_A375_sh37_dtct_lncRNA:1	16	Gene TSTD2	C9orf87, TSTD2, PLI09724	thiosulfate sulfurtransferase (rhodanese)-like domain containing 2	NM_152296, NCT22753685.1, NCT22769021.1, NCT22533393.0, NCT19233.3	1555430_at, 213161_at	NP_689518.4, EAW65593.1, EAW65595.1, EAW65594.1, EAW65591.1
GeneID:686	NCBP1	9	100,393,705	100,436,030	40,326	+	1	2_A375_sh37_dtct_lncRNA:1:7892	28	upstream	0	1	16	16	1	2_A375_sh37_dtct_lncRNA:1	16	Gene NCBP1	NCBP1, NCBP, Sto1, CBP80, MGC20687	nuclear cap binding protein subunit 1, 80kDa	NM_002486, NCT22753560.0, NCT19232.2, NCT19849864.1	209319_at, 209320_s_at	NP_002477.1, EAW65543.1, EAW65552.1, EAW65553.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:7507	XPA	9	100,437,191	100,459,691	22,500	-	2	1_A375_pNL7_minus_lncRNA::1::5556, 2_A375_pNL97_plus_lncRNA::1::7993	267, 331	in gene, in gene	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene XPA	XP1, XPAC, XPA	xeroderma pigmentosum, complementation group A	NM_000380, NR_027302, hCT19311.3	205672_at, 232967_at	NP_000371.1, EAW58855.1
GeneID:51531	C9orf156	9	100,666,772	100,684,852	18,080	-	2	1_A375_pNL7_minus_lncRNA::1::5557, 2_A375_pNL97_plus_lncRNA::1::7995	212, 116	in gene, in gene	1	1	36	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene C9orf156	HSPC219, NAP1, C9orf156	chromosome 9 open reading frame 156	NM_016481, hCT21115.3, hCT2353390.0, hCT1965005.1	222186_at, 222195_s_at, 47530_at	NP_057565.3, EAW58860.1, EAW58858.1, EAW58859.1
GeneID:55363	HEMGN	9	100,689,073	100,707,134	18,061	-	2	1_A375_pNL7_minus_lncRNA::1::5557, 2_A375_pNL97_plus_lncRNA::1::7995	22494, 22398	downstream, downstream	1	1	36	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene HEMGN	EDAG, EDAG-1, HEMGN	hemogen	NM_197978, NM_018437, hCT2273945.0, hCT2353376.0, hCT1776286.1	223669_at, 223670_s_at	NP_932095.1, NP_060907.2, EAW58861.1, EAW58862.1, EAW58863.1
GeneID:10541	ANP32B	9	100,745,489	100,778,225	32,736	+	4	1_A375_pNL7_minus_lncRNA::1::5558, 2_A375_pNL97_plus_lncRNA::1::7996, 2_A375_pNL97_plus_lncRNA::1::7997, 2_A375_pNL97_plus_lncRNA::1::7998	-17, -2001, 207, 1647	upstream, upstream, in gene, in gene	1	1	14	19.33	3	2_A375_pNL97_plus_lncRNA::1	21	Gene ANP32B	PHAPI2, SSP29, APRIL, ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	NM_006401, hCT21112.3, hCT2353386.0	201305_x_at, 201306_s_at	NP_006392.1, EAW58864.1, EAW58865.1
GeneID:9830	TRIM14	9	100,831,563	100,881,488	49,925	-	1	2_A375_pNL97_plus_lncRNA::1::7999	208	in gene	0	1	18	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene TRIM14	KIAA0129, TRIM14	tripartite motif containing 14	NM_014788, NM_033219, NM_033220, hCT2273683.0, hCT2273684.0, hCT2273685.0, hCT2273686.0, hCT2273687.0, hCT2273688.0, hCT2273689.0, hCT2273691.0, hCT2273693.0	203147_s_at, 203148_s_at, 210846_x_at, 211044_at, 231934_at	NP_055603.2, NP_150088.1, NP_150089.1, EAW58872.1, EAW58873.1, EAW58877.1, EAW58870.1, EAW58871.1, EAW58874.1, EAW58875.1, EAW58876.1, EAW58878.1
GeneID:7464	CORO2A	9	100,883,257	100,954,956	71,699	-	2	2_A375_pNL97_plus_lncRNA::1::7999, 2_A375_pNL97_plus_lncRNA::1::8000	73676, -564	downstream, upstream	0	1	15	19	2	2_A375_pNL97_plus_lncRNA::1	22	Gene CORO2A	CORO2A, WDR2, DKFZp686G19226, IR10, CLIPINB	coronin, actin binding protein, 2A	NM_052820, NM_003389, hCT21111.2, hCT2273720.0, hCT1776431.1	205538_at, 227177_at	NP_438171.1, NP_003380.3, EAW58879.1, EAW58880.1, EAW58881.1
GeneID:55357	TBC1D2	9	100,961,280	101,018,003	56,723	-	2	2_A375_pNL97_plus_lncRNA::1::8000, 2_A375_pNL97_plus_lncRNA::1::8001	62483, -205	downstream, upstream	0	1	14.5	21	2	2_A375_pNL97_plus_lncRNA::1	26	Gene TBC1D2	FLJ42782, PARIS1, TBC1D2A, FLJ16244, TBC1D2, FLJ10702, PARIS-1, DKFZp761D1823	TBC1 domain family, member 2	NM_018421, hCT21114.3, hCT2273712.0, hCT2273715.0, hCT2273717.0, hCT2353388.0, hCT2353389.0, hCT1960320.1	222173_s_at	NP_060891.3, EAW58887.1, EAW58882.1, EAW58884.1, EAW58885.1, EAW58888.1, EAW58883.1, EAW58886.1
GeneID:9568	GABBR2	9	101,050,364	101,471,479	421,115	-	2	2_A375_pNL97_plus_lncRNA::1::8002, 2_A375_pNL97_plus_lncRNA::1::8003	133319, -1513	in gene, upstream	0	1	16.5	21	2	2_A375_pNL97_plus_lncRNA::1	24	Gene GABBR2	GPR51, HRIHFB2099, FLJ36928, GPRC3B, GABABR2, HG20, GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	NM_005458, hCT2273704.0, hCT2273707.0, hCT2273709.0	209990_s_at, 209991_x_at, 211679_x_at, 217077_s_at	NP_005449.5, EAW58889.1, EAW58890.1, EAW58891.1
GeneID:85365	ALG2	9	101,978,707	101,984,246	5,539	-	2	1_A375_pNL7_minus_lncRNA::1::5559, 2_A375_pNL97_plus_lncRNA::1::8004	193, -74	in gene, upstream	1	1	18	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene ALG2	NET38, FLJ14511, ALG2, hALPG2, CDGIi	asparagine-linked glycosylation 2, alpha-1,3-mannosyltransferase homolog (S. cerevisiae)	NM_033087, NR_024532, hCT21325.2, hCT2282517.0, hCT2282522.0, hCT2353370.0	225621_at, 226166_at	NP_149078.1, EAW58908.1, EAW58909.1, EAW58910.1, EAW58911.1
GeneID:10952	SEC61B	9	101,984,570	101,992,901	8,331	+	2	1_A375_pNL7_minus_lncRNA::1::5559, 2_A375_pNL97_plus_lncRNA::1::8004	-517, -250	upstream, upstream	1	1	18	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene SEC61B	SEC61B		NM_006808, hCT1961554.1	203133_at, 244700_at	NP_006799.1, EAW58912.1
GeneID:8013	NR4A3	9	102,584,137	102,629,173	45,036	+	4	1_A375_pNL7_minus_lncRNA::1::5561, 2_A375_pNL97_plus_lncRNA::1::8006, 2_A375_pNL97_plus_lncRNA::1::8007, 2_A375_pNL97_plus_lncRNA::1::8008	51943, -2313, -9, 51911	downstream, upstream, upstream, downstream	1	1	15.33	18.67	3	2_A375_pNL97_plus_lncRNA::1	19	Gene NR4A3	CHN, NOR1, NR4A3, TEC, MINOR, CSMF	nuclear receptor subfamily 4, group A, member 3	NM_006981, NM_173199, NM_173200, hCT19909.3, hCT2282270.0, hCT2282272.0, hCT1964997.1	207978_s_at, 209959_at, 216979_at	NP_008912.2, NP_775291.1, NP_775292.1, EAW58916.1, EAW58917.1, EAW58918.1, EAW58915.1
GeneID:55014	STX17	9	102,668,915	102,736,818	67,903	+	1	1_A375_pNL7_minus_lncRNA::1::5562	169	in gene	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene STX17	MGC126613, MGC126615, STX17, MGC102796, FLJ20651	syntaxin 17	NM_017919, hCT2282280.0	218666_s_at, 222708_s_at	NP_060389.2, EAW58920.1
GeneID:23071	ERP44	9	102,741,461	102,861,330	119,869	-	2	1_A375_pNL7_minus_lncRNA::1::5563, 2_A375_pNL97_plus_lncRNA::1::8009	-30, -110	upstream, upstream	1	1	25	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene ERP44	ERP44, PDIA10, KIAA0573, TXNDC4	endoplasmic reticulum protein 44	NM_015051, hCT2353379.0, hCT1776381.2	208957_at, 208958_at, 208959_s_at	NP_055866.1, EAW58923.1, EAW58922.1
GeneID:27130	INVS	9	102,861,511	103,063,426	201,915	+	2	1_A375_pNL7_minus_lncRNA::1::5563, 2_A375_pNL97_plus_lncRNA::1::8009	-151, -71	upstream, upstream	1	1	25	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene INVS	NPH2, INV, INVS, KIAA0573, MGC133081, MGC133080, NPHP2	inversin	NM_183245, NM_014425, hCT19906.3, hCT2282283.0, hCT2282287.0	210114_at, 211054_at, 211055_s_at	NP_899068.1, NP_055240.2, EAW58924.1, EAW58925.1, EAW58926.1
GeneID:54881	TEX10	9	103,064,357	103,115,259	50,902	-	1	2_A375_pNL97_plus_lncRNA::1::8010	155	in gene	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TEX10	bA208F1.2, FLJ31157, TEX10, FLJ20287, FLJ34350	testis expressed 10	NM_017746, NM_001161584, hCT19905.3, hCT2282483.0, hCT1961146.0	1558702_at, 218104_at	NP_060216.2, NP_001155056.1, EAW58927.1, EAW58928.1, EAW58929.1
GeneID:100507449	LOC100507449	9	103,115,318	103,116,360	1,042	+	1	2_A375_pNL97_plus_lncRNA::1::8010	-214	upstream	0	1	14	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100507449		hypothetical LOC100507449	XR_113246, XR_108986, XR_114282		
GeneID:91283	C9orf30	9	103,189,642	103,213,513	23,871	+	1	2_A375_pNL97_plus_lncRNA::1::8011	2150	in gene	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene C9orf30	L8, FLJ34973, C9orf30, MGC17337	chromosome 9 open reading frame 30	NM_080655, hCT19907.3, hCT2273692.0, hCT1640986.1	1552277_a_at	NP_542386.1, EAW58933.1, EAW58932.1, EAW58934.1
GeneID:54534	MRPL50	9	104,152,249	104,160,919	8,670	-	1	2_A375_pNL97_plus_lncRNA::1::8012	119	in gene	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene MRPL50	MRPL50, FLJ20493, MRP-L50, FLJ21990	mitochondrial ribosomal protein L50	NM_019051, hCT1776756.2	225580_at, 225581_s_at	NP_061924.1, EAW58948.1
GeneID:7743	ZNF189	9	104,161,163	104,172,942	11,779	+	1	2_A375_pNL97_plus_lncRNA::1::8012	-363	upstream	0	1	12	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene ZNF189	ZNF189	zinc finger protein 189	NM_197977, NM_003452, hCT20169.3, hCT2273725.0	207513_s_at	NP_932094.1, NP_003443.2, EAW58949.1, EAW58950.1
GeneID:100507465	LOC100507465	9	104,231,661	104,243,788	12,127	+	1	2_A375_pNL97_plus_lncRNA::1::8013	17187	downstream	0	1	19	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene LOC100507465		hypothetical LOC100507465	XR_108987		
GeneID:84302	C9orf125	9	104,237,608	104,249,475	11,867	-	1	2_A375_pNL97_plus_lncRNA::1::8013	627	in gene	0	1	19	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene C9orf125	MGC12992, C9orf125	chromosome 9 open reading frame 125	NM_032342, hCT1967489.1, hCT1640795.3	224458_at	NP_115718.1, EAW58954.1, EAW58953.1
GeneID:56254	RNF20	9	104,296,133	104,325,626	29,493	+	1	2_A375_pNL97_plus_lncRNA::1::8014	3195	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene RNF20	KIAA2779, BRE1A, hBRE1, MGC129667, FLJ11189, MGC129668, RNF20, BRE1, FLJ20382	ring finger protein 20	NM_019592, hCT20172.2, hCT2273420.0, hCT1960319.1	222683_at	NP_062538.5, EAW58957.1, EAW58955.1, EAW58956.1
GeneID:116443	GRIN3A	9	104,331,634	104,500,862	169,228	-	4	1_A375_pNL7_minus_lncRNA::1::5564, 1_A375_pNL7_minus_lncRNA::1::5565, 2_A375_pNL97_plus_lncRNA::1::8015, 2_A375_pNL97_plus_lncRNA::1::8016	110254, 1676, 110266, 1662	in gene, in gene, in gene, in gene	1	1	17	23	2	2_A375_pNL97_plus_lncRNA::1	29	Gene GRIN3A	NR3A, NMDAR-L, GRIN3A, FLJ45414	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	NM_133445, hCT20173.3, hCT2274175.0, hCT2353385.0	233171_at, 233220_at	NP_597702.2, EAW58958.1, EAW58959.1, EAW58960.1
GeneID:10592	SMC2	9	106,856,541	106,903,700	47,159	+	2	1_A375_pNL7_minus_lncRNA::1::5567, 2_A375_pNL97_plus_lncRNA::1::8019	-77, -173	upstream, upstream	1	1	15	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SMC2	hCAP-E, FLJ10093, SMC2L1, CAPE, SMC2, CAP-E	structural maintenance of chromosomes 2	NM_006444, NM_001042550, NM_001042551, hCT2273849.0, hCT2273850.0, hCT2353371.0, hCT18786.2, hCT1964988.1	204240_s_at, 213253_at	NP_006435.2, NP_001036015.1, NP_001036016.1, EAW58975.1, EAW58976.1, EAW58977.1, EAW58973.1, EAW58974.1
GeneID:25934	NIPSNAP3A	9	107,509,969	107,522,403	12,434	+	1	2_A375_pNL97_plus_lncRNA::1::8021	-193	upstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene NIPSNAP3A	MGC14553, DKFZp564D177, TASSC, HSPC299, FLJ13953, NIPSNAP3A, NIPSNAP4	nipsnap homolog 3A (C. elegans)	NM_015469, hCT1814660.1	224436_s_at	NP_056284.1, EAW58990.1
GeneID:23446	SLC44A1	9	108,006,929	108,153,682	146,753	+	2	1_A375_pNL7_minus_lncRNA::1::5569, 2_A375_pNL97_plus_lncRNA::1::8023	-252, -273	upstream, upstream	1	1	14	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SLC44A1	CTL1, CD92, SLC44A1, CDW92, RP11-287A8.1, CHTL1	solute carrier family 44, member 1	NM_080546, hCT20211.4, hCT2274232.0, hCT2274233.0, hCT2274234.0, hCT1809244.1	224595_at, 224596_at, 228485_s_at, 228486_at	NP_536856.2, EAW58998.1, EAW58995.1, EAW58996.1, EAW58997.1, EAW58999.1
GeneID:83856	FSD1L	9	108,210,315	108,311,385	101,070	+	2	1_A375_pNL7_minus_lncRNA::1::5570, 2_A375_pNL97_plus_lncRNA::1::8024	-235, -224	upstream, upstream	1	1	17	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene FSD1L	MGC45564, FSD1NL, FSD1CL, FSD1L, CCDC10, CSDUFD1, MIR1	fibronectin type III and SPRY domain containing 1-like	NM_207647, NM_031919, NM_001145313, hCT1776426.2	223985_at, 230904_at, 242586_at, 242607_at	NP_997530.2, NP_114125.1, NP_001138785.1, EAW59000.1
GeneID:5887	RAD23B	9	110,045,544	110,094,470	48,926	+	2	2_A375_pNL97_plus_lncRNA::1::8027, 2_A375_pNL97_plus_lncRNA::1::8028	24, 664	in gene, in gene	0	1	12.5	21	2	2_A375_pNL97_plus_lncRNA::1	23	Gene RAD23B	HR23B, P58, HHR23B, RAD23B	RAD23 homolog B (S. cerevisiae)	NM_002874, hCT2353391.0, hCT5699.2	201222_s_at, 201223_s_at, 223598_at	NP_002865.1, EAW59016.1, EAW59017.1
GeneID:9314	KLF4	9	110,247,133	110,252,047	4,914	-	1	1_A375_pNL7_minus_lncRNA::1::5573	911	in gene	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene KLF4	KLF4, GKLF, EZF	Kruppel-like factor 4 (gut)	NM_004235, hCT2274551.0, hCT2274553.0, hCT1776150.2	220266_s_at, 221841_s_at	NP_004226.3, EAW59019.1, EAW59020.1, EAW59021.1
GeneID:8518	IKBKAP	9	111,629,800	111,696,608	66,808	-	3	1_A375_pNL7_minus_lncRNA::1::5576, 2_A375_pNL97_plus_lncRNA::1::8036, 2_A375_pNL97_plus_lncRNA::1::8037	48352, 48352, 240	in gene, in gene, in gene	1	1	18	22	2	2_A375_pNL97_plus_lncRNA::1	26	Gene IKBKAP	FD, IKI3, IKAP, TOT1, IKBKAP, DKFZp781H1425, ELP1, FLJ12497, DYS	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	NM_003640, hCT20054.3, hCT2276660.0, hCT2276664.0, hCT1958819.1, hCT1958820.1	202490_at, 202491_s_at	NP_003631.2, EAW59029.1, EAW59027.1, EAW59028.1, EAW59030.1, EAW59031.1
GeneID:54942	C9orf6	9	111,696,673	111,703,238	6,565	+	1	2_A375_pNL97_plus_lncRNA::1::8037	-305	upstream	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene C9orf6	FLJ20457, CG-8, C9orf6	chromosome 9 open reading frame 6	NM_017832, hCT20057.3, hCT2353372.0, hCT1965001.1	218998_at	NP_060302.1, EAW59033.1, EAW59032.1, EAW59034.1
GeneID:8727	CTNNAL1	9	111,704,851	111,775,764	70,913	-	1	2_A375_pNL97_plus_lncRNA::1::8037	79396	downstream	0	1	17	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CTNNAL1	CLLP, FLJ08121, CTNNAL1, alpha-CATU	catenin (cadherin-associated protein), alpha-like 1	NM_003798, hCT20055.2, hCT2276655.0, hCT2353392.0	202468_s_at	NP_003789.1, EAW59036.1, EAW59035.1, EAW59037.1
GeneID:23731	C9orf5	9	111,777,415	111,882,225	104,810	-	1	2_A375_pNL97_plus_lncRNA::1::8038	-63	upstream	0	1	12	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene C9orf5	FLJ23668, CG-2, FLJ33224, C9orf5, CG2	chromosome 9 open reading frame 5	NM_032012, hCT2276650.1, hCT2276653.1	223005_s_at, 223006_s_at, 223007_s_at, 223008_s_at, 227631_at	NP_114401.2, EAW59039.1, EAW59038.1
GeneID:54566	EPB41L4B	9	111,934,254	112,083,021	148,767	-	1	2_A375_pNL97_plus_lncRNA::1::8039	75933	in gene	0	1	8	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene EPB41L4B	FLJ21596, EPB41L4B, DKFZp761N1814, CG1	erythrocyte membrane protein band 4.1 like 4B	NM_019114, NM_018424, hCT2276639.0, hCT2276641.0, hCT1776398.1, hCT1776399.2	220161_s_at, 220524_at, 223426_s_at, 223427_s_at, 223659_at, 233098_s_at	NP_061987.3, NP_060894.2, EAW59041.1, EAW59042.1, EAW59043.1, EAW59044.1
GeneID:5774	PTPN3	9	112,137,974	112,260,593	122,619	-	4	1_A375_pNL7_minus_lncRNA::1::5579, 1_A375_pNL7_minus_lncRNA::1::5580, 2_A375_pNL97_plus_lncRNA::1::8040, 2_A375_pNL97_plus_lncRNA::1::8041	50641, 28129, 50577, 28033	in gene, in gene, in gene, in gene	1	1	19	18.5	2	2_A375_pNL97_plus_lncRNA::1	21	Gene PTPN3	PTPN3, DKFZp686N0569, PTPH1	protein tyrosine phosphatase, non-receptor type 3	NM_002829, NM_001145368, NM_001145369, NM_001145370, NM_001145371, NM_001145372, NR_026918, hCT2276634.0, hCT18732.3, hCT1958113.1	203997_at, 227944_at	NP_002820.3, NP_001138840.1, NP_001138841.1, NP_001138842.1, NP_001138843.1, NP_001138844.1, EAW59045.1, EAW59046.1, EAW59047.1
GeneID:114299	PALM2	9	112,403,068	112,713,756	310,688	+	3	1_A375_pNL7_minus_lncRNA::1::5581, 1_A375_pNL7_minus_lncRNA::1::5582, 2_A375_pNL97_plus_lncRNA::1::8042	125668, 175924, 125668	in gene, in gene, in gene	1	1	24.5	22.5	2	1_A375_pNL7_minus_lncRNA::1	27	Gene PALM2	AKAP2, PALM2	paralemmin 2	NM_001037293, NM_053016	1553502_a_at	NP_001032370.1, NP_443749.5
GeneID:445815	PALM2-AKAP2	9	112,542,577	112,934,792	392,215	+	1	1_A375_pNL7_minus_lncRNA::1::5582	36415	in gene	1	0	22	21	1	1_A375_pNL7_minus_lncRNA::1	22	Gene PALM2-AKAP2	AKAP2, PALM2-AKAP2, DKFZp686H1946	PALM2-AKAP2 readthrough	NM_147150, NM_007203		NP_671492.1, NP_009134.1
GeneID:7295	TXN	9	113,006,310	113,018,778	12,468	-	2	1_A375_pNL7_minus_lncRNA::1::5583, 2_A375_pNL97_plus_lncRNA::1::8043	266, 186	in gene, in gene	1	1	20	17	1	1_A375_pNL7_minus_lncRNA::1	20	Gene TXN	DKFZp686B1993, TRX, TRX1, MGC61975, TXN	thioredoxin	NM_003329, hCT19918.2, hCT1961561.1	208864_s_at, 216609_at	NP_003320.2, EAW59060.1, EAW59059.1
GeneID:79987	SVEP1	9	113,127,528	113,342,160	214,632	-	2	1_A375_pNL7_minus_lncRNA::1::5584, 2_A375_pNL97_plus_lncRNA::1::8044	688, 720	in gene, in gene	1	1	20	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene SVEP1	FLJ90719, SELOB, CCP22, FLJ16013, C9orf13, POLYDOM, SVEP1, SEL-OB	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	NM_153366	1553129_at, 1566721_at, 1566722_a_at, 213247_at, 219552_at, 224543_at	NP_699197.3
GeneID:4593	MUSK	9	113,431,051	113,563,278	132,227	+	1	1_A375_pNL7_minus_lncRNA::1::5585	76373	in gene	1	0	18	9	1	1_A375_pNL7_minus_lncRNA::1	18	Gene MUSK	MGC126324, MGC126323, MUSK	muscle, skeletal, receptor tyrosine kinase	NM_005592, NM_001166280, NM_001166281, hCT19913.3, hCT2274214.0, hCT2274215.0	207632_at, 207633_s_at, 241122_s_at	NP_005583.1, NP_001159752.1, NP_001159753.1, EAW59065.1, EAW59066.1, EAW59067.1
GeneID:548645	DNAJC25	9	114,393,632	114,416,631	22,999	+	2	1_A375_pNL7_minus_lncRNA::1::5586, 2_A375_pNL97_plus_lncRNA::1::8045	-96, -64	upstream, upstream	1	1	32	17	1	1_A375_pNL7_minus_lncRNA::1	32	Gene DNAJC25	bA16L21.2.1, DNAJC25	DnaJ (Hsp40) homolog, subfamily C , member 25	NM_001015882	226859_at	NP_001015882.2
GeneID:552891	DNAJC25-GNG10	9	114,393,666	114,432,509	38,843	+	2	1_A375_pNL7_minus_lncRNA::1::5586, 2_A375_pNL97_plus_lncRNA::1::8045	-130, -98	upstream, upstream	1	1	32	17	1	1_A375_pNL7_minus_lncRNA::1	32	Gene DNAJC25-GNG10	DNAJC25-GNG10		NM_004125		NP_004116.2
GeneID:158401	C9orf84	9	114,448,901	114,545,779	96,878	-	1	2_A375_pNL97_plus_lncRNA::1::8046	40067	in gene	0	1	13	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene C9orf84	FLJ44067, MGC43661, FLJ32779, C9orf84	chromosome 9 open reading frame 84	NM_173521, NM_001080551, hCT2277068.1, hCT2277069.1, hCT1648384.4	1553920_at, 233504_at	NP_775792.3, NP_001074020.1, EAW59088.1, EAW59089.1, EAW59090.1
GeneID:7357	UGCG	9	114,659,206	114,695,439	36,233	+	1	1_A375_pNL7_minus_lncRNA::1::5587	-374	upstream	1	0	18	13	1	1_A375_pNL7_minus_lncRNA::1	18	Gene UGCG	UGCG, GLCT1, GCS	UDP-glucose ceramide glucosyltransferase	NM_003358, hCT18741.2, hCT1961553.1	204881_s_at, 221765_at, 224967_at	NP_003349.1, EAW59091.1, EAW59092.1
GeneID:84263	HSDL2	9	115,142,351	115,234,684	92,333	+	1	2_A375_pNL97_plus_lncRNA::1::8047	-239	upstream	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene HSDL2	FLJ25855, C9orf99, SDR13C1, MGC10940, HSDL2	hydroxysteroid dehydrogenase like 2	NM_032303, hCT19938.3, hCT2274348.0, hCT2353380.0, hCT1965000.1	1559128_at, 209512_at, 209513_s_at, 215436_at	NP_115679.2, EAW59106.1, EAW59104.1, EAW59105.1, EAW59107.1
GeneID:58493	C9orf80	9	115,448,786	115,480,387	31,601	-	1	2_A375_pNL97_plus_lncRNA::1::8048	99	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C9orf80	SSBIP1, MISE, HSPC043, C9orf80, SOSSC, hSSBIP1	chromosome 9 open reading frame 80	NM_021218, hCT1776779.3	1560558_at, 223558_at, 223559_s_at	NP_067041.1, EAW59113.1
GeneID:401548	SNX30	9	115,513,134	115,637,267	124,133	+	1	1_A375_pNL7_minus_lncRNA::1::5588	-334	upstream	1	0	16	15	1	1_A375_pNL7_minus_lncRNA::1	16	Gene SNX30	FLJ35589, FLJ45069, FLJ34280, ATG24A, FLJ44686, FLJ46577, FLJ26481, SNX30	sorting nexin family member 30	NM_001012994	226249_at	NP_001013012.1
GeneID:23307	FKBP15	9	115,927,800	115,983,641	55,841	-	1	2_A375_pNL97_plus_lncRNA::1::8050	57	in gene	0	1	11	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene FKBP15	FKBP133, KIAA0674, FKBP15	FK506 binding protein 15, 133kDa	NM_015258	1568717_a_at, 212663_at, 242574_at, 31826_at, 76897_s_at	NP_056073.1
GeneID:1317	SLC31A1	9	115,983,808	116,026,772	42,964	+	1	2_A375_pNL97_plus_lncRNA::1::8050	-224	upstream	0	1	11	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SLC31A1	COPT1, SLC31A1, MGC75487, hCTR1, CTR1	solute carrier family 31 (copper transporters), member 1	NM_001859, hCT2316510.0, hCT2316513.0, hCT1951158.1	203971_at, 235013_at, 236217_at	NP_001850.1, EAW87359.1, EAW87357.1, EAW87358.1
GeneID:246184	CDC26	9	116,029,288	116,037,869	8,581	-	1	2_A375_pNL97_plus_lncRNA::1::8051	77	in gene	0	1	23	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene CDC26	CDC26, ANAPC12, C9orf17, APC12	cell division cycle 26 homolog (S. cerevisiae)	NM_139286, hCT1823796.1, hCT1951159.1	225422_at	NP_644815.1, EAW87360.1, EAW87361.1
GeneID:9128	PRPF4	9	116,037,974	116,055,056	17,082	+	1	2_A375_pNL97_plus_lncRNA::1::8051	-182	upstream	0	1	23	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene PRPF4	PRP4, PRPF4, HPRP4P, HPRP4, Prp4p	PRP4 pre-mRNA processing factor 4 homolog (yeast)	NM_004697, hCT20353.2, hCT1951172.1	209161_at, 209162_s_at	NP_004688.2, EAW87362.1, EAW87363.1
GeneID:114987	WDR31	9	116,077,930	116,102,620	24,690	-	1	2_A375_pNL97_plus_lncRNA::1::8052	-68	upstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene WDR31	FLJ35921, WDR31	WD repeat domain 31	NM_001012361, NM_145241, hCT20352.3, hCT2316821.0, hCT2356971.0, hCT2356972.0, hCT2356973.0, hCT1951171.1	229516_at, 241919_x_at	NP_001012361.1, NP_660284.1, EAW87368.1, EAW87370.1, EAW87371.1, EAW87373.1, EAW87369.1, EAW87372.1
GeneID:54836	BSPRY	9	116,111,812	116,133,513	21,701	+	1	2_A375_pNL97_plus_lncRNA::1::8052	-9124	upstream	0	1	16	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene BSPRY	BSPRY, FLJ20150	B-box and SPRY domain containing	NM_017688, hCT20346.3	218792_s_at, 222746_s_at	NP_060158.2, EAW87374.1
GeneID:210	ALAD	9	116,148,592	116,163,618	15,026	-	2	1_A375_pNL7_minus_lncRNA::1::5590, 2_A375_pNL97_plus_lncRNA::1::8053	-9246, -9262	upstream, upstream	1	1	29	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene ALAD	PBGS, ALADH, ALAD, MGC5057	aminolevulinate, delta-, dehydratase	NM_000031, hCT20345.3, hCT2316853.0	218487_at, 218489_s_at	NP_000022.3, EAW87379.1, EAW87380.1
GeneID:54107	POLE3	9	116,169,515	116,173,029	3,514	-	2	1_A375_pNL7_minus_lncRNA::1::5590, 2_A375_pNL97_plus_lncRNA::1::8053	165, 149	in gene, in gene	1	1	29	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene POLE3	POLE3, CHRAC17, p17, CHARAC17, YBL1	polymerase (DNA directed), epsilon 3 (p17 subunit)	NM_017443, NR_027261, hCT20349.3, hCT2316849.0	208828_at	NP_059139.3, EAW87381.1, EAW87382.1
GeneID:257169	C9orf43	9	116,173,022	116,191,882	18,860	+	2	1_A375_pNL7_minus_lncRNA::1::5590, 2_A375_pNL97_plus_lncRNA::1::8053	-158, -142	upstream, upstream	1	1	29	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene C9orf43	MGC17358, C9orf43	chromosome 9 open reading frame 43	NM_152786, hCT2316520.0, hCT2348620.0, hCT2348621.0, hCT2356967.0	1554280_a_at	NP_689999.1, EAW87385.1, EAW87383.1, EAW87384.1, EAW87386.1
GeneID:85301	COL27A1	9	116,918,231	117,072,975	154,744	+	2	1_A375_pNL7_minus_lncRNA::1::5591, 2_A375_pNL97_plus_lncRNA::1::8055	68105, 21817	in gene, in gene	1	1	15	11	2	1_A375_pNL7_minus_lncRNA::1	17	Gene COL27A1	MGC11337, COL27A1, KIAA1870, FLJ11895	collagen, type XXVII, alpha 1	NM_032888, hCT2316330.1, hCT2316331.1, hCT2316333.1, hCT2356946.0	1564008_at, 225292_at, 225293_at, 230603_at, 237452_at	NP_116277.2, EAW87411.1, EAW87412.1, EAW87413.1, EAW87414.1
GeneID:100505521	LOC100505521	9	117,659,547	117,664,893	5,346	+	1	2_A375_pNL97_plus_lncRNA::1::8056	-3259	upstream	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene LOC100505521		hypothetical LOC100505521	XR_113241, XR_108993, XR_114289		
GeneID:944	TNFSF8	9	117,665,124	117,692,770	27,646	-	1	2_A375_pNL97_plus_lncRNA::1::8056	36482	downstream	0	1	11	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene TNFSF8	CD153, CD30LG, MGC138144, TNFSF8, CD30L	tumor necrosis factor (ligand) superfamily, member 8	NM_001244, hCT21020.3, hCT2316413.0	207216_at	NP_001235.1, EAW87433.1, EAW87432.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Internal Transcripts Count	Internal Transcripts	Internal Pos.	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
GeneID:23371	TNC	9	117,782,855	117,880,466	97,611	-	3	1_A275_shL7_dhrus_lncRNA:1:-5983, 2_A275_shL67_dhrs_lncRNA:1:-5987, 2_A275_shL67_dhrs_lncRNA:1:-5994	5975, 6662, 36	up gene, ut gene, nt gene	1	1	30.5	34.5	2	2_A275_shL97_dhrs_lncRNA:1	61	Gene TNC	GMEM, MGC167028, CP, 150-225, JI, TNC, TN-C, HXB, TN	Tenascin C	NM_002160, XCT210182, 2, XCT1935170.1	201643_at, 216003_at	NP_002151.2, EAW67435.1, EAW67434.1
GeneID:50514	T-Dec	9	117,900,097	118,164,823	260,226	+	3	1_A275_shL7_dhrus_lncRNA:1:-5594, 2_A275_shL67_dhrs_lncRNA:1:-5599, 2_A275_shL67_dhrs_lncRNA:1:-5600	2317711, 120952, 2317711	up gene, ut gene, nt gene	1	1	15	19	2	2_A275_shL97_dhrs_lncRNA:1	19	Gene DEC1	DEC1, CTS9	deleted in encephalopathy cancer 1	NM_017414, XCT2316268.0, XCT1622465.1	220781_at	NP_059134.1, EAW67437.1, EAW67436.1
GeneID:23245	ASTN2	9	119,167,504	120,177,217	989,813	-	3	1_A275_shL7_dhrus_lncRNA:1:-5597, 2_A275_shL67_dhrs_lncRNA:1:-5592, 2_A275_shL67_dhrs_lncRNA:1:-5596	6687537, 716453, 680725	up gene, ut gene, nt gene	1	1	15	15.5	2	2_A275_shL97_dhrs_lncRNA:1	17	Gene ASTN2	ASTN2, BAETK191, KIAA0634	astrotactin 2	NM_001184734, NM_001184735, NM_014010, NM_198186, NM_198187, NM_198188, XCT2340938.0	1554016_at, 208692_at, 215407_s_at	NP_001171663.1, NP_001171664.1, NP_937611.1, NP_054726.2, NP_937629.2, NP_937630.3, EAW67444.1
GeneID:23264	TKIM22	9	119,449,561	119,463,979	13,988	+	1	2_A275_shL67_dhrs_lncRNA:1:-5595	11263	up gene	0	1	13	15	1	2_A275_shL97_dhrs_lncRNA:1	15	Gene TKIM22	HT2A, TKIM22, TKTIP, LGMD2H, BBS11	Bardet-Biedl syndrome 11	NM_001099679, NM_012110, XCT1553.2, XCT1801883.1	203546_s_at, 209233_at	NP_001093149.1, NP_036342.2, EAW67446.1, EAW67447.1
GeneID:7099	TLR4	9	120,466,460	120,479,765	13,306	+	1	1_A275_shL7_dhrus_lncRNA:1:-5599	-572	upstream	1	0	17	10	1	1_A275_shL7_dhrus_lnc RNA:1	17	Gene TLR4	TOLL, TLR4, CD284, ARMD10, TOLL	toll-like receptor 4	NM_024166, NM_024166, NM_138554	1552798_a_at, 224341_s_at, 242066_x_at	NP_612564.1
GeneID:6320	DBC1	9	121,928,995	122,131,709	202,831	-	1	2_A275_shL67_dhrs_lncRNA:1:-5596	-1461	upstream	0	1	9	14	1	2_A275_shL97_dhrs_lncRNA:1	14	Gene DBC1	DBC1/R1, FAMSA, DBC1	deleted in bladder cancer 1	NM_014618, XCT2316398.0, XCT1552.1	1555437_at	NP_055633.2, EAW67456.1, EAW67455.1
GeneID:5755	CDK5RAP2	9	123,151,147	123,342,037	191,290	-	2	1_A275_shL7_dhrus_lncRNA:1:-5602, 2_A275_shL67_dhrs_lncRNA:1:-5597	1766771, 176901	up gene, ut gene	1	1	44	49	1	2_A275_shL97_dhrs_lncRNA:1	49	Gene CDK5RAP2	DKFZp686O1070, Cep215, DKFZp686B1070, CDK5RAP2, MCPH3, KIAA1633, Ct6	CDK5 regulatory subunit associated protein 2	NM_018249, NM_001011649, XCT2316481.1, XCT2316502.1, XCT2356993.0, XCT2396984.0, XCT1559585.3, XCT1860607.2	203553_s_at, 213560_s_at, 221416_x_at, 243163_at	NP_060719.0, NP_001011649.1, EAW67458.1, EAW67459.1, EAW67460.1, EAW67461.1, EAW67457.1, EAW67462.1, EAW67463.1
GeneID:5711	PSMD5	9	123,576,331	123,605,206	28,875	-	2	1_A275_shL7_dhrus_lncRNA:1:-5603, 2_A275_shL67_dhrs_lncRNA:1:-5598	-202, -56	upstream, downstream	1	1	16	16	1	2_A275_shL97_dhrs_lncRNA:1	16	Gene PSMD5	KIAA0072, SSB, MGC23145, PSMD5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	NM_002807, XCT21506.2	203477_at, 213596_at	NP_002030.1, EAW67471.1
GeneID:53039	LOC25303	9	123,605,320	123,616,651	11,331	+	2	1_A275_shL7_dhrus_lncRNA:1:-5603, 2_A275_shL67_dhrs_lncRNA:1:-5596	66, -40	up gene, downstream	1	1	16	16	1	2_A275_shL97_dhrs_lncRNA:1	16	Gene LOC253039	DKFZp27C191	hypothetical LOC253039	NM_024455	1555092_s_at, 231626_at, 239656_at, 241268_at	NP_076949.2, EAW67455.1, EAW67457.1
GeneID:5147	PHF19	9	123,617,931	123,639,606	21,675	-	3	1_A275_shL7_dhrus_lncRNA:1:-5604, 2_A275_shL67_dhrs_lncRNA:1:-5599, 2_A275_shL67_dhrs_lncRNA:1:-5601	822, 1153, 554	up gene, ut gene, upstream	1	1	12.5	16.5	2	2_A275_shL97_dhrs_lncRNA:1	19	Gene PHF19	MGC139712, MGC133995, MTF2L1, PHF19, PCL3, MGC149712, MGC23829	PHD finger protein 19	NM_015651, NM_001008836, XCT21851.3, XCT2171010, XCT2171312.1, XCT2171313.1	228533_at, 237211_at, 237212_s_at	NP_056965.1, NP_001008836.1, EAW67478.1, EAW67476.1, EAW67477.1, EAW67478.1
GeneID:7185	TRAP1	9	123,664,671	123,691,451	26,780	-	4	1_A275_shL7_dhrus_lncRNA:1:-5605, 2_A275_shL67_dhrs_lncRNA:1:-5609, 2_A275_shL67_dhrs_lncRNA:1:-5571, 2_A275_shL67_dhrs_lncRNA:1:-5600	15193, 5547, 15193, 9627	up gene, ut gene, nt gene, ut gene	1	1	23	22.5	2	2_A275_shL97_dhrs_lncRNA:1	27	Gene TRAP1	EB96, MGC10352, TRAP1	TNF receptor-associated factor 1	NM_001190845, NM_001160947, NM_005656, XCT21503.3	208599_at, 228116_at	NP_001177574.1, NP_001177576.1, NP_005639.1, EAW67479.1
GeneID:7027	CS	9	123,714,613	123,812,554	97,941	-	1	2_A275_shL67_dhrs_lncRNA:1:-5573	89370	downstream	0	1	10	17	1	2_A275_shL97_dhrs_lncRNA:1	17	Gene CS	MGC142298, FLJ37622, CPAMD4, FLJ10816, CS	complement component 5	NM_007135, XCT21504.3	203503_at	NP_001726.2, EAW67460.1
GeneID:51552	RAB14	9	123,840,415	123,864,265	23,850	-	1	1_A275_shL7_dhrus_lncRNA:1:-5607	-19	upstream	1	0	24	16	1	1_A275_shL7_dhrus_lnc RNA:1	24	Gene RAB14	RAB14, RBP, RAB-14	RAB14, member RAS oncogene family	NM_016322, XCT21503.2, XCT1951751.1	209277_s_at, 209926_s_at, 211503_s_at	NP_057409.2, EAW67455.1, EAW67457.1
GeneID:934	QSN	9	124,030,390	124,093,120	62,730	+	2	1_A275_shL7_dhrus_lncRNA:1:-5610, 2_A275_shL67_dhrs_lncRNA:1:-5576	10676, 10604	up gene, ut gene	1	1	16	16.5	2	1_A275_shL7_dhrus_lnc RNA:1	16	Gene QSN	DKFZp313J0716, QSN	gelsolin (amyloidosis, Finnish type)	NM_198252, NM_000177, NM_001127662, NM_001127663, NM_001127665, NM_001127666, NM_001127667, XCT16894.4, XCT1951951.2, XCT1951952.1	200696_s_at, 214090_s_at	NP_937851.1, NP_000166.1, NP_001121134.1, NP_001121135.1, NP_001121136.1, NP_001121137.1, NP_001121138.1, NP_001121139.1, EAW67480.1, EAW67482.1, EAW67481.1
GeneID:128088	LOC1001128084	9	124,042,136	124,049,119	6,983	-	2	1_A275_shL7_dhrus_lncRNA:1:-5610, 2_A275_shL67_dhrs_lncRNA:1:-5578	6063, 4735	downstream, up gene	1	1	16	16.5	2	1_A275_shL7_dhrus_lnc RNA:1	16	Gene LOC100128084		hypothetical LOC100128084	XM_001714574, XM_001719711, XM_001728677		XP_001714626.1, XP_001719761.1, XP_001728620.1
GeneID:6340	STOM	9	124,101,253	124,132,845	31,192	-	2	1_A275_shL7_dhrus_lncRNA:1:-5611, 2_A275_shL67_dhrs_lncRNA:1:-5577	-1023, -1623	upstream, upstream	1	1	62	65	1	1_A275_shL7_dhrus_lnc RNA:1	63	Gene STOM	STOM, BND7, EPB7, EPB72	stomatin	NM_198194, NM_004099, XCT21501.2, XCT2117264.0	201060_s_at, 201061_s_at, 201062_at	NP_937677.1, NP_004090.4, EAW67493.1, EAW67494.1
GeneID:55125	TTLL11	9	124,554,204	124,653,665	271,681	+	4	1_A275_shL7_dhrus_lncRNA:1:-5612, 2_A275_shL67_dhrs_lncRNA:1:-5611, 2_A275_shL67_dhrs_lncRNA:1:-5578, 2_A275_shL67_dhrs_lncRNA:1:-5602	121999, 333, 121935, 317	up gene, ut gene, up gene, ut gene	1	1	22.5	19	2	1_A275_shL7_dhrus_lnc RNA:1	25	Gene TTLL11	TTLL11, bA240H19.1, C9orf20	tubulin tyrosine ligase-like family, member 11	NM_198252, NM_001139482, XCT2316268.2, XCT2165059.0, XCT2165160.0, XCT2356979.0, XCT1649041.3	231197_at	NP_938232.2, NP_001132914.1, EAW67509.1, EAW67507.1, EAW67508.1, EAW67509.1, EAW67505.1
GeneID:7772	ZBTB6	9	125,070,335	125,073,609	3,274	-	2	1_A275_shL7_dhrus_lncRNA:1:-5616, 2_A275_shL67_dhrs_lncRNA:1:-5592	7697, 3799	downstream, downstream	1	1	17	17	1	2_A275_shL97_dhrs_lncRNA:1	17	Gene ZBTB6	ZNF652, ZID, ZBTB6	zinc finger and BTB domain containing 6	NM_006626, XCT22213.3	209368_at	NP_006617.1, EAW67552.1
GeneID:7654	ZBTB26	9	125,680,376	125,693,779	13,401	-	2	1_A275_shL7_dhrus_lncRNA:1:-5617, 2_A275_shL67_dhrs_lncRNA:1:-5593	-205, -172	upstream, downstream	1	1	19	25	1	2_A275_shL97_dhrs_lncRNA:1	25	Gene ZBTB26	KIAA1972, bcke1, ZNF481, ZBTB26	zinc finger and BTB domain containing 26	NM_020824	1554973_s_at, 221162_at	NP_065875.1
GeneID:3637	RABGAP1	9	125,703,268	125,807,147	163,839	+	2	1_A275_shL7_dhrus_lncRNA:1:-5617, 2_A275_shL67_dhrs_lncRNA:1:-5593	4304, 8336	downstream, downstream	1	1	19	25	1	2_A275_shL97_dhrs_lncRNA:1	25	Gene RABGAP1	RP11-123N2.2, GAPCENA, RABGAP1, TBC1D11, DKFZp686D2123	RAB GTPase activating protein 1	NM_012197, XCT2316730.1, XCT2376732.1, XCT2376733.1, XCT2376734.0	204029_s_at, 213213_at, 213570_s_at	NP_036329.2, EAW67556.1, EAW67554.1, EAW67555.1, EAW67557.1
GeneID:7706	DENND1A	9	126,141,933	126,692,817	550,884	-	2	1_A275_shL7_dhrus_lncRNA:1:-5618, 2_A275_shL67_dhrs_lncRNA:1:-5594	1621, 1853	downstream, up gene	1	1	19	17	1	2_A275_shL97_dhrs_lncRNA:1	19	Gene DENND1A	DENND1A, FLJ35464, RP11-230L22.2, KIAA1605, FAM31A	DENN/MADD domain containing 1A	NM_020946, NM_024630, XCT2370466.2, XCT2370467.2, XCT2370468.0, XCT2370564.0, XCT2370565.0, XCT1912.4, XCT1912.5	219763_at, 226589_at	NP_065977.2, NP_079092.2, EAW67569.1, EAW67570.1, EAW67572.1, EAW67573.1, EAW67571.1, EAW67574.1, EAW67575.1
GeneID:693	PSMB7	9	127,115,744	127,177,721	61,977	-	3	1_A275_shL7_dhrus_lncRNA:1:-5620, 2_A275_shL67_dhrs_lncRNA:1:-5621, 2_A275_shL67_dhrs_lncRNA:1:-5599	22392, 135, -135	up gene, upstream, upstream	1	1	20	14	2	1_A275_shL7_dhrus_lnc RNA:1	21	Gene PSMB7	PSMB7, Z	proteasome (prosome, macropain) subunit, beta type, 7	NM_002799, XCT2035413, XCT1909901.1	200795_at, 246601_at	NP_002790.1, EAW67552.1, EAW67553.1
GeneID:4893	NRAS1	9	127,264,703	127,333,976	248,873	-	2	1_A275_shL7_dhrus_lncRNA:1:-5622, 2_A275_shL67_dhrs_lncRNA:1:-5600	-152, -152	upstream, upstream	1	1	48	38	1	1_A275_shL7_dhrus_lnc RNA:1	48	Gene NRAS1	NRAK1, GCNF, RTR, GCNP1, NRS1	nuclear receptor subfamily 6, group A, member 1	NM_033134, NM_001466, XCT2036803.0, XCT2170633.0, XCT1657666.1	207743_s_at, 210291_at, 210292_s_at	NP_031917.2, NP_001466.2, EAW67593.1, EAW67594.1
GeneID:6291	LOC100506607	9	127,322,902	127,333,206	2,304	+	2	1_A275_shL7_dhrus_lncRNA:1:-5622, 2_A275_shL67_dhrs_lncRNA:1:-5599	1326, 1326	up gene, ut gene	1	1	48	38	1	1_A275_shL7_dhrus_lnc RNA:1	48	Gene LOC100506607		hypothetical LOC100506607	XR_108996, XR_114282		
GeneID:69611	OLFML2A	9	127,329,437	127,377,161	37,724	+	2	1_A275_shL7_dhrus_lncRNA:1:-5622, 2_A275_shL67_dhrs_lncRNA:1:-5599	5709, 5709	upstream, upstream	1	1	48	38	1	1_A275_shL7_dhrus_lnc RNA:1	48	Gene OLFML2A	FRO34016, FLJ00237, OLFML2A	olfactomedin-like 2A	NM_182487, XCT2316951.1, XCT2199552.1	213079_at	NP_872242.2, EAW67596.1, EAW67597.1
GeneID:51551	WDR38	9	127,615,755	127,620,190	4,435	+	2	1_A275_shL7_dhrus_lncRNA:1:-5623, 2_A275_shL67_dhrs_lncRNA:1:-5600	5427, 5643	downstream, downstream	1	1	21	21	1	2_A275_shL97_dhrs_lncRNA:1	21	Gene WDR38	WDR38	WD repeat domain 38	NM_001045476	243800_at, 244109_at	NP_001038941.1
GeneID:1224	RPL38	9	127,620,158	127,624,240	4,082	-	2	1_A275_shL7_dhrus_lncRNA:1:-5623, 2_A275_shL67_dhrs_lncRNA:1:-5599	-68, -160	up gene, upstream	1	1	21	21	1	2_A275_shL97_dhrs_lncRNA:1	21	Gene RPL38	RPL38, L38	ribosomal protein L38	NM_007209, XCT2317857.1, XCT2317858.1, XCT2317859.1	200002_at	NP_001140.1, EAW67602.1, EAW67600.1, EAW67601.1
GeneID:1573	ARPC5L	9	127,631,464	127,639,696	8,232	+	2	1_A275_shL7_dhrus_lncRNA:1:-5623, 2_A275_shL67_dhrs_lncRNA:1:-5601	-7282, -7054	upstream, upstream	1	1	21	21	1	2_A275_shL97_dhrs_lncRNA:1	21	Gene ARPC5L	ARPC5L, ARC16-2, MGC3038	actin related protein 2/3 complex, subunit 5-like	NM_030978, XCT2035845, XCT2195855.1	203966_s_at, 223101_s_at, 226514_at, 226515_at, 226516_s_at	NP_112240.1, EAW67603.1, EAW67602.1
GeneID:930	GOLGA1	9	127,640,573	127,703,586	62,813	-	2	1_A275_shL7_dhrus_lncRNA:1:-5624, 2_A275_shL67_dhrs_lncRNA:1:-5600	-38, 90	upstream, up gene	1	1	19	17	1	1_A275_shL7_dhrus_lnc RNA:1	19	Gene GOLGA1	GOLGA1, golgin-97, MGC13154	golgi autoantigen, golgin subfamily a, 1	NM_002077, XCT2317858.1, XCT16526.3	200366_s_at, 200367_s_at, 200368_s_at	NP_002068.1, EAW67606.1, EAW67605.1
GeneID:9235	SCAI	9	127,704,557	127,905,535	200,978	-	2	1_A275_shL7_dhrus_lncRNA:1:-5624, 2_A275_shL67_dhrs_lncRNA:1:-5600	202414, 202342	downstream, downstream	1	1	18	17	1	1_A275_shL7_dhrus_lnc RNA:1	19	Gene SCAI	MGC120325, MET40, C9orf126, SCAI, FLJ38664, FLJ11756, MGC120325, MGC120326	suppressor of cancer cell invasion	NM_172600, NM_001146377, FLJ38664, XCT2316268.1, XCT2440840.0	241754_at	NP_776961.2, NP_001139349.1, EAW67608.1, EAW67609.1
GeneID:537	PPP6C	9	127,908,652	127,953,218	43,366	-	2	1_A275_shL7_dhrus_lncRNA:1:-5625, 2_A275_shL67_dhrs_lncRNA:1:-5602	-6, 56	upstream, up gene	1	1	21	20	1	1_A275_shL7_dhrus_lnc RNA:1	21	Gene PPP6C	PPP6C, MGC12286, FLJ36646, PP6	protein phosphatase 6, catalytic subunit	NM_002721, NM_001122355, NM_001122366, XCT2036242.3, XCT2396949.0, XCT 1659606.1, XCT1660424.1	203529_at, 208153_s_at, 208154_x_at	NP_002721.1, NP_001116827.1, NP_001116828.1, EAW67611.1, EAW67612.1, EAW67613.1
GeneID:6240	RABEPK	9	127,962,621	127,995,435	33,017	+	1	2_A275_shL67_dhrs_lncRNA:1:-5602	43571	downstream	0	1	16	21	1	2_A275_shL97_dhrs_lncRNA:1	21	Gene RABEPK	p40, RABEPK, DKFZp686P1077, RABAP40, bA530N3.1	Rab9 effector protein with kelch motifs	NM_001174152, NM_001174153, NM_030633, XCT2036324.3, XCT2396951.0, XCT2396952.0, XCT2396953.0, XCT1659609.1, XCT1660429.1	1555021_at, 203190_at	NP_001167622.1, NP_001167624.1, NP_001116826.1, EAW67616.1, EAW67617.1, EAW67619.1, EAW67615.1, EAW67618.1, EAW67620.1
GeneID:3098	HSPA8	3	127,997,127	128,003,661	6,534	-	2	1_A275_shL67_dhrs_lncRNA:1:-5603	269	up gene	0	1	16	21	1	2_A275_shL97_dhrs_lncRNA:1	21	Gene HSPA8	BIP, HSP72, HSPA8, GRP78, FLJ26106	heat shock 70 kDa protein 8 /glucose-regulated protein 78 kDa	NM_006597, XCT2036324.4, XCT1659573.1	201150_s_at, 208683_at	NP_006588.3, EAW67621.1, EAW67622.1
GeneID:6130	QKI7VDI	9	128,024,111	128,127,290	103,179	+	2	1_A275_shL7_dhrus_lncRNA:1:-5626, 2_A275_shL67_dhrs_lncRNA:1:-5604	149, 177	up gene, ut gene	1	1	16	20	1	2_A275_shL97_dhrs_lncRNA:1	20	Gene QKI7VDI	MGC135547, MGC135548, RAP6, KIAA1521, QAPVDI, DKFZp434C212, QAPEX3	GTPase activating protein and VPS9 domains 1	NM_015625, XCT20527.2, XCT2396948.0, XCT2396949.0, XCT2396950.0, XCT2396951.0, XCT1659610.1, XCT1660431.1	212602_s_at, 212604_s_at, 214669_x_at	NP_056440.2, EAW67624.1, EAW67626.1, EAW67627.1, EAW67628.1, EAW67622.1, EAW67625.1, EAW67626.1
GeneID:1145	LOC81145	9	128,506,656	128,508,625	2,198	-	1	2_A275_shL67_dhrs_lncRNA:1:-5606	441	up gene	0	1	12	14	1	2_A275_shL97_dhrs_lncRNA:1	14	Gene LOC81145		erythrocyte transmembrane protein	XR_108997, XR_114283	230752_at	
GeneID:390	PBX3	9	128,509,617	128,727,699	220,039	+	2	1_A275_shL7_dhrus_lncRNA:1:-5606, 2_A275_shL67_dhrs_lncRNA:1:-5606	1233, 165300	upstream, up gene	0	1	11.5	15.5	2	2_A275_shL97_dhrs_lncRNA:1	17	Gene PBX3	PBX3		NM_006195, NM_001134776, NM_001134777, NM_001134778, XCT20526.3, XCT2195777.0, XCT2195779.0, XCT2195781.1	204062_at	NP_006181.1, NP_001128250.1, EAW67638.1, EAW67636.1, EAW67637.1, EAW67638.1
GeneID:8653	PAM12SB	9	129,056,126	129,292,519	160,191	+	1	2_A275_shL67_dhrs_lncRNA:1:-5606	160424	downstream	0	1	12	16	1	2_A275_shL97_dhrs_lncRNA:1	16	Gene PAM12SB	PAM, FLJ00001, PAM12SB, C9orf25	Rimbp family sequence similarity 129, member B	NM_032449, NM_001011703, XCT2170052.0, XCT2170053.0	1554055_at, 221607_s_at, 221626_s_at	NP_115827.1, NP_001011703.1, EAW67639.1, EAW67640.1
GeneID:648	RALGPS1	9	129,877,053	129,955,448	356,362	+	3	1_A275_shL7_dhrus_lncRNA:1:-5100, 2_A275_shL67_dhrs_lncRNA:1:-5101, 2_A275_shL67_dhrs_lncRNA:1:-5107	154531, 205163, 205747	up gene, ut gene, downstream	0	1	12.33	16.33	2	2_A275_shL97_dhrs_lncRNA:1	25	Gene RALGPS1	RALGPS1A, RALGEP2, RASGEP2, KIAA0351, RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	NM_001197726, NM_001100728, NM_001100730, NM_014636, XCT16940.3, XCT1659645.1, XCT1659646.1, XCT1659646.2	1554749_at, 1555452_at, 1555453_at, 1555454_at, 204599_at	NP_001177655.1, NP_001177656.1, NP_055451.1, NP_001177659.1, EAW67645.1, EAW67646.1, EAW67647.1, EAW67648.1
GeneID:3452	ANGPTL2	9	128,648,626	128,655,044	33,416	-	1	2_A275_shL67_dhrs_lncRNA:1:-5101	-172	upstream	0	1	14	19	1	2_A275_shL97_dhrs_lncRNA:1	19	Gene ANGPTL2	ANGPTL2, HARP, MGC5689, ARP2	angiopoietin-like 2	NM_012098, XCT2317100.0, XCT2396921.0, XCT2396932.0, XCT1659612.1	213001_at, 213004_at, 213005_s_at	NP_036230.1, EAW67650.1, EAW67649.1, EAW67652.1
GeneID:632	ZNF79	9	130,166,653	130,207,651	20,998	+	1	2_A275_shL67_dhrs_lncRNA:1:-5102	165	up gene	0	1	11	21	1	2_A275_shL97_dhrs_lncRNA:1	21	Gene ZNF79	pT7, ZNF79	zinc finger protein 79	NM_007135, XCT2317741.1	214138_at, 216462_s_at, 216469_s_at	NP_008964.2, EAW67665.1
GeneID:4655	PAM12SB	9	130,297,616	130,341,266	73,650	-	2	1_A275_shL7_dhrus_lncRNA:1:-5104, 2_A275_shL67_dhrs_lncRNA:1:-5103	19764, 11540	up gene, upstream	0	1	11	11	2	2_A275_shL97_dhrs_lncRNA:1	20	Gene PAM12SB	C9orf66, FLJ22151, PLJ22295, PAM12SB	Rimbp family sequence similarity 129, member B	NM_022833, NM_001033834, XCT2197190.0, XCT2396936.0, XCT2396937.0, XCT9922.2	221019_at, 233074_s_at	NP_073744.2, NP_001029006.1, EAW67676.1, EAW67677.1, EAW67678.1
GeneID:9360	LOC100390603	9	130,316,656	130,316,841	2,093	-	1	2_A275_shL67_dhrs_lncRNA:1:-5104	-2563	upstream	0	1	10	20	1	2_A275_shL97_dhrs_lncRNA:1	20	Gene LOC100390603		hypothetical protein LOC100390603	XM_002119609		NP_002119697.1
GeneID:26207	C9orf117	9	130,369,271	130,476,203	7,022	+	1	1_A275_shL7_dhrus_lncRNA:1:-5629	6617	downstream	1	0	16	12	1	1_A275_shL7_dhrus_lnc RNA:1	16	Gene C9orf117	C9orf117	chromosome 9 open reading frame 117	NM_001123932, XCT2336808.0, XCT1657.1	1557899_at, 1557901_s_at, 241172_at	NP_001120520.2, EAW67682.1, EAW67683.1, EAW67684.1
GeneID:5524	PTRH1	9	130,476,227	130,477,636	1,709	-	1	1_A275_shL7_dhrus_lncRNA:1:-5624	-46	up gene	1	0	16	12	1	1_A275_shL7_dhrus_lnc RNA:1	16	Gene PTRH1	MGC31999, PTRH, C9orf115, PTRH1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	NM_001082913, XCT2396977.0, XCT9921.2	1555432_at, 225514_at	NP_001076382.1, EAW67685.1, EAW67686.1
GeneID:54245	TTC16	9	130,476,356	130,493,879	15,521	+	1	1_A275_shL7_dhrus_lncRNA:1:-5624	-170	upstream	1	0	16	12	1	1_A275_shL7_dhrus_lnc RNA:1	16	Gene TTC16	FLJ32150, TTC16	tetratricopeptide repeat domain 16	NM_148963, XCT2337092.0, XCT2396982.0, XCT1659620.1	1554643_at, 1554644_s_at	NP_683763.2, EAW67687.1, EAW67688.1, EAW67689.1
GeneID:9044	SH2D3C	9	130,500,596	130,541,048	40,452	-	2	1_A275_shL7_dhrus_lncRNA:1:-5630, 2_A275_shL67_dhrs_lncRNA:1:-5105	27015, 27126	up gene, ut gene	1	1	17	24	1	2_A275_shL97_dhrs_lncRNA:1	28	Gene SH2D3C	FLJ39664, CHAT, SH2D3C, PRO34858	SH2 domain containing 3C	NM_170600, NM_005489, NM_001142531, NM_001142532, NM_001142534, XCT1659631.1	1552987_at, 1553001_at, 210162_s_at, 210163_at, 210164_s_at	NP_733745.1, NP_005480.2, NP_001129693.1, EAW67722.1, EAW67724.1, EAW67725.1, EAW67723.1, EAW67726.1
GeneID:5293	PIP5KL1	9	130,663,805	130,693,076	9,296	-	1	2_A275_shL67_dhrs_lncRNA:1:-5107	4795	upstream	1	0	13	17	1	2_A275_shL97_dhrs_lncRNA:1	17	Gene PIP5KL1	PIP5KL1, PIPKH, bA203J24.5, MGC94624	phosphatidylinositol-4-phosphate 5-kinase-like 1	NM_183462, NM_001135219, XCT2396770.0, XCT2396771.0, XCT2396980.0, XCT2396981.0, XCT2396982.0, XCT2396983.0, XCT9926.2	1557613_at, 1557614_s_at	NP_001128691.1, EAW67727.1, EAW67728.1, EAW67727.1, EAW67723.1, EAW67728.1, EAW67726.1
GeneID:5032	DPM2	9	130,697,274	130,700,763	3,389	-	1	1_A275_shL7_dhrus_lncRNA:1:-5107	691	up gene	0	1	13	17	1	2_A275_shL97_dhrs_lncRNA:1	17	Gene DPM2	MGC111183, MGC21599, DPM2, FLJ90013	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit	NM_003863	200291_at	NP_003854.1
GeneID:99665	PAM16DA	9	130,702,891	130,743,812	39,981	+	1	2_A275_shL67_dhrs_lncRNA:1:-5107	42940	downstream	0	1	13	17	1	2_A275_shL97_dhrs_lncRNA:1	17	Gene PAM16DA	PAM16DA, bA203J24.7, EEG1, C9orf132, MGC30653	Rimbp family sequence similarity 16A, member A	NM_032305, NM_001032354, XCT2197417.0, XCT9923.3, XCT1659650.0	212400_at	NP_878080.1, NP_001030331.1, EAW67731.1, EAW67732.1, EAW67733.1
GeneID:53355	NAIF1	9	130,823,512	130,829,599	6,087	-	1	1_A275_shL7_dhrus_lncRNA:1:-5108	-47	upstream	1	0	13	16	1	1_A275_shL7_dhrus_lnc RNA:1	16	Gene NAIF1	DKFZp762G199, C9orf80, RP11-236D10.2, bA735C10.2, NAIF1	nuclear apoptosis inducing factor 1	NM_178596, XCT2317431.1, XCT2396933.0, XCT9219.2	1554664_at, 221525_at	NP_839481.1, EAW67736.1, EAW67733.1, EAW67737.1
GeneID:14709	SLC25A25	9	130,830,479	130,871,524	41,045	+	1	2_A275_shL7_dhrus_lncRNA:1:-5108	-783	upstream	1	0	13	16	1	1_A275_shL7_dhrus_lnc RNA:1	16	Gene SLC25A25	RP11-295F17.4, SCAMC-2, MGC103135, bA541B6, SLC25A25, MGC119317, MGC119318, MGC119319, MGC119320	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	NM_052901, NM_001005641, NM_001005642, NM_001005643, XCT6708.2, XCT1909547.1	1557655_at, 1557656_s_at, 1557657_s_at, 1557658_s_at	NP_443132.2, NP_001005641.1, NP_001005642.1, NP_001005643.1, EAW67737.1
GeneID:10228601	LOC100228601	9	130,873,450	130,881,013	7,563	-	2	1_A275_shL7_dhrus_lncRNA:1:-5621, 2_A275_shL67_dhrs_lncRNA:1:-5108	4035, 9035	upstream, upstream	1	1	32	33	1	1_A275_shL7_dhrus_lnc RNA:1	33	Gene LOC100228601	FLJ42733, DKFZp686O0137	hypothetical LOC100228601	NR_033374		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:80142	PTGES2	9	130,882,972	130,890,712	7,740	-	2	1_A375_pNL7_minus_lncRNA::1::5631, 2_A375_pNL97_plus_lncRNA::1::8109	664, 664	in gene, in gene	1	1	32	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene PTGES2	mPGES-2, FLJ14038, MGC11289, PGES2, PTGES2, C9orf15, GBF1	prostaglandin E synthase 2	NM_025072, NR_027811, NR_027812, hCT2319740.0, hCT2357047.0, hCT2357048.0, hCT2357049.0, hCT1824483.2, hCT1950565.1	218083_at	NP_079348.1, EAW87742.1, EAW87743.1, EAW87744.1, EAW87745.1, EAW87746.1, EAW87741.1
GeneID:389791	LOC389791	9	130,890,808	130,892,913	2,105	+	2	1_A375_pNL7_minus_lncRNA::1::5631, 2_A375_pNL97_plus_lncRNA::1::8109	-760, -760	upstream, upstream	1	1	32	33	1	2_A375_pNL97_plus_lncRNA::1	33	Gene LOC389791		hypothetical LOC389791	NR_024425, hCT2317803.0		EAW87747.1
GeneID:25792	CIZ1	9	130,928,344	130,966,662	38,318	-	4	1_A375_pNL7_minus_lncRNA::1::5632, 1_A375_pNL7_minus_lncRNA::1::5633, 2_A375_pNL97_plus_lncRNA::1::8110, 2_A375_pNL97_plus_lncRNA::1::8111	12742, 11206, 12710, 11366	in gene, in gene, in gene, in gene	1	1	38.5	42	2	2_A375_pNL97_plus_lncRNA::1	61	Gene CIZ1	NP94, LSFR1, CIZ1, ZNF356	CDKN1A interacting zinc finger protein 1	NM_012127, NM_001131015, NM_001131016, NM_001131017, NM_001131018, hCT2319728.1, hCT2319730.1, hCT2319732.1, hCT2319734.1, hCT2319735.1, hCT2319737.1, hCT2356962.0	205516_x_at, 211358_s_at, 213976_at, 213977_s_at	NP_036259.2, NP_001124487.1, NP_001124488.1, NP_001124489.1, NP_001124490.1, EAW87756.1, EAW87752.1, EAW87753.1, EAW87754.1, EAW87755.1, EAW87757.1, EAW87758.1
GeneID:1759	DNM1	9	130,965,663	131,017,527	51,864	+	1	1_A375_pNL7_minus_lncRNA::1::5633	-10207	upstream	1	0	18	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene DNM1	DNM1, DNM	dynamin 1	NM_001005336, NM_004408, hCT1827278.2, hCT1954875.1	215116_s_at	NP_001005336.1, NP_004399.2, EAW87759.1, EAW87760.1
GeneID:26995	TRUB2	9	131,071,396	131,084,697	13,301	-	4	1_A375_pNL7_minus_lncRNA::1::5634, 1_A375_pNL7_minus_lncRNA::1::5635, 2_A375_pNL97_plus_lncRNA::1::8112, 2_A375_pNL97_plus_lncRNA::1::8113	14505, -247, 14521, -263	downstream, upstream, downstream, upstream	1	1	25	25	2	2_A375_pNL97_plus_lncRNA::1	37	Gene TRUB2	CLONE24922, RP11-339B21.1, TRUB2	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	NM_015679, hCT2356968.0, hCT2356969.0, hCT9615.3, hCT1950582.1	223109_at	NP_056494.1, EAW87771.1, EAW87770.1, EAW87772.1, EAW87773.1
GeneID:51117	COQ4	9	131,084,791	131,096,351	11,560	+	2	1_A375_pNL7_minus_lncRNA::1::5635, 2_A375_pNL97_plus_lncRNA::1::8113	153, 169	in gene, in gene	1	1	32	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene COQ4	CGI-92, COQ4	coenzyme Q4 homolog (S. cerevisiae)	NM_016035, hCT2317827.1, hCT2317829.1, hCT2317832.1, hCT2341107.0, hCT2357023.0	218328_at, 226931_at	NP_057119.2, EAW87776.1, EAW87774.1, EAW87775.1, EAW87777.1, EAW87778.1
GeneID:100506065	LOC100506065	9	131,173,854	131,182,503	8,649	+	1	2_A375_pNL97_plus_lncRNA::1::8114	8576	in gene	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100506065		hypothetical LOC100506065	XR_108948		
GeneID:51148	CERCAM	9	131,182,759	131,199,630	16,871	+	1	2_A375_pNL97_plus_lncRNA::1::8114	-327	upstream	0	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene CERCAM	CEECAM1, CERCAM, MGC149620, MGC149621, GLT25D3	cerebral endothelial cell adhesion molecule	NM_016174, hCT2317598.0, hCT2317601.0, hCT9619.3, hCT1950583.1	224794_s_at, 227381_at	NP_057258.3, EAW87789.1, EAW87787.1, EAW87788.1, EAW87790.1
GeneID:6709	SPTAN1	9	131,314,866	131,395,941	81,075	+	1	2_A375_pNL97_plus_lncRNA::1::8115	238	in gene	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SPTAN1	SPTA2, FLJ17738, FLJ44613, EIEE5, NEAS, SPTAN1, (ALPHA)II-SPECTRIN	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	NM_003127, NM_001130438, hCT2317615.0, hCT2317616.0, hCT2317617.0, hCT2317618.0, hCT2317620.0, hCT2357042.0, hCT2357043.0, hCT2357044.0, hCT32307.3	208611_s_at, 214925_s_at, 214926_at, 215235_at, 241150_at	NP_003118.2, NP_001123910.1, EAW87805.1, EAW87807.1, EAW87809.1, EAW87811.1, EAW87806.1, EAW87808.1, EAW87810.1, EAW87812.1, EAW87813.1
GeneID:10444	ZER1	9	131,492,065	131,534,198	42,133	-	2	1_A375_pNL7_minus_lncRNA::1::5636, 2_A375_pNL97_plus_lncRNA::1::8116	-314, -106	upstream, upstream	1	1	17	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene ZER1	ZER1, C9orf60, ZYG11BL, ZYG, Hzyg, RP11-545E17.4	zer-1 homolog (C. elegans)	NM_006336, hCT2317665.0, hCT2317666.0, hCT2317669.0	202448_s_at, 202452_at, 202456_s_at, 230358_at	NP_006327.2, EAW87829.1, EAW87830.1, EAW87831.1
GeneID:54662	TBC1D13	9	131,549,510	131,572,711	23,201	+	2	1_A375_pNL7_minus_lncRNA::1::5637, 2_A375_pNL97_plus_lncRNA::1::8117	31274, -6	downstream, upstream	1	1	21.5	20.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene TBC1D13	TBC1D13, FLJ10743, RP11-545E17.5	TBC1 domain family, member 13	NM_018201, hCT2317636.0, hCT2357071.0, hCT1827290.2, hCT1950567.1, hCT1950568.1	218596_at, 44696_at	NP_060671.3, EAW87834.1, EAW87832.1, EAW87833.1, EAW87835.1, EAW87836.1
GeneID:2021	ENDOG	9	131,580,779	131,584,955	4,176	+	2	1_A375_pNL7_minus_lncRNA::1::5637, 2_A375_pNL97_plus_lncRNA::1::8118	5, 11237	in gene, downstream	1	1	19	18.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene ENDOG	ENDOG, FLJ27463	endonuclease G	NM_004435, hCT21763.3	204824_at	NP_004426.2, EAW87837.1
GeneID:51490	C9orf114	9	131,584,345	131,592,085	7,740	-	2	1_A375_pNL7_minus_lncRNA::1::5637, 2_A375_pNL97_plus_lncRNA::1::8118	11301, 69	downstream, in gene	1	1	19	18.5	2	1_A375_pNL7_minus_lncRNA::1	25	Gene C9orf114	RP11-545E17.7, C9orf114, MGC29492, HSPC109, DKFZp566D143	chromosome 9 open reading frame 114	NM_016390, hCT21765.3, hCT1950620.1	218565_at, 222674_at	NP_057474.2, EAW87839.1, EAW87838.1
GeneID:883	CCBL1	9	131,595,392	131,644,354	48,962	-	3	1_A375_pNL7_minus_lncRNA::1::5638, 2_A375_pNL97_plus_lncRNA::1::8118, 2_A375_pNL97_plus_lncRNA::1::8119	98, 52338, 98	in gene, downstream, in gene	1	1	30.5	33.5	2	1_A375_pNL7_minus_lncRNA::1	48	Gene CCBL1	FLJ95217, CCBL1, KAT1, GTK, KATI, MGC29624	cysteine conjugate-beta lyase, cytoplasmic	NM_004059, NM_001122671, NM_001122672, hCT1950619.1, hCT1965685.1	1570650_at, 1570651_at, 206037_at	NP_004050.3, NP_001116143.1, NP_001116144.1, EAW87840.1, EAW87841.1
GeneID:56262	LRRC8A	9	131,644,391	131,680,318	35,927	+	3	1_A375_pNL7_minus_lncRNA::1::5638, 1_A375_pNL7_minus_lncRNA::1::5639, 2_A375_pNL97_plus_lncRNA::1::8119	-135, 10361, -135	upstream, in gene, upstream	1	1	33	30	2	1_A375_pNL7_minus_lncRNA::1	48	Gene LRRC8A	AGM5, FLJ41617, KIAA1437, FLJ10337, LRRC8, LRRC8A	leucine rich repeat containing 8 family, member A	NM_001127244, NM_019594, NM_001127245, hCT1643880.2, hCT1964773.1	224624_at, 233487_s_at	NP_001120716.1, NP_062540.2, NP_001120717.1, EAW87842.1, EAW87843.1
GeneID:254295	PHYHD1	9	131,683,174	131,704,320	21,146	+	2	1_A375_pNL7_minus_lncRNA::1::5640, 2_A375_pNL97_plus_lncRNA::1::8120	26874, 26842	downstream, downstream	1	1	21	21	1	1_A375_pNL7_minus_lncRNA::1	21	Gene PHYHD1	MGC16638, PHYHD1	phytanoyl-CoA dioxygenase domain containing 1	NM_174933, NM_001100876, NM_001100877, hCT2356958.0, hCT2356959.0, hCT2356960.0, hCT2356961.0, hCT1963069.1	226846_at	NP_777593.2, NP_001094346.1, NP_001094347.1, EAW87844.1, EAW87846.1, EAW87848.1, EAW87845.1, EAW87847.1
GeneID:22845	DOLK	9	131,707,809	131,710,012	2,203	-	2	1_A375_pNL7_minus_lncRNA::1::5640, 2_A375_pNL97_plus_lncRNA::1::8120	-36, -4	upstream, upstream	1	1	21	21	1	1_A375_pNL7_minus_lncRNA::1	21	Gene DOLK	SEC59, DOLK, DK, KIAA1094, TMEM15, CDG1M, DK1	dolichol kinase	NM_014908, hCT19540.3	204488_at	NP_055723.1, EAW87849.1
GeneID:23511	NUP188	9	131,709,977	131,769,374	59,397	+	2	1_A375_pNL7_minus_lncRNA::1::5640, 2_A375_pNL97_plus_lncRNA::1::8120	71, 39	in gene, in gene	1	1	21	21	1	1_A375_pNL7_minus_lncRNA::1	21	Gene NUP188	KIAA0169, NUP188, FLJ21639	nucleoporin 188kDa	NM_015354, hCT2356957.0, hCT2356956.0, hCT1827303.2, hCT1827304.2	212691_at, 214675_at, 217601_at	NP_056169.1, EAW87852.1, EAW87850.1, EAW87851.1, EAW87853.1
GeneID:56904	SH3GLB2	9	131,770,313	131,790,579	20,266	-	1	2_A375_pNL97_plus_lncRNA::1::8121	-8141	upstream	0	1	18	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene SH3GLB2	SH3GLB2, PP9455, PP6569, KIAA1848	SH3-domain GRB2-like endophilin B2	NM_020145, hCT21777.3, hCT2357006.0, hCT2357007.0, hCT2357008.0, hCT1954931.1, hCT1954932.1, hCT1954933.1	218813_s_at, 224432_at, 224907_s_at	NP_064530.1, EAW87854.1, EAW87855.1, EAW87858.1, EAW87859.1, EAW87860.1, EAW87856.1, EAW87857.1
GeneID:84895	FAM73B	9	131,799,253	131,834,351	35,098	+	2	2_A375_pNL97_plus_lncRNA::1::8121, 2_A375_pNL97_plus_lncRNA::1::8122	-533, 44299	upstream, downstream	0	1	14	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene FAM73B	FLJ00199, C9orf54, FLJ14596, FAM73B	family with sequence similarity 73, member B	NM_032809, hCT2317569.0, hCT2317570.0, hCT2317571.0, hCT2317572.0, hCT2357056.0, hCT2357057.0	226356_at	NP_116198.2, EAW87863.1, EAW87861.1, EAW87864.1, EAW87865.1, EAW87866.1, EAW87862.1
GeneID:57171	DOLPP1	9	131,843,383	131,852,717	9,334	+	1	2_A375_pNL97_plus_lncRNA::1::8122	169	in gene	0	1	10	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene DOLPP1	DOLPP1, LSFR2	dolichyl pyrophosphate phosphatase 1	NM_020438, NM_001135917, hCT21775.2, hCT2357002.0, hCT2357003.0, hCT2357004.0, hCT1965688.1, hCT1965691.1	221817_at	NP_065171.2, NP_001129389.1, EAW87869.1, EAW87870.1, EAW87871.1, EAW87872.1, EAW87867.1, EAW87868.1
GeneID:389792	IER5L	9	131,937,831	131,940,540	2,709	-	1	2_A375_pNL97_plus_lncRNA::1::8123	4060	downstream	0	1	23	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene IER5L	MGC70833, bA247A12.2, IER5L	immediate early response 5-like	NM_203434	226552_at, 226559_at	NP_982258.2
GeneID:100506190	LOC100506190	9	132,245,730	132,267,406	21,676	+	3	2_A375_pNL97_plus_lncRNA::1::8125, 2_A375_pNL97_plus_lncRNA::1::8126, 2_A375_pNL97_plus_lncRNA::1::8127	-9378, 6867, 12565	upstream, in gene, in gene	0	1	14	16.67	3	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100506190		hypothetical LOC100506190	XR_113260, XR_113259, XR_108960, XR_108958, XR_108957, XR_108959, XR_114306, XR_114305		
GeneID:100128077	LOC100128077	9	132,252,760	132,253,362	602	+	2	2_A375_pNL97_plus_lncRNA::1::8126, 2_A375_pNL97_plus_lncRNA::1::8127	-163, 5555	upstream, downstream	0	1	17	17	2	2_A375_pNL97_plus_lncRNA::1	19	Gene LOC100128077		hypothetical LOC100128077	XR_113258, XR_108956, XR_114304		
GeneID:28989	METTL11A	9	132,388,435	132,397,879	9,444	+	2	1_A375_pNL7_minus_lncRNA::1::5641, 2_A375_pNL97_plus_lncRNA::1::8128	16045, 16013	downstream, downstream	1	1	213	204	1	1_A375_pNL7_minus_lncRNA::1	213	Gene METTL11A	NRMT, NTM1A, METTL11A, C9orf32, AD-003	methyltransferase like 11A	NM_014064, hCT21770.1, hCT2321311.0, hCT1950622.1	223368_s_at, 223369_at	NP_054783.2, EAW87895.1, EAW87893.1, EAW87894.1
GeneID:140459	ASB6	9	132,396,883	132,404,444	7,561	-	2	1_A375_pNL7_minus_lncRNA::1::5641, 2_A375_pNL97_plus_lncRNA::1::8128	-36, -4	upstream, upstream	1	1	213	204	1	1_A375_pNL7_minus_lncRNA::1	213	Gene ASB6	MGC1024, FLJ20548, ASB6	ankyrin repeat and SOCS box containing 6	NM_177999, NM_017873, hCT21776.4, hCT2321495.1, hCT2321497.1, hCT2357014.0, hCT1686779.3	221657_s_at, 222524_s_at	NP_821066.1, NP_060343.1, EAW87897.1, EAW87898.1, EAW87899.1, EAW87900.1, EAW87896.1
GeneID:51450	PRRX2	9	132,427,920	132,484,953	57,033	+	1	2_A375_pNL97_plus_lncRNA::1::8129	47520	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PRRX2	PRRX2, PMX2, MGC19843, PRX2	paired related homeobox 2	NM_016307, hCT21769.3	219729_at	NP_057391.1, EAW87901.1
GeneID:100506231	LOC100506231	9	132,475,173	132,480,957	5,784	-	1	2_A375_pNL97_plus_lncRNA::1::8129	5517	in gene	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene LOC100506231		hypothetical LOC100506231	XR_108961		
GeneID:27348	TOR1B	9	132,565,432	132,573,560	8,128	+	1	2_A375_pNL97_plus_lncRNA::1::8132	40	in gene	0	1	10	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene TOR1B	DQ1, TOR1B, MGC4386	torsin family 1, member B (torsin B)	NM_014506, hCT21779.3	209593_s_at	NP_055321.1, EAW87906.1
GeneID:1861	TOR1A	9	132,575,221	132,586,441	11,220	-	3	1_A375_pNL7_minus_lncRNA::1::5644, 2_A375_pNL97_plus_lncRNA::1::8132, 2_A375_pNL97_plus_lncRNA::1::8133	73, 20969, 41	in gene, downstream, in gene	1	1	15.5	23.5	2	2_A375_pNL97_plus_lncRNA::1	27	Gene TOR1A	DYT1, DQ2, TOR1A	torsin family 1, member A (torsin A)	NM_000113, hCT21768.2, hCT1950621.1	1554649_at, 202348_s_at, 202349_at	NP_000104.1, EAW87907.1, EAW87908.1
GeneID:51759	C9orf78	9	132,589,564	132,597,572	8,008	-	2	1_A375_pNL7_minus_lncRNA::1::5644, 2_A375_pNL97_plus_lncRNA::1::8133	11204, 11172	downstream, downstream	1	1	21	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene C9orf78	HSPC220, C9orf78, bA409K20.3	chromosome 9 open reading frame 78	NM_016520, hCT1950598.1, hCT19541.3	218116_at	NP_057604.1, EAW87909.1, EAW87910.1
GeneID:100289200	LOC100289200	9	133,028,161	133,072,949	44,788	+	2	1_A375_pNL7_minus_lncRNA::1::5645, 2_A375_pNL97_plus_lncRNA::1::8134	32991, 32943	in gene, in gene	1	1	29	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene LOC100289200		hemicentin-2-like	XM_002342856		XP_002342897.1
GeneID:25	ABL1	9	133,589,268	133,763,062	173,794	+	2	1_A375_pNL7_minus_lncRNA::1::5646, 2_A375_pNL97_plus_lncRNA::1::8135	52364, 120940	in gene, in gene	1	1	15.5	16	2	1_A375_pNL7_minus_lncRNA::1	19	Gene ABL1	bcr/abl, JTK7, c-ABL, ABL1, p150, v-abl, ABL	c-abl oncogene 1, non-receptor tyrosine kinase	NM_007313, NM_005157, hCT2323164.0, hCT1950600.1, hCT19568.3	202123_s_at	NP_009297.2, NP_005148.2, EAW87947.1, EAW87948.1, EAW87949.1
GeneID:83543	AIF1L	9	133,971,863	133,998,539	26,676	+	2	1_A375_pNL7_minus_lncRNA::1::5647, 2_A375_pNL97_plus_lncRNA::1::8136	29033, 29129	downstream, downstream	1	1	29	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene AIF1L	AIF1L, MGC29466, FLJ12783, C9orf58, IBA2	allograft inflammatory factor 1-like	NM_001185095, NM_001185096, NM_031426, NR_033701, hCT21364.2, hCT1950618.1	223074_s_at, 223075_s_at	NP_001172024.1, NP_001172025.1, NP_113614.1, EAW87958.1, EAW87959.1
GeneID:8021	NUP214	9	134,000,981	134,109,091	108,110	+	2	1_A375_pNL7_minus_lncRNA::1::5647, 2_A375_pNL97_plus_lncRNA::1::8136	-65, 11	upstream, in gene	1	1	29	32	1	2_A375_pNL97_plus_lncRNA::1	32	Gene NUP214	MGC104525, N214, D9S46E, CAN, NUP214, CAIN	nucleoporin 214kDa	NM_005085, hCT21359.3, hCT2323176.0, hCT2356933.0, hCT1950614.1	202155_s_at	NP_005076.3, EAW87962.1, EAW87960.1, EAW87961.1, EAW87963.1
GeneID:84726	BAT2L1	9	134,305,477	134,375,578	70,101	+	2	1_A375_pNL7_minus_lncRNA::1::5649, 2_A375_pNL97_plus_lncRNA::1::8138	72907, 72859	downstream, downstream	1	1	37	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene BAT2L1	BAT2L1, KIAA0515, PRRC2B, LQFBS-1, BAT2L, DKFZp781F05101, DKFZp781K12107, MGC10526	HLA-B associated transcript 2-like 1	NM_013318	212068_s_at, 212069_s_at, 223793_at	NP_037450.2
GeneID:10585	POMT1	9	134,378,289	134,399,193	20,904	+	2	1_A375_pNL7_minus_lncRNA::1::5649, 2_A375_pNL97_plus_lncRNA::1::8138	95, 47	in gene, in gene	1	1	37	45	1	2_A375_pNL97_plus_lncRNA::1	45	Gene POMT1	FLJ37239, MDDGA1, LGMD2K, RT, MDDGB1, POMT1, MDDGC1	protein-O-mannosyltransferase 1	NM_001077366, NM_001077365, NM_007171, NM_001136113, NM_001136114, hCT1823332.2, hCT1950602.1, hCT1959916.1, hCT1959918.1, hCT1959919.1	218476_at	NP_001070834.1, NP_001070833.1, NP_009102.3, NP_001129585.1, NP_001129586.1, EAW87974.1, EAW87975.1, EAW87976.1, EAW87977.1, EAW87978.1
GeneID:9442	MED27	9	134,735,499	134,955,253	219,754	-	2	2_A375_pNL97_plus_lncRNA::1::8143, 2_A375_pNL97_plus_lncRNA::1::8144	119173, -75	in gene, upstream	0	1	13	19	2	2_A375_pNL97_plus_lncRNA::1	21	Gene MED27	MED27, TRAP37, MGC11274, CRSP8, CRSP34, CRAP34	mediator complex subunit 27	NM_004269, hCT2317465.0, hCT2317466.0, hCT2317468.0, hCT2357075.0, hCT19241.2	215371_at, 221598_s_at, 51176_at	NP_004260.2, EAW87991.1, EAW87989.1, EAW87990.1, EAW87992.1, EAW87993.1
GeneID:23064	SETX	9	135,136,827	135,230,372	93,545	-	1	1_A375_pNL7_minus_lncRNA::1::5653	132	in gene	1	0	20	13	1	1_A375_pNL7_minus_lncRNA::1	20	Gene SETX	bA479K20.2, FLJ43459, SETX, FLJ12840, KIAA0625, ALS4, AOA2, SCAR1, DKFZp781B151	senataxin	NM_015046, hCT2317459.0, hCT2317460.0, hCT2317462.0, hCT2317463.0	201964_at, 201965_s_at, 232229_at	NP_055861.3, EAW87997.1, EAW87998.1, EAW87999.1, EAW88000.1
GeneID:389799	C9orf171	9	135,285,611	135,448,675	163,064	+	2	1_A375_pNL7_minus_lncRNA::1::5654, 2_A375_pNL97_plus_lncRNA::1::8146	171973, 172021	downstream, downstream	1	1	64	82	1	2_A375_pNL97_plus_lncRNA::1	82	Gene C9orf171	C9orf171, FLJ46082, MGC148067	chromosome 9 open reading frame 171	NM_207417, hCT2357061.0, hCT1653189.3		NP_997300.1, EAW88004.1, EAW88003.1
GeneID:56751	BARHL1	9	135,457,993	135,465,640	7,647	+	2	1_A375_pNL7_minus_lncRNA::1::5654, 2_A375_pNL97_plus_lncRNA::1::8146	-409, -361	upstream, upstream	1	1	64	82	1	2_A375_pNL97_plus_lncRNA::1	82	Gene BARHL1	BARHL1	BarH-like homeobox 1	NM_020064, hCT22644.3	224092_at	NP_064448.1, EAW88005.1
GeneID:64794	DDX31	9	135,469,676	135,545,788	76,112	-	1	2_A375_pNL97_plus_lncRNA::1::8147	540	in gene	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene DDX31	FLJ13633, FLJ14578, DDX31, FLJ23349	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	NM_022779, NM_138620, hCT22646.3, hCT1965707.1, hCT1965708.1, hCT1965709.1	1553181_at, 219328_at	NP_073616.6, NP_619526.1, EAW88006.1, EAW88007.1, EAW88008.1, EAW88009.1
GeneID:9329	GTF3C4	9	135,545,728	135,565,471	19,743	+	1	2_A375_pNL97_plus_lncRNA::1::8147	-480	upstream	0	1	13	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene GTF3C4	TFIII90, TFIIIC290, GTF3C4, FLJ21002, TFIIICDELTA, KAT12, MGC138450, TFIIIC90	general transcription factor IIIC, polypeptide 4, 90kDa	NM_012204, hCT22641.3, hCT2356940.0	219198_at	NP_036336.2, EAW88011.1, EAW88010.1
GeneID:9328	GTF3C5	9	135,906,062	135,933,890	27,828	+	1	1_A375_pNL7_minus_lncRNA::1::5655	322	in gene	1	0	21	15	1	1_A375_pNL7_minus_lncRNA::1	21	Gene GTF3C5	TFIIICepsilon, TFIIIC2-63, TFIIIC63, GTF3C5, FLJ20857	general transcription factor IIIC, polypeptide 5, 63kDa	NM_012087, NM_001122823, hCT22635.3, hCT2357054.0, hCT2357055.0, hCT1950633.1	217876_at, 233173_x_at	NP_036219.2, NP_001116295.1, EAW88026.1, EAW88027.1, EAW88028.1, EAW88029.1
GeneID:6838	SURF6	9	136,197,552	136,203,047	5,495	-	2	1_A375_pNL7_minus_lncRNA::1::5656, 2_A375_pNL97_plus_lncRNA::1::8148	-25, -57	upstream, upstream	1	1	80	86	1	2_A375_pNL97_plus_lncRNA::1	86	Gene SURF6	SURF6, FLJ30322, RRP14	surfeit 6	NM_006753, hCT19295.3	225038_s_at	NP_006744.2, EAW88055.1
GeneID:6837	MED22	9	136,207,744	136,214,972	7,228	-	4	1_A375_pNL7_minus_lncRNA::1::5656, 1_A375_pNL7_minus_lncRNA::1::5657, 2_A375_pNL97_plus_lncRNA::1::8148, 2_A375_pNL97_plus_lncRNA::1::8149	11900, -68, 11868, -68	downstream, upstream, downstream, upstream	1	1	54	63	2	2_A375_pNL97_plus_lncRNA::1	86	Gene MED22	MGC48682, MED22, MED24, SURF5	mediator complex subunit 22	NM_181491, NM_133640, hCT2335787.1, hCT2335788.1, hCT2335789.1, hCT2335790.1, hCT2335791.1	206593_s_at	NP_852468.1, NP_598395.1, EAW88056.1, EAW88057.1, EAW88059.1, EAW88060.1, EAW88058.1
GeneID:6130	RPL7A	9	136,215,069	136,218,280	3,211	+	2	1_A375_pNL7_minus_lncRNA::1::5657, 2_A375_pNL97_plus_lncRNA::1::8149	-29, -29	upstream, upstream	1	1	28	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene RPL7A	SURF3, TRUP, RPL7A, L7A	ribosomal protein L7a	NM_000972, hCT2335565.1, hCT2335566.1, hCT2335567.1, hCT2335568.1, hCT2335569.1, hCT2348626.1	217740_x_at, 224930_x_at	NP_000963.1, EAW88061.1, EAW88062.1, EAW88063.1, EAW88064.1, EAW88065.1, EAW88066.1
GeneID:26820	SNORD24	9	136,216,251	136,216,325	74	+	2	1_A375_pNL7_minus_lncRNA::1::5657, 2_A375_pNL97_plus_lncRNA::1::8149	-1211, -1211	upstream, upstream	1	1	28	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene SNORD24	RNU24, U24, SNORD24	small nucleolar RNA, C/D box 24	NR_002447		
GeneID:26814	SNORD36B	9	136,216,949	136,217,019	70	+	2	1_A375_pNL7_minus_lncRNA::1::5657, 2_A375_pNL97_plus_lncRNA::1::8149	-1909, -1909	upstream, upstream	1	1	28	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene SNORD36B	RNU36B, SNORD36B, U36b	small nucleolar RNA, C/D box 36B	NR_000017		
GeneID:26815	SNORD36A	9	136,217,311	136,217,382	71	+	2	1_A375_pNL7_minus_lncRNA::1::5657, 2_A375_pNL97_plus_lncRNA::1::8149	-2271, -2271	upstream, upstream	1	1	28	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene SNORD36A	SNORD36A, RNU36A, U36a	small nucleolar RNA, C/D box 36A	NR_002448		
GeneID:26813	SNORD36C	9	136,217,701	136,217,768	67	+	2	1_A375_pNL7_minus_lncRNA::1::5657, 2_A375_pNL97_plus_lncRNA::1::8149	-2661, -2661	upstream, upstream	1	1	28	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene SNORD36C	SNORD36C, U36c, RNU36C	small nucleolar RNA, C/D box 36C	NR_000016		
GeneID:6834	SURF1	9	136,218,666	136,223,361	4,695	-	2	1_A375_pNL7_minus_lncRNA::1::5657, 2_A375_pNL97_plus_lncRNA::1::8149	8321, 8321	downstream, downstream	1	1	28	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene SURF1	SURF1	surfeit 1	NM_003172, hCT19291.4	204295_at, 217646_at	NP_003163.1, EAW88067.1
GeneID:6835	SURF2	9	136,223,421	136,228,040	4,619	+	2	1_A375_pNL7_minus_lncRNA::1::5657, 2_A375_pNL97_plus_lncRNA::1::8149	-8381, -8381	upstream, upstream	1	1	28	40	1	2_A375_pNL97_plus_lncRNA::1	40	Gene SURF2	SURF2, SURF-2	surfeit 2	NM_017503, hCT2335562.1, hCT19292.3, hCT1962453.2	205224_at	NP_059973.3, EAW88068.1, EAW88069.1, EAW88070.1
GeneID:6836	SURF4	9	136,228,340	136,242,970	14,630	-	3	1_A375_pNL7_minus_lncRNA::1::5658, 1_A375_pNL7_minus_lncRNA::1::5659, 2_A375_pNL97_plus_lncRNA::1::8150	666, -38, -102	in gene, upstream, upstream	1	1	51	58	1	2_A375_pNL97_plus_lncRNA::1	58	Gene SURF4	MGC102753, SURF4, ERV29, FLJ22993	surfeit 4	NM_033161, hCT1971125.2, hCT1971129.2, hCT2356989.0, hCT19294.4	222977_at, 222978_at, 222979_s_at	NP_149351.1, EAW88072.1, EAW88071.1, EAW88073.1, EAW88074.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervals Count	Intervals	Intervals Dists to Start	Intervals Pos.	[A]	[R]	[C]	[G]	Acc Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ENSG00000169436	C9orf66	9	136,243,264	136,271,220	27,956	+	3	1_A375_shN7_dhrus_bioRNA:1:36558,1_A375_shN7_dhrus_bioRNA:1:36592,1_A375_shN37_ghrs_bioRNA:1:36181	460,-276,212	upstream, upstream, upstream	1	1	51	56	1	2_A375_shN37_ghrs_bioRNA:1	95	Gene C9orf66	RP11-244N20.6, MGC45336, SQ4271, C9orf66, B4521	Chromosome 9 open reading frame 66	NM_152710, NCT12340936.0, NCT23409857.0, NCT23409858.0, NCT23409859.0, NCT23409860.0, NCT23409861.0, NCT23409862.0, NCT16302.4	1564727_at, 238603_at	NP_714621.2; EAN66550.1; EAN65078.1, EAN65079.1, EAN65080.1, EAN65081.1, EAN65076.1, EAN65078.1
Gene:ENSG00000171100	REXO4	9	136,271,156	136,283,164	11,976	-	2	1_A375_shN7_dhrus_bioRNA:1:36992,2_A375_shN37_ghrs_bioRNA:1:4183	-100, -122	upstream, upstream	1	1	20	29	1	2_A375_shN37_ghrs_bioRNA:1	29	Gene REXO4	REXO, XRN2, XRN2CH, REXO4	REXO4, RNA exonuclease 4 homolog (S. cerevisiae)	NM_020383, NCT16296.2	210767_at	NP_065118.2; EAN65082.1
Gene:ENSG00000171083	ADAMTS13	9	136,279,459	136,324,555	45,096	+	2	1_A375_shN7_dhrus_bioRNA:1:36992,2_A375_shN37_ghrs_bioRNA:1:4183	3505, 3037	in gene, us gene	1	1	20	29	1	2_A375_shN37_ghrs_bioRNA:1	29	Gene ADAMTS13	MGC116500, C9orf5, TTP, VWFCP, FLJ42883, vWF-CP, DKFZp434C2322, MGC116499, ADAMTS13	ADAM metallopeptidase with thrombospondin type 1 motif, 13	NM_139025, NM_139027, NM_139026, NM_030954, NCT23355715.0, NCT23355716.0, NCT23355717.0, NCT23355718.0, NCT23355719.0, NCT23355720.0, NCT23370343.0, NCT23370344.0	2352206_at, 2230644_at	NP_620594.1, NP_620596.2; NP_620595.1, EAN65555.1, EAN65556.1, EAN65557.1, EAN65554.1, EAN65555.1, EAN65556.1
Gene:ENSG00000171848	ADAMTSL2	9	136,297,256	136,440,641	143,385	+	1	1_A375_shN37_ghrs_bioRNA:1:36152	28776	in gene	0	1	13	17	1	2_A375_shN37_ghrs_bioRNA:1	17	Gene ADAMTSL2	ADAMTSL2, KIAA0605, FLJ45164	ADAMTS-like 2	NM_014964, NM_001145120, NCT16731.1, NCT23396800.0, NCT16282.3	2056529_at	NP_055972.2, NP_001128792.1, EAN65098.1, EAN65099.1, EAN65097.1
Gene:ENSG00000171410	UAV2	9	136,627,016	136,637,496	230,480	-	3	1_A375_shN7_dhrus_bioRNA:1:36961,1_A375_shN7_dhrus_bioRNA:1:36964,2_A375_shN37_ghrs_bioRNA:1:4132,2_A375_shN37_ghrs_bioRNA:1:4134	1190, 117942, 1030	in gene, us gene, in gene, in gene	1	1	13	20.5	2	2_A375_shN37_ghrs_bioRNA:1	21	Gene VAV2	VAV2		NM_003371, NM_001134088, NCT12872.2, NCT23384324.0, NCT23385330.0	208539_at, 208537_s_at, 208063_at	NP_003362.2, NP_001127670.1, EAN65107.1, EAN65108.1, EAN65109.1
Gene:ENSG00000169555	NCRNA00084	9	136,690,561	136,696,719	6,158	+	2	1_A375_shN7_dhrus_bioRNA:1:36962,2_A375_shN37_ghrs_bioRNA:1:4130	-33, -33	upstream, upstream	1	1	32	62	1	2_A375_shN37_ghrs_bioRNA:1	62	Gene NCRNA00084	bA379F20.2, NCRNA00084, LPJ477, FLJ35340	non-protein coding RNA 84	NR_015427	2032455_s_at, 212567_at, 212565_s_at	
Gene:ENSG00000169558	BRD3	9	136,695,427	136,933,141	237,714	-	2	1_A375_shN7_dhrus_bioRNA:1:36962,2_A375_shN37_ghrs_bioRNA:1:4130	42612, 42613	downstream, downstream	1	1	52	62	1	2_A375_shN37_ghrs_bioRNA:1	62	Gene BRD3	BRD3, FLJ22227, RING3L, ORFX, KIAA0043, FLH01326	bromodomain containing 3	NM_007371, NCT21250.3, NCT23382930.0, NCT23382931.0, NCT23382932.0, NCT23382933.0, NCT23382934.0, NCT23382935.0, NCT23382936.0	1555028_at, 203625_at	NP_031397.1, EAN65115.1, EAN65113.1, EAN65114.1
Gene:ENSG00000171091	WDR5	9	137,001,210	137,029,094	23,884	+	4	1_A375_shN7_dhrus_bioRNA:1:36963,1_A375_shN7_dhrus_bioRNA:1:36964,1_A375_shN7_dhrus_bioRNA:1:36966,1_A375_shN37_ghrs_bioRNA:1:4127	-262, 26582, 216, 26622	upstream, downstream, upstream, downstream	1	1	22.5	25.5	2	2_A375_shN37_ghrs_bioRNA:1	29	Gene WDR5	WDR5, BIG-3, SWD3	WD repeat domain 5	NM_017588, NM_052821, NCT23178898.0, NCT23178900.0, NCT23179901.0, NCT23179902.0	2203355_s_at, 226170_at	NP_060058.1, NP_439172.1, EAN65117.1, EAN65118.1, EAN65119.1, EAN65120.1
Gene:ENSG00000231916	RNU6ATAC	9	137,029,552	137,029,656	124	-	2	1_A375_shN7_dhrus_bioRNA:1:36964,2_A375_shN37_ghrs_bioRNA:1:4130	-106, -366	upstream, upstream	1	1	22	22	1	1_A375_shN7_dhrus_bioRNA:1	22	Gene RNU6ATAC	RNU6ATAC, RNU6ATAC1, U6ATAC	RNA, U6 atac small nuclear (U12-dependent splicing)	NR_023344		
Gene:ENSG00000170428	OLFM1	9	137,967,058	138,013,030	45,941	+	4	1_A375_shN7_dhrus_bioRNA:1:36963,1_A375_shN7_dhrus_bioRNA:1:36966,1_A375_shN7_dhrus_bioRNA:1:36967,1_A375_shN7_dhrus_bioRNA:1:36968,2_A375_shN37_ghrs_bioRNA:1:4127	23227, 2418, 19535, 23343	in gene, us gene, in gene, in gene, us gene	1	1	17	23	2	2_A375_shN37_ghrs_bioRNA:1	29	Gene OLFM1	OlfM, OLFM1, AMY, NOE1, NOELIN1	olfactomedin 1	NM_006334, NM_014279, NCT23179600.0, NCT23179602.0, NCT11283.3, NCT16903.3	208991_at, 219824_at, 213131_at	NP_006325.1, NP_055096.1, EAN65142.1, EAN65143.1, EAN65144.1, EAN65145.1
Gene:ENSG00000231161	LOC100506589	9	138,354,564	138,364,095	9,531	-	2	1_A375_shN7_dhrus_bioRNA:1:36967,2_A375_shN37_ghrs_bioRNA:1:4132	-2649, -2617	upstream, upstream	1	1	23	22	1	1_A375_shN7_dhrus_bioRNA:1	33	Gene LOC100506589		hypothetical LOC100506589	XR_113269, XR_109557, XR_114316		
Gene:ENSG00000231555	KIAA0649	9	138,371,646	138,380,729	9,091	+	2	1_A375_shN7_dhrus_bioRNA:1:36967,2_A375_shN37_ghrs_bioRNA:1:4132	-4704, -4736	upstream, upstream	1	1	23	22	1	1_A375_shN7_dhrus_bioRNA:1	33	Gene KIAA0649	RP11-426A6.8, KIAA0649	KIAA0649	NM_014611, NCT16377.5, NCT19807.1	2018553_at	NP_055626.2; EAN65151.1, EAN65150.1
Gene:ENSG00000138162	C9orf116	9	138,387,026	138,391,761	4,735	-	2	1_A375_shN7_dhrus_bioRNA:1:36968,2_A375_shN37_ghrs_bioRNA:1:4132	-791, -791	upstream, upstream	1	1	128	149	1	2_A375_shN37_ghrs_bioRNA:1	149	Gene C9orf116	FLJ10345, C9orf116, MGC20761	Chromosome 9 open reading frame 116	NM_144954, NM_001040265, NCT19882.2, NCT23217.0	221649_at, 1554427_at	NP_653351.1, NP_001041720.1; EAN65154.1, EAN65155.1
Gene:ENSG00000131116	MRPS2	9	138,392,463	138,399,819	7,356	+	2	1_A375_shN7_dhrus_bioRNA:1:36968,2_A375_shN37_ghrs_bioRNA:1:4132	-28, -28	in gene, in gene	1	1	128	149	1	2_A375_shN37_ghrs_bioRNA:1	149	Gene MRPS2	CGI-61, MRP52, MRP-S2, S2-mt	mitochondrial ribosomal protein S2	NM_016034, NCT16552.2, NCT19824.1	218001_at	NP_057118.1, EAN65152.1, EAN65153.1
Gene:ENSG00000232252	LOC40231	9	138,668,123	138,668,644	8,321	+	1	1_A375_shN37_ghrs_bioRNA:1:4135	13541	downstream	0	1	12	21	1	2_A375_shN37_ghrs_bioRNA:1	21	Gene LOC402382		hypothetical protein LOC402382	XM_378382		XP_378092.5
Gene:ENSG00000120129	C9orf69	9	139,006,427	139,010,731	6,304	-	3	1_A375_shN7_dhrus_bioRNA:1:36965,1_A375_shN7_dhrus_bioRNA:1:36966,2_A375_shN37_ghrs_bioRNA:1:4132	8067, 4975, 139	downstream, in gene, us gene	0	1	14	20.33	3	2_A375_shN37_ghrs_bioRNA:1	23	Gene C9orf69	C9orf69, bA525N9.1	Chromosome 9 open reading frame 69	NM_152633	2049652_at	NP_690046.2
Gene:ENSG00000231607	LOC10013998	9	139,014,397	139,016,209	1,842	+	2	1_A375_shN7_dhrus_bioRNA:1:36966,2_A375_shN37_ghrs_bioRNA:1:4132	-7711, -7773	upstream, upstream	0	1	14.5	20	2	2_A375_shN37_ghrs_bioRNA:1	23	Gene LOC100129989		hypothetical LOC100129989	XR_112272, XR_109559, XR_114316		
Gene:ENSG00000169551	GPSM1	9	139,221,932	139,254,057	32,125	+	1	1_A375_shN7_dhrus_bioRNA:1:36968	17676	in gene	0	1	16	23	1	2_A375_shN37_ghrs_bioRNA:1	23	Gene GPSM1	GPSM1, AGS3, DKFZp727d151	G-protein signaling modulator 1	NM_015597, NM_001143838, NM_001143839, NCT23161542.2, NCT23161543.2, NCT23161544.2, NCT23161545.1, NCT16259.4	1554259_at, 206043_at	NP_056412.2, NP_001138110.1, NP_001138111.1, EAN65216.1, EAN65217.1, EAN65218.1
Gene:ENSG00000214221	SNAPC4	9	139,270,029	139,292,889	22,860	-	1	1_A375_shN37_ghrs_bioRNA:1:4132	-1691	upstream	0	1	14	15	1	2_A375_shN37_ghrs_bioRNA:1	16	Gene SNAPC4	FLJ13451, SNAP190, SNAPC4, PTF alpha	small nuclear RNA activating complex, polypeptide 4, 190 kDa	NM_003086, NCT23155846.0, NCT23155847.0, NCT16521.4	203855_s_at, 213629_s_at	NP_003072.2, EAN65227.1, EAN65228.1, EAN65229.1
Gene:ENSG00000165507	SDCCAG33	9	139,296,374	139,303,054	6,680	-	1	1_A375_shN7_dhrus_bioRNA:1:36968	10174	downstream	0	1	14	16	1	2_A375_shN37_ghrs_bioRNA:1	16	Gene SDCCAG3	NY-CO-3, SDCCAG3	serologically defined colon cancer antigen 3	NM_006643, NM_001163707, NM_001163708, NCT23165311.1, NCT23165312.1, NCT23165313.1, NCT23165314.1, NCT23165315.1, NCT23165316.1, NCT23165317.1, NCT23165318.1	216527_at, 2030056_at, 2051111_at	NP_006634.3, NP_001034796.1, NP_001034797.1, EAN65230.1, EAN65231.1, EAN65232.1, EAN65129.1
Gene:ENSG00000231221	PNPCA	9	139,305,116	139,316,213	13,097	+	1	1_A375_shN37_ghrs_bioRNA:1:4139	10236	downstream	0	1	14	15	1	2_A375_shN37_ghrs_bioRNA:1	16	Gene PNPCA	INPPSE, PNPCA, PLC99258, KIAA0123, MGC104187, dJ34A16.2	peptidase (mitochondrial processing) alpha	NM_015160, NCT16195.3	212655_at	NP_055975.1, EAN65232.1
Gene:ENSG00000169623	INPPSE	9	139,323,071	139,334,296	11,165	+	2	1_A375_shN7_dhrus_bioRNA:1:36970,2_A375_shN37_ghrs_bioRNA:1:4130	1848, 1848	in gene, us gene	0	1	20	28	1	2_A375_shN37_ghrs_bioRNA:1	28	Gene INPPSE	FLJ36737, RP11-413M2.10, SEC16L, KIAA0310, SEC16A, p250	inositol polyphosphate-5-phosphatase, 72 kDa	NM_018952, NCT23165323.0, NCT23165324.0, NCT23165325.0, NCT23165326.0, NCT16051.3	2047056_at	NP_061845.2, EAN65233.1, EAN65233.1, EAN65234.1
Gene:ENSG00000169918	SEC16A	9	139,334,946	139,377,507	42,561	-	2	1_A375_shN7_dhrus_bioRNA:1:36970,2_A375_shN37_ghrs_bioRNA:1:4130	43295, 43295	downstream, downstream	1	1	20	34	1	2_A375_shN37_ghrs_bioRNA:1	34	Gene SEC16A	FLJ36737, RP11-413M2.10, SEC16L, KIAA0310, SEC16A, p250	SEC16 homolog A (S. cerevisiae)	NM_014866	219696_s_at	NP_056651.1
Gene:ENSG00000156311	FAM69B	9	139,697,024	139,819,170	122,146	+	3	1_A375_shN7_dhrus_bioRNA:1:36971,2_A375_shN37_ghrs_bioRNA:1:4171,2_A375_shN37_ghrs_bioRNA:1:4172	13728, 16272, 13744	downstream, downstream, downstream	1	1	16.5	25	2	2_A375_shN37_ghrs_bioRNA:1	34	Gene FAM69B	MGC20262, FAM69B, C9orf126, pp9977	family with sequence similarity 69, member B	NM_152421, NCT23399898.0, NCT16776.3	2060400_at, 227652_at, 236052_at, 236053_s_at	NP_689634.2, EAN65234.1, EAN65232.1
Gene:ENSG00000214873	SNHG7	9	139,819,046	139,822,836	3,790	+	3	1_A375_shN7_dhrus_bioRNA:1:36971,2_A375_shN37_ghrs_bioRNA:1:4171,2_A375_shN37_ghrs_bioRNA:1:4172	-116, 1380, -132	upstream, us gene, upstream	1	1	16.5	25	2	2_A375_shN37_ghrs_bioRNA:1	34	Gene SNHG7	SNHG7, MGC16037, NCRNA00061	small nucleolar RNA host gene 7 (non-protein coding)	NR_003672, NR_024542, NR_024543	1552724_at, 1555619_at, 236090_s_at	
Gene:ENSG00000177624	SNORA43	9	139,820,556	139,820,689	133	-	3	1_A375_shN7_dhrus_bioRNA:1:36971,2_A375_shN37_ghrs_bioRNA:1:4171,2_A375_shN37_ghrs_bioRNA:1:4172	-2060, -1607, -3079	upstream, upstream, upstream	1	1	16.5	25	2	2_A375_shN37_ghrs_bioRNA:1	34	Gene SNORA43	SNORA43, ACA43	small nucleolar RNA, H/ACA box 43	NR_002975		
Gene:ENSG00000177656	SNORA17	9	139,821,198	139,821,331	132	-	3	1_A375_shN7_dhrus_bioRNA:1:36971,2_A375_shN37_ghrs_bioRNA:1:4171,2_A375_shN37_ghrs_bioRNA:1:4172	-1421, 35, -1627	upstream, in gene, upstream	1	1	16.5	25	2	2_A375_shN37_ghrs_bioRNA:1	34	Gene SNORA17	ACA17, SNORA17	small nucleolar RNA, H/ACA box 17	NR_002955		
Gene:ENSG00000214332	LCN10	9	139,832,619	139,837,811	5,192	-	2	1_A375_shN7_dhrus_bioRNA:1:36971,2_A375_shN37_ghrs_bioRNA:1:4172	18659, 18643	downstream, downstream	1	1	26	34	1	2_A375_shN37_ghrs_bioRNA:1	34	Gene LCN10	LCN10	lipocalin 10	NM_001001712	2056071_at	NP_001001712.2
Gene:ENSG00000169654	C9orf66	9	139,702,374	139,735,639	33,265	+	6	1_A375_shN7_dhrus_bioRNA:1:36972,1_A375_shN7_dhrus_bioRNA:1:36973,1_A375_shN7_dhrus_bioRNA:1:36974,2_A375_shN37_ghrs_bioRNA:1:4173,2_A375_shN37_ghrs_bioRNA:1:4174,2_A375_shN37_ghrs_bioRNA:1:4175,2_A375_shN37_ghrs_bioRNA:1:4176	28652, 40990, 41370, 44554, 45026, 41214	downstream, downstream, downstream, downstream, downstream, downstream	1	1	22.67	21.33	3	1_A375_shN7_dhrus_bioRNA:1	33	Gene C9orf66	RBEL1, bA216L13.9, FLJ13045, FLJ10191, pp5570, KIAA1804, Fbh1, C9orf66	Chromosome 9 open reading frame 66	NM_001173955, NM_001173956, NM_024716, NCT23161581.1, NCT23161582.1, NCT23161583.1, NCT23161584.1, NCT23358270.0	219525_at, 2231995_s_at, 226377_at	NP_001167459.1, NP_001167460.1, NP_078994.2, EAN65262.1, EAN65263.1, EAN65264.1, EAN65265.1, EAN65266.1, EAN65266.1
Gene:ENSG00000169813	C9orf172	9	139,735,557	139,741,797	2,930	+	9	1_A375_shN7_dhrus_bioRNA:1:36972,1_A375_shN7_dhrus_bioRNA:1:36973,1_A375_shN7_dhrus_bioRNA:1:36974,2_A375_shN37_ghrs_bioRNA:1:4173,2_A375_shN37_ghrs_bioRNA:1:4174,2_A375_shN37_ghrs_bioRNA:1:4175,2_A375_shN37_ghrs_bioRNA:1:4176,2_A375_shN37_ghrs_bioRNA:1:4177,2_A375_shN37_ghrs_bioRNA:1:4178	-1811, 3997, 4077, -1939, 3533, 455	upstream, downstream, downstream, upstream, downstream, downstream	1	1	22.67	21.33	3	1_A375_shN7_dhrus_bioRNA:1	33	Gene C9orf172	C9orf172	Chromosome 9 open reading frame 172	NM_001080552		NP_001073551.2
Gene:ENSG00000214861	PHYHD1	9	139,743,256	139,745,990	2,734	+	9	1_A375_shN7_dhrus_bioRNA:1:36972,1_A375_shN7_dhrus_bioRNA:1:36973,1_A375_shN7_dhrus_bioRNA:1:36974,2_A375_shN37_ghrs_bioRNA:1:4173,2_A375_shN37_ghrs_bioRNA:1:4174,2_A375_shN37_ghrs_bioRNA:1:4175,2_A375_shN37_ghrs_bioRNA:1:4176,2_A375_shN37_ghrs_bioRNA:1:4177,2_A375_shN37_ghrs_bioRNA:1:4178	6200, -792, 466, 6126, 382	upstream, upstream, in gene, upstream, upstream, in gene	1	1	22.67	21.33	3	1_A375_shN7_dhrus_bioRNA:1	33	Gene PHYP1	PHYH, RP11-216L13.10, CGI-202, PHYT1, DKFZp566M170, HSPC141, MAJ-NL1.2.10	phosphoinositides phosphatase 1	NM_014172, NM_001135561, NCT23162250.0, NCT23162272.0, NCT23162280.0, NCT23162331.0	2222071_s_at, 225663_s_at	NP_054892.2, NP_001128331.1, EAN65239.1, EAN65240.1, EAN65241.1, EAN65242.1
Gene:ENSG00000169826	MAMDC4	9	139,748,818	139,783,251	34,433	+	7	1_A375_shN7_dhrus_bioRNA:1:36972,1_A375_shN7_dhrus_bioRNA:1:36973,1_A375_shN7_dhrus_bioRNA:1:36974,2_A375_shN37_ghrs_bioRNA:1:4172,2_A375_shN37_ghrs_bioRNA:1:4173,2_A375_shN37_ghrs_bioRNA:1:4174,2_A375_shN37_ghrs_bioRNA:1:4175,2_A375_shN37_ghrs_bioRNA:1:4176,2_A375_shN37_ghrs_bioRNA:1:4177	4763, -4355, 3075, 8951, 4419, 3171, 16013	upstream, downstream, downstream, downstream, downstream, downstream	1	1	20.5	21.25	4	1_A375_shN7_dhrus_bioRNA:1	33	Gene MAMDC4	MAMDC4, AEGP, DKFZp434M1411	MAM domain containing 4	NM_206820, NCT23182340.0, NCT23185005.0, NCT16777.2	228473_at	NP_996813.2, EAN65263.1, EAN65263.1, EAN65264.1
Gene:ENSG00000169721	EDF1	9	139,786,571	139,790,738	4,167	-	1	1_A375_shN7_dhrus_bioRNA:1:36976	-84	upstream	0	1	16	21	1	2_A375_shN37_ghrs_bioRNA:1	21	Gene EDF1	MGC9055, EDF-1, EDF1, MBF1	endothelial differentiation-related factor 1	NM_003792, NM_153200, NCT23178100.0, NCT23178101.0, NCT16801.1	208055_at, 208056_s_at	NP_003783.1, NP_694580.1, EAN65266.1, EAN65267.1, EAN65268.1
Gene:ENSG00000166166	TRAP2	9	139,790,955	139,821,067	40,152	+	2	1_A375_shN7_dhrus_bioRNA:1:36976,2_A375_shN37_ghrs_bioRNA:1:4139	-3925, 15355	upstream, in gene	0	1	14.5	17.5	2	2_A375_shN37_ghrs_bioRNA:1	16	Gene TRAP2	MGC45012, TRAP3, TRAP, TRAP2	TNF receptor-associated factor 2	NM_021138, NCT23182342.0, NCT23182345.0, NCT23182347.0, NCT23182348.0, NCT16779.2, NCT19819.0, NCT23181.0	204612_at	NP_065881.2, EAN65268.1, EAN65269.1, EAN65270.1, EAN65269.1
Gene:ENSG00000214861	FBXW5	9	139,834,687	139,839,173	4,286	-	3	1_A375_shN7_dhrus_bioRNA:1:36976,2_A375_shN37_ghrs_bioRNA:1:4179,2_A375_shN37_ghrs_bioRNA:1:4180	-27, -27, 5015	upstream, upstream, upstream	1	1	19	21.5	2	1_A375_shN7_dhrus_bioRNA:1	27	Gene FBXW5	MGC20982, DKFZp434B208, FBXW5, RP11-228P13.10, Fbw5	F-box and WD repeat domain containing 5	NM_018998, NCT23187987.0, NCT23187988.0, NCT23187989.0, NCT23187990.0, NCT23187991.0, NCT23187992.0, NCT23187993.0, NCT23187994.0, NCT23187995.0, NCT16195.2, NCT19803.1	2220550_s_at	NP_061871.1, EAN65268.1, EAN65268.1, EAN65269.1, EAN65270.1, EAN65271.1, EAN65272.1, EAN65273.1, EAN65274.1, EAN65275.1, EAN65276.1, EAN65315.1
Gene:ENSG00000169782	CSG	9	139,839,998	139,841,426	1,728	+	3	1_A375_shN7_dhrus_bioRNA:1:36976,2_A375_shN37_ghrs_bioRNA:1:4179,2_A375_shN37_ghrs_bioRNA:1:4180	-486, -486, 4990	upstream, upstream, downstream	1	1	19	21.5	2	1_A375_shN7_dhrus_bioRNA:1	27	Gene CSG	MGC142166, CSG, CdC	complement component 5, gamma polypeptide	NM_006606, NCT16512.4	2103224_at	NP_006597.2, EAN65316.1
Gene:ENSG00000156256	LCN12	9	139,846,766	139,849,849	3,181	+	3	1_A375_shN7_dhrus_bioRNA:1:36976,2_A375_shN37_ghrs_bioRNA:1:4179,2_A375_shN37_ghrs_bioRNA:1:4180	7565, -2050	upstream, upstream	1	1	19	21.5	2	1_A375_shN7_dhrus_bioRNA:1	27	Gene LCN12	MGC49035, LCN12, MGC33733	lipocalin 12	NM_015536, NCT23430162.0, NCT23495300.1, NCT23495631.1, NCT23509205.0	230717_at	NP_056351.2; EAN65320.1, EAN65317.1, EAN65318.1, EAN65319.1
Gene:ENSG00000214274	ABCA2	9	139,901,656	139,923,274	21,668	+	1	1_A375_shN37_ghrs_bioRNA:1:4180	-274	upstream	0	1	12	19	1	2_A375_shN37_ghrs_bioRNA:1	19	Gene ABCA2	ABC2, MGC129761, ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	NM_212533, NM_0016095, NCT23167196.0, NCT23167197.0, NCT16115.4	2109393_at, 2101103_s_at, 212772_s_at	NP_997668.1, NP_001597.2; EAN65321.1, EAN65322.1, EAN65323.1
Gene:ENSG00000169813	C9orf139	9	139,921,916	139,931,234	9,318	+	2	1_A375_shN37_ghrs_bioRNA:1:4180,2_A375_shN37_ghrs_bioRNA:1:4182	1732, 16724	in gene, downstream	0	1	10.5	16	2	2_A375_shN37_ghrs_bioRNA:1	19	Gene C9orf139	FLJ42809, C9orf139, FLJ35268	Chromosome 9 open reading frame 139	NM_207311, NCT23182370.0		NP_997394.1, EAN65324.1
Gene:ENSG00000156232	FUT7	9	139,924,636	139,927,292	2,656	-	1	1_A375_shN37_ghrs_bioRNA:1:4180	3648	downstream	0	1	12	19	1	2_A375_shN37_ghrs_bioRNA:1	19	Gene FUT7	FUT7, FucT-VII	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	NM_004479	2103506_at, 2103506_at	NP_004470.1
Gene:ENSG00000156650	NPDC1	9	139,933,909	139,940,876	6,767	-	2	1_A375_shN7_dhrus_bioRNA:1:36976,2_A375_shN37_ghrs_bioRNA:1:4180,2_A375_shN37_ghrs_bioRNA:1:4182	17028, 36	downstream, in gene	0	1	10.5	16	2	2_A375_shN37_ghrs_bioRNA:1	19	Gene NPDC1	CAB-, CAB, CAB-1, CAB1, DKFZp586J0323, NPDC1	neural proliferation, differentiation and control, 1	NM_015392, NCT23167155.1	2103596_at	NP_056207.2; EAN65328.1
Gene:ENSG00000214854	ENTPD2	9	139,942,553	139,946,305	3,932	+	1	1_A375_shN37_ghrs_bioRNA:1:4182	1565	downstream	0	1	10	17	1	2_A375_shN37_ghrs_bioRNA:1	17	Gene ENTPD2	ENTPD2, NTPDase-2, CD39L1	ectonucleoside triphosphate diphosphohydrolase 2	NM_003665, NM_001246, NCT19812.5, NCT23173.3	207272_s_at, 205430_at	NP_003656.1, NP_001237.1, EAN65330.1, EAN65331.1
Gene:ENSG00000214866	C9orf140	9	139,946,579	139,953,025	6,446	+	1	1_A375_shN37_ghrs_bioRNA:1:4183	260	in gene	0	1	9	19	1	2_A375_shN37_ghrs_bioRNA:1	19	Gene C9orf140	C9orf140, p423.3	Chromosome 9 open reading frame 140	NM_174940, NCT12931.2, NCT23183419.0	2070777_at	NP_777597.2, EAN65332.1, EAN65333.1
Gene:ENSG00000131373	UAP1L1	9	139,971,953	139,974,990	7,037	+	1	1_A375_shN37_ghrs_bioRNA:1:4183	7165	upstream	0	1	9	19	1	2_A375_shN37_ghrs_bioRNA:1	19	Gene UAP1L1	UAP1L1, RP11-229P13.16	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1	NM_007359, NCT23293.2, NCT23182660.0, NCT23570970.0, NCT23570969.0	2047553_at	NP_031922.2, EAN65340.1, EAN65340.1, EAN65342.1, EAN65343.1
Gene:ENSG00000165832	ANAPC2	9	140,099,236	140,063,057	13,821	-	2	1_A375_shN7_dhrus_bioRNA:1:36976,2_A375_shN37_ghrs_bioRNA:1:4184	48,17	in gene, us gene	1	1	46	29	1	1_A375_shN7_dhrus_bioRNA:1	46	Gene ANAPC2	RP11-330D14.3, ANAPC2, APC2	anaphase promoting complex subunit 2	NM_013366, NCT17555.3	2018553_at	NP_037486.1, EAN65361.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:8636	SSNA1	9	140,083,054	140,084,822	1,768	+	2	1_A375_pNL7_minus_lncRNA::1::5676, 2_A375_pNL97_plus_lncRNA::1::8184	-46, -14	upstream, upstream	1	1	46	29	1	1_A375_pNL7_minus_lncRNA::1	46	Gene SSNA1	NA14, N14, SSNA1, NA-14	Sjogren syndrome nuclear autoantigen 1	NM_003731, hCT2318329.0, hCT2318330.0	210378_s_at	NP_003722.2, EAW88362.1, EAW88363.1
GeneID:286262	C9orf75	9	140,086,069	140,094,980	8,911	-	2	1_A375_pNL7_minus_lncRNA::1::5676, 2_A375_pNL97_plus_lncRNA::1::8184	11972, 11940	downstream, downstream	1	1	46	29	1	1_A375_pNL7_minus_lncRNA::1	46	Gene C9orf75	MGC131933, RP11-350O14.7, C9orf75, DFNB79, FLJ90254, TPRN	chromosome 9 open reading frame 75	NM_173691, NM_001128228, hCT1963586.1	225891_at	NP_775962.2, NP_001121700.1, EAW88364.1
GeneID:142680	SLC34A3	9	140,125,209	140,131,006	5,797	+	2	1_A375_pNL7_minus_lncRNA::1::5677, 2_A375_pNL97_plus_lncRNA::1::8185	9831, 10519	downstream, downstream	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SLC34A3	HHRH, SLC34A3, NPTIIc, FLJ38680	solute carrier family 34 (sodium phosphate), member 3	NM_080877, NM_001177316, NM_001177317	1552510_at, 1569926_s_at	NP_543153.1, NP_001170787.1, NP_001170788.1
GeneID:10383	TUBB2C	9	140,135,711	140,138,159	2,448	+	2	1_A375_pNL7_minus_lncRNA::1::5677, 2_A375_pNL97_plus_lncRNA::1::8185	-671, 17	upstream, in gene	1	1	20	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene TUBB2C	TUBB2C, TUBB2	tubulin, beta 2C	NM_006088, hCT2317736.0, hCT2317740.1, hCT87437.4	208977_x_at, 213726_x_at	NP_006079.1, EAW88369.1, EAW88368.1, EAW88370.1
GeneID:401565	FAM166A	9	140,138,037	140,142,222	4,185	-	3	1_A375_pNL7_minus_lncRNA::1::5677, 1_A375_pNL7_minus_lncRNA::1::5678, 2_A375_pNL97_plus_lncRNA::1::8185	7182, -7010, 6494	downstream, upstream, downstream	1	1	18.5	19	2	2_A375_pNL97_plus_lncRNA::1	23	Gene FAM166A	FAM166A, FLJ40100, HSD46	family with sequence similarity 166, member A	NM_001001710, hCT2357050.0, hCT88120.2	1562778_at, 233971_at	NP_001001710.1, EAW88372.1, EAW88371.1
GeneID:100129722	LOC100129722	9	140,144,671	140,147,949	3,278	-	3	1_A375_pNL7_minus_lncRNA::1::5677, 1_A375_pNL7_minus_lncRNA::1::5678, 2_A375_pNL97_plus_lncRNA::1::8185	12909, -1263, 12221	downstream, upstream, downstream	1	1	18.5	19	2	2_A375_pNL97_plus_lncRNA::1	23	Gene LOC100129722		hypothetical LOC100129722	XR_113276, XR_110100, XR_114322		
GeneID:441476	C9orf173	9	140,145,730	140,147,934	2,204	+	2	1_A375_pNL7_minus_lncRNA::1::5678, 2_A375_pNL97_plus_lncRNA::1::8185	3502, -10002	downstream, upstream	1	1	18.5	19	2	2_A375_pNL97_plus_lncRNA::1	23	Gene C9orf173	FLJ40246, C9orf173	chromosome 9 open reading frame 173	NM_001004353, hCT2357045.0, hCT2357046.0, hCT88119.3	1566908_at	NP_001004353.2, EAW88374.1, EAW88375.1, EAW88376.1
GeneID:25920	COBRA1	9	140,149,759	140,168,000	18,241	+	1	1_A375_pNL7_minus_lncRNA::1::5678	-527	upstream	1	0	17	15	1	1_A375_pNL7_minus_lncRNA::1	17	Gene COBRA1	NELFB, NELF-B, DKFZp586B0519, COBRA1, KIAA1182	cofactor of BRCA1	NM_015456, hCT2317747.0, hCT1775127.2	202757_at	NP_056271.2, EAW88378.1, EAW88377.1
GeneID:54932	EXD3	9	140,201,348	140,317,714	116,366	-	1	1_A375_pNL7_minus_lncRNA::1::5679	94898	in gene	1	0	37	17	1	1_A375_pNL7_minus_lncRNA::1	37	Gene EXD3	MGC131904, mut-7, EXD3, FLJ20433, MGC74981, FLJ30442	exonuclease 3'-5' domain containing 3	NM_017820, hCT2348595.0, hCT2348596.0, hCT2348597.0, hCT2348598.0	1555914_a_at, 220838_at, 241363_at	NP_060290.3, EAW88383.1, EAW88381.1, EAW88382.1, EAW88384.1
GeneID:92715	WDR85	9	140,449,361	140,473,387	24,026	-	2	1_A375_pNL7_minus_lncRNA::1::5680, 2_A375_pNL97_plus_lncRNA::1::8186	-5, -21	upstream, upstream	1	1	62	76	1	2_A375_pNL97_plus_lncRNA::1	76	Gene WDR85	C9orf112, WDR85, RP11-48C7.3, FLJ90634	WD repeat domain 85	NM_138778, hCT2357009.0, hCT19591.1	225586_at	NP_620133.1, EAW88401.1, EAW88400.1
GeneID:116225	ZMYND19	9	140,476,531	140,484,937	8,406	-	2	1_A375_pNL7_minus_lncRNA::1::5680, 2_A375_pNL97_plus_lncRNA::1::8186	11545, 11529	downstream, downstream	1	1	62	76	1	2_A375_pNL97_plus_lncRNA::1	76	Gene ZMYND19	RP11-48C7.4, MIZIP, ZMYND19	zinc finger, MYND-type containing 19	NM_138462, hCT19596.3	227477_at	NP_612471.1, EAW88402.1
GeneID:100133077	LOC100133077	9	140,762,377	140,787,022	24,645	-	3	1_A375_pNL7_minus_lncRNA::1::5681, 2_A375_pNL97_plus_lncRNA::1::8187, 2_A375_pNL97_plus_lncRNA::1::8188	1646, 7854, 1614	in gene, in gene, in gene	1	1	33	41	2	2_A375_pNL97_plus_lncRNA::1	45	Gene LOC100133077		hypothetical LOC100133077	XR_110101, XR_114324		
GeneID:774	CACNA1B	9	140,772,241	141,019,076	246,835	+	3	1_A375_pNL7_minus_lncRNA::1::5681, 2_A375_pNL97_plus_lncRNA::1::8187, 2_A375_pNL97_plus_lncRNA::1::8188	13135, 6927, 13167	in gene, in gene, in gene	1	1	33	41	2	2_A375_pNL97_plus_lncRNA::1	45	Gene CACNA1B	CACNA1B, Cav2.2, CACNL1A5, BIII, CACNN	calcium channel, voltage-dependent, N type, alpha 1B subunit	NM_000718, hCT2317811.1, hCT2317818.1, hCT2356976.0, hCT2356977.0	207162_s_at, 235781_at	NP_000709.1, EAW88417.1, EAW88415.1, EAW88416.1, EAW88418.1
GeneID:5613	PRKX	X	3,522,384	3,631,675	109,291	-	1	2_A375_pNL97_plus_lncRNA::1::8189	15659	in gene	0	1	9	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene PRKX	PRKX, PKX1	protein kinase, X-linked	NM_005044, hCT2254209.0, hCT2254211.0, hCT9547.3	204060_s_at	NP_005035.1, EAW98727.1, EAW98726.1, EAW98728.1
GeneID:389906	LOC389906	X	3,735,576	3,761,935	26,359	-	1	2_A375_pNL97_plus_lncRNA::1::8190	28783	downstream	0	1	12	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene LOC389906	FLJ20463	hypothetical LOC389906	NR_034031	1564639_at, 1569629_x_at	
GeneID:6907	TBL1X	X	9,431,335	9,687,780	256,445	+	2	1_A375_pNL7_minus_lncRNA::1::5684, 2_A375_pNL97_plus_lncRNA::1::8194	-199, -199	upstream, upstream	1	1	36	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene TBL1X	SMAP55, TBL1, EBI, TBL1X	transducin (beta)-like 1X-linked	NM_005647, NM_001139466, NM_001139467, NM_001139468, hCT2254778.0, hCT2254782.0	1570293_at, 201867_s_at, 201868_s_at, 201869_s_at, 213400_s_at, 213401_s_at	NP_005638.1, NP_001132938.1, NP_001132939.1, NP_001132940.1, EAW98771.1, EAW98772.1
GeneID:4281	MID1	X	10,413,350	10,851,809	438,459	-	1	1_A375_pNL7_minus_lncRNA::1::5685	248961	in gene	1	0	16	8	1	1_A375_pNL7_minus_lncRNA::1	16	Gene MID1	RNF59, TRIM18, GBBB1, FLJ57031, FLJ76288, OSX, MIDIN, OGS1, FLJ58683, BBBG1, ZNFXY, XPRF, FXY, OS, MID1	midline 1 (Opitz/BBB syndrome)	NM_001098624, NM_000381, NM_033290, NM_033289, NM_001193277, NM_001193278, NM_001193279, NM_001193280, NM_001193281, hCT1955346.0, hCT2254889.0, hCT2254891.0	203636_at, 203637_s_at	NP_001092094.1, NP_000372.1, NP_150632.1, NP_150631.1, NP_001180206.1, NP_001180207.1, NP_001180208.1, NP_001180209.1, NP_001180210.1, EAW98779.1, EAW98780.1, EAW98781.1
GeneID:10943	MSL3	X	11,776,278	11,793,872	17,594	+	1	2_A375_pNL97_plus_lncRNA::1::8195	-374	upstream	0	1	10	12	1	2_A375_pNL97_plus_lncRNA::1	12	Gene MSL3	MSL3, MSL3L1, DKFZp586J1822	male-specific lethal 3 homolog (Drosophila)	NM_078628, NM_078629, NM_006800, NM_001193270, hCT1954608.1, hCT2358244.0, hCT2358245.0, hCT401192.1	207551_s_at, 214009_at	NP_523352.1, NP_523353.2, NP_006791.2, NP_001180199.1, EAW98799.1, EAW98801.1, EAW98800.1, EAW98802.1
GeneID:9758	FRMPD4	X	12,156,585	12,742,642	586,057	+	5	1_A375_pNL7_minus_lncRNA::1::5687, 1_A375_pNL7_minus_lncRNA::1::5688, 2_A375_pNL97_plus_lncRNA::1::8197, 2_A375_pNL97_plus_lncRNA::1::8198, 2_A375_pNL97_plus_lncRNA::1::8199	410407, 582711, 410359, 586391, 582807	in gene, in gene, in gene, in gene, in gene	1	1	14.67	28	3	2_A375_pNL97_plus_lncRNA::1	41	Gene FRMPD4	PDZD10, PDZK10, MGC142262, MGC142260, FRMPD4, KIAA0316	FERM and PDZ domain containing 4	NM_014728, hCT2340422.0	215052_at	NP_055543.2, EAW98804.1
GeneID:54960	GEMIN8	X	14,024,845	14,048,035	23,190	-	1	2_A375_pNL97_plus_lncRNA::1::8200	-61	upstream	0	1	13	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene GEMIN8	GEMIN8, FLJ20514, FAM51A1, FLJ43072	gem (nuclear organelle) associated protein 8	NM_017856, NM_001042480, NM_001042479, hCT10768.2, hCT1954576.0, hCT1954577.0, hCT1954578.0, hCT2256504.0, hCT2358263.0	219252_s_at, 222854_s_at, 230758_at	NP_060326.1, NP_001035945.1, NP_001035944.1, EAW98851.1, EAW98852.1, EAW98855.1, EAW98853.1, EAW98854.1, EAW98856.1
GeneID:2742	GLRA2	X	14,547,420	14,749,934	202,514	+	1	1_A375_pNL7_minus_lncRNA::1::5689	164	in gene	1	0	17	12	1	1_A375_pNL7_minus_lncRNA::1	17	Gene GLRA2	GLR, GLRA2	glycine receptor, alpha 2	NM_002063, NM_001118885, NM_001118886, NM_001171942, hCT2254972.0, hCT2254974.0, hCT5798.3	207462_at	NP_002054.1, NP_001112357.1, NP_001112358.1, NP_001165413.1, EAW98858.1, EAW98859.1, EAW98860.1
GeneID:140462	ASB9	X	15,262,109	15,288,569	26,460	-	1	1_A375_pNL7_minus_lncRNA::1::5691	36621	downstream	1	0	14	8	1	1_A375_pNL7_minus_lncRNA::1	14	Gene ASB9	DKFZp564L0862, ASB9, MGC4954, FLJ20636	ankyrin repeat and SOCS box containing 9	NM_001031739, NM_024087, NM_001168530, NM_001168531, hCT2255527.0, hCT2255529.0, hCT2255531.0, hCT2358274.0, hCT2358275.0, hCT2358276.0, hCT6782.3	205673_s_at	NP_001026909.1, NP_076992.1, NP_001162002.1, NP_001162003.1, EAW98873.1, EAW98874.1, EAW98870.1, EAW98871.1, EAW98872.1, EAW98875.1, EAW98876.1
GeneID:57393	TMEM27	X	15,645,441	15,683,154	37,713	-	2	1_A375_pNL7_minus_lncRNA::1::5692, 2_A375_pNL97_plus_lncRNA::1::8202	-9902, -10094	upstream, upstream	1	1	14	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene TMEM27	NX-17, NX17, TMEM27	transmembrane protein 27	NM_020665, hCT6771.2	223784_at	NP_065716.1, EAW98894.1
GeneID:94056	SYAP1	X	16,737,707	16,780,807	43,100	+	2	1_A375_pNL7_minus_lncRNA::1::5693, 2_A375_pNL97_plus_lncRNA::1::8204	52405, 52389	downstream, downstream	1	1	18	17	1	1_A375_pNL7_minus_lncRNA::1	18	Gene SYAP1	DKFZp686K221, FLJ14495, FLJ44185, SYAP1, PRO3113	synapse associated protein 1, SAP47 homolog (Drosophila)	NM_032796, NR_033181, hCT22666.3	225154_at	NP_116185.2, EAW98917.1
GeneID:55787	CXorf15	X	16,804,555	16,862,642	58,087	+	1	1_A375_pNL7_minus_lncRNA::1::5694	-315	upstream	1	0	17	17	1	1_A375_pNL7_minus_lncRNA::1	17	Gene CXorf15	FLJ33481, FIAT, TXLNG, ELRG, MGC126621, LSR5, MGC126625, CXorf15, FLJ11209	chromosome X open reading frame 15	NM_018360, NM_001168683, hCT11182.2	1557954_at, 219969_at, 227520_at	NP_060830.2, NP_001162154.1, EAW98918.1
GeneID:5256	PHKA2	X	18,910,416	19,002,480	92,064	-	1	2_A375_pNL97_plus_lncRNA::1::8205	-453	upstream	0	1	11	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene PHKA2	PHK, GSD9A, PYK, XLG2, XLG, MGC133071, PHKA2, PYKL	phosphorylase kinase, alpha 2 (liver)	NM_000292, hCT10652.3	1559705_s_at, 1560358_at, 209438_at, 209439_s_at	NP_000283.1, EAW98951.1
GeneID:10149	GPR64	X	19,007,425	19,140,755	133,330	-	1	2_A375_pNL97_plus_lncRNA::1::8205	137822	downstream	0	1	11	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene GPR64	GPR64, EDDM6, MGC138738, TM7LN2, FLJ00282, MGC138739, MGC104454, HE6	G protein-coupled receptor 64	NM_001079858, NM_001079859, NM_001079860, NM_001184833, NM_001184834, NM_001184835, NM_001184836, NM_001184837, NM_005756, hCT1955330.1, hCT2256198.0, hCT2358236.0, hCT2358237.0, hCT2358238.0, hCT2358239.0	206002_at	NP_001073327.1, NP_001073328.1, NP_001073329.1, NP_001171762.1, NP_001171763.1, NP_001171764.1, NP_005747.2, NP_001171765.1, NP_001171766.1, EAW98952.1, EAW98953.1, EAW98954.1, EAW98955.1, EAW98956.1, EAW98957.1
GeneID:51360	MBTPS2	X	21,857,656	21,903,541	45,885	+	1	2_A375_pNL97_plus_lncRNA::1::8209	72	in gene	0	1	15	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene MBTPS2	S2P, FLJ32174, MBTPS2, IFAP	membrane-bound transcription factor peptidase, site 2	NM_015884, hCT9812.1	1554604_at, 206473_at	NP_056968.1, EAW98982.1
GeneID:6303	SAT1	X	23,801,275	23,804,327	3,052	+	1	2_A375_pNL97_plus_lncRNA::1::8211	1925	in gene	0	1	3	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene SAT1	KFSD, SSAT-1, DC21, SAT1, KFSDX, SAT, SSAT	spermidine/spermine N1-acetyltransferase 1	NM_002970, NR_027783, hCT1964111.0, hCT8939.2	203455_s_at, 210592_s_at, 213988_s_at	NP_002961.1, EAW98999.1, EAW99000.1
GeneID:1968	EIF2S3	X	24,073,065	24,096,927	23,862	+	1	1_A375_pNL7_minus_lncRNA::1::5699	-201	upstream	1	0	19	15	1	1_A375_pNL7_minus_lncRNA::1	19	Gene EIF2S3	EIF2G, EIF2gamma, eIF-2gA, EIF2S3, EIF2	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	NM_001415, hCT1781292.2, hCT2256483.0, hCT2256484.0	205321_at, 224935_at, 224936_at	NP_001406.1, EAW99010.1, EAW99011.1, EAW99012.1
GeneID:257397	MAP3K7IP3	X	30,845,559	30,907,511	61,952	-	1	1_A375_pNL7_minus_lncRNA::1::5701	-52	upstream	1	0	15	12	1	1_A375_pNL7_minus_lncRNA::1	15	Gene MAP3K7IP3	MAP3K7IP3, TAB3, NAP1, MGC45404	TGF-beta activated kinase 1/MAP3K7 binding protein 3	NM_152787, hCT1644516.4, hCT2345101.0, hCT2358252.0	1552927_at, 1552928_s_at, 1558518_at, 227357_at	NP_690000.2, EAW99057.1, EAW99058.1, EAW99059.1
GeneID:6103	RPGR	X	38,128,423	38,186,788	58,365	-	2	1_A375_pNL7_minus_lncRNA::1::5703, 2_A375_pNL97_plus_lncRNA::1::8215	-60, -76	upstream, upstream	1	1	47	41	1	1_A375_pNL7_minus_lncRNA::1	47	Gene RPGR	XLRP3, COD1, CORDX1, RP15, PCDX, CRD, orf15, RPGR, RP3	retinitis pigmentosa GTPase regulator	NM_000328, NM_001034853, hCT1953023.1, hCT2262321.0, hCT2353419.0, hCT2353420.0	207624_s_at	NP_000319.1, NP_001030025.1, EAW59441.1, EAW59442.1, EAW59443.1, EAW59444.1
GeneID:58526	MID1IP1	X	38,660,685	38,665,785	5,100	+	1	2_A375_pNL97_plus_lncRNA::1::8216	3747	in gene	0	1	12	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene MID1IP1	THRSPL, MIG12, MID1IP1, G12-like, STRAIT11499, S14R, FLJ10386	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	NM_021242, NM_001098790, NM_001098791, hCT1787694.2, hCT2262393.0	218251_at	NP_067065.1, NP_001092260.1, NP_001092261.1, EAW59435.1, EAW59436.1
GeneID:54880	BCOR	X	39,910,499	40,036,582	126,083	-	1	2_A375_pNL97_plus_lncRNA::1::8217	1190	in gene	0	1	13	16	1	2_A375_pNL97_plus_lncRNA::1	16	Gene BCOR	ANOP2, FLJ20285, FLJ38041, MAA2, MGC131961, MGC71031, KIAA1575, MCOPS2, BCOR	BCL6 co-repressor	NM_017745, NM_001123383, NM_001123384, NM_001123385, hCT2267840.0, hCT2267841.0, hCT2267842.0, hCT2267843.0, hCT2267844.0, hCT2267845.0	219433_at, 223566_s_at, 223915_at, 223916_s_at	NP_060215.4, NP_001116855.1, NP_001116856.1, NP_001116857.1, EAW59427.1, EAW59429.1, EAW59425.1, EAW59426.1, EAW59428.1, EAW59430.1
GeneID:8239	USP9X	X	40,944,888	41,095,832	150,944	+	1	2_A375_pNL97_plus_lncRNA::1::8218	-1000	upstream	0	1	13	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene USP9X	FAM, FAF, DFFRX, USP9X	ubiquitin specific peptidase 9, X-linked	NM_001039590, NM_001039591, hCT1965609.1, hCT1965610.1, hCT1965611.1, hCT2263560.0, hCT2263564.0, hCT2263567.0, hCT9440.2	201099_at, 201100_s_at, 229573_at	NP_001034679.2, NP_001034680.2, EAW59407.1, EAW59408.1, EAW59409.1, EAW59411.1, EAW59406.1, EAW59410.1, EAW59412.1
GeneID:4128	MAOA	X	43,515,409	43,606,068	90,659	+	2	1_A375_pNL7_minus_lncRNA::1::5704, 2_A375_pNL97_plus_lncRNA::1::8219	-1425, -1409	upstream, upstream	1	1	21	22	1	2_A375_pNL97_plus_lncRNA::1	22	Gene MAOA	MAOA		NM_000240, hCT2261987.0, hCT2261988.0, hCT7868.3	204388_s_at, 204389_at, 212741_at	NP_000231.1, EAW59383.1, EAW59381.1, EAW59382.1
GeneID:8241	RBM10	X	47,004,631	47,046,212	41,581	+	4	1_A375_pNL7_minus_lncRNA::1::5707, 1_A375_pNL7_minus_lncRNA::1::5708, 2_A375_pNL97_plus_lncRNA::1::8221, 2_A375_pNL97_plus_lncRNA::1::8222	45513, 48201, 45481, 48073	downstream, downstream, downstream, downstream	1	1	26.5	32	2	2_A375_pNL97_plus_lncRNA::1	37	Gene RBM10	KIAA0122, ZRANB5, MGC997, GPATCH9, TARPS, RBM10, DXS8237E, GPATC9, FLJ40796, MGC1132	RNA binding motif protein 10	NM_005676, NM_152856, hCT1953017.1, hCT1953018.1, hCT2353405.0, hCT2353406.0, hCT2353407.0	208984_x_at, 215089_s_at, 217221_x_at	NP_005667.2, NP_690595.1, EAW59284.1, EAW59285.1, EAW59286.1, EAW59287.1, EAW59283.1
GeneID:7317	UBA1	X	47,050,199	47,074,527	24,328	+	6	1_A375_pNL7_minus_lncRNA::1::5707, 1_A375_pNL7_minus_lncRNA::1::5708, 1_A375_pNL7_minus_lncRNA::1::5709, 2_A375_pNL97_plus_lncRNA::1::8221, 2_A375_pNL97_plus_lncRNA::1::8222, 2_A375_pNL97_plus_lncRNA::1::8223	-55, 2633, 27769, -87, 2505, 27769	upstream, in gene, downstream, upstream, in gene, downstream	1	1	23.33	31	3	2_A375_pNL97_plus_lncRNA::1	37	Gene UBA1	A1S9T, MGC4781, GXP1, UBA1, UBE1, AMCX1, A1ST, UBE1X, SMAX2, A1S9, POC20, UBA1A	ubiquitin-like modifier activating enzyme 1	NM_153280, NM_003334, hCT1953019.2, hCT1968275.1, hCT2255373.0, hCT8456.4	1555387_at, 200964_at	NP_695012.1, NP_003325.2, EAW59290.1, EAW59291.1, EAW59292.1, EAW59293.1
GeneID:5127	CDK16	X	47,077,528	47,089,396	11,868	+	2	1_A375_pNL7_minus_lncRNA::1::5709, 2_A375_pNL97_plus_lncRNA::1::8223	440, 440	in gene, in gene	1	1	17	29	1	2_A375_pNL97_plus_lncRNA::1	29	Gene CDK16	PCTAIRE, PCTK1, PCTGAIRE, FLJ16665, CDK16, PCTAIRE1	cyclin-dependent kinase 16	NM_033018, NM_006201, NM_001170460, hCT1953016.1, hCT2255376.0, hCT2255380.0, hCT2255382.0, hCT8454.3	207239_s_at, 208823_s_at, 208824_x_at	NP_148978.2, NP_006192.1, NP_001163931.1, EAW59294.1, EAW59295.1, EAW59296.1, EAW59297.1, EAW59298.1
GeneID:7592	ZNF41	X	47,305,561	47,342,345	36,784	-	1	1_A375_pNL7_minus_lncRNA::1::5711	-183	upstream	1	0	16	9	1	1_A375_pNL7_minus_lncRNA::1	16	Gene ZNF41	MRX89, ZNF41, MGC8941	zinc finger protein 41	NM_007130, NM_153380, hCT1966749.1, hCT1966750.1, hCT2288105.0, hCT2288108.0, hCT2288112.0, hCT2288114.0, hCT2288118.0, hCT22886.4, hCT2353412.0	1553216_at, 1553217_s_at, 214904_at	NP_009061.1, NP_700359.1, EAW59300.1, EAW59301.1, EAW59305.1, EAW59306.1, EAW59302.1, EAW59303.1, EAW59304.1, EAW59307.1, EAW59308.1
GeneID:203414	CXorf24	X	47,333,966	47,343,288	9,322	+	1	1_A375_pNL7_minus_lncRNA::1::5711	8562	in gene	1	0	16	9	1	1_A375_pNL7_minus_lncRNA::1	16	Gene CXorf24	CXorf24	chromosome X open reading frame 24	XR_113303, XR_110617, XR_115509	239034_at	
GeneID:6853	SYN1	X	47,431,300	47,479,256	47,956	-	3	1_A375_pNL7_minus_lncRNA::1::5713, 1_A375_pNL7_minus_lncRNA::1::5714, 2_A375_pNL97_plus_lncRNA::1::8224	37411, -168, -104	in gene, upstream, upstream	1	1	19	25	2	2_A375_pNL97_plus_lncRNA::1	37	Gene SYN1	SYN1, SYN1a, SYN1b, SYNI	synapsin I	NM_133499, NM_006950, hCT1966742.0, hCT20305.3	1553264_a_at, 221914_at	NP_598006.1, NP_008881.2, EAW59313.1, EAW59314.1
GeneID:7076	TIMP1	X	47,441,690	47,446,190	4,500	+	1	1_A375_pNL7_minus_lncRNA::1::5713	155	in gene	1	0	13	13	1	1_A375_pNL7_minus_lncRNA::1	13	Gene TIMP1	CLGI, FLJ90373, TIMP1, TIMP, EPA, HCI, EPO	TIMP metallopeptidase inhibitor 1	NM_003254, hCT20301.2, hCT2257036.0	201666_at	NP_003245.1, EAW59315.1, EAW59316.1
GeneID:5199	CFP	X	47,483,612	47,489,704	6,092	-	2	1_A375_pNL7_minus_lncRNA::1::5714, 2_A375_pNL97_plus_lncRNA::1::8224	10280, 10344	downstream, downstream	1	1	25	37	1	2_A375_pNL97_plus_lncRNA::1	37	Gene CFP	PFC, PROPERDIN, CFP, PFD, BFD	complement factor properdin	NM_001145252, NM_002621, hCT20298.2, hCT2288063.0, hCT2288065.0, hCT2353413.0	206380_s_at	NP_001138724.1, NP_002612.1, EAW59317.1, EAW59318.1, EAW59319.1, EAW59320.1
GeneID:5935	RBM3	X	48,432,836	48,436,804	3,968	+	1	2_A375_pNL97_plus_lncRNA::1::8226	-68	upstream	0	1	7	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene RBM3	RBM3, RNPL, IS1-RNPL	RNA binding motif (RNP1, RRM) protein 3	NM_006743, hCT10885.3, hCT1958688.1, hCT1958691.1, hCT2352401.0	208319_s_at, 222026_at	NP_006734.1, EAW50767.1, EAW50765.1, EAW50766.1, EAW50768.1
GeneID:100506703	LOC100506703	X	48,435,420	48,439,550	4,130	-	1	2_A375_pNL97_plus_lncRNA::1::8226	6782	downstream	0	1	7	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene LOC100506703		hypothetical LOC100506703	XR_110616, XR_115510		
GeneID:64743	WDR13	X	48,455,880	48,463,582	7,702	+	1	1_A375_pNL7_minus_lncRNA::1::5716	40	in gene	1	0	17	10	1	1_A375_pNL7_minus_lncRNA::1	17	Gene WDR13	FLJ20563, WDR13, DKFZp779C2057, MG21	WD repeat domain 13	NM_017883, NM_001166426, NR_029427, hCT10908.3, hCT2263829.0, hCT2263832.0	222138_s_at	NP_060353.2, NP_001159898.1, EAW50760.1, EAW50761.1, EAW50762.1
GeneID:27238	GPKOW	X	48,969,022	48,980,079	11,057	-	2	1_A375_pNL7_minus_lncRNA::1::5717, 2_A375_pNL97_plus_lncRNA::1::8227	-129, -145	upstream, upstream	1	1	16	13	1	1_A375_pNL7_minus_lncRNA::1	16	Gene GPKOW	T54, GPKOW, Spp2, GPATCH5, GPATC5	G patch domain and KOW motifs	NM_015698, hCT10901.2	203776_at	NP_056513.2, EAW50694.1
GeneID:79917	MAGIX	X	49,019,181	49,023,836	4,655	+	1	1_A375_pNL7_minus_lncRNA::1::5718	3635	in gene	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene MAGIX	MAGIX, JM10, MGC138889, PDZX, FLJ21687	MAGI family member, X-linked	NM_001099681, NM_001099680, NM_001099682, NM_024859, hCT1640222.3, hCT2263895.0, hCT2263897.0	1563318_s_at, 1565559_at, 1565562_at, 219965_s_at, 222944_s_at, 234927_s_at	NP_001093151.1, NP_001093150.1, NP_001093152.1, NP_079135.2, EAW50691.1, EAW50692.1, EAW50693.1
GeneID:5355	PLP2	X	49,028,184	49,031,469	3,285	+	1	1_A375_pNL7_minus_lncRNA::1::5718	-5368	upstream	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene PLP2	PLP2, A4LSB, MGC126187, A4	proteolipid protein 2 (colonic epithelium-enriched)	NM_002668, hCT10900.3, hCT2263898.0	201136_at	NP_002659.1, EAW50690.1, EAW50689.1
GeneID:4007	PRICKLE3	X	49,031,906	49,042,776	10,870	-	1	1_A375_pNL7_minus_lncRNA::1::5718	19960	downstream	1	0	17	13	1	1_A375_pNL7_minus_lncRNA::1	17	Gene PRICKLE3	PRICKLE3, LMO6	prickle homolog 3 (Drosophila)	NM_006150, hCT10903.2, hCT1958711.0, hCT2262036.0	217349_s_at	NP_006141.2, EAW50688.1, EAW50686.1, EAW50687.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[A]	[B]	[C]	[D]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:6855	SYP	X	49,044,265	49,056,661	12,396	-	2	1_A375_pNL7_minus_lncRNA::1::5719, 2_A375_pNL97_plus_lncRNA::1::8228	21, 21	in gene, in gene	1	1	22	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene SYP	SYP, MRXSYP	synaptophysin	NM_003179, hCT2344593.0, hCT2344594.0	213200_at	NP_003170.1, EAW50685.1, EAW50684.1
GeneID:778	CACNA1F	X	49,061,523	49,089,833	28,310	-	2	1_A375_pNL7_minus_lncRNA::1::5719, 2_A375_pNL97_plus_lncRNA::1::8228	33193, 33193	downstream, downstream	1	1	22	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene CACNA1F	COD3, CSNBX2, CSNB2, Cav1.4, COD4, CORDX3, AIED, OA2, JM8, CORDX, JMC8, CACNA1F, CSNB2A	calcium channel, voltage-dependent, L type, alpha 1F subunit	NM_005183, hCT2344595.0, hCT2344596.0, hCT2344597.0, hCT2344598.0, hCT2344599.0, hCT2344600.0, hCT2344601.0	208377_s_at	NP_005174.2, EAW50677.1, EAW50679.1, EAW50680.1, EAW50681.1, EAW50682.1, EAW50678.1, EAW50683.1
GeneID:57477	SHROOM4	X	50,334,642	50,557,044	222,402	-	1	2_A375_pNL97_plus_lncRNA::1::8229	-1180	upstream	0	1	11	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene SHROOM4	SHAP, SHROOM4, KIAA1202	shroom family member 4	NR_027121, NM_020717, hCT1950655.1, hCT2271748.0	244625_at	NP_065768.2, EAW89917.1, EAW89916.1
GeneID:23708	GSPT2	X	51,486,481	51,489,328	2,847	+	2	1_A375_pNL7_minus_lncRNA::1::5720, 2_A375_pNL97_plus_lncRNA::1::8230	-65, -65	upstream, upstream	1	1	15	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene GSPT2	ERF3B, GSPT2, FLJ10441, GST2, eRF3b	G1 to S phase transition 2	NM_018094, hCT1786750.2	205541_s_at	NP_060564.2, EAW62898.1
GeneID:9500	MAGED1	X	51,546,155	51,645,450	99,295	+	1	1_A375_pNL7_minus_lncRNA::1::5721	-171	upstream	1	0	14	13	1	1_A375_pNL7_minus_lncRNA::1	14	Gene MAGED1	NRAGE, MAGED1, DLXIN-1	melanoma antigen family D, 1	NM_006986, NM_001005332, NM_001005333, hCT2263980.0, hCT2263981.0	209014_at	NP_008917.3, NP_001005332.1, NP_001005333.1, EAW62896.1, EAW62897.1
GeneID:8242	KDM5C	X	53,220,503	53,254,604	34,101	-	1	2_A375_pNL97_plus_lncRNA::1::8233	236	in gene	0	1	9	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene KDM5C	KDM5C, MRXSJ, JARID1C, DXS1272E, MRXJ, XE169, SMCX	lysine (K)-specific demethylase 5C	NM_004187, NM_001146702, hCT10226.3, hCT2357607.0	202383_at, 239207_at	NP_004178.2, NP_001140174.1, EAW93145.1, EAW93146.1
GeneID:23096	IQSEC2	X	53,262,058	53,350,522	88,464	-	2	2_A375_pNL97_plus_lncRNA::1::8233, 2_A375_pNL97_plus_lncRNA::1::8234	96154, 57647	downstream, in gene	0	1	11	17	2	2_A375_pNL97_plus_lncRNA::1	19	Gene IQSEC2	MRX1, BRAG1, KIAA0522, IQSEC2	IQ motif and Sec7 domain 2	NM_015075, NM_001111125, NR_024449	214619_at, 229640_at	NP_055890.1, NP_001104595.1
GeneID:10075	HUWE1	X	53,559,063	53,713,673	154,610	-	1	2_A375_pNL97_plus_lncRNA::1::8235	2633	in gene	0	1	5	19	1	2_A375_pNL97_plus_lncRNA::1	19	Gene HUWE1	MULE, ARF-BP1, lb772, HUWE1, LASU1, KIAA0312, HSPC272, UREB1, HECTH9	HECT, UBA and WWE domain containing 1	NM_031407, hCT2284385.1, hCT2284388.1, hCT2284390.1, hCT2284391.1, hCT2284393.1, hCT2284394.1, hCT2284397.1	207783_x_at, 208598_s_at, 208599_at, 214673_s_at, 236294_at	NP_113584.3, EAW93160.1, EAW93161.1, EAW93162.1, EAW93164.1, EAW93165.1, EAW93163.1, EAW93166.1
GeneID:90121	TSR2	X	54,466,853	54,471,730	4,877	+	1	2_A375_pNL97_plus_lncRNA::1::8236	-181	upstream	0	1	12	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene TSR2	WGG1, MGC20451, TSR2, DT1P1A10	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	NM_058163, hCT1967993.1, hCT9370.2	213079_at	NP_477511.1, EAW93177.1, EAW93178.1
GeneID:2245	FGD1	X	54,471,887	54,522,599	50,712	-	1	2_A375_pNL97_plus_lncRNA::1::8236	55927	downstream	0	1	12	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene FGD1	FGD1, AAS, ZFYVE3, FGDY, MRXS16	FYVE, RhoGEF and PH domain containing 1	NM_004463, hCT2279116.0, hCT2279117.0, hCT8782.2	204819_at	NP_004454.2, EAW93181.1, EAW93179.1, EAW93180.1
GeneID:169981	SPIN3	X	57,002,803	57,021,988	19,185	-	1	2_A375_pNL97_plus_lncRNA::1::8238	132	in gene	0	1	11	13	1	2_A375_pNL97_plus_lncRNA::1	13	Gene SPIN3	MGC40395, SPIN3, FLJ54952, SPIN-3, bA445O16.1, FLJ41127	spindlin family, member 3	NM_001010862, NR_027139, hCT1792819.2, hCT2278864.0	1554098_at, 1554099_a_at, 1555882_at, 1555883_s_at	NP_001010862.2, EAW93237.1, EAW93236.1
GeneID:139285	FAM123B	X	63,404,997	63,425,624	20,627	-	2	1_A375_pNL7_minus_lncRNA::1::5722, 2_A375_pNL97_plus_lncRNA::1::8239	-136, -168	upstream, upstream	1	1	22	18	1	1_A375_pNL7_minus_lncRNA::1	22	Gene FAM123B	AMER1, OSCS, FLJ39827, WTX, FAM123B	family with sequence similarity 123B	NM_152424, hCT2267544.1	1552882_a_at	NP_689637.3, EAX05415.1
GeneID:1947	EFNB1	X	68,048,840	68,062,007	13,167	+	1	2_A375_pNL97_plus_lncRNA::1::8240	8	in gene	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene EFNB1	MGC8782, LERK2, EFNB1, EFL3, CFNS, Elk-L, EPLG2, CFND	ephrin-B1	NM_004429, hCT2269902.0, hCT6094.3	202711_at	NP_004420.1, EAX05370.1, EAX05371.1
GeneID:1741	DLG3	X	69,664,705	69,725,340	60,635	+	2	1_A375_pNL7_minus_lncRNA::1::5723, 1_A375_pNL7_minus_lncRNA::1::5724	-129, 32671	upstream, in gene	1	0	17	12.5	2	1_A375_pNL7_minus_lncRNA::1	17	Gene DLG3	SAP102, XLMR, KIAA1232, DLG3, MRX, MRX90, NEDLG	discs, large homolog 3 (Drosophila)	NM_021120, NM_020730, NM_001166278, hCT2268578.0, hCT2268582.0, hCT2268583.0, hCT2268585.0, hCT2358972.0, hCT6375.3	207732_s_at, 212727_at, 212728_at, 212729_at	NP_066943.2, NP_065781.1, NP_001159750.1, EAX05333.1, EAX05334.1, EAX05336.1, EAX05335.1, EAX05337.1, EAX05338.1
GeneID:29934	SNX12	X	70,280,788	70,288,231	7,443	-	2	1_A375_pNL7_minus_lncRNA::1::5725, 2_A375_pNL97_plus_lncRNA::1::8241	-185, -153	upstream, upstream	1	1	23	19	1	1_A375_pNL7_minus_lncRNA::1	23	Gene SNX12	SNX12, MGC118983, MGC118982	sorting nexin 12	NM_013346, hCT2267911.0, hCT2267913.0, hCT2267914.0	224684_at, 231723_at	NP_037478.2, EAX05323.1, EAX05324.1, EAX05325.1
GeneID:9203	ZMYM3	X	70,459,474	70,475,047	15,573	-	2	1_A375_pNL7_minus_lncRNA::1::5726, 2_A375_pNL97_plus_lncRNA::1::8242	999, 1063	in gene, in gene	1	1	29	28	1	1_A375_pNL7_minus_lncRNA::1	29	Gene ZMYM3	ZMYM3, XFIM, MYM, ZNF261, KIAA0385, ZNF198L2, DXS6673E	zinc finger, MYM-type 3	NM_201599, NM_005096, NM_001171162, NM_001171163, hCT1969232.0, hCT1969233.1, hCT9430.2	1554171_at, 1554172_a_at, 207559_s_at	NP_963893.1, NP_005087.1, NP_001164633.1, NP_001164634.1, EAX05301.1, EAX05302.1, EAX05303.1
GeneID:5303	PIN4	X	71,401,526	71,483,814	82,288	+	1	2_A375_pNL97_plus_lncRNA::1::8243	74	in gene	0	1	12	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene PIN4	MGC138486, PAR14, EPVH, PIN4, PAR17	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	NM_006223, NM_001170747, NR_033187, hCT201193.2	204571_x_at	NP_006214.2, NP_001164218.1, EAW71812.1
GeneID:6191	RPS4X	X	71,492,453	71,497,141	4,688	-	2	1_A375_pNL7_minus_lncRNA::1::5727, 2_A375_pNL97_plus_lncRNA::1::8244	-11, 21	upstream, in gene	1	1	45	52	1	2_A375_pNL97_plus_lncRNA::1	52	Gene RPS4X	RPS4X, S4, SCR10, CCG2, RPS4, SCAR, DXS306, FLJ40595	ribosomal protein S4, X-linked	NM_001007, hCT2272246.0, hCT2272247.0, hCT9696.3	200933_x_at, 213347_x_at	NP_000998.1, EAW71816.1, EAW71815.1, EAW71817.1
GeneID:4435	CITED1	X	71,521,488	71,527,037	5,549	-	2	1_A375_pNL7_minus_lncRNA::1::5728, 2_A375_pNL97_plus_lncRNA::1::8245	125, 189	in gene, in gene	1	1	22	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CITED1	MSG1, CITED1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	NM_004143, NM_001144885, NM_001144886, NM_001144887, hCT2272243.0, hCT2272244.0, hCT8661.3	207144_s_at	NP_004134.2, NP_001138357.1, NP_001138358.1, NP_001138359.1, EAW71818.1, EAW71820.1, EAW71819.1
GeneID:55869	HDAC8	X	71,549,366	71,792,953	243,587	-	1	2_A375_pNL97_plus_lncRNA::1::8246	111161	in gene	0	1	9	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene HDAC8	CDA07, HDAC8, RPD3, HDACL1, HD8	histone deacetylase 8	NM_001166448, NM_018486, NM_001166418, NM_001166419, NM_001166422, NM_001166420, hCT2272239.0, hCT2272240.0, hCT2272242.0, hCT9698.2	223345_at, 223908_at, 223909_s_at	NP_001159920.1, NP_060956.1, NP_001159890.1, NP_001159891.1, NP_001159894.1, NP_001159892.1, EAW71821.1, EAW71822.1, EAW71823.1, EAW71824.1
GeneID:22	ABCB7	X	74,273,105	74,376,132	103,027	-	1	1_A375_pNL7_minus_lncRNA::1::5730	100	in gene	1	0	20	14	1	1_A375_pNL7_minus_lncRNA::1	20	Gene ABCB7	ABC7, ABCB7, Atm1p, EST140535, ASAT	ATP-binding cassette, sub-family B (MDR/TAP), member 7	NM_004299, hCT10436.3, hCT2272048.0, hCT2343412.0, hCT2343413.0, hCT2343414.0, hCT2358232.0	209620_s_at	NP_004290.2, EAW98634.1, EAW98632.1, EAW98633.1, EAW98636.1, EAW98637.1, EAW98635.1
GeneID:139596	UPRT	X	74,493,894	74,524,732	30,838	+	1	2_A375_pNL97_plus_lncRNA::1::8248	58	in gene	0	1	9	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene UPRT	FUR1, MGC23937, UPRT, DKFZp781E1243, UPP	uracil phosphoribosyltransferase (FUR1) homolog (S.cerevisiae)	NM_145052, NR_030774, hCT11406.3, hCT1966372.1	226199_at	NP_659489.1, EAW98631.1, EAW98630.1
GeneID:5230	PGK1	X	77,359,666	77,382,324	22,658	+	1	1_A375_pNL7_minus_lncRNA::1::5731	46	in gene	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene PGK1	MGC117307, MGC142128, PGK1, PGKA, MGC8947, MIG10	phosphoglycerate kinase 1	NM_000291, hCT11106.3, hCT1950114.2, hCT2274608.1	200737_at, 200738_s_at, 217356_s_at, 217383_at, 227068_at	NP_000282.1, EAW98604.1, EAW98602.1, EAW98603.1
GeneID:695	BTK	X	100,604,435	100,641,212	36,777	-	2	1_A375_pNL7_minus_lncRNA::1::5732, 2_A375_pNL97_plus_lncRNA::1::8249	-4644, -4676	upstream, upstream	1	1	23	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene BTK	AT, PSCTK1, MGC126262, ATK, IMD1, BTK, BPK, MGC126261, XLA, AGMX1	Bruton agammaglobulinemia tyrosine kinase	NM_000061, hCT11477.1, hCT1954588.1, hCT2358868.0	205504_at	NP_000052.1, EAX02856.1, EAX02857.1, EAX02858.1
GeneID:6173	RPL36A	X	100,645,948	100,650,783	4,835	+	2	1_A375_pNL7_minus_lncRNA::1::5732, 2_A375_pNL97_plus_lncRNA::1::8249	-92, -60	upstream, upstream	1	1	23	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene RPL36A	RPL36A, RPL44, MGC72020, L44L, MIG6, L36A	ribosomal protein L36a	NM_021029, hCT2265339.0, hCT2265340.0, hCT2265341.0	201406_at	NP_066357.1, EAX02859.1, EAX02860.1, EAX02861.1
GeneID:2717	GLA	X	100,652,779	100,663,001	10,222	-	2	1_A375_pNL7_minus_lncRNA::1::5732, 2_A375_pNL97_plus_lncRNA::1::8249	17145, 17113	downstream, downstream	1	1	23	30	1	2_A375_pNL97_plus_lncRNA::1	30	Gene GLA	GALA, GLA	galactosidase, alpha	NM_000169, hCT11478.2, hCT1954590.1	214430_at	NP_000160.1, EAX02862.1, EAX02863.1
GeneID:401612	MCART6	X	103,343,898	103,401,708	57,810	-	4	1_A375_pNL7_minus_lncRNA::1::5733, 1_A375_pNL7_minus_lncRNA::1::5734, 2_A375_pNL97_plus_lncRNA::1::8250, 2_A375_pNL97_plus_lncRNA::1::8251	188, -9300, 204, -9380	in gene, upstream, in gene, upstream	1	1	20	28	2	2_A375_pNL97_plus_lncRNA::1	32	Gene MCART6	MCART6, DKFZp686O1267	mitochondrial carrier triple repeat 6	NM_001012755	1561578_s_at, 1561660_at	NP_001012773.2
GeneID:139231	CXorf39	X	103,411,301	103,436,127	24,826	+	4	1_A375_pNL7_minus_lncRNA::1::5733, 1_A375_pNL7_minus_lncRNA::1::5734, 2_A375_pNL97_plus_lncRNA::1::8250, 2_A375_pNL97_plus_lncRNA::1::8251	-9781, -293, -9797, -213	upstream, upstream, upstream, upstream	1	1	20	28	2	2_A375_pNL97_plus_lncRNA::1	32	Gene CXorf39	FAM199X, CXorf39	family with sequence similarity 199, X-linked	NM_207318, hCT2280924.0, hCT2280925.0, hCT2280927.0, hCT2280929.0	225216_at, 227133_at, 242781_at	NP_997201.1, EAX02757.1, EAX02758.1, EAX02759.1, EAX02760.1
GeneID:5716	PSMD10	X	107,327,437	107,334,848	7,411	-	1	1_A375_pNL7_minus_lncRNA::1::5735	-32	upstream	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene PSMD10	dJ889N15.2, PSMD10, p28(GANK), p28	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	NM_002814, NM_170750, hCT12776.3, hCT1962546.1	1554577_a_at, 219485_s_at	NP_002805.1, NP_736606.1, EAX02697.1, EAX02698.1
GeneID:115201	ATG4A	X	107,334,934	107,397,896	62,962	+	1	1_A375_pNL7_minus_lncRNA::1::5735	-54	upstream	1	0	14	12	1	1_A375_pNL7_minus_lncRNA::1	14	Gene ATG4A	ATG4A, AUTL2, APG4A	ATG4 autophagy related 4 homolog A (S. cerevisiae)	NM_178270, NM_052936, hCT12779.3, hCT1966461.1, hCT1966462.1, hCT1966463.1, hCT2280713.0, hCT2280714.0, hCT2280715.0, hCT2355676.0	213115_at	NP_840054.1, NP_443168.2, EAX02689.1, EAX02691.1, EAX02693.1, EAX02695.1, EAX02690.1, EAX02692.1, EAX02694.1, EAX02696.1
GeneID:9949	AMMECR1	X	109,437,414	109,683,461	246,047	-	1	2_A375_pNL97_plus_lncRNA::1::8253	45157	in gene	0	1	6	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene AMMECR1	AMMECR1, AMMERC1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	NM_015365, NM_001025580, NM_001171689, hCT11378.3	1553219_a_at, 204976_s_at, 226421_at, 236760_at	NP_056180.1, NP_001020751.1, NP_001165160.1, EAX02663.1
GeneID:6170	RPL39	X	118,920,469	118,925,606	5,137	-	1	2_A375_pNL97_plus_lncRNA::1::8254	198	in gene	0	1	12	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene RPL39	RPL39, L39	ribosomal protein L39	NM_001000, hCT2286179.0, hCT2286181.0, hCT2286182.0	208695_s_at	NP_000991.1, EAW89849.1, EAW89847.1, EAW89848.1
GeneID:26779	SNORA69	X	118,921,316	118,921,447	131	-	1	2_A375_pNL97_plus_lncRNA::1::8254	-3961	upstream	0	1	12	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene SNORA69	U69, RNU69, U69A, SNORA69	small nucleolar RNA, H/ACA box 69	NR_002584		
GeneID:7737	RNF113A	X	119,004,495	119,005,791	1,296	-	1	2_A375_pNL97_plus_lncRNA::1::8255	-46	upstream	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene RNF113A	ZNF183, RNF113A, Cwc24, RNF113	ring finger protein 113A	NM_006978, hCT13586.2	209565_at	NP_008909.1, EAW89841.1
GeneID:4694	NDUFA1	X	119,005,734	119,010,629	4,895	+	1	2_A375_pNL97_plus_lncRNA::1::8255	103	in gene	0	1	11	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene NDUFA1	ZNF183, MWFE, NDUFA1, CI-MWFE	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	NM_004541, hCT14289.2	202298_at	NP_004532.1, EAW89840.1
GeneID:79576	NKAP	X	119,059,013	119,077,735	18,722	-	1	1_A375_pNL7_minus_lncRNA::1::5736	39	in gene	1	0	14	13	1	1_A375_pNL7_minus_lncRNA::1	14	Gene NKAP	NKAP, FLJ22626	NFKB activating protein	NM_024528, hCT14294.2	223439_at	NP_078804.2, EAW89838.1
GeneID:28985	MCTS1	X	119,737,744	119,755,014	17,270	+	1	2_A375_pNL97_plus_lncRNA::1::8256	26064	downstream	0	1	6	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene MCTS1	MCT1, MCTS1, MCT-1, FLJ39637	malignant T cell amplified sequence 1	NM_014060, NM_001137554, hCT1816107.1, hCT2253759.0	218163_at	NP_054779.1, NP_001131026.1, EAX11874.1, EAX11875.1
GeneID:29071	C1GALT1C1	X	119,759,529	119,764,005	4,476	-	1	2_A375_pNL97_plus_lncRNA::1::8256	197	in gene	0	1	6	17	1	2_A375_pNL97_plus_lncRNA::1	17	Gene C1GALT1C1	MGC19947, COSMC, MST143, C38H2-L1, C1GALT1C1, HSPC067, C1GALT2	C1GALT1-specific chaperone 1	NM_152692, NM_001011551, hCT32025.2	1555573_at, 219283_at, 238969_at	NP_689905.1, NP_001011551.1, EAX11873.1
GeneID:4952	OCRL	X	128,674,252	128,726,533	52,281	+	2	1_A375_pNL7_minus_lncRNA::1::5737, 2_A375_pNL97_plus_lncRNA::1::8257	-12, 20	upstream, in gene	1	1	34	28	1	1_A375_pNL7_minus_lncRNA::1	34	Gene OCRL	NPHL2, INPP5F, OCRL1, LOCR, OCRL	oculocerebrorenal syndrome of Lowe	NM_001587, NM_000276, hCT11785.2, hCT2253443.0, hCT2253445.0	203446_s_at, 208316_s_at	NP_001578.2, NP_000267.2, EAX11830.1, EAX11831.1, EAX11832.1
GeneID:9131	AIFM1	X	129,263,337	129,299,861	36,524	-	2	1_A375_pNL7_minus_lncRNA::1::5738, 2_A375_pNL97_plus_lncRNA::1::8258	-267, -219	upstream, upstream	1	1	24	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene AIFM1	COXPD6, AIF, AIFM1, MGC111425, PDCD8	apoptosis-inducing factor, mitochondrion-associated, 1	NM_145813, NM_001130846, NM_001130847, NM_004208, NM_145812, hCT12083.3, hCT1967914.1, hCT2253686.0	205512_s_at	NP_665812.1, NP_001124318.1, NP_665811.1, NP_001124319.1, NP_004199.1, EAX11811.1, EAX11810.1, EAX11812.1
GeneID:9363	RAB33A	X	129,305,773	129,318,844	13,071	+	2	1_A375_pNL7_minus_lncRNA::1::5738, 2_A375_pNL97_plus_lncRNA::1::8258	-5645, -5693	upstream, upstream	1	1	24	26	1	2_A375_pNL97_plus_lncRNA::1	26	Gene RAB33A	RAB33A, MGC1488, RabS10	RAB33A, member RAS oncogene family	NM_004794, hCT12089.3	206039_at	NP_004785.1, EAX11808.1
GeneID:56180	MOSPD1	X	134,021,662	134,049,297	27,635	-	1	1_A375_pNL7_minus_lncRNA::1::5739	49	in gene	1	0	15	16	1	1_A375_pNL7_minus_lncRNA::1	15	Gene MOSPD1	DJ473B4, MOSPD1	motile sperm domain containing 1	NM_019556, hCT2253259.0, hCT2253260.0	1557455_s_at, 218853_s_at	NP_062456.1, EAX11743.1, EAX11744.1
GeneID:203522	DDX26B	X	134,654,555	134,716,460	61,905	+	1	2_A375_pNL97_plus_lncRNA::1::8259	-155	upstream	0	1	17	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene DDX26B	DKFZp686G0470, DDX26B, FLJ41215, MGC88298	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	NM_182540, hCT2359693.0, hCT2359694.0, hCT5784.4	227485_at	NP_872346.3, EAX11727.1, EAX11725.1, EAX11726.1
GeneID:541465	CT45A6	X	134,963,215	134,971,244	8,029	-	1	2_A375_pNL97_plus_lncRNA::1::8261	-4532	upstream	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene CT45A6	CT45-6, CT45A6, CT45.6, CT45A4	cancer/testis antigen family 45, member A6	NM_001017438		NP_001017438.1
GeneID:55511	SAGE1	X	134,975,785	134,995,220	19,435	+	1	2_A375_pNL97_plus_lncRNA::1::8261	-9	upstream	0	1	13	23	1	2_A375_pNL97_plus_lncRNA::1	23	Gene SAGE1	SAGE1, CT14, SAGE	sarcoma antigen 1	NM_018666, hCT24294.2	220793_at	NP_061136.2, EAW88486.1
GeneID:10479	SLC9A6	X	135,067,583	135,129,428	61,845	+	1	2_A375_pNL97_plus_lncRNA::1::8262	1	in gene	0	1	10	20	1	2_A375_pNL97_plus_lncRNA::1	20	Gene SLC9A6	MRSA, SLC9A6, NHE6, KIAA0267	solute carrier family 9 (sodium/hydrogen exchanger), member 6	NM_001042537, NM_006359, NM_001177651, hCT2251570.0, hCT24293.2	203909_at	NP_001036002.1, NP_006350.1, NP_001171122.1, EAW88481.1, EAW88482.1
GeneID:3149	HMGB3	X	150,151,763	150,159,248	7,485	+	2	1_A375_pNL7_minus_lncRNA::1::5743, 2_A375_pNL97_plus_lncRNA::1::8264	-83, -115	upstream, upstream	1	1	27	28	1	2_A375_pNL97_plus_lncRNA::1	28	Gene HMGB3	HMG2A, HMGB3, MGC90319, HMG4	high mobility group box 3	NM_005342, hCT1953033.1, hCT30487.3	203744_at, 225601_at	NP_005333.2, EAW99398.1, EAW99397.1
GeneID:1260	CNGA2	X	150,903,218	150,914,036	10,818	+	1	2_A375_pNL97_plus_lncRNA::1::8265	18830	downstream	0	1	12	18	1	2_A375_pNL97_plus_lncRNA::1	18	Gene CNGA2	FLJ46312, CNG2, CNGA2, OCNCa, CNCA1, OCNC1, CNCA, OCNCALPHA	cyclic nucleotide gated channel alpha 2	NM_005140, hCT29954.3		NP_005131.1, EAW99409.1
GeneID:1069	CETN2	X	151,995,871	151,999,301	3,430	-	1	2_A375_pNL97_plus_lncRNA::1::8266	-187	upstream	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene CETN2	CEN2, CETN2, CALT	centrin, EF-hand protein, 2	NM_004344, hCT30824.2	209194_at	NP_004335.1, EAW72900.1
GeneID:50814	NSDHL	X	151,999,511	152,037,907	38,396	+	1	2_A375_pNL97_plus_lncRNA::1::8266	-23	upstream	0	1	10	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene NSDHL	XAP104, SDR31E1, NSDHL, H105E3	NAD(P) dependent steroid dehydrogenase-like	NM_015922, NM_001129765, hCT2286452.0, hCT2355080.0, hCT30825.3	209279_s_at, 215093_at	NP_057006.1, NP_001123237.1, EAW72897.1, EAW72898.1, EAW72899.1
GeneID:3897	L1CAM	X	153,126,971	153,141,399	14,428	-	2	1_A375_pNL7_minus_lncRNA::1::5744, 2_A375_pNL97_plus_lncRNA::1::8267	391, 375	in gene, in gene	1	1	29	46	1	2_A375_pNL97_plus_lncRNA::1	46	Gene L1CAM	L1CAM, S10, HSAS1, MASA, MIC5, HSAS, CD171, SPG1, N-CAML1, CAML1	L1 cell adhesion molecule	NM_000425, NM_024003, NM_001143963, hCT2291422.0, hCT2291423.0, hCT2291425.0	204584_at, 204585_s_at	NP_000416.1, NP_076493.1, NP_001137435.1, EAW72787.1, EAW72788.1, EAW72789.1
GeneID:2316	FLNA	X	153,576,900	153,603,006	26,106	-	2	1_A375_pNL7_minus_lncRNA::1::5745, 2_A375_pNL97_plus_lncRNA::1::8268	3374, 3326	in gene, in gene	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene FLNA	ABP-280, FLN1, DKFZp434P031, NHBP, OPD, XMVD, XLVD, FLN, CVD1, MNS, FMD, ABPX, OPD1, FLNA, OPD2	filamin A, alpha	NM_001456, NM_001110556, hCT1958082.1, hCT2291391.0, hCT2291392.0, hCT2291393.0, hCT32611.2	200859_x_at, 213746_s_at, 214752_x_at	NP_001447.2, NP_001104026.1, EAW72744.1, EAW72746.1, EAW72747.1, EAW72748.1, EAW72745.1
GeneID:2010	EMD	X	153,607,597	153,609,883	2,286	+	2	1_A375_pNL7_minus_lncRNA::1::5745, 2_A375_pNL97_plus_lncRNA::1::8268	-7965, -7917	upstream, upstream	1	1	24	27	1	2_A375_pNL97_plus_lncRNA::1	27	Gene EMD	EMD, EDMD, LEMD5, STA	emerin	NM_000117, hCT1966414.1, hCT32613.2	209477_at	NP_000108.1, EAW72743.1, EAW72742.1
GeneID:100507387	LOC100507387	X	153,625,054	153,627,361	2,307	-	2	1_A375_pNL7_minus_lncRNA::1::5746, 2_A375_pNL97_plus_lncRNA::1::8269	721, 769	in gene, in gene	1	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene LOC100507387		hypothetical LOC100507387	XR_110937, XR_115614		
GeneID:6134	RPL10	X	153,626,571	153,630,680	4,109	+	3	1_A375_pNL7_minus_lncRNA::1::5746, 2_A375_pNL97_plus_lncRNA::1::8269, 2_A375_pNL97_plus_lncRNA::1::8270	69, 21, 13237	in gene, in gene, downstream	1	1	13	19.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene RPL10	L10, FLJ23544, DXS648E, FLJ27072, DXS648, DKFZp686J1851, RPL10, QM, NOV	ribosomal protein L10	NM_006013, NR_026898, hCT2296095.0, hCT2296096.0, hCT2296098.0, hCT2296100.0, hCT2296101.0, hCT2296104.0	1569188_s_at, 200724_at, 200725_x_at, 221989_at	NP_006004.2, EAW72741.1, EAW72736.1, EAW72737.1, EAW72739.1, EAW72740.1, EAW72738.1
GeneID:26778	SNORA70	X	153,628,622	153,628,756	134	+	2	1_A375_pNL7_minus_lncRNA::1::5746, 2_A375_pNL97_plus_lncRNA::1::8269	-1982, -2030	upstream, upstream	1	1	16	24	1	2_A375_pNL97_plus_lncRNA::1	24	Gene SNORA70	U70, DXS648E, SNORA70, RNU70	small nucleolar RNA, H/ACA box 70	NR_000011		
GeneID:1774	DNASE1L1	X	153,629,579	153,640,427	10,848	-	3	1_A375_pNL7_minus_lncRNA::1::5746, 2_A375_pNL97_plus_lncRNA::1::8269, 2_A375_pNL97_plus_lncRNA::1::8270	13787, 13835, 619	downstream, downstream, in gene	1	1	13	19.5	2	2_A375_pNL97_plus_lncRNA::1	24	Gene DNASE1L1	DNASE1L1, DNASEX, DNL1L, XIB, DNAS1L1	deoxyribonuclease I-like 1	NM_006730, NM_001009932, NM_001009933, NM_001009934, hCT1958052.1, hCT1958053.0, hCT1959908.1, hCT1959909.1, hCT1959910.1	203912_s_at	NP_006721.1, NP_001009932.1, NP_001009933.1, NP_001009934.1, EAW72734.1, EAW72735.1, EAW72731.1, EAW72732.1, EAW72733.1
GeneID:6901	TAZ	X	153,639,877	153,650,065	10,188	+	1	2_A375_pNL97_plus_lncRNA::1::8270	-69	upstream	0	1	10	15	1	2_A375_pNL97_plus_lncRNA::1	15	Gene TAZ	CMD3A, EFE2, BTHS, LVNCX, Taz1, G4.5, FLJ27390, TAZ, XAP-2, EFE	tafazzin	NM_000116, NM_181312, NM_181311, NM_181313, NR_024048, hCT1959897.1, hCT1959898.1, hCT1959899.1, hCT1959900.1, hCT1959901.1, hCT1959902.1, hCT2296110.0, hCT2296112.0, hCT2296113.0, hCT2355088.0, hCT2355089.0, hCT2355090.0, hCT2355091.0, hCT32610.3	203977_at, 37278_at	NP_000107.1, NP_851829.1, NP_851828.1, NP_851830.1, EAW72722.1, EAW72724.1, EAW72717.1, EAW72718.1, EAW72719.1, EAW72720.1, EAW72721.1, EAW72723.1, EAW72725.1, EAW72726.1, EAW72727.1, EAW72728.1, EAW72729.1, EAW72730.1
GeneID:116442	RAB39B	X	154,487,526	154,493,852	6,326	-	2	1_A375_pNL7_minus_lncRNA::1::5747, 2_A375_pNL97_plus_lncRNA::1::8271	92, 124	in gene, in gene	1	1	17	21	1	2_A375_pNL97_plus_lncRNA::1	21	Gene RAB39B	RAB39B, MRX72		NM_171998, hCT9100.2	230075_at, 238695_s_at	NP_741995.1, EAW72626.1
GeneID:55217	TMLHE	X	154,718,672	154,842,622	123,950	-	1	2_A375_pNL97_plus_lncRNA::1::8272	446	in gene	0	1	14	14	1	2_A375_pNL97_plus_lncRNA::1	14	Gene TMLHE	TMLHE, FLJ10727, TMLH, XAP130, BBOX2	trimethyllysine hydroxylase, epsilon	NM_001184797, NM_018196, hCT1958051.1, hCT2273001.0, hCT8662.3	1554206_at, 218790_s_at, 222744_s_at	NP_001171726.1, NP_060666.1, EAW55873.1, EAW55874.1, EAW55875.1

Table 9B. Genes differentially bound by AR

TAble 9B lists the genes that are differentially bound by AR in the presence or absence of AR as determines via MACS.

Annotations:

[1] 1_pNL7_minus_increased::1 Present

[2] 2_pNL97_plus_increased::1 Present

[3] 1_pNL7_minus_increased::1 AvgPeak

[4] 2_pNL97_plus_increased::1 AvgPeak

Table 9B

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[1]	[2]	[3]	[4]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID: 81669	CCNL2	1	1,321,091	1,334,718	13,627	+	1	2_pNL97_plus_increased::1:1:0	-80666	upstream	0	1	11	38	1	2_pNL97_plus_increased::1	30	Gene CCNL2	HLA-ISO, ANXA6B, CCNM, IBR1B, PCEE, DKFZp761A1210, HDLA-ISO, DKFZp762C165, CCNL2	cyclin L2	NM_030937, NM_001039577, hCT1502.2, hCT1609975.2, hCT1954521.1, hCT1954522.1, hCT1954522.1, hCT2275736.0, hCT2275739.0	225555_x_at	NP_112199.2, NP_001034666.1, EAW56212.1, EAW56213.1, EAW56215.1, EAW56217.1, EAW56211.1, EAW56214.1, EAW56216.1
GeneID: 148413	LOC144413	1	1,334,910	1,337,426	2,516	+	1	2_pNL97_plus_increased::1:1:0	7874	downstream	0	1	11	38	1	2_pNL97_plus_increased::1	30	Gene LOC148413		hypothetical LOC148413	NR_015434	225920_at, 225934_at	
GeneID: 55052	MRPL20	21	1,337,276	1,342,693	5,417	-	1	2_pNL97_plus_increased::1:1:0	-91	upstream	0	1	11	38	1	2_pNL97_plus_increased::1	30	Gene MRPL20	MGC74465, MRP-L20, MGC4779, L20mt, MRPL20	mitochondrial ribosomal protein L20	NM_017971, hCT11496.3, hCT1954901.1, hCT1954902.1	220526_s_at, 220527_at, 224883_s_at	NP_060441.2, EAW56208.1, EAW56207.1, EAW56209.1
GeneID: 55450	CAMK2N1	21	20,808,884	20,812,728	3,844	-	1	2_pNL97_plus_increased::1:1:2	-2051	in gene	0	1	5	18	1	2_pNL97_plus_increased::1	18	Gene CAMK2N1	RP11-443M16.1, CAMK2N1, MGC22256, PRO1489	calcium/calmodulin-dependent protein kinase II inhibitor 1	NM_018584, hCT1955778.2, hCT2842804	210309_at, 228302_x_at, 229163_at	NP_061854.2, EAW84924.1, EAW84923.1
GeneID: 127396	ZNF684	1	40,997,233	41,013,841	16,608	+	1	2_pNL97_plus_increased::1:1:3	127	in gene	0	1	9	21	1	2_pNL97_plus_increased::1	21	Gene ZNF684	ZNF684, MGC27466	zinc finger protein 684	NM_152373, hCT12963.3, hCT2335695.0	232563_at, 244398_x_at	NP_689586.3, EAX07208.1, EAX07209.1
GeneID: 84042	HPDL	1	45,782,545	45,794,347	11,802	+	1	2_pNL97_plus_increased::1:1:4	479	in gene	0	1	8	22	1	2_pNL97_plus_increased::1	22	Gene HPDL	MGC15668, HPDL, RP4-534D1.1, GLOXD1, 4-HPPD-L	4-hydroxyphenylpyruvate dioxygenase-like	NM_032756, hCT1633803.1	229332_at	NP_116145.1, EAX07802.1
GeneID: 4585	MUTYH	1	45,794,914	45,806,142	11,228	-	1	2_pNL97_plus_increased::1:1:4	13118	downstream	0	1	8	22	1	2_pNL97_plus_increased::1	22	Gene MUTYH	MYH, MGC4416, CYP2C, MUTYH	mutY homolog (E. coli)	NM_012222, NM_001048171, NM_001048172, NM_001048173, NM_001048174, NM_001128425, hCT1810872.3, hCT1966772.1, hCT2359120.0, hCT2359121.0, hCT2359122.0, hCT2359123.0, hCT2359124.0, hCT2359125.0, hCT2359126.0, hCT2359127.0, hCT2359128.0	207727_s_at	NP_036354.1, NP_001041636.1, NP_001041637.1, NP_001041638.1, NP_001041639.1, NP_001121097.1, EAX06991.1, EAX06992.1, EAX06993.1, EAX06994.1, EAX06995.1, EAX06996.1, EAX06997.1, EAX07001.1, EAX06998.1, EAX06999.1, EAX07000.1
GeneID: 10207	INADL	1	62,208,149	62,629,592	421,443	+	1	2_pNL97_plus_increased::1:1:5	250955	in gene	0	1	8	23	1	2_pNL97_plus_increased::1	23	Gene INADL	INADL, FLJ28982, PATJ, hINADL, Cipp	InaD-like (Drosophila)	NM_176877, hCT1951994.2, hCT2344414.1, hCT2334417.1, hCT2344418.1	214493_s_at, 214765_at, 222681_s_at, 232041_at, 238173_at	NP_795352.2, EAX06598.1, EAX06593.1, EAX06594.1, EAX06595.1
GeneID: 10542	HBXIP	1	110,943,875	110,950,546	6,671	-	1	2_pNL97_plus_increased::1:1:6	306	in gene	0	1	14	28	1	2_pNL97_plus_increased::1	28	Gene HBXIP	XIP, HBXIP, MGC71071	hepatitis B virus x interacting protein	NM_006402, hCT31507.3	202299_s_at, 202300_at	NP_006383.2, EAX06447.1
GeneID: 126868	C1orf161	1	116,654,376	116,677,861	23,485	+	1	2_pNL97_plus_increased::1:1:7	11320	in gene	0	1	7	18	1	2_pNL97_plus_increased::1	18	Gene C1orf161	MAB21L3, FLJ38716, RP5-1185H19.1, C1orf161	chromosome 1 open reading frame 161	NM_152367, hCT2278531.1, hCT2344824.0	1553333_at	NP_689580.2, EAW56643.1, EAW56642.1
GeneID: 6282	S100A11	1	152,004,982	152,009,511	4,529	-	1	2_pNL97_plus_increased::1:1:8	7703	downstream	0	1	10	22	1	2_pNL97_plus_increased::1	22	Gene S100A11	MLN70, S100D	S100 calcium binding protein A11	NM_005620, hCT7662.2	200660_at	NP_005611.1, EAX03392.1
GeneID: 2494	NR5A2	1	199,996,770	200,146,552	149,782	+	1	2_pNL97_plus_increased::1:1:10	152038	downstream	0	1	14	18	1	2_pNL97_plus_increased::1	18	Gene NR5A2	FTZ-F1beta, FTF, NR5A2, hB1F, LRH-1, hB1F-2, LRH1, CPF, B1F2, B1F, FTZ-F1	nuclear receptor subfamily 5, group A, member 2	NM_003822, NM_205860, hCT10323.3, hCT1951270.1, hCT2323911.0, hCT2323912.0	1560469_at, 208337_s_at, 208343_s_at, 210174_at	NP_003813.1, NP_995582.1, EAW81305.1, EAW81306.1, EAW81307.1, EAW81308.1
GeneID: 100188847	LOC100188847	10	93,066,719	93,299,337	232,618	-	1	2_pNL97_plus_increased::1:1:12	27721	in gene	0	1	8	19	1	2_pNL97_plus_increased::1	19	Gene LOC100188847		hypothetical LOC100188847	NR_024467		
GeneID: 143279	HECTD2	10	93,170,090	93,274,528	104,424	+	1	2_pNL97_plus_increased::1:1:12	101520	in gene	0	1	8	19	1	2_pNL97_plus_increased::1	19	Gene HECTD2	HECTD2, FLJ16050	HECT domain containing 2	NM_173497, NM_182765, hCT2348869.1, hCT2351051.0, hCT2352328.0	1565699_at, 227568_at, 238863_at	NP_775768.2, NP_877497.2, EAW50109.1, EAW50110.1, EAW50111.1
GeneID: 3632	INPP5A	10	134,351,353	134,596,984	245,631	+	1	2_pNL97_plus_increased::1:1:13	253015	downstream	0	1	8	25	1	2_pNL97_plus_increased::1	25	Gene INPP5A	INPP5A, MGC116949, DKFZp434A1721, SPTASE, MGC116947	inositol polyphosphate-5-phosphatase, 40kDa	NM_005539, hCT2289563.0, hCT2389566.0	1554757_a_at, 203096_at	NP_005530.3, EAW61306.1, EAW61307.1
GeneID: 84504	NKX6-2	10	134,599,328	134,599,537	1,217	-	1	2_pNL97_plus_increased::1:1:12	-6831	upstream	0	1	8	25	1	2_pNL97_plus_increased::1	25	Gene NKX6-2	NKX6B, NKX6-2, NKX6.2, GTX, MGC126884	NK6 homeobox 2	NM_177400, hCT1780459.2	235832_at	NP_796374.1, EAW61308.1
GeneID: 55128	TRIM68	11	4,619,902	4,629,437	9,535	-	1	2_pNL97_plus_increased::1:1:14	189	in gene	0	1	5	16	1	2_pNL97_plus_increased::1	16	Gene TRIM68	MGC12870, SS-56, FLJ10361, TRIM68, SS56, RNF137, GC109	tripartite motif containing 68	NM_018073, hCT2270464.0, hCT13687.3	219405_at	NP_060543.5, EAW68834.1, EAW68835.1
GeneID: 8495	PPFIBP2	11	7,535,001	7,674,991	139,990	+	1	2_pNL97_plus_increased::1:1:15	98663	in gene	0	1	8	21	1	2_pNL97_plus_increased::1	21	Gene PPFIBP2	GSDT, PPFIBP2, DKFZp781K06120, MGC42541	PTPRF interacting protein, binding protein 2 (liprin beta 2)	NM_003621, hCT2270376.8, hCT2270377.0, hCT13046.3	212841_s_at, 215959_at	NP_003612.2, EAW68654.1, EAW68652.1, EAW68653.1
GeneID: 9152	SLC6A5	11	20,628,946	20,676,610	55,664	+	1	2_pNL97_plus_increased::1:1:16	484	in gene	0	1	15	29	1	2_pNL97_plus_increased::1	29	Gene SLC6A5	SLC6A5, GLYT-2, GLYT2, NET1	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	NM_004211, hCT14449.3	210810_s_at	NP_004202.2, EAW68330.1
GeneID: 57586	SYT13	11	45,201,353	45,307,884	46,031	-	1	1_pNL7_minus_increased::1:1:1	28551	in gene	1	0	23	13	1	1_pNL7_minus_increased::1	23	Gene SYT13	KIAA1427, SYT13	synaptotagmin XIII	NM_020826, hCT2267606.0, hCT16513.2	221894_at, 236066_at	NP_065877.1, EAW68044.1, EAW68043.1
GeneID: 4978	OPCML	11	132,284,875	133,402,483	1,117,528	-	1	2_pNL97_plus_increased::1:1:17	610008	in gene	0	1	12	21	1	2_pNL97_plus_increased::1	21	Gene OPCML	OPCM, OBCAM, IGLON1, opioid binding protein/cell adhesion molecule-like	opioid binding protein/cell adhesion molecule-like	NM_002545, NM_001012393, hCT1953785.1, hCT2335283.0	206215_at, 214111_at	NP_002536.1, NP_001012393.1, EAW67884.1, EAW67885.1
GeneID: 100128095	LOC100128095	11	132,526,971	133,402,878	875,907	+	1	2_pNL97_plus_increased::1:1:17	257424	in gene	0	1	12	21	1	2_pNL97_plus_increased::1	21	Gene LOC100128095		hypothetical LOC100128095	XR_110538, XR_114543		
GeneID: 440073	IQSEC3	12	178,049	287,626	111,577	+	1	2_pNL97_plus_increased::1:1:18	-9517	upstream	0	1	10	21	1	2_pNL97_plus_increased::1	21	Gene IQSEC3	MGC38156, KIAA1110, IQSEC3	IQ motif and Sec7 domain 3	NM_015232, NM_001170738, hCT2280268.0, hCT2286262.0, hCT2286264.0, hCT2286266.0, hCT2286267.0	1556872_s_at, 213834_at, 242694_at	NP_056047.1, NP_001164268.1, EAW68869.1, EAW68881.1, EAW68883.1, EAW68984.1, EAW68982.1
GeneID: 50846	DHH	12	49,483,204	49,488,602	5,398	-	1	2_pNL97_plus_increased::1:1:19	-2618	in gene	0	1	9	20	1	2_pNL97_plus_increased::1	20	Gene DHH	DHH, MGC35145, HHG-3	desert hedgehog homolog (Drosophila)	NM_021044, hCT22771.4	1552730_at	NP_066382.1, EAW58839.1
GeneID: 55716	LMBR1L	12	49,490,922	49,504,688	13,758	-	1	2_pNL97_plus_increased::1:1:19	10696	downstream	0	1	9	20	1	2_pNL97_plus_increased::1	20	Gene LMBR1L	FLJ36251, LMBR1L, KIAA1174, LIMR, FLJ10494	limb region 1 homolog (mouse)-like	NM_018113, hCT2300483.8, hCT2300484.0, hCT2300485.0, hCT2300486.0, hCT2300487.0, hCT2300488.0, hCT2315266.0, hCT2352387.0	220836_s_at	NP_060583.2, EAW58040.1, EAW58041.1, EAW58044.1, EAW58046.1, EAW58047.1, EAW58042.1, EAW58043.1, EAW58045.1
GeneID: 6541	SLC7A1	13	30,083,551	30,169,825	86,274	-	1	2_pNL97_plus_increased::1:1:21	12241	in gene	0	1	11	28	1	2_pNL97_plus_increased::1	20	Gene SLC7A1	REC1L, ATRC1, CAT-1, SLC7A1, HCAT1, ERR	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	NM_003045, hCT16944.3, hCT1957870.1	206566_at, 212280_at, 212282_at, 212285_s_at, 215979_s_at	NP_003036.1, EAX08444.1, EAX08443.1
GeneID: 79621	RNASEH2B	13	51,483,892	51,544,596	60,704	+	1	2_pNL97_plus_increased::1:1:22	288	in gene	0	1	11	28	1	2_pNL97_plus_increased::1	20	Gene RNASEH2B	FLJ11712, DLEU8, AGS2, RNASEH2B	ribonuclease H2, subunit B	NM_024570, NM_001142279, hCT1954794.1, hCT19951.2	215040_at, 219056_at, 229210_at, 233156_at	NP_078846.2, NP_001135751.1, EAX08863.1, EAX08864.1
GeneID: 114798	SLITRK1	13	84,451,343	84,456,528	5,185	-	1	2_pNL97_plus_increased::1:1:23	2416	in gene	0	1	14	21	1	2_pNL97_plus_increased::1	21	Gene SLITRK1	TTM, LRR012, KIAA1910, SLITRK1, RP11-245N17.1, FLJ44428, KIAA0918	SLIT and NTRK-like family, member 1	NM_052910, hCT1647464.1	230734_at	NP_443142.1, EAW80608.1
GeneID: 10160	FARP1	13	98,795,434	99,102,023	306,589	+	1	2_pNL97_plus_increased::1:1:24	159556	in gene	0	1	7	14	1	2_pNL97_plus_increased::1	14	Gene FARP1	CDEP, MGC37400, FARP1, PLEKHC2	PERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	NM_005766, NM_001801715, hCT1952354.0	1562425_at, 1562426_a_at, 201910_at, 201911_s_at, 227996_at, 239246_at	NP_005757.1, NP_001801715.2, EAX08862.1
GeneID: 23348	DOCK9	13	99,445,741	99,738,660	292,919	-	1	2_pNL97_plus_increased::1:1:25	-732	upstream	0	1	10	28	1	2_pNL97_plus_increased::1	20	Gene DOCK9	DKFZp686N04132, DKFZp686C11110, FLJ45282, ZIZIMIN1, ZIZI, FLJ44528, DKFZp686D2047, FLJ11949, FLJ45601, FLJ16744, KIAA1058, DOCK9, KIAA1085	dedicator of cytokinesis 9	NM_015296, NM_001130048, NM_001130049, NM_001130050, hCT20870.4, hCT2302280.1, hCT2302291.1, hCT2302292.1, hCT2302293.0, ZIZI, FLJ44528, hCT2302296.1, hCT2302297.1, hCT2302298.1, hCT2302299.1, hCT2302300.1, hCT2340461.0	212538_at, 215041_s_at, 215237_at, 215238_s_at, 232874_at	NP_056111.1, NP_001123528.1, NP_001123521.1, NP_001123522.1, EAX08994.1, EAX09003.1, EAX08995.1, EAX08996.1, EAX08997.1, EAX08998.1, EAX08999.1, EAX09000.1, EAX09004.1, EAX09005.1, EAX09001.1, EAX09002.1
GeneID: 2259	FGF14	13	102,373,205	103,054,124	680,919	-	1	2_pNL97_plus_increased::1:1:26	-4028	upstream	0	1	12	28	1	2_pNL97_plus_increased::1	28	Gene FGF14	SCA27, FHF4, MGC119129, FGF14	fibroblast growth factor 14	NM_175929, NM_004115, hCT19152.3, hCT2301958.0	221310_at, 230288_at, 231523_at	NP_787125.1, NP_004106.1, EAX09054.1, EAX09055.1
GeneID: 283481	LOC283481	13	103,046,928	103,048,055	1,127	+	1	2_pNL97_plus_increased::1:1:26	11216	downstream	0	1	12	28	1	2_pNL97_plus_increased::1	28	Gene LOC283481		hypothetical LOC283481	NR_036437	231351_at, 243225_at	
GeneID: 100289410	LOC100289410	13	113,621,786	113,622,952	1,154	-	1	2_pNL97_plus_increased::1:1:28	-152	upstream	0	1	9	23	1	2_pNL97_plus_increased::1	23	Gene LOC100289410	MCF2L-AS1	MCF2L antisense RNA 1 (non-protein coding)	NR_034002		
GeneID: 23263	MCF2L	13	113,622,757	113,752,862	130,105	+	1	2_pNL97_plus_increased::1:1:26	347	in gene	0	1	8	23	1	2_pNL97_plus_increased::1	23	Gene MCF2L	FLJ12122, ARHGEF14, KIAA0362, OST, DBS, MCF.2L	MCF.2 cell line derived transforming sequence-like	NM_024979, NM_001112732, hCT1813208.1, hCT19020.3, hCT2302466.1, hCT2340540.0, hCT2340541.0, hCT2359370.0	1552743_at, 1559427_at, 1563808_at, 1563809_a_at, 212935_at, 220464_at, 239630_at, besT_at	NP_076255.3, NP_001106203.1, EAX09175.1, EAX09176.1, EAX09177.1, EAX09179.1, EAX09178.1, EAX09180.1
GeneID: 91875	TTC5	14	20,757,290	20,774,153	16,863	-	1	2_pNL97_plus_increased::1:1:28	73	in gene	0	1	8	26	43	1	43	Gene TTC5	Strap, TTC5	tetratricopeptide repeat domain 5	NM_138376, hCT2354235.0, hCT2354236.0, hCT31744.3	226557_at	NP_612385.2, EAW66480.1, EAW66481.1, EAW66482.1
GeneID: 57820	CCNB1IP1	14	20,779,529	20,801,457	21,928	-	1	2_pNL97_plus_increased::1:1:28	27377	downstream	0	1	8	26	43	1	43	Gene CCNB1IP1	HEI10, C14orf18	cyclin B1 interacting protein 1	NM_182849, NM_182851, NM_021178, NM_182852, hCT2304666.0	217988_at	NP_378269.1, NP_878271.1, NP_067001.3, NP_878272.1, EAW66479.1
GeneID: 55449	C14orf167	14	24,407,840	24,424,298	16,458	-	1	2_pNL97_plus_increased::1:1:31	954	in gene	0	1	8	29	57	1	57	Gene C14orf167	C14orf167, PRO1488	chromosome 14 open reading frame 167	NR_023921, NR_023922, NR_023923, NR_023924	227446_s_at	
GeneID: 10901	DHRS4	14	24,422,905	24,438,488	15,583	+	1	2_pNL97_plus_increased::1:1:31	379	in gene	0	1	8	29	57	1	57	Gene DHRS4	FLJ11008, SDR2C1, SCAD-SRL, NRDR, SDR2C2, SDR-SRL, DHRS4	dehydrogenase/reductase (SDR family) member 4	NM_021004	216021_at	NP_066284.2
GeneID: 5583	PRKCH	14	61,788,515	62,017,698	229,183	+	1	1_pNL7_minus_increased::1:1:3	34333	in gene	1	0	19	6	1	1_pNL7_minus_increased::1	19	Gene PRKCH	nPKC-eta, PRKCL, MGC26269, PKC-L, PKCL, MGC5363, PRKCH	protein kinase C, eta	NM_006255, hCT13455.2, hCT2336287.0, hCT2356070.0	206899_at, 210764_at	NP_006246.2, EAW68801.1, EAW68800.1, EAW68802.1
GeneID: 53844	CSNK1G1	15	64,457,710	64,648,442	190,726	-	1	2_pNL97_plus_increased::1:1:33	666	in gene	0	1	7	22	1	2_pNL97_plus_increased::1	22	Gene CSNK1G1	CSNK1G1		NM_022048	220640_at, 221673_s_at, 226888_at, 231929_s_at	NP_071331.2
GeneID: 9768	KIAA0101	15	64,657,193	64,673,702	16,509	-	1	2_pNL97_plus_increased::1:1:33	25926	downstream	0	1	7	22	1	2_pNL97_plus_increased::1	22	Gene KIAA0101	FLJ53702, L5, KIAA0101, OEATC1, OEATC-1, p15(PAF), PAF, NSSATP9	KIAA0101	NM_014736, NM_001029989	202503_s_at, 211713_x_at	NP_055551.1, NP_001025169.1
GeneID: 10391	CORO2B	15	88,808,879	89,020,145	111,266	+	1	2_pNL97_plus_increased::1:1:34	75345	in gene	0	1	8	19	1	2_pNL97_plus_increased::1	19	Gene CORO2B	KIAA0925, CORO2B, CLIPINC	coronin, actin binding protein, 2B	NM_006091, NM_001190456, NM_001190457, hCT14924.2, hCT2288947.0	209789_at	NP_006082.3, NP_001177385.1, NP_001177386.1, EAW77822.1, EAW77823.1
GeneID: 5151	PDE8A	15	85,525,205	85,682,373	157,168	+	1	2_pNL97_plus_increased::1:1:36	142283	in gene	0	1	7	16	1	2_pNL97_plus_increased::1	16	Gene PDE8A	HsT19550, PDE8A, FLJ16150	phosphodiesterase 8A	NM_002605, NM_172434, hCT2268955.0, hCT2268956.0, hCT2268959.0, hCT2358631.0, hCT2358632.0, hCT2358633.0	1552831_a_at, 212521_s_at, 212522_at, 239874_at	NP_002596.1, NP_775856.1, EAX01966.1, EAX01967.1, EAX01969.1, EAX01970.1, EAX01965.1, EAX01969.1
GeneID: 51704	GPRC5B	16	19,870,293	19,896,151	25,858	-	1	2_pNL97_plus_increased::1:1:37	-665	upstream	0	1	5	14	1	2_pNL97_plus_increased::1	14	Gene GPRC5B	GPRC5B, RAIG2, RAIG-2	G protein-coupled receptor, family C, group 5, member B	NM_016235, hCT19628991.1, hCT2273609.0, hCT2273610.0, hCT2329264.4	203631_s_at, 203632_s_at, 225511_at, 228313_at	NP_057319.1, EAW50302.1, EAW50303.1, EAW50304.1, EAW50305.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[1]	[2]	[3]	[4]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:26470	SEZ6L2	16	29,882,488	29,910,588	28,100	-	1	2_pNL97_plus_increase.t::1::38	-344	upstream	0	1	14	21	1	2_pNL97_plus_increased::1	21	Gene SEZ6L2	SEZ6L2, FLJ90517, PSK-1	seizure related 6 homolog (mouse)-like 2	NM_012410, NM_201575, NM_001114899, NM_001114100, hCT1809240.3	216739_x_at, 223458_at, 233237_s_at, 238404_x_at, 238406_x_at	NP_036542.1, NP_963869.2, NP_001107571.1, NP_001107572.1, EAW79973.1
GeneID:252882	ASPHD1	16	29,912,147	29,917,377	5,230	+	1	2_pNL97_plus_increase.t::1::38	-723	upstream	0	1	14	21	1	2_pNL97_plus_increased::1	21	Gene ASPHD1	ASPHD1	aspartate beta-hydroxylase domain containing 1	NM_181718, hCT1830508.3, hCT2355982.0	1553997_a_at, 214993_at	NP_858069.2, EAW79972.1, EAW79971.1
GeneID:253980	KCTD13	16	29,917,960	29,937,545	19,585	-	1	2_pNL97_plus_increase.t::1::38	26121	downstream	0	1	14	21	1	2_pNL97_plus_increased::1	21	Gene KCTD13	hBACURD1, POLDIP1, PDIP1, PKSG86, KCTD13	potassium channel tetramerisation domain containing 13	NM_178863, hCT1809247.1, hCT2355969.0	221889_at, 45653_at	NP_849194.1, EAW79969.1, EAW79970.1
GeneID:26000	TBC1D10B	16	30,368,422	30,381,522	13,100	-	1	2_pNL97_plus_increase.t::1::39	-8362	upstream	0	1	7	25	1	2_pNL97_plus_increased::1	25	Gene TBC1D10B	TBC1D10B, FP2461, DKFZp434P1750	TBC1 domain family, member 10B	NM_015527, hCT2280281.1, hCT2280282.1, hCT2352522.0	220947_s_at	NP_056342.3, EAW52258.1, EAW52256.1, EAW52257.1
GeneID:28895	MYLPF	16	30,380,123	30,389,310	9,187	+	1	2_pNL97_plus_increase.t::1::39	3701	downstream	0	1	7	25	1	2_pNL97_plus_increased::1	25	Gene MYLPF	DKFZp779D0757, MYL11, MRLC2, MYLPF, HUMMLC2B, MGC13450	myosin light chain, phosphorylatable, fast skeletal muscle	NM_013292, hCT1759993.1, hCT2282500.0	205163_at	NP_037424.2, EAW52254.1, EAW52255.1
GeneID:1731	1-Sep	16	30,389,456	30,394,171	4,715	-	1	2_pNL97_plus_increase.t::1::39	4347	in gene	0	1	7	25	1	2_pNL97_plus_increased::1	25	Gene SEPT1	MGC20394, SEPT1, LARP, SEP1, DIFF6, PNUTL3	septin 1	NM_052838, hCT1759999.0, hCT2280279.0	227552_at	NP_443870.1, EAW52252.1, EAW52253.1
GeneID:4669	NAGLU	17	40,687,951	40,698,467	8,516	+	1	2_pNL97_plus_increase.t::1::40	17521	downstream	0	1	8	21	1	2_pNL97_plus_increased::1	21	Gene NAGLU	NAG, UPHS2, MPS3B, MPS-IIIB, NAGLU	N-acetylglucosaminidase, alpha	NM_000263, hCT2292129.8, hCT6764.2	204360_s_at, 215888_at	NP_000254.2, EAW68832.1, EAW68833.1
GeneID:3292	HSD17B1	17	40,703,984	40,707,232	3,248	+	1	2_pNL97_plus_increase.t::1::40	1488	in gene	0	1	8	21	1	2_pNL97_plus_increased::1	21	Gene HSD17B1	HSD17, EDH7B2, MGC138140, HSD17B1, SDR28C1, EDHB17	hydroxysteroid (17-beta) dehydrogenase 1	NM_000413, hCT7687.2	205829_at, 228595_at	NP_000404.2, EAW68838.1
GeneID:100290596	LOC100290566	17	40,704,454	40,706,766	2,312	-	1	2_pNL97_plus_increase.t::1::40	1294	in gene	0	1	8	21	1	2_pNL97_plus_increased::1	21	Gene LOC100290566		hypothetical LOC100290566	XR_111701, XR_109384, XR_115184		
GeneID:80347	COASY	17	40,714,092	40,718,295	4,203	+	1	2_pNL97_plus_increase.t::1::40	8628	upstream	0	1	8	21	1	2_pNL97_plus_increased::1	21	Gene COASY	COASY, FLJ35178, UKR1, NBP, PPAT, pCoV-2, DPCK	CoA synthase	NM_001042529, NM_025233, NM_001042530, NM_001042531, NM_001042532, hCT2292131.0, hCT2292132.0, hCT6019.2	201913_s_at	NP_001035994.1, NP_079509.5, NP_001035995.1, NP_001035996.1, NP_001035997.2, EAW68838.1, EAW68839.1, EAW68840.1
GeneID:124871	FLJ40194	17	47,325,605	47,336,027	10,422	+	1	2_pNL97_plus_increase.t::1::41	12267	downstream	0	1	10	18	1	2_pNL97_plus_increased::1	18	Gene FLJ40194		hypothetical FLJ40194	NR_034181, hCT2285872.0		EAW94685.1
GeneID:100489467	LOC100489467	17	70,399,463	70,508,943	109,480	-	3	2_pNL97_plus_increase.t::1::42, 2_pNL97_plus_increase.t::1::43, 2_pNL97_plus_increase.t::1::44	188015, 161663, 239	in gene, in gene, in gene	0	1	12.67	324	3	2_pNL97_plus_increased::1	448	Gene LOC100489467	FLJ20478, FLJ26252	hypothetical LOC100489467	NR_036488		
GeneID:400619	FLJ36484	17	70,584,180	70,636,611	42,431	-	1	2_pNL97_plus_increase.t::1::44	47907	downstream	0	1	23	447	1	2_pNL97_plus_increased::1	447	Gene FLJ36484		hypothetical LOC400619	NR_033876		
GeneID:10982	MAPRE2	18	32,556,892	32,722,378	165,486	+	1	1_pNL7_minus_increase.t::1::4	2244	in gene	1	0	17	8	1	1_pNL7_minus_increased::1	17	Gene MAPRE2	RP1, EB2, EB1, MAPRE2	microtubule-associated protein RP/EB family, member 2	NM_014268, NM_001142826, NM_001143827, NR_026570, hCT1549.3, hCT1951928.1, hCT2316441.0, hCT2316443.0, hCT2316444.0	202501_at, 211536_at, 213489_at	NP_055883.1, NP_001137288.1, NP_001137289.1, EAX01336.1, EAX01337.1, EAX01339.1, EAX01338.1, EAX01340.1
GeneID:498	ATP5A1	18	43,664,110	43,684,199	20,089	-	1	2_pNL97_plus_increase.t::1::46	-121	upstream	0	1	6	16	1	2_pNL97_plus_increased::1	16	Gene ATP5A1	ATP5A1, MOM3, ATPM, ATP5A, ATP5AL2, OMR, hATP1, ORM	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	NM_004046, NM_001001937	1568891_at, 213738_s_at	NP_004037.1, NP_001001937.1
GeneID:115106	HAUS1	18	43,684,298	43,708,299	24,001	+	1	2_pNL97_plus_increase.t::1::46	22	in gene	0	1	6	16	1	2_pNL97_plus_increased::1	16	Gene HAUS1	HAUS1, FLJ21894, HEIC, HEI-C, FLJ40084, CCDC5, Hs71461	HAUS augmin-like complex, subunit 1	NR_026978, NM_138443, hCT1816418.1	225297_at	NP_612452.1, EAX01469.1
GeneID:22859	LPHN1	19	14,258,548	14,316,997	58,448	-	1	2_pNL97_plus_increase.t::1::47	-1275	upstream	0	1	40	55	1	2_pNL97_plus_increased::1	55	Gene LPHN1	LEC2, LPHN1, CL1, CIRL1	latrophilin 1	NM_014921, NM_001008701, hCT18961.2, hCT2284835.0, hCT2284836.0, hCT2284838.0, hCT2356542.0, hCT2356543.0	203488_at, 219145_at, 47568_at	NP_055736.2, NP_001008701.1, EAW64404.1, EAW64406.1, EAW64408.1, EAW64409.1, EAW64405.1, EAW64407.1
GeneID:11136	SLC7A9	19	33,321,417	33,360,683	39,266	-	1	2_pNL97_plus_increase.t::1::48	-1525	upstream	0	1	3	14	1	2_pNL97_plus_increased::1	14	Gene SLC7A9	FLJ49301, BAT1, CSNU3, SLC7A9	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	NM_014270, NM_001126335	220135_s_at	NP_055085.1, NP_001119807.1
GeneID:84992	CCDC123	19	33,369,904	33,462,969	92,965	-	1	2_pNL97_plus_increase.t::1::48	100961	downstream	0	1	3	14	1	2_pNL97_plus_increased::1	14	Gene CCDC123	FLJ14644, CCDC123	coiled-coil domain containing 123	NM_032816	1553732_s_at, 1554512_a_at, 1554513_s_at, 1563599_s_at, 1563919_a_at, 232106_s_at	NP_116205.3
GeneID:57655	GRAMD1A	19	35,491,246	35,517,373	26,127	+	1	2_pNL97_plus_increase.t::1::50	754	in gene	0	1	7	19	1	2_pNL97_plus_increased::1	19	Gene GRAMD1A	FLJ40346, FLJ22411, GRAMD1A, KIAA1533	GRAM domain containing 1A	NM_020895, NM_001130189	224807_at, 244008_at	NP_065946.2, NP_001129671.1
GeneID:4856	NOVA2	19	46,442,771	46,476,657	33,886	-	1	2_pNL97_plus_increase.t::1::51	20721	in gene	0	1	17	34	1	2_pNL97_plus_increased::1	34	Gene NOVA2	ANOVA, NOVA2, NOVA3	neuro-oncological ventral antigen 2	NM_002516, hCT11890.3	206476_s_at, 209477_s_at	NP_002507.1, EAW57397.1
GeneID:9853	ASAP2	2	9,346,894	9,545,812	198,918	+	1	2_pNL97_plus_increase.t::1::52	171938	in gene	0	1	7	20	1	2_pNL97_plus_increased::1	20	Gene ASAP2	PAG3, CENTB3, KIAA0400, PAP, ASAP2, DDEF2, SHAG1, Pap-alpha, AMAP2, FLJ42910	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	NM_003887, NM_001135191, hCT1994190.1, hCT1967490.1, hCT2276915.0, hCT2276917.0, hCT2358456.0	206414_s_at	NP_003870.1, NP_001128663.1, EAX01803.1, EAX01804.1, EAX01805.1, EAX01806.1, EAX01802.1
GeneID:55818	KDM3A	2	98,998,271	99,219,839	51,568	+	1	2_pNL97_plus_increase.t::1::55	1057	in gene	0	1	9	21	1	2_pNL97_plus_increased::1	21	Gene KDM3A	DKFZp686P07111, TSGA, KIAA0742, JHDM2A, KDM3A, JMJD1A, JMJD1, DKFZp686A24246, JHMD2A	lysine (K)-specific demethylase 3A	NM_018433, NM_001146088, hCT1819953.2, hCT2358409.0, hCT2358410.0, hCT2358411.0	212689_s_at	NP_060903.2, NP_001140160.1, EAW99453.1, EAW99454.1, EAW99455.1, EAW99456.1
GeneID:10619	RBCK1	20	388,709	411,610	22,901	+	1	1_pNL7_minus_increase.t::1::7	23483	downstream	1	0	16	8	1	1_pNL7_minus_increased::1	16	Gene RBCK1	XAP3, RBCK2, HOIL-1, HOIL1, XAP4, C20orf18, UBCE7IP3, RNF54, ZRANB4, RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	NM_031229, NM_006462	207713_s_at, 221827_at	NP_112586.2, NP_006453.1
GeneID:128637	TBC1D20	20	416,124	443,187	27,063	-	1	1_pNL7_minus_increase.t::1::7	28995	downstream	1	0	16	8	1	1_pNL7_minus_increased::1	16	Gene TBC1D20	FLJ45119, TBC1D20, C20orf140	TBC1 domain family, member 20	NM_144628, hCT2359534.0, hCT2359535.0, hCT31128.3	226409_at, 228664_at	NP_653229.1, EAX10872.1, EAX10870.1, EAX10871.1
GeneID:50861	STMN3	20	62,271,961	62,284,768	13,719	-	1	2_pNL97_plus_increase.t::1::59	140	in gene	0	1	12	26	1	2_pNL97_plus_increased::1	26	Gene STMN3	SCLIP, STMN3	stathmin-like 3	NM_015894, hCT2312478.1, hCT2312420.1	218287_s_at, 222557_at	NP_056978.2, EAW75250.1, EAW75249.1
GeneID:51750	RTEL1	20	62,289,647	62,327,601	37,954	+	1	2_pNL97_plus_increase.t::1::59	-5087	upstream	0	1	12	26	1	2_pNL97_plus_increased::1	26	Gene RTEL1	RTEL, DKFZp434C012, KIAA1088, bK319A7.3, RTEL1, C20orf41, NHL	regulator of telomere elongation helicase 1	NM_016434, NM_032957	206467_x_at	NP_057518.1, NP_116575.2
GeneID:375223	LHFPL4	3	9,540,045	9,585,486	55,441	-	1	2_pNL97_plus_increase.t::1::60	1390	in gene	0	1	13	42	1	2_pNL97_plus_increased::1	42	Gene LHFPL4	LHFPL4, MGC133162	lipoma HMGIC fusion partner-like 4	NM_198580, hCT12651.2	223422_at	NP_940962.1, EAW63964.1
GeneID:28512	NKIRAS1	3	23,933,572	23,958,507	24,935	+	1	2_pNL97_plus_increase.t::1::61	189	in gene	0	1	16	26	1	2_pNL97_plus_increased::1	26	Gene NKIRAS	NKIRAS1, kappaB-Ras1, KBRAS1	NFKB inhibitor interacting Ras-like 1	NM_020345, hCT2277984.0, hCT2277986.0	225930_at	NP_065078.1, EAW64336.1, EAW64335.1
GeneID:6138	RPL15	3	23,958,639	23,962,334	3,695	+	1	2_pNL97_plus_increase.t::1::61	-271	upstream	0	1	16	26	1	2_pNL97_plus_increased::1	26	Gene RPL15	RPLY10, L15, MGC88063, RPL10, RPL10, RPL15, FLJ26304, EC45	ribosomal protein L15	NM_002948, hCT2277499.0, hCT2277503.0, hCT2277501.0	221475_s_at, 221476_s_at, 240886_at	NP_002939.2, EAW64339.1, EAW64337.1, EAW64338.1
GeneID:100505901	LOC100505901	3	23,961,600	23,962,515	28,915	-	1	2_pNL97_plus_increase.t::1::61	24147	downstream	0	1	16	26	1	2_pNL97_plus_increased::1	26	Gene LOC100505901		hypothetical LOC100505901	XR_110045, XR_113484		
GeneID:7068	THRB	3	24,158,644	24,536,313	377,669	-	1	2_pNL97_plus_increase.t::1::62	129497	in gene	0	1	5	19	1	2_pNL97_plus_increased::1	19	Gene THRB	THRB2, THRB1, MGC126109, GRTH, THR1, NR1A2, ERBA2, PRTH, MGC126110, ERBA-BETA, THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	NM_000461, NM_001128176, NM_001128177, hCT1957628.1, hCT2277950.0, hCT2277953.0, hCT2277954.0, hCT2354171.0, hCT6550.3	207644_at, 228716_at, 229657_at	NP_000452.2, NP_001121648.1, NP_001121649.1, EAW64345.1, EAW64348.1, EAW64350.1, EAW64346.1, EAW64347.1, EAW64349.1
GeneID:2272	FHIT	3	59,735,036	61,237,133	1,502,097	-	1	2_pNL97_plus_increase.t::1::63	973901	in gene	0	1	9	17	1	2_pNL97_plus_increased::1	17	Gene FHIT	FRA3B, AP3Aase, FHIT	fragile histidine triad gene	NM_002012, NM_001166243, hCT2279841.1, hCT2279845.2	206492_at	NP_002003.1, NP_001159715.1, EAW65283.1, EAW65284.1
GeneID:317649	EIF4E3	3	71,728,440	71,883,924	75,484	-	1	1_pNL7_minus_increase.t::1::8	64148	in gene	1	0	17	2	1	1_pNL7_minus_increased::1	17	Gene EIF4E3	MGC39820, EIF4E3	eukaryotic translation initiation factor 4E family member 3	NM_173359, NM_001134649, NM_001134650, NM_001134651, hCT1642689.3, hCT1954495.1	225839_at, 225940_at, 225941_at, 238461_at	NP_775495.1, NP_001128121.1, NP_001128122.1, NP_001128123.1, EAW55503.1, EAW55504.1
GeneID:84383	CHCHD6	3	126,423,118	126,679,244	256,126	+	1	2_pNL97_plus_increase.t::1::96	-174	upstream	0	1	11	24	1	2_pNL97_plus_increased::1	24	Gene CHCHD6	CHCHD6, MGC13016	coiled-coil-helix-coiled-coil-helix domain containing 6	NM_032343, hCT1960348.1	224462_s_at	NP_115719.1, EAW79352.1
GeneID:100132481	LOC100132481	3	126,426,195	126,427,493	1,298	+	1	2_pNL97_plus_increase.t::1::96	3251	upstream	0	1	11	24	1	2_pNL97_plus_increased::1	24	Gene LOC100132481		hypothetical LOC100132481	XR_112533, XR_108479, XR_113589		
GeneID:26577	PCOLCE2	3	142,536,702	142,608,045	71,343	-	1	2_pNL97_plus_increase.t::1::98	25561	in gene	0	1	5	19	1	2_pNL97_plus_increased::1	19	Gene PCOLCE2	PCPE2, PCOLCE2	procollagen C-endopeptidase enhancer 2	NM_013363, hCT12585.2, hCT2318687.0	219295_s_at	NP_037495.1, EAW78961.1, EAW78962.1
GeneID:100507647	LOC100507647	3	160,213,705	160,215,712	2,007	-	1	2_pNL97_plus_increase.t::1::99	1680	in gene	0	1	4	17	1	2_pNL97_plus_increased::1	17	Gene LOC100507647		hypothetical LOC100507647	XR_112567, XR_108508, XR_113535		
GeneID:3842	KPNA4	3	160,217,962	160,283,376	65,414	-	1	2_pNL97_plus_increase.t::1::99	69344	downstream	0	1	4	17	1	2_pNL97_plus_increased::1	17	Gene KPNA4	SRP3, KPNA4, MGC26703, QIP1, IPOA3, MGC12217	karyopherin alpha 4 (importin alpha 3)	NM_002268, hCT2318441.0, hCT2318442.0, hCT8274.4	209853_at, 225267_at, 225268_at	NP_002259.1, EAW78632.1, EAW78631.1, EAW78633.1
GeneID:1400	CRMP1	4	5,822,491	5,894,765	72,274	-	1	2_pNL97_plus_increase.t::1::70	11553	in gene	0	1	13	32	1	2_pNL97_plus_increased::1	32	Gene CRMP1	DPYSL1, DRP-1, DRP1, CRMP1, ULIP-3, CRMP-1	collapsin response mediator protein 1	NM_001313, NM_001014809, hCT2254151.8, hCT2356267.0, hCT2356268.0, hCT2356269.0, hCT31148.2	202517_at	NP_001304.1, NP_001014809.1, EAW62403.1, EAW62404.1, EAW62406.1, EAW62407.1, EAW62405.1
GeneID:100507292	LOC100507292	4	5,869,059	5,891,958	22,899	-	1	2_pNL97_plus_increase.t::1::70	8726	in gene	0	1	13	32	1	2_pNL97_plus_increased::1	32	Gene LOC100507292		hypothetical LOC100507292	XR_112612, XR_108540		
GeneID:55330	CNO	4	6,717,842	6,719,387	1,545	+	1	2_pNL97_plus_increase.t::1::71	11318	downstream	0	1	6	18	1	2_pNL97_plus_increased::1	18	Gene CNO	FLJ11238, BCA84L, CNO	cappuccino homolog (mouse)	NM_018366	223431_at	NP_060836.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	[1]	[2]	[3]	[4]	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PRO'T
GeneID:10885	EDIL3	5	83,238,126	83,680,611	442,485	-	1	1_pNL7_minus_increase:c:1:-9	412403	in gene	1	0	22	10	1	1_pNL7_minus_increased:1	22	Gene EDIL3	MGC26267, DEL1, EDIL3	EGF-like repeats and discoidin I-like domains 3	NM_005711, hCT1957909.1, hCT2357899.0, hCT28350.3	1558643_s_at, 207379_at, 225275_at	NP_005702.3, EAW85916.1, EAW85917.1, EAW85918.1
GeneID:4001	LMNB1	5	126,112,833	126,172,709	59,876	+	1	2_pNL97_plus_increase:c:1:-74	1567	in gene	0	1	12	16	1	2_pNL97_plus_increased:1	16	Gene LMNB1	MGC111419, ADLD, LMN2, LMNB, LMN, LMNB1	lamin B1	NM_005573, hCT1816864, hCT2352214.0	203276_at	NP_005564.1, EAW48846.1, EAW48845.1
GeneID:94081	SFXN1	5	174,905,514	174,955,021	50,107	+	1	1_pNL7_minus_increase:c:1:-10	39446	in gene	1	0	20	9	1	1_pNL7_minus_increased:1	20	Gene SFXN1	SFXN1, FLJ12876	sideroflexin 1	NM_022754, hCT1821032.3, hCT2251939.1, hCT2251942.2, hCT2251943.2, hCT2353763.0, hCT2353764.0	216392_x_at, 230069_at	NP_073591.2, EAW61372.1, EAW61378.1, EAW61371.1, EAW61373.1, EAW61375.1, EAW61374.1
GeneID:114781	BTBD9	6	38,136,227	38,687,924	471,697	-	1	2_pNL97_plus_increase:c:1:-76	410228	in gene	0	1	15	33	1	2_pNL97_plus_increased:1	33	Gene BTBD9	MGC126520, MGC126519, BTBD9, MGC126517, FLJ32845, DJ322312.1, KIAA1880	BTB (POZ) domain containing 9	NM_052892, NM_001099272, NM_152733, NM_001172418, hCT2344016.0, hCT2349263.0, hCT2349264.0	1553375_at, 229987_at, 234682_at, 235248_at	NP_443125.1, NP_001092742.1, NP_689946.2, NP_001165889.1, EAX03959.1, EAX03960.1, EAX03961.1
GeneID:2740	GLP1R	6	39,016,557	39,055,520	38,963	+	1	2_pNL97_plus_increase:c:1:-77	39795	downstream	0	1	4	17	1	2_pNL97_plus_increased:1	17	Gene GLP1R	MGC138331, GLP1R	glucagon-like peptide 1 receptor	NM_002062, hCT2282514.0, hCT2282516.0, hCT2358871.0, hCT2358872.0, hCT2358873.0	206390_s_at, 206391_s_at, 206480_at, 206481_s_at, 211232_x_at	NP_002053.3, EAX03970.1, EAX03971.1, EAX03972.1, EAX03973.1, EAX03974.1
GeneID:59845	ABCC10	6	43,399,489	43,418,163	18,674	+	1	1_pNL7_minus_increase:c:1:-11	-4289	upstream	1	0	23	9	1	1_pNL7_minus_increased:1	23	Gene ABCC10	EST182763, MRP7, ABCC10, SMRP7	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	NM_033450, hCT1967874.1, hCT1969068.1, hCT1969069.1, hCT2358821.0, hCT2358822.0, hCT18074.4	213485_s_at, 215873_x_at	NP_256261.2, EAX04180.1, EAX04181.1, EAX04182.1, EAX04184.1, EAX04185.1, EAX04182.1
GeneID:114327	EFHC1	6	52,284,994	52,360,583	75,589	+	1	2_pNL97_plus_increase:c:1:-79	3966	in gene	0	1	6	18	1	2_pNL97_plus_increased:1	18	Gene EFHC1	FLJ37269, EFHC1, EJM, EJM1, dJ304B14.2, FLJ10466, JAE, EJA1	EF-hand domain (C-terminal) containing 1	NM_018100, NR_033327, NM_001172428, hCT2286825.0, hCT12282.4, hCT1963344.1	219833_s_at, 225656_at, 231026_at	NP_060570.2, NP_001165891.1, EAX04370.1, EAX04371.1, EAX04372.1
GeneID:26238	TIAM2	6	155,411,423	155,578,857	167,434	+	1	1_pNL7_minus_increase:c:1:-12	36961	in gene	1	0	28	11	1	1_pNL7_minus_increased:1	26	Gene TIAM2	TIAM-2, STEF, FLJ41865, TIAM2	T-cell lymphoma invasion and metastasis 2	NM_012454, NM_001010927, hCT2330615.0, hCT1953626.2	219950_s_at, 222842_s_at	NP_036586.2, NP_001010927.1, EAW47682.1, EAW47683.1
GeneID:222608	VSTM2A	7	54,610,019	54,636,948	26,929	+	2	2_pNL97_plus_increase:c:1:-88, 2_pNL97_plus_increase:c:1:-81	93, 1085	in gene, in gene	0	1	8	21.5	2	2_pNL97_plus_increased:1	23	Gene VSTM2A	VSTM2A, MGC33330, VSTM2	V-set and transmembrane domain containing 2A	NM_182546, hCT2349460.0, hCT2352427.0, hCT1644444.4	1554530_at	NP_872352.2, EAW50954.1, EAW50952.1, EAW50953.1
GeneID:10960	CCP90	7	99,686,583	99,689,823	3,240	+	1	2_pNL97_plus_increase:c:1:-82	11721	downstream	0	1	13	28	1	2_pNL97_plus_increased:1	28	Gene CCP90	CSN6, CCP90, MOV34-34KD	CCP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	NM_006833, hCT2321627.0, hCT2321628.0	201435_s_at, 213564_at	NP_006824.2, EAW76601.1, EAW76602.1
GeneID:4176	MCM7	7	99,690,404	99,699,427	9,023	-	1	2_pNL97_plus_increase:c:1:-82	1123	in gene	0	1	13	28	1	2_pNL97_plus_increased:1	28	Gene MCM7	PNAS146, P1-1-MCM3, MCM2, CDC47, P1CDC47, P85MCM, MCM7	minichromosome maintenance complex component 7	NM_182776, NM_005916, hCT2320828.0, hCT2320829.0, hCT2355610.0	208795_s_at, 210983_s_at	NP_877577.1, NP_005907.3, EAW76598.1, EAW76599.1, EAW76600.1
GeneID:407014	MIR25	7	99,691,183	99,691,266	83	-	1	2_pNL97_plus_increase:c:1:-82	-7038	upstream	0	1	13	28	1	2_pNL97_plus_increased:1	28	Gene MIR25	miR-25, MIR25, MIRN25, hsa-mir-25	microRNA 25	NR_029498		
GeneID:407050	MIR93	7	99,691,391	99,691,470	79	-	1	2_pNL97_plus_increase:c:1:-82	-6834	upstream	0	1	13	28	1	2_pNL97_plus_increased:1	28	Gene MIR93	MIR93, hsa-mir-93, MIRN9, MIRN93, miR-93	microRNA 93	NR_029510		
GeneID:406900	MIR106B	7	99,691,616	99,691,697	81	-	1	2_pNL97_plus_increase:c:1:-82	-6607	upstream	0	1	13	28	1	2_pNL97_plus_increased:1	28	Gene MIR106B	MIRN106B, MIR106B	microRNA 106b	NR_029831		
GeneID:9179	AP4M1	7	99,699,130	99,704,803	5,673	+	1	2_pNL97_plus_increase:c:1:-82	-826	upstream	0	1	13	28	1	2_pNL97_plus_increased:1	28	Gene AP4M1	MU-ARP2, MU-4, CPSQ3, AP4M1	adaptor-related protein complex 4, mu 1 subunit	NM_004722, hCT2321632.8, hCT2321633.0, hCT2321634.0, hCT2355580.0	209837_at	NP_004713.2, EAW76597.1, EAW76594.1, EAW76595.1, EAW76596.1
GeneID:9878	TAF6	7	99,704,693	99,717,481	12,788	-	1	2_pNL97_plus_increase:c:1:-82	19177	downstream	0	1	13	28	1	2_pNL97_plus_increased:1	28	Gene TAF6	TAFII85, TAFII70, TAF6, TAFII80, DKFZp781E21155, MGC8964, TAF(II)80, TAF2E	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa	NM_001198415, NM_005641, NM_139315, NR_033792, hCT2320823.0, hCT2320824.0, hCT2320825.0, hCT2320826.0, hCT2320827.0	203572_s_at	NP_001177344.1, NP_005632.1, NP_647476.1, EAW76588.1, EAW76589.1, EAW76590.1, EAW76591.1, EAW76592.1
GeneID:91584	PLXNA4	7	131,888,091	132,333,447	525,356	-	1	2_pNL97_plus_increase:c:1:-84	297062	in gene	0	1	1	15	1	2_pNL97_plus_increased:1	15	Gene PLXNA4	PLXNA4B, PRO34003, PLXNA4, FLJ35026, PLXNA4A, FLJ38287, FAYV2820, PLEXA4, KIAA1556, DKFZp434G0625, DKFZp566C0546	plexin A4	NM_181775, NM_020911, NM_001105543, hCT2305642.1, hCT2340967.1, hCT2348157.0, hCT2348158.1	234859_at	NP_981440.2, NP_065982.1, NP_001099813.1, EAW83793.1, EAW83795.1, EAW83796.1, EAW83794.1
GeneID:5157	PDGFRL	8	17,433,942	17,500,642	66,700	+	1	2_pNL97_plus_increase:c:1:-85	72378	downstream	0	1	4	14	1	2_pNL97_plus_increased:1	14	Gene PDGFRL	PDGRL, PRLTS, PDGFRL	platelet-derived growth factor receptor-like	NM_006207, hCT18894.3	205236_at	NP_006198.1, EAW63811.1
GeneID:57589	MTUS1	8	17,501,303	17,658,426	157,123	-	1	2_pNL97_plus_increase:c:1:-85	152106	in gene	0	1	4	14	1	2_pNL97_plus_increased:1	14	Gene MTUS1	MP44, FLJ14295, DKFZp564D1519, KIAA1288, MTUS1, ATIP, MTSG1, ATBP, DKFZp686F20243	microtubule associated tumor suppressor 1	NM_001001931, NM_001001925, NM_001001924, NM_020749, NM_001166393, hCT2273592.0, hCT2273592.0, hCT2273594.0, hCT2353924.0, hCT2353925.0, hCT18898.2	212093_s_at, 212095_s_at, 212096_s_at, 235576_at	NP_001001931.1, NP_001001925.1, NP_065800.1, NP_001159865.1, NP_001001924.1, EAW63808.1, EAW63804.1, EAW63805.1, EAW63806.1, EAW63807.1, EAW63809.1, EAW63810.1
GeneID:137886	UBXN2B	8	59,323,823	59,364,060	40,237	+	1	2_pNL97_plus_increase:c:1:-90	81	in gene	0	1	8	18	1	2_pNL97_plus_increased:1	18	Gene UBXN2B	UBXN2B, p37	UBX domain protein 2B	NM_001077619	212834_at, 238903_at	NP_001071087.1
GeneID:54332	GDAP1	8	75,262,618	75,279,345	16,727	+	1	2_pNL97_plus_increase:c:1:-87	134	in gene	0	1	34	62	1	2_pNL97_plus_increased:1	62	Gene GDAP1	CMTRIA, GDAP1, CMT4A, CMT4	ganglioside-induced differentiation-associated protein 1	NM_018972, NM_001040875, hCT2356859.0, hCT13925.3	221279_at, 226269_at, 226271_at	NP_061845.2, NP_001035808.1, EAW87032.1, EAW87033.1
GeneID:51650	PI15	8	75,736,772	75,767,204	30,432	+	1	1_pNL7_minus_increase:c:1:-13	-1764	upstream	1	0	21	5	1	1_pNL7_minus_increased:1	21	Gene PI15	PI3T1, PI3T1, PI15, DKFZp686F0366, CRISP6	peptidase inhibitor 15	NM_015886, hCT13927.2	207938_at, 229947_at	NP_056970.1, EAW87037.1
GeneID:23245	ASTN2	9	119,187,504	120,177,317	989,813	-	1	2_pNL97_plus_increase:c:1:-93	455013	in gene	0	1	6	16	1	2_pNL97_plus_increased:1	16	Gene ASTN2	ASTN2, bA67K19.1, KIAA0634	astrotactin 2	NM_001184734, NM_001184735, NM_014010, NM_198186, NM_198187, NM_198188, hCT2340955.0	1554898_at, 209693_at, 215467_s_at	NP_001170663.1, NP_001170664.1, NP_937831.1, NP_054729.3, NP_937829.3, NP_937830.3, EAW87444.1
GeneID:9758	FRMPD4	X	12,156,585	12,742,642	586,057	+	1	2_pNL97_plus_increase:c:1:-94	585391	in gene	0	1	2	15	1	2_pNL97_plus_increased:1	15	Gene FRMPD4	PDZD10, PDZK10, MGC142262, MGC142260, FRMPD4, KIAA0316	FERM and PDZ domain containing 4	NM_014728, hCT2340422.8	215052_at	NP_055543.2, EAW86804.1
GeneID:28985	MCTS1	X	119,737,744	119,755,014	17,270	+	1	2_pNL97_plus_increase:c:1:-95	28064	downstream	0	1	6	17	1	2_pNL97_plus_increased:1	17	Gene MCTS1	MCT1, MCTS1, MCT-1, FLJ39637	malignant T cell amplified sequence 1	NM_014060, NM_001137554, hCT1816107.1, hCT2353759.0	218163_at	NP_054779.1, NP_001131026.1, EAX11674.1, EAX11675.1
GeneID:29071	C1GALT1C1	X	119,759,529	119,764,005	4,476	-	1	2_pNL97_plus_increase:c:1:-95	197	in gene	0	1	6	17	1	2_pNL97_plus_increased:1	17	Gene C1GALT1C1	MGC19947, CCSMC, MST143, C1GH3-L1, C1GALT1C1, HSPC067, C1GALT2	C1GALT1-specific chaperone 1	NM_152692, NM_001011551, hCT32025.2	1555573_at, 219283_at, 238989_at	NP_689905.1, NP_001011551.1, EAX11673.1

Table 9C. Genes differentially bound by AR

TAble 9C lists the genes differentially bound by AR (Table 9B) with corresponding fold change and significance of differential gene expression values after expression of *SLNCR1* (Schmidt, K., et al., Cell Rep, 2016. 15(9): p. 2025-37).

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Table 9C

Gene Name	1_pNL7_minus_increased::1 Present	2_pNL97_plus_increased::1 Present	1_pNL7_minus_increased::1 AvgPeak	2_pNL97_plus_increased::1 AvgPeak	ActReg Count	SLNCR1 expression log2 fold change	p-value	adj p-value	
GDAP1	0	1	34	62	1	-0.699898507	2.58E-08	1.40E-05	ganglioside-induced differentiation-associated protein 1
THRB	0	1	5	19	1	-0.479368194	0.002249816	0.166984157	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)
PCOLCE2	0	1	5	19	1	0.468088099	0.003249261	0.21207433	procollagen C-endopeptidase enhancer 2
ATP5A1	0	1	6	16	1	0.276149923	0.005584057	0.294087818	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
KIAA0101	0	1	7	22	1	0.318803769	0.013220699	0.45443443	PCNA-binding protein that acts as a regulator of DNA repair during DNA replication
S100A11	0	1	10	22	1	0.305228961	0.01548303	0.487722702	S100 calcium binding protein A11
RPL15	0	1	16	26	1	0.22809349	0.025879897	0.60927634	ribosomal protein L15
CSNK1G1	0	1	7	22	1	-0.34157479	0.028421574	0.630556221	casein kinase 1 gamma 1 (cell cycle regulator)
LMNB1	0	1	12	16	1	0.198825239	0.043025642	0.751392111	lamin B1
HBXIP	0	1	14	28	1	0.223073561	0.051592665	0.806701876	
MCM7	0	1	13	28	1	0.187559645	0.055161351	0.821223937	
COASY	0	1	8	21	1	0.192082112	0.056173882	0.82584662	
LMBR1L	0	1	9	20	1	-0.269708634	0.063244722	0.859748758	
ASTN2	0	1	6	16	1	-0.402366995	0.066151642	0.876829428	
COPS6	0	1	13	28	1	0.194059436	0.069176407	0.890415975	
MCTS1	0	1	6	17	1	0.224275348	0.07308559	0.905475208	
KDM3A	0	1	9	21	1	-0.202523962	0.073184676	0.905475208	
SFXN1	1	0	20	9	1	0.184675668	0.073243992	0.905475208	
GRAMD1A	0	1	7	19	1	0.168758122	0.097817225	1	
EDIL3	1	0	22	10	1	0.391361005	0.144216284	1	
AP4M1	0	1	13	28	1	0.201776057	0.146321644	1	
CAMK2N1	0	1	5	18	1	0.168341856	0.154680759	1	
RNASEH2B	0	1	11	20	1	0.224295614	0.160050274	1	
PPFIBP2	0	1	8	21	1	-0.609228373	0.171620653	1	
CCNL2	0	1	11	30	1	0.133419151	0.174696457	1	
RBCK1	1	0	16	8	1	0.145388583	0.184966387	1	
PLXNA4	0	1	1	15	1	-0.221362292	0.21533469	1	
C1GALT1C1	0	1	6	17	1	0.182691837	0.228920525	1	
ASAP2	0	1	7	20	1	-0.238816657	0.242009765	1	
C14orf167	0	1	29	57	1	0.219564031	0.243088131	1	
HECTD2	0	1	8	19	1	-0.223054099	0.253680141	1	
DHH	0	1	9	20	1	-0.711557983	0.280679989	1	
EFHC1	0	1	6	18	1	-0.159660974	0.289818567	1	
EIF4E3	1	0	17	2	1	0.340752998	0.308892043	1	
PI15	1	0	21	5	1	-0.309599087	0.319097816	1	
HAUS1	0	1	6	16	1	0.179047648	0.326861447	1	
MRPL20	0	1	11	30	1	0.124871763	0.337070425	1	
SLITRK1	0	1	14	21	1	-0.149424388	0.349884425	1	
TIAM2	1	0	26	11	1	-0.175031146	0.351281249	1	
DHRS4	0	1	29	57	1	0.226649903	0.374405448	1	
CNO	0	1	6	18	1	0.11907978	0.378337431	1	
SLC7A9	0	1	3	14	1	#NAME?	0.386377895	1	
HPDL	0	1	8	22	1	0.127977151	0.392926857	1	
MTUS1	0	1	4	14	1	-0.150497167	0.396772697	1	
CHCHD6	0	1	11	24	1	0.124457939	0.398752117	1	
KPNA4	0	1	4	17	1	0.082988089	0.400676856	1	
NAGLU	0	1	8	21	1	0.09584457	0.426327138	1	
FARP1	0	1	7	14	1	0.079789599	0.439865184	1	
CRMP1	0	1	13	32	1	-0.163458892	0.449276481	1	
NKIRAS1	0	1	16	26	1	0.112131497	0.44932458	1	
UBXN2B	0	1	8	18	1	-0.09192269	0.454559961	1	
TRIM68	0	1	5	16	1	-0.129682046	0.455687174	1	
FRMPD4	0	1	2	15	1	-0.387205256	0.466568255	1	
STMN3	0	1	12	26	1	-0.150316684	0.483655487	1	
TTC5	0	1	26	43	1	-0.102647144	0.487857533	1	
MCF2L	0	1	9	23	1	0.085074916	0.503182742	1	
TAF6	0	1	13	28	1	0.076499589	0.513540392	1	
SEZ6L2	0	1	14	21	1	0.08505456	0.528238343	1	
TBC1D20	1	0	16	8	1	-0.067249265	0.56851042	1	
CCDC123	0	1	3	14	1	-0.068497599	0.572068609	1	

Gene Name	1_pNL97_minus_increased::1 Present	2_pNL97_plus_increased::1 Present	1_pNL97_minus_increased::1 AvgPeak	2_pNL97_plus_increased::1 AvgPeak	ActReg Count	SLNCR1 expression log2 fold change	p-value	adj p-value	
SEPT1	0	1	7	25	1	0.219498808	0.595983481	1	
HSD17B1	0	1	8	21	1	0.118471626	0.598714195	1	
DOCK9	0	1	10	20	1	-0.081246143	0.59889568	1	
INADL	0	1	8	23	1	-0.075290885	0.639039574	1	
INPP5A	0	1	8	25	1	0.061166716	0.657672796	1	
CORO2B	0	1	6	19	1	-0.060599498	0.683078584	1	
NR5A2	0	1	14	18	1	-0.20612523	0.684212653	1	
C1orf161	0	1	7	18	1	-1.546268658	0.733381366	1	
MAPRE2	1	0	17	8	1	0.042244998	0.738748169	1	
MIR25	0	1	13	28	1	-0.187120195	0.744340535	1	
NOVA2	0	1	17	34	1	-0.773269907	0.74832979	1	
MIR93	0	1	13	28	1	-0.474667535	0.754361271	1	
ABCC10	1	0	23	9	1	-0.040517692	0.759525596	1	
PDE8A	0	1	7	16	1	-0.038280621	0.75976843	1	
GPRC5B	0	1	5	14	1	0.064790803	0.769377724	1	
PDGFRL	0	1	4	14	1	0.158858885	0.781643314	1	
BTBD9	0	1	15	33	1	-0.034697274	0.809327463	1	
MUTYH	0	1	8	22	1	0.033486706	0.832862805	1	
LPHN1	0	1	40	55	1	-0.023846391	0.856115296	1	
SLC7A1	0	1	11	20	1	0.013171373	0.858119317	1	
MYLPF	0	1	7	25	1	0.944473225	0.870613889	1	
CCNB1IP1	0	1	26	43	1	-0.01027329	0.898344499	1	
FGF14	0	1	12	28	1	-0.232832827	0.902533446	1	
RTEL1	0	1	12	26	1	-0.064559992	0.913913636	1	
KCTD13	0	1	14	21	1	0.009843565	0.926534407	1	
TBC1D10B	0	1	7	25	1	0.009537252	0.940813595	1	
SLC6A5	0	1	15	29	1	Inf	0.948090223	1	
ZNF684	0	1	9	21	1	-0.016030634	0.952550861	1	
ASPHD1	0	1	14	21	1	-0.000671224	0.954949191	1	
IQSEC3	0	1	10	21	1	0.153672308	0.987900963	1	
PRKCH	1	0	19	6	1	0.005118462	0.993471305	1	
NKX6-2	0	1	8	25	1	#NAME?	1	1	
SYT13	1	0	23	13	1	#NAME?	1	1	
OPCML	0	1	12	21	1	#NAME?	1	1	
LHFPL4	0	1	13	42	1	0.309987673	1	1	
FHIT	0	1	6	17	1	-0.076150874	1	1	
VSTM2A	0	1	8	21.5	2	-0.821011634	1	1	
MIR106B	0	1	13	28	1	-0.098374499	1	1	
GLP1R	0	1	4	17	1	NA	NA	NA	
LOC148413	0	1	11	30	1	#N/A	#N/A	#N/A	
LOC100188947	0	1	8	19	1	#N/A	#N/A	#N/A	
LOC100128095	0	1	12	21	1	#N/A	#N/A	#N/A	
LOC283481	0	1	12	28	1	#N/A	#N/A	#N/A	
LOC100289410	0	1	9	23	1	#N/A	#N/A	#N/A	
LOC100290566	0	1	8	21	1	#N/A	#N/A	#N/A	
FLJ40194	0	1	10	18	1	#N/A	#N/A	#N/A	
LOC100499467	0	1	12.67	324	3	#N/A	#N/A	#N/A	
FLJ26484	0	1	23	447	1	#N/A	#N/A	#N/A	
LOC100505901	0	1	16	26	1	#N/A	#N/A	#N/A	
LOC100132481	0	1	11	24	1	#N/A	#N/A	#N/A	
LOC100507647	0	1	4	17	1	#N/A	#N/A	#N/A	
LOC100507292	0	1	13	32	1	#N/A	#N/A	#N/A	

Table 10. Genes bound by AR and regulated by SLNCR

Table 10 lists the genes bound by AR and regulated by SLNCR. RNA-Seq differential expression was taken from Tables 6A-6C, and AR ChIP-Seq values were taken from Table 9A. The table lists only those genes that are significantly dysregulated by *SLNCR* knockdown and bound by AR.

Annotations:

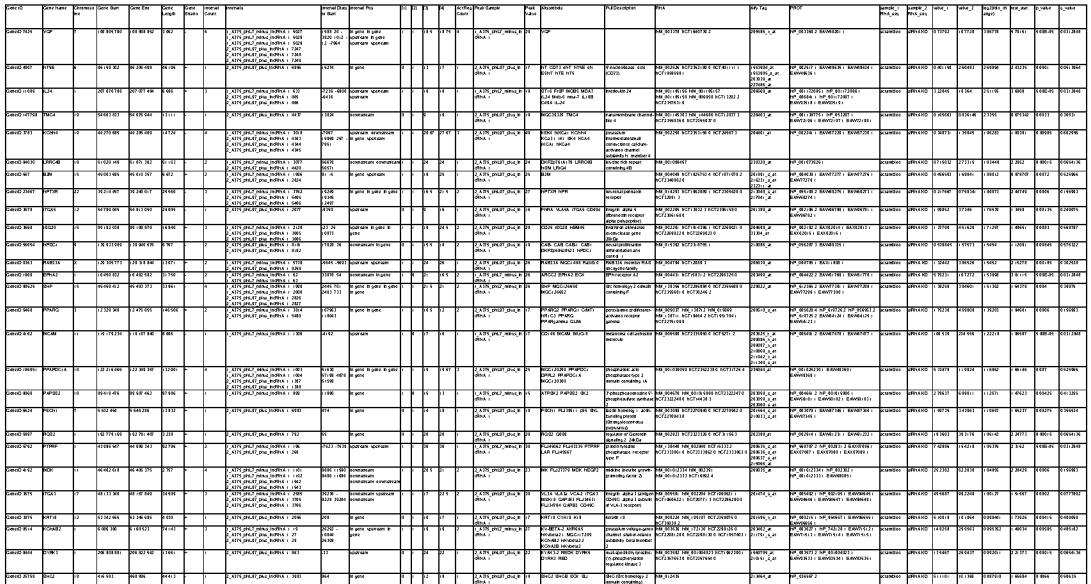
[1] 1_A375_pNL7_minus_lncRNA::1 Present

[2] 2_A375_pNL97_plus_lncRNA::1 Present

[3] 1_A375_pNL7_minus_lncRNA::1 AvgPeak

[4] 2_A375_pNL97_plus_lncRNA::1 AvgPeak

Table 10



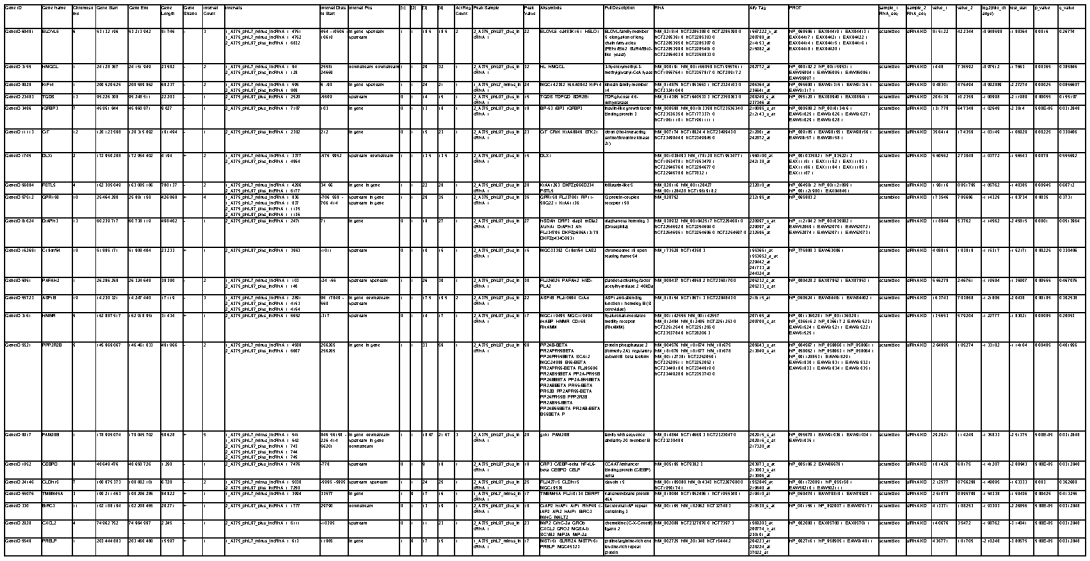


Table 11. AR and EGR1 active regions as determined via ChIP-Seq

Table 11 lists the AR and EGR1 active regions as determinied via ChIP-Seq. EGR1 ChIP-Seq was performed from A375 melanoma cells. The table also contains AR ChIP-Seq active regions (Table 7) to enable comparative analyses.

1_A375_pNL7_minus_lncRNA_AR = AR ChIP-seq from vector control

2_A375_pNL97_plus_lncRNA_AR = AR ChIP-seq from SLNCR1-expressing vector

4_A375_EGR1 = EGR1 ChIP-seq

Table 11

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GeneCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1	1	713,862	714,400	538	2	14.529	15.471	7.176	25	28	14	1	2	2	LOC100288069, LOC100287934	-63, -7189	upstream, upstream	ActReg chr1 #1	1	1	0
2	1	858,150	858,759	609	1	4.421	7.263	10.684	7	15	15	0	2	3	LOC284600, FLJ39609, SAMD11	11639, -3637, -2667	downstream, upstream, upstream	ActReg chr1 #2	0	0	1
3	1	871,728	872,760	1,032	1	3.704	3.656	11.719	8	7	17	1	0	2	SAMD11, NOC2L	11123, 22435	in gene, downstream	ActReg chr1 #3	0	0	1
4	1	875,945	876,617	672	1	6.857	8.143	12	10	15	16	1	0	2	SAMD11, NOC2L	15160, 18398	in gene, downstream	ActReg chr1 #4	0	0	1
5	1	878,186	878,692	506	1	4.562	9.938	11.125	9	14	18	1	0	2	SAMD11, NOC2L	17318, 16240	in gene, downstream	ActReg chr1 #5	0	0	1
6	1	894,244	895,424	1,180	1	9.378	14.73	3.917	19	25	9	1	3	3	NOC2L, KLHL17, PLEKHN1	-155, -1133, -7043	upstream, upstream, upstream	ActReg chr1 #6	0	1	0
7	1	895,655	896,170	515	1	9.333	12.562	0	17	22	0	1	3	3	NOC2L, KLHL17, PLEKHN1	-1233, -55, -5965	upstream, upstream, upstream	ActReg chr1 #7	0	1	0
8	1	896,737	897,298	561	1	5.647	6.059	11	11	9	17	1	3	3	NOC2L, KLHL17, PLEKHN1	-2338, 1050, -4860	upstream, in gene, upstream	ActReg chr1 #8	0	0	1
9	1	899,049	899,607	558	1	2.647	3.941	14.118	6	6	20	1	2	3	NOC2L, KLHL17, PLEKHN1	-4649, 3361, -2549	upstream, in gene, upstream	ActReg chr1 #9	0	0	1
10	1	901,566	902,644	1,078	1	6.5	10.735	14.677	14	16	23	1	2	4	NOC2L, KLHL17, PLEKHN1, C1orf170	-7426, 6138, 228, 15368	upstream, downstream, in gene, downstream	ActReg chr1 #10	0	0	1
11	1	911,288	911,879	591	1	6	6.632	13.105	10	12	19	0	0	2	PLEKHN1, C1orf170	9706, 5890	downstream, in gene	ActReg chr1 #11	0	0	1
12	1	913,749	914,340	591	1	2.176	3.579	11.21	3	5	14	0	0	2	PLEKHN1, C1orf170	12167, 3429	downstream, in gene	ActReg chr1 #12	0	0	1
13	1	935,841	936,619	778	2	11.5	11.25	5.958	23	22	9	1	1	1	HES4	-678	upstream	ActReg chr1 #13	1	1	0
14	1	938,750	939,312	562	1	4.556	3.667	10.722	7	7	15	0	1	2	HES4, ISG15	-3479, -9816	upstream, upstream	ActReg chr1 #14	0	0	1
15	1	982,217	983,099	882	1	3.593	3.04	10.852	6	7	14	2	0	1	AGRN	27,155	in gene	ActReg chr1 #15	0	0	1
16	1	986,761	987,433	672	1	4.524	3.476	11.429	6	5	16	0	0	1	AGRN	31,594	in gene	ActReg chr1 #16	0	0	1
17	1	989,076	989,624	548	1	3.824	6.706	11.353	6	11	18	0	0	1	AGRN	33,847	in gene	ActReg chr1 #17	0	0	1
18	1	994,361	995,383	1,022	2	13.188	12.469	7.3	24	23	21	1	0	1	AGRN	39,369	downstream	ActReg chr1 #18	1	1	0
19	1	999,152	1,000,115	963	1	7.967	9.767	13.3	15	16	17	1	0	2	AGRN, LOC401934	44130, 10054	downstream, downstream	ActReg chr1 #19	0	0	1
20	1	1,021,259	1,021,737	478	1	4.8	5.533	12.933	8	8	19	0	0	1	C1orf159	30,238	in gene	ActReg chr1 #20	0	0	1
21	1	1,051,234	1,051,988	754	2	9	11.087	1.706	18	21	3	1	1	1	C1orf159	125	in gene	ActReg chr1 #21	1	1	0
22	1	1,057,059	1,058,263	1,204	1	4.757	6.459	11.703	10	12	17	0	1	1	C1orf159	-5,925	upstream	ActReg chr1 #22	0	0	1
23	1	1,078,730	1,079,131	401	1	1.818	1.417	11.25	2	2	16	0	0	0				ActReg chr1 #23	0	0	1
24	1	1,080,161	1,080,667	506	1	2.917	4.267	12.733	5	8	18	0	0	0				ActReg chr1 #24	0	0	1
25	1	1,086,688	1,087,468	780	1	3.043	3.84	14.28	6	7	23	0	0	0				ActReg chr1 #25	0	0	1
26	1	1,093,005	1,094,378	1,373	3	7.814	9.698	13.163	14	16	24	1	0	2	MIR200B, MIR200A	-8793, -9552	upstream, upstream	ActReg chr1 #26	0	1	1
27	1	1,100,137	1,100,742	605	1	3.947	5.474	13.21	6	7	18	1	3	5	MIR200B, MIR200A, MIR429, LOC100506376, TTLL10	-2045, -2804, -3946, 14496, -8847	upstream, upstream, upstream, downstream, upstream	ActReg chr1 #27	0	0	1
28	1	1,102,845	1,103,261	416	1	3.538	5	11.231	5	6	16	0	4	5	MIR200B, MIR200A, MIR429, LOC100506376, TTLL10	569, -190, -1332, 11882, -6233	downstream, upstream, upstream, downstream, upstream	ActReg chr1 #28	0	0	1
29	1	1,114,070	1,114,685	615	1	3.632	4.474	12.947	6	6	22	0	1	3	MIR429, LOC100506376, TTLL10	9992, 558, 5091	downstream, in gene, in gene	ActReg chr1 #29	0	0	1
30	1	1,115,323	1,115,858	535	1	1.556	2.176	12.647	2	4	21	1	1	2	LOC100506376, TTLL10	-655, 6304	upstream, in gene	ActReg chr1 #30	0	0	1
31	1	1,120,468	1,120,858	390	1	3.5	8	12.5	5	11	17	0	1	2	LOC100506376, TTLL10	-5728, 11377	upstream, in gene	ActReg chr1 #31	0	0	1
32	1	1,138,788	1,139,638	850	1	2.423	6.385	14.154	4	11	19	0	1	3	TTLL10, TNFRSF18, TNFRSF4	29927, 2876, 10299	downstream, in gene, downstream	ActReg chr1 #32	0	0	1
33	1	1,145,761	1,146,444	683	1	3.8	5.048	10.667	7	7	13	1	1	3	TNFRSF18, TNFRSF4, SDF4	-4013, 3410, 21345	upstream, downstream, downstream	ActReg chr1 #33	0	0	1
34	1	1,147,100	1,147,647	547	1	2.533	5.588	13.177	7	11	19	1	2	3	TNFRSF18, TNFRSF4, SDF4	-5284, 2139, 20074	upstream, in gene, downstream	ActReg chr1 #34	0	0	1
35	1	1,151,445	1,152,028	583	1	1.882	2.917	13.278	5	5	18	0	1	3	TNFRSF18, TNFRSF4, SDF4	-9647, -2224, 15711	upstream, upstream, downstream	ActReg chr1 #35	0	0	1
36	1	1,152,937	1,153,389	452	1	4.154	3.643	11	7	5	18	1	1	2	TNFRSF4, SDF4	-3651, 14284	upstream, in gene	ActReg chr1 #36	0	0	1
37	1	1,157,474	1,158,110	636	1	1.857	3.688	11.368	3	7	15	0	0	3	TNFRSF4, SDF4, B3GALT6	-8280, 9655, -9837	upstream, in gene, upstream	ActReg chr1 #37	0	0	1
38	1	1,173,227	1,174,153	926	1	10.69	12.966	9.276	17	18	14	1	1	3	SDF4, B3GALT6, FAM132A	-6243, 6061, 8412	upstream, downstream, downstream	ActReg chr1 #38	0	1	0
39	1	1,174,493	1,175,810	1,317	1	4.6	6.833	15.095	8	10	22	0	1	3	SDF4, B3GALT6, FAM132A	-7704, 7522, 6951	upstream, downstream, downstream	ActReg chr1 #39	0	0	1
40	1	1,182,505	1,183,158	653	1	3.3	6.65	12.25	5	10	19	1	1	2	FAM132A, UBE2J2	-729, 26403	upstream, downstream	ActReg chr1 #40	0	0	1
41	1	1,207,914	1,208,913	999	1	5.484	6.645	14.065	8	13	23	1	1	2	UBE2J2, SCNN1D	821, -9076	in gene, upstream	ActReg chr1 #41	0	0	1
42	1	1,209,597	1,210,274	677	1	6.636	7.318	10.136	10	9	17	1	2	2	UBE2J2, SCNN1D	-701, -7554	upstream, upstream	ActReg chr1 #42	0	0	1
43	1	1,217,227	1,218,100	873	1	7.407	8	10.741	10	14	17	0	1	3	UBE2J2, SCNN1D, ACAP3	-8429, 174, 25606	upstream, in gene, downstream	ActReg chr1 #43	0	0	1
44	1	1,221,010	1,221,765	755	1	4.875	4.565	14.792	7	9	23	0	0	2	SCNN1D, ACAP3	3898, 21882	in gene, downstream	ActReg chr1 #44	0	0	1
45	1	1,222,170	1,222,829	659	1	3.619	3.19	15	6	5	21	0	0	2	SCNN1D, ACAP3	5010, 20770	in gene, downstream	ActReg chr1 #45	0	0	1
46	1	1,234,197	1,235,470	1,273	3	10.4	10.525	11.6	23	30	15	0	0	3	SCNN1D, ACAP3, PUSL1	17344, 8436, -9161	downstream, in gene, upstream	ActReg chr1 #46	1	1	1
47	1	1,240,651	1,241,099	448	1	5.714	8.214	11.857	8	11	16	0	2	3	ACAP3, PUSL1, CPSF3L	2394, -3119, 19171	in gene, upstream, downstream	ActReg chr1 #47	0	0	1
48	1	1,243,346	1,244,607	1,261	2	10.308	11.487	6.564	23	22	15	1	2	3	ACAP3, PUSL1, CPSF3L	-707, -18, 16070	upstream, upstream, downstream	ActReg chr1 #48	1	1	0
49	1	1,263,666	1,264,283	617	1	4.105	5.737	13.053	7	9	18	0	2	4	CPSF3L, GLTPD1, TAS1R3, DVL1	-3928, 3831, -2752, 20518	upstream, in gene, upstream, downstream	ActReg chr1 #49	0	0	1
50	1	1,266,195	1,267,311	1,116	1	5.486	5.8	12.514	9	11	18	2	2	4	CPSF3L, GLTPD1, TAS1R3, DVL1	-6707, 6610, 27, 17739	upstream, downstream, in gene, downstream	ActReg chr1 #50	0	0	1
51	1	1,267,676	1,268,515	839	1	6.741	7.296	14.518	10	11	20	1	1	4	CPSF3L, GLTPD1, TAS1R3, DVL1	-8049, 7952, 1369, 16397	upstream, downstream, in gene, downstream	ActReg chr1 #51	0	0	1
52	1	1,268,530	1,269,558	1,028	1	7.344	7.219	11.562	13	15	15	1	1	4	CPSF3L, GLTPD1, TAS1R3, DVL1	-8998, 8901, 2318, 15448	upstream, downstream, in gene, downstream	ActReg chr1 #52	0	0	1
53	1	1,273,554	1,274,295	741	1	5.261	3.19	12.043	11	6	17	0	0	3	GLTPD1, TAS1R3, DVL1	13781, 7198, 10568	downstream, downstream, in gene	ActReg chr1 #53	0	0	1
54	1	1,306,101	1,307,092	991	1	5.677	3.44	12.613	10	6	19	0	0	2	LOC100506404, AURKAIP1	3021, 4222	in gene, downstream	ActReg chr1 #54	0	0	1
55	1	1,309,212	1,311,238	2,026	4	12.641	12.828	9.516	46	49	19	1	1	3	LOC100506404, AURKAIP1, CCNL2	6650, 593, 24493	in gene, in gene, downstream	ActReg chr1 #55	1	1	1
56	1	1,334,555	1,336,092	1,537	1	10.271	12.521	6.667	17	17	13	1	2	3	CCNL2, LOC148413, MRPL20	-605, 413, 7370	upstream, in gene, downstream	ActReg chr1 #56	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
57	1	1,342,139	1,343,495	1,356	1	7.558	14.326	6.419	11	30	13	1	2	3	CCNL2, LOC148413, MRPL20	-8099, 7907, -124	upstream, downstream, upstream	ActReg chr1 #57	0	1	0
58	1	1,354,555	1,355,088	533	1	4	1.941	11.706	7	4	17	1	2	2	hCG_20426, TMEM88B	1829, -6687	in gene, upstream	ActReg chr1 #58	0	0	1
59	1	1,365,677	1,366,023	346	1	4.455	5.727	10.818	6	9	15	0	1	4	hCG_20426, TMEM88B, LOC100288271, VWA1	-9200, 4342, 4050, -5053	upstream, downstream, downstream, upstream	ActReg chr1 #59	0	0	1
60	1	1,366,928	1,367,551	623	1	3.579	5.316	11.579	5	10	17	0	2	3	TMEM88B, LOC100288271, VWA1	5731, 2661, -3664	downstream, in gene, upstream	ActReg chr1 #60	0	0	1
61	1	1,371,650	1,372,098	448	1	6	4.286	9.786	8	6	15	0	2	3	TMEM88B, LOC100288271, VWA1	10366, -1974, 971	downstream, upstream, in gene	ActReg chr1 #61	0	0	1
62	1	1,372,660	1,373,095	435	1	5.143	7.071	12.071	8	9	19	0	2	3	TMEM88B, LOC100288271, VWA1	11369, -2977, 1974	downstream, upstream, in gene	ActReg chr1 #62	0	0	1
63	1	1,374,413	1,374,765	352	1	3.818	3.091	12.182	6	6	19	1	1	2	LOC100288271, VWA1	-4689, 3686	upstream, in gene	ActReg chr1 #63	0	0	1
64	1	1,376,820	1,377,321	501	1	3.688	7.875	13.062	5	11	20	0	1	3	LOC100288271, VWA1, ATAD3C	-7170, 6167, -7999	upstream, in gene, upstream	ActReg chr1 #64	0	0	1
65	1	1,391,015	1,391,378	363	1	1.8	3.545	11.818	3	6	17	0	0	1	ATAD3C	6,127	in gene	ActReg chr1 #65	0	0	1
66	1	1,395,737	1,396,166	429	1	2.214	4.357	11.643	6	6	15	1	0	1	ATAD3C	10,882	in gene	ActReg chr1 #66	0	0	1
67	1	1,398,093	1,398,531	438	1	4.071	3.462	12.5	6	6	19	0	0	2	ATAD3C, ATAD3B	13243, -8852	in gene, upstream	ActReg chr1 #67	0	0	1
68	1	1,406,700	1,407,293	593	1	11.167	13.5	7.765	15	24	10	1	1	2	ATAD3C, ATAD3B	21927, -168	downstream, upstream	ActReg chr1 #68	0	1	0
69	1	1,430,520	1,431,097	577	1	3.556	5.889	11.889	7	11	21	0	0	1	ATAD3B	23,644	in gene	ActReg chr1 #69	0	0	1
70	1	1,446,826	1,447,685	859	3	13.963	14.926	8.739	20	25	18	1	1	1	ATAD3A	-268	upstream	ActReg chr1 #70	1	1	1
71	1	1,470,084	1,470,440	356	1	1.833	2.2	10.727	4	4	15	1	0	3	ATAD3A, C1orf70, SSU72	22739, 5478, 40000	downstream, in gene, downstream	ActReg chr1 #71	0	0	1
72	1	1,471,344	1,472,073	729	1	5.522	4.217	14.043	11	6	22	1	0	3	ATAD3A, C1orf70, SSU72	24185, 4032, 38554	downstream, in gene, downstream	ActReg chr1 #72	0	0	1
73	1	1,476,380	1,476,916	536	1	5.118	4.529	12.823	8	6	20	1	1	3	ATAD3A, C1orf70, SSU72	29125, -908, 33614	downstream, upstream, downstream	ActReg chr1 #73	0	0	1
74	1	1,477,573	1,478,226	653	1	4.65	6.85	11.45	8	9	14	0	1	3	ATAD3A, C1orf70, SSU72	30376, -2159, 32363	downstream, upstream, in gene	ActReg chr1 #74	0	0	1
75	1	1,490,482	1,491,070	588	1	5.611	7.5	12.056	8	11	17	0	0	1	SSU72	19,486	in gene	ActReg chr1 #75	0	0	1
76	1	1,510,002	1,510,774	772	3	11	12.375	12.682	22	27	22	1	1	1	SSU72	-126	upstream	ActReg chr1 #76	1	1	1
77	1	1,536,749	1,537,323	574	1	2.778	5.667	11.667	5	9	17	0	1	1	LOC643988	-1,566	upstream	ActReg chr1 #77	0	0	1
78	1	1,563,336	1,564,141	805	1	5.16	6.44	12.88	8	11	18	1	1	3	MIB2, MMP23B, CDK11B	12943, -3822, 26735	in gene, upstream, downstream	ActReg chr1 #78	0	0	1
79	1	1,590,202	1,590,809	607	2	10.158	11.105	7.263	18	17	12	1	1	2	CDK11B, RP11-345P4.4	-32, 33738	upstream, downstream	ActReg chr1 #79	1	1	0
80	1	1,618,485	1,618,982	497	1	3.562	4.75	10.312	6	7	20	0	0	1	RP11-345P4.4	5,510	in gene	ActReg chr1 #80	0	0	1
81	1	1,623,948	1,624,773	825	2	9.923	14.462	3.692	23	27	7	1	1	2	RP11-345P4.4, CDK11A	-117, 31431	upstream, downstream	ActReg chr1 #81	1	1	0
82	1	1,822,872	1,823,558	686	1	5.136	5.5	11.909	7	9	18	1	1	1	GNB1	-720	upstream	ActReg chr1 #82	0	0	1
83	1	1,847,041	1,847,587	546	1	3.824	4.824	11	6	8	13	0	1	2	CALML6, TMEM52	1048, 3426	in gene, downstream	ActReg chr1 #83	0	0	1
84	1	1,849,735	1,850,256	521	1	4.188	5.438	10.812	6	9	20	1	1	2	CALML6, TMEM52	3729, 745	downstream, in gene	ActReg chr1 #84	0	0	1
85	1	1,851,259	1,851,963	704	1	5.636	4.409	11.954	10	7	17	1	1	2	CALML6, TMEM52	5345, -871	downstream, upstream	ActReg chr1 #85	0	0	1
86	1	1,900,038	1,900,659	621	1	3.438	4.263	12.263	5	7	17	0	0	1	KIAA1751	34,928	in gene	ActReg chr1 #86	0	0	1
87	1	1,901,741	1,902,296	555	1	4.588	4.765	13	8	7	17	0	0	1	KIAA1751	33,258	in gene	ActReg chr1 #87	0	0	1
88	1	1,952,956	1,953,586	630	1	3.2	7	12.35	4	14	20	0	1	1	GABRD	2,503	in gene	ActReg chr1 #88	0	0	1
89	1	1,959,105	1,959,613	508	1	2.867	3.733	12.933	5	6	20	1	0	1	GABRD	8,591	in gene	ActReg chr1 #89	0	0	1
90	1	1,981,201	1,981,557	356	1	7.545	5.364	11.273	10	8	15	1	1	1	PRKCZ	-530	upstream	ActReg chr1 #90	0	0	1
91	1	2,007,031	2,007,423	392	1	4.75	4.417	13.083	7	6	17	0	0	1	PRKCZ	25,318	in gene	ActReg chr1 #91	0	0	1
92	1	2,064,986	2,065,580	594	1	9.526	9.789	11.474	14	17	16	1	0	1	PRKCZ	83,374	in gene	ActReg chr1 #92	0	0	1
93	1	2,066,258	2,067,799	1,541	2	10.5	11.938	7.271	16	24	14	1	0	1	PRKCZ	85,119	in gene	ActReg chr1 #93	1	1	0
94	1	2,100,495	2,101,109	614	1	1.471	2.526	10.842	2	5	15	0	0	1	PRKCZ	118,893	in gene	ActReg chr1 #94	0	0	1
95	1	2,110,264	2,110,780	516	1	3.5	2.75	13.438	5	5	23	0	0	4	PRKCZ, LOC100506504, C1orf86, LOC100128003	128613, 4970, 28650, 14502	in gene, downstream, downstream, downstream	ActReg chr1 #95	0	0	1
96	1	2,111,340	2,111,804	464	1	1.5	4.786	12.5	2	7	20	0	0	4	PRKCZ, LOC100506504, C1orf86, LOC100128003	129663, 3920, 27600, 13452	in gene, downstream, downstream, downstream	ActReg chr1 #96	0	0	1
97	1	2,120,843	2,121,583	740	1	11.565	8.696	7.522	20	12	13	1	1	4	PRKCZ, LOC100506504, C1orf86, LOC100128003	139304, -5721, 17959, 3811	downstream, upstream, in gene, in gene	ActReg chr1 #97	1	0	0
98	1	2,134,220	2,134,744	524	1	5.75	4.25	11.938	11	6	17	0	0	2	C1orf86, LOC100128003	4690, -9458	in gene, upstream	ActReg chr1 #98	0	0	1
99	1	2,135,048	2,135,609	561	1	3.312	8.588	11.823	7	11	17	0	0	1	C1orf86	3,844	in gene	ActReg chr1 #99	0	0	1
100	1	2,137,184	2,137,635	451	1	9.467	3.2	11.733	15	6	16	1	1	1	C1orf86	1,763	in gene	ActReg chr1 #100	0	0	1
101	1	2,139,099	2,139,729	630	1	4.526	7.25	11.25	8	14	17	0	1	1	C1orf86	-242	upstream	ActReg chr1 #101	0	0	1
102	1	2,145,509	2,146,665	1,156	1	3.444	7.306	12.611	7	17	18	0	1	1	C1orf86	-6,915	upstream	ActReg chr1 #102	0	0	1
103	1	2,158,043	2,158,553	510	1	6.438	3.5	14.938	11	5	24	1	1	1	SKI	-1,836	upstream	ActReg chr1 #103	0	0	1
104	1	2,162,283	2,162,864	581	1	11.611	10.222	5.222	18	13	10	0	1	1	SKI	2,439	in gene	ActReg chr1 #104	1	0	0
105	1	2,199,343	2,199,950	607	1	3.895	5.316	11.474	5	8	17	0	0	1	SKI	39,512	in gene	ActReg chr1 #105	0	0	1
106	1	2,202,142	2,202,798	656	1	1.733	4.381	10.524	3	7	14	0	0	1	SKI	42,336	in gene	ActReg chr1 #106	0	0	1
107	1	2,223,851	2,224,514	663	1	4.762	5.714	12.286	8	10	19	0	0	1	SKI	64,048	in gene	ActReg chr1 #107	0	0	1
108	1	2,243,990	2,244,721	731	1	3.652	4.217	12.043	5	7	18	0	0	2	SKI, MORN1	84221, 78638	downstream, downstream	ActReg chr1 #108	0	0	1
109	1	2,248,911	2,249,997	1,086	1	5.088	2.529	11.912	11	6	17	1	0	2	SKI, MORN1	89320, 73539	downstream, downstream	ActReg chr1 #109	0	0	1
110	1	2,251,878	2,252,677	799	1	3.96	2.375	13.44	7	5	19	0	0	1	MORN1	70,716	downstream	ActReg chr1 #110	0	0	1
111	1	2,254,906	2,255,548	642	1	2	3.133	11.35	4	5	18	1	0	1	MORN1	67,766	in gene	ActReg chr1 #111	0	0	1
112	1	2,259,073	2,259,751	678	1	3.412	2.421	11.238	6	4	16	1	0	1	MORN1	63,581	in gene	ActReg chr1 #112	0	0	1
113	1	2,260,190	2,260,775	585	1	2.263	2.053	11.368	4	4	16	0	0	1	MORN1	62,511	in gene	ActReg chr1 #113	0	0	1
114	1	2,264,519	2,265,258	739	1	4.304	1.476	10.957	6	2	17	0	0	1	MORN1	58,105	in gene	ActReg chr1 #114	0	0	1
115	1	2,267,168	2,267,848	680	1	4.955	4.045	12.864	8	7	17	0	0	1	MORN1	55,485	in gene	ActReg chr1 #115	0	0	1
116	1	2,271,513	2,272,327	814	1	5.364	4.2	12.538	8	7	18	0	0	1	MORN1	51,073	in gene	ActReg chr1 #116	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
117	1	2,275,442	2,275,889	447	1	4	5.5	10.571	6	9	15	0	0	1	MORN1	47,328	in gene	ActReg chr1 #117	0	0	1
118	1	2,276,684	2,277,292	608	1	6.053	2.947	14.368	13	4	23	1	0	1	MORN1	46,005	in gene	ActReg chr1 #118	0	0	1
119	1	2,313,003	2,313,786	783	1	4.917	7.087	12.083	10	15	15	0	0	2	MORN1, RER1	9599, -9820	in gene, upstream	ActReg chr1 #119	0	0	1
120	1	2,313,855	2,314,386	531	1	5.353	5	11.706	8	10	16	0	0	2	MORN1, RER1	8873, -9094	in gene, upstream	ActReg chr1 #120	0	0	1
121	1	2,344,067	2,345,246	1,179	1	8.167	11	9.323	14	16	17	1	1	2	RER1, PEX10	21442, -646	downstream, upstream	ActReg chr1 #121	0	1	0
122	1	2,347,484	2,347,961	477	1	2.467	4.643	13.4	4	8	20	0	1	1	PEX10	-3,712	upstream	ActReg chr1 #122	0	0	1
123	1	2,350,082	2,350,585	503	1	4.333	8.467	11.6	9	10	15	0	1	1	PEX10	-6,323	upstream	ActReg chr1 #123	0	0	1
124	1	2,358,440	2,358,982	542	1	4.294	6.235	12.177	6	9	19	0	0	0				ActReg chr1 #124	0	0	1
125	1	2,364,265	2,364,748	483	1	3.667	2.933	13.733	5	6	20	0	0	0				ActReg chr1 #125	0	0	1
126	1	2,365,173	2,365,813	640	1	2.65	2.3	13.25	4	4	22	0	0	0				ActReg chr1 #126	0	0	1
127	1	2,375,572	2,376,053	481	1	2.5	1.933	13.2	4	3	19	1	0	0				ActReg chr1 #127	0	0	1
128	1	2,385,091	2,385,753	662	1	2.25	3.6	12	4	5	21	0	0	0				ActReg chr1 #128	0	0	1
129	1	2,388,429	2,389,448	1,019	1	4.929	4.906	12.062	9	12	17	0	0	0				ActReg chr1 #129	0	0	1
130	1	2,392,428	2,393,069	641	1	3.4	3.15	12.45	7	7	20	0	0	0				ActReg chr1 #130	0	0	1
131	1	2,396,607	2,397,078	471	1	3.308	3.667	10.8	6	6	18	0	0	0				ActReg chr1 #131	0	0	1
132	1	2,397,383	2,398,039	656	1	3.6	5.75	13.55	6	8	21	0	0	1	PLCH2	-10,043	upstream	ActReg chr1 #132	0	0	1
133	1	2,398,065	2,398,509	444	1	5.286	6.143	12.571	8	9	18	0	0	1	PLCH2	-9,467	upstream	ActReg chr1 #133	0	0	1
134	1	2,403,734	2,404,115	381	1	2.75	4.167	12.5	5	8	17	0	1	1	PLCH2	-3,830	upstream	ActReg chr1 #134	0	0	1
135	1	2,405,339	2,405,781	442	1	4	8.429	11.286	6	11	16	0	1	1	PLCH2	-2,194	upstream	ActReg chr1 #135	0	0	1
136	1	2,407,234	2,408,228	994	1	3.71	3.6	12.806	7	8	17	0	1	1	PLCH2	-23	upstream	ActReg chr1 #136	0	0	1
137	1	2,409,443	2,410,211	768	1	2.556	4.5	13.458	3	9	18	1	1	1	PLCH2	2,073	in gene	ActReg chr1 #137	0	0	1
138	1	2,411,050	2,411,728	678	1	4.4	4.81	13.571	7	9	19	1	0	1	PLCH2	3,635	in gene	ActReg chr1 #138	0	0	1
139	1	2,418,189	2,418,709	520	1	6.438	5.188	12.375	9	7	17	0	0	1	PLCH2	10,695	in gene	ActReg chr1 #139	0	0	1
140	1	2,421,961	2,422,494	533	1	4.562	6.438	12.312	8	8	20	0	0	1	PLCH2	14,473	in gene	ActReg chr1 #140	0	0	1
141	1	2,434,000	2,434,906	906	1	3.321	2.929	11.143	8	5	16	2	0	2	PLCH2, PANK4	26699, 23582	in gene, downstream	ActReg chr1 #141	0	0	1
142	1	2,435,773	2,436,360	587	1	2.647	3.789	11.105	5	5	15	1	0	2	PLCH2, PANK4	28312, 21969	in gene, downstream	ActReg chr1 #142	0	0	1
143	1	2,441,176	2,441,961	785	1	5.4	2.273	14.04	9	4	23	0	0	2	PLCH2, PANK4	33814, 16467	downstream, in gene	ActReg chr1 #143	0	0	1
144	1	2,442,209	2,442,831	622	1	11.895	4.211	12.947	3	6	18	0	0	2	PLCH2, PANK4	34766, 15515	downstream, in gene	ActReg chr1 #144	0	0	1
145	1	2,449,836	2,450,535	699	1	2.182	2.095	11.636	5	4	15	1	0	2	PANK4, HES5	7850, 11499	in gene, downstream	ActReg chr1 #145	0	0	1
146	1	2,456,997	2,458,417	1,420	3	15.773	16.364	8.5	35	39	18	1	1	2	PANK4, HES5	328, 3977	in gene, downstream	ActReg chr1 #146	1	1	1
147	1	2,464,092	2,464,852	760	1	4.792	4.375	12.167	10	9	17	0	2	2	PANK4, HES5	-6437, -2788	upstream, upstream	ActReg chr1 #147	0	0	1
148	1	2,473,272	2,473,711	439	1	4.786	4.429	13.071	8	8	16	0	0	1	LOC115110	10,793	downstream	ActReg chr1 #148	0	0	1
149	1	2,476,288	2,477,108	820	1	3	3.885	12.462	5	9	16	0	0	1	LOC115110	7,586	downstream	ActReg chr1 #149	0	0	1
150	1	2,477,838	2,478,304	466	1	7.333	7.533	12.933	9	12	19	1	0	3	LOC115110, LOC100133445, TNFRSF14	6213, 10377, -9734	downstream, downstream, upstream	ActReg chr1 #150	0	0	1
151	1	2,488,777	2,489,314	537	1	3.176	4.882	10.471	4	6	18	0	3	4	LOC115110, LOC100133445, TNFRSF14, LOC100506589	-4761, -597, 1240, -8929	upstream, upstream, in gene, upstream	ActReg chr1 #151	0	0	1
152	1	2,500,563	2,500,923	360	1	2.273	2.182	9.364	3	3	13	0	0	2	TNFRSF14, LOC100506589	12938, 2769	downstream, in gene	ActReg chr1 #152	0	0	1
153	1	2,527,038	2,527,465	427	1	1.769	2.636	11.357	4	4	17	1	0	2	C1orf93, MMEL1	9002, 37230	downstream, in gene	ActReg chr1 #153	0	0	1
154	1	2,527,882	2,528,759	877	1	5	3.308	13.407	8	6	17	0	0	2	C1orf93, MMEL1	10071, 36161	downstream, in gene	ActReg chr1 #154	0	0	1
155	1	2,573,950	2,575,090	1,140	1	10.722	6.944	8.167	18	13	16	1	0	2	MMEL1, LOC100287898	-10039, 131710	upstream, in gene	ActReg chr1 #155	1	0	0
156	1	2,575,753	2,576,435	682	1	1.857	2.19	12.476	3	3	16	0	0	1	LOC100287898	130,136	in gene	ActReg chr1 #156	0	0	1
157	1	2,694,347	2,694,872	525	1	2.5	3	11.5	5	5	18	0	0	1	LOC100287898	11,621	in gene	ActReg chr1 #157	0	0	1
158	1	2,716,691	2,717,331	640	1	2.55	3.75	11.15	5	5	15	1	0	0				ActReg chr1 #158	0	0	1
159	1	2,720,842	2,721,140	298	1	1.667	2.889	10	2	5	13	0	0	0				ActReg chr1 #159	0	0	1
160	1	2,729,570	2,730,120	550	1	3.625	2.824	13.471	7	5	22	0	0	0				ActReg chr1 #160	0	0	1
161	1	2,737,550	2,738,151	601	1	3.333	3.053	11.474	6	5	17	0	0	0				ActReg chr1 #161	0	0	1
162	1	2,738,448	2,739,003	555	1	3.533	2.941	12.412	5	5	18	0	0	0				ActReg chr1 #162	0	0	1
163	1	2,749,027	2,749,491	464	1	3.154	1.667	10.929	7	4	16	0	0	0				ActReg chr1 #163	0	0	1
164	1	2,782,277	2,783,467	1,190	1	4.343	3.297	12.108	11	7	20	0	0	0				ActReg chr1 #164	0	0	1
165	1	2,784,525	2,784,914	389	1	2.5	2.083	12	4	4	17	0	0	0				ActReg chr1 #165	0	0	1
166	1	2,791,327	2,791,709	382	1	3.75	1.833	10.417	5	3	15	0	0	0				ActReg chr1 #166	0	0	1
167	1	2,799,843	2,800,622	779	1	2.091	3.083	12.458	4	5	20	0	0	0				ActReg chr1 #167	0	0	1
168	1	2,847,476	2,848,287	811	1	2.32	5.8	12.28	4	10	22	1	0	0				ActReg chr1 #168	0	0	1
169	1	2,851,319	2,851,880	561	1	2.733	3.333	10.667	5	5	14	0	0	0				ActReg chr1 #169	0	0	1
170	1	2,882,951	2,883,401	450	1	3.417	4.714	10.286	6	7	16	0	0	0				ActReg chr1 #170	0	0	1
171	1	2,896,885	2,897,357	472	1	4.133	5.5	10.667	6	8	16	0	0	0				ActReg chr1 #171	0	0	1
172	1	2,929,243	2,930,003	760	1	2	4.263	10.75	3	7	15	1	0	1	ACTRT2	-8,423	upstream	ActReg chr1 #172	0	0	1
173	1	2,944,669	2,945,139	470	1	3.933	3.2	10.4	6	5	16	0	0	1	ACTRT2	6,858	downstream	ActReg chr1 #173	0	0	1
174	1	2,984,324	2,984,730	406	1	4.167	1.917	11.833	5	3	14	1	2	2	FLJ42875, PRDM16	-238, -1215	upstream, upstream	ActReg chr1 #174	0	0	1
175	1	3,012,986	3,013,427	441	1	3.214	3.286	14.429	5	5	24	0	0	1	PRDM16	27,464	in gene	ActReg chr1 #175	0	0	1
176	1	3,021,766	3,022,073	307	1	1	3	12	1	3	14	0	0	1	PRDM16	36,177	in gene	ActReg chr1 #176	0	0	1
177	1	3,031,814	3,032,309	495	1	3.143	2.533	13.533	5	4	17	0	0	1	PRDM16	46,319	in gene	ActReg chr1 #177	0	0	1
178	1	3,157,958	3,158,542	584	1	3.278	5.889	13.056	6	11	17	1	0	1	PRDM16	172,508	in gene	ActReg chr1 #178	0	0	1
179	1	3,163,860	3,164,198	338	1	5.556	4.364	10.273	8	7	14	1	0	1	PRDM16	178,287	in gene	ActReg chr1 #179	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
180	1	3,179,404	3,180,237	833	1	2.385	3.462	12.039	5	7	17	0	0	1	PRDM16	194,078	in gene	ActReg chr1 #180	0	0	1
181	1	3,195,664	3,196,185	521	1	3.867	7	13.438	7	12	18	1	0	1	PRDM16	210,182	in gene	ActReg chr1 #181	0	0	1
182	1	3,201,417	3,201,883	466	1	2.571	2.778	12.429	4	4	16	0	0	1	PRDM16	215,908	in gene	ActReg chr1 #182	0	0	1
183	1	3,228,425	3,229,044	619	1	4.368	4	13.263	7	7	18	0	0	1	PRDM16	242,992	in gene	ActReg chr1 #183	0	0	1
184	1	3,289,429	3,289,942	513	1	4.875	3.867	11.438	7	5	15	0	0	1	PRDM16	303,943	in gene	ActReg chr1 #184	0	0	1
185	1	3,308,229	3,308,581	352	1	1.364	1.182	11.454	2	2	16	0	0	1	PRDM16	322,663	in gene	ActReg chr1 #185	0	0	1
186	1	3,328,989	3,329,530	541	1	2.706	3.176	11.177	4	5	16	1	0	1	PRDM16	343,517	in gene	ActReg chr1 #186	0	0	1
187	1	3,344,669	3,345,324	655	1	1.368	3.524	11.857	2	6	19	0	0	1	PRDM16	359,254	in gene	ActReg chr1 #187	0	0	1
188	1	3,379,814	3,380,240	426	1	5.231	1.769	12.385	11	3	17	0	0	1	ARHGEF16	8,880	in gene	ActReg chr1 #188	0	0	1
189	1	3,384,642	3,385,260	618	1	4.842	4.737	11.105	8	6	16	0	0	1	ARHGEF16	13,804	in gene	ActReg chr1 #189	0	0	1
190	1	3,388,327	3,388,996	669	1	5.619	6.762	13.048	7	10	21	0	0	1	ARHGEF16	17,514	in gene	ActReg chr1 #190	0	0	1
191	1	3,389,790	3,390,195	405	1	2.167	3.615	13.769	3	5	22	0	0	1	ARHGEF16	18,845	in gene	ActReg chr1 #191	0	0	1
192	1	3,413,340	3,414,152	812	1	3.538	4.269	14.731	6	8	22	0	0	1	MEGF6	114,313	in gene	ActReg chr1 #192	0	0	1
193	1	3,418,583	3,419,516	933	1	6.379	8.724	12.379	12	19	18	0	0	1	MEGF6	109,010	in gene	ActReg chr1 #193	0	0	1
194	1	3,425,174	3,425,733	559	1	3.556	4.333	11.778	7	7	15	1	0	1	MEGF6	102,606	in gene	ActReg chr1 #194	0	0	1
195	1	3,426,206	3,426,881	675	1	4.35	6.182	12.682	9	11	20	1	0	1	MEGF6	101,516	in gene	ActReg chr1 #195	0	0	1
196	1	3,427,089	3,427,508	419	1	7.692	6.231	11.308	10	8	18	1	0	1	MEGF6	100,761	in gene	ActReg chr1 #196	0	0	1
197	1	3,427,790	3,428,250	460	1	4.286	4.857	11.714	7	10	20	1	0	1	MEGF6	100,039	in gene	ActReg chr1 #197	0	0	1
198	1	3,435,718	3,436,138	420	1	1.364	4.308	13.923	3	6	18	1	0	1	MEGF6	92,131	in gene	ActReg chr1 #198	0	0	1
199	1	3,437,560	3,437,867	307	1	6.9	3.8	12.4	11	6	17	0	0	1	MEGF6	90,346	in gene	ActReg chr1 #199	0	0	1
200	1	3,464,902	3,465,375	473	1	6.429	3.5	11.214	10	10	18	0	0	1	MEGF6	62,921	in gene	ActReg chr1 #200	0	0	1
201	1	3,469,774	3,470,300	526	1	2.133	2.857	11.688	4	6	15	0	0	2	MEGF6, MIR551A	58022, 7317	in gene, downstream	ActReg chr1 #201	0	0	1
202	1	3,473,851	3,474,320	469	1	4.667	2.8	12.467	8	5	19	0	0	2	MEGF6, MIR551A	53974, 3269	in gene, downstream	ActReg chr1 #202	0	0	1
203	1	3,493,933	3,494,655	722	1	1.682	5.273	12.364	3	9	21	0	0	1	MEGF6	33,765	in gene	ActReg chr1 #203	0	0	1
204	1	3,500,427	3,500,802	375	1	3.833	2.833	13.083	5	6	21	1	0	1	MEGF6	27,445	in gene	ActReg chr1 #204	0	0	1
205	1	3,514,722	3,515,205	483	1	2.867	4.933	13.333	5	6	19	0	0	1	MEGF6	13,096	in gene	ActReg chr1 #205	0	0	1
206	1	3,568,029	3,568,556	527	1	2.824	4.118	12.294	4	8	17	1	2	2	WDR8, TP73	-1621, -837	upstream, upstream	ActReg chr1 #206	0	0	1
207	1	3,590,907	3,591,593	686	1	1.467	2.318	13	4	5	21	0	1	2	TP73, LOC100506635	22121, 720	in gene, downstream	ActReg chr1 #207	0	0	1
208	1	3,602,619	3,603,064	445	1	3.143	3.091	10.571	5	4	15	0	0	1	TP73	33,712	in gene	ActReg chr1 #208	0	0	1
209	1	3,606,550	3,607,173	623	1	3	2.474	11.2	5	4	15	1	0	1	TP73	37,732	in gene	ActReg chr1 #209	0	0	1
210	1	3,634,462	3,634,959	497	1	4.125	4.125	11.812	7	8	16	1	0	1	TP73	65,581	in gene	ActReg chr1 #210	0	0	1
211	1	3,643,780	3,644,761	981	1	2.607	5.167	13.5	5	10	18	0	0	2	TP73, KIAA0495	75141, 19667	in gene, downstream	ActReg chr1 #211	0	0	1
212	1	3,647,168	3,647,738	570	1	3.222	2.722	12.167	5	4	17	0	0	2	TP73, KIAA0495	78324, 16484	in gene, downstream	ActReg chr1 #212	0	0	1
213	1	3,712,675	3,713,375	700	2	11.381	12.905	3.714	19	20	5	1	1	1	LRRC47	43	in gene	ActReg chr1 #213	1	1	0
214	1	3,773,500	3,774,236	736	2	11.522	8.957	11.454	18	13	15	1	2	2	KIAA0562, DFFB	-71, 23	upstream, in gene	ActReg chr1 #214	1	0	1
215	1	3,817,294	3,818,114	820	1	8.346	12.885	8.192	12	20	11	1	2	2	C1orf174, LOC100133612	-847, 736	upstream, in gene	ActReg chr1 #215	0	1	0
216	1	3,820,144	3,820,555	411	1	1.727	5.231	12.154	3	6	16	0	1	2	C1orf174, LOC100133612	-3492, 3381	upstream, in gene	ActReg chr1 #216	0	0	1
217	1	3,830,809	3,831,807	998	1	2.774	3.806	10.968	4	6	17	0	0	1	LOC100133612	14,340	in gene	ActReg chr1 #217	0	0	1
218	1	4,028,784	4,029,366	582	1	9.167	12.944	2.667	15	24	5	0	0	0				ActReg chr1 #218	0	1	0
219	1	4,143,433	4,144,131	698	1	4.591	11.227	6.136	7	16	9	0	0	0				ActReg chr1 #219	0	1	0
220	1	4,527,219	4,527,702	483	1	3.4	2.867	10.4	5	4	14	0	0	0				ActReg chr1 #220	0	0	1
221	1	4,696,297	4,697,491	1,194	1	5.892	14.865	6.189	9	25	10	0	0	0				ActReg chr1 #221	0	1	0
222	1	4,719,661	4,720,121	460	1	5	3.357	11.429	8	5	17	0	0	1	AJAP1	4,786	in gene	ActReg chr1 #222	0	0	1
223	1	4,787,159	4,787,579	420	1	3.308	3.692	10.923	4	5	13	0	0	1	AJAP1	72,264	in gene	ActReg chr1 #223	0	0	1
224	1	6,051,797	6,053,045	1,248	2	12.342	16.667	3.857	23	36	7	1	1	1	NPHP4	110	in gene	ActReg chr1 #224	1	1	0
225	1	6,076,000	6,076,687	687	1	7	11	6.682	11	16	11	0	0	1	KCNAB2	-10,037	upstream	ActReg chr1 #225	0	1	0
226	1	6,100,871	6,101,435	564	1	1.882	2.765	13.588	3	4	20	0	0	1	KCNAB2	14,773	in gene	ActReg chr1 #226	0	0	1
227	1	6,112,112	6,113,268	1,156	2	11.556	13.417	2	27	22	4	0	0	1	KCNAB2	26,310	in gene	ActReg chr1 #227	1	1	0
228	1	6,131,677	6,132,387	710	1	5.13	5.087	10.87	9	8	17	1	0	1	KCNAB2	45,652	in gene	ActReg chr1 #228	0	0	1
229	1	6,138,643	6,139,161	518	1	4	3.75	11.938	7	7	18	0	0	1	KCNAB2	52,522	in gene	ActReg chr1 #229	0	0	1
230	1	6,181,392	6,181,873	481	1	5.667	5.133	12.2	10	7	16	0	0	1	CHD5	58,562	in gene	ActReg chr1 #230	0	0	1
231	1	6,188,054	6,188,540	486	1	4.8	5.733	12	7	8	17	1	0	1	CHD5	51,897	in gene	ActReg chr1 #231	0	0	1
232	1	6,189,778	6,190,210	432	1	2.5	2.929	11.286	4	4	16	0	0	1	CHD5	50,200	in gene	ActReg chr1 #232	0	0	1
233	1	6,217,215	6,218,802	1,587	2	8.92	14.44	6.277	22	23	12	0	0	1	CHD5	22,186	in gene	ActReg chr1 #233	1	1	0
234	1	6,221,430	6,222,491	1,061	2	17.515	20.606	3.034	33	42	7	0	0	1	CHD5	18,234	in gene	ActReg chr1 #234	1	1	0
235	1	6,226,373	6,226,933	560	1	5.8	4.647	10.235	12	8	13	0	0	1	CHD5	13,541	in gene	ActReg chr1 #235	0	0	1
236	1	6,259,129	6,260,192	1,063	2	26.559	35.235	8.912	84	108	17	1	2	2	RPL22, RNF207	19, -6529	in gene, upstream	ActReg chr1 #236	1	1	0
237	1	6,269,147	6,269,834	687	1	10.864	15.364	6.545	19	27	12	1	0	2	RPL22, RNF207	-9811, 3301	upstream, in gene	ActReg chr1 #237	0	1	0
238	1	6,296,246	6,296,722	476	1	4.533	10.067	5.867	6	15	11	1	2	3	ICMT, C1orf211, HES3	-440, -1384, -7768	upstream, upstream, upstream	ActReg chr1 #238	0	1	0
239	1	6,301,897	6,302,379	482	1	2.733	7.2	11.533	5	11	18	1	2	4	ICMT, C1orf211, HES3, GPR153	-6094, 4270, -2114, 18897	upstream, downstream, upstream, downstream	ActReg chr1 #239	0	0	1
240	1	6,305,133	6,306,058	925	3	13.241	12.621	8.793	36	27	17	1	1	4	ICMT, C1orf211, HES3, GPR153	-9551, 7727, 1343, 15440	upstream, downstream, in gene, downstream	ActReg chr1 #240	1	1	1
241	1	6,306,076	6,306,851	775	1	5.8	4.76	12.96	9	11	26	1	1	3	C1orf211, HES3, GPR153	8595, 2211, 14572	downstream, downstream, downstream	ActReg chr1 #241	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
242	1	6,310,018	6,310,601	583	1	4	5.056	11.611	6	8	15	1	0	2	HES3, GPR153	6057, 10726	downstream, in gene	ActReg chr1 #242	0	0	1
243	1	6,322,120	6,322,755	635	1	7.55	5.8	11.7	10	11	15	0	2	3	GPR153, ACOT7, UNQ6193	-1402, 131389, -4078	upstream, downstream, upstream	ActReg chr1 #243	0	0	1
244	1	6,332,934	6,334,239	1,305	2	8.925	10.75	8.675	14	15	19	0	0	2	ACOT7, UNQ6193	120240, 7071	in gene, downstream	ActReg chr1 #244	0	1	1
245	1	6,336,686	6,337,300	614	1	4.158	5.158	13.316	7	7	22	0	0	2	ACOT7, UNQ6193	116833, 10478	in gene, downstream	ActReg chr1 #245	0	0	1
246	1	6,339,582	6,340,323	741	1	3.591	4.875	11.708	8	7	22	1	0	1	ACOT7	113,874	in gene	ActReg chr1 #246	0	0	1
247	1	6,490,958	6,491,205	247	1	3.25	4.75	11	5	6	14	0	1	2	ESPN, MIR4252	6233, -1125	in gene, upstream	ActReg chr1 #247	0	0	1
248	1	6,503,797	6,504,284	487	1	5.667	2.733	12.933	10	6	18	0	0	1	ESPN	19,192	in gene	ActReg chr1 #248	0	0	1
249	1	6,506,951	6,507,730	779	1	8.125	14.417	6	14	25	9	1	0	1	ESPN	22,492	in gene	ActReg chr1 #249	0	1	0
250	1	6,535,372	6,535,946	574	1	7.286	6	13.667	11	9	24	0	0	2	TNFRSF25, PLEKHG5	-9404, 44410	upstream, in gene	ActReg chr1 #250	0	0	1
251	1	6,546,047	6,546,732	685	1	4.227	6.5	11.091	10	12	18	0	0	1	PLEKHG5	33,680	in gene	ActReg chr1 #251	0	0	1
252	1	6,550,720	6,551,180	460	1	7.733	6.692	14.867	14	10	25	1	0	1	PLEKHG5	29,119	in gene	ActReg chr1 #252	0	0	1
253	1	6,556,706	6,557,335	629	1	3.526	8.474	11.79	7	15	18	0	0	1	PLEKHG5	23,049	in gene	ActReg chr1 #253	0	0	1
254	1	6,564,982	6,565,512	530	1	4.765	4	11.765	6	6	21	0	0	1	PLEKHG5	14,822	in gene	ActReg chr1 #254	0	0	1
255	1	6,613,807	6,615,100	1,293	2	27.75	30.825	6.225	93	110	15	1	2	2	NOL9, TAS1R1	205, -885	in gene, upstream	ActReg chr1 #255	1	1	0
256	1	6,662,196	6,663,581	1,385	1	12.698	9.698	6.324	24	20	13	1	1	1	KLHL21	41	in gene	ActReg chr1 #256	1	0	0
257	1	6,673,268	6,673,834	566	1	7.278	12.444	3.353	13	21	7	1	1	1	PHF13	-205	upstream	ActReg chr1 #257	0	1	0
258	1	6,760,807	6,762,473	1,666	2	38.423	42.346	4.308	169	181	9	1	1	1	DNAJC11	326	in gene	ActReg chr1 #258	1	1	0
259	1	7,106,253	7,106,865	612	1	8.684	11.579	1.842	15	23	5	0	0	2	CAMTA1, LOC100505910	261175, 5205	in gene, downstream	ActReg chr1 #259	0	1	0
260	1	7,135,189	7,136,179	990	2	14.806	15.452	3.71	39	30	7	0	0	1	CAMTA1	290,300	in gene	ActReg chr1 #260	1	1	0
261	1	7,325,799	7,326,684	885	2	12.111	10.518	6.037	21	18	14	0	0	1	CAMTA1	480,857	in gene	ActReg chr1 #261	1	1	0
262	1	7,373,017	7,373,752	735	1	5.261	9.565	3.5	13	12	6	0	0	1	CAMTA1	528,000	in gene	ActReg chr1 #262	0	1	0
263	1	7,496,644	7,497,282	638	1	3.5	3.9	12.95	6	6	21	0	0	1	CAMTA1	651,579	in gene	ActReg chr1 #263	0	0	1
264	1	7,500,014	7,500,567	553	1	5.118	3.824	10.294	11	5	14	0	0	1	CAMTA1	654,906	in gene	ActReg chr1 #264	0	0	1
265	1	7,578,448	7,578,861	413	1	4.769	2.846	10.769	8	4	16	0	0	1	CAMTA1	733,270	in gene	ActReg chr1 #265	0	0	1
266	1	7,620,802	7,621,839	1,037	1	3.467	3.733	13.312	6	8	19	0	0	1	CAMTA1	775,936	in gene	ActReg chr1 #266	0	0	1
267	1	7,676,182	7,677,489	1,307	2	11.585	15.39	4.59	30	34	8	0	0	1	CAMTA1	831,451	in gene	ActReg chr1 #267	1	1	0
268	1	7,844,755	7,845,141	386	1	7.417	6	10	10	9	15	1	1	2	VAMP3, PER3	13619, 185	downstream, in gene	ActReg chr1 #268	0	0	1
269	1	8,014,046	8,014,659	613	1	12	9.15	11.15	19	12	15	1	1	1	PARK7	-7,362	upstream	ActReg chr1 #269	1	0	0
270	1	8,021,108	8,022,272	1,164	2	14.405	21.216	5.194	35	47	10	1	1	1	PARK7	-24	upstream	ActReg chr1 #270	1	1	0
271	1	8,086,067	8,087,530	1,463	2	11.587	14.696	5.079	25	27	10	1	1	1	ERRFI1	-405	upstream	ActReg chr1 #271	1	1	0
272	1	8,137,217	8,137,798	581	1	8.167	12	3.944	11	21	5	0	0	0				ActReg chr1 #272	0	1	0
273	1	8,181,224	8,181,902	678	1	11.857	9	6.714	19	13	10	0	0	0				ActReg chr1 #273	1	0	0
274	1	8,214,676	8,215,224	548	1	10.882	7.118	3.846	22	14	6	0	0	0				ActReg chr1 #274	1	0	0
275	1	8,229,126	8,229,876	750	1	8.348	11.783	3.87	16	18	10	0	0	0				ActReg chr1 #275	0	1	0
276	1	8,257,801	8,258,519	718	1	9.455	14.546	9.136	16	24	17	0	0	0				ActReg chr1 #276	0	1	0
277	1	8,377,831	8,378,549	718	1	7.182	13.591	7.318	13	19	15	1	1	1	SLC45A1	-6,200	upstream	ActReg chr1 #277	0	1	0
278	1	8,418,600	8,419,462	862	1	5	5.407	11.741	10	11	16	1	0	1	RERE	458,668	in gene	ActReg chr1 #278	0	0	1
279	1	8,431,480	8,431,947	467	1	5.6	6	10.667	7	9	16	0	0	1	RERE	445,986	in gene	ActReg chr1 #279	0	0	1
280	1	8,484,051	8,485,176	1,125	2	8.029	11.114	4.686	16	20	8	1	0	1	RERE	393,086	in gene	ActReg chr1 #280	1	1	0
281	1	8,560,170	8,560,514	344	1	3.182	4	11.091	5	5	16	0	0	1	RERE	317,357	in gene	ActReg chr1 #281	0	0	1
282	1	8,763,319	8,763,896	577	1	10	12.944	5.25	15	23	8	1	0	1	RERE	114,092	in gene	ActReg chr1 #282	0	1	0
283	1	8,799,976	8,800,662	686	2	8.429	13.143	3.111	15	23	4	0	0	1	RERE	77,380	in gene	ActReg chr1 #283	1	1	0
284	1	8,937,767	8,939,489	1,722	4	10.87	11.111	9.611	21	20	23	1	2	2	ENO1, LOC100505975	152, -266	in gene, upstream	ActReg chr1 #284	1	1	1
285	1	8,950,875	8,951,178	303	1	5.8	3.9	9.9	8	6	13	0	0	0				ActReg chr1 #285	0	0	1
286	1	9,073,570	9,073,924	354	1	2.182	5.273	12.182	3	7	17	0	0	1	SLC2A7	12,657	in gene	ActReg chr1 #286	0	0	1
287	1	9,099,037	9,099,538	501	1	3.688	4.75	13.375	6	9	20	1	0	1	SLC2A5	49,223	in gene	ActReg chr1 #287	0	0	1
288	1	9,242,047	9,242,753	706	1	11.13	7.261	5.739	17	12	10	1	0	1	LOC727721	14,640	in gene	ActReg chr1 #288	1	0	0
289	1	9,488,754	9,489,369	615	1	11.632	13.158	6.789	21	23	10	1	1	1	LOC100506022	-6	upstream	ActReg chr1 #289	0	1	0
290	1	9,775,596	9,776,177	581	1	4	5.188	12	6	7	15	1	0	1	PIK3CD	64,096	in gene	ActReg chr1 #290	0	0	1
291	1	9,781,441	9,782,237	796	1	5.125	5.583	15.167	9	8	21	0	0	2	PIK3CD, CLSTN1	70049, 102711	in gene, downstream	ActReg chr1 #291	0	0	1
292	1	9,784,598	9,785,084	486	1	4.733	3.933	12.933	7	6	20	0	0	2	PIK3CD, CLSTN1	73051, 99709	in gene, downstream	ActReg chr1 #292	0	0	1
293	1	9,903,141	9,903,546	405	1	3.25	5.75	13.417	6	9	21	0	0	1	CTNNBIP1	66,973	downstream	ActReg chr1 #293	0	0	1
294	1	9,970,515	9,971,270	755	1	6.591	11.542	5.087	10	17	10	1	1	1	CTNNBIP1	-576	upstream	ActReg chr1 #294	0	1	0
295	1	10,002,889	10,003,833	944	3	13.724	9.586	9.552	25	22	16	1	2	2	LZIC, NMNAT1	-535, -125	upstream, upstream	ActReg chr1 #295	1	1	1
296	1	10,270,297	10,270,857	560	1	10	7.111	7.25	15	9	11	1	1	1	KIF1B	-187	upstream	ActReg chr1 #296	1	0	0
297	1	10,458,507	10,459,783	1,276	3	13.225	16.3	10.45	28	33	18	1	2	2	LOC100287506, PGD	-190, 60	upstream, in gene	ActReg chr1 #297	1	1	1
298	1	10,490,008	10,490,815	807	2	16.44	16.04	3.2	33	38	6	1	1	2	PGD, APITD1	31326, 252	downstream, in gene	ActReg chr1 #298	1	1	0
299	1	10,532,183	10,532,988	805	2	12.8	13.08	5.16	22	22	9	1	2	2	DFFA, PEX14	28, -2418	in gene, upstream	ActReg chr1 #299	1	1	0
300	1	10,534,575	10,535,374	799	2	13.72	14.52	3.045	29	34	5	1	2	2	DFFA, PEX14	-2361, -29	upstream, upstream	ActReg chr1 #300	1	1	0
301	1	10,689,617	10,690,303	686	1	3.81	4.333	11.857	7	7	18	0	0	2	PEX14, CASZ1	154957, 166747	in gene, downstream	ActReg chr1 #301	0	0	1
302	1	10,700,135	10,700,770	635	1	3.1	3.45	12.25	9	6	18	1	0	2	PEX14, CASZ1	165449, 156255	downstream, in gene	ActReg chr1 #302	0	0	1
303	1	10,707,248	10,707,746	498	1	4.75	2.4	12.688	7	5	23	1	0	1	CASZ1	149,210	in gene	ActReg chr1 #303	0	0	1
304	1	10,713,303	10,713,894	591	1	2.267	4.368	14.368	4	6	19	1	0	1	CASZ1	143,109	in gene	ActReg chr1 #304	0	0	1
305	1	10,716,081	10,716,426	345	1	2.909	2	12	5	3	16	0	0	1	CASZ1	140,454	in gene	ActReg chr1 #305	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
306	1	10,734,649	10,735,157	508	1	4.438	4.846	11.75	8	7	17	0	0	1	CASZ1	121,804	in gene	ActReg chr1 #306	0	0	1
307	1	10,764,219	10,764,690	471	1	2.267	3.533	11.4	4	6	17	1	0	1	CASZ1	92,253	in gene	ActReg chr1 #307	0	0	1
308	1	10,848,606	10,849,098	492	1	5.562	3.938	10.875	9	7	16	0	0	1	CASZ1	7,855	in gene	ActReg chr1 #308	0	0	1
309	1	10,856,437	10,857,148	711	2	14.591	15.773	4.5	33	32	9	1	1	1	CASZ1	-85	upstream	ActReg chr1 #309	1	1	0
310	1	10,895,826	10,896,426	600	1	5.474	5.684	13.79	10	8	27	1	0	0				ActReg chr1 #310	0	0	1
311	1	11,006,467	11,006,839	372	1	2.636	4	12.636	4	8	18	0	0	1	C1orf127	35,441	in gene	ActReg chr1 #311	0	0	1
312	1	11,039,305	11,039,967	662	1	13.05	5.45	2.938	19	10	9	0	1	1	C1orf127	2,458	in gene	ActReg chr1 #312	1	0	0
313	1	11,072,219	11,073,206	987	2	16.032	16.355	6.233	33	31	19	1	1	1	TARDBP	33	in gene	ActReg chr1 #313	1	1	0
314	1	11,159,358	11,160,085	727	1	7.957	12.391	7.913	14	18	17	1	1	2	EXOSC10, MTOR	217, 162887	in gene, downstream	ActReg chr1 #314	0	1	0
315	1	11,333,192	11,334,187	995	2	11.032	11	6	18	17	14	1	1	1	UBIAD1	434	in gene	ActReg chr1 #315	1	1	0
316	1	11,533,542	11,534,177	635	1	9.65	10.35	2.692	19	17	5	0	1	1	PTCHD2	-5,436	upstream	ActReg chr1 #316	1	0	0
317	1	11,538,702	11,539,827	1,125	2	10.971	11.429	5.03	19	22	9	1	1	1	PTCHD2	-31	upstream	ActReg chr1 #317	1	1	0
318	1	11,539,895	11,540,715	820	1	8.346	13.577	7.692	15	22	13	1	1	1	PTCHD2	1,010	in gene	ActReg chr1 #318	0	1	0
319	1	11,561,258	11,561,931	673	1	3.211	3.619	11.857	6	7	15	1	0	1	PTCHD2	22,299	in gene	ActReg chr1 #319	0	0	1
320	1	11,596,674	11,597,111	437	1	2.846	2.846	12.231	5	4	16	1	0	1	PTCHD2	57,597	in gene	ActReg chr1 #320	0	0	1
321	1	11,610,224	11,611,433	1,209	2	23.868	25.947	3.103	57	68	5	0	0	0				ActReg chr1 #321	1	1	0
322	1	11,657,550	11,658,102	552	1	3.312	2	10.471	7	3	14	0	0	0				ActReg chr1 #322	0	0	1
323	1	11,695,942	11,696,547	605	2	13.474	10.895	3.947	22	16	6	0	0	0				ActReg chr1 #323	1	1	0
324	1	11,740,571	11,741,511	940	1	8.167	11.467	7.333	14	21	10	1	0	2	FBXO6, MAD2L2	16891, 10637	downstream, in gene	ActReg chr1 #324	0	1	0
325	1	11,766,255	11,766,859	604	1	2.632	5.368	12.947	4	9	21	0	0	1	C1orf187	14,776	in gene	ActReg chr1 #325	0	0	1
326	1	11,779,475	11,780,006	531	1	7.294	10.177	11.529	10	16	18	1	1	2	C1orf187, LOC100506086	27959, -2296	in gene, upstream	ActReg chr1 #326	0	0	1
327	1	11,795,878	11,796,878	1,000	1	7.067	7.645	11.097	11	15	15	1	1	1	AGTRAP	236	in gene	ActReg chr1 #327	0	0	1
328	1	11,826,034	11,826,900	866	1	3.037	5.519	11.852	5	10	18	0	1	2	LOC100506273, C1orf167	4623, -338	in gene, upstream	ActReg chr1 #328	0	0	1
329	1	11,844,205	11,844,905	700	1	4.35	4.955	12.909	6	7	18	0	0	4	C1orf167, LOC100506310, LOC100506116, MTHFR	17750, 6012, 4675, 21605	downstream, in gene, in gene, downstream	ActReg chr1 #329	0	0	1
330	1	11,847,717	11,848,419	702	1	4.955	6	11.364	8	9	17	0	0	4	C1orf167, LOC100506310, LOC100506116, MTHFR	21263, 9525, 8188, 18092	downstream, in gene, in gene, in gene	ActReg chr1 #330	0	0	1
331	1	11,865,382	11,866,464	1,082	2	11.588	9.118	7.588	25	14	16	1	2	2	MTHFR, CLCN6	237, -284	in gene, upstream	ActReg chr1 #331	1	0	1
332	1	11,919,116	11,919,999	883	2	12	15.259	5.852	27	27	10	1	1	1	NPPB	-565	upstream	ActReg chr1 #332	1	1	0
333	1	11,958,626	11,959,154	528	1	4.312	6.312	11.875	8	10	14	0	0	1	RNU5E	-9,321	upstream	ActReg chr1 #333	0	0	1
334	1	11,967,753	11,969,246	1,493	3	13.478	14.043	9.457	38	27	17	0	1	1	RNU5E	288	downstream	ActReg chr1 #334	1	1	1
335	1	11,969,588	11,970,431	843	2	12.423	10.577	5	24	24	12	0	1	2	RNU5E, KIAA2013	1798, 16471	downstream, downstream	ActReg chr1 #335	1	1	0
336	1	11,989,712	11,990,358	646	1	8.05	10.85	3.05	17	19	5	0	2	2	KIAA2013, PLOD1	-3555, -4711	upstream, upstream	ActReg chr1 #336	0	1	0
337	1	12,039,846	12,040,789	943	1	8.593	11.655	6.759	17	18	14	1	1	2	PLOD1, MFN2	45571, 79	downstream, in gene	ActReg chr1 #337	0	1	0
338	1	12,066,978	12,067,541	563	1	4.941	2.176	12.941	8	4	18	0	0	1	MFN2	27,021	in gene	ActReg chr1 #338	0	0	1
339	1	12,081,637	12,082,325	688	1	3.2	5.526	12.762	7	5	17	0	1	2	MFN2, MIIP	41743, 2469	downstream, in gene	ActReg chr1 #339	0	0	1
340	1	12,202,685	12,203,308	623	1	4.6	2.722	11.45	8	5	19	0	0	1	TNFRSF8	79,562	in gene	ActReg chr1 #340	0	0	1
341	1	12,227,288	12,227,885	597	1	5.684	5.211	10.053	11	9	14	1	1	1	TNFRSF1B	526	in gene	ActReg chr1 #341	0	0	1
342	1	12,244,728	12,245,168	440	1	3.429	2.714	14.571	6	5	21	0	0	1	TNFRSF1B	17,888	in gene	ActReg chr1 #342	0	0	1
343	1	12,289,465	12,290,405	940	2	12.667	16.933	4.083	33	39	11	1	1	2	LOC390998, VPS13D	-8771, -178	upstream, upstream	ActReg chr1 #343	1	1	0
344	1	12,290,533	12,291,099	566	1	7.353	9.941	6.824	9	16	10	2	1	2	LOC390998, VPS13D	-9652, 703	upstream, in gene	ActReg chr1 #344	0	1	0
345	1	12,538,507	12,539,231	724	1	12.773	7.591	3.909	18	11	7	0	0	1	VPS13D	248,756	in gene	ActReg chr1 #345	1	0	0
346	1	12,600,199	12,600,879	680	1	3.19	4.333	11.952	6	7	17	1	0	0				ActReg chr1 #346	0	0	1
347	1	12,609,004	12,609,988	984	1	7	11.161	7.032	17	17	15	0	0	0				ActReg chr1 #347	0	1	0
348	1	12,655,873	12,656,377	504	1	7	13.333	5.933	10	23	10	1	0	1	DHRS3	21,695	in gene	ActReg chr1 #348	0	1	0
349	1	12,676,793	12,677,412	619	1	6.2	10.15	9.5	9	19	15	1	1	1	DHRS3	718	in gene	ActReg chr1 #349	0	1	0
350	1	13,789,072	13,789,565	493	1	3.8	2.333	11.467	6	3	17	0	0	0				ActReg chr1 #350	0	0	1
351	1	14,746,887	14,747,264	377	1	4.75	5.167	11.417	9	7	17	0	0	0				ActReg chr1 #351	0	0	1
352	1	15,370,374	15,370,733	359	1	1	5	11.091	1	7	16	0	0	1	RP1-21O18.1	445,340	in gene	ActReg chr1 #352	0	0	1
353	1	15,653,263	15,653,713	450	1	2.643	7.5	11.143	5	11	18	0	0	1	FHAD1	79,720	in gene	ActReg chr1 #353	0	0	1
354	1	15,664,004	15,664,748	744	1	10.478	13.435	6.435	17	27	13	0	0	1	FHAD1	90,608	in gene	ActReg chr1 #354	0	1	0
355	1	15,678,716	15,679,370	654	1	12.619	10.809	4.05	21	15	6	0	0	1	FHAD1	105,275	in gene	ActReg chr1 #355	0	1	0
356	1	15,735,553	15,736,011	458	1	7	7.071	10.5	11	8	17	1	1	1	ERHD2	-609	upstream	ActReg chr1 #356	0	0	1
357	1	15,799,018	15,799,389	371	1	3.909	7.364	12.636	5	10	16	0	1	2	CELA2A, CELA2B	15980, -3393	downstream, upstream	ActReg chr1 #357	0	0	1
358	1	15,852,809	15,853,633	824	2	17.5	14.115	5.462	35	28	10	1	2	2	CASP9, DNAJC16	-2431, -131	upstream, upstream	ActReg chr1 #358	1	1	0
359	1	16,058,727	16,059,218	491	1	3.267	4.533	11.533	5	7	17	0	1	3	PLEKHM2, SLC25A34, TMEM82	48145, -3837, -9945	in gene, upstream, upstream	ActReg chr1 #359	0	0	1
360	1	16,062,903	16,063,490	587	1	6.842	5.158	14.895	13	7	23	0	2	3	PLEKHM2, SLC25A34, TMEM82	52369, 387, -5721	downstream, in gene, upstream	ActReg chr1 #360	0	0	1
361	1	16,161,859	16,162,793	934	1	8.655	7.259	12.655	13	13	23	1	0	1	hCG_2008140	12,316	in gene	ActReg chr1 #361	0	0	1
362	1	16,270,824	16,271,550	726	1	2.19	5.727	14.682	6	11	19	1	0	2	SPEN, ZBTB17	96828, 31440	downstream, in gene	ActReg chr1 #362	0	0	1
363	1	16,320,524	16,321,003	479	1	4.133	5.733	11.8	6	11	19	0	0	1	C1orf64	-9,968	upstream	ActReg chr1 #363	0	0	1
364	1	16,351,461	16,351,791	330	1	3.1	4.8	12	4	6	17	0	1	2	HSPB7, CLCNKA	-6341, 3140	upstream, in gene	ActReg chr1 #364	0	0	1
365	1	16,355,735	16,356,225	490	1	5.438	5.812	12	10	9	15	0	0	1	CLCNKA	7,494	in gene	ActReg chr1 #365	0	0	1
366	1	16,402,268	16,403,887	1,619	2	11.098	11.843	6.765	19	22	10	0	1	1	FAM131C	-2,950	upstream	ActReg chr1 #366	1	1	0
367	1	16,448,925	16,449,863	938	1	12.4	9.4	6.767	26	17	11	0	0	1	EPHA2	33,188	downstream	ActReg chr1 #367	1	0	0
368	1	16,459,450	16,459,958	508	1	3.312	6.625	13.75	6	10	21	0	0	1	EPHA2	22,878	in gene	ActReg chr1 #368	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
369	1	16,464,429	16,465,022	593	1	6.389	5.5	10.833	10	9	14	1	0	1	EPHA2	17,857	in gene	ActReg chr1 #369	0	0	1
370	1	16,466,679	16,467,137	458	1	8.2	4.733	12	11	7	18	0	0	1	EPHA2	15,674	in gene	ActReg chr1 #370	0	0	1
371	1	16,470,643	16,471,275	632	1	6	4.75	12.3	8	7	15	0	0	1	EPHA2	11,623	in gene	ActReg chr1 #371	0	0	1
372	1	16,481,326	16,481,846	520	1	5.562	10.875	10.75	9	15	18	1	2	2	EPHA2, LOC100506484	996, -144	in gene, upstream	ActReg chr1 #372	0	0	1
373	1	16,481,916	16,482,788	872	2	10.107	9.429	8.893	16	16	20	1	2	2	EPHA2, LOC100506484	230, 622	in gene, in gene	ActReg chr1 #373	1	0	1
374	1	16,483,458	16,484,041	583	1	3.778	3.056	10.111	8	5	15	0	2	2	EPHA2, LOC100506484	-1167, 2019	upstream, in gene	ActReg chr1 #374	0	0	1
375	1	16,499,431	16,500,472	1,041	1	7.062	11.312	6.75	13	18	12	0	0	0				ActReg chr1 #375	0	1	0
376	1	16,535,009	16,535,702	693	1	4.095	7.381	11.286	6	10	15	0	0	1	ARHGEF19	3,749	in gene	ActReg chr1 #376	0	0	1
377	1	16,536,616	16,537,122	506	1	4.875	3.375	11.188	9	7	19	0	1	1	ARHGEF19	2,235	in gene	ActReg chr1 #377	0	0	1
378	1	16,557,837	16,558,506	669	1	5.048	5.905	10.905	5	7	15	0	0	1	C1orf89	5,488	downstream	ActReg chr1 #378	0	0	1
379	1	16,678,343	16,679,533	1,190	3	13.703	10.46	9.27	24	15	17	1	1	1	FBXO42	10	in gene	ActReg chr1 #379	1	1	1
380	1	16,693,244	16,694,428	1,184	2	15.46	15.919	5.973	36	37	13	1	1	1	C1orf144	253	in gene	ActReg chr1 #380	1	1	0
381	1	16,766,615	16,767,825	1,210	2	12.5	16.421	8.658	36	39	16	1	2	2	SPATA21, NECAP2	-3301, 53	upstream, in gene	ActReg chr1 #381	1	1	0
382	1	16,938,892	16,940,781	1,889	2	20.339	23.881	17.271	53	59	43	1	1	1	NBPF1	146	in gene	ActReg chr1 #382	0	1	1
383	1	16,951,975	16,952,892	917	1	14.179	9.893	18.786	21	14	33	0	0	0				ActReg chr1 #383	0	0	1
384	1	16,955,713	16,957,033	1,320	1	7.268	8.512	12.878	17	13	21	0	0	0				ActReg chr1 #384	0	0	1
385	1	16,957,209	16,958,871	1,662	1	9.154	7.673	16.404	16	16	27	0	0	0				ActReg chr1 #385	0	0	1
386	1	16,970,452	16,971,624	1,172	3	19	18.541	15.595	47	42	37	1	0	0				ActReg chr1 #386	1	1	1
387	1	17,022,892	17,023,990	1,098	1	4.677	5.941	13.323	8	10	19	1	0	0				ActReg chr1 #387	0	0	1
388	1	17,026,422	17,028,818	2,396	3	14.427	15.48	12.32	48	51	22	1	0	0				ActReg chr1 #388	1	1	1
389	1	17,030,798	17,031,683	885	1	9.071	7.607	13.25	15	10	16	0	0	0				ActReg chr1 #389	0	0	1
390	1	17,035,784	17,036,619	835	1	8.231	8.038	13.885	13	14	22	0	0	0				ActReg chr1 #390	0	0	1
391	1	17,045,008	17,045,868	860	1	5.815	7.481	13.111	9	11	19	0	0	0				ActReg chr1 #391	0	0	1
392	1	17,222,558	17,222,887	329	2	8.364	14.727	11.546	12	23	17	1	2	2	LOC100506687, RNU1-2	-6561, 247	upstream, downstream	ActReg chr1 #392	0	1	1
393	1	17,222,970	17,223,254	284	1	6.111	11	12.222	8	14	16	0	2	2	LOC100506687, RNU1-2	-6951, 637	upstream, downstream	ActReg chr1 #393	0	0	1
394	1	17,230,781	17,232,286	1,505	3	24.957	27.575	10.489	94	112	24	1	0	1	RNU1-2	9,058	downstream	ActReg chr1 #394	1	1	1
395	1	17,239,581	17,241,312	1,731	3	10.964	11.146	11.846	21	25	24	1	1	1	CROCC	-7,999	upstream	ActReg chr1 #395	1	1	1
396	1	17,250,742	17,253,334	2,592	1	5.84	6.383	13.889	10	15	24	0	1	1	CROCC	3,593	in gene	ActReg chr1 #396	0	0	1
397	1	17,264,632	17,265,344	712	1	5.1	7.043	13.739	10	10	20	0	0	1	CROCC	16,543	in gene	ActReg chr1 #397	0	0	1
398	1	17,273,036	17,273,768	732	1	4.435	6.478	15.13	10	11	23	0	0	1	CROCC	24,957	in gene	ActReg chr1 #398	0	0	1
399	1	17,274,810	17,275,507	697	1	4.273	5.227	12.364	8	8	19	0	0	1	CROCC	26,713	in gene	ActReg chr1 #399	0	0	1
400	1	17,331,587	17,332,096	509	1	7.375	4.375	11.062	10	6	17	1	0	1	ATP13A2	6,582	in gene	ActReg chr1 #400	0	0	1
401	1	17,445,264	17,445,939	675	1	5.619	4.429	11.667	7	7	17	1	1	1	PADI2	347	in gene	ActReg chr1 #401	0	0	1
402	1	17,475,652	17,476,082	430	1	2.615	4.538	13.077	4	7	21	1	0	0				ActReg chr1 #402	0	0	1
403	1	17,511,345	17,512,018	673	1	2.529	5.857	11.667	5	10	14	0	0	1	LOC400743	-9,140	upstream	ActReg chr1 #403	0	0	1
404	1	17,620,161	17,621,008	847	1	7.654	10.577	3.083	12	16	7	0	0	1	PADI3	44,991	downstream	ActReg chr1 #404	0	1	0
405	1	17,668,412	17,668,969	557	1	6.389	4.111	11.444	10	8	16	0	0	1	PADI4	34,000	in gene	ActReg chr1 #405	0	0	1
406	1	17,743,650	17,744,031	381	1	2.182	5.636	10.818	3	9	16	0	0	1	RCC2	22,380	in gene	ActReg chr1 #406	0	0	1
407	1	17,765,396	17,766,271	875	1	8.407	11.074	5.375	15	18	14	1	1	1	RCC2	387	in gene	ActReg chr1 #407	0	1	0
408	1	17,802,815	17,803,231	416	1	4.1	4.308	10.308	6	6	17	0	0	0				ActReg chr1 #408	0	0	1
409	1	17,871,844	17,872,519	675	1	11.191	6.524	3.619	20	11	6	0	0	1	ARHGEF10L	5,851	in gene	ActReg chr1 #409	1	0	0
410	1	17,964,938	17,965,423	485	1	3.267	1.8	12.067	6	3	15	0	0	1	ARHGEF10L	98,850	in gene	ActReg chr1 #410	0	0	1
411	1	18,003,328	18,003,746	418	1	2.273	3.786	10.143	4	6	15	0	0	1	ARHGEF10L	137,207	in gene	ActReg chr1 #411	0	0	1
412	1	18,157,817	18,158,756	939	2	12.6	15.833	1.684	28	32	2	0	0	1	ACTL8	8,809	downstream	ActReg chr1 #412	1	1	0
413	1	18,245,705	18,246,881	1,176	2	12.811	15.73	4.917	30	32	9	0	0	0				ActReg chr1 #413	1	1	0
414	1	18,437,057	18,437,737	680	1	2.429	3.048	11.333	5	6	15	1	0	1	IGSF21	3,157	in gene	ActReg chr1 #414	0	0	1
415	1	19,031,431	19,031,831	400	1	3.182	3.417	11.083	5	6	15	0	0	1	PAX7	74,131	in gene	ActReg chr1 #415	0	0	1
416	1	19,228,989	19,229,471	482	1	12.133	11.4	4.333	21	14	8	1	2	3	ALDH4A1, MIR1290, IFFO2	63, -5588, 53596	in gene, upstream, downstream	ActReg chr1 #416	1	0	0
417	1	19,252,550	19,253,311	761	1	10.087	15.478	4.261	14	22	7	0	0	1	IFFO2	29,896	in gene	ActReg chr1 #417	0	1	0
418	1	19,258,669	19,259,660	991	2	10.065	9.677	4.387	19	16	11	0	0	1	IFFO2	23,662	in gene	ActReg chr1 #418	1	1	0
419	1	19,281,444	19,282,430	986	1	6.033	11.767	6.067	10	17	19	1	1	1	IFFO2	889	in gene	ActReg chr1 #419	0	1	0
420	1	19,536,388	19,537,307	919	2	13.714	11.929	5.036	28	19	8	1	1	2	UBR4, KIAA0090	-101, 41199	upstream, downstream	ActReg chr1 #420	1	1	0
421	1	19,577,657	19,578,671	1,014	3	14.281	17.094	10.742	36	36	17	1	2	2	KIAA0090, MRTO4	-118, 89	upstream, in gene	ActReg chr1 #421	1	1	1
422	1	19,653,417	19,654,019	602	1	4.105	2.882	10.263	6	5	15	0	0	1	PQLC2	14,978	in gene	ActReg chr1 #422	0	0	1
423	1	20,002,155	20,003,587	1,432	2	15.556	18.022	5	39	50	10	0	0	2	HTR6, TMCO4	11091, 123539	in gene, downstream	ActReg chr1 #423	1	1	0
424	1	20,685,169	20,686,039	870	2	9.926	9.926	4	24	13	5	0	0	2	VWA5B1, LOC339505	68192, 69683	downstream, downstream	ActReg chr1 #424	1	1	0
425	1	20,697,690	20,698,942	1,252	2	12.128	18.692	2.258	32	42	5	0	0	1	LOC339505	56,971	in gene	ActReg chr1 #425	1	1	0
426	1	20,737,631	20,738,364	733	1	8.261	11.957	4.091	16	18	9	0	0	1	LOC339505	17,290	in gene	ActReg chr1 #426	0	1	0
427	1	20,812,919	20,813,501	582	1	6.389	9.167	11.222	11	12	14	1	1	1	CAMK2N1	-482	upstream	ActReg chr1 #427	0	0	1
428	1	20,820,850	20,821,860	1,010	1	8	11.444	3.719	16	18	9	0	0	2	CAMK2N1, MUL1	-8627, 13319	upstream, downstream	ActReg chr1 #428	0	1	0
429	1	20,834,206	20,835,152	946	3	12.2	11.767	8.9	22	19	13	1	1	1	MUL1	-5	upstream	ActReg chr1 #429	1	1	1
430	1	20,920,265	20,920,629	364	1	1.727	3.727	11.364	3	5	16	0	0	1	CDA	5,003	in gene	ActReg chr1 #430	0	0	1
431	1	20,987,434	20,988,064	630	1	9.4	11	8.1	14	15	13	1	1	3	PINK1, DDOST, KIF17	27801, 288, 56568	downstream, in gene, downstream	ActReg chr1 #431	0	1	0
432	1	21,112,583	21,113,374	791	1	11.875	9.167	5.5	21	17	9	1	1	1	HP1BP3	203	in gene	ActReg chr1 #432	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
433	1	21,362,169	21,362,528	359	1	4.083	7.75	11.5	5	12	16	0	0	1	EIF4G3	140,992	in gene	ActReg chr1 #433	0	0	1
434	1	21,588,054	21,588,746	692	1	8.045	12.364	6.545	12	19	11	0	1	2	ECE1, LOC100506824	83634, -4175	in gene, upstream	ActReg chr1 #434	0	1	0
435	1	21,780,369	21,780,858	489	2	10.533	9.6	2.133	16	14	3	0	0	1	NBPF3	13,982	in gene	ActReg chr1 #435	1	1	0
436	1	21,836,002	21,836,358	356	1	3.273	4	10.454	5	5	14	1	1	1	ALPL	322	in gene	ActReg chr1 #436	0	0	1
437	1	21,934,601	21,935,157	556	1	2.471	1.533	13.706	4	2	23	0	0	1	RAP1GAP	60,977	in gene	ActReg chr1 #437	0	0	1
438	1	21,974,111	21,975,008	897	2	16.517	14.621	2.88	34	30	6	0	0	1	RAP1GAP	21,297	in gene	ActReg chr1 #438	1	1	0
439	1	21,985,377	21,986,331	954	2	13.586	14.448	6.103	19	30	13	1	0	1	RAP1GAP	10,002	in gene	ActReg chr1 #439	1	1	0
440	1	21,994,852	21,995,371	519	1	4.062	7.25	12.062	7	11	16	1	1	2	RAP1GAP, USP48	745, 114577	in gene, downstream	ActReg chr1 #440	0	0	1
441	1	22,032,920	22,033,464	544	1	11.588	6.333	1.357	23	10	2	0	0	1	USP48	76,496	in gene	ActReg chr1 #441	1	0	0
442	1	22,108,760	22,110,465	1,705	2	12.907	14.407	5.698	19	25	14	1	1	1	USP48	76	in gene	ActReg chr1 #442	1	1	0
443	1	22,177,962	22,178,372	410	1	3.846	2.308	12.231	7	4	17	0	0	1	HSPG2	44,637	in gene	ActReg chr1 #443	0	0	1
444	1	22,186,634	22,187,123	489	1	3.667	2.867	11.667	5	6	16	0	0	1	HSPG2	35,926	in gene	ActReg chr1 #444	0	0	1
445	1	22,263,895	22,264,502	607	1	11.368	11.947	6.929	18	19	11	0	0	0				ActReg chr1 #445	1	0	0
446	1	22,266,149	22,266,924	775	2	13.333	14.125	3.789	26	23	7	0	0	0				ActReg chr1 #446	1	1	0
447	1	22,351,100	22,352,190	1,090	1	10.294	11.647	5.588	18	17	9	1	1	1	HSPC157	-62	upstream	ActReg chr1 #447	0	1	0
448	1	22,459,953	22,460,499	546	1	2.118	2.294	11	4	4	13	0	0	1	WNT4	9,293	in gene	ActReg chr1 #448	0	0	1
449	1	22,538,756	22,539,210	454	1	1.857	2.357	11.643	5	4	19	0	0	0				ActReg chr1 #449	0	0	1
450	1	22,778,096	22,779,149	1,053	2	7.697	10.848	7.455	12	16	15	1	1	1	ZBTB40	278	in gene	ActReg chr1 #450	0	1	1
451	1	22,937,354	22,938,821	1,467	2	24.304	26.413	3.854	72	79	7	0	0	1	EPHA8	48,083	downstream	ActReg chr1 #451	1	1	0
452	1	23,039,860	23,040,312	452	1	6.357	4.643	11.857	8	6	17	0	0	1	EPHB2	2,755	in gene	ActReg chr1 #452	0	0	1
453	1	23,345,447	23,346,231	784	2	11.75	12.5	4.5	22	23	9	1	2	2	LOC729059, KDM1A	-3496, -102	upstream, upstream	ActReg chr1 #453	1	1	0
454	1	23,557,849	23,558,241	392	1	1.615	5.308	10.538	3	7	15	0	0	0				ActReg chr1 #454	0	0	1
455	1	23,670,911	23,671,604	693	1	8.045	10.409	1.882	14	19	3	1	1	1	HNRNPR	-404	upstream	ActReg chr1 #455	0	1	0
456	1	23,694,556	23,695,867	1,311	2	12.22	10.683	9.317	20	18	16	1	2	2	ZNF436, C1orf213	1146, -253	in gene, upstream	ActReg chr1 #456	1	0	1
457	1	23,703,416	23,704,177	761	1	9.042	11.75	5.583	17	20	9	0	1	3	ZNF436, C1orf213, TCEA3	-7439, 8332, 47465	upstream, downstream, downstream	ActReg chr1 #457	0	1	0
458	1	23,857,005	23,858,292	1,287	2	7.775	10.35	6.744	15	20	15	1	1	1	E2F2	65	in gene	ActReg chr1 #458	0	1	1
459	1	23,865,980	23,866,645	665	1	7.714	11.143	3.619	11	16	6	0	0	1	E2F2	-8,599	upstream	ActReg chr1 #459	0	1	0
460	1	23,999,481	24,000,565	1,084	2	16.412	17.529	1.906	32	36	4	0	1	1	LOC729856	2,755	downstream	ActReg chr1 #460	1	1	0
461	1	24,017,962	24,018,697	735	2	10	13.696	10.706	19	25	20	1	1	1	RPL11	35	in gene	ActReg chr1 #461	0	1	1
462	1	24,069,356	24,070,367	1,011	1	8.742	12.839	5.267	16	23	12	1	1	1	TCEB3	5	in gene	ActReg chr1 #462	0	1	0
463	1	24,125,765	24,127,698	1,933	2	11.083	13.483	8.069	20	32	17	1	1	3	LYPLA2, GALE, HMGCL	9085, 563, 25218	downstream, in gene, downstream	ActReg chr1 #463	1	1	0
464	1	24,151,567	24,152,128	561	1	9.222	10.111	11.389	18	19	17	0	1	1	HMGCL	102	in gene	ActReg chr1 #464	0	0	1
465	1	24,285,937	24,286,373	436	1	9.214	9.857	11.857	14	13	18	1	1	2	PNRC2, SFRS13A	-146, 20798	upstream, downstream	ActReg chr1 #465	0	0	1
466	1	24,306,432	24,307,204	772	3	12.04	13.36	11.421	23	28	21	1	1	1	SFRS13A	135	in gene	ActReg chr1 #466	1	1	1
467	1	24,377,967	24,378,391	424	1	12.308	9.846	1	16	15	1	0	0	1	MYOM3	60,486	downstream	ActReg chr1 #467	0	1	0
468	1	24,483,421	24,483,851	430	1	3.143	2.769	11	5	5	17	0	0	1	IL28RA	30,115	in gene	ActReg chr1 #468	0	0	1
469	1	24,620,330	24,621,345	1,015	2	12.935	13.344	3.419	33	18	7	0	0	0				ActReg chr1 #469	1	1	0
470	1	24,691,839	24,692,517	678	2	9.679	12.571	4.125	22	19	7	0	0	2	GRHL3, C1orf201	46266, 35871	downstream, in gene	ActReg chr1 #470	1	1	0
471	1	24,739,756	24,740,226	470	1	7.267	9.333	13.8	9	12	19	1	1	1	NIPAL3	-2,254	upstream	ActReg chr1 #471	0	0	1
472	1	24,741,750	24,742,874	1,124	2	11.229	10.943	4.5	20	28	7	1	1	1	NIPAL3	67	in gene	ActReg chr1 #472	1	1	0
473	1	24,782,483	24,782,982	499	1	4	4.643	11.875	7	7	17	0	0	1	NIPAL3	40,487	in gene	ActReg chr1 #473	0	0	1
474	1	25,071,759	25,072,189	430	1	9.769	11.615	12.538	13	14	20	1	1	1	CLIC4	214	in gene	ActReg chr1 #474	0	0	1
475	1	25,174,233	25,174,992	759	1	6.833	9.5	12.292	10	16	18	1	0	1	CLIC4	102,852	downstream	ActReg chr1 #475	0	0	1
476	1	25,255,670	25,256,052	382	1	4.25	7.583	12.667	10	15	16	1	0	1	RUNX3	35,640	in gene	ActReg chr1 #476	0	0	1
477	1	25,275,780	25,276,340	560	1	12.647	9.941	6.312	20	15	11	0	0	1	RUNX3	15,441	in gene	ActReg chr1 #477	1	0	0
478	1	25,285,613	25,286,616	1,003	1	9.129	11.548	4.258	13	20	11	0	0	1	RUNX3	5,387	in gene	ActReg chr1 #478	0	1	0
479	1	25,343,890	25,344,728	838	1	8.269	10.385	7.962	13	16	14	0	0	0				ActReg chr1 #479	0	1	0
480	1	25,348,919	25,350,000	1,081	1	11.471	8.912	6.294	17	15	13	0	0	0				ActReg chr1 #480	1	0	0
481	1	25,429,703	25,430,216	513	1	4.125	5.312	12.375	6	7	23	0	0	0				ActReg chr1 #481	0	0	1
482	1	25,451,533	25,451,931	398	1	4.75	4.667	10.667	6	6	17	0	0	0				ActReg chr1 #482	0	0	1
483	1	25,493,889	25,494,566	677	1	9.429	12.333	5.5	14	21	11	0	0	0				ActReg chr1 #483	0	1	0
484	1	25,572,878	25,573,470	592	1	7.444	10.722	4.778	11	21	9	1	1	1	C1orf63	811	in gene	ActReg chr1 #484	0	1	0
485	1	25,573,519	25,574,747	1,228	3	7.816	10.132	11.816	16	16	21	1	1	1	C1orf63	-148	upstream	ActReg chr1 #485	0	1	1
486	1	25,664,731	25,665,141	410	1	8.846	5.769	9.846	13	9	13	1	1	2	RHD, TMEM50A	65955, 125	downstream, in gene	ActReg chr1 #486	0	0	1
487	1	25,894,800	25,896,991	2,191	2	9.559	10.882	6.355	15	20	14	0	0	1	LDLRAP1	25,819	downstream	ActReg chr1 #487	1	1	0
488	1	25,942,583	25,942,976	393	1	5	7.769	10.462	8	11	16	1	1	1	MAN1C1	-1,180	upstream	ActReg chr1 #488	0	0	1
489	1	26,146,168	26,147,276	1,108	2	11.571	9.314	8.343	17	18	17	1	1	3	SEPN1, FAM54B, LOC646471	20055, 325, 3375	downstream, in gene, in gene	ActReg chr1 #489	1	0	1
490	1	26,219,987	26,220,337	350	1	4.545	5.364	11.182	7	7	16	0	0	1	STMN1	13,206	in gene	ActReg chr1 #490	0	0	1
491	1	26,232,234	26,232,549	315	1	5.4	4.5	10.2	7	8	12	1	1	1	STMN1	977	in gene	ActReg chr1 #491	0	0	1
492	1	26,324,298	26,325,197	899	2	14.179	12.429	5.179	26	30	8	1	1	1	PAFAH2	-99	upstream	ActReg chr1 #492	1	1	0
493	1	26,354,660	26,355,779	1,119	2	10.686	13.086	5.771	18	26	11	0	0	2	EXTL1, SLC30A2	6948, 17385	in gene, downstream	ActReg chr1 #493	1	1	0
494	1	26,361,499	26,362,424	925	2	16.345	13.966	8.793	33	22	12	1	0	2	EXTL1, SLC30A2	13690, 10643	in gene, downstream	ActReg chr1 #494	1	1	0
495	1	26,437,186	26,438,913	1,727	2	12.796	13.87	7.467	25	26	17	1	1	1	PDIK1L	393	in gene	ActReg chr1 #495	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
496	1	26,495,996	26,496,758	762	2	11.542	12.583	8.25	25	26	14	1	3	4	GRRP1, LOC100128346, ZNF593, CNKSR1	10866, 1935, -11, -7604	downstream, in gene, upstream, upstream	ActReg chr1 #496	1	1	0
497	1	26,509,514	26,509,921	407	1	2.1	5.154	12.077	4	6	16	0	1	2	CNKSR1, CATSPER4	5736, -7402	in gene, upstream	ActReg chr1 #497	0	0	1
498	1	26,560,014	26,560,969	955	1	10.533	9.233	8.5	15	15	16	1	1	1	CCDC21	-202	upstream	ActReg chr1 #498	1	0	0
499	1	26,601,948	26,603,204	1,256	1	11.975	8.5	5.5	19	16	10	0	1	3	CCDC21, SH3BGRL3, UBXN11	41883, -3637, 42180	in gene, upstream, downstream	ActReg chr1 #499	1	0	0
500	1	26,606,101	26,607,029	928	2	7.69	12.931	11.724	14	19	23	1	1	3	CCDC21, SH3BGRL3, UBXN11	45872, 352, 38191	downstream, in gene, downstream	ActReg chr1 #500	0	1	1
501	1	26,663,185	26,663,796	611	1	7.105	2.611	13.579	8	6	22	1	0	1	AIM1L	17,131	in gene	ActReg chr1 #501	0	0	1
502	1	26,734,602	26,735,795	1,193	2	18.135	26.405	3.472	50	71	6	0	1	1	LIN28	-2,071	upstream	ActReg chr1 #502	1	1	0
503	1	26,737,722	26,738,304	582	1	5.526	2.833	14.105	11	5	19	1	1	1	LIN28	744	in gene	ActReg chr1 #503	0	0	1
504	1	26,758,334	26,759,193	859	3	14.185	15.556	9.407	30	29	20	1	1	2	LIN28, DHDDS	21494, -39	downstream, upstream	ActReg chr1 #504	1	1	1
505	1	26,797,578	26,798,751	1,173	2	9.833	12.917	8.194	17	20	14	1	1	2	DHDDS, HMGN2	39362, -738	downstream, upstream	ActReg chr1 #505	1	1	0
506	1	26,826,581	26,827,601	1,020	2	10.469	11.844	8.094	19	18	15	1	0	0				ActReg chr1 #506	1	1	0
507	1	26,881,882	26,882,606	724	1	8.652	11.304	4	14	17	7	0	1	2	RPS6KA1, MIR1976	25995, 1211	in gene, downstream	ActReg chr1 #507	0	1	0
508	1	26,946,780	26,948,294	1,514	3	13.167	16.896	8.292	29	30	14	1	0	0				ActReg chr1 #508	1	1	1
509	1	27,018,495	27,020,112	1,617	2	17.235	20.706	4.961	39	58	10	0	1	1	ARID1A	-3,219	upstream	ActReg chr1 #509	1	1	0
510	1	27,021,675	27,022,445	770	3	15	20.167	10.571	31	45	17	1	1	1	ARID1A	-462	upstream	ActReg chr1 #510	1	1	1
511	1	27,114,493	27,115,081	588	1	7.684	7.474	13.947	12	14	20	1	1	2	ARID1A, PIGV	92265, 301	downstream, in gene	ActReg chr1 #511	0	0	1
512	1	27,183,055	27,183,796	741	1	3.217	2.714	12.13	6	6	18	0	1	2	ZDHHC18, SFN	30224, -6208	downstream, upstream	ActReg chr1 #512	0	0	1
513	1	27,189,490	27,190,216	726	1	6.565	4.913	12	9	7	19	1	1	2	ZDHHC18, SFN	36652, 220	downstream, in gene	ActReg chr1 #513	0	0	1
514	1	27,191,092	27,192,084	992	1	10.032	13.097	9.484	16	18	14	1	1	2	ZDHHC18, SFN	38387, 1955	downstream, downstream	ActReg chr1 #514	0	1	0
515	1	27,215,955	27,216,924	969	3	11.8	12.667	15.933	23	19	29	1	1	2	GPN2, GPATCH3	430, 10523	in gene, downstream	ActReg chr1 #515	1	1	1
516	1	27,248,018	27,248,754	736	1	10.522	12.913	7.727	16	23	14	1	2	2	NR0B2, NUDC	-7819, 162	upstream, in gene	ActReg chr1 #516	0	1	0
517	1	27,278,028	27,278,907	879	1	2.444	3.741	12.815	5	6	20	0	0	2	NUDC, C1orf172	30243, 8434	downstream, in gene	ActReg chr1 #517	0	0	1
518	1	27,328,178	27,328,963	785	1	10.36	12.96	4.167	18	26	8	0	0	2	TRNP1, FAM46B	8375, 10763	downstream, downstream	ActReg chr1 #518	0	1	0
519	1	27,335,609	27,336,446	837	1	6.692	10.462	4.12	13	14	7	0	0	2	TRNP1, FAM46B	15832, 3306	downstream, in gene	ActReg chr1 #519	0	1	0
520	1	27,396,635	27,397,109	474	1	3.067	2.615	10.933	4	4	18	0	0	0				ActReg chr1 #520	0	0	1
521	1	27,426,957	27,427,541	584	1	4.056	8.167	10.5	7	13	13	0	0	1	SLC9A1	54,202	in gene	ActReg chr1 #521	0	0	1
522	1	27,560,743	27,561,388	645	1	12.1	7.5	5	21	12	11	1	1	1	WDTC1	58	in gene	ActReg chr1 #522	1	0	0
523	1	27,648,266	27,649,088	822	3	13.962	14.231	11.077	27	30	19	1	2	2	TMEM222, LOC644961	41, -1688	in gene, upstream	ActReg chr1 #523	1	1	1
524	1	27,671,897	27,672,309	412	1	4.154	4.923	11.154	5	8	17	0	0	3	TMEM222, SYTL1, MAP3K6	23467, 3620, 21234	downstream, in gene, downstream	ActReg chr1 #524	0	0	1
525	1	27,675,520	27,676,643	1,123	2	8.278	12.139	8.944	15	17	20	1	0	2	SYTL1, MAP3K6	7598, 17256	in gene, downstream	ActReg chr1 #525	0	1	1
526	1	27,679,600	27,680,043	443	1	5.429	3.5	10.571	8	6	15	0	0	2	SYTL1, MAP3K6	11338, 13516	in gene, downstream	ActReg chr1 #526	0	0	1
527	1	27,718,657	27,719,368	711	1	8.773	12.636	5.6	14	20	12	1	1	2	CD164L2, GPR3	-9207, -140	upstream, upstream	ActReg chr1 #527	0	1	0
528	1	27,816,247	27,817,374	1,127	2	11.629	12.171	4.758	15	23	12	1	1	1	WASF2	-141	upstream	ActReg chr1 #528	1	1	0
529	1	27,875,299	27,876,094	795	1	4	4.217	12.417	6	7	21	0	0	1	AHDC1	54,447	in gene	ActReg chr1 #529	0	0	1
530	1	27,877,258	27,877,908	650	1	4.15	2.9	11.3	5	5	17	0	0	1	AHDC1	52,560	in gene	ActReg chr1 #530	0	0	1
531	1	27,974,712	27,975,284	572	1	3.611	3.389	11.278	7	6	18	0	1	1	LOC729973	-913	upstream	ActReg chr1 #531	0	0	1
532	1	27,998,329	27,999,374	1,045	1	8.061	12.333	3.333	14	19	8	0	1	1	IFI6	-127	upstream	ActReg chr1 #532	0	1	0
533	1	28,208,921	28,209,321	400	1	8.923	5.846	12.154	13	9	19	0	0	2	C1orf38, RPA2	10066, 32115	in gene, downstream	ActReg chr1 #533	0	0	1
534	1	28,470,910	28,471,645	735	2	11.304	15.522	1.5	20	35	2	0	0	1	PTAFR	49,170	downstream	ActReg chr1 #534	1	1	0
535	1	28,520,072	28,520,736	664	1	4.667	4.143	11.333	10	7	16	0	1	2	PTAFR, DNAJC8	43, 39138	in gene, downstream	ActReg chr1 #535	0	0	1
536	1	28,585,911	28,586,567	656	1	6.81	10.143	10.905	11	16	14	1	1	1	SESN2	233	in gene	ActReg chr1 #536	0	0	1
537	1	28,640,296	28,640,773	477	1	8.867	10.333	6.933	11	15	11	0	0	0				ActReg chr1 #537	0	1	0
538	1	28,672,525	28,673,196	671	1	9.952	2.286	2.667	17	3	5	0	0	0				ActReg chr1 #538	1	0	0
539	1	28,845,169	28,845,674	505	1	7	8.062	11.5	11	12	18	1	0	3	RCC1, SNHG3, RNU105A	12966, 12966, 10351	in gene, downstream, downstream	ActReg chr1 #539	0	0	1
540	1	28,879,083	28,880,127	1,044	1	9.75	13.156	4.719	18	26	10	1	0	0				ActReg chr1 #540	0	1	0
541	1	28,908,002	28,908,787	785	2	12.917	12.417	14.083	20	22	26	1	5	6	SNHG12, SNORD99, SNORA61, SNORA44, SNORA16A, RAB42	-28, -3060, -1989, -1370, -829, -10318	upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr1 #541	0	1	1
542	1	28,974,483	28,975,784	1,301	2	13.317	13.268	8.61	28	23	13	0	2	2	TAF12, RNU11	-5529, 21	upstream, in gene	ActReg chr1 #542	1	1	0
543	1	28,994,805	28,995,345	540	1	12.765	10.353	5.294	21	18	11	0	1	1	GMEB1	-169	upstream	ActReg chr1 #543	1	0	0
544	1	29,062,788	29,063,946	1,158	2	20.861	17.306	3.889	54	35	10	1	1	1	YTHDF2	234	in gene	ActReg chr1 #544	1	1	0
545	1	29,213,261	29,213,933	672	1	9.571	12.571	6.15	13	20	13	1	1	1	EPB41	-6	upstream	ActReg chr1 #545	0	1	0
546	1	29,448,474	29,449,036	562	1	6.167	6.889	9.944	11	10	13	1	1	2	EPB41, TMEM200B	235152, 1666	downstream, in gene	ActReg chr1 #546	0	0	1
547	1	29,507,780	29,508,792	1,012	1	8.065	15.258	6.433	14	24	13	1	1	1	SFRS4	351	in gene	ActReg chr1 #547	0	1	0
548	1	29,520,578	29,521,041	463	1	2.929	2.3	11.857	4	3	16	0	0	1	MECR	36,645	in gene	ActReg chr1 #548	0	0	1
549	1	29,557,143	29,557,756	613	1	8.947	11.79	7.947	12	18	12	1	2	2	MECR, PTPRJ	5, -5579	in gene, upstream	ActReg chr1 #549	0	1	0
550	1	30,042,486	30,043,436	950	2	15.1	13.5	1.917	30	28	4	0	0	0				ActReg chr1 #550	1	1	0
551	1	30,112,255	30,113,136	881	1	6.643	10.393	4.731	13	15	9	0	0	0				ActReg chr1 #551	0	1	0
552	1	30,171,552	30,171,903	351	1	3.455	2.818	11.091	4	4	16	0	0	0				ActReg chr1 #552	0	0	1
553	1	30,181,710	30,183,141	1,431	1	8.111	11.6	4.409	16	22	7	0	0	0				ActReg chr1 #553	0	1	0
554	1	30,208,823	30,210,063	1,240	2	12.769	12.615	3	26	32	7	0	0	0				ActReg chr1 #554	1	1	0
555	1	30,273,185	30,273,652	467	1	1.857	2.308	10.5	4	4	16	0	0	0				ActReg chr1 #555	0	0	1
556	1	30,447,282	30,448,484	1,202	2	12.105	14.21	3.613	36	34	6	0	0	0				ActReg chr1 #556	1	1	0
557	1	31,084,565	31,085,264	699	1	8.591	11.954	2.05	14	19	3	0	0	0				ActReg chr1 #557	0	1	0
558	1	31,191,532	31,192,230	698	1	13.364	11.773	9.909	20	17	16	1	1	2	MATN1, LOC100129196	4551, 262	in gene, in gene	ActReg chr1 #558	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
559	1	31,205,244	31,206,090	846	1	8.556	12.704	3.074	13	20	4	0	0	3	MATN1, LOC100129196, LAPTM5	-9235, 14048, 25016	upstream, downstream, in gene	ActReg chr1 #559	0	1	0
560	1	31,229,317	31,230,145	828	2	14.885	14.615	4.731	32	27	7	0	1	1	LAPTM5	952	in gene	ActReg chr1 #560	1	1	0
561	1	31,249,728	31,250,298	570	1	4.778	3.533	13.389	7	5	20	0	0	0				ActReg chr1 #561	0	0	1
562	1	31,270,675	31,271,320	645	1	7.75	10.85	5.35	11	14	12	0	0	0				ActReg chr1 #562	0	1	0
563	1	31,288,903	31,290,274	1,371	1	9.512	11.954	6.186	19	20	13	0	0	0				ActReg chr1 #563	0	1	0
564	1	31,296,592	31,297,486	894	2	11.429	13.143	8.321	22	19	16	0	0	0				ActReg chr1 #564	1	1	0
565	1	31,380,352	31,381,116	764	1	5.875	7.708	10.958	8	12	16	1	1	1	SDC3	746	in gene	ActReg chr1 #565	0	0	1
566	1	31,381,875	31,382,253	378	1	6.417	6.75	13	8	9	19	1	1	1	SDC3	-584	upstream	ActReg chr1 #566	0	0	1
567	1	31,635,365	31,636,013	648	2	10.45	10.65	2.947	16	21	5	0	0	0				ActReg chr1 #567	1	1	0
568	1	31,654,365	31,655,839	1,474	3	14.152	12.87	8.261	27	26	16	1	0	1	NKAIN1	57,632	in gene	ActReg chr1 #568	1	1	1
569	1	31,769,128	31,769,776	648	1	6.75	13.8	7.4	9	25	15	1	2	2	SNRNP40, ZCCHC17	192, -390	in gene, upstream	ActReg chr1 #569	0	1	0
570	1	31,769,781	31,770,263	482	1	8.667	9.933	11.733	13	13	18	1	2	2	SNRNP40, ZCCHC17	-378, 180	upstream, in gene	ActReg chr1 #570	0	0	1
571	1	31,867,344	31,868,085	741	1	11.913	7.957	4.565	18	17	7	0	0	0				ActReg chr1 #571	1	0	0
572	1	31,906,771	31,908,254	1,483	2	11.152	10.826	5.978	21	25	10	0	0	1	SERINC2	21,549	in gene	ActReg chr1 #572	1	1	0
573	1	31,913,673	31,913,981	308	1	4.889	3.889	11.444	6	5	15	0	0	1	SERINC2	27,864	downstream	ActReg chr1 #573	0	0	1
574	1	32,042,409	32,042,896	487	1	7.533	7.333	14.2	9	11	19	0	1	1	TINAGL1	566	in gene	ActReg chr1 #574	0	0	1
575	1	32,054,224	32,054,624	400	1	1.917	4.462	10.846	3	9	18	1	0	1	TINAGL1	12,338	downstream	ActReg chr1 #575	0	0	1
576	1	32,109,903	32,111,036	1,133	3	12.686	18.143	10.086	21	33	27	1	1	2	PEF1, COL16A1	369, 59299	in gene, downstream	ActReg chr1 #576	1	1	1
577	1	32,155,296	32,156,022	726	1	7.391	12.783	3.826	13	24	6	0	0	1	COL16A1	14,109	in gene	ActReg chr1 #577	0	1	0
578	1	32,180,814	32,181,670	856	2	9.667	9.741	8.963	15	15	18	0	0	0				ActReg chr1 #578	1	0	1
579	1	32,182,623	32,183,379	756	1	9.917	12.25	3.667	20	21	5	0	0	1	BAI2	46,647	downstream	ActReg chr1 #579	0	1	0
580	1	32,189,148	32,190,350	1,202	2	17.368	17.432	3.737	36	42	8	0	0	1	BAI2	39,899	downstream	ActReg chr1 #580	1	1	0
581	1	32,230,013	32,230,457	444	1	8.929	6.643	12.286	12	14	18	1	2	2	BAI2, MIR4254	-587, -5899	upstream, upstream	ActReg chr1 #581	0	0	1
582	1	32,253,465	32,254,496	1,031	2	19.454	13.333	5.152	39	26	10	1	0	1	SPOCD1	27,600	downstream	ActReg chr1 #582	1	1	0
583	1	32,404,051	32,404,514	463	1	11.667	8.267	7.867	16	13	15	1	1	1	PTP4A2	-294	upstream	ActReg chr1 #583	1	0	0
584	1	32,537,923	32,538,928	1,005	2	13.387	14.097	8.903	22	21	16	1	1	1	TMEM39B	-78	upstream	ActReg chr1 #584	1	1	0
585	1	32,573,327	32,574,509	1,182	1	8.25	11.622	3.824	13	20	6	1	1	2	TMEM39B, KPNA6	35415, 274	downstream, in gene	ActReg chr1 #585	0	1	0
586	1	32,644,742	32,645,683	941	1	13.172	9.724	7.517	18	17	18	1	1	2	KPNA6, TXLNA	71568, -133	downstream, upstream	ActReg chr1 #586	1	0	0
587	1	32,670,811	32,671,829	1,018	2	10.375	10.625	12.469	15	15	31	1	2	6	TXLNA, CCDC28B, IQCC, DCDC2B, LOC100507457, C1orf91	-25975, 5118, 84, -3375, 9738, 16606	downstream, downstream, in gene, upstream, downstream, downstream	ActReg chr1 #587	1	0	1
588	1	32,701,619	32,702,318	699	2	11.136	10.454	3.421	20	18	6	0	0	1	EIF3I	13,997	downstream	ActReg chr1 #588	1	1	0
589	1	32,716,476	32,717,307	831	1	4.615	5.538	13.231	7	11	22	0	1	2	FAM167B, LCK	4073, 51	downstream, in gene	ActReg chr1 #589	0	0	1
590	1	32,757,629	32,758,621	992	2	7.935	11.645	7.414	17	20	20	1	1	2	LCK, HDAC1	41285, 417	downstream, in gene	ActReg chr1 #590	0	1	1
591	1	32,803,527	32,804,009	482	1	8.667	6.067	10.6	11	9	17	0	1	2	HDAC1, MARCKSL1	46060, -1934	downstream, upstream	ActReg chr1 #591	0	0	1
592	1	32,817,097	32,817,819	722	1	8.318	11.227	7	13	20	15	1	0	1	LOC100128071	10,386	downstream	ActReg chr1 #592	0	1	0
593	1	32,859,429	32,860,659	1,230	1	9.395	13.658	5.974	15	20	11	1	1	1	BSDC1	18	in gene	ActReg chr1 #593	0	1	0
594	1	33,235,365	33,235,937	572	1	4.444	6.111	14.389	6	9	24	1	0	2	KIAA1522, YARS	28139, 47982	in gene, downstream	ActReg chr1 #594	0	0	1
595	1	33,282,504	33,283,792	1,288	3	18.95	24.45	8	68	86	17	1	2	2	YARS, S100P6P	485, -28	in gene, upstream	ActReg chr1 #595	1	1	1
596	1	33,351,540	33,352,014	474	1	5.067	4.067	10.8	9	6	19	1	1	2	HPCA, TMEM54	-321, 15176	upstream, downstream	ActReg chr1 #596	0	0	1
597	1	33,438,279	33,438,889	610	1	5.579	9.211	4.316	9	17	6	1	0	1	RNF19B	-8,298	upstream	ActReg chr1 #597	0	1	0
598	1	33,546,652	33,547,534	882	1	5.607	9.964	12.929	8	14	19	1	1	1	ADC	379	in gene	ActReg chr1 #598	0	0	1
599	1	33,564,979	33,565,686	707	1	6.136	11.682	4.455	12	17	9	0	0	1	ADC	18,618	in gene	ActReg chr1 #599	0	1	0
600	1	33,592,434	33,593,544	1,110	2	26.714	34.857	3.714	93	114	7	1	0	1	ADC	46,275	downstream	ActReg chr1 #600	1	1	0
601	1	33,626,629	33,627,555	926	1	9.069	10.448	5.517	14	15	9	0	0	1	TRIM62	20,579	in gene	ActReg chr1 #601	0	1	0
602	1	33,709,735	33,710,528	793	1	12.12	8.52	3.56	16	13	7	0	0	0				ActReg chr1 #602	1	0	0
603	1	33,713,696	33,714,219	523	1	12.588	10.294	3.588	25	19	6	0	0	1	ZNF362	-8,217	upstream	ActReg chr1 #603	1	0	0
604	1	33,896,448	33,897,059	611	1	10.05	7	3.111	22	15	5	1	0	0				ActReg chr1 #604	1	0	0
605	1	33,899,116	33,899,880	764	1	13.833	9.458	2.381	28	17	5	0	0	0				ActReg chr1 #605	1	0	0
606	1	33,908,777	33,909,765	988	1	10.677	7.161	4.968	16	11	10	0	0	0				ActReg chr1 #606	1	0	0
607	1	34,089,958	34,090,514	556	1	3	3.176	13.647	5	6	20	1	0	1	CSMD2	541,207	in gene	ActReg chr1 #607	0	0	1
608	1	35,174,993	35,175,738	745	2	9.174	13.217	3	17	28	6	0	0	0				ActReg chr1 #608	1	1	0
609	1	35,246,801	35,247,479	678	1	5.952	12.429	8.19	10	22	14	1	1	1	GJB3	350	in gene	ActReg chr1 #609	0	1	0
610	1	35,324,571	35,325,999	1,428	2	34.178	31.6	2.73	133	136	5	1	1	2	C1orf212, DLGAP3	132, 45699	in gene, downstream	ActReg chr1 #610	1	1	0
611	1	35,331,639	35,332,441	802	1	9.72	10.56	12.92	15	16	18	1	1	2	C1orf212, DLGAP3	-6623, 38944	upstream, in gene	ActReg chr1 #611	0	0	1
612	1	35,369,949	35,370,313	364	1	2.833	4.75	10.5	5	6	14	0	1	1	DLGAP3	853	in gene	ActReg chr1 #612	0	0	1
613	1	35,389,867	35,391,142	1,275	2	13.5	16.125	5	31	43	10	0	0	0				ActReg chr1 #613	1	1	0
614	1	35,395,491	35,395,924	433	1	4.615	6.308	12.538	11	12	18	1	0	0				ActReg chr1 #614	0	0	1
615	1	35,450,473	35,451,244	771	3	9.167	10.042	8.174	14	18	16	1	1	2	LOC100506144, ZMYM6	90, 46711	in gene, downstream	ActReg chr1 #615	1	1	1
616	1	35,497,027	35,497,833	806	2	11.4	11.68	4.7	17	20	7	1	1	1	ZMYM6	139	in gene	ActReg chr1 #616	1	1	0
617	1	35,658,098	35,659,045	947	3	10.133	11.667	7.652	15	19	19	1	1	1	SFPQ	172	in gene	ActReg chr1 #617	1	1	1
618	1	36,022,692	36,023,640	948	2	9.655	12.345	15.172	15	25	25	1	2	2	KIAA0319L, NCDN	-129, -227	upstream, upstream	ActReg chr1 #618	0	1	1
619	1	36,042,740	36,043,358	618	1	4.211	3.105	12.79	7	5	19	1	0	1	TFAP2E	4,078	in gene	ActReg chr1 #619	0	0	1
620	1	36,106,793	36,107,502	709	2	10.636	9.955	4.682	22	19	7	1	1	1	PSMB2	-4	upstream	ActReg chr1 #620	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
621	1	36,116,207	36,116,946	739	1	6.478	10.435	2.667	14	14	4	0	0	1	PSMB2	-9,433	upstream	ActReg chr1 #621	0	1	0
622	1	36,125,913	36,127,333	1,420	2	11.911	15.111	4.841	36	43	12	0	0	0				ActReg chr1 #622	1	1	0
623	1	36,184,078	36,184,958	880	2	8.852	11.63	8.63	14	14	18	1	1	1	C1orf216	272	in gene	ActReg chr1 #623	0	1	1
624	1	36,234,795	36,235,198	403	1	8	7.333	12	12	10	19	1	1	1	CLSPN	555	in gene	ActReg chr1 #624	0	0	1
625	1	36,342,215	36,343,071	856	2	9.462	11.462	3	19	16	4	0	1	1	EIF2C1	-6,167	upstream	ActReg chr1 #625	1	1	0
626	1	36,396,508	36,397,233	725	1	6.217	12.913	7.7	9	22	16	1	1	2	EIF2C1, EIF2C3	48060, 98	downstream, in gene	ActReg chr1 #626	0	1	0
627	1	36,553,938	36,555,134	1,196	2	20.108	22.351	7.405	51	54	12	1	1	3	TEKT2, ADPRHL2, COL8A2	4860, 83, 11314	downstream, in gene, downstream	ActReg chr1 #627	1	1	0
628	1	36,565,507	36,565,931	424	1	6.077	4.923	11.385	8	6	16	0	1	2	ADPRHL2, COL8A2	11266, 131	downstream, in gene	ActReg chr1 #628	0	0	1
629	1	36,591,210	36,591,779	569	1	5.529	7.111	11.778	9	10	17	1	0	0				ActReg chr1 #629	0	0	1
630	1	36,616,117	36,616,839	722	1	7.565	11.652	5.652	12	16	10	0	2	2	TRAPPC3, MAP7D1	-1411, -5325	upstream, upstream	ActReg chr1 #630	0	1	0
631	1	36,689,402	36,690,576	1,174	3	11.27	13.892	11.676	25	24	24	1	1	1	THRAP3	-28	upstream	ActReg chr1 #631	1	1	1
632	1	36,765,530	36,766,116	586	1	10.79	7.579	3.615	15	11	5	0	1	2	THRAP3, C1orf113	75806, -6171	in gene, upstream	ActReg chr1 #632	1	0	0
633	1	36,786,351	36,786,967	616	1	3.789	4.368	13.421	7	6	19	1	0	2	C1orf113, FAM176B	14665, 3096	in gene, downstream	ActReg chr1 #633	0	0	1
634	1	36,817,501	36,818,797	1,296	1	8.878	11.78	4.951	15	18	8	0	0	1	STK40	33,336	in gene	ActReg chr1 #634	0	1	0
635	1	36,839,805	36,840,914	1,109	2	12.086	12.114	4.971	20	21	13	0	0	2	STK40, LOC100506594	11126, 7739	in gene, in gene	ActReg chr1 #635	1	1	0
636	1	36,851,857	36,852,735	878	2	11.778	13.963	5.074	19	25	8	1	1	3	STK40, LOC100506594, LSM10	-811, 19676, 11197	upstream, downstream, downstream	ActReg chr1 #636	1	1	0
637	1	36,863,023	36,863,775	752	2	12.652	11.609	7.696	23	19	12	1	1	1	LSM10	94	in gene	ActReg chr1 #637	1	1	0
638	1	36,866,291	36,866,722	431	1	6.5	6.143	10.857	9	10	16	0	1	1	LSM10	-3,013	upstream	ActReg chr1 #638	0	0	1
639	1	36,929,460	36,930,414	954	2	17.667	21.267	7.167	47	55	12	1	1	2	MRPS15, CSF3R	103, 18978	in gene, downstream	ActReg chr1 #639	1	1	0
640	1	37,068,900	37,069,574	674	1	9.429	15	1.643	19	32	3	0	0	0				ActReg chr1 #640	0	1	0
641	1	37,389,541	37,390,389	848	1	9.731	15.269	2.423	17	31	4	0	0	1	GRIK3	109,879	in gene	ActReg chr1 #641	0	1	0
642	1	37,431,524	37,432,480	956	2	13.9	21.767	4.667	28	47	9	0	0	1	GRIK3	67,842	in gene	ActReg chr1 #642	1	1	0
643	1	37,486,139	37,486,719	580	2	9.778	9.125	1.846	18	17	4	0	0	1	GRIK3	13,415	in gene	ActReg chr1 #643	1	1	0
644	1	37,498,111	37,498,509	398	1	2.077	1.769	11.462	3	3	16	1	1	1	GRIK3	1,534	in gene	ActReg chr1 #644	0	0	1
645	1	37,720,951	37,721,518	567	1	9.889	10.333	2.706	16	16	5	0	0	0				ActReg chr1 #645	0	1	0
646	1	37,875,753	37,876,845	1,092	1	7.5	12.706	3.724	12	29	8	0	0	0				ActReg chr1 #646	0	1	0
647	1	37,913,029	37,913,612	583	1	3.944	6.056	10.722	6	10	17	0	0	1	LOC728431	26,727	downstream	ActReg chr1 #647	0	0	1
648	1	37,945,059	37,946,031	972	1	8.7	9.933	7.933	18	15	15	0	1	2	LOC728431, ZC3H12A	-5498, 5426	upstream, in gene	ActReg chr1 #648	0	1	0
649	1	38,022,426	38,022,780	354	1	3.182	2.818	11.091	5	5	14	1	2	3	SNIP1, DNALI1, GNL2	-2700, 83, 38983	upstream, in gene, downstream	ActReg chr1 #649	0	0	1
650	1	38,027,287	38,027,698	411	1	7.154	7.385	12.154	9	9	16	0	1	3	SNIP1, DNALI1, GNL2	-7589, 4972, 34094	upstream, in gene, downstream	ActReg chr1 #650	0	0	1
651	1	38,096,219	38,096,640	421	1	4.357	4.5	13.214	6	6	21	0	0	1	RSPO1	4,062	in gene	ActReg chr1 #651	0	0	1
652	1	38,157,047	38,158,512	1,465	2	10.674	11.587	7.109	18	21	14	1	2	2	C1orf109, CDCA8	-1587, -380	upstream, upstream	ActReg chr1 #652	1	1	0
653	1	38,227,032	38,227,386	354	1	2	3.818	12.454	3	6	18	1	0	1	EPHA10	3,615	in gene	ActReg chr1 #653	0	0	1
654	1	38,229,522	38,231,062	1,540	2	11.75	14.167	7.625	25	36	18	1	1	1	EPHA10	532	in gene	ActReg chr1 #654	1	1	0
655	1	38,273,679	38,274,273	594	2	12.526	16.053	4.529	22	30	9	1	2	4	MANEAL, YRDC, C1orf122, MTF1	14202, -111, 503, 51316	downstream, upstream, in gene, downstream	ActReg chr1 #655	1	1	0
656	1	38,324,807	38,326,182	1,375	3	11.837	11.767	10.349	19	22	21	1	1	2	MTF1, INPP5B	-202, 87235	upstream, downstream	ActReg chr1 #656	1	1	1
657	1	38,455,077	38,456,298	1,221	3	43.763	48.947	7.816	172	183	19	1	1	2	SF3A3, FHL3	74, 15547	in gene, downstream	ActReg chr1 #657	1	1	1
658	1	38,477,875	38,478,979	1,104	2	10.2	13.2	7.429	17	23	13	1	2	2	FHL3, UTP11L	-7193, 43	upstream, in gene	ActReg chr1 #658	1	1	0
659	1	38,496,409	38,497,047	638	1	4.3	7.65	13.2	10	16	22	0	0	1	UTP11L	18,344	downstream	ActReg chr1 #659	0	0	1
660	1	38,512,771	38,513,055	284	1	9	8	12.875	12	11	16	1	1	1	POU3F1	-463	upstream	ActReg chr1 #660	0	0	1
661	1	38,529,748	38,530,664	916	1	10.586	13.793	4.241	21	22	9	0	0	0				ActReg chr1 #661	0	1	0
662	1	38,541,485	38,542,355	870	2	12.63	13.333	4.667	28	28	8	0	0	0				ActReg chr1 #662	1	1	0
663	1	38,550,370	38,550,703	333	1	5.9	3.4	12.4	7	4	15	0	0	0				ActReg chr1 #663	0	0	1
664	1	38,672,715	38,673,295	580	1	4.278	3	11.889	7	5	18	0	0	0				ActReg chr1 #664	0	0	1
665	1	39,266,636	39,267,109	473	1	2.917	6.2	12.267	4	10	19	0	0	0				ActReg chr1 #665	0	0	1
666	1	39,456,612	39,457,224	612	1	7.684	11.526	3.769	15	21	6	1	1	1	AKIRIN1	2	in gene	ActReg chr1 #666	0	1	0
667	1	39,874,128	39,874,592	464	1	3.2	4.733	10.6	7	7	17	1	1	2	MACF1, KIAA0754	327242, -816	in gene, upstream	ActReg chr1 #667	0	0	1
668	1	39,899,554	39,899,821	267	1	1	2.429	9.625	1	3	13	0	0	1	MACF1	352,569	in gene	ActReg chr1 #668	0	0	1
669	1	40,042,471	40,043,250	779	2	11.208	11.917	1.933	18	20	4	1	1	3	PABPC4, LOC100506950, SNORA55	-339, 12091, -9678	upstream, downstream, upstream	ActReg chr1 #669	1	1	0
670	1	40,264,744	40,265,245	501	1	10	7.8	5.133	16	12	7	0	0	1	LOC100287437	10,340	downstream	ActReg chr1 #670	1	0	0
671	1	40,348,697	40,349,483	786	2	8.36	9.92	9.955	14	21	16	1	1	1	TRIT1	87	in gene	ActReg chr1 #671	0	1	1
672	1	40,420,615	40,421,445	830	2	7.692	10	11.808	13	14	17	1	1	1	MFSD2A	246	in gene	ActReg chr1 #672	0	1	1
673	1	40,421,699	40,422,178	479	1	4.6	5.2	12.867	7	10	18	0	1	1	MFSD2A	1,154	in gene	ActReg chr1 #673	0	0	1
674	1	40,626,658	40,627,856	1,198	3	11.46	11.514	10.667	22	26	19	1	1	1	RLF	216	in gene	ActReg chr1 #674	1	1	1
675	1	40,723,333	40,724,423	1,090	3	15.706	11.794	9.029	28	26	17	2	1	2	TMCO2, ZMPSTE24	10305, 145	downstream, in gene	ActReg chr1 #675	1	1	1
676	1	40,839,765	40,840,854	1,089	2	9.147	10.706	5.529	18	15	11	1	1	2	LOC100286988, SMAP2	52234, 581	in gene, in gene	ActReg chr1 #676	1	1	0
677	1	40,853,497	40,853,996	499	1	4.312	4.5	9.688	8	7	12	0	0	2	LOC100286988, SMAP2	18797, 14018	in gene, in gene	ActReg chr1 #677	0	0	1
678	1	40,915,396	40,916,258	862	1	7.63	13.889	4.407	14	23	9	1	1	1	ZNF643	-510	upstream	ActReg chr1 #678	0	1	0
679	1	40,942,796	40,943,339	543	1	8.882	9.294	3.333	17	13	6	1	1	1	ZNF642	-235	upstream	ActReg chr1 #679	1	0	0
680	1	40,973,994	40,974,884	890	2	13.071	11.536	10.179	21	16	17	1	1	1	DEM1	6	in gene	ActReg chr1 #680	1	1	0
681	1	40,996,958	40,997,706	748	1	4.792	13.375	4.522	9	21	9	1	1	1	ZNF684	99	in gene	ActReg chr1 #681	0	1	0
682	1	41,091,415	41,092,244	829	1	7.385	12.269	5.455	17	19	11	0	0	1	RIMS3	39,495	in gene	ActReg chr1 #682	0	1	0
683	1	41,157,024	41,157,920	896	1	8.103	12.552	8.552	12	21	18	1	2	2	LOC100130557, NFYC	461, 230	in gene, in gene	ActReg chr1 #683	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
684	1	41,284,094	41,284,591	497	1	3.375	6.562	14.25	5	9	22	1	0	1	KCNQ4	34,658	in gene	ActReg chr1 #684	0	0	1
685	1	41,292,837	41,293,371	534	1	3.75	4.625	13.938	6	8	23	0	0	1	KCNQ4	43,420	in gene	ActReg chr1 #685	0	0	1
686	1	41,303,718	41,304,536	818	1	5.52	9.68	13.68	6	14	20	1	0	1	KCNQ4	54,443	in gene	ActReg chr1 #686	0	0	1
687	1	41,384,967	41,385,682	715	1	13.046	8.045	2.6	19	13	4	0	0	0				ActReg chr1 #687	1	0	0
688	1	41,444,553	41,445,649	1,096	2	8.206	10.206	9.118	16	16	15	1	1	1	CTPS	94	in gene	ActReg chr1 #688	0	1	1
689	1	41,979,802	41,980,486	684	1	9.091	12.591	2.111	14	25	4	0	0	1	HIVEP3	404,352	in gene	ActReg chr1 #689	0	1	0
690	1	42,248,744	42,249,560	816	1	12.32	9.88	4.8	18	16	7	0	0	1	HIVEP3	135,344	in gene	ActReg chr1 #690	1	0	0
691	1	42,275,924	42,277,290	1,366	3	12.535	12.512	2.216	32	26	5	0	0	1	HIVEP3	107,889	in gene	ActReg chr1 #691	1	1	0
692	1	42,312,175	42,312,858	683	1	12.714	8.857	1.118	20	13	3	0	0	2	HIVEP3, LOC100507198	71980, 25374	in gene, downstream	ActReg chr1 #692	1	0	0
693	1	42,316,989	42,317,597	608	1	7.944	10.21	1.286	13	14	2	0	0	2	HIVEP3, LOC100507198	67203, 20597	in gene, in gene	ActReg chr1 #693	0	1	0
694	1	42,335,615	42,336,333	718	1	11.348	10.348	3.294	21	14	5	0	1	2	HIVEP3, LOC100507198	48522, 1916	in gene, in gene	ActReg chr1 #694	1	0	0
695	1	42,383,621	42,384,437	816	1	6.72	9.6	4.32	12	13	9	1	1	1	HIVEP3	467	in gene	ActReg chr1 #695	0	1	0
696	1	42,386,223	42,386,765	542	1	10.941	4.294	4.154	21	8	7	0	1	1	HIVEP3	-1,998	upstream	ActReg chr1 #696	1	0	0
697	1	42,401,577	42,402,356	779	2	12.773	10.667	2.5	29	18	5	0	0	0				ActReg chr1 #697	1	1	0
698	1	42,800,672	42,801,484	812	1	8.923	12.346	6.56	14	23	17	1	1	1	FOXJ3	-175	upstream	ActReg chr1 #698	0	1	0
699	1	42,845,405	42,846,088	683	2	12	12	3.368	18	19	5	1	1	1	RIMKLA	-722	upstream	ActReg chr1 #699	1	1	0
700	1	42,921,810	42,922,871	1,061	2	9.303	14.364	10.364	14	22	22	1	3	3	ZMYND12, PPCS, LOC100507214	-402, 167, -6617	upstream, in gene, upstream	ActReg chr1 #700	0	1	1
701	1	42,995,569	42,996,146	577	1	14.5	9.611	1.778	29	23	2	0	1	1	CCDC30	-4,703	upstream	ActReg chr1 #701	1	0	0
702	1	43,123,533	43,124,621	1,088	3	10.941	13.059	9.794	20	22	20	1	1	2	CCDC30, PPIH	123517, 29	downstream, in gene	ActReg chr1 #702	1	1	1
703	1	43,205,647	43,206,368	721	1	1.55	3.87	10.696	2	7	16	0	1	2	CLDN19, LEPRE1	-82, 26748	upstream, downstream	ActReg chr1 #703	0	0	1
704	1	43,232,437	43,233,403	966	1	9.733	10.4	16.167	18	18	30	1	2	2	LEPRE1, C1orf50	-165, 4	upstream, in gene	ActReg chr1 #704	0	0	1
705	1	43,311,760	43,313,061	1,301	1	7.561	11.024	6.95	14	17	15	1	1	2	ERMAP, ZNF691	29634, 130	downstream, in gene	ActReg chr1 #705	0	1	0
706	1	43,365,418	43,366,100	682	1	4.524	11.905	3.947	7	17	8	0	0	0				ActReg chr1 #706	0	1	0
707	1	43,389,904	43,390,500	596	1	10.263	11.316	12.79	18	17	20	1	0	1	SLC2A1	34,645	downstream	ActReg chr1 #707	0	0	1
708	1	43,424,202	43,425,079	877	2	10.37	12.37	6.037	14	20	11	1	2	2	SLC2A1, FLJ32224	207, -80	in gene, upstream	ActReg chr1 #708	1	1	0
709	1	43,814,713	43,815,363	650	1	6	11.476	7.095	11	20	12	1	0	2	MPL, CDC20	11563, -9588	in gene, upstream	ActReg chr1 #709	0	1	0
710	1	43,832,651	43,833,161	510	1	11.688	13.125	12.5	16	19	19	1	1	2	CDC20, ELOVL1	8280, 793	downstream, in gene	ActReg chr1 #710	0	0	1
711	1	43,855,060	43,855,982	922	3	11.552	11.724	9.207	17	24	20	1	2	2	MED8, C1orf84	-38, -35	upstream, upstream	ActReg chr1 #711	1	1	1
712	1	43,917,064	43,917,521	457	1	3.643	6.214	12.857	5	9	15	0	1	2	KIAA0467, HYI	28495, 2368	in gene, in gene	ActReg chr1 #712	0	0	1
713	1	43,988,680	43,989,445	765	2	13.667	14.417	2.235	30	30	3	0	1	1	PTPRF	-7,485	upstream	ActReg chr1 #713	1	1	0
714	1	44,084,996	44,085,931	935	1	2.483	5.552	11.552	4	10	16	0	0	1	PTPRF	88,916	in gene	ActReg chr1 #714	0	0	1
715	1	44,299,907	44,301,783	1,876	3	8.655	10.828	2.608	21	18	5	0	0	1	ST3GAL3	127,627	in gene	ActReg chr1 #715	1	1	0
716	1	44,395,080	44,395,774	694	1	11.762	11.619	3.333	24	22	6	0	1	2	ST3GAL3, ARTN	222209, -3565	in gene, upstream	ActReg chr1 #716	1	0	0
717	1	44,411,761	44,412,886	1,125	3	13.057	14.314	9.857	25	25	17	1	1	2	ARTN, IPO13	13331, -155	downstream, upstream	ActReg chr1 #717	1	1	1
718	1	44,433,895	44,434,603	708	1	12.954	10.954	2.6	24	17	5	0	2	3	IPO13, DPH2, ATP6V0B	21771, -1404, -6353	downstream, upstream, upstream	ActReg chr1 #718	1	0	0
719	1	44,446,658	44,447,207	549	1	5.706	3.765	13.353	8	6	20	0	1	3	DPH2, ATP6V0B, B4GALT2	11279, 6330, 2066	downstream, downstream, in gene	ActReg chr1 #719	0	0	1
720	1	44,489,715	44,490,370	655	1	3.667	5.905	11.095	6	10	19	0	0	1	SLC6A9	7,092	in gene	ActReg chr1 #720	0	0	1
721	1	44,496,049	44,496,676	627	1	7.8	11.45	7.75	12	18	14	1	1	1	SLC6A9	772	in gene	ActReg chr1 #721	0	1	0
722	1	44,678,818	44,679,363	545	1	15.059	12.235	7.647	30	25	14	1	1	2	DMAP1, ERI3	-35, 141849	upstream, downstream	ActReg chr1 #722	1	0	0
723	1	44,705,251	44,705,672	421	1	3.077	5.385	12.154	8	8	16	0	0	1	ERI3	115,478	in gene	ActReg chr1 #723	0	0	1
724	1	44,793,222	44,793,935	713	1	11.682	8.091	3.273	17	12	6	0	0	1	ERI3	27,361	in gene	ActReg chr1 #724	1	0	0
725	1	44,997,531	44,998,316	785	2	12.52	13.96	2.167	26	29	4	0	0	1	RNF220	126,963	in gene	ActReg chr1 #725	1	1	0
726	1	45,097,206	45,097,705	499	1	10.625	11.062	11.625	18	16	21	1	0	1	RNF220	226,495	in gene	ActReg chr1 #726	0	0	1
727	1	45,187,135	45,188,195	1,060	3	13.529	13.588	7.935	27	27	18	0	0	2	C1orf228, RNU5D	47271, 9175	in gene, downstream	ActReg chr1 #727	1	1	1
728	1	45,196,534	45,197,312	778	2	11.72	14.36	4.68	21	34	11	0	1	3	C1orf228, RNU5D, KIF2C	56529, -83, -8567	downstream, upstream, upstream	ActReg chr1 #728	1	1	0
729	1	45,204,070	45,204,545	475	1	3.8	6.733	10.6	5	11	17	0	2	2	RNU5D, KIF2C	-7467, -1183	upstream, upstream	ActReg chr1 #729	0	0	1
730	1	45,240,634	45,241,778	1,144	3	9.972	9.972	11.722	23	24	24	1	5	7	KIF2C, RPS8, SNORD55, SNORD46, SNORD38A, SNORD38B, BEST4	35716, -40, -331, -958, -2308, -2856, 12220	downstream, upstream, upstream, upstream, upstream, upstream, upstream, downstream	ActReg chr1 #730	1	1	1
731	1	45,266,207	45,266,658	451	1	5.867	6.467	9.8	10	9	16	1	2	3	PLK3, TCTEX1D4, BTBD19	396, 6525, -7722	in gene, downstream, upstream	ActReg chr1 #731	0	0	1
732	1	45,285,114	45,286,589	1,475	2	11.717	13.761	7.804	31	35	11	0	0	2	BTBD19, PTCH2	11697, 22765	downstream, in gene	ActReg chr1 #732	1	1	0
733	1	45,288,163	45,288,974	811	1	3.68	3.04	11.52	8	8	15	0	0	2	BTBD19, PTCH2	14414, 20048	downstream, in gene	ActReg chr1 #733	0	0	1
734	1	45,451,807	45,452,717	910	2	17.379	22.69	5.379	47	57	10	1	1	1	EIF2B3	99	in gene	ActReg chr1 #734	1	1	0
735	1	45,476,288	45,478,190	1,902	2	13.233	17.45	3.912	46	43	10	1	2	3	HECTD3, URQD, ZSWIM5	-212, -566, 195011	upstream, upstream, downstream	ActReg chr1 #735	1	1	0
736	1	45,769,481	45,769,901	420	1	9.846	16.083	14.538	16	22	21	1	1	1	hCG_1820661	109	in gene	ActReg chr1 #736	0	0	1
737	1	45,792,434	45,793,421	987	1	4.774	12.032	9.742	8	22	15	1	1	2	HPDL, MUTYH	382, 13215	in gene, downstream	ActReg chr1 #737	0	1	0
738	1	45,956,350	45,957,020	670	1	6	7.714	12.238	11	14	19	1	1	3	TESK2, CCDC163P, MMACHC	155, 9066, -9171	in gene, downstream, upstream	ActReg chr1 #738	0	0	1
739	1	45,965,393	45,966,259	866	2	14.963	15.333	4.37	32	32	8	1	2	3	TESK2, CCDC163P, MMACHC	-8986, -75, -30	upstream, upstream, upstream	ActReg chr1 #739	1	1	0
740	1	45,986,853	45,988,003	1,150	2	8.694	13.111	10.235	17	25	22	1	1	1	PRDX1	181	in gene	ActReg chr1 #740	0	1	1
741	1	46,049,198	46,050,139	941	3	15.207	12.31	7.897	28	18	17	1	1	1	NASP	-49	upstream	ActReg chr1 #741	1	1	1
742	1	46,151,763	46,153,365	1,602	3	10.72	11.16	9.143	18	21	14	1	2	3	GPBP1L1, TMEM69, IPP	-262, -1283, 63921	upstream, upstream, downstream	ActReg chr1 #742	1	1	1
743	1	46,153,474	46,154,145	671	1	7.238	11.191	7.278	12	17	10	0	2	3	GPBP1L1, TMEM69, IPP	-1507, -38, 62676	upstream, upstream, downstream	ActReg chr1 #743	0	1	0
744	1	46,215,754	46,216,800	1,046	2	9.758	13.242	8.697	16	19	22	1	1	1	IPP	208	in gene	ActReg chr1 #744	0	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
745	1	46,597,966	46,598,875	909	3	14.821	19.536	9.643	36	42	15	1	1	1	PIK3R3	288	in gene	ActReg chr1 #745	1	1	1
746	1	46,600,351	46,600,935	584	1	8.789	10.316	2.571	14	16	3	0	1	1	PIK3R3	-1,935	upstream	ActReg chr1 #746	0	1	0
747	1	46,663,724	46,664,095	371	1	5.818	7.636	11	10	10	16	0	1	2	POMGNT1, C1orf190	22068, -5097	in gene, upstream	ActReg chr1 #747	0	0	1
748	1	46,668,663	46,669,305	642	1	11	9.65	12.8	15	16	20	1	1	2	POMGNT1, C1orf190	16993, -22	in gene, upstream	ActReg chr1 #748	0	0	1
749	1	46,713,176	46,713,769	593	2	15.421	15.158	5.316	29	36	10	0	1	1	RAD54L	105	in gene	ActReg chr1 #749	1	1	0
750	1	46,767,286	46,768,893	1,607	2	11.12	13.74	6.25	19	21	11	1	2	2	LRRC41, UQCRH	949, -1291	in gene, upstream	ActReg chr1 #750	1	1	0
751	1	46,768,912	46,769,714	802	1	12.84	8.84	5	20	18	8	1	2	2	LRRC41, UQCRH	-275, -67	upstream, upstream	ActReg chr1 #751	1	0	0
752	1	46,954,743	46,955,306	563	1	5.833	5.444	10.833	9	10	17	1	0	0				ActReg chr1 #752	0	0	1
753	1	46,956,897	46,957,448	551	1	1.688	2.765	9.706	3	5	12	1	0	0				ActReg chr1 #753	0	0	1
754	1	47,184,250	47,185,300	1,050	2	19.394	17.424	4.5	45	41	9	1	1	1	KIAA0494	-39	upstream	ActReg chr1 #754	1	1	0
755	1	47,201,113	47,201,999	886	2	13.821	12.107	2.231	23	20	4	0	0	0				ActReg chr1 #755	1	1	0
756	1	47,644,778	47,645,375	597	1	4.5	12.944	5.889	7	20	8	0	0	1	PDZK1IP1	10,695	downstream	ActReg chr1 #756	0	1	0
757	1	47,696,484	47,696,967	483	1	4.467	4.733	12.667	7	8	18	1	1	1	TAL1	-1,282	upstream	ActReg chr1 #757	0	0	1
758	1	47,779,422	47,780,018	596	2	11.632	10.421	6.737	20	18	14	1	1	1	STIL	99	in gene	ActReg chr1 #758	1	1	0
759	1	47,902,717	47,904,079	1,362	1	8.023	13.046	3.865	15	22	10	1	2	2	MGC12982, FOXD2	-3085, 1709	upstream, in gene	ActReg chr1 #759	0	1	0
760	1	48,043,088	48,044,397	1,309	2	9.756	10.78	6.244	17	16	12	0	0	0				ActReg chr1 #760	1	1	0
761	1	48,681,220	48,682,153	933	1	6.552	11.69	2.167	10	17	4	0	1	1	SLC5A9	-6,671	upstream	ActReg chr1 #761	0	1	0
762	1	48,937,241	48,937,839	598	2	10.21	7.789	7.526	16	11	13	1	1	1	SPATA6	336	in gene	ActReg chr1 #762	1	0	1
763	1	48,959,626	48,960,762	1,136	2	11	11.829	3.556	18	18	7	0	0	0				ActReg chr1 #763	1	1	0
764	1	48,996,252	48,997,388	1,136	2	15.833	15.028	3.611	36	37	6	0	0	1	AGBL4	1,492,806	downstream	ActReg chr1 #764	1	1	0
765	1	49,084,792	49,085,583	791	1	7.52	11.44	4.267	13	18	8	0	0	1	AGBL4	1,404,439	in gene	ActReg chr1 #765	0	1	0
766	1	49,318,448	49,319,254	806	2	12.36	12.84	2.048	23	22	3	0	0	1	AGBL4	1,170,775	in gene	ActReg chr1 #766	1	1	0
767	1	49,817,396	49,817,913	517	1	10.375	6.5	2.714	15	11	6	0	0	1	AGBL4	671,972	in gene	ActReg chr1 #767	1	0	0
768	1	50,733,590	50,734,269	679	2	12	10.524	1.538	26	19	3	0	0	0				ActReg chr1 #768	1	1	0
769	1	50,745,509	50,746,172	663	2	8.7	10.4	3.1	16	21	5	0	0	0				ActReg chr1 #769	1	1	0
770	1	50,774,327	50,775,043	716	2	12.13	14	4.348	24	29	7	0	0	0				ActReg chr1 #770	1	1	0
771	1	50,881,093	50,881,639	546	1	2.625	3.462	12.059	3	6	19	1	0	1	DMRTA2	7,775	downstream	ActReg chr1 #771	0	0	1
772	1	51,425,610	51,426,363	753	2	10.13	13.174	5.087	19	21	10	1	1	2	FAF1, CDKN2C	-50, -8381	upstream, upstream	ActReg chr1 #772	1	1	0
773	1	51,433,803	51,435,092	1,289	1	7.675	13.325	5.657	12	23	11	1	1	2	FAF1, CDKN2C	-8511, 80	upstream, in gene	ActReg chr1 #773	0	1	0
774	1	51,701,624	51,702,836	1,212	2	11.526	7.316	9.389	19	15	20	1	1	1	RNF11	285	in gene	ActReg chr1 #774	1	0	1
775	1	51,810,819	51,811,341	522	1	4.812	4	11.375	8	6	17	1	1	2	TTC39A, EPS15	-295, 173915	upstream, downstream	ActReg chr1 #775	0	0	1
776	1	52,006,810	52,007,526	716	1	11.696	10.348	1.85	17	15	5	0	0	0				ActReg chr1 #776	1	0	0
777	1	52,035,069	52,036,118	1,049	1	11.546	10.061	2.034	16	16	5	0	0	0				ActReg chr1 #777	1	0	0
778	1	52,082,700	52,083,741	1,041	1	13.562	11.125	6.5	22	17	13	0	1	1	OSBPL9	673	in gene	ActReg chr1 #778	1	0	0
779	1	52,194,903	52,195,492	589	1	8.789	9.526	8.263	11	17	14	1	0	1	OSBPL9	112,650	in gene	ActReg chr1 #779	0	1	0
780	1	52,498,747	52,499,604	857	3	11.963	11.556	10.63	17	21	17	1	1	2	TXNDC12, KTI12	21872, 297	in gene, in gene	ActReg chr1 #780	1	1	1
781	1	52,520,590	52,521,397	807	1	9.64	13.28	5.12	14	21	13	1	2	2	TXNDC12, BTF3L4	54, -864	in gene, upstream	ActReg chr1 #781	0	1	0
782	1	52,521,644	52,522,610	966	2	12.233	11.533	4.7	17	20	9	1	2	2	TXNDC12, BTF3L4	-1080, 270	upstream, in gene	ActReg chr1 #782	1	1	0
783	1	52,825,679	52,826,272	593	1	3.211	4.947	11.79	6	7	15	0	0	1	CC2D1B	5,889	in gene	ActReg chr1 #783	0	0	1
784	1	52,869,271	52,870,569	1,298	2	10.439	12.439	4.576	18	17	12	1	2	2	ORC1L, PRPF38A	223, -299	in gene, upstream	ActReg chr1 #784	1	1	0
785	1	53,163,848	53,164,298	350	1	5.636	10.091	9.818	11	13	14	1	1	1	C1orf163	-85	upstream	ActReg chr1 #785	0	0	1
786	1	53,386,925	53,387,469	544	1	7.118	8.529	15.588	9	14	24	1	2	2	ECHDC2, SCP2	249, -5704	in gene, upstream	ActReg chr1 #786	0	0	1
787	1	53,480,240	53,480,932	692	2	9.636	11.046	1.611	19	22	3	0	0	1	SCP2	87,685	in gene	ActReg chr1 #787	1	1	0
788	1	53,541,204	53,541,797	593	1	2.278	2.368	12.579	4	6	20	0	0	1	PODN	13,615	in gene	ActReg chr1 #788	0	0	1
789	1	53,556,351	53,556,908	557	1	5.056	4.833	12.722	8	10	19	0	0	2	PODN, SLC1A7	28744, 51660	downstream, in gene	ActReg chr1 #789	0	0	1
790	1	53,662,433	53,663,161	728	1	6.364	12.273	5.636	8	16	10	1	1	1	CPT2	696	in gene	ActReg chr1 #790	0	1	0
791	1	53,685,770	53,686,535	765	3	12.958	13.458	11.5	19	22	21	1	1	3	CPT2, C1orf123, MAGOH	24051, 137, 18055	downstream, in gene, downstream	ActReg chr1 #791	1	1	1
792	1	53,703,849	53,704,585	736	3	9.739	14.217	8.826	15	27	16	1	2	3	MAGOH, LOC100507564, LRP8	-10, -65, 89604	upstream, upstream, downstream	ActReg chr1 #792	1	1	1
793	1	53,791,032	53,793,088	2,056	1	8.344	12.846	6.723	18	21	13	1	1	1	LRP8	1,761	in gene	ActReg chr1 #793	0	1	0
794	1	53,793,124	53,793,596	472	1	5.429	3.929	11.286	7	6	18	1	1	1	LRP8	461	in gene	ActReg chr1 #794	0	0	1
795	1	54,059,404	54,060,005	601	1	2.368	4.632	12.895	4	7	20	0	0	1	GLIS1	140,173	in gene	ActReg chr1 #795	0	0	1
796	1	54,203,969	54,204,479	510	1	6.364	4.467	11.933	9	8	17	1	1	1	GLIS1	-4,347	upstream	ActReg chr1 #796	0	0	1
797	1	54,303,337	54,304,612	1,275	2	19.975	27.025	7.618	50	78	16	1	1	1	TMEM48	251	in gene	ActReg chr1 #797	1	1	0
798	1	54,354,933	54,356,014	1,081	2	17.353	21.647	4.471	48	56	7	1	2	2	YIPF1, DIO1	-20, -4388	upstream, upstream	ActReg chr1 #798	1	1	0
799	1	54,518,504	54,519,866	1,362	2	9.143	12.643	5.595	22	20	11	1	2	2	TMEM59, C1orf83	-74, -89	upstream, upstream	ActReg chr1 #799	1	1	0
800	1	54,655,108	54,655,533	425	1	2.692	4.538	12.077	6	6	16	0	0	1	CYB5RL	10,426	in gene	ActReg chr1 #800	0	0	1
801	1	54,665,821	54,666,450	629	1	7.35	11.95	9.15	12	20	13	1	2	2	CYB5RL, MRPL37	-389, 295	upstream, in gene	ActReg chr1 #801	0	1	0
802	1	54,830,722	54,831,449	727	1	6.591	9.773	3.263	13	13	6	0	0	1	SSBP3	41,007	in gene	ActReg chr1 #802	0	1	0
803	1	55,181,064	55,181,844	780	1	9.083	13.625	8.208	14	25	14	1	1	2	C1orf175, TTC4	74027, -41	downstream, upstream	ActReg chr1 #803	0	1	0
804	1	55,211,078	55,211,601	523	1	4.125	3.562	11.5	7	5	18	0	0	1	TTC4	29,944	downstream	ActReg chr1 #804	0	0	1
805	1	55,229,823	55,230,417	594	1	12.684	8.474	12.263	19	15	17	1	1	1	PARS2	106	in gene	ActReg chr1 #805	0	0	1
806	1	55,269,354	55,269,986	632	1	7.7	10.9	1.812	15	15	3	0	2	2	TTC22, C1orf177	-2729, -2066	upstream, upstream	ActReg chr1 #806	0	1	0
807	1	55,319,074	55,319,453	379	1	5.909	6.818	12	8	10	16	0	0	1	DHCR24	33,658	in gene	ActReg chr1 #807	0	0	1
808	1	55,680,861	55,681,596	735	1	9.174	12.826	7.889	14	21	15	1	2	2	USP24, LOC100507634	-189, 148	upstream, in gene	ActReg chr1 #808	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GeneCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
809	1	55,894,612	55,895,530	918	2	10.828	11.966	1.571	16	20	3	0	0	0				ActReg chr1 #809	1	1	0
810	1	56,129,038	56,129,449	411	1	8	9.462	0	11	14	0	0	0	0				ActReg chr1 #810	0	1	0
811	1	57,142,245	57,142,838	593	1	9.667	11.389	1.647	15	22	3	0	0	1	PRKAA2	31,551	in gene	ActReg chr1 #811	0	1	0
812	1	57,833,762	57,834,155	393	1	4.583	2	11.167	7	3	15	0	0	1	DAB1	882,253	in gene	ActReg chr1 #812	0	0	1
813	1	58,898,371	58,898,731	360	1	3.818	2.1	11.909	6	3	19	0	0	0				ActReg chr1 #813	0	0	1
814	1	59,012,174	59,012,830	656	1	10.15	13.95	5.55	19	23	11	1	1	1	OMA1	-56	upstream	ActReg chr1 #814	0	1	0
815	1	59,165,508	59,165,959	451	1	8.214	7	12.286	15	9	18	0	1	1	MYSM1	14	in gene	ActReg chr1 #815	0	0	1
816	1	59,192,794	59,193,603	809	2	9.769	11.5	2.808	18	17	5	0	0	0				ActReg chr1 #816	1	1	0
817	1	59,197,522	59,198,074	552	2	9.706	10.059	3.429	15	17	6	0	0	0				ActReg chr1 #817	1	1	0
818	1	59,220,722	59,221,611	889	1	9.571	13.786	3.214	14	21	5	0	0	0				ActReg chr1 #818	0	1	0
819	1	59,247,401	59,248,223	822	1	11.24	9.12	4.2	16	15	6	1	2	2	JUN, LOC100131060	1973, -3011	in gene, upstream	ActReg chr1 #819	1	0	0
820	1	59,248,615	59,248,969	354	1	6.818	6.909	12.636	9	10	17	1	2	2	JUN, LOC100131060	993, -2031	in gene, upstream	ActReg chr1 #820	0	0	1
821	1	59,249,054	59,251,191	2,137	3	11.269	10.851	9.119	20	20	18	1	2	2	JUN, LOC100131060	-337, -701	upstream, upstream	ActReg chr1 #821	1	1	1
822	1	59,314,106	59,315,049	943	2	10.5	12.2	3.043	15	25	7	0	0	1	LOC100131060	63,754	in gene	ActReg chr1 #822	1	1	0
823	1	59,616,445	59,617,421	976	1	9.194	10.806	1.706	16	16	3	0	1	1	LOC729467	-4,454	upstream	ActReg chr1 #823	0	1	0
824	1	59,920,452	59,921,173	721	1	11.909	7.136	3.238	18	14	6	0	0	1	FGGY	158,187	in gene	ActReg chr1 #824	1	0	0
825	1	59,942,790	59,943,388	598	1	7.056	13.5	1.462	10	23	2	0	0	1	FGGY	180,464	in gene	ActReg chr1 #825	0	1	0
826	1	60,135,449	60,136,073	624	1	5.5	12.55	2.235	8	22	5	0	0	1	FGGY	373,136	in gene	ActReg chr1 #826	0	1	0
827	1	60,144,440	60,144,981	541	1	9.412	8.471	1.75	18	13	2	0	0	1	FGGY	382,085	in gene	ActReg chr1 #827	1	0	0
828	1	60,196,301	60,197,374	1,073	2	10.667	10.454	5.424	25	17	10	0	0	1	FGGY	434,212	in gene	ActReg chr1 #828	1	1	0
829	1	61,508,567	61,508,944	377	1	4.667	6.833	10.417	7	11	13	1	0	0				ActReg chr1 #829	0	0	1
830	1	62,190,366	62,191,299	933	2	13.633	14.433	6.633	32	30	16	1	1	1	TM2D1	263	in gene	ActReg chr1 #830	1	1	0
831	1	62,458,852	62,459,515	663	1	4.1	13.35	1.15	8	23	2	0	0	1	INADL	251,034	in gene	ActReg chr1 #831	0	1	0
832	1	62,784,169	62,784,809	640	1	3.882	8	12.25	6	15	16	1	1	1	KANK4	594	in gene	ActReg chr1 #832	0	0	1
833	1	62,901,687	62,903,033	1,346	3	10.452	10.667	11.833	19	19	23	1	1	1	USP1	385	in gene	ActReg chr1 #833	0	1	1
834	1	63,154,123	63,154,659	536	1	5.176	9.882	4.412	9	16	7	1	1	1	DOCK7	-422	upstream	ActReg chr1 #834	0	1	0
835	1	63,787,940	63,788,275	335	1	8.1	8.5	10.7	10	13	16	1	1	1	FOXD3	-623	upstream	ActReg chr1 #835	0	0	1
836	1	63,833,135	63,833,772	637	1	6.8	13.15	4.3	11	22	6	1	1	1	ALG6	192	in gene	ActReg chr1 #836	0	1	0
837	1	63,988,602	63,989,646	1,044	2	15.424	14.727	5.333	39	42	13	0	2	2	ITGB3BP, EFCAB7	-289, 111	upstream, in gene	ActReg chr1 #837	1	1	0
838	1	64,058,705	64,059,772	1,067	3	10.121	13.788	7.167	16	22	16	1	1	1	PGM1	291	in gene	ActReg chr1 #838	1	1	1
839	1	64,127,668	64,129,099	1,431	1	12.222	7.889	3.902	19	14	9	0	0	1	PGM1	69,436	downstream	ActReg chr1 #839	1	0	0
840	1	64,434,846	64,435,526	680	2	10.182	12	2.222	17	21	4	0	0	1	ROR1	195,496	in gene	ActReg chr1 #840	1	1	0
841	1	64,509,494	64,510,134	640	1	10.2	6.3	1.722	17	13	3	0	0	1	ROR1	270,124	in gene	ActReg chr1 #841	1	0	0
842	1	64,542,884	64,543,579	695	1	8.842	12.286	3.4	16	17	7	0	0	1	ROR1	303,541	in gene	ActReg chr1 #842	0	1	0
843	1	64,598,672	64,599,608	936	1	8	12.414	3.923	16	19	9	0	0	1	ROR1	359,450	in gene	ActReg chr1 #843	0	1	0
844	1	64,935,465	64,936,028	563	1	9.059	11.059	6.917	12	14	11	1	1	1	CACHD1	-730	upstream	ActReg chr1 #844	0	1	0
845	1	65,210,917	65,211,340	423	1	10	5.385	8.077	15	9	14	1	1	1	RAVER2	350	in gene	ActReg chr1 #845	1	0	0
846	1	65,533,376	65,534,072	696	2	6.591	9.773	9	11	17	18	2	0	1	MIR101-1	-9,533	upstream	ActReg chr1 #846	0	1	1
847	1	65,640,031	65,640,633	602	1	7.158	10	1.75	9	20	2	0	0	1	AK3L1	27,100	in gene	ActReg chr1 #847	0	1	0
848	1	65,720,174	65,720,746	572	1	10.333	7.667	10.111	16	12	17	1	0	1	DNAJC6	-9,970	upstream	ActReg chr1 #848	0	0	1
849	1	65,729,867	65,730,707	840	2	10.5	9.769	2.857	18	19	6	0	1	1	DNAJC6	-143	upstream	ActReg chr1 #849	1	1	0
850	1	65,775,319	65,775,895	576	2	16.667	13.444	4.056	30	24	7	1	0	2	DNAJC6, LOC100505510	45177, 11321	in gene, downstream	ActReg chr1 #850	1	1	0
851	1	65,924,590	65,925,440	850	2	7.37	10.63	2.45	17	17	3	0	0	1	LEPR	38,767	in gene	ActReg chr1 #851	1	1	0
852	1	66,488,495	66,489,183	688	2	11.286	11.381	1.75	23	22	2	0	0	1	PDE4B	230,646	in gene	ActReg chr1 #852	1	1	0
853	1	66,727,776	66,728,498	722	2	12.348	10.261	2.158	23	16	5	0	0	1	PDE4B	469,944	in gene	ActReg chr1 #853	1	1	0
854	1	66,736,715	66,737,265	550	1	11	7.412	1.111	16	12	2	0	0	1	PDE4B	478,797	in gene	ActReg chr1 #854	1	0	0
855	1	66,802,859	66,803,215	356	1	4.091	4.727	9.545	6	7	13	0	0	1	PDE4B	544,844	in gene	ActReg chr1 #855	0	0	1
856	1	66,987,415	66,987,917	502	1	8.188	12.562	1	11	18	1	0	0	0				ActReg chr1 #856	0	1	0
857	1	67,390,206	67,391,599	1,393	2	8.341	13.5	9.333	15	22	18	1	2	2	WDR78, MIER1	-332, 324	upstream, in gene	ActReg chr1 #857	0	1	1
858	1	67,519,458	67,520,227	769	2	11.667	9.167	9.458	17	13	14	1	1	1	SLC35D1	238	in gene	ActReg chr1 #858	1	0	1
859	1	67,865,406	67,866,037	631	1	12.75	8.3	2.579	22	16	8	0	0	2	IL12RB2, SERBP1	92674, 30402	downstream, downstream	ActReg chr1 #859	1	0	0
860	1	67,895,759	67,896,734	975	3	14.533	9.233	8.8	27	15	19	1	1	1	SERBP1	-123	upstream	ActReg chr1 #860	1	1	1
861	1	68,298,318	68,299,211	893	1	8.929	10.857	6.214	12	16	14	1	2	2	GNG12, LOC100289178	391, 778	in gene, in gene	ActReg chr1 #861	0	1	0
862	1	68,299,214	68,299,698	484	1	5.8	10.133	6.133	12	16	10	1	2	2	GNG12, LOC100289178	-301, 1470	upstream, in gene	ActReg chr1 #862	0	1	0
863	1	68,353,832	68,354,603	771	2	14.375	12.375	3.421	32	26	10	0	0	1	LOC100289178	56,231	in gene	ActReg chr1 #863	1	1	0
864	1	68,578,005	68,579,165	1,160	1	10.806	7.417	3.472	20	19	8	0	0	2	LOC100289178, GPR177	280599, 119699	in gene, in gene	ActReg chr1 #864	1	0	0
865	1	68,796,270	68,797,163	893	2	12.821	11.25	1.545	23	21	3	0	0	0				ActReg chr1 #865	1	1	0
866	1	68,849,577	68,850,314	737	1	9.391	12.217	1	13	15	1	0	0	0				ActReg chr1 #866	0	1	0
867	1	68,962,277	68,963,127	850	1	8.769	12.808	4.808	14	23	9	1	1	1	DEPDC1	97	in gene	ActReg chr1 #867	0	1	0
868	1	69,777,744	69,778,174	430	1	1.462	2.692	12.462	2	5	19	0	0	0				ActReg chr1 #868	0	0	1
869	1	70,137,212	70,137,707	495	1	9.188	9.562	4	13	16	9	0	0	0				ActReg chr1 #869	0	1	0
870	1	70,503,605	70,504,218	613	1	13.79	10.21	2.6	24	20	3	0	0	1	LRRC7	278,053	in gene	ActReg chr1 #870	1	0	0
871	1	70,670,949	70,671,823	874	1	11.185	12.963	3.593	20	22	8	1	2	2	LRRC40, SFRS11	-25, 21	upstream, in gene	ActReg chr1 #871	0	1	0
872	1	70,686,922	70,687,437	515	1	8.75	13.125	8.688	12	18	14	1	0	1	SFRS11	15,814	in gene	ActReg chr1 #872	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
873	1	70,819,593	70,821,024	1,431	3	8.733	10.533	9.372	19	17	15	1	2	2	ANKRD13C, HHLA3	109, -185	in gene, upstream	ActReg chr1 #873	1	1	1
874	1	70,876,299	70,877,260	961	1	10.7	13	9.036	14	20	16	1	1	1	CTH	-122	upstream	ActReg chr1 #874	0	1	0
875	1	71,546,483	71,547,356	873	2	14.518	14.482	3.565	32	30	8	1	1	1	ZRANB2	53	in gene	ActReg chr1 #875	1	1	0
876	1	72,749,173	72,749,875	702	1	11.909	9.318	6.364	16	15	13	1	1	1	NEGR1	-1,247	upstream	ActReg chr1 #876	1	0	0
877	1	74,967,876	74,968,778	902	2	17.5	25.679	1.462	43	62	2	0	0	1	TNNI3K	304,380	in gene	ActReg chr1 #877	1	1	0
878	1	76,138,395	76,139,069	674	1	5.476	12.952	3.619	9	21	8	0	0	0				ActReg chr1 #878	0	1	0
879	1	76,190,093	76,190,649	556	2	8.941	11.941	11.823	15	17	17	1	1	1	ACADM	328	in gene	ActReg chr1 #879	0	1	1
880	1	76,251,543	76,252,233	690	1	4.476	11.182	6.3	9	16	16	0	4	4	RABGGTB, SNORD45C, SNORD45A, SNORD45B	2, -869, -1686, -3274	in gene, upstream, upstream, upstream	ActReg chr1 #880	0	1	0
881	1	76,262,597	76,263,004	407	1	3	8.833	11.667	4	10	18	1	1	5	RABGGTB, SNORD45C, SNORD45A, SNORD45B, MSH4	10914, 10043, 9226, 7638, 170	downstream, downstream, downstream, downstream, in gene	ActReg chr1 #881	0	0	1
882	1	77,333,881	77,334,537	656	1	8.238	10.619	5.619	14	15	10	1	1	1	ST6GALNAC5	1,023	in gene	ActReg chr1 #882	0	1	0
883	1	77,502,059	77,502,801	742	1	7.785	12.957	2.471	13	24	4	0	0	1	ST6GALNAC5	169,244	in gene	ActReg chr1 #883	0	1	0
884	1	77,505,296	77,506,034	738	1	12.522	9.957	3.522	29	15	7	0	0	1	ST6GALNAC5	172,479	in gene	ActReg chr1 #884	1	0	0
885	1	77,684,674	77,685,293	619	1	7.053	11.421	6.211	12	21	12	1	1	1	PIGK	149	in gene	ActReg chr1 #885	0	1	0
886	1	78,147,881	78,148,782	901	1	7.5	10.571	2.889	11	15	7	1	1	1	ZZZ3	12	in gene	ActReg chr1 #886	0	1	0
887	1	78,148,892	78,149,599	707	1	10.546	12.5	7.238	15	18	16	1	1	1	ZZZ3	-902	upstream	ActReg chr1 #887	0	1	0
888	1	78,262,223	78,262,712	489	1	11.333	6.8	2.455	13	9	3	0	0	1	FAM73A	17,158	in gene	ActReg chr1 #888	1	0	0
889	1	78,470,024	78,470,678	654	1	9.2	10.2	2.3	13	16	6	0	1	1	DNAJB4	-285	upstream	ActReg chr1 #889	0	1	0
890	1	78,677,799	78,678,169	370	1	2.833	3.273	10.091	6	5	15	0	0	0				ActReg chr1 #890	0	0	1
891	1	80,519,217	80,519,607	390	1	5	2.583	10.833	9	7	15	0	0	0				ActReg chr1 #891	0	0	1
892	1	81,640,525	81,641,066	541	1	5.118	10	2.882	7	15	7	0	0	0				ActReg chr1 #892	0	1	0
893	1	81,702,960	81,703,579	619	1	11.947	6.842	1	18	9	1	0	0	0				ActReg chr1 #893	1	0	0
894	1	81,879,972	81,880,537	565	1	4.812	8.353	1.909	8	16	3	0	0	0				ActReg chr1 #894	0	1	0
895	1	82,266,810	82,267,358	548	1	7.941	11.647	4.706	12	20	9	1	1	1	LPHN2	1,002	in gene	ActReg chr1 #895	0	1	0
896	1	82,385,964	82,386,390	426	1	7.769	10.462	1	11	14	1	0	0	1	LPHN2	120,095	in gene	ActReg chr1 #896	0	1	0
897	1	84,464,533	84,465,265	732	2	9	11.739	4.304	16	20	8	1	1	1	TTLL7	-66	upstream	ActReg chr1 #897	1	1	0
898	1	84,944,493	84,945,037	544	1	7.706	8.706	3.765	13	16	8	1	1	1	RPF1	-155	upstream	ActReg chr1 #898	0	1	0
899	1	85,724,946	85,725,309	363	1	6.545	5.909	12	10	8	15	1	1	2	C1orf52, BCL10	228, 17460	in gene, downstream	ActReg chr1 #899	0	0	1
900	1	85,749,501	85,749,890	389	1	3.385	2.333	10.385	5	3	14	0	1	2	BCL10, LOC646626	-7108, 7572	upstream, downstream	ActReg chr1 #900	0	0	1
901	1	85,985,946	85,987,770	1,824	2	12.123	13.018	4.86	22	28	10	0	0	1	DDAH1	57,188	in gene	ActReg chr1 #901	1	1	0
902	1	86,042,207	86,042,531	324	1	6.364	6.909	9.727	8	10	14	1	2	2	DDAH1, CYR61	1677, -4075	in gene, upstream	ActReg chr1 #902	0	0	1
903	1	86,861,471	86,861,813	342	1	4.364	7.727	9.818	9	13	14	1	1	1	ODF2L	383	in gene	ActReg chr1 #903	0	0	1
904	1	86,952,418	86,953,352	934	2	8	11.034	2.043	16	16	3	0	0	1	CLCA1	18,359	in gene	ActReg chr1 #904	1	1	0
905	1	87,379,546	87,380,022	476	1	6.429	9.133	2.429	9	13	4	1	2	2	SEP15, HS2ST1	323, -551	in gene, upstream	ActReg chr1 #905	0	1	0
906	1	87,900,932	87,901,570	638	1	5.4	9.7	2.471	11	18	4	0	0	0				ActReg chr1 #906	0	1	0
907	1	89,149,599	89,150,182	583	1	4.579	8.632	5.211	8	14	8	1	1	1	PKN2	-32	upstream	ActReg chr1 #907	0	1	0
908	1	89,356,947	89,357,624	677	2	8.312	10.905	8.3	16	22	17	1	1	1	GTF2B	16	in gene	ActReg chr1 #908	0	1	1
909	1	89,457,903	89,458,469	566	1	5.056	9.944	6.611	8	16	11	1	2	2	CCBL2, RBM3XL1	457, 457	in gene, in gene	ActReg chr1 #909	0	1	0
910	1	90,460,375	90,461,096	721	2	10.348	10.87	2.6	18	15	5	1	1	1	ZNF326	57	in gene	ActReg chr1 #910	1	1	0
911	1	91,487,325	91,487,682	357	1	6.583	9	11.75	10	13	17	1	2	2	ZNF644, LOC100505857	168, -221	in gene, upstream	ActReg chr1 #911	0	0	1
912	1	91,870,015	91,870,599	584	2	11	11.158	3.667	21	22	8	1	1	1	HFM1	119	in gene	ActReg chr1 #912	1	1	0
913	1	92,292,649	92,293,679	1,030	1	6.438	12.719	1.667	13	22	3	0	0	1	TGFBR3	58,623	in gene	ActReg chr1 #913	0	1	0
914	1	92,350,895	92,351,470	575	1	7.889	10.389	4.667	10	14	8	1	1	1	TGFBR3	605	in gene	ActReg chr1 #914	0	1	0
915	1	92,545,988	92,546,420	432	1	6.769	10.077	5.364	10	14	9	1	2	2	LOC646817, BTBD8	-5236, 342	upstream, in gene	ActReg chr1 #915	0	1	0
916	1	92,764,098	92,764,633	535	3	9.875	8	8	15	17	14	1	2	2	GLMN, RPAP2	201, -157	in gene, upstream	ActReg chr1 #916	1	1	1
917	1	93,297,097	93,298,189	1,092	2	44.765	44.941	5.818	156	158	13	1	2	4	RPL5, SNORD21, SNORA66, FAM69A	49, -5203, -8633, 129436	in gene, upstream, upstream, downstream	ActReg chr1 #917	1	1	0
918	1	93,544,388	93,545,115	727	1	9.136	12.818	5.955	13	23	8	1	1	1	MTF2	-41	upstream	ActReg chr1 #918	0	1	0
919	1	93,645,694	93,646,499	805	2	10.962	11.462	4.654	21	21	9	1	2	2	TMED5, CCDC18	150, 176	in gene, in gene	ActReg chr1 #919	1	1	0
920	1	94,071,306	94,071,857	551	1	10.882	7.706	2.8	18	14	5	0	0	2	BCAR3, LOC100129046	75804, 14056	in gene, downstream	ActReg chr1 #920	1	0	0
921	1	94,146,054	94,146,545	491	1	12	8.143	3.385	15	12	8	1	1	1	BCAR3	1,071	in gene	ActReg chr1 #921	1	0	0
922	1	94,312,694	94,313,456	762	1	9.458	6.417	14	14	13	23	2	1	1	MIR760	687	downstream	ActReg chr1 #922	0	0	1
923	1	94,790,840	94,791,591	751	2	8.625	10.5	1	17	14	1	0	0	1	LOC100505940	77,801	in gene	ActReg chr1 #923	1	1	0
924	1	95,045,155	95,045,722	567	1	7.882	9.941	5	15	15	7	0	0	0				ActReg chr1 #924	0	1	0
925	1	95,071,302	95,071,823	521	1	11.688	7.188	2.833	19	12	5	0	0	0				ActReg chr1 #925	1	0	0
926	1	95,538,128	95,538,933	805	1	10.68	14.16	6.44	20	21	12	1	1	1	ALG14	-23	upstream	ActReg chr1 #926	0	1	0
927	1	95,849,954	95,850,628	674	2	10.667	11.286	4.812	16	21	8	0	0	0				ActReg chr1 #927	1	1	0
928	1	96,541,965	96,542,518	553	1	10.412	6.706	1.8	19	11	3	0	0	0				ActReg chr1 #928	1	0	0
929	1	97,452,334	97,453,506	1,172	2	13.784	13.622	2.545	29	21	4	0	0	0				ActReg chr1 #929	1	1	0
930	1	98,385,910	98,387,079	1,169	3	12.46	12.595	13.162	22	20	30	1	1	1	DPYD	121	in gene	ActReg chr1 #930	1	1	1
931	1	98,510,730	98,511,298	568	1	8.333	10.778	4.533	11	14	11	1	2	2	FLJ35409, MIR137	0, 713	in gene, downstream	ActReg chr1 #931	0	1	0
932	1	98,511,461	98,512,255	794	1	6.417	11.667	5.417	12	20	11	1	2	2	FLJ35409, MIR137	-844, -131	upstream, upstream	ActReg chr1 #932	0	1	0
933	1	98,513,488	98,514,370	882	2	14	23.036	2.438	36	60	3	0	2	2	FLJ35409, MIR137	-2915, -2202	upstream, upstream	ActReg chr1 #933	1	1	0
934	1	98,789,131	98,789,906	775	1	9.333	10.667	3.938	14	14	6	0	0	0				ActReg chr1 #934	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
935	1	98,853,813	98,854,513	700	1	5.773	10.5	3.2	10	18	8	0	0	0				ActReg chr1 #935	0	1	0
936	1	100,147,924	100,148,428	504	1	6.5	10.188	1.167	11	14	2	0	0	1	PALMD	36,745	in gene	ActReg chr1 #936	0	1	0
937	1	100,315,143	100,316,025	882	3	11.407	14.037	10.28	15	22	23	1	1	1	AGL	-56	upstream	ActReg chr1 #937	1	1	1
938	1	100,435,189	100,435,990	801	1	13.56	17.12	6.52	23	33	15	1	2	2	LOC730081, SLC35A3	249, 49	in gene, in gene	ActReg chr1 #938	0	1	0
939	1	100,503,181	100,504,108	927	3	12.138	14.241	7.793	19	28	18	1	1	1	HIAT1	-145	upstream	ActReg chr1 #939	1	1	1
940	1	100,598,093	100,599,088	995	2	12.065	11	3.806	17	26	6	1	2	2	SASS6, CCDC76	-79, -116	upstream, upstream	ActReg chr1 #940	1	1	0
941	1	100,817,802	100,818,678	876	2	10.37	12.407	6.926	19	17	13	1	1	1	CDC14A	217	in gene	ActReg chr1 #941	1	1	0
942	1	101,250,880	101,251,685	805	2	15.769	12.538	3.591	37	30	8	0	0	0				ActReg chr1 #942	1	1	0
943	1	101,361,346	101,361,647	301	1	8.111	6.667	9.444	9	10	14	1	2	2	EXTL2, SLC30A7	-1078, -136	upstream, upstream	ActReg chr1 #943	0	0	1
944	1	101,491,168	101,491,887	719	1	8.391	11.391	7.522	16	18	16	1	2	2	DPH5, LOC100506051	-165, 93	upstream, in gene	ActReg chr1 #944	0	1	0
945	1	101,972,907	101,973,572	665	1	9.857	6.571	3.562	15	11	8	0	0	0				ActReg chr1 #945	1	0	0
946	1	102,370,724	102,371,170	446	1	6.5	9.429	2	10	18	2	0	0	1	OLFM3	91,843	in gene	ActReg chr1 #946	0	1	0
947	1	102,462,106	102,462,984	878	2	17.357	19.5	3.429	37	52	7	0	1	1	OLFM3	245	in gene	ActReg chr1 #947	1	1	0
948	1	104,843,499	104,843,809	310	1	2.7	1.4	9.5	4	2	13	0	0	0				ActReg chr1 #948	0	0	1
949	1	106,206,629	106,207,426	797	1	6.28	10.52	3.292	11	15	7	0	0	0				ActReg chr1 #949	0	1	0
950	1	106,220,999	106,221,444	445	1	10.286	7.357	1.8	15	10	2	0	0	0				ActReg chr1 #950	1	0	0
951	1	107,479,739	107,480,207	468	1	9.467	9.133	1	16	13	1	0	0	0				ActReg chr1 #951	1	0	0
952	1	107,598,924	107,600,385	1,461	3	10.957	13.022	10.304	16	25	16	1	1	1	PRMT6	387	in gene	ActReg chr1 #952	1	1	1
953	1	107,677,919	107,678,695	776	2	12	12.68	1.833	22	26	3	0	1	1	NTNG1	-4,322	upstream	ActReg chr1 #953	1	1	0
954	1	108,533,173	108,533,792	619	1	7.05	10.1	1.636	14	19	2	0	0	0				ActReg chr1 #954	0	1	0
955	1	108,591,940	108,592,477	537	1	9.875	11.875	1.3	14	21	2	0	0	0				ActReg chr1 #955	0	1	0
956	1	108,742,924	108,743,829	905	1	7.63	11.107	4.607	14	19	13	1	1	1	SLC25A24	-402	upstream	ActReg chr1 #956	0	1	0
957	1	109,289,114	109,289,626	512	1	12	11.5	12.625	15	15	19	1	1	2	FNDC7, STXBP3	33814, 85	downstream, in gene	ActReg chr1 #957	0	0	1
958	1	109,419,200	109,420,027	827	2	9.846	10.192	4	18	15	10	1	1	1	GPSM2	10	in gene	ActReg chr1 #958	1	1	0
959	1	109,583,850	109,584,865	1,015	2	10.438	8.645	11.233	17	18	23	1	1	1	WDR47	493	in gene	ActReg chr1 #959	1	0	1
960	1	109,618,286	109,619,022	736	2	9.609	10.13	6.87	17	21	8	1	1	1	TAF13	-30	upstream	ActReg chr1 #960	1	1	0
961	1	109,632,887	109,633,829	942	2	22.833	23.933	5.433	66	64	12	1	1	2	TMEM167B, SCARNA2	-45, -8457	upstream, upstream	ActReg chr1 #961	1	1	0
962	1	109,642,298	109,643,520	1,222	2	14.256	17.769	8.077	39	45	15	1	1	3	TMEM167B, SCARNA2, C1orf194	9506, 94, 13570	downstream, in gene, downstream	ActReg chr1 #962	1	1	0
963	1	109,783,272	109,783,702	430	1	13.077	11.385	11.462	17	16	17	0	0	2	SARS, CELSR2	26972, -9154	downstream, upstream	ActReg chr1 #963	0	0	1
964	1	109,792,821	109,793,535	714	1	4.045	6.909	13.046	7	10	21	1	1	1	CELSR2	537	in gene	ActReg chr1 #964	0	0	1
965	1	109,798,053	109,798,718	665	1	3.2	2.938	11.8	5	5	16	0	0	1	CELSR2	5,744	in gene	ActReg chr1 #965	0	0	1
966	1	109,842,078	109,843,219	1,141	1	7.4	11.417	7.556	17	21	15	0	0	2	MYBPHL, SORT1	7015, 97915	in gene, downstream	ActReg chr1 #966	0	1	0
967	1	110,008,730	110,009,493	763	1	10.833	7.833	5	16	14	9	1	1	1	SYPL2	11	in gene	ActReg chr1 #967	1	0	0
968	1	110,025,720	110,027,514	1,794	3	20.286	22.071	8.9	69	84	15	1	1	3	SYPL2, ATXN7L2, CYB561D1	17517, 56, -10041	downstream, in gene, upstream	ActReg chr1 #968	1	1	0
969	1	110,035,971	110,037,264	1,293	3	22	22.15	8.95	68	75	17	1	1	2	ATXN7L2, CYB561D1	10056, -41	downstream, upstream	ActReg chr1 #969	1	1	1
970	1	110,162,533	110,163,028	495	1	9.733	8.667	11.8	12	17	16	1	2	2	GNAT2, AMPD2	-7075, 321	upstream, in gene	ActReg chr1 #970	0	0	1
971	1	110,254,719	110,255,410	691	1	2.667	2.667	12	6	5	17	0	1	2	LOC100506210, GSTM5	4350, 200	downstream, in gene	ActReg chr1 #971	0	0	1
972	1	110,394,864	110,395,548	684	2	11.762	11.762	4.857	24	22	7	0	0	0				ActReg chr1 #972	1	1	0
973	1	110,526,907	110,528,089	1,182	2	11.135	9.973	8.541	15	21	13	1	1	1	AHCYL1	190	in gene	ActReg chr1 #973	1	1	0
974	1	110,698,347	110,699,207	860	2	13.111	13.778	2.269	21	24	4	0	0	1	SLC6A17	5,645	in gene	ActReg chr1 #974	1	1	0
975	1	110,880,557	110,882,252	1,695	2	11.34	13.075	7.396	28	19	15	2	1	1	RBM15	-541	upstream	ActReg chr1 #975	1	1	0
976	1	110,883,553	110,884,217	664	1	7.35	11	3.25	11	15	5	0	1	1	RBM15	1,940	in gene	ActReg chr1 #976	0	1	0
977	1	110,949,698	110,950,675	977	1	8.467	17.267	7.267	14	28	13	1	1	1	HBXIP	360	in gene	ActReg chr1 #977	0	1	0
978	1	111,019,544	111,020,175	631	1	11.5	9.55	2.389	19	17	7	0	0	0				ActReg chr1 #978	1	0	0
979	1	111,080,707	111,081,148	441	1	2.077	4.077	12.538	3	6	19	0	0	0				ActReg chr1 #979	0	0	1
980	1	111,085,203	111,086,125	922	2	15.103	16.035	2.296	33	39	4	0	0	0				ActReg chr1 #980	1	1	0
981	1	111,097,804	111,098,488	684	1	7.333	13.714	8.905	13	30	14	1	0	0				ActReg chr1 #981	0	1	0
982	1	111,216,519	111,217,091	572	1	1.6	3.333	11.611	3	5	17	1	1	1	KCNA3	850	in gene	ActReg chr1 #982	0	0	1
983	1	111,289,020	111,289,986	966	2	15.387	20.71	2.133	37	52	4	0	0	0				ActReg chr1 #983	1	1	0
984	1	111,506,497	111,507,335	838	1	8.462	10.962	5	13	15	10	1	1	1	C1orf103	-350	upstream	ActReg chr1 #984	0	1	0
985	1	111,682,817	111,683,504	687	1	7.952	11.667	9.143	13	19	14	1	2	2	DRAM2, CEPT1	-322, 911	upstream, in gene	ActReg chr1 #985	0	1	0
986	1	112,281,698	112,282,114	416	1	6.231	7.462	11.615	8	13	17	1	1	2	C1orf183, LOC100506343	16513, -557	in gene, upstream	ActReg chr1 #986	0	0	1
987	1	112,297,753	112,298,721	968	2	13.419	13.613	7.258	25	23	13	1	2	3	C1orf183, LOC100506343, DDX20	182, 15774, 47	in gene, downstream, in gene	ActReg chr1 #987	1	1	0
988	1	112,375,780	112,376,594	814	2	15.2	14.84	1.3	28	32	4	0	0	1	KCND3	155,590	in gene	ActReg chr1 #988	1	1	0
989	1	112,407,102	112,407,956	854	1	7.185	12.741	3.28	18	23	6	0	0	1	KCND3	124,248	in gene	ActReg chr1 #989	0	1	0
990	1	112,714,676	112,715,450	774	2	13	17.25	2.762	30	36	5	0	0	0				ActReg chr1 #990	1	1	0
991	1	112,794,220	112,794,866	646	2	12.65	10.55	2.947	24	16	6	0	0	0				ActReg chr1 #991	1	1	0
992	1	112,928,696	112,929,185	489	1	3.929	4.25	11.938	7	8	17	0	0	1	CTTNBP2NL	-9,860	upstream	ActReg chr1 #992	0	0	1
993	1	113,161,463	113,162,867	1,404	2	11.386	10.75	6.273	20	18	13	1	2	2	ST7L, CAPZA1	-125, 90	upstream, in gene	ActReg chr1 #993	1	1	0
994	1	113,216,705	113,217,795	1,090	2	7.529	13.971	7.765	13	23	16	1	1	2	CAPZA1, MOV10	55175, 202	downstream, in gene	ActReg chr1 #994	0	1	1
995	1	113,247,110	113,248,223	1,113	2	9.324	11.529	5.441	19	18	10	0	1	3	MOV10, RHOC, PPM1J	30618, 2359, 10284	downstream, in gene, downstream	ActReg chr1 #995	1	1	0
996	1	113,249,254	113,249,679	425	1	6.769	5.923	11.692	9	8	19	1	1	3	MOV10, RHOC, PPM1J	32418, 559, 8484	downstream, in gene, downstream	ActReg chr1 #996	0	0	1
997	1	113,286,197	113,286,807	610	1	2.167	1.895	10.368	4	4	15	1	1	1	LOC128322	-4,215	upstream	ActReg chr1 #997	0	0	1
998	1	113,497,573	113,499,223	1,350	2	11.167	14.976	8.619	21	30	25	2	2	2	SLC16A1, LOC100506392	427, -472	in gene, upstream	ActReg chr1 #998	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
999	1	113,615,114	113,616,415	1,301	2	13.55	19.7	6.211	25	40	15	1	1	1	LRIG2	-67	upstream	ActReg chr1 #999	1	1	0
1000	1	113,999,421	113,999,929	508	1	7.062	9.875	1.273	12	14	3	0	0	1	MAGI3	66,200	in gene	ActReg chr1 #1000	0	1	0
1001	1	114,301,669	114,302,456	787	2	8.381	10.667	11.375	14	14	15	1	1	2	PHTF1, RSBN1	-285, 53008	upstream, downstream	ActReg chr1 #1001	0	1	1
1002	1	114,446,999	114,448,380	1,381	2	15.512	14.302	4.605	33	29	8	1	2	3	LOC100287722, AP4B1, DCLRE1B	48432, 52, -226	downstream, in gene, upstream	ActReg chr1 #1002	1	1	0
1003	1	114,471,606	114,472,527	921	2	15.483	12	4.8	30	21	13	1	1	1	HIPK1	70	in gene	ActReg chr1 #1003	1	1	0
1004	1	114,656,159	114,657,192	1,033	1	11.667	11.061	5.152	15	15	10	0	0	1	SYT6	39,797	in gene	ActReg chr1 #1004	1	0	0
1005	1	114,672,945	114,673,805	860	1	8.333	10.556	3.652	12	14	8	0	0	1	SYT6	23,097	in gene	ActReg chr1 #1005	0	1	0
1006	1	114,888,996	114,889,610	614	1	8.684	12.737	7.062	11	22	10	0	0	0				ActReg chr1 #1006	0	1	0
1007	1	115,052,876	115,053,375	499	1	8.867	8.333	12.6	11	10	24	1	1	1	TRIM33	656	in gene	ActReg chr1 #1007	0	0	1
1008	1	115,299,957	115,300,852	875	1	10.786	12.571	8.821	14	19	18	0	1	1	CSDE1	277	in gene	ActReg chr1 #1008	0	1	0
1009	1	115,322,845	115,323,606	761	1	12.917	9.25	11.167	24	14	15	1	1	1	SIKE1	83	in gene	ActReg chr1 #1009	1	0	0
1010	1	115,721,708	115,722,570	862	2	12.482	10.482	2.63	23	22	6	0	0	0				ActReg chr1 #1010	1	1	0
1011	1	115,842,757	115,843,449	692	1	11.333	7.714	2.056	17	12	3	0	0	1	NGF	37,754	in gene	ActReg chr1 #1011	1	0	0
1012	1	115,880,096	115,880,623	527	1	6.176	7.235	13.765	12	10	18	1	2	2	NGF, LOC100506434	498, -1444	in gene, upstream	ActReg chr1 #1012	0	0	1
1013	1	115,902,791	115,903,184	393	1	2.75	3.083	12.417	6	4	15	0	0	0				ActReg chr1 #1013	0	0	1
1014	1	115,973,257	115,973,887	630	1	10.526	12.737	1.667	18	23	2	0	0	0				ActReg chr1 #1014	0	1	0
1015	1	116,214,318	116,214,609	291	1	7	6.889	12.556	10	8	17	0	0	1	VANGL1	29,889	in gene	ActReg chr1 #1015	0	0	1
1016	1	116,270,055	116,270,696	641	1	11.55	8.25	2.9	17	12	5	0	0	1	CASQ2	41,051	in gene	ActReg chr1 #1016	1	0	0
1017	1	116,270,704	116,271,097	393	1	12	5.417	1	19	11	1	0	0	1	CASQ2	40,526	in gene	ActReg chr1 #1017	1	0	0
1018	1	116,665,476	116,666,089	613	1	4	11.684	1.389	7	18	2	0	0	1	C1orf161	11,406	in gene	ActReg chr1 #1018	0	1	0
1019	1	116,694,581	116,695,164	583	2	9.667	11.778	11.125	13	21	23	1	0	0				ActReg chr1 #1019	0	1	1
1020	1	116,915,328	116,915,964	636	1	9.4	8.1	14.3	18	12	23	1	1	1	ATP1A1	-149	upstream	ActReg chr1 #1020	0	0	1
1021	1	116,916,416	116,916,772	356	1	6.583	6.5	10.667	9	10	16	1	1	1	ATP1A1	799	in gene	ActReg chr1 #1021	0	0	1
1022	1	116,975,621	116,976,647	1,026	1	11.719	12.031	4.276	17	20	7	0	0	0				ActReg chr1 #1022	0	1	0
1023	1	117,046,919	117,047,603	684	1	10.571	8.905	2.9	16	17	5	0	1	2	LOC100506459, CD58	-5427, 66454	upstream, downstream	ActReg chr1 #1023	1	0	0
1024	1	117,051,331	117,052,117	786	1	7.75	10.708	2.833	14	14	5	0	0	2	LOC100506459, CD58	-9890, 61991	upstream, downstream	ActReg chr1 #1024	0	1	0
1025	1	117,113,179	117,113,856	677	1	9.773	11.5	7.273	13	20	10	1	1	2	CD58, IGSF3	198, 96797	in gene, downstream	ActReg chr1 #1025	0	1	0
1026	1	117,320,281	117,320,940	659	1	4.762	10.619	1.235	6	18	2	0	0	1	CD2	23,524	downstream	ActReg chr1 #1026	0	1	0
1027	1	117,416,488	117,417,117	629	1	10.474	7.737	1	17	11	1	0	0	0				ActReg chr1 #1027	1	0	0
1028	1	117,664,190	117,664,815	625	1	8.05	7.65	12.7	10	13	18	1	2	2	TRIM45, LOC100506478	-91, -6964	upstream, upstream	ActReg chr1 #1028	0	0	1
1029	1	117,714,321	117,714,960	639	1	5.5	11.2	3.95	9	19	8	0	0	1	VTCN1	38,909	in gene	ActReg chr1 #1029	0	1	0
1030	1	117,833,404	117,834,009	605	1	9.895	6.789	1.333	16	13	2	0	0	0				ActReg chr1 #1030	1	0	0
1031	1	117,910,032	117,910,362	330	1	7.1	9.3	10.1	9	13	13	1	1	1	MAN1A2	112	in gene	ActReg chr1 #1031	0	0	1
1032	1	119,471,334	119,472,147	813	2	11.16	10.52	1.75	18	20	2	0	0	1	TBX15	60,439	in gene	ActReg chr1 #1032	1	1	0
1033	1	119,721,630	119,722,098	468	1	3.643	2.867	12.467	6	4	16	0	0	0				ActReg chr1 #1033	0	0	1
1034	1	120,085,023	120,085,977	954	2	15.567	14.5	3.476	34	40	9	0	0	0				ActReg chr1 #1034	1	1	0
1035	1	120,146,012	120,146,654	642	1	5.25	9.95	3.312	8	15	5	0	1	1	LOC644242	-4,419	upstream	ActReg chr1 #1035	0	1	0
1036	1	120,190,412	120,191,303	891	1	6.643	10.786	7.75	12	16	17	1	1	1	ZNF697	-467	upstream	ActReg chr1 #1036	0	1	0
1037	1	120,254,392	120,254,733	341	1	6.545	10.364	10.909	11	15	16	1	1	1	PHGDH	143	in gene	ActReg chr1 #1037	0	0	1
1038	1	120,611,907	120,612,288	381	1	8.75	11.667	6.75	15	18	11	1	1	1	NOTCH2	179	in gene	ActReg chr1 #1038	0	1	0
1039	1	121,138,050	121,138,419	369	1	5	5.455	8.818	7	9	12	1	0	0				ActReg chr1 #1039	0	0	1
1040	1	142,618,430	142,619,257	827	2	14.577	12.577	11.808	29	28	26	1	0	0				ActReg chr1 #1040	1	1	0
1041	1	143,467,448	143,467,947	499	2	7.938	10.062	4.062	16	14	7	1	0	0				ActReg chr1 #1041	1	1	0
1042	1	144,532,889	144,534,647	1,758	2	30.454	30.8	19.382	82	84	50	1	0	0				ActReg chr1 #1042	1	0	1
1043	1	144,594,050	144,594,499	449	1	9.786	9.643	6.231	14	13	12	1	0	0				ActReg chr1 #1043	1	0	0
1044	1	144,890,733	144,892,793	2,060	1	13.594	15.141	3.492	27	31	13	0	0	1	PDE4DIP	184,316	in gene	ActReg chr1 #1044	0	1	0
1045	1	144,930,241	144,933,460	3,219	3	15.15	19.94	14.14	31	41	37	1	0	1	PDE4DIP	144,229	in gene	ActReg chr1 #1045	1	1	1
1046	1	145,007,670	145,012,854	5,184	1	15.037	13.086	7.299	32	28	20	0	1	2	PDE4DIP, LOC100505971	65817, -6211	in gene, upstream	ActReg chr1 #1046	1	0	0
1047	1	145,038,899	145,040,877	1,978	1	22.839	28.726	22.758	39	46	45	1	0	1	PDE4DIP	36,191	in gene	ActReg chr1 #1047	0	0	1
1048	1	145,041,812	145,043,841	2,029	1	19.141	16.406	7.203	42	35	15	0	0	1	PDE4DIP	33,253	in gene	ActReg chr1 #1048	1	0	0
1049	1	145,091,349	145,092,989	1,640	1	12.902	16.628	9.784	29	38	16	0	1	1	SEC22B	-4,238	upstream	ActReg chr1 #1049	0	1	0
1050	1	145,382,170	145,383,344	1,174	3	13.649	15.973	10.46	30	35	30	1	1	1	LOC100505987	-359	upstream	ActReg chr1 #1050	1	1	1
1051	1	145,395,175	145,396,464	1,289	3	11.775	14.25	13.59	29	27	40	0	0	0				ActReg chr1 #1051	1	1	1
1052	1	145,396,619	145,398,264	1,645	4	13.745	10.804	11.902	24	17	27	0	0	0				ActReg chr1 #1052	1	1	1
1053	1	145,398,888	145,399,711	823	3	12.16	11.52	11.36	21	20	27	0	0	0				ActReg chr1 #1053	1	1	1
1054	1	145,470,192	145,471,049	857	1	9.593	12.593	6	19	23	10	1	3	3	POLR3GL, ANKRD34A, LIX1L	-233, 112, -6465	upstream, in gene, upstream	ActReg chr1 #1054	0	1	0
1055	1	145,473,009	145,474,505	1,496	1	10.83	12.617	12.787	19	19	19	1	2	3	POLR3GL, ANKRD34A, LIX1L	-3370, 3249, -3328	upstream, in gene, upstream	ActReg chr1 #1055	0	0	1
1056	1	145,476,776	145,477,268	492	1	7.533	11.6	11.467	12	18	21	1	2	3	POLR3GL, ANKRD34A, LIX1L	-6635, 6514, -63	upstream, downstream, upstream	ActReg chr1 #1056	0	0	1
1057	1	145,507,235	145,508,221	986	2	11.667	11.733	5.767	22	17	10	1	1	3	LIX1L, RBM8A, PEX11B	30643, 90, -8437	downstream, in gene, upstream	ActReg chr1 #1057	1	1	0
1058	1	145,515,012	145,517,505	2,493	2	11.244	11.526	9.038	24	19	20	1	2	3	RBM8A, PEX11B, ITGA10	8620, 93, -8732	downstream, in gene, upstream	ActReg chr1 #1058	1	1	0
1059	1	145,533,047	145,533,597	550	1	2.647	6.588	12.353	4	11	18	0	0	2	PEX11B, ITGA10	17157, 8332	downstream, in gene	ActReg chr1 #1059	0	0	1
1060	1	145,548,796	145,549,280	484	1	3.688	6.867	12.375	6	12	19	0	1	2	ITGA10, ANKRD35	24048, -171	downstream, upstream	ActReg chr1 #1060	0	0	1
1061	1	145,575,356	145,576,284	928	1	10.207	14.207	6	18	23	9	1	1	2	ANKRD35, PIAS3	26611, -168	downstream, upstream	ActReg chr1 #1061	0	1	0
1062	1	145,588,509	145,589,759	1,250	2	12.026	9.897	11.921	18	19	22	1	1	3	PIAS3, NUDT17, POLR3C	13146, 301, 21750	downstream, in gene, downstream	ActReg chr1 #1062	1	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1063	1	145,610,534	145,611,380	846	2	11.692	16	7.615	21	28	14	2	2	2	POLR3C, RNF115	-73, -79	upstream, upstream	ActReg chr1 #1063	1	1	0
1064	1	146,373,488	146,373,870	382	1	4.182	9.917	5.5	7	16	8	1	2	2	LOC100505723, LOC100505752	714, 124	in gene, in gene	ActReg chr1 #1064	0	1	0
1065	1	146,555,861	146,556,968	1,107	2	21.6	22.143	10.257	54	67	21	1	0	0				ActReg chr1 #1065	1	1	0
1066	1	146,642,971	146,644,828	1,857	2	12.19	14.448	8.294	27	29	14	1	2	2	PRKAB2, LOC100505794	230, -427	in gene, upstream	ActReg chr1 #1066	1	1	0
1067	1	146,696,706	146,697,475	769	1	5.625	10.75	6.5	10	14	12	0	1	1	FMO5	140	in gene	ActReg chr1 #1067	0	1	0
1068	1	146,713,837	146,715,089	1,252	2	10.282	13.59	8.128	21	24	18	1	1	1	CHD1L	172	in gene	ActReg chr1 #1068	1	1	0
1069	1	146,976,165	146,976,959	794	1	11.958	6.417	3.917	16	11	7	0	0	0				ActReg chr1 #1069	1	0	0
1070	1	147,006,071	147,006,709	638	1	8.95	12.8	3.15	14	23	6	0	1	1	BCL9	-6,792	upstream	ActReg chr1 #1070	0	1	0
1071	1	147,070,652	147,071,849	1,197	2	12.316	16.053	7.375	22	27	15	1	0	1	BCL9	58,068	in gene	ActReg chr1 #1071	1	1	0
1072	1	147,141,680	147,143,071	1,391	2	13.349	15.07	10.256	25	25	18	1	1	1	ACP6	259	in gene	ActReg chr1 #1072	1	1	0
1073	1	147,148,697	147,149,274	577	1	7.944	11	1.083	14	16	2	0	1	1	ACP6	-6,351	upstream	ActReg chr1 #1073	0	1	0
1074	1	147,152,684	147,153,154	470	1	3.467	3.267	11.267	6	6	16	0	0	0				ActReg chr1 #1074	0	0	1
1075	1	147,222,216	147,223,414	1,198	2	16.216	16.486	4.306	39	41	9	0	0	1	GJA5	22,669	downstream	ActReg chr1 #1075	1	1	0
1076	1	147,715,686	147,716,506	820	1	7.12	6.2	14.16	12	9	19	0	0	0				ActReg chr1 #1076	0	0	1
1077	1	147,718,293	147,719,372	1,079	1	6.412	6.647	14.529	10	11	22	1	0	0				ActReg chr1 #1077	0	0	1
1078	1	147,735,294	147,736,374	1,080	3	14.588	13.618	8.941	40	32	17	1	0	0				ActReg chr1 #1078	1	1	1
1079	1	147,806,103	147,807,500	1,397	2	16.5	23.932	6.795	40	62	15	1	0	0				ActReg chr1 #1079	1	1	0
1080	1	148,000,426	148,001,027	601	3	10.353	11.421	15.79	20	24	33	1	0	1	NBPF14	25,122	downstream	ActReg chr1 #1080	1	1	1
1081	1	148,241,227	148,241,748	521	2	9.938	7.455	13.5	19	12	26	1	0	1	LOC100288142	119,694	downstream	ActReg chr1 #1081	1	0	1
1082	1	148,556,171	148,556,514	343	1	10.454	9.364	14.182	16	15	21	1	1	1	NBPF15	-1,846	upstream	ActReg chr1 #1082	0	0	1
1083	1	148,556,525	148,557,158	633	1	12.7	17.6	6.471	27	36	14	1	1	1	NBPF15	-1,347	upstream	ActReg chr1 #1083	0	1	0
1084	1	148,847,950	148,848,429	479	1	6.933	10.733	2.2	10	16	4	0	0	0				ActReg chr1 #1084	0	1	0
1085	1	148,849,989	148,850,383	394	1	6.25	10.25	1	10	15	1	0	0	0				ActReg chr1 #1085	0	1	0
1086	1	148,853,753	148,853,987	234	1	1.571	3	12.25	2	5	17	1	0	0				ActReg chr1 #1086	0	0	1
1087	1	148,854,049	148,854,502	453	1	6.5	5.857	16.143	9	9	27	1	0	1	FLJ37786	-10,181	upstream	ActReg chr1 #1087	0	0	1
1088	1	148,854,638	148,854,981	343	1	3.727	2.545	9.455	5	3	13	1	0	1	FLJ37786	-9,647	upstream	ActReg chr1 #1088	0	0	1
1089	1	148,927,737	148,928,452	715	2	13.478	19.478	20.261	23	42	44	0	0	0				ActReg chr1 #1089	0	1	1
1090	1	148,928,675	148,928,906	231	1	4.857	4.714	12.857	6	6	17	0	0	0				ActReg chr1 #1090	0	0	1
1091	1	148,929,537	148,929,967	430	1	9.077	7.077	16.615	13	12	26	0	0	0				ActReg chr1 #1091	0	0	1
1092	1	149,222,280	149,225,467	3,187	3	21.798	19.818	15.808	49	42	52	1	1	1	RNU1-5	348	downstream	ActReg chr1 #1092	1	1	1
1093	1	149,284,575	149,284,838	263	1	8.875	5	11.75	12	7	15	0	0	1	LOC388692	15,230	downstream	ActReg chr1 #1093	0	0	1
1094	1	149,298,498	149,298,892	394	1	11.417	14.667	14.833	18	19	20	0	0	2	LOC388692, RP11-403I13.9	19219, 14459	downstream, downstream	ActReg chr1 #1094	0	0	1
1095	1	149,684,120	149,684,435	315	1	10.4	8.4	14.4	14	11	20	0	0	1	LOC644634	8,417	downstream	ActReg chr1 #1095	0	0	1
1096	1	149,857,350	149,857,870	520	1	5.812	7.25	11.688	9	12	16	1	3	3	HIST2H2BE, HIST2H2AC, HIST2H2AB	622, -915, 1856	in gene, upstream, downstream	ActReg chr1 #1096	0	0	1
1097	1	149,857,940	149,860,136	2,196	4	14.536	13.246	11.667	24	28	36	1	3	3	HIST2H2BE, HIST2H2AC, HIST2H2AB	-806, 513, 428	upstream, downstream, in gene	ActReg chr1 #1097	1	1	1
1098	1	149,899,270	149,900,041	771	3	13.333	11.417	10.875	23	18	22	1	1	4	LOC100507640, SV2A, SF3B4, MTMR11	26119, -10221, 47, 9136	downstream, upstream, in gene, downstream	ActReg chr1 #1098	1	1	1
1099	1	149,910,857	149,911,620	763	1	9.875	12.375	5.6	15	18	10	0	1	2	MTMR11, OTUD7B	-2447, 71448	upstream, downstream	ActReg chr1 #1099	0	1	0
1100	1	149,978,609	149,979,443	834	1	15.115	11.923	4.556	28	25	7	0	0	1	OTUD7B	3,660	in gene	ActReg chr1 #1100	1	0	0
1101	1	149,982,021	149,983,054	1,033	1	11.906	10.75	8.062	23	16	14	1	1	1	OTUD7B	149	in gene	ActReg chr1 #1101	1	0	0
1102	1	150,039,079	150,040,191	1,112	1	11.441	15.529	6.206	17	27	12	1	1	1	VPS45	293	in gene	ActReg chr1 #1102	0	1	0
1103	1	150,206,583	150,207,824	1,241	1	8.692	12.718	6.974	19	19	12	1	1	1	ANP32E	1,301	in gene	ActReg chr1 #1103	0	1	0
1104	1	150,207,849	150,208,979	1,130	1	13.657	9.857	5.4	21	15	11	1	1	1	ANP32E	90	in gene	ActReg chr1 #1104	1	0	0
1105	1	150,240,464	150,241,843	1,379	1	9.465	12.046	8	17	19	15	1	2	3	CA14, APH1A, C1orf54	10935, 379, -4030	downstream, in gene, upstream	ActReg chr1 #1105	0	1	0
1106	1	150,335,001	150,336,751	1,750	2	9.345	10.927	6.927	19	17	13	1	1	2	PRPF3, RPRD2	41948, -1114	downstream, upstream	ActReg chr1 #1106	1	1	0
1107	1	150,459,448	150,460,280	832	2	10.615	15.538	5.231	20	29	8	0	1	1	TARS2	-56	upstream	ActReg chr1 #1107	1	1	0
1108	1	150,522,167	150,522,730	563	1	4.833	6.556	11.667	7	10	17	1	2	2	ADAMTSL4, MIR4257	550, -1957	in gene, upstream	ActReg chr1 #1108	0	0	1
1109	1	150,530,680	150,531,743	1,063	1	4.727	6.606	13.879	7	11	19	0	0	2	ADAMTSL4, MIR4257	9313, 6806	in gene, downstream	ActReg chr1 #1109	0	0	1
1110	1	150,533,680	150,534,455	775	1	8.417	11.125	12.958	12	19	19	1	0	2	ADAMTSL4, MIR4257	12169, 9662	downstream, downstream	ActReg chr1 #1110	0	0	1
1111	1	150,550,906	150,552,240	1,334	1	9.976	12.191	7	14	16	14	1	1	1	MCL1	563	in gene	ActReg chr1 #1111	0	1	0
1112	1	150,583,900	150,584,593	693	2	14.091	13.5	4.864	28	24	10	0	0	0				ActReg chr1 #1112	1	1	0
1113	1	150,849,226	150,849,834	608	1	10.737	9.789	5.158	17	16	8	1	1	1	ARNT	-344	upstream	ActReg chr1 #1113	1	0	0
1114	1	150,867,969	150,868,624	655	1	13	13.95	1.737	22	29	3	0	0	0				ActReg chr1 #1114	0	1	0
1115	1	150,898,363	150,899,114	751	2	11.75	11.5	5.792	18	21	10	1	1	1	SETDB1	-77	upstream	ActReg chr1 #1115	1	1	0
1116	1	150,949,593	150,950,311	718	1	14.087	16.217	6.696	29	35	13	0	2	2	LASS2, ANXA9	-2512, -4547	upstream, upstream	ActReg chr1 #1116	0	1	0
1117	1	150,980,558	150,981,396	838	1	13.192	8.923	8.115	19	15	13	1	2	2	FAM63A, PRUNE	-123, 4	upstream, in gene	ActReg chr1 #1117	1	0	0
1118	1	151,019,784	151,021,408	1,624	2	11.804	10.098	8.56	20	19	16	1	1	3	BNIPL, C1orf56, CDC42SE1	11567, 337, 11529	downstream, in gene, downstream	ActReg chr1 #1118	1	0	1
1119	1	151,042,659	151,043,800	1,141	3	12.886	13.829	7.371	29	25	14	1	1	2	MLLT11, GABPB2	11078, 149	downstream, in gene	ActReg chr1 #1119	1	1	1
1120	1	151,104,342	151,105,217	875	1	2.893	5.25	11.071	7	11	22	1	0	1	SEMA6C	14,361	in gene	ActReg chr1 #1120	0	0	1
1121	1	151,105,663	151,106,277	614	1	4.75	3.2	12.45	8	5	22	1	0	1	SEMA6C	13,170	in gene	ActReg chr1 #1121	0	0	1
1122	1	151,114,903	151,115,441	538	1	3	3.412	14.588	5	5	23	0	0	1	SEMA6C	3,968	in gene	ActReg chr1 #1122	0	0	1
1123	1	151,117,886	151,119,072	1,186	1	6	7.605	12.421	9	12	16	1	1	1	SEMA6C	661	in gene	ActReg chr1 #1123	0	0	1
1124	1	151,137,988	151,138,984	996	2	16.936	15	4.645	37	27	13	0	2	5	TNFAIP8L2, LYSMD1, SCNM1, TMOD4, VPS72	9381, -62, -31, 10061, 24154	downstream, upstream, upstream, downstream, downstream	ActReg chr1 #1124	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1125	1	151,162,081	151,163,111	1,030	2	19.5	17.125	4.968	56	50	8	0	1	2	VPS72, PIP5K1A	44, -8425	in gene, upstream	ActReg chr1 #1125	1	1	0
1126	1	151,170,472	151,171,775	1,303	2	15.95	14.05	6.541	31	31	12	1	1	2	VPS72, PIP5K1A	-8483, 102	upstream, in gene	ActReg chr1 #1126	1	1	0
1127	1	151,226,731	151,227,523	792	1	11.52	14.4	10	18	27	13	0	1	2	PIP5K1A, PSMD4	56106, -70	downstream, upstream	ActReg chr1 #1127	0	1	0
1128	1	151,253,408	151,255,463	2,055	3	27.54	27.723	10.292	96	107	18	1	2	3	LOC100507670, ZNF687, PI4KB	330, -356, 44289	in gene, upstream, downstream	ActReg chr1 #1128	1	1	1
1129	1	151,259,837	151,260,787	950	1	6.467	8	11.867	11	15	18	0	1	3	LOC100507670, ZNF687, PI4KB	-5547, 5521, 38412	upstream, in gene, downstream	ActReg chr1 #1129	0	0	1
1130	1	151,262,092	151,263,105	1,013	1	6.719	6.406	13.031	13	10	21	0	1	3	LOC100507670, ZNF687, PI4KB	-7833, 7807, 36126	upstream, in gene, downstream	ActReg chr1 #1130	0	0	1
1131	1	151,371,631	151,372,702	1,071	3	15.242	13.636	8.455	30	21	20	1	2	3	PSMB4, LOC100505497, POGZ	125, 714, 59775	in gene, in gene, downstream	ActReg chr1 #1131	1	1	1
1132	1	151,373,196	151,374,189	993	1	8.161	11.065	4.097	14	15	8	0	2	3	PSMB4, LOC100505497, POGZ	1651, -812, 58249	in gene, upstream, downstream	ActReg chr1 #1132	0	1	0
1133	1	151,512,501	151,513,571	1,070	1	10.471	13.147	11.265	16	25	16	1	2	3	CGN, TUFT1, MIR554	29174, 255, -5236	downstream, in gene, upstream	ActReg chr1 #1133	0	1	0
1134	1	151,546,984	151,548,013	1,029	1	9.312	14.781	4.464	17	28	10	0	0	1	TUFT1	34,717	in gene	ActReg chr1 #1134	0	1	0
1135	1	151,551,027	151,552,573	1,546	1	9.792	11.458	2.714	20	17	5	0	0	1	TUFT1	39,019	in gene	ActReg chr1 #1135	0	1	0
1136	1	151,584,244	151,585,316	1,072	2	11	12.588	6.647	19	17	16	1	1	1	SNX27	118	in gene	ActReg chr1 #1136	1	1	0
1137	1	151,735,709	151,736,266	557	1	15.889	15.111	14.111	26	26	24	1	2	3	MRPL9, QAZ3, TDRKH	53, 542, 27023	in gene, in gene, downstream	ActReg chr1 #1137	0	0	1
1138	1	151,762,650	151,763,248	598	1	12.368	14.21	15.895	20	19	25	1	1	2	TDRKH, LINGO4	61, 14933	in gene, downstream	ActReg chr1 #1138	0	0	1
1139	1	151,773,734	151,775,067	1,333	1	3.225	4.135	12.512	7	9	20	0	0	2	LINGO4, RORC	3482, 29948	in gene, downstream	ActReg chr1 #1139	0	0	1
1140	1	151,798,079	151,798,906	827	1	3.308	6.077	13.615	7	12	19	0	0	1	RORC	5,856	in gene	ActReg chr1 #1140	0	0	1
1141	1	151,811,798	151,812,921	1,123	2	9.714	15.314	11.314	19	31	22	2	3	4	RORC, C2CD4D, LOC100132111, THEM5	-8011, 674, 1414, 13814	upstream, in gene, in gene, downstream	ActReg chr1 #1141	0	1	1
1142	1	151,813,486	151,814,155	669	1	11.191	9.619	2.154	16	16	4	0	1	4	RORC, C2CD4D, LOC100132111, THEM5	-9472, -787, 2875, 12353	upstream, upstream, in gene, downstream	ActReg chr1 #1142	1	0	0
1143	1	151,881,599	151,882,697	1,098	2	16.514	14.857	8.829	34	25	15	1	1	1	THEM4	-35	upstream	ActReg chr1 #1143	1	1	0
1144	1	151,918,105	151,919,735	1,630	2	10.294	12.392	1.804	21	26	4	0	0	0				ActReg chr1 #1144	1	1	0
1145	1	151,952,507	151,953,346	839	1	7.333	11.704	2.423	13	18	5	0	0	1	S100A10	13,788	downstream	ActReg chr1 #1145	0	1	0
1146	1	151,964,495	151,967,103	2,608	2	10.222	13.123	7.42	16	32	15	2	1	1	S100A10	915	in gene	ActReg chr1 #1146	0	1	1
1147	1	152,001,371	152,002,143	772	1	5.5	12.5	3.364	10	22	6	0	0	1	S100A11	7,754	downstream	ActReg chr1 #1147	0	1	0
1148	1	152,006,787	152,007,579	792	1	6.375	11.875	5.5	11	15	9	0	1	1	S100A11	2,328	in gene	ActReg chr1 #1148	0	1	0
1149	1	152,009,209	152,009,659	450	1	8.786	12.357	12.214	13	18	21	1	1	1	S100A11	77	in gene	ActReg chr1 #1149	0	0	1
1150	1	152,009,789	152,010,293	504	1	3.188	6.938	12.5	5	11	17	0	1	1	S100A11	-530	upstream	ActReg chr1 #1150	0	0	1
1151	1	152,020,196	152,021,349	1,153	2	14.917	12.889	6.636	25	26	16	0	0	0				ActReg chr1 #1151	1	1	0
1152	1	152,083,068	152,083,829	761	1	10	14.5	15.583	14	21	27	1	0	1	TCHH	3,108	in gene	ActReg chr1 #1152	0	0	1
1153	1	152,160,993	152,162,118	1,125	2	10	14.057	9.914	16	22	18	1	0	0				ActReg chr1 #1153	0	1	1
1154	1	152,191,511	152,191,990	479	1	3.533	5.867	12.067	5	8	15	0	0	1	HRNR	4,919	in gene	ActReg chr1 #1154	0	0	1
1155	1	152,216,878	152,217,953	1,075	2	10.882	11.735	2	19	18	2	0	0	0				ActReg chr1 #1155	1	1	0
1156	1	152,277,178	152,277,465	287	1	1.556	2.222	11.667	2	5	15	0	0	2	FLG, LOC339400	20358, -8614	in gene, upstream	ActReg chr1 #1156	0	0	1
1157	1	153,072,689	153,073,096	407	1	11.231	8	1	19	13	1	0	1	1	SPRR2E	-5,891	upstream	ActReg chr1 #1157	1	0	0
1158	1	153,394,682	153,395,609	927	2	13.931	18.586	2	30	45	4	0	0	1	S100A7A	6,145	in gene	ActReg chr1 #1158	1	1	0
1159	1	153,416,325	153,416,776	451	1	3.929	1.5	10.571	6	2	16	0	1	1	S100A7L2	-4,047	upstream	ActReg chr1 #1159	0	0	1
1160	1	153,424,691	153,425,444	753	2	13.708	13.667	2.619	30	27	4	0	0	1	S100A7	8,070	downstream	ActReg chr1 #1160	1	1	0
1161	1	153,462,462	153,463,542	1,080	1	10.353	11.647	7.5	16	16	11	0	0	0				ActReg chr1 #1161	0	1	0
1162	1	153,505,692	153,506,898	1,206	2	11.079	12.184	8.711	24	19	17	0	2	4	LOC100505623, S100A6, S100A5, S100A4	233, 2422, 7946, 11987	in gene, downstream, downstream, downstream	ActReg chr1 #1162	1	1	0
1163	1	153,507,469	153,509,633	2,164	3	13.853	13.323	10.162	25	29	21	1	2	4	LOC100505623, S100A6, S100A5, S100A4	2489, 166, 5690, 9731	downstream, in gene, downstream, downstream	ActReg chr1 #1163	1	1	1
1164	1	153,517,190	153,518,175	985	1	10.3	14.033	7.667	17	23	17	0	2	5	LOC100505623, S100A6, S100A5, S100A4, S100A3	11620, -8965, -3441, 600, 4052	downstream, upstream, upstream, upstream, in gene, downstream	ActReg chr1 #1164	0	1	0
1165	1	153,538,004	153,539,888	1,884	2	11.288	13.034	7.121	22	23	17	0	1	1	S100A2	-640	upstream	ActReg chr1 #1165	1	1	0
1166	1	153,540,021	153,541,549	1,528	2	11.167	12.625	7.917	23	18	15	0	1	1	S100A2	-2,479	upstream	ActReg chr1 #1166	1	1	0
1167	1	153,580,794	153,583,415	2,621	2	11.976	15.11	7.284	21	27	19	0	1	3	S100A16, S100A14, S100A13	3410, 6686, 24464	in gene, downstream, downstream	ActReg chr1 #1167	1	1	0
1168	1	153,585,164	153,585,736	572	1	8.611	7.778	13.944	13	11	21	0	1	3	S100A16, S100A14, S100A13	64, 3340, 21118	in gene, downstream, downstream	ActReg chr1 #1168	0	0	1
1169	1	153,599,308	153,600,221	913	2	12.786	10.714	12.5	17	16	19	0	2	3	S100A13, S100A1, C1orf77	6804, -1109, -6761	in gene, upstream, upstream	ActReg chr1 #1169	1	0	1
1170	1	153,605,958	153,607,020	1,062	2	7.485	12.697	9.364	14	21	17	1	2	3	S100A13, S100A1, C1orf77	79, 5616, -36	in gene, downstream, upstream	ActReg chr1 #1170	0	1	1
1171	1	153,630,964	153,631,537	573	1	8.944	12	13.056	12	20	18	1	1	2	SNAPIN, ILF2	105, 12229	in gene, downstream	ActReg chr1 #1171	0	0	1
1172	1	153,643,500	153,644,035	535	1	17	11	14.412	27	17	27	1	2	3	SNAPIN, ILF2, NPR1	12622, -288, -7397	downstream, upstream, upstream	ActReg chr1 #1172	0	0	1
1173	1	153,699,795	153,700,535	740	2	10.478	9.909	6.174	19	21	11	1	1	1	INTS3	-402	upstream	ActReg chr1 #1173	1	1	0
1174	1	153,772,815	153,773,496	681	1	4.333	3.056	14.286	8	5	22	0	0	2	LOC343052, GATAD2B	6732, 122296	in gene, downstream	ActReg chr1 #1174	0	0	1
1175	1	153,774,640	153,775,266	626	1	4.15	5.5	13	7	9	22	0	0	2	LOC343052, GATAD2B	8530, 120498	in gene, downstream	ActReg chr1 #1175	0	0	1
1176	1	153,914,210	153,914,779	569	1	5.471	5.647	13.177	7	10	19	1	0	2	DENND4B, CRTC2	4660, 16549	in gene, downstream	ActReg chr1 #1176	0	0	1
1177	1	153,918,000	153,919,638	1,638	2	17.726	18.608	6.979	55	58	17	1	1	2	DENND4B, CRTC2	335, 12224	in gene, downstream	ActReg chr1 #1177	1	1	0
1178	1	153,930,070	153,931,529	1,459	3	14.391	11.609	8.591	27	20	16	1	1	3	CRTC2, SLC39A1, CREB3L4	244, 9389, -9598	in gene, downstream, upstream	ActReg chr1 #1178	1	1	1
1179	1	153,935,581	153,936,689	1,108	1	12.571	11.086	6.514	18	15	11	1	2	3	CRTC2, SLC39A1, CREB3L4	-5092, 4053, -4262	upstream, in gene, upstream	ActReg chr1 #1179	0	1	0
1180	1	153,939,516	153,940,035	519	1	10	11.294	12.588	16	16	16	1	2	4	CRTC2, SLC39A1, CREB3L4, JTB	-8732, 413, -622, 10676	upstream, in gene, upstream, downstream	ActReg chr1 #1180	0	0	1
1181	1	153,949,338	153,950,678	1,340	3	13.309	12.214	10.643	22	19	19	1	1	4	SLC39A1, CREB3L4, JTB, RAB13	-9820, 9611, 443, 8798	upstream, downstream, in gene, downstream	ActReg chr1 #1181	1	1	1
1182	1	153,962,812	153,963,653	841	1	9.222	14	8.556	14	21	17	1	2	3	RAB13, RPS27, NUP210L	-4426, -7, 164360	upstream, upstream, downstream	ActReg chr1 #1182	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1183	1	154,070,437	154,070,819	382	1	2.333	3.833	11.25	3	5	15	0	0	1	NUP210L	56,964	in gene	ActReg chr1 #1183	0	0	1
1184	1	154,154,775	154,156,189	1,414	3	13.068	11.182	9.818	23	20	20	1	0	2	TPM3, MIR190B	9127, 10737	in gene, downstream	ActReg chr1 #1184	1	1	1
1185	1	154,167,622	154,168,164	542	1	4	4.235	10.412	5	7	14	0	2	3	TPM3, MIR190B, C1orf189	-3284, -1674, 10916	upstream, upstream, downstream	ActReg chr1 #1185	0	0	1
1186	1	154,192,495	154,193,605	1,110	1	9.8	12.771	8.343	19	20	16	1	2	2	C1orf43, UBAP2L	223, 395	in gene, in gene	ActReg chr1 #1186	0	1	0
1187	1	154,298,256	154,299,386	1,130	1	9.514	11.286	5.771	16	16	12	1	1	2	AQP10, ATP8B2	5229, 785	downstream, in gene	ActReg chr1 #1187	0	1	0
1188	1	154,377,401	154,378,005	604	1	10.316	8.737	10.263	19	11	16	1	1	1	IL6R	34	in gene	ActReg chr1 #1188	0	0	1
1189	1	154,378,048	154,379,038	990	1	9.194	11.645	9.935	14	17	16	1	1	1	IL6R	874	in gene	ActReg chr1 #1189	0	1	0
1190	1	154,406,927	154,407,433	506	1	4.25	3.875	10.75	6	7	18	0	0	1	IL6R	29,511	in gene	ActReg chr1 #1190	0	0	1
1191	1	154,531,130	154,532,421	1,291	2	13.244	12.293	7.075	21	22	18	1	1	2	UBE2Q1, CHRNB2	-655, -8482	upstream, upstream	ActReg chr1 #1191	1	1	0
1192	1	154,539,445	154,541,107	1,662	2	12.442	16.173	5.66	33	40	11	1	1	2	UBE2Q1, CHRNB2	-9156, 19	upstream, in gene	ActReg chr1 #1192	1	1	0
1193	1	154,580,019	154,580,975	956	1	9.967	12.933	4.367	15	19	10	1	0	1	ADAR	19,959	in gene	ActReg chr1 #1193	0	1	0
1194	1	154,599,730	154,600,712	982	2	9.387	12.29	11.645	18	18	17	1	1	1	ADAR	235	in gene	ActReg chr1 #1194	0	1	1
1195	1	154,714,276	154,714,830	554	1	5.529	4	11.059	9	7	16	0	0	1	KCNN3	128,201	in gene	ActReg chr1 #1195	0	0	1
1196	1	154,786,909	154,787,605	696	1	2.684	3	10.454	5	5	17	0	0	1	KCNN3	55,497	in gene	ActReg chr1 #1196	0	0	1
1197	1	154,819,313	154,819,861	548	1	5.588	4.529	10.471	9	6	14	0	0	1	KCNN3	23,167	in gene	ActReg chr1 #1197	0	0	1
1198	1	154,908,704	154,910,382	1,678	2	17.868	19.038	6.472	40	41	16	1	1	2	PMVK, PBXIP1	-59, 19024	upstream, downstream	ActReg chr1 #1198	1	1	0
1199	1	154,933,753	154,935,125	1,372	3	13.814	15.395	8.14	27	38	25	1	2	3	PBXIP1, PYGO2, SHC1	-5872, -181, 12520	upstream, upstream, downstream	ActReg chr1 #1199	1	1	1
1200	1	154,941,005	154,941,638	633	1	3.4	6.4	13.75	7	12	25	0	3	4	PYGO2, SHC1, CKS1B, MIR4258	-7063, 5638, -5797, -6848	upstream, in gene, upstream, upstream	ActReg chr1 #1200	0	0	1
1201	1	154,942,921	154,944,121	1,200	1	11.703	13.919	7.595	20	24	14	0	2	4	PYGO2, SHC1, CKS1B, MIR4258	-9263, 3438, -3597, -4648	upstream, in gene, upstream, upstream	ActReg chr1 #1201	0	1	0
1202	1	154,955,308	154,956,043	735	1	12.043	17.826	5.696	20	36	9	0	1	4	SHC1, CKS1B, MIR4258, FLAD1	-5716, 8557, 7506, -95	upstream, downstream, downstream, upstream	ActReg chr1 #1202	0	1	0
1203	1	154,973,157	154,975,020	1,863	4	14.603	17.069	10.125	36	31	24	2	1	3	FLAD1, LENEP, ZBTB7B	18318, 8026, -1024	downstream, downstream, upstream	ActReg chr1 #1203	1	1	1
1204	1	154,975,676	154,976,955	1,279	2	12.325	10.975	10.225	20	19	21	1	1	2	LENEP, ZBTB7B	downstream, in gene	ActReg chr1 #1204	1	0	1
1205	1	154,983,972	154,984,732	760	1	3.955	6.435	12.565	8	11	20	0	0	2	ZBTB7B, DCST2	9240, 21905	in gene, downstream	ActReg chr1 #1205	0	0	1
1206	1	154,989,570	154,990,517	947	1	13.379	13.897	15.414	20	21	22	1	0	2	ZBTB7B, DCST2	14931, 16214	in gene, downstream	ActReg chr1 #1206	0	0	1
1207	1	155,021,058	155,021,728	670	1	3.571	4.667	11.286	5	8	15	0	1	3	DCST1, LOC100505666, ADAM15	15093, 15026, -2369	in gene, in gene, upstream	ActReg chr1 #1207	0	0	1
1208	1	155,022,251	155,023,734	1,483	2	16.956	11.826	9.067	32	24	19	1	1	3	DCST1, LOC100505666, ADAM15	16692, 13427, -770	in gene, in gene, upstream	ActReg chr1 #1208	1	0	1
1209	1	155,024,014	155,024,616	602	1	10.842	8.579	13.526	19	16	17	1	1	3	DCST1, LOC100505666, ADAM15	18015, 12104, 553	downstream, in gene, in gene	ActReg chr1 #1209	0	0	1
1210	1	155,029,954	155,030,706	752	1	5.478	7.565	14.478	8	10	23	0	1	4	DCST1, LOC100505666, ADAM15, EFNA4	24030, 6089, 6568, -5883	downstream, in gene, in gene, upstream	ActReg chr1 #1210	0	0	1
1211	1	155,032,497	155,033,011	514	1	5.938	5.188	12.312	11	8	19	0	1	4	DCST1, LOC100505666, ADAM15, EFNA4	26454, 3665, 5992, -3459	downstream, in gene, in gene, upstream	ActReg chr1 #1211	0	0	1
1212	1	155,034,561	155,035,012	451	1	3.143	4.857	14.643	5	8	20	1	2	3	LOC100505666, ADAM15, EFNA4	1633, 11024, -1427	in gene, in gene, upstream	ActReg chr1 #1212	0	0	1
1213	1	155,035,292	155,036,667	1,375	1	9.907	13.698	9.186	16	26	15	1	2	3	LOC100505666, ADAM15, EFNA4	440, 12217, -234	in gene, downstream, upstream	ActReg chr1 #1213	0	1	0
1214	1	155,052,367	155,053,269	902	1	3.714	8.071	13.571	7	16	19	1	1	1	EFNA3	1,470	in gene	ActReg chr1 #1214	0	0	1
1215	1	155,056,644	155,057,266	622	1	9.211	9.737	12.053	14	13	15	1	0	1	EFNA3	5,607	in gene	ActReg chr1 #1215	0	0	1
1216	1	155,058,147	155,058,520	373	1	6.545	8.364	14.909	8	12	21	1	0	1	EFNA3	6,985	in gene	ActReg chr1 #1216	0	0	1
1217	1	155,063,896	155,064,476	580	1	5.944	9.333	12.556	11	15	20	0	0	1	EFNA3	12,838	downstream	ActReg chr1 #1217	0	0	1
1218	1	155,065,994	155,067,008	1,014	1	5.031	7.031	10.875	10	12	15	0	0	1	EFNA3	15,153	downstream	ActReg chr1 #1218	0	0	1
1219	1	155,098,746	155,100,313	1,567	2	9.163	13.51	10.531	16	23	21	1	1	2	EFNA1, RAG1AP1	-820, -8759	upstream, upstream	ActReg chr1 #1219	0	1	1
1220	1	155,100,797	155,102,892	2,095	2	9.576	8.909	8.561	18	16	15	0	2	3	EFNA1, RAG1AP1, DPM3	1495, -6444, 111152	in gene, upstream, downstream	ActReg chr1 #1220	1	0	1
1221	1	155,107,504	155,108,984	1,480	3	7.761	11.913	11.913	13	17	24	1	1	3	EFNA1, RAG1AP1, DPM3	7895, -44, 4752	downstream, upstream, downstream	ActReg chr1 #1221	0	1	1
1222	1	155,112,098	155,113,366	1,268	1	11.872	13.513	8.667	22	22	13	1	1	3	EFNA1, RAG1AP1, DPM3	12383, 4444, 264	downstream, downstream, in gene	ActReg chr1 #1222	0	1	0
1223	1	155,145,013	155,146,985	1,972	2	30.21	29.823	8.355	156	142	18	1	2	2	KRTCAP2, TRIM46	-195, -361	upstream, upstream	ActReg chr1 #1223	1	1	0
1224	1	155,156,265	155,156,739	474	1	4.267	6.067	13.467	6	9	20	0	0	4	TRIM46, MUC1, MIR92B, THBS3	10142, 6198, -8466, 21188	in gene, downstream, upstream, downstream	ActReg chr1 #1224	0	0	1
1225	1	155,163,121	155,165,003	1,882	2	10.983	13.136	9.237	20	21	15	2	3	5	TRIM46, MUC1, MIR92B, THBS3, LOC100129268	17702, -1362, -906, 13628, -6531	downstream, upstream, upstream, downstream, upstream	ActReg chr1 #1225	1	1	0
1226	1	155,178,565	155,179,094	529	1	10.688	9.625	11.875	15	12	17	1	2	3	THBS3, LOC100129268, MTX1	-1139, 8236, 339	upstream, downstream, in gene	ActReg chr1 #1226	0	0	1
1227	1	155,196,396	155,198,112	1,716	1	10.111	13.185	7.537	16	21	20	1	0	1	GBA	17,399	downstream	ActReg chr1 #1227	0	1	0
1228	1	155,214,176	155,215,155	979	3	12.258	14.387	13.613	23	28	26	0	1	2	GBA, FAM189B	-12, 10609	upstream, downstream	ActReg chr1 #1228	1	1	1
1229	1	155,220,216	155,220,994	778	2	6.48	11.88	9.4	14	22	21	1	1	3	GBA, FAM189B, SCAMP3	-5952, 4669, 11590	upstream, in gene, downstream	ActReg chr1 #1229	0	1	1
1230	1	155,225,036	155,225,840	804	1	10.64	11.88	14.6	18	20	24	1	1	3	FAM189B, SCAMP3, CLK2	-164, 6757, 17843	upstream, downstream, downstream	ActReg chr1 #1230	0	0	1
1231	1	155,231,621	155,232,556	935	1	11.379	14.31	10.483	15	27	16	1	2	3	FAM189B, SCAMP3, CLK2	-6814, 107, 11193	upstream, in gene, downstream	ActReg chr1 #1231	0	1	0
1232	1	155,246,699	155,248,610	1,911	2	7.85	12.533	8.55	15	21	24	1	2	2	CLK2, HCN3	-4373, 280	upstream, in gene	ActReg chr1 #1232	0	1	1
1233	1	155,278,046	155,279,356	1,310	2	11.878	13.854	6.927	22	27	14	1	2	2	PKLR, FDPS	-7476, 162	upstream, in gene	ActReg chr1 #1233	1	1	0
1234	1	155,290,644	155,291,454	810	1	4.28	8.36	13.2	10	12	18	1	2	3	FDPS, C1orf104, RUSC1	12510, 2889, 409	downstream, in gene, in gene	ActReg chr1 #1234	0	0	1
1235	1	155,293,529	155,294,753	1,224	1	10.436	11.974	11.846	15	20	16	1	1	3	FDPS, C1orf104, RUSC1	15602, -203, 3501	downstream, downstream, in gene	ActReg chr1 #1235	0	1	0
1236	1	155,296,388	155,297,004	616	1	4.526	6.947	13.158	6	11	21	0	1	4	FDPS, C1orf104, RUSC1, ASH1L	18157, -2758, 6056, 235628	downstream, upstream, in gene, downstream	ActReg chr1 #1236	0	0	1
1237	1	155,531,766	155,533,346	1,580	2	14.88	16.28	7.08	46	48	14	1	2	2	ASH1L, LOC645676	-232, 784	upstream, in gene	ActReg chr1 #1237	1	1	0
1238	1	155,657,803	155,659,182	1,379	3	17.023	23.884	14.581	53	70	27	1	2	2	YY1AP1, DAP3	299, -382	in gene, upstream	ActReg chr1 #1238	1	1	1
1239	1	155,714,828	155,715,658	830	1	9.269	14.423	6.923	17	25	17	1	1	3	DAP3, LOC100505728, GON4L	56369, 530, 111729	downstream, in gene, downstream	ActReg chr1 #1239	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1240	1	155,826,490	155,827,535	1,045	2	19.212	22.909	6.7	46	66	18	0	2	2	GON4L, SYT11	-40, -2248	upstream, upstream	ActReg chr1 #1240	1	1	0
1241	1	155,829,813	155,830,676	863	1	8.741	13.037	7.815	17	22	14	1	2	2	GON4L, SYT11	-3272, 984	upstream, in gene	ActReg chr1 #1241	0	1	0
1242	1	155,903,592	155,904,681	1,089	3	12.5	15.559	10.971	27	28	18	1	2	3	KIAA0907, SCARNA4, RXFP4	52, -8259, -7344	in gene, upstream, upstream	ActReg chr1 #1242	1	1	1
1243	1	155,911,381	155,912,556	1,175	1	10.189	7.703	13.649	16	14	21	0	2	3	KIAA0907, RXFP4, ARHGEF2	-7780, 488, 36368	upstream, in gene, downstream	ActReg chr1 #1243	0	0	1
1244	1	155,920,533	155,921,109	576	1	7.611	7.056	14.111	10	12	18	1	0	2	RXFP4, ARHGEF2	9341, 27515	downstream, in gene	ActReg chr1 #1244	0	0	1
1245	1	155,935,900	155,936,684	784	1	6.24	7.64	11.68	10	11	19	0	0	1	ARHGEF2	12,044	in gene	ActReg chr1 #1245	0	0	1
1246	1	155,940,174	155,941,039	865	1	11.148	7.741	4.909	19	17	8	0	0	1	ARHGEF2	7,730	in gene	ActReg chr1 #1246	1	0	0
1247	1	156,023,488	156,025,234	1,746	3	14.185	14.6	8.635	26	30	19	1	3	3	UBQLN4, ROBLD3, RAB25	-845, -156, -6605	upstream, upstream, upstream	ActReg chr1 #1247	1	1	1
1248	1	156,046,159	156,047,551	1,392	1	4.721	5.419	12.139	12	10	20	1	0	2	RAB25, MEX3A	15889, 4934	downstream, in gene	ActReg chr1 #1248	0	0	1
1249	1	156,074,602	156,075,294	692	1	8.81	11.905	9.048	12	17	14	0	0	1	LMNA	-9,513	upstream	ActReg chr1 #1249	0	1	0
1250	1	156,083,705	156,086,002	2,297	2	11.194	13.764	9.347	22	26	17	1	1	1	LMNA	392	in gene	ActReg chr1 #1250	1	1	0
1251	1	156,092,209	156,093,040	831	1	9.615	11.654	5.192	15	17	10	0	0	1	LMNA	8,163	in gene	ActReg chr1 #1251	0	1	0
1252	1	156,095,807	156,097,296	1,489	2	14.702	11.915	5.702	24	19	11	0	0	1	LMNA	12,090	in gene	ActReg chr1 #1252	1	1	0
1253	1	156,104,505	156,105,123	618	1	6.65	4.8	11.45	10	11	16	0	0	1	LMNA	20,353	in gene	ActReg chr1 #1253	0	0	1
1254	1	156,105,700	156,106,281	581	1	8.333	4.278	13.889	16	7	21	1	0	1	LMNA	21,529	in gene	ActReg chr1 #1254	0	0	1
1255	1	156,163,245	156,164,373	1,128	1	7.152	12.686	8.2	12	20	13	1	1	1	SLC25A44	79	in gene	ActReg chr1 #1255	0	1	0
1256	1	156,213,747	156,215,011	1,264	1	4.65	7.85	13.45	8	12	21	0	1	4	PMF1, BGLAP, PAQR6, SMG5	31595, 2428, 3464, 38241	downstream, downstream, in gene, downstream	ActReg chr1 #1256	0	0	1
1257	1	156,230,329	156,231,168	839	1	9.037	14.37	4.444	16	23	8	0	0	1	SMG5	21,872	in gene	ActReg chr1 #1257	0	1	0
1258	1	156,308,017	156,308,843	826	1	11.192	12.115	3.615	18	20	6	1	3	3	CCT3, LOC100505747, C1orf182	-235, -1401, 1325	upstream, upstream, in gene	ActReg chr1 #1258	0	1	0
1259	1	156,346,683	156,347,314	631	1	5.2	7.25	15.1	8	12	28	0	0	1	RHBG	7,995	in gene	ActReg chr1 #1259	0	0	1
1260	1	156,357,369	156,358,013	644	1	6.85	8.75	12.6	9	11	19	1	0	1	RHBG	18,688	downstream	ActReg chr1 #1260	0	0	1
1261	1	156,383,635	156,384,769	1,134	1	10.694	14.222	7.417	20	28	13	0	1	3	C1orf61, LOC100505765, MIR9-1	14982, -1517, 6019	in gene, upstream, downstream	ActReg chr1 #1261	0	1	0
1262	1	156,390,973	156,391,946	973	3	14.677	11.032	9.484	27	19	18	1	1	3	C1orf61, LOC100505765, MIR9-1	7725, -8774, -1238	in gene, upstream, upstream	ActReg chr1 #1262	1	1	1
1263	1	156,425,795	156,427,206	1,411	2	12.5	12.523	6.727	19	24	16	1	0	1	MEF2D	44,029	downstream	ActReg chr1 #1263	1	1	0
1264	1	156,437,600	156,438,191	591	1	5	4.526	12.421	8	7	21	0	0	1	MEF2D	32,634	in gene	ActReg chr1 #1264	0	0	1
1265	1	156,469,841	156,471,702	1,861	2	15.155	18.259	6.807	37	41	14	1	1	1	MEF2D	-242	upstream	ActReg chr1 #1265	1	1	0
1266	1	156,472,739	156,473,630	891	1	11.148	15.741	4.12	21	27	7	0	1	1	MEF2D	-2,655	upstream	ActReg chr1 #1266	0	1	0
1267	1	156,474,422	156,476,016	1,594	3	19.16	19.28	8.62	52	49	23	1	1	1	MEF2D	-4,690	upstream	ActReg chr1 #1267	1	1	1
1268	1	156,521,353	156,522,189	836	1	12.154	14.577	7.115	22	29	12	0	0	1	IQGAP3	20,625	in gene	ActReg chr1 #1268	0	1	0
1269	1	156,561,561	156,562,073	512	1	15.25	15.25	13.75	22	19	19	1	1	3	TTC24, APOA1BP, GPATCH4	12298, 259, 9453	downstream, in gene, downstream	ActReg chr1 #1269	0	0	1
1270	1	156,570,847	156,572,256	1,409	3	9.311	11	6.844	15	20	19	0	1	2	APOA1BP, GPATCH4	9993, -281	downstream, upstream	ActReg chr1 #1270	1	1	1
1271	1	156,593,520	156,594,530	1,010	1	6.438	12	12.656	13	21	19	1	0	1	HAPLN2	4,939	in gene	ActReg chr1 #1271	0	0	1
1272	1	156,611,842	156,612,614	772	1	11.042	8.625	14.875	16	15	25	1	1	1	BCAN	488	in gene	ActReg chr1 #1272	0	0	1
1273	1	156,617,046	156,617,696	650	1	6.333	5.619	12.857	11	9	25	1	0	1	BCAN	5,631	in gene	ActReg chr1 #1273	0	0	1
1274	1	156,621,343	156,622,266	923	1	10.517	13.931	6.793	16	23	12	0	0	1	BCAN	10,064	in gene	ActReg chr1 #1274	0	1	0
1275	1	156,629,678	156,630,745	1,067	2	14.758	16.121	7	25	28	12	0	0	2	BCAN, NES	18471, 16978	downstream, downstream	ActReg chr1 #1275	1	1	0
1276	1	156,630,750	156,632,673	1,923	2	12.918	15.393	7.436	24	34	15	0	0	2	BCAN, NES	19971, 15478	downstream, downstream	ActReg chr1 #1276	1	1	0
1277	1	156,646,307	156,647,581	1,274	1	8.641	14.487	8.286	17	19	16	1	1	1	NES	245	in gene	ActReg chr1 #1277	0	1	0
1278	1	156,674,631	156,675,273	642	1	9.05	8.25	11.25	17	16	15	1	1	1	CRABP2	423	in gene	ActReg chr1 #1278	0	0	1
1279	1	156,675,490	156,676,741	1,251	1	5.744	6.513	12.128	10	11	19	1	1	1	CRABP2	-740	upstream	ActReg chr1 #1279	0	0	1
1280	1	156,697,764	156,699,230	1,466	2	13.733	13.044	7.047	33	31	15	1	2	3	ISG20L2, C1orf66, MRPL24	-792, 234, 12426	upstream, in gene, downstream	ActReg chr1 #1280	1	1	0
1281	1	156,710,147	156,711,654	1,507	2	14.761	13.468	8.213	36	26	17	1	1	3	C1orf66, MRPL24, HDGF	12637, 23, 11340	downstream, in gene, downstream	ActReg chr1 #1281	1	1	0
1282	1	156,717,553	156,719,125	1,572	1	10.347	11.714	6.816	15	20	13	0	1	2	MRPL24, HDGF	-7416, 3901	upstream, in gene	ActReg chr1 #1282	0	1	0
1283	1	156,721,361	156,722,401	1,040	2	26.303	28.212	6.091	78	81	12	1	1	1	HDGF	359	in gene	ActReg chr1 #1283	1	1	0
1284	1	156,736,120	156,737,894	1,774	3	17.054	19.893	9.893	41	45	15	1	1	1	PRCC	-267	upstream	ActReg chr1 #1284	1	1	1
1285	1	156,814,652	156,815,715	1,063	1	3.5	3.559	13.823	7	7	23	1	0	2	NTRK1, INSRR	29641, 13483	in gene, in gene	ActReg chr1 #1285	0	0	1
1286	1	156,843,433	156,843,976	543	1	3.706	6.471	12.941	7	9	16	0	0	1	NTRK1	58,162	in gene	ActReg chr1 #1286	0	0	1
1287	1	156,862,644	156,863,152	508	1	3.875	3.438	12.688	5	8	17	0	1	1	PEAR1	-625	upstream	ActReg chr1 #1287	0	0	1
1288	1	156,877,878	156,878,812	934	1	6.759	4.724	13.414	10	10	19	1	0	1	PEAR1	14,822	in gene	ActReg chr1 #1288	0	0	1
1289	1	156,890,322	156,891,025	703	1	6.318	3.591	13.364	10	7	22	1	1	2	PEAR1, C1orf92	27150, 249	downstream, in gene	ActReg chr1 #1289	0	0	1
1290	1	156,897,038	156,897,584	546	1	6.706	9.529	13	11	18	19	1	0	3	C1orf92, ARHGEF11, MIR765	6887, 117851, 8725	in gene, downstream, downstream	ActReg chr1 #1290	0	0	1
1291	1	156,915,701	156,916,772	1,071	1	10.235	11.853	3.882	19	18	8	0	0	2	ARHGEF11, MIR765	98926, -10200	in gene, upstream	ActReg chr1 #1291	0	1	0
1292	1	157,107,533	157,108,913	1,380	3	13.395	12.93	11.139	20	24	18	1	1	1	ETV3	160	in gene	ActReg chr1 #1292	1	1	1
1293	1	157,164,648	157,165,628	980	1	3.633	4.9	11.867	6	9	16	1	0	0				ActReg chr1 #1293	0	0	1
1294	1	158,007,446	158,008,265	819	1	13.962	9.615	3.458	27	15	8	0	0	2	KIRREL, LOC100505785	44792, 12510	in gene, downstream	ActReg chr1 #1294	1	0	0
1295	1	158,038,591	158,039,118	527	1	1.7	3.375	10.765	2	6	16	0	0	1	KIRREL	75,791	in gene	ActReg chr1 #1295	0	0	1
1296	1	158,114,580	158,115,483	903	1	8.536	11.857	2.609	18	16	5	0	1	1	hCG_1654703	-4,601	upstream	ActReg chr1 #1296	0	1	0
1297	1	158,115,670	158,116,541	871	1	8.296	14.37	4.741	14	27	9	0	1	1	hCG_1654703	-5,675	upstream	ActReg chr1 #1297	0	1	0
1298	1	158,150,546	158,151,608	1,062	2	8.212	12.242	13.152	15	20	19	1	1	1	CD1D	1,340	in gene	ActReg chr1 #1298	0	1	1
1299	1	158,969,271	158,970,070	799	2	11.6	11.32	4.12	18	22	8	0	0	1	IFI16	-10,012	upstream	ActReg chr1 #1299	1	1	0
1300	1	159,046,261	159,047,577	1,316	1	9.61	13.634	3.179	14	24	7	0	1	1	AIM2	-272	upstream	ActReg chr1 #1300	0	1	0
1301	1	159,061,033	159,061,976	943	2	12.414	12.034	1.889	16	19	4	0	0	0				ActReg chr1 #1301	1	1	0
1302	1	159,140,750	159,141,311	561	1	3.647	4.647	13.294	7	9	19	1	1	1	CADM3	-347	upstream	ActReg chr1 #1302	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1303	1	159,145,022	159,145,943	921	2	16.035	13.034	1.63	34	29	3	0	0	1	CADM3	4,105	in gene	ActReg chr1 #1303	1	1	0
1304	1	159,146,463	159,147,725	1,262	2	23.875	26.625	2.969	82	83	5	0	0	1	CADM3	5,717	in gene	ActReg chr1 #1304	1	1	0
1305	1	159,171,863	159,172,419	556	1	3.833	2.889	10.333	5	6	14	0	2	3	CADM3, LOC100131825, DARC	30764, 53, -2369	in gene, in gene, upstream	ActReg chr1 #1305	0	0	1
1306	1	159,464,721	159,465,027	306	1	5.8	5.3	10.7	8	8	13	0	0	0				ActReg chr1 #1306	0	0	1
1307	1	159,750,419	159,751,281	862	1	13.778	14.556	14.074	19	23	22	1	1	1	DUSP23	91	in gene	ActReg chr1 #1307	0	0	1
1308	1	159,774,403	159,775,410	1,007	2	11.452	13.613	2.903	20	25	6	0	1	1	FCRL6	2,733	in gene	ActReg chr1 #1308	1	1	0
1309	1	159,824,698	159,825,150	452	1	9.929	9.286	12.357	18	12	21	1	1	2	C1orf204, VSIG8	213, 7523	in gene, in gene	ActReg chr1 #1309	0	0	1
1310	1	159,879,929	159,880,746	817	1	6.731	11.423	3.692	11	17	7	0	0	1	TAGLN2	14,947	downstream	ActReg chr1 #1310	0	1	0
1311	1	159,893,975	159,895,798	1,823	3	15.105	15.895	8.982	33	33	26	1	1	2	TAGLN2, IGSF9	398, 20500	in gene, downstream	ActReg chr1 #1311	1	1	1
1312	1	160,000,771	160,002,245	1,474	2	10.783	13	5.304	23	25	12	1	1	2	PIGM, KCNJ10	275, 38543	in gene, downstream	ActReg chr1 #1312	1	1	0
1313	1	160,031,571	160,032,499	928	1	4.31	6.897	11.069	7	12	17	0	0	1	KCNJ10	8,016	in gene	ActReg chr1 #1313	0	0	1
1314	1	160,053,942	160,054,699	757	1	5.083	10.208	13.625	8	16	18	1	0	2	KCNJ9, IGSF8	2960, 14088	in gene, downstream	ActReg chr1 #1314	0	0	1
1315	1	160,068,015	160,068,520	505	1	4.312	9.625	11.25	9	14	18	1	1	2	KCNJ9, IGSF8	16907, 141	downstream, in gene	ActReg chr1 #1315	0	0	1
1316	1	160,175,147	160,176,359	1,212	1	8.474	12.447	8.324	14	20	18	1	1	3	CASQ1, PEA15, DCAF8	15468, 628, 56597	downstream, in gene, downstream	ActReg chr1 #1316	0	1	0
1317	1	160,231,702	160,232,593	891	3	12.056	13.571	14.893	22	20	31	1	2	3	DCAF8, LOC100287049, LOC100505665	203, 9443, 629	in gene, in gene, in gene	ActReg chr1 #1317	1	1	1
1318	1	160,254,505	160,255,316	811	2	13.04	11.92	7.8	23	26	15	0	1	2	PEX19, COPA	31, 58444	in gene, downstream	ActReg chr1 #1318	1	1	0
1319	1	160,369,677	160,370,335	658	1	3.9	6	11.05	7	9	16	1	1	1	VANGL2	-358	upstream	ActReg chr1 #1319	0	0	1
1320	1	160,795,809	160,796,495	686	2	11.857	12.524	1.778	24	25	4	0	0	2	LY9, CD244	30224, 36540	in gene, downstream	ActReg chr1 #1320	1	1	0
1321	1	161,008,435	161,008,966	531	1	4.917	4.75	11.706	9	8	16	1	1	3	TSTD1, USF1, ARHGAP30	74, 7057, 31060	in gene, downstream, downstream	ActReg chr1 #1321	0	0	1
1322	1	161,019,012	161,019,506	494	1	6.267	4.667	11.267	8	7	18	0	1	2	USF1, ARHGAP30	-3502, 20501	upstream, in gene	ActReg chr1 #1322	0	0	1
1323	1	161,087,190	161,088,317	1,127	3	12.371	12.771	11.857	23	16	24	1	2	3	PFDN2, NIT1, DEDD	113, -109, 14725	in gene, upstream, downstream	ActReg chr1 #1323	1	1	1
1324	1	161,093,853	161,094,437	584	1	3.714	6.895	10.421	7	9	17	0	1	3	PFDN2, NIT1, DEDD	-6279, 6283, 8333	upstream, in gene, in gene	ActReg chr1 #1324	0	0	1
1325	1	161,101,934	161,103,158	1,224	2	12.658	13.921	4.294	29	26	9	1	1	2	NIT1, DEDD	14684, -68	downstream, upstream	ActReg chr1 #1325	1	1	0
1326	1	161,123,595	161,124,219	624	2	10.79	13.947	12	18	25	18	0	2	2	UFC1, USP21	373, -5347	in gene, upstream	ActReg chr1 #1326	0	1	1
1327	1	161,128,389	161,129,903	1,514	3	10.766	10.702	8.913	18	16	17	1	2	3	UFC1, USP21, PPOX	5612, -108, -7035	downstream, upstream, upstream	ActReg chr1 #1327	1	1	1
1328	1	161,130,441	161,131,165	724	1	4.955	6.682	12.454	8	11	18	0	2	4	UFC1, USP21, PPOX, B4GALT3	7269, 1549, -5378, 16511	downstream, in gene, upstream, downstream	ActReg chr1 #1328	0	0	1
1329	1	161,135,469	161,137,078	1,609	2	18.94	22.92	9.58	59	63	13	1	1	4	UFC1, USP21, PPOX, B4GALT3	12739, 7019, 92, 11041	downstream, downstream, in gene, downstream	ActReg chr1 #1329	1	1	0
1330	1	161,160,509	161,161,163	654	1	3.286	5.905	12.809	7	10	18	0	0	2	ADAMTS4, NDUFS2	8009, -8269	in gene, upstream	ActReg chr1 #1330	0	0	1
1331	1	161,163,342	161,163,916	574	1	7.5	6.722	10.833	12	11	15	0	1	2	ADAMTS4, NDUFS2	5216, -5476	in gene, upstream	ActReg chr1 #1331	0	0	1
1332	1	161,167,662	161,168,414	752	1	5	6.652	13.957	9	10	20	0	2	2	ADAMTS4, NDUFS2	807, -1067	in gene, upstream	ActReg chr1 #1332	0	0	1
1333	1	161,171,788	161,172,654	866	1	11.482	15.815	10.741	16	26	17	1	1	2	ADAMTS4, NDUFS2	-3376, 3116	upstream, in gene	ActReg chr1 #1333	0	1	0
1334	1	161,195,364	161,196,497	1,133	1	7.514	11.943	6.943	13	19	15	0	2	4	FCER1G, APOA2, TOMM40L, NR1I3	10843, -2512, 97, 12070	downstream, upstream, in gene, downstream	ActReg chr1 #1334	0	1	0
1335	1	161,348,677	161,349,299	622	2	9.368	9.947	3.316	20	21	5	0	0	0				ActReg chr1 #1335	1	1	0
1336	1	161,359,288	161,360,704	1,416	3	10.711	11.644	5.951	19	25	12	1	0	1	LOC100505703	-9,203	upstream	ActReg chr1 #1336	1	1	0
1337	1	161,368,779	161,370,163	1,384	3	13.605	14.907	12.976	24	24	27	1	1	1	LOC100505703	272	in gene	ActReg chr1 #1337	1	1	1
1338	1	161,391,517	161,392,166	649	3	10.667	9.905	9.632	16	21	19	0	0	1	LOC100505703	22,642	in gene	ActReg chr1 #1338	1	1	1
1339	1	161,409,557	161,410,039	482	1	7.867	10.467	14.133	12	14	21	1	0	0				ActReg chr1 #1339	0	0	1
1340	1	161,410,041	161,410,690	649	1	7.143	10	7.048	13	18	13	1	0	0				ActReg chr1 #1340	0	1	0
1341	1	161,468,351	161,468,943	592	1	10.579	11.21	1	18	20	1	0	1	1	FCGR2A	-6,558	upstream	ActReg chr1 #1341	0	1	0
1342	1	161,493,441	161,493,988	547	1	9.588	8.706	14.235	16	12	24	1	1	2	FCGR2A, HSPA6	18509, -322	downstream, upstream	ActReg chr1 #1342	0	0	1
1343	1	161,499,973	161,500,300	327	1	6.5	8.1	13.6	10	10	19	1	0	1	HSPA6	6,100	downstream	ActReg chr1 #1343	0	0	1
1344	1	161,500,512	161,501,191	679	2	5.955	10.273	8.636	14	15	15	1	0	1	HSPA6	6,815	downstream	ActReg chr1 #1344	0	1	1
1345	1	161,509,606	161,510,303	697	3	13.524	16.667	11.095	25	33	22	0	0	1	FCGR3A	10,459	downstream	ActReg chr1 #1345	1	1	1
1346	1	161,691,504	161,692,274	770	2	13.083	16.167	5.455	32	34	12	0	1	2	FCRLA, FCRLB	15127, -568	downstream, upstream	ActReg chr1 #1346	1	1	0
1347	1	161,695,350	161,696,905	1,555	3	14.082	14.792	10.347	29	25	22	1	0	1	FCRLB	3,670	in gene	ActReg chr1 #1347	1	1	1
1348	1	161,699,853	161,700,497	644	1	13.95	9.3	2.85	19	13	5	0	0	1	FCRLB	7,718	downstream	ActReg chr1 #1348	1	0	0
1349	1	161,719,114	161,720,391	1,277	3	14.375	15.525	8.175	31	29	22	1	1	1	DUSP12	171	in gene	ActReg chr1 #1349	1	1	1
1350	1	161,735,813	161,736,506	693	2	12.524	12.905	9	21	21	13	0	1	2	DUSP12, ATF6	16578, 75	downstream, in gene	ActReg chr1 #1350	1	1	0
1351	1	161,942,781	161,943,284	503	1	2.688	5.375	11.125	6	9	17	0	0	1	OLFML2B	50,612	downstream	ActReg chr1 #1351	0	0	1
1352	1	161,972,775	161,973,478	703	1	11.682	12.454	5.455	15	19	8	0	0	1	OLFML2B	20,518	in gene	ActReg chr1 #1352	0	1	0
1353	1	162,024,817	162,025,428	611	1	8.474	12.737	4.158	10	19	7	0	0	0				ActReg chr1 #1353	0	1	0
1354	1	162,279,845	162,280,755	910	2	15.393	14.536	2.174	30	33	5	0	0	1	NOS1AP	240,719	in gene	ActReg chr1 #1354	1	1	0
1355	1	162,374,409	162,375,111	702	1	10.773	6.182	3.684	19	12	7	0	0	1	SH2D1B	7,168	in gene	ActReg chr1 #1355	1	0	0
1356	1	162,467,487	162,468,437	950	3	12.8	12.433	7.8	21	28	17	1	1	1	UHMK1	998	in gene	ActReg chr1 #1356	1	1	1
1357	1	162,530,343	162,532,491	2,148	3	10.746	13.672	7.033	20	28	24	1	1	1	UAP1	121	in gene	ActReg chr1 #1357	1	1	1
1358	1	162,575,169	162,575,815	646	1	7.1	10.3	1.818	13	16	3	0	0	1	UAP1	44,196	downstream	ActReg chr1 #1358	0	1	0
1359	1	162,602,585	162,603,378	793	1	8.8	10.64	2.4	16	17	5	0	1	1	DDR2	753	in gene	ActReg chr1 #1359	0	1	0
1360	1	162,889,223	162,889,800	577	1	5.222	6.889	11.389	7	11	14	0	0	0				ActReg chr1 #1360	0	0	1
1361	1	162,993,274	162,993,834	560	1	3.5	4.611	11.278	6	7	16	0	0	0				ActReg chr1 #1361	0	0	1
1362	1	163,005,438	163,006,123	685	1	10.636	10.046	1.4	18	18	2	0	0	0				ActReg chr1 #1362	1	0	0
1363	1	163,017,602	163,018,553	951	1	7.034	10.345	4.552	14	16	9	0	0	0				ActReg chr1 #1363	0	1	0
1364	1	163,291,197	163,292,301	1,104	2	21.057	25.657	8.743	51	66	18	1	1	1	NUF2	26	in gene	ActReg chr1 #1364	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1365	1	163,468,876	163,469,146	270	1	2.25	2.125	9.125	5	3	11	0	0	0				ActReg chr1 #1365	0	0	1
1366	1	164,527,728	164,528,329	601	1	10.632	8.158	3.053	17	14	5	0	1	1	PBX1	-774	upstream	ActReg chr1 #1366	1	0	0
1367	1	164,573,308	164,573,609	301	1	2	4.8	10.5	4	6	15	0	0	1	PBX1	44,656	in gene	ActReg chr1 #1367	0	0	1
1368	1	165,131,967	165,132,734	767	1	13.625	16.375	3.375	24	40	6	0	0	0				ActReg chr1 #1368	0	1	0
1369	1	165,508,346	165,509,261	915	2	11.793	10.345	3.154	20	21	5	0	1	2	LOC400794, LRRC52	42538, -4675	in gene, upstream	ActReg chr1 #1369	1	1	0
1370	1	165,599,682	165,601,140	1,458	3	10.533	12.556	9.044	23	20	17	1	1	1	MGST3	-39	upstream	ActReg chr1 #1370	1	1	1
1371	1	165,667,390	165,668,248	858	1	13.444	11.259	9.208	19	19	18	1	1	1	ALDH9A1	81	in gene	ActReg chr1 #1371	1	0	0
1372	1	165,737,712	165,738,582	870	2	13.111	13.148	8.037	27	21	13	1	2	2	TMCO1, LOC100147773	-12, -19	upstream, upstream	ActReg chr1 #1372	1	1	0
1373	1	165,797,405	165,797,995	590	1	10.684	8.789	3.684	15	13	6	1	1	1	UCK2	810	in gene	ActReg chr1 #1373	1	0	0
1374	1	165,910,408	165,910,980	572	1	4.176	5.278	13.444	6	9	21	1	0	0				ActReg chr1 #1374	0	0	1
1375	1	165,918,556	165,919,183	627	1	13.65	11.35	3.4	22	18	6	0	0	0				ActReg chr1 #1375	1	0	0
1376	1	165,977,696	165,978,037	341	1	5.364	2	10.727	7	3	14	0	0	0				ActReg chr1 #1376	0	0	1
1377	1	166,135,923	166,136,959	1,036	2	9.5	9.906	2.933	17	19	5	1	1	1	FAM78B	-483	upstream	ActReg chr1 #1377	1	1	0
1378	1	166,139,711	166,141,121	1,410	2	11.889	12.911	2.22	21	23	5	0	1	1	FAM78B	-4,458	upstream	ActReg chr1 #1378	1	1	0
1379	1	166,245,066	166,245,499	433	1	4.692	6.308	12.769	6	9	19	0	0	0				ActReg chr1 #1379	0	0	1
1380	1	166,312,491	166,312,912	421	1	4.769	1.111	10.692	9	2	17	0	0	0				ActReg chr1 #1380	0	0	1
1381	1	166,785,619	166,786,380	761	1	4.25	4.417	12.375	7	8	18	0	0	0				ActReg chr1 #1381	0	0	1
1382	1	166,808,127	166,808,872	745	1	9.913	13.125	5.75	17	24	9	1	1	1	POGK	-225	upstream	ActReg chr1 #1382	0	1	0
1383	1	166,844,669	166,846,004	1,335	3	15.5	13.976	7.806	38	35	17	1	1	1	TADA1	318	in gene	ActReg chr1 #1383	1	1	1
1384	1	166,921,361	166,922,185	824	2	12.769	12.192	1.647	23	22	2	0	0	1	IL6R2	22,788	in gene	ActReg chr1 #1384	1	1	0
1385	1	167,090,432	167,091,184	752	1	8.333	9.667	11.542	12	14	17	1	0	1	DUSP27	26,721	in gene	ActReg chr1 #1385	0	0	1
1386	1	167,105,307	167,106,043	736	1	9.826	12.913	3.048	16	22	5	0	0	1	DUSP27	41,588	downstream	ActReg chr1 #1386	0	1	0
1387	1	167,126,242	167,126,834	592	1	8.833	12.389	2.538	13	21	5	0	0	0				ActReg chr1 #1387	0	1	0
1388	1	167,164,987	167,165,594	607	1	12.579	7.368	4.333	22	11	7	0	0	0				ActReg chr1 #1388	1	0	0
1389	1	167,189,195	167,190,554	1,359	3	13.976	13.405	9.548	27	21	16	1	1	1	POU2F1	-269	upstream	ActReg chr1 #1389	1	1	1
1390	1	167,190,944	167,191,914	970	2	10.032	10.516	5.323	22	15	8	1	1	1	POU2F1	1,286	in gene	ActReg chr1 #1390	1	1	0
1391	1	167,408,288	167,408,893	605	1	7.263	4.526	11.579	12	8	17	1	0	1	CD247	79,257	in gene	ActReg chr1 #1391	0	0	1
1392	1	167,486,497	167,487,252	755	1	10.652	15.783	6.043	17	23	11	0	1	1	CD247	973	in gene	ActReg chr1 #1392	0	1	0
1393	1	167,522,516	167,523,010	494	1	13	11.438	4.188	18	18	8	1	1	1	CREG1	293	in gene	ActReg chr1 #1393	1	0	0
1394	1	167,532,377	167,533,555	1,178	1	10.324	13.432	2.781	20	22	6	0	0	1	CREG1	-9,910	upstream	ActReg chr1 #1394	0	1	0
1395	1	167,683,273	167,685,154	1,881	4	14.542	15.661	8.593	31	39	21	2	1	2	RCSD1, MPZL1	84739, -6974	downstream, upstream	ActReg chr1 #1395	1	1	1
1396	1	167,690,417	167,691,715	1,298	1	12.049	16.024	6.415	16	26	10	1	1	1	MPZL1	-121	upstream	ActReg chr1 #1396	0	1	0
1397	1	167,904,597	167,906,862	2,265	4	10	11.409	10.62	16	21	30	1	2	2	BRP44, DCAF6	549, -179	in gene, upstream	ActReg chr1 #1397	1	1	1
1398	1	168,106,307	168,106,753	446	1	9.143	10.5	12	12	16	17	1	1	1	GPR161	-906	upstream	ActReg chr1 #1398	0	0	1
1399	1	168,147,582	168,149,061	1,479	1	8.66	13.575	8.319	13	23	21	1	1	1	TIPRL	150	in gene	ActReg chr1 #1399	0	1	0
1400	1	168,195,317	168,195,842	525	1	10.235	11.118	13.706	16	17	18	1	1	1	SFT2D2	324	in gene	ActReg chr1 #1400	0	0	1
1401	1	168,206,137	168,206,841	704	1	11.591	13.182	2.85	19	21	7	0	0	1	SFT2D2	11,234	in gene	ActReg chr1 #1401	0	1	0
1402	1	168,290,001	168,290,694	693	1	10.954	10.5	2.364	15	18	4	0	0	1	TBX19	40,069	downstream	ActReg chr1 #1402	0	1	0
1403	1	168,435,146	168,435,873	727	1	11.826	10.13	1.619	16	18	4	0	0	0				ActReg chr1 #1403	1	0	0
1404	1	168,445,739	168,446,954	1,215	1	10.684	10.342	2.516	18	18	5	0	0	0				ActReg chr1 #1404	1	0	0
1405	1	168,592,137	168,592,822	685	1	11.524	8.048	1.5	16	14	3	0	0	0				ActReg chr1 #1405	1	0	0
1406	1	168,678,246	168,679,848	1,602	1	10.88	8.12	4.2	16	15	8	0	0	1	DPT	19,395	in gene	ActReg chr1 #1406	1	0	0
1407	1	168,688,385	168,689,221	836	2	12.615	10.923	2.231	26	21	5	0	0	1	DPT	9,639	in gene	ActReg chr1 #1407	1	1	0
1408	1	169,074,691	169,075,838	1,147	1	8.057	12.886	6.533	13	21	14	1	1	1	ATP1B1	-683	upstream	ActReg chr1 #1408	0	1	0
1409	1	169,075,844	169,076,483	639	1	10.15	14.5	4.5	18	20	9	1	1	1	ATP1B1	216	in gene	ActReg chr1 #1409	0	1	0
1410	1	169,085,024	169,085,808	784	1	11.32	13.4	3.88	20	23	6	0	0	1	ATP1B1	9,469	in gene	ActReg chr1 #1410	0	1	0
1411	1	169,132,229	169,133,005	776	1	10.375	8.75	1.765	16	17	3	0	0	1	NME7	204,569	in gene	ActReg chr1 #1411	1	0	0
1412	1	169,280,993	169,281,889	896	2	18.679	26.786	2.208	50	73	4	0	0	1	NME7	55,745	in gene	ActReg chr1 #1412	1	1	0
1413	1	169,564,801	169,565,406	605	1	9.611	11.778	4.412	19	20	7	0	0	2	F5, SELP	-9334, 34274	upstream, in gene	ActReg chr1 #1413	0	1	0
1414	1	169,763,744	169,764,527	783	2	13.24	12.92	5.88	18	23	10	1	2	2	C1orf156, C1orf112	-104, -415	upstream, upstream	ActReg chr1 #1414	1	1	0
1415	1	169,862,846	169,863,568	722	2	12.522	14.783	4.5	22	35	9	1	1	1	SCYL3	-131	upstream	ActReg chr1 #1415	1	1	0
1416	1	169,968,348	169,968,975	627	1	5	11.4	2.231	9	16	4	0	0	1	KIFAP3	75,218	in gene	ActReg chr1 #1416	0	1	0
1417	1	170,043,180	170,044,246	1,066	2	16.333	13.454	4.818	26	23	12	1	1	1	KIFAP3	166	in gene	ActReg chr1 #1417	1	1	0
1418	1	170,083,495	170,084,993	1,498	2	10.468	13.809	2.048	31	37	4	0	0	0				ActReg chr1 #1418	1	1	0
1419	1	170,265,755	170,266,250	495	1	10.062	8.938	2.562	16	16	5	0	0	0				ActReg chr1 #1419	1	0	0
1420	1	170,489,576	170,490,002	426	1	10.923	8.077	1.125	14	14	2	0	0	0				ActReg chr1 #1420	1	0	0
1421	1	170,500,683	170,501,988	1,305	3	14.951	13.561	7.317	28	31	20	0	1	1	GORAB	72	in gene	ActReg chr1 #1421	1	1	1
1422	1	170,630,355	170,630,804	449	1	6.571	3.5	11.643	12	5	20	1	2	2	PRRX1, LOC100127910	-2734, -5768	upstream, upstream	ActReg chr1 #1422	0	0	1
1423	1	170,667,753	170,668,275	522	1	5.625	11.688	4.429	10	19	8	0	0	1	PRRX1	34,701	in gene	ActReg chr1 #1423	0	1	0
1424	1	170,677,077	170,677,702	625	1	11	8.3	2.077	17	12	3	0	0	1	PRRX1	44,076	in gene	ActReg chr1 #1424	1	0	0
1425	1	170,776,307	170,777,107	800	2	12.12	10.8	4.08	25	14	6	0	0	0				ActReg chr1 #1425	1	1	0
1426	1	171,196,818	171,197,252	434	1	10.643	7.929	1.778	15	12	2	0	0	0				ActReg chr1 #1426	1	0	0
1427	1	171,206,481	171,207,207	726	1	3.783	4.261	10.957	8	7	15	0	0	0				ActReg chr1 #1427	0	0	1
1428	1	171,282,841	171,283,485	644	1	6.15	11.25	2.692	10	18	4	0	1	1	FMO4	-323	upstream	ActReg chr1 #1428	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1429	1	171,453,903	171,455,296	1,393	2	11.364	10.204	4.146	26	22	12	1	1	1	BAT2L2	-67	upstream	ActReg chr1 #1429	1	1	0
1430	1	171,710,559	171,711,862	1,303	3	18.61	19.659	8.878	52	45	29	1	1	1	VAMP4	169	in gene	ActReg chr1 #1430	1	1	1
1431	1	171,763,105	171,763,936	831	2	12.423	10.269	2.412	24	23	4	0	0	1	METTL13	12,759	in gene	ActReg chr1 #1431	1	1	0
1432	1	171,810,068	171,811,417	1,349	4	9.762	12.262	12.571	18	22	22	1	1	1	DNM3	121	in gene	ActReg chr1 #1432	1	1	1
1433	1	171,813,384	171,814,092	708	1	11.227	6.227	2.765	15	8	5	0	0	1	DNM3	5,117	in gene	ActReg chr1 #1433	1	0	0
1434	1	172,412,648	172,413,817	1,169	2	28.444	30.389	5.686	74	100	8	1	1	2	C1orf105, PIGC	23404, -2	in gene, upstream	ActReg chr1 #1434	1	1	0
1435	1	172,501,104	172,502,978	1,874	3	15.356	14.763	9.661	33	26	28	1	1	1	C1orf9	-219	upstream	ActReg chr1 #1435	1	1	1
1436	1	172,557,781	172,558,543	762	2	13.417	11.458	3.118	23	17	5	0	0	1	C1orf9	55,902	in gene	ActReg chr1 #1436	1	1	0
1437	1	172,578,534	172,579,121	587	1	10.444	5.833	1	17	9	1	0	0	1	C1orf9	76,567	in gene	ActReg chr1 #1437	1	0	0
1438	1	172,607,748	172,609,165	1,417	2	17.591	14.523	2.786	49	35	7	0	0	0				ActReg chr1 #1438	1	1	0
1439	1	172,623,541	172,624,129	588	1	6.368	11.579	4.737	9	15	7	0	1	1	FASLG	-4,350	upstream	ActReg chr1 #1439	0	1	0
1440	1	172,668,150	172,668,807	657	1	11.381	7.905	2.778	17	14	4	0	0	0				ActReg chr1 #1440	1	0	0
1441	1	172,902,971	172,903,837	866	2	11.741	11.444	2.481	17	20	4	0	0	0				ActReg chr1 #1441	1	1	0
1442	1	172,917,404	172,918,151	747	1	8.375	13.542	4.364	21	29	7	0	0	0				ActReg chr1 #1442	0	1	0
1443	1	172,968,285	172,968,948	663	1	12.429	6.81	2.333	25	12	4	0	0	0				ActReg chr1 #1443	1	0	0
1444	1	173,031,159	173,031,829	670	1	16.095	17.476	3	32	32	7	0	0	0				ActReg chr1 #1444	0	1	0
1445	1	173,091,990	173,092,599	609	1	11.053	7.263	3.308	18	10	6	0	0	0				ActReg chr1 #1445	1	0	0
1446	1	173,238,487	173,239,152	665	1	11.714	9.714	2.625	18	13	3	0	0	1	LOC100506023	207,475	in gene	ActReg chr1 #1446	1	0	0
1447	1	173,445,689	173,446,324	635	1	7.8	11	8.1	16	16	14	1	2	2	LOC100506023, PRDX6	288, -480	in gene, upstream	ActReg chr1 #1447	0	1	0
1448	1	173,683,646	173,684,610	964	2	14.645	13.129	7.138	26	32	12	1	1	1	KLHL20	48	in gene	ActReg chr1 #1448	1	1	0
1449	1	173,793,174	173,794,377	1,203	2	14.71	12.237	8.237	26	25	13	1	2	2	CENPL, DARS2	2, -22	in gene, upstream	ActReg chr1 #1449	1	1	0
1450	1	173,836,482	173,837,918	1,436	3	12.409	14.182	12.068	21	28	22	1	12	14	DARS2, LOC100506046, GAS5, SNORD81, SNORD47, SNORD80, SNORD79, SNORD78, SNORD44, SNORD77, SNORD76, SNORD75, SNORD74, ZBTB37	45403, 5910, -75, -3845, -3617, -3159, -2632, -2376, -2034, -1691, -1347, -1124, -317, -293	downstream, downstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr1 #1450	1	1	1
1451	1	173,839,390	173,840,072	682	1	7.091	12.409	2.857	11	18	4	0	12	13	LOC100506046, GAS5, SNORD81, SNORD47, SNORD80, SNORD79, SNORD78, SNORD44, SNORD77, SNORD76, SNORD75, SNORD74, ZBTB37	8441, -2606, -6376, -6148, -5690, -5163, -4907, -4565, -4222, -3878, -3655, -2848, 2238	downstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, in gene	ActReg chr1 #1451	0	1	0
1452	1	173,990,651	173,991,948	1,297	1	9.878	15.585	7.359	22	25	15	1	0	0				ActReg chr1 #1452	0	1	0
1453	1	174,021,092	174,021,703	611	1	7.368	10.684	3.312	13	19	6	0	0	0				ActReg chr1 #1453	0	1	0
1454	1	174,128,035	174,129,378	1,343	2	10.524	12.548	10.738	18	20	24	1	1	1	RABGAP1L	72	in gene	ActReg chr1 #1454	0	1	1
1455	1	174,367,081	174,367,703	622	1	7.947	10.368	4.684	15	14	7	0	0	1	RABGAP1L	238,758	in gene	ActReg chr1 #1455	0	1	0
1456	1	174,628,840	174,629,386	546	1	8.294	10.823	3.235	14	17	6	0	0	1	RABGAP1L	500,479	in gene	ActReg chr1 #1456	0	1	0
1457	1	174,968,200	174,969,725	1,525	4	13.085	14.617	9.383	30	28	17	1	1	2	LOC100506087, CACYBP	35057, 391	downstream, in gene	ActReg chr1 #1457	1	1	1
1458	1	175,138,263	175,139,739	1,476	2	11.022	12.935	4.13	19	19	8	0	0	1	KIAA0040	23,228	in gene	ActReg chr1 #1458	1	1	0
1459	1	175,166,099	175,167,218	1,119	1	10.6	6.229	3	20	10	7	0	1	1	KIAA0040	-4,429	upstream	ActReg chr1 #1459	1	0	0
1460	1	175,568,423	175,568,928	506	1	5.25	4.562	14.938	9	8	25	1	0	1	TNR	144,076	in gene	ActReg chr1 #1460	0	0	1
1461	1	175,642,214	175,643,280	1,066	1	8.697	12.576	2.8	13	22	5	0	0	1	TNR	70,005	in gene	ActReg chr1 #1461	0	1	0
1462	1	175,694,578	175,695,471	893	2	13.25	18.964	3	34	43	7	0	0	1	TNR	17,728	in gene	ActReg chr1 #1462	1	1	0
1463	1	175,711,949	175,713,154	1,205	2	10.868	11.816	3.657	25	22	8	0	1	1	TNR	201	in gene	ActReg chr1 #1463	1	1	0
1464	1	176,175,805	176,177,141	1,336	2	10.929	11.238	7.25	18	21	12	1	1	1	RFWD2	-103	upstream	ActReg chr1 #1464	1	1	0
1465	1	176,486,493	176,487,053	560	1	8.167	11.167	3	11	22	5	0	0	1	PAPPA2	54,466	in gene	ActReg chr1 #1465	0	1	0
1466	1	177,177,954	177,178,993	1,039	2	13.031	14.75	2.621	28	33	7	0	0	1	FAM5B	37,840	in gene	ActReg chr1 #1466	1	1	0
1467	1	177,198,886	177,199,368	482	1	4.333	7.533	10.4	8	13	17	0	0	1	FAM5B	58,494	in gene	ActReg chr1 #1467	0	0	1
1468	1	177,225,308	177,225,989	681	1	11.682	11.091	2.636	18	15	7	0	0	1	FAM5B	85,015	in gene	ActReg chr1 #1468	1	0	0
1469	1	177,278,976	177,280,167	1,191	2	11.474	11.579	2.722	22	23	5	0	0	0				ActReg chr1 #1469	1	1	0
1470	1	177,568,160	177,568,729	569	2	10.889	9.278	2.929	22	17	5	0	0	0				ActReg chr1 #1470	1	1	0
1471	1	178,021,869	178,022,549	680	1	10.667	11.809	5.095	15	16	9	0	0	0				ActReg chr1 #1471	0	1	0
1472	1	178,062,114	178,064,182	2,068	2	12.719	14.406	5.593	32	31	10	1	2	2	LOC100302401, RASAL2	-20, 264	upstream, in gene	ActReg chr1 #1472	1	1	0
1473	1	178,095,811	178,096,394	583	2	12	11.278	3.889	23	18	5	0	0	1	RASAL2	33,238	in gene	ActReg chr1 #1473	1	1	0
1474	1	178,386,919	178,387,601	682	1	14.476	9	1	26	16	1	0	0	1	RASAL2	324,396	in gene	ActReg chr1 #1474	1	0	0
1475	1	178,505,777	178,506,696	919	1	11.31	8.966	5.241	18	17	8	0	1	1	C1orf220	-5,695	upstream	ActReg chr1 #1475	1	0	0
1476	1	178,511,037	178,512,761	1,724	3	11.333	12.537	8.944	17	20	18	1	1	1	C1orf220	-32	upstream	ActReg chr1 #1476	1	1	1
1477	1	178,583,413	178,584,084	671	2	10.952	9.905	5.895	18	16	13	0	0	0				ActReg chr1 #1477	1	1	0
1478	1	178,693,890	178,694,316	426	1	8.462	11.077	7.231	10	17	13	1	1	1	RALGPS2	-197	upstream	ActReg chr1 #1478	0	1	0
1479	1	178,994,553	178,995,054	501	1	11.875	15.5	6.467	18	28	12	1	1	1	FAM20B	-271	upstream	ActReg chr1 #1479	0	1	0
1480	1	178,995,280	178,996,294	1,014	2	9.906	10.062	5.071	19	18	10	1	1	1	FAM20B	713	in gene	ActReg chr1 #1480	1	1	0
1481	1	179,050,554	179,051,697	1,143	2	12.167	12.583	6.361	19	19	13	1	1	2	FAM20B, TOR3A	56051, 13	downstream, in gene	ActReg chr1 #1481	1	1	0
1482	1	179,107,879	179,108,295	416	1	5.462	7	12.615	7	9	16	0	0	1	ABL2	90,732	in gene	ActReg chr1 #1482	0	0	1
1483	1	179,262,284	179,263,242	958	3	12.467	11.167	8.567	18	17	18	1	1	1	SOAT1	-254	upstream	ActReg chr1 #1483	1	1	1
1484	1	179,334,719	179,335,537	818	1	10.962	12.5	6.654	15	25	10	1	1	1	C1orf125	273	in gene	ActReg chr1 #1484	0	1	0
1485	1	179,519,575	179,520,900	1,325	2	11.571	13.309	2.61	23	22	6	0	0	2	C1orf125, NPHS2	185382, 24847	in gene, in gene	ActReg chr1 #1485	1	1	0
1486	1	179,782,251	179,783,304	1,053	1	4.394	7.03	11.818	10	14	22	0	0	1	FAM163A	70,479	in gene	ActReg chr1 #1486	0	0	1
1487	1	179,786,814	179,787,390	576	1	2.667	5.222	14.444	4	9	20	0	0	1	FAM163A	74,804	downstream	ActReg chr1 #1487	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIsIandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1488	1	179,850,907	179,852,507	1,600	3	14.98	15.22	11.94	29	24	21	1	2	2	TOR1AIP2, TOR1AIP1	-4766, 287	upstream, in gene	ActReg chr1 #1488	1	1	1
1489	1	179,923,541	179,924,600	1,059	1	10.636	15.939	7.273	18	30	14	1	1	1	CEP350	162	in gene	ActReg chr1 #1489	0	1	0
1490	1	180,151,712	180,152,424	712	1	2.286	6.217	13.348	3	12	18	0	0	1	QSOX1	28,100	in gene	ActReg chr1 #1490	0	0	1
1491	1	180,197,902	180,198,420	518	1	6.938	8.062	11.375	11	10	15	1	1	1	LHX4	-1,281	upstream	ActReg chr1 #1491	0	0	1
1492	1	180,471,077	180,472,434	1,357	2	15.048	18.024	8.333	31	35	15	1	1	1	ACBD6	267	in gene	ActReg chr1 #1492	1	1	0
1493	1	180,601,013	180,602,030	1,017	2	10.062	10.969	6.688	17	19	10	1	1	1	XPR1	375	in gene	ActReg chr1 #1493	1	1	0
1494	1	180,889,445	180,889,839	394	1	1.917	2.083	12.083	3	3	17	0	0	1	KIAA1614	7,329	in gene	ActReg chr1 #1494	0	0	1
1495	1	180,904,611	180,905,572	961	1	3.567	3.367	11.367	9	6	19	1	0	1	KIAA1614	22,778	in gene	ActReg chr1 #1495	0	0	1
1496	1	180,923,443	180,923,874	431	1	4.286	5.071	12	6	9	16	1	0	1	KIAA1614	41,345	downstream	ActReg chr1 #1496	0	0	1
1497	1	180,991,095	180,992,192	1,097	1	9.971	12.829	10.257	15	20	16	2	1	1	STX6	403	in gene	ActReg chr1 #1497	0	1	0
1498	1	181,057,215	181,058,628	1,413	3	12.622	14.444	9.513	24	32	19	1	1	1	IER5	283	in gene	ActReg chr1 #1498	1	1	1
1499	1	181,058,718	181,059,307	589	1	8	11.474	8.111	10	19	13	1	1	1	IER5	1,374	in gene	ActReg chr1 #1499	0	1	0
1500	1	181,074,645	181,075,264	619	1	12	12.05	5.3	16	20	10	1	0	0				ActReg chr1 #1500	0	1	0
1501	1	181,287,162	181,287,541	379	1	4.167	3.417	12.75	8	5	18	1	0	0				ActReg chr1 #1501	0	0	1
1502	1	181,314,600	181,315,238	638	1	3.35	3.6	12.15	7	6	17	0	0	0				ActReg chr1 #1502	0	0	1
1503	1	182,204,685	182,205,968	1,283	2	11.65	10.275	5.825	16	18	12	0	0	0				ActReg chr1 #1503	1	1	0
1504	1	182,557,924	182,558,779	855	1	7.115	11.846	5.615	11	17	9	0	1	2	RNASEL, RGS16	-2243, 15197	upstream, downstream	ActReg chr1 #1504	0	1	0
1505	1	182,572,961	182,573,898	937	2	11.621	14.069	10.241	19	24	17	1	1	1	RGS16	119	in gene	ActReg chr1 #1505	1	1	0
1506	1	182,583,784	182,584,621	837	2	10.231	10.231	8.5	16	17	14	1	1	1	LOC284648	-73	upstream	ActReg chr1 #1506	1	1	0
1507	1	182,720,925	182,722,548	1,623	2	11.726	12.118	2.9	22	23	8	0	0	0				ActReg chr1 #1507	1	1	0
1508	1	182,758,279	182,759,314	1,035	1	9.25	15.094	7.719	19	30	16	1	1	1	NPL	-2,598	upstream	ActReg chr1 #1508	0	1	0
1509	1	182,807,877	182,809,247	1,370	1	9.524	11.809	7.268	16	18	15	1	1	2	NPL, DHX9	47168, 123	downstream, in gene	ActReg chr1 #1509	0	1	0
1510	1	182,991,214	182,992,225	1,011	1	7.469	11.188	7.719	14	18	18	1	1	1	LAMC1	-876	upstream	ActReg chr1 #1510	0	1	0
1511	1	182,992,878	182,993,695	817	2	11.12	13.12	4.52	22	22	11	1	1	1	LAMC1	691	in gene	ActReg chr1 #1511	1	1	0
1512	1	183,203,390	183,204,383	993	1	12.29	10.419	3.968	19	16	8	0	0	1	LAMC2	48,712	in gene	ActReg chr1 #1512	1	0	0
1513	1	183,246,880	183,249,547	2,667	1	10.607	11.738	5.952	19	19	19	0	0	1	NMNAT2	139,524	in gene	ActReg chr1 #1513	0	1	0
1514	1	183,258,192	183,258,763	571	1	4.389	4.611	13.556	7	7	18	0	0	1	NMNAT2	129,260	in gene	ActReg chr1 #1514	0	0	1
1515	1	183,318,152	183,319,579	1,427	1	8.386	11.932	4.35	18	20	11	0	0	1	NMNAT2	68,872	in gene	ActReg chr1 #1515	0	1	0
1516	1	183,385,253	183,387,845	2,592	2	14.123	19.407	5.141	32	48	11	1	1	1	NMNAT2	1,188	in gene	ActReg chr1 #1516	1	1	0
1517	1	183,439,896	183,442,392	2,496	2	12.218	15.192	8.064	23	32	21	1	2	2	LOC100506298, SMG7	-10, -362	upstream, upstream	ActReg chr1 #1517	1	1	0
1518	1	183,569,154	183,569,829	675	1	14.762	11.476	2.167	31	20	6	0	0	1	NCF2	-9,435	upstream	ActReg chr1 #1518	1	0	0
1519	1	183,604,457	183,605,660	1,203	3	12.378	12.432	11.351	25	20	23	1	2	4	ARPC5, LOC100292409, RGL1, APOBEC4	-73, 3349, -150, 17390	upstream, downstream, upstream, downstream	ActReg chr1 #1519	1	1	1
1520	1	183,912,020	183,912,717	697	1	9.091	11.409	3.429	18	18	6	0	0	1	GLT25D2	94,495	in gene	ActReg chr1 #1520	0	1	0
1521	1	184,005,280	184,006,168	888	1	3.192	6.536	12.821	7	10	19	1	1	1	GLT25D2	1,139	in gene	ActReg chr1 #1521	0	0	1
1522	1	184,020,376	184,021,656	1,280	2	10.85	14.8	5.65	25	30	11	1	1	1	TSEN15	205	in gene	ActReg chr1 #1522	1	1	0
1523	1	184,168,109	184,169,535	1,426	1	12.159	9.932	2.032	18	18	4	0	0	0				ActReg chr1 #1523	1	0	0
1524	1	184,584,259	184,585,024	765	2	10.667	11.125	4.5	17	21	7	0	0	1	C1orf21	228,491	in gene	ActReg chr1 #1524	1	1	0
1525	1	184,591,231	184,592,092	861	1	13.37	8.889	5.28	22	14	9	0	0	1	C1orf21	235,511	in gene	ActReg chr1 #1525	1	0	0
1526	1	184,723,079	184,724,863	1,784	3	11.764	13.836	10.018	20	26	20	1	1	1	EDEM3	70	in gene	ActReg chr1 #1526	1	1	1
1527	1	184,836,197	184,836,705	508	1	11.312	10.438	2	14	14	3	0	0	1	FAM129A	-107,231	in gene	ActReg chr1 #1527	1	0	0
1528	1	185,014,288	185,015,298	1,010	1	10.781	8.406	6.034	18	13	11	1	1	1	RNF2	242	in gene	ActReg chr1 #1528	1	0	0
1529	1	185,125,465	185,127,014	1,549	2	10.551	10.959	10.553	16	16	18	1	2	2	C1orf25, C1orf26	-123, 47	upstream, in gene	ActReg chr1 #1529	0	1	1
1530	1	185,285,252	185,287,138	1,886	1	9.655	13.407	7.39	15	24	16	1	1	1	IVNS1ABP	266	in gene	ActReg chr1 #1530	0	1	0
1531	1	185,342,948	185,343,629	681	1	12.381	10.191	3.263	20	15	5	0	0	0				ActReg chr1 #1531	1	0	0
1532	1	185,378,651	185,379,867	1,216	2	11.737	11.816	2.355	19	22	5	0	0	0				ActReg chr1 #1532	1	1	0
1533	1	185,452,812	185,454,003	1,191	2	12.405	13.46	2.903	23	27	8	0	0	0				ActReg chr1 #1533	1	1	0
1534	1	185,615,215	185,615,753	538	1	8.765	10.941	0	14	16	0	0	0	0				ActReg chr1 #1534	0	1	0
1535	1	185,703,150	185,703,964	814	1	10.32	15.36	6.88	18	31	10	1	1	1	HMCN1	-126	upstream	ActReg chr1 #1535	0	1	0
1536	1	185,759,262	185,760,106	844	1	9.259	10.778	2.944	14	16	6	0	0	1	HMCN1	56,001	in gene	ActReg chr1 #1536	0	1	0
1537	1	186,152,199	186,153,143	944	1	10.31	7.793	3.893	18	14	9	0	0	1	HMCN1	448,988	in gene	ActReg chr1 #1537	1	0	0
1538	1	186,156,539	186,157,890	1,351	2	15.512	14.721	3.463	23	29	9	0	0	1	HMCN1	453,531	in gene	ActReg chr1 #1538	1	1	0
1539	1	186,177,813	186,178,549	736	1	12	10	4	18	17	8	0	0	0				ActReg chr1 #1539	1	0	0
1540	1	186,205,514	186,206,710	1,196	2	13.297	11.46	3.387	25	23	6	0	0	0				ActReg chr1 #1540	1	1	0
1541	1	186,343,998	186,345,178	1,180	2	16.811	16.378	7.946	35	23	17	1	2	2	TPR, C1orf27	-131, -302	upstream, upstream	ActReg chr1 #1541	1	1	0
1542	1	186,447,583	186,448,139	556	2	8.222	10.333	1.778	17	16	2	0	0	0				ActReg chr1 #1542	1	1	0
1543	1	186,649,632	186,650,187	555	1	7.444	10.556	6.333	12	16	10	1	1	1	PTGS2	-350	upstream	ActReg chr1 #1543	0	1	0
1544	1	187,660,424	187,661,137	713	2	10.727	12	1.167	23	20	2	0	0	0				ActReg chr1 #1544	1	1	0
1545	1	187,811,583	187,812,221	638	1	10.6	6.55	3.8	16	10	8	0	0	0				ActReg chr1 #1545	1	0	0
1546	1	188,639,781	188,640,490	709	1	11.182	15.136	1.941	19	29	4	0	0	0				ActReg chr1 #1546	0	1	0
1547	1	188,826,665	188,827,320	655	1	3.8	3.75	14.45	6	7	21	0	0	0				ActReg chr1 #1547	0	0	1
1548	1	188,856,935	188,858,040	1,105	2	12.353	13.794	2.387	21	20	7	0	0	0				ActReg chr1 #1548	1	1	0
1549	1	189,586,015	189,586,350	335	1	10.727	7.273	2.182	15	10	3	0	0	0				ActReg chr1 #1549	1	0	0
1550	1	189,627,581	189,627,995	414	1	10.846	8.077	2.818	12	12	4	0	0	0				ActReg chr1 #1550	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1551	1	189,991,730	189,992,369	639	1	10.1	7.6	1.467	20	15	2	0	0	0				ActReg chr1 #1551	1	0	0
1552	1	190,751,075	190,751,419	344	1	3.3	5.8	12.6	5	8	16	0	0	1	LOC440704	-9,391	upstream	ActReg chr1 #1552	0	0	1
1553	1	192,194,946	192,195,455	509	1	10.467	9.333	1.857	16	14	2	0	0	0				ActReg chr1 #1553	1	0	0
1554	1	192,500,122	192,500,627	505	1	5.625	10.562	2.188	7	18	4	0	0	0				ActReg chr1 #1554	0	1	0
1555	1	192,519,829	192,520,621	792	2	11.72	11	1.75	18	25	3	0	0	0				ActReg chr1 #1555	1	1	0
1556	1	192,777,124	192,778,604	1,480	1	9.435	11.891	6.884	20	20	12	1	1	1	RGS2	-305	upstream	ActReg chr1 #1556	0	1	0
1557	1	193,027,357	193,029,430	2,073	3	12.8	14.815	10.141	34	35	24	1	2	2	UCHL5, TROVE2	128, -159	in gene, upstream	ActReg chr1 #1557	1	1	1
1558	1	193,073,889	193,074,988	1,099	2	8.882	11.588	6.5	15	20	18	1	1	1	GLRX2	806	in gene	ActReg chr1 #1558	0	1	1
1559	1	193,090,546	193,091,709	1,163	3	14.194	14.361	12.833	25	24	24	1	1	1	CDC73	39	in gene	ActReg chr1 #1559	1	1	1
1560	1	193,210,424	193,211,529	1,105	1	4.545	6	12.371	7	11	19	0	0	1	CDC73	119,888	in gene	ActReg chr1 #1560	0	0	1
1561	1	193,427,649	193,428,353	704	1	12	9.455	1.125	15	18	2	0	0	0				ActReg chr1 #1561	1	0	0
1562	1	193,527,452	193,528,059	607	1	7.684	10.421	1.385	11	14	2	0	0	0				ActReg chr1 #1562	0	1	0
1563	1	194,828,234	194,828,545	311	1	5.2	4.9	10	7	10	13	0	0	0				ActReg chr1 #1563	0	0	1
1564	1	195,023,326	195,023,850	524	1	5.933	5.118	13.647	11	7	21	0	0	0				ActReg chr1 #1564	0	0	1
1565	1	195,633,516	195,634,175	659	1	12.55	8.4	2	24	11	2	0	0	0				ActReg chr1 #1565	1	0	0
1566	1	195,917,361	195,917,825	464	1	3.667	5.667	11.067	6	9	17	0	0	0				ActReg chr1 #1566	0	0	1
1567	1	196,149,657	196,150,854	1,197	1	14.474	10.026	2.667	33	19	7	0	0	0				ActReg chr1 #1567	1	0	0
1568	1	196,577,019	196,578,844	1,825	2	10.544	12.737	6.316	21	21	19	1	1	1	KCNT2	-432	upstream	ActReg chr1 #1568	1	1	0
1569	1	196,902,644	196,903,432	788	1	5.28	7.48	12.64	8	11	22	0	0	1	CFHR2	-9,896	upstream	ActReg chr1 #1569	0	0	1
1570	1	197,115,134	197,116,335	1,201	2	11.974	15.632	7.289	26	28	14	0	1	2	ASPM, ZBTB41	90, 53938	in gene, downstream	ActReg chr1 #1570	1	1	0
1571	1	197,169,911	197,171,123	1,212	1	10.026	15.895	7.027	17	37	17	1	1	1	ZBTB41	-845	upstream	ActReg chr1 #1571	0	1	0
1572	1	197,871,326	197,872,391	1,065	2	16.971	16.941	5.061	36	39	12	1	1	2	C1orf53, LHX9	176, -9777	in gene, upstream	ActReg chr1 #1572	1	1	0
1573	1	197,880,496	197,881,095	599	1	6.947	6.684	11.632	10	11	19	1	1	2	C1orf53, LHX9	9113, -840	downstream, upstream	ActReg chr1 #1573	0	0	1
1574	1	197,886,668	197,887,264	596	1	8.316	9.737	13.105	13	16	21	1	0	1	LHX9	5,331	in gene	ActReg chr1 #1574	0	0	1
1575	1	197,987,588	197,988,502	914	1	9.536	12.321	2.643	18	21	6	0	0	0				ActReg chr1 #1575	0	1	0
1576	1	198,090,034	198,090,833	799	1	9.88	13.28	2.714	17	19	8	0	0	0				ActReg chr1 #1576	0	1	0
1577	1	198,126,312	198,126,861	549	2	5.647	11.471	10.615	10	17	18	1	1	1	NEK7	478	in gene	ActReg chr1 #1577	0	1	1
1578	1	198,412,371	198,413,031	660	2	11.238	12.857	3	21	31	5	0	0	0				ActReg chr1 #1578	1	1	0
1579	1	198,682,298	198,682,787	489	1	4.188	9.25	2.6	6	16	3	0	0	1	PTPRC	74,405	in gene	ActReg chr1 #1579	0	1	0
1580	1	198,850,221	198,850,806	585	1	11.556	9.056	2	20	13	3	0	0	0				ActReg chr1 #1580	1	0	0
1581	1	199,711,466	199,712,323	857	2	14.778	13.963	3.733	30	39	7	0	0	0				ActReg chr1 #1581	1	1	0
1582	1	200,008,284	200,008,990	706	1	9.227	12.591	5.591	17	17	10	1	0	1	NR5A2	11,867	in gene	ActReg chr1 #1582	0	1	0
1583	1	200,044,600	200,045,064	464	1	10.067	4.4	1.583	18	8	3	0	0	1	NR5A2	48,062	in gene	ActReg chr1 #1583	1	0	0
1584	1	200,116,909	200,117,492	583	1	5.611	7.111	11.222	8	12	15	1	0	1	NR5A2	120,430	in gene	ActReg chr1 #1584	0	0	1
1585	1	200,149,121	200,150,594	1,473	1	6.333	12.022	3.804	14	18	8	0	0	1	NR5A2	153,087	downstream	ActReg chr1 #1585	0	1	0
1586	1	200,589,428	200,590,354	926	2	13.828	12.172	7.103	24	21	14	1	1	1	KIF14	-29	upstream	ActReg chr1 #1586	1	1	0
1587	1	200,638,343	200,639,558	1,215	3	12.579	17.79	10.629	26	32	21	1	1	1	DDX59	176	in gene	ActReg chr1 #1587	1	1	1
1588	1	200,707,971	200,708,793	822	2	8.565	13.88	9.96	13	25	19	1	1	1	CAMSAP1L1	-304	upstream	ActReg chr1 #1588	0	1	1
1589	1	200,849,250	200,849,969	719	1	9.182	14.273	4.409	18	24	6	0	0	1	GPR25	7,443	downstream	ActReg chr1 #1589	0	1	0
1590	1	200,859,495	200,860,936	1,441	3	14.156	17.156	8.711	32	36	20	1	1	1	C1orf106	-424	upstream	ActReg chr1 #1590	1	1	1
1591	1	200,885,149	200,885,619	470	1	2.2	4.467	11.933	4	7	17	0	1	2	C1orf106, C1orf81	-24745, -1204	downstream, upstream	ActReg chr1 #1591	0	0	1
1592	1	200,940,763	200,941,952	1,189	1	4.189	4.821	12.5	8	9	22	0	0	2	C1orf81, KIF21B	54769, 51471	downstream, in gene	ActReg chr1 #1592	0	0	1
1593	1	200,951,332	200,952,135	803	1	5.083	3.48	12	8	6	15	0	0	1	KIF21B	41,095	in gene	ActReg chr1 #1593	0	0	1
1594	1	200,969,016	200,969,759	743	1	4.783	6.043	12.913	8	12	20	1	0	1	KIF21B	23,441	in gene	ActReg chr1 #1594	0	0	1
1595	1	201,017,471	201,018,108	637	1	6.15	5.45	13.65	9	11	20	0	0	1	CACNA1S	63,905	in gene	ActReg chr1 #1595	0	0	1
1596	1	201,030,997	201,031,515	518	1	5.625	6.25	13.25	10	10	17	0	0	1	CACNA1S	50,438	in gene	ActReg chr1 #1596	0	0	1
1597	1	201,040,332	201,040,891	559	1	5.118	3.529	10.706	7	6	16	0	0	1	CACNA1S	41,083	in gene	ActReg chr1 #1597	0	0	1
1598	1	201,084,268	201,084,963	695	1	5.591	5.909	15.5	9	9	25	1	1	2	CACNA1S, ASCL5	-2921, 14754	upstream, in gene	ActReg chr1 #1598	0	0	1
1599	1	201,185,495	201,186,007	512	1	2.917	3.533	11.25	4	6	15	0	0	1	IGFN1	25,798	in gene	ActReg chr1 #1599	0	0	1
1600	1	201,198,824	201,199,844	1,020	2	12.656	9.75	4.438	19	17	8	0	0	1	IGFN1	39,381	downstream	ActReg chr1 #1600	1	1	0
1601	1	201,224,129	201,225,007	878	1	6	5.815	13.63	9	10	18	0	0	0				ActReg chr1 #1601	0	0	1
1602	1	201,228,819	201,229,327	508	1	4.875	4.875	13.062	8	7	17	0	0	0				ActReg chr1 #1602	0	0	1
1603	1	201,243,942	201,244,508	566	1	10.118	7.706	15.588	18	13	26	0	0	1	PKP1	-8,355	upstream	ActReg chr1 #1603	0	0	1
1604	1	201,252,391	201,253,481	1,090	1	4.788	4.794	15.088	10	8	23	1	1	1	PKP1	356	in gene	ActReg chr1 #1604	0	0	1
1605	1	201,279,551	201,280,587	1,036	1	13.242	12.727	5.848	21	17	9	0	0	1	PKP1	27,489	in gene	ActReg chr1 #1605	1	0	0
1606	1	201,294,107	201,294,749	642	1	4.3	5.8	15.1	9	8	22	0	0	1	PKP1	41,848	in gene	ActReg chr1 #1606	0	0	1
1607	1	201,333,480	201,334,053	573	1	2.333	3.294	13.278	4	6	25	0	0	1	TNNT2	13,039	in gene	ActReg chr1 #1607	0	0	1
1608	1	201,419,849	201,420,644	795	1	9.44	13.16	5.68	12	20	10	0	0	0				ActReg chr1 #1608	0	1	0
1609	1	201,430,178	201,431,728	1,550	2	14.021	12.435	5.458	30	23	9	0	0	1	PHLDA3	7,346	downstream	ActReg chr1 #1609	1	1	0
1610	1	201,437,394	201,439,179	1,785	1	9.518	13.054	8.696	19	19	18	1	1	1	PHLDA3	13	in gene	ActReg chr1 #1610	0	1	0
1611	1	201,450,010	201,451,181	1,171	1	6.667	7.622	12.568	15	15	19	1	0	1	CSRP1	25,792	downstream	ActReg chr1 #1611	0	0	1
1612	1	201,457,899	201,458,934	1,035	2	10.656	11.406	6.25	21	22	14	0	0	1	CSRP1	17,971	in gene	ActReg chr1 #1612	1	1	0
1613	1	201,463,392	201,464,003	611	1	4.05	4.05	11.2	6	8	19	0	0	1	CSRP1	12,690	in gene	ActReg chr1 #1613	0	0	1
1614	1	201,475,674	201,476,737	1,063	3	11.206	12.059	9.794	23	21	19	1	2	2	CSRP1, LOC100506590	182, -1032	in gene, upstream	ActReg chr1 #1614	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1615	1	201,520,814	201,521,560	746	2	12.478	14.739	4.522	25	31	8	0	0	0				ActReg chr1 #1615	1	1	0
1616	1	201,562,139	201,563,179	1,040	2	13.333	14.242	6.781	27	24	14	0	0	0				ActReg chr1 #1616	1	1	0
1617	1	201,563,219	201,564,846	1,627	1	8.686	13.706	5.26	22	25	10	0	0	0				ActReg chr1 #1617	0	1	0
1618	1	201,617,735	201,618,498	763	1	6.917	12.208	7.417	12	21	14	1	1	1	NAV1	666	in gene	ActReg chr1 #1618	0	1	0
1619	1	201,682,280	201,683,021	741	1	7.522	13.261	2.783	13	23	5	0	0	1	NAV1	65,200	in gene	ActReg chr1 #1619	0	1	0
1620	1	201,797,805	201,798,907	1,102	2	25.235	28.765	7.481	72	78	16	1	1	2	NAV1, IPO9	180906, 68	downstream, in gene	ActReg chr1 #1620	1	1	0
1621	1	201,865,631	201,866,466	835	1	5.815	7.259	10.741	9	13	19	0	0	2	SHISA4, LMOD1	8251, 49668	downstream, in gene	ActReg chr1 #1621	0	0	1
1622	1	201,924,126	201,925,327	1,201	3	10.395	11.158	9.026	23	21	23	1	1	2	LMOD1, TIMM17A	-9010, 107	upstream, in gene	ActReg chr1 #1622	1	1	1
1623	1	201,951,741	201,952,800	1,059	1	9.515	13.177	5.677	20	23	12	1	1	1	RNPEP	504	in gene	ActReg chr1 #1623	0	1	0
1624	1	201,979,543	201,980,605	762	1	4.261	6.739	12.261	9	11	16	0	2	3	RNPEP, LOC100289488, ELF3	28458, -986, 534	downstream, upstream, in gene	ActReg chr1 #1624	0	0	1
1625	1	201,982,053	201,982,695	642	1	4.2	5.3	12.35	6	8	18	0	2	3	RNPEP, LOC100289488, ELF3	30608, -3136, 2684	downstream, upstream, in gene	ActReg chr1 #1625	0	0	1
1626	1	201,986,970	201,987,582	612	1	4.474	9.789	11.684	7	15	16	0	0	2	LOC100289488, ELF3	-8038, 7586	upstream, downstream	ActReg chr1 #1626	0	0	1
1627	1	202,091,985	202,092,721	736	1	4.652	5.783	12.913	9	8	19	0	1	2	GPR37L1, ARL8A	324, 21513	in gene, downstream	ActReg chr1 #1627	0	0	1
1628	1	202,096,862	202,097,773	911	1	3.655	5.241	13	5	9	20	0	0	2	GPR37L1, ARL8A	5288, 16549	in gene, downstream	ActReg chr1 #1628	0	0	1
1629	1	202,146,193	202,147,249	1,056	1	4.879	4.121	12.485	10	7	18	0	0	0				ActReg chr1 #1629	0	0	1
1630	1	202,310,736	202,311,492	756	2	9.958	11.636	5.45	16	22	11	1	2	2	UBE2T, PPP1R12B	-20, -6716	upstream, upstream	ActReg chr1 #1630	1	1	0
1631	1	202,317,467	202,318,703	1,236	1	12.769	11.41	7.921	20	19	15	1	2	2	UBE2T, PPP1R12B	-6991, 255	upstream, in gene	ActReg chr1 #1631	1	0	0
1632	1	202,358,609	202,358,908	299	1	2.778	1.778	10	4	3	13	0	0	1	PPP1R12B	40,928	in gene	ActReg chr1 #1632	0	0	1
1633	1	202,582,115	202,582,579	464	1	3.786	2.714	10.071	6	4	17	0	0	1	SYT2	97,204	in gene	ActReg chr1 #1633	0	0	1
1634	1	202,612,724	202,613,450	726	1	3.739	4.826	13.13	6	9	18	1	0	1	SYT2	66,464	in gene	ActReg chr1 #1634	0	0	1
1635	1	202,625,761	202,627,161	1,400	2	13.186	13.698	4.93	26	24	10	0	0	1	SYT2	53,090	in gene	ActReg chr1 #1635	1	1	0
1636	1	202,649,406	202,650,222	816	1	6.154	11.731	4.269	15	17	7	0	0	1	SYT2	29,737	in gene	ActReg chr1 #1636	0	1	0
1637	1	202,661,852	202,662,974	1,122	2	19.086	24.286	2.143	58	63	5	0	0	1	SYT2	17,138	in gene	ActReg chr1 #1637	1	1	0
1638	1	202,678,709	202,679,167	458	1	3.571	5.714	12.357	7	8	16	1	1	1	SYT2	613	in gene	ActReg chr1 #1638	0	0	1
1639	1	202,775,986	202,776,477	491	1	8.4	12.133	13.733	13	15	22	1	2	2	KDM5B, LOC100506696	1318, -3843	in gene, upstream	ActReg chr1 #1639	0	0	1
1640	1	202,777,008	202,777,846	838	1	9.538	13.269	5.04	16	20	12	1	2	2	KDM5B, LOC100506696	122, -2647	in gene, upstream	ActReg chr1 #1640	0	1	0
1641	1	202,779,399	202,780,895	1,496	3	12.022	10.543	13.196	23	22	25	1	2	3	KDM5B, LOC100506696, LOC641515	-2598, 73, -9238	upstream, in gene, upstream	ActReg chr1 #1641	1	1	1
1642	1	202,829,898	202,831,364	1,466	2	10.065	8.696	8.174	16	12	18	1	0	0				ActReg chr1 #1642	1	0	1
1643	1	202,895,764	202,896,654	890	2	9.964	13.071	12.321	16	21	23	1	1	1	KLHL12	162	in gene	ActReg chr1 #1643	0	1	1
1644	1	202,926,782	202,927,750	968	2	7.548	13.774	7.484	15	21	18	1	1	2	ADIPOR1, CYB5R1	434, 9138	in gene, downstream	ActReg chr1 #1644	0	1	1
1645	1	202,976,085	202,977,130	1,045	1	9.727	12.606	7.121	22	18	13	1	1	1	TMEM183A	73	in gene	ActReg chr1 #1645	0	1	0
1646	1	202,995,614	202,996,078	464	1	10.867	8.133	13	14	13	22	1	0	2	TMEM183A, LOC100507405	19312, -9998	downstream, upstream	ActReg chr1 #1646	0	0	1
1647	1	203,017,190	203,017,747	557	1	6	10.588	11.765	8	15	14	0	1	2	LOC100507405, PPFIA4	11624, -2843	downstream, upstream	ActReg chr1 #1647	0	0	1
1648	1	203,027,978	203,028,704	726	1	7.696	6	11.348	16	8	15	0	0	1	PPFIA4	8,030	in gene	ActReg chr1 #1648	0	0	1
1649	1	203,053,515	203,054,227	712	1	6.682	6.045	13.046	9	9	17	0	1	2	PPFIA4, MYOG	33560, 1506	downstream, in gene	ActReg chr1 #1649	0	0	1
1650	1	203,096,950	203,098,120	1,170	2	10.568	12	11.108	18	21	20	1	1	1	ADORA1	699	in gene	ActReg chr1 #1650	0	1	1
1651	1	203,247,242	203,248,464	1,222	1	8.289	11.342	5.053	13	20	13	0	0	1	LOC100506775	-8,427	upstream	ActReg chr1 #1651	0	1	0
1652	1	203,274,570	203,275,531	961	1	7.567	11.8	12.433	13	19	21	1	2	2	LOC730227, BTG2	-597, 386	upstream, in gene	ActReg chr1 #1652	0	0	1
1653	1	203,296,347	203,297,139	792	1	6.32	9.84	11.76	10	17	19	1	0	0				ActReg chr1 #1653	0	0	1
1654	1	203,429,499	203,429,973	474	1	11.667	10.8	12.2	16	16	21	0	0	0				ActReg chr1 #1654	0	0	1
1655	1	203,433,742	203,434,342	600	1	6.474	6.474	12.474	10	10	20	0	0	0				ActReg chr1 #1655	0	0	1
1656	1	203,456,444	203,457,386	942	2	11.433	11.033	14.333	17	15	23	1	1	2	PRELP, OPTC	12032, -6356	in gene, upstream	ActReg chr1 #1656	1	0	1
1657	1	203,503,411	203,504,211	800	2	13.44	12.24	4.348	25	22	8	0	0	0				ActReg chr1 #1657	1	1	0
1658	1	203,527,172	203,528,397	1,225	2	14.895	12.842	4.297	33	23	10	0	0	0				ActReg chr1 #1658	1	1	0
1659	1	203,559,277	203,560,335	1,058	2	15.152	14.848	5.636	33	22	9	0	0	0				ActReg chr1 #1659	1	1	0
1660	1	203,772,811	203,773,170	359	1	4.091	5.182	10.727	6	8	16	0	0	2	ZC3H11A, ZBED6	8239, 6339	in gene, downstream	ActReg chr1 #1660	0	0	1
1661	1	203,830,138	203,831,308	1,170	3	14.568	20.946	8.081	35	46	15	1	1	2	ZC3H11A, SNRPE	65972, -17	downstream, upstream	ActReg chr1 #1661	1	1	1
1662	1	204,041,436	204,042,082	646	1	3	3.8	10.143	6	6	18	1	1	1	SOX13	-487	upstream	ActReg chr1 #1662	0	0	1
1663	1	204,042,651	204,043,925	1,274	2	12.125	10.75	7.925	18	17	13	1	1	1	SOX13	1,042	in gene	ActReg chr1 #1663	1	1	0
1664	1	204,092,116	204,092,789	673	1	6.714	4.762	11.952	14	8	15	0	0	2	SOX13, ETNK2	50206, 28855	in gene, downstream	ActReg chr1 #1664	0	0	1
1665	1	204,094,979	204,095,640	661	1	4.8	8.15	14.65	10	12	20	0	0	2	SOX13, ETNK2	53063, 25998	in gene, downstream	ActReg chr1 #1665	0	0	1
1666	1	204,099,115	204,099,709	594	1	6.056	5.353	13.944	11	8	19	0	0	2	SOX13, ETNK2	57166, 21895	downstream, downstream	ActReg chr1 #1666	0	0	1
1667	1	204,346,414	204,347,479	1,065	1	10.576	7.576	14.727	18	12	21	1	0	1	LOC127841	-8,099	upstream	ActReg chr1 #1667	0	0	1
1668	1	204,380,430	204,381,077	647	1	9.8	13.15	11.65	15	17	16	1	1	1	PPP1R15B	191	in gene	ActReg chr1 #1668	0	0	1
1669	1	204,386,349	204,387,282	933	1	9.483	12.034	5.69	13	17	9	0	1	2	PPP1R15B, PIK3C2B	-5871, 72659	upstream, downstream	ActReg chr1 #1669	0	1	0
1670	1	204,475,427	204,476,533	1,106	2	11.735	9.971	12.206	24	19	28	0	0	1	MDM4	-9,531	upstream	ActReg chr1 #1670	1	0	1
1671	1	204,485,046	204,486,025	979	1	14.323	9.323	9.194	23	16	15	1	1	1	MDM4	24	in gene	ActReg chr1 #1671	1	0	0
1672	1	204,586,905	204,588,050	1,145	1	4.944	4.694	12.861	9	9	17	0	0	2	LRRN2, LOC100506855	67120, -8426	in gene, upstream	ActReg chr1 #1672	0	0	1
1673	1	204,607,840	204,608,278	438	1	2.929	4	11.714	4	9	20	0	0	2	LRRN2, LOC100506855	46538, 12156	in gene, downstream	ActReg chr1 #1673	0	0	1
1674	1	204,616,185	204,617,589	1,404	2	20.204	22.454	3.705	68	81	11	0	0	1	LRRN2	37,710	in gene	ActReg chr1 #1674	1	1	0
1675	1	204,653,513	204,654,329	816	1	6	7.12	14	8	10	19	1	1	1	LRRN2	676	in gene	ActReg chr1 #1675	0	0	1
1676	1	204,732,693	204,733,469	776	1	9.833	14	5.5	14	30	9	0	0	0				ActReg chr1 #1676	0	1	0
1677	1	204,806,148	204,807,366	1,218	2	15.132	16.684	3.028	32	37	8	0	0	1	NFASC	8,975	in gene	ActReg chr1 #1677	1	1	0
1678	1	204,915,518	204,916,105	587	1	4.105	4.211	12.316	6	6	20	0	0	1	NFASC	118,029	in gene	ActReg chr1 #1678	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1679	1	204,958,236	204,959,610	1,374	1	7.047	11.605	8.093	13	21	14	0	0	1	NFASC	161,141	in gene	ActReg chr1 #1679	0	1	0
1680	1	205,090,604	205,091,792	1,188	2	19.892	19.919	6.758	49	50	13	0	1	1	RBBP5	-48	upstream	ActReg chr1 #1680	1	1	0
1681	1	205,179,966	205,181,540	1,574	3	9.66	14.6	10.857	18	26	22	1	1	1	DSTYK	-26	upstream	ActReg chr1 #1681	1	1	1
1682	1	205,227,610	205,228,419	809	1	9.846	11.846	4.692	16	19	11	0	0	2	TMCC2, LOC100506871	30976, -8622	in gene, upstream	ActReg chr1 #1682	0	1	0
1683	1	205,252,872	205,254,477	1,605	3	12.76	12.68	7.56	19	27	16	0	0	0				ActReg chr1 #1683	1	1	1
1684	1	205,307,182	205,307,635	453	1	3.786	5	10.571	6	7	18	0	0	1	KLHDC8A	18,631	in gene	ActReg chr1 #1684	0	0	1
1685	1	205,409,244	205,409,970	726	1	5.739	5.565	13.348	8	9	18	0	0	2	LOC100506918, MIR135B	15607, 7919	in gene, downstream	ActReg chr1 #1685	0	0	1
1686	1	205,417,884	205,418,780	896	1	12.857	9.5	4.929	17	14	9	0	2	3	LOC100506918, MIR135B, LOC284577	6882, -806, -6713	in gene, upstream, upstream	ActReg chr1 #1686	1	0	0
1687	1	205,424,732	205,425,493	761	1	5.75	5.792	12.292	9	9	17	1	3	3	LOC100506918, MIR135B, LOC284577	102, -7586, 67	in gene, upstream, in gene	ActReg chr1 #1687	0	0	1
1688	1	205,426,767	205,428,718	1,951	3	15.512	16.623	3.918	36	54	8	0	2	3	LOC100506918, MIR135B, LOC284577	-2528, -10216, 2697	upstream, upstream, in gene	ActReg chr1 #1688	1	1	0
1689	1	205,495,081	205,495,916	835	1	4.115	7.385	12.308	7	10	19	0	0	1	CDK18	21,814	in gene	ActReg chr1 #1689	0	0	1
1690	1	205,497,783	205,498,899	1,116	1	9.343	8.6	14.886	16	17	24	1	0	1	CDK18	24,657	in gene	ActReg chr1 #1690	0	0	1
1691	1	205,538,731	205,539,467	736	1	5.913	5.739	11.957	10	12	15	0	1	1	MFSD4	987	in gene	ActReg chr1 #1691	0	0	1
1692	1	205,600,776	205,601,703	927	3	11.483	16.345	8.407	32	38	18	1	1	1	ELK4	761	in gene	ActReg chr1 #1692	1	1	1
1693	1	205,630,684	205,631,478	794	1	3.16	2.167	11.56	6	4	20	0	0	1	SLC45A3	18,549	in gene	ActReg chr1 #1693	0	0	1
1694	1	205,649,812	205,650,453	641	1	5.65	4.25	10.95	10	8	14	1	1	1	SLC45A3	-502	upstream	ActReg chr1 #1694	0	0	1
1695	1	205,718,228	205,718,857	629	1	6.15	8.7	12.75	11	14	26	1	1	1	NUCKS1	819	in gene	ActReg chr1 #1695	0	0	1
1696	1	205,719,194	205,719,821	627	1	8.75	12.55	8.4	12	19	14	1	1	1	NUCKS1	-146	upstream	ActReg chr1 #1696	0	1	0
1697	1	205,744,000	205,745,050	1,050	2	12.364	14.303	4.939	29	26	9	1	1	1	RAB7L1	85	in gene	ActReg chr1 #1697	1	1	0
1698	1	205,774,568	205,775,083	515	1	4.188	6.933	11.25	6	13	16	0	1	2	SLC41A1, LOC100131354	7336, -7043	in gene, upstream	ActReg chr1 #1698	0	0	1
1699	1	205,782,031	205,782,939	908	1	9.143	14.5	8	16	25	14	1	2	2	SLC41A1, LOC100131354	-324, 617	upstream, in gene	ActReg chr1 #1699	0	1	0
1700	1	205,902,243	205,903,553	1,310	2	11.61	13.805	4.769	22	24	8	0	0	1	SLC26A9	9,690	in gene	ActReg chr1 #1700	1	1	0
1701	1	206,275,444	206,276,072	628	1	6.05	10.75	4.5	9	17	7	0	0	1	LOC100505650	12,441	downstream	ActReg chr1 #1701	0	1	0
1702	1	206,643,288	206,645,009	1,721	2	13.444	12.093	7.833	25	27	15	0	1	2	SRGAP2, IKBKE	127952, 562	downstream, in gene	ActReg chr1 #1702	1	1	0
1703	1	206,785,329	206,786,289	960	3	20.067	24.433	8.267	51	53	16	1	1	1	LGTN	95	in gene	ActReg chr1 #1703	1	1	1
1704	1	206,808,324	206,809,398	1,074	2	10.061	14.333	15.485	24	22	34	1	1	1	DYRK3	-20	upstream	ActReg chr1 #1704	0	1	1
1705	1	206,857,738	206,858,311	573	1	3.444	10.944	3.182	6	22	5	1	1	1	MAPKAPK2	-265	upstream	ActReg chr1 #1705	0	1	0
1706	1	206,859,121	206,859,968	847	1	7.333	7.074	11.37	13	12	17	1	1	1	MAPKAPK2	1,255	in gene	ActReg chr1 #1706	0	0	1
1707	1	206,902,696	206,903,140	444	1	7.214	4.714	11.643	10	9	18	0	0	1	MAPKAPK2	44,629	in gene	ActReg chr1 #1707	0	0	1
1708	1	207,063,205	207,064,731	1,526	3	12.128	11.234	3.632	19	18	7	0	1	1	IL24	-6,820	upstream	ActReg chr1 #1708	1	1	0
1709	1	207,108,743	207,109,118	375	1	4.727	5	12	9	7	16	0	0	1	PIGR	10,881	in gene	ActReg chr1 #1709	0	0	1
1710	1	207,194,251	207,195,430	1,179	1	9.081	12.027	3.595	14	18	6	0	0	1	C1orf116	11,261	in gene	ActReg chr1 #1710	0	1	0
1711	1	207,226,149	207,227,101	952	2	8.345	12.345	9.931	14	20	16	1	2	2	YOD1, PFKFB2	-2203, 5	upstream, in gene	ActReg chr1 #1711	0	1	1
1712	1	207,369,451	207,369,803	352	1	5.364	4.818	10	7	8	13	0	0	1	LOC100129101	125,847	in gene	ActReg chr1 #1712	0	0	1
1713	1	207,377,938	207,379,259	1,321	2	8.463	8.512	2.722	15	18	6	0	0	1	LOC100129101	116,876	in gene	ActReg chr1 #1713	1	1	0
1714	1	207,392,137	207,392,769	632	1	8.75	10.7	1.667	12	18	2	0	0	1	LOC100129101	103,021	in gene	ActReg chr1 #1714	0	1	0
1715	1	207,627,398	207,627,899	501	1	4.867	7.533	12.533	6	12	16	1	1	1	CR2	3	in gene	ActReg chr1 #1715	0	0	1
1716	1	208,204,126	208,204,612	486	1	5	2	12.25	7	3	19	0	0	1	PLXNA2	213,296	in gene	ActReg chr1 #1716	0	0	1
1717	1	208,280,911	208,282,034	1,123	2	12.429	11.886	3.719	20	16	7	0	0	1	PLXNA2	136,193	in gene	ActReg chr1 #1717	1	1	0
1718	1	208,357,380	208,358,213	833	1	7.962	12.269	4.84	16	20	8	0	0	1	PLXNA2	59,869	in gene	ActReg chr1 #1718	0	1	0
1719	1	208,502,540	208,503,210	670	1	6.938	11.857	1.533	14	20	2	0	0	0				ActReg chr1 #1719	0	1	0
1720	1	208,648,776	208,649,395	619	1	7.211	11.21	1.562	11	20	3	0	0	0				ActReg chr1 #1720	0	1	0
1721	1	208,661,844	208,662,139	295	1	4	2.111	11.333	5	3	14	0	0	0				ActReg chr1 #1721	0	0	1
1722	1	208,842,096	208,842,945	849	2	13.444	20.926	2.556	40	55	5	0	0	0				ActReg chr1 #1722	1	1	0
1723	1	208,922,169	208,922,783	614	1	5.737	10.632	3.684	11	17	6	0	0	0				ActReg chr1 #1723	0	1	0
1724	1	209,212,623	209,213,568	945	2	10.767	12	1.188	19	20	2	0	0	0				ActReg chr1 #1724	1	1	0
1725	1	209,323,216	209,324,297	1,081	2	16.765	22.882	1.96	48	69	4	0	0	0				ActReg chr1 #1725	1	1	0
1726	1	209,414,756	209,415,409	653	1	8.5	12.55	2.833	14	20	6	0	0	0				ActReg chr1 #1726	0	1	0
1727	1	209,491,821	209,492,469	648	1	11.85	9.85	3.4	17	15	6	0	0	0				ActReg chr1 #1727	1	0	0
1728	1	209,542,005	209,542,888	883	1	7.714	10.75	3.5	15	17	7	0	0	0				ActReg chr1 #1728	0	1	0
1729	1	209,575,837	209,576,534	697	1	6.409	11.636	3.375	10	22	7	0	0	0				ActReg chr1 #1729	0	1	0
1730	1	209,824,292	209,825,069	777	1	14.875	11.833	3.917	27	21	6	0	1	1	LAMB3	1,140	in gene	ActReg chr1 #1730	1	0	0
1731	1	209,826,231	209,827,328	1,097	1	7.4	12.286	2.577	13	22	6	0	1	1	LAMB3	-959	upstream	ActReg chr1 #1731	0	1	0
1732	1	209,956,756	209,957,151	395	1	3.917	8	11.5	7	10	16	0	1	3	TRAF3IP3, C1orf74, IRF6	27559, 937, 22526	downstream, in gene, downstream	ActReg chr1 #1732	0	0	1
1733	1	209,978,892	209,979,699	807	1	6.52	7.4	12.08	11	11	17	1	1	1	IRF6	184	in gene	ActReg chr1 #1733	0	0	1
1734	1	210,000,966	210,001,763	797	1	11	14.6	8.8	17	29	14	1	1	1	C1orf107	52	in gene	ActReg chr1 #1734	0	1	0
1735	1	210,013,019	210,013,962	943	2	11.067	11.133	2.75	21	22	6	0	0	1	C1orf107	12,178	in gene	ActReg chr1 #1735	1	1	0
1736	1	210,052,605	210,053,418	813	2	11.846	11.308	3.692	18	21	7	0	0	0				ActReg chr1 #1736	1	1	0
1737	1	210,099,180	210,099,803	623	1	5.947	11	2.471	9	21	4	0	0	0				ActReg chr1 #1737	0	1	0
1738	1	210,110,219	210,112,263	2,044	3	11.547	15.016	4.765	48	53	11	1	1	1	SYT14	-297	upstream	ActReg chr1 #1738	1	1	0
1739	1	210,152,047	210,152,390	343	1	3	5.273	10.818	4	8	14	0	0	1	SYT14	40,680	in gene	ActReg chr1 #1739	0	0	1
1740	1	210,159,017	210,159,410	393	1	5.333	3.833	10.833	7	5	16	0	0	1	SYT14	47,675	in gene	ActReg chr1 #1740	0	0	1
1741	1	210,247,897	210,248,842	945	2	12.433	13.4	4.143	24	23	10	0	0	1	SYT14	136,831	in gene	ActReg chr1 #1741	1	1	0
1742	1	210,303,037	210,303,592	555	1	7.222	10.222	2.455	11	16	4	0	0	1	SYT14	191,776	in gene	ActReg chr1 #1742	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1743	1	210,305,791	210,306,507	716	1	11.304	9.13	1.909	21	18	3	0	0	1	SYT14	194,611	in gene	ActReg chr1 #1743	1	0	0
1744	1	210,386,273	210,387,313	1,040	2	10.938	11.594	2.667	18	25	6	0	0	0				ActReg chr1 #1744	1	1	0
1745	1	210,406,391	210,407,348	957	2	12.7	11	8.538	17	19	15	2	2	2	C1orf133, SERTAD4	597,674	in gene, in gene	ActReg chr1 #1745	1	0	1
1746	1	210,465,539	210,466,467	928	3	11.31	12.759	10.483	24	22	16	1	0	0				ActReg chr1 #1746	1	1	1
1747	1	210,502,243	210,502,801	558	1	12.412	14.353	14.588	17	16	20	1	1	1	HHAT	926	in gene	ActReg chr1 #1747	0	0	1
1748	1	210,546,793	210,548,132	1,339	2	14.905	15.024	6.8	35	35	16	0	0	1	HHAT	45,866	in gene	ActReg chr1 #1748	1	1	0
1749	1	210,566,704	210,567,556	852	1	10.741	13.704	4.259	18	25	7	0	0	1	HHAT	65,534	in gene	ActReg chr1 #1749	0	1	0
1750	1	210,612,096	210,613,001	905	1	11.483	8.862	3	18	14	5	0	0	1	HHAT	110,952	in gene	ActReg chr1 #1750	1	0	0
1751	1	210,770,732	210,772,046	1,314	2	12.024	15.659	2.846	21	26	6	0	0	1	HHAT	269,793	in gene	ActReg chr1 #1751	1	1	0
1752	1	210,899,635	210,900,540	905	2	12.429	14.286	2.393	21	29	4	0	0	1	KCNH1	407,370	in gene	ActReg chr1 #1752	1	1	0
1753	1	210,912,822	210,913,525	703	1	10.5	11.636	2.267	18	21	3	0	0	1	KCNH1	394,284	in gene	ActReg chr1 #1753	0	1	0
1754	1	211,307,188	211,307,958	770	1	9.083	12.792	5.05	16	21	8	1	1	1	KCNH1	-116	upstream	ActReg chr1 #1754	0	1	0
1755	1	211,431,837	211,432,603	766	2	11.833	10.625	7.417	17	21	11	1	1	1	RCOR3	-488	upstream	ActReg chr1 #1755	1	1	0
1756	1	211,433,451	211,434,072	621	1	11.79	8.579	9.158	21	13	14	1	1	1	RCOR3	1,053	in gene	ActReg chr1 #1756	1	0	0
1757	1	211,750,869	211,753,261	2,392	3	9.213	13.387	7.58	15	21	20	1	1	1	SLC30A1	34	in gene	ActReg chr1 #1757	0	1	1
1758	1	211,765,189	211,766,126	937	2	9.724	14	2.885	19	28	6	0	0	0				ActReg chr1 #1758	1	1	0
1759	1	211,816,704	211,817,360	656	1	3.952	6.524	14.381	6	11	24	0	0	0				ActReg chr1 #1759	0	0	1
1760	1	211,848,439	211,849,248	809	1	9.962	12.615	10	21	22	17	1	1	1	NEK2	124	in gene	ActReg chr1 #1760	0	1	0
1761	1	211,908,434	211,909,661	1,227	1	13.816	10	3.485	20	13	7	0	0	1	LPGAT1	95,067	downstream	ActReg chr1 #1761	1	0	0
1762	1	212,204,074	212,205,255	1,181	2	10.838	12.838	2.733	28	32	6	0	1	2	INTS7, DTL	4220, -4255	in gene, upstream	ActReg chr1 #1762	1	1	0
1763	1	212,208,440	212,209,478	1,038	1	11.454	13.273	7	21	21	11	1	2	2	INTS7, DTL	-75, 40	upstream, in gene	ActReg chr1 #1763	0	1	0
1764	1	212,457,770	212,460,216	2,446	4	14.487	15.342	8.292	30	33	20	1	1	1	PPP2R5A	114	in gene	ActReg chr1 #1764	1	1	1
1765	1	212,643,156	212,644,022	866	2	12.926	14.926	3.148	26	28	8	0	0	0				ActReg chr1 #1765	1	1	0
1766	1	212,655,079	212,656,977	1,898	2	12.864	13.186	6.818	30	23	18	0	0	0				ActReg chr1 #1766	1	1	0
1767	1	212,658,164	212,659,952	1,788	2	11.679	12.857	6.125	20	32	11	0	0	0				ActReg chr1 #1767	1	1	0
1768	1	212,687,269	212,688,065	796	1	5.2	6.8	13.04	9	11	20	1	0	0				ActReg chr1 #1768	0	0	1
1769	1	212,732,014	212,732,890	876	1	9.407	14.074	5.667	14	25	12	1	1	1	ATF3	-6,245	upstream	ActReg chr1 #1769	0	1	0
1770	1	212,780,110	212,780,646	536	1	6.941	6.118	11.294	11	12	15	1	0	1	ATF3	41,681	in gene	ActReg chr1 #1770	0	0	1
1771	1	212,780,847	212,782,429	1,582	3	10.306	10.674	9	17	18	17	1	0	1	ATF3	42,941	in gene	ActReg chr1 #1771	1	1	1
1772	1	212,782,826	212,783,296	470	1	10.2	9.2	12.267	16	14	19	1	0	1	ATF3	44,364	in gene	ActReg chr1 #1772	0	0	1
1773	1	212,844,716	212,845,607	891	1	13.25	6.607	6.148	21	11	9	0	0	0				ActReg chr1 #1773	1	0	0
1774	1	212,873,304	212,874,094	790	1	8.88	5.44	14.72	17	15	24	1	1	1	BATF3	-372	upstream	ActReg chr1 #1774	0	0	1
1775	1	212,933,689	212,934,260	571	1	5.167	3.5	13.167	8	9	19	0	0	1	NSL1	31,165	in gene	ActReg chr1 #1775	0	0	1
1776	1	212,964,687	212,965,580	893	3	14.607	14.607	11	28	26	23	1	2	2	NSL1, TATDN3	6, -37	in gene, upstream	ActReg chr1 #1776	1	1	1
1777	1	213,030,835	213,032,573	1,738	2	10.556	12.315	13.482	14	22	32	1	2	3	C1orf227, LGK1, FLVCR1	-10713, -224, 107	upstream, upstream, in gene	ActReg chr1 #1777	0	1	1
1778	1	213,089,942	213,090,590	648	1	8.55	12.6	5.15	15	18	8	0	0	0				ActReg chr1 #1778	0	1	0
1779	1	213,149,890	213,150,443	553	1	3.471	6.235	10.647	6	11	18	0	0	1	VASH2	26,279	in gene	ActReg chr1 #1779	0	0	1
1780	1	213,188,907	213,189,380	473	1	10.933	13.2	6.067	16	21	9	1	1	1	ANGEL2	25	in gene	ActReg chr1 #1780	0	1	0
1781	1	213,224,012	213,225,225	1,213	1	11.71	13.684	6.053	23	28	16	1	1	1	RPS6KC1	30	in gene	ActReg chr1 #1781	0	1	0
1782	1	213,500,471	213,501,186	715	2	11.348	11.391	2.75	24	22	5	0	0	0				ActReg chr1 #1782	1	1	0
1783	1	213,862,473	213,863,039	566	1	11.765	9.647	3.412	15	13	7	0	0	0				ActReg chr1 #1783	1	0	0
1784	1	214,146,269	214,146,984	715	1	12.696	9.348	3.261	20	14	5	0	1	1	LOC100505832	-7,018	upstream	ActReg chr1 #1784	1	0	0
1785	1	214,156,499	214,157,017	518	1	3.938	6.062	12.125	7	12	21	1	1	1	PROX1	-5,102	upstream	ActReg chr1 #1785	0	0	1
1786	1	214,280,491	214,281,128	637	1	5.158	11.35	4.3	8	18	7	0	0	0				ActReg chr1 #1786	0	1	0
1787	1	214,296,438	214,297,162	724	2	10.478	10.174	3.261	18	20	7	0	0	0				ActReg chr1 #1787	1	1	0
1788	1	214,454,443	214,455,113	670	1	11.857	11.524	5.176	25	20	10	1	1	1	SMYD2	213	in gene	ActReg chr1 #1788	0	1	0
1789	1	214,600,804	214,601,765	961	1	13.633	9.6	2.28	26	21	3	0	0	1	PTPN14	123,740	in gene	ActReg chr1 #1789	1	0	0
1790	1	214,619,983	214,620,845	862	2	10.37	13.074	2.238	16	24	5	0	0	1	PTPN14	104,610	in gene	ActReg chr1 #1790	1	1	0
1791	1	214,723,871	214,725,118	1,247	2	9.769	10.82	10.744	15	17	19	2	1	1	PTPN14	530	in gene	ActReg chr1 #1791	0	1	1
1792	1	214,776,138	214,777,179	1,041	1	9.5	17.031	6.781	21	32	14	1	1	2	CENPF, FAM108A4	126, 5925	in gene, downstream	ActReg chr1 #1792	0	1	0
1793	1	215,631,359	215,632,043	684	1	9.136	11.818	1.467	14	25	2	0	0	0				ActReg chr1 #1793	0	1	0
1794	1	215,740,277	215,741,447	1,170	2	12.649	10.838	8.595	21	22	15	1	1	1	KCTD3	127	in gene	ActReg chr1 #1794	1	1	0
1795	1	216,896,474	216,897,234	760	1	15.583	8.708	5.75	35	20	12	0	0	1	ESRRG	414,243	in gene	ActReg chr1 #1795	1	0	0
1796	1	217,102,890	217,103,564	674	1	5.286	11.667	2.889	11	18	4	0	0	1	ESRRG	207,870	in gene	ActReg chr1 #1796	0	1	0
1797	1	217,262,802	217,263,423	621	2	9.789	10.263	3	17	17	5	1	0	1	ESRRG	47,985	in gene	ActReg chr1 #1797	1	1	0
1798	1	217,803,966	217,804,913	947	2	12	10.767	3.897	20	16	11	1	2	2	GPATCH2, SPATA17	-30, -256	upstream, upstream	ActReg chr1 #1798	1	1	0
1799	1	217,833,541	217,834,210	669	2	12	13.143	2.154	23	25	4	0	0	1	SPATA17	29,180	in gene	ActReg chr1 #1799	1	1	0
1800	1	218,080,572	218,081,358	786	1	9.44	11.92	1.706	18	22	3	0	0	0				ActReg chr1 #1800	0	1	0
1801	1	218,337,623	218,338,415	792	2	7.28	13	10	11	18	16	1	0	0				ActReg chr1 #1801	0	1	1
1802	1	218,435,405	218,436,130	725	1	9.565	13.87	2.571	17	26	4	0	0	0				ActReg chr1 #1802	0	1	0
1803	1	218,457,840	218,459,132	1,292	3	13.85	12.825	10.95	26	27	21	1	1	1	RRP15	-143	upstream	ActReg chr1 #1803	1	1	1
1804	1	218,599,132	218,600,056	924	1	9.862	10.172	1.889	18	17	3	0	0	1	TGFB2	80,203	in gene	ActReg chr1 #1804	0	1	0
1805	1	218,671,302	218,672,194	892	1	10.964	6.893	2.88	17	14	5	0	0	0				ActReg chr1 #1805	1	0	0
1806	1	218,758,239	218,760,022	1,783	2	10.339	11.071	2.956	17	18	7	0	0	0				ActReg chr1 #1806	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1807	1	218,833,906	218,834,661	755	2	13.833	9.292	1.455	25	18	2	0	0	0				ActReg chr1 #1807	1	1	0
1808	1	219,047,453	219,048,112	659	1	10.809	10.048	1	21	17	1	0	0	0				ActReg chr1 #1808	1	0	0
1809	1	219,261,904	219,262,757	853	2	11.889	10.24	6.308	24	17	16	0	0	0				ActReg chr1 #1809	1	1	0
1810	1	219,346,932	219,348,035	1,103	2	10.886	10.743	5.2	24	17	12	1	1	1	LYPLAL1	291	in gene	ActReg chr1 #1810	1	1	0
1811	1	219,559,054	219,559,508	454	1	9.929	8.214	2.167	15	13	3	0	0	0				ActReg chr1 #1811	1	0	0
1812	1	219,634,259	219,635,016	757	2	11.333	11.542	1.471	18	24	2	0	0	0				ActReg chr1 #1812	1	1	0
1813	1	219,813,231	219,814,700	1,469	1	10.065	11.543	3.912	16	20	8	0	0	0				ActReg chr1 #1813	0	1	0
1814	1	219,834,977	219,835,625	648	1	7.2	10.8	1.75	13	19	3	0	0	0				ActReg chr1 #1814	0	1	0
1815	1	219,873,183	219,873,848	665	1	12.571	8.19	5.19	21	12	9	0	0	0				ActReg chr1 #1815	1	0	0
1816	1	219,943,975	219,944,990	1,015	1	16	13.129	3.423	35	31	6	0	0	0				ActReg chr1 #1816	1	0	0
1817	1	220,262,810	220,263,733	923	2	11.138	14.724	3.552	25	30	8	0	2	2	BPNT1, IARS2	-80, -4184	upstream, upstream	ActReg chr1 #1817	1	1	0
1818	1	220,267,079	220,267,949	870	1	6.5	13.926	8.273	10	21	15	1	2	2	BPNT1, IARS2	-4323, 59	upstream, in gene	ActReg chr1 #1818	0	1	0
1819	1	220,445,105	220,446,235	1,130	1	10.886	13.686	7.824	19	23	15	1	1	1	RAB3GAP2	173	in gene	ActReg chr1 #1819	0	1	0
1820	1	220,543,302	220,544,010	708	1	9.091	12.818	3.211	14	18	6	0	0	0				ActReg chr1 #1820	0	1	0
1821	1	220,636,022	220,636,354	332	1	4.455	7.273	11.636	10	9	17	0	0	0				ActReg chr1 #1821	0	0	1
1822	1	220,636,593	220,637,039	446	1	3.643	4.643	12.214	6	6	17	0	0	0				ActReg chr1 #1822	0	0	1
1823	1	220,701,570	220,702,856	1,286	2	12.475	11.025	7.342	17	17	14	1	1	1	MARK1	645	in gene	ActReg chr1 #1823	1	1	0
1824	1	221,052,997	221,053,784	787	2	9.417	12.292	11.792	17	22	19	1	1	1	HLX	647	in gene	ActReg chr1 #1824	0	1	1
1825	1	221,290,493	221,291,421	928	1	7.517	12	2	18	24	4	0	0	0				ActReg chr1 #1825	0	1	0
1826	1	221,508,364	221,509,403	1,039	1	11.25	9.625	2.935	19	16	5	0	1	1	LOC400804	755	in gene	ActReg chr1 #1826	1	0	0
1827	1	221,911,750	221,913,492	1,742	2	14.63	16.074	5.333	36	34	9	0	1	1	DUSP10	2,840	in gene	ActReg chr1 #1827	1	1	0
1828	1	221,915,412	221,917,127	1,715	2	13.333	11.518	4.962	27	22	8	1	1	1	DUSP10	-808	upstream	ActReg chr1 #1828	1	1	0
1829	1	221,996,861	221,997,926	1,065	2	10.559	12.853	3.033	16	27	6	0	0	0				ActReg chr1 #1829	1	1	0
1830	1	222,012,954	222,013,655	701	1	12.727	10.591	4.4	24	19	7	0	0	0				ActReg chr1 #1830	1	0	0
1831	1	222,031,969	222,032,593	624	1	9.368	10.158	4.368	15	20	8	0	0	0				ActReg chr1 #1831	0	1	0
1832	1	222,134,928	222,135,649	721	1	11.739	9.783	1.188	18	17	2	0	0	0				ActReg chr1 #1832	1	0	0
1833	1	222,161,003	222,161,769	766	1	8.25	13.375	2.789	17	26	6	0	0	0				ActReg chr1 #1833	0	1	0
1834	1	222,167,297	222,168,129	832	1	10.231	15.154	3.136	17	22	8	0	0	0				ActReg chr1 #1834	0	1	0
1835	1	222,223,059	222,223,446	387	1	4.75	9.667	13.167	9	11	20	0	0	0				ActReg chr1 #1835	0	0	1
1836	1	222,560,471	222,561,271	800	1	5.48	12.08	2	11	17	4	0	0	0				ActReg chr1 #1836	0	1	0
1837	1	222,790,817	222,791,229	412	1	10	8.333	12	14	13	20	2	1	1	MIA3	-421	upstream	ActReg chr1 #1837	0	0	1
1838	1	222,817,034	222,818,123	1,089	3	14.059	12.088	10	26	20	20	1	0	1	MIA3	26,134	in gene	ActReg chr1 #1838	1	1	1
1839	1	222,885,698	222,887,004	1,306	3	12.975	17.025	10.125	25	34	23	1	2	2	AIDA, C1orf58	-487, 445	upstream, in gene	ActReg chr1 #1839	1	1	1
1840	1	222,987,145	222,989,116	1,971	2	11.312	12.541	4.721	18	22	12	1	0	0				ActReg chr1 #1840	1	1	0
1841	1	223,092,127	223,092,952	825	1	9.038	11.423	3.2	13	17	8	0	0	1	DISP1	-9,244	upstream	ActReg chr1 #1841	0	1	0
1842	1	223,189,537	223,190,652	1,115	2	10.029	6.412	8.765	17	14	19	0	0	0				ActReg chr1 #1842	1	0	1
1843	1	223,254,701	223,255,199	498	1	7.933	8.467	13.733	12	15	20	1	0	0				ActReg chr1 #1843	0	0	1
1844	1	223,397,715	223,398,189	474	1	4	3.333	12.533	6	5	20	0	0	1	SUSD4	139,592	in gene	ActReg chr1 #1844	0	0	1
1845	1	223,673,430	223,674,513	1,083	1	8.824	11.559	5.147	19	17	8	0	0	0				ActReg chr1 #1845	0	1	0
1846	1	223,840,013	223,840,714	701	1	11.818	11.091	3.238	24	19	8	0	0	1	CAPN8	13,073	in gene	ActReg chr1 #1846	1	0	0
1847	1	223,888,260	223,889,282	1,022	1	12.469	11.719	5.781	21	20	10	0	1	1	CAPN2	-524	upstream	ActReg chr1 #1847	1	0	0
1848	1	223,894,801	223,895,865	1,064	1	11.121	9.667	5	15	15	9	0	0	1	CAPN2	6,038	in gene	ActReg chr1 #1848	1	0	0
1849	1	223,902,383	223,903,569	1,186	2	11.595	11.216	2.344	17	19	5	0	0	1	CAPN2	13,681	in gene	ActReg chr1 #1849	1	1	0
1850	1	223,952,666	223,953,443	777	1	8.36	11.68	3.818	12	20	8	0	0	1	CAPN2	63,759	in gene	ActReg chr1 #1850	0	1	0
1851	1	224,033,782	224,034,470	688	1	9.682	7.864	13.636	15	13	22	1	1	2	TP53BP2, LOC100506213	-452, 7409	upstream, downstream	ActReg chr1 #1851	0	0	1
1852	1	224,063,908	224,064,679	771	1	11.458	8.917	1.556	18	17	2	0	0	0				ActReg chr1 #1852	1	0	0
1853	1	224,075,511	224,076,286	775	1	11.625	9.625	5.833	18	15	12	0	0	0				ActReg chr1 #1853	1	0	0
1854	1	224,180,123	224,180,641	518	1	17.235	10.882	7	36	21	13	1	1	1	LOC100288102	-36	upstream	ActReg chr1 #1854	1	0	0
1855	1	224,301,419	224,302,596	1,177	1	12.892	11.595	7.757	21	25	18	1	1	1	FBXO28	216	in gene	ActReg chr1 #1855	1	0	0
1856	1	224,370,369	224,371,859	1,490	1	10.891	12.717	5.773	16	21	12	1	1	1	DEGS1	186	in gene	ActReg chr1 #1856	0	1	0
1857	1	224,517,461	224,518,456	995	2	14.774	16.839	8.806	31	30	18	1	1	1	NVL	-86	upstream	ActReg chr1 #1857	1	1	0
1858	1	224,544,242	224,545,334	1,092	1	10.618	16.323	6.061	16	25	16	1	1	1	CNIH4	193	in gene	ActReg chr1 #1858	0	1	0
1859	1	224,621,391	224,622,146	755	1	8	10.583	7.273	12	16	15	1	2	2	WDR26, LOC100506354	233, -846	in gene, upstream	ActReg chr1 #1859	0	1	0
1860	1	224,622,409	224,623,271	862	2	19.963	23.259	5.259	39	47	9	1	2	2	WDR26, LOC100506354	-839, 226	upstream, in gene	ActReg chr1 #1860	1	1	0
1861	1	224,685,540	224,686,708	1,168	1	12.583	8.333	4.5	24	17	8	0	0	1	LOC100506354	63,510	in gene	ActReg chr1 #1861	1	0	0
1862	1	224,752,094	224,753,641	1,547	2	14.429	17.184	4.886	32	30	9	0	0	0				ActReg chr1 #1862	1	1	0
1863	1	224,803,678	224,805,302	1,624	1	7.098	9.667	14.274	14	17	21	2	1	1	CNIH3	311	in gene	ActReg chr1 #1863	0	0	1
1864	1	224,895,273	224,896,427	1,154	1	9.778	12.028	4.028	17	17	8	0	0	1	CNIH3	91,671	in gene	ActReg chr1 #1864	0	1	0
1865	1	224,920,711	224,921,808	1,097	1	8.618	12.118	3.059	16	21	6	0	0	1	CNIH3	117,080	in gene	ActReg chr1 #1865	0	1	0
1866	1	225,116,986	225,117,912	926	3	12.483	11.172	10.259	21	21	25	1	1	1	DNAH14	93	in gene	ActReg chr1 #1866	1	1	1
1867	1	225,614,423	225,616,792	2,369	3	10.405	13.527	4.946	19	21	11	1	1	1	LBR	912	in gene	ActReg chr1 #1867	1	1	0
1868	1	225,619,029	225,619,567	538	1	5.176	5.941	13.177	9	9	20	0	1	1	LBR	-2,779	upstream	ActReg chr1 #1868	0	0	1
1869	1	225,652,607	225,653,100	493	1	6.75	8.375	11.375	9	14	17	0	0	0				ActReg chr1 #1869	0	0	1
1870	1	225,844,990	225,845,755	765	1	8.75	10.833	2.227	15	18	5	0	1	1	ENAH	-4,527	upstream	ActReg chr1 #1870	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1871	1	225,857,850	225,859,527	1,677	2	13.321	13.207	4.091	22	23	10	0	0	0				ActReg chr1 #1871	1	1	0
1872	1	225,954,934	225,956,859	1,925	1	8.5	12.65	6.85	13	22	17	0	0	1	SRP9	-9,619	upstream	ActReg chr1 #1872	0	1	0
1873	1	225,959,791	225,960,407	616	1	12.526	5.737	4.133	21	8	7	0	1	1	SRP9	-5,416	upstream	ActReg chr1 #1873	1	0	0
1874	1	225,964,759	225,966,161	1,402	2	16.591	21.727	6.864	57	77	17	1	1	1	SRP9	-55	upstream	ActReg chr1 #1874	1	1	0
1875	1	226,064,813	226,065,921	1,108	1	7.943	12.886	6.886	14	25	10	0	0	2	TMEM63A, LEFTY1	5053, 11469	in gene, downstream	ActReg chr1 #1875	0	1	0
1876	1	226,067,535	226,068,618	1,083	1	11.441	7.971	7.824	17	13	12	0	1	2	TMEM63A, LEFTY1	2344, 8760	in gene, downstream	ActReg chr1 #1876	1	0	0
1877	1	226,069,698	226,071,334	1,636	2	12.196	12.667	10	18	21	19	1	1	2	TMEM63A, LEFTY1	-96, 6320	upstream, downstream	ActReg chr1 #1877	1	1	0
1878	1	226,109,107	226,110,053	946	1	4.138	7.233	13.967	6	12	20	0	1	1	PYCR2	2,385	in gene	ActReg chr1 #1878	0	0	1
1879	1	226,111,477	226,112,252	775	2	11.417	12.208	10.917	19	23	18	1	1	1	PYCR2	101	in gene	ActReg chr1 #1879	0	1	1
1880	1	226,128,068	226,128,832	764	1	3.208	7.833	13.792	4	13	18	0	1	1	LEFTY2	633	in gene	ActReg chr1 #1880	0	0	1
1881	1	226,216,050	226,216,582	532	1	4.529	4.706	11.059	7	7	16	0	0	0				ActReg chr1 #1881	0	0	1
1882	1	226,249,290	226,249,944	654	1	12.45	10.7	8.353	19	16	15	1	1	2	H3F3A, LOC100506398	-804, 34803	upstream, downstream	ActReg chr1 #1882	1	0	0
1883	1	226,250,283	226,250,915	632	1	9.3	8.5	14.25	15	13	25	1	1	2	H3F3A, LOC100506398	178, 33821	in gene, downstream	ActReg chr1 #1883	0	0	1
1884	1	226,270,534	226,272,114	1,580	2	12.02	12.429	11.98	19	21	21	1	0	1	LOC100506398	13,096	in gene	ActReg chr1 #1884	0	1	1
1885	1	226,298,003	226,298,951	948	2	11.033	10.2	8.433	17	15	15	1	0	0				ActReg chr1 #1885	1	0	1
1886	1	226,373,832	226,374,877	1,045	3	12.375	11.938	9.469	18	16	17	1	1	1	ACSD3	69	in gene	ActReg chr1 #1886	1	1	1
1887	1	226,496,262	226,497,193	931	2	9.862	14.414	5.154	21	33	10	1	1	1	LIN9	471	in gene	ActReg chr1 #1887	1	1	0
1888	1	226,595,304	226,595,984	680	2	11.286	10.429	3.421	19	17	6	1	1	1	PARP1	157	in gene	ActReg chr1 #1888	1	1	0
1889	1	226,789,911	226,790,367	456	1	7	6.571	11.214	12	10	20	0	0	1	C1orf95	53,638	in gene	ActReg chr1 #1889	0	0	1
1890	1	226,890,645	226,891,577	932	1	8.276	15.621	5.621	18	25	12	1	0	1	ITPKB	35,765	in gene	ActReg chr1 #1890	0	1	0
1891	1	227,002,585	227,003,389	804	1	15.48	13.6	3.76	32	26	11	0	0	0				ActReg chr1 #1891	1	0	0
1892	1	227,118,665	227,119,260	595	1	11.889	9.778	4.333	22	15	7	0	0	1	CABC1	-8,976	upstream	ActReg chr1 #1892	1	0	0
1893	1	227,126,994	227,128,620	1,626	4	12.255	13.569	11.078	17	29	23	1	1	1	CABC1	-131	upstream	ActReg chr1 #1893	1	1	1
1894	1	227,152,529	227,153,030	501	1	3.188	4.438	11.375	5	8	15	0	0	1	CABC1	24,841	in gene	ActReg chr1 #1894	0	0	1
1895	1	227,161,899	227,162,639	740	1	2.913	4.348	11.652	5	8	15	0	0	1	CABC1	34,331	in gene	ActReg chr1 #1895	0	0	1
1896	1	227,166,548	227,167,281	733	1	3.435	4.13	12.174	8	9	22	0	0	1	CABC1	38,976	in gene	ActReg chr1 #1896	0	0	1
1897	1	227,167,760	227,168,777	1,017	1	4.312	4.258	12.469	7	9	17	0	0	2	CABC1, CDC42BPA	40330, 337558	in gene, downstream	ActReg chr1 #1897	0	0	1
1898	1	227,505,786	227,506,240	454	1	10.533	13.533	12.4	13	21	24	1	1	1	CDC42BPA	-187	upstream	ActReg chr1 #1898	0	0	1
1899	1	227,544,717	227,545,578	861	2	11.741	10.111	6.158	19	26	14	0	0	0				ActReg chr1 #1899	1	1	0
1900	1	227,566,351	227,567,408	1,057	2	10.667	12.788	1.906	17	21	5	0	0	0				ActReg chr1 #1900	1	1	0
1901	1	227,728,545	227,728,986	441	1	5.615	7.077	12.538	8	12	16	0	0	0				ActReg chr1 #1901	0	0	1
1902	1	227,729,208	227,730,006	798	1	6.52	11.32	6.88	12	17	10	1	0	0				ActReg chr1 #1902	0	1	0
1903	1	227,749,020	227,749,413	393	1	3.692	2.615	11.538	6	6	18	1	1	1	ZNF678	-2,004	upstream	ActReg chr1 #1903	0	0	1
1904	1	227,751,075	227,751,844	769	1	9.125	12.667	7.25	14	18	10	1	1	1	ZNF678	239	in gene	ActReg chr1 #1904	0	1	0
1905	1	227,916,360	227,917,285	925	1	6.724	10.586	11.621	14	22	17	1	2	3	LOC100130093, JMJD4, SNAP47	582, 6290, -5875	in gene, downstream, upstream	ActReg chr1 #1905	0	0	1
1906	1	227,922,531	227,923,422	891	3	14.333	15.518	12.444	26	24	23	1	2	3	LOC100130093, JMJD4, SNAP47	6736, 136, 279	downstream, in gene, in gene	ActReg chr1 #1906	1	1	1
1907	1	227,928,935	227,929,530	595	1	2.5	5.167	14.833	4	7	22	0	1	3	LOC100130093, JMJD4, SNAP47	12992, -6120, 6535	downstream, upstream, in gene	ActReg chr1 #1907	0	0	1
1908	1	227,951,215	227,951,809	594	1	5.263	7.842	12.947	7	12	19	0	0	1	SNAP47	28,815	in gene	ActReg chr1 #1908	0	0	1
1909	1	227,968,826	227,969,378	552	1	6.471	5.889	11.722	11	9	17	0	0	1	SNAP47	46,405	downstream	ActReg chr1 #1909	0	0	1
1910	1	227,975,248	227,975,917	669	1	5.429	6.952	11.667	8	10	19	1	0	1	SNAP47	52,885	downstream	ActReg chr1 #1910	0	0	1
1911	1	227,976,095	227,977,060	965	1	4.774	6.484	14.806	8	10	29	1	0	1	SNAP47	53,880	downstream	ActReg chr1 #1911	0	0	1
1912	1	227,981,239	227,982,056	817	1	4.385	5.346	13.962	10	11	20	0	0	0				ActReg chr1 #1912	0	0	1
1913	1	228,076,357	228,077,060	703	1	4.273	6.091	11.591	8	10	15	0	0	0				ActReg chr1 #1913	0	0	1
1914	1	228,109,042	228,110,322	1,280	1	3.825	4.7	13.45	8	8	19	0	0	1	WNT9A	25,994	in gene	ActReg chr1 #1914	0	0	1
1915	1	228,111,086	228,111,641	555	1	3.235	3.471	13.765	6	7	20	0	0	1	WNT9A	24,313	in gene	ActReg chr1 #1915	0	0	1
1916	1	228,112,523	228,113,200	677	1	4.211	5.333	13.429	9	8	21	1	0	1	WNT9A	22,815	in gene	ActReg chr1 #1916	0	0	1
1917	1	228,122,177	228,123,282	1,105	2	12.471	12.794	4.323	24	22	10	0	0	1	WNT9A	12,947	in gene	ActReg chr1 #1917	1	1	0
1918	1	228,136,030	228,136,901	871	1	7.893	8.179	11.964	14	12	16	1	1	1	WNT9A	-789	upstream	ActReg chr1 #1918	0	0	1
1919	1	228,158,806	228,158,990	184	1	1.833	1.833	10.167	2	2	12	0	0	1	LOC648262	6,965	downstream	ActReg chr1 #1919	0	0	1
1920	1	228,226,226	228,227,029	803	1	2.56	6	11.88	5	11	16	0	0	1	WNT3A	31,875	in gene	ActReg chr1 #1920	0	0	1
1921	1	228,246,401	228,246,995	594	1	3.056	5.111	10.5	5	9	15	1	0	1	WNT3A	51,946	in gene	ActReg chr1 #1921	0	0	1
1922	1	228,252,379	228,253,015	636	1	3.8	6.4	13.55	6	10	24	0	0	2	WNT3A, LOC100506571	57945, 11554	downstream, downstream	ActReg chr1 #1922	0	0	1
1923	1	228,269,757	228,271,242	1,485	2	7.957	12.255	8.222	20	19	18	1	2	2	LOC100506571, ARF1	-6248, 138	upstream, in gene	ActReg chr1 #1923	0	1	1
1924	1	228,284,248	228,285,184	936	1	6.633	4.667	12.133	11	7	17	0	0	4	ARF1, C1orf35, LOC100506628, MRPL55	14355, 6306, 20066, 12297	in gene, downstream, downstream, downstream	ActReg chr1 #1924	0	0	1
1925	1	228,286,260	228,286,686	426	1	2.769	8.615	14.385	4	16	21	0	0	4	ARF1, C1orf35, LOC100506628, MRPL55	16112, 4549, 18309, 10540	in gene, downstream, downstream, downstream	ActReg chr1 #1925	0	0	1
1926	1	228,289,339	228,290,489	1,150	1	7	9.139	13.361	12	15	22	1	1	4	ARF1, C1orf35, LOC100506628, MRPL55	19553, 1108, 14868, 7099	downstream, in gene, downstream, downstream	ActReg chr1 #1926	0	0	1
1927	1	228,290,612	228,291,409	797	1	12.28	15.96	5.625	19	30	11	1	1	4	ARF1, C1orf35, LOC100506628, MRPL55	20649, 12, 13772, 6003	downstream, in gene, downstream, downstream	ActReg chr1 #1927	0	1	0
1928	1	228,293,324	228,294,413	1,089	1	4.294	4.794	11.912	9	7	20	0	1	4	ARF1, C1orf35, LOC100506628, MRPL55	23507, -2846, 10914, 3145	downstream, upstream, in gene, downstream	ActReg chr1 #1928	0	0	1
1929	1	228,296,585	228,297,476	891	3	11.786	13.929	10.821	27	28	16	1	2	4	ARF1, C1orf35, LOC100506628, MRPL55	26669, -6008, 7752, -17	downstream, upstream, in gene, upstream	ActReg chr1 #1929	1	1	1
1930	1	228,327,490	228,328,682	1,192	2	14.973	11.73	10.351	25	23	15	1	1	2	GUK1, GJC2	157, -9467	in gene, upstream	ActReg chr1 #1930	1	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1931	1	228,337,606	228,338,727	1,121	1	6.286	7.829	12.8	10	14	20	0	1	2	GUK1, GJC2	10237, 613	downstream, in gene	ActReg chr1 #1931	0	0	1
1932	1	228,344,357	228,345,005	648	1	3.1	4.05	14.05	5	7	19	0	0	4	GUK1, GJC2, LOC100506642, C1orf69	16752, 7128, 7868, -5748	downstream, in gene, downstream, upstream	ActReg chr1 #1932	0	0	1
1933	1	228,349,676	228,351,433	1,757	1	5.236	5.545	13.255	10	11	21	0	2	3	GJC2, LOC100506642, C1orf69	13001, 1995, -2875	downstream, downstream, upstream	ActReg chr1 #1933	0	0	1
1934	1	228,353,095	228,354,103	1,008	2	22.258	25.323	5.194	54	65	10	1	2	3	GJC2, LOC100506642, C1orf69	16046, -1050, 170	downstream, upstream, in gene	ActReg chr1 #1934	1	1	0
1935	1	228,396,610	228,397,133	523	1	5.312	3.125	13.25	9	4	21	0	1	1	OBSCN	1,010	in gene	ActReg chr1 #1935	0	0	1
1936	1	228,444,215	228,444,884	669	1	3.95	4.235	14.143	6	7	18	0	0	1	OBSCN	48,688	in gene	ActReg chr1 #1936	0	0	1
1937	1	228,464,029	228,465,134	1,105	1	5.371	6.686	12.114	11	14	17	1	0	1	OBSCN	68,720	in gene	ActReg chr1 #1937	0	0	1
1938	1	228,467,307	228,468,150	843	1	6.692	4.808	13	13	7	18	1	0	1	OBSCN	71,867	in gene	ActReg chr1 #1938	0	0	1
1939	1	228,470,790	228,471,383	593	1	5.167	5.111	14.444	9	7	23	0	0	1	OBSCN	75,225	in gene	ActReg chr1 #1939	0	0	1
1940	1	228,493,869	228,494,669	800	1	3.68	5.88	13.52	10	9	22	0	0	1	OBSCN	98,408	in gene	ActReg chr1 #1940	0	0	1
1941	1	228,503,332	228,504,815	1,483	1	3.778	4.739	15.63	7	11	27	1	0	1	OBSCN	108,212	in gene	ActReg chr1 #1941	0	0	1
1942	1	228,521,862	228,522,388	526	1	4.25	3.125	13.188	8	5	17	0	0	1	OBSCN	126,264	in gene	ActReg chr1 #1942	0	0	1
1943	1	228,528,306	228,529,206	900	1	5.286	5.429	13.071	8	11	17	0	0	1	OBSCN	132,895	in gene	ActReg chr1 #1943	0	0	1
1944	1	228,538,753	228,539,233	480	1	4.6	2.5	12.2	7	4	18	0	0	1	OBSCN	143,132	in gene	ActReg chr1 #1944	0	0	1
1945	1	228,547,789	228,548,584	795	1	4.4	5.76	12.8	8	9	19	1	0	1	OBSCN	152,325	in gene	ActReg chr1 #1945	0	0	1
1946	1	228,563,036	228,563,793	757	1	3.81	5.167	11.958	8	8	18	0	0	1	OBSCN	167,553	in gene	ActReg chr1 #1946	0	0	1
1947	1	228,564,160	228,565,362	1,202	1	3.5	4.132	11.263	9	10	16	0	0	1	OBSCN	168,900	in gene	ActReg chr1 #1947	0	0	1
1948	1	228,644,747	228,647,277	2,530	2	11.544	14.987	7.09	28	27	14	1	2	2	HIST3H2A, HIST3H2BB	-452, 204	upstream, in gene	ActReg chr1 #1948	1	1	0
1949	1	228,657,187	228,657,762	575	1	3.571	2.875	12.611	5	5	20	1	0	0				ActReg chr1 #1949	0	0	1
1950	1	228,673,964	228,675,335	1,371	2	27.442	32.279	9.474	66	84	19	1	1	1	RNF187	-419	upstream	ActReg chr1 #1950	1	1	0
1951	1	228,688,499	228,689,341	842	1	8.769	11.885	5.5	14	19	10	0	0	2	RNF187, LOC100129084	13852, 10738	downstream, downstream	ActReg chr1 #1951	0	1	0
1952	1	228,742,887	228,743,425	538	1	3.294	3.647	11.412	5	6	17	1	0	4	RN5S1, RN5S2, RN5S3, RN5S4	2977, 5218, 7459, 9700	downstream, downstream, downstream, downstream, downstream	ActReg chr1 #1952	0	0	1
1953	1	228,771,081	228,771,390	309	1	5.222	3.889	12.111	10	6	15	1	5	9	RN5S8, RN5S9, RN5S10, RN5S11, RN5S12, RN5S13, RN5S14, RN5S15, RN5S16	-9461, -7222, -4980, -2739, -499, 1726, 3967, 6198, 8439	upstream, upstream, upstream, upstream, upstream, upstream, downstream, downstream, downstream, downstream, downstream	ActReg chr1 #1953	0	0	1
1954	1	228,782,376	228,784,278	1,902	4	12.034	13	8.441	21	23	16	1	4	5	RN5S13, RN5S14, RN5S15, RN5S16, RN5S17	-10366, -8125, -5884, 3653, -1422	upstream, upstream, upstream, upstream, upstream	ActReg chr1 #1954	1	1	0
1955	1	228,870,580	228,871,569	989	1	6.968	10.484	6.586	17	20	12	1	1	1	RHOU	205	in gene	ActReg chr1 #1955	0	1	0
1956	1	228,918,181	228,919,116	935	1	8.862	10.621	2.52	13	19	5	0	0	0				ActReg chr1 #1956	0	1	0
1957	1	228,977,800	228,978,454	654	1	14.1	10.45	5.8	28	15	9	0	0	0				ActReg chr1 #1957	1	0	0
1958	1	229,038,647	229,039,671	1,024	1	7.375	11.688	7.125	12	19	12	0	0	0				ActReg chr1 #1958	0	1	0
1959	1	229,073,422	229,074,293	871	1	8.778	13.482	8.704	13	23	14	0	0	0				ActReg chr1 #1959	0	1	0
1960	1	229,159,256	229,160,053	797	1	10.96	9.04	5.56	17	12	8	0	0	0				ActReg chr1 #1960	1	0	0
1961	1	229,230,487	229,231,278	791	1	12.24	8.12	4.5	21	16	8	0	0	0				ActReg chr1 #1961	1	0	0
1962	1	229,283,431	229,283,823	392	1	2.75	4.833	13.583	4	7	21	0	0	0				ActReg chr1 #1962	0	0	1
1963	1	229,334,912	229,335,882	970	1	8.355	10.387	4.71	13	16	9	0	0	0				ActReg chr1 #1963	0	1	0
1964	1	229,406,450	229,407,193	743	1	6.391	11.783	5.1	11	18	8	1	1	1	RAB4A	-58	upstream	ActReg chr1 #1964	0	1	0
1965	1	229,477,971	229,479,095	1,124	1	10.543	14.057	7.5	18	22	19	1	1	1	C1orf96	155	in gene	ActReg chr1 #1965	0	1	0
1966	1	229,543,197	229,543,897	700	1	4.455	5.545	12.682	8	10	20	1	0	0				ActReg chr1 #1966	0	0	1
1967	1	229,566,149	229,566,961	812	1	13.04	10.12	7.76	20	22	13	0	0	1	ACTA1	3,288	downstream	ActReg chr1 #1967	1	0	0
1968	1	229,567,679	229,568,240	561	1	5	6.389	15	9	12	22	1	1	2	ACTA1, NUP133	1884, 76129	in gene, downstream	ActReg chr1 #1968	0	0	1
1969	1	229,568,553	229,569,017	464	1	5.357	8	12.714	9	11	17	1	1	2	ACTA1, NUP133	1058, 75303	in gene, downstream	ActReg chr1 #1969	0	0	1
1970	1	229,569,261	229,570,189	928	1	3.786	5.414	13.69	10	8	23	1	1	2	ACTA1, NUP133	118, 74363	in gene, downstream	ActReg chr1 #1970	0	0	1
1971	1	229,643,585	229,644,554	969	2	10.633	17.333	15.133	19	30	28	1	1	2	NUP133, ABCB10	19, 50373	in gene, downstream	ActReg chr1 #1971	0	1	1
1972	1	229,694,194	229,695,606	1,412	3	14.886	17.454	6.341	32	40	19	1	1	1	ABCB10	-458	upstream	ActReg chr1 #1972	1	1	1
1973	1	229,761,595	229,762,531	936	3	14.4	15.6	11.8	33	37	19	1	2	2	TAF5L, URB2	-269, 82	upstream, in gene	ActReg chr1 #1973	1	1	1
1974	1	229,799,422	229,800,654	1,232	2	15.154	18.077	5.528	37	35	11	0	0	1	URB2	38,057	downstream	ActReg chr1 #1974	1	1	0
1975	1	229,979,453	229,980,113	660	1	11.429	5.857	1.75	18	9	3	0	0	0				ActReg chr1 #1975	1	0	0
1976	1	230,208,823	230,209,638	815	1	11.692	8.923	5.269	15	13	12	0	0	1	GALNT2	6,274	in gene	ActReg chr1 #1976	1	0	0
1977	1	230,240,304	230,241,074	770	1	10.167	14.542	5.087	16	22	8	0	0	1	GALNT2	37,733	in gene	ActReg chr1 #1977	0	1	0
1978	1	230,439,376	230,440,131	755	1	10.917	13.042	3.222	16	26	5	0	0	0				ActReg chr1 #1978	0	1	0
1979	1	230,443,626	230,444,368	742	1	12.913	16.087	3.682	31	32	6	0	0	0				ActReg chr1 #1979	0	1	0
1980	1	230,468,252	230,468,821	569	1	5.556	4.889	13.611	10	9	19	1	0	1	PGBD5	44,855	in gene	ActReg chr1 #1980	0	0	1
1981	1	230,472,524	230,473,248	724	1	3.13	4.391	11.348	7	8	16	0	0	1	PGBD5	40,505	in gene	ActReg chr1 #1981	0	0	1
1982	1	230,526,265	230,526,585	320	1	1.9	3.4	12.1	3	5	15	0	0	0				ActReg chr1 #1982	0	0	1
1983	1	230,562,188	230,563,535	1,347	2	12.143	14.429	5.128	27	27	12	1	0	0				ActReg chr1 #1983	1	1	0
1984	1	230,572,294	230,572,777	483	1	1.923	2.571	12	3	5	18	0	0	0				ActReg chr1 #1984	0	0	1
1985	1	230,777,455	230,778,900	1,445	2	60.333	59.867	7.211	253	237	16	1	1	1	COG2	-25	upstream	ActReg chr1 #1985	1	1	0
1986	1	230,839,482	230,840,021	539	1	5.294	6.235	11.059	8	9	16	0	0	2	COG2, AGT	61549, 10585	downstream, in gene	ActReg chr1 #1986	0	0	1
1987	1	230,992,426	230,993,425	999	1	9.581	13.226	3.296	16	25	6	0	0	1	C1orf198	12,410	in gene	ActReg chr1 #1987	0	1	0
1988	1	230,994,455	230,995,269	814	1	8.346	10.538	5.077	13	16	9	0	0	1	C1orf198	10,473	in gene	ActReg chr1 #1988	0	1	0
1989	1	231,114,323	231,115,308	985	3	16.097	13.839	9.519	30	29	19	1	2	2	TTC13, ARV1	-197, -8	upstream, upstream	ActReg chr1 #1989	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
1990	1	231,228,750	231,229,713	963	1	12.3	6.967	4.233	17	11	12	0	0	0				ActReg chr1 #1990	1	0	0
1991	1	231,274,613	231,276,199	1,586	2	11.46	15.34	4.841	23	29	12	0	0	0				ActReg chr1 #1991	1	1	0
1992	1	231,296,149	231,296,974	825	1	4.615	3.72	12.846	8	6	19	1	1	1	TRIM67	-2,113	upstream	ActReg chr1 #1992	0	0	1
1993	1	231,297,649	231,299,038	1,389	3	12	16.023	8.81	26	35	19	1	1	1	TRIM67	-331	upstream	ActReg chr1 #1993	1	1	1
1994	1	231,346,967	231,347,738	771	1	11	9.083	7.75	17	18	14	0	0	1	TRIM67	48,678	in gene	ActReg chr1 #1994	1	0	0
1995	1	231,376,672	231,377,536	864	1	9.821	11.607	12.464	17	17	20	1	2	2	C1orf131, GNPAT	-180, 185	upstream, in gene	ActReg chr1 #1995	0	0	1
1996	1	231,428,230	231,428,576	346	1	5.273	2.818	11.818	8	6	19	0	0	0				ActReg chr1 #1996	0	0	1
1997	1	231,451,405	231,451,923	518	1	5.688	5.125	10.875	9	8	17	0	0	0				ActReg chr1 #1997	0	0	1
1998	1	231,472,951	231,474,543	1,592	2	11.22	15.14	10.46	28	28	20	1	2	2	EXOC8, C1orf124	-169, 65	upstream, in gene	ActReg chr1 #1998	0	1	1
1999	1	231,647,737	231,648,363	626	1	11.85	7.95	2.533	21	11	4	0	0	0				ActReg chr1 #1999	1	0	0
2000	1	231,663,741	231,664,883	1,142	3	13.028	17.861	9.083	25	38	16	1	2	2	TSNAX-DISC1, TSNAX	-87, -87	upstream, upstream	ActReg chr1 #2000	1	1	1
2001	1	231,762,555	231,763,151	596	1	11.316	8.789	14.737	15	15	25	1	1	2	TSNAX-DISC1, DISC1	98454, 292	in gene, in gene	ActReg chr1 #2001	0	0	1
2002	1	232,182,071	232,182,964	893	1	10.607	11.143	2.214	14	15	4	0	0	2	TSNAX-DISC1, DISC1	518118, 419956	downstream, downstream	ActReg chr1 #2002	0	1	0
2003	1	232,505,026	232,506,025	999	1	9.29	12.742	3.613	17	19	5	0	0	0				ActReg chr1 #2003	0	1	0
2004	1	232,508,138	232,509,357	1,219	1	10.763	15.21	5.553	21	26	10	0	0	0				ActReg chr1 #2004	0	1	0
2005	1	232,514,195	232,514,732	537	1	7.294	6	13.177	11	11	19	0	0	0				ActReg chr1 #2005	0	0	1
2006	1	232,520,664	232,521,551	887	1	10.643	12.143	5.607	18	20	12	0	0	0				ActReg chr1 #2006	0	1	0
2007	1	232,673,823	232,674,373	550	1	11.556	11.389	3.529	17	18	6	0	0	0				ActReg chr1 #2007	0	1	0
2008	1	232,839,927	232,841,095	1,168	1	14.946	10.919	2.371	26	24	7	0	0	0				ActReg chr1 #2008	1	0	0
2009	1	232,902,981	232,903,839	858	1	8.846	11.654	2.923	15	19	5	0	0	0				ActReg chr1 #2009	0	1	0
2010	1	232,909,110	232,909,367	257	1	6.875	4.5	10.75	10	6	14	0	0	0				ActReg chr1 #2010	0	0	1
2011	1	233,085,609	233,086,659	1,050	1	12.364	9.152	9.583	18	14	16	1	1	1	C1orf57	-236	upstream	ActReg chr1 #2011	1	0	0
2012	1	233,126,366	233,127,054	688	1	4.571	6.136	11.227	9	9	16	0	0	1	PCNXL2	304,749	in gene	ActReg chr1 #2012	0	0	1
2013	1	233,248,499	233,249,827	1,328	2	13.405	14.833	2.75	29	24	5	0	0	1	PCNXL2	182,296	in gene	ActReg chr1 #2013	1	1	0
2014	1	233,463,756	233,464,445	689	1	5.333	9.762	1.647	11	14	2	1	1	1	KIAA1804	586	in gene	ActReg chr1 #2014	0	1	0
2015	1	233,679,162	233,680,036	874	2	14.179	16.143	1.926	26	34	3	0	0	0				ActReg chr1 #2015	1	1	0
2016	1	234,040,963	234,041,648	685	1	10.429	8.857	11.571	14	15	17	1	1	1	SLC35F3	626	in gene	ActReg chr1 #2016	0	0	1
2017	1	234,129,283	234,129,951	668	1	8.684	12.7	4.1	13	22	9	0	0	1	SLC35F3	88,938	in gene	ActReg chr1 #2017	0	1	0
2018	1	234,321,665	234,322,363	698	1	10.095	11.714	5.143	16	19	11	0	0	1	SLC35F3	281,335	in gene	ActReg chr1 #2018	0	1	0
2019	1	234,349,663	234,350,207	544	1	5.588	11.765	3.059	10	20	6	1	0	1	SLC35F3	309,256	in gene	ActReg chr1 #2019	0	1	0
2020	1	234,353,389	234,354,299	910	1	11.429	8.357	4.615	16	16	8	0	0	1	SLC35F3	313,165	in gene	ActReg chr1 #2020	1	0	0
2021	1	234,508,709	234,509,825	1,116	3	15.314	15.257	10.333	36	28	24	1	2	2	LOC100506778, C1orf61	112, -162	in gene, upstream	ActReg chr1 #2021	1	1	1
2022	1	234,663,672	234,664,608	936	1	6.321	10.9	1.833	9	16	4	0	0	1	LOC100506795	3,385	in gene	ActReg chr1 #2022	0	1	0
2023	1	234,792,417	234,794,444	2,027	2	10.857	12.016	3.778	23	23	8	0	0	0				ActReg chr1 #2023	1	1	0
2024	1	234,857,999	234,859,366	1,367	1	12.209	8	3.821	16	13	8	0	1	1	LOC100506810	-1,107	upstream	ActReg chr1 #2024	1	0	0
2025	1	234,915,922	234,916,835	913	1	12.931	13.31	18.172	21	18	36	0	0	0				ActReg chr1 #2025	0	0	1
2026	1	235,001,700	235,002,687	987	1	14.567	10.533	4.433	19	17	7	0	0	0				ActReg chr1 #2026	1	0	0
2027	1	235,054,908	235,055,277	369	1	5.083	6.583	12.75	9	9	21	0	0	0				ActReg chr1 #2027	0	0	1
2028	1	235,068,785	235,069,732	947	1	7.9	13.6	4.867	14	25	11	0	0	0				ActReg chr1 #2028	0	1	0
2029	1	235,110,018	235,111,467	1,449	2	12.111	13.489	3.023	25	23	7	0	0	0				ActReg chr1 #2029	1	1	0
2030	1	235,115,899	235,117,323	1,424	2	13.644	13.378	5.578	29	21	9	0	0	0				ActReg chr1 #2030	1	1	0
2031	1	235,125,150	235,125,598	448	1	4.429	6.929	11.786	6	11	16	0	0	0				ActReg chr1 #2031	0	0	1
2032	1	235,132,866	235,133,623	757	1	13.043	11.217	3.565	24	18	6	0	0	0				ActReg chr1 #2032	1	0	0
2033	1	235,147,294	235,148,609	1,315	2	12.286	10.095	6.385	23	23	12	0	0	0				ActReg chr1 #2033	1	1	0
2034	1	235,270,879	235,271,524	645	1	5.571	6.476	12	9	10	16	0	0	1	TOMM20	21,055	downstream	ActReg chr1 #2034	0	0	1
2035	1	235,291,625	235,292,712	1,087	3	14.588	14.618	11.677	25	31	28	1	2	3	TOMM20, SNORA14B, RBM34	88, -916, 32403	in gene, upstream, downstream	ActReg chr1 #2035	1	1	1
2036	1	235,324,134	235,325,056	922	1	11.966	15.207	6.069	19	27	10	1	1	2	RBM34, ARID4B	-24, 166937	upstream, downstream	ActReg chr1 #2036	0	1	0
2037	1	235,491,170	235,492,622	1,452	1	10.2	11.956	8.409	16	20	17	1	2	2	ARID4B, GGPS1	-364, 143	upstream, in gene	ActReg chr1 #2037	0	1	0
2038	1	235,530,408	235,531,480	1,072	1	8.848	11.97	7.061	20	17	16	0	1	1	TBCE	216	in gene	ActReg chr1 #2038	0	1	0
2039	1	235,667,347	235,668,887	1,540	3	14.438	16.521	8.854	28	28	19	1	1	1	B3GALNT2	-336	upstream	ActReg chr1 #2039	1	1	1
2040	1	235,672,997	235,673,357	360	1	4	2.909	11.454	6	4	17	0	1	1	B3GALNT2	-5,396	upstream	ActReg chr1 #2040	0	0	1
2041	1	235,757,763	235,758,345	582	1	3.556	4.778	14.111	6	9	18	0	0	1	GNG4	56,000	in gene	ActReg chr1 #2041	0	0	1
2042	1	235,799,559	235,800,056	497	1	5.8	9.733	11.667	10	14	16	0	0	1	GNG4	14,247	in gene	ActReg chr1 #2042	0	0	1
2043	1	235,804,785	235,806,706	1,921	2	11.833	12.167	8.067	21	23	20	1	0	1	GNG4	8,309	in gene	ActReg chr1 #2043	1	1	0
2044	1	236,029,361	236,030,922	1,561	3	11.878	11.245	8.286	19	16	20	1	1	1	LYST	79	in gene	ActReg chr1 #2044	1	1	1
2045	1	236,046,308	236,047,417	1,109	1	9.647	12.647	4	15	18	9	0	0	0				ActReg chr1 #2045	0	1	0
2046	1	236,066,189	236,066,975	786	1	12.125	7.333	3.714	20	13	9	0	0	0				ActReg chr1 #2046	1	0	0
2047	1	236,081,241	236,081,967	726	1	8.304	12.261	5.652	13	16	11	0	0	0				ActReg chr1 #2047	0	1	0
2048	1	236,156,718	236,157,231	513	1	4.625	7.5	12.5	8	10	19	1	0	1	NID1	71,507	in gene	ActReg chr1 #2048	0	0	1
2049	1	236,162,152	236,163,535	1,383	2	11.721	11.977	5.135	20	20	10	0	0	1	NID1	65,638	in gene	ActReg chr1 #2049	1	1	0
2050	1	236,188,960	236,189,833	873	1	7.321	11.857	4.179	11	15	7	0	0	1	NID1	39,085	in gene	ActReg chr1 #2050	0	1	0
2051	1	236,227,167	236,229,144	1,977	1	10.419	12.806	9.129	23	26	21	1	1	1	NID1	326	in gene	ActReg chr1 #2051	0	1	0
2052	1	236,291,972	236,292,646	674	1	8.571	11.809	5.762	13	21	13	0	0	0				ActReg chr1 #2052	0	1	0
2053	1	236,444,960	236,445,373	413	1	8.692	11.154	12.769	11	15	21	1	1	1	ERO1LB	173	in gene	ActReg chr1 #2053	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2054	1	236,449,704	236,451,015	1,311	2	8.805	13.171	3	15	23	8	0	1	1	ERO1LB	-5,020	upstream	ActReg chr1 #2054	1	1	0
2055	1	236,686,695	236,688,310	1,615	2	9.46	13.34	12.766	15	27	31	1	1	2	LGALS8, LOC100287902	5937, 306	in gene, in gene	ActReg chr1 #2055	0	1	1
2056	1	236,909,983	236,910,654	671	1	11.524	8.619	3.619	21	15	7	0	0	1	ACTN2	60,548	in gene	ActReg chr1 #2056	1	0	0
2057	1	236,958,016	236,959,275	1,259	2	10.325	13.425	9.1	16	18	17	1	1	1	MTR	64	in gene	ActReg chr1 #2057	0	1	1
2058	1	237,368,090	237,368,637	547	1	4.471	6.118	13.412	9	10	21	0	0	1	RYR2	162,661	in gene	ActReg chr1 #2058	0	0	1
2059	1	237,922,298	237,923,531	1,233	2	14.897	14.18	2.914	35	27	6	0	0	1	RYR2	717,212	in gene	ActReg chr1 #2059	1	1	0
2060	1	237,945,908	237,946,616	708	1	4.727	11.091	1.9	8	17	3	0	0	1	RYR2	740,560	in gene	ActReg chr1 #2060	0	1	0
2061	1	238,036,593	238,037,671	1,078	1	13.588	15.059	2.591	27	25	5	0	0	1	ZP4	17,090	downstream	ActReg chr1 #2061	0	1	0
2062	1	238,041,905	238,043,138	1,233	1	10.436	6.231	3.625	16	13	5	0	0	1	ZP4	11,701	in gene	ActReg chr1 #2062	1	0	0
2063	1	238,054,844	238,055,909	1,065	2	11.588	13.118	2.121	24	22	4	0	1	1	ZP4	-1,154	upstream	ActReg chr1 #2063	1	1	0
2064	1	238,066,986	238,067,769	783	2	13.917	12.125	1.905	26	20	4	0	0	0				ActReg chr1 #2064	1	1	0
2065	1	238,226,046	238,227,352	1,306	2	13	16.317	4.919	35	37	9	0	0	0				ActReg chr1 #2065	1	1	0
2066	1	238,251,611	238,252,675	1,064	2	13.588	11.765	2.941	23	21	5	0	0	0				ActReg chr1 #2066	1	1	0
2067	1	238,571,974	238,573,127	1,153	2	15.278	12.889	2.758	30	30	6	0	0	0				ActReg chr1 #2067	1	1	0
2068	1	238,769,951	238,770,669	718	1	13.217	10	2.412	23	16	5	0	0	0				ActReg chr1 #2068	1	0	0
2069	1	238,810,992	238,811,699	707	2	13.864	12.591	1.368	22	27	2	0	0	0				ActReg chr1 #2069	1	1	0
2070	1	239,977,490	239,978,336	846	1	12.444	9.185	3.889	20	16	6	0	0	1	CHRM3	185,540	in gene	ActReg chr1 #2070	1	0	0
2071	1	240,021,225	240,021,896	671	2	10.429	11.286	2.8	21	23	4	0	0	1	CHRM3	229,187	in gene	ActReg chr1 #2071	1	1	0
2072	1	240,107,213	240,107,667	454	1	4.214	4.5	10.286	6	7	16	0	0	0				ActReg chr1 #2072	0	0	1
2073	1	240,255,314	240,256,238	924	2	12.379	7.31	11.448	16	11	19	1	1	1	FMN2	591	in gene	ActReg chr1 #2073	1	0	1
2074	1	240,256,281	240,256,849	568	1	8.389	5.611	15.111	13	9	30	1	1	1	FMN2	1,380	in gene	ActReg chr1 #2074	0	0	1
2075	1	240,925,903	240,926,373	470	1	3.769	2.667	9.8	7	4	18	0	0	0				ActReg chr1 #2075	0	0	1
2076	1	241,319,909	241,320,367	458	1	9.538	12.929	1.9	13	20	3	0	0	1	RGS7	200,340	in gene	ActReg chr1 #2076	0	1	0
2077	1	241,486,524	241,487,369	845	2	10.963	18.63	2	22	45	4	0	0	1	RGS7	33,532	in gene	ActReg chr1 #2077	1	1	0
2078	1	241,520,078	241,520,640	562	1	8.389	11.778	2.545	14	19	4	1	1	1	RGS7	119	in gene	ActReg chr1 #2078	0	1	0
2079	1	241,586,857	241,587,742	885	3	12.926	12.815	10.167	24	20	16	1	0	0				ActReg chr1 #2079	1	1	1
2080	1	241,587,816	241,588,298	482	1	9.867	7.533	11.067	14	11	16	1	0	0				ActReg chr1 #2080	0	0	1
2081	1	241,682,159	241,683,412	1,253	3	10.641	16.231	8.385	24	34	19	1	1	1	FH	300	in gene	ActReg chr1 #2081	1	1	1
2082	1	241,754,476	241,756,129	1,653	2	9.327	13.885	2.182	20	26	5	0	0	2	KMO, OPN3	59622, 48399	in gene, downstream	ActReg chr1 #2082	1	1	0
2083	1	241,870,283	241,871,312	1,029	1	7.438	12.219	3.227	22	20	5	0	0	1	WDR64	-55,217	in gene	ActReg chr1 #2083	0	1	0
2084	1	242,010,894	242,011,947	1,053	2	15.424	16.061	8.909	28	29	15	1	1	1	EXO1	-73	upstream	ActReg chr1 #2084	1	1	0
2085	1	242,120,926	242,121,330	404	1	7.462	3.385	12.538	9	6	19	0	1	1	BECN1L1	59	in gene	ActReg chr1 #2085	0	0	1
2086	1	242,121,339	242,122,024	685	1	5.727	4.818	11.5	11	9	15	0	1	1	BECN1L1	612	in gene	ActReg chr1 #2086	0	0	1
2087	1	242,687,027	242,687,619	592	1	5.684	6.632	13.895	8	9	21	1	1	1	PLD5	675	in gene	ActReg chr1 #2087	0	0	1
2088	1	242,852,739	242,853,194	455	1	4.583	5.5	11.643	7	8	16	0	0	0				ActReg chr1 #2088	0	0	1
2089	1	242,927,185	242,927,522	337	1	2.273	1.909	10.454	3	3	15	0	0	0				ActReg chr1 #2089	0	0	1
2090	1	243,010,596	243,011,118	522	2	11.188	10.125	2.938	20	14	5	0	0	0				ActReg chr1 #2090	1	1	0
2091	1	243,053,314	243,053,836	522	1	10.312	3.312	6.5	17	7	10	1	0	0				ActReg chr1 #2091	1	0	0
2092	1	243,418,160	243,419,740	1,580	2	10.755	13.837	7.417	19	24	16	1	2	2	CEP170, SDCCAG8	-242, -370	upstream, upstream	ActReg chr1 #2092	1	1	0
2093	1	243,432,779	243,433,386	607	1	8.421	10.737	4.125	11	17	9	0	0	1	SDCCAG8	13,762	in gene	ActReg chr1 #2093	0	1	0
2094	1	244,012,128	244,013,206	1,078	1	8.765	10.706	3.242	14	17	8	1	1	1	AKT3	-6,114	upstream	ActReg chr1 #2094	0	1	0
2095	1	244,014,198	244,015,016	818	1	7.654	10.039	6.522	14	14	16	1	0	1	AKT3	-8,054	upstream	ActReg chr1 #2095	0	1	0
2096	1	244,067,077	244,067,827	750	2	14.478	12.826	1.4	28	28	2	0	0	0				ActReg chr1 #2096	1	1	0
2097	1	244,137,500	244,138,614	1,114	2	13.4	17.229	2.296	31	35	4	0	0	1	LOC339529	57,353	in gene	ActReg chr1 #2097	1	1	0
2098	1	244,211,142	244,211,574	432	1	9.615	10.462	13.231	15	13	21	1	1	2	LOC339529, ZNF238	130654, -3203	downstream, upstream	ActReg chr1 #2098	0	0	1
2099	1	244,212,795	244,213,082	287	1	4.111	8.222	11.333	5	10	15	0	1	2	LOC339529, ZNF238	132234, -1623	downstream, upstream	ActReg chr1 #2099	0	0	1
2100	1	244,327,049	244,327,886	837	1	10.615	12.154	2.88	16	17	6	0	0	0				ActReg chr1 #2100	0	1	0
2101	1	244,377,245	244,378,083	838	1	13.852	9.741	4.296	23	17	8	0	0	0				ActReg chr1 #2101	1	0	0
2102	1	244,516,919	244,517,486	567	1	10.056	11.5	6.667	16	17	12	0	1	1	C1orf100	1,265	in gene	ActReg chr1 #2102	0	1	0
2103	1	244,614,211	244,615,320	1,109	2	10.382	13.5	13.147	16	25	22	1	1	2	ADSS, C1orf101	648, -9908	in gene, upstream	ActReg chr1 #2103	0	1	1
2104	1	244,816,451	244,817,075	624	1	8.158	8.947	15.263	14	16	24	1	1	1	PPPDE1	411	in gene	ActReg chr1 #2104	0	0	1
2105	1	244,997,689	244,998,937	1,248	2	11.051	11.487	7.821	19	19	18	1	1	2	FAM36A, NCRNA00201	-326, 11930	upstream, downstream	ActReg chr1 #2105	1	1	0
2106	1	245,026,799	245,028,736	1,937	3	11.607	14.262	8.617	21	24	23	1	1	1	HNRNPU	60	in gene	ActReg chr1 #2106	1	1	1
2107	1	245,132,876	245,134,902	2,026	3	10.095	14.286	8.508	22	34	16	1	1	1	EFCAB2	718	in gene	ActReg chr1 #2107	1	1	1
2108	1	245,589,836	245,590,357	521	1	4.562	3.143	10.812	7	7	16	0	0	1	KIF26B	271,809	in gene	ActReg chr1 #2108	0	0	1
2109	1	245,748,495	245,749,206	711	1	12.227	10.454	2.5	17	16	6	0	0	1	KIF26B	430,563	in gene	ActReg chr1 #2109	1	0	0
2110	1	245,851,888	245,852,385	497	1	2.125	4.125	15.5	4	7	26	1	0	1	KIF26B	533,849	in gene	ActReg chr1 #2110	0	0	1
2111	1	245,966,001	245,966,843	842	2	9.5	11.5	4.269	16	18	7	0	0	1	SMYD3	704,222	in gene	ActReg chr1 #2111	1	1	0
2112	1	246,675,446	246,675,954	508	1	2.875	2.929	13.25	5	5	19	0	1	1	SMYD3	-5,056	upstream	ActReg chr1 #2112	0	0	1
2113	1	246,729,581	246,730,122	541	1	12.882	13.118	14.059	20	20	20	1	2	2	TFB2M, CNST	-286, 212	upstream, in gene	ActReg chr1 #2113	0	0	1
2114	1	246,810,372	246,811,126	754	1	13.478	12.174	4	25	20	6	0	0	1	CNST	81,110	in gene	ActReg chr1 #2114	1	0	0
2115	1	247,094,852	247,095,968	1,116	1	11.4	17.686	7.594	20	36	13	1	1	1	AHCTF1	-684	upstream	ActReg chr1 #2115	0	1	0
2116	1	247,241,501	247,242,338	837	3	11.444	10.259	9.185	19	18	20	1	1	1	ZNF670	196	in gene	ActReg chr1 #2116	1	1	1
2117	1	247,250,751	247,251,281	530	1	5.176	4.059	15.647	9	5	24	0	0	1	ZNF670	-8,901	upstream	ActReg chr1 #2117	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2118	1	247,267,005	247,267,820	815	1	8.385	13.154	9.346	18	25	18	1	1	2	ZNF669, C1orf229	262, 8307	in gene, downstream	ActReg chr1 #2118	0	1	0
2119	1	247,275,599	247,276,115	516	1	6.875	4.562	12.812	10	6	21	1	1	2	ZNF669, C1orf229	-8183, -138	upstream, upstream	ActReg chr1 #2119	0	0	1
2120	1	247,278,467	247,279,212	745	1	5.609	6.217	11.522	8	12	15	1	1	1	C1orf229	-5,120	upstream	ActReg chr1 #2120	0	0	1
2121	1	247,282,214	247,282,893	679	1	4.571	4.714	11.667	10	8	17	0	1	1	C1orf229	-6,834	upstream	ActReg chr1 #2121	0	0	1
2122	1	247,373,564	247,374,464	900	2	9.517	10.138	9.407	20	15	13	1	0	0				ActReg chr1 #2122	1	1	0
2123	1	247,494,179	247,496,032	1,853	3	11.448	11.379	7.632	25	19	20	1	1	1	ZNF496	-60	upstream	ActReg chr1 #2123	1	1	1
2124	1	247,505,781	247,506,521	740	1	4.826	11.435	2.045	9	18	4	0	0	0				ActReg chr1 #2124	0	1	0
2125	1	247,802,533	247,803,341	808	2	13.04	10.96	2.739	20	22	6	1	1	1	LOC100507070	1,228	in gene	ActReg chr1 #2125	1	1	0
2126	1	248,020,436	248,021,137	701	2	10.364	11.454	3.438	15	16	5	1	1	1	TRIM58	285	in gene	ActReg chr1 #2126	1	1	0
2127	1	248,100,314	248,100,845	531	1	8.176	11.647	7.118	12	21	13	1	1	1	OR2L13	86	in gene	ActReg chr1 #2127	0	1	0
2128	1	249,119,632	249,121,201	1,569	1	10.469	13.347	7.449	18	25	18	1	2	2	SH3BP5L, MIR3124	-262, -160	upstream, upstream	ActReg chr1 #2128	0	1	0
2129	1	249,131,944	249,133,610	1,666	2	13.538	15.788	10.462	25	34	17	1	1	1	ZNF672	247	in gene	ActReg chr1 #2129	1	1	0
2130	1	249,151,837	249,153,820	1,983	3	14.823	16.177	8.242	36	39	16	1	1	2	ZNF672, ZNF692	20298, 487	downstream, in gene	ActReg chr1 #2130	1	1	0
2131	1	249,166,960	249,168,959	1,999	3	15.113	12.903	12.783	29	25	37	1	0	0				ActReg chr1 #2131	1	1	1
2132	1	249,199,964	249,200,761	797	1	10.8	18.08	8.84	17	33	21	1	1	1	PGBD2	-80	upstream	ActReg chr1 #2132	0	1	0
2133	10	1,033,819	1,034,707	888	2	14.857	15.071	6.643	36	32	13	1	2	2	LOC100288619, GTPBP4	18, -86	in gene, upstream	ActReg chr10 #2133	1	1	0
2134	10	1,094,527	1,095,459	932	2	9.433	11.9	5.917	14	21	14	1	2	3	C10orf110, IDI1, WDR37	26416, 68, -7783	downstream, in gene, upstream	ActReg chr10 #2134	1	1	0
2135	10	2,256,270	2,256,706	436	1	8.429	5.357	2	14	10	3	0	0	0				ActReg chr10 #2135	1	0	0
2136	10	2,274,645	2,275,049	404	1	7.769	13.615	1	12	23	1	0	0	0				ActReg chr10 #2136	0	1	0
2137	10	3,006,602	3,006,993	391	1	5.167	10.583	2.556	7	15	3	0	0	0				ActReg chr10 #2137	0	1	0
2138	10	3,389,803	3,390,300	497	1	4.067	9.733	3.2	8	16	6	0	0	0				ActReg chr10 #2138	0	1	0
2139	10	3,966,424	3,966,985	561	1	5.222	9.056	2.667	10	17	4	0	0	0				ActReg chr10 #2139	0	1	0
2140	10	4,746,238	4,746,688	450	2	9.333	10.6	1	15	15	1	0	0	0				ActReg chr10 #2140	1	1	0
2141	10	4,925,384	4,926,028	644	2	10.55	9.25	1.412	18	16	3	0	0	0				ActReg chr10 #2141	1	1	0
2142	10	5,359,580	5,360,058	478	1	9.667	5.267	1.75	15	8	2	0	0	0				ActReg chr10 #2142	1	0	0
2143	10	5,553,512	5,553,844	332	1	1	2.3	11.6	1	3	15	0	0	0				ActReg chr10 #2143	0	0	1
2144	10	6,019,336	6,020,084	748	1	11.87	8.043	4.714	20	13	9	1	1	1	IL15RA	432	in gene	ActReg chr10 #2144	1	0	0
2145	10	6,130,601	6,131,054	453	2	10.357	9.857	1	17	17	1	1	1	1	RBM17	-122	upstream	ActReg chr10 #2145	1	1	0
2146	10	6,224,723	6,225,018	295	1	2.889	3.889	9.889	4	5	14	0	0	1	PFKFB3	38,027	in gene	ActReg chr10 #2146	0	0	1
2147	10	6,244,624	6,245,152	528	1	10	9.765	13.059	17	15	24	1	0	1	PFKFB3	58,045	in gene	ActReg chr10 #2147	0	0	1
2148	10	6,755,072	6,756,128	1,056	3	10.059	11.235	1.833	23	22	3	0	0	0				ActReg chr10 #2148	1	1	0
2149	10	7,029,265	7,029,773	508	1	5.875	12.25	3.812	11	17	7	0	0	0				ActReg chr10 #2149	0	1	0
2150	10	7,691,885	7,692,384	499	1	8.438	10.438	2	14	15	3	0	0	1	ITIH5	16,827	in gene	ActReg chr10 #2150	0	1	0
2151	10	7,860,107	7,861,055	948	2	13.414	13.172	4.552	29	23	11	1	1	1	TAF3	-92	upstream	ActReg chr10 #2151	1	1	0
2152	10	12,084,692	12,085,396	704	2	10.046	11.273	2.75	20	19	7	1	1	1	UPF2	-21	upstream	ActReg chr10 #2152	1	1	0
2153	10	13,203,058	13,203,817	759	2	14.292	9.667	4.9	27	18	8	1	1	1	MCM10	-117	upstream	ActReg chr10 #2153	1	1	0
2154	10	13,390,169	13,390,619	450	1	6.462	9.214	8.769	10	15	14	0	1	1	SEPHS1	-114	upstream	ActReg chr10 #2154	0	1	0
2155	10	13,404,664	13,405,058	394	1	8	9.769	2.273	13	16	3	0	0	0				ActReg chr10 #2155	0	1	0
2156	10	13,628,482	13,629,327	845	2	21.038	24.154	5.308	58	69	9	1	1	1	PRPF18	-35	upstream	ActReg chr10 #2156	1	1	0
2157	10	13,754,833	13,755,320	487	1	9.067	9.4	1.615	12	14	2	0	0	1	FRMD4A	617,790	in gene	ActReg chr10 #2157	0	1	0
2158	10	14,035,194	14,035,640	446	1	7.429	10	1.75	12	16	2	0	0	1	FRMD4A	537,449	in gene	ActReg chr10 #2158	0	1	0
2159	10	14,195,502	14,195,951	449	1	10.786	7.5	3.545	13	12	5	0	0	1	FRMD4A	177,140	in gene	ActReg chr10 #2159	1	0	0
2160	10	14,286,726	14,287,467	741	2	11.174	10.261	2	20	20	3	0	0	1	FRMD4A	85,770	in gene	ActReg chr10 #2160	1	1	0
2161	10	14,439,028	14,439,486	458	1	10.143	7.643	2	15	11	3	0	0	0				ActReg chr10 #2161	1	0	0
2162	10	14,880,781	14,881,239	458	1	4.143	5.286	11.714	6	7	19	1	2	2	CDNF, HSPA14	-1027, 749	upstream, in gene	ActReg chr10 #2162	0	0	1
2163	10	15,902,324	15,902,861	537	2	8.824	11.059	2.071	13	14	3	1	1	1	FAM188A	-73	upstream	ActReg chr10 #2163	1	1	0
2164	10	16,654,242	16,654,635	393	1	9.417	8.5	1.667	15	14	2	0	0	1	RSU1	205,015	in gene	ActReg chr10 #2164	1	0	0
2165	10	17,155,736	17,156,201	465	1	4.4	10.667	1.556	7	15	2	0	0	1	CUBN	15,848	in gene	ActReg chr10 #2165	0	1	0
2166	10	17,243,165	17,243,758	593	2	7.947	10.21	9.667	15	14	17	1	1	1	TRDMT1	609	in gene	ActReg chr10 #2166	0	1	1
2167	10	17,271,152	17,271,795	643	2	6.9	10.85	14.1	11	20	22	1	2	2	LOC100507347, VIM	-2576, 1215	upstream, in gene	ActReg chr10 #2167	0	1	1
2168	10	17,280,538	17,280,979	441	1	4.643	9.929	3.5	8	15	6	0	0	1	VIM	10,500	downstream	ActReg chr10 #2168	0	1	0
2169	10	17,495,580	17,495,940	360	1	4.167	4.833	11.833	7	7	16	1	1	1	ST8SIA6	494	in gene	ActReg chr10 #2169	0	0	1
2170	10	17,685,722	17,686,494	772	2	9.5	12.375	6.375	18	22	11	1	1	1	STAM	-16	upstream	ActReg chr10 #2170	1	1	0
2171	10	21,814,555	21,815,003	448	1	9.429	6.357	4.143	14	13	6	1	1	2	C10orf140, MLLT10	-168, -8323	upstream, upstream	ActReg chr10 #2171	1	0	0
2172	10	22,518,018	22,518,741	723	2	9.955	9.136	10.591	15	16	26	1	0	0				ActReg chr10 #2172	1	0	1
2173	10	22,726,033	22,726,418	385	1	3.417	6.583	11.75	9	12	15	1	2	2	LOC100499489, LOC100289455	633, 210	in gene, in gene	ActReg chr10 #2173	0	0	1
2174	10	24,078,879	24,079,577	698	2	16.364	13.6	1	41	30	1	0	0	1	KIAA1217	95,553	in gene	ActReg chr10 #2174	1	1	0
2175	10	24,115,214	24,115,898	684	1	5.714	11.857	1.278	11	26	2	0	0	1	KIAA1217	131,881	in gene	ActReg chr10 #2175	0	1	0
2176	10	24,624,705	24,625,013	308	1	4.444	3.333	11.111	6	5	14	0	0	1	KIAA1217	641,184	in gene	ActReg chr10 #2176	0	0	1
2177	10	25,463,158	25,465,096	1,938	4	11.869	16	5.873	29	35	16	1	2	2	LOC100128811, GPR158	1078, -163	in gene, upstream	ActReg chr10 #2177	1	1	0
2178	10	26,506,385	26,506,708	323	1	2	1	12.2	3	1	16	1	1	2	MYO3A, GAD2	283544, 1310	downstream, in gene	ActReg chr10 #2178	0	0	1
2179	10	27,149,480	27,150,033	553	2	4.941	9.471	6.647	9	16	14	1	1	1	ABI1	260	in gene	ActReg chr10 #2179	0	1	1
2180	10	27,194,459	27,194,788	329	1	1.273	3.636	10.546	2	5	14	0	0	0				ActReg chr10 #2180	0	0	1
2181	10	27,443,095	27,443,492	397	1	9.231	6.538	5.385	13	11	10	1	2	2	YME1L1, MASTL	28, -460	in gene, upstream	ActReg chr10 #2181	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2182	10	27,541,642	27,541,952	310	1	7.1	10.5	8.3	11	13	12	1	0	1	LOC100288039	-10,128	upstream	ActReg chr10 #2182	0	0	1
2183	10	27,792,860	27,793,563	703	1	7.545	12.364	6.909	12	23	12	1	1	1	RAB18	-38	upstream	ActReg chr10 #2183	0	1	0
2184	10	30,092,325	30,092,911	586	1	7.167	10.778	2.294	8	18	4	0	0	0				ActReg chr10 #2184	0	1	0
2185	10	30,451,873	30,452,113	240	1	3.4	1.857	10.571	4	2	12	0	0	0				ActReg chr10 #2185	0	0	1
2186	10	31,073,845	31,074,447	602	1	6.421	11.316	3.765	12	15	7	1	0	0				ActReg chr10 #2186	0	1	0
2187	10	31,320,513	31,321,035	522	1	4.062	9.062	5.333	9	16	10	1	1	2	ZNF438, LOC100507663	92, -9028	in gene, upstream	ActReg chr10 #2187	0	1	0
2188	10	31,893,412	31,893,981	569	1	11.412	7.765	2.471	19	9	5	0	0	0				ActReg chr10 #2188	1	0	0
2189	10	31,958,394	31,958,793	399	1	7.308	10.846	2.111	12	17	3	0	0	0				ActReg chr10 #2189	0	1	0
2190	10	32,039,359	32,039,692	333	1	2	5.364	9.364	4	8	13	0	0	0				ActReg chr10 #2190	0	0	1
2191	10	32,635,032	32,635,498	466	1	8.867	6.8	3.2	13	9	5	1	1	1	EPC1	848	in gene	ActReg chr10 #2191	1	0	0
2192	10	33,624,007	33,624,388	381	1	7.833	7	12.75	12	10	16	1	1	1	NRP1	-364	upstream	ActReg chr10 #2192	0	0	1
2193	10	34,524,380	34,524,906	526	2	10.353	12	1	19	25	1	0	0	1	PARD3	579,610	in gene	ActReg chr10 #2193	1	1	0
2194	10	34,999,299	34,999,839	540	1	4.312	9.625	2.571	7	17	4	0	0	1	PARD3	104,684	in gene	ActReg chr10 #2194	0	1	0
2195	10	35,379,082	35,379,927	845	2	17.615	15.269	2.739	40	32	5	1	1	1	CUL2	-210	upstream	ActReg chr10 #2195	1	1	0
2196	10	35,931,017	35,931,544	527	2	10.625	9.562	3.812	15	15	5	1	1	1	FZD8	-918	upstream	ActReg chr10 #2196	1	1	0
2197	10	38,299,627	38,300,113	486	1	6.867	10.6	12.333	9	15	17	1	1	1	ZNF33A	292	in gene	ActReg chr10 #2197	0	0	1
2198	10	43,249,703	43,250,366	663	1	2.2	3.65	14.35	3	6	24	1	1	1	LOC100505906	2,722	in gene	ActReg chr10 #2198	0	0	1
2199	10	43,277,679	43,278,570	891	2	8.357	11.714	6.25	16	19	12	1	1	1	BMS1	170	in gene	ActReg chr10 #2199	1	1	0
2200	10	43,428,870	43,429,237	367	1	2.818	2	11.091	5	3	16	1	0	0				ActReg chr10 #2200	0	0	1
2201	10	43,567,468	43,567,748	280	1	2.889	2.333	11.556	4	3	15	0	1	1	RET	-4,909	upstream	ActReg chr10 #2201	0	0	1
2202	10	43,778,218	43,779,382	1,164	2	10.5	16.306	4.139	21	27	7	0	0	0				ActReg chr10 #2202	1	1	0
2203	10	43,779,569	43,780,296	727	2	7.826	12.609	6.261	19	28	14	0	0	0				ActReg chr10 #2203	1	1	0
2204	10	43,846,229	43,846,693	464	1	1.75	3.267	11.133	2	6	16	1	0	0				ActReg chr10 #2204	0	0	1
2205	10	43,892,675	43,893,082	407	1	7	5.333	10.333	10	6	16	1	0	1	HNRNPF	11,818	in gene	ActReg chr10 #2205	0	0	1
2206	10	44,101,733	44,102,370	637	2	5.25	8.8	7.6	11	16	15	1	1	1	ZNF485	196	in gene	ActReg chr10 #2206	0	1	1
2207	10	44,144,087	44,144,703	616	1	6.579	10.105	2.059	9	16	3	1	1	1	ZNF32	-69	upstream	ActReg chr10 #2207	0	1	0
2208	10	44,185,723	44,186,063	340	1	6.545	4.364	11.273	8	8	15	1	0	0				ActReg chr10 #2208	0	0	1
2209	10	44,796,582	44,796,993	411	1	5.385	10	2.5	7	16	4	0	0	1	LOC100130539	8,583	downstream	ActReg chr10 #2209	0	1	0
2210	10	45,202,099	45,202,560	461	1	9.8	10.333	2.4	15	17	4	0	0	0				ActReg chr10 #2210	0	1	0
2211	10	46,951,196	46,951,663	467	1	7.467	10	2.8	10	16	4	0	1	2	LOC100507539, SYT15	-43, 19172	upstream, downstream	ActReg chr10 #2211	0	1	0
2212	10	46,969,883	46,970,413	530	1	6.412	6.235	12	10	11	19	1	1	2	LOC100507539, SYT15	18676, 453	downstream, in gene	ActReg chr10 #2212	0	0	1
2213	10	46,998,982	46,999,834	852	1	6.846	6.269	13.5	10	8	19	0	0	1	GPRIN2	5,862	in gene	ActReg chr10 #2213	0	0	1
2214	10	47,594,087	47,594,802	715	1	7.545	11.636	3.421	13	18	5	0	0	0				ActReg chr10 #2214	0	1	0
2215	10	47,605,931	47,606,452	521	1	9.875	5	1.667	16	8	4	0	0	0				ActReg chr10 #2215	1	0	0
2216	10	47,644,012	47,644,323	311	1	3.125	3	9.4	6	3	13	0	0	0				ActReg chr10 #2216	0	0	1
2217	10	48,485,601	48,485,901	300	1	5.222	6	11.667	7	7	14	0	0	0				ActReg chr10 #2217	0	0	1
2218	10	49,953,782	49,954,127	345	1	2.125	3.636	10.364	3	5	15	0	0	1	WDFY4	60,436	in gene	ActReg chr10 #2218	0	0	1
2219	10	50,605,849	50,606,500	651	2	11.048	9.762	5.619	21	17	9	1	1	1	DRGX	-6,267	upstream	ActReg chr10 #2219	1	1	0
2220	10	50,814,775	50,815,909	1,134	2	9.5	13.889	4.829	26	27	8	0	2	2	CHAT, SLC18A3	-1799, -3005	upstream, upstream	ActReg chr10 #2220	1	1	0
2221	10	50,887,496	50,887,887	391	1	5.917	5.5	11.667	9	8	17	1	1	1	C10orf53	7	in gene	ActReg chr10 #2221	0	0	1
2222	10	50,970,270	50,970,724	454	1	8.867	9.867	1.867	15	15	4	1	1	1	OGDHL	-72	upstream	ActReg chr10 #2222	1	0	0
2223	10	51,572,144	51,572,530	386	1	6.083	6.583	10.833	13	9	15	1	0	3	TIMM23B, MSMB, NCOA4	200958, 22784, 7229	in gene, downstream, in gene	ActReg chr10 #2223	0	0	1
2224	10	52,383,355	52,383,805	450	1	10.429	6.929	2.545	15	11	4	1	1	1	SGMS1	157	in gene	ActReg chr10 #2224	1	0	0
2225	10	52,383,975	52,385,289	1,314	2	9.146	12.585	4.27	23	30	8	1	1	1	SGMS1	-895	upstream	ActReg chr10 #2225	1	1	0
2226	10	53,592,628	53,593,215	587	1	7.667	11.667	1.4	12	20	2	0	0	1	PRKG1	841,976	in gene	ActReg chr10 #2226	0	1	0
2227	10	59,908,532	59,909,143	611	2	10.737	10.684	2.2	16	18	4	0	0	0				ActReg chr10 #2227	1	1	0
2228	10	59,935,678	59,936,124	446	1	9.357	10.357	1	14	17	1	0	0	0				ActReg chr10 #2228	0	1	0
2229	10	60,144,873	60,145,519	646	2	5.5	10.8	12.45	8	19	17	1	1	1	TFAM	20	in gene	ActReg chr10 #2229	0	1	1
2230	10	60,208,090	60,208,441	351	1	1.571	2.818	11.454	2	4	16	0	0	0				ActReg chr10 #2230	0	0	1
2231	10	60,936,527	60,936,960	433	1	3.857	2.786	10.071	6	4	17	1	1	1	PHYHIPL	395	in gene	ActReg chr10 #2231	0	0	1
2232	10	61,665,327	61,665,717	390	1	5.667	4	10.25	8	5	14	1	1	1	CCDC6	1,296	in gene	ActReg chr10 #2232	0	0	1
2233	10	61,665,810	61,666,851	1,041	2	27.727	31.531	2.677	91	98	7	1	1	1	CCDC6	488	in gene	ActReg chr10 #2233	1	1	0
2234	10	63,212,625	63,212,929	304	1	2.2	1.111	9.7	3	2	14	1	1	1	TMEM26	431	in gene	ActReg chr10 #2234	0	0	1
2235	10	64,492,639	64,493,078	439	1	10.857	4.5	1	17	8	1	0	0	0				ActReg chr10 #2235	1	0	0
2236	10	64,563,923	64,564,345	422	1	9.769	4.692	1.231	15	7	2	1	1	2	ADO, EGR2	-382, 14793	upstream, downstream	ActReg chr10 #2236	1	0	0
2237	10	64,675,782	64,676,545	763	1	8.833	10.958	2.375	14	20	4	0	0	0				ActReg chr10 #2237	0	1	0
2238	10	64,693,983	64,694,458	475	1	6.067	9.4	1.333	14	15	3	0	0	0				ActReg chr10 #2238	0	1	0
2239	10	65,281,281	65,281,555	274	1	3.25	7.125	10.625	5	12	14	1	1	1	REEP3	295	in gene	ActReg chr10 #2239	0	0	1
2240	10	66,227,584	66,228,076	492	1	10.438	4.812	1.333	16	7	2	0	0	0				ActReg chr10 #2240	1	0	0
2241	10	69,523,782	69,524,502	720	2	6.864	9.636	10.381	12	15	18	1	0	0				ActReg chr10 #2241	0	1	1
2242	10	69,644,140	69,644,545	405	1	7.154	8.846	13.154	11	12	22	1	1	1	SIRT1	-85	upstream	ActReg chr10 #2242	0	0	1
2243	10	69,895,958	69,896,571	613	1	9.263	5.368	1.867	18	9	3	0	0	1	MYPN	27,014	in gene	ActReg chr10 #2243	1	0	0
2244	10	69,913,312	69,913,762	450	1	11.067	5.067	1	20	9	1	0	0	1	MYPN	44,287	in gene	ActReg chr10 #2244	1	0	0
2245	10	70,166,382	70,167,350	968	2	14.067	14.933	4.7	29	28	9	1	1	2	RUFY2, DNA2	185, 65013	in gene, downstream	ActReg chr10 #2245	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2246	10	70,231,327	70,231,633	306	1	5.9	2.6	9.3	9	3	14	1	1	1	DNA2	399	in gene	ActReg chr10 #2246	0	0	1
2247	10	70,319,966	70,320,420	454	2	10.533	8.867	10.733	14	12	15	1	1	1	TET1	76	in gene	ActReg chr10 #2247	1	0	1
2248	10	70,715,459	70,716,445	986	2	8.867	9.067	6.733	19	18	13	1	1	2	DDX50, DDX21	54918, 60	downstream, in gene	ActReg chr10 #2248	1	1	0
2249	10	70,748,293	70,748,936	643	1	5	12.45	2.4	9	17	4	1	1	3	DDX21, LOC100507126, KIAA1279	32722, 14205, 137	downstream, in gene, in gene	ActReg chr10 #2249	0	1	0
2250	10	70,939,500	70,940,245	745	1	12.957	10.913	6.174	24	20	14	1	1	2	VPS26A, SUPV3L1	55964, -121	downstream, upstream	ActReg chr10 #2250	1	0	0
2251	10	71,252,575	71,252,898	323	1	1.778	5.091	9.273	3	7	13	0	0	1	TSPAN15	41,510	in gene	ActReg chr10 #2251	0	0	1
2252	10	71,265,754	71,266,049	295	1	3.9	2.7	8.8	5	5	13	0	0	1	TSPAN15	54,675	in gene	ActReg chr10 #2252	0	0	1
2253	10	71,327,437	71,328,025	588	2	10.889	10.611	3.917	21	16	6	0	0	1	NEUROG3	5,479	downstream	ActReg chr10 #2253	1	1	0
2254	10	71,629,186	71,629,765	579	1	7.444	11.5	1.4	10	16	2	0	0	1	COL13A1	67,831	in gene	ActReg chr10 #2254	0	1	0
2255	10	72,575,986	72,576,448	462	1	2.714	9.133	4.5	6	16	8	1	1	1	SGPL1	513	in gene	ActReg chr10 #2255	0	1	0
2256	10	73,554,668	73,555,923	1,255	2	13.282	16.846	3	32	42	9	0	0	1	CDH23	398,604	in gene	ActReg chr10 #2256	1	1	0
2257	10	73,619,978	73,620,564	586	2	10.167	11.111	2.167	15	15	3	0	0	1	PSAP	-9,189	upstream	ActReg chr10 #2257	1	1	0
2258	10	73,625,735	73,626,046	311	1	1.889	2.667	10.333	3	4	13	0	0	0				ActReg chr10 #2258	0	0	1
2259	10	74,033,033	74,034,054	1,021	3	8.062	9.844	8.938	13	22	16	1	1	1	DDIT4	-134	upstream	ActReg chr10 #2259	0	1	1
2260	10	74,035,873	74,036,137	264	1	4.375	2.125	10.375	6	3	14	0	1	1	DDIT4	2,328	downstream	ActReg chr10 #2260	0	0	1
2261	10	74,078,642	74,078,949	307	1	7.9	7.1	10.5	9	9	14	1	0	0				ActReg chr10 #2261	0	0	1
2262	10	74,114,279	74,115,096	817	2	11.2	12.08	4.56	17	18	10	1	1	1	DNAJB12	220	in gene	ActReg chr10 #2262	1	1	0
2263	10	74,856,250	74,857,123	873	2	12.179	13.75	6.964	25	26	14	1	1	1	P4HA1	46	in gene	ActReg chr10 #2263	1	1	0
2264	10	74,927,516	74,928,129	613	1	10.85	9.05	5.7	18	14	12	1	2	2	ECD, FAM149B1	31, -55	in gene, upstream	ActReg chr10 #2264	1	0	0
2265	10	75,173,460	75,173,929	469	1	8.4	7.733	11	14	10	18	1	1	2	ANXA7, ZMYND17	147, 19625	in gene, downstream	ActReg chr10 #2265	0	0	1
2266	10	75,255,195	75,255,485	290	1	5.556	4.444	11.667	8	5	16	1	2	3	PPP3CB, LOC100507259, USP54	442, -170, 80093	in gene, upstream, downstream	ActReg chr10 #2266	0	0	1
2267	10	75,255,644	75,256,099	455	1	7	8.733	5.25	11	17	9	1	2	3	PPP3CB, LOC100507259, USP54	-89, 361, 79562	upstream, in gene, downstream	ActReg chr10 #2267	0	1	0
2268	10	75,489,959	75,490,699	740	2	9.087	12.826	5.412	15	24	11	1	0	0				ActReg chr10 #2268	1	1	0
2269	10	75,936,164	75,936,800	636	1	8.5	10.2	10.15	13	16	14	1	0	1	ADK	25,517	in gene	ActReg chr10 #2269	0	1	0
2270	10	76,586,113	76,586,565	452	2	9.429	10.714	1.4	15	18	2	1	1	1	MYST4	-40	upstream	ActReg chr10 #2270	1	1	0
2271	10	76,867,712	76,868,121	409	1	1.923	6.308	10.308	3	12	13	0	2	2	DUSP13, SAMD8	1054, -3477	in gene, upstream	ActReg chr10 #2271	0	0	1
2272	10	76,969,992	76,970,856	864	2	15.593	13.778	6.28	36	26	16	1	1	1	VDAC2	512	in gene	ActReg chr10 #2272	1	1	0
2273	10	76,995,068	76,995,375	307	1	4.7	6.3	11.5	7	8	15	1	1	2	VDAC2, COMTD1	25309, 549	downstream, in gene	ActReg chr10 #2273	0	0	1
2274	10	77,161,328	77,161,842	514	1	6.5	12.25	6.357	11	19	10	1	2	2	ZNF503, C10orf41	-72, 299	upstream, in gene	ActReg chr10 #2274	0	1	0
2275	10	77,161,851	77,162,390	539	1	6.118	10.118	3.118	10	17	5	1	2	2	ZNF503, C10orf41	-607, 834	upstream, in gene	ActReg chr10 #2275	0	1	0
2276	10	77,162,859	77,163,263	404	1	5.75	10.75	4.25	9	17	6	1	2	2	ZNF503, C10orf41	-1548, 1775	upstream, in gene	ActReg chr10 #2276	0	1	0
2277	10	77,533,144	77,533,612	468	1	11.133	7.4	2.077	17	11	3	0	0	1	C10orf11	-9,141	upstream	ActReg chr10 #2277	1	0	0
2278	10	79,056,910	79,057,600	690	1	8.636	13.182	3	12	28	5	0	0	1	KCNMA1	340,322	in gene	ActReg chr10 #2278	0	1	0
2279	10	79,087,803	79,088,704	901	2	14.241	15.517	1.552	30	36	4	0	0	1	KCNMA1	309,324	in gene	ActReg chr10 #2279	1	1	0
2280	10	79,110,294	79,110,841	547	1	11.059	9.824	1.417	18	18	3	0	0	1	KCNMA1	287,010	in gene	ActReg chr10 #2280	1	0	0
2281	10	79,152,260	79,153,086	826	2	11.72	11.32	5.24	20	19	7	0	0	1	KCNMA1	244,904	in gene	ActReg chr10 #2281	1	1	0
2282	10	79,265,198	79,266,169	971	2	11.467	10.033	1.429	21	16	3	0	0	1	KCNMA1	131,894	in gene	ActReg chr10 #2282	1	1	0
2283	10	79,273,334	79,274,258	924	1	7.483	10.897	2.88	16	16	6	0	0	1	KCNMA1	123,781	in gene	ActReg chr10 #2283	0	1	0
2284	10	79,276,327	79,276,672	345	1	4	9.909	10.909	6	6	15	0	0	1	KCNMA1	121,078	in gene	ActReg chr10 #2284	0	0	1
2285	10	79,291,039	79,291,988	949	1	14.2	10.533	2.917	21	18	7	0	0	1	KCNMA1	106,064	in gene	ActReg chr10 #2285	1	0	0
2286	10	79,342,301	79,343,082	781	1	12.04	9.32	3.24	20	15	7	0	0	1	KCNMA1	54,886	in gene	ActReg chr10 #2286	1	0	0
2287	10	79,421,149	79,421,855	706	2	10.773	12	3.773	16	17	6	0	0	0				ActReg chr10 #2287	1	1	0
2288	10	79,608,700	79,609,468	768	2	12.167	12.417	5.625	20	21	12	0	0	1	DLG5	77,264	in gene	ActReg chr10 #2288	1	1	0
2289	10	79,685,502	79,686,260	758	1	4.417	7.458	14	9	13	22	1	2	2	DLG5, LOC100128292	467, -689	in gene, upstream	ActReg chr10 #2289	0	0	1
2290	10	79,788,913	79,789,951	1,038	2	13.281	13.812	4.621	24	23	7	1	2	2	POLR3A, RPS24	-134, -4086	upstream, upstream	ActReg chr10 #2290	1	1	0
2291	10	79,793,379	79,793,773	394	1	11.667	10.833	16.25	15	16	26	1	2	2	POLR3A, RPS24	4278, 58	upstream, in gene	ActReg chr10 #2291	0	0	1
2292	10	80,015,088	80,016,550	1,462	1	7.196	12.13	4.022	18	21	8	0	0	1	LOC100132987	7,573	downstream	ActReg chr10 #2292	0	1	0
2293	10	80,023,051	80,023,952	901	1	12.357	8.464	3.607	19	16	6	0	0	0				ActReg chr10 #2293	1	0	0
2294	10	80,321,148	80,321,598	450	1	3.929	4.929	11.214	6	8	16	0	0	0				ActReg chr10 #2294	0	0	1
2295	10	80,516,268	80,517,324	1,056	2	11.97	12.636	3.242	24	19	6	0	0	0				ActReg chr10 #2295	1	1	0
2296	10	80,732,043	80,733,537	1,494	2	10.021	12.021	5	19	19	8	0	0	1	LOC283050	94,415	in gene	ActReg chr10 #2296	1	1	0
2297	10	80,827,031	80,827,587	556	1	10.667	12.611	3.25	16	19	6	1	2	2	LOC283050, ZMIZ1	-104, -1483	upstream, upstream	ActReg chr10 #2297	0	1	0
2298	10	80,830,653	80,831,004	351	1	3.455	9.273	10.727	4	13	13	1	2	2	LOC283050, ZMIZ1	-3623, 2036	upstream, in gene	ActReg chr10 #2298	0	0	1
2299	10	80,841,328	80,841,953	625	1	10.7	12.9	7.7	15	17	10	0	0	1	ZMIZ1	12,848	in gene	ActReg chr10 #2299	0	1	0
2300	10	80,908,631	80,909,617	986	1	8.71	10.548	7.29	15	18	12	0	0	1	ZMIZ1	80,332	in gene	ActReg chr10 #2300	0	1	0
2301	10	81,042,050	81,042,463	413	1	5.583	2.583	14	8	4	21	0	0	1	ZMIZ1	213,464	in gene	ActReg chr10 #2301	0	0	1
2302	10	81,053,068	81,053,658	590	1	3.889	3.944	11.667	10	6	18	0	0	1	ZMIZ1	224,571	in gene	ActReg chr10 #2302	0	0	1
2303	10	81,060,374	81,060,861	487	1	4.533	9.067	14.133	8	14	20	0	0	1	ZMIZ1	231,825	in gene	ActReg chr10 #2303	0	0	1
2304	10	81,080,446	81,081,765	1,319	2	13.595	17.571	3.952	32	36	8	0	0	1	ZMIZ1	252,313	downstream	ActReg chr10 #2304	1	1	0
2305	10	81,106,949	81,107,776	827	1	7.154	12.846	3.591	12	17	7	2	1	1	PPIF	142	in gene	ActReg chr10 #2305	0	1	0
2306	10	81,196,320	81,196,732	412	1	5.846	5.308	12.385	9	10	17	0	0	1	ZCCHC24	8,857	in gene	ActReg chr10 #2306	0	0	1
2307	10	81,197,693	81,198,283	590	1	12.526	10.79	6.842	18	16	11	0	0	1	ZCCHC24	7,395	in gene	ActReg chr10 #2307	1	0	0
2308	10	81,205,323	81,205,969	646	1	13.6	8.05	4.7	25	18	10	1	1	1	ZCCHC24	-263	upstream	ActReg chr10 #2308	1	0	0
2309	10	81,664,146	81,665,170	1,024	2	11.406	12.406	6.688	16	26	12	1	1	1	LOC100288974	4	in gene	ActReg chr10 #2309	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2310	10	81,838,242	81,838,683	441	1	12.154	7.462	10.385	16	12	15	1	2	2	LOC219347, C10orf57	487, 36	in gene, in gene	ActReg chr10 #2310	1	0	0
2311	10	81,886,835	81,887,239	404	1	7.615	10.692	4.4	10	15	7	0	1	1	PLAC9	-5,221	upstream	ActReg chr10 #2311	0	1	0
2312	10	81,965,056	81,965,749	693	1	9.045	12.091	3.615	14	16	5	1	2	2	ANXA11, LOC439990	-74, -2077	upstream, upstream	ActReg chr10 #2312	0	1	0
2313	10	82,168,460	82,168,918	458	1	10.643	7.071	13.214	13	11	19	1	1	1	C10orf58	447	in gene	ActReg chr10 #2313	0	0	1
2314	10	82,289,458	82,290,098	640	1	3	4.2	10.1	6	9	14	0	0	2	TSPAN14, SH2D4B	75740, -7880	downstream, upstream	ActReg chr10 #2314	0	0	1
2315	10	83,330,451	83,331,090	639	1	3.706	2.7	12	9	7	18	0	0	0				ActReg chr10 #2315	0	0	1
2316	10	83,429,427	83,429,732	305	1	3.8	1.75	11.3	5	2	14	0	0	0				ActReg chr10 #2316	0	0	1
2317	10	83,635,243	83,635,799	556	1	3	3.176	14.177	4	7	21	1	1	1	NRG3	451	in gene	ActReg chr10 #2317	0	0	1
2318	10	83,737,858	83,738,539	681	2	11.429	11.714	1.75	22	20	2	0	0	1	NRG3	103,128	in gene	ActReg chr10 #2318	1	1	0
2319	10	84,972,378	84,973,086	708	1	7.864	10.273	3.062	11	16	7	0	0	0				ActReg chr10 #2319	0	1	0
2320	10	85,417,112	85,417,532	420	1	2.615	1.615	11.077	3	3	17	0	0	0				ActReg chr10 #2320	0	0	1
2321	10	85,899,002	85,899,829	827	1	10.423	12.462	3.667	15	20	6	1	1	1	GHITM	230	in gene	ActReg chr10 #2321	0	1	0
2322	10	85,916,560	85,917,016	456	1	7	10.5	5	12	16	8	0	0	1	GHITM	17,603	downstream	ActReg chr10 #2322	0	1	0
2323	10	86,050,979	86,051,773	794	2	19.542	31.208	2.278	53	78	5	0	0	1	LOC170425	11,640	in gene	ActReg chr10 #2323	1	1	0
2324	10	86,331,009	86,331,446	437	1	2.692	3.769	12.385	4	6	20	0	0	0				ActReg chr10 #2324	0	0	1
2325	10	87,661,202	87,661,761	559	1	7.611	10.611	1.786	14	16	3	0	0	1	GRID1	464,769	in gene	ActReg chr10 #2325	0	1	0
2326	10	87,963,214	87,964,211	997	1	7.774	9.258	3.839	17	16	11	0	0	1	GRID1	162,538	in gene	ActReg chr10 #2326	0	1	0
2327	10	88,066,310	88,066,842	532	1	10.25	11.25	5.688	17	21	9	0	0	1	GRID1	59,674	in gene	ActReg chr10 #2327	0	1	0
2328	10	88,136,493	88,137,077	584	1	5.167	3.176	10.278	8	7	14	1	0	0				ActReg chr10 #2328	0	0	1
2329	10	88,160,490	88,161,046	556	1	5.412	5.412	10.588	9	8	15	1	0	0				ActReg chr10 #2329	0	0	1
2330	10	88,281,085	88,282,109	1,024	1	12.625	10.219	3.467	18	21	9	1	1	1	WAPAL	-56	upstream	ActReg chr10 #2330	1	0	0
2331	10	88,313,100	88,313,872	772	1	9.208	12.25	1.905	18	20	4	0	0	0				ActReg chr10 #2331	0	1	0
2332	10	88,319,598	88,320,075	477	1	3.667	1.8	10.067	5	3	15	0	0	0				ActReg chr10 #2332	0	0	1
2333	10	88,515,596	88,516,258	662	1	10.286	8.15	7.412	15	11	12	1	1	1	BMPR1A	-469	upstream	ActReg chr10 #2333	1	0	0
2334	10	88,705,902	88,706,382	480	1	4.4	2.462	12.133	7	4	17	0	0	1	MMRN2	11,283	in gene	ActReg chr10 #2334	0	0	1
2335	10	88,730,901	88,731,890	989	1	9.484	14.323	6.484	16	27	11	1	2	4	SNCG, LOC100133190, C10orf116, AGAP11	13107, -327, 3207, 897	downstream, upstream, downstream, in gene	ActReg chr10 #2335	0	1	0
2336	10	88,854,273	88,854,782	509	3	11	10	10.182	19	17	16	1	2	2	GLUD1, FAM35A	249, -426	in gene, upstream	ActReg chr10 #2336	1	1	1
2337	10	88,854,928	88,855,691	763	3	10	11.667	10.25	18	17	15	1	2	2	GLUD1, FAM35A	-533, 356	upstream, in gene	ActReg chr10 #2337	1	1	1
2338	10	89,264,249	89,265,403	1,154	2	11.389	12.194	9.806	18	19	14	1	1	1	MINPP1	603	in gene	ActReg chr10 #2338	1	1	0
2339	10	89,345,643	89,346,382	739	2	12.261	8.435	1.143	22	19	2	0	0	0				ActReg chr10 #2339	1	1	0
2340	10	89,395,419	89,396,246	827	1	9.154	11.808	2.84	17	17	5	0	0	0				ActReg chr10 #2340	0	1	0
2341	10	89,419,534	89,419,940	406	1	9.615	9.615	13.538	12	15	22	1	1	1	PAPSS2	261	in gene	ActReg chr10 #2341	0	0	1
2342	10	89,430,960	89,431,713	753	1	11.583	7.625	2.682	15	13	5	0	0	1	PAPSS2	11,860	in gene	ActReg chr10 #2342	1	0	0
2343	10	89,577,602	89,578,405	803	1	8.68	11.6	7.92	15	17	15	1	1	1	ATAD1	-86	upstream	ActReg chr10 #2343	0	1	0
2344	10	89,604,808	89,605,393	585	1	6.889	11.111	2.625	13	16	3	0	0	0				ActReg chr10 #2344	0	1	0
2345	10	89,622,584	89,623,645	1,061	2	11.03	8.636	6.576	20	19	13	1	2	2	KILLIN, PTEN	80, -81	in gene, upstream	ActReg chr10 #2345	1	1	0
2346	10	89,912,232	89,913,007	775	1	12.875	8.208	5	23	12	11	0	0	0				ActReg chr10 #2346	1	0	0
2347	10	90,145,444	90,145,853	409	1	4.333	10.167	3.375	6	16	7	0	0	1	RNLS	197,434	in gene	ActReg chr10 #2347	0	1	0
2348	10	90,234,274	90,234,795	521	1	9.375	6.812	2.143	14	9	5	0	0	1	RNLS	108,548	in gene	ActReg chr10 #2348	0	1	0
2349	10	90,342,816	90,343,218	402	1	5.154	3.077	9.923	8	5	17	1	2	2	RNLS, LIPJ	65, -3502	in gene, upstream	ActReg chr10 #2349	0	0	1
2350	10	90,487,995	90,488,564	569	1	5.167	7.056	11.556	9	11	15	0	0	1	LIPK	3,978	in gene	ActReg chr10 #2350	0	0	1
2351	10	90,639,861	90,640,960	1,099	3	10.743	13.2	8.257	21	21	18	1	1	1	STAMBPL1	384	in gene	ActReg chr10 #2351	1	1	1
2352	10	91,111,806	91,112,497	691	2	13.318	14.35	1.059	25	33	2	0	0	1	LOC100507575	-9,735	upstream	ActReg chr10 #2352	1	1	0
2353	10	91,174,223	91,175,367	1,144	1	8.583	12.722	5.778	15	22	12	1	1	1	IFIT5	470	in gene	ActReg chr10 #2353	0	1	0
2354	10	91,294,913	91,295,346	433	1	2.778	2.769	10.077	4	4	16	1	1	1	SLC16A12	184	in gene	ActReg chr10 #2354	0	0	1
2355	10	91,403,790	91,405,275	1,485	1	6.935	11.109	5	13	17	9	1	1	1	PANK1	683	in gene	ActReg chr10 #2355	0	1	0
2356	10	91,460,788	91,462,346	1,558	2	11.98	11.51	4.878	25	29	10	1	1	1	KIF20B	200	in gene	ActReg chr10 #2356	1	1	0
2357	10	91,621,423	91,622,106	683	1	9.048	11	1.438	14	14	2	0	0	0				ActReg chr10 #2357	0	1	0
2358	10	91,664,405	91,665,118	713	1	9.636	11.409	2.682	17	20	5	0	0	0				ActReg chr10 #2358	0	1	0
2359	10	92,346,899	92,347,527	628	1	8.4	9.9	1.333	13	19	4	0	0	0				ActReg chr10 #2359	0	1	0
2360	10	92,381,241	92,381,744	503	1	6.375	10.312	1	10	16	1	0	0	0				ActReg chr10 #2360	0	1	0
2361	10	92,534,841	92,535,468	627	1	8.6	11.55	2.643	12	21	4	0	0	1	HTR7	82,517	in gene	ActReg chr10 #2361	0	1	0
2362	10	92,631,132	92,632,026	894	1	10.143	11.679	6.385	19	20	17	0	1	1	RPP30	-130	upstream	ActReg chr10 #2362	0	1	0
2363	10	92,887,052	92,887,576	524	1	8.312	11.562	2.5	13	17	3	0	0	0				ActReg chr10 #2363	0	1	0
2364	10	92,923,087	92,923,551	464	1	5.929	10.071	5	8	15	6	0	0	0				ActReg chr10 #2364	0	1	0
2365	10	92,950,807	92,951,375	568	1	9.778	7.222	1.364	15	12	2	0	0	0				ActReg chr10 #2365	1	0	0
2366	10	93,169,098	93,169,897	799	1	10.2	10.24	7.542	14	15	14	1	1	2	LOC100188947, HECTD2	129840, -599	in gene, upstream	ActReg chr10 #2366	1	0	0
2367	10	93,271,017	93,271,877	860	1	4.037	10.667	1.75	8	19	3	0	0	2	LOC100188947, HECTD2	27890, 101351	in gene, in gene	ActReg chr10 #2367	0	1	0
2368	10	93,334,538	93,335,497	959	1	7.167	12.7	4.667	13	21	8	0	0	0				ActReg chr10 #2368	0	1	0
2369	10	93,368,396	93,368,720	324	1	5.2	5.8	9.9	7	7	13	0	0	0				ActReg chr10 #2369	0	0	1
2370	10	93,411,947	93,412,699	752	1	7.348	12.913	1.923	14	22	4	0	0	0				ActReg chr10 #2370	0	1	0
2371	10	93,646,884	93,647,765	881	1	7.704	12.815	7	11	20	14	1	0	0				ActReg chr10 #2371	0	1	0
2372	10	93,667,838	93,669,130	1,292	2	24.854	26.244	5.415	79	85	13	1	1	1	FGFBP3	774	in gene	ActReg chr10 #2372	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2373	10	93,683,182	93,683,956	774	1	12.083	9.917	5.167	22	21	9	1	1	1	BTAF1	-167	upstream	ActReg chr10 #2373	1	0	0
2374	10	94,050,499	94,051,374	875	2	12.407	12	6.741	24	21	12	1	2	2	CPEB3, MARCH5	-61, 16	upstream, in gene	ActReg chr10 #2374	1	1	0
2375	10	94,146,941	94,147,756	815	2	13.769	15.577	3.8	33	35	6	0	0	0				ActReg chr10 #2375	1	1	0
2376	10	94,167,051	94,167,895	844	2	10.577	11.192	2.08	15	20	4	0	0	0				ActReg chr10 #2376	1	1	0
2377	10	94,351,138	94,351,733	595	2	9.778	10.389	8.389	17	15	15	1	1	1	KIF11	-1,390	upstream	ActReg chr10 #2377	1	1	0
2378	10	94,449,668	94,450,385	717	1	7.5	12.091	6.95	10	17	14	1	1	1	HHEX	345	in gene	ActReg chr10 #2378	0	1	0
2379	10	94,651,867	94,652,641	774	1	7.16	12.28	2.545	12	23	5	0	0	1	EXOC6	57,784	in gene	ActReg chr10 #2379	0	1	0
2380	10	94,968,328	94,969,001	673	2	11.905	10.857	3.35	20	20	7	0	0	0				ActReg chr10 #2380	1	1	0
2381	10	95,241,678	95,242,592	914	2	14.885	14.483	5.714	28	30	10	0	1	1	MYOF	-61	upstream	ActReg chr10 #2381	1	1	0
2382	10	95,255,713	95,256,744	1,031	2	10.812	11.312	3.419	19	22	7	1	1	1	CEP55	-141	upstream	ActReg chr10 #2382	1	1	0
2383	10	95,462,004	95,462,739	735	1	12.652	14.13	7.391	24	28	17	1	1	1	C10orf4	-42	upstream	ActReg chr10 #2383	0	1	0
2384	10	95,511,586	95,512,130	544	1	9.706	11.412	1	15	19	1	0	1	1	LGI1	-5,708	upstream	ActReg chr10 #2384	0	1	0
2385	10	95,653,236	95,653,903	667	1	8.429	11.905	3.905	16	21	7	1	1	1	TMEM20	-161	upstream	ActReg chr10 #2385	0	1	0
2386	10	95,751,509	95,752,252	743	2	11.565	10.739	2.158	17	22	4	0	1	1	PLCE1	-1,866	upstream	ActReg chr10 #2386	1	1	0
2387	10	95,825,935	95,826,805	870	2	16.593	23.148	2	37	60	4	0	0	1	PLCE1	72,624	in gene	ActReg chr10 #2387	1	1	0
2388	10	95,875,340	95,876,113	773	1	9.667	13.875	2	26	35	3	0	0	1	PLCE1	121,980	in gene	ActReg chr10 #2388	0	1	0
2389	10	95,984,271	95,984,827	556	1	8.882	13	3	14	22	6	0	0	1	PLCE1	230,803	in gene	ActReg chr10 #2389	0	1	0
2390	10	96,122,325	96,123,030	705	2	13	12.091	6.727	25	18	13	1	1	1	NOC3L	6	in gene	ActReg chr10 #2390	1	1	0
2391	10	96,305,531	96,305,995	464	1	8.667	11.733	6.867	13	18	11	1	1	2	TBC1D12, HELLS	143577, 189	downstream, in gene	ActReg chr10 #2391	0	1	0
2392	10	96,943,026	96,944,021	995	2	12.194	13.742	6.516	22	26	12	1	0	1	C10orf129	-10,434	upstream	ActReg chr10 #2392	1	1	0
2393	10	96,990,663	96,991,021	358	1	3.182	5.636	11.182	5	9	16	0	0	2	C10orf129, PDLIM1	36885, 59939	downstream, downstream	ActReg chr10 #2393	0	0	1
2394	10	97,151,604	97,152,222	618	2	11.579	13.263	1.5	19	26	2	0	0	1	SORBS1	169,258	in gene	ActReg chr10 #2394	1	1	0
2395	10	97,153,679	97,154,363	684	1	11.667	9.952	1.091	22	18	2	0	0	1	SORBS1	167,150	in gene	ActReg chr10 #2395	1	0	0
2396	10	97,415,986	97,416,794	808	1	13.2	10	8.48	22	15	14	1	1	2	ALDH18A1, TCTN3	177, 37510	in gene, downstream	ActReg chr10 #2396	1	0	0
2397	10	97,453,435	97,454,123	688	3	9.818	12.682	9.955	17	21	14	1	1	1	TCTN3	121	in gene	ActReg chr10 #2397	1	1	1
2398	10	97,667,188	97,668,026	838	1	9.115	12.231	8.458	16	21	16	1	1	1	C10orf131	-115	upstream	ActReg chr10 #2398	0	1	0
2399	10	97,802,935	97,803,662	727	1	9.739	11.043	3.632	14	15	9	1	1	2	LOC728558, CCNJ	46655, 139	in gene, in gene	ActReg chr10 #2399	0	1	0
2400	10	97,803,766	97,804,395	629	1	10.65	8.45	5.9	16	12	10	1	1	2	LOC728558, CCNJ	45873, 921	in gene, in gene	ActReg chr10 #2400	1	0	0
2401	10	97,849,311	97,850,634	1,323	2	11.571	14.762	5.55	25	26	14	1	1	1	LOC728558	-19	upstream	ActReg chr10 #2401	1	1	0
2402	10	97,889,288	97,890,756	1,468	3	10.348	14.326	8	19	31	20	1	1	1	ZNF518A	550	in gene	ActReg chr10 #2402	1	1	1
2403	10	98,255,690	98,256,682	992	2	12.355	19.742	1.967	25	45	4	0	0	1	TLL2	17,497	in gene	ActReg chr10 #2403	1	1	0
2404	10	98,273,200	98,273,939	739	1	8.043	11.174	7.565	14	18	12	1	1	2	TLL2, TM9SF3	114, 73240	in gene, downstream	ActReg chr10 #2404	0	1	0
2405	10	98,479,857	98,480,174	317	1	4.6	4.6	13.1	6	7	18	1	1	1	PIK3AP1	264	in gene	ActReg chr10 #2405	0	0	1
2406	10	98,841,240	98,842,011	771	1	9.917	14.917	4.333	19	30	7	0	0	1	SLIT1	104,058	in gene	ActReg chr10 #2406	0	1	0
2407	10	98,929,157	98,929,705	548	1	3.529	5.588	10.823	6	7	14	0	0	1	SLIT1	16,252	in gene	ActReg chr10 #2407	0	0	1
2408	10	98,945,991	98,946,429	438	1	1.538	2.462	10.308	2	4	15	1	1	1	SLIT1	-527	upstream	ActReg chr10 #2408	0	0	1
2409	10	98,970,931	98,971,302	371	1	4.25	2.833	11.25	7	4	17	0	0	0				ActReg chr10 #2409	0	0	1
2410	10	99,078,465	99,079,361	896	2	12.143	12.25	4.357	25	20	7	1	1	1	FRAT1	-109	upstream	ActReg chr10 #2410	1	1	0
2411	10	99,093,314	99,093,997	683	1	8.4	10.095	6.647	12	18	14	1	1	1	FRAT2	803	in gene	ActReg chr10 #2411	0	1	0
2412	10	99,094,271	99,094,913	642	2	12.191	10.571	5.857	23	19	11	1	1	1	FRAT2	-134	upstream	ActReg chr10 #2412	1	1	0
2413	10	99,185,729	99,186,879	1,150	1	6.2	10.857	4.818	11	19	9	1	1	2	PCAM1, EXOSC1	277, 19464	in gene, downstream	ActReg chr10 #2413	0	1	0
2414	10	99,257,415	99,258,325	910	1	10.893	10.036	7.393	14	19	16	1	2	2	MMS19, UBTD1	496, -898	in gene, upstream	ActReg chr10 #2414	1	0	0
2415	10	99,301,856	99,303,419	1,563	3	10.225	10.674	4.186	18	21	9	0	0	1	UBTD1	43,869	in gene	ActReg chr10 #2415	1	1	0
2416	10	99,332,231	99,332,647	416	1	6	10.077	10.154	9	16	17	0	1	2	UBTD1, ANKRD2	75671, 183	downstream, in gene	ActReg chr10 #2416	0	0	1
2417	10	99,446,522	99,447,697	1,175	3	12.297	11.784	9.459	22	21	21	1	1	1	AVPI1	-94	upstream	ActReg chr10 #2417	1	1	1
2418	10	99,473,651	99,474,162	511	1	7.625	11.75	9.467	13	20	17	1	1	2	MARVELD1, LOC100270710	441, 19392	in gene, downstream	ActReg chr10 #2418	0	1	0
2419	10	99,486,302	99,486,996	694	1	11.909	8.273	4.25	18	12	11	0	0	3	MARVELD1, LOC100270710, ZFYVE27	13184, 6649, -10229	downstream, in gene, upstream	ActReg chr10 #2419	1	0	0
2420	10	99,496,419	99,497,385	966	2	10.633	11.733	9.433	16	18	12	1	2	2	LOC100270710, ZFYVE27	-3604, 24	upstream, in gene	ActReg chr10 #2420	1	1	0
2421	10	99,561,387	99,561,929	542	1	4	4.588	11	7	7	15	0	0	0				ActReg chr10 #2421	0	0	1
2422	10	99,570,162	99,570,873	711	1	8.045	12.636	3.5	14	18	6	0	0	0				ActReg chr10 #2422	0	1	0
2423	10	99,602,395	99,603,571	1,176	2	10.784	15.081	2	26	28	4	0	1	2	LOC100505561, GOLGA7B	6572, -7013	in gene, upstream	ActReg chr10 #2423	1	1	0
2424	10	99,620,909	99,621,717	808	1	8.48	13.28	3.875	15	23	6	0	1	3	GOLGA7B, CRTAC1, LOC100128300	11317, 169272, -6576	in gene, downstream, upstream	ActReg chr10 #2424	0	1	0
2425	10	99,641,800	99,643,033	1,233	2	15.79	10.421	5.658	29	23	11	0	0	1	CRTAC1	148,169	in gene	ActReg chr10 #2425	1	1	0
2426	10	99,649,062	99,649,905	843	1	8.692	14.308	3.84	15	26	7	0	0	1	CRTAC1	141,102	in gene	ActReg chr10 #2426	0	1	0
2427	10	99,651,145	99,651,599	454	1	3.929	3.143	12.286	6	7	18	0	0	1	CRTAC1	139,213	in gene	ActReg chr10 #2427	0	0	1
2428	10	99,751,447	99,752,176	729	1	8.391	14.087	1.867	15	27	2	0	0	1	CRTAC1	38,774	in gene	ActReg chr10 #2428	0	1	0
2429	10	99,789,386	99,789,900	514	1	4.375	6.438	13.25	7	10	20	1	1	1	CRTAC1	942	in gene	ActReg chr10 #2429	0	0	1
2430	10	99,814,841	99,816,992	2,151	2	19.221	23.073	2.545	73	103	6	0	0	0				ActReg chr10 #2430	1	1	0
2431	10	99,846,866	99,847,548	682	2	11.095	10.714	4.45	21	20	11	0	0	0				ActReg chr10 #2431	1	1	0
2432	10	99,894,176	99,894,754	578	2	9.316	9.158	7.316	18	14	11	1	1	1	C10orf28	84	in gene	ActReg chr10 #2432	1	1	0
2433	10	100,006,635	100,007,480	845	1	7.5	11.269	3.731	11	16	6	0	0	2	C10orf28, LOXL4	112676, 20950	downstream, downstream	ActReg chr10 #2433	0	1	0
2434	10	100,029,147	100,029,748	601	1	9.947	12.158	4.421	15	19	9	0	1	1	LOXL4	-1,440	upstream	ActReg chr10 #2434	0	1	0
2435	10	100,059,002	100,059,626	624	1	11.35	7.444	3.2	21	13	4	0	0	0				ActReg chr10 #2435	1	0	0
2436	10	100,082,439	100,083,582	1,143	1	8.714	13.6	3.2	16	31	6	0	0	0				ActReg chr10 #2436	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2437	10	100,113,066	100,113,904	838	1	6.615	10.654	2.88	11	15	5	0	0	0				ActReg chr10 #2437	0	1	0
2438	10	100,189,254	100,189,867	613	1	5.105	4.211	12.842	8	6	19	0	0	1	HPS1	17,144	in gene	ActReg chr10 #2438	0	0	1
2439	10	100,248,151	100,249,084	933	1	7.414	12.621	2.154	12	23	3	0	0	1	HPSE2	747,015	in gene	ActReg chr10 #2439	0	1	0
2440	10	101,294,511	101,294,971	460	1	2.25	2.308	13.357	3	6	18	1	1	1	NKX2-3	2,051	in gene	ActReg chr10 #2440	0	0	1
2441	10	101,380,846	101,381,666	820	2	11.923	10	13.615	26	19	28	1	1	1	SLC25A28	-1,035	upstream	ActReg chr10 #2441	1	0	1
2442	10	101,418,376	101,419,374	998	1	9.806	11.194	4.793	16	22	9	1	1	1	ENTPD7	-388	upstream	ActReg chr10 #2442	0	1	0
2443	10	101,945,442	101,946,148	706	1	9.714	12.682	6.409	14	23	14	1	1	2	ERLIN1, CHUK	19, 43549	in gene, downstream	ActReg chr10 #2443	0	1	0
2444	10	102,027,110	102,027,681	571	1	10.833	16.389	6.389	16	35	11	1	1	2	CWF19L1, BLOC1S2	42, 19044	in gene, downstream	ActReg chr10 #2444	0	1	0
2445	10	102,046,143	102,046,654	511	1	10.688	11.812	11.688	16	14	19	1	1	2	BLOC1S2, PKD2L1	41, 43845	in gene, downstream	ActReg chr10 #2445	0	0	1
2446	10	102,084,770	102,085,480	710	1	9.591	11.818	2.8	21	23	5	0	0	1	PKD2L1	5,118	in gene	ActReg chr10 #2446	0	1	0
2447	10	102,098,853	102,099,169	316	1	4.3	6.2	10.3	8	8	15	0	0	2	PKD2L1, SCD	-8768, -7761	upstream, upstream	ActReg chr10 #2447	0	0	1
2448	10	102,105,979	102,107,785	1,806	2	9.491	12.491	5.842	22	24	11	1	1	1	SCD	110	in gene	ActReg chr10 #2448	1	1	0
2449	10	102,266,302	102,266,943	641	1	5.421	11.7	1.118	9	25	2	0	0	1	SEC31B	12,973	in gene	ActReg chr10 #2449	0	1	0
2450	10	102,295,195	102,295,978	783	2	16.04	17.56	5.05	34	48	11	0	2	2	NDUFB8, HIF1AN	-5950, -55	upstream, upstream	ActReg chr10 #2450	1	1	0
2451	10	102,440,193	102,441,001	808	2	10.36	13.12	5.7	23	22	9	1	0	0				ActReg chr10 #2451	1	1	0
2452	10	102,586,538	102,587,142	604	1	9.368	12.368	9.474	14	18	18	1	0	1	PAX2	81,372	in gene	ActReg chr10 #2452	0	1	0
2453	10	102,672,732	102,673,262	530	1	9.059	7.765	12.118	13	12	17	1	1	1	FAM178A	671	in gene	ActReg chr10 #2453	0	0	1
2454	10	102,746,366	102,747,555	1,189	2	9.289	12.658	7.921	18	22	16	1	2	4	SEMA4G, MRPL43, C10orf2, LZTS2	14674, 312, -333, -10005	downstream, in gene, upstream, upstream	ActReg chr10 #2454	1	1	0
2455	10	102,758,293	102,759,311	1,018	1	10.312	12.344	6.312	14	18	12	1	1	2	C10orf2, LZTS2	11509, 1837	downstream, in gene	ActReg chr10 #2455	0	1	0
2456	10	102,766,251	102,767,079	828	1	6.846	6.5	14.192	11	10	22	1	0	1	LZTS2	9,700	in gene	ActReg chr10 #2456	0	0	1
2457	10	102,768,346	102,768,923	577	1	6.5	13.167	6.167	11	19	9	0	0	2	LZTS2, PDZD7	11669, 22245	downstream, downstream	ActReg chr10 #2457	0	1	0
2458	10	102,791,323	102,792,921	1,598	1	12.86	9.94	7.04	22	19	14	1	2	2	PDZD7, SFXN3	-1243, 1126	upstream, in gene	ActReg chr10 #2458	1	0	0
2459	10	102,820,935	102,821,444	509	1	9.312	7.688	14.375	16	10	24	1	2	2	KAZALD1, LOC100505670	190, -4867	in gene, upstream	ActReg chr10 #2459	0	0	1
2460	10	102,825,775	102,826,480	705	1	9.591	10.046	13.091	13	17	18	1	1	2	KAZALD1, LOC100505670	5128, 71	downstream, in gene	ActReg chr10 #2460	0	0	1
2461	10	102,840,580	102,841,358	778	2	10.542	13.25	3.273	18	22	8	0	0	1	TLX1NB	49,934	downstream	ActReg chr10 #2461	1	1	0
2462	10	102,845,475	102,846,253	778	2	10.708	15.792	5	21	26	9	0	0	1	TLX1NB	45,039	downstream	ActReg chr10 #2462	1	1	0
2463	10	103,113,145	103,114,406	1,261	2	13.05	13.525	4.375	22	22	9	1	1	1	BTRC	-50	upstream	ActReg chr10 #2463	1	1	0
2464	10	103,124,310	103,124,796	486	3	12.933	19.333	18.667	25	41	41	0	0	1	BTRC	10,728	in gene	ActReg chr10 #2464	1	1	1
2465	10	103,326,080	103,326,427	347	1	2.3	2.9	13.091	4	4	18	1	0	1	BTRC	212,428	downstream	ActReg chr10 #2465	0	0	1
2466	10	103,453,722	103,454,839	1,117	1	9.743	10.886	4.794	15	18	10	1	1	1	FBXW4	463	in gene	ActReg chr10 #2466	0	1	0
2467	10	103,542,548	103,543,669	1,121	2	9.545	10.914	8.943	18	19	19	1	2	3	FGF8, NPM3, MGEA5	-7349, 62, 35114	upstream, in gene, downstream	ActReg chr10 #2467	0	1	1
2468	10	103,577,904	103,578,785	881	2	15.607	15.464	4.786	34	33	9	1	2	3	MGEA5, LOC100289509, KCNIP2	-122, -481, 25333	upstream, upstream, downstream	ActReg chr10 #2468	1	1	0
2469	10	103,590,521	103,591,048	527	1	7.706	15	13.059	12	25	20	1	0	2	LOC100289509, KCNIP2	11959, 12893	downstream, in gene	ActReg chr10 #2469	0	0	1
2470	10	103,600,341	103,601,920	1,579	2	15.22	17.24	5.98	37	51	15	0	1	2	KCNIP2, C10orf76	2547, 214802	in gene, downstream	ActReg chr10 #2470	1	1	0
2471	10	103,815,446	103,816,412	966	2	15.1	16.433	5.1	33	34	9	1	1	2	C10orf76, HPS6	3, -9218	in gene, upstream	ActReg chr10 #2471	1	1	0
2472	10	103,824,653	103,825,810	1,157	1	9.472	10.833	2.531	14	19	8	1	1	2	C10orf76, HPS6	-9299, 84	upstream, in gene	ActReg chr10 #2472	0	1	0
2473	10	103,892,129	103,893,947	1,818	3	12.375	17.089	7.696	38	35	19	1	1	1	PPRC1	251	in gene	ActReg chr10 #2473	1	1	1
2474	10	103,911,655	103,912,678	1,023	1	8.812	12.469	7.625	17	21	13	1	1	2	PPRC1, NOLC1	19379, 233	downstream, in gene	ActReg chr10 #2474	0	1	0
2475	10	103,989,657	103,990,398	741	1	6.652	11.13	11.348	16	19	17	1	0	2	ELOVL3, PITX3	3884, 11204	downstream, in gene	ActReg chr10 #2475	0	0	1
2476	10	104,000,495	104,001,021	526	1	4.688	3.438	12	7	7	17	1	2	2	PITX3, GBF1	473, -4551	in gene, upstream	ActReg chr10 #2476	0	0	1
2477	10	104,005,019	104,005,561	542	1	11.294	7.235	7.824	20	13	15	1	2	2	PITX3, GBF1	-4059, -19	upstream, upstream	ActReg chr10 #2477	1	0	0
2478	10	104,121,392	104,121,827	435	1	7.5	10.214	1.556	12	18	2	0	0	1	GBF1	116,300	in gene	ActReg chr10 #2478	0	1	0
2479	10	104,153,604	104,154,859	1,255	1	9.615	12.59	8.564	16	21	14	1	1	2	NFKB2, PSD	2, 24670	in gene, downstream	ActReg chr10 #2479	0	1	0
2480	10	104,179,186	104,179,863	677	1	10.619	11.143	4.714	21	17	7	1	2	4	PSD, FBXL15, LOC100286939, CUEDC2	-623, -47, 3369, 12899	upstream, upstream, downstream, downstream	ActReg chr10 #2480	0	1	0
2481	10	104,180,284	104,181,719	1,435	2	17.511	19.533	7.956	47	60	17	1	3	4	PSD, FBXL15, LOC100286939, CUEDC2	-2100, 1430, 1892, 11422	upstream, in gene, downstream, downstream	ActReg chr10 #2481	1	1	0
2482	10	104,191,917	104,192,769	852	2	12.704	11.296	6.926	21	26	13	1	2	4	FBXL15, LOC100286939, CUEDC2, MIR146B	12772, -9450, 80, -3926	downstream, upstream, in gene, upstream	ActReg chr10 #2482	1	1	0
2483	10	104,261,880	104,262,883	1,003	1	9.719	11.562	5.655	20	22	12	1	2	2	ACTR1A, SUFU	131, -1338	in gene, upstream	ActReg chr10 #2483	0	1	0
2484	10	104,263,342	104,263,967	625	1	13.579	10.842	2.944	23	14	6	1	2	2	ACTR1A, SUFU	-1142, -65	upstream, upstream	ActReg chr10 #2484	1	0	0
2485	10	104,405,225	104,406,102	877	1	11.852	10.37	4.593	20	15	8	0	1	1	TRIM8	1,411	in gene	ActReg chr10 #2485	1	0	0
2486	10	104,425,569	104,426,037	468	1	3.857	6.143	12.5	6	10	18	0	0	2	TRIM8, ARL3	21551, 48387	downstream, downstream	ActReg chr10 #2486	0	0	1
2487	10	104,429,181	104,429,649	468	1	5.133	6.2	11.267	6	8	16	0	0	1	ARL3	44,775	downstream	ActReg chr10 #2487	0	0	1
2488	10	104,473,399	104,475,052	1,653	2	6.327	8.481	11.712	13	15	18	1	2	2	ARL3, SFXN2	-35, -73	upstream, upstream	ActReg chr10 #2488	0	1	1
2489	10	104,613,729	104,614,508	779	1	10.667	16.875	5.273	15	34	9	1	1	1	C10orf32	151	in gene	ActReg chr10 #2489	0	1	0
2490	10	104,952,440	104,953,029	589	1	7.158	10.105	6.4	12	15	9	1	1	1	NT5C2	322	in gene	ActReg chr10 #2490	0	1	0
2491	10	105,001,020	105,001,609	589	1	11.316	9.053	4.389	16	13	8	0	1	1	hCG_2024410	-4,330	upstream	ActReg chr10 #2491	1	0	0
2492	10	105,025,217	105,025,910	693	1	10.714	14.333	3.444	15	28	5	0	0	0				ActReg chr10 #2492	0	1	0
2493	10	105,032,542	105,033,350	808	2	13.346	15.769	2.154	30	42	4	0	1	1	INA	-3,974	upstream	ActReg chr10 #2493	1	1	0
2494	10	105,037,854	105,039,072	1,218	2	10.923	15.462	6.526	32	37	20	1	1	1	INA	1,543	in gene	ActReg chr10 #2494	1	1	0
2495	10	105,110,150	105,111,204	1,054	3	8.818	7.939	6.576	16	21	15	1	1	1	PCGF6	214	in gene	ActReg chr10 #2495	1	1	1
2496	10	105,127,564	105,128,225	661	1	11.571	13.333	7.381	15	19	16	2	1	1	TAF5	170	in gene	ActReg chr10 #2496	0	1	0
2497	10	105,156,045	105,156,723	678	1	6.476	9.19	11.381	9	16	15	1	3	4	TAF5, USMG5, MIR1307, PCCD11	28660, -161, -2226, -28	downstream, upstream, upstream, upstream	ActReg chr10 #2497	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2498	10	105,157,172	105,157,607	435	1	3.357	8	10.429	6	11	19	0	3	4	TAF5, USMG5, MIR1307, PCDD11	29665, -1166, -3231, 977	downstream, upstream, upstream, in gene	ActReg chr10 #2498	0	0	1
2499	10	105,211,514	105,212,151	637	1	8.4	9.45	13.55	13	12	23	1	2	4	PCDH11, CALHM2, LOC100505820, CALHM1	55420, 330, -771, 6816	downstream, in gene, upstream, downstream	ActReg chr10 #2499	0	0	1
2500	10	105,315,590	105,316,041	451	1	5.5	5.571	11.5	8	8	18	0	0	1	NEURL	62,080	in gene	ActReg chr10 #2500	0	0	1
2501	10	105,372,488	105,372,871	383	1	5.917	8.25	12.167	8	12	20	0	0	1	SH3PXD2A	242,485	in gene	ActReg chr10 #2501	0	0	1
2502	10	105,419,824	105,421,203	1,379	3	12.116	12.767	11.139	22	18	21	1	0	1	SH3PXD2A	194,651	in gene	ActReg chr10 #2502	1	1	1
2503	10	105,506,297	105,507,556	1,259	2	10.825	12.85	6.925	20	24	17	0	1	2	SH3PXD2A, LOC100505839	108238, 389	in gene, in gene	ActReg chr10 #2503	1	1	0
2504	10	105,516,171	105,516,726	555	1	5.412	6.353	11.118	11	10	14	0	0	2	SH3PXD2A, LOC100505839	98716, 9911	in gene, downstream	ActReg chr10 #2504	0	0	1
2505	10	105,558,259	105,558,619	360	1	6.091	4.636	11.818	16	6	15	0	0	1	SH3PXD2A	56,725	in gene	ActReg chr10 #2505	0	0	1
2506	10	105,560,087	105,561,031	944	1	9.367	12.033	5.931	18	21	11	0	0	1	SH3PXD2A	54,605	in gene	ActReg chr10 #2506	0	1	0
2507	10	105,587,452	105,589,006	1,554	2	9.939	10.408	3.064	16	20	8	0	0	1	SH3PXD2A	26,935	in gene	ActReg chr10 #2507	1	1	0
2508	10	105,621,090	105,621,825	735	1	6.522	9.652	1.625	11	15	2	0	0	1	SH3PXD2A	-6,293	upstream	ActReg chr10 #2508	0	1	0
2509	10	105,655,071	105,655,863	792	1	7.12	12.48	2.19	12	20	3	0	0	1	OBFC1	22,578	in gene	ActReg chr10 #2509	0	1	0
2510	10	105,695,879	105,696,254	375	1	3	2.455	11.364	4	4	16	0	0	0				ActReg chr10 #2510	0	0	1
2511	10	105,869,573	105,870,283	710	1	12.182	8.682	2.227	18	15	4	0	0	0				ActReg chr10 #2511	1	0	0
2512	10	105,881,379	105,881,954	575	1	11.278	11	4.111	17	13	9	1	1	2	C10orf78, C10orf79	-150, 110454	upstream, downstream	ActReg chr10 #2512	1	0	0
2513	10	105,991,491	105,992,294	803	1	7.28	13.12	4.8	11	23	11	1	1	1	C10orf79	228	in gene	ActReg chr10 #2513	0	1	0
2514	10	106,014,141	106,015,107	966	2	10.129	10.419	8.903	15	15	16	1	1	1	GSTO1	672	in gene	ActReg chr10 #2514	0	1	1
2515	10	106,059,323	106,060,697	1,374	1	7.884	11.488	4.721	16	18	8	0	0	1	GSTO2	31,379	downstream	ActReg chr10 #2515	0	1	0
2516	10	106,088,760	106,089,735	975	2	13.806	13.581	3.935	26	21	7	0	0	2	ITPRIP, LOC100505856	44416, 6125	in gene, downstream	ActReg chr10 #2516	1	1	0
2517	10	106,097,667	106,098,905	1,238	2	18.763	21.842	4.868	52	52	14	1	1	1	ITPRIP	4,623	upstream	ActReg chr10 #2517	1	1	0
2518	10	106,307,718	106,308,341	623	1	10.579	11.79	2.1	21	19	3	0	0	0				ActReg chr10 #2518	0	1	0
2519	10	106,399,941	106,400,244	303	1	3.778	4.778	10.222	6	7	15	1	1	1	SORCS3	-767	upstream	ActReg chr10 #2519	0	0	1
2520	10	106,583,819	106,584,847	1,028	2	20.969	29.406	2.607	61	80	6	0	0	1	SORCS3	183,474	in gene	ActReg chr10 #2520	1	1	0
2521	10	106,697,218	106,697,847	629	1	10.895	10.474	4.312	18	19	6	0	0	1	SORCS3	296,673	in gene	ActReg chr10 #2521	1	0	0
2522	10	108,174,019	108,174,349	330	1	1.8	3.4	10.5	3	4	15	0	0	0				ActReg chr10 #2522	0	0	1
2523	10	109,305,332	109,306,010	678	1	10	10.286	3.81	12	16	6	0	0	0				ActReg chr10 #2523	0	1	0
2524	10	109,710,068	109,710,384	316	1	1.222	3	11.8	2	4	15	0	0	0				ActReg chr10 #2524	0	0	1
2525	10	111,694,585	111,695,238	653	1	8.095	11.286	4.619	12	17	8	0	0	0				ActReg chr10 #2525	0	1	0
2526	10	111,766,552	111,767,526	974	2	10.484	11.258	6.323	17	20	15	1	1	1	ADD3	1,313	in gene	ActReg chr10 #2526	1	1	0
2527	10	111,767,732	111,768,306	574	1	4.778	8.389	13.944	8	11	20	1	1	1	ADD3	2,293	in gene	ActReg chr10 #2527	0	0	1
2528	10	111,836,523	111,836,979	456	1	5	9.714	1	8	15	1	0	0	1	ADD3	71,025	in gene	ActReg chr10 #2528	0	1	0
2529	10	111,966,968	111,967,636	668	1	12.143	6.429	4	20	13	8	1	1	1	MXI1	-61	upstream	ActReg chr10 #2529	1	0	0
2530	10	111,970,139	111,970,803	664	1	9.714	10.714	4.45	16	17	12	1	0	1	MXI1	3,108	in gene	ActReg chr10 #2530	0	1	0
2531	10	112,091,130	112,091,677	547	1	4.824	2.235	12.647	7	4	21	0	0	0				ActReg chr10 #2531	0	0	1
2532	10	112,167,216	112,168,146	930	1	8.621	9.931	5.3	14	14	9	0	0	0				ActReg chr10 #2532	0	1	0
2533	10	112,173,781	112,174,803	1,022	2	9.844	9.562	3.375	18	19	5	0	0	0				ActReg chr10 #2533	1	1	0
2534	10	112,185,493	112,186,211	718	1	11.217	4.652	3.25	18	8	5	0	0	0				ActReg chr10 #2534	1	0	0
2535	10	112,257,030	112,257,770	740	1	7.826	12.696	4.909	11	17	9	1	1	1	DUSP5	-225	upstream	ActReg chr10 #2535	0	1	0
2536	10	112,258,112	112,258,717	605	1	7.421	10.842	7.211	10	16	11	1	1	1	DUSP5	789	in gene	ActReg chr10 #2536	0	1	0
2537	10	112,285,431	112,285,981	550	1	8.294	10.235	4.333	13	16	7	0	0	0				ActReg chr10 #2537	0	1	0
2538	10	112,295,607	112,296,531	924	2	11.448	12.379	3.897	17	17	7	0	0	0				ActReg chr10 #2538	1	1	0
2539	10	112,326,787	112,327,923	1,136	2	16.571	19.286	6.971	40	43	15	1	1	1	SMC3	-94	upstream	ActReg chr10 #2539	1	1	0
2540	10	112,431,689	112,432,672	983	2	13.677	9.967	4.741	26	21	9	1	0	1	RBM20	28,025	in gene	ActReg chr10 #2540	1	1	0
2541	10	112,533,835	112,534,554	719	2	10.954	11.182	3.438	15	23	5	0	0	1	RBM20	130,039	in gene	ActReg chr10 #2541	1	1	0
2542	10	112,678,226	112,679,285	1,059	3	13.576	12.939	7.697	23	27	15	1	2	2	NCRNA00081, SHOC2	369, -546	in gene, upstream	ActReg chr10 #2542	1	1	1
2543	10	112,993,275	112,993,699	424	1	9.214	5.929	2	14	9	3	0	0	0				ActReg chr10 #2543	1	0	0
2544	10	113,515,947	113,516,773	826	1	7.154	12.538	2.72	12	23	5	0	0	0				ActReg chr10 #2544	0	1	0
2545	10	113,766,498	113,767,490	992	1	10.419	7.645	1.792	15	11	4	0	0	0				ActReg chr10 #2545	1	0	0
2546	10	113,799,620	113,800,027	407	1	6.417	10.25	1	8	13	1	0	0	0				ActReg chr10 #2546	0	1	0
2547	10	113,943,149	113,944,003	854	2	10.407	13.148	5.926	21	26	12	1	1	1	GPAM	-51	upstream	ActReg chr10 #2547	1	1	0
2548	10	114,206,132	114,207,244	1,112	3	9.143	12.657	11.314	19	17	23	1	2	2	ZDHHC6, VTI1A	-16, -68	upstream, upstream	ActReg chr10 #2548	1	1	1
2549	10	114,393,746	114,394,267	521	1	11	4.667	3.111	16	8	4	0	1	2	VTI1A, MIR4295	187250, 77	in gene, in gene	ActReg chr10 #2549	1	0	0
2550	10	114,719,005	114,719,601	596	1	6.474	9.684	1.909	12	16	3	0	0	1	TCF7L2	9,294	in gene	ActReg chr10 #2550	0	1	0
2551	10	114,751,309	114,752,380	1,071	2	12.818	10.333	5.455	23	20	12	0	0	1	TCF7L2	41,835	in gene	ActReg chr10 #2551	1	1	0
2552	10	115,144,819	115,145,357	538	1	10.588	7.765	3.471	16	10	6	0	0	0				ActReg chr10 #2552	1	0	0
2553	10	115,195,995	115,196,631	636	1	3.3	10.5	3.45	9	15	9	0	0	0				ActReg chr10 #2553	0	1	0
2554	10	115,438,624	115,440,363	1,739	3	10.618	13.673	8.291	17	24	18	1	1	1	CASP7	558	in gene	ActReg chr10 #2554	1	1	1
2555	10	115,613,842	115,614,387	545	1	10.765	8.882	5.765	15	14	10	1	2	2	DCLRE1A, NHLRC2	-255, -277	upstream, upstream	ActReg chr10 #2555	1	0	0
2556	10	115,614,410	115,615,052	642	1	9.95	11.65	5.368	14	18	10	1	2	2	DCLRE1A, NHLRC2	-872, 340	upstream, in gene	ActReg chr10 #2556	0	1	0
2557	10	115,738,506	115,738,956	420	1	3.818	2.923	11	6	5	15	0	0	0				ActReg chr10 #2557	0	0	1
2558	10	115,933,387	115,934,162	775	1	7.958	11.375	9.625	15	20	16	1	3	3	C10orf118, MIR2110, TDRD1	590, 164, -5255	in gene, downstream, upstream	ActReg chr10 #2558	0	1	0
2559	10	115,999,534	115,999,980	446	1	1.5	2.643	13.143	3	5	19	1	1	2	TDRD1, VWA2	60728, 739	downstream, in gene	ActReg chr10 #2559	0	0	1
2560	10	116,105,218	116,106,655	1,437	2	10.046	7.977	8	16	13	17	0	0	1	AFAP1L2	58,579	in gene	ActReg chr10 #2560	1	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2561	10	116,149,058	116,149,635	577	1	12.222	13.167	1.25	20	24	2	0	0	1	AFAP1L2	15,169	in gene	ActReg chr10 #2561	0	1	0
2562	10	116,154,296	116,155,274	978	1	8.742	10.677	2.581	14	14	5	0	0	1	AFAP1L2	9,730	in gene	ActReg chr10 #2562	0	1	0
2563	10	116,163,792	116,164,296	504	1	7.312	4.25	12.312	10	7	21	1	1	1	AFAP1L2	471	in gene	ActReg chr10 #2563	0	0	1
2564	10	116,697,747	116,698,226	479	1	11.8	12.8	4.333	16	19	5	1	1	1	TRUB1	34	in gene	ActReg chr10 #2564	1	0	0
2565	10	117,376,126	117,376,492	366	1	2.5	2.5	10.417	4	4	15	0	0	1	ATRNL1	523,185	in gene	ActReg chr10 #2565	0	0	1
2566	10	117,923,142	117,923,519	377	1	5	3.818	10.364	7	6	13	0	0	1	GFRA1	109,796	in gene	ActReg chr10 #2566	0	0	1
2567	10	117,943,134	117,943,610	476	1	12.4	11.467	4.929	19	15	9	0	0	1	GFRA1	89,754	in gene	ActReg chr10 #2567	1	0	0
2568	10	118,368,939	118,369,274	335	1	2.7	6.5	11.8	4	10	14	1	0	1	PNLIPRP1	18,616	downstream	ActReg chr10 #2568	0	0	1
2569	10	118,501,062	118,501,508	446	1	7.143	3.786	10.429	10	5	14	1	1	1	HSPA12A	800	in gene	ActReg chr10 #2569	0	0	1
2570	10	118,764,263	118,764,793	530	1	9.5	11.125	3.625	16	15	6	1	1	1	KIAA1598	560	in gene	ActReg chr10 #2570	0	1	0
2571	10	118,900,543	118,900,845	302	1	2.7	4.9	10.7	4	6	15	0	1	1	VAX1	-2,882	upstream	ActReg chr10 #2571	0	0	1
2572	10	118,934,689	118,935,407	718	1	7.864	8.727	12.409	13	13	17	1	0	0				ActReg chr10 #2572	0	0	1
2573	10	118,946,161	118,946,862	701	1	11.727	9.273	4.368	22	14	10	0	0	0				ActReg chr10 #2573	1	0	0
2574	10	118,976,025	118,976,747	722	2	8.174	11.739	11.435	15	20	19	1	0	1	KCNK18	19,386	downstream	ActReg chr10 #2574	0	1	1
2575	10	118,976,779	118,977,333	554	1	8.176	6.588	10.647	11	9	16	1	0	1	KCNK18	20,056	downstream	ActReg chr10 #2575	0	0	1
2576	10	119,134,891	119,135,561	670	1	10.667	12.238	8.778	16	21	13	1	1	1	PDZD8	-289	upstream	ActReg chr10 #2576	0	1	0
2577	10	119,202,394	119,203,069	675	1	11.191	6	5.524	20	10	11	0	0	0				ActReg chr10 #2577	1	0	0
2578	10	119,739,800	119,740,301	501	1	5	11.562	1.556	8	14	4	0	0	0				ActReg chr10 #2578	0	1	0
2579	10	120,011,358	120,011,979	621	2	10.7	10.2	5.5	17	16	9	0	0	0				ActReg chr10 #2579	1	1	0
2580	10	120,248,149	120,248,639	490	1	9.267	11.667	4.429	15	20	8	0	0	0				ActReg chr10 #2580	0	1	0
2581	10	120,322,804	120,323,252	448	1	9	9.643	3.714	13	14	7	0	0	0				ActReg chr10 #2581	0	1	0
2582	10	120,353,723	120,356,048	2,325	4	9.863	13.192	9.205	21	24	18	1	1	1	PRLHR	275	in gene	ActReg chr10 #2582	1	1	1
2583	10	120,513,517	120,514,974	1,457	2	12.311	11.822	9.267	20	19	13	1	1	1	C10orf46	513	in gene	ActReg chr10 #2583	1	1	0
2584	10	120,739,496	120,740,114	618	1	3.176	3.368	11.947	5	6	15	0	0	0				ActReg chr10 #2584	0	0	1
2585	10	120,839,870	120,840,645	775	1	9.56	10.2	5.4	16	13	9	1	1	1	EIF3A	77	in gene	ActReg chr10 #2585	0	1	0
2586	10	120,937,826	120,938,488	662	1	11	9.85	7.25	17	14	13	1	1	1	PROX3	188	in gene	ActReg chr10 #2586	1	0	0
2587	10	121,258,524	121,259,428	904	1	8.138	11.793	3.778	13	17	6	0	0	1	RGS10	43,246	downstream	ActReg chr10 #2587	0	1	0
2588	10	121,278,403	121,278,749	346	1	6.3	5.5	11.5	9	6	16	0	0	1	RGS10	23,646	in gene	ActReg chr10 #2588	0	0	1
2589	10	121,356,064	121,357,085	1,021	2	8.094	12.812	10.812	14	20	20	1	1	1	TIAL1	-33	upstream	ActReg chr10 #2589	0	1	1
2590	10	121,427,117	121,428,418	1,301	1	9.829	13.61	4.463	16	20	7	0	0	1	BAG3	16,885	in gene	ActReg chr10 #2590	0	1	0
2591	10	121,484,940	121,485,434	494	1	7.133	8.4	11.267	12	12	16	1	1	1	INPP5F	-422	upstream	ActReg chr10 #2591	0	0	1
2592	10	121,651,620	121,652,509	889	1	12.111	8.778	5.667	20	15	9	1	1	1	SEC23IP	-159	upstream	ActReg chr10 #2592	1	0	0
2593	10	121,890,675	121,891,274	599	2	9.158	12.368	2.467	20	23	4	0	0	0				ActReg chr10 #2593	1	1	0
2594	10	122,146,720	122,147,430	710	1	5.87	10.609	2.227	12	14	4	0	0	0				ActReg chr10 #2594	0	1	0
2595	10	122,216,731	122,217,398	667	1	8.429	5.524	12	9	9	18	1	1	1	PPAPDC1A	598	in gene	ActReg chr10 #2595	0	0	1
2596	10	122,220,206	122,220,943	737	1	8.565	13.13	3.091	17	25	6	0	0	1	PPAPDC1A	4,108	in gene	ActReg chr10 #2596	0	1	0
2597	10	122,267,738	122,268,522	784	2	11.16	10.76	3.083	20	23	6	0	0	1	PPAPDC1A	51,664	in gene	ActReg chr10 #2597	1	1	0
2598	10	122,273,446	122,273,969	523	1	12	6.875	2.4	20	11	3	0	0	1	PPAPDC1A	57,241	in gene	ActReg chr10 #2598	1	0	0
2599	10	122,610,482	122,611,330	848	2	9.407	13.63	7.148	16	28	11	1	2	2	LOC283089, WDR11	-215, 219	upstream, in gene	ActReg chr10 #2599	1	1	0
2600	10	122,708,564	122,708,920	356	1	3.182	7	10.273	5	11	13	1	0	0				ActReg chr10 #2600	0	0	1
2601	10	122,802,444	122,803,051	607	1	8.895	11.105	5.778	13	20	10	0	0	0				ActReg chr10 #2601	0	1	0
2602	10	122,828,428	122,829,246	818	2	9.52	11.72	2.957	15	19	5	0	0	0				ActReg chr10 #2602	1	1	0
2603	10	123,687,389	123,688,128	739	2	10.542	10.542	4.958	21	14	9	1	2	2	ATE1, LOC100130887	-212, -69	upstream, upstream	ActReg chr10 #2603	1	1	0
2604	10	123,702,412	123,702,847	435	1	8	12.385	2.167	10	17	3	0	0	1	LOC100130887	14,802	in gene	ActReg chr10 #2604	0	1	0
2605	10	123,733,717	123,735,323	1,606	3	18.98	21.62	4.8	66	74	15	1	1	1	NSMCE4A	223	in gene	ActReg chr10 #2605	1	1	1
2606	10	123,872,726	123,873,423	697	2	9.455	11.864	12.909	14	20	22	1	0	1	TACC2	124,385	in gene	ActReg chr10 #2606	0	1	1
2607	10	123,900,253	123,901,240	987	2	15.516	13.387	2.962	30	26	5	0	0	1	TACC2	152,057	in gene	ActReg chr10 #2607	1	1	0
2608	10	124,091,304	124,091,859	555	1	7	12.177	3	12	18	6	0	0	1	BTBD16	60,760	in gene	ActReg chr10 #2608	0	1	0
2609	10	124,228,388	124,229,200	812	1	10.28	13.2	4.417	14	20	8	0	0	1	HTRA1	7,753	in gene	ActReg chr10 #2609	0	1	0
2610	10	124,254,156	124,254,828	672	1	13.143	9	5.095	22	15	9	0	0	1	HTRA1	33,451	in gene	ActReg chr10 #2610	1	0	0
2611	10	124,545,607	124,546,357	750	2	12.522	12.043	2.889	27	25	6	0	0	0				ActReg chr10 #2611	1	1	0
2612	10	124,638,807	124,639,684	877	1	6.786	12.357	7.519	9	20	16	1	1	1	FAM24B	-88	upstream	ActReg chr10 #2612	0	1	0
2613	10	124,670,853	124,672,221	1,368	2	26.286	31.214	3.738	88	95	7	0	1	1	FAM24A	1,320	in gene	ActReg chr10 #2613	1	1	0
2614	10	124,713,369	124,714,398	1,029	1	11.75	14.844	6.906	23	22	14	1	1	1	C10orf88	36	in gene	ActReg chr10 #2614	0	1	0
2615	10	124,739,589	124,740,433	844	2	10.385	10.039	4.522	24	21	10	1	1	1	PSTK	455	in gene	ActReg chr10 #2615	1	1	0
2616	10	124,767,678	124,768,960	1,282	1	10.244	11.39	9.585	18	18	17	1	2	2	IKZF5, ACADSB	-8, -110	upstream, upstream	ActReg chr10 #2616	0	1	0
2617	10	124,913,397	124,914,711	1,314	2	8.61	11.317	7.537	15	19	19	1	1	2	HMX2, BUB3	6416, 294	downstream, in gene	ActReg chr10 #2617	0	1	1
2618	10	125,220,153	125,220,519	366	1	1	1.75	9.5	1	3	14	0	0	0				ActReg chr10 #2618	0	0	1
2619	10	125,374,253	125,375,121	868	2	9.963	15.259	4.36	22	27	8	0	0	0				ActReg chr10 #2619	1	1	0
2620	10	125,851,988	125,852,575	587	1	4.294	5.389	11.389	7	8	17	1	0	0				ActReg chr10 #2620	0	0	1
2621	10	125,978,078	125,978,554	476	1	3.267	7.867	12.6	6	11	18	0	0	0				ActReg chr10 #2621	0	0	1
2622	10	126,077,432	126,077,811	379	1	4.917	8.583	12.5	6	10	19	1	0	1	OAT	29,924	downstream	ActReg chr10 #2622	0	0	1
2623	10	126,137,281	126,137,709	428	1	3.667	6	11.077	6	8	18	1	1	1	NKX1-2	1,055	in gene	ActReg chr10 #2623	0	0	1
2624	10	126,240,131	126,240,701	570	1	4.706	3.562	12.235	8	6	18	0	0	1	LHPP	90,075	in gene	ActReg chr10 #2624	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2625	10	126,305,724	126,306,267	543	1	3.067	5.588	12.882	6	8	23	0	0	2	LHPP, FAM53B	155654, 126935	downstream, downstream	ActReg chr10 #2625	0	0	1
2626	10	126,356,988	126,357,525	537	1	3.294	3.588	12.412	6	6	17	0	0	1	FAM53B	75,674	in gene	ActReg chr10 #2626	0	0	1
2627	10	126,479,635	126,480,750	1,115	1	10.086	11.343	7.629	17	20	15	1	1	2	METTL10, FAM175B	247, -10162	in gene, upstream	ActReg chr10 #2627	0	1	0
2628	10	126,489,982	126,490,631	649	1	8.667	11.238	7.524	18	17	14	1	1	2	METTL10, FAM175B	-9867, -48	upstream, upstream	ActReg chr10 #2628	0	1	0
2629	10	126,686,245	126,686,779	534	1	7.688	4.938	13.5	12	6	19	1	0	1	CTBP2	163,112	in gene	ActReg chr10 #2629	0	0	1
2630	10	126,847,288	126,847,813	525	1	6.118	9	9.444	10	16	14	1	1	1	CTBP2	2,074	in gene	ActReg chr10 #2630	0	1	0
2631	10	126,850,670	126,851,156	486	1	4.667	4.267	11.933	7	8	17	1	1	1	CTBP2	-1,289	upstream	ActReg chr10 #2631	0	0	1
2632	10	126,889,508	126,890,139	631	1	6.842	11.79	1.882	14	17	3	0	0	0				ActReg chr10 #2632	0	1	0
2633	10	127,511,459	127,512,415	956	2	14.414	19.138	5.931	29	47	14	1	2	2	UROS, BCCIP	-100, -167	upstream, upstream	ActReg chr10 #2633	1	1	0
2634	10	127,583,420	127,586,027	2,607	3	16.354	18.341	20.134	28	38	50	1	1	1	FANK1	-385	upstream	ActReg chr10 #2634	0	1	1
2635	10	127,750,850	127,751,853	1,003	1	9.452	11.032	5.323	15	16	9	0	0	1	ADAM12	325,776	in gene	ActReg chr10 #2635	0	1	0
2636	10	127,887,691	127,888,277	586	1	8.667	14.667	3.188	13	29	5	0	0	1	ADAM12	189,143	in gene	ActReg chr10 #2636	0	1	0
2637	10	128,148,385	128,149,193	808	1	10.08	13.12	3.722	21	22	6	0	0	1	C10orf90	61,221	in gene	ActReg chr10 #2637	0	1	0
2638	10	128,330,315	128,330,972	657	1	10.25	7.75	2	19	14	3	0	0	0				ActReg chr10 #2638	1	0	0
2639	10	128,352,570	128,353,128	558	1	6.389	11.722	3.714	11	16	5	0	0	0				ActReg chr10 #2639	0	1	0
2640	10	128,915,306	128,915,857	551	1	9.529	11.118	1	18	17	1	0	0	1	DOCK1	146,616	in gene	ActReg chr10 #2640	0	1	0
2641	10	129,283,384	129,284,001	617	1	10.1	14.4	4.95	22	27	9	0	0	0				ActReg chr10 #2641	0	1	0
2642	10	129,355,092	129,355,684	592	2	9.158	9.579	2.579	14	19	5	0	0	1	NPS	7,775	downstream	ActReg chr10 #2642	1	1	0
2643	10	129,398,489	129,399,359	870	2	13.741	16.815	1.731	25	34	3	0	0	0				ActReg chr10 #2643	1	1	0
2644	10	129,537,276	129,537,702	426	1	5.071	4.714	13.714	8	7	18	1	2	2	LOC387720, FOXI2	-2229, 1951	upstream, in gene	ActReg chr10 #2644	0	0	1
2645	10	129,823,840	129,824,298	458	1	2.533	1.769	12.2	4	4	18	0	0	1	PTPRE	118,744	in gene	ActReg chr10 #2645	0	0	1
2646	10	129,895,995	129,896,418	423	1	1.846	5.643	11	3	9	14	0	0	1	MKI67	28,262	in gene	ActReg chr10 #2646	0	0	1
2647	10	130,726,291	130,726,725	434	1	2.846	3	10.571	5	6	17	0	0	0				ActReg chr10 #2647	0	0	1
2648	10	130,777,631	130,778,100	469	1	1	2.357	12.133	1	4	21	0	0	0				ActReg chr10 #2648	0	0	1
2649	10	130,795,986	130,796,289	303	1	5.2	1	10.8	6	1	15	0	0	0				ActReg chr10 #2649	0	0	1
2650	10	131,504,205	131,504,706	501	1	4.25	3	12.125	7	5	17	0	0	1	MGMT	239,001	in gene	ActReg chr10 #2650	0	0	1
2651	10	131,566,717	131,567,195	478	1	2.1	2.4	11	3	3	14	0	0	1	MGMT	301,502	downstream	ActReg chr10 #2651	0	0	1
2652	10	131,567,204	131,567,568	364	1	3.727	1.667	11.546	6	2	15	0	0	1	MGMT	301,932	downstream	ActReg chr10 #2652	0	0	1
2653	10	131,609,361	131,609,683	322	1	3	7.6	12.7	4	11	17	0	0	1	LOC100506006	20,726	downstream	ActReg chr10 #2653	0	0	1
2654	10	131,661,411	131,662,075	664	1	10.15	14.05	8.467	19	23	13	0	0	1	EBF3	100,348	in gene	ActReg chr10 #2654	0	1	0
2655	10	131,749,420	131,750,134	714	1	11.591	8.591	6.636	17	13	9	0	0	1	EBF3	12,314	in gene	ActReg chr10 #2655	1	0	0
2656	10	131,766,804	131,767,229	425	1	2.154	1.333	10.692	4	2	17	1	1	1	EBF3	-4,925	upstream	ActReg chr10 #2656	0	0	1
2657	10	131,820,553	131,821,491	938	1	6	11.862	5.517	13	19	9	0	0	0				ActReg chr10 #2657	0	1	0
2658	10	131,863,094	131,864,009	915	1	7.241	11.621	4.103	13	18	11	0	0	1	LOC387723	45,530	in gene	ActReg chr10 #2658	0	1	0
2659	10	131,908,295	131,910,125	1,830	2	12.232	15.053	7.947	25	26	18	1	1	1	LOC387723	-129	upstream	ActReg chr10 #2659	1	1	0
2660	10	132,098,634	132,100,316	1,682	3	11.75	9.923	18.308	19	21	36	0	0	0				ActReg chr10 #2660	1	1	1
2661	10	132,365,567	132,366,000	433	1	2	3.364	11.214	3	5	16	1	0	0				ActReg chr10 #2661	0	0	1
2662	10	132,728,084	132,728,641	557	1	1.438	2.529	10.111	3	3	16	0	0	0				ActReg chr10 #2662	0	0	1
2663	10	132,734,133	132,734,610	477	1	3.133	2.1	9.533	5	3	15	0	0	0				ActReg chr10 #2663	0	0	1
2664	10	132,768,794	132,769,190	396	1	2.846	2.417	10.077	4	4	15	0	0	1	MIR378C	-8,061	upstream	ActReg chr10 #2664	0	0	1
2665	10	132,882,633	132,883,000	367	1	3.625	7.273	11.182	6	10	18	0	0	1	TCERG1L	227,168	downstream	ActReg chr10 #2665	0	0	1
2666	10	132,977,003	132,977,380	377	1	2.833	2.333	11.417	5	3	14	0	0	1	TCERG1L	132,793	in gene	ActReg chr10 #2666	0	0	1
2667	10	133,075,832	133,076,264	432	1	3	2.769	11.286	5	5	18	0	0	1	TCERG1L	33,936	in gene	ActReg chr10 #2667	0	0	1
2668	10	133,152,557	133,153,083	526	1	7.25	10.5	2.615	12	17	4	0	0	0				ActReg chr10 #2668	0	1	0
2669	10	133,934,302	133,934,600	298	1	2.5	4.3	10.8	4	6	15	0	0	1	JAKMIP3	16,138	in gene	ActReg chr10 #2669	0	0	1
2670	10	133,946,372	133,947,235	863	1	3.769	5.115	11.815	6	6	17	0	0	1	JAKMIP3	28,490	in gene	ActReg chr10 #2670	0	0	1
2671	10	133,981,806	133,982,287	481	1	3.467	3.333	11.733	5	5	19	0	0	1	JAKMIP3	63,733	in gene	ActReg chr10 #2671	0	0	1
2672	10	133,982,368	133,983,178	810	1	6.538	6.769	11.692	14	11	22	0	0	1	JAKMIP3	64,460	in gene	ActReg chr10 #2672	0	0	1
2673	10	134,009,691	134,010,642	951	1	3.517	4.133	10.967	7	10	14	0	0	1	DPYSL4	9,752	in gene	ActReg chr10 #2673	0	0	1
2674	10	134,016,731	134,017,267	536	1	5.294	4.353	13.706	9	5	21	0	0	2	DPYSL4, STK32C	16585, 104478	in gene, downstream	ActReg chr10 #2674	0	0	1
2675	10	134,021,208	134,021,803	595	1	3.526	4.263	10.263	6	6	15	0	0	2	DPYSL4, STK32C	21091, 99972	downstream, in gene	ActReg chr10 #2675	0	0	1
2676	10	134,036,515	134,037,612	1,097	1	7.194	5.088	11.794	14	10	17	0	0	1	STK32C	84,414	in gene	ActReg chr10 #2676	0	0	1
2677	10	134,039,965	134,040,396	431	1	6.357	1.429	12.5	10	2	20	1	0	1	STK32C	81,297	in gene	ActReg chr10 #2677	0	0	1
2678	10	134,120,369	134,120,832	463	1	4.467	4.8	10.6	6	8	17	1	1	1	STK32C	877	in gene	ActReg chr10 #2678	0	0	1
2679	10	134,133,519	134,134,188	669	1	4.05	10.952	4.278	8	17	8	0	0	1	LOC100506057	11,520	downstream	ActReg chr10 #2679	0	1	0
2680	10	134,145,045	134,146,093	1,048	3	9.606	12.182	11.121	17	23	20	1	2	2	LOC100506057, LRRC27	-196, -45	upstream, upstream	ActReg chr10 #2680	1	1	1
2681	10	134,202,432	134,203,197	765	1	1.958	5.625	12.708	4	13	17	0	0	2	LRRC27, PWWP2B	57200, -7888	downstream, upstream	ActReg chr10 #2681	0	0	1
2682	10	134,213,445	134,213,784	339	1	3.2	4.9	12.5	5	7	17	0	0	1	PWWP2B	2,912	in gene	ActReg chr10 #2682	0	0	1
2683	10	134,222,132	134,222,670	538	1	5.588	3.118	12.235	8	5	16	0	0	1	PWWP2B	11,699	in gene	ActReg chr10 #2683	0	0	1
2684	10	134,222,706	134,223,127	421	1	4.308	2.444	12.308	6	4	15	0	0	1	PWWP2B	12,214	in gene	ActReg chr10 #2684	0	0	1
2685	10	134,230,671	134,231,214	543	1	2.824	4.059	12.059	5	7	18	0	0	1	PWWP2B	20,240	in gene	ActReg chr10 #2685	0	0	1
2686	10	134,251,910	134,252,586	676	1	2.368	2.737	11.048	4	5	16	0	1	1	C10orf91	-6,466	upstream	ActReg chr10 #2686	0	0	1
2687	10	134,259,383	134,260,131	748	1	2.542	4.125	12.625	5	8	17	0	1	1	C10orf91	1,043	in gene	ActReg chr10 #2687	0	0	1
2688	10	134,264,419	134,264,864	445	1	3.143	4	13.857	4	5	20	0	0	1	C10orf91	5,927	downstream	ActReg chr10 #2688	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2689	10	134,265,132	134,266,056	924	1	4.31	5.429	11.897	7	12	16	0	0	1	C10orf91	6,880	downstream	ActReg chr10 #2689	0	0	1
2690	10	134,268,789	134,269,312	523	1	4	5.529	11.412	6	8	14	0	0	1	C10orf91	10,336	downstream	ActReg chr10 #2690	0	0	1
2691	10	134,271,167	134,271,870	703	1	4.318	5.591	12.454	9	9	19	0	0	1	C10orf91	12,804	downstream	ActReg chr10 #2691	0	0	1
2692	10	134,272,206	134,272,753	547	1	7.824	6.882	11.882	11	9	18	0	0	0				ActReg chr10 #2692	0	0	1
2693	10	134,274,110	134,274,589	479	1	4.067	3	10.8	6	4	16	0	0	0				ActReg chr10 #2693	0	0	1
2694	10	134,279,451	134,279,969	518	1	8.647	3.294	11.765	14	7	17	0	0	0				ActReg chr10 #2694	0	0	1
2695	10	134,290,740	134,291,314	574	1	2.588	4.5	13.778	5	9	20	0	0	0				ActReg chr10 #2695	0	0	1
2696	10	134,300,891	134,301,631	740	1	3.217	5.435	12.957	5	10	17	0	0	0				ActReg chr10 #2696	0	0	1
2697	10	134,302,470	134,303,227	757	1	5	6.522	12.217	9	13	16	0	0	0				ActReg chr10 #2697	0	0	1
2698	10	134,457,428	134,458,116	688	1	3.773	2.727	11.909	7	5	16	0	0	1	INPP5A	106,419	in gene	ActReg chr10 #2698	0	0	1
2699	10	134,467,394	134,468,012	618	1	3.211	6.421	11.421	6	10	15	0	0	1	INPP5A	116,350	in gene	ActReg chr10 #2699	0	0	1
2700	10	134,542,091	134,542,607	516	1	4	4.562	12.875	6	8	17	0	0	1	INPP5A	190,996	in gene	ActReg chr10 #2700	0	0	1
2701	10	134,549,542	134,550,438	896	1	2.786	4.393	12.571	5	8	21	1	0	1	INPP5A	198,637	in gene	ActReg chr10 #2701	0	0	1
2702	10	134,573,746	134,574,103	357	1	3.909	6.818	12.454	5	8	17	0	0	1	INPP5A	222,571	in gene	ActReg chr10 #2702	0	0	1
2703	10	134,606,001	134,607,129	1,128	2	5.771	12.029	9.2	12	25	14	1	1	2	INPP5A, NKX6-2	255212, -7028	downstream, upstream	ActReg chr10 #2703	0	1	1
2704	10	134,625,426	134,626,026	600	1	4.632	4.421	11.316	10	6	16	0	0	1	C10orf92	48,665	in gene	ActReg chr10 #2704	0	0	1
2705	10	134,640,664	134,640,972	308	1	5.4	6.5	11.6	7	9	14	0	0	1	C10orf92	33,573	in gene	ActReg chr10 #2705	0	0	1
2706	10	134,648,205	134,649,094	889	1	4.5	2.48	11.75	7	4	16	0	0	1	C10orf92	25,742	in gene	ActReg chr10 #2706	0	0	1
2707	10	134,649,617	134,650,043	426	1	2.556	5.154	11.692	3	8	18	0	0	1	C10orf92	24,561	in gene	ActReg chr10 #2707	0	0	1
2708	10	134,662,466	134,663,071	605	1	4.444	4.222	11.5	6	7	16	0	0	1	C10orf92	11,623	in gene	ActReg chr10 #2708	0	0	1
2709	10	134,663,229	134,663,720	491	1	3.625	2.938	10.875	6	5	17	0	0	1	C10orf92	10,917	in gene	ActReg chr10 #2709	0	0	1
2710	10	134,664,382	134,664,869	487	1	4.154	3.562	11.5	6	5	19	0	0	1	C10orf92	9,766	in gene	ActReg chr10 #2710	0	0	1
2711	10	134,675,333	134,675,809	476	1	2.8	2.067	13.333	4	4	21	0	1	2	C10orf92, LOC100506209	-1180, 65428	upstream, downstream	ActReg chr10 #2711	0	0	1
2712	10	134,681,150	134,681,554	404	1	1.154	1.75	10.846	2	3	16	0	1	2	C10orf92, LOC100506209	-6961, 59647	upstream, in gene	ActReg chr10 #2712	0	0	1
2713	10	134,682,564	134,682,956	392	1	5.25	4	11.083	8	6	16	1	0	2	C10orf92, LOC100506209	-8369, 58239	upstream, in gene	ActReg chr10 #2713	0	0	1
2714	10	134,694,829	134,695,439	610	1	3.895	2.647	10.263	5	5	14	0	0	1	LOC100506209	45,865	in gene	ActReg chr10 #2714	0	0	1
2715	10	134,719,579	134,719,916	337	1	2.8	2.909	11.273	5	4	14	1	0	1	LOC100506209	21,252	in gene	ActReg chr10 #2715	0	0	1
2716	10	134,724,480	134,724,804	324	1	1.286	2.364	10.546	3	3	15	0	0	1	LOC100506209	16,357	in gene	ActReg chr10 #2716	0	0	1
2717	10	134,727,219	134,727,623	404	1	3.538	3.692	11.308	6	7	15	0	0	1	LOC100506209	13,578	in gene	ActReg chr10 #2717	0	0	1
2718	10	134,730,336	134,731,079	743	1	2.833	2.727	11.625	8	5	17	0	0	1	LOC100506209	10,292	in gene	ActReg chr10 #2718	0	0	1
2719	10	134,733,179	134,733,737	558	1	4.611	4.556	12.222	6	7	16	1	0	2	LOC100506209, C10orf93	7541, 22631	in gene, downstream	ActReg chr10 #2719	0	0	1
2720	10	134,734,704	134,735,132	428	1	6.231	2.385	11.308	8	3	18	0	0	2	LOC100506209, C10orf93	6081, 21171	in gene, downstream	ActReg chr10 #2720	0	0	1
2721	10	134,741,771	134,742,219	448	1	3	4.5	11.857	4	8	17	0	1	2	LOC100506209, C10orf93	-996, 14094	upstream, downstream	ActReg chr10 #2721	0	0	1
2722	10	134,778,916	134,779,481	565	2	10.059	11	2.765	19	18	5	1	2	2	LOC100289424, LOC399829	-415, 160	upstream, in gene	ActReg chr10 #2722	1	1	0
2723	10	134,786,365	134,787,547	1,182	1	4.946	4.243	13.649	9	8	21	0	0	2	LOC100289424, LOC399829	-8173, 7918	upstream, in gene	ActReg chr10 #2723	0	0	1
2724	10	134,795,844	134,796,244	400	1	4.25	6	10.917	6	10	16	0	0	1	LOC399829	17,006	downstream	ActReg chr10 #2724	0	0	1
2725	10	134,798,245	134,799,064	819	1	3.24	4.24	11.64	6	7	17	0	0	1	LOC399829	19,616	downstream	ActReg chr10 #2725	0	0	1
2726	10	134,807,241	134,807,916	675	1	3.619	4.524	10.762	6	6	15	1	0	0				ActReg chr10 #2726	0	0	1
2727	10	134,829,342	134,830,089	747	1	2.5	3.042	13.208	4	6	19	0	0	0				ActReg chr10 #2727	0	0	1
2728	10	134,893,323	134,893,969	646	2	9.4	11	9.6	18	18	17	1	1	2	LOC100128127, GPR123	6491, -7763	downstream, upstream	ActReg chr10 #2728	0	1	1
2729	10	134,910,569	134,911,047	478	1	5.467	3.2	12.533	11	5	19	0	0	1	GPR123	9,399	in gene	ActReg chr10 #2729	0	0	1
2730	10	134,926,763	134,927,213	450	1	1	3.308	11.857	1	6	18	1	0	1	GPR123	25,579	in gene	ActReg chr10 #2730	0	0	1
2731	10	134,953,239	134,953,616	377	1	4.833	4.5	10.083	7	6	14	0	0	1	GPR123	52,018	downstream	ActReg chr10 #2731	0	0	1
2732	10	134,955,101	134,955,820	719	1	2.227	3.913	10.87	5	7	15	1	0	1	GPR123	54,051	downstream	ActReg chr10 #2732	0	0	1
2733	10	134,972,134	134,972,910	776	1	3.292	3.792	13.958	5	6	19	1	1	1	KNDC1	-1,449	upstream	ActReg chr10 #2733	0	0	1
2734	10	134,974,562	134,974,977	415	1	3.923	6.462	11.538	6	10	16	0	1	1	KNDC1	798	in gene	ActReg chr10 #2734	0	0	1
2735	10	134,980,651	134,981,115	464	1	7	8.214	11.786	8	12	18	1	0	1	KNDC1	6,912	in gene	ActReg chr10 #2735	0	0	1
2736	10	134,999,727	135,000,230	503	1	4.312	4.312	11.25	6	8	16	1	0	1	KNDC1	26,007	in gene	ActReg chr10 #2736	0	0	1
2737	10	135,010,795	135,011,401	606	1	4.474	4.053	12.105	6	7	21	0	0	1	KNDC1	37,127	in gene	ActReg chr10 #2737	0	0	1
2738	10	135,011,597	135,012,279	682	1	4.762	5.762	13.286	7	9	17	0	0	1	KNDC1	37,967	in gene	ActReg chr10 #2738	0	0	1
2739	10	135,013,506	135,014,119	613	1	4.421	7.263	11.737	8	12	15	0	0	1	KNDC1	39,841	in gene	ActReg chr10 #2739	0	0	1
2740	10	135,015,111	135,015,543	432	1	3.538	3.769	12.923	5	6	17	1	0	1	KNDC1	41,356	in gene	ActReg chr10 #2740	0	0	1
2741	10	135,026,285	135,027,223	938	1	4.379	5.621	13.069	7	7	20	0	0	1	KNDC1	52,783	in gene	ActReg chr10 #2741	0	0	1
2742	10	135,039,727	135,040,024	297	1	3.111	2.222	11.111	4	4	13	1	1	2	KNDC1, UTF1	65904, -3903	in gene, upstream	ActReg chr10 #2742	0	0	1
2743	10	135,061,794	135,062,262	468	1	2.111	5.5	13.714	4	7	21	0	1	2	VENTX, MIR202	10620, -904	downstream, upstream	ActReg chr10 #2743	0	0	1
2744	10	135,071,824	135,072,747	923	1	6.552	7.483	11.414	11	15	17	0	1	2	ADAM8, LOC100506167	18122, -5278	downstream, upstream	ActReg chr10 #2744	0	0	1
2745	10	135,091,098	135,092,908	1,810	2	8.491	10.93	7.561	17	25	18	0	1	3	ADAM8, LOC100506167, TUBGCP2	-1596, 14440, 30641	upstream, in gene, downstream	ActReg chr10 #2745	0	1	1
2746	10	135,106,159	135,107,218	1,059	1	8.212	11.546	6.394	12	17	12	0	0	1	TUBGCP2	15,956	in gene	ActReg chr10 #2746	0	1	0
2747	10	135,109,234	135,109,787	553	1	5.412	3.941	12.235	11	6	18	0	0	1	TUBGCP2	13,134	in gene	ActReg chr10 #2747	0	0	1
2748	10	135,132,063	135,132,548	485	1	9.938	5.375	11.438	14	10	19	1	0	3	TUBGCP2, ZNF511, CALY	-9661, 9882, 18170	upstream, downstream, downstream	ActReg chr10 #2748	0	0	1
2749	10	135,149,129	135,149,564	435	1	6	5.923	12.231	8	8	17	1	1	1	CALY	1,129	in gene	ActReg chr10 #2749	0	0	1
2750	10	135,164,958	135,165,435	477	1	3.714	5.333	12.4	9	8	16	0	0	2	PRAP1, C10orf125	4352, 6333	in gene, downstream	ActReg chr10 #2750	0	0	1
2751	10	135,165,666	135,166,112	446	1	1.538	4.286	14.214	4	7	23	0	0	3	PRAP1, C10orf125, ECHS1	5045, 5640, 21019	in gene, downstream, downstream	ActReg chr10 #2751	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2752	10	135,170,302	135,171,041	739	1	4.667	8.458	11.833	7	12	16	1	1	3	PRAP1, C10orf125, ECHS1	9827, 858, 16237	downstream, in gene, downstream	ActReg chr10 #2752	0	0	1
2753	10	135,171,681	135,172,335	654	1	3.65	3.9	12.95	8	7	19	1	1	3	PRAP1, C10orf125, ECHS1	11164, -479, 14900	downstream, upstream, downstream	ActReg chr10 #2753	0	0	1
2754	10	135,190,219	135,190,648	429	1	3.333	3.923	12.769	6	5	18	0	2	2	ECHS1, PAOX	-3525, -2308	upstream, upstream	ActReg chr10 #2754	0	0	1
2755	10	135,191,841	135,192,344	503	1	10.933	9.4	12.667	14	14	19	1	2	2	ECHS1, PAOX	-5184, -649	upstream, upstream	ActReg chr10 #2755	0	0	1
2756	10	135,205,051	135,205,485	434	1	1.929	4.214	10.929	3	6	15	0	1	2	PAOX, MTG1	12527, -2353	downstream, upstream	ActReg chr10 #2756	0	0	1
2757	10	135,207,530	135,208,171	641	2	6.4	11.4	9.5	10	20	15	1	1	2	PAOX, MTG1	15109, 229	downstream, in gene	ActReg chr10 #2757	0	1	1
2758	10	135,267,171	135,267,518	347	1	3.1	2.6	11.9	4	3	16	0	0	0				ActReg chr10 #2758	0	0	1
2759	10	135,270,865	135,271,796	931	1	5.345	5.724	13.276	10	8	22	2	0	0				ActReg chr10 #2759	0	0	1
2760	10	135,341,512	135,342,288	776	1	3.333	3.458	12.542	8	8	18	1	1	1	CYP2E1	1,033	in gene	ActReg chr10 #2760	0	0	1
2761	11	189,325	190,472	1,147	3	17.889	15.083	20.2	31	30	47	0	2	2	SCGB1C1, ODF3	-3182, -686	upstream, upstream	ActReg chr11 #2761	1	1	1
2762	11	195,027	195,740	713	1	4.955	6.182	12.546	8	11	16	0	2	3	SCGB1C1, ODF3, BET1L	2303, -1378, 12039	downstream, upstream, downstream	ActReg chr11 #2762	0	0	1
2763	11	289,853	290,289	436	1	3.571	3.571	9.357	5	7	15	1	1	3	NLRP6, ATHL1, IFITM5	11501, 933, 8455	downstream, in gene, downstream	ActReg chr11 #2763	0	0	1
2764	11	355,747	356,143	396	1	9.833	11.667	9.583	13	17	16	1	0	0				ActReg chr11 #2764	0	0	1
2765	11	364,199	365,035	836	2	16.962	17.038	6	43	43	12	0	1	1	B4GALNT4	-5,178	upstream	ActReg chr11 #2765	1	1	0
2766	11	396,947	397,244	297	1	6	5.444	10.111	9	8	12	1	0	2	PKP3, SIGIRR	2878, 20302	in gene, downstream	ActReg chr11 #2766	0	0	1
2767	11	448,153	448,664	511	1	7.188	10.75	3.812	12	16	6	0	2	2	ANO9, PTDSS2	-6397, -1872	upstream, upstream	ActReg chr11 #2767	0	1	0
2768	11	449,854	450,711	857	2	9.889	14.111	5.125	21	31	8	1	1	2	ANO9, PTDSS2	-8271, 2	upstream, in gene	ActReg chr11 #2768	1	1	0
2769	11	500,309	500,721	412	1	2.167	4.909	10.077	3	10	14	0	0	2	PTDSS2, RNH1	50235, 6758	downstream, in gene	ActReg chr11 #2769	0	0	1
2770	11	534,682	535,014	332	1	4.727	3.545	10.546	6	5	15	1	2	2	HRAS, LRRC56	702, -2674	in gene, upstream	ActReg chr11 #2770	0	0	1
2771	11	536,898	537,624	726	2	8.591	12.318	11.591	13	23	18	1	2	2	HRAS, LRRC56	-1711, -261	upstream, upstream	ActReg chr11 #2771	0	1	1
2772	11	575,569	575,915	346	1	5.125	5.818	10.818	8	13	17	1	4	4	LOC100506211, MIR210, LOC143666, PHRF1	-7322, -7544, 143, -741	upstream, upstream, in gene, upstream	ActReg chr11 #2772	0	0	1
2773	11	597,919	598,229	310	1	4.4	2.6	10.5	6	7	13	0	0	1	PHRF1	21,591	in gene	ActReg chr11 #2773	0	0	1
2774	11	660,485	660,823	338	1	1.9	3.1	10.4	3	5	14	1	0	1	DEAF1	35,086	in gene	ActReg chr11 #2774	0	0	1
2775	11	702,782	703,271	489	1	6.812	6.25	12.125	10	10	15	0	2	3	DEAF1, TMEM80, EPS8L2	-7286, 7410, -3094	upstream, in gene, upstream	ActReg chr11 #2775	0	0	1
2776	11	794,618	794,960	342	1	3.273	4.273	10.636	5	6	15	0	1	3	CEND1, SLC25A22, LRDD	-4663, 3480, 10461	upstream, in gene, downstream	ActReg chr11 #2776	0	0	1
2777	11	800,660	800,921	261	1	3.75	2	10.375	5	3	12	1	1	3	SLC25A22, LRDD, RPLP2	-2521, 4460, -9146	upstream, in gene, upstream	ActReg chr11 #2777	0	0	1
2778	11	802,610	803,002	392	1	3.083	2.25	12.417	6	3	17	0	3	4	SLC25A22, LRDD, RPLP2, SNORA52	-4537, 2444, -7130, -8875	upstream, in gene, upstream, upstream	ActReg chr11 #2778	0	0	1
2779	11	805,327	805,635	308	1	7.7	5.8	11.9	10	9	14	1	4	4	SLC25A22, LRDD, RPLP2, SNORA52	-7212, -231, -4455, -6200	upstream, upstream, upstream, upstream	ActReg chr11 #2779	0	0	1
2780	11	809,118	810,102	984	3	11.258	9.548	7.71	17	17	14	1	3	4	LRDD, RPLP2, SNORA52, PNPLA2	-4360, -326, -2071, -9291	upstream, upstream, upstream, upstream	ActReg chr11 #2780	1	1	1
2781	11	834,819	835,367	548	1	11.059	9.118	7.176	19	15	8	0	2	5	PNPLA2, EFCAB4A, CD151, POLR2L, TSPAN4	16192, 7508, 2141, 7436, -7731	downstream, downstream, in gene, downstream, upstream	ActReg chr11 #2781	1	0	0
2782	11	836,978	837,573	595	1	3.368	5	12.053	8	7	17	0	1	4	EFCAB4A, CD151, POLR2L, TSPAN4	9690, 4323, 5254, -5549	downstream, in gene, downstream, upstream	ActReg chr11 #2782	0	0	1
2783	11	841,300	841,787	487	1	5.533	5.6	10.867	9	7	16	0	2	4	EFCAB4A, CD151, POLR2L, TSPAN4	13958, 8591, 986, -1281	downstream, downstream, in gene, upstream	ActReg chr11 #2783	0	0	1
2784	11	842,280	843,068	788	2	23.087	23.375	1	55	54	1	1	2	3	CD151, POLR2L, TSPAN4	9722, -145, -150	downstream, upstream, upstream	ActReg chr11 #2784	1	1	0
2785	11	1,079,941	1,080,419	478	1	2.867	2.533	10.6	5	3	16	0	0	1	MUC2	5,305	in gene	ActReg chr11 #2785	0	0	1
2786	11	1,085,453	1,086,009	556	1	2.059	3.176	12.412	4	6	21	0	0	1	MUC2	10,856	in gene	ActReg chr11 #2786	0	0	1
2787	11	1,213,134	1,213,646	512	1	8	5.312	18.25	12	10	30	0	0	0				ActReg chr11 #2787	0	0	1
2788	11	1,246,136	1,246,626	490	1	7.438	11.438	5.938	10	15	11	0	1	1	MUC5B	2,086	in gene	ActReg chr11 #2788	0	1	0
2789	11	1,330,674	1,331,527	853	1	10.963	7.741	7.15	14	15	15	1	2	2	TOLLIP, LOC255512	-208, 162	upstream, in gene	ActReg chr11 #2789	1	0	0
2790	11	1,391,850	1,392,174	324	1	1	3.3	11.8	1	5	15	0	0	0				ActReg chr11 #2790	0	0	1
2791	11	1,417,691	1,418,141	450	1	2.417	3.3	11.143	4	5	18	0	0	1	BRSK2	6,787	in gene	ActReg chr11 #2791	0	0	1
2792	11	1,434,907	1,435,159	252	1	2.375	3.571	9.375	3	5	12	0	0	1	BRSK2	23,904	in gene	ActReg chr11 #2792	0	0	1
2793	11	1,594,942	1,595,265	323	1	2.455	3.333	9.545	4	4	13	0	2	2	DUSP8, LOC338651	-1953, 1132	upstream, in gene	ActReg chr11 #2793	0	0	1
2794	11	1,768,859	1,769,236	377	1	2.455	6.333	10.667	4	8	16	1	1	2	LOC402778, CTSD	302, 16175	in gene, downstream	ActReg chr11 #2794	0	0	1
2795	11	1,772,248	1,772,849	601	1	5.474	2.842	10.526	9	4	13	0	1	2	LOC402778, CTSD	-3199, 12674	upstream, downstream	ActReg chr11 #2795	0	0	1
2796	11	1,782,304	1,782,723	419	1	3.583	6.571	12	6	9	18	0	1	1	CTSD	2,709	in gene	ActReg chr11 #2796	0	0	1
2797	11	1,847,042	1,847,453	411	1	5.167	3.273	12.833	8	5	18	1	0	1	SYT8	-8,427	upstream	ActReg chr11 #2797	0	0	1
2798	11	1,853,621	1,853,940	319	1	5	4.8	11.4	7	10	15	0	2	2	SYT8, TNNI2	-1894, -6453	upstream, upstream	ActReg chr11 #2798	0	0	1
2799	11	1,884,351	1,884,964	613	1	5.85	11.2	6.333	10	18	9	0	1	2	LSP1, MIR4298	10457, -3891	in gene, upstream	ActReg chr11 #2799	0	1	0
2800	11	1,903,185	1,903,642	457	1	1.929	1.857	9.929	4	3	15	1	0	1	LSP1	29,213	in gene	ActReg chr11 #2800	0	0	1
2801	11	1,968,269	1,969,355	1,086	2	12.382	18.853	4.607	33	51	8	1	1	2	TNNT3, MRPL23	28013, 310	downstream, in gene	ActReg chr11 #2801	1	1	0
2802	11	1,978,070	1,978,370	300	1	1.25	1.889	10.2	2	3	14	1	0	1	MRPL23	9,718	downstream	ActReg chr11 #2802	0	0	1
2803	11	2,030,029	2,030,450	421	1	2.231	2.818	10.538	3	4	15	0	0	0				ActReg chr11 #2803	0	0	1
2804	11	2,184,102	2,184,444	342	1	2.8	1.5	11	3	2	16	0	2	3	INS-IGF2, INS, TH	-1834, -1834, 8762	upstream, upstream, downstream	ActReg chr11 #2804	0	0	1
2805	11	2,185,576	2,185,966	390	1	2.636	4.167	10.833	5	6	16	0	2	3	INS-IGF2, INS, TH	-3332, -3332, 7264	upstream, upstream, in gene	ActReg chr11 #2805	0	0	1
2806	11	2,187,023	2,187,372	349	1	2.273	3.636	11.454	5	5	15	1	2	3	INS-IGF2, INS, TH	-4758, -4758, 5838	upstream, upstream, in gene	ActReg chr11 #2806	0	0	1
2807	11	2,421,327	2,422,214	887	2	12	9.607	9.643	23	15	16	1	1	3	CD81, TSSC4, TRPM5	23223, -1753, 22505	downstream, upstream, downstream	ActReg chr11 #2807	1	1	0
2808	11	2,428,023	2,428,404	381	1	11.875	2.917	10.75	2	5	16	0	0	3	CD81, TSSC4, TRPM5	29666, 4690, 16062	downstream, downstream, in gene	ActReg chr11 #2808	0	0	1
2809	11	2,487,004	2,487,370	366	1	1.667	2.75	10	3	4	16	0	0	1	KCNQ1	20,966	in gene	ActReg chr11 #2809	0	0	1
2810	11	2,537,071	2,537,393	322	1	1.6	5.2	11	2	8	14	0	0	1	KCNQ1	71,011	in gene	ActReg chr11 #2810	0	0	1
2811	11	2,552,482	2,552,924	442	1	4.769	3.923	10.231	7	5	16	0	0	1	KCNQ1	86,482	in gene	ActReg chr11 #2811	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2812	11	2,556,910	2,557,485	575	1	2.167	4.375	11	3	7	15	0	0	1	KCNQ1	90,976	in gene	ActReg chr11 #2812	0	0	1
2813	11	2,561,184	2,561,525	341	1	2.909	3.273	9.455	5	5	15	0	0	1	KCNQ1	95,133	in gene	ActReg chr11 #2813	0	0	1
2814	11	2,720,844	2,721,330	486	1	4.733	5.6	11.067	9	10	19	1	1	2	KCNQ1, KCNQ1OT1	254866, 141	in gene, in gene	ActReg chr11 #2814	0	0	1
2815	11	2,810,734	2,811,086	352	1	3.455	5	11.636	6	8	17	0	0	1	KCNQ1	344,689	in gene	ActReg chr11 #2815	0	0	1
2816	11	2,822,780	2,823,195	415	1	2.667	1.692	11.692	4	3	18	0	0	1	KCNQ1	356,766	in gene	ActReg chr11 #2816	0	0	1
2817	11	2,842,024	2,842,409	385	1	3.75	3.417	10.167	5	5	15	0	0	1	KCNQ1	375,995	in gene	ActReg chr11 #2817	0	0	1
2818	11	2,862,781	2,863,336	555	1	1.882	4.222	10.611	3	6	15	0	0	1	KCNQ1	396,837	in gene	ActReg chr11 #2818	0	0	1
2819	11	2,866,779	2,867,410	631	1	4.25	5.75	11.85	8	9	16	0	0	1	KCNQ1	400,873	in gene	ActReg chr11 #2819	0	0	1
2820	11	2,906,279	2,907,071	792	2	6.042	10.708	9.8	10	15	15	1	1	2	CDKN1C, SLC22A18AS	320, 18500	in gene, downstream	ActReg chr11 #2820	0	1	1
2821	11	2,943,196	2,943,499	303	1	3.3	2.4	10.3	6	4	13	1	0	2	SLC22A18, PHLDA2	22396, 7303	in gene, downstream	ActReg chr11 #2821	0	0	1
2822	11	2,950,222	2,950,709	487	1	7.2	13.133	3.538	12	19	6	1	1	2	SLC22A18, PHLDA2	29514, 185	downstream, in gene	ActReg chr11 #2822	0	1	0
2823	11	2,952,375	2,952,687	312	1	3.7	2	9.8	5	3	13	0	1	2	SLC22A18, PHLDA2	31580, -1881	downstream, upstream	ActReg chr11 #2823	0	0	1
2824	11	3,078,358	3,078,993	635	2	7.35	9	10.6	12	16	16	1	1	1	CARS	6	in gene	ActReg chr11 #2824	0	1	1
2825	11	3,862,596	3,863,100	504	1	7.467	9.733	6.533	12	18	9	1	1	1	RHOG	-635	upstream	ActReg chr11 #2825	0	1	0
2826	11	4,115,874	4,116,302	428	1	11.923	9.769	3.538	16	13	5	1	1	2	STIM1, RRM1	239155, 164	downstream, in gene	ActReg chr11 #2826	0	1	0
2827	11	4,629,020	4,629,513	493	1	3.5	10.75	3	5	16	4	1	1	1	TRIM68	171	in gene	ActReg chr11 #2827	0	1	0
2828	11	6,411,540	6,411,971	431	1	5.5	8.571	10.143	9	11	16	1	1	3	SMPD1, APBB1, LOC100506137	111, 28889, 7822	in gene, downstream, downstream	ActReg chr11 #2828	0	0	1
2829	11	6,502,334	6,503,174	840	2	8.481	9.778	6.292	14	16	11	1	3	3	TRIM3, ARFIP2, FXC1	-7549, -159, 77	upstream, upstream, in gene	ActReg chr11 #2829	1	1	0
2830	11	7,621,404	7,621,966	562	1	5.222	12.889	3.235	8	21	5	0	0	1	PPFIBP2	86,684	in gene	ActReg chr11 #2830	0	1	0
2831	11	7,672,243	7,672,842	599	1	9.895	5.579	3.412	17	10	6	0	0	1	PPFIBP2	137,541	in gene	ActReg chr11 #2831	1	0	0
2832	11	8,040,880	8,041,210	330	1	3.9	4.5	9.4	5	7	14	1	0	0				ActReg chr11 #2832	0	0	1
2833	11	8,244,744	8,245,405	661	1	8.7	12	2.2	15	18	4	0	0	1	LMO1	40,332	downstream	ActReg chr11 #2833	0	1	0
2834	11	8,319,856	8,320,167	311	1	2	1	9.3	3	1	13	0	0	0				ActReg chr11 #2834	0	0	1
2835	11	8,394,546	8,394,888	342	1	3.273	1.818	9.727	5	3	12	0	0	0				ActReg chr11 #2835	0	0	1
2836	11	8,430,013	8,430,624	611	2	10.7	8.05	3.2	19	15	4	0	0	1	STK33	185,185	in gene	ActReg chr11 #2836	1	1	0
2837	11	8,703,979	8,704,649	670	1	11.286	6.81	5.476	20	14	8	1	3	3	RPL27A, SNORA3, SNORA45	319, -1460, -2672	in gene, upstream, upstream	ActReg chr11 #2837	1	0	0
2838	11	8,986,151	8,986,701	550	1	8.765	6.059	11.823	12	7	22	1	1	1	TMEM9B	-437	upstream	ActReg chr11 #2838	0	0	1
2839	11	9,385,688	9,386,266	578	1	5.944	12.833	3.333	10	23	6	1	0	0				ActReg chr11 #2839	0	1	0
2840	11	9,406,028	9,406,318	290	1	7.111	6.333	11.667	10	7	14	1	1	1	IPO7	4	in gene	ActReg chr11 #2840	0	0	1
2841	11	9,481,817	9,482,561	744	1	8.833	10.583	5.583	14	13	9	1	2	2	LOC644656, ZNF143	56, -323	in gene, upstream	ActReg chr11 #2841	0	1	0
2842	11	9,635,524	9,635,988	464	1	10.786	10.643	5.143	16	18	8	1	0	0				ActReg chr11 #2842	1	0	0
2843	11	10,325,834	10,326,744	910	3	10.556	13.929	5.286	19	30	12	1	1	1	ADM	-353	upstream	ActReg chr11 #2843	1	1	1
2844	11	10,511,965	10,512,777	812	1	9.346	11.308	3	13	14	6	0	0	1	AMPD3	40,503	in gene	ActReg chr11 #2844	0	1	0
2845	11	10,562,564	10,563,061	497	1	11.333	10.4	3.3	14	15	6	1	2	2	RNF141, LOC100129827	-38, 25	upstream, in gene	ActReg chr11 #2845	0	1	0
2846	11	10,746,736	10,747,285	549	1	10.235	5.941	2.071	20	9	6	0	0	0				ActReg chr11 #2846	1	0	0
2847	11	10,829,698	10,830,223	525	1	5.562	10.25	6.812	10	16	12	1	2	2	EIF4G2, SNORD97	622, -6805	in gene, upstream	ActReg chr11 #2847	0	1	0
2848	11	11,413,283	11,413,733	450	1	10.5	6.357	4.857	18	10	6	0	0	1	GALNTL4	230,053	in gene	ActReg chr11 #2848	1	0	0
2849	11	11,863,214	11,863,638	424	1	8.538	7.923	11.308	9	11	15	1	1	1	USP47	456	in gene	ActReg chr11 #2849	0	0	1
2850	11	12,029,562	12,029,951	389	1	2.083	3.5	11.25	4	6	16	1	1	1	DKK3	1,161	in gene	ActReg chr11 #2850	0	0	1
2851	11	12,309,189	12,309,901	712	1	11.909	7.5	5.524	19	11	9	0	1	1	MICALCL	1,098	in gene	ActReg chr11 #2851	1	0	0
2852	11	12,695,542	12,696,067	525	1	9.118	8.118	1.615	18	12	3	1	1	1	TEAD1	-165	upstream	ActReg chr11 #2852	1	0	0
2853	11	13,237,381	13,238,204	823	1	7.6	10.08	3.12	13	13	7	0	0	0				ActReg chr11 #2853	0	1	0
2854	11	13,299,638	13,300,032	394	1	9.923	9.077	6.231	15	13	9	1	1	1	ARNTL	510	in gene	ActReg chr11 #2854	1	0	0
2855	11	14,358,619	14,359,108	489	1	8.562	10.188	1	14	20	1	0	0	1	RRAS2	27,189	in gene	ActReg chr11 #2855	0	1	0
2856	11	14,380,389	14,381,289	900	2	13.714	23.464	2.714	30	59	5	1	0	1	RRAS2	5,213	in gene	ActReg chr11 #2856	1	1	0
2857	11	14,521,153	14,521,617	464	1	8.929	12.643	2.714	14	20	5	0	1	2	COPB1, PSMA1	56, 143795	in gene, downstream	ActReg chr11 #2857	0	1	0
2858	11	14,541,589	14,542,377	788	3	17.96	18.32	5.92	39	39	13	1	0	1	PSMA1	123,197	in gene	ActReg chr11 #2858	1	1	1
2859	11	15,900,258	15,900,770	512	1	10.5	11.562	1	17	23	1	0	0	0				ActReg chr11 #2859	0	1	0
2860	11	16,759,848	16,760,510	662	1	7.35	13.25	3.65	14	20	7	1	1	1	C11orf58	31	in gene	ActReg chr11 #2860	0	1	0
2861	11	17,229,020	17,229,750	730	1	6.217	5.652	11.13	13	9	16	1	0	0				ActReg chr11 #2861	0	0	1
2862	11	18,127,180	18,128,715	1,535	3	15.625	13.271	3.705	37	36	8	1	1	1	SAAL1	-309	upstream	ActReg chr11 #2862	1	1	0
2863	11	18,132,470	18,133,135	665	1	7.619	11.619	2.188	18	18	4	0	1	2	SAAL1, MRGPRX3	-5164, -9700	upstream, upstream	ActReg chr11 #2863	0	1	0
2864	11	18,416,020	18,416,491	471	1	4.933	8.867	11.8	9	10	17	1	1	1	LDHA	319	in gene	ActReg chr11 #2864	0	0	1
2865	11	18,471,738	18,472,066	328	1	1.2	3.167	9.818	2	4	13	0	1	2	LDHC, LDHAL6A	38049, -5472	in gene, upstream	ActReg chr11 #2865	0	0	1
2866	11	18,548,082	18,548,748	666	1	12.095	10.286	5.286	23	15	10	1	1	2	TSG101, UEVLD	74, 61866	in gene, downstream	ActReg chr11 #2866	1	0	0
2867	11	18,655,630	18,656,235	605	1	10.316	8.421	5.632	16	14	8	1	1	1	SPTY2D1	88	in gene	ActReg chr11 #2867	1	0	0
2868	11	18,857,829	18,858,478	649	1	9.5	6.5	3.333	17	14	6	0	0	0				ActReg chr11 #2868	1	0	0
2869	11	19,940,655	19,941,357	702	2	10.546	10.454	2.4	16	18	6	0	0	1	NAV2	568,735	in gene	ActReg chr11 #2869	1	1	0
2870	11	20,133,827	20,134,548	721	1	5.727	11.773	2.682	12	16	5	0	0	1	NAV2	761,916	in gene	ActReg chr11 #2870	0	1	0
2871	11	20,180,067	20,181,050	983	2	11.533	18.033	4.3	26	37	8	1	1	1	DBX1	1,312	in gene	ActReg chr11 #2871	1	1	0
2872	11	20,621,073	20,621,755	682	1	6.333	15.905	1.5	15	29	3	0	1	1	SLC6A5	468	in gene	ActReg chr11 #2872	0	1	0
2873	11	22,214,117	22,214,577	460	1	3.5	5.357	10.643	6	8	17	1	1	1	ANO5	-375	upstream	ActReg chr11 #2873	0	0	1
2874	11	22,358,958	22,359,761	803	1	7.76	14.6	2.4	12	30	5	0	1	1	SLC17A6	-308	upstream	ActReg chr11 #2874	0	1	0
2875	11	23,674,859	23,675,125	266	1	4.857	2.8	10.75	8	4	13	0	0	0				ActReg chr11 #2875	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2876	11	25,372,859	25,373,145	286	1	2.778	3.556	10.889	4	7	14	0	0	0				ActReg chr11 #2876	0	0	1
2877	11	27,255,651	27,256,203	552	1	6.529	10.529	3.533	10	18	5	0	0	0				ActReg chr11 #2877	0	1	0
2878	11	27,740,595	27,741,283	688	2	10.182	9.842	6.238	20	16	11	1	1	1	BDNF	2,666	in gene	ActReg chr11 #2878	1	1	0
2879	11	27,741,480	27,742,599	1,119	2	14.543	19.086	3.818	32	43	6	1	1	1	BDNF	1,566	in gene	ActReg chr11 #2879	1	1	0
2880	11	27,742,912	27,743,383	471	1	5	10.067	3.933	7	13	7	1	1	1	BDNF	458	in gene	ActReg chr11 #2880	0	1	0
2881	11	27,743,675	27,744,104	429	1	11.357	7	1.625	15	13	2	1	1	1	BDNF	-284	upstream	ActReg chr11 #2881	1	0	0
2882	11	27,926,045	27,926,486	441	1	7.714	10.714	1	9	16	1	0	0	0				ActReg chr11 #2882	0	1	0
2883	11	28,129,717	28,130,116	399	1	5.769	10.231	4.231	8	14	6	0	2	2	KIF18A, METT5D1	-170, 118	upstream, in gene	ActReg chr11 #2883	0	1	0
2884	11	28,723,643	28,724,036	393	1	5.385	10.154	2	8	14	3	0	0	0				ActReg chr11 #2884	0	1	0
2885	11	29,303,598	29,304,218	620	2	7.526	13.579	1.286	17	29	3	0	0	0				ActReg chr11 #2885	1	1	0
2886	11	31,391,112	31,391,683	571	1	7.889	9.556	5.389	11	16	11	1	2	2	DCDC1, DNAJC24	-76, 20	upstream, in gene	ActReg chr11 #2886	0	1	0
2887	11	31,990,676	31,991,398	722	1	11.783	6.435	3.429	17	12	7	0	0	0				ActReg chr11 #2887	1	0	0
2888	11	31,996,156	31,996,781	625	2	10.5	8.85	2.294	21	19	4	0	0	0				ActReg chr11 #2888	1	1	0
2889	11	32,109,430	32,110,407	977	1	10.71	7.258	2.29	17	13	7	0	1	1	RCN1	-2,559	upstream	ActReg chr11 #2889	1	0	0
2890	11	32,219,407	32,220,378	971	2	9.607	11.5	2.722	20	22	6	0	0	0				ActReg chr11 #2890	1	1	0
2891	11	32,456,096	32,456,461	365	1	9.167	9.333	10.833	13	13	17	1	2	2	WT1, WIT1	809, -1007	in gene, upstream	ActReg chr11 #2891	0	0	1
2892	11	32,909,906	32,910,228	322	1	2.3	2.444	10.4	3	4	12	0	1	1	QSER1	4,725	upstream	ActReg chr11 #2892	0	0	1
2893	11	32,913,792	32,914,353	561	1	10.833	6.333	3.444	21	10	6	1	1	1	QSER1	-720	upstream	ActReg chr11 #2893	1	0	0
2894	11	32,914,823	32,915,431	608	1	8.947	7.105	11.526	15	11	16	1	1	1	QSER1	335	in gene	ActReg chr11 #2894	0	0	1
2895	11	33,036,911	33,037,741	830	3	11.923	9.615	10.8	20	19	23	1	1	1	DEPDC7	-84	upstream	ActReg chr11 #2895	1	1	1
2896	11	33,060,605	33,061,768	1,163	2	12.297	13.324	6.784	19	28	13	1	1	2	DEPDC7, TCP11L1	23776, 223	downstream, in gene	ActReg chr11 #2896	1	1	0
2897	11	33,232,964	33,233,651	687	1	10.238	8.286	1.571	18	13	2	0	0	0				ActReg chr11 #2897	1	0	0
2898	11	33,278,816	33,280,282	1,466	1	9.63	11.109	7.778	15	17	13	1	1	1	HIPK3	581	in gene	ActReg chr11 #2898	0	1	0
2899	11	33,654,677	33,655,834	1,157	2	10.639	9.389	3.781	16	14	8	0	0	1	C11orf41	91,378	in gene	ActReg chr11 #2899	1	1	0
2900	11	33,691,751	33,693,031	1,280	2	9.275	8.475	2.419	16	13	5	0	0	1	C11orf41	128,514	in gene	ActReg chr11 #2900	1	1	0
2901	11	33,703,857	33,704,492	635	1	8.25	12.25	2.294	11	19	3	0	0	1	C11orf41	140,297	downstream	ActReg chr11 #2901	0	1	0
2902	11	33,742,895	33,744,536	1,641	2	8.039	10.726	3.638	14	17	6	0	0	1	CD59	14,310	in gene	ActReg chr11 #2902	1	1	0
2903	11	33,757,646	33,758,750	1,104	2	9.676	8.147	7.618	17	16	19	1	1	2	CD59, FBXO3	-173, 37873	upstream, downstream	ActReg chr11 #2903	1	0	1
2904	11	33,795,379	33,796,025	646	1	5.85	5.35	14.35	9	8	26	1	2	2	FBXO3, LOC100507109	369, -2032	in gene, upstream	ActReg chr11 #2904	0	0	1
2905	11	33,823,957	33,824,713	756	1	8.458	12.917	3.792	12	23	6	0	0	0				ActReg chr11 #2905	0	1	0
2906	11	33,933,955	33,934,847	892	2	12.111	15.889	2.739	27	29	5	0	0	0				ActReg chr11 #2906	1	1	0
2907	11	34,072,908	34,073,533	625	2	12.895	11.368	6.053	22	19	13	1	1	1	CAPRIN1	-10	upstream	ActReg chr11 #2907	1	1	0
2908	11	34,126,598	34,127,556	958	1	11.767	16.767	7.2	24	34	11	1	1	2	CAPRIN1, NAT10	53847, -34	downstream, upstream	ActReg chr11 #2908	0	1	0
2909	11	34,236,419	34,236,951	532	1	7.5	12	4.812	12	19	8	0	0	1	ABTB2	142,870	in gene	ActReg chr11 #2909	0	1	0
2910	11	34,272,635	34,273,166	531	1	9.294	11.294	4.375	13	15	8	0	0	1	ABTB2	106,655	in gene	ActReg chr11 #2910	0	1	0
2911	11	34,323,729	34,324,610	881	1	6.786	12.464	3.393	13	23	9	0	0	1	ABTB2	55,386	in gene	ActReg chr11 #2911	0	1	0
2912	11	34,352,605	34,353,487	882	1	15.536	7.857	2.75	29	15	5	0	0	1	ABTB2	26,509	in gene	ActReg chr11 #2912	1	0	0
2913	11	34,360,671	34,361,231	560	1	10.167	8.056	2	16	12	3	0	0	1	ABTB2	18,604	in gene	ActReg chr11 #2913	1	0	0
2914	11	34,380,291	34,380,918	627	1	11.947	12.053	4.789	17	19	8	1	1	1	ABTB2	-1,049	upstream	ActReg chr11 #2914	0	1	0
2915	11	34,417,529	34,418,252	723	2	12.087	12.348	2.286	18	23	4	0	0	0				ActReg chr11 #2915	1	1	0
2916	11	34,460,479	34,460,796	317	1	10	10.8	17.5	14	14	23	1	1	1	CAT	165	in gene	ActReg chr11 #2916	0	0	1
2917	11	34,675,372	34,676,873	1,501	3	10.362	12.106	2.8	18	24	5	0	0	1	EHF	33,534	in gene	ActReg chr11 #2917	1	1	0
2918	11	34,938,071	34,938,504	433	1	10.929	8.857	12.143	16	11	18	1	2	2	APIP, PDHX	-348, 610	upstream, in gene	ActReg chr11 #2918	0	0	1
2919	11	35,124,835	35,125,398	563	1	6.471	10.353	3.529	9	14	6	0	0	0				ActReg chr11 #2919	0	1	0
2920	11	35,160,112	35,161,534	1,422	2	9.159	11.341	9.818	15	25	23	1	2	2	LOC100507144, CD44	-1249, 406	upstream, in gene	ActReg chr11 #2920	0	1	1
2921	11	35,187,994	35,188,717	723	2	13.217	12.13	3.783	21	23	7	0	0	1	CD44	27,938	in gene	ActReg chr11 #2921	1	1	0
2922	11	35,453,335	35,453,656	321	1	3.2	3	11.5	5	6	15	0	0	1	PAMR1	93,681	in gene	ActReg chr11 #2922	0	0	1
2923	11	35,640,473	35,641,704	1,231	2	10.846	11.795	6.359	19	20	15	1	1	1	FJX1	1,353	in gene	ActReg chr11 #2923	1	1	0
2924	11	35,683,599	35,684,752	1,153	1	9.472	12.778	5.406	17	20	13	1	1	1	TRIM44	-178	upstream	ActReg chr11 #2924	0	1	0
2925	11	35,747,341	35,748,185	844	2	16.077	15.731	2.611	41	39	5	0	0	1	TRIM44	63,410	in gene	ActReg chr11 #2925	1	1	0
2926	11	36,013,029	36,013,597	568	1	8.765	10.235	1.824	13	18	4	0	0	1	LDLRAD3	47,701	in gene	ActReg chr11 #2926	0	1	0
2927	11	36,023,670	36,024,278	608	1	6.789	12.737	2.333	12	22	3	0	0	1	LDLRAD3	58,362	in gene	ActReg chr11 #2927	0	1	0
2928	11	36,170,919	36,171,798	879	2	13.593	14.482	4.259	32	24	9	0	0	1	LDLRAD3	205,746	in gene	ActReg chr11 #2928	1	1	0
2929	11	36,310,696	36,311,374	678	1	10.381	12.238	4.762	16	20	7	0	2	2	COMMD9, PRR5L	-36, -6690	upstream, upstream	ActReg chr11 #2929	0	1	0
2930	11	36,453,060	36,453,861	801	1	8.6	11.92	2.909	20	20	6	0	0	1	PRR5L	135,735	in gene	ActReg chr11 #2930	0	1	0
2931	11	36,531,001	36,532,299	1,298	3	23.146	30.366	8.625	63	93	22	1	1	1	TRAF6	172	in gene	ActReg chr11 #2931	1	1	1
2932	11	36,615,753	36,616,333	580	2	10.177	12.333	2.588	18	19	6	0	1	2	RAG2, C11orf74	3786, -50	in gene, upstream	ActReg chr11 #2932	1	1	0
2933	11	37,525,538	37,526,117	579	2	9.556	9.611	1.765	13	19	3	0	0	0				ActReg chr11 #2933	1	1	0
2934	11	37,810,043	37,810,479	436	1	8.214	9.857	2.083	10	18	3	0	0	0				ActReg chr11 #2934	0	1	0
2935	11	39,214,178	39,214,480	302	1	2.4	1	12.333	4	1	16	0	0	0				ActReg chr11 #2935	0	0	1
2936	11	39,307,135	39,307,464	329	1	2.364	2.6	8.636	3	5	12	0	0	0				ActReg chr11 #2936	0	0	1
2937	11	39,354,552	39,355,135	583	1	2.588	2.588	13.222	4	5	17	0	0	0				ActReg chr11 #2937	0	0	1
2938	11	40,409,845	40,410,435	590	1	5.316	9.211	1	9	17	1	0	0	0				ActReg chr11 #2938	0	1	0
2939	11	40,898,698	40,899,340	642	1	12.1	6.75	2.15	20	10	4	0	0	1	LOC100507187	582,749	in gene	ActReg chr11 #2939	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
2940	11	42,902,896	42,903,303	407	1	2.583	2.333	11.231	4	4	17	0	0	0				ActReg chr11 #2940	0	0	1
2941	11	43,333,087	43,334,069	982	3	33.419	40.484	6.276	103	128	14	1	1	1	APIS	73	in gene	ActReg chr11 #2941	1	1	1
2942	11	43,380,202	43,380,969	767	3	11.083	13.625	9.35	25	20	17	1	1	1	TTC17	150	in gene	ActReg chr11 #2942	1	1	1
2943	11	43,598,367	43,599,139	772	2	12.8	14.32	2.44	32	28	4	0	2	3	LOC100507261, LOC100131381, MIR129-2	7897, -1776, -4191	downstream, upstream, upstream	ActReg chr11 #2943	1	1	0
2944	11	43,638,821	43,639,516	695	1	8.143	12.619	2.25	13	19	5	0	0	0				ActReg chr11 #2944	0	1	0
2945	11	43,665,355	43,666,257	902	2	13.321	17.286	5.286	34	36	11	0	0	0				ActReg chr11 #2945	1	1	0
2946	11	43,890,302	43,891,055	753	2	12.542	10.917	1.857	21	16	5	0	0	1	LOC100507282	-9,616	upstream	ActReg chr11 #2946	1	1	0
2947	11	43,901,866	43,902,908	1,042	2	9.774	16.25	6.938	19	34	13	1	1	1	ALKBH3	30	in gene	ActReg chr11 #2947	1	1	0
2948	11	43,941,977	43,942,809	832	2	12.192	12.115	3.654	24	22	7	0	1	2	ALKBH3, LOC100507300	40036, 83	downstream, in gene	ActReg chr11 #2948	1	1	0
2949	11	44,087,364	44,088,331	967	2	13	12.633	9.9	26	19	18	1	1	2	ACCSL, ACCS	18316, 118	downstream, in gene	ActReg chr11 #2949	1	1	0
2950	11	44,116,855	44,117,686	831	1	11.962	8.423	4.56	21	17	12	1	1	1	EXT2	171	in gene	ActReg chr11 #2950	1	0	0
2951	11	44,505,423	44,505,937	514	1	3.125	3.875	11.875	5	8	22	0	0	0				ActReg chr11 #2951	0	0	1
2952	11	45,119,252	45,120,236	984	2	12.258	15.839	4.806	26	29	14	0	0	1	PRDM11	4,180	in gene	ActReg chr11 #2952	1	1	0
2953	11	45,202,460	45,202,934	474	1	6.267	7.667	13	10	12	18	1	0	1	PRDM11	87,133	in gene	ActReg chr11 #2953	0	0	1
2954	11	45,233,940	45,234,413	473	1	5.067	5.333	13.4	7	7	23	1	1	2	PRDM11, LOC100507338	118612, -456	in gene, upstream	ActReg chr11 #2954	0	0	1
2955	11	45,247,954	45,248,525	571	1	4.5	4.611	10.5	7	8	14	0	0	1	PRDM11	132,675	downstream	ActReg chr11 #2955	0	0	1
2956	11	45,280,933	45,281,723	790	1	14.875	6.708	2.348	23	13	4	0	0	1	SYT13	26,556	in gene	ActReg chr11 #2956	1	0	0
2957	11	45,565,199	45,566,062	863	2	14.852	15.741	2.667	35	35	5	0	0	0				ActReg chr11 #2957	1	1	0
2958	11	45,601,852	45,602,609	757	2	11.5	11.833	1.789	18	22	4	0	0	0				ActReg chr11 #2958	1	1	0
2959	11	45,825,546	45,827,583	2,037	4	12.889	9.889	8.556	39	22	18	1	1	1	SLC35C1	941	in gene	ActReg chr11 #2959	1	1	1
2960	11	45,868,561	45,869,497	936	2	6.148	12.276	10.552	10	24	15	1	1	1	CRY2	360	in gene	ActReg chr11 #2960	0	1	1
2961	11	45,894,315	45,894,964	649	1	12.4	12.6	3.1	20	20	7	0	0	1	CRY2	25,970	in gene	ActReg chr11 #2961	0	1	0
2962	11	45,906,501	45,907,143	642	1	8.05	11.95	4.105	13	19	7	1	1	2	CRY2, MAPK8IP1	38153, -380	downstream, upstream	ActReg chr11 #2962	0	1	0
2963	11	45,920,455	45,921,650	1,195	2	11.838	11.54	7.611	25	22	14	1	0	3	MAPK8IP1, C11orf94, PEX16	13850, 7781, 18622	in gene, downstream, downstream	ActReg chr11 #2963	1	1	0
2964	11	45,921,929	45,922,352	423	1	10.077	5.308	13.154	14	8	17	1	0	3	MAPK8IP1, C11orf94, PEX16	14938, 6693, 17534	in gene, downstream, downstream	ActReg chr11 #2964	0	0	1
2965	11	45,938,909	45,940,466	1,557	3	10.326	10.082	10.122	23	17	20	1	2	2	PEX16, GYLTL1B	-13, -3509	upstream, upstream	ActReg chr11 #2965	1	1	1
2966	11	46,164,522	46,165,036	514	1	2.875	4.429	10.938	4	7	17	1	0	0				ActReg chr11 #2966	0	0	1
2967	11	46,258,675	46,259,641	966	2	12	11.333	6.167	21	18	12	1	0	0				ActReg chr11 #2967	1	1	0
2968	11	46,260,480	46,261,011	531	1	9.353	9.941	13.177	14	15	19	1	0	0				ActReg chr11 #2968	0	0	1
2969	11	46,367,299	46,367,682	383	1	3.167	3.583	11.167	6	7	14	1	0	1	DGKZ	12,751	in gene	ActReg chr11 #2969	0	0	1
2970	11	46,384,143	46,385,670	1,527	2	10.188	11.333	6.104	24	18	11	0	0	1	DGKZ	30,167	in gene	ActReg chr11 #2970	1	1	0
2971	11	46,410,828	46,412,103	1,275	3	10.55	11.925	11.475	20	19	19	1	1	4	DGKZ, MDK, CHRM4, AMBRA1	-56726, 8847, -3358, 201449	downstream, downstream, upstream, downstream	ActReg chr11 #2971	1	1	1
2972	11	46,413,840	46,415,113	1,273	2	9.175	12.35	8.103	21	23	16	1	1	3	MDK, CHRM4, AMBRA1	11858, -6369, 198438	downstream, upstream, downstream	ActReg chr11 #2972	1	1	0
2973	11	46,521,083	46,521,396	313	1	2.889	4.125	11.2	4	6	14	0	0	1	AMBRA1	91,675	in gene	ActReg chr11 #2973	0	0	1
2974	11	46,564,309	46,564,708	399	1	3.364	1.833	10.154	5	6	14	0	0	1	AMBRA1	48,406	in gene	ActReg chr11 #2974	0	0	1
2975	11	46,614,990	46,616,141	1,151	2	15.028	18.611	3.071	38	49	6	1	1	2	AMBRA1, HARBI1	-2651, 23212	upstream, downstream	ActReg chr11 #2975	1	1	0
2976	11	46,638,417	46,639,659	1,242	3	9.769	10.256	6.179	19	19	17	1	2	2	HARBI1, KIAA0652	-261, 212	upstream, in gene	ActReg chr11 #2976	1	1	1
2977	11	46,717,891	46,718,276	385	1	1.222	4.25	10.083	2	6	17	0	1	2	ARHGAP1, ZNF408	4037, -4234	in gene, upstream	ActReg chr11 #2977	0	0	1
2978	11	46,721,886	46,722,734	848	3	10.259	13.963	9.615	14	23	17	1	2	2	ARHGAP1, ZNF408	-190, -7	upstream, upstream	ActReg chr11 #2978	1	1	1
2979	11	46,866,963	46,868,447	1,484	2	14.848	14.457	4.891	44	35	13	1	2	3	CKAP5, LOC100507401, LRP4	138, -252, 72468	in gene, upstream, downstream	ActReg chr11 #2979	1	1	0
2980	11	47,199,050	47,199,712	662	1	7.524	7.905	13	11	11	23	1	1	2	ARFGAP2, PACSIN3	-962, 8629	upstream, in gene	ActReg chr11 #2980	0	0	1
2981	11	47,207,017	47,207,615	598	1	10.278	12.722	6.833	14	18	11	1	1	2	ARFGAP2, PACSIN3	-8897, 694	upstream, in gene	ActReg chr11 #2981	0	1	0
2982	11	47,208,009	47,208,664	655	1	12.15	7.5	4.2	20	12	9	1	1	2	ARFGAP2, PACSIN3	-9917, -326	upstream, upstream	ActReg chr11 #2982	1	0	0
2983	11	47,270,114	47,270,889	775	1	10.542	13.375	7.667	16	23	14	1	2	3	DDB2, ACP2, NR1H3	34008, -44, 52	downstream, upstream, in gene	ActReg chr11 #2983	0	1	0
2984	11	47,290,503	47,291,177	674	1	7.571	11.238	5.143	12	15	10	1	1	2	NR1H3, MADD	20391, -87	downstream, upstream	ActReg chr11 #2984	0	1	0
2985	11	47,353,454	47,353,888	434	1	3.286	5.214	11.643	5	8	15	0	0	2	MADD, MYBPC3	62744, 20582	downstream, in gene	ActReg chr11 #2985	0	0	1
2986	11	47,380,279	47,380,691	412	1	3.538	4.231	13.385	5	6	18	0	1	2	MYBPC3, SPI1	-6232, 19642	upstream, in gene	ActReg chr11 #2986	0	0	1
2987	11	47,400,037	47,400,403	366	1	1.909	5.273	12.909	3	7	19	1	1	2	SPI1, LOC100507417	-93, 16971	upstream, downstream	ActReg chr11 #2987	0	0	1
2988	11	47,429,555	47,430,099	544	1	13.647	10.647	4.6	26	21	7	1	1	1	SLC39A13	-219	upstream	ActReg chr11 #2988	1	0	0
2989	11	47,447,539	47,448,574	1,035	1	9.438	10.781	5.781	16	16	14	1	1	2	SLC39A13, PSMC3	18010, -32	downstream, upstream	ActReg chr11 #2989	0	1	0
2990	11	47,485,952	47,486,475	523	1	7.647	13.294	2.214	9	23	3	0	0	1	CUGBP1	88,579	downstream	ActReg chr11 #2990	0	1	0
2991	11	47,573,936	47,575,154	1,218	2	10.237	13.158	6.556	21	23	15	1	1	1	CUGBP1	247	in gene	ActReg chr11 #2991	1	1	0
2992	11	47,586,532	47,586,951	419	1	9.846	6.077	11.923	13	8	14	1	1	2	PTPMT1, KBTBD4	-241, 13826	upstream, downstream	ActReg chr11 #2992	0	0	1
2993	11	47,600,101	47,600,974	873	3	13.444	13	12.518	27	23	21	1	3	4	PTPMT1, KBTBD4, NDUFS3, FAM180B	13555, 30, -25, -7693	downstream, in gene, upstream, upstream	ActReg chr11 #2993	1	1	1
2994	11	47,869,425	47,870,318	893	3	9.893	12.893	12.964	18	23	22	1	1	1	NUP160	186	in gene	ActReg chr11 #2994	1	1	1
2995	11	47,968,433	47,969,322	889	2	11.143	9.893	3.28	18	14	6	0	0	0				ActReg chr11 #2995	1	1	0
2996	11	47,970,970	47,971,324	354	1	2.909	2.727	11.636	4	4	16	0	0	0				ActReg chr11 #2996	0	0	1
2997	11	48,012,802	48,013,302	500	1	10.267	5.733	3.2	18	7	6	0	0	1	PTPRJ	10,942	in gene	ActReg chr11 #2997	1	0	0
2998	11	48,014,809	48,015,375	566	1	11.389	8.111	3.824	20	11	7	0	0	1	PTPRJ	12,982	in gene	ActReg chr11 #2998	1	0	0
2999	11	48,076,677	48,077,833	1,156	1	8.528	10.833	3.971	14	16	7	0	0	1	PTPRJ	75,145	in gene	ActReg chr11 #2999	0	1	0
3000	11	49,229,741	49,230,024	283	1	2.778	7.333	12.333	5	9	16	1	1	1	FOLH1	340	in gene	ActReg chr11 #3000	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3001	11	49,819,635	49,819,924	289	1	2.333	2.333	8.444	3	4	12	0	0	0				ActReg chr11 #3001	0	0	1
3002	11	50,227,006	50,227,406	400	1	2.077	4.462	9.615	5	7	17	1	0	0				ActReg chr11 #3002	0	0	1
3003	11	50,257,240	50,257,636	396	1	9.154	8.077	10.692	12	10	18	1	0	0				ActReg chr11 #3003	0	0	1
3004	11	55,640,074	55,641,127	1,053	2	9.903	10.848	5.727	14	20	13	1	0	1	SPRYD5	-10,173	upstream	ActReg chr11 #3004	1	1	0
3005	11	56,169,380	56,169,988	608	1	4.316	2.25	13.421	7	4	24	0	0	0				ActReg chr11 #3005	0	0	1
3006	11	56,700,224	56,700,837	613	1	5.6	11.4	1.412	9	21	2	0	0	0				ActReg chr11 #3006	0	1	0
3007	11	57,092,111	57,093,432	1,321	3	16.171	16.976	7.158	46	59	19	1	1	2	TNKS1BP1, SSRP1	-358, 10580	upstream, downstream	ActReg chr11 #3007	1	1	1
3008	11	57,102,739	57,103,599	860	1	11.185	9.556	3.889	22	15	7	1	2	2	SSRP1, P2RX3	182, -2780	in gene, upstream	ActReg chr11 #3008	1	0	0
3009	11	57,146,833	57,147,761	928	2	14.103	15.345	3.966	26	27	9	0	1	3	P2RX3, PRG3, PRG2	41348, 1326, 10833	downstream, in gene, downstream	ActReg chr11 #3009	1	1	0
3010	11	57,313,271	57,313,745	474	1	2.154	5.867	12.2	3	7	17	0	0	2	SMTNL1, UBE2L6	3394, 21945	in gene, downstream	ActReg chr11 #3010	0	0	1
3011	11	57,335,248	57,336,045	797	1	7.04	12.04	7.12	9	18	14	1	1	1	UBE2L6	-193	upstream	ActReg chr11 #3011	0	1	0
3012	11	57,336,777	57,337,330	553	1	10.882	6.529	5	16	10	7	0	1	1	UBE2L6	-1,600	upstream	ActReg chr11 #3012	1	0	0
3013	11	57,365,497	57,365,948	451	1	2.778	4	12	5	7	16	0	1	1	SERPING1	695	in gene	ActReg chr11 #3013	0	0	1
3014	11	57,414,270	57,415,009	739	1	3.375	8.25	12.542	7	12	20	1	1	3	LOC100507106, MIR130A, YPEL4	8789, 5968, 2778	in gene, downstream, in gene	ActReg chr11 #3014	0	0	1
3015	11	57,424,780	57,425,477	697	2	11.091	13.318	9.263	17	24	19	1	2	4	LOC100507106, YPEL4, CLP1, ZDHHC5	19278, -7711, -88, -10346	downstream, upstream, upstream, upstream	ActReg chr11 #3015	0	1	1
3016	11	57,508,474	57,509,206	732	2	14.087	15.174	9.652	22	30	16	1	1	3	TMX2, C11orf51, BTBD18	28798, 118, 10413	downstream, in gene, downstream	ActReg chr11 #3016	1	1	0
3017	11	57,652,516	57,653,492	976	2	15.4	19.7	3.143	36	49	5	0	0	0				ActReg chr11 #3017	1	1	0
3018	11	57,688,371	57,688,884	513	1	3.812	2.727	11.125	6	4	17	0	0	0				ActReg chr11 #3018	0	0	1
3019	11	58,345,705	58,346,500	795	1	12.68	11.2	5.88	22	16	13	1	3	3	LPXN, ZFP91-CNTF, ZFP91	-463, -485, -485	upstream, upstream, upstream	ActReg chr11 #3019	1	0	0
3020	11	58,409,240	58,409,786	546	2	13.118	9	3.812	25	15	8	0	0	0				ActReg chr11 #3020	1	1	0
3021	11	58,672,522	58,673,033	511	1	7.25	11	5.875	10	18	9	1	0	0				ActReg chr11 #3021	0	1	0
3022	11	58,830,374	58,830,855	481	1	2.867	3.067	14.133	4	4	20	1	1	2	LOC283194, LOC100506773	-4689, 64167	upstream, in gene	ActReg chr11 #3022	0	0	1
3023	11	58,909,867	58,910,603	736	1	8.043	13.565	7.304	11	27	12	1	1	1	FAM111A	-83	upstream	ActReg chr11 #3023	0	1	0
3024	11	59,317,677	59,318,759	1,082	3	10.529	10.235	15.412	18	14	27	0	0	0				ActReg chr11 #3024	1	1	1
3025	11	59,327,469	59,328,055	586	2	11.056	7	12.222	15	11	18	1	0	0				ActReg chr11 #3025	1	0	1
3026	11	59,382,958	59,383,821	863	1	10.741	11.963	3.037	19	18	7	2	2	2	OSBP, LOC100507411	228, -246	in gene, upstream	ActReg chr11 #3026	0	1	0
3027	11	59,521,895	59,523,461	1,566	2	11.122	12.755	6.652	22	18	15	1	1	1	STX3	146	in gene	ActReg chr11 #3027	1	1	0
3028	11	59,554,354	59,554,988	634	1	10.737	9	1.188	21	12	2	0	0	1	STX3	32,154	in gene	ActReg chr11 #3028	1	0	0
3029	11	59,577,846	59,578,536	690	1	10.046	10.727	10.909	16	19	19	1	1	2	STX3, MRPL16	55659, 154	downstream, in gene	ActReg chr11 #3029	0	1	0
3030	11	59,787,695	59,787,961	266	1	2.286	2.5	12.875	4	3	17	0	0	0				ActReg chr11 #3030	0	0	1
3031	11	60,282,509	60,283,143	634	1	11.45	9.85	7.947	21	12	12	1	1	2	MS4A12, MS4A13	22575, -60	downstream, upstream	ActReg chr11 #3031	1	0	0
3032	11	60,386,086	60,386,396	310	1	2.4	4.889	10.889	3	6	13	0	0	1	C11orf64	3,017	in gene	ActReg chr11 #3032	0	0	1
3033	11	60,534,845	60,535,435	590	1	4.368	5.947	10.737	6	9	15	1	0	1	MS4A15	10,800	in gene	ActReg chr11 #3033	0	0	1
3034	11	60,640,347	60,641,108	761	1	8.625	11.792	5.583	12	17	11	0	0	1	ZP1	5,712	in gene	ActReg chr11 #3034	0	1	0
3035	11	60,673,797	60,674,520	723	1	9	11.273	3.955	16	19	8	1	2	2	PRPF19, TMEM109	-97, -7213	upstream, upstream	ActReg chr11 #3035	0	1	0
3036	11	60,681,623	60,682,142	519	1	9.312	10.5	12.125	12	15	17	1	1	3	PRPF19, TMEM109, TMEM132A	-7821, 511, -10031	upstream, in gene, upstream	ActReg chr11 #3036	0	0	1
3037	11	60,691,382	60,692,129	747	1	10.125	14.958	7.375	24	28	14	1	1	2	TMEM109, TMEM132A	10384, -158	downstream, upstream	ActReg chr11 #3037	0	1	0
3038	11	60,699,223	60,699,710	487	1	2.6	5.533	11.6	4	8	18	0	0	3	TMEM109, TMEM132A, SLC15A3	18095, 7553, 19791	downstream, in gene, downstream	ActReg chr11 #3038	0	0	1
3039	11	60,928,570	60,929,542	972	2	12.355	7.613	1.571	21	18	4	1	1	1	VPS37C	-140	upstream	ActReg chr11 #3039	1	1	0
3040	11	61,100,189	61,101,128	939	2	12.9	14.367	9.167	33	22	15	1	2	2	DDB1, DAK	8, 4	in gene, in gene	ActReg chr11 #3040	1	1	0
3041	11	61,129,193	61,130,272	1,079	1	8.029	11.147	6.824	13	16	13	1	2	2	CYBASC3, TMEM138	23, 259	in gene, in gene	ActReg chr11 #3041	0	1	0
3042	11	61,159,700	61,160,402	702	1	13.364	11.909	6.682	24	18	11	1	1	2	TMEM216, CPSF7	219, 37413	in gene, downstream	ActReg chr11 #3042	1	0	0
3043	11	61,197,000	61,197,984	984	3	10.871	12.258	6.968	17	18	16	1	2	2	CPSF7, SDHAF2	-28, -105	upstream, upstream	ActReg chr11 #3043	1	1	1
3044	11	61,275,533	61,276,125	592	1	4.278	5.167	13.056	7	8	21	1	1	2	LRRC10B, SYT7	-443, 72469	upstream, downstream	ActReg chr11 #3044	0	0	1
3045	11	61,283,836	61,284,342	506	1	3.875	4.688	12.438	6	6	19	1	0	2	LRRC10B, SYT7	7817, 64209	downstream, in gene	ActReg chr11 #3045	0	0	1
3046	11	61,312,403	61,313,651	1,248	2	15.051	16.436	3.842	45	37	10	0	0	1	SYT7	35,271	in gene	ActReg chr11 #3046	1	1	0
3047	11	61,334,370	61,335,644	1,274	3	20.077	21.897	7.41	68	69	14	1	0	1	SYT7	13,291	in gene	ActReg chr11 #3047	1	1	1
3048	11	61,348,765	61,349,356	591	2	15.368	18.263	7.941	36	38	15	1	1	1	SYT7	-762	upstream	ActReg chr11 #3048	1	1	0
3049	11	61,355,235	61,355,779	544	1	4.235	2.765	12.118	8	5	18	1	1	1	SYT7	-7,209	upstream	ActReg chr11 #3049	0	0	1
3050	11	61,517,148	61,517,757	609	1	6.632	6.316	12.158	12	8	16	0	1	3	DAGLA, C11orf9, DKFZP434K028	69542, -2669, 7684	downstream, upstream, downstream	ActReg chr11 #3050	0	0	1
3051	11	61,536,742	61,537,256	514	1	3.812	1.867	14.875	6	3	22	0	1	2	C11orf9, LOC100507482	16878, 2599	in gene, downstream	ActReg chr11 #3051	0	0	1
3052	11	61,559,745	61,560,710	965	3	15.2	15.6	9.067	31	36	14	1	3	5	C11orf9, C11orf10, MIR611, FEN1, FADS1	40106, -142, -194, 77, 24302	downstream, upstream, upstream, in gene, downstream	ActReg chr11 #3052	1	1	1
3053	11	61,582,731	61,583,416	685	1	9.762	9.905	13.286	13	13	18	1	2	2	FADS1, MIR1908	1456, -361	in gene, upstream	ActReg chr11 #3053	0	0	1
3054	11	61,583,792	61,584,661	869	2	11.63	10.148	5.926	17	14	10	1	2	2	FADS1, MIR1908	303, -1514	in gene, upstream	ActReg chr11 #3054	1	1	0
3055	11	61,609,835	61,610,353	518	1	2.417	3.625	11.188	3	5	16	0	0	1	FADS2	14,381	in gene	ActReg chr11 #3055	0	0	1
3056	11	61,630,063	61,630,493	430	1	2.462	3.308	12.077	3	5	15	0	0	1	FADS2	34,565	in gene	ActReg chr11 #3056	0	0	1
3057	11	61,657,993	61,658,951	958	2	8.067	10.933	7.867	19	18	15	1	1	2	FADS3, RAB3IL1	534, 26525	in gene, downstream	ActReg chr11 #3057	1	1	0
3058	11	61,664,221	61,665,674	1,453	2	10.63	11.696	4.089	21	16	11	0	1	2	FADS3, RAB3IL1	-5941, 20050	upstream, in gene	ActReg chr11 #3058	1	1	0
3059	11	61,734,807	61,736,022	1,215	2	9.579	10.974	6.868	17	16	16	1	1	2	BEST1, FTH1	18058, -282	downstream, upstream	ActReg chr11 #3059	1	1	0
3060	11	61,780,169	61,780,895	726	1	10.5	14.364	3.455	15	22	6	0	0	0				ActReg chr11 #3060	0	1	0
3061	11	61,793,031	61,793,752	721	1	8.364	11.364	6.727	15	21	14	0	0	0				ActReg chr11 #3061	0	1	0
3062	11	61,890,996	61,891,921	925	1	11.345	8.207	7.483	15	14	17	1	1	1	INCENP	13	in gene	ActReg chr11 #3062	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3063	11	61,897,073	61,897,819	746	1	4.957	5.826	11.783	8	13	16	0	0	1	INCENP	6,001	in gene	ActReg chr11 #3063	0	0	1
3064	11	61,908,275	61,908,744	469	1	4.133	4.533	11.467	7	7	14	0	0	1	INCENP	17,064	in gene	ActReg chr11 #3064	0	0	1
3065	11	62,012,508	62,013,236	728	2	11.957	12.217	4.565	23	23	9	0	0	1	SCGB1D2	3,148	downstream	ActReg chr11 #3065	1	1	0
3066	11	62,104,468	62,105,333	865	1	5.259	11.704	6.926	11	23	14	1	1	1	ASRGL1	126	in gene	ActReg chr11 #3066	0	1	0
3067	11	62,230,584	62,231,193	609	1	5.368	9.474	3.846	9	15	6	0	0	1	AHNAK	83,444	in gene	ActReg chr11 #3067	0	1	0
3068	11	62,312,532	62,314,205	1,673	1	9.06	9.75	12.096	15	15	19	1	1	1	AHNAK	964	in gene	ActReg chr11 #3068	0	0	1
3069	11	62,314,721	62,315,225	504	1	6.267	7.333	11.933	10	12	21	1	1	1	AHNAK	-641	upstream	ActReg chr11 #3069	0	0	1
3070	11	62,320,441	62,321,890	1,449	1	11.196	10.065	6.174	17	15	14	0	1	2	AHNAK, EEF1G	-6833, 20295	upstream, downstream	ActReg chr11 #3070	1	0	0
3071	11	62,342,018	62,342,403	385	1	8.75	4.667	11.583	11	7	16	0	1	2	EEF1G, TUT1	-750, 16899	upstream, downstream	ActReg chr11 #3071	0	0	1
3072	11	62,358,598	62,359,772	1,174	2	20.861	17.778	7.083	60	35	12	1	1	3	TUT1, MTA2, EML3	-76, 10118, 21052	upstream, downstream, downstream	ActReg chr11 #3072	1	1	0
3073	11	62,368,791	62,369,784	993	1	8.806	11.226	8.065	13	18	15	1	1	3	TUT1, MTA2, EML3	-10178, 16, 10950	upstream, in gene, downstream	ActReg chr11 #3073	0	1	0
3074	11	62,389,140	62,390,004	864	1	8.519	12.407	5	12	19	12	1	1	4	EML3, ROM1, B3GAT3, GANAB	-9335, 9359, -124, 24532	upstream, downstream, upstream, downstream	ActReg chr11 #3074	0	1	0
3075	11	62,413,431	62,414,407	976	2	7.129	10.355	10.484	15	17	16	1	1	2	GANAB, INTS5	185, 6855	in gene, downstream	ActReg chr11 #3075	0	1	1
3076	11	62,432,011	62,434,114	2,103	4	9.864	10.954	13.758	16	19	32	1	3	5	C11orf48, METTL12, SNORA57, C11orf83, UBXN1	6179, 283, 168, -6064, 13465	in gene, in gene, downstream, upstream, downstream	ActReg chr11 #3076	1	1	1
3077	11	62,438,566	62,439,926	1,360	3	10.595	11.143	12.857	21	18	19	1	2	5	C11orf48, METTL12, SNORA57, C11orf83, UBXN1	-5, 6467, 6352, 120, 7281	upstream, downstream, downstream, in gene, downstream	ActReg chr11 #3077	1	1	1
3078	11	62,446,140	62,446,543	403	1	10.615	11.385	11.462	15	17	17	1	2	4	C11orf48, C11orf83, UBXN1, LRRN4CL	-7100, 7215, 186, 10859	upstream, downstream, in gene, downstream	ActReg chr11 #3078	0	0	1
3079	11	62,476,819	62,477,636	817	2	9.192	10	5.885	17	14	15	1	2	3	BSCL2, GNG3, HNRNPUL2	-181, 2113, 17594	upstream, downstream, downstream	ActReg chr11 #3079	1	1	0
3080	11	62,493,824	62,494,324	500	1	9.25	11.312	3.6	14	20	5	1	2	2	HNRNPUL2, TTC9C	747, -1878	in gene, upstream	ActReg chr11 #3080	0	1	0
3081	11	62,494,701	62,495,359	658	2	7.8	11.9	11.526	11	16	19	1	2	2	HNRNPUL2, TTC9C	-209, -922	upstream, upstream	ActReg chr11 #3081	0	1	1
3082	11	62,538,022	62,539,518	1,496	2	11.109	12.804	5.065	16	21	11	1	1	2	POLR2G, TAF6L	9759, -105	downstream, upstream	ActReg chr11 #3082	1	1	0
3083	11	62,554,375	62,555,487	1,112	2	12.471	12.765	9.29	21	21	17	1	1	4	TAF6L, TMEM179B, TMEM223, NXF1	16056, 57, 4555, 18033	downstream, in gene, downstream, downstream	ActReg chr11 #3083	1	1	0
3084	11	62,558,900	62,559,985	1,085	3	10.559	13.235	10.147	18	28	19	1	1	4	TAF6L, TMEM179B, TMEM223, NXF1	20567, 4568, 44, 13522	downstream, downstream, in gene, downstream	ActReg chr11 #3084	1	1	1
3085	11	62,572,473	62,573,286	813	3	13.346	12.154	9.885	28	21	22	1	1	2	NXF1, STX5	85, 26681	in gene, downstream	ActReg chr11 #3085	1	1	1
3086	11	62,598,632	62,600,157	1,525	3	12.553	11.575	6.63	23	24	14	1	1	3	STX5, WDR74, RNU2-2	166, 8234, 9839	in gene, downstream, downstream	ActReg chr11 #3086	1	1	0
3087	11	62,606,379	62,607,372	993	2	9.097	12.806	9.742	17	18	19	1	3	3	STX5, WDR74, RNU2-2	-7315, 753, 2358	upstream, in gene, downstream	ActReg chr11 #3087	0	1	1
3088	11	62,608,541	62,609,727	1,186	3	19.351	17.568	19.568	58	63	60	0	2	4	STX5, WDR74, RNU2-2, SNHG1	-9574, -1506, 99, 14226	upstream, upstream, in gene, downstream	ActReg chr11 #3088	1	1	1
3089	11	62,622,968	62,623,959	991	1	9.839	13.774	6.903	15	21	13	1	10	10	SNHG1, SNORD22, SNORD31, SNORD30, SNORD29, SNORD28, SNORD27, SNORD26, SNORD25, SLC3A2	-103, -2956, -2598, -2259, -2023, -1296, -908, -625, -360, -55	upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr11 #3089	0	1	0
3090	11	62,647,767	62,649,277	1,510	3	16.723	21.894	9.689	35	48	21	1	0	1	SLC3A2	25,004	in gene	ActReg chr11 #3090	1	1	1
3091	11	62,694,183	62,694,851	668	1	2.316	1.538	11.191	4	2	16	1	1	1	CHRM1	-5,505	upstream	ActReg chr11 #3091	0	0	1
3092	11	62,747,379	62,748,279	900	2	11.857	12.964	3.704	24	19	6	0	0	1	SLC22A6	4,640	in gene	ActReg chr11 #3092	1	1	0
3093	11	63,334,464	63,335,229	765	1	8.125	10.583	1.222	14	15	2	0	1	2	HRASLS2, PLA2G16	-3991, 47095	upstream, downstream	ActReg chr11 #3093	0	1	0
3094	11	63,438,682	63,439,532	850	2	12.889	11.148	6.769	27	18	11	1	1	2	ATL3, RTN3	-24, -9815	upstream, upstream	ActReg chr11 #3094	1	1	0
3095	11	63,449,200	63,450,132	932	1	6.517	10.103	6.077	10	19	12	1	1	1	RTN3	744	in gene	ActReg chr11 #3095	0	1	0
3096	11	63,581,083	63,581,445	362	1	7.833	9.167	11	12	12	16	1	1	1	C11orf84	341	in gene	ActReg chr11 #3096	0	0	1
3097	11	63,683,743	63,684,414	671	1	4.667	5.381	12.048	7	10	18	1	1	2	MARK2, RCOR2	77678, 238	downstream, in gene	ActReg chr11 #3097	0	0	1
3098	11	63,686,990	63,687,490	500	1	4.333	3.812	11.938	7	6	19	0	1	2	MARK2, RCOR2	80840, -2924	downstream, upstream	ActReg chr11 #3098	0	0	1
3099	11	63,687,705	63,688,371	666	1	3.381	4	12.143	5	9	15	0	1	2	MARK2, RCOR2	81638, -3722	downstream, upstream	ActReg chr11 #3099	0	0	1
3100	11	63,728,489	63,729,173	684	1	4.143	5.714	11.429	10	10	14	0	0	1	NAA40	22,389	downstream	ActReg chr11 #3100	0	0	1
3101	11	63,741,751	63,742,649	898	1	7.643	13.321	6.107	12	24	11	1	1	1	COX8A	121	in gene	ActReg chr11 #3101	0	1	0
3102	11	63,753,542	63,754,668	1,126	3	10.171	10.314	9.886	19	19	18	1	1	2	COX8A, OTUB1	12026, 780	downstream, in gene	ActReg chr11 #3102	1	1	1
3103	11	63,771,173	63,771,668	495	1	3.533	7.333	12.867	7	10	19	0	0	2	OTUB1, MACROD1	18095, 162165	downstream, in gene	ActReg chr11 #3103	0	0	1
3104	11	63,775,193	63,775,660	467	1	2.154	4.733	12.2	3	6	16	1	0	2	OTUB1, MACROD1	22101, 158159	downstream, in gene	ActReg chr11 #3104	0	0	1
3105	11	63,775,722	63,776,419	697	1	5.682	9.682	9.182	10	15	12	1	0	2	OTUB1, MACROD1	22745, 157515	downstream, in gene	ActReg chr11 #3105	0	1	0
3106	11	63,785,510	63,785,864	354	1	2.727	3	13.818	4	4	20	0	0	1	MACROD1	147,898	in gene	ActReg chr11 #3106	0	0	1
3107	11	63,789,609	63,789,958	349	1	2.455	5	11.273	3	8	17	0	0	1	MACROD1	143,802	in gene	ActReg chr11 #3107	0	0	1
3108	11	63,796,170	63,796,998	828	1	4.846	3.125	10.846	11	9	17	0	0	1	MACROD1	137,001	in gene	ActReg chr11 #3108	0	0	1
3109	11	63,801,939	63,802,473	534	1	2.562	6.059	13.412	5	9	21	0	0	1	MACROD1	131,379	in gene	ActReg chr11 #3109	0	0	1
3110	11	63,804,227	63,805,003	776	1	2.864	4.083	11.25	4	9	16	1	0	1	MACROD1	128,970	in gene	ActReg chr11 #3110	0	0	1
3111	11	63,849,917	63,850,430	513	1	2.933	3.75	11.188	7	8	16	0	0	1	MACROD1	83,412	in gene	ActReg chr11 #3111	0	0	1
3112	11	63,918,278	63,918,848	570	1	2.882	4.056	10.611	4	7	15	0	0	1	MACROD1	15,022	in gene	ActReg chr11 #3112	0	0	1
3113	11	63,920,498	63,920,927	429	1	4.769	6.692	10.923	8	10	14	0	0	1	MACROD1	12,873	in gene	ActReg chr11 #3113	0	0	1
3114	11	63,952,537	63,953,381	844	2	7.63	11.704	11.185	10	20	17	1	1	1	STIP1	-628	upstream	ActReg chr11 #3114	0	1	1
3115	11	63,974,504	63,975,050	546	1	5.529	5.941	11.294	9	8	15	1	1	2	STIP1, FERMT3	21190, 625	downstream, in gene	ActReg chr11 #3115	0	0	1
3116	11	63,987,781	63,988,634	853	1	6.077	5.538	16.346	13	9	25	0	1	4	FERMT3, TRPT1, NUDT22, DNAJC4	14055, 5519, -5531, -9546	in gene, downstream, upstream, upstream	ActReg chr11 #3116	0	0	1
3117	11	63,993,901	63,994,698	797	1	8.44	7.64	12.4	17	14	16	1	3	5	FERMT3, TRPT1, NUDT22, DNAJC4, VEGFB	20147, -573, 561, -3454, -7967	downstream, upstream, in gene, upstream, upstream	ActReg chr11 #3117	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3118	11	64,007,961	64,008,711	750	1	7.542	8.75	13.208	11	13	21	1	2	5	DNAJC4, VEGFB, FKBP2, PPP1R14B, LOC100507590	10583, 6070, -77, 6077, -6275	downstream, downstream, upstream, downstream, upstream	ActReg chr11 #3118	0	0	1
3119	11	64,008,925	64,009,475	550	1	7.056	7.389	14.222	12	10	27	1	2	6	DNAJC4, VEGFB, FKBP2, PPP1R14B, LOC100507590, PLCB3	11447, 6934, 787, 5213, -5411, -9795	downstream, downstream, in gene, downstream, upstream, upstream	ActReg chr11 #3119	0	0	1
3120	11	64,013,146	64,013,770	624	2	11.8	10.3	9.7	19	15	18	1	3	5	VEGFB, FKBP2, PPP1R14B, LOC100507590, PLCB3	11192, 5045, 955, -1153, -5537	downstream, downstream, in gene, upstream, upstream	ActReg chr11 #3120	1	0	1
3121	11	64,014,440	64,015,287	847	1	9.769	15.115	7.308	17	24	14	1	3	5	VEGFB, FKBP2, PPP1R14B, LOC100507590, PLCB3	12597, 6450, -450, 252, -4132	downstream, downstream, upstream, in gene, upstream	ActReg chr11 #3121	0	1	0
3122	11	64,022,028	64,022,513	485	1	4.6	4.667	13.467	8	7	18	0	0	3	PPP1R14B, LOC100507590, PLCB3	-7857, 7659, 3275	upstream, downstream, in gene	ActReg chr11 #3122	0	0	1
3123	11	64,023,451	64,023,879	428	1	3.714	2.857	11.143	8	4	17	0	0	3	PPP1R14B, LOC100507590, PLCB3	-9252, 9054, 4670	upstream, downstream, in gene	ActReg chr11 #3123	0	0	1
3124	11	64,030,753	64,031,291	538	1	7.125	6.062	12.75	13	8	20	0	0	2	PLCB3, BAD	12027, 21154	in gene, downstream	ActReg chr11 #3124	0	0	1
3125	11	64,031,329	64,032,055	726	1	4.727	4.227	14.909	7	7	27	0	0	2	PLCB3, BAD	12697, 20484	in gene, downstream	ActReg chr11 #3125	0	0	1
3126	11	64,036,778	64,037,853	1,075	1	9.879	12.333	7.182	15	20	17	1	0	2	PLCB3, BAD	18320, 14861	in gene, downstream	ActReg chr11 #3126	0	1	0
3127	11	64,055,523	64,056,042	519	1	2.125	4.625	13.562	3	7	17	1	2	3	BAD, GPR137, KCNK4	-3606, 3971, -3011	upstream, in gene, upstream	ActReg chr11 #3127	0	0	1
3128	11	64,067,923	64,068,870	947	2	7.2	10	8.3	10	17	15	1	2	3	KCNK4, C11orf20, ESRRA	9603, 533, -4648	downstream, in gene, upstream	ActReg chr11 #3128	0	1	1
3129	11	64,084,439	64,085,979	1,540	2	15.333	15.771	9.458	32	30	18	1	2	3	ESRRA, TRMT112, PRDX5	12165, -176, -360	downstream, upstream, upstream	ActReg chr11 #3129	1	1	0
3130	11	64,099,858	64,100,156	298	1	2.778	3.778	12	3	5	16	0	0	1	CCDC88B	-7,683	upstream	ActReg chr11 #3130	0	0	1
3131	11	64,109,433	64,109,886	453	1	2.357	4.5	12.714	5	7	18	1	1	1	CCDC88B	1,969	in gene	ActReg chr11 #3131	0	0	1
3132	11	64,118,582	64,119,151	569	1	2.176	4.056	11.444	4	7	14	0	1	2	CCDC88B, RPS6KA4	11176, -7759	in gene, upstream	ActReg chr11 #3132	0	0	1
3133	11	64,120,006	64,120,826	820	1	5.64	4.76	14.92	8	9	24	0	1	2	CCDC88B, RPS6KA4	12726, -6209	in gene, upstream	ActReg chr11 #3133	0	0	1
3134	11	64,120,925	64,121,813	888	1	5.143	6.964	13.321	9	13	18	0	1	2	CCDC88B, RPS6KA4	13679, -5256	in gene, upstream	ActReg chr11 #3134	0	0	1
3135	11	64,129,091	64,129,474	383	1	4.917	3.083	11.75	7	5	17	0	2	3	CCDC88B, RPS6KA4, MIR1237	21592, 2657, -6792	downstream, in gene, upstream	ActReg chr11 #3135	0	0	1
3136	11	64,137,305	64,137,982	677	1	3.762	5.857	11.191	6	8	16	1	1	2	RPS6KA4, MIR1237	11018, 1569	in gene, downstream	ActReg chr11 #3136	0	0	1
3137	11	64,328,175	64,328,790	615	1	2.824	3.474	12.684	5	7	16	0	0	1	SLC22A11	5,384	in gene	ActReg chr11 #3137	0	0	1
3138	11	64,360,784	64,361,259	475	1	4.867	3.2	11.867	7	7	18	0	0	1	SLC22A12	2,739	in gene	ActReg chr11 #3138	0	0	1
3139	11	64,479,647	64,480,104	457	1	2.8	3.933	12.067	4	6	16	2	0	1	NRXN2	10,785	in gene	ActReg chr11 #3139	0	0	1
3140	11	64,503,910	64,504,464	554	1	1.765	3.588	11	3	8	14	0	0	2	RASGRP2, PYGM	8741, 24000	in gene, downstream	ActReg chr11 #3140	0	0	1
3141	11	64,509,760	64,510,162	402	1	3.25	4.615	12.615	6	7	17	1	0	2	RASGRP2, PYGM	2967, 18226	in gene, downstream	ActReg chr11 #3141	0	0	1
3142	11	64,510,345	64,511,159	814	1	5	5.2	12.16	7	8	19	1	1	2	RASGRP2, PYGM	2176, 17435	in gene, downstream	ActReg chr11 #3142	0	0	1
3143	11	64,511,397	64,511,786	389	1	6.917	9.75	11.75	12	13	16	1	1	2	RASGRP2, PYGM	1337, 16596	in gene, downstream	ActReg chr11 #3143	0	0	1
3144	11	64,557,280	64,557,787	507	1	3.375	1.545	11.25	5	2	16	0	0	1	MAP4K2	13,180	in gene	ActReg chr11 #3144	0	0	1
3145	11	64,577,763	64,578,513	750	1	9.391	12.348	5.913	18	25	12	1	2	2	MAP4K2, MEN1	-7425, 628	upstream, in gene	ActReg chr11 #3145	0	1	0
3146	11	64,601,507	64,602,152	645	1	4.4	6.55	11	6	11	16	0	0	1	CDC42BPG	10,212	in gene	ActReg chr11 #3146	0	0	1
3147	11	64,623,423	64,624,499	1,076	2	9.912	11.059	9.529	16	17	14	0	0	1	EHD1	22,230	in gene	ActReg chr11 #3147	0	1	1
3148	11	64,631,429	64,632,254	825	1	4.48	4.565	11.92	8	6	17	0	0	1	EHD1	14,350	in gene	ActReg chr11 #3148	0	0	1
3149	11	64,645,349	64,646,739	1,390	3	9.721	12.512	12.395	15	22	20	1	1	1	EHD1	147	in gene	ActReg chr11 #3149	0	1	1
3150	11	64,656,069	64,656,894	825	1	4.762	6.28	12.68	8	12	23	0	2	4	EHD1, MIR192, MIR194-2, ATG2A	-10290, 2237, 2430, 28241	upstream, downstream, downstream, downstream, downstream	ActReg chr11 #3150	0	0	1
3151	11	64,660,946	64,661,946	1,000	1	5.935	6.645	13.129	11	17	19	0	2	3	MIR192, MIR194-2, ATG2A	-2728, -2535, 23276	upstream, upstream, downstream	ActReg chr11 #3151	0	0	1
3152	11	64,662,203	64,663,054	851	1	2.593	6.593	11.259	4	12	15	1	2	3	MIR192, MIR194-2, ATG2A	-3910, -3717, 22094	upstream, upstream, in gene	ActReg chr11 #3152	0	0	1
3153	11	64,668,203	64,668,620	417	1	3.077	4.615	12.769	5	8	20	0	0	3	MIR192, MIR194-2, ATG2A	-9693, -9500, 16311	upstream, upstream, in gene	ActReg chr11 #3153	0	0	1
3154	11	64,678,145	64,678,589	444	1	3.385	5.538	11.769	4	8	19	0	0	1	ATG2A	6,355	in gene	ActReg chr11 #3154	0	0	1
3155	11	64,683,633	64,685,385	1,752	2	9.164	10.782	5.038	18	20	11	1	2	2	ATG2A, PPP2R5B	213, -7634	in gene, upstream	ActReg chr11 #3155	1	1	0
3156	11	64,691,113	64,692,536	1,423	2	21.023	27.546	4.791	49	66	10	1	2	3	ATG2A, PPP2R5B, GPHA2	-7102, -319, 11536	upstream, upstream, downstream	ActReg chr11 #3156	1	1	0
3157	11	64,745,029	64,745,610	581	2	9	10.833	2.929	18	17	7	0	1	2	C11orf85, BATF2	-5961, 19198	upstream, downstream	ActReg chr11 #3157	1	1	0
3158	11	64,780,997	64,782,417	1,420	2	11.909	12.068	8.268	17	21	16	1	1	1	ARL2	121	in gene	ActReg chr11 #3158	1	1	0
3159	11	64,794,488	64,795,622	1,134	2	37.111	46.444	3.556	92	120	8	1	1	2	ARL2, SNX15	13469, 145	downstream, in gene	ActReg chr11 #3159	1	1	0
3160	11	64,803,032	64,803,581	549	1	2.882	5.471	11.529	5	9	15	0	1	3	SNX15, SAC3D1, NAALADL1	8396, -5070, 22703	in gene, upstream, downstream	ActReg chr11 #3160	0	0	1
3161	11	64,851,063	64,851,875	812	2	9.885	11.039	10.923	16	22	17	1	2	3	CDCA5, ZFPL1, LOC100130348	146, -225, 5034	in gene, upstream, downstream	ActReg chr11 #3161	0	1	1
3162	11	64,855,371	64,855,872	501	1	4.438	4	10.188	6	6	17	0	2	4	CDCA5, ZFPL1, LOC100130348, C11orf2	-4006, 3927, 882, -8062	upstream, in gene, downstream, upstream	ActReg chr11 #3162	0	0	1
3163	11	64,863,338	64,863,964	626	2	10.947	9.895	9.895	17	16	17	1	2	3	ZFPL1, LOC100130348, C11orf2	11957, -7148, -32	downstream, upstream, upstream	ActReg chr11 #3163	1	0	1
3164	11	64,883,964	64,885,752	1,788	3	8.732	11.643	11.482	16	18	25	1	2	6	C11orf2, TM7SF2, ZNHIT2, FAU, MRPL49, SYVN1	21175, 5517, 312, 4814, -4870, 17145	downstream, downstream, in gene, downstream, upstream, downstream	ActReg chr11 #3164	0	1	1
3165	11	64,889,207	64,890,196	989	1	10.258	13.323	8.387	14	25	15	1	3	5	TM7SF2, ZNHIT2, FAU, MRPL49, SYVN1	10360, -4531, -29, -27, 12302	downstream, upstream, upstream, upstream, downstream	ActReg chr11 #3165	0	1	0
3166	11	64,901,643	64,902,832	1,189	2	11.622	12.811	8.135	17	24	18	1	1	2	MRPL49, SYVN1	12509, -234	downstream, upstream	ActReg chr11 #3166	1	1	0
3167	11	65,028,822	65,029,584	762	1	7	11.708	8.333	10	19	15	1	1	1	POLA2	-229	upstream	ActReg chr11 #3167	0	1	0
3168	11	65,082,198	65,082,780	582	1	6	10.889	4.706	10	21	7	1	1	1	CDC42EP2	158	in gene	ActReg chr11 #3168	0	1	0
3169	11	65,084,331	65,084,811	480	1	4.933	5.933	13.133	6	10	19	0	1	1	CDC42EP2	2,240	in gene	ActReg chr11 #3169	0	0	1
3170	11	65,121,402	65,122,087	685	1	7.909	11.454	5.045	13	16	9	1	1	2	DPF2, TIGD3	20398, -538	downstream, upstream	ActReg chr11 #3170	0	1	0
3171	11	65,124,034	65,124,496	462	1	2.714	4.214	12.143	4	7	17	0	1	2	DPF2, TIGD3	22919, 1983	downstream, in gene	ActReg chr11 #3171	0	0	1
3172	11	65,149,053	65,150,779	1,726	1	9.63	12.574	5.407	16	20	17	0	2	2	SLC25A45, FRMD8	226, -4125	in gene, upstream	ActReg chr11 #3172	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3173	11	65,153,578	65,154,730	1,152	3	10.694	14.25	7.583	25	30	13	1	2	2	SLC25A45, FRMD8	-4012, 113	upstream, in gene	ActReg chr11 #3173	1	1	1
3174	11	65,157,678	65,158,594	916	2	10.897	10	5.828	22	15	10	0	0	2	SLC25A45, FRMD8	-7994, 4095	upstream, in gene	ActReg chr11 #3174	1	1	0
3175	11	65,161,374	65,161,882	508	1	7.125	6.375	13.812	11	10	21	0	0	1	FRMD8	7,587	in gene	ActReg chr11 #3175	0	0	1
3176	11	65,188,726	65,189,134	408	1	4.308	11.154	3.833	6	19	6	0	1	2	FRMD8, NEAT1	34889, -1339	downstream, upstream	ActReg chr11 #3176	0	1	0
3177	11	65,189,397	65,191,569	2,172	3	9.588	10.5	10.485	20	21	19	2	1	2	FRMD8, NEAT1	36442, 214	downstream, in gene	ActReg chr11 #3177	1	1	1
3178	11	65,194,157	65,194,967	810	1	10.92	4.28	4.636	15	6	9	0	0	1	NEAT1	4,293	downstream	ActReg chr11 #3178	1	0	0
3179	11	65,213,021	65,213,862	841	1	7.889	7.963	13.333	12	15	20	0	1	1	MIR612	1,512	downstream	ActReg chr11 #3179	0	0	1
3180	11	65,215,939	65,216,459	520	1	4.062	6.938	10.875	6	10	14	0	0	1	MIR612	4,270	downstream	ActReg chr11 #3180	0	0	1
3181	11	65,239,312	65,240,025	713	2	9.955	10.409	4.524	20	20	12	0	0	1	LOC100507645	27,583	in gene	ActReg chr11 #3181	1	1	0
3182	11	65,243,991	65,245,398	1,407	2	9.364	9.841	8	15	16	18	1	0	1	LOC100507645	22,557	in gene	ActReg chr11 #3182	0	1	1
3183	11	65,255,160	65,256,123	963	2	9.6	8.367	7.067	14	19	12	0	0	2	LOC100507645, MALAT1	11610, -9592	in gene, upstream	ActReg chr11 #3183	1	1	0
3184	11	65,258,884	65,259,675	791	1	12.667	10.667	5	20	16	8	0	1	2	LOC100507645, MALAT1	7972, -5954	in gene, upstream	ActReg chr11 #3184	1	0	0
3185	11	65,264,661	65,265,409	748	2	11.833	14.625	8.958	20	25	12	1	2	2	LOC100507645, MALAT1	2216, -198	in gene, upstream	ActReg chr11 #3185	1	1	0
3186	11	65,321,514	65,321,994	480	1	5.667	3.533	12.667	10	5	22	1	0	1	LTBP3	3,945	in gene	ActReg chr11 #3186	0	0	1
3187	11	65,337,178	65,338,330	1,152	2	12	16.778	8.028	21	33	12	1	3	3	SSSCA1, FAM89B, EHBP1L1	-189, -2066, -5755	upstream, upstream, upstream	ActReg chr11 #3187	1	1	0
3188	11	65,348,957	65,349,796	839	1	3.308	3.074	11.926	7	5	15	0	0	3	SSSCA1, FAM89B, EHBP1L1	11433, 9556, 5867	downstream, downstream, in gene	ActReg chr11 #3188	0	0	1
3189	11	65,360,857	65,361,569	712	1	5.783	4.783	11.609	9	8	21	0	1	3	EHBP1L1, KCNK7, MAP3K11	17704, 2254, 20507	downstream, in gene, downstream	ActReg chr11 #3189	0	0	1
3190	11	65,380,978	65,381,878	900	1	7.321	7.286	11.5	10	16	19	1	2	2	MAP3K11, PCNXL3	292, -2355	in gene, upstream	ActReg chr11 #3190	0	0	1
3191	11	65,382,301	65,383,257	956	2	20.967	21	2.074	60	56	6	1	2	2	MAP3K11, PCNXL3	-1059, -1004	upstream, upstream	ActReg chr11 #3191	1	1	0
3192	11	65,386,934	65,387,502	568	1	3.389	4.444	15.333	7	7	23	0	1	2	MAP3K11, PCNXL3	-5498, 3435	upstream, in gene	ActReg chr11 #3192	0	0	1
3193	11	65,393,175	65,393,584	409	1	3.923	5.308	12.538	6	8	18	0	0	1	PCNXL3	9,596	in gene	ActReg chr11 #3193	0	0	1
3194	11	65,397,113	65,397,608	495	1	5.438	3.938	12.062	10	8	14	0	0	2	PCNXL3, SIPA1	13577, -8218	in gene, upstream	ActReg chr11 #3194	0	0	1
3195	11	65,402,634	65,403,101	467	1	5.214	3.714	11.643	8	7	18	1	1	2	PCNXL3, SIPA1	19084, -2711	in gene, upstream	ActReg chr11 #3195	0	0	1
3196	11	65,405,812	65,406,312	500	1	7	6.688	12	11	8	20	0	1	2	PCNXL3, SIPA1	22279, 484	downstream, in gene	ActReg chr11 #3196	0	0	1
3197	11	65,409,659	65,410,215	556	1	2.944	6.389	12.5	5	9	16	1	0	2	PCNXL3, SIPA1	26154, 4359	downstream, in gene	ActReg chr11 #3197	0	0	1
3198	11	65,430,201	65,431,217	1,016	2	10.375	8	7.92	17	14	16	1	1	1	RELA	-266	upstream	ActReg chr11 #3198	1	0	1
3199	11	65,479,149	65,480,033	884	1	9.786	14.107	7.071	18	25	11	1	1	2	KAT5, RNASEH2C	102, 8818	in gene, downstream	ActReg chr11 #3199	0	1	0
3200	11	65,487,301	65,488,454	1,153	2	13.029	13.444	8.353	24	25	12	1	1	2	KAT5, RNASEH2C	8388, 532	downstream, in gene	ActReg chr11 #3200	1	1	0
3201	11	65,511,348	65,511,837	489	1	5.667	11	13	9	13	18	0	0	0				ActReg chr11 #3201	0	0	1
3202	11	65,545,071	65,548,168	3,097	3	8.464	10.598	12.814	20	26	21	1	2	3	DKFZp761E198, OVOL1, LOC100507675	1203, -7910, 11720	in gene, upstream, downstream	ActReg chr11 #3202	1	1	1
3203	11	65,549,025	65,549,669	644	1	6.3	4.9	12.25	9	8	21	1	2	3	DKFZp761E198, OVOL1, LOC100507675	-1525, -5182, 8992	upstream, upstream, downstream	ActReg chr11 #3203	0	0	1
3204	11	65,549,681	65,550,106	425	1	5.692	4.692	14.308	8	8	19	0	2	3	DKFZp761E198, OVOL1, LOC100507675	-2071, -4636, 8446	upstream, upstream, downstream	ActReg chr11 #3204	0	0	1
3205	11	65,576,908	65,577,454	546	1	3.176	3.941	11.647	5	5	15	0	0	0				ActReg chr11 #3205	0	0	1
3206	11	65,600,532	65,602,220	1,688	2	8.868	11.793	9.528	27	28	15	1	1	1	SNX32	-34	upstream	ActReg chr11 #3206	0	1	1
3207	11	65,624,239	65,626,135	1,896	2	11.881	14.237	9.393	27	29	19	1	2	4	SNX32, CFL1, MUS81, EFEMP2	23777, 617, -2685, 15153	downstream, in gene, upstream, downstream	ActReg chr11 #3207	1	1	0
3208	11	65,626,487	65,628,861	2,374	2	29.162	32.959	9.781	129	133	18	1	2	4	SNX32, CFL1, MUS81, EFEMP2	26264, -1870, -198, 12666	downstream, upstream, upstream, upstream, downstream	ActReg chr11 #3208	1	1	0
3209	11	65,634,203	65,634,980	777	1	4.64	5	13.24	8	8	19	0	0	3	CFL1, MUS81, EFEMP2	-8787, 6719, 5749	upstream, downstream, in gene	ActReg chr11 #3209	0	0	1
3210	11	65,640,812	65,641,535	723	1	11.546	12.818	14.682	18	17	25	1	2	4	MUS81, EFEMP2, CTSW, FIBP	13301, -833, -6111, 14837	downstream, upstream, upstream, downstream	ActReg chr11 #3210	0	0	1
3211	11	65,649,858	65,650,921	1,063	1	7.03	6.2	12.636	12	12	20	0	1	5	EFEMP2, CTSW, FIBP, CCDC85B, FOSL1	-10049, 3105, 5621, -7486, 17608	upstream, in gene, downstream, upstream, downstream	ActReg chr11 #3211	0	0	1
3212	11	65,655,240	65,657,108	1,868	3	11.483	12.966	10.672	22	27	21	1	2	4	CTSW, FIBP, CCDC85B, FOSL1	8890, -164, -1701, 11823	downstream, upstream, upstream, downstream	ActReg chr11 #3212	1	1	1
3213	11	65,657,943	65,659,703	1,760	3	11.055	12	13.291	21	23	22	1	2	4	CTSW, FIBP, CCDC85B, FOSL1	11539, -2813, 948, 9174	downstream, upstream, in gene, downstream	ActReg chr11 #3213	1	1	1
3214	11	65,661,504	65,662,031	527	1	8.353	9.941	11.765	11	16	20	0	1	3	FIBP, CCDC85B, FOSL1	-5757, 3892, 6230	upstream, downstream, in gene	ActReg chr11 #3214	0	0	1
3215	11	65,664,095	65,664,620	525	1	7.706	3.5	11.765	12	5	17	0	0	3	FIBP, CCDC85B, FOSL1	-8347, 6482, 3640	upstream, downstream, in gene	ActReg chr11 #3215	0	0	1
3216	11	65,666,913	65,668,226	1,313	2	8.244	13.878	11.439	14	25	19	1	1	2	CCDC85B, FOSL1	9694, 428	downstream, in gene	ActReg chr11 #3216	0	1	1
3217	11	65,670,479	65,671,294	815	1	11.52	10.16	5.16	18	14	9	0	1	1	FOSL1	-2,889	upstream	ActReg chr11 #3217	1	0	0
3218	11	65,678,010	65,678,410	400	1	2.083	4	10.308	3	6	16	0	0	2	C11orf68, DRAP1	8321, -8518	downstream, upstream	ActReg chr11 #3218	0	0	1
3219	11	65,678,756	65,679,411	655	1	8.65	6.6	11	13	10	16	0	1	2	C11orf68, DRAP1	7448, -7645	downstream, upstream	ActReg chr11 #3219	0	0	1
3220	11	65,682,289	65,683,780	1,491	2	12.489	11.745	7.596	29	21	13	0	1	2	C11orf68, DRAP1	3497, -3694	downstream, upstream	ActReg chr11 #3220	1	1	0
3221	11	65,684,929	65,685,526	597	1	12.056	9.611	15.056	18	13	24	1	2	2	C11orf68, DRAP1	1304, -1501	in gene, upstream	ActReg chr11 #3221	0	0	1
3222	11	65,686,409	65,687,412	1,003	2	32.871	35.194	4.2	106	113	7	1	2	2	C11orf68, DRAP1	-379, 182	upstream, in gene	ActReg chr11 #3222	1	1	0
3223	11	65,687,451	65,688,150	699	1	6.909	9.364	12	12	16	16	1	2	2	C11orf68, DRAP1	-1269, 1072	upstream, in gene	ActReg chr11 #3223	0	0	1
3224	11	65,695,979	65,696,344	365	1	4	3	10.546	5	6	14	0	0	2	C11orf68, DRAP1	-9630, 9433	upstream, downstream	ActReg chr11 #3224	0	0	1
3225	11	65,714,620	65,715,069	449	1	5.929	2.643	11.143	10	4	16	0	1	1	TSGA10IP	1,729	in gene	ActReg chr11 #3225	0	0	1
3226	11	65,728,576	65,729,737	1,161	2	28.946	30.054	6.138	103	96	11	0	1	2	TSGA10IP, SART1	16041, -4	downstream, upstream	ActReg chr11 #3226	1	1	0
3227	11	65,769,219	65,770,224	1,005	2	14.323	16.516	7.517	30	27	14	1	2	3	EIF1AD, BANF1, CST6	-143, 171, -9741	upstream, in gene, upstream	ActReg chr11 #3227	1	1	0
3228	11	65,792,396	65,792,854	458	1	1.909	4.143	11.786	3	6	16	0	1	1	CATSPER1	1,363	in gene	ActReg chr11 #3228	0	0	1
3229	11	65,819,351	65,820,381	1,030	2	12.094	11.906	8.062	25	20	14	1	2	2	GAL3ST3, SF3B2	-3215, 50	upstream, in gene	ActReg chr11 #3229	1	1	0
3230	11	66,024,617	66,026,468	1,851	2	9.069	11.241	8.431	17	19	16	1	1	2	KLC2, RAB1B	777, -10514	in gene, upstream	ActReg chr11 #3230	0	1	1
3231	11	66,034,343	66,036,141	1,798	1	7.232	10.893	7.589	14	15	15	3	1	3	KLC2, RAB1B, CNIH2	10477, -814, -10454	in gene, upstream, upstream	ActReg chr11 #3231	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3232	11	66,049,880	66,050,341	461	1	7	9.067	12.8	10	15	21	1	0	4	RAB1B, CNIH2, YIF1A, TMEM151A	14054, 4414, 6528, -9263	downstream, in gene, downstream, upstream	ActReg chr11 #3232	0	0	1
3233	11	66,056,000	66,058,043	2,043	2	10.238	13.234	6.25	26	24	12	1	2	3	CNIH2, YIF1A, TMEM151A	11325, -383, -2352	downstream, upstream, upstream	ActReg chr11 #3233	1	1	0
3234	11	66,102,761	66,103,307	546	1	10.706	10.412	12.059	13	13	18	0	1	3	RIN1, BRMS1, B3GNT1	966, 9548, 12127	in gene, downstream, downstream	ActReg chr11 #3234	0	0	1
3235	11	66,103,615	66,105,022	1,407	3	11.568	15.159	10.204	33	44	15	0	1	3	RIN1, BRMS1, B3GNT1	-318, 8264, 10843	upstream, downstream, downstream	ActReg chr11 #3235	1	1	1
3236	11	66,112,105	66,112,800	695	2	12.546	8.5	10.046	20	16	16	1	2	3	RIN1, BRMS1, B3GNT1	-8452, 130, 2709	upstream, in gene, downstream	ActReg chr11 #3236	1	0	1
3237	11	66,113,956	66,115,035	1,079	1	8.758	6.03	12.121	16	12	18	2	2	3	RIN1, BRMS1, B3GNT1	-10495, -1913, 666	upstream, upstream, in gene	ActReg chr11 #3237	0	0	1
3238	11	66,115,312	66,115,960	648	2	11.8	9.65	12.05	21	14	21	1	2	2	BRMS1, B3GNT1	-3054, -475	upstream, upstream	ActReg chr11 #3238	1	0	1
3239	11	66,138,420	66,139,368	948	1	8.667	12.1	10.7	14	17	18	1	1	1	SLC29A2	397	in gene	ActReg chr11 #3239	0	1	0
3240	11	66,176,031	66,176,655	624	1	10.4	7.85	5.9	16	18	12	1	1	1	LOC100505504	-322	upstream	ActReg chr11 #3240	1	0	0
3241	11	66,185,150	66,190,672	5,522	4	32.272	40.11	5.598	235	262	16	1	1	2	LOC100505504, NPAS4	11246, -564	downstream, upstream	ActReg chr11 #3241	1	1	1
3242	11	66,205,843	66,206,860	1,017	2	15.625	13.344	8.062	34	28	15	0	1	1	MRPL11	-41	upstream	ActReg chr11 #3242	1	1	0
3243	11	66,210,897	66,211,483	586	1	9.278	10.611	3.056	13	15	7	0	1	1	MRPL11	-4,880	upstream	ActReg chr11 #3243	0	1	0
3244	11	66,243,189	66,243,887	698	1	4.818	8.227	13.682	11	17	21	1	1	3	PELI3, LOC100505554, DPP3	9202, 4168, -4342	in gene, downstream, upstream	ActReg chr11 #3244	0	0	1
3245	11	66,247,270	66,248,433	1,163	2	12.778	13.5	6.306	28	20	12	1	2	3	PELI3, LOC100505554, DPP3	13515, -145, -29	downstream, upstream, upstream	ActReg chr11 #3245	1	1	0
3246	11	66,314,350	66,314,799	449	1	2.462	6.071	10.214	4	8	19	1	2	2	ZDHHC24, ACTN3	-903, 183	upstream, in gene	ActReg chr11 #3246	0	0	1
3247	11	66,383,829	66,384,364	535	1	8.294	10.235	13.471	12	16	19	1	1	1	RBM14	43	in gene	ActReg chr11 #3247	0	0	1
3248	11	66,445,181	66,445,791	610	1	10.684	10.474	14.316	14	14	23	1	1	2	RBM4B, SPTBN2	-211, 43384	upstream, downstream	ActReg chr11 #3248	0	0	1
3249	11	66,529,460	66,530,312	852	1	7.63	12	2.667	11	18	5	1	0	1	C11orf80	17,679	in gene	ActReg chr11 #3249	0	1	0
3250	11	66,623,091	66,624,318	1,227	2	9.237	10.395	5.237	19	16	12	1	1	3	RCE1, PC, LRFN4	12821, 102143, -1172	downstream, in gene, upstream	ActReg chr11 #3250	1	1	0
3251	11	66,625,036	66,625,971	935	1	4.893	7.517	12.724	12	13	17	1	1	2	PC, LRFN4	100344, 627	in gene, in gene	ActReg chr11 #3251	0	0	1
3252	11	66,626,862	66,627,365	503	1	3.5	2.688	12.75	6	5	19	1	1	2	PC, LRFN4	98734, 2237	in gene, in gene	ActReg chr11 #3252	0	0	1
3253	11	66,628,009	66,629,112	1,103	1	6.206	5.031	13	14	10	19	0	0	2	PC, LRFN4	97287, 3684	in gene, downstream	ActReg chr11 #3253	0	0	1
3254	11	66,659,388	66,660,212	824	2	21.769	22.846	3.545	45	57	7	0	0	1	PC	66,047	in gene	ActReg chr11 #3254	1	1	0
3255	11	66,725,553	66,726,106	553	1	7.706	13.118	7.529	12	22	11	1	1	1	PC	18	in gene	ActReg chr11 #3255	0	1	0
3256	11	66,738,203	66,738,793	590	1	12.526	14.158	2.579	22	25	4	0	1	1	C11orf86	-4,256	upstream	ActReg chr11 #3256	0	1	0
3257	11	67,048,667	67,049,694	1,027	1	2.969	4.844	12.25	6	6	16	0	1	2	ADRBK1, ANKRD13D	15275, -7582	in gene, upstream	ActReg chr11 #3257	0	0	1
3258	11	67,050,042	67,050,529	487	1	4.375	4.562	11.5	6	6	16	0	1	2	ADRBK1, ANKRD13D	16380, -6477	in gene, upstream	ActReg chr11 #3258	0	0	1
3259	11	67,055,860	67,056,585	725	1	8.087	11.652	7.87	11	18	13	1	1	2	ADRBK1, ANKRD13D	22317, -540	downstream, upstream	ActReg chr11 #3259	0	1	0
3260	11	67,070,670	67,071,516	846	2	13.154	15.115	3.591	27	32	10	1	1	2	ANKRD13D, SSH3	14331, 174	downstream, in gene	ActReg chr11 #3260	1	1	0
3261	11	67,084,656	67,085,247	591	1	9.167	11.611	12.556	16	14	17	1	1	2	SSH3, LOC100130987	14032, -359	downstream, downstream	ActReg chr11 #3261	0	0	1
3262	11	67,132,355	67,133,112	757	1	4.391	4.609	10.826	7	8	18	0	0	2	LOC100130987, CLCF1	47423, 8915	in gene, in gene	ActReg chr11 #3262	0	0	1
3263	11	67,141,332	67,142,190	858	2	11.778	12.482	6	16	21	11	1	1	2	LOC100130987, CLCF1	56451, -113	in gene, upstream	ActReg chr11 #3263	1	1	0
3264	11	67,159,014	67,159,657	643	1	8.35	13.4	9.25	15	21	15	1	1	3	LOC100130987, RAD9A, PPP1CA	74025, -88, 10041	downstream, upstream, downstream	ActReg chr11 #3264	0	1	0
3265	11	67,185,884	67,186,756	872	1	3.571	4.5	12.393	6	6	18	0	0	3	TBC1D10C, ATPGD1, RPS6KB2	14908, 3171, -9615	downstream, in gene, upstream	ActReg chr11 #3265	0	0	1
3266	11	67,195,379	67,196,370	991	1	9.29	13.548	8	13	29	14	1	1	4	ATPGD1, RPS6KB2, PTPRCAP, CORO1B	12725, -61, 9279, 15389	downstream, upstream, downstream, downstream	ActReg chr11 #3266	0	1	0
3267	11	67,236,487	67,237,235	748	2	13.217	14	9.13	25	29	16	1	1	2	CASP4, TMEM134	14043, -130	downstream, upstream	ActReg chr11 #3267	1	1	0
3268	11	67,250,233	67,250,979	746	1	8.25	10.5	5.042	20	15	11	1	1	2	AIP, PITPNM1	101, 22237	in gene, downstream	ActReg chr11 #3268	0	1	0
3269	11	67,275,039	67,276,419	1,380	2	10.114	10.864	8.159	21	16	13	1	2	3	PITPNM1, CDK2AP2, CABP2	-2896, 373, 15170	upstream, in gene, downstream	ActReg chr11 #3269	1	1	0
3270	11	67,283,957	67,284,582	625	1	4.75	4.05	11.55	7	6	15	0	0	2	CDK2AP2, CABP2	-8167, 6630	upstream, downstream	ActReg chr11 #3270	0	0	1
3271	11	67,373,986	67,374,803	817	1	8.8	13.96	9.24	20	28	16	1	2	2	LOC100505621, NDUFV1	-217, 71	upstream, in gene	ActReg chr11 #3271	0	1	0
3272	11	67,383,032	67,383,603	571	1	4.222	4.444	12.556	7	8	15	1	0	2	LOC100505621, NDUFV1	-9140, 8994	upstream, downstream	ActReg chr11 #3272	0	0	1
3273	11	67,396,351	67,397,209	858	1	10.259	9.556	11.963	18	18	18	1	1	2	NUDT8, TBX10	621, 10251	in gene, downstream	ActReg chr11 #3273	0	0	1
3274	11	67,406,916	67,407,755	839	1	6.304	6.962	12.923	15	14	19	0	1	3	NUDT8, TBX10, ACY3	-9934, -304, 10795	upstream, upstream, downstream	ActReg chr11 #3274	0	0	1
3275	11	67,431,639	67,432,154	515	1	4.062	2.25	11.438	7	5	20	0	0	1	ALDH3B2	16,789	in gene	ActReg chr11 #3275	0	0	1
3276	11	67,433,845	67,434,338	493	1	4.188	4.812	11.875	8	8	15	0	0	1	ALDH3B2	14,594	in gene	ActReg chr11 #3276	0	0	1
3277	11	67,478,728	67,479,080	352	1	2.25	1	9.091	3	1	15	1	0	0				ActReg chr11 #3277	0	0	1
3278	11	67,723,209	67,723,558	349	1	3.727	9.364	1	6	13	1	1	1	1	LOC100132261	157	in gene	ActReg chr11 #3278	0	1	0
3279	11	67,770,523	67,770,959	436	1	3.714	6.643	11.214	7	8	15	1	2	2	UNC93B1, ALDH3B1	852, -5307	in gene, upstream	ActReg chr11 #3279	0	0	1
3280	11	67,777,522	67,778,153	631	1	8.65	11.9	7.9	12	22	11	0	2	2	UNC93B1, ALDH3B1	-6244, 1789	upstream, in gene	ActReg chr11 #3280	0	1	0
3281	11	67,786,295	67,786,889	594	1	6.579	4.842	12.737	10	9	21	0	0	1	ALDH3B1	10,544	in gene	ActReg chr11 #3281	0	0	1
3282	11	67,795,266	67,796,037	771	1	10.333	11.875	5.75	21	20	11	0	1	2	ALDH3B1, NDUFS8	19603, -2433	in gene, upstream	ActReg chr11 #3282	0	1	0
3283	11	67,800,413	67,800,909	496	1	5.188	4.188	12.375	9	7	15	0	2	3	ALDH3B1, NDUFS8, TCIRG1	24613, 2577, -5822	downstream, in gene, upstream	ActReg chr11 #3283	0	0	1
3284	11	67,800,955	67,801,665	710	1	4.783	3.957	11.913	7	6	19	0	1	3	ALDH3B1, NDUFS8, TCIRG1	25262, 3226, -5173	downstream, in gene, upstream	ActReg chr11 #3284	0	0	1
3285	11	67,805,878	67,806,412	534	1	8.471	9.471	11.059	12	12	16	1	1	3	ALDH3B1, NDUFS8, TCIRG1	30097, 8061, -338	downstream, downstream, upstream	ActReg chr11 #3285	0	0	1
3286	11	67,980,886	67,981,915	1,029	3	9.906	10.516	8.344	18	27	21	1	1	1	SUV420H1	-616	upstream	ActReg chr11 #3286	1	1	1
3287	11	67,982,249	67,982,797	548	1	7.059	11.177	13.118	13	15	18	1	1	1	SUV420H1	-1,739	upstream	ActReg chr11 #3287	0	0	1
3288	11	68,039,133	68,039,999	866	1	8.852	11.333	6.25	14	20	15	1	1	1	C11orf24	-97	upstream	ActReg chr11 #3288	0	1	0
3289	11	68,205,256	68,205,872	616	1	4.316	5.474	12.684	7	9	17	1	0	1	LRP5	125,456	in gene	ActReg chr11 #3289	0	0	1
3290	11	68,213,970	68,214,408	438	1	3.6	6.214	13.429	5	11	19	0	0	1	LRP5	134,081	in gene	ActReg chr11 #3290	0	0	1
3291	11	68,214,413	68,215,078	665	1	7.667	6	9.762	13	9	13	0	0	1	LRP5	134,637	in gene	ActReg chr11 #3291	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3292	11	68,227,392	68,228,062	670	1	10.714	11	14.048	17	18	24	1	1	1	SAPS3	-459	upstream	ActReg chr11 #3292	0	0	1
3293	11	68,426,544	68,427,115	571	1	7.5	12.111	3.706	11	20	7	0	0	0				ActReg chr11 #3293	0	1	0
3294	11	68,670,843	68,672,070	1,227	3	12.59	11.82	12.026	27	31	27	1	2	2	MRPL21, IGHM5P2	-153, 137	upstream, in gene	ActReg chr11 #3294	1	1	1
3295	11	68,778,614	68,779,168	554	1	4	3.611	10.389	7	7	16	1	1	1	MRGPRF	1,959	in gene	ActReg chr11 #3295	0	0	1
3296	11	68,924,646	68,925,480	834	1	7.692	8.308	11.885	12	13	17	1	0	0				ActReg chr11 #3296	0	0	1
3297	11	68,984,954	68,985,471	517	1	7.062	5.438	12.188	10	9	20	0	0	0				ActReg chr11 #3297	0	0	1
3298	11	69,065,621	69,066,923	1,302	1	12.61	11.39	6.951	22	17	12	0	0	1	MYEOV	4,650	downstream	ActReg chr11 #3298	1	0	0
3299	11	69,068,788	69,069,953	1,165	1	16.622	14.297	4.27	30	22	8	0	0	1	MYEOV	7,748	downstream	ActReg chr11 #3299	1	0	0
3300	11	69,149,536	69,150,394	858	2	17.846	17.556	4.37	43	43	9	0	0	0				ActReg chr11 #3300	1	1	0
3301	11	69,167,337	69,167,980	643	1	10.9	8.55	1.7	22	15	3	0	0	0				ActReg chr11 #3301	1	0	0
3302	11	69,192,570	69,193,012	442	1	3.143	6.929	13	5	9	20	0	0	0				ActReg chr11 #3302	0	0	1
3303	11	69,195,250	69,195,751	501	1	3.5	5.625	12.812	6	8	20	0	0	0				ActReg chr11 #3303	0	0	1
3304	11	69,230,766	69,231,245	479	1	5.867	9.267	15	9	14	20	0	0	1	LOC100505834	-9,434	upstream	ActReg chr11 #3304	0	0	1
3305	11	69,231,682	69,232,331	649	1	7.95	12.95	3.632	12	19	6	0	0	1	LOC100505834	-8,433	upstream	ActReg chr11 #3305	0	1	0
3306	11	69,258,142	69,258,791	649	1	6.333	7.81	13.619	10	15	23	1	0	0				ActReg chr11 #3306	0	0	1
3307	11	69,290,793	69,291,251	458	1	3.786	2.077	11.429	5	3	15	0	0	0				ActReg chr11 #3307	0	0	1
3308	11	69,300,369	69,300,919	550	1	3.353	5.647	12.294	5	8	17	0	0	0				ActReg chr11 #3308	0	0	1
3309	11	69,407,760	69,408,125	365	1	4.909	3.182	11.273	6	4	17	0	0	0				ActReg chr11 #3309	0	0	1
3310	11	69,458,633	69,459,370	737	1	9.739	9.783	12.304	16	18	18	1	0	1	CCND1	3,128	in gene	ActReg chr11 #3310	0	0	1
3311	11	69,462,613	69,463,002	389	1	3	2.083	12.75	5	3	17	0	0	1	CCND1	6,934	in gene	ActReg chr11 #3311	0	0	1
3312	11	69,489,696	69,490,353	657	2	13.952	13.952	11.952	28	28	17	1	1	1	ORAOV1	141	in gene	ActReg chr11 #3312	0	1	1
3313	11	69,588,463	69,589,106	643	1	3.4	3.55	14.3	5	6	22	1	1	1	FGF4	1,387	in gene	ActReg chr11 #3313	0	0	1
3314	11	69,611,359	69,611,698	339	1	3.636	2.455	11.273	7	5	14	0	0	0				ActReg chr11 #3314	0	0	1
3315	11	69,632,198	69,633,039	841	1	3.846	5.923	12.923	7	13	21	1	1	1	FGF3	1,574	in gene	ActReg chr11 #3315	0	0	1
3316	11	69,648,855	69,649,497	642	1	3.75	3.95	13.4	5	5	23	0	0	0				ActReg chr11 #3316	0	0	1
3317	11	70,005,738	70,006,753	1,015	2	9.906	10.062	5.594	16	15	10	0	0	1	ANO1	81,837	in gene	ActReg chr11 #3317	1	1	0
3318	11	70,049,273	70,049,724	451	1	7.929	9.857	12.286	11	12	16	1	1	1	FADD	229	in gene	ActReg chr11 #3318	0	0	1
3319	11	70,079,363	70,080,184	821	2	14.44	10.76	3.04	26	20	6	0	0	0				ActReg chr11 #3319	1	1	0
3320	11	70,244,050	70,244,605	555	1	10.823	10.529	12.647	19	18	19	1	1	1	CTTN	-285	upstream	ActReg chr11 #3320	0	0	1
3321	11	70,244,686	70,244,969	283	1	7.333	7.556	9.889	11	12	13	1	1	1	CTTN	215	in gene	ActReg chr11 #3321	0	0	1
3322	11	70,320,431	70,321,009	578	1	2.833	3.889	11.222	5	6	17	0	0	1	SHANK2	615,088	in gene	ActReg chr11 #3322	0	0	1
3323	11	70,332,398	70,332,851	453	1	3.786	5.071	11.571	5	8	16	1	0	1	SHANK2	603,184	in gene	ActReg chr11 #3323	0	0	1
3324	11	70,351,090	70,351,930	840	1	2.231	2.269	11.731	4	4	17	0	0	1	SHANK2	584,298	in gene	ActReg chr11 #3324	0	0	1
3325	11	70,374,256	70,374,625	369	1	2.5	3.917	12.833	5	6	18	0	0	1	SHANK2	561,368	in gene	ActReg chr11 #3325	0	0	1
3326	11	70,390,571	70,390,880	309	1	2.125	5.4	12.5	3	8	17	0	0	1	SHANK2	545,083	in gene	ActReg chr11 #3326	0	0	1
3327	11	70,426,458	70,427,314	856	1	4.37	6.037	11.444	11	13	15	0	0	1	SHANK2	508,922	in gene	ActReg chr11 #3327	0	0	1
3328	11	70,452,879	70,453,428	549	1	2.059	3.941	12.059	4	8	24	0	0	1	SHANK2	482,655	in gene	ActReg chr11 #3328	0	0	1
3329	11	70,495,877	70,497,593	1,716	2	21.132	26.962	3.68	74	91	9	0	0	1	SHANK2	439,073	in gene	ActReg chr11 #3329	1	1	0
3330	11	70,509,043	70,509,428	385	1	3.667	5.75	11.667	4	9	16	0	0	1	SHANK2	426,573	in gene	ActReg chr11 #3330	0	0	1
3331	11	70,571,959	70,572,371	412	1	1.615	3	9.462	3	4	16	0	0	1	SHANK2	363,643	in gene	ActReg chr11 #3331	0	0	1
3332	11	70,813,657	70,814,089	432	1	2.615	2.929	10.357	5	4	16	0	0	1	SHANK2	-121,955	in gene	ActReg chr11 #3332	0	0	1
3333	11	70,819,147	70,819,558	411	1	5.231	2.167	10.923	8	4	15	0	0	1	SHANK2	116,456	in gene	ActReg chr11 #3333	0	0	1
3334	11	71,072,758	71,074,085	1,327	1	10.881	11.905	2.476	17	19	6	0	0	0				ActReg chr11 #3334	0	1	0
3335	11	71,342,697	71,343,066	369	1	2.818	3	9.727	5	4	13	0	0	0				ActReg chr11 #3335	0	0	1
3336	11	71,485,674	71,486,081	407	1	2.308	5.308	10.308	3	9	14	0	0	0				ActReg chr11 #3336	0	0	1
3337	11	71,498,482	71,498,764	282	1	6.222	6.667	10	9	9	13	1	1	1	FAM86C	66	in gene	ActReg chr11 #3337	0	0	1
3338	11	71,639,298	71,640,342	1,044	2	13.312	13.031	6.688	20	20	11	0	1	1	RNF121	52	in gene	ActReg chr11 #3338	1	1	0
3339	11	71,724,164	71,724,535	371	1	2.818	8.182	12.273	7	12	16	0	0	1	NUMA1	67,224	in gene	ActReg chr11 #3339	0	0	1
3340	11	71,751,556	71,753,241	1,685	2	15.269	15.154	4.347	31	28	9	0	0	1	NUMA1	39,175	in gene	ActReg chr11 #3340	1	1	0
3341	11	71,791,646	71,792,292	646	1	6.81	10.809	5.857	9	15	12	1	2	3	NUMA1, MIR3165, LRTOMT	-396, -8621, 587	upstream, upstream, in gene	ActReg chr11 #3341	0	1	0
3342	11	71,813,914	71,814,454	540	1	4.588	11.059	11.941	7	16	20	1	1	3	LRTOMT, C11orf59, C11orf51	22802, 249, 9638	in gene, in gene, downstream	ActReg chr11 #3342	0	0	1
3343	11	71,835,310	71,835,676	366	1	3	2.364	12	4	3	16	0	0	0				ActReg chr11 #3343	0	0	1
3344	11	71,933,932	71,934,697	765	2	12.333	11.083	6.958	25	24	16	1	1	2	FOLR2, INPPL1	6495, -1568	downstream, upstream	ActReg chr11 #3344	1	1	0
3345	11	71,961,051	71,961,455	404	1	5	5.385	10.077	6	7	16	0	2	2	PHOX2A, LOC220077	-6033, 1099	upstream, in gene	ActReg chr11 #3345	0	0	1
3346	11	72,092,030	72,092,587	557	1	3.944	4.222	9.444	7	7	16	0	0	1	CLPB	53,360	in gene	ActReg chr11 #3346	0	0	1
3347	11	72,145,004	72,145,999	995	2	10.194	12.258	5.484	22	21	10	1	1	1	CLPB	67	in gene	ActReg chr11 #3347	1	1	0
3348	11	72,339,907	72,340,492	585	1	6.722	4.294	12.889	11	6	17	0	0	1	PDE2A	45,295	in gene	ActReg chr11 #3348	0	0	1
3349	11	72,387,805	72,388,541	736	2	9.696	14	9.522	14	28	18	0	1	2	PDE2A, ARAP1	-2679, 75261	upstream, downstream	ActReg chr11 #3349	0	1	1
3350	11	72,427,716	72,428,098	382	1	2.6	4.167	12.667	5	7	16	0	0	1	ARAP1	35,527	in gene	ActReg chr11 #3350	0	0	1
3351	11	72,504,719	72,505,446	727	1	9.391	12.174	6.762	17	23	16	1	1	1	STARD10	-332	upstream	ActReg chr11 #3351	0	1	0
3352	11	72,524,747	72,526,206	1,459	2	12.956	13.444	7	28	23	13	1	1	1	ATG16L2	25	in gene	ActReg chr11 #3352	1	1	0
3353	11	72,852,689	72,853,238	549	1	5.588	8.412	12.353	8	12	20	1	1	1	FCHSD2	180	in gene	ActReg chr11 #3353	0	0	1
3354	11	73,087,805	73,088,508	703	1	9.545	12.818	4.444	15	21	6	1	1	2	ARHGEF17, RELT	68493, 751	downstream, in gene	ActReg chr11 #3354	0	1	0
3355	11	73,096,042	73,096,528	486	1	2.4	3.462	10.2	6	6	17	0	0	1	RELT	8,880	in gene	ActReg chr11 #3355	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3356	11	73,105,266	73,105,645	379	1	4.167	6.5	12.583	6	9	18	0	0	1	RELT	18,050	in gene	ActReg chr11 #3356	0	0	1
3357	11	73,308,774	73,310,026	1,252	2	10.077	10.462	5.795	16	20	11	1	1	1	FAM168A	-172	upstream	ActReg chr11 #3357	1	1	0
3358	11	73,490,392	73,491,099	707	2	11.046	11.364	5.455	22	20	8	1	0	1	MRPL48	-8,172	upstream	ActReg chr11 #3358	1	1	0
3359	11	73,498,637	73,499,397	760	2	10.375	12.292	5.917	19	25	9	1	1	1	MRPL48	100	in gene	ActReg chr11 #3359	1	1	0
3360	11	73,587,411	73,588,484	1,073	1	8.853	11.412	6.226	14	17	12	1	2	2	CHCHD8, PAAF1	-57, -86	upstream, upstream	ActReg chr11 #3360	0	1	0
3361	11	73,694,294	73,694,808	514	1	9.5	9.25	11.938	12	13	16	1	1	1	UCP2	-662	upstream	ActReg chr11 #3361	0	0	1
3362	11	73,748,228	73,748,883	655	1	8.4	12.3	1.5	13	24	2	0	0	1	C2CD3	133,509	in gene	ActReg chr11 #3362	0	1	0
3363	11	73,881,671	73,882,848	1,177	2	9.973	14.189	6.838	19	24	12	1	2	2	C2CD3, PPME1	-195, -109	upstream, upstream	ActReg chr11 #3363	1	1	0
3364	11	73,987,853	73,988,367	514	1	6.688	9.75	3.312	8	16	5	0	0	1	P4HA3	34,589	in gene	ActReg chr11 #3364	0	1	0
3365	11	74,109,586	74,110,330	744	1	12.522	10.696	6.529	23	19	14	1	1	1	PGM2L1	-456	upstream	ActReg chr11 #3365	1	0	0
3366	11	74,128,742	74,129,549	807	2	15.84	16.2	4.96	26	28	8	0	0	0				ActReg chr11 #3366	1	1	0
3367	11	74,204,219	74,204,981	762	2	11.125	10.625	4.958	19	19	10	1	2	2	LIPT2, LOC100287896	155, 115	in gene, in gene	ActReg chr11 #3367	1	1	0
3368	11	74,459,472	74,460,260	788	2	16.75	16.96	4.955	41	39	9	1	1	1	RNF169	-47	upstream	ActReg chr11 #3368	1	1	0
3369	11	74,460,437	74,460,901	464	1	6.4	7.333	11.467	9	10	16	1	1	1	RNF169	756	in gene	ActReg chr11 #3369	0	0	1
3370	11	74,465,570	74,466,132	562	1	11.529	6.235	4.267	15	9	7	0	0	1	RNF169	5,938	in gene	ActReg chr11 #3370	1	0	0
3371	11	74,560,574	74,561,341	767	1	9.042	12.375	3.917	12	18	8	0	0	2	RNF169, XRRA1	101044, 99275	downstream, in gene	ActReg chr11 #3371	0	1	0
3372	11	74,659,728	74,660,559	831	1	7.346	15	7.269	11	28	13	1	2	2	XRRA1, SPCS2	89, -149	in gene, upstream	ActReg chr11 #3372	0	1	0
3373	11	74,904,299	74,904,867	568	1	3.111	3.333	11.722	6	6	17	0	0	1	SLCO2B1	42,543	in gene	ActReg chr11 #3373	0	0	1
3374	11	74,925,187	74,926,240	1,053	2	21.788	22.364	3.8	66	61	7	0	0	1	SLCO2B1	63,673	downstream	ActReg chr11 #3374	1	1	0
3375	11	74,944,543	74,945,554	1,011	2	14.156	17.219	2.923	32	40	6	0	1	1	LOC100507050	-6,374	upstream	ActReg chr11 #3375	1	1	0
3376	11	75,101,277	75,101,593	316	1	3	2.9	9.8	6	5	12	0	0	2	RPS3, SNORD15A	-9127, -10000	upstream, upstream	ActReg chr11 #3376	0	0	1
3377	11	75,110,225	75,111,047	822	3	10.423	11.346	8.769	18	20	19	1	3	3	RPS3, SNORD15A, SNORD15B	74, -799, -4829	in gene, upstream, upstream	ActReg chr11 #3377	1	1	1
3378	11	75,259,661	75,260,359	698	1	10.227	12.318	3.421	16	18	6	0	0	0				ActReg chr11 #3378	0	1	0
3379	11	75,273,209	75,273,891	682	1	4.227	7.818	11.727	8	12	17	1	1	1	SERPINH1	380	in gene	ActReg chr11 #3379	0	0	1
3380	11	75,479,224	75,480,029	805	3	13.2	12.84	8.76	27	28	19	1	1	1	DGAT2	-152	upstream	ActReg chr11 #3380	1	1	1
3381	11	75,525,360	75,526,590	1,230	1	8.895	11.342	5.611	13	20	11	2	2	2	LOC100506113, UVRAG	-133, -237	upstream, upstream	ActReg chr11 #3381	0	1	0
3382	11	75,864,137	75,865,036	899	1	7.464	11.179	3.316	14	19	9	0	0	1	UVRAG	338,374	downstream	ActReg chr11 #3382	0	1	0
3383	11	75,882,228	75,882,698	470	1	2.75	2.667	11.6	4	4	18	0	0	0				ActReg chr11 #3383	0	0	1
3384	11	75,916,954	75,917,473	519	1	3.059	6.412	11.177	7	9	17	1	1	1	WNT11	361	in gene	ActReg chr11 #3384	0	0	1
3385	11	75,919,704	75,920,713	1,009	2	9.312	12.594	6.625	18	19	11	1	1	1	WNT11	-2,634	upstream	ActReg chr11 #3385	1	1	0
3386	11	75,946,189	75,947,566	1,377	3	11.698	12.744	14.954	22	19	30	1	0	0				ActReg chr11 #3386	1	1	1
3387	11	76,090,955	76,092,839	1,884	3	21.152	22.407	4.211	93	101	15	1	2	2	PRKRIR, LOC100506127	-17, -463	upstream, upstream	ActReg chr11 #3387	1	1	0
3388	11	76,155,303	76,156,302	999	1	9.677	12.677	5	20	19	9	1	1	1	C11orf30	-267	upstream	ActReg chr11 #3388	0	1	0
3389	11	76,288,435	76,289,060	625	1	6.9	10.85	6.6	9	17	9	0	0	0				ActReg chr11 #3389	0	1	0
3390	11	76,289,311	76,289,949	638	1	9.3	11.55	2.25	13	17	4	0	0	0				ActReg chr11 #3390	0	1	0
3391	11	76,411,300	76,412,245	945	1	7.828	10.483	5.179	15	16	9	0	0	0				ActReg chr11 #3391	0	1	0
3392	11	76,427,754	76,428,175	421	1	5.154	3.769	10.154	8	6	13	0	0	0				ActReg chr11 #3392	0	0	1
3393	11	76,430,523	76,431,085	562	1	3.833	3.294	13.611	6	5	20	0	0	0				ActReg chr11 #3393	0	0	1
3394	11	76,435,161	76,435,835	674	2	9.81	11.333	3.25	18	20	6	0	0	0				ActReg chr11 #3394	1	1	0
3395	11	76,784,208	76,785,006	798	2	6.64	12.2	9.92	11	18	15	0	0	1	CAPN5	6,615	in gene	ActReg chr11 #3395	0	1	1
3396	11	76,804,052	76,804,539	487	1	3.333	3.533	11.467	7	6	20	0	0	2	CAPN5, OMP	26303, -9591	in gene, upstream	ActReg chr11 #3396	0	0	1
3397	11	77,185,264	77,185,786	522	1	10.25	11.5	5.938	17	19	12	1	1	1	PAK1	-417	upstream	ActReg chr11 #3397	0	1	0
3398	11	77,300,288	77,300,847	559	1	5.667	10.333	4.062	9	16	6	1	1	1	AQP11	-113	upstream	ActReg chr11 #3398	0	1	0
3399	11	77,348,437	77,349,217	780	2	10.36	11.76	6.4	17	22	13	1	1	1	CLNS1A	24	in gene	ActReg chr11 #3399	1	1	0
3400	11	77,530,307	77,530,924	617	2	9.158	9.316	2.421	16	16	4	0	2	2	RSF1, C11orf67	1265, -1593	in gene, upstream	ActReg chr11 #3400	1	1	0
3401	11	77,705,424	77,706,503	1,079	2	11.177	11.765	6.324	18	25	10	1	1	1	INTS4	-246	upstream	ActReg chr11 #3401	1	1	0
3402	11	77,850,197	77,851,082	885	2	9.286	10.643	10.393	18	22	16	1	1	1	ALG8	60	in gene	ActReg chr11 #3402	0	1	1
3403	11	77,899,254	77,900,767	1,513	2	15.106	18.979	7.66	47	67	15	1	2	2	KCTD21, USP35	-346, 152	upstream, in gene	ActReg chr11 #3403	1	1	0
3404	11	78,285,109	78,286,135	1,026	1	9.312	11.688	5.75	14	17	13	1	1	1	NARS2	287	in gene	ActReg chr11 #3404	0	1	0
3405	11	78,349,708	78,350,099	391	1	1.667	6.167	11.25	3	8	18	0	0	0				ActReg chr11 #3405	0	0	1
3406	11	79,151,271	79,151,579	308	1	3.111	5.111	11.333	4	6	16	1	1	1	ODZ4	270	in gene	ActReg chr11 #3406	0	0	1
3407	11	82,782,629	82,783,329	700	1	10.954	13.091	4.364	15	23	10	0	2	3	RAB30, LOC100506233, LOC100506259	-95, -140, 7945	upstream, upstream, downstream	ActReg chr11 #3407	0	1	0
3408	11	82,904,459	82,906,036	1,577	2	9.388	11.388	5.878	18	17	11	1	2	3	PCF11, LOC100506282, ANKRD42	37110, -543, -44	downstream, upstream, upstream	ActReg chr11 #3408	1	1	0
3409	11	82,996,584	82,997,942	1,358	3	21.357	25.286	7.452	58	76	18	1	1	1	CCDC90B	114	in gene	ActReg chr11 #3409	1	1	1
3410	11	84,019,458	84,019,889	431	1	3.769	3.167	12.923	6	5	16	0	0	1	DLG2	1,318,641	in gene	ActReg chr11 #3410	0	0	1
3411	11	84,425,217	84,425,760	543	1	12.706	7.529	1.176	24	14	2	0	0	1	DLG2	912,826	in gene	ActReg chr11 #3411	1	0	0
3412	11	84,912,109	84,912,582	473	1	1.615	2	11.4	3	4	17	0	0	1	DLG2	425,969	in gene	ActReg chr11 #3412	0	0	1
3413	11	85,339,127	85,339,853	726	1	12.565	7.522	5.261	19	13	10	1	2	2	DLG2, TMEM126B	-1176, -132	upstream, upstream	ActReg chr11 #3413	1	0	0
3414	11	85,358,669	85,359,251	582	1	10.889	13.722	7.556	15	20	14	1	1	2	TMEM126A, CREBZF	-3, 17222	upstream, downstream	ActReg chr11 #3414	0	1	0
3415	11	85,375,845	85,376,212	367	1	10	7.727	12.364	14	12	19	1	1	2	TMEM126A, CREBZF	17065, 154	downstream, in gene	ActReg chr11 #3415	0	0	1
3416	11	85,429,892	85,430,643	751	2	11.739	14.435	1.533	24	26	3	0	0	1	SYTL2	91,911	in gene	ActReg chr11 #3416	1	1	0
3417	11	85,565,531	85,566,073	542	1	7.118	11.353	4.176	10	22	7	1	2	2	LOC100506308, CCDC83	184, -342	in gene, upstream	ActReg chr11 #3417	0	1	0
3418	11	85,601,047	85,601,573	526	1	10.412	7.353	1.733	17	11	3	0	0	1	CCDC83	35,166	in gene	ActReg chr11 #3418	1	0	0
3419	11	85,779,906	85,780,341	435	1	13.308	8.308	8.308	19	11	11	1	1	1	PICALM	-15	upstream	ActReg chr11 #3419	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3420	11	85,828,012	85,828,550	538	1	10.118	7.059	1.5	17	10	4	0	0	0				ActReg chr11 #3420	1	0	0
3421	11	85,885,017	85,886,059	1,042	1	9.818	11	3.781	15	17	8	0	0	0				ActReg chr11 #3421	0	1	0
3422	11	85,955,304	85,956,290	986	2	11.516	16.581	5	17	29	10	2	1	1	EED	-18	upstream	ActReg chr11 #3422	1	1	0
3423	11	86,012,900	86,013,679	779	1	14.625	11.125	3.042	25	20	6	0	1	1	C11orf73	36	in gene	ActReg chr11 #3423	1	0	0
3424	11	86,170,714	86,171,431	717	1	5	10.826	4.304	8	15	5	0	0	1	ME3	212,606	in gene	ActReg chr11 #3424	0	1	0
3425	11	86,343,597	86,344,501	904	2	14.464	11.179	4	29	17	7	0	0	1	ME3	39,629	in gene	ActReg chr11 #3425	1	1	0
3426	11	86,382,680	86,383,773	1,093	3	7.824	11.059	9.824	15	19	16	1	1	1	ME3	452	in gene	ActReg chr11 #3426	1	1	1
3427	11	86,706,053	86,706,380	327	1	4.4	3.3	10	6	4	14	0	0	1	LOC100506368	39,553	in gene	ActReg chr11 #3427	0	0	1
3428	11	87,489,120	87,489,813	693	2	8.182	10.909	1.944	15	22	3	0	0	0				ActReg chr11 #3428	1	1	0
3429	11	87,802,310	87,802,645	335	1	3.9	2.4	12.3	6	3	16	0	0	0				ActReg chr11 #3429	0	0	1
3430	11	88,070,478	88,071,248	770	2	8.875	10.375	10.542	15	20	18	1	1	1	CTSC	78	in gene	ActReg chr11 #3430	0	1	1
3431	11	88,428,695	88,429,616	921	1	9.286	14.69	2.393	15	29	5	0	0	1	GRM5	367,661	in gene	ActReg chr11 #3431	0	1	0
3432	11	88,437,499	88,438,135	636	1	10.8	10.15	1	19	15	1	0	0	1	GRM5	358,999	in gene	ActReg chr11 #3432	1	0	0
3433	11	88,442,635	88,443,172	537	1	9.118	9.294	3.118	15	16	5	0	0	1	GRM5	353,913	in gene	ActReg chr11 #3433	0	1	0
3434	11	88,901,348	88,902,071	723	1	11.954	8.318	2.4	19	13	5	0	0	1	TYR	-9,331	upstream	ActReg chr11 #3434	1	0	0
3435	11	89,955,906	89,956,851	945	1	7.31	11.966	4.636	13	16	9	1	1	1	CHORDC1	154	in gene	ActReg chr11 #3435	0	1	0
3436	11	91,957,584	91,958,089	505	1	7.188	6.625	11.625	10	10	18	1	0	0				ActReg chr11 #3436	0	0	1
3437	11	91,959,764	91,960,098	334	1	2.364	6.818	10.909	4	10	13	1	0	0				ActReg chr11 #3437	0	0	1
3438	11	92,930,530	92,931,525	995	1	8.226	11.871	3.516	13	19	8	1	1	1	SLC36A4	68	in gene	ActReg chr11 #3438	0	1	0
3439	11	93,214,328	93,214,739	411	1	1.615	4.923	11.385	3	6	20	0	0	1	C11orf75	62,013	in gene	ActReg chr11 #3439	0	0	1
3440	11	93,394,455	93,395,458	1,003	1	8.031	11.469	5.806	15	20	12	1	1	1	KIAA1731	140	in gene	ActReg chr11 #3440	0	1	0
3441	11	93,474,447	93,475,028	581	2	8.833	10.222	13.278	10	16	19	1	3	9	SNORD6, SNORA1, SNORA8, SNORD5, SNORA18, MIR1304, SNORA40, TAF1D, C11orf54	-9998, -9438, -9072, -8271, -7974, -7807, -6335, -34, -56	upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr11 #3441	0	1	1
3442	11	93,517,369	93,518,279	910	1	8.172	11.862	8.448	13	17	15	1	1	1	MED17	419	in gene	ActReg chr11 #3442	0	1	0
3443	11	94,501,079	94,501,911	832	2	16.885	16.385	3.708	34	35	8	1	1	1	AMOTL1	-13	upstream	ActReg chr11 #3443	1	1	0
3444	11	94,523,567	94,524,283	716	1	11.318	10.182	3.833	14	16	6	0	0	1	AMOTL1	22,417	in gene	ActReg chr11 #3444	1	0	0
3445	11	94,535,551	94,536,407	856	1	13.444	11.667	3.667	23	17	7	0	0	1	AMOTL1	34,471	in gene	ActReg chr11 #3445	1	0	0
3446	11	94,612,692	94,613,955	1,263	2	19.7	19.225	2.353	74	69	4	0	0	1	AMOTL1	111,815	downstream	ActReg chr11 #3446	1	1	0
3447	11	94,800,040	94,801,034	994	1	8.968	10.71	3.935	14	19	8	1	1	1	SFRS2B	481	in gene	ActReg chr11 #3447	0	1	0
3448	11	94,822,554	94,822,904	350	1	3.091	9.273	11.636	4	13	18	1	1	1	ENDOD1	-245	upstream	ActReg chr11 #3448	0	0	1
3449	11	94,866,128	94,866,635	507	1	5.438	11.188	1.167	8	17	2	0	0	1	ENDOD1	43,407	downstream	ActReg chr11 #3449	0	1	0
3450	11	94,883,846	94,884,973	1,127	2	12.8	7.114	9.543	23	11	16	1	0	0				ActReg chr11 #3450	1	0	1
3451	11	95,289,619	95,290,166	547	1	10.765	6.562	2	19	12	3	0	0	0				ActReg chr11 #3451	1	0	0
3452	11	95,449,484	95,449,930	446	1	10.071	5.571	1	15	7	1	0	0	0				ActReg chr11 #3452	1	0	0
3453	11	95,522,313	95,523,856	1,543	1	9.417	15.083	8.188	18	26	17	1	2	2	FAM76B, CEP57	-130, -558	upstream, upstream	ActReg chr11 #3453	0	1	0
3454	11	95,656,837	95,657,639	802	2	12.8	14.72	5.04	22	33	13	1	1	1	MTMR2	133	in gene	ActReg chr11 #3454	1	1	0
3455	11	95,747,130	95,747,734	604	1	10.263	7.316	2.111	14	11	5	0	0	1	MAML2	328,912	in gene	ActReg chr11 #3455	1	0	0
3456	11	95,855,819	95,856,343	524	1	8.062	11.438	2.812	12	16	4	0	0	1	MAML2	220,283	in gene	ActReg chr11 #3456	0	1	0
3457	11	95,889,246	95,889,932	686	1	10.091	12.318	4.864	17	25	8	0	0	1	MAML2	186,755	in gene	ActReg chr11 #3457	0	1	0
3458	11	96,074,358	96,075,193	835	1	11.731	9.077	6.808	18	16	13	0	2	2	MAML2, MIR1260B	1569, 173	in gene, downstream	ActReg chr11 #3458	1	0	0
3459	11	96,232,771	96,233,111	340	1	3	2.5	9.9	5	4	15	0	0	0				ActReg chr11 #3459	0	0	1
3460	11	96,471,230	96,471,544	314	1	1.429	1.8	10.8	2	3	16	0	0	0				ActReg chr11 #3460	0	0	1
3461	11	97,616,518	97,616,975	457	1	2.286	4.143	11.857	4	6	16	0	0	0				ActReg chr11 #3461	0	0	1
3462	11	101,111,911	101,112,285	374	1	3	2.182	12.182	4	3	17	0	0	0				ActReg chr11 #3462	0	0	1
3463	11	101,312,422	101,312,871	449	1	5.571	10.714	1.4	9	14	2	0	0	1	TRPC6	142,013	downstream	ActReg chr11 #3463	0	1	0
3464	11	101,980,725	101,981,405	680	1	7.19	11.571	2.308	12	16	4	1	1	1	YAP1	-127	upstream	ActReg chr11 #3464	0	1	0
3465	11	102,115,503	102,116,135	632	1	10.7	9.15	3.75	19	15	7	0	0	0				ActReg chr11 #3465	1	0	0
3466	11	102,217,554	102,218,323	769	2	8.417	12.375	7.042	13	19	14	1	1	2	BIRC3, BIRC2	29744, -28	downstream, upstream	ActReg chr11 #3466	0	1	1
3467	11	102,323,014	102,323,699	685	2	10.333	9.05	4.5	16	16	8	1	2	2	TMEM123, LOC727869	419, -294	in gene, upstream	ActReg chr11 #3467	1	1	0
3468	11	102,463,532	102,464,167	635	1	9.45	7.4	2.562	16	9	4	0	0	1	MMP20	32,214	in gene	ActReg chr11 #3468	1	0	0
3469	11	102,714,050	102,714,718	668	1	10.5	5.4	3.909	19	8	5	0	1	2	LOC100288077, MMP3	59977, -42	downstream, upstream	ActReg chr11 #3469	0	1	0
3470	11	102,979,807	102,980,480	673	1	10.773	11.182	3.778	13	17	7	0	1	1	DYNC2H1	-17	upstream	ActReg chr11 #3470	0	1	0
3471	11	105,763,145	105,764,086	941	2	16.207	21.035	1.944	36	58	3	0	0	0				ActReg chr11 #3471	1	1	0
3472	11	105,228,083	105,228,765	682	1	9.19	11.714	4.778	11	19	8	0	0	0				ActReg chr11 #3472	0	1	0
3473	11	105,543,652	105,544,384	732	2	11.478	9.217	2.1	25	21	4	0	0	1	GRIA4	63,218	in gene	ActReg chr11 #3473	1	1	0
3474	11	105,590,008	105,590,549	541	1	4.941	11.118	1.733	7	18	3	0	0	1	GRIA4	109,478	in gene	ActReg chr11 #3474	0	1	0
3475	11	105,892,528	105,893,491	963	2	8.867	11.233	6.767	14	18	15	1	1	1	KIAA1826	-55	upstream	ActReg chr11 #3475	0	1	1
3476	11	106,889,305	106,890,331	1,026	2	13.562	22.781	6.25	22	44	11	1	1	1	GUCY1A2	-647	upstream	ActReg chr11 #3476	1	1	0
3477	11	107,433,504	107,434,099	595	1	11.21	6.842	1.333	20	9	2	0	1	1	ALKBH8	2,660	in gene	ActReg chr11 #3477	1	0	0
3478	11	107,435,873	107,436,699	826	1	8.44	11.88	4.4	13	18	7	0	1	1	ALKBH8	175	in gene	ActReg chr11 #3478	0	1	0
3479	11	107,570,022	107,570,807	785	1	7.174	12	2.667	13	16	4	0	0	1	SLN	12,373	downstream	ActReg chr11 #3479	0	1	0
3480	11	107,729,190	107,729,508	318	1	6.3	7.5	10	8	11	14	1	1	1	SLC35F2	565	in gene	ActReg chr11 #3480	0	0	1
3481	11	107,799,158	107,799,587	429	1	5.143	10.429	8.143	8	14	13	1	1	1	RAB39	95	in gene	ActReg chr11 #3481	0	1	0
3482	11	108,093,646	108,094,189	543	2	5.882	9.412	9.059	9	15	18	1	2	2	NPAT, ATM	-552, 358	upstream, in gene	ActReg chr11 #3482	0	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3483	11	108,463,506	108,463,861	355	1	3.182	4.273	10.454	4	7	14	1	1	1	EXPH5	691	in gene	ActReg chr11 #3483	0	0	1
3484	11	109,512,152	109,512,786	634	2	10.35	11.25	3.611	24	22	7	0	0	0				ActReg chr11 #3484	1	1	0
3485	11	109,730,008	109,730,611	603	1	7.158	10.632	1.579	12	23	2	0	0	0				ActReg chr11 #3485	0	1	0
3486	11	111,249,976	111,250,290	314	1	1.889	5.3	10.8	3	7	14	0	1	1	POU2AF1	24	in gene	ActReg chr11 #3486	0	0	1
3487	11	111,317,245	111,317,714	469	1	9.6	3.667	3.182	17	5	5	0	0	1	LOC644277	18,256	in gene	ActReg chr11 #3487	1	0	0
3488	11	111,636,642	111,637,051	409	1	5.917	7.25	11.417	7	10	14	1	1	1	PPP2R1B	323	in gene	ActReg chr11 #3488	0	0	1
3489	11	111,749,300	111,750,186	886	2	8.214	9.75	2.75	18	15	6	1	3	3	ALG9, FDXACB1, C11orf1	-7438, 410, -205	upstream, in gene, upstream	ActReg chr11 #3489	1	1	0
3490	11	112,541,961	112,542,445	484	1	5.267	4.533	10.467	7	8	15	0	0	0				ActReg chr11 #3490	0	0	1
3491	11	112,604,626	112,605,444	818	2	13.115	12.077	1.955	27	28	3	0	0	0				ActReg chr11 #3491	1	1	0
3492	11	112,831,795	112,832,358	563	1	4.944	9.944	4.611	8	16	7	1	1	1	NCAM1	81	in gene	ActReg chr11 #3492	0	1	0
3493	11	113,185,252	113,185,835	583	1	6.333	13.333	3.125	11	21	5	1	1	1	TTC12	292	in gene	ActReg chr11 #3493	0	1	0
3494	11	113,316,923	113,317,940	1,017	1	10.781	10.781	4.097	18	18	9	0	0	2	DRD2, MIR4301	28570, 3379	in gene, downstream	ActReg chr11 #3494	0	1	0
3495	11	113,318,312	113,319,468	1,156	2	13.056	11.722	3	23	19	8	0	1	2	DRD2, MIR4301	27111, 1920	in gene, downstream	ActReg chr11 #3495	1	1	0
3496	11	113,344,372	113,345,907	1,535	2	21.229	25.375	6.17	59	74	12	1	1	1	DRD2	862	in gene	ActReg chr11 #3496	1	1	0
3497	11	113,519,962	113,520,403	441	1	4.786	2.214	11.929	7	4	17	0	0	0				ActReg chr11 #3497	0	0	1
3498	11	113,535,251	113,536,289	1,038	1	5.879	11.485	1.429	14	18	2	0	0	0				ActReg chr11 #3498	0	1	0
3499	11	113,545,797	113,546,476	679	1	5.238	11	3	9	18	5	0	0	0				ActReg chr11 #3499	0	1	0
3500	11	113,644,126	113,644,898	772	2	13.48	11.24	3.2	32	29	6	1	2	2	ZW10, CLDN25	-87, -6006	upstream, upstream	ActReg chr11 #3500	1	1	0
3501	11	113,861,703	113,863,019	1,316	2	11.195	15.39	2.778	32	39	5	0	0	1	HTR3A	16,564	downstream	ActReg chr11 #3501	1	1	0
3502	11	113,906,797	113,907,255	458	1	5.929	7.857	10.929	8	12	15	1	0	0				ActReg chr11 #3502	0	0	1
3503	11	114,165,676	114,166,204	528	1	5.875	9.875	3.5	9	14	7	0	1	2	NNMT, LOC100506941	-595, 2922	upstream, downstream	ActReg chr11 #3503	0	1	0
3504	11	114,219,263	114,219,708	445	1	4.769	9.5	3.429	8	16	5	0	0	0				ActReg chr11 #3504	0	1	0
3505	11	114,270,508	114,271,960	1,452	1	8.444	12.089	7.93	14	21	15	1	2	2	C11orf21, RBM7	-95, -150	upstream, upstream	ActReg chr11 #3505	0	1	0
3506	11	114,309,834	114,311,070	1,236	2	12.447	15.71	4.5	22	32	9	1	1	1	REXO2	344	in gene	ActReg chr11 #3506	1	1	0
3507	11	114,800,158	114,800,495	337	1	4.091	2.273	10	6	3	13	0	0	0				ActReg chr11 #3507	0	0	1
3508	11	115,093,113	115,093,528	415	1	10.615	6.615	1.615	14	9	3	0	0	1	CADM1	281,921	in gene	ActReg chr11 #3508	1	0	0
3509	11	115,171,837	115,172,255	418	1	4.231	10.462	2.583	6	14	4	0	0	1	CADM1	203,195	in gene	ActReg chr11 #3509	0	1	0
3510	11	115,371,294	115,371,758	464	1	10.333	4.6	1.357	12	7	2	0	0	1	CADM1	3,715	in gene	ActReg chr11 #3510	1	0	0
3511	11	115,373,578	115,374,138	560	1	9.529	10.235	5.588	13	19	11	1	1	1	CADM1	1,383	in gene	ActReg chr11 #3511	0	1	0
3512	11	115,374,703	115,375,650	947	2	10.533	11.367	5.31	20	17	10	1	1	1	CADM1	65	in gene	ActReg chr11 #3512	1	1	0
3513	11	115,529,992	115,530,479	487	1	2.333	7	13.8	6	14	18	1	0	0				ActReg chr11 #3513	0	0	1
3514	11	115,572,111	115,572,413	302	1	2.667	2.444	11.222	4	6	14	0	0	0				ActReg chr11 #3514	0	0	1
3515	11	115,587,426	115,588,239	813	1	7.12	11.84	6.64	13	19	12	0	0	0				ActReg chr11 #3515	0	1	0
3516	11	115,740,478	115,740,959	481	1	3.667	6.267	10.8	6	9	18	0	0	0				ActReg chr11 #3516	0	0	1
3517	11	115,812,112	115,812,855	743	1	12.478	10.826	2.05	17	16	6	0	0	0				ActReg chr11 #3517	1	0	0
3518	11	116,433,483	116,434,776	1,293	1	12.175	12	3.564	18	18	8	0	0	0				ActReg chr11 #3518	1	0	0
3519	11	116,476,175	116,477,038	863	2	12.407	16.518	4.407	26	32	7	0	0	0				ActReg chr11 #3519	1	1	0
3520	11	116,563,162	116,563,666	504	1	5.125	5	11.625	6	8	18	0	0	0				ActReg chr11 #3520	0	0	1
3521	11	116,706,397	116,706,859	462	1	4.267	4.733	10.733	6	8	18	1	1	3	APOC3, APOA1, SIK3	6004, 1710, 262365	downstream, in gene, downstream	ActReg chr11 #3521	0	0	1
3522	11	116,897,488	116,898,131	643	1	11.6	8.2	1.167	21	13	2	0	0	1	SIK3	71,184	in gene	ActReg chr11 #3522	1	0	0
3523	11	116,943,180	116,943,829	649	1	11.35	7	1.5	16	10	3	0	0	1	SIK3	25,489	in gene	ActReg chr11 #3523	1	0	0
3524	11	117,048,859	117,050,184	1,325	3	17.548	21.929	9.757	61	69	24	1	1	2	PAFAH1B2, SIDT2	34521, -418	downstream, upstream	ActReg chr11 #3524	1	1	1
3525	11	117,102,319	117,103,588	1,269	2	18.375	17.075	2.933	53	54	7	2	2	2	PCSK7, RNF214	-142, -451	upstream, upstream	ActReg chr11 #3525	1	1	0
3526	11	117,186,810	117,187,478	668	3	11.667	13.048	8.2	21	20	13	1	1	1	BACE1	-172	upstream	ActReg chr11 #3526	1	1	1
3527	11	117,198,282	117,199,112	830	1	5.962	11.039	7.808	10	18	11	1	1	2	CEP164, LOC100129201	126, 8650	in gene, downstream	ActReg chr11 #3527	0	1	0
3528	11	117,329,307	117,329,671	364	1	2.417	2.667	12.667	4	4	17	0	0	1	DSCAML1	338,487	in gene	ActReg chr11 #3528	0	0	1
3529	11	117,396,480	117,396,815	335	1	1.727	3.727	11.454	3	6	15	0	0	1	DSCAML1	271,329	in gene	ActReg chr11 #3529	0	0	1
3530	11	117,467,649	117,468,560	911	2	9.593	10.607	3.071	17	16	5	0	0	1	DSCAML1	199,872	in gene	ActReg chr11 #3530	1	1	0
3531	11	117,619,508	117,619,914	406	1	2.692	3	11.077	4	5	17	0	0	1	DSCAML1	48,265	in gene	ActReg chr11 #3531	0	0	1
3532	11	118,187,170	118,187,940	770	1	9.667	12.75	4.292	16	19	7	0	0	1	CD3E	12,260	downstream	ActReg chr11 #3532	0	1	0
3533	11	118,229,880	118,230,604	724	1	6.913	14.565	5.524	11	30	11	1	1	2	CD3G, UBE4A	15183, -60	downstream, upstream	ActReg chr11 #3533	0	1	0
3534	11	118,271,624	118,272,912	1,288	2	10.825	11.4	8.725	17	16	14	1	1	2	UBE4A, ATP5L	41966, 164	downstream, in gene	ActReg chr11 #3534	1	1	0
3535	11	118,305,241	118,305,892	651	1	8.667	12.143	3.667	12	21	6	1	2	2	MGC13053, MLL	355, -1639	in gene, upstream	ActReg chr11 #3535	0	1	0
3536	11	118,305,925	118,307,354	1,429	2	14.068	14.227	7.029	32	28	16	1	2	2	MGC13053, MLL	-718, -566	upstream, upstream	ActReg chr11 #3536	1	1	0
3537	11	118,404,932	118,405,325	393	1	8.083	6.083	11.333	12	10	17	0	0	4	MLL, TTC36, TMEM25, C11orf60	97923, 6918, 3325, 31663	downstream, downstream, in gene, downstream	ActReg chr11 #3537	0	0	1
3538	11	118,478,663	118,479,745	1,082	3	13.029	11.941	8.941	26	17	19	1	1	2	ARCN1, PHLDB1	36102, 1991	downstream, in gene	ActReg chr11 #3538	1	1	1
3539	11	118,560,644	118,561,339	695	1	12.619	7.333	6.095	21	13	11	0	0	0				ActReg chr11 #3539	1	0	0
3540	11	118,661,843	118,662,382	539	1	5.941	12.177	9.176	10	18	13	1	1	1	DDX6	-140	upstream	ActReg chr11 #3540	0	1	0
3541	11	118,772,694	118,773,069	375	1	1.6	3.75	11	2	7	17	0	0	2	CXCR5, BCL9L	18340, 8732	downstream, in gene	ActReg chr11 #3541	0	0	1
3542	11	118,790,225	118,791,056	831	1	10.962	11.808	5.385	19	22	8	0	0	1	BCL9L	-9,027	upstream	ActReg chr11 #3542	0	1	0
3543	11	118,796,542	118,797,107	565	1	14.889	10.778	3.889	23	18	8	1	0	0				ActReg chr11 #3543	1	0	0
3544	11	118,798,663	118,801,141	2,478	3	11.61	13.454	5.818	25	24	17	0	0	0				ActReg chr11 #3544	1	1	1
3545	11	118,809,116	118,810,060	944	2	8.533	10.9	3.533	15	18	5	0	0	0				ActReg chr11 #3545	1	1	0
3546	11	118,827,437	118,828,119	682	1	4.619	4.476	11.191	10	7	17	0	1	1	UPK2	770	in gene	ActReg chr11 #3546	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3547	11	118,868,260	118,869,215	955	1	8.483	11.448	8.69	14	17	14	1	1	1	CCDC84	-115	upstream	ActReg chr11 #3547	0	1	0
3548	11	118,889,182	118,890,049	867	1	9.429	9.536	14.786	14	14	26	1	2	4	CCDC84, RPS25, TRAPPC4, SLC37A4	20763, -558, 374, 12001	downstream, upstream, in gene, downstream	ActReg chr11 #3548	0	0	1
3549	11	118,938,055	118,938,970	915	2	9.321	13.536	7.5	16	22	16	1	1	1	VPS11	19	in gene	ActReg chr11 #3549	0	1	1
3550	11	118,955,238	118,955,899	661	1	12.6	11	7.35	18	18	10	1	1	3	VPS11, HMBS, H2AFX	17075, -19, 10609	downstream, upstream, downstream	ActReg chr11 #3550	1	0	0
3551	11	118,964,769	118,965,438	669	1	6.7	8.7	14.35	14	13	22	1	1	3	HMBS, H2AFX, DPAGT1	9516, 1074, 7682	downstream, in gene, downstream	ActReg chr11 #3551	0	0	1
3552	11	118,965,553	118,966,705	1,152	3	13.306	13.333	10.111	26	22	20	1	1	3	HMBS, H2AFX, DPAGT1	10542, 48, 6656	downstream, in gene, downstream	ActReg chr11 #3552	1	1	1
3553	11	118,972,062	118,973,525	1,463	2	11.457	14.283	5.409	19	25	11	1	3	4	HMBS, H2AFX, DPAGT1, C2CD2L	17206, -6616, -8, -5300	downstream, upstream, upstream, upstream	ActReg chr11 #3553	1	1	0
3554	11	119,089,169	119,089,668	499	2	9.938	9.4	2.917	15	17	5	0	0	1	CBL	12,428	in gene	ActReg chr11 #3554	1	1	0
3555	11	119,187,474	119,187,968	494	1	8.583	9	11.667	13	13	18	1	1	2	CBL, MCAM	110681, 169	downstream, in gene	ActReg chr11 #3555	0	0	1
3556	11	119,191,609	119,192,252	643	1	11.65	10.1	6.15	17	16	9	1	1	1	MCAM	-4,090	upstream	ActReg chr11 #3556	1	0	0
3557	11	119,204,752	119,205,735	983	2	8.419	10.613	6.833	15	17	20	1	1	3	RNF26, MFRP, C1QTNF5	6, 12140, 12140	in gene, downstream, downstream	ActReg chr11 #3557	0	1	1
3558	11	119,363,629	119,365,515	1,886	2	14.649	21.305	4.136	51	60	8	0	0	1	LOC100499227	112,084	in gene	ActReg chr11 #3558	1	1	0
3559	11	119,389,214	119,390,099	885	2	14.107	14.929	4.095	27	35	8	0	0	0				ActReg chr11 #3559	1	1	0
3560	11	119,438,653	119,439,891	1,238	1	5.359	10.154	4.265	11	20	8	0	0	0				ActReg chr11 #3560	0	1	0
3561	11	119,505,046	119,505,500	454	1	3.692	1.571	13	5	3	19	0	0	1	PVRL1	94,162	downstream	ActReg chr11 #3561	0	0	1
3562	11	119,599,799	119,600,534	735	1	8	15.043	4.565	14	24	10	1	1	2	PVRL1, LOC100507077	-731, -10255	upstream, upstream	ActReg chr11 #3562	0	1	0
3563	11	119,644,469	119,645,867	1,398	2	13.454	14.25	4.049	30	32	7	0	0	0				ActReg chr11 #3563	1	1	0
3564	11	120,081,279	120,082,458	1,179	2	10	11.027	5.111	24	20	10	1	1	1	OAF	121	in gene	ActReg chr11 #3564	1	1	0
3565	11	120,088,292	120,089,317	1,025	1	11.5	13.188	4.714	21	19	10	0	0	1	OAF	7,057	in gene	ActReg chr11 #3565	0	1	0
3566	11	120,175,822	120,176,257	435	1	5.143	3.286	10.429	7	5	16	0	0	1	POU2F3	65,088	in gene	ActReg chr11 #3566	0	0	1
3567	11	120,195,534	120,196,557	1,023	2	18.25	21.469	3.12	37	45	6	1	1	2	POU2F3, TMEM136	85094, 29	downstream, in gene	ActReg chr11 #3567	1	1	0
3568	11	120,302,691	120,303,322	631	1	10.368	4.222	1.583	18	8	3	0	0	1	ARHGEF12	95,060	in gene	ActReg chr11 #3568	1	0	0
3569	11	120,434,744	120,435,402	658	1	6.048	4.286	12.714	10	9	17	1	0	0				ActReg chr11 #3569	0	0	1
3570	11	120,485,028	120,485,447	419	1	4.231	1.615	10.385	6	3	16	0	0	0				ActReg chr11 #3570	0	0	1
3571	11	120,953,263	120,953,787	524	1	7.125	12.312	1.75	10	20	2	0	0	1	TBCEL	58,722	in gene	ActReg chr11 #3571	0	1	0
3572	11	121,964,421	121,964,742	321	1	6.9	12.1	1	11	16	1	0	0	3	LOC100507145, LOC399959, MIR12551	328998, 109189, 5971	in gene, in gene, downstream	ActReg chr11 #3572	0	1	0
3573	11	122,012,348	122,012,831	483	1	10.267	5.867	2.733	17	8	5	0	0	3	LOC100507145, LOC399959, MIRLET7A2	280990, 61181, 4712	in gene, in gene, downstream	ActReg chr11 #3573	1	0	0
3574	11	122,073,680	122,074,192	512	1	7.875	10.625	3.062	14	15	6	0	1	2	LOC100507145, LOC399959	219643, -166	in gene, upstream	ActReg chr11 #3574	0	1	0
3575	11	122,144,184	122,144,798	614	1	10.474	9.053	2	19	17	4	0	0	1	LOC100507145	149,088	in gene	ActReg chr11 #3575	1	0	0
3576	11	122,451,855	122,452,412	557	1	10.118	12.294	2.647	16	21	4	0	0	0				ActReg chr11 #3576	0	1	0
3577	11	122,526,700	122,527,607	907	1	8.071	10.857	7.769	13	14	13	1	1	1	UBASH3B	755	in gene	ActReg chr11 #3577	0	1	0
3578	11	122,574,552	122,575,156	604	1	7.684	10.947	2.684	12	21	5	0	0	1	UBASH3B	48,456	in gene	ActReg chr11 #3578	0	1	0
3579	11	122,851,618	122,853,041	1,423	2	13.454	14.5	3	29	30	6	1	1	1	BSX	50	in gene	ActReg chr11 #3579	1	1	0
3580	11	122,932,314	122,933,231	917	1	9.862	9.966	13.724	15	14	22	1	4	5	HSPA8, SNORD14E, SNORD14D, SNORD14C, ASAM	72, -3908, -3069, -2642, 133235	in gene, upstream, upstream, upstream, downstream	ActReg chr11 #3580	0	0	1
3581	11	123,059,378	123,059,894	516	1	11.562	9.25	2.357	16	14	4	0	0	1	ASAM	6,371	in gene	ActReg chr11 #3581	1	0	0
3582	11	123,524,188	123,525,411	1,223	2	11.359	14.82	6.923	28	27	13	1	1	1	SCN3B	516	in gene	ActReg chr11 #3582	1	1	0
3583	11	123,611,819	123,612,761	942	2	9.069	10.483	7.345	18	18	12	1	1	1	ZNF202	73	in gene	ActReg chr11 #3583	1	1	0
3584	11	123,940,000	123,940,614	614	1	9.95	5.15	3.842	16	9	8	0	0	0				ActReg chr11 #3584	1	0	0
3585	11	124,041,615	124,042,085	470	1	10.467	8.8	8.6	14	13	12	0	0	0				ActReg chr11 #3585	1	0	0
3586	11	124,471,935	124,472,627	692	2	14.136	13.954	2.4	28	34	4	0	0	1	PANX3	-9,172	upstream	ActReg chr11 #3586	1	1	0
3587	11	124,492,330	124,493,082	752	2	11.304	11.043	8.565	16	18	13	1	1	2	PANX3, TBRG1	11253, -36	downstream, upstream	ActReg chr11 #3587	1	1	0
3588	11	124,669,441	124,669,932	491	1	6.667	9.933	8.2	13	17	13	1	2	3	C11orf61, UNQ565, LOC100507283	613, -9721, -638	in gene, upstream, upstream	ActReg chr11 #3588	0	1	0
3589	11	124,670,076	124,670,598	522	1	8.941	11.706	3.812	12	16	8	1	2	2	C11orf61, LOC100507283	-38, 13	upstream, in gene	ActReg chr11 #3589	0	1	0
3590	11	124,761,273	124,761,694	421	1	5	2.538	11.462	6	4	17	0	0	2	ROBO3, ROBO4	26178, 6348	downstream, in gene	ActReg chr11 #3590	0	0	1
3591	11	124,823,661	124,824,489	828	2	10.115	9.231	7.769	16	17	10	1	1	1	CCDC15	58	in gene	ActReg chr11 #3591	1	1	0
3592	11	124,940,529	124,941,379	850	1	8.667	12.37	5.926	14	18	12	0	0	1	SLC37A2	7,941	in gene	ActReg chr11 #3592	0	1	0
3593	11	124,945,413	124,946,288	875	1	6.333	12.407	5.185	10	17	8	0	0	1	SLC37A2	12,857	in gene	ActReg chr11 #3593	0	1	0
3594	11	125,104,692	125,105,781	1,089	1	7.706	10.471	2.765	14	15	7	0	0	1	PKNOX2	70,677	in gene	ActReg chr11 #3594	0	1	0
3595	11	125,132,856	125,134,170	1,314	2	9.78	12.488	6.195	19	18	12	0	0	1	PKNOX2	98,954	in gene	ActReg chr11 #3595	1	1	0
3596	11	125,462,263	125,463,703	1,440	2	10.024	12.044	4.953	17	28	14	1	1	2	EI24, STT3A	23685, 244	downstream, in gene	ActReg chr11 #3596	1	1	0
3597	11	125,495,216	125,496,087	871	2	11.111	14.37	11.667	16	23	25	1	1	2	STT3A, CHEK1	32912, 615	downstream, in gene	ActReg chr11 #3597	0	1	1
3598	11	125,932,609	125,933,302	693	2	16.952	13.381	4.846	36	27	9	1	1	1	CDON	232	in gene	ActReg chr11 #3598	1	1	0
3599	11	126,080,929	126,082,033	1,104	1	8.294	14.353	6.029	15	25	10	1	2	2	RPUSD4, FAM118B	106, -138	in gene, upstream	ActReg chr11 #3599	0	1	0
3600	11	126,138,488	126,139,369	881	2	9.893	12.893	8.929	17	24	11	1	2	3	FAM118B, SRPR, FOXRED1	57309, -51, -127	downstream, upstream, upstream	ActReg chr11 #3600	1	1	0
3601	11	126,173,426	126,174,340	914	2	13.241	7.759	9.103	23	15	15	1	1	2	TIRAP, DCPS	20901, 236	downstream, in gene	ActReg chr11 #3601	1	0	1
3602	11	126,223,227	126,224,116	889	1	10.393	7.286	6.217	18	13	10	0	2	3	DCPS, FLJ39051, ST3GAL4	50024, 1811, -2425	downstream, in gene, upstream	ActReg chr11 #3602	1	0	0
3603	11	126,338,493	126,339,017	524	1	3	3.941	10.529	4	6	13	0	0	1	KIRREL3	532,011	in gene	ActReg chr11 #3603	0	0	1
3604	11	126,413,372	126,416,657	3,285	4	18.126	21.087	3.214	63	68	8	0	0	1	KIRREL3	455,752	in gene	ActReg chr11 #3604	1	1	0
3605	11	126,430,742	126,432,174	1,432	2	14.578	17.644	2.882	32	30	8	0	0	1	KIRREL3	439,308	in gene	ActReg chr11 #3605	1	1	0
3606	11	126,462,510	126,463,633	1,123	1	9.514	11.257	5.2	16	15	8	0	0	1	KIRREL3	407,695	in gene	ActReg chr11 #3606	0	1	0
3607	11	126,464,703	126,465,189	486	1	3.5	3.25	11.688	5	7	18	0	0	1	KIRREL3	405,820	in gene	ActReg chr11 #3607	0	0	1
3608	11	126,588,019	126,588,617	598	1	12.947	11.579	3.158	24	17	5	0	0	1	KIRREL3	282,448	in gene	ActReg chr11 #3608	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3609	11	126,660,474	126,660,976	502	1	5.75	11.688	2.429	15	19	5	0	0	1	KIRREL3	210,041	in gene	ActReg chr11 #3609	0	1	0
3610	11	126,838,664	126,839,677	1,013	1	6.806	12.355	3.88	11	18	8	0	0	1	KIRREL3	31,596	in gene	ActReg chr11 #3610	0	1	0
3611	11	126,905,749	126,906,654	905	1	9.536	13.179	2.333	17	20	4	0	0	0				ActReg chr11 #3611	0	1	0
3612	11	126,968,258	126,969,079	821	2	12	10.56	3.32	20	19	5	0	0	0				ActReg chr11 #3612	1	1	0
3613	11	127,909,254	127,910,049	795	2	10.16	8.64	2.13	18	20	4	0	0	0				ActReg chr11 #3613	1	1	0
3614	11	127,931,221	127,931,672	451	1	7.5	10.929	2.857	10	13	5	0	0	0				ActReg chr11 #3614	0	1	0
3615	11	128,079,980	128,080,815	835	1	12.923	7.038	1.167	21	9	2	0	0	0				ActReg chr11 #3615	1	0	0
3616	11	128,085,124	128,085,698	574	1	3.111	2.556	12.944	4	5	19	0	0	0				ActReg chr11 #3616	0	0	1
3617	11	128,158,210	128,159,422	1,212	3	11.324	12.486	2.129	21	22	5	0	0	0				ActReg chr11 #3617	1	1	0
3618	11	128,234,761	128,235,523	762	2	16.792	16.625	3.211	38	31	6	0	0	0				ActReg chr11 #3618	1	1	0
3619	11	128,391,916	128,393,058	1,142	1	8.333	11.528	2.794	14	21	6	1	0	1	ETS1	64,966	in gene	ActReg chr11 #3619	0	1	0
3620	11	128,556,715	128,557,152	437	1	6.643	9.643	11.786	9	15	18	0	1	2	LOC100507392, FLI1	8985, -5456	downstream, upstream	ActReg chr11 #3620	0	0	1
3621	11	129,013,112	129,013,748	636	1	10.9	8.25	3.077	23	19	5	0	0	1	RICS	48,663	in gene	ActReg chr11 #3621	1	0	0
3622	11	129,321,195	129,321,798	603	1	9.526	12.105	1.684	16	20	3	0	0	1	BARX2	75,615	in gene	ActReg chr11 #3622	0	1	0
3623	11	129,399,999	129,400,919	920	1	6.483	10.241	2.778	13	15	5	0	0	0				ActReg chr11 #3623	0	1	0
3624	11	129,508,974	129,509,670	696	1	7.273	12.227	2.417	13	18	4	0	0	0				ActReg chr11 #3624	0	1	0
3625	11	129,512,787	129,513,751	964	1	9.667	11.367	3.1	15	18	7	0	0	0				ActReg chr11 #3625	0	1	0
3626	11	129,872,152	129,873,121	969	1	11.355	9.097	7.067	20	19	12	1	2	2	PRDM10, NCRNA00167	94, 117	in gene, in gene	ActReg chr11 #3626	1	0	0
3627	11	130,318,413	130,318,820	407	1	10.923	6.538	11.615	16	13	18	1	1	1	ADAMTS15	-253	upstream	ActReg chr11 #3627	0	0	1
3628	11	130,453,676	130,454,270	594	1	8.944	11.278	4.111	12	16	7	0	0	0				ActReg chr11 #3628	0	1	0
3629	11	130,500,864	130,501,478	614	1	10.45	6.9	2.4	19	13	4	0	0	0				ActReg chr11 #3629	1	0	0
3630	11	130,607,527	130,608,232	705	1	8.545	12.773	3.273	12	17	6	0	0	0				ActReg chr11 #3630	0	1	0
3631	11	130,717,531	130,718,074	543	1	11.118	7.647	1.941	22	14	4	0	0	1	LOC100507431	14,200	in gene	ActReg chr11 #3631	1	0	0
3632	11	130,785,929	130,786,813	884	2	12	12.296	4.667	20	23	12	1	1	1	SNX19	11	in gene	ActReg chr11 #3632	1	1	0
3633	11	131,934,180	131,935,508	1,328	2	11.829	12.463	1.462	18	22	2	0	0	1	NTM	694,473	in gene	ActReg chr11 #3633	1	1	0
3634	11	132,046,765	132,047,953	1,188	2	8.676	12.838	2.579	27	26	5	0	0	1	NTM	806,988	in gene	ActReg chr11 #3634	1	1	0
3635	11	132,187,969	132,189,024	1,055	2	18.151	25.091	1.474	49	65	3	0	0	1	NTM	948,125	in gene	ActReg chr11 #3635	1	1	0
3636	11	132,783,761	132,784,936	1,175	1	6.278	12.243	3.762	12	21	7	0	0	2	OPCML, LOC100128095	618055, 257377	in gene, in gene	ActReg chr11 #3636	0	1	0
3637	11	133,067,202	133,067,961	759	2	11.609	14.043	3.381	24	32	5	0	0	2	OPCML, LOC100128095	334822, 540610	in gene, in gene	ActReg chr11 #3637	1	1	0
3638	11	133,213,938	133,214,414	476	1	9.867	10.067	3.2	15	16	6	0	0	2	OPCML, LOC100128095	188227, 687205	in gene, in gene	ActReg chr11 #3638	1	0	0
3639	11	133,790,811	133,791,374	563	1	2.722	3.611	12.778	4	7	21	1	0	2	LOC646543, IGSF9B	-8835, 35788	upstream, in gene	ActReg chr11 #3639	0	0	1
3640	11	133,804,322	133,805,287	965	1	9.7	14.067	8.433	21	24	15	0	0	1	IGSF9B	22,076	in gene	ActReg chr11 #3640	0	1	0
3641	11	133,906,892	133,908,020	1,128	1	8.286	10.829	4.438	13	20	8	1	0	1	LOC100128239	5,289	in gene	ActReg chr11 #3641	0	1	0
3642	11	134,093,461	134,094,890	1,429	1	9.422	11.622	7.829	17	17	17	1	2	2	NCAPD3, VPS26B	251, -386	in gene, upstream	ActReg chr11 #3642	0	1	0
3643	11	134,095,259	134,095,811	552	1	8.056	8.556	11.944	15	13	18	1	2	2	NCAPD3, VPS26B	-1109, 974	upstream, in gene	ActReg chr11 #3643	0	0	1
3644	11	134,122,996	134,123,753	757	3	13.792	11.75	8.708	23	22	15	2	2	3	VPS26B, THYN1, ACAD8	28813, -114, -60	downstream, upstream, upstream	ActReg chr11 #3644	1	1	1
3645	11	134,288,159	134,288,990	831	2	9.04	12.346	3.85	15	27	7	0	1	1	B3GAT1	-6,762	upstream	ActReg chr11 #3645	1	1	0
3646	11	134,344,007	134,344,522	515	1	3.312	2.562	12.438	4	4	21	0	0	1	LOC283177	37,888	in gene	ActReg chr11 #3646	0	0	1
3647	11	134,346,158	134,346,905	747	2	11.143	12.304	5.6	23	23	10	0	0	1	LOC283177	40,155	in gene	ActReg chr11 #3647	1	1	0
3648	11	134,353,107	134,353,513	406	1	1	2.083	10.385	1	3	16	0	0	1	LOC283177	46,934	in gene	ActReg chr11 #3648	0	0	1
3649	11	134,401,128	134,401,586	458	1	4.5	4.357	11.071	6	6	16	0	0	0				ActReg chr11 #3649	0	0	1
3650	11	134,534,614	134,535,106	492	1	4.5	7.938	13.062	6	13	19	1	0	0				ActReg chr11 #3650	0	0	1
3651	11	134,713,328	134,713,801	473	1	1.533	3.333	11.8	3	5	19	0	0	0				ActReg chr11 #3651	0	0	1
3652	11	134,818,898	134,819,638	740	2	10.261	16.391	2.87	17	32	6	0	0	0				ActReg chr11 #3652	1	1	0
3653	11	134,897,243	134,897,840	597	1	6.105	11.105	0	10	20	0	0	0	0				ActReg chr11 #3653	0	1	0
3654	11	134,921,324	134,921,581	257	1	3.375	1.875	12.25	5	3	15	0	0	0				ActReg chr11 #3654	0	0	1
3655	11	134,945,666	134,945,951	285	1	2.5	5.875	11.75	4	8	14	0	0	0				ActReg chr11 #3655	0	0	1
3656	12	322,235	322,594	359	1	2.417	5.75	11.833	5	8	14	0	1	2	SLC6A12, SLC6A13	957, 49625	in gene, downstream	ActReg chr12 #3656	0	0	1
3657	12	498,329	499,176	847	1	8.778	12.037	4.37	13	21	8	1	2	2	KDM5A, CCDC77	-132, 236	upstream, in gene	ActReg chr12 #3657	0	1	0
3658	12	678,839	679,977	1,138	2	13.056	9.444	8.889	20	15	18	1	0	2	B4GALNT3, NINJ2	109865, 93347	downstream, in gene	ActReg chr12 #3658	1	0	1
3659	12	695,698	696,148	450	1	3.071	2.786	11	5	5	17	0	0	1	NINJ2	76,832	in gene	ActReg chr12 #3659	0	0	1
3660	12	741,081	741,879	798	1	10.32	4.64	3.28	14	9	8	0	1	2	NINJ2, LOC100049716	31275, 1423	in gene, in gene	ActReg chr12 #3660	1	0	0
3661	12	861,256	861,910	654	1	12	9.1	5.882	26	15	13	1	1	1	WNK1	-506	upstream	ActReg chr12 #3661	1	0	0
3662	12	862,306	863,319	1,013	2	10.097	8.065	11.724	16	16	23	1	1	1	WNK1	723	in gene	ActReg chr12 #3662	1	0	1
3663	12	1,058,260	1,059,357	1,097	1	9.176	12.412	9.969	18	18	15	1	1	1	RAD52	55	in gene	ActReg chr12 #3663	0	1	0
3664	12	1,325,403	1,325,785	382	1	10.833	2.833	0	18	5	0	0	0	1	ERC1	225,190	in gene	ActReg chr12 #3664	1	0	0
3665	12	1,701,877	1,702,613	736	1	11.826	9.957	7.478	17	14	11	1	1	1	FBXL14	1,086	in gene	ActReg chr12 #3665	1	0	0
3666	12	1,702,912	1,703,327	415	1	6.308	6.917	12.154	13	11	19	1	1	1	FBXL14	212	in gene	ActReg chr12 #3666	0	0	1
3667	12	1,714,224	1,715,377	1,153	2	10.771	10.75	2.844	16	17	6	0	0	0				ActReg chr12 #3667	1	1	0
3668	12	1,936,891	1,937,422	531	1	4.941	6.412	13.588	7	8	18	0	0	2	CACNA2D4, LRTM2	90714, 7723	in gene, in gene	ActReg chr12 #3668	0	0	1
3669	12	1,939,938	1,940,823	885	1	10.333	18.963	6.481	20	36	11	0	0	2	CACNA2D4, LRTM2	87490, 10947	in gene, in gene	ActReg chr12 #3669	0	1	0
3670	12	1,944,882	1,945,479	597	1	5	3.111	11.947	10	7	16	0	0	2	CACNA2D4, LRTM2	82690, 15747	in gene, in gene	ActReg chr12 #3670	0	0	1
3671	12	2,017,204	2,017,749	545	1	3.235	3.533	11.765	4	5	15	1	0	1	CACNA2D4	10,394	in gene	ActReg chr12 #3671	0	0	1
3672	12	2,113,041	2,114,118	1,077	2	16	20.677	4.735	42	48	12	1	1	1	DCP1B	98	in gene	ActReg chr12 #3672	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3673	12	2,238,123	2,238,724	601	1	7.211	10.947	3.533	12	16	7	0	0	1	CACNA1C	76,007	in gene	ActReg chr12 #3673	0	1	0
3674	12	2,457,290	2,457,776	486	1	4.154	4.667	12.333	8	6	18	0	0	1	CACNA1C	295,117	in gene	ActReg chr12 #3674	0	0	1
3675	12	2,861,457	2,862,938	1,481	2	26.065	25.087	6.429	90	92	16	1	0	1	LOC283440	18,638	downstream	ActReg chr12 #3675	1	1	0
3676	12	2,999,458	3,000,536	1,078	2	8.273	11.515	9.879	15	22	22	1	1	2	C12orf32, TULP3	13632, -36	downstream, upstream	ActReg chr12 #3676	0	1	1
3677	12	3,067,477	3,068,156	679	1	7.952	12	4.476	18	18	10	1	1	1	TEAD4	-662	upstream	ActReg chr12 #3677	0	1	0
3678	12	3,128,119	3,128,693	574	1	5.444	6.611	13.611	11	11	20	0	0	1	TEAD4	59,928	in gene	ActReg chr12 #3678	0	0	1
3679	12	3,246,092	3,246,676	584	1	2.714	4.111	11.944	4	8	17	0	0	1	TSPAN9	59,863	in gene	ActReg chr12 #3679	0	0	1
3680	12	3,378,784	3,379,349	565	1	1.833	4.667	10.944	3	10	15	0	0	1	TSPAN9	192,545	in gene	ActReg chr12 #3680	0	0	1
3681	12	3,413,440	3,414,395	955	1	9.533	12.633	6.567	15	18	14	0	1	1	LOC100128253	-4,527	upstream	ActReg chr12 #3681	0	1	0
3682	12	3,441,211	3,441,845	634	1	10.45	10.75	1.769	18	18	3	0	0	0				ActReg chr12 #3682	0	1	0
3683	12	3,562,394	3,562,868	474	1	5.8	4.267	10.467	9	6	15	0	0	0				ActReg chr12 #3683	0	0	1
3684	12	3,601,116	3,602,012	896	1	7.962	14.036	9.5	15	22	17	1	2	2	LOC100129223, PRMT8	421, 1139	in gene, in gene	ActReg chr12 #3684	0	1	0
3685	12	3,861,837	3,862,323	486	1	7.933	8.4	11.067	10	15	18	1	1	1	EFCAB4B	286	in gene	ActReg chr12 #3685	0	0	1
3686	12	4,380,087	4,380,660	573	1	4.067	4.267	11.056	7	6	16	1	1	1	CCND2	-2,529	upstream	ActReg chr12 #3686	0	0	1
3687	12	4,381,796	4,382,237	441	1	4	2.538	10.538	6	5	18	1	1	1	CCND2	-886	upstream	ActReg chr12 #3687	0	0	1
3688	12	4,647,344	4,648,260	916	2	10.724	9.897	5.069	16	14	10	1	2	2	C12orf4, RAD51AP1	-165, -148	upstream, upstream	ActReg chr12 #3688	1	1	0
3689	12	4,713,756	4,714,447	691	1	7.182	10.318	6.045	12	16	9	0	0	1	DYRK4	14,857	in gene	ActReg chr12 #3689	0	1	0
3690	12	5,998,045	5,998,651	606	1	3.105	2.824	12	6	5	17	0	0	1	ANO2	57,050	in gene	ActReg chr12 #3690	0	0	1
3691	12	6,202,055	6,202,876	821	1	10.4	13.44	7.083	14	21	15	0	0	1	VWF	31,371	in gene	ActReg chr12 #3691	0	1	0
3692	12	6,276,811	6,277,546	735	1	12.783	14.174	3.087	19	27	5	0	0	0				ActReg chr12 #3692	0	1	0
3693	12	6,309,498	6,309,847	349	1	11.909	5.182	12.091	16	8	20	1	1	1	CD9	117	in gene	ActReg chr12 #3693	0	0	1
3694	12	6,338,515	6,339,319	804	1	8.48	11.84	2.957	13	19	5	0	0	1	CD9	29,362	in gene	ActReg chr12 #3694	0	1	0
3695	12	6,472,624	6,473,212	588	1	3.059	5.389	12.056	4	9	17	1	0	1	SCNN1A	13,605	in gene	ActReg chr12 #3695	0	0	1
3696	12	6,492,699	6,493,859	1,160	1	8.135	12.568	8.973	16	20	15	1	2	2	SCNN1A, LTBR	-6756, -78	upstream, upstream	ActReg chr12 #3696	0	1	0
3697	12	6,579,393	6,580,037	644	1	9.1	12	10.5	15	21	17	1	1	2	TAPBPL, VAMP1	18538, 128	downstream, in gene	ActReg chr12 #3697	0	0	1
3698	12	6,586,733	6,587,145	412	1	3.455	1.846	10.231	5	4	17	1	1	1	VAMP1	-7,096	upstream	ActReg chr12 #3698	0	0	1
3699	12	6,641,481	6,644,365	2,884	3	10.467	13.778	7.244	17	26	17	1	1	3	NCAPD2, GAPDH, IFFO1	39625, -734, 22326	downstream, upstream, downstream	ActReg chr12 #3699	1	1	1
3700	12	6,646,231	6,647,406	1,175	1	8.703	10.784	7.432	15	20	12	0	0	3	NCAPD2, GAPDH, IFFO1	43520, 3161, 18431	downstream, in gene, downstream	ActReg chr12 #3700	0	1	0
3701	12	6,648,976	6,649,815	839	1	5.5	9.577	13.039	8	18	20	1	0	3	NCAPD2, GAPDH, IFFO1	46097, 5738, 15854	downstream, downstream, in gene	ActReg chr12 #3701	0	0	1
3702	12	6,676,989	6,677,697	708	1	8.348	11.217	12.87	11	15	21	1	1	2	NOP2, CHD4	137, 39208	in gene, downstream	ActReg chr12 #3702	0	0	1
3703	12	6,716,194	6,716,630	436	1	7.769	9.231	13	13	14	18	1	1	1	CHD4	139	in gene	ActReg chr12 #3703	0	0	1
3704	12	6,729,996	6,730,457	461	1	5.143	6.143	13.786	8	9	25	1	0	1	LPAR5	15,071	in gene	ActReg chr12 #3704	0	0	1
3705	12	6,772,001	6,772,910	909	2	10.071	9.679	5	19	19	8	1	1	2	ING4, ZNF384	-147, 26221	upstream, downstream	ActReg chr12 #3705	1	1	0
3706	12	6,798,106	6,799,131	1,025	2	11.969	12.312	3.607	20	18	8	1	1	2	ZNF384, C12orf53	58, 11194	in gene, downstream	ActReg chr12 #3706	1	1	0
3707	12	6,832,856	6,833,729	873	2	14.821	13.786	8.75	33	30	18	1	1	1	COPS7A	142	in gene	ActReg chr12 #3707	1	1	0
3708	12	6,861,906	6,862,814	908	1	9.5	12.821	10.393	17	18	17	2	1	1	MLF2	276	in gene	ActReg chr12 #3708	0	1	0
3709	12	6,937,805	6,938,967	1,162	2	12.306	11.306	7.371	20	16	15	1	1	3	CD4, GPR162, LEPREL2	39748, 7423, 814	downstream, downstream, in gene	ActReg chr12 #3709	1	1	0
3710	12	6,950,016	6,950,529	513	1	3.882	3.118	11.823	6	6	19	0	1	3	LEPREL2, GNB3, CDCA3	12700, 897, 10184	downstream, in gene, downstream	ActReg chr12 #3710	0	0	1
3711	12	6,961,166	6,962,100	934	2	15.552	19.517	5.345	35	46	10	1	2	3	GNB3, CDCA3, USP5	12258, -1177, 348	downstream, upstream, in gene	ActReg chr12 #3711	1	1	0
3712	12	6,976,586	6,977,023	437	1	7.231	8.231	11.077	10	12	19	1	1	3	USP5, TPI1, SPSB2	15519, 220, 5717	downstream, in gene, downstream	ActReg chr12 #3712	0	0	1
3713	12	6,982,271	6,983,326	1,055	1	10.636	13.182	5.545	17	21	16	1	1	3	USP5, TPI1, SPSB2	21513, 6214, -277	downstream, downstream, upstream	ActReg chr12 #3713	0	1	0
3714	12	6,999,704	7,000,568	864	2	10.296	8.926	3.667	17	17	7	1	0	0				ActReg chr12 #3714	1	1	0
3715	12	7,046,587	7,047,903	1,316	3	26.463	28.829	13.756	106	111	22	1	2	4	ATN1, RNU7, C12orf57, PTPN6	13619, -5734, -5958, -8495	in gene, upstream, upstream, upstream	ActReg chr12 #3715	1	1	1
3716	12	7,052,917	7,054,096	1,179	3	12.054	11.324	10.514	24	20	21	1	3	4	ATN1, RNU7, C12orf57, PTPN6	19880, 527, 303, -2234	downstream, downstream, in gene, upstream	ActReg chr12 #3716	1	1	1
3717	12	7,070,230	7,071,771	1,541	2	10.875	11.771	8.083	25	18	14	0	3	7	PTPN6, LOC100507644, MIR200C, MIR141, PHB2, SCARNA12, EMG1	15260, -1409, -1862, -2260, 8916, 5769, -8944	downstream, upstream, upstream, upstream, downstream, downstream, downstream, upstream	ActReg chr12 #3717	1	1	0
3718	12	7,076,739	7,077,212	473	1	5.643	4.857	12.571	7	9	21	0	2	8	PTPN6, LOC100507644, MIR200C, MIR141, PHB2, SCARNA12, EMG1, LPCAT3	21235, 4566, 4113, 3715, 2941, -206, -2969, 48867	downstream, downstream, downstream, downstream, in gene, upstream, upstream, downstream	ActReg chr12 #3718	0	0	1
3719	12	7,079,091	7,080,354	1,263	3	11.9	12.9	12.675	21	22	26	1	3	8	PTPN6, LOC100507644, MIR200C, MIR141, PHB2, SCARNA12, EMG1, LPCAT3	23982, 7313, 6860, 6462, 194, -2953, -222, 46120	downstream, downstream, downstream, downstream, in gene, upstream, upstream, downstream	ActReg chr12 #3719	1	1	1
3720	12	7,260,841	7,261,269	428	1	5.692	5.923	11.077	9	11	16	0	2	2	C1RL, UNQ2963	814, 151	in gene, in gene	ActReg chr12 #3720	0	0	1
3721	12	7,341,024	7,342,952	1,928	3	11.82	14.148	6.525	35	39	16	2	1	1	PEX5	229	in gene	ActReg chr12 #3721	1	1	1
3722	12	7,521,836	7,522,391	555	1	7.059	11.588	3.25	11	17	6	0	0	1	CD163L1	74,636	in gene	ActReg chr12 #3722	0	1	0
3723	12	8,167,349	8,168,057	708	1	8.409	14.546	2.571	17	31	6	0	0	0				ActReg chr12 #3723	0	1	0
3724	12	8,179,275	8,180,109	834	2	11.308	14.692	6.25	24	33	9	0	1	1	FOXJ2	-5,667	upstream	ActReg chr12 #3724	1	1	0
3725	12	8,184,798	8,185,256	458	1	7.4	12.667	4.333	12	24	7	1	1	1	FOXJ2	-332	upstream	ActReg chr12 #3725	0	1	0
3726	12	8,234,200	8,235,283	1,083	2	10.323	16.265	4.529	24	25	10	1	1	1	NECAP1	-66	upstream	ActReg chr12 #3726	1	1	0
3727	12	8,405,014	8,405,251	237	1	4.25	2.875	11.5	5	4	15	0	0	0				ActReg chr12 #3727	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3728	12	8,556,931	8,557,261	330	1	1	3.8	11	1	6	17	0	0	0				ActReg chr12 #3728	0	0	1
3729	12	9,090,547	9,090,970	423	1	3	8.769	0	5	12	0	0	0	2	PHC1, M6PR	23442, 11494	in gene, downstream	ActReg chr12 #3729	0	1	0
3730	12	9,102,026	9,103,034	1,008	2	9.032	12.774	6.774	21	19	11	1	1	2	PHC1, M6PR	35214, -278	downstream, upstream	ActReg chr12 #3730	1	1	0
3731	12	9,216,677	9,217,386	709	1	11.773	7.773	5.25	19	11	8	1	2	3	C12orf33, LOC144571, A2M	635, -742, 51527	in gene, upstream, downstream	ActReg chr12 #3731	1	0	0
3732	12	9,218,919	9,219,233	314	1	2.875	4.6	11.4	4	6	15	0	2	3	C12orf33, LOC144571, A2M	-1410, 1303, 49482	upstream, in gene, downstream	ActReg chr12 #3732	0	0	1
3733	12	9,487,560	9,488,070	510	1	4.5	4.625	13.312	7	6	21	0	0	0				ActReg chr12 #3733	0	0	1
3734	12	9,492,927	9,493,465	538	1	11.294	8.765	4.118	19	15	7	0	0	0				ActReg chr12 #3734	1	0	0
3735	12	9,516,779	9,517,738	959	1	9.167	11.033	3.1	14	15	5	0	0	0				ActReg chr12 #3735	0	1	0
3736	12	10,306,027	10,306,468	441	1	7.5	9.286	10.786	10	16	15	0	0	1	OLR1	18,543	downstream	ActReg chr12 #3736	0	0	1
3737	12	10,765,842	10,766,572	730	2	10.652	14.478	6.739	23	29	11	1	1	2	MAGOHB, STYK1	-24, 60684	upstream, downstream	ActReg chr12 #3737	1	1	0
3738	12	10,874,406	10,875,562	1,156	3	12.139	9.611	8.562	26	16	21	1	1	1	CSDA	969	in gene	ActReg chr12 #3738	1	1	1
3739	12	10,902,425	10,902,931	506	1	11.25	9.5	1.545	15	12	2	0	1	1	LOC100506226	-155	upstream	ActReg chr12 #3739	1	0	0
3740	12	11,323,778	11,324,360	582	1	10.444	9	11	13	14	15	1	2	2	PRR4, PRH1	144, 141	in gene, in gene	ActReg chr12 #3740	0	0	1
3741	12	11,652,725	11,654,647	1,924	4	20.617	26.483	9.3	91	116	22	1	0	0				ActReg chr12 #3741	1	1	1
3742	12	11,801,500	11,802,412	912	2	10	11.138	3.043	17	19	7	1	1	1	ETV6	-832	upstream	ActReg chr12 #3742	1	1	0
3743	12	11,872,496	11,873,145	649	1	8.15	11.3	3.3	13	16	6	0	0	1	ETV6	70,032	in gene	ActReg chr12 #3743	0	1	0
3744	12	12,161,679	12,163,916	2,237	2	9.343	11.143	3.5	22	18	8	0	0	0				ActReg chr12 #3744	1	1	0
3745	12	12,419,623	12,420,540	917	3	10.464	14.107	9.571	20	25	26	1	1	1	LRP6	-270	upstream	ActReg chr12 #3745	1	1	1
3746	12	12,509,704	12,510,681	977	2	12.933	8.567	10.033	26	18	17	1	3	3	MANSC1, LOH12CR2, LOH12CR1	-7023, -191, 172	upstream, upstream, in gene	ActReg chr12 #3746	1	0	1
3747	12	12,551,228	12,551,868	640	1	7.5	11.85	4.706	12	17	8	0	0	1	LOH12CR1	41,528	in gene	ActReg chr12 #3747	0	1	0
3748	12	12,764,394	12,765,051	657	1	11.4	9.25	7.65	21	14	12	1	1	1	CREBL2	-109	upstream	ActReg chr12 #3748	1	0	0
3749	12	12,836,848	12,838,272	1,424	2	13.333	12.222	1.688	21	27	4	0	0	1	GPR19	11,561	in gene	ActReg chr12 #3749	1	1	0
3750	12	12,869,834	12,870,647	813	2	10.56	10.04	7.24	18	24	13	1	1	2	CDKN1B, APOLD1	-62, -8611	upstream, upstream	ActReg chr12 #3750	1	1	0
3751	12	12,877,766	12,879,089	1,323	3	8.146	11.317	6.366	19	22	13	1	1	2	CDKN1B, APOLD1	8125, -424	downstream, upstream	ActReg chr12 #3751	1	1	1
3752	12	12,879,448	12,879,999	551	1	10.235	6.059	1.889	17	11	3	0	1	2	CDKN1B, APOLD1	9421, 872	downstream, in gene	ActReg chr12 #3752	1	0	0
3753	12	13,034,373	13,034,960	587	1	8.889	10.944	4.944	14	19	9	0	0	1	GPRC5A	-9,290	upstream	ActReg chr12 #3753	0	1	0
3754	12	13,043,437	13,044,786	1,349	3	11.214	11.905	9.054	16	18	19	1	1	1	GPRC5A	155	in gene	ActReg chr12 #3754	1	1	1
3755	12	13,153,375	13,153,904	529	1	10.882	9.059	9.706	16	17	12	2	1	1	HEBP1	-396	upstream	ActReg chr12 #3755	0	0	1
3756	12	13,196,945	13,197,987	1,042	2	11.242	12.576	8.242	20	24	16	1	1	1	KIAA1467	151	in gene	ActReg chr12 #3756	1	1	0
3757	12	13,254,378	13,255,456	1,078	1	7.882	13.677	3.559	19	26	7	1	1	1	GSG1	1,702	in gene	ActReg chr12 #3757	0	1	0
3758	12	13,880,319	13,881,127	808	2	7.962	10.385	0	16	16	0	0	0	1	GRIN2B	252,299	in gene	ActReg chr12 #3758	1	1	0
3759	12	14,410,373	14,411,297	924	2	16.759	13.69	3.31	37	35	6	0	0	0				ActReg chr12 #3759	1	1	0
3760	12	14,923,537	14,924,282	745	2	11.043	11.478	7.5	22	17	13	1	2	2	HIST4H4, H2AFJ	156, -3361	in gene, upstream	ActReg chr12 #3760	1	1	0
3761	12	15,431,842	15,432,697	855	1	8.577	13.577	4.038	16	22	7	0	0	0				ActReg chr12 #3761	0	1	0
3762	12	15,475,546	15,475,885	339	1	5.182	7.273	10.909	7	8	16	1	1	1	PTPRO	228	in gene	ActReg chr12 #3762	0	0	1
3763	12	15,841,130	15,841,755	625	1	7.947	12.21	3.737	11	20	7	0	0	1	EPS8	101,068	in gene	ActReg chr12 #3763	0	1	0
3764	12	15,854,092	15,854,676	584	1	6.833	10.389	1	10	15	1	0	0	1	EPS8	88,126	in gene	ActReg chr12 #3764	0	1	0
3765	12	15,910,735	15,911,246	511	1	9.125	10.375	2.062	16	20	5	0	0	1	EPS8	31,520	in gene	ActReg chr12 #3765	0	1	0
3766	12	15,941,797	15,942,945	1,148	3	7.667	10.694	10.194	14	16	16	1	1	1	EPS8	139	in gene	ActReg chr12 #3766	0	1	1
3767	12	16,034,643	16,035,996	1,353	3	11.357	11.786	7.667	20	18	16	1	1	1	STRAP	31	in gene	ActReg chr12 #3767	1	1	1
3768	12	17,250,601	17,250,776	175	1	5.2	9.4	13.6	6	12	16	0	0	0				ActReg chr12 #3768	0	0	1
3769	12	18,876,576	18,877,146	570	1	6.278	9.444	2	11	17	3	0	0	1	PLCZ1	14,057	in gene	ActReg chr12 #3769	0	1	0
3770	12	19,002,009	19,002,535	526	1	9.353	4.824	1	15	9	1	0	0	0				ActReg chr12 #3770	1	0	0
3771	12	19,592,434	19,593,268	834	2	5.038	10.808	8	7	17	18	1	1	1	AEBP2	243	in gene	ActReg chr12 #3771	0	1	1
3772	12	19,593,460	19,593,827	367	1	5.75	3.917	9.25	8	7	14	1	1	1	AEBP2	1,035	in gene	ActReg chr12 #3772	0	0	1
3773	12	19,864,828	19,865,540	712	2	13.609	15.391	1.824	27	30	4	0	0	0				ActReg chr12 #3773	1	1	0
3774	12	19,948,176	19,948,622	446	1	4.25	9.5	1.786	7	13	3	0	0	0				ActReg chr12 #3774	0	1	0
3775	12	20,255,131	20,255,521	390	1	2.5	5	11.385	4	6	15	0	0	1	LOC100506393	87,707	downstream	ActReg chr12 #3775	0	0	1
3776	12	20,365,409	20,366,212	803	2	13.04	9.6	2.375	19	23	4	0	0	0				ActReg chr12 #3776	1	1	0
3777	12	21,513,945	21,514,235	290	1	1.667	1.778	10.444	3	2	14	0	0	1	SLCO1A2	34,281	in gene	ActReg chr12 #3777	0	0	1
3778	12	21,810,416	21,810,864	448	1	9.286	10.571	11.357	17	13	15	1	1	1	LDHB	149	in gene	ActReg chr12 #3778	0	0	1
3779	12	22,199,190	22,199,465	275	1	6.444	7.667	11.778	8	10	16	1	1	1	CMAS	168	in gene	ActReg chr12 #3779	0	0	1
3780	12	22,488,594	22,489,049	455	1	9.286	7.429	1.273	16	11	3	1	1	1	ST8SIA1	-1,173	upstream	ActReg chr12 #3780	1	0	0
3781	12	22,589,807	22,590,593	786	1	8.24	12.04	2.92	14	20	6	0	0	0				ActReg chr12 #3781	0	1	0
3782	12	22,696,739	22,697,965	1,226	2	13.947	16.658	5.514	28	35	13	1	1	1	KIAA0528	100	in gene	ActReg chr12 #3782	1	1	0
3783	12	22,777,896	22,778,965	1,069	1	9.091	11.576	6.636	15	16	11	1	1	1	ETNK1	354	in gene	ActReg chr12 #3783	0	1	0
3784	12	22,875,058	22,875,654	596	1	4.421	9.737	2.167	9	17	4	0	0	0				ActReg chr12 #3784	0	1	0
3785	12	24,103,310	24,104,241	931	1	7.241	12.207	2	16	20	3	0	0	1	SOX5	611,605	in gene	ActReg chr12 #3785	0	1	0
3786	12	24,909,561	24,910,265	704	1	8.5	10.364	2.625	13	17	4	0	0	0				ActReg chr12 #3786	0	1	0
3787	12	25,403,566	25,404,636	1,070	2	12.333	11.697	3.321	22	22	8	0	1	1	KRAS	-247	upstream	ActReg chr12 #3787	1	1	0
3788	12	25,610,907	25,611,642	735	2	10.043	10.826	2.214	21	17	3	0	0	0				ActReg chr12 #3788	1	1	0
3789	12	25,619,721	25,620,362	641	1	8.85	10.6	2.167	12	18	4	0	0	1	IFLTD1	181,447	downstream	ActReg chr12 #3789	0	1	0
3790	12	26,037,167	26,037,897	730	1	2.5	5.391	11.13	8	9	16	0	0	0				ActReg chr12 #3790	0	0	1
3791	12	26,163,137	26,164,077	940	1	10.966	6.069	1.476	18	9	2	0	1	2	RASSF8, LOC100506529	36919, -1104	in gene, upstream	ActReg chr12 #3791	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3792	12	26,279,329	26,279,797	468	1	10.286	11.714	4	14	15	6	1	1	1	BHLHE41	-1,560	upstream	ActReg chr12 #3792	0	1	0
3793	12	26,427,427	26,428,179	752	1	9.261	11.348	3.95	18	19	7	0	0	0				ActReg chr12 #3793	0	1	0
3794	12	26,470,953	26,471,658	705	2	11.273	11.364	1.765	25	17	3	0	0	0				ActReg chr12 #3794	1	1	0
3795	12	26,844,345	26,845,000	655	1	11	8.905	1.615	21	16	2	0	0	1	ITPR2	141,459	in gene	ActReg chr12 #3795	1	0	0
3796	12	26,984,808	26,985,947	1,139	1	7.088	11	3.69	13	16	7	1	1	1	ITPR2	754	in gene	ActReg chr12 #3796	0	1	0
3797	12	27,091,174	27,091,681	507	1	8.875	13.188	11.938	13	22	17	1	2	2	C12orf11, FGFR1OP2	-173, 122	upstream, in gene	ActReg chr12 #3797	0	0	1
3798	12	27,175,353	27,175,940	587	1	6.158	10.21	6.211	10	17	10	1	1	2	TM7SF3, MED21	-8307, 163	upstream, in gene	ActReg chr12 #3798	0	1	0
3799	12	27,396,615	27,397,445	830	1	7.731	12.192	4.923	13	26	7	1	1	1	STK38L	-48	upstream	ActReg chr12 #3799	0	1	0
3800	12	27,397,472	27,397,944	472	1	4.133	10.933	3.733	5	17	6	1	1	1	STK38L	630	in gene	ActReg chr12 #3800	0	1	0
3801	12	27,863,403	27,864,222	819	2	14.52	12.72	8.96	28	25	13	1	1	1	MRPS35	106	in gene	ActReg chr12 #3801	1	1	0
3802	12	28,342,778	28,344,163	1,385	2	12.046	14.091	6.886	18	29	13	1	0	0				ActReg chr12 #3802	1	1	0
3803	12	28,756,084	28,756,483	399	1	6.077	11.538	2.111	9	18	3	0	0	0				ActReg chr12 #3803	0	1	0
3804	12	28,912,156	28,912,790	634	1	10.4	11.25	2.462	19	17	4	0	0	0				ActReg chr12 #3804	0	1	0
3805	12	29,265,153	29,265,753	600	1	5.167	10.5	6.167	7	15	9	0	0	0				ActReg chr12 #3805	0	1	0
3806	12	29,793,607	29,794,463	856	2	11.846	11.269	3.84	18	21	10	0	0	1	TMTC1	143,657	in gene	ActReg chr12 #3806	1	1	0
3807	12	29,894,372	29,895,034	662	2	9.55	10.8	1.5	18	21	2	0	0	1	TMTC1	42,989	in gene	ActReg chr12 #3807	1	1	0
3808	12	29,936,288	29,936,593	305	1	8.6	7.9	9.5	13	11	14	1	1	1	TMTC1	1,252	in gene	ActReg chr12 #3808	0	0	1
3809	12	30,179,645	30,180,105	460	1	9.933	6.667	1.333	15	10	2	0	0	0				ActReg chr12 #3809	1	0	0
3810	12	30,323,154	30,323,466	312	1	1	3.7	9.9	1	5	12	1	0	0				ActReg chr12 #3810	0	0	1
3811	12	30,354,021	30,354,542	521	1	2.625	2.429	13.125	4	4	16	1	0	0				ActReg chr12 #3811	0	0	1
3812	12	30,948,402	30,949,450	1,048	2	9.97	14	11.758	17	22	18	1	1	1	LOC100287314	949	in gene	ActReg chr12 #3812	0	1	1
3813	12	30,949,826	30,950,330	504	1	6.8	9.933	5.467	8	16	12	1	1	1	LOC100287314	2,101	in gene	ActReg chr12 #3813	0	1	0
3814	12	31,079,688	31,080,469	781	1	5.542	12.042	6.583	10	18	10	1	1	1	TSPAN11	240	in gene	ActReg chr12 #3814	0	1	0
3815	12	31,237,259	31,237,524	265	1	1	4.625	9.75	1	6	11	0	0	1	DDX11	10,612	in gene	ActReg chr12 #3815	0	0	1
3816	12	31,272,077	31,272,548	471	1	4.333	6.8	11.933	6	10	18	0	0	1	OVOS2	86,776	in gene	ActReg chr12 #3816	0	0	1
3817	12	31,477,476	31,478,509	1,033	3	10.688	11.344	8.375	15	14	20	1	2	2	FAM60A, FLJ13224	1167, 742	in gene, in gene	ActReg chr12 #3817	1	1	1
3818	12	31,478,656	31,479,292	636	1	8.75	11.5	9.05	12	17	12	1	2	2	FAM60A, FLJ13224	185, 1724	in gene, downstream	ActReg chr12 #3818	0	1	0
3819	12	31,811,765	31,812,903	1,138	2	22.222	23.333	4.971	50	51	10	0	0	1	C12orf72	12,240	in gene	ActReg chr12 #3819	1	1	0
3820	12	31,881,817	31,882,609	792	1	11.52	15.88	4.12	19	23	8	1	1	1	AMN1	-105	upstream	ActReg chr12 #3820	0	1	0
3821	12	31,902,009	31,902,542	533	1	11.118	8.353	3.8	18	13	6	0	0	0				ActReg chr12 #3821	1	0	0
3822	12	32,111,935	32,112,619	684	2	10.286	12.364	5.65	17	22	10	1	1	1	C12orf35	-76	upstream	ActReg chr12 #3822	1	1	0
3823	12	32,204,263	32,204,997	734	2	10.304	10.739	3.176	21	17	5	0	0	0				ActReg chr12 #3823	1	1	0
3824	12	32,242,433	32,242,999	566	1	9.824	11.412	1.75	13	21	2	0	0	0				ActReg chr12 #3824	0	1	0
3825	12	32,259,508	32,260,448	940	2	10.5	11.2	6.241	19	18	11	1	1	1	BICD1	-207	upstream	ActReg chr12 #3825	1	1	0
3826	12	32,552,203	32,553,010	807	1	8.56	13.16	5.44	14	21	12	1	0	0				ActReg chr12 #3826	0	1	0
3827	12	32,831,849	32,832,944	1,095	2	11.559	13.647	5.182	19	20	13	1	1	1	DNM1L	259	in gene	ActReg chr12 #3827	1	1	0
3828	12	32,908,082	32,909,347	1,265	1	13.625	8.425	7.615	21	14	18	1	1	2	DNM1L, YARS2	76577, 160	downstream, in gene	ActReg chr12 #3828	1	0	0
3829	12	33,205,842	33,206,182	340	1	3	5.6	9.273	4	9	15	0	0	0				ActReg chr12 #3829	0	0	1
3830	12	33,228,084	33,228,595	511	1	1.333	1.933	13.625	3	3	20	0	0	0				ActReg chr12 #3830	0	0	1
3831	12	33,591,910	33,592,494	584	1	2.8	4.778	11.722	5	10	18	1	1	1	SYT10	552	in gene	ActReg chr12 #3831	0	0	1
3832	12	33,615,513	33,615,933	420	1	1	2.2	10.923	1	4	16	0	0	0				ActReg chr12 #3832	0	0	1
3833	12	34,175,205	34,175,657	452	1	7.786	13.429	3.857	14	19	7	1	1	1	ALG10	215	in gene	ActReg chr12 #3833	0	1	0
3834	12	38,710,197	38,710,809	612	3	9.105	11.474	8.316	18	22	17	1	1	1	ALG10B	-54	upstream	ActReg chr12 #3834	1	1	1
3835	12	38,778,357	38,779,123	766	2	13.917	9.5	3.526	25	14	8	0	0	0				ActReg chr12 #3835	1	1	0
3836	12	39,298,948	39,300,170	1,222	2	11.158	11.947	7.132	19	20	11	1	1	1	CPNE8	-139	upstream	ActReg chr12 #3836	1	1	0
3837	12	39,835,972	39,837,383	1,411	1	7.318	11.727	3.267	14	17	10	1	1	1	KIF21A	515	in gene	ActReg chr12 #3837	0	1	0
3838	12	40,410,648	40,411,233	585	1	9.316	12.21	1	12	24	1	0	0	1	SLC2A13	88,721	in gene	ActReg chr12 #3838	0	1	0
3839	12	42,538,265	42,538,779	514	1	7.688	11.688	3.812	12	17	11	1	1	1	GXYLT1	151	in gene	ActReg chr12 #3839	0	1	0
3840	12	42,630,979	42,631,479	500	1	9.6	7.571	3.231	17	13	6	1	1	1	YAF2	925	in gene	ActReg chr12 #3840	1	0	0
3841	12	42,982,632	42,983,584	952	3	15.467	18.7	7.593	30	35	17	1	1	1	PRICKLE1	464	in gene	ActReg chr12 #3841	1	1	1
3842	12	43,004,718	43,005,065	347	1	3.273	2.1	11.454	5	4	17	0	0	0				ActReg chr12 #3842	0	0	1
3843	12	43,253,350	43,253,972	622	1	3.632	10.526	2.632	7	16	5	0	0	0				ActReg chr12 #3843	0	1	0
3844	12	43,315,578	43,316,173	595	1	11.526	8.947	2.895	17	15	6	0	0	0				ActReg chr12 #3844	1	0	0
3845	12	44,152,370	44,152,915	545	1	7.294	10.882	6.294	12	18	11	1	2	2	PUS7L, IRAK4	-46, -105	upstream, upstream	ActReg chr12 #3845	0	1	0
3846	12	44,363,557	44,364,156	599	1	9.556	10.278	2.5	14	18	5	0	0	1	TMEM117	133,894	in gene	ActReg chr12 #3846	0	1	0
3847	12	45,270,021	45,271,149	1,128	1	7.871	12.429	5.969	12	18	12	1	0	1	NELL2	37,126	in gene	ActReg chr12 #3847	0	1	0
3848	12	45,609,368	45,610,065	697	3	14	10.409	7.955	26	18	15	1	2	2	PLEKHA9, ANO6	73, -54	in gene, upstream	ActReg chr12 #3848	1	1	1
3849	12	45,610,078	45,610,859	781	1	11.36	6.6	7.16	16	9	11	1	2	2	PLEKHA9, ANO6	-679, 698	upstream, in gene	ActReg chr12 #3849	1	0	0
3850	12	45,809,034	45,809,828	794	2	16.48	12.16	2.88	36	28	5	0	0	1	ANO6	199,661	in gene	ActReg chr12 #3850	1	1	0
3851	12	45,832,666	45,833,258	592	1	7.789	11.895	2.263	13	20	5	0	0	1	ANO6	223,192	in gene	ActReg chr12 #3851	0	1	0
3852	12	45,862,718	45,863,255	537	1	3.824	3.294	10.882	6	6	18	0	0	0				ActReg chr12 #3852	0	0	1
3853	12	46,031,397	46,031,867	470	1	10.643	5.429	1.091	14	7	2	0	0	0				ActReg chr12 #3853	1	0	0
3854	12	46,121,088	46,121,810	722	1	10.043	14.696	5.304	20	29	9	1	2	2	LOC400027, ARID2	255, -2171	in gene, upstream	ActReg chr12 #3854	0	1	0
3855	12	46,122,418	46,122,999	581	1	9.944	10.167	3.688	16	18	7	1	2	2	LOC400027, ARID2	-1004, -912	upstream, upstream	ActReg chr12 #3855	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3856	12	46,333,479	46,333,930	451	1	7.214	10.071	1.875	11	15	4	0	0	1	SFRS2IP	50,697	in gene	ActReg chr12 #3856	0	1	0
3857	12	46,383,501	46,384,968	1,467	2	13.478	10.891	6.13	27	23	11	1	1	1	SFRS2IP	167	in gene	ActReg chr12 #3857	1	1	0
3858	12	46,385,362	46,386,092	730	1	12.174	8.957	7	23	14	15	1	1	1	SFRS2IP	-1,326	upstream	ActReg chr12 #3858	1	0	0
3859	12	46,411,765	46,412,178	413	1	1.538	4.615	13.154	2	6	20	0	0	0				ActReg chr12 #3859	0	0	1
3860	12	46,662,255	46,663,271	1,016	1	11.719	13.75	8.719	19	23	14	1	1	1	SLC38A1	445	in gene	ActReg chr12 #3860	0	1	0
3861	12	46,765,730	46,766,710	980	1	5.933	10.867	7.6	9	18	17	1	1	1	SLC38A2	425	in gene	ActReg chr12 #3861	0	1	0
3862	12	46,777,240	46,778,139	899	2	13.679	14.643	7.964	23	29	16	1	1	1	LOC100288798	-3,841	upstream	ActReg chr12 #3862	1	1	0
3863	12	46,917,738	46,918,388	650	1	9	13.2	7.4	14	20	12	0	0	1	LOC100288798	136,533	in gene	ActReg chr12 #3863	0	1	0
3864	12	46,943,360	46,944,031	671	2	11.191	11.143	1.118	20	21	2	0	0	1	LOC100288798	162,165	in gene	ActReg chr12 #3864	1	1	0
3865	12	47,224,848	47,225,413	565	1	3.278	7.556	10	4	10	12	1	1	2	LOC100288798, SLC38A4	443600, -5350	in gene, upstream	ActReg chr12 #3865	0	0	1
3866	12	47,479,489	47,479,896	407	1	6.917	11.167	1.25	12	15	2	0	1	1	AMIGO2	-5,958	upstream	ActReg chr12 #3866	0	1	0
3867	12	48,099,282	48,100,005	723	1	9.696	12.391	7.304	16	21	11	1	1	2	RPAP3, P11	201, 19712	in gene, downstream	ActReg chr12 #3867	0	1	0
3868	12	48,129,229	48,129,769	540	1	2.412	4.294	11.823	4	6	17	0	0	2	P11, RAPGEF3	-10144, 23390	upstream, in gene	ActReg chr12 #3868	0	0	1
3869	12	48,130,419	48,131,178	759	1	3.583	4.125	12.875	7	8	23	0	0	1	RAPGEF3	22,091	in gene	ActReg chr12 #3869	0	0	1
3870	12	48,134,275	48,134,895	620	1	4.105	5.158	12.263	7	7	20	0	0	1	RAPGEF3	18,304	in gene	ActReg chr12 #3870	0	0	1
3871	12	48,357,019	48,357,785	766	1	6.417	13.5	7	10	25	12	1	1	2	TMEM106C, COL2A1	72, 40883	in gene, downstream	ActReg chr12 #3871	0	1	0
3872	12	48,429,179	48,429,584	405	1	7.385	8.462	10.385	11	13	16	0	0	1	SENP1	70,260	downstream	ActReg chr12 #3872	0	0	1
3873	12	48,499,546	48,500,504	958	2	9.433	10.133	10.483	19	19	19	1	2	2	SENP1, PFKM	-384, 369	upstream, in gene	ActReg chr12 #3873	0	1	1
3874	12	48,591,514	48,592,363	849	1	8.407	13.185	5.185	13	18	12	1	1	2	DKFZP779L1853, OR10AD1	-208, 5137	upstream, downstream	ActReg chr12 #3874	0	1	0
3875	12	48,914,232	48,914,528	296	1	1	4	9.9	1	5	13	0	1	1	OR8S1	-5,035	upstream	ActReg chr12 #3875	0	0	1
3876	12	49,075,415	49,076,260	845	3	10.815	11.778	11.482	16	19	21	1	1	2	C12orf41, LOC144438	198, 10392	in gene, downstream	ActReg chr12 #3876	1	1	1
3877	12	49,110,100	49,111,327	1,227	2	9.553	12.842	13.053	18	19	22	1	1	2	CCNT1, LOC255411	68, -10505	in gene, upstream	ActReg chr12 #3877	0	1	1
3878	12	49,245,469	49,246,549	1,080	2	11.735	14.647	4.516	25	25	9	1	1	2	DDX23, RND1	-52, 13644	upstream, downstream	ActReg chr12 #3878	1	1	0
3879	12	49,297,576	49,298,262	686	2	11.857	11.667	3.143	22	23	4	0	1	1	CCDC65	26	in gene	ActReg chr12 #3879	1	1	0
3880	12	49,350,886	49,351,723	837	3	12.654	13.462	9.462	21	22	15	1	1	2	ARF3, WNT10B	-52, 14337	upstream, downstream	ActReg chr12 #3880	1	1	1
3881	12	49,363,866	49,364,336	470	1	4.067	4.133	12.333	7	7	16	1	1	2	WNT10B, WNT1	1540, -8135	in gene, upstream	ActReg chr12 #3881	0	0	1
3882	12	49,365,838	49,366,519	681	1	4.952	6.316	12.048	9	12	18	0	2	2	WNT10B, WNT1	-537, -6058	upstream, upstream	ActReg chr12 #3882	0	0	1
3883	12	49,372,031	49,372,898	867	1	3.643	5.714	12.143	6	13	16	1	2	2	WNT10B, WNT1	-6823, 228	upstream, in gene	ActReg chr12 #3883	0	0	1
3884	12	49,453,964	49,455,258	1,294	3	14.575	17.475	8.85	37	35	15	1	1	2	MLL2, RHEBL1	-5504, 9164	upstream, downstream	ActReg chr12 #3884	1	1	1
3885	12	49,485,809	49,486,393	784	1	5.083	14.167	6.125	9	20	11	1	1	2	DHH, LMBR1L	2601, 18679	in gene, downstream	ActReg chr12 #3885	0	1	0
3886	12	49,504,200	49,504,940	740	1	8.478	11.783	5.739	15	18	12	1	1	2	LMBR1L, LOC100288366	110, -9587	in gene, upstream	ActReg chr12 #3886	0	1	0
3887	12	49,523,934	49,525,271	1,337	2	9.571	7.952	11.191	16	12	21	1	1	2	LOC100288366, TUBA1B	10445, 702	in gene, in gene	ActReg chr12 #3887	1	0	1
3888	12	49,582,178	49,582,696	518	1	7.875	5.375	12.188	12	11	19	1	1	2	LOC100289104, TUBA1A	31086, 424	in gene, in gene	ActReg chr12 #3888	0	0	1
3889	12	49,627,989	49,628,616	627	1	11.65	8.35	3.529	20	14	7	1	0	1	LOC100293962	30,237	in gene	ActReg chr12 #3889	1	0	0
3890	12	49,658,305	49,659,691	1,386	3	9.721	11.861	7.8	17	19	20	1	2	2	LOC100293962, TUBA1C	-459, 133	upstream, in gene	ActReg chr12 #3890	1	1	1
3891	12	49,690,494	49,691,014	520	1	5.235	6.294	12.588	9	10	19	1	1	1	PRPH	1,845	in gene	ActReg chr12 #3891	0	0	1
3892	12	49,716,686	49,717,443	757	1	6	11.417	7.083	12	17	11	1	1	2	TROAP, C1QL4	93, 13907	in gene, downstream	ActReg chr12 #3892	0	1	0
3893	12	49,730,498	49,731,089	591	1	6.056	10.111	13.278	9	14	18	1	1	3	TROAP, C1QL4, DNAJC22	13822, 178, -10248	downstream, in gene, upstream	ActReg chr12 #3893	0	0	1
3894	12	49,733,022	49,733,342	320	1	5.7	5.2	10.7	7	7	15	0	1	3	TROAP, C1QL4, DNAJC22	16211, -2211, -7859	downstream, upstream, upstream	ActReg chr12 #3894	0	0	1
3895	12	49,735,308	49,736,069	761	1	4.833	1.5	11.708	8	2	19	1	2	3	TROAP, C1QL4, DNAJC22	18717, -4717, -5353	downstream, upstream, upstream	ActReg chr12 #3895	0	0	1
3896	12	49,740,614	49,741,618	1,004	1	9.548	12	7.323	14	19	13	1	1	2	C1QL4, DNAJC22	-10145, 75	upstream, in gene	ActReg chr12 #3896	0	1	0
3897	12	49,742,952	49,743,337	385	1	5.091	5.25	11.167	9	7	15	0	1	1	DNAJC22	2,103	in gene	ActReg chr12 #3897	0	0	1
3898	12	49,761,094	49,761,472	378	1	6.364	4.182	10	9	8	18	1	1	1	SPATS2	595	in gene	ActReg chr12 #3898	0	0	1
3899	12	49,829,133	49,829,426	293	1	1.625	1	10.556	2	1	15	0	0	1	SPATS2	68,591	in gene	ActReg chr12 #3899	0	0	1
3900	12	49,933,190	49,933,750	560	1	4.714	7.824	11.882	8	11	15	1	1	1	KCNH3	530	in gene	ActReg chr12 #3900	0	0	1
3901	12	49,951,241	49,951,708	467	1	3.929	5.571	12.357	5	8	17	0	0	2	KCNH3, MCRS1	18534, 10437	in gene, downstream	ActReg chr12 #3901	0	0	1
3902	12	49,961,468	49,962,129	661	2	6.81	11.095	9.333	11	16	20	1	1	2	KCNH3, MCRS1	28858, 113	downstream, in gene	ActReg chr12 #3902	0	1	1
3903	12	50,134,820	50,135,604	784	1	11.125	13.125	7.5	17	23	13	1	1	1	TMBIM6	-81	upstream	ActReg chr12 #3903	0	1	0
3904	12	50,185,521	50,185,922	401	1	1.692	4	11.231	3	5	17	1	0	1	NCKAP5L	36,487	in gene	ActReg chr12 #3904	0	0	1
3905	12	50,190,397	50,190,919	522	1	2.071	5.176	13.588	3	7	20	0	0	1	NCKAP5L	31,550	in gene	ActReg chr12 #3905	0	0	1
3906	12	50,221,149	50,221,768	619	1	4.55	7.25	11.5	5	11	15	1	2	3	NCKAP5L, LOC100286844, BCDIN3D	750, -868, 15454	in gene, upstream, downstream	ActReg chr12 #3906	0	0	1
3907	12	50,236,031	50,237,262	1,231	2	10.744	10.154	6.564	17	21	14	1	1	2	LOC100286844, BCDIN3D	14320, 266	downstream, in gene	ActReg chr12 #3907	1	1	0
3908	12	50,248,236	50,248,654	418	1	4.385	2.923	10.538	7	4	17	0	0	0				ActReg chr12 #3908	0	0	1
3909	12	50,360,951	50,361,664	713	1	12.957	11.87	10.304	20	16	15	1	1	3	AQP2, AQP5, AQP6	16783, 6028, -5313	downstream, downstream, upstream	ActReg chr12 #3909	1	0	0
3910	12	50,450,490	50,451,167	677	1	5.476	11.952	6.619	11	18	10	1	1	1	ACCN2	-659	upstream	ActReg chr12 #3910	0	1	0
3911	12	50,505,882	50,506,352	470	1	13.867	13.333	13.867	21	15	22	1	1	2	GPD1, C12orf62	8316, 217	downstream, in gene	ActReg chr12 #3911	0	0	1
3912	12	50,898,427	50,899,078	651	1	11.857	11.809	3.524	16	15	7	1	1	1	DIP2B	-16	upstream	ActReg chr12 #3912	1	0	0
3913	12	51,419,762	51,420,584	822	1	10.077	8.5	14.538	12	12	20	1	1	1	SLC11A2	1,885	in gene	ActReg chr12 #3913	0	0	1
3914	12	51,441,409	51,442,499	1,090	2	11.618	12.147	5.324	25	22	10	1	1	1	LETMD1	-130	upstream	ActReg chr12 #3914	1	1	0
3915	12	51,476,919	51,477,742	823	1	11.923	8.808	7.038	21	14	12	1	1	2	CSRNP2, TFCP2	3, 89596	in gene, downstream	ActReg chr12 #3915	1	0	0
3916	12	51,566,590	51,567,388	798	1	12.92	11.4	6.24	21	18	11	1	1	1	TFCP2	-63	upstream	ActReg chr12 #3916	1	0	0
3917	12	51,664,359	51,665,138	779	1	9.667	10.667	5.087	16	16	8	1	1	2	SMAGP, BIN2	-546, 53190	upstream, downstream	ActReg chr12 #3917	0	1	0
3918	12	51,818,455	51,819,219	764	2	9.875	8.542	9.583	20	19	18	1	1	1	SLC4A8	243	in gene	ActReg chr12 #3918	1	0	1
3919	12	51,986,536	51,987,689	1,153	2	9.778	13.361	3.143	18	31	6	0	1	1	SCN8A	2,092	in gene	ActReg chr12 #3919	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3920	12	52,258,132	52,258,550	418	1	2.769	2.615	12.077	5	4	19	1	0	0				ActReg chr12 #3920	0	0	1
3921	12	52,431,295	52,431,746	451	1	6.867	4.933	10.8	11	8	20	1	0	1	LOC100506166	4,785	in gene	ActReg chr12 #3921	0	0	1
3922	12	52,444,494	52,445,616	1,122	3	11.257	11.286	9.226	23	23	20	1	1	2	LOC100506166, NR4A1	18320, -136	in gene, upstream	ActReg chr12 #3922	1	1	1
3923	12	52,462,802	52,463,969	1,167	2	16.27	14.243	5.857	38	27	12	1	1	2	NR4A1, C12orf44	18194, -373	downstream, upstream	ActReg chr12 #3923	1	1	0
3924	12	52,540,206	52,541,994	1,788	3	11.089	8.839	9.571	22	25	15	0	0	0				ActReg chr12 #3924	1	1	1
3925	12	52,585,491	52,586,525	1,034	2	7.125	12.219	9.219	11	28	16	0	1	1	KRT80	-224	upstream	ActReg chr12 #3925	0	1	1
3926	12	52,596,606	52,597,465	859	1	10.556	12.074	5.407	19	20	9	0	1	2	LOC283403, LOC283404	7572, -7679	downstream, upstream	ActReg chr12 #3926	0	1	0
3927	12	52,609,109	52,609,875	766	1	11.667	9.25	5.083	20	15	7	0	1	2	LOC283403, LOC283404	-4885, 4778	upstream, in gene	ActReg chr12 #3927	1	0	0
3928	12	52,643,925	52,644,661	736	1	3	3.227	11.783	6	6	18	1	0	1	KRT7	17,339	downstream	ActReg chr12 #3928	0	0	1
3929	12	52,679,884	52,680,360	476	1	3	4.2	12.6	4	7	18	0	0	1	KRT81	5,177	in gene	ActReg chr12 #3929	0	0	1
3930	12	52,754,524	52,755,028	504	1	4.562	3.938	11	7	7	18	0	0	1	KRT85	6,533	in gene	ActReg chr12 #3930	0	0	1
3931	12	52,784,802	52,785,194	392	1	8.417	2.091	12	11	4	18	0	1	2	KRT84, KRT82	-5581, 15178	upstream, downstream	ActReg chr12 #3931	0	0	1
3932	12	52,916,186	52,916,652	466	1	5.533	5.8	11.8	9	7	17	0	1	1	KRT5	-2,176	upstream	ActReg chr12 #3932	0	0	1
3933	12	52,934,159	52,934,743	584	1	3.556	3.722	10.889	5	6	14	0	0	1	KRT71	12,480	downstream	ActReg chr12 #3933	0	0	1
3934	12	53,129,154	53,129,537	383	1	2.111	2.833	10.167	3	7	16	0	0	0				ActReg chr12 #3934	0	0	1
3935	12	53,134,995	53,135,916	921	2	14.138	19.172	3.429	30	42	8	0	0	0				ActReg chr12 #3935	1	1	0
3936	12	53,342,391	53,343,186	795	1	6.84	11.24	5.44	10	17	12	1	1	1	KRT18	133	in gene	ActReg chr12 #3936	0	1	0
3937	12	53,439,986	53,440,970	984	1	6.484	10.71	6.967	10	19	11	1	1	3	EIF4B, LOC283335, TENC1	40416, 7744, -332	downstream, in gene, upstream	ActReg chr12 #3937	0	1	0
3938	12	53,447,833	53,448,340	507	1	2.688	3.5	11.688	6	6	20	1	1	3	LOC283335, TENC1, SPRYD3	156, 7276, 25118	in gene, in gene, downstream	ActReg chr12 #3938	0	0	1
3939	12	53,453,069	53,454,038	969	1	4.467	4.367	12.5	10	7	18	0	1	3	LOC283335, TENC1, SPRYD3	-5331, 12743, 19651	upstream, in gene, downstream	ActReg chr12 #3939	0	0	1
3940	12	53,454,497	53,455,178	681	1	3.571	5.941	12.809	7	10	20	0	1	3	LOC283335, TENC1, SPRYD3	-6615, 14027, 18367	upstream, in gene, downstream	ActReg chr12 #3940	0	0	1
3941	12	53,573,970	53,574,720	750	1	5.458	11.333	5.25	8	19	10	1	2	2	CSAD, ZNF740	85, -190	in gene, upstream	ActReg chr12 #3941	0	1	0
3942	12	53,574,766	53,575,318	552	2	6.529	12.529	9.647	10	22	17	1	2	3	CSAD, ZNF740, ITGB7	-612, 507, 25958	upstream, in gene, downstream	ActReg chr12 #3942	0	1	1
3943	12	53,612,964	53,614,003	1,039	2	11.562	10.281	6.344	18	18	12	1	0	1	RARG	12,553	in gene	ActReg chr12 #3943	1	1	0
3944	12	53,661,735	53,662,317	582	1	11.722	9.833	6.389	16	17	11	1	1	1	ESPL1	-57	upstream	ActReg chr12 #3944	1	0	0
3945	12	53,688,991	53,689,698	707	1	7.957	12.435	7.522	10	24	13	1	2	3	ESPL1, PFDN5, C12orf10	27261, 109, -4126	downstream, in gene, upstream	ActReg chr12 #3945	0	1	0
3946	12	53,693,108	53,694,080	972	1	12.097	14.613	7.484	20	28	19	1	1	4	ESPL1, PFDN5, C12orf10, AAAS	31511, 4359, 124, 21818	downstream, downstream, in gene, downstream	ActReg chr12 #3946	0	1	0
3947	12	53,714,647	53,715,953	1,306	2	38.171	43.854	6.902	138	153	18	1	1	2	AAAS, SP7	112, 14704	in gene, downstream	ActReg chr12 #3947	1	1	0
3948	12	53,846,060	53,846,598	538	1	7.647	11	5.176	13	19	11	1	1	2	PRR13, PCBP2	10896, 443	downstream, in gene	ActReg chr12 #3948	0	1	0
3949	12	53,876,477	53,876,912	435	1	6.214	8.143	11.071	8	13	15	0	0	2	PCBP2, MAP3K12	30808, 16750	downstream, in gene	ActReg chr12 #3949	0	0	1
3950	12	53,894,547	53,895,795	1,248	2	13.564	15.462	7.459	24	30	17	1	2	3	MAP3K12, TARBP2, NPFF	-1727, 466, 6251	upstream, in gene, downstream	ActReg chr12 #3950	1	1	0
3951	12	54,019,640	54,020,473	833	2	12.808	12.192	5.462	25	26	10	1	1	1	ATF7	143	in gene	ActReg chr12 #3951	1	1	0
3952	12	54,052,707	54,053,238	531	1	7.25	10.375	1.267	10	17	2	0	0	1	ATP5G2	17,540	downstream	ActReg chr12 #3952	0	1	0
3953	12	54,069,512	54,070,425	913	2	17.571	17.929	8.464	33	47	16	1	1	1	ATP5G2	544	in gene	ActReg chr12 #3953	1	1	0
3954	12	54,088,530	54,088,946	416	1	3.692	3.7	10.692	5	6	15	0	0	0				ActReg chr12 #3954	0	0	1
3955	12	54,121,004	54,121,918	914	2	12.357	21.393	4.85	20	46	7	0	1	1	CALCOCO1	-154	upstream	ActReg chr12 #3955	1	1	0
3956	12	54,192,226	54,192,872	646	1	12.9	9.65	3.833	21	15	5	0	0	0				ActReg chr12 #3956	1	0	0
3957	12	54,332,307	54,333,509	1,202	2	13.553	14.921	4.857	22	26	11	1	1	1	HOXC13	332	in gene	ActReg chr12 #3957	1	1	0
3958	12	54,379,760	54,380,279	519	1	9.75	10.125	12.375	15	13	19	1	2	3	HOXC11, HOXC10, MIR196A2	13109, 1073, -5503	downstream, in gene, upstream	ActReg chr12 #3958	0	0	1
3959	12	54,391,006	54,391,439	433	1	7.643	11.071	7.071	12	14	11	0	1	3	HOXC10, MIR196A2, HOXC9	12276, 5700, -2655	downstream, downstream, upstream	ActReg chr12 #3959	0	1	0
3960	12	54,411,673	54,412,532	859	1	6.222	13.593	8.111	11	28	14	1	3	4	HOXC8, HOXC4, HOXC5, HOXC6	9212, 1460, 1460, 1460	downstream, in gene, in gene, in gene	ActReg chr12 #3960	0	1	0
3961	12	54,426,899	54,427,547	648	2	5.15	10.8	10.2	7	16	19	1	1	4	HOXC4, HOXC5, HOXC6, MIR615	16581, 16581, 16581, -511	in gene, in gene, downstream, upstream	ActReg chr12 #3961	0	1	1
3962	12	54,519,740	54,520,292	552	1	7.222	11.333	6.056	11	15	12	1	1	2	FLJ12825, LOC400043	67978, 161	downstream, in gene	ActReg chr12 #3962	0	1	0
3963	12	54,608,297	54,609,192	895	1	8.75	18.821	3.88	21	46	9	0	0	0				ActReg chr12 #3963	0	1	0
3964	12	54,673,975	54,675,034	1,059	2	13.727	8.576	10.091	21	18	18	1	3	3	CBX5, HNRNPA1, LOC100506653	-589, 16, -5183	upstream, in gene, upstream	ActReg chr12 #3964	1	0	1
3965	12	54,754,051	54,755,103	1,052	1	7.875	10.438	2.778	15	20	6	0	0	3	COPZ1, GPR84, ZNF385A	35666, 3693, 30506	downstream, downstream, downstream	ActReg chr12 #3965	0	1	0
3966	12	54,822,229	54,822,853	624	1	6.25	10.55	4.95	9	16	7	0	0	1	ITGA5	-9,491	upstream	ActReg chr12 #3966	0	1	0
3967	12	54,867,131	54,867,684	553	2	10.389	8.444	10.167	17	13	19	0	1	1	GTSF1	-21	upstream	ActReg chr12 #3967	1	0	1
3968	12	54,943,266	54,943,848	582	1	6.889	7.278	13.056	12	10	20	0	1	2	NCKAP1L, PDE1B	52082, 380	downstream, in gene	ActReg chr12 #3968	0	0	1
3969	12	54,986,845	54,987,414	569	1	6.5	11.667	3.111	11	21	4	0	1	1	PPP1R1A	-4,686	upstream	ActReg chr12 #3969	0	1	0
3970	12	55,328,948	55,329,574	626	1	9.95	7.2	1.188	17	11	2	0	0	0				ActReg chr12 #3970	1	0	0
3971	12	55,413,461	55,414,266	805	2	15.04	15.28	2.84	33	31	5	0	1	1	NEUROD4	134	in gene	ActReg chr12 #3971	1	1	0
3972	12	55,786,229	55,786,581	352	1	4.909	3	12	6	7	16	0	0	1	OR6C65	-7,908	upstream	ActReg chr12 #3972	0	0	1
3973	12	56,109,482	56,110,113	631	1	10.6	12.65	7.3	16	21	11	1	3	4	ITGA7, BLOC1S1, RDH5, CD63	-3708, -23, -4354, 13113	upstream, upstream, upstream, downstream	ActReg chr12 #3973	0	1	0
3974	12	56,114,711	56,115,461	750	2	10.875	10.125	3.75	19	19	10	0	2	5	ITGA7, BLOC1S1, RDH5, CD63, LOC100506701	-8997, 5266, 935, 7824, -7802	upstream, downstream, in gene, downstream, upstream	ActReg chr12 #3974	1	1	0
3975	12	56,121,652	56,122,391	739	1	10.913	9.13	5.957	18	15	11	1	2	4	BLOC1S1, RDH5, CD63, LOC100506701	12201, 7870, 889, -867	downstream, downstream, in gene, upstream	ActReg chr12 #3975	1	0	0
3976	12	56,122,930	56,123,365	435	1	9.786	11	11.214	15	18	16	1	2	4	BLOC1S1, RDH5, CD63, LOC100506701	13327, 8996, -237, 259	downstream, downstream, downstream, in gene	ActReg chr12 #3976	0	0	1
3977	12	56,223,070	56,224,263	1,193	3	12.605	11.947	7.395	20	18	18	2	2	4	ORMDL2, DNAJC14, LOC440104, MMP19	11860, -246, 274, 13069	downstream, upstream, in gene, downstream	ActReg chr12 #3977	1	1	1
3978	12	56,226,692	56,227,385	693	1	2.7	7.571	11.952	6	12	16	0	1	3	DNAJC14, LOC440104, MMP19	-3618, 3646, 9697	upstream, in gene, downstream	ActReg chr12 #3978	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
3979	12	56,320,934	56,321,405	471	1	12.429	8.857	4.071	18	12	5	1	2	2	WIBG, DGKA	528, -3777	in gene, upstream	ActReg chr12 #3979	1	0	0
3980	12	56,325,912	56,326,336	424	1	7.786	5.643	11.643	13	8	19	1	2	2	WIBG, DGKA	-4427, 1178	upstream, in gene	ActReg chr12 #3980	0	0	1
3981	12	56,367,296	56,368,127	831	1	15.846	12.231	6.038	28	19	17	1	2	4	SILV, CDK2, RAB5B, LOC100131294	-7885, 7155, -151, 7140	upstream, downstream, upstream, downstream	ActReg chr12 #3981	1	0	0
3982	12	56,400,699	56,401,451	752	2	11.833	11.083	5.292	23	22	9	1	0	1	SUOX	10,032	downstream	ActReg chr12 #3982	1	1	0
3983	12	56,435,497	56,436,152	655	3	14.1	13.75	9.6	21	23	15	1	1	2	IKZF4, RPS26	21135, 138	downstream, in gene	ActReg chr12 #3983	1	1	1
3984	12	56,472,739	56,473,995	1,256	1	8.231	12.82	9.282	14	21	16	1	1	1	ERBB3	-525	upstream	ActReg chr12 #3984	0	1	0
3985	12	56,474,099	56,475,106	1,007	1	9.719	10.375	8.31	13	15	16	1	1	1	ERBB3	710	in gene	ActReg chr12 #3985	0	1	0
3986	12	56,497,857	56,499,293	1,436	1	11.659	14.523	7.727	21	28	13	1	1	2	ERBB3, PA2G4	24683, 472	downstream, in gene	ActReg chr12 #3986	0	1	0
3987	12	56,511,659	56,512,411	752	3	10.304	15.478	9.87	22	23	20	1	2	4	PA2G4, RPL41, ZC3H10, ESYT1	13932, 1661, 5, -9951	downstream, downstream, in gene, upstream	ActReg chr12 #3987	1	1	1
3988	12	56,545,966	56,546,619	653	2	10.9	11.45	3.8	21	20	6	1	2	4	ESYT1, MYL6B, MYL6, SMARCC2	24306, -43, -5808, 37059	downstream, upstream, upstream, downstream	ActReg chr12 #3988	1	1	0
3989	12	56,583,191	56,584,238	1,047	1	8.97	11.212	6.065	16	26	13	1	1	1	SMARCC2	-363	upstream	ActReg chr12 #3989	0	1	0
3990	12	56,617,692	56,619,046	1,354	2	12.279	16.023	4.154	33	42	9	1	3	3	RNF41, OSFC2B, SLC39A5	-2634, 244, -5451	upstream, in gene, upstream	ActReg chr12 #3990	1	1	0
3991	12	56,651,369	56,652,622	1,253	1	7.974	10.564	4.667	13	16	9	1	1	2	ANKRD52, COQ10A	148, -8647	in gene, upstream	ActReg chr12 #3991	0	1	0
3992	12	56,660,376	56,660,886	510	1	6.875	11.438	6.062	12	14	11	1	1	3	ANKRD52, COQ10A, CS	-8488, -11, 33544	upstream, upstream, downstream	ActReg chr12 #3992	0	1	0
3993	12	56,709,419	56,710,527	1,108	2	7.794	11.647	11	14	19	19	1	1	2	CNPY2, PAN2	155, 17864	in gene, downstream	ActReg chr12 #3993	0	1	1
3994	12	56,861,940	56,862,850	910	2	17.931	16.448	6.724	45	42	13	0	1	2	SPRYD4, GLS2	94, 19786	in gene, downstream	ActReg chr12 #3994	1	1	0
3995	12	56,882,226	56,882,644	418	1	5.462	7.923	12.385	8	11	17	1	1	1	GLS2	-254	upstream	ActReg chr12 #3995	0	0	1
3996	12	56,972,848	56,973,295	447	1	9.714	7.714	3.357	15	11	4	0	0	1	RBMS2	57,462	in gene	ActReg chr12 #3996	1	0	0
3997	12	57,023,846	57,024,794	948	3	18.69	25	7.345	52	68	17	1	0	2	BAZ2A, ATP5B	5843, 15532	in gene, downstream	ActReg chr12 #3997	1	1	1
3998	12	57,028,540	57,029,272	732	2	13.435	14.522	3.826	30	29	7	1	1	4	BAZ2A, ATP5B, SNORD59B, SNORD59A	1257, 10946, 8632, 9979	in gene, downstream, downstream, downstream	ActReg chr12 #3998	1	1	0
3999	12	57,039,372	57,040,196	824	1	7.654	12.846	7.038	12	17	12	1	3	4	BAZ2A, ATP5B, SNORD59B, SNORD59A	-9621, 68, -2246, -899	upstream, in gene, upstream, upstream	ActReg chr12 #3999	0	1	0
4000	12	57,080,888	57,082,230	1,342	3	7.857	10.905	7.969	17	19	15	1	1	1	PTGES3	519	in gene	ActReg chr12 #4000	1	1	1
4001	12	57,118,690	57,119,491	801	1	8.28	13.56	6.88	16	24	13	1	1	2	NACA, PRIM1	256, 27056	in gene, downstream	ActReg chr12 #4001	0	1	0
4002	12	57,443,384	57,444,067	683	1	9.091	12.091	2.714	17	18	4	0	1	2	MYO1A, TMEM194A	168, 28849	in gene, downstream	ActReg chr12 #4002	0	1	0
4003	12	57,481,269	57,482,570	1,301	2	9.244	12.732	9.805	17	20	17	1	1	3	TMEM194A, NAB2, STAT6	-9345, -758, 23277	upstream, upstream, downstream	ActReg chr12 #4003	0	1	1
4004	12	57,568,939	57,569,902	963	1	2.6	4.107	12.167	5	8	18	1	0	1	LRP1	47,138	in gene	ActReg chr12 #4004	0	0	1
4005	12	57,632,654	57,633,295	641	2	12.5	13	7.85	23	19	11	1	1	3	SHMT2, NDUFA4L2, STAC3	9618, 1571, 11995	downstream, in gene, downstream	ActReg chr12 #4005	1	1	0
4006	12	57,633,662	57,634,121	459	1	6.667	7.267	12.2	9	10	16	1	1	3	SHMT2, NDUFA4L2, STAC3	10535, 654, 11078	downstream, in gene, downstream	ActReg chr12 #4006	0	0	1
4007	12	57,634,209	57,634,666	457	1	11.643	9.357	13.214	17	12	19	1	1	3	SHMT2, NDUFA4L2, STAC3	11081, 108, 10532	downstream, in gene, downstream	ActReg chr12 #4007	0	0	1
4008	12	57,635,762	57,637,381	1,619	2	22	25.98	6.471	86	85	16	2	1	3	SHMT2, NDUFA4L2, STAC3	13215, -2026, 8398	downstream, upstream, downstream	ActReg chr12 #4008	1	1	0
4009	12	57,850,006	57,850,537	531	1	6.118	9.118	10.882	11	13	17	0	2	3	INHBC, INHBE, GLI1	21728, 1175, -3647	downstream, in gene, upstream	ActReg chr12 #4009	0	0	1
4010	12	57,852,813	57,853,925	1,112	2	9.029	11.029	5.286	17	21	9	1	1	3	INHBC, INHBE, GLI1	24826, 4273, -549	downstream, downstream, upstream	ActReg chr12 #4010	1	1	0
4011	12	57,854,521	57,854,975	454	1	5.071	4.643	10.571	8	7	18	0	1	3	INHBC, INHBE, GLI1	26205, 5652, 830	downstream, downstream, in gene	ActReg chr12 #4011	0	0	1
4012	12	57,881,092	57,882,166	1,074	2	9.939	10.879	5.697	16	17	11	1	2	2	ARHGAP9, MARS	-7996, -222	upstream, upstream	ActReg chr12 #4012	1	1	0
4013	12	57,913,519	57,914,506	987	1	6.29	11.774	8.258	10	17	13	2	3	5	MARS, DDIT3, MIR616, MIR616, MIR06, DCTN2	32161, 288, -970, -2647, 26966	downstream, in gene, upstream, upstream, downstream	ActReg chr12 #4013	0	1	0
4014	12	58,014,317	58,015,024	707	1	3.818	3.318	10.864	6	6	16	1	1	3	GEFT, SLC26A10, B4GALNT1	10707, 977, 12315	downstream, in gene, downstream	ActReg chr12 #4014	0	0	1
4015	12	58,119,838	58,121,396	1,558	4	8.388	10.265	10.213	17	13	18	1	1	3	OS9, AGAP2, hCG_2014417	32879, 15323, 594	downstream, in gene, in gene	ActReg chr12 #4015	1	1	1
4016	12	58,131,118	58,131,623	505	1	8.375	7.812	15.812	12	12	28	1	1	3	AGAP2, hCG_2014417, TSPAN31	4570, 11347, -7414	in gene, downstream, upstream	ActReg chr12 #4016	0	0	1
4017	12	58,138,056	58,139,100	1,044	1	10.938	9.031	3.969	18	18	7	0	2	4	AGAP2, TSPAN31, CDK4, MARCH9	-2638, -206, 7586, -10322	upstream, upstream, downstream, upstream	ActReg chr12 #4017	1	0	0
4018	12	58,159,497	58,160,918	1,421	1	7.636	12.796	8.773	14	24	15	1	2	4	MARCH9, CYP27B1, METTL1, FAM119B	11307, 769, 5707, -6176	downstream, in gene, downstream, upstream	ActReg chr12 #4018	0	1	0
4019	12	58,165,458	58,166,954	1,496	4	11.872	16.787	11.702	28	41	22	2	3	4	CYP27B1, METTL1, FAM119B, TSFM	-5230, -292, -177, -10322	upstream, upstream, upstream, upstream	ActReg chr12 #4019	1	1	1
4020	12	58,176,112	58,177,191	1,079	2	41.647	43.824	4.576	144	150	9	0	1	2	FAM119B, TSFM	10268, 123	downstream, in gene	ActReg chr12 #4020	1	1	0
4021	12	58,239,525	58,240,562	1,037	2	11.781	8.281	10.75	17	14	22	1	1	2	CTDSP2, LOC100506805	704, 9167	in gene, downstream	ActReg chr12 #4021	1	0	1
4022	12	58,282,290	58,283,111	821	1	7	12.154	3.52	13	21	6	0	0	2	LOC100289282, LOC100289313	9654, 16328	downstream, downstream	ActReg chr12 #4022	0	1	0
4023	12	58,334,481	58,335,238	757	1	10.958	5.792	4.708	17	12	10	0	2	2	LOC100506844, XRCC6BP1	-4912, -586	upstream, upstream	ActReg chr12 #4023	1	0	0
4024	12	58,460,859	58,461,728	869	2	13.214	10.107	3.24	21	14	8	0	0	0				ActReg chr12 #4024	1	1	0
4025	12	58,819,154	58,819,876	722	1	11.174	5.565	2.118	19	9	5	0	0	0				ActReg chr12 #4025	1	0	0
4026	12	58,894,764	58,895,346	582	1	4.5	11.833	3	9	16	7	0	0	0				ActReg chr12 #4026	0	1	0
4027	12	58,902,851	58,903,267	416	1	10.923	8.077	1.333	18	11	3	0	0	0				ActReg chr12 #4027	1	0	0
4028	12	59,313,831	59,314,461	630	2	11.421	6.842	9.632	17	9	17	1	1	1	LRIG3	116	in gene	ActReg chr12 #4028	1	0	1
4029	12	59,430,701	59,431,328	627	1	11.3	8.5	3.5	15	14	4	0	0	0				ActReg chr12 #4029	1	0	0
4030	12	59,482,419	59,482,971	552	1	9.176	2.214	2	14	5	3	0	0	0				ActReg chr12 #4030	1	0	0
4031	12	59,991,114	59,991,561	447	1	7.429	10.143	2.462	12	14	4	0	0	0				ActReg chr12 #4031	0	1	0
4032	12	60,366,657	60,367,243	586	1	9	10.111	1	12	17	1	0	0	0				ActReg chr12 #4032	0	1	0
4033	12	62,653,480	62,654,562	1,082	3	47.029	51.735	9.862	168	173	16	1	1	1	USP15	-166	upstream	ActReg chr12 #4033	1	1	1
4034	12	62,996,016	62,997,763	1,747	4	12.655	12.618	10	21	22	18	1	2	3	MON2, C12orf61, MIRLET7I	136292, 325, -577	downstream, in gene, upstream	ActReg chr12 #4034	1	1	1
4035	12	63,025,499	63,026,857	1,358	2	8.558	12.954	8.395	17	29	18	1	0	0				ActReg chr12 #4035	0	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4036	12	63,118,627	63,119,242	615	1	7.421	11.263	5.882	15	17	10	0	0	1	PPM1H	209,731	in gene	ActReg chr12 #4036	0	1	0
4037	12	63,125,673	63,126,408	735	1	12	8.391	3.211	20	16	6	0	0	1	PPM1H	202,625	in gene	ActReg chr12 #4037	1	0	0
4038	12	63,177,489	63,178,343	854	1	12.704	10.667	5.074	23	18	10	0	0	1	PPM1H	150,749	in gene	ActReg chr12 #4038	1	0	0
4039	12	63,179,702	63,180,543	841	1	8.577	9.962	3.737	15	19	6	0	0	1	PPM1H	148,543	in gene	ActReg chr12 #4039	0	1	0
4040	12	63,327,791	63,328,481	690	1	7.727	11.591	7.364	13	21	15	1	1	1	PPM1H	529	in gene	ActReg chr12 #4040	0	1	0
4041	12	64,173,571	64,174,240	669	2	8.048	12.952	8.143	13	22	15	1	1	1	TMEM5	268	in gene	ActReg chr12 #4041	0	1	1
4042	12	64,237,321	64,238,581	1,260	2	13.359	11.359	5.771	23	14	14	1	1	1	SRGAP1	-590	upstream	ActReg chr12 #4042	1	1	0
4043	12	64,615,582	64,616,638	1,056	1	15.576	10.212	7.576	25	18	12	1	1	1	C12orf66	-34	upstream	ActReg chr12 #4043	1	0	0
4044	12	64,798,274	64,798,765	491	1	10.267	13.733	6.933	12	20	11	1	1	1	XPOT	286	in gene	ActReg chr12 #4044	0	1	0
4045	12	64,845,542	64,846,442	900	1	10.429	9.179	7.923	17	16	14	1	1	2	XPOT, TBK1	47759, 55	downstream, in gene	ActReg chr12 #4045	1	0	0
4046	12	65,214,966	65,215,521	555	1	10.667	9.944	2.2	16	13	3	0	0	1	TBC1D30	40,654	in gene	ActReg chr12 #4046	1	0	0
4047	12	65,218,840	65,219,395	555	1	3.353	8.611	10.389	11	12	13	1	0	1	TBC1D30	44,528	in gene	ActReg chr12 #4047	0	0	1
4048	12	65,219,823	65,220,683	860	2	14.778	15.037	3	36	28	6	0	0	1	TBC1D30	45,664	in gene	ActReg chr12 #4048	1	1	0
4049	12	65,514,854	65,515,289	435	1	2.385	7.385	10.462	4	10	15	1	1	1	WIF1	275	in gene	ActReg chr12 #4049	0	0	1
4050	12	66,042,783	66,043,205	422	1	10.571	9.5	1.429	16	14	3	0	1	1	LOC100507065	-6,842	upstream	ActReg chr12 #4050	1	0	0
4051	12	66,088,824	66,089,547	723	1	10.783	7.609	1.4	17	12	2	0	0	0				ActReg chr12 #4051	1	0	0
4052	12	66,217,178	66,219,192	2,014	3	10.079	12.984	6.367	19	29	14	1	1	1	HMGA2	-55	upstream	ActReg chr12 #4052	1	1	0
4053	12	66,219,413	66,219,821	408	1	7.538	7.231	11.846	10	9	16	1	1	1	HMGA2	1,377	in gene	ActReg chr12 #4053	0	0	1
4054	12	66,563,149	66,564,148	999	2	13.161	14.839	8.29	26	29	13	1	1	1	TMBIM4	159	in gene	ActReg chr12 #4054	1	1	0
4055	12	66,695,963	66,696,763	800	1	5.08	12.04	2.833	8	20	6	0	1	1	HELB	7	in gene	ActReg chr12 #4055	0	1	0
4056	12	67,027,445	67,028,002	557	2	8.222	11.167	2	18	20	3	0	0	1	GRIP1	45,202	in gene	ActReg chr12 #4056	1	1	0
4057	12	67,134,024	67,134,561	537	1	6.375	9.882	1.375	11	15	2	0	0	0				ActReg chr12 #4057	0	1	0
4058	12	67,587,224	67,588,246	1,022	2	14.438	20.562	2.737	36	50	6	0	0	0				ActReg chr12 #4058	1	1	0
4059	12	67,662,496	67,663,809	1,313	2	13.643	11.048	9.976	24	23	17	1	1	1	CAND1	91	in gene	ActReg chr12 #4059	1	1	0
4060	12	67,828,569	67,829,062	493	1	10.438	10.812	3.333	14	15	5	0	0	0				ActReg chr12 #4060	0	1	0
4061	12	68,141,438	68,143,212	1,774	2	11.232	10.857	2.296	22	21	6	0	0	0				ActReg chr12 #4061	1	1	0
4062	12	69,080,311	69,081,200	889	2	13.786	14.964	7.821	25	29	12	1	2	2	LOC100507250, NUP107	-172, 24	upstream, in gene	ActReg chr12 #4062	1	1	0
4063	12	69,753,350	69,753,792	442	1	10.857	10.214	12.143	17	14	18	1	1	3	LYZ, LOC100507296, YEATS4	11437, 4507, 39	downstream, in gene, in gene	ActReg chr12 #4063	0	0	1
4064	12	69,979,037	69,979,636	599	1	10.263	13.053	10.474	13	22	15	1	1	2	FRS2, CCT2	115207, 128	downstream, in gene	ActReg chr12 #4064	0	1	0
4065	12	70,215,588	70,216,078	490	1	9.933	8.733	2.769	17	12	5	0	1	2	RAB3IP, C12orf28	83202, -3465	in gene, upstream	ActReg chr12 #4065	1	0	0
4066	12	70,446,661	70,447,189	528	1	7.062	11.062	3.375	12	14	6	0	0	0				ActReg chr12 #4066	0	1	0
4067	12	70,636,328	70,637,281	953	2	7.733	13.367	9.7	12	19	19	1	2	2	LOC100507317, CNOT2	310, 27	in gene, in gene	ActReg chr12 #4067	0	1	1
4068	12	71,003,517	71,004,063	546	1	8	11.588	3.929	13	19	7	1	0	1	PTPRB	27,429	in gene	ActReg chr12 #4068	0	1	0
4069	12	71,313,243	71,314,483	1,240	2	9.667	10.846	4.5	16	17	9	0	1	1	PTPRR	721	in gene	ActReg chr12 #4069	1	1	0
4070	12	71,833,445	71,834,128	683	1	10.952	11.524	5.476	18	20	8	1	1	1	LGR5	-27	upstream	ActReg chr12 #4070	0	1	0
4071	12	72,056,615	72,057,809	1,194	1	11.676	9.405	6.583	17	17	15	1	2	2	ZFC3H1, THAP2	537, -572	in gene, upstream	ActReg chr12 #4071	1	0	0
4072	12	72,079,704	72,080,270	566	1	9.722	12.389	6.333	14	21	12	1	1	2	THAP2, TMEM19	22203, 109	downstream, in gene	ActReg chr12 #4072	0	1	0
4073	12	72,332,327	72,333,076	749	2	12.826	14.435	3.15	26	31	6	0	1	1	TPH2	75	in gene	ActReg chr12 #4073	1	1	0
4074	12	72,374,695	72,375,504	809	2	12.44	10.24	1.917	21	18	3	0	0	1	TPH2	42,473	in gene	ActReg chr12 #4074	1	1	0
4075	12	72,666,343	72,667,016	673	1	12.476	13.238	7.571	21	21	13	1	2	2	LOC283392, TRHDE	610, 150	in gene, in gene	ActReg chr12 #4075	0	1	0
4076	12	73,993,039	73,993,509	470	1	4.067	9.867	1	6	14	1	0	0	0				ActReg chr12 #4076	0	1	0
4077	12	74,686,260	74,686,920	660	1	6.762	10.857	6.571	12	18	12	0	1	1	LOC100507377	-179	upstream	ActReg chr12 #4077	0	1	0
4078	12	74,931,454	74,931,917	463	2	9.8	8.867	9	15	12	16	1	1	1	LOC552889	134	in gene	ActReg chr12 #4078	1	0	1
4079	12	75,571,748	75,572,269	521	2	10	9.4	1.429	14	16	2	0	0	1	KCNC2	31,503	in gene	ActReg chr12 #4079	1	1	0
4080	12	75,602,702	75,603,676	974	1	9.167	12.067	4.708	18	20	9	1	1	1	KCNC2	322	in gene	ActReg chr12 #4080	0	1	0
4081	12	75,723,610	75,724,465	855	2	13.333	15.482	5.12	25	38	13	1	2	2	CAPS2, GLIPR1L1	-201, -4426	upstream, upstream	ActReg chr12 #4081	1	1	0
4082	12	75,728,096	75,728,804	708	1	9.739	9.391	5	18	14	9	0	2	2	CAPS2, GLIPR1L1	-4614, -13	upstream, upstream	ActReg chr12 #4082	0	1	0
4083	12	75,822,586	75,822,849	263	1	2.333	3.667	9.222	3	5	12	0	0	1	GLIPR1L2	37,828	downstream	ActReg chr12 #4083	0	0	1
4084	12	75,904,967	75,905,791	824	2	11	13.2	2.6	24	21	5	1	1	2	GLIPR1, KRR1	30866, 39	downstream, in gene	ActReg chr12 #4084	1	1	0
4085	12	76,160,460	76,161,091	631	1	5.6	11.05	1.778	9	20	3	0	0	0				ActReg chr12 #4085	0	1	0
4086	12	76,326,754	76,327,381	597	1	9.947	6.842	1	20	10	1	0	1	1	LOC100289143	-5,703	upstream	ActReg chr12 #4086	1	0	0
4087	12	76,338,081	76,338,773	692	1	12.714	8.524	2.8	20	12	6	0	0	1	LOC100289143	5,642	in gene	ActReg chr12 #4087	1	0	0
4088	12	76,414,023	76,414,676	653	1	11.55	11.3	2.4	17	20	5	0	0	1	PHLDA1	11,207	downstream	ActReg chr12 #4088	1	0	0
4089	12	76,424,854	76,426,608	1,754	4	10.055	11.982	9.618	18	18	20	1	1	1	PHLDA1	-175	upstream	ActReg chr12 #4089	1	1	1
4090	12	76,576,903	76,577,852	949	1	9.897	11.069	3.692	17	17	7	0	0	0				ActReg chr12 #4090	0	1	0
4091	12	76,953,083	76,954,028	945	2	8.3	10.8	8.633	15	15	15	1	1	1	OSBPL8	34	in gene	ActReg chr12 #4091	0	1	1
4092	12	77,005,323	77,005,851	528	1	5.25	9.375	4.067	9	15	7	0	0	0				ActReg chr12 #4092	0	1	0
4093	12	77,272,707	77,273,289	582	1	7	10.556	7.778	10	17	12	1	1	1	CSRP2	-199	upstream	ActReg chr12 #4093	0	1	0
4094	12	77,336,536	77,337,032	496	1	7.25	11.562	3.667	11	16	6	0	0	0				ActReg chr12 #4094	0	1	0
4095	12	77,527,122	77,528,043	921	2	15.897	17.724	3.958	37	43	7	0	0	0				ActReg chr12 #4095	1	1	0
4096	12	78,241,551	78,242,249	698	1	7.682	10.682	1.176	10	16	2	0	0	1	NAV3	16,831	in gene	ActReg chr12 #4096	0	1	0
4097	12	79,955,350	79,955,706	356	1	5.455	4.091	11.182	7	7	16	0	0	0				ActReg chr12 #4097	0	0	1
4098	12	79,958,526	79,959,166	640	1	3.8	3.889	14.2	7	6	24	0	0	0				ActReg chr12 #4098	0	0	1
4099	12	80,328,244	80,329,604	1,360	3	12.465	15.465	8.238	24	32	16	1	1	1	PPP1R12A	311	in gene	ActReg chr12 #4099	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4100	12	80,457,772	80,458,469	697	1	11.954	5.864	2.4	18	9	4	0	0	0				ActReg chr12 #4100	1	0	0
4101	12	82,751,781	82,752,874	1,093	2	37.765	35.735	6.029	125	107	11	1	2	2	CCDC59, C12orf26	257, 51	in gene, in gene	ActReg chr12 #4101	1	1	0
4102	12	82,867,066	82,867,375	309	1	6	5.6	10.7	9	5	14	0	0	1	C12orf26	114,944	in gene	ActReg chr12 #4102	0	0	1
4103	12	83,081,245	83,081,703	458	1	5.8	9.6	6.067	8	14	8	1	1	1	TMTC2	540	in gene	ActReg chr12 #4103	0	1	0
4104	12	83,122,314	83,122,806	492	1	7.133	6.133	11.667	12	7	14	0	0	1	TMTC2	41,626	in gene	ActReg chr12 #4104	0	0	1
4105	12	85,305,103	85,306,934	1,831	4	11.561	12.368	7.382	19	27	21	3	1	1	SLC6A15	588	in gene	ActReg chr12 #4105	1	1	1
4106	12	85,410,097	85,410,683	586	1	11.444	9.529	1	22	19	1	0	0	1	TSPAN19	19,665	in gene	ActReg chr12 #4106	1	0	0
4107	12	85,486,261	85,487,280	1,019	2	13.094	12.438	2.25	21	25	4	0	0	1	LRRIQ1	56,671	in gene	ActReg chr12 #4107	1	1	0
4108	12	85,673,758	85,674,765	1,007	2	11.875	14.156	6.188	24	25	14	1	1	1	ALX1	225	in gene	ActReg chr12 #4108	1	1	0
4109	12	87,822,955	87,823,470	515	1	5.75	9.938	1.5	7	16	2	0	0	0				ActReg chr12 #4109	0	1	0
4110	12	87,833,689	87,834,337	648	2	8.667	11.048	1.4	16	17	2	0	0	0				ActReg chr12 #4110	1	1	0
4111	12	88,177,921	88,178,631	710	1	6.909	11.046	1.474	12	24	3	0	0	0				ActReg chr12 #4111	0	1	0
4112	12	88,429,086	88,429,833	747	2	13.417	11.125	5.167	23	20	9	1	2	2	C12orf50, C12orf29	-6283, 191	upstream, in gene	ActReg chr12 #4112	1	1	0
4113	12	88,535,384	88,536,395	1,011	1	9.906	14.094	4.25	16	26	8	1	2	2	CEP290, TMTC3	104, -184	in gene, upstream	ActReg chr12 #4113	0	1	0
4114	12	88,692,467	88,693,061	594	1	10.105	10.263	2.867	14	17	6	0	0	0				ActReg chr12 #4114	0	1	0
4115	12	88,693,195	88,694,007	812	2	10.68	9.68	1.647	19	19	3	0	0	0				ActReg chr12 #4115	1	1	0
4116	12	88,718,863	88,719,475	612	1	10.947	8.368	4.167	14	14	7	0	0	0				ActReg chr12 #4116	1	0	0
4117	12	88,814,155	88,814,783	628	2	10.842	10.474	1	21	18	1	0	0	0				ActReg chr12 #4117	1	1	0
4118	12	88,974,112	88,974,637	525	1	9.647	5.667	5.882	14	8	11	1	1	1	KITLG	-124	upstream	ActReg chr12 #4118	1	0	0
4119	12	89,458,456	89,459,137	681	2	9.636	9.182	2.143	20	21	4	0	0	0				ActReg chr12 #4119	1	1	0
4120	12	89,511,185	89,511,633	448	1	9	10.929	1.833	13	13	3	0	0	0				ActReg chr12 #4120	0	1	0
4121	12	89,619,017	89,619,884	867	1	11.815	10.296	2.24	18	17	5	0	0	0				ActReg chr12 #4121	1	0	0
4122	12	89,744,294	89,744,946	652	1	5.15	9.8	6.85	8	17	10	0	1	1	DUSP6	1,676	in gene	ActReg chr12 #4122	0	1	0
4123	12	89,745,185	89,746,068	883	2	12.963	11.852	8.444	18	20	15	1	1	1	DUSP6	670	in gene	ActReg chr12 #4123	1	1	0
4124	12	89,746,251	89,746,933	682	1	12.571	9.286	9.143	24	13	14	1	1	1	DUSP6	-296	upstream	ActReg chr12 #4124	1	0	0
4125	12	89,747,751	89,748,246	495	1	9.4	10.6	10.933	13	13	19	1	1	1	DUSP6	-1,702	upstream	ActReg chr12 #4125	0	0	1
4126	12	89,784,373	89,785,467	1,094	2	10.941	10.441	1.75	16	17	4	0	0	0				ActReg chr12 #4126	1	1	0
4127	12	89,833,624	89,834,253	629	1	11	8.65	3.75	18	14	6	0	0	1	WDR51B	85,839	in gene	ActReg chr12 #4127	1	0	0
4128	12	89,919,240	89,920,347	1,107	2	35.147	30.5	7.742	101	90	15	1	2	2	WDR51B, GALNT4	-16, -1258	upstream, upstream	ActReg chr12 #4128	1	1	0
4129	12	90,101,249	90,101,672	423	1	4	11.154	6.385	5	17	9	1	1	1	LOC338758	-1,272	upstream	ActReg chr12 #4129	0	1	0
4130	12	90,101,849	90,102,321	472	1	8.4	8.267	13.867	12	10	23	1	1	1	LOC338758	-647	upstream	ActReg chr12 #4130	0	0	1
4131	12	90,103,227	90,103,993	766	2	10.833	12.125	9.167	15	18	16	1	1	1	LOC338758	878	in gene	ActReg chr12 #4131	1	1	0
4132	12	90,162,805	90,163,544	739	1	12.696	8.304	3.13	22	12	5	0	0	0				ActReg chr12 #4132	1	0	0
4133	12	90,484,944	90,485,388	444	1	11.571	10.429	2.143	15	15	3	0	0	0				ActReg chr12 #4133	0	1	0
4134	12	90,727,498	90,728,070	572	1	10	7	2.688	15	11	5	0	0	0				ActReg chr12 #4134	1	0	0
4135	12	90,804,583	90,804,865	282	1	2.222	1.222	9.444	4	2	13	0	0	0				ActReg chr12 #4135	0	0	1
4136	12	90,904,630	90,905,307	677	1	9.095	11.143	1.941	13	21	3	0	0	0				ActReg chr12 #4136	0	1	0
4137	12	92,530,644	92,531,516	872	1	10.741	5.519	2	17	10	3	0	0	1	BTG1	8,593	downstream	ActReg chr12 #4137	1	0	0
4138	12	92,539,336	92,540,536	1,200	2	10.351	10.189	5.297	16	21	10	1	1	1	BTG1	-263	upstream	ActReg chr12 #4138	1	1	0
4139	12	92,683,194	92,683,773	579	1	7.556	9.278	1	14	15	1	0	0	0				ActReg chr12 #4139	0	1	0
4140	12	92,763,382	92,763,978	596	2	7.789	10.737	1.077	13	18	2	0	0	0				ActReg chr12 #4140	1	1	0
4141	12	92,800,217	92,800,663	446	1	3.5	2	9.571	6	3	15	0	0	0				ActReg chr12 #4141	0	0	1
4142	12	92,932,741	92,933,435	694	1	8.286	11.048	1.75	12	21	2	0	0	0				ActReg chr12 #4142	0	1	0
4143	12	92,952,449	92,953,317	868	1	8.037	10.667	1.8	14	18	2	0	0	0				ActReg chr12 #4143	0	1	0
4144	12	93,043,441	93,044,080	639	1	7.2	10.9	2.154	10	16	3	0	0	0				ActReg chr12 #4144	0	1	0
4145	12	93,323,127	93,323,651	524	2	6.882	10.059	9.882	11	18	19	1	1	1	EEA1	-282	upstream	ActReg chr12 #4145	0	1	1
4146	12	93,547,103	93,547,560	457	1	9.533	4.333	3.467	14	7	5	0	0	0				ActReg chr12 #4146	1	0	0
4147	12	93,623,139	93,623,958	819	1	9.92	5.32	1.533	14	10	2	0	0	0				ActReg chr12 #4147	1	0	0
4148	12	93,770,980	93,771,716	736	1	8.348	15.739	7.87	14	35	12	1	1	1	NUDT4	-353	upstream	ActReg chr12 #4148	0	1	0
4149	12	93,781,564	93,782,037	473	1	9.133	7.533	2.3	13	11	3	0	0	1	NUDT4	10,099	in gene	ActReg chr12 #4149	1	0	0
4150	12	93,861,145	93,861,793	648	1	9.143	10.524	7.619	16	21	13	1	1	1	MRPL42	199	in gene	ActReg chr12 #4150	0	1	0
4151	12	93,963,829	93,965,174	1,345	3	13.643	14.071	9.571	29	23	17	1	2	2	LOC144481, SOCS2	1477, 903	in gene, in gene	ActReg chr12 #4151	1	1	1
4152	12	94,070,792	94,071,932	1,140	2	10.314	10.943	2.324	16	15	5	1	1	1	CRADD	211	in gene	ActReg chr12 #4152	1	1	0
4153	12	94,212,489	94,213,224	735	1	10	12.13	1.842	16	19	4	0	0	1	CRADD	141,705	in gene	ActReg chr12 #4153	0	1	0
4154	12	94,358,613	94,359,310	697	1	6.727	11.318	3.591	12	18	6	0	0	0				ActReg chr12 #4154	0	1	0
4155	12	94,376,337	94,377,319	982	1	11.226	8.355	2.56	19	18	5	0	0	0				ActReg chr12 #4155	1	0	0
4156	12	94,534,439	94,535,098	659	1	2.526	3.7	12.7	4	5	19	0	1	1	PLXNC1	-7,731	upstream	ActReg chr12 #4156	0	0	1
4157	12	94,543,303	94,543,782	479	1	5.467	5.667	10.4	11	7	15	1	1	1	PLXNC1	1,043	in gene	ActReg chr12 #4157	0	0	1
4158	12	94,852,981	94,854,347	1,366	2	12.349	12.767	5.95	22	20	11	1	2	2	CCDC41, LOC144486	100, -115	in gene, upstream	ActReg chr12 #4158	1	1	0
4159	12	95,009,623	95,010,578	955	2	10.967	10.2	3.933	18	16	5	0	0	1	TMCC3	34,224	in gene	ActReg chr12 #4159	1	1	0
4160	12	95,038,219	95,038,915	696	1	11.046	8.636	4.375	17	15	6	0	0	1	TMCC3	5,757	in gene	ActReg chr12 #4160	1	0	0
4161	12	95,397,135	95,397,888	753	2	14.167	10.75	5.208	35	19	7	1	1	1	NDUFA12	0	in gene	ActReg chr12 #4161	1	1	0
4162	12	95,466,605	95,467,855	1,250	2	12.897	14.667	6.308	35	37	13	1	1	2	NR2C1, FGD6	174, 144010	in gene, downstream	ActReg chr12 #4162	1	1	0
4163	12	95,610,784	95,612,412	1,628	2	8.314	10.235	6.275	17	16	17	1	2	2	FGD6, VEZT	-358, 76	upstream, in gene	ActReg chr12 #4163	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4164	12	95,805,090	95,805,868	778	2	9.708	9.625	2.261	22	15	4	0	0	0				ActReg chr12 #4164	1	1	0
4165	12	95,867,486	95,868,211	725	2	12.217	15.261	7.955	26	35	12	1	1	1	METAP2	26	in gene	ActReg chr12 #4165	1	1	0
4166	12	96,184,965	96,185,428	463	1	10.5	6.857	3.75	16	10	6	1	1	1	NTN4	-660	upstream	ActReg chr12 #4166	1	0	0
4167	12	96,271,355	96,271,776	421	1	10.5	5.714	1	14	8	1	0	0	1	CCDC38	64,863	in gene	ActReg chr12 #4167	1	0	0
4168	12	96,428,752	96,430,058	1,306	3	10.78	12.878	7.073	23	28	20	1	1	1	LTA4H	-40	upstream	ActReg chr12 #4168	1	1	1
4169	12	96,502,755	96,503,173	418	1	3.385	2.846	13.154	5	6	22	0	0	0				ActReg chr12 #4169	0	0	1
4170	12	96,529,834	96,530,365	531	1	10.75	12	3.333	18	16	5	0	0	0				ActReg chr12 #4170	0	1	0
4171	12	96,792,958	96,793,646	688	2	9.545	11.409	11.5	15	16	21	1	1	1	CDK17	1,064	in gene	ActReg chr12 #4171	0	1	1
4172	12	97,070,529	97,070,919	390	1	1.25	2.167	8.417	2	3	14	0	0	1	C12orf63	28,971	in gene	ActReg chr12 #4172	0	0	1
4173	12	97,300,682	97,301,442	760	2	10.792	9.375	7.318	16	15	16	1	1	1	NEDD1	61	in gene	ActReg chr12 #4173	1	1	0
4174	12	98,231,183	98,231,725	542	1	5.882	8.294	1	12	15	1	0	0	0				ActReg chr12 #4174	0	1	0
4175	12	98,690,419	98,691,027	608	1	8.158	9.632	2	11	19	3	0	0	0				ActReg chr12 #4175	0	1	0
4176	12	98,746,131	98,746,712	581	1	6.389	10.611	2.333	10	17	5	0	0	0				ActReg chr12 #4176	0	1	0
4177	12	98,811,904	98,812,695	791	1	11.56	6.96	2.8	17	9	5	0	0	0				ActReg chr12 #4177	1	0	0
4178	12	98,896,938	98,898,257	1,319	3	10.341	10.78	15.073	26	18	26	1	1	2	LOC643770, LOC100128191	30, 12407	in gene, downstream	ActReg chr12 #4178	1	1	1
4179	12	98,908,820	98,910,685	1,865	2	8.983	11.431	7.633	16	17	17	1	2	2	LOC100128191, TMPO	252, 401	in gene, in gene	ActReg chr12 #4179	0	1	1
4180	12	98,987,086	98,988,138	1,052	1	12.606	10.697	9.818	24	21	16	1	2	2	SLC25A3, SNORA53	209, -5801	in gene, upstream	ActReg chr12 #4180	1	0	0
4181	12	99,038,550	99,039,612	1,062	3	9.121	8.879	7.667	15	15	18	1	2	2	IKBIP, APAF1	-492, 3	upstream, in gene	ActReg chr12 #4181	1	1	1
4182	12	99,072,192	99,072,557	365	1	4.333	3	11.75	6	6	14	0	0	1	APAF1	33,296	in gene	ActReg chr12 #4182	0	0	1
4183	12	99,207,919	99,208,471	552	1	7.176	10.177	1	10	15	1	0	0	1	ANKS1B	1,170,237	in gene	ActReg chr12 #4183	0	1	0
4184	12	99,290,507	99,291,179	672	1	4.857	10.524	3.118	8	14	7	0	0	1	ANKS1B	1,087,589	in gene	ActReg chr12 #4184	0	1	0
4185	12	99,848,993	99,849,598	605	1	9.333	8.111	1.692	17	12	3	0	0	1	ANKS1B	529,137	in gene	ActReg chr12 #4185	1	0	0
4186	12	100,378,759	100,379,076	317	1	3.4	2.7	9.6	5	4	14	1	1	1	ANKS1B	-485	upstream	ActReg chr12 #4186	0	0	1
4187	12	100,536,267	100,536,620	353	1	5.273	6.818	11.546	7	11	18	1	1	1	UHRF1BP1L	199	in gene	ActReg chr12 #4187	0	0	1
4188	12	100,932,866	100,933,647	781	2	12.292	13.25	3	31	29	6	0	0	1	NR1H4	65,577	in gene	ActReg chr12 #4188	1	1	0
4189	12	100,967,032	100,968,116	1,084	1	8.676	11.882	7.176	14	20	11	1	1	2	NR1H4, GAS2L3	99895, 85	downstream, in gene	ActReg chr12 #4189	0	1	0
4190	12	101,081,910	101,082,826	916	2	8.931	10.517	3	17	19	5	0	0	0				ActReg chr12 #4190	1	1	0
4191	12	101,219,951	101,220,622	671	2	11.238	9.19	1.231	19	16	2	0	0	1	ANO4	31,912	in gene	ActReg chr12 #4191	1	1	0
4192	12	101,421,058	101,421,559	501	1	2.133	3.154	12.333	4	5	17	0	0	1	ANO4	232,934	in gene	ActReg chr12 #4192	0	0	1
4193	12	101,693,774	101,694,205	431	1	9.846	6.308	1.538	14	9	2	0	0	1	UTP20	20,084	in gene	ActReg chr12 #4193	1	0	0
4194	12	101,801,284	101,801,920	636	1	9.4	12	8.85	11	16	14	1	1	1	ARL1	-30	upstream	ActReg chr12 #4194	0	1	0
4195	12	102,091,719	102,092,342	623	1	10.368	11.21	8.263	15	18	13	1	1	1	CHPT1	613	in gene	ActReg chr12 #4195	0	1	0
4196	12	102,270,776	102,271,991	1,215	2	8.158	11.895	6.632	16	16	15	1	1	1	DRAM1	278	in gene	ActReg chr12 #4196	0	1	1
4197	12	102,329,849	102,330,709	860	2	9.556	13.111	2.714	14	21	5	0	0	0				ActReg chr12 #4197	1	1	0
4198	12	102,513,414	102,514,276	862	1	10.482	12.778	5.593	16	21	9	1	2	2	NUP37, C12orf48	-1484, -111	upstream, upstream	ActReg chr12 #4198	0	1	0
4199	12	103,352,347	103,352,678	331	1	2.727	6.182	10.454	4	10	16	1	1	1	ASCL1	1,060	in gene	ActReg chr12 #4199	0	0	1
4200	12	103,889,498	103,889,950	452	1	3.643	10.5	6.429	7	16	11	1	1	1	C12orf42	25	in gene	ActReg chr12 #4200	0	1	0
4201	12	103,954,304	103,954,828	524	1	12.765	10.294	1.889	26	19	4	0	0	0				ActReg chr12 #4201	1	0	0
4202	12	103,968,958	103,969,605	647	2	10.762	11.619	4.333	24	21	10	0	0	0				ActReg chr12 #4202	1	1	0
4203	12	104,195,673	104,196,633	960	1	10.4	9.267	3.7	16	16	7	0	0	1	NT5DC3	38,822	in gene	ActReg chr12 #4203	1	0	0
4204	12	104,350,492	104,351,353	861	2	13.074	13.444	7.37	23	26	15	1	1	3	HSP90B1, C12orf73, TDG	-26733, 71, -8671	downstream, in gene, upstream	ActReg chr12 #4204	1	1	0
4205	12	104,359,208	104,360,124	916	3	13.321	16.75	7.893	24	37	14	1	1	2	C12orf73, TDG	-8673, 73	upstream, in gene	ActReg chr12 #4205	1	1	1
4206	12	104,457,724	104,458,695	971	1	7.935	12.581	9.323	13	22	18	1	1	1	HCFC2	-27	upstream	ActReg chr12 #4206	0	1	0
4207	12	104,680,353	104,681,062	709	1	7.636	12.091	4.222	12	19	11	1	0	1	TXNRD1	71,148	in gene	ActReg chr12 #4207	0	1	0
4208	12	104,682,214	104,683,029	815	1	5.04	12.4	3.8	8	19	6	1	0	1	TXNRD1	73,062	in gene	ActReg chr12 #4208	0	1	0
4209	12	104,850,242	104,850,904	662	2	10.4	10.15	6.111	18	19	11	1	1	1	CHST11	-119	upstream	ActReg chr12 #4209	1	1	0
4210	12	104,851,711	104,852,209	498	1	4	9.688	14.062	5	13	19	1	1	1	CHST11	1,268	in gene	ActReg chr12 #4210	0	0	1
4211	12	105,113,290	105,113,778	488	1	3.933	2.867	11.933	7	6	18	0	0	1	CHST11	262,842	in gene	ActReg chr12 #4211	0	0	1
4212	12	105,501,145	105,502,001	856	1	11.037	14.333	6.52	20	24	18	1	1	1	KIAA1033	81	in gene	ActReg chr12 #4212	0	1	0
4213	12	105,651,080	105,651,661	581	1	10.333	11.389	1.923	16	22	3	0	0	0				ActReg chr12 #4213	0	1	0
4214	12	106,696,139	106,697,286	1,147	3	14.389	15.417	9.722	28	30	18	1	1	1	TCP11L2	131	in gene	ActReg chr12 #4214	1	1	1
4215	12	106,751,211	106,752,142	931	2	9.69	12.379	8.276	20	20	22	1	1	1	POLR3B	240	in gene	ActReg chr12 #4215	0	1	1
4216	12	107,167,593	107,168,843	1,250	3	12.359	13.923	8.359	23	22	14	1	2	2	LOC100287944, RIC8B	478, -181	in gene, upstream	ActReg chr12 #4216	1	1	1
4217	12	107,348,605	107,348,934	329	1	5.727	4.091	9	8	5	14	0	1	1	C12orf23	-775	upstream	ActReg chr12 #4217	0	0	1
4218	12	107,349,357	107,350,388	1,031	1	7.281	10.844	3.438	10	17	9	1	1	1	C12orf23	328	in gene	ActReg chr12 #4218	0	1	0
4219	12	107,486,766	107,487,968	1,202	2	6.921	11.579	6.526	11	16	13	1	1	1	CRY1	231	in gene	ActReg chr12 #4219	0	1	1
4220	12	108,079,355	108,080,094	739	2	9.522	12.696	9.783	15	18	19	1	1	1	PWP1	134	in gene	ActReg chr12 #4220	0	1	1
4221	12	108,237,427	108,237,951	524	1	3.438	4.875	11.312	5	8	14	1	0	0				ActReg chr12 #4221	0	0	1
4222	12	108,238,907	108,239,322	415	1	2.385	2.692	10.308	4	3	15	1	0	0				ActReg chr12 #4222	0	0	1
4223	12	108,343,217	108,343,539	322	1	1.3	1.375	10.7	2	2	15	0	0	0				ActReg chr12 #4223	0	0	1
4224	12	108,349,887	108,350,474	587	1	8.579	10.632	2.846	14	17	5	0	0	0				ActReg chr12 #4224	0	1	0
4225	12	108,523,397	108,523,851	454	1	2.786	2.857	14.214	4	6	19	1	1	1	WSCD2	113	in gene	ActReg chr12 #4225	0	0	1
4226	12	108,588,052	108,588,610	558	1	3.611	10.389	2.231	5	17	4	0	0	1	WSCD2	64,820	in gene	ActReg chr12 #4226	0	1	0
4227	12	108,607,968	108,608,765	797	2	11.88	13.44	2.84	20	29	6	0	0	1	WSCD2	84,855	in gene	ActReg chr12 #4227	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4228	12	108,622,250	108,623,128	878	2	9.481	10.407	3.926	14	16	8	0	0	1	WSCD2	99,178	in gene	ActReg chr12 #4228	1	1	0
4229	12	108,819,199	108,819,677	478	1	2.2	5.2	11.2	3	7	17	0	0	0				ActReg chr12 #4229	0	0	1
4230	12	108,954,392	108,955,251	859	2	12.074	11.778	9.63	22	18	16	1	2	2	SART3, ISCU	344, -1473	in gene, upstream	ActReg chr12 #4230	1	0	1
4231	12	109,037,613	109,038,252	639	1	11.85	9	2.9	19	16	5	0	0	2	SELPLG, CORO1C	-10262, 87363	upstream, downstream	ActReg chr12 #4231	1	0	0
4232	12	109,084,969	109,086,330	1,361	2	9.071	11.976	4.238	15	19	12	0	0	1	CORO1C	39,646	in gene	ActReg chr12 #4232	1	1	0
4233	12	109,124,608	109,125,313	705	1	6.913	11.087	5	9	18	13	1	1	1	CORO1C	335	in gene	ActReg chr12 #4233	0	1	0
4234	12	109,125,357	109,125,826	469	1	7.533	6	11.667	10	11	21	1	1	1	CORO1C	-296	upstream	ActReg chr12 #4234	0	0	1
4235	12	109,248,126	109,248,804	678	1	11.182	11.954	7.773	17	18	14	0	0	1	SSH1	2,894	in gene	ActReg chr12 #4235	0	1	0
4236	12	109,283,922	109,284,492	570	1	10.444	5.056	3	20	10	5	0	0	1	DAO	10,350	in gene	ActReg chr12 #4236	1	0	0
4237	12	109,458,369	109,459,253	884	2	15.148	17.667	4.577	32	37	7	0	0	0				ActReg chr12 #4237	1	1	0
4238	12	109,489,981	109,491,228	1,247	2	8.077	12.667	10.846	20	25	32	1	2	2	LOC100131733, USP30	1166, 224	in gene, in gene	ActReg chr12 #4238	0	1	1
4239	12	109,530,951	109,531,751	800	2	18.72	15.68	7	45	35	11	1	2	3	USP30, ALKBH2, UNG	40971, -58, -4064	downstream, upstream, upstream	ActReg chr12 #4239	1	1	0
4240	12	109,535,024	109,536,504	1,480	3	10.522	10.63	9.196	25	23	17	1	2	3	USP30, ALKBH2, UNG	45384, -4471, 349	downstream, upstream, in gene	ActReg chr12 #4240	1	1	1
4241	12	109,702,739	109,703,240	501	1	3.25	3.938	11.875	5	7	19	0	0	1	ACACB	125,787	in gene	ActReg chr12 #4241	0	0	1
4242	12	109,914,870	109,915,919	1,049	3	12.758	15.333	9.833	26	33	19	1	2	2	KCTD10, UBE3B	-239, -45	upstream, upstream	ActReg chr12 #4242	1	1	1
4243	12	109,982,573	109,983,398	825	1	11.115	7.654	3.462	15	11	6	0	0	2	UBE3B, MMAB	67546, 28373	downstream, downstream	ActReg chr12 #4243	1	0	0
4244	12	110,010,697	110,011,572	875	2	14.074	17.074	5.038	28	33	11	1	2	2	MMAB, MVK	224, -366	in gene, upstream	ActReg chr12 #4244	1	1	0
4245	12	110,148,356	110,149,140	784	1	13.333	10.292	3.042	22	14	5	0	1	1	C12orf34	-3,439	upstream	ActReg chr12 #4245	1	0	0
4246	12	110,337,609	110,338,727	1,118	2	13.914	17.057	5.686	27	41	10	1	1	1	TCHP	89	in gene	ActReg chr12 #4246	1	1	0
4247	12	110,353,074	110,353,644	570	1	3.056	2.692	9.444	5	6	14	0	0	1	TCHP	15,280	in gene	ActReg chr12 #4247	0	0	1
4248	12	110,384,889	110,385,437	548	1	8.588	11.529	1.533	12	16	2	0	0	1	GIT2	49,031	in gene	ActReg chr12 #4248	0	1	0
4249	12	110,436,572	110,437,497	925	2	23.276	22.138	3.583	64	57	8	1	2	2	GIT2, ANKRD13A	-2840, -201	upstream, upstream	ActReg chr12 #4249	1	1	0
4250	12	110,486,125	110,486,672	547	1	9.647	10.647	5.812	14	14	10	1	0	2	ANKRD13A, C12orf76	49163, 19102	downstream, in gene	ActReg chr12 #4250	0	1	0
4251	12	110,718,365	110,718,898	533	2	11.647	8.294	15	19	14	25	1	1	1	ATP2A2	-401	upstream	ActReg chr12 #4251	1	0	1
4252	12	110,841,001	110,841,725	724	1	8.136	11.727	8.4	12	21	17	1	1	1	ANAPC7	172	in gene	ActReg chr12 #4252	0	1	0
4253	12	110,905,776	110,906,480	704	2	10	12.818	10	18	20	20	1	2	2	GPN3, C12orf24	398, -104	in gene, upstream	ActReg chr12 #4253	0	1	1
4254	12	110,939,592	110,940,376	784	3	11.083	11.542	11.542	16	21	20	1	2	2	VPS29, RAD9B	-68, -21	upstream, upstream	ActReg chr12 #4254	1	1	1
4255	12	111,016,373	111,016,973	600	1	11.842	6.474	4.789	19	11	8	0	0	1	PPTC7	4,391	in gene	ActReg chr12 #4255	1	0	0
4256	12	111,051,544	111,052,296	752	2	12.083	8.917	11.708	17	15	19	1	1	1	TCTN1	88	in gene	ActReg chr12 #4256	1	0	1
4257	12	111,114,006	111,114,636	630	1	2.8	1.824	10.6	5	3	14	0	0	1	HVCN1	13,296	in gene	ActReg chr12 #4257	0	0	1
4258	12	111,758,411	111,758,766	355	1	5.636	5.727	11.182	9	8	17	1	0	1	CUX2	286,760	in gene	ActReg chr12 #4258	0	0	1
4259	12	111,806,239	111,807,391	1,152	2	15.167	10.889	6.735	26	22	10	1	1	1	FAM109A	110	in gene	ActReg chr12 #4259	1	1	0
4260	12	111,834,637	111,835,403	766	2	14.917	14.167	5.826	33	29	10	1	0	1	SH2B3	-8,732	upstream	ActReg chr12 #4260	1	1	0
4261	12	111,836,817	111,837,695	878	1	10.63	8.519	2.05	15	17	4	0	1	1	SH2B3	-6,496	upstream	ActReg chr12 #4261	1	0	0
4262	12	111,843,145	111,843,548	403	1	8.583	8.917	11.917	12	12	16	1	1	1	SH2B3	-406	upstream	ActReg chr12 #4262	0	0	1
4263	12	111,851,157	111,852,336	1,179	1	8.919	12.838	6	16	18	11	0	0	1	SH2B3	7,994	in gene	ActReg chr12 #4263	0	1	0
4264	12	112,035,888	112,036,350	462	1	7.786	10.571	6.214	10	14	8	1	1	1	ATXN2	1,361	in gene	ActReg chr12 #4264	0	1	0
4265	12	112,037,380	112,037,985	605	1	9.842	8.053	8.684	16	11	12	1	1	1	ATXN2	-202	upstream	ActReg chr12 #4265	1	0	0
4266	12	112,279,452	112,280,506	1,054	3	11.636	16.303	7.406	30	33	21	1	2	2	C12orf47, MAPKAPK5	727, -300	in gene, upstream	ActReg chr12 #4266	1	1	1
4267	12	112,450,512	112,451,993	1,481	2	12.826	10.522	8.239	21	19	12	1	2	2	TMEM116, ERP29	-229, 100	upstream, in gene	ActReg chr12 #4267	1	1	0
4268	12	112,545,977	112,547,047	1,070	1	9.147	13.235	7.088	18	26	21	1	1	1	NAA25	123	in gene	ActReg chr12 #4268	0	1	0
4269	12	112,554,388	112,554,868	480	2	9.933	10.133	5.333	16	15	7	0	0	2	NAA25, TRAFD1	-7993, -8721	upstream, upstream	ActReg chr12 #4269	1	1	0
4270	12	112,622,320	112,622,674	354	1	4.364	2.273	11.273	6	4	15	1	0	1	C12orf51	197,399	in gene	ActReg chr12 #4270	0	0	1
4271	12	112,820,090	112,820,777	687	1	6.636	12.5	3.8	13	18	7	1	1	1	C12orf51	-537	upstream	ActReg chr12 #4271	0	1	0
4272	12	112,846,786	112,847,577	791	1	8.542	10.875	6.208	17	15	9	1	1	3	LOC100506435, RPL6, PTPN11	8780, 262, -9355	downstream, in gene, upstream	ActReg chr12 #4272	0	1	0
4273	12	112,856,285	112,856,953	668	1	13.667	8.048	6.143	20	12	12	1	1	2	RPL6, PTPN11	-9176, 83	upstream, in gene	ActReg chr12 #4273	1	0	0
4274	12	113,102,192	113,102,989	797	2	15.88	16.2	2.381	32	34	5	0	0	0				ActReg chr12 #4274	1	1	0
4275	12	113,228,922	113,229,987	1,065	2	15	17.235	4.161	31	35	7	0	1	1	RPH3A	-95	upstream	ActReg chr12 #4275	1	1	0
4276	12	113,306,053	113,306,824	771	2	11.917	12.125	4.333	24	22	9	0	0	1	RPH3A	76,889	in gene	ActReg chr12 #4276	1	1	0
4277	12	113,384,361	113,384,685	324	1	4.3	4	10.4	5	5	13	0	0	1	OAS3	8,274	in gene	ActReg chr12 #4277	0	0	1
4278	12	113,400,939	113,401,324	385	1	3.667	4.75	11	5	7	17	0	0	1	OAS3	24,882	in gene	ActReg chr12 #4278	0	0	1
4279	12	113,565,353	113,565,978	625	1	3.562	5.421	11.053	7	9	15	0	0	1	RASAL1	8,379	in gene	ActReg chr12 #4279	0	0	1
4280	12	113,622,633	113,623,899	1,266	3	13.59	13.872	9.359	29	28	16	1	2	3	DDX54, C12orf52, IQCD	18, -289, 35614	in gene, upstream, downstream	ActReg chr12 #4280	1	1	1
4281	12	113,772,810	113,773,412	602	1	10.526	9.789	2.053	19	16	4	1	1	1	SLC24A6	-186	upstream	ActReg chr12 #4281	1	0	0
4282	12	113,795,967	113,796,960	993	2	13.281	13.906	6.769	24	22	12	1	1	1	PLBD2	92	in gene	ActReg chr12 #4282	1	1	0
4283	12	113,859,732	113,860,416	684	1	11.909	10.046	5.545	24	17	14	0	1	1	SOSL	-142	upstream	ActReg chr12 #4283	1	0	0
4284	12	113,905,291	113,906,019	728	1	3.652	4.87	11.783	8	12	18	1	1	2	LHX5, LOC100506452	4222, -4153	in gene, upstream	ActReg chr12 #4284	0	0	1
4285	12	113,908,877	113,909,389	512	1	2.733	4	12.562	6	7	17	1	2	2	LHX5, LOC100506452	744, -675	in gene, upstream	ActReg chr12 #4285	0	0	1
4286	12	113,917,565	113,918,489	924	2	9.621	12.621	3.231	21	25	5	1	0	2	LHX5, LOC100506452	-8150, 8219	upstream, in gene	ActReg chr12 #4286	1	1	0
4287	12	114,039,094	114,040,086	992	1	10.097	14.194	2.391	17	27	5	0	0	0				ActReg chr12 #4287	0	1	0
4288	12	114,403,827	114,404,614	787	1	7.12	11.48	6	16	17	9	1	1	1	RBM19	-44	upstream	ActReg chr12 #4288	0	1	0
4289	12	114,878,513	114,878,940	427	1	2.875	1.25	12.077	4	2	18	1	0	0				ActReg chr12 #4289	0	0	1
4290	12	114,922,888	114,923,178	290	1	1.625	2	10.556	2	2	13	0	0	0				ActReg chr12 #4290	0	0	1
4291	12	115,103,669	115,104,009	340	1	4.091	1	9.727	5	1	14	1	0	1	TBX3	18,130	downstream	ActReg chr12 #4291	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4292	12	115,121,791	115,122,479	688	1	9.818	12	7.591	14	18	12	1	1	1	TBX3	-166	upstream	ActReg chr12 #4292	0	1	0
4293	12	115,211,792	115,212,466	674	1	9.429	11.143	1.278	17	17	3	0	0	0				ActReg chr12 #4293	0	1	0
4294	12	115,353,742	115,354,355	613	2	11	11.421	3	20	21	4	0	0	0				ActReg chr12 #4294	1	1	0
4295	12	115,371,085	115,371,874	789	2	10.64	12.12	1.7	22	25	3	0	0	0				ActReg chr12 #4295	1	1	0
4296	12	115,374,587	115,375,351	764	1	5.125	9.875	1.615	12	13	3	0	0	0				ActReg chr12 #4296	0	1	0
4297	12	115,593,189	115,594,104	915	1	8.929	11.786	2.88	14	20	5	0	0	0				ActReg chr12 #4297	0	1	0
4298	12	115,779,102	115,779,726	624	1	5.85	10.2	2.833	12	18	5	0	0	0				ActReg chr12 #4298	0	1	0
4299	12	115,877,994	115,878,684	690	2	12.381	10.952	3.714	23	15	6	0	0	0				ActReg chr12 #4299	1	1	0
4300	12	117,039,223	117,039,887	664	1	5.476	9.619	4.235	10	17	9	0	0	0				ActReg chr12 #4300	0	1	0
4301	12	117,175,627	117,176,374	747	1	10.348	13.739	3.429	23	34	7	1	2	2	C12orf49, RNFT2	-157, -96	upstream, upstream	ActReg chr12 #4301	0	1	0
4302	12	117,250,728	117,251,866	1,138	1	11	15.657	4.87	15	22	9	0	0	1	RNFT2	75,201	in gene	ActReg chr12 #4302	0	1	0
4303	12	117,256,714	117,257,433	719	1	9.045	11.5	2.864	12	16	5	1	0	1	RNFT2	80,977	in gene	ActReg chr12 #4303	0	1	0
4304	12	117,295,782	117,296,376	594	2	10.167	12.333	2.667	20	21	4	0	0	2	RNFT2, HRK	119983, 23153	downstream, downstream	ActReg chr12 #4304	1	1	0
4305	12	117,354,527	117,355,030	503	1	7.312	9.75	1.25	11	16	2	0	0	1	FBXW8	6,017	in gene	ActReg chr12 #4305	0	1	0
4306	12	117,536,183	117,536,596	413	1	5.154	5.846	12.692	9	11	17	1	1	1	TESC	862	in gene	ActReg chr12 #4306	0	0	1
4307	12	117,536,637	117,536,999	362	1	8.333	12.833	10.417	12	17	12	1	1	1	TESC	433	in gene	ActReg chr12 #4307	0	0	1
4308	12	117,551,119	117,551,481	362	1	2.3	3.545	12.818	4	5	19	0	0	0				ActReg chr12 #4308	0	0	1
4309	12	118,432,024	118,432,965	941	1	12.033	9.533	3.667	18	15	6	0	0	0				ActReg chr12 #4309	1	0	0
4310	12	118,573,548	118,574,819	1,271	2	10.55	10.125	6.4	15	18	15	1	1	2	LOC100506570, PEBP1	9204, 313	in gene, in gene	ActReg chr12 #4310	1	1	0
4311	12	118,810,344	118,811,258	914	2	20.357	13.929	3.296	46	29	11	1	2	2	TAOK3, SUDS3	-51, -3557	upstream, upstream	ActReg chr12 #4311	1	1	0
4312	12	118,814,072	118,814,589	517	1	8.688	12.5	4.462	12	17	8	1	2	2	TAOK3, SUDS3	-3580, -28	upstream, upstream	ActReg chr12 #4312	0	1	0
4313	12	119,498,686	119,499,583	897	2	13	16.25	2.857	28	36	6	0	0	1	SRRM4	79,738	in gene	ActReg chr12 #4313	1	1	0
4314	12	120,314,466	120,315,353	887	1	9	13.926	6.846	15	23	15	1	1	1	CIT	183	in gene	ActReg chr12 #4314	0	1	0
4315	12	120,427,079	120,427,489	410	1	10.538	9.538	2.917	17	16	5	1	1	1	CCDC64	-364	upstream	ActReg chr12 #4315	1	0	0
4316	12	120,427,634	120,428,398	764	2	12.625	10.167	7.273	18	18	14	1	1	1	CCDC64	368	in gene	ActReg chr12 #4316	1	1	0
4317	12	120,524,568	120,525,402	834	2	12.769	12.885	4.308	21	18	7	1	0	2	CCDC64, RAB35	97337, 29658	in gene, downstream	ActReg chr12 #4317	1	1	0
4318	12	120,632,090	120,633,407	1,317	3	11.512	13.293	5.341	25	25	15	1	2	3	GCN1L1, RPLP0, LOC100506649	-235, 6266, -6363	upstream, downstream, upstream	ActReg chr12 #4318	1	1	1
4319	12	120,638,325	120,639,635	1,310	3	54.073	61.244	11.171	202	217	29	1	3	4	GCN1L1, RPLP0, LOC100506649, PXN	-6467, 34, -131, 64583	upstream, in gene, upstream, downstream	ActReg chr12 #4319	1	1	1
4320	12	120,652,375	120,652,860	485	1	2.467	3.133	10.867	4	5	17	0	0	2	LOC100506649, PXN	13506, 50946	downstream, in gene	ActReg chr12 #4320	0	0	1
4321	12	120,669,053	120,669,937	884	1	11.393	9.714	4.464	17	14	8	0	0	1	PXN	34,068	in gene	ActReg chr12 #4321	1	0	0
4322	12	120,703,652	120,704,154	502	1	11.6	6.133	7.733	15	8	13	1	1	1	PXN	-340	upstream	ActReg chr12 #4322	1	0	0
4323	12	120,715,643	120,716,349	506	1	2.364	2.933	11.467	3	4	17	0	0	0				ActReg chr12 #4323	0	0	1
4324	12	120,729,397	120,731,445	2,048	5	12.641	14.656	9.938	46	56	20	0	0	2	3	RNU4-2, RNU4-1, SIRT4	-715, 619, -9703	upstream, downstream, upstream	ActReg chr12 #4324	1	1	1
4325	12	120,739,865	120,740,576	711	2	12.043	12.857	4.174	28	27	11	0	1	2	RNU4-1, SIRT4	-9180, 96	upstream, in gene	ActReg chr12 #4325	1	1	0
4326	12	120,784,864	120,785,491	627	1	3.2	3.45	11.9	6	6	17	0	0	1	MSH1	21,781	in gene	ActReg chr12 #4326	0	0	1
4327	12	120,883,856	120,884,666	810	3	11.48	15.84	10.48	20	28	18	1	2	3	COX6A1, TRIAP1, GATC	8357, -46, 20	downstream, upstream, in gene	ActReg chr12 #4327	1	1	1
4328	12	120,907,227	120,908,053	826	2	13	14.5	7.04	27	32	11	1	2	3	GATC, SFRS9, DYNLL1	23399, -82, -20	downstream, upstream, upstream	ActReg chr12 #4328	1	1	0
4329	12	120,933,746	120,934,531	785	1	7.28	10	8.52	14	17	13	1	1	3	DYNLL1, LOC100506668, COQ5	26478, -395, 32826	in gene, upstream, downstream	ActReg chr12 #4329	0	1	0
4330	12	120,966,570	120,967,367	797	1	8.48	12.2	5.348	16	18	10	1	2	2	COQ5, RNF10	-4, -5164	upstream, upstream	ActReg chr12 #4330	0	1	0
4331	12	120,972,106	120,972,563	457	1	7.5	11.714	3.071	14	16	6	1	2	2	COQ5, RNF10	-5370, 202	upstream, in gene	ActReg chr12 #4331	0	1	0
4332	12	121,124,338	121,124,872	534	1	11.647	9.235	10.765	18	12	16	1	1	1	MLEC	-344	upstream	ActReg chr12 #4332	0	0	1
4333	12	121,176,875	121,177,484	609	1	3.526	4.421	12.105	6	6	17	1	0	1	ACADS	13,608	in gene	ActReg chr12 #4333	0	0	1
4334	12	121,342,102	121,342,575	473	1	9.333	13.4	6.4	12	23	9	1	1	1	UNQ1887	-187	upstream	ActReg chr12 #4334	0	1	0
4335	12	121,344,754	121,345,683	929	2	7.966	10.552	3.414	15	17	7	0	1	1	UNQ1887	-3,067	upstream	ActReg chr12 #4335	1	1	0
4336	12	121,476,365	121,477,364	999	2	21.129	16.1	4.455	53	35	11	0	1	1	OASL	-84	upstream	ActReg chr12 #4336	1	1	0
4337	12	121,711,835	121,712,279	444	1	5.357	4.214	9.357	8	7	14	1	0	1	CAMKK2	24,054	in gene	ActReg chr12 #4337	0	0	1
4338	12	121,733,953	121,734,388	435	1	5.077	8.769	12.231	9	12	21	1	1	1	CAMKK2	1,941	in gene	ActReg chr12 #4338	0	0	1
4339	12	121,789,569	121,790,542	973	2	14	10.3	4.966	24	20	10	1	1	1	ANAPC5	1,957	in gene	ActReg chr12 #4339	1	1	0
4340	12	121,832,066	121,832,361	295	1	3.333	5.667	9.667	5	8	12	0	1	1	RNF34	-5,689	upstream	ActReg chr12 #4340	0	0	1
4341	12	121,904,768	121,905,969	1,201	3	9.447	10.553	10.3	25	21	15	1	0	1	KDM2B	113,552	in gene	ActReg chr12 #4341	1	1	1
4342	12	122,231,373	122,232,448	1,075	2	9.088	11.941	9.794	21	16	23	1	1	2	RHOF, LOC338799	-316, 9480	upstream, downstream	ActReg chr12 #4342	0	1	1
4343	12	122,234,779	122,235,560	781	1	13.56	8.56	6.84	24	15	12	1	2	3	RHOF, LOC338799, SETD1B	-3575, 6221, -7469	upstream, in gene, upstream	ActReg chr12 #4343	1	0	0
4344	12	122,235,655	122,236,340	685	1	7.952	11.524	5.524	11	15	9	0	2	3	RHOF, LOC338799, SETD1B	-4403, 5393, -6641	upstream, in gene, upstream	ActReg chr12 #4344	0	1	0
4345	12	122,250,109	122,250,615	506	1	6.062	8.438	11.312	10	11	18	1	0	2	LOC338799, SETD1B	-8972, 7724	upstream, in gene	ActReg chr12 #4345	0	0	1
4346	12	122,326,150	122,327,177	1,027	2	12.656	11.938	4.906	28	21	7	1	2	2	HPD, PSMD9	-146, 17	upstream, in gene	ActReg chr12 #4346	1	1	0
4347	12	122,516,021	122,516,644	623	1	9.7	13.1	2	17	23	3	1	1	2	LOC100506691, MLXIP	10345, -428	downstream, upstream	ActReg chr12 #4347	0	1	0
4348	12	122,710,254	122,710,923	669	2	11.381	6.524	9.476	19	14	17	1	1	2	DIABLO, VPS33A	1480, 40480	in gene, downstream	ActReg chr12 #4348	1	0	1
4349	12	122,750,358	122,751,554	1,196	3	11.579	15.184	8.737	28	27	18	1	1	2	VPS33A, CLIP1	112, 156160	in gene, downstream	ActReg chr12 #4349	1	1	1
4350	12	123,237,063	123,237,692	629	2	11.158	12.263	15.632	15	18	28	1	1	1	DENR	6	in gene	ActReg chr12 #4350	0	1	1
4351	12	123,339,606	123,340,203	597	1	3.895	2.842	11.053	7	5	17	0	0	2	HIP1R, VPS37B	19865, 40808	in gene, downstream	ActReg chr12 #4351	0	0	1
4352	12	123,343,665	123,344,251	586	1	6	4.278	12.056	10	6	17	0	0	2	HIP1R, VPS37B	23919, 36754	in gene, downstream	ActReg chr12 #4352	0	0	1
4353	12	123,380,380	123,381,196	816	2	12.346	13	5.846	27	31	11	1	1	1	VPS37B	-76	upstream	ActReg chr12 #4353	1	1	0
4354	12	123,428,923	123,430,181	1,258	2	12.275	11.75	4.475	23	21	8	0	0	1	ABCB9	30,200	in gene	ActReg chr12 #4354	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4355	12	123,458,842	123,460,105	1,263	2	19.025	16.725	7.325	33	37	10	1	3	4	ABCB9, OGFOD2, ARL6IP4, PITPNM2	279, 119, -5407, 135502	in gene, in gene, upstream, downstream	ActReg chr12 #4355	1	1	0
4356	12	123,464,392	123,464,948	556	1	7.824	6.824	12.471	12	10	15	1	2	4	ABCB9, OGFOD2, ARL6IP4, PITPNM2	-4918, 5316, -210, 130305	upstream, downstream, upstream, downstream	ActReg chr12 #4356	0	0	1
4357	12	123,466,283	123,466,963	680	1	4.762	6.333	11.381	11	12	17	0	2	4	ABCB9, OGFOD2, ARL6IP4, PITPNM2	-6871, 7269, 1743, 128352	upstream, downstream, in gene, downstream	ActReg chr12 #4357	0	0	1
4358	12	123,570,205	123,571,152	947	1	9.233	9.733	3.833	13	17	8	0	0	2	PITPNM2, LOC100507091	24297, 4747	in gene, downstream	ActReg chr12 #4358	0	1	0
4359	12	123,573,958	123,574,754	796	2	11.32	10	2.391	21	19	5	0	0	2	PITPNM2, LOC100507091	20619, 8425	in gene, downstream	ActReg chr12 #4359	1	1	0
4360	12	123,610,908	123,611,755	847	1	13.704	10.111	3.062	23	18	5	0	0	0				ActReg chr12 #4360	1	0	0
4361	12	123,634,667	123,635,074	407	1	4.923	6.385	12.077	6	9	18	1	0	1	MPHOSPH9	71,571	downstream	ActReg chr12 #4361	0	0	1
4362	12	123,717,131	123,717,930	799	3	12.28	12.8	8.8	22	29	15	1	1	1	C12orf65	-314	upstream	ActReg chr12 #4362	1	1	1
4363	12	123,717,989	123,718,492	503	1	7.933	7.6	14.333	13	11	23	1	1	1	C12orf65	396	in gene	ActReg chr12 #4363	0	0	1
4364	12	123,750,368	123,751,607	1,239	1	4.692	5.057	11.744	9	7	18	0	0	2	C12orf65, CDK2AP1	33143, 5700	downstream, in gene	ActReg chr12 #4364	0	0	1
4365	12	123,752,524	123,753,408	884	1	5.107	4.464	11.857	9	12	18	0	0	1	CDK2AP1	3,721	in gene	ActReg chr12 #4365	0	0	1
4366	12	123,920,709	123,921,187	478	1	10.8	9.133	10	14	11	16	1	1	1	RILPL2	316	in gene	ActReg chr12 #4366	0	0	1
4367	12	124,068,664	124,069,540	876	2	14.643	20.214	5.179	33	45	10	1	1	1	TMED2	26	in gene	ActReg chr12 #4367	1	1	0
4368	12	124,085,962	124,087,043	1,081	3	14.294	12.853	12.912	28	25	28	1	1	3	TMED2, LOC100507130, DDX55	17426, 14062, -170	downstream, in gene, upstream	ActReg chr12 #4368	1	1	1
4369	12	124,117,793	124,118,718	925	2	12.179	13.821	8.179	21	32	13	1	2	2	EIF2B1, GTF2H3	68, -126	in gene, upstream	ActReg chr12 #4369	1	1	0
4370	12	124,155,505	124,155,872	367	1	7.5	10.583	12.833	9	13	16	1	1	1	TCTN2	28	in gene	ActReg chr12 #4370	0	0	1
4371	12	124,676,291	124,677,228	937	1	8.759	11.172	4.759	14	17	8	0	0	0				ActReg chr12 #4371	0	1	0
4372	12	124,773,765	124,774,654	889	1	8.407	12.667	4.556	11	21	7	0	1	1	FAM101A	499	in gene	ActReg chr12 #4372	0	1	0
4373	12	124,791,669	124,792,145	476	1	3.933	6.867	11	6	11	18	0	0	1	FAM101A	18,197	in gene	ActReg chr12 #4373	0	0	1
4374	12	124,793,152	124,793,656	504	1	2.875	4.812	11.438	5	7	15	0	0	1	FAM101A	19,694	in gene	ActReg chr12 #4374	0	0	1
4375	12	124,819,187	124,819,967	780	1	2.684	4.125	12.167	5	7	17	0	0	1	NCOR2	232,433	in gene	ActReg chr12 #4375	0	0	1
4376	12	124,826,247	124,826,700	453	1	4.643	4.786	11.643	7	7	16	0	0	1	NCOR2	225,537	in gene	ActReg chr12 #4376	0	0	1
4377	12	124,844,211	124,844,879	668	1	3.706	3.81	12.095	7	9	18	0	0	1	NCOR2	207,465	in gene	ActReg chr12 #4377	0	0	1
4378	12	124,848,466	124,848,993	527	1	3.062	4.471	10.588	5	9	15	0	0	1	NCOR2	203,281	in gene	ActReg chr12 #4378	0	0	1
4379	12	124,881,021	124,881,796	775	1	4.16	3.12	10.8	9	7	18	0	0	1	NCOR2	170,602	in gene	ActReg chr12 #4379	0	0	1
4380	12	124,890,105	124,890,572	467	1	3.143	6.214	13.467	6	9	23	0	0	1	NCOR2	161,672	in gene	ActReg chr12 #4380	0	0	1
4381	12	124,965,726	124,966,172	446	1	5.929	9.786	11.929	8	13	18	0	0	1	NCOR2	86,061	in gene	ActReg chr12 #4381	0	0	1
4382	12	124,984,891	124,985,440	549	1	3.444	3.833	10.889	5	7	13	0	0	1	NCOR2	66,845	in gene	ActReg chr12 #4382	0	0	1
4383	12	125,026,589	125,027,121	532	1	6.059	4.412	10.823	11	8	14	0	0	1	NCOR2	25,155	in gene	ActReg chr12 #4383	0	0	1
4384	12	125,050,986	125,051,633	647	1	6.05	11.4	8.45	10	20	11	1	1	1	NCOR2	701	in gene	ActReg chr12 #4384	0	1	0
4385	12	125,052,182	125,052,721	539	2	12.706	17.529	5	24	33	9	1	1	1	NCOR2	-441	upstream	ActReg chr12 #4385	1	1	0
4386	12	125,110,682	125,111,401	719	1	7.565	11.217	3.435	11	18	7	0	0	0				ActReg chr12 #4386	0	1	0
4387	12	125,165,882	125,166,867	985	1	9.484	12.355	3.862	16	19	10	0	0	0				ActReg chr12 #4387	0	1	0
4388	12	125,211,588	125,212,400	812	2	10.72	12	4.52	16	21	7	0	0	0				ActReg chr12 #4388	1	1	0
4389	12	125,226,641	125,227,253	612	1	3.118	4.053	10.895	6	6	14	0	0	0				ActReg chr12 #4389	0	0	1
4390	12	125,244,710	125,245,153	443	1	4.462	4.643	10.857	9	9	18	0	0	0				ActReg chr12 #4390	0	0	1
4391	12	125,398,493	125,399,893	1,400	3	16.091	18.204	11.204	42	45	23	1	1	2	LOC100288312, UBC	5110, 384	downstream, in gene	ActReg chr12 #4391	1	1	1
4392	12	125,401,493	125,402,460	967	1	15.133	8.067	2	32	19	5	0	1	2	LOC100288312, UBC	7893, -2399	downstream, upstream	ActReg chr12 #4392	1	0	0
4393	12	125,406,127	125,406,553	426	1	9.077	8.308	11.308	13	11	20	0	1	2	LOC100288312, UBC	12257, -6763	downstream, upstream	ActReg chr12 #4393	0	0	1
4394	12	125,411,685	125,412,821	1,136	2	11.4	8.4	12.323	27	14	25	1	0	0				ActReg chr12 #4394	1	0	1
4395	12	125,423,913	125,424,837	924	1	14.069	11.345	15.586	25	20	25	0	0	1	DHX37	49,292	downstream	ActReg chr12 #4395	0	0	1
4396	12	125,425,124	125,425,866	742	1	11.261	8.217	6.217	18	13	12	0	0	1	DHX37	48,172	downstream	ActReg chr12 #4396	1	0	0
4397	12	125,434,397	125,435,255	858	1	3.593	3.259	13.222	8	6	22	0	0	1	DHX37	38,841	in gene	ActReg chr12 #4397	0	0	1
4398	12	125,533,851	125,534,751	900	1	7.571	11.357	5.643	11	18	8	1	0	0				ActReg chr12 #4398	0	1	0
4399	12	125,834,377	125,834,947	570	1	1.438	1.778	10.667	2	3	15	0	0	1	TMEM132B	23,500	in gene	ActReg chr12 #4399	0	0	1
4400	12	126,536,139	126,536,648	509	1	10.5	7.688	1.154	16	13	2	0	0	0				ActReg chr12 #4400	1	0	0
4401	12	126,895,459	126,896,010	551	1	10.529	5.938	2.765	18	9	4	0	0	0				ActReg chr12 #4401	1	0	0
4402	12	127,544,629	127,545,646	1,017	1	8.5	14.312	2.9	14	22	7	0	0	0				ActReg chr12 #4402	0	1	0
4403	12	127,610,277	127,610,865	588	1	11.222	9.944	5	16	19	8	0	0	0				ActReg chr12 #4403	1	0	0
4404	12	127,675,615	127,676,053	438	1	9.357	3.615	1.111	16	7	2	0	0	0				ActReg chr12 #4404	1	0	0
4405	12	127,715,203	127,715,821	618	1	10.158	13.053	3.833	13	22	7	0	0	0				ActReg chr12 #4405	0	1	0
4406	12	127,874,202	127,875,044	842	2	10.333	13.63	1.652	23	29	3	0	0	0				ActReg chr12 #4406	1	1	0
4407	12	127,969,950	127,970,552	602	1	8.579	9.789	1.944	13	15	4	0	0	0				ActReg chr12 #4407	0	1	0
4408	12	128,043,870	128,044,809	939	1	8.233	12.8	4.167	14	27	12	0	0	0				ActReg chr12 #4408	0	1	0
4409	12	129,454,410	129,454,838	428	1	1.333	4.154	12.846	2	8	16	0	0	1	GLT1D1	116,543	in gene	ActReg chr12 #4409	0	0	1
4410	12	130,387,541	130,387,910	369	1	1.6	1.818	11.333	2	3	15	1	1	1	TMEM132D	487	in gene	ActReg chr12 #4410	0	0	1
4411	12	130,645,323	130,645,649	326	1	2	2	10.1	2	4	13	1	2	2	FLJ31485, FZD10	737, -1546	in gene, upstream	ActReg chr12 #4411	0	0	1
4412	12	130,649,580	130,649,840	260	1	1.625	2.429	10.375	2	3	13	0	1	2	FLJ31485, FZD10	-3487, 2678	upstream, in gene	ActReg chr12 #4412	0	0	1
4413	12	131,260,622	131,261,676	1,054	2	11.727	13.485	5.219	24	26	12	0	0	0				ActReg chr12 #4413	1	1	0
4414	12	131,355,941	131,356,382	441	1	8.769	10.538	9.083	11	15	13	1	1	1	RAN	-456	upstream	ActReg chr12 #4414	0	1	0
4415	12	131,468,134	131,468,747	613	1	8.526	11.632	2.833	12	19	4	0	0	2	GPR133, LOC100128540	29988, 6133	in gene, downstream	ActReg chr12 #4415	0	1	0
4416	12	131,529,097	131,530,098	1,001	2	11.194	13.774	7.323	22	26	10	1	0	1	GPR133	91,145	in gene	ActReg chr12 #4416	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4417	12	131,590,000	131,590,621	621	1	3.211	5.368	12.474	5	9	18	0	0	1	GPR133	151,858	in gene	AdReg chr12 #4417	0	0	1
4418	12	131,615,628	131,616,145	517	1	2.688	4.688	12.438	4	8	16	0	0	1	GPR133	177,434	in gene	AdReg chr12 #4418	0	0	1
4419	12	131,622,823	131,623,313	490	1	4.467	2	12.667	7	5	19	1	0	1	GPR133	184,616	in gene	AdReg chr12 #4419	0	0	1
4420	12	131,623,315	131,624,550	1,235	1	2.667	2.091	12.077	5	5	18	1	0	1	GPR133	185,480	in gene	AdReg chr12 #4420	0	0	1
4421	12	131,759,643	131,759,974	331	1	3.545	2.5	11.364	6	3	17	0	0	0				AdReg chr12 #4421	0	0	1
4422	12	131,852,966	131,853,602	636	1	3.6	2.65	12.25	6	4	16	0	1	1	LOC338797	2,714	downstream	AdReg chr12 #4422	0	0	1
4423	12	132,071,058	132,071,811	753	1	2.565	7.083	12.708	5	13	20	0	0	0				AdReg chr12 #4423	0	0	1
4424	12	132,094,783	132,095,408	625	1	4.4	2.5	12.15	6	6	19	0	0	0				AdReg chr12 #4424	0	0	1
4425	12	132,102,441	132,103,387	946	2	11.172	14.379	5.889	26	35	12	0	0	0				AdReg chr12 #4425	1	1	0
4426	12	132,186,539	132,186,969	430	1	7	5.846	11.462	10	6	17	0	0	1	SFRS8	-8,881	upstream	AdReg chr12 #4426	0	0	1
4427	12	132,194,917	132,196,094	1,177	2	11.639	16.417	10.486	26	26	20	1	1	1	SFRS8	-130	upstream	AdReg chr12 #4427	1	1	0
4428	12	132,268,372	132,269,341	969	2	11.167	9.586	2.875	15	18	7	0	0	1	SFRS8	73,221	in gene	AdReg chr12 #4428	1	1	0
4429	12	132,269,393	132,270,028	635	1	8.4	9.85	2.368	14	18	4	0	0	1	SFRS8	74,075	in gene	AdReg chr12 #4429	0	1	0
4430	12	132,270,605	132,271,302	697	1	6.773	7.773	12.227	11	12	17	0	0	1	SFRS8	75,318	in gene	AdReg chr12 #4430	0	0	1
4431	12	132,312,498	132,313,167	669	2	14.286	12.737	1.545	35	26	2	1	1	1	MMP17	-109	upstream	AdReg chr12 #4431	1	1	0
4432	12	132,336,685	132,337,377	692	1	6.045	4.227	11.591	9	8	17	0	0	1	MMP17	24,090	downstream	AdReg chr12 #4432	0	0	1
4433	12	132,352,809	132,353,219	410	1	4.538	5	12.385	6	7	17	0	0	0				AdReg chr12 #4433	0	0	1
4434	12	132,380,170	132,380,621	451	1	7.929	5.571	13	14	10	18	2	1	1	ULK1	1,116	in gene	AdReg chr12 #4434	0	0	1
4435	12	132,386,505	132,387,323	818	1	4.48	4.48	9.92	8	7	12	0	0	1	ULK1	7,635	in gene	AdReg chr12 #4435	0	0	1
4436	12	132,399,912	132,400,862	950	1	4.621	4.862	11.414	7	9	16	0	0	1	ULK1	21,108	in gene	AdReg chr12 #4436	0	0	1
4437	12	132,402,147	132,402,580	433	1	4.538	4	13.692	6	7	20	0	0	1	ULK1	23,084	in gene	AdReg chr12 #4437	0	0	1
4438	12	132,414,493	132,414,994	501	1	8.25	5.188	12.875	12	8	24	1	1	2	ULK1, PUS1	35464, 998	downstream, in gene	AdReg chr12 #4438	0	0	1
4439	12	132,548,165	132,548,545	380	1	3.083	2.333	11.583	5	5	17	0	0	1	EP400	113,847	in gene	AdReg chr12 #4439	0	0	1
4440	12	132,618,097	132,618,885	788	1	4.68	4.2	10.6	6	7	20	0	0	1	DDX51	10,389	downstream	AdReg chr12 #4440	0	0	1
4441	12	132,625,390	132,626,113	723	1	3.435	5.391	10.565	5	14	15	0	1	2	DDX51, NOC4L	3129, -3242	in gene, upstream	AdReg chr12 #4441	0	0	1
4442	12	132,628,665	132,629,323	658	2	12.526	12.476	6.895	24	27	12	1	2	2	DDX51, NOC4L	-114, 1	upstream, in gene	AdReg chr12 #4442	1	1	0
4443	12	132,631,687	132,632,370	683	1	4.619	4	12.667	8	6	19	0	1	2	DDX51, NOC4L	-3148, 3035	upstream, in gene	AdReg chr12 #4443	0	0	1
4444	12	132,656,073	132,657,001	928	1	4.034	4.586	11.241	7	8	15	0	0	0				AdReg chr12 #4444	0	0	1
4445	12	132,660,588	132,661,138	550	1	3.059	3.588	11.529	5	9	15	0	0	0				AdReg chr12 #4445	0	0	1
4446	12	132,666,231	132,666,725	494	1	2.812	4.75	11.125	4	10	18	0	0	0				AdReg chr12 #4446	0	0	1
4447	12	132,700,046	132,700,438	392	1	3.417	8.333	13.833	6	13	20	0	0	1	GALNT9	-9,669	upstream	AdReg chr12 #4447	0	0	1
4448	12	132,834,178	132,834,706	528	1	5.125	5.167	13.438	8	5	20	1	0	1	GALNT9	71,463	in gene	AdReg chr12 #4448	0	0	1
4449	12	132,835,086	132,835,727	641	1	5.1	2.05	11.45	9	4	17	0	0	1	GALNT9	70,499	in gene	AdReg chr12 #4449	0	0	1
4450	12	132,837,217	132,837,603	386	1	5	4.417	11.167	9	6	16	1	0	1	GALNT9	68,495	in gene	AdReg chr12 #4450	0	0	1
4451	12	132,864,070	132,864,545	475	1	4.4	6.067	11.4	6	10	17	0	0	2	GALNT9, LOC100130238	41598, 12330	in gene, downstream	AdReg chr12 #4451	0	0	1
4452	12	132,895,005	132,895,627	622	1	5.8	4.7	12.9	10	8	21	0	0	1	GALNT9	10,589	in gene	AdReg chr12 #4452	0	0	1
4453	12	132,905,481	132,905,986	505	1	6.375	5.938	13.062	10	9	23	1	1	1	GALNT9	172	in gene	AdReg chr12 #4453	0	0	1
4454	12	132,913,714	132,914,300	586	1	4	6.444	11.222	7	13	15	0	0	1	GALNT9	-8,102	upstream	AdReg chr12 #4454	0	0	1
4455	12	132,918,820	132,919,390	570	1	2.118	6.353	13.588	4	9	19	0	0	0				AdReg chr12 #4455	0	0	1
4456	12	132,930,766	132,931,403	637	1	5.3	4.4	12.8	7	7	18	0	0	0				AdReg chr12 #4456	0	0	1
4457	12	132,936,680	132,937,207	527	1	5.625	3.125	14.812	8	4	26	0	0	0				AdReg chr12 #4457	0	0	1
4458	12	132,962,853	132,963,586	733	1	5	3.25	11.783	9	5	16	0	0	0				AdReg chr12 #4458	0	0	1
4459	12	132,971,783	132,972,300	517	1	4.125	3.812	10.938	10	8	14	0	0	0				AdReg chr12 #4459	0	0	1
4460	12	132,983,691	132,984,405	714	1	4.227	5.727	11.864	8	10	17	1	0	0				AdReg chr12 #4460	0	0	1
4461	12	132,991,068	132,991,698	630	1	6.1	5.55	12.45	11	10	20	1	0	0				AdReg chr12 #4461	0	0	1
4462	12	133,010,160	133,010,726	566	1	3.944	6.167	10.833	5	8	15	2	0	0				AdReg chr12 #4462	0	0	1
4463	12	133,027,242	133,027,804	562	1	3.235	4.062	12.823	6	7	20	0	1	1	LOC100506978	-7,499	upstream	AdReg chr12 #4463	0	0	1
4464	12	133,030,355	133,030,811	456	1	4.429	5.5	11.857	7	8	14	0	1	1	LOC100506978	-4,439	upstream	AdReg chr12 #4464	0	0	1
4465	12	133,042,022	133,042,394	372	1	4.818	3.909	11	7	6	14	0	0	1	LOC100506978	7,186	downstream	AdReg chr12 #4465	0	0	1
4466	12	133,052,032	133,052,418	386	1	7.692	7.538	11.462	12	10	17	0	0	0				AdReg chr12 #4466	0	0	1
4467	12	133,072,124	133,072,641	517	1	4.941	4.235	10.412	10	5	16	0	0	1	FBRSL1	5,225	in gene	AdReg chr12 #4467	0	0	1
4468	12	133,074,559	133,075,082	523	1	1.941	5.529	11.823	3	9	17	0	0	1	FBRSL1	7,663	in gene	AdReg chr12 #4468	0	0	1
4469	12	133,076,300	133,076,799	499	1	5.467	4.133	12.2	11	6	16	0	0	2	FBRSL1, LOC100506996	9392, -9659	in gene, upstream	AdReg chr12 #4469	0	0	1
4470	12	133,083,414	133,084,028	614	1	4.474	3.684	11.737	8	7	19	0	1	2	FBRSL1, LOC100506996	16564, -2487	in gene, upstream	AdReg chr12 #4470	0	0	1
4471	12	133,084,724	133,085,630	906	1	4.808	5.536	12.607	8	8	19	0	1	2	FBRSL1, LOC100506996	18020, -1031	in gene, upstream	AdReg chr12 #4471	0	0	1
4472	12	133,103,776	133,104,188	412	1	1.375	1.923	15.077	2	3	26	0	0	1	FBRSL1	36,825	in gene	AdReg chr12 #4472	0	0	1
4473	12	133,126,716	133,127,243	527	1	3.235	2.667	11.529	6	4	16	0	1	2	FBRSL1, LOC100507023	59822, -805	in gene, upstream	AdReg chr12 #4473	0	0	1
4474	12	133,140,542	133,141,128	586	1	3	3	10.842	4	5	15	1	0	2	FBRSL1, LOC100507023	73678, 13051	in gene, downstream	AdReg chr12 #4474	0	0	1
4475	12	133,162,057	133,162,501	444	1	3.286	3.286	12	5	6	14	1	0	1	FBRSL1	95,122	downstream	AdReg chr12 #4475	0	0	1
4476	12	133,180,232	133,180,937	705	1	3.5	4.773	14.546	6	10	22	1	0	1	LOC100507055	6,399	in gene	AdReg chr12 #4476	0	0	1
4477	12	133,263,713	133,264,478	765	2	14.783	12.409	1	34	28	1	1	2	2	POLE, PXMP2	-150, -97	upstream, upstream	AdReg chr12 #4477	1	1	0
4478	12	133,286,756	133,287,600	844	3	9.292	9.077	9.364	16	18	18	1	1	2	PXMP2, PGAM5	22986, -215	downstream, upstream	AdReg chr12 #4478	1	1	1
4479	12	133,338,752	133,339,139	387	1	10	7.538	7.923	16	11	13	1	1	2	ANKLE2, GOLGA3	-494, 66481	upstream, downstream	AdReg chr12 #4479	1	0	0
4480	12	133,360,515	133,360,982	467	1	4.786	4.286	12.357	8	7	18	0	0	1	GOLGA3	44,678	in gene	AdReg chr12 #4480	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4481	12	133,365,557	133,365,917	360	1	1.778	4.818	12.273	3	7	17	1	0	1	GOLGA3	39,689	in gene	AdReg chr12 #4481	0	0	1
4482	12	133,370,253	133,370,540	287	1	4.778	3.222	10.667	6	5	13	1	0	1	GOLGA3	35,030	in gene	AdReg chr12 #4482	0	0	1
4483	12	133,405,361	133,405,831	470	1	10.533	13.6	4.6	16	24	7	1	1	1	GOLGA3	-170	upstream	AdReg chr12 #4483	0	1	0
4484	12	133,464,233	133,464,911	678	2	10.905	9.571	6.381	17	14	10	1	1	1	CHFR	-568	upstream	AdReg chr12 #4484	1	1	0
4485	12	133,532,642	133,533,209	567	1	6.353	14.765	4.533	9	27	7	1	1	1	ZNF605	-33	upstream	AdReg chr12 #4485	0	1	0
4486	12	133,562,532	133,563,259	727	1	7.952	12.454	7.955	15	21	12	1	1	1	ZNF26	-161	upstream	AdReg chr12 #4486	0	1	0
4487	12	133,656,426	133,657,941	1,515	2	11.766	14.319	7.545	20	24	15	1	1	1	ZNF140	146	in gene	AdReg chr12 #4487	1	1	0
4488	12	133,706,600	133,707,012	412	1	9.231	8.077	12.538	11	13	21	1	2	2	hCG_1646157, ZNF10	253, -408	in gene, upstream	AdReg chr12 #4488	0	0	1
4489	12	133,757,693	133,758,437	744	1	7.217	13.083	6.556	13	23	11	1	1	1	ZNF268	70	in gene	AdReg chr12 #4489	0	1	0
4490	13	19,726,925	19,727,461	536	1	3.824	2.385	10.118	7	4	14	0	0	0				AdReg chr13 #4490	0	0	1
4491	13	19,755,647	19,756,295	648	1	5.286	3.333	11.714	9	5	17	0	1	1	TUBA3C	-35	upstream	AdReg chr13 #4491	0	0	1
4492	13	19,879,554	19,879,920	366	1	3.125	2.909	10.182	4	3	15	0	0	0				AdReg chr13 #4492	0	0	1
4493	13	20,160,825	20,161,517	692	1	9.318	12.409	3.591	15	21	5	0	0	0				AdReg chr13 #4493	0	1	0
4494	13	20,191,633	20,191,964	331	1	2.9	6.5	11.2	5	9	15	0	0	0				AdReg chr13 #4494	0	0	1
4495	13	20,207,887	20,208,617	730	1	8.348	11.13	5.913	12	15	11	1	1	1	MPHOSPH8	464	in gene	AdReg chr13 #4495	0	1	0
4496	13	20,356,825	20,357,456	631	1	6.3	10	4.35	9	15	8	1	1	1	PSPC1	-57	upstream	AdReg chr13 #4496	0	1	0
4497	13	20,437,461	20,438,222	761	3	14.875	15.917	8.667	29	34	16	1	2	2	ZMYM5, LOC400099	-65, 717	upstream, in gene	AdReg chr13 #4497	1	1	1
4498	13	20,531,452	20,532,230	778	1	8.76	10.6	7.52	15	15	12	1	1	1	ZMYM2	-969	upstream	AdReg chr13 #4498	0	1	0
4499	13	20,735,154	20,736,005	851	1	13.074	6.926	6.375	19	11	10	1	1	1	GJA3	-396	upstream	AdReg chr13 #4499	1	0	0
4500	13	20,993,789	20,994,677	888	1	9.464	11.857	5	15	17	8	0	0	1	CRYL1	105,779	in gene	AdReg chr13 #4500	0	1	0
4501	13	21,100,112	21,100,781	669	1	7.476	12.191	3.571	15	18	5	1	1	1	CRYL1	-434	upstream	AdReg chr13 #4501	0	1	0
4502	13	21,347,235	21,348,392	1,157	3	9.417	13.028	9.25	18	18	20	1	1	2	N6AMT2, XPO4	244, 129100	in gene, downstream	AdReg chr13 #4502	1	1	1
4503	13	21,634,350	21,634,854	504	1	10.875	6.688	6.417	16	10	10	1	1	1	LATS2	1,120	in gene	AdReg chr13 #4503	1	0	0
4504	13	21,635,286	21,635,988	702	2	11.273	8.727	2.941	18	17	4	1	1	1	LATS2	85	in gene	AdReg chr13 #4504	1	1	0
4505	13	21,750,084	21,751,217	1,133	3	13.457	14.086	11.629	27	29	27	1	2	2	SKA3, MRP63	91, 278	in gene, in gene	AdReg chr13 #4505	1	1	1
4506	13	21,871,624	21,873,077	1,453	2	31.133	36.889	7.111	141	160	15	1	1	2	LOC650794, LOC100505610	8, 50510	in gene, downstream	AdReg chr13 #4506	1	1	0
4507	13	21,894,770	21,895,064	294	1	2.778	3.111	12.556	4	4	16	1	0	1	LOC100505610	27,943	in gene	AdReg chr13 #4507	0	0	1
4508	13	22,177,782	22,178,585	803	1	8.16	13	9.44	14	18	12	1	1	1	EPHA1	172	in gene	AdReg chr13 #4508	0	1	0
4509	13	22,826,574	22,826,920	346	1	3.545	2	10.727	5	5	14	0	0	1	LOC100506622	42,323	in gene	AdReg chr13 #4509	0	0	1
4510	13	23,514,113	23,514,682	569	1	3.875	2.647	10.588	6	6	13	0	0	0				AdReg chr13 #4510	0	0	1
4511	13	23,535,858	23,536,327	469	1	2.667	3.067	11.933	4	5	19	0	0	0				AdReg chr13 #4511	0	0	1
4512	13	23,708,886	23,709,474	588	1	2	3.474	10.368	3	5	15	0	0	0				AdReg chr13 #4512	0	0	1
4513	13	23,716,147	23,716,713	566	1	3.833	5.667	13.333	7	11	23	0	0	0				AdReg chr13 #4513	0	0	1
4514	13	24,007,212	24,008,219	1,007	2	10.774	8.355	6.968	17	15	17	0	1	2	SACS, LOC100506680	126, 14605	in gene, downstream	AdReg chr13 #4514	1	0	1
4515	13	24,041,286	24,041,749	463	1	4.571	12.5	2.929	6	19	5	0	1	1	LOC100506697	-2,134	upstream	AdReg chr13 #4515	0	1	0
4516	13	24,144,154	24,144,757	603	1	9.368	11.474	2.789	14	20	4	0	1	1	TNFRSF19	-268	upstream	AdReg chr13 #4516	0	1	0
4517	13	24,153,349	24,153,998	649	1	6.8	13	8.55	10	18	12	1	0	1	TNFRSF19	8,950	in gene	AdReg chr13 #4517	0	1	0
4518	13	24,462,916	24,464,514	1,598	2	35.82	40.3	5.188	176	189	11	1	2	3	MIPEP, PCOTH, RP11-45B20.2	-128, 687, 7410	upstream, in gene, downstream	AdReg chr13 #4518	1	1	0
4519	13	24,553,224	24,554,162	938	2	11.069	12.517	5.739	18	19	11	1	0	0				AdReg chr13 #4519	1	1	0
4520	13	24,734,325	24,735,251	926	1	6	9.862	8.207	12	15	18	1	2	2	SPATA13, MIR2276	-73, -1767	upstream, upstream	AdReg chr13 #4520	0	1	0
4521	13	25,086,101	25,087,260	1,159	1	13.889	9.889	8.296	25	17	16	1	1	1	PARP4	268	in gene	AdReg chr13 #4521	1	0	0
4522	13	25,496,364	25,497,459	1,095	1	14.059	11.5	5.438	22	17	9	1	1	1	CENPJ	174	in gene	AdReg chr13 #4522	1	0	0
4523	13	25,592,851	25,593,190	339	1	5.636	6.455	10.636	7	8	14	1	0	0				AdReg chr13 #4523	0	0	1
4524	13	25,850,849	25,851,308	459	2	13.143	9.071	1.333	23	16	2	0	0	1	MTMR6	10,626	in gene	AdReg chr13 #4524	1	1	0
4525	13	25,860,649	25,862,156	1,507	2	22.425	25.979	4.932	80	90	12	1	1	1	MTMR6	302	in gene	AdReg chr13 #4525	1	1	0
4526	13	25,875,278	25,876,484	1,206	3	11.79	12.895	6.211	31	28	14	1	1	1	NUPL1	215	in gene	AdReg chr13 #4526	1	1	1
4527	13	26,067,985	26,068,444	459	1	9.714	10.571	1	12	14	1	0	0	1	ATP8A2	122,005	in gene	AdReg chr13 #4527	0	1	0
4528	13	26,760,198	26,761,025	827	1	8	13.154	5.692	17	25	15	1	0	0				AdReg chr13 #4528	0	1	0
4529	13	26,795,777	26,796,856	1,079	2	10.788	13.152	8.939	20	24	19	1	1	1	RNF6	192	in gene	AdReg chr13 #4529	1	1	0
4530	13	27,082,834	27,083,374	540	1	10.353	11.765	1.429	13	24	2	0	0	0				AdReg chr13 #4530	0	1	0
4531	13	27,131,360	27,131,726	366	1	10	6.083	6.5	15	8	10	1	0	0				AdReg chr13 #4531	1	0	0
4532	13	27,269,992	27,270,655	663	1	4.8	2.059	10.85	10	4	14	0	0	2	WASF3, LOC100506956	83226, 8286	downstream, in gene	AdReg chr13 #4532	0	0	1
4533	13	27,588,623	27,589,275	652	1	3.45	4.75	12.1	5	8	15	0	0	0				AdReg chr13 #4533	0	0	1
4534	13	27,609,852	27,610,624	772	1	8.08	13.64	3.273	13	21	6	0	0	0				AdReg chr13 #4534	0	1	0
4535	13	27,704,145	27,704,410	265	1	2.375	5.125	9.875	3	7	14	0	0	1	USP12	41,756	in gene	AdReg chr13 #4535	0	0	1
4536	13	27,746,045	27,746,644	599	2	9.789	11.263	4.667	19	16	8	0	1	1	USP12	-311	upstream	AdReg chr13 #4536	1	1	0
4537	13	27,769,385	27,769,909	524	2	10.5	9.938	2.875	16	14	5	0	0	0				AdReg chr13 #4537	1	1	0
4538	13	27,825,159	27,826,149	990	3	10.194	12.258	11.161	19	18	22	1	3	3	RPL21, SNORD102, SNORA27	-38, -3547, -3884	upstream, upstream, upstream	AdReg chr13 #4538	1	1	1
4539	13	27,845,075	27,845,643	568	1	7.389	11.222	3.444	10	17	6	1	1	1	RASL11A	895	in gene	AdReg chr13 #4539	0	1	0
4540	13	27,961,415	27,961,687	272	1	2.375	5	10.875	3	6	14	0	0	0				AdReg chr13 #4540	0	0	1
4541	13	28,024,064	28,025,021	957	2	11.467	9.5	9.621	19	15	18	1	1	1	MTIF3	197	in gene	AdReg chr13 #4541	1	0	1
4542	13	28,033,603	28,034,274	671	1	7.81	9.8	15.809	13	14	28	0	0	1	MTIF3	-9,199	upstream	AdReg chr13 #4542	0	0	1
4543	13	28,366,120	28,367,735	1,615	2	11.02	16.88	5.347	35	45	11	1	1	1	GSX1	147	in gene	AdReg chr13 #4543	1	1	0
4544	13	28,368,889	28,369,367	478	1	2	2.933	11.733	3	4	16	0	1	1	GSX1	2,348	downstream	AdReg chr13 #4544	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4545	13	28,502,372	28,502,942	570	1	4.235	4.824	10.941	7	11	15	2	0	1	PDX1	8,489	downstream	ActReg chr13 #4545	0	0	1
4546	13	29,068,217	29,068,650	433	1	7	6	11.643	10	8	16	1	1	1	FLT1	832	in gene	ActReg chr13 #4546	0	0	1
4547	13	29,114,577	29,115,203	626	1	7.95	12	3.462	16	20	6	0	0	0				ActReg chr13 #4547	0	1	0
4548	13	29,148,617	29,149,236	619	1	9.737	13.526	3.778	14	24	6	0	0	0				ActReg chr13 #4548	0	1	0
4549	13	29,198,040	29,199,220	1,180	1	8.649	12.243	4.784	12	18	11	0	0	0				ActReg chr13 #4549	0	1	0
4550	13	30,010,046	30,010,706	660	1	4.81	11.048	5.048	9	15	7	0	0	1	MTUS2	411,628	in gene	ActReg chr13 #4550	0	1	0
4551	13	30,156,777	30,157,923	1,146	1	6.118	12.917	4	11	20	8	0	0	1	SLC7A1	12,475	in gene	ActReg chr13 #4551	0	1	0
4552	13	30,307,291	30,307,823	532	1	10.765	8.647	3.294	14	13	5	0	0	0				ActReg chr13 #4552	1	0	0
4553	13	30,314,327	30,314,626	299	1	4	2.4	10.5	5	3	14	0	0	0				ActReg chr13 #4553	0	0	1
4554	13	30,424,237	30,424,506	269	1	10.75	6.25	11.75	14	7	14	1	1	1	UBL3	449	in gene	ActReg chr13 #4554	0	0	1
4555	13	30,963,663	30,964,256	593	1	9.737	9.526	2.625	14	15	5	0	0	0				ActReg chr13 #4555	0	1	0
4556	13	31,151,433	31,152,046	613	1	6.263	11.684	1.353	11	21	3	0	0	0				ActReg chr13 #4556	0	1	0
4557	13	31,191,373	31,192,707	1,334	3	10.571	13.024	6.452	20	26	17	1	1	1	USPL1	210	in gene	ActReg chr13 #4557	1	1	1
4558	13	31,247,687	31,248,855	1,168	3	11.472	12.444	10.056	19	19	27	1	0	0				ActReg chr13 #4558	1	1	1
4559	13	31,305,794	31,306,398	604	1	1.824	3.611	10.056	3	7	12	0	1	1	ALOX5AP	-3,573	upstream	ActReg chr13 #4559	0	0	1
4560	13	31,317,117	31,318,286	1,169	2	12.135	14.405	3	20	31	6	0	0	1	ALOX5AP	8,032	in gene	ActReg chr13 #4560	1	1	0
4561	13	31,403,135	31,403,950	815	2	15.885	15.423	4.615	31	26	9	0	0	0				ActReg chr13 #4561	1	1	0
4562	13	31,446,393	31,446,720	327	1	4.727	7.273	10	6	12	15	0	0	1	LOC100507084	8,869	in gene	ActReg chr13 #4562	0	0	1
4563	13	31,579,230	31,579,700	470	1	5.267	3.933	11	8	7	13	0	0	0				ActReg chr13 #4563	0	0	1
4564	13	31,735,623	31,736,908	1,285	2	8.65	10.9	8.05	18	17	19	1	1	1	HSPH1	-148	upstream	ActReg chr13 #4564	1	1	0
4565	13	32,605,465	32,606,033	568	1	9.944	6.167	8.389	16	10	13	1	2	2	LOC100507099, FRY	31, 312	in gene, in gene	ActReg chr13 #4565	1	0	0
4566	13	32,885,354	32,885,770	416	1	4.692	2.692	11.692	7	4	16	1	2	2	ZAR1L, BRCA2	529, -4055	in gene, upstream	ActReg chr13 #4566	0	0	1
4567	13	32,889,303	32,889,831	528	1	7.647	10.529	7.765	11	17	12	1	2	2	ZAR1L, BRCA2	-3476, -50	upstream, upstream	ActReg chr13 #4567	0	1	0
4568	13	32,889,841	32,890,287	446	1	10.214	5.857	5.714	12	8	10	1	2	2	ZAR1L, BRCA2	-3973, 447	upstream, in gene	ActReg chr13 #4568	1	0	0
4569	13	33,002,003	33,002,520	517	1	8.188	6.688	11.812	13	10	16	1	1	2	N4BP2L1, N4BP2L2	54, 110675	in gene, downstream	ActReg chr13 #4569	0	0	1
4570	13	33,112,339	33,113,571	1,232	2	22.615	20.18	4	59	62	11	0	1	1	N4BP2L2	-19	upstream	ActReg chr13 #4570	1	1	0
4571	13	34,021,115	34,021,818	703	2	9.409	11.864	2.9	17	24	4	0	0	0				ActReg chr13 #4571	1	1	0
4572	13	34,116,736	34,117,301	565	1	10.333	9.5	4.722	17	15	7	1	0	0				ActReg chr13 #4572	1	0	0
4573	13	34,184,388	34,185,048	660	1	11.1	6.5	5.312	19	11	9	0	0	0				ActReg chr13 #4573	1	0	0
4574	13	34,256,165	34,256,530	365	1	3.875	3.727	12.182	5	7	17	0	0	0				ActReg chr13 #4574	0	0	1
4575	13	34,391,857	34,392,640	783	2	11.72	11.2	7.16	27	21	14	1	1	1	RFC3	42	in gene	ActReg chr13 #4575	1	1	0
4576	13	34,730,906	34,731,614	708	1	12.864	9.273	5.571	20	15	10	0	0	0				ActReg chr13 #4576	1	0	0
4577	13	34,921,775	34,922,545	770	1	12.75	3.75	1.875	21	8	4	0	0	0				ActReg chr13 #4577	1	0	0
4578	13	35,486,950	35,487,651	701	1	12.636	11.046	4.955	25	24	7	0	0	0				ActReg chr13 #4578	1	0	0
4579	13	35,500,559	35,501,109	550	2	11.286	14.941	0	20	26	0	0	0	0				ActReg chr13 #4579	1	1	0
4580	13	36,290,874	36,291,199	325	1	4.5	8.1	11.9	6	10	15	0	0	0				ActReg chr13 #4580	0	0	1
4581	13	36,429,576	36,430,279	703	1	6.909	12	1.955	14	21	3	0	0	1	DCLK1	275,537	in gene	ActReg chr13 #4581	0	1	0
4582	13	36,919,911	36,920,204	293	1	9.111	10.556	10.444	11	16	13	1	1	2	SPG20, LOC100507135	24260, -518	in gene, upstream	ActReg chr13 #4582	0	0	1
4583	13	36,920,207	36,921,175	968	2	11.586	14.9	4.533	24	25	11	1	1	2	SPG20, LOC100507135	23626, 116	in gene, in gene	ActReg chr13 #4583	1	1	0
4584	13	37,292,057	37,292,658	601	1	10.632	11.21	3.105	15	17	5	0	0	0				ActReg chr13 #4584	0	1	0
4585	13	37,393,655	37,394,319	664	1	4.857	10.857	8	7	17	13	1	1	1	RFXAP	648	in gene	ActReg chr13 #4585	0	1	0
4586	13	37,572,841	37,573,946	1,105	2	35.294	37.912	4.382	136	126	10	1	2	3	ALG5, EXOSC8, FAM48A	111, -1285, 60457	in gene, upstream, downstream	ActReg chr13 #4586	1	1	0
4587	13	37,574,491	37,575,210	719	2	11	11.565	8.565	20	19	13	1	2	3	ALG5, EXOSC8, FAM48A	-1346, 172, 59000	upstream, in gene, downstream	ActReg chr13 #4587	1	1	0
4588	13	37,643,827	37,644,318	491	1	3.733	6.933	11.2	6	14	17	0	0	1	FAM48A	-10,222	upstream	ActReg chr13 #4588	0	0	1
4589	13	39,248,208	39,248,922	714	2	12.773	9.381	1.4	26	21	2	0	0	0				ActReg chr13 #4589	1	1	0
4590	13	39,462,483	39,462,958	475	1	9.2	9.667	1.857	12	17	3	0	0	1	FREM2	201,547	downstream	ActReg chr13 #4590	0	1	0
4591	13	39,611,686	39,612,867	1,181	2	13.324	17.811	5.973	32	42	12	2	2	2	C13orf23, NHLRC3	-24, -179	upstream, upstream	ActReg chr13 #4591	1	1	0
4592	13	40,414,255	40,414,840	585	1	11.111	8.722	3.5	19	13	5	0	0	0				ActReg chr13 #4592	1	0	0
4593	13	40,676,890	40,677,423	533	1	5.941	11.529	4.353	8	21	7	0	0	0				ActReg chr13 #4593	0	1	0
4594	13	40,738,070	40,738,578	508	1	5.133	12.5	2.125	8	19	5	0	0	0				ActReg chr13 #4594	0	1	0
4595	13	40,742,491	40,743,277	786	1	7.68	10.88	3.368	13	17	5	0	0	0				ActReg chr13 #4595	0	1	0
4596	13	40,976,402	40,976,923	521	1	10.125	2.875	1	17	5	1	0	0	1	LOC646982	78,481	in gene	ActReg chr13 #4596	1	0	0
4597	13	41,027,648	41,028,320	672	2	9.8	9.682	3.091	18	16	4	0	0	1	LOC646982	27,159	in gene	ActReg chr13 #4597	1	1	0
4598	13	41,238,698	41,239,959	1,261	2	9.949	11.41	4.108	16	22	7	1	1	1	FOXO1	1,406	in gene	ActReg chr13 #4598	1	1	0
4599	13	41,344,926	41,345,718	792	3	12.08	11.88	13.4	25	25	25	1	1	1	MRPS31	25	in gene	ActReg chr13 #4599	1	1	1
4600	13	41,495,333	41,496,252	919	2	9.25	10.893	8.214	17	18	15	1	0	1	ELF1	97,716	downstream	ActReg chr13 #4600	0	1	1
4601	13	41,634,046	41,636,301	2,255	4	9.859	13.225	9.662	29	24	19	1	1	1	WBP4	-524	upstream	ActReg chr13 #4601	1	1	1
4602	13	41,706,077	41,707,301	1,224	2	8.59	12.18	7.833	25	27	12	1	1	1	KBTBD6	247	in gene	ActReg chr13 #4602	0	1	1
4603	13	41,768,212	41,769,062	850	2	10.852	11.037	5.2	18	28	11	1	1	1	KBTBD7	65	in gene	ActReg chr13 #4603	1	1	0
4604	13	41,884,910	41,886,018	1,108	3	10.857	9.429	11.281	21	17	21	1	1	1	NAA16	123	in gene	ActReg chr13 #4604	1	1	1
4605	13	42,031,097	42,031,525	428	1	5.214	9	14	9	12	22	1	1	1	C13orf15	-231	upstream	ActReg chr13 #4605	0	0	1
4606	13	42,534,787	42,535,611	824	1	9.32	12.08	9.56	18	16	17	1	2	2	KIAA0564, LOC100507240	22, -106	in gene, upstream	ActReg chr13 #4606	0	1	0
4607	13	42,615,103	42,615,489	386	1	7	9.846	9.769	9	15	15	1	1	1	DGKH	-7,593	upstream	ActReg chr13 #4607	0	0	1
4608	13	42,623,411	42,623,753	342	1	10.454	10.091	10.636	14	13	16	1	1	1	DGKH	693	in gene	ActReg chr13 #4608	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4609	13	43,051,830	43,052,152	322	1	4.8	5.2	10.1	7	7	14	0	0	0				ActReg chr13 #4609	0	0	1
4610	13	43,284,461	43,284,993	532	1	10.118	9.529	2.167	15	17	4	0	0	0				ActReg chr13 #4610	0	1	0
4611	13	43,565,982	43,566,554	572	1	5	5.667	12.778	7	8	18	1	1	1	EPSTI1	109	in gene	ActReg chr13 #4611	0	0	1
4612	13	43,632,070	43,632,767	697	1	9.619	10.476	2.625	14	13	5	0	0	1	DNAJC15	35,056	in gene	ActReg chr13 #4612	0	1	0
4613	13	44,379,108	44,379,727	619	1	7.412	9	3.105	13	18	5	0	0	0				ActReg chr13 #4613	0	1	0
4614	13	44,453,069	44,453,633	564	2	10.222	10.833	11.111	15	15	18	1	2	2	CCDC122, C13orf31	475, -69	in gene, upstream	ActReg chr13 #4614	1	0	1
4615	13	44,706,724	44,707,420	696	1	8.857	12.238	4.143	12	22	7	0	0	1	LOC100507253	-9,392	upstream	ActReg chr13 #4615	0	1	0
4616	13	44,715,764	44,716,241	477	1	8.933	11.933	10.933	16	16	15	1	1	1	LOC100507253	-462	upstream	ActReg chr13 #4616	0	0	1
4617	13	44,733,637	44,734,359	722	1	8.273	12.091	1.5	18	25	3	0	0	1	LOC100507253	17,534	downstream	ActReg chr13 #4617	0	1	0
4618	13	44,817,019	44,817,762	743	1	12.75	9.167	3.792	21	13	6	0	0	0				ActReg chr13 #4618	1	0	0
4619	13	45,151,990	45,152,493	503	1	6.562	8.812	12.5	9	13	22	1	2	2	TSC22D1, LOC641467	-1540, 2212	upstream, in gene	ActReg chr13 #4619	0	0	1
4620	13	45,165,208	45,165,803	595	1	2.062	2.091	11.632	3	3	17	0	0	0				ActReg chr13 #4620	0	0	1
4621	13	45,391,080	45,391,604	524	1	5.375	12.062	4.625	11	16	7	0	0	0				ActReg chr13 #4621	0	1	0
4622	13	45,393,054	45,393,806	752	1	8.583	12.167	2.773	13	21	6	0	0	0				ActReg chr13 #4622	0	1	0
4623	13	45,491,697	45,493,080	1,383	3	12.628	12.674	10.767	20	25	37	0	0	0				ActReg chr13 #4623	1	1	1
4624	13	45,563,213	45,564,144	931	3	11.276	9.724	12.345	18	18	22	1	2	2	NUP1P1, KIAA1704	-65, -9	upstream, upstream	ActReg chr13 #4624	1	1	1
4625	13	45,915,102	45,915,802	700	3	9.818	14.546	11.454	18	26	21	1	3	4	LOC100287803, TPT1, SNORA31, LOC100190939	4451, -155, -3708, -28	in gene, upstream, upstream, upstream	ActReg chr13 #4625	1	1	1
4626	13	45,991,569	45,992,784	1,215	1	7.763	11.842	8	13	20	15	1	2	2	SLC25A30, LOC100507293	340, 217	in gene, in gene	ActReg chr13 #4626	0	1	0
4627	13	46,038,624	46,039,883	1,259	1	8.4	11.6	6.763	16	20	13	1	1	1	COG3	182	in gene	ActReg chr13 #4627	0	1	0
4628	13	46,626,546	46,627,213	667	1	9.667	10.667	6.238	14	21	13	1	1	2	ZC3H13, CPB2	15, 52332	in gene, downstream	ActReg chr13 #4628	0	1	0
4629	13	47,127,709	47,128,460	751	1	12.292	8.042	8.583	20	13	12	1	1	1	LRCH1	788	in gene	ActReg chr13 #4629	1	0	0
4630	13	47,370,583	47,371,327	744	2	7.696	9.783	10.348	12	13	18	1	1	1	ESD	412	in gene	ActReg chr13 #4630	0	1	1
4631	13	48,235,068	48,235,679	611	2	8.737	7.842	2.273	18	15	4	0	0	0				ActReg chr13 #4631	1	1	0
4632	13	48,574,821	48,575,951	1,130	2	7.829	11.543	9.429	13	17	17	1	1	1	SUCLA2	76	in gene	ActReg chr13 #4632	0	1	1
4633	13	48,611,419	48,612,545	1,126	2	14.556	15.611	8.636	26	26	23	1	1	1	NUDT15	279	in gene	ActReg chr13 #4633	1	1	0
4634	13	48,668,765	48,669,700	935	2	27.6	33.633	8.633	83	99	15	1	1	1	MED4	8	in gene	ActReg chr13 #4634	1	1	0
4635	13	48,784,181	48,784,824	643	1	11.4	6.55	1.667	20	14	3	0	0	0				ActReg chr13 #4635	1	0	0
4636	13	49,020,655	49,021,152	497	1	9.938	4.875	1.444	15	9	2	0	1	2	RB1, LPAR6	143020, -2063	in gene, upstream	ActReg chr13 #4636	1	0	0
4637	13	49,106,482	49,107,515	1,033	2	10.406	9.562	13.25	18	17	25	1	1	1	RCBTB2	318	in gene	ActReg chr13 #4637	1	0	1
4638	13	49,323,696	49,324,360	664	1	6.952	10.714	1.364	11	19	2	0	0	0				ActReg chr13 #4638	0	1	0
4639	13	49,466,337	49,467,383	1,046	2	15.031	12.344	2.167	31	22	5	0	0	0				ActReg chr13 #4639	1	1	0
4640	13	49,550,260	49,550,642	382	1	12.083	9.583	15.167	16	13	24	1	1	1	FNDC3A	403	in gene	ActReg chr13 #4640	0	0	1
4641	13	50,017,828	50,018,837	1,009	1	9.581	11.613	7.742	17	18	13	1	2	2	CAB39L, SETDB2	-111, -97	upstream, upstream	ActReg chr13 #4641	0	1	0
4642	13	50,070,232	50,070,810	578	1	7.944	11.556	4.643	12	19	8	1	1	2	SETDB2, PHF11	52092, 720	downstream, in gene	ActReg chr13 #4642	0	1	0
4643	13	50,143,605	50,143,907	302	1	3	3.4	9.6	6	4	13	0	0	1	RCBTB1	15,963	in gene	ActReg chr13 #4643	0	0	1
4644	13	50,366,525	50,367,230	705	2	13.727	14.546	6.25	27	28	11	1	1	1	KPNA3	180	in gene	ActReg chr13 #4644	1	1	0
4645	13	50,509,809	50,510,931	1,122	2	18.971	24.629	6.971	47	75	13	1	1	1	C13orf1	256	in gene	ActReg chr13 #4645	1	1	0
4646	13	50,697,948	50,699,390	1,442	3	8.956	12.822	7.644	15	29	15	1	1	1	DLEU2	1,008	in gene	ActReg chr13 #4646	1	1	0
4647	13	50,985,360	50,985,892	532	1	7.941	10.588	5.235	13	13	10	0	0	0				ActReg chr13 #4647	0	1	0
4648	13	51,199,982	51,200,580	598	1	4.158	10.632	1.5	7	15	2	0	0	0				ActReg chr13 #4648	0	1	0
4649	13	51,483,542	51,484,867	1,325	1	7.071	13.857	5.842	11	20	15	1	1	1	RNASEH2B	312	in gene	ActReg chr13 #4649	0	1	0
4650	13	51,722,552	51,723,015	463	1	1.533	4.467	12.133	3	7	15	0	1	1	LOC647166	346	in gene	ActReg chr13 #4650	0	0	1
4651	13	52,026,902	52,027,317	415	1	10.308	7.769	10.846	13	10	17	1	2	2	INTS6, LOC100507398	166, -368	in gene, upstream	ActReg chr13 #4651	0	0	1
4652	13	52,377,513	52,378,130	617	1	7.684	12.21	6.368	12	17	10	1	2	3	DHRS12, LOC100507413, RP11-327P2.4	472, 88, 41465	in gene, in gene, downstream	ActReg chr13 #4652	0	1	0
4653	13	52,378,135	52,378,750	615	1	8.056	11.263	5.389	13	18	10	1	2	3	DHRS12, LOC100507413, RP11-327P2.4	-149, 709, 40844	upstream, in gene, downstream	ActReg chr13 #4653	0	1	0
4654	13	52,702,714	52,703,160	446	1	4.429	5.786	12.214	7	8	16	1	1	2	NEK5, NEK3	277, 31059	in gene, downstream	ActReg chr13 #4654	0	0	1
4655	13	52,768,281	52,768,844	563	1	10.389	11.389	13.111	17	19	24	1	0	0				ActReg chr13 #4655	0	0	1
4656	13	53,024,145	53,025,071	926	2	9.655	11.517	4.931	15	18	8	1	2	2	VPS36, CKAP2	155, -4887	in gene, upstream	ActReg chr13 #4656	1	1	0
4657	13	53,029,077	53,030,285	1,208	1	8.053	10.29	6.152	15	17	12	1	2	2	VPS36, CKAP2	-4918, 186	upstream, in gene	ActReg chr13 #4657	0	1	0
4658	13	53,174,069	53,174,408	339	1	3	4.091	11.091	4	6	14	1	0	0				ActReg chr13 #4658	0	0	1
4659	13	53,191,105	53,192,048	943	1	8.103	11.931	6.16	11	21	9	1	1	1	HNRNPA1L2	-29	upstream	ActReg chr13 #4659	0	1	0
4660	13	53,226,147	53,227,518	1,371	2	11.333	12.976	6.385	24	38	12	1	1	2	HNRNPA1L2, SUGT1	35227, 1	downstream, in gene	ActReg chr13 #4660	1	1	0
4661	13	53,424,393	53,425,640	1,247	2	10.256	12.462	7.111	15	18	14	1	1	1	PCDH8	-2,242	upstream	ActReg chr13 #4661	1	1	0
4662	13	53,775,643	53,776,538	895	1	2.792	4.786	12.821	7	8	21	1	0	0				ActReg chr13 #4662	0	0	1
4663	13	53,982,933	53,983,476	543	1	3.375	2.7	12.412	6	3	17	0	0	0				ActReg chr13 #4663	0	0	1
4664	13	54,026,604	54,026,927	323	1	0	1	9.8	0	1	13	0	0	0				ActReg chr13 #4664	0	0	1
4665	13	56,150,793	56,151,072	279	1	1.222	3.333	9.556	2	4	12	0	0	0				ActReg chr13 #4665	0	0	1
4666	13	57,309,823	57,310,214	391	1	4.538	12.308	11.385	8	18	20	0	0	0				ActReg chr13 #4666	0	0	1
4667	13	57,860,584	57,861,119	535	1	4.312	4.438	12.812	6	6	17	0	0	0				ActReg chr13 #4667	0	0	1
4668	13	59,078,383	59,078,747	364	1	2.273	2.727	10.546	4	5	13	0	0	0				ActReg chr13 #4668	0	0	1
4669	13	59,347,467	59,347,774	307	1	4.222	2.667	10.889	7	4	12	0	0	0				ActReg chr13 #4669	0	0	1
4670	13	59,433,328	59,433,667	339	1	3	4	12.636	6	5	19	0	0	0				ActReg chr13 #4670	0	0	1
4671	13	60,737,687	60,738,467	780	1	10.12	12.72	6.04	18	27	9	1	1	1	DIAPH3	42	in gene	ActReg chr13 #4671	0	1	0
4672	13	61,237,712	61,238,153	441	1	2.385	4.5	11.857	4	6	16	0	0	0				ActReg chr13 #4672	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4673	13	61,687,434	61,688,016	582	1	3.353	3.167	12.5	5	5	17	0	0	0				ActReg chr13 #4673	0	0	1
4674	13	62,269,168	62,269,696	528	1	11.235	6.941	1.846	18	14	3	0	0	0				ActReg chr13 #4674	1	0	0
4675	13	63,216,918	63,217,779	861	2	10.407	13.37	2.815	24	24	7	0	0	0				ActReg chr13 #4675	1	1	0
4676	13	64,009,795	64,010,330	535	1	7.188	10.688	1.357	11	17	2	0	0	0				ActReg chr13 #4676	0	1	0
4677	13	64,649,609	64,650,379	770	1	6.917	11.125	5.783	14	19	12	0	0	0				ActReg chr13 #4677	0	1	0
4678	13	64,651,239	64,651,994	755	1	12.522	9.13	3.227	20	14	6	0	0	0				ActReg chr13 #4678	1	0	0
4679	13	65,125,879	65,126,427	548	1	7.824	11.412	1.375	15	16	2	0	0	0				ActReg chr13 #4679	0	1	0
4680	13	65,499,675	65,500,015	340	1	5.727	6.727	11.364	10	9	14	0	0	0				ActReg chr13 #4680	0	0	1
4681	13	66,114,479	66,114,921	442	1	10.643	6.429	1	19	11	1	0	0	0				ActReg chr13 #4681	1	0	0
4682	13	66,418,625	66,418,941	316	1	5.222	2.778	12	6	4	14	0	0	0				ActReg chr13 #4682	0	0	1
4683	13	67,804,218	67,805,078	860	2	13.148	12.518	2.962	21	18	7	1	2	2	PCDH9, LOC730236	-180, -67	upstream, upstream	ActReg chr13 #4683	1	1	0
4684	13	68,343,463	68,344,387	924	1	7.655	10.207	6.345	11	18	13	0	0	0				ActReg chr13 #4684	0	1	0
4685	13	69,795,905	69,796,301	396	1	9.5	10.167	5.583	12	14	8	0	0	0				ActReg chr13 #4685	0	1	0
4686	13	71,641,497	71,641,865	368	1	3.833	1.833	9.333	5	2	14	0	0	0				ActReg chr13 #4686	0	0	1
4687	13	72,958,877	72,959,407	530	1	9.235	6.875	1.417	16	10	2	0	0	0				ActReg chr13 #4687	1	0	0
4688	13	73,301,088	73,302,331	1,243	3	12.436	13.949	10.615	31	30	19	1	2	2	C13orf37, C13orf34	229, -333	in gene, upstream	ActReg chr13 #4688	1	1	1
4689	13	73,911,147	73,911,510	363	1	10.182	3.818	2.636	15	5	4	0	0	0				ActReg chr13 #4689	1	0	0
4690	13	74,707,838	74,708,309	471	1	7.533	9.4	5	11	15	9	1	1	1	KLF12	-7	upstream	ActReg chr13 #4690	0	1	0
4691	13	74,709,791	74,710,545	754	1	7.875	10.292	7.083	17	15	11	1	1	1	KLF12	-2,102	upstream	ActReg chr13 #4691	0	1	0
4692	13	74,784,917	74,785,532	615	2	11.421	15.053	1.545	18	29	3	0	0	0				ActReg chr13 #4692	1	1	0
4693	13	76,055,508	76,056,947	1,439	1	9	10.311	6.022	16	18	13	1	1	1	TBC1D4	23	in gene	ActReg chr13 #4693	0	1	0
4694	13	76,092,448	76,093,078	630	1	3.211	2.833	11.05	5	5	15	0	0	1	COMMD6	19,228	downstream	ActReg chr13 #4694	0	0	1
4695	13	76,111,575	76,112,575	1,000	2	11.355	14.129	4.433	23	32	9	1	1	1	COMMD6	-84	upstream	ActReg chr13 #4695	1	1	0
4696	13	76,123,314	76,124,335	1,021	2	10.969	13.844	5.812	22	22	12	1	1	1	UCHL3	-103	upstream	ActReg chr13 #4696	1	1	0
4697	13	76,210,480	76,211,273	793	2	10.72	7.4	10.92	22	11	17	1	0	1	LMO7	16,306	in gene	ActReg chr13 #4697	1	0	1
4698	13	76,567,844	76,568,295	451	1	9.714	10.571	2.143	16	19	3	0	0	0				ActReg chr13 #4698	0	1	0
4699	13	76,593,423	76,594,287	864	1	6.37	12.926	4.2	10	18	5	0	0	0				ActReg chr13 #4699	0	1	0
4700	13	77,566,073	77,566,645	572	1	10.111	11.833	8.611	17	18	18	1	1	1	CLN5	300	in gene	ActReg chr13 #4700	0	1	0
4701	13	77,900,404	77,901,627	1,223	1	8.316	11.947	5.816	17	25	12	1	1	1	MYCBP2	162	in gene	ActReg chr13 #4701	0	1	0
4702	13	77,903,095	77,903,957	862	2	12.889	11.926	5.889	20	24	11	1	1	1	MYCBP2	-2,349	upstream	ActReg chr13 #4702	1	1	0
4703	13	78,427,829	78,428,468	639	1	10.15	6.4	1	18	12	1	0	0	1	LOC100505518	35,076	in gene	ActReg chr13 #4703	1	0	0
4704	13	78,492,424	78,493,092	668	1	11.333	9.19	3.19	18	12	5	1	1	2	LOC100505518, EDNRB	99686, 208	downstream, in gene	ActReg chr13 #4704	1	0	0
4705	13	79,702,237	79,702,796	559	2	8.556	8.778	1.091	14	17	2	0	0	0				ActReg chr13 #4705	1	1	0
4706	13	79,980,137	79,981,070	933	1	6.552	13.069	6.536	13	19	13	1	2	2	RBM26, LOC100505538	-680, 120	upstream, in gene	ActReg chr13 #4706	0	1	0
4707	13	80,205,323	80,205,726	403	1	5.583	11.667	1	9	20	1	0	0	0				ActReg chr13 #4707	0	1	0
4708	13	80,561,366	80,561,978	612	1	9.947	6.211	3.316	16	11	7	0	0	0				ActReg chr13 #4708	1	0	0
4709	13	80,563,189	80,563,710	521	1	11.938	9	2.667	16	13	4	0	0	0				ActReg chr13 #4709	1	0	0
4710	13	80,614,575	80,615,296	721	2	13.13	12.217	1	23	22	1	0	0	0				ActReg chr13 #4710	1	1	0
4711	13	80,914,373	80,914,855	482	1	7.6	6.467	11.267	12	10	16	1	1	1	SPRY2	472	in gene	ActReg chr13 #4711	0	0	1
4712	13	80,915,062	80,915,632	570	1	5.444	9.111	14.389	10	14	29	1	1	1	SPRY2	-261	upstream	ActReg chr13 #4712	0	0	1
4713	13	80,916,687	80,917,635	948	1	6.833	9.867	3.9	14	18	6	0	1	1	SPRY2	-2,075	upstream	ActReg chr13 #4713	0	1	0
4714	13	80,953,480	80,953,914	434	1	10.462	6.923	2.692	17	11	4	0	0	0				ActReg chr13 #4714	1	0	0
4715	13	81,042,844	81,043,382	538	1	9.529	6.353	2	15	10	5	0	0	0				ActReg chr13 #4715	1	0	0
4716	13	81,622,080	81,622,509	429	1	11	11.214	1	14	13	1	0	0	0				ActReg chr13 #4716	1	0	0
4717	13	81,738,613	81,738,963	350	1	4	3.545	10.091	6	6	14	0	0	0				ActReg chr13 #4717	0	0	1
4718	13	83,314,662	83,314,952	290	1	5.111	1.111	10.667	7	2	14	0	0	0				ActReg chr13 #4718	0	0	1
4719	13	84,073,223	84,073,948	725	2	10.318	12.364	2.286	15	20	4	0	0	0				ActReg chr13 #4719	1	1	0
4720	13	84,187,636	84,188,075	439	1	2.5	8.357	10.714	4	11	18	0	0	0				ActReg chr13 #4720	0	0	1
4721	13	84,453,349	84,454,887	1,538	1	6.792	12.604	6.458	14	21	21	1	1	1	SLITRK1	2,410	in gene	ActReg chr13 #4721	0	1	0
4722	13	84,455,825	84,456,663	838	2	15.654	21.615	4.042	37	50	10	0	1	1	SLITRK1	284	in gene	ActReg chr13 #4722	1	1	0
4723	13	84,660,236	84,661,047	811	1	12.64	13.24	6.72	19	20	15	0	0	0				ActReg chr13 #4723	0	1	0
4724	13	85,405,856	85,406,289	433	1	4.286	3	13	6	5	18	0	0	0				ActReg chr13 #4724	0	0	1
4725	13	85,439,874	85,440,589	715	1	6.045	10.409	1	12	17	1	0	0	0				ActReg chr13 #4725	0	1	0
4726	13	85,468,727	85,469,269	542	1	2.588	7.176	11.941	4	14	18	0	0	0				ActReg chr13 #4726	0	0	1
4727	13	85,887,709	85,888,400	691	1	8.409	13.409	1.438	12	27	2	0	0	0				ActReg chr13 #4727	0	1	0
4728	13	85,888,588	85,889,327	739	2	9.043	10.391	1.667	17	18	3	0	0	0				ActReg chr13 #4728	1	1	0
4729	13	86,004,925	86,005,423	498	1	4.438	4.5	12.438	8	6	21	0	0	0				ActReg chr13 #4729	0	0	1
4730	13	86,160,435	86,161,185	750	1	8	9.583	2.364	11	13	5	0	0	0				ActReg chr13 #4730	0	1	0
4731	13	86,225,235	86,226,049	814	1	9.846	7.36	2.769	16	12	7	0	0	0				ActReg chr13 #4731	1	0	0
4732	13	87,233,956	87,234,599	643	1	7.4	11.25	2.353	13	19	5	0	0	0				ActReg chr13 #4732	0	1	0
4733	13	87,444,042	87,444,852	810	2	22.72	21.08	7.36	52	48	11	0	0	0				ActReg chr13 #4733	1	1	0
4734	13	87,731,881	87,733,155	1,274	1	11.175	8.6	6.5	15	12	11	0	0	0				ActReg chr13 #4734	1	0	0
4735	13	88,150,726	88,151,458	732	2	12	13.043	2.1	22	26	3	0	0	1	hCG_1795283	172,126	in gene	ActReg chr13 #4735	1	1	0
4736	13	88,213,799	88,214,158	359	1	1.75	3	8.727	2	4	11	0	0	1	hCG_1795283	109,240	in gene	ActReg chr13 #4736	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4737	13	88,323,176	88,324,281	1,105	1	10.735	14.559	6.529	23	28	11	1	2	2	hCG_1795283, SLITRK5	-510, -1142	upstream, upstream	ActReg chr13 #4737	0	1	0
4738	13	88,462,467	88,463,616	1,149	2	11.556	15.611	7.656	23	26	16	0	0	0				ActReg chr13 #4738	1	1	0
4739	13	88,606,549	88,606,989	440	1	9.5	7.143	1	15	12	1	0	0	0				ActReg chr13 #4739	1	0	0
4740	13	88,943,971	88,944,396	425	1	5	5.538	11.615	9	8	17	0	0	0				ActReg chr13 #4740	0	0	1
4741	13	89,815,246	89,815,909	663	1	13.476	11.238	3.333	31	21	6	0	0	0				ActReg chr13 #4741	1	0	0
4742	13	90,378,847	90,379,437	590	2	10.316	10.895	1.333	21	16	2	0	0	0				ActReg chr13 #4742	1	1	0
4743	13	91,147,029	91,147,508	479	1	2.733	4.333	18.867	6	7	25	0	0	0				ActReg chr13 #4743	0	0	1
4744	13	92,001,220	92,001,648	428	1	4.846	10.923	4.769	7	18	8	1	7	7	MIR17HG, MIR17, MIR18A, MIR19A, MIR20A, MIR19B1, MIR92A1	1360, -1425, -1571, -1711, -1885, -2012, -2134	in gene, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr13 #4744	0	1	0
4745	13	92,051,068	92,051,874	806	1	5.769	5.385	12.577	10	7	18	1	1	1	GPC5	536	in gene	ActReg chr13 #4745	0	0	1
4746	13	93,495,757	93,496,395	638	1	7.25	9.8	2.25	11	17	4	0	0	1	GPC5	1,445,141	in gene	ActReg chr13 #4746	0	1	0
4747	13	93,803,302	93,804,089	787	1	10.958	9.708	0	14	14	0	0	0	0				ActReg chr13 #4747	1	0	0
4748	13	93,822,155	93,822,887	732	2	14.043	11.565	3.391	31	22	6	0	0	0				ActReg chr13 #4748	1	1	0
4749	13	93,869,679	93,870,501	822	1	7.231	11.077	1.455	17	19	3	0	0	1	GPC6	-8,988	upstream	ActReg chr13 #4749	0	1	0
4750	13	93,878,663	93,881,075	2,412	4	11.68	14.4	8.746	20	24	19	1	1	1	GPC6	791	in gene	ActReg chr13 #4750	1	1	1
4751	13	93,900,744	93,901,331	587	1	7.722	12.778	3.556	11	21	5	0	0	1	GPC6	21,959	in gene	ActReg chr13 #4751	0	1	0
4752	13	93,901,656	93,902,338	682	1	11	9.864	1	15	13	1	0	0	1	GPC6	22,919	in gene	ActReg chr13 #4752	1	0	0
4753	13	94,016,355	94,016,895	540	1	7.438	13.625	3.182	11	25	5	0	0	1	GPC6	137,547	in gene	ActReg chr13 #4753	0	1	0
4754	13	94,499,204	94,499,825	621	1	8.947	10.632	1.917	16	20	3	0	0	1	GPC6	620,436	in gene	ActReg chr13 #4754	0	1	0
4755	13	94,981,893	94,982,582	689	1	7.19	10.714	3.238	11	18	6	0	0	1	GPC6	1,103,159	in gene	ActReg chr13 #4755	0	1	0
4756	13	95,248,197	95,248,696	499	1	10.867	16.6	14	15	24	20	1	2	2	TGDS, GPR180	65, -5658	in gene, upstream	ActReg chr13 #4756	0	0	1
4757	13	95,253,679	95,254,561	882	1	9.679	11.857	8.036	14	15	13	1	2	2	TGDS, GPR180	-5609, 16	upstream, in gene	ActReg chr13 #4757	0	1	0
4758	13	95,363,078	95,363,595	517	1	5.75	9.812	12.25	9	13	21	1	2	2	SOX21, LOC100507533	1053, -1634	in gene, upstream	ActReg chr13 #4758	0	0	1
4759	13	95,620,274	95,620,987	713	1	4.864	6.727	12.5	8	9	16	1	0	0				ActReg chr13 #4759	0	0	1
4760	13	95,752,590	95,753,418	828	2	10.808	10.808	3.562	17	18	5	0	0	1	ABCC4	200,683	in gene	ActReg chr13 #4760	1	1	0
4761	13	95,952,873	95,953,791	918	2	11.893	13.714	6.5	23	26	10	1	1	1	ABCC4	355	in gene	ActReg chr13 #4761	1	1	0
4762	13	96,187,394	96,188,230	836	2	13.615	13.346	3.346	23	25	7	0	0	1	CLDN10	101,959	in gene	ActReg chr13 #4762	1	1	0
4763	13	96,295,802	96,296,699	897	1	11	11.821	5.926	19	16	11	1	1	1	DZIP1	707	in gene	ActReg chr13 #4763	0	1	0
4764	13	96,328,718	96,329,855	1,137	2	12.171	14.029	9.514	17	25	18	1	2	2	LOC100289274, DNAJC3	-125, -107	upstream, upstream	ActReg chr13 #4764	1	1	0
4765	13	96,743,498	96,743,889	391	1	11.25	5.083	13.083	14	8	20	1	1	1	HS6ST3	600	in gene	ActReg chr13 #4765	0	0	1
4766	13	97,646,125	97,646,869	744	2	11.478	9.478	9.783	23	18	15	1	1	1	OXGR1	107	in gene	ActReg chr13 #4766	1	0	1
4767	13	97,655,262	97,655,771	509	1	10.812	5.062	1	17	9	1	0	0	1	OXGR1	-8,912	upstream	ActReg chr13 #4767	1	0	0
4768	13	97,907,021	97,907,504	483	1	10.133	8	1.846	17	14	3	0	0	1	MBNL2	32,688	in gene	ActReg chr13 #4768	1	0	0
4769	13	97,947,629	97,948,204	575	1	9.944	3.647	1.125	15	6	2	0	0	1	MBNL2	73,342	in gene	ActReg chr13 #4769	1	0	0
4770	13	98,019,171	98,019,688	517	1	6.625	10.25	3.438	12	17	6	0	0	1	MBNL2	144,855	in gene	ActReg chr13 #4770	0	1	0
4771	13	98,047,649	98,048,510	861	2	9.692	15.5	1	18	33	1	0	0	1	MBNL2	173,505	downstream	ActReg chr13 #4771	1	1	0
4772	13	98,085,253	98,086,303	1,050	1	12	10.25	3.5	21	16	7	1	1	1	RAP2A	-697	upstream	ActReg chr13 #4772	1	0	0
4773	13	98,300,898	98,301,365	467	1	11.643	11.143	1.538	17	14	3	0	0	0				ActReg chr13 #4773	1	0	0
4774	13	98,371,940	98,372,535	595	1	4.5	10.5	1.267	7	19	2	0	0	0				ActReg chr13 #4774	0	1	0
4775	13	98,432,570	98,433,244	674	2	11.048	11.762	2.571	19	17	5	0	0	0				ActReg chr13 #4775	1	1	0
4776	13	99,128,582	99,129,260	678	1	11.286	13.619	4.571	22	24	6	0	0	1	STK24	100,475	in gene	ActReg chr13 #4776	0	1	0
4777	13	99,161,723	99,162,282	559	1	10.389	6.167	3.5	18	10	5	0	0	1	STK24	67,394	in gene	ActReg chr13 #4777	1	0	0
4778	13	99,739,049	99,739,887	838	1	5.923	13.115	5.115	10	20	12	1	1	1	DOCK9	-808	upstream	ActReg chr13 #4778	0	1	0
4779	13	99,852,537	99,853,291	754	1	9.708	13.25	9.083	15	26	19	1	2	2	LOC100289373, UBAC2	97, 255	in gene, in gene	ActReg chr13 #4779	0	1	0
4780	13	100,153,093	100,154,029	936	2	13.793	11.724	5.069	26	18	14	1	1	1	TM9SF2	-167	upstream	ActReg chr13 #4780	1	1	0
4781	13	100,448,170	100,448,902	732	2	11.87	14.261	2.333	21	23	4	0	0	1	CLYBL	189,617	in gene	ActReg chr13 #4781	1	1	0
4782	13	100,740,757	100,741,651	894	3	10.321	12.429	8.571	24	18	18	1	2	2	LOC100507636, PCCA	-7, -65	upstream, upstream	ActReg chr13 #4782	1	1	1
4783	13	100,934,583	100,934,937	354	1	2.857	3.7	11.818	4	5	16	0	0	1	PCCA	193,491	in gene	ActReg chr13 #4783	0	0	1
4784	13	101,240,723	101,241,719	996	2	11.968	16.323	4.222	36	35	10	1	1	2	A2LD1, LOC100507654	-175, -8850	upstream, upstream	ActReg chr13 #4784	1	1	0
4785	13	102,118,098	102,118,719	621	1	9.842	8.158	2.778	21	11	4	0	0	1	ITGB1	13,442	in gene	ActReg chr13 #4785	1	0	0
4786	13	102,497,793	102,498,278	485	1	10.933	6.067	1.727	16	9	3	0	0	1	FGF14	556,089	in gene	ActReg chr13 #4786	1	0	0
4787	13	102,568,492	102,568,979	487	1	4.733	2.4	13	6	6	19	1	0	1	FGF14	485,389	in gene	ActReg chr13 #4787	0	0	1
4788	13	102,571,681	102,572,305	624	2	8.789	10.947	4.438	15	17	9	0	0	1	FGF14	482,131	in gene	ActReg chr13 #4788	1	1	0
4789	13	103,052,186	103,053,201	1,015	2	6.875	10.094	9.438	14	15	19	1	2	3	FGF14, LOC283480, LOC283481	1431, -5824, 5765	in gene, upstream, downstream	ActReg chr13 #4789	0	1	1
4790	13	103,057,853	103,058,496	643	1	6.333	14.905	3.4	12	28	6	0	1	2	FGF14, LOC283481	-4050, 11246	upstream, downstream	ActReg chr13 #4790	0	1	0
4791	13	103,248,888	103,249,542	654	1	9.381	11.905	7.625	15	19	11	1	1	1	TPP2	-71	upstream	ActReg chr13 #4791	0	1	0
4792	13	103,425,489	103,426,643	1,154	2	11.25	9.417	11.611	19	14	19	1	1	2	C13orf27, KDELC1	83, 25338	in gene, downstream	ActReg chr13 #4792	1	0	1
4793	13	103,450,913	103,451,711	798	1	8.292	12.75	7.708	11	20	13	1	2	2	KDELC1, BIVM	92, -87	in gene, upstream	ActReg chr13 #4793	0	1	0
4794	13	103,451,805	103,452,527	722	1	6.565	11.696	6.435	10	17	10	1	2	2	KDELC1, BIVM	-762, 767	upstream, in gene	ActReg chr13 #4794	0	1	0
4795	13	103,497,764	103,498,580	816	1	12.36	15.52	11	26	31	17	1	1	2	BIVM, ERCC5	46773, -2	downstream, upstream	ActReg chr13 #4795	0	1	0
4796	13	104,038,496	104,039,344	848	2	18.185	21.815	2.8	51	58	4	0	0	0				ActReg chr13 #4796	1	1	0
4797	13	104,695,312	104,696,062	750	2	10.783	10.391	3.923	18	18	7	0	0	0				ActReg chr13 #4797	1	1	0
4798	13	105,102,017	105,102,784	767	1	5.25	11.958	2.111	10	20	4	0	0	0				ActReg chr13 #4798	0	1	0
4799	13	105,311,315	105,312,153	838	2	12	11.577	3.167	23	19	8	0	0	0				ActReg chr13 #4799	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4800	13	105,490,030	105,490,716	686	1	3.579	11.095	4.905	7	18	12	0	0	0				ActReg chr13 #4800	0	1	0
4801	13	106,239,947	106,240,782	835	2	12.423	14	2.684	33	33	5	0	0	0				ActReg chr13 #4801	1	1	0
4802	13	106,294,735	106,295,478	743	2	12.652	12.783	3.25	21	21	6	0	0	0				ActReg chr13 #4802	1	1	0
4803	13	106,426,150	106,427,057	907	1	7.071	12.393	2.826	10	19	5	0	0	0				ActReg chr13 #4803	0	1	0
4804	13	106,643,582	106,644,575	993	2	11.839	11.452	5.583	24	20	13	0	0	0				ActReg chr13 #4804	1	1	0
4805	13	106,803,510	106,804,441	931	1	11.586	8.966	4.828	19	21	9	0	0	0				ActReg chr13 #4805	1	0	0
4806	13	106,828,491	106,829,161	670	1	9.381	10.809	1	17	16	1	0	0	0				ActReg chr13 #4806	0	1	0
4807	13	107,028,180	107,029,739	1,559	1	7.837	12.796	5.408	16	22	11	0	1	1	LOC728192	48	in gene	ActReg chr13 #4807	0	1	0
4808	13	107,124,161	107,124,905	744	1	6.87	10.652	3.391	13	15	6	0	0	0				ActReg chr13 #4808	0	1	0
4809	13	107,160,031	107,160,575	544	1	10.941	11.765	4.824	17	17	7	0	0	1	EFNB2	27,034	in gene	ActReg chr13 #4809	0	1	0
4810	13	107,165,322	107,166,144	822	1	11.615	9.231	3	17	14	7	0	0	1	EFNB2	21,604	in gene	ActReg chr13 #4810	1	0	0
4811	13	107,219,658	107,220,544	886	1	10.464	11.643	9.321	18	18	17	1	1	1	ARGLU1	413	in gene	ActReg chr13 #4811	0	1	0
4812	13	108,516,698	108,517,749	1,051	2	11.303	12.333	1.667	23	24	3	0	1	1	FAM155A	2,237	in gene	ActReg chr13 #4812	1	1	0
4813	13	108,772,632	108,773,088	456	1	4.933	9.733	2.071	8	14	4	0	0	0				ActReg chr13 #4813	0	1	0
4814	13	108,870,295	108,871,205	910	2	10.724	13.138	6.069	21	24	13	1	2	2	LIG4, ABHD13	-54, -13	upstream, upstream	ActReg chr13 #4814	1	1	0
4815	13	108,929,782	108,930,452	670	1	9	11.238	2.647	17	21	7	0	0	1	TNFSF13B	8,140	in gene	ActReg chr13 #4815	0	1	0
4816	13	109,554,579	109,555,300	721	1	10.304	11.478	3.647	15	17	8	0	0	1	MYO16	306,439	in gene	ActReg chr13 #4816	0	1	0
4817	13	109,637,364	109,638,016	652	1	9.333	12.619	2.619	18	16	5	0	0	1	MYO16	389,190	in gene	ActReg chr13 #4817	0	1	0
4818	13	109,639,549	109,640,351	802	1	9.08	11.92	4.56	13	18	7	0	0	1	MYO16	391,450	in gene	ActReg chr13 #4818	0	1	0
4819	13	109,833,066	109,833,677	611	1	6.579	11.368	2.333	10	17	4	0	0	1	MYO16	584,871	in gene	ActReg chr13 #4819	0	1	0
4820	13	109,895,521	109,896,279	758	1	11.913	9	2.591	17	12	6	0	0	0				ActReg chr13 #4820	1	0	0
4821	13	110,056,806	110,057,209	403	1	5.167	6.667	11.167	8	10	16	0	0	0				ActReg chr13 #4821	0	0	1
4822	13	110,374,301	110,374,797	496	1	4.062	4.188	12.375	6	5	20	0	0	0				ActReg chr13 #4822	0	0	1
4823	13	110,434,259	110,437,041	2,782	3	12.391	14.483	7.828	24	22	20	1	1	1	IRS2	3,264	in gene	ActReg chr13 #4823	1	1	1
4824	13	110,443,379	110,443,988	609	1	6.632	10.263	2.8	12	18	4	0	1	1	IRS2	-4,769	upstream	ActReg chr13 #4824	0	1	0
4825	13	110,492,474	110,493,317	843	1	10.926	15.704	4.407	19	30	8	0	0	0				ActReg chr13 #4825	0	1	0
4826	13	110,650,936	110,651,797	861	1	8.815	12.222	1.292	13	20	2	0	0	0				ActReg chr13 #4826	0	1	0
4827	13	110,658,267	110,659,222	955	2	12.867	12.933	4.433	24	19	11	0	0	0				ActReg chr13 #4827	1	1	0
4828	13	110,679,699	110,680,857	1,158	1	14.917	9.083	3.861	30	18	8	0	0	0				ActReg chr13 #4828	1	0	0
4829	13	110,746,745	110,747,713	968	2	12.613	13.613	1.643	23	32	4	0	0	0				ActReg chr13 #4829	1	1	0
4830	13	110,760,396	110,761,650	1,254	1	11.154	13.462	6.263	17	21	13	0	0	0				ActReg chr13 #4830	0	1	0
4831	13	110,790,123	110,790,857	734	1	13.043	14.565	7.5	20	25	13	1	0	0				ActReg chr13 #4831	0	1	0
4832	13	110,918,240	110,918,649	409	1	1.6	3.308	12.154	2	7	17	1	0	1	COL4A1	41,052	in gene	ActReg chr13 #4832	0	0	1
4833	13	110,958,614	110,960,684	2,070	3	11.431	11.492	9.968	18	18	27	1	2	2	COL4A1, COL4A2	-153, 18	upstream, in gene	ActReg chr13 #4833	1	1	1
4834	13	110,971,546	110,973,006	1,460	2	14.652	13.109	5.2	26	23	12	0	0	1	COL4A2	12,645	in gene	ActReg chr13 #4834	1	1	0
4835	13	111,065,538	111,066,377	839	1	7.154	7.154	12.385	13	11	18	0	0	1	COL4A2	106,326	in gene	ActReg chr13 #4835	0	0	1
4836	13	111,151,696	111,153,138	1,442	2	10.911	11.4	3.2	21	19	7	0	0	1	COL4A2	192,786	in gene	ActReg chr13 #4836	1	1	0
4837	13	111,157,557	111,158,549	992	1	5.065	5.806	10.032	7	11	15	0	0	1	COL4A2	198,422	in gene	ActReg chr13 #4837	0	0	1
4838	13	111,178,004	111,178,422	418	1	4	7.692	13.615	7	12	20	0	0	1	RAB20	35,858	in gene	ActReg chr13 #4838	0	0	1
4839	13	111,213,308	111,214,113	805	1	7.077	11.5	8.96	12	19	18	1	1	1	RAB20	361	in gene	ActReg chr13 #4839	0	1	0
4840	13	111,267,337	111,268,850	1,513	3	12.404	12.66	11.744	22	19	20	1	1	1	CARKD	85	in gene	ActReg chr13 #4840	1	1	1
4841	13	111,277,759	111,278,634	875	1	2.731	5.143	11.107	5	7	16	1	0	1	CARKD	10,188	in gene	ActReg chr13 #4841	0	0	1
4842	13	111,294,523	111,295,281	758	1	4.583	6.458	13.083	6	11	18	1	0	2	CARKD, CARS2	26894, 63578	downstream, in gene	ActReg chr13 #4842	0	0	1
4843	13	111,364,791	111,366,064	1,273	2	11.475	12.3	12.725	19	20	26	1	2	2	CARS2, ING1	-6947, 344	upstream, in gene	ActReg chr13 #4843	0	1	1
4844	13	111,366,979	111,368,119	1,140	2	8.886	10.657	10.029	15	13	19	1	1	2	CARS2, ING1	-9069, 2466	upstream, in gene	ActReg chr13 #4844	0	1	1
4845	13	111,464,306	111,464,846	540	1	4	4.941	12.471	7	7	19	1	0	0				ActReg chr13 #4845	0	0	1
4846	13	111,465,041	111,465,460	419	1	3.923	5.231	13.692	6	8	22	1	0	0				ActReg chr13 #4846	0	0	1
4847	13	111,521,668	111,523,194	1,526	1	10.34	15.234	5.766	23	26	10	0	1	2	C13orf29, ANKRD10	224, 44985	in gene, downstream	ActReg chr13 #4847	0	1	0
4848	13	111,566,849	111,568,387	1,538	3	9.292	11.125	10.581	18	26	23	1	1	1	ANKRD10	-202	upstream	ActReg chr13 #4848	0	1	1
4849	13	111,605,701	111,606,244	543	1	6.412	6.235	12.353	9	9	16	0	0	1	LOC100505512	17,963	in gene	ActReg chr13 #4849	0	0	1
4850	13	111,607,286	111,607,645	359	1	8.545	15	11.091	11	21	14	0	0	1	LOC100505512	16,470	in gene	ActReg chr13 #4850	0	0	1
4851	13	111,747,193	111,747,806	613	1	4.421	9.211	15.684	6	13	29	0	0	0				ActReg chr13 #4851	0	0	1
4852	13	111,766,803	111,767,152	349	1	7.909	7.727	11	13	9	15	0	1	1	ARHGEF7	-647	upstream	ActReg chr13 #4852	0	0	1
4853	13	111,805,372	111,806,885	1,513	3	12.729	15.062	8.104	27	30	27	1	1	2	ARHGEF7, LOC100505533	38504, -204	in gene, upstream	ActReg chr13 #4853	1	1	1
4854	13	112,110,192	112,110,903	711	1	3.545	5.909	11.636	6	9	19	0	0	0				ActReg chr13 #4854	0	0	1
4855	13	112,113,953	112,114,440	487	1	2.6	3.333	13.133	4	5	17	0	0	0				ActReg chr13 #4855	0	0	1
4856	13	112,135,088	112,135,588	500	1	2.933	3.125	12.438	7	5	20	0	0	0				ActReg chr13 #4856	0	0	1
4857	13	112,200,637	112,201,057	420	1	3	2.571	11	4	4	20	1	0	0				ActReg chr13 #4857	0	0	1
4858	13	112,275,610	112,276,121	511	1	5.125	5.312	12.375	8	8	20	1	0	0				ActReg chr13 #4858	0	0	1
4859	13	112,297,731	112,298,222	491	1	4	2.267	11.133	6	3	15	0	0	0				ActReg chr13 #4859	0	0	1
4860	13	112,322,305	112,322,712	407	1	2.75	3.167	12.667	5	5	14	0	0	0				ActReg chr13 #4860	0	0	1
4861	13	112,333,103	112,333,632	529	1	3.353	3.471	13.647	6	6	20	0	0	0				ActReg chr13 #4861	0	0	1
4862	13	112,343,479	112,343,918	439	1	2.538	3.071	10	4	5	15	0	0	0				ActReg chr13 #4862	0	0	1
4863	13	112,353,069	112,353,863	794	1	2.6	3	12.36	5	5	21	0	0	0				ActReg chr13 #4863	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GeneCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4864	13	112,547,982	112,548,892	910	1	2.8	3.958	11.536	7	9	17	1	0	0				ActReg chr13 #4864	0	0	1
4865	13	112,665,038	112,665,701	663	1	2.81	3.905	11.238	4	6	16	0	0	0				ActReg chr13 #4865	0	0	1
4866	13	112,690,647	112,691,232	585	1	2.789	5.211	11.368	5	8	18	1	0	0				ActReg chr13 #4866	0	0	1
4867	13	112,712,546	112,712,937	391	1	1.833	2.917	11.333	3	5	18	1	0	1	SOX1	-9,172	upstream	ActReg chr13 #4867	0	0	1
4868	13	112,984,831	112,985,471	640	1	2.7	6.2	10.75	5	10	14	1	0	0				ActReg chr13 #4868	0	0	1
4869	13	112,997,040	112,997,491	451	1	5.286	4.357	11.643	7	8	15	1	0	0				ActReg chr13 #4869	0	0	1
4870	13	113,106,815	113,107,451	636	1	7.8	3.2	14.05	11	4	20	0	0	0				ActReg chr13 #4870	0	0	1
4871	13	113,120,616	113,121,326	710	1	3.95	2.632	12.182	6	5	18	0	0	0				ActReg chr13 #4871	0	0	1
4872	13	113,241,537	113,242,876	1,339	3	11.341	13.854	10	16	22	19	2	1	1	TUBGCP3	275	in gene	ActReg chr13 #4872	1	1	1
4873	13	113,486,591	113,487,090	499	1	5.438	4.25	12.812	7	6	17	1	0	1	ATP11A	142,197	in gene	ActReg chr13 #4873	0	0	1
4874	13	113,530,737	113,531,304	567	1	2.833	4.111	11.778	5	5	16	0	0	1	ATP11A	186,377	in gene	ActReg chr13 #4874	0	0	1
4875	13	113,543,256	113,543,957	701	1	2	4.5	11.364	4	8	19	0	1	2	ATP11A, LOC100506063	198963, -5130	downstream, upstream	ActReg chr13 #4875	0	0	1
4876	13	113,588,433	113,589,026	593	1	3.789	5.579	16	6	8	25	0	0	1	LOC100506063	39,993	in gene	ActReg chr13 #4876	0	0	1
4877	13	113,622,742	113,623,455	713	1	4.955	12.954	10.454	9	23	17	1	2	2	LOC100289410, MCF2L	-146, 341	upstream, in gene	ActReg chr13 #4877	0	1	0
4878	13	113,648,427	113,648,933	506	1	4	5.312	13.062	6	8	23	1	0	1	MCF2L	25,923	in gene	ActReg chr13 #4878	0	0	1
4879	13	113,648,942	113,649,567	625	1	5.526	3.263	16.737	8	7	26	1	0	1	MCF2L	26,497	in gene	ActReg chr13 #4879	0	0	1
4880	13	113,660,264	113,660,749	485	1	4.357	5.333	12.467	8	8	16	0	0	1	MCF2L	37,749	in gene	ActReg chr13 #4880	0	0	1
4881	13	113,664,724	113,665,227	503	1	2.308	7.188	14	4	10	20	0	0	1	MCF2L	42,218	in gene	ActReg chr13 #4881	0	0	1
4882	13	113,668,307	113,668,789	482	1	4.467	3.429	14	7	6	24	0	0	1	MCF2L	45,791	in gene	ActReg chr13 #4882	0	0	1
4883	13	113,675,812	113,676,660	848	1	5.231	7.038	12.846	8	9	22	1	0	1	MCF2L	53,479	in gene	ActReg chr13 #4883	0	0	1
4884	13	113,687,744	113,688,417	673	1	3.429	7.318	12.818	6	12	18	1	0	1	MCF2L	65,323	in gene	ActReg chr13 #4884	0	0	1
4885	13	113,696,229	113,696,678	449	1	6.071	7.429	15.071	9	11	26	0	0	1	MCF2L	73,696	in gene	ActReg chr13 #4885	0	0	1
4886	13	113,697,157	113,697,781	624	1	4.368	6.105	16	7	9	26	0	0	1	MCF2L	74,712	in gene	ActReg chr13 #4886	0	0	1
4887	13	113,701,904	113,702,292	388	1	4.833	5.917	13.5	5	9	18	1	0	1	MCF2L	79,341	in gene	ActReg chr13 #4887	0	0	1
4888	13	113,710,079	113,710,514	435	1	4.571	5.571	11.929	7	7	21	0	0	1	MCF2L	87,539	in gene	ActReg chr13 #4888	0	0	1
4889	13	113,718,293	113,719,435	1,142	1	6.556	13.083	6.361	11	25	13	0	0	1	MCF2L	96,107	in gene	ActReg chr13 #4889	0	1	0
4890	13	113,720,007	113,720,555	548	1	4.8	5.882	13.235	8	8	19	0	0	1	MCF2L	97,524	in gene	ActReg chr13 #4890	0	0	1
4891	13	113,720,934	113,721,584	650	1	5.3	4.95	12.5	8	10	18	1	0	1	MCF2L	98,502	in gene	ActReg chr13 #4891	0	0	1
4892	13	113,728,344	113,728,747	403	1	2.462	3.083	12.231	5	5	19	0	0	1	MCF2L	105,788	in gene	ActReg chr13 #4892	0	0	1
4893	13	113,731,795	113,732,328	533	1	2.824	2.929	12.882	4	5	18	0	0	1	MCF2L	109,304	in gene	ActReg chr13 #4893	0	0	1
4894	13	113,732,493	113,733,227	734	1	3.524	5.174	11.826	7	9	17	0	0	1	MCF2L	110,103	in gene	ActReg chr13 #4894	0	0	1
4895	13	113,761,011	113,761,337	326	1	3.5	4	10.1	4	6	14	0	1	2	MCF2L, F7	138417, 1069	downstream, in gene	ActReg chr13 #4895	0	0	1
4896	13	113,769,796	113,770,309	513	1	3.625	3.312	11.812	6	5	16	0	1	2	F7, F10	9947, -7061	in gene, upstream	ActReg chr13 #4896	0	0	1
4897	13	113,775,758	113,776,882	1,124	1	4.531	4.914	12.943	8	9	25	0	1	2	F7, F10	16215, -793	downstream, upstream	ActReg chr13 #4897	0	0	1
4898	13	113,784,128	113,784,806	678	1	4.682	8.318	13.364	8	11	26	1	0	2	F7, F10	24362, 7354	downstream, in gene	ActReg chr13 #4898	0	0	1
4899	13	113,798,205	113,799,002	797	1	3.917	5.64	11.52	7	9	14	0	0	1	F10	21,490	in gene	ActReg chr13 #4899	0	0	1
4900	13	113,838,955	113,839,459	504	1	4.188	4.875	11.25	7	8	17	0	0	2	PCID2, LOC100506079	23822, 4103	in gene, downstream	ActReg chr13 #4900	0	0	1
4901	13	113,841,260	113,842,043	783	1	10.458	12.375	3.083	15	20	6	0	1	2	PCID2, LOC100506079	21378, 1659	in gene, downstream	ActReg chr13 #4901	0	1	0
4902	13	113,842,351	113,843,005	654	1	9.85	11.4	10.45	18	22	14	0	1	2	PCID2, LOC100506079	20351, 632	in gene, in gene	ActReg chr13 #4902	0	1	0
4903	13	113,862,299	113,863,581	1,282	3	14.65	16.275	10.75	33	29	23	1	2	2	PCID2, CUL4A	89, -146	in gene, upstream	ActReg chr13 #4903	1	1	1
4904	13	113,950,614	113,951,734	1,120	3	15.229	18.057	7.941	37	36	20	1	1	1	LAMP1	-295	upstream	ActReg chr13 #4904	1	1	1
4905	13	114,004,785	114,005,779	994	1	3.966	4.276	12.29	9	9	19	0	0	1	GRTP1	13,181	in gene	ActReg chr13 #4905	0	0	1
4906	13	114,020,286	114,020,790	504	1	4.357	2.562	12.188	7	4	15	0	1	1	GRTP1	-2,075	upstream	ActReg chr13 #4906	0	0	1
4907	13	114,047,550	114,048,452	902	2	9.276	11.414	9.357	23	22	14	1	0	0				ActReg chr13 #4907	1	1	0
4908	13	114,060,058	114,060,740	682	1	4.591	4.227	12.364	9	8	18	0	0	0				ActReg chr13 #4908	0	0	1
4909	13	114,061,122	114,062,512	1,390	1	4.585	3.833	13.209	10	8	19	0	0	0				ActReg chr13 #4909	0	0	1
4910	13	114,064,360	114,066,499	2,139	3	9.104	10.06	9.881	20	15	18	0	0	1	ADPRHL1	42,410	downstream	ActReg chr13 #4910	0	1	1
4911	13	114,067,418	114,067,963	545	1	2.938	5.529	11.823	6	10	22	2	0	1	ADPRHL1	40,149	downstream	ActReg chr13 #4911	0	0	1
4912	13	114,068,081	114,068,678	597	1	4.526	5.789	12.368	7	9	19	1	0	1	ADPRHL1	39,460	downstream	ActReg chr13 #4912	0	0	1
4913	13	114,076,883	114,077,460	577	1	3.667	2.294	11.278	7	4	17	0	0	1	ADPRHL1	30,668	in gene	ActReg chr13 #4913	0	0	1
4914	13	114,087,195	114,087,692	497	1	4.188	4.312	12.625	7	7	21	0	0	1	ADPRHL1	20,396	in gene	ActReg chr13 #4914	0	0	1
4915	13	114,099,446	114,100,031	585	1	7.778	4.222	11.556	15	6	19	0	0	1	ADPRHL1	8,101	in gene	ActReg chr13 #4915	0	0	1
4916	13	114,145,004	114,146,263	1,259	2	10.205	14.462	4.097	22	38	7	2	2	2	DCUN1D2, TMCO3	-610, 325	upstream, in gene	ActReg chr13 #4916	1	1	0
4917	13	114,200,976	114,201,531	555	1	6.471	4.294	13.235	10	7	19	0	0	1	TMCO3	55,945	in gene	ActReg chr13 #4917	0	0	1
4918	13	114,261,764	114,263,096	1,332	1	4.561	3.659	13.317	7	7	20	0	0	1	TFDP1	23,427	in gene	ActReg chr13 #4918	0	0	1
4919	13	114,310,196	114,311,157	961	1	4.233	6.633	13.3	8	10	23	0	1	1	ATP4B	1,837	in gene	ActReg chr13 #4919	0	0	1
4920	13	114,312,407	114,313,511	1,104	1	1.971	5.086	16.714	4	14	24	0	1	2	ATP4B, GRK1	-446, -8635	upstream, upstream	ActReg chr13 #4920	0	0	1
4921	13	114,321,962	114,322,722	760	1	4.542	5.727	11.083	6	12	16	0	1	2	ATP4B, GRK1	-9829, 748	upstream, in gene	ActReg chr13 #4921	0	0	1
4922	13	114,323,617	114,324,528	911	1	3	4.464	11.893	5	9	18	0	1	1	GRK1	2,478	in gene	ActReg chr13 #4922	0	0	1
4923	13	114,427,294	114,428,299	1,005	1	3.968	8.25	14.625	7	12	25	1	1	1	GRK1	1,750	in gene	ActReg chr13 #4923	0	0	1
4924	13	114,429,501	114,430,576	1,075	1	5.441	9.706	12.765	11	16	19	1	0	1	GRK1	3,992	in gene	ActReg chr13 #4924	0	0	1
4925	13	114,437,272	114,438,101	829	1	5	4.308	11.269	8	6	17	1	0	1	GRK1	11,640	in gene	ActReg chr13 #4925	0	0	1
4926	13	114,450,473	114,451,020	547	1	3.706	3	10.882	7	5	15	0	0	1	LOC100130386	3,316	downstream	ActReg chr13 #4926	0	0	1
4927	13	114,478,314	114,479,418	1,104	1	6.059	7.265	13.853	10	11	23	0	0	1	FAM70B	16,650	in gene	ActReg chr13 #4927	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4928	13	114,487,888	114,488,782	894	2	14.5	12.714	3.786	26	26	7	0	0	1	FAM70B	26,119	in gene	ActReg chr13 #4928	1	1	0
4929	13	114,503,382	114,504,798	1,416	1	5.091	4.105	13.477	11	9	21	0	0	1	FAM70B	41,874	in gene	ActReg chr13 #4929	0	0	1
4930	13	114,509,973	114,510,421	448	1	2.083	5.429	14	4	10	24	1	0	1	FAM70B	47,981	in gene	ActReg chr13 #4930	0	0	1
4931	13	114,513,537	114,514,168	631	1	3.368	3.895	12.526	6	7	20	0	0	2	FAM70B, GAS6	51636, 53194	in gene, downstream	ActReg chr13 #4931	0	0	1
4932	13	114,523,539	114,525,586	2,047	4	12.406	13.453	12	24	25	19	1	0	2	FAM70B, GAS6	62346, 42484	downstream, in gene	ActReg chr13 #4932	1	1	1
4933	13	114,540,385	114,541,206	821	1	14.28	13.16	10.72	20	20	15	0	1	2	GAS6, FLJ41484	26251, -4498	in gene, upstream	ActReg chr13 #4933	1	0	0
4934	13	114,542,786	114,543,435	649	1	3.789	5.55	12.35	8	7	16	0	1	2	GAS6, FLJ41484	23936, -2183	in gene, upstream	ActReg chr13 #4934	0	0	1
4935	13	114,546,199	114,546,793	594	1	4.474	4.579	10.263	9	7	14	1	1	2	GAS6, FLJ41484	20550, 1203	in gene, in gene	ActReg chr13 #4935	0	0	1
4936	13	114,576,999	114,577,563	564	1	3.2	7.529	11.941	6	12	15	0	0	3	GAS6, LOC100506394, FLJ44054	-10235, 10131, -9329	upstream, downstream, upstream	ActReg chr13 #4936	0	0	1
4937	13	114,580,196	114,580,874	678	1	3.762	5.286	10.952	6	10	17	0	1	1	FLJ44054	-6,075	upstream	ActReg chr13 #4937	0	0	1
4938	13	114,586,864	114,587,403	539	1	5.941	3.118	11.059	9	5	18	1	1	1	FLJ44054	523	in gene	ActReg chr13 #4938	0	0	1
4939	13	114,620,279	114,620,832	553	1	6.667	5.222	15.111	9	8	20	0	0	1	FLJ44054	33,945	in gene	ActReg chr13 #4939	0	0	1
4940	13	114,742,953	114,743,596	643	1	5.45	5.75	11.6	8	9	17	1	0	1	RASA3	154,821	downstream	ActReg chr13 #4940	0	0	1
4941	13	114,744,533	114,745,226	693	1	4.455	3.545	11.136	7	6	18	0	0	1	RASA3	153,216	downstream	ActReg chr13 #4941	0	0	1
4942	13	114,795,238	114,795,792	554	1	4.882	6	13.294	7	8	21	0	0	1	RASA3	102,580	in gene	ActReg chr13 #4942	0	0	1
4943	13	114,821,175	114,821,809	634	1	4.3	6.7	11.55	8	11	16	0	0	1	RASA3	76,603	in gene	ActReg chr13 #4943	0	0	1
4944	13	114,829,594	114,832,498	2,904	3	11	12.396	9.275	24	22	18	0	0	1	RASA3	67,049	in gene	ActReg chr13 #4944	1	1	1
4945	13	114,893,541	114,895,021	1,180	3	12.27	11.865	9.097	25	24	18	0	0	1	RASA3	3,664	in gene	ActReg chr13 #4945	1	1	1
4946	13	114,896,394	114,897,743	1,349	2	10.809	14.905	10.619	17	25	17	1	1	1	RASA3	1,027	in gene	ActReg chr13 #4946	0	1	1
4947	13	115,000,051	115,001,082	1,031	2	13.25	12.781	4.406	24	21	7	1	1	1	CDC16	204	in gene	ActReg chr13 #4947	1	1	0
4948	13	115,046,415	115,047,342	927	2	9.379	10.793	7.429	23	19	19	1	1	2	CDC16, UPF3A	46516, -200	downstream, upstream	ActReg chr13 #4948	0	1	1
4949	13	115,047,512	115,047,874	362	1	10.167	5.917	10.333	15	7	17	1	1	2	CDC16, UPF3A	47331, 615	downstream, in gene	ActReg chr13 #4949	0	0	1
4950	13	115,079,469	115,080,439	970	1	10.4	15.833	8.562	19	28	17	1	1	2	UPF3A, ZNF828	32876, -11	downstream, upstream	ActReg chr13 #4950	0	1	0
4951	14	19,469,010	19,469,497	487	1	6	9.933	3.133	11	16	5	0	0	0				ActReg chr14 #4951	0	1	0
4952	14	20,773,639	20,774,403	764	2	10.75	20	4.667	26	43	7	0	1	2	TTC5, CCNB1IP1	132, 27436	in gene, downstream	ActReg chr14 #4952	1	1	0
4953	14	20,811,097	20,811,938	841	2	11.222	8.778	11.741	27	20	27	0	2	3	CCNB1IP1, RPPH1, PARP2	-10060, 53, -256	upstream, in gene, upstream	ActReg chr14 #4953	1	0	1
4954	14	20,937,398	20,937,982	584	1	7.444	10.278	6.722	12	20	11	0	1	2	TMEM55B, PNP	-8053, 152	upstream, in gene	ActReg chr14 #4954	0	1	0
4955	14	21,078,133	21,078,674	541	1	5.294	5.647	11.177	8	10	19	1	0	0				ActReg chr14 #4955	0	0	1
4956	14	21,093,284	21,093,737	453	1	7.714	7.214	14.143	11	11	19	1	0	0				ActReg chr14 #4956	0	0	1
4957	14	21,100,054	21,101,005	951	1	7.5	11.333	3.233	10	16	6	1	0	1	OR6S1	9,321	downstream	ActReg chr14 #4957	0	1	0
4958	14	21,151,012	21,151,408	396	1	7.167	7.25	11.25	13	11	17	1	2	2	ANG, RNASE4	-1126, -1162	upstream, upstream	ActReg chr14 #4958	0	0	1
4959	14	21,439,460	21,439,975	515	1	6.625	9.875	3.857	9	16	7	1	0	0				ActReg chr14 #4959	0	1	0
4960	14	21,571,647	21,572,448	801	2	12.769	13.039	5.231	27	30	9	1	1	2	ZNF219, C14orf176	816, 4951	in gene, downstream	ActReg chr14 #4960	1	1	0
4961	14	21,924,171	21,925,028	857	1	9.148	14.037	3	15	22	6	1	0	1	RAB2B	20,533	downstream	ActReg chr14 #4961	0	1	0
4962	14	21,944,895	21,945,812	917	2	20.172	28.552	2.92	54	77	7	1	2	2	RAB2B, TOX4	-221, 18	upstream, in gene	ActReg chr14 #4962	1	1	0
4963	14	21,979,170	21,979,940	770	2	12.625	13.167	3.095	26	33	7	1	1	2	METTL3, SALL2	-98, 25782	upstream, downstream	ActReg chr14 #4963	1	1	0
4964	14	23,005,806	23,006,337	531	1	8.059	9.941	2.615	14	19	4	0	8	18	TRA@, TRAJ17, TRAJ16, TRAJ15, TRAJ14, TRAJ13, TRAJ12, TRAJ11, TRAJ10, TRAJ9, TRAJ8, TRAJ7, TRAJ6, TRAJ5, TRAJ4, TRAJ3, TRAJ2, TRAJ1	916014, 10259, 8584, 7491, 6793, 6045, 5182, 4619, 3626, 1569, 979, -496, -1945, -3119, -5071, -6051, -6944, -7910	in gene, downstream, downstream, downstream, downstream, downstream, downstream, downstream, downstream, downstream, downstream, downstream, downstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr14 #4964	0	1	0
4965	14	23,299,065	23,299,472	407	1	5.077	8.308	10.615	6	11	15	1	2	2	MRPL52, MMP14	176, -6525	in gene, upstream	ActReg chr14 #4965	0	0	1
4966	14	23,314,990	23,315,352	362	1	3.818	5.273	11.182	5	7	14	1	0	1	MMP14	9,378	in gene	ActReg chr14 #4966	0	0	1
4967	14	23,356,251	23,356,929	678	2	10.636	11.727	2.952	28	24	5	1	0	2	LRP10, REM2	15630, 4158	downstream, in gene	ActReg chr14 #4967	1	1	0
4968	14	23,398,784	23,399,192	408	1	10.385	8.538	13.538	18	11	22	1	1	2	LOC100505758, PRMT5	10479, -327	downstream, upstream	ActReg chr14 #4968	0	0	1
4969	14	23,450,492	23,450,956	464	1	3	4.333	12.2	6	8	16	1	1	2	JUB, C14orf93	1127, 28636	in gene, downstream	ActReg chr14 #4969	0	0	1
4970	14	23,475,821	23,476,770	949	2	11.1	11.7	5.6	19	23	14	1	0	1	C14orf93	3,065	in gene	ActReg chr14 #4970	1	1	0
4971	14	23,563,944	23,564,307	363	1	7.091	7.909	9.182	9	11	13	1	2	3	ACIN1, C14orf119, LOC100128908	698, -663, 10046	in gene, upstream, downstream	ActReg chr14 #4971	0	0	1
4972	14	23,584,081	23,584,609	528	1	11.118	9.471	1.6	15	13	2	0	0	3	LOC100128908, CEBPE, SLC7A8	-10174, 4129, 68504	upstream, downstream, downstream	ActReg chr14 #4972	1	0	0
4973	14	23,771,046	23,771,416	370	1	6.818	4.727	12	9	8	17	1	2	2	PPP1R3E, BCL2L2	826, -4781	in gene, upstream	ActReg chr14 #4973	0	0	1
4974	14	23,829,478	23,829,808	330	1	1	2.25	10.8	1	3	13	0	1	2	SLC22A17, EFS	-7563, 5199	upstream, in gene	ActReg chr14 #4974	0	0	1
4975	14	23,938,218	23,938,755	537	1	7.125	9.294	3.786	14	15	7	0	1	1	NGDN	-412	upstream	ActReg chr14 #4975	0	1	0
4976	14	24,422,675	24,423,686	1,011	2	13.844	24	6.5	29	57	14	1	2	2	C14orf167, DHRS4	1118, 215	in gene, in gene	ActReg chr14 #4976	1	1	0
4977	14	24,505,338	24,506,405	1,067	2	11.765	9.118	3.559	23	23	8	1	1	1	DHRS4L1	161	in gene	ActReg chr14 #4977	1	1	0
4978	14	24,521,359	24,521,949	590	1	11.333	9.556	8.222	15	14	14	1	1	2	DHRS4L1, LRRC16B	15944, 448	downstream, in gene	ActReg chr14 #4978	1	0	0
4979	14	24,629,989	24,630,411	422	1	6.846	12.154	3.308	10	15	5	0	1	2	RNF31, IRF9	13541, -222	downstream, upstream	ActReg chr14 #4979	0	1	0
4980	14	24,682,492	24,682,897	405	1	10.538	9.308	11.077	13	11	17	1	2	4	TSSK4, CHMP4A, MDP1, NEDD8	7768, 491, 2547, 18882	downstream, in gene, downstream, downstream	ActReg chr14 #4980	0	0	1
4981	14	24,684,810	24,685,404	594	1	12.167	8.944	3.667	16	14	5	0	2	4	TSSK4, CHMP4A, MDP1, NEDD8	10181, -1922, 134, 16469	downstream, upstream, in gene, downstream	ActReg chr14 #4981	1	0	0
4982	14	24,701,656	24,702,164	508	1	7.75	10.312	4.438	11	16	6	1	2	3	NEDD8, GMPR2, TINF2	-334, 262, 9970	upstream, in gene, downstream	ActReg chr14 #4982	0	1	0
4983	14	24,740,439	24,741,044	605	1	7.842	11.053	5.789	11	14	8	1	1	2	TOM1, RABGGTA	-8325, 62	upstream, in gene	ActReg chr14 #4983	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
4984	14	24,768,675	24,769,336	661	2	8.3	11.35	6.5	15	24	11	1	2	3	DHRS1, C14orf21, CIDEB	34, -93, 11571	in gene, upstream, downstream	ActReg chr14 #4984	1	1	0
4985	14	24,836,221	24,836,972	751	2	10.583	10.375	6.25	17	15	10	1	1	1	NFATC4	451	in gene	ActReg chr14 #4985	1	1	0
4986	14	24,982,125	24,982,663	538	1	4.294	9.471	1.429	7	14	2	0	1	1	CMA1	-4,923	upstream	ActReg chr14 #4986	0	1	0
4987	14	27,432,833	27,433,340	507	1	4.067	9.467	1.6	6	15	2	0	0	0				ActReg chr14 #4987	0	1	0
4988	14	29,237,433	29,237,715	282	1	3.556	5.222	11.222	4	7	15	1	2	2	FOXG1, C14orf23	1287, -4336	in gene, upstream	ActReg chr14 #4988	0	0	1
4989	14	30,692,442	30,693,032	590	1	7.684	11.632	3.412	11	21	6	0	0	0				ActReg chr14 #4989	0	1	0
4990	14	31,343,995	31,344,343	348	1	4.727	6.818	12.454	7	8	16	1	1	2	COCH, LOC100506071	428, 14744	in gene, downstream	ActReg chr14 #4990	0	0	1
4991	14	31,889,473	31,890,224	751	2	17.696	20	5.696	44	51	10	1	0	0				ActReg chr14 #4991	1	1	0
4992	14	32,670,438	32,671,680	1,242	1	7.538	10.872	4	12	16	8	1	0	0				ActReg chr14 #4992	0	1	0
4993	14	32,672,260	32,672,954	694	1	8.333	14.524	6.905	11	26	15	1	0	0				ActReg chr14 #4993	0	1	0
4994	14	34,206,486	34,206,997	511	1	7	9.438	2.154	11	17	3	0	0	1	NPAS3	798,282	in gene	ActReg chr14 #4994	0	1	0
4995	14	34,844,381	34,844,986	605	1	6.556	10.684	0	14	16	0	0	0	0				ActReg chr14 #4995	0	1	0
4996	14	36,003,927	36,005,030	1,103	2	11.714	16.486	6.229	27	31	10	1	1	2	INSM2, RALGAPA1	1230, 273954	in gene, downstream	ActReg chr14 #4996	1	1	0
4997	14	36,295,069	36,295,722	653	2	11.429	8.55	5.071	15	16	9	1	1	1	BRMS1L	-202	upstream	ActReg chr14 #4997	1	1	0
4998	14	36,994,144	36,994,599	455	1	2.167	2.867	10.8	3	6	17	1	1	2	NKX2-1, LOC100506237	-4941, 5850	upstream, downstream	ActReg chr14 #4998	0	0	1
4999	14	37,135,398	37,135,739	341	1	3.4	5.5	11.6	5	9	15	1	0	1	PAX9	8,795	in gene	ActReg chr14 #4999	0	0	1
5000	14	37,207,462	37,208,010	548	1	9.235	8.235	3.2	17	15	6	0	0	1	SLC25A21	434,129	in gene	ActReg chr14 #5000	1	0	0
5001	14	39,735,966	39,736,820	854	2	13.741	16.741	6.852	29	36	12	1	1	1	CTAGE5	1,917	in gene	ActReg chr14 #5001	1	1	0
5002	14	39,900,569	39,900,962	393	1	3.308	5.615	11.077	6	9	16	1	1	1	FBXO33	939	in gene	ActReg chr14 #5002	0	0	1
5003	14	39,901,235	39,902,338	1,103	2	16.343	14.286	3.394	43	40	6	1	1	1	FBXO33	-82	upstream	ActReg chr14 #5003	1	1	0
5004	14	41,754,335	41,754,919	584	2	9.882	10.053	1	18	18	1	0	0	0				ActReg chr14 #5004	1	1	0
5005	14	42,078,879	42,079,508	629	1	9.95	5.7	6.45	18	11	10	0	1	1	LRFN5	2,429	in gene	ActReg chr14 #5005	1	0	0
5006	14	45,603,175	45,603,977	802	2	14.13	17.88	3.4	36	49	5	1	2	2	FKBP3, FANCM	156, -1560	in gene, upstream	ActReg chr14 #5006	1	1	0
5007	14	45,722,205	45,722,938	733	2	11.783	12	4.957	22	21	7	1	1	1	C14orf106	54	in gene	ActReg chr14 #5007	1	1	0
5008	14	46,517,278	46,517,916	638	1	5.75	12.3	1.5	13	24	2	0	0	0				ActReg chr14 #5008	0	1	0
5009	14	49,770,467	49,771,212	745	2	13	16.913	1.5	28	39	3	0	0	0				ActReg chr14 #5009	1	1	0
5010	14	50,052,880	50,053,385	505	1	5.75	5.688	12	9	10	18	1	2	2	RPS29, RN7SL1	-38, -166	upstream, upstream	ActReg chr14 #5010	0	0	1
5011	14	50,065,044	50,066,010	966	2	8.5	14.567	11.333	19	29	19	1	1	1	PPIL5	112	in gene	ActReg chr14 #5011	0	1	1
5012	14	50,100,640	50,101,373	733	1	11.174	9.043	5.895	16	11	13	1	1	2	C14orf104, POLE2	942, 53929	in gene, downstream	ActReg chr14 #5012	1	0	0
5013	14	50,159,574	50,160,122	548	1	9.235	12.471	2.312	14	22	4	1	2	2	POLE2, KLHDC1	-4913, 25	upstream, in gene	ActReg chr14 #5013	0	1	0
5014	14	50,234,383	50,235,167	784	2	18.208	16.833	3	37	36	5	1	1	1	KLHDC2	-12	upstream	ActReg chr14 #5014	1	1	0
5015	14	50,319,366	50,319,934	568	1	11.823	6	4.353	20	9	7	1	1	2	SDCCAG1, RN7SL2	-111, 9917	upstream, downstream	ActReg chr14 #5015	1	0	0
5016	14	50,359,358	50,359,993	635	2	10.2	10.25	8.3	14	15	15	1	1	1	ARF6	-61	upstream	ActReg chr14 #5016	0	1	1
5017	14	50,469,773	50,470,385	612	1	9.474	10.105	6.444	13	14	12	1	1	2	C14orf182, LOC100506463	4159, 565	in gene, in gene	ActReg chr14 #5017	0	1	0
5018	14	50,778,374	50,779,149	775	2	12.542	14.583	6.583	26	30	11	1	2	2	L2HGDH, ATP5S	186, -286	in gene, upstream	ActReg chr14 #5018	1	1	0
5019	14	51,561,252	51,562,080	828	1	8.038	11.577	5.731	15	19	12	1	1	2	TRIM9, LOC100506566	756, 5991	in gene, downstream	ActReg chr14 #5019	0	1	0
5020	14	51,605,896	51,606,498	602	1	7.684	9.368	2.632	14	17	4	0	0	0				ActReg chr14 #5020	0	1	0
5021	14	52,282,700	52,283,560	860	1	4.074	10.593	4.222	7	16	7	0	0	0				ActReg chr14 #5021	0	1	0
5022	14	52,294,508	52,295,174	666	1	9.048	11.238	1.81	16	19	4	0	0	0				ActReg chr14 #5022	0	1	0
5023	14	52,535,435	52,535,932	497	1	4.467	4.067	13.533	7	7	20	1	1	1	NID2	263	in gene	ActReg chr14 #5023	0	0	1
5024	14	53,427,758	53,428,247	489	1	9.733	4.267	2.111	17	9	3	0	0	1	FERMT2	-10,187	upstream	ActReg chr14 #5024	1	0	0
5025	14	53,684,115	53,684,564	449	1	5.143	9.857	4.643	7	14	8	0	0	0				ActReg chr14 #5025	0	1	0
5026	14	54,720,155	54,720,767	612	1	8.947	10.421	3.077	12	16	5	0	0	0				ActReg chr14 #5026	0	1	0
5027	14	54,955,504	54,955,922	418	1	10.615	9.615	2.75	19	14	4	1	1	1	GMFB	31	in gene	ActReg chr14 #5027	0	1	0
5028	14	55,016,437	55,017,112	675	1	9.286	10.476	1.5	18	17	2	0	0	0				ActReg chr14 #5028	0	1	0
5029	14	55,031,749	55,032,322	573	1	6.444	5.944	11.222	10	9	17	1	1	1	SAMD4A	-2,602	upstream	ActReg chr14 #5029	0	0	1
5030	14	55,493,572	55,494,204	632	1	5.118	5.842	14.579	8	10	24	1	2	2	WDHD1, SOCS4	-69, 44	upstream, in gene	ActReg chr14 #5030	0	0	1
5031	14	56,046,436	56,046,979	543	2	8.647	9.059	2.692	17	17	5	1	2	2	C14orf33, KTN1	103, -218	in gene, upstream	ActReg chr14 #5031	1	1	0
5032	14	56,269,766	56,270,294	528	1	6.875	11.938	1	9	17	1	0	1	1	C14orf34	-6,638	upstream	ActReg chr14 #5032	0	1	0
5033	14	57,045,967	57,047,098	1,131	2	30.771	32.514	2.6	67	73	4	1	1	1	C14orf101	21	in gene	ActReg chr14 #5033	1	1	0
5034	14	57,264,696	57,265,002	306	1	1	2.5	9.8	1	4	14	1	0	1	OTX2	12,335	downstream	ActReg chr14 #5034	0	0	1
5035	14	58,666,445	58,667,011	566	2	8.556	10.222	4	14	21	7	1	1	1	ACTR10	-105	upstream	ActReg chr14 #5035	1	1	0
5036	14	59,688,187	59,688,884	697	1	5.091	11	2.6	7	16	5	0	0	1	DAAM1	33,136	in gene	ActReg chr14 #5036	0	1	0
5037	14	59,950,436	59,951,197	761	1	8.391	12.609	9.609	15	20	15	1	2	2	C14orf149, JKAMP	257, -345	in gene, upstream	ActReg chr14 #5037	0	1	0
5038	14	60,286,348	60,286,659	311	1	4.4	1	10.9	5	1	13	0	0	1	RTN1	51,054	in gene	ActReg chr14 #5038	0	0	1
5039	14	60,558,287	60,559,109	822	1	8.192	11.615	5	13	20	8	1	1	1	C14orf135	69	in gene	ActReg chr14 #5039	0	1	0
5040	14	60,952,452	60,952,720	268	1	4.875	6.625	13.375	6	10	18	1	1	1	C14orf39	178	in gene	ActReg chr14 #5040	0	0	1
5041	14	61,115,396	61,116,334	938	1	11.103	7.31	5.621	20	11	10	1	1	1	SIX1	290	in gene	ActReg chr14 #5041	1	0	0
5042	14	61,123,902	61,124,323	421	1	7.5	9.714	2.786	10	14	5	1	0	1	SIX1	-7,957	upstream	ActReg chr14 #5042	0	1	0
5043	14	61,619,499	61,619,969	470	1	5.133	10.2	3.571	10	14	6	0	0	0				ActReg chr14 #5043	0	1	0
5044	14	61,822,548	61,823,193	645	1	10.75	3.7	2.5	19	6	4	0	0	1	PRKCH	34,355	in gene	ActReg chr14 #5044	1	0	0
5045	14	62,020,274	62,021,278	1,004	1	10.581	12.419	1.2	20	19	2	0	0	1	PRKCH	232,261	downstream	ActReg chr14 #5045	0	1	0
5046	14	62,029,002	62,030,144	1,142	1	8.167	12.917	4.444	14	20	11	0	1	1	FLJ22447	-7,741	upstream	ActReg chr14 #5046	0	1	0
5047	14	62,128,878	62,129,649	771	2	12.708	12.792	4.25	19	23	8	0	0	1	FLJ22447	91,949	downstream	ActReg chr14 #5047	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5048	14	62,162,168	62,162,786	618	1	7.15	8.25	14.85	11	12	22	1	1	1	HIF1A	358	in gene	ActReg chr14 #5048	0	0	1
5049	14	62,331,162	62,331,571	409	1	1	3.364	10.692	1	4	18	1	0	0				ActReg chr14 #5049	0	0	1
5050	14	62,431,822	62,432,269	447	1	9	9.786	1.75	11	12	2	0	0	0				ActReg chr14 #5050	0	1	0
5051	14	62,584,117	62,584,459	342	1	2.6	4.909	10	3	7	14	1	1	1	FLJ43390	213	in gene	ActReg chr14 #5051	0	0	1
5052	14	64,061,783	64,062,130	347	1	2.364	3.727	9.636	3	5	12	1	0	1	WDR89	46,635	downstream	ActReg chr14 #5052	0	0	1
5053	14	64,804,993	64,805,363	370	1	5.545	4.636	10.909	9	8	16	1	1	2	ESR2, LOC441687	90, 9151	in gene, downstream	ActReg chr14 #5053	0	0	1
5054	14	64,805,494	64,806,062	568	1	3.667	10.889	3.333	6	16	5	1	1	2	ESR2, LOC441687	-510, 8551	upstream, downstream	ActReg chr14 #5054	0	1	0
5055	14	64,970,712	64,971,181	469	1	9.533	11.667	6.267	14	16	11	1	2	2	ZBTB25, ZBTB1	-392, -346	upstream, upstream	ActReg chr14 #5055	0	1	0
5056	14	65,207,852	65,208,251	399	1	1.667	2.667	11.333	3	4	15	0	0	2	PLEKHG3, SPTB	36858, 81815	in gene, downstream	ActReg chr14 #5056	0	0	1
5057	14	65,273,189	65,273,674	485	1	6.333	10.067	2.769	8	16	4	0	0	1	SPTB	16,435	in gene	ActReg chr14 #5057	0	1	0
5058	14	65,453,399	65,454,029	630	1	8.75	11.7	6.65	13	18	9	1	1	1	FNTB	207	in gene	ActReg chr14 #5058	0	1	0
5059	14	66,783,485	66,783,801	316	1	2.1	1	8.4	3	1	13	0	0	0				ActReg chr14 #5059	0	0	1
5060	14	66,974,253	66,975,149	896	2	10.286	12.893	8.786	17	19	14	1	1	2	C14orf53, GPHN	21592, 576	downstream, in gene	ActReg chr14 #5060	1	1	0
5061	14	67,708,148	67,708,764	616	1	7.263	11.316	7.842	10	19	12	1	1	1	MPP5	435	in gene	ActReg chr14 #5061	0	1	0
5062	14	67,826,327	67,827,347	1,020	2	30.094	30.344	6.031	86	71	9	1	2	2	ATP6V1D, EIF2S1	-246, -197	upstream, upstream	ActReg chr14 #5062	1	1	0
5063	14	67,880,632	67,881,413	781	1	6.56	9.56	2.909	12	17	5	0	1	1	PLEK2	-2,194	upstream	ActReg chr14 #5063	0	1	0
5064	14	67,999,613	68,000,157	544	1	4.643	9.412	4.091	7	15	6	1	1	1	PLEKHH1	-123	upstream	ActReg chr14 #5064	0	1	0
5065	14	68,140,986	68,141,826	840	2	11.556	12.222	6.148	20	28	11	1	1	2	VTI1B, RDH11	196, 21104	in gene, downstream	ActReg chr14 #5065	1	1	0
5066	14	68,205,505	68,206,281	776	2	7.792	9.875	1	18	14	1	0	0	2	RDH12, ZFYVE26	57290, 77413	downstream, downstream	ActReg chr14 #5066	1	1	0
5067	14	68,644,445	68,644,871	426	1	4.286	9.571	1	7	15	1	0	0	1	RAD51L1	358,162	in gene	ActReg chr14 #5067	0	1	0
5068	14	69,014,806	69,015,468	662	1	7.381	10.381	3.083	10	16	4	0	0	1	RAD51L1	728,641	in gene	ActReg chr14 #5068	0	1	0
5069	14	69,409,772	69,410,307	535	1	2.235	3.235	11.882	4	5	18	0	0	1	ACTN1	36,044	in gene	ActReg chr14 #5069	0	0	1
5070	14	69,417,818	69,418,395	577	1	5.778	10.444	3.222	8	18	6	0	0	1	ACTN1	27,977	in gene	ActReg chr14 #5070	0	1	0
5071	14	69,657,977	69,658,540	563	2	9.667	9.611	4.222	15	17	6	1	1	1	EXD2	64	in gene	ActReg chr14 #5071	1	1	0
5072	14	70,233,541	70,233,980	439	1	10.692	7.308	8.615	15	9	13	1	2	3	LOC100289511, SFRS5, SLC10A1	670, -69, 30246	in gene, upstream, downstream	ActReg chr14 #5072	1	0	0
5073	14	70,345,989	70,346,285	296	1	2.889	3.222	9	4	5	11	1	1	1	SMOC1	-6	upstream	ActReg chr14 #5073	0	0	1
5074	14	70,519,764	70,520,253	489	1	7.733	10.067	1.867	12	18	3	0	0	1	SLC8A3	135,779	in gene	ActReg chr14 #5074	0	1	0
5075	14	70,826,133	70,826,796	663	2	10.905	11.333	3.421	17	20	7	1	1	2	COX16, SYNJ2BP	-20, 57343	upstream, downstream	ActReg chr14 #5075	1	1	0
5076	14	71,323,473	71,323,972	499	1	6.625	8.625	2	13	16	2	0	0	0				ActReg chr14 #5076	0	1	0
5077	14	73,074,539	73,075,811	1,272	2	7.975	8.2	2.324	15	16	4	0	0	0				ActReg chr14 #5077	1	1	0
5078	14	73,493,670	73,494,284	614	1	9.579	8.789	2.5	18	15	4	1	1	1	ZFYVE1	-57	upstream	ActReg chr14 #5078	1	0	0
5079	14	73,957,544	73,957,865	321	1	4.4	7.4	11.7	6	10	16	1	1	2	HEATR4, C14orf169	67947, 60	in gene, in gene	ActReg chr14 #5079	0	0	1
5080	14	74,033,126	74,033,499	373	1	5.455	3	11.182	7	5	14	0	2	2	HEATR4, ACOT2	-7661, -2460	upstream, upstream	ActReg chr14 #5080	0	0	1
5081	14	74,079,126	74,079,694	568	1	9.778	5.444	3.118	18	10	6	1	1	1	ACOT6	-4,138	upstream	ActReg chr14 #5081	1	0	0
5082	14	74,353,532	74,353,909	377	1	4.75	9.167	10.25	8	12	14	1	1	2	PTGR2, ZNF410	35186, 134	downstream, in gene	ActReg chr14 #5082	0	0	1
5083	14	74,413,569	74,413,943	374	1	1.571	1.182	10.546	2	2	16	0	1	2	FAM161B, COQ6	3079, -2887	in gene, upstream	ActReg chr14 #5083	0	0	1
5084	14	74,707,634	74,708,129	495	1	2.8	4.938	12	6	10	19	1	1	1	VSX2	1,706	in gene	ActReg chr14 #5084	0	0	1
5085	14	74,769,265	74,770,067	802	3	11.68	8.12	6.92	21	15	16	1	1	1	ABCD4	101	in gene	ActReg chr14 #5085	1	1	1
5086	14	74,892,337	74,892,831	494	1	9.333	9.2	2.364	14	12	4	1	1	1	TMEM90A	221	in gene	ActReg chr14 #5086	1	0	0
5087	14	75,086,407	75,087,014	607	1	8.526	10.684	4.765	13	15	9	0	1	1	LTBP2	-7,676	upstream	ActReg chr14 #5087	0	1	0
5088	14	75,348,254	75,348,857	603	2	10.579	9.053	6.947	19	16	11	1	1	1	DLST	-39	upstream	ActReg chr14 #5088	1	1	0
5089	14	75,725,588	75,726,392	804	2	9.68	11.84	2.25	20	16	4	1	0	0				ActReg chr14 #5089	1	1	0
5090	14	75,745,044	75,746,028	984	3	13.645	16.452	8	23	29	18	1	2	2	FOS, LOC100287415	55, 1295	in gene, in gene	ActReg chr14 #5090	1	1	1
5091	14	76,012,875	76,013,190	315	1	3.6	3.1	11.3	6	4	15	1	0	1	BATF	24,248	in gene	ActReg chr14 #5091	0	0	1
5092	14	76,451,947	76,452,441	494	1	9.8	7.533	4	16	13	6	1	2	2	TGFB3, C14orf179	-4102, 98	upstream, in gene	ActReg chr14 #5092	1	0	0
5093	14	76,599,133	76,599,953	820	2	10.423	14.423	2.333	18	29	5	0	0	0				ActReg chr14 #5093	1	1	0
5094	14	77,339,632	77,339,935	303	1	5	2.222	11.222	6	4	14	0	0	1	C14orf166B	47,058	downstream	ActReg chr14 #5094	0	0	1
5095	14	77,370,349	77,371,129	780	1	5.667	11.125	4.542	9	14	8	0	0	0				ActReg chr14 #5095	0	1	0
5096	14	77,492,615	77,492,962	347	1	6.091	8.455	12.182	9	16	15	1	1	1	C14orf4	2,246	in gene	ActReg chr14 #5096	0	0	1
5097	14	77,498,992	77,499,569	577	1	6.611	9.5	2.833	10	15	5	2	1	1	C14orf4	-4,246	upstream	ActReg chr14 #5097	0	1	0
5098	14	77,599,547	77,600,714	1,167	2	12.784	21.622	5.027	39	53	10	0	0	1	ZDHHC22	8,004	in gene	ActReg chr14 #5098	1	1	0
5099	14	77,674,872	77,675,434	562	1	12.111	13.667	4.176	21	26	6	0	0	1	TMEM63C	27,051	in gene	ActReg chr14 #5099	0	1	0
5100	14	77,706,573	77,706,910	337	1	1.7	2.5	10.7	2	6	14	0	0	1	TMEM63C	58,639	in gene	ActReg chr14 #5100	0	0	1
5101	14	77,708,221	77,709,024	803	1	5.462	9.269	1.7	10	15	3	0	0	1	TMEM63C	60,520	in gene	ActReg chr14 #5101	0	1	0
5102	14	77,769,293	77,769,773	480	1	7.667	13.067	1.5	12	22	2	0	0	1	POMT2	17,692	in gene	ActReg chr14 #5102	0	1	0
5103	14	77,784,184	77,784,659	475	1	10.067	2.167	2.667	14	3	4	0	1	2	POMT2, GSTZ1	2804, -2809	in gene, upstream	ActReg chr14 #5103	1	0	0
5104	14	77,787,251	77,787,903	652	1	6.75	11.9	5.25	10	18	9	1	2	2	POMT2, GSTZ1	-352, 347	upstream, in gene	ActReg chr14 #5104	0	1	0
5105	14	78,986,026	78,986,724	698	2	10.318	8.864	1.556	20	16	2	0	0	1	NRXN3	116,282	in gene	ActReg chr14 #5105	1	1	0
5106	14	79,329,437	79,329,960	523	1	11.235	7.353	2.429	18	14	3	0	0	1	NRXN3	459,605	in gene	ActReg chr14 #5106	1	0	0
5107	14	79,485,230	79,485,711	481	1	6.733	9.133	1.692	11	15	3	0	0	1	NRXN3	615,377	in gene	ActReg chr14 #5107	0	1	0
5108	14	79,511,635	79,511,973	338	1	10.182	8.8	1	15	12	1	0	0	1	NRXN3	641,711	in gene	ActReg chr14 #5108	1	0	0
5109	14	79,627,806	79,628,432	626	2	9.5	10.45	1.4	20	18	2	0	0	1	NRXN3	758,026	in gene	ActReg chr14 #5109	1	1	0
5110	14	81,407,699	81,408,533	834	2	9.923	15.039	3.5	21	33	6	1	1	1	C14orf145	-2,232	upstream	ActReg chr14 #5110	1	1	0
5111	14	81,687,383	81,687,793	410	1	5.615	9.923	3.692	8	17	9	1	2	2	GTF2A1, LOC100506659	-13, 26	upstream, in gene	ActReg chr14 #5111	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5112	14	82,541,878	82,542,330	452	1	9.5	9	1.6	17	13	2	0	0	0				ActReg chr14 #5112	1	0	0
5113	14	85,997,511	85,998,299	788	1	7.875	11.292	5.375	12	14	9	1	2	2	LOC100506731, FLRT2	-1436, 1417	upstream, in gene	ActReg chr14 #5113	0	1	0
5114	14	87,598,219	87,598,642	423	1	4.692	9.385	3.2	7	16	5	0	0	0				ActReg chr14 #5114	0	1	0
5115	14	88,237,454	88,238,014	560	1	28.823	34.133	57.353	60	58	105	0	0	0				ActReg chr14 #5115	0	0	1
5116	14	89,017,491	89,018,247	756	2	12.583	13.217	6.625	24	33	10	1	0	1	PTPN21	5,254	in gene	ActReg chr14 #5116	1	1	0
5117	14	89,290,889	89,291,252	363	1	7.182	9.909	12.273	10	12	16	1	1	1	TTC8	92	in gene	ActReg chr14 #5117	0	0	1
5118	14	89,443,999	89,444,699	700	2	11.409	12	0	23	23	0	0	0	0				ActReg chr14 #5118	1	1	0
5119	14	89,448,543	89,449,425	882	2	8.857	13.393	1.269	17	26	2	0	0	0				ActReg chr14 #5119	1	1	0
5120	14	89,450,162	89,450,610	448	1	5.643	9.286	1.75	8	13	2	0	0	0				ActReg chr14 #5120	0	1	0
5121	14	89,506,740	89,507,378	638	1	6.85	9.9	4.368	12	19	7	0	0	0				ActReg chr14 #5121	0	1	0
5122	14	89,603,753	89,604,359	606	1	5.316	9.105	2.312	8	17	4	0	0	0				ActReg chr14 #5122	0	1	0
5123	14	90,420,817	90,421,705	888	2	10	9.857	4.821	17	17	10	1	2	2	C14orf143, TDP1	-172, -985	upstream, upstream	ActReg chr14 #5123	1	1	0
5124	14	90,421,779	90,422,661	882	2	10.75	11.679	4.25	23	18	9	1	2	2	C14orf143, TDP1	-1131, -26	upstream, upstream	ActReg chr14 #5124	1	1	0
5125	14	90,863,260	90,863,733	473	1	7.133	5.867	11.467	12	8	19	1	1	1	CALM1	169	in gene	ActReg chr14 #5125	0	0	1
5126	14	90,961,194	90,962,435	1,241	2	10.205	17	3	30	35	6	0	0	0				ActReg chr14 #5126	1	1	0
5127	14	91,268,444	91,268,782	338	1	1.909	4.636	12.273	3	6	17	0	0	1	TTC7B	14,148	in gene	ActReg chr14 #5127	0	0	1
5128	14	91,580,164	91,580,739	575	1	7.778	12.111	3.944	13	20	6	0	1	1	C14orf159	94	in gene	ActReg chr14 #5128	0	1	0
5129	14	91,699,906	91,700,461	555	1	3.909	4.188	12.235	6	8	17	1	0	2	C14orf159, GPR68	119826, 20041	downstream, in gene	ActReg chr14 #5129	0	0	1
5130	14	91,731,121	91,731,419	298	1	1.444	1	10.111	3	1	13	1	0	1	CCDC88C	152,863	downstream	ActReg chr14 #5130	0	0	1
5131	14	91,790,361	91,790,722	361	1	4.5	4.833	10.25	7	7	15	0	0	1	CCDC88C	93,592	in gene	ActReg chr14 #5131	0	0	1
5132	14	91,976,421	91,977,198	777	2	11.375	11.125	8	18	18	13	1	1	1	SMEK1	-165	upstream	ActReg chr14 #5132	1	1	0
5133	14	92,506,148	92,506,749	601	1	11.111	8.167	5.056	18	13	9	1	1	1	TRIP11	-45	upstream	ActReg chr14 #5133	1	0	0
5134	14	92,572,786	92,573,464	678	2	12.571	13.095	1.765	29	32	3	1	1	2	ATXN3, NDUFB1	-160, 15028	upstream, downstream	ActReg chr14 #5134	1	1	0
5135	14	92,587,645	92,588,801	1,156	2	12.46	15.27	6.865	34	24	13	1	2	2	NDUFB1, CPSF2	-70, -106	upstream, upstream	ActReg chr14 #5135	1	1	0
5136	14	92,980,342	92,980,821	479	1	7	10.733	8.933	10	13	13	1	1	1	RIN3	456	in gene	ActReg chr14 #5136	0	1	0
5137	14	93,371,935	93,372,465	530	1	12.059	7.647	1	18	12	1	0	0	0				ActReg chr14 #5137	1	0	0
5138	14	93,380,322	93,381,002	680	2	12.571	13.143	1.643	26	29	2	0	0	1	CHGA	-8,783	upstream	ActReg chr14 #5138	1	1	0
5139	14	93,383,388	93,383,727	339	1	2	1.636	11.091	2	2	16	0	1	1	CHGA	-5,888	upstream	ActReg chr14 #5139	0	0	1
5140	14	93,389,543	93,390,256	713	2	11.046	11.5	4.857	20	20	10	1	1	1	CHGA	454	in gene	ActReg chr14 #5140	1	1	0
5141	14	93,896,637	93,896,973	336	1	6.545	1.364	9.545	9	2	14	1	0	1	KIAA1409	97,240	in gene	ActReg chr14 #5141	0	0	1
5142	14	94,425,670	94,426,310	640	2	10.9	10.65	3.05	15	15	5	0	1	2	ASB2, LOC100506919	-2223, 2868	upstream, in gene	ActReg chr14 #5142	1	1	0
5143	14	94,492,311	94,492,883	572	2	13.353	16.611	4.5	26	31	9	1	1	1	OTUB2	-127	upstream	ActReg chr14 #5143	1	1	0
5144	14	94,808,318	94,808,926	608	1	6.526	11.737	2.455	10	18	4	0	0	0				ActReg chr14 #5144	0	1	0
5145	14	95,120,410	95,120,990	580	1	5.278	10.111	3.611	7	19	5	0	0	0				ActReg chr14 #5145	0	1	0
5146	14	95,727,032	95,727,590	558	1	10.111	10.667	1.778	14	17	2	0	0	1	CLMN	58,934	in gene	ActReg chr14 #5146	1	0	0
5147	14	95,826,567	95,827,043	476	2	10.4	6.867	7.2	13	10	12	1	0	0				ActReg chr14 #5147	1	0	1
5148	14	95,973,342	95,973,725	383	1	4.833	10.167	2.75	7	13	5	0	0	0				ActReg chr14 #5148	0	1	0
5149	14	96,328,391	96,329,100	709	2	16.773	19.273	1	38	49	1	0	0	0				ActReg chr14 #5149	1	1	0
5150	14	96,342,214	96,342,467	253	1	3.5	2.286	10.75	4	4	13	1	1	1	LOC100507043	-389	upstream	ActReg chr14 #5150	0	0	1
5151	14	96,967,929	96,968,675	746	2	4.292	10.917	8.25	6	15	14	1	1	1	PAPOLA	-418	upstream	ActReg chr14 #5151	0	1	1
5152	14	97,406,324	97,406,879	555	1	6.765	10.353	1.308	11	17	2	0	0	0				ActReg chr14 #5152	0	1	0
5153	14	98,179,285	98,179,748	463	1	7.2	9.067	2.2	12	17	3	0	0	0				ActReg chr14 #5153	0	1	0
5154	14	98,565,861	98,566,348	487	1	8.267	10.133	1.182	12	13	2	0	0	0				ActReg chr14 #5154	0	1	0
5155	14	100,019,927	100,020,227	300	1	2.8	1.333	10.4	4	2	14	0	0	1	CCDC85C	50,650	in gene	ActReg chr14 #5155	0	0	1
5156	14	100,070,738	100,071,388	650	1	12.1	7.2	5.833	17	10	10	1	2	2	CCDC85C, LOC100507108	-336, 170	upstream, in gene	ActReg chr14 #5156	1	0	0
5157	14	100,224,684	100,225,374	690	1	11.143	7.714	2.368	20	13	5	0	0	0				ActReg chr14 #5157	1	0	0
5158	14	100,599,098	100,599,467	369	1	1.833	2.833	8.917	3	4	15	0	0	1	EVL	67,531	in gene	ActReg chr14 #5158	0	0	1
5159	14	100,751,944	100,752,257	313	1	8	11	12.6	10	13	16	1	0	2	YY1, SLC25A29	46998, 20760	downstream, downstream	ActReg chr14 #5159	0	0	1
5160	14	100,842,617	100,843,221	604	1	11	4.842	1.8	19	8	3	0	1	2	WDR25, LOC100507124	100164, -4374	in gene, upstream	ActReg chr14 #5160	1	0	0
5161	14	100,952,707	100,953,272	565	1	8.471	11.588	2.077	14	17	4	0	0	2	WDR25, LOC100507124	110204, 5696	in gene, downstream	ActReg chr14 #5161	0	1	0
5162	14	101,017,205	101,017,608	403	1	3.385	2.462	9.538	5	6	14	0	0	1	BEGAIN	18,725	in gene	ActReg chr14 #5162	0	0	1
5163	14	101,104,657	101,105,136	479	1	1	1.571	10.333	1	4	16	0	0	0				ActReg chr14 #5163	0	0	1
5164	14	101,539,453	101,540,084	631	1	11.9	5.55	6.5	25	8	12	0	0	7	MIR541, MIR409, MIR412, MIR369, MIR410, MIR656, LOC100507257	8936, 8131, 7984, 7833, 7519, 6707, 3520	downstream, downstream, downstream, downstream, downstream, downstream, downstream	ActReg chr14 #5164	1	0	0
5165	14	101,544,502	101,544,780	278	1	2.556	2.556	10.444	3	5	15	0	0	1	LOC100507257	8,393	downstream	ActReg chr14 #5165	0	0	1
5166	14	101,617,811	101,618,076	265	1	3.875	10.5	12.375	5	13	14	0	0	0				ActReg chr14 #5166	0	0	1
5167	14	101,620,005	101,620,503	498	1	8.067	9.733	3.231	12	16	6	0	0	0				ActReg chr14 #5167	0	1	0
5168	14	102,027,977	102,028,345	368	1	2.818	5.091	11.546	4	7	16	1	3	3	DIO3OS, MIR1247, DIO3	-6148, -1402, 473	upstream, upstream, in gene	ActReg chr14 #5168	0	0	1
5169	14	102,155,377	102,155,848	471	1	3.133	1.357	11.533	5	2	19	0	0	0				ActReg chr14 #5169	0	0	1
5170	14	102,414,154	102,414,998	844	1	10.462	12.885	5.577	21	18	10	1	0	0				ActReg chr14 #5170	0	1	0
5171	14	102,427,163	102,427,583	420	1	4.923	6.769	10.308	7	11	17	0	1	1	DYNC1H1	-3,492	upstream	ActReg chr14 #5171	0	0	1
5172	14	102,553,255	102,553,509	254	1	6.375	6.286	10.625	10	10	16	1	0	1	HSP90AA1	52,704	in gene	ActReg chr14 #5172	0	0	1
5173	14	102,601,908	102,602,197	289	1	2.444	1.556	9.667	3	2	12	0	1	2	HSP90AA1, WDR20	4034, -4160	in gene, upstream	ActReg chr14 #5173	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5174	14	102,771,246	102,771,758	512	1	9.938	5.5	3.875	17	8	7	1	1	1	RAGE	29	in gene	ActReg chr14 #5174	1	0	0
5175	14	102,780,453	102,781,008	555	1	6.824	10.235	4.294	13	16	6	1	1	2	RAGE, ZNF839	-9199, -5366	upstream, upstream	ActReg chr14 #5175	0	1	0
5176	14	102,828,986	102,829,555	549	1	4.176	9.588	6.154	7	16	11	1	2	2	CINP, TECPR2	-7, -40	upstream, upstream	ActReg chr14 #5176	0	1	0
5177	14	102,991,473	102,991,965	492	1	10.6	4.467	1.375	17	7	2	0	0	0				ActReg chr14 #5177	1	0	0
5178	14	103,217,454	103,217,823	369	1	4.444	1.909	12.182	6	2	17	0	0	0				ActReg chr14 #5178	0	0	1
5179	14	103,507,799	103,508,164	365	1	4.167	4	9.75	6	6	16	0	0	1	CDC42BPB	15,761	in gene	ActReg chr14 #5179	0	0	1
5180	14	103,687,941	103,688,250	309	1	2.444	1	12.556	4	1	16	0	0	0				ActReg chr14 #5180	0	0	1
5181	14	103,851,403	103,852,004	601	1	5.947	9.316	12.632	10	12	16	1	1	1	MARK3	2	in gene	ActReg chr14 #5181	0	0	1
5182	14	103,983,567	103,983,876	309	1	2.143	4.1	10.4	4	6	15	0	0	1	CKB	5,449	downstream	ActReg chr14 #5182	0	0	1
5183	14	103,996,688	103,997,225	537	1	10.765	9.118	2.588	18	12	6	0	1	2	CKB, TRMT61A	-7786, 1447	upstream, in gene	ActReg chr14 #5183	1	0	0
5184	14	104,013,400	104,013,816	416	1	4.077	4.154	10.615	6	8	16	0	0	2	TRMT61A, BAG5	18099, 15543	downstream, downstream	ActReg chr14 #5184	0	0	1
5185	14	104,028,528	104,029,263	735	1	6.435	12.304	5	10	20	10	1	2	2	BAG5, C14orf153	256, -404	in gene, upstream	ActReg chr14 #5185	0	1	0
5186	14	104,029,355	104,029,621	266	1	9.5	5.875	11	15	11	15	1	2	2	BAG5, C14orf153	-337, 189	upstream, in gene	ActReg chr14 #5186	0	0	1
5187	14	104,073,314	104,073,808	494	1	4.733	9.733	5.933	6	14	9	0	0	0				ActReg chr14 #5187	0	1	0
5188	14	104,387,447	104,388,302	855	2	11.556	12.518	6.5	30	21	15	1	2	2	C14orf2, TDRD9	29, -6943	in gene, upstream	ActReg chr14 #5188	1	1	0
5189	14	104,599,638	104,600,005	367	1	3.556	2.545	10.917	5	4	17	0	1	1	KIF26A	-5,239	upstream	ActReg chr14 #5189	0	0	1
5190	14	104,604,263	104,604,550	287	1	2.444	4.556	9.889	5	6	12	1	1	1	KIF26A	-654	upstream	ActReg chr14 #5190	0	0	1
5191	14	104,633,452	104,633,859	407	1	1.667	2.545	13.769	2	4	18	0	0	1	KIF26A	28,595	in gene	ActReg chr14 #5191	0	0	1
5192	14	104,667,496	104,668,041	545	1	2.818	2.235	11.647	5	4	18	0	0	0				ActReg chr14 #5192	0	0	1
5193	14	104,678,605	104,679,029	424	1	2.154	2	10	4	3	15	0	0	0				ActReg chr14 #5193	0	0	1
5194	14	104,970,488	104,970,799	311	1	2.8	5.6	8.9	4	8	11	0	0	0				ActReg chr14 #5194	0	0	1
5195	14	105,038,436	105,038,877	441	1	2.385	1.667	11.077	4	2	18	0	1	1	C14orf180	-7,400	upstream	ActReg chr14 #5195	0	0	1
5196	14	105,065,098	105,065,567	469	1	1.929	3.5	12.5	3	5	17	0	1	3	C14orf180, LOC100288144, TMEM179	19276, -5934, 5765	downstream, upstream, in gene	ActReg chr14 #5196	0	0	1
5197	14	105,070,116	105,070,418	302	1	4.111	3.444	11.556	5	6	14	1	1	1	TMEM179	830	in gene	ActReg chr14 #5197	0	0	1
5198	14	105,100,029	105,100,340	311	1	3.9	2.8	10.5	5	4	14	0	0	0				ActReg chr14 #5198	0	0	1
5199	14	105,145,725	105,146,120	395	1	4	3.417	10.538	6	5	14	0	0	1	INF2	-10,021	upstream	ActReg chr14 #5199	0	0	1
5200	14	105,201,512	105,202,012	500	1	3.733	3.467	12	7	5	17	0	0	1	ADSSL1	11,228	in gene	ActReg chr14 #5200	0	0	1
5201	14	105,258,685	105,259,097	412	1	2.167	4.769	10.615	4	7	15	0	0	2	AKT1, ZBTB42	3189, -8042	in gene, upstream	ActReg chr14 #5201	0	0	1
5202	14	105,282,097	105,282,633	536	1	10.294	15.177	6.176	15	30	12	1	1	1	MGC23270	-5,173	upstream	ActReg chr14 #5202	0	1	0
5203	14	105,363,717	105,364,042	325	1	1.875	3.222	8.8	3	6	11	0	0	1	KIAA0284	32,225	downstream	ActReg chr14 #5203	0	0	1
5204	14	105,414,485	105,414,983	498	1	3.929	2.375	10.125	7	4	17	0	0	1	AHNAK2	29,960	in gene	ActReg chr14 #5204	0	0	1
5205	14	105,491,164	105,491,545	381	1	11	6.833	4	16	10	6	0	1	1	CDCA4	-3,929	upstream	ActReg chr14 #5205	1	0	0
5206	14	105,560,063	105,560,525	462	1	3.067	4.267	11.867	6	6	15	1	0	0				ActReg chr14 #5206	0	0	1
5207	14	105,781,665	105,782,052	387	1	6.333	6.5	12.25	9	12	18	1	1	1	PACS2	777	in gene	ActReg chr14 #5207	0	0	1
5208	14	105,793,406	105,793,741	335	1	2.273	2.333	10.182	5	4	12	0	0	1	PACS2	12,492	in gene	ActReg chr14 #5208	0	0	1
5209	14	105,824,535	105,824,998	463	1	2.154	3.6	10.533	4	5	16	0	0	1	PACS2	43,685	in gene	ActReg chr14 #5209	0	0	1
5210	14	105,890,217	105,890,507	290	1	2.667	2.667	9.444	3	3	13	0	2	3	LOC100507437, MTA1, LOC100128343	-4270, 4176, -402	upstream, in gene, upstream	ActReg chr14 #5210	0	0	1
5211	14	105,907,361	105,907,740	379	1	2	2.364	12.364	3	5	18	0	0	1	MTA1	21,364	in gene	ActReg chr14 #5211	0	0	1
5212	14	105,930,972	105,931,456	484	1	1.643	3	11.625	2	5	15	1	0	2	MTA1, CRIP2	45028, -9917	in gene, upstream	ActReg chr14 #5212	0	0	1
5213	14	105,935,536	105,936,077	541	1	3	3	10.706	4	6	15	1	1	2	MTA1, CRIP2	49620, -5325	in gene, upstream	ActReg chr14 #5213	0	0	1
5214	14	105,956,096	105,956,865	769	1	6.04	6.4	11.72	10	10	19	1	1	3	CRIP2, CRIP1, C14orf80	15349, 3223, -40	downstream, downstream, upstream	ActReg chr14 #5214	0	0	1
5215	14	105,957,016	105,957,738	722	2	10.522	10	3	14	15	6	1	1	2	CRIP1, C14orf80	4120, 857	downstream, in gene	ActReg chr14 #5215	1	1	0
5216	14	105,965,582	105,966,103	521	1	8.062	11.312	5.75	11	15	12	0	0	1	C14orf80	9,322	downstream	ActReg chr14 #5216	0	1	0
5217	14	106,135,257	106,135,569	312	1	2.5	1.778	12	3	3	15	0	0	1	IGH@	1,152,638	in gene	ActReg chr14 #5217	0	0	1
5218	14	106,267,238	106,268,088	850	2	15.808	14.731	1.118	39	37	2	0	0	1	IGH@	1,020,388	in gene	ActReg chr14 #5218	1	1	0
5219	14	106,392,397	106,392,732	335	1	1.625	2.1	10.2	3	3	16	0	1	4	IGH@, IGHD2-2, KIAA0125, IGHD1-1	895487, -9849, 8726, 7187	in gene, upstream, in gene, upstream	ActReg chr14 #5219	0	0	1
5220	14	106,915,984	106,916,337	353	1	6.909	11.182	2.556	9	17	5	1	0	2	IGH@, IGHV3-43	371891, 10484	in gene, downstream	ActReg chr14 #5220	0	1	0
5221	14	106,938,338	106,938,766	428	2	9.231	8.077	11.385	13	12	17	1	1	2	IGH@, C14orf98	349499, 97	in gene, in gene	ActReg chr14 #5221	1	0	1
5222	15	20,487,710	20,488,217	507	1	8.75	13.062	14.375	12	18	21	0	0	0				ActReg chr15 #5222	0	0	1
5223	15	20,505,856	20,506,283	427	1	3.214	3.786	11.071	6	5	15	0	0	0				ActReg chr15 #5223	0	0	1
5224	15	20,546,549	20,546,906	357	1	7.636	4.818	16.364	11	8	26	0	0	0				ActReg chr15 #5224	0	0	1
5225	15	20,550,061	20,550,701	640	1	5.55	5.8	15.25	8	10	26	0	0	0				ActReg chr15 #5225	0	0	1
5226	15	20,554,168	20,555,425	1,257	1	6.15	6.4	18.6	10	11	27	0	0	0				ActReg chr15 #5226	0	0	1
5227	15	20,561,662	20,564,248	2,586	1	7.63	8.556	17.988	15	22	28	1	0	0				ActReg chr15 #5227	0	0	1
5228	15	20,851,034	20,851,930	896	1	11.357	15.464	4.5	26	33	8	0	0	0				ActReg chr15 #5228	0	1	0
5229	15	21,915,889	21,916,570	681	1	12.143	9.095	4.05	17	15	5	0	0	0				ActReg chr15 #5229	1	0	0
5230	15	22,387,250	22,387,746	496	1	5.25	9.938	8.923	9	15	14	0	0	1	OR4N4	5,025	downstream	ActReg chr15 #5230	0	1	0
5231	15	22,503,400	22,503,815	415	1	5.308	5.923	12.077	9	10	15	0	0	1	MIR1268	9,673	downstream	ActReg chr15 #5231	0	0	1
5232	15	22,546,529	22,546,855	326	1	5.6	7.5	13.6	8	13	18	1	1	1	LOC646396	127	in gene	ActReg chr15 #5232	0	0	1
5233	15	22,832,999	22,833,975	976	2	12.6	10.967	5.897	18	21	10	1	1	1	TUBGCP5	92	in gene	ActReg chr15 #5233	1	1	0
5234	15	22,954,928	22,955,328	400	1	2.6	3.769	10.385	3	5	17	0	0	1	CYFIP1	62,444	in gene	ActReg chr15 #5234	0	0	1
5235	15	23,033,860	23,034,682	822	1	8.24	6.96	12.44	12	13	21	1	1	2	NIPA2, NIPA1	156, 52572	in gene, downstream	ActReg chr15 #5235	0	0	1
5236	15	23,890,447	23,890,924	477	1	3.533	2.667	13.133	9	4	15	0	1	1	MAGEL2	2,308	in gene	ActReg chr15 #5236	0	0	1
5237	15	24,323,627	24,324,103	476	1	2.4	2.467	9.2	4	3	13	0	0	0				ActReg chr15 #5237	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5238	15	25,017,844	25,018,796	952	2	13.333	14.7	3.633	29	39	7	1	0	0				ActReg chr15 #5238	1	1	0
5239	15	25,123,228	25,123,815	587	1	7.263	10.632	4.947	14	17	8	1	0	1	SNRPN	54,727	in gene	ActReg chr15 #5239	0	1	0
5240	15	25,463,076	25,463,438	362	1	4.455	2.273	12.454	9	3	17	0	6	14	SNRPN, SNORD115@, SNORD115-21, SNORD115-22, PAR4, SNORD115-23, HBII-52-24, SNORD115-25, SNORD115-26, HBII-52-27, HBII-52-28, SNORD115-29, SNORD115-30, SNORD115-31	394463, 47387, 10027, 8192, 6418, 6314, 4451, 2569, -507, -2393, -4244, -5136, -7093, -8999	in gene, in gene, downstream, downstream, downstream, downstream, downstream, downstream, upstream, upstream, upstream, upstream, upstream	ActReg chr15 #5240	0	0	1
5241	15	25,485,708	25,486,521	813	1	2.381	2.105	11.68	5	3	14	0	5	14	SNRPN, SNORD115@, SNORD115-33, SNORD115-34, SNORD115-35, SNORD115-36, SNORD115-37, SNORD115-38, SNORD115-39, SNORD115-40, SNORD115-41, SNORD115-42, SNORD115-43, SNORD115-44	417320, 70244, 10129, 8580, 6720, 4882, 2981, 1129, -779, -2647, -4511, -6378, -8231, -9892	in gene, in gene, downstream, downstream, downstream, downstream, downstream, downstream, upstream, upstream, upstream, upstream, upstream	ActReg chr15 #5241	0	0	1
5242	15	25,495,060	25,495,454	394	1	2	4.833	11.25	4	7	17	0	2	9	SNRPN, SNORD115@, SNORD115-38, SNORD115-39, SNORD115-40, SNORD115-41, SNORD115-42, SNORD115-43, SNORD115-44	426463, 79387, 10272, 8364, 6496, 4632, 2765, 912, -749	in gene, in gene, downstream, downstream, downstream, downstream, downstream, downstream, upstream	ActReg chr15 #5242	0	0	1
5243	15	25,749,025	25,750,146	1,121	1	7.971	10.657	3.242	17	17	6	0	0	0				ActReg chr15 #5243	0	1	0
5244	15	26,327,190	26,327,822	632	2	7.5	12.55	11.85	9	20	17	1	0	0				ActReg chr15 #5244	0	1	1
5245	15	26,543,153	26,543,651	498	1	1.6	3.312	11.875	2	5	19	0	0	0				ActReg chr15 #5245	0	0	1
5246	15	26,873,985	26,874,588	603	1	5.056	10.778	7.222	9	16	10	1	0	1	GABRB3	144,649	in gene	ActReg chr15 #5246	0	1	0
5247	15	27,663,348	27,663,778	430	1	4.571	2.214	10.786	7	4	16	0	0	1	GABRG3	447,134	in gene	ActReg chr15 #5247	0	0	1
5248	15	27,687,235	27,687,529	294	1	1.667	1.143	10.222	3	2	14	0	0	1	GABRG3	470,953	in gene	ActReg chr15 #5248	0	0	1
5249	15	27,710,087	27,710,711	624	1	11.105	8.895	1.5	18	13	2	0	0	1	GABRG3	493,970	in gene	ActReg chr15 #5249	1	0	0
5250	15	27,837,234	27,837,909	675	1	10.667	11.191	2.875	18	19	5	0	0	0				ActReg chr15 #5250	0	1	0
5251	15	28,088,543	28,089,849	1,306	2	8.583	12.366	4.737	18	17	9	0	0	1	OCA2	255,262	in gene	ActReg chr15 #5251	1	1	0
5252	15	28,344,020	28,344,473	453	1	1.875	3.143	11.571	3	5	19	1	1	1	OCA2	212	in gene	ActReg chr15 #5252	0	0	1
5253	15	28,700,952	28,702,471	1,519	1	6.917	7.583	15.833	11	14	25	1	0	0				ActReg chr15 #5253	0	0	1
5254	15	29,130,082	29,130,888	806	1	4.2	6	11.72	7	10	17	1	0	0				ActReg chr15 #5254	0	0	1
5255	15	29,269,394	29,270,418	1,024	2	17	18.188	3.531	44	43	8	0	0	1	APBA2	56,066	in gene	ActReg chr15 #5255	1	1	0
5256	15	29,407,881	29,408,352	471	1	2.231	3.467	11.867	4	6	18	1	0	2	APBA2, FAM189A1	194276, 454811	in gene, downstream	ActReg chr15 #5256	0	0	1
5257	15	29,424,164	29,424,642	478	1	1.667	3.154	11.667	3	5	18	0	0	1	FAM189A1	438,524	in gene	ActReg chr15 #5257	0	0	1
5258	15	29,425,618	29,425,979	361	1	2.545	3.364	11.636	4	6	15	0	0	1	FAM189A1	437,129	in gene	ActReg chr15 #5258	0	0	1
5259	15	29,741,182	29,741,930	748	1	7.125	12.25	2.708	14	22	5	0	0	1	FAM189A1	121,371	in gene	ActReg chr15 #5259	0	1	0
5260	15	29,783,006	29,783,407	402	1	1.923	2.385	10.538	3	3	15	0	0	1	FAM189A1	79,721	in gene	ActReg chr15 #5260	0	0	1
5261	15	30,114,760	30,115,394	634	1	6.7	12.35	4.667	13	21	9	1	1	1	TJP1	-371	upstream	ActReg chr15 #5261	0	1	0
5262	15	30,917,759	30,918,100	341	1	9.364	4.545	2	15	7	2	0	1	1	ARHGAP11B	-950	upstream	ActReg chr15 #5262	1	0	0
5263	15	31,195,604	31,196,442	838	2	15.615	23.5	5.739	39	52	11	1	1	1	MTMR15	-32	upstream	ActReg chr15 #5263	1	1	0
5264	15	31,593,317	31,593,846	529	1	3.429	6.562	11.375	5	10	15	0	0	0				ActReg chr15 #5264	0	0	1
5265	15	31,621,666	31,621,919	253	1	2.571	3.143	11.143	3	5	13	1	0	1	KLF13	2,709	in gene	ActReg chr15 #5265	0	0	1
5266	15	32,137,574	32,137,911	337	1	2	1	10.7	3	1	15	0	0	0				ActReg chr15 #5266	0	0	1
5267	15	32,976,033	32,976,875	842	1	11.115	9.692	1.214	15	15	2	0	0	1	SCG5	42,584	in gene	ActReg chr15 #5267	1	0	0
5268	15	33,243,850	33,244,620	770	2	10.542	9.917	2.913	17	17	7	0	0	1	FMN1	115,850	in gene	ActReg chr15 #5268	1	1	0
5269	15	33,446,845	33,447,765	920	1	12.36	7.92	1.75	21	14	2	0	0	1	LOC100506959	39,542	in gene	ActReg chr15 #5269	1	0	0
5270	15	33,570,857	33,571,531	674	1	11	11.762	2.05	15	23	4	0	0	0				ActReg chr15 #5270	0	1	0
5271	15	33,840,047	33,840,560	513	1	10.688	10.875	3.625	18	17	6	0	0	1	RYR3	237,126	in gene	ActReg chr15 #5271	0	1	0
5272	15	34,013,149	34,013,633	484	2	10.25	12.188	1.545	17	21	2	0	0	1	RYR3	410,214	in gene	ActReg chr15 #5272	1	1	0
5273	15	34,152,854	34,153,436	582	1	12.056	8	2.056	21	16	5	0	0	2	RYR3, AVEN	549968, 178158	in gene, downstream	ActReg chr15 #5273	1	0	0
5274	15	34,330,528	34,330,819	291	1	7.7	9.4	11.7	10	13	17	1	1	2	AVEN, CHRM5	630, 69584	in gene, in gene	ActReg chr15 #5274	0	0	1
5275	15	34,339,580	34,340,577	997	1	9.656	11.438	4.267	16	20	7	0	0	2	AVEN, CHRM5	-8775, 78989	upstream, in gene	ActReg chr15 #5275	0	1	0
5276	15	34,516,879	34,517,685	806	1	10.6	10.68	7	16	15	11	0	1	2	TMEM85, SLC12A6	37, 112983	in gene, downstream	ActReg chr15 #5276	0	1	0
5277	15	34,634,918	34,635,756	838	2	9.462	11.923	4.292	16	22	8	0	3	3	SLC12A6, NOP10, C15orf55	-5072, 25, -2729	upstream, in gene, upstream	ActReg chr15 #5277	1	1	0
5278	15	34,659,484	34,660,178	694	2	11.136	10.909	4.905	19	18	10	1	1	2	C15orf55, LPCAT4	21765, -436	downstream, upstream	ActReg chr15 #5278	1	1	0
5279	15	34,875,832	34,876,681	849	1	7.519	13.667	8.538	13	22	17	1	1	1	GOLGA8B	-485	upstream	ActReg chr15 #5279	0	1	0
5280	15	35,045,096	35,045,999	903	2	11.821	16.821	3.524	25	33	6	0	1	1	GJD2	1,142	in gene	ActReg chr15 #5280	1	1	0
5281	15	35,086,735	35,087,160	425	1	1.769	7	11.923	4	10	19	0	1	1	ACTC1	980	in gene	ActReg chr15 #5281	0	0	1
5282	15	35,129,335	35,129,810	475	1	10.267	9.267	2.067	19	17	4	0	0	0				ActReg chr15 #5282	1	0	0
5283	15	35,261,524	35,262,492	968	2	40.1	40.833	5.933	124	132	11	1	1	2	AQR, ZNF770	-13, 18489	upstream, downstream	ActReg chr15 #5283	1	1	0
5284	15	35,280,162	35,281,207	1,045	2	12.969	12.906	5.2	27	23	12	1	1	1	ZNF770	-187	upstream	ActReg chr15 #5284	1	1	0
5285	15	35,585,495	35,586,131	636	2	10.05	11.7	1.421	19	21	2	0	0	0				ActReg chr15 #5285	1	1	0
5286	15	35,837,960	35,838,877	917	2	11.857	11.464	4.964	22	17	8	1	2	2	ATPBD4, LOC100507466	-14, 22	upstream, in gene	ActReg chr15 #5286	1	1	0
5287	15	36,030,518	36,031,077	559	1	7.333	11.167	1.25	11	22	2	0	0	1	LOC100507466	192,401	in gene	ActReg chr15 #5287	0	1	0
5288	15	36,166,296	36,166,991	695	1	12.273	8.364	1	25	13	1	0	0	0				ActReg chr15 #5288	1	0	0
5289	15	36,813,729	36,814,471	742	1	6.913	10.826	1.75	14	21	3	0	0	0				ActReg chr15 #5289	0	1	0
5290	15	36,871,136	36,871,927	791	2	11.04	14.2	4.8	16	25	8	1	1	1	C15orf41	-281	upstream	ActReg chr15 #5290	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5291	15	38,116,951	38,117,455	504	1	10.375	7.312	1.812	17	13	3	0	0	0				ActReg chr15 #5291	1	0	0
5292	15	38,422,283	38,422,936	653	1	5.7	11	2.25	8	15	4	0	0	0				ActReg chr15 #5292	0	1	0
5293	15	38,543,938	38,544,792	854	3	10.039	11.5	10.154	15	16	16	1	1	1	SPRED1	-687	upstream	ActReg chr15 #5293	1	1	1
5294	15	38,746,018	38,746,923	905	3	12.5	14.25	8.893	29	31	18	1	1	1	FAM98B	142	in gene	ActReg chr15 #5294	1	1	1
5295	15	39,178,636	39,179,343	707	2	12.227	12.682	1	23	24	1	0	0	0				ActReg chr15 #5295	1	1	0
5296	15	39,464,006	39,464,636	630	1	6.842	12.421	3.588	12	19	7	0	0	0				ActReg chr15 #5296	0	1	0
5297	15	39,464,767	39,465,601	834	1	8.444	12.333	3.826	17	23	6	0	0	0				ActReg chr15 #5297	0	1	0
5298	15	39,469,311	39,470,205	894	1	7.893	11	2.708	14	18	5	0	0	0				ActReg chr15 #5298	0	1	0
5299	15	39,487,861	39,488,661	800	1	8.48	11.96	1.545	12	21	3	0	0	0				ActReg chr15 #5299	0	1	0
5300	15	39,527,457	39,528,055	598	1	9.722	8.167	1.714	17	13	3	0	0	0				ActReg chr15 #5300	1	0	0
5301	15	39,561,571	39,562,060	489	1	6.533	11.667	1	10	16	1	0	0	0				ActReg chr15 #5301	0	1	0
5302	15	39,696,739	39,697,534	795	2	10.833	13.292	2.684	22	25	6	0	0	0				ActReg chr15 #5302	1	1	0
5303	15	39,872,853	39,873,742	889	2	10.75	13.286	13.393	21	23	22	1	1	1	THBS1	17	in gene	ActReg chr15 #5303	0	1	1
5304	15	39,874,415	39,874,894	479	1	9.067	10	12.133	11	13	20	0	1	1	THBS1	1,374	in gene	ActReg chr15 #5304	0	0	1
5305	15	39,875,942	39,876,813	871	2	14.482	9.519	6.185	23	22	9	0	0	1	THBS1	3,097	in gene	ActReg chr15 #5305	1	1	0
5306	15	39,937,853	39,938,384	531	1	6.824	3.059	13.177	9	5	22	0	0	1	FSIP1	136,921	in gene	ActReg chr15 #5306	0	0	1
5307	15	40,069,574	40,070,325	751	2	10.783	12	3.435	19	23	6	0	0	1	FSIP1	5,090	in gene	ActReg chr15 #5307	1	1	0
5308	15	40,074,742	40,075,363	621	2	5.1	11.15	8.9	9	17	16	1	1	1	FSIP1	-13	upstream	ActReg chr15 #5308	0	1	1
5309	15	40,212,188	40,213,116	928	1	10.034	11.552	8.621	14	18	12	1	2	2	GPR176, LOC100505534	441, -559	in gene, upstream	ActReg chr15 #5309	0	1	0
5310	15	40,268,417	40,269,131	714	1	8.955	10.046	7.048	13	15	13	1	0	1	EIF2AK4	42,427	in gene	ActReg chr15 #5310	0	1	0
5311	15	40,330,651	40,331,775	1,124	1	8.686	10.829	5.371	17	17	10	1	2	3	EIF2AK4, SRP14, LOC100131089	104866, 176, -299	downstream, in gene, upstream	ActReg chr15 #5311	0	1	0
5312	15	40,390,659	40,391,486	827	1	9.64	10.92	3.4	20	17	6	0	0	1	BMF	10,003	in gene	ActReg chr15 #5312	0	1	0
5313	15	40,400,969	40,401,674	705	2	17.227	15.546	2.75	38	32	6	1	1	1	BMF	-246	upstream	ActReg chr15 #5313	1	1	0
5314	15	40,452,837	40,453,761	924	2	17.759	16	6.448	34	42	12	1	1	1	BUB1B	89	in gene	ActReg chr15 #5314	1	1	0
5315	15	40,558,288	40,558,965	677	1	5.381	7.333	11.571	10	11	17	0	0	1	PAK6	48,997	in gene	ActReg chr15 #5315	0	0	1
5316	15	40,574,369	40,575,065	696	1	6.857	12.381	5.35	9	21	8	1	1	3	PAK6, LOC100131244, PLCB2	65088, 70, 25457	downstream, in gene, downstream	ActReg chr15 #5316	0	1	0
5317	15	40,615,056	40,615,926	870	2	40.556	45.222	5.571	109	126	10	1	1	2	LOC100505573, C15orf52	-1692, 17677	upstream, downstream	ActReg chr15 #5317	1	1	0
5318	15	40,627,440	40,627,923	483	1	5.6	3.643	11.2	8	6	19	0	0	2	LOC100505573, C15orf52	10498, 5487	downstream, in gene	ActReg chr15 #5318	0	0	1
5319	15	40,629,538	40,630,130	592	1	5.944	5.389	12.722	11	10	18	0	0	1	C15orf52	3,334	in gene	ActReg chr15 #5319	0	0	1
5320	15	40,659,317	40,659,816	499	1	4.286	6.188	11.938	10	9	17	1	0	1	DISP2	9,132	in gene	ActReg chr15 #5320	0	0	1
5321	15	40,660,721	40,661,171	450	1	2.929	6	12.214	5	9	16	1	0	1	DISP2	10,512	in gene	ActReg chr15 #5321	0	0	1
5322	15	40,661,301	40,661,736	435	1	2.615	3.643	10.429	4	6	17	0	0	1	DISP2	11,084	in gene	ActReg chr15 #5322	0	0	1
5323	15	40,732,034	40,732,593	559	1	6.176	5.188	12.823	8	10	18	0	1	1	BAHD1	-1,098	upstream	ActReg chr15 #5323	0	0	1
5324	15	40,751,414	40,752,059	645	1	3.75	4.75	11.8	5	7	18	0	0	1	BAHD1	18,325	in gene	ActReg chr15 #5324	0	0	1
5325	15	40,861,388	40,862,068	680	1	8.762	10.571	13.809	18	19	19	1	2	2	C15orf57, RPUSD2	-4476, 191	upstream, in gene	ActReg chr15 #5325	0	0	1
5326	15	40,885,821	40,887,111	1,290	2	7.902	11.439	9.634	19	21	21	1	1	1	CASC5	19	in gene	ActReg chr15 #5326	0	1	1
5327	15	41,047,229	41,047,688	459	1	8.333	11.133	9.267	11	15	16	1	1	2	FAM82A2, GCHFR	0, -8827	in gene, upstream	ActReg chr15 #5327	0	1	0
5328	15	41,055,651	41,056,697	1,046	1	8.719	7.969	13.375	17	19	20	1	2	4	FAM82A2, GCHFR, DNAJC17, C15orf62	-8716, -111, 43502, -5985	upstream, upstream, downstream, upstream	ActReg chr15 #5328	0	0	1
5329	15	41,099,010	41,100,227	1,217	2	11.947	13.71	7.184	21	20	12	1	2	3	DNAJC17, ZFYVE19, PPP1R14D	58, 344, 21289	in gene, in gene, downstream	ActReg chr15 #5329	1	1	0
5330	15	41,186,088	41,186,897	809	2	12.2	9.56	9.4	17	12	17	1	1	1	VPS18	-136	upstream	ActReg chr15 #5330	1	0	1
5331	15	41,198,488	41,199,181	693	1	7.455	10.954	11.136	10	15	16	0	1	2	VPS18, LOC100505662	12206, -175	downstream, upstream	ActReg chr15 #5331	0	0	1
5332	15	41,199,260	41,199,692	432	1	7.429	4.357	11.857	10	6	20	0	1	2	VPS18, LOC100505662	12848, 467	downstream, in gene	ActReg chr15 #5332	0	0	1
5333	15	41,221,379	41,221,855	476	1	6.643	6.786	13.714	11	10	18	1	1	1	DLL4	86	in gene	ActReg chr15 #5333	0	0	1
5334	15	41,408,057	41,409,095	1,038	2	26.394	31.182	5.393	77	104	10	1	1	1	INO80	-236	upstream	ActReg chr15 #5334	1	1	0
5335	15	41,522,611	41,523,904	1,293	2	16.244	22.732	6.878	47	55	13	1	2	2	EXD1, CHP	-362, -180	upstream, upstream	ActReg chr15 #5335	1	1	0
5336	15	41,575,918	41,576,534	616	2	9.684	11.737	10.895	18	17	17	1	1	2	CHP, LOC729082	52789, 25	downstream, in gene	ActReg chr15 #5336	0	1	1
5337	15	41,624,194	41,625,447	1,253	2	11.308	13.667	7.872	22	21	14	1	2	2	CIP5, NUSAP1	-1, -106	upstream, upstream	ActReg chr15 #5337	1	1	0
5338	15	41,694,244	41,694,940	696	3	10.429	10.286	11.316	18	19	21	1	1	1	NDUFAF1	50	in gene	ActReg chr15 #5338	1	1	1
5339	15	41,709,450	41,709,930	480	1	9.8	8.6	11.467	14	12	19	1	1	1	RTF1	388	in gene	ActReg chr15 #5339	0	0	1
5340	15	41,795,186	41,795,768	582	1	3	4.111	13.667	5	9	18	1	0	2	ITPKA, LTK	9355, 10608	in gene, downstream	ActReg chr15 #5340	0	0	1
5341	15	41,836,113	41,836,742	629	1	10.3	11.1	12.45	16	16	23	1	1	1	RPAP1	37	in gene	ActReg chr15 #5341	0	0	1
5342	15	41,877,203	41,877,790	587	1	6.333	10.444	3.533	8	17	8	1	0	1	TYRO3	26,276	downstream	ActReg chr15 #5342	0	1	0
5343	15	42,149,336	42,149,844	508	1	2.812	4.375	12.062	4	6	15	0	0	4	JMJD7-PLA2G4B, PLA2G4B, SPTBN5, MIR4310	29307, 18579, 36685, 9159	downstream, downstream, in gene, downstream	ActReg chr15 #5343	0	0	1
5344	15	42,170,406	42,170,987	581	1	2.778	1.889	13.333	5	3	18	0	0	1	SPTBN5	15,579	in gene	ActReg chr15 #5344	0	0	1
5345	15	42,186,327	42,187,293	966	1	11.733	7.167	8.633	15	11	13	0	2	3	SPTBN5, LOC100289090, EHD4	-535, 485, 77945	upstream, in gene, downstream	ActReg chr15 #5345	1	0	0
5346	15	42,328,513	42,328,964	451	1	3.214	6.071	13.357	7	8	21	0	0	0				ActReg chr15 #5346	0	0	1
5347	15	42,349,051	42,350,286	1,235	2	11.026	17	4.487	32	38	7	0	0	1	PLA2G4D	37,084	downstream	ActReg chr15 #5347	1	1	0
5348	15	42,376,937	42,377,411	474	1	6.6	4.067	11.8	10	6	15	0	0	1	PLA2G4D	9,578	in gene	ActReg chr15 #5348	0	0	1
5349	15	42,385,345	42,386,076	731	1	2.955	5	11.454	7	7	17	0	1	1	PLA2G4D	1,042	in gene	ActReg chr15 #5349	0	0	1
5350	15	42,386,438	42,386,934	496	1	3.917	4.267	11.4	6	6	17	0	1	1	PLA2G4D	66	in gene	ActReg chr15 #5350	0	0	1
5351	15	42,565,261	42,566,119	858	2	11.593	10.111	8.37	17	16	13	2	2	2	TMEM87A, GANC	65, -676	in gene, upstream	ActReg chr15 #5351	1	1	0
5352	15	42,782,961	42,783,682	721	1	7.652	10.652	7.304	11	13	13	1	1	1	SNAP23	-4,514	upstream	ActReg chr15 #5352	0	1	0
5353	15	42,840,572	42,841,297	725	2	10.783	10.13	14.609	18	15	25	1	2	2	LRRC57, HAUS2	68, -77	in gene, upstream	ActReg chr15 #5353	1	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5354	15	42,867,481	42,867,797	316	1	3.4	7	10.7	7	9	15	1	1	2	HAUS2, STARD9	26628, -218	downstream, upstream	ActReg chr15 #5354	0	0	1
5355	15	43,051,342	43,051,684	342	1	4.545	2.182	12	7	4	16	0	0	1	TTBK2	161,494	in gene	ActReg chr15 #5355	0	0	1
5356	15	43,212,758	43,213,880	1,122	1	7.086	10.514	6.057	14	17	12	1	1	1	TTBK2	-312	upstream	ActReg chr15 #5356	0	1	0
5357	15	43,425,440	43,426,460	1,020	2	10.625	10.562	5.531	17	18	10	1	1	1	TMEM62	228	in gene	ActReg chr15 #5357	1	1	0
5358	15	43,541,877	43,542,318	441	1	11.786	9.143	2.571	17	13	4	0	0	1	TGM5	16,958	in gene	ActReg chr15 #5358	1	0	0
5359	15	43,621,925	43,622,914	989	2	9.387	11.387	8.516	15	17	16	1	2	2	LCMT2, ADAL	472, -453	in gene, upstream	ActReg chr15 #5359	0	1	1
5360	15	43,662,307	43,663,958	1,651	3	10.177	10.353	9.54	20	17	22	1	2	2	ZSCAN29, TUBGCP4	-874, -181	upstream, upstream	ActReg chr15 #5360	1	1	1
5361	15	43,732,989	43,733,549	560	1	9.611	7.118	1.8	16	13	3	0	0	1	TP53BP1	69,438	in gene	ActReg chr15 #5361	1	0	0
5362	15	43,802,924	43,803,721	797	2	7.8	10.44	9.76	9	14	17	1	2	2	TP53BP1, MAP1A	-615, -6484	upstream, upstream	ActReg chr15 #5362	0	1	1
5363	15	44,038,719	44,039,137	418	1	6.286	10.857	3.786	8	14	5	1	1	1	PDIA3	338	in gene	ActReg chr15 #5363	0	1	0
5364	15	44,116,501	44,117,171	670	1	8.714	11.238	5.048	17	19	10	1	2	2	MFAP1, WDR76	115, -2276	in gene, upstream	ActReg chr15 #5364	0	1	0
5365	15	44,203,278	44,203,837	559	1	8.941	10.471	1.412	13	14	2	0	0	1	FRMD5	283,872	in gene	ActReg chr15 #5365	0	1	0
5366	15	44,205,309	44,205,973	664	1	9.476	14.095	1.706	14	21	3	0	0	1	FRMD5	281,788	in gene	ActReg chr15 #5366	0	1	0
5367	15	44,394,597	44,395,522	925	2	12.552	9.759	2.25	18	17	3	0	0	1	FRMD5	92,370	in gene	ActReg chr15 #5367	1	1	0
5368	15	44,487,276	44,487,921	645	2	12.4	11.7	9.4	23	23	15	1	1	1	FRMD5	-169	upstream	ActReg chr15 #5368	1	1	0
5369	15	44,781,501	44,782,329	828	2	8.154	10.423	2.654	18	21	5	0	0	1	CTDSPL2	62,336	in gene	ActReg chr15 #5369	1	1	0
5370	15	44,828,417	44,829,141	724	3	10.909	12.091	9	20	17	16	1	2	3	CTDSPL2, LOC645212, EIF3J	109200, 342, -487	downstream, in gene, upstream	ActReg chr15 #5370	1	1	1
5371	15	44,829,267	44,830,236	969	2	11.367	10.433	6.233	16	15	14	1	2	3	CTDSPL2, LOC645212, EIF3J	110172, -630, 485	downstream, upstream, in gene	ActReg chr15 #5371	1	1	0
5372	15	44,955,248	44,956,199	951	2	10.833	14.4	9.867	16	23	16	1	1	2	SPG11, PATL2	153, 13363	in gene, downstream	ActReg chr15 #5372	0	1	1
5373	15	45,003,285	45,004,166	881	3	11.929	13.107	9.286	19	25	15	1	1	1	B2M	40	in gene	ActReg chr15 #5373	1	1	1
5374	15	45,076,513	45,077,202	689	2	12.667	10.429	3.154	23	18	5	0	0	0				ActReg chr15 #5374	1	1	0
5375	15	45,145,510	45,145,881	371	1	11.182	7.182	1.182	15	10	2	0	0	0				ActReg chr15 #5375	1	0	0
5376	15	45,248,770	45,249,104	334	1	1.75	2.9	12.7	3	5	16	0	1	1	C15orf43	57	in gene	ActReg chr15 #5376	0	0	1
5377	15	45,315,225	45,315,663	438	1	6.357	11.929	12.357	10	18	18	1	1	1	SORD	142	in gene	ActReg chr15 #5377	0	0	1
5378	15	45,408,877	45,409,606	729	1	4	3.652	10.957	8	6	15	1	2	3	DUOX2, DUOXA2, DUOXA1	-2882, 2718, 12816	upstream, in gene, downstream	ActReg chr15 #5378	0	0	1
5379	15	45,471,648	45,472,081	433	1	8.143	8.714	10.143	12	12	15	0	0	1	SHF	21,509	in gene	ActReg chr15 #5379	0	0	1
5380	15	45,490,509	45,491,320	811	3	12.32	10.96	11.72	17	20	26	1	1	1	SHF	2,459	in gene	ActReg chr15 #5380	1	1	1
5381	15	45,492,332	45,493,588	1,256	4	12.513	9.821	11	26	22	19	0	1	1	SHF	413	in gene	ActReg chr15 #5381	1	1	1
5382	15	45,694,011	45,695,345	1,334	1	12.214	11.619	8.351	22	19	17	1	1	1	SPATA5L1	159	in gene	ActReg chr15 #5382	1	0	0
5383	15	45,722,465	45,722,895	430	1	9.154	6.846	12	13	9	18	1	2	3	SPATA5L1, C15orf48, MIR147B	28161, -83, -2568	downstream, upstream, upstream	ActReg chr15 #5383	0	0	1
5384	15	45,742,935	45,743,255	320	1	3.9	1.6	11.4	7	2	14	0	0	0				ActReg chr15 #5384	0	0	1
5385	15	45,748,390	45,749,244	854	1	8.308	13.538	4.346	17	20	10	0	0	0				ActReg chr15 #5385	0	1	0
5386	15	45,879,053	45,880,052	999	2	13.452	15	6.548	26	26	13	1	1	1	PLDN	135	in gene	ActReg chr15 #5386	1	1	0
5387	15	46,501,897	46,502,215	318	1	1.75	3.9	10.1	3	7	14	0	0	0				ActReg chr15 #5387	0	0	1
5388	15	48,214,124	48,214,471	347	1	2.364	2.111	9.364	4	3	13	0	0	0				ActReg chr15 #5388	0	0	1
5389	15	48,482,744	48,483,641	897	2	14.964	16.786	2.632	32	35	5	0	1	1	CTXN2	-675	upstream	ActReg chr15 #5389	1	1	0
5390	15	48,623,217	48,624,648	1,431	4	9.956	14.533	6.659	17	30	14	1	1	1	DUT	311	in gene	ActReg chr15 #5390	1	1	1
5391	15	48,717,135	48,717,635	500	1	3.812	13.312	4.308	6	17	8	0	0	1	FBN1	220,600	in gene	ActReg chr15 #5391	0	1	0
5392	15	48,725,666	48,726,318	652	1	10.9	8.3	2.526	18	11	4	0	0	1	FBN1	211,993	in gene	ActReg chr15 #5392	1	0	0
5393	15	48,937,449	48,938,091	642	1	4.8	11.55	5.722	8	18	10	1	2	2	FBN1, LOC100506059	215, -1084	in gene, upstream	ActReg chr15 #5393	0	1	0
5394	15	49,015,455	49,015,963	508	1	10.562	8.688	1.583	15	13	3	0	0	0				ActReg chr15 #5394	1	0	0
5395	15	49,102,923	49,103,393	470	1	7.933	10.333	10.733	11	13	16	2	2	2	CEP152, LOC100506104	185, 263	in gene, in gene	ActReg chr15 #5395	0	0	1
5396	15	49,150,940	49,151,433	493	1	2.75	9.188	0	6	16	0	0	0	1	SHC4	104,455	in gene	ActReg chr15 #5396	0	1	0
5397	15	49,169,749	49,170,956	1,207	1	5.921	12.737	5.833	13	25	14	1	1	2	SHC4, EID1	85289, 62	in gene, in gene	ActReg chr15 #5397	0	1	0
5398	15	49,221,618	49,222,383	765	1	8.208	10.875	2.792	13	16	6	0	0	1	SHC4	33,641	in gene	ActReg chr15 #5398	0	1	0
5399	15	49,338,205	49,339,130	925	2	10.931	8.966	10.769	18	17	16	1	1	1	SECISBP2L	93	in gene	ActReg chr15 #5399	1	0	1
5400	15	49,447,146	49,448,233	1,087	2	9.735	14.265	4.559	17	28	10	1	2	2	COPS2, GALK2	165, -287	in gene, upstream	ActReg chr15 #5400	1	1	0
5401	15	49,912,823	49,913,605	782	3	10.56	12.48	8.32	18	23	22	1	2	2	C15orf33, DTWD1	-96, -12	upstream, upstream	ActReg chr15 #5401	1	1	1
5402	15	50,429,423	50,430,081	658	1	12.429	12.571	2.789	23	21	5	0	0	0				ActReg chr15 #5402	0	1	0
5403	15	50,474,678	50,475,109	431	1	5.071	6.143	12.643	7	10	18	1	1	1	SLC27A2	500	in gene	ActReg chr15 #5403	0	0	1
5404	15	50,647,026	50,647,768	742	3	11.348	10.087	10.391	16	20	20	1	3	3	GABPB1, FLJ10038, LOC100129387	208, -321, 1026	in gene, upstream, in gene	ActReg chr15 #5404	1	1	1
5405	15	50,716,190	50,716,944	754	1	12.875	9.583	6.792	23	14	11	1	1	1	USP8	-12	upstream	ActReg chr15 #5405	1	0	0
5406	15	50,978,527	50,978,867	340	1	7.727	11	10.454	12	15	14	1	1	1	TRPM7	315	in gene	ActReg chr15 #5406	0	0	1
5407	15	51,177,561	51,178,465	904	1	6.241	9.724	3.621	13	15	7	0	0	0				ActReg chr15 #5407	0	1	0
5408	15	51,200,701	51,201,425	724	1	11.696	8.739	8.304	16	14	13	1	1	1	AP4E1	117	in gene	ActReg chr15 #5408	1	0	0
5409	15	51,633,528	51,633,902	374	1	3.333	4.917	11	6	8	17	1	2	3	CYP19A1, LOC100506192, GLDN	-2920, 4591, 2	upstream, downstream, in gene	ActReg chr15 #5409	0	0	1
5410	15	51,913,931	51,914,657	726	1	7.478	12.435	3.304	10	21	8	1	1	1	DMXL2	673	in gene	ActReg chr15 #5410	0	1	0
5411	15	51,973,200	51,974,095	895	2	17.357	23.821	4.964	47	62	10	1	1	1	SCG3	97	in gene	ActReg chr15 #5411	1	1	0
5412	15	52,263,480	52,264,374	894	2	11.429	14.464	6.643	25	31	13	1	1	1	LEO1	31	in gene	ActReg chr15 #5412	1	1	0
5413	15	52,311,036	52,311,640	604	1	11.263	10.316	13.474	15	20	22	1	1	1	MAPK6	-73	upstream	ActReg chr15 #5413	0	0	1
5414	15	52,332,223	52,332,683	460	1	6.4	11.8	2.8	10	16	4	0	0	1	MAPK6	21,042	in gene	ActReg chr15 #5414	0	1	0
5415	15	52,471,341	52,471,843	502	1	8.562	10.75	8.625	13	19	14	1	1	2	GNB5, LOC100129973	11973, -604	in gene, upstream	ActReg chr15 #5415	0	1	0
5416	15	52,820,194	52,820,932	738	1	9.217	12.522	5.391	15	21	9	1	1	1	MYO5A	684	in gene	ActReg chr15 #5416	0	1	0
5417	15	52,970,910	52,971,333	423	1	9.143	4.429	12.286	12	6	14	1	1	1	KIAA1370	-501	upstream	ActReg chr15 #5417	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIsIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5418	15	53,076,273	53,076,688	415	1	5.462	6.538	12	7	8	17	1	0	1	ONECUT1	5,729	in gene	ActReg chr15 #5418	0	0	1
5419	15	53,082,599	53,083,044	445	1	3.929	3.833	12.214	7	6	20	1	1	1	ONECUT1	-612	upstream	ActReg chr15 #5419	0	0	1
5420	15	53,087,107	53,087,433	326	1	3	2.8	10.5	5	5	15	1	1	1	ONECUT1	-5,061	upstream	ActReg chr15 #5420	0	0	1
5421	15	53,363,983	53,365,338	1,355	2	23.476	29.191	3.079	89	109	5	0	0	0				ActReg chr15 #5421	1	1	0
5422	15	53,484,689	53,485,918	1,229	2	9.289	14.158	1.923	28	35	5	0	0	0				ActReg chr15 #5422	1	1	0
5423	15	53,600,431	53,600,977	546	1	8.941	13.177	3.188	12	19	5	0	0	0				ActReg chr15 #5423	0	1	0
5424	15	53,620,183	53,621,086	903	2	12.036	14.464	1.792	29	27	3	0	0	0				ActReg chr15 #5424	1	1	0
5425	15	54,754,437	54,754,905	468	1	2.714	2.583	10.5	5	4	15	0	0	1	UNC13C	449,570	in gene	ActReg chr15 #5425	0	0	1
5426	15	55,488,771	55,489,555	784	2	11.25	13.625	8.833	23	24	18	1	1	2	RSL24D1, RAB27A	68, 92838	in gene, downstream	ActReg chr15 #5426	1	1	0
5427	15	55,571,784	55,572,430	646	1	8.65	11.65	2.316	16	21	5	0	0	1	RAB27A	9,894	in gene	ActReg chr15 #5427	0	1	0
5428	15	55,610,858	55,611,782	924	2	12.31	13.69	6.552	25	25	14	1	2	2	LOC100506294, PIGB	21, 187	in gene, in gene	ActReg chr15 #5428	1	1	0
5429	15	55,699,812	55,700,820	1,008	1	8.774	11.065	6.667	14	16	13	1	2	3	CCPG1, FLJ27352, DYX1C1	258, -430, 100116	in gene, upstream, downstream	ActReg chr15 #5429	0	1	0
5430	15	55,739,627	55,739,952	325	1	2.9	4.1	11.8	4	5	16	0	0	1	DYX1C1	60,643	in gene	ActReg chr15 #5430	0	0	1
5431	15	56,199,835	56,200,483	648	1	8.286	11.857	2.143	15	26	3	0	0	1	NEDD4	85,676	in gene	ActReg chr15 #5431	0	1	0
5432	15	56,209,044	56,209,516	472	1	9.933	8.067	2.1	16	12	3	0	0	1	NEDD4	76,555	in gene	ActReg chr15 #5432	1	0	0
5433	15	56,538,122	56,538,543	421	1	5.846	10	2.583	8	14	4	0	1	1	RFX7	-2,849	upstream	ActReg chr15 #5433	0	1	0
5434	15	56,853,831	56,854,133	302	1	11.875	5.889	10.333	3	8	13	0	0	0				ActReg chr15 #5434	0	0	1
5435	15	57,178,999	57,180,029	1,030	2	11	11.5	5.621	19	20	13	1	0	1	LOC145783	31,183	in gene	ActReg chr15 #5435	1	1	0
5436	15	57,210,054	57,211,163	1,109	2	9.882	16.206	12.294	15	29	24	1	2	2	LOC145783, TCF12	89, -225	in gene, upstream	ActReg chr15 #5436	0	1	1
5437	15	57,829,081	57,829,677	596	1	10.053	11.053	2.684	18	18	4	0	0	1	CGNL1	99,196	in gene	ActReg chr15 #5437	0	1	0
5438	15	57,998,506	57,999,115	609	1	10.526	10.842	7.421	16	19	14	1	1	2	GCOM1, GRINL1A	114708, -91	in gene, upstream	ActReg chr15 #5438	1	0	0
5439	15	58,472,036	58,472,980	944	1	8.966	11.828	1.846	14	17	4	0	0	1	AQP9	42,100	in gene	ActReg chr15 #5439	0	1	0
5440	15	59,062,789	59,064,455	1,666	2	7.519	11.923	6.3	20	24	15	1	2	2	LOC100506466, FAM63B	-444, 229	upstream, in gene	ActReg chr15 #5440	0	1	1
5441	15	59,397,407	59,397,892	485	1	4.875	8.812	11.625	11	16	16	1	1	2	RNF111, CCNB2	117784, 329	downstream, in gene	ActReg chr15 #5441	0	0	1
5442	15	59,664,446	59,665,516	1,070	2	9.676	9.118	10.194	15	15	22	1	1	1	MYO1E	90	in gene	ActReg chr15 #5442	1	0	1
5443	15	59,949,300	59,949,907	607	1	10.737	12.526	9.842	17	20	14	1	1	2	GTF2A2, BNIP2	134, 32039	in gene, downstream	ActReg chr15 #5443	0	1	0
5444	15	59,981,035	59,981,885	850	1	10.923	9.231	6.885	15	19	12	1	1	1	BNIP2	182	in gene	ActReg chr15 #5444	1	0	0
5445	15	59,982,000	59,982,296	296	1	7.333	5.222	11.889	10	7	17	0	1	1	BNIP2	-506	upstream	ActReg chr15 #5445	0	0	1
5446	15	60,144,703	60,145,095	392	1	6.615	3.154	10.769	9	5	13	0	0	0				ActReg chr15 #5446	0	0	1
5447	15	60,184,992	60,185,761	769	1	8.6	13.28	3.174	12	21	6	0	0	0				ActReg chr15 #5447	0	1	0
5448	15	60,297,426	60,297,874	448	1	7.571	11.429	7.929	10	13	13	1	1	1	FOXB1	1,229	in gene	ActReg chr15 #5448	0	1	0
5449	15	60,297,961	60,298,491	530	1	6.562	7.688	12.938	11	11	18	1	1	1	FOXB1	1,805	downstream	ActReg chr15 #5449	0	0	1
5450	15	60,654,776	60,655,308	532	1	6.882	10.706	1.308	12	17	3	0	0	1	ANXA2	35,143	in gene	ActReg chr15 #5450	0	1	0
5451	15	60,663,150	60,664,138	988	2	11.581	13.258	3.174	20	25	8	0	0	1	ANXA2	26,541	in gene	ActReg chr15 #5451	1	1	0
5452	15	60,666,009	60,667,349	1,340	1	10.619	8.857	3.895	15	20	7	0	0	1	ANXA2	23,506	in gene	ActReg chr15 #5452	1	0	0
5453	15	60,685,063	60,685,721	658	1	12.4	7.45	1.778	23	12	3	0	0	1	ANXA2	4,793	in gene	ActReg chr15 #5453	1	0	0
5454	15	60,700,438	60,701,106	668	2	12.286	11.714	1	19	21	1	0	0	0				ActReg chr15 #5454	1	1	0
5455	15	60,770,881	60,771,770	889	2	10.296	15.518	9.63	18	23	14	1	1	2	NARG2, RORA	19, 750177	in gene, downstream	ActReg chr15 #5455	1	1	0
5456	15	61,467,222	61,467,735	513	1	6.357	9.125	2.444	11	16	3	0	0	1	RORA	54,024	in gene	ActReg chr15 #5456	0	1	0
5457	15	61,657,146	61,657,681	535	1	5.647	1.818	11.059	7	4	15	0	0	0				ActReg chr15 #5457	0	0	1
5458	15	61,876,592	61,877,085	493	1	7.8	10.067	1.6	11	17	2	0	0	0				ActReg chr15 #5458	0	1	0
5459	15	62,411,427	62,412,118	691	2	13.809	12.857	1.588	24	24	2	0	0	0				ActReg chr15 #5459	1	1	0
5460	15	62,682,678	62,683,009	331	1	9.273	10.454	2	13	16	2	1	0	0				ActReg chr15 #5460	0	1	0
5461	15	62,898,398	62,899,440	1,042	2	12.242	14.939	2.793	24	28	5	0	0	0				ActReg chr15 #5461	1	1	0
5462	15	62,939,523	62,940,141	618	1	13.526	7.105	1	24	12	1	0	2	2	MGC15885, TLN2	-2452, 322	upstream, in gene	ActReg chr15 #5462	1	0	0
5463	15	63,178,683	63,179,193	510	1	10.25	8.25	2.25	18	10	4	0	0	0				ActReg chr15 #5463	1	0	0
5464	15	63,310,584	63,311,977	1,393	2	10.477	10.841	3.302	15	16	7	0	0	0				ActReg chr15 #5464	1	1	0
5465	15	63,413,436	63,414,761	1,325	3	15.786	15.262	7.1	53	48	18	1	1	1	LACTB	66	in gene	ActReg chr15 #5465	1	1	1
5466	15	63,449,323	63,450,047	724	1	10.364	14.091	6.85	13	26	10	1	1	1	RPS27L	56	in gene	ActReg chr15 #5466	0	1	0
5467	15	63,478,222	63,478,882	660	1	10.952	8.048	2.952	21	14	5	0	1	1	RAB8B	-3,176	upstream	ActReg chr15 #5467	1	0	0
5468	15	63,616,061	63,616,905	844	1	9.63	11.963	5.04	16	18	10	0	0	1	CA12	57,592	in gene	ActReg chr15 #5468	0	1	0
5469	15	63,640,166	63,640,939	773	1	9.125	7.792	5.375	14	14	11	0	0	1	CA12	33,523	in gene	ActReg chr15 #5469	1	0	0
5470	15	63,795,892	63,797,125	1,233	3	10.564	12.282	8.528	25	28	17	1	1	1	USP3	-302	upstream	ActReg chr15 #5470	1	1	1
5471	15	64,162,354	64,163,520	1,166	2	20.514	26.432	5.297	62	77	14	0	1	1	MIR422A	281	downstream	ActReg chr15 #5471	1	1	0
5472	15	64,385,688	64,386,796	1,108	2	11.343	12.429	6.143	22	20	13	1	2	2	FAM96A, SNX1	-35, -1935	upstream, upstream	ActReg chr15 #5472	1	1	0
5473	15	64,387,915	64,388,621	706	2	12.091	8.273	8.818	20	15	15	1	2	2	FAM96A, SNX1	-2061, 91	upstream, in gene	ActReg chr15 #5473	1	0	1
5474	15	64,454,884	64,455,929	1,045	2	15.969	15.469	7.281	33	29	16	1	1	3	SNX22, PPIB, CSNK1G1	11490, -52, 193036	downstream, upstream, downstream	ActReg chr15 #5474	1	1	0
5475	15	64,647,591	64,648,920	1,329	3	7.366	9.902	6.707	17	22	14	1	1	2	CSNK1G1, KIAA0101	187, 25447	in gene, downstream	ActReg chr15 #5475	1	1	1
5476	15	64,673,118	64,674,033	915	1	7.241	11.655	4.207	11	19	8	0	2	2	KIAA0101, TRIP4	127, -6428	in gene, upstream	ActReg chr15 #5476	0	1	0
5477	15	64,679,649	64,680,362	713	2	12.727	12.864	8.091	23	26	17	1	2	2	KIAA0101, TRIP4	-6303, 2	upstream, in gene	ActReg chr15 #5477	1	1	0
5478	15	64,752,263	64,752,988	725	2	10.409	11.909	3.444	22	22	7	1	0	1	TRIP4	72,622	downstream	ActReg chr15 #5478	1	1	0
5479	15	65,068,527	65,068,951	424	1	4.769	6.077	11.846	7	9	19	1	1	1	RBPMS2	-969	upstream	ActReg chr15 #5479	0	0	1
5480	15	65,117,284	65,118,389	1,105	1	8.206	11.823	5.419	12	24	10	0	1	1	PIF1	2	in gene	ActReg chr15 #5480	0	1	0
5481	15	65,127,764	65,128,535	771	2	10.625	9.625	4.739	16	15	10	1	1	2	PIF1, PLEKHO2	-10311, -5933	upstream, upstream	ActReg chr15 #5481	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5482	15	65,133,323	65,133,946	623	1	4.5	7.737	13.105	7	17	21	1	1	1	PLEKHO2	-448	upstream	ActReg chr15 #5482	0	0	1
5483	15	65,176,103	65,176,906	803	1	4.56	10.08	5.364	8	18	8	0	0	0				ActReg chr15 #5483	0	1	0
5484	15	65,321,515	65,322,111	596	1	11	9.5	6.833	16	14	8	1	1	1	MTFMT	164	in gene	ActReg chr15 #5484	1	0	0
5485	15	65,361,321	65,361,983	662	1	8.05	11.65	3	11	17	5	0	2	2	RASL12, KBTBD13	-1264, -7502	upstream, upstream	ActReg chr15 #5485	0	1	0
5486	15	65,425,763	65,426,592	829	2	9.115	12.615	3.182	19	22	7	1	1	1	PDCD7	-3	upstream	ActReg chr15 #5486	1	1	0
5487	15	65,477,315	65,477,668	353	1	6.091	10.909	10.636	9	14	13	1	1	1	CLPX	72	in gene	ActReg chr15 #5487	0	0	1
5488	15	65,477,700	65,477,968	268	1	7.625	7.125	11.625	11	10	14	1	1	1	CLPX	-271	upstream	ActReg chr15 #5488	0	0	1
5489	15	65,587,904	65,588,612	708	2	19.13	15	5.238	46	33	13	0	1	3	PARP16, RNU5A, RNU5B-1	-9240, -131, -8757	upstream, upstream, upstream	ActReg chr15 #5489	1	1	0
5490	15	65,596,607	65,597,840	1,233	1	7.974	10.436	4.529	15	16	15	0	1	2	RNU5A, RNU5B-1	8834, 208	downstream, downstream	ActReg chr15 #5490	0	1	0
5491	15	65,677,530	65,678,229	699	1	9.182	7.545	11.091	14	15	17	0	1	2	IGDCC3, IGDCC4	-7501, 37531	upstream, in gene	ActReg chr15 #5491	0	0	1
5492	15	65,809,237	65,810,616	1,379	3	49.279	53.791	7.907	176	189	23	1	1	1	DPP8	109	in gene	ActReg chr15 #5492	1	1	1
5493	15	65,822,753	65,823,422	669	1	8.6	13.2	16.05	12	21	26	1	1	1	PTPLAD1	260	in gene	ActReg chr15 #5493	0	0	1
5494	15	65,903,038	65,904,079	1,041	3	11.424	16.454	7.758	24	38	20	1	1	1	C15orf44	-89	upstream	ActReg chr15 #5494	1	1	1
5495	15	66,084,035	66,084,397	362	1	8.182	5.091	12.546	10	6	15	1	1	1	DENND4A	415	in gene	ActReg chr15 #5495	0	0	1
5496	15	66,084,515	66,085,256	741	2	18.478	20.522	9.913	41	37	24	1	1	1	DENND4A	-254	upstream	ActReg chr15 #5496	1	1	0
5497	15	66,125,231	66,125,677	446	1	6.5	11.357	5.3	11	15	8	0	0	0				ActReg chr15 #5497	0	1	0
5498	15	66,161,234	66,162,054	820	2	10.154	15.615	12.538	13	26	24	1	1	1	RAB11A	-152	upstream	ActReg chr15 #5498	0	1	1
5499	15	66,244,452	66,247,249	2,797	3	16.977	19.759	4.057	50	52	9	0	0	1	MEGF11	300,225	in gene	ActReg chr15 #5499	1	1	0
5500	15	66,296,780	66,297,838	1,058	2	15.061	12.152	3.067	35	28	6	0	0	1	MEGF11	248,766	in gene	ActReg chr15 #5500	1	1	0
5501	15	66,299,158	66,299,974	816	2	13.077	14.577	2.2	24	32	5	0	0	1	MEGF11	246,509	in gene	ActReg chr15 #5501	1	1	0
5502	15	66,544,900	66,545,547	647	1	4	10.95	3.059	7	17	5	1	1	1	MEGF11	852	in gene	ActReg chr15 #5502	0	1	0
5503	15	66,678,757	66,679,300	543	1	9.529	12.294	5.176	15	21	8	1	1	1	MAP2K1	-183	upstream	ActReg chr15 #5503	0	1	0
5504	15	66,789,648	66,790,762	1,114	2	10.229	11.257	7.469	16	29	21	1	2	8	MAP2K1, SNAPC5, RPL4, SNORD18C, SNORD18B, SNORD16, SNORD18A, ZWILCH	110994, -59, 6979, 3451, 4224, 5043, 5447, -7226	downstream, upstream, downstream, downstream, downstream, downstream, downstream, upstream	ActReg chr15 #5504	1	1	0
5505	15	66,913,213	66,913,665	452	1	4.467	9.667	4.4	8	13	7	0	0	0				ActReg chr15 #5505	0	1	0
5506	15	66,914,230	66,914,550	320	1	3.111	3.2	9.7	4	5	14	1	0	0				ActReg chr15 #5506	0	0	1
5507	15	66,993,668	66,994,765	1,097	3	11.412	10.5	6.656	22	19	16	1	1	1	SMAD6	-458	upstream	ActReg chr15 #5507	1	1	1
5508	15	67,058,129	67,058,810	681	1	9.762	11.714	2.2	15	18	4	0	0	1	SMAD6	63,795	in gene	ActReg chr15 #5508	0	1	0
5509	15	67,061,625	67,062,023	398	1	2.091	4.308	9.769	4	7	14	0	0	1	SMAD6	67,150	in gene	ActReg chr15 #5509	0	0	1
5510	15	67,134,111	67,134,678	567	1	5.833	11.611	5.167	13	15	9	1	0	0				ActReg chr15 #5510	0	1	0
5511	15	67,316,082	67,317,192	1,110	1	10.171	7.286	4.697	17	11	9	0	0	0				ActReg chr15 #5511	1	0	0
5512	15	67,383,357	67,384,008	651	1	12.191	10.952	3	19	19	5	0	0	1	SMAD3	25,487	in gene	ActReg chr15 #5512	1	0	0
5513	15	67,476,760	67,477,164	404	1	3.538	6.154	11.923	5	8	19	0	0	1	SMAD3	118,767	in gene	ActReg chr15 #5513	0	0	1
5514	15	67,546,566	67,547,544	978	2	14	16.7	8.8	31	38	15	1	2	2	AAGAB, IQCH	19, -83	in gene, upstream	ActReg chr15 #5514	1	1	0
5515	15	67,812,981	67,813,476	495	1	9.5	5.188	4.75	15	8	7	1	2	2	LOC100506686, C15orf61	954, -294	in gene, upstream	ActReg chr15 #5515	1	0	0
5516	15	67,834,667	67,835,096	429	1	10.462	8.385	7.077	14	11	13	1	1	1	MAP2K5	-140	upstream	ActReg chr15 #5516	1	0	0
5517	15	68,113,180	68,113,797	617	1	8.5	13.4	7.3	15	23	11	1	1	1	LBXCOR1	-4,453	upstream	ActReg chr15 #5517	0	1	0
5518	15	68,132,394	68,133,216	822	1	11.423	12.462	6	17	22	13	1	1	2	LBXCOR1, RNU6-1	14864, -422	downstream, upstream	ActReg chr15 #5518	0	1	0
5519	15	68,548,963	68,549,670	707	1	5.591	5.909	12.818	8	9	17	0	0	0				ActReg chr15 #5519	0	0	1
5520	15	68,569,538	68,571,241	1,703	2	15.377	15.925	8.038	27	32	14	1	1	1	FEM1B	248	in gene	ActReg chr15 #5520	1	1	0
5521	15	68,608,302	68,608,733	431	1	3.462	3.308	11.462	5	5	16	0	0	1	ITGA11	115,975	in gene	ActReg chr15 #5521	0	0	1
5522	15	68,664,591	68,665,177	586	1	11.611	5.667	6.389	18	9	12	0	0	1	ITGA11	59,608	in gene	ActReg chr15 #5522	1	0	0
5523	15	68,870,344	68,871,043	699	2	11.864	10.954	11.136	18	14	21	1	0	0				ActReg chr15 #5523	0	1	1
5524	15	68,871,657	68,872,149	492	1	8.667	8.467	13.8	12	14	21	1	0	0				ActReg chr15 #5524	0	0	1
5525	15	69,366,387	69,367,213	826	1	8.962	13.538	5.5	14	21	7	1	1	1	TMEM84	-6,390	upstream	ActReg chr15 #5525	0	1	0
5526	15	69,452,695	69,453,213	518	1	5.75	7.188	10.938	10	11	14	1	1	1	GLCE	-19	upstream	ActReg chr15 #5526	0	0	1
5527	15	69,706,281	69,707,454	1,173	1	8.444	13.194	5	14	25	10	1	2	3	PAQR5, LOC145694, KIF23	115573, 501, 179	downstream, in gene, in gene	ActReg chr15 #5527	0	1	0
5528	15	69,744,648	69,745,725	1,077	3	10.485	14.939	11.97	19	28	29	1	1	2	KIF23, RPLP1	38498, 27	downstream, in gene	ActReg chr15 #5528	1	1	1
5529	15	70,006,443	70,007,115	672	1	11.238	10.286	2.714	20	14	5	0	0	0				ActReg chr15 #5529	1	0	0
5530	15	70,053,067	70,054,099	1,032	2	11.469	13.531	2.148	22	25	4	0	0	0				ActReg chr15 #5530	1	1	0
5531	15	70,264,757	70,266,189	1,432	2	15.867	21.156	3.644	45	66	8	0	0	0				ActReg chr15 #5531	1	1	0
5532	15	70,268,103	70,269,552	1,449	2	8.578	14	2.651	21	28	7	0	0	0				ActReg chr15 #5532	1	1	0
5533	15	70,389,605	70,390,197	592	1	8.056	11.611	4.333	12	17	7	1	1	1	TLE3	355	in gene	ActReg chr15 #5533	0	1	0
5534	15	70,488,437	70,489,049	612	1	6.421	5.263	11.79	9	10	19	0	0	0				ActReg chr15 #5534	0	0	1
5535	15	70,563,436	70,564,355	919	2	13.241	13.207	3.034	26	25	5	0	0	0				ActReg chr15 #5535	1	1	0
5536	15	70,667,337	70,667,865	528	1	13.562	11.812	5.688	20	17	10	0	0	0				ActReg chr15 #5536	1	0	0
5537	15	70,717,518	70,719,393	1,875	2	9.305	11.915	2.286	30	27	7	0	0	0				ActReg chr15 #5537	1	1	0
5538	15	70,766,630	70,768,620	1,990	2	9.435	12.403	5.081	17	23	12	0	0	0				ActReg chr15 #5538	1	1	0
5539	15	70,784,634	70,785,487	853	2	12.407	13.63	5.333	27	24	12	0	0	0				ActReg chr15 #5539	1	1	0
5540	15	70,786,118	70,786,598	480	1	7.4	8.2	13.333	10	10	21	0	0	0				ActReg chr15 #5540	0	0	1
5541	15	70,797,246	70,798,317	1,071	1	6.471	11.177	7.676	10	15	15	0	0	0				ActReg chr15 #5541	0	1	0
5542	15	71,151,773	71,152,461	688	1	2.526	5.5	11.727	4	10	19	0	1	1	LARP6	-5,619	upstream	ActReg chr15 #5542	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5543	15	71,184,701	71,185,449	748	1	10.75	10.542	5.292	16	20	12	1	2	2	THAP10, LRRC49	-322, 88	upstream, in gene	ActReg chr15 #5543	1	0	0
5544	15	71,587,241	71,588,222	981	1	6.1	12.067	2.913	12	21	5	0	0	1	THSD4	153,943	in gene	ActReg chr15 #5544	0	1	0
5545	15	72,522,464	72,524,247	1,783	3	10.214	11.518	8.982	17	17	24	1	1	2	PKM2, PARP6	329, 40273	in gene, downstream	ActReg chr15 #5545	1	1	1
5546	15	72,564,509	72,565,728	1,219	3	29.333	33.821	5.108	118	122	17	1	1	1	PARP6	-1,490	upstream	ActReg chr15 #5546	1	1	1
5547	15	72,611,645	72,613,075	1,430	3	10.489	13.622	6.273	26	27	12	1	1	1	BRUNOL6	165	in gene	ActReg chr15 #5547	1	1	0
5548	15	72,667,936	72,668,772	836	2	14.148	14.815	6.741	28	29	12	1	2	2	HEXA, C15orf34	166, -100	in gene, upstream	ActReg chr15 #5548	1	1	0
5549	15	72,766,179	72,767,000	821	1	9.76	14.08	8.458	14	20	14	1	1	1	ARIH1	-78	upstream	ActReg chr15 #5549	0	1	0
5550	15	72,767,205	72,767,917	712	1	7.682	15.682	6.909	10	26	16	1	1	1	ARIH1	894	in gene	ActReg chr15 #5550	0	1	0
5551	15	72,978,133	72,978,883	750	1	9.417	11.833	6.417	15	18	13	1	1	1	BBS4	-18	upstream	ActReg chr15 #5551	0	1	0
5552	15	73,075,577	73,076,686	1,109	2	10.143	16.4	8.229	25	31	14	1	1	1	ADPGK	-5	upstream	ActReg chr15 #5552	1	1	0
5553	15	73,344,006	73,344,594	588	1	4.25	10.389	5.071	6	19	9	1	1	1	NEO1	-525	upstream	ActReg chr15 #5553	0	1	0
5554	15	73,631,495	73,631,948	453	1	1.286	2.857	11.357	2	6	18	0	0	1	HCN4	29,884	in gene	ActReg chr15 #5554	0	0	1
5555	15	73,638,848	73,639,632	784	2	11.76	17.68	5.833	22	35	10	0	0	1	HCN4	22,365	in gene	ActReg chr15 #5555	1	1	0
5556	15	73,680,365	73,680,686	321	1	4.2	5.5	11.3	7	4	16	0	0	0				ActReg chr15 #5556	0	0	1
5557	15	73,924,972	73,925,408	436	1	4	10.357	6.143	7	18	11	1	1	1	NPTN	563	in gene	ActReg chr15 #5557	0	1	0
5558	15	74,115,142	74,115,922	780	2	14.417	17.5	2.773	36	43	6	0	0	0				ActReg chr15 #5558	1	1	0
5559	15	74,143,583	74,144,875	1,292	2	14.415	20.585	5.122	37	58	9	0	0	0				ActReg chr15 #5559	1	1	0
5560	15	74,189,983	74,190,696	713	1	8.696	13.261	4.478	16	21	9	0	0	1	TBC1D21	24,371	downstream	ActReg chr15 #5560	0	1	0
5561	15	74,284,313	74,285,408	1,095	2	31.486	30.971	4.086	108	111	7	1	2	2	STOML1, PML	-225, -2154	upstream, upstream	ActReg chr15 #5561	1	1	0
5562	15	74,324,724	74,325,274	550	1	6.471	3.471	11.941	12	7	16	0	0	1	PML	37,985	in gene	ActReg chr15 #5562	0	0	1
5563	15	74,336,911	74,337,424	513	1	3.75	5.812	11.688	7	9	14	0	0	1	PML	50,153	in gene	ActReg chr15 #5563	0	0	1
5564	15	74,420,413	74,420,874	461	1	6	4.8	11.733	8	8	17	1	2	2	LOC283731, ISLR2	976, -1072	in gene, upstream	ActReg chr15 #5564	0	0	1
5565	15	74,425,034	74,425,533	499	1	6.4	9.133	13.8	9	14	21	1	1	2	LOC283731, ISLR2	-3664, 3568	upstream, in gene	ActReg chr15 #5565	0	0	1
5566	15	74,425,889	74,426,227	338	1	3.5	6	13.1	5	9	15	1	1	2	LOC283731, ISLR2	-4439, 4343	upstream, in gene	ActReg chr15 #5566	0	0	1
5567	15	74,471,339	74,472,979	1,640	1	9.314	14.118	5.137	18	23	12	0	0	2	ISLR, STRA6	6072, 29212	downstream, in gene	ActReg chr15 #5567	0	1	0
5568	15	74,483,108	74,483,506	398	1	2.333	4.5	12.25	3	7	18	0	0	1	STRA6	18,064	in gene	ActReg chr15 #5568	0	0	1
5569	15	74,492,975	74,494,075	1,100	1	8.147	11.853	7.172	15	18	13	0	0	1	STRA6	7,846	in gene	ActReg chr15 #5569	0	1	0
5570	15	74,556,975	74,558,121	1,146	2	11.833	20.194	2.472	24	39	5	0	0	1	CCDC33	28,881	in gene	ActReg chr15 #5570	1	1	0
5571	15	74,583,375	74,584,733	1,358	2	15.452	19.357	6.143	37	36	16	0	0	1	CCDC33	55,387	in gene	ActReg chr15 #5571	1	1	0
5572	15	74,607,012	74,607,524	512	1	3.571	4.375	12.375	5	7	17	0	0	1	CCDC33	78,601	in gene	ActReg chr15 #5572	0	0	1
5573	15	74,631,705	74,632,166	461	1	5.133	3.8	10.467	8	6	15	0	0	2	CCDC33, CYP11A1	103268, 28146	downstream, in gene	ActReg chr15 #5573	0	0	1
5574	15	74,665,684	74,666,835	1,151	2	5.667	9.083	9.972	8	14	16	1	1	2	CYP11A1, LOC729739	-6178, 19462	upstream, downstream	ActReg chr15 #5574	0	1	1
5575	15	74,702,678	74,703,236	558	1	4.333	4	11.833	7	6	15	1	0	1	SEMA7A	23,342	in gene	ActReg chr15 #5575	0	0	1
5576	15	74,838,475	74,838,971	496	1	10.133	11	12.867	16	17	19	0	0	1	ARID3B	5,175	in gene	ActReg chr15 #5576	0	0	1
5577	15	74,892,096	74,892,566	470	1	5.733	6.077	11.867	11	9	19	0	0	2	ARID3B, CLK3	58783, -8382	downstream, upstream	ActReg chr15 #5577	0	0	1
5578	15	74,906,927	74,908,561	1,634	1	12.863	10.392	6.689	19	18	13	1	0	1	CLK3	7,031	in gene	ActReg chr15 #5578	1	0	0
5579	15	74,987,941	74,988,692	751	1	14.565	10.261	7.739	26	15	14	1	1	1	EDC3	70	in gene	ActReg chr15 #5579	1	0	0
5580	15	75,016,206	75,016,833	627	1	6.15	11.75	2.15	8	18	4	0	1	1	CYP1A1	1,358	in gene	ActReg chr15 #5580	0	1	0
5581	15	75,018,080	75,019,376	1,296	2	9.732	13.683	10.024	21	28	19	1	1	1	CYP1A1	-851	upstream	ActReg chr15 #5581	0	1	1
5582	15	75,131,629	75,132,202	573	1	2.941	3.167	11.5	7	5	16	0	0	3	CPLX3, ULK3, SCAMP2	12964, 3637, 33755	downstream, in gene, downstream	ActReg chr15 #5582	0	0	1
5583	15	75,135,550	75,136,079	529	1	8.765	7.412	13.235	14	14	23	1	1	2	ULK3, SCAMP2	-262, 29856	upstream, downstream	ActReg chr15 #5583	0	0	1
5584	15	75,182,011	75,183,223	1,212	2	10.79	9.184	6.632	22	16	21	1	1	2	MPI, C15orf17	207, 16845	in gene, downstream	ActReg chr15 #5584	1	0	1
5585	15	75,198,811	75,200,007	1,196	2	9.711	10.895	5.237	13	21	13	1	1	2	MPI, C15orf17	16999, 53	downstream, in gene	ActReg chr15 #5585	1	1	0
5586	15	75,229,783	75,230,874	1,091	2	13.177	11.323	7.9	20	19	14	1	1	1	COX5A	167	in gene	ActReg chr15 #5586	1	1	0
5587	15	75,248,159	75,250,077	1,918	3	10.467	10.85	7.517	22	19	21	1	1	1	RPP25	657	in gene	ActReg chr15 #5587	1	1	1
5588	15	75,251,244	75,251,777	533	1	2.059	2.353	10.118	3	4	16	1	1	1	RPP25	-1,735	upstream	ActReg chr15 #5588	0	0	1
5589	15	75,276,098	75,276,814	716	2	11.909	10	3.111	22	19	5	0	0	0				ActReg chr15 #5589	1	1	0
5590	15	75,287,338	75,287,890	552	2	13.118	12.412	5.938	20	22	8	1	1	1	SCAMP5	-262	upstream	ActReg chr15 #5590	1	1	0
5591	15	75,289,935	75,290,240	305	1	4.3	5.6	11.4	5	8	17	0	1	1	SCAMP5	2,211	in gene	ActReg chr15 #5591	0	0	1
5592	15	75,315,664	75,316,308	644	2	8.35	11.35	9.737	13	20	19	1	1	2	SCAMP5, PPCDC	28110, 59	downstream, in gene	ActReg chr15 #5592	0	1	1
5593	15	75,335,582	75,336,466	884	1	9.286	11.929	4.792	17	20	7	0	0	1	PPCDC	20,097	in gene	ActReg chr15 #5593	0	1	0
5594	15	75,470,910	75,471,434	524	1	2.692	3.059	10.588	6	5	19	1	0	0				ActReg chr15 #5594	0	0	1
5595	15	75,474,630	75,475,630	1,000	2	6.968	14.71	10.95	14	22	17	0	0	0				ActReg chr15 #5595	0	1	1
5596	15	75,494,221	75,495,093	872	1	9.259	12.037	5.769	13	19	11	1	1	1	C15orf39	436	in gene	ActReg chr15 #5596	0	1	0
5597	15	75,628,315	75,628,868	553	1	6.111	8.778	11.333	10	15	16	1	1	1	COMMD4	217	in gene	ActReg chr15 #5597	0	0	1
5598	15	75,640,759	75,641,299	540	1	5	10.059	13.177	7	14	18	1	1	4	COMMD4, NEIL1, MIR631, MAN2C1	12655, 1698, 4997, 19912	downstream, in gene, downstream, downstream	ActReg chr15 #5598	0	0	1
5599	15	75,660,001	75,661,152	1,151	2	10.528	12.583	11.694	20	22	26	1	1	2	MAN2C1, SIN3A	365, 87548	in gene, downstream	ActReg chr15 #5599	0	1	1
5600	15	75,747,625	75,748,181	556	1	4.471	5.471	15.941	7	7	24	1	1	1	SIN3A	221	in gene	ActReg chr15 #5600	0	0	1
5601	15	75,917,610	75,918,616	1,006	2	7.774	13.484	11.032	11	25	16	1	1	1	SNUPN	606	in gene	ActReg chr15 #5601	0	1	1
5602	15	75,931,868	75,933,167	1,299	2	11.732	11.1	9.561	18	19	14	1	1	2	IMP3, SNX33	147, -8831	in gene, upstream	ActReg chr15 #5602	1	0	1
5603	15	75,974,162	75,975,136	974	1	1.789	3.107	12	3	6	17	1	0	1	CSPG4	30,540	in gene	ActReg chr15 #5603	0	0	1
5604	15	75,987,457	75,988,297	840	1	10.308	10.692	5.308	14	14	9	0	0	1	CSPG4	17,312	in gene	ActReg chr15 #5604	0	1	0
5605	15	75,988,420	75,989,731	1,311	2	8.756	10.293	5.902	20	19	10	0	0	1	CSPG4	16,114	in gene	ActReg chr15 #5605	1	1	0
5606	15	76,001,681	76,002,111	430	1	5.538	9.231	10.846	7	14	18	0	0	1	CSPG4	3,293	in gene	ActReg chr15 #5606	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5607	15	76,005,386	76,006,388	1,002	2	11	14.161	4.355	18	24	9	0	1	2	CSPG4, ODF3L1	-698, -10432	upstream, upstream	ActReg chr15 #5607	1	1	0
5608	15	76,031,219	76,031,647	428	1	3.231	7	12.923	5	11	19	1	0	0				ActReg chr15 #5608	0	0	1
5609	15	76,184,117	76,184,644	527	1	9.176	7.647	1	15	12	1	0	0	1	UBE2Q2	48,758	in gene	ActReg chr15 #5609	1	0	0
5610	15	76,195,815	76,196,653	838	2	10.231	12.5	13.5	18	18	20	1	1	2	UBE2Q2, FBXO22	60612, 34	downstream, in gene	ActReg chr15 #5610	0	1	1
5611	15	76,269,299	76,269,655	356	1	2.545	3.364	10.727	4	5	14	0	0	1	NRG4	55,308	in gene	ActReg chr15 #5611	0	0	1
5612	15	76,603,304	76,603,977	673	3	11.333	10	14.191	16	19	22	1	1	1	ETFA	170	in gene	ActReg chr15 #5612	1	1	1
5613	15	76,631,835	76,632,418	583	1	2.412	5.895	10.579	4	12	20	1	0	2	ISL2, SCAPER	2979, 544091	in gene, downstream	ActReg chr15 #5613	0	0	1
5614	15	77,247,053	77,247,570	517	2	8.5	9.812	2	17	14	3	0	1	2	RCN2, LOC100506704	23349, 512	downstream, in gene	ActReg chr15 #5614	1	1	0
5615	15	77,271,399	77,272,385	986	1	4.839	5.161	11.323	8	10	15	0	0	0				ActReg chr15 #5615	0	0	1
5616	15	77,327,712	77,328,184	472	1	4.4	6.2	11.8	6	14	16	0	0	2	PSTPIP1, TSPAN3	40483, 35622	in gene, downstream	ActReg chr15 #5616	0	0	1
5617	15	77,363,164	77,363,887	723	2	12.696	10.739	1.429	25	19	2	1	1	1	TSPAN3	45	in gene	ActReg chr15 #5617	1	1	0
5618	15	77,712,152	77,712,548	396	1	2.385	10.077	2.625	4	17	3	1	1	1	HMG20A	-893	upstream	ActReg chr15 #5618	0	1	0
5619	15	77,835,446	77,836,243	797	2	10.12	13.24	9.36	19	21	17	0	0	0				ActReg chr15 #5619	1	1	0
5620	15	77,841,367	77,842,083	716	1	4.478	4.13	11	8	7	15	0	0	0				ActReg chr15 #5620	0	0	1
5621	15	77,906,504	77,907,331	827	1	5.4	6.846	11.462	10	11	16	1	0	1	LINGO1	17,792	in gene	ActReg chr15 #5621	0	0	1
5622	15	77,907,954	77,908,655	701	1	3.682	2.409	11.227	5	5	15	1	0	1	LINGO1	16,405	in gene	ActReg chr15 #5622	0	0	1
5623	15	77,994,503	77,995,471	968	2	13.833	13.667	3.833	22	27	7	0	0	0				ActReg chr15 #5623	1	1	0
5624	15	78,179,392	78,179,939	547	1	3.75	4.353	10.167	7	7	15	0	0	0				ActReg chr15 #5624	0	0	1
5625	15	78,267,967	78,268,408	441	1	5	4.833	14.071	9	8	21	0	0	0				ActReg chr15 #5625	0	0	1
5626	15	78,280,664	78,280,967	303	1	4.2	7.5	12	5	10	17	0	0	2	LOC91450, TBC1D2B	5752, 89179	downstream, downstream	ActReg chr15 #5626	0	0	1
5627	15	78,441,476	78,442,163	687	1	9.667	12.952	3.9	16	26	13	1	1	1	IDH3A	100	in gene	ActReg chr15 #5627	0	1	0
5628	15	78,591,673	78,592,222	549	1	11.118	10.941	6	15	14	9	0	1	1	WDR61	-7	upstream	ActReg chr15 #5628	1	0	0
5629	15	78,729,852	78,730,644	792	3	10.92	10.92	12.6	17	19	28	1	1	1	IREB2	-270	upstream	ActReg chr15 #5629	1	1	1
5630	15	78,799,931	78,800,570	639	1	5.35	7.85	13.2	10	11	19	1	1	2	IREB2, AGPHD1	69732, 344	downstream, in gene	ActReg chr15 #5630	0	0	1
5631	15	78,912,429	78,912,919	490	1	2.533	2.077	12.4	4	3	17	1	1	2	CHRNA3, CHRNB4	963, 20913	in gene, downstream	ActReg chr15 #5631	0	0	1
5632	15	78,932,851	78,933,521	670	1	2.944	4.308	12.857	6	7	20	1	1	1	CHRNB4	401	in gene	ActReg chr15 #5632	0	0	1
5633	15	79,063,626	79,063,952	326	1	1.1	5.4	10.8	2	8	14	0	0	1	ADAMTS7	39,984	in gene	ActReg chr15 #5633	0	0	1
5634	15	79,070,481	79,070,797	316	1	5.5	3.7	9.3	8	5	11	0	0	1	ADAMTS7	33,134	in gene	ActReg chr15 #5634	0	0	1
5635	15	79,290,291	79,290,631	340	1	4.091	4	11.454	7	5	17	0	0	1	RASGRF1	92,754	in gene	ActReg chr15 #5635	0	0	1
5636	15	79,575,835	79,576,515	680	1	10.727	13.727	4.1	21	25	7	1	2	3	LOC729911, LOC100506846, ANKRD34C	3187, -19, 1029	in gene, upstream, in gene	ActReg chr15 #5636	0	1	0
5637	15	79,603,391	79,604,172	781	2	7.75	10.88	8.958	16	17	13	1	1	1	TMED3	290	in gene	ActReg chr15 #5637	0	1	1
5638	15	80,188,788	80,189,948	1,160	3	8.75	12	10.562	18	21	24	1	1	2	MTHFS, ST20	2, 26709	in gene, downstream	ActReg chr15 #5638	1	1	1
5639	15	80,215,386	80,216,301	915	2	11	11.207	10.034	21	16	18	1	2	2	ST20, C15orf37	234, 730	in gene, in gene	ActReg chr15 #5639	0	1	1
5640	15	80,303,410	80,304,028	618	1	6.842	10.895	3.474	10	17	7	0	0	0				ActReg chr15 #5640	0	1	0
5641	15	80,364,553	80,365,141	588	1	9.444	6.333	1.714	16	12	3	0	0	1	ZFAND6	12,826	in gene	ActReg chr15 #5641	1	0	0
5642	15	80,557,206	80,557,937	731	2	11.391	13.522	3.278	19	26	6	0	0	1	LOC283688	76,576	in gene	ActReg chr15 #5642	1	1	0
5643	15	80,609,620	80,610,474	854	1	10.111	12.667	5.217	17	20	10	0	0	1	LOC283688	24,100	in gene	ActReg chr15 #5643	0	1	0
5644	15	80,707,108	80,707,560	452	1	9.143	11.929	2.1	11	20	3	0	0	1	ARNT2	10,642	in gene	ActReg chr15 #5644	0	1	0
5645	15	80,728,721	80,729,481	760	1	8.833	12	4.125	13	17	5	0	0	2	ARNT2, LOC100133746	32409, 8127	in gene, in gene	ActReg chr15 #5645	0	1	0
5646	15	80,872,069	80,872,937	868	1	12.704	9.852	3.741	24	21	9	0	0	1	ARNT2	175,811	in gene	ActReg chr15 #5646	1	0	0
5647	15	81,071,618	81,073,471	1,853	3	11.597	13.035	9.684	28	20	18	1	1	1	KIAA1199	832	in gene	ActReg chr15 #5647	1	1	1
5648	15	81,247,942	81,248,619	677	1	6.714	12.191	3.714	10	21	6	0	0	1	KIAA1199	176,568	downstream	ActReg chr15 #5648	0	1	0
5649	15	81,281,506	81,282,283	777	1	7.083	12.083	9.583	13	17	15	1	1	1	MESDC2	311	in gene	ActReg chr15 #5649	0	1	0
5650	15	81,293,231	81,293,643	412	1	9.308	5.538	9.615	12	8	15	1	1	1	MESDC1	142	in gene	ActReg chr15 #5650	0	0	1
5651	15	81,295,371	81,295,786	415	1	4.154	5.385	9.846	6	9	16	1	1	1	MESDC1	2,283	in gene	ActReg chr15 #5651	0	0	1
5652	15	81,384,388	81,385,183	795	1	7.042	11.333	2.417	12	18	4	0	0	1	LOC647020	25,707	in gene	ActReg chr15 #5652	0	1	0
5653	15	81,473,539	81,474,842	1,303	1	8.605	11.85	2.708	17	22	7	0	0	0				ActReg chr15 #5653	0	1	0
5654	15	81,528,222	81,528,902	680	1	9.636	13.273	2.476	13	20	5	0	0	1	IL16	39,343	in gene	ActReg chr15 #5654	0	1	0
5655	15	82,180,203	82,180,653	450	1	10.643	6.286	2.7	13	9	5	0	0	0				ActReg chr15 #5655	1	0	0
5656	15	82,337,414	82,338,203	789	1	6.833	11.792	5.75	10	18	12	1	1	1	MEX3B	553	in gene	ActReg chr15 #5656	0	1	0
5657	15	82,554,777	82,555,347	570	1	8.667	9.722	14.167	12	15	21	1	2	2	EFTUD1, FAM154B	42, -90	in gene, upstream	ActReg chr15 #5657	0	0	1
5658	15	82,824,960	82,825,126	266	2	18.444	24.444	3.444	27	37	5	1	1	1	RPS17	-128	upstream	ActReg chr15 #5658	1	1	0
5659	15	83,315,727	83,316,719	992	2	11.387	8.226	7.71	20	15	13	1	1	1	CPEB1	505	in gene	ActReg chr15 #5659	1	0	1
5660	15	83,331,456	83,332,895	1,439	2	12.444	17.4	6.209	30	36	15	0	0	1	AP3B2	46,460	in gene	ActReg chr15 #5660	1	1	0
5661	15	83,378,229	83,379,073	844	2	10.741	13.63	4.88	17	26	7	1	1	2	AP3B2, LOC338963	-16, 4094	upstream, downstream	ActReg chr15 #5661	1	1	0
5662	15	83,501,775	83,502,554	779	1	10.833	6.667	4	16	11	8	0	0	2	WHAMM, LOC100505647	24191, 10032	in gene, downstream	ActReg chr15 #5662	1	0	0
5663	15	83,679,561	83,680,991	1,430	3	31.136	32.886	10.209	99	102	22	1	1	2	C15orf40, BTBD1	117, 55830	in gene, downstream	ActReg chr15 #5663	1	1	1
5664	15	83,735,396	83,736,282	886	2	9.815	12.704	3.737	14	20	9	1	1	1	BTBD1	267	in gene	ActReg chr15 #5664	1	1	0
5665	15	83,952,182	83,952,598	416	1	4.231	6.538	10.231	6	10	15	1	1	1	BNC1	1,078	in gene	ActReg chr15 #5665	0	0	1
5666	15	84,828,175	84,828,445	270	1	1.625	1.25	11.5	2	2	16	0	0	0				ActReg chr15 #5666	0	0	1
5667	15	85,043,498	85,043,691	193	1	1.667	1	10.333	2	1	14	1	0	0				ActReg chr15 #5667	0	0	1
5668	15	85,113,451	85,114,518	1,067	2	7.273	10.485	7.645	12	22	14	1	1	1	LOC100506874	-1,439	upstream	ActReg chr15 #5668	0	1	1
5669	15	85,143,622	85,144,931	1,309	1	6.073	11.049	8.432	11	16	12	1	1	1	ZSCAN2	27	in gene	ActReg chr15 #5669	0	1	0
5670	15	85,259,027	85,259,690	663	3	12.191	11.381	11.762	24	15	20	1	1	1	SEC11A	316	in gene	ActReg chr15 #5670	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5671	15	85,290,674	85,291,394	720	1	7.348	10.696	8.435	10	14	13	1	1	1	ZNF592	-784	upstream	ActReg chr15 #5671	0	1	0
5672	15	85,523,353	85,524,999	1,646	3	15.423	18.75	7.84	31	41	18	1	1	1	PDE8A	-1,029	upstream	ActReg chr15 #5672	1	1	1
5673	15	85,667,136	85,667,785	649	1	3.833	10.191	2.25	7	16	8	0	0	1	PDE8A	142,255	in gene	ActReg chr15 #5673	0	1	0
5674	15	85,873,192	85,873,742	550	1	5.235	10.235	1.25	10	14	2	0	0	0				ActReg chr15 #5674	0	1	0
5675	15	87,891,816	87,892,297	481	1	9.733	6.533	1.867	20	11	3	0	0	0				ActReg chr15 #5675	1	0	0
5676	15	88,709,418	88,710,009	591	1	8.722	12.167	3.647	18	20	6	0	0	1	NTRK3	89,948	in gene	ActReg chr15 #5676	0	1	0
5677	15	88,766,220	88,766,664	444	1	2.071	3.429	11.643	4	5	17	0	0	1	NTRK3	33,219	in gene	ActReg chr15 #5677	0	0	1
5678	15	88,820,137	88,820,627	490	1	1.933	4.8	11.133	3	7	17	0	0	1	LOC283738	24,436	downstream	ActReg chr15 #5678	0	0	1
5679	15	89,010,217	89,011,343	1,126	1	9.4	13.886	7.571	17	22	13	1	2	2	MRPL46, MRPS11	-147, 96	upstream, in gene	ActReg chr15 #5679	0	1	0
5680	15	89,067,394	89,067,691	297	1	3.444	5.333	9.111	5	7	12	0	0	1	DET1	22,370	in gene	ActReg chr15 #5680	0	0	1
5681	15	89,089,603	89,090,341	738	2	18.565	15.87	4.043	42	39	8	0	1	1	DET1	-60	upstream	ActReg chr15 #5681	1	1	0
5682	15	89,129,723	89,130,412	689	1	12.182	9.182	1.333	24	16	2	0	0	0				ActReg chr15 #5682	1	0	0
5683	15	89,148,247	89,149,586	1,339	3	14.667	14.452	10.5	33	39	15	1	2	2	MIR1179, MIR7-2	-2422, -6140	upstream, upstream	ActReg chr15 #5683	1	1	1
5684	15	89,164,151	89,165,146	995	2	7.548	9.613	10.032	14	17	19	1	1	2	MIR7-2, AEN	9592, 121	downstream, in gene	ActReg chr15 #5684	0	1	1
5685	15	89,181,705	89,182,613	908	3	14.393	14.393	8.429	24	29	18	0	1	2	AEN, ISG20	17632, 120	downstream, in gene	ActReg chr15 #5685	1	1	1
5686	15	89,192,465	89,193,237	772	1	8.875	13.542	6.792	14	20	11	0	0	1	ISG20	10,812	in gene	ActReg chr15 #5686	0	1	0
5687	15	89,333,754	89,334,602	848	1	10.963	7.111	2.55	19	12	5	0	0	0				ActReg chr15 #5687	1	0	0
5688	15	89,456,320	89,456,836	516	1	10.588	7.824	5.235	16	10	10	1	1	1	MFGE8	85	in gene	ActReg chr15 #5688	1	0	0
5689	15	89,630,719	89,631,907	1,188	2	10.184	10.947	6.447	16	16	15	1	1	1	ABHD2	-68	upstream	ActReg chr15 #5689	1	1	0
5690	15	89,647,463	89,647,944	481	1	2.867	4.733	11.2	3	7	21	0	0	1	ABHD2	16,322	in gene	ActReg chr15 #5690	0	0	1
5691	15	89,710,454	89,711,608	1,124	2	11.657	9.314	2.886	20	15	6	0	0	1	ABHD2	79,665	in gene	ActReg chr15 #5691	1	1	0
5692	15	89,769,875	89,770,421	546	1	7.941	10.706	4.412	12	17	10	0	1	1	RLBP1	-5,226	upstream	ActReg chr15 #5692	0	1	0
5693	15	89,864,024	89,864,479	455	1	3.643	3.857	10.286	5	6	14	0	0	2	FANCI, POLG	77057, 13775	downstream, in gene	ActReg chr15 #5693	0	0	1
5694	15	89,877,595	89,878,906	1,311	3	15.293	17.488	12.488	35	38	25	1	2	2	POLG, LOC100506983	-224, -252	upstream, upstream	ActReg chr15 #5694	1	1	1
5695	15	89,903,350	89,903,897	547	1	3.357	5.765	11.471	6	10	20	1	1	1	MIR9-3	-7,625	upstream	ActReg chr15 #5695	0	0	1
5696	15	89,904,535	89,905,759	1,224	2	11.684	15.605	6.417	26	29	14	1	1	1	MIR9-3	-6,101	upstream	ActReg chr15 #5696	1	1	0
5697	15	89,907,522	89,908,592	1,070	2	11.909	10.212	6.545	19	17	11	0	1	1	MIR9-3	-3,191	upstream	ActReg chr15 #5697	1	1	0
5698	15	89,910,190	89,910,822	632	1	4.05	2.526	13.9	8	5	19	1	1	1	MIR9-3	-742	upstream	ActReg chr15 #5698	0	0	1
5699	15	89,962,407	89,963,268	861	1	8.963	13.037	3.346	19	25	8	0	0	0				ActReg chr15 #5699	0	1	0
5700	15	89,973,669	89,974,423	754	1	9.174	11.652	4.565	13	19	8	1	0	0				ActReg chr15 #5700	0	1	0
5701	15	90,118,263	90,119,636	1,373	3	10.767	11.233	8.047	23	16	23	1	1	1	C15orf42	131	in gene	ActReg chr15 #5701	1	1	1
5702	15	90,327,635	90,328,180	545	1	4.176	4.588	11.882	7	11	18	0	0	2	MESP2, ANPEP	8318, 30165	downstream, downstream	ActReg chr15 #5702	0	0	1
5703	15	90,347,113	90,347,896	783	1	5.417	5.083	11.542	8	8	15	0	0	1	ANPEP	10,568	in gene	ActReg chr15 #5703	0	0	1
5704	15	90,357,390	90,357,856	466	1	5.429	7	9.467	8	9	14	1	1	1	ANPEP	449	in gene	ActReg chr15 #5704	0	0	1
5705	15	90,365,518	90,365,934	416	1	9.077	9.231	12	15	13	17	0	1	2	ANPEP, AP3S2	-7654, 71891	upstream, downstream	ActReg chr15 #5705	0	0	1
5706	15	90,436,787	90,437,763	976	2	13.839	15.581	9.387	34	30	17	1	1	3	AP3S2, LOC100507010, C15orf38	342, 5480, 18947	in gene, downstream, downstream	ActReg chr15 #5706	1	1	0
5707	15	90,567,166	90,567,483	317	1	1.667	3.8	12.4	2	5	16	0	0	0				ActReg chr15 #5707	0	0	1
5708	15	90,586,299	90,586,810	511	1	3.625	2.312	11.625	5	4	15	0	0	0				ActReg chr15 #5708	0	0	1
5709	15	90,588,489	90,589,087	598	1	4.353	2.056	13.167	8	3	18	0	0	0				ActReg chr15 #5709	0	0	1
5710	15	90,686,628	90,686,944	316	1	6.7	6.2	10.9	10	9	16	0	0	0				ActReg chr15 #5710	0	0	1
5711	15	90,698,773	90,699,176	403	1	1.667	2.692	11.462	2	5	17	0	0	0				ActReg chr15 #5711	0	0	1
5712	15	90,762,820	90,763,608	788	1	2.652	2.958	11.042	5	7	17	0	0	2	SEMA4B, CIB1	35062, 14065	in gene, downstream	ActReg chr15 #5712	0	0	1
5713	15	90,771,681	90,772,089	408	1	4.333	2.25	12.167	6	4	18	0	1	3	SEMA4B, CIB1, C15orf58	43733, 5394, -5602	in gene, downstream, upstream	ActReg chr15 #5713	0	0	1
5714	15	90,776,604	90,777,349	745	1	6.208	11	5.125	11	16	9	1	2	3	SEMA4B, CIB1, C15orf58	48824, 303, -511	downstream, in gene, upstream	ActReg chr15 #5714	0	1	0
5715	15	90,808,375	90,809,204	829	1	10.385	12.654	8	17	25	12	1	2	3	TTLL13, NGRN, LOC100507029	16025, -106, -7397	downstream, upstream, upstream	ActReg chr15 #5715	0	1	0
5716	15	90,895,402	90,895,852	450	1	9.286	10.857	10.357	15	16	18	1	1	1	ZNF774	150	in gene	ActReg chr15 #5716	0	0	1
5717	15	91,445,400	91,445,965	565	1	11	5.625	5	22	10	9	1	1	2	FES, MAN2A2	18017, -1738	downstream, upstream	ActReg chr15 #5717	1	0	0
5718	15	91,446,237	91,446,772	535	1	6.353	6.353	14.118	9	10	21	1	1	2	FES, MAN2A2	18839, -916	downstream, upstream	ActReg chr15 #5718	0	0	1
5719	15	91,474,832	91,476,252	1,420	2	21.523	26.5	7.068	61	76	17	1	2	3	MAN2A2, UNC45A, HDDC3	28122, 2132, 232	downstream, in gene, in gene	ActReg chr15 #5719	1	1	0
5720	15	91,493,260	91,494,041	781	1	3.8	7.417	11.625	9	10	13	0	1	3	UNC45A, LOC100288997, RCCD1	20240, 4823, -4456	in gene, downstream, upstream	ActReg chr15 #5720	0	0	1
5721	15	91,537,287	91,538,377	1,090	2	9.235	11.152	6.562	18	20	13	1	1	3	PRC1, LOC100507118, VPS33B	-28, 28229, 28001	upstream, downstream, downstream	ActReg chr15 #5721	1	1	0
5722	15	91,881,892	91,882,559	667	1	7.9	12.8	2.1	16	23	3	0	0	0				ActReg chr15 #5722	0	1	0
5723	15	92,058,477	92,059,118	641	2	11.05	11.2	4.8	20	17	9	0	0	0				ActReg chr15 #5723	1	1	0
5724	15	92,380,198	92,380,521	323	1	2.333	1.667	9.2	3	3	14	0	0	0				ActReg chr15 #5724	0	0	1
5725	15	92,395,777	92,396,288	511	1	7.062	11.062	5.188	12	14	9	1	1	1	SLCO3A1	-906	upstream	ActReg chr15 #5725	0	1	0
5726	15	92,555,047	92,555,665	618	1	8.211	10.632	3.947	12	14	7	0	0	1	SLCO3A1	158,418	in gene	ActReg chr15 #5726	0	1	0
5727	15	92,937,311	92,937,626	315	1	2.1	1.889	10.2	3	3	14	1	1	1	ST8SIA2	328	in gene	ActReg chr15 #5727	0	0	1
5728	15	93,254,596	93,255,002	406	1	1	1.571	12.833	1	3	22	0	1	1	UNQ6190	-2,625	upstream	ActReg chr15 #5728	0	0	1
5729	15	93,352,100	93,353,067	967	2	11.567	12.767	6.3	22	22	15	1	0	0				ActReg chr15 #5729	1	1	0
5730	15	93,524,495	93,525,024	529	1	11.588	8.882	1	16	11	1	0	0	1	CHD2	81,208	in gene	ActReg chr15 #5730	1	0	0
5731	15	93,587,934	93,588,437	503	1	2.5	2.812	13.062	4	5	19	1	0	1	RGMA	44,258	in gene	ActReg chr15 #5731	0	0	1
5732	15	93,590,831	93,591,325	494	1	4	3.533	11.8	6	6	18	0	0	1	RGMA	41,365	in gene	ActReg chr15 #5732	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5733	15	93,615,791	93,616,195	404	1	5.154	4.615	11.231	6	7	18	1	0	1	RGMA	16,450	in gene	ActReg chr15 #5733	0	0	1
5734	15	93,616,512	93,616,994	482	1	4.562	4.938	12.188	8	6	19	1	0	1	RGMA	15,690	in gene	ActReg chr15 #5734	0	0	1
5735	15	93,997,994	93,998,311	317	1	1.75	3.7	10.4	2	5	15	0	0	0				ActReg chr15 #5735	0	0	1
5736	15	94,372,512	94,373,358	846	1	11.963	12.259	2.176	25	21	4	0	0	0				ActReg chr15 #5736	1	0	0
5737	15	94,443,416	94,444,599	1,183	1	7.351	12.135	5.892	12	16	10	0	0	0				ActReg chr15 #5737	0	1	0
5738	15	94,569,538	94,570,165	627	1	10.947	8.895	3.316	19	14	5	0	0	0				ActReg chr15 #5738	1	0	0
5739	15	95,753,497	95,754,242	745	1	8.417	11	1.667	14	24	3	0	0	0				ActReg chr15 #5739	0	1	0
5740	15	95,790,154	95,790,976	822	2	10.115	13.731	1.842	18	24	5	0	0	0				ActReg chr15 #5740	1	1	0
5741	15	96,816,666	96,817,451	785	1	10.04	14.8	4.273	19	24	10	0	0	2	LOC644192, LOC100506754	53532, 53351	in gene, downstream	ActReg chr15 #5741	0	1	0
5742	15	96,899,998	96,900,701	703	3	9.955	10.864	7.318	18	18	18	1	1	1	LOC728800	-2,544	upstream	ActReg chr15 #5742	1	1	1
5743	15	96,903,004	96,903,434	430	1	2.929	6.167	11.357	5	9	14	1	1	1	LOC728800	326	in gene	ActReg chr15 #5743	0	0	1
5744	15	98,418,466	98,419,308	842	2	15.692	14.5	3.615	30	29	9	0	1	1	LOC91948	-1,228	upstream	ActReg chr15 #5744	1	1	0
5745	15	98,503,267	98,504,273	1,006	2	11.968	16.806	3.774	25	30	8	1	1	1	ARRDC4	-163	upstream	ActReg chr15 #5745	1	1	0
5746	15	98,706,435	98,706,785	350	1	2.875	3.364	11.091	6	5	15	0	0	0				ActReg chr15 #5746	0	0	1
5747	15	98,964,479	98,964,909	430	1	4.143	8	12.429	7	11	17	1	0	0				ActReg chr15 #5747	0	0	1
5748	15	99,091,303	99,091,845	542	1	10.529	10.412	5.588	13	15	9	1	0	0				ActReg chr15 #5748	0	1	0
5749	15	99,396,299	99,396,833	534	1	8.824	10.941	1.909	15	19	3	0	0	1	IGF1R	203,805	in gene	ActReg chr15 #5749	0	1	0
5750	15	99,439,393	99,440,442	1,049	1	11.438	6.969	4.516	18	12	11	0	0	1	IGF1R	247,156	in gene	ActReg chr15 #5750	1	0	0
5751	15	99,531,335	99,531,749	414	1	2.692	1.846	11	4	2	16	0	0	1	LOC145814	19,482	in gene	ActReg chr15 #5751	0	0	1
5752	15	99,645,793	99,646,370	577	1	10.556	14.333	2	15	21	5	1	1	1	SYNM	795	in gene	ActReg chr15 #5752	0	1	0
5753	15	99,663,785	99,664,367	584	1	12.389	10.889	6.5	19	15	10	0	0	1	SYNM	18,789	in gene	ActReg chr15 #5753	1	0	0
5754	15	99,730,201	99,730,519	318	1	2.25	2	9.5	3	4	13	0	0	1	TTC23	59,455	in gene	ActReg chr15 #5754	0	0	1
5755	15	99,789,543	99,790,107	564	1	10.353	13.235	4.353	17	23	9	0	2	2	TTC23, LRRC28	-10, -1827	upstream, upstream	ActReg chr15 #5755	0	1	0
5756	15	100,468,645	100,469,165	520	1	12.438	9.75	5.938	20	15	10	0	0	0				ActReg chr15 #5756	1	0	0
5757	15	100,889,806	100,890,717	911	1	10.107	12.036	7.821	18	18	11	1	1	2	ADAMTS17, FLJ42289	-8078, 662	upstream, in gene	ActReg chr15 #5757	0	1	0
5758	15	101,226,179	101,227,205	1,026	1	7.219	12.062	6.031	16	18	9	0	0	0				ActReg chr15 #5758	0	1	0
5759	15	101,261,849	101,262,594	745	1	10.417	11.917	3.727	23	20	7	0	0	0				ActReg chr15 #5759	0	1	0
5760	15	101,304,214	101,304,815	601	1	5.684	5.421	10.79	8	9	16	0	0	0				ActReg chr15 #5760	0	0	1
5761	15	101,420,697	101,421,227	530	1	5.471	8.353	12.765	9	15	17	1	1	2	LOC145757, ALDH1A3	18914, 953	downstream, in gene	ActReg chr15 #5761	0	0	1
5762	15	101,431,083	101,432,386	1,303	1	10.317	14.098	6.35	16	21	16	0	0	2	ALDH1A3, LOC100507452	11725, 27754	in gene, downstream	ActReg chr15 #5762	0	1	0
5763	15	101,458,101	101,459,481	1,380	2	8.326	11.558	6.14	14	19	16	1	2	3	ALDH1A3, LOC100507452, LRRK1	38782, 697, -669	downstream, in gene, upstream	ActReg chr15 #5763	0	1	1
5764	15	101,605,385	101,605,842	457	1	6.5	6	10.286	12	8	13	0	0	1	LRRK1	146,153	in gene	ActReg chr15 #5764	0	0	1
5765	15	101,791,943	101,792,918	975	2	11.4	11.667	3.357	20	19	7	1	1	1	CHSY1	-293	upstream	ActReg chr15 #5765	1	1	0
5766	15	101,834,799	101,836,242	1,443	2	17.267	18.933	5.465	42	43	12	1	1	2	SNRPA1, PCSK6	-60, 194667	upstream, downstream	ActReg chr15 #5766	1	1	0
5767	15	102,075,391	102,076,097	706	1	3.45	5.043	10.087	7	9	14	0	0	0				ActReg chr15 #5767	0	0	1
5768	15	102,152,910	102,153,332	422	1	4.909	3.462	12.923	8	6	17	0	0	0				ActReg chr15 #5768	0	0	1
5769	15	102,191,885	102,193,091	1,206	1	7.605	11.579	6.974	15	17	17	1	1	2	TM2D3, TARSL2	106, 72157	in gene, downstream	ActReg chr15 #5769	0	1	0
5770	15	102,317,347	102,317,772	425	1	3.077	1.167	11.077	5	2	17	0	0	1	LOC100507518	4,525	downstream	ActReg chr15 #5770	0	0	1
5771	15	102,351,091	102,351,637	546	1	6.529	9.765	1	10	17	1	0	1	2	OR4F6, OR4F15	5441, -7026	downstream, upstream	ActReg chr15 #5771	0	1	0
5772	16	103,179	103,836	657	1	11.45	11.2	6.632	16	19	9	1	2	3	POLR3K, SNRNP25, RHBDF1	125, -322, 19122	in gene, upstream, downstream	ActReg chr16 #5772	0	1	0
5773	16	111,781	112,336	555	1	3.529	5.882	11.588	7	9	17	1	0	3	POLR3K, SNRNP25, RHBDF1	-8426, 8229, 10571	upstream, downstream, in gene	ActReg chr16 #5773	0	0	1
5774	16	114,527	115,218	691	1	4.545	5.864	12.682	7	11	17	0	0	2	SNRNP25, RHBDF1	11043, 7757	downstream, in gene	ActReg chr16 #5774	0	0	1
5775	16	118,151	118,843	692	1	12.619	11.524	7.429	18	22	13	0	0	2	RHBDF1, MPG	4132, -8521	in gene, upstream	ActReg chr16 #5775	1	0	0
5776	16	122,632	123,394	762	1	7.125	11.417	3.826	12	19	8	1	2	2	RHBDF1, MPG	-384, -4005	upstream, upstream	ActReg chr16 #5776	0	1	0
5777	16	127,229	128,235	1,006	1	8.219	9.375	12.25	14	16	16	1	2	3	RHBDF1, MPG, C16orf35	-5103, 714, 60840	upstream, in gene, downstream	ActReg chr16 #5777	0	0	1
5778	16	129,876	130,325	449	1	2.357	3.769	11.857	8	5	18	0	1	3	RHBDF1, MPG, C16orf35	-7471, 3082, 58572	upstream, in gene, downstream	ActReg chr16 #5778	0	0	1
5779	16	278,990	279,832	842	2	12.154	13.115	8.24	19	24	15	1	3	3	LUC7L, LOC100129478, ITFG3	38, -1118, -5390	in gene, upstream, upstream	ActReg chr16 #5779	1	1	0
5780	16	319,106	319,655	549	1	5.294	4.706	13.353	8	7	19	0	0	2	ITFG3, RGS11	34579, 6534	downstream, in gene	ActReg chr16 #5780	0	0	1
5781	16	323,345	323,902	557	1	3	2.529	11.941	4	4	18	0	2	4	ITFG3, RGS11, ARHGDIG, PDIA2	38822, 2291, -6983, -9495	downstream, in gene, upstream, upstream	ActReg chr16 #5781	0	0	1
5782	16	324,347	324,902	555	1	3.944	3.167	9.667	7	5	14	1	2	4	ITFG3, RGS11, ARHGDIG, PDIA2	39823, 1290, -5982, -8494	downstream, in gene, upstream, upstream	ActReg chr16 #5782	0	0	1
5783	16	330,965	331,542	577	1	4.556	3.375	13.5	9	6	22	1	3	4	RGS11, ARHGDIG, PDIA2, AXIN1	-5339, 647, -1865, 71211	upstream, in gene, upstream, downstream	ActReg chr16 #5783	0	0	1
5784	16	354,145	354,579	434	1	2.455	3.308	11.385	5	5	17	1	0	1	AXIN1	48,102	in gene	ActReg chr16 #5784	0	0	1
5785	16	377,057	377,965	908	1	10.464	14.607	7.321	15	26	16	0	0	1	AXIN1	24,953	in gene	ActReg chr16 #5785	0	1	0
5786	16	390,357	390,876	519	1	2.938	2.875	11.188	4	9	14	0	0	1	AXIN1	11,848	in gene	ActReg chr16 #5786	0	0	1
5787	16	404,540	405,216	676	1	3.409	6.318	12.273	6	10	18	0	1	1	AXIN1	-2,414	upstream	ActReg chr16 #5787	0	0	1
5788	16	408,864	409,377	513	1	6.471	2.765	11.765	9	5	21	0	1	2	AXIN1, MRPL28	-6656, 11420	upstream, downstream	ActReg chr16 #5788	0	0	1
5789	16	411,663	412,280	617	1	8.294	9.053	14.947	18	18	25	1	0	3	AXIN1, MRPL28, TMEM8A	-9507, 8569, 19979	upstream, downstream, downstream	ActReg chr16 #5789	0	0	1
5790	16	414,329	415,164	835	1	5.154	5.24	10.731	10	10	19	0	0	2	MRPL28, TMEM8A	5794, 17204	downstream, downstream	ActReg chr16 #5790	0	0	1
5791	16	425,764	426,346	582	1	5.867	4.833	12.722	9	10	17	1	2	3	MRPL28, TMEM8A, LOC100134368	-5515, 5895, -6186	upstream, in gene, upstream	ActReg chr16 #5791	0	0	1
5792	16	427,193	427,919	726	1	1.783	5.348	12.087	3	12	15	1	2	3	MRPL28, TMEM8A, LOC100134368	-7016, 4394, -4685	upstream, in gene, upstream	ActReg chr16 #5792	0	0	1
5793	16	431,063	431,632	569	1	4.833	5.611	10.167	6	8	14	1	2	2	TMEM8A, LOC100134368	603, -894	in gene, upstream	ActReg chr16 #5793	0	0	1
5794	16	474,742	475,616	874	1	12.893	9.929	6.25	22	16	12	1	1	1	RAB11FIP3	-489	upstream	ActReg chr16 #5794	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5795	16	476,410	476,810	400	1	6.769	7.692	11.385	9	11	18	1	1	1	RAB11FIP3	942	in gene	ActReg chr16 #5795	0	0	1
5796	16	508,031	508,424	393	1	2.769	4.615	10.692	4	6	16	0	0	1	RAB11FIP3	32,559	in gene	ActReg chr16 #5796	0	0	1
5797	16	532,433	532,875	442	1	4.692	4.786	12.643	7	9	19	1	0	1	RAB11FIP3	56,986	in gene	ActReg chr16 #5797	0	0	1
5798	16	576,580	577,776	1,196	2	12.486	13.108	7.086	23	24	13	1	2	3	RAB11FIP3, C16orf10, SOLH	101510, 229, -678	downstream, in gene, upstream	ActReg chr16 #5798	1	1	0
5799	16	578,179	579,014	835	2	7.346	10.846	9.846	11	15	16	0	2	4	RAB11FIP3, C16orf10, SOLH, LOC100507047	102928, -1189, 740, -10354	downstream, upstream, in gene, upstream	ActReg chr16 #5799	0	1	1
5800	16	584,883	585,633	750	1	4.958	7.75	11.667	11	15	17	0	2	4	C16orf10, SOLH, LOC100507047, MIR3176	-7851, 7402, -3692, -8019	upstream, in gene, upstream, upstream	ActReg chr16 #5800	0	0	1
5801	16	586,159	586,824	665	1	4.667	6.19	11.571	7	9	15	0	2	4	C16orf10, SOLH, LOC100507047, MIR3176	-9084, 8635, -2459, -6786	upstream, in gene, upstream, upstream	ActReg chr16 #5801	0	0	1
5802	16	587,391	588,242	851	1	4.296	3.333	11.704	6	6	18	1	2	4	C16orf10, SOLH, LOC100507047, MIR3176	-10409, 9960, -1134, -5461	upstream, in gene, upstream, upstream	ActReg chr16 #5802	0	0	1
5803	16	590,568	591,322	754	1	3.783	4.435	13.435	9	7	23	1	2	3	SOLH, LOC100507047, MIR3176	13089, 1995, -2332	in gene, downstream, upstream	ActReg chr16 #5803	0	0	1
5804	16	598,480	599,233	753	1	5.542	5.417	11.417	10	9	18	0	0	3	SOLH, LOC100507047, MIR3176	21000, 9906, 5579	in gene, downstream, downstream	ActReg chr16 #5804	0	0	1
5805	16	599,453	599,877	424	1	1.75	3.571	11.929	4	6	16	0	0	3	SOLH, LOC100507047, MIR3176	21809, 10715, 6388	in gene, downstream, downstream	ActReg chr16 #5805	0	0	1
5806	16	601,689	602,183	494	1	5.375	3.062	11.125	8	5	17	0	0	3	SOLH, MIR3176, C16orf11	24080, 8659, -8486	in gene, downstream, upstream	ActReg chr16 #5806	0	0	1
5807	16	604,102	604,572	470	1	4	5.714	12.286	5	8	18	0	1	2	SOLH, C16orf11	26481, -6085	in gene, upstream	ActReg chr16 #5807	0	0	1
5808	16	605,676	606,402	726	1	3.905	4.478	11.174	7	10	17	0	1	2	SOLH, C16orf11	28183, -4383	downstream, upstream	ActReg chr16 #5808	0	0	1
5809	16	606,506	606,879	373	1	2.727	4.364	12.636	4	6	17	0	1	2	SOLH, C16orf11	28836, -3730	downstream, upstream	ActReg chr16 #5809	0	0	1
5810	16	608,367	609,229	862	1	3.889	3.045	11.778	7	8	20	0	1	3	SOLH, C16orf11, NHLRC4	30942, -1624, -8234	downstream, upstream, upstream	ActReg chr16 #5810	0	0	1
5811	16	609,653	610,055	402	1	5.462	1.167	12.308	7	2	19	1	2	4	SOLH, C16orf11, NHLRC4, PIGQ	31998, -568, -7178, -10150	downstream, upstream, upstream, upstream	ActReg chr16 #5811	0	0	1
5812	16	610,913	611,408	495	1	3.6	2.533	10.8	6	4	17	1	2	4	SOLH, C16orf11, NHLRC4, PIGQ	33304, 738, -5872, -8844	downstream, in gene, upstream, upstream	ActReg chr16 #5812	0	0	1
5813	16	613,568	614,065	497	1	2.167	3	12.438	3	5	18	0	2	4	SOLH, C16orf11, NHLRC4, PIGQ	35960, 3394, -3216, -6188	downstream, in gene, upstream, upstream	ActReg chr16 #5813	0	0	1
5814	16	615,128	615,583	455	1	4.571	4.643	11	7	8	17	2	2	3	C16orf11, NHLRC4, PIGQ	4933, -1677, -4649	in gene, upstream, upstream	ActReg chr16 #5814	0	0	1
5815	16	615,877	616,308	431	1	2.077	5.385	13.154	3	9	20	1	2	3	C16orf11, NHLRC4, PIGQ	5670, -940, -3912	downstream, upstream, upstream	ActReg chr16 #5815	0	0	1
5816	16	617,664	618,614	950	1	4.593	4.167	13.067	8	7	16	0	2	3	C16orf11, NHLRC4, PIGQ	7717, 1107, -1865	downstream, in gene, upstream	ActReg chr16 #5816	0	0	1
5817	16	627,919	628,690	771	1	3.25	3.125	13.083	6	5	19	0	0	2	NHLRC4, PIGQ	11272, 8300	downstream, in gene	ActReg chr16 #5817	0	0	1
5818	16	630,097	630,552	455	1	3.857	2.786	11.143	5	4	18	1	0	2	PIGQ, RAB40C	10320, -9033	in gene, upstream	ActReg chr16 #5818	0	0	1
5819	16	632,540	633,291	751	1	3.542	2.583	11.625	8	5	17	0	1	2	PIGQ, RAB40C	12911, -6442	in gene, upstream	ActReg chr16 #5819	0	0	1
5820	16	633,440	634,007	567	1	6	3.444	12.611	10	6	16	1	1	2	PIGQ, RAB40C	13719, -5634	in gene, upstream	ActReg chr16 #5820	0	0	1
5821	16	642,430	642,960	530	1	6.176	4.882	11.588	10	6	16	0	0	2	PIGQ, RAB40C	22691, 3338	downstream, in gene	ActReg chr16 #5821	0	0	1
5822	16	665,212	665,603	391	1	4.364	2.667	10.5	6	4	16	0	0	1	RAB40C	24,050	in gene	ActReg chr16 #5822	0	0	1
5823	16	675,910	676,569	659	1	5.45	3.55	11.85	8	8	19	1	1	3	RAB40C, WFIKKN1, C16orf13	36882, -4773, 10108	in gene, upstream, downstream	ActReg chr16 #5823	0	0	1
5824	16	680,909	681,449	540	1	3.882	4.176	12.471	6	6	17	0	2	5	RAB40C, WFIKKN1, C16orf13, LOC100287175, LOC100130285	41822, 167, 5168, -5638, 10556	downstream, in gene, downstream, upstream, downstream	ActReg chr16 #5824	0	0	1
5825	16	685,919	687,110	1,191	3	17.237	20.105	11.838	43	46	31	1	3	6	RAB40C, WFIKKN1, C16orf13, LOC100287175, LOC100130285, FAM195A	47157, 5502, -167, -303, 5221, -5335	downstream, downstream, upstream, upstream, downstream, upstream	ActReg chr16 #5825	1	1	1
5826	16	687,489	688,202	713	1	2.864	6.864	12.727	5	11	20	0	3	6	RAB40C, WFIKKN1, C16orf13, LOC100287175, LOC100130285, FAM195A	45488, 6833, -1498, 1028, 3890, -4004	downstream, downstream, upstream, in gene, downstream, upstream	ActReg chr16 #5826	0	0	1
5827	16	691,458	691,824	366	1	9.455	9.818	12.636	13	13	20	1	3	7	WFIKKN1, C16orf13, LOC100287175, LOC100130285, FAM195A, LOC100507146, WDR90	10629, -5294, 4824, 94, -208, 7388, -7722	downstream, upstream, downstream, in gene, upstream, upstream, downstream, upstream	ActReg chr16 #5827	0	0	1
5828	16	715,832	716,201	369	1	3.417	5.667	11.833	5	9	15	0	2	4	WDR90, LOC100507167, RHOT2, RHBDL1	16653, 2056, -2117, -10059	in gene, downstream, upstream, upstream	ActReg chr16 #5828	0	0	1
5829	16	717,798	719,238	1,440	2	7.289	9.156	10.293	12	24	21	1	2	4	WDR90, LOC100507167, RHOT2, RHBDL1	19155, 4558, 385, -7557	downstream, downstream, in gene, upstream	ActReg chr16 #5829	0	1	1
5830	16	722,784	724,014	1,230	1	4.487	5	13.718	8	10	22	0	2	6	WDR90, LOC100507167, RHOT2, RHBDL1, STUB1, JMJD8	24036, 9439, 5266, -2676, -6716, 11040	downstream, downstream, in gene, upstream, upstream, downstream	ActReg chr16 #5830	0	0	1
5831	16	724,319	725,193	874	1	4.214	6.821	11.607	9	11	16	0	2	7	WDR90, LOC100507167, RHOT2, RHBDL1, STUB1, JMJD8, WDR24	25393, 10796, 6623, -1319, -5359, 9683, 15644	downstream, downstream, downstream, upstream, upstream, downstream, downstream	ActReg chr16 #5831	0	0	1
5832	16	726,500	727,319	819	1	3	5.048	13.88	5	10	19	0	2	6	WDR90, RHOT2, RHBDL1, STUB1, JMJD8, WDR24	27546, 8776, 834, -3206, 7530, 13491	downstream, downstream, in gene, upstream, downstream, downstream	ActReg chr16 #5832	0	0	1
5833	16	728,906	729,663	757	1	6.261	7.174	12.609	10	14	19	1	1	5	RHOT2, RHBDL1, STUB1, JMJD8, WDR24	11151, 3209, -831, 5155, 11116	downstream, downstream, upstream, downstream, downstream	ActReg chr16 #5833	0	0	1
5834	16	732,104	732,904	800	1	7.52	8.6	11.4	11	15	17	1	2	6	RHOT2, RHBDL1, STUB1, JMJD8, WDR24, FBXL16	14371, 6429, 2389, 1935, 7896, 23321	downstream, downstream, in gene, in gene, downstream, downstream	ActReg chr16 #5834	0	0	1
5835	16	733,301	734,724	1,423	2	9.956	10.133	7.976	17	22	17	1	1	6	RHOT2, RHBDL1, STUB1, JMJD8, WDR24, FBXL16	15879, 7937, 3897, 427, 6388, 21813	downstream, downstream, downstream, in gene, downstream, downstream	ActReg chr16 #5835	0	1	1
5836	16	734,984	735,525	541	1	8.812	7.353	16	17	12	24	1	1	5	RHBDL1, STUB1, JMJD8, WDR24, FBXL16	9179, 5139, -815, 5146, 20571	downstream, downstream, upstream, in gene, downstream	ActReg chr16 #5836	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5837	16	739,809	740,712	903	1	8.679	12.571	9.607	17	22	15	1	2	4	STUB1, JMJD8, WDR24, FBXL16	10145, -5821, 140, 15565	downstream, upstream, in gene, downstream	ActReg chr16 #5837	0	1	0
5838	16	750,851	751,359	508	1	4.933	5.533	12.133	7	10	17	1	1	2	FBXL16, LOC100287301	4720, -6208	in gene, upstream	ActReg chr16 #5838	0	0	1
5839	16	753,413	754,090	677	1	3.667	5.524	15.238	7	10	23	0	2	2	FBXL16, LOC100287301	2074, -3562	in gene, upstream	ActReg chr16 #5839	0	0	1
5840	16	756,315	756,680	365	1	3.25	3.667	12.667	5	5	17	1	2	3	FBXL16, LOC100287301, METRN	-672, -816, -8676	upstream, upstream, upstream	ActReg chr16 #5840	0	0	1
5841	16	759,246	760,117	871	1	4.63	4.923	11	9	7	14	0	3	3	FBXL16, LOC100287301, METRN	-3856, 2368, -5492	upstream, downstream, upstream	ActReg chr16 #5841	0	0	1
5842	16	761,449	762,055	606	1	8.105	6.684	11.632	15	10	15	0	2	4	FBXL16, LOC100287301, METRN, FAM173A	-5927, 4439, -3421, -9406	upstream, downstream, upstream, upstream	ActReg chr16 #5842	0	0	1
5843	16	763,743	764,130	387	1	4.308	5.077	13.692	6	7	22	0	2	5	FBXL16, LOC100287301, METRN, FAM173A, CCDC78	-8111, 6623, -1237, -7222, 12537	upstream, downstream, upstream, upstream, downstream	ActReg chr16 #5843	0	0	1
5844	16	767,008	767,582	574	1	7	5.778	12.056	9	8	19	1	2	5	LOC100287301, METRN, FAM173A, CCDC78, HAGHL	9982, 2122, -3863, 9178, -9663	downstream, in gene, upstream, downstream, upstream	ActReg chr16 #5844	0	0	1
5845	16	767,689	768,453	764	1	4.833	7.083	13.5	10	12	22	0	1	5	LOC100287301, METRN, FAM173A, CCDC78, HAGHL	10758, 2898, -3087, 8402, -8887	downstream, downstream, upstream, downstream, upstream	ActReg chr16 #5845	0	0	1
5846	16	770,872	771,526	654	1	10.476	13.857	3.263	15	23	8	1	2	5	METRN, FAM173A, CCDC78, HAGHL, NARFL	6026, 41, 5274, -5759, 19798	downstream, in gene, downstream, upstream, downstream	ActReg chr16 #5846	0	1	0
5847	16	771,841	772,605	764	1	4.455	5.111	11.609	8	10	16	1	2	5	METRN, FAM173A, CCDC78, HAGHL, NARFL	7050, 1065, 4250, -4735, 18774	downstream, in gene, downstream, upstream, downstream	ActReg chr16 #5847	0	0	1
5848	16	774,232	774,617	385	1	7.25	5.5	12.333	9	8	18	0	2	5	METRN, FAM173A, CCDC78, HAGHL, NARFL	9251, 3266, 2049, -2534, 16573	downstream, downstream, in gene, upstream, downstream	ActReg chr16 #5848	0	0	1
5849	16	775,688	776,536	848	1	6.808	7.885	12	11	15	18	1	2	5	METRN, FAM173A, CCDC78, HAGHL, NARFL	10939, 4954, 361, -846, 14885	downstream, downstream, in gene, upstream, downstream	ActReg chr16 #5849	0	0	1
5850	16	778,937	779,465	528	1	4.588	5.647	10.294	7	7	18	1	2	4	FAM173A, CCDC78, HAGHL, NARFL	8043, -2728, 2243, 11796	downstream, upstream, in gene, downstream	ActReg chr16 #5850	0	0	1
5851	16	790,202	791,351	1,149	2	7.917	8.139	9.222	21	18	18	1	1	1	NARFL	221	in gene	ActReg chr16 #5851	0	1	1
5852	16	811,462	812,602	1,140	1	2.382	3.286	12.943	6	7	20	0	1	3	MSLN, MSLNL, MIR662	1267, 20894, -8151	in gene, downstream, upstream	ActReg chr16 #5852	0	0	1
5853	16	815,942	816,312	370	1	3	2.455	12.546	4	3	15	0	1	3	MSLN, MSLNL, MIR662	5362, 16799, -4056	in gene, downstream, upstream	ActReg chr16 #5853	0	0	1
5854	16	816,538	817,384	846	1	4.852	3.28	13.593	7	7	19	0	1	3	MSLN, MSLNL, MIR662	6196, 15965, -3222	in gene, downstream, upstream	ActReg chr16 #5854	0	0	1
5855	16	819,960	820,387	427	1	1.786	2.071	12.929	3	4	18	0	1	3	MSLN, MSLNL, MIR662	9408, 12753, -10	downstream, in gene, upstream	ActReg chr16 #5855	0	0	1
5856	16	824,112	824,905	793	1	3.68	4.64	11.52	6	7	16	0	0	3	MSLN, MSLNL, MIR662	13743, 8418, 4325	downstream, in gene, downstream	ActReg chr16 #5856	0	0	1
5857	16	825,174	825,786	612	1	3.333	2	10.737	6	2	14	0	0	4	MSLN, MSLNL, MIR662, RPUSD1	14715, 7446, 5297, 12903	downstream, in gene, downstream, downstream	ActReg chr16 #5857	0	0	1
5858	16	832,830	833,617	787	1	7	5.56	14.36	14	11	21	1	2	3	MSLNL, RPUSD1, CHTF18	-297, 5160, -5399	upstream, downstream, upstream	ActReg chr16 #5858	0	0	1
5859	16	834,265	834,962	697	1	3.778	3.818	11.591	7	6	15	0	2	3	MSLNL, RPUSD1, CHTF18	-1687, 3770, -4009	upstream, downstream, upstream	ActReg chr16 #5859	0	0	1
5860	16	838,455	839,082	627	1	7.7	12.25	8.353	13	26	13	1	3	4	MSLNL, RPUSD1, CHTF18, GNG13	-5842, -385, 146, 11965	upstream, upstream, in gene, downstream	ActReg chr16 #5860	0	1	0
5861	16	844,104	844,725	621	1	3.895	4.579	11.158	6	10	14	0	1	3	RPUSD1, CHTF18, GNG13	-6031, 5792, 6319	upstream, in gene, downstream	ActReg chr16 #5861	0	0	1
5862	16	845,673	846,399	726	1	5.773	7.545	12.682	6	13	19	0	1	4	RPUSD1, CHTF18, GNG13, PRR25	-7653, 7414, 4697, -9407	upstream, in gene, downstream, upstream	ActReg chr16 #5862	0	0	1
5863	16	849,018	849,762	744	1	2.364	4.625	12.417	5	7	21	0	2	3	CHTF18, GNG13, PRR25	10768, 1343, -6053	downstream, in gene, upstream	ActReg chr16 #5863	0	0	1
5864	16	850,214	850,659	445	1	4.286	6.571	11.786	6	9	17	1	2	3	CHTF18, GNG13, PRR25	11814, 297, -5007	downstream, in gene, upstream	ActReg chr16 #5864	0	0	1
5865	16	851,195	851,927	732	1	3.625	5.174	12.13	6	9	18	0	2	3	CHTF18, GNG13, PRR25	12939, -828, -3882	downstream, upstream, upstream	ActReg chr16 #5865	0	0	1
5866	16	855,455	856,290	835	1	3.926	3.8	12.444	7	9	20	0	2	3	CHTF18, GNG13, PRR25	17250, -5139, 429	downstream, upstream, in gene	ActReg chr16 #5866	0	0	1
5867	16	866,965	867,533	568	1	2.4	4.111	11.222	4	6	17	1	0	1	PRR25	11,806	downstream	ActReg chr16 #5867	0	0	1
5868	16	878,372	878,782	410	1	2.4	4.333	13.25	4	6	17	0	0	0				ActReg chr16 #5868	0	0	1
5869	16	880,472	880,938	466	1	4.867	2.667	12.933	6	5	22	0	0	0				ActReg chr16 #5869	0	0	1
5870	16	894,465	895,298	833	1	5	3.577	14.231	9	5	25	1	0	1	LMF1	136,437	downstream	ActReg chr16 #5870	0	0	1
5871	16	901,665	902,187	522	1	2.75	4.875	11.75	4	7	18	0	0	1	LMF1	129,392	downstream	ActReg chr16 #5871	0	0	1
5872	16	905,125	905,835	710	1	2.684	3.364	14.864	4	8	24	0	0	1	LMF1	125,838	in gene	ActReg chr16 #5872	0	0	1
5873	16	918,338	918,671	333	1	2	3.6	11.3	2	5	14	0	0	1	LMF1	112,814	in gene	ActReg chr16 #5873	0	0	1
5874	16	918,891	919,481	590	1	2.429	3.385	14.167	3	7	22	0	0	1	LMF1	112,132	in gene	ActReg chr16 #5874	0	0	1
5875	16	929,480	929,922	442	1	2.846	1.786	12.571	6	3	16	0	0	1	LMF1	101,617	in gene	ActReg chr16 #5875	0	0	1
5876	16	959,156	959,716	560	1	2.944	5.056	11.667	5	7	17	1	0	1	LMF1	71,882	in gene	ActReg chr16 #5876	0	0	1
5877	16	967,723	968,226	503	1	5.562	3.188	10.312	7	5	12	1	0	1	LMF1	63,344	in gene	ActReg chr16 #5877	0	0	1
5878	16	1,020,168	1,021,126	958	1	8.8	12.233	9.033	15	21	21	1	0	1	LMF1	10,671	in gene	ActReg chr16 #5878	0	1	0
5879	16	1,033,182	1,033,643	461	1	5.8	5.067	13.267	12	6	16	1	2	2	LMF1, SOX8	-2094, 1604	upstream, in gene	ActReg chr16 #5879	0	0	1
5880	16	1,034,390	1,034,722	332	1	2.091	2	10.727	4	3	13	1	1	2	LMF1, SOX8	-3238, 2748	upstream, in gene	ActReg chr16 #5880	0	0	1
5881	16	1,035,638	1,036,349	711	1	3.1	3.15	9.591	6	8	16	0	1	2	LMF1, SOX8	-4675, 4185	upstream, in gene	ActReg chr16 #5881	0	0	1
5882	16	1,037,796	1,038,289	493	1	3.333	3.455	11.6	6	6	18	0	1	2	LMF1, SOX8	-6724, 6234	upstream, downstream	ActReg chr16 #5882	0	0	1
5883	16	1,038,743	1,039,350	607	1	1.818	2.789	12.737	2	6	20	0	1	2	LMF1, SOX8	-7728, 7238	upstream, downstream	ActReg chr16 #5883	0	0	1
5884	16	1,049,694	1,050,282	588	1	2.632	3.368	11.421	7	6	19	0	0	0				ActReg chr16 #5884	0	0	1
5885	16	1,050,567	1,051,047	480	1	2.667	2.733	12.067	4	6	19	0	0	0				ActReg chr16 #5885	0	0	1
5886	16	1,053,560	1,054,208	648	1	4.143	7.857	11.524	6	12	17	0	0	0				ActReg chr16 #5886	0	0	1
5887	16	1,062,823	1,063,767	944	1	5.276	5.931	12.276	8	9	18	0	0	0				ActReg chr16 #5887	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5888	16	1,071,043	1,071,783	740	1	3.565	5.737	12.478	6	9	20	1	0	0				ActReg chr16 #5888	0	0	1
5889	16	1,071,785	1,072,250	465	1	2.786	4	12.357	6	6	18	0	0	0				ActReg chr16 #5889	0	0	1
5890	16	1,080,359	1,081,178	819	1	2.84	6.28	11.36	5	10	18	1	0	0				ActReg chr16 #5890	0	0	1
5891	16	1,086,504	1,086,940	436	1	2.385	5.769	12.923	5	11	16	0	0	0				ActReg chr16 #5891	0	0	1
5892	16	1,088,172	1,088,606	434	1	2.769	6.154	10.692	4	9	16	1	0	0				ActReg chr16 #5892	0	0	1
5893	16	1,093,692	1,094,053	361	1	2.917	3.583	11	4	6	16	0	0	0				ActReg chr16 #5893	0	0	1
5894	16	1,094,392	1,094,851	459	1	2.2	4.8	11.467	3	7	17	0	0	0				ActReg chr16 #5894	0	0	1
5895	16	1,096,037	1,096,579	542	1	4.118	3.765	12.941	7	5	17	0	0	0				ActReg chr16 #5895	0	0	1
5896	16	1,096,843	1,097,348	505	1	3.562	6.062	12.25	9	8	16	0	0	0				ActReg chr16 #5896	0	0	1
5897	16	1,104,465	1,105,015	550	1	5	5.294	11.294	8	8	17	0	0	1	LOC146336	23,991	downstream	ActReg chr16 #5897	0	0	1
5898	16	1,105,767	1,106,214	447	1	4.214	3.286	12.929	6	5	18	0	0	1	LOC146336	22,741	downstream	ActReg chr16 #5898	0	0	1
5899	16	1,107,576	1,108,135	559	1	3.556	4.6	10.5	5	9	14	1	0	1	LOC146336	20,876	downstream	ActReg chr16 #5899	0	0	1
5900	16	1,116,384	1,116,847	463	1	4.733	4.267	10.6	8	7	18	1	1	2	LOC146336, SSTR5	12116, -6141	in gene, upstream	ActReg chr16 #5900	0	0	1
5901	16	1,118,853	1,119,311	458	1	1.125	4.143	11.143	2	5	16	0	1	2	LOC146336, SSTR5	9649, -3674	in gene, upstream	ActReg chr16 #5901	0	0	1
5902	16	1,128,378	1,128,831	453	1	3.571	4.143	12.143	6	6	16	1	1	3	LOC146336, SSTR5, C1QTNF8	127, 5848, 17640	in gene, in gene, downstream	ActReg chr16 #5902	0	0	1
5903	16	1,128,909	1,129,419	510	1	5	4.875	11.438	7	7	15	1	1	3	LOC146336, SSTR5, C1QTNF8	-433, 6408, 17080	upstream, in gene, downstream	ActReg chr16 #5903	0	0	1
5904	16	1,129,814	1,130,647	833	1	4.385	3.846	12.039	6	8	17	1	1	3	LOC146336, SSTR5, C1QTNF8	-1499, 7474, 16014	upstream, in gene, downstream	ActReg chr16 #5904	0	0	1
5905	16	1,131,673	1,132,199	526	1	5.235	1.667	10.235	7	3	15	0	1	3	LOC146336, SSTR5, C1QTNF8	-3205, 9180, 14308	upstream, downstream, downstream	ActReg chr16 #5905	0	0	1
5906	16	1,132,553	1,133,008	455	1	4.5	4.214	12.643	6	7	17	0	1	3	LOC146336, SSTR5, C1QTNF8	-4049, 10024, 13464	upstream, downstream, downstream	ActReg chr16 #5906	0	0	1
5907	16	1,139,504	1,140,052	548	1	4.412	4.176	11.823	6	7	16	1	0	3	SSTR5, C1QTNF8, GS85	17022, 6466, 20917	downstream, in gene, downstream	ActReg chr16 #5907	0	0	1
5908	16	1,146,657	1,147,752	1,095	1	4.281	4.294	13.529	9	8	19	0	1	2	C1QTNF8, GS85	-960, 13491	upstream, in gene	ActReg chr16 #5908	0	0	1
5909	16	1,153,162	1,153,942	780	1	4	4.25	13.792	8	8	18	1	1	2	C1QTNF8, GS85	-7308, 7143	upstream, in gene	ActReg chr16 #5909	0	0	1
5910	16	1,157,683	1,158,212	529	1	4.588	4.412	11.882	7	6	17	0	1	1	GS85	2,748	in gene	ActReg chr16 #5910	0	0	1
5911	16	1,174,915	1,175,409	494	1	3	3.214	11.8	6	6	18	0	0	0				ActReg chr16 #5911	0	0	1
5912	16	1,179,520	1,180,678	1,158	1	3.378	2.812	13.919	9	6	19	1	0	0				ActReg chr16 #5912	0	0	1
5913	16	1,192,940	1,193,320	380	1	2.1	3.417	11.583	3	4	20	0	0	1	CACNA1H	-10,111	upstream	ActReg chr16 #5913	0	0	1
5914	16	1,207,440	1,208,252	812	1	3.64	5.32	13.08	8	8	19	2	0	1	CACNA1H	4,605	in gene	ActReg chr16 #5914	0	0	1
5915	16	1,212,777	1,213,392	615	1	4.947	8.474	13.526	9	13	16	0	0	1	CACNA1H	9,843	in gene	ActReg chr16 #5915	0	0	1
5916	16	1,216,983	1,217,507	524	1	5.529	2.154	12.706	9	4	22	1	0	1	CACNA1H	14,004	in gene	ActReg chr16 #5916	0	0	1
5917	16	1,219,456	1,219,939	483	1	3.643	5.125	13.312	6	9	18	1	0	1	CACNA1H	16,456	in gene	ActReg chr16 #5917	0	0	1
5918	16	1,221,943	1,222,498	555	1	4.389	4.611	12.556	6	8	20	1	0	1	CACNA1H	18,979	in gene	ActReg chr16 #5918	0	0	1
5919	16	1,230,025	1,230,676	651	1	3.25	3	11.4	4	6	14	1	0	1	CACNA1H	27,109	in gene	ActReg chr16 #5919	0	0	1
5920	16	1,230,685	1,231,320	635	1	2.85	6.7	13.05	6	10	19	0	0	1	CACNA1H	27,761	in gene	ActReg chr16 #5920	0	0	1
5921	16	1,234,011	1,234,688	677	1	5.762	6.955	11.318	10	11	16	0	0	1	CACNA1H	31,108	in gene	ActReg chr16 #5921	0	0	1
5922	16	1,236,332	1,236,811	479	1	4.667	6.733	11.467	7	10	16	1	0	1	CACNA1H	33,330	in gene	ActReg chr16 #5922	0	0	1
5923	16	1,236,858	1,237,631	773	1	6.292	4.062	12.375	10	7	17	1	0	1	CACNA1H	34,003	in gene	ActReg chr16 #5923	0	0	1
5924	16	1,253,975	1,254,659	684	1	4.136	3.571	9.909	8	7	14	2	0	1	CACNA1H	51,076	in gene	ActReg chr16 #5924	0	0	1
5925	16	1,258,448	1,259,088	640	1	5.45	5.3	13.2	8	9	22	0	0	1	CACNA1H	55,527	in gene	ActReg chr16 #5925	0	0	1
5926	16	1,260,956	1,261,573	617	1	3.35	4.75	10.65	5	9	14	0	0	1	CACNA1H	58,023	in gene	ActReg chr16 #5926	0	0	1
5927	16	1,262,052	1,263,249	1,197	1	4.833	3.162	13.622	10	7	20	0	0	2	CACNA1H, TPSG1	59409, 12604	in gene, downstream	ActReg chr16 #5927	0	0	1
5928	16	1,264,446	1,265,586	1,140	1	2.6	2.229	12.806	4	4	18	1	0	2	CACNA1H, TPSG1	61775, 10238	in gene, downstream	ActReg chr16 #5928	0	0	1
5929	16	1,267,328	1,268,225	897	1	3.276	4.517	14.483	9	8	23	1	0	2	CACNA1H, TPSG1	64535, 7478	in gene, downstream	ActReg chr16 #5929	0	0	1
5930	16	1,270,980	1,271,566	586	1	3.333	3.889	12.667	4	6	19	0	0	3	CACNA1H, TPSG1, TPSB2	68032, 3981, 8912	in gene, downstream, downstream	ActReg chr16 #5930	0	0	1
5931	16	1,350,728	1,351,489	761	1	7.333	6.75	12.25	13	10	19	0	0	1	UBE2I	-8,072	upstream	ActReg chr16 #5931	0	0	1
5932	16	1,358,749	1,359,526	777	2	18.16	17.96	7.35	40	33	15	1	1	1	UBE2I	-43	upstream	ActReg chr16 #5932	1	1	0
5933	16	1,362,924	1,363,445	521	1	1.733	4.867	12.312	3	8	18	0	0	1	UBE2I	4,004	in gene	ActReg chr16 #5933	0	0	1
5934	16	1,382,957	1,383,344	387	1	7	4.667	11.583	11	6	18	1	1	2	UBE2I, BAIAP3	-23970, -1513	downstream, upstream	ActReg chr16 #5934	0	0	1
5935	16	1,392,356	1,393,074	718	1	3.364	8.091	10.954	6	13	15	2	0	3	BAIAP3, C16orf42, GNPTG	8052, 9158, -9185	in gene, downstream, upstream	ActReg chr16 #5935	0	0	1
5936	16	1,393,258	1,393,759	501	1	6.667	9.533	13.667	9	15	20	2	0	3	BAIAP3, C16orf42, GNPTG	8845, 8365, -8392	in gene, downstream, upstream	ActReg chr16 #5936	0	0	1
5937	16	1,397,889	1,399,013	1,124	1	3.618	6.657	12.343	6	11	16	1	1	3	BAIAP3, C16orf42, GNPTG	13788, 3422, -3449	in gene, downstream, upstream	ActReg chr16 #5937	0	0	1
5938	16	1,400,736	1,402,465	1,729	2	8.8	11.418	6.545	16	21	15	1	2	3	BAIAP3, C16orf42, GNPTG	16937, 273, -300	downstream, in gene, upstream	ActReg chr16 #5938	0	1	1
5939	16	1,406,899	1,407,616	717	1	2.783	4.826	11.826	6	8	18	0	1	4	BAIAP3, C16orf42, GNPTG, UNKL	22594, -5384, 5357, 57448	downstream, upstream, in gene, downstream	ActReg chr16 #5939	0	0	1
5940	16	1,413,468	1,413,905	437	1	3.214	6.643	11.643	5	11	18	0	0	2	GNPTG, UNKL	11786, 51019	downstream, in gene	ActReg chr16 #5940	0	0	1
5941	16	1,416,192	1,416,810	618	1	3.2	6.15	11.8	6	12	16	0	0	2	GNPTG, UNKL	14601, 48204	downstream, in gene	ActReg chr16 #5941	0	0	1
5942	16	1,470,152	1,471,222	1,070	2	11.485	13.879	9.97	27	25	15	1	1	2	UNKL, C16orf91	-5982, 8658	upstream, in gene	ActReg chr16 #5942	1	1	0
5943	16	1,478,548	1,479,121	573	1	2.176	2.556	12.556	4	4	19	1	1	2	C16orf91, CCDC154	511, 15656	in gene, downstream	ActReg chr16 #5943	0	0	1
5944	16	1,482,998	1,483,438	440	1	1.786	1.857	12.286	3	3	16	1	1	2	C16orf91, CCDC154	-3873, 11272	upstream, downstream	ActReg chr16 #5944	0	0	1
5945	16	1,487,405	1,488,417	1,012	1	3.613	5.344	11.719	6	11	16	1	0	3	C16orf91, CCDC154, CLCN7	-8566, 6579, 37174	upstream, in gene, downstream	ActReg chr16 #5945	0	0	1
5946	16	1,492,502	1,493,151	649	1	1.692	4.842	10.85	3	8	14	0	1	2	CCDC154, CLCN7	1664, 32259	in gene, downstream	ActReg chr16 #5946	0	0	1
5947	16	1,496,086	1,496,555	469	1	3.267	3.8	11.267	6	6	17	0	1	2	CCDC154, CLCN7	-1830, 28765	upstream, in gene	ActReg chr16 #5947	0	0	1
5948	16	1,497,602	1,498,167	565	1	1.769	6.882	13.765	3	12	22	2	1	2	CCDC154, CLCN7	-3394, 27201	upstream, in gene	ActReg chr16 #5948	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5949	16	1,501,520	1,502,191	671	1	5.095	4.095	13.476	9	9	18	0	1	2	CCDC154, CLCN7	-7365, 23230	upstream, in gene	ActReg chr16 #5949	0	0	1
5950	16	1,524,705	1,525,399	694	1	9.571	13	4.706	19	26	9	1	1	1	CLCN7	33	in gene	ActReg chr16 #5950	0	1	0
5951	16	1,544,275	1,544,695	420	1	3.846	4.6	10.692	5	8	17	1	2	2	C16orf38, TELO2	-6017, 1133	upstream, in gene	ActReg chr16 #5951	0	0	1
5952	16	1,551,304	1,552,442	1,138	1	3.542	3.429	12.371	7	6	20	0	0	2	TELO2, IFT140	8521, 110236	in gene, downstream	ActReg chr16 #5952	0	0	1
5953	16	1,580,598	1,581,168	570	1	2.267	2.333	10.778	4	4	14	0	1	2	IFT140, TMEM204	81226, -3348	in gene, upstream	ActReg chr16 #5953	0	0	1
5954	16	1,581,472	1,581,856	384	1	4.083	3.154	11.846	7	5	17	0	1	2	IFT140, TMEM204	80445, -2567	in gene, upstream	ActReg chr16 #5954	0	0	1
5955	16	1,583,764	1,584,287	523	1	4.062	4.188	12.375	7	5	18	1	1	2	IFT140, TMEM204	78084, -206	in gene, upstream	ActReg chr16 #5955	0	0	1
5956	16	1,601,373	1,601,977	604	1	3.111	3.647	11.579	5	6	16	0	0	2	IFT140, TMEM204	60434, 17444	in gene, in gene	ActReg chr16 #5956	0	0	1
5957	16	1,695,812	1,696,553	741	2	11.478	11.652	3.636	17	18	8	0	0	1	CRAMP1L	31,541	in gene	ActReg chr16 #5957	1	1	0
5958	16	1,706,209	1,706,899	690	1	3.571	5.143	12.476	6	7	16	2	0	1	CRAMP1L	41,913	in gene	ActReg chr16 #5958	0	0	1
5959	16	1,755,502	1,756,739	1,237	2	11.41	12.128	4.138	21	19	11	0	1	2	HN1L, MAPK8IP3	27842, -101	downstream, upstream	ActReg chr16 #5959	1	1	0
5960	16	1,796,475	1,797,173	698	1	7.364	10.636	13.182	11	17	21	1	0	1	MAPK8IP3	40,603	in gene	ActReg chr16 #5960	0	0	1
5961	16	1,814,341	1,814,901	560	1	4.5	5.118	13.823	7	7	22	1	0	4	MAPK8IP3, NME3, MRPS34, EME2	58400, 7089, 8519, -8608	in gene, downstream, downstream, upstream	ActReg chr16 #5961	0	0	1
5962	16	1,819,185	1,819,641	456	1	4.857	7.286	13.643	7	11	22	0	2	5	MAPK8IP3, NME3, MRPS34, EME2, SPSB3	63192, 2297, 3727, -3816, 13168	in gene, downstream, downstream, upstream, downstream	ActReg chr16 #5962	0	0	1
5963	16	1,819,679	1,820,492	813	1	5.654	5.654	11.923	12	9	17	1	2	5	MAPK8IP3, NME3, MRPS34, EME2, SPSB3	63864, 1625, 3055, -3144, 12496	in gene, downstream, downstream, upstream, downstream	ActReg chr16 #5963	0	0	1
5964	16	1,820,538	1,821,151	613	1	9.579	9.474	12.316	12	13	17	1	3	5	MAPK8IP3, NME3, MRPS34, EME2, SPSB3	64623, 866, 2296, -2385, 11737	downstream, in gene, downstream, upstream, downstream	ActReg chr16 #5964	0	0	1
5965	16	1,821,831	1,822,561	730	1	8.609	12.913	3.727	13	20	6	1	3	5	MAPK8IP3, NME3, MRPS34, EME2, SPSB3	65975, -486, 944, -1033, 10385	downstream, upstream, in gene, upstream, downstream	ActReg chr16 #5965	0	1	0
5966	16	1,822,702	1,823,493	791	2	9.2	15.12	9	13	30	20	1	3	6	MAPK8IP3, NME3, MRPS34, EME2, SPSB3, NUBP2	66876, -1387, 43, -132, 9484, -9836	downstream, upstream, in gene, upstream, downstream, upstream	ActReg chr16 #5966	0	1	1
5967	16	1,825,705	1,826,304	599	1	4.526	6.158	12.263	8	10	17	0	4	6	MAPK8IP3, NME3, MRPS34, EME2, SPSB3, NUBP2	69783, -4294, -2854, 2775, 6577, -6929	downstream, upstream, upstream, in gene, downstream, upstream	ActReg chr16 #5967	0	0	1
5968	16	1,828,183	1,828,782	599	1	3.474	5.368	10.158	7	9	14	0	3	6	MAPK8IP3, NME3, MRPS34, EME2, SPSB3, NUBP2	72261, -6772, -5342, 5253, 4099, -4451	downstream, upstream, upstream, downstream, in gene, upstream	ActReg chr16 #5968	0	0	1
5969	16	1,829,453	1,829,993	540	1	4.412	5.529	12.647	6	8	18	0	2	6	MAPK8IP3, NME3, MRPS34, EME2, SPSB3, NUBP2	73502, -8013, -6583, 6494, 2858, -3210	downstream, upstream, upstream, downstream, in gene, upstream	ActReg chr16 #5969	0	0	1
5970	16	1,832,536	1,833,254	718	1	8.217	14.217	8.087	13	26	12	1	2	5	MRPS34, EME2, SPSB3, NUBP2, IGFALS	-9755, 9666, -314, -38, 12014	upstream, downstream, upstream, upstream, downstream	ActReg chr16 #5970	0	1	0
5971	16	1,836,299	1,836,831	532	1	2.562	3.812	13.188	4	7	18	1	1	3	SPSB3, NUBP2, IGFALS	-3984, 3632, 8344	upstream, in gene, downstream	ActReg chr16 #5971	0	0	1
5972	16	1,843,840	1,844,942	1,102	1	5.24	5	11.257	11	9	15	0	1	2	NUBP2, IGFALS	11458, 518	downstream, in gene	ActReg chr16 #5972	0	0	1
5973	16	1,867,601	1,868,739	1,138	1	4.429	4.528	11.111	8	8	14	0	0	2	HAGH, FAHD1	9025, -9055	in gene, upstream	ActReg chr16 #5973	0	0	1
5974	16	1,870,869	1,871,510	641	1	2.85	3.75	12.25	4	8	19	0	1	2	HAGH, FAHD1	6006, -6036	in gene, upstream	ActReg chr16 #5974	0	0	1
5975	16	1,876,704	1,877,694	990	3	11.065	20.097	10.552	18	45	18	1	2	3	HAGH, FAHD1, C16orf73	-4, -26, 44980	upstream, upstream, downstream	ActReg chr16 #5975	1	1	1
5976	16	1,959,104	1,959,539	435	1	3.643	6.357	11.071	5	10	17	0	0	1	HS3ST6	8,910	downstream	ActReg chr16 #5976	0	0	1
5977	16	1,963,327	1,964,127	800	1	3.72	3.52	10.84	7	5	14	0	0	1	HS3ST6	4,504	in gene	ActReg chr16 #5977	0	0	1
5978	16	1,982,411	1,983,113	702	1	5.773	3.429	11.364	7	7	15	0	0	1	SEPX1	10,532	downstream	ActReg chr16 #5978	0	0	1
5979	16	1,992,935	1,993,502	567	1	8.412	7.529	12.353	13	11	17	1	1	2	SEPX1, RPL3L	76, 11461	in gene, downstream	ActReg chr16 #5979	0	0	1
5980	16	2,009,145	2,009,994	849	3	12.407	14.926	8.63	26	34	18	1	6	8	RPL3L, NDUFB10, RPS2, SNORA10, SNORA64, SNHG9, SNORA78, RNF151	-4890, 52, 5258, 2898, 3538, -5428, -5616, -7306	upstream, in gene, downstream, downstream, downstream, upstream, upstream, upstream	ActReg chr16 #5980	1	1	1
5981	16	2,014,565	2,015,258	693	1	10.857	9.667	18.333	17	16	31	1	7	9	RPL3L, NDUFB10, RPS2, SNORA10, SNORA64, SNHG9, SNORA78, RNF151, TBL3	-10232, 5394, -84, -2444, -1804, -86, -274, -1964, -7153	upstream, downstream, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr16 #5981	0	0	1
5982	16	2,021,575	2,022,526	951	2	14.345	14.483	8.069	28	32	15	1	2	9	NDUFB10, RPS2, SNORA10, SNORA64, SNHG9, SNORA78, RNF151, TBL3, NOXO1	12533, -7223, -9583, 8943, 7053, 6865, 5175, -14, 9390	downstream, upstream, upstream, upstream, downstream, downstream, downstream, upstream, downstream	ActReg chr16 #5982	1	1	0
5983	16	2,027,585	2,028,514	929	1	6.185	3.931	13.207	11	10	19	1	1	4	RNF151, TBL3, NOXO1, GFER	11174, 5985, 3391, -6101	downstream, in gene, downstream, upstream	ActReg chr16 #5983	0	0	1
5984	16	2,028,628	2,029,157	529	1	3.882	3.353	10.588	7	5	16	2	2	4	RNF151, TBL3, NOXO1, GFER	12017, 6828, 2548, -5258	downstream, downstream, downstream, upstream	ActReg chr16 #5984	0	0	1
5985	16	2,029,500	2,031,121	1,621	1	4.216	4.647	13.902	9	8	21	1	2	4	TBL3, NOXO1, GFER, SYNGR3	8246, 1130, -3840, -9658	downstream, in gene, upstream, upstream	ActReg chr16 #5985	0	0	1
5986	16	2,033,515	2,034,082	567	1	10.889	13.611	9.5	18	22	16	1	3	4	TBL3, NOXO1, GFER, SYNGR3	11734, -2358, -352, -6170	downstream, upstream, upstream, upstream	ActReg chr16 #5986	0	1	0
5987	16	2,040,483	2,040,978	495	1	4.6	5.867	13.067	6	10	21	1	1	4	NOXO1, GFER, SYNGR3, ZNF598	-9290, 6580, 762, 19033	upstream, downstream, in gene, downstream	ActReg chr16 #5987	0	0	1
5988	16	2,048,971	2,050,509	1,538	1	4.125	4.458	12.75	9	8	18	0	0	2	SYNGR3, ZNF598	9772, 10023	downstream, in gene	ActReg chr16 #5988	0	0	1
5989	16	2,054,109	2,055,285	1,176	1	4.73	5.595	12.054	9	9	18	1	0	2	SYNGR3, ZNF598	14729, 5066	downstream, in gene	ActReg chr16 #5989	0	0	1
5990	16	2,059,809	2,060,621	812	1	12.28	15.44	8.24	19	27	16	1	1	2	ZNF598, NPW	-452, -9306	upstream, upstream	ActReg chr16 #5990	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
5991	16	2,072,993	2,073,799	806	1	10.92	9.04	7.52	19	15	12	0	1	2	NPW, SLC9A3R2	3875, -3492	downstream, upstream	ActReg chr16 #5991	1	0	0
5992	16	2,075,053	2,075,602	549	1	4.412	5.059	12.706	5	8	19	0	1	2	NPW, SLC9A3R2	5806, -1561	downstream, upstream	ActReg chr16 #5992	0	0	1
5993	16	2,082,513	2,084,096	1,583	2	10.14	12.46	11.2	15	17	18	0	0	2	SLC9A3R2, NTHL1	6416, 14563	in gene, downstream	ActReg chr16 #5993	0	1	1
5994	16	2,085,143	2,086,027	884	1	7.5	6.214	12.929	12	11	18	0	0	2	SLC9A3R2, NTHL1	8697, 12282	in gene, downstream	ActReg chr16 #5994	0	0	1
5995	16	2,097,466	2,098,181	715	2	11.609	11.043	7.318	17	15	10	1	2	3	SLC9A3R2, NTHL1, TSC2	20935, 44, -167	downstream, in gene, upstream	ActReg chr16 #5995	1	1	0
5996	16	2,111,517	2,112,061	544	1	4.118	4.647	13.765	6	9	20	0	0	1	TSC2	13,799	in gene	ActReg chr16 #5996	0	0	1
5997	16	2,123,039	2,123,795	756	1	4.292	6	12.25	8	11	15	0	0	1	TSC2	25,427	in gene	ActReg chr16 #5997	0	0	1
5998	16	2,124,046	2,124,502	456	1	6.857	5.5	13.286	11	8	19	0	0	1	TSC2	26,284	in gene	ActReg chr16 #5998	0	0	1
5999	16	2,126,465	2,127,372	907	1	2.893	3.429	12.25	6	6	23	0	0	1	TSC2	28,928	in gene	ActReg chr16 #5999	0	0	1
6000	16	2,141,695	2,142,076	381	1	2.75	7	17.5	4	10	26	1	1	3	TSC2, PKD1, MIR1225	43895, 44014, -1600	downstream, in gene, upstream	ActReg chr16 #6000	0	0	1
6001	16	2,143,286	2,143,837	551	1	3.412	2.059	12.823	9	5	20	0	1	3	TSC2, PKD1, MIR1225	45571, 42338, -3276	downstream, in gene, upstream	ActReg chr16 #6001	0	0	1
6002	16	2,165,590	2,165,876	286	1	2.111	1.667	9.778	3	3	12	1	0	2	PKD1, LOC100287400	20166, 10194	in gene, downstream	ActReg chr16 #6002	0	0	1
6003	16	2,202,443	2,203,267	824	1	9.192	15.962	7.769	16	31	14	0	3	4	RAB26, LOC100507303, SNORD60, TRAF7	4204, 2504, 2251, -2944	in gene, downstream, downstream, upstream	ActReg chr16 #6003	0	1	0
6004	16	2,204,973	2,205,606	633	1	11.7	11.25	14.4	17	16	26	1	3	4	RAB26, LOC100507303, SNORD60, TRAF7	6638, 70, -183, -510	downstream, in gene, upstream, upstream	ActReg chr16 #6004	0	0	1
6005	16	2,209,107	2,210,185	1,078	1	3.559	5	12.412	6	7	21	0	2	4	RAB26, LOC100507303, SNORD60, TRAF7	10995, -4287, -4540, 3847	downstream, upstream, upstream, in gene	ActReg chr16 #6005	0	0	1
6006	16	2,213,315	2,214,032	717	1	3.905	5.409	11.727	6	10	16	1	0	4	RAB26, LOC100507303, SNORD60, TRAF7	15022, -8314, -8567, 7874	downstream, upstream, upstream, in gene	ActReg chr16 #6006	0	0	1
6007	16	2,217,198	2,218,430	1,232	1	4.553	5.079	12	9	8	18	0	0	2	TRAF7, CASKIN1	12015, 28651	in gene, downstream	ActReg chr16 #6007	0	0	1
6008	16	2,221,160	2,221,639	479	1	2.867	4.667	11.8	8	6	17	0	0	2	TRAF7, CASKIN1	15600, 25066	in gene, downstream	ActReg chr16 #6008	0	0	1
6009	16	2,236,545	2,237,155	610	1	3.421	4.263	12.947	6	6	20	1	0	2	TRAF7, CASKIN1	31051, 9615	downstream, in gene	ActReg chr16 #6009	0	0	1
6010	16	2,240,683	2,241,618	935	1	3.214	5.276	12.586	6	11	20	0	0	1	CASKIN1	5,315	in gene	ActReg chr16 #6010	0	0	1
6011	16	2,255,030	2,256,328	1,298	2	16.22	16.171	9.39	43	35	22	1	1	4	CASKIN1, MLST8, C16orf79, PGP	-9214, 229, 5332, 9143	upstream, in gene, downstream, downstream	ActReg chr16 #6011	1	1	0
6012	16	2,256,750	2,257,371	621	1	4.632	9.105	11.263	8	18	15	0	1	3	MLST8, C16orf79, PGP	1610, 3951, 7762	in gene, downstream, downstream	ActReg chr16 #6012	0	0	1
6013	16	2,259,761	2,260,431	670	1	4.571	5.81	12.762	7	8	18	0	1	3	MLST8, C16orf79, PGP	4646, 915, 4726	downstream, in gene, downstream	ActReg chr16 #6013	0	0	1
6014	16	2,264,940	2,265,615	675	1	5.476	10.476	4.571	11	14	10	1	2	4	MLST8, C16orf79, PGP, E4F1	9827, -4266, -455, -8290	downstream, downstream, upstream, upstream	ActReg chr16 #6014	0	1	0
6015	16	2,286,180	2,286,747	567	1	4.647	3.176	12.294	6	7	18	1	1	3	E4F1, DNASE1L2, DCI	12896, -5, 15139	downstream, upstream, downstream	ActReg chr16 #6015	0	0	1
6016	16	2,317,638	2,319,116	1,478	4	16.152	15.239	10.689	43	41	19	1	2	3	RNPS1, MIR940, ABCA3	-263, -3371, 72370	upstream, upstream, downstream	ActReg chr16 #6016	1	1	1
6017	16	2,326,117	2,326,633	516	1	2.938	4.25	11.125	5	7	17	0	0	3	RNPS1, MIR940, ABCA3	-8261, 4627, 64372	upstream, downstream, in gene	ActReg chr16 #6017	0	0	1
6018	16	2,334,798	2,335,581	783	1	3.364	4.125	12.75	6	7	18	0	0	1	ABCA3	55,558	in gene	ActReg chr16 #6018	0	0	1
6019	16	2,336,212	2,336,722	510	1	4.125	5	10.188	7	7	13	0	0	1	ABCA3	54,280	in gene	ActReg chr16 #6019	0	0	1
6020	16	2,358,574	2,358,999	425	1	3.769	2.231	9.846	6	3	16	0	0	1	ABCA3	31,961	in gene	ActReg chr16 #6020	0	0	1
6021	16	2,390,776	2,391,242	466	1	10.533	11.133	5.533	17	15	9	1	1	1	ABCA3	-262	upstream	ActReg chr16 #6021	0	1	0
6022	16	2,478,768	2,479,303	535	1	8.529	9.125	16	12	12	24	1	1	1	CCNF	-360	upstream	ActReg chr16 #6022	0	0	1
6023	16	2,510,386	2,510,781	395	1	6.167	5.25	12	9	10	17	1	1	2	CCNF, C16orf59	31188, 468	downstream, in gene	ActReg chr16 #6023	0	0	1
6024	16	2,510,948	2,511,548	600	1	2.529	4.167	14.167	4	6	20	0	1	3	CCNF, C16orf59, NTN3	31853, 1133, -10252	downstream, in gene, upstream	ActReg chr16 #6024	0	0	1
6025	16	2,517,878	2,518,675	797	1	6.56	10.72	5.4	11	17	12	1	2	4	CCNF, C16orf59, NTN3, TBC1D24	38881, 8161, -3224, -6871	downstream, downstream, upstream, upstream	ActReg chr16 #6025	0	1	0
6026	16	2,518,868	2,519,492	624	1	9.55	4.6	10.9	15	9	16	0	2	3	C16orf59, NTN3, TBC1D24	9065, -2320, -5967	downstream, upstream, upstream	ActReg chr16 #6026	0	0	1
6027	16	2,522,898	2,523,522	624	1	6.75	7	10.55	11	11	14	1	2	3	C16orf59, NTN3, TBC1D24	13095, 1710, -1937	downstream, in gene, upstream	ActReg chr16 #6027	0	0	1
6028	16	2,523,981	2,524,590	609	1	8.158	13.105	8.667	12	21	12	1	2	3	C16orf59, NTN3, TBC1D24	14170, 2785, -862	downstream, downstream, upstream	ActReg chr16 #6028	0	1	0
6029	16	2,546,087	2,547,331	1,244	1	5.974	3.368	12.385	15	6	17	1	0	1	TBC1D24	21,562	in gene	ActReg chr16 #6029	0	0	1
6030	16	2,551,838	2,552,339	501	1	3.312	4.5	13.688	6	7	19	0	0	1	TBC1D24	26,941	in gene	ActReg chr16 #6030	0	0	1
6031	16	2,570,789	2,571,264	475	1	4.267	3.2	12.133	8	5	17	1	1	3	ATP6V0C, AMDHD2, CEMIP1	7073, 663, 23051	downstream, in gene, downstream	ActReg chr16 #6031	0	0	1
6032	16	2,577,689	2,578,835	1,146	1	4.528	6.028	11.722	9	17	19	1	0	5	ATP6V0C, AMDHD2, CEMIP1, MIR3178, PDPK1	14309, 7899, 15815, 3744, -9708	downstream, in gene, downstream, downstream, upstream	ActReg chr16 #6032	0	0	1
6033	16	2,581,569	2,582,092	523	1	10.062	9.875	13.688	14	18	21	1	2	4	AMDHD2, CEMIP1, MIR3178, PDPK1	11467, 12247, 176, -6140	downstream, in gene, downstream, upstream	ActReg chr16 #6033	0	0	1
6034	16	2,653,071	2,654,003	932	3	10.931	14.862	10.414	17	24	19	1	1	2	PDPK1, PRO0461	65567, 152	downstream, in gene	ActReg chr16 #6034	1	1	1
6035	16	2,732,067	2,732,838	771	2	13.375	12.75	7.375	23	20	13	1	1	2	LOC100507321, KCTD5	-9012, -43	upstream, upstream	ActReg chr16 #6035	1	1	0
6036	16	2,748,558	2,748,970	412	1	3	5.385	10.538	7	8	15	0	0	1	KCTD5	16,269	in gene	ActReg chr16 #6036	0	0	1
6037	16	2,765,558	2,766,036	478	1	8.733	9.933	14.933	15	16	21	1	0	2	KCTD5, PRSS27	33302, 4755	downstream, in gene	ActReg chr16 #6037	0	0	1
6038	16	2,787,212	2,787,696	484	1	2.467	3.067	11	4	4	17	0	0	1	LOC100128788	15,147	in gene	ActReg chr16 #6038	0	0	1
6039	16	2,801,792	2,803,107	1,315	3	10.548	10.286	9.308	22	21	17	1	2	2	LOC100128788, SRRM2	152, 119	in gene, in gene	ActReg chr16 #6039	1	1	1
6040	16	2,903,138	2,903,564	426	1	3.385	4.308	13	5	6	20	1	0	1	PRSS22	4,820	in gene	ActReg chr16 #6040	0	0	1
6041	16	2,909,591	2,910,239	648	1	5.15	5.75	11.85	10	9	20	0	1	1	PRSS22	-1,744	upstream	ActReg chr16 #6041	0	0	1
6042	16	2,910,802	2,911,629	827	2	11.423	12.962	5.192	17	28	11	0	1	1	PRSS22	-3,044	upstream	ActReg chr16 #6042	1	1	0
6043	16	2,917,787	2,918,701	914	3	9.552	13.241	7.517	17	24	18	1	0	1	PRSS22	-10,073	upstream	ActReg chr16 #6043	1	1	1
6044	16	2,933,241	2,933,945	704	1	8.409	7.864	12.364	12	14	19	1	1	1	FLYWCH2	397	in gene	ActReg chr16 #6044	0	0	1
6045	16	2,946,691	2,947,065	374	1	3.545	4	13.909	5	5	18	0	0	1	FLYWCH2	13,682	in gene	ActReg chr16 #6045	0	0	1
6046	16	2,954,920	2,955,587	667	1	6.524	7	14.619	10	12	23	1	1	2	FLYWCH2, FLYWCH1	22057, -6727	downstream, upstream	ActReg chr16 #6046	0	0	1
6047	16	2,961,543	2,962,218	675	2	10.667	12.333	4.947	22	22	10	1	1	1	FLYWCH1	-100	upstream	ActReg chr16 #6047	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6048	16	2,979,555	2,980,020	465	1	4	6.429	11.786	5	8	15	0	0	1	FLYWCH1	17,807	in gene	ActReg chr16 #6048	0	0	1
6049	16	3,003,733	3,004,074	341	1	4.636	3	11.364	7	5	17	0	0	1	FLYWCH1	41,923	downstream	ActReg chr16 #6049	0	0	1
6050	16	3,013,815	3,014,330	515	1	5.5	7.312	14	9	11	19	1	2	3	KREMEN2, PAQR4, PKMYT1	-145, -5270, 16402	upstream, upstream, downstream	ActReg chr16 #6050	0	0	1
6051	16	3,018,510	3,019,446	936	3	13.172	14.448	9.815	26	28	18	1	1	3	KREMEN2, PAQR4, PKMYT1	4761, -364, 11496	downstream, upstream, downstream	ActReg chr16 #6051	1	1	1
6052	16	3,019,621	3,020,498	877	1	9.704	9.741	13.852	16	12	19	1	1	3	KREMEN2, PAQR4, PKMYT1	5842, 717, 10415	downstream, in gene, downstream	ActReg chr16 #6052	0	0	1
6053	16	3,022,894	3,023,328	434	1	5.214	4.214	12.5	8	7	19	0	0	3	KREMEN2, PAQR4, PKMYT1	8894, 3769, 7363	downstream, in gene, in gene	ActReg chr16 #6053	0	0	1
6054	16	3,023,959	3,024,800	841	1	4.704	8.074	11.556	8	17	17	0	0	3	KREMEN2, PAQR4, PKMYT1	10162, 5037, 6095	downstream, downstream, in gene	ActReg chr16 #6054	0	0	1
6055	16	3,029,416	3,029,928	512	1	2.875	7.75	12.125	5	10	17	1	1	3	PAQR4, PKMYT1, LOC283875	10330, 802, -9383	downstream, in gene, upstream	ActReg chr16 #6055	0	0	1
6056	16	3,030,210	3,031,027	817	2	7.32	12.64	8.56	9	18	19	1	1	3	PAQR4, PKMYT1, LOC283875	11276, -144, -8437	downstream, upstream, upstream	ActReg chr16 #6056	0	1	1
6057	16	3,035,811	3,036,325	514	1	3.062	6.938	13.438	6	10	19	0	2	2	PKMYT1, LOC283875	-5594, -2987	upstream, upstream	ActReg chr16 #6057	0	0	1
6058	16	3,038,023	3,038,835	812	1	3.56	3	11.6	7	6	16	0	1	2	PKMYT1, LOC283875	-7955, -626	upstream, upstream	ActReg chr16 #6058	0	0	1
6059	16	3,050,488	3,050,975	487	1	5.2	2.533	13.333	7	5	19	0	1	2	LOC283875, LOC100507378	11676, -570	downstream, upstream	ActReg chr16 #6059	0	0	1
6060	16	3,057,453	3,057,808	355	1	6	3.091	13.546	7	5	19	0	1	3	LOC100507378, CLDN9, CLDN6	6329, -4827, 10558	downstream, upstream, downstream	ActReg chr16 #6060	0	0	1
6061	16	3,063,104	3,064,102	998	1	7.094	5.406	13.188	11	9	18	1	2	5	CLDN9, CLDN6, TNFRSF12A, HCFC1R1, THOC6	1146, 4585, -6710, 10684, -10429	in gene, downstream, upstream, downstream, upstream	ActReg chr16 #6061	0	0	1
6062	16	3,068,153	3,068,466	313	1	4.8	4	10.7	7	5	15	1	3	6	CLDN9, CLDN6, TNFRSF12A, HCFC1R1, THOC6, CCDC64B	5852, -121, -2004, 5978, -5723, 17233	downstream, upstream, upstream, downstream, upstream, downstream	ActReg chr16 #6062	0	0	1
6063	16	3,070,543	3,072,215	1,672	4	9.885	11.558	9.269	21	19	15	1	4	6	CLDN9, CLDN6, TNFRSF12A, HCFC1R1, THOC6, CCDC64B	8922, -3191, 1066, 2908, -2653, 14163	downstream, upstream, in gene, downstream, upstream, downstream	ActReg chr16 #6063	1	1	1
6064	16	3,073,388	3,074,602	1,214	3	10.974	10.447	13.579	21	21	22	1	3	7	CLDN9, CLDN6, TNFRSF12A, HCFC1R1, THOC6, CCDC64B, LOC100128770	11538, -5807, 3682, 292, -37, 11547, -5487	downstream, upstream, downstream, in gene, upstream, downstream, upstream	ActReg chr16 #6064	1	1	1
6065	16	3,077,266	3,077,830	564	1	5.056	2.833	11.944	9	5	20	0	2	6	CLDN6, TNFRSF12A, HCFC1R1, THOC6, CCDC64B, LOC100128770	-9360, 7235, -3261, 3516, 7994, -4934	upstream, downstream, upstream, in gene, downstream, upstream	ActReg chr16 #6065	0	0	1
6066	16	3,080,914	3,081,697	783	1	4.88	4.32	9.92	8	7	16	0	2	5	TNFRSF12A, HCFC1R1, THOC6, CCDC64B, LOC100128770	10992, -7018, 7273, 4237, -1177	downstream, upstream, downstream, in gene, upstream	ActReg chr16 #6066	0	0	1
6067	16	3,095,978	3,096,444	466	1	5.286	7.143	12.357	11	13	17	1	1	3	LOC100128770, MMP25, LOC100507419	13729, -471, 13153	downstream, upstream, downstream	ActReg chr16 #6067	0	0	1
6068	16	3,156,109	3,156,646	537	1	5.765	10	7	13	15	10	1	1	2	MGC3771, ZNF205	9222, -6186	downstream, upstream	ActReg chr16 #6068	0	1	0
6069	16	3,174,106	3,175,133	1,027	2	12.719	12.25	7.438	23	21	13	1	0	4	MGC3771, ZNF205, LOC100507458, ZNF213	-9020, 12056, 10259, 10438	upstream, downstream, downstream, upstream	ActReg chr16 #6069	1	1	0
6070	16	3,193,791	3,194,449	658	1	5.3	3.238	11.667	11	6	16	0	0	2	LOC100507458, ZNF213	-9242, 9063	upstream, downstream	ActReg chr16 #6070	0	0	1
6071	16	3,195,216	3,195,690	474	1	3.4	3.733	11.067	6	6	17	0	0	1	ZNF213	10,396	downstream	ActReg chr16 #6071	0	0	1
6072	16	3,200,071	3,201,168	1,097	3	13.147	10	14.323	26	15	28	2	0	1	ZNF213	15,562	downstream	ActReg chr16 #6072	1	1	1
6073	16	3,202,337	3,203,234	897	2	8.25	12.357	8.286	12	18	19	0	0	1	ZNF213	17,728	downstream	ActReg chr16 #6073	0	1	1
6074	16	3,208,611	3,209,336	725	1	9.909	10.454	12.046	14	12	16	1	0	0				ActReg chr16 #6074	0	0	1
6075	16	3,232,481	3,233,385	904	1	10.357	10.036	13.857	19	15	18	1	0	0				ActReg chr16 #6075	0	0	1
6076	16	3,239,282	3,239,912	630	2	10.9	8	12.45	14	12	25	1	0	0				ActReg chr16 #6076	1	0	1
6077	16	3,241,295	3,242,191	896	1	8.929	5.786	13.929	16	13	24	0	0	0				ActReg chr16 #6077	0	0	1
6078	16	3,284,606	3,285,210	604	1	8.211	8.526	12.632	12	14	16	1	1	2	ZNF200, MEFV	549, 21719	in gene, downstream	ActReg chr16 #6078	0	0	1
6079	16	3,314,062	3,314,909	847	1	9.462	10.885	14.577	14	17	24	1	2	2	MEFV, FLJ39639	-7858, 717	upstream, in gene	ActReg chr16 #6079	0	0	1
6080	16	3,354,964	3,356,211	1,247	3	8.077	11.59	9.029	18	17	15	1	2	2	TIGD7, ZNF75A	-4187, 154	upstream, in gene	ActReg chr16 #6080	1	1	1
6081	16	3,414,697	3,415,425	728	1	9.435	11.304	6.826	13	15	13	1	0	2	OR2C1, MTRNR2L4	9172, 7222	downstream, downstream	ActReg chr16 #6081	0	1	0
6082	16	3,450,552	3,451,700	1,148	3	13.25	13.861	11.333	27	30	22	1	2	2	ZNF434, ZNF174	-101, -64	upstream, upstream	ActReg chr16 #6082	1	1	1
6083	16	3,507,348	3,508,248	900	2	9.893	10.75	8.111	17	19	17	1	0	1	NAT15	14,130	in gene	ActReg chr16 #6083	1	1	0
6084	16	3,550,457	3,551,344	887	2	12.893	13.714	7.821	24	24	12	2	2	2	C16orf90, CLUAP1	-5479, -63	upstream, upstream	ActReg chr16 #6084	1	1	0
6085	16	3,600,237	3,600,626	389	1	3.083	1.75	11.083	5	3	14	0	0	1	NLRC3	26,961	in gene	ActReg chr16 #6085	0	0	1
6086	16	3,611,639	3,612,269	630	1	3.25	3.2	12.95	6	5	17	0	0	1	NLRC3	15,438	in gene	ActReg chr16 #6086	0	0	1
6087	16	3,646,230	3,646,686	456	1	2.462	3.286	12.357	4	5	18	0	0	1	BTBD12	15,127	in gene	ActReg chr16 #6087	0	0	1
6088	16	3,661,061	3,661,756	695	2	9.571	6.714	11.056	17	14	19	1	1	1	BTBD12	177	in gene	ActReg chr16 #6088	1	0	1
6089	16	3,702,074	3,702,518	444	1	3.857	3.643	11.643	7	5	18	0	1	2	DNASE1, TRAP1	-644, 65302	upstream, downstream	ActReg chr16 #6089	0	0	1
6090	16	3,766,915	3,768,062	1,147	1	9.6	11.914	6.4	15	20	13	1	1	2	TRAP1, CREBBP	110, 162633	in gene, downstream	ActReg chr16 #6090	0	1	0
6091	16	3,929,261	3,929,807	546	1	9.765	8.765	6.353	15	14	9	1	1	1	CREBBP	587	in gene	ActReg chr16 #6091	1	0	0
6092	16	3,931,081	3,931,672	591	1	5.278	6.611	13.833	10	12	21	1	1	1	CREBBP	-1,255	upstream	ActReg chr16 #6092	0	0	1
6093	16	4,233,442	4,234,229	787	2	10.833	10.875	7.875	17	18	14	1	0	1	SRL	58,346	downstream	ActReg chr16 #6093	1	1	0
6094	16	4,303,224	4,304,340	1,116	2	8.714	10.886	9.824	14	18	18	1	1	2	LOC100507501, TFAP4	8, 19219	in gene, downstream	ActReg chr16 #6094	0	1	1
6095	16	4,321,551	4,322,215	664	1	9.905	11.286	4.714	17	25	9	2	1	1	TFAP4	1,118	in gene	ActReg chr16 #6095	0	1	0
6096	16	4,356,346	4,356,846	500	1	3.733	7	12.625	6	9	18	0	0	0				ActReg chr16 #6096	0	0	1
6097	16	4,366,632	4,367,362	730	1	7.13	9.435	11.652	11	14	16	1	0	0				ActReg chr16 #6097	0	0	1
6098	16	4,393,120	4,393,745	625	1	4.85	5.05	11.1	10	7	17	0	0	2	GLIS2, Magmas	11207, 7868	downstream, in gene	ActReg chr16 #6098	0	0	1
6099	16	4,411,318	4,411,886	568	1	2.471	5	11.667	4	7	15	0	0	2	CORO7, VASN	55037, -10247	in gene, upstream	ActReg chr16 #6099	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6100	16	4,424,598	4,425,063	465	1	3.733	2.077	11.8	6	3	16	0	0	2	CORO7, VASN	41809, 2981	in gene, in gene	ActReg chr16 #6100	0	0	1
6101	16	4,441,562	4,441,975	413	1	1.923	4.923	11.385	3	7	17	0	0	2	CORO7, VASN	24871, 19919	in gene, downstream	ActReg chr16 #6101	0	0	1
6102	16	4,452,499	4,452,927	428	1	7.385	8	12.538	11	11	18	0	0	1	CORO7	13,926	in gene	ActReg chr16 #6102	0	0	1
6103	16	4,475,216	4,476,260	1,044	2	13.454	13.727	8.909	26	23	16	1	1	2	CORO7, DNAJA3	-9099, -120	upstream, upstream	ActReg chr16 #6103	1	1	0
6104	16	4,525,740	4,527,081	1,341	2	9.619	7.286	8.19	14	15	18	1	2	2	NMRAL1, HMOX2	-1514, 1691	upstream, in gene	ActReg chr16 #6104	1	0	1
6105	16	4,588,407	4,589,116	709	1	9.045	12.364	6.864	13	22	11	1	1	1	C16orf5	55	in gene	ActReg chr16 #6105	0	1	0
6106	16	4,663,640	4,664,191	551	1	10	6.765	11.941	13	14	18	1	1	1	FAM100A	1,012	in gene	ActReg chr16 #6106	0	0	1
6107	16	4,664,435	4,666,480	2,045	4	10.297	11.312	9.733	22	19	19	1	1	2	FAM100A, MGRN1	-530, -9369	upstream, upstream	ActReg chr16 #6107	1	1	1
6108	16	4,674,129	4,675,085	956	2	10.233	14.767	5.448	16	23	10	1	1	3	FAM100A, MGRN1, LOC100507570	-9680, -219, 16017	upstream, upstream, downstream	ActReg chr16 #6108	1	1	0
6109	16	4,732,791	4,733,547	756	1	5.292	4.409	11.583	5	10	17	1	0	1	MGRN1	58,343	in gene	ActReg chr16 #6109	0	0	1
6110	16	4,741,552	4,742,494	942	1	3.724	3.517	11.793	7	5	17	0	1	3	MGRN1, NUDT16L1, ANKS3	67197, -1671, 42140	downstream, upstream, downstream	ActReg chr16 #6110	0	0	1
6111	16	4,743,147	4,743,629	482	1	5.6	9.467	12.267	8	12	19	1	1	3	MGRN1, NUDT16L1, ANKS3	68562, -306, 40775	downstream, upstream, downstream	ActReg chr16 #6111	0	0	1
6112	16	4,747,670	4,748,605	935	1	3.407	3.828	11.172	7	9	15	0	0	3	MGRN1, NUDT16L1, ANKS3	73311, 4443, 36026	downstream, downstream, in gene	ActReg chr16 #6112	0	0	1
6113	16	4,751,860	4,752,639	779	1	3.5	3.458	11.958	6	7	16	0	0	2	NUDT16L1, ANKS3	8555, 31914	downstream, in gene	ActReg chr16 #6113	0	0	1
6114	16	4,783,840	4,784,618	778	1	10.12	11.88	5.143	13	17	9	1	2	2	ANKS3, C16orf71	-66, -60	upstream, upstream	ActReg chr16 #6114	0	1	0
6115	16	4,792,914	4,793,359	445	1	2.214	3.643	10.929	3	5	17	0	0	3	ANKS3, C16orf71, ZNF500	-8973, 8847, 24030	upstream, in gene, downstream	ActReg chr16 #6115	0	0	1
6116	16	4,816,941	4,817,675	734	2	13.043	16.13	8	26	26	16	1	1	2	ZNF500, SEPT12	-142, 21091	upstream, downstream	ActReg chr16 #6116	1	1	0
6117	16	4,896,692	4,897,176	484	1	7.333	5.8	12.133	12	7	19	1	2	2	GLYR1, UBN1	569, -978	in gene, upstream	ActReg chr16 #6117	0	0	1
6118	16	4,909,156	4,910,456	1,300	2	11.825	12.55	3.077	18	24	7	0	0	1	UBN1	11,894	in gene	ActReg chr16 #6118	1	1	0
6119	16	4,943,058	4,943,931	873	1	3.308	3.778	12.259	6	7	17	0	0	1	PPL	43,642	in gene	ActReg chr16 #6119	0	0	1
6120	16	4,968,531	4,968,929	398	1	2.385	3.923	10.308	5	7	16	0	0	1	PPL	18,406	in gene	ActReg chr16 #6120	0	0	1
6121	16	4,992,956	4,993,760	804	1	7.615	11.462	5.462	14	16	10	0	1	1	PPL	-6,222	upstream	ActReg chr16 #6121	0	1	0
6122	16	4,994,380	4,995,191	811	1	9.88	10.76	5.56	18	16	9	0	1	1	PPL	-7,649	upstream	ActReg chr16 #6122	0	1	0
6123	16	4,995,648	4,996,133	485	1	12.562	3.875	6.438	21	8	11	0	0	1	PPL	-8,754	upstream	ActReg chr16 #6123	1	0	0
6124	16	5,008,492	5,008,952	460	1	5.643	11.143	11.929	11	14	17	0	1	1	SEC14L5	404	in gene	ActReg chr16 #6124	0	0	1
6125	16	5,075,348	5,075,770	422	1	2.462	1.182	13.769	4	3	19	0	0	3	SEC14L5, NAGPA, LOC100507589	67241, 8383, -8144	downstream, in gene, upstream	ActReg chr16 #6125	0	0	1
6126	16	5,127,254	5,127,648	394	1	1.667	2.077	11.385	2	4	17	0	0	2	ALG1, FAM86A	5641, 20338	in gene, downstream	ActReg chr16 #6126	0	0	1
6127	16	7,484,066	7,484,385	319	1	1	2.4	9.7	1	3	14	0	0	1	A2BP1	1,415,093	in gene	ActReg chr16 #6127	0	0	1
6128	16	8,076,347	8,077,041	694	2	9.1	14.273	1	17	31	1	0	0	0				ActReg chr16 #6128	1	1	0
6129	16	8,241,653	8,242,424	771	2	11.917	11.708	1	20	24	1	0	0	0				ActReg chr16 #6129	1	1	0
6130	16	8,396,142	8,396,810	668	2	9.81	12	1.083	18	26	2	0	0	0				ActReg chr16 #6130	1	1	0
6131	16	8,715,390	8,715,863	473	1	7.533	9.2	10.533	12	12	18	1	1	1	C16orf68	99	in gene	ActReg chr16 #6131	0	0	1
6132	16	8,891,301	8,892,003	702	1	12.591	15.227	4.727	18	27	8	1	2	2	TMEM186, PMM2	-147, -18	upstream, upstream	ActReg chr16 #6132	0	1	0
6133	16	8,958,319	8,958,757	438	1	7.286	7.857	9.714	10	11	16	0	1	2	CARHSP1, LOC100507655	4325, -744	in gene, upstream	ActReg chr16 #6133	0	0	1
6134	16	8,960,257	8,960,947	690	1	3.381	4.105	10.714	7	7	14	0	2	2	CARHSP1, LOC100507655	2261, -2808	in gene, upstream	ActReg chr16 #6134	0	0	1
6135	16	9,025,585	9,026,244	659	2	10.191	10.524	2.85	24	20	6	0	0	1	USP7	31,427	in gene	ActReg chr16 #6135	1	1	0
6136	16	10,275,419	10,276,172	753	1	5.167	6.167	11.5	13	13	18	1	1	1	GRIN2A	816	in gene	ActReg chr16 #6136	0	0	1
6137	16	10,652,668	10,653,178	510	1	9.75	7.812	13.188	14	10	18	0	0	1	EMP2	21,616	in gene	ActReg chr16 #6137	0	0	1
6138	16	10,746,824	10,747,335	511	1	6	6.438	10.75	8	12	16	0	0	1	TEKT5	41,723	in gene	ActReg chr16 #6138	0	0	1
6139	16	10,837,460	10,838,033	573	1	10.056	13	7.056	16	25	10	1	1	1	NUBP1	48	in gene	ActReg chr16 #6139	0	1	0
6140	16	10,862,189	10,862,538	349	1	3.2	4.545	9.455	4	7	13	0	0	2	NUBP1, FAM18A	24665, 50258	in gene, in gene	ActReg chr16 #6140	0	0	1
6141	16	10,921,572	10,922,052	480	1	5.733	6.267	13.867	8	10	23	0	0	1	FAM18A	-9,191	upstream	ActReg chr16 #6141	0	0	1
6142	16	10,972,036	10,973,361	1,325	2	9.756	9.683	7.075	14	20	13	1	1	1	CIITA	1,643	in gene	ActReg chr16 #6142	1	1	0
6143	16	10,988,737	10,989,578	841	1	10.692	8.577	4.308	18	14	8	0	0	1	CIITA	18,102	in gene	ActReg chr16 #6143	1	0	0
6144	16	11,038,005	11,038,751	746	3	13	11.783	9.435	26	22	22	1	2	3	DEXI, LOC100505564, CLEC16A	-2121, 3802, 33	upstream, downstream, in gene	ActReg chr16 #6144	1	1	1
6145	16	11,271,817	11,272,567	750	1	2.957	3.478	10.739	5	6	15	1	0	1	CLEC16A	233,847	in gene	ActReg chr16 #6145	0	0	1
6146	16	11,504,673	11,505,107	434	1	4	4.538	13.308	7	6	20	0	0	1	LOC400499	97,927	in gene	ActReg chr16 #6146	0	0	1
6147	16	11,517,518	11,518,082	564	1	4.611	5.222	13.389	7	10	19	0	0	1	LOC400499	85,017	in gene	ActReg chr16 #6147	0	0	1
6148	16	11,555,885	11,556,425	540	1	1.941	2.706	11.529	3	4	18	0	0	1	LOC400499	46,662	in gene	ActReg chr16 #6148	0	0	1
6149	16	11,620,869	11,621,312	443	1	2.5	1.714	10.857	4	4	17	0	0	0				ActReg chr16 #6149	0	0	1
6150	16	11,890,887	11,891,999	1,112	3	13.941	17.061	11.154	37	48	16	1	0	0				ActReg chr16 #6150	1	1	1
6151	16	12,009,392	12,010,414	1,022	2	11.031	11.031	8	21	18	15	1	1	1	GSPT1	616	in gene	ActReg chr16 #6151	1	1	0
6152	16	12,069,978	12,070,697	719	1	8.652	11.261	8.136	13	15	14	1	1	2	TNFRSF17, RUNDC2A	11373, -265	downstream, upstream	ActReg chr16 #6152	0	1	0
6153	16	12,755,471	12,756,084	613	1	9.421	12.526	3.733	15	22	6	0	0	1	CPPED1	141,967	in gene	ActReg chr16 #6153	0	1	0
6154	16	12,896,998	12,898,185	1,187	3	12.946	17.081	8.568	30	33	19	1	1	1	CPPED1	153	in gene	ActReg chr16 #6154	1	1	1
6155	16	13,130,441	13,130,901	460	1	10.071	7.929	1.571	17	11	2	0	0	1	SHISA9	135,194	in gene	ActReg chr16 #6155	1	0	0
6156	16	13,203,847	13,204,752	905	1	8.679	12.679	2.45	13	21	5	0	0	1	SHISA9	208,822	in gene	ActReg chr16 #6156	0	1	0
6157	16	13,385,589	13,386,290	701	2	9.727	11.091	2.286	15	21	4	0	0	0				ActReg chr16 #6157	1	1	0
6158	16	14,013,828	14,014,333	505	1	10.333	7.867	12.2	13	10	17	1	1	1	ERCC4	66	in gene	ActReg chr16 #6158	0	0	1
6159	16	14,051,122	14,052,107	985	2	11.839	10.516	4.296	19	16	9	0	0	1	ERCC4	37,600	downstream	ActReg chr16 #6159	1	1	0
6160	16	14,164,656	14,165,232	576	2	7.222	11.778	10.235	13	16	20	1	1	1	MKL2	-252	upstream	ActReg chr16 #6160	0	1	1
6161	16	14,379,117	14,380,233	1,116	3	12.2	12.029	10.543	23	27	30	1	0	0				ActReg chr16 #6161	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6162	16	14,493,325	14,493,857	532	1	9.647	7.059	6.294	17	14	9	0	0	0				ActReg chr16 #6162	1	0	0
6163	16	14,595,319	14,595,965	646	1	7.8	13.95	4.5	12	27	7	0	0	1	PARN	128,482	in gene	ActReg chr16 #6163	0	1	0
6164	16	14,605,015	14,605,792	777	1	10.52	7.96	1.389	15	11	2	0	0	1	PARN	118,721	in gene	ActReg chr16 #6164	1	0	0
6165	16	14,726,414	14,727,418	1,004	1	12.097	9.903	7.767	18	16	15	1	2	2	PARN, BFAR	-2792, 248	upstream, in gene	ActReg chr16 #6165	1	0	0
6166	16	15,052,485	15,053,248	763	2	12.458	8.75	2.333	24	16	3	0	0	1	NPIP	21,566	downstream	ActReg chr16 #6166	1	1	0
6167	16	15,149,181	15,149,591	410	1	5.923	8.231	10.923	10	10	16	1	1	2	NTAN1, RRN3	447, 38772	in gene, downstream	ActReg chr16 #6167	0	0	1
6168	16	15,489,438	15,490,221	783	2	11.12	7.88	4.8	19	18	8	1	1	1	MPV17L	218	in gene	ActReg chr16 #6168	1	1	0
6169	16	15,527,991	15,528,633	642	1	7.5	11.65	6.35	15	17	12	1	1	1	C16orf45	-13	upstream	ActReg chr16 #6169	0	1	0
6170	16	15,528,754	15,529,125	371	1	8.583	7.083	11.5	14	11	16	1	1	1	C16orf45	614	in gene	ActReg chr16 #6170	0	0	1
6171	16	15,684,500	15,685,303	803	2	10.6	10.68	2	19	21	4	0	0	2	C16orf45, KIAA0430	156576, 52122	downstream, downstream	ActReg chr16 #6171	1	1	0
6172	16	15,693,346	15,694,125	779	1	10.25	7.458	3.684	16	13	7	0	0	1	KIAA0430	43,288	in gene	ActReg chr16 #6172	1	0	0
6173	16	15,762,869	15,763,219	350	1	1.909	2.727	10.727	3	4	16	0	0	1	NDE1	25,920	in gene	ActReg chr16 #6173	0	0	1
6174	16	15,766,331	15,767,023	692	1	8.591	12.636	2.944	14	20	6	0	0	1	NDE1	29,553	in gene	ActReg chr16 #6174	0	1	0
6175	16	15,981,907	15,982,751	844	2	10.885	9.208	9.154	19	15	17	1	1	1	C16orf83	118	in gene	ActReg chr16 #6175	1	0	1
6176	16	16,326,267	16,326,498	231	1	7.125	11.375	0	10	16	0	1	1	2	ABCC6, NOMO3	-9054, -7	upstream, upstream	ActReg chr16 #6176	0	1	0
6177	16	16,459,200	16,459,462	262	1	2.222	2.667	13.111	3	4	18	1	0	0				ActReg chr16 #6177	0	0	1
6178	16	16,891,120	16,891,689	569	1	10.833	5.833	1.909	17	8	3	0	0	0				ActReg chr16 #6178	1	0	0
6179	16	16,922,480	16,923,413	933	1	9.862	6.483	2.045	14	10	4	0	0	0				ActReg chr16 #6179	1	0	0
6180	16	16,951,865	16,952,346	481	1	10	10.933	2.8	15	15	4	0	0	0				ActReg chr16 #6180	0	1	0
6181	16	17,232,457	17,233,361	904	2	11.929	12.286	3.773	25	22	7	0	0	2	XYLT1, LOC100506171	331829, 4548	in gene, downstream	ActReg chr16 #6181	1	1	0
6182	16	17,243,544	17,244,437	893	2	17.929	22	2.308	49	57	5	0	0	1	XYLT1	320,748	in gene	ActReg chr16 #6182	1	1	0
6183	16	17,259,845	17,260,513	668	1	8.762	14.476	5.571	18	24	7	0	0	1	XYLT1	304,559	in gene	ActReg chr16 #6183	0	1	0
6184	16	17,271,889	17,272,647	758	2	10.292	15.125	5.333	27	30	9	0	0	1	XYLT1	292,470	in gene	ActReg chr16 #6184	1	1	0
6185	16	17,491,222	17,491,743	521	1	5.562	10	3.333	10	17	5	0	0	1	XYLT1	73,256	in gene	ActReg chr16 #6185	0	1	0
6186	16	17,498,775	17,499,764	989	1	12.129	11.194	5.581	18	23	9	0	0	1	XYLT1	65,469	in gene	ActReg chr16 #6186	1	0	0
6187	16	17,877,574	17,878,534	960	2	14.433	11.867	2.407	25	23	5	0	0	0				ActReg chr16 #6187	1	1	0
6188	16	18,133,723	18,134,350	627	1	5.35	10.1	2.833	11	17	6	0	0	0				ActReg chr16 #6188	0	1	0
6189	16	18,801,095	18,802,126	1,031	3	12.875	12.844	10.656	23	22	18	1	1	2	RPS15A, ARL6IP1	46, 11247	in gene, downstream	ActReg chr16 #6189	1	1	1
6190	16	18,812,284	18,813,721	1,437	3	20.911	28.378	10.8	70	85	27	1	1	2	ARL6IP1, SMG1	-145, 124724	upstream, downstream	ActReg chr16 #6190	1	1	1
6191	16	19,078,622	19,079,455	833	2	12	11.615	5.385	20	18	9	1	1	2	TMC7, COQ7	83782, 121	downstream, in gene	ActReg chr16 #6191	1	1	0
6192	16	19,124,723	19,125,542	819	1	8.154	10.654	5.192	12	14	12	1	1	1	ITPRIPL2	-122	upstream	ActReg chr16 #6192	0	1	0
6193	16	19,125,710	19,126,877	1,167	2	8.028	13.111	13.028	13	23	22	1	1	1	ITPRIPL2	1,039	in gene	ActReg chr16 #6193	0	1	1
6194	16	19,178,892	19,179,522	630	1	7.95	10.9	5.429	14	19	9	1	1	1	SYT17	-431	upstream	ActReg chr16 #6194	0	1	0
6195	16	19,179,653	19,180,015	362	1	6.273	10.364	11.454	8	13	16	1	1	1	SYT17	196	in gene	ActReg chr16 #6195	0	0	1
6196	16	19,318,668	19,319,834	1,166	2	17	20.139	2.125	43	45	5	0	0	1	LOC728276	22,146	downstream	ActReg chr16 #6196	1	1	0
6197	16	19,534,958	19,535,480	522	1	6.625	11.688	5.375	11	18	9	1	2	2	GDE1, CPI10	-1769, 40	upstream, in gene	ActReg chr16 #6197	0	1	0
6198	16	19,566,310	19,567,425	1,115	1	7.914	11.886	7.914	15	19	16	1	1	2	CPI10, C16orf62	31688, -173	downstream, upstream	ActReg chr16 #6198	0	1	0
6199	16	19,728,965	19,729,887	922	1	6.643	13.893	8.286	10	23	16	1	2	2	C16orf88, IQCK	66, 1648	in gene, in gene	ActReg chr16 #6199	0	1	0
6200	16	19,894,979	19,895,449	470	1	4.214	4.75	15.429	7	7	28	1	1	1	GPRC5B	937	in gene	ActReg chr16 #6200	0	0	1
6201	16	20,752,796	20,753,474	678	1	8.636	17.409	7	20	37	13	1	1	1	THUMPD1	64	in gene	ActReg chr16 #6201	0	1	0
6202	16	20,817,290	20,818,849	1,559	3	10.918	9.714	8.347	28	18	19	1	2	3	ACSM3, ERI2, LOC81691	42757, -274, 302	downstream, upstream, in gene	ActReg chr16 #6202	1	1	1
6203	16	20,911,876	20,912,654	778	2	8.417	10.75	11.708	15	20	19	1	2	3	DCUN1D3, LOC100506372, LYRM1	-704, 13425, 708	upstream, downstream, in gene	ActReg chr16 #6203	0	1	1
6204	16	21,060,225	21,060,539	314	1	2.889	2.556	9.778	4	5	12	0	0	1	DNAH3	110,380	in gene	ActReg chr16 #6204	0	0	1
6205	16	21,170,692	21,171,052	360	1	1.727	2.909	11	3	6	15	0	2	2	DNAH3, TMEM159	-110, 960	upstream, in gene	ActReg chr16 #6205	0	0	1
6206	16	21,371,327	21,371,629	302	1	3.1	1.625	7.6	5	2	12	0	0	1	RUNDC2B	12,994	in gene	ActReg chr16 #6206	0	0	1
6207	16	21,531,360	21,531,905	545	2	12.056	13.722	8.214	17	29	16	1	0	0				ActReg chr16 #6207	1	1	0
6208	16	21,566,593	21,567,137	544	1	4.059	6.235	10.118	6	10	13	0	0	0				ActReg chr16 #6208	0	0	1
6209	16	21,610,275	21,611,214	939	3	11.759	13.034	7.643	18	28	19	1	1	1	METTL9	-112	upstream	ActReg chr16 #6209	1	1	1
6210	16	21,696,308	21,696,800	492	1	6.688	11.375	4.125	8	18	6	0	0	1	OTOA	6,719	in gene	ActReg chr16 #6210	0	1	0
6211	16	21,964,122	21,965,006	884	2	12.571	13.286	5.857	21	21	16	0	1	1	UCCRC2	-45	upstream	ActReg chr16 #6211	1	1	0
6212	16	22,017,939	22,019,337	1,398	2	10.568	11.182	5.31	18	18	11	1	2	2	C16orf85, C16orf52	-6207, -818	upstream, upstream	ActReg chr16 #6212	1	1	0
6213	16	22,201,077	22,201,916	839	1	7.577	13.654	5.577	12	26	10	1	0	1	LOC100288072	24,592	in gene	ActReg chr16 #6213	0	1	0
6214	16	22,206,818	22,207,325	507	1	10.929	13.533	18	20	22	32	0	0	1	LOC100288072	30,167	downstream	ActReg chr16 #6214	0	0	1
6215	16	22,217,176	22,218,759	1,583	2	10.46	15.32	4.676	18	31	9	1	1	1	EEF2K	375	in gene	ActReg chr16 #6215	1	1	0
6216	16	22,308,160	22,309,925	1,765	3	10.821	12.589	10.25	20	22	33	1	1	2	EEF2K, POLR3E	91450, 301	downstream, in gene	ActReg chr16 #6216	1	1	1
6217	16	22,337,986	22,338,659	673	1	1.952	4.857	13.048	3	7	18	0	0	1	POLR3E	29,581	in gene	ActReg chr16 #6217	0	0	1
6218	16	22,448,144	22,448,549	405	1	9.385	6.538	11.154	16	9	16	1	0	0				ActReg chr16 #6218	0	0	1
6219	16	22,625,016	22,626,437	1,421	2	11.089	12.689	3.25	20	21	6	0	0	0				ActReg chr16 #6219	1	1	0
6220	16	22,651,977	22,653,056	1,079	2	14.059	15.441	3.5	22	29	10	0	0	0				ActReg chr16 #6220	1	1	0
6221	16	22,734,267	22,734,891	624	1	3.5	4.75	13.25	5	7	20	0	0	0				ActReg chr16 #6221	0	0	1
6222	16	22,824,642	22,825,276	634	1	2.789	5.632	11.684	5	7	17	1	1	1	HS3ST2	-901	upstream	ActReg chr16 #6222	0	0	1
6223	16	22,899,977	22,900,591	614	1	4.053	10.263	1.526	7	14	3	0	0	1	HS3ST2	74,424	in gene	ActReg chr16 #6223	0	1	0
6224	16	23,037,910	23,038,709	799	2	11.88	14.76	2.24	29	28	5	0	0	0				ActReg chr16 #6224	1	1	0
6225	16	23,182,731	23,183,318	587	1	4.278	11.333	2.833	6	17	5	0	0	0				ActReg chr16 #6225	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6226	16	23,185,801	23,186,414	613	1	9.842	11.947	3.571	13	18	7	0	0	1	SCNN1G	-7,933	upstream	ActReg chr16 #6226	0	1	0
6227	16	23,194,146	23,194,587	441	1	4.692	1.917	12.769	9	4	17	1	1	1	SCNN1G	326	in gene	ActReg chr16 #6227	0	0	1
6228	16	23,197,206	23,197,709	503	1	3.458	6.312	11.125	8	8	19	1	0	1	SCNN1G	3,417	in gene	ActReg chr16 #6228	0	0	1
6229	16	23,382,671	23,383,192	521	1	2.562	4.25	12.875	4	10	20	0	0	1	SCNN1B	69,340	in gene	ActReg chr16 #6229	0	0	1
6230	16	23,568,208	23,569,120	912	2	11.69	12.579	8.111	23	20	13	1	2	2	EARS2, UBFD1	52, -198	in gene, upstream	ActReg chr16 #6230	1	1	0
6231	16	23,606,906	23,608,179	1,273	2	32.075	30.875	4.156	122	114	8	1	1	2	NDUFAB1, PALB2	97, 45136	in gene, downstream	ActReg chr16 #6231	1	1	0
6232	16	23,652,257	23,653,183	926	2	16.679	21.179	8.786	40	48	18	1	2	2	PALB2, DCTN5	-42, -87	upstream, upstream	ActReg chr16 #6232	1	1	0
6233	16	23,689,695	23,690,965	1,270	3	11.225	21.525	7.9	32	59	24	1	1	3	DCTN5, LOC100506587, PLK1	37523, 8998, 129	downstream, downstream, in gene	ActReg chr16 #6233	1	1	1
6234	16	23,723,960	23,724,360	400	1	1.5	1.917	12.154	2	3	16	1	1	1	ERN2	661	in gene	ActReg chr16 #6234	0	0	1
6235	16	23,766,116	23,766,582	466	1	3.214	2.643	11.357	5	3	14	1	1	1	CHP2	401	in gene	ActReg chr16 #6235	0	0	1
6236	16	23,848,322	23,848,680	358	1	4.091	3.364	9.545	7	5	14	0	1	1	PRKCB	1,201	in gene	ActReg chr16 #6236	0	0	1
6237	16	23,985,489	23,986,117	628	1	6.6	10.8	4.35	14	16	9	0	0	1	PRKCB	138,503	in gene	ActReg chr16 #6237	0	1	0
6238	16	24,189,714	24,190,352	638	1	8.05	10	2.471	15	21	6	0	0	1	PRKCB	342,733	in gene	ActReg chr16 #6238	0	1	0
6239	16	24,266,991	24,267,735	744	2	12.304	14.478	5.565	24	28	8	1	1	1	CACNG3	487	in gene	ActReg chr16 #6239	1	1	0
6240	16	24,550,312	24,551,060	748	1	9.435	12.957	5.435	15	23	9	1	1	1	RBBP6	-222	upstream	ActReg chr16 #6240	0	1	0
6241	16	24,618,404	24,618,730	326	1	2	1.8	11.1	3	3	16	0	0	0				ActReg chr16 #6241	0	0	1
6242	16	24,680,487	24,681,251	764	2	8.792	12.696	3.091	21	24	5	0	1	1	FLJ45256	1,514	in gene	ActReg chr16 #6242	1	1	0
6243	16	24,740,549	24,741,118	569	1	9	10.647	4.333	16	17	7	1	1	1	TNRC6A	-216	upstream	ActReg chr16 #6243	0	1	0
6244	16	24,869,377	24,870,367	990	2	13.633	13.233	3.136	25	29	6	0	0	1	SLC5A11	12,320	in gene	ActReg chr16 #6244	1	1	0
6245	16	25,026,835	25,027,184	349	1	5.364	6.091	13.727	7	11	19	0	1	1	ARHGAP17	-334	upstream	ActReg chr16 #6245	0	0	1
6246	16	25,059,702	25,060,625	923	2	11.483	14.897	2.185	28	37	4	0	0	0				ActReg chr16 #6246	1	1	0
6247	16	25,268,589	25,269,228	639	1	11.15	7.2	3.176	16	11	7	1	1	1	ZKSCAN2	-53	upstream	ActReg chr16 #6247	1	0	0
6248	16	27,214,403	27,215,793	1,390	2	18.116	17.698	7.814	46	63	12	1	1	1	JMJD5	291	in gene	ActReg chr16 #6248	1	1	0
6249	16	27,279,867	27,280,696	829	2	8.962	11.192	8	14	16	15	1	2	2	NSMCE1, FLJ21408	-168, 114	upstream, in gene	ActReg chr16 #6249	0	1	1
6250	16	27,443,501	27,443,955	454	1	8.429	7.643	10.929	12	14	15	0	0	1	IL21R	30,245	in gene	ActReg chr16 #6250	0	0	1
6251	16	27,738,088	27,738,760	672	1	12.143	11	5.905	25	18	15	0	0	1	KIAA0556	176,956	in gene	ActReg chr16 #6251	1	0	0
6252	16	27,806,957	27,808,236	1,279	2	15.35	21.8	3.6	30	55	6	0	0	1	GSG1L	267,234	in gene	ActReg chr16 #6252	1	1	0
6253	16	27,852,454	27,852,908	454	1	3.231	4	12.538	4	7	17	0	0	1	GSG1L	222,134	in gene	ActReg chr16 #6253	0	0	1
6254	16	28,270,183	28,270,677	494	1	3	5.867	14.067	4	9	18	1	0	0				ActReg chr16 #6254	0	0	1
6255	16	28,312,323	28,312,769	446	1	1.5	5.214	10.429	2	9	17	0	0	2	LOC100506705, SBK1	-9161, 8706	upstream, in gene	ActReg chr16 #6255	0	0	1
6256	16	28,314,940	28,315,977	1,037	2	10.219	14.242	5.364	23	28	9	0	0	1	SBK1	11,618	in gene	ActReg chr16 #6256	1	1	0
6257	16	28,503,132	28,503,823	691	1	8	11.454	3.864	17	22	10	1	2	3	CLN3, APOBR48R, IL27	146, -2516, 14678	in gene, upstream, downstream	ActReg chr16 #6257	0	1	0
6258	16	28,833,763	28,834,259	496	2	9.467	11.467	13	15	16	19	1	1	1	ATXN2L	-403	upstream	ActReg chr16 #6258	0	1	1
6259	16	28,835,208	28,835,887	679	1	9.048	13.762	8.667	13	23	16	1	1	1	ATXN2L	1,133	in gene	ActReg chr16 #6259	0	1	0
6260	16	28,846,491	28,847,288	797	1	3.88	5.92	11.16	7	11	18	0	0	2	ATXN2L, TUFM	12475, 10840	in gene, downstream	ActReg chr16 #6260	0	0	1
6261	16	28,857,051	28,858,232	1,181	2	10.189	14	8.943	24	30	16	1	1	2	ATXN2L, TUFM	23227, 88	downstream, in gene	ActReg chr16 #6261	1	1	0
6262	16	28,874,481	28,875,273	792	1	10.88	12.32	6.48	17	19	14	1	1	1	SH2B1	-201	upstream	ActReg chr16 #6262	0	1	0
6263	16	28,891,314	28,891,742	428	1	7.923	7	12.923	10	8	19	1	2	3	SH2B1, ATP2A1, LOC100289092	16450, 1719, -287	downstream, in gene, upstream	ActReg chr16 #6263	0	0	1
6264	16	28,915,808	28,916,585	777	1	2.28	5.92	11.24	4	11	20	0	0	2	ATP2A1, RABEP2	26387, 20336	downstream, in gene	ActReg chr16 #6264	0	0	1
6265	16	28,916,926	28,917,572	646	1	3.571	4	12.667	6	6	19	0	0	2	ATP2A1, RABEP2	27440, 19283	downstream, in gene	ActReg chr16 #6265	0	0	1
6266	16	28,936,707	28,937,068	361	1	9.091	4	12.818	11	6	18	1	2	2	RABEP2, CD19	-355, -6373	upstream, upstream	ActReg chr16 #6266	0	0	1
6267	16	28,985,731	28,986,546	815	1	12.76	17.08	9.24	22	32	12	1	1	3	NFATC2IP, SPNS1, LAT	23820, 42, -10009	downstream, in gene, upstream	ActReg chr16 #6267	0	1	0
6268	16	29,301,768	29,302,499	731	1	8.826	11.217	4.348	14	18	7	0	0	0				ActReg chr16 #6268	0	1	0
6269	16	29,624,595	29,625,071	476	2	10.2	10	5.667	14	15	11	1	0	0				ActReg chr16 #6269	1	1	0
6270	16	29,801,273	29,802,710	1,437	3	8.6	12.044	12.889	16	19	24	1	1	2	ZG16, KIF22	12430, -67	downstream, upstream	ActReg chr16 #6270	1	1	1
6271	16	29,816,411	29,817,177	766	2	9.917	12.417	12.5	18	21	20	1	2	3	KIF22, MAZ, PRRT2	14736, -1061, -6615	downstream, upstream, upstream	ActReg chr16 #6271	0	1	1
6272	16	29,818,609	29,819,770	1,161	1	10.278	12.861	9.583	15	20	16	1	2	4	KIF22, MAZ, PRRT2, C16orf53	17131, 1334, -4220, -8339	downstream, in gene, upstream, upstream	ActReg chr16 #6272	0	1	0
6273	16	29,821,195	29,822,080	885	1	9.857	8.214	5.571	14	14	12	0	2	5	KIF22, MAZ, PRRT2, C16orf53, MVP	19579, 3782, -1772, -5891, -10150	downstream, in gene, upstream, upstream, upstream	ActReg chr16 #6273	1	0	0
6274	16	29,822,286	29,823,403	1,117	1	10.143	11.943	6.714	22	17	11	1	2	5	KIF22, MAZ, PRRT2, C16orf53, MVP	20786, 4989, -565, -4684, -8943	downstream, downstream, upstream, upstream, upstream	ActReg chr16 #6274	0	1	0
6275	16	29,827,045	29,827,681	636	1	10.65	12.6	6	17	19	9	1	2	4	MAZ, PRRT2, C16orf53, MVP	9508, 3954, -165, -4424	downstream, downstream, upstream, upstream	ActReg chr16 #6275	0	1	0
6276	16	29,855,896	29,856,399	503	1	4.562	3.438	12.938	6	6	20	1	0	1	MVP	24,360	in gene	ActReg chr16 #6276	0	0	1
6277	16	29,873,782	29,875,310	1,528	2	22.708	28.917	4.277	61	76	10	1	2	3	CDIPT, LOC440356, SEZ6L2	52, -458, 36034	in gene, upstream, downstream	ActReg chr16 #6277	1	1	0
6278	16	29,888,374	29,888,813	439	1	3.357	2.583	12.143	5	4	18	1	0	2	LOC440356, SEZ6L2	13589, 21987	downstream, in gene	ActReg chr16 #6278	0	0	1
6279	16	29,910,834	29,912,145	1,311	1	6.1	11.22	5.073	14	21	10	1	2	3	SEZ6L2, ASPHD1, KCTD13	-909, -658, 26056	upstream, upstream, downstream	ActReg chr16 #6279	0	1	0
6280	16	29,912,485	29,913,133	648	1	4.6	6.8	12.65	7	12	15	1	2	3	SEZ6L2, ASPHD1, KCTD13	-2229, 662, 24736	upstream, in gene, downstream	ActReg chr16 #6280	0	0	1
6281	16	29,937,323	29,938,441	1,118	2	6.486	9.6	7.412	10	18	16	1	1	1	KCTD13	-337	upstream	ActReg chr16 #6281	0	1	1
6282	16	29,999,069	29,999,589	520	1	3.933	4.118	12.765	5	6	18	1	0	3	TAOK2, HIRIP3, INO80E	14107, 8083, -8202	in gene, downstream, upstream	ActReg chr16 #6282	0	0	1
6283	16	30,006,413	30,008,030	1,617	2	9.56	12.46	9.62	21	18	18	1	2	4	TAOK2, HIRIP3, INO80E, DOC2A	21999, 191, -310, 15180	downstream, in gene, upstream, downstream	ActReg chr16 #6283	1	1	0
6284	16	30,014,929	30,015,397	468	1	4.2	3.267	11.133	6	6	18	0	0	3	HIRIP3, INO80E, DOC2A	-7751, 7632, 7238	upstream, in gene, downstream	ActReg chr16 #6284	0	0	1
6285	16	30,036,408	30,037,022	614	1	5	5.368	12.158	9	8	16	0	1	2	C16orf92, FAM57B	2060, 5471	downstream, in gene	ActReg chr16 #6285	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6286	16	30,075,310	30,075,893	583	1	5.167	7.222	10.5	8	10	13	0	0	1	ALDOA	11,110	in gene	ActReg chr16 #6286	0	0	1
6287	16	30,076,196	30,077,354	1,158	2	12.222	11.056	8.389	24	18	12	1	0	1	ALDOA	12,284	in gene	ActReg chr16 #6287	1	1	0
6288	16	30,102,066	30,104,233	2,167	3	8.358	10.823	9.746	23	33	16	1	3	5	PPP4C, TBX6, YPEL3, LOC100271831, LOC100506914	15764, 56, 4388, -1916, -4602	downstream, in gene, downstream, upstream, upstream	ActReg chr16 #6288	1	1	1
6289	16	30,107,766	30,108,169	403	1	5.692	7.308	10.846	8	12	17	1	3	5	TBX6, YPEL3, LOC100271831, LOC100506914, GDPD3	-4762, -430, 2902, 216, 16911	upstream, upstream, in gene, in gene, downstream	ActReg chr16 #6289	0	0	1
6290	16	30,133,633	30,134,013	380	1	4.545	4.727	12.273	7	8	18	0	1	3	LOC100271831, GDPD3, MAPK3	28758, -8945, 807	downstream, upstream, in gene	ActReg chr16 #6290	0	0	1
6291	16	30,199,345	30,199,679	334	1	5.3	4.2	11.7	7	5	16	0	2	4	CORO1A, BOLA2B, GIYD1, SULT1A3	4781, 6115, -5705, -6231	in gene, downstream, upstream, upstream	ActReg chr16 #6291	0	0	1
6292	16	30,366,278	30,367,526	1,248	2	11.692	11.205	6.641	20	19	14	1	1	2	CD2BP2, TBC1D10B	-220, 14620	upstream, downstream	ActReg chr16 #6292	1	1	0
6293	16	30,370,440	30,371,036	596	1	3.611	3.667	12.111	8	5	20	0	1	2	CD2BP2, TBC1D10B	-4056, 10784	upstream, in gene	ActReg chr16 #6293	0	0	1
6294	16	30,389,185	30,390,272	1,087	2	5.903	10.118	9.882	12	25	16	1	0	3	TBC1D10B, MYLPF, SEPT1	-8206, 3605, 4443	upstream, downstream, in gene	ActReg chr16 #6294	0	1	1
6295	16	30,429,562	30,430,141	579	1	6.222	9.5	12.556	12	18	18	1	0	2	ZNF771, DCTPP1	11116, 11522	in gene, downstream	ActReg chr16 #6295	0	0	1
6296	16	30,440,945	30,441,543	598	1	10.053	10.368	9.263	13	16	13	1	1	1	DCTPP1	129	in gene	ActReg chr16 #6296	0	1	0
6297	16	30,456,454	30,457,209	755	1	10.826	13.652	9.174	19	21	14	1	1	1	SEPHS2	393	in gene	ActReg chr16 #6297	0	1	0
6298	16	30,485,376	30,485,685	309	1	1.75	1.7	11.3	2	2	15	1	1	1	ITGAL	1,547	in gene	ActReg chr16 #6298	0	0	1
6299	16	30,538,117	30,538,835	718	1	12.773	12.091	12.409	18	19	17	1	2	5	ITGAL, ZNF768, LOC100506960, ZNF747, LOC100506973	-54493, -566, 329, 7718, -7915	downstream, upstream, in gene, downstream, upstream	ActReg chr16 #6299	0	0	1
6300	16	30,546,343	30,547,003	660	1	4.1	12.2	5.2	7	17	7	1	2	4	ZNF768, LOC100506960, ZNF747, LOC100506973	-8763, 8526, -479, 282	upstream, downstream, upstream, in gene	ActReg chr16 #6300	0	1	0
6301	16	30,547,102	30,547,461	359	1	4.5	3.5	10.083	6	6	16	0	2	4	ZNF768, LOC100506960, ZNF747, LOC100506973	-9371, 9134, -1087, 890	upstream, downstream, upstream, in gene	ActReg chr16 #6301	0	0	1
6302	16	30,569,054	30,569,913	859	1	8.074	10.556	8.148	13	19	13	1	1	1	ZNF764	159	in gene	ActReg chr16 #6302	0	1	0
6303	16	30,581,234	30,581,661	427	1	6.615	3.077	13.846	8	4	22	1	1	1	ZNF688	2,281	in gene	ActReg chr16 #6303	0	0	1
6304	16	30,620,982	30,622,186	1,204	2	10.737	14.579	7.556	22	29	11	1	1	1	ZNF689	98	in gene	ActReg chr16 #6304	1	1	0
6305	16	30,661,499	30,662,424	925	2	12.552	12.759	4.148	24	25	10	1	1	2	PRR14, LOC100506988	-280, -9026	upstream, upstream	ActReg chr16 #6305	1	1	0
6306	16	30,669,010	30,670,913	1,903	2	20.667	17.267	7.286	37	35	16	1	2	3	PRR14, LOC100506988, FBRS	7720, -1026, -5817	downstream, upstream, upstream	ActReg chr16 #6306	1	1	0
6307	16	30,678,278	30,679,161	883	1	2.704	2.68	9.963	5	4	14	0	0	2	LOC100506988, FBRS	7732, 2941	downstream, in gene	ActReg chr16 #6307	0	0	1
6308	16	30,709,188	30,710,338	1,150	2	10.583	11.528	7.861	18	20	16	1	2	2	LOC730183, SRCAP	47, -699	in gene, upstream	ActReg chr16 #6308	0	1	1
6309	16	30,759,187	30,759,694	507	1	8.5	9	11.625	14	14	20	1	1	3	SRCAP, PHKG2, C16orf93	48978, -180, 14102	downstream, upstream, downstream	ActReg chr16 #6309	0	0	1
6310	16	30,772,634	30,773,215	581	1	7.778	10.056	12.611	13	12	19	1	2	3	PHKG2, C16orf93, RNF40	13304, 618, -706	downstream, in gene, upstream	ActReg chr16 #6310	0	0	1
6311	16	30,786,538	30,787,769	1,231	3	10.46	13.053	9.474	19	23	19	1	0	2	RNF40, ZNF629	13523, 11370	downstream, downstream	ActReg chr16 #6311	1	1	1
6312	16	30,798,341	30,798,915	574	1	6.611	12	9.111	9	19	13	1	1	1	ZNF629	-105	upstream	ActReg chr16 #6312	0	1	0
6313	16	30,816,655	30,816,994	339	1	10.546	8.727	12.091	13	10	15	1	0	0				ActReg chr16 #6313	0	0	1
6314	16	30,817,018	30,817,334	316	1	5.6	5.6	9.8	10	9	12	1	0	0				ActReg chr16 #6314	0	0	1
6315	16	30,885,942	30,887,082	1,140	3	13.583	11.914	12.778	23	26	26	1	0	0				ActReg chr16 #6315	1	1	1
6316	16	30,905,502	30,906,104	602	2	11.474	15.632	7.158	22	28	13	1	3	3	BCL7C, MIR762, CTF1	-404, 579, -2125	upstream, downstream, upstream	ActReg chr16 #6316	1	1	0
6317	16	30,932,599	30,932,932	333	1	3.273	3.273	10.454	5	8	15	0	2	2	NCRNA00095, FBXL19	1825, -3131	in gene, upstream	ActReg chr16 #6317	0	0	1
6318	16	30,932,941	30,934,924	1,983	2	11.29	13.581	5.694	30	27	9	1	2	2	NCRNA00095, FBXL19	658, -1964	in gene, upstream	ActReg chr16 #6318	1	1	0
6319	16	30,968,193	30,969,521	1,328	3	13.195	16.78	6.308	36	45	15	1	1	3	FBXL19, ORAI3, SETD1A	32961, 8452, 242	downstream, downstream, in gene	ActReg chr16 #6319	1	1	1
6320	16	30,969,854	30,970,315	461	1	3.4	4.4	10.133	6	8	16	1	1	3	FBXL19, ORAI3, SETD1A	34188, 9679, 1469	downstream, downstream, in gene	ActReg chr16 #6320	0	0	1
6321	16	30,996,387	30,997,008	621	1	6.526	3.684	11.263	14	9	15	0	1	3	SETD1A, HSD3B7, STX1B	28082, 178, 25132	downstream, in gene, downstream	ActReg chr16 #6321	0	0	1
6322	16	31,044,185	31,045,013	828	1	12.154	8.423	10.115	20	17	15	1	1	1	STX4	-304	upstream	ActReg chr16 #6322	1	0	0
6323	16	31,072,759	31,073,283	524	1	4.692	4.294	12.588	9	7	17	1	0	1	ZNF668	12,620	in gene	ActReg chr16 #6323	0	0	1
6324	16	31,084,170	31,086,049	1,879	3	18.271	24.237	8.153	41	53	19	1	2	3	ZNF668, ZNF646, POL3S	-532, -634, 15021	in gene, upstream, downstream	ActReg chr16 #6324	1	1	1
6325	16	31,119,353	31,120,294	941	2	7.433	8.467	11.9	14	21	20	1	1	3	BCKDK, MYST1, LOC100507092	161, -9162, -9458	in gene, upstream, upstream	ActReg chr16 #6325	0	1	1
6326	16	31,190,808	31,192,100	1,292	3	12.488	16.073	16.122	20	37	28	1	1	1	FUS	23	in gene	ActReg chr16 #6326	1	1	1
6327	16	31,227,665	31,228,361	696	1	4.545	6.316	13.636	6	15	22	1	2	2	TRIM72, PYDC1	2671, 385	in gene, in gene	ActReg chr16 #6327	0	0	1
6328	16	31,453,967	31,454,832	865	1	11.148	13.444	8.259	17	26	12	1	1	2	LOC100507110, ZNF843	11001, -51	in gene, upstream	ActReg chr16 #6328	0	1	0
6329	16	31,470,117	31,471,368	1,251	3	10.846	9.949	14.128	18	20	31	1	2	2	LOC100507110, ARMC5	-5342, 425	upstream, in gene	ActReg chr16 #6329	1	1	1
6330	16	31,477,588	31,478,276	688	1	2.571	4.167	11.954	5	7	18	0	1	2	ARMC5, TGFB1I1	7615, -5544	in gene, upstream	ActReg chr16 #6330	0	0	1
6331	16	31,519,313	31,520,155	842	2	9.231	14.538	12.292	14	27	19	1	1	1	C16orf58	-28	upstream	ActReg chr16 #6331	0	1	1
6332	16	31,724,428	31,724,885	457	1	6.429	7.214	11.214	11	9	18	1	1	2	C16orf67, ZNF720	12722, 106	downstream, in gene	ActReg chr16 #6332	0	0	1
6333	16	31,885,134	31,885,559	425	1	8.385	9.923	11.231	11	12	17	1	1	1	ZNF267	267	in gene	ActReg chr16 #6333	0	0	1
6334	16	32,096,853	32,097,145	292	1	2.667	3	9.111	4	4	11	1	0	0				ActReg chr16 #6334	0	0	1
6335	16	32,489,718	32,490,031	313	1	1.7	1.5	10.3	3	2	14	1	0	0				ActReg chr16 #6335	0	0	1
6336	16	32,648,844	32,649,850	1,006	1	4.323	4.806	12.323	8	8	18	0	0	0				ActReg chr16 #6336	0	0	1
6337	16	32,823,056	32,823,354	298	1	6	2.222	9.444	7	4	13	1	0	0				ActReg chr16 #6337	0	0	1
6338	16	33,040,099	33,040,396	297	1	1	3.111	9.889	1	5	13	1	0	0				ActReg chr16 #6338	0	0	1
6339	16	33,351,268	33,351,553	285	1	2.111	4	12.333	3	5	16	0	0	0				ActReg chr16 #6339	0	0	1
6340	16	33,483,085	33,483,501	416	1	1.857	5.846	11.846	3	9	19	1	0	0				ActReg chr16 #6340	0	0	1
6341	16	33,569,290	33,570,285	995	1	6.484	8.71	12.742	9	12	20	0	1	1	LOC401847	103	in gene	ActReg chr16 #6341	0	0	1
6342	16	33,626,876	33,627,591	715	1	4.091	5	12.043	7	10	16	0	0	0				ActReg chr16 #6342	0	0	1
6343	16	34,489,750	34,490,207	457	1	6.143	10.571	12.714	9	14	21	0	0	0				ActReg chr16 #6343	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6344	16	34,545,715	34,546,146	431	1	3.077	3.571	10.286	5	5	16	0	0	0				ActReg chr16 #6344	0	0	1
6345	16	34,578,705	34,578,978	273	1	1.571	4.111	9.667	3	5	13	0	0	0				ActReg chr16 #6345	0	0	1
6346	16	34,586,672	34,587,168	496	2	6.062	10.375	7.625	9	19	13	1	0	0				ActReg chr16 #6346	0	1	1
6347	16	34,741,517	34,741,849	332	1	5	3.1	11.1	8	6	14	1	1	1	LOC100130700	-843	upstream	ActReg chr16 #6347	0	0	1
6348	16	34,969,077	34,969,375	298	1	2.889	1.4	9.556	4	2	13	0	0	0				ActReg chr16 #6348	0	0	1
6349	16	46,462,307	46,462,721	414	1	1	1.364	11.231	1	2	16	1	0	0				ActReg chr16 #6349	0	0	1
6350	16	46,654,984	46,655,442	458	1	8.429	9.929	13.643	12	13	23	1	1	1	SHCBP1	98	in gene	ActReg chr16 #6350	0	0	1
6351	16	46,666,917	46,667,463	546	1	4.176	4.4	10.059	8	8	14	0	0	0				ActReg chr16 #6351	0	0	1
6352	16	46,723,182	46,724,480	1,298	1	6.707	12.878	5.976	11	23	13	1	2	2	VPS35, ORC6L	-687, 273	upstream, in gene	ActReg chr16 #6352	0	1	0
6353	16	46,823,853	46,824,457	604	3	10.21	10.632	9.316	19	19	19	1	0	0				ActReg chr16 #6353	1	1	1
6354	16	46,917,579	46,918,475	896	2	9	13.464	8.16	16	23	16	1	1	1	GPT2	-281	upstream	ActReg chr16 #6354	1	1	0
6355	16	47,077,118	47,077,559	441	1	4.643	2	10.929	8	3	19	0	0	0				ActReg chr16 #6355	0	0	1
6356	16	47,089,160	47,089,679	519	1	4.214	6.125	13.938	8	8	22	0	0	0				ActReg chr16 #6356	0	0	1
6357	16	47,494,509	47,495,548	1,039	1	8.969	11.281	5.333	13	15	11	1	2	2	ITFG1, PHKB	-10, -182	upstream, upstream	ActReg chr16 #6357	0	1	0
6358	16	47,821,520	47,822,089	569	1	9.889	5.222	3.111	18	10	4	0	0	0				ActReg chr16 #6358	1	0	0
6359	16	48,004,007	48,004,664	657	2	10.1	14.75	1.5	19	32	2	0	0	0				ActReg chr16 #6359	1	1	0
6360	16	48,047,289	48,047,895	606	1	9.474	12.526	4.692	13	21	9	0	0	0				ActReg chr16 #6360	0	1	0
6361	16	48,115,408	48,116,462	1,054	1	7.636	10.546	5.062	15	20	11	0	0	1	ABCC12	64,746	downstream	ActReg chr16 #6361	0	1	0
6362	16	48,149,193	48,149,676	483	1	3	1.857	12.4	5	4	17	0	0	1	ABCC12	31,247	in gene	ActReg chr16 #6362	0	0	1
6363	16	48,156,817	48,157,637	820	1	9.731	14.808	3.962	19	29	14	0	0	1	ABCC12	23,454	in gene	ActReg chr16 #6363	0	1	0
6364	16	48,160,674	48,161,429	755	1	11.913	9.652	4.783	20	15	8	0	0	1	ABCC12	19,630	in gene	ActReg chr16 #6364	1	0	0
6365	16	48,277,869	48,278,680	811	2	12.76	17	5.652	23	29	11	1	1	2	ABCC11, LONP2	-9186, 63	upstream, in gene	ActReg chr16 #6365	1	1	0
6366	16	48,478,475	48,479,498	1,023	2	9.433	12.094	3.31	25	25	8	0	0	0				ActReg chr16 #6366	1	1	0
6367	16	48,952,288	48,953,015	727	1	8.261	12.696	3.565	14	19	6	0	0	0				ActReg chr16 #6367	0	1	0
6368	16	49,160,983	49,161,471	488	1	9.133	11.467	1.8	13	20	3	0	0	0				ActReg chr16 #6368	0	1	0
6369	16	49,191,675	49,192,539	864	2	23.926	25.296	3.167	62	70	6	0	0	0				ActReg chr16 #6369	1	1	0
6370	16	49,635,479	49,635,968	489	1	2.312	5.688	10.812	4	9	17	0	0	1	ZNF423	225,195	in gene	ActReg chr16 #6370	0	0	1
6371	16	49,665,490	49,665,809	319	1	1.556	2	12.9	3	3	17	0	0	1	ZNF423	195,269	in gene	ActReg chr16 #6371	0	0	1
6372	16	49,869,571	49,870,130	559	1	1.917	1.882	10.823	3	3	13	0	0	1	ZNF423	-8,932	upstream	ActReg chr16 #6372	0	0	1
6373	16	49,892,642	49,893,025	383	1	2.333	4.083	11.5	4	6	17	1	0	0				ActReg chr16 #6373	0	0	1
6374	16	50,058,615	50,059,631	1,016	2	24.125	23.781	5.906	69	66	13	1	1	1	TMEM188	-66	upstream	ActReg chr16 #6374	1	1	0
6375	16	50,186,522	50,187,067	545	2	10.882	10.647	6.294	18	17	10	0	2	2	LOC100505488, PAPD5	173, -35	in gene, upstream	ActReg chr16 #6375	1	1	0
6376	16	50,279,448	50,279,874	426	1	6.077	5.833	10.429	10	9	19	1	0	0				ActReg chr16 #6376	0	0	1
6377	16	50,325,552	50,326,196	644	1	2.25	4.3	11.35	6	6	14	0	0	1	ADCY7	4,051	in gene	ActReg chr16 #6377	0	0	1
6378	16	50,331,336	50,332,034	698	1	5.318	3.773	12.864	10	6	20	0	0	1	ADCY7	9,862	in gene	ActReg chr16 #6378	0	0	1
6379	16	50,582,972	50,583,325	353	1	5.667	4	11.364	8	8	16	1	1	1	NKD1	907	in gene	ActReg chr16 #6379	0	0	1
6380	16	50,840,147	50,840,707	560	1	10.111	10.833	2.667	14	17	4	0	0	1	CYLD	64,466	downstream	ActReg chr16 #6380	0	1	0
6381	16	51,197,904	51,198,671	767	1	13.667	11	4.625	25	20	11	0	0	0				ActReg chr16 #6381	1	0	0
6382	16	51,534,097	51,534,680	583	1	8.5	10.111	1	17	19	1	0	0	0				ActReg chr16 #6382	0	1	0
6383	16	51,670,569	51,671,411	842	2	12.308	11.5	2.64	18	20	6	0	0	0				ActReg chr16 #6383	1	1	0
6384	16	51,914,493	51,915,128	635	1	4.95	10.75	1.5	11	18	3	0	0	0				ActReg chr16 #6384	0	1	0
6385	16	52,513,845	52,514,285	440	1	3.385	4.214	9.714	6	5	14	0	0	1	TOX3	67,649	in gene	ActReg chr16 #6385	0	0	1
6386	16	52,692,091	52,692,500	409	1	2.154	1.923	11.615	3	4	15	0	0	0				ActReg chr16 #6386	0	0	1
6387	16	52,765,221	52,765,830	609	1	3.263	2.895	11.842	5	4	16	0	0	0				ActReg chr16 #6387	0	0	1
6388	16	53,088,467	53,089,053	586	2	6.889	10.167	13.889	12	17	22	1	1	1	CHD9	-185	upstream	ActReg chr16 #6388	0	1	1
6389	16	53,132,778	53,133,317	539	1	10.882	8.706	3.625	15	15	6	0	0	1	CHD9	44,102	in gene	ActReg chr16 #6389	1	0	0
6390	16	53,164,463	53,165,057	594	1	7.368	12.263	3.909	11	19	5	1	0	1	CHD9	75,815	in gene	ActReg chr16 #6390	0	1	0
6391	16	53,165,455	53,166,006	551	1	8.941	10.765	6.706	16	18	12	1	0	1	CHD9	76,785	in gene	ActReg chr16 #6391	0	1	0
6392	16	53,407,345	53,407,780	435	1	2.643	4.929	11.071	5	8	17	1	1	1	LOC643802	-2,661	upstream	ActReg chr16 #6392	0	0	1
6393	16	53,468,069	53,469,186	1,117	2	10.371	12.486	5.818	22	18	13	1	1	1	RBL2	276	in gene	ActReg chr16 #6393	1	1	0
6394	16	53,537,202	53,537,948	746	1	11.391	8.391	6.048	16	18	14	1	1	1	AKTIP	-405	upstream	ActReg chr16 #6394	1	0	0
6395	16	53,737,402	53,738,410	1,008	1	8.219	12.438	4.812	17	23	11	1	2	2	RPGRIP1L, FTO	-135, 31	upstream, in gene	ActReg chr16 #6395	0	1	0
6396	16	54,114,280	54,114,969	689	2	11.667	11.095	1.294	17	18	2	0	0	1	FTO	376,749	in gene	ActReg chr16 #6396	1	1	0
6397	16	54,319,200	54,319,854	654	1	6.476	11.714	7.389	11	19	11	1	1	1	IRX3	851	in gene	ActReg chr16 #6397	0	1	0
6398	16	54,320,866	54,321,410	544	2	9.765	5.118	10.588	14	7	15	1	1	1	IRX3	-760	upstream	ActReg chr16 #6398	1	0	1
6399	16	54,342,025	54,342,358	333	1	3.7	1.111	11.8	4	2	17	0	0	0				ActReg chr16 #6399	0	0	1
6400	16	54,407,435	54,408,244	809	1	10.32	11.2	4.261	15	15	7	0	0	0				ActReg chr16 #6400	0	1	0
6401	16	55,452,279	55,452,969	690	1	7.318	10.727	2.053	13	17	5	0	0	0				ActReg chr16 #6401	0	1	0
6402	16	55,513,335	55,513,721	386	1	3.75	9.917	11.583	7	14	20	1	1	1	MMP2	447	in gene	ActReg chr16 #6402	0	0	1
6403	16	55,572,820	55,573,259	439	1	10.857	4	0	18	5	0	0	0	1	LPCAT2	30,126	in gene	ActReg chr16 #6403	1	0	0
6404	16	56,047,614	56,048,557	943	2	21.633	22.533	1.412	63	60	2	0	0	0				ActReg chr16 #6404	1	1	0
6405	16	56,384,319	56,384,880	561	1	1.5	2.944	10.5	2	5	13	0	0	1	GNAO1	159,348	in gene	ActReg chr16 #6405	0	0	1
6406	16	56,387,213	56,387,778	565	1	3.389	5.167	13.722	5	9	22	0	0	2	GNAO1, AMFR	162244, 71949	in gene, downstream	ActReg chr16 #6406	0	0	1
6407	16	56,484,816	56,485,690	874	1	9.852	10.407	7.222	14	14	15	1	2	2	NUDT21, OGFOD1	8, -171	in gene, upstream	ActReg chr16 #6407	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6408	16	56,553,434	56,554,083	649	1	7.857	9.381	11.905	14	13	16	1	1	1	BBS2	250	in gene	ActReg chr16 #6408	0	0	1
6409	16	56,623,265	56,623,964	699	1	5.714	4.4	11.809	11	10	17	1	1	1	MT3	347	in gene	ActReg chr16 #6409	0	0	1
6410	16	56,640,926	56,641,675	749	1	8.125	11.042	3.792	12	17	7	0	1	1	MT2A	-1,178	upstream	ActReg chr16 #6410	0	1	0
6411	16	56,641,900	56,642,838	938	1	8.69	13.586	7.897	15	24	14	1	1	1	MT2A	-109	upstream	ActReg chr16 #6411	0	1	0
6412	16	56,681,713	56,682,220	507	1	2.5	2.938	14.25	4	4	22	0	1	3	MT1A, MT1B, MT1F	9388, -3845, -9889	downstream, upstream, upstream	ActReg chr16 #6412	0	0	1
6413	16	56,696,810	56,697,191	381	1	1	3.125	10.333	1	5	15	1	1	4	MT1B, MT1F, MT1G, MT1H	11189, 5145, 4977, -6726	downstream, downstream, downstream, upstream	ActReg chr16 #6413	0	0	1
6414	16	56,763,956	56,764,497	541	2	11.118	10.412	12.059	18	14	18	1	2	2	LOC100505742, NUP93	-246, 209	upstream, in gene	ActReg chr16 #6414	1	0	1
6415	16	56,965,867	56,966,488	621	1	10.526	13.579	13.421	16	22	17	1	1	1	HERPUD1	429	in gene	ActReg chr16 #6415	0	0	1
6416	16	57,034,127	57,034,847	720	1	12.727	9.5	5.955	21	11	17	0	0	1	NLRC5	11,077	in gene	ActReg chr16 #6416	1	0	0
6417	16	57,278,449	57,279,351	902	2	13.429	12.893	6.833	29	25	14	1	1	2	RSPRY1, ARL2BP	58659, -138	downstream, upstream	ActReg chr16 #6417	1	1	0
6418	16	57,334,121	57,335,005	884	2	8.926	16.482	13.889	14	32	29	0	0	0				ActReg chr16 #6418	0	1	1
6419	16	57,406,236	57,406,906	670	1	5.857	5.714	12.619	12	10	18	0	1	2	CCL22, CX3CL1	13876, 157	downstream, in gene	ActReg chr16 #6419	0	0	1
6420	16	57,481,158	57,481,861	703	2	11.5	11.773	7.682	20	17	14	1	2	2	CIAPIN1, COQ9	-140, 160	upstream, in gene	ActReg chr16 #6420	1	1	0
6421	16	57,496,138	57,496,979	841	3	25.154	26.923	9.545	72	80	20	1	1	3	COQ9, POLR2C, DOK4	15209, 7, 23827	downstream, in gene, downstream	ActReg chr16 #6421	1	1	1
6422	16	57,650,160	57,650,561	401	1	5.308	3.154	10.538	8	4	16	0	1	1	GPR56	-3,550	upstream	ActReg chr16 #6422	0	0	1
6423	16	57,657,316	57,658,133	817	1	7.44	13.96	3.36	14	26	8	0	0	1	GPR56	3,814	in gene	ActReg chr16 #6423	0	1	0
6424	16	57,661,936	57,662,548	612	1	10.421	7.842	11.105	17	15	14	0	0	1	GPR56	8,332	in gene	ActReg chr16 #6424	0	0	1
6425	16	57,667,778	57,668,705	927	1	11.862	10.517	6.414	19	18	11	0	0	1	GPR56	14,331	in gene	ActReg chr16 #6425	1	0	0
6426	16	57,796,367	57,797,029	662	1	5.333	4.81	11.905	8	7	18	0	0	2	KATNB1, KIFC3	27038, 39741	downstream, in gene	ActReg chr16 #6426	0	0	1
6427	16	57,809,436	57,809,849	413	1	2.692	7.769	11	5	12	17	0	0	1	KIFC3	26,797	in gene	ActReg chr16 #6427	0	0	1
6428	16	57,836,348	57,837,400	1,052	1	7.364	14.515	6.276	16	24	10	1	2	2	KIFC3, LOC388282	-435, -7675	upstream, upstream	ActReg chr16 #6428	0	1	0
6429	16	58,060,311	58,061,496	1,185	1	7.892	7.784	12.838	14	16	18	1	1	2	C16orf57, MMP15	25598, 1621	downstream, in gene	ActReg chr16 #6429	0	0	1
6430	16	58,118,482	58,118,979	497	1	3.188	3.25	10.375	6	5	19	0	0	0				ActReg chr16 #6430	0	0	1
6431	16	58,162,984	58,163,813	829	1	8.769	14.269	10	15	23	13	1	1	1	C16orf80	-102	upstream	ActReg chr16 #6431	0	1	0
6432	16	58,231,888	58,232,395	507	2	13.812	16.938	6.625	26	28	9	0	1	1	CSNK2A2	-359	upstream	ActReg chr16 #6432	1	1	0
6433	16	58,425,852	58,427,057	1,205	2	17.368	26.579	7.158	51	74	16	1	1	1	GINS3	156	in gene	ActReg chr16 #6433	1	1	0
6434	16	58,534,961	58,535,791	830	1	5.077	5.846	11.885	8	10	19	1	1	2	NDRG4, LOC100505804	37827, 1329	in gene, in gene	ActReg chr16 #6434	0	0	1
6435	16	58,548,951	58,549,909	958	2	10	11.633	8.867	17	22	17	1	1	3	NDRG4, SETD6, CNOT1	51881, 47, 114320	downstream, in gene, downstream	ActReg chr16 #6435	0	1	1
6436	16	58,718,255	58,718,973	718	1	12.409	12.318	6.727	18	19	9	1	1	1	SLC38A7	60	in gene	ActReg chr16 #6436	1	0	0
6437	16	58,767,495	58,768,651	1,156	2	19.611	20.611	5.706	53	56	12	1	1	1	GOT2	173	in gene	ActReg chr16 #6437	1	1	0
6438	16	58,824,557	58,824,992	435	1	3.5	4.071	11.5	7	5	15	0	0	0				ActReg chr16 #6438	0	0	1
6439	16	59,912,321	59,912,928	607	1	6.842	11.79	2.077	11	19	4	0	0	0				ActReg chr16 #6439	0	1	0
6440	16	60,676,726	60,677,285	559	1	9.889	6.611	1.4	17	12	2	0	0	0				ActReg chr16 #6440	1	0	0
6441	16	61,162,762	61,163,313	551	1	3.412	8.824	2.353	5	17	4	0	0	0				ActReg chr16 #6441	0	1	0
6442	16	62,717,626	62,718,025	399	1	1.462	2.538	11.231	3	4	14	0	0	0				ActReg chr16 #6442	0	0	1
6443	16	64,195,157	64,195,826	669	1	11.809	6.571	2	21	13	3	0	0	0				ActReg chr16 #6443	1	0	0
6444	16	65,038,491	65,038,909	418	1	2.6	3.615	10.769	4	5	17	0	0	1	CDH11	117,219	in gene	ActReg chr16 #6444	0	0	1
6445	16	65,427,045	65,427,609	564	1	9.118	12.529	5.529	16	21	10	0	0	1	LOC283867	182,876	in gene	ActReg chr16 #6445	0	1	0
6446	16	66,115,537	66,116,356	819	2	8.038	11.231	2.318	17	16	4	0	0	0				ActReg chr16 #6446	1	1	0
6447	16	66,164,978	66,165,746	768	2	13.833	17.792	2.583	31	38	5	0	0	0				ActReg chr16 #6447	1	1	0
6448	16	66,394,683	66,395,155	472	1	6.067	3.8	11.733	9	6	16	0	1	1	CDH5	-5,606	upstream	ActReg chr16 #6448	0	0	1
6449	16	66,583,499	66,584,310	811	1	9	13.56	6.542	14	23	14	1	2	2	TK2, CKLF	411, -2562	in gene, upstream	ActReg chr16 #6449	0	1	0
6450	16	66,586,153	66,586,976	823	1	13.192	12.269	8.731	23	22	17	1	2	2	TK2, CKLF	-2249, 98	upstream, in gene	ActReg chr16 #6450	1	0	0
6451	16	66,639,413	66,639,881	468	1	4.2	8.267	11.867	9	10	18	1	1	2	CMTM3, CMTM4	1445, 90963	in gene, downstream	ActReg chr16 #6451	0	0	1
6452	16	66,729,739	66,730,107	368	1	5.636	6	12.636	9	7	17	1	1	1	CMTM4	687	in gene	ActReg chr16 #6452	0	0	1
6453	16	66,834,983	66,835,497	514	1	4.125	4	12.312	6	6	15	1	1	2	CCDC79, NAE1	283, 29639	in gene, downstream	ActReg chr16 #6453	0	0	1
6454	16	66,864,460	66,865,237	777	1	11.583	9.542	4.667	16	13	8	1	1	1	NAE1	31	in gene	ActReg chr16 #6454	1	0	0
6455	16	66,906,810	66,907,557	747	1	12.375	10.083	7.458	19	17	13	1	1	1	PDP2	-7,253	upstream	ActReg chr16 #6455	1	0	0
6456	16	66,914,139	66,914,983	844	2	11.037	12.333	10.296	18	26	15	1	1	2	PDP2, LOC100505926	125, -8106	in gene, upstream	ActReg chr16 #6456	0	1	1
6457	16	66,955,565	66,956,234	669	1	1.85	7.286	12.143	3	11	20	1	1	3	CDH16, RRAD, FAM96B	-3133, 3540, 12421	upstream, in gene, downstream	ActReg chr16 #6457	0	0	1
6458	16	66,967,977	66,968,909	932	2	9.724	11.759	9.897	18	19	18	1	2	3	RRAD, FAM96B, CES2	-9004, -123, 96	upstream, upstream, in gene	ActReg chr16 #6458	0	1	1
6459	16	67,013,099	67,013,429	330	1	3.6	5	12.1	6	7	14	0	0	2	CES3, CES8	18132, -9228	downstream, upstream	ActReg chr16 #6459	0	0	1
6460	16	67,176,258	67,176,565	307	1	2.667	4.667	11.667	4	6	15	0	0	2	C16orf70, B3GNT9	32496, 8491	in gene, downstream	ActReg chr16 #6460	0	0	1
6461	16	67,194,412	67,195,053	641	1	8.7	5.35	11.45	13	9	16	0	3	5	B3GNT9, TRADD, FBXL8, HSF4, NOL3	-9830, -920, 841, -2556, -9673	upstream, upstream, in gene, upstream, upstream	ActReg chr16 #6461	0	0	1
6462	16	67,207,827	67,208,560	733	1	11.348	13.826	9.652	17	26	15	1	0	5	FBXL8, HSF4, NOL3, KIAA0895L, EXOC3L	14302, 10905, 3788, 9690, 15914	downstream, downstream, in gene, downstream, downstream	ActReg chr16 #6462	0	1	0
6463	16	67,208,697	67,209,304	607	1	3.947	7.263	11.737	5	10	17	1	0	4	HSF4, NOL3, KIAA0895L, EXOC3L	11712, 4595, 8883, 15107	downstream, in gene, downstream, downstream	ActReg chr16 #6463	0	0	1
6464	16	67,219,138	67,219,756	618	1	11.526	13.632	5.316	19	25	12	1	2	4	NOL3, KIAA0895L, EXOC3L, E2F4	15042, -1564, 4660, -6621	downstream, upstream, in gene, upstream	ActReg chr16 #6464	0	1	0
6465	16	67,225,495	67,226,779	1,284	1	7.275	12.375	5.725	15	24	10	0	3	5	KIAA0895L, EXOC3L, E2F4, ELMO3, MIR328	-8254, -2030, 69, -6891, 10161	upstream, upstream, in gene, upstream, downstream	ActReg chr16 #6465	0	1	0
6466	16	67,260,247	67,261,488	1,241	2	9.641	12.436	8.205	16	32	17	1	2	3	LRRC29, TMEM208, FHOD1	34, -149, 20558	in gene, upstream, downstream	ActReg chr16 #6466	0	1	1
6467	16	67,263,941	67,264,765	824	1	3.375	5.52	11.24	6	9	16	0	1	3	LRRC29, TMEM208, FHOD1	-3452, 3337, 17072	upstream, downstream, in gene	ActReg chr16 #6467	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6468	16	67,279,794	67,280,269	475	1	10.933	8.2	12.267	14	14	16	1	2	2	FHOD1, SLC9A5	1394, -2824	in gene, upstream	ActReg chr16 #6468	0	0	1
6469	16	67,302,019	67,302,556	537	1	11.5	5.875	2.125	21	11	3	0	0	2	SLC9A5, PLEKHG4	19432, -9126	in gene, upstream	ActReg chr16 #6469	1	0	0
6470	16	67,312,622	67,314,292	1,670	2	11.404	16.865	6.976	37	43	10	1	1	3	SLC9A5, PLEKHG4, KCTD19	30602, 2044, 47204	downstream, in gene, downstream	ActReg chr16 #6470	1	1	0
6471	16	67,318,805	67,319,699	894	1	3.107	3.926	11.107	6	7	18	0	0	2	PLEKHG4, KCTD19	7839, 41409	in gene, downstream	ActReg chr16 #6471	0	0	1
6472	16	67,345,366	67,346,457	1,091	1	8.188	11.118	3.548	20	15	7	0	0	1	KCTD19	14,750	in gene	ActReg chr16 #6472	0	1	0
6473	16	67,499,532	67,500,168	636	1	9.85	11.3	7.25	14	18	11	0	0	1	ATP6V0D1	15,239	in gene	ActReg chr16 #6473	0	1	0
6474	16	67,514,709	67,516,164	1,455	1	9.935	12.978	5.86	16	23	13	1	2	2	ATP6V0D1, AQRP	-347, 2280	upstream, downstream	ActReg chr16 #6474	0	1	0
6475	16	67,554,864	67,555,923	1,059	2	11.364	12.121	6	20	23	12	0	1	2	LOC100505942, FAM65A	7158, -7324	in gene, upstream	ActReg chr16 #6475	1	1	0
6476	16	67,581,690	67,582,222	532	1	3.294	6.529	13	5	9	21	0	0	1	FAM65A	19,239	downstream	ActReg chr16 #6476	0	0	1
6477	16	67,595,871	67,596,572	701	2	11.727	10.409	3.842	26	19	7	1	1	1	CTCF	-89	upstream	ActReg chr16 #6477	1	1	0
6478	16	67,596,904	67,597,584	680	1	9.25	11.857	6.81	14	19	12	1	1	1	CTCF	934	in gene	ActReg chr16 #6478	0	1	0
6479	16	67,685,763	67,686,774	1,011	1	6.097	10.935	6.161	11	16	10	1	0	3	RLTPR, ACD, PARD6A	7238, 8450, -8583	in gene, downstream, upstream	ActReg chr16 #6479	0	1	0
6480	16	67,693,734	67,694,497	763	1	8.625	8.542	14.875	12	14	24	1	3	5	RLTPR, ACD, PARD6A, C16orf48, C16orf86	15085, 603, -736, 6513, -6602	downstream, in gene, upstream, downstream, upstream	ActReg chr16 #6480	0	0	1
6481	16	67,700,572	67,701,525	953	2	6.7	11.3	14.633	12	16	30	1	3	6	RLTPR, ACD, PARD6A, C16orf48, C16orf86, GFOD2	22018, -6330, 6197, -420, 331, 52225	downstream, upstream, downstream, upstream, in gene, downstream	ActReg chr16 #6481	0	1	1
6482	16	67,763,868	67,764,406	538	1	4.471	5.706	12.765	7	7	18	0	0	1	RANBP10	76,418	in gene	ActReg chr16 #6482	0	0	1
6483	16	67,840,199	67,841,252	1,053	3	12.454	13.667	8.848	30	25	16	1	2	2	RANBP10, TSNAXIP1	-170, -285	upstream, upstream	ActReg chr16 #6483	1	1	1
6484	16	67,867,395	67,868,054	659	1	10.05	12	7.55	19	18	12	1	0	3	TSNAXIP1, CENPT, THAP11	26714, 13637, -8489	downstream, in gene, upstream	ActReg chr16 #6484	0	1	0
6485	16	67,876,338	67,876,955	617	1	12.632	11.895	4.556	21	16	6	1	2	3	CENPT, THAP11, NUTF2	4715, 433, -4173	in gene, in gene, upstream	ActReg chr16 #6485	1	0	0
6486	16	67,880,413	67,881,379	966	2	9.032	12.452	5.667	20	29	9	1	2	3	CENPT, THAP11, NUTF2	465, 4683, 77	in gene, downstream, in gene	ActReg chr16 #6486	1	1	0
6487	16	67,906,592	67,907,384	792	1	6.76	12.04	6.88	13	21	13	1	1	2	NUTF2, EDC4	26169, -11	downstream, upstream	ActReg chr16 #6487	0	1	0
6488	16	67,969,070	67,970,186	1,116	1	10	11.857	7.657	15	18	12	1	2	5	PSKH1, CTRL, PSMB10, LCAT, SLC12A4	42453, -3863, 1125, 8387, 32969	downstream, upstream, in gene, downstream, downstream	ActReg chr16 #6488	0	1	0
6489	16	67,984,953	67,985,809	856	1	4.815	3.28	11.296	8	7	16	0	1	2	LCAT, SLC12A4	-7366, 17216	upstream, in gene	ActReg chr16 #6489	0	0	1
6490	16	68,000,179	68,000,934	755	1	6	6.667	12.458	15	11	21	0	1	2	SLC12A4, DPEP3	2041, 13896	in gene, downstream	ActReg chr16 #6490	0	0	1
6491	16	68,027,029	68,027,537	508	1	9.875	8.438	14.062	13	11	21	1	0	1	DPEP2	6,081	in gene	ActReg chr16 #6491	0	0	1
6492	16	68,056,311	68,057,500	1,189	2	10.703	13.027	9.432	25	19	16	1	2	2	DDX28, DUS2L	865, -299	in gene, upstream	ActReg chr16 #6492	0	1	1
6493	16	68,118,333	68,119,094	761	2	6.333	11	12.25	10	18	18	1	1	2	DUS2L, NFATC3	61509, -662	downstream, upstream	ActReg chr16 #6493	0	1	1
6494	16	68,119,326	68,119,881	555	1	9.889	9.5	1.625	18	13	2	1	1	2	DUS2L, NFATC3	62399, 228	downstream, in gene	ActReg chr16 #6494	1	0	0
6495	16	68,278,637	68,279,668	1,031	2	11.281	15.438	6.844	25	28	13	1	1	2	ESRP2, PLA2G15	-9016, -95	upstream, upstream	ActReg chr16 #6495	1	1	0
6496	16	68,289,042	68,289,571	529	1	1.857	2.647	12.118	4	4	18	0	0	2	PLA2G15, SLC7A6	10059, -9117	in gene, upstream	ActReg chr16 #6496	0	0	1
6497	16	68,297,736	68,299,160	1,424	1	7.614	12.136	6.615	13	26	14	1	1	2	PLA2G15, SLC7A6	19201, 25	downstream, in gene	ActReg chr16 #6497	0	1	0
6498	16	68,344,429	68,345,557	1,128	2	8.571	12.571	7.486	18	20	13	1	2	3	SLC7A6, SLC7A6OS, PRMT7	46570, -125, 116	downstream, upstream, in gene	ActReg chr16 #6498	1	1	0
6499	16	68,388,807	68,389,299	492	1	4.333	4.462	11.733	7	9	18	0	0	2	PRMT7, SMPD3	44176, 93356	in gene, downstream	ActReg chr16 #6499	0	0	1
6500	16	68,477,807	68,478,506	699	2	12.273	14.454	1.889	24	32	4	0	0	1	SMPD3	4,253	in gene	ActReg chr16 #6500	1	1	0
6501	16	68,481,105	68,481,695	590	1	4.833	7.333	11.722	7	9	17	1	1	1	SMPD3	1,009	in gene	ActReg chr16 #6501	0	0	1
6502	16	68,481,760	68,483,458	1,698	3	10.611	15.704	7.812	20	28	18	1	1	1	SMPD3	-200	upstream	ActReg chr16 #6502	1	1	1
6503	16	68,573,020	68,573,407	387	1	7.583	5.833	12.667	10	9	16	1	1	1	ZFP90	-448	upstream	ActReg chr16 #6503	0	0	1
6504	16	68,678,964	68,679,355	391	1	2.75	5	11.667	4	6	18	1	1	1	CDH3	1,008	in gene	ActReg chr16 #6504	0	0	1
6505	16	68,701,922	68,702,734	812	2	10.88	10.08	2.826	19	16	5	0	0	1	CDH3	24,177	in gene	ActReg chr16 #6505	1	1	0
6506	16	69,107,113	69,107,811	698	1	8.364	13.591	4.682	13	22	8	0	0	1	TMCO7	229,953	in gene	ActReg chr16 #6506	0	1	0
6507	16	69,165,766	69,166,136	370	1	7	9.364	9.909	10	13	15	0	2	2	CHTF8, CIRH1A	-542, -548	in gene, upstream	ActReg chr16 #6507	0	0	1
6508	16	69,200,036	69,200,628	592	1	10.444	6.222	4.944	16	9	7	0	0	1	CIRH1A	33,833	in gene	ActReg chr16 #6508	1	0	0
6509	16	69,220,456	69,221,335	879	2	11.037	10.704	6.28	17	20	16	1	1	1	SNTB2	-155	upstream	ActReg chr16 #6509	1	1	0
6510	16	69,359,581	69,359,982	401	1	3.615	4.846	11.769	5	7	18	0	0	4	VPS4A, LOC100506031, COG8, PDF	14494, 16576, 13745, 4717	downstream, in gene, downstream, downstream	ActReg chr16 #6510	0	0	1
6511	16	69,363,522	69,364,859	1,337	2	11.244	11.293	9.1	18	21	20	1	1	5	VPS4A, LOC100506031, COG8, PDF, NIP7	18903, 12167, 9336, 308, -9356	downstream, in gene, in gene, in gene, upstream	ActReg chr16 #6511	0	1	1
6512	16	69,372,856	69,374,013	1,157	2	14.833	19.389	6.194	42	44	11	1	3	5	LOC100506031, COG8, PDF, NIP7, TMED6	2923, 92, -8936, -112, 12278	in gene, in gene, upstream, upstream, downstream	ActReg chr16 #6512	1	1	0
6513	16	69,383,622	69,383,962	340	1	4.6	4.3	11	6	6	15	0	2	4	LOC100506031, NIP7, TMED6, TERF2	-7435, 10246, 1920, 36081	upstream, downstream, in gene, downstream	ActReg chr16 #6513	0	0	1
6514	16	69,457,989	69,459,019	1,030	1	7.469	13.875	6.188	13	22	9	1	1	1	CY55B	6	in gene	ActReg chr16 #6514	0	1	0
6515	16	69,564,621	69,565,082	461	1	6.786	11.929	6.923	11	18	12	0	0	0				ActReg chr16 #6515	0	1	0
6516	16	69,599,537	69,599,951	414	1	4.615	10.692	6.273	8	14	13	1	2	2	NFAT5, MIR1538	747, 27	in gene, in gene	ActReg chr16 #6516	0	1	0
6517	16	69,760,178	69,760,994	816	1	7.5	11.115	7.154	13	17	13	1	1	1	NQO1	-53	upstream	ActReg chr16 #6517	0	1	0
6518	16	69,788,361	69,789,179	818	2	7.4	14.44	12.8	11	28	19	1	2	2	NOB1, WWP2	59, -7504	in gene, upstream	ActReg chr16 #6518	0	1	1
6519	16	70,285,417	70,286,361	944	2	27.276	27.517	7.478	79	82	16	1	1	2	EXOSC6, AARS	-56, 37523	upstream, downstream	ActReg chr16 #6519	1	1	0
6520	16	70,323,049	70,323,586	537	1	9.412	6.941	14	14	13	25	1	1	2	AARS, DDX19B	95, -9755	in gene, upstream	ActReg chr16 #6520	0	0	1
6521	16	70,332,862	70,333,480	618	2	9.85	10.35	6.053	16	17	9	0	1	2	AARS, DDX19B	-9759, 99	upstream, in gene	ActReg chr16 #6521	1	1	0
6522	16	70,380,534	70,381,268	734	3	11.391	12.696	11.391	24	21	23	1	2	2	LOC100506083, DDX19A	-223, 77	upstream, in gene	ActReg chr16 #6522	1	1	1
6523	16	70,414,795	70,416,018	1,223	1	4.974	5.658	13.921	9	10	18	1	0	2	DDX19A, ST3GAL2	34582, 57585	downstream, in gene	ActReg chr16 #6523	0	0	1
6524	16	70,472,891	70,473,767	876	3	15.821	20.821	10.56	34	45	20	1	1	1	ST3GAL2	-338	upstream	ActReg chr16 #6524	1	1	1
6525	16	70,487,912	70,489,019	1,107	3	20.294	24.029	11.5	49	71	22	1	1	1	FUK	-33	upstream	ActReg chr16 #6525	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6526	16	70,491,187	70,491,864	677	1	12.286	10.667	3.095	19	13	6	0	0	1	FUK	3,027	in gene	ActReg chr16 #6526	1	0	0
6527	16	70,508,713	70,509,275	562	1	9.706	5	14	13	7	25	0	0	2	FUK, COG4	20496, 48463	in gene, downstream	ActReg chr16 #6527	0	0	1
6528	16	70,514,593	70,515,601	1,008	1	3.033	6.774	11.387	7	10	19	0	0	2	FUK, COG4	26599, 42360	downstream, in gene	ActReg chr16 #6528	0	0	1
6529	16	70,557,560	70,558,184	624	1	6.95	10.3	10.05	11	16	14	1	3	3	COG4, SF3B3, SNORD111B	-415, 181, -5533	upstream, in gene, upstream	ActReg chr16 #6529	0	1	0
6530	16	70,690,520	70,690,933	413	1	3.692	2.615	11.154	8	4	17	0	0	2	IL34, MTSS1L	76928, 29228	in gene, downstream	ActReg chr16 #6530	0	0	1
6531	16	70,696,054	70,696,429	375	1	3.833	4.5	13	8	7	17	0	0	2	IL34, MTSS1L	82443, 23713	downstream, in gene	ActReg chr16 #6531	0	0	1
6532	16	70,834,643	70,835,377	734	1	10.261	12.087	8.913	19	21	17	1	1	2	VAC14, HYDIN	51, 429559	in gene, downstream	ActReg chr16 #6532	0	1	0
6533	16	70,895,357	70,896,372	1,015	1	12.031	13.25	4.258	23	23	9	0	0	1	HYDIN	368,705	in gene	ActReg chr16 #6533	0	1	0
6534	16	70,971,882	70,972,860	978	1	8.733	6.167	13.533	13	10	21	0	0	1	HYDIN	292,198	in gene	ActReg chr16 #6534	0	0	1
6535	16	71,020,561	71,022,363	1,802	2	16.75	16.321	5.196	39	39	11	0	0	1	HYDIN	243,107	in gene	ActReg chr16 #6535	1	1	0
6536	16	71,052,826	71,053,688	862	2	14.926	18.704	3.25	27	39	7	0	0	1	HYDIN	211,312	in gene	ActReg chr16 #6536	1	1	0
6537	16	71,322,742	71,323,451	709	2	11.954	9.864	8	21	17	15	1	1	1	FTSJD1	413	in gene	ActReg chr16 #6537	1	1	0
6538	16	71,349,966	71,350,558	592	1	9.444	11.5	2.222	17	22	4	0	0	0				ActReg chr16 #6538	0	1	0
6539	16	71,475,152	71,475,629	477	1	3.2	4.667	12	5	7	19	1	0	1	ZNF23	20,727	downstream	ActReg chr16 #6539	0	0	1
6540	16	71,495,601	71,496,623	1,022	3	10	15.656	7.812	22	32	22	1	2	2	ZNF23, LOC100506105	5, -86	in gene, upstream	ActReg chr16 #6540	1	1	1
6541	16	71,501,025	71,502,309	1,284	2	17.025	19.875	3.423	47	52	8	0	1	3	ZNF23, LOC100506105, ZNF19	-5550, 5469, 21587	upstream, downstream, downstream	ActReg chr16 #6541	1	1	0
6542	16	71,508,653	71,509,244	591	1	7.667	10.833	4.611	11	18	8	0	0	1	ZNF19	14,306	in gene	ActReg chr16 #6542	0	1	0
6543	16	71,518,060	71,518,705	645	1	10.8	11.65	7.1	15	17	11	0	0	1	ZNF19	4,872	in gene	ActReg chr16 #6543	0	1	0
6544	16	71,598,670	71,599,059	389	1	4.917	8	9.917	7	11	15	0	1	2	LOC100132529, TAT	-828, 12134	upstream, downstream	ActReg chr16 #6544	0	0	1
6545	16	71,599,180	71,599,482	302	1	9.778	9.111	11.333	13	12	15	0	1	2	LOC100132529, TAT	-361, 11667	upstream, downstream	ActReg chr16 #6545	0	0	1
6546	16	71,842,151	71,843,133	982	3	11.9	12.133	10.033	21	26	18	1	1	1	AP1G1	334	in gene	ActReg chr16 #6546	1	1	1
6547	16	71,879,558	71,880,249	691	1	9.714	13.524	8.667	14	19	13	1	1	1	ATXN1L	4	in gene	ActReg chr16 #6547	0	1	0
6548	16	71,928,994	71,929,746	752	1	9.826	15.913	8.478	14	27	13	1	1	2	ATXN1L, KIAA0174	49471, -76	downstream, upstream	ActReg chr16 #6548	0	1	0
6549	16	72,042,293	72,043,114	821	3	11.615	11.115	11.346	25	21	22	1	1	2	PKD1L3, DHODH	-8826, 60	upstream, in gene	ActReg chr16 #6549	1	1	1
6550	16	72,127,184	72,128,342	1,158	3	10.194	10.833	8.306	19	22	13	1	2	2	TXNL4B, DHX38	452, 148	in gene, in gene	ActReg chr16 #6550	1	1	1
6551	16	72,325,667	72,326,126	459	1	6.286	11	1.8	7	18	3	0	0	0				ActReg chr16 #6551	0	1	0
6552	16	72,961,445	72,961,974	529	1	6.467	12.75	4.5	10	21	8	0	0	1	ZFHX3	130,825	in gene	ActReg chr16 #6552	0	1	0
6553	16	73,049,505	73,049,958	453	1	3.571	7.5	12.286	6	9	21	0	1	2	ZFHX3, LOC100506152	42803, -3453	in gene, upstream	ActReg chr16 #6553	0	0	1
6554	16	73,054,192	73,054,895	703	2	14.091	10.591	1.688	28	24	5	0	0	2	ZFHX3, LOC100506152	37991, -8265	in gene, upstream	ActReg chr16 #6554	1	1	0
6555	16	73,100,770	73,101,392	622	1	4.895	6.333	14.316	7	13	18	1	0	1	ZFHX3	-8,547	upstream	ActReg chr16 #6555	0	0	1
6556	16	74,173,385	74,173,791	406	1	1.571	2.143	11.667	3	3	16	0	0	0				ActReg chr16 #6556	0	0	1
6557	16	74,330,423	74,331,135	712	1	11.591	13.318	13.773	23	19	24	1	1	2	PSMD7, LOC100506201	98, 25491	in gene, downstream	ActReg chr16 #6557	0	0	1
6558	16	74,407,325	74,407,817	492	1	4	1.833	12.812	6	3	18	0	2	2	NPIPL2, LOC100507666	-4301, -4301	upstream, upstream	ActReg chr16 #6558	0	0	1
6559	16	74,640,692	74,641,209	517	1	10.438	8.875	13.438	15	10	21	1	1	2	GLG1, LOC100132346	92, 6169	in gene, downstream	ActReg chr16 #6559	0	0	1
6560	16	74,700,353	74,700,720	367	1	10.636	10.364	10.273	15	14	15	1	1	2	RFWD3, MLKL	243, 34253	in gene, downstream	ActReg chr16 #6560	0	0	1
6561	16	74,747,319	74,748,142	823	1	4.269	3.115	12.577	9	5	17	0	0	1	FA2H	60,999	in gene	ActReg chr16 #6561	0	0	1
6562	16	75,018,378	75,018,977	599	1	10.895	12.737	12.21	18	18	15	1	1	1	WDR59	340	in gene	ActReg chr16 #6562	0	0	1
6563	16	75,147,388	75,147,892	504	1	2.167	3.75	12.062	3	6	18	0	0	2	ZNRF1, LDHD	114725, 3025	downstream, in gene	ActReg chr16 #6563	0	0	1
6564	16	75,181,980	75,182,666	686	1	11.5	13.454	7.19	18	25	13	1	1	1	ZFP1	-98	upstream	ActReg chr16 #6564	0	1	0
6565	16	75,240,408	75,240,958	550	1	3.059	3.882	13.177	5	7	18	0	1	1	CTRB2	389	in gene	ActReg chr16 #6565	0	0	1
6566	16	75,268,891	75,269,429	538	1	4.529	3.882	14.471	7	6	22	1	0	2	LOC100506281, BCAR1	8473, 32791	downstream, in gene	ActReg chr16 #6566	0	0	1
6567	16	75,272,040	75,272,679	639	1	10.9	10.2	11.1	17	17	15	0	0	2	LOC100506281, BCAR1	11672, 29592	downstream, in gene	ActReg chr16 #6567	0	0	1
6568	16	75,277,569	75,278,373	804	1	5.28	5.6	13.24	7	11	20	0	0	1	BCAR1	23,980	in gene	ActReg chr16 #6568	0	0	1
6569	16	75,279,048	75,279,735	687	1	9.286	7.524	13.381	14	14	22	0	0	1	BCAR1	22,560	in gene	ActReg chr16 #6569	0	0	1
6570	16	75,281,207	75,281,662	455	1	3.571	7.214	13.857	5	10	22	0	0	1	BCAR1	20,517	in gene	ActReg chr16 #6570	0	0	1
6571	16	75,298,811	75,299,537	726	1	6.136	7.391	12.174	9	12	17	1	1	1	BCAR1	2,777	in gene	ActReg chr16 #6571	0	0	1
6572	16	75,466,759	75,467,255	496	1	9.8	9.933	14.867	13	11	24	1	1	1	CFDP1	380	in gene	ActReg chr16 #6572	0	0	1
6573	16	75,497,887	75,498,970	1,083	2	10.118	13.147	5.824	16	23	15	1	1	2	TMEM170A, CHST6	156, 30498	in gene, downstream	ActReg chr16 #6573	1	1	0
6574	16	75,550,762	75,551,381	619	1	7.684	10.368	12.421	11	15	19	1	0	0				ActReg chr16 #6574	0	0	1
6575	16	75,589,582	75,590,544	962	2	10.367	13.667	6.733	21	24	15	1	1	2	TMEM231, GABARAPL2	107, -10186	in gene, upstream	ActReg chr16 #6575	1	1	0
6576	16	75,600,682	75,601,102	420	1	5.538	9	11.231	8	12	17	1	1	1	GABARAPL2	643	in gene	ActReg chr16 #6576	0	0	1
6577	16	75,681,172	75,682,555	1,383	2	9.116	13.419	9	14	20	22	1	2	2	KARS, TERF2IP	-278, 228	upstream, in gene	ActReg chr16 #6577	0	1	1
6578	16	76,838,882	76,839,535	653	1	11.85	10.25	3.333	22	12	7	0	0	0				ActReg chr16 #6578	1	0	0
6579	16	76,980,842	76,981,392	550	1	9.059	11.823	2.571	11	21	5	0	0	0				ActReg chr16 #6579	0	1	0
6580	16	77,246,623	77,247,154	531	1	4.2	9.118	10.177	6	13	13	1	0	1	SYCE1L	13,539	in gene	ActReg chr16 #6580	0	0	1
6581	16	77,247,213	77,247,944	731	1	10.478	13.217	4.136	13	23	6	0	0	1	SYCE1L	14,229	downstream	ActReg chr16 #6581	0	1	0
6582	16	77,818,338	77,818,872	534	1	2.375	4	11.125	6	6	14	0	1	1	VAT1L	-3,878	upstream	ActReg chr16 #6582	0	0	1
6583	16	77,821,897	77,822,893	996	1	7.548	12.097	7.808	14	18	13	1	1	1	VAT1L	-88	upstream	ActReg chr16 #6583	0	1	0
6584	16	78,079,547	78,080,554	1,007	3	19.375	30.125	7.438	53	71	15	1	0	0				ActReg chr16 #6584	1	1	1
6585	16	78,133,029	78,134,271	1,242	3	17.842	16.947	11.368	38	42	22	1	1	1	WWOX	99	in gene	ActReg chr16 #6585	1	1	1
6586	16	79,406,389	79,406,902	513	1	8.188	10.688	2.5	14	18	5	0	0	0				ActReg chr16 #6586	0	1	0
6587	16	79,634,519	79,635,705	1,186	2	8.568	13.297	7.081	12	21	18	1	1	1	MAF	-490	upstream	ActReg chr16 #6587	0	1	1
6588	16	79,662,205	79,662,850	645	1	6.238	10.905	1.875	9	16	4	0	0	0				ActReg chr16 #6588	0	1	0
6589	16	79,681,365	79,682,023	658	1	11.286	9.857	3.619	20	16	7	0	0	0				ActReg chr16 #6589	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6590	16	79,685,061	79,685,782	721	2	11.909	11.046	2.955	20	16	5	0	0	0				ActReg chr16 #6590	1	1	0
6591	16	79,692,039	79,692,679	640	1	11.05	9.15	1.647	17	13	3	0	0	0				ActReg chr16 #6591	1	0	0
6592	16	80,039,964	80,040,793	829	1	5.038	10.385	1.625	8	15	3	0	0	0				ActReg chr16 #6592	0	1	0
6593	16	80,060,821	80,061,596	775	2	9.917	11.667	4.8	18	22	10	0	0	0				ActReg chr16 #6593	1	1	0
6594	16	80,574,368	80,575,177	809	1	10.077	14.077	6.269	20	25	13	1	1	1	DYNLRB2	-82	upstream	ActReg chr16 #6594	0	1	0
6595	16	81,039,823	81,041,398	1,575	3	22.367	27.204	15.551	93	78	29	1	2	2	C16orf61, CENPN	-108, 507	upstream, in gene	ActReg chr16 #6595	1	1	1
6596	16	81,348,185	81,348,850	665	3	9.81	13.809	7.6	14	24	19	1	1	1	GAN	-54	upstream	ActReg chr16 #6596	1	1	1
6597	16	81,434,607	81,435,519	912	1	10	7.571	3.5	16	13	6	0	0	0				ActReg chr16 #6597	1	0	0
6598	16	81,741,296	81,741,769	473	1	3.467	5	13.667	5	7	18	0	0	1	CMIP	262,757	in gene	ActReg chr16 #6598	0	0	1
6599	16	81,763,946	81,764,466	520	1	8.25	4	11.312	13	7	15	0	0	0				ActReg chr16 #6599	0	0	1
6600	16	81,779,409	81,780,294	885	2	9.214	11.536	5.214	18	20	8	0	0	0				ActReg chr16 #6600	1	1	0
6601	16	82,203,343	82,204,232	889	2	10.536	13.107	6.519	16	21	14	1	1	1	MPHOSPH6	42	in gene	ActReg chr16 #6601	1	1	0
6602	16	82,591,606	82,591,971	365	1	5.083	3	9.5	9	4	15	0	0	0				ActReg chr16 #6602	0	0	1
6603	16	82,661,333	82,662,233	900	1	9.214	13.071	6.679	16	20	13	1	1	1	CDH13	1,205	in gene	ActReg chr16 #6603	0	1	0
6604	16	82,667,567	82,668,232	665	1	11	7.095	2.895	18	12	5	0	0	1	CDH13	7,321	in gene	ActReg chr16 #6604	1	0	0
6605	16	83,170,633	83,171,294	661	1	5.55	11.45	4.15	11	16	8	0	0	1	CDH13	510,385	in gene	ActReg chr16 #6605	0	1	0
6606	16	83,546,607	83,547,373	766	1	11.042	7.917	1.882	15	11	3	0	0	2	CDH13, MIR3182	886412, 5039	in gene, downstream	ActReg chr16 #6606	1	0	0
6607	16	83,595,250	83,596,055	805	2	10.96	16.8	2.062	25	34	4	0	0	1	CDH13	935,074	in gene	ActReg chr16 #6607	1	1	0
6608	16	83,734,986	83,735,667	681	1	12.524	11.381	5.238	22	17	10	0	0	1	CDH13	1,074,748	in gene	ActReg chr16 #6608	1	0	0
6609	16	83,751,247	83,752,095	848	1	8	11.577	1.789	12	17	2	0	0	1	CDH13	1,091,093	in gene	ActReg chr16 #6609	0	1	0
6610	16	83,959,771	83,960,283	512	1	3.75	6.938	11.5	7	8	15	0	0	1	MLYCD	27,297	downstream	ActReg chr16 #6610	0	0	1
6611	16	83,969,497	83,970,045	548	1	3.294	2.059	11.706	6	3	15	0	0	0				ActReg chr16 #6611	0	0	1
6612	16	83,986,128	83,987,130	1,002	2	16.774	16.613	8.097	29	32	12	0	0	1	OSGIN1	5,957	in gene	ActReg chr16 #6612	1	1	0
6613	16	84,150,283	84,151,513	1,230	2	7.158	11.5	7.333	14	17	19	1	1	2	MBTPS1, HSDL1	-381, 27902	upstream, downstream	ActReg chr16 #6613	0	1	1
6614	16	84,178,955	84,179,220	265	1	8.5	7.375	11.625	10	9	13	1	2	2	HSDL1, LRRC50	-287, 222	upstream, in gene	ActReg chr16 #6614	0	0	1
6615	16	84,220,250	84,220,883	633	1	8.7	14.1	7.1	12	19	13	1	2	4	LRRC50, TAF1C, ADAD2, LOC654780	41701, 96, -4157, 10093	downstream, in gene, upstream, downstream	ActReg chr16 #6615	0	1	0
6616	16	84,224,629	84,224,971	342	1	1.455	4.273	11.546	2	6	18	1	2	3	TAF1C, ADAD2, LOC654780	-4138, 77, 5859	upstream, in gene, downstream	ActReg chr16 #6616	0	0	1
6617	16	84,261,806	84,262,734	928	1	8.103	10.828	5.724	15	20	10	0	0	1	KCNG4	11,086	in gene	ActReg chr16 #6617	0	1	0
6618	16	84,327,911	84,328,421	510	1	6.438	4.5	11.125	12	7	16	1	1	1	WFDC1	-235	upstream	ActReg chr16 #6618	0	0	1
6619	16	84,538,666	84,539,148	482	1	6.267	10	11.733	13	13	18	1	1	1	KIAA1609	-619	upstream	ActReg chr16 #6619	0	0	1
6620	16	84,636,568	84,637,594	1,026	1	12.406	9.704	4.719	25	18	10	0	0	1	COTL1	14,588	in gene	ActReg chr16 #6620	1	0	0
6621	16	84,839,960	84,841,142	1,182	1	7.811	11.054	4.667	15	15	9	0	0	0				ActReg chr16 #6621	0	1	0
6622	16	84,872,055	84,872,541	486	1	3.867	5.6	13.2	7	9	19	0	0	1	CRISPLD2	18,711	in gene	ActReg chr16 #6622	0	0	1
6623	16	84,918,179	84,919,184	1,005	1	6.065	11.484	3.724	14	17	10	0	0	1	CRISPLD2	65,094	in gene	ActReg chr16 #6623	0	1	0
6624	16	84,963,488	84,963,998	510	1	4.875	3.812	12.5	7	7	23	0	0	0				ActReg chr16 #6624	0	0	1
6625	16	84,967,367	84,967,937	570	1	3.389	6.389	11.778	7	11	15	0	0	0				ActReg chr16 #6625	0	0	1
6626	16	85,044,587	85,044,907	320	1	5.2	4.6	10	10	6	14	1	1	1	ZDHHC7	594	in gene	ActReg chr16 #6626	0	0	1
6627	16	85,123,043	85,123,352	309	1	3.889	6.778	12.889	6	9	16	0	0	2	KIAA0513, FAM92B	61787, 22917	in gene, downstream	ActReg chr16 #6627	0	0	1
6628	16	85,143,785	85,144,173	388	1	2.75	2.5	12.25	4	4	15	0	1	1	FAM92B	2,135	in gene	ActReg chr16 #6628	0	0	1
6629	16	85,152,174	85,152,491	317	1	2.7	4.1	11.8	5	5	16	0	1	1	FAM92B	-6,218	upstream	ActReg chr16 #6629	0	0	1
6630	16	85,196,167	85,196,573	406	1	5.75	4.833	13	9	7	20	1	1	2	LOC100506467, LOC123855	6225, -6761	in gene, upstream	ActReg chr16 #6630	0	0	1
6631	16	85,204,897	85,205,409	512	1	5.062	5	13	10	8	22	1	2	2	LOC100506467, LOC123855	-2558, 2022	upstream, in gene	ActReg chr16 #6631	0	0	1
6632	16	85,283,054	85,283,677	623	1	5.474	3.053	13.263	10	5	19	0	0	0				ActReg chr16 #6632	0	0	1
6633	16	85,320,651	85,321,274	623	1	5.632	9.526	12.263	10	20	22	1	0	1	TMEM148	4,701	downstream	ActReg chr16 #6633	0	0	1
6634	16	85,346,500	85,347,000	500	1	3.357	3.867	12.4	6	5	17	0	0	0				ActReg chr16 #6634	0	0	1
6635	16	85,390,438	85,390,920	482	1	3.733	4.733	12.133	6	8	19	0	0	0				ActReg chr16 #6635	0	0	1
6636	16	85,446,453	85,446,927	474	1	5.067	1.545	11	6	3	17	0	0	0				ActReg chr16 #6636	0	0	1
6637	16	85,478,812	85,479,335	523	1	2.647	2.375	11.471	5	4	16	0	0	0				ActReg chr16 #6637	0	0	1
6638	16	85,486,942	85,487,387	445	1	1.571	5.5	12.429	2	6	16	0	0	0				ActReg chr16 #6638	0	0	1
6639	16	85,558,477	85,558,917	440	1	4.786	3.929	12.071	7	7	17	0	0	0				ActReg chr16 #6639	0	0	1
6640	16	85,586,864	85,588,132	1,268	2	9.5	8.9	4.906	18	17	9	1	0	0				ActReg chr16 #6640	1	1	0
6641	16	85,643,941	85,644,786	845	1	6	11.731	8.308	10	16	11	2	1	1	KIAA0182	-666	upstream	ActReg chr16 #6641	0	1	0
6642	16	85,665,203	85,665,886	683	1	2.857	5	11.714	5	7	19	0	0	1	KIAA0182	20,515	in gene	ActReg chr16 #6642	0	0	1
6643	16	85,666,867	85,667,366	499	1	3.562	2.875	11.625	7	5	18	2	0	1	KIAA0182	22,087	in gene	ActReg chr16 #6643	0	0	1
6644	16	85,685,488	85,685,879	391	1	7.583	5.583	11.917	10	8	19	0	0	1	KIAA0182	40,654	in gene	ActReg chr16 #6644	0	0	1
6645	16	85,687,149	85,687,798	649	1	7	6.4	11.05	10	8	15	0	0	1	KIAA0182	42,444	in gene	ActReg chr16 #6645	0	0	1
6646	16	85,688,968	85,689,393	425	1	2.692	3	10.538	4	5	14	0	0	1	KIAA0182	44,151	in gene	ActReg chr16 #6646	0	0	1
6647	16	85,695,136	85,695,701	565	1	3.278	4.556	10.5	6	7	15	0	0	1	KIAA0182	50,389	in gene	ActReg chr16 #6647	0	0	1
6648	16	85,768,540	85,768,920	380	1	2.75	3.083	13	5	4	21	0	0	2	C16orf74, MIR1910	15959, 6576	in gene, downstream	ActReg chr16 #6648	0	0	1
6649	16	85,783,781	85,784,164	383	1	6.417	5.583	11.583	9	7	17	1	1	2	C16orf74, MIR1910	717, -8666	in gene, upstream	ActReg chr16 #6649	0	0	1
6650	16	85,833,027	85,833,729	702	1	13.864	13.227	7.864	26	20	13	1	2	3	COX4NB, LOC100506521, COX4I1	-230, 7357, 182	upstream, downstream, in gene	ActReg chr16 #6650	0	1	0
6651	16	85,932,068	85,932,652	584	1	3.222	3.722	11.944	5	7	18	1	1	1	IRF8	-414	upstream	ActReg chr16 #6651	0	0	1
6652	16	85,988,465	85,989,155	690	1	2.476	3.5	11.909	5	6	18	0	0	0				ActReg chr16 #6652	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6653	16	86,060,331	86,060,641	310	1	1.4	4.5	9.5	2	6	14	0	0	0				ActReg chr16 #6653	0	0	1
6654	16	86,062,775	86,063,128	353	1	2	2.182	11.454	3	4	15	0	0	0				ActReg chr16 #6654	0	0	1
6655	16	86,078,765	86,079,120	355	1	3.091	3.545	10.091	4	5	15	0	0	0				ActReg chr16 #6655	0	0	1
6656	16	86,127,744	86,128,333	589	1	2.316	3.412	11.895	4	7	19	0	0	0				ActReg chr16 #6656	0	0	1
6657	16	86,371,030	86,371,438	408	1	3.154	5	9.692	5	6	12	0	0	1	LOC732275	8,051	in gene	ActReg chr16 #6657	0	0	1
6658	16	86,427,373	86,428,048	675	1	6.333	11.905	3	9	18	6	0	0	0				ActReg chr16 #6658	0	1	0
6659	16	86,432,220	86,432,756	536	1	12.177	6.824	1	18	9	1	0	0	0				ActReg chr16 #6659	1	0	0
6660	16	86,438,314	86,438,763	449	1	4.286	4.714	10.643	6	7	17	0	0	0				ActReg chr16 #6660	0	0	1
6661	16	86,524,559	86,525,669	1,110	2	10.514	10.143	4.441	18	18	10	0	0	1	FLJ34515	17,352	in gene	ActReg chr16 #6661	1	1	0
6662	16	86,544,940	86,545,379	439	1	4.385	5.786	11.429	6	8	16	1	2	2	FLJ34515, FOXF1	-2693, 1026	upstream, in gene	ActReg chr16 #6662	0	0	1
6663	16	86,561,885	86,562,512	627	1	3.7	2.65	11.8	6	4	16	0	0	1	MTHFSD	26,643	downstream	ActReg chr16 #6663	0	0	1
6664	16	86,697,923	86,699,035	1,112	2	12.029	12.382	3.882	20	22	7	0	0	0				ActReg chr16 #6664	1	1	0
6665	16	86,805,621	86,806,332	711	1	10.773	5.773	2.643	20	10	6	0	0	0				ActReg chr16 #6665	1	0	0
6666	16	86,922,336	86,922,875	539	1	5.118	9.882	1.267	8	15	2	0	0	0				ActReg chr16 #6666	0	1	0
6667	16	86,980,468	86,980,989	521	1	3.062	4.688	12.625	5	6	17	0	0	0				ActReg chr16 #6667	0	0	1
6668	16	86,984,528	86,986,308	1,780	2	13.125	17.5	3.5	23	29	6	0	0	0				ActReg chr16 #6668	1	1	0
6669	16	87,350,280	87,351,330	1,050	3	10.515	10.606	9.273	14	15	15	1	1	1	LOC100506581	190	in gene	ActReg chr16 #6669	1	1	1
6670	16	87,379,450	87,379,908	458	1	4.267	2.8	10.533	6	5	15	0	0	1	FBXO31	46,029	in gene	ActReg chr16 #6670	0	0	1
6671	16	87,417,371	87,418,010	639	2	9.158	11.95	21.947	19	23	39	1	0	2	FBXO31, MAP1LC3B	8018, -8111	in gene, upstream	ActReg chr16 #6671	0	1	1
6672	16	87,425,045	87,426,251	1,206	2	11.605	11.079	5.609	19	21	13	1	2	2	FBXO31, MAP1LC3B	60, -153	in gene, upstream	ActReg chr16 #6672	1	1	0
6673	16	87,526,533	87,526,973	440	1	12.077	5.615	4	19	9	7	0	1	1	ZCCHC14	-1,293	upstream	ActReg chr16 #6673	1	0	0
6674	16	87,583,978	87,584,808	830	1	4.8	4.115	11.808	8	6	17	1	0	0				ActReg chr16 #6674	0	0	1
6675	16	87,615,915	87,616,758	843	2	8.923	10.846	9.5	14	16	22	0	0	0				ActReg chr16 #6675	0	1	1
6676	16	87,641,433	87,642,877	1,444	2	16.022	18.578	5.622	35	41	13	0	0	1	JPH3	5,656	in gene	ActReg chr16 #6676	1	1	0
6677	16	87,661,090	87,661,622	532	1	2.938	3.938	11.812	5	5	18	0	0	1	JPH3	24,857	in gene	ActReg chr16 #6677	0	0	1
6678	16	87,694,749	87,695,744	995	2	9.219	14.406	3.677	16	35	6	0	0	1	JPH3	58,747	in gene	ActReg chr16 #6678	1	1	0
6679	16	87,718,608	87,719,191	583	1	4.2	5.278	15.056	9	6	21	1	0	2	JPH3, LOC100129215	82400, 10854	in gene, downstream	ActReg chr16 #6679	0	0	1
6680	16	87,721,002	87,721,515	513	1	3.25	2.625	11.75	4	5	16	0	0	2	JPH3, LOC100129215	84759, 8495	in gene, downstream	ActReg chr16 #6680	0	0	1
6681	16	87,724,751	87,725,160	409	1	3.846	2.583	12.077	7	3	17	0	0	3	JPH3, LOC100129215, LOC100129637	88456, 4798, 14335	in gene, downstream, downstream	ActReg chr16 #6681	0	0	1
6682	16	87,727,506	87,728,350	844	1	2.565	4.269	11.808	5	9	17	0	1	3	JPH3, LOC100129215, LOC100129637	91429, 1825, 11362	in gene, in gene, downstream	ActReg chr16 #6682	0	0	1
6683	16	87,823,447	87,824,238	791	2	4.8	10.44	6.6	10	18	16	0	0	0				ActReg chr16 #6683	0	1	1
6684	16	87,828,113	87,828,659	546	1	1.714	2.706	11.177	3	4	20	0	0	0				ActReg chr16 #6684	0	0	1
6685	16	87,835,256	87,835,659	403	1	4	2.6	12.231	6	4	19	0	0	0				ActReg chr16 #6685	0	0	1
6686	16	87,856,949	87,857,424	475	1	3.267	1.786	13.133	6	3	21	0	1	2	SLC7A5, LOC100506670	45914, -6775	downstream, upstream	ActReg chr16 #6686	0	0	1
6687	16	87,861,904	87,862,355	451	1	3.571	3.929	11.929	6	6	19	0	1	2	SLC7A5, LOC100506670	40971, -1832	downstream, upstream	ActReg chr16 #6687	0	0	1
6688	16	87,868,626	87,869,261	635	1	5	3.9	11.05	9	6	16	0	0	2	SLC7A5, LOC100506670	34157, 4982	in gene, downstream	ActReg chr16 #6688	0	0	1
6689	16	87,869,782	87,870,458	676	1	4.667	2.81	11.571	9	5	18	0	0	2	SLC7A5, LOC100506670	32980, 6159	in gene, downstream	ActReg chr16 #6689	0	0	1
6690	16	87,965,090	87,966,143	1,053	1	9.344	11.469	7.906	19	17	12	0	0	1	CA5A	4,496	in gene	ActReg chr16 #6690	0	1	0
6691	16	87,984,061	87,985,209	1,148	2	9.583	17.417	7.194	25	38	11	1	1	1	BANP	-403	upstream	ActReg chr16 #6691	1	1	0
6692	16	88,365,510	88,366,942	1,432	2	12.682	13.386	7.659	29	25	14	0	0	0				ActReg chr16 #6692	1	1	0
6693	16	88,456,289	88,456,876	587	1	2.882	3	11.556	4	5	15	0	0	0				ActReg chr16 #6693	0	0	1
6694	16	88,465,944	88,466,496	552	1	2.333	2.2	12.167	4	4	19	0	0	0				ActReg chr16 #6694	0	0	1
6695	16	88,492,289	88,492,860	571	1	2.941	3	13.235	5	5	17	0	1	1	ZNF469	-1,305	upstream	ActReg chr16 #6695	0	0	1
6696	16	88,509,337	88,510,159	822	1	7.077	11.115	9.72	11	15	17	0	0	2	ZNF469, ZFPM1	15869, -10266	downstream, upstream	ActReg chr16 #6696	0	1	0
6697	16	88,518,798	88,519,403	605	1	8.474	3.737	12.21	12	6	17	1	1	1	ZFPM1	-914	upstream	ActReg chr16 #6697	0	0	1
6698	16	88,529,129	88,530,041	912	1	2.593	4.321	11.679	4	7	22	0	0	1	ZFPM1	9,571	in gene	ActReg chr16 #6698	0	0	1
6699	16	88,539,885	88,540,241	356	1	5.909	4	11.636	9	9	15	1	0	1	ZFPM1	20,049	in gene	ActReg chr16 #6699	0	0	1
6700	16	88,557,186	88,558,093	907	1	2.474	2.429	10.893	5	5	16	1	0	1	ZFPM1	37,625	in gene	ActReg chr16 #6700	0	0	1
6701	16	88,567,117	88,567,544	427	1	3.846	5.385	12	9	8	18	0	0	1	ZFPM1	47,316	in gene	ActReg chr16 #6701	0	0	1
6702	16	88,593,753	88,594,257	504	1	9.125	6.562	10.938	13	10	15	0	0	1	ZFPM1	73,991	in gene	ActReg chr16 #6702	0	0	1
6703	16	88,601,763	88,602,220	457	1	5.5	5.643	11.643	8	7	18	0	0	1	ZFPM1	81,977	downstream	ActReg chr16 #6703	0	0	1
6704	16	88,626,561	88,628,274	1,713	2	14.226	17.076	5.48	37	34	9	0	0	1	ZC3H18	-9,372	upstream	ActReg chr16 #6704	1	1	0
6705	16	88,698,626	88,699,175	547	1	1.833	1.647	13	3	2	17	0	1	2	ZC3H18, IL17C	62112, -6100	downstream, upstream	ActReg chr16 #6705	0	0	1
6706	16	88,700,161	88,700,978	817	1	5.12	3.76	13.52	9	7	19	1	1	3	ZC3H18, IL17C, CYBA	63780, -4432, 16888	downstream, upstream, downstream	ActReg chr16 #6706	0	0	1
6707	16	88,704,814	88,705,438	624	1	2.947	4.368	11.526	4	7	15	0	1	3	ZC3H18, IL17C, CYBA	68337, 125, 12331	downstream, in gene, downstream	ActReg chr16 #6707	0	0	1
6708	16	88,705,678	88,706,332	654	1	2.579	4.85	13.05	6	7	19	1	1	3	ZC3H18, IL17C, CYBA	69216, 1004, 11452	downstream, in gene, downstream	ActReg chr16 #6708	0	0	1
6709	16	88,709,043	88,709,520	477	1	2.8	6.467	11.533	4	10	16	1	0	3	IL17C, CYBA, MVD	4280, 8176, 20214	downstream, downstream, downstream	ActReg chr16 #6709	0	0	1
6710	16	88,713,960	88,714,282	322	1	1.875	5.5	11.7	3	7	14	0	0	3	IL17C, CYBA, MVD	9120, 3336, 15374	downstream, in gene, downstream	ActReg chr16 #6710	0	0	1
6711	16	88,717,767	88,718,471	704	1	6.238	5.318	14.409	11	9	23	1	1	2	CYBA, MVD	-662, 11376	upstream, downstream	ActReg chr16 #6711	0	0	1
6712	16	88,721,716	88,722,265	549	1	5.118	2.333	13.059	7	5	17	2	1	3	CYBA, MVD, MGC23284	-4533, 7505, -7791	upstream, in gene, upstream	ActReg chr16 #6712	0	0	1
6713	16	88,761,456	88,762,073	617	1	5.474	4.421	10.684	12	8	13	0	0	3	MGC23284, SNAI3, RNF166	31983, -8882, 11065	downstream, upstream, downstream	ActReg chr16 #6713	0	0	1
6714	16	88,765,066	88,765,823	757	1	7.261	4.478	13	14	7	19	1	1	2	RNF166, CTU2	7385, -7447	in gene, upstream	ActReg chr16 #6714	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6715	16	88,789,838	88,790,319	481	1	3.167	3.467	11.933	5	5	16	0	1	3	CTU2, FAM38A, LOC100289580	17187, 61294, -7510	downstream, in gene, upstream	ActReg chr16 #6715	0	0	1
6716	16	88,793,210	88,793,793	583	1	3.059	3.842	13.526	5	7	22	1	1	2	FAM38A, LOC100289580	57871, -4087	in gene, upstream	ActReg chr16 #6716	0	0	1
6717	16	88,798,486	88,799,101	615	1	4.556	4.947	15.474	7	9	25	0	1	2	FAM38A, LOC100289580	52579, 1205	in gene, in gene	ActReg chr16 #6717	0	0	1
6718	16	88,800,796	88,801,461	665	1	2.45	6.095	11.048	5	10	13	0	0	3	FAM38A, LOC100289580, FLJ40448	50244, 3540, -8047	in gene, in gene, upstream	ActReg chr16 #6718	0	0	1
6719	16	88,810,181	88,811,092	911	1	5.5	4.214	13.679	9	6	19	0	1	3	FAM38A, LOC100289580, FLJ40448	40736, 13048, 1461	in gene, downstream, in gene	ActReg chr16 #6719	0	0	1
6720	16	88,816,693	88,817,086	393	1	3	3.818	13.667	5	5	19	0	0	2	FAM38A, FLJ40448	34483, 7714	in gene, downstream	ActReg chr16 #6720	0	0	1
6721	16	88,834,469	88,835,201	732	1	4.476	4.739	10.957	8	9	17	0	0	1	FAM38A	16,537	in gene	ActReg chr16 #6721	0	0	1
6722	16	88,851,705	88,852,462	757	2	11.417	12.208	4.842	18	18	10	1	1	1	FAM38A	-711	upstream	ActReg chr16 #6722	1	1	0
6723	16	88,869,553	88,870,291	738	2	10.391	13.478	2.652	25	24	5	1	1	3	CDT1, APRT, GALNS	-264, 8420, 53452	upstream, downstream, downstream	ActReg chr16 #6723	1	1	0
6724	16	88,870,842	88,871,442	600	1	7.895	6.211	11.947	14	9	15	0	1	3	CDT1, APRT, GALNS	956, 7200, 52232	in gene, downstream, downstream	ActReg chr16 #6724	0	0	1
6725	16	88,872,564	88,873,731	1,167	1	5.432	6.784	12.405	11	11	16	0	1	3	CDT1, APRT, GALNS	2961, 5195, 50227	in gene, downstream, downstream	ActReg chr16 #6725	0	0	1
6726	16	88,873,866	88,874,715	849	1	5.577	7.423	14.154	9	11	24	0	0	3	CDT1, APRT, GALNS	4104, 4052, 49084	in gene, downstream, downstream	ActReg chr16 #6726	0	0	1
6727	16	88,875,830	88,876,530	700	1	5.636	7.409	11.591	10	13	17	0	1	3	CDT1, APRT, GALNS	5994, 2162, 47194	downstream, in gene, downstream	ActReg chr16 #6727	0	0	1
6728	16	88,877,499	88,879,295	1,796	4	16.5	13.571	9.821	31	31	23	1	1	3	CDT1, APRT, GALNS	8211, -55, 44977	downstream, upstream, downstream	ActReg chr16 #6728	1	1	1
6729	16	88,882,443	88,882,957	514	1	6.312	5.562	12.875	11	8	21	1	1	3	CDT1, APRT, GALNS	12514, -4358, 40674	downstream, upstream, in gene	ActReg chr16 #6729	0	0	1
6730	16	88,923,162	88,924,046	884	1	9.464	12.857	6.679	13	23	13	1	2	3	GALNS, TRAPPC2L, PABPN1L	-230, 98, 9410	upstream, in gene, downstream	ActReg chr16 #6730	0	1	0
6731	16	88,930,746	88,931,565	819	1	3.474	2.375	13.923	5	5	18	0	2	4	GALNS, TRAPPC2L, PABPN1L, CBFA2T3	-7781, 7649, 1859, 112246	upstream, downstream, in gene, downstream	ActReg chr16 #6731	0	0	1
6732	16	88,931,983	88,932,733	750	1	2.478	4.217	13.957	4	6	20	0	1	4	GALNS, TRAPPC2L, PABPN1L, CBFA2T3	-8984, 8852, 656, 111043	upstream, downstream, in gene, downstream	ActReg chr16 #6732	0	0	1
6733	16	88,947,781	88,948,324	543	1	3.882	6.765	12.412	7	10	16	1	0	1	CBFA2T3	95,349	in gene	ActReg chr16 #6733	0	0	1
6734	16	88,951,199	88,952,002	803	1	2.654	4.731	12.692	5	10	21	1	0	1	CBFA2T3	91,801	in gene	ActReg chr16 #6734	0	0	1
6735	16	88,958,054	88,958,713	659	1	2.632	3.05	12.25	5	5	17	1	0	1	CBFA2T3	85,018	in gene	ActReg chr16 #6735	0	0	1
6736	16	88,963,266	88,964,157	891	1	3.318	4.926	13.407	6	10	19	1	0	1	CBFA2T3	79,690	in gene	ActReg chr16 #6736	0	0	1
6737	16	88,964,171	88,964,715	544	1	3	3.294	13.294	5	5	18	0	0	1	CBFA2T3	78,958	in gene	ActReg chr16 #6737	0	0	1
6738	16	88,967,630	88,968,518	888	1	5.536	3.481	12.821	8	6	21	0	0	1	CBFA2T3	75,327	in gene	ActReg chr16 #6738	0	0	1
6739	16	88,969,376	88,970,060	684	1	4.045	2.455	11.091	8	5	15	0	0	1	CBFA2T3	73,683	in gene	ActReg chr16 #6739	0	0	1
6740	16	88,973,494	88,974,044	550	1	1.5	3	11.647	2	4	16	0	0	1	CBFA2T3	69,632	in gene	ActReg chr16 #6740	0	0	1
6741	16	88,976,210	88,976,666	456	1	2.643	7.857	11.214	4	12	15	1	0	1	CBFA2T3	66,963	in gene	ActReg chr16 #6741	0	0	1
6742	16	88,988,127	88,989,246	1,119	1	3.743	6.629	13.029	6	12	23	0	0	1	CBFA2T3	54,715	in gene	ActReg chr16 #6742	0	0	1
6743	16	88,994,300	88,995,347	1,047	1	4.424	4.545	12.303	8	8	18	1	0	1	CBFA2T3	48,578	in gene	ActReg chr16 #6743	0	0	1
6744	16	88,999,278	88,999,709	431	1	3.154	4.692	11	5	6	17	1	1	2	CBFA2T3, LOC100129697	43908, -7056	in gene, upstream	ActReg chr16 #6744	0	0	1
6745	16	89,004,403	89,005,006	603	1	5.167	4.053	12.895	10	7	17	0	1	2	CBFA2T3, LOC100129697	38697, -1845	in gene, upstream	ActReg chr16 #6745	0	0	1
6746	16	89,006,624	89,007,236	612	1	4.05	3.8	10.5	7	6	16	1	1	2	CBFA2T3, LOC100129697	36471, 381	in gene, in gene	ActReg chr16 #6746	0	0	1
6747	16	89,022,734	89,023,355	621	1	3.947	3.368	12.105	7	5	16	0	0	2	CBFA2T3, LOC100129697	20357, 16495	in gene, downstream	ActReg chr16 #6747	0	0	1
6748	16	89,025,146	89,025,648	502	1	4.125	5.625	12.125	6	8	15	0	0	2	CBFA2T3, LOC100129697	18004, 18848	in gene, downstream	ActReg chr16 #6748	0	0	1
6749	16	89,039,274	89,039,787	513	1	2.923	3.188	12.562	5	5	17	0	0	1	CBFA2T3	3,871	in gene	ActReg chr16 #6749	0	0	1
6750	16	89,050,089	89,050,601	512	1	2.438	2.25	13.438	5	5	18	0	1	1	CBFA2T3	-6,944	upstream	ActReg chr16 #6750	0	0	1
6751	16	89,055,977	89,056,481	504	1	4.25	4.062	12.938	7	7	20	0	0	0				ActReg chr16 #6751	0	0	1
6752	16	89,075,675	89,076,575	900	1	8.536	13.143	5.571	13	21	9	0	0	0				ActReg chr16 #6752	0	1	0
6753	16	89,082,170	89,083,699	1,529	2	13.729	15.375	3.659	27	35	11	0	0	0				ActReg chr16 #6753	1	1	0
6754	16	89,103,345	89,104,483	1,138	1	8.028	10.667	8.361	16	16	15	0	0	1	LOC100506183	15,459	downstream	ActReg chr16 #6754	0	1	0
6755	16	89,105,688	89,106,583	895	1	2.739	4.536	10.893	6	7	15	0	0	1	LOC100506183	13,238	downstream	ActReg chr16 #6755	0	0	1
6756	16	89,118,363	89,119,055	692	1	4.364	9.091	11.954	7	12	17	1	1	1	LOC100506183	664	in gene	ActReg chr16 #6756	0	0	1
6757	16	89,121,222	89,121,646	424	1	6.615	2.462	12.769	11	4	17	0	1	1	LOC100506183	-2,061	upstream	ActReg chr16 #6757	0	0	1
6758	16	89,121,833	89,122,378	545	1	2.412	5.824	10.412	4	11	12	0	1	1	LOC100506183	-2,732	upstream	ActReg chr16 #6758	0	0	1
6759	16	89,124,624	89,125,276	652	1	2.5	2.6	13.1	3	5	21	0	1	1	LOC100506183	-5,577	upstream	ActReg chr16 #6759	0	0	1
6760	16	89,133,046	89,133,598	552	1	1.7	2.235	12.882	2	5	19	0	0	0				ActReg chr16 #6760	0	0	1
6761	16	89,219,970	89,220,628	658	1	3.65	4.9	14.05	7	8	22	0	1	2	ACSF3, C16orf81	60045, -5329	in gene, upstream	ActReg chr16 #6761	0	0	1
6762	16	89,223,098	89,223,808	710	1	3.957	5.059	12.435	6	9	21	0	1	2	ACSF3, C16orf81	63199, -2175	downstream, upstream	ActReg chr16 #6762	0	0	1
6763	16	89,227,343	89,227,777	434	1	5.143	5.5	11.643	6	7	19	0	1	2	ACSF3, C16orf81	67306, 1932	downstream, in gene	ActReg chr16 #6763	0	0	1
6764	16	89,233,329	89,233,888	559	1	6.222	7.778	12.889	14	13	18	0	1	2	C16orf81, CDH15	7980, -4555	downstream, upstream	ActReg chr16 #6764	0	0	1
6765	16	89,238,808	89,239,244	436	1	3.5	5.786	13	6	8	17	0	1	2	C16orf81, CDH15	13398, 863	downstream, in gene	ActReg chr16 #6765	0	0	1
6766	16	89,242,552	89,243,142	590	1	4.895	2.579	14.21	7	4	19	0	0	1	CDH15	4,684	in gene	ActReg chr16 #6766	0	0	1
6767	16	89,244,892	89,245,426	534	1	4.235	4.647	12.412	7	7	17	1	0	1	CDH15	6,996	in gene	ActReg chr16 #6767	0	0	1
6768	16	89,261,261	89,261,642	381	1	5.25	4.167	12.667	9	5	17	0	0	3	CDH15, LOC146429, LOC100506202	23288, 5078, 5275	in gene, downstream, downstream	ActReg chr16 #6768	0	0	1
6769	16	89,283,787	89,284,543	756	1	8.609	11.261	10.348	14	16	15	1	1	1	ZNF778	54	in gene	ActReg chr16 #6769	0	1	0
6770	16	89,306,993	89,307,577	584	2	13.611	16.833	4.111	27	30	8	0	0	0				ActReg chr16 #6770	1	1	0
6771	16	89,307,631	89,307,983	352	1	8.364	9.182	10.091	11	12	15	0	0	0				ActReg chr16 #6771	0	0	1
6772	16	89,340,313	89,340,934	621	1	6.8	4.35	12	12	7	17	0	0	1	ANKRD11	216,346	in gene	ActReg chr16 #6772	0	0	1
6773	16	89,361,735	89,362,091	356	1	4.182	2.364	11.182	5	3	15	0	1	2	ANKRD11, LOC100506251	195056, -2003	in gene, upstream	ActReg chr16 #6773	0	0	1
6774	16	89,386,319	89,387,474	1,155	1	8.889	12.833	7.417	13	22	11	0	1	2	ANKRD11, LOC100287036	170073, -645	in gene, upstream	ActReg chr16 #6774	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6775	16	89,573,810	89,574,232	422	1	6.462	6.538	10.615	9	9	14	1	1	2	LOC100506268, SPG7	16288, -784	downstream, upstream	ActReg chr16 #6775	0	0	1
6776	16	89,575,045	89,575,640	595	1	5.222	11.389	6.944	8	17	10	1	1	2	LOC100506268, SPG7	17609, 537	downstream, in gene	ActReg chr16 #6776	0	1	0
6777	16	89,611,694	89,612,032	338	1	2.333	1.909	10.636	4	3	16	0	0	1	SPG7	37,058	in gene	ActReg chr16 #6777	0	0	1
6778	16	89,626,532	89,628,222	1,690	2	8.077	10.385	9.423	20	16	19	1	2	3	SPG7, RPL13, SNORD68	52572, 287, -461	downstream, in gene, upstream	ActReg chr16 #6778	0	1	1
6779	16	89,631,459	89,632,720	1,261	2	7.769	12.077	11.385	15	19	20	1	1	4	SPG7, RPL13, SNORD68, CPNE7	57284, 4999, 4251, -10087	downstream, downstream, downstream, upstream	ActReg chr16 #6779	0	1	1
6780	16	89,637,686	89,638,183	497	1	4.875	6.3	12	8	10	18	0	1	3	RPL13, SNORD68, CPNE7	10844, 10096, -4242	downstream, downstream, upstream	ActReg chr16 #6780	0	0	1
6781	16	89,668,716	89,669,304	588	1	8.278	6.444	13.167	12	9	17	0	0	1	CPNE7	26,834	downstream	ActReg chr16 #6781	0	0	1
6782	16	89,681,612	89,682,208	596	1	3	3.842	11.316	6	8	15	0	1	1	DPEP1	2,194	in gene	ActReg chr16 #6782	0	0	1
6783	16	89,712,279	89,712,628	349	1	4	5.727	12.727	6	12	19	0	0	2	DPEP1, CHMP1A	32737, 11676	downstream, in gene	ActReg chr16 #6783	0	0	1
6784	16	89,760,169	89,760,657	488	1	4.467	6.2	14.133	7	9	21	0	0	2	CDK10, SPATA2L	7337, 7686	in gene, downstream	ActReg chr16 #6784	0	0	1
6785	16	89,763,573	89,764,100	527	1	4.412	5.176	11.235	10	7	17	0	0	3	CDK10, SPATA2L, C16orf7	10760, 4263, 23558	downstream, in gene, downstream	ActReg chr16 #6785	0	0	1
6786	16	89,766,478	89,766,976	498	1	9.25	8.188	13.062	13	13	21	0	1	3	CDK10, SPATA2L, C16orf7	13651, 1372, 20667	downstream, in gene, downstream	ActReg chr16 #6786	0	0	1
6787	16	89,774,428	89,775,175	747	1	3.875	6	14.292	6	9	21	0	2	3	SPATA2L, C16orf7, LOC100128881	-6702, 12593, -3463	upstream, in gene, upstream	ActReg chr16 #6787	0	0	1
6788	16	89,777,310	89,777,885	575	1	3.867	3.056	11.722	7	5	17	1	1	4	SPATA2L, C16orf7, LOC100128881, ZNF276	-9498, 9797, -667, -9796	upstream, in gene, upstream, upstream	ActReg chr16 #6788	0	0	1
6789	16	89,778,161	89,778,874	713	1	4.8	6.136	13.636	7	10	18	1	1	3	C16orf7, LOC100128881, ZNF276	8877, 253, -8876	in gene, in gene, upstream	ActReg chr16 #6789	0	0	1
6790	16	89,787,063	89,787,964	901	2	16.286	14.643	4.185	36	23	8	1	2	3	C16orf7, LOC100128881, ZNF276	-119, 9249, 120	upstream, downstream, in gene	ActReg chr16 #6790	1	1	0
6791	16	89,788,677	89,789,221	544	1	6.647	6.706	14.177	10	10	19	1	2	3	C16orf7, LOC100128881, ZNF276	-1555, 10685, 1556	upstream, downstream, in gene	ActReg chr16 #6791	0	0	1
6792	16	89,789,440	89,789,937	497	1	4.562	8.125	12.75	8	12	21	0	2	3	C16orf7, LOC100128881, ZNF276	-2294, 11424, 2295	upstream, downstream, in gene	ActReg chr16 #6792	0	0	1
6793	16	89,854,399	89,854,874	475	1	2.667	2.133	11.467	5	4	18	0	0	1	FANCA	28,429	in gene	ActReg chr16 #6793	0	0	1
6794	16	89,882,828	89,883,349	521	1	11.125	10.25	5.375	16	16	10	1	1	1	FANCA	-23	upstream	ActReg chr16 #6794	1	0	0
6795	16	89,894,932	89,895,261	329	1	4.3	10.3	0	6	15	0	1	1	1	SPIRE2	189	in gene	ActReg chr16 #6795	0	1	0
6796	16	89,898,435	89,898,854	419	1	7	6.154	10.077	9	9	14	0	0	1	SPIRE2	3,737	in gene	ActReg chr16 #6796	0	0	1
6797	16	89,938,845	89,939,519	674	1	5.286	4.81	13.476	13	8	19	1	1	2	SPIRE2, TCF25	44275, -812	downstream, upstream	ActReg chr16 #6797	0	0	1
6798	16	89,957,657	89,958,161	504	1	3.062	4.688	12.062	5	9	16	0	0	1	TCF25	17,915	in gene	ActReg chr16 #6798	0	0	1
6799	16	89,978,730	89,979,273	543	1	3.471	7.882	12.882	5	12	17	0	1	2	TCF25, MC1R	39007, -5286	downstream, upstream	ActReg chr16 #6799	0	0	1
6800	16	89,985,329	89,986,120	791	1	9.92	6.48	12.56	13	13	17	1	2	3	TCF25, MC1R, TUBB3	45730, 1437, -4021	downstream, in gene, upstream	ActReg chr16 #6800	0	0	1
6801	16	89,988,236	89,989,243	1,007	2	8.645	10.258	9.097	13	17	21	1	1	2	MC1R, TUBB3	4452, -1006	downstream, upstream	ActReg chr16 #6801	0	1	1
6802	16	90,014,619	90,015,281	662	2	14.571	24.952	6.529	38	56	12	1	1	1	DEF8	-201	upstream	ActReg chr16 #6802	1	1	0
6803	16	90,020,214	90,020,717	503	1	5.875	2.75	9.875	10	5	12	0	0	1	DEF8	5,314	in gene	ActReg chr16 #6803	0	0	1
6804	16	90,028,149	90,028,548	399	1	8.692	4.846	12.308	13	7	17	0	0	2	DEF8, CENPBD1	13197, 10594	in gene, downstream	ActReg chr16 #6804	0	0	1
6805	16	90,038,324	90,038,696	372	1	7.667	11.167	10.833	11	14	15	1	1	2	DEF8, CENPBD1	23359, 432	downstream, in gene	ActReg chr16 #6805	0	0	1
6806	16	90,058,875	90,059,368	493	1	4.062	2.938	9.812	7	5	15	0	0	0				ActReg chr16 #6806	0	0	1
6807	16	90,087,162	90,087,882	720	2	11.565	10.652	3.636	21	15	7	0	2	3	DBNDD1, GAS8, C16orf3	-1585, -1486, 8787	upstream, upstream, downstream	ActReg chr16 #6807	1	1	0
6808	16	90,113,119	90,113,896	777	1	5.24	6.4	11.6	7	11	14	0	1	3	GAS8, LOC100130015, PRDM7	24499, 674, 28831	downstream, in gene, downstream	ActReg chr16 #6808	0	0	1
6809	17	15,912	16,295	383	1	4.25	3	11.083	5	5	17	0	0	0				ActReg chr17 #6809	0	0	1
6810	17	206,347	206,862	515	1	1.688	4.312	11.938	3	7	20	1	1	1	RPH3AL	-3,971	upstream	ActReg chr17 #6810	0	0	1
6811	17	234,942	235,348	406	1	3.538	3.692	10.385	6	5	15	1	0	0				ActReg chr17 #6811	0	0	1
6812	17	617,570	618,519	949	2	16.828	13.655	7.69	36	28	12	1	1	1	VPS53	52	in gene	ActReg chr17 #6812	1	1	0
6813	17	685,083	686,007	924	3	12.759	13.724	8.931	19	28	19	1	2	2	GLOD4, RNMTL1	26, 32	in gene, in gene	ActReg chr17 #6813	1	1	1
6814	17	706,261	706,708	447	1	3.571	2.643	13.429	6	3	20	0	0	1	NXN	176,526	in gene	ActReg chr17 #6814	0	0	1
6815	17	899,535	900,859	1,324	2	8.561	12.659	10.171	18	24	20	1	2	3	TIMM22, LOC100506836, ABR	-160, -5610, 190419	upstream, upstream, downstream	ActReg chr17 #6815	0	1	1
6816	17	922,258	922,664	406	1	2.385	4.462	10.538	5	6	15	0	0	2	ABR, MIR3183	168155, 3338	in gene, downstream	ActReg chr17 #6816	0	0	1
6817	17	930,538	930,948	410	1	3.231	3.154	10.769	5	4	16	0	1	2	ABR, MIR3183	159873, -4944	in gene, upstream	ActReg chr17 #6817	0	0	1
6818	17	974,566	975,119	553	1	2.312	4.824	11.529	4	6	15	0	0	1	ABR	115,774	in gene	ActReg chr17 #6818	0	0	1
6819	17	1,011,207	1,011,709	502	1	7.667	8.8	12.333	14	12	16	1	0	1	ABR	79,158	in gene	ActReg chr17 #6819	0	0	1
6820	17	1,013,571	1,015,320	1,749	1	10.056	12.056	4.231	20	18	11	0	0	1	ABR	76,171	in gene	ActReg chr17 #6820	0	1	0
6821	17	1,054,190	1,054,899	709	1	13.091	7.591	3.842	30	12	8	0	0	1	ABR	36,072	in gene	ActReg chr17 #6821	1	0	0
6822	17	1,090,242	1,090,858	616	1	11.316	9.474	7	19	14	10	0	1	1	ABR	66	in gene	ActReg chr17 #6822	1	0	0
6823	17	1,106,742	1,107,213	471	1	6.733	8.933	15.667	10	14	23	1	0	0				ActReg chr17 #6823	0	0	1
6824	17	1,162,432	1,163,153	721	1	7.87	10.957	2.957	13	18	6	1	0	0				ActReg chr17 #6824	0	1	0
6825	17	1,226,590	1,227,052	462	1	9.667	12.6	5.4	15	24	8	0	0	0				ActReg chr17 #6825	0	1	0
6826	17	1,302,888	1,303,739	851	2	6.077	9.769	10	12	16	21	1	1	1	YWHAE	243	in gene	ActReg chr17 #6826	0	1	1
6827	17	1,389,080	1,389,978	898	3	11.607	17.769	8.333	28	34	17	1	0	2	MYO1C, INPP5K	6472, 30653	in gene, downstream	ActReg chr17 #6827	1	1	1
6828	17	1,394,269	1,394,738	469	1	8.8	10.267	12.2	11	13	20	1	1	2	MYO1C, INPP5K	1498, 25679	in gene, downstream	ActReg chr17 #6828	0	0	1
6829	17	1,466,002	1,466,535	536	2	17.706	15.353	3.867	36	30	7	1	1	2	PITPNA, LOC100507036	-160, 13711	upstream, in gene	ActReg chr17 #6829	1	1	0
6830	17	1,494,118	1,494,829	711	1	7.182	8.952	12.364	13	12	18	0	0	1	SLC43A2	37,657	in gene	ActReg chr17 #6830	0	0	1
6831	17	1,524,599	1,525,089	490	1	3.25	3.875	11.312	4	6	17	0	0	1	SLC43A2	7,286	in gene	ActReg chr17 #6831	0	0	1
6832	17	1,533,130	1,533,648	518	1	6	5.875	12.812	7	9	19	1	1	2	SLC43A2, SCARF1	-1259, 15652	upstream, downstream	ActReg chr17 #6832	0	0	1
6833	17	1,551,616	1,552,128	512	1	7.529	8.765	11.177	11	14	15	1	2	3	SCARF1, RILP, PRPF8	-2831, 1520, 36304	upstream, in gene, downstream	ActReg chr17 #6833	0	0	1
6834	17	1,552,827	1,553,586	759	1	6.417	8.583	11.167	10	13	17	1	2	3	SCARF1, RILP, PRPF8	-4165, 186, 34970	upstream, in gene, downstream	ActReg chr17 #6834	0	0	1
6835	17	1,587,865	1,588,543	678	2	5.333	11.238	10.048	9	18	17	1	1	1	PRPF8	-28	upstream	ActReg chr17 #6835	0	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6836	17	1,619,152	1,621,220	2,068	3	13.169	15.369	7.742	24	28	22	1	4	4	TLCD2, C17orf91, MIR22, WDR81	-6524, -620, -2905, 569	upstream, upstream, upstream, in gene	ActReg chr17 #6836	1	1	1
6837	17	1,630,392	1,631,090	698	1	6.318	4	12.273	8	8	16	0	0	1	WDR81	10,924	in gene	ActReg chr17 #6837	0	0	1
6838	17	1,636,897	1,637,780	883	1	3.208	4.36	11.63	6	8	21	1	0	2	WDR81, SERPINF2	17521, -8792	in gene, upstream	ActReg chr17 #6838	0	0	1
6839	17	1,665,574	1,666,212	638	1	4.9	6.25	12.2	6	11	17	0	1	2	SERPINF2, SERPINF1	19763, 634	downstream, in gene	ActReg chr17 #6839	0	0	1
6840	17	1,846,100	1,846,700	600	1	3.842	2.842	12	9	6	18	0	0	1	RTN4RL1	81,778	in gene	ActReg chr17 #6840	0	0	1
6841	17	1,932,891	1,934,334	1,443	3	19.667	20.622	8.622	61	77	17	1	2	2	RTN4RL1, DPH1	-5434, 181	upstream, in gene	ActReg chr17 #6841	1	1	1
6842	17	1,944,519	1,945,831	1,312	2	11.878	10.829	8.634	21	24	17	1	1	4	DPH1, OVCA2, MIR132, MIR212	11744, -102, 8127, 8499	in gene, upstream, downstream, downstream	ActReg chr17 #6842	1	1	0
6843	17	1,954,715	1,955,045	330	1	4.818	3.909	11.727	6	8	15	1	3	6	DPH1, OVCA2, MIR132, MIR212, HIC1, SMG6	21449, 9603, -1578, -1206, -3513, 252189	downstream, downstream, upstream, upstream, upstream, downstream	ActReg chr17 #6843	0	0	1
6844	17	2,239,503	2,240,700	1,197	1	8.27	10.324	11.162	16	19	17	1	4	4	TSR1, SNORD91B, SNORD91A, SGSM2	577, -7597, -6437, -705	in gene, upstream, upstream, upstream	ActReg chr17 #6844	0	0	1
6845	17	2,262,427	2,263,169	742	1	13	10.542	5.042	22	16	9	0	0	1	SGSM2	21,992	in gene	ActReg chr17 #6845	1	0	0
6846	17	2,265,918	2,266,364	446	1	4.083	4	12.143	6	6	17	1	0	1	SGSM2	25,335	in gene	ActReg chr17 #6846	0	0	1
6847	17	2,282,961	2,283,531	570	1	2.278	5.133	10.111	4	10	12	0	0	2	SGSM2, MNT	42440, 21012	in gene, downstream	ActReg chr17 #6847	0	0	1
6848	17	2,295,616	2,297,196	1,580	1	9.38	13.24	6.114	15	21	16	1	0	1	MNT	7,852	in gene	ActReg chr17 #6848	0	1	0
6849	17	2,300,022	2,300,442	420	1	5.462	5.154	12	6	12	18	0	0	2	MNT, LOC284009	4026, 18498	in gene, downstream	ActReg chr17 #6849	0	0	1
6850	17	2,304,047	2,305,502	1,455	2	29.956	56.4	4.281	83	116	8	1	1	2	MNT, LOC284009	-516, 13956	upstream, downstream	ActReg chr17 #6850	1	1	0
6851	17	2,317,911	2,318,311	400	1	2.385	3.818	10.154	3	6	16	0	1	2	LOC284009, METT10D	619, 97089	in gene, downstream	ActReg chr17 #6851	0	0	1
6852	17	2,496,317	2,497,026	709	1	6.348	12.783	4.85	13	24	10	1	1	1	PAFAH1B1	-252	upstream	ActReg chr17 #6852	0	1	0
6853	17	2,593,507	2,593,818	311	1	3.556	3.778	12.333	4	5	15	1	0	2	PAFAH1B1, KIAA0664	96739, 21265	downstream, in gene	ActReg chr17 #6853	0	0	1
6854	17	2,614,832	2,615,552	720	2	11.478	12.348	6.947	23	27	11	1	1	1	KIAA0664	-265	upstream	ActReg chr17 #6854	1	1	0
6855	17	2,653,102	2,653,636	534	1	9.471	12.941	3.118	18	25	6	1	1	1	MIR1253	-1,893	upstream	ActReg chr17 #6855	0	1	0
6856	17	2,858,215	2,858,944	729	2	10.261	10.348	1.955	23	19	4	0	0	1	RAP1GAP2	158,847	in gene	ActReg chr17 #6856	1	1	0
6857	17	2,863,297	2,864,130	833	1	9.333	15.769	7.231	17	27	14	0	0	1	RAP1GAP2	163,981	in gene	ActReg chr17 #6857	0	1	0
6858	17	2,878,674	2,879,196	522	2	9.625	12	4.312	14	19	8	0	0	1	RAP1GAP2	179,203	in gene	ActReg chr17 #6858	1	1	0
6859	17	2,951,890	2,952,505	615	1	8.579	11.79	5.316	13	17	7	1	0	0				ActReg chr17 #6859	0	1	0
6860	17	3,301,158	3,301,595	437	1	9.667	12.154	4.385	17	20	7	0	1	1	OR1E1	328	in gene	ActReg chr17 #6860	0	1	0
6861	17	3,336,561	3,336,986	425	1	8.462	11.923	4.923	14	18	7	0	1	2	OR1E2, SPATA22	362, 38369	in gene, downstream	ActReg chr17 #6861	0	1	0
6862	17	3,434,894	3,436,222	1,328	2	6.317	9.561	9.415	18	14	21	1	0	1	TRPV3	25,731	in gene	ActReg chr17 #6862	1	0	1
6863	17	3,558,382	3,558,943	561	1	3.067	3.529	10.588	6	7	15	0	0	2	CTNS, TAX1BP3	18900, 13311	in gene, downstream	ActReg chr17 #6863	0	0	1
6864	17	3,563,660	3,564,034	374	1	4.167	4.583	11	6	6	17	0	0	3	CTNS, TAX1BP3, TMEM93	24085, 8126, -8243	in gene, downstream, upstream	ActReg chr17 #6864	0	0	1
6865	17	3,571,231	3,572,500	1,269	2	9.6	11.675	10.4	13	20	20	1	2	5	CTNS, TAX1BP3, TMEM93, P2RX5, LOC100506618	32103, 108, -225, 27718, 10705	downstream, in gene, upstream, downstream, downstream	ActReg chr17 #6865	0	1	1
6866	17	3,626,635	3,627,920	1,285	3	19.45	21.825	12.825	47	52	20	1	1	2	ITGAE, GSG2	77260, 80	in gene, in gene	ActReg chr17 #6866	1	1	1
6867	17	3,749,186	3,749,952	766	1	8.125	12.542	7.625	18	23	13	1	1	1	C17orf85	-29	upstream	ActReg chr17 #6867	0	1	0
6868	17	3,807,869	3,808,221	352	1	6.818	1.9	10.364	9	3	14	0	0	1	P2RX1	11,915	in gene	ActReg chr17 #6868	0	0	1
6869	17	3,831,378	3,831,857	479	1	3.933	4.2	12.133	6	9	15	0	0	1	ATP2A3	56,119	in gene	ActReg chr17 #6869	0	0	1
6870	17	4,046,206	4,047,248	1,042	1	9.788	12.636	8.152	20	23	12	1	2	2	ZZEF1, CYB5D2	-474, 265	upstream, in gene	ActReg chr17 #6870	0	1	0
6871	17	4,390,658	4,391,151	493	1	5.067	5.733	12.267	8	8	18	0	0	1	SPNS3	53,685	in gene	ActReg chr17 #6871	0	0	1
6872	17	4,395,949	4,397,126	1,177	2	12.351	16.108	3.676	30	39	8	0	1	2	SPNS3, SPNS2	59318, -5592	downstream, upstream	ActReg chr17 #6872	1	1	0
6873	17	4,436,120	4,436,695	575	1	6.444	8.778	12.722	12	15	17	0	0	2	SPNS2, MYBBP1A	34278, 22274	in gene, downstream	ActReg chr17 #6873	0	0	1
6874	17	4,453,258	4,454,214	956	1	3.148	5.7	12.967	5	8	18	0	0	2	MYBBP1A, GGT6	4945, 10140	in gene, downstream	ActReg chr17 #6874	0	0	1
6875	17	4,458,036	4,458,689	653	1	8.333	9.429	11.619	12	18	16	1	1	2	MYBBP1A, GGT6	319, 5514	in gene, downstream	ActReg chr17 #6875	0	0	1
6876	17	4,478,899	4,479,468	569	1	3.222	3.889	10.222	5	7	13	0	0	1	SMTNL2	-8,093	upstream	ActReg chr17 #6876	0	0	1
6877	17	4,490,524	4,490,979	455	1	3.154	4	10.133	5	6	16	0	0	1	SMTNL2	3,475	in gene	ActReg chr17 #6877	0	0	1
6878	17	4,606,970	4,607,794	824	1	9	13.039	9.385	15	21	13	1	2	2	PELP1, ARRB2	250, -6407	in gene, upstream	ActReg chr17 #6878	0	1	0
6879	17	4,634,284	4,635,250	966	2	12.267	11.167	5.9	20	19	15	1	1	4	ARRB2, MED11, CXCL16, ZMYND15	20978, 44, 8456, -8552	downstream, in gene, downstream, upstream	ActReg chr17 #6879	1	1	0
6880	17	4,692,766	4,694,067	1,301	1	6.854	11.439	5.78	13	18	14	1	4	5	TM4SF5, VMO1, GLTPD2, LOC100288822, PSMB6	18229, -3687, 1162, 459, -6041	downstream, upstream, in gene, in gene, upstream	ActReg chr17 #6880	0	1	0
6881	17	4,793,557	4,793,994	437	1	6.786	3	11.5	10	6	18	0	0	3	MINK1, CHRNE, C17orf107	57140, 12594, -9173	in gene, downstream, upstream	ActReg chr17 #6881	0	0	1
6882	17	4,850,897	4,851,859	962	2	10.567	12.033	10.733	20	17	25	1	3	4	SLC25A11, RNF167, PFN1, ENO3	-7916, 7748, 447, -3006	upstream, downstream, in gene, upstream	ActReg chr17 #6882	0	1	1
6883	17	4,853,516	4,854,094	578	1	10.778	11.222	13.389	15	19	22	1	2	4	RNF167, PFN1, ENO3, SPAG7	10175, -1980, -579, 17327	downstream, upstream, upstream, downstream	ActReg chr17 #6883	0	0	1
6884	17	4,870,187	4,870,514	327	1	11.5	11.3	11.8	14	15	16	1	1	3	ENO3, SPAG7, CAMTA2	15966, 782, 20610	downstream, in gene, downstream	ActReg chr17 #6884	0	0	1
6885	17	4,872,095	4,873,094	999	2	11.594	9.656	6.25	18	16	12	0	1	2	SPAG7, CAMTA2	-1462, 18366	upstream, in gene	ActReg chr17 #6885	1	1	0
6886	17	4,877,100	4,877,524	424	1	1.727	4.556	11	3	7	18	0	1	2	SPAG7, CAMTA2	-6180, 13648	upstream, in gene	ActReg chr17 #6886	0	0	1
6887	17	4,890,180	4,891,397	1,217	3	19.184	18.316	7.342	48	48	14	1	1	3	CAMTA2, INCA1, KIF1C	172, 10117, -10455	in gene, downstream, upstream	ActReg chr17 #6887	1	1	1
6888	17	4,900,576	4,901,956	1,380	2	18.932	17.091	7.35	70	59	12	1	2	3	CAMTA2, INCA1, KIF1C	-10306, -361, 23	upstream, upstream, in gene	ActReg chr17 #6888	1	1	0
6889	17	5,000,334	5,001,168	834	1	3.375	2.417	11.808	8	4	17	1	0	2	ZFP3, ZNF232	18997, 25646	downstream, downstream	ActReg chr17 #6889	0	0	1
6890	17	5,014,705	5,015,426	721	2	10.826	10.435	9.13	16	18	12	1	1	2	ZNF232, LOC100506676	11332, 302	in gene, in gene	ActReg chr17 #6890	1	1	0
6891	17	5,035,372	5,035,767	395	1	2.3	1.917	15.917	3	3	22	0	0	2	ZNF232, USP6	-9172, 3882	upstream, in gene	ActReg chr17 #6891	0	0	1
6892	17	5,094,691	5,095,921	1,230	2	37.263	41.947	8.895	129	145	16	1	2	2	ZNF594, LOC100130950	-128, -73	upstream, upstream	ActReg chr17 #6892	1	1	0
6893	17	5,342,000	5,342,919	919	2	12.379	16.759	4.643	26	30	14	1	1	3	RPAIN, C1QBP, DHX33	19498, 12, 29722	downstream, in gene, downstream	ActReg chr17 #6893	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6894	17	5,371,919	5,372,793	874	2	13	13.518	7.238	24	24	15	1	1	2	DHX33, DERL2	-175, 17141	upstream, downstream	ActReg chr17 #6894	1	1	0
6895	17	5,388,918	5,389,460	542	1	7.294	10.882	6.647	10	16	10	1	2	2	DERL2, MIS12	308, -1058	in gene, upstream	ActReg chr17 #6895	0	1	0
6896	17	5,389,775	5,390,567	792	2	7.88	11.04	10.625	14	17	17	1	2	2	DERL2, MIS12	-674, -76	upstream, upstream	ActReg chr17 #6896	0	1	1
6897	17	5,404,111	5,404,592	481	1	6.2	6.933	11.8	9	9	20	1	1	3	MIS12, LOC728392, NLRP1	14104, -32, 83481	downstream, upstream, downstream	ActReg chr17 #6897	0	0	1
6898	17	5,430,032	5,430,627	595	1	9.526	11.79	6.053	18	20	10	0	0	1	NLRP1	57,503	in gene	ActReg chr17 #6898	0	1	0
6899	17	5,496,651	5,497,433	782	1	8.417	15.667	4.875	17	26	9	0	0	1	NLRP1	-9,210	upstream	ActReg chr17 #6899	0	1	0
6900	17	5,592,299	5,592,918	619	1	2.706	2.895	11.105	6	5	14	0	0	0				ActReg chr17 #6900	0	0	1
6901	17	5,969,419	5,970,155	736	1	7	11.435	2.909	12	24	5	0	1	1	WSCD1	-4,147	upstream	ActReg chr17 #6901	0	1	0
6902	17	6,172,618	6,173,415	797	2	13.68	16.48	2.8	31	34	5	0	0	0				ActReg chr17 #6902	1	1	0
6903	17	6,206,814	6,207,615	1,001	2	17.871	20.839	2.538	40	47	4	0	0	0				ActReg chr17 #6903	1	1	0
6904	17	6,268,500	6,269,267	767	1	6.167	11.667	4.833	10	17	8	0	0	0				ActReg chr17 #6904	0	1	0
6905	17	6,347,293	6,348,019	726	1	8.652	10	12.261	11	17	18	1	1	3	AIPL1, FAM84A, PITPNM3	-9137, -139, 112221	upstream, upstream, downstream	ActReg chr17 #6905	0	0	1
6906	17	6,429,503	6,430,111	608	1	11.842	11.105	2.4	18	17	4	0	0	1	PITPNM3	30,070	in gene	ActReg chr17 #6906	1	0	0
6907	17	6,543,854	6,544,778	924	3	15.793	12.862	9.517	33	22	15	1	2	3	KIAA0753, TXNDC17, MED31	-69, 94, 10638	upstream, in gene, downstream	ActReg chr17 #6907	1	1	1
6908	17	6,554,757	6,555,588	831	1	9.231	11.5	9.577	14	14	14	1	2	3	TXNDC17, MED31, C17orf100	10950, -218, 113	downstream, upstream, in gene	ActReg chr17 #6908	0	1	0
6909	17	6,572,194	6,573,063	869	1	12.185	11.518	3.741	18	19	6	0	0	0				ActReg chr17 #6909	1	0	0
6910	17	6,616,332	6,616,929	597	1	5	2.882	13.895	7	4	20	1	1	1	SLC13A5	110	in gene	ActReg chr17 #6910	0	0	1
6911	17	6,915,374	6,916,323	949	2	13.033	13.867	4.833	25	27	10	1	3	7	LOC100506713, ALOX12, RNASEK, C17orf49, LOC100506755, MIR195, MIR497	-180, 16464, 50, -2225, 7125, 5172, 5493	upstream, downstream, in gene, upstream, downstream, downstream, downstream	ActReg chr17 #6911	1	1	0
6912	17	6,917,336	6,918,575	1,239	2	12.462	13.256	6.526	30	32	13	1	4	8	LOC100506713, ALOX12, RNASEK, C17orf49, LOC100506755, MIR195, MIR497, BCL6B	-2287, 18571, 2157, -118, 5018, 3065, 3386, -8414	upstream, downstream, downstream, upstream, downstream, downstream, downstream, upstream	ActReg chr17 #6912	1	1	0
6913	17	6,946,613	6,947,094	481	1	2.533	4.4	12.133	4	6	19	1	1	2	SLC16A13, SLC16A11	7459, 389	downstream, in gene	ActReg chr17 #6913	0	0	1
6914	17	6,953,965	6,954,265	300	1	3	3.333	11.222	6	5	14	0	1	1	SLC16A11	-6,873	upstream	ActReg chr17 #6914	0	0	1
6915	17	6,963,641	6,964,219	578	1	10.278	10.389	2.778	18	14	6	0	0	0				ActReg chr17 #6915	1	0	0
6916	17	7,077,115	7,077,646	531	1	4	2.647	10.706	5	6	13	1	0	1	ASGR1	5,503	in gene	ActReg chr17 #6916	0	0	1
6917	17	7,117,923	7,118,847	924	1	11.929	15.107	3.821	22	26	9	1	1	4	DLG4, ACADVL, MIR324, DVL2	4984, -4768, 8313, 19478	in gene, upstream, downstream, downstream	ActReg chr17 #6917	0	1	0
6918	17	7,122,922	7,124,024	1,102	2	9.676	12.559	11.353	16	20	26	1	2	4	DLG4, ACADVL, MIR324, DVL2	-104, 320, 3225, 14390	upstream, in gene, downstream, downstream	ActReg chr17 #6918	0	1	1
6919	17	7,137,485	7,138,344	859	2	12.556	13.667	5.556	19	20	12	1	1	5	ACADVL, DVL2, PHF23, GABARAP, DULLARD	14761, -51, 4911, 7839, 17345	downstream, upstream, upstream, downstream, downstream, downstream	ActReg chr17 #6919	1	1	0
6920	17	7,142,469	7,143,258	789	2	9.958	12.042	8.375	16	20	18	1	3	4	DVL2, PHF23, GABARAP, DULLARD	-5000, -38, 2890, 12396	upstream, upstream, downstream, downstream	ActReg chr17 #6920	0	1	1
6921	17	7,154,951	7,156,201	1,250	3	10.231	12.128	12.054	18	20	23	1	2	4	GABARAP, DULLARD, C17orf81, CLDN7	-9823, -317, 204, 10936	upstream, upstream, in gene, downstream	ActReg chr17 #6921	1	1	1
6922	17	7,184,094	7,184,793	699	1	6.045	7.364	11.727	13	13	18	1	1	3	SLC2A4, LOC100506772, YBX2	-611, 2947, 13433	upstream, downstream, downstream	ActReg chr17 #6922	0	0	1
6923	17	7,192,972	7,193,504	532	1	2.438	3.529	11.765	3	6	20	1	1	3	SLC2A4, LOC100506772, YBX2	8184, -5848, 4638	downstream, upstream, in gene	ActReg chr17 #6923	0	0	1
6924	17	7,198,193	7,198,597	404	1	4.077	4.846	12.538	6	7	19	1	1	2	SLC2A4, YBX2	13341, -519	downstream, upstream	ActReg chr17 #6924	0	0	1
6925	17	7,210,103	7,211,190	1,087	1	6.412	11.088	5.471	9	17	10	1	1	3	EIF5A, GPS2, NEURL4	328, 8012, 21992	in gene, downstream, downstream	ActReg chr17 #6925	0	1	0
6926	17	7,217,925	7,218,480	555	2	7.438	14.647	9.294	13	28	18	1	1	3	EIF5A, GPS2, NEURL4	7884, 456, 14456	downstream, in gene, downstream	ActReg chr17 #6926	0	1	1
6927	17	7,218,596	7,219,479	883	1	5.815	8.667	12.259	9	16	21	1	1	3	EIF5A, GPS2, NEURL4	8719, -379, 13601	downstream, upstream, in gene	ActReg chr17 #6927	0	0	1
6928	17	7,232,619	7,233,372	753	1	9.609	13.043	8.652	18	26	16	1	3	3	NEURL4, LOC390760, ACAP1	-357, -776, -6855	upstream, upstream, upstream	ActReg chr17 #6928	0	1	0
6929	17	7,254,999	7,255,802	803	2	11.56	15.04	7.292	17	25	15	1	2	3	ACAP1, KCTD11, TMEM95	15552, 192, -3097	downstream, in gene, upstream	ActReg chr17 #6929	1	1	0
6930	17	7,287,717	7,288,191	474	1	2.364	4	12.357	3	7	16	1	0	2	TNK1, PLSCR3	3589, 9889	in gene, downstream	ActReg chr17 #6930	0	0	1
6931	17	7,297,264	7,297,786	522	1	3.812	6.938	11.312	7	9	17	1	1	3	TNK1, PLSCR3, C17orf81	13160, 318, 9893	downstream, in gene, downstream	ActReg chr17 #6931	0	0	1
6932	17	7,382,995	7,383,590	595	2	5.579	11.684	12.333	9	16	25	0	2	3	ZBTB4, AMAC1L3, POLR2A	4276, -1429, -4558	in gene, upstream, upstream	ActReg chr17 #6932	0	1	1
6933	17	7,386,414	7,388,499	2,085	3	35.354	34.892	9.328	201	176	22	1	3	3	ZBTB4, AMAC1L3, POLR2A	112, 2735, -394	in gene, downstream, upstream	ActReg chr17 #6933	1	1	1
6934	17	7,452,547	7,453,070	523	1	4.25	7.562	14	6	14	20	1	2	3	TNFSF12, TNFSF12-TNFSF13, TNFSF13	433, 392, -8801	in gene, in gene, upstream	ActReg chr17 #6934	0	0	1
6935	17	7,475,566	7,476,821	1,255	1	8.974	14.718	8.231	14	22	14	1	1	6	SENP3, EIF4A1, SNORA48, SNORD10, SNORA67, CD68	10874, 136, -1838, -3936, -5080, -6612	downstream, in gene, upstream, upstream, upstream, upstream	ActReg chr17 #6935	0	1	0
6936	17	7,482,512	7,483,647	1,135	1	10.057	11.8	5.029	17	18	10	0	4	8	SENP3, EIF4A1, SNORA48, SNORD10, SNORA67, CD68, MPDU1, SOX15	17760, 7022, 5048, 2950, 1806, 274, -3886, 10409	downstream, downstream, downstream, downstream, downstream, in gene, upstream, downstream	ActReg chr17 #6936	0	1	0
6937	17	7,485,992	7,486,530	538	1	7.235	6.882	12.882	9	12	21	1	1	8	EIF4A1, SNORA48, SNORD10, SNORA67, CD68, MPDU1, SOX15, FXR2	10204, 8230, 6132, 4988, 3456, -704, 7227, 31954	downstream, downstream, downstream, downstream, downstream, upstream, downstream, downstream	ActReg chr17 #6937	0	0	1
6938	17	7,486,658	7,487,965	1,307	1	10.575	11.8	9.475	17	22	17	1	1	8	EIF4A1, SNORA48, SNORD10, SNORA67, CD68, MPDU1, SOX15, FXR2	11254, 9280, 7182, 6038, 4506, 346, 6177, 30904	downstream, downstream, downstream, downstream, downstream, in gene, downstream, downstream	ActReg chr17 #6938	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
6939	17	7,553,784	7,554,440	656	1	5.429	10.905	3.095	11	20	6	1	1	1	ATP1B2	-142	upstream	ActReg chr17 #6939	0	1	0
6940	17	7,589,216	7,590,391	1,175	2	11.108	10.514	5.622	16	17	12	1	3	3	TP53, LOC100506809, WRAP53	1060, -181, 414	in gene, upstream, in gene	ActReg chr17 #6940	1	1	0
6941	17	7,607,923	7,608,654	731	1	12.435	11.696	6.348	25	19	11	1	1	2	WRAP53, EFNB3	18899, -232	downstream, upstream	ActReg chr17 #6941	1	0	0
6942	17	7,615,231	7,615,852	621	1	3.65	4.45	13	6	9	18	0	1	3	WRAP53, EFNB3, DNAH2	26152, 7021, -7498	downstream, downstream, upstream	ActReg chr17 #6942	0	0	1
6943	17	7,620,112	7,621,137	1,025	2	14.406	16.812	6.594	29	43	11	1	1	2	EFNB3, DNAH2	12104, -2415	downstream, upstream	ActReg chr17 #6943	1	1	0
6944	17	7,739,141	7,739,697	556	1	7.471	8.059	11.823	10	11	15	1	1	2	DNAH2, KDM6B	116380, -3816	downstream, upstream	ActReg chr17 #6944	0	0	1
6945	17	7,739,784	7,740,696	912	2	21.143	18.75	3.115	52	47	7	1	1	2	DNAH2, KDM6B	117201, -2995	downstream, upstream	ActReg chr17 #6945	1	1	0
6946	17	7,744,892	7,746,702	1,810	3	12.491	11.947	9.263	22	19	18	1	1	2	DNAH2, KDM6B	122758, 2562	downstream, in gene	ActReg chr17 #6946	1	1	1
6947	17	7,746,890	7,748,157	1,267	1	8.333	11.077	6.897	16	18	12	1	0	2	DNAH2, KDM6B	124484, 4288	downstream, in gene	ActReg chr17 #6947	0	1	0
6948	17	7,748,390	7,748,984	594	1	6.667	6.333	13.278	10	11	18	1	0	2	KDM6B, TMEM88	5452, -9697	in gene, upstream	ActReg chr17 #6948	0	0	1
6949	17	7,758,349	7,759,011	662	1	5.143	6.19	10.619	8	10	15	1	3	4	KDM6B, TMEM88, LSMD1, CYB5D1	15445, 296, 2492, -2384	downstream, in gene, downstream, upstream	ActReg chr17 #6949	0	0	1
6950	17	7,760,091	7,762,136	2,045	4	9.219	12.234	9.062	21	25	16	1	3	4	KDM6B, TMEM88, LSMD1, CYB5D1	17878, 2729, 59, 49	downstream, downstream, in gene, in gene	ActReg chr17 #6950	1	1	1
6951	17	7,788,751	7,789,730	979	2	9.613	9.935	7.129	15	22	11	1	1	1	CHD3	1,117	in gene	ActReg chr17 #6951	1	1	0
6952	17	7,819,490	7,819,927	437	1	10.692	10.692	14.308	16	18	20	1	1	4	CHD3, SCARNA21, LOC284023, KCNAB3	31585, 10267, -443, 13045	downstream, downstream, upstream, downstream	ActReg chr17 #6952	0	0	1
6953	17	7,982,461	7,982,981	520	1	9.688	7.941	10.294	16	15	15	1	0	2	ALOX12B, MIR4314	8300, -8653	in gene, upstream	ActReg chr17 #6953	0	0	1
6954	17	7,982,982	7,983,728	746	1	7.435	10.739	5.652	10	15	10	1	0	2	ALOX12B, MIR4314	7666, -8019	in gene, upstream	ActReg chr17 #6954	0	1	0
6955	17	8,013,553	8,014,037	484	1	5.133	6.267	12.333	9	9	19	1	0	2	ALOXE3, HES7	8439, 13615	in gene, downstream	ActReg chr17 #6955	0	0	1
6956	17	8,022,175	8,022,654	479	1	7.467	9.933	11.8	9	13	17	1	1	2	ALOXE3, HES7	-180, 4996	upstream, downstream	ActReg chr17 #6956	0	0	1
6957	17	8,022,702	8,024,524	1,822	3	10.123	8.632	9.228	25	19	19	1	1	2	ALOXE3, HES7	-1379, 3797	upstream, downstream	ActReg chr17 #6957	1	1	1
6958	17	8,025,757	8,026,776	1,019	2	7.625	8.656	9.5	12	17	18	1	2	2	ALOXE3, HES7	-4032, 1144	upstream, in gene	ActReg chr17 #6958	0	1	1
6959	17	8,028,657	8,029,329	672	2	12.286	7.714	11.619	20	15	22	1	2	2	ALOXE3, HES7	-6759, -1583	upstream, upstream	ActReg chr17 #6959	1	0	1
6960	17	8,041,867	8,043,164	1,297	3	12.725	9.6	9.925	28	18	20	0	0	1	PER1	13,208	downstream	ActReg chr17 #6960	1	1	1
6961	17	8,043,968	8,044,382	414	1	3.923	2.769	11	6	5	14	0	0	1	PER1	11,578	in gene	ActReg chr17 #6961	0	0	1
6962	17	8,076,489	8,077,475	986	2	13.677	15.258	6	22	32	13	0	2	2	TMEM107, SNORD118	2732, -76	in gene, upstream	ActReg chr17 #6962	1	1	0
6963	17	8,079,542	8,080,016	474	1	11.133	10.067	11.667	15	13	15	1	2	2	TMEM107, SNORD118	-65, -2873	upstream, upstream	ActReg chr17 #6963	0	0	1
6964	17	8,089,211	8,091,492	2,281	3	12.806	11.875	14.083	26	27	31	1	1	2	TMEM107, C17orf59	-10637, 3213	upstream, downstream	ActReg chr17 #6964	1	1	1
6965	17	8,092,219	8,094,000	1,781	2	10.625	14.643	7.611	23	32	13	1	1	1	C17orf59	455	in gene	ActReg chr17 #6965	1	1	0
6966	17	8,103,282	8,103,909	627	1	6.1	11.95	5.45	10	16	10	0	0	2	C17orf59, AURKB	-10031, 10288	upstream, downstream	ActReg chr17 #6966	0	1	0
6967	17	8,123,909	8,127,344	3,435	6	10.421	12.346	12.766	23	32	36	2	1	2	C17orf44, C17orf68	1735, 25787	in gene, downstream	ActReg chr17 #6967	1	1	1
6968	17	8,129,820	8,130,562	742	1	8.833	11.667	13.542	16	20	23	0	1	2	C17orf44, C17orf68	-2830, 21222	upstream, in gene	ActReg chr17 #6968	0	0	1
6969	17	8,191,654	8,192,594	940	1	7	12.103	9.345	10	18	15	1	1	2	SLC25A35, RANGRF	6046, 155	in gene, in gene	ActReg chr17 #6969	0	1	0
6970	17	8,214,325	8,214,735	410	1	4.077	5.385	10.308	7	7	15	0	1	1	ARHGEF15	974	in gene	ActReg chr17 #6970	0	0	1
6971	17	8,286,052	8,287,374	1,322	3	43.707	51.463	7.951	155	171	22	1	1	2	RPL26, RNF222	-148, 14431	upstream, downstream	ActReg chr17 #6971	1	1	1
6972	17	8,295,703	8,296,390	687	1	3.682	4.318	11.227	7	7	17	1	0	2	RPL26, RNF222	-9481, 5098	upstream, in gene	ActReg chr17 #6972	0	0	1
6973	17	8,762,275	8,763,219	944	2	14.759	12.931	5.138	28	29	8	0	0	1	PIK3R6	8,247	in gene	ActReg chr17 #6973	1	1	0
6974	17	8,791,386	8,791,854	468	1	3.385	5	11.333	5	9	15	1	0	1	PIK3R5	77,404	in gene	ActReg chr17 #6974	0	0	1
6975	17	8,818,721	8,819,530	809	2	12.08	12.8	5.64	17	19	8	0	0	1	PIK3R5	49,899	in gene	ActReg chr17 #6975	1	1	0
6976	17	8,924,016	8,924,482	466	1	6.4	8.2	12.533	9	12	20	1	1	1	NTN1	-610	upstream	ActReg chr17 #6976	0	0	1
6977	17	8,993,983	8,994,431	448	1	2.75	3	11	4	4	17	0	0	1	NTN1	69,348	in gene	ActReg chr17 #6977	0	0	1
6978	17	9,081,491	9,081,790	299	1	1	2.778	11.889	1	4	15	0	0	1	NTN1	156,781	in gene	ActReg chr17 #6978	0	0	1
6979	17	9,478,737	9,479,449	712	2	11.273	11.182	4.545	18	15	7	1	2	2	STX8, WDR16	182, -851	in gene, upstream	ActReg chr17 #6979	1	1	0
6980	17	9,579,917	9,580,566	649	1	12.7	11.1	6.2	16	20	11	0	0	1	USP43	31,291	in gene	ActReg chr17 #6980	1	0	0
6981	17	9,820,263	9,820,686	423	1	3.769	3.154	10.692	6	4	17	0	0	1	GAS7	281,394	in gene	ActReg chr17 #6981	0	0	1
6982	17	9,880,543	9,881,051	508	1	10.938	5.188	0	20	10	0	0	0	1	GAS7	221,071	in gene	ActReg chr17 #6982	1	0	0
6983	17	10,018,273	10,019,156	883	1	7.519	11.222	5.37	15	17	8	0	0	1	GAS7	83,154	in gene	ActReg chr17 #6983	0	1	0
6984	17	10,100,753	10,101,297	544	1	5.235	6.059	12.353	10	12	20	1	1	1	GAS7	843	in gene	ActReg chr17 #6984	0	0	1
6985	17	10,173,498	10,174,271	773	2	10.292	12.292	3.583	17	21	6	0	0	0				ActReg chr17 #6985	1	1	0
6986	17	10,600,449	10,601,322	873	1	8.519	14.963	9.091	14	28	14	1	2	2	SCO1, C17orf48	0, -42	in gene, upstream	ActReg chr17 #6986	0	1	0
6987	17	10,748,357	10,748,686	329	1	4.3	5.5	9.9	6	9	14	0	1	1	hCG_1776018	-7,103	upstream	ActReg chr17 #6987	0	0	1
6988	17	11,023,401	11,023,712	311	1	1.375	2.2	10.4	2	3	14	0	0	0				ActReg chr17 #6988	0	0	1
6989	17	11,462,338	11,462,756	418	1	2.636	2.727	10.615	4	5	13	0	0	1	SHISA6	317,807	in gene	ActReg chr17 #6989	0	0	1
6990	17	11,756,907	11,757,822	915	1	7.357	12.286	2.667	15	19	6	0	0	1	DNAH9	255,616	in gene	ActReg chr17 #6990	0	1	0
6991	17	11,900,261	11,901,493	1,232	2	11.237	10.974	5.316	16	17	12	1	1	1	ZNF18	-188	upstream	ActReg chr17 #6991	1	1	0
6992	17	12,693,018	12,693,454	436	1	7.143	7.357	12.143	12	9	19	1	1	1	RICH2	407	in gene	ActReg chr17 #6992	0	0	1
6993	17	12,920,617	12,921,613	996	2	10.968	12.323	7.903	19	22	13	1	1	1	ELAC2	266	in gene	ActReg chr17 #6993	1	1	0
6994	17	13,464,895	13,465,839	944	1	10.867	12.7	3.04	14	21	5	0	0	1	HS3ST3A1	39,877	in gene	ActReg chr17 #6994	0	1	0
6995	17	13,503,719	13,504,307	588	1	6.167	10.778	5.286	11	17	8	1	1	1	HS3ST3A1	1,231	in gene	ActReg chr17 #6995	0	1	0
6996	17	13,504,947	13,505,603	656	1	7.381	8.238	15.095	12	12	23	1	1	1	HS3ST3A1	569	in gene	ActReg chr17 #6996	0	0	1
6997	17	13,972,329	13,973,250	921	2	9.172	13.138	9.828	17	19	25	1	2	2	LOC100506989, COX10	-14, 70	upstream, in gene	ActReg chr17 #6997	0	1	1
6998	17	15,009,723	15,010,391	668	1	6.905	11.571	1.812	14	27	3	0	0	0				ActReg chr17 #6998	0	1	0
6999	17	15,165,499	15,166,831	1,332	2	7.857	11.691	9.881	15	16	20	1	1	1	PMP22	2,479	in gene	ActReg chr17 #6999	0	1	1
7000	17	15,295,505	15,296,708	1,203	2	8.026	11.947	3.857	18	22	8	0	0	0				ActReg chr17 #7000	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7001	17	15,333,368	15,333,757	389	1	2.333	2.583	10.833	4	4	16	0	0	1	CDRT4	37,363	downstream	ActReg chr17 #7001	0	0	1
7002	17	15,393,473	15,394,611	1,138	1	10.6	9.8	3.657	16	14	8	0	0	0				ActReg chr17 #7002	1	0	0
7003	17	15,602,760	15,603,160	400	1	9.25	8	5.167	13	12	10	1	1	1	ZNF286A	69	in gene	ActReg chr17 #7003	1	0	0
7004	17	15,824,036	15,824,669	633	1	7.789	11.79	3.143	11	17	5	0	0	0				ActReg chr17 #7004	0	1	0
7005	17	15,902,199	15,903,324	1,125	1	8.971	11.943	7.406	21	22	17	1	2	2	ZSWIM7, TTC19	245, -21	in gene, upstream	ActReg chr17 #7005	0	1	0
7006	17	16,119,580	16,119,942	362	1	5.75	6.167	9.75	8	8	14	1	2	2	NCOR1, PIGL	-887, -748	upstream, upstream	ActReg chr17 #7006	0	0	1
7007	17	16,284,181	16,284,995	814	2	7.269	10.808	6.6	12	16	14	1	1	1	UBB	221	in gene	ActReg chr17 #7007	0	1	1
7008	17	16,341,520	16,342,711	1,191	2	7.486	11.838	9.297	14	19	21	1	4	6	TRPV2, NCRNA00188, SNORD49B, SNORD49A, SNORD65, C17orf76	23259, -186, -708, -1235, -2425, 53365	downstream, upstream, upstream, upstream, upstream, downstream	ActReg chr17 #7008	0	1	1
7009	17	16,471,872	16,472,682	810	2	9.308	10.385	10.269	15	20	15	1	1	1	ZNF287	243	in gene	ActReg chr17 #7009	0	1	1
7010	17	16,492,391	16,492,901	510	1	11.25	8.188	11.688	20	11	15	1	0	0				ActReg chr17 #7010	0	0	1
7011	17	16,556,382	16,557,452	1,070	2	7.912	11.118	8.969	19	18	20	1	1	1	ZNF624	250	in gene	ActReg chr17 #7011	0	1	1
7012	17	16,837,591	16,838,268	677	1	4.19	5.619	10.476	6	9	13	0	1	2	TBC1D27, TNFRSF13B	-2111, 37473	upstream, downstream	ActReg chr17 #7012	0	0	1
7013	17	16,900,633	16,901,239	606	1	3.053	3.105	12.79	4	6	17	0	0	0				ActReg chr17 #7013	0	0	1
7014	17	16,946,386	16,947,164	778	1	6.917	10.083	1.792	10	14	5	1	1	1	MPRIP	668	in gene	ActReg chr17 #7014	0	1	0
7015	17	17,108,813	17,110,054	1,241	1	9.59	13.487	6.118	17	24	15	2	1	2	PLD6, FLCN	213, 31069	in gene, downstream	ActReg chr17 #7015	0	1	0
7016	17	17,139,628	17,141,369	1,741	2	21.148	26.018	4.222	78	86	8	1	1	2	FLCN, COPS3	4, 44093	in gene, downstream	ActReg chr17 #7016	1	1	0
7017	17	17,380,214	17,380,788	574	2	12	11.278	8.333	19	18	15	1	1	1	MED9	201	in gene	ActReg chr17 #7017	1	1	0
7018	17	17,398,623	17,398,963	340	1	4.909	5.909	11.909	7	8	19	1	1	3	MED9, RASD1, PEMT	18493, 914, 96201	downstream, in gene, downstream	ActReg chr17 #7018	0	0	1
7019	17	17,432,082	17,432,663	581	1	4.833	4.222	11.222	7	8	15	0	0	1	PEMT	62,622	in gene	ActReg chr17 #7019	0	0	1
7020	17	17,494,085	17,495,589	1,504	3	13.17	15.254	9.319	37	36	20	1	1	1	PEMT	157	in gene	ActReg chr17 #7020	1	1	1
7021	17	17,596,603	17,597,726	1,123	1	9.353	12.343	6.629	16	18	11	1	0	1	RAI1	12,377	in gene	ActReg chr17 #7021	0	1	0
7022	17	17,614,651	17,615,200	549	1	8.333	12	11.389	11	18	17	0	0	1	RAI1	30,138	in gene	ActReg chr17 #7022	0	0	1
7023	17	17,696,218	17,696,967	749	1	5.333	2.905	11.917	8	5	18	0	0	1	RAI1	111,805	in gene	ActReg chr17 #7023	0	0	1
7024	17	17,699,251	17,699,934	683	1	3.095	4.571	11.667	4	9	16	0	0	1	RAI1	114,805	in gene	ActReg chr17 #7024	0	0	1
7025	17	17,716,526	17,717,332	806	1	3.64	8.72	13.08	7	14	18	0	1	3	RAI1, SREBF1, MIR33B	132142, 23396, 316	downstream, in gene, downstream	ActReg chr17 #7025	0	0	1
7026	17	17,717,554	17,717,951	397	1	5	3.333	12.5	7	6	17	0	1	3	RAI1, SREBF1, MIR33B	132965, 22573, -507	downstream, in gene, upstream	ActReg chr17 #7026	0	0	1
7027	17	17,739,520	17,740,287	767	2	11.042	10.333	11.25	15	16	18	1	1	2	SREBF1, TOM1L2	422, 135881	in gene, downstream	ActReg chr17 #7027	1	0	1
7028	17	17,875,340	17,876,397	1,057	2	12.273	10.121	5.5	28	23	12	1	2	2	TOM1L2, LRRC48	-84, -259	upstream, upstream	ActReg chr17 #7028	1	1	0
7029	17	17,928,789	17,930,133	1,344	2	13.357	15.119	3.949	25	28	9	0	0	2	LRRC48, ATPAF2	53334, 13019	downstream, in gene	ActReg chr17 #7029	1	1	0
7030	17	17,936,749	17,937,118	369	1	13.727	11.091	2	22	15	2	0	1	2	ATPAF2, C17orf39	5547, -5678	in gene, upstream	ActReg chr17 #7030	1	0	0
7031	17	17,942,137	17,943,077	940	2	12.133	13.3	6.586	22	22	10	1	2	2	ATPAF2, C17orf39	-127, -4	upstream, upstream	ActReg chr17 #7031	1	1	0
7032	17	17,990,892	17,991,543	651	2	10.8	12.95	9.7	18	26	15	1	1	1	DRG2	-66	upstream	ActReg chr17 #7032	1	1	0
7033	17	18,085,865	18,087,369	1,504	3	11.809	10.298	11.159	20	19	22	1	1	2	MYO15A, ALKBH5	74597, -250	downstream, upstream	ActReg chr17 #7033	1	1	1
7034	17	18,138,340	18,138,743	403	1	6.833	4.083	12.917	10	8	20	0	0	2	LLGL1, FLII	9605, 25514	in gene, downstream	ActReg chr17 #7034	0	0	1
7035	17	18,150,459	18,150,893	434	1	1.8	4.429	11.429	2	7	18	1	0	2	LLGL1, FLII	21740, 11379	downstream, in gene	ActReg chr17 #7035	0	0	1
7036	17	18,161,309	18,162,247	938	3	11.633	11.7	7.9	20	21	17	1	2	2	FLII, SMCR7	277, -2070	in gene, upstream	ActReg chr17 #7036	1	1	1
7037	17	18,163,285	18,164,405	1,120	2	13.971	17	7.879	35	36	13	1	2	2	FLII, SMCR7	-1790, -3	upstream, upstream	ActReg chr17 #7037	1	1	0
7038	17	18,167,153	18,167,787	634	1	3.3	3.65	15.95	8	8	25	1	1	3	FLII, SMCR7, TOP3A	-5415, 3622, 50851	upstream, in gene, downstream	ActReg chr17 #7038	0	0	1
7039	17	18,217,703	18,218,915	1,212	2	8.711	14.263	11.526	12	27	19	1	2	2	TOP3A, SMCR8	12, -285	in gene, upstream	ActReg chr17 #7039	0	1	1
7040	17	18,883,418	18,883,873	455	1	2.667	7.067	11.867	4	10	17	0	0	2	SLC5A10, FAM83G	28167, 24415	in gene, in gene	ActReg chr17 #7040	0	0	1
7041	17	18,967,066	18,967,250	184	1	5.333	5.167	14	7	6	17	1	2	2	SNORD38-1, SNORD38-2	1933, 291	downstream, downstream	ActReg chr17 #7041	0	0	1
7042	17	19,220,383	19,221,639	1,256	2	15.9	17.55	4.333	49	61	9	0	0	1	EPN2	80,321	in gene	ActReg chr17 #7042	1	1	0
7043	17	19,285,793	19,286,400	607	1	6.579	4.579	11.316	9	7	16	0	0	2	MAPK7, MFAP4	5062, 4397	in gene, downstream	ActReg chr17 #7043	0	0	1
7044	17	19,411,095	19,412,014	919	1	9.621	8.828	11.31	19	21	18	1	0	0				ActReg chr17 #7044	0	0	1
7045	17	19,551,340	19,552,654	1,314	2	8.976	13.366	11.268	14	20	22	1	1	1	ALDH3A2	-67	upstream	ActReg chr17 #7045	0	1	1
7046	17	19,557,649	19,558,090	441	1	4.571	3.286	13	8	5	17	0	0	1	ALDH3A2	5,805	in gene	ActReg chr17 #7046	0	0	1
7047	17	19,648,265	19,648,773	508	1	3.125	2.938	12	6	6	21	1	0	1	ALDH3A1	3,227	in gene	ActReg chr17 #7047	0	0	1
7048	17	19,655,921	19,656,831	910	1	10.857	13.536	6.643	24	24	13	0	1	1	ALDH3A1	-4,630	upstream	ActReg chr17 #7048	0	1	0
7049	17	19,881,311	19,881,736	425	1	6.571	6.786	10.786	10	11	17	1	1	1	AKAP10	-394	upstream	ActReg chr17 #7049	0	0	1
7050	17	19,967,151	19,968,131	980	2	11.097	10.161	3.355	14	19	6	0	0	0				ActReg chr17 #7050	1	1	0
7051	17	20,825,543	20,826,022	479	1	7.4	10.933	1.273	10	17	2	0	0	1	LOC100507263	30,120	in gene	ActReg chr17 #7051	0	1	0
7052	17	20,895,526	20,895,961	435	1	5.308	5.769	12.231	10	9	17	0	0	1	USP22	50,609	downstream	ActReg chr17 #7052	0	0	1
7053	17	20,900,220	20,900,736	516	1	4.706	4.529	10.765	10	8	15	0	0	1	USP22	45,874	downstream	ActReg chr17 #7053	0	0	1
7054	17	20,946,652	20,947,268	616	2	10.2	7.9	8.6	20	17	18	1	1	1	USP22	-608	upstream	ActReg chr17 #7054	1	0	1
7055	17	21,002,052	21,002,943	891	1	7.481	10.852	3.519	12	16	8	0	0	0				ActReg chr17 #7055	0	1	0
7056	17	21,029,973	21,030,703	730	1	11.739	10.217	7.304	17	16	11	1	1	1	DHRS7B	80	in gene	ActReg chr17 #7056	1	0	0
7057	17	21,116,790	21,118,215	1,425	3	14.444	11.689	6.814	31	29	13	1	1	1	TMEM11	406	in gene	ActReg chr17 #7057	1	1	1
7058	17	21,190,643	21,192,215	1,572	2	13.49	11.612	5.083	24	20	11	0	0	1	MAP2K3	3,461	in gene	ActReg chr17 #7058	1	1	0
7059	17	21,198,362	21,199,286	924	1	6.517	6.724	13.069	11	12	19	0	0	1	MAP2K3	10,856	in gene	ActReg chr17 #7059	0	0	1
7060	17	21,199,545	21,200,464	919	1	5.759	8.345	12.552	10	12	19	0	0	1	MAP2K3	12,036	in gene	ActReg chr17 #7060	0	0	1
7061	17	21,207,300	21,208,658	1,358	1	5.643	7.857	16.143	10	12	26	0	0	1	MAP2K3	20,011	in gene	ActReg chr17 #7061	0	0	1
7062	17	21,221,209	21,222,716	1,507	1	6.894	6.255	14.447	14	11	23	0	0	1	MAP2K3	33,994	downstream	ActReg chr17 #7062	0	0	1
7063	17	21,226,038	21,227,324	1,286	2	15.3	12.325	14.3	25	19	24	0	0	1	MAP2K3	38,713	downstream	ActReg chr17 #7063	1	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7064	17	21,240,702	21,241,492	790	1	7.04	9.32	17.44	11	16	32	0	0	0				ActReg chr17 #7064	0	0	1
7065	17	21,246,139	21,247,780	1,641	1	9.481	9.442	14.519	18	18	21	0	0	0				ActReg chr17 #7065	0	0	1
7066	17	21,248,014	21,249,005	991	1	7.355	8.968	14	9	15	26	0	0	0				ActReg chr17 #7066	0	0	1
7067	17	21,251,960	21,254,154	2,194	1	5.043	7.029	12.899	9	15	23	0	0	0				ActReg chr17 #7067	0	0	1
7068	17	21,295,639	21,295,993	354	1	3	2.364	11.636	5	3	16	0	0	1	KCNJ12	16,117	in gene	ActReg chr17 #7068	0	0	1
7069	17	21,303,289	21,304,158	869	1	7.852	10.63	13.259	10	17	20	0	0	1	KCNJ12	24,024	in gene	ActReg chr17 #7069	0	0	1
7070	17	21,304,191	21,304,605	414	1	9.385	9.846	17.308	12	14	26	0	0	1	KCNJ12	24,699	in gene	ActReg chr17 #7070	0	0	1
7071	17	21,305,655	21,306,511	856	1	12.074	10.778	14.444	22	18	21	0	0	1	KCNJ12	26,384	in gene	ActReg chr17 #7071	0	0	1
7072	17	21,307,082	21,309,709	2,627	1	9.805	10.207	16.963	21	17	31	0	0	1	KCNJ12	28,696	in gene	ActReg chr17 #7072	0	0	1
7073	17	21,313,156	21,315,297	2,141	1	10.672	11.134	16.09	21	21	34	0	0	1	KCNJ12	34,527	in gene	ActReg chr17 #7073	0	0	1
7074	17	21,315,505	21,317,587	2,082	1	8.923	8.938	17.908	18	15	29	0	0	1	KCNJ12	36,847	in gene	ActReg chr17 #7074	0	0	1
7075	17	21,317,676	21,319,656	1,980	1	8.274	10.323	19.468	15	18	33	1	0	1	KCNJ12	38,967	in gene	ActReg chr17 #7075	0	0	1
7076	17	21,319,709	21,320,857	1,148	1	6.694	5.556	13.417	12	11	23	1	0	1	KCNJ12	40,584	in gene	ActReg chr17 #7076	0	0	1
7077	17	21,323,810	21,325,162	1,352	1	6.619	4.69	13.452	15	10	22	0	0	1	KCNJ12	44,787	downstream	ActReg chr17 #7077	0	0	1
7078	17	21,325,185	21,327,882	2,697	1	6.75	8.06	15.131	12	16	25	0	0	1	KCNJ12	46,834	downstream	ActReg chr17 #7078	0	0	1
7079	17	21,415,216	21,415,669	453	1	5.786	3.857	12.929	7	5	18	1	0	0				ActReg chr17 #7079	0	0	1
7080	17	21,454,253	21,454,995	742	2	4.13	7.826	7.783	7	17	15	1	1	1	C17orf51	317	in gene	ActReg chr17 #7080	0	1	1
7081	17	21,559,212	21,559,799	587	1	6.056	6.5	13.333	8	10	19	0	0	0				ActReg chr17 #7081	0	0	1
7082	17	21,831,195	21,831,577	382	1	3	4.583	10.25	5	7	17	0	0	1	FAM27L	6,016	downstream	ActReg chr17 #7082	0	0	1
7083	17	21,903,099	21,903,296	197	1	20.571	16.143	36.571	27	22	49	0	1	1	FLJ36000	-865	upstream	ActReg chr17 #7083	0	0	1
7084	17	21,904,639	21,904,972	333	1	8.727	10.273	15.727	16	17	28	0	1	1	FLJ36000	743	in gene	ActReg chr17 #7084	0	0	1
7085	17	25,290,170	25,290,636	466	1	6.867	4.583	12.467	9	8	21	1	0	0				ActReg chr17 #7085	0	0	1
7086	17	25,336,031	25,336,455	424	1	3.643	5.143	9.571	6	7	16	0	0	0				ActReg chr17 #7086	0	0	1
7087	17	25,620,859	25,621,993	1,134	2	10.722	12.917	7.083	18	21	14	1	1	1	WSB1	320	in gene	ActReg chr17 #7087	1	1	0
7088	17	25,680,341	25,681,130	789	2	7.8	11.6	6.958	19	16	19	1	0	0				ActReg chr17 #7088	0	1	1
7089	17	25,798,336	25,799,331	995	2	11.469	12.75	3.156	18	20	5	0	1	1	KSR1	-203	upstream	ActReg chr17 #7089	1	1	0
7090	17	26,089,719	26,090,504	785	2	8.625	15.88	2.579	20	40	4	0	0	1	NOS2	37,444	in gene	ActReg chr17 #7090	1	1	0
7091	17	26,104,007	26,104,883	876	2	11.296	11.518	4.333	18	21	7	0	0	1	NOS2	23,110	in gene	ActReg chr17 #7091	1	1	0
7092	17	26,301,726	26,302,856	1,130	1	9.917	12.139	4.706	16	19	9	0	0	0				ActReg chr17 #7092	0	1	0
7093	17	26,335,142	26,336,168	1,026	2	19.844	21.219	2.333	50	64	4	0	0	0				ActReg chr17 #7093	1	1	0
7094	17	26,368,381	26,368,915	534	2	12.059	14.588	5.538	24	28	9	1	1	1	NLK	-1,040	upstream	ActReg chr17 #7094	1	1	0
7095	17	26,645,238	26,646,774	1,536	3	10.188	13.125	10.708	16	22	24	2	1	2	TMEM97, IFT20	-115, 16489	upstream, downstream	ActReg chr17 #7095	1	1	1
7096	17	26,661,972	26,663,434	1,462	2	10.935	13.478	7.13	20	22	14	1	2	3	TMEM97, IFT20, TNFAIP1	16582, -208, 155	downstream, upstream, in gene	ActReg chr17 #7096	1	1	0
7097	17	26,684,092	26,685,104	1,012	2	19.531	22.469	6.156	50	54	11	1	2	4	POLDIP2, TMEM199, SEBOX, VTN	5, -89, 7667, 12775	in gene, upstream, downstream, downstream	ActReg chr17 #7097	1	1	0
7098	17	26,700,487	26,701,203	716	1	9.045	11.636	2.591	13	24	5	0	2	3	SEBOX, VTN, SARM1	-8580, -3472, 1858	upstream, upstream, in gene	ActReg chr17 #7098	0	1	0
7099	17	26,711,226	26,711,721	495	1	4.438	4	11.75	7	7	16	1	0	2	SARM1, SLC46A1	12486, 21755	in gene, downstream	ActReg chr17 #7099	0	0	1
7100	17	26,731,834	26,732,523	689	1	4.227	3.227	12.591	6	5	18	1	1	2	SARM1, SLC46A1	33191, 1050	downstream, in gene	ActReg chr17 #7100	0	0	1
7101	17	26,732,955	26,733,787	832	1	11.192	8.5	5.385	15	12	10	1	1	2	SARM1, SLC46A1	34384, -143	downstream, upstream	ActReg chr17 #7101	1	0	0
7102	17	26,861,812	26,862,290	478	1	2.071	4.6	11.933	3	7	22	0	0	1	FOXN1	11,092	in gene	ActReg chr17 #7102	0	0	1
7103	17	26,925,568	26,927,105	1,537	1	12.674	8.367	6.327	20	14	16	1	2	3	SPAG5, LOC100506436, FLJ25006	-280, 528, 14875	upstream, in gene, downstream	ActReg chr17 #7103	1	0	0
7104	17	26,988,708	26,989,510	802	1	10	11.36	8	15	21	13	1	2	2	SDF2, SUPT6H	-176, -193	upstream, upstream	ActReg chr17 #7104	0	1	0
7105	17	27,043,909	27,044,868	959	2	9.567	10.7	9.8	16	15	18	1	7	8	PROCA1, RAB34, RPL23A, SNORD42B, SNORD4A, SNORD42A, SNORD4B, TLCD1	-5516, 898, -2612, -3180, -5212, -6060, -6311, 9561	upstream, in gene, upstream, upstream, upstream, upstream, downstream, downstream	ActReg chr17 #7105	0	1	1
7106	17	27,046,363	27,047,366	1,003	1	11.25	9.969	8.438	19	17	15	1	7	9	PROCA1, RAB34, RPL23A, SNORD42B, SNORD4A, SNORD42A, SNORD4B, TLCD1, NEK8	-7992, -1578, -136, -704, -2736, -3584, -3835, 7085, -8968	upstream, upstream, upstream, downstream, upstream, upstream, upstream, upstream, downstream, upstream	ActReg chr17 #7106	1	0	0
7107	17	27,051,364	27,053,283	1,919	3	7.136	10.3	8.483	16	16	20	1	6	8	RAB34, RPL23A, SNORD42B, SNORD4A, SNORD42A, SNORD4B, TLCD1, NEK8	-7037, 5323, 4755, 2723, 1875, 1624, 1626, -3509	upstream, downstream, downstream, downstream, downstream, downstream, downstream, in gene, upstream	ActReg chr17 #7107	0	1	1
7108	17	27,053,373	27,054,204	831	2	6.885	11.538	11	11	21	23	1	2	8	RAB34, RPL23A, SNORD42B, SNORD4A, SNORD42A, SNORD4B, TLCD1, NEK8	-8502, 6788, 6220, 4188, 3340, 3089, 161, -2044	upstream, downstream, downstream, downstream, downstream, downstream, downstream, in gene, upstream	ActReg chr17 #7108	0	1	1
7109	17	27,085,542	27,086,077	535	1	3.125	4.688	13.5	5	7	23	0	0	2	TRAF4, C17orf63	14786, 84032	downstream, in gene	ActReg chr17 #7109	0	0	1
7110	17	27,181,389	27,182,577	1,188	2	8.622	16.081	5.273	18	27	13	1	1	3	ERAL1, MIR451, MIR144	-60, 6475, 6653	upstream, downstream, downstream	ActReg chr17 #7110	1	1	0
7111	17	27,278,343	27,279,730	1,387	1	12.233	9.116	5.302	18	20	12	2	1	2	PHF12, SEZ6	-528, 54045	upstream, downstream	ActReg chr17 #7111	1	0	0
7112	17	27,331,008	27,331,984	976	1	9.097	11.161	7.935	22	16	12	0	1	1	SEZ6	1,585	in gene	ActReg chr17 #7112	0	1	0
7113	17	27,332,729	27,333,594	865	2	12.704	14.185	4.64	32	31	8	1	1	1	SEZ6	-80	upstream	ActReg chr17 #7113	1	1	0
7114	17	27,334,453	27,335,481	1,028	2	13.719	11.469	3.897	30	23	6	0	1	1	SEZ6	-1,886	upstream	ActReg chr17 #7114	1	1	0
7115	17	27,441,614	27,443,001	1,387	1	3.605	4.512	11.628	11	8	16	0	0	1	MYO18A	65,100	in gene	ActReg chr17 #7115	0	0	1
7116	17	27,459,723	27,460,563	840	2	11.231	7.192	9.269	20	13	19	0	0	1	MYO18A	47,264	in gene	ActReg chr17 #7116	1	0	1
7117	17	27,478,370	27,479,030	660	1	10.95	11.9	3.75	18	23	5	0	0	1	MYO18A	28,707	in gene	ActReg chr17 #7117	0	1	0
7118	17	27,481,730	27,483,133	1,403	1	8	12.302	6.951	13	21	12	0	0	1	MYO18A	24,976	in gene	ActReg chr17 #7118	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7119	17	27,522,608	27,523,230	622	1	7.316	12	2.105	11	20	4	0	0	0				ActReg chr17 #7119	0	1	0
7120	17	27,567,765	27,568,719	954	1	6	13.233	3.429	11	20	8	0	1	1	CRYBA1	-5,633	upstream	ActReg chr17 #7120	0	1	0
7121	17	27,620,786	27,621,707	921	1	9.103	14.054	7.92	16	26	14	1	1	1	NUP1P2	-80	upstream	ActReg chr17 #7121	0	1	0
7122	17	27,893,034	27,893,938	904	1	4.429	9.893	8.143	7	17	14	1	2	3	ABHD15, TP53I13, GIT1	556, -2253, 23124	in gene, upstream, downstream	ActReg chr17 #7122	0	1	0
7123	17	27,916,641	27,917,289	648	1	10.1	12.15	2.769	17	23	4	1	2	2	GIT1, ANKRD13B	-355, -3562	upstream, upstream	ActReg chr17 #7123	0	1	0
7124	17	27,920,769	27,921,823	1,054	1	9.719	11.875	6.875	16	18	11	1	2	2	GIT1, ANKRD13B	-4686, 769	upstream, in gene	ActReg chr17 #7124	0	1	0
7125	17	28,087,975	28,088,555	580	2	7.889	12.389	8.556	16	19	18	1	0	1	SSH2	168,753	in gene	ActReg chr17 #7125	0	1	1
7126	17	28,256,632	28,257,620	988	2	7.806	10.194	8.452	14	15	20	1	2	2	SSH2, EFCAB5	-108, 252	upstream, in gene	ActReg chr17 #7126	0	1	1
7127	17	28,703,655	28,704,482	827	1	6.346	11.385	1.792	10	17	3	0	1	1	CPD	-1,916	upstream	ActReg chr17 #7127	0	1	0
7128	17	28,705,246	28,706,542	1,296	3	9.366	13.024	7.1	18	24	17	1	1	1	CPD	-90	upstream	ActReg chr17 #7128	1	1	1
7129	17	28,715,243	28,715,787	544	1	5.059	4.067	11.706	8	9	14	0	0	1	CPD	9,531	in gene	ActReg chr17 #7129	0	0	1
7130	17	28,803,779	28,804,973	1,194	2	31.081	30.676	4.973	102	100	10	1	1	2	CPD, GOSR1	98392, -50	downstream, upstream	ActReg chr17 #7130	1	1	0
7131	17	28,877,444	28,878,321	877	1	10.444	8.741	5.519	15	14	10	0	0	1	TBC1D29	-8,702	upstream	ActReg chr17 #7131	1	0	0
7132	17	28,882,473	28,882,847	374	1	5.273	6	11.454	6	7	16	0	1	1	TBC1D29	-3,924	upstream	ActReg chr17 #7132	0	0	1
7133	17	28,898,600	28,898,960	360	1	3.667	5.455	10.546	7	7	16	0	0	2	TBC1D29, LOC100506480	12196, 4719	downstream, downstream	ActReg chr17 #7133	0	0	1
7134	17	28,927,009	28,927,868	859	1	9.962	13.615	8.038	18	25	13	1	0	0				ActReg chr17 #7134	0	1	0
7135	17	29,034,957	29,035,672	715	2	15.636	17	4.364	23	30	8	1	0	0				ActReg chr17 #7135	1	1	0
7136	17	29,035,687	29,036,143	456	2	14.643	18.857	2.889	23	34	4	1	0	0				ActReg chr17 #7136	1	1	0
7137	17	29,151,358	29,151,833	475	1	14.4	9.6	7.231	22	15	12	1	2	2	CRLF3, ATAD5	183, -7425	in gene, upstream	ActReg chr17 #7137	1	0	0
7138	17	29,158,521	29,159,545	1,024	2	12.531	16.562	5.906	24	33	10	1	2	2	CRLF3, ATAD5	-7255, 13	upstream, in gene	ActReg chr17 #7138	1	1	0
7139	17	29,232,931	29,233,792	861	2	10.593	12	6.815	18	19	11	1	1	1	C17orf42	-75	upstream	ActReg chr17 #7139	1	1	0
7140	17	29,378,804	29,379,458	654	1	13.762	9.048	4.905	20	13	7	0	0	0				ActReg chr17 #7140	1	0	0
7141	17	29,740,844	29,741,442	598	1	11.316	10.526	3.684	20	17	8	0	0	1	RAB11FIP4	22,501	in gene	ActReg chr17 #7141	1	0	0
7142	17	29,799,086	29,799,671	585	1	12.278	9.222	7	19	13	9	0	0	1	RAB11FIP4	80,736	in gene	ActReg chr17 #7142	1	0	0
7143	17	29,815,390	29,815,814	424	1	2.714	7.214	10.286	5	15	16	1	0	1	RAB11FIP4	96,960	in gene	ActReg chr17 #7143	0	0	1
7144	17	29,826,892	29,827,632	740	1	7.913	11.174	2.696	12	14	6	0	0	1	RAB11FIP4	108,620	in gene	ActReg chr17 #7144	0	1	0
7145	17	29,851,698	29,852,147	449	1	5.5	6.714	11.714	8	9	17	0	0	1	RAB11FIP4	133,280	in gene	ActReg chr17 #7145	0	0	1
7146	17	29,876,788	29,877,621	833	3	10.538	17.115	17	22	34	40	2	0	1	MIR193A	-9,811	upstream	ActReg chr17 #7146	1	1	1
7147	17	29,907,328	29,908,454	1,126	1	13.583	8.361	4.472	20	14	8	0	0	1	MIR365-2	5,461	downstream	ActReg chr17 #7147	1	0	0
7148	17	29,920,696	29,921,137	441	1	3.786	6.143	11.143	6	8	17	0	0	0				ActReg chr17 #7148	0	0	1
7149	17	29,923,191	29,924,755	1,564	1	9.204	11.388	4.5	18	20	11	0	0	0				ActReg chr17 #7149	0	1	0
7150	17	30,048,794	30,050,367	1,573	2	11.837	12.531	3.275	24	19	6	0	0	0				ActReg chr17 #7150	1	1	0
7151	17	30,468,867	30,469,710	843	2	11.308	10.808	3.654	20	23	11	1	1	1	RHOT1	-185	upstream	ActReg chr17 #7151	1	1	0
7152	17	30,601,713	30,602,703	990	2	10.355	11.516	5.258	22	20	9	0	0	1	RHBDL3	9,013	in gene	ActReg chr17 #7152	1	1	0
7153	17	30,668,953	30,669,501	548	2	7.824	11.823	12.882	12	19	26	1	1	3	C17orf75, MIR632, ZNF207	-38, -7901, -7930	upstream, upstream, upstream	ActReg chr17 #7153	0	1	1
7154	17	30,771,185	30,772,096	911	1	8.759	10.034	6.414	14	18	10	1	1	1	PSMD11	138	in gene	ActReg chr17 #7154	0	1	0
7155	17	31,399,376	31,400,397	1,021	1	8.312	13.781	3.033	20	27	7	0	0	1	ACCN1	1,083,939	in gene	ActReg chr17 #7155	0	1	0
7156	17	31,469,472	31,470,470	998	2	18.188	17.5	4.455	38	34	7	0	0	1	ACCN1	1,013,854	in gene	ActReg chr17 #7156	1	1	0
7157	17	31,594,099	31,595,215	1,116	2	11.086	10.514	3.059	17	17	5	0	0	1	ACCN1	889,168	in gene	ActReg chr17 #7157	1	1	0
7158	17	31,654,999	31,655,779	780	2	8.72	12.68	2.5	17	28	5	0	0	1	ACCN1	828,436	in gene	ActReg chr17 #7158	1	1	0
7159	17	32,907,229	32,908,330	1,101	1	3.906	3.559	13.543	7	8	24	1	2	2	C17orf102, TMEM132E	-1391, 11	upstream, in gene	ActReg chr17 #7159	0	0	1
7160	17	33,030,342	33,031,189	847	2	12.808	11.231	4.143	23	21	6	0	0	0				ActReg chr17 #7160	1	1	0
7161	17	33,122,972	33,123,386	414	1	2.615	5.231	11.308	4	8	15	0	0	0				ActReg chr17 #7161	0	0	1
7162	17	33,124,556	33,125,210	654	1	5.8	12.2	4.5	12	24	7	0	0	0				ActReg chr17 #7162	0	1	0
7163	17	33,288,047	33,288,870	823	3	11.462	16.038	7.192	19	34	17	1	2	2	CCT6B, ZNF830	70, -91	in gene, upstream	ActReg chr17 #7163	1	1	1
7164	17	33,390,497	33,391,036	539	1	10.062	9.062	3.875	18	13	8	0	0	1	RFFL	25,528	in gene	ActReg chr17 #7164	1	0	0
7165	17	33,446,198	33,447,039	841	2	9.5	8.846	9.423	14	13	21	1	2	2	RAD51L3, FNDC8	270, -2013	in gene, upstream	ActReg chr17 #7165	1	0	1
7166	17	33,468,670	33,469,702	1,032	2	18.303	14.879	6.788	39	35	10	1	2	2	NLE1, UNC45B	136, -5650	in gene, upstream	ActReg chr17 #7166	1	1	0
7167	17	33,568,923	33,569,470	547	1	10.882	7.529	5.882	16	11	9	1	1	1	SLFN5	-890	upstream	ActReg chr17 #7167	1	0	0
7168	17	33,569,470	33,570,277	807	1	5.692	11.385	6.885	12	16	13	1	1	1	SLFN5	-213	upstream	ActReg chr17 #7168	0	1	0
7169	17	33,570,354	33,571,013	659	1	4.5	11.3	5.1	7	21	11	1	1	1	SLFN5	612	in gene	ActReg chr17 #7169	0	1	0
7170	17	33,700,589	33,700,986	397	1	10.167	10.083	4.083	15	12	5	2	1	1	SLFN11	-67	upstream	ActReg chr17 #7170	1	0	0
7171	17	33,775,289	33,775,666	377	1	5.25	6.333	12.25	8	9	17	1	1	1	SLFN13	379	in gene	ActReg chr17 #7171	0	0	1
7172	17	33,905,350	33,906,051	701	1	10.682	11.546	13.364	18	19	20	1	1	4	LOC100506761, SNORD7, PEX12, AP2B1	10573, 5024, -44, -8582	downstream, downstream, upstream, upstream	ActReg chr17 #7172	0	0	1
7173	17	34,070,439	34,071,435	996	2	19.323	17	4.484	40	42	9	0	0	2	RASL10B, GAS2L2	12258, 8960	downstream, downstream	ActReg chr17 #7173	1	1	0
7174	17	34,093,421	34,094,017	596	1	5	5.526	11.158	8	11	15	1	0	2	C17orf50, MMP28	5803, 28921	downstream, in gene	ActReg chr17 #7174	0	0	1
7175	17	34,135,774	34,136,844	1,070	2	14.206	18.529	7	27	38	14	1	1	1	TAF15	-179	upstream	ActReg chr17 #7175	1	1	0
7176	17	34,819,552	34,820,291	739	2	11.292	14.167	5.25	26	30	10	1	0	0				ActReg chr17 #7176	1	1	0
7177	17	34,838,329	34,839,360	1,031	1	6.455	11.424	6.303	12	17	11	1	1	1	ZNHIT3	-3,629	upstream	ActReg chr17 #7177	0	1	0
7178	17	34,842,040	34,843,128	1,088	2	16.794	17.5	4.5	46	48	8	1	1	2	ZNHIT3, MYO19	111, 48721	in gene, downstream	ActReg chr17 #7178	1	1	0
7179	17	34,890,192	34,891,844	1,652	1	8.077	11.365	9.423	19	16	24	1	2	3	MYO19, PIGW, GGNBP2	287, -385, -9719	in gene, upstream, upstream	ActReg chr17 #7179	0	1	0
7180	17	34,900,151	34,900,695	544	1	8.529	11	11.588	11	14	17	1	1	3	MYO19, PIGW, GGNBP2	-9118, 9020, -314	upstream, downstream, upstream	ActReg chr17 #7180	0	0	1
7181	17	34,901,268	34,901,974	706	2	12.227	11.636	7.091	25	17	14	1	1	3	MYO19, PIGW, GGNBP2	-10316, 10218, 884	upstream, downstream, in gene	ActReg chr17 #7181	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7182	17	34,957,713	34,958,786	1,073	1	10.735	9.941	14.235	23	17	24	1	1	2	DHRS11, MRM1	10023, 224	downstream, in gene	ActReg chr17 #7182	0	0	1
7183	17	35,054,180	35,054,820	640	1	7.15	11.55	4.308	10	18	8	0	0	0				ActReg chr17 #7183	0	1	0
7184	17	35,060,003	35,060,843	840	2	12.462	13.039	6.385	23	23	11	1	0	0				ActReg chr17 #7184	1	1	0
7185	17	35,134,155	35,135,026	871	2	11.148	13.37	2.059	23	21	4	0	0	0				ActReg chr17 #7185	1	1	0
7186	17	35,206,896	35,207,513	617	1	8.368	12.842	3.684	10	20	8	0	0	0				ActReg chr17 #7186	0	1	0
7187	17	35,278,607	35,279,248	641	1	8.6	12.1	7.35	12	18	14	0	0	0				ActReg chr17 #7187	0	1	0
7188	17	35,303,323	35,303,731	408	1	3.75	5.769	12.154	6	10	18	1	1	2	LHX1, AATF	9028, -2648	downstream, upstream	ActReg chr17 #7188	0	0	1
7189	17	35,305,666	35,306,831	1,165	1	8.611	14.444	7.056	14	23	12	1	1	2	LHX1, AATF	11749, 73	downstream, in gene	ActReg chr17 #7189	0	1	0
7190	17	35,715,677	35,716,111	434	1	6.357	9.786	11.143	9	12	16	1	0	1	ACACA	51,008	in gene	ActReg chr17 #7190	0	0	1
7191	17	35,767,216	35,767,636	420	1	8.538	7.692	14.923	13	11	21	1	2	2	ACACA, TADA2A	-524, 449	upstream, in gene	ActReg chr17 #7191	0	0	1
7192	17	35,843,412	35,844,125	713	1	11.5	9.364	2.381	17	14	5	0	1	2	TADA2A, DUSP14	76791, -6183	downstream, upstream	ActReg chr17 #7192	1	0	0
7193	17	35,969,155	35,969,747	592	1	9.111	11.833	4.556	11	17	6	1	1	2	SYNRG, DDX52	35, 34036	in gene, downstream	ActReg chr17 #7193	0	1	0
7194	17	36,003,120	36,003,670	550	1	6.941	10.765	6.176	9	18	10	1	1	1	DDX52	92	in gene	ActReg chr17 #7194	0	1	0
7195	17	36,208,845	36,209,704	859	1	6.296	10.407	1.667	11	19	2	0	0	0				ActReg chr17 #7195	0	1	0
7196	17	36,507,358	36,507,948	590	1	7.316	10.526	9.154	10	21	14	1	1	2	GPR179, SOCS7	-7960, -352	upstream, upstream	ActReg chr17 #7196	0	1	0
7197	17	36,585,166	36,585,629	463	1	7.857	5.214	14.214	13	8	22	1	0	0				ActReg chr17 #7197	0	0	1
7198	17	36,760,572	36,761,023	451	1	6.857	5.143	11.429	10	7	18	0	1	1	SRCIN1	1,386	in gene	ActReg chr17 #7198	0	0	1
7199	17	36,761,225	36,761,600	375	1	3.167	4.917	11.417	4	8	16	0	1	1	SRCIN1	771	in gene	ActReg chr17 #7199	0	0	1
7200	17	36,830,572	36,831,018	446	1	8.429	10.643	5.214	10	17	9	1	1	1	C17orf96	592	in gene	ActReg chr17 #7200	0	1	0
7201	17	36,905,601	36,906,122	521	1	12.125	11.438	13.938	17	14	17	1	2	2	PCGF2, PSMB3	-1303, -3141	upstream, upstream	ActReg chr17 #7201	0	0	1
7202	17	36,907,854	36,909,809	1,955	3	15.787	15.279	9.525	53	49	22	2	2	2	PCGF2, PSMB3	-4273, -171	upstream, upstream	ActReg chr17 #7202	1	1	1
7203	17	36,955,005	36,955,886	881	2	7.714	13.821	4.679	17	23	10	1	1	2	PIP4K2B, CWC25	713, 26144	in gene, downstream	ActReg chr17 #7203	1	1	0
7204	17	36,956,017	36,956,609	592	1	11.632	9.474	7.526	23	18	12	1	1	2	PIP4K2B, CWC25	-155, 25276	upstream, downstream	ActReg chr17 #7204	1	0	0
7205	17	36,981,332	36,981,976	644	3	13.3	15.05	8	27	28	19	1	1	2	CWC25, C17orf98	-65, 15988	upstream, downstream	ActReg chr17 #7205	1	1	1
7206	17	37,009,353	37,010,488	1,135	2	7.743	13.543	6.971	20	24	14	1	2	2	RPL23, SNORA21	133, -672	in gene, upstream	ActReg chr17 #7206	0	1	1
7207	17	37,025,501	37,026,933	1,432	2	8.178	10.756	9.178	16	18	16	1	1	1	LASP1	105	in gene	ActReg chr17 #7207	0	1	1
7208	17	37,030,875	37,031,254	379	1	5.417	4.667	10.417	7	7	13	0	0	1	LASP1	4,952	in gene	ActReg chr17 #7208	0	0	1
7209	17	37,157,880	37,158,778	898	1	12.464	8.929	4	17	14	7	0	0	0				ActReg chr17 #7209	1	0	0
7210	17	37,213,009	37,213,538	529	1	9.412	10.529	14.353	13	18	22	0	1	3	FLJ43826, LOC100131347, PLXDC1	27114, 1, 94629	downstream, in gene, downstream	ActReg chr17 #7210	0	0	1
7211	17	37,309,753	37,310,270	517	1	9	9.562	13.062	14	15	21	0	1	2	PLXDC1, ARL5C	-2109, 12403	upstream, downstream	ActReg chr17 #7211	0	0	1
7212	17	37,310,397	37,311,124	727	3	9.957	11.217	10.826	17	19	20	0	1	2	PLXDC1, ARL5C	-2858, 11654	upstream, downstream	ActReg chr17 #7212	1	1	1
7213	17	37,365,903	37,366,593	690	1	6.318	7.818	14.091	9	11	24	1	0	2	RPL19, STAC2	9712, 15792	downstream, downstream	ActReg chr17 #7213	0	0	1
7214	17	37,556,954	37,558,253	1,299	1	11.585	7.561	7.525	15	14	15	1	1	2	FBXL20, MED1	306, 49924	in gene, downstream	ActReg chr17 #7214	1	0	0
7215	17	37,748,185	37,749,307	1,122	2	9.657	11.771	4.971	20	18	10	0	0	0				ActReg chr17 #7215	1	1	0
7216	17	37,762,084	37,762,653	569	1	4.588	4.706	11.765	8	6	18	1	1	1	NEUROD2	1,807	in gene	ActReg chr17 #7216	0	0	1
7217	17	37,774,470	37,775,106	636	1	7.3	15.05	4.15	14	22	8	1	0	1	PPP1R1B	-8,391	upstream	ActReg chr17 #7217	0	1	0
7218	17	37,793,214	37,793,825	611	1	8.5	8.85	17.8	11	14	36	1	1	2	PPP1R1B, STARD3	10340, 186	downstream, in gene	ActReg chr17 #7218	0	0	1
7219	17	37,826,156	37,826,511	355	1	9.182	5.909	11	12	8	17	0	1	4	STARD3, TCAP, PNMT, PGAP3	33000, 4734, 1826, 17977	downstream, downstream, in gene, downstream	ActReg chr17 #7219	0	0	1
7220	17	37,827,793	37,828,321	528	1	4.059	5.294	13.118	7	7	21	0	0	4	STARD3, TCAP, PNMT, PGAP3	34724, 6458, 3550, 16253	downstream, downstream, downstream, in gene	ActReg chr17 #7220	0	0	1
7221	17	37,833,879	37,834,355	476	1	2.533	4.867	11.8	5	8	20	0	0	2	PNMT, PGAP3	9610, 10193	downstream, in gene	ActReg chr17 #7221	0	0	1
7222	17	37,886,261	37,886,872	611	2	9	11.263	7.737	13	16	16	1	2	3	ERBB2, C17orf37, GRB7	42173, 222, -7621	downstream, in gene, upstream	ActReg chr17 #7222	0	1	1
7223	17	37,902,875	37,903,297	422	1	2.643	4.929	10.571	3	8	16	0	0	1	GRB7	8,899	in gene	ActReg chr17 #7223	0	0	1
7224	17	37,909,790	37,911,324	1,534	3	11.208	11.688	7.812	22	27	16	1	0	2	GRB7, IKZF3	16370, 109884	downstream, downstream	ActReg chr17 #7224	1	1	1
7225	17	38,083,671	38,084,204	533	1	9.176	11.529	5.588	14	20	12	1	1	2	GSDMB, ORMDL3	-9034, -83	upstream, upstream	ActReg chr17 #7225	0	1	0
7226	17	38,119,419	38,119,867	448	1	3.5	4.071	12.071	6	7	16	0	1	1	GSDMA	417	in gene	ActReg chr17 #7226	0	0	1
7227	17	38,136,454	38,137,548	1,094	2	25.235	29.029	8.029	83	85	11	1	1	2	GSDMA, PSMD3	17775, -59	downstream, upstream	ActReg chr17 #7227	1	1	0
7228	17	38,167,248	38,167,626	378	1	2	3.417	10.167	4	6	15	0	1	2	CSF3, MED24	-4177, 43452	upstream, downstream	ActReg chr17 #7228	0	0	1
7229	17	38,219,146	38,219,902	756	2	12.095	12.696	7.55	21	25	15	1	1	2	MED24, THRA	-8635, 1078	upstream, in gene	ActReg chr17 #7229	1	1	0
7230	17	38,228,237	38,228,806	569	1	6.278	9.222	12.333	9	12	18	0	0	1	THRA	10,075	in gene	ActReg chr17 #7230	0	0	1
7231	17	38,256,277	38,257,138	861	1	12.852	9.815	5.481	21	14	11	1	1	2	THRA, NR1D1	38261, 266	downstream, in gene	ActReg chr17 #7231	1	0	0
7232	17	38,279,302	38,280,152	850	1	8.615	11.231	6	15	16	14	1	1	1	MSL1	937	in gene	ActReg chr17 #7232	0	1	0
7233	17	38,470,774	38,471,350	576	2	11.889	11.611	7.056	18	19	11	0	0	1	RARA	5,639	in gene	ActReg chr17 #7233	1	1	0
7234	17	38,532,001	38,532,412	411	1	4.75	8.25	11.75	7	12	15	0	0	0				ActReg chr17 #7234	0	0	1
7235	17	38,573,547	38,574,726	1,179	2	12.054	12.54	5.455	20	25	10	1	1	1	TOP2A	66	in gene	ActReg chr17 #7235	1	1	0
7236	17	38,677,405	38,677,984	579	1	6.579	5.211	9.895	11	7	14	0	0	0				ActReg chr17 #7236	0	0	1
7237	17	38,692,808	38,693,345	537	1	2.588	4.824	11.294	4	8	19	0	0	0				ActReg chr17 #7237	0	0	1
7238	17	38,803,879	38,804,667	788	1	7.375	10.375	9.542	11	15	14	1	1	2	SMARCE1, KRT222	-170, 17143	upstream, downstream	ActReg chr17 #7238	0	1	0
7239	17	39,254,677	39,255,143	466	1	2.733	9.4	3.889	6	13	5	0	2	2	KRTAP4-8, KRTAP4-9	-535, -6731	upstream, upstream	ActReg chr17 #7239	0	1	0
7240	17	39,305,665	39,306,107	442	1	2.692	4.923	11.538	5	6	16	0	1	3	KRTAP4-6, KRTAP4-5, KRTAP4-4	-9147, 168, 11097	upstream, in gene, downstream	ActReg chr17 #7240	0	0	1
7241	17	39,559,953	39,560,744	791	2	11.16	13.08	2.792	18	24	6	0	2	2	KRT31, LOC100505782	-6504, 1680	upstream, in gene	ActReg chr17 #7241	1	1	0
7242	17	39,770,276	39,770,774	498	1	4	6.8	14.533	6	10	24	0	1	2	KRT16, KRT17	-1446, 10357	upstream, downstream	ActReg chr17 #7242	0	0	1
7243	17	39,792,771	39,793,439	668	1	2.643	3.3	13.35	5	7	17	0	0	0				ActReg chr17 #7243	0	0	1
7244	17	39,811,597	39,812,269	672	1	4.095	3.19	12.429	6	6	15	0	0	0				ActReg chr17 #7244	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7245	17	39,814,955	39,815,675	720	1	5.136	4.545	11.909	9	6	18	0	0	0				ActReg chr17 #7245	0	0	1
7246	17	39,821,747	39,822,676	929	2	10.897	10.483	4.552	20	18	11	1	0	0				ActReg chr17 #7246	1	1	0
7247	17	39,834,609	39,835,782	1,173	2	14.757	15.081	3.2	34	29	8	0	0	1	EIF1	-9,932	upstream	ActReg chr17 #7247	1	1	0
7248	17	39,844,902	39,845,833	931	1	8.586	12.138	16.276	14	19	29	1	1	1	EIF1	240	in gene	ActReg chr17 #7248	0	0	1
7249	17	39,890,259	39,891,250	991	1	6.71	6.71	14.935	10	9	21	1	1	1	HAP1	144	in gene	ActReg chr17 #7249	0	0	1
7250	17	39,957,469	39,957,910	441	1	7.429	5.714	13.357	9	12	22	0	0	1	SC65	10,762	downstream	ActReg chr17 #7250	0	0	1
7251	17	39,966,951	39,969,221	2,270	3	11.352	15.817	8.114	19	36	14	1	2	2	SC65, FKBP10	365, -876	in gene, upstream	ActReg chr17 #7251	1	1	1
7252	17	40,020,946	40,021,808	862	2	7.852	11.926	9.28	13	18	19	1	1	2	KLHL11, ACLY	252, 53895	in gene, downstream	ActReg chr17 #7252	0	1	1
7253	17	40,074,662	40,076,004	1,342	1	8.19	6.857	13.405	15	12	24	1	1	1	ACLY	-61	upstream	ActReg chr17 #7253	0	0	1
7254	17	40,086,319	40,087,112	793	2	9.56	10.8	4.16	14	15	8	1	1	1	TTC25	-173	upstream	ActReg chr17 #7254	1	1	0
7255	17	40,168,911	40,170,210	1,299	2	12.659	18.098	7.707	33	32	16	1	2	4	DNAJC7, NKIRAS2, ZNF385C, LOC100507628	155, -34, 11147, 20484	in gene, upstream, downstream, downstream	ActReg chr17 #7255	1	1	0
7256	17	40,171,520	40,172,494	974	2	31.484	34.419	6.677	96	108	13	1	2	4	DNAJC7, NKIRAS2, ZNF385C, LOC100507628	-2292, 2413, 8700, 18037	upstream, in gene, downstream, downstream	ActReg chr17 #7256	1	1	0
7257	17	40,192,350	40,192,849	499	1	2.938	4.375	14.688	4	8	26	1	2	2	LOC100507628, LOC100507656	-2555, 2530	upstream, in gene	ActReg chr17 #7257	0	0	1
7258	17	40,306,717	40,307,874	1,157	2	8.027	10.622	7.541	13	18	17	1	1	2	RAB5C, KCNH4	-273, 26001	upstream, downstream	ActReg chr17 #7258	0	1	1
7259	17	40,331,923	40,333,628	1,705	2	11.509	16.377	8.906	26	40	15	1	1	3	KCNH4, HCRT, GHDC	521, 4695, 13775	in gene, downstream, downstream	ActReg chr17 #7259	1	1	0
7260	17	40,345,987	40,347,044	1,057	2	23.546	32.364	3.548	69	89	5	0	1	3	HCRT, GHDC, STAT5B	-9045, 35, 81909	upstream, in gene, downstream	ActReg chr17 #7260	1	1	0
7261	17	40,418,852	40,419,344	492	1	10	9.533	2.2	16	15	3	0	0	1	STAT5B	9,326	in gene	ActReg chr17 #7261	1	0	0
7262	17	40,439,155	40,439,851	696	1	9.682	11.636	4.588	16	26	8	0	1	1	STAT5A	-62	upstream	ActReg chr17 #7262	0	1	0
7263	17	40,440,904	40,441,693	789	1	6	4.667	12.25	10	7	18	1	1	1	STAT5A	1,733	in gene	ActReg chr17 #7263	0	0	1
7264	17	40,540,093	40,541,159	1,066	2	19.618	21.118	7.618	45	54	17	1	1	1	STAT3	-113	upstream	ActReg chr17 #7264	1	1	0
7265	17	40,556,823	40,557,335	512	1	3.133	5.25	11	5	7	17	1	0	1	PTRF	18,259	in gene	ActReg chr17 #7265	0	0	1
7266	17	40,610,599	40,611,593	994	2	9.129	10.258	12.286	16	16	28	1	1	1	ATP6V0A1	234	in gene	ActReg chr17 #7266	0	1	1
7267	17	40,690,237	40,690,562	325	1	4.636	3.4	10.091	9	5	14	0	1	1	NAGLU	2,448	in gene	ActReg chr17 #7267	0	0	1
7268	17	40,705,149	40,705,868	719	1	4.739	12.565	5.435	8	21	8	1	2	4	NAGLU, HSD17B1, LOC100290566, COASY	17557, 1524, 1258, -8584	downstream, in gene, in gene, upstream	ActReg chr17 #7268	0	1	0
7269	17	40,706,331	40,706,842	511	2	11.188	10.188	12.938	14	13	21	1	3	4	NAGLU, HSD17B1, LOC100290566, COASY	18635, 2602, 180, -7506	downstream, in gene, in gene, upstream	ActReg chr17 #7269	1	0	1
7270	17	40,718,633	40,719,584	951	1	10	10.933	11.5	16	16	17	1	1	3	COASY, MLX, PSMC3IP	5016, 30, 10639	downstream, in gene, downstream	ActReg chr17 #7270	0	1	0
7271	17	40,761,692	40,762,212	520	1	7.059	7.867	12.118	13	12	18	1	2	2	FAM134C, TUBG1	-507, 594	upstream, in gene	ActReg chr17 #7271	0	0	1
7272	17	40,811,290	40,811,815	525	1	6.647	7.118	11.412	11	9	17	1	1	2	TUBG2, PLEKHH3	286, 17496	in gene, downstream	ActReg chr17 #7272	0	0	1
7273	17	40,829,056	40,830,341	1,285	1	9	13.268	3.882	16	19	8	0	2	3	PLEKHH3, CCR10, CNTNAP1	-650, 4147, -4934	upstream, downstream, upstream	ActReg chr17 #7273	0	1	0
7274	17	40,831,506	40,832,488	982	2	14.258	15.935	9.871	28	27	14	1	3	3	PLEKHH3, CCR10, CNTNAP1	-2949, 1848, -2635	upstream, in gene, upstream	ActReg chr17 #7274	1	1	0
7275	17	40,913,366	40,913,816	450	1	3.4	4.643	11.429	5	6	17	1	2	2	LOC100190938, RAMP2	-316, 379	upstream, in gene	ActReg chr17 #7275	0	0	1
7276	17	40,936,402	40,936,941	539	1	4.824	3.688	11.529	9	11	17	1	0	2	VPS25, WNK4	11217, 4022	downstream, in gene	ActReg chr17 #7276	0	0	1
7277	17	40,950,309	40,951,056	747	1	10.609	12	4.905	17	21	9	1	2	3	WNK4, CCDC56, CNTD1	18033, 22, -172	downstream, in gene, upstream	ActReg chr17 #7277	0	1	0
7278	17	40,975,790	40,976,642	852	1	11.667	10.037	8.889	20	16	13	1	1	2	BECN1, PSME3	94, -9207	in gene, upstream	ActReg chr17 #7278	1	0	0
7279	17	40,984,780	40,986,238	1,458	2	10.533	10.111	8.146	21	15	13	1	1	2	BECN1, PSME3	-9199, 86	upstream, in gene	ActReg chr17 #7279	1	1	0
7280	17	41,149,859	41,150,903	1,044	3	10.094	12.812	10.312	24	20	26	1	1	3	RUNDC1, RPL27, IFI35	17799, -65, -8388	downstream, upstream, upstream	ActReg chr17 #7280	1	1	1
7281	17	41,162,706	41,163,591	885	1	4.607	9.893	1.885	11	14	4	0	0	3	RPL27, IFI35, VAT1	12702, 4379, 11311	downstream, in gene, downstream	ActReg chr17 #7281	0	1	0
7282	17	41,173,724	41,174,746	1,022	2	11.656	12.375	6.656	24	20	13	1	2	3	IFI35, VAT1, RND2	15466, 224, -3023	downstream, in gene, upstream	ActReg chr17 #7282	1	1	0
7283	17	41,278,473	41,278,927	454	1	4.583	5.714	13.429	7	10	24	1	2	2	BRCA1, NBR2	-1200, 1100	upstream, in gene	ActReg chr17 #7283	0	0	1
7284	17	41,392,392	41,393,576	1,184	2	14.946	13.6	6.243	30	30	12	1	0	0				ActReg chr17 #7284	1	1	0
7285	17	41,438,212	41,439,151	939	3	11.586	13.931	10.414	26	29	22	1	0	1	LOC100130581	27,585	downstream	ActReg chr17 #7285	1	1	1
7286	17	41,444,834	41,446,022	1,188	2	13.486	15.108	4.595	32	36	7	1	0	1	LOC100130581	20,838	downstream	ActReg chr17 #7286	1	1	0
7287	17	41,476,195	41,476,656	461	1	6.857	10.143	11.643	12	12	18	1	1	2	LOC100130581, ARL4D	-10159, 72	upstream, in gene	ActReg chr17 #7287	0	0	1
7288	17	41,496,139	41,496,923	784	1	10.083	11.583	6.958	17	16	10	0	0	0				ActReg chr17 #7288	0	1	0
7289	17	41,519,968	41,520,608	640	1	8.667	10.143	2.222	15	19	4	0	1	1	MIR2117	-1,886	upstream	ActReg chr17 #7289	0	1	0
7290	17	41,560,831	41,561,665	834	2	17.889	15.926	5.963	45	37	12	1	1	1	DHX8	-86	upstream	ActReg chr17 #7290	1	1	0
7291	17	41,788,436	41,788,810	374	1	1.75	4.667	12.583	3	8	20	0	0	0				ActReg chr17 #7291	0	0	1
7292	17	41,910,630	41,911,042	412	1	4.846	5.077	11.769	7	11	16	1	1	1	MPP3	-289	upstream	ActReg chr17 #7292	0	0	1
7293	17	41,985,410	41,985,891	481	1	3.308	5.267	10.867	5	7	16	0	1	2	MPP2, C17orf88	-537, -8926	upstream, upstream	ActReg chr17 #7293	0	0	1
7294	17	42,030,348	42,030,964	616	1	3.105	3	12.105	6	5	15	1	0	1	PYY	51,181	in gene	ActReg chr17 #7294	0	0	1
7295	17	42,084,576	42,085,183	607	1	5.579	9.842	11.579	9	15	16	1	1	3	PYY, NAGS, TMEM101	-3042, 2847, 7466	upstream, in gene, downstream	ActReg chr17 #7295	0	0	1
7296	17	42,091,955	42,092,712	757	1	10.042	16.042	8.167	20	30	11	2	1	2	NAGS, TMEM101	10301, 12	downstream, in gene	ActReg chr17 #7296	0	1	0
7297	17	42,168,442	42,169,000	558	1	4.056	5.444	12.333	8	9	20	0	0	1	HDAC5	32,293	in gene	ActReg chr17 #7297	0	0	1
7298	17	42,188,117	42,188,714	597	1	9.632	5	11	15	9	16	0	0	1	HDAC5	12,599	in gene	ActReg chr17 #7298	0	0	1
7299	17	42,200,174	42,200,614	440	1	6.071	4.857	11.143	9	7	18	1	1	1	HDAC5	620	in gene	ActReg chr17 #7299	0	0	1
7300	17	42,200,967	42,201,681	714	2	12.409	9.905	3.81	26	15	8	1	1	1	HDAC5	-310	upstream	ActReg chr17 #7300	1	1	0
7301	17	42,215,238	42,216,141	903	2	11.464	14.464	5.64	21	26	10	0	1	1	C17orf53	-3,585	upstream	ActReg chr17 #7301	1	1	0
7302	17	42,219,013	42,219,742	729	2	11.318	14.136	6.045	17	26	8	1	1	1	C17orf53	103	in gene	ActReg chr17 #7302	1	1	0
7303	17	42,285,717	42,286,411	694	1	7.045	11.409	4.455	15	18	8	0	0	1	UBTF	12,186	in gene	ActReg chr17 #7303	0	1	0
7304	17	42,298,596	42,299,015	419	1	11.769	7.333	4.231	20	11	7	1	1	1	UBTF	-555	upstream	ActReg chr17 #7304	1	0	0
7305	17	42,342,011	42,342,361	350	1	2.8	2.636	11.909	4	3	15	0	0	1	SLC4A1	3,316	in gene	ActReg chr17 #7305	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7306	17	42,385,587	42,386,237	650	3	12.8	10.55	9.75	22	17	18	1	1	1	RUNDC3A	-15	upstream	ActReg chr17 #7306	1	1	1
7307	17	42,401,525	42,402,742	1,217	3	13.684	17.237	9.061	32	36	23	2	1	2	RUNDC3A, SLC25A39	16206, 84	downstream, in gene	ActReg chr17 #7307	1	1	1
7308	17	42,403,997	42,404,735	738	2	17	11.739	3.842	43	31	7	0	1	2	RUNDC3A, SLC25A39	18439, -2149	downstream, upstream	ActReg chr17 #7308	1	1	0
7309	17	42,429,529	42,430,380	851	1	3.385	5.259	11.593	6	9	18	0	0	2	GRN, FAM171A2	7463, 11281	in gene, downstream	ActReg chr17 #7309	0	0	1
7310	17	42,446,316	42,446,716	400	1	2.833	5.417	12.417	5	8	21	0	1	2	FAM171A2, ITGA2B	-5281, 20357	upstream, downstream	ActReg chr17 #7310	0	0	1
7311	17	42,580,439	42,581,285	846	1	8.519	12.741	5.852	11	19	11	1	1	1	GPATCH8	95	in gene	ActReg chr17 #7311	0	1	0
7312	17	42,633,698	42,634,756	1,058	2	10.394	11.121	3.667	16	16	8	1	1	1	FZD2	-698	upstream	ActReg chr17 #7312	1	1	0
7313	17	42,766,686	42,767,810	1,124	3	10.75	10.861	10.556	14	20	21	1	1	1	CCDC43	-83	upstream	ActReg chr17 #7313	1	1	1
7314	17	42,785,646	42,786,704	1,058	2	11.606	14.152	4.364	19	31	10	1	1	1	DBF4B	199	in gene	ActReg chr17 #7314	1	1	0
7315	17	42,826,152	42,826,610	458	1	2.2	5.1	12	3	5	17	0	1	3	DBF4B, LOC100505943, ADAM11	40405, 50, -10187	in gene, in gene, upstream	ActReg chr17 #7315	0	0	1
7316	17	42,835,694	42,836,118	424	1	3.769	3.615	10.923	6	4	14	1	1	3	DBF4B, LOC100505943, ADAM11	49930, 9575, -662	downstream, downstream, upstream	ActReg chr17 #7316	0	0	1
7317	17	42,836,706	42,837,373	667	1	5.95	6	12.3	12	8	16	1	1	3	DBF4B, LOC100505943, ADAM11	51063, 10708, 471	downstream, downstream, in gene	ActReg chr17 #7317	0	0	1
7318	17	42,852,054	42,853,107	1,043	1	9.182	9.909	13.394	13	14	20	1	0	1	ADAM11	16,017	in gene	ActReg chr17 #7318	0	0	1
7319	17	42,976,600	42,977,317	717	1	12.826	12.217	9.217	23	20	12	1	2	3	EFTUD2, CCDC103, GFAP	35, -196, 15956	in gene, upstream, downstream	ActReg chr17 #7319	0	1	0
7320	17	43,005,274	43,005,775	501	1	5.125	4.812	11.312	8	6	18	0	0	1	KIF18B	19,558	in gene	ActReg chr17 #7320	0	0	1
7321	17	43,024,706	43,025,642	936	1	9.172	13.621	10.448	13	26	19	1	1	1	KIF18B	-92	upstream	ActReg chr17 #7321	0	1	0
7322	17	43,044,311	43,044,943	632	1	4.25	4.45	12.35	8	7	18	1	1	1	C1QL1	1,017	in gene	ActReg chr17 #7322	0	0	1
7323	17	43,045,963	43,046,365	402	1	3.333	9	11.75	4	11	16	1	1	1	C1QL1	-520	upstream	ActReg chr17 #7323	0	0	1
7324	17	43,138,019	43,138,982	963	1	11.867	12.933	5.533	20	23	8	1	2	2	DCAKD, NMT1	-27, -180	upstream, upstream	ActReg chr17 #7324	0	1	0
7325	17	43,208,981	43,209,522	541	1	5.471	10.823	10.647	8	15	14	1	2	2	PLCD3, ACBD4	640, -716	in gene, upstream	ActReg chr17 #7325	0	0	1
7326	17	43,222,122	43,222,604	482	1	3	5.733	12.6	7	7	19	1	1	2	ACBD4, HEXIM1	12396, -2321	downstream, upstream	ActReg chr17 #7326	0	0	1
7327	17	43,224,700	43,226,306	1,606	2	10.922	16.216	9.706	29	36	22	1	1	2	ACBD4, HEXIM1	15536, 819	downstream, in gene	ActReg chr17 #7327	0	1	1
7328	17	43,238,312	43,239,805	1,493	2	11.935	8.978	11.152	20	16	18	1	1	3	HEXIM1, HEXIM2, LOC100505972	14374, 794, 9794	downstream, in gene, downstream	ActReg chr17 #7328	1	0	1
7329	17	43,247,894	43,248,670	776	1	9.167	12.167	6.875	12	23	11	0	1	2	HEXIM2, LOC100505972	10018, 570	downstream, in gene	ActReg chr17 #7329	0	1	0
7330	17	43,249,367	43,250,734	1,367	2	12.465	16.977	5.837	28	34	11	0	1	2	HEXIM2, LOC100505972	11786, -1198	downstream, upstream	ActReg chr17 #7330	1	1	0
7331	17	43,298,549	43,298,964	415	1	3.538	5.308	9.538	5	8	16	1	1	1	FMNL1	-536	upstream	ActReg chr17 #7331	0	0	1
7332	17	43,394,487	43,395,154	667	1	11.333	9.762	6.55	17	16	13	1	1	1	MAP3K14	-406	upstream	ActReg chr17 #7332	1	0	0
7333	17	43,448,829	43,449,515	686	1	9.909	12.318	4.227	16	22	9	1	0	0				ActReg chr17 #7333	0	1	0
7334	17	43,473,912	43,474,423	511	1	1.733	3.625	12.5	3	6	16	1	0	1	ARHGAP27	28,845	in gene	ActReg chr17 #7334	0	0	1
7335	17	43,480,340	43,480,829	489	1	2.071	3.2	13.467	5	5	21	0	0	1	ARHGAP27	22,428	in gene	ActReg chr17 #7335	0	0	1
7336	17	43,482,859	43,483,362	503	1	2.333	5.625	12	4	10	19	1	0	1	ARHGAP27	19,902	in gene	ActReg chr17 #7336	0	0	1
7337	17	43,861,976	43,862,671	695	1	6.045	6.409	13.273	9	10	19	1	1	1	CRHR1	677	in gene	ActReg chr17 #7337	0	0	1
7338	17	43,912,068	43,912,528	460	1	5.857	3.571	11	9	5	17	0	0	3	CRHR1, LOC100128977, IMP5	50652, 60581, -9958	in gene, downstream, upstream	ActReg chr17 #7338	0	0	1
7339	17	43,922,451	43,922,896	445	1	4.857	5.857	12.429	7	8	17	0	1	3	CRHR1, LOC100128977, IMP5	61027, 50206, 417	downstream, in gene, in gene	ActReg chr17 #7339	0	0	1
7340	17	43,931,667	43,932,051	384	1	2	4.25	11.833	3	7	18	0	0	2	LOC100128977, IMP5	41020, 9603	in gene, downstream	ActReg chr17 #7340	0	0	1
7341	17	43,935,207	43,936,060	853	2	10.423	12.462	3.682	24	23	9	0	0	1	LOC100128977	37,246	in gene	ActReg chr17 #7341	1	1	0
7342	17	43,971,336	43,972,074	738	2	11.652	10.783	4.696	17	20	10	1	3	3	LOC100128977, MAPT, LOC100130148	1174, -43, -1444	in gene, upstream, upstream	ActReg chr17 #7342	1	1	0
7343	17	44,089,553	44,090,201	648	1	2	2.789	11.95	5	6	16	0	0	1	MAPT	118,129	in gene	ActReg chr17 #7343	0	0	1
7344	17	44,271,033	44,271,568	535	1	14.412	12.294	14.353	19	20	22	1	1	2	KIAA1267, LOC644246	31440, 361	in gene, in gene	ActReg chr17 #7344	0	0	1
7345	17	44,847,944	44,848,561	617	1	5.263	6.947	11.316	9	10	16	1	0	1	WNT3	47,830	in gene	ActReg chr17 #7345	0	0	1
7346	17	44,961,026	44,961,687	661	1	4.2	2.895	10.25	8	5	14	0	0	1	WNT9B	32,388	downstream	ActReg chr17 #7346	0	0	1
7347	17	45,000,004	45,000,913	909	2	13.357	16.143	8.357	22	34	18	1	1	1	GOSR2	-28	upstream	ActReg chr17 #7347	1	1	0
7348	17	45,041,228	45,042,261	1,033	2	9.5	10.594	2.759	19	23	6	0	0	0				ActReg chr17 #7348	1	1	0
7349	17	45,144,460	45,145,120	660	2	12.905	12.381	4.533	26	24	8	0	1	1	LOC100506214	64	in gene	ActReg chr17 #7349	1	1	0
7350	17	45,177,441	45,177,809	368	1	6.364	4.818	12.818	10	8	19	1	0	0				ActReg chr17 #7350	0	0	1
7351	17	45,234,087	45,234,505	418	1	10.923	9.231	20.846	19	15	36	0	0	1	CDC27	32,369	in gene	ActReg chr17 #7351	0	0	1
7352	17	45,236,925	45,237,249	324	1	1.545	7	10.909	3	10	14	0	0	1	CDC27	29,578	in gene	ActReg chr17 #7352	0	0	1
7353	17	45,249,257	45,249,422	165	1	19.8	20.6	36.4	24	24	44	0	0	1	CDC27	17,326	in gene	ActReg chr17 #7353	0	0	1
7354	17	45,315,526	45,315,984	458	1	7.143	5.214	15.643	10	8	24	0	0	0				ActReg chr17 #7354	0	0	1
7355	17	45,331,110	45,331,744	634	1	10.25	6.65	6.895	15	11	13	1	1	1	ITGB3	219	in gene	ActReg chr17 #7355	1	0	0
7356	17	45,357,586	45,358,342	756	1	7.875	11.167	4.375	13	19	8	0	0	1	ITGB3	26,756	in gene	ActReg chr17 #7356	0	1	0
7357	17	45,371,888	45,373,107	1,219	1	6.947	12.447	5.316	11	17	10	0	0	2	ITGB3, LOC100506252	41289, 10554	in gene, downstream	ActReg chr17 #7357	0	1	0
7358	17	45,400,799	45,401,981	1,182	1	10.946	10.189	7.054	19	18	12	1	1	1	C17orf57	43	in gene	ActReg chr17 #7358	1	0	0
7359	17	45,726,496	45,727,124	628	1	10.2	9.3	12.65	18	13	19	1	1	1	KPNB1	-465	upstream	ActReg chr17 #7359	0	0	1
7360	17	45,773,046	45,773,556	510	1	3.688	3.25	11.375	6	4	17	2	1	1	TBKBP1	671	in gene	ActReg chr17 #7360	0	0	1
7361	17	45,855,759	45,856,128	369	1	4.25	2.917	10.25	6	4	16	1	0	0				ActReg chr17 #7361	0	0	1
7362	17	45,862,669	45,863,703	1,034	2	17.344	18.594	5.444	45	46	13	0	0	0				ActReg chr17 #7362	1	1	0
7363	17	45,893,856	45,894,342	486	1	3.562	5.938	12.312	7	9	19	0	0	3	LOC100506269, OSBPL7, MRPL10	11628, 5048, 14804	in gene, in gene, downstream	ActReg chr17 #7363	0	0	1
7364	17	45,898,715	45,899,621	906	3	19.679	18.241	8.379	51	41	18	0	1	4	LOC100506269, OSBPL7, MRPL10, LRRC46	16697, -21, 9735, -9825	in gene, upstream, downstream, upstream	ActReg chr17 #7364	1	1	1
7365	17	45,925,104	45,925,512	408	1	3.667	4.923	12	6	7	16	1	1	2	SCRN2, SP6	-6609, 7932	upstream, in gene	ActReg chr17 #7365	0	0	1
7366	17	45,949,805	45,950,146	341	1	3.818	2.167	11.727	6	3	15	1	0	0				ActReg chr17 #7366	0	0	1
7367	17	45,957,388	45,957,747	359	1	2.636	2.727	10.909	5	4	16	0	0	0				ActReg chr17 #7367	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7368	17	45,972,954	45,974,258	1,304	2	16.244	19.805	5.171	44	56	9	1	2	3	LOC100506295, SP2, LOC100506325	-428, 90, 45119	upstream, in gene, downstream	ActReg chr17 #7368	1	1	0
7369	17	46,047,930	46,049,273	1,343	1	9.31	13.738	6.341	17	20	14	1	1	1	CDK5RAP3	172	in gene	ActReg chr17 #7369	0	1	0
7370	17	46,100,846	46,101,734	888	1	7.036	8.643	14.556	15	16	25	1	0	1	COPZ2	13,862	downstream	ActReg chr17 #7370	0	0	1
7371	17	46,114,204	46,114,545	341	1	7.364	4.818	11	13	8	16	1	2	2	COPZ2, MIR152	778, 239	in gene, downstream	ActReg chr17 #7371	0	0	1
7372	17	46,124,825	46,126,138	1,313	3	9.146	11.317	10.415	19	18	19	1	1	2	COPZ2, NFE2L1	-10329, -205	upstream, upstream	ActReg chr17 #7372	1	1	1
7373	17	46,178,220	46,179,131	911	1	10.75	9.393	4.462	18	15	10	1	2	2	CBX1, SNX11	208, -6245	in gene, upstream	ActReg chr17 #7373	1	0	0
7374	17	46,184,413	46,185,446	1,033	1	6.485	10.121	6.879	9	14	14	1	2	2	CBX1, SNX11	-6046, 9	upstream, in gene	ActReg chr17 #7374	0	1	0
7375	17	46,687,586	46,688,390	804	2	10.8	10	7.2	18	16	13	1	2	4	hCG_2042068, HOXB6, HOXB7, HOXB8	20165, -5654, 395, 4313	downstream, upstream, in gene, downstream	ActReg chr17 #7375	1	1	0
7376	17	46,800,850	46,801,605	755	1	11.5	9.208	5.235	20	19	8	3	3	4	PRAC, C17orf93, MIR3185, HOXB13	-1345, 685, 610, 4884	upstream, in gene, downstream, downstream	ActReg chr17 #7376	1	0	0
7377	17	46,985,478	46,985,978	500	1	11.467	10.933	12.6	16	21	20	1	1	1	UBE2Z	-3	upstream	ActReg chr17 #7377	0	0	1
7378	17	47,021,914	47,022,711	797	1	10.92	12.44	6	15	20	11	1	1	1	SNF8	-158	upstream	ActReg chr17 #7378	0	1	0
7379	17	47,049,526	47,050,261	735	1	7.783	11.609	2.174	11	21	5	0	1	1	GIP	-3,938	upstream	ActReg chr17 #7379	0	1	0
7380	17	47,269,172	47,270,211	1,039	3	12.727	12.515	13.788	26	21	39	1	0	0				ActReg chr17 #7380	1	1	1
7381	17	47,337,680	47,338,560	880	1	4.536	12	4.464	10	18	8	1	0	1	FLJ40194	12,515	downstream	ActReg chr17 #7381	0	1	0
7382	17	47,438,717	47,439,185	468	1	8.067	10.8	11.2	12	14	15	1	1	1	ZNF652	884	in gene	ActReg chr17 #7382	0	0	1
7383	17	47,513,156	47,513,598	442	1	4.923	4.308	10.923	7	7	18	0	0	0				ActReg chr17 #7383	0	0	1
7384	17	47,519,260	47,519,692	432	1	2.889	6	10.643	4	7	15	0	0	0				ActReg chr17 #7384	0	0	1
7385	17	47,572,719	47,573,082	363	1	2.818	6.818	12.454	5	10	18	1	1	2	NGFR, LOC100288866	245, 78526	in gene, downstream	ActReg chr17 #7385	0	0	1
7386	17	47,573,248	47,573,841	593	1	5.211	6.737	12.053	8	11	18	1	1	2	NGFR, LOC100288866	889, 77882	in gene, downstream	ActReg chr17 #7386	0	0	1
7387	17	47,655,876	47,656,327	451	1	3.385	5	11	4	8	17	0	1	2	LOC100288866, NXPH3	-4675, 2803	upstream, in gene	ActReg chr17 #7387	0	0	1
7388	17	47,784,938	47,786,086	1,148	2	22.333	25.194	6.917	48	56	12	0	1	2	SLC35B1, FAM117A	-230, 56006	upstream, downstream	ActReg chr17 #7388	1	1	0
7389	17	47,865,851	47,866,834	983	1	9.731	13.516	9.839	15	21	18	1	1	1	MYST2	271	in gene	ActReg chr17 #7389	0	1	0
7390	17	47,928,848	47,929,509	661	1	6.45	5.048	10.571	9	8	17	1	1	2	TAC4, FLJ45513	-3799, 5906	upstream, downstream	ActReg chr17 #7390	0	0	1
7391	17	47,939,867	47,940,342	475	1	3.333	5.933	14.067	5	9	23	0	0	0				ActReg chr17 #7391	0	0	1
7392	17	48,004,052	48,004,787	735	2	11.391	11.391	6.773	20	22	12	0	0	0				ActReg chr17 #7392	1	1	0
7393	17	48,048,979	48,049,599	620	1	5.368	4.895	13	8	9	18	1	1	1	DLX4	2,727	in gene	ActReg chr17 #7393	0	0	1
7394	17	48,104,644	48,106,241	1,597	1	8.98	13.72	6.94	18	23	16	0	0	0				ActReg chr17 #7394	0	1	0
7395	17	48,123,821	48,124,838	1,017	1	4.875	10.688	6.688	10	15	11	0	0	2	LOC284080, ITGA3	8774, -9011	downstream, upstream	ActReg chr17 #7395	0	1	0
7396	17	48,145,474	48,145,926	452	1	6.5	9.214	11	9	14	16	0	0	1	ITGA3	12,360	in gene	ActReg chr17 #7396	0	0	1
7397	17	48,156,802	48,157,441	639	1	4	7.4	12.65	6	12	20	0	0	1	ITGA3	23,781	in gene	ActReg chr17 #7397	0	0	1
7398	17	48,172,177	48,173,532	1,355	2	9	14.833	6.78	24	30	15	1	1	2	ITGA3, PDK2	39514, 158	downstream, in gene	ActReg chr17 #7398	1	1	0
7399	17	48,226,588	48,227,099	511	1	6.688	5.188	12.438	10	8	17	1	1	1	PPP1R9B	1,034	in gene	ActReg chr17 #7399	0	0	1
7400	17	48,228,429	48,229,891	1,462	2	12.13	11.152	4.848	30	27	9	1	1	1	PPP1R9B	-1,283	upstream	ActReg chr17 #7400	1	1	0
7401	17	48,277,966	48,278,662	696	1	9.091	8.364	14.227	18	13	27	1	1	2	COL1A1, LOC100506522	686, 15706	in gene, in gene	ActReg chr17 #7401	0	0	1
7402	17	48,474,507	48,475,399	892	2	13.857	14	7.536	29	24	12	1	1	1	LRRC59	-39	upstream	ActReg chr17 #7402	1	1	0
7403	17	48,542,553	48,543,236	683	1	2.059	4.182	9.909	3	7	14	0	0	2	ACSF2, CHAD	39375, 3333	in gene, in gene	ActReg chr17 #7403	0	0	1
7404	17	48,555,749	48,556,709	960	2	20.533	23.867	5.321	55	53	10	1	1	3	ACSF2, CHAD, RSAD1	52710, -10002, 39	downstream, upstream, in gene	ActReg chr17 #7404	1	1	0
7405	17	48,559,678	48,560,360	682	2	12.773	11.364	5.35	29	26	17	0	0	2	ACSF2, RSAD1	56500, 3829	downstream, in gene	ActReg chr17 #7405	1	1	0
7406	17	48,686,708	48,687,382	674	1	4.714	3.619	12.238	7	5	19	0	0	1	CACNA1G	48,596	in gene	ActReg chr17 #7406	0	0	1
7407	17	48,714,219	48,714,551	332	1	4.5	4.4	12.2	7	7	17	0	1	2	CACNA1G, ABCC3	75936, 2167	downstream, in gene	ActReg chr17 #7407	0	0	1
7408	17	48,716,004	48,717,114	1,110	1	9.029	15.029	3.485	13	23	8	0	0	1	ABCC3	4,341	in gene	ActReg chr17 #7408	0	1	0
7409	17	48,796,763	48,797,495	732	1	8.261	10.783	5.19	11	16	12	1	1	1	LUC7L3	203	in gene	ActReg chr17 #7409	0	1	0
7410	17	48,917,502	48,917,945	443	1	3.571	2.636	12.214	5	5	18	1	0	1	WFIKKN2	5,118	in gene	ActReg chr17 #7410	0	0	1
7411	17	48,943,317	48,944,262	945	1	7.414	11.433	6.9	15	18	14	1	2	2	TOB1, LOC400604	-2376, -108	upstream, upstream	ActReg chr17 #7411	0	1	0
7412	17	48,970,598	48,971,413	815	1	9.417	13.2	6.125	19	23	10	0	0	0				ActReg chr17 #7412	0	1	0
7413	17	49,010,632	49,011,298	666	1	12	9.238	3.778	20	13	7	0	0	1	LOC100506609	11,109	downstream	ActReg chr17 #7413	1	0	0
7414	17	49,230,552	49,231,528	976	2	10.419	13.774	17.032	23	31	46	1	2	2	NME1-NME2, NME1	120, 120	in gene, in gene	ActReg chr17 #7414	0	1	1
7415	17	49,243,545	49,244,906	1,361	1	8.233	11.93	6.1	13	20	14	1	1	4	NME1-NME2, NME1, NME2, MBTD1	13305, 13305, 1334, 93202	in gene, downstream, in gene, downstream	ActReg chr17 #7415	0	1	0
7416	17	49,337,182	49,338,077	895	2	20.321	16.071	6.643	46	40	13	1	2	2	MBTD1, UTP18	-202, -268	upstream, upstream	ActReg chr17 #7416	1	1	0
7417	17	49,430,035	49,431,158	1,123	1	6.943	10.714	3.057	12	15	5	0	0	0				ActReg chr17 #7417	0	1	0
7418	17	50,238,211	50,238,738	527	1	6.875	11.188	1.533	12	21	3	0	1	1	CA10	-1,097	upstream	ActReg chr17 #7418	0	1	0
7419	17	53,045,592	53,046,304	712	1	9.217	12.565	12.391	15	19	17	1	2	3	TOM1L1, COX11, STXBP4	67896, 116, -178	downstream, in gene, upstream	ActReg chr17 #7419	0	0	1
7420	17	53,239,401	53,240,084	683	2	10.667	11.238	2.667	21	19	5	0	0	1	STXBP4	193,616	in gene	ActReg chr17 #7420	1	1	0
7421	17	53,535,811	53,536,803	992	2	11.355	10.323	4.889	18	16	10	0	0	0				ActReg chr17 #7421	1	1	0
7422	17	54,397,857	54,398,304	447	1	3	10.357	1.3	4	15	2	0	0	1	ANKFN1	167,244	in gene	ActReg chr17 #7422	0	1	0
7423	17	54,990,620	54,991,823	1,203	2	8.921	11.684	10.263	12	17	25	1	1	1	TRIM25	188	in gene	ActReg chr17 #7423	0	1	1
7424	17	55,162,022	55,162,526	504	1	9	13.667	6.867	12	23	13	1	1	1	AKAP1	-279	upstream	ActReg chr17 #7424	0	1	0
7425	17	55,288,899	55,289,514	615	1	7.526	10.737	1.222	11	16	2	0	0	0				ActReg chr17 #7425	0	1	0
7426	17	55,557,896	55,558,507	611	1	8.368	11.21	2.529	14	17	5	0	0	1	MSI2	224,270	in gene	ActReg chr17 #7426	0	1	0
7427	17	55,926,952	55,928,139	1,187	2	28.108	31.838	7.838	92	88	15	1	1	1	MRPS23	-146	upstream	ActReg chr17 #7427	1	1	0
7428	17	55,976,402	55,976,962	560	1	8.556	10.056	12.278	12	16	22	0	0	1	CUEDC1	4,068	in gene	ActReg chr17 #7428	0	0	1
7429	17	55,980,252	55,980,651	399	1	11.846	6.846	11.308	14	10	18	0	1	1	CUEDC1	299	in gene	ActReg chr17 #7429	0	0	1
7430	17	56,013,125	56,013,807	682	1	13.048	5.762	4.333	25	9	8	0	0	0				ActReg chr17 #7430	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7431	17	56,083,763	56,085,378	1,615	4	10.451	11.961	8.608	20	20	22	1	1	1	SFRS1	137	in gene	ActReg chr17 #7431	1	1	1
7432	17	56,190,254	56,190,862	608	1	10.947	6.421	4.211	15	9	7	0	0	0				ActReg chr17 #7432	1	0	0
7433	17	56,197,351	56,198,149	798	2	16.4	14.56	2.68	35	29	5	0	0	0				ActReg chr17 #7433	1	1	0
7434	17	56,249,547	56,250,178	631	1	4.7	10.3	3.211	10	20	5	0	0	1	OR4D2	2,845	downstream	ActReg chr17 #7434	0	1	0
7435	17	56,296,182	56,297,184	1,002	2	10.312	13.531	5.484	17	26	10	1	1	1	MKS1	283	in gene	ActReg chr17 #7435	1	1	0
7436	17	56,400,280	56,400,727	447	1	5.5	1.917	11.571	8	3	17	0	1	3	BZRAP1, LOC100506779, MIR142	5649, -2308, 8176	in gene, upstream, downstream	ActReg chr17 #7436	0	0	1
7437	17	56,410,241	56,410,686	445	1	3.231	5.462	11.846	5	8	17	0	2	3	BZRAP1, LOC100506779, MIR142	-4311, 7652, -1784	upstream, in gene, upstream	ActReg chr17 #7437	0	0	1
7438	17	56,429,120	56,430,455	1,335	2	8.762	10.976	5.463	18	19	14	1	1	3	LOC100506779, SUPT4H1, RNF43	26976, -224, 65144	in gene, upstream, downstream	ActReg chr17 #7438	1	1	0
7439	17	56,708,893	56,709,801	908	2	13.172	10.138	6.929	23	18	14	0	0	1	TEX14	60,069	in gene	ActReg chr17 #7439	1	1	0
7440	17	56,736,438	56,737,152	714	2	11.478	12.348	6.826	23	22	13	1	0	1	TEX14	32,621	in gene	ActReg chr17 #7440	1	1	0
7441	17	56,743,765	56,744,631	866	1	8.222	12.037	3.538	17	19	6	0	0	1	TEX14	25,218	in gene	ActReg chr17 #7441	0	1	0
7442	17	56,756,613	56,757,497	884	2	10.444	12	5.185	21	22	10	0	0	1	TEX14	12,361	in gene	ActReg chr17 #7442	1	1	0
7443	17	56,832,618	56,833,410	792	2	11.76	13.24	3.579	20	22	6	1	1	1	PPM1E	-218	upstream	ActReg chr17 #7443	1	1	0
7444	17	57,183,311	57,183,729	418	1	10.769	5.385	5.3	16	8	10	1	2	3	TRIM37, LOC100506847, SKA2	746, -331, 49280	in gene, upstream, downstream	ActReg chr17 #7444	1	0	0
7445	17	57,183,790	57,184,328	538	1	11.412	10.588	12.647	14	13	16	1	2	3	TRIM37, LOC100506847, SKA2	207, 208, 48741	in gene, in gene, downstream	ActReg chr17 #7445	0	0	1
7446	17	57,233,797	57,234,238	441	1	5.231	11.538	2.692	7	13	5	0	3	3	SKA2, MIR301A, PRR11	-1217, -5435, 1157	upstream, upstream, in gene	ActReg chr17 #7446	0	1	0
7447	17	57,287,385	57,287,789	404	1	6.692	10.385	10.308	10	15	16	1	1	2	PRR11, C17orf71	54727, 216	downstream, in gene	ActReg chr17 #7447	0	0	1
7448	17	57,297,741	57,298,550	809	1	7.24	10.44	5.16	9	14	9	1	1	2	C17orf71, GDPD1	10774, 317	downstream, in gene	ActReg chr17 #7448	0	1	0
7449	17	57,432,307	57,433,249	942	1	10.367	11.3	2.654	16	16	5	0	0	1	YPEL2	23,725	in gene	ActReg chr17 #7449	0	1	0
7450	17	57,642,496	57,643,320	824	3	10.962	12.885	9.385	19	25	17	1	1	1	DHX40	22	in gene	ActReg chr17 #7450	1	1	1
7451	17	57,696,364	57,697,188	824	2	12.846	11.923	5.462	24	16	11	1	1	1	CLTC	-274	upstream	ActReg chr17 #7451	1	1	0
7452	17	57,920,405	57,921,224	819	1	10.154	7.385	4.692	17	13	9	0	1	2	TMEM49, MIR21	135951, 2187	downstream, downstream	ActReg chr17 #7452	1	0	0
7453	17	57,922,957	57,923,422	465	1	11	5.857	3.786	17	8	5	0	0	2	TMEM49, MIR21	138326, 4562	downstream, downstream	ActReg chr17 #7453	1	0	0
7454	17	57,930,546	57,931,147	601	1	5.789	9.211	3.529	10	15	6	0	0	1	TUBD1	59,460	downstream	ActReg chr17 #7454	0	1	0
7455	17	57,970,205	57,970,891	686	2	10.954	13.546	10.318	23	24	18	1	2	2	TUBD1, RPS6KB1	-242, 105	upstream, in gene	ActReg chr17 #7455	0	1	1
7456	17	58,216,170	58,216,738	568	1	5.333	7.833	12.444	8	10	18	2	0	0				ActReg chr17 #7456	0	0	1
7457	17	58,216,796	58,217,785	989	2	11.452	16.484	5.774	28	33	9	1	0	1	CA4	-10,012	upstream	ActReg chr17 #7457	1	1	0
7458	17	58,218,197	58,219,305	1,108	1	8.176	11.971	8.286	15	19	13	1	0	1	CA4	-8,551	upstream	ActReg chr17 #7458	0	1	0
7459	17	58,226,922	58,227,516	594	1	5	5.556	12.389	6	10	21	1	1	1	CA4	-83	upstream	ActReg chr17 #7459	0	0	1
7460	17	58,468,631	58,470,259	1,628	1	8.157	11.412	7.667	15	17	12	1	1	1	USP32	141	in gene	ActReg chr17 #7460	0	1	0
7461	17	58,602,877	58,603,988	1,111	3	11.257	10	9.914	18	17	19	1	1	1	APPBP2	148	in gene	ActReg chr17 #7461	1	1	1
7462	17	58,676,933	58,678,259	1,326	2	7.878	10.854	8.341	14	18	18	1	1	1	PPM1D	42	in gene	ActReg chr17 #7462	0	1	1
7463	17	59,328,298	59,328,915	617	1	6.421	12.21	3.316	8	17	6	0	0	1	BCAS3	573,434	in gene	ActReg chr17 #7463	0	1	0
7464	17	59,389,525	59,390,156	631	1	11.15	10.9	3.647	14	18	7	0	0	1	BCAS3	634,668	in gene	ActReg chr17 #7464	0	1	0
7465	17	59,398,599	59,399,206	607	2	13.105	10.389	3.158	22	18	6	0	0	1	BCAS3	643,730	in gene	ActReg chr17 #7465	1	1	0
7466	17	59,466,885	59,467,645	760	1	4.217	5.217	11.609	6	10	16	0	0	3	BCAS3, LOC645722, TBX2	712093, 21651, -9992	in gene, downstream, upstream	ActReg chr17 #7466	0	0	1
7467	17	59,489,460	59,490,152	692	2	7.682	12.091	11.318	11	17	18	1	2	3	LOC645722, TBX2, C17orf82	-890, 12549, 694	upstream, downstream, in gene	ActReg chr17 #7467	0	1	1
7468	17	59,532,208	59,533,067	859	1	2.762	3.217	12.074	7	5	17	1	1	1	TBX4	-1,170	upstream	ActReg chr17 #7468	0	0	1
7469	17	59,887,134	59,887,705	571	1	5.222	10	3.056	8	19	6	0	0	1	BRIP1	53,501	in gene	ActReg chr17 #7469	0	1	0
7470	17	60,004,690	60,005,555	865	2	12.815	10.667	5.704	23	16	12	1	1	1	INTS2	255	in gene	ActReg chr17 #7470	1	1	0
7471	17	60,142,863	60,143,550	687	2	10.952	11.333	7.238	20	20	13	1	1	1	MED13	-563	upstream	ActReg chr17 #7471	1	1	0
7472	17	60,501,021	60,501,610	589	1	5.263	9.947	5	10	17	9	1	1	2	EFCAB3, METTL2A	53736, 69	downstream, in gene	ActReg chr17 #7472	0	1	0
7473	17	60,704,377	60,705,294	917	2	10.138	10.586	10.586	15	13	17	1	1	1	MRC2	73	in gene	ActReg chr17 #7473	1	0	1
7474	17	60,769,384	60,770,095	711	1	5.136	3.045	12.773	9	6	18	0	0	2	MRC2, MARCH10	64977, 115966	in gene, downstream	ActReg chr17 #7474	0	0	1
7475	17	60,771,495	60,772,504	1,009	2	11.29	13.258	5.968	18	21	10	0	0	2	MRC2, MARCH10	67237, 113706	downstream, downstream	ActReg chr17 #7475	1	1	0
7476	17	60,839,202	60,839,877	675	1	6	11.286	4.385	8	19	7	0	0	1	10-Mar	46,166	in gene	ActReg chr17 #7476	0	1	0
7477	17	60,869,411	60,869,983	572	1	10.235	15.882	2.6	15	26	4	0	0	1	10-Mar	16,008	in gene	ActReg chr17 #7477	0	1	0
7478	17	61,352,548	61,353,288	740	2	10.174	11.13	0	20	24	0	0	0	1	TANC2	266,020	in gene	ActReg chr17 #7478	1	1	0
7479	17	61,433,453	61,434,094	641	1	11.05	11.45	2.667	21	21	5	0	0	1	TANC2	346,875	in gene	ActReg chr17 #7479	1	0	0
7480	17	61,524,079	61,524,541	462	1	8.214	12.429	12.643	15	21	20	1	1	1	CYB561	-588	upstream	ActReg chr17 #7480	0	0	1
7481	17	61,538,074	61,538,600	526	1	7.471	11.823	3.235	12	19	5	0	0	0				ActReg chr17 #7481	0	1	0
7482	17	61,627,084	61,628,333	1,249	3	10.769	10.872	7.081	17	15	16	1	1	2	KCNH6, DCAF7	27013, -114	downstream, upstream	ActReg chr17 #7482	1	1	1
7483	17	61,677,796	61,678,544	748	3	12.957	10.348	9.783	23	20	22	1	1	2	DCAF7, TACO1	50348, -61	downstream, upstream	ActReg chr17 #7483	1	1	1
7484	17	61,818,721	61,819,494	773	1	9.696	11.783	11.043	14	16	17	1	1	2	STRADA, CCDC47	198, 31956	in gene, downstream	ActReg chr17 #7484	0	0	1
7485	17	61,850,637	61,851,245	608	1	12.105	12.842	4.632	20	19	11	1	2	2	CCDC47, DDX42	147, -626	in gene, upstream	ActReg chr17 #7485	1	0	0
7486	17	61,851,334	61,851,834	500	1	10.867	10.667	5.667	16	13	10	1	2	2	CCDC47, DDX42	-496, 17	upstream, in gene	ActReg chr17 #7486	1	0	0
7487	17	61,904,606	61,905,448	842	1	8.556	13.148	6.778	16	22	14	1	2	4	DDX42, FTSJ3, PSMC5, SMARCD2	53460, 4, 217, 15324	downstream, in gene, in gene, downstream	ActReg chr17 #7487	0	1	0
7488	17	61,919,937	61,920,529	592	2	12.333	17.222	3.278	23	33	6	1	1	1	SMARCD2	118	in gene	ActReg chr17 #7488	1	1	0
7489	17	61,994,024	61,994,708	684	1	3	1.462	44.191	7	2	60	0	2	2	CSHL1, GH1	-5748, 1832	upstream, downstream	ActReg chr17 #7489	0	0	1
7490	17	62,024,977	62,025,715	738	1	2.913	6.522	11.522	6	10	20	0	0	1	SCN4A	24,932	in gene	ActReg chr17 #7490	0	0	1
7491	17	62,049,673	62,050,679	1,006	1	3.097	4.935	12.419	5	9	16	0	1	1	SCN4A	102	in gene	ActReg chr17 #7491	0	0	1
7492	17	62,051,307	62,052,281	974	2	11.4	12.367	4.267	19	17	7	0	1	1	SCN4A	-1,516	upstream	ActReg chr17 #7492	1	1	0
7493	17	62,067,508	62,068,003	495	1	6.25	6.688	12.125	12	10	15	0	0	1	C17orf72	-7,956	upstream	ActReg chr17 #7493	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7494	17	62,076,219	62,076,698	479	1	4.733	2.867	11.933	6	4	17	0	1	2	C17orf72, ICAM2	747, 21536	in gene, downstream	ActReg chr17 #7494	0	0	1
7495	17	62,222,845	62,224,251	1,406	3	10.909	15.341	13.432	23	27	34	1	2	3	SNORD104, SNORA76, TEX2	110, -151, 117105	downstream, upstream, downstream	ActReg chr17 #7495	1	1	1
7496	17	62,340,469	62,341,363	894	2	19.964	26.393	4.407	57	71	10	1	1	1	TEX2	-263	upstream	ActReg chr17 #7496	1	1	0
7497	17	62,403,371	62,404,196	825	1	8.962	11.231	4.115	12	18	8	0	2	2	LOC100506961, PECAM1	-5742, -2578	upstream, upstream	ActReg chr17 #7497	0	1	0
7498	17	62,492,926	62,493,640	714	1	5.565	12.261	4.619	10	19	10	1	1	3	POLG2, DDX5, CCDC45	-99, 9201, -9875	upstream, downstream, upstream	ActReg chr17 #7498	0	1	0
7499	17	62,502,122	62,502,669	547	1	10.059	9.235	15.412	15	16	30	1	2	3	POLG2, DDX5, CCDC45	-9211, 89, -763	upstream, in gene, upstream	ActReg chr17 #7499	0	0	1
7500	17	62,502,719	62,503,722	1,003	2	7.188	12.969	9.875	13	24	21	1	2	3	POLG2, DDX5, CCDC45	-10036, -736, 62	upstream, upstream, in gene	ActReg chr17 #7500	0	1	1
7501	17	62,675,815	62,676,380	565	1	12.529	9.588	3.667	18	13	7	0	0	0				ActReg chr17 #7501	1	0	0
7502	17	62,702,925	62,703,745	820	1	6.538	11.5	3.923	14	19	11	0	0	0				ActReg chr17 #7502	0	1	0
7503	17	62,776,897	62,777,266	369	1	1.833	1.273	11.091	3	2	15	1	1	1	LOC146880	1,036	in gene	ActReg chr17 #7503	0	0	1
7504	17	62,930,511	62,930,793	282	1	2.889	5.222	11.556	5	7	15	0	0	0				ActReg chr17 #7504	0	0	1
7505	17	62,971,228	62,972,450	1,222	3	12.718	12.077	13.333	25	19	26	1	0	0				ActReg chr17 #7505	1	1	1
7506	17	62,986,962	62,987,627	665	1	8.476	14.238	7.842	15	26	13	0	0	0				ActReg chr17 #7506	0	1	0
7507	17	62,988,404	62,989,036	632	2	11.75	10.6	1.545	25	20	2	0	0	0				ActReg chr17 #7507	1	1	0
7508	17	63,074,440	63,075,004	564	1	9.118	13.118	2.824	13	20	4	0	0	0				ActReg chr17 #7508	0	1	0
7509	17	63,084,775	63,085,284	509	1	9.5	11.25	3.438	16	15	5	0	0	0				ActReg chr17 #7509	1	0	0
7510	17	63,250,236	63,250,787	551	1	7.889	11.222	1.143	13	23	2	0	0	0				ActReg chr17 #7510	0	1	0
7511	17	63,466,635	63,467,130	495	1	4.6	5.6	11.6	8	9	17	0	0	0				ActReg chr17 #7511	0	0	1
7512	17	64,271,637	64,272,325	688	2	11.273	10.636	1.471	24	24	2	0	0	0				ActReg chr17 #7512	1	1	0
7513	17	64,299,163	64,299,734	571	1	8	9.389	12.056	13	15	16	1	1	1	PRKCA	522	in gene	ActReg chr17 #7513	0	0	1
7514	17	64,489,348	64,490,339	991	1	11.839	8.774	2.476	18	16	4	0	0	1	PRKCA	190,917	in gene	ActReg chr17 #7514	1	0	0
7515	17	64,505,338	64,505,941	603	1	8.316	10.158	2.75	12	15	4	0	0	1	PRKCA	206,713	in gene	ActReg chr17 #7515	0	1	0
7516	17	64,536,074	64,536,879	805	2	11.16	11.2	5	18	26	9	0	0	1	PRKCA	237,550	in gene	ActReg chr17 #7516	1	1	0
7517	17	64,825,532	64,826,184	652	1	10.952	15.571	6.095	19	35	8	0	0	0				ActReg chr17 #7517	0	1	0
7518	17	64,993,230	64,993,823	593	1	2.059	2.944	11.111	3	5	16	0	0	1	CACNG4	32,513	in gene	ActReg chr17 #7518	0	0	1
7519	17	65,020,616	65,021,117	501	1	3.667	4	12.4	6	5	16	0	0	1	CACNG4	59,853	in gene	ActReg chr17 #7519	0	0	1
7520	17	65,362,172	65,363,030	858	2	10.037	12.407	11	21	24	24	1	1	1	PSMD12	120	in gene	ActReg chr17 #7520	0	1	1
7521	17	65,713,659	65,714,418	759	1	10.042	12.667	7.542	19	21	14	1	2	2	LOC100507049, NOL11	-294, -23	upstream, upstream	ActReg chr17 #7521	0	1	0
7522	17	65,821,277	65,821,785	508	1	9.938	8.438	4.467	16	11	7	1	1	1	BPTF	-249	upstream	ActReg chr17 #7522	1	0	0
7523	17	66,015,737	66,016,537	800	3	13.56	14.08	16.8	24	29	41	1	0	0				ActReg chr17 #7523	1	1	1
7524	17	66,031,605	66,032,536	931	2	9.103	11.69	11.31	14	22	19	1	1	1	KPNA2	222	in gene	ActReg chr17 #7524	0	1	1
7525	17	66,095,558	66,096,035	477	1	2.867	2	11.267	5	3	19	0	1	1	LOC100499466	-1,900	upstream	ActReg chr17 #7525	0	0	1
7526	17	66,243,603	66,244,132	529	1	11.647	10.412	13.412	16	13	24	1	1	1	AM22	-278	upstream	ActReg chr17 #7526	0	0	1
7527	17	66,376,987	66,377,802	815	2	9.962	10	2.188	16	19	3	0	0	1	ARSG	122,071	in gene	ActReg chr17 #7527	1	1	0
7528	17	66,395,909	66,396,943	1,034	2	11.469	10.719	4.355	18	16	9	0	0	1	ARSG	141,103	in gene	ActReg chr17 #7528	1	1	0
7529	17	66,431,723	66,432,585	862	1	10.407	7.037	4.769	16	12	9	0	0	1	WIPI1	21,499	in gene	ActReg chr17 #7529	1	0	0
7530	17	66,507,945	66,509,066	1,121	2	11.314	15.114	5.688	21	26	9	1	1	1	PRKAR1A	395	in gene	ActReg chr17 #7530	1	1	0
7531	17	66,596,117	66,596,630	513	1	6.438	10	13.125	11	13	21	1	1	1	FAM20A	722	in gene	ActReg chr17 #7531	0	0	1
7532	17	66,690,894	66,691,918	1,024	2	10.625	12.062	2.594	18	17	4	0	0	0				ActReg chr17 #7532	1	1	0
7533	17	66,694,133	66,694,709	576	1	10.389	4.444	1	15	7	1	0	0	0				ActReg chr17 #7533	1	0	0
7534	17	66,905,089	66,905,582	493	1	9	9.6	2.333	14	14	4	0	0	1	ABCA8	46,198	in gene	ActReg chr17 #7534	0	1	0
7535	17	67,535,840	67,536,234	394	1	7.154	10.077	1.636	11	15	3	0	0	1	MAP2K6	125,199	in gene	ActReg chr17 #7535	0	1	0
7536	17	67,759,453	67,760,273	820	2	12.308	11.962	2.6	29	30	5	0	0	0				ActReg chr17 #7536	1	1	0
7537	17	67,866,161	67,866,753	592	1	10.368	10.79	2.278	16	17	3	0	0	0				ActReg chr17 #7537	0	1	0
7538	17	68,165,019	68,165,468	449	1	8.357	10.929	7.5	11	17	11	1	2	2	FLJ36644, KCNJ2	300, -433	in gene, upstream	ActReg chr17 #7538	0	1	0
7539	17	68,192,594	68,193,300	706	2	12.682	14.182	2	27	27	3	0	0	0				ActReg chr17 #7539	1	1	0
7540	17	68,401,727	68,402,312	585	1	12.158	9	1	22	12	1	0	0	0				ActReg chr17 #7540	1	0	0
7541	17	69,067,996	69,068,445	449	1	10.357	11.571	2	16	16	3	0	0	0				ActReg chr17 #7541	0	1	0
7542	17	69,408,900	69,409,403	503	1	5.2	9.667	1.25	9	17	2	0	0	0				ActReg chr17 #7542	0	1	0
7543	17	69,437,139	69,437,663	524	1	10.562	12.375	2.688	15	20	6	0	0	0				ActReg chr17 #7543	0	1	0
7544	17	70,026,435	70,026,943	508	1	6.8	10.067	2.467	9	15	5	0	0	0				ActReg chr17 #7544	0	1	0
7545	17	70,117,581	70,118,106	525	1	5.25	6.062	11.75	9	9	14	1	2	2	FLJ37644, SOX9	-5686, 682	upstream, in gene	ActReg chr17 #7545	0	0	1
7546	17	70,461,597	70,462,116	519	1	9.706	5.824	2.6	18	10	4	0	0	1	LOC100499467	127,087	in gene	ActReg chr17 #7546	1	0	0
7547	17	70,567,912	70,568,972	1,060	1	11.03	12.061	5.455	15	17	9	0	0	1	LOC100499467	20,501	in gene	ActReg chr17 #7547	0	1	0
7548	17	70,611,641	70,612,391	750	1	11.417	12.083	7.458	19	21	13	0	0	1	FLJ26484	24,595	in gene	ActReg chr17 #7548	0	1	0
7549	17	70,613,564	70,615,005	1,441	1	10.556	13.756	5.545	17	24	11	0	0	1	FLJ26484	22,327	in gene	ActReg chr17 #7549	0	1	0
7550	17	70,627,460	70,628,958	1,498	1	11.717	12.761	6.886	18	25	13	0	0	1	FLJ26484	8,402	in gene	ActReg chr17 #7550	0	1	0
7551	17	70,651,827	70,652,952	1,125	2	11.8	10.314	3.562	19	21	6	0	0	1	SLC39A11	436,464	in gene	ActReg chr17 #7551	1	1	0
7552	17	70,657,501	70,658,585	1,084	2	10.719	12.5	4.821	20	21	10	0	0	1	SLC39A11	430,810	in gene	ActReg chr17 #7552	1	1	0
7553	17	70,680,071	70,680,955	884	2	12	11.296	2.636	19	16	5	0	0	1	SLC39A11	408,340	in gene	ActReg chr17 #7553	1	1	0
7554	17	70,720,537	70,721,358	821	1	7	9.846	1.75	11	14	3	0	0	1	SLC39A11	367,906	in gene	ActReg chr17 #7554	0	1	0
7555	17	71,189,125	71,189,663	538	1	7.75	12.25	3.667	12	20	6	1	1	1	COG1	221	in gene	ActReg chr17 #7555	0	1	0
7556	17	71,281,284	71,282,106	822	1	4.04	6.04	12.24	8	10	17	1	0	1	CDC42EP4	26,448	in gene	ActReg chr17 #7556	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7557	17	71,287,715	71,288,651	936	1	10.897	12.448	4.286	17	20	7	0	0	1	CDC42EP4	19,960	in gene	ActReg chr17 #7557	0	1	0
7558	17	71,307,741	71,308,260	519	1	7.706	11.294	11.588	10	17	18	1	1	1	CDC42EP4	143	in gene	ActReg chr17 #7558	0	0	1
7559	17	71,451,506	71,451,936	430	1	6	3	10.714	9	5	16	0	0	1	SDK2	188,506	in gene	ActReg chr17 #7559	0	0	1
7560	17	71,551,137	71,551,684	547	1	1.867	3.294	11.647	3	5	15	0	0	1	SDK2	88,817	in gene	ActReg chr17 #7560	0	0	1
7561	17	71,567,667	71,568,201	534	1	2.118	3.647	11.588	4	6	16	0	0	1	SDK2	72,293	in gene	ActReg chr17 #7561	0	0	1
7562	17	71,640,120	71,640,557	437	1	3.667	3.571	10.714	6	7	17	1	1	1	SDK2	-111	upstream	ActReg chr17 #7562	0	0	1
7563	17	71,788,315	71,788,675	360	1	3.583	4.5	11.833	6	7	15	0	0	1	C17orf54	36,181	in gene	ActReg chr17 #7563	0	0	1
7564	17	72,176,386	72,176,752	366	1	4.545	1	9.909	7	1	14	0	0	0				ActReg chr17 #7564	0	0	1
7565	17	72,199,359	72,200,283	924	3	20.172	23.414	10.621	53	71	17	1	1	3	RPL38, MGC16275, TTYH2	26, 9639, -9875	in gene, downstream, upstream	ActReg chr17 #7565	1	1	1
7566	17	72,348,209	72,348,952	743	1	3.714	4.13	11.957	6	8	16	1	0	2	KIF19, BTBD17	26229, 9378	in gene, downstream	ActReg chr17 #7566	0	0	1
7567	17	72,349,407	72,349,867	460	1	3.067	3.333	12	5	5	18	0	0	2	KIF19, BTBD17	27286, 8321	in gene, downstream	ActReg chr17 #7567	0	0	1
7568	17	72,368,193	72,368,666	473	1	4.714	5.143	12.071	6	7	18	1	0	1	GPR142	4,784	in gene	ActReg chr17 #7568	0	0	1
7569	17	72,390,331	72,390,654	323	1	1.8	1	10.6	2	1	14	0	0	0				ActReg chr17 #7569	0	0	1
7570	17	72,427,579	72,428,020	441	1	7.214	7.143	11.786	10	9	18	1	1	1	GPRC5C	132	in gene	ActReg chr17 #7570	0	0	1
7571	17	72,439,117	72,439,518	401	1	2.111	5.083	10.917	3	8	15	0	0	1	GPRC5C	11,650	in gene	ActReg chr17 #7571	0	0	1
7572	17	72,606,001	72,606,731	730	1	7.217	13.13	2.318	14	20	4	0	0	1	CD300E	13,435	downstream	ActReg chr17 #7572	0	1	0
7573	17	72,667,033	72,668,034	1,001	2	26.125	29.125	6.387	79	79	14	1	1	1	RAB37	277	in gene	ActReg chr17 #7573	1	1	0
7574	17	72,772,205	72,772,874	669	1	7.905	12.095	7.905	15	23	17	1	2	3	SLC9A3R1, NAT9, TMEM104	27776, -69, -83	downstream, upstream, upstream	ActReg chr17 #7574	0	1	0
7575	17	72,834,929	72,835,421	492	1	1.846	3.786	11.8	3	7	16	0	0	2	TMEM104, GRIN2C	62553, 20832	in gene, downstream	ActReg chr17 #7575	0	0	1
7576	17	72,856,903	72,857,331	428	1	4.769	1.273	13.923	7	2	21	1	1	2	GRIN2C, FDXR	-1110, 12039	upstream, downstream	ActReg chr17 #7576	0	0	1
7577	17	72,862,140	72,862,932	792	1	6.32	6.56	13.2	11	9	22	0	1	2	GRIN2C, FDXR	-6529, 6620	upstream, in gene	ActReg chr17 #7577	0	0	1
7578	17	72,945,657	72,946,186	529	1	4	4.588	11.059	6	7	17	0	0	2	OTOP3, C17orf28	14024, 22979	downstream, downstream	ActReg chr17 #7578	0	0	1
7579	17	72,948,557	72,948,973	416	1	3	4	12.692	4	6	17	0	0	2	OTOP3, C17orf28	16868, 20135	downstream, in gene	ActReg chr17 #7579	0	0	1
7580	17	72,978,069	72,978,984	915	1	8.759	10.69	8.655	13	17	13	1	1	2	C17orf28, CDR2L	-9626, -5201	upstream, upstream	ActReg chr17 #7580	0	1	0
7581	17	73,008,202	73,009,258	1,056	3	11.758	12.182	11	19	22	20	1	1	2	CDR2L, ICT1	25003, -50	downstream, upstream	ActReg chr17 #7581	1	1	1
7582	17	73,029,645	73,031,660	2,015	3	14.762	14.444	15.714	31	24	31	1	0	1	ATP5H	12,422	downstream	ActReg chr17 #7582	1	1	1
7583	17	73,042,738	73,043,418	680	1	10.25	10.191	8.368	15	15	13	1	2	2	ATP5H, KCTD2	-4, -201	upstream, upstream	ActReg chr17 #7583	0	1	0
7584	17	73,120,169	73,120,949	780	1	9.542	11.5	6.917	14	18	11	0	0	2	ARMC7, NT5C	14477, 7318	in gene, downstream	ActReg chr17 #7584	0	1	0
7585	17	73,124,553	73,125,275	722	1	6.318	6.5	13.546	8	8	23	1	0	3	ARMC7, NT5C, HN1	18832, 2963, 25861	in gene, downstream, downstream	ActReg chr17 #7585	0	0	1
7586	17	73,127,412	73,128,037	625	1	8.15	12.3	5.529	12	19	10	1	1	3	ARMC7, NT5C, HN1	21642, 153, 23051	downstream, in gene, downstream	ActReg chr17 #7586	0	1	0
7587	17	73,178,133	73,178,555	422	1	1.667	7.538	11.308	3	11	19	1	1	1	SUMO2	754	in gene	ActReg chr17 #7587	0	0	1
7588	17	73,201,020	73,202,403	1,383	3	18.932	18.454	8.318	53	55	17	1	1	1	NUP85	114	in gene	ActReg chr17 #7588	1	1	1
7589	17	73,235,883	73,236,490	607	1	3.333	3.812	10.842	6	8	14	0	0	2	NUP85, GGA3	34589, 22258	downstream, in gene	ActReg chr17 #7589	0	0	1
7590	17	73,257,055	73,258,322	1,267	3	10.425	11.95	10.154	18	18	19	1	2	4	GGA3, MRPS7, MIF4GD, LOC100287042	756, -61, 9615, -9692	in gene, upstream, downstream, upstream	ActReg chr17 #7590	1	1	1
7591	17	73,266,485	73,267,213	728	1	5.87	7.174	15.174	11	12	28	1	2	5	GGA3, MRPS7, MIF4GD, LOC100287042, SLC25A19	-8405, 9100, 454, -531, 18681	upstream, downstream, in gene, upstream, downstream	ActReg chr17 #7591	0	0	1
7592	17	73,282,613	73,282,968	355	1	4.182	3.273	10.909	7	4	14	0	0	1	SLC25A19	2,740	in gene	ActReg chr17 #7592	0	0	1
7593	17	73,285,009	73,286,041	1,032	3	12.875	9.656	10.469	23	14	20	1	1	1	SLC25A19	5	in gene	ActReg chr17 #7593	1	1	1
7594	17	73,452,460	73,453,429	969	1	8.5	7.9	11.767	18	13	17	1	1	1	KIAA0195	280	in gene	ActReg chr17 #7594	0	0	1
7595	17	73,481,895	73,482,465	570	1	3.111	2.611	11.5	5	4	15	0	0	1	KIAA0195	29,516	in gene	ActReg chr17 #7595	0	0	1
7596	17	73,500,200	73,500,829	629	1	4.105	6	10.579	7	9	13	1	0	2	KIAA0195, CASKIN2	47850, 11113	downstream, in gene	ActReg chr17 #7596	0	0	1
7597	17	73,511,675	73,513,421	1,746	2	13.873	12.982	7.109	28	38	12	1	2	3	CASKIN2, TSEN54, LLGL2	-921, -61, -9235	upstream, upstream, upstream	ActReg chr17 #7597	1	1	0
7598	17	73,570,594	73,571,073	479	1	2.833	4.267	12.867	7	7	20	0	0	1	LLGL2	49,050	in gene	ActReg chr17 #7598	0	0	1
7599	17	73,583,630	73,584,055	425	1	2.923	4.692	12.077	4	7	17	1	0	0				ActReg chr17 #7599	0	0	1
7600	17	73,597,329	73,597,842	513	1	7.312	7.125	12.625	13	9	21	0	0	0				ActReg chr17 #7600	0	0	1
7601	17	73,627,087	73,628,011	924	1	4.897	3.897	12.138	9	7	18	1	1	2	RECQL5, LOC643008	35720, -1965	in gene, upstream	ActReg chr17 #7601	0	0	1
7602	17	73,629,059	73,630,179	1,120	1	7.657	9.486	11.486	12	14	18	0	1	2	RECQL5, LOC643008	33650, 105	in gene, in gene	ActReg chr17 #7602	0	0	1
7603	17	73,663,021	73,663,700	679	1	11.238	12.571	5	18	22	8	1	2	2	RECQL5, SAP30BP	-91, -39	upstream, upstream	ActReg chr17 #7603	0	1	0
7604	17	73,687,385	73,688,375	990	1	7.806	11.484	5.806	11	19	12	0	0	1	SAP30BP	24,481	in gene	ActReg chr17 #7604	0	1	0
7605	17	73,717,618	73,718,023	405	1	3.846	7.846	11.615	7	10	17	1	1	1	ITGB4	304	in gene	ActReg chr17 #7605	0	0	1
7606	17	73,739,584	73,740,171	587	1	6.421	4.368	12.895	9	9	20	0	0	1	ITGB4	22,361	in gene	ActReg chr17 #7606	0	0	1
7607	17	73,750,019	73,750,664	645	1	5.1	6.2	13.4	6	9	18	1	0	2	ITGB4, GALK1	32825, 10939	in gene, downstream	ActReg chr17 #7607	0	0	1
7608	17	73,754,135	73,754,809	674	1	5.238	4.81	13.667	9	10	20	0	0	2	ITGB4, GALK1	36956, 6808	downstream, in gene	ActReg chr17 #7608	0	0	1
7609	17	73,775,563	73,776,176	613	2	11.263	11.421	8.947	17	21	18	1	2	2	H3F3B, UNK	-9, -4812	upstream, upstream	ActReg chr17 #7609	1	1	0
7610	17	73,780,458	73,781,680	1,222	2	15.105	13.842	6.447	26	22	11	1	2	2	H3F3B, UNK	-5209, 388	upstream, in gene	ActReg chr17 #7610	1	1	0
7611	17	73,805,665	73,806,369	704	1	4.909	8.136	11.364	8	16	17	0	0	1	UNK	25,336	in gene	ActReg chr17 #7611	0	0	1
7612	17	73,819,296	73,819,844	548	1	2.5	3.222	13.944	4	5	17	0	1	3	UNK, LOC100507191, UNC13D	38889, -1499, 21228	in gene, upstream, downstream	ActReg chr17 #7612	0	0	1
7613	17	73,821,841	73,822,317	476	1	1.357	4.267	11.733	2	5	17	0	1	3	UNK, LOC100507191, UNC13D	41398, -4008, 18719	downstream, upstream, downstream	ActReg chr17 #7613	0	0	1
7614	17	73,851,342	73,852,201	859	1	11.222	9.407	7.333	17	15	14	1	1	1	WBP2	-270	upstream	ActReg chr17 #7614	1	0	0
7615	17	73,871,624	73,873,092	1,468	2	6.152	12.978	9.543	10	20	20	0	1	1	TRIM47	2,298	in gene	ActReg chr17 #7615	0	1	1
7616	17	73,873,274	73,874,768	1,494	1	9.045	11.34	5	20	18	10	1	1	1	TRIM47	635	in gene	ActReg chr17 #7616	0	1	0
7617	17	73,913,590	73,914,069	479	1	3.8	4.467	12.067	6	7	17	1	0	1	FBF1	23,290	in gene	ActReg chr17 #7617	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7618	17	73,915,937	73,916,465	528	1	6.75	5.438	12.75	12	10	18	0	0	1	FBF1	20,918	in gene	ActReg chr17 #7618	0	0	1
7619	17	73,936,674	73,937,454	780	1	9.292	11	8.542	16	17	13	1	1	2	FBF1, ACOX1	55, 38451	in gene, downstream	ActReg chr17 #7619	0	1	0
7620	17	73,974,623	73,975,400	777	2	7.32	9.8	7.68	11	14	14	1	2	2	ACOX1, C17orf106	504, -290	in gene, upstream	ActReg chr17 #7620	0	1	1
7621	17	73,996,462	73,997,205	743	1	4.174	4.348	11	8	8	16	0	1	3	C17orf106, CDK3, EVPL	21532, -154, 26674	downstream, upstream, downstream	ActReg chr17 #7621	0	0	1
7622	17	74,013,641	74,014,201	560	1	1.941	5.412	13	3	8	17	0	0	1	EVPL	9,586	in gene	ActReg chr17 #7622	0	0	1
7623	17	74,018,260	74,018,882	622	1	2.2	3.85	12	4	9	20	1	0	1	EVPL	4,936	in gene	ActReg chr17 #7623	0	0	1
7624	17	74,068,189	74,069,058	869	3	13.536	14.214	8.036	29	34	16	1	3	4	SRP68, GALR2, ZACN, EXOC7	-16, -2269, -6640, 31245	upstream, upstream, upstream, downstream	ActReg chr17 #7624	1	1	1
7625	17	74,072,072	74,072,889	817	1	4.542	6.56	12.52	9	10	20	1	3	4	SRP68, GALR2, ZACN, EXOC7	-3873, 1588, -2783, 27388	upstream, in gene, upstream, downstream	ActReg chr17 #7625	0	0	1
7626	17	74,085,050	74,085,602	552	1	1	4.667	14	1	9	20	0	0	2	ZACN, EXOC7	10063, 14542	downstream, in gene	ActReg chr17 #7626	0	0	1
7627	17	74,128,058	74,128,531	473	1	4	2.467	11.4	7	4	17	0	0	2	FOXJ1, LOC100507218	9086, -8343	downstream, upstream	ActReg chr17 #7627	0	0	1
7628	17	74,236,819	74,237,440	621	3	10.2	9.8	9.85	20	18	15	1	1	1	RNF157	-739	upstream	ActReg chr17 #7628	1	1	1
7629	17	74,247,931	74,249,557	1,626	2	9.608	14.569	3.431	37	44	7	0	0	0				ActReg chr17 #7629	1	1	0
7630	17	74,270,031	74,270,486	455	1	6.643	4.214	11.571	10	6	17	0	0	2	FAM100B, QRICH2	8972, 33503	downstream, in gene	ActReg chr17 #7630	0	0	1
7631	17	74,276,049	74,276,734	685	1	6.476	4.524	11.809	10	8	15	0	0	2	FAM100B, QRICH2	15105, 27370	downstream, in gene	ActReg chr17 #7631	0	0	1
7632	17	74,379,606	74,380,370	764	1	5.958	8.583	12.5	11	13	18	1	1	2	SPHK1, UBE2O	-702, 69300	upstream, downstream	ActReg chr17 #7632	0	0	1
7633	17	74,382,848	74,383,659	811	1	5.038	4.962	13.615	7	8	20	0	1	2	SPHK1, UBE2O	2563, 66035	in gene, downstream	ActReg chr17 #7633	0	0	1
7634	17	74,468,052	74,468,827	775	1	5.375	4.042	11.875	12	6	17	1	0	2	AANAT, RHBDF2	19006, 29069	downstream, in gene	ActReg chr17 #7634	0	0	1
7635	17	74,494,205	74,494,723	518	1	3.412	6.118	11.177	6	8	15	0	0	1	RHBDF2	5,044	in gene	ActReg chr17 #7635	0	0	1
7636	17	74,553,332	74,554,484	1,152	2	9.889	9.583	6.278	18	17	13	2	4	6	LOC100507230, LOC100507246, SNORD1C, SNORD1B, SNORD1A, ST6GALNAC2	12208, 62, -966, -3282, -3807, 28237	downstream, in gene, upstream, upstream, upstream, downstream	ActReg chr17 #7636	1	1	0
7637	17	74,580,848	74,581,299	451	1	4.417	3.417	12.5	6	5	18	1	1	1	ST6GALNAC2	1,072	in gene	ActReg chr17 #7637	0	0	1
7638	17	74,581,730	74,582,321	591	1	9.889	10.944	3.333	14	16	7	1	1	1	ST6GALNAC2	120	in gene	ActReg chr17 #7638	0	1	0
7639	17	74,721,906	74,722,787	881	1	9.857	13.536	5.821	16	24	10	1	2	4	JMJD6, C17orf95, SFRS2, MIR636	535, -604, 11066, 10284	in gene, upstream, downstream, downstream	ActReg chr17 #7639	0	1	0
7640	17	74,732,849	74,733,649	800	1	12.16	11.52	15.12	16	18	23	1	3	5	JMJD6, C17orf95, SFRS2, MIR636, MFSD11	-10368, 10299, 163, -619, -534	upstream, downstream, in gene, upstream, upstream	ActReg chr17 #7640	0	0	1
7641	17	74,787,409	74,787,953	544	1	5.882	10.941	3.118	10	21	7	0	0	0				ActReg chr17 #7641	0	1	0
7642	17	74,868,377	74,869,216	839	2	11.815	12.148	3.583	20	25	7	0	0	1	MGAT5B	3,998	in gene	ActReg chr17 #7642	1	1	0
7643	17	74,899,044	74,899,609	565	1	2.467	2.412	12.118	5	5	15	0	0	1	MGAT5B	34,528	in gene	ActReg chr17 #7643	0	0	1
7644	17	74,905,828	74,906,729	901	1	9.071	13.25	6.357	22	25	11	0	0	1	MGAT5B	41,480	in gene	ActReg chr17 #7644	0	1	0
7645	17	74,970,534	74,971,238	704	1	3.364	4.955	12	6	9	18	0	0	0				ActReg chr17 #7645	0	0	1
7646	17	75,084,301	75,085,174	873	2	18.296	19.926	8.296	38	43	13	1	2	2	C17orf86, SCARNA16	12, -652	in gene, upstream	ActReg chr17 #7646	1	1	0
7647	17	75,136,193	75,136,849	656	1	9.1	8.85	11.5	12	14	14	1	1	1	SEC14L1	-484	upstream	ActReg chr17 #7647	0	0	1
7648	17	75,242,770	75,243,457	687	2	10.5	10.182	11.954	19	19	17	1	0	0				ActReg chr17 #7648	1	0	1
7649	17	75,250,768	75,251,913	1,145	2	14.083	12.194	4.972	25	24	9	1	0	0				ActReg chr17 #7649	1	1	0
7650	17	75,281,600	75,282,563	963	2	7.968	12.742	7.774	15	24	14	0	0	1	9-Sep	4,589	in gene	ActReg chr17 #7650	0	1	1
7651	17	75,282,662	75,283,713	1,051	1	8.485	10.758	8.061	14	14	12	0	0	1	9-Sep	5,695	in gene	ActReg chr17 #7651	0	1	0
7652	17	75,283,812	75,284,737	925	1	8.793	10.966	6.172	13	18	13	0	0	1	9-Sep	6,782	in gene	ActReg chr17 #7652	0	1	0
7653	17	75,317,699	75,318,163	464	1	9.929	10.214	11.929	16	19	15	0	0	1	9-Sep	40,439	in gene	ActReg chr17 #7653	0	0	1
7654	17	75,318,422	75,320,022	1,600	3	11.08	11.72	6.837	16	20	20	0	0	1	9-Sep	41,730	in gene	ActReg chr17 #7654	1	1	1
7655	17	75,360,293	75,360,533	240	1	4.857	9.714	10.286	7	13	12	0	0	1	9-Sep	82,921	in gene	ActReg chr17 #7655	0	0	1
7656	17	75,361,554	75,362,267	713	1	13.954	11.409	4.773	22	21	10	0	0	1	9-Sep	84,418	in gene	ActReg chr17 #7656	1	0	0
7657	17	75,421,765	75,422,760	995	1	10.645	9.548	8.484	17	14	12	0	0	1	9-Sep	144,770	in gene	ActReg chr17 #7657	1	0	0
7658	17	75,451,210	75,452,722	1,512	1	9.894	12.277	6.915	19	19	11	0	0	2	SEPT9, LOC100507304	174474, 11180	in gene, downstream	ActReg chr17 #7658	0	1	0
7659	17	75,730,205	75,730,869	664	1	5.333	5.095	10.238	8	8	13	0	0	0				ActReg chr17 #7659	0	0	1
7660	17	75,848,836	75,849,837	1,001	1	3.839	6.452	13.065	7	12	19	0	0	0				ActReg chr17 #7660	0	0	1
7661	17	75,883,621	75,884,418	797	1	7.48	11.48	3.96	14	20	8	1	1	1	FLJ45079	-3,850	upstream	ActReg chr17 #7661	0	1	0
7662	17	75,954,321	75,954,853	532	1	8	8.941	11.647	13	16	21	1	0	0				ActReg chr17 #7662	0	0	1
7663	17	76,100,679	76,101,086	407	1	3.917	4.333	11.75	7	7	16	1	0	2	TNRC6C, TMC6	100564, 27606	in gene, downstream	ActReg chr17 #7663	0	0	1
7664	17	76,107,674	76,108,241	567	1	3.889	5.667	11.778	7	9	15	0	0	2	TNRC6C, TMC6	107639, 20531	downstream, downstream	ActReg chr17 #7664	0	0	1
7665	17	76,120,735	76,121,198	463	1	6.867	5.6	12.733	12	8	18	0	1	2	TMC6, TMC8	7522, -5893	in gene, upstream	ActReg chr17 #7665	0	0	1
7666	17	76,123,249	76,123,751	502	1	5.8	6.312	11.375	10	7	14	0	1	2	TMC6, TMC8	4988, -3359	in gene, upstream	ActReg chr17 #7666	0	0	1
7667	17	76,166,688	76,167,027	339	1	5.091	7	10.909	7	10	14	0	1	3	C17orf99, SYNGR2, TK1	24423, 2186, 16428	downstream, in gene, downstream	ActReg chr17 #7667	0	0	1
7668	17	76,182,788	76,183,559	771	1	9.75	18.75	5.818	23	44	11	1	2	2	TK1, AFMID	112, -225	in gene, upstream	ActReg chr17 #7668	0	1	0
7669	17	76,209,930	76,210,961	1,031	3	12.562	15.125	10.25	23	28	20	1	1	3	AFMID, BIRC5, EPR1	27047, 168, 10338	downstream, in gene, in gene	ActReg chr17 #7669	1	1	1
7670	17	76,232,104	76,233,043	939	1	3.071	3.667	12.172	4	11	15	0	0	1	LOC283999	5,182	in gene	ActReg chr17 #7670	0	0	1
7671	17	76,248,771	76,249,325	554	1	5.412	7.941	12.294	9	13	18	0	0	0				ActReg chr17 #7671	0	0	1
7672	17	76,249,914	76,250,925	1,011	2	11.812	11.5	7.5	19	22	18	1	0	0				ActReg chr17 #7672	1	1	0
7673	17	76,259,432	76,259,877	445	1	3.643	5	12.214	7	7	18	0	0	0				ActReg chr17 #7673	0	0	1
7674	17	76,290,318	76,291,282	964	1	7.333	11.767	4.133	10	17	8	0	0	0				ActReg chr17 #7674	0	1	0
7675	17	76,356,618	76,357,255	637	1	8.65	11.75	9.75	12	21	13	1	1	1	SOCS3	-778	upstream	ActReg chr17 #7675	0	1	0
7676	17	76,360,865	76,361,423	558	1	11.823	11.235	8.176	19	19	15	0	1	1	SOCS3	-4,986	upstream	ActReg chr17 #7676	0	1	0
7677	17	76,462,563	76,463,680	1,117	1	5.914	11.514	7.257	13	21	11	0	0	1	DNAH17	110,355	in gene	ActReg chr17 #7677	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7678	17	76,835,988	76,837,669	1,681	2	23.472	25.358	7.34	98	101	15	1	1	1	USP36	141	in gene	ActReg chr17 #7678	1	1	0
7679	17	76,852,039	76,852,567	528	1	2.688	3.867	10.312	4	7	13	1	0	1	TIMP2	69,169	in gene	ActReg chr17 #7679	0	0	1
7680	17	76,879,037	76,880,668	1,631	1	9.451	12.451	7.961	15	17	12	0	0	1	TIMP2	41,620	in gene	ActReg chr17 #7680	0	1	0
7681	17	76,925,870	76,926,223	353	1	2.2	5.818	10.546	3	9	15	0	1	1	TIMP2	-4,574	upstream	ActReg chr17 #7681	0	0	1
7682	17	76,929,207	76,929,954	747	1	8.208	14.042	5.875	12	21	10	0	0	1	TIMP2	-8,108	upstream	ActReg chr17 #7682	0	1	0
7683	17	76,968,656	76,969,436	780	1	6.458	6.833	12.417	10	13	19	0	0	1	LGALS3BP	7,015	in gene	ActReg chr17 #7683	0	0	1
7684	17	76,996,572	76,997,267	695	1	3.364	2.818	11.227	5	5	15	0	0	1	CANT1	8,980	in gene	ActReg chr17 #7684	0	0	1
7685	17	77,019,897	77,020,473	576	1	4.167	3.722	12.722	8	5	22	1	1	2	LOC100507410, C1QTNF1	3517, -66	in gene, upstream	ActReg chr17 #7685	0	0	1
7686	17	77,020,841	77,021,382	541	1	2.353	6.824	12.177	4	10	18	1	2	2	LOC100507410, C1QTNF1	2591, 860	in gene, in gene	ActReg chr17 #7686	0	0	1
7687	17	77,086,988	77,087,367	379	1	3.667	2.583	11.583	5	5	16	0	0	2	ENGASE, hCG_1776007	16158, 391386	downstream, in gene	ActReg chr17 #7687	0	0	1
7688	17	77,092,986	77,093,536	550	1	1.812	1.733	9.944	4	2	13	1	0	2	ENGASE, hCG_1776007	22242, 385302	downstream, in gene	ActReg chr17 #7688	0	0	1
7689	17	77,102,461	77,103,020	559	1	3.056	2.812	10.889	5	4	19	0	0	1	hCG_1776007	375,823	in gene	ActReg chr17 #7689	0	0	1
7690	17	77,106,351	77,106,803	452	1	2.2	3	12.357	3	5	19	0	0	1	hCG_1776007	371,986	in gene	ActReg chr17 #7690	0	0	1
7691	17	77,112,999	77,113,575	576	1	3.278	2.5	13.167	5	4	22	0	0	1	hCG_1776007	365,276	in gene	ActReg chr17 #7691	0	0	1
7692	17	77,140,023	77,140,459	436	1	4.357	3.154	12.214	6	5	18	0	0	1	hCG_1776007	338,322	in gene	ActReg chr17 #7692	0	0	1
7693	17	77,146,956	77,147,320	364	1	3.455	5.636	10.727	6	9	13	0	0	1	hCG_1776007	331,425	in gene	ActReg chr17 #7693	0	0	1
7694	17	77,150,785	77,151,418	633	1	3.895	3.462	11.053	7	6	17	0	0	1	hCG_1776007	327,462	in gene	ActReg chr17 #7694	0	0	1
7695	17	77,152,500	77,153,265	765	1	3.625	2.235	11.5	7	5	17	0	0	1	hCG_1776007	325,681	in gene	ActReg chr17 #7695	0	0	1
7696	17	77,179,724	77,180,163	439	1	3.571	4.286	11.214	6	6	17	1	0	1	hCG_1776007	298,820	in gene	ActReg chr17 #7696	0	0	1
7697	17	77,188,378	77,189,177	799	1	7.48	14.52	7.88	12	26	14	0	0	1	hCG_1776007	289,786	in gene	ActReg chr17 #7697	0	1	0
7698	17	77,290,296	77,291,115	819	2	11.577	16.154	5	25	31	8	0	0	1	hCG_1776007	187,858	in gene	ActReg chr17 #7698	1	1	0
7699	17	77,409,575	77,410,077	502	1	1	5.533	11.333	1	9	18	0	0	1	hCG_1776007	68,737	in gene	ActReg chr17 #7699	0	0	1
7700	17	77,453,539	77,453,933	394	1	5	2.25	11.667	7	4	15	0	0	1	hCG_1776007	24,827	in gene	ActReg chr17 #7700	0	0	1
7701	17	77,689,622	77,690,355	733	1	4.048	3.696	10.478	8	9	14	0	0	0				ActReg chr17 #7701	0	0	1
7702	17	77,704,591	77,705,075	484	1	2.533	4	10.6	4	6	17	0	1	1	ENPP7	-49	upstream	ActReg chr17 #7702	0	0	1
7703	17	77,768,642	77,769,199	557	1	3.706	4.438	11.118	6	10	13	0	2	3	CBX2, CBX8, LOC100507425	16943, 1995, -5477	downstream, in gene, upstream	ActReg chr17 #7703	0	0	1
7704	17	77,774,716	77,775,336	620	1	5.4	9.95	12	9	14	16	1	2	2	CBX8, LOC100507425	-4111, 629	upstream, in gene	ActReg chr17 #7704	0	0	1
7705	17	77,784,724	77,785,722	998	2	7.226	11.774	9.516	11	19	17	1	0	1	LOC100507425	10,826	downstream	ActReg chr17 #7705	0	1	1
7706	17	77,928,245	77,928,769	524	1	2.333	4	11.529	3	7	18	0	0	1	TBC1D16	81,140	in gene	ActReg chr17 #7706	0	0	1
7707	17	77,964,550	77,965,108	558	1	3.882	5.588	11.353	7	9	16	0	0	1	TBC1D16	44,818	in gene	ActReg chr17 #7707	0	0	1
7708	17	78,037,755	78,038,618	863	2	9.704	10.889	6.704	24	19	15	0	0	1	CCDC40	27,751	in gene	ActReg chr17 #7708	1	1	0
7709	17	78,086,897	78,087,241	344	1	3.091	3.4	14.091	6	6	19	0	0	1	GAA	11,714	in gene	ActReg chr17 #7709	0	0	1
7710	17	78,155,005	78,155,551	546	1	4.471	4.824	10.765	7	8	16	1	0	1	CARD14	2,997	in gene	ActReg chr17 #7710	0	0	1
7711	17	78,167,199	78,167,649	450	1	2	3.667	13.2	4	5	24	0	0	1	CARD14	-15,143	in gene	ActReg chr17 #7711	0	0	1
7712	17	78,184,323	78,184,841	518	1	5.625	4.812	12.25	7	7	16	1	0	3	CARD14, SGSH, SLC26A11	32301, 9617, -9618	downstream, in gene, upstream	ActReg chr17 #7712	0	0	1
7713	17	78,193,278	78,194,353	1,075	1	6.441	10.794	2.966	11	22	7	1	2	2	SGSH, SLC26A11	384, -385	in gene, upstream	ActReg chr17 #7713	0	1	0
7714	17	78,235,047	78,235,610	563	1	6.765	9.941	10.118	9	15	13	1	1	2	SLC26A11, RNF213	41128, 661	downstream, in gene	ActReg chr17 #7714	0	1	0
7715	17	78,388,520	78,390,045	1,525	3	10.021	10.957	10.915	19	20	19	1	3	3	LOC100294362, FLJ35220, LOC100507440	-314, 315, -1935	upstream, in gene, upstream	ActReg chr17 #7715	1	1	1
7716	17	78,414,717	78,415,447	730	1	8.217	13	4.091	12	27	7	0	0	1	FLJ35220	26,115	downstream	ActReg chr17 #7716	0	1	0
7717	17	78,418,547	78,418,925	378	1	4.273	3.917	13.083	7	5	21	0	0	1	FLJ35220	29,769	downstream	ActReg chr17 #7717	0	0	1
7718	17	78,418,965	78,419,500	535	1	3.882	3.235	12.882	7	5	17	0	0	1	FLJ35220	30,265	downstream	ActReg chr17 #7718	0	0	1
7719	17	78,428,103	78,429,141	1,038	1	7.844	11.719	8.844	12	18	17	1	0	0				ActReg chr17 #7719	0	1	0
7720	17	78,454,905	78,455,548	643	1	5.25	3.85	11.85	7	7	19	0	1	1	NPTX1	-4,822	upstream	ActReg chr17 #7720	0	0	1
7721	17	78,518,360	78,519,397	1,037	2	10.788	15.121	4.788	25	26	7	1	1	1	RPTOR	253	in gene	ActReg chr17 #7721	1	1	0
7722	17	78,623,053	78,624,123	1,070	1	6.455	10.879	4.406	11	17	8	0	0	1	RPTOR	104,963	in gene	ActReg chr17 #7722	0	1	0
7723	17	78,774,995	78,775,400	405	1	2.154	3.462	12.154	3	5	18	1	0	1	RPTOR	256,572	in gene	ActReg chr17 #7723	0	0	1
7724	17	78,806,670	78,807,427	757	1	6.208	12.75	4.917	10	19	8	0	0	1	RPTOR	288,423	in gene	ActReg chr17 #7724	0	1	0
7725	17	78,847,310	78,847,967	657	1	11.8	15.85	5.6	22	25	10	0	0	1	RPTOR	329,013	in gene	ActReg chr17 #7725	0	1	0
7726	17	78,865,896	78,866,627	731	1	6.87	13.478	5.522	10	20	14	0	0	1	RPTOR	347,636	in gene	ActReg chr17 #7726	0	1	0
7727	17	78,914,266	78,914,811	545	1	4.412	2.471	13.471	8	6	22	0	1	2	RPTOR, LOC100128105	395913, 1295	in gene, in gene	ActReg chr17 #7727	0	0	1
7728	17	78,914,987	78,915,477	490	1	4	3.357	11.6	6	6	19	1	1	2	RPTOR, LOC100128105	396607, 601	in gene, in gene	ActReg chr17 #7728	0	0	1
7729	17	78,937,560	78,938,119	559	1	3.286	4.111	12.167	5	8	21	2	0	1	RPTOR	419,214	in gene	ActReg chr17 #7729	0	0	1
7730	17	78,938,682	78,939,296	614	1	2.5	5.95	10.6	5	7	15	0	0	1	RPTOR	420,364	in gene	ActReg chr17 #7730	0	0	1
7731	17	78,955,882	78,956,788	906	1	4	4.536	12.714	11	8	20	0	0	1	CHMP6	-9,306	upstream	ActReg chr17 #7731	0	0	1
7732	17	78,971,281	78,971,778	497	1	4.938	4.375	11.75	8	6	19	0	1	2	CHMP6, LOC100129503	5888, -6530	in gene, upstream	ActReg chr17 #7732	0	0	1
7733	17	78,973,868	78,974,760	892	1	3.556	4.5	14.214	7	7	23	0	1	2	CHMP6, LOC100129503	8673, -3745	downstream, upstream	ActReg chr17 #7733	0	0	1
7734	17	78,976,763	78,977,117	354	1	3.364	8	10.364	9	11	14	0	1	2	CHMP6, LOC100129503	11299, -1119	downstream, upstream	ActReg chr17 #7734	0	0	1
7735	17	79,012,007	79,012,690	683	1	3.095	3.714	13.809	6	6	18	0	1	2	FLJ90757, BAIAP2	-3829, 3401	upstream, in gene	ActReg chr17 #7735	0	0	1
7736	17	79,022,539	79,023,079	540	1	4.765	4.471	14.294	9	8	21	0	0	1	BAIAP2	13,862	in gene	ActReg chr17 #7736	0	0	1
7737	17	79,041,366	79,041,867	501	1	2.188	4.562	11.625	4	9	19	0	0	1	BAIAP2	32,669	in gene	ActReg chr17 #7737	0	0	1
7738	17	79,069,072	79,069,469	397	1	10.583	10.833	11.667	13	17	15	0	0	1	BAIAP2	60,323	in gene	ActReg chr17 #7738	0	0	1
7739	17	79,071,039	79,071,757	718	1	9.348	6.957	12.478	14	10	20	0	0	1	BAIAP2	62,451	in gene	ActReg chr17 #7739	0	0	1
7740	17	79,092,067	79,092,820	753	1	3.826	4.348	12.652	6	8	18	0	1	5	BAIAP2, AATK, MIR657, MIR3065, MIR338	83496, 47429, 6730, -7234, 7306	downstream, in gene, downstream, upstream, downstream	ActReg chr17 #7740	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7741	17	79,094,376	79,095,122	746	1	3.783	4	13.478	6	7	19	1	1	5	BAIAP2, AATK, MIR657, MIR3065, MIR338	85802, 45123, 4424, -4928, 5000	downstream, in gene, downstream, upstream, downstream	ActReg chr17 #7741	0	0	1
7742	17	79,095,296	79,095,913	617	1	2.75	3.55	13.1	5	7	20	1	1	5	BAIAP2, AATK, MIR657, MIR3065, MIR338	86657, 44268, 3569, -4073, 4145	downstream, in gene, downstream, upstream, downstream	ActReg chr17 #7742	0	0	1
7743	17	79,098,188	79,098,738	550	1	4.235	6	11.353	6	10	18	0	3	6	BAIAP2, AATK, MIR657, MIR3065, MIR338, MIR1250	89516, 41409, 710, -1214, 1286, 8645	downstream, in gene, downstream, upstream, downstream, downstream	ActReg chr17 #7743	0	0	1
7744	17	79,100,129	79,100,793	664	1	3.588	3.5	10.45	6	5	15	0	3	6	BAIAP2, AATK, MIR657, MIR3065, MIR338, MIR1250	91514, 39411, -1288, 784, -712, 6647	downstream, in gene, upstream, downstream, upstream, downstream	ActReg chr17 #7744	0	0	1
7745	17	79,101,975	79,102,545	570	1	4.167	5.722	11.111	6	8	15	0	3	5	AATK, MIR657, MIR3065, MIR338, MIR1250	37612, -3087, 2583, -2511, 4848	in gene, upstream, downstream, upstream, downstream	ActReg chr17 #7745	0	0	1
7746	17	79,117,977	79,118,445	468	1	3.267	2.133	10.067	5	4	17	0	1	2	AATK, LOC100507494	21661, 427	in gene, in gene	ActReg chr17 #7746	0	0	1
7747	17	79,161,224	79,161,819	595	1	4.944	2.529	10.278	8	4	13	0	0	2	LOC388428, AZI1	22214, 35230	downstream, downstream	ActReg chr17 #7747	0	0	1
7748	17	79,163,419	79,163,945	526	1	4.882	5.294	13.177	8	10	23	0	0	2	LOC388428, AZI1	24375, 33069	downstream, in gene	ActReg chr17 #7748	0	0	1
7749	17	79,166,586	79,167,096	510	1	3.5	3.312	10.75	5	5	17	0	0	2	LOC388428, AZI1	27534, 29910	downstream, in gene	ActReg chr17 #7749	0	0	1
7750	17	79,168,712	79,169,552	840	1	3.231	5.269	12.769	7	10	20	0	0	1	AZI1	27,619	in gene	ActReg chr17 #7750	0	0	1
7751	17	79,173,682	79,174,444	762	1	2.056	5.125	11.708	5	6	18	0	0	1	AZI1	22,688	in gene	ActReg chr17 #7751	0	0	1
7752	17	79,206,866	79,207,837	971	1	2.72	4.967	11.5	5	9	16	0	1	2	C17orf56, C17orf89	5540, -5760	in gene, upstream	ActReg chr17 #7752	0	0	1
7753	17	79,219,286	79,219,907	621	1	3.684	4.8	13	7	9	20	0	1	3	C17orf56, C17orf89, SLC38A10	-6705, 6485, 49500	upstream, downstream, in gene	ActReg chr17 #7753	0	0	1
7754	17	79,219,935	79,220,741	806	1	4.96	3.375	12.577	11	7	19	0	1	3	C17orf56, C17orf89, SLC38A10	-7447, 7227, 48758	upstream, downstream, in gene	ActReg chr17 #7754	0	0	1
7755	17	79,234,400	79,234,983	583	1	6	6.111	11.684	11	13	16	0	0	1	SLC38A10	34,405	in gene	ActReg chr17 #7755	0	0	1
7756	17	79,268,363	79,268,845	482	1	8.2	8.2	13.467	15	12	20	1	1	2	SLC38A10, C17orf55	492, 14444	in gene, downstream	ActReg chr17 #7756	0	0	1
7757	17	79,288,754	79,289,295	541	1	5.647	3.412	13.235	10	6	19	0	1	2	C17orf55, TMEM105	-5976, 15450	upstream, in gene	ActReg chr17 #7757	0	0	1
7758	17	79,320,050	79,320,890	840	1	7.269	7.192	13.731	12	14	21	1	0	0				ActReg chr17 #7758	0	0	1
7759	17	79,362,249	79,362,771	522	1	3.231	4.625	13.375	5	6	17	0	2	2	LOC100130370, LOC100507520	-5063, 2177	upstream, in gene	ActReg chr17 #7759	0	0	1
7760	17	79,367,552	79,368,314	762	2	10.417	9.792	3.75	21	20	7	1	2	2	LOC100507520, BAHCC1	-3246, -5607	upstream, upstream	ActReg chr17 #7760	1	1	0
7761	17	79,368,561	79,369,124	563	1	10.778	8.611	2.706	16	9	4	1	2	2	LOC100507520, BAHCC1	-4155, -4698	upstream, upstream	ActReg chr17 #7761	1	0	0
7762	17	79,369,738	79,370,720	982	1	7.968	10.484	5.367	16	16	10	1	2	2	LOC100507520, BAHCC1	-5542, -3311	upstream, upstream	ActReg chr17 #7762	0	1	0
7763	17	79,380,320	79,381,065	745	1	4.417	2.583	11.917	7	4	18	1	0	1	BAHCC1	7,152	in gene	ActReg chr17 #7763	0	0	1
7764	17	79,390,400	79,391,086	686	1	5.182	4.955	13.273	8	9	18	0	0	1	BAHCC1	17,203	in gene	ActReg chr17 #7764	0	0	1
7765	17	79,394,052	79,394,571	519	1	4	5	11.75	7	8	18	0	0	1	BAHCC1	20,771	in gene	ActReg chr17 #7765	0	0	1
7766	17	79,401,200	79,401,581	381	1	3.417	4	11.25	5	7	17	0	0	1	BAHCC1	27,850	in gene	ActReg chr17 #7766	0	0	1
7767	17	79,401,991	79,402,677	686	1	1.952	2.762	12.238	4	4	16	0	0	1	BAHCC1	28,794	in gene	ActReg chr17 #7767	0	0	1
7768	17	79,419,454	79,419,901	447	1	3.357	1.538	12.286	5	2	19	0	1	2	BAHCC1, MIR3186	46137, -1463	in gene, upstream	ActReg chr17 #7768	0	0	1
7769	17	79,425,276	79,426,047	771	1	5	3.792	13.583	8	8	17	1	1	2	BAHCC1, MIR3186	52121, -7447	in gene, upstream	ActReg chr17 #7769	0	0	1
7770	17	79,434,256	79,434,828	572	1	3.722	4.944	12.556	6	6	20	0	0	1	BAHCC1	61,002	downstream	ActReg chr17 #7770	0	0	1
7771	17	79,466,529	79,467,037	508	1	3.4	5	12.333	5	6	17	0	0	2	LOC100507545, ACTG1	12473, 13044	in gene, downstream	ActReg chr17 #7771	0	0	1
7772	17	79,478,832	79,480,005	1,173	2	5.703	12.243	7.906	14	19	17	1	1	2	LOC100507545, ACTG1	25108, 409	in gene, in gene	ActReg chr17 #7772	0	1	1
7773	17	79,480,128	79,481,215	1,087	2	8.353	12.059	8.312	15	17	14	1	1	2	LOC100507545, ACTG1	26361, -844	in gene, upstream	ActReg chr17 #7773	0	1	1
7774	17	79,491,062	79,491,665	603	1	4.526	6.737	10.684	8	11	14	0	1	2	LOC100507545, FSCN2	37053, -4054	in gene, upstream	ActReg chr17 #7774	0	0	1
7775	17	79,492,876	79,493,562	686	1	3.476	4.429	11.667	7	8	15	0	1	2	LOC100507545, FSCN2	38909, -2198	downstream, upstream	ActReg chr17 #7775	0	0	1
7776	17	79,494,890	79,496,589	1,699	1	6.038	6.189	11.962	11	14	19	1	1	2	LOC100507545, FSCN2	41429, 322	downstream, in gene	ActReg chr17 #7776	0	0	1
7777	17	79,501,155	79,502,120	965	1	3.964	3.4	11.5	8	9	17	0	0	3	LOC100507545, FSCN2, C17orf70	47327, 6220, 17792	downstream, in gene, downstream	ActReg chr17 #7777	0	0	1
7778	17	79,505,909	79,506,387	478	1	2.857	2.692	12.067	5	5	17	0	0	2	FSCN2, C17orf70	10731, 13281	downstream, downstream	ActReg chr17 #7778	0	0	1
7779	17	79,507,658	79,508,419	761	1	4.25	3.958	10.958	6	7	17	0	0	2	FSCN2, C17orf70	12621, 11391	downstream, in gene	ActReg chr17 #7779	0	0	1
7780	17	79,514,027	79,514,538	511	1	3.938	9.375	12.062	7	12	19	0	0	3	FSCN2, C17orf70, NPLOC4	18865, 5147, 89856	downstream, in gene, downstream	ActReg chr17 #7780	0	0	1
7781	17	79,604,109	79,604,486	377	1	8	6.833	11.333	13	13	19	0	2	2	NPLOC4, TSPAN10	-159, -5052	upstream, upstream	ActReg chr17 #7781	0	0	1
7782	17	79,612,079	79,612,726	647	1	3.556	4.7	13.9	7	7	20	0	0	3	NPLOC4, TSPAN10, PDE6G	-8264, 3053, 11205	upstream, in gene, downstream	ActReg chr17 #7782	0	0	1
7783	17	79,622,202	79,622,623	421	1	1.923	3.308	14	3	6	21	0	1	3	TSPAN10, PDE6G, C17orf90	13063, 1195, 11206	downstream, in gene, downstream	ActReg chr17 #7783	0	0	1
7784	17	79,622,993	79,623,554	561	1	4.778	3.056	14.111	8	6	19	0	1	3	TSPAN10, PDE6G, C17orf90	13924, 334, 10345	downstream, in gene, downstream	ActReg chr17 #7784	0	0	1
7785	17	79,632,310	79,632,780	470	1	6.733	8.067	11.867	9	13	19	0	2	3	PDE6G, C17orf90, CCDC137	-8938, 1073, -1216	upstream, in gene, upstream	ActReg chr17 #7785	0	0	1
7786	17	79,633,286	79,634,295	1,009	2	7.29	12.839	11.581	15	21	18	1	2	3	PDE6G, C17orf90, CCDC137	-10183, -172, 29	upstream, upstream, in gene	ActReg chr17 #7786	0	1	1
7787	17	79,650,482	79,651,640	1,158	3	10.806	10.333	8.576	20	17	19	1	2	3	CCDC137, ARL16, HGS	17300, -107, 41	downstream, upstream, in gene	ActReg chr17 #7787	1	1	1
7788	17	79,654,050	79,654,561	511	1	3.625	6.625	12.125	7	11	16	0	1	2	ARL16, HGS	-3351, 3285	upstream, in gene	ActReg chr17 #7788	0	0	1
7789	17	79,669,790	79,670,854	1,064	2	12.059	11.147	8.353	21	21	17	1	1	3	HGS, MRPL12, SLC25A10	19302, -85, -9049	downstream, upstream, upstream	ActReg chr17 #7789	1	1	0
7790	17	79,674,940	79,675,512	572	1	4.167	5.625	13.389	7	10	24	0	1	3	HGS, MRPL12, SLC25A10	24206, 4819, -4145	downstream, downstream, upstream	ActReg chr17 #7790	0	0	1
7791	17	79,677,190	79,677,727	537	1	4.688	7.25	12.875	10	12	19	0	1	3	HGS, MRPL12, SLC25A10	26438, 7051, -1913	downstream, downstream, upstream	ActReg chr17 #7791	0	0	1
7792	17	79,683,159	79,683,918	759	1	2.263	3.5	13.417	4	6	20	0	0	2	MRPL12, SLC25A10	13131, 4167	downstream, in gene	ActReg chr17 #7792	0	0	1
7793	17	79,765,815	79,766,203	388	1	5.333	2.5	12	8	4	14	0	0	1	GCGR	3,999	in gene	ActReg chr17 #7793	0	0	1
7794	17	79,770,655	79,771,524	869	1	2.893	3.885	10.857	5	10	15	1	0	2	GCGR, FAM195B	9079, 20078	in gene, downstream	ActReg chr17 #7794	0	0	1
7795	17	79,782,628	79,783,093	465	1	2.857	4	12.714	5	5	16	0	0	3	FAM195B, DYSFIP1, LOC100505927	8307, 10066, -9110	in gene, downstream, upstream	ActReg chr17 #7795	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7796	17	79,790,201	79,790,779	578	1	6.056	8.333	11.111	10	13	14	1	3	3	FAM195B, DYSFIP1, LOC100505927	677, 2436, -1480	in gene, downstream, upstream	ActReg chr17 #7796	0	0	1
7797	17	79,809,209	79,809,623	414	1	3.385	6.615	12.308	5	9	19	0	0	2	LOC100505927, P4HB	17446, 9128	downstream, in gene	ActReg chr17 #7797	0	0	1
7798	17	79,818,575	79,819,404	829	1	8.577	11.385	6.962	13	24	14	1	1	2	P4HB, ARHGDIA	-445, 10293	upstream, downstream	ActReg chr17 #7798	0	1	0
7799	17	79,824,744	79,826,681	1,937	2	8.183	10.517	13.233	18	18	22	1	1	2	P4HB, ARHGDIA	-7168, 3570	upstream, in gene	ActReg chr17 #7799	0	1	1
7800	17	79,829,126	79,830,646	1,520	3	16.319	15.447	7.511	41	40	17	1	1	1	ARHGDIA	-604	upstream	ActReg chr17 #7800	1	1	1
7801	17	79,860,832	79,861,539	707	1	5.522	4.565	12.565	10	7	17	1	1	4	ANAPC11, NPB, PCYT2, SIRT7	11586, 1113, 8155, 14873	downstream, downstream, in gene, downstream	ActReg chr17 #7801	0	0	1
7802	17	79,864,324	79,864,867	543	1	2.176	4.353	11.235	9	8	13	0	0	4	ANAPC11, NPB, PCYT2, SIRT7	14996, 4523, 4745, 11463	downstream, downstream, in gene, downstream	ActReg chr17 #7802	0	0	1
7803	17	79,870,190	79,870,935	745	1	3.652	4.522	12.696	6	9	18	0	1	4	NPB, PCYT2, SIRT7, MAFG	10490, -1222, 5496, 15026	downstream, upstream, in gene, downstream	ActReg chr17 #7803	0	0	1
7804	17	79,878,365	79,878,848	483	1	5.625	3.875	11.75	9	6	19	0	2	4	PCYT2, SIRT7, MAFG, LOC92659	-9266, -2548, 6982, -7099	upstream, upstream, in gene, upstream	ActReg chr17 #7804	0	0	1
7805	17	79,885,472	79,886,022	550	2	10.778	14.778	4.706	21	25	7	1	2	4	SIRT7, MAFG, LOC92659, PYCR1	-9689, -159, 42, 9221	upstream, upstream, in gene, downstream	ActReg chr17 #7805	1	1	0
7806	17	79,886,103	79,886,698	595	1	6.684	10.842	12.474	10	15	16	1	2	3	MAFG, LOC92659, PYCR1	-812, 695, 8568	upstream, in gene, downstream	ActReg chr17 #7806	0	0	1
7807	17	79,892,817	79,893,228	411	1	3.385	4.846	11.846	7	7	18	1	2	4	MAFG, LOC92659, PYCR1, MYADML2	-7434, 7317, 1946, 12087	upstream, downstream, in gene, downstream	ActReg chr17 #7807	0	0	1
7808	17	79,897,767	79,898,233	466	1	3.857	2.071	13.143	7	5	18	0	1	3	LOC92659, PYCR1, MYADML2	12295, -3032, 7109	downstream, upstream, in gene	ActReg chr17 #7808	0	0	1
7809	17	79,914,278	79,915,120	842	1	3.962	6.462	14	7	10	19	1	0	2	MYADML2, NOTUM	-9590, 4358	upstream, in gene	ActReg chr17 #7809	0	0	1
7810	17	79,916,991	79,917,404	413	1	3.615	9.077	11.615	6	14	15	1	1	1	NOTUM	1,860	in gene	ActReg chr17 #7810	0	0	1
7811	17	79,920,414	79,920,880	466	1	4	2.143	12.4	6	4	17	1	1	1	NOTUM	-1,590	upstream	ActReg chr17 #7811	0	0	1
7812	17	79,949,799	79,950,909	1,110	1	2.455	3.412	12.559	4	8	18	0	0	1	ASPSCR1	14,926	in gene	ActReg chr17 #7812	0	0	1
7813	17	79,953,535	79,954,145	610	1	2.684	4.35	12	4	8	16	0	0	1	ASPSCR1	18,414	in gene	ActReg chr17 #7813	0	0	1
7814	17	79,961,245	79,962,072	827	2	11.192	11.923	9.846	18	19	19	1	0	1	ASPSCR1	26,232	in gene	ActReg chr17 #7814	1	1	0
7815	17	79,962,988	79,963,523	535	1	3.882	8.471	11.588	6	11	14	0	0	1	ASPSCR1	27,829	in gene	ActReg chr17 #7815	0	0	1
7816	17	79,965,934	79,966,580	646	1	3.053	4.75	12.35	5	6	21	0	0	2	ASPSCR1, STRA13	30831, 14516	in gene, downstream	ActReg chr17 #7816	0	0	1
7817	17	79,970,258	79,970,794	536	1	3.294	2.071	11.647	5	3	18	0	0	2	ASPSCR1, STRA13	35100, 10247	in gene, downstream	ActReg chr17 #7817	0	0	1
7818	17	79,973,112	79,973,733	621	1	2.95	2.45	11.15	5	4	15	0	0	3	ASPSCR1, STRA13, LRRC45	37996, 7351, -7858	in gene, downstream, upstream	ActReg chr17 #7818	0	0	1
7819	17	79,975,988	79,976,415	427	1	4.769	5.692	13.615	7	9	19	0	1	3	ASPSCR1, STRA13, LRRC45	40775, 4572, -5079	downstream, downstream, upstream	ActReg chr17 #7819	0	0	1
7820	17	79,978,062	79,978,580	518	1	5.438	5.938	11.375	10	10	15	0	2	3	ASPSCR1, STRA13, LRRC45	42895, 2452, -2959	downstream, in gene, upstream	ActReg chr17 #7820	0	0	1
7821	17	79,980,195	79,980,778	583	1	7.889	12.278	11.611	12	19	18	1	2	4	ASPSCR1, STRA13, LRRC45, RAC3	45060, 287, -794, -9046	downstream, in gene, upstream, upstream	ActReg chr17 #7821	0	0	1
7822	17	79,982,653	79,983,325	672	1	3.81	4.238	14.286	7	7	20	0	3	4	ASPSCR1, STRA13, LRRC45, RAC3	47563, -2216, 1709, -6543	downstream, upstream, in gene, upstream	ActReg chr17 #7822	0	0	1
7823	17	79,987,805	79,989,141	1,336	2	9.381	9.881	13.429	22	24	23	1	2	4	STRA13, LRRC45, RAC3, DCXR	-7700, 7193, -1059, 7100	upstream, in gene, upstream, downstream	ActReg chr17 #7823	0	1	1
7824	17	79,991,177	79,991,809	632	1	3.143	4.2	12.55	5	6	22	0	1	3	LRRC45, RAC3, DCXR	10213, 1961, 4080	downstream, in gene, downstream	ActReg chr17 #7824	0	0	1
7825	17	79,994,710	79,995,780	1,070	2	9.529	11.206	7.176	21	16	13	1	1	4	LRRC45, RAC3, DCXR, RFNG	13965, 5713, 328, 14405	downstream, downstream, in gene, downstream	ActReg chr17 #7825	1	1	0
7826	17	80,005,970	80,006,507	537	1	3.176	3.471	11.706	6	6	18	0	1	3	RFNG, GPS1, DUS1L	3412, -3525, 17442	in gene, upstream, downstream	ActReg chr17 #7826	0	0	1
7827	17	80,013,575	80,014,068	493	1	5.643	5.867	12.733	10	10	16	0	1	3	RFNG, GPS1, DUS1L	-4171, 4058, 9859	upstream, in gene, downstream	ActReg chr17 #7827	0	0	1
7828	17	80,014,265	80,015,160	895	1	3.393	6.321	12.429	7	9	18	0	1	3	RFNG, GPS1, DUS1L	-5062, 4949, 8968	upstream, in gene, downstream	ActReg chr17 #7828	0	0	1
7829	17	80,016,170	80,017,073	903	1	4.321	5.5	14.536	7	8	21	0	1	3	RFNG, GPS1, DUS1L	-6971, 6858, 7059	upstream, downstream, in gene	ActReg chr17 #7829	0	0	1
7830	17	80,022,424	80,023,054	630	1	6.4	6.3	10.75	10	9	14	1	1	2	GPS1, DUS1L	12976, 941	downstream, in gene	ActReg chr17 #7830	0	0	1
7831	17	80,037,972	80,038,755	783	1	5.6	7.32	12.56	11	10	23	1	0	1	FASN	17,743	in gene	ActReg chr17 #7831	0	0	1
7832	17	80,045,674	80,046,585	911	1	3.75	7.393	12.786	6	11	20	1	0	1	FASN	9,977	in gene	ActReg chr17 #7832	0	0	1
7833	17	80,051,205	80,051,663	458	1	4.786	6	14.143	6	8	23	0	0	2	FASN, CCDC57	4672, 119255	in gene, downstream	ActReg chr17 #7833	0	0	1
7834	17	80,053,797	80,054,523	726	1	7.636	8.5	13.864	12	12	19	1	1	2	FASN, CCDC57	1946, 116529	in gene, downstream	ActReg chr17 #7834	0	0	1
7835	17	80,054,703	80,055,583	880	2	9.926	8.593	8.115	15	14	17	1	1	2	FASN, CCDC57	963, 115546	in gene, downstream	ActReg chr17 #7835	1	0	1
7836	17	80,062,698	80,063,768	1,070	1	4.875	3.531	12.03	8	8	17	0	1	2	FASN, CCDC57	-7127, 107456	upstream, in gene	ActReg chr17 #7836	0	0	1
7837	17	80,074,129	80,074,538	409	1	3.923	2.231	11.769	7	3	16	0	0	1	CCDC57	96,356	in gene	ActReg chr17 #7837	0	0	1
7838	17	80,170,308	80,171,081	773	1	6.75	12.542	4.353	12	21	9	1	1	1	CCDC57	-5	upstream	ActReg chr17 #7838	0	1	0
7839	17	80,173,651	80,175,544	1,893	2	8.915	10.983	10.051	15	19	17	0	1	1	CCDC57	-3,908	upstream	ActReg chr17 #7839	0	1	1
7840	17	80,182,623	80,182,981	358	1	2.417	4.917	10.083	4	7	16	0	1	1	SLC16A3	-3,491	upstream	ActReg chr17 #7840	0	0	1
7841	17	80,193,398	80,194,086	688	1	4.955	5.727	11.273	8	8	15	0	0	2	SLC16A3, CSNK1D	7449, 37831	in gene, downstream	ActReg chr17 #7841	0	0	1
7842	17	80,254,906	80,256,524	1,618	3	10.667	13.255	8.333	18	25	21	0	0	0				ActReg chr17 #7842	1	1	1
7843	17	80,268,527	80,269,050	523	1	4	5.688	11.875	6	7	15	0	0	2	CD7, SECTM1	6692, 23133	downstream, downstream	ActReg chr17 #7843	0	0	1
7844	17	80,275,161	80,275,869	708	1	4.95	4.818	12	9	9	16	0	1	2	CD7, SECTM1	-35, 16406	upstream, downstream	ActReg chr17 #7844	0	0	1
7845	17	80,342,714	80,343,244	530	1	5.941	6.706	11.765	9	17	18	0	0	2	UTS2R, C17orf101	10778, 33534	downstream, downstream	ActReg chr17 #7845	0	0	1
7846	17	80,344,518	80,345,024	506	1	2	5.625	10.875	5	8	17	0	0	1	C17orf101	31,742	downstream	ActReg chr17 #7846	0	0	1
7847	17	80,345,825	80,346,500	675	1	5.8	8.667	13.667	10	13	24	1	0	1	C17orf101	30,351	downstream	ActReg chr17 #7847	0	0	1
7848	17	80,376,207	80,376,797	590	2	13.833	15.778	4.083	25	31	9	1	3	3	C17orf101, HEXDC, LOC100505970	11, 250, -6872	in gene, in gene, upstream	ActReg chr17 #7848	1	1	0
7849	17	80,396,730	80,397,318	588	1	4.389	4.579	13.105	8	8	21	1	0	2	HEXDC, C17orf62	20772, 11683	in gene, downstream	ActReg chr17 #7849	0	0	1
7850	17	80,403,491	80,403,940	449	1	2.429	3.417	12.357	3	6	18	0	0	2	HEXDC, C17orf62	27463, 4992	downstream, in gene	ActReg chr17 #7850	0	0	1
7851	17	80,415,788	80,416,628	840	2	9.923	11.5	5.458	14	19	10	1	2	2	C17orf62, NARF	-7501, 148	upstream, in gene	ActReg chr17 #7851	1	1	0
7852	17	80,452,289	80,452,998	709	1	10.773	8.409	14.818	16	13	26	0	0	1	NARF	36,583	downstream	ActReg chr17 #7852	0	0	1
7853	17	80,476,779	80,477,637	858	1	5	11.593	1.952	9	16	5	1	1	1	FOXK2	-386	upstream	ActReg chr17 #7853	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7854	17	80,605,807	80,606,535	728	1	7.364	12.739	6.222	15	22	14	1	1	3	WDR45L, LOC100506019, RAB40B	240, 8586, 50427	in gene, downstream, downstream	ActReg chr17 #7854	0	1	0
7855	17	80,620,216	80,620,853	637	1	3.45	3.526	12.45	5	6	17	0	1	2	LOC100506019, RAB40B	-5777, 36064	upstream, in gene	ActReg chr17 #7855	0	0	1
7856	17	80,622,410	80,622,814	404	1	3.5	5.75	11.917	5	7	18	0	0	2	LOC100506019, RAB40B	-7855, 33986	upstream, in gene	ActReg chr17 #7856	0	0	1
7857	17	80,655,480	80,655,908	428	1	3.643	3.571	13.714	10	6	21	1	1	1	RAB40B	904	in gene	ActReg chr17 #7857	0	0	1
7858	17	80,668,119	80,668,764	645	1	5.15	4.7	12.7	7	8	17	0	1	1	FN3KRP	-6,141	upstream	ActReg chr17 #7858	0	0	1
7859	17	80,709,620	80,710,252	632	2	13.05	12.85	5.385	25	25	10	1	1	2	FN3K, TBCD	16484, -4	downstream, upstream	ActReg chr17 #7859	1	1	0
7860	17	80,943,837	80,944,439	602	1	8.5	10	3.474	14	16	5	0	0	1	B3GNTL1	65,548	in gene	ActReg chr17 #7860	0	1	0
7861	17	81,008,457	81,009,108	651	1	5.05	11.05	3.7	8	21	6	1	1	1	B3GNTL1	904	in gene	ActReg chr17 #7861	0	1	0
7862	17	81,044,600	81,045,479	879	1	1.893	3.577	12.214	3	9	19	1	0	1	METRNL	7,472	in gene	ActReg chr17 #7862	0	0	1
7863	17	81,054,264	81,054,815	551	1	2.588	3	12.235	4	4	20	0	0	1	METRNL	16,972	downstream	ActReg chr17 #7863	0	0	1
7864	17	81,056,469	81,057,079	610	1	3.684	2.438	10.737	7	6	15	0	0	1	METRNL	19,207	downstream	ActReg chr17 #7864	0	0	1
7865	17	81,068,310	81,068,794	484	1	2	3.4	13	4	6	19	0	0	0				ActReg chr17 #7865	0	0	1
7866	18	267,774	268,310	536	1	8.471	12.118	9.412	13	19	12	1	1	1	THOC1	17	in gene	ActReg chr18 #7866	0	1	0
7867	18	657,790	658,446	656	2	6.476	11.238	7.333	10	20	13	1	2	3	CLUL1, C18orf56, TYMS	61120, 222, 514	downstream, in gene, in gene	ActReg chr18 #7867	0	1	1
7868	18	903,552	904,295	743	2	18.708	16.667	2.722	39	39	6	0	1	1	ADCYAP1	-1,021	upstream	ActReg chr18 #7868	1	1	0
7869	18	905,101	905,369	268	1	2.875	3.375	9.625	4	5	13	1	1	1	ADCYAP1	291	in gene	ActReg chr18 #7869	0	0	1
7870	18	1,094,383	1,094,909	526	2	8.062	11.062	1	16	16	1	0	0	0				ActReg chr18 #7870	1	1	0
7871	18	2,571,271	2,571,804	533	1	12.062	13.688	5.2	19	22	10	1	2	2	METTL4, NDC80	-48, 27	upstream, in gene	ActReg chr18 #7871	0	1	0
7872	18	2,627,871	2,628,336	465	1	5.867	10.133	1.667	10	15	3	0	0	0				ActReg chr18 #7872	0	1	0
7873	18	2,655,688	2,656,507	819	1	6.458	9.44	5.167	10	16	10	1	2	2	LOC645158, SMCHD1	-2866, 211	upstream, in gene	ActReg chr18 #7873	0	1	0
7874	18	2,905,822	2,906,378	556	1	4.562	8.833	4.5	8	15	7	1	0	1	EMILIN2	59,072	in gene	ActReg chr18 #7874	0	1	0
7875	18	3,247,245	3,247,945	700	2	9.364	12.046	7.409	20	18	12	1	1	2	MYL12A, LOC100505577	67, 14250	in gene, downstream	ActReg chr18 #7875	1	1	0
7876	18	3,261,561	3,262,700	1,139	2	13.472	14.944	4.067	26	32	8	1	2	3	MYL12A, LOC100505577, MYL12B	-14602, -285, 19	downstream, upstream, in gene	ActReg chr18 #7876	1	1	0
7877	18	3,297,097	3,297,848	751	2	21.13	23.174	2.818	50	56	4	0	0	0				ActReg chr18 #7877	1	1	0
7878	18	3,448,028	3,448,630	602	1	10.263	4.737	6.526	18	7	10	1	0	1	TGIF1	36,257	in gene	ActReg chr18 #7878	1	0	0
7879	18	3,451,899	3,452,176	277	1	3.333	6.333	11	6	8	14	1	0	1	TGIF1	39,965	in gene	ActReg chr18 #7879	0	0	1
7880	18	5,237,892	5,238,369	477	1	9.133	6.4	4	14	11	6	1	2	2	C18orf18, LOC339290	-102, 31	upstream, in gene	ActReg chr18 #7880	1	0	0
7881	18	8,608,988	8,609,615	627	2	10.65	7.65	3.25	17	11	5	1	1	1	RAB12	-142	upstream	ActReg chr18 #7881	1	1	0
7882	18	8,685,494	8,686,131	637	1	8.9	12.15	3.15	16	24	4	0	0	0				ActReg chr18 #7882	0	1	0
7883	18	8,705,579	8,705,860	281	1	2.625	10.667	0	4	15	0	1	0	0				ActReg chr18 #7883	0	1	0
7884	18	8,989,908	8,990,181	273	1	2.111	3.111	10	3	4	13	0	0	0				ActReg chr18 #7884	0	0	1
7885	18	9,136,175	9,137,078	903	2	9.214	13.321	3.75	17	24	8	1	1	2	NDUFV2, ANKRD12	33998, -132	downstream, upstream	ActReg chr18 #7885	1	1	0
7886	18	9,913,905	9,914,255	350	1	10.182	9.818	6.364	15	13	9	1	1	1	VAPA	125	in gene	ActReg chr18 #7886	1	0	0
7887	18	10,907,156	10,907,419	263	1	1.125	1.833	8.625	2	2	12	0	0	1	FAM38B	241,474	in gene	ActReg chr18 #7887	0	0	1
7888	18	11,688,963	11,689,378	415	1	7.385	10.692	3.692	10	16	5	1	1	1	GNAL	34	in gene	ActReg chr18 #7888	0	1	0
7889	18	11,851,035	11,851,710	675	1	11.762	8.095	6	17	12	11	1	1	2	GNAL, CHMP1B	162236, -17	in gene, upstream	ActReg chr18 #7889	1	0	0
7890	18	11,908,382	11,908,921	539	1	7.235	9.412	7.062	12	14	13	1	1	1	MPPE1	-10	upstream	ActReg chr18 #7890	0	1	0
7891	18	11,989,679	11,989,965	286	1	2.778	1.556	9.222	4	3	13	0	0	1	IMPA2	8,367	in gene	ActReg chr18 #7891	0	0	1
7892	18	12,307,298	12,307,999	701	1	7.905	12.381	3.333	11	18	7	1	1	1	TUBB6	-609	upstream	ActReg chr18 #7892	0	1	0
7893	18	12,419,941	12,420,351	410	1	6.083	11.667	7.75	10	14	10	1	0	1	SLMO1	12,251	in gene	ActReg chr18 #7893	0	1	0
7894	18	12,702,333	12,703,261	928	2	10.552	15.552	7.103	24	29	11	1	2	2	CEP76, PSMG2	-94, -267	upstream, upstream	ActReg chr18 #7894	1	1	0
7895	18	12,991,209	12,991,719	510	1	8.875	10.125	6.375	13	13	10	1	1	2	SEH1L, CEP192	43481, 103	downstream, in gene	ActReg chr18 #7895	0	1	0
7896	18	13,452,051	13,452,362	311	1	3.7	3.222	10.4	5	4	15	0	0	1	C18orf1	233,420	in gene	ActReg chr18 #7896	0	0	1
7897	18	13,726,186	13,726,991	805	1	8.4	14.84	6.56	15	28	9	1	2	2	C18orf19, RNMT	3, -116	in gene, upstream	ActReg chr18 #7897	0	1	0
7898	18	19,180,193	19,180,944	751	1	8.826	12.435	7.565	13	18	12	1	1	1	ESCO1	125	in gene	ActReg chr18 #7898	0	1	0
7899	18	19,191,806	19,192,703	897	2	24.571	30	4.038	75	75	10	1	1	1	SNRPD1	-6	upstream	ActReg chr18 #7899	1	1	0
7900	18	19,731,998	19,732,389	391	1	2.846	10.615	3.333	6	18	7	0	0	0				ActReg chr18 #7900	0	1	0
7901	18	19,748,955	19,749,250	295	1	5.2	3.9	10.2	8	5	15	1	2	2	LOC100128893, GATA6	-173, -314	upstream, upstream	ActReg chr18 #7901	0	0	1
7902	18	20,065,545	20,066,221	676	2	11.905	8.19	0	23	17	0	0	0	0				ActReg chr18 #7902	1	1	0
7903	18	20,160,029	20,160,659	630	2	14.05	13.25	1.308	34	26	2	0	0	0				ActReg chr18 #7903	1	1	0
7904	18	21,017,658	21,018,124	466	1	4.667	9.733	3.067	8	16	5	1	1	1	C18orf45	34	in gene	ActReg chr18 #7904	0	1	0
7905	18	21,083,099	21,083,751	652	2	13.286	17.286	3.789	27	41	8	1	1	1	C18orf8	-37	upstream	ActReg chr18 #7905	1	1	0
7906	18	21,296,258	21,297,011	753	2	18.739	16.044	0	47	36	0	0	0	1	LAMA3	27,072	in gene	ActReg chr18 #7906	1	1	0
7907	18	21,656,127	21,656,734	607	1	5.947	10.579	1.583	8	20	2	0	0	1	TTC39C	83,693	in gene	ActReg chr18 #7907	0	1	0
7908	18	21,977,549	21,978,020	471	1	8.867	11.6	5.867	12	15	8	1	1	1	OSBPL1A	6	in gene	ActReg chr18 #7908	0	1	0
7909	18	22,006,165	22,006,727	562	1	10.833	7.722	3.611	16	10	6	1	1	1	IMPACT	-163	upstream	ActReg chr18 #7909	1	0	0
7910	18	23,317,492	23,318,122	630	1	5.15	9.7	2.294	9	16	4	0	0	0				ActReg chr18 #7910	0	1	0
7911	18	23,670,182	23,671,418	1,236	2	11.816	15	6.289	30	25	12	1	1	1	SS18	-189	upstream	ActReg chr18 #7911	1	1	0
7912	18	23,806,268	23,807,041	773	1	7.24	9.68	6.842	11	14	14	1	1	1	TAF4B	245	in gene	ActReg chr18 #7912	0	1	0
7913	18	25,199,084	25,199,574	490	1	10.333	4.867	2.133	15	7	3	0	0	0				ActReg chr18 #7913	1	0	0
7914	18	28,591,207	28,591,751	544	1	8.706	5.824	1.857	16	9	2	0	0	1	DSC3	31,302	in gene	ActReg chr18 #7914	1	0	0
7915	18	29,259,209	29,259,730	521	1	7.438	10.25	1.417	9	15	2	0	1	2	B4GALT6, LOC100507120	5217, -5580	in gene, upstream	ActReg chr18 #7915	0	1	0
7916	18	29,522,754	29,523,238	484	1	4.5	10	4.214	6	17	7	1	1	1	KIAA1012	95	in gene	ActReg chr18 #7916	0	1	0
7917	18	29,952,314	29,952,912	598	1	8.895	8.053	1.714	16	13	2	0	0	1	FAM59A	97,834	in gene	ActReg chr18 #7917	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7918	18	32,558,824	32,559,459	635	1	10.5	3.55	2.4	17	8	5	0	1	1	MAPRE2	2,249	in gene	ActReg chr18 #7918	1	0	0
7919	18	32,621,375	32,621,828	453	1	6.133	10	5.867	9	16	8	1	0	1	MAPRE2	64,709	in gene	ActReg chr18 #7919	0	1	0
7920	18	32,869,882	32,870,730	848	2	15.593	14.889	4.846	34	34	9	1	1	1	ZNF397OS	-110	upstream	ActReg chr18 #7920	1	1	0
7921	18	32,923,990	32,924,479	489	1	9.933	4	4.133	14	5	6	1	1	1	ZNF24	192	in gene	ActReg chr18 #7921	1	0	0
7922	18	33,077,354	33,078,143	789	2	10.625	11.458	6.917	15	19	11	1	1	1	INO80C	207	in gene	ActReg chr18 #7922	1	1	0
7923	18	33,355,910	33,356,396	486	1	10.067	7.933	1	15	12	1	0	0	0				ActReg chr18 #7923	1	0	0
7924	18	33,647,009	33,647,599	590	1	11.833	10.333	5.667	17	13	10	1	1	1	RPRD1A	69	in gene	ActReg chr18 #7924	1	0	0
7925	18	33,709,048	33,710,148	1,100	2	10.771	17.286	7.771	20	29	12	1	2	2	SLC39A6, ELP2	-241, -289	upstream, upstream	ActReg chr18 #7925	1	1	0
7926	18	33,756,637	33,757,163	526	1	4.588	8.706	1	7	15	1	0	0	1	ELP2	47,013	downstream	ActReg chr18 #7926	0	1	0
7927	18	34,849,540	34,851,203	1,663	2	14.288	23.827	2.614	52	74	9	0	0	1	BRUNOL4	295,629	in gene	ActReg chr18 #7927	1	1	0
7928	18	35,063,413	35,063,993	580	2	9.611	10	3.944	16	20	6	0	0	1	BRUNOL4	82,297	in gene	ActReg chr18 #7928	1	1	0
7929	18	35,144,722	35,145,246	524	1	8.938	10.625	4.562	15	16	6	1	1	1	BRUNOL4	1,016	in gene	ActReg chr18 #7929	0	1	0
7930	18	36,298,319	36,298,973	654	2	6.85	10.4	11.35	11	16	15	0	0	0				ActReg chr18 #7930	0	1	1
7931	18	38,448,157	38,448,529	372	1	4.167	10.5	0	8	18	0	0	0	0				ActReg chr18 #7931	0	1	0
7932	18	39,754,865	39,755,544	679	2	10.762	13.809	1.75	20	24	3	0	0	0				ActReg chr18 #7932	1	1	0
7933	18	40,125,768	40,126,192	424	1	10.154	5.769	0	17	10	0	0	0	0				ActReg chr18 #7933	1	0	0
7934	18	40,719,527	40,719,882	355	1	3	4.091	10.273	5	5	14	0	0	0				ActReg chr18 #7934	0	0	1
7935	18	42,747,533	42,748,128	595	1	8.421	5.632	1.077	18	8	2	0	0	0				ActReg chr18 #7935	1	0	0
7936	18	42,748,991	42,749,982	991	2	11	9.484	1.45	16	16	2	0	0	0				ActReg chr18 #7936	1	1	0
7937	18	43,062,202	43,062,923	721	1	10.478	6.739	1	14	13	1	0	0	0				ActReg chr18 #7937	1	0	0
7938	18	43,546,936	43,547,480	544	2	13	10.177	8.529	22	16	14	1	1	1	KIAA1632	97	in gene	ActReg chr18 #7938	1	0	1
7939	18	43,684,164	43,684,690	526	1	3.812	11.062	4.733	6	16	8	1	2	2	ATP5A1, HAUS1	-228, 129	upstream, in gene	ActReg chr18 #7939	0	1	0
7940	18	43,753,211	43,754,382	1,171	2	22.568	24.054	6.054	64	63	10	1	1	1	C18orf25	-192	upstream	ActReg chr18 #7940	1	1	0
7941	18	44,076,929	44,077,608	679	2	12.053	10.857	2.737	23	21	4	0	0	1	LOXHD1	159,728	in gene	ActReg chr18 #7941	1	1	0
7942	18	44,082,317	44,082,911	594	1	7.438	9.889	4.333	13	15	7	0	0	1	LOXHD1	154,382	in gene	ActReg chr18 #7942	0	1	0
7943	18	44,116,489	44,116,922	433	1	12.308	10.077	3.385	17	16	6	0	0	1	LOXHD1	120,291	in gene	ActReg chr18 #7943	1	0	0
7944	18	44,212,565	44,213,250	685	2	9.682	7.909	1.9	18	17	3	0	0	1	LOXHD1	24,089	in gene	ActReg chr18 #7944	1	1	0
7945	18	44,337,279	44,337,800	521	1	6	8.824	2.235	11	16	4	2	1	1	ST8SIA5	-500	upstream	ActReg chr18 #7945	0	1	0
7946	18	44,519,423	44,520,042	619	1	6.05	9.8	1.125	12	19	2	0	1	1	KATNAL2	-7,055	upstream	ActReg chr18 #7946	0	1	0
7947	18	45,816,912	45,817,355	443	1	3.571	8.286	4.286	6	15	7	0	0	0				ActReg chr18 #7947	0	1	0
7948	18	46,066,079	46,066,432	353	1	6.75	6.333	10.333	9	7	15	1	1	1	KIAA0427	828	in gene	ActReg chr18 #7948	0	0	1
7949	18	46,067,082	46,067,949	867	1	8	10.704	3.64	13	15	10	1	1	1	KIAA0427	2,088	in gene	ActReg chr18 #7949	0	1	0
7950	18	46,166,224	46,166,512	288	1	2	2.222	10.667	3	3	14	0	0	1	KIAA0427	100,941	in gene	ActReg chr18 #7950	0	0	1
7951	18	46,256,467	46,256,828	361	1	2.5	2.273	13.727	4	5	20	0	0	1	KIAA0427	191,220	in gene	ActReg chr18 #7951	0	0	1
7952	18	47,112,112	47,112,743	631	1	6.25	11.1	2.312	8	23	4	0	0	1	LIPG	24,000	in gene	ActReg chr18 #7952	0	1	0
7953	18	47,339,702	47,340,170	468	1	5.067	6.4	11.467	9	12	18	1	2	3	ACAA2, SCARNA17, MYO5B	315, -457, 381515	in gene, upstream, downstream	ActReg chr18 #7953	0	0	1
7954	18	47,424,660	47,425,393	733	2	10.391	11.636	1.071	20	28	2	0	0	1	MYO5B	296,425	in gene	ActReg chr18 #7954	1	1	0
7955	18	47,794,767	47,795,156	389	1	3.083	1.143	10.667	4	2	15	1	1	2	CCDC11, MSD1	-2096, 13183	upstream, downstream	ActReg chr18 #7955	0	0	1
7956	18	48,494,286	48,494,787	501	1	10.688	8.688	1.308	19	12	2	1	1	1	ELAC1	149	in gene	ActReg chr18 #7956	1	0	0
7957	18	48,724,294	48,724,835	541	1	7.941	9.353	5.529	12	16	9	1	1	1	MEX3C	-513	upstream	ActReg chr18 #7957	0	1	0
7958	18	48,760,355	48,760,856	501	1	3.308	9.2	1.4	5	15	2	0	0	0				ActReg chr18 #7958	0	1	0
7959	18	49,052,281	49,052,798	517	1	5.938	9.812	1.455	9	16	2	0	0	0				ActReg chr18 #7959	0	1	0
7960	18	49,224,724	49,225,018	294	1	1.444	2	11.222	2	2	15	0	0	0				ActReg chr18 #7960	0	0	1
7961	18	49,686,961	49,687,428	467	1	9.667	7.583	1.929	16	13	3	0	0	0				ActReg chr18 #7961	1	0	0
7962	18	49,763,823	49,764,390	567	1	10.278	7.167	2.375	15	11	3	0	0	0				ActReg chr18 #7962	1	0	0
7963	18	51,795,593	51,796,085	492	1	8.133	11.2	5.467	11	14	10	1	1	1	POLI	-10	upstream	ActReg chr18 #7963	0	1	0
7964	18	51,883,990	51,884,467	477	1	6.2	9.333	7.267	10	15	11	1	2	2	STARD6, C18orf54	-3285, -943	upstream, upstream	ActReg chr18 #7964	0	1	0
7965	18	52,942,647	52,943,237	590	1	6.211	8.737	2.471	10	17	4	0	0	1	TCF4	312,918	in gene	ActReg chr18 #7965	0	1	0
7966	18	53,256,998	53,257,432	434	1	8.077	7	11.385	13	11	17	1	1	1	TCF4	-1,355	upstream	ActReg chr18 #7966	0	0	1
7967	18	54,318,259	54,319,006	747	1	10.652	9	6.545	16	17	13	1	2	2	LOC100505499, WDR7	-127, 16	upstream, in gene	ActReg chr18 #7967	1	0	0
7968	18	55,114,138	55,114,836	698	2	11.182	10.773	2.381	21	20	5	0	0	1	ONECUT2	11,570	in gene	ActReg chr18 #7968	1	1	0
7969	18	55,289,011	55,289,645	634	1	8.95	4.85	5.8	18	10	10	1	1	2	NARS, LOC100505549	-151, -8254	upstream, upstream	ActReg chr18 #7969	1	0	0
7970	18	55,470,641	55,471,008	367	1	3.25	2.167	11.083	6	3	14	1	1	1	ATP8B1	-497	upstream	ActReg chr18 #7970	0	0	1
7971	18	55,852,106	55,852,581	475	1	7.571	11.333	3.933	13	18	7	0	0	1	NEDD4L	140,724	in gene	ActReg chr18 #7971	0	1	0
7972	18	56,246,368	56,246,868	500	1	10.125	6.812	2.7	16	10	4	0	0	1	ALPK2	49,571	in gene	ActReg chr18 #7972	1	0	0
7973	18	56,272,693	56,273,248	555	1	4.278	9.5	2.722	7	16	4	0	0	1	ALPK2	23,219	in gene	ActReg chr18 #7973	0	1	0
7974	18	56,435,899	56,436,195	296	1	4.4	4.1	10.7	8	6	14	1	0	0				ActReg chr18 #7974	0	0	1
7975	18	56,806,739	56,807,833	1,094	1	6.265	11.559	5.559	14	18	11	1	1	1	SEC11C	161	in gene	ActReg chr18 #7975	0	1	0
7976	18	58,330,309	58,330,895	586	1	6.5	10.944	2.056	10	16	3	0	0	0				ActReg chr18 #7976	0	1	0
7977	18	60,189,666	60,190,412	746	2	10.826	12.261	5.043	18	24	7	1	1	1	ZCCHC2	-619	upstream	ActReg chr18 #7977	1	1	0
7978	18	60,381,956	60,382,672	716	2	11.636	10.5	1.8	19	21	3	1	1	1	PHLPP1	-358	upstream	ActReg chr18 #7978	1	1	0
7979	18	61,034,366	61,035,300	934	3	13.033	11.967	8.417	30	22	19	1	1	1	KDSR	-327	upstream	ActReg chr18 #7979	1	1	1
7980	18	61,637,187	61,637,694	507	1	10.4	7.067	7.667	15	10	13	1	1	2	HMGD, SERPINB8	20852, 177	downstream, in gene	ActReg chr18 #7980	1	0	0
7981	18	67,711,884	67,712,311	427	1	5.769	11.231	1.923	8	16	4	0	0	1	RTTN	160,865	in gene	ActReg chr18 #7981	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
7982	18	67,872,623	67,873,563	940	2	10.448	15.379	6.259	18	29	11	1	1	1	RTTN	-131	upstream	ActReg chr18 #7982	1	1	0
7983	18	70,497,144	70,497,905	761	2	9.792	11.292	1.692	25	21	2	0	0	1	NETO1	37,286	in gene	ActReg chr18 #7983	1	1	0
7984	18	71,575,441	71,576,014	573	2	10.778	10.889	1.5	24	22	2	0	0	0				ActReg chr18 #7984	1	1	0
7985	18	72,163,468	72,163,907	439	1	11.143	10	6.571	15	15	10	1	1	1	CNDP2	187	in gene	ActReg chr18 #7985	1	0	0
7986	18	72,264,835	72,265,356	521	1	6.875	10.25	5.812	12	15	9	1	1	1	LOC400657	-24	upstream	ActReg chr18 #7986	0	1	0
7987	18	72,919,920	72,920,486	566	1	9.722	8.833	5.167	17	14	7	1	2	2	ZADH2, TSHZ1	1078, -2528	in gene, upstream	ActReg chr18 #7987	1	0	0
7988	18	73,120,759	73,121,371	612	2	11.526	9.737	2.632	21	14	4	0	0	1	C18orf62	18,524	downstream	ActReg chr18 #7988	1	1	0
7989	18	74,420,369	74,420,673	304	1	4.9	3.8	9.1	7	7	11	0	0	0				ActReg chr18 #7989	0	0	1
7990	18	74,533,799	74,534,223	424	1	3.231	10.385	5.1	5	16	7	1	1	1	ZNF236	-2,105	upstream	ActReg chr18 #7990	0	1	0
7991	18	75,680,787	75,681,085	298	1	2.889	7.556	10.222	5	9	14	0	0	0				ActReg chr18 #7991	0	0	1
7992	18	75,883,554	75,883,959	405	1	2.889	1.727	10.167	4	3	16	0	0	0				ActReg chr18 #7992	0	0	1
7993	18	77,280,045	77,280,356	311	1	3.2	1.75	10.4	5	2	15	1	0	1	NFATC1	124,428	in gene	ActReg chr18 #7993	0	0	1
7994	18	77,284,709	77,284,996	287	1	1.444	4.778	10.222	2	7	14	1	0	1	NFATC1	129,080	in gene	ActReg chr18 #7994	0	0	1
7995	18	77,307,361	77,307,913	552	1	2.529	3.5	11.353	4	6	18	1	0	1	LOC100127987	31,727	downstream	ActReg chr18 #7995	0	0	1
7996	18	77,438,925	77,439,997	1,072	2	13.879	13.212	5.633	25	25	9	1	1	1	CTDP1	-540	upstream	ActReg chr18 #7996	1	1	0
7997	18	77,558,564	77,558,885	321	1	1.571	1.2	10.2	3	2	14	1	0	0				ActReg chr18 #7997	0	0	1
7998	18	77,721,414	77,721,765	351	1	2.182	2.091	10.454	4	4	16	0	1	2	PQLC1, HSBP1L1	-9936, -2993	upstream, upstream	ActReg chr18 #7998	0	0	1
7999	18	77,831,574	77,832,053	479	1	1	1.733	8.6	1	3	16	0	0	1	LOC100506070	4,557	in gene	ActReg chr18 #7999	0	0	1
8000	19	266,931	267,734	803	2	12.4	14.52	6.955	22	30	13	1	0	0				ActReg chr19 #8000	1	1	0
8001	19	306,552	307,147	595	1	2.158	4.059	11.053	3	7	15	1	0	1	MIER2	37,942	in gene	ActReg chr19 #8001	0	0	1
8002	19	308,708	309,021	313	1	2.333	5.444	9.556	3	7	12	1	0	1	MIER2	35,927	in gene	ActReg chr19 #8002	0	0	1
8003	19	342,545	343,906	1,361	2	9.256	10.721	3.075	15	17	7	0	1	1	MIER2	1,566	in gene	ActReg chr19 #8003	1	1	0
8004	19	344,914	345,424	510	1	8.812	5.25	11.688	12	7	16	1	1	1	MIER2	-378	upstream	ActReg chr19 #8004	0	0	1
8005	19	377,924	378,520	596	1	1.667	3	12.278	4	6	20	0	1	1	THEG	-2,213	upstream	ActReg chr19 #8005	0	0	1
8006	19	430,800	431,093	293	1	5	3.333	10	7	5	13	0	0	1	SHC2	30,050	in gene	ActReg chr19 #8006	0	0	1
8007	19	459,566	460,326	760	1	6.667	12.042	5	12	18	7	1	1	2	SHC2, ODF3L2	1050, 15037	in gene, downstream	ActReg chr19 #8007	0	1	0
8008	19	463,295	463,984	689	1	4.909	3.684	10.5	8	7	17	1	1	2	SHC2, ODF3L2	-2643, 11344	upstream, in gene	ActReg chr19 #8008	0	0	1
8009	19	488,461	489,524	1,063	2	12.727	12.333	6	26	24	12	1	1	1	MADCAM1	-7,498	upstream	ActReg chr19 #8009	1	1	0
8010	19	498,528	498,905	377	1	2.5	2	9.833	4	3	14	0	1	2	MADCAM1, C19orf20	2226, -8781	in gene, upstream	ActReg chr19 #8010	0	0	1
8011	19	506,524	507,135	611	1	9.421	14.895	5.895	15	25	9	1	1	2	MADCAM1, C19orf20	10339, -668	downstream, upstream	ActReg chr19 #8011	0	1	0
8012	19	507,147	508,137	990	3	11.226	14.903	9.452	19	23	15	2	1	2	MADCAM1, C19orf20	11152, 145	downstream, in gene	ActReg chr19 #8012	1	1	1
8013	19	523,500	523,735	235	1	1.286	1.833	11.286	2	3	13	1	0	2	C19orf20, CDC34	16120, -8116	downstream, upstream	ActReg chr19 #8013	0	0	1
8014	19	531,890	532,483	593	1	6.211	6.842	11.158	10	13	16	1	1	1	CDC34	453	in gene	ActReg chr19 #8014	0	0	1
8015	19	547,234	547,816	582	1	2.611	3.556	12.444	4	6	19	0	0	2	CDC34, QZMM	15792, 3498	downstream, in gene	ActReg chr19 #8015	0	0	1
8016	19	573,066	573,529	463	1	9.643	10.5	11.143	15	16	16	1	1	1	BSG	1,972	in gene	ActReg chr19 #8016	0	0	1
8017	19	581,970	582,423	453	1	2.273	2.214	12.071	4	4	19	0	1	2	BSG, HCN2	10871, -7697	in gene, upstream	ActReg chr19 #8017	0	0	1
8018	19	584,697	585,134	437	1	2.786	5.357	11.143	6	12	19	1	1	2	BSG, HCN2	13590, -4978	downstream, upstream	ActReg chr19 #8018	0	0	1
8019	19	588,435	589,256	821	1	7.346	5.962	14.385	13	11	19	1	1	2	BSG, HCN2	17520, -1048	downstream, upstream	ActReg chr19 #8019	0	0	1
8020	19	591,055	591,673	618	1	7.368	8.579	10.79	14	12	14	1	1	2	BSG, HCN2	20039, 1471	downstream, in gene	ActReg chr19 #8020	0	0	1
8021	19	608,421	608,919	498	1	1.933	6.067	13.533	5	8	16	0	0	2	HCN2, POLRMT	18777, 24898	in gene, downstream	ActReg chr19 #8021	0	0	1
8022	19	619,713	620,407	694	1	2.6	6.524	12.667	5	12	17	1	0	2	HCN2, POLRMT	30167, 13508	downstream, in gene	ActReg chr19 #8022	0	0	1
8023	19	639,162	639,623	461	1	7.467	6.867	11.667	11	10	18	2	2	3	POLRMT, FGF22, RNF126	-5824, -534, 23841	upstream, upstream, downstream	ActReg chr19 #8023	0	0	1
8024	19	640,192	641,098	906	1	5.586	5.103	11.414	9	10	17	2	2	3	POLRMT, FGF22, RNF126	-7077, 719, 22588	upstream, in gene, downstream	ActReg chr19 #8024	0	0	1
8025	19	652,568	653,572	1,004	1	2.935	4.3	11.75	5	8	17	1	0	2	FGF22, RNF126	13144, 10163	downstream, in gene	ActReg chr19 #8025	0	0	1
8026	19	658,556	659,459	903	1	4.621	6.379	11.31	8	8	17	0	0	1	RNF126	4,226	in gene	ActReg chr19 #8026	0	0	1
8027	19	679,273	679,996	723	1	5.409	5.5	15.182	8	12	22	1	0	2	FSTL3, PRSSL1	3245, 15827	in gene, downstream	ActReg chr19 #8027	0	0	1
8028	19	698,897	699,781	884	1	1.773	3.72	10.214	3	8	14	0	1	2	PRSSL1, PALM	-3878, -9614	upstream, upstream	ActReg chr19 #8028	0	0	1
8029	19	719,525	719,908	383	1	3.833	2.583	12.417	6	3	21	1	0	1	PALM	10,763	in gene	ActReg chr19 #8029	0	0	1
8030	19	727,411	728,512	1,101	1	3.171	5.457	12.314	7	9	19	1	0	1	PALM	19,008	in gene	ActReg chr19 #8030	0	0	1
8031	19	735,919	736,473	554	1	3.588	2.588	11.412	6	4	18	1	0	1	PALM	27,243	in gene	ActReg chr19 #8031	0	0	1
8032	19	739,853	740,425	572	1	4.167	6	11.778	6	8	18	1	0	1	PALM	31,186	in gene	ActReg chr19 #8032	0	0	1
8033	19	747,460	748,202	742	1	3.773	3.478	12.522	6	6	20	0	1	2	PALM, C19orf21	38878, -3315	in gene, upstream	ActReg chr19 #8033	0	0	1
8034	19	796,626	797,441	815	2	10.731	9.654	7.346	20	19	13	1	1	1	PTBP1	-559	upstream	ActReg chr19 #8034	1	1	0
8035	19	798,505	799,116	611	1	4.684	5.056	11.895	7	12	17	1	1	1	PTBP1	1,418	in gene	ActReg chr19 #8035	0	0	1
8036	19	801,111	801,842	731	1	6.696	5.478	15.304	12	8	24	0	0	1	PTBP1	4,084	in gene	ActReg chr19 #8036	0	0	1
8037	19	831,599	832,099	500	1	4.875	5.5	13.125	8	9	19	0	0	3	LPPR3, AZU1, PRTN3	-9897, 4018, -9136	upstream, in gene, upstream	ActReg chr19 #8037	0	0	1
8038	19	846,169	846,689	520	1	6.235	4.235	12.294	9	8	18	1	1	2	PRTN3, ELANE	5444, -5862	in gene, upstream	ActReg chr19 #8038	0	0	1
8039	19	873,589	874,079	490	1	4.733	5.733	11.533	7	8	19	0	0	2	CFD, MED16	14169, 19384	downstream, in gene	ActReg chr19 #8039	0	0	1
8040	19	876,909	877,326	417	1	3.923	4.077	13.538	5	5	20	0	0	1	MED16	16,101	in gene	ActReg chr19 #8040	0	0	1
8041	19	879,874	880,383	509	1	4.333	2.267	12.2	6	5	19	0	0	1	MED16	13,090	in gene	ActReg chr19 #8041	0	0	1
8042	19	881,850	882,243	393	1	2.769	3.154	11.462	4	4	15	0	0	1	MED16	11,172	in gene	ActReg chr19 #8042	0	0	1
8043	19	892,926	893,895	969	3	10.903	11.548	10	24	18	17	1	1	2	MED16, C19orf22	-192, 19815	upstream, downstream	ActReg chr19 #8043	1	1	1
8044	19	925,046	926,033	987	2	11	17.355	6.5	20	40	13	2	1	2	KISS1R, ARID3A	8197, -498	downstream, upstream	ActReg chr19 #8044	1	1	0
8045	19	954,937	955,268	331	1	1.182	2.8	10	2	5	13	0	0	1	ARID3A	29,065	in gene	ActReg chr19 #8045	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8046	19	955,390	955,699	309	1	2.4	2.111	9	4	3	11	0	0	1	ARID3A	29,507	in gene	ActReg chr19 #8046	0	0	1
8047	19	993,983	994,391	408	1	2.923	3.231	10.615	4	6	14	1	1	2	WDR18, GRIN3B	9859, -6250	in gene, upstream	ActReg chr19 #8047	0	0	1
8048	19	996,504	996,840	336	1	4.091	6.727	11	7	10	16	1	1	2	WDR18, GRIN3B	12344, -3765	downstream, upstream	ActReg chr19 #8048	0	0	1
8049	19	1,020,934	1,022,057	1,123	2	12.857	14.257	5.5	21	27	11	1	2	2	C19orf6, CNN2	-554, -4803	upstream, upstream	ActReg chr19 #8049	1	1	0
8050	19	1,039,632	1,040,376	744	2	10.522	13.304	5.652	21	27	10	1	1	2	CNN2, ABCA7	13706, -98	downstream, upstream	ActReg chr19 #8050	1	1	0
8051	19	1,095,139	1,095,622	483	1	6.8	10.2	8.533	9	16	13	1	1	3	HMHA1, POLR2E, GPX4	28206, 11, -8556	downstream, in gene, upstream	ActReg chr19 #8051	0	1	0
8052	19	1,109,782	1,110,064	282	1	2.778	1.444	10.778	4	2	14	1	0	2	GPX4, SBNO2	5987, 64359	downstream, in gene	ActReg chr19 #8052	0	0	1
8053	19	1,113,264	1,113,657	393	1	3	6.727	10.091	4	9	14	0	0	2	GPX4, SBNO2	9539, 60807	downstream, in gene	ActReg chr19 #8053	0	0	1
8054	19	1,131,202	1,131,815	613	1	2.353	6.526	11.21	4	9	16	0	0	1	SBNO2	42,774	in gene	ActReg chr19 #8054	0	0	1
8055	19	1,160,046	1,160,641	595	1	2.316	2.737	10.21	4	4	13	0	0	1	SBNO2	13,939	in gene	ActReg chr19 #8055	0	0	1
8056	19	1,170,419	1,170,925	506	1	10.938	7.25	3.812	17	9	6	0	0	1	SBNO2	3,610	in gene	ActReg chr19 #8056	1	0	0
8057	19	1,238,777	1,239,238	461	1	2.636	5	11.533	4	8	15	0	2	3	C19orf26, ATP5D, MIDN	-1017, -2742, -9545	upstream, upstream, upstream	ActReg chr19 #8057	0	0	1
8058	19	1,255,606	1,255,917	311	1	3.2	3.3	9.5	5	7	13	1	0	1	MIDN	7,209	in gene	ActReg chr19 #8058	0	0	1
8059	19	1,265,841	1,266,512	671	1	9.381	11.048	7.095	12	20	13	1	1	4	MIDN, C19orf23, CIRBP, C19orf24	17624, 4083, -3091, -9344	downstream, downstream, upstream, upstream	ActReg chr19 #8059	0	1	0
8060	19	1,266,840	1,267,326	486	1	11.6	10.933	6.636	19	14	11	1	1	4	MIDN, C19orf23, CIRBP, C19orf24	18531, 3176, -2184, -8437	downstream, downstream, upstream, upstream	ActReg chr19 #8060	1	0	0
8061	19	1,272,011	1,272,353	342	1	3.091	3.909	9.818	4	5	14	0	2	3	C19orf23, CIRBP, C19orf24	-1923, 2915, -3338	upstream, in gene, upstream	ActReg chr19 #8061	0	0	1
8062	19	1,293,045	1,293,460	415	1	2.385	3.75	9.462	4	6	13	0	1	2	EFNA2, LOC100506781	7084, -7016	in gene, upstream	ActReg chr19 #8062	0	0	1
8063	19	1,383,113	1,384,190	1,077	3	10.546	11.454	13.727	16	22	30	1	1	2	MUM1, NDUFS7	28675, -232	downstream, upstream	ActReg chr19 #8063	1	1	1
8064	19	1,388,495	1,388,983	488	1	3.067	2.615	10.8	5	4	18	0	0	2	NDUFS7, GAMT	4856, 12813	in gene, downstream	ActReg chr19 #8064	0	0	1
8065	19	1,409,073	1,409,545	472	1	3.133	6.267	11.933	6	10	15	0	1	2	GAMT, DAZAP1	-7757, 1725	upstream, in gene	ActReg chr19 #8065	0	0	1
8066	19	1,437,919	1,438,764	845	2	22.444	25.37	6.667	63	75	11	1	2	3	DAZAP1, RPS15, LOC100506822	30757, -22, -2503	downstream, upstream, upstream	ActReg chr19 #8066	1	1	0
8067	19	1,452,169	1,452,727	558	1	4.824	3.471	12.118	8	5	15	0	1	2	APC2, LOC100506848	2300, 10316	in gene, downstream	ActReg chr19 #8067	0	0	1
8068	19	1,472,266	1,472,709	443	1	2.786	2.857	12.286	4	5	19	0	0	4	APC2, LOC100506848, C19orf25, PCSK4	22339, -9723, 6741, 17920	in gene, upstream, downstream, downstream	ActReg chr19 #8068	0	0	1
8069	19	1,507,500	1,508,295	795	2	13.64	19.125	5.24	30	44	9	1	0	2	REEP6, ADAMTSL5	16732, 5291	downstream, in gene	ActReg chr19 #8069	1	1	0
8070	19	1,513,778	1,514,140	362	1	3.182	4.727	11.636	7	7	14	1	1	1	ADAMTSL5	-771	upstream	ActReg chr19 #8070	0	0	1
8071	19	1,652,640	1,653,339	699	1	7.524	12.546	5.5	13	24	8	0	1	1	TCF3	-663	upstream	ActReg chr19 #8071	0	1	0
8072	19	1,676,650	1,677,032	382	1	2.545	2.4	10.833	4	3	16	0	0	0				ActReg chr19 #8072	0	0	1
8073	19	1,843,685	1,844,176	491	1	2.538	3.133	12.267	4	5	18	0	0	2	REXO1, KLF16	4522, 19634	in gene, downstream	ActReg chr19 #8073	0	0	1
8074	19	1,848,406	1,848,838	432	1	11.286	10.786	4.857	20	17	7	1	1	2	REXO1, KLF16	-170, 14942	upstream, downstream	ActReg chr19 #8074	1	0	0
8075	19	1,875,748	1,876,673	925	2	12.586	12.207	9.138	27	24	14	1	0	1	FAM108A1	9,308	downstream	ActReg chr19 #8075	1	1	0
8076	19	1,909,739	1,909,967	228	1	2.429	5.429	11	3	7	13	0	0	2	SCAMP4, ADAT3	4480, 4436	in gene, in gene	ActReg chr19 #8076	0	0	1
8077	19	1,962,646	1,963,049	403	1	3.625	4.667	10.692	5	9	15	0	0	2	CSNK1G2, C19orf34	21686, -8299	in gene, upstream	ActReg chr19 #8077	0	0	1
8078	19	1,971,259	1,971,638	379	1	2.556	1	10	3	1	15	0	0	1	CSNK1G2	30,287	in gene	ActReg chr19 #8078	0	0	1
8079	19	2,055,892	2,056,202	310	1	3	4.2	9.1	4	6	12	0	1	1	MKNK2	-4,804	upstream	ActReg chr19 #8079	0	0	1
8080	19	2,059,424	2,060,224	800	2	11.462	7.846	6.885	18	19	14	0	0	1	MKNK2	-8,581	upstream	ActReg chr19 #8080	1	1	0
8081	19	2,061,374	2,062,041	667	2	9.476	11.857	5.667	16	21	10	1	0	1	MOBKL2A	34,562	downstream	ActReg chr19 #8081	1	1	0
8082	19	2,095,930	2,096,673	743	1	8.375	12.25	4.438	14	25	13	1	2	3	MOBKL2A, C19orf36, AP3D1	-32, -567, 55255	upstream, upstream, downstream	ActReg chr19 #8082	0	1	0
8083	19	2,120,467	2,120,754	287	1	2.167	2.333	11.667	4	3	14	1	0	1	AP3D1	30,946	in gene	ActReg chr19 #8083	0	0	1
8084	19	2,249,422	2,249,729	307	1	1.8	2.6	11.5	3	4	14	0	2	4	SF3A2, AMH, MIR4321, JSRP1	12759, 462, -1063, 6847	downstream, in gene, upstream, downstream	ActReg chr19 #8084	0	0	1
8085	19	2,269,401	2,269,803	402	1	8.615	10	3.923	12	13	5	1	1	2	OAZ1, C19orf55	82, 12579	in gene, downstream	ActReg chr19 #8085	0	1	0
8086	19	2,337,961	2,338,379	418	1	2	2.538	11.923	4	4	18	0	0	2	LSM7, SPPL2B	-9556, 9541	upstream, in gene	ActReg chr19 #8086	0	0	1
8087	19	2,427,276	2,427,911	635	1	10.25	9.45	8.8	19	12	14	1	1	3	TMPRSS9, TIMM13, LMNB2	37809, 282, 29365	downstream, in gene, downstream	ActReg chr19 #8087	1	0	0
8088	19	2,431,529	2,431,808	279	1	1.556	2.667	9.333	2	4	13	0	1	3	TMPRSS9, TIMM13, LMNB2	41884, -3793, 25290	downstream, upstream, in gene	ActReg chr19 #8088	0	0	1
8089	19	2,475,923	2,476,805	882	1	5.464	9.857	5.481	8	15	11	1	1	1	GADD45B	241	in gene	ActReg chr19 #8089	0	1	0
8090	19	2,494,049	2,495,185	1,136	2	8.8	15.143	6.829	15	30	15	1	0	0				ActReg chr19 #8090	1	1	0
8091	19	2,722,973	2,723,396	423	1	10.214	5	5.071	18	8	7	1	1	2	DIRAS1, SLC39A3	-1794, 16890	upstream, downstream	ActReg chr19 #8091	1	0	0
8092	19	2,739,951	2,740,614	663	2	11.286	11.667	2.833	19	20	6	1	1	1	SLC39A3	-208	upstream	ActReg chr19 #8092	1	1	0
8093	19	2,752,968	2,753,273	305	1	3.556	3	11.333	5	4	14	0	0	1	SGTA	30,294	downstream	ActReg chr19 #8093	0	0	1
8094	19	2,807,472	2,807,831	359	1	2.545	1.667	10.909	4	2	14	1	0	1	THOP1	22,145	in gene	ActReg chr19 #8094	0	0	1
8095	19	2,810,038	2,810,479	441	1	1.071	2.714	10.429	2	4	18	1	0	2	THOP1, ZNF554	24752, -9614	in gene, upstream	ActReg chr19 #8095	0	0	1
8096	19	2,812,774	2,813,473	699	1	2.5	2.714	11.5	4	5	17	0	1	2	THOP1, ZNF554	27617, -6749	in gene, upstream	ActReg chr19 #8096	0	0	1
8097	19	2,819,421	2,820,235	814	2	29.231	28.885	5.263	91	86	9	1	1	2	THOP1, ZNF554	34322, -44	downstream, upstream	ActReg chr19 #8097	1	1	0
8098	19	2,840,899	2,841,466	567	2	10.294	11.765	5.176	17	16	12	1	1	2	ZNF554, ZNF555	21310, -251	downstream, upstream	ActReg chr19 #8098	1	1	0
8099	19	2,944,966	2,945,702	736	2	8.957	10.261	5.571	23	19	12	1	1	1	ZNF77	-365	upstream	ActReg chr19 #8099	1	1	0
8100	19	3,005,369	3,005,936	567	1	3.667	3.556	11.722	6	7	15	0	0	1	TLE2	41,981	in gene	ActReg chr19 #8100	0	0	1
8101	19	3,027,999	3,028,485	486	1	2.462	5.125	12.438	4	6	21	1	0	1	TLE2	19,391	in gene	ActReg chr19 #8101	0	0	1
8102	19	3,035,226	3,036,766	1,540	2	7.958	10.979	6.065	15	18	11	2	0	1	TLE2	11,637	in gene	ActReg chr19 #8102	1	1	0
8103	19	3,053,309	3,053,741	432	1	5.143	4.286	11.429	6	6	18	0	1	2	TLE2, AES	-5892, 9439	upstream, in gene	ActReg chr19 #8103	0	0	1
8104	19	3,116,244	3,116,977	733	1	2.348	3.826	12.348	5	7	21	0	0	1	GNA11	22,202	in gene	ActReg chr19 #8104	0	0	1
8105	19	3,171,884	3,172,718	834	1	9.462	12.154	8.769	16	20	17	0	1	2	GNA15, S1PR4	36110, -6435	downstream, upstream	ActReg chr19 #8105	0	1	0
8106	19	3,177,252	3,177,696	444	1	7.5	9.571	11.071	12	13	16	0	1	2	S1PR4, NCLN	-1262, -8401	upstream, upstream	ActReg chr19 #8106	0	0	1
8107	19	3,178,404	3,178,828	424	1	2.25	3	11.385	4	5	18	1	2	2	S1PR4, NCLN	-120, -7259	upstream, upstream	ActReg chr19 #8107	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8108	19	3,179,050	3,179,766	716	1	3.636	6.15	13.091	7	13	19	1	2	2	S1PR4, NCLN	672, -6467	in gene, upstream	ActReg chr19 #8108	0	0	1
8109	19	3,189,563	3,190,195	632	1	6.75	3.895	13.85	9	6	25	1	0	2	S1PR4, NCLN	11143, 4004	downstream, in gene	ActReg chr19 #8109	0	0	1
8110	19	3,210,307	3,211,029	722	1	5.136	7.545	13.546	9	13	18	0	0	1	NCLN	24,793	downstream	ActReg chr19 #8110	0	0	1
8111	19	3,243,673	3,244,851	1,178	2	14.703	22.216	3.027	32	53	6	0	0	1	BRUNOL5	19,561	in gene	ActReg chr19 #8111	1	1	0
8112	19	3,275,277	3,276,001	724	1	5.565	7.957	11.435	11	14	19	1	0	1	BRUNOL5	50,938	in gene	ActReg chr19 #8112	0	0	1
8113	19	3,360,441	3,361,240	799	1	11.68	10.44	9.8	17	17	13	1	1	1	NFIC	1,224	in gene	ActReg chr19 #8113	1	0	0
8114	19	3,396,972	3,398,131	1,159	1	11.917	7.861	5.528	16	13	12	0	0	1	NFIC	37,935	in gene	ActReg chr19 #8114	1	0	0
8115	19	3,434,465	3,435,602	1,137	3	11.743	11.6	12.457	17	25	28	1	0	1	NFIC	75,417	in gene	ActReg chr19 #8115	1	1	1
8116	19	3,450,737	3,451,527	790	1	10.68	8.16	5.261	16	13	8	0	0	1	NFIC	91,516	in gene	ActReg chr19 #8116	1	0	0
8117	19	3,453,666	3,454,095	429	1	4.308	3.846	11.769	5	6	14	1	0	1	NFIC	94,264	in gene	ActReg chr19 #8117	0	0	1
8118	19	3,500,188	3,501,325	1,137	2	11.194	17.083	9.412	27	36	18	1	2	2	DOHH, FZR1	182, -5539	in gene, upstream	ActReg chr19 #8118	1	1	0
8119	19	3,505,572	3,506,233	661	1	13.05	9.45	8	24	15	17	1	2	2	DOHH, FZR1	-4964, -393	upstream, upstream	ActReg chr19 #8119	1	0	0
8120	19	3,536,478	3,537,324	846	1	6.519	8	11.111	10	17	15	0	1	3	FZR1, C19orf28, C19orf71	30606, 20670, -2254	downstream, downstream, upstream	ActReg chr19 #8120	0	0	1
8121	19	3,537,868	3,538,282	414	1	6.846	7	13.923	10	13	21	0	1	3	FZR1, C19orf28, C19orf71	31780, 19496, -1080	downstream, downstream, upstream	ActReg chr19 #8121	0	0	1
8122	19	3,544,921	3,545,419	498	1	3.5	5.938	10.938	5	10	20	0	0	3	FZR1, C19orf28, C19orf71	38875, 12401, 6015	downstream, in gene, downstream	ActReg chr19 #8122	0	0	1
8123	19	3,557,388	3,558,223	835	2	13.423	14.692	3.955	27	27	6	1	1	1	C19orf28	-234	upstream	ActReg chr19 #8123	1	1	0
8124	19	3,572,335	3,572,975	640	2	9.45	11	6	16	24	10	1	1	1	HMG20B	-288	upstream	ActReg chr19 #8124	1	1	0
8125	19	3,607,215	3,608,055	840	1	6.269	6.731	12.385	10	13	21	1	1	2	TBXA2R, C19orf29	-804, 19178	upstream, downstream	ActReg chr19 #8125	0	0	1
8126	19	3,614,869	3,615,487	618	1	3.211	3.263	14.684	6	7	22	0	0	2	TBXA2R, C19orf29	-8347, 11635	upstream, in gene	ActReg chr19 #8126	0	0	1
8127	19	3,618,445	3,619,055	610	1	3.333	4.105	12.105	9	8	19	0	0	1	C19orf29	8,063	in gene	ActReg chr19 #8127	0	0	1
8128	19	3,626,307	3,627,308	1,001	3	16.613	19.742	12.516	44	42	23	1	1	2	C19orf29, PIP5K1C	6, 73638	in gene, downstream	ActReg chr19 #8128	1	1	1
8129	19	3,638,226	3,638,597	371	1	4.727	4.25	10.75	6	6	15	0	0	1	PIP5K1C	62,034	in gene	ActReg chr19 #8129	0	0	1
8130	19	3,638,857	3,639,398	541	1	4	4.471	9.765	6	8	15	0	0	1	PIP5K1C	61,318	in gene	ActReg chr19 #8130	0	0	1
8131	19	3,644,234	3,644,725	491	1	4.333	3	11.667	7	5	19	0	0	1	PIP5K1C	55,966	in gene	ActReg chr19 #8131	0	0	1
8132	19	3,671,190	3,671,663	473	1	3.733	4.2	12.667	7	8	20	0	0	1	PIP5K1C	29,019	in gene	ActReg chr19 #8132	0	0	1
8133	19	3,683,170	3,683,761	591	1	4.167	5.389	11.556	7	7	16	0	0	1	PIP5K1C	16,980	in gene	ActReg chr19 #8133	0	0	1
8134	19	3,688,103	3,688,674	571	1	2.909	3.389	10.278	6	5	14	1	0	1	PIP5K1C	12,057	in gene	ActReg chr19 #8134	0	0	1
8135	19	3,707,973	3,708,460	487	1	4.867	2.692	12.933	7	5	20	0	0	1	PIP5K1C	-7,771	upstream	ActReg chr19 #8135	0	0	1
8136	19	3,721,189	3,721,934	745	2	11.652	12.8	11.043	20	24	16	1	1	1	TJP3	-6,813	upstream	ActReg chr19 #8136	1	1	0
8137	19	3,761,414	3,761,773	359	1	12.182	10.909	12.636	17	13	15	1	2	3	APBA3, MRPL54, RAX2	80, -1072, 10626	in gene, upstream, downstream	ActReg chr19 #8137	0	0	1
8138	19	3,777,526	3,778,435	909	1	3.929	4.103	13.448	7	7	18	0	1	3	MRPL54, RAX2, MATK	15315, -5761, 23830	downstream, upstream, in gene	ActReg chr19 #8138	0	0	1
8139	19	3,784,927	3,785,374	447	1	2.357	4.714	11.5	3	6	15	1	0	1	MATK	16,660	in gene	ActReg chr19 #8139	0	0	1
8140	19	3,810,827	3,811,393	566	1	5.444	4.278	10.278	10	7	13	1	0	2	MATK, ZFR2	-9300, 57917	upstream, in gene	ActReg chr19 #8140	0	0	1
8141	19	3,821,818	3,822,426	608	1	5.286	6.353	13	8	13	22	1	0	1	ZFR2	46,905	in gene	ActReg chr19 #8141	0	0	1
8142	19	3,838,508	3,839,103	595	1	3.944	4.833	12.444	7	7	17	0	0	1	ZFR2	30,222	in gene	ActReg chr19 #8142	0	0	1
8143	19	3,876,826	3,877,406	580	2	10.889	17.444	3.556	18	36	6	0	1	2	ZFR2, ATCAY	-8089, -3502	upstream, upstream	ActReg chr19 #8143	1	1	0
8144	19	3,946,348	3,946,795	447	1	1.5	4	11.071	2	5	17	0	0	1	ITGB1BP3	13,470	downstream	ActReg chr19 #8144	0	0	1
8145	19	3,963,995	3,964,308	313	1	4.3	2.4	12	6	3	14	0	1	2	DAPK3, MIR637	5675, -2641	in gene, upstream	ActReg chr19 #8145	0	0	1
8146	19	3,985,140	3,985,735	595	1	10.263	8.211	7.105	15	10	11	1	2	2	EEF2, SNORD37	24, -2867	in gene, upstream	ActReg chr19 #8146	1	0	0
8147	19	4,057,866	4,058,227	361	1	6.091	7.818	9.455	11	10	13	0	0	1	ZBTB7A	8,770	in gene	ActReg chr19 #8147	0	0	1
8148	19	4,094,685	4,095,132	447	1	4.929	3.286	11.357	7	5	15	0	0	1	MAP2K2	29,218	in gene	ActReg chr19 #8148	0	0	1
8149	19	4,112,263	4,112,693	430	1	3.615	4.231	13.538	6	6	20	0	0	1	MAP2K2	11,648	in gene	ActReg chr19 #8149	0	0	1
8150	19	4,124,136	4,124,496	360	1	6.091	8.727	12.909	9	12	18	1	1	1	MAP2K2	-190	upstream	ActReg chr19 #8150	0	0	1
8151	19	4,145,566	4,146,281	715	2	12.652	10.696	4.913	24	15	9	0	1	1	CREB3L3	-7,706	upstream	ActReg chr19 #8151	1	1	0
8152	19	4,181,730	4,182,975	1,245	2	8.553	13.763	7.971	13	22	18	1	2	3	CREB3L3, SIRT6, ANKRD24	28723, 244, -999	downstream, in gene, upstream	ActReg chr19 #8152	0	1	1
8153	19	4,199,774	4,200,293	519	1	4.412	5.941	11.235	7	9	15	0	0	1	ANKRD24	16,682	in gene	ActReg chr19 #8153	0	0	1
8154	19	4,207,606	4,207,947	341	1	1.909	4.727	13.364	3	7	17	0	0	1	ANKRD24	24,425	in gene	ActReg chr19 #8154	0	0	1
8155	19	4,224,313	4,224,774	461	1	3.467	3.867	11.867	7	6	17	0	1	2	ANKRD24, EBI3	41192, -4997	in gene, upstream	ActReg chr19 #8155	0	0	1
8156	19	4,246,485	4,247,419	934	2	12.448	12.724	4.034	29	26	9	1	1	2	EBI3, CCDC94	17412, -159	downstream, upstream	ActReg chr19 #8156	1	1	0
8157	19	4,323,525	4,323,899	374	1	3.3	6.273	11.364	5	10	16	0	0	2	FSD1, STAP2	19121, 15135	in gene, downstream	ActReg chr19 #8157	0	0	1
8158	19	4,360,608	4,361,095	487	1	6.375	6	11.938	9	9	17	0	0	2	MPND, SH3GL1	17327, 39620	downstream, in gene	ActReg chr19 #8158	0	0	1
8159	19	4,361,240	4,361,814	574	1	5	5.389	10.5	9	8	13	1	0	2	MPND, SH3GL1	18003, 38944	downstream, in gene	ActReg chr19 #8159	0	0	1
8160	19	4,374,218	4,375,353	1,135	3	11.657	11.086	9.143	20	25	16	0	0	1	SH3GL1	25,686	in gene	ActReg chr19 #8160	1	1	1
8161	19	4,447,711	4,448,262	551	1	6.611	3.389	13.167	10	5	20	0	0	2	CHAF1A, UBXN6	45326, 9805	downstream, in gene	ActReg chr19 #8161	0	0	1
8162	19	4,472,515	4,472,943	428	1	3.692	3.583	12.077	6	5	15	1	1	1	HDGF2	474	in gene	ActReg chr19 #8162	0	0	1
8163	19	4,516,721	4,517,298	577	1	3.556	5.056	10.944	6	12	14	0	1	2	PLIN4, PLIN5	707, 18199	in gene, downstream	ActReg chr19 #8163	0	0	1
8164	19	4,534,649	4,535,251	602	1	3.842	5.316	14.263	7	8	21	1	1	3	PLIN5, LRG1, SEMA6B	258, 5086, 23553	in gene, downstream, downstream	ActReg chr19 #8164	0	0	1
8165	19	4,580,214	4,580,805	591	1	4.316	3.333	12.579	6	6	17	1	0	0				ActReg chr19 #8165	0	0	1
8166	19	4,584,001	4,585,312	1,311	2	7.512	9	10.512	16	20	16	1	0	0				ActReg chr19 #8166	0	1	1
8167	19	4,639,806	4,640,271	465	1	6.467	5.867	10.867	9	9	15	1	1	1	TNFAIP8L1	511	in gene	ActReg chr19 #8167	0	0	1
8168	19	4,683,919	4,684,206	287	1	1.667	4.667	12	3	6	17	0	0	2	DPP9, LOC100131094	39793, 4768	in gene, in gene	ActReg chr19 #8168	0	0	1
8169	19	4,691,054	4,691,532	478	1	2.857	6.933	10.267	5	11	18	0	0	2	DPP9, LOC100131094	32562, 11999	in gene, downstream	ActReg chr19 #8169	0	0	1
8170	19	4,694,308	4,694,982	674	1	8.714	11.286	4.81	17	21	13	0	0	2	DPP9, LOC100131094	29210, 15351	in gene, downstream	ActReg chr19 #8170	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8171	19	4,722,857	4,724,383	1,526	3	18.565	16.66	11.34	43	35	31	1	1	1	DPP9	235	in gene	ActReg chr19 #8171	1	1	1
8172	19	4,744,438	4,745,338	900	1	11.036	12.214	3.607	21	21	6	0	0	0				ActReg chr19 #8172	0	1	0
8173	19	4,768,739	4,771,274	2,535	2	32.279	58.544	6.684	179	207	15	0	2	2	C19orf30, MIR7-3	889, -676	in gene, upstream	ActReg chr19 #8173	1	1	0
8174	19	4,791,031	4,792,337	1,306	2	22.098	20.512	6.293	54	53	17	1	2	3	LOC100506984, FEM1A, LOC100507004	-432, -44, 9594	upstream, upstream, downstream	ActReg chr19 #8174	1	1	0
8175	19	4,792,363	4,792,914	551	1	7.588	7.647	14.353	11	11	21	1	2	3	LOC100506984, FEM1A, LOC100507004	-1386, 910, 8640	upstream, in gene, downstream	ActReg chr19 #8175	0	0	1
8176	19	4,812,737	4,813,621	884	1	13.185	8.333	3.769	20	17	10	0	0	1	TICAM1	18,558	downstream	ActReg chr19 #8176	1	0	0
8177	19	4,831,486	4,832,124	638	1	11.8	13.95	7.05	20	23	13	1	1	2	TICAM1, PLIN3	-68, 35975	upstream, downstream	ActReg chr19 #8177	0	1	0
8178	19	4,851,989	4,852,537	548	1	5.5	2.941	11.471	9	5	20	1	0	1	PLIN3	15,517	in gene	ActReg chr19 #8178	0	0	1
8179	19	4,866,846	4,867,165	319	1	3.7	7.6	9.9	5	11	15	0	1	1	PLIN3	775	in gene	ActReg chr19 #8179	0	0	1
8180	19	4,869,976	4,870,485	509	1	11.875	8.125	3.812	19	13	5	0	1	1	PLIN3	-2,450	upstream	ActReg chr19 #8180	1	0	0
8181	19	4,968,359	4,969,198	839	2	12.308	12.538	7.818	22	27	14	1	1	2	UHRF1, KDM4B	59268, -346	downstream, upstream	ActReg chr19 #8181	1	1	0
8182	19	4,981,369	4,981,971	602	1	3.842	3.105	12.526	7	6	18	0	0	1	KDM4B	12,546	in gene	ActReg chr19 #8182	0	0	1
8183	19	5,022,341	5,022,745	404	1	3.417	4.167	11.417	5	6	17	0	0	1	KDM4B	53,419	in gene	ActReg chr19 #8183	0	0	1
8184	19	5,036,769	5,037,453	684	1	11.809	12.905	5	21	23	7	1	0	1	KDM4B	67,987	in gene	ActReg chr19 #8184	0	1	0
8185	19	5,047,654	5,048,447	793	1	7.25	8.333	11.792	14	17	15	2	0	1	KDM4B	78,926	in gene	ActReg chr19 #8185	0	0	1
8186	19	5,103,947	5,104,406	459	1	2.357	4.214	11.143	3	9	17	0	0	2	KDM4B, LOC100507052	135052, -9563	in gene, upstream	ActReg chr19 #8186	0	0	1
8187	19	5,114,004	5,114,641	637	1	3	4.35	13.4	5	10	21	0	1	2	KDM4B, LOC100507052	145198, 583	in gene, in gene	ActReg chr19 #8187	0	0	1
8188	19	5,119,462	5,119,927	465	1	2.357	2.929	11.571	4	7	16	1	0	2	KDM4B, LOC100507052	150570, 5955	in gene, downstream	ActReg chr19 #8188	0	0	1
8189	19	5,122,575	5,123,112	537	1	4.765	4.647	10.765	7	6	16	0	0	2	KDM4B, LOC100507052	153719, 9104	in gene, downstream	ActReg chr19 #8189	0	0	1
8190	19	5,130,981	5,131,356	375	1	4.182	4.364	12.818	5	7	16	0	0	1	KDM4B	162,044	in gene	ActReg chr19 #8190	0	0	1
8191	19	5,134,276	5,135,107	831	1	4.731	4.154	11.692	9	6	17	2	0	1	KDM4B	165,567	in gene	ActReg chr19 #8191	0	0	1
8192	19	5,135,296	5,135,678	382	1	4.75	3.083	12.333	6	5	16	1	0	1	KDM4B	166,363	in gene	ActReg chr19 #8192	0	0	1
8193	19	5,135,775	5,136,210	435	1	3.286	3.429	11.571	5	6	15	0	0	1	KDM4B	166,868	in gene	ActReg chr19 #8193	0	0	1
8194	19	5,151,110	5,151,699	589	1	2.556	3.778	10.5	5	6	13	1	0	2	KDM4B, LOC100507080	182280, 17839	in gene, downstream	ActReg chr19 #8194	0	0	1
8195	19	5,228,507	5,228,872	365	1	2	2.5	12.833	4	3	17	0	0	1	PTPRS	112,125	in gene	ActReg chr19 #8195	0	0	1
8196	19	5,232,790	5,233,213	423	1	4.462	5.308	13.462	8	10	16	0	0	1	PTPRS	107,813	in gene	ActReg chr19 #8196	0	0	1
8197	19	5,269,222	5,269,700	478	1	2.6	3.25	11.533	4	5	17	0	0	1	PTPRS	71,353	in gene	ActReg chr19 #8197	0	0	1
8198	19	5,288,508	5,288,960	452	1	2.667	7.933	10.733	5	11	16	0	0	1	PTPRS	52,080	in gene	ActReg chr19 #8198	0	0	1
8199	19	5,290,370	5,291,120	750	1	6.435	7.043	11.217	10	12	14	1	0	1	PTPRS	50,069	in gene	ActReg chr19 #8199	0	0	1
8200	19	5,345,725	5,346,534	809	2	13	11.692	2.423	20	25	5	0	1	1	PTPRS	-5,315	upstream	ActReg chr19 #8200	1	1	0
8201	19	5,403,750	5,404,654	904	2	18.179	21.429	4.92	45	58	8	0	0	0				ActReg chr19 #8201	1	1	0
8202	19	5,434,830	5,435,828	998	1	13.387	9.323	4.8	20	16	10	0	0	0				ActReg chr19 #8202	1	0	0
8203	19	5,622,503	5,623,438	935	2	9.103	11.483	10.034	16	16	18	1	2	2	SAFB2, SAFB	-32, -194	upstream, upstream	ActReg chr19 #8203	0	1	1
8204	19	5,679,958	5,681,079	1,121	2	13.057	13.486	9.029	27	21	17	1	2	3	C19orf70, HSD11B1L, RPL36	393, -517, -9754	in gene, upstream, upstream	ActReg chr19 #8204	1	1	0
8205	19	5,689,829	5,690,968	1,139	3	15.114	16.2	13.743	27	34	29	1	1	4	C19orf70, HSD11B1L, RPL36, LONP1	-9487, 9363, 126, 29778	upstream, downstream, in gene, downstream	ActReg chr19 #8205	1	1	1
8206	19	5,696,358	5,696,783	425	1	4.692	10	14	6	14	19	0	0	3	HSD11B1L, RPL36, LONP1	15535, 6298, 23606	downstream, downstream, in gene	ActReg chr19 #8206	0	0	1
8207	19	5,719,897	5,720,899	1,002	3	9.875	12.812	10.188	20	19	17	1	2	2	LONP1, TMEM146	-222, -290	upstream, upstream	ActReg chr19 #8207	1	1	1
8208	19	5,783,751	5,784,200	449	1	1.538	4	11.571	3	6	16	0	1	3	TMEM146, PRR22, DUS3L	63287, 801, 7274	downstream, in gene, downstream	ActReg chr19 #8208	0	0	1
8209	19	5,790,328	5,791,578	1,250	3	12.641	14.333	8.795	26	27	16	1	2	2	PRR22, DUS3L	-6177, 296	upstream, in gene	ActReg chr19 #8209	1	1	1
8210	19	5,827,893	5,828,757	864	2	11.63	10.741	8.083	18	18	14	1	0	2	NRTN, FUT6	4507, 11417	in gene, downstream	ActReg chr19 #8210	1	1	0
8211	19	5,913,775	5,914,471	696	1	6.682	12.273	6.227	13	21	12	0	1	4	NDUFA11, VMAC, CAPS, RANBP3	-10099, 9271, -70, 64197	upstream, downstream, upstream, downstream	ActReg chr19 #8211	0	1	0
8212	19	5,977,574	5,978,002	428	1	7.385	9.231	13.846	11	12	20	1	1	1	RANBP3	532	in gene	ActReg chr19 #8212	0	0	1
8213	19	6,087,768	6,088,432	664	1	11.714	8.143	3.381	17	13	5	0	0	1	RFX2	22,564	in gene	ActReg chr19 #8213	1	0	0
8214	19	6,198,964	6,199,803	839	2	10.346	11.615	11.308	16	23	16	1	1	2	ACSBG2, LOC100507094	63673, 157	downstream, in gene	ActReg chr19 #8214	0	1	1
8215	19	6,230,312	6,230,895	583	1	2.833	4.278	11.611	4	6	16	2	0	1	MLLT1	49,356	in gene	ActReg chr19 #8215	0	0	1
8216	19	6,233,362	6,233,774	412	1	4	4.1	12.154	7	6	17	0	0	1	MLLT1	46,391	in gene	ActReg chr19 #8216	0	0	1
8217	19	6,361,591	6,362,057	466	1	12	10.6	10.133	18	14	14	1	1	1	CLPP	361	in gene	ActReg chr19 #8217	0	0	1
8218	19	6,424,708	6,425,672	964	1	10.067	13.433	6.667	15	21	15	2	1	2	KHSRP, SLC25A41	-368, 8600	upstream, downstream	ActReg chr19 #8218	0	1	0
8219	19	6,459,709	6,460,870	1,161	2	11.73	14.351	5.2	25	30	8	1	2	3	SLC25A23, CRB3, DENND1C	-508, -3971, 21509	upstream, upstream, downstream	ActReg chr19 #8219	1	1	0
8220	19	6,464,368	6,464,820	452	1	2.714	2.273	10.786	5	3	18	1	2	3	SLC25A23, CRB3, DENND1C	-4813, 334, 17204	upstream, in gene, downstream	ActReg chr19 #8220	0	0	1
8221	19	6,495,949	6,496,323	374	1	2.333	2.875	13	4	4	18	1	1	2	TUBB4, MIR220B	6194, 177	in gene, downstream	ActReg chr19 #8221	0	0	1
8222	19	6,504,427	6,505,322	895	1	8.357	13.107	3.52	21	25	7	0	1	2	TUBB4, MIR220B	-2544, 8915	upstream, downstream	ActReg chr19 #8222	0	1	0
8223	19	6,530,784	6,531,421	637	1	10.05	10.45	7.8	17	15	13	1	1	1	TNFSF9	92	in gene	ActReg chr19 #8223	1	0	0
8224	19	6,564,296	6,564,944	648	2	14.3	11.15	3	28	18	5	0	0	0				ActReg chr19 #8224	1	1	0
8225	19	6,590,682	6,591,260	578	1	11.611	7.333	8.722	19	10	12	1	1	1	CD70	192	in gene	ActReg chr19 #8225	1	0	0
8226	19	6,692,755	6,693,142	387	1	4.333	2.417	12.917	7	3	17	0	0	1	C3	27,714	in gene	ActReg chr19 #8226	0	0	1
8227	19	6,733,243	6,733,726	483	1	3.929	3.2	11.867	6	5	19	0	1	2	GPR108, TRIP10	4149, -6223	in gene, upstream	ActReg chr19 #8227	0	0	1
8228	19	6,737,080	6,738,183	1,103	2	14.771	15.314	4.029	26	36	8	1	2	2	GPR108, TRIP10	2, -2076	in gene, upstream	ActReg chr19 #8228	1	1	0
8229	19	6,947,621	6,948,153	532	1	10.688	8.812	1.812	19	16	3	0	0	1	EMR1	60,305	downstream	ActReg chr19 #8229	1	0	0
8230	19	7,196,857	7,197,606	749	2	10.417	13.958	5.158	23	24	10	1	0	1	INSR	96,780	in gene	ActReg chr19 #8230	1	1	0
8231	19	7,459,809	7,460,246	437	1	4.308	6.692	12.308	6	10	15	1	1	1	ARHGEF18	28	in gene	ActReg chr19 #8231	0	0	1
8232	19	7,524,279	7,525,113	834	1	5.538	4.923	11.808	6	7	17	0	0	1	ARHGEF18	64,697	in gene	ActReg chr19 #8232	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8233	19	7,542,121	7,542,591	470	1	3.429	4.571	12.071	6	7	19	1	1	3	ARHGEF18, LOC100128573, PEX11G	82357, -4109, 11549	downstream, upstream, in gene	ActReg chr19 #8233	0	0	1
8234	19	7,574,358	7,575,097	739	2	11.522	13	6.739	16	27	12	0	1	2	C19orf45, ZNF358	12282, -6277	downstream, upstream	ActReg chr19 #8234	1	1	0
8235	19	7,587,031	7,587,918	887	2	14.964	18	7.321	37	40	13	1	1	2	ZNF358, MCOLN1	6470, -22	downstream, upstream	ActReg chr19 #8235	1	1	0
8236	19	7,598,095	7,599,434	1,339	2	9	13.476	5.524	25	29	11	1	1	2	MCOLN1, PNPLA6	11268, -274	in gene, upstream	ActReg chr19 #8236	1	1	0
8237	19	7,599,876	7,601,098	1,222	3	13.5	16.132	9.421	25	33	17	1	1	2	MCOLN1, PNPLA6	12991, 1449	downstream, in gene	ActReg chr19 #8237	1	1	1
8238	19	7,621,759	7,622,229	470	1	2.933	4.467	11.4	4	7	17	1	0	1	PNPLA6	22,956	in gene	ActReg chr19 #8238	0	0	1
8239	19	7,627,154	7,628,343	1,189	2	11.027	15.081	3.464	23	36	8	0	0	1	PNPLA6	28,710	downstream	ActReg chr19 #8239	1	1	0
8240	19	7,661,623	7,662,185	562	1	4.333	3.111	12.444	7	6	16	1	1	1	KIAA1543	1,116	in gene	ActReg chr19 #8240	0	0	1
8241	19	7,670,103	7,670,548	445	1	5.286	5.286	9.786	8	9	16	0	0	1	KIAA1543	9,537	in gene	ActReg chr19 #8241	0	0	1
8242	19	7,677,005	7,677,339	334	1	6.1	7.1	11.6	8	11	13	1	0	2	KIAA1543, XAB2	16384, 17267	in gene, downstream	ActReg chr19 #8242	0	0	1
8243	19	7,894,491	7,895,121	630	2	10.5	10.8	4.053	23	18	6	0	1	1	EVI5L	-355	upstream	ActReg chr19 #8243	1	1	0
8244	19	7,916,157	7,916,687	530	1	2.353	3.917	11.471	4	6	19	0	0	1	EVI5L	21,261	in gene	ActReg chr19 #8244	0	0	1
8245	19	7,922,230	7,922,874	644	1	2.684	3.7	11.65	5	5	14	0	0	1	EVI5L	27,391	in gene	ActReg chr19 #8245	0	0	1
8246	19	7,923,737	7,924,354	617	1	2.333	4.25	9	3	8	13	0	0	2	EVI5L, FLJ22184	28884, 15281	in gene, downstream	ActReg chr19 #8246	0	0	1
8247	19	7,933,490	7,933,961	471	1	5.667	7.133	12.2	8	10	15	1	0	2	EVI5L, FLJ22184	38564, 5601	downstream, in gene	ActReg chr19 #8247	0	0	1
8248	19	7,936,564	7,937,023	459	1	6.429	7.714	11.214	10	11	16	1	1	2	EVI5L, FLJ22184	41632, 2533	downstream, in gene	ActReg chr19 #8248	0	0	1
8249	19	7,944,212	7,944,681	469	1	2.538	5.2	9.067	4	9	16	0	1	2	FLJ22184, LRRC8E	-5120, -8944	upstream, upstream	ActReg chr19 #8249	0	0	1
8250	19	7,968,020	7,968,964	944	2	9.8	11.9	8.357	17	19	17	1	1	2	LRRC8E, MAP2K7	15102, -273	downstream, upstream	ActReg chr19 #8250	0	1	1
8251	19	7,979,402	7,979,985	583	1	3	6.389	11.056	4	9	17	0	2	4	MAP2K7, LOC100507588, SNAPC2, CTXN1	10928, -1460, -5501, 11358	downstream, upstream, upstream, downstream	ActReg chr19 #8251	0	0	1
8252	19	7,984,887	7,985,417	530	1	12.529	10.882	11.412	22	16	17	1	1	5	MAP2K7, LOC100507588, SNAPC2, CTXN1, TIMM44	16387, 3999, -42, 5899, 23556	downstream, downstream, upstream, downstream, downstream	ActReg chr19 #8252	0	0	1
8253	19	7,985,708	7,986,143	435	1	5.692	9.385	13	9	14	20	1	1	5	MAP2K7, LOC100507588, SNAPC2, CTXN1, TIMM44	17160, 4772, 731, 5126, 22783	downstream, downstream, in gene, downstream, downstream	ActReg chr19 #8253	0	0	1
8254	19	7,992,471	7,993,114	643	1	4.316	6.45	12.55	7	10	16	0	1	4	LOC100507588, SNAPC2, CTXN1, TIMM44	11639, 7598, -1741, 15916	downstream, downstream, upstream, in gene	ActReg chr19 #8254	0	0	1
8255	19	8,115,055	8,115,777	722	1	4.565	4.913	12.87	7	8	22	1	1	1	CCL25	-2,518	upstream	ActReg chr19 #8255	0	0	1
8256	19	8,130,625	8,131,045	420	1	4.615	5.385	12.231	6	8	17	0	0	2	CCL25, FBN3	12901, 81550	downstream, in gene	ActReg chr19 #8256	0	0	1
8257	19	8,154,608	8,155,047	439	1	2	5.714	10.714	3	7	16	0	0	1	FBN3	57,558	in gene	ActReg chr19 #8257	0	0	1
8258	19	8,206,295	8,206,618	323	1	3.7	3.1	9.9	5	5	13	0	0	1	FBN3	5,929	in gene	ActReg chr19 #8258	0	0	1
8259	19	8,213,186	8,213,708	522	1	3.688	4.067	10.625	6	9	14	0	1	1	FBN3	-1,062	upstream	ActReg chr19 #8259	0	0	1
8260	19	8,273,266	8,273,823	557	1	4.529	8.059	11.294	7	11	18	1	1	1	LASS4	-673	upstream	ActReg chr19 #8260	0	0	1
8261	19	8,372,367	8,373,738	1,371	2	13.581	13.465	5.1	26	23	10	1	1	2	CD320, NDUFA7	188, 13228	in gene, downstream	ActReg chr19 #8261	1	1	0
8262	19	8,385,475	8,386,560	1,085	2	9.5	11.618	8.618	14	20	17	1	2	3	NDUFA7, RPS28, KANK3	263, -367, 22129	in gene, upstream, downstream	ActReg chr19 #8262	0	1	1
8263	19	8,407,653	8,408,295	642	1	5.6	4.75	12.75	8	10	21	1	1	1	KANK3	172	in gene	ActReg chr19 #8263	0	0	1
8264	19	8,429,076	8,429,733	657	1	9.81	11.143	7.619	14	22	13	1	1	2	ANGPTL4, LOC100507567	393, 26165	in gene, downstream	ActReg chr19 #8264	0	1	0
8265	19	8,509,828	8,510,794	966	1	7.9	10.5	13.933	11	16	24	1	1	2	MARCH2, HNRNPM	32124, 508	downstream, in gene	ActReg chr19 #8265	0	0	1
8266	19	8,570,601	8,571,400	799	1	3.8	5.72	14.36	9	9	26	1	1	2	PRAM1, ZNF414	-3462, 8048	upstream, downstream	ActReg chr19 #8266	0	0	1
8267	19	8,657,255	8,657,938	683	1	5.476	3.65	14.762	9	8	19	1	0	1	ADAMTS10	17,992	in gene	ActReg chr19 #8267	0	0	1
8268	19	8,808,548	8,809,055	507	1	4.667	4.286	11.6	6	6	21	1	1	1	ACTL9	371	in gene	ActReg chr19 #8268	0	0	1
8269	19	8,841,605	8,842,288	683	1	6.762	11.476	3.952	10	22	8	0	1	1	OR2Z1	555	in gene	ActReg chr19 #8269	0	1	0
8270	19	8,942,534	8,943,368	834	3	9.731	17.269	7.885	18	31	22	1	0	2	ZNF558, MBD3L1	-9386, -10318	upstream, upstream	ActReg chr19 #8270	1	1	1
8271	19	9,084,153	9,084,560	407	1	10	9.615	3.154	16	14	5	0	0	1	MUC16	7,662	in gene	ActReg chr19 #8271	1	0	0
8272	19	9,186,187	9,186,820	633	2	10.15	11.2	1.526	20	23	3	0	0	0				ActReg chr19 #8272	1	1	0
8273	19	9,250,820	9,251,519	699	1	4.667	10.762	4.19	8	15	9	1	1	1	ZNF317	113	in gene	ActReg chr19 #8273	0	1	0
8274	19	9,373,139	9,373,436	297	1	2.778	2.111	9.889	5	3	13	0	0	0				ActReg chr19 #8274	0	0	1
8275	19	9,420,218	9,420,712	494	1	4.75	9.875	2.643	6	17	4	1	1	1	ZNF699	-4,670	upstream	ActReg chr19 #8275	0	1	0
8276	19	9,517,391	9,518,088	697	2	9.818	5.455	8.364	15	9	17	1	0	1	ZNF266	28,495	downstream	ActReg chr19 #8276	1	0	1
8277	19	9,545,917	9,546,365	448	1	9.929	6.357	5.929	15	11	9	1	1	1	ZNF266	93	in gene	ActReg chr19 #8277	1	0	0
8278	19	9,785,348	9,786,139	791	2	12	10.167	6.435	21	16	12	1	1	1	ZNF562	33	in gene	ActReg chr19 #8278	1	1	0
8279	19	9,787,968	9,788,272	304	1	1.5	2.222	9.3	2	4	12	0	1	1	ZNF562	-2,344	upstream	ActReg chr19 #8279	0	0	1
8280	19	9,878,855	9,879,860	1,005	2	11.323	11.613	8.161	20	17	11	1	1	1	ZNF846	53	in gene	ActReg chr19 #8280	1	1	0
8281	19	9,929,055	9,929,862	807	3	10.269	11.808	10.538	18	23	17	1	1	2	FBXL12, UBL5	273, -9110	in gene, upstream	ActReg chr19 #8281	1	1	1
8282	19	9,959,210	9,959,890	680	1	3.143	4.19	10.905	7	6	15	0	0	2	PIN1, OLFM2	13551, 87520	in gene, downstream	ActReg chr19 #8282	0	0	1
8283	19	10,049,685	10,050,642	957	2	9.5	12.733	3.833	16	25	10	0	1	1	OLFM2	-3,093	upstream	ActReg chr19 #8283	1	1	0
8284	19	10,172,321	10,173,423	1,102	2	16.382	21.235	3.265	34	40	6	1	0	0				ActReg chr19 #8284	1	1	0
8285	19	10,220,634	10,221,684	1,050	1	5.31	7.545	11.212	11	12	14	1	4	7	ANGPTL6, PPAN, PPAN-P2RY11, SNORD105, SNORD105B, P2RY11, EIF3G	-7734, 4194, 4088, 2832, 734, -1038, 9440	upstream, in gene, in gene, downstream, downstream, upstream, downstream	ActReg chr19 #8285	0	0	1
8286	19	10,223,885	10,225,834	1,949	3	10.295	9.984	11.41	18	19	17	1	1	6	PPAN, PPAN-P2RY11, SNORD105, SNORD105B, P2RY11, EIF3G	7894, 7788, 6532, 4434, 2662, 5740	downstream, in gene, downstream, downstream, in gene, downstream	ActReg chr19 #8286	1	1	1
8287	19	10,229,966	10,230,965	999	1	10.968	13.032	6.484	20	24	10	1	1	5	PPAN, PPAN-P2RY11, SNORD105B, P2RY11, EIF3G	13500, 13394, 10040, 8268, 134	downstream, downstream, downstream, downstream, in gene	ActReg chr19 #8287	0	1	0
8288	19	10,246,367	10,246,846	479	1	4.8	3.933	10.6	6	7	16	0	0	1	DNMT1	59,149	in gene	ActReg chr19 #8288	0	0	1
8289	19	10,268,821	10,269,376	555	1	3.167	5	12	6	8	16	0	0	1	DNMT1	36,657	in gene	ActReg chr19 #8289	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8290	19	10,304,695	10,306,053	1,358	1	10.302	12.233	8.024	17	23	14	1	1	1	DNMT1	381	in gene	ActReg chr19 #8290	0	1	0
8291	19	10,337,713	10,338,502	789	1	7.52	12.48	8.08	11	23	12	0	1	2	S1PR2, MIR4322	3841, -2982	in gene, upstream	ActReg chr19 #8291	0	1	0
8292	19	10,340,638	10,341,857	1,219	3	12.795	13.128	9.769	26	23	18	1	2	2	S1PR2, MIR4322	701, 158	in gene, downstream	ActReg chr19 #8292	1	1	1
8293	19	10,362,498	10,363,264	766	1	7.083	13.417	9.042	12	25	13	1	1	1	MRPL4	241	in gene	ActReg chr19 #8293	0	1	0
8294	19	10,380,686	10,381,796	1,110	2	7.943	11.8	10.714	14	17	16	1	1	2	MRPL4, ICAM1	18601, -276	downstream, upstream	ActReg chr19 #8294	0	1	1
8295	19	10,400,279	10,402,614	2,335	3	9.233	10.699	13.699	21	27	25	1	1	3	ICAM1, ICAM4, ICAM5	19929, 3796, 791	downstream, downstream, in gene	ActReg chr19 #8295	0	1	1
8296	19	10,404,197	10,404,816	619	1	6.368	7.105	13.158	12	10	21	1	0	3	ICAM1, ICAM4, ICAM5	22989, 6856, 3851	downstream, downstream, in gene	ActReg chr19 #8296	0	0	1
8297	19	10,404,870	10,405,663	793	1	3	7.333	12.875	6	12	21	1	0	4	ICAM1, ICAM4, ICAM5, ZGLP1	23749, 7616, 4611, 14967	downstream, downstream, in gene, downstream	ActReg chr19 #8297	0	0	1
8298	19	10,426,020	10,426,917	897	1	8.214	12.393	13.857	14	18	23	1	2	3	ZGLP1, FDX1L, RAVER1	-6235, 223, 17846	upstream, in gene, downstream	ActReg chr19 #8298	0	0	1
8299	19	10,433,225	10,434,299	1,074	1	3.774	6.909	11.333	10	11	16	1	1	2	FDX1L, RAVER1	-7071, 10552	upstream, in gene	ActReg chr19 #8299	0	0	1
8300	19	10,439,315	10,439,912	597	1	6.895	6.632	13.316	10	8	21	0	0	2	RAVER1, ICAM3	4701, 10732	in gene, downstream	ActReg chr19 #8300	0	0	1
8301	19	10,443,269	10,446,136	2,867	4	11.798	14.809	9.663	20	30	20	1	1	2	RAVER1, ICAM3	-388, 5643	upstream, in gene	ActReg chr19 #8301	1	1	1
8302	19	10,475,085	10,475,788	703	1	3.136	6.455	11.954	7	9	18	0	0	1	TYK2	15,812	in gene	ActReg chr19 #8302	0	0	1
8303	19	10,475,830	10,476,439	609	1	3.842	2.471	11.79	7	4	19	0	0	1	TYK2	15,114	in gene	ActReg chr19 #8303	0	0	1
8304	19	10,490,858	10,491,955	1,097	2	9.882	11.794	9.441	16	19	23	1	1	2	TYK2, CDC37	-158, 22865	upstream, downstream	ActReg chr19 #8304	0	1	1
8305	19	10,513,816	10,515,392	1,576	3	14.22	16.1	11.16	26	30	19	1	2	2	CDC37, MIR1181	-333, -390	upstream, upstream	ActReg chr19 #8305	1	1	1
8306	19	10,526,204	10,527,986	1,782	3	12.732	15.268	9.286	27	38	19	1	1	1	PDE4A	-4,238	upstream	ActReg chr19 #8306	1	1	1
8307	19	10,530,058	10,531,145	1,087	3	12.765	14.912	10.794	24	29	18	1	1	1	PDE4A	-732	upstream	ActReg chr19 #8307	1	1	1
8308	19	10,531,318	10,531,962	644	1	7.6	9.35	10.5	14	15	15	1	1	1	PDE4A	307	in gene	ActReg chr19 #8308	0	0	1
8309	19	10,534,800	10,535,649	849	1	9.111	9	12.63	12	15	20	1	0	1	PDE4A	3,891	in gene	ActReg chr19 #8309	0	0	1
8310	19	10,602,013	10,602,719	706	1	4.045	7.091	12.091	8	12	19	1	0	1	KEAP1	11,688	in gene	ActReg chr19 #8310	0	0	1
8311	19	10,612,460	10,613,947	1,487	3	13.348	14.826	10.109	24	26	22	1	1	2	KEAP1, S1PR5	851, 15465	in gene, downstream	ActReg chr19 #8311	1	1	1
8312	19	10,614,058	10,614,583	525	1	8.125	8.5	11.438	14	13	17	1	1	2	KEAP1, S1PR5	-266, 14348	upstream, downstream	ActReg chr19 #8312	0	0	1
8313	19	10,668,166	10,669,003	837	1	4.346	4.269	12.462	6	7	17	1	0	4	ATG4D, MIR1238, KRI1, CDKN2D	13937, 5786, 8118, 11071	downstream, downstream, in gene, downstream	ActReg chr19 #8313	0	0	1
8314	19	10,676,293	10,676,889	596	1	12.889	12.444	10.556	20	20	20	1	1	3	KRI1, CDKN2D, AP1M2	111, 3064, 21400	in gene, downstream, downstream	ActReg chr19 #8314	0	1	0
8315	19	10,679,513	10,680,565	1,052	2	13.758	15.182	5.935	32	30	11	1	2	3	KRI1, CDKN2D, AP1M2	-3337, -384, 17952	upstream, upstream, downstream	ActReg chr19 #8315	1	1	0
8316	19	10,691,940	10,692,721	781	1	10.542	8.833	13.583	19	13	17	1	0	1	AP1M2	5,661	in gene	ActReg chr19 #8316	0	0	1
8317	19	10,713,112	10,713,705	593	1	11.684	8.889	7.789	19	12	12	1	1	1	SLC44A2	287	in gene	ActReg chr19 #8317	1	0	0
8318	19	10,746,995	10,747,712	717	1	3.652	7.174	12.174	7	12	16	1	0	1	SLC44A2	34,232	in gene	ActReg chr19 #8318	0	0	1
8319	19	10,764,106	10,765,394	1,288	3	17.2	17.3	10.725	44	36	18	1	2	3	SLC44A2, LOC147727, ILF3	51629, -202, -187	downstream, upstream, upstream	ActReg chr19 #8319	1	1	1
8320	19	10,798,094	10,799,247	1,153	1	4.667	8.472	12.694	9	16	22	0	0	1	ILF3	33,733	in gene	ActReg chr19 #8320	0	0	1
8321	19	10,805,604	10,807,214	1,610	3	12.52	14.56	9.64	20	25	21	0	1	2	ILF3, QTRT1	41472, -5703	downstream, upstream	ActReg chr19 #8321	1	1	1
8322	19	10,811,792	10,812,942	1,150	3	10.972	12.333	11.722	24	18	23	1	1	2	ILF3, QTRT1	47430, 255	downstream, in gene	ActReg chr19 #8322	1	1	1
8323	19	10,822,828	10,824,053	1,225	1	5.421	4.406	13.053	11	9	20	1	2	3	QTRT1, DNM2, MIR638	11328, -5289, -5640	in gene, upstream, upstream	ActReg chr19 #8323	0	0	1
8324	19	10,827,478	10,828,913	1,435	1	13.2	14.956	5.089	25	30	11	1	2	3	QTRT1, DNM2, MIR638	16083, -554, -885	downstream, upstream, upstream	ActReg chr19 #8324	0	1	0
8325	19	10,860,129	10,860,689	560	1	7.647	5.353	13.823	11	7	19	0	0	1	DNM2	31,680	in gene	ActReg chr19 #8325	0	0	1
8326	19	10,913,613	10,914,262	649	1	3.5	5.8	12.5	6	9	15	0	1	2	DNM2, LOC100507081	85208, -7078	in gene, upstream	ActReg chr19 #8326	0	0	1
8327	19	10,919,362	10,920,435	1,073	2	10.636	12.364	6.758	23	23	14	0	1	3	DNM2, LOC100507081, MIR199A1	91169, -1117, 8274	in gene, upstream, downstream	ActReg chr19 #8327	1	1	0
8328	19	10,926,235	10,927,258	1,023	1	5.594	4.656	12.688	9	7	17	0	1	3	DNM2, LOC100507081, MIR199A1	98017, 5731, 1426	in gene, downstream, downstream	ActReg chr19 #8328	0	0	1
8329	19	10,941,809	10,942,361	552	1	2.353	3.706	12.118	4	6	15	0	0	2	DNM2, TMED1	113356, 4898	in gene, downstream	ActReg chr19 #8329	0	0	1
8330	19	10,945,349	10,947,700	2,351	3	12.658	13.712	13.288	26	31	25	1	1	2	DNM2, TMED1	117795, 459	downstream, in gene	ActReg chr19 #8330	1	1	1
8331	19	10,981,108	10,981,673	565	1	4.944	8	12.5	10	15	21	1	1	2	C19orf38, CARM1	22284, -863	downstream, upstream	ActReg chr19 #8331	0	0	1
8332	19	10,982,839	10,983,284	445	1	5.571	5.214	14.071	8	6	21	1	1	2	C19orf38, CARM1	23955, 808	downstream, in gene	ActReg chr19 #8332	0	0	1
8333	19	11,019,450	11,019,971	521	1	5.294	4.941	11.235	8	7	17	0	0	1	CARM1	37,457	in gene	ActReg chr19 #8333	0	0	1
8334	19	11,024,221	11,024,730	509	1	6.062	6.562	13	10	8	17	0	0	2	CARM1, YIPF2	42222, 14882	in gene, downstream	ActReg chr19 #8334	0	0	1
8335	19	11,025,590	11,027,117	1,527	1	7.583	9.25	12.792	13	20	17	0	0	2	CARM1, YIPF2	44100, 13004	in gene, downstream	ActReg chr19 #8335	0	0	1
8336	19	11,030,907	11,031,979	1,072	1	7.706	8.441	14.735	13	12	22	1	1	3	CARM1, YIPF2, C19orf52	49190, 7914, -7981	in gene, downstream, upstream	ActReg chr19 #8336	0	0	1
8337	19	11,034,079	11,034,957	878	1	6.929	5.786	13.75	10	9	21	0	1	3	CARM1, YIPF2, C19orf52	52265, 4839, -4906	downstream, in gene, upstream	ActReg chr19 #8337	0	0	1
8338	19	11,038,864	11,040,417	1,553	3	10.02	13	9.714	20	30	23	1	2	3	CARM1, YIPF2, C19orf52	57387, -283, 216	downstream, upstream, in gene	ActReg chr19 #8338	1	1	1
8339	19	11,070,866	11,071,566	700	2	8.545	12.182	11.727	12	25	25	1	1	1	SMARCA4	-382	upstream	ActReg chr19 #8339	0	1	1
8340	19	11,096,883	11,097,456	573	1	6.333	5.889	13.722	10	12	19	0	0	1	SMARCA4	25,571	in gene	ActReg chr19 #8340	0	0	1
8341	19	11,128,340	11,128,889	549	1	3.941	5.118	15	7	6	23	0	0	1	SMARCA4	57,016	in gene	ActReg chr19 #8341	0	0	1
8342	19	11,132,156	11,132,759	603	1	7.526	3.5	13.684	10	10	22	0	0	1	SMARCA4	60,859	in gene	ActReg chr19 #8342	0	0	1
8343	19	11,170,855	11,171,387	532	1	6.188	3.875	13.188	9	6	20	1	0	1	SMARCA4	99,523	in gene	ActReg chr19 #8343	0	0	1
8344	19	11,199,597	11,201,063	1,466	2	10.957	8.913	9.881	19	15	17	1	1	1	LDLR	273	in gene	ActReg chr19 #8344	1	0	1
8345	19	11,201,118	11,201,948	830	2	9.962	13.885	11.077	21	22	17	1	1	1	LDLR	1,476	in gene	ActReg chr19 #8345	0	1	1
8346	19	11,202,072	11,202,893	821	1	10.231	7.769	3.5	17	17	7	0	1	1	LDLR	2,425	in gene	ActReg chr19 #8346	1	0	0
8347	19	11,238,556	11,239,002	446	1	6.786	3.857	11.429	10	5	15	0	0	1	LDLR	38,722	in gene	ActReg chr19 #8347	0	0	1
8348	19	11,249,163	11,250,128	965	2	11.724	13.767	9.767	17	23	15	0	0	2	LDLR, SPC24	49588, 16839	downstream, downstream	ActReg chr19 #8348	1	1	0
8349	19	11,253,300	11,254,489	1,189	3	13.054	14.432	12.54	23	27	23	0	0	2	LDLR, SPC24	53837, 12590	downstream, downstream	ActReg chr19 #8349	1	1	1
8350	19	11,265,994	11,266,883	889	2	11.107	16.286	12.071	17	32	20	1	1	2	SPC24, KANK2	46, 41805	in gene, downstream	ActReg chr19 #8350	0	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIsIandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8351	19	11,304,169	11,305,167	998	1	3.724	4.033	14.516	7	9	20	1	0	2	KANK2, DOCK6	3575,68489	in gene, downstream	ActReg chr19 #8351	0	0	1
8352	19	11,352,138	11,352,927	789	1	4.833	4.5	12.083	11	8	19	0	1	2	DOCK6, LOC55908	20625, 2237	in gene, in gene	ActReg chr19 #8352	0	0	1
8353	19	11,372,371	11,372,988	617	1	8.158	9.421	14.053	12	16	25	1	1	1	DOCK6	478	in gene	ActReg chr19 #8353	0	0	1
8354	19	11,404,342	11,405,035	693	1	7.955	12.727	6.545	10	22	11	1	1	1	TSPAN16	-2,136	upstream	ActReg chr19 #8354	0	1	0
8355	19	11,480,097	11,481,003	906	1	10.286	15.929	3.821	18	29	6	0	1	3	LPPR2, C19orf59, EPOR	14488, -4833, 14468	downstream, upstream, downstream	ActReg chr19 #8355	0	1	0
8356	19	11,483,604	11,484,147	543	1	4.294	8.471	11.529	7	12	14	0	1	3	LPPR2, C19orf59, EPOR	17813, -1508, 11143	downstream, upstream, downstream	ActReg chr19 #8356	0	0	1
8357	19	11,529,139	11,530,000	861	1	7.778	8.222	12.593	12	16	20	2	1	2	RGL3, CCDC151	449, 16411	in gene, downstream	ActReg chr19 #8357	0	0	1
8358	19	11,532,919	11,533,749	830	1	1.773	4.577	12.115	5	8	18	1	1	2	RGL3, CCDC151	-3316, 12646	upstream, in gene	ActReg chr19 #8358	0	0	1
8359	19	11,545,574	11,546,960	1,386	2	12.419	12.395	8.605	18	21	16	1	2	2	CCDC151, PRKCSH	-287, -2	upstream, upstream	ActReg chr19 #8359	1	1	0
8360	19	11,556,785	11,557,470	685	1	4.048	5.762	15.286	9	8	24	0	0	2	PRKCSH, ELAVL3	10858, 34676	in gene, downstream	ActReg chr19 #8360	0	0	1
8361	19	11,559,067	11,559,793	726	1	5.478	5.739	12.609	9	12	18	0	0	2	PRKCSH, ELAVL3	13161, 32373	in gene, downstream	ActReg chr19 #8361	0	0	1
8362	19	11,559,870	11,560,441	571	1	6.889	5.167	13.222	12	6	20	1	0	2	PRKCSH, ELAVL3	13886, 31648	in gene, downstream	ActReg chr19 #8362	0	0	1
8363	19	11,590,877	11,591,309	432	1	7.214	5.5	12.929	9	8	20	1	1	2	ELAVL3, ZNF653	710, 25645	in gene, downstream	ActReg chr19 #8363	0	0	1
8364	19	11,592,530	11,593,935	1,405	3	12.364	12.5	11.341	21	22	20	1	1	2	ELAVL3, ZNF653	-1429, 23506	upstream, downstream	ActReg chr19 #8364	1	1	1
8365	19	11,597,229	11,598,009	780	1	3.542	3.583	13.708	8	7	22	0	1	2	ELAVL3, ZNF653	-5816, 19119	upstream, in gene	ActReg chr19 #8365	0	0	1
8366	19	11,616,766	11,617,361	595	1	6.895	9.263	11.684	9	14	17	1	1	2	ZNF653, ECSIT	-325, 22924	upstream, in gene	ActReg chr19 #8366	0	0	1
8367	19	11,639,262	11,640,321	1,059	3	12.559	11.823	10.294	24	16	22	1	1	2	ECSIT, CNN1	196, -9788	in gene, upstream	ActReg chr19 #8367	1	1	1
8368	19	11,664,513	11,665,359	846	1	5.44	6.038	14.308	8	10	25	0	0	2	CNN1, ELOF1	15357, 5115	downstream, in gene	ActReg chr19 #8368	0	0	1
8369	19	11,669,526	11,670,522	996	1	8.71	14	8.839	13	24	18	1	1	2	CNN1, ELOF1	20445, 27	downstream, in gene	ActReg chr19 #8369	0	1	0
8370	19	11,687,993	11,689,519	1,526	1	8.479	9.042	11.354	14	16	17	1	1	1	ACP5	1,045	in gene	ActReg chr19 #8370	0	0	1
8371	19	11,708,059	11,708,870	811	1	13.846	12.808	11.308	25	21	19	1	1	1	ZNF627	229	in gene	ActReg chr19 #8371	1	0	0
8372	19	11,805,208	11,806,238	1,030	1	7.5	11.719	5.875	14	19	10	1	0	0				ActReg chr19 #8372	0	1	0
8373	19	11,877,437	11,878,505	1,068	2	14.588	13.177	3.559	25	22	6	1	1	1	ZNF441	156	in gene	ActReg chr19 #8373	1	1	0
8374	19	11,908,334	11,908,860	526	1	4.812	11.062	3.75	8	16	6	0	1	1	ZNF491	-794	upstream	ActReg chr19 #8374	0	1	0
8375	19	11,909,301	11,909,975	674	1	11.619	6.286	5.571	17	10	10	1	1	1	ZNF491	247	in gene	ActReg chr19 #8375	1	0	0
8376	19	11,959,478	11,960,000	522	1	6.188	8.706	10.588	9	15	17	1	1	1	LOC100507095	178	in gene	ActReg chr19 #8376	0	0	1
8377	19	11,998,318	11,999,257	939	2	10.966	12	6.586	19	18	13	1	1	1	ZNF69	117	in gene	ActReg chr19 #8377	1	1	0
8378	19	12,035,466	12,036,398	932	1	11.31	14.897	10.552	19	29	15	1	1	1	ZNF700	32	in gene	ActReg chr19 #8378	0	1	0
8379	19	12,098,456	12,098,881	425	1	8	8.643	13.357	10	10	19	1	1	2	ZNF763, LOC100507111	22799, 185	downstream, in gene	ActReg chr19 #8379	0	0	1
8380	19	12,145,962	12,146,564	602	1	5.211	10.421	14.158	9	13	21	1	1	3	LOC100507111, ZNF433, ZNF878	47780, 262, 20864	in gene, in gene, downstream	ActReg chr19 #8380	0	0	1
8381	19	12,163,289	12,163,997	708	3	10.182	11.773	8.909	20	18	16	1	0	2	LOC100507111, ZNF878	65160, 3484	downstream, in gene	ActReg chr19 #8381	1	1	1
8382	19	12,175,198	12,176,188	990	1	6.806	10.839	7.185	13	16	13	1	1	2	ZNF878, ZNF844	-8566, 147	upstream, in gene	ActReg chr19 #8382	0	1	0
8383	19	12,250,640	12,251,064	424	1	6.154	8.154	13.077	9	11	18	1	1	2	ZNF20, ZNF625	288, 16677	in gene, downstream	ActReg chr19 #8383	0	0	1
8384	19	12,266,953	12,267,912	959	1	9.4	11.9	4.633	14	17	12	1	2	2	ZNF625, ZNF136	97, -6440	in gene, upstream	ActReg chr19 #8384	0	1	0
8385	19	12,443,890	12,444,302	412	1	6.923	7.615	12.077	13	10	18	1	1	1	ZNF563	438	in gene	ActReg chr19 #8385	0	0	1
8386	19	12,476,114	12,477,169	1,055	2	11.273	9.303	6.433	18	20	12	1	1	1	ZNF442	-166	upstream	ActReg chr19 #8386	1	1	0
8387	19	12,511,235	12,512,247	1,012	1	11.419	10.129	7.774	17	14	14	1	1	1	ZNF799	347	in gene	ActReg chr19 #8387	1	0	0
8388	19	12,551,529	12,552,115	586	1	12.5	8.444	5	18	12	8	1	1	1	ZNF443	104	in gene	ActReg chr19 #8388	1	0	0
8389	19	12,624,179	12,624,931	752	1	3.348	4.875	13.125	8	7	23	1	0	0				ActReg chr19 #8389	0	0	1
8390	19	12,661,762	12,662,935	1,173	1	14.056	15.611	9.333	23	32	16	1	1	1	ZNF564	8	in gene	ActReg chr19 #8390	0	1	0
8391	19	12,721,673	12,722,144	471	1	15.333	11.333	15.267	22	14	23	1	2	2	ZNF490, ZNF791	-285, 176	upstream, in gene	ActReg chr19 #8391	0	0	1
8392	19	12,777,242	12,777,927	685	1	8.545	8.909	11.727	13	11	16	1	2	4	MAN2B1, WDR83, C19orf56, DHPS	7, -34, 2881, 15093	in gene, upstream, downstream, downstream	ActReg chr19 #8392	0	0	1
8393	19	12,779,869	12,781,206	1,337	3	12.691	12.905	9.31	18	21	14	1	3	5	MAN2B1, WDR83, C19orf56, DHPS, LOC100507285	-2946, 2919, -72, 12140, -9080	upstream, in gene, upstream, downstream, upstream	ActReg chr19 #8393	1	1	1
8394	19	12,806,957	12,807,878	921	2	10.621	14.207	15.379	20	22	30	1	1	5	LOC100507285, LOC648044, FBXW9, TNPO2, SNORD41	17800, 8605, 38, 27393, 9915	downstream, downstream, in gene, downstream, downstream	ActReg chr19 #8394	0	1	1
8395	19	12,812,312	12,813,166	854	1	5.037	7.444	14.444	8	10	23	0	1	3	FBXW9, TNPO2, SNORD41	-5284, 22071, 4593	upstream, in gene, downstream	ActReg chr19 #8395	0	0	1
8396	19	12,833,223	12,833,951	728	1	10.909	14.364	5.364	24	26	10	1	1	2	TNPO2, C19orf43	1223, 11942	in gene, downstream	ActReg chr19 #8396	0	1	0
8397	19	12,847,761	12,849,019	1,258	2	10.897	15.231	6.128	16	34	12	1	2	2	C19orf43, ASNA1	-2861, 84	upstream, in gene	ActReg chr19 #8397	1	1	0
8398	19	12,857,930	12,858,624	694	1	2.409	5.091	11.182	5	9	16	0	1	2	ASNA1, BEST2	9971, -5130	in gene, upstream	ActReg chr19 #8398	0	0	1
8399	19	12,885,613	12,886,763	1,150	3	16.194	16.056	9.333	49	43	20	1	1	1	HOOK2	246	in gene	ActReg chr19 #8399	1	1	1
8400	19	12,888,571	12,889,605	1,034	1	10	12.424	6.424	16	21	15	1	1	1	HOOK2	-2,654	upstream	ActReg chr19 #8400	0	1	0
8401	19	12,892,529	12,894,135	1,606	2	14.56	17.7	5.94	39	54	14	1	1	2	HOOK2, JUNB	-6898, -8978	upstream, upstream	ActReg chr19 #8401	1	1	0
8402	19	12,900,578	12,903,960	3,382	5	14.476	13.571	8.548	31	26	29	2	1	2	JUNB, PRDX2	-41, 10425	upstream, downstream	ActReg chr19 #8402	1	1	1
8403	19	12,904,023	12,905,203	1,180	2	14.189	12.135	8.568	22	27	15	1	1	2	JUNB, PRDX2	2303, 8081	downstream, downstream	ActReg chr19 #8403	1	1	0
8404	19	12,911,789	12,913,337	1,548	3	16.458	17.065	15.5	26	33	32	1	2	3	JUNB, PRDX2, RNASEH2A	10253, 131, -4865	downstream, in gene, upstream	ActReg chr19 #8404	1	1	1
8405	19	12,942,702	12,944,069	1,367	2	18.861	22.605	5.93	48	63	10	1	2	3	RTBDN, LOC100507305, MAST1	2845, 6860, -5874	in gene, in gene, upstream	ActReg chr19 #8405	1	1	0
8406	19	12,945,021	12,945,554	533	1	8	7.941	13.118	13	12	21	1	2	3	RTBDN, LOC100507305, MAST1	943, 8762, -3972	in gene, downstream, upstream	ActReg chr19 #8406	0	0	1
8407	19	12,945,932	12,946,508	576	1	4.778	7.444	11.389	6	12	19	0	2	3	RTBDN, LOC100507305, MAST1	10, 9695, -3039	in gene, downstream, upstream	ActReg chr19 #8407	0	0	1
8408	19	12,946,855	12,947,673	818	1	11.12	15.56	5.16	18	34	8	0	2	3	RTBDN, LOC100507305, MAST1	-1034, 10739, -1995	upstream, downstream, upstream	ActReg chr19 #8408	0	1	0
8409	19	12,958,009	12,959,083	1,074	1	13.588	10.677	11.794	22	16	20	1	0	1	MAST1	9,287	in gene	ActReg chr19 #8409	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8410	19	12,978,090	12,978,665	575	1	3.444	5.611	14.333	7	8	25	1	0	2	MAST1, DNASE2	29118, 13958	in gene, downstream	ActReg chr19 #8410	0	0	1
8411	19	12,991,312	12,992,562	1,250	2	8.769	10.564	9.846	14	22	15	1	1	4	MAST1, DNASE2, KLF1, GCDH	42678, 398, 6080, -10037	downstream, in gene, downstream, upstream	ActReg chr19 #8411	0	1	1
8412	19	12,996,676	12,997,117	441	1	6.077	4.154	16.077	9	7	26	1	3	3	DNASE2, KLF1, GCDH	-4561, 1121, -5078	upstream, in gene, upstream	ActReg chr19 #8412	0	0	1
8413	19	13,001,345	13,003,107	1,762	2	21.709	23.782	7.481	83	81	14	1	2	4	DNASE2, KLF1, GCDH, SYCE2	-9891, -4209, 252, 27860	upstream, upstream, in gene, downstream	ActReg chr19 #8413	1	1	0
8414	19	13,048,431	13,049,925	1,494	3	15.702	16.319	14.043	34	33	27	1	3	4	FARSA, CALR, LOC100507328, RAD23A	-4620, -236, 29027, -7476	upstream, upstream, downstream, upstream	ActReg chr19 #8414	1	1	1
8415	19	13,067,078	13,068,416	1,338	2	11.619	11.309	6.476	18	20	15	1	1	3	LOC100507328, RAD23A, GADD45GIP1	10458, 11093, 303	in gene, downstream, in gene	ActReg chr19 #8415	1	1	0
8416	19	13,095,208	13,096,765	1,557	2	12.312	12.542	7.104	19	21	17	0	0	2	DAND5, NFIX	15554, -10598	downstream, upstream	ActReg chr19 #8416	1	1	0
8417	19	13,105,360	13,106,352	992	1	11.161	11.484	7.259	24	24	10	0	1	1	NFIX	-728	upstream	ActReg chr19 #8417	1	0	0
8418	19	13,106,750	13,108,028	1,278	1	8.675	12.275	10	16	22	20	1	1	1	NFIX	805	in gene	ActReg chr19 #8418	0	1	0
8419	19	13,121,137	13,121,643	506	1	3.071	5.188	12.562	6	8	15	1	0	1	NFIX	14,806	in gene	ActReg chr19 #8419	0	0	1
8420	19	13,166,531	13,167,144	613	1	9.316	10.053	13.368	13	13	19	0	0	1	NFIX	60,253	in gene	ActReg chr19 #8420	0	0	1
8421	19	13,179,159	13,180,363	1,204	1	4.368	3.417	13.053	9	6	17	0	0	1	NFIX	73,177	in gene	ActReg chr19 #8421	0	0	1
8422	19	13,180,875	13,181,970	1,095	1	3.03	3.382	12.441	9	7	17	0	0	1	NFIX	74,838	in gene	ActReg chr19 #8422	0	0	1
8423	19	13,189,398	13,189,924	526	1	3	4.647	12.823	5	7	21	0	0	1	NFIX	83,077	in gene	ActReg chr19 #8423	0	0	1
8424	19	13,192,224	13,192,996	772	1	6.88	5.826	12.12	14	6	23	0	0	1	NFIX	86,026	in gene	ActReg chr19 #8424	0	0	1
8425	19	13,202,341	13,202,908	567	1	3.059	4.846	11.177	5	9	17	0	0	2	NFIX, LYL1	96040, 11057	in gene, downstream	ActReg chr19 #8425	0	0	1
8426	19	13,210,320	13,210,762	442	1	2.357	2.769	11.786	4	4	19	1	0	3	NFIX, LYL1, TRMT1	103957, 3140, 17022	downstream, in gene, downstream	ActReg chr19 #8426	0	0	1
8427	19	13,213,063	13,214,382	1,319	1	7.024	7.475	15.927	11	12	26	1	1	3	NFIX, LYL1, TRMT1	107138, -41, 13841	downstream, upstream, downstream	ActReg chr19 #8427	0	0	1
8428	19	13,215,320	13,216,041	721	1	5.13	5.913	12.348	7	12	20	1	1	3	NFIX, LYL1, TRMT1	109096, -1999, 11883	downstream, upstream, downstream	ActReg chr19 #8428	0	0	1
8429	19	13,220,075	13,220,772	697	1	3.545	5.227	12	5	8	16	0	1	3	LYL1, TRMT1, NACC1	-6742, 7140, -8686	upstream, in gene, upstream	ActReg chr19 #8429	0	0	1
8430	19	13,227,041	13,228,080	1,039	3	13.5	17.188	9.844	31	35	18	1	2	2	TRMT1, NACC1	5, -1549	in gene, upstream	ActReg chr19 #8430	1	1	1
8431	19	13,232,638	13,233,258	620	1	4.8	5	12.4	8	7	19	0	1	2	TRMT1, NACC1	-5385, 3839	upstream, in gene	ActReg chr19 #8431	0	0	1
8432	19	13,260,195	13,265,374	5,179	7	17.472	16.64	10.706	51	47	29	1	2	3	NACC1, STX10, IER2	33675, -1797, 1502	downstream, upstream, in gene	ActReg chr19 #8432	1	1	1
8433	19	13,273,540	13,275,007	1,467	1	9.844	12.467	9.178	16	24	18	1	0	1	IER2	12,991	downstream	ActReg chr19 #8433	0	1	0
8434	19	13,275,024	13,276,156	1,132	2	12.4	11.6	7.143	17	17	13	0	0	1	IER2	14,308	downstream	ActReg chr19 #8434	1	1	0
8435	19	13,297,372	13,297,786	414	1	3.455	5.154	12	7	7	19	0	0	0				ActReg chr19 #8435	0	0	1
8436	19	13,321,636	13,322,502	866	1	7.37	6.667	12.074	13	9	16	0	0	1	CACNA1A	295,205	in gene	ActReg chr19 #8436	0	0	1
8437	19	13,322,594	13,323,208	614	1	4.895	2.895	13.474	7	4	21	0	0	1	CACNA1A	294,373	in gene	ActReg chr19 #8437	0	0	1
8438	19	13,371,909	13,372,674	765	2	13.708	12	2.957	22	21	6	0	0	1	CACNA1A	244,983	in gene	ActReg chr19 #8438	1	1	0
8439	19	13,552,404	13,553,659	1,255	2	17.846	21.872	3.359	44	55	7	0	0	1	CACNA1A	64,243	in gene	ActReg chr19 #8439	1	1	0
8440	19	13,572,526	13,574,971	2,445	3	9.987	16.079	4.392	30	47	10	0	0	1	CACNA1A	43,526	in gene	ActReg chr19 #8440	1	1	0
8441	19	13,842,190	13,842,886	696	2	7.136	12.091	12.546	14	19	26	0	0	0				ActReg chr19 #8441	0	1	1
8442	19	13,858,158	13,859,001	843	2	12	13.577	10.654	20	22	20	1	1	1	CCDC130	-174	upstream	ActReg chr19 #8442	0	1	1
8443	19	13,874,899	13,875,389	490	1	10.933	14.8	7.467	14	21	14	1	1	3	CCDC130, MRH, C19orf53	16391, -193, -10113	downstream, upstream, upstream	ActReg chr19 #8443	0	1	0
8444	19	13,884,803	13,886,485	1,682	2	12.635	18.288	7.827	41	57	17	1	1	2	MRH, C19orf53	10307, 387	downstream, in gene	ActReg chr19 #8444	1	1	0
8445	19	13,905,393	13,906,466	1,073	1	10.294	12.088	7.419	17	21	14	1	1	1	ZSWIM4	-345	upstream	ActReg chr19 #8445	0	1	0
8446	19	13,928,277	13,928,844	567	1	6.188	6.333	13.444	10	9	19	0	0	1	ZSWIM4	22,286	in gene	ActReg chr19 #8446	0	0	1
8447	19	13,940,943	13,941,477	534	1	7.765	6.882	12.353	11	10	21	1	0	5	ZSWIM4, LOC284454, MIR24-2, MIR27A, MIR23A	34936, 5893, 5963, 6121, 6263	in gene, downstream, downstream, downstream, downstream	ActReg chr19 #8447	0	0	1
8448	19	13,943,933	13,944,960	1,027	1	10.091	9.333	14.636	19	15	28	1	3	5	ZSWIM4, LOC284454, MIR24-2, MIR27A, MIR23A	38172, 2657, 2727, 2885, 3027	downstream, downstream, downstream, downstream, downstream, downstream	ActReg chr19 #8448	0	0	1
8449	19	13,946,726	13,948,094	1,368	2	11.048	12.833	11.548	19	23	21	0	4	5	ZSWIM4, LOC284454, MIR24-2, MIR27A, MIR23A	41136, -307, -237, -79, 63	downstream, upstream, upstream, upstream, in gene	ActReg chr19 #8449	1	0	1
8450	19	13,949,551	13,952,719	3,168	3	12.768	13.495	11.04	25	23	30	0	4	5	ZSWIM4, LOC284454, MIR24-2, MIR27A, MIR23A	44861, -4032, -3962, -3804, -3662	downstream, upstream, upstream, upstream, upstream, upstream	ActReg chr19 #8450	1	1	1
8451	19	13,957,099	13,959,103	2,004	3	12.555	13.339	9.403	29	20	21	0	0	4	LOC284454, MIR24-2, MIR27A, MIR23A	-10998, -10928, -10770, -10628	upstream, upstream, upstream, upstream	ActReg chr19 #8451	1	1	1
8452	19	13,961,579	13,962,749	1,170	2	12.333	14.472	5.25	26	27	12	0	0	0				ActReg chr19 #8452	1	1	0
8453	19	13,990,828	13,991,539	711	1	13.546	12.909	9.4	21	19	14	1	0	4	MIR181C, MIR181D, NANOS3, C19orf57	5670, 5494, 3233, 25726	downstream, downstream, in gene, downstream	ActReg chr19 #8453	0	1	0
8454	19	13,997,789	13,998,505	716	1	5.435	5.609	11.043	8	9	18	0	0	2	NANOS3, C19orf57	10197, 18762	downstream, in gene	ActReg chr19 #8454	0	0	1
8455	19	14,013,864	14,014,607	743	2	12.217	14.565	2.636	29	31	6	0	2	2	C19orf57, CC2D1A	2674, -2721	in gene, upstream	ActReg chr19 #8455	1	1	0
8456	19	14,016,799	14,017,781	982	2	11.871	10.387	10.355	20	14	14	1	2	2	C19orf57, CC2D1A	-381, 334	upstream, in gene	ActReg chr19 #8456	0	1	1
8457	19	14,029,687	14,030,078	391	1	3.75	4.5	14.583	6	6	24	0	0	1	CC2D1A	12,926	in gene	ActReg chr19 #8457	0	0	1
8458	19	14,041,903	14,042,817	914	1	3.828	4.931	11.552	8	7	16	0	0	2	CC2D1A, PODNL1	25404, 21844	downstream, in gene	ActReg chr19 #8458	0	0	1
8459	19	14,046,253	14,046,832	579	1	5.5	3.5	12.278	11	6	16	0	0	2	CC2D1A, PODNL1	29586, 17662	downstream, in gene	ActReg chr19 #8459	0	0	1
8460	19	14,070,716	14,071,598	882	1	8.571	6.607	12.643	16	9	22	0	1	3	PODNL1, DCAF15, RFX1	-6953, 7838, 45977	upstream, in gene, downstream	ActReg chr19 #8460	0	0	1
8461	19	14,076,273	14,076,862	589	1	4.588	4.722	12.722	8	6	20	0	0	2	DCAF15, RFX1	13248, 40567	downstream, in gene	ActReg chr19 #8461	0	0	1
8462	19	14,077,192	14,077,933	741	1	2.87	4.87	14.478	6	7	22	0	0	2	DCAF15, RFX1	14243, 39572	downstream, in gene	ActReg chr19 #8462	0	0	1
8463	19	14,097,087	14,097,696	609	1	3.85	4	11.8	8	6	17	0	0	1	RFX1	19,743	in gene	ActReg chr19 #8463	0	0	1
8464	19	14,116,818	14,118,226	1,408	4	14.182	16.614	12.136	26	38	28	1	1	1	RFX1	-388	upstream	ActReg chr19 #8464	1	1	1
8465	19	14,138,940	14,139,432	492	1	5.125	4.308	10.938	7	6	14	0	2	2	RLN3, IL27RA	169, -3076	in gene, upstream	ActReg chr19 #8465	0	0	1
8466	19	14,142,422	14,143,348	926	1	9.379	9.241	14.862	17	14	30	1	1	2	RLN3, IL27RA	3868, 623	downstream, in gene	ActReg chr19 #8466	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8467	19	14,169,571	14,170,129	558	1	5.647	6.882	11.118	9	12	15	0	1	2	IL27RA, PALM3	27588, 121	downstream, in gene	ActReg chr19 #8467	0	0	1
8468	19	14,182,975	14,183,538	563	1	7.722	7.278	13.389	13	12	20	1	1	2	LOC113230, C19orf67	-565, 13183	upstream, downstream	ActReg chr19 #8468	0	0	1
8469	19	14,185,104	14,185,647	543	1	5.882	10.294	11.706	8	13	16	1	1	2	LOC113230, C19orf67	1554, 11064	in gene, downstream	ActReg chr19 #8469	0	0	1
8470	19	14,192,097	14,192,994	897	2	9	13.107	9.964	23	23	21	1	0	4	LOC113230, C19orf67, SAMD1, PRKACA	8724, 3894, 8687, 36014	downstream, in gene, downstream, downstream	ActReg chr19 #8470	0	1	1
8471	19	14,218,204	14,219,174	970	1	3.839	4.097	11.452	6	8	18	0	0	1	PRKACA	9,870	in gene	ActReg chr19 #8471	0	0	1
8472	19	14,229,212	14,230,020	808	1	9.692	12.192	9.923	14	17	15	1	1	2	PRKACA, ASF1B	-1057, 17824	upstream, downstream	ActReg chr19 #8472	0	1	0
8473	19	14,230,983	14,231,478	495	1	4.4	3.4	13.133	6	5	18	0	1	2	PRKACA, ASF1B	-2671, 16210	upstream, in gene	ActReg chr19 #8473	0	0	1
8474	19	14,246,992	14,248,661	1,669	4	11.654	13.019	11.039	21	22	22	1	2	3	ASF1B, LOC100507373, LPHN1	-386, -154, 69171	upstream, upstream, downstream	ActReg chr19 #8474	1	1	1
8475	19	14,260,846	14,261,444	598	1	3.368	5.105	14.579	5	9	24	0	0	2	LOC100507373, LPHN1	13165, 55852	in gene, in gene	ActReg chr19 #8475	0	0	1
8476	19	14,270,823	14,271,439	616	1	2.588	8.526	12.316	6	12	20	0	0	2	LOC100507373, LPHN1	23151, 45866	in gene, in gene	ActReg chr19 #8476	0	0	1
8477	19	14,273,492	14,274,551	1,059	1	4.879	7.667	12.727	7	16	19	1	0	2	LOC100507373, LPHN1	26041, 42976	in gene, in gene	ActReg chr19 #8477	0	0	1
8478	19	14,275,533	14,276,320	787	1	3.96	7.04	12.6	10	12	17	0	0	2	LOC100507373, LPHN1	27946, 41071	in gene, in gene	ActReg chr19 #8478	0	0	1
8479	19	14,293,716	14,294,810	1,094	1	4.059	3.704	13.206	8	9	20	0	0	1	LPHN1	22,734	in gene	ActReg chr19 #8479	0	0	1
8480	19	14,317,539	14,318,876	1,337	2	20.537	31.317	5.5	40	55	14	1	1	1	LPHN1	-1,210	upstream	ActReg chr19 #8480	1	1	0
8481	19	14,486,357	14,486,929	572	1	4.389	4.389	11.222	8	9	14	0	1	2	CD97, LOC100507396	-5570, -8388	upstream, upstream	ActReg chr19 #8481	0	0	1
8482	19	14,491,999	14,493,144	1,145	2	7.611	11.278	8.833	14	16	17	0	2	2	CD97, LOC100507396	358, -2460	in gene, upstream	ActReg chr19 #8482	0	1	1
8483	19	14,504,153	14,504,691	538	1	3.706	4	13.235	6	7	18	0	0	2	CD97, LOC100507396	12209, 9391	in gene, downstream	ActReg chr19 #8483	0	0	1
8484	19	14,516,559	14,517,066	507	1	8.75	8.188	12.312	14	14	18	1	0	2	CD97, DDX39	24599, 13359	in gene, downstream	ActReg chr19 #8484	0	0	1
8485	19	14,517,168	14,517,701	533	1	5.059	8.176	15.059	7	14	23	1	0	2	CD97, DDX39	25221, 12737	in gene, downstream	ActReg chr19 #8485	0	0	1
8486	19	14,521,027	14,522,100	1,073	1	7.212	7.394	14.091	11	12	20	0	0	2	CD97, DDX39	29350, 8608	downstream, in gene	ActReg chr19 #8486	0	0	1
8487	19	14,529,707	14,530,365	658	1	10.9	9.75	13	14	14	21	1	1	1	DDX39	135	in gene	ActReg chr19 #8487	0	0	1
8488	19	14,544,403	14,546,197	1,794	3	10.071	9.357	11.821	22	18	22	1	1	1	PKN1	1,134	in gene	ActReg chr19 #8488	1	0	1
8489	19	14,574,672	14,575,158	486	1	4.267	7.4	11.067	7	10	15	0	0	2	PKN1, PTGER1	30749, 11259	in gene, downstream	ActReg chr19 #8489	0	0	1
8490	19	14,590,725	14,591,484	759	1	10.087	7.304	16	16	10	27	1	1	4	PKN1, PTGER1, GIPC1, LOC100130932	46938, -4930, 15840, 8654	downstream, upstream, in gene, upstream	ActReg chr19 #8490	0	0	1
8491	19	14,628,807	14,629,318	511	1	15.438	9.312	18.25	22	16	32	1	1	1	DNAJB1	139	in gene	ActReg chr19 #8491	0	0	1
8492	19	14,630,287	14,631,377	1,090	2	12.971	13.441	5.029	23	24	10	0	1	3	DNAJB1, MIR639, TECR	-1631, -9523, -9550	upstream, upstream, upstream	ActReg chr19 #8492	1	1	0
8493	19	14,639,488	14,640,906	1,418	1	9.333	10.556	12.556	20	19	19	1	2	2	MIR639, TECR	-158, -185	upstream, upstream	ActReg chr19 #8493	0	0	1
8494	19	14,671,987	14,672,406	419	1	2.083	3.308	13.615	4	5	21	0	0	2	TECR, NDUFB7	31814, 10690	in gene, downstream	ActReg chr19 #8494	0	0	1
8495	19	14,673,465	14,673,985	520	1	4.294	5.941	12.412	8	9	16	0	0	2	TECR, NDUFB7	33343, 9161	in gene, downstream	ActReg chr19 #8495	0	0	1
8496	19	14,674,058	14,674,844	786	1	5.917	6.167	11.5	8	11	15	0	0	2	TECR, NDUFB7	34069, 8435	in gene, downstream	ActReg chr19 #8496	0	0	1
8497	19	14,675,584	14,676,602	1,018	1	5.906	5.219	13.406	10	9	26	1	0	2	TECR, NDUFB7	35711, 6793	in gene, downstream	ActReg chr19 #8497	0	0	1
8498	19	14,682,214	14,683,391	1,177	3	26.417	32.25	9.694	83	99	19	1	1	2	TECR, NDUFB7	42420, 84	downstream, in gene	ActReg chr19 #8498	1	1	1
8499	19	15,121,483	15,122,127	644	1	5.2	5.5	12.8	10	8	23	1	1	1	CCDC105	266	in gene	ActReg chr19 #8499	0	0	1
8500	19	15,126,445	15,127,351	906	1	11.107	19.857	4.167	23	37	9	0	0	1	CCDC105	5,359	in gene	ActReg chr19 #8500	0	1	0
8501	19	15,197,598	15,198,711	1,113	1	7.029	12.543	5.353	18	25	8	0	1	1	OR1I1	277	in gene	ActReg chr19 #8501	0	1	0
8502	19	15,219,726	15,220,588	862	1	5.444	6.37	11.111	10	10	18	0	1	2	SYDE1, ILVBL	1943, 16420	in gene, downstream	ActReg chr19 #8502	0	0	1
8503	19	15,235,845	15,236,863	1,018	2	11.903	15.742	12.032	21	25	21	1	1	1	ILVBL	223	in gene	ActReg chr19 #8503	0	1	1
8504	19	15,271,387	15,272,458	1,071	1	5.176	6.676	14.441	9	13	19	0	0	1	NOTCH3	39,870	in gene	ActReg chr19 #8504	0	0	1
8505	19	15,289,117	15,290,083	966	1	6.065	7.161	12.516	10	12	21	0	0	1	NOTCH3	22,192	in gene	ActReg chr19 #8505	0	0	1
8506	19	15,297,422	15,298,264	842	1	4.077	4.885	12.385	7	7	18	0	0	1	NOTCH3	13,949	in gene	ActReg chr19 #8506	0	0	1
8507	19	15,324,426	15,325,002	576	1	4.222	5.556	12.389	7	8	20	0	0	0				ActReg chr19 #8507	0	0	1
8508	19	15,441,691	15,442,509	818	1	9.462	14.039	6.833	17	21	15	1	0	0				ActReg chr19 #8508	0	1	0
8509	19	15,465,754	15,466,188	434	1	5.786	4.5	13.5	9	7	22	0	0	1	AKAP8	24,632	in gene	ActReg chr19 #8509	0	0	1
8510	19	15,480,580	15,481,279	699	1	6.381	4.762	12.857	12	7	18	0	0	2	AKAP8, AKAP8L	9674, 48904	in gene, downstream	ActReg chr19 #8510	0	0	1
8511	19	15,489,515	15,491,515	2,000	3	10.71	13.677	8.458	27	27	20	1	1	2	AKAP8, AKAP8L	88, 39318	in gene, downstream	ActReg chr19 #8511	1	1	1
8512	19	15,529,222	15,530,286	1,064	2	16.273	12.939	6.727	29	24	10	1	1	2	AKAP8L, WIZ	79, 31008	in gene, downstream	ActReg chr19 #8512	1	1	0
8513	19	15,535,580	15,536,368	788	1	3.56	5.92	13.84	6	10	21	1	1	2	AKAP8L, WIZ	-6141, 24788	upstream, in gene	ActReg chr19 #8513	0	0	1
8514	19	15,543,438	15,544,097	659	2	18.048	25.333	7.941	32	55	12	1	0	1	WIZ	16,995	in gene	ActReg chr19 #8514	1	1	0
8515	19	15,547,462	15,547,957	495	1	4.733	5.067	12.667	7	10	21	0	0	1	WIZ	13,053	in gene	ActReg chr19 #8515	0	0	1
8516	19	15,586,364	15,587,343	979	1	3.613	4.581	11.387	5	7	20	0	0	1	PGLYRP2	3,462	in gene	ActReg chr19 #8516	0	0	1
8517	19	15,661,974	15,662,586	612	1	5.737	8.842	13.421	8	17	19	1	0	1	CYP4F22	42,944	in gene	ActReg chr19 #8517	0	0	1
8518	19	15,666,598	15,667,806	1,208	1	10.108	11.838	6.514	20	21	13	0	0	1	CYP4F22	47,866	downstream	ActReg chr19 #8518	0	1	0
8519	19	15,687,744	15,688,541	797	1	10.84	15.48	4.44	22	27	8	0	0	0				ActReg chr19 #8519	0	1	0
8520	19	15,733,954	15,735,149	1,195	2	13.297	15.46	4.656	29	41	12	0	0	1	CYP4F8	8,522	in gene	ActReg chr19 #8520	1	1	0
8521	19	15,739,844	15,740,278	434	1	7.692	7.538	11.769	13	10	19	0	0	1	CYP4F8	14,032	in gene	ActReg chr19 #8521	0	0	1
8522	19	15,880,213	15,880,958	745	1	9.522	15.13	5.652	17	30	8	0	0	1	LOC388514	10,213	in gene	ActReg chr19 #8522	0	1	0
8523	19	15,947,309	15,948,082	773	2	10.792	12.917	11.583	19	27	24	1	0	1	UCA1	7,938	downstream	ActReg chr19 #8523	0	1	1
8524	19	16,109,023	16,109,540	517	1	3.118	2.714	13.177	4	5	22	0	0	0				ActReg chr19 #8524	0	0	1
8525	19	16,129,619	16,130,222	603	1	6.158	5.316	11.316	8	10	14	0	1	2	LOC126536, LOC100507483	3476, -632	in gene, upstream	ActReg chr19 #8525	0	0	1
8526	19	16,130,811	16,131,275	464	1	4.8	5.333	14.867	8	10	24	0	1	2	LOC126536, LOC100507483	4599, 491	in gene, in gene	ActReg chr19 #8526	0	0	1
8527	19	16,133,509	16,133,990	481	1	5.733	2.643	12.933	10	5	22	0	0	3	LOC126536, LOC100507483, FLJ25328	7305, 3197, -9537	in gene, downstream, upstream	ActReg chr19 #8527	0	0	1
8528	19	16,134,108	16,134,487	379	1	6.833	9.333	11.833	11	13	15	0	0	3	LOC126536, LOC100507483, FLJ25328	7853, 3745, -8989	in gene, downstream, upstream	ActReg chr19 #8528	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8529	19	16,161,824	16,162,729	905	2	11.552	10.966	7.931	22	19	14	0	0	1	FLJ25328	18,990	downstream	ActReg chr19 #8529	1	1	0
8530	19	16,221,881	16,223,022	1,141	2	10.75	11.944	7.611	18	23	12	1	1	2	TPM4, RAB8A	44134, -39	downstream, upstream	ActReg chr19 #8530	1	1	0
8531	19	16,238,417	16,239,626	1,209	1	4.816	5.316	12.579	9	12	22	0	1	2	RAB8A, HSH2D	16531, -5817	in gene, upstream	ActReg chr19 #8531	0	0	1
8532	19	16,271,326	16,272,394	1,068	2	13.677	12.647	5.676	22	22	10	0	0	2	HSH2D, CIB3	27022, 12426	downstream, downstream	ActReg chr19 #8532	1	1	0
8533	19	16,308,178	16,309,134	956	1	13.1	6.6	8.414	21	12	15	1	1	2	FAM32A, AP1M1	12421, -9	downstream, upstream	ActReg chr19 #8533	1	0	0
8534	19	16,315,093	16,315,674	581	1	5	4	10.111	8	6	13	0	0	1	AP1M1	6,718	in gene	ActReg chr19 #8534	0	0	1
8535	19	16,318,477	16,318,957	480	1	2.467	5.733	12.733	4	9	19	0	0	1	AP1M1	10,052	in gene	ActReg chr19 #8535	0	0	1
8536	19	16,335,188	16,335,654	466	1	5.733	4.4	12.8	9	6	18	0	0	1	AP1M1	26,756	in gene	ActReg chr19 #8536	0	0	1
8537	19	16,337,930	16,339,099	1,169	1	5.333	6.556	14.111	10	11	18	0	0	1	AP1M1	29,849	in gene	ActReg chr19 #8537	0	0	1
8538	19	16,344,372	16,344,856	484	1	6.467	5.867	12.133	9	8	17	0	0	1	AP1M1	35,949	in gene	ActReg chr19 #8538	0	0	1
8539	19	16,404,306	16,404,992	686	1	11.818	7.773	5.727	18	15	10	0	0	0				ActReg chr19 #8539	1	0	0
8540	19	16,435,024	16,435,401	377	1	5.667	4.417	12.583	7	6	21	1	1	1	KLF2	-439	upstream	ActReg chr19 #8540	0	0	1
8541	19	16,448,521	16,450,408	1,887	2	10.237	13.441	10.508	21	19	22	0	0	0				ActReg chr19 #8541	0	1	1
8542	19	16,466,170	16,466,954	784	1	9.6	10.92	12.68	18	15	20	1	0	1	EPS15L1	116,200	downstream	ActReg chr19 #8542	0	0	1
8543	19	16,491,704	16,492,689	985	1	5.29	4.71	11.097	8	8	15	0	0	1	EPS15L1	90,566	in gene	ActReg chr19 #8543	0	0	1
8544	19	16,515,947	16,516,833	886	1	3.929	3.536	10.893	6	7	16	0	0	1	EPS15L1	66,372	in gene	ActReg chr19 #8544	0	0	1
8545	19	16,606,639	16,607,607	968	2	13.667	17.8	11.833	24	35	21	1	2	2	CALR3, C19orf44	-120, -82	upstream, upstream	ActReg chr19 #8545	0	1	1
8546	19	16,630,861	16,631,754	893	1	3.607	5.12	13.286	8	11	18	0	0	2	C19orf44, CHERP	24102, 21956	in gene, in gene	ActReg chr19 #8546	0	0	1
8547	19	16,635,888	16,636,396	508	1	6.75	5.938	12.562	11	9	20	1	0	2	C19orf44, CHERP	28937, 17121	downstream, in gene	ActReg chr19 #8547	0	0	1
8548	19	16,640,855	16,641,588	733	1	7	4.826	12.609	10	10	18	1	0	2	C19orf44, CHERP	34016, 12042	downstream, in gene	ActReg chr19 #8548	0	0	1
8549	19	16,643,223	16,644,242	1,019	1	5.156	6.875	13.906	9	10	19	1	0	1	CHERP	9,531	in gene	ActReg chr19 #8549	0	0	1
8550	19	16,652,769	16,653,842	1,073	3	11.818	13.061	13.273	19	25	23	1	1	2	CHERP, SLC35E1	-42, 29888	upstream, downstream	ActReg chr19 #8550	1	1	1
8551	19	16,687,392	16,688,216	824	1	3.609	6.5	13.077	6	9	17	0	1	2	SLC35E1, MED26	-4611, 51211	upstream, in gene	ActReg chr19 #8551	0	0	1
8552	19	16,738,281	16,738,790	509	1	4.875	12.188	10.062	7	18	14	1	1	2	MED26, LOC100507522	480, 18267	in gene, downstream	ActReg chr19 #8552	0	0	1
8553	19	16,739,074	16,739,913	839	2	9.577	12.769	10.36	18	21	21	1	1	2	MED26, LOC100507522	-478, 17309	upstream, downstream	ActReg chr19 #8553	0	1	1
8554	19	16,770,530	16,771,946	1,416	2	17.023	13.273	8.767	37	31	18	1	2	2	C19orf42, TMEM38A	-270, -700	upstream, upstream	ActReg chr19 #8554	1	1	0
8555	19	16,838,027	16,838,664	637	1	4.6	4.7	12.9	9	9	21	0	0	1	NWD1	7,558	in gene	ActReg chr19 #8555	0	0	1
8556	19	16,850,203	16,850,929	726	1	7.261	14.304	3.5	11	29	6	0	0	1	NWD1	19,779	in gene	ActReg chr19 #8556	0	1	0
8557	19	16,869,187	16,870,591	1,404	1	8.093	15.07	7.605	16	33	18	0	0	1	NWD1	39,102	in gene	ActReg chr19 #8557	0	1	0
8558	19	16,918,345	16,919,120	775	1	4.458	4.75	11.333	8	9	16	1	0	1	NWD1	87,945	in gene	ActReg chr19 #8558	0	0	1
8559	19	16,979,958	16,981,015	1,057	1	4.167	6.188	12.061	6	10	18	0	0	1	SIN3B	40,268	in gene	ActReg chr19 #8559	0	0	1
8560	19	16,983,401	16,984,238	837	1	5.962	3.077	13.115	9	5	17	0	0	1	SIN3B	43,601	in gene	ActReg chr19 #8560	0	0	1
8561	19	16,986,789	16,987,802	1,013	1	7.419	8.903	14.452	10	16	23	1	0	1	SIN3B	47,077	in gene	ActReg chr19 #8561	0	0	1
8562	19	16,988,602	16,989,206	604	1	7.316	7.526	12.474	10	12	17	1	0	1	SIN3B	48,686	in gene	ActReg chr19 #8562	0	0	1
8563	19	16,991,543	16,992,151	608	1	4.947	6.105	14.526	9	9	24	0	0	2	SIN3B, F2RL3	51629, -7979	downstream, upstream	ActReg chr19 #8563	0	0	1
8564	19	16,999,619	17,000,536	917	1	6.857	5.296	11.714	12	10	16	1	1	3	SIN3B, F2RL3, CPAMD8	59859, 251, 137548	downstream, in gene, downstream	ActReg chr19 #8564	0	0	1
8565	19	17,125,563	17,126,046	483	1	4.6	3.933	10.8	6	7	14	0	0	1	CPAMD8	11,821	in gene	ActReg chr19 #8565	0	0	1
8566	19	17,185,198	17,186,779	1,581	2	16.082	23.918	8.388	60	80	15	1	2	2	HAUS8, MYO9B	355, -603	in gene, upstream	ActReg chr19 #8566	1	1	0
8567	19	17,190,331	17,191,483	1,152	1	9.167	11.167	6.278	14	23	10	0	1	2	HAUS8, MYO9B	-4564, 4316	upstream, in gene	ActReg chr19 #8567	0	1	0
8568	19	17,202,246	17,202,808	562	1	6	4.412	12.647	8	7	18	0	0	1	MYO9B	15,936	in gene	ActReg chr19 #8568	0	0	1
8569	19	17,213,064	17,213,579	515	1	5.688	6.875	11.75	8	10	18	1	0	1	MYO9B	26,730	in gene	ActReg chr19 #8569	0	0	1
8570	19	17,218,134	17,219,334	1,200	2	14.421	12.21	6.553	22	20	13	0	0	1	MYO9B	32,143	in gene	ActReg chr19 #8570	1	1	0
8571	19	17,246,065	17,246,868	803	1	12.72	8.76	5.72	20	13	10	0	0	1	MYO9B	59,875	in gene	ActReg chr19 #8571	1	0	0
8572	19	17,291,767	17,292,348	581	1	4.778	7	13.111	9	10	16	0	0	1	MYO9B	105,466	in gene	ActReg chr19 #8572	0	0	1
8573	19	17,305,739	17,306,541	802	1	4.76	5.76	13.88	11	10	21	0	0	1	MYO9B	119,549	in gene	ActReg chr19 #8573	0	0	1
8574	19	17,312,755	17,313,432	677	1	6.81	7.762	12.714	9	10	19	0	0	1	MYO9B	126,502	in gene	ActReg chr19 #8574	0	0	1
8575	19	17,315,998	17,316,871	873	1	5.607	5.214	13.107	9	8	19	1	0	2	MYO9B, USE1	129843, -9721	in gene, upstream	ActReg chr19 #8575	0	0	1
8576	19	17,322,086	17,322,651	565	1	2.733	4	13.353	4	9	20	1	1	2	MYO9B, USE1	135777, -3787	in gene, upstream	ActReg chr19 #8576	0	0	1
8577	19	17,325,753	17,326,538	785	1	9.56	14.88	9.16	18	29	13	1	1	2	MYO9B, USE1	139554, -10	downstream, upstream	ActReg chr19 #8577	0	1	0
8578	19	17,336,747	17,337,802	1,055	3	16.061	15.515	13.182	37	38	26	1	1	3	USE1, OCEL1, NR2F6	11119, 219, 18877	downstream, in gene, downstream	ActReg chr19 #8578	1	1	1
8579	19	17,346,090	17,346,916	826	2	11.833	14.308	6.278	23	28	13	1	0	2	OCEL1, NR2F6	9448, 9648	downstream, in gene	ActReg chr19 #8579	1	1	0
8580	19	17,357,270	17,357,869	599	1	8.053	6.737	12.421	11	11	20	1	1	2	NR2F6, USHBP1	-1418, 17975	upstream, downstream	ActReg chr19 #8580	0	0	1
8581	19	17,358,994	17,359,702	708	1	7.591	13	8.909	11	19	12	0	1	2	NR2F6, USHBP1	-3197, 16196	upstream, downstream	ActReg chr19 #8581	0	1	0
8582	19	17,402,573	17,404,271	1,698	2	7.755	10.679	9.189	14	17	18	1	0	2	ANKLE1, ABHD8	10968, 10860	downstream, in gene	ActReg chr19 #8582	0	1	1
8583	19	17,413,462	17,414,678	1,216	3	11.842	13.763	10.21	33	30	18	1	3	3	ABHD8, MRPL34, DDA1	212, -2407, -6267	in gene, upstream, upstream	ActReg chr19 #8583	1	1	1
8584	19	17,416,003	17,417,499	1,496	2	10.022	13.283	9.217	19	24	22	1	3	3	ABHD8, MRPL34, DDA1	-2469, 274, -3586	upstream, in gene, upstream	ActReg chr19 #8584	0	1	1
8585	19	17,419,970	17,420,864	894	2	7.25	12.071	11.286	11	19	17	1	2	3	ABHD8, MRPL34, DDA1	-6135, 3940, 80	upstream, downstream, in gene	ActReg chr19 #8585	0	1	1
8586	19	17,435,512	17,436,010	498	1	4.688	3.125	13.625	8	6	20	0	0	2	DDA1, ANO8	15424, 9877	downstream, in gene	ActReg chr19 #8586	0	0	1
8587	19	17,437,962	17,438,812	850	1	5.192	6	14.462	8	13	19	1	0	3	DDA1, ANO8, GTPBP3	18050, 7251, -9969	downstream, in gene, upstream	ActReg chr19 #8587	0	0	1
8588	19	17,444,704	17,446,426	1,722	2	13.537	15.296	5.462	36	37	17	2	2	2	ANO8, GTPBP3	73, -2791	in gene, upstream	ActReg chr19 #8588	1	1	0
8589	19	17,447,255	17,449,156	1,901	3	10.883	14.783	8.617	22	31	16	2	2	2	ANO8, GTPBP3	-2567, -151	upstream, upstream	ActReg chr19 #8589	1	1	1
8590	19	17,496,561	17,497,067	506	1	5.688	7.312	12.25	9	12	20	0	0	1	PLVAP	-8,677	upstream	ActReg chr19 #8590	0	0	1
8591	19	17,529,968	17,531,731	1,763	2	11.854	12.782	7.055	19	22	15	1	1	2	LOC100507535, FAM125A	14299, -63	in gene, upstream	ActReg chr19 #8591	1	1	0
8592	19	17,585,985	17,587,044	1,059	2	11.182	11.394	6.667	17	19	11	0	0	1	SLC27A1	5,214	in gene	ActReg chr19 #8592	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIsIandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8593	19	17,618,392	17,619,436	1,044	1	9.788	14.121	5.667	15	22	13	0	2	3	SLC27A1, LOC100507551, PQLS	37614, -5641, -3518	downstream, upstream, upstream	ActReg chr19 #8593	0	1	0
8594	19	17,622,028	17,623,463	1,435	3	16.489	16.2	13.378	34	35	22	1	1	3	SLC27A1, LOC100507551, PQLS	41445, -9472, 313	downstream, upstream, in gene	ActReg chr19 #8594	1	1	1
8595	19	17,649,528	17,650,862	1,334	3	11.952	12.238	8.881	22	19	18	1	0	1	FAM129C	16,085	in gene	ActReg chr19 #8595	1	1	1
8596	19	17,665,739	17,667,466	1,727	4	16.444	20.093	10.365	37	36	25	1	1	2	FAM129C, GLT25D1	32492, 91	downstream, in gene	ActReg chr19 #8596	1	1	1
8597	19	17,691,363	17,691,825	462	1	3.714	5	13.143	5	7	16	1	0	1	GLT25D1	25,083	in gene	ActReg chr19 #8597	0	0	1
8598	19	17,693,394	17,693,949	555	1	3.412	3.941	13.294	7	6	21	0	0	1	GLT25D1	27,160	in gene	ActReg chr19 #8598	0	0	1
8599	19	17,716,613	17,717,625	1,012	1	13.581	15.581	9.067	28	28	20	1	0	1	UNC13A	81,889	in gene	ActReg chr19 #8599	0	1	0
8600	19	17,757,938	17,758,528	590	1	4.842	6.632	10.842	7	11	15	1	0	1	UNC13A	40,775	in gene	ActReg chr19 #8600	0	0	1
8601	19	17,759,710	17,760,330	620	1	6.35	3.5	10.4	8	6	14	0	0	1	UNC13A	38,988	in gene	ActReg chr19 #8601	0	0	1
8602	19	17,790,316	17,791,654	1,338	2	11.286	12.595	7	22	20	17	1	0	1	UNC13A	8,023	in gene	ActReg chr19 #8602	1	1	0
8603	19	17,792,134	17,793,615	1,481	3	12.087	13.239	8.37	27	25	16	0	0	1	UNC13A	6,134	in gene	ActReg chr19 #8603	1	1	1
8604	19	17,797,071	17,799,825	2,754	3	16.384	21.802	9.927	34	44	21	2	1	1	UNC13A	560	in gene	ActReg chr19 #8604	1	1	1
8605	19	17,829,461	17,830,490	1,029	1	9.875	12.5	6.844	16	18	16	1	1	1	MAP1S	-328	upstream	ActReg chr19 #8605	0	1	0
8606	19	17,830,633	17,831,259	626	1	9.737	8.947	14.632	12	14	20	1	1	1	MAP1S	643	in gene	ActReg chr19 #8606	0	0	1
8607	19	17,836,386	17,837,184	798	1	4.88	3.32	13	11	5	20	1	0	1	MAP1S	6,482	in gene	ActReg chr19 #8607	0	0	1
8608	19	17,838,002	17,838,553	551	1	5.353	6.882	13	7	10	19	1	0	1	MAP1S	7,974	in gene	ActReg chr19 #8608	0	0	1
8609	19	17,843,690	17,844,364	674	1	4.238	6.476	11.905	6	9	16	0	0	1	MAP1S	13,724	in gene	ActReg chr19 #8609	0	0	1
8610	19	17,875,107	17,875,429	322	1	5.8	5.4	11.2	7	7	15	0	0	1	FCHO1	16,741	in gene	ActReg chr19 #8610	0	0	1
8611	19	17,881,147	17,881,593	446	1	3.429	4.786	13	5	9	17	0	0	1	FCHO1	22,843	in gene	ActReg chr19 #8611	0	0	1
8612	19	17,918,416	17,919,005	589	1	4	3.444	11.389	8	6	15	1	1	3	B3GNT3, LOC100507578, INSL3	12791, 400, 13610	in gene, in gene, downstream	ActReg chr19 #8612	0	0	1
8613	19	17,931,876	17,932,513	637	1	5.714	5.35	10.6	7	10	16	1	1	3	B3GNT3, INSL3, JAK3	26275, 126, 26647	downstream, in gene, downstream	ActReg chr19 #8613	0	0	1
8614	19	17,941,985	17,942,608	623	1	5.211	4	14.368	8	8	23	1	0	2	INSL3, JAK3	-9976, 16545	upstream, in gene	ActReg chr19 #8614	0	0	1
8615	19	17,953,037	17,954,398	1,361	1	8.476	10.595	14.595	23	19	26	1	0	1	JAK3	5,124	in gene	ActReg chr19 #8615	0	0	1
8616	19	17,970,145	17,971,432	1,287	3	13.45	13.325	11.725	23	24	31	1	2	2	RPL18A, SNORA68	57, -2609	in gene, upstream	ActReg chr19 #8616	1	1	1
8617	19	17,974,889	17,975,573	684	1	7	8.333	11.667	14	14	16	0	2	3	RPL18A, SNORA68, SLC5A5	4500, 1834, -7551	downstream, downstream, upstream	ActReg chr19 #8617	0	0	1
8618	19	17,983,398	17,984,026	628	1	2.526	6.421	10.684	4	10	17	1	1	3	RPL18A, SNORA68, SLC5A5	12981, 10315, 930	downstream, downstream, in gene	ActReg chr19 #8618	0	0	1
8619	19	17,984,394	17,985,043	649	1	3.75	4.9	11.8	6	8	16	1	1	1	SLC5A5	1,936	in gene	ActReg chr19 #8619	0	0	1
8620	19	17,991,400	17,991,855	455	1	1.929	3.929	13.071	3	5	17	0	0	1	SLC5A5	8,845	in gene	ActReg chr19 #8620	0	0	1
8621	19	17,992,365	17,992,905	540	1	5.235	8.118	14.059	8	12	21	0	0	1	SLC5A5	9,853	in gene	ActReg chr19 #8621	0	0	1
8622	19	17,999,979	18,001,347	1,368	2	19.861	25.419	7.395	60	72	11	0	0	1	SLC5A5	17,881	in gene	ActReg chr19 #8622	1	1	0
8623	19	18,043,146	18,044,218	1,072	2	13.939	14.454	9.364	23	24	14	1	1	1	CCDC124	-142	upstream	ActReg chr19 #8623	1	1	0
8624	19	18,078,297	18,078,822	525	1	5.706	5.765	14.941	12	9	22	1	0	1	KCNN1	16,448	in gene	ActReg chr19 #8624	0	0	1
8625	19	18,119,318	18,120,107	789	1	5.96	7.44	11.76	9	11	18	1	0	2	KCNN1, ARRDC2	57601, 7768	downstream, in gene	ActReg chr19 #8625	0	0	1
8626	19	18,220,032	18,220,669	637	1	4.95	6.15	10.8	9	9	14	1	0	1	MAST3	11,747	in gene	ActReg chr19 #8626	0	0	1
8627	19	18,221,018	18,221,502	484	1	9.533	9.067	12.333	14	12	16	1	0	1	MAST3	12,657	in gene	ActReg chr19 #8627	0	0	1
8628	19	18,248,128	18,248,619	491	1	3.062	3.846	12.312	6	7	21	0	0	1	MAST3	39,770	in gene	ActReg chr19 #8628	0	0	1
8629	19	18,267,306	18,268,247	941	1	7.103	8.345	14.172	13	11	24	0	0	2	MAST3, PIK3R2	59173, 3760	downstream, in gene	ActReg chr19 #8629	0	0	1
8630	19	18,279,529	18,280,089	560	1	6.294	7.059	14.353	12	11	23	1	1	2	PIK3R2, IFI30	15793, -4770	in gene, upstream	ActReg chr19 #8630	0	0	1
8631	19	18,285,823	18,286,160	337	1	6.455	9.182	12.818	8	12	19	0	1	2	PIK3R2, IFI30	21975, 1412	downstream, in gene	ActReg chr19 #8631	0	0	1
8632	19	18,336,299	18,336,895	596	1	6.111	6.333	12.167	10	8	17	1	0	1	PDE4C	22,413	in gene	ActReg chr19 #8632	0	0	1
8633	19	18,343,208	18,345,360	2,152	3	26.791	33.478	9.045	72	81	17	1	0	1	PDE4C	14,726	in gene	ActReg chr19 #8633	1	1	1
8634	19	18,367,873	18,369,334	1,461	1	4.364	7.178	15.867	9	12	25	1	0	2	PDE4C, KIAA1683	-9593, 16716	upstream, in gene	ActReg chr19 #8634	0	0	1
8635	19	18,371,231	18,372,106	875	1	6.607	8.679	11.929	10	17	16	0	0	1	KIAA1683	13,651	in gene	ActReg chr19 #8635	0	0	1
8636	19	18,375,174	18,375,973	799	1	6.32	3.24	14.6	11	7	19	0	0	1	KIAA1683	9,746	in gene	ActReg chr19 #8636	0	0	1
8637	19	18,377,747	18,378,327	580	1	5.778	6.278	12.056	8	9	18	0	0	1	KIAA1683	7,282	in gene	ActReg chr19 #8637	0	0	1
8638	19	18,385,539	18,386,418	879	1	11.037	13.185	7.63	16	21	10	0	2	3	KIAA1683, JUND, MIR3188	-659, 6454, -6909	upstream, downstream, upstream	ActReg chr19 #8638	0	1	0
8639	19	18,390,142	18,390,672	530	1	9.235	10.177	13.588	15	17	22	1	3	3	KIAA1683, JUND, MIR3188	-5088, 2025, -2480	upstream, downstream, upstream	ActReg chr19 #8639	0	0	1
8640	19	18,390,825	18,391,729	904	1	10.84	11.286	7.107	17	20	18	1	3	3	KIAA1683, JUND, MIR3188	-5958, 1155, -1610	upstream, in gene, upstream	ActReg chr19 #8640	0	1	0
8641	19	18,392,396	18,393,681	1,285	2	12.275	8.4	10.179	24	12	22	1	3	3	KIAA1683, JUND, MIR3188	-7719, -606, 151	upstream, upstream, downstream	ActReg chr19 #8641	1	0	1
8642	19	18,402,089	18,404,414	2,325	2	12.708	16.25	8.056	28	37	17	1	0	2	JUND, MIR3188	-10819, 10364	upstream, downstream	ActReg chr19 #8642	1	1	0
8643	19	18,411,708	18,412,502	794	1	10.92	13.44	9.56	24	24	17	0	0	1	LSM4	21,896	downstream	ActReg chr19 #8643	0	1	0
8644	19	18,417,009	18,417,740	731	1	5.957	7.13	10.783	10	9	15	0	0	1	LSM4	16,627	downstream	ActReg chr19 #8644	0	0	1
8645	19	18,418,775	18,419,541	766	1	2.652	5.5	15.667	6	7	22	0	0	1	LSM4	14,843	in gene	ActReg chr19 #8645	0	0	1
8646	19	18,420,004	18,421,002	998	1	7.387	5.613	13.258	13	7	19	1	0	1	LSM4	13,498	in gene	ActReg chr19 #8646	0	0	1
8647	19	18,422,592	18,423,390	798	1	4.08	6.56	13.96	6	11	22	0	0	1	LSM4	11,010	in gene	ActReg chr19 #8647	0	0	1
8648	19	18,433,483	18,434,480	997	2	11.774	11.419	8.452	18	21	18	1	1	1	LSM4	20	in gene	ActReg chr19 #8648	1	0	1
8649	19	18,439,191	18,439,859	668	1	9.714	12.191	5.476	16	20	13	0	1	1	LSM4	-5,524	upstream	ActReg chr19 #8649	0	1	0
8650	19	18,451,367	18,452,199	832	1	10.077	10.192	15.154	14	13	22	1	1	1	PGPEP1	375	in gene	ActReg chr19 #8650	0	0	1
8651	19	18,470,487	18,470,912	425	1	5	4.714	10.714	8	7	16	0	0	1	PGPEP1	19,291	in gene	ActReg chr19 #8651	0	0	1
8652	19	18,484,901	18,485,649	748	1	14	12.435	2.6	25	21	8	0	0	1	PGPEP1	33,867	downstream	ActReg chr19 #8652	1	0	0
8653	19	18,527,232	18,530,386	3,154	3	10.889	12.98	10.023	21	21	27	1	1	1	SSBP4	-1,412	upstream	ActReg chr19 #8653	1	1	1
8654	19	18,530,646	18,531,375	729	1	10.826	11.435	11.522	17	16	17	1	1	1	SSBP4	789	in gene	ActReg chr19 #8654	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8655	19	18,535,895	18,536,692	797	1	5.08	2.96	14.12	8	6	22	0	0	2	SSBP4, ISYNA1	6072, 12818	in gene, downstream	ActReg chr19 #8655	0	0	1
8656	19	18,541,311	18,541,852	541	1	4.412	7.882	14.235	6	13	18	0	0	2	SSBP4, ISYNA1	11360, 7530	in gene, downstream	ActReg chr19 #8656	0	0	1
8657	19	18,542,178	18,542,804	626	1	5.842	6.923	13.421	9	15	25	0	0	2	SSBP4, ISYNA1	12270, 6620	in gene, downstream	ActReg chr19 #8657	0	0	1
8658	19	18,545,614	18,546,381	767	1	2.667	5.583	13.125	5	8	18	1	0	3	SSBP4, ISYNA1, ELL	15776, 3114, 86940	downstream, in gene, downstream	ActReg chr19 #8658	0	0	1
8659	19	18,546,747	18,547,894	1,147	1	5.972	10.167	14.583	9	15	23	1	1	3	SSBP4, ISYNA1, ELL	17099, 1791, 85617	downstream, in gene, downstream	ActReg chr19 #8659	0	0	1
8660	19	18,549,005	18,549,953	948	1	9.567	5.2	14.733	13	8	22	1	1	3	SSBP4, ISYNA1, ELL	19258, -368, 83458	downstream, upstream, downstream	ActReg chr19 #8660	0	0	1
8661	19	18,580,329	18,580,921	592	1	6.889	5.611	13.944	10	7	19	0	0	1	ELL	52,312	in gene	ActReg chr19 #8661	0	0	1
8662	19	18,595,887	18,596,643	756	1	3.542	6.5	10.625	5	10	14	0	0	1	ELL	36,672	in gene	ActReg chr19 #8662	0	0	1
8663	19	18,598,603	18,599,423	820	1	5	7.24	12.12	10	12	17	0	0	1	ELL	33,924	in gene	ActReg chr19 #8663	0	0	1
8664	19	18,630,765	18,631,681	916	2	13.828	12.241	5	26	28	10	0	1	1	ELL	1,715	in gene	ActReg chr19 #8664	1	1	0
8665	19	18,632,302	18,633,797	1,495	2	37.766	36.723	5.565	125	120	16	1	1	2	ELL, FKBP8	-112, 21334	upstream, downstream	ActReg chr19 #8665	1	1	0
8666	19	18,642,826	18,643,658	832	1	4.538	6.654	12.654	7	11	17	0	0	2	ELL, FKBP8	-10305, 11141	upstream, in gene	ActReg chr19 #8666	0	0	1
8667	19	18,682,219	18,683,217	998	1	12.903	13.806	8.677	23	28	14	1	1	2	C19orf50, UBA52	14146, 104	downstream, in gene	ActReg chr19 #8667	0	1	0
8668	19	18,698,824	18,700,746	1,922	2	21.433	24.7	7.767	69	76	14	1	1	2	C19orf60, CRLF1	290, 17875	in gene, downstream	ActReg chr19 #8668	1	1	0
8669	19	18,702,637	18,703,273	636	1	5.75	5.4	12.15	9	9	17	0	0	2	C19orf60, CRLF1	3460, 14705	in gene, downstream	ActReg chr19 #8669	0	0	1
8670	19	18,716,022	18,716,590	568	1	6.556	9.167	12.889	11	13	17	1	2	2	CRLF1, TMEM59L	1354, -7376	in gene, upstream	ActReg chr19 #8670	0	0	1
8671	19	18,718,085	18,719,030	945	1	8.586	8.897	11.862	15	15	17	1	2	2	CRLF1, TMEM59L	-897, -5125	upstream, upstream	ActReg chr19 #8671	0	0	1
8672	19	18,722,532	18,723,620	1,088	1	6.467	7.853	12.853	12	12	16	1	2	2	CRLF1, TMEM59L	-5416, -606	upstream, upstream	ActReg chr19 #8672	0	0	1
8673	19	18,747,865	18,748,270	405	1	7	5.077	13.308	9	6	18	0	1	1	KLHL26	229	in gene	ActReg chr19 #8673	0	0	1
8674	19	18,770,373	18,772,232	1,859	1	10.393	12.672	10.034	31	22	20	1	0	1	KLHL26	23,464	in gene	ActReg chr19 #8674	0	1	0
8675	19	18,773,237	18,774,211	974	1	6.71	6.355	13.065	11	9	17	0	0	1	KLHL26	25,886	in gene	ActReg chr19 #8675	0	0	1
8676	19	18,819,861	18,820,851	990	1	5.097	6.71	12.645	10	10	20	0	0	1	CRTC1	25,931	in gene	ActReg chr19 #8676	0	0	1
8677	19	18,846,051	18,846,881	830	1	4.077	5.385	12.115	7	9	18	0	0	1	CRTC1	52,041	in gene	ActReg chr19 #8677	0	0	1
8678	19	18,854,034	18,854,900	866	1	6.074	4.222	15.37	11	7	26	0	0	1	CRTC1	60,042	in gene	ActReg chr19 #8678	0	0	1
8679	19	18,855,906	18,856,840	934	1	3.793	3.793	14.483	7	7	26	0	0	1	CRTC1	61,948	in gene	ActReg chr19 #8679	0	0	1
8680	19	18,857,438	18,858,011	573	1	2.222	3.118	14.5	3	5	24	0	0	1	CRTC1	63,299	in gene	ActReg chr19 #8680	0	0	1
8681	19	18,872,359	18,873,261	902	1	4.893	4.357	11.714	9	11	17	1	0	1	CRTC1	78,385	in gene	ActReg chr19 #8681	0	0	1
8682	19	18,874,492	18,875,189	697	1	9.773	12.046	13.227	14	19	20	0	0	1	CRTC1	80,415	in gene	ActReg chr19 #8682	0	0	1
8683	19	18,878,818	18,879,420	602	1	4.667	5.5	13.444	9	8	18	0	0	1	CRTC1	84,694	in gene	ActReg chr19 #8683	0	0	1
8684	19	18,879,721	18,880,792	1,071	1	5.273	5.727	14.061	10	10	20	0	0	1	CRTC1	85,831	in gene	ActReg chr19 #8684	0	0	1
8685	19	18,885,743	18,887,463	1,720	1	6.278	7.407	14.463	11	17	23	1	0	2	CRTC1, COMP	92178, 15511	in gene, downstream	ActReg chr19 #8685	0	0	1
8686	19	18,890,857	18,891,790	933	1	4.207	3.739	12.862	8	9	21	0	0	2	CRTC1, COMP	96898, 10791	in gene, downstream	ActReg chr19 #8686	0	0	1
8687	19	18,901,266	18,902,318	1,052	1	6.758	5.545	13.879	11	11	20	1	1	2	CRTC1, COMP	107367, 322	downstream, in gene	ActReg chr19 #8687	0	0	1
8688	19	18,911,441	18,912,170	729	1	4.043	5.391	12.13	6	9	20	0	0	1	COMP	-9,691	upstream	ActReg chr19 #8688	0	0	1
8689	19	18,918,533	18,919,076	543	1	6.412	4.824	13.059	10	7	19	0	0	0				ActReg chr19 #8689	0	0	1
8690	19	18,942,202	18,943,213	1,011	2	12.188	9.781	4.962	27	15	9	1	1	1	UPF1	-37	upstream	ActReg chr19 #8690	1	1	0
8691	19	18,966,392	18,967,484	1,092	1	5.118	4.912	13.529	10	9	20	0	0	1	UPF1	24,194	in gene	ActReg chr19 #8691	0	0	1
8692	19	18,975,690	18,976,394	704	1	3.864	4.579	11.182	8	7	15	0	0	4	UPF1, LASS1-GDF1, GDF1, LASS1	33298, 30911, 30911, 30911	in gene, downstream, downstream, downstream	ActReg chr19 #8692	0	0	1
8693	19	18,994,747	18,995,137	390	1	8.769	4.385	11.308	12	9	16	0	0	3	LASS1-GDF1, GDF1, LASS1	12011, 12011, 12011	in gene, in gene, in gene	ActReg chr19 #8693	0	0	1
8694	19	19,005,106	19,006,184	1,078	1	10	11.471	11.735	19	22	19	1	3	4	LASS1-GDF1, GDF1, LASS1, COPE	1308, 1308, 1308, 24554	in gene, in gene, in gene, downstream	ActReg chr19 #8694	0	0	1
8695	19	19,015,250	19,016,324	1,074	1	2.833	9.382	12.853	7	15	20	0	0	4	LASS1-GDF1, GDF1, LASS1, COPE	-8834, -8834, -8834, 14412	upstream, upstream, upstream, in gene	ActReg chr19 #8695	0	0	1
8696	19	19,029,649	19,031,037	1,388	2	13.861	13.93	7.558	22	26	13	1	2	3	COPE, DDX49, HOMER3	-144, -141, 21698	upstream, upstream, downstream	ActReg chr19 #8696	1	1	0
8697	19	19,032,298	19,033,451	1,153	1	5.111	5.889	12.917	10	10	17	0	2	3	COPE, DDX49, HOMER3	-2675, 2390, 19167	upstream, in gene, downstream	ActReg chr19 #8697	0	0	1
8698	19	19,038,602	19,039,189	587	1	7.056	6.444	11.778	11	10	15	0	0	3	COPE, DDX49, HOMER3	-8696, 8411, 13146	upstream, in gene, downstream	ActReg chr19 #8698	0	0	1
8699	19	19,039,982	19,040,473	491	1	6.2	4.4	12.133	10	7	17	1	0	3	COPE, DDX49, HOMER3	-10028, 9743, 11814	upstream, downstream, in gene	ActReg chr19 #8699	0	0	1
8700	19	19,041,881	19,042,851	970	1	3.645	4.774	11.355	7	8	18	1	0	2	DDX49, HOMER3	11882, 9675	downstream, in gene	ActReg chr19 #8700	0	0	1
8701	19	19,050,994	19,051,553	559	1	8.778	10.722	13.611	13	16	17	1	1	1	HOMER3	768	in gene	ActReg chr19 #8701	0	0	1
8702	19	19,059,288	19,060,086	798	1	4.84	5.84	12.48	7	10	21	0	1	1	HOMER3	-7,646	upstream	ActReg chr19 #8702	0	0	1
8703	19	19,144,179	19,144,964	785	2	14.8	13.32	5.56	26	24	10	1	2	2	SFRS14, ARMC6	-191, 100	upstream, in gene	ActReg chr19 #8703	1	1	0
8704	19	19,153,382	19,154,496	1,114	1	3.794	5.914	11.886	7	11	17	0	0	2	SFRS14, ARMC6	-9559, 9468	upstream, in gene	ActReg chr19 #8704	0	0	1
8705	19	19,162,863	19,163,387	524	1	5.25	5.6	12.938	8	12	21	0	0	1	ARMC6	18,654	in gene	ActReg chr19 #8705	0	0	1
8706	19	19,169,722	19,170,433	711	1	3.478	4.348	12.217	6	7	16	0	1	2	ARMC6, SLC25A42	25606, -4726	downstream, upstream	ActReg chr19 #8706	0	0	1
8707	19	19,173,858	19,175,076	1,218	1	9.2	13.895	8.263	17	22	14	1	1	2	ARMC6, SLC25A42	29996, -336	downstream, upstream	ActReg chr19 #8707	0	1	0
8708	19	19,248,541	19,249,126	585	1	8	7.737	11.526	10	13	17	1	1	3	TMEM161A, LOC729991-MEF2B, MEF2B	434, 54567, 32265	in gene, downstream, downstream	ActReg chr19 #8708	0	0	1
8709	19	19,256,208	19,257,126	918	1	3.379	5.552	14.448	6	7	24	1	1	3	TMEM161A, LOC729991-MEF2B, MEF2B	-7400, 46733, 24431	upstream, in gene, in gene	ActReg chr19 #8709	0	0	1
8710	19	19,271,427	19,271,959	532	1	5.75	4.188	13.188	10	5	20	0	0	2	LOC729991-MEF2B, MEF2B	31707, 9405	in gene, in gene	ActReg chr19 #8710	0	0	1
8711	19	19,280,909	19,281,741	832	1	5.462	8.154	12	8	13	23	1	1	3	LOC729991-MEF2B, MEF2B, LOC729991	22075, -227, 22075	in gene, upstream, downstream	ActReg chr19 #8711	0	0	1
8712	19	19,296,370	19,296,932	562	1	4.438	6.111	12.889	9	10	20	0	1	3	LOC729991-MEF2B, LOC729991, RFXANK	6749, 6749, -6557	in gene, in gene, upstream	ActReg chr19 #8712	0	0	1
8713	19	19,302,305	19,303,980	1,675	3	19.365	22.365	9.942	54	49	20	2	3	4	LOC729991-MEF2B, LOC729991, RFXANK, NR2C2AP	258, 258, 134, 11096	in gene, in gene, in gene, downstream	ActReg chr19 #8713	1	1	1
8714	19	19,313,563	19,314,566	1,003	3	12.5	13.625	12.406	24	27	17	1	1	3	RFXANK, NR2C2AP, NCAN	11056, 174, -8718	downstream, in gene, upstream	ActReg chr19 #8714	1	1	1
8715	19	19,325,501	19,326,258	757	1	12.917	10.958	8.417	27	23	16	0	0	1	NCAN	3,097	in gene	ActReg chr19 #8715	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8716	19	19,334,746	19,335,132	386	1	6.583	4.75	12.25	11	7	16	0	0	1	NCAN	12,157	in gene	ActReg chr19 #8716	0	0	1
8717	19	19,348,712	19,349,343	631	1	4	4.053	12.526	6	7	17	0	0	1	NCAN	26,245	in gene	ActReg chr19 #8717	0	0	1
8718	19	19,431,012	19,432,215	1,203	2	10.432	18.865	8.595	15	27	14	1	2	2	SF4, KIAA0892	-306, -17	upstream, upstream	ActReg chr19 #8718	1	1	0
8719	19	19,445,516	19,446,332	816	1	5.72	6.4	12.2	10	9	16	0	0	1	KIAA0892	14,294	in gene	ActReg chr19 #8719	0	0	1
8720	19	19,495,866	19,496,730	864	1	11.889	11.593	14.185	17	18	22	1	1	1	GATAD2A	-344	upstream	ActReg chr19 #8720	0	0	1
8721	19	19,496,853	19,497,645	792	1	6.12	6.92	13	9	11	22	1	1	1	GATAD2A	607	in gene	ActReg chr19 #8721	0	0	1
8722	19	19,515,896	19,516,662	766	2	14.583	14	7.65	33	32	14	1	0	1	GATAD2A	19,637	in gene	ActReg chr19 #8722	1	1	0
8723	19	19,613,713	19,614,399	686	1	5.333	6.095	11	7	8	16	0	0	1	GATAD2A	117,414	in gene	ActReg chr19 #8723	0	0	1
8724	19	19,626,541	19,627,669	1,128	2	8.943	12.857	15.657	20	29	24	1	2	3	GATAD2A, TSSK6, NDUFA13	130463, -636, 86	downstream, upstream, in gene	ActReg chr19 #8724	0	1	1
8725	19	19,650,403	19,650,815	412	1	2.5	5.75	13.917	3	5	21	1	1	2	YJEFN3, CILP2	10939, 1535	downstream, in gene	ActReg chr19 #8725	0	0	1
8726	19	19,654,364	19,655,180	816	1	4.577	5.731	14.115	7	10	22	1	0	2	YJEFN3, CILP2	15102, 5698	downstream, in gene	ActReg chr19 #8726	0	0	1
8727	19	19,657,456	19,658,138	682	1	2.706	3.571	12.667	5	5	18	0	0	2	YJEFN3, CILP2	18127, 8723	downstream, downstream	ActReg chr19 #8727	0	0	1
8728	19	19,660,507	19,661,512	1,005	1	6.25	4.719	12.969	10	7	24	0	0	1	CILP2	11,935	downstream	ActReg chr19 #8728	0	0	1
8729	19	19,701,701	19,702,788	1,087	2	11.323	12.294	4.556	23	25	10	0	0	1	PBX4	27,195	in gene	ActReg chr19 #8729	1	1	0
8730	19	19,739,396	19,740,006	610	1	6.474	9.684	12.947	13	14	20	1	1	3	PBX4, LPAR2, GMIP	-10262, -662, 14754	upstream, upstream, downstream	ActReg chr19 #8730	0	0	1
8731	19	19,760,288	19,760,888	600	1	4.947	7.053	13.947	7	11	23	0	1	2	GMIP, ATP13A1	-6133, 13915	upstream, in gene	ActReg chr19 #8731	0	0	1
8732	19	19,773,811	19,774,249	438	1	8.643	11.857	11.929	11	16	17	1	2	2	ATP13A1, ZNF101	473, -5633	in gene, upstream	ActReg chr19 #8732	0	0	1
8733	19	19,853,556	19,854,346	790	1	3.217	3.583	11.24	5	6	16	0	1	2	ZNF14, LOC100287160	-10030, 2318	upstream, downstream	ActReg chr19 #8733	0	0	1
8734	19	19,860,360	19,861,996	1,636	1	4.51	4.262	13.255	10	8	21	0	1	2	LOC100287160, LOC284440	-4909, 26044	upstream, downstream	ActReg chr19 #8734	0	0	1
8735	19	19,886,746	19,887,988	1,242	2	15.462	16.923	9.231	32	39	19	0	1	1	LOC284440	-145	upstream	ActReg chr19 #8735	1	1	0
8736	19	20,149,773	20,150,480	707	1	10.091	11	7.591	18	15	12	1	1	1	ZNF682	151	in gene	ActReg chr19 #8736	0	1	0
8737	19	20,162,477	20,163,765	1,288	2	11.375	17.35	4.375	24	36	6	1	0	0				ActReg chr19 #8737	1	1	0
8738	19	21,182,426	21,183,129	703	1	7.273	13.773	8.136	11	27	14	0	0	0				ActReg chr19 #8738	0	1	0
8739	19	21,203,269	21,204,028	759	1	7.261	14.348	9	11	26	13	0	1	1	ZNF430	222	in gene	ActReg chr19 #8739	0	1	0
8740	19	21,511,704	21,512,419	715	1	11.826	10.217	3.579	21	14	7	0	1	1	ZNF708	151	in gene	ActReg chr19 #8740	1	0	0
8741	19	21,657,782	21,658,125	343	1	8.2	7.727	11	13	12	14	1	0	1	LOC400680	-8,564	upstream	ActReg chr19 #8741	0	0	1
8742	19	21,949,794	21,950,545	751	3	9.13	10.957	9.409	19	16	19	1	1	1	ZNF100	261	in gene	ActReg chr19 #8742	1	1	1
8743	19	22,018,411	22,018,969	558	1	5.765	8.941	12.882	10	15	21	1	1	1	ZNF43	280	in gene	ActReg chr19 #8743	0	0	1
8744	19	22,444,601	22,444,927	326	1	3.5	3.9	11.9	5	6	17	1	0	0				ActReg chr19 #8744	0	0	1
8745	19	22,604,846	22,605,511	665	1	8.81	10.667	6.476	15	17	12	0	1	1	ZNF98	-30	upstream	ActReg chr19 #8745	0	1	0
8746	19	22,700,734	22,701,259	525	1	3.176	2.706	11.353	5	6	14	1	0	0				ActReg chr19 #8746	0	0	1
8747	19	22,785,490	22,786,219	729	1	4.385	2.522	11.609	7	4	19	0	0	1	LOC440518	6,795	in gene	ActReg chr19 #8747	0	0	1
8748	19	22,792,697	22,793,354	657	1	2.579	2.167	12.095	3	3	17	0	0	2	LOC440518, LOC374890	13966, 13748	downstream, downstream	ActReg chr19 #8748	0	0	1
8749	19	22,806,061	22,806,891	830	1	4.12	6.769	12.885	8	12	18	1	1	1	LOC374890	-297	in gene	ActReg chr19 #8749	0	0	1
8750	19	23,253,432	23,254,339	907	1	7.586	8.276	11.517	13	13	19	2	0	0				ActReg chr19 #8750	0	0	1
8751	19	23,299,827	23,300,409	582	1	8.778	5.25	12.278	13	11	23	1	1	1	ZNF730	235	in gene	ActReg chr19 #8751	0	0	1
8752	19	23,386,726	23,387,123	397	1	2.182	4.333	11.917	3	6	19	1	0	0				ActReg chr19 #8752	0	0	1
8753	19	23,432,619	23,433,607	988	2	9.258	11.258	8.552	16	23	20	0	0	1	LOC100132815	23,919	downstream	ActReg chr19 #8753	0	1	1
8754	19	23,653,477	23,654,348	871	1	5.852	10.037	12.333	12	15	18	1	0	0				ActReg chr19 #8754	0	0	1
8755	19	23,945,443	23,946,449	1,006	2	9.742	14	8.194	17	21	12	1	1	1	ZNF681	-4,253	upstream	ActReg chr19 #8755	1	1	0
8756	19	23,954,709	23,955,881	1,172	1	9.676	14.946	3.457	18	23	6	0	0	0				ActReg chr19 #8756	0	1	0
8757	19	24,059,966	24,060,506	540	1	3.588	5.706	13.823	6	8	20	0	0	0				ActReg chr19 #8757	0	0	1
8758	19	24,097,305	24,098,183	878	1	7.893	11.429	8.607	16	18	17	0	1	1	ZNF726	60	in gene	ActReg chr19 #8758	0	1	0
8759	19	24,154,638	24,155,306	668	1	4.714	4	12.762	8	5	16	1	0	0				ActReg chr19 #8759	0	0	1
8760	19	24,236,686	24,237,907	1,221	1	10.132	14.842	2.528	16	25	5	0	0	0				ActReg chr19 #8760	0	1	0
8761	19	24,360,731	24,361,164	433	1	2.417	2.429	11.929	3	5	15	0	0	0				ActReg chr19 #8761	0	0	1
8762	19	28,284,635	28,285,509	874	1	11.429	11	8.286	17	14	11	1	2	2	LOC148189, LOC100506694	-224, 697	upstream, in gene	ActReg chr19 #8762	0	1	0
8763	19	29,820,146	29,820,988	842	2	12.885	18.654	4.5	32	42	7	0	0	0				ActReg chr19 #8763	1	1	0
8764	19	29,920,505	29,920,831	326	1	2.8	4.1	12.5	4	7	15	0	0	0				ActReg chr19 #8764	0	0	1
8765	19	29,930,631	29,931,010	379	1	1.111	2.167	12.417	2	4	17	0	0	0				ActReg chr19 #8765	0	0	1
8766	19	30,096,737	30,097,502	765	1	6.043	12.826	6.696	10	20	10	1	1	1	POP4	-51	upstream	ActReg chr19 #8766	0	1	0
8767	19	30,136,855	30,137,349	494	1	10.812	8.812	2.733	18	13	6	0	0	0				ActReg chr19 #8767	1	0	0
8768	19	30,165,627	30,166,286	659	1	3.9	4.167	10.762	7	7	14	1	0	1	PLEKHF1	9,629	in gene	ActReg chr19 #8768	0	0	1
8769	19	30,169,485	30,169,932	447	1	4.143	3.429	13	6	6	17	0	0	1	PLEKHF1	13,381	downstream	ActReg chr19 #8769	0	0	1
8770	19	30,298,018	30,298,465	447	1	2.929	4	11.571	4	5	13	0	1	1	CCNE1	-4,660	upstream	ActReg chr19 #8770	0	0	1
8771	19	30,323,497	30,324,053	556	1	4.188	3.941	9.412	7	6	13	0	0	1	CCNE1	20,874	downstream	ActReg chr19 #8771	0	0	1
8772	19	30,696,127	30,696,486	359	1	2.727	2.182	10.083	4	4	14	0	0	0				ActReg chr19 #8772	0	0	1
8773	19	31,118,627	31,119,089	462	1	12.357	7.857	4.357	16	10	6	0	0	0				ActReg chr19 #8773	1	0	0
8774	19	31,899,202	31,899,675	473	1	7.929	10.5	1.167	10	15	2	0	0	0				ActReg chr19 #8774	0	1	0
8775	19	31,991,430	31,991,751	321	1	1.25	1.75	9.4	2	2	14	0	0	0				ActReg chr19 #8775	0	0	1
8776	19	32,836,216	32,837,112	896	1	7.214	11.357	5.857	13	17	11	1	1	1	ZNF507	150	in gene	ActReg chr19 #8776	0	1	0
8777	19	32,896,187	32,896,710	523	1	6.294	9.882	11	10	13	14	1	1	1	DPY19L3	-207	upstream	ActReg chr19 #8777	0	0	1
8778	19	33,071,760	33,072,818	1,058	2	11.879	10.727	6.062	17	22	10	1	1	1	PDCD5	185	in gene	ActReg chr19 #8778	1	1	0
8779	19	33,143,304	33,143,668	364	1	2.727	0	9.909	5	0	14	0	0	1	ANKRD27	22,616	in gene	ActReg chr19 #8779	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8780	19	33,182,423	33,182,953	530	1	11.353	9.412	5.062	16	13	8	1	1	1	NUDT19	-179	upstream	ActReg chr19 #8780	1	0	0
8781	19	33,355,113	33,355,756	643	1	4.2	3.45	12	8	6	16	0	0	1	SLC7A9	5,249	in gene	ActReg chr19 #8781	0	0	1
8782	19	33,462,570	33,463,512	942	2	13.138	20.759	6.828	33	56	12	1	2	3	CCDC123, C19orf40, RHPN2	-172, -107, 92783	upstream, upstream, downstream	ActReg chr19 #8782	1	1	0
8783	19	33,667,538	33,668,814	1,276	3	14.375	14.85	18	24	27	34	1	0	1	WDR88	45,178	downstream	ActReg chr19 #8783	1	1	1
8784	19	33,710,134	33,710,748	614	1	12.158	11.526	7.526	16	18	12	0	0	1	SLC7A10	6,315	in gene	ActReg chr19 #8784	0	1	0
8785	19	33,718,108	33,718,499	391	1	2.615	3.692	10.385	4	6	15	1	1	1	SLC7A10	-1,547	upstream	ActReg chr19 #8785	0	0	1
8786	19	33,741,929	33,742,663	734	1	4.043	2	11.522	6	4	15	0	0	0				ActReg chr19 #8786	0	0	1
8787	19	33,766,014	33,766,652	638	1	4.15	4.389	11.4	8	8	15	0	0	0				ActReg chr19 #8787	0	0	1
8788	19	33,766,833	33,767,386	553	1	6.176	6.118	12.353	9	10	16	0	0	0				ActReg chr19 #8788	0	0	1
8789	19	33,772,265	33,772,826	561	1	3.235	7	13.118	4	11	21	0	0	0				ActReg chr19 #8789	0	0	1
8790	19	33,791,969	33,792,330	361	1	5.182	6.818	13.182	6	8	19	1	2	2	CEBPA, LOC80054	1281, -1614	in gene, upstream	ActReg chr19 #8790	0	0	1
8791	19	33,793,678	33,794,088	410	1	6.846	7.231	10.231	10	10	16	1	2	2	CEBPA, LOC80054	-453, 120	upstream, in gene	ActReg chr19 #8791	0	0	1
8792	19	33,794,369	33,794,831	462	1	2.143	4.429	12.857	5	7	20	1	2	2	CEBPA, LOC80054	-1170, 837	upstream, in gene	ActReg chr19 #8792	0	0	1
8793	19	33,878,185	33,879,213	1,028	1	1.968	4.031	11.906	4	8	16	1	0	2	CEBPG, PEPD	14090, 134100	downstream, in gene	ActReg chr19 #8793	0	0	1
8794	19	33,881,374	33,882,249	875	1	3.179	4.071	10.571	5	6	15	0	0	2	CEBPG, PEPD	17202, 130988	downstream, in gene	ActReg chr19 #8794	0	0	1
8795	19	33,893,004	33,893,483	479	1	5.333	1.733	11.533	7	3	18	0	0	1	PEPD	119,556	in gene	ActReg chr19 #8795	0	0	1
8796	19	33,897,424	33,897,930	506	1	6.5	5.875	12.562	9	10	19	0	0	1	PEPD	115,122	in gene	ActReg chr19 #8796	0	0	1
8797	19	34,008,791	34,009,429	638	1	4.55	2.35	12.15	9	5	19	0	0	1	PEPD	3,689	in gene	ActReg chr19 #8797	0	0	1
8798	19	34,035,934	34,036,358	424	1	3.5	3.357	10.429	5	6	15	0	0	0				ActReg chr19 #8798	0	0	1
8799	19	34,071,765	34,072,132	367	1	3	2	11	4	3	14	0	0	0				ActReg chr19 #8799	0	0	1
8800	19	34,113,771	34,114,372	601	1	1.765	2.684	10.158	4	4	14	1	1	1	CHST8	1,210	in gene	ActReg chr19 #8800	0	0	1
8801	19	34,174,948	34,175,664	716	1	9.182	12.773	5.455	18	23	11	1	0	1	CHST8	62,445	in gene	ActReg chr19 #8801	0	1	0
8802	19	34,181,161	34,181,637	476	1	2.571	3.467	12.867	4	5	19	0	0	1	CHST8	68,538	in gene	ActReg chr19 #8802	0	0	1
8803	19	34,231,503	34,232,264	761	1	8.458	13.125	3.304	13	21	7	0	0	1	CHST8	119,022	in gene	ActReg chr19 #8803	0	1	0
8804	19	34,258,423	34,259,271	848	2	12.37	12.593	2.704	24	20	4	0	0	1	CHST8	145,986	in gene	ActReg chr19 #8804	1	1	0
8805	19	34,302,133	34,302,656	523	1	2.294	3.133	11.118	4	5	19	1	0	1	KCTD15	14,643	in gene	ActReg chr19 #8805	0	0	1
8806	19	34,310,570	34,312,079	1,509	2	9.638	12.34	8.468	16	20	16	1	0	1	KCTD15	23,573	downstream	ActReg chr19 #8806	0	1	1
8807	19	34,378,805	34,379,174	369	1	3.4	5	10	5	8	14	0	0	0				ActReg chr19 #8807	0	0	1
8808	19	34,625,074	34,625,842	768	1	14.333	8.458	8.208	28	12	18	1	0	0				ActReg chr19 #8808	1	0	0
8809	19	34,662,662	34,663,341	679	1	8.952	12.571	6.095	15	19	11	1	1	1	LSM14A	-351	upstream	ActReg chr19 #8809	0	1	0
8810	19	34,723,764	34,724,380	616	1	11.947	9.263	3.412	17	13	6	0	0	1	LSM14A	60,720	downstream	ActReg chr19 #8810	1	0	0
8811	19	34,849,829	34,850,719	890	1	9.815	12.444	6.481	19	19	12	1	1	2	KIAA0355, GPI	104818, -5371	downstream, upstream	ActReg chr19 #8811	0	1	0
8812	19	34,894,984	34,895,723	739	2	7.565	10.435	10.348	14	19	16	1	1	2	GPI, PDCD2L	39708, 50	downstream, in gene	ActReg chr19 #8812	0	1	1
8813	19	34,984,089	34,984,678	589	1	2.316	2.263	10	3	4	14	0	0	1	WTIP	11,503	in gene	ActReg chr19 #8813	0	0	1
8814	19	34,988,665	34,989,135	470	1	3.071	2	11.733	5	3	18	1	0	1	WTIP	16,020	in gene	ActReg chr19 #8814	0	0	1
8815	19	34,992,499	34,992,909	410	1	4.462	4.923	11.462	6	10	17	0	0	1	WTIP	19,824	downstream	ActReg chr19 #8815	0	0	1
8816	19	35,167,620	35,169,055	1,435	3	11.704	14.068	6.558	20	20	14	1	1	1	ZNF302	-230	upstream	ActReg chr19 #8816	1	1	1
8817	19	35,221,900	35,222,526	626	1	1.8	2.412	10.421	3	5	14	0	1	1	ZNF181	-3,267	upstream	ActReg chr19 #8817	0	0	1
8818	19	35,263,912	35,264,441	529	1	8.5	11.375	7.133	13	18	13	1	1	1	ZNF599	-42	upstream	ActReg chr19 #8818	0	1	0
8819	19	35,395,783	35,396,463	680	1	3.095	4.286	10.905	6	7	14	1	0	0				ActReg chr19 #8819	0	0	1
8820	19	35,454,943	35,455,358	415	1	8.231	11.615	11	12	14	15	1	1	1	ZNF792	-197	upstream	ActReg chr19 #8820	0	0	1
8821	19	35,512,231	35,512,994	763	1	3.292	3.333	11.208	6	6	20	1	0	2	GRAMD1A, SCN1B	21366, -8980	in gene, upstream	ActReg chr19 #8821	0	0	1
8822	19	35,530,648	35,531,170	522	1	2.846	4	11.647	6	7	17	0	1	2	SCN1B, HPN	9317, -501	in gene, upstream	ActReg chr19 #8822	0	0	1
8823	19	35,531,593	35,532,031	438	1	2.077	2.25	12.154	4	3	17	1	1	2	SCN1B, HPN	10220, 402	downstream, in gene	ActReg chr19 #8823	0	0	1
8824	19	35,550,487	35,550,952	465	1	3.733	5.333	11.333	10	9	17	1	0	2	HPN, LOC100128675	19309, 46489	in gene, in gene	ActReg chr19 #8824	0	0	1
8825	19	35,566,364	35,567,135	771	1	2.143	4.75	13.333	3	10	20	0	0	2	HPN, LOC100128675	35339, 30459	downstream, in gene	ActReg chr19 #8825	0	0	1
8826	19	35,596,067	35,597,612	1,545	2	11.438	11.667	6.675	18	21	13	0	1	2	LOC100128675, FXYD3	369, -9893	in gene, upstream	ActReg chr19 #8826	1	1	0
8827	19	35,605,833	35,606,477	644	1	4.389	12.55	4.5	9	17	9	0	1	3	LOC100128675, FXYD3, LGI4	-8947, -577, 20023	upstream, upstream, downstream	ActReg chr19 #8827	0	1	0
8828	19	35,615,880	35,616,285	405	1	7.333	8	13	10	11	19	0	0	2	FXYD3, LGI4	9350, 10096	downstream, in gene	ActReg chr19 #8828	0	0	1
8829	19	35,645,594	35,646,039	445	1	7.929	5.857	11.286	12	8	15	1	1	2	FXYD7, FXYD5	11662, 191	downstream, in gene	ActReg chr19 #8829	0	0	1
8830	19	35,715,734	35,716,181	447	1	4.308	3.786	12	8	6	16	1	0	2	LOC100506239, FAM187B	22887, 3671	downstream, in gene	ActReg chr19 #8830	0	0	1
8831	19	35,739,245	35,739,777	532	1	4.235	3.647	12.706	6	5	17	1	1	1	LSR	-48	upstream	ActReg chr19 #8831	0	0	1
8832	19	35,740,218	35,740,467	249	1	3.75	2.75	11	5	4	13	1	1	1	LSR	783	in gene	ActReg chr19 #8832	0	0	1
8833	19	35,782,863	35,783,301	438	1	2.929	5	12	5	8	17	0	1	2	HAMP, MAG	9672, 44	downstream, in gene	ActReg chr19 #8833	0	0	1
8834	19	35,800,679	35,801,267	588	1	4.389	7.611	11.111	8	11	16	1	0	1	MAG	17,935	in gene	ActReg chr19 #8834	0	0	1
8835	19	35,809,540	35,810,439	899	1	13.679	8.964	4	25	16	8	0	0	2	MAG, CD22	26951, -10083	downstream, upstream	ActReg chr19 #8835	1	0	0
8836	19	35,896,139	35,896,606	467	1	4.643	10.643	2.538	9	16	4	0	0	0				ActReg chr19 #8836	0	1	0
8837	19	36,024,739	36,025,307	568	1	2.706	3.118	12.471	4	6	20	1	2	3	SBSN, GAPDHS, LOC100506469	-5770, 709, 11394	upstream, in gene, downstream	ActReg chr19 #8837	0	0	1
8838	19	36,049,165	36,049,666	501	1	3.25	4.375	12.688	5	8	17	1	0	1	ATP4A	5,145	in gene	ActReg chr19 #8838	0	0	1
8839	19	36,103,293	36,103,992	699	3	10.091	15.046	8.227	19	29	18	1	1	1	HAUS5	-4	upstream	ActReg chr19 #8839	1	1	1
8840	19	36,119,535	36,120,274	739	2	13.913	12.435	5.696	26	25	9	1	1	2	HAUS5, RBM42	16258, -76	downstream, upstream	ActReg chr19 #8840	1	1	0
8841	19	36,135,269	36,135,870	601	1	5.833	4.889	12.056	10	11	16	1	1	3	RBM42, ETV2, COX6B1	15589, 2922, -3556	downstream, in gene, upstream	ActReg chr19 #8841	0	0	1
8842	19	36,192,947	36,193,925	978	2	11.613	13.935	7.903	26	24	14	1	0	1	ZBTB32	-10,394	upstream	ActReg chr19 #8842	1	1	0
8843	19	36,206,219	36,206,980	761	1	4.125	7.208	11.708	7	11	16	1	2	2	ZBTB32, MLL4	2769, -2322	in gene, upstream	ActReg chr19 #8843	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8844	19	36,207,507	36,208,732	1,225	3	9.579	11.974	13.105	16	19	31	1	1	2	ZBTB32, MLL4	4289, -802	downstream, upstream	ActReg chr19 #8844	1	1	1
8845	19	36,209,337	36,209,817	480	1	3.933	5.667	11.6	7	10	15	1	1	2	ZBTB32, MLL4	5747, 656	downstream, in gene	ActReg chr19 #8845	0	0	1
8846	19	36,210,749	36,211,175	426	1	1.769	2.071	10.571	3	3	15	1	1	2	ZBTB32, MLL4	7132, 2041	downstream, in gene	ActReg chr19 #8846	0	0	1
8847	19	36,213,104	36,213,534	430	1	3.462	4.538	13.769	4	7	18	0	0	2	ZBTB32, MLL4	9489, 4398	downstream, in gene	ActReg chr19 #8847	0	0	1
8848	19	36,228,998	36,229,643	645	1	5.9	5.947	11.75	9	9	18	1	1	5	MLL4, TMEM149, U2AF1L4, PSENEN, LIN37	20399, 4031, 7016, -7174, -10192	in gene, downstream, downstream, upstream, upstream	ActReg chr19 #8848	0	0	1
8849	19	36,248,258	36,248,705	447	1	5.786	5.429	11.429	9	10	17	0	2	3	LIN37, HSPB6, C19orf55	8969, -551, -563	downstream, upstream, upstream	ActReg chr19 #8849	0	0	1
8850	19	36,288,852	36,289,239	387	1	1.917	2.8	11.75	4	4	16	0	0	2	SNX26, PRODH2	22628, 15156	downstream, downstream	ActReg chr19 #8850	0	0	1
8851	19	36,297,494	36,297,939	445	1	4.857	2.643	11	10	5	17	0	0	1	PRODH2	6,485	in gene	ActReg chr19 #8851	0	0	1
8852	19	36,319,372	36,320,225	853	2	14.333	16.63	5.852	30	39	15	0	0	1	NPHS1	23,097	in gene	ActReg chr19 #8852	1	1	0
8853	19	36,336,042	36,336,843	801	1	5.48	7.52	13.44	10	13	19	1	0	1	NPHS1	6,453	in gene	ActReg chr19 #8853	0	0	1
8854	19	36,370,452	36,371,359	907	2	17.143	18.429	2.84	35	41	5	0	0	2	APLP1, NFKBID	11504, 20647	downstream, downstream	ActReg chr19 #8854	1	1	0
8855	19	36,422,143	36,422,651	508	1	9.188	8.188	12.938	14	13	19	1	1	1	LRFN3	-5,625	upstream	ActReg chr19 #8855	0	0	1
8856	19	36,450,182	36,450,835	653	1	4.55	5.75	16	12	8	29	1	0	0				ActReg chr19 #8856	0	0	1
8857	19	36,454,246	36,454,946	700	1	9.545	13.136	2.294	18	25	4	0	0	0				ActReg chr19 #8857	0	1	0
8858	19	36,466,251	36,467,192	941	2	12.517	11.414	2.96	25	20	7	0	0	0				ActReg chr19 #8858	1	1	0
8859	19	36,485,644	36,486,524	880	2	9.074	12.593	9.615	13	18	18	2	1	2	SDHAF1, C19orf46	-6, 13588	upstream, downstream	ActReg chr19 #8859	0	1	1
8860	19	36,500,050	36,500,957	907	1	10.214	9.964	6.107	17	15	14	1	1	3	C19orf46, ALKBH6, CLIP3	-831, 4638, 23272	upstream, in gene, downstream	ActReg chr19 #8860	1	0	0
8861	19	36,523,641	36,524,119	478	1	3.333	6.733	12.333	5	11	18	1	1	2	CLIP3, THAP8	-105, 21784	upstream, downstream	ActReg chr19 #8861	0	0	1
8862	19	36,544,637	36,545,566	929	2	9.276	12.655	10.207	15	18	18	1	2	2	THAP8, WDR62	563, -682	in gene, upstream	ActReg chr19 #8862	0	1	1
8863	19	36,594,100	36,594,722	622	1	4.3	4.85	13.05	7	7	20	0	1	3	WDR62, LOC728361, POLR2I	48628, -7694, 11795	in gene, upstream, downstream	ActReg chr19 #8863	0	0	1
8864	19	36,605,463	36,606,274	811	1	12.346	10.885	5.769	23	15	10	1	2	4	WDR62, LOC728361, POLR2I, TBCB	60085, 3763, 338, -20	downstream, downstream, in gene, upstream	ActReg chr19 #8864	1	0	0
8865	19	36,618,465	36,619,257	792	1	7.625	8.25	12.792	15	12	16	1	0	1	TBCB	12,973	downstream	ActReg chr19 #8865	0	0	1
8866	19	36,630,253	36,631,290	1,037	3	15.625	18.406	10.531	38	40	21	1	1	1	CAPNS1	-147	upstream	ActReg chr19 #8866	1	1	1
8867	19	36,705,072	36,706,380	1,308	1	9.024	13.293	5	15	22	10	1	2	2	ZNF565, ZNF146	260, 222	in gene, in gene	ActReg chr19 #8867	0	1	0
8868	19	36,869,413	36,870,353	940	2	11.69	11.483	8.379	25	16	17	1	1	1	ZFP14	195	in gene	ActReg chr19 #8868	1	1	0
8869	19	36,909,068	36,909,805	737	1	6.522	9.87	12.826	10	15	17	1	2	2	ZFP82, LOC644189	114, -3003	in gene, upstream	ActReg chr19 #8869	0	0	1
8870	19	36,979,715	36,981,028	1,313	1	6.683	11.073	4.415	11	16	9	1	2	2	ZNF566, LOC728752	92, -158	in gene, upstream	ActReg chr19 #8870	0	1	0
8871	19	37,063,831	37,064,473	642	2	9	10.05	9.5	16	13	20	1	0	1	ZNF529	32,026	in gene	ActReg chr19 #8871	1	0	1
8872	19	37,328,744	37,329,312	568	1	11.167	8.722	6.533	16	14	10	1	1	2	LOC284408, ZNF790	40941, 256	downstream, in gene	ActReg chr19 #8872	1	0	0
8873	19	37,406,754	37,407,665	911	1	11.929	7.179	7.192	16	11	11	1	2	2	ZNF829, ZNF568	-16, -25	upstream, upstream	ActReg chr19 #8873	1	0	0
8874	19	37,502,952	37,503,402	450	1	1.786	2.917	10.571	3	5	13	0	0	0				ActReg chr19 #8874	0	0	1
8875	19	37,547,612	37,547,976	364	1	2.273	3.083	10.417	5	5	15	0	0	0				ActReg chr19 #8875	0	0	1
8876	19	37,568,805	37,569,315	510	1	11.438	11.125	12.438	18	18	17	1	1	1	ZNF420	-322	upstream	ActReg chr19 #8876	0	0	1
8877	19	37,708,509	37,709,567	1,058	1	10.273	13	7.586	15	21	16	1	1	2	ZNF585B, ZNF383	-7587, -8328	upstream, upstream	ActReg chr19 #8877	0	1	0
8878	19	37,825,082	37,825,832	750	1	6.333	11.333	6.458	9	16	13	1	1	2	LOC100507342, HKR1	16655, -123	downstream, upstream	ActReg chr19 #8878	0	1	0
8879	19	37,861,660	37,862,570	910	1	8.655	13.931	5.552	15	26	8	1	1	2	HKR1, ZNF527	36535, 56	downstream, in gene	ActReg chr19 #8879	0	1	0
8880	19	38,042,326	38,042,776	450	1	5.286	4.385	12.214	7	7	18	0	2	3	ZNF793, DKFZp761D1918, LOC100507433	44710, -2484, 2700	downstream, upstream, in gene	ActReg chr19 #8880	0	0	1
8881	19	38,269,681	38,270,578	897	1	13.25	9.429	5.821	21	14	13	1	1	1	ZNF573	101	in gene	ActReg chr19 #8881	1	0	0
8882	19	38,308,029	38,308,574	545	1	3.929	2.4	13.353	7	4	21	1	1	1	LOC644554	411	in gene	ActReg chr19 #8882	0	0	1
8883	19	38,345,923	38,346,445	522	1	2.375	3.438	9.938	5	6	13	1	0	0				ActReg chr19 #8883	0	0	1
8884	19	38,397,395	38,398,019	624	1	8.5	10.9	5	17	17	10	1	2	2	WDR87, SIPA1L3	-390, -161	upstream, upstream	ActReg chr19 #8884	0	1	0
8885	19	38,662,816	38,663,284	468	1	2.667	3.933	10.8	5	6	17	0	0	1	SIPA1L3	265,182	in gene	ActReg chr19 #8885	0	0	1
8886	19	38,663,811	38,664,215	404	1	2.455	5.375	11.667	4	8	17	0	0	1	SIPA1L3	266,145	in gene	ActReg chr19 #8886	0	0	1
8887	19	38,795,735	38,796,265	530	1	4.647	3.353	11.765	8	6	20	0	1	2	YIF1B, C19orf33	10606, 1196	in gene, downstream	ActReg chr19 #8887	0	0	1
8888	19	38,797,854	38,798,434	580	1	3.143	4.056	12.944	5	5	16	0	0	2	YIF1B, C19orf33	8447, 3355	in gene, downstream	ActReg chr19 #8888	0	0	1
8889	19	38,864,770	38,865,917	1,147	2	9.143	10.143	5.343	19	18	10	1	1	3	CATSPERG, PSMD8, GGN	38900, 153, 13325	downstream, in gene, downstream	ActReg chr19 #8889	1	1	0
8890	19	38,893,537	38,894,071	534	1	8.438	10.938	6.75	11	15	10	1	1	3	SPRED3, FAM98C, RASGRP4	12865, 29, 23141	downstream, in gene, downstream	ActReg chr19 #8890	0	1	0
8891	19	38,908,837	38,909,328	491	1	9.6	5.533	11.667	12	8	18	1	0	2	FAM98C, RASGRP4	15507, 7863	downstream, in gene	ActReg chr19 #8891	0	0	1
8892	19	38,945,483	38,946,267	784	2	10.292	14.833	6.312	21	33	9	0	0	1	RYR1	21,535	in gene	ActReg chr19 #8892	1	1	0
8893	19	39,028,559	39,028,995	436	1	1.643	3.643	10.643	3	5	16	0	0	1	RYR1	104,437	in gene	ActReg chr19 #8893	0	0	1
8894	19	39,051,922	39,052,623	701	1	2.9	4.045	10.5	5	7	14	1	0	1	RYR1	127,932	in gene	ActReg chr19 #8894	0	0	1
8895	19	39,055,434	39,055,811	377	1	4.375	5.333	12	5	8	20	1	0	1	RYR1	131,282	in gene	ActReg chr19 #8895	0	0	1
8896	19	39,109,181	39,110,167	986	1	7.71	11.742	8.452	14	21	14	1	2	2	MAP4K1, EIF3K	-1031, -48	upstream, upstream	ActReg chr19 #8896	0	1	0
8897	19	39,137,879	39,138,600	721	2	10.609	13.87	8.619	20	21	20	1	1	1	ACTN4	-88	upstream	ActReg chr19 #8897	0	1	1
8898	19	39,148,347	39,148,841	494	1	8	10.688	11.8	12	16	2	0	0	1	ACTN4	10,267	in gene	ActReg chr19 #8898	0	1	0
8899	19	39,173,926	39,174,864	938	2	12.276	10.552	5.345	18	15	9	0	0	1	ACTN4	36,068	in gene	ActReg chr19 #8899	1	1	0
8900	19	39,182,237	39,183,320	1,083	2	9.912	10.794	5.735	15	14	13	0	0	1	ACTN4	44,451	in gene	ActReg chr19 #8900	1	1	0
8901	19	39,311,987	39,312,520	533	1	3.647	6.667	12.353	7	12	20	0	0	4	LGALS4, ECH1, LOC100507591, LOC100289396	-8513, 10244, 6189, 4184	upstream, in gene, downstream, in gene	ActReg chr19 #8901	0	0	1
8902	19	39,342,862	39,343,561	699	1	9.955	12.182	6.409	16	21	11	1	1	1	HNRNPL	-232	upstream	ActReg chr19 #8902	0	1	0
8903	19	39,359,626	39,361,403	1,777	3	11.036	12.618	9.127	35	37	17	1	0	2	RINL, SIRT2	8380, 29988	in gene, downstream	ActReg chr19 #8903	1	1	1
8904	19	39,389,802	39,390,790	988	2	10.935	13.129	6.323	17	22	13	1	2	3	SIRT2, NFKBIB, LOC643669	206, -319, 12502	in gene, upstream, downstream	ActReg chr19 #8904	1	1	0
8905	19	39,402,007	39,402,584	577	1	3.5	5.444	10.722	6	8	15	0	1	3	NFKBIB, LOC643669, SARS2	11680, 503, 19241	downstream, in gene, downstream	ActReg chr19 #8905	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8906	19	39,481,888	39,482,310	422	1	4.714	2.786	10.643	7	4	19	0	0	0				ActReg chr19 #8906	0	0	1
8907	19	39,561,282	39,562,047	765	2	11.565	14.304	3.435	17	25	8	0	0	0				ActReg chr19 #8907	1	1	0
8908	19	39,564,074	39,564,790	716	2	13.864	11.091	3.25	23	19	5	0	0	0				ActReg chr19 #8908	1	1	0
8909	19	39,675,483	39,675,962	479	1	2.714	4	10.067	4	7	16	0	0	1	PAK4	59,302	downstream	ActReg chr19 #8909	0	0	1
8910	19	39,714,196	39,714,969	773	2	13.708	14.546	3.261	31	28	6	0	0	0				ActReg chr19 #8910	1	1	0
8911	19	39,738,596	39,739,024	428	1	2	1.556	10.769	3	3	16	1	1	1	IL28B	-3,199	upstream	ActReg chr19 #8911	0	0	1
8912	19	39,832,089	39,833,083	994	2	33.968	33.581	5.217	106	116	8	1	2	2	GMFG, SAMD4B	-5860, -522	upstream, upstream	ActReg chr19 #8912	1	1	0
8913	19	39,881,258	39,882,566	1,308	2	11.073	13.537	8.146	18	22	12	1	2	3	SAMD4B, PAF1, MED29	48804, -233, -51	downstream, upstream, upstream	ActReg chr19 #8913	1	1	0
8914	19	39,902,555	39,903,677	1,122	2	13.8	15.314	8.571	23	27	12	1	1	2	ZFP36, PLEKHG2	5629, -634	downstream, upstream	ActReg chr19 #8914	1	1	0
8915	19	39,926,044	39,926,840	796	1	7.64	12.24	9.96	13	21	15	1	1	3	PLEKHG2, RPS16, SUPT5H	22692, 176, -9744	downstream, in gene, upstream	ActReg chr19 #8915	0	1	0
8916	19	39,935,926	39,936,520	594	1	10.421	10.421	10.263	17	13	13	1	1	2	RPS16, SUPT5H	-9605, 37	upstream, in gene	ActReg chr19 #8916	0	0	1
8917	19	39,971,237	39,971,882	645	1	13.55	12.9	6.9	16	17	13	1	1	2	SUPT5H, TIMM50	35373, 507	downstream, in gene	ActReg chr19 #8917	1	0	0
8918	19	40,030,574	40,031,026	452	1	11.357	9.5	7.857	15	14	11	2	2	2	EID2B, EID2	-7306, 38	upstream, in gene	ActReg chr19 #8918	1	0	0
8919	19	40,089,604	40,090,382	778	2	10.75	12.5	1	21	22	1	0	1	1	LGALS13	-3,176	upstream	ActReg chr19 #8919	1	1	0
8920	19	40,135,715	40,136,955	1,240	2	13.763	16.526	2	27	36	4	0	0	1	LGALS16	-10,223	upstream	ActReg chr19 #8920	1	1	0
8921	19	40,324,215	40,324,853	638	1	6.789	7.6	14.15	12	11	23	1	1	2	DYRK1B, FBL	307, 12520	in gene, downstream	ActReg chr19 #8921	0	0	1
8922	19	40,420,040	40,420,394	354	1	4.636	3.364	10.273	8	5	17	0	0	1	FCGBP	20,316	in gene	ActReg chr19 #8922	0	0	1
8923	19	40,476,546	40,477,340	794	1	8.083	13.042	7.708	12	23	12	1	1	1	PSMC4	-130	upstream	ActReg chr19 #8923	0	1	0
8924	19	40,596,285	40,597,033	748	1	6.583	11.667	5.333	12	23	8	1	1	1	ZNF780A	186	in gene	ActReg chr19 #8924	0	1	0
8925	19	40,626,624	40,627,413	789	2	13.24	8.68	1.96	28	20	3	0	0	0				ActReg chr19 #8925	1	1	0
8926	19	40,697,876	40,698,606	730	1	7.348	9.87	12.304	13	12	19	1	1	1	MAP3K10	590	in gene	ActReg chr19 #8926	0	0	1
8927	19	40,725,456	40,726,253	797	1	9.76	13.56	1.909	16	23	3	0	1	4	MAP3K10, TTC9B, CNTD2, AKT2	28203, -1548, 6743, 65411	downstream, upstream, downstream, downstream	ActReg chr19 #8927	0	1	0
8928	19	40,728,255	40,728,789	534	1	6.176	3.176	12.529	8	5	18	1	1	4	MAP3K10, TTC9B, CNTD2, AKT2	30871, -4216, 4075, 62743	downstream, upstream, in gene, downstream	ActReg chr19 #8928	0	0	1
8929	19	40,738,880	40,739,284	404	1	1.1	5.231	13.615	2	8	19	0	1	2	CNTD2, AKT2	-6485, 52183	upstream, in gene	ActReg chr19 #8929	0	0	1
8930	19	40,827,114	40,827,929	815	1	4.826	3.76	12.96	10	7	23	0	0	1	C19orf47	26,772	in gene	ActReg chr19 #8930	0	0	1
8931	19	40,854,081	40,854,790	709	1	11.227	13.954	4.421	20	25	9	1	2	2	C19orf47, PLD3	-142, 103	upstream, in gene	ActReg chr19 #8931	0	1	0
8932	19	40,926,706	40,927,219	513	1	11.125	11.938	12.75	17	16	18	1	1	2	PRX, SERTAD1	-7691, 4970	upstream, downstream	ActReg chr19 #8932	0	0	1
8933	19	40,971,295	40,972,943	1,648	1	9.51	11.712	7.308	17	21	15	1	2	2	BLVRB, SPTBN4	-394, -1007	upstream, upstream	ActReg chr19 #8933	0	1	0
8934	19	41,034,964	41,035,494	530	1	6.118	8.294	12.235	8	14	20	1	0	1	SPTBN4	62,103	in gene	ActReg chr19 #8934	0	0	1
8935	19	41,060,161	41,060,548	387	1	3.25	2.25	11.417	6	5	16	1	0	1	SPTBN4	87,228	in gene	ActReg chr19 #8935	0	0	1
8936	19	41,063,031	41,063,439	408	1	4.308	4.923	11.154	6	8	16	0	0	1	SPTBN4	90,109	in gene	ActReg chr19 #8936	0	0	1
8937	19	41,082,427	41,083,319	892	2	10.607	13.75	3.429	21	34	6	1	1	2	SPTBN4, SHKBP1	109747, 116	downstream, in gene	ActReg chr19 #8937	1	1	0
8938	19	41,110,596	41,111,957	1,361	2	9.524	10.143	10.191	15	15	23	1	0	1	LTBP4	12,204	in gene	ActReg chr19 #8938	1	0	1
8939	19	41,115,606	41,115,896	290	1	6	6	13.333	8	8	17	1	0	1	LTBP4	16,679	in gene	ActReg chr19 #8939	0	0	1
8940	19	41,116,072	41,117,457	1,385	2	9.744	12.419	5.302	21	19	11	0	0	1	LTBP4	17,692	in gene	ActReg chr19 #8940	1	1	0
8941	19	41,119,002	41,119,647	645	1	5	8.3	14.8	8	13	23	1	0	1	LTBP4	20,252	in gene	ActReg chr19 #8941	0	0	1
8942	19	41,120,039	41,120,636	597	1	7.944	11.278	8.389	11	17	14	1	0	1	LTBP4	21,265	in gene	ActReg chr19 #8942	0	1	0
8943	19	41,221,337	41,223,178	1,841	3	10.724	9.586	5.224	21	16	12	2	2	3	ADCK4, ITPKC, LOC100507668	533, -751, 16952	in gene, upstream, downstream	ActReg chr19 #8943	1	1	0
8944	19	41,223,630	41,224,320	690	1	4.455	4.455	11.773	6	10	20	0	2	3	ADCK4, ITPKC, LOC100507668	-1185, 967, 15234	upstream, in gene, in gene	ActReg chr19 #8944	0	0	1
8945	19	41,315,700	41,316,118	418	1	2.769	5.538	10.538	4	9	16	0	1	2	EGLN2, CYP2A	10861, 1509	downstream, in gene	ActReg chr19 #8945	0	0	1
8946	19	41,769,871	41,770,740	869	1	8.037	13.148	5	15	21	11	1	1	2	AXL, HNRNPUL1	45197, 1914	downstream, in gene	ActReg chr19 #8946	0	1	0
8947	19	41,815,760	41,816,618	858	2	13.074	11.741	8.63	24	22	17	1	1	2	HNRNPUL1, CCDC97	47798, 95	downstream, in gene	ActReg chr19 #8947	1	1	0
8948	19	41,827,602	41,828,340	738	1	7.739	10.304	4.304	11	15	10	0	0	2	CCDC97, TGFB1	11877, 31860	in gene, downstream	ActReg chr19 #8948	0	1	0
8949	19	41,828,906	41,830,004	1,098	1	7.735	11.618	8.559	14	18	13	0	0	2	CCDC97, TGFB1	13361, 30376	in gene, downstream	ActReg chr19 #8949	0	1	0
8950	19	41,833,576	41,834,240	664	1	9.667	9.905	11.333	15	13	15	0	0	2	CCDC97, TGFB1	17814, 25923	downstream, downstream	ActReg chr19 #8950	0	0	1
8951	19	41,847,649	41,847,979	330	1	3.5	4	11.7	5	5	15	0	0	1	TGFB1	12,017	in gene	ActReg chr19 #8951	0	0	1
8952	19	41,869,694	41,870,315	621	1	9.4	10.4	4.9	14	16	10	1	2	3	TGFB1, B9D2, TMEM91	-10173, 74, 133	upstream, in gene, in gene	ActReg chr19 #8952	0	1	0
8953	19	41,945,292	41,946,411	1,119	2	19.6	21.971	7.143	65	61	14	1	2	3	ATP5SL, C19orf69, LOC100505495	-8, -3212, 60703	upstream, upstream, downstream	ActReg chr19 #8953	1	1	0
8954	19	41,951,579	41,951,920	341	1	2.778	1	9.818	4	1	14	0	1	3	ATP5SL, C19orf69, LOC100505495	-5906, 2686, 54805	upstream, downstream, downstream	ActReg chr19 #8954	0	0	1
8955	19	42,123,223	42,123,950	727	2	11.261	10.348	4.435	18	19	9	0	0	1	CEACAM4	9,856	downstream	ActReg chr19 #8955	1	1	0
8956	19	42,317,432	42,317,992	560	2	10.944	12.167	2.647	21	23	4	0	0	1	CEACAM3	17,178	downstream	ActReg chr19 #8956	1	1	0
8957	19	42,363,491	42,364,460	969	2	11.3	9.167	5.9	17	17	11	1	1	3	DMRTC2, RPS19, LOC100505604	14889, -13, 9306	downstream, upstream, downstream	ActReg chr19 #8957	1	1	0
8958	19	42,388,010	42,388,749	739	1	7.826	12.652	6	10	21	13	1	1	2	CD79A, ARHGEF1	7189, 1112	downstream, in gene	ActReg chr19 #8958	0	1	0
8959	19	42,391,704	42,392,408	704	1	8.136	12	6.409	17	21	11	0	0	2	CD79A, ARHGEF1	10866, 4789	downstream, in gene	ActReg chr19 #8959	0	1	0
8960	19	42,396,069	42,397,057	988	1	5.241	4.968	12.097	9	8	21	0	0	1	ARHGEF1	9,296	in gene	ActReg chr19 #8960	0	0	1
8961	19	42,443,912	42,444,245	333	1	10.1	4	10.5	12	6	14	1	0	1	LOC100505585	16,832	downstream	ActReg chr19 #8961	0	0	1
8962	19	42,455,732	42,456,219	487	1	4.267	6.727	11.667	6	10	19	0	0	1	RABAC1	7,553	downstream	ActReg chr19 #8962	0	0	1
8963	19	42,474,218	42,474,824	606	1	2.667	5.474	10.737	5	10	15	0	0	1	ATP1A3	23,861	in gene	ActReg chr19 #8963	0	0	1
8964	19	42,500,978	42,501,814	836	1	9.5	15.731	5.769	14	31	10	1	1	2	ATP1A3, GRIK5	-3014, 68561	upstream, downstream	ActReg chr19 #8964	0	1	0
8965	19	42,644,054	42,644,952	898	2	18.179	18.107	3.731	39	41	7	0	2	3	POU2F2, LOC100505622, MIR4323	-7873, 7796, -6838	upstream, downstream, upstream	ActReg chr19 #8965	1	1	0
8966	19	42,646,988	42,648,275	1,287	2	19.075	24.125	3.405	52	65	7	0	0	3	LOC100505622, MIR4323, LOC100505639	10924, -9966, -9090	downstream, upstream, upstream	ActReg chr19 #8966	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
8967	19	42,680,102	42,680,563	461	1	3.429	4.143	11.357	6	7	15	0	0	0				ActReg chr19 #8967	0	0	1
8968	19	42,720,853	42,721,495	642	1	9.1	10.65	5.55	13	21	8	1	2	2	DEDD2, ZNF526	639, -3318	in gene, upstream	ActReg chr19 #8968	0	1	0
8969	19	42,722,439	42,723,266	827	1	9.808	8.038	7.423	14	13	10	0	2	2	DEDD2, ZNF526	-1039, -1640	upstream, upstream	ActReg chr19 #8969	1	0	0
8970	19	42,724,408	42,724,850	442	1	13.571	9.857	12.143	22	14	19	1	2	3	DEDD2, ZNF526, GSK3A	-2816, 137, 22107	upstream, in gene, downstream	ActReg chr19 #8970	0	0	1
8971	19	42,746,697	42,747,771	1,074	2	15.364	16.636	7.125	23	25	11	1	2	3	GSK3A, LOC100132272, ERF	-498, 307, 12075	upstream, in gene, downstream	ActReg chr19 #8971	1	1	0
8972	19	42,748,608	42,749,574	966	2	10.581	11.806	3.065	16	17	5	1	2	3	GSK3A, LOC100132272, ERF	-2355, 2164, 10218	upstream, in gene, downstream	ActReg chr19 #8972	1	1	0
8973	19	42,758,001	42,758,750	749	1	8.391	12.043	7.467	13	21	11	1	1	2	LOC100132272, ERF	11448, 934	downstream, in gene	ActReg chr19 #8973	0	1	0
8974	19	42,772,608	42,773,462	854	2	11.296	13.111	5.407	22	23	10	1	0	0				ActReg chr19 #8974	1	1	0
8975	19	42,775,863	42,776,575	712	1	4.227	7.5	13.182	7	13	20	0	0	0				ActReg chr19 #8975	0	0	1
8976	19	42,781,896	42,782,582	686	1	6.762	3.619	13	12	6	19	0	1	1	CIC	-6,578	upstream	ActReg chr19 #8976	0	0	1
8977	19	42,783,911	42,785,197	1,286	2	13.05	14.925	6.7	24	31	13	1	1	1	CIC	-4,263	upstream	ActReg chr19 #8977	1	1	0
8978	19	42,787,068	42,788,082	1,014	1	8.406	12.969	6.375	17	20	10	0	1	1	CIC	-1,242	upstream	ActReg chr19 #8978	0	1	0
8979	19	42,806,164	42,807,039	875	3	11.778	11.407	10.778	22	17	17	1	3	4	CIC, LOC100505682, PAFAH1B3, PRR19	17784, 1681, 351, 317	downstream, in gene, in gene, in gene	ActReg chr19 #8979	1	1	1
8980	19	42,817,313	42,818,338	1,025	2	6	9.469	8.2	9	17	14	1	1	3	LOC100505682, PRR19, TMEM145	-9543, 11541, 348	upstream, downstream, in gene	ActReg chr19 #8980	0	1	1
8981	19	42,900,993	42,901,825	832	1	6.538	13.077	7.346	10	22	11	1	1	2	CNFN, LIPE	-6965, 30169	upstream, downstream	ActReg chr19 #8981	0	1	0
8982	19	42,927,218	42,928,334	1,116	2	8.457	11.771	9.457	9	18	21	1	0	2	LIPE, CXCL17	3802, 19360	in gene, downstream	ActReg chr19 #8982	0	1	1
8983	19	43,105,666	43,106,590	924	1	9.143	13.964	5.643	18	26	10	0	1	1	CEACAM8	-7,046	upstream	ActReg chr19 #8983	0	1	0
8984	19	43,469,488	43,469,926	438	1	9	5.714	2.214	13	9	4	0	0	1	PSG11	60,924	in gene	ActReg chr19 #8984	1	0	0
8985	19	43,624,640	43,625,162	522	2	10.765	9.647	1	19	14	1	0	0	0				ActReg chr19 #8985	1	1	0
8986	19	43,857,578	43,858,010	432	1	2.231	1.909	11.846	4	5	16	0	1	2	PRG1, CD177	4586, -31	downstream, upstream	ActReg chr19 #8986	0	0	1
8987	19	43,943,080	43,943,581	501	1	12.8	10.933	1.5	22	17	2	0	0	0				ActReg chr19 #8987	1	0	0
8988	19	43,968,276	43,968,732	456	1	5.385	8.286	11.929	8	11	17	1	1	1	LYPD3	1,327	in gene	ActReg chr19 #8988	0	0	1
8989	19	43,979,280	43,979,763	483	1	5.067	7.733	12.733	9	10	22	1	0	2	LYPD3, PHLDB3	-9690, 29464	upstream, in gene	ActReg chr19 #8989	0	0	1
8990	19	44,005,715	44,006,048	333	1	4.545	2.545	10.636	6	4	15	1	0	2	PHLDB3, ETHE1	3104, 25515	in gene, downstream	ActReg chr19 #8990	0	0	1
8991	19	44,029,575	44,030,177	602	1	9.368	12.158	3.105	13	23	6	0	2	2	ETHE1, ZNF575	1520, -7464	in gene, upstream	ActReg chr19 #8991	0	1	0
8992	19	44,030,980	44,031,792	812	2	13.68	12.2	5.48	30	24	10	1	2	2	ETHE1, ZNF575	10, -5954	in gene, upstream	ActReg chr19 #8992	1	1	0
8993	19	44,036,641	44,037,597	956	1	6.379	11.241	9.207	14	18	18	1	2	3	ETHE1, ZNF575, XRCC1	-5723, -221, 42611	upstream, upstream, downstream	ActReg chr19 #8993	0	1	0
8994	19	44,099,839	44,101,043	1,204	2	15.921	16.368	7.289	37	28	10	1	2	2	IRGQ, ZNF576	-154, -103	upstream, upstream	ActReg chr19 #8994	1	1	0
8995	19	44,123,193	44,124,433	1,240	4	12.128	15.205	9.73	20	24	18	1	1	3	ZNF428, SRRM5, CADM4	201, 7560, 20178	in gene, downstream, downstream	ActReg chr19 #8995	1	1	1
8996	19	44,173,994	44,174,511	517	1	10	9.312	12.375	13	14	17	0	1	1	PLAUR	250	in gene	ActReg chr19 #8996	0	0	1
8997	19	44,269,032	44,269,861	829	1	10.731	12.385	6.615	14	25	13	0	0	2	C19orf61, KCNN4	-10304, 15963	upstream, downstream	ActReg chr19 #8997	0	1	0
8998	19	44,284,741	44,285,946	1,205	1	9.378	11.784	4.108	14	18	12	0	1	1	KCNN4	66	in gene	ActReg chr19 #8998	0	1	0
8999	19	44,292,960	44,293,734	774	2	16.44	17.8	2.75	34	40	4	0	0	2	KCNN4, LYPD5	-7938, 31461	upstream, downstream	ActReg chr19 #8999	1	1	0
9000	19	44,405,710	44,406,451	741	1	12	11.13	4.045	18	16	7	1	1	1	LOC100505715	-123	upstream	ActReg chr19 #9000	1	0	0
9001	19	44,506,689	44,507,691	1,002	1	8.226	12.903	5.226	14	21	9	1	2	3	ZNF155, LOC100505743, ZNF230	18835, -202, 113	downstream, upstream, in gene	ActReg chr19 #9001	0	1	0
9002	19	44,598,213	44,598,824	611	1	7.474	12.526	5.158	11	15	9	1	1	2	ZNF284, ZNF224	22221, 36	downstream, in gene	ActReg chr19 #9002	0	1	0
9003	19	44,617,078	44,617,711	633	1	11.35	11.1	3.2	19	18	5	1	2	3	ZNF224, LOC100379224, ZNF225	18912, -58, -154	downstream, upstream, upstream	ActReg chr19 #9003	1	0	0
9004	19	44,763,802	44,764,441	639	2	17.4	15	5.8	37	30	10	1	1	1	ZNF233	45	in gene	ActReg chr19 #9004	1	1	0
9005	19	44,808,708	44,809,277	569	2	9.706	10.177	9.059	14	16	15	1	1	1	ZNF235	186	in gene	ActReg chr19 #9005	0	1	1
9006	19	45,003,988	45,005,040	1,052	3	9.758	14.606	11.788	14	24	18	1	1	2	ZNF180, CEACAM20	60, 29034	in gene, downstream	ActReg chr19 #9006	1	1	1
9007	19	45,016,774	45,017,438	664	1	5.2	10.4	3.7	8	17	6	0	0	1	CEACAM20	16,442	in gene	ActReg chr19 #9007	0	1	0
9008	19	45,245,033	45,245,746	713	1	13.591	6.818	5.45	24	13	8	0	1	1	BCL3	-6,589	upstream	ActReg chr19 #9008	1	0	0
9009	19	45,429,718	45,430,035	317	1	6.8	3.7	10.4	9	5	13	0	0	1	APOC1	11,955	downstream	ActReg chr19 #9009	0	0	1
9010	19	45,457,800	45,459,088	1,288	2	10.65	12.6	6.289	20	24	13	1	1	3	APOC4, APOC2, CLPTM1	12949, 9201, -194	downstream, downstream, upstream	ActReg chr19 #9010	1	1	0
9011	19	45,492,987	45,493,505	518	1	5.294	5.118	11.706	8	13	21	0	0	1	CLPTM1	34,608	in gene	ActReg chr19 #9011	0	0	1
9012	19	45,582,093	45,582,874	781	1	11.917	13.333	6.583	22	24	11	1	2	3	SFRS16, ZNF296, GEMIN7	40185, -2795, -35	downstream, upstream, upstream	ActReg chr19 #9012	0	1	0
9013	19	45,595,642	45,596,709	1,067	1	6.767	13.677	5.529	20	26	12	1	1	2	GEMIN7, LRRC68	13657, -41	downstream, upstream	ActReg chr19 #9013	0	1	0
9014	19	45,716,120	45,716,796	676	1	6.333	6.19	12.191	10	10	19	0	0	1	EXOC3L2	21,011	in gene	ActReg chr19 #9014	0	0	1
9015	19	45,829,311	45,829,923	612	1	8.5	11.35	7.3	12	23	9	0	1	1	CKM	-3,384	upstream	ActReg chr19 #9015	0	1	0
9016	19	45,844,051	45,844,472	421	1	4.538	2.917	11.077	7	6	20	1	1	1	KLC3	263	in gene	ActReg chr19 #9016	0	0	1
9017	19	45,867,234	45,868,391	1,157	1	3.63	5.467	11.667	9	9	16	1	0	1	ERCC2	6,033	in gene	ActReg chr19 #9017	0	0	1
9018	19	45,873,335	45,874,354	1,019	2	18.375	18.219	6.031	47	47	13	1	1	2	ERCC2, PPP1R13L	1, 35763	in gene, downstream	ActReg chr19 #9018	1	1	0
9019	19	45,901,185	45,901,777	592	1	11.389	7.611	5.556	20	13	7	1	0	3	PPP1R13L, CD3EAP, ERCC1	8126, -7986, 25696	in gene, upstream, downstream	ActReg chr19 #9019	1	0	0
9020	19	45,908,506	45,910,424	1,918	3	32.4	37.617	8.617	133	146	19	2	2	3	PPP1R13L, CD3EAP, ERCC1	142, -2, 17712	in gene, upstream, downstream	ActReg chr19 #9020	1	1	1
9021	19	45,926,665	45,927,668	1,003	2	10.129	11.806	10.323	15	21	15	1	1	1	ERCC1	11	in gene	ActReg chr19 #9021	0	1	1
9022	19	45,946,443	45,946,939	496	1	11.2	8.733	12.533	18	12	16	1	0	0				ActReg chr19 #9022	0	0	1
9023	19	45,953,306	45,954,789	1,483	2	12.957	16.404	3.841	29	30	9	1	0	0				ActReg chr19 #9023	1	1	0
9024	19	45,958,841	45,959,864	1,023	2	12.594	14.625	6.31	22	31	15	0	0	0				ActReg chr19 #9024	1	1	0
9025	19	45,981,228	45,982,502	1,274	2	12.75	15.175	5.025	32	32	13	0	0	2	FOSB, RTN2	10612, 18448	downstream, downstream	ActReg chr19 #9025	1	1	0
9026	19	45,988,400	45,989,045	645	1	11.35	11.65	9.2	23	27	14	0	0	2	FOSB, RTN2	17469, 11591	downstream, in gene	ActReg chr19 #9026	0	1	0
9027	19	45,998,819	46,000,220	1,401	2	9.535	13.395	6.143	20	25	12	1	2	2	RTN2, FLJ40125	794, -2212	in gene, upstream	ActReg chr19 #9027	1	1	0
9028	19	46,009,466	46,010,181	715	2	10.13	8.87	10.826	14	12	17	1	1	3	RTN2, FLJ40125, VASP	-9510, 8092, -865	upstream, downstream, upstream	ActReg chr19 #9028	1	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9029	19	46,010,216	46,011,087	871	2	16.577	21.926	6.741	40	50	14	1	1	3	RTN2, FLJ40125, VASP	-10338, 8920, -37	upstream, downstream, upstream	ActReg chr19 #9029	1	1	0
9030	19	46,045,490	46,046,168	678	1	8.81	12.381	2.737	13	20	6	0	0	1	OPA3	42,293	in gene	ActReg chr19 #9030	0	1	0
9031	19	46,047,243	46,047,933	690	1	11	8.286	3.95	22	14	8	0	0	1	OPA3	40,534	in gene	ActReg chr19 #9031	1	0	0
9032	19	46,084,105	46,085,362	1,257	1	12.128	9.333	2.784	18	14	5	0	0	2	OPA3, GPR4	3389, 20733	in gene, downstream	ActReg chr19 #9032	1	0	0
9033	19	46,087,716	46,088,659	943	2	15.448	19.069	6.931	39	46	12	1	1	2	OPA3, GPR4	-65, 17279	upstream, downstream	ActReg chr19 #9033	1	1	0
9034	19	46,094,120	46,094,763	643	1	5.75	6.1	12.8	8	12	17	1	1	2	OPA3, GPR4	-6319, 11025	upstream, in gene	ActReg chr19 #9034	0	0	1
9035	19	46,145,022	46,145,919	897	2	10.357	12.179	7.536	15	19	14	1	2	3	EMI2, MIR330, LOC100287177	3305, -3125, 522	in gene, upstream, in gene	ActReg chr19 #9035	0	1	1
9036	19	46,194,810	46,196,295	1,485	1	8.936	12.723	8.702	13	19	14	1	2	3	GIPR, SNRPD2, QPCTL	24050, -109, -189	downstream, upstream, upstream	ActReg chr19 #9036	0	1	0
9037	19	46,220,390	46,221,285	895	2	17.036	17.536	6.857	38	42	17	1	0	1	FBXO46	13,314	in gene	ActReg chr19 #9037	1	1	0
9038	19	46,269,500	46,269,977	477	1	4.533	4.867	11.067	7	8	18	1	0	3	LOC388553, SIX5, DMPK	26784, 2759, 16077	downstream, in gene, downstream	ActReg chr19 #9038	0	0	1
9039	19	46,270,983	46,271,519	536	1	7.25	7.25	17.25	9	10	28	1	1	3	LOC388553, SIX5, DMPK	28297, 1246, 14564	downstream, in gene, downstream	ActReg chr19 #9039	0	0	1
9040	19	46,272,977	46,273,924	947	1	8.467	8.267	13.467	12	16	19	1	1	3	LOC388553, SIX5, DMPK	30496, -953, 12365	downstream, upstream, in gene	ActReg chr19 #9040	0	0	1
9041	19	46,280,263	46,281,195	932	1	4.759	3.655	11.759	9	6	15	1	0	3	SIX5, DMPK, DMWD	-8232, 5086, 15331	upstream, in gene, downstream	ActReg chr19 #9041	0	0	1
9042	19	46,319,486	46,320,463	977	1	4.29	4.29	10.645	6	8	16	0	1	2	RSPH6A, SYMPK	-1369, 46574	upstream, in gene	ActReg chr19 #9042	0	0	1
9043	19	46,365,950	46,367,049	1,099	1	10.057	13.286	8.571	18	22	15	1	2	2	SYMPK, FOXA3	49, -1019	in gene, upstream	ActReg chr19 #9043	0	1	0
9044	19	46,387,194	46,387,716	522	1	4	7.941	11.588	6	13	17	1	1	2	IRF2BP1, MYPOP	1921, 18407	in gene, downstream	ActReg chr19 #9044	0	0	1
9045	19	46,387,936	46,388,667	731	1	5.476	6.174	12.174	8	11	18	1	1	2	IRF2BP1, MYPOP	1075, 17561	in gene, downstream	ActReg chr19 #9045	0	0	1
9046	19	46,388,750	46,389,234	484	1	10.067	10.733	4.364	15	18	7	1	1	2	IRF2BP1, MYPOP	384, 16870	in gene, downstream	ActReg chr19 #9046	0	1	0
9047	19	46,389,310	46,390,450	1,140	2	11.361	14.833	7.394	20	27	13	2	1	2	IRF2BP1, MYPOP	-504, 15982	upstream, downstream	ActReg chr19 #9047	1	1	0
9048	19	46,405,928	46,406,379	451	1	9.214	10.5	8.214	11	13	14	1	1	1	MYPOP	-291	upstream	ActReg chr19 #9048	0	1	0
9049	19	46,430,782	46,431,474	692	2	9.955	12.046	3.409	27	23	8	0	0	0				ActReg chr19 #9049	1	1	0
9050	19	46,442,940	46,443,402	462	1	2.571	3.9	10.733	4	6	20	0	0	1	NOVA2	33,486	in gene	ActReg chr19 #9050	0	0	1
9051	19	46,455,610	46,456,627	1,017	1	8.125	17.375	8	17	34	11	1	0	1	NOVA2	20,559	in gene	ActReg chr19 #9051	0	1	0
9052	19	46,464,011	46,464,454	443	1	6.571	7	10.286	14	12	17	0	0	1	NOVA2	12,425	in gene	ActReg chr19 #9052	0	0	1
9053	19	46,571,645	46,572,412	767	1	6.167	14	2.708	9	24	5	0	0	0				ActReg chr19 #9053	0	1	0
9054	19	46,721,198	46,722,011	813	2	16.32	16.8	3.88	29	36	8	0	0	1	DKFZp434J0226	8,105	downstream	ActReg chr19 #9054	1	1	0
9055	19	46,885,181	46,885,589	408	1	2.455	2.917	12.077	6	4	18	0	0	1	PPP5C	35,091	in gene	ActReg chr19 #9055	0	0	1
9056	19	46,997,892	46,998,759	867	1	2.407	3.5	11.407	4	7	17	1	1	2	LOC100506012, PNMAL2	106132, 844	in gene, in gene	ActReg chr19 #9056	0	0	1
9057	19	47,103,708	47,104,489	781	2	14.68	15.8	8.318	28	27	14	1	2	2	LOC100506012, CALM3	359, -414	in gene, upstream	ActReg chr19 #9057	1	1	0
9058	19	47,163,975	47,164,310	335	1	7.3	9.2	12.8	10	11	18	1	2	2	DACT3, LOC100506068	253, -593	in gene, upstream	ActReg chr19 #9058	0	0	1
9059	19	47,177,642	47,178,234	592	1	2.833	3.889	12.833	5	6	21	0	0	2	LOC100506068, PRKD2	13203, 42446	downstream, in gene	ActReg chr19 #9059	0	0	1
9060	19	47,220,299	47,220,904	605	1	11.368	11.632	9.263	15	21	14	1	1	3	PRKD2, MIR320E, STRN4	-217, -7999, 29119	upstream, upstream, downstream	ActReg chr19 #9060	0	1	0
9061	19	47,227,710	47,228,136	426	1	5.214	5.143	12.929	7	7	22	0	1	2	PRKD2, STRN4	-7539, 21797	upstream, in gene	ActReg chr19 #9061	0	0	1
9062	19	47,260,350	47,260,817	467	1	8	6.2	11.733	11	10	19	1	0	1	FKRP	11,280	in gene	ActReg chr19 #9062	0	0	1
9063	19	47,287,865	47,288,685	820	2	13.577	13.654	5.115	25	24	12	0	0	1	SLC1A5	3,567	in gene	ActReg chr19 #9063	1	1	0
9064	19	47,291,504	47,292,149	645	2	9.2	6.75	11.7	15	10	19	1	1	1	SLC1A5	16	in gene	ActReg chr19 #9064	1	0	1
9065	19	47,296,446	47,296,967	521	1	11	7.235	2.308	19	10	5	0	1	1	SLC1A5	-4,864	upstream	ActReg chr19 #9065	1	0	0
9066	19	47,353,993	47,354,640	647	1	9.1	11.35	4.3	18	22	18	1	1	1	AP2S1	-113	upstream	ActReg chr19 #9066	0	1	0
9067	19	47,359,817	47,360,370	553	1	11.471	9	4.235	18	14	7	0	1	1	AP2S1	-5,890	upstream	ActReg chr19 #9067	1	0	0
9068	19	47,542,181	47,542,880	699	1	5.5	4.955	14.136	8	9	18	0	0	2	NPAS1, TMEM160	18387, 9352	in gene, downstream	ActReg chr19 #9068	0	0	1
9069	19	47,544,307	47,544,830	523	1	3.25	2.875	11.562	7	5	18	0	0	2	NPAS1, TMEM160	20425, 7314	in gene, downstream	ActReg chr19 #9069	0	0	1
9070	19	47,551,627	47,552,257	630	1	10.95	17	3.25	21	36	8	1	1	2	NPAS1, TMEM160	27799, -60	downstream, upstream	ActReg chr19 #9070	0	1	0
9071	19	47,615,259	47,615,860	601	1	9.474	9.789	8.053	12	16	15	1	1	1	ZC3H4	1,450	in gene	ActReg chr19 #9071	0	1	0
9072	19	47,633,728	47,634,431	703	1	11.636	8.682	5.5	17	15	9	1	1	1	SAE1	-1	upstream	ActReg chr19 #9072	1	0	0
9073	19	47,746,018	47,746,500	482	1	4.667	5.8	10.933	7	9	16	1	0	1	BBC3	-10,236	upstream	ActReg chr19 #9073	0	0	1
9074	19	47,759,400	47,759,952	552	1	10.471	15.471	7.882	15	30	15	1	1	1	CCDC9	-55	upstream	ActReg chr19 #9074	0	1	0
9075	19	47,767,496	47,767,937	441	1	4.273	4	11.5	7	6	16	1	0	1	CCDC9	7,985	in gene	ActReg chr19 #9075	0	0	1
9076	19	47,776,454	47,777,102	648	1	10.3	12.85	6.3	17	18	11	1	1	2	CCDC9, PRR24	17047, -1364	downstream, upstream	ActReg chr19 #9076	0	1	0
9077	19	47,792,674	47,793,104	430	1	12.077	8.077	2.538	18	11	6	0	0	0				ActReg chr19 #9077	1	0	0
9078	19	47,818,451	47,819,067	616	1	11.053	9.579	3.842	16	16	8	0	0	1	C5AR1	5,655	in gene	ActReg chr19 #9078	1	0	0
9079	19	47,843,951	47,844,983	1,032	1	3.393	3.406	12	6	6	17	0	0	2	GPR77, DHX34	4096, -8071	in gene, upstream	ActReg chr19 #9079	0	0	1
9080	19	47,875,773	47,876,389	616	1	3.45	2.7	11.5	5	4	19	0	0	1	DHX34	23,543	in gene	ActReg chr19 #9080	0	0	1
9081	19	47,882,915	47,883,446	531	1	6.125	2.8	11.688	12	5	18	0	0	1	DHX34	30,642	in gene	ActReg chr19 #9081	0	0	1
9082	19	47,939,915	47,941,644	1,729	2	11.074	10.37	5.926	24	21	14	0	0	1	SLC8A2	34,528	in gene	ActReg chr19 #9082	1	1	0
9083	19	47,947,308	47,948,086	778	2	14.625	14.042	3.696	25	29	8	0	0	1	SLC8A2	27,610	in gene	ActReg chr19 #9083	1	1	0
9084	19	47,973,000	47,973,455	455	1	6.214	5.5	11.5	10	7	18	0	1	2	SLC8A2, KPTN	2080, 14294	in gene, downstream	ActReg chr19 #9084	0	0	1
9085	19	47,987,094	47,987,793	699	1	14.046	14.454	4.636	23	27	8	1	2	3	KPTN, LOC100505681, NAPA	78, -27, 31054	in gene, upstream, downstream	ActReg chr19 #9085	0	1	0
9086	19	48,017,891	48,018,866	975	1	11.167	11.667	7.2	16	18	11	1	1	2	NAPA, ZNF541	119, 40735	in gene, downstream	ActReg chr19 #9086	0	1	0
9087	19	48,047,699	48,048,452	753	1	4.208	3.125	12.875	7	5	17	1	0	1	ZNF541	11,038	in gene	ActReg chr19 #9087	0	0	1
9088	19	48,111,264	48,112,151	887	2	7.679	10.429	10	15	18	19	1	1	1	GLTSCR1	254	in gene	ActReg chr19 #9088	0	1	1
9089	19	48,226,057	48,226,892	835	1	5.077	10.154	1.95	8	14	4	0	0	1	EHD2	9,873	in gene	ActReg chr19 #9089	0	1	0
9090	19	48,246,249	48,247,327	1,078	3	12.546	13.909	10.636	23	23	15	1	1	2	EHD2, GLTSCR2	30187, -2005	downstream, upstream	ActReg chr19 #9090	1	1	1
9091	19	48,277,058	48,277,544	486	1	11.333	10.533	3.467	15	14	5	0	2	2	LOC729626, SEPW1	-5204, -4541	upstream, upstream	ActReg chr19 #9091	1	0	0
9092	19	48,281,201	48,282,284	1,083	3	12.382	14.618	12.735	26	35	18	1	1	2	LOC729626, SEPW1	-9645, -100	upstream, upstream	ActReg chr19 #9092	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9093	19	48,613,562	48,614,227	665	1	7.762	10.714	4.158	13	20	8	0	1	2	PLA2G4C, LIG1	215, 59666	in gene, downstream	ActReg chr19 #9093	0	1	0
9094	19	48,673,160	48,674,128	968	3	8.567	11.8	8.667	18	24	18	1	2	2	LIG1, C19orf68	-84, -1566	upstream, upstream	ActReg chr19 #9094	1	1	1
9095	19	48,824,971	48,825,569	598	2	10.421	13.105	11.263	13	21	22	1	2	2	CCDC114, EMP3	-1938, -3359	upstream, upstream	ActReg chr19 #9095	0	1	1
9096	19	48,866,187	48,866,871	684	2	14.381	13.095	7.476	27	25	14	1	2	2	TMEM143, SYNGR4	657, -1128	in gene, upstream	ActReg chr19 #9096	1	1	0
9097	19	48,899,762	48,900,149	387	1	1	2.833	11.25	1	4	15	0	2	2	KDELR1, GRIN2D	-5145, 1823	upstream, in gene	ActReg chr19 #9097	0	0	1
9098	19	48,948,697	48,949,476	779	1	10.32	13.52	6.04	16	23	11	1	1	3	GRIN2D, GRWD1, KCNJ14	50954, 56, -9680	downstream, in gene, upstream	ActReg chr19 #9098	0	1	0
9099	19	48,957,652	48,958,072	420	1	3.769	2.923	12.077	6	5	19	0	1	3	GRIN2D, GRWD1, KCNJ14	59730, 8832, -904	downstream, downstream, upstream	ActReg chr19 #9099	0	0	1
9100	19	49,099,308	49,099,777	469	1	3.1	1.75	11.267	4	3	17	0	0	2	SULT2B1, FAM83E	44113, 17152	in gene, downstream	ActReg chr19 #9100	0	0	1
9101	19	49,119,134	49,119,558	424	1	6.571	8.429	12.857	10	12	18	0	2	4	FAM83E, SPACA4, RPL18, SPHK2	-2652, 9346, 3087, -3202	upstream, downstream, in gene, upstream	ActReg chr19 #9101	0	0	1
9102	19	49,121,775	49,123,178	1,403	2	11.386	12.25	9.227	18	21	17	1	3	3	FAM83E, RPL18, SPHK2	-5782, -43, -72	upstream, upstream, upstream	ActReg chr19 #9102	0	1	1
9103	19	49,129,228	49,129,690	462	1	3.214	6.286	12.643	6	8	21	0	1	3	RPL18, SPHK2, DBP	-7026, 6911, 11180	upstream, in gene, downstream	ActReg chr19 #9103	0	0	1
9104	19	49,132,497	49,133,448	951	1	5.467	6.133	12.567	9	9	20	1	0	3	SPHK2, DBP, CA11	10424, 7667, 16479	in gene, downstream, downstream	ActReg chr19 #9104	0	0	1
9105	19	49,140,662	49,141,647	985	2	14.677	16.032	7.774	35	33	14	1	1	3	SPHK2, DBP, CA11	18606, -515, 8297	downstream, upstream, downstream	ActReg chr19 #9105	1	1	0
9106	19	49,147,904	49,148,632	728	1	10.783	8.609	4.333	20	15	9	0	2	2	DBP, CA11	-7629, 1183	upstream, in gene	ActReg chr19 #9106	1	0	0
9107	19	49,149,327	49,150,140	813	2	14.4	14.8	5.16	29	26	10	0	1	2	DBP, CA11	-9094, -282	upstream, upstream	ActReg chr19 #9107	1	1	0
9108	19	49,173,805	49,174,156	351	1	2.455	3	10.091	5	4	14	1	1	1	NTN5	2,284	in gene	ActReg chr19 #9108	0	0	1
9109	19	49,223,683	49,224,692	1,009	2	12	13.129	6.032	20	22	10	1	1	2	MAMSTR, RASIP1	-1211, 19783	upstream, in gene	ActReg chr19 #9109	1	1	0
9110	19	49,229,294	49,229,628	334	1	2.9	2.3	12.4	4	4	18	0	1	2	MAMSTR, RASIP1	-6485, 14509	upstream, in gene	ActReg chr19 #9110	0	0	1
9111	19	49,256,156	49,256,857	701	1	3.273	6.524	10.318	7	11	14	1	3	3	IZUMO1, FUT1, FGF21	-6340, 2141, -2838	upstream, in gene, upstream	ActReg chr19 #9111	0	0	1
9112	19	49,298,312	49,299,213	901	2	18.808	17.286	6.25	46	38	10	1	0	1	BCAT2	15,558	in gene	ActReg chr19 #9112	1	1	0
9113	19	49,375,351	49,375,870	519	1	7.25	10.812	12.438	11	15	16	1	2	3	PLEKHA4, PPP1R15A, TULP2	-3726, -39, 26386	upstream, upstream, downstream	ActReg chr19 #9113	0	0	1
9114	19	49,429,064	49,429,410	346	1	5.364	4.455	10.909	8	6	15	0	0	2	NUCB1, DHDH	25930, -7702	downstream, upstream	ActReg chr19 #9114	0	0	1
9115	19	49,468,356	49,469,642	1,286	3	10.375	11.925	8.8	21	21	21	1	1	3	BAX, FTL, GYS1	10882, 433, 27611	downstream, in gene, downstream	ActReg chr19 #9115	1	1	1
9116	19	49,496,599	49,497,377	778	2	14.64	11.92	7.28	28	21	11	1	2	2	GYS1, RUVBL2	-378, -168	upstream, upstream	ActReg chr19 #9116	1	1	0
9117	19	49,588,267	49,589,255	988	2	11.065	14.065	6.032	18	23	12	1	1	1	SNRNP70	296	in gene	ActReg chr19 #9117	1	1	0
9118	19	49,621,806	49,622,672	866	2	17.704	17.296	7.667	37	34	15	1	2	4	SNRNP70, LIN7B, C19orf73, PPFIA3	33774, 4621, 158, -424	downstream, downstream, in gene, upstream	ActReg chr19 #9118	1	1	0
9119	19	49,652,683	49,654,318	1,635	2	14.686	16.569	8.725	27	26	15	1	1	3	PPFIA3, HRC, TRPM4	30837, 5181, -7552	in gene, downstream, upstream	ActReg chr19 #9119	1	1	0
9120	19	49,655,143	49,655,520	377	1	4.833	4.667	11.5	7	6	19	1	1	3	PPFIA3, HRC, TRPM4	32668, 3350, -5721	downstream, in gene, upstream	ActReg chr19 #9120	0	0	1
9121	19	49,866,907	49,867,420	513	1	6.375	2.812	13.125	9	5	20	1	2	2	TEAD2, DKKL1	-1449, 121	upstream, in gene	ActReg chr19 #9121	0	0	1
9122	19	49,939,628	49,940,221	593	1	3.176	3.389	11.944	5	5	19	1	0	3	LOC100507003, SLC17A7, PIH1D1	10236, 4884, 15191	downstream, in gene, downstream	ActReg chr19 #9122	0	0	1
9123	19	49,946,419	49,947,416	997	2	13.097	9.9	8.194	25	21	13	1	1	3	SLC17A7, PIH1D1, ALDH16A1	-2109, 8198, -9556	upstream, downstream, upstream	ActReg chr19 #9123	1	1	0
9124	19	49,956,292	49,957,239	947	2	11.448	7.643	8.448	24	14	17	1	2	2	PIH1D1, ALDH16A1	-1650, 292	upstream, in gene	ActReg chr19 #9124	1	0	1
9125	19	49,967,148	49,967,559	411	1	4.154	3.462	10.923	5	5	16	1	0	2	ALDH16A1, FLT3LG	10880, -10133	in gene, upstream	ActReg chr19 #9125	0	0	1
9126	19	49,977,039	49,977,562	523	1	7.438	10.688	11.375	13	15	17	0	1	2	ALDH16A1, FLT3LG	20827, -186	downstream, upstream	ActReg chr19 #9126	0	0	1
9127	19	49,981,858	49,982,618	760	2	16.522	20.652	3.591	42	53	8	0	0	3	ALDH16A1, FLT3LG, RPL13A	25765, 4752, -8627	downstream, in gene, upstream	ActReg chr19 #9127	1	1	0
9128	19	49,990,548	49,991,203	655	1	8	10.809	15.857	11	17	29	2	5	8	FLT3LG, RPL13A, SNORD32A, SNORD33, SNORD34, SNORD35A, RPS11, SNORD35B	13389, 10, -2348, -2999, -3289, -3557, -8759, -10101	downstream, in gene, upstream, upstream, upstream, upstream, upstream, upstream	ActReg chr19 #9128	0	0	1
9129	19	49,999,428	49,999,951	523	1	10.062	7.562	13.938	15	11	19	1	2	9	FLT3LG, RPL13A, SNORD32A, SNORD33, SNORD34, SNORD35A, RPS11, SNORD35B, MIR150	22203, 8824, 6466, 5815, 5525, 5257, 55, -1287, 4436	downstream, downstream, downstream, downstream, downstream, downstream, downstream, in gene, upstream, downstream	ActReg chr19 #9129	0	0	1
9130	19	50,116,647	50,118,000	1,353	1	9.143	12.571	4.342	17	21	12	0	0	1	PRR12	22,411	in gene	ActReg chr19 #9130	0	1	0
9131	19	50,143,080	50,144,315	1,235	2	14.079	12.79	6.114	30	25	12	1	2	2	RRAS, SCAF1	-297, -1685	upstream, upstream	ActReg chr19 #9131	1	1	0
9132	19	50,144,792	50,145,627	835	2	14.5	10.885	8.962	32	20	16	1	2	2	RRAS, SCAF1	-1809, -173	upstream, upstream	ActReg chr19 #9132	1	1	0
9133	19	50,161,170	50,161,755	585	1	3.944	5.167	11.444	7	8	17	0	1	3	SCAF1, IRF3, BCL2L12	16080, 7670, -6937	in gene, downstream, upstream	ActReg chr19 #9133	0	0	1
9134	19	50,165,203	50,165,714	511	1	4.375	6.75	11.5	8	10	19	0	1	3	SCAF1, IRF3, BCL2L12	20076, 3674, -2941	downstream, in gene, upstream	ActReg chr19 #9134	0	0	1
9135	19	50,220,648	50,221,266	618	2	14.526	14.368	4.632	28	30	12	0	0	1	CPT1C	26,556	downstream	ActReg chr19 #9135	1	1	0
9136	19	50,248,345	50,248,881	536	1	2.941	4.235	11.118	5	5	17	0	0	1	TSKS	17,902	in gene	ActReg chr19 #9136	0	0	1
9137	19	50,295,956	50,296,441	485	1	5	4.2	11.333	10	7	18	0	0	1	AP2A1	26,018	in gene	ActReg chr19 #9137	0	0	1
9138	19	50,316,417	50,317,283	866	2	13.407	12.37	2.36	23	24	5	1	2	3	AP2A1, FUZ, MED25	46670, -283, -4686	downstream, upstream, upstream	ActReg chr19 #9138	1	1	0
9139	19	50,322,304	50,322,789	485	1	6.25	3.75	11.875	9	6	15	0	2	2	FUZ, MED25	-5979, 1010	upstream, in gene	ActReg chr19 #9139	0	0	1
9140	19	50,339,051	50,339,515	464	1	4.786	1.714	11.071	9	3	17	0	0	2	MED25, LOC100506033	17747, 15650	in gene, downstream	ActReg chr19 #9140	0	0	1
9141	19	50,353,948	50,354,583	635	1	7.7	10.85	5.077	14	18	7	1	2	4	LOC100506033, PTOV1, LOC100506002, PNKP	668, -151, 8279, 16553	in gene, upstream, downstream, downstream	ActReg chr19 #9141	0	1	0
9142	19	50,362,881	50,363,477	596	1	6.444	4.889	12.889	8	7	20	0	1	5	LOC100506033, PTOV1, LOC100506002, PNKP, AKT1S1	-8246, 8763, -635, 7639, 17465	upstream, in gene, upstream, downstream, downstream	ActReg chr19 #9142	0	0	1
9143	19	50,372,831	50,373,480	649	1	8.381	10.333	15.238	13	18	28	1	2	4	PTOV1, PNKP, AKT1S1, TBC1D17	18739, -2337, 7489, -7527	downstream, upstream, in gene, upstream	ActReg chr19 #9143	0	0	1
9144	19	50,379,338	50,381,030	1,692	3	11.264	12.358	8.472	21	19	17	1	2	3	PNKP, AKT1S1, TBC1D17	-9366, 460, -498	upstream, in gene, upstream	ActReg chr19 #9144	1	1	1
9145	19	50,392,810	50,393,396	586	1	2.111	5.056	11.389	3	8	18	1	0	2	TBC1D17, IL4I1	12421, 39659	downstream, in gene	ActReg chr19 #9145	0	0	1
9146	19	50,411,430	50,412,244	814	1	5.48	5.56	11.8	10	10	16	0	0	2	IL4I1, NUP62	20925, 21151	in gene, in gene	ActReg chr19 #9146	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9147	19	50,431,933	50,433,105	1,172	3	9.216	13.297	9.081	16	28	15	1	3	3	IL4I1, NUP62, ATF5	243, 469, 560	in gene, in gene, in gene	ActReg chr19 #9147	1	1	1
9148	19	50,489,558	50,492,534	2,976	2	39.215	51.849	4.124	257	320	10	0	0	1	VRK3	37,759	in gene	ActReg chr19 #9148	1	1	0
9149	19	50,829,121	50,829,896	775	1	4.368	8.917	13.792	15	14	19	1	0	1	KCNC3	3,126	in gene	ActReg chr19 #9149	0	0	1
9150	19	50,836,501	50,837,182	681	2	13.588	8.286	14.524	22	15	23	1	1	1	KCNC3	-4,207	upstream	ActReg chr19 #9150	1	0	1
9151	19	50,879,280	50,879,729	449	1	10.5	8.929	11.286	14	14	17	1	1	2	NR1H2, POLD1	-181, -8089	upstream, upstream	ActReg chr19 #9151	0	0	1
9152	19	50,919,944	50,920,497	553	1	3.941	4.235	11.294	6	7	14	0	1	2	POLD1, SPIB	32627, -1975	in gene, upstream	ActReg chr19 #9152	0	0	1
9153	19	50,970,356	50,970,966	610	1	2.667	3.263	11.053	6	4	15	0	0	3	MYBPC2, FAM71E1, C19orf83	34501, 9342, -9075	downstream, in gene, upstream	ActReg chr19 #9153	0	0	1
9154	19	51,011,258	51,011,657	399	1	4.923	6.077	9.385	7	8	15	0	0	3	JOSD2, ASPDH, LRRC4B	2888, 6490, 59845	in gene, downstream, downstream	ActReg chr19 #9154	0	0	1
9155	19	51,014,134	51,015,139	1,005	2	12.469	14.062	6.625	24	24	17	1	1	3	JOSD2, ASPDH, LRRC4B	-291, 3311, 56666	upstream, downstream, downstream	ActReg chr19 #9155	1	1	0
9156	19	51,017,549	51,017,939	390	1	6.5	6.083	13.25	11	10	18	0	2	3	JOSD2, ASPDH, LRRC4B	-3399, 203, 53558	upstream, in gene, downstream	ActReg chr19 #9156	0	0	1
9157	19	51,135,557	51,135,908	351	1	4.727	4.091	9.727	7	6	14	0	0	1	SYT3	7,360	in gene	ActReg chr19 #9157	0	0	1
9158	19	51,142,114	51,142,698	584	1	6.222	6	12.889	9	9	20	1	1	1	SYT3	686	in gene	ActReg chr19 #9158	0	0	1
9159	19	51,161,604	51,162,391	787	1	9.417	11.875	5.708	13	16	8	1	0	2	LOC342918, SHANK1	9295, 58198	in gene, downstream	ActReg chr19 #9159	0	1	0
9160	19	51,198,664	51,199,333	669	1	5.85	6.333	12.762	11	11	23	1	0	1	SHANK1	21,197	in gene	ActReg chr19 #9160	0	0	1
9161	19	51,205,620	51,205,978	358	1	4.5	2.727	11.273	10	4	14	0	0	1	SHANK1	14,396	in gene	ActReg chr19 #9161	0	0	1
9162	19	51,228,402	51,228,864	462	1	9.533	10.8	11.667	15	17	19	1	1	2	SHANK1, CLEC11A	-8438, 2028	upstream, in gene	ActReg chr19 #9162	0	0	1
9163	19	51,293,407	51,294,120	713	1	2.8	2.739	10.826	4	5	16	0	1	4	ACPT, C19orf48, SNORD88B, SNORD88A	91, 14211, 8619, 9029	in gene, downstream, downstream, downstream	ActReg chr19 #9163	0	0	1
9164	19	51,301,051	51,302,033	982	1	5.581	5.774	14.129	11	10	23	0	2	5	ACPT, C19orf48, SNORD88B, SNORD88A, SNORD88C	7870, 6432, 840, 1250, 4136	downstream, in gene, downstream, downstream, downstream, downstream	ActReg chr19 #9164	0	0	1
9165	19	51,302,368	51,302,951	583	1	2.579	5.684	12.526	6	9	20	0	2	5	ACPT, C19orf48, SNORD88B, SNORD88A, SNORD88C	8987, 5315, -277, 133, 3019	downstream, in gene, upstream, downstream, downstream, downstream	ActReg chr19 #9165	0	0	1
9166	19	51,307,480	51,308,455	975	3	19.29	25.742	12.226	43	62	24	1	4	5	ACPT, C19orf48, SNORD88B, SNORD88A, SNORD88C	14295, 7, -5555, -5175, -2289	downstream, in gene, upstream, upstream, upstream	ActReg chr19 #9166	1	1	1
9167	19	51,373,454	51,374,204	750	2	12.391	12.87	5.818	19	22	11	0	1	2	KLK3, KLK2	15658, -2860	downstream, upstream	ActReg chr19 #9167	1	1	0
9168	19	51,521,924	51,522,491	567	1	4.176	5.176	9.353	7	9	12	1	1	4	KLK9, KLK10, KLK11, KLK12	-9317, 1224, 9083, 15941	upstream, in gene, downstream, downstream	ActReg chr19 #9168	0	0	1
9169	19	51,857,346	51,857,676	330	1	7.5	5.3	10.6	11	6	15	0	0	1	ETFB	12,161	in gene	ActReg chr19 #9169	0	0	1
9170	19	51,867,404	51,868,100	696	1	7.136	13.909	5.091	11	24	13	0	1	3	ETFB, CLDND2, NKG7	1920, 4505, 8208	in gene, downstream, downstream	ActReg chr19 #9170	0	1	0
9171	19	51,870,870	51,871,387	517	1	8.625	6.812	13.062	15	12	21	1	2	3	ETFB, CLDND2, NKG7	-1456, 1129, 4832	upstream, in gene, downstream	ActReg chr19 #9171	0	0	1
9172	19	51,925,089	51,925,743	654	2	10.8	14.85	5.2	23	33	8	1	1	2	SIGLEC10, LOC100129083	-4359, 6256	upstream, downstream	ActReg chr19 #9172	1	1	0
9173	19	51,951,237	51,951,604	367	1	1	5.545	11.364	1	7	17	0	0	1	SIGLEC8	10,288	downstream	ActReg chr19 #9173	0	0	1
9174	19	51,983,594	51,984,402	808	1	7.4	13.56	4.64	16	22	8	0	0	1	CEACAM18	4,160	in gene	ActReg chr19 #9174	0	1	0
9175	19	52,056,282	52,057,058	776	2	9.92	12.4	3.48	25	25	6	0	0	0				ActReg chr19 #9175	1	1	0
9176	19	52,074,097	52,074,711	614	1	12.368	9.211	3.263	19	14	5	1	1	1	ZNF175	-127	upstream	ActReg chr19 #9176	1	0	0
9177	19	52,097,494	52,098,139	645	1	10.55	14.05	8	18	24	10	1	1	2	ZNF175, FLJ30403	23285, -183	downstream, upstream	ActReg chr19 #9177	0	1	0
9178	19	52,111,031	52,111,899	868	2	14.185	16.259	2.421	33	37	4	0	0	1	SIGLEC5	22,262	downstream	ActReg chr19 #9178	1	1	0
9179	19	52,531,413	52,531,998	585	1	10.5	12.722	6.722	15	19	12	1	1	2	ZNF614, ZNF432	-25, 20368	upstream, downstream	ActReg chr19 #9179	0	1	0
9180	19	52,693,299	52,693,861	562	1	4.889	6.556	10.667	7	9	16	1	1	1	PPP2R1A	525	in gene	ActReg chr19 #9180	0	0	1
9181	19	52,800,463	52,801,119	656	2	8.05	10.45	8.1	12	18	14	1	1	2	ZNF766, ZNF480	27967, 365	downstream, in gene	ActReg chr19 #9181	0	1	1
9182	19	53,496,016	53,496,345	329	1	4.5	3.9	11.7	8	5	15	0	0	0				ActReg chr19 #9182	0	0	1
9183	19	54,023,724	54,024,519	795	1	11.4	9.68	4.32	20	14	7	2	1	1	ZNF331	-56	upstream	ActReg chr19 #9183	1	0	0
9184	19	54,040,701	54,041,266	565	1	3.278	7	11.889	9	10	15	1	0	1	ZNF331	16,806	in gene	ActReg chr19 #9184	0	0	1
9185	19	54,406,127	54,406,980	853	2	10.482	16.593	2.8	21	30	5	0	0	2	PRKCG, CACNG7	21086, -9518	in gene, upstream	ActReg chr19 #9185	1	1	0
9186	19	54,412,744	54,413,195	451	1	4.429	3.214	12.571	7	4	18	1	1	2	PRKCG, CACNG7	27502, -3102	downstream, upstream	ActReg chr19 #9186	0	0	1
9187	19	54,430,571	54,431,613	1,042	2	12.25	15.719	3.769	25	37	9	0	0	1	CACNG7	15,021	in gene	ActReg chr19 #9187	1	1	0
9188	19	54,483,045	54,483,574	529	1	9	12.75	5.438	13	21	9	1	1	2	CACNG8, MIR935	17015, -2252	in gene, upstream	ActReg chr19 #9188	0	1	0
9189	19	54,493,000	54,493,614	614	1	4.556	5.421	11.474	7	11	14	0	1	3	CACNG8, MIR935, CACNG6	27013, 7746, -2235	downstream, downstream, upstream	ActReg chr19 #9189	0	0	1
9190	19	54,605,778	54,606,443	665	2	10.905	12.667	11.048	20	24	15	1	2	3	OSCAR, NDUFA3, TFPT	-1962, -50, 12945	upstream, upstream, downstream	ActReg chr19 #9190	0	1	1
9191	19	54,618,354	54,619,489	1,135	2	11.583	16.111	7.5	24	30	11	1	2	3	NDUFA3, TFPT, PRPF31	12761, 134, 131	downstream, in gene, in gene	ActReg chr19 #9191	1	1	0
9192	19	54,641,257	54,641,657	400	1	8.167	5.583	14	11	9	19	1	1	2	PRPF31, CNOT3	22667, 21	downstream, in gene	ActReg chr19 #9192	0	0	1
9193	19	54,662,796	54,663,537	741	1	6.409	12.478	6.652	9	19	11	1	1	3	CNOT3, LENG1, TMC4	21730, 280, 13778	downstream, in gene, downstream	ActReg chr19 #9193	0	1	0
9194	19	54,671,822	54,672,288	466	1	5.267	6.4	11	10	9	18	0	0	3	LENG1, TMC4, MBOAT7	-8609, 4889, 21678	upstream, in gene, downstream	ActReg chr19 #9194	0	0	1
9195	19	54,704,375	54,705,071	696	1	10.818	10.682	11.364	14	15	15	1	1	2	TSEN34, RPS9	10604, -3	downstream, upstream	ActReg chr19 #9195	0	0	1
9196	19	54,744,087	54,744,410	323	1	3.8	3	10.8	5	5	14	0	1	2	LILRA6, LILRB5	2476, 16919	in gene, downstream	ActReg chr19 #9196	0	0	1
9197	19	54,815,490	54,816,256	766	2	9.917	11.792	1.647	18	18	3	0	0	1	LILRA5	8,536	downstream	ActReg chr19 #9197	1	1	0
9198	19	54,944,974	54,945,398	424	1	3.364	4.154	9.846	5	6	14	0	0	1	TTYH1	18,551	in gene	ActReg chr19 #9198	0	0	1
9199	19	54,945,892	54,946,398	506	1	2.933	4.067	12.2	5	6	15	0	0	1	TTYH1	19,510	in gene	ActReg chr19 #9199	0	0	1
9200	19	54,959,240	54,961,088	1,848	2	9.31	13.483	7.224	16	27	18	1	1	1	LENG8	99	in gene	ActReg chr19 #9200	1	1	0
9201	19	54,974,560	54,976,303	1,743	2	11.909	11.146	5.08	20	18	12	1	1	3	LENG8, LENG9, CDC42EP5	15366, -537, 8991	downstream, upstream, downstream	ActReg chr19 #9201	1	1	0
9202	19	54,982,353	54,982,796	443	1	3.429	6	12.071	5	7	16	1	2	3	LENG8, LENG9, CDC42EP5	22509, -7680, 1848	downstream, upstream, in gene	ActReg chr19 #9202	0	0	1
9203	19	55,028,508	55,029,131	623	2	8.75	14.1	2.412	15	29	6	0	0	1	LAIR2	14,806	downstream	ActReg chr19 #9203	1	1	0
9204	19	55,195,609	55,196,346	737	2	14	18.609	2.619	32	45	4	0	0	0				ActReg chr19 #9204	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9205	19	55,555,888	55,556,533	645	1	3.6	3.2	11.25	5	7	15	0	1	2	GP6, RDH13	-6578, 24704	upstream, in gene	ActReg chr19 #9205	0	0	1
9206	19	55,607,576	55,608,106	530	1	2.625	3.25	11.235	4	5	17	0	0	2	EPS8L1, PPP1R12C	20620, 21086	downstream, in gene	ActReg chr19 #9206	0	0	1
9207	19	55,609,901	55,610,714	813	1	3.76	4.4	11.52	8	7	17	0	0	1	PPP1R12C	18,620	in gene	ActReg chr19 #9207	0	0	1
9208	19	55,690,148	55,691,981	1,833	2	9.158	13.702	6.07	22	22	12	1	1	2	SYT5, PTPRH	656, 29810	in gene, downstream	ActReg chr19 #9208	1	1	0
9209	19	55,700,415	55,701,333	918	2	13.31	12.828	2.759	25	22	5	0	0	2	SYT5, PTPRH	-9154, 20000	upstream, in gene	ActReg chr19 #9209	1	1	0
9210	19	55,727,551	55,729,019	1,468	2	19.261	23.783	6.717	41	48	10	1	1	2	PTPRH, TMEM86B	-7411, 12347	upstream, downstream	ActReg chr19 #9210	1	1	0
9211	19	55,769,210	55,769,546	336	1	5.727	10.091	12.091	10	13	15	1	1	2	SAPS1, HSPBP1	660, 22373	in gene, downstream	ActReg chr19 #9211	0	0	1
9212	19	55,769,953	55,771,159	1,206	3	15.784	15.514	6.167	25	31	17	1	1	2	SAPS1, HSPBP1	-518, 21195	upstream, downstream	ActReg chr19 #9212	1	1	1
9213	19	55,791,328	55,791,901	573	1	8.235	10.444	10.944	14	20	16	1	2	2	HSPBP1, BRSK1	137, -3920	in gene, upstream	ActReg chr19 #9213	0	0	1
9214	19	55,872,399	55,872,933	534	1	3.529	4.059	11.353	4	8	15	0	2	3	COX6B2, FAM71E2, IL11	-6484, 1954, 9148	upstream, in gene, downstream	ActReg chr19 #9214	0	0	1
9215	19	55,873,194	55,873,721	527	1	3.571	1.875	11.312	5	2	16	1	2	3	COX6B2, FAM71E2, IL11	-7275, 1163, 8357	upstream, in gene, downstream	ActReg chr19 #9215	0	0	1
9216	19	55,887,796	55,888,281	485	1	6.8	4.733	9.333	13	8	15	0	2	4	IL11, TMEM190, LOC388564, RPL28	-6224, -166, 7589, -9262	upstream, upstream, downstream, upstream	ActReg chr19 #9216	0	0	1
9217	19	55,897,076	55,897,736	660	1	10.476	11.952	14.143	16	22	23	1	2	3	TMEM190, LOC388564, RPL28	9202, -1779, 106	downstream, upstream, in gene	ActReg chr19 #9217	0	0	1
9218	19	55,918,867	55,920,085	1,218	2	11	12.237	5.486	17	21	11	1	1	1	UBE2S	-151	upstream	ActReg chr19 #9218	1	1	0
9219	19	55,944,323	55,944,644	321	1	5.2	2.4	12.5	7	4	18	1	0	1	SHISA7	9,747	in gene	ActReg chr19 #9219	0	0	1
9220	19	55,948,045	55,949,392	1,347	2	14.167	20.238	5.538	45	52	16	0	0	1	SHISA7	5,512	in gene	ActReg chr19 #9220	1	1	0
9221	19	55,953,311	55,953,725	414	1	4.75	4.538	10	6	6	16	1	1	1	SHISA7	712	in gene	ActReg chr19 #9221	0	0	1
9222	19	55,959,103	55,959,446	343	1	8.091	7.273	9.455	10	9	14	0	1	2	SHISA7, ISOC2	-5044, 13775	upstream, downstream	ActReg chr19 #9222	0	0	1
9223	19	55,974,720	55,975,236	516	1	1.133	5.118	11.706	2	9	14	0	1	1	ISOC2	-1,929	upstream	ActReg chr19 #9223	0	0	1
9224	19	55,987,467	55,988,178	711	1	10.454	12.773	7.048	18	21	11	1	1	2	ZNF628, NAT14	123, -8772	in gene, upstream	ActReg chr19 #9224	0	1	0
9225	19	55,988,205	55,988,909	704	2	16.636	22.909	3.762	28	40	8	1	1	2	ZNF628, NAT14	858, -8037	in gene, upstream	ActReg chr19 #9225	1	1	0
9226	19	56,030,346	56,031,782	1,436	2	11.222	17.578	2.867	19	38	5	0	0	2	SSC5D, SBK2	31194, 17371	downstream, downstream	ActReg chr19 #9226	1	1	0
9227	19	56,092,232	56,093,293	1,061	1	6.454	12	5.581	12	20	16	0	1	2	ZNF579, FIZ1	-551, 18131	upstream, downstream	ActReg chr19 #9227	0	1	0
9228	19	56,110,641	56,111,808	1,167	3	12.529	14.162	8.703	32	24	14	1	2	2	FIZ1, ZNF524	-331, -506	upstream, upstream	ActReg chr19 #9228	1	1	1
9229	19	56,150,382	56,150,876	494	1	10.867	11.333	2.733	17	13	4	0	2	3	ZNF580, ZNF581, CCDC106	-1763, -4357, -8325	upstream, upstream, upstream	ActReg chr19 #9229	1	0	0
9230	19	56,151,604	56,152,392	788	1	8.56	11.92	14.2	15	19	22	1	3	3	ZNF580, ZNF581, CCDC106	-394, -2988, -6956	upstream, upstream, upstream	ActReg chr19 #9230	0	0	1
9231	19	56,154,107	56,155,173	1,066	1	10	10.971	6.094	18	23	11	2	3	3	ZNF580, ZNF581, CCDC106	2248, -346, -4314	in gene, upstream, upstream	ActReg chr19 #9231	0	1	0
9232	19	56,155,764	56,156,615	851	1	6.185	9	11.593	13	12	16	1	2	4	ZNF580, ZNF581, CCDC106, U2AF2	3797, 1203, -2765, -9227	downstream, in gene, upstream, upstream	ActReg chr19 #9232	0	0	1
9233	19	56,158,887	56,160,246	1,359	4	17.976	21.119	12.881	39	44	32	1	2	4	ZNF580, ZNF581, CCDC106, U2AF2	7174, 4580, 612, -5850	downstream, downstream, in gene, upstream	ActReg chr19 #9233	1	1	1
9234	19	56,186,267	56,186,872	605	2	10.421	13.105	4.778	21	19	11	1	1	2	U2AF2, EPN1	21153, 8	downstream, in gene	ActReg chr19 #9234	1	1	0
9235	19	56,215,222	56,215,546	324	1	2	2.4	11.6	3	4	15	1	0	2	EPN1, NLRP9	28823, 34384	downstream, downstream	ActReg chr19 #9235	0	0	1
9236	19	56,320,429	56,321,137	708	1	12.546	8.227	1.625	20	17	3	0	0	1	NLRP11	27,345	in gene	ActReg chr19 #9236	1	0	0
9237	19	56,530,219	56,530,641	422	1	6.231	11.538	1.846	8	17	3	0	0	1	NLRP5	19,338	in gene	ActReg chr19 #9237	0	1	0
9238	19	56,614,419	56,614,975	556	1	5.353	4.706	11.588	9	8	19	1	0	1	ZNF787	17,952	in gene	ActReg chr19 #9238	0	0	1
9239	19	56,631,740	56,632,129	389	1	7.615	6.385	10.692	10	9	18	1	1	1	ZNF787	715	in gene	ActReg chr19 #9239	0	0	1
9240	19	56,652,091	56,652,687	596	1	8.368	13.947	6.211	15	28	9	1	1	1	ZNF444	-167	upstream	ActReg chr19 #9240	0	1	0
9241	19	56,763,967	56,764,583	616	1	10.55	7	7	18	15	14	0	0	1	ZSCAN5D	12,502	downstream	ActReg chr19 #9241	1	0	0
9242	19	56,825,876	56,826,851	975	1	10.742	11.484	6.774	14	18	11	1	0	1	LOC100506374	13,058	downstream	ActReg chr19 #9242	0	1	0
9243	19	56,915,158	56,915,666	508	1	7.812	9.25	10.438	13	12	16	1	1	2	BC036928, ZNF583	10367, 29	downstream, in gene	ActReg chr19 #9243	0	0	1
9244	19	57,049,709	57,050,145	436	1	10.154	11.571	10.5	15	20	19	1	1	3	ZNF471, ZFP28, LOC100506419	30715, -390, 28855	downstream, upstream, downstream	ActReg chr19 #9244	0	1	0
9245	19	57,078,327	57,079,250	923	1	6.483	10.379	5.655	11	18	11	1	2	2	LOC100506419, ZNF470	-6, -102	upstream, upstream	ActReg chr19 #9245	0	1	0
9246	19	57,106,456	57,107,107	651	1	7.381	9.905	6.55	9	18	11	1	1	1	ZNF71	117	in gene	ActReg chr19 #9246	0	1	0
9247	19	57,149,041	57,151,160	2,119	2	29.742	35.03	3	134	144	7	1	1	1	LOC147670	-4,427	upstream	ActReg chr19 #9247	1	1	0
9248	19	57,175,100	57,175,695	595	1	3.056	6.526	12	8	9	16	1	0	2	LOC147670, ZNF835	20870, 8849	downstream, in gene	ActReg chr19 #9248	0	0	1
9249	19	57,182,959	57,183,530	571	1	4.722	7.722	11.222	8	11	18	1	1	1	ZNF835	1,002	in gene	ActReg chr19 #9249	0	0	1
9250	19	57,349,210	57,349,666	456	1	4.733	6.133	11.267	7	12	17	0	3	3	ZIM2, PEG3, MIMT1	2659, 2656, -2832	in gene, in gene, upstream	ActReg chr19 #9250	0	0	1
9251	19	57,350,003	57,350,341	338	1	4.636	4.182	12.364	6	6	15	1	3	3	ZIM2, PEG3, MIMT1	1925, 1922, -2098	in gene, in gene, upstream	ActReg chr19 #9251	0	0	1
9252	19	57,702,365	57,703,183	818	1	6.846	11.5	5.846	9	15	11	1	1	1	ZNF264	-94	upstream	ActReg chr19 #9252	0	1	0
9253	19	57,741,886	57,742,404	518	1	3.5	2.882	11.588	6	5	16	1	1	3	ZNF264, AURKC, ZNF805	39277, -232, -9908	downstream, upstream, upstream	ActReg chr19 #9253	0	0	1
9254	19	57,751,608	57,752,454	846	2	11.037	11.741	6.308	18	23	9	1	1	2	AURKC, ZNF805	9654, -22	downstream, upstream	ActReg chr19 #9254	1	1	0
9255	19	57,791,328	57,792,202	874	1	10.286	13.393	9.821	17	26	18	1	1	1	ZNF460	-88	upstream	ActReg chr19 #9255	0	1	0
9256	19	57,862,241	57,862,901	660	1	11.5	9.55	6.1	18	14	13	1	1	1	ZNF304	-74	upstream	ActReg chr19 #9256	1	0	0
9257	19	57,874,350	57,875,238	888	2	10.786	11.321	3.84	18	23	7	1	1	2	ZNF304, ZNF547	12149, -97	downstream, upstream	ActReg chr19 #9257	1	1	0
9258	19	57,900,882	57,901,647	765	2	10.375	11.417	4.958	15	16	9	1	1	2	ZNF547, ZNF548	26373, 46	downstream, in gene	ActReg chr19 #9258	1	1	0
9259	19	57,922,323	57,923,084	761	1	10.333	11.375	7.542	20	15	14	1	1	2	ZNF548, ZNF17	21485, 174	downstream, in gene	ActReg chr19 #9259	0	1	0
9260	19	57,946,326	57,946,950	624	1	10.95	12.6	10.3	18	21	17	1	1	1	ZNF749	-55	upstream	ActReg chr19 #9260	0	1	0
9261	19	58,038,774	58,039,181	407	1	6.692	5.462	11.846	12	9	17	1	1	1	ZNF549	284	in gene	ActReg chr19 #9261	0	0	1
9262	19	58,090,080	58,090,770	690	1	9.952	10.636	2.909	15	19	4	1	2	2	ZNF416, ZIK1	-182, -5203	upstream, upstream	ActReg chr19 #9262	0	1	0
9263	19	58,094,538	58,095,919	1,381	2	5.279	9.907	9.465	9	18	18	1	2	2	ZNF416, ZIK1	-4985, -400	upstream, upstream	ActReg chr19 #9263	0	1	1
9264	19	58,193,134	58,193,827	693	1	8.227	11.227	8.091	16	19	11	1	1	2	ZSCAN4, ZNF551	13177, 123	downstream, in gene	ActReg chr19 #9264	0	1	0
9265	19	58,238,699	58,239,137	438	1	9.429	6.286	11.5	12	11	16	1	1	1	ZNF671	77	in gene	ActReg chr19 #9265	0	0	1
9266	19	58,331,066	58,331,495	429	1	6.714	6.857	12.5	10	12	20	1	1	1	ZNF552	-4,999	upstream	ActReg chr19 #9266	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9267	19	58,458,858	58,459,582	724	2	10.454	9.955	3	21	22	10	1	1	1	ZNF256	-143	upstream	ActReg chr19 #9267	1	1	0
9268	19	58,513,756	58,514,463	707	1	10.182	8.773	7.545	15	12	11	1	2	2	ZNF606, LOC100128398	605, -153	in gene, upstream	ActReg chr19 #9268	1	0	0
9269	19	58,520,930	58,521,539	609	2	10.105	9.842	11.368	15	18	16	1	1	2	ZNF606, LOC100128398	-6520, 6972	upstream, downstream	ActReg chr19 #9269	0	1	1
9270	19	58,544,640	58,545,013	373	1	2.25	2.5	9.833	3	5	13	1	1	1	ZSCAN1	-608	upstream	ActReg chr19 #9270	0	0	1
9271	19	58,554,251	58,554,698	447	1	3.071	4	11.643	6	6	18	1	0	1	ZSCAN1	9,040	in gene	ActReg chr19 #9271	0	0	1
9272	19	58,570,850	58,571,306	456	1	5.714	5	12.429	10	7	17	1	1	2	ZSCAN1, ZNF135	25644, 471	downstream, in gene	ActReg chr19 #9272	0	0	1
9273	19	58,665,992	58,666,820	828	1	11.039	11.808	8.346	17	16	15	1	1	1	ZNF329	-4,258	upstream	ActReg chr19 #9273	0	1	0
9274	19	58,694,792	58,695,317	525	1	8.688	10.625	11.562	14	16	18	1	1	1	ZNF274	658	in gene	ActReg chr19 #9274	0	0	1
9275	19	58,739,782	58,740,656	874	2	12.518	9.222	12.37	23	14	23	1	1	1	ZNF544	149	in gene	ActReg chr19 #9275	1	0	1
9276	19	58,789,839	58,791,267	1,428	1	7.956	11	7.6	13	16	17	1	2	2	LOC100506561, ZNF8	-396, 235	upstream, in gene	ActReg chr19 #9276	0	1	0
9277	19	58,816,275	58,817,233	958	2	12.5	12.033	6	23	23	15	1	1	2	ZNF8, LOC100506584	26436, 11	downstream, in gene	ActReg chr19 #9277	1	1	0
9278	19	58,838,081	58,839,110	1,029	2	18.562	18.125	5.344	34	34	8	1	1	1	ZSCAN22	210	in gene	ActReg chr19 #9278	1	1	0
9279	19	58,873,116	58,874,620	1,504	3	11.617	12.17	9.681	22	22	19	1	1	4	A1BG, NCRNA00181, ZNF497, ZNF837	-9003, 10532, 252, 18521	upstream, downstream, in gene, downstream	ActReg chr19 #9279	1	1	1
9280	19	58,891,303	58,892,653	1,350	3	9.667	12.548	7.619	21	25	18	1	2	2	ZNF837, RPS5	411, -6658	in gene, upstream	ActReg chr19 #9280	1	1	1
9281	19	58,897,573	58,898,983	1,410	2	7.864	11.75	13.364	17	20	17	1	2	3	ZNF837, RPS5, LOC100506612	-5889, -358, -9179	upstream, upstream, upstream	ActReg chr19 #9281	0	1	1
9282	19	58,912,093	58,912,661	568	1	7.111	6.778	12.778	12	9	24	1	2	5	RPS5, LOC100506612, LOC100506657, LOC100506634, ZNF584	13741, 4920, 892, 6286, -7686	downstream, downstream, in gene, downstream, upstream	ActReg chr19 #9282	0	0	1
9283	19	58,912,682	58,913,228	546	1	6.412	10.647	4.235	13	18	6	1	2	5	RPS5, LOC100506612, LOC100506657, LOC100506634, ZNF584	14319, 5498, 314, 5708, -7108	downstream, downstream, in gene, downstream, upstream	ActReg chr19 #9283	0	1	0
9284	19	58,919,562	58,920,807	1,245	3	13.538	11.641	12.128	23	18	18	1	3	3	LOC100506657, LOC100506634, ZNF584	-6915, -1521, 121	upstream, upstream, in gene	ActReg chr19 #9284	1	1	1
9285	19	58,962,466	58,963,548	1,082	3	6.061	10.091	12.121	11	17	17	1	1	1	ZNF324B	36	in gene	ActReg chr19 #9285	0	1	1
9286	19	58,987,375	58,988,132	757	1	9.917	9.417	10.75	17	14	14	1	1	2	ZNF324, ZNF446	9341, -42	downstream, upstream	ActReg chr19 #9286	0	0	1
9287	19	59,025,146	59,025,736	590	1	6.895	11.895	5.684	13	22	9	1	1	2	SLC27A5, ZBTB45	-2009, 5480	upstream, in gene	ActReg chr19 #9287	0	1	0
9288	19	59,030,396	59,031,784	1,388	3	12.727	13.954	10.75	25	27	20	1	2	2	SLC27A5, ZBTB45	-7658, -169	upstream, upstream	ActReg chr19 #9288	1	1	1
9289	19	59,066,080	59,066,778	698	2	8.545	11.954	13.046	16	16	21	1	2	5	TRIM28, CHMP2A, UBE2M, LOC100131691, MZF1	10593, 57, 3914, -4163, 18513	downstream, in gene, downstream, upstream, downstream	ActReg chr19 #9289	0	1	1
9290	19	59,069,891	59,070,773	882	1	12.148	7.926	4.741	20	14	9	1	3	5	TRIM28, CHMP2A, UBE2M, LOC100131691, MZF1	14496, -3846, 11, -260, 14610	downstream, upstream, in gene, upstream, downstream	ActReg chr19 #9290	1	0	0
9291	19	59,086,739	59,087,537	798	1	8.92	7.48	12.64	14	18	18	1	2	3	LOC100131691, MZF1, MGC2752	16546, -2196, 372	downstream, upstream, in gene	ActReg chr19 #9291	0	0	1
9292	2	11,475	11,905	430	1	5.071	7.357	9.571	8	10	16	0	0	0				ActReg chr2 #9292	0	0	1
9293	2	45,448	45,831	383	1	1.25	3.5	10.417	2	6	15	1	1	1	FAM110C	949	in gene	ActReg chr2 #9293	0	0	1
9294	2	264,614	265,214	600	1	10	6.833	5.5	16	12	8	1	2	2	SH3YL1, ACP1	-846, 45	upstream, in gene	ActReg chr2 #9294	1	0	0
9295	2	429,511	429,967	456	1	3.857	3.571	11.5	6	6	18	0	0	0				ActReg chr2 #9295	0	0	1
9296	2	566,972	567,451	479	1	3.933	5.4	10.6	6	7	15	0	0	0				ActReg chr2 #9296	0	0	1
9297	2	628,789	629,071	282	1	7	7.222	10.556	8	11	13	1	0	0				ActReg chr2 #9297	0	0	1
9298	2	677,164	677,713	549	1	9.353	10.647	11.941	14	15	20	1	1	1	TMEM18	1	in gene	ActReg chr2 #9298	0	0	1
9299	2	888,934	889,249	315	1	6.4	3.9	9.2	8	5	13	0	0	0				ActReg chr2 #9299	0	0	1
9300	2	1,595,602	1,596,044	442	1	3.786	2.857	11.5	6	6	18	1	0	0				ActReg chr2 #9300	0	0	1
9301	2	1,770,772	1,771,130	358	1	5.636	5.727	11.273	7	9	14	0	0	0				ActReg chr2 #9301	0	0	1
9302	2	1,971,644	1,972,107	463	1	1.923	2.733	9.933	4	5	16	0	0	1	MYT1L	363,170	in gene	ActReg chr2 #9302	0	0	1
9303	2	2,332,547	2,333,029	482	1	7.533	10.733	1.636	11	19	3	0	1	2	MYT1L, LOC730811	2257, 9784	in gene, downstream	ActReg chr2 #9303	0	1	0
9304	2	2,617,039	2,617,548	509	1	11.062	10.938	6.125	20	17	9	0	0	0				ActReg chr2 #9304	0	1	0
9305	2	2,667,184	2,667,553	369	1	2	4.083	10.417	3	5	16	0	0	0				ActReg chr2 #9305	0	0	1
9306	2	2,830,249	2,830,573	324	1	1.8	2.7	9.8	4	4	13	0	0	0				ActReg chr2 #9306	0	0	1
9307	2	3,149,318	3,149,804	486	1	2.333	2.714	11.333	3	5	15	0	1	1	LOC100132738	-3,831	upstream	ActReg chr2 #9307	0	0	1
9308	2	3,381,057	3,382,262	1,205	2	10.568	12.351	8.108	18	20	13	1	2	2	TSSC1, TTC15	-6, -1787	upstream, upstream	ActReg chr2 #9308	1	1	0
9309	2	3,383,243	3,383,975	732	1	10.087	12.609	9.913	17	20	14	1	2	2	TSSC1, TTC15	-1956, 163	upstream, in gene	ActReg chr2 #9309	0	1	0
9310	2	3,522,312	3,523,640	1,328	2	9.146	11.927	12.05	17	20	23	1	1	1	ADI1	374	in gene	ActReg chr2 #9310	0	1	1
9311	2	3,584,077	3,584,773	696	1	13.682	9.545	3.273	27	20	5	0	1	2	LOC100506014, RNASEH1	-2628, 21515	upstream, downstream	ActReg chr2 #9311	1	0	0
9312	2	3,605,585	3,606,363	778	1	9.792	9.667	13.458	13	19	20	1	2	2	RNASEH1, LOC100506054	-34, -2	upstream, upstream	ActReg chr2 #9312	0	0	1
9313	2	3,622,442	3,623,250	808	3	13.24	13.96	9.292	34	24	17	1	1	1	RPS7	-7	upstream	ActReg chr2 #9313	1	1	1
9314	2	4,416,572	4,416,839	267	1	1	2.778	11.889	1	4	15	0	0	0				ActReg chr2 #9314	0	0	1
9315	2	4,931,697	4,932,179	482	1	2.667	5.267	12.667	4	7	19	0	0	0				ActReg chr2 #9315	0	0	1
9316	2	6,646,068	6,646,943	875	2	10.259	12.741	2.042	17	21	4	0	0	0				ActReg chr2 #9316	1	1	0
9317	2	6,696,926	6,697,376	450	1	4.333	10.267	2.1	6	14	4	0	0	0				ActReg chr2 #9317	0	1	0
9318	2	7,373,174	7,373,810	636	1	6.737	10.2	1	13	16	1	0	0	0				ActReg chr2 #9318	0	1	0
9319	2	7,759,546	7,760,938	1,392	3	8.636	10.159	1.971	24	18	4	0	0	0				ActReg chr2 #9319	1	1	0
9320	2	7,888,906	7,889,650	744	1	7.217	11	3.353	11	18	5	0	0	0				ActReg chr2 #9320	0	1	0
9321	2	8,738,222	8,739,416	1,194	2	14.351	12.081	3.759	33	29	9	0	0	0				ActReg chr2 #9321	1	1	0
9322	2	9,211,008	9,211,705	697	2	13.364	11.046	1.75	25	25	3	0	0	0				ActReg chr2 #9322	1	1	0
9323	2	9,224,464	9,225,192	728	1	10.652	4.957	3.565	15	8	6	0	0	0				ActReg chr2 #9323	1	0	0
9324	2	9,252,070	9,252,861	791	2	12.125	13.833	8	22	22	18	0	0	0				ActReg chr2 #9324	1	1	0
9325	2	9,305,606	9,306,174	568	1	9.412	11.412	3.588	13	14	7	0	0	0				ActReg chr2 #9325	0	1	0
9326	2	9,319,441	9,320,536	1,095	1	8.412	10.677	3.147	14	15	6	0	0	0				ActReg chr2 #9326	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GeneCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9327	2	9,330,766	9,331,642	876	2	11.333	13.037	5.926	22	19	10	0	0	0				ActReg chr2 #9327	1	1	0
9328	2	9,374,437	9,375,409	972	1	8.533	12.8	5.633	15	20	9	0	0	1	ASAP2	28,029	in gene	ActReg chr2 #9328	0	1	0
9329	2	9,375,585	9,376,305	720	1	9.227	11.136	4.591	13	15	9	0	0	1	ASAP2	29,051	in gene	ActReg chr2 #9329	0	1	0
9330	2	9,427,506	9,428,791	1,285	3	9.55	13.075	3.27	20	27	6	0	0	1	ASAP2	81,254	in gene	ActReg chr2 #9330	1	1	0
9331	2	9,518,434	9,519,133	699	1	4.571	12.762	6.238	7	20	13	0	0	1	ASAP2	171,889	in gene	ActReg chr2 #9331	0	1	0
9332	2	9,562,699	9,563,920	1,221	1	10.395	14.605	8.684	21	31	14	1	2	2	ITGB1BP1, CPSF3	334, -559	in gene, upstream	ActReg chr2 #9332	0	1	0
9333	2	9,695,161	9,696,424	1,263	2	10.6	10.75	5.474	17	19	12	1	1	1	ADAM17	125	in gene	ActReg chr2 #9333	1	1	0
9334	2	9,770,882	9,771,789	907	2	9.179	10.643	8.179	17	16	15	1	1	1	YWHAQ	-229	upstream	ActReg chr2 #9334	1	1	0
9335	2	9,778,320	9,778,978	658	1	7.619	11	5.143	12	21	10	0	1	1	YWHAQ	-7,543	upstream	ActReg chr2 #9335	0	1	0
9336	2	9,892,517	9,893,823	1,306	2	10.95	12.9	3.3	15	21	5	0	0	1	LOC100506386	17,300	downstream	ActReg chr2 #9336	1	1	0
9337	2	9,941,055	9,941,624	569	1	6.056	10.778	12.611	9	19	22	0	0	0				ActReg chr2 #9337	0	0	1
9338	2	9,983,299	9,984,031	732	1	9.5	13.5	7.682	13	22	11	1	1	1	TAF1B	94	in gene	ActReg chr2 #9338	0	1	0
9339	2	10,149,706	10,150,458	752	1	1.263	5.478	12.652	2	9	17	0	0	1	GRHL1	58,290	downstream	ActReg chr2 #9339	0	0	1
9340	2	10,202,942	10,203,327	385	1	2.667	4.333	11.333	4	7	17	0	0	2	KLF11, CYS1	19452, 17404	downstream, in gene	ActReg chr2 #9340	0	0	1
9341	2	10,206,278	10,206,634	356	1	3.182	4.636	10	4	7	13	0	0	1	CYS1	14,082	in gene	ActReg chr2 #9341	0	0	1
9342	2	10,261,895	10,263,478	1,583	3	14.449	20.388	9.894	40	53	21	1	1	1	RRM2	-9	upstream	ActReg chr2 #9342	1	1	1
9343	2	10,275,735	10,276,666	931	2	12.207	13.897	4.25	21	24	8	0	1	2	RRM2, C2orf48	13505, -5309	downstream, upstream	ActReg chr2 #9343	1	1	0
9344	2	10,396,187	10,396,717	530	1	5	2.333	10.647	9	4	17	0	0	0				ActReg chr2 #9344	0	0	1
9345	2	10,429,822	10,430,622	800	2	11.68	14.04	2.88	23	28	5	0	0	0				ActReg chr2 #9345	1	1	0
9346	2	10,443,846	10,444,633	787	1	7.5	10.75	7.524	12	15	15	1	1	1	HPCAL1	1,199	in gene	ActReg chr2 #9346	0	1	0
9347	2	10,451,913	10,453,178	1,265	1	11.256	14.949	1.611	17	24	3	0	0	1	HPCAL1	9,505	in gene	ActReg chr2 #9347	0	1	0
9348	2	10,545,329	10,546,139	810	1	6.96	12.96	6.68	10	21	10	0	0	1	HPCAL1	102,694	in gene	ActReg chr2 #9348	0	1	0
9349	2	10,637,770	10,638,478	708	1	8.955	11.727	6.409	12	20	10	0	0	0				ActReg chr2 #9349	0	1	0
9350	2	10,829,522	10,830,346	824	1	7.615	9.962	6.154	14	15	9	1	1	1	NOL10	178	in gene	ActReg chr2 #9350	0	1	0
9351	2	10,979,876	10,980,578	702	2	10.954	10.864	5.955	15	18	11	0	0	0				ActReg chr2 #9351	1	1	0
9352	2	10,985,854	10,986,281	427	1	5.786	2.429	11.071	8	4	17	0	0	0				ActReg chr2 #9352	0	0	1
9353	2	11,041,181	11,041,915	734	1	5.435	11.913	6.545	9	17	15	0	0	0				ActReg chr2 #9353	0	1	0
9354	2	11,059,047	11,059,630	583	1	3.722	5.056	12.444	6	7	17	0	0	1	KCNF1	7,275	downstream	ActReg chr2 #9354	0	0	1
9355	2	11,076,151	11,076,785	634	1	11.25	12.9	3.5	19	21	5	0	0	0				ActReg chr2 #9355	0	1	0
9356	2	11,295,496	11,296,298	802	1	6.68	11.84	5.458	13	18	9	1	1	2	C2orf50, PQLC3	22718, 357	downstream, in gene	ActReg chr2 #9356	0	1	0
9357	2	11,483,683	11,484,390	707	1	9.045	10.409	7.273	13	18	16	1	2	2	ROCK2, LOC650157	675, -7717	in gene, upstream	ActReg chr2 #9357	0	1	0
9358	2	11,514,413	11,515,399	986	2	10.258	10.581	4.29	15	18	9	0	0	1	LOC650157	23,153	downstream	ActReg chr2 #9358	1	1	0
9359	2	11,606,074	11,607,210	1,136	2	8.5	12.306	6.429	20	26	14	1	1	1	E2F6	-345	upstream	ActReg chr2 #9359	1	1	0
9360	2	11,758,788	11,759,309	521	1	3.25	3.188	12.25	5	4	18	1	0	1	GREB1	84,806	in gene	ActReg chr2 #9360	0	0	1
9361	2	11,799,889	11,800,468	579	1	2.444	3.294	12.889	5	6	19	0	0	1	NTSR2	10,151	in gene	ActReg chr2 #9361	0	0	1
9362	2	11,809,654	11,810,440	786	2	13.96	16.92	7.818	34	39	16	1	1	1	NTSR2	282	in gene	ActReg chr2 #9362	1	1	0
9363	2	11,883,932	11,884,915	983	2	13.065	12.645	3.5	32	21	6	0	1	1	LPIN1	-2,317	upstream	ActReg chr2 #9363	1	1	0
9364	2	11,970,060	11,970,688	628	1	8.85	11.9	5.25	13	20	8	0	0	2	LPIN1, MIR4262	83634, 6738	downstream, downstream	ActReg chr2 #9364	0	1	0
9365	2	12,260,250	12,261,172	922	1	9.517	10.793	3.517	14	16	8	0	0	1	LOC100506457	13,961	in gene	ActReg chr2 #9365	0	1	0
9366	2	12,309,207	12,310,209	1,002	1	7.656	9.219	3.552	12	16	6	0	0	0				ActReg chr2 #9366	0	1	0
9367	2	12,647,189	12,647,944	755	2	11.292	12.625	4.238	20	23	8	0	0	0				ActReg chr2 #9367	1	1	0
9368	2	12,748,082	12,748,566	484	1	9.333	7.2	1.667	17	15	2	0	0	0				ActReg chr2 #9368	1	0	0
9369	2	14,322,903	14,323,248	345	1	2.818	3.182	12	5	4	15	0	0	0				ActReg chr2 #9369	0	0	1
9370	2	15,701,097	15,701,753	656	2	11.2	10.35	4.214	17	16	7	1	1	1	NBAS	29	in gene	ActReg chr2 #9370	1	1	0
9371	2	15,731,476	15,732,493	1,017	2	9.938	13.75	10.375	16	27	18	1	1	1	DDX1	214	in gene	ActReg chr2 #9371	0	1	1
9372	2	16,431,443	16,431,818	375	1	3.667	3.583	9.5	6	5	13	0	0	0				ActReg chr2 #9372	0	0	1
9373	2	16,727,277	16,727,825	548	2	9.765	8.353	2.2	19	16	3	0	0	1	FAM49A	77,736	downstream	ActReg chr2 #9373	1	1	0
9374	2	17,374,768	17,375,202	434	1	2.083	4.286	12.071	4	7	17	0	0	0				ActReg chr2 #9374	0	0	1
9375	2	17,699,345	17,699,885	540	1	10.177	10.412	2.533	16	15	6	0	1	1	RAD51AP2	91	in gene	ActReg chr2 #9375	1	0	0
9376	2	17,719,968	17,720,737	769	1	12.48	10.04	3.778	26	22	9	1	1	1	VSNL1	-1,455	upstream	ActReg chr2 #9376	1	0	0
9377	2	17,721,204	17,721,633	429	1	12	8.571	7.857	18	12	13	1	1	1	VSNL1	-389	upstream	ActReg chr2 #9377	1	0	0
9378	2	18,741,562	18,742,312	750	2	12.208	11.5	5.056	23	23	8	1	1	2	RDH14, NT5C1B	22, 28901	in gene, downstream	ActReg chr2 #9378	1	1	0
9379	2	19,278,546	19,279,222	676	1	6.286	11.191	1.75	9	15	3	0	0	0				ActReg chr2 #9379	0	1	0
9380	2	19,319,018	19,320,027	1,009	1	9.194	12.645	3.741	16	20	6	0	0	0				ActReg chr2 #9380	0	1	0
9381	2	19,320,558	19,321,393	835	1	12.154	8.192	4.192	21	15	7	0	0	0				ActReg chr2 #9381	1	0	0
9382	2	19,384,753	19,385,116	363	1	9.545	5	10.727	10	7	15	0	0	0				ActReg chr2 #9382	0	0	1
9383	2	19,386,825	19,387,722	897	2	9.714	13.393	4.333	21	20	10	0	0	0				ActReg chr2 #9383	1	1	0
9384	2	19,547,349	19,548,195	846	2	11.37	10.704	9.259	19	15	14	1	0	1	OSR1	10,600	downstream	ActReg chr2 #9384	1	1	0
9385	2	19,871,417	19,872,127	710	1	11.409	5.227	2.545	14	11	6	0	0	0				ActReg chr2 #9385	1	0	0
9386	2	19,902,026	19,902,679	653	1	7.35	13.85	1.647	12	21	2	0	0	0				ActReg chr2 #9386	0	1	0
9387	2	20,001,056	20,001,679	623	1	12.05	8.4	5.55	25	13	10	0	0	0				ActReg chr2 #9387	1	0	0
9388	2	20,101,201	20,102,201	1,000	2	14.645	13.516	8.194	27	24	12	1	1	2	TTC32, WDR35	46, 88183	in gene, downstream	ActReg chr2 #9388	1	1	0
9389	2	20,189,268	20,190,339	1,071	3	10.412	11.5	7.618	21	19	17	1	1	2	WDR35, MATN3	81, 22652	in gene, downstream	ActReg chr2 #9389	1	1	1
9390	2	20,379,397	20,379,901	504	1	3.667	3.333	12.2	6	5	19	0	0	0				ActReg chr2 #9390	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIsIandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9391	2	20,423,442	20,423,987	545	1	7.647	6.471	11.118	13	9	15	1	2	2	SDC1, LOC100131373	1480, -1321	in gene, upstream	ActReg chr2 #9391	0	0	1
9392	2	20,442,330	20,442,687	357	1	4.5	4.9	10.182	6	7	14	0	0	1	PUM2	84,636	downstream	ActReg chr2 #9392	0	0	1
9393	2	20,549,968	20,550,514	546	1	7.118	13.118	5.824	14	21	10	1	0	0				ActReg chr2 #9393	0	1	0
9394	2	20,550,526	20,551,404	878	1	10	10.393	3.481	16	21	9	1	0	0				ActReg chr2 #9394	1	0	0
9395	2	20,647,014	20,648,097	1,083	1	8.471	12.5	6.242	17	25	13	1	1	1	RHOB	720	in gene	ActReg chr2 #9395	0	1	0
9396	2	20,777,307	20,778,199	892	1	8.071	14.607	6.857	19	27	11	0	0	0				ActReg chr2 #9396	0	1	0
9397	2	20,778,582	20,779,569	987	1	13.452	9.968	6.419	23	17	14	0	0	0				ActReg chr2 #9397	1	0	0
9398	2	20,798,784	20,799,127	343	1	5.364	4.182	11.909	7	8	17	0	0	0				ActReg chr2 #9398	0	0	1
9399	2	20,845,050	20,845,557	507	1	4	3.188	10.875	8	5	19	0	0	1	HS1BP3	5,561	in gene	ActReg chr2 #9399	0	0	1
9400	2	20,850,599	20,851,274	675	1	8.714	12.333	9	13	20	17	1	1	1	HS1BP3	-72	upstream	ActReg chr2 #9400	0	1	0
9401	2	21,022,326	21,023,193	867	2	11.482	14.111	4.56	23	27	8	1	1	1	C2orf43	68	in gene	ActReg chr2 #9401	1	1	0
9402	2	21,079,925	21,080,426	501	1	5	2.062	10.188	7	3	14	0	0	0				ActReg chr2 #9402	0	0	1
9403	2	23,078,251	23,079,125	874	1	4.222	11.704	3.889	8	20	6	0	0	0				ActReg chr2 #9403	0	1	0
9404	2	23,582,491	23,583,282	791	1	12.2	7.56	3.25	20	11	6	0	0	0				ActReg chr2 #9404	1	0	0
9405	2	23,747,034	23,747,678	644	2	9.55	9.6	4.55	19	18	7	0	0	1	KLHL29	139,058	in gene	ActReg chr2 #9405	1	1	0
9406	2	23,797,738	23,798,172	434	1	3.273	5	13.077	5	9	20	0	0	1	KLHL29	189,657	in gene	ActReg chr2 #9406	0	0	1
9407	2	23,913,263	23,913,716	453	1	3.214	2.643	12.357	5	5	20	1	0	1	KLHL29	305,191	in gene	ActReg chr2 #9407	0	0	1
9408	2	23,943,806	23,944,577	771	1	4	3.292	10.48	6	6	15	0	0	0				ActReg chr2 #9408	0	0	1
9409	2	24,149,554	24,150,410	856	1	11.704	14.518	8.741	23	24	14	1	1	1	ATAD2B	-48	upstream	ActReg chr2 #9409	0	1	0
9410	2	24,240,129	24,240,656	527	1	5.375	4.429	10.562	9	8	16	0	0	1	MFSD2B	7,439	in gene	ActReg chr2 #9410	0	0	1
9411	2	24,298,775	24,299,573	798	3	12.36	12.84	8.24	24	24	16	1	1	2	SF3B14, TP53I3	140, 8554	in gene, downstream	ActReg chr2 #9411	1	1	1
9412	2	24,306,854	24,308,078	1,224	2	24.395	22.263	7.553	52	43	12	1	1	2	SF3B14, TP53I3	-8152, 262	upstream, in gene	ActReg chr2 #9412	1	1	0
9413	2	24,345,774	24,346,605	831	2	9.962	11.192	3.577	15	19	7	1	2	2	PRN4, LOC375190	-38, -161	upstream, upstream	ActReg chr2 #9413	1	1	0
9414	2	24,454,239	24,454,816	577	1	13.158	8.526	1.636	19	12	2	0	1	2	ITSN2, LOC100507630	128870, -5125	in gene, upstream	ActReg chr2 #9414	1	0	0
9415	2	24,583,016	24,583,771	755	1	10.217	9.696	4.25	16	13	8	1	1	1	ITSN2	4	in gene	ActReg chr2 #9415	0	1	0
9416	2	24,713,630	24,713,921	291	1	3.7	6.111	9.7	7	9	14	1	0	0				ActReg chr2 #9416	0	0	1
9417	2	24,931,391	24,931,980	589	1	10.053	4.526	1.778	19	8	2	0	0	1	NCOA1	124,339	in gene	ActReg chr2 #9417	1	0	0
9418	2	25,015,662	25,017,073	1,411	2	9.386	12.341	8.163	19	18	14	1	2	2	C2orf79, CENPO	-116, 34	upstream, in gene	ActReg chr2 #9418	1	1	0
9419	2	25,194,444	25,194,925	481	1	8.333	8.6	12.8	14	15	18	1	2	2	DNAJC27, LOC729723	140, -297	in gene, upstream	ActReg chr2 #9419	0	0	1
9420	2	25,326,009	25,326,638	629	1	8.75	11.9	5.3	15	19	8	0	0	1	EFR3B	61,350	in gene	ActReg chr2 #9420	0	1	0
9421	2	25,391,704	25,392,016	312	1	2.8	5.8	10.9	4	7	14	1	1	2	EFR3B, POMC	126887, -301	downstream, upstream	ActReg chr2 #9421	0	0	1
9422	2	25,474,485	25,474,944	459	1	2	5.6	12.733	3	5	16	1	0	1	DNMT3A	90,745	in gene	ActReg chr2 #9422	0	0	1
9423	2	25,537,432	25,537,871	439	1	4.214	4.286	11.071	5	8	16	0	0	1	DNMT3A	27,808	in gene	ActReg chr2 #9423	0	0	1
9424	2	25,565,128	25,565,901	773	2	13.5	14.792	6.583	23	29	11	1	1	1	DNMT3A	-55	upstream	ActReg chr2 #9424	1	1	0
9425	2	25,813,678	25,814,192	514	1	3.938	4.375	10.688	7	9	15	0	0	1	DTNB	82,568	in gene	ActReg chr2 #9425	0	0	1
9426	2	25,896,764	25,897,210	446	1	6.929	10.5	6.5	12	15	10	1	1	1	DTNB	-484	upstream	ActReg chr2 #9426	0	1	0
9427	2	26,220,426	26,220,981	555	1	8	11.353	3.529	12	16	6	0	0	1	LOC729769	3,099	downstream	ActReg chr2 #9427	0	1	0
9428	2	26,256,693	26,257,451	758	1	10.083	13.042	7.348	16	23	13	1	2	2	LOC391358, RAB10	-5591, 343	upstream, in gene	ActReg chr2 #9428	0	1	0
9429	2	26,467,048	26,468,508	1,460	3	11.422	12.556	8.422	20	30	18	2	2	2	HADHA, HADHB	-184, 162	upstream, in gene	ActReg chr2 #9429	1	1	1
9430	2	26,539,640	26,539,913	273	1	5.444	3.556	12.778	7	5	17	0	0	1	GPR113	29,909	in gene	ActReg chr2 #9430	0	0	1
9431	2	26,568,528	26,569,391	863	2	11.704	11.778	9	18	17	15	1	2	2	GPR113, SELI	726, 5	in gene, in gene	ActReg chr2 #9431	1	1	0
9432	2	26,698,701	26,699,305	604	1	3.579	2.211	12.579	6	3	23	0	0	1	OTOF	82,563	in gene	ActReg chr2 #9432	0	0	1
9433	2	26,699,895	26,700,382	487	1	3.133	3.933	11.533	5	7	18	0	0	1	OTOF	81,428	in gene	ActReg chr2 #9433	0	0	1
9434	2	26,916,149	26,916,645	496	1	5.562	3.688	11	10	6	18	1	1	1	KCNK3	816	in gene	ActReg chr2 #9434	0	0	1
9435	2	26,918,914	26,919,734	820	1	12.2	10.28	4.32	18	17	7	0	0	1	KCNK3	3,743	in gene	ActReg chr2 #9435	1	0	0
9436	2	26,980,689	26,981,130	441	1	10.5	10.643	3.643	15	16	5	0	1	1	C2orf18	-6,233	upstream	ActReg chr2 #9436	0	1	0
9437	2	27,008,400	27,009,255	855	2	11.963	11.63	5.778	24	19	16	1	1	2	C2orf18, CENPA	21685, -55	downstream, upstream	ActReg chr2 #9437	1	1	0
9438	2	27,061,148	27,062,239	1,091	2	12.853	15.882	2.643	29	33	5	0	0	1	DPYSL5	-9,276	upstream	ActReg chr2 #9438	1	1	0
9439	2	27,071,198	27,071,745	547	1	7	5.889	14	10	12	25	1	0	1	DPYSL5	502	in gene	ActReg chr2 #9439	0	0	1
9440	2	27,193,076	27,193,865	789	1	10.44	12.48	7.235	17	19	13	1	1	1	MAPRE3	-55	upstream	ActReg chr2 #9440	0	1	0
9441	2	27,216,192	27,217,161	969	2	13.387	22.613	1.333	27	53	2	0	0	1	MAPRE3	23,151	in gene	ActReg chr2 #9441	1	1	0
9442	2	27,255,702	27,256,465	763	2	10.083	11.375	10.125	13	22	18	1	1	2	MAPRE3, TMEM214	62558, 309	downstream, in gene	ActReg chr2 #9442	0	1	1
9443	2	27,273,286	27,274,582	1,296	3	15.025	13.525	15.225	23	22	27	2	1	2	TMEM214, AGBL5	18160, -557	downstream, upstream	ActReg chr2 #9443	1	1	1
9444	2	27,293,983	27,294,867	884	1	9.071	10.607	4.364	14	19	8	1	2	3	AGBL5, LOC100128731, EMILIN1	19934, 142, -7010	downstream, in gene, upstream	ActReg chr2 #9444	0	1	0
9445	2	27,305,267	27,306,123	856	1	3.778	4.815	11.815	7	9	18	1	1	2	EMILIN1, KHK	4260, -3916	in gene, upstream	ActReg chr2 #9445	0	0	1
9446	2	27,306,305	27,306,919	614	1	3.737	5.053	11.79	7	9	19	0	1	2	EMILIN1, KHK	5177, -2999	in gene, upstream	ActReg chr2 #9446	0	0	1
9447	2	27,308,329	27,309,622	1,293	2	9.744	13.525	6.917	24	20	17	1	1	2	EMILIN1, KHK	7540, -636	in gene, upstream	ActReg chr2 #9447	1	1	0
9448	2	27,350,765	27,351,285	520	1	2.6	4.125	10.938	6	6	13	0	0	4	CGREF1, ABHD1, PREB, C2orf53	-9030, 4568, 6517, 11307	upstream, in gene, downstream, downstream	ActReg chr2 #9448	0	0	1
9449	2	27,357,258	27,357,848	590	2	14.667	12.167	5.722	24	21	9	1	1	3	ABHD1, PREB, C2orf53	10896, -11, 4779	downstream, upstream, downstream	ActReg chr2 #9449	1	1	0
9450	2	27,359,862	27,360,639	777	1	2.476	4.391	12.458	5	8	18	0	2	3	ABHD1, PREB, C2orf53	13593, -2708, 2082	downstream, upstream, in gene	ActReg chr2 #9450	0	0	1
9451	2	27,434,886	27,435,641	755	2	11	10.652	7.429	16	16	12	1	3	3	SLC5A6, C2orf28, CAD	-88, 364, -4995	upstream, in gene, upstream	ActReg chr2 #9451	1	1	0
9452	2	27,485,367	27,485,937	570	1	6.5	8.111	11.222	11	12	15	1	1	1	SLC30A3	308	in gene	ActReg chr2 #9452	0	0	1
9453	2	27,528,994	27,529,891	897	1	3.964	7.679	11.893	7	12	17	1	1	3	TRIM54, UCN, MPV17	24145, 1688, 16527	in gene, downstream, downstream	ActReg chr2 #9453	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9454	2	27,545,662	27,546,296	634	2	13.55	13	10.1	21	20	17	0	1	2	MPV17, GTF3C2	-10, 33889	upstream, downstream	ActReg chr2 #9454	1	0	1
9455	2	27,578,967	27,579,760	793	1	10.32	11.72	6.92	17	16	11	1	2	3	GTF3C2, LOC100505605, EIF2B4	505, 250, 13961	in gene, in gene, downstream	ActReg chr2 #9455	0	1	0
9456	2	27,592,572	27,594,058	1,486	2	20.766	25	7.936	66	74	14	1	2	4	LOC100505605, EIF2B4, SNX17, ZNF513	14202, 9, -74, 10278	downstream, in gene, upstream, downstream	ActReg chr2 #9456	1	1	0
9457	2	27,600,084	27,600,522	438	1	3.714	9.286	11.857	5	13	16	0	1	4	EIF2B4, SNX17, ZNF513, PPM1G	-6979, 6914, 3290, 32193	upstream, downstream, in gene, downstream	ActReg chr2 #9457	0	0	1
9458	2	27,600,891	27,601,828	937	1	5.933	7.033	12.9	11	10	20	1	1	4	EIF2B4, SNX17, ZNF513, PPM1G	-8035, 7970, 2234, 31137	upstream, downstream, in gene, downstream	ActReg chr2 #9458	0	0	1
9459	2	27,851,548	27,852,140	592	1	8.632	11.895	4.684	17	21	8	0	2	3	ZNF512, CCDC121, GPN1	45951, 54, 329	downstream, in gene, in gene	ActReg chr2 #9459	0	1	0
9460	2	27,942,872	27,943,657	785	2	12	10.4	2.565	17	17	5	0	0	0				ActReg chr2 #9460	1	1	0
9461	2	27,994,248	27,995,085	837	3	9.462	10.154	8.208	15	19	16	1	1	2	MRPL33, RBKS	82, 118557	in gene, downstream	ActReg chr2 #9461	1	1	1
9462	2	28,093,289	28,094,229	940	2	15.138	11.552	1.963	27	26	3	0	0	1	RBKS	19,464	in gene	ActReg chr2 #9462	1	1	0
9463	2	28,236,384	28,237,001	617	2	9.35	10.1	1.312	18	17	2	0	0	1	BRE	123,210	in gene	ActReg chr2 #9463	1	1	0
9464	2	28,612,866	28,614,166	1,300	1	8	11.55	6.795	15	18	13	1	1	2	FLJ31356, FOSL2	4023, -2263	in gene, upstream	ActReg chr2 #9464	0	1	0
9465	2	28,615,061	28,615,975	914	2	11.552	12.241	5.75	26	23	9	1	2	2	FLJ31356, FOSL2	2021, -261	in gene, upstream	ActReg chr2 #9465	1	1	0
9466	2	28,634,779	28,635,286	507	1	4	3.75	11.375	7	7	17	0	0	1	FOSL2	19,253	in gene	ActReg chr2 #9466	0	0	1
9467	2	28,662,339	28,663,000	661	1	2.6	2.2	10.75	5	4	15	0	0	0				ActReg chr2 #9467	0	0	1
9468	2	28,695,419	28,695,939	520	1	3.5	3.529	11.059	6	6	15	0	0	0				ActReg chr2 #9468	0	0	1
9469	2	28,806,658	28,807,933	1,275	1	12.026	10.615	2.41	22	19	5	0	0	1	PLB1	88,357	in gene	ActReg chr2 #9469	1	0	0
9470	2	28,814,650	28,815,054	404	1	5	5.385	10.769	7	8	16	0	0	1	PLB1	95,914	in gene	ActReg chr2 #9470	0	0	1
9471	2	28,833,226	28,834,590	1,364	1	9.833	14.309	3.378	17	24	7	0	0	1	PLB1	114,970	in gene	ActReg chr2 #9471	0	1	0
9472	2	28,940,145	28,941,003	858	2	12.222	14.259	4.105	27	30	9	0	0	1	LOC100505774	18,456	in gene	ActReg chr2 #9472	1	1	0
9473	2	28,973,780	28,974,920	1,140	2	11.556	13.778	3.774	22	32	9	1	1	1	PPP1CB	-264	upstream	ActReg chr2 #9473	1	1	0
9474	2	29,092,785	29,093,625	840	2	12.115	12.885	10.8	23	24	18	1	1	1	TRMT61B	-30	upstream	ActReg chr2 #9474	1	1	0
9475	2	29,116,950	29,117,877	927	2	17.621	22.552	4.464	38	47	9	1	1	1	WDR43	-120	upstream	ActReg chr2 #9475	1	1	0
9476	2	29,337,248	29,337,976	728	1	6.565	10.565	3.762	12	14	6	1	1	1	CLIP4	-696	upstream	ActReg chr2 #9476	0	1	0
9477	2	29,338,613	29,339,587	974	1	6.742	10.71	4.038	11	15	10	1	1	1	CLIP4	792	in gene	ActReg chr2 #9477	0	1	0
9478	2	29,437,943	29,438,482	539	1	3.118	2.562	12.118	5	4	17	0	0	1	ALK	706,220	in gene	ActReg chr2 #9478	0	0	1
9479	2	29,516,591	29,517,301	710	1	13.318	11	1.941	30	17	3	0	0	1	ALK	627,486	in gene	ActReg chr2 #9479	1	0	0
9480	2	29,970,728	29,971,583	855	2	16.154	14.923	1.833	35	35	3	0	0	1	ALK	173,277	in gene	ActReg chr2 #9480	1	1	0
9481	2	30,142,388	30,144,507	2,119	3	11.212	18.515	7.348	27	41	19	1	1	1	ALK	985	in gene	ActReg chr2 #9481	1	1	1
9482	2	30,248,506	30,249,817	1,311	2	16.829	18.488	5.139	37	37	10	0	0	0				ActReg chr2 #9482	1	1	0
9483	2	30,369,021	30,369,715	694	1	10.818	14.273	2.818	22	26	7	1	1	1	YPEL5	-382	upstream	ActReg chr2 #9483	0	1	0
9484	2	30,607,960	30,608,839	879	2	12.321	15.964	3.667	29	36	7	0	0	0				ActReg chr2 #9484	1	1	0
9485	2	30,669,858	30,670,686	828	2	5.88	10.56	11.48	9	20	17	1	1	1	LCLAT1	149	in gene	ActReg chr2 #9485	0	1	1
9486	2	31,330,232	31,331,049	817	2	14.962	17.385	3.192	37	38	5	0	0	1	GALNT14	30,931	in gene	ActReg chr2 #9486	1	1	0
9487	2	31,331,533	31,332,131	598	1	6.579	10.737	1.6	11	19	3	0	0	1	GALNT14	29,739	in gene	ActReg chr2 #9487	0	1	0
9488	2	31,360,969	31,361,784	815	2	11.48	10.4	5.667	16	14	11	1	1	1	GALNT14	195	in gene	ActReg chr2 #9488	1	1	0
9489	2	31,456,545	31,457,254	709	2	12.864	10.227	3.409	25	20	6	1	1	1	EHD3	19	in gene	ActReg chr2 #9489	1	1	0
9490	2	31,457,507	31,457,851	344	1	8.4	11.2	12.6	13	16	18	1	1	1	EHD3	799	in gene	ActReg chr2 #9490	0	0	1
9491	2	31,805,689	31,806,108	419	1	1.923	6.385	12.769	3	13	16	1	1	1	SRD5A2	142	in gene	ActReg chr2 #9491	0	0	1
9492	2	32,235,776	32,236,640	864	3	13.714	19.321	8.259	27	43	18	1	1	1	MEMO1	-510	upstream	ActReg chr2 #9492	1	1	1
9493	2	32,264,641	32,265,221	580	3	10.444	12.722	9.889	16	23	18	1	1	1	DPY30	-87	upstream	ActReg chr2 #9493	1	1	1
9494	2	32,390,459	32,391,221	762	3	13.042	11.542	10.75	25	24	20	1	1	2	SPAST, SLC30A6	102160, -70	downstream, upstream	ActReg chr2 #9494	1	1	1
9495	2	32,581,580	32,582,650	1,070	2	10.818	12.394	8.061	18	20	17	1	1	1	BIRC6	19	in gene	ActReg chr2 #9495	1	1	0
9496	2	32,852,418	32,852,931	513	1	5.438	6.625	11.75	11	11	16	1	1	2	BIRC6, TTC27	270578, -413	downstream, upstream	ActReg chr2 #9496	0	0	1
9497	2	33,294,669	33,295,839	1,170	2	8.111	9.361	4.7	18	14	12	0	0	1	LTBP1	122,885	in gene	ActReg chr2 #9497	1	1	0
9498	2	33,359,175	33,359,709	534	1	10.5	10.688	1.667	16	18	2	0	0	1	LTBP1	187,073	in gene	ActReg chr2 #9498	0	1	0
9499	2	33,500,683	33,501,269	586	1	8.556	12	3	17	20	5	0	0	1	LTBP1	328,607	in gene	ActReg chr2 #9499	0	1	0
9500	2	33,600,096	33,600,845	749	1	7.375	10.625	3.474	14	18	7	0	0	1	LTBP1	428,101	in gene	ActReg chr2 #9500	0	1	0
9501	2	33,700,745	33,701,194	449	1	10.786	6.357	2.5	18	8	3	0	0	1	RASGRP3	39,553	in gene	ActReg chr2 #9501	1	0	0
9502	2	33,823,821	33,825,100	1,279	2	10.45	11.41	5.8	17	17	10	1	1	1	FAM98A	-98	upstream	ActReg chr2 #9502	1	1	0
9503	2	34,035,156	34,035,604	448	1	7.286	9.929	1.455	11	15	4	0	0	0				ActReg chr2 #9503	0	1	0
9504	2	34,803,518	34,804,217	699	1	14.046	5.5	2	29	10	3	0	0	0				ActReg chr2 #9504	1	0	0
9505	2	34,877,661	34,878,215	554	1	10.333	7.722	1	23	13	1	0	0	0				ActReg chr2 #9505	1	0	0
9506	2	35,966,465	35,967,172	707	2	10.227	11.727	1.882	22	21	3	0	0	0				ActReg chr2 #9506	1	1	0
9507	2	36,400,872	36,401,679	807	1	12.24	8.96	1.474	18	16	3	0	0	0				ActReg chr2 #9507	1	0	0
9508	2	36,584,663	36,585,486	823	1	11.615	10.692	3.25	18	15	9	1	2	2	LOC100288911, CRIM1	-2361, 1677	upstream, in gene	ActReg chr2 #9508	1	0	0
9509	2	36,654,710	36,655,443	733	1	7.913	13.043	3.182	12	22	5	0	0	1	CRIM1	71,679	in gene	ActReg chr2 #9509	0	1	0
9510	2	37,035,577	37,035,986	409	1	3.077	2.833	12.846	7	4	18	1	0	1	VIT	111,948	in gene	ActReg chr2 #9510	0	0	1
9511	2	37,458,249	37,459,294	1,045	1	6.812	13.094	7.645	12	18	14	1	2	2	CEBPZ, C2orf56	-31, -3	upstream, upstream	ActReg chr2 #9511	0	1	0
9512	2	37,552,064	37,552,628	564	1	11	10.278	5.056	20	14	6	1	0	1	PRKD3	-8,124	upstream	ActReg chr2 #9512	1	0	0
9513	2	37,603,616	37,604,438	822	2	10.039	12.039	2.44	19	17	5	0	0	1	QPCT	32,274	downstream	ActReg chr2 #9513	1	1	0
9514	2	37,606,855	37,607,413	558	1	8.059	11.118	4.176	12	17	8	0	0	1	QPCT	35,381	downstream	ActReg chr2 #9514	0	1	0
9515	2	37,797,936	37,798,586	650	1	10.6	9.15	2	16	13	3	0	0	0				ActReg chr2 #9515	1	0	0
9516	2	37,898,119	37,898,714	595	1	8.333	9.056	12.889	13	14	18	1	1	1	CDC42EP3	910	in gene	ActReg chr2 #9516	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9517	2	37,898,927	37,900,290	1,363	2	9.14	11.349	5.535	18	18	11	1	1	1	CDC42EP3	-282	upstream	ActReg chr2 #9517	1	1	0
9518	2	38,007,268	38,008,138	870	1	8.296	11.963	4.762	11	17	10	0	0	0				ActReg chr2 #9518	0	1	0
9519	2	38,152,246	38,153,082	836	1	10.615	13.615	9.269	16	19	17	1	1	1	FAM82A1	202	in gene	ActReg chr2 #9519	0	1	0
9520	2	38,302,676	38,303,284	608	1	4.211	4.211	13.316	6	6	17	1	1	2	FAM82A1, CYP1B1	150518, 343	downstream, in gene	ActReg chr2 #9520	0	0	1
9521	2	38,303,884	38,304,570	686	1	10.381	12.905	3.789	14	19	7	1	1	2	FAM82A1, CYP1B1	151765, -904	downstream, upstream	ActReg chr2 #9521	0	1	0
9522	2	38,373,609	38,374,367	758	1	7.783	10.565	4.13	14	15	7	0	0	1	C2orf58	15,741	in gene	ActReg chr2 #9522	0	1	0
9523	2	38,429,973	38,430,952	979	2	11.419	11.419	3.037	18	18	6	0	0	0				ActReg chr2 #9523	1	1	0
9524	2	38,604,038	38,604,811	773	2	11.833	14.125	3.043	25	26	5	1	1	1	ATL2	8	in gene	ActReg chr2 #9524	1	1	0
9525	2	38,624,330	38,624,854	524	1	7.688	8.625	15.562	10	11	26	0	0	0				ActReg chr2 #9525	0	0	1
9526	2	38,763,005	38,763,592	587	1	7.158	10.842	6.474	13	18	12	1	0	0				ActReg chr2 #9526	0	1	0
9527	2	38,829,351	38,829,742	391	1	8.917	3.667	10.333	13	7	16	1	1	1	HNRPLL	632	in gene	ActReg chr2 #9527	0	0	1
9528	2	38,917,606	38,918,052	446	1	10.571	5.214	3.214	16	7	5	0	0	1	GALM	24,777	in gene	ActReg chr2 #9528	1	0	0
9529	2	38,978,161	38,978,786	625	1	12.7	14.2	14.7	16	24	29	1	1	1	SFRS7	163	in gene	ActReg chr2 #9529	0	0	1
9530	2	39,102,561	39,103,276	715	2	11.636	13.773	5.818	17	24	11	1	2	2	DHX57, MORN2	103, -185	in gene, upstream	ActReg chr2 #9530	1	1	0
9531	2	39,347,920	39,348,470	550	1	12.471	12.765	8.471	20	21	16	1	1	1	SOS1	-591	upstream	ActReg chr2 #9531	0	1	0
9532	2	39,351,170	39,352,046	876	3	18.926	16.074	13.444	49	42	21	1	1	1	SOS1	-4,004	upstream	ActReg chr2 #9532	1	1	1
9533	2	39,597,132	39,597,661	529	1	10.5	7.438	1.818	18	12	2	0	0	1	MAP4K3	66,823	in gene	ActReg chr2 #9533	1	0	0
9534	2	40,006,023	40,006,445	422	1	8.615	9.077	9.846	11	13	15	1	1	1	THUMPD2	182	in gene	ActReg chr2 #9534	0	0	1
9535	2	40,885,983	40,886,552	569	1	6.778	9.222	0	13	17	0	0	0	0				ActReg chr2 #9535	0	1	0
9536	2	42,018,340	42,019,244	904	2	13.643	17.179	1.826	31	36	3	0	0	0				ActReg chr2 #9536	1	1	0
9537	2	42,063,835	42,064,815	980	2	20.226	19.613	1.455	46	44	3	0	0	0				ActReg chr2 #9537	1	1	0
9538	2	42,067,502	42,068,748	1,246	2	20.41	27.872	4.359	64	95	10	2	0	0				ActReg chr2 #9538	1	1	0
9539	2	42,396,504	42,397,053	549	1	10.059	5.765	10.529	14	9	14	1	1	1	EML4	288	in gene	ActReg chr2 #9539	0	0	1
9540	2	42,568,111	42,568,795	684	1	12.381	9.095	4.81	22	15	9	0	0	2	EML4, COX7A2L	171963, 19903	downstream, downstream	ActReg chr2 #9540	1	0	0
9541	2	42,568,939	42,570,536	1,597	2	11.84	11.02	5.442	20	19	12	0	0	2	EML4, COX7A2L	173247, 18619	downstream, downstream	ActReg chr2 #9541	1	1	0
9542	2	42,587,961	42,588,799	838	1	10.846	11.846	4.154	17	18	7	1	1	1	COX7A2L	-24	upstream	ActReg chr2 #9542	0	1	0
9543	2	42,652,044	42,652,425	381	1	2.364	3.667	9	4	6	13	0	0	0				ActReg chr2 #9543	0	0	1
9544	2	42,994,695	42,995,229	534	1	11.929	3.812	11.875	3	6	15	0	1	2	OXER1, HAAO	-3561, 24789	upstream, in gene	ActReg chr2 #9544	0	0	1
9545	2	43,037,312	43,038,697	1,385	3	8.659	14.432	8.705	21	24	21	2	0	0				ActReg chr2 #9545	1	1	1
9546	2	43,268,433	43,269,207	774	1	8	10.792	3.542	13	17	7	0	0	0				ActReg chr2 #9546	0	1	0
9547	2	43,277,313	43,277,659	346	1	2.3	4.5	12.8	5	7	18	0	0	0				ActReg chr2 #9547	0	0	1
9548	2	43,358,575	43,359,032	457	1	7.643	9.143	11.714	11	15	19	0	0	0				ActReg chr2 #9548	0	0	1
9549	2	43,361,355	43,361,980	625	1	3.368	4.421	10.158	7	6	14	0	0	0				ActReg chr2 #9549	0	0	1
9550	2	43,425,147	43,425,794	647	1	3.294	3.786	9.952	6	6	13	0	0	0				ActReg chr2 #9550	0	0	1
9551	2	43,446,479	43,447,513	1,034	1	8.812	12.188	5.031	19	24	13	0	1	2	ZFP36L2, LOC100129726	6749, -7354	downstream, upstream	ActReg chr2 #9551	0	1	0
9552	2	43,452,115	43,453,145	1,030	1	8.688	11.562	6.5	14	19	12	1	2	3	ZFP36L2, LOC100129726, THADA	1115, -1720, 370555	in gene, upstream, downstream	ActReg chr2 #9552	0	1	0
9553	2	43,454,306	43,455,120	814	1	9.76	10.2	8.583	13	13	14	1	2	3	ZFP36L2, LOC100129726, THADA	-968, 363, 368472	upstream, in gene, downstream	ActReg chr2 #9553	1	0	0
9554	2	43,520,725	43,521,435	710	2	17.864	13.364	1.235	41	25	2	0	0	1	THADA	302,105	in gene	ActReg chr2 #9554	1	1	0
9555	2	43,822,771	43,823,697	926	2	11.621	13.069	9.345	20	21	15	1	1	1	THADA	-49	upstream	ActReg chr2 #9555	1	1	0
9556	2	44,065,307	44,065,674	367	1	2.667	2.583	13.167	6	5	16	0	2	2	ABCG5, ABCG8	468, -613	in gene, upstream	ActReg chr2 #9556	0	0	1
9557	2	44,222,535	44,223,753	1,218	2	18.447	15.921	5.135	44	32	11	1	1	1	LRPPRC	0	in gene	ActReg chr2 #9557	1	1	0
9558	2	44,243,216	44,244,021	805	2	13.68	11.2	2.75	29	22	4	0	0	0				ActReg chr2 #9558	1	1	0
9559	2	44,327,361	44,328,264	903	1	9.286	14.571	4.821	16	27	9	0	0	0				ActReg chr2 #9559	0	1	0
9560	2	44,395,328	44,396,330	1,002	1	6.375	10.5	4.812	10	15	12	1	1	1	PPM1B	-171	upstream	ActReg chr2 #9560	0	1	0
9561	2	44,588,369	44,589,464	1,095	1	12.059	8.088	7.735	21	16	18	1	2	2	PREPL, C2orf34	85, -127	in gene, upstream	ActReg chr2 #9561	1	0	0
9562	2	45,020,402	45,020,961	559	1	6.375	9.389	1.278	11	19	3	0	0	0				ActReg chr2 #9562	0	1	0
9563	2	45,165,589	45,165,905	316	1	4.9	2.1	11.3	7	3	15	1	2	3	LOC100506088, LOC100506108, SIX3	-2957, 3270, -3290	upstream, downstream, upstream	ActReg chr2 #9563	0	0	1
9564	2	45,182,173	45,183,005	832	1	4.654	8.385	11.538	10	16	21	1	0	1	SIX3	13,552	downstream	ActReg chr2 #9564	0	0	1
9565	2	45,186,014	45,186,627	613	1	8.85	11.1	5.15	17	17	6	0	0	0				ActReg chr2 #9565	0	1	0
9566	2	45,240,359	45,240,725	366	1	1.818	4.545	11.454	3	6	14	1	1	1	SIX2	-4,000	upstream	ActReg chr2 #9566	0	0	1
9567	2	46,078,621	46,079,424	803	2	11.538	9.077	4.846	17	18	8	0	0	1	PRKCE	199,979	in gene	ActReg chr2 #9567	1	1	0
9568	2	46,165,964	46,166,808	844	1	10.192	7.923	2.529	14	12	5	0	0	1	PRKCE	287,343	in gene	ActReg chr2 #9568	1	0	0
9569	2	46,325,614	46,326,449	835	2	8.654	9.692	1.909	16	16	4	0	0	1	PRKCE	446,988	in gene	ActReg chr2 #9569	1	1	0
9570	2	46,398,365	46,398,930	565	1	7.611	12.056	4.944	11	17	8	0	0	1	PRKCE	519,604	in gene	ActReg chr2 #9570	0	1	0
9571	2	46,443,452	46,444,046	594	1	5.105	10.526	2.842	8	17	5	0	0	0				ActReg chr2 #9571	0	1	0
9572	2	46,525,534	46,526,354	820	1	6.038	7.5	13.346	9	14	17	1	1	1	EPAS1	1,403	in gene	ActReg chr2 #9572	0	0	1
9573	2	46,707,639	46,708,161	522	1	6	6.471	13.118	10	8	21	1	1	1	LOC388946	1,196	in gene	ActReg chr2 #9573	0	0	1
9574	2	46,708,524	46,709,183	659	1	5.75	11.45	2.556	9	20	4	0	1	1	LOC388946	2,149	in gene	ActReg chr2 #9574	0	1	0
9575	2	46,727,114	46,727,916	802	1	7.696	12.92	5.36	15	24	10	0	0	0				ActReg chr2 #9575	0	1	0
9576	2	46,768,760	46,769,203	443	1	8.5	9.286	10.929	11	16	16	0	2	2	FLJ41757, RHOQ	160, -886	in gene, upstream	ActReg chr2 #9576	0	0	1
9577	2	47,136,611	47,137,331	720	1	8.773	12.182	2.864	21	21	5	0	0	2	LOC100506177, MCFD2	10557, 32023	downstream, in gene	ActReg chr2 #9577	0	1	0
9578	2	47,167,639	47,168,088	449	1	6.643	8.357	11.214	8	12	16	1	2	2	MCFD2, TTC7A	1131, -450	in gene, upstream	ActReg chr2 #9578	0	0	1
9579	2	47,213,717	47,214,109	392	1	7.333	7.167	12.583	10	9	18	0	0	1	TTC7A	45,600	in gene	ActReg chr2 #9579	0	0	1
9580	2	47,221,250	47,221,804	554	1	4.941	1.667	11	8	3	14	0	0	1	TTC7A	53,214	in gene	ActReg chr2 #9580	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9581	2	47,312,819	47,313,525	706	1	10.591	7.5	5.421	17	13	10	0	0	2	TTC7A, C2orf61	144859, 69345	downstream, downstream	ActReg chr2 #9581	1	0	0
9582	2	47,403,075	47,404,440	1,365	3	12.429	11.881	14.024	20	20	24	1	1	1	CALM2	-17	upstream	ActReg chr2 #9582	1	1	1
9583	2	47,425,842	47,426,549	707	1	10.318	13.136	2	15	20	3	0	0	0				ActReg chr2 #9583	0	1	0
9584	2	47,499,128	47,499,911	783	1	12.12	10.68	7.84	20	15	13	1	0	0				ActReg chr2 #9584	1	0	0
9585	2	47,629,946	47,630,954	1,008	2	10.375	10.906	7.312	19	17	15	1	1	1	MSH2	187	in gene	ActReg chr2 #9585	1	1	0
9586	2	47,798,042	47,799,199	1,157	2	14.972	17.083	7.083	32	32	10	1	1	1	KCNK12	-1,150	upstream	ActReg chr2 #9586	1	1	0
9587	2	48,010,137	48,010,696	559	2	8.222	11.222	7.647	11	21	14	1	1	1	MSH6	195	in gene	ActReg chr2 #9587	0	1	1
9588	2	48,667,357	48,668,074	717	2	9.043	11.304	9.565	12	19	18	1	1	1	KLRAQ1	-193	upstream	ActReg chr2 #9588	0	1	1
9589	2	48,793,575	48,793,996	421	1	3.846	10.308	1.6	6	14	4	0	1	1	STON1-GTF2A1L	-2,374	upstream	ActReg chr2 #9589	0	1	0
9590	2	51,180,045	51,180,730	685	1	10.809	6.81	2.857	20	9	5	0	0	1	NRXN1	79,287	in gene	ActReg chr2 #9590	1	0	0
9591	2	51,258,953	51,259,876	923	2	13.759	20.276	4.889	28	53	9	0	1	1	NRXN1	260	in gene	ActReg chr2 #9591	1	1	0
9592	2	51,378,705	51,379,264	559	1	4.611	4.944	11.722	8	9	18	0	0	0				ActReg chr2 #9592	0	0	1
9593	2	51,808,778	51,809,511	733	1	12.826	8.043	3.571	21	13	6	0	0	0				ActReg chr2 #9593	1	0	0
9594	2	52,233,956	52,234,438	482	1	4.133	10.533	7.267	6	15	13	0	0	0				ActReg chr2 #9594	0	1	0
9595	2	53,580,363	53,580,909	546	1	11.471	8.647	3.294	17	13	6	0	0	0				ActReg chr2 #9595	1	0	0
9596	2	53,780,657	53,781,376	719	1	3.522	2.783	11.348	7	5	19	0	0	0				ActReg chr2 #9596	0	0	1
9597	2	54,013,641	54,014,664	1,023	1	9.875	13.688	5.719	17	21	10	1	2	3	ASB3, LOC100302652, ERLEC1	-73, 73018, 84	upstream, in gene, in gene	ActReg chr2 #9597	0	1	0
9598	2	54,330,794	54,331,272	478	1	6.6	8.8	2.733	9	13	5	0	0	0				ActReg chr2 #9598	0	1	0
9599	2	54,342,383	54,343,247	864	2	8	10.444	9.846	14	16	19	1	1	1	ACYP2	405	in gene	ActReg chr2 #9599	0	1	1
9600	2	54,709,628	54,710,152	524	1	11.235	7.235	4.529	18	10	9	0	0	1	SPTBN1	26,436	in gene	ActReg chr2 #9600	1	0	0
9601	2	54,950,241	54,951,302	1,061	1	12.848	11.515	6	19	15	11	1	1	1	EML6	-1,378	upstream	ActReg chr2 #9601	1	0	0
9602	2	55,130,979	55,131,835	856	1	10.154	13.615	4.682	16	23	7	0	0	1	EML6	179,258	in gene	ActReg chr2 #9602	0	1	0
9603	2	55,275,957	55,276,642	685	2	14.727	11.727	4.381	23	20	9	1	1	1	RTN4	1,435	in gene	ActReg chr2 #9603	1	1	0
9604	2	55,496,039	55,496,797	758	1	11.565	10.522	8.947	18	22	16	1	1	1	MTIF2	-34	upstream	ActReg chr2 #9604	1	0	0
9605	2	55,646,622	55,647,362	740	2	12.333	9.75	11.792	21	17	25	1	1	1	CCDC88A	65	in gene	ActReg chr2 #9605	1	0	1
9606	2	55,844,397	55,845,217	820	2	11.154	12.039	6	19	21	11	1	1	1	SMEK2	-11	upstream	ActReg chr2 #9606	1	1	0
9607	2	56,150,238	56,150,679	441	1	2.857	3.643	11.071	4	8	16	1	1	1	EFEMP1	474	in gene	ActReg chr2 #9607	0	0	1
9608	2	58,069,565	58,070,136	571	1	3.444	8.722	2.222	5	18	3	0	0	0				ActReg chr2 #9608	0	1	0
9609	2	58,077,547	58,077,914	367	1	3.182	2.364	11.636	6	3	16	0	0	0				ActReg chr2 #9609	0	0	1
9610	2	58,273,436	58,274,553	1,117	1	11.657	9.829	7.697	18	15	16	1	1	1	VRK2	217	in gene	ActReg chr2 #9610	1	0	0
9611	2	58,468,080	58,468,844	764	1	10.458	6.417	4.792	15	10	9	1	1	1	FANCL	53	in gene	ActReg chr2 #9611	1	0	0
9612	2	58,787,794	58,788,301	507	1	10.625	5.125	2.417	15	7	5	0	0	1	FLJ30838	40,159	in gene	ActReg chr2 #9612	1	0	0
9613	2	58,828,109	58,828,613	504	1	5.625	10.25	2.312	12	16	5	0	0	1	FLJ30838	80,473	in gene	ActReg chr2 #9613	0	1	0
9614	2	60,687,919	60,688,281	362	1	5	4.091	10.546	7	5	15	1	0	1	BCL11A	92,533	in gene	ActReg chr2 #9614	0	0	1
9615	2	61,107,949	61,108,986	1,037	1	6.344	10.938	7.034	12	19	11	1	2	2	FLJ16341, REL	-18, -285	upstream, upstream	ActReg chr2 #9615	0	1	0
9616	2	61,199,912	61,200,475	563	1	2.75	3.294	11.941	4	4	18	0	0	1	PUS10	45,172	in gene	ActReg chr2 #9616	0	0	1
9617	2	61,243,882	61,245,291	1,409	2	27.432	25.095	5.233	78	65	10	0	2	2	PUS10, PEX13	779, -226	in gene, upstream	ActReg chr2 #9617	1	1	0
9618	2	61,403,564	61,404,505	941	3	11.357	12.724	8.136	17	31	19	1	1	1	AHSA2	-521	upstream	ActReg chr2 #9618	1	1	1
9619	2	61,698,412	61,698,846	434	1	8.231	9.077	13	11	12	21	0	1	2	USP34, XPO1	-780, 66789	upstream, downstream	ActReg chr2 #9619	0	0	1
9620	2	61,765,189	61,765,815	626	1	8.947	11.21	2.632	12	18	5	1	1	1	XPO1	-84	upstream	ActReg chr2 #9620	0	1	0
9621	2	61,991,214	61,991,993	779	2	7.417	12	12.042	13	16	18	1	0	0				ActReg chr2 #9621	0	1	1
9622	2	62,081,148	62,082,307	1,159	1	9.378	12.351	5.432	17	17	11	1	1	1	FAM161A	-449	upstream	ActReg chr2 #9622	0	1	0
9623	2	62,115,339	62,116,107	768	3	10.542	11.917	15.542	22	19	28	1	1	1	CCT4	68	in gene	ActReg chr2 #9623	1	1	1
9624	2	62,132,406	62,133,101	695	2	10.864	10.818	6.773	21	18	12	0	1	1	COMMD1	-50	upstream	ActReg chr2 #9624	1	1	0
9625	2	62,266,296	62,266,887	591	2	9.789	9.368	2.421	21	19	4	0	0	1	COMMD1	133,788	in gene	ActReg chr2 #9625	1	1	0
9626	2	62,282,718	62,283,331	613	1	11	13.6	1.75	16	21	3	0	0	1	COMMD1	150,221	in gene	ActReg chr2 #9626	0	1	0
9627	2	62,932,312	62,932,843	531	1	10.765	9.941	5.059	15	14	8	1	0	1	EHBP1	31,591	in gene	ActReg chr2 #9627	1	0	0
9628	2	62,932,955	62,933,203	248	1	3.875	5.25	12.5	5	7	15	1	0	1	EHBP1	32,093	in gene	ActReg chr2 #9628	0	0	1
9629	2	63,282,675	63,283,218	543	1	3.176	5.353	12.529	6	8	17	1	1	3	EHBP1, LOC100132215, OTX1	381960, -7290, 4981	downstream, upstream, in gene	ActReg chr2 #9629	0	0	1
9630	2	63,815,390	63,816,347	957	3	12.8	10.867	9.6	20	22	21	1	2	2	C2orf86, MDH1	-17, -254	upstream, upstream	ActReg chr2 #9630	1	1	1
9631	2	64,067,635	64,069,123	1,488	2	11.149	11.575	7.383	22	23	11	1	1	1	UGP2	281	in gene	ActReg chr2 #9631	1	1	0
9632	2	64,455,001	64,455,992	991	2	22.387	18.355	5.032	65	47	12	0	1	1	LOC100507006	-92	upstream	ActReg chr2 #9632	1	1	0
9633	2	64,500,560	64,501,480	920	2	11.345	10.586	2.778	18	21	6	0	0	0				ActReg chr2 #9633	1	1	0
9634	2	64,575,783	64,576,377	594	1	4.389	11.5	1.929	6	18	4	0	0	0				ActReg chr2 #9634	0	1	0
9635	2	64,586,752	64,587,682	930	1	9.1	12	3.733	13	18	8	0	0	0				ActReg chr2 #9635	0	1	0
9636	2	64,751,010	64,752,080	1,070	1	8.061	11.697	7.121	13	19	11	1	1	1	AFTPH	106	in gene	ActReg chr2 #9636	0	1	0
9637	2	64,880,739	64,881,087	348	1	9.5	6.9	13.2	14	9	18	1	1	2	SERTAD2, LOC730184	133, 9167	in gene, downstream	ActReg chr2 #9637	0	0	1
9638	2	64,977,645	64,979,346	1,701	1	8.038	11.377	5.755	14	23	13	1	0	0				ActReg chr2 #9638	0	1	0
9639	2	65,034,369	65,035,035	666	2	9.25	11.45	1.571	20	21	2	0	0	0				ActReg chr2 #9639	1	1	0
9640	2	65,058,309	65,059,015	706	1	9.636	11.182	4.182	14	15	7	0	0	0				ActReg chr2 #9640	0	1	0
9641	2	65,212,249	65,213,144	895	1	10.429	8.536	2.333	14	15	3	0	1	1	SLC1A4	-2,883	upstream	ActReg chr2 #9641	1	0	0
9642	2	65,356,969	65,357,673	704	2	13.227	9.409	2.636	26	20	5	2	1	1	RAB1A	114	in gene	ActReg chr2 #9642	1	1	0
9643	2	65,454,897	65,455,452	555	1	7.529	10.941	7.706	10	15	11	1	1	1	ACTR2	345	in gene	ActReg chr2 #9643	0	1	0
9644	2	65,658,807	65,659,179	372	1	4.083	7.667	11.25	11	10	14	1	1	1	SPRED2	663	in gene	ActReg chr2 #9644	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9645	2	65,659,497	65,660,202	705	2	8.773	11.273	4.773	20	20	7	1	1	1	SPRED2	-193	upstream	ActReg chr2 #9645	1	1	0
9646	2	65,662,667	65,663,376	709	2	11.773	12.091	4.818	23	20	7	1	1	1	SPRED2	-3,365	upstream	ActReg chr2 #9646	1	1	0
9647	2	66,661,695	66,662,568	873	2	12.357	11.25	4.179	23	22	7	2	2	2	LOC730198, MEIS1	-622, -401	upstream, upstream	ActReg chr2 #9647	1	1	0
9648	2	67,096,177	67,096,656	479	1	7.2	9.733	1.222	11	16	2	0	0	0				ActReg chr2 #9648	0	1	0
9649	2	67,115,675	67,116,336	661	1	9.095	10.857	5.667	14	18	13	0	0	0				ActReg chr2 #9649	0	1	0
9650	2	67,624,488	67,625,084	596	1	7.944	9.556	4.667	12	15	7	1	1	1	ETAA1	344	in gene	ActReg chr2 #9650	0	1	0
9651	2	67,691,014	67,691,514	500	1	9.4	9.5	1.857	16	16	2	0	0	0				ActReg chr2 #9651	1	0	0
9652	2	68,289,866	68,290,476	610	1	5.684	11.105	7.312	13	17	15	0	1	1	C1D	-12	upstream	ActReg chr2 #9652	0	1	0
9653	2	68,383,893	68,385,436	1,543	2	17.792	20.188	6.778	60	61	15	1	2	2	WDR92, PNO1	-8, -341	upstream, upstream	ActReg chr2 #9653	1	1	0
9654	2	68,547,300	68,547,871	571	1	9.824	13.353	2	16	22	3	1	1	1	CNRIP1	-402	upstream	ActReg chr2 #9654	0	1	0
9655	2	68,660,164	68,660,613	449	1	4	3.643	11.214	6	6	15	0	0	0				ActReg chr2 #9655	0	0	1
9656	2	68,694,026	68,695,100	1,074	2	13.758	16.546	7.303	21	30	11	1	2	2	FBXO48, APLF	-173, -128	upstream, upstream	ActReg chr2 #9656	1	1	0
9657	2	69,056,309	69,056,777	468	1	11.067	7.533	5.467	20	10	7	0	0	1	ARHGAP25	94,630	downstream	ActReg chr2 #9657	1	0	0
9658	2	69,220,674	69,221,445	771	1	6.167	14.375	1.792	8	24	3	0	0	0				ActReg chr2 #9658	0	1	0
9659	2	69,405,122	69,405,757	635	2	11.316	10.368	3.368	21	20	6	0	0	1	ANTXR1	165,163	in gene	ActReg chr2 #9659	1	1	0
9660	2	69,534,342	69,534,788	446	1	10.214	9.857	11.429	14	14	17	1	0	0				ActReg chr2 #9660	0	0	1
9661	2	69,664,148	69,665,026	878	2	9.143	12.056	8.893	15	17	16	1	1	1	NFU1	166	in gene	ActReg chr2 #9661	0	1	1
9662	2	69,869,433	69,870,232	799	1	6.84	11.04	4.565	11	19	9	1	1	1	AAK1	1,145	in gene	ActReg chr2 #9662	0	1	0
9663	2	69,871,550	69,872,104	554	1	5.882	10.722	5.467	10	17	9	1	1	1	AAK1	-850	upstream	ActReg chr2 #9663	0	1	0
9664	2	69,968,690	69,969,685	995	1	10.71	9.677	6.484	16	16	14	1	1	1	ANXA4	60	in gene	ActReg chr2 #9664	1	0	0
9665	2	70,056,285	70,057,574	1,289	3	10.268	10.415	11.756	16	19	22	1	1	2	ANXA4, GMCL1	87802, 111	downstream, in gene	ActReg chr2 #9665	0	1	1
9666	2	70,141,345	70,141,845	500	1	8	11.4	12.667	12	14	17	1	1	2	SNRNP27, MXD1	20505, -608	downstream, upstream	ActReg chr2 #9666	0	0	1
9667	2	70,142,034	70,143,049	1,015	1	7.375	8.156	12.031	16	13	17	1	1	2	SNRNP27, MXD1	21451, 338	downstream, in gene	ActReg chr2 #9667	0	0	1
9668	2	70,313,248	70,314,676	1,428	2	7.978	10.644	7	18	17	14	1	2	2	LOC400960, PCBP1	185, -623	in gene, upstream	ActReg chr2 #9668	1	1	0
9669	2	70,314,682	70,315,656	974	1	9.484	11.032	6.733	15	19	13	1	2	2	LOC400960, PCBP1	-1022, 584	upstream, in gene	ActReg chr2 #9669	0	1	0
9670	2	70,351,334	70,351,667	333	1	7.4	3.7	10.7	11	5	14	1	1	1	LOC100133985	948	in gene	ActReg chr2 #9670	0	0	1
9671	2	70,368,926	70,369,359	433	1	8.071	7.714	11.857	13	11	21	1	0	1	C2orf42	49,009	downstream	ActReg chr2 #9671	0	0	1
9672	2	70,369,569	70,370,252	683	1	10.191	12.571	6.368	18	26	11	1	0	1	C2orf42	48,241	downstream	ActReg chr2 #9672	0	1	0
9673	2	70,375,327	70,375,850	523	1	3.176	3.133	13	4	5	21	0	0	1	C2orf42	42,563	downstream	ActReg chr2 #9673	0	0	1
9674	2	70,417,520	70,418,435	915	2	9.931	9.966	13.276	15	17	24	1	1	1	C2orf42	174	in gene	ActReg chr2 #9674	0	1	1
9675	2	70,485,170	70,485,828	658	1	7.714	10.381	6.19	11	16	10	1	2	3	TIA1, MIR1285-2, PCYOX1	-9720, -5362, 268	upstream, upstream, in gene	ActReg chr2 #9675	0	1	0
9676	2	70,520,248	70,521,186	938	2	11.967	8.7	6.9	21	17	13	1	1	2	SNRPG, FAM136A	152, 8503	in gene, downstream	ActReg chr2 #9676	1	1	0
9677	2	70,528,431	70,529,253	822	2	10.115	14.615	11.769	12	29	19	1	1	2	SNRPG, FAM136A	-7973, 378	upstream, in gene	ActReg chr2 #9677	0	1	1
9678	2	70,780,259	70,781,841	1,582	3	11.245	8.673	8.245	27	18	19	1	1	1	TGFA	55	in gene	ActReg chr2 #9678	1	1	1
9679	2	70,823,287	70,824,349	1,062	1	10.576	8.182	4.5	17	13	7	0	0	0				ActReg chr2 #9679	1	0	0
9680	2	70,914,034	70,914,432	398	1	7.692	11.308	3.462	9	17	6	0	0	1	ADD2	81,142	in gene	ActReg chr2 #9680	0	1	0
9681	2	71,098,625	71,099,297	672	1	10.667	11.238	6.571	18	15	12	1	0	0				ActReg chr2 #9681	0	1	0
9682	2	71,128,212	71,128,864	652	1	9.952	11.143	12.524	14	16	19	1	1	1	VAX2	818	in gene	ActReg chr2 #9682	0	0	1
9683	2	71,174,582	71,175,235	653	1	7.524	11.857	3.35	11	21	5	0	0	1	ATP6V1B1	11,910	in gene	ActReg chr2 #9683	0	1	0
9684	2	71,221,216	71,222,680	1,464	2	21.217	27.413	8.045	78	99	17	1	1	2	ANKRD53, TEX261	16373, 53	downstream, in gene	ActReg chr2 #9684	1	1	0
9685	2	71,295,084	71,296,182	1,098	3	13.647	13.559	9.882	21	24	23	1	1	1	NAGK	225	in gene	ActReg chr2 #9685	1	1	1
9686	2	71,356,867	71,357,968	1,101	2	10.941	13.265	7.735	23	24	16	1	2	2	MCEE, MPHOSPH10	-23, -27	upstream, upstream	ActReg chr2 #9686	1	1	0
9687	2	71,503,449	71,504,177	728	1	10.826	12.652	6.304	14	20	13	1	0	0				ActReg chr2 #9687	1	0	0
9688	2	71,559,071	71,559,510	439	1	8.571	9	10.714	12	13	16	1	1	1	ZNF638	401	in gene	ActReg chr2 #9688	0	0	1
9689	2	71,574,453	71,576,309	1,856	3	11.207	15.793	2.353	23	29	5	0	0	1	ZNF638	16,492	in gene	ActReg chr2 #9689	1	1	0
9690	2	71,971,176	71,971,828	652	1	10.95	10.6	4.15	19	18	6	0	0	0				ActReg chr2 #9690	1	0	0
9691	2	72,070,350	72,071,073	723	1	11.609	7.783	4.609	23	11	8	0	0	0				ActReg chr2 #9691	1	0	0
9692	2	72,083,566	72,084,343	777	1	8.375	11.583	5.091	16	19	10	0	0	0				ActReg chr2 #9692	0	1	0
9693	2	72,109,520	72,110,687	1,167	3	13.139	14.806	8.25	27	25	16	0	0	0				ActReg chr2 #9693	1	1	1
9694	2	72,341,140	72,341,500	360	1	3.455	6.818	11.546	5	9	16	0	0	0				ActReg chr2 #9694	0	0	1
9695	2	72,342,431	72,343,421	990	2	9.387	11.71	5.133	19	17	14	0	0	0				ActReg chr2 #9695	1	1	0
9696	2	72,372,062	72,372,521	459	1	6.067	5.8	10.733	8	8	17	1	1	1	CYP26B1	2,672	in gene	ActReg chr2 #9696	0	0	1
9697	2	73,005,571	73,005,970	399	1	8.167	9.583	2.333	12	14	3	0	0	1	EXOC6B	47,407	in gene	ActReg chr2 #9697	0	1	0
9698	2	73,052,527	73,053,430	903	2	10.821	12.037	7.679	18	25	12	1	1	1	EXOC6B	199	in gene	ActReg chr2 #9698	1	1	0
9699	2	73,110,257	73,111,109	852	2	16.222	16.704	1.739	34	36	3	0	1	1	SPR	-3,829	upstream	ActReg chr2 #9699	1	1	0
9700	2	73,114,238	73,114,932	694	1	8.227	12.727	5.4	14	22	13	1	1	1	SPR	73	in gene	ActReg chr2 #9700	0	1	0
9701	2	73,190,828	73,191,230	402	1	3.917	8.083	12.75	6	11	18	0	0	1	SFXN5	107,936	in gene	ActReg chr2 #9701	0	0	1
9702	2	73,216,949	73,217,677	728	1	3.087	2.632	11.739	5	4	17	0	0	1	SFXN5	81,652	in gene	ActReg chr2 #9702	0	0	1
9703	2	73,297,960	73,298,818	858	1	10.963	8.815	7.231	15	13	13	1	1	2	SFXN5, RAB11FIP5	576, 41757	in gene, downstream	ActReg chr2 #9703	1	0	0
9704	2	73,441,170	73,442,036	866	3	9.852	10.185	12.63	18	18	29	1	1	2	NOTO, SMYD5	12217, 237	downstream, in gene	ActReg chr2 #9704	1	1	1
9705	2	73,460,485	73,462,095	1,610	3	10.96	13.1	9.08	19	19	17	1	2	3	SMYD5, C2orf7, CCT7	19924, -934, -74	downstream, upstream, upstream	ActReg chr2 #9705	1	1	1
9706	2	73,511,515	73,511,874	359	1	6	10.083	12.75	8	14	20	1	1	2	LOC100507133, EGR4	41, 9135	in gene, downstream	ActReg chr2 #9706	0	0	1
9707	2	73,517,949	73,519,428	1,479	2	8.596	14.936	7.561	22	28	14	1	1	2	LOC100507133, EGR4	7035, 2141	downstream, in gene	ActReg chr2 #9707	1	1	0
9708	2	73,612,995	73,613,589	594	1	6.667	12.833	10.278	10	19	14	1	1	1	ALMS1	406	in gene	ActReg chr2 #9708	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9709	2	73,964,261	73,965,183	922	2	13.25	13.643	5.375	23	23	10	1	1	1	TPRKB	-205	upstream	ActReg chr2 #9709	1	1	0
9710	2	74,007,001	74,007,593	592	1	9.368	12.579	5.526	16	26	10	1	2	2	DUSP11, C2orf78	-13, -4019	upstream, upstream	ActReg chr2 #9710	0	1	0
9711	2	74,055,776	74,056,525	749	1	8	11.5	5.25	13	18	9	1	1	1	STAMBP	64	in gene	ActReg chr2 #9711	0	1	0
9712	2	74,057,924	74,058,374	450	1	12.286	8.929	3.143	16	12	6	0	1	1	STAMBP	2,063	in gene	ActReg chr2 #9712	1	0	0
9713	2	74,079,117	74,079,780	663	1	11.143	8	2.444	17	10	3	0	0	1	STAMBP	23,362	in gene	ActReg chr2 #9713	1	0	0
9714	2	74,153,820	74,154,380	560	2	6.765	11.667	9.778	11	18	20	1	1	2	ACTG2, DGUOK	34007, 147	downstream, in gene	ActReg chr2 #9714	0	1	1
9715	2	74,328,696	74,329,283	587	1	3.438	4.895	11.368	7	8	15	0	0	1	TET3	55,539	in gene	ActReg chr2 #9715	0	0	1
9716	2	74,347,093	74,348,114	1,021	2	27.469	34.312	5.581	79	106	11	1	0	0				ActReg chr2 #9716	1	1	0
9717	2	74,374,393	74,375,846	1,453	2	27.239	30.848	4.462	103	136	8	1	2	3	BOLA3, LOC100507171, MOBKL1B	-80, -47, 30876	upstream, upstream, downstream	ActReg chr2 #9717	1	1	0
9718	2	74,425,470	74,426,104	634	1	9.8	10.6	6.15	17	18	10	1	1	1	MTHFD2	97	in gene	ActReg chr2 #9718	0	1	0
9719	2	74,619,034	74,619,563	529	1	11.471	8	3.5	16	16	6	1	1	2	DCTN1, LOC100189589	-84, 6453	upstream, in gene	ActReg chr2 #9719	1	0	0
9720	2	74,648,325	74,648,992	667	1	7.571	11.381	4.722	12	18	8	1	3	4	C2orf81, LOC100130009, WDR54, RTKN	-3814, -3089, -227, 20402	upstream, upstream, upstream, downstream	ActReg chr2 #9720	0	1	0
9721	2	74,663,690	74,664,152	462	1	3.786	5	12.214	5	11	19	1	0	1	RTKN	5,139	in gene	ActReg chr2 #9721	0	0	1
9722	2	74,666,888	74,668,405	1,517	2	11.83	16.234	8.766	29	40	13	1	1	1	RTKN	1,414	in gene	ActReg chr2 #9722	1	1	0
9723	2	74,681,780	74,682,672	892	1	10.893	12.464	6.321	23	20	13	1	2	3	ING3DB, WBP1, MOGS	27, -3351, 10311	in gene, upstream, downstream	ActReg chr2 #9723	0	1	0
9724	2	74,684,707	74,685,114	407	1	6	8	11.417	8	11	17	1	1	3	ING3DB, WBP1, MOGS	2711, -667, 7627	in gene, upstream, downstream	ActReg chr2 #9724	0	0	1
9725	2	74,699,274	74,700,232	958	3	12.6	10.533	10.967	20	22	20	1	2	4	MOGS, MRPL53, CCDC142, TTC31	-7216, 174, 10604, -10447	upstream, in gene, downstream, upstream	ActReg chr2 #9725	1	1	1
9726	2	74,709,114	74,710,738	1,624	3	12.922	12.941	11.02	19	23	20	1	2	3	MRPL53, CCDC142, TTC31	-9999, 431, -274	upstream, in gene, upstream	ActReg chr2 #9726	1	1	1
9727	2	74,724,856	74,725,393	537	1	6.529	7.412	12.177	10	13	15	1	1	4	TTC31, LBX2, hCG_1811732, PCGF1	14924, 5319, -4620, 9697	downstream, in gene, upstream, downstream	ActReg chr2 #9727	0	0	1
9728	2	74,734,027	74,735,041	1,014	3	13.562	19	10.281	28	38	22	1	3	4	LBX2, hCG_1811732, PCGF1, TLX2	4091, 4790, 287, -7062	upstream, downstream, in gene, upstream	ActReg chr2 #9728	1	1	1
9729	2	74,756,206	74,757,601	1,395	2	8	10.296	11.182	16	27	19	1	3	4	DCX1, AUP1, HTRA2, LOXL3	-3495, 71, 371, 24159	upstream, in gene, in gene, downstream	ActReg chr2 #9729	0	1	1
9730	2	74,780,174	74,780,827	653	1	10.05	9.9	11.55	15	17	17	0	2	3	LOXL3, DOK1, C2orf65	562, -1360, 94664	in gene, upstream, downstream	ActReg chr2 #9730	0	0	1
9731	2	74,781,286	74,781,784	498	1	5.4	7.533	11.6	8	14	17	1	2	3	LOXL3, DOK1, C2orf65	-473, -325, 93629	upstream, upstream, downstream	ActReg chr2 #9731	0	0	1
9732	2	74,782,119	74,782,586	467	1	4.929	5.429	12.857	9	10	19	1	2	3	LOXL3, DOK1, C2orf65	-1290, 492, 92812	upstream, in gene, downstream	ActReg chr2 #9732	0	0	1
9733	2	74,881,461	74,882,124	663	1	7.381	7.81	14.381	12	11	20	1	2	2	C2orf65, SEMA4F	-6628, 399	upstream, in gene	ActReg chr2 #9733	0	0	1
9734	2	75,061,437	75,062,527	1,090	2	8.882	11.853	9.353	16	22	18	1	1	1	HK2	2,200	in gene	ActReg chr2 #9734	0	1	1
9735	2	75,144,861	75,145,810	949	1	11.2	10.2	3.077	18	16	5	0	0	0				ActReg chr2 #9735	1	0	0
9736	2	75,274,854	75,275,461	607	1	12.737	8.105	1.308	22	16	3	0	0	1	TACR1	151,488	in gene	ActReg chr2 #9736	1	0	0
9737	2	75,427,083	75,427,691	608	1	4.947	6.947	10.632	10	12	15	1	1	1	TACR1	-742	upstream	ActReg chr2 #9737	0	0	1
9738	2	75,818,943	75,819,781	838	2	13.259	15.778	1.36	29	38	3	0	0	0				ActReg chr2 #9738	1	1	0
9739	2	75,833,019	75,833,683	664	1	7.3	11.429	3.286	14	17	5	0	0	0				ActReg chr2 #9739	0	1	0
9740	2	75,873,486	75,874,293	807	2	9.84	13.36	6.28	17	21	13	1	1	1	MRPL19	-20	upstream	ActReg chr2 #9740	1	1	0
9741	2	75,937,414	75,938,346	932	1	9.724	11.931	4.862	19	23	12	1	1	1	C2orf3	231	in gene	ActReg chr2 #9741	0	1	0
9742	2	76,098,824	76,099,898	1,074	2	9.97	11.97	3.636	20	20	8	0	0	0				ActReg chr2 #9742	1	1	0
9743	2	77,185,601	77,186,344	743	2	9.696	13.13	2.1	20	20	4	0	0	1	LRRTM4	563,530	in gene	ActReg chr2 #9743	1	1	0
9744	2	78,768,719	78,769,742	1,023	2	14.062	16.344	4	39	40	7	0	0	0				ActReg chr2 #9744	1	1	0
9745	2	81,708,145	81,709,376	1,231	2	9.692	10.615	5.706	17	20	12	0	0	0				ActReg chr2 #9745	1	1	0
9746	2	81,810,439	81,811,001	562	1	4.176	4.941	11.647	6	8	16	0	0	0				ActReg chr2 #9746	0	0	1
9747	2	81,885,337	81,885,808	471	1	11.2	8.2	3	19	12	4	0	0	0				ActReg chr2 #9747	1	0	0
9748	2	82,212,172	82,212,575	403	1	1.455	3	10.167	2	4	15	0	0	0				ActReg chr2 #9748	0	0	1
9749	2	83,212,746	83,213,540	794	1	3.48	3.667	11.24	6	6	16	0	0	0				ActReg chr2 #9749	0	0	1
9750	2	83,407,927	83,408,457	530	1	2.933	2.714	12.235	5	4	17	0	0	0				ActReg chr2 #9750	0	0	1
9751	2	84,541,917	84,542,356	439	1	10	4.071	4.308	14	6	6	0	0	0				ActReg chr2 #9751	1	0	0
9752	2	84,685,914	84,687,002	1,088	3	14.265	15.412	8.441	40	37	14	1	1	1	SUCLG1	128	in gene	ActReg chr2 #9752	1	1	1
9753	2	84,968,026	84,968,928	902	1	6.586	11.414	6.724	10	25	15	0	0	1	DNAH6	224,898	in gene	ActReg chr2 #9753	0	1	0
9754	2	85,132,396	85,133,696	1,300	2	7	11.366	7.175	10	19	16	2	1	1	TMSB10	283	in gene	ActReg chr2 #9754	0	1	1
9755	2	85,152,635	85,153,611	976	2	13.419	12.774	5.613	21	24	10	0	0	0				ActReg chr2 #9755	1	1	0
9756	2	85,153,720	85,154,520	800	1	10.44	8.08	5.92	15	11	10	0	0	0				ActReg chr2 #9756	1	0	0
9757	2	85,554,843	85,555,657	814	2	11.923	11.577	8.5	20	18	18	1	1	1	TGOLN2	124	in gene	ActReg chr2 #9757	1	1	0
9758	2	85,580,961	85,582,198	1,237	1	8.289	13.237	5.333	14	21	11	1	2	2	RETSAT, ELMOD3	242, -264	in gene, upstream	ActReg chr2 #9758	0	1	0
9759	2	85,647,630	85,648,173	543	1	8.059	13.118	3.647	11	21	6	0	0	1	CAPG	-10,225	upstream	ActReg chr2 #9759	0	1	0
9760	2	85,664,507	85,665,085	578	1	6.333	11.5	4.882	11	21	10	1	0	1	SH2D6	2,878	in gene	ActReg chr2 #9760	0	1	0
9761	2	85,765,430	85,767,294	1,864	3	10.397	11.345	8.914	21	19	22	1	1	3	MAT2A, LOC100507238, GGCX	74, 7030, 22295	in gene, downstream, downstream	ActReg chr2 #9761	1	1	1
9762	2	85,788,439	85,788,826	387	1	8.917	7.75	13.917	12	10	20	1	1	1	GGCX	25	in gene	ActReg chr2 #9762	0	0	1
9763	2	85,811,677	85,812,208	531	1	8.765	9.647	11.882	15	13	17	1	1	2	VAMP8, VAMP5	7328, 411	downstream, in gene	ActReg chr2 #9763	0	0	1
9764	2	85,822,269	85,823,246	977	1	6.452	11.258	4.69	15	17	8	1	1	4	VAMP5, RNF181, TMEM150A, C2orf68	11226, -80, 7065, 16422	downstream, upstream, downstream, downstream	ActReg chr2 #9764	0	1	0
9765	2	85,829,489	85,830,405	916	1	9.172	14.379	5.414	13	23	10	1	1	4	VAMP5, RNF181, TMEM150A, C2orf68	18416, 7110, -125, 9232	downstream, downstream, upstream, downstream	ActReg chr2 #9765	0	1	0
9766	2	85,838,529	85,839,742	1,213	2	8.73	11.108	9.361	16	21	21	1	2	3	TMEM150A, C2orf68, USP39	-9313, 44, -4148	upstream, in gene, upstream	ActReg chr2 #9766	0	1	1
9767	2	85,886,485	85,887,094	609	1	2.789	7	11.79	4	12	18	0	0	1	SFTPB	9,075	in gene	ActReg chr2 #9767	0	0	1
9768	2	85,889,869	85,890,472	603	1	9.263	14	6.263	15	24	12	0	0	1	SFTPB	5,694	in gene	ActReg chr2 #9768	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9769	2	85,999,303	86,000,021	718	2	11.409	13.773	5.455	23	26	10	0	0	1	ATOH8	18,753	in gene	ActReg chr2 #9769	1	1	0
9770	2	86,006,046	86,006,699	653	1	5.476	5.095	11.714	8	9	15	0	0	1	ATOH8	25,463	in gene	ActReg chr2 #9770	0	0	1
9771	2	86,120,534	86,121,223	689	1	8	13	3.75	18	19	5	0	1	1	ST3GAL5	4,721	upstream	ActReg chr2 #9771	0	1	0
9772	2	86,129,228	86,129,977	749	1	6.957	10.87	3.688	12	13	7	0	0	0				ActReg chr2 #9772	0	1	0
9773	2	86,332,397	86,333,662	1,265	2	13.538	14.641	6.081	25	28	14	1	2	2	POLR1A, PTCD3	249, -276	in gene, upstream	ActReg chr2 #9773	1	1	0
9774	2	86,527,392	86,528,593	1,201	2	13.368	14.895	3.606	22	26	9	0	0	1	REEP1	57,214	in gene	ActReg chr2 #9774	1	1	0
9775	2	86,667,736	86,668,338	602	1	11.053	10.947	6.263	17	16	12	1	1	1	KDM3A	-234	upstream	ActReg chr2 #9775	1	0	0
9776	2	86,669,085	86,669,763	678	1	3.4	13.546	1.842	9	21	3	1	1	1	KDM3A	1,153	in gene	ActReg chr2 #9776	0	1	0
9777	2	86,789,597	86,790,566	969	2	11.935	13.871	5.75	29	24	12	1	1	1	VPS24	539	in gene	ActReg chr2 #9777	1	1	0
9778	2	87,317,745	87,317,969	224	1	2.286	1.571	9.286	3	2	12	0	0	0				ActReg chr2 #9778	0	0	1
9779	2	87,579,381	87,579,697	316	1	4.7	4.4	12.5	7	7	17	0	0	0				ActReg chr2 #9779	0	0	1
9780	2	88,417,356	88,418,006	650	1	8.8	9.9	5.875	17	17	9	0	0	2	SMYD1, FABP1	50299, 9897	downstream, downstream	ActReg chr2 #9780	0	1	0
9781	2	88,438,654	88,439,115	461	1	4.8	9.6	0	6	14	0	0	0	0				ActReg chr2 #9781	0	1	0
9782	2	88,927,188	88,927,868	680	1	11.333	10.809	7	16	14	16	1	2	2	EIF2AK3, LOC100507360	434, 489	upstream, in gene	ActReg chr2 #9782	1	0	0
9783	2	88,990,616	88,991,517	901	2	12.607	12.786	6.929	24	25	12	1	1	1	RPIA	-110	upstream	ActReg chr2 #9783	1	1	0
9784	2	89,185,354	89,185,817	463	1	1	1.923	19.214	1	3	35	0	1	3	LOC100294406, IGK@, IGKV4-1	537379, 444851, 497	in gene, in gene, in gene	ActReg chr2 #9784	0	0	1
9785	2	90,414,023	90,414,303	280	1	6.125	6.625	13.75	8	9	18	1	0	0				ActReg chr2 #9785	0	0	1
9786	2	91,669,955	91,670,618	663	1	7.85	4.7	11.9	13	9	20	1	0	0				ActReg chr2 #9786	0	0	1
9787	2	91,762,786	91,764,338	1,552	1	19.667	18.375	25.354	37	29	39	0	0	0				ActReg chr2 #9787	0	0	1
9788	2	91,775,168	91,778,785	3,617	1	12.693	13.833	23.614	30	30	57	1	0	0				ActReg chr2 #9788	0	0	1
9789	2	91,843,938	91,844,270	332	1	3	6.6	16.9	5	9	23	0	0	1	LOC100506191	-8,728	upstream	ActReg chr2 #9789	0	0	1
9790	2	91,844,430	91,844,931	501	1	9.25	7.125	11.938	13	10	17	0	0	1	LOC100506191	-9,304	upstream	ActReg chr2 #9790	0	0	1
9791	2	91,953,923	91,954,933	1,010	2	9.161	9.29	3.355	19	16	6	0	0	0				ActReg chr2 #9791	1	1	0
9792	2	95,424,981	95,425,512	531	1	10.529	10.294	1.222	15	19	2	0	0	0				ActReg chr2 #9792	0	1	0
9793	2	95,787,413	95,787,863	450	1	8.929	10.857	7.071	12	18	11	1	1	1	MRPS5	116	in gene	ActReg chr2 #9793	0	1	0
9794	2	95,831,110	95,831,863	753	2	9.174	9.087	9.13	13	17	12	1	2	2	ZNF514, ZNF2	-6223, 303	upstream, in gene	ActReg chr2 #9794	0	1	1
9795	2	95,942,374	95,942,919	545	1	2.154	3.765	10.588	4	6	13	0	1	1	PROM2	2,445	in gene	ActReg chr2 #9795	0	0	1
9796	2	95,999,365	95,999,915	550	1	9.941	6.706	4.294	18	13	10	0	0	1	KCNIP3	36,568	in gene	ActReg chr2 #9796	1	0	0
9797	2	96,068,199	96,068,877	678	1	4.1	10.667	7	6	21	10	1	1	1	FAHD2A	90	in gene	ActReg chr2 #9797	0	1	0
9798	2	96,917,454	96,917,881	427	1	10.538	13.077	2.625	18	21	3	0	0	2	LOC285033, TMEM127	11690, 14084	downstream, in gene	ActReg chr2 #9798	0	1	0
9799	2	97,001,339	97,001,905	566	2	10.556	9.167	4.125	17	15	9	1	1	2	ITPRIPL1, NCAPH	10560, 138	downstream, in gene	ActReg chr2 #9799	1	1	0
9800	2	97,073,031	97,073,668	637	1	7.05	11.15	1.9	11	16	3	0	0	0				ActReg chr2 #9800	0	1	0
9801	2	97,222,462	97,223,151	689	2	11.909	9.682	5.227	20	19	7	0	0	1	ARID5A	20,342	downstream	ActReg chr2 #9801	1	1	0
9802	2	97,303,851	97,304,517	666	2	11.952	11.238	7.048	20	24	14	1	2	2	KIAA1310, FER1L5	-69, -4390	upstream, upstream	ActReg chr2 #9802	1	1	0
9803	2	97,481,780	97,482,353	573	1	10.111	6.556	2.722	20	10	5	1	2	3	CNNM4, LOC100506036, CNNM3	55427, -1896, 75	downstream, upstream, in gene	ActReg chr2 #9803	1	0	0
9804	2	97,525,855	97,526,512	657	1	2.333	3.375	11.667	4	6	15	0	1	2	ANKRD39, SEMA4C	-2427, 9552	upstream, in gene	ActReg chr2 #9804	0	0	1
9805	2	97,527,052	97,527,506	454	1	1.846	5.214	11.143	3	10	15	1	1	2	ANKRD39, SEMA4C	-3523, 8456	upstream, in gene	ActReg chr2 #9805	0	0	1
9806	2	98,262,282	98,262,741	459	1	4.571	6.643	11.786	7	9	15	1	2	3	UBTFL6, COX5B, ACTR1B	-7424, -10, 18050	upstream, upstream, downstream	ActReg chr2 #9806	0	0	1
9807	2	98,280,354	98,280,979	625	1	12.053	7.579	2.929	23	15	5	1	1	1	ACTR1B	-105	upstream	ActReg chr2 #9807	1	0	0
9808	2	99,124,213	99,124,675	462	1	2.667	5.6	12	4	11	18	0	0	1	INPP4A	63,123	in gene	ActReg chr2 #9808	0	0	1
9809	2	99,224,479	99,225,000	521	1	4.118	10.059	6.765	9	16	10	1	2	2	C2orf64, UNC50	-216, -303	in gene, upstream	ActReg chr2 #9809	0	1	0
9810	2	99,771,504	99,771,827	323	1	8	7.4	9.2	12	10	11	1	2	3	TSGA10, C2orf15, LIPT1	-478, 13480, 247	upstream, downstream, in gene	ActReg chr2 #9810	0	0	1
9811	2	99,797,280	99,797,796	516	1	9.647	10.471	4.667	14	18	9	1	2	2	MITD1, MRPL30	-46, -40	upstream, upstream	ActReg chr2 #9811	0	1	0
9812	2	99,953,555	99,954,101	546	1	13.353	8	3.471	20	14	5	1	2	2	TXNDC9, EIF5B	-968, -6	upstream, upstream	ActReg chr2 #9812	1	0	0
9813	2	100,498,206	100,498,726	520	1	9	3.235	2.062	14	5	4	0	0	1	AFF3	260,571	in gene	ActReg chr2 #9813	1	0	0
9814	2	101,042,902	101,043,219	317	1	1.667	3.7	9.6	3	5	12	0	0	1	CHST10	-8,969	upstream	ActReg chr2 #9814	0	0	1
9815	2	101,087,235	101,087,884	649	2	8.5	9.85	1.231	17	18	2	0	1	1	NMS	615	in gene	ActReg chr2 #9815	1	1	0
9816	2	101,461,939	101,462,234	295	1	1.889	4.556	10.222	3	6	14	0	0	1	NPAS2	25,473	in gene	ActReg chr2 #9816	0	0	1
9817	2	101,736,942	101,737,640	698	2	7.818	10	2.5	16	17	5	0	0	1	TBC1D8	30,555	in gene	ActReg chr2 #9817	1	1	0
9818	2	102,063,223	102,063,841	618	2	10	8.6	1	23	18	1	0	0	1	RFX8	27,633	in gene	ActReg chr2 #9818	1	1	0
9819	2	102,133,629	102,134,234	605	1	11.158	7.842	2.375	17	11	4	0	0	0				ActReg chr2 #9819	1	0	0
9820	2	105,953,594	105,954,140	546	1	7.824	9.882	3.412	12	18	5	1	3	3	TGFBRAP1, LOC100506473, C2orf49	-7719, -1862, -146	upstream, upstream, upstream	ActReg chr2 #9820	0	1	0
9821	2	106,535,603	106,536,501	898	1	11.929	8.214	3.6	18	21	7	0	0	0				ActReg chr2 #9821	1	0	0
9822	2	106,731,226	106,732,328	1,102	2	10.171	11.371	2.771	22	19	5	0	0	1	UXS1	79,018	in gene	ActReg chr2 #9822	1	1	0
9823	2	106,927,159	106,927,490	331	1	3.364	1.333	9.091	5	2	14	0	0	0				ActReg chr2 #9823	0	0	1
9824	2	109,150,369	109,150,736	367	1	7.182	7.091	11.091	9	10	14	1	1	1	LIMS1	-305	upstream	ActReg chr2 #9824	0	0	1
9825	2	109,335,645	109,336,238	593	1	10.79	12	5.579	17	20	10	1	1	1	RANBP2	4	in gene	ActReg chr2 #9825	0	1	0
9826	2	109,745,156	109,745,746	590	1	3.889	10.833	4.071	7	19	7	1	2	2	LOC100287216, SH3RF3	1124, -546	in gene, upstream	ActReg chr2 #9826	0	1	0
9827	2	109,746,473	109,746,814	341	1	7.9	9.5	12	12	12	15	1	2	2	LOC100287216, SH3RF3	-68, 646	upstream, in gene	ActReg chr2 #9827	0	0	1
9828	2	109,830,385	109,830,850	465	1	4.6	11.2	3.8	9	17	6	0	0	1	SH3RF3	84,620	in gene	ActReg chr2 #9828	0	1	0
9829	2	109,859,436	109,859,895	459	1	5.077	10.214	2	8	17	3	0	0	2	SH3RF3, LOC100506574	113668, -8213	in gene, upstream	ActReg chr2 #9829	0	1	0
9830	2	110,962,313	110,962,626	313	1	5.3	4.889	9.8	8	11	14	1	1	2	NPHP1, NCRNA00116	170, 18048	in gene, downstream	ActReg chr2 #9830	0	0	1
9831	2	111,435,420	111,436,021	601	1	6.211	11.368	4.526	11	18	7	2	1	1	BUB1	-36	upstream	ActReg chr2 #9831	0	1	0
9832	2	111,858,269	111,858,894	625	2	12	12.4	1.643	26	24	4	0	0	2	ACOXL, FLJ44006	368431, 13181	in gene, in gene	ActReg chr2 #9832	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9833	2	112,641,346	112,642,094	748	2	7.391	8.174	10.391	11	15	17	1	1	1	ANAPC1	21	in gene	ActReg chr2 #9833	0	1	1
9834	2	113,032,721	113,033,616	895	2	7.25	11.071	9.286	13	19	14	1	1	1	ZC3H6	-10	upstream	ActReg chr2 #9834	0	1	1
9835	2	113,240,360	113,240,667	307	1	6	3	10.778	8	4	15	1	1	1	TTL	770	in gene	ActReg chr2 #9835	0	0	1
9836	2	113,299,346	113,300,174	828	1	9.077	10.885	6.269	13	17	11	1	1	2	TTL, POLR1B	60017, 268	downstream, in gene	ActReg chr2 #9836	0	1	0
9837	2	113,398,164	113,398,872	708	1	8.909	11.136	2.5	12	18	5	0	1	2	FLJ42351, SLC20A1	5239, -5009	downstream, upstream	ActReg chr2 #9837	0	1	0
9838	2	113,403,322	113,404,227	905	2	6.241	9.552	6.333	13	15	17	1	2	2	FLJ42351, SLC20A1	-2017, 247	upstream, in gene	ActReg chr2 #9838	0	1	1
9839	2	113,521,895	113,522,572	677	2	8.81	11.286	5.238	15	23	9	1	1	2	CKAP2L, IL1A	21, 20738	in gene, downstream	ActReg chr2 #9839	1	1	0
9840	2	113,561,452	113,562,021	569	1	11.889	6.444	3	16	10	4	0	0	0				ActReg chr2 #9840	1	0	0
9841	2	113,638,702	113,639,259	557	1	7.882	11.529	1.857	13	19	2	0	0	0				ActReg chr2 #9841	0	1	0
9842	2	113,678,456	113,679,039	583	1	7.056	10.556	3.389	11	17	7	0	0	1	IL1F7	8,199	downstream	ActReg chr2 #9842	0	1	0
9843	2	113,997,511	113,997,820	309	1	8	5.222	10.333	11	7	14	0	1	3	PAX8, LOC654433, LOC100506707	38833, 3819, 2019	in gene, in gene, in gene	ActReg chr2 #9843	0	0	1
9844	2	113,998,293	113,998,954	661	2	10.048	12.333	1.353	16	21	3	0	0	3	PAX8, LOC654433, LOC100506707	37875, 4777, 2977	in gene, in gene, downstream	ActReg chr2 #9844	1	1	0
9845	2	114,340,988	114,341,773	785	2	18.24	18.792	5.25	30	33	10	1	1	2	FAM138B, MIR1302-3	6421, -707	downstream, upstream	ActReg chr2 #9845	1	1	0
9846	2	115,200,103	115,200,618	515	1	10.188	7.938	3.571	14	13	6	0	1	1	DPP10	461	in gene	ActReg chr2 #9846	1	0	0
9847	2	118,571,774	118,572,574	800	2	25.12	26.52	4.4	69	73	8	1	1	1	DDX18	-81	upstream	ActReg chr2 #9847	1	1	0
9848	2	119,593,459	119,593,764	305	1	4.4	4.2	9	6	6	13	1	0	1	EN1	12,148	downstream	ActReg chr2 #9848	0	0	1
9849	2	119,863,731	119,864,429	698	1	9.227	11.591	1	21	23	1	0	0	0				ActReg chr2 #9849	0	1	0
9850	2	119,924,613	119,925,014	401	1	10.917	8.417	2.917	15	11	4	0	0	1	C1QL2	-8,342	upstream	ActReg chr2 #9850	1	0	0
9851	2	120,770,118	120,770,913	795	2	15.64	22.56	5.68	38	53	12	1	1	1	EPB41L5	-89	upstream	ActReg chr2 #9851	1	1	0
9852	2	120,891,796	120,892,193	397	1	7.385	10.385	2	11	15	3	0	0	1	EPB41L5	121,390	in gene	ActReg chr2 #9852	0	1	0
9853	2	120,996,484	120,996,911	427	1	7.154	5	11.077	10	6	16	0	0	0				ActReg chr2 #9853	0	0	1
9854	2	121,132,979	121,133,299	320	1	1.714	2.25	10.4	3	3	14	0	0	0				ActReg chr2 #9854	0	0	1
9855	2	121,195,830	121,196,097	267	1	2.25	3.25	10	3	4	13	0	0	0				ActReg chr2 #9855	0	0	1
9856	2	122,287,612	122,288,652	1,040	3	9.939	10.818	7.879	23	23	18	1	1	3	CLASP1, RNU4ATAC, LOC100506849	118920, -324, 15897	in gene, upstream, downstream	ActReg chr2 #9856	1	1	1
9857	2	122,512,856	122,513,572	716	2	16.304	13.957	6.391	37	29	11	1	1	1	TSN	93	in gene	ActReg chr2 #9857	1	1	0
9858	2	127,414,024	127,414,497	473	1	3.818	8.933	1.583	5	15	2	1	1	1	GYPC	576	in gene	ActReg chr2 #9858	0	1	0
9859	2	127,728,922	127,729,240	318	1	4.3	6.1	9.4	7	9	13	0	0	0				ActReg chr2 #9859	0	0	1
9860	2	127,976,306	127,976,702	396	1	4.833	9.917	8.083	7	16	12	1	0	0				ActReg chr2 #9860	0	1	0
9861	2	128,051,273	128,051,674	401	1	6.083	5.333	10.25	10	9	15	1	1	2	ERCC3, LOC100506904	279, 8452	in gene, downstream	ActReg chr2 #9861	0	0	1
9862	2	128,399,623	128,399,957	334	1	2.6	2.571	12.3	4	4	17	0	1	3	MYO7B, LIMS2, GPR17	106412, 39570, -3649	downstream, in gene, upstream	ActReg chr2 #9862	0	0	1
9863	2	128,458,742	128,459,189	447	1	7.071	7	9.429	9	12	15	1	1	2	SFT2D3, WDR33	368, 109796	in gene, downstream	ActReg chr2 #9863	0	0	1
9864	2	128,848,328	128,849,223	895	3	13.607	11.857	8.643	23	25	16	1	1	1	UGGT1	21	in gene	ActReg chr2 #9864	1	1	1
9865	2	129,103,366	129,103,685	319	1	1	1	9	1	1	13	1	0	0				ActReg chr2 #9865	0	0	1
9866	2	129,116,680	129,117,025	345	1	3.909	5.3	9.636	6	8	14	0	0	0				ActReg chr2 #9866	0	0	1
9867	2	129,222,764	129,223,183	419	1	3.923	1.917	10.231	5	3	15	0	0	0				ActReg chr2 #9867	0	0	1
9868	2	130,938,776	130,939,422	646	2	8.4	9.7	5.2	16	19	7	1	2	3	SMPD4, FAM128B, TUBA3E	1224, -402, 16935	in gene, upstream, downstream	ActReg chr2 #9868	1	1	0
9869	2	131,100,091	131,100,856	765	1	8.583	12.292	3.917	17	20	7	1	2	2	CCDC115, IMP4	-551, -16	upstream, upstream	ActReg chr2 #9869	0	1	0
9870	2	131,583,590	131,584,044	454	1	5.286	5.071	11.643	6	7	18	0	0	0				ActReg chr2 #9870	0	0	1
9871	2	132,250,299	132,250,807	508	1	5.75	10.688	5.375	8	14	9	1	1	2	TUBA3D, FAM128A	16887, -489	downstream, upstream	ActReg chr2 #9871	0	1	0
9872	2	133,075,887	133,077,101	1,214	2	11.579	11.816	3.351	24	20	8	0	1	1	ZNF806	1,819	downstream	ActReg chr2 #9872	1	1	0
9873	2	133,104,568	133,105,416	848	2	12.222	11.444	6.846	24	21	11	0	1	1	LOC339742	-1,798	upstream	ActReg chr2 #9873	1	1	0
9874	2	133,246,524	133,247,155	631	2	11.1	9.1	2	17	16	4	0	0	1	GPR39	72,692	in gene	ActReg chr2 #9874	1	1	0
9875	2	133,784,318	133,784,780	462	1	6.6	8.933	2.467	12	13	4	0	0	1	NCKAP5	541,482	in gene	ActReg chr2 #9875	0	1	0
9876	2	133,821,293	133,821,800	507	2	11.688	11.875	2.154	20	20	4	0	0	1	NCKAP5	504,485	in gene	ActReg chr2 #9876	1	1	0
9877	2	134,575,822	134,576,252	430	1	5.769	11.077	3.385	9	17	5	0	0	0				ActReg chr2 #9877	0	1	0
9878	2	135,788,354	135,788,957	603	2	10.5	10.278	1.545	17	18	2	0	1	1	YSK4	-6,407	upstream	ActReg chr2 #9878	1	1	0
9879	2	137,285,127	137,285,581	454	1	8.071	14.214	2.846	13	25	4	0	0	0				ActReg chr2 #9879	0	1	0
9880	2	138,829,727	138,830,425	698	2	12.682	13.046	1.917	28	27	3	0	0	0				ActReg chr2 #9880	1	1	0
9881	2	139,259,435	139,259,747	312	1	6.2	5.444	11.3	8	7	16	1	1	1	SPOPL	241	in gene	ActReg chr2 #9881	0	0	1
9882	2	139,899,543	139,900,067	524	1	9.562	9.125	0	16	15	0	0	0	0				ActReg chr2 #9882	1	0	0
9883	2	140,879,478	140,880,121	643	2	10.35	11.65	1	22	24	1	0	0	0				ActReg chr2 #9883	1	1	0
9884	2	142,314,936	142,315,328	392	1	9.231	4.308	1	15	7	1	0	0	1	LRP1B	574,138	in gene	ActReg chr2 #9884	1	0	0
9885	2	143,637,716	143,638,156	440	1	10.214	4.857	1	16	7	1	0	0	1	KYNU	2,741	in gene	ActReg chr2 #9885	1	0	0
9886	2	149,289,006	149,289,336	330	1	3.9	2.667	11.4	11	4	14	0	0	0				ActReg chr2 #9886	0	0	1
9887	2	149,402,780	149,403,083	303	1	4.9	4.6	8.6	8	6	11	1	1	1	EPC2	371	in gene	ActReg chr2 #9887	0	0	1
9888	2	150,444,057	150,444,620	563	1	7.833	10.222	6.688	14	19	10	0	2	2	MMADHC, LOC642340	-8,466	upstream, in gene	ActReg chr2 #9888	0	1	0
9889	2	151,061,026	151,061,509	483	1	6	9.867	2.4	8	17	4	0	0	0				ActReg chr2 #9889	0	1	0
9890	2	151,342,500	151,343,190	690	1	5.381	11.857	4.286	9	18	7	1	1	1	RND3	1,335	in gene	ActReg chr2 #9890	0	1	0
9891	2	152,265,981	152,266,713	732	2	13.522	14.478	7.273	26	31	13	1	1	1	RIF1	-50	upstream	ActReg chr2 #9891	1	1	0
9892	2	152,616,723	152,617,043	320	1	2.2	1.444	9.8	4	2	14	0	0	0				ActReg chr2 #9892	0	0	1
9893	2	153,031,827	153,032,836	1,009	2	9.812	12	6.969	17	20	17	1	1	1	STAM2	175	in gene	ActReg chr2 #9893	0	1	1
9894	2	153,056,962	153,057,605	643	1	12.15	5.474	3.211	25	10	7	0	0	0				ActReg chr2 #9894	1	0	0
9895	2	153,312,811	153,313,230	419	1	5.462	9.231	1.917	8	14	4	0	0	1	FMNL2	121,269	in gene	ActReg chr2 #9895	0	1	0
9896	2	153,573,878	153,575,346	1,468	3	15.435	21.13	7.543	41	44	18	1	2	2	PRPF40A, ARL6IP6	-637, 189	upstream, in gene	ActReg chr2 #9896	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9897	2	156,604,681	156,605,088	407	1	2.308	3.308	10	3	8	14	0	0	0				ActReg chr2 #9897	0	0	1
9898	2	157,189,058	157,189,596	538	1	10.938	8.938	6.688	15	15	8	1	1	1	NR4A2	-40	upstream	ActReg chr2 #9898	1	0	0
9899	2	157,197,960	157,198,253	293	1	7.889	3.111	10.222	11	5	12	1	0	1	NR4A2	-8,819	upstream	ActReg chr2 #9899	0	0	1
9900	2	161,098,285	161,098,696	411	1	8.462	11.462	2.308	14	16	5	0	0	0				ActReg chr2 #9900	0	1	0
9901	2	161,469,803	161,470,344	541	1	7.882	9.588	1.812	14	17	3	0	0	0				ActReg chr2 #9901	0	1	0
9902	2	162,016,780	162,017,366	586	1	10.944	7.667	5.167	18	11	8	1	0	1	TANK	23,607	in gene	ActReg chr2 #9902	1	0	0
9903	2	162,164,678	162,165,367	689	2	6.381	9.81	11.524	11	18	19	1	1	1	PSMD14	236	in gene	ActReg chr2 #9903	0	1	1
9904	2	163,696,915	163,697,768	853	2	17.074	18.482	2.895	43	48	6	0	1	1	KCNH7	-2,101	upstream	ActReg chr2 #9904	1	1	0
9905	2	166,810,052	166,810,789	737	2	13.957	9.652	3.739	27	16	7	1	1	2	TTC21B, LOC100506134	-72, 20053	upstream, downstream	ActReg chr2 #9905	1	1	0
9906	2	170,681,092	170,681,731	639	1	6.1	10.6	2.412	10	21	4	1	2	2	METTL5, UBR3	-58, -2607	upstream, upstream	ActReg chr2 #9906	0	1	0
9907	2	171,785,247	171,786,038	791	2	11.92	14.4	2.059	24	28	4	1	1	1	GORASP2	-69	upstream	ActReg chr2 #9907	1	1	0
9908	2	172,947,779	172,948,189	410	1	2	1.636	10	3	3	15	1	1	2	MAP1D, DLX1	83180, -2224	downstream, upstream	ActReg chr2 #9908	0	0	1
9909	2	172,949,355	172,949,932	577	2	9.889	7.5	7.944	13	12	13	1	1	2	MAP1D, DLX1	84839, -565	downstream, upstream	ActReg chr2 #9909	1	0	1
9910	2	172,959,966	172,960,568	602	1	9.737	10.105	4.947	14	15	9	1	0	2	DLX1, DLX2	10059, 7211	downstream, downstream	ActReg chr2 #9910	0	1	0
9911	2	173,114,540	173,114,984	444	1	9.714	4.5	3.2	14	7	5	0	0	0				ActReg chr2 #9911	1	0	0
9912	2	174,016,296	174,016,882	586	2	10.167	9.667	1.625	19	17	2	0	0	1	ZAK	76,024	in gene	ActReg chr2 #9912	1	1	0
9913	2	174,218,864	174,220,362	1,498	2	7.979	15.787	3.308	19	40	10	1	1	1	CDCA7	52	in gene	ActReg chr2 #9913	1	1	0
9914	2	175,574,142	175,574,641	499	1	1.429	1.286	11.688	3	3	19	0	0	0				ActReg chr2 #9914	0	0	1
9915	2	176,952,846	176,953,445	599	2	10.368	11.947	6.158	19	22	13	1	2	2	EVX2, HOXD13	-4455, -4387	upstream, upstream	ActReg chr2 #9915	1	1	0
9916	2	176,957,804	176,958,155	351	1	6.455	9.909	4.818	11	15	8	1	2	3	EVX2, HOXD13, HOXD12	-9289, 447, -6551	upstream, in gene, upstream	ActReg chr2 #9916	0	1	0
9917	2	177,024,670	177,025,003	333	1	1.909	1.273	8.727	3	2	12	1	1	3	MIR10B, HOXD4, HOXD3	9805, 8723, -3969	downstream, downstream, upstream	ActReg chr2 #9917	0	0	1
9918	2	177,134,007	177,134,389	382	1	6	7.75	12.333	8	11	16	1	1	1	MTX2	75	in gene	ActReg chr2 #9918	0	0	1
9919	2	177,418,754	177,419,340	586	1	3.556	11.333	1.636	7	16	2	0	0	0				ActReg chr2 #9919	0	1	0
9920	2	178,128,105	178,128,637	532	1	10.438	10.188	5.438	19	13	9	1	2	2	NFE2L2, MIR3128	1488, -7633	in gene, upstream	ActReg chr2 #9920	1	0	0
9921	2	178,483,244	178,483,972	728	1	7.652	11.522	5.739	12	19	11	1	1	2	TTC30A, PDE11A	86, 489458	in gene, downstream	ActReg chr2 #9921	0	1	0
9922	2	178,976,630	178,978,026	1,396	2	10.364	16.341	5.703	34	35	10	1	2	2	PDE11A, RBM45	-4262, 146	upstream, in gene	ActReg chr2 #9922	1	1	0
9923	2	179,269,024	179,269,607	583	1	6.737	8.947	3.889	13	20	5	0	0	2	OSBPL6, LOC100506831	209941, -9337	downstream, upstream	ActReg chr2 #9923	0	1	0
9924	2	179,278,323	179,278,720	397	1	8.167	10	3.385	12	16	5	1	1	1	LOC100506831	-131	upstream	ActReg chr2 #9924	0	1	0
9925	2	180,871,697	180,872,219	522	1	11.438	7.125	5.833	16	10	7	1	1	1	CWC22	-178	upstream	ActReg chr2 #9925	1	0	0
9926	2	180,882,314	180,882,695	381	1	9	4.75	1	13	9	1	0	0	0				ActReg chr2 #9926	1	0	0
9927	2	182,321,702	182,322,276	574	1	10.611	8.333	4.667	15	14	10	1	1	1	ITGA4	370	in gene	ActReg chr2 #9927	1	0	0
9928	2	182,542,378	182,543,430	1,052	2	12.454	17.333	4.655	30	38	11	0	1	1	NEUROD1	2,477	in gene	ActReg chr2 #9928	1	1	0
9929	2	182,548,595	182,548,955	360	1	2.091	3.909	8.818	5	7	12	1	1	1	NEUROD1	-3,394	upstream	ActReg chr2 #9929	0	0	1
9930	2	182,549,849	182,550,424	575	1	10.111	7.778	2.353	15	13	4	0	1	1	NEUROD1	-4,755	upstream	ActReg chr2 #9930	1	0	0
9931	2	183,580,721	183,581,260	539	2	11.529	9.588	9.882	15	14	13	1	1	1	DNAJC10	-9	upstream	ActReg chr2 #9931	1	0	1
9932	2	187,350,447	187,351,175	728	2	9.522	9.957	3.087	21	15	6	1	1	1	ZC3H15	-74	upstream	ActReg chr2 #9932	1	1	0
9933	2	187,454,492	187,455,183	691	1	4.682	11.318	7.773	6	18	11	1	1	1	ITGAV	47	in gene	ActReg chr2 #9933	0	1	0
9934	2	189,156,085	189,156,558	473	1	9.4	7.8	2.091	13	10	3	1	2	2	GULP1, MIR561	-1069, -5898	upstream, upstream	ActReg chr2 #9934	1	0	0
9935	2	189,809,203	189,809,570	367	1	2.3	4.167	11.5	4	6	14	0	0	0				ActReg chr2 #9935	0	0	1
9936	2	190,627,037	190,627,635	598	1	9.421	10.21	3.833	16	14	6	0	1	2	OSGEPL1, ORMDL1	588, 21761	in gene, downstream	ActReg chr2 #9936	1	0	0
9937	2	191,184,109	191,185,073	964	2	9.133	13.733	2.188	22	28	3	1	1	1	HIBCH	180	in gene	ActReg chr2 #9937	1	1	0
9938	2	191,878,629	191,879,121	492	1	7.2	8.867	14.067	10	12	20	1	1	1	STAT1	101	in gene	ActReg chr2 #9938	0	0	1
9939	2	191,884,950	191,885,596	646	1	11.5	8.65	6.15	17	12	12	1	1	2	STAT1, STAT4	-6297, 130652	upstream, downstream	ActReg chr2 #9939	1	0	0
9940	2	192,542,651	192,543,115	464	1	7.6	4.667	11.6	10	7	17	1	1	1	OBFC2A	85	in gene	ActReg chr2 #9940	0	0	1
9941	2	194,367,095	194,367,450	355	1	6.545	10.273	8.455	9	15	12	0	0	0				ActReg chr2 #9941	0	1	0
9942	2	196,398,815	196,399,429	614	1	10.05	8.95	0	16	14	0	0	0	0				ActReg chr2 #9942	1	0	0
9943	2	197,503,958	197,504,866	908	2	6.269	10.828	2.476	15	17	5	1	1	1	CCDC150	56	in gene	ActReg chr2 #9943	1	1	0
9944	2	198,364,314	198,365,039	725	2	13.174	9.87	6.739	25	17	10	1	2	2	HSPD1, HSPE1	322, -45	in gene, upstream	ActReg chr2 #9944	1	1	0
9945	2	198,380,416	198,381,084	668	2	7.905	12.809	10.048	13	23	17	1	1	1	MOBKL3	430	in gene	ActReg chr2 #9945	0	1	1
9946	2	198,570,109	198,570,446	337	1	8.364	7.273	10.364	11	11	14	1	1	1	MARS2	190	in gene	ActReg chr2 #9946	0	0	1
9947	2	200,180,052	200,180,634	582	1	5.222	10.222	0	9	15	0	0	0	1	SATB2	155,646	in gene	ActReg chr2 #9947	0	1	0
9948	2	200,323,541	200,324,791	1,250	2	12.308	15.513	6.769	27	32	13	1	1	3	SATB2, LOC100288092, FLJ32063	111823, 1743, -8655	in gene, in gene, upstream	ActReg chr2 #9948	1	1	0
9949	2	200,819,985	200,820,922	937	2	11.276	12.69	5.179	32	20	10	1	2	2	C2orf60, C2orf47	6, 413	in gene, in gene	ActReg chr2 #9949	1	1	0
9950	2	201,374,688	201,375,139	451	1	9.667	8.667	4.417	16	11	7	1	1	1	KCTD18	-121	upstream	ActReg chr2 #9950	1	0	0
9951	2	201,527,433	201,527,872	439	1	5.143	9.714	3.5	8	13	5	0	0	1	AOX1	76,921	in gene	ActReg chr2 #9951	0	1	0
9952	2	201,675,899	201,676,818	919	4	9.655	8.552	10.586	17	15	18	1	1	1	BZW1	-289	upstream	ActReg chr2 #9952	1	1	1
9953	2	201,710,038	201,710,356	318	1	2.875	4.6	10.6	6	6	15	0	0	1	CLK1	19,270	downstream	ActReg chr2 #9953	0	0	1
9954	2	201,936,352	201,936,947	595	1	11.421	8.579	4.529	20	12	9	1	2	2	FAM126B, NDUFB3	-257, 187	upstream, in gene	ActReg chr2 #9954	1	0	0
9955	2	201,980,704	201,981,539	835	1	7.815	10.63	4.231	14	18	12	1	1	1	CFLAR	305	in gene	ActReg chr2 #9955	0	1	0
9956	2	202,316,040	202,316,491	451	1	12.214	8.857	5.9	17	12	11	1	2	2	TRAK2, STRADB	54, -127	in gene, upstream	ActReg chr2 #9956	1	0	0
9957	2	202,645,419	202,646,158	739	1	10.696	7.565	6.143	15	12	13	1	1	1	ALS2	107	in gene	ActReg chr2 #9957	1	0	0
9958	2	202,899,787	202,900,611	824	1	5.731	12.269	10.077	8	18	16	1	1	1	FZD7	889	in gene	ActReg chr2 #9958	0	1	0
9959	2	203,130,235	203,130,883	648	2	10.667	11.476	4.857	16	19	9	1	1	1	NOP58	44	in gene	ActReg chr2 #9959	1	1	0
9960	2	203,776,009	203,776,733	724	2	10.864	8.591	2.667	15	19	4	1	2	2	WDR12, ALS2CR8	578, -607	in gene, upstream	ActReg chr2 #9960	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
9961	2	204,103,321	204,104,097	776	2	14.12	17.08	6.52	27	34	12	1	2	2	LOC100507265, CYP20A1	-1033, 545	upstream, in gene	ActReg chr2 #9961	1	1	0
9962	2	204,193,422	204,193,839	417	1	4.154	5.462	12.615	7	8	19	1	1	1	ABI2	627	in gene	ActReg chr2 #9962	0	0	1
9963	2	204,884,336	204,884,800	464	1	10.333	6.267	1	16	7	1	0	0	0				ActReg chr2 #9963	1	0	0
9964	2	206,514,970	206,515,453	483	1	11	8.6	2.417	20	12	4	0	0	0				ActReg chr2 #9964	1	0	0
9965	2	206,544,785	206,545,296	511	1	11.062	7.438	3.091	21	12	4	0	1	1	NRP2	-2,184	upstream	ActReg chr2 #9965	1	0	0
9966	2	206,950,438	206,950,882	444	1	6.429	10.643	5.917	9	13	8	1	2	2	INO80D, LOC729570	246, 1340	in gene, in gene	ActReg chr2 #9966	0	1	0
9967	2	208,067,187	208,067,873	686	1	10.818	8	1	24	13	1	0	0	0				ActReg chr2 #9967	1	0	0
9968	2	208,352,446	208,353,137	691	2	14.182	13.227	2.909	32	27	6	0	0	0				ActReg chr2 #9968	1	1	0
9969	2	208,489,440	208,490,326	886	2	10.393	11.143	5.885	18	17	8	1	1	1	FAM119A	90	in gene	ActReg chr2 #9969	1	1	0
9970	2	209,130,354	209,131,207	853	2	16.889	17.333	4.185	47	43	10	1	1	2	LOC100507475, PIKFYVE	10823, -211	downstream, upstream	ActReg chr2 #9970	1	1	0
9971	2	210,636,171	210,636,795	624	1	8.211	12.526	4.625	12	20	8	1	1	1	UNC80	-234	upstream	ActReg chr2 #9971	0	1	0
9972	2	215,275,568	215,276,069	501	1	7.188	13.812	3	12	26	4	0	1	2	SPAG16, VWC2L	1126702, -643	downstream, upstream	ActReg chr2 #9972	0	1	0
9973	2	216,871,036	216,871,512	476	1	4.067	9.533	3.667	6	13	5	0	0	1	MREG	7,072	in gene	ActReg chr2 #9973	0	1	0
9974	2	217,236,668	217,238,028	1,360	2	11.767	15.588	3.676	28	41	8	1	1	1	4-Mar	-598	upstream	ActReg chr2 #9974	1	1	0
9975	2	217,238,235	217,238,735	500	2	8.438	11.125	1.692	15	20	2	0	1	1	4-Mar	-1,735	upstream	ActReg chr2 #9975	1	1	0
9976	2	217,276,717	217,277,612	895	2	11	10.143	6.714	16	16	12	1	1	1	SMARCAL1	27	in gene	ActReg chr2 #9976	1	1	0
9977	2	217,363,325	217,363,909	584	1	11.684	7.895	6.842	24	12	14	1	2	2	LOC100507554, RPL37A	-148, 97	upstream, in gene	ActReg chr2 #9977	1	0	0
9978	2	218,142,431	218,142,941	510	1	5.438	10.875	1	12	17	1	0	0	1	DIRC3	478,630	downstream	ActReg chr2 #9978	0	1	0
9979	2	219,260,628	219,261,492	864	2	10.741	18.407	4.458	21	37	8	0	2	3	SLC11A1, CTDSP1, MIR26B	14308, -3418, -6309	in gene, upstream, upstream	ActReg chr2 #9979	1	1	0
9980	2	219,264,158	219,264,885	727	2	11.043	15.13	2.471	30	38	6	1	2	3	SLC11A1, CTDSP1, MIR26B	17769, 43, -2848	downstream, in gene, upstream	ActReg chr2 #9980	1	1	0
9981	2	219,773,660	219,774,240	580	1	10.895	9.789	4.267	19	15	7	1	0	0				ActReg chr2 #9981	1	0	0
9982	2	219,826,631	219,828,303	1,672	2	11.654	16.481	4.347	22	28	10	1	1	1	CDK5R2	3,069	downstream	ActReg chr2 #9982	1	1	0
9983	2	219,856,379	219,856,908	529	1	9.647	4.706	5.176	17	7	7	0	2	3	FEV, CRYBA2, MIR375	-6264, 1484, 9787	upstream, in gene, downstream	ActReg chr2 #9983	1	0	0
9984	2	219,910,497	219,911,279	782	2	11.708	11.75	1.8	26	24	5	0	1	2	CCDC108, IHH	-4643, 14350	upstream, downstream	ActReg chr2 #9984	1	1	0
9985	2	219,989,548	219,990,483	935	2	9.2	10.6	2.333	14	18	4	0	0	1	NHEJ1	35,422	in gene	ActReg chr2 #9985	1	1	0
9986	2	220,083,177	220,083,918	741	1	7.696	10.522	8.957	14	14	12	1	1	3	ZFAND2B, ABCD6, ATG9A	12009, 125, 10814	downstream, in gene, downstream	ActReg chr2 #9986	0	1	0
9987	2	220,093,883	220,094,538	655	1	10.857	8.286	4.211	17	15	8	1	2	3	ATG9A, ANKZF1, GLB1L	151, -269, 15921	in gene, upstream, downstream	ActReg chr2 #9987	1	0	0
9988	2	220,109,923	220,110,585	662	2	8.45	11	10.1	9	15	17	1	2	4	ANKZF1, GLB1L, STK16, TUBA4A	15775, -123, 62, 8384	downstream, upstream, in gene, downstream	ActReg chr2 #9988	0	1	1
9989	2	220,144,174	220,144,574	400	1	5.583	3.083	12	7	6	17	1	1	2	DNAJB2, PTPRN	334, 29769	in gene, downstream	ActReg chr2 #9989	0	0	1
9990	2	220,172,763	220,173,682	919	2	13.414	15.034	5.75	24	30	10	2	1	1	PTPRN	921	in gene	ActReg chr2 #9990	1	1	0
9991	2	220,196,163	220,196,733	570	1	8.235	11.235	2.875	13	19	5	1	1	1	RESP18	1,451	in gene	ActReg chr2 #9991	0	1	0
9992	2	220,253,030	220,253,588	558	1	11.118	8.118	2	20	15	3	0	1	1	DNPEP	-647	upstream	ActReg chr2 #9992	1	0	0
9993	2	220,269,105	220,269,640	535	1	1.6	2.286	10.882	2	4	15	0	0	0				ActReg chr2 #9993	0	0	1
9994	2	220,330,637	220,330,977	340	1	3.545	1.909	9.545	5	3	14	0	0	1	SPEG	31,107	in gene	ActReg chr2 #9994	0	0	1
9995	2	220,360,567	220,360,853	286	1	4.333	4.667	10.667	7	7	14	0	1	3	SPEG, LOC100507611, GMPPA	61010, 20889, -2877	downstream, in gene, upstream	ActReg chr2 #9995	0	0	1
9996	2	220,379,634	220,380,111	477	1	2.2	2.467	11.067	4	3	18	0	2	3	LOC100507611, GMPPA, ACCN4	1727, 16285, 980	in gene, downstream, in gene	ActReg chr2 #9996	0	0	1
9997	2	220,546,343	220,546,834	491	1	11.533	4.267	2.2	17	6	3	0	0	0				ActReg chr2 #9997	1	0	0
9998	2	220,571,468	220,572,131	663	1	9.05	12.571	1.778	15	20	3	0	0	0				ActReg chr2 #9998	0	1	0
9999	2	221,989,490	221,990,017	527	1	6.118	9	3.2	11	17	5	0	0	0				ActReg chr2 #9999	0	1	0
10000	2	223,520,406	223,521,197	791	1	7.36	11.8	4.28	15	19	7	1	1	1	FARSB	26	in gene	ActReg chr2 #10000	0	1	0
10001	2	223,573,959	223,574,378	419	1	9.462	10.385	2.6	11	14	4	0	0	1	MOGAT1	57,711	in gene	ActReg chr2 #10001	0	1	0
10002	2	223,725,529	223,726,031	502	1	12.812	7	4.143	20	10	8	1	1	1	ACSL3	48	in gene	ActReg chr2 #10002	1	0	0
10003	2	224,401,202	224,401,640	438	1	10.357	11.643	2	14	16	3	0	0	0				ActReg chr2 #10003	1	0	0
10004	2	224,760,234	224,760,873	639	1	6.3	9.85	1.625	10	21	3	0	0	1	WDFY1	49,499	in gene	ActReg chr2 #10004	0	1	0
10005	2	224,809,786	224,810,335	549	2	8.529	11.529	4.059	16	21	8	1	1	1	WDFY1	-8	upstream	ActReg chr2 #10005	1	1	0
10006	2	224,821,868	224,822,673	805	1	5.208	12.24	5.12	13	21	8	1	1	1	MRPL44	149	in gene	ActReg chr2 #10006	0	1	0
10007	2	224,907,023	224,907,460	437	1	10.071	9.214	0	16	14	0	0	1	1	SERPINE2	-3,205	upstream	ActReg chr2 #10007	1	0	0
10008	2	225,984,843	225,985,386	543	1	5.824	10.118	1.312	10	18	2	0	0	0				ActReg chr2 #10008	0	1	0
10009	2	226,785,720	226,786,112	392	1	5.923	9.154	1	9	13	1	0	0	0				ActReg chr2 #10009	0	1	0
10010	2	226,802,316	226,802,960	644	2	12	11.25	3.286	20	19	4	0	0	0				ActReg chr2 #10010	1	1	0
10011	2	227,661,817	227,662,150	333	1	1.6	3.636	8.909	2	6	12	1	1	1	IRS1	1,523	in gene	ActReg chr2 #10011	0	0	1
10012	2	227,675,588	227,676,227	639	2	8.389	13.45	2.182	13	23	4	0	0	0				ActReg chr2 #10012	1	1	0
10013	2	228,336,365	228,337,261	896	2	29.25	28	3.5	89	90	7	1	1	1	AGFG1	-75	upstream	ActReg chr2 #10013	1	1	0
10014	2	228,727,402	228,727,930	528	1	7.562	11.188	3.846	10	14	5	0	0	1	WDR69	-8,661	upstream	ActReg chr2 #10014	0	1	0
10015	2	230,579,443	230,580,270	827	2	9.846	12.808	4.154	19	19	7	1	1	1	DNER	-570	upstream	ActReg chr2 #10015	1	1	0
10016	2	231,577,168	231,577,763	595	2	17.737	18.684	5.1	37	39	8	1	1	1	CAB39	-92	upstream	ActReg chr2 #10016	1	1	0
10017	2	231,735,278	231,735,659	381	1	2.833	1.5	9.25	4	2	15	0	0	1	ITM2C	5,847	in gene	ActReg chr2 #10017	0	0	1
10018	2	231,773,216	231,773,843	627	1	9.95	11.8	1.15	12	16	2	0	0	1	GPR55	16,412	in gene	ActReg chr2 #10018	0	1	0
10019	2	231,828,545	231,829,227	382	1	4.75	2.667	9.833	7	4	14	0	0	0				ActReg chr2 #10019	0	0	1
10020	2	231,917,368	231,917,981	613	1	7.579	10	3.706	10	15	7	1	1	2	C2orf72, PSMD1	15393, -3904	downstream, upstream	ActReg chr2 #10020	0	1	0
10021	2	231,920,929	231,922,094	1,165	2	34.583	37.472	5.417	113	104	10	1	1	2	C2orf72, PSMD1	19230, -67	downstream, upstream	ActReg chr2 #10021	1	1	0
10022	2	232,229,680	232,230,337	657	2	14.381	10.571	2.235	24	15	3	0	0	0				ActReg chr2 #10022	1	1	0
10023	2	232,252,929	232,253,750	821	2	9.32	9.84	5.48	18	13	9	0	1	1	B3GNT7	-6,996	upstream	ActReg chr2 #10023	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10024	2	232,328,514	232,328,877	363	1	5.636	8.455	10.636	7	10	13	1	3	4	NCL, SNORA75, SNORD20, SNORD82	510, -8048, -7461, -5542	in gene, upstream, upstream, upstream	ActReg chr2 #10024	0	0	1
10025	2	232,526,891	232,527,289	398	1	6	10.583	3.25	8	15	6	1	0	0				ActReg chr2 #10025	0	1	0
10026	2	232,531,019	232,531,597	578	1	6.944	11.444	7.111	10	15	10	0	0	0				ActReg chr2 #10026	0	1	0
10027	2	232,570,935	232,572,737	1,802	3	10.544	14.105	6.839	28	34	16	1	1	1	PTMA	-1,399	upstream	ActReg chr2 #10027	1	1	1
10028	2	232,572,827	232,573,646	819	2	10.538	8.346	7.038	13	17	13	1	1	1	PTMA	1	in gene	ActReg chr2 #10028	1	1	0
10029	2	232,575,484	232,575,809	325	1	3.091	5	9.545	7	9	12	1	1	1	PTMA	2,411	in gene	ActReg chr2 #10029	0	0	1
10030	2	232,645,462	232,646,418	956	2	5.533	10.433	7.033	10	19	14	1	2	2	PDE6D, COPS7B	34, -5222	in gene, upstream	ActReg chr2 #10030	0	1	1
10031	2	232,650,724	232,651,581	857	2	9.115	14.154	5.72	21	22	12	1	2	2	PDE6D, COPS7B	-5178, -10	upstream, upstream	ActReg chr2 #10031	1	1	0
10032	2	233,180,028	233,180,760	732	2	8.217	11.174	3.667	16	18	6	0	0	1	DIS3L2	354,101	in gene	ActReg chr2 #10032	1	1	0
10033	2	233,303,911	233,304,212	301	1	1.444	1.889	10.556	2	4	16	0	0	0				ActReg chr2 #10033	0	0	1
10034	2	233,311,131	233,311,510	379	1	1.75	1.917	9.667	2	3	14	0	0	1	ALPI	-9,513	upstream	ActReg chr2 #10034	0	0	1
10035	2	233,415,121	233,415,428	307	1	10.6	11.4	11.5	15	13	14	1	2	3	CHRNG, TIGD1, EIF4E2	10837, -48, -83	downstream, upstream, upstream	ActReg chr2 #10035	0	0	1
10036	2	234,821,205	234,822,004	799	2	11.2	16.48	2.19	23	39	4	0	1	1	TRPM8	-4,439	upstream	ActReg chr2 #10036	1	1	0
10037	2	235,087,125	235,087,947	822	2	12.385	14.615	4.423	31	30	6	0	0	0				ActReg chr2 #10037	1	1	0
10038	2	235,244,267	235,244,650	383	1	5.917	11	2.75	8	13	3	0	0	0				ActReg chr2 #10038	0	1	0
10039	2	237,195,732	237,196,231	499	1	7.312	9.812	2.438	12	19	4	0	0	0				ActReg chr2 #10039	0	1	0
10040	2	237,994,126	237,994,827	701	2	9.955	13.546	6.409	18	28	10	1	1	1	COPS8	392	in gene	ActReg chr2 #10040	1	1	0
10041	2	238,136,104	238,136,721	617	1	9.316	11.053	1.778	14	19	2	0	0	0				ActReg chr2 #10041	0	1	0
10042	2	238,341,126	238,341,835	709	1	7.182	11.591	3.95	10	19	8	0	0	0				ActReg chr2 #10042	0	1	0
10043	2	238,383,726	238,384,864	1,138	2	17.111	17.528	4.176	46	46	7	1	0	0				ActReg chr2 #10043	1	1	0
10044	2	238,472,343	238,472,917	574	1	7.778	11.111	4.278	13	17	6	0	1	2	MLPH, PRLH	76752, -2587	downstream, upstream	ActReg chr2 #10044	0	1	0
10045	2	238,484,713	238,485,072	359	1	2.333	1.2	9.909	4	2	13	0	0	2	PRLH, RAB17	9675, 14877	downstream, in gene	ActReg chr2 #10045	0	0	1
10046	2	238,807,104	238,807,810	706	2	9.87	11.043	2.65	20	20	7	0	0	1	RAMP1	39,270	in gene	ActReg chr2 #10046	1	1	0
10047	2	238,864,310	238,864,703	393	1	5.667	2.4	10.917	8	4	17	1	0	0				ActReg chr2 #10047	0	0	1
10048	2	238,875,281	238,875,793	512	1	9	6.25	2.333	16	10	3	1	1	1	UBE2F	-163	upstream	ActReg chr2 #10048	1	0	0
10049	2	238,969,140	238,969,711	571	1	3.889	10.333	5.389	7	19	10	1	1	1	SCLY	-207	upstream	ActReg chr2 #10049	0	1	0
10050	2	238,969,791	238,970,100	309	1	6.8	6	10.8	10	8	14	1	1	1	SCLY	313	in gene	ActReg chr2 #10050	0	0	1
10051	2	239,037,400	239,037,670	270	1	1.6	1.667	10.444	2	3	12	1	0	2	ESPNL, KLHL30	28584, -9828	in gene, upstream	ActReg chr2 #10051	0	0	1
10052	2	239,038,247	239,038,557	310	1	1.143	4.111	10.111	2	6	14	0	0	2	ESPNL, KLHL30	29451, -8961	in gene, upstream	ActReg chr2 #10052	0	0	1
10053	2	239,165,067	239,165,685	618	2	12.526	16.526	3.056	30	32	5	0	0	1	PER2	31,831	in gene	ActReg chr2 #10053	1	1	0
10054	2	239,197,300	239,197,839	539	2	9.765	9.647	4.812	17	16	8	1	1	1	PER2	-362	upstream	ActReg chr2 #10054	1	1	0
10055	2	239,552,609	239,553,111	502	1	10.933	8.6	3	14	11	6	0	0	0				ActReg chr2 #10055	1	0	0
10056	2	239,592,972	239,593,525	553	1	9.941	6.824	1.25	16	11	2	0	0	0				ActReg chr2 #10056	1	0	0
10057	2	239,670,270	239,670,970	700	2	10.454	11.091	2.167	21	19	3	0	0	0				ActReg chr2 #10057	1	1	0
10058	2	239,907,544	239,907,820	276	1	1.333	4.667	11.111	2	6	14	0	0	0				ActReg chr2 #10058	0	0	1
10059	2	240,196,687	240,197,298	611	1	6.579	11.684	6.053	9	18	13	1	0	1	HDAC4	125,651	in gene	ActReg chr2 #10059	0	1	0
10060	2	240,323,064	240,323,610	546	2	11.353	9.353	4.529	15	15	9	1	1	1	HDAC4	-694	upstream	ActReg chr2 #10060	1	1	0
10061	2	240,964,695	240,965,078	383	1	10	11.333	4.9	13	18	8	1	1	2	NDUFA10, OR6B2	-67, 4960	upstream, downstream	ActReg chr2 #10061	0	1	0
10062	2	241,279,234	241,280,039	805	1	2.304	3.04	11.96	4	6	17	0	0	0				ActReg chr2 #10062	0	0	1
10063	2	241,286,461	241,286,975	514	1	2.5	2.562	14	4	4	17	0	0	0				ActReg chr2 #10063	0	0	1
10064	2	241,288,070	241,288,460	390	1	1.833	3.083	12.417	3	5	18	0	0	0				ActReg chr2 #10064	0	0	1
10065	2	241,516,940	241,517,545	605	1	1.6	4.789	11.263	3	9	14	0	0	2	RNPEPL1, CAPN10	9138, -8903	in gene, upstream	ActReg chr2 #10065	0	0	1
10066	2	241,721,281	241,722,082	801	1	4.12	6.88	11.08	6	10	18	1	0	1	KIF1A	37,943	in gene	ActReg chr2 #10066	0	0	1
10067	2	241,836,569	241,837,029	460	1	3.867	3.667	12.133	6	6	16	0	1	1	C2orf54	-1,226	upstream	ActReg chr2 #10067	0	0	1
10068	2	241,859,854	241,860,485	631	1	3.35	3.95	11.15	5	6	17	0	0	0				ActReg chr2 #10068	0	0	1
10069	2	241,885,454	241,885,737	283	1	1.571	5.333	10.333	2	7	14	0	0	1	LOC200772	21,273	downstream	ActReg chr2 #10069	0	0	1
10070	2	241,902,717	241,903,020	303	1	2.5	1.778	10.1	4	4	13	0	0	1	LOC200772	4,000	in gene	ActReg chr2 #10070	0	0	1
10071	2	241,937,619	241,937,958	339	1	11.636	7.364	11.091	16	10	16	1	1	1	SNED1	-467	upstream	ActReg chr2 #10071	0	0	1
10072	2	242,041,480	242,042,101	621	1	12.053	9.737	9.526	18	18	17	1	1	3	SNED1, MTERFD2, PASK	103535, -43, 47088	downstream, upstream, upstream, downstream	ActReg chr2 #10072	1	0	0
10073	2	242,211,134	242,211,704	570	2	8.444	8.5	2.059	16	16	3	1	0	1	HDLBP	43,835	in gene	ActReg chr2 #10073	1	1	0
10074	2	242,254,097	242,255,148	1,051	2	12.727	14	5.207	34	27	9	1	2	2	HDLBP, SEPT2	632, -101	in gene, upstream	ActReg chr2 #10074	1	1	0
10075	2	242,447,812	242,448,542	730	1	8.727	11.318	3.474	15	19	7	1	1	1	STK25	-143	upstream	ActReg chr2 #10075	0	1	0
10076	2	242,480,976	242,481,281	305	1	5.1	2.6	9.9	7	4	12	1	0	1	BOKAS	17,430	downstream	ActReg chr2 #10076	0	0	1
10077	2	242,501,606	242,502,037	431	1	3.091	4.692	11.154	6	8	15	0	1	2	BOKAS, BOK	-3263, 3629	upstream, in gene	ActReg chr2 #10077	0	0	1
10078	2	242,658,883	242,659,145	262	1	1.333	2.5	10.125	2	4	12	0	0	1	ING5	17,558	in gene	ActReg chr2 #10078	0	0	1
10079	2	242,683,055	242,683,426	371	1	2.75	2.333	10.667	4	3	15	0	0	1	D2HGDH	9,210	in gene	ActReg chr2 #10079	0	0	1
10080	2	242,691,498	242,692,057	559	1	1.533	1.692	13.118	3	3	16	0	0	1	D2HGDH	17,747	in gene	ActReg chr2 #10080	0	0	1
10081	2	242,716,505	242,716,790	285	1	1.5	5.444	12.667	2	6	16	0	1	2	D2HGDH, GAL3ST2	42617, 407	downstream, in gene	ActReg chr2 #10081	0	0	1
10082	2	242,794,579	242,794,869	290	1	3.333	2.111	10.667	4	3	15	1	0	1	PDCD1	6,334	in gene	ActReg chr2 #10082	0	0	1
10083	2	242,796,407	242,796,898	491	1	3.688	2.2	13.062	6	3	16	0	0	1	PDCD1	4,406	in gene	ActReg chr2 #10083	0	0	1
10084	2	242,801,255	242,801,545	290	1	4.667	2	12	7	3	15	0	1	1	PDCD1	-342	upstream	ActReg chr2 #10084	0	0	1
10085	2	242,811,738	242,812,068	330	1	1.455	1.5	9	2	3	12	0	1	1	C2orf85	17	in gene	ActReg chr2 #10085	0	0	1
10086	2	242,875,012	242,875,322	310	1	5	5	11.778	6	7	15	1	0	0				ActReg chr2 #10086	0	0	1
10087	2	242,889,972	242,890,349	377	1	1	1.364	11.833	1	4	15	0	0	0				ActReg chr2 #10087	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10088	20	278,728	279,240	512	1	7.875	9.312	11.75	12	12	17	1	2	2	C20orf96, ZCCHC3	-7594, 780	upstream, in gene	ActReg chr20 #10088	0	0	1
10089	20	304,854	305,671	817	1	8.846	12.615	7.423	16	22	12	1	2	2	LOC100507459, SOX12	634, -977	in gene, upstream	ActReg chr20 #10089	0	1	0
10090	20	307,834	308,345	511	1	5.625	9.375	10.438	8	15	16	1	2	2	LOC100507459, SOX12	-2193, 1850	upstream, in gene	ActReg chr20 #10090	0	0	1
10091	20	361,412	361,793	381	1	6.583	11	11.667	9	18	19	1	1	1	TRIB3	284	in gene	ActReg chr20 #10091	0	0	1
10092	20	387,823	388,604	781	1	9.958	10.875	4.783	22	18	10	1	1	2	TRIB3, RBCK1	26905, -496	downstream, upstream	ActReg chr20 #10092	0	1	0
10093	20	401,470	402,093	623	1	3.316	7.5	13.5	7	10	23	0	0	1	RBCK1	13,072	in gene	ActReg chr20 #10093	0	0	1
10094	20	411,901	412,598	697	1	11.954	4.318	5.632	16	8	11	0	0	2	RBCK1, TBC1D20	23540, 30938	downstream, downstream	ActReg chr20 #10094	1	0	0
10095	20	524,001	525,114	1,113	2	12.441	11.735	4.29	21	22	11	1	1	1	CSNK2A1	-75	upstream	ActReg chr20 #10095	1	1	0
10096	20	655,828	656,654	826	1	8.115	10.423	4.8	12	18	10	1	1	1	SCRT2	582	in gene	ActReg chr20 #10096	0	1	0
10097	20	680,346	680,726	380	1	2.556	3.333	10.917	5	5	14	0	0	0				ActReg chr20 #10097	0	0	1
10098	20	813,935	814,759	824	2	13.154	10.385	5.808	29	18	11	1	1	1	FAM110A	-9	upstream	ActReg chr20 #10098	1	1	0
10099	20	825,443	825,885	442	1	3.846	3.923	12.308	5	6	18	1	0	1	FAM110A	11,308	in gene	ActReg chr20 #10099	0	0	1
10100	20	859,347	859,801	454	1	8.357	12.357	3.083	12	22	5	0	0	1	ANGPT4	37,386	in gene	ActReg chr20 #10100	0	1	0
10101	20	1,098,624	1,099,911	1,287	2	10.537	12.415	7.756	23	28	16	1	0	1	PSMF1	5,361	in gene	ActReg chr20 #10101	1	1	0
10102	20	1,206,978	1,207,266	288	1	4.556	6.556	11.778	7	11	14	1	1	1	RAD21L1	358	in gene	ActReg chr20 #10102	0	0	1
10103	20	1,288,835	1,289,209	374	1	2.1	4.455	12.364	3	6	18	0	0	2	SNPH, SDCBP2	42062, 20816	in gene, downstream	ActReg chr20 #10103	0	0	1
10104	20	1,293,184	1,293,700	516	1	4	3.824	11.823	7	6	19	1	0	2	SNPH, SDCBP2	46482, 16396	downstream, in gene	ActReg chr20 #10104	0	0	1
10105	20	1,293,729	1,294,158	429	1	3.462	5.923	12.923	5	11	17	1	0	2	SNPH, SDCBP2	46983, 15895	downstream, in gene	ActReg chr20 #10105	0	0	1
10106	20	1,305,676	1,306,681	1,005	1	6.871	11.194	5.258	11	16	10	1	1	3	SDCBP2, LOC100507495, LOC100288764	3660, 124, 11377	in gene, in gene, downstream	ActReg chr20 #10106	0	1	0
10107	20	1,396,498	1,397,354	856	1	10.111	13.259	2.13	21	22	5	0	0	0				ActReg chr20 #10107	0	1	0
10108	20	1,446,885	1,447,966	1,081	2	10.303	13.727	5.576	25	25	10	1	1	2	NSFL1C, SIRPB2	992, 24808	in gene, downstream	ActReg chr20 #10108	1	1	0
10109	20	1,464,910	1,465,351	441	1	7.286	10.429	4.125	10	17	5	0	0	1	SIRPB2	7,103	in gene	ActReg chr20 #10109	0	1	0
10110	20	1,757,536	1,758,462	926	2	18.241	20.241	4.552	50	55	9	1	0	1	LOC100289473	4,838	in gene	ActReg chr20 #10110	1	1	0
10111	20	1,808,461	1,809,173	712	1	6.682	12.136	4.182	12	20	7	0	0	0				ActReg chr20 #10111	0	1	0
10112	20	1,876,400	1,877,051	651	1	6.15	5.1	11.95	9	8	17	0	1	1	SIRPA	1,912	in gene	ActReg chr20 #10112	0	0	1
10113	20	1,986,271	1,987,050	779	2	13.36	13.2	1.467	29	27	4	0	0	0				ActReg chr20 #10113	1	1	0
10114	20	2,082,188	2,084,315	2,127	3	30.909	32.818	8.015	97	93	18	1	1	1	STK35	723	in gene	ActReg chr20 #10114	1	1	1
10115	20	2,187,968	2,188,686	718	1	7.857	11.304	9.826	14	16	19	1	1	1	LOC388780	361	in gene	ActReg chr20 #10115	0	1	0
10116	20	2,363,191	2,364,062	871	1	9.185	11.593	2.522	16	18	6	0	1	1	TGM6	2,072	in gene	ActReg chr20 #10116	0	1	0
10117	20	2,450,800	2,451,767	967	3	12.733	13.633	11.033	22	25	20	1	2	2	SNRPB, SNORD119	216, -7590	in gene, upstream	ActReg chr20 #10117	1	1	1
10118	20	2,489,129	2,490,008	879	2	11.704	9.963	8.704	18	13	14	2	1	1	ZNF343	210	in gene	ActReg chr20 #10118	1	1	0
10119	20	2,539,358	2,539,664	306	1	4	2.9	13.7	8	5	17	1	0	1	TMC2	22,258	in gene	ActReg chr20 #10119	0	0	1
10120	20	2,632,652	2,633,732	1,080	1	9.353	13.677	6.618	14	24	19	1	7	8	NOP56, MIR1292, SNORD110, SNORA51, SNORD86, SNORD56, SNORD57, IDH3B	-62, -231, -1666, -2521, -3551, -4078, -4393, 11651	upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, downstream	ActReg chr20 #10120	0	1	0
10121	20	2,644,445	2,645,267	822	1	9.885	12.731	5.462	16	23	10	1	1	7	NOP56, SNORD110, SNORA51, SNORD86, SNORD56, SNORD57, IDH3B	11602, 9998, 9143, 8113, 7586, 7271, -13	downstream, downstream, downstream, downstream, downstream, downstream, downstream, upstream	ActReg chr20 #10121	0	1	0
10122	20	2,776,065	2,776,576	511	1	4.846	6	10.125	9	9	14	0	0	1	CPXM1	4,972	in gene	ActReg chr20 #10122	0	0	1
10123	20	2,797,126	2,797,476	350	1	3.2	7.091	11.273	7	10	15	0	2	2	C20orf141, LOC100288797	1644, 325	downstream, in gene	ActReg chr20 #10123	0	0	1
10124	20	2,820,807	2,821,470	663	1	12.45	8.45	11.55	19	12	16	1	2	2	FAM113A, VPS16	194, -235	in gene, upstream	ActReg chr20 #10124	0	0	1
10125	20	2,851,194	2,851,878	684	1	10.636	7.864	2.789	20	12	4	0	0	2	VPS16, PTPRA	30163, 6695	downstream, in gene	ActReg chr20 #10125	1	0	0
10126	20	2,853,168	2,853,660	492	1	8	8.8	12.133	10	12	19	1	0	2	VPS16, PTPRA	32041, 8573	downstream, in gene	ActReg chr20 #10126	0	0	1
10127	20	3,049,568	3,050,278	710	2	11.522	10.783	6	22	24	11	0	1	1	OXT	-2,343	upstream	ActReg chr20 #10127	1	1	0
10128	20	3,064,525	3,064,959	434	1	4.462	3.077	11.615	6	5	19	0	1	1	AVP	628	in gene	ActReg chr20 #10128	0	0	1
10129	20	3,139,936	3,141,016	1,080	2	15.029	9.471	8.824	25	21	18	1	2	3	UBOX5, FASTKD5, ProSAP/PI	64, 56, 8731	in gene, in gene, downstream	ActReg chr20 #10129	1	0	1
10130	20	3,154,056	3,155,108	1,052	2	12.909	11.879	7.438	30	22	15	1	1	1	ProSAP/PI	-5,375	upstream	ActReg chr20 #10130	1	1	0
10131	20	3,184,724	3,185,246	522	1	8.938	8.312	10.938	11	14	15	1	2	2	DDRGK1, ITPA	310, -5071	in gene, upstream	ActReg chr20 #10131	0	0	1
10132	20	3,219,456	3,220,595	1,139	2	12.528	13.611	6.167	21	23	12	1	1	2	SLC4A11, C20orf194	-138, 168230	upstream, downstream	ActReg chr20 #10132	1	1	0
10133	20	3,256,008	3,256,407	399	1	2.833	2.833	12.667	4	6	20	0	0	1	C20orf194	132,048	in gene	ActReg chr20 #10133	0	0	1
10134	20	3,451,047	3,452,278	1,231	2	10.632	13.816	5.158	17	25	14	1	1	2	ATRN, LOC100507610	-5, -8980	upstream, upstream	ActReg chr20 #10134	1	1	0
10135	20	3,652,416	3,653,001	585	1	5.895	4.368	10.105	9	8	17	1	0	2	GFRA4, ADAM33	-8662, 10030	upstream, in gene	ActReg chr20 #10135	0	0	1
10136	20	3,653,033	3,653,609	576	1	3.2	5.778	12.333	5	6	18	1	0	2	GFRA4, ADAM33	-9275, 9417	upstream, in gene	ActReg chr20 #10136	0	0	1
10137	20	3,672,432	3,673,020	588	1	4.611	2	10.722	6	3	15	0	0	2	ADAM33, SIGLEC1	-9988, 15049	upstream, in gene	ActReg chr20 #10137	0	0	1
10138	20	3,673,179	3,674,024	845	1	3.56	4.407	12.556	5	8	16	0	0	1	SIGLEC1	14,174	in gene	ActReg chr20 #10138	0	0	1
10139	20	3,674,156	3,674,554	398	1	4	4.333	13.25	6	7	18	0	0	1	SIGLEC1	13,420	in gene	ActReg chr20 #10139	0	0	1
10140	20	3,747,774	3,748,811	1,037	1	6.939	7.818	12.879	11	11	21	1	1	2	C20orf27, SPEF1	160, 13810	in gene, downstream	ActReg chr20 #10140	0	0	1
10141	20	3,758,183	3,758,576	393	1	4.667	7.083	12.25	6	9	19	1	0	3	C20orf27, SPEF1, CENPB	-9927, 3723, 8958	upstream, in gene, downstream	ActReg chr20 #10141	0	0	1
10142	20	3,776,045	3,776,983	938	2	9.414	11.793	10.241	13	18	22	2	1	2	CENPB, CDC25B	-9177, 113	upstream, in gene	ActReg chr20 #10142	0	1	1
10143	20	3,781,096	3,781,683	587	1	4.944	3.889	10.389	8	7	14	0	0	1	CDC25B	4,988	in gene	ActReg chr20 #10143	0	0	1
10144	20	3,792,163	3,792,988	825	1	15	11.44	5.48	26	24	10	0	0	2	CDC25B, C20orf29	16174, -8628	downstream, upstream	ActReg chr20 #10144	1	0	0
10145	20	3,800,652	3,801,762	1,110	2	12.114	12.971	5.8	21	22	11	1	1	1	C20orf29	4	in gene	ActReg chr20 #10145	1	1	0
10146	20	3,804,370	3,805,151	781	1	6.5	3.292	11.875	10	5	15	0	0	1	C20orf29	3,557	in gene	ActReg chr20 #10146	0	0	1
10147	20	3,826,785	3,828,030	1,245	4	7.684	11.632	11.29	15	18	17	1	1	1	MAVS	-42	upstream	ActReg chr20 #10147	0	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10148	20	3,869,292	3,870,247	955	2	8.567	12.7	10.2	18	21	24	1	1	1	PANK2	283	in gene	ActReg chr20 #10148	0	1	1
10149	20	4,047,930	4,048,600	670	1	8.524	10.905	5.143	16	16	9	0	0	0				ActReg chr20 #10149	0	1	0
10150	20	4,116,751	4,117,526	775	1	6.708	11.708	4.208	12	18	8	0	0	0				ActReg chr20 #10150	0	1	0
10151	20	4,153,083	4,153,424	341	1	5.182	6.818	13.273	8	10	21	1	0	1	SMOX	23,803	in gene	ActReg chr20 #10151	0	0	1
10152	20	4,387,120	4,387,933	813	1	6.92	13.4	4.04	13	23	8	0	0	0				ActReg chr20 #10152	0	1	0
10153	20	4,536,008	4,536,638	630	1	12.105	9.684	1.929	21	19	5	0	0	0				ActReg chr20 #10153	1	0	0
10154	20	4,543,769	4,544,697	928	2	9.897	13.069	3.417	23	35	6	0	0	0				ActReg chr20 #10154	1	1	0
10155	20	4,646,650	4,647,150	500	1	10.312	6.938	1.688	15	10	3	0	0	0				ActReg chr20 #10155	1	0	0
10156	20	4,663,860	4,664,484	624	1	6.55	9.9	2.05	10	19	3	0	1	1	PRNP	-2,625	upstream	ActReg chr20 #10156	0	1	0
10157	20	5,093,330	5,094,282	952	2	14.133	15.3	8.567	27	32	15	1	2	3	C20orf30, PCNA, PCNAAS	-73, 13462, -6426	upstream, downstream, upstream	ActReg chr20 #10157	1	1	0
10158	20	5,099,795	5,100,855	1,060	1	7.242	12.212	9.485	10	22	21	1	3	4	C20orf30, PCNA, PCNAAS, CDS2	-6592, 6943, 93, -7157	upstream, in gene, in gene, upstream	ActReg chr20 #10158	0	1	0
10159	20	5,380,533	5,381,366	833	2	11.692	13.462	1.571	25	26	2	0	0	0				ActReg chr20 #10159	1	1	0
10160	20	5,824,768	5,825,366	598	1	9.368	12.21	3.278	16	24	7	0	0	1	C20orf196	94,024	in gene	ActReg chr20 #10160	0	1	0
10161	20	5,891,727	5,892,771	1,044	2	17.379	24.212	4.036	33	65	11	1	1	1	CHGB	275	in gene	ActReg chr20 #10161	1	1	0
10162	20	5,930,812	5,931,399	587	1	10.79	8.684	9.526	14	14	14	1	2	2	TRMT6, MCM8	68, -193	in gene, upstream	ActReg chr20 #10162	1	0	0
10163	20	6,103,314	6,104,055	741	1	8.957	10.913	6.435	15	16	14	1	1	1	FERMT1	507	in gene	ActReg chr20 #10163	0	1	0
10164	20	6,472,885	6,473,813	928	1	6.759	13.276	1.333	12	21	4	0	0	0				ActReg chr20 #10164	0	1	0
10165	20	6,481,489	6,482,331	842	1	13.462	10	1	21	16	1	0	0	0				ActReg chr20 #10165	1	0	0
10166	20	6,665,490	6,666,151	661	1	9.19	10.429	2.071	15	18	3	0	0	0				ActReg chr20 #10166	0	1	0
10167	20	6,748,604	6,748,911	307	1	6	8.3	15.8	7	11	23	1	1	1	BMP2	12	in gene	ActReg chr20 #10167	0	0	1
10168	20	6,750,318	6,751,110	792	1	11.52	10.28	6	24	16	11	1	1	1	BMP2	1,969	in gene	ActReg chr20 #10168	1	0	0
10169	20	7,176,216	7,176,751	535	1	6.471	10.765	1.562	11	19	3	0	0	0				ActReg chr20 #10169	0	1	0
10170	20	7,588,828	7,589,342	514	1	10.188	7.312	2.133	16	10	4	0	0	0				ActReg chr20 #10170	1	0	0
10171	20	7,831,365	7,832,110	745	1	11.435	7.435	1.769	18	13	4	0	0	0				ActReg chr20 #10171	1	0	0
10172	20	7,905,295	7,906,038	743	2	10	8.391	2.182	21	18	3	0	0	1	HAO1	15,427	in gene	ActReg chr20 #10172	1	1	0
10173	20	7,999,809	8,000,825	1,016	3	10.613	11.387	7.633	16	18	20	1	1	1	TMX4	76	in gene	ActReg chr20 #10173	1	1	1
10174	20	8,054,045	8,054,462	417	1	6.846	11.769	1	11	16	1	0	0	0				ActReg chr20 #10174	0	1	0
10175	20	8,525,745	8,526,417	672	2	10.667	10.429	2	18	18	3	0	0	1	PLCB1	412,785	in gene	ActReg chr20 #10175	1	1	0
10176	20	8,736,952	8,737,501	549	1	8.706	10.941	2.75	14	19	5	0	0	1	PLCB1	623,930	in gene	ActReg chr20 #10176	0	1	0
10177	20	9,049,715	9,050,261	546	1	9.647	10	6.583	16	14	13	1	1	1	PLCB4	287	in gene	ActReg chr20 #10177	1	0	0
10178	20	10,020,721	10,021,271	550	1	10.294	12.235	1.231	21	19	2	0	0	2	LOC100131208, ANKRD5	179155, 5299	in gene, in gene	ActReg chr20 #10178	0	1	0
10179	20	10,040,764	10,041,485	721	2	10.652	10.739	1.944	20	16	4	0	0	2	LOC100131208, ANKRD5	159027, 25427	in gene, downstream	ActReg chr20 #10179	1	1	0
10180	20	10,073,557	10,074,352	795	1	11.8	7.28	2.619	17	12	5	0	0	1	LOC100131208	126,197	in gene	ActReg chr20 #10180	1	0	0
10181	20	10,152,819	10,153,176	357	1	7.818	9.364	11.273	11	12	14	1	0	1	LOC100131208	47,154	in gene	ActReg chr20 #10181	0	0	1
10182	20	10,198,354	10,199,089	735	1	7.13	12.609	8.304	10	20	14	1	2	2	LOC100131208, SNAP25	1430, -756	in gene, upstream	ActReg chr20 #10182	0	1	0
10183	20	10,199,395	10,200,659	1,264	2	18.051	22.769	3.108	50	57	7	1	2	2	LOC100131208, SNAP25	124, 550	in gene, in gene	ActReg chr20 #10183	1	1	0
10184	20	10,413,997	10,415,580	1,583	2	13.735	13.674	5.708	25	27	19	1	2	2	MKKS, C20orf94	78, -1163	in gene, upstream	ActReg chr20 #10184	1	1	0
10185	20	10,579,107	10,579,566	459	1	11.214	7.857	2.357	14	12	3	0	0	1	C20orf94	163,385	in gene	ActReg chr20 #10185	1	0	0
10186	20	10,654,582	10,655,304	722	1	7.783	11.826	3.842	15	18	9	1	1	1	JAG1	-249	upstream	ActReg chr20 #10186	0	1	0
10187	20	10,686,373	10,687,209	836	2	10.923	11.885	3.792	19	21	8	0	0	0				ActReg chr20 #10187	1	1	0
10188	20	10,982,325	10,983,023	698	2	9.409	10.409	2.5	14	20	4	0	0	0				ActReg chr20 #10188	1	1	0
10189	20	10,999,454	10,999,801	347	1	4.455	5.273	9.182	8	7	12	0	0	0				ActReg chr20 #10189	0	0	1
10190	20	11,098,169	11,099,031	862	2	11.259	13.556	1.438	21	26	2	0	0	0				ActReg chr20 #10190	1	1	0
10191	20	11,159,539	11,160,158	619	1	10.632	4.842	1	20	9	1	0	0	0				ActReg chr20 #10191	1	0	0
10192	20	11,627,195	11,627,665	470	1	1.857	3.733	11.133	3	5	17	0	0	0				ActReg chr20 #10192	0	0	1
10193	20	12,709,856	12,710,517	661	2	10.191	10.333	4	20	18	6	0	0	0				ActReg chr20 #10193	1	1	0
10194	20	13,201,110	13,201,473	363	1	3.545	7.417	11	5	9	15	1	1	1	ISM1	-1,127	upstream	ActReg chr20 #10194	0	0	1
10195	20	13,765,206	13,765,902	696	2	8.773	12.864	9.182	15	20	17	1	2	2	ESF1, C20orf7	-22, -118	upstream, upstream	ActReg chr20 #10195	0	1	1
10196	20	14,269,114	14,269,859	745	1	11.333	6.417	2.312	18	10	5	0	0	1	MACROD2	293,340	in gene	ActReg chr20 #10196	1	0	0
10197	20	14,845,604	14,846,261	657	1	5.45	10.25	2.588	8	21	4	0	0	1	MACROD2	869,786	in gene	ActReg chr20 #10197	0	1	0
10198	20	15,679,947	15,680,616	669	1	14.095	10.714	3.238	28	25	6	0	0	1	MACROD2	1,704,135	in gene	ActReg chr20 #10198	1	0	0
10199	20	16,197,186	16,197,738	552	1	4.941	10.941	2.5	8	16	3	0	0	0				ActReg chr20 #10199	0	1	0
10200	20	16,553,818	16,554,469	651	1	10.857	13.238	7.048	18	22	13	1	1	1	KIF16B	-65	upstream	ActReg chr20 #10200	0	1	0
10201	20	16,555,165	16,555,901	736	1	12.391	9.087	4.522	19	12	9	1	1	1	KIF16B	-1,455	upstream	ActReg chr20 #10201	1	0	0
10202	20	16,710,195	16,711,121	926	2	21.724	27.483	7.966	60	76	14	1	1	1	SNRPB2	49	in gene	ActReg chr20 #10202	1	1	0
10203	20	16,844,228	16,845,237	1,009	1	10.484	13.258	4.033	17	20	10	0	0	0				ActReg chr20 #10203	0	1	0
10204	20	17,010,314	17,011,014	700	1	7.909	11.682	2.429	15	17	5	0	0	0				ActReg chr20 #10204	0	1	0
10205	20	17,064,245	17,064,856	611	1	8.211	10.526	2.312	11	20	5	0	0	0				ActReg chr20 #10205	0	1	0
10206	20	17,207,095	17,207,505	410	1	8.769	10.154	4.091	14	16	6	1	1	1	PCSK2	-331	upstream	ActReg chr20 #10206	0	1	0
10207	20	17,207,811	17,208,847	1,036	2	11.419	15.375	4.25	22	30	8	1	1	1	PCSK2	698	in gene	ActReg chr20 #10207	1	1	0
10208	20	17,397,735	17,398,480	745	2	11.435	12.696	2.1	25	31	3	0	0	1	PCSK2	190,476	in gene	ActReg chr20 #10208	1	1	0
10209	20	17,591,597	17,592,138	541	1	4.235	5.824	11.765	5	9	16	0	0	2	DSTN, RRBP1	41268, 71061	downstream, downstream	ActReg chr20 #10209	0	0	1
10210	20	17,596,016	17,596,564	548	1	3.875	2.765	12.765	6	4	19	0	0	2	DSTN, RRBP1	45691, 66638	downstream, in gene	ActReg chr20 #10210	0	0	1
10211	20	17,836,678	17,837,153	475	1	8.533	13.733	2.154	12	22	4	0	0	0				ActReg chr20 #10211	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10212	20	17,862,528	17,864,193	1,665	2	10.623	12.377	7.623	20	22	15	0	0	0				ActReg chr20 #10212	1	1	0
10213	20	17,948,947	17,950,330	1,383	2	12.302	16.309	8.814	23	30	19	1	3	3	SNX5, SNORD17, C20orf72	-148, -6049, -124	upstream, upstream, upstream	ActReg chr20 #10213	1	1	0
10214	20	18,038,093	18,038,428	335	1	4.9	6.8	11.1	6	9	16	1	1	1	OVOL2	261	in gene	ActReg chr20 #10214	0	0	1
10215	20	18,118,042	18,118,957	915	4	18.035	19.414	10.448	44	44	17	1	2	2	PET117, CSRP2BP	0, -4369	in gene, upstream	ActReg chr20 #10215	1	1	1
10216	20	18,268,174	18,269,454	1,280	2	7.85	12.825	10.1	15	21	20	1	1	1	ZNF133	-307	upstream	ActReg chr20 #10216	0	1	1
10217	20	18,393,773	18,394,249	476	1	10.133	7.467	1.714	18	10	3	0	0	1	C20orf12	53,818	in gene	ActReg chr20 #10217	1	0	0
10218	20	18,447,536	18,448,597	1,061	2	11.697	13.061	9.091	24	24	14	1	3	3	C20orf12, POLR3F, MIR3192	-237, 33, -3193	upstream, in gene, upstream	ActReg chr20 #10218	1	1	0
10219	20	18,477,507	18,478,101	594	1	6.5	10.944	5.667	8	19	10	1	1	1	RBBP9	83	in gene	ActReg chr20 #10219	0	1	0
10220	20	18,487,992	18,488,707	715	2	12.609	10.043	6.043	21	13	10	1	1	1	SEC23B	161	in gene	ActReg chr20 #10220	1	1	0
10221	20	18,568,227	18,568,878	651	1	7.9	8.9	3.474	11	16	7	1	1	1	DTD1	-4	upstream	ActReg chr20 #10221	0	1	0
10222	20	19,063,514	19,064,347	833	2	13.538	13.154	2.35	23	25	4	0	0	0				ActReg chr20 #10222	1	1	0
10223	20	19,620,410	19,620,767	357	1	4.364	1.9	12	7	3	17	0	0	1	SLC24A3	427,298	in gene	ActReg chr20 #10223	0	0	1
10224	20	19,997,611	19,998,610	999	2	10.194	13.645	7.839	25	26	12	1	1	1	NAA20	173	in gene	ActReg chr20 #10224	1	1	0
10225	20	20,032,673	20,033,501	828	1	9.16	9.2	13.24	15	16	18	1	1	2	CRNKL1, C20orf26	3603, -71	in gene, upstream	ActReg chr20 #10225	0	0	1
10226	20	20,675,738	20,676,523	785	2	10.8	11.12	2	25	25	4	0	0	1	RALGAPA2	17,136	in gene	ActReg chr20 #10226	1	1	0
10227	20	21,083,540	21,083,969	429	1	4.083	3.615	10.714	7	5	18	1	0	0				ActReg chr20 #10227	0	0	1
10228	20	21,283,539	21,284,684	1,145	2	13.333	9	4.886	25	15	11	1	1	1	XRN2	169	in gene	ActReg chr20 #10228	1	1	0
10229	20	21,416,628	21,417,144	516	1	7.125	10.75	2.133	11	14	3	0	0	0				ActReg chr20 #10229	0	1	0
10230	20	21,486,283	21,486,611	328	1	6.2	7.8	10.9	9	13	14	1	0	1	NKX2-2	8,217	downstream	ActReg chr20 #10230	0	0	1
10231	20	21,686,743	21,687,086	343	1	3.5	3.364	10.636	6	5	14	1	1	1	PAX1	617	in gene	ActReg chr20 #10231	0	0	1
10232	20	22,567,270	22,567,644	374	1	2.091	3.727	11.636	3	4	16	1	1	2	C20orf56, FOXA2	-8177, -1356	upstream, upstream	ActReg chr20 #10232	0	0	1
10233	20	22,785,754	22,786,559	775	2	11.042	11.583	3.792	21	22	7	0	0	0				ActReg chr20 #10233	1	1	0
10234	20	22,999,913	23,000,259	346	1	3.636	2.818	10.454	6	5	14	0	0	0				ActReg chr20 #10234	0	0	1
10235	20	23,238,474	23,239,426	952	1	7.367	12.3	1.815	13	20	4	0	0	0				ActReg chr20 #10235	0	1	0
10236	20	23,330,650	23,331,574	924	1	7.966	10.724	6.793	16	20	12	1	1	2	NXT1, LOC100505683	-261, 7530	upstream, downstream	ActReg chr20 #10236	0	1	0
10237	20	23,341,979	23,342,765	786	2	12.48	15.72	5.286	25	23	12	1	2	3	NXT1, LOC100505683, GZF1	10999, -3730, -2649	downstream, upstream, upstream	ActReg chr20 #10237	1	1	0
10238	20	23,343,005	23,343,630	625	1	5.1	4.9	10.65	7	7	14	1	2	3	NXT1, LOC100505683, GZF1	11944, -4675, -1704	downstream, upstream, upstream	ActReg chr20 #10238	0	0	1
10239	20	24,236,995	24,237,347	352	1	2.182	4.545	9.818	6	7	15	0	0	0				ActReg chr20 #10239	0	0	1
10240	20	24,615,412	24,616,116	704	1	4.864	10.273	4.136	8	18	7	0	0	1	TMEM90B	165,929	in gene	ActReg chr20 #10240	0	1	0
10241	20	24,972,561	24,973,776	1,215	3	12.237	10.737	9.184	24	16	17	1	1	1	C20orf3	257	in gene	ActReg chr20 #10241	1	1	1
10242	20	25,035,278	25,036,434	1,156	2	13.306	16.278	3.139	35	32	6	0	0	1	ACSS1	3,760	in gene	ActReg chr20 #10242	1	1	0
10243	20	25,037,586	25,038,180	594	1	8.579	8.474	13.579	12	17	23	1	1	1	ACSS1	1,733	in gene	ActReg chr20 #10243	0	0	1
10244	20	25,038,977	25,039,534	557	1	4.647	6.765	12.177	7	10	15	1	1	1	ACSS1	361	in gene	ActReg chr20 #10244	0	0	1
10245	20	25,159,360	25,160,155	795	2	10.52	11.32	4.316	17	20	12	0	0	0				ActReg chr20 #10245	1	1	0
10246	20	25,175,767	25,176,660	893	1	8.071	12.107	7.333	13	18	15	2	1	1	ENTPD6	-126	upstream	ActReg chr20 #10246	0	1	0
10247	20	25,203,725	25,204,425	700	2	12.227	12.182	4.286	19	19	8	0	0	1	ENTPD6	27,736	in gene	ActReg chr20 #10247	1	1	0
10248	20	25,218,068	25,218,904	836	1	11.192	13.769	3.231	17	27	7	0	0	1	PYGB	-10,220	upstream	ActReg chr20 #10248	0	1	0
10249	20	25,262,694	25,263,226	532	1	5.688	6.188	12.188	10	11	17	0	0	1	PYGB	34,254	in gene	ActReg chr20 #10249	0	0	1
10250	20	25,263,822	25,264,532	710	1	4.545	6.318	14.591	9	10	19	0	0	1	PYGB	35,471	in gene	ActReg chr20 #10250	0	0	1
10251	20	25,272,796	25,273,419	623	1	5.5	7.05	11.9	8	11	17	0	0	2	PYGB, ABHD12	44401, 98370	in gene, downstream	ActReg chr20 #10251	0	0	1
10252	20	25,278,040	25,278,472	432	1	3.357	8.857	11.714	5	12	19	0	0	2	PYGB, ABHD12	49550, 93221	in gene, in gene	ActReg chr20 #10252	0	0	1
10253	20	25,290,232	25,290,889	657	1	6.333	11.619	6.286	10	18	11	0	0	1	ABHD12	80,917	in gene	ActReg chr20 #10253	0	1	0
10254	20	25,370,361	25,370,937	576	1	6.222	8.278	10.778	8	12	15	1	1	1	ABHD12	828	in gene	ActReg chr20 #10254	0	0	1
10255	20	25,387,889	25,388,744	855	1	8.778	13.778	5.37	16	26	7	1	1	1	GINS1	-7	upstream	ActReg chr20 #10255	0	1	0
10256	20	25,477,552	25,478,323	771	1	13.542	13.042	3	26	24	5	0	0	1	NINL	88,216	in gene	ActReg chr20 #10256	1	0	0
10257	20	25,603,845	25,605,278	1,433	3	11.386	11.614	12.909	21	19	26	1	1	1	NANP	87	in gene	ActReg chr20 #10257	1	1	1
10258	20	25,676,823	25,677,866	1,043	2	13.03	15.515	4.97	27	28	9	1	1	1	ZNF337	125	in gene	ActReg chr20 #10258	1	1	0
10259	20	25,755,288	25,755,575	287	1	3.25	1.111	8.889	5	2	11	0	0	1	FAM182B	26,496	in gene	ActReg chr20 #10259	0	0	1
10260	20	25,958,545	25,958,885	340	1	2.364	1.125	9.364	4	2	14	0	0	0				ActReg chr20 #10260	0	0	1
10261	20	29,428,757	29,429,148	391	1	3.917	3.833	13.833	7	8	20	0	0	0				ActReg chr20 #10261	0	0	1
10262	20	30,101,944	30,102,771	827	3	11.962	11.923	8.846	24	17	23	1	1	1	HM13	116	in gene	ActReg chr20 #10262	1	1	1
10263	20	30,160,362	30,160,990	628	1	10.421	9.105	6	21	13	10	1	0	1	HM13	58,435	downstream	ActReg chr20 #10263	1	0	0
10264	20	30,180,972	30,181,946	974	1	8.267	11.967	3.6	13	19	7	0	0	0				ActReg chr20 #10264	0	1	0
10265	20	30,310,523	30,312,070	1,547	4	10.571	11.694	9.327	17	21	18	2	1	1	BCL2L1	-640	upstream	ActReg chr20 #10265	1	1	1
10266	20	30,326,668	30,327,464	796	2	10.6	10.92	6.818	19	18	12	1	1	1	TPX2	162	in gene	ActReg chr20 #10266	1	1	0
10267	20	30,432,320	30,432,816	496	1	2.214	3.5	10.75	5	6	17	1	1	3	MYLK2, FOXS1, C20orf57	25390, 852, 13549	downstream, in gene, downstream	ActReg chr20 #10267	0	0	1
10268	20	30,457,912	30,458,650	738	1	8.043	11.217	4.75	13	17	11	1	2	2	DUSP15, TTLL9	198, -224	in gene, upstream	ActReg chr20 #10268	0	1	0
10269	20	30,556,119	30,556,851	732	3	23.391	30.174	12.522	56	71	20	1	1	1	XKR7	680	in gene	ActReg chr20 #10269	1	1	1
10270	20	30,697,137	30,697,914	777	1	13.458	6.833	4.75	22	11	8	0	1	2	HCK, TM9SF4	57534, 216	downstream, in gene	ActReg chr20 #10270	1	0	0
10271	20	30,777,409	30,777,877	468	1	4.417	5.4	12.143	7	7	15	1	0	1	PLAGL2	17,903	downstream	ActReg chr20 #10271	0	0	1
10272	20	30,795,490	30,796,279	789	1	10.667	10	4.947	16	15	10	1	2	2	PLAGL2, POFUT1	-338, 188	upstream, in gene	ActReg chr20 #10272	1	0	0
10273	20	30,945,277	30,946,429	1,152	2	11.611	14.611	6.343	23	21	13	1	2	2	LOC100506402, ASXL1	-5994, -294	upstream, upstream	ActReg chr20 #10273	1	1	0
10274	20	31,051,068	31,052,205	1,137	2	10.25	14.333	7.694	15	26	12	0	0	1	C20orf112	19,652	in gene	ActReg chr20 #10274	1	1	0
10275	20	31,060,327	31,060,673	346	1	5.333	4.364	11.636	7	5	16	0	0	1	C20orf112	10,788	in gene	ActReg chr20 #10275	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10276	20	31,070,385	31,070,751	366	1	7.182	11.818	8.091	9	17	14	1	1	2	C20orf112, LOC100506597	720, 53883	in gene, downstream	ActReg chr20 #10276	0	1	0
10277	20	31,115,287	31,115,827	540	1	3.706	2.625	10.765	7	4	15	0	0	1	LOC100506597	8,894	in gene	ActReg chr20 #10277	0	0	1
10278	20	31,260,868	31,261,226	358	1	2.727	2.182	11.273	4	3	14	0	0	0				ActReg chr20 #10278	0	0	1
10279	20	31,264,274	31,264,652	378	1	4.083	3.333	10.917	7	5	15	0	0	0				ActReg chr20 #10279	0	0	1
10280	20	31,366,195	31,366,879	684	1	5.947	5.81	11.191	10	8	16	0	0	1	DNMT3B	16,346	in gene	ActReg chr20 #10280	0	0	1
10281	20	31,499,073	31,499,515	442	1	3.692	4	12.538	5	6	19	0	0	1	EFCAB8	52,565	in gene	ActReg chr20 #10281	0	0	1
10282	20	31,560,323	31,560,930	607	1	2.316	5.316	10.158	5	9	14	0	0	0				ActReg chr20 #10282	0	0	1
10283	20	31,780,664	31,781,339	675	2	12.381	13.048	2	21	22	4	0	0	0				ActReg chr20 #10283	1	1	0
10284	20	31,797,485	31,798,073	588	1	9.333	14.389	2.5	17	26	5	0	1	1	C20orf71	-7,356	upstream	ActReg chr20 #10284	0	1	0
10285	20	31,988,921	31,989,745	824	3	11.231	11.346	9.654	20	21	16	1	1	2	CDK5RAP1, SNTA1	4, 42365	in gene, downstream	ActReg chr20 #10285	1	1	1
10286	20	32,254,643	32,256,236	1,593	3	9.94	11.64	8.42	15	20	19	1	1	4	NECAB3, C20orf144, C20orf134, E2F1	6825, 5319, 1135, 18771	in gene, downstream, in gene, downstream	ActReg chr20 #10286	1	1	1
10287	20	32,307,692	32,308,506	814	1	7.56	14.8	6.88	12	31	13	1	1	1	PXMP4	37	in gene	ActReg chr20 #10287	0	1	0
10288	20	32,378,508	32,379,291	783	1	3.875	3.875	12.792	6	6	21	1	0	1	ZNF341	59,091	in gene	ActReg chr20 #10288	0	0	1
10289	20	32,398,638	32,399,356	718	1	11	15.046	3.095	27	33	8	1	1	1	CHMP4B	-113	upstream	ActReg chr20 #10289	0	1	0
10290	20	32,533,234	32,533,895	661	2	12.143	11.191	3.2	21	19	6	0	0	0				ActReg chr20 #10290	1	1	0
10291	20	32,581,254	32,582,051	797	1	11	11.44	8.059	20	16	16	1	2	2	LOC100505490, RALY	510, -80	in gene, upstream	ActReg chr20 #10291	0	1	0
10292	20	32,699,434	32,700,468	1,034	1	8.062	11.531	4.656	12	18	9	1	1	1	EIF2S2	134	in gene	ActReg chr20 #10292	0	1	0
10293	20	32,890,091	32,891,625	1,534	3	22.688	27.771	9.792	76	88	19	1	0	1	AHCY	8,750	in gene	ActReg chr20 #10293	1	1	1
10294	20	32,902,138	32,902,952	814	1	9.154	13.308	4.308	13	23	6	0	1	1	AHCY	-2,937	upstream	ActReg chr20 #10294	0	1	0
10295	20	32,950,845	32,951,483	638	1	10.65	11.1	7.25	19	21	12	1	1	1	ITCH	102	in gene	ActReg chr20 #10295	0	1	0
10296	20	33,103,145	33,104,870	1,725	2	11.833	13.389	8.685	21	21	19	1	1	2	ITCH, DYNLRB1	152945, -197	downstream, upstream	ActReg chr20 #10296	0	1	1
10297	20	33,112,993	33,114,312	1,319	2	12.244	13.902	4.054	24	31	8	0	0	1	DYNLRB1	9,448	in gene	ActReg chr20 #10297	1	1	0
10298	20	33,145,915	33,146,708	793	1	12.04	14.2	6.92	21	27	12	1	0	2	MAP1LC3A, PIGU	111619, 118778	in gene, downstream	ActReg chr20 #10298	0	1	0
10299	20	33,264,600	33,265,421	821	1	12.039	16.577	5.731	18	31	13	1	1	1	PIGU	79	in gene	ActReg chr20 #10299	0	1	0
10300	20	33,297,115	33,297,626	511	1	8.875	9.562	13.625	13	15	20	1	1	3	TP53INP2, NCOA6, LOC100505514	5222, 116063, -5232	in gene, downstream, upstream	ActReg chr20 #10300	0	0	1
10301	20	33,460,376	33,461,139	763	1	7.833	13.292	5.417	12	24	9	1	2	2	GGT7, ACSS2	-96, -2009	upstream, upstream	ActReg chr20 #10301	0	1	0
10302	20	33,494,880	33,496,662	1,782	2	9.786	11.589	5.214	17	17	12	0	0	1	ACSS2	33,005	in gene	ActReg chr20 #10302	1	1	0
10303	20	33,542,988	33,544,231	1,243	3	14.205	14.538	13.125	24	27	20	1	2	2	GSS, MYH7B	-8, -95	upstream, upstream	ActReg chr20 #10303	1	1	1
10304	20	33,571,677	33,572,470	793	1	4.409	3.56	13.04	9	6	18	0	1	2	MYH7B, MIR499	28369, -6106	in gene, upstream	ActReg chr20 #10304	0	0	1
10305	20	33,572,492	33,573,523	1,031	1	4.969	5.781	12.406	9	9	18	0	1	2	MYH7B, MIR499	29303, -5172	in gene, upstream	ActReg chr20 #10305	0	0	1
10306	20	33,590,319	33,591,491	1,172	1	4.703	4.73	11.973	9	7	16	0	0	2	MYH7B, TRPC4AP	47201, 89713	downstream, in gene	ActReg chr20 #10306	0	0	1
10307	20	33,679,866	33,681,331	1,465	2	11.391	12.087	7.935	20	21	16	2	1	1	TRPC4AP	20	in gene	ActReg chr20 #10307	1	1	0
10308	20	33,786,898	33,787,784	886	1	5.107	10.214	4.917	8	15	8	0	0	0				ActReg chr20 #10308	0	1	0
10309	20	33,814,889	33,815,892	1,003	2	14.903	16.903	5	24	33	8	1	1	1	MMP24	851	in gene	ActReg chr20 #10309	1	1	0
10310	20	33,864,160	33,864,779	619	1	8.1	3.55	11.35	13	7	15	0	0	3	MMP24, EIF6, FAM83C	49930, 8125, 15756	in gene, downstream, downstream	ActReg chr20 #10310	0	0	1
10311	20	33,865,667	33,866,079	412	1	7.917	9.5	15.917	11	12	26	2	0	3	MMP24, EIF6, FAM83C	51334, 6721, 14352	downstream, downstream, downstream	ActReg chr20 #10311	0	0	1
10312	20	33,871,495	33,873,085	1,590	1	10.775	14.041	9.776	23	21	19	1	1	3	MMP24, EIF6, FAM83C	57751, 304, 7935	downstream, in gene, downstream	ActReg chr20 #10312	0	1	0
10313	20	33,874,520	33,875,939	1,419	1	4.6	5.778	12.933	7	13	20	0	1	3	MMP24, EIF6, FAM83C	60690, -2635, 4996	downstream, upstream, in gene	ActReg chr20 #10313	0	0	1
10314	20	33,892,957	33,894,600	1,643	2	13.519	13.692	6.059	29	28	13	0	0	1	UQCC	106,167	in gene	ActReg chr20 #10314	1	1	0
10315	20	33,895,542	33,896,888	1,346	1	6.905	10.976	4.381	10	17	7	0	0	1	UQCC	103,730	in gene	ActReg chr20 #10315	0	1	0
10316	20	34,042,825	34,043,710	885	2	11.63	7.333	17.815	17	12	26	1	2	2	MIR1289-1, CEP250	-1348, 44	upstream, in gene	ActReg chr20 #10316	1	0	1
10317	20	34,091,846	34,092,624	778	1	4.833	8	12.167	8	13	16	0	0	1	CEP250	49,012	in gene	ActReg chr20 #10317	0	0	1
10318	20	34,129,606	34,130,184	578	1	6.5	8.222	17.722	8	13	32	1	1	1	ERGIC3	117	in gene	ActReg chr20 #10318	0	0	1
10319	20	34,188,498	34,188,950	452	1	2.929	6.5	11.5	4	9	17	1	0	0				ActReg chr20 #10319	0	0	1
10320	20	34,203,404	34,204,384	980	2	11.903	12.516	9.387	19	23	17	1	1	2	SPAG4, CPNE1	85, 48954	in gene, downstream	ActReg chr20 #10320	1	1	0
10321	20	34,205,375	34,205,885	510	1	5.562	2.625	12.75	8	4	18	1	1	2	SPAG4, CPNE1	1821, 47218	in gene, downstream	ActReg chr20 #10321	0	0	1
10322	20	34,207,116	34,207,748	632	1	9.45	10.95	12.1	15	20	19	1	0	2	SPAG4, CPNE1	3623, 45416	in gene, downstream	ActReg chr20 #10322	0	0	1
10323	20	34,240,714	34,241,252	538	1	3.765	3.647	13.353	4	9	21	0	0	2	CPNE1, RBM12	11865, 11855	in gene, in gene	ActReg chr20 #10323	0	0	1
10324	20	34,252,396	34,253,024	628	1	13.85	16.8	16.35	17	26	27	1	2	3	CPNE1, RBM12, NFS1	138, 128, 34564	in gene, in gene, downstream	ActReg chr20 #10324	0	0	1
10325	20	34,286,841	34,287,811	970	1	11.516	15.129	10.806	22	23	16	1	2	3	NFS1, ROMO1, RBM39	-52, 94, 42867	upstream, in gene, downstream	ActReg chr20 #10325	0	1	0
10326	20	34,329,796	34,330,905	1,109	2	10.029	11.912	12.647	21	22	20	1	1	1	RBM39	-157	upstream	ActReg chr20 #10326	0	1	1
10327	20	34,356,931	34,357,626	695	1	11.048	12.333	3.952	22	25	6	0	1	1	PHF20	-2,645	upstream	ActReg chr20 #10327	0	1	0
10328	20	34,541,441	34,543,028	1,587	3	15.49	15.612	12.286	31	27	21	1	1	2	PHF20, SCAND1	182311, 194	downstream, in gene	ActReg chr20 #10328	1	1	1
10329	20	34,638,343	34,639,213	870	3	10.185	10.333	14.2	17	16	24	1	1	1	LOC647979	104	in gene	ActReg chr20 #10329	1	1	1
10330	20	34,652,580	34,653,475	895	1	6.25	9.036	13.857	12	15	21	1	0	0				ActReg chr20 #10330	0	0	1
10331	20	34,673,261	34,674,136	875	1	9.296	11.741	2.84	14	16	5	0	0	0				ActReg chr20 #10331	0	1	0
10332	20	34,679,775	34,680,334	559	1	7.778	7.167	11.167	13	12	20	1	0	0				ActReg chr20 #10332	0	0	1
10333	20	34,680,761	34,681,940	1,179	1	9	13.081	7.784	14	23	14	1	0	0				ActReg chr20 #10333	0	1	0
10334	20	34,823,692	34,824,812	1,120	3	11.4	14.971	11.343	19	29	23	1	1	2	EPB41L1, C20orf4	123904, -195	downstream, upstream	ActReg chr20 #10334	1	1	1
10335	20	34,894,539	34,895,364	825	1	3.538	3.92	15.423	7	7	24	1	0	0				ActReg chr20 #10335	0	0	1
10336	20	34,948,711	34,949,154	443	1	2.143	4.929	11.429	4	7	16	0	0	0				ActReg chr20 #10336	0	0	1
10337	20	34,972,622	34,973,959	1,337	2	10.929	18	4.714	24	42	8	0	0	0				ActReg chr20 #10337	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10338	20	35,011,775	35,014,175	2,400	2	9.137	16.733	4.333	44	60	11	0	0	1	DLGAP4	17,531	in gene	ActReg chr20 #10338	1	1	0
10339	20	35,029,595	35,030,096	501	1	4.688	3.4	10.688	8	5	18	0	0	1	DLGAP4	34,401	in gene	ActReg chr20 #10339	0	0	1
10340	20	35,064,025	35,065,043	1,018	1	9.219	10.531	10.938	16	15	16	1	0	1	DLGAP4	69,090	in gene	ActReg chr20 #10340	0	0	1
10341	20	35,068,069	35,068,974	905	1	5.143	5.357	12.25	10	15	18	0	0	1	DLGAP4	73,077	in gene	ActReg chr20 #10341	0	0	1
10342	20	35,075,013	35,075,816	803	1	5.96	5.48	13.68	10	9	19	0	0	1	DLGAP4	79,970	in gene	ActReg chr20 #10342	0	0	1
10343	20	35,169,214	35,169,635	421	1	3.143	8.214	11.286	6	12	17	1	1	1	MYL9	-473	upstream	ActReg chr20 #10343	0	0	1
10344	20	35,169,949	35,170,275	326	1	6	5.818	13	7	8	17	0	1	1	MYL9	215	in gene	ActReg chr20 #10344	0	0	1
10345	20	35,233,547	35,234,948	1,401	2	12.727	15.159	10.432	26	33	24	1	1	2	C20orf24, SLA2	80, 40311	in gene, downstream	ActReg chr20 #10345	1	1	0
10346	20	35,305,063	35,305,935	872	1	6.296	2.615	14.074	10	5	22	0	0	1	NDRG3	68,982	in gene	ActReg chr20 #10346	0	0	1
10347	20	35,401,858	35,403,006	1,148	1	8.857	13.286	15.229	22	21	20	1	1	2	DSN1, C20orf117	-202, 89655	upstream, downstream	ActReg chr20 #10347	0	0	1
10348	20	35,421,681	35,422,920	1,239	1	5.974	5.59	14.103	10	9	26	1	0	1	C20orf117	69,787	in gene	ActReg chr20 #10348	0	0	1
10349	20	35,435,288	35,435,933	645	1	3.5	5.05	12.4	7	8	21	0	0	1	C20orf117	56,477	in gene	ActReg chr20 #10349	0	0	1
10350	20	35,443,736	35,444,697	961	1	6.433	7.7	15.733	10	11	24	1	0	1	C20orf117	47,871	in gene	ActReg chr20 #10350	0	0	1
10351	20	35,467,447	35,467,768	321	1	2.889	8.9	13.7	5	11	19	1	0	1	C20orf117	24,480	in gene	ActReg chr20 #10351	0	0	1
10352	20	35,490,841	35,491,192	351	1	11.273	5.364	13.182	15	7	19	1	1	1	C20orf117	1,071	in gene	ActReg chr20 #10352	0	0	1
10353	20	35,492,387	35,492,902	515	1	7.312	13.25	11.812	12	22	16	1	1	1	C20orf117	-557	upstream	ActReg chr20 #10353	0	0	1
10354	20	35,579,129	35,579,681	552	1	7.5	7.556	10.944	13	10	14	1	1	1	SAMHD1	841	in gene	ActReg chr20 #10354	0	0	1
10355	20	35,579,874	35,580,545	671	1	10.381	10.809	14	16	16	21	1	1	1	SAMHD1	37	in gene	ActReg chr20 #10355	0	0	1
10356	20	35,723,497	35,724,964	1,467	3	10.391	13.413	9.522	18	24	18	1	1	2	RBL1, C20orf132	180, 83744	in gene, downstream	ActReg chr20 #10356	1	1	1
10357	20	35,808,422	35,808,406	1,984	3	24.113	26.855	8.516	95	96	22	1	2	2	C20orf132, RPN2	560, -42	in gene, upstream	ActReg chr20 #10357	1	1	1
10358	20	35,917,786	35,918,670	884	2	10.607	14.321	8.964	21	26	21	1	1	1	MANBAL	177	in gene	ActReg chr20 #10358	0	1	1
10359	20	35,971,707	35,972,511	804	1	13.28	15.56	4.2	24	30	6	0	1	1	SRC	-979	upstream	ActReg chr20 #10359	0	1	0
10360	20	36,017,777	36,018,528	751	1	5.292	5.625	12.125	9	12	18	0	0	1	SRC	45,064	in gene	ActReg chr20 #10360	0	0	1
10361	20	36,026,576	36,027,309	733	1	3.087	5.174	13.174	5	8	18	0	0	1	SRC	53,854	in gene	ActReg chr20 #10361	0	0	1
10362	20	36,149,410	36,149,977	567	1	3.647	4.647	12.529	7	8	20	1	1	2	BLCAP, NNAT	6640, 86	in gene, in gene	ActReg chr20 #10362	0	0	1
10363	20	36,155,757	36,157,158	1,401	3	28.432	32.568	11.841	82	88	28	1	1	2	BLCAP, NNAT	-124, 6850	upstream, downstream	ActReg chr20 #10363	1	1	1
10364	20	36,201,110	36,201,967	857	2	11.593	16.741	4.037	23	30	9	0	0	0				ActReg chr20 #10364	1	1	0
10365	20	36,254,614	36,256,222	1,608	2	18.64	19.08	1.705	63	62	4	0	0	0				ActReg chr20 #10365	1	1	0
10366	20	36,322,222	36,322,789	567	1	7.778	9.611	12.278	10	16	20	1	1	1	CTNNBL1	71	in gene	ActReg chr20 #10366	0	0	1
10367	20	36,515,215	36,515,718	503	1	3.333	6.5	11.438	6	10	16	0	0	0				ActReg chr20 #10367	0	0	1
10368	20	36,519,667	36,520,207	540	1	3.118	2.706	13.941	6	4	22	0	0	0				ActReg chr20 #10368	0	0	1
10369	20	36,522,696	36,523,176	480	1	5	2.667	11.333	8	8	20	0	0	1	VSTM2L	-8,563	upstream	ActReg chr20 #10369	0	0	1
10370	20	36,529,673	36,530,295	622	2	13.684	13.737	8.421	22	18	13	0	1	1	VSTM2L	-1,515	upstream	ActReg chr20 #10370	1	1	0
10371	20	36,530,306	36,531,077	771	2	17.917	17.083	5.083	31	27	11	1	1	1	VSTM2L	-808	upstream	ActReg chr20 #10371	1	1	0
10372	20	36,532,608	36,533,268	660	1	3.714	4.857	13.143	7	8	20	0	1	1	VSTM2L	1,439	in gene	ActReg chr20 #10372	0	0	1
10373	20	36,534,491	36,535,163	672	1	2.95	2.714	10.333	6	5	15	0	0	1	VSTM2L	3,328	in gene	ActReg chr20 #10373	0	0	1
10374	20	36,542,920	36,543,885	965	1	4.067	4.633	12.5	8	7	20	0	0	1	VSTM2L	11,903	in gene	ActReg chr20 #10374	0	0	1
10375	20	36,661,279	36,662,631	1,352	2	8.744	12.814	10.095	15	26	18	1	2	2	KIAA0406, RPRD1B	-122, 7	upstream, in gene	ActReg chr20 #10375	0	1	1
10376	20	36,763,992	36,764,868	876	1	3.786	6.143	12.429	9	13	17	0	0	1	TGM2	29,270	in gene	ActReg chr20 #10376	0	0	1
10377	20	36,780,604	36,781,598	994	1	8.645	13.71	6.71	14	20	9	0	0	1	TGM2	12,599	in gene	ActReg chr20 #10377	0	1	0
10378	20	36,841,045	36,841,743	698	1	3.864	5.409	11.636	5	7	15	0	0	1	KIAA1755	47,780	in gene	ActReg chr20 #10378	0	0	1
10379	20	36,899,377	36,900,463	1,086	1	12.147	8.794	5.971	23	20	10	0	0	0				ActReg chr20 #10379	1	0	0
10380	20	36,903,988	36,904,761	773	1	12.583	11.75	2.353	22	14	4	0	0	0				ActReg chr20 #10380	1	0	0
10381	20	37,047,272	37,047,854	582	1	6.722	9.611	14.111	9	12	19	0	0	3	LOC388796, SNORA71B, SNORA71A	16455, 6415, 8523	downstream, downstream, downstream	ActReg chr20 #10381	0	0	1
10382	20	37,063,286	37,064,422	1,136	3	17.528	19.583	9.389	44	45	25	1	4	5	LOC388796, SNORA71B, SNORA71A, SNORA71C, SNORA71D	164, -9876, -7768, -5407, -1212	in gene, upstream, upstream, upstream, upstream	ActReg chr20 #10382	1	1	1
10383	20	37,074,843	37,076,383	1,540	3	19.688	21.708	11.167	69	84	20	1	3	3	SNHG11, SNORA39, SNORA60	316, -1113, -2399	in gene, upstream, upstream	ActReg chr20 #10383	1	1	1
10384	20	37,274,335	37,275,601	1,266	2	8.325	10.425	8.475	19	23	19	1	0	1	C20orf95	44,391	in gene	ActReg chr20 #10384	0	1	1
10385	20	37,308,323	37,309,875	1,552	2	25.396	27.167	2.667	79	77	4	0	0	0				ActReg chr20 #10385	1	1	0
10386	20	37,314,070	37,315,485	1,415	2	16.318	19.864	1.939	49	51	6	0	0	0				ActReg chr20 #10386	1	1	0
10387	20	37,320,287	37,322,343	2,056	2	20.246	23.815	5.143	62	80	12	0	0	0				ActReg chr20 #10387	1	1	0
10388	20	37,352,501	37,352,955	454	1	5.154	2.231	14.571	8	4	23	1	1	1	SLC32A1	-377	upstream	ActReg chr20 #10388	0	0	1
10389	20	37,356,574	37,357,362	788	1	4.375	8.76	14.48	8	15	20	1	0	1	SLC32A1	3,863	in gene	ActReg chr20 #10389	0	0	1
10390	20	37,376,802	37,377,611	809	1	11.96	13.88	8.2	18	20	14	1	1	1	ACTR5	109	in gene	ActReg chr20 #10390	0	1	0
10391	20	37,393,157	37,394,043	886	1	7	11.333	4	14	19	8	0	0	1	ACTR5	16,503	in gene	ActReg chr20 #10391	0	1	0
10392	20	37,433,682	37,434,262	580	1	2.778	2.111	12.056	5	3	21	1	1	1	PPP1R16B	-376	upstream	ActReg chr20 #10392	0	0	1
10393	20	37,464,413	37,464,982	569	1	4	6.222	12	6	10	20	1	0	1	PPP1R16B	30,349	in gene	ActReg chr20 #10393	0	0	1
10394	20	37,518,268	37,519,756	1,488	2	13.447	15.255	8.191	29	30	18	0	0	1	PPP1R16B	84,664	in gene	ActReg chr20 #10394	1	1	0
10395	20	37,525,629	37,526,588	959	1	10.667	13.6	3.321	15	19	8	0	0	1	PPP1R16B	91,760	in gene	ActReg chr20 #10395	0	1	0
10396	20	37,554,399	37,555,820	1,421	3	11.444	13.578	13.022	20	21	24	1	1	2	PPP1R16B, FAM83D	120761, 154	downstream, in gene	ActReg chr20 #10396	1	1	1
10397	20	37,590,375	37,591,624	1,249	2	10.923	13.692	13.051	20	23	21	1	1	2	FAM83D, DHX35	36044, 18	downstream, in gene	ActReg chr20 #10397	0	1	1
10398	20	37,669,564	37,670,119	555	1	6.611	3.778	11.833	11	5	20	0	0	1	DHX35	78,860	downstream	ActReg chr20 #10398	0	0	1
10399	20	37,678,257	37,679,207	950	2	7.833	13.133	10.2	15	22	20	1	0	1	DHX35	87,751	downstream	ActReg chr20 #10399	0	1	1
10400	20	37,779,095	37,779,518	423	1	3.308	2.462	11.615	4	3	18	0	0	0				ActReg chr20 #10400	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10401	20	39,193,358	39,194,309	951	1	9.433	12.3	3.233	16	20	7	0	0	0				ActReg chr20 #10401	0	1	0
10402	20	39,311,568	39,312,451	883	1	4.192	7.143	12.429	6	14	17	1	0	1	MAFB	5,867	downstream	ActReg chr20 #10402	0	0	1
10403	20	39,318,299	39,318,865	566	1	8.389	4.5	12.556	11	6	17	1	1	1	MAFB	-706	upstream	ActReg chr20 #10403	0	0	1
10404	20	39,589,923	39,592,002	2,079	3	10.308	12.815	9.016	19	20	19	0	0	0				ActReg chr20 #10404	1	1	1
10405	20	39,631,557	39,632,828	1,271	1	13.41	10.359	5.103	23	17	9	0	0	1	LOC100128988	22,766	in gene	ActReg chr20 #10405	1	0	0
10406	20	39,633,173	39,634,194	1,021	1	7.375	10.844	5.406	12	15	8	0	0	1	LOC100128988	24,257	in gene	ActReg chr20 #10406	0	1	0
10407	20	39,635,858	39,636,383	525	1	7.75	7.562	13.312	11	13	17	0	0	1	LOC100128988	26,694	in gene	ActReg chr20 #10407	0	0	1
10408	20	39,656,905	39,658,660	1,755	3	14.618	13.273	12.255	24	27	34	1	1	2	LOC100128988, TOP1	48356, 320	downstream, in gene	ActReg chr20 #10408	1	1	1
10409	20	39,700,865	39,701,394	529	1	6.188	12.25	1	11	20	1	0	0	1	TOP1	43,667	in gene	ActReg chr20 #10409	0	1	0
10410	20	39,765,033	39,765,635	602	1	9.632	10	14.053	13	12	25	1	2	2	LOC100505725, PLCG1	1306, -827	in gene, upstream	ActReg chr20 #10410	0	0	1
10411	20	39,769,430	39,770,533	1,103	1	9.829	12.057	5.343	20	26	13	0	1	2	LOC100505725, PLCG1	-3341, 3820	upstream, in gene	ActReg chr20 #10411	0	1	0
10412	20	39,945,207	39,946,169	962	2	13.621	11.9	7.28	21	23	19	1	0	0				ActReg chr20 #10412	1	1	0
10413	20	39,957,883	39,958,731	848	2	10.462	13.407	6.481	21	24	9	0	0	0				ActReg chr20 #10413	1	1	0
10414	20	39,985,937	39,986,852	915	1	5.552	4.103	12.966	9	7	17	0	0	2	LPIN3, EMILIN3	16834, 9104	in gene, downstream	ActReg chr20 #10414	0	0	1
10415	20	39,989,423	39,990,260	837	1	5.308	5.154	11.269	8	10	16	0	0	2	LPIN3, EMILIN3	20281, 5657	downstream, in gene	ActReg chr20 #10415	0	0	1
10416	20	40,272,006	40,272,732	726	1	13.182	6.773	3.7	23	13	7	0	0	0				ActReg chr20 #10416	1	0	0
10417	20	40,321,199	40,322,637	1,438	2	13.956	17.089	6.533	29	32	11	1	0	0				ActReg chr20 #10417	1	1	0
10418	20	40,627,787	40,628,136	349	1	3.091	2.545	13.182	4	5	18	1	0	0				ActReg chr20 #10418	0	0	1
10419	20	41,236,196	41,236,625	429	1	1.111	2	11	2	3	16	0	0	1	PTPRT	582,147	in gene	ActReg chr20 #10419	0	0	1
10420	20	42,086,189	42,087,080	891	3	12.25	13.821	13.143	20	25	29	1	1	1	SFRS6	130	in gene	ActReg chr20 #10420	1	1	1
10421	20	42,142,540	42,143,802	1,262	1	5	3.872	13.538	10	7	20	1	1	1	LSM8TL	118	in gene	ActReg chr20 #10421	0	0	1
10422	20	42,218,897	42,219,855	958	2	12.9	15.267	7.4	31	30	14	1	1	2	SGK2, IFT52	31690, -203	downstream, upstream	ActReg chr20 #10422	1	1	0
10423	20	42,285,693	42,286,541	848	2	10.444	15.889	14.667	19	30	29	1	0	2	IFT52, MYBL2	66538, -9592	downstream, upstream	ActReg chr20 #10423	0	1	1
10424	20	42,342,272	42,342,829	557	1	4.667	1.412	12.778	8	3	18	0	0	1	MYBL2	46,841	in gene	ActReg chr20 #10424	0	0	1
10425	20	42,471,227	42,471,658	431	1	5.5	3.571	12.714	10	6	16	0	0	0				ActReg chr20 #10425	0	0	1
10426	20	42,553,686	42,554,431	745	1	9.913	12.913	6.318	15	24	10	0	0	1	TOX2	10,566	in gene	ActReg chr20 #10426	0	1	0
10427	20	42,603,748	42,604,486	738	1	11.087	14.217	3.4	19	29	7	0	0	1	TOX2	60,625	in gene	ActReg chr20 #10427	0	1	0
10428	20	42,660,577	42,661,217	640	1	4.35	3.875	12.8	12	7	22	0	0	1	TOX2	117,405	in gene	ActReg chr20 #10428	0	0	1
10429	20	42,788,070	42,788,647	577	1	5.167	9.389	14.5	8	15	22	1	0	1	JPH2	27,960	in gene	ActReg chr20 #10429	0	0	1
10430	20	42,815,285	42,815,814	529	1	2.412	4	12.941	4	8	17	0	1	2	JPH2, C20orf111	669, 23882	in gene, downstream	ActReg chr20 #10430	0	0	1
10431	20	42,838,945	42,840,008	1,063	2	10	12.212	12.333	20	21	18	1	2	2	C20orf111, LOC100505783	-45, -37	upstream, upstream	ActReg chr20 #10431	0	1	1
10432	20	42,876,295	42,877,456	1,161	2	12	16.361	4.889	19	39	9	1	1	1	GDAP1L1	967	in gene	ActReg chr20 #10432	1	1	0
10433	20	42,892,556	42,893,925	1,369	2	11.837	14.465	4.128	29	31	11	0	0	1	GDAP1L1	17,332	in gene	ActReg chr20 #10433	1	1	0
10434	20	42,939,199	42,940,250	1,051	3	15.454	17.333	9.939	35	34	18	1	1	1	FITM2	165	in gene	ActReg chr20 #10434	1	1	1
10435	20	43,056,770	43,057,841	1,071	2	15.03	21.788	2.516	38	48	5	0	0	1	HNF4A	72,864	in gene	ActReg chr20 #10435	1	1	0
10436	20	43,104,104	43,105,339	1,235	1	11.29	12.737	7.514	21	23	13	1	1	1	TTPAL	174	in gene	ActReg chr20 #10436	0	1	0
10437	20	43,124,188	43,125,244	1,056	1	10.848	12.303	2.552	16	18	8	0	0	2	TTPAL, SERINC3	20169, 26010	downstream, downstream	ActReg chr20 #10437	0	1	0
10438	20	43,150,224	43,150,947	723	1	9.043	13.217	8.261	15	22	13	1	1	2	SERINC3, PKIG	141, -9851	in gene, upstream	ActReg chr20 #10438	0	1	0
10439	20	43,201,293	43,201,996	703	1	11.046	9.636	2.579	16	12	5	0	0	1	PKIG	41,208	in gene	ActReg chr20 #10439	1	0	0
10440	20	43,343,182	43,343,746	564	1	5.889	5.611	12.278	10	9	24	0	1	1	WISP2	-421	upstream	ActReg chr20 #10440	0	0	1
10441	20	43,353,200	43,354,036	836	1	4.917	4.038	12	11	7	20	0	0	1	WISP2	9,733	in gene	ActReg chr20 #10441	0	0	1
10442	20	43,357,315	43,358,141	826	1	14.04	9.36	3.263	24	20	5	0	0	1	WISP2	13,843	downstream	ActReg chr20 #10442	1	0	0
10443	20	43,379,323	43,379,699	376	1	2.667	4	13.083	3	5	19	1	0	2	KCNK15, RIMS4	5023, 59401	in gene, downstream	ActReg chr20 #10443	0	0	1
10444	20	43,396,779	43,397,392	613	1	3.842	6.368	13.158	6	10	18	0	0	1	RIMS4	41,827	in gene	ActReg chr20 #10444	0	0	1
10445	20	43,399,650	43,400,121	471	1	1.857	3.571	11.714	5	6	20	0	0	1	RIMS4	39,027	in gene	ActReg chr20 #10445	0	0	1
10446	20	43,405,376	43,406,338	962	2	12.065	17.032	2.571	22	40	5	0	0	1	RIMS4	33,055	in gene	ActReg chr20 #10446	1	1	0
10447	20	43,407,890	43,409,392	1,502	2	13.936	16.617	4.383	44	49	9	0	0	1	RIMS4	30,271	in gene	ActReg chr20 #10447	1	1	0
10448	20	43,513,659	43,514,868	1,209	1	8.447	13.868	3.919	14	21	8	1	1	1	YWHAB	-81	upstream	ActReg chr20 #10448	0	1	0
10449	20	43,538,514	43,539,183	669	2	9.524	12.857	11.238	11	20	18	1	1	2	YWHAB, PABPC1L	24504, 145	downstream, in gene	ActReg chr20 #10449	0	1	1
10450	20	43,588,586	43,589,462	876	1	8.778	11.778	8.741	16	18	16	1	2	3	TOMM34, LOC100505826, STK4	90, 6075, -6096	in gene, downstream, upstream	ActReg chr20 #10450	0	1	0
10451	20	43,594,498	43,595,537	1,039	2	11.062	13.938	10.219	18	24	18	1	3	3	TOMM34, LOC100505826, STK4	-5903, 82, -103	upstream, in gene, upstream	ActReg chr20 #10451	1	1	0
10452	20	43,716,772	43,717,372	600	1	13.722	12.222	4.059	22	20	7	0	0	2	STK4, KCNS1	121952, 12681	downstream, downstream	ActReg chr20 #10452	1	0	0
10453	20	43,729,582	43,729,967	385	1	5.417	5.333	12	6	12	19	1	1	2	KCNS1, WFDC5	-21, 14029	upstream, downstream	ActReg chr20 #10453	0	0	1
10454	20	43,864,196	43,865,077	881	1	5.259	7.074	14.593	8	9	20	0	0	0				ActReg chr20 #10454	0	0	1
10455	20	43,921,742	43,922,680	938	1	10.655	13.069	12.724	19	21	18	1	0	1	MATN4	14,756	in gene	ActReg chr20 #10455	0	1	0
10456	20	43,944,715	43,945,249	534	1	2.176	7.588	13.059	5	11	17	1	0	3	MATN4, RBPJL, SDC4	-8015, 9491, 32082	upstream, in gene, downstream	ActReg chr20 #10456	0	0	1
10457	20	43,976,158	43,977,093	935	1	11.933	9.333	7.7	17	17	16	1	1	1	SDC4	439	in gene	ActReg chr20 #10457	1	0	0
10458	20	43,991,042	43,992,570	1,528	2	12.894	15.298	9.435	24	31	17	1	2	3	SYS1, SYS1-DBNDD2, TP53TG5	105, -34, 15151	in gene, upstream, downstream	ActReg chr20 #10458	1	1	0
10459	20	44,023,276	44,024,066	790	1	6.88	7.76	11.16	11	12	16	0	0	1	SYS1-DBNDD2	31,831	in gene	ActReg chr20 #10459	0	0	1
10460	20	44,047,702	44,048,267	565	1	4.059	6.556	11.944	7	11	17	0	0	3	SYS1-DBNDD2, DBNDD2, PIGT	56144, 13313, 3277	downstream, downstream, in gene	ActReg chr20 #10460	0	0	1
10461	20	44,098,687	44,099,556	869	1	6.964	8.643	10.5	12	15	14	1	1	1	WFDC2	727	in gene	ActReg chr20 #10461	0	0	1
10462	20	44,364,434	44,365,024	590	1	5.053	2.526	12.737	8	4	19	0	0	0				ActReg chr20 #10462	0	0	1
10463	20	44,409,857	44,410,498	641	1	11.1	9.6	3.3	18	15	7	0	0	1	WFDC3	10,370	in gene	ActReg chr20 #10463	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10464	20	44,420,253	44,420,941	688	1	11.818	14.864	5.864	18	28	11	1	2	2	WFDC3, DNTTIP1	-50, 21	upstream, in gene	ActReg chr20 #10464	0	1	0
10465	20	44,440,762	44,441,814	1,052	2	14.697	14.667	10.212	25	22	13	1	1	2	DNTTIP1, UBE2C	20712, 33	downstream, in gene	ActReg chr20 #10465	1	1	0
10466	20	44,452,567	44,453,185	618	1	6.2	6.95	12.95	11	10	20	1	0	3	UBE2C, TNNC2, SNX21	11621, 3077, -9594	downstream, in gene, upstream	ActReg chr20 #10466	0	0	1
10467	20	44,461,828	44,463,820	1,992	2	11.194	14.403	7.508	19	28	16	1	2	3	TNNC2, SNX21, ACOT8	-6871, 354, 23211	upstream, in gene, downstream	ActReg chr20 #10467	1	1	0
10468	20	44,485,406	44,486,518	1,112	3	13.771	12.086	10.314	21	22	22	0	2	2	ACOT8, ZSWIM3	73, -300	in gene, upstream	ActReg chr20 #10468	1	1	1
10469	20	44,518,876	44,520,716	1,840	3	11.121	12.121	13.483	24	25	25	1	3	5	ZSWIM1, C20orf165, NEURL2, CTSA, PLTP	9948, -3558, 105, 205, 20990	downstream, upstream, in gene, in gene, downstream	ActReg chr20 #10469	1	1	1
10470	20	44,533,316	44,533,900	584	1	5	8.111	12.611	7	11	16	0	0	2	CTSA, PLTP	14017, 7178	downstream, in gene	ActReg chr20 #10470	0	0	1
10471	20	44,539,644	44,541,175	1,531	2	9.583	11.354	11.354	16	22	22	2	1	1	PLTP	377	in gene	ActReg chr20 #10471	0	1	1
10472	20	44,562,780	44,563,774	994	3	12.355	13.161	21.29	20	26	37	1	1	1	PCIF1	-40	upstream	ActReg chr20 #10472	1	1	1
10473	20	44,599,663	44,601,518	1,855	3	18.965	20.862	18.035	35	40	66	1	1	1	ZNF335	243	in gene	ActReg chr20 #10473	1	1	1
10474	20	44,641,972	44,642,901	929	1	5.414	7.931	12.69	10	13	23	2	1	3	MMP9, LOC100128028, SLC12A5	4889, 8276, -7893	in gene, in gene, upstream	ActReg chr20 #10474	0	0	1
10475	20	44,655,239	44,658,560	3,321	4	11.173	13.827	8.913	30	34	22	1	1	2	LOC100128028, SLC12A5	-6187, 6570	upstream, in gene	ActReg chr20 #10475	1	1	1
10476	20	44,668,780	44,670,319	1,539	2	14.521	19.917	5.479	39	34	13	0	0	1	SLC12A5	19,220	in gene	ActReg chr20 #10476	1	1	0
10477	20	44,685,603	44,686,165	562	1	7.118	12.294	13.588	10	18	18	1	0	2	SLC12A5, NCOA5	35555, 32696	in gene, downstream	ActReg chr20 #10477	0	0	1
10478	20	44,687,181	44,687,923	742	1	3.87	3.773	11.739	6	6	15	1	0	2	SLC12A5, NCOA5	37223, 31028	in gene, downstream	ActReg chr20 #10478	0	0	1
10479	20	44,717,723	44,718,979	1,256	2	11.9	13.4	8.424	20	31	19	1	1	1	NCOA5	229	in gene	ActReg chr20 #10479	1	1	0
10480	20	44,720,289	44,721,048	759	1	3.913	3.913	13	6	7	19	0	1	1	NCOA5	-2,088	upstream	ActReg chr20 #10480	0	0	1
10481	20	44,728,009	44,728,433	424	1	6.769	7.385	13	10	12	17	0	0	1	NCOA5	-9,641	upstream	ActReg chr20 #10481	0	0	1
10482	20	44,767,560	44,768,048	488	1	2.733	3.769	13.267	5	9	18	0	0	1	CD40	20,898	downstream	ActReg chr20 #10482	0	0	1
10483	20	44,768,692	44,769,309	617	1	3.125	6.263	13.79	8	9	23	0	0	0				ActReg chr20 #10483	0	0	1
10484	20	44,857,385	44,860,251	2,866	2	21.281	24.213	5.13	61	64	13	0	0	1	CDH22	21,516	in gene	ActReg chr20 #10484	1	1	0
10485	20	44,921,498	44,922,347	849	2	12.407	15.815	3.115	21	33	5	0	0	0				ActReg chr20 #10485	1	1	0
10486	20	44,983,687	44,984,358	671	1	5.333	7.381	11.238	7	11	16	0	0	1	SLC35C2	9,042	in gene	ActReg chr20 #10486	0	0	1
10487	20	44,992,207	44,993,160	953	2	9.033	11.133	11.138	13	18	27	1	1	2	SLC35C2, ELMO2	381, 42588	in gene, downstream	ActReg chr20 #10487	0	1	1
10488	20	45,034,512	45,035,998	1,486	2	14.739	14.022	7.609	24	23	15	1	1	1	ELMO2	16	in gene	ActReg chr20 #10488	1	1	0
10489	20	45,141,769	45,142,575	806	1	8.72	12.24	6.68	15	21	11	1	1	1	ZNF334	22	in gene	ActReg chr20 #10489	0	1	0
10490	20	45,152,503	45,153,080	577	1	11.611	13.056	2.333	21	21	4	0	0	0				ActReg chr20 #10490	0	1	0
10491	20	45,174,042	45,175,047	1,005	1	3.969	6.062	11.875	7	11	18	0	0	1	C20orf123	4,669	in gene	ActReg chr20 #10491	0	0	1
10492	20	45,259,687	45,260,470	783	1	8.667	16.875	3.542	17	42	6	0	0	1	SLC13A3	53,046	in gene	ActReg chr20 #10492	0	1	0
10493	20	45,354,307	45,355,175	868	1	3.556	4.889	12.518	6	8	17	0	0	1	SLC2A10	16,462	in gene	ActReg chr20 #10493	0	0	1
10494	20	45,959,867	45,960,851	984	1	10.065	14.065	5.968	20	26	10	0	0	1	ZMYND8	25,115	in gene	ActReg chr20 #10494	0	1	0
10495	20	45,987,369	45,988,166	797	1	12.4	13.28	12.36	18	19	18	0	1	2	ZMYND8, LOC100505963	-2293, 6462	upstream, downstream	ActReg chr20 #10495	0	0	1
10496	20	46,020,712	46,022,101	1,389	2	12.023	11.977	4.738	18	20	9	0	0	0				ActReg chr20 #10496	1	1	0
10497	20	46,311,057	46,311,720	663	1	5.333	3.857	14.619	7	6	23	0	0	1	SULF2	103,972	in gene	ActReg chr20 #10497	0	0	1
10498	20	46,352,765	46,353,178	413	1	7	10.769	13	10	15	18	0	0	1	SULF2	62,389	in gene	ActReg chr20 #10498	0	0	1
10499	20	46,414,630	46,415,178	548	1	9.059	7.824	11.412	13	12	16	1	1	1	SULF2	456	in gene	ActReg chr20 #10499	0	0	1
10500	20	46,438,234	46,439,408	1,174	1	10.919	14.514	5.811	26	32	11	0	0	0				ActReg chr20 #10500	0	1	0
10501	20	46,496,412	46,496,996	584	1	3.105	5.474	13	5	7	20	0	0	0				ActReg chr20 #10501	0	0	1
10502	20	46,537,441	46,537,981	540	1	4	5.875	13.562	7	8	20	0	0	0				ActReg chr20 #10502	0	0	1
10503	20	46,579,710	46,580,863	1,153	1	8.944	12	7.057	13	20	13	1	1	1	LOC100505983	743	in gene	ActReg chr20 #10503	0	1	0
10504	20	46,687,554	46,688,021	467	1	5.071	5.571	13.643	8	10	18	0	0	0				ActReg chr20 #10504	0	0	1
10505	20	46,823,101	46,823,806	705	1	3	4	12.591	7	8	18	0	0	0				ActReg chr20 #10505	0	0	1
10506	20	46,958,512	46,959,184	672	1	9.571	11.714	2.476	13	20	5	0	0	0				ActReg chr20 #10506	0	1	0
10507	20	46,968,397	46,968,875	478	1	4.067	3.933	12.733	7	6	19	0	0	0				ActReg chr20 #10507	0	0	1
10508	20	46,971,495	46,972,204	709	1	5.364	4.636	13.182	11	6	18	0	0	0				ActReg chr20 #10508	0	0	1
10509	20	47,029,166	47,029,795	629	1	6.55	3.45	11.05	10	6	15	0	0	0				ActReg chr20 #10509	0	0	1
10510	20	47,083,146	47,083,837	691	1	2.476	5.857	12.429	5	8	19	0	0	0				ActReg chr20 #10510	0	0	1
10511	20	47,139,473	47,140,785	1,312	2	12.805	14.878	5.707	32	37	10	0	0	0				ActReg chr20 #10511	1	1	0
10512	20	47,145,043	47,145,631	588	1	4.222	4.889	12.111	6	7	15	0	0	0				ActReg chr20 #10512	0	0	1
10513	20	47,236,450	47,237,287	837	1	10.136	9.231	11.846	21	17	16	0	0	1	PREX1	207,552	downstream	ActReg chr20 #10513	0	0	1
10514	20	47,252,810	47,253,304	494	1	4.333	6.067	15.667	7	9	25	1	0	1	PREX1	191,363	in gene	ActReg chr20 #10514	0	0	1
10515	20	47,254,971	47,255,730	759	1	9.917	14.042	6.5	14	25	16	0	0	1	PREX1	189,070	in gene	ActReg chr20 #10515	0	1	0
10516	20	47,391,156	47,391,734	578	1	5.333	5.722	11.667	7	8	18	0	0	1	PREX1	52,975	in gene	ActReg chr20 #10516	0	0	1
10517	20	47,392,654	47,393,087	433	1	4.833	4.667	13.083	8	8	19	0	0	1	PREX1	51,535	in gene	ActReg chr20 #10517	0	0	1
10518	20	47,401,770	47,402,224	454	1	3	4.071	11.5	4	6	18	0	0	1	PREX1	42,423	in gene	ActReg chr20 #10518	0	0	1
10519	20	47,443,713	47,444,231	518	1	6.75	6.25	12.125	10	9	18	1	1	1	PREX1	448	in gene	ActReg chr20 #10519	0	0	1
10520	20	47,470,012	47,471,168	1,156	1	9.333	11.622	6.216	17	19	14	0	0	0				ActReg chr20 #10520	0	1	0
10521	20	47,662,246	47,663,367	1,121	1	11.229	12.143	14.257	19	23	24	1	1	2	ARFGEF2, CSE1L	124531, -32	downstream, upstream	ActReg chr20 #10521	0	0	1
10522	20	47,803,504	47,804,275	771	1	9.833	11.083	5.5	14	16	8	1	1	1	STAU1	1,015	in gene	ActReg chr20 #10522	0	1	0
10523	20	47,804,746	47,805,554	808	2	12	14.08	7.19	25	26	13	1	1	1	STAU1	-246	upstream	ActReg chr20 #10523	1	1	0
10524	20	47,864,648	47,865,323	675	1	6.667	5.429	11.238	9	8	16	0	0	2	DDX27, ZNFX1	29153, 29771	downstream, in gene	ActReg chr20 #10524	0	0	1
10525	20	47,894,301	47,895,657	1,356	3	14.256	14.512	9.429	23	34	24	1	5	5	ZNFX1, C20orf199, SNORD12C, SNORD12B, SNORD12	-223, 264, -503, -1871, -2241	upstream, in gene, upstream, upstream, upstream	ActReg chr20 #10525	1	1	1
10526	20	48,016,372	48,017,375	1,003	1	7.645	10.677	3.24	11	15	8	0	0	1	KCNB1	82,308	in gene	ActReg chr20 #10526	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10527	20	48,098,613	48,099,750	1,137	2	12.917	15.139	7.5	24	32	14	1	1	1	KCNB1	0	in gene	ActReg chr20 #10527	1	1	0
10528	20	48,100,698	48,101,306	608	3	12.421	11.316	10.947	22	24	20	1	1	1	KCNB1	-1,821	upstream	ActReg chr20 #10528	1	1	1
10529	20	48,178,773	48,179,437	664	1	7.143	9.571	13.524	13	13	24	0	0	1	PTGIS	5,602	in gene	ActReg chr20 #10529	0	0	1
10530	20	48,183,961	48,184,574	613	1	5.632	5.316	13.053	10	8	22	1	1	1	PTGIS	440	in gene	ActReg chr20 #10530	0	0	1
10531	20	48,227,239	48,228,233	994	2	11.871	12.548	8.355	20	23	14	0	1	1	LOC728671	-4,676	upstream	ActReg chr20 #10531	1	1	0
10532	20	48,278,067	48,278,858	791	1	10	10.76	3.095	14	15	6	0	0	1	B4GALT5	51,959	in gene	ActReg chr20 #10532	0	1	0
10533	20	48,329,771	48,330,233	462	1	9.5	6.143	12.5	14	10	22	1	1	1	B4GALT5	419	in gene	ActReg chr20 #10533	0	0	1
10534	20	48,330,503	48,330,867	364	1	13.182	10.454	11.636	20	16	18	1	1	1	B4GALT5	-264	upstream	ActReg chr20 #10534	0	0	1
10535	20	48,334,044	48,334,985	941	1	6.9	11.567	3.679	16	19	10	0	1	1	B4GALT5	-4,093	upstream	ActReg chr20 #10535	0	1	0
10536	20	48,391,461	48,392,311	850	1	14.385	10.154	4.154	27	14	8	0	0	0				ActReg chr20 #10536	1	0	0
10537	20	48,428,365	48,430,214	1,849	2	9.448	12.741	8.603	14	21	16	1	1	1	SLC9A8	39	in gene	ActReg chr20 #10537	0	1	1
10538	20	48,503,044	48,503,687	643	1	6.45	4.6	12.15	10	10	19	0	0	1	SLC9A8	74,115	in gene	ActReg chr20 #10538	0	0	1
10539	20	48,503,877	48,505,078	1,201	3	12.676	12.324	10.514	22	19	16	0	0	1	SLC9A8	75,227	in gene	ActReg chr20 #10539	1	1	1
10540	20	48,531,762	48,532,862	1,100	2	14.765	16.147	7.647	34	38	15	1	1	1	SPATA2	-232	upstream	ActReg chr20 #10540	1	1	0
10541	20	48,552,466	48,553,767	1,301	2	11.098	12.927	6.316	23	19	18	1	1	1	RNF114	202	in gene	ActReg chr20 #10541	1	1	0
10542	20	48,605,677	48,606,888	1,211	1	8.184	13.421	7.395	14	22	14	0	0	1	SNAI1	6,769	downstream	ActReg chr20 #10542	0	1	0
10543	20	48,632,701	48,633,200	499	1	4.062	4.938	11.625	8	7	15	0	0	0				ActReg chr20 #10543	0	0	1
10544	20	48,635,947	48,637,467	1,520	1	9.681	11.681	7.468	13	17	16	0	0	0				ActReg chr20 #10544	0	1	0
10545	20	48,669,650	48,670,081	431	1	3.333	4.714	11.857	5	8	18	0	0	0				ActReg chr20 #10545	0	0	1
10546	20	48,690,890	48,691,178	288	1	6.444	6.556	12.111	8	9	17	0	0	2	TMEM189-UBE2V1, UBE2V1	79301, 41460	downstream, downstream	ActReg chr20 #10546	0	0	1
10547	20	48,732,166	48,733,165	999	1	9.839	13.194	5.967	16	25	12	0	1	3	TMEM189-UBE2V1, UBE2V1, TMEM189	37670, -171, 37670	in gene, upstream, downstream	ActReg chr20 #10547	0	1	0
10548	20	48,754,737	48,756,097	1,360	2	13.442	13.558	7.163	23	25	14	0	0	2	TMEM189-UBE2V1, TMEM189	14918, 14918	in gene, in gene	ActReg chr20 #10548	1	1	0
10549	20	48,757,614	48,758,083	469	1	3.6	7.733	13.067	7	11	19	0	0	2	TMEM189-UBE2V1, TMEM189	12487, 12487	in gene, in gene	ActReg chr20 #10549	0	0	1
10550	20	48,850,127	48,851,123	996	1	5.387	5.355	12.065	9	11	20	0	0	0				ActReg chr20 #10550	0	0	1
10551	20	48,859,215	48,860,154	939	2	18.828	14.724	13.172	32	20	23	0	0	0				ActReg chr20 #10551	1	0	1
10552	20	48,860,429	48,861,463	1,034	1	10.031	14.281	8.281	16	23	20	0	0	0				ActReg chr20 #10552	0	1	0
10553	20	48,866,863	48,867,387	524	1	3.625	8.688	14.25	5	12	22	0	0	0				ActReg chr20 #10553	0	0	1
10554	20	48,883,181	48,884,662	1,481	2	10.217	11.674	8.5	17	18	13	0	1	1	LOC100506115	-114	upstream	ActReg chr20 #10554	1	1	0
10555	20	48,886,999	48,887,556	557	1	6.056	5.278	11	9	8	16	0	0	1	LOC100506115	3,242	in gene	ActReg chr20 #10555	0	0	1
10556	20	49,055,487	49,056,548	1,061	1	14.235	13.735	7	22	23	14	0	0	0				ActReg chr20 #10556	0	1	0
10557	20	49,056,898	49,057,775	877	2	13.482	12.37	4.815	22	21	11	0	0	0				ActReg chr20 #10557	1	1	0
10558	20	49,126,203	49,127,255	1,052	1	11.485	9.424	8.455	19	16	14	1	1	1	PTPN1	-162	upstream	ActReg chr20 #10558	1	0	0
10559	20	49,177,709	49,178,701	992	1	7.323	13.452	3.44	14	24	11	0	0	2	PTPN1, LOC100506153	51314, 16373	in gene, downstream	ActReg chr20 #10559	0	1	0
10560	20	49,261,635	49,262,627	992	3	10.194	15.161	9.258	18	23	18	0	1	2	FAM65C, LOC100506175	-8705, 123	upstream, in gene	ActReg chr20 #10560	1	1	1
10561	20	49,347,543	49,348,429	886	2	10.857	8.179	9.321	20	12	25	1	1	1	PARD6B	-95	upstream	ActReg chr20 #10561	1	0	1
10562	20	49,481,962	49,482,708	746	1	3.391	4.913	12.348	7	7	17	0	0	1	BCAS4	70,868	in gene	ActReg chr20 #10562	0	0	1
10563	20	49,547,862	49,548,766	904	2	13.643	14.607	8.571	20	28	14	1	1	2	ADNP, DPM1	-787, 26746	upstream, downstream	ActReg chr20 #10563	1	1	0
10564	20	49,574,650	49,576,328	1,678	2	13.321	16.66	10.698	20	32	19	1	2	2	DPM1, MOCS3	-429, 126	upstream, in gene	ActReg chr20 #10564	1	1	0
10565	20	49,596,654	49,597,954	1,300	1	10.22	12.317	8.415	18	22	17	0	0	0				ActReg chr20 #10565	0	1	0
10566	20	49,638,854	49,640,646	1,792	2	11.236	13.782	10.878	16	22	20	1	1	1	KCNG1	-90	upstream	ActReg chr20 #10566	0	1	1
10567	20	49,650,116	49,650,667	551	1	13.882	12	1.643	30	21	3	0	0	0				ActReg chr20 #10567	1	0	0
10568	20	49,922,879	49,923,787	908	2	8.931	11.241	10.862	16	18	23	0	0	0				ActReg chr20 #10568	0	1	1
10569	20	49,961,165	49,963,120	1,955	1	9.951	11.344	5.705	15	23	10	0	0	0				ActReg chr20 #10569	0	1	0
10570	20	49,970,906	49,971,860	954	1	9.7	13.467	4.3	15	21	7	0	0	0				ActReg chr20 #10570	0	1	0
10571	20	49,976,815	49,978,050	1,235	2	12.82	11.282	5.282	21	18	11	0	0	0				ActReg chr20 #10571	1	1	0
10572	20	49,982,406	49,983,898	1,492	2	11.5	12.065	6.391	18	19	17	0	0	0				ActReg chr20 #10572	1	1	0
10573	20	49,985,075	49,985,817	742	1	12.652	13.522	4.87	19	22	8	0	0	0				ActReg chr20 #10573	0	1	0
10574	20	50,041,655	50,042,585	930	2	15.103	18.793	7.345	34	47	14	0	0	1	NFATC2	137,048	in gene	ActReg chr20 #10574	1	1	0
10575	20	50,048,564	50,049,080	516	1	4.875	11.812	11.625	9	16	14	0	0	1	NFATC2	130,346	in gene	ActReg chr20 #10575	0	0	1
10576	20	50,053,971	50,054,956	985	2	12.871	13.774	5.258	23	24	8	0	0	1	NFATC2	124,705	in gene	ActReg chr20 #10576	1	1	0
10577	20	50,108,471	50,109,260	789	1	4.44	5.72	11	9	9	18	1	0	1	NFATC2	70,303	in gene	ActReg chr20 #10577	0	0	1
10578	20	50,113,773	50,115,183	1,410	2	12.659	12.818	4.932	23	22	10	0	0	1	NFATC2	64,690	in gene	ActReg chr20 #10578	1	1	0
10579	20	50,170,217	50,171,549	1,332	1	8.854	11.366	4.902	16	17	10	0	0	1	NFATC2	8,285	in gene	ActReg chr20 #10579	0	1	0
10580	20	50,178,815	50,179,326	511	1	14.25	11.25	12.438	22	17	20	1	1	1	NFATC2	98	in gene	ActReg chr20 #10580	0	0	1
10581	20	50,179,878	50,180,930	1,052	2	11.364	11.091	3.909	18	21	7	0	1	1	NFATC2	-1,236	upstream	ActReg chr20 #10581	1	1	0
10582	20	50,416,635	50,417,220	585	1	7	13.368	6.737	10	22	9	1	1	1	SALL4	2,121	in gene	ActReg chr20 #10582	0	1	0
10583	20	50,555,298	50,556,079	781	2	12.292	10.917	3.167	22	21	6	0	0	0				ActReg chr20 #10583	1	1	0
10584	20	50,807,245	50,809,287	2,042	2	12.891	12.516	6.21	25	23	14	1	1	1	ZFP64	258	in gene	ActReg chr20 #10584	1	1	0
10585	20	52,199,345	52,199,871	526	1	9.5	11.438	2.5	14	19	3	0	1	1	ZNF217	28	in gene	ActReg chr20 #10585	0	1	0
10586	20	52,515,556	52,516,956	1,400	2	12.093	12.628	4.326	20	24	9	0	0	0				ActReg chr20 #10586	1	1	0
10587	20	52,523,408	52,524,138	730	1	12.87	8.435	3.095	19	14	7	0	0	0				ActReg chr20 #10587	1	0	0
10588	20	52,534,095	52,534,822	727	1	9.435	12.435	4.913	16	22	9	0	0	0				ActReg chr20 #10588	0	1	0
10589	20	52,739,791	52,740,749	958	2	14.433	12.967	2.269	27	24	4	0	0	0				ActReg chr20 #10589	1	1	0
10590	20	52,749,059	52,750,351	1,292	2	15.7	12.15	2.8	27	16	5	0	0	0				ActReg chr20 #10590	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GeneCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10591	20	52,755,505	52,756,171	666	2	12.667	11.809	3.857	20	18	8	0	0	0				ActReg chr20 #10591	1	1	0
10592	20	52,824,071	52,825,189	1,118	2	14.794	19.343	6.758	29	45	12	1	1	1	PFDN4	128	in gene	ActReg chr20 #10592	1	1	0
10593	20	52,867,339	52,867,879	540	1	12.647	5.647	5.588	20	9	12	0	0	0				ActReg chr20 #10593	1	0	0
10594	20	52,883,589	52,884,663	1,074	2	17.242	15.182	3.516	35	29	8	0	0	0				ActReg chr20 #10594	1	1	0
10595	20	52,901,497	52,902,261	764	1	7.375	10.5	3.1	13	17	7	0	0	0				ActReg chr20 #10595	0	1	0
10596	20	54,686,920	54,687,580	660	1	7.9	12.95	1.688	13	23	3	0	0	0				ActReg chr20 #10596	0	1	0
10597	20	54,903,690	54,904,586	896	2	14.929	17.821	3.64	26	36	6	0	0	0				ActReg chr20 #10597	1	1	0
10598	20	54,912,021	54,912,382	361	1	2.364	4	11.091	4	5	15	0	0	0				ActReg chr20 #10598	0	0	1
10599	20	54,919,049	54,919,493	444	1	5.571	8.143	12.357	7	13	19	1	0	0				ActReg chr20 #10599	0	0	1
10600	20	54,934,720	54,935,682	962	1	8.387	14.71	6.5	14	25	16	0	1	2	C20orf108, AURKA	1218, 32150	in gene, downstream	ActReg chr20 #10600	0	1	0
10601	20	54,966,940	54,968,154	1,214	2	20.368	21.105	9.237	56	59	14	1	2	2	AURKA, CSTF1	-196, 120	upstream, in gene	ActReg chr20 #10601	1	1	0
10602	20	55,043,034	55,044,034	1,000	3	13.688	14.812	12.094	34	26	41	1	1	2	CASS4, C20orf43	56366, -113	downstream, upstream	ActReg chr20 #10602	1	1	1
10603	20	55,201,234	55,202,168	934	1	3.621	4.655	12.241	7	7	19	1	1	1	TFAP2C	-2,657	upstream	ActReg chr20 #10603	0	0	1
10604	20	55,205,076	55,206,937	1,861	2	8.828	13.483	9.93	15	24	20	1	1	1	TFAP2C	1,648	in gene	ActReg chr20 #10604	0	1	1
10605	20	55,277,513	55,279,237	1,724	1	8.278	14	4.63	20	22	9	0	0	0				ActReg chr20 #10605	0	1	0
10606	20	55,362,867	55,363,810	943	1	8.167	12.3	4.31	13	21	9	0	0	0				ActReg chr20 #10606	0	1	0
10607	20	55,411,933	55,412,397	464	1	3.6	4.2	12.133	5	7	18	0	0	0				ActReg chr20 #10607	0	0	1
10608	20	55,446,911	55,447,477	566	1	2	4.944	12.056	4	8	15	0	0	0				ActReg chr20 #10608	0	0	1
10609	20	55,551,486	55,552,165	679	1	4.409	6.136	10.954	8	9	16	0	0	0				ActReg chr20 #10609	0	0	1
10610	20	55,574,909	55,576,793	1,884	2	10.305	13.712	5.017	16	23	10	0	0	0				ActReg chr20 #10610	1	1	0
10611	20	55,580,300	55,580,796	496	1	5.067	9.067	10.933	6	12	13	0	0	0				ActReg chr20 #10611	0	0	1
10612	20	55,605,543	55,606,825	1,282	2	11.725	11.6	6.27	24	20	12	0	0	0				ActReg chr20 #10612	1	1	0
10613	20	55,613,861	55,614,875	1,014	1	8.968	12.161	3.731	12	18	6	0	0	0				ActReg chr20 #10613	0	1	0
10614	20	55,622,140	55,623,470	1,330	1	7.786	12.119	5.476	14	19	11	0	0	0				ActReg chr20 #10614	0	1	0
10615	20	55,651,025	55,651,778	753	1	9.583	13.042	6.875	12	21	11	0	0	0				ActReg chr20 #10615	0	1	0
10616	20	55,668,519	55,669,051	532	1	6.5	2.5	13.375	11	4	20	0	0	0				ActReg chr20 #10616	0	0	1
10617	20	55,765,455	55,766,565	1,110	1	10.257	12.743	4.543	18	19	10	0	0	1	BMP7	75,697	in gene	ActReg chr20 #10617	0	1	0
10618	20	55,770,208	55,771,155	947	1	8.7	16.333	6.433	19	33	11	0	0	1	BMP7	71,026	in gene	ActReg chr20 #10618	0	1	0
10619	20	55,780,599	55,781,403	804	1	14.56	10.6	4.8	22	21	9	0	0	1	BMP7	60,706	in gene	ActReg chr20 #10619	1	0	0
10620	20	55,840,120	55,841,147	1,027	1	4.938	6.219	15.375	8	17	25	1	1	1	BMP7	1,074	in gene	ActReg chr20 #10620	0	0	1
10621	20	55,841,388	55,842,124	736	1	6.957	9.087	14.826	11	14	24	1	1	1	BMP7	-49	upstream	ActReg chr20 #10621	0	0	1
10622	20	55,876,052	55,876,555	503	1	3.438	5.562	11.5	7	10	18	0	0	0				ActReg chr20 #10622	0	0	1
10623	20	55,926,038	55,926,795	757	2	9.542	12.417	11.5	19	22	17	1	1	3	SPO11, RAE1, MTRNR2L3	21585, 271, 8462	downstream, in gene, downstream	ActReg chr20 #10623	0	1	1
10624	20	55,960,270	55,960,911	641	1	3.9	6.45	15.95	6	9	25	0	1	3	RAE1, LOC100291105, RBM38	34445, 7528, -5873	downstream, in gene, upstream	ActReg chr20 #10624	0	0	1
10625	20	55,962,302	55,962,900	598	1	4.842	3.263	11.053	10	6	17	0	1	3	RAE1, LOC100291105, RBM38	36456, 5517, -3862	downstream, in gene, upstream	ActReg chr20 #10625	0	0	1
10626	20	55,967,200	55,967,993	793	1	5.28	5.88	12.96	10	9	19	0	2	2	LOC100291105, RBM38	522, 1133	in gene, in gene	ActReg chr20 #10626	0	0	1
10627	20	55,979,587	55,980,344	757	1	4.87	5.652	15.348	8	11	24	0	0	1	RBM38	13,502	in gene	ActReg chr20 #10627	0	0	1
10628	20	55,980,836	55,981,392	556	1	4.059	6.294	12.941	8	14	18	0	0	1	RBM38	14,651	in gene	ActReg chr20 #10628	0	0	1
10629	20	55,986,628	55,987,369	741	1	3.652	3.913	11.696	6	7	16	0	0	1	RBM38	20,535	downstream	ActReg chr20 #10629	0	0	1
10630	20	55,988,881	55,989,733	852	1	4.333	7.519	11.704	7	11	15	0	0	1	RBM38	22,844	downstream	ActReg chr20 #10630	0	0	1
10631	20	55,990,013	55,990,634	621	1	5.85	6.211	11.65	10	10	18	0	0	1	RBM38	23,860	downstream	ActReg chr20 #10631	0	0	1
10632	20	56,010,422	56,011,747	1,325	3	11.61	13.476	9.167	17	20	18	0	0	0				ActReg chr20 #10632	1	1	1
10633	20	56,165,003	56,165,589	586	1	5.167	6.833	12.889	7	13	22	0	0	0				ActReg chr20 #10633	0	0	1
10634	20	56,175,525	56,176,559	1,034	1	13.562	14.781	5.1	22	24	13	0	0	1	ZBP1	19,590	downstream	ActReg chr20 #10634	0	1	0
10635	20	56,191,522	56,192,132	610	1	4.474	7.737	10.947	6	11	15	0	0	1	ZBP1	3,805	in gene	ActReg chr20 #10635	0	0	1
10636	20	56,192,140	56,192,535	395	1	8	5.833	12.167	10	8	15	0	0	1	ZBP1	3,295	in gene	ActReg chr20 #10636	0	0	1
10637	20	56,236,721	56,237,300	579	1	5.222	6.611	12.889	9	10	21	0	0	1	PMEPA1	49,531	in gene	ActReg chr20 #10637	0	0	1
10638	20	56,238,543	56,239,498	955	1	8.267	5.793	14.967	13	13	23	1	0	1	PMEPA1	47,521	in gene	ActReg chr20 #10638	0	0	1
10639	20	56,273,035	56,274,534	1,499	2	10.34	11.447	4.681	20	21	9	0	0	1	PMEPA1	12,757	in gene	ActReg chr20 #10639	1	1	0
10640	20	56,284,831	56,286,000	1,169	2	19.568	21	3.394	47	48	8	1	1	1	PMEPA1	1,126	in gene	ActReg chr20 #10640	1	1	0
10641	20	56,289,633	56,290,132	499	1	8	6.133	12.533	10	10	17	0	1	1	PMEPA1	-3,341	upstream	ActReg chr20 #10641	0	0	1
10642	20	56,293,363	56,294,265	902	2	15.571	16.071	4.48	33	31	9	1	1	1	PMEPA1	-7,273	upstream	ActReg chr20 #10642	1	1	0
10643	20	56,347,210	56,348,306	1,096	2	13.588	12.588	5.529	19	22	11	0	0	0				ActReg chr20 #10643	1	1	0
10644	20	56,357,751	56,358,627	876	1	5.25	8.185	14.107	9	15	20	0	0	0				ActReg chr20 #10644	0	0	1
10645	20	56,566,217	56,567,578	1,361	2	14.048	15.191	5.61	33	32	10	0	0	0				ActReg chr20 #10645	1	1	0
10646	20	56,585,389	56,586,094	705	1	5.045	7.182	11.273	9	11	17	0	0	0				ActReg chr20 #10646	0	0	1
10647	20	56,592,191	56,595,264	3,073	3	13.103	13.196	7.175	23	27	14	0	0	0				ActReg chr20 #10647	1	1	0
10648	20	56,621,607	56,623,763	2,156	2	20.448	23.597	3.262	56	68	6	0	0	0				ActReg chr20 #10648	1	1	0
10649	20	56,661,692	56,662,973	1,281	1	8.289	12.025	4.184	12	19	11	0	0	0				ActReg chr20 #10649	0	1	0
10650	20	56,663,012	56,663,837	825	1	8.84	13.92	5.045	16	23	10	0	0	0				ActReg chr20 #10650	0	1	0
10651	20	56,677,235	56,678,565	1,330	1	12	13.357	3.805	22	22	7	0	0	0				ActReg chr20 #10651	0	1	0
10652	20	56,754,316	56,755,178	862	1	11.556	13.074	4.37	23	20	8	1	0	0				ActReg chr20 #10652	0	1	0
10653	20	56,781,021	56,781,452	431	1	4.571	3.231	12.143	7	5	16	1	0	0				ActReg chr20 #10653	0	0	1
10654	20	57,014,888	57,015,592	704	1	9.955	11.591	1.789	14	21	3	0	0	1	VAPB	50,995	in gene	ActReg chr20 #10654	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10655	20	57,037,026	57,037,568	542	1	5.824	5.353	11.059	8	10	19	0	0	1	APCDD1L	52,652	in gene	ActReg chr20 #10655	0	0	1
10656	20	57,197,578	57,199,446	1,868	1	16.431	12.328	7.345	29	25	17	0	0	1	LOC149773	108,077	downstream	ActReg chr20 #10656	1	0	0
10657	20	57,220,438	57,221,226	788	1	7.44	12	5.16	11	17	8	0	1	2	MGC4294, STX16	11005, -5496	downstream, upstream	ActReg chr20 #10657	0	1	0
10658	20	57,225,834	57,227,205	1,371	3	13.395	16.907	14.512	31	42	28	1	1	1	STX16	191	in gene	ActReg chr20 #10658	1	1	1
10659	20	57,268,516	57,268,997	481	1	8.067	9.133	13.6	12	14	20	1	1	1	NPEPL1	894	in gene	ActReg chr20 #10659	0	0	1
10660	20	57,294,230	57,294,920	690	1	5.591	4.364	13.909	7	8	23	0	0	1	NPEPL1	26,713	downstream	ActReg chr20 #10660	0	0	1
10661	20	57,365,333	57,366,353	1,020	1	10.094	13.75	4.875	18	22	9	0	0	0				ActReg chr20 #10661	0	1	0
10662	20	57,370,133	57,370,657	524	1	3.294	5.706	11.882	7	8	19	0	0	0				ActReg chr20 #10662	0	0	1
10663	20	57,379,127	57,379,687	560	1	3.562	4.833	12.167	6	8	16	0	0	0				ActReg chr20 #10663	0	0	1
10664	20	57,386,436	57,387,152	716	1	10.682	11.227	12.682	15	16	20	0	0	3	MIR296, MIR298, GNASAS	5955, 6574, 39164	downstream, downstream, downstream	ActReg chr20 #10664	0	0	1
10665	20	57,390,814	57,391,711	897	1	4.679	5.786	15.786	11	9	28	0	2	3	MIR296, MIR298, GNASAS	1487, 2106, 34696	downstream, downstream, downstream	ActReg chr20 #10665	0	0	1
10666	20	57,427,403	57,428,512	1,109	1	6.559	5.545	11.971	13	11	17	2	1	2	GNASAS, GNAS	-1999, 13162	upstream, in gene	ActReg chr20 #10666	0	0	1
10667	20	57,429,013	57,429,631	618	1	5.947	4.316	13.895	8	8	21	1	1	2	GNASAS, GNAS	-3364, 14527	upstream, in gene	ActReg chr20 #10667	0	0	1
10668	20	57,430,688	57,431,178	490	1	4.812	2.938	16.188	8	5	25	1	1	2	GNASAS, GNAS	-4975, 16138	upstream, in gene	ActReg chr20 #10668	0	0	1
10669	20	57,581,089	57,582,520	1,431	2	8.318	12.114	9.075	14	19	22	1	1	1	CTSZ	505	in gene	ActReg chr20 #10669	0	1	1
10670	20	57,606,834	57,607,587	753	2	12.208	14.375	7.708	25	27	14	1	1	3	TUBB1, ATP5E, SLMO2	12901, 212, 10691	downstream, in gene, downstream	ActReg chr20 #10670	1	1	0
10671	20	57,616,881	57,619,280	2,399	2	12.667	12.32	5.632	24	18	15	1	1	2	ATP5E, SLMO2	-10658, -179	upstream, upstream	ActReg chr20 #10671	1	1	0
10672	20	57,637,959	57,639,366	1,407	1	10.818	7.432	3.341	16	14	9	0	0	0				ActReg chr20 #10672	1	0	0
10673	20	57,708,617	57,709,993	1,376	2	13.698	16	5.419	28	35	11	0	0	1	LOC100287547	20,599	in gene	ActReg chr20 #10673	1	1	0
10674	20	57,716,831	57,717,884	1,053	2	13.818	21.303	5.273	41	49	9	0	0	1	LOC100287547	12,547	in gene	ActReg chr20 #10674	1	1	0
10675	20	57,765,939	57,767,555	1,616	1	4.549	5.059	12.843	7	10	18	1	1	1	ZNF831	672	in gene	ActReg chr20 #10675	0	0	1
10676	20	57,795,833	57,796,764	931	1	11.069	9.793	3.172	15	15	5	0	0	1	ZNF831	30,223	in gene	ActReg chr20 #10676	1	0	0
10677	20	57,817,633	57,818,266	633	1	6.368	12.053	1.867	10	22	3	0	0	1	ZNF831	51,874	in gene	ActReg chr20 #10677	0	1	0
10678	20	57,822,840	57,823,836	996	1	11.677	7.419	2.045	17	14	4	0	0	1	ZNF831	57,263	in gene	ActReg chr20 #10678	1	0	0
10679	20	57,875,582	57,876,094	512	1	2.4	5.125	12.188	4	8	17	1	1	1	EDN3	339	in gene	ActReg chr20 #10679	0	0	1
10680	20	58,072,373	58,073,633	1,260	2	11.425	10.9	1.973	18	18	5	0	0	0				ActReg chr20 #10680	1	1	0
10681	20	58,148,625	58,149,254	629	1	3.1	3.85	11.9	4	7	17	0	0	0				ActReg chr20 #10681	0	0	1
10682	20	58,154,095	58,154,553	458	1	4.071	2	12.357	6	4	18	0	0	0				ActReg chr20 #10682	0	0	1
10683	20	58,179,129	58,179,632	503	1	1.4	2.643	12.5	2	5	21	1	1	1	PHACTR3	-223	upstream	ActReg chr20 #10683	0	0	1
10684	20	58,180,220	58,180,777	557	1	2.556	2.222	13.889	4	4	21	1	1	1	PHACTR3	895	in gene	ActReg chr20 #10684	0	0	1
10685	20	58,186,431	58,186,829	398	1	4.462	5.231	10.846	6	7	15	0	0	1	PHACTR3	7,027	in gene	ActReg chr20 #10685	0	0	1
10686	20	58,319,981	58,320,486	505	1	5.375	4.562	11.312	9	7	17	0	0	1	PHACTR3	140,630	in gene	ActReg chr20 #10686	0	0	1
10687	20	58,340,263	58,341,348	1,085	2	14.323	17.147	4.857	32	32	7	0	0	1	PHACTR3	161,202	in gene	ActReg chr20 #10687	1	1	0
10688	20	58,513,617	58,514,764	1,147	2	5.861	10.111	12.606	9	17	22	1	2	3	SYCP2, C20orf177, PPP1R3D	-6981, 5371, 1162	upstream, in gene, in gene	ActReg chr20 #10688	0	1	1
10689	20	58,515,100	58,516,251	1,151	2	13.556	12.611	8.222	23	18	15	1	1	3	SYCP2, C20orf177, PPP1R3D	-8466, 6856, -323	upstream, in gene, upstream	ActReg chr20 #10689	1	1	0
10690	20	58,625,571	58,626,021	450	1	4.929	5.714	13	7	7	19	0	1	1	C20orf197	-5,184	upstream	ActReg chr20 #10690	0	0	1
10691	20	58,824,533	58,825,025	492	1	11.562	8.5	2.643	19	11	6	0	0	0				ActReg chr20 #10691	1	0	0
10692	20	59,087,532	59,088,213	681	1	6.571	13.143	1.812	10	25	4	0	0	0				ActReg chr20 #10692	0	1	0
10693	20	59,158,478	59,159,353	875	2	12.222	17.222	1.941	23	37	4	0	0	0				ActReg chr20 #10693	1	1	0
10694	20	59,163,738	59,165,341	1,603	2	8.94	13.46	2.74	30	36	6	0	0	0				ActReg chr20 #10694	1	1	0
10695	20	59,631,630	59,631,917	287	1	2	3.222	12.222	3	4	14	0	0	0				ActReg chr20 #10695	0	0	1
10696	20	59,875,342	59,875,823	481	1	4.933	3	12.667	7	6	19	0	0	1	CDH4	48,023	in gene	ActReg chr20 #10696	0	0	1
10697	20	59,906,731	59,907,173	442	1	3	8.071	12.429	5	10	19	0	0	1	CDH4	79,393	in gene	ActReg chr20 #10697	0	0	1
10698	20	59,945,022	59,945,642	620	1	2.35	2.9	10.35	6	4	14	0	0	1	CDH4	117,773	in gene	ActReg chr20 #10698	0	0	1
10699	20	60,010,617	60,011,065	448	1	2	4	10.786	3	7	15	0	0	1	CDH4	183,282	in gene	ActReg chr20 #10699	0	0	1
10700	20	60,074,810	60,075,317	507	1	3.75	5.062	12.125	6	9	19	0	0	1	CDH4	247,504	in gene	ActReg chr20 #10700	0	0	1
10701	20	60,105,587	60,106,349	762	1	8.75	13.625	3.75	16	29	6	0	0	1	CDH4	278,409	in gene	ActReg chr20 #10701	0	1	0
10702	20	60,113,261	60,114,024	763	1	2.647	4.875	11.833	5	10	19	0	0	1	CDH4	286,083	in gene	ActReg chr20 #10702	0	0	1
10703	20	60,183,181	60,183,946	765	1	10.708	14.167	4.75	17	26	8	0	0	1	CDH4	356,004	in gene	ActReg chr20 #10703	0	1	0
10704	20	60,190,985	60,191,611	626	1	4.947	2.789	10.842	7	4	16	0	0	1	CDH4	363,739	in gene	ActReg chr20 #10704	0	0	1
10705	20	60,203,402	60,203,878	476	1	1.667	3.867	11.333	3	6	17	0	0	1	CDH4	376,081	in gene	ActReg chr20 #10705	0	0	1
10706	20	60,237,773	60,238,424	651	1	4	5.6	12.5	6	9	17	0	0	1	CDH4	410,539	in gene	ActReg chr20 #10706	0	0	1
10707	20	60,243,947	60,244,367	420	1	2.615	4.692	11.769	7	6	17	0	0	1	CDH4	416,598	in gene	ActReg chr20 #10707	0	0	1
10708	20	60,254,697	60,255,300	603	1	2.947	3.889	13.579	4	6	17	0	0	1	CDH4	427,439	in gene	ActReg chr20 #10708	0	0	1
10709	20	60,305,659	60,306,939	1,280	1	2.4	2.914	12.05	5	7	16	0	0	1	CDH4	478,740	in gene	ActReg chr20 #10709	0	0	1
10710	20	60,312,588	60,313,261	673	1	2.476	4.095	13.429	4	7	18	0	0	1	CDH4	485,365	in gene	ActReg chr20 #10710	0	0	1
10711	20	60,336,819	60,337,312	493	1	3.25	2	11.875	4	3	18	0	0	1	CDH4	509,506	in gene	ActReg chr20 #10711	0	0	1
10712	20	60,360,198	60,360,757	559	1	3.176	2.8	11.588	5	7	14	0	0	1	CDH4	532,918	in gene	ActReg chr20 #10712	0	0	1
10713	20	60,377,626	60,378,372	746	1	4.667	3.85	11.417	7	6	21	0	0	1	CDH4	550,440	in gene	ActReg chr20 #10713	0	0	1
10714	20	60,378,767	60,379,283	516	1	3.438	4.625	11.562	6	7	15	0	0	1	CDH4	551,466	in gene	ActReg chr20 #10714	0	0	1
10715	20	60,428,987	60,429,663	676	1	3.714	2.524	10.571	6	5	16	0	0	1	CDH4	601,766	in gene	ActReg chr20 #10715	0	0	1
10716	20	60,439,751	60,440,146	395	1	2.833	2.545	11.833	4	5	18	0	0	1	CDH4	612,389	in gene	ActReg chr20 #10716	0	0	1
10717	20	60,449,433	60,450,134	701	1	4.591	2.864	11.5	8	5	18	0	0	1	CDH4	622,224	in gene	ActReg chr20 #10717	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10718	20	60,450,530	60,451,413	883	1	4.926	4.889	13.037	7	8	20	0	0	1	CDH4	623,412	in gene	ActReg chr20 #10718	0	0	1
10719	20	60,456,045	60,456,934	889	1	4.714	5.643	13.286	8	9	18	1	0	1	CDH4	628,930	in gene	ActReg chr20 #10719	0	0	1
10720	20	60,470,830	60,471,716	886	1	4.821	7.071	11.679	11	14	15	0	0	1	CDH4	643,714	in gene	ActReg chr20 #10720	0	0	1
10721	20	60,472,807	60,473,394	587	1	4.556	5.111	14.333	9	10	21	0	0	1	CDH4	645,541	in gene	ActReg chr20 #10721	0	0	1
10722	20	60,477,166	60,477,734	568	1	6.944	4.611	12.333	13	9	21	0	0	1	CDH4	649,891	in gene	ActReg chr20 #10722	0	0	1
10723	20	60,485,318	60,485,893	575	1	3.778	5.389	13.611	5	11	22	0	0	1	CDH4	658,046	in gene	ActReg chr20 #10723	0	0	1
10724	20	60,499,739	60,500,564	825	1	7	6.538	14.846	14	12	22	0	0	1	CDH4	672,592	in gene	ActReg chr20 #10724	0	0	1
10725	20	60,505,929	60,506,455	526	1	6	3.188	12.438	9	7	21	0	0	1	CDH4	678,633	in gene	ActReg chr20 #10725	0	0	1
10726	20	60,509,005	60,509,597	592	1	5.778	4.667	11.389	8	8	16	0	0	1	CDH4	681,742	in gene	ActReg chr20 #10726	0	0	1
10727	20	60,516,189	60,517,579	1,390	1	5.744	4.293	12.364	9	8	19	0	0	1	CDH4	689,325	downstream	ActReg chr20 #10727	0	0	1
10728	20	60,528,342	60,529,157	815	1	5.577	5.423	11.115	8	9	16	0	1	1	MIR1257	-31	upstream	ActReg chr20 #10728	0	0	1
10729	20	60,545,171	60,545,803	632	1	13.2	10.15	5.421	18	17	11	2	0	1	TAF4	95,379	downstream	ActReg chr20 #10729	1	0	0
10730	20	60,578,680	60,579,256	576	1	3.5	4.111	12.833	5	6	20	0	0	1	TAF4	61,898	in gene	ActReg chr20 #10730	0	0	1
10731	20	60,589,003	60,589,881	878	1	4.63	4.593	12.444	7	8	20	0	0	1	TAF4	51,424	in gene	ActReg chr20 #10731	0	0	1
10732	20	60,604,771	60,605,437	666	1	2.75	5.75	12.05	4	8	18	0	0	1	TAF4	35,762	in gene	ActReg chr20 #10732	0	0	1
10733	20	60,636,139	60,636,515	376	1	3.667	7.4	10.917	7	10	15	0	0	1	TAF4	4,539	in gene	ActReg chr20 #10733	0	0	1
10734	20	60,642,689	60,643,086	397	1	5.833	6.333	11.833	8	8	17	0	1	1	TAF4	-2,021	upstream	ActReg chr20 #10734	0	0	1
10735	20	60,660,095	60,660,686	591	1	6	3.053	11.737	9	6	16	0	0	0				ActReg chr20 #10735	0	0	1
10736	20	60,693,574	60,694,095	521	1	4.312	3.5	13.938	5	5	20	0	1	1	LSM14B	-3,683	upstream	ActReg chr20 #10736	0	0	1
10737	20	60,708,016	60,708,705	689	1	4.682	2.81	13.091	7	5	23	0	0	2	LSM14B, PSMA7	10843, 10114	in gene, downstream	ActReg chr20 #10737	0	0	1
10738	20	60,710,727	60,711,263	536	1	4.062	5.75	13.688	5	9	21	0	0	3	LSM14B, PSMA7, SS18L1	13478, 7479, -7827	downstream, downstream, upstream	ActReg chr20 #10738	0	0	1
10739	20	60,719,149	60,719,810	661	1	8.684	12.714	7.778	16	21	16	1	2	3	LSM14B, PSMA7, SS18L1	21962, -1005, 657	downstream, upstream, in gene	ActReg chr20 #10739	0	1	0
10740	20	60,723,566	60,724,040	474	1	2.267	5	12.133	3	8	17	0	1	2	PSMA7, SS18L1	-5329, 4981	upstream, in gene	ActReg chr20 #10740	0	0	1
10741	20	60,757,448	60,758,606	1,158	3	13.417	16.028	11.686	27	30	26	1	1	2	SS18L1, GTPBP5	39205, -54	downstream, upstream	ActReg chr20 #10741	1	1	1
10742	20	60,776,197	60,776,671	474	1	4.929	5.786	13.5	8	8	19	1	0	1	GTPBP5	18,353	in gene	ActReg chr20 #10742	0	0	1
10743	20	60,791,636	60,792,615	979	1	5.821	6.387	11.677	10	11	15	1	0	1	HRH3	3,198	in gene	ActReg chr20 #10743	0	0	1
10744	20	60,793,041	60,794,193	1,152	1	4.778	6.444	13.056	9	10	19	1	1	1	HRH3	1,706	in gene	ActReg chr20 #10744	0	0	1
10745	20	60,797,265	60,798,046	781	1	4.208	5.833	11.292	7	9	14	0	1	2	HRH3, FLJ44790	-2332, -9361	upstream, upstream	ActReg chr20 #10745	0	0	1
10746	20	60,801,393	60,802,146	753	1	4	4.5	11.583	8	8	17	0	2	2	HRH3, FLJ44790	-6446, -5247	upstream, upstream	ActReg chr20 #10746	0	0	1
10747	20	60,807,215	60,807,741	526	1	5.125	5.071	13.375	8	8	17	0	2	2	FLJ44790, OSBPL2	462, -6102	in gene, upstream	ActReg chr20 #10747	0	0	1
10748	20	60,824,948	60,825,344	396	1	3.615	6.846	11.615	4	8	18	0	0	1	OSBPL2	11,566	in gene	ActReg chr20 #10748	0	0	1
10749	20	60,844,806	60,845,392	586	1	4.176	4.278	12.944	7	6	22	0	0	1	OSBPL2	31,519	in gene	ActReg chr20 #10749	0	0	1
10750	20	60,872,839	60,873,254	415	1	4.692	6.692	12.846	8	10	19	0	1	2	OSBPL2, ADRM1	59466, -4981	downstream, upstream	ActReg chr20 #10750	0	0	1
10751	20	60,876,885	60,878,244	1,359	2	13.721	14.628	7.784	25	39	16	1	1	3	OSBPL2, ADRM1, LAMA5	63984, -463, 64804	downstream, upstream, downstream	ActReg chr20 #10751	1	1	0
10752	20	60,878,465	60,880,647	2,182	1	8.397	11.735	9.868	15	18	20	1	1	3	OSBPL2, ADRM1, LAMA5	65976, 1529, 62812	downstream, in gene, downstream	ActReg chr20 #10752	0	1	0
10753	20	60,881,361	60,882,134	773	1	6.792	5.042	14.375	12	11	23	0	0	2	ADRM1, LAMA5	3720, 60621	in gene, downstream	ActReg chr20 #10753	0	0	1
10754	20	60,882,543	60,883,161	618	1	7.842	7.263	16.053	11	10	23	1	0	2	ADRM1, LAMA5	4825, 59516	in gene, downstream	ActReg chr20 #10754	0	0	1
10755	20	60,884,708	60,885,223	515	1	4.312	8.688	12	9	12	19	0	0	2	ADRM1, LAMA5	6938, 57403	downstream, in gene	ActReg chr20 #10755	0	0	1
10756	20	60,885,588	60,886,775	1,187	1	4.811	4.973	14.595	8	9	25	1	0	2	ADRM1, LAMA5	8154, 56187	downstream, in gene	ActReg chr20 #10756	0	0	1
10757	20	60,886,963	60,887,680	717	1	4.913	5.261	13.696	6	9	23	0	0	2	ADRM1, LAMA5	9294, 55047	downstream, in gene	ActReg chr20 #10757	0	0	1
10758	20	60,891,189	60,892,350	1,161	1	6.639	6.194	14.389	10	11	26	0	0	2	ADRM1, LAMA5	13742, 50599	downstream, in gene	ActReg chr20 #10758	0	0	1
10759	20	60,898,291	60,899,292	1,001	1	3.286	5.548	14.129	6	9	25	0	0	1	LAMA5	43,577	in gene	ActReg chr20 #10759	0	0	1
10760	20	60,902,623	60,904,178	1,555	1	4.184	3.634	12.367	9	8	19	0	0	1	LAMA5	38,968	in gene	ActReg chr20 #10760	0	0	1
10761	20	60,904,440	60,906,198	1,758	1	4.873	6.833	11.854	11	14	18	1	0	1	LAMA5	37,049	in gene	ActReg chr20 #10761	0	0	1
10762	20	60,906,363	60,906,990	627	1	5	7.55	13.2	7	11	19	1	0	1	LAMA5	35,692	in gene	ActReg chr20 #10762	0	0	1
10763	20	60,907,424	60,908,533	1,109	1	5	5.829	13	8	11	19	0	0	1	LAMA5	34,390	in gene	ActReg chr20 #10763	0	0	1
10764	20	60,908,968	60,909,780	812	1	4.8	4.36	15.2	9	8	21	0	0	1	LAMA5	32,994	in gene	ActReg chr20 #10764	0	0	1
10765	20	60,920,857	60,922,325	1,468	1	5.109	5.217	13.935	10	8	20	0	1	2	LAMA5, LOC100506553	20777, -6471	in gene, upstream	ActReg chr20 #10765	0	0	1
10766	20	60,925,072	60,925,782	710	1	4.045	6.273	11.5	6	12	15	0	1	2	LAMA5, LOC100506553	16941, -2635	in gene, upstream	ActReg chr20 #10766	0	0	1
10767	20	60,930,310	60,931,035	725	1	4	4.381	12.591	6	11	17	0	1	2	LAMA5, LOC100506553	11696, 2610	in gene, in gene	ActReg chr20 #10767	0	0	1
10768	20	60,931,591	60,932,654	1,063	1	7.939	5.697	11.667	13	11	16	0	0	2	LAMA5, LOC100506553	10246, 4060	in gene, downstream	ActReg chr20 #10768	0	0	1
10769	20	60,932,913	60,933,646	733	1	6.696	5.696	12.522	11	10	20	0	0	2	LAMA5, LOC100506553	9089, 5217	in gene, downstream	ActReg chr20 #10769	0	0	1
10770	20	60,933,794	60,934,532	738	1	4.773	8.087	12.739	14	12	19	0	0	2	LAMA5, LOC100506553	8205, 6101	in gene, downstream	ActReg chr20 #10770	0	0	1
10771	20	60,936,111	60,936,623	512	1	5.688	3.312	11.875	10	6	18	0	0	2	LAMA5, LOC100506553	6001, 8305	in gene, downstream	ActReg chr20 #10771	0	0	1
10772	20	60,942,547	60,943,743	1,196	1	7.892	8.811	15.973	12	12	24	1	1	1	LAMA5	-777	upstream	ActReg chr20 #10772	0	0	1
10773	20	60,944,048	60,944,573	525	1	8.562	9.312	12	11	14	20	0	1	1	LAMA5	-1,942	upstream	ActReg chr20 #10773	0	0	1
10774	20	60,944,819	60,945,530	711	1	9.727	10.136	11.591	15	14	17	0	1	1	LAMA5	-2,806	upstream	ActReg chr20 #10774	0	0	1
10775	20	60,945,632	60,946,724	1,092	1	5.667	5.686	11.6	12	10	17	0	1	1	LAMA5	-3,810	upstream	ActReg chr20 #10775	0	0	1
10776	20	60,948,934	60,949,571	637	1	5.4	8.35	11.75	10	11	18	1	1	1	LAMA5	-6,884	upstream	ActReg chr20 #10776	0	0	1
10777	20	60,953,314	60,953,838	524	1	5.312	7.438	12.312	8	11	19	1	0	2	RPS21, CABLES2	-8545, 28763	upstream, downstream	ActReg chr20 #10777	0	0	1
10778	20	60,961,448	60,962,265	817	2	11.04	12.32	13.92	19	20	24	1	1	2	RPS21, CABLES2	-265, 20483	upstream, downstream	ActReg chr20 #10778	0	1	1
10779	20	60,965,880	60,967,186	1,306	1	6.683	6.61	15.561	10	10	24	0	0	2	RPS21, CABLES2	4412, 15806	downstream, in gene	ActReg chr20 #10779	0	0	1
10780	20	60,967,625	60,968,733	1,108	1	4.529	5.441	15.235	7	11	22	0	0	2	RPS21, CABLES2	6058, 14160	downstream, in gene	ActReg chr20 #10780	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10781	20	60,971,213	60,972,895	1,682	1	4.288	6.173	14.538	9	12	23	1	0	2	RPS21, CABLES2	9933, 10285	downstream, in gene	ActReg chr20 #10781	0	0	1
10782	20	60,977,315	60,978,156	841	1	3.423	3.308	15.769	5	6	24	0	0	2	CABLES2, C20orf151	4604, 24894	in gene, downstream	ActReg chr20 #10782	0	0	1
10783	20	60,979,774	60,980,433	659	1	5.524	6.952	12.191	10	13	14	0	1	2	CABLES2, C20orf151	2236, 22526	in gene, downstream	ActReg chr20 #10783	0	0	1
10784	20	60,980,525	60,981,162	637	1	7.3	8	12.75	11	13	20	0	1	2	CABLES2, C20orf151	1496, 21786	in gene, downstream	ActReg chr20 #10784	0	0	1
10785	20	60,982,345	60,983,154	809	2	14.44	19.28	8.208	38	42	11	1	1	2	CABLES2, C20orf151	-410, 19880	upstream, downstream	ActReg chr20 #10785	1	1	0
10786	20	60,986,175	60,986,689	514	1	4.118	3.353	16.529	6	9	26	0	1	2	CABLES2, C20orf151	-4093, 16197	upstream, in gene	ActReg chr20 #10786	0	0	1
10787	20	60,987,488	60,988,345	857	1	6.519	5.037	13.37	9	8	18	0	1	2	CABLES2, C20orf151	-5577, 14713	upstream, in gene	ActReg chr20 #10787	0	0	1
10788	20	60,988,749	60,989,756	1,007	1	4.6	3.226	16.581	8	6	27	0	1	2	CABLES2, C20orf151	-6913, 13377	upstream, in gene	ActReg chr20 #10788	0	0	1
10789	20	60,989,973	60,991,200	1,227	1	5.179	4.237	14.846	10	9	23	0	0	2	CABLES2, C20orf151	-8247, 12043	upstream, in gene	ActReg chr20 #10789	0	0	1
10790	20	60,991,393	60,992,341	948	1	4.054	6.517	13.345	8	12	19	1	0	2	CABLES2, C20orf151	-9528, 10762	upstream, in gene	ActReg chr20 #10790	0	0	1
10791	20	60,994,278	60,995,349	1,071	1	5.152	3.939	13.97	9	7	19	0	0	1	C20orf151	7,816	in gene	ActReg chr20 #10791	0	0	1
10792	20	60,997,844	60,998,309	465	1	6.2	4.4	13.4	8	7	21	0	0	1	C20orf151	4,553	in gene	ActReg chr20 #10792	0	0	1
10793	20	60,999,754	61,000,994	1,240	1	4.949	3.846	13.974	10	7	20	0	1	1	C20orf151	2,255	in gene	ActReg chr20 #10793	0	0	1
10794	20	61,001,448	61,002,662	1,214	1	3.895	3.027	12.5	7	6	17	0	1	1	C20orf151	574	in gene	ActReg chr20 #10794	0	0	1
10795	20	61,004,094	61,004,909	815	1	4.038	5.192	13.423	7	8	19	0	1	1	C20orf151	-1,872	upstream	ActReg chr20 #10795	0	0	1
10796	20	61,012,851	61,013,819	968	1	4.5	1.893	15.833	9	5	26	0	0	0				ActReg chr20 #10796	0	0	1
10797	20	61,016,316	61,017,286	970	1	5.968	5.774	11.258	12	9	15	0	0	0				ActReg chr20 #10797	0	0	1
10798	20	61,020,361	61,021,183	822	1	3.909	5.96	11.04	7	9	15	0	0	0				ActReg chr20 #10798	0	0	1
10799	20	61,021,495	61,022,138	643	1	5.15	4.5	12	8	8	16	0	0	0				ActReg chr20 #10799	0	0	1
10800	20	61,023,683	61,024,453	770	1	3.708	4.833	12.542	6	9	18	0	0	0				ActReg chr20 #10800	0	0	1
10801	20	61,032,912	61,034,267	1,355	1	4.25	5.69	13.786	10	8	21	0	0	1	GATA5	17,457	downstream	ActReg chr20 #10801	0	0	1
10802	20	61,039,110	61,039,814	704	1	6.318	3.476	13.227	10	6	19	0	0	1	GATA5	11,564	in gene	ActReg chr20 #10802	0	0	1
10803	20	61,041,002	61,041,694	692	1	4.81	5.667	13.857	7	10	20	1	0	1	GATA5	9,678	in gene	ActReg chr20 #10803	0	0	1
10804	20	61,043,347	61,044,139	792	1	3.211	2.833	13.24	8	5	17	0	0	1	GATA5	7,283	in gene	ActReg chr20 #10804	0	0	1
10805	20	61,045,619	61,046,245	626	1	3.3	3.1	13.8	6	5	19	0	0	1	GATA5	5,094	in gene	ActReg chr20 #10805	0	0	1
10806	20	61,047,188	61,047,648	460	1	3.533	4.667	12.467	7	6	18	0	0	1	GATA5	3,608	in gene	ActReg chr20 #10806	0	0	1
10807	20	61,050,399	61,050,818	419	1	1.538	6.857	10.286	3	9	17	1	1	1	GATA5	418	in gene	ActReg chr20 #10807	0	0	1
10808	20	61,051,188	61,051,710	522	1	5.562	5.5	10.438	10	8	12	1	1	1	GATA5	-423	upstream	ActReg chr20 #10808	0	0	1
10809	20	61,055,372	61,056,147	775	1	4.75	3.333	12.042	8	5	17	0	1	1	GATA5	-4,733	upstream	ActReg chr20 #10809	0	0	1
10810	20	61,058,604	61,060,366	1,762	1	4.673	7.364	13.673	8	11	26	0	0	1	GATA5	-8,459	upstream	ActReg chr20 #10810	0	0	1
10811	20	61,064,526	61,065,805	1,279	1	5.325	7.475	12.775	9	10	18	0	0	0				ActReg chr20 #10811	0	0	1
10812	20	61,067,528	61,068,826	1,298	1	5.45	4.263	15.25	10	9	22	0	0	0				ActReg chr20 #10812	0	0	1
10813	20	61,070,788	61,071,594	806	1	4.64	6.32	13	10	9	17	0	0	0				ActReg chr20 #10813	0	0	1
10814	20	61,071,601	61,072,626	1,025	1	3.103	4.469	11.344	6	8	17	0	0	0				ActReg chr20 #10814	0	0	1
10815	20	61,076,612	61,078,153	1,541	1	6.208	12.208	8.667	12	18	17	0	0	0				ActReg chr20 #10815	0	1	0
10816	20	61,082,319	61,082,826	507	1	1	2.312	12.062	1	5	17	0	0	0				ActReg chr20 #10816	0	0	1
10817	20	61,142,932	61,143,412	480	1	4.533	3.933	12.467	8	6	19	0	1	3	C20orf200, C20orf166, MIR1-1	5596, -4488, -8341	in gene, upstream, upstream	ActReg chr20 #10817	0	0	1
10818	20	61,144,004	61,144,719	715	1	7.682	3.818	13.046	15	6	20	0	2	3	C20orf200, C20orf166, MIR1-1	4407, -3299, -7152	in gene, upstream, upstream	ActReg chr20 #10818	0	0	1
10819	20	61,144,835	61,145,281	446	1	5.5	3.714	11.071	6	8	15	0	2	3	C20orf200, C20orf166, MIR1-1	3710, -2602, -6455	in gene, upstream, upstream	ActReg chr20 #10819	0	0	1
10820	20	61,145,825	61,146,516	691	1	4.429	4.714	14	7	7	21	0	3	3	C20orf200, C20orf166, MIR1-1	2598, -1490, -5343	in gene, upstream, upstream	ActReg chr20 #10820	0	0	1
10821	20	61,151,852	61,153,229	1,377	1	5.674	7.093	13.372	9	14	20	1	2	4	C20orf200, C20orf166, MIR1-1, MIR133A2	-3772, 4880, 1027, -9579	upstream, in gene, downstream, upstream	ActReg chr20 #10821	0	0	1
10822	20	61,154,605	61,155,870	1,265	1	4.436	7.436	13.974	8	13	21	0	2	4	C20orf200, C20orf166, MIR1-1, MIR133A2	-6469, 7577, 3724, -6882	upstream, in gene, downstream, upstream	ActReg chr20 #10822	0	0	1
10823	20	61,158,021	61,158,878	857	1	3.542	6.615	14.577	7	10	19	0	1	4	C20orf200, C20orf166, MIR1-1, MIR133A2	-9681, 10789, 6936, -3670	upstream, in gene, downstream, upstream	ActReg chr20 #10823	0	0	1
10824	20	61,162,532	61,163,855	1,323	1	4.488	5.154	13.171	7	9	18	0	1	3	C20orf166, MIR133A2, LOC100131174	15533, 1074, -9604	in gene, downstream, upstream	ActReg chr20 #10824	0	0	1
10825	20	61,171,580	61,172,388	808	1	4.462	8.538	15.962	8	14	24	0	1	3	C20orf166, MIR133A2, LOC100131174	24324, 9865, -813	downstream, downstream, upstream	ActReg chr20 #10825	0	0	1
10826	20	61,172,772	61,174,664	1,892	3	10.017	11.559	8.186	24	27	15	0	1	2	C20orf166, LOC100131174	26058, 921	downstream, in gene	ActReg chr20 #10826	1	1	1
10827	20	61,177,381	61,178,028	647	1	8.15	6.053	12.9	13	10	18	0	0	2	C20orf166, LOC100131174	30044, 4907	downstream, downstream	ActReg chr20 #10827	0	0	1
10828	20	61,200,138	61,201,522	1,384	2	7.349	13.628	9.14	13	23	18	1	0	0				ActReg chr20 #10828	0	1	1
10829	20	61,203,952	61,204,453	501	1	4.692	3.5	12.188	8	5	17	0	0	0				ActReg chr20 #10829	0	0	1
10830	20	61,265,715	61,266,297	582	1	4.353	3.278	14.444	7	7	21	0	1	3	LOC100505735, RP11-93B14.6, SLCO4A1	882, 8650, -7791	in gene, downstream, upstream	ActReg chr20 #10830	0	0	1
10831	20	61,266,450	61,267,005	555	1	5.235	5.294	14.882	10	7	24	0	2	3	LOC100505735, RP11-93B14.6, SLCO4A1	1603, 7929, -7070	in gene, downstream, upstream	ActReg chr20 #10831	0	0	1
10832	20	61,272,260	61,272,869	609	1	4.053	8.737	12.895	8	12	18	0	2	3	LOC100505735, RP11-93B14.6, SLCO4A1	7440, 2092, -1233	downstream, in gene, upstream	ActReg chr20 #10832	0	0	1
10833	20	61,274,319	61,275,075	756	1	7.333	9.667	13.667	16	14	23	1	2	3	LOC100505735, RP11-93B14.6, SLCO4A1	9573, -41, 900	downstream, upstream, in gene	ActReg chr20 #10833	0	0	1
10834	20	61,284,165	61,284,796	631	1	5.895	9	13.895	9	13	21	0	0	3	RP11-93B14.6, SLCO4A1, hCG_2018279	-9824, 10683, 13493	upstream, in gene, downstream	ActReg chr20 #10834	0	0	1
10835	20	61,286,953	61,287,526	573	1	8.944	5.167	12.167	12	8	20	0	0	2	SLCO4A1, hCG_2018279	13442, 10734	in gene, downstream	ActReg chr20 #10835	0	0	1
10836	20	61,287,748	61,288,596	848	1	6.5	9.462	16.923	15	17	27	1	0	2	SLCO4A1, hCG_2018279	14375, 9801	in gene, downstream	ActReg chr20 #10836	0	0	1
10837	20	61,288,625	61,289,111	486	1	9.533	8.733	12.8	14	10	19	1	0	2	SLCO4A1, hCG_2018279	15071, 9105	in gene, downstream	ActReg chr20 #10837	0	0	1
10838	20	61,297,563	61,300,782	3,219	3	11.109	15.723	10.792	20	26	25	0	1	2	SLCO4A1, hCG_2018279	25375, -1199	in gene, upstream	ActReg chr20 #10838	1	1	1
10839	20	61,316,056	61,316,501	445	1	5.071	5.643	12.286	9	10	21	0	0	0				ActReg chr20 #10839	0	0	1
10840	20	61,318,505	61,319,375	870	1	5.889	8.593	13.333	11	14	24	0	0	0				ActReg chr20 #10840	0	0	1
10841	20	61,333,012	61,333,727	715	1	6.182	7.136	13.454	11	12	19	0	1	1	NTSR1	-6,820	upstream	ActReg chr20 #10841	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10842	20	61,334,335	61,336,340	2,005	1	11.048	15.079	9.286	21	26	17	0	1	1	NTSR1	-4,852	upstream	ActReg chr20 #10842	0	1	0
10843	20	61,342,958	61,343,590	632	1	5.6	5.7	11.05	10	10	18	0	0	1	NTSR1	3,085	in gene	ActReg chr20 #10843	0	0	1
10844	20	61,343,723	61,344,571	848	1	4.231	6.731	12.039	7	8	22	0	0	1	NTSR1	3,958	in gene	ActReg chr20 #10844	0	0	1
10845	20	61,348,001	61,348,671	670	1	6.9	6.7	12.65	11	9	21	0	0	1	NTSR1	8,147	in gene	ActReg chr20 #10845	0	0	1
10846	20	61,355,116	61,355,803	687	1	6.353	5.286	13.952	11	7	19	0	0	1	NTSR1	15,270	in gene	ActReg chr20 #10846	0	0	1
10847	20	61,358,850	61,359,417	567	1	4	6.529	15.412	6	11	25	0	0	1	NTSR1	18,944	in gene	ActReg chr20 #10847	0	0	1
10848	20	61,370,733	61,373,665	2,932	3	12.413	14.272	8.315	24	31	18	0	0	1	NTSR1	32,010	in gene	ActReg chr20 #10848	1	1	1
10849	20	61,374,973	61,375,518	545	1	4.294	5	15.765	6	10	23	0	0	1	NTSR1	35,056	in gene	ActReg chr20 #10849	0	0	1
10850	20	61,393,644	61,394,222	578	1	3	5	11.833	5	7	14	0	0	1	NTSR1	53,744	in gene	ActReg chr20 #10850	0	0	1
10851	20	61,394,628	61,395,363	735	1	2.273	6.043	12.217	6	10	17	0	0	1	NTSR1	54,806	downstream	ActReg chr20 #10851	0	0	1
10852	20	61,396,122	61,396,665	543	1	5.353	4	14.647	7	7	22	0	0	1	NTSR1	56,204	downstream	ActReg chr20 #10852	0	0	1
10853	20	61,406,199	61,407,024	825	1	5.769	7.038	10.577	10	11	14	0	1	1	LOC100505843	-2,459	upstream	ActReg chr20 #10853	0	0	1
10854	20	61,407,404	61,408,084	680	1	6.714	7.81	11.857	12	11	18	0	1	1	LOC100505843	-1,326	upstream	ActReg chr20 #10854	0	0	1
10855	20	61,417,672	61,418,334	662	1	7.65	6.7	16.9	12	10	25	0	0	2	LOC100505843, C20orf20	8933, -9802	downstream, upstream	ActReg chr20 #10855	0	0	1
10856	20	61,420,100	61,420,927	827	1	5.64	4.48	12.76	8	10	21	0	1	1	C20orf20	-7,292	upstream	ActReg chr20 #10856	0	0	1
10857	20	61,424,889	61,425,770	881	1	10.821	11.286	14.607	17	16	21	0	1	1	C20orf20	-2,476	upstream	ActReg chr20 #10857	0	0	1
10858	20	61,425,865	61,427,264	1,399	2	10.091	11.886	10.454	18	24	22	1	1	2	C20orf20, OGFR	-1241, -9613	upstream, upstream	ActReg chr20 #10858	0	1	1
10859	20	61,441,041	61,442,487	1,446	1	4.205	6.533	13.644	7	13	26	0	1	3	C20orf20, OGFR, COL9A3	13959, 5587, -6650	downstream, in gene, upstream	ActReg chr20 #10859	0	0	1
10860	20	61,443,971	61,444,606	635	1	6.053	7	15.684	11	12	20	1	1	2	OGFR, COL9A3	8111, -4126	in gene, upstream	ActReg chr20 #10860	0	0	1
10861	20	61,445,441	61,445,957	516	1	6.875	11.062	13.938	9	15	19	0	1	2	OGFR, COL9A3	9522, -2715	downstream, upstream	ActReg chr20 #10861	0	0	1
10862	20	61,447,551	61,448,275	724	1	7.591	8.435	15.435	14	12	24	1	1	2	OGFR, COL9A3	11736, -501	downstream, upstream	ActReg chr20 #10862	0	0	1
10863	20	61,448,394	61,450,735	2,341	2	9.041	12.836	11	17	19	19	1	1	2	OGFR, COL9A3	13387, 1150	downstream, in gene	ActReg chr20 #10863	0	1	1
10864	20	61,451,086	61,452,514	1,428	1	8.556	9.489	13.578	15	18	21	0	0	2	OGFR, COL9A3	15623, 3386	downstream, in gene	ActReg chr20 #10864	0	0	1
10865	20	61,452,721	61,453,504	783	1	7	5.24	11.88	12	9	17	0	0	2	OGFR, COL9A3	16935, 4698	downstream, in gene	ActReg chr20 #10865	0	0	1
10866	20	61,457,376	61,458,493	1,117	1	3.771	6.371	11.771	7	11	17	0	0	1	COL9A3	9,520	in gene	ActReg chr20 #10866	0	0	1
10867	20	61,458,827	61,459,478	651	1	3.25	5.6	12.75	5	10	16	0	0	1	COL9A3	10,738	in gene	ActReg chr20 #10867	0	0	1
10868	20	61,460,079	61,461,395	1,316	1	6.073	5.049	12.512	10	10	21	0	0	1	COL9A3	12,323	in gene	ActReg chr20 #10868	0	0	1
10869	20	61,471,599	61,472,294	695	1	5.364	8.773	13.318	9	12	22	1	1	3	COL9A3, TCFL5, DPH3B	23532, 21169, -4530	in gene, downstream, upstream	ActReg chr20 #10869	0	0	1
10870	20	61,511,546	61,512,025	479	1	7.067	3.933	12.267	10	7	19	1	0	1	DIDO1	57,519	in gene	ActReg chr20 #10870	0	0	1
10871	20	61,512,275	61,512,853	578	1	5.278	3.5	14.444	10	8	23	1	0	1	DIDO1	56,740	in gene	ActReg chr20 #10871	0	0	1
10872	20	61,512,898	61,513,498	600	1	7	4.611	11.278	12	9	14	1	0	1	DIDO1	56,106	in gene	ActReg chr20 #10872	0	0	1
10873	20	61,542,513	61,542,933	420	1	6.077	6.846	13.308	8	9	18	1	0	1	DIDO1	26,581	in gene	ActReg chr20 #10873	0	0	1
10874	20	61,556,716	61,557,567	851	1	6.885	10.808	7.385	11	16	12	1	0	1	DIDO1	12,163	in gene	ActReg chr20 #10874	0	1	0
10875	20	61,568,599	61,569,478	879	3	11.857	10.593	11.667	20	18	20	1	2	2	DIDO1, C20orf11	266, -403	in gene, upstream	ActReg chr20 #10875	1	1	1
10876	20	61,569,634	61,570,453	819	1	7.68	11.92	6.818	12	17	12	1	2	2	DIDO1, C20orf11	-739, 602	upstream, in gene	ActReg chr20 #10876	0	1	0
10877	20	61,585,132	61,585,846	714	1	5.727	9	11.454	9	12	16	0	1	2	C20orf11, SLC17A9	16048, 1490	downstream, in gene	ActReg chr20 #10877	0	0	1
10878	20	61,587,509	61,588,485	976	1	2.222	4.774	11.935	4	9	18	0	0	2	C20orf11, SLC17A9	18556, 3998	downstream, in gene	ActReg chr20 #10878	0	0	1
10879	20	61,592,662	61,593,474	812	1	3.654	4.231	11.192	7	8	18	0	0	1	SLC17A9	9,069	in gene	ActReg chr20 #10879	0	0	1
10880	20	61,594,296	61,595,454	1,158	1	4.861	4.886	13.389	8	8	22	0	0	1	SLC17A9	10,876	in gene	ActReg chr20 #10880	0	0	1
10881	20	61,603,864	61,604,765	901	1	6.821	5.429	14	12	10	21	0	0	1	SLC17A9	20,315	downstream	ActReg chr20 #10881	0	0	1
10882	20	61,609,356	61,610,193	837	1	6.346	2.958	10.385	10	6	14	0	0	1	SLC17A9	25,775	downstream	ActReg chr20 #10882	0	0	1
10883	20	61,611,184	61,611,973	789	1	5.476	4.72	13.56	12	9	19	0	0	0				ActReg chr20 #10883	0	0	1
10884	20	61,612,736	61,613,296	560	1	4	6	12.333	7	8	15	0	0	0				ActReg chr20 #10884	0	0	1
10885	20	61,627,138	61,627,787	649	1	4.7	4.35	13.6	8	7	19	0	0	1	BHLHE23	10,925	downstream	ActReg chr20 #10885	0	0	1
10886	20	61,636,925	61,637,786	861	1	6.852	6.852	16.296	10	12	27	1	2	2	BHLHE23, LOC63930	1032, -3380	in gene, upstream	ActReg chr20 #10886	0	0	1
10887	20	61,639,546	61,641,550	2,004	1	4.952	5.667	11.905	11	11	16	1	2	2	BHLHE23, LOC63930	-2161, -187	upstream, upstream	ActReg chr20 #10887	0	0	1
10888	20	61,648,511	61,649,884	1,373	1	5.767	5.465	13.302	15	10	21	0	0	1	LOC63930	8,462	in gene	ActReg chr20 #10888	0	0	1
10889	20	61,656,887	61,657,830	943	1	5.133	8.933	12.633	9	16	16	0	0	2	LOC63930, NCRNA00029	16623, 11022	in gene, downstream	ActReg chr20 #10889	0	0	1
10890	20	61,661,834	61,662,368	534	1	3.824	6.529	11.706	6	12	15	0	1	3	LOC63930, NCRNA00029, LOC100144597	21366, 6279, -7262	in gene, downstream, upstream	ActReg chr20 #10890	0	0	1
10891	20	61,666,405	61,667,179	774	1	4.087	5.542	15.667	9	9	23	1	2	3	LOC63930, NCRNA00029, LOC100144597	26057, 1588, -2571	in gene, in gene, upstream	ActReg chr20 #10891	0	0	1
10892	20	61,687,087	61,687,718	631	1	5.4	7.1	14.7	9	10	26	0	0	2	LOC63930, LOC100144597	46667, 18039	in gene, downstream	ActReg chr20 #10892	0	0	1
10893	20	61,687,912	61,688,417	505	1	2.8	6.312	12.938	5	9	21	0	0	2	LOC63930, LOC100144597	47429, 18801	in gene, downstream	ActReg chr20 #10893	0	0	1
10894	20	61,692,057	61,692,570	513	1	8.188	8.062	12.25	11	12	18	0	0	2	LOC63930, LOC100144597	51578, 22950	in gene, downstream	ActReg chr20 #10894	0	0	1
10895	20	61,700,913	61,701,672	759	2	11.833	15.917	4.682	21	35	9	0	0	1	LOC63930	60,557	in gene	ActReg chr20 #10895	1	1	0
10896	20	61,704,567	61,705,181	614	1	3.5	6.632	10.79	7	10	14	0	0	1	LOC63930	64,139	in gene	ActReg chr20 #10896	0	0	1
10897	20	61,712,575	61,714,670	2,095	4	14.591	19	10.697	43	47	18	0	0	1	LOC63930	72,857	in gene	ActReg chr20 #10897	1	1	1
10898	20	61,715,187	61,715,971	784	1	4.36	6.76	12.36	8	11	17	0	0	1	LOC63930	74,844	in gene	ActReg chr20 #10898	0	0	1
10899	20	61,716,442	61,717,167	725	1	4	4.609	12.87	10	8	18	0	0	2	LOC63930, HAR1B	76069, 16867	downstream, downstream	ActReg chr20 #10899	0	0	1
10900	20	61,718,090	61,718,610	520	1	7.375	6.438	12.375	11	10	18	1	0	2	LOC63930, HAR1B	77615, 15321	downstream, downstream	ActReg chr20 #10900	0	0	1
10901	20	61,723,113	61,724,016	903	1	5.286	6.423	13.714	9	13	21	0	0	3	LOC63930, HAR1B, HAR1A	82829, 10107, -9080	downstream, downstream, upstream	ActReg chr20 #10901	0	0	1
10902	20	61,728,179	61,728,957	778	1	3.682	3.875	11.542	5	8	17	0	1	2	HAR1B, HAR1A	5103, -4076	in gene, upstream	ActReg chr20 #10902	0	0	1
10903	20	61,732,007	61,732,767	760	1	4.913	2.429	13.217	8	5	21	0	2	2	HAR1B, HAR1A	1284, -257	in gene, upstream	ActReg chr20 #10903	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10904	20	61,733,157	61,733,876	719	1	9.364	12.864	11.546	14	17	17	1	2	2	HAR1B, HAR1A	155, 872	in gene, in gene	ActReg chr20 #10904	0	0	1
10905	20	61,735,861	61,736,379	518	1	2.062	5.688	13.625	4	9	18	0	1	2	HAR1B, HAR1A	-2449, 3476	upstream, downstream	ActReg chr20 #10905	0	0	1
10906	20	61,737,025	61,737,745	720	1	3.909	5.682	12.136	7	6	18	0	1	2	HAR1B, HAR1A	-3714, 4741	upstream, downstream	ActReg chr20 #10906	0	0	1
10907	20	61,738,520	61,739,003	483	1	4.6	5.133	12.6	8	8	16	0	1	2	HAR1B, HAR1A	-5090, 6117	upstream, downstream	ActReg chr20 #10907	0	0	1
10908	20	61,747,157	61,748,390	1,233	1	8.564	13.128	6.923	14	22	11	0	0	0				ActReg chr20 #10908	0	1	0
10909	20	61,749,473	61,750,200	727	1	6.818	9.591	11.227	10	15	14	0	0	0				ActReg chr20 #10909	0	0	1
10910	20	61,765,044	61,766,026	982	1	4.567	5.704	12.065	10	9	20	0	0	0				ActReg chr20 #10910	0	0	1
10911	20	61,780,157	61,780,682	525	1	3.941	4.176	11.471	6	7	19	0	0	0				ActReg chr20 #10911	0	0	1
10912	20	61,781,997	61,782,421	424	1	3.923	5.308	12.077	5	8	18	0	0	0				ActReg chr20 #10912	0	0	1
10913	20	61,783,552	61,784,838	1,286	1	3.39	6.61	12.683	5	11	22	0	0	0				ActReg chr20 #10913	0	0	1
10914	20	61,791,260	61,791,891	631	1	4.3	4.25	14.75	7	7	19	0	0	0				ActReg chr20 #10914	0	0	1
10915	20	61,798,968	61,799,533	565	1	5.556	4.562	11.333	9	9	17	0	0	0				ActReg chr20 #10915	0	0	1
10916	20	61,807,357	61,808,512	1,155	1	5.162	8.27	11.946	11	15	17	1	1	1	MIR124-3	-1,918	upstream	ActReg chr20 #10916	0	0	1
10917	20	61,813,898	61,814,656	758	1	7.042	4.208	14.417	11	9	24	0	0	1	MIR124-3	4,425	downstream	ActReg chr20 #10917	0	0	1
10918	20	61,821,939	61,822,799	860	1	2.852	2.045	13.518	5	5	22	1	0	1	YTHDF1	25,169	downstream	ActReg chr20 #10918	0	0	1
10919	20	61,847,602	61,848,378	776	1	9.708	12.25	12.333	16	18	22	1	1	1	YTHDF1	-452	upstream	ActReg chr20 #10919	0	0	1
10920	20	61,866,773	61,868,008	1,235	1	5.692	7.487	14.769	10	12	31	0	2	3	BIRC7, MIR3196, NKAIN4	114, -2741, 18502	in gene, upstream, downstream	ActReg chr20 #10920	0	0	1
10921	20	61,877,966	61,878,601	635	1	2.85	6.6	16.45	7	12	25	1	1	4	BIRC7, MIR3196, NKAIN4, FLJ16779	11007, 8152, 7609, -7047	downstream, downstream, in gene, upstream	ActReg chr20 #10921	0	0	1
10922	20	61,878,963	61,879,867	904	1	5.214	6.214	14.107	8	11	20	0	1	4	BIRC7, MIR3196, NKAIN4, FLJ16779	12139, 9284, 6477, -5915	downstream, downstream, in gene, upstream	ActReg chr20 #10922	0	0	1
10923	20	61,886,090	61,886,915	825	1	4.308	5.308	15.308	7	8	22	1	2	2	NKAIN4, FLJ16779	-610, 1172	upstream, in gene	ActReg chr20 #10923	0	0	1
10924	20	61,891,632	61,892,713	1,081	1	5.5	4.412	15.206	9	8	25	0	1	2	NKAIN4, FLJ16779	-6280, 6842	upstream, in gene	ActReg chr20 #10924	0	0	1
10925	20	61,916,988	61,917,832	844	1	4.444	5.963	12.556	8	10	16	1	2	3	ARFGAP1, MIR4326, COL20A1	13245, -750, -7128	in gene, upstream, upstream	ActReg chr20 #10925	0	0	1
10926	20	61,921,836	61,922,811	975	1	4.2	7	11.133	8	10	16	0	1	3	ARFGAP1, MIR4326, COL20A1	18158, 4163, -2215	downstream, downstream, upstream	ActReg chr20 #10926	0	0	1
10927	20	61,925,944	61,926,755	811	1	6.962	4.615	13.154	15	7	23	0	1	3	ARFGAP1, MIR4326, COL20A1	22184, 8189, 1811	downstream, downstream, in gene	ActReg chr20 #10927	0	0	1
10928	20	61,928,207	61,928,639	432	1	2.308	4.923	11.846	3	6	18	0	0	3	ARFGAP1, MIR4326, COL20A1	24258, 10263, 3885	downstream, downstream, in gene	ActReg chr20 #10928	0	0	1
10929	20	61,937,987	61,938,786	799	1	4.48	5.52	12.36	7	8	19	0	0	1	COL20A1	13,848	in gene	ActReg chr20 #10929	0	0	1
10930	20	61,940,654	61,942,122	1,468	1	4.196	5.848	12.674	7	10	19	0	0	1	COL20A1	16,850	in gene	ActReg chr20 #10930	0	0	1
10931	20	61,942,857	61,943,292	435	1	4.308	3.333	13.846	8	5	19	0	0	1	COL20A1	18,536	in gene	ActReg chr20 #10931	0	0	1
10932	20	61,951,803	61,952,351	548	1	3	8	12.647	5	10	18	0	0	1	COL20A1	27,539	in gene	ActReg chr20 #10932	0	0	1
10933	20	61,952,839	61,954,096	1,257	1	3.865	6.333	13.256	7	9	19	1	0	1	COL20A1	28,929	in gene	ActReg chr20 #10933	0	0	1
10934	20	61,957,723	61,958,467	744	1	4.042	3.792	13.625	8	7	21	0	0	1	COL20A1	33,557	in gene	ActReg chr20 #10934	0	0	1
10935	20	61,961,457	61,962,115	658	1	3.143	5.095	11.571	5	9	15	0	0	1	COL20A1	37,248	in gene	ActReg chr20 #10935	0	0	1
10936	20	61,974,592	61,975,329	737	1	3.333	4.458	14.667	6	6	25	0	0	1	CHRNA4	17,735	in gene	ActReg chr20 #10936	0	0	1
10937	20	61,976,328	61,977,254	926	1	3	3.345	12.862	6	8	17	0	0	1	CHRNA4	15,904	in gene	ActReg chr20 #10937	0	0	1
10938	20	61,977,808	61,978,477	669	1	3.105	5.238	11.286	5	11	17	1	0	1	CHRNA4	14,555	in gene	ActReg chr20 #10938	0	0	1
10939	20	61,978,501	61,979,996	1,495	1	3.044	4.37	13.891	6	9	22	1	0	1	CHRNA4	13,447	in gene	ActReg chr20 #10939	0	0	1
10940	20	61,980,983	61,981,583	600	1	5.316	3.667	12.526	7	6	17	1	0	1	CHRNA4	11,412	in gene	ActReg chr20 #10940	0	0	1
10941	20	61,982,756	61,983,638	882	1	4.519	4.111	12.741	8	6	18	0	0	1	CHRNA4	9,498	in gene	ActReg chr20 #10941	0	0	1
10942	20	61,987,842	61,988,323	481	1	4.067	5.8	14.933	6	8	26	0	0	1	CHRNA4	4,613	in gene	ActReg chr20 #10942	0	0	1
10943	20	61,989,344	61,990,044	700	1	3.35	5	12.182	6	6	20	0	0	1	CHRNA4	3,001	in gene	ActReg chr20 #10943	0	0	1
10944	20	61,990,467	61,991,074	607	1	2.316	4.737	12.895	5	7	16	0	0	1	CHRNA4	1,925	in gene	ActReg chr20 #10944	0	0	1
10945	20	61,993,031	61,993,655	624	1	5.211	4.474	13.895	8	7	26	1	1	1	CHRNA4	-648	upstream	ActReg chr20 #10945	0	0	1
10946	20	61,997,919	61,998,521	602	1	4.368	4.737	12.79	8	7	19	0	1	1	CHRNA4	-5,525	upstream	ActReg chr20 #10946	0	0	1
10947	20	62,004,961	62,005,561	600	1	4.111	4.667	11.611	7	8	14	0	0	0				ActReg chr20 #10947	0	0	1
10948	20	62,006,128	62,006,801	673	1	5	5.762	12.333	9	9	20	0	0	0				ActReg chr20 #10948	0	0	1
10949	20	62,010,604	62,011,123	519	1	3.938	7.375	13.188	11	12	20	0	0	0				ActReg chr20 #10949	0	0	1
10950	20	62,017,508	62,018,405	897	1	3.429	4.28	11	6	7	14	0	0	0				ActReg chr20 #10950	0	0	1
10951	20	62,024,241	62,024,997	756	1	4.833	1.9	12.958	10	6	18	0	0	0				ActReg chr20 #10951	0	0	1
10952	20	62,031,014	62,031,894	880	1	3.667	4.704	13.185	6	8	18	1	0	1	KCNQ2	72,539	downstream	ActReg chr20 #10952	0	0	1
10953	20	62,035,741	62,036,322	581	1	4.941	4.474	14.684	9	6	22	0	0	1	KCNQ2	67,962	downstream	ActReg chr20 #10953	0	0	1
10954	20	62,036,685	62,037,767	1,082	1	3.303	4.559	12.706	8	9	19	2	0	1	KCNQ2	66,767	downstream	ActReg chr20 #10954	0	0	1
10955	20	62,039,210	62,039,710	500	1	4.733	2.2	12.133	7	3	17	0	0	1	KCNQ2	64,533	in gene	ActReg chr20 #10955	0	0	1
10956	20	62,041,309	62,042,075	766	1	3.238	4.5	14.208	6	8	24	0	0	1	KCNQ2	62,301	in gene	ActReg chr20 #10956	0	0	1
10957	20	62,042,089	62,042,837	748	1	5.174	4.043	11.391	10	8	17	0	0	1	KCNQ2	61,530	in gene	ActReg chr20 #10957	0	0	1
10958	20	62,048,652	62,049,615	963	1	4.967	7.933	15.4	10	14	21	0	0	1	KCNQ2	54,860	in gene	ActReg chr20 #10958	0	0	1
10959	20	62,050,208	62,050,974	766	1	4.458	3.958	12.667	6	6	18	0	0	1	KCNQ2	53,402	in gene	ActReg chr20 #10959	0	0	1
10960	20	62,052,533	62,053,645	1,112	1	2.6	4.057	13.943	6	8	20	1	0	1	KCNQ2	50,904	in gene	ActReg chr20 #10960	0	0	1
10961	20	62,060,994	62,061,712	718	1	3.81	6.545	12.364	7	9	14	0	0	1	KCNQ2	42,840	in gene	ActReg chr20 #10961	0	0	1
10962	20	62,070,758	62,072,116	1,358	1	4.692	4.095	15.5	10	9	25	0	0	1	KCNQ2	32,556	in gene	ActReg chr20 #10962	0	0	1
10963	20	62,083,020	62,084,104	1,084	1	4.324	4.118	12.206	10	6	21	0	0	1	KCNQ2	20,431	in gene	ActReg chr20 #10963	0	0	1
10964	20	62,086,044	62,086,815	771	1	5.417	5.75	11.958	11	9	15	1	0	1	KCNQ2	17,564	in gene	ActReg chr20 #10964	0	0	1
10965	20	62,089,463	62,090,152	689	1	8.591	7.091	13.046	13	10	19	0	0	1	KCNQ2	14,186	in gene	ActReg chr20 #10965	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
10966	20	62,094,915	62,095,958	1,043	1	5.094	7.188	13.344	8	12	24	0	0	1	KCNQ2	8,557	in gene	ActReg chr20 #10966	0	0	1
10967	20	62,096,783	62,097,858	1,075	1	4.375	4.794	12.147	7	12	15	1	0	1	KCNQ2	6,673	in gene	ActReg chr20 #10967	0	0	1
10968	20	62,101,085	62,102,857	1,772	1	5.818	4.875	13.625	12	8	21	1	1	1	KCNQ2	2,022	in gene	ActReg chr20 #10968	0	0	1
10969	20	62,104,521	62,105,316	795	1	5.88	7.52	13.8	8	14	22	0	1	1	KCNQ2	-925	upstream	ActReg chr20 #10969	0	0	1
10970	20	62,106,367	62,107,013	646	1	12.191	10.286	8.762	21	15	12	0	1	1	KCNQ2	-2,697	upstream	ActReg chr20 #10970	1	0	0
10971	20	62,109,739	62,110,452	713	1	7.136	9.773	12.773	13	15	18	0	1	2	KCNQ2, EEF1A2	-6102, 20410	upstream, downstream	ActReg chr20 #10971	0	0	1
10972	20	62,110,501	62,111,394	893	1	5.607	4.321	12.429	11	7	19	1	1	2	KCNQ2, EEF1A2	-6954, 19558	upstream, downstream	ActReg chr20 #10972	0	0	1
10973	20	62,112,993	62,114,116	1,123	1	4.943	4.686	13.457	10	8	19	0	0	2	KCNQ2, EEF1A2	-9561, 16951	upstream, downstream	ActReg chr20 #10973	0	0	1
10974	20	62,116,279	62,116,699	420	1	4.231	2.923	14.538	5	4	20	0	0	1	EEF1A2	14,016	downstream	ActReg chr20 #10974	0	0	1
10975	20	62,117,761	62,118,236	475	1	4.786	4.143	14.429	7	7	24	0	0	1	EEF1A2	12,507	downstream	ActReg chr20 #10975	0	0	1
10976	20	62,119,940	62,120,392	452	1	5.714	6.286	13.929	10	8	24	1	0	1	EEF1A2	10,339	in gene	ActReg chr20 #10976	0	0	1
10977	20	62,125,708	62,126,615	907	1	6.5	3.643	12.893	9	6	20	1	0	1	EEF1A2	4,344	in gene	ActReg chr20 #10977	0	0	1
10978	20	62,129,156	62,130,054	898	1	10.786	12.571	7.107	17	20	11	0	1	1	EEF1A2	900	in gene	ActReg chr20 #10978	0	1	0
10979	20	62,130,972	62,131,719	747	1	5.458	6.583	12.958	10	10	16	0	1	1	EEF1A2	-840	upstream	ActReg chr20 #10979	0	0	1
10980	20	62,133,916	62,134,531	615	1	4.65	4.3	13.8	9	9	22	0	1	1	EEF1A2	-3,718	upstream	ActReg chr20 #10980	0	0	1
10981	20	62,148,754	62,150,233	1,479	1	5.196	5.63	13.043	9	10	24	0	1	2	PPDPF, PTK6	-2640, 19214	upstream, downstream	ActReg chr20 #10981	0	0	1
10982	20	62,153,549	62,154,175	626	1	6.789	7.842	13.316	13	14	21	0	1	2	PPDPF, PTK6	1729, 14845	downstream, downstream	ActReg chr20 #10982	0	0	1
10983	20	62,161,069	62,162,528	1,459	1	5.543	5.326	15.609	12	10	24	0	0	3	PPDPF, PTK6, SRMS	9665, 6909, 17059	downstream, in gene, downstream	ActReg chr20 #10983	0	0	1
10984	20	62,168,591	62,169,698	1,107	1	9.057	9.543	13.057	17	16	19	1	1	2	PTK6, SRMS	-437, 9713	upstream, downstream	ActReg chr20 #10984	0	0	1
10985	20	62,171,007	62,171,634	627	1	7	4.25	14.65	11	7	23	0	1	2	PTK6, SRMS	-2613, 7537	upstream, downstream	ActReg chr20 #10985	0	0	1
10986	20	62,171,950	62,173,000	1,050	1	5.545	5.273	16.273	9	8	28	0	1	2	PTK6, SRMS	-3768, 6382	upstream, in gene	ActReg chr20 #10986	0	0	1
10987	20	62,175,416	62,176,264	848	1	8.889	9.667	14.148	13	16	24	0	1	3	PTK6, SRMS, C20orf195	-7133, 3017, -8533	upstream, in gene, upstream	ActReg chr20 #10987	0	0	1
10988	20	62,178,602	62,179,158	556	1	3.529	4.118	13.941	7	7	20	1	2	3	PTK6, SRMS, C20orf195	-10173, -23, -5493	upstream, upstream, upstream	ActReg chr20 #10988	0	0	1
10989	20	62,193,457	62,194,218	761	1	3.583	5.75	13.167	6	11	21	1	0	2	C20orf195, PRIC285	9464, 11755	downstream, in gene	ActReg chr20 #10989	0	0	1
10990	20	62,194,432	62,195,679	1,247	1	7.641	6.821	12.256	13	11	20	1	0	2	C20orf195, PRIC285	10682, 10537	downstream, in gene	ActReg chr20 #10990	0	0	1
10991	20	62,195,754	62,197,794	2,040	1	7.391	6.094	12.875	11	10	18	1	0	2	C20orf195, PRIC285	12401, 8818	downstream, in gene	ActReg chr20 #10991	0	0	1
10992	20	62,198,091	62,199,263	1,172	1	7.25	8.667	14.111	12	13	24	1	0	1	PRIC285	6,915	in gene	ActReg chr20 #10992	0	0	1
10993	20	62,203,371	62,204,647	1,276	1	8.7	10.275	12.3	14	14	21	1	1	1	PRIC285	1,583	in gene	ActReg chr20 #10993	0	0	1
10994	20	62,205,743	62,206,160	417	1	11.308	9.077	14.231	16	16	24	1	1	1	PRIC285	-359	upstream	ActReg chr20 #10994	0	0	1
10995	20	62,221,254	62,222,314	1,060	1	5.576	4.061	14.303	11	6	25	1	0	1	GMEB2	36,597	in gene	ActReg chr20 #10995	0	0	1
10996	20	62,258,445	62,259,169	724	2	10.571	11.87	13.8	15	20	24	1	2	2	GMEB2, LOC100505771	-426, 220	upstream, in gene	ActReg chr20 #10996	0	1	1
10997	20	62,273,902	62,274,481	579	1	5.556	5.889	12	8	9	23	1	0	1	STMN3	10,589	in gene	ActReg chr20 #10997	0	0	1
10998	20	62,276,469	62,277,097	628	1	9.05	14.15	5.7	16	26	10	0	0	1	STMN3	7,997	in gene	ActReg chr20 #10998	0	1	0
10999	20	62,283,150	62,283,848	698	1	6.682	7.409	12.773	9	11	23	1	2	2	STMN3, RTEL1	1281, -6148	in gene, upstream	ActReg chr20 #10999	0	0	1
11000	20	62,284,477	62,285,373	896	1	6.185	12.464	10	12	26	15	1	2	2	STMN3, RTEL1	-145, -4722	upstream, upstream	ActReg chr20 #11000	0	1	0
11001	20	62,289,283	62,290,667	1,384	2	11.07	17.395	11.814	21	27	27	2	2	2	STMN3, RTEL1	-5195, 328	upstream, in gene	ActReg chr20 #11001	0	1	1
11002	20	62,295,905	62,296,592	687	1	4.952	3.238	12.714	7	5	21	0	0	1	RTEL1	6,601	in gene	ActReg chr20 #11002	0	0	1
11003	20	62,312,610	62,313,610	1,000	1	6.774	11.677	14.032	11	19	21	0	0	1	RTEL1	23,463	in gene	ActReg chr20 #11003	0	0	1
11004	20	62,316,775	62,318,343	1,568	1	4.469	8.224	16.551	9	15	27	2	0	2	RTEL1, TNFRSF6B	27912, -8729	in gene, upstream	ActReg chr20 #11004	0	0	1
11005	20	62,322,188	62,322,989	801	1	6.04	5.4	11.68	9	9	14	0	1	3	RTEL1, TNFRSF6B, ARFRP1	32941, -3700, 16767	in gene, upstream, downstream	ActReg chr20 #11005	0	0	1
11006	20	62,325,993	62,327,114	1,121	1	4.571	7.143	15.6	9	12	27	0	1	3	RTEL1, TNFRSF6B, ARFRP1	56908, 265, 12802	in gene, in gene, downstream	ActReg chr20 #11006	0	0	1
11007	20	62,327,137	62,329,024	1,887	1	7.102	7.661	14.542	12	14	23	1	1	4	RTEL1, TNFRSF6B, ARFRP1, ZGPAT	58433, 1792, 11275, -10714	downstream, in gene, downstream, upstream	ActReg chr20 #11007	0	0	1
11008	20	62,329,165	62,329,807	642	1	5.55	9.8	14.2	9	14	21	0	0	4	RTEL1, TNFRSF6B, ARFRP1, ZGPAT	59839, 3198, 9869, -9308	downstream, in gene, downstream, upstream	ActReg chr20 #11008	0	0	1
11009	20	62,330,275	62,331,140	865	1	12.222	9.852	9.111	20	15	18	0	0	4	RTEL1, TNFRSF6B, ARFRP1, ZGPAT	41060, 4419, 8648, -8087	downstream, downstream, in gene, upstream	ActReg chr20 #11009	1	0	0
11010	20	62,331,339	62,332,370	1,031	1	4.594	9.375	13.219	7	14	22	0	1	4	RTEL1, TNFRSF6B, ARFRP1, ZGPAT	42207, 5566, 7501, -6940	downstream, downstream, in gene, upstream	ActReg chr20 #11010	0	0	1
11011	20	62,338,311	62,339,626	1,315	2	13.171	14.098	8.61	32	37	23	1	2	3	TNFRSF6B, ARFRP1, ZGPAT	12680, 387, 174	downstream, in gene, in gene	ActReg chr20 #11011	1	1	0
11012	20	62,339,648	62,340,237	589	1	7.789	6.684	14.105	13	11	24	1	2	3	TNFRSF6B, ARFRP1, ZGPAT	13654, -587, 1148	downstream, upstream, in gene	ActReg chr20 #11012	0	0	1
11013	20	62,369,849	62,370,349	500	1	6.625	5.125	12.375	9	7	18	1	2	4	ZGPAT, LIME1, SLC2A4RG, ZBTB46	31305, 2121, -1112, 66757	downstream, in gene, upstream, downstream	ActReg chr20 #11013	0	0	1
11014	20	62,371,884	62,372,734	850	1	11	11.115	14.269	17	15	24	1	1	4	ZGPAT, LIME1, SLC2A4RG, ZBTB46	33515, 4331, 1098, 64547	downstream, downstream, in gene, downstream	ActReg chr20 #11014	0	0	1
11015	20	62,376,267	62,377,208	941	1	3	5.379	12.138	6	8	23	0	0	4	ZGPAT, LIME1, SLC2A4RG, ZBTB46	37943, 8759, 5526, 60119	downstream, downstream, downstream, in gene	ActReg chr20 #11015	0	0	1
11016	20	62,378,933	62,380,005	1,072	1	5.059	7.029	13.765	9	11	22	0	0	3	LIME1, SLC2A4RG, ZBTB46	11491, 8258, 57387	downstream, downstream, in gene	ActReg chr20 #11016	0	0	1
11017	20	62,384,473	62,385,075	602	1	2.737	4.882	10.158	5	10	14	1	0	2	SLC2A4RG, ZBTB46	13563, 52082	downstream, in gene	ActReg chr20 #11017	0	0	1
11018	20	62,406,351	62,407,486	1,135	1	4.286	5.114	12	9	8	22	1	0	1	ZBTB46	29,938	in gene	ActReg chr20 #11018	0	0	1
11019	20	62,421,408	62,422,467	1,059	1	4.912	6.853	12.794	9	9	18	1	0	1	ZBTB46	14,919	in gene	ActReg chr20 #11019	0	0	1
11020	20	62,431,691	62,432,418	727	1	7.565	6.545	15.087	10	11	24	0	0	1	ZBTB46	4,802	in gene	ActReg chr20 #11020	0	0	1
11021	20	62,465,531	62,466,197	666	1	4	7.667	15.191	7	12	22	0	0	1	C20orf181	13,801	in gene	ActReg chr20 #11021	0	0	1
11022	20	62,474,602	62,475,426	824	1	5.769	5.56	12.5	9	9	15	0	0	1	C20orf181	4,651	in gene	ActReg chr20 #11022	0	0	1
11023	20	62,476,336	62,476,850	514	1	3.812	6.062	13.688	8	9	19	0	0	1	C20orf181	3,072	in gene	ActReg chr20 #11023	0	0	1
11024	20	62,477,496	62,477,957	461	1	8.467	11.067	12	13	15	19	0	1	1	C20orf181	1,939	in gene	ActReg chr20 #11024	0	0	1
11025	20	62,485,553	62,486,475	922	1	4.655	4.897	14.276	8	9	23	0	2	2	C20orf181, C20orf135	-6349, -6552	upstream, upstream	ActReg chr20 #11025	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11026	20	62,486,528	62,487,279	751	1	3	6.083	12.042	6	9	14	0	2	3	C20orf181, C20orf135, TPD52L2	-7238, -5663, -9687	upstream, upstream, upstream	ActReg chr20 #11026	0	0	1
11027	20	62,493,337	62,493,889	552	1	6.056	5.556	17.5	10	8	33	1	2	2	C20orf135, TPD52L2	1047, -2977	in gene, upstream	ActReg chr20 #11027	0	0	1
11028	20	62,495,254	62,497,300	2,046	3	10.062	11.984	10.375	17	20	16	1	1	2	C20orf135, TPD52L2	3711, -513	downstream, upstream	ActReg chr20 #11028	1	1	1
11029	20	62,516,586	62,517,234	648	1	6.9	4.05	13	10	7	21	0	0	2	TPD52L2, DNAJC5	20320, -9608	in gene, upstream	ActReg chr20 #11029	0	0	1
11030	20	62,525,996	62,526,585	589	1	13.944	9.167	9.875	24	14	14	1	1	2	TPD52L2, DNAJC5	29700, -228	downstream, upstream	ActReg chr20 #11030	1	0	0
11031	20	62,551,454	62,551,946	492	1	3.438	8.75	11.188	5	12	15	2	2	3	DNAJC5, MIR941-2, MIR941-1	25182, 794, 263	in gene, downstream, downstream	ActReg chr20 #11031	0	0	1
11032	20	62,570,335	62,571,135	800	1	3.48	4.292	11.6	6	8	20	1	1	4	DNAJC5, UCKL1, MIR1914, MIR647	44217, 17065, 2162, 3344	downstream, downstream, downstream, downstream	ActReg chr20 #11032	0	0	1
11033	20	62,571,449	62,572,955	1,506	2	6.34	8.83	14.106	9	22	29	1	2	4	DNAJC5, UCKL1, MIR1914, MIR647	45684, 15598, 695, 1877	downstream, in gene, downstream, downstream	ActReg chr20 #11033	0	1	1
11034	20	62,575,588	62,576,305	717	1	6.318	7.409	13.864	10	12	18	1	2	4	UCKL1, MIR1914, MIR647, UCKL1AS	11854, -3049, -1867, -8791	in gene, upstream, upstream, upstream	ActReg chr20 #11034	0	0	1
11035	20	62,580,306	62,580,921	615	1	7.368	6.211	12.21	11	12	16	0	3	5	UCKL1, MIR1914, MIR647, UCKL1AS, ZNF512B	7187, -7716, -6534, -4124, 20605	in gene, upstream, upstream, upstream, downstream	ActReg chr20 #11035	0	0	1
11036	20	62,581,907	62,582,850	943	1	4.833	5.667	12.867	8	10	19	0	1	5	UCKL1, MIR1914, MIR647, UCKL1AS, ZNF512B	5422, -9481, -8299, -2359, 18840	in gene, upstream, upstream, upstream, downstream	ActReg chr20 #11036	0	0	1
11037	20	62,586,771	62,588,342	1,571	2	12.326	17.224	8.49	29	31	16	1	2	3	UCKL1, UCKL1AS, ZNF512B	244, 2819, 13662	in gene, in gene, downstream	ActReg chr20 #11037	1	1	0
11038	20	62,588,349	62,588,923	574	1	8.889	8.833	13.556	15	12	19	1	1	3	UCKL1, UCKL1AS, ZNF512B	-836, 3899, 12582	upstream, downstream, in gene	ActReg chr20 #11038	0	0	1
11039	20	62,594,951	62,595,992	1,041	1	5.812	4.344	14.062	6	11	21	1	1	4	UCKL1, UCKL1AS, ZNF512B, SAMD10	-7671, 10734, 5747, 15524	upstream, downstream, in gene, downstream	ActReg chr20 #11039	0	0	1
11040	20	62,598,093	62,598,670	577	1	4.778	6.333	12.667	8	10	20	0	0	3	UCKL1AS, ZNF512B, SAMD10	13644, 2837, 12614	downstream, in gene, downstream	ActReg chr20 #11040	0	0	1
11041	20	62,611,377	62,612,984	1,607	2	12.62	19.3	8.76	29	47	14	1	2	2	SAMD10, PRPF6	-1185, -251	upstream, upstream	ActReg chr20 #11041	1	1	0
11042	20	62,658,842	62,659,650	808	1	2.96	5.462	12.154	6	10	19	0	1	2	PRPF6, NCRNA00176	46815, -6451	in gene, upstream	ActReg chr20 #11042	0	0	1
11043	20	62,669,637	62,671,405	1,768	3	7.057	10.818	12.018	13	17	27	1	0	3	PRPF6, NCRNA00176, SOX18	58090, 4824, 10458	downstream, in gene, downstream	ActReg chr20 #11043	0	1	1
11044	20	62,671,475	62,672,085	610	1	7.053	8	12.79	11	11	16	0	0	3	PRPF6, NCRNA00176, SOX18	59349, 6083, 9199	downstream, downstream, downstream	ActReg chr20 #11044	0	0	1
11045	20	62,673,136	62,674,089	953	1	4.567	7.633	12.667	10	12	21	1	0	3	PRPF6, NCRNA00176, SOX18	61181, 7915, 7367	downstream, downstream, downstream	ActReg chr20 #11045	0	0	1
11046	20	62,681,247	62,682,611	1,364	1	5.372	8.116	12.605	9	14	22	1	2	3	NCRNA00176, SOX18, TCEA2	16232, -950, -6510	downstream, upstream, upstream	ActReg chr20 #11046	0	0	1
11047	20	62,682,928	62,683,515	587	1	6.611	7.444	11.556	10	12	16	0	2	2	SOX18, TCEA2	-2242, -5218	upstream, upstream	ActReg chr20 #11047	0	0	1
11048	20	62,686,951	62,687,878	927	1	3.714	6.276	12.103	9	10	16	0	2	2	SOX18, TCEA2	-6435, -1025	upstream, upstream	ActReg chr20 #11048	0	0	1
11049	20	62,693,375	62,695,234	1,859	4	9.712	12.831	12.327	33	38	20	1	0	2	TCEA2, RGS19	5865, 17020	in gene, downstream	ActReg chr20 #11049	1	1	1
11050	20	62,696,905	62,697,504	599	1	7.684	8.158	12.21	14	12	19	0	0	2	TCEA2, RGS19	8765, 14120	in gene, downstream	ActReg chr20 #11050	0	0	1
11051	20	62,700,129	62,701,589	1,460	1	6.356	8.022	15.067	10	12	22	0	0	3	TCEA2, RGS19, OPRL1	12420, 10465, -10629	in gene, downstream, upstream	ActReg chr20 #11051	0	0	1
11052	20	62,703,274	62,704,294	1,020	1	5.188	6.031	11.281	9	11	15	0	1	3	TCEA2, RGS19, OPRL1	15345, 7540, -7704	downstream, downstream, upstream	ActReg chr20 #11052	0	0	1
11053	20	62,704,713	62,706,222	1,509	1	3.522	7.426	11.787	7	14	16	1	1	4	TCEA2, RGS19, OPRL1, C20orf201	17028, 5857, -6021, 10245	downstream, in gene, upstream, downstream	ActReg chr20 #11053	0	0	1
11054	20	62,709,364	62,710,222	858	1	5.074	5.481	11.778	7	7	15	0	2	4	TCEA2, RGS19, OPRL1, C20orf201	21354, 1531, -1695, 5919	downstream, in gene, upstream, downstream	ActReg chr20 #11054	0	0	1
11055	20	62,710,569	62,711,157	588	1	4.722	7.5	11.5	8	11	18	1	2	4	TCEA2, RGS19, OPRL1, C20orf201	22424, 461, -625, 4849	downstream, in gene, upstream, downstream	ActReg chr20 #11055	0	0	1
11056	20	62,736,250	62,736,831	581	1	5.929	5.667	11.889	10	8	18	0	1	2	OPRL1, NPBWR2	25052, 1644	downstream, downstream	ActReg chr20 #11056	0	0	1
11057	20	62,737,236	62,738,300	1,064	1	5.364	8.303	11.546	11	14	17	1	1	2	OPRL1, NPBWR2	26280, 416	downstream, in gene	ActReg chr20 #11057	0	0	1
11058	20	62,740,528	62,741,185	657	1	4.238	4.333	12.809	6	9	21	0	1	2	OPRL1, NPBWR2	29368, -2672	downstream, upstream	ActReg chr20 #11058	0	0	1
11059	20	62,743,298	62,743,931	633	1	6.812	5.316	12.105	11	8	18	0	1	1	NPBWR2	-5,430	upstream	ActReg chr20 #11059	0	0	1
11060	20	62,750,580	62,751,722	1,142	1	4.944	4.75	12.583	7	10	21	0	0	0				ActReg chr20 #11060	0	0	1
11061	20	62,785,354	62,786,529	1,175	1	5.216	6.595	11.946	10	14	17	0	0	1	MYT1	-9,886	upstream	ActReg chr20 #11061	0	0	1
11062	20	62,793,004	62,793,822	818	2	12.84	17.24	5.72	28	38	9	0	1	1	MYT1	-2,414	upstream	ActReg chr20 #11062	1	1	0
11063	20	62,797,614	62,798,664	1,050	2	5.273	11.333	10.394	11	26	20	0	1	1	MYT1	2,312	in gene	ActReg chr20 #11063	0	1	1
11064	20	62,816,952	62,817,504	552	1	4.722	4.444	11.444	8	6	19	0	0	1	MYT1	21,401	in gene	ActReg chr20 #11064	0	0	1
11065	20	62,823,227	62,824,416	1,189	1	8.421	13.29	6.816	19	21	12	0	0	1	MYT1	27,994	in gene	ActReg chr20 #11065	0	1	0
11066	20	62,836,379	62,837,670	1,291	1	10.732	13.293	6.39	16	20	16	0	0	1	MYT1	41,197	in gene	ActReg chr20 #11066	0	1	0
11067	20	62,863,098	62,863,837	739	1	3.739	4.435	11.565	7	7	18	0	0	1	MYT1	67,640	in gene	ActReg chr20 #11067	0	0	1
11068	20	62,886,245	62,887,374	1,129	2	14.257	13.4	3.967	29	33	7	1	1	1	PCMTD2	-239	upstream	ActReg chr20 #11068	1	1	0
11069	21	9,439,134	9,439,803	669	1	2.9	5.714	14.952	5	12	25	1	0	0				ActReg chr21 #11069	0	0	1
11070	21	9,855,877	9,857,423	1,546	1	7.271	5.208	14.75	14	15	24	0	0	0				ActReg chr21 #11070	0	0	1
11071	21	9,877,386	9,877,715	329	1	3.3	5.667	14	5	8	19	0	0	0				ActReg chr21 #11071	0	0	1
11072	21	9,878,143	9,878,774	631	1	4.5	3.35	11.25	8	8	15	0	0	0				ActReg chr21 #11072	0	0	1
11073	21	9,878,864	9,879,665	801	1	4.68	4.739	11.6	9	8	16	0	0	0				ActReg chr21 #11073	0	0	1
11074	21	9,903,770	9,904,151	381	1	3.778	8.333	11.333	6	13	14	0	0	1	LOC100132288	64,625	downstream	ActReg chr21 #11074	0	0	1
11075	21	9,907,923	9,908,578	655	1	4.333	8.905	14.048	8	14	20	0	0	1	LOC100132288	60,335	in gene	ActReg chr21 #11075	0	0	1
11076	21	9,908,660	9,909,540	880	1	5.407	4.731	17.286	13	9	31	2	0	1	LOC100132288	59,485	in gene	ActReg chr21 #11076	0	0	1
11077	21	9,909,635	9,910,066	431	1	7.231	6.923	13.769	12	12	22	1	0	1	LOC100132288	58,735	in gene	ActReg chr21 #11077	0	0	1
11078	21	9,911,712	9,912,524	812	1	5.542	10.423	18.5	10	18	30	1	0	1	LOC100132288	56,467	in gene	ActReg chr21 #11078	0	0	1
11079	21	10,991,178	10,991,507	329	1	3.6	5.2	10.8	5	6	15	1	1	1	TPTE	-422	upstream	ActReg chr21 #11079	0	0	1
11080	21	11,059,524	11,059,977	453	1	6.5	8.714	18.357	9	13	31	0	2	2	BAGE3, BAGE	-1427, 67	upstream, in gene	ActReg chr21 #11080	0	0	1
11081	21	11,108,487	11,113,208	4,721	1	15.306	16.061	21.939	44	41	48	0	0	0				ActReg chr21 #11081	0	0	1
11082	21	11,128,083	11,129,507	1,424	1	7.444	11	14.6	18	21	32	0	0	0				ActReg chr21 #11082	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11083	21	11,143,460	11,146,695	3,235	1	15.604	18.564	18.545	29	33	41	0	0	0				ActReg chr21 #11083	0	0	1
11084	21	11,168,444	11,169,258	814	1	16.038	15.769	20.308	29	24	40	0	0	0				ActReg chr21 #11084	0	0	1
11085	21	11,169,834	11,170,646	812	1	15.76	16.28	9.76	25	23	22	0	0	0				ActReg chr21 #11085	0	1	0
11086	21	15,457,293	15,457,460	167	1	16	15.6	17.2	21	20	22	0	0	0				ActReg chr21 #11086	0	0	1
11087	21	16,437,893	16,438,408	515	1	5.562	8.812	5.188	10	14	8	1	1	1	NRIP1	-1,024	upstream	ActReg chr21 #11087	0	1	0
11088	21	18,835,767	18,836,260	493	1	6.062	8.938	1	10	16	1	0	0	0				ActReg chr21 #11088	0	1	0
11089	21	19,060,933	19,061,725	792	2	8.417	14.792	2.905	21	30	5	0	0	0				ActReg chr21 #11089	1	1	0
11090	21	19,191,349	19,192,217	868	2	15.741	18.148	3.778	48	42	6	1	1	1	C21orf91	-80	upstream	ActReg chr21 #11090	1	1	0
11091	21	26,979,501	26,980,090	589	1	11	13.556	6.444	14	21	10	1	1	1	MRPL39	6	in gene	ActReg chr21 #11091	0	1	0
11092	21	27,512,449	27,513,027	578	1	10.778	6.889	3.176	17	12	6	0	0	1	APP	30,400	in gene	ActReg chr21 #11092	1	0	0
11093	21	29,186,625	29,187,079	454	1	9	10.143	1	12	14	1	0	0	0				ActReg chr21 #11093	0	1	0
11094	21	30,365,004	30,365,470	466	1	9.286	12	4.357	16	19	9	1	1	1	RNF160	40	in gene	ActReg chr21 #11094	0	1	0
11095	21	30,445,524	30,446,445	921	1	8.31	14	7.034	17	27	11	1	2	2	CCT8, C21orf7	26, -6889	in gene, upstream	ActReg chr21 #11095	0	1	0
11096	21	30,672,059	30,672,912	853	1	7.444	10.667	2.231	15	18	5	0	1	1	BACH1	1,265	in gene	ActReg chr21 #11096	0	1	0
11097	21	31,028,971	31,029,349	378	1	9.833	5.333	4.417	14	7	6	0	0	1	GRIK1	283,122	in gene	ActReg chr21 #11097	1	0	0
11098	21	31,311,840	31,312,195	355	1	1.857	3.833	9.333	3	6	14	1	1	1	GRIK1	265	in gene	ActReg chr21 #11098	0	0	1
11099	21	33,650,955	33,651,715	760	1	9.75	16.042	8.042	20	34	17	1	1	1	C21orf45	41	in gene	ActReg chr21 #11099	0	1	0
11100	21	33,941,554	33,942,276	722	1	6.609	10.043	6.739	11	13	9	1	0	1	TCP10L	15,930	downstream	ActReg chr21 #11100	0	1	0
11101	21	33,969,254	33,970,221	967	2	19.067	16.867	3.167	53	40	7	0	0	1	C21orf59	15,181	downstream	ActReg chr21 #11101	1	1	0
11102	21	33,984,608	33,985,210	602	1	10.737	11.579	6.316	13	17	8	1	1	1	C21orf59	9	in gene	ActReg chr21 #11102	0	1	0
11103	21	34,100,459	34,101,157	698	1	8	11.546	3.895	13	21	8	1	2	3	SYNJ1, LOC100506215, C21orf66	-457, 383, 43361	upstream, in gene, downstream	ActReg chr21 #11103	0	1	0
11104	21	34,143,785	34,144,766	981	2	15.8	18.367	3.621	36	46	8	1	2	2	C21orf66, C21orf49	-106, -136	upstream, upstream	ActReg chr21 #11104	1	1	0
11105	21	34,696,712	34,697,270	558	1	8.412	11.118	6.647	14	18	10	1	1	1	IFNAR1	-223	upstream	ActReg chr21 #11105	0	1	0
11106	21	34,752,798	34,753,355	557	1	8.778	7.278	3.5	19	13	5	0	0	0				ActReg chr21 #11106	1	0	0
11107	21	34,776,396	34,776,900	504	1	5.875	10.875	4.375	9	16	8	1	1	1	IFNGR2	1,446	in gene	ActReg chr21 #11107	0	1	0
11108	21	34,852,446	34,852,986	540	1	9	6.235	3.588	15	12	6	1	1	2	TMEM50B, DNAJC28	-435, 11307	upstream, downstream	ActReg chr21 #11108	1	0	0
11109	21	35,395,124	35,395,621	497	1	4.062	11	1.7	7	16	3	0	0	0				ActReg chr21 #11109	0	1	0
11110	21	35,987,323	35,988,027	704	2	15.909	16.818	2.357	33	36	4	1	1	1	RCAN1	-293	upstream	ActReg chr21 #11110	1	1	0
11111	21	37,432,532	37,433,027	495	1	10	5.688	6.5	16	8	9	1	1	2	SETD4, CBR1	37, -9506	in gene, upstream	ActReg chr21 #11111	1	0	0
11112	21	38,445,205	38,446,460	1,255	2	11.026	8.923	6.282	22	17	14	1	2	2	PIGP, TTC3	-374, 261	upstream, in gene	ActReg chr21 #11112	1	1	0
11113	21	39,649,250	39,650,183	933	1	10	5.586	2.238	15	11	4	0	0	1	KCNJ15	21,052	in gene	ActReg chr21 #11113	1	0	0
11114	21	40,159,700	40,160,247	547	1	7.647	10.647	1.417	13	15	3	0	0	0				ActReg chr21 #11114	0	1	0
11115	21	40,817,640	40,818,248	608	1	9.474	6.632	3.842	17	13	7	1	2	2	LCA5L, SH3BGR	-1816, 147	upstream, in gene	ActReg chr21 #11115	1	0	0
11116	21	42,878,808	42,879,175	367	1	2.083	2.833	11.25	4	4	15	1	1	1	TMPRSS2	1,094	in gene	ActReg chr21 #11116	0	0	1
11117	21	43,160,920	43,161,352	432	1	4.714	2.692	12.429	9	4	19	1	0	1	RIPK4	26,113	in gene	ActReg chr21 #11117	0	0	1
11118	21	43,309,006	43,309,528	522	1	3.688	9.625	3.438	8	13	5	0	0	2	PRDM15, C2CD2	-9676, 64732	upstream, in gene	ActReg chr21 #11118	0	1	0
11119	21	43,857,721	43,858,563	842	1	9.259	12.593	5.519	17	21	9	0	0	1	UBASH3A	34,123	in gene	ActReg chr21 #11119	0	1	0
11120	21	44,299,128	44,299,955	827	3	9.538	10.039	10.039	20	19	19	1	1	1	WDR4	137	in gene	ActReg chr21 #11120	1	1	1
11121	21	44,393,887	44,395,023	1,136	2	13.778	16.639	5.242	37	42	13	1	1	1	PKNOX1	-188	upstream	ActReg chr21 #11121	1	1	0
11122	21	44,495,160	44,496,031	871	1	10.037	8.074	5.808	15	11	13	1	1	1	CBS	877	in gene	ActReg chr21 #11122	1	0	0
11123	21	44,630,064	44,630,493	429	1	7.231	10.308	3.308	10	13	5	0	0	0				ActReg chr21 #11123	0	1	0
11124	21	44,717,469	44,717,883	414	1	3.538	3.231	12.077	5	6	17	0	0	0				ActReg chr21 #11124	0	0	1
11125	21	44,816,256	44,816,649	393	1	2.923	5.727	10.385	4	8	16	0	0	0				ActReg chr21 #11125	0	0	1
11126	21	44,838,397	44,838,776	379	1	4.667	3.833	10.25	8	5	16	0	0	1	SIK1	8,416	in gene	ActReg chr21 #11126	0	0	1
11127	21	45,209,132	45,209,715	583	1	4.389	11.278	5.056	6	20	12	1	1	1	RRP1	5	in gene	ActReg chr21 #11127	0	1	0
11128	21	45,622,428	45,622,992	564	1	9.444	5.167	4.667	17	9	9	1	0	0				ActReg chr21 #11128	1	0	0
11129	21	45,648,695	45,649,127	432	1	3.364	1.333	9.857	4	2	15	0	0	1	ICOSLG	11,923	in gene	ActReg chr21 #11129	0	0	1
11130	21	45,759,099	45,759,641	542	1	9.941	8.824	4.941	16	14	11	1	1	2	C21orf2, LOC100505684	-85, 3635	upstream, downstream	ActReg chr21 #11130	1	0	0
11131	21	45,819,818	45,820,252	434	1	1.4	3.1	10.154	2	5	15	0	0	1	TRPM2	46,551	in gene	ActReg chr21 #11131	0	0	1
11132	21	45,972,079	45,972,446	367	1	1.556	7.375	10.636	2	10	15	0	1	3	C21orf29, KRTAP10-2, KRTAP10-3	159233, -874, 6381	in gene, upstream, downstream	ActReg chr21 #11132	0	0	1
11133	21	46,021,510	46,021,814	304	1	1.111	1.778	10.222	2	3	12	0	1	3	C21orf29, KRTAP10-6, KRTAP10-7	109833, -9276, 1165	in gene, upstream, in gene	ActReg chr21 #11133	0	0	1
11134	21	46,184,281	46,184,655	374	1	2.125	3.333	12.25	4	7	15	0	0	1	UBE2G2	37,270	downstream	ActReg chr21 #11134	0	0	1
11135	21	46,221,275	46,221,972	697	1	6.682	12.318	4.048	11	23	10	1	1	2	UBE2G2, SUMO3	115, 16421	in gene, downstream	ActReg chr21 #11135	0	1	0
11136	21	46,293,431	46,294,359	928	3	9.793	11.31	7.286	18	19	18	1	1	1	PTTG1IP	-154	upstream	ActReg chr21 #11136	1	1	1
11137	21	46,311,717	46,312,131	414	1	3.846	4.231	11.308	5	7	17	0	0	1	ITGB2	36,829	in gene	ActReg chr21 #11137	0	0	1
11138	21	46,359,456	46,360,060	604	1	5.158	9.895	5.053	9	17	9	1	2	3	LOC100505746, C21orf67, C21orf70	18792, 70, -197	downstream, in gene, upstream	ActReg chr21 #11138	0	1	0
11139	21	46,406,669	46,407,063	394	1	4.091	2.583	9.667	6	4	12	0	0	2	C21orf70, NCRNA00163	46911, 7135	downstream, downstream	ActReg chr21 #11139	0	0	1
11140	21	46,418,340	46,418,631	291	1	4.556	2.889	12.333	6	4	14	0	1	2	NCRNA00163, NCRNA00162	-4484, 6157	upstream, downstream	ActReg chr21 #11140	0	0	1
11141	21	46,707,740	46,708,147	407	1	4.308	7	9.385	6	12	15	1	2	2	POFUT2, LOC642852	-132, -24	upstream, upstream	ActReg chr21 #11141	0	0	1
11142	21	46,783,819	46,784,308	489	1	10.8	7.667	5.2	13	11	9	0	0	0				ActReg chr21 #11142	1	0	0
11143	21	46,824,333	46,824,650	317	1	2.143	2.375	11.2	4	3	15	1	1	1	COL18A1	-606	upstream	ActReg chr21 #11143	0	0	1
11144	21	46,847,959	46,848,350	391	1	4.091	4.583	11.167	6	7	17	1	1	2	COL18A1, NCRNA00175	23057, -3169	in gene, upstream	ActReg chr21 #11144	0	0	1
11145	21	46,888,006	46,888,479	473	1	3.571	4.929	11.071	7	8	16	0	0	1	COL18A1	63,145	in gene	ActReg chr21 #11145	0	0	1
11146	21	46,931,891	46,932,219	328	1	2.9	2.8	10.6	4	4	15	1	0	2	COL18A1, SLC19A1	106958, 30296	in gene, downstream	ActReg chr21 #11146	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11147	21	46,948,013	46,948,255	242	1	1.167	1	11.143	2	1	13	0	0	1	SLC19A1	14,217	in gene	ActReg chr21 #11147	0	0	1
11148	21	46,960,233	46,960,541	308	1	2.571	2.778	10.444	3	4	14	0	1	1	SLC19A1	1,964	in gene	ActReg chr21 #11148	0	0	1
11149	21	46,971,683	46,972,166	483	1	2.667	7.133	13.133	4	10	21	0	0	1	SLC19A1	-9,573	upstream	ActReg chr21 #11149	0	0	1
11150	21	46,975,511	46,976,031	520	2	8.438	11.125	7.688	13	15	14	1	0	0				ActReg chr21 #11150	0	1	1
11151	21	46,999,108	46,999,534	426	1	3.556	5.154	10.923	5	9	18	0	0	0				ActReg chr21 #11151	0	0	1
11152	21	47,065,536	47,066,235	699	2	13.773	14.364	1.556	35	36	2	0	0	0				ActReg chr21 #11152	1	1	0
11153	21	47,401,901	47,402,211	310	1	2.7	4.2	9	4	6	13	0	1	1	COL6A1	593	in gene	ActReg chr21 #11153	0	0	1
11154	21	47,442,616	47,442,927	311	1	3.5	3.6	9.5	5	6	14	0	0	0				ActReg chr21 #11154	0	0	1
11155	21	47,684,646	47,685,232	586	1	3.778	4.111	10.778	6	7	15	0	0	1	MCM3AP	20,297	in gene	ActReg chr21 #11155	0	0	1
11156	21	47,705,700	47,706,476	776	1	8.917	11.833	6.87	13	16	15	1	2	2	MCM3AP, C21orf57	-852, -179	upstream, upstream	ActReg chr21 #11156	0	1	0
11157	21	48,055,400	48,056,297	897	2	12.786	9.5	5.24	21	20	11	1	1	1	PRMT2	321	in gene	ActReg chr21 #11157	1	1	0
11158	22	17,001,572	17,001,858	286	1	1.778	1	10.889	2	1	14	1	0	0				ActReg chr22 #11158	0	0	1
11159	22	17,652,113	17,653,158	1,045	2	11.818	15.273	4.2	21	34	9	1	1	3	CECR5, CECR4, CECR1	-6458, 12356, 38144	upstream, downstream, downstream	ActReg chr22 #11159	1	1	0
11160	22	18,455,392	18,456,063	671	1	6.762	10.333	4.762	9	19	8	0	0	2	MICAL3, MIR648	51598, 8000	in gene, downstream	ActReg chr22 #11160	0	1	0
11161	22	18,484,002	18,485,046	1,044	2	34.906	32.156	3.719	86	75	6	1	0	1	MICAL3	22,801	in gene	ActReg chr22 #11161	1	1	0
11162	22	18,560,173	18,561,048	875	1	7.741	13.259	6.593	14	19	11	1	1	1	PEX26	-76	upstream	ActReg chr22 #11162	0	1	0
11163	22	18,592,855	18,593,397	542	1	5.294	4.647	12.059	7	7	21	1	1	1	TUBA8	-327	upstream	ActReg chr22 #11163	0	0	1
11164	22	18,893,299	18,893,688	389	1	5.583	7.083	10.25	8	10	16	1	1	2	DGCR6, PRODH	-243, 30321	upstream, downstream	ActReg chr22 #11164	0	0	1
11165	22	19,017,776	19,018,065	289	1	0	1.6	9.222	0	2	13	1	1	4	LOC100506454, DGCR10, LOC402036, DGCR2	16054, 7783, 2642, 92047	in gene, downstream, downstream, downstream	ActReg chr22 #11165	0	0	1
11166	22	19,108,897	19,109,471	574	1	3.941	9.471	5.647	6	15	8	1	1	3	DGCR2, DGCR14, TSSK2	783, 23006, -9137	in gene, downstream, upstream	ActReg chr22 #11166	0	1	0
11167	22	19,158,765	19,159,377	612	1	10.947	10.316	7.737	16	13	12	1	0	2	SLC25A1, CLTCL1	7230, 120168	downstream, downstream	ActReg chr22 #11167	1	0	0
11168	22	19,189,317	19,190,098	781	2	7.5	13.667	4.579	16	24	9	0	0	1	CLTCL1	89,532	in gene	ActReg chr22 #11168	1	1	0
11169	22	19,419,677	19,420,335	658	3	9.429	10.191	7.286	15	15	15	1	2	3	HIRA, MRPL40, C22orf39	upstream, upstream, downstream	ActReg chr22 #11169	1	1	1
11170	22	19,434,232	19,434,674	442	1	10.714	3.643	2.25	14	5	4	1	2	3	C22orf39, LOC100506503, UFD1L	1302, -963, 32285	in gene, upstream, downstream	ActReg chr22 #11170	1	0	0
11171	22	19,466,559	19,467,199	640	2	10.35	11.35	3.6	17	18	6	1	2	2	UFD1L, CDC45L	-141, -535	upstream, upstream	ActReg chr22 #11171	1	1	0
11172	22	19,788,262	19,788,531	269	1	1	3.333	12.375	1	4	15	0	0	1	GNB1L	54,066	in gene	ActReg chr22 #11172	0	0	1
11173	22	19,842,135	19,842,903	768	1	7.792	11.455	7.333	12	16	11	1	2	2	GNB1L, C22orf29	-57, -148	upstream, upstream	ActReg chr22 #11173	0	1	0
11174	22	20,004,494	20,004,870	376	1	3.182	2.5	11.917	5	4	16	1	2	2	ARVCF, C22orf25	-373, -3949	upstream, upstream	ActReg chr22 #11174	0	0	1
11175	22	20,104,349	20,105,079	730	2	10.957	10.217	1.579	24	20	2	1	2	3	DGCR8, TRMT2A, RANBP1	36959, 54, -310	downstream, in gene, upstream	ActReg chr22 #11175	1	1	0
11176	22	20,118,313	20,119,055	742	1	7.522	15.348	3.167	13	29	5	1	1	2	RANBP1, ZDHHC8	13660, -680	downstream, downstream	ActReg chr22 #11176	0	1	0
11177	22	20,119,748	20,120,049	301	1	4.333	8.222	11.333	7	11	16	1	1	2	RANBP1, ZDHHC8	14874, 534	downstream, in gene	ActReg chr22 #11177	0	0	1
11178	22	20,175,543	20,175,956	413	1	1.727	1.462	10.385	5	2	13	0	0	0				ActReg chr22 #11178	0	0	1
11179	22	20,191,821	20,192,178	357	1	3.727	4.273	12.273	5	6	16	0	1	1	LOC150197	-1,856	upstream	ActReg chr22 #11179	0	0	1
11180	22	20,199,105	20,199,652	547	1	3.176	2.071	12.118	5	4	21	0	0	1	LOC150197	5,523	downstream	ActReg chr22 #11180	0	0	1
11181	22	20,219,877	20,220,195	318	1	1.3	3.7	10.9	2	7	14	0	0	1	RTN4R	35,780	downstream	ActReg chr22 #11181	0	0	1
11182	22	20,861,570	20,862,190	620	2	8.053	11	8.579	16	19	14	1	1	1	MED15	-6	upstream	ActReg chr22 #11182	1	1	0
11183	22	21,212,833	21,213,458	625	2	11.474	11	1.824	25	21	3	1	2	2	PI4KA, SNAP29	-75, -147	upstream, upstream	ActReg chr22 #11183	1	1	0
11184	22	21,319,944	21,320,298	354	1	1.667	3.091	11.454	2	5	15	1	1	2	LOC100507329, AIFM3	8741, 703	downstream, in gene	ActReg chr22 #11184	0	0	1
11185	22	21,336,045	21,336,880	835	2	8.269	12.731	8.731	15	18	20	1	1	2	AIFM3, LZTR1	17044, -96	downstream, upstream	ActReg chr22 #11185	0	1	1
11186	22	21,351,552	21,352,003	451	1	2.75	1.933	10.667	5	3	15	0	1	3	LZTR1, THAP7, FLJ39582	15219, 4627, -4434	in gene, downstream, upstream	ActReg chr22 #11186	0	0	1
11187	22	21,355,713	21,356,648	935	3	9.793	10.138	11.379	18	21	19	1	2	3	LZTR1, THAP7, FLJ39582	19622, 224, -31	downstream, in gene, upstream	ActReg chr22 #11187	1	1	1
11188	22	21,363,778	21,364,406	628	1	8.526	12.947	4.421	14	21	9	0	2	3	THAP7, FLJ39582, P2RX6	-7688, 7881, -5350	upstream, in gene, upstream	ActReg chr22 #11188	0	1	0
11189	22	21,800,427	21,800,700	273	1	2	1.75	12	4	2	14	1	0	1	HIC2	28,870	in gene	ActReg chr22 #11189	0	0	1
11190	22	21,983,289	21,984,700	1,411	2	15.204	17.864	4.095	42	38	12	1	2	3	UBE2L3, YDJC, CCDC116	62037, 346, -3092	downstream, in gene, upstream	ActReg chr22 #11190	1	1	0
11191	22	22,006,671	22,007,066	395	1	2.091	6.083	12.667	3	9	17	1	2	3	SDF2L1, MIR301B, MIR130B	10326, -402, -725	downstream, upstream, upstream	ActReg chr22 #11191	0	0	1
11192	22	22,020,165	22,020,692	527	2	11.875	10.562	10.812	17	13	14	1	1	1	PPIL2	155	in gene	ActReg chr22 #11192	1	0	1
11193	22	22,336,865	22,337,274	409	1	1.833	5.667	11.75	2	9	16	1	1	2	TOP3B, PRAMEL	78, 48324	in gene, downstream	ActReg chr22 #11193	0	0	1
11194	22	23,230,080	23,230,363	283	1	1	1.375	10.889	1	2	14	0	3	5	IGL@, IGLV3-1, IGLL5, IGLJ1, IGLC1	849747, 7129, 261, -5740, -7334	in gene, downstream, in gene, upstream, upstream	ActReg chr22 #11194	0	0	1
11195	22	23,499,872	23,500,195	323	1	2.8	2.364	10.273	4	3	14	0	0	1	RAB36	12,520	in gene	ActReg chr22 #11195	0	0	1
11196	22	24,093,408	24,093,668	260	1	9.556	5.333	10.889	14	8	14	1	1	2	ZNF70, VPREB3	-259, 3092	upstream, downstream	ActReg chr22 #11196	0	0	1
11197	22	24,110,160	24,110,569	409	1	4.923	7.154	10.077	9	11	15	1	2	3	C22orf15, CHCHD10, MMP11	5156, -223, -4672	downstream, upstream, upstream	ActReg chr22 #11197	0	0	1
11198	22	24,191,740	24,192,032	292	1	7.6	7	10	9	8	12	1	1	1	SLC2A11	-7,173	upstream	ActReg chr22 #11198	0	0	1
11199	22	24,256,020	24,256,411	391	1	5.667	7.083	10.25	7	12	15	1	0	0				ActReg chr22 #11199	0	0	1
11200	22	24,359,448	24,360,159	711	1	9.364	12.046	3.75	18	19	6	0	1	1	LOC729852	-7,724	upstream	ActReg chr22 #11200	0	1	0
11201	22	24,551,384	24,551,689	305	1	3.1	4	11.1	5	8	14	1	0	1	CABIN1	143,771	in gene	ActReg chr22 #11201	0	0	1
11202	22	24,820,799	24,821,125	326	1	1.909	2.727	11.182	3	3	16	1	1	3	CYTSA, ADORA2A, C22orf45	154176, -2568, 69821	downstream, upstream, downstream	ActReg chr22 #11202	0	0	1
11203	22	24,836,511	24,836,956	445	1	3.643	3.214	11.714	5	5	17	0	0	2	ADORA2A, C22orf45	13203, 54050	in gene, in gene	ActReg chr22 #11203	0	0	1
11204	22	24,951,461	24,952,134	673	2	6.048	11.524	7	9	16	14	1	2	2	C22orf13, SNRPD3	-522, 179	upstream, in gene	ActReg chr22 #11204	0	1	1
11205	22	25,271,791	25,272,360	569	1	8.111	12.5	3.2	14	23	5	0	0	1	SGSM1	69,939	in gene	ActReg chr22 #11205	0	1	0
11206	22	26,143,052	26,143,691	639	1	11	7	3.15	16	14	6	0	0	1	MYO18B	5,251	in gene	ActReg chr22 #11206	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11207	22	26,908,196	26,908,701	505	1	9.333	9.867	5.4	14	15	10	1	2	2	TFIP11, LOC100507599	-11, -28	upstream, upstream	ActReg chr22 #11207	0	1	0
11208	22	27,345,090	27,345,748	658	2	9.1	11.15	2.25	20	20	4	0	0	0				ActReg chr22 #11208	1	1	0
11209	22	27,471,161	27,471,719	558	1	9.5	8.611	2.167	18	16	3	0	0	0				ActReg chr22 #11209	1	0	0
11210	22	27,508,990	27,509,610	620	1	12.4	9.1	3	20	14	7	0	0	0				ActReg chr22 #11210	1	0	0
11211	22	27,608,460	27,609,061	601	1	7.789	10.579	2	12	16	2	0	0	0				ActReg chr22 #11211	0	1	0
11212	22	27,803,327	27,803,569	242	1	1.75	1.875	11	3	3	13	0	0	0				ActReg chr22 #11212	0	0	1
11213	22	28,122,569	28,123,101	532	1	6.5	10.875	2.875	10	18	4	0	0	0				ActReg chr22 #11213	0	1	0
11214	22	29,663,223	29,663,523	300	1	5.8	6.8	9.2	8	9	12	1	2	3	EMID1, RHBDD3, EWSR1	61420, 541, -625	downstream, in gene, upstream	ActReg chr22 #11214	0	0	1
11215	22	29,663,633	29,664,581	948	2	14.033	17.833	5.862	32	41	12	1	2	3	EMID1, RHBDD3, EWSR1	62154, -193, 109	downstream, upstream, in gene	ActReg chr22 #11215	1	1	0
11216	22	29,702,048	29,703,294	1,246	2	9.564	12.692	4.514	16	19	9	1	1	3	EWSR1, GAS2L1, RASL10A	38673, -326, 9077	downstream, upstream, downstream	ActReg chr22 #11216	1	1	0
11217	22	29,714,153	29,714,466	313	1	2.3	3.6	11.7	3	6	16	0	1	3	GAS2L1, RASL10A, AP1B1	11312, -2561, 70263	downstream, upstream, downstream	ActReg chr22 #11217	0	0	1
11218	22	29,949,402	29,950,173	771	2	12.333	10.208	3.708	24	25	6	1	1	2	THOC5, NIPSNAP1	-51, 27357	upstream, downstream	ActReg chr22 #11218	1	1	0
11219	22	29,999,650	29,999,999	349	1	6.2	5.9	11.9	11	7	16	1	1	1	NF2	279	in gene	ActReg chr22 #11219	0	0	1
11220	22	30,112,050	30,113,531	1,481	2	14.804	19.696	4.804	52	55	12	0	1	1	CABP7	-3,554	upstream	ActReg chr22 #11220	1	1	0
11221	22	30,162,891	30,163,689	798	1	7.28	12.4	3.8	14	24	8	1	2	2	ZMAT5, UQCR10	-321, -68	upstream, upstream	ActReg chr22 #11221	0	1	0
11222	22	30,195,085	30,195,636	551	1	10.235	7.235	5.125	15	10	8	0	0	1	ASCC2	38,894	in gene	ActReg chr22 #11222	1	0	0
11223	22	30,622,162	30,622,619	457	1	3	11.357	3.308	5	17	6	0	0	0				ActReg chr22 #11223	0	1	0
11224	22	30,752,488	30,753,073	585	1	7.278	10.944	6	11	19	11	1	2	2	SF3A1, CCDC157	133, 153	in gene, in gene	ActReg chr22 #11224	0	1	0
11225	22	30,819,957	30,820,485	528	1	13.882	9.824	3.353	21	18	6	1	1	2	SEC14L2, MTP18	27288, -1499	in gene, upstream	ActReg chr22 #11225	1	0	0
11226	22	30,855,089	30,855,810	721	2	9.522	12.13	3	19	20	5	0	0	1	SEC14L3	12,585	in gene	ActReg chr22 #11226	1	1	0
11227	22	31,091,012	31,091,365	353	1	2.909	1.778	12.273	4	3	16	1	1	1	OSBP2	395	in gene	ActReg chr22 #11227	0	0	1
11228	22	31,198,467	31,199,287	820	2	15.8	16.28	3.833	29	33	9	1	0	1	OSBP2	108,084	in gene	ActReg chr22 #11228	1	1	0
11229	22	31,202,127	31,202,929	802	2	14.92	15.32	3.261	28	28	5	0	0	1	OSBP2	111,735	in gene	ActReg chr22 #11229	1	1	0
11230	22	31,280,521	31,280,828	307	1	1.111	2.778	9.111	2	3	11	0	0	1	OSBP2	189,881	in gene	ActReg chr22 #11230	0	0	1
11231	22	31,364,852	31,365,672	820	2	11.923	11.808	5.4	33	20	12	1	2	2	MORC2, TUG1	-1075, -372	upstream, upstream	ActReg chr22 #11231	1	1	0
11232	22	31,480,799	31,481,248	449	1	7.533	5	9.733	11	10	16	1	0	1	SMTN	3,718	in gene	ActReg chr22 #11232	0	0	1
11233	22	31,885,791	31,886,364	573	1	9.278	11.611	2.533	13	19	3	1	2	2	EIF4ENIF1, SFI1	-203, -6184	upstream, upstream	ActReg chr22 #11233	0	1	0
11234	22	32,026,372	32,027,319	947	3	9.483	10.517	9.69	16	20	18	1	1	1	PISD	-55	upstream	ActReg chr22 #11234	1	1	1
11235	22	32,145,632	32,146,537	905	2	10.138	10.655	5.586	17	25	10	1	2	2	C22orf30, DEPDC5	36, -3985	in gene, upstream	ActReg chr22 #11235	1	1	0
11236	22	32,499,778	32,500,675	897	1	7.857	14.607	2	15	27	4	0	0	1	SLC5A1	61,207	in gene	ActReg chr22 #11236	0	1	0
11237	22	32,502,783	32,503,318	535	1	7	11.412	2.938	10	14	5	0	0	1	SLC5A1	64,031	in gene	ActReg chr22 #11237	0	1	0
11238	22	32,555,199	32,555,493	294	1	1.6	1.4	8.9	2	2	13	0	1	1	C22orf42	-103	upstream	ActReg chr22 #11238	0	0	1
11239	22	32,602,395	32,602,771	376	1	2.583	7.167	11.167	4	11	16	0	1	1	RFPL2	-1,865	upstream	ActReg chr22 #11239	0	0	1
11240	22	32,870,317	32,871,164	847	3	8.808	11.308	6.846	14	19	14	1	1	1	FBXO7	33	in gene	ActReg chr22 #11240	1	1	1
11241	22	32,928,024	32,929,067	1,043	1	7.152	11.454	7.485	16	17	14	0	0	1	SYN3	525,832	in gene	ActReg chr22 #11241	0	1	0
11242	22	33,192,741	33,193,345	604	1	10.421	6.474	2.579	20	10	4	0	1	2	SYN3, TIMP3	261334, -3759	in gene, upstream	ActReg chr22 #11242	1	0	0
11243	22	34,318,284	34,318,599	315	1	1.875	2.6	8.9	4	4	12	1	1	1	LARGE	-2,025	upstream	ActReg chr22 #11243	0	0	1
11244	22	35,653,077	35,653,887	810	2	8.24	15.4	2.84	17	31	6	1	1	1	HMGXB4	37	in gene	ActReg chr22 #11244	1	1	0
11245	22	35,695,741	35,696,895	1,154	2	7.667	12.028	4.97	13	20	11	1	1	2	HMGXB4, TOM1	42873, 1050	downstream, in gene	ActReg chr22 #11245	1	1	0
11246	22	35,772,750	35,773,322	572	1	10.556	5.611	5.667	17	9	11	0	1	1	HMOX1	-4,024	upstream	ActReg chr22 #11246	1	0	0
11247	22	36,680,168	36,680,413	245	1	3.571	1.429	12.571	4	3	14	0	0	1	MYH9	103,773	in gene	ActReg chr22 #11247	0	0	1
11248	22	36,851,234	36,851,612	378	1	2.8	4.364	11.909	4	6	15	1	0	0				ActReg chr22 #11248	0	0	1
11249	22	36,859,780	36,860,213	433	1	3.615	3.692	11.846	6	5	17	0	0	1	TXN2	17,691	downstream	ActReg chr22 #11249	0	0	1
11250	22	36,877,287	36,877,806	519	2	8.938	9.312	10.4	12	17	18	0	1	2	TXN2, FOXRED2	141, 25602	in gene, downstream	ActReg chr22 #11250	0	1	1
11251	22	36,924,924	36,925,434	510	1	9.938	6.812	6.312	15	11	8	1	1	1	EIF3D	98	in gene	ActReg chr22 #11251	1	0	0
11252	22	36,942,894	36,943,457	563	1	4.833	10.778	2.462	9	18	4	0	0	0				ActReg chr22 #11252	0	1	0
11253	22	37,039,949	37,040,862	913	2	12.667	18.036	2.95	33	36	5	0	0	1	CACNG2	58,498	in gene	ActReg chr22 #11253	1	1	0
11254	22	37,055,879	37,056,507	628	1	6.579	11.053	2.375	12	18	5	0	0	1	CACNG2	42,710	in gene	ActReg chr22 #11254	0	1	0
11255	22	37,099,318	37,099,857	539	2	10.118	8.471	2.583	16	17	4	1	1	1	CACNG2	-684	upstream	ActReg chr22 #11255	1	1	0
11256	22	37,121,495	37,121,787	292	1	3.111	1.875	9.778	7	3	12	0	0	0				ActReg chr22 #11256	0	0	1
11257	22	37,583,940	37,584,291	351	1	1.909	3.455	9.364	4	6	12	0	1	1	C1QTNF6	215	in gene	ActReg chr22 #11257	0	0	1
11258	22	37,731,000	37,731,443	443	1	3	4.571	13.143	5	6	16	1	0	0				ActReg chr22 #11258	0	0	1
11259	22	38,004,231	38,005,159	928	2	16.483	17.759	4.069	32	36	8	1	1	1	GGA1	214	in gene	ActReg chr22 #11259	1	1	0
11260	22	38,081,989	38,082,734	745	2	10.913	13.826	6.217	23	26	12	1	1	2	LGALS1, NOL12	10748, 17	downstream, in gene	ActReg chr22 #11260	1	1	0
11261	22	38,165,054	38,165,538	484	1	4.733	4.375	10.5	8	7	18	0	0	1	TRIOBP	72,301	in gene	ActReg chr22 #11261	0	0	1
11262	22	38,239,927	38,240,691	764	1	8.042	13.292	4.364	15	18	7	1	3	4	ANKRD54, MIR658, MIR659, EIF3L	44, 69, 3472, -5061	in gene, in gene, downstream, upstream	ActReg chr22 #11262	0	1	0
11263	22	38,245,108	38,245,861	753	2	7.625	11.375	10.25	12	19	18	1	4	4	ANKRD54, MIR658, MIR659, EIF3L	-5131, -5106, -1703, 114	upstream, upstream, upstream, in gene	ActReg chr22 #11263	0	1	1
11264	22	38,300,846	38,301,769	923	1	11.966	7.828	4.172	18	15	7	1	1	1	MICALL1	-1,039	upstream	ActReg chr22 #11264	1	0	0
11265	22	38,363,560	38,364,879	1,319	1	11.293	8.951	5.976	16	15	11	0	0	2	POLR2F, SOX10	14545, 16320	in gene, downstream	ActReg chr22 #11265	1	0	0
11266	22	38,373,535	38,374,147	612	1	6.15	8.75	14.7	11	15	21	0	0	3	POLR2F, SOX10, LOC100131530	24167, 6698, -8329	downstream, in gene, upstream	ActReg chr22 #11266	0	0	1
11267	22	38,378,834	38,380,206	1,372	2	8.163	10.674	8.821	13	16	18	1	2	2	SOX10, LOC100131530	1019, -2650	in gene, upstream	ActReg chr22 #11267	0	1	1
11268	22	38,414,629	38,415,256	627	1	7.947	8.684	10.632	11	13	13	0	0	0				ActReg chr22 #11268	0	0	1
11269	22	38,426,407	38,427,956	1,549	1	7.562	13.167	6.333	14	22	14	0	0	0				ActReg chr22 #11269	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11270	22	38,429,498	38,430,882	1,384	1	7.705	11.704	7.205	14	18	12	0	0	0				ActReg chr22 #11270	0	1	0
11271	22	38,435,406	38,435,963	557	1	4.412	7.941	12.471	7	11	19	0	0	0				ActReg chr22 #11271	0	0	1
11272	22	38,751,186	38,751,487	301	1	1.667	3.5	9.556	4	6	12	0	0	0				ActReg chr22 #11272	0	0	1
11273	22	39,052,386	39,052,756	370	1	6.727	4.455	11.182	8	6	15	1	2	2	RP1-199H16.1, CSY1	63, -87	in gene, upstream	ActReg chr22 #11273	0	0	1
11274	22	39,077,420	39,078,404	984	3	35.677	39.645	7.226	112	130	16	1	2	5	CBY1, LOC100506326, TOMM22, LOC100506349, JOSD1	25254, -137, -42, 21129, 18547	downstream, upstream, upstream, downstream, downstream	ActReg chr22 #11274	1	1	1
11275	22	39,096,775	39,097,303	528	1	11.125	11.375	4.4	20	20	6	1	3	3	LOC100506349, JOSD1, GTPBP1	2002, -580, -4768	in gene, upstream, upstream	ActReg chr22 #11275	0	1	0
11276	22	39,101,444	39,102,193	749	2	10.826	10.174	2.059	19	17	5	1	3	3	LOC100506349, JOSD1, GTPBP1	-2777, -5359, 11	upstream, upstream, in gene	ActReg chr22 #11276	1	1	0
11277	22	39,151,340	39,152,640	1,300	3	9.805	8.5	5.182	23	20	13	1	1	1	SUN2	-43	upstream	ActReg chr22 #11277	1	1	0
11278	22	39,190,079	39,190,597	518	1	8.706	6.294	1.333	15	8	3	1	1	1	DNAL4	-177	upstream	ActReg chr22 #11278	1	0	0
11279	22	39,220,296	39,221,130	834	2	12.269	15.423	2.4	25	27	4	0	0	1	NPTXR	19,304	in gene	ActReg chr22 #11279	1	1	0
11280	22	39,227,241	39,227,757	516	1	4.875	11.188	5.312	8	16	8	0	0	1	NPTXR	12,518	in gene	ActReg chr22 #11280	0	1	0
11281	22	39,268,265	39,268,725	460	1	7.769	10.786	4.857	13	18	7	1	1	2	LOC100506361, CBX6	21306, -237	downstream, upstream	ActReg chr22 #11281	0	1	0
11282	22	39,312,741	39,313,245	504	1	7	9.467	3	11	16	4	0	0	0				ActReg chr22 #11282	0	1	0
11283	22	39,715,055	39,715,881	826	2	6.231	11.192	10.346	10	19	24	1	5	5	RPL3, SNORD83B, SNORD83A, RNU86, SNORD43	202, -5552, -4156, -2567, -350	in gene, upstream, upstream, upstream, upstream	ActReg chr22 #11283	0	1	1
11284	22	39,795,378	39,796,092	714	2	15.636	16.364	7.136	32	36	13	1	1	1	MAP3K7IP1	-24	upstream	ActReg chr22 #11284	1	1	0
11285	22	39,874,025	39,874,922	897	3	10.429	10.75	8.714	20	15	15	0	0	2	MGAT3, LOC100506493	21148, 3027	in gene, downstream	ActReg chr22 #11285	1	1	1
11286	22	39,924,922	39,925,674	752	1	9.708	6.5	5.958	17	11	9	0	0	2	ATF4, RPS19BP1	8729, 3562	downstream, in gene	ActReg chr22 #11286	1	0	0
11287	22	39,941,361	39,942,836	1,475	2	11.783	14.522	3.78	27	34	9	0	0	0				ActReg chr22 #11287	1	1	0
11288	22	40,076,793	40,077,188	395	1	3.538	2.615	12.231	5	5	16	0	0	1	CACNA1I	110,232	in gene	ActReg chr22 #11288	0	0	1
11289	22	40,111,879	40,112,248	369	1	1.6	2.364	11.546	2	3	14	0	0	0				ActReg chr22 #11289	0	0	1
11290	22	40,742,245	40,742,705	460	1	9.929	10.071	7.286	12	14	12	1	1	1	ADSL	-29	upstream	ActReg chr22 #11290	1	0	0
11291	22	41,032,450	41,033,423	973	2	10.133	10.333	3.867	20	17	8	1	1	1	MKL1	-246	upstream	ActReg chr22 #11291	1	1	0
11292	22	41,047,959	41,048,511	552	1	9.118	8.118	10.823	11	12	16	0	0	0				ActReg chr22 #11292	0	0	1
11293	22	41,252,946	41,253,368	422	1	8.615	9.923	11.385	11	14	16	1	2	3	ST13, XPNPEP3, DNAJB7	-470, 63, 4973	upstream, in gene, downstream	ActReg chr22 #11293	0	0	1
11294	22	41,592,765	41,593,431	666	1	5.095	8.333	12.619	8	13	19	1	0	1	L3MBTL2	-8,215	upstream	ActReg chr22 #11294	0	0	1
11295	22	41,682,042	41,682,640	598	1	8.053	11.684	4	15	26	9	1	1	1	RANGAP1	-125	upstream	ActReg chr22 #11295	0	1	0
11296	22	41,716,796	41,717,067	271	1	3.111	4.333	10.444	5	6	15	0	0	1	ZC3H7B	19,364	in gene	ActReg chr22 #11296	0	0	1
11297	22	41,842,518	41,843,319	801	3	10.8	11.6	11.08	17	16	23	1	1	1	TOB2	109	in gene	ActReg chr22 #11297	1	1	1
11298	22	41,864,542	41,865,443	901	2	10	10.586	4.586	16	16	9	1	2	2	PHF5A, ACO2	-284, -137	upstream, upstream	ActReg chr22 #11298	1	1	0
11299	22	41,939,915	41,940,521	606	1	12.21	9.895	3.429	20	15	6	1	1	1	POLR3H	261	in gene	ActReg chr22 #11299	1	0	0
11300	22	42,062,719	42,063,093	374	1	6.833	11.667	7.5	10	17	10	1	0	3	XRCC6, NHP2L1, LOC100506562	45611, 22007, 10346	downstream, downstream, downstream	ActReg chr22 #11300	0	1	0
11301	22	42,196,370	42,196,935	565	1	4.333	7.722	12.444	7	14	19	1	1	2	MEI1, CCDC134	101134, -26	downstream, upstream	ActReg chr22 #11301	0	0	1
11302	22	42,222,546	42,222,853	307	1	2	4.9	9.9	3	7	15	0	1	2	CCDC134, SREBF2	26021, -6407	downstream, upstream	ActReg chr22 #11302	0	0	1
11303	22	42,228,373	42,229,345	972	2	18.484	12.194	3.29	39	30	6	1	1	2	CCDC134, SREBF2	32181, -247	downstream, upstream	ActReg chr22 #11303	1	1	0
11304	22	42,342,573	42,343,478	905	2	13.286	16.786	7.607	32	39	12	1	2	2	CENPM, LOC339674	123, -5166	in gene, upstream	ActReg chr22 #11304	1	1	0
11305	22	42,486,242	42,486,674	432	1	7.462	5.231	10.462	10	10	15	1	3	4	C22orf32, NDUFA6, LOC100287153, LOC100132273	10759, 430, -479, -479	downstream, in gene, upstream, upstream	ActReg chr22 #11305	0	0	1
11306	22	42,567,892	42,568,903	1,011	2	9.406	8.188	2.3	14	15	5	0	0	1	TCF20	43,048	in gene	ActReg chr22 #11306	1	1	0
11307	22	43,010,624	43,011,862	1,238	3	11.051	12.256	10.026	24	22	24	1	2	3	POLDIP3, RNU12, CYB5R3	-281, -8, 34162	upstream, upstream, downstream	ActReg chr22 #11307	1	1	1
11308	22	43,150,642	43,151,099	457	1	7.143	10.786	3.333	11	15	4	0	0	0				ActReg chr22 #11308	0	1	0
11309	22	43,484,698	43,485,674	976	2	15.645	22.258	1.821	33	53	3	1	1	1	TTLL1	248	in gene	ActReg chr22 #11309	1	1	0
11310	22	44,208,156	44,208,708	552	1	7.222	10.5	3.722	10	15	7	1	1	1	EFCAB6	-215	upstream	ActReg chr22 #11310	0	1	0
11311	22	44,263,506	44,264,231	725	2	8.87	13.391	3.5	20	28	5	0	1	1	SULT4A1	-5,490	upstream	ActReg chr22 #11311	1	1	0
11312	22	44,350,938	44,351,622	684	2	7.455	10.046	9	17	14	12	1	1	2	PNPLA3, SAMM50	31661, 19	downstream, in gene	ActReg chr22 #11312	1	1	0
11313	22	44,694,322	44,694,638	316	1	2.7	3.5	10.3	4	5	13	0	0	1	KIAA1644	14,251	in gene	ActReg chr22 #11313	0	0	1
11314	22	44,806,582	44,806,845	263	1	1.125	1.875	10.375	2	4	13	0	0	0				ActReg chr22 #11314	0	0	1
11315	22	45,020,767	45,021,175	408	1	4.385	3.308	10	6	6	14	0	0	0				ActReg chr22 #11315	0	0	1
11316	22	45,130,385	45,130,870	485	1	2.8	3.867	11.667	5	7	15	0	0	2	PRR5, PRR5-ARHGAP8	66034, 32245	in gene, in gene	ActReg chr22 #11316	0	0	1
11317	22	45,243,770	45,244,214	444	1	2.444	3.571	10.643	4	6	14	0	0	2	PRR5-ARHGAP8, ARHGAP8	145610, 95554	in gene, in gene	ActReg chr22 #11317	0	0	1
11318	22	45,371,223	45,371,902	679	2	11.714	12.191	4.278	21	24	8	0	1	2	PHF21B, LOC100506695	34247, -3397	in gene, upstream	ActReg chr22 #11318	1	1	0
11319	22	45,475,874	45,476,537	663	1	8.684	11.7	1.812	14	19	4	0	0	0				ActReg chr22 #11319	0	1	0
11320	22	45,559,323	45,559,746	423	1	6.214	5.857	10.071	10	7	16	1	2	2	LOC100506714, NUP50	128, -192	in gene, upstream	ActReg chr22 #11320	0	0	1
11321	22	45,705,287	45,705,658	371	1	3.727	8.909	10.727	5	12	17	1	1	1	FAM118A	391	in gene	ActReg chr22 #11321	0	0	1
11322	22	46,068,097	46,068,824	727	1	3.773	10.046	2.9	6	15	6	1	1	1	ATXN10	782	in gene	ActReg chr22 #11322	0	1	0
11323	22	46,281,835	46,282,164	329	1	1.3	1.857	11.8	2	2	15	0	0	0				ActReg chr22 #11323	0	0	1
11324	22	46,330,910	46,331,428	518	1	5.824	9.824	11.353	8	16	15	0	0	1	WNT7B	41,839	in gene	ActReg chr22 #11324	0	0	1
11325	22	46,338,399	46,338,774	375	1	2.917	5.25	10	5	7	15	0	1	2	WNT7B, LOC100506756	34422, -7250	in gene, upstream	ActReg chr22 #11325	0	0	1
11326	22	46,364,636	46,365,429	793	1	6.56	11.92	5.2	12	18	11	0	0	2	WNT7B, LOC100506756	7976, 19196	in gene, in gene	ActReg chr22 #11326	0	1	0
11327	22	46,383,094	46,383,447	353	1	3.727	1.5	10.546	5	3	13	0	0	0				ActReg chr22 #11327	0	0	1
11328	22	46,392,933	46,393,296	363	1	2.455	4.818	11.182	4	6	17	0	0	0				ActReg chr22 #11328	0	0	1
11329	22	46,480,873	46,481,369	496	1	8.867	6.667	11.733	15	8	17	0	1	1	LOC400931	-756	upstream	ActReg chr22 #11329	0	0	1
11330	22	46,481,696	46,482,388	692	2	10.591	6.864	8.455	17	11	15	1	1	1	LOC400931	165	in gene	ActReg chr22 #11330	1	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11331	22	46,508,901	46,509,496	595	1	3.833	5.444	12.167	5	8	18	0	2	3	LOC400931, MIRLET7A3, MIRLET7B	27321, 569, -368	in gene, downstream, upstream	ActReg chr22 #11331	0	0	1
11332	22	46,692,402	46,693,110	708	2	12.318	11.954	4.364	22	20	8	1	2	3	TTC38, CN5H6.4, GTSE1	28895, -199, 118	downstream, upstream, in gene	ActReg chr22 #11332	1	1	0
11333	22	46,731,270	46,732,034	764	1	8.167	14.708	3.958	14	29	7	1	1	2	GTSE1, TRMU	39014, 354	downstream, in gene	ActReg chr22 #11333	0	1	0
11334	22	46,849,931	46,850,514	583	1	8.056	11	2.688	10	15	4	0	0	1	CELSR1	82,845	in gene	ActReg chr22 #11334	0	1	0
11335	22	47,158,098	47,158,869	771	2	8.792	11.917	6	17	18	11	1	1	1	TBC1D22A	-35	upstream	ActReg chr22 #11335	1	1	0
11336	22	47,605,801	47,606,075	274	1	1.667	2	11.25	2	4	15	0	0	0				ActReg chr22 #11336	0	0	1
11337	22	48,027,225	48,027,995	770	1	7.292	11.542	3.13	12	23	5	1	1	1	RP11-191L9.1	-292	upstream	ActReg chr22 #11337	0	1	0
11338	22	49,032,782	49,033,136	354	1	1.8	3	10.091	2	5	12	0	0	1	FAM19A5	147,671	in gene	ActReg chr22 #11338	0	0	1
11339	22	49,039,961	49,040,542	581	1	5.611	10.778	3.556	10	18	5	0	0	1	FAM19A5	154,963	in gene	ActReg chr22 #11339	0	1	0
11340	22	49,047,222	49,047,527	305	1	1.6	2	9.9	3	4	13	0	0	1	FAM19A5	162,086	in gene	ActReg chr22 #11340	0	0	1
11341	22	49,098,193	49,098,938	745	1	11.609	9.261	5.696	17	12	10	0	0	1	FAM19A5	213,277	in gene	ActReg chr22 #11341	1	0	0
11342	22	49,116,771	49,117,087	316	1	2.556	1.111	9.111	3	2	12	0	0	1	FAM19A5	231,641	in gene	ActReg chr22 #11342	0	0	1
11343	22	49,145,315	49,145,650	335	1	4	2.2	11.3	5	3	14	1	0	1	FAM19A5	260,194	in gene	ActReg chr22 #11343	0	0	1
11344	22	49,546,126	49,546,427	301	1	2	1	9.667	4	1	13	0	0	0				ActReg chr22 #11344	0	0	1
11345	22	49,768,835	49,769,268	433	1	5.385	3.923	11.077	8	9	16	0	0	0				ActReg chr22 #11345	0	0	1
11346	22	49,812,125	49,812,571	446	1	3.667	1.417	11.857	5	3	19	1	0	0				ActReg chr22 #11346	0	0	1
11347	22	49,970,976	49,971,417	441	1	2	3.154	11.643	3	5	20	0	0	0				ActReg chr22 #11347	0	0	1
11348	22	50,008,831	50,009,221	390	1	2.455	3.778	11.923	4	5	18	1	1	2	LOC100506932, C22orf34	338, 42164	in gene, downstream	ActReg chr22 #11348	0	0	1
11349	22	50,032,728	50,033,006	278	1	1.667	2.5	10	3	4	12	0	0	1	C22orf34	18,323	in gene	ActReg chr22 #11349	0	0	1
11350	22	50,128,944	50,129,393	449	1	3.929	10.214	3.714	7	16	5	0	0	0				ActReg chr22 #11350	0	1	0
11351	22	50,465,991	50,466,583	592	1	8.556	12.056	5.111	11	17	7	0	0	1	TTLL8	26,768	in gene	ActReg chr22 #11351	0	1	0
11352	22	50,469,651	50,470,080	429	1	2.786	2	11.357	5	3	17	1	0	1	TTLL8	23,190	in gene	ActReg chr22 #11352	0	0	1
11353	22	50,614,887	50,615,237	350	1	1	2	10.091	1	3	16	1	0	2	PANX2, TRABD	5902, -9298	in gene, upstream	ActReg chr22 #11353	0	0	1
11354	22	50,628,804	50,629,128	324	1	2.9	2.8	9.9	4	4	12	1	0	1	TRABD	4,606	in gene	ActReg chr22 #11354	0	0	1
11355	22	50,683,013	50,683,743	730	2	7.636	12.636	10.454	13	19	14	1	1	3	TUBGCP6, HDAC10, MAPK12	22, 6456, 16711	in gene, downstream, downstream	ActReg chr22 #11355	0	1	1
11356	22	50,714,345	50,714,709	364	1	3.909	1.9	10.727	5	3	15	0	1	2	MAPK11, PLXNB2	-5748, 31474	upstream, in gene	ActReg chr22 #11356	0	0	1
11357	22	50,722,613	50,722,943	330	1	2.7	2.6	11	5	4	13	0	0	1	PLXNB2	23,223	in gene	ActReg chr22 #11357	0	0	1
11358	22	50,724,647	50,725,005	358	1	4.091	3.714	10.727	6	5	14	0	0	1	PLXNB2	21,175	in gene	ActReg chr22 #11358	0	0	1
11359	22	50,735,347	50,735,694	347	1	3.636	3.444	11.546	6	5	17	0	0	1	PLXNB2	10,481	in gene	ActReg chr22 #11359	0	0	1
11360	22	50,765,532	50,766,366	834	2	9.538	10.84	3.812	19	17	6	1	1	1	FAM116B	-460	upstream	ActReg chr22 #11360	1	1	0
11361	22	50,920,257	50,920,650	393	1	4.917	5	10.5	7	7	15	1	3	3	SBF1, ADM2, MIOX	-6989, 441, -4760	upstream, in gene, upstream	ActReg chr22 #11361	0	0	1
11362	22	50,964,473	50,965,236	763	1	8.167	11.25	5.955	13	16	12	1	1	4	NCAPH2, SCO2, TYMP, ODF3B	18209, 14, 3660, 6154	downstream, in gene, in gene, downstream	ActReg chr22 #11362	0	1	0
11363	22	50,969,227	50,969,602	375	1	7.75	4.917	11.25	9	6	15	1	3	4	NCAPH2, SCO2, TYMP, ODF3B	22769, -4546, -900, 1594	downstream, upstream, upstream, in gene	ActReg chr22 #11363	0	0	1
11364	22	51,038,174	51,038,947	773	2	10.72	13.04	3.45	20	23	6	1	1	1	MAPK8IP2	-571	upstream	ActReg chr22 #11364	1	1	0
11365	22	51,066,157	51,066,434	277	1	4.4	4.125	9.778	5	7	12	1	2	2	LOC100506900, ARSA	-3969, 312	upstream, in gene	ActReg chr22 #11365	0	0	1
11366	3	238,829	239,229	400	1	2.333	4.167	13.25	4	6	20	1	2	2	LOC642891, CHL1	61, 379	in gene, in gene	ActReg chr3 #11366	0	0	1
11367	3	577,429	578,349	920	2	12.862	18.965	3.565	35	52	7	0	0	0				ActReg chr3 #11367	1	1	0
11368	3	754,952	755,391	439	1	11.308	9.615	1	14	14	1	0	0	0				ActReg chr3 #11368	1	0	0
11369	3	1,220,505	1,221,193	688	1	11.5	7.545	3.2	18	12	6	0	0	1	CNTN6	86,220	in gene	ActReg chr3 #11369	1	0	0
11370	3	2,125,169	2,125,615	446	1	1.929	3.571	9.5	3	7	13	0	0	0				ActReg chr3 #11370	0	0	1
11371	3	2,393,837	2,394,272	435	1	3.214	3.769	11.643	5	7	19	0	0	1	CNTN4	251,807	in gene	ActReg chr3 #11371	0	0	1
11372	3	3,168,052	3,169,211	1,159	2	9	13.222	7.171	18	27	18	1	1	1	TRNT1	31	in gene	ActReg chr3 #11372	0	1	1
11373	3	3,220,867	3,221,929	1,062	2	33.636	43.636	4.406	102	127	13	1	1	1	CRBN	3	in gene	ActReg chr3 #11373	1	1	0
11374	3	4,344,592	4,345,426	834	1	10.154	7.769	5.423	16	13	9	1	1	1	SETMAR	21	in gene	ActReg chr3 #11374	1	0	0
11375	3	4,508,493	4,509,219	726	2	15.565	17.13	7.562	34	35	11	1	1	1	SUMF1	110	in gene	ActReg chr3 #11375	1	1	0
11376	3	4,534,524	4,535,320	796	2	11.56	10.68	9.04	19	16	16	1	1	1	ITPR1	-110	upstream	ActReg chr3 #11376	1	1	0
11377	3	4,994,591	4,995,438	847	2	11.333	12.37	3.125	18	22	5	0	0	0				ActReg chr3 #11377	1	1	0
11378	3	5,019,604	5,020,263	659	1	6.714	11.809	7.286	11	20	15	1	1	1	BHLHE40	-1,164	upstream	ActReg chr3 #11378	0	1	0
11379	3	5,163,429	5,164,785	1,356	2	45.191	51.809	6.541	189	203	13	1	1	1	ARL8B	177	in gene	ActReg chr3 #11379	1	1	0
11380	3	6,951,983	6,952,733	750	2	9.739	9.435	2.667	17	17	6	0	0	1	GRM7	49,556	in gene	ActReg chr3 #11380	1	1	0
11381	3	7,031,174	7,031,783	609	1	10.632	7.105	1	16	11	1	0	0	1	GRM7	128,676	in gene	ActReg chr3 #11381	1	0	0
11382	3	7,546,822	7,547,292	470	1	6.5	10.857	2.385	12	17	4	0	0	1	GRM7	644,255	in gene	ActReg chr3 #11382	0	1	0
11383	3	7,610,421	7,610,715	294	1	2.286	1.889	10.778	3	3	15	0	0	1	GRM7	707,766	in gene	ActReg chr3 #11383	0	0	1
11384	3	8,019,565	8,020,441	876	1	10.037	15.889	4.519	17	28	7	0	0	0				ActReg chr3 #11384	0	1	0
11385	3	8,543,080	8,543,729	649	1	7.75	13.15	6.25	11	22	9	1	2	2	LOC100288428, LMCD1	-60, -107	upstream, upstream	ActReg chr3 #11385	0	1	0
11386	3	8,671,048	8,671,794	746	2	10.043	15.826	5.095	23	32	11	0	0	1	C3orf32	22,316	in gene	ActReg chr3 #11386	1	1	0
11387	3	8,834,654	8,835,395	741	1	9.75	14.125	5.583	18	27	9	0	0	0				ActReg chr3 #11387	0	1	0
11388	3	9,004,623	9,005,437	814	1	13.08	7.92	5.52	21	19	11	1	1	1	RAD18	129	in gene	ActReg chr3 #11388	1	0	0
11389	3	9,438,114	9,439,208	1,094	1	7.912	13.529	6.794	18	21	14	1	3	4	THUMPD3, LOC440944, LOC100507618, SETD5	33944, 513, 91, -742	downstream, in gene, in gene, upstream	ActReg chr3 #11389	0	1	0
11390	3	9,439,520	9,439,967	447	1	6.571	7.143	10.286	12	12	18	1	3	3	LOC440944, LOC100507618, SETD5	-569, -991, 340	upstream, upstream, in gene	ActReg chr3 #11390	0	0	1
11391	3	9,464,290	9,464,875	585	1	9.056	6.611	2.389	16	13	4	0	0	1	SETD5	25,179	in gene	ActReg chr3 #11391	1	0	0
11392	3	9,593,782	9,594,408	626	1	7.75	21.85	5.3	13	42	8	1	1	1	LHFPL4	1,391	in gene	ActReg chr3 #11392	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11393	3	9,773,031	9,773,740	709	1	5.682	10.182	7	10	16	19	1	1	2	CPNE9, BRPF1	27875, -49	downstream, upstream	ActReg chr3 #11393	0	1	0
11394	3	9,833,843	9,834,993	1,150	2	8.972	12.5	9.694	15	21	17	1	2	2	TADA3, ARPC4	2, 191	in gene, in gene	ActReg chr3 #11394	0	1	1
11395	3	9,932,004	9,932,777	773	2	11.875	15.667	8.083	23	29	14	1	1	1	JAGN1	119	in gene	ActReg chr3 #11395	1	1	0
11396	3	9,974,627	9,975,821	1,194	2	11.054	15.46	6.108	19	36	13	1	1	2	IL17RC, CRELD1	16460, -300	in gene, upstream	ActReg chr3 #11396	1	1	0
11397	3	9,987,697	9,989,657	1,960	3	20.377	26.279	9.984	59	84	21	1	0	2	CRELD1, PRRT3	13153, 5401	downstream, in gene	ActReg chr3 #11397	1	1	1
11398	3	10,027,987	10,028,963	976	2	11.419	14.871	6.097	26	31	11	0	2	2	TMEM111, LOC442075	47, -120	in gene, upstream	ActReg chr3 #11398	1	1	0
11399	3	10,067,728	10,068,468	740	2	14.739	18.391	7.304	33	43	11	1	1	1	FANCD2	-15	upstream	ActReg chr3 #11399	1	1	0
11400	3	10,183,402	10,183,960	558	1	11.294	8.353	12.941	16	13	19	1	1	1	VHL	362	in gene	ActReg chr3 #11400	0	0	1
11401	3	10,206,589	10,207,065	476	1	9.533	10.267	10.533	16	15	19	1	1	1	IRAK2	264	in gene	ActReg chr3 #11401	0	0	1
11402	3	10,247,195	10,248,252	1,057	1	7.636	11.879	4.355	13	17	9	0	0	1	IRAK2	41,160	in gene	ActReg chr3 #11402	0	1	0
11403	3	10,362,511	10,363,169	658	1	9.286	13.095	5.429	18	29	8	1	1	3	SEC13, ATP2B2, MIR378B	18, 184428, -9073	in gene, downstream, upstream	ActReg chr3 #11403	0	1	0
11404	3	10,384,317	10,384,841	524	1	4.941	4.882	11.823	10	9	19	0	0	1	ATP2B2	162,689	in gene	ActReg chr3 #11404	0	0	1
11405	3	10,500,462	10,503,169	2,707	2	20.224	26.671	5.014	117	119	12	0	0	1	ATP2B2	45,453	in gene	ActReg chr3 #11405	1	1	0
11406	3	10,539,935	10,540,688	753	1	3.75	3.667	11.125	10	5	16	0	0	1	ATP2B2	6,957	in gene	ActReg chr3 #11406	0	0	1
11407	3	10,599,152	10,600,332	1,180	2	10.838	10.865	5	20	16	10	0	0	0				ActReg chr3 #11407	1	1	0
11408	3	10,636,427	10,637,165	738	2	12.652	10.174	1.368	27	17	3	0	0	0				ActReg chr3 #11408	1	1	0
11409	3	10,641,843	10,643,301	1,458	1	6.739	11.761	6.609	11	17	13	0	0	0				ActReg chr3 #11409	0	1	0
11410	3	10,683,257	10,684,074	817	2	10.231	11.846	2.304	19	17	5	0	0	0				ActReg chr3 #11410	1	1	0
11411	3	10,795,436	10,796,235	799	2	10.84	19.48	3.8	25	43	8	0	0	1	LOC285370	10,042	downstream	ActReg chr3 #11411	1	1	0
11412	3	11,005,769	11,006,751	982	2	12.2	15.967	3.05	24	28	5	0	0	0				ActReg chr3 #11412	1	1	0
11413	3	11,138,190	11,138,810	620	1	6.474	12.263	3.737	15	17	7	0	0	0				ActReg chr3 #11413	0	1	0
11414	3	11,609,314	11,610,513	1,199	2	12.892	14.189	3.086	26	26	6	1	1	2	VGLL4, LOC100133039	152307, -3964	in gene, upstream	ActReg chr3 #11414	1	1	0
11415	3	11,651,350	11,651,852	502	1	8.688	12.562	2.75	16	23	4	0	0	1	VGLL4	110,619	in gene	ActReg chr3 #11415	0	1	0
11416	3	11,887,586	11,888,927	1,341	2	47.366	46.439	6.795	193	174	13	1	1	1	C3orf31	96	in gene	ActReg chr3 #11416	1	1	0
11417	3	12,196,797	12,197,896	1,099	2	11.059	10.794	4.107	20	25	9	0	0	2	SYN2, TIMP4	151479, 3306	in gene, in gene	ActReg chr3 #11417	1	1	0
11418	3	12,437,009	12,437,553	544	1	9.235	4.294	0	14	7	0	0	0	1	PPARG	107,932	in gene	ActReg chr3 #11418	1	0	0
11419	3	12,447,203	12,447,680	477	1	4.933	10.267	3.071	7	17	5	0	0	1	PPARG	118,092	in gene	ActReg chr3 #11419	0	1	0
11420	3	12,525,501	12,526,448	947	2	10.933	11.7	6.5	19	19	11	1	1	1	TSEN2	43	in gene	ActReg chr3 #11420	1	1	0
11421	3	12,598,103	12,599,064	961	2	13.433	14.2	5.967	22	26	13	1	1	1	MKRN2	-11	upstream	ActReg chr3 #11421	1	1	0
11422	3	12,705,033	12,706,207	1,174	3	15.111	17.111	8.829	35	45	17	1	1	1	RAF1	80	in gene	ActReg chr3 #11422	1	1	1
11423	3	12,882,656	12,883,650	994	1	7.906	15.094	6.6	13	28	13	1	2	3	CAND2, RPL32, SNORA7A	44982, -72, -1204	downstream, upstream, upstream	ActReg chr3 #11423	0	1	0
11424	3	12,976,492	12,977,057	565	1	5	6.667	13	9	10	18	1	0	1	IQSEC1	137,843	in gene	ActReg chr3 #11424	0	0	1
11425	3	12,989,820	12,991,265	1,445	1	7.652	11.957	5.07	15	18	14	0	0	1	IQSEC1	124,075	in gene	ActReg chr3 #11425	0	1	0
11426	3	12,994,015	12,994,375	360	1	2	2.417	10.5	4	3	12	0	0	1	IQSEC1	120,422	in gene	ActReg chr3 #11426	0	0	1
11427	3	13,034,222	13,034,900	678	1	8.81	6.714	13.429	15	12	19	1	0	1	IQSEC1	80,056	in gene	ActReg chr3 #11427	0	0	1
11428	3	13,035,938	13,037,072	1,134	3	18.229	22.4	8.514	48	71	16	1	0	1	IQSEC1	78,112	in gene	ActReg chr3 #11428	1	1	1
11429	3	13,096,040	13,096,939	899	1	8.071	10.75	8.16	14	19	13	0	0	1	IQSEC1	18,128	in gene	ActReg chr3 #11429	0	1	0
11430	3	13,182,632	13,184,552	1,920	2	11.95	20.117	4.679	37	56	11	0	0	0				ActReg chr3 #11430	1	1	0
11431	3	13,318,068	13,318,537	469	1	3.133	4.067	10.667	5	6	16	0	0	0				ActReg chr3 #11431	0	0	1
11432	3	13,322,144	13,322,653	509	1	2.25	2	11.625	4	3	14	0	0	0				ActReg chr3 #11432	0	0	1
11433	3	13,326,990	13,327,433	443	1	1.929	2.357	11.214	4	4	15	0	0	0				ActReg chr3 #11433	0	0	1
11434	3	13,534,546	13,534,997	451	1	2.286	3.857	11.357	4	5	15	0	0	1	HDAC11	13,056	in gene	ActReg chr3 #11434	0	0	1
11435	3	13,558,426	13,559,014	588	1	4.105	2.474	9.632	8	4	15	0	0	0				ActReg chr3 #11435	0	0	1
11436	3	13,612,726	13,613,234	508	1	3.75	3.375	11.625	5	5	15	0	0	1	FBLN2	22,355	in gene	ActReg chr3 #11436	0	0	1
11437	3	13,695,077	13,695,409	332	1	6	3.5	12	8	5	16	0	1	2	LOC100293612, LOC285375	704, 3022	in gene, in gene	ActReg chr3 #11437	0	0	1
11438	3	13,919,996	13,920,379	383	1	3.083	4.167	11.25	4	7	16	1	1	1	WNT7A	1,431	in gene	ActReg chr3 #11438	0	0	1
11439	3	13,976,356	13,976,732	376	1	3	1.625	10.909	4	3	17	0	1	1	LOC100132526	1,991	in gene	ActReg chr3 #11439	0	0	1
11440	3	14,078,510	14,078,998	488	1	3.083	4	13.067	4	5	19	0	0	0				ActReg chr3 #11440	0	0	1
11441	3	14,165,391	14,167,772	2,381	2	8.608	14.351	7.437	14	23	15	1	2	2	CHCHD4, TMEM43	-210, 141	upstream, in gene	ActReg chr3 #11441	0	1	1
11442	3	14,175,252	14,175,759	507	1	2.533	6.062	12.062	4	9	18	0	0	2	CHCHD4, TMEM43	-9134, 9065	upstream, in gene	ActReg chr3 #11442	0	0	1
11443	3	14,219,621	14,220,605	984	2	10.4	14.1	6	21	24	11	1	2	2	XPC, LSM3	59, -115	in gene, upstream	ActReg chr3 #11443	1	1	0
11444	3	14,306,626	14,307,390	764	1	6.609	9.739	4.95	12	13	9	0	0	0				ActReg chr3 #11444	0	1	0
11445	3	14,334,845	14,335,154	309	1	3.6	2.5	11.2	5	4	17	0	0	0				ActReg chr3 #11445	0	0	1
11446	3	14,388,491	14,389,010	519	1	4.062	2.688	11.125	5	6	14	0	0	0				ActReg chr3 #11446	0	0	1
11447	3	14,454,366	14,454,738	372	1	3.333	6.25	12.167	5	9	20	0	0	1	SLC6A6	10,446	in gene	ActReg chr3 #11447	0	0	1
11448	3	14,473,551	14,474,367	816	2	12.8	12	4.368	23	15	8	0	0	1	SLC6A6	29,853	in gene	ActReg chr3 #11448	1	1	0
11449	3	14,493,507	14,494,878	1,371	1	8.762	12	7.976	14	18	15	0	0	1	SLC6A6	50,086	in gene	ActReg chr3 #11449	0	1	0
11450	3	14,550,499	14,551,137	638	1	9.7	8.4	12.45	13	14	18	0	0	1	GRIP2	32,770	in gene	ActReg chr3 #11450	0	0	1
11451	3	14,605,609	14,606,841	1,232	1	8.105	12.105	7.053	13	18	11	0	0	0				ActReg chr3 #11451	0	1	0
11452	3	14,639,318	14,641,072	1,754	2	23.927	31.927	2.636	74	99	7	0	0	0				ActReg chr3 #11452	1	1	0
11453	3	14,663,379	14,663,741	362	1	4.091	5	11.727	6	6	15	0	0	0				ActReg chr3 #11453	0	0	1
11454	3	14,814,113	14,814,668	555	1	2.286	2.625	10.823	4	5	15	0	0	1	C3orf20	97,784	in gene	ActReg chr3 #11454	0	0	1
11455	3	14,918,546	14,919,222	676	1	3.667	4.905	12.333	7	7	21	0	0	1	FGD5	58,415	in gene	ActReg chr3 #11455	0	0	1
11456	3	14,988,550	14,988,963	413	1	5.846	12.385	8.385	8	18	14	1	3	3	LOC100505673, LOC100505641, NR2C2	1175, 644, -480	in gene, in gene, upstream	ActReg chr3 #11456	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11457	3	15,140,253	15,141,179	926	2	17.172	18.828	7.069	46	43	14	1	1	1	ZFYVE20	-61	upstream	ActReg chr3 #11457	1	1	0
11458	3	15,247,731	15,248,375	644	1	10.2	13.5	4.9	13	23	7	1	1	1	CAPN7	320	in gene	ActReg chr3 #11458	0	1	0
11459	3	15,310,760	15,311,540	780	1	12.625	9.792	5.042	24	19	8	0	0	2	LOC100505696, SH3BP5	15991, 71751	downstream, in gene	ActReg chr3 #11459	1	0	0
11460	3	15,342,072	15,343,131	1,059	2	10.152	14.727	4	21	29	7	0	0	1	SH3BP5	40,300	in gene	ActReg chr3 #11460	1	1	0
11461	3	15,352,112	15,352,689	577	1	7.278	10.722	1.625	12	16	3	0	0	1	SH3BP5	30,501	in gene	ActReg chr3 #11461	0	1	0
11462	3	15,373,034	15,374,415	1,381	2	14.302	17.395	5.091	33	28	13	1	0	1	SH3BP5	9,177	in gene	ActReg chr3 #11462	1	1	0
11463	3	15,468,366	15,469,431	1,065	1	7.424	10.424	8.061	10	14	11	1	2	2	METTL6, EAF1	144, -166	in gene, upstream	ActReg chr3 #11463	0	1	0
11464	3	15,693,647	15,694,169	522	1	3.625	4.4	10.375	5	7	12	0	0	2	BTD, LOC100505737	50653, -10088	downstream, upstream	ActReg chr3 #11464	0	0	1
11465	3	15,900,424	15,900,969	545	1	9	11.118	8.059	14	18	12	1	1	1	ANKRD28	357	in gene	ActReg chr3 #11465	0	1	0
11466	3	15,901,441	15,902,029	588	1	9.167	11.333	4.889	15	18	10	1	1	1	ANKRD28	-682	upstream	ActReg chr3 #11466	0	1	0
11467	3	16,024,444	16,025,160	716	1	11.261	9.957	3.235	19	14	5	0	0	0				ActReg chr3 #11467	1	0	0
11468	3	16,306,031	16,306,881	850	1	13.741	9.963	8.704	24	19	13	1	2	2	DPH3, OXNAD1	40, -211	in gene, upstream	ActReg chr3 #11468	1	0	0
11469	3	16,468,632	16,469,164	532	1	10.412	8.294	3.471	19	15	6	0	0	1	RFTN1	86,324	in gene	ActReg chr3 #11469	1	0	0
11470	3	16,625,005	16,625,562	557	1	11.294	7.941	2.062	20	10	4	0	0	1	DAZL	21,723	downstream	ActReg chr3 #11470	1	0	0
11471	3	16,930,530	16,931,201	671	1	11.238	5.286	3.353	16	9	7	0	0	1	PLCL2	4,413	in gene	ActReg chr3 #11471	1	0	0
11472	3	17,522,598	17,522,947	349	1	3.455	7	10.727	5	9	15	0	0	1	TBC1D5	261,468	in gene	ActReg chr3 #11472	0	0	1
11473	3	18,960,580	18,961,012	432	1	9.692	10.154	2.846	14	14	4	0	0	0				ActReg chr3 #11473	0	1	0
11474	3	19,189,326	19,189,848	522	1	8.25	12	3.429	13	17	6	1	1	1	KCNH8	-430	upstream	ActReg chr3 #11474	0	1	0
11475	3	19,190,030	19,190,705	675	2	10.238	10.238	2	16	17	3	1	1	1	KCNH8	350	in gene	ActReg chr3 #11475	1	1	0
11476	3	19,190,722	19,191,608	886	2	14.37	15.037	1.545	29	32	3	0	1	1	KCNH8	1,148	in gene	ActReg chr3 #11476	1	1	0
11477	3	19,988,267	19,989,401	1,134	2	9.943	10.857	12.286	17	19	25	1	1	1	RAB5A	262	in gene	ActReg chr3 #11477	0	1	1
11478	3	20,227,314	20,227,981	667	1	10.619	12.857	5.095	16	23	8	1	1	1	SGOL1	36	in gene	ActReg chr3 #11478	0	1	0
11479	3	22,413,710	22,414,059	349	1	5.182	3.909	11.273	8	6	16	1	1	1	LOC100505836	135	in gene	ActReg chr3 #11479	0	0	1
11480	3	22,458,363	22,458,696	333	1	2.636	4	11	5	5	15	0	0	0				ActReg chr3 #11480	0	0	1
11481	3	22,626,869	22,627,555	686	2	11.273	10.136	1.538	21	17	3	0	0	0				ActReg chr3 #11481	1	1	0
11482	3	23,244,674	23,245,124	450	1	9.143	9.786	7.077	14	17	13	1	2	2	LOC100505877, UBE2E2	-830, 115	upstream, in gene	ActReg chr3 #11482	0	1	0
11483	3	23,726,972	23,727,733	761	1	10.708	4.958	3.091	16	13	5	0	0	0				ActReg chr3 #11483	1	0	0
11484	3	23,957,973	23,959,377	1,404	2	9.091	16.046	11.546	16	26	24	1	2	3	NKIRAS1, RPL15, LOC100505901	-138, 36, 23840	upstream, in gene, downstream	ActReg chr3 #11484	0	1	1
11485	3	23,987,310	23,988,107	797	1	7.44	12.08	3.231	14	16	6	1	2	2	LOC100505901, NR1D2	-5193, 957	upstream, in gene	ActReg chr3 #11485	0	1	0
11486	3	24,197,862	24,198,524	662	1	12.2	8.9	1	23	17	1	0	0	1	THRB	338,120	in gene	ActReg chr3 #11486	1	0	0
11487	3	24,262,263	24,263,270	1,007	1	8.25	12.094	3.357	15	20	6	0	0	1	THRB	273,547	in gene	ActReg chr3 #11487	0	1	0
11488	3	24,406,585	24,407,133	548	1	3.412	11	1.188	5	19	2	0	0	1	THRB	129,454	in gene	ActReg chr3 #11488	0	1	0
11489	3	24,513,716	24,514,326	610	1	5.895	11.579	2.154	10	21	3	0	0	1	THRB	22,292	in gene	ActReg chr3 #11489	0	1	0
11490	3	24,535,431	24,536,620	1,189	3	9.568	11.162	10.595	18	17	20	1	1	1	THRB	288	in gene	ActReg chr3 #11490	1	1	1
11491	3	24,549,746	24,550,346	600	1	9.947	4.789	1.333	16	8	2	0	0	0				ActReg chr3 #11491	1	0	0
11492	3	24,563,570	24,564,125	555	1	4.529	10	4.059	7	15	6	1	0	0				ActReg chr3 #11492	0	1	0
11493	3	24,871,231	24,871,712	481	1	3.75	3.438	11.625	5	5	16	1	0	0				ActReg chr3 #11493	0	0	1
11494	3	25,705,519	25,706,059	540	1	8.471	10	6.545	16	18	9	1	1	1	TOP2B	-1	upstream	ActReg chr3 #11494	0	1	0
11495	3	25,831,193	25,831,945	752	1	11.708	7	4.429	16	9	7	0	2	2	NGLY1, OXSM	-39, 6	upstream, in gene	ActReg chr3 #11495	1	0	0
11496	3	25,893,217	25,893,585	368	1	3.636	3	9.727	4	4	15	0	0	1	LOC285326	21,785	downstream	ActReg chr3 #11496	0	0	1
11497	3	25,987,332	25,987,640	308	1	2	2.222	10.556	3	3	13	0	0	0				ActReg chr3 #11497	0	0	1
11498	3	27,156,121	27,156,673	552	1	10.278	6.706	1.941	21	14	3	0	0	0				ActReg chr3 #11498	1	0	0
11499	3	27,524,705	27,525,352	647	1	11.25	8.15	3	16	13	5	1	0	0				ActReg chr3 #11499	1	0	0
11500	3	27,525,628	27,526,416	788	1	9.08	11.68	4.333	15	15	7	1	0	0				ActReg chr3 #11500	0	1	0
11501	3	27,575,111	27,576,375	1,264	2	16.026	16.949	1.786	44	42	6	0	0	0				ActReg chr3 #11501	1	1	0
11502	3	27,763,393	27,764,084	691	2	11.048	9.19	7.4	18	16	14	1	1	1	EOMES	47	in gene	ActReg chr3 #11502	1	1	0
11503	3	27,799,389	27,800,145	756	2	10.667	10.333	1.583	21	19	3	0	0	0				ActReg chr3 #11503	1	1	0
11504	3	30,327,339	30,327,998	659	2	13.75	12.85	3.65	27	23	6	0	0	0				ActReg chr3 #11504	1	1	0
11505	3	30,389,037	30,389,803	766	1	6.333	11.167	2.652	13	16	4	0	0	0				ActReg chr3 #11505	0	1	0
11506	3	30,696,691	30,697,460	769	1	7.958	11.75	2.136	11	18	4	0	0	1	TGFBR2	49,081	in gene	ActReg chr3 #11506	0	1	0
11507	3	31,118,370	31,119,310	940	2	11.483	11.379	2.56	21	21	5	0	0	0				ActReg chr3 #11507	1	1	0
11508	3	31,329,635	31,330,604	969	1	8.3	11.433	2.963	14	19	6	0	0	0				ActReg chr3 #11508	0	1	0
11509	3	31,418,532	31,419,063	531	1	6.438	9.312	1.4	11	16	2	0	0	0				ActReg chr3 #11509	0	1	0
11510	3	31,573,072	31,574,511	1,439	3	10.422	13.178	11.822	19	20	22	1	1	1	STT3B	-700	upstream	ActReg chr3 #11510	1	1	1
11511	3	31,978,553	31,979,281	728	2	11.565	12.304	2	19	20	5	0	0	1	OSBPL10	44,425	in gene	ActReg chr3 #11511	1	1	0
11512	3	32,022,556	32,023,717	1,161	2	9.541	11.135	4.595	17	18	10	1	2	2	OSBPL10, ZNF860	206, -130	in gene, upstream	ActReg chr3 #11512	1	1	0
11513	3	32,147,605	32,148,271	666	1	13.381	7.524	7.05	21	15	11	1	1	1	GPD1L	-65	upstream	ActReg chr3 #11513	1	0	0
11514	3	32,268,294	32,268,846	552	1	11.412	5.588	1.778	18	8	2	0	0	0				ActReg chr3 #11514	1	0	0
11515	3	32,543,873	32,544,247	374	1	10	8.636	12.818	15	13	17	1	1	1	CMTM6	343	in gene	ActReg chr3 #11515	0	0	1
11516	3	32,611,764	32,612,767	1,003	1	8.097	11.355	7.806	15	15	17	1	1	1	DYNC1LI1	101	in gene	ActReg chr3 #11516	0	1	0
11517	3	32,726,169	32,727,189	1,020	3	8.594	12.844	6.571	17	27	15	1	1	1	CNOT10	-19	upstream	ActReg chr3 #11517	1	1	1
11518	3	33,137,878	33,139,226	1,348	1	7.405	10.833	6.595	13	17	16	1	2	2	GLB1, TMPPE	142, -259	in gene, upstream	ActReg chr3 #11518	0	1	0
11519	3	33,155,246	33,156,295	1,049	1	7.121	12.515	3.677	12	21	8	1	1	1	CRTAP	320	in gene	ActReg chr3 #11519	0	1	0
11520	3	33,481,980	33,482,696	716	1	7.304	12.13	7.789	11	16	13	2	1	1	UBP1	-441	upstream	ActReg chr3 #11520	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11521	3	33,700,205	33,701,280	1,075	2	12.265	11.265	2.194	22	17	4	0	0	1	CLASP2	59,106	in gene	ActReg chr3 #11521	1	1	0
11522	3	33,759,436	33,760,262	826	2	12.423	10.077	5.423	19	18	11	1	1	1	CLASP2	-1	upstream	ActReg chr3 #11522	1	1	0
11523	3	33,839,754	33,840,598	844	2	10.44	12.84	14.64	13	19	21	1	1	1	PDCD6IP	125	in gene	ActReg chr3 #11523	0	1	1
11524	3	35,681,222	35,681,702	480	1	6.2	7.4	11.6	11	13	19	1	2	2	LOC100130503, ARPP-21	717, -2387	in gene, upstream	ActReg chr3 #11524	0	0	1
11525	3	36,421,674	36,422,552	878	2	10.296	11.926	6.8	14	18	12	1	1	1	STAC	16	in gene	ActReg chr3 #11525	1	1	0
11526	3	36,718,712	36,719,439	727	1	11.304	7.739	1.647	18	13	3	0	0	0				ActReg chr3 #11526	1	0	0
11527	3	37,033,957	37,035,420	1,463	2	11.6	11.733	5.356	22	20	10	1	2	2	EPM2AIP1, MLH1	107, -153	in gene, upstream	ActReg chr3 #11527	1	1	0
11528	3	37,204,401	37,205,215	814	1	7.04	11.84	2.125	13	18	4	0	0	1	LRRFIP2	13,043	in gene	ActReg chr3 #11528	0	1	0
11529	3	37,217,307	37,218,391	1,084	2	9.606	13	4.731	22	21	11	1	1	1	LRRFIP2	2	in gene	ActReg chr3 #11529	1	1	0
11530	3	37,284,308	37,285,242	934	3	12.138	11.207	10.793	23	19	14	1	1	1	GOLGA4	93	in gene	ActReg chr3 #11530	1	1	1
11531	3	37,661,421	37,662,342	921	2	8.103	14.586	3.276	16	30	8	0	0	1	ITGA9	168,068	in gene	ActReg chr3 #11531	1	1	0
11532	3	37,734,746	37,735,603	857	1	6.815	10.407	2.5	10	16	6	0	0	1	ITGA9	241,361	in gene	ActReg chr3 #11532	0	1	0
11533	3	37,903,629	37,904,324	695	2	8.455	10.546	5.364	16	19	10	1	1	1	CTDSPL	307	in gene	ActReg chr3 #11533	1	1	0
11534	3	37,950,711	37,951,243	532	1	7	13	3.941	12	23	5	0	0	1	CTDSPL	47,308	in gene	ActReg chr3 #11534	0	1	0
11535	3	37,977,677	37,978,160	483	1	9.2	11.333	3.929	14	15	7	0	0	1	CTDSPL	74,249	in gene	ActReg chr3 #11535	0	1	0
11536	3	38,178,804	38,179,695	891	1	11.107	8.321	3.381	17	18	7	2	2	2	ACAA1, MYD88	-516, -720	upstream, upstream	ActReg chr3 #11536	1	0	0
11537	3	38,179,787	38,180,481	694	1	11.136	8.409	6.364	17	15	9	1	2	2	ACAA1, MYD88	-1401, 165	upstream, in gene	ActReg chr3 #11537	1	0	0
11538	3	38,387,866	38,388,644	778	2	11.84	13.72	9.52	22	27	14	1	1	1	XYLB	4	in gene	ActReg chr3 #11538	1	1	0
11539	3	38,521,198	38,521,566	368	1	7.909	5.818	11.454	11	10	16	0	0	1	ACVR2B	25,592	in gene	ActReg chr3 #11539	0	0	1
11540	3	38,690,579	38,690,992	413	1	2.385	5.385	13.308	5	8	18	1	1	1	SCN5A	379	in gene	ActReg chr3 #11540	0	0	1
11541	3	38,846,914	38,847,885	971	2	23.433	23.2	3.269	60	60	6	0	0	0				ActReg chr3 #11541	1	1	0
11542	3	39,079,660	39,080,402	742	1	6.696	10.565	1.588	10	15	3	0	0	0				ActReg chr3 #11542	0	1	0
11543	3	39,145,456	39,145,887	431	1	6.308	3.364	10.846	8	5	16	0	1	3	WDR48, GORASP1, TTC21A	52164, 3459, -3481	downstream, in gene, upstream	ActReg chr3 #11543	0	0	1
11544	3	39,148,799	39,149,826	1,027	2	12.242	10.242	7.037	24	21	15	1	2	2	GORASP1, TTC21A	-182, 160	upstream, in gene	ActReg chr3 #11544	1	1	0
11545	3	39,188,197	39,189,264	1,067	1	11.303	12.182	4.667	23	19	11	0	0	2	TTC21A, CSRNP1	39578, 6372	downstream, in gene	ActReg chr3 #11545	0	1	0
11546	3	39,193,204	39,194,798	1,594	2	12.34	12.36	7.86	23	29	14	1	1	1	CSRNP1	1,101	in gene	ActReg chr3 #11546	1	1	0
11547	3	39,207,556	39,208,373	817	1	8.84	11	3.783	13	14	7	0	0	0				ActReg chr3 #11547	0	1	0
11548	3	39,228,523	39,229,024	501	1	2	5.562	11.188	4	8	19	0	0	1	XIRP1	5,304	in gene	ActReg chr3 #11548	0	0	1
11549	3	39,424,641	39,425,951	1,310	3	9.65	11.675	8.6	17	22	17	1	1	1	SLC25A38	481	in gene	ActReg chr3 #11549	1	1	1
11550	3	39,448,029	39,448,527	498	1	11.562	10.75	8	16	14	12	1	3	4	SLC25A38, RPSA, SNORA6, SNORA62	23463, 74, -1604, -4267	downstream, in gene, upstream, upstream	ActReg chr3 #11550	1	0	0
11551	3	39,680,739	39,681,241	502	1	10.933	9.467	1.5	21	15	2	0	0	0				ActReg chr3 #11551	1	0	0
11552	3	40,300,002	40,300,657	655	1	9.95	7.9	2	21	14	4	0	0	2	MYRIP, FLJ33065	449026, 50860	in gene, in gene	ActReg chr3 #11552	1	0	0
11553	3	40,350,715	40,351,461	746	2	13.25	15.042	7.375	25	30	13	1	2	2	FLJ33065, EIF1B	101, -85	in gene, upstream	ActReg chr3 #11553	1	1	0
11554	3	40,518,308	40,518,839	531	1	6	12.75	5.188	8	19	9	1	1	1	ZNF619	-31	upstream	ActReg chr3 #11554	0	1	0
11555	3	40,565,835	40,567,178	1,343	2	12.191	11.476	7.595	21	20	15	1	1	2	ZNF620, ZNF621	18976, 130	downstream, in gene	ActReg chr3 #11555	1	1	0
11556	3	41,012,730	41,013,721	991	2	9.345	10	2.476	17	16	7	0	0	0				ActReg chr3 #11556	1	1	0
11557	3	41,240,431	41,241,411	980	3	9.69	10.677	9.037	16	18	21	1	1	1	CTNNB1	-21	upstream	ActReg chr3 #11557	1	1	1
11558	3	42,003,237	42,004,064	827	2	14.308	14.769	3.692	27	28	9	1	2	2	ULK4, LOC100287063	10, 736	in gene, in gene	ActReg chr3 #11558	1	1	0
11559	3	42,121,861	42,122,596	735	1	11.348	5.304	3.261	15	8	6	0	0	1	LOC100287063	119,314	in gene	ActReg chr3 #11559	1	0	0
11560	3	42,341,369	42,342,091	722	1	9.739	14.261	1.778	18	26	2	0	0	0				ActReg chr3 #11560	0	1	0
11561	3	42,539,627	42,540,048	421	1	3.077	5	10.077	4	7	13	0	1	1	VIPR1	-4,267	upstream	ActReg chr3 #11561	0	0	1
11562	3	42,581,509	42,582,042	533	1	4.688	5.625	12.5	7	10	18	0	0	2	VIPR1, SEC22C	37671, 41653	downstream, downstream	ActReg chr3 #11562	0	0	1
11563	3	42,622,981	42,624,253	1,272	2	11.79	12	6.308	19	19	15	1	1	2	SEC22C, SS18L2	-189, -8681	upstream, upstream	ActReg chr3 #11563	1	1	0
11564	3	42,641,745	42,642,486	741	2	12.391	9.435	13.783	17	15	26	1	1	2	SS18L2, NKTR	9817, -32	downstream, upstream	ActReg chr3 #11564	1	0	1
11565	3	42,695,151	42,695,755	604	1	7.579	7.842	11.579	10	10	18	1	1	2	NKTR, ZBTB47	53306, 277	downstream, in gene	ActReg chr3 #11565	0	0	1
11566	3	42,704,077	42,704,696	619	1	2.842	4.684	10.632	5	9	15	0	0	1	ZBTB47	9,210	in gene	ActReg chr3 #11566	0	0	1
11567	3	42,738,343	42,739,140	797	1	3.783	4.4	12.96	7	8	16	0	0	2	KBTBD5, HHATL	11730, 5578	downstream, in gene	ActReg chr3 #11567	0	0	1
11568	3	42,742,472	42,743,586	1,114	2	14.629	11.257	6.6	25	22	11	0	1	3	KBTBD5, HHATL, CCDC13	16018, 1290, 71716	downstream, in gene, downstream	ActReg chr3 #11568	1	1	0
11569	3	42,814,400	42,815,113	713	1	12.652	7.739	5.636	23	14	10	1	1	2	CCDC13, HIGD1A	-11, 31271	upstream, downstream	ActReg chr3 #11569	1	0	0
11570	3	42,845,558	42,846,429	871	1	7.481	11.482	9.111	11	14	15	1	2	2	HIGD1A, CCBP2	34, -4971	in gene, upstream	ActReg chr3 #11570	0	1	0
11571	3	42,860,911	42,861,803	892	1	6.25	9.357	3.652	10	15	9	0	0	1	CCBP2	10,393	in gene	ActReg chr3 #11571	0	1	0
11572	3	42,921,995	42,923,002	1,007	1	10.516	12.29	8.613	13	17	12	1	1	1	CYP8B1	-4,865	upstream	ActReg chr3 #11572	0	1	0
11573	3	43,001,677	43,002,323	646	2	12.65	13.85	1.5	28	32	2	0	0	0				ActReg chr3 #11573	1	1	0
11574	3	43,197,138	43,197,777	639	1	7.4	10.6	4.55	13	18	9	0	0	0				ActReg chr3 #11574	0	1	0
11575	3	43,405,387	43,405,933	546	1	2.875	1.941	11.647	5	3	16	1	0	1	ANO10	257,900	downstream	ActReg chr3 #11575	0	0	1
11576	3	43,673,573	43,674,431	858	2	12.615	11.538	2.917	20	21	5	0	0	0				ActReg chr3 #11576	1	1	0
11577	3	43,837,470	43,838,060	590	1	7.474	12.421	3.316	10	23	5	0	0	0				ActReg chr3 #11577	0	1	0
11578	3	43,995,205	43,995,823	618	1	9.316	13.053	2.778	15	22	6	0	0	0				ActReg chr3 #11578	0	1	0
11579	3	44,040,260	44,041,207	947	2	8.724	11	8	12	15	16	1	0	0				ActReg chr3 #11579	0	1	1
11580	3	44,177,916	44,178,487	571	2	16.667	19.222	1.692	28	34	3	0	0	0				ActReg chr3 #11580	1	1	0
11581	3	44,282,989	44,283,533	544	1	1.875	4.25	11.882	3	8	18	1	1	1	C3orf77	-117	upstream	ActReg chr3 #11581	0	0	1
11582	3	44,379,744	44,380,670	926	2	11.345	10.379	14.625	20	18	28	1	1	2	C3orf77, C3orf23	96829, 596	downstream, in gene	ActReg chr3 #11582	1	0	1
11583	3	44,519,093	44,519,466	373	1	4	10.083	3.917	7	13	6	1	1	1	ZNF445	-117	upstream	ActReg chr3 #11583	0	1	0
11584	3	44,551,717	44,552,295	578	1	3.444	11.056	3.778	8	19	6	0	1	1	ZNF852	126	in gene	ActReg chr3 #11584	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11585	3	44,574,029	44,574,876	847	2	9.692	13.538	3.84	23	24	6	0	0	0				ActReg chr3 #11585	1	1	0
11586	3	44,666,172	44,666,821	649	2	12.524	12	3.95	16	20	8	1	1	1	ZNF197	-15	upstream	ActReg chr3 #11586	1	1	0
11587	3	44,753,886	44,754,348	462	1	9.8	12.2	5.667	13	20	10	1	1	1	ZNF502	-18	upstream	ActReg chr3 #11587	0	1	0
11588	3	44,803,127	44,803,470	343	1	13	10	12.454	18	16	19	1	2	2	KIAA1143, KIF15	-125, 89	upstream, in gene	ActReg chr3 #11588	0	0	1
11589	3	44,902,720	44,903,278	558	1	7.056	7.278	9.778	15	11	13	1	2	3	KIF15, MIR564, TMEM42	99790, -381, -409	downstream, upstream, upstream	ActReg chr3 #11589	0	0	1
11590	3	44,903,284	44,903,593	309	1	5.8	9.2	10.5	12	11	15	1	2	3	KIF15, MIR564, TMEM42	100229, 58, 30	downstream, in gene, in gene	ActReg chr3 #11590	0	0	1
11591	3	44,942,934	44,943,376	442	1	3.214	2.857	10.714	5	4	16	0	0	1	TGM4	27,057	in gene	ActReg chr3 #11591	0	0	1
11592	3	45,147,182	45,147,884	702	2	11.091	11.182	1.333	21	18	2	0	0	1	CDCP1	40,381	in gene	ActReg chr3 #11592	1	1	0
11593	3	45,165,274	45,166,189	915	1	10.69	8.31	3.708	17	14	8	0	0	1	CDCP1	22,183	in gene	ActReg chr3 #11593	1	0	0
11594	3	45,195,715	45,196,860	1,145	1	8.886	14.771	3.943	20	22	9	0	0	1	CDCP1	-8,373	upstream	ActReg chr3 #11594	0	1	0
11595	3	45,208,290	45,209,436	1,146	2	12.143	14.543	4.657	22	30	11	0	0	0				ActReg chr3 #11595	1	1	0
11596	3	45,515,403	45,515,859	456	1	6.714	10.714	4.857	10	13	7	0	0	1	LARS2	85,556	in gene	ActReg chr3 #11596	0	1	0
11597	3	45,550,532	45,551,192	660	1	12.65	10.8	3.583	20	15	6	0	0	1	LARS2	120,787	in gene	ActReg chr3 #11597	1	0	0
11598	3	45,698,088	45,698,654	566	1	8.824	12.177	5.615	12	23	9	0	0	1	LIMD1	62,048	in gene	ActReg chr3 #11598	0	1	0
11599	3	45,730,152	45,731,156	1,004	3	13.032	18.484	15.032	24	33	36	2	2	3	LIMD1, LOC644714, SACM1L	94331, -280, -100	downstream, upstream, upstream	ActReg chr3 #11599	1	1	1
11600	3	45,837,429	45,837,857	428	1	5.357	12.286	12.929	9	17	17	1	1	1	SLC6A20	392	in gene	ActReg chr3 #11600	0	0	1
11601	3	45,859,120	45,860,273	1,153	2	10.333	8.5	2.714	17	15	6	0	0	1	LZTFL1	23,925	downstream	ActReg chr3 #11601	1	1	0
11602	3	45,883,231	45,884,007	776	2	11.56	11.76	6.76	17	21	11	1	1	1	LZTFL1	2	in gene	ActReg chr3 #11602	1	1	0
11603	3	46,036,988	46,037,694	706	1	11.136	10.364	5.727	17	16	12	1	1	1	FYCO1	-34	upstream	ActReg chr3 #11603	1	0	0
11604	3	46,791,957	46,792,556	599	1	4	3.947	12	6	7	19	1	1	2	PRSS45, LOC100288960	-6011, 6101	upstream, downstream	ActReg chr3 #11604	0	0	1
11605	3	46,919,300	46,919,999	699	1	3.143	3.762	11.238	8	8	14	0	1	1	PTH1R	413	in gene	ActReg chr3 #11605	0	0	1
11606	3	46,924,037	46,924,480	443	1	5.429	3.857	11.071	9	5	16	1	0	1	PTH1R	5,022	in gene	ActReg chr3 #11606	0	0	1
11607	3	46,946,928	46,947,789	861	1	3.333	2.19	13.778	6	4	18	0	0	1	PTH1R	28,122	downstream	ActReg chr3 #11607	0	0	1
11608	3	47,017,597	47,018,889	1,292	2	11.366	14.829	6.317	25	25	16	1	2	2	CCDC12, NBEAL2	27, -2930	in gene, upstream	ActReg chr3 #11608	1	1	0
11609	3	47,043,190	47,043,681	491	1	4	4.438	11.938	5	6	17	0	0	1	NBEAL2	22,262	in gene	ActReg chr3 #11609	0	0	1
11610	3	47,044,062	47,044,707	645	1	2.778	5.81	11.619	5	12	16	0	0	1	NBEAL2	23,211	in gene	ActReg chr3 #11610	0	0	1
11611	3	47,046,473	47,046,997	524	1	3.25	3.125	13.375	5	5	18	0	0	1	NBEAL2	25,562	in gene	ActReg chr3 #11611	0	0	1
11612	3	47,205,395	47,206,212	817	2	11.885	14	5.96	25	25	15	1	2	2	SETD2, FLJ39534	-336, -57	upstream, upstream	ActReg chr3 #11612	1	1	0
11613	3	47,288,930	47,289,383	453	1	5.857	2.143	10.929	8	3	17	0	0	2	FLJ39534, KIF9	83296, 35181	downstream, in gene	ActReg chr3 #11613	0	0	1
11614	3	47,324,008	47,324,670	662	1	11.05	14.1	5.85	16	25	10	1	2	2	KIF9, KLHL18	-2, 9	upstream, in gene	ActReg chr3 #11614	0	1	0
11615	3	47,421,674	47,423,248	1,574	3	12.122	9.571	10.98	16	19	16	1	1	1	PTPN23	-30	upstream	ActReg chr3 #11615	1	1	1
11616	3	47,452,959	47,453,798	839	1	4.077	4.407	12.074	6	10	17	0	0	2	PTPN23, SCAP	30887, 64067	in gene, downstream	ActReg chr3 #11616	0	0	1
11617	3	47,458,826	47,459,343	517	1	2.125	2.417	13.375	4	6	19	0	0	2	PTPN23, SCAP	36593, 58361	downstream, in gene	ActReg chr3 #11617	0	0	1
11618	3	47,465,114	47,465,674	560	1	2.667	4.722	11.778	4	8	17	0	0	1	SCAP	52,051	in gene	ActReg chr3 #11618	0	0	1
11619	3	47,516,873	47,517,851	978	1	7.067	11.467	6.84	12	17	14	1	1	1	SCAP	83	in gene	ActReg chr3 #11619	0	1	0
11620	3	47,563,541	47,564,206	665	1	10.476	7.667	7.429	18	14	14	0	0	1	C3orf75	-8,674	upstream	ActReg chr3 #11620	1	0	0
11621	3	47,844,239	47,845,357	1,118	2	10.4	10.486	6.429	17	18	12	1	1	1	DHX30	399	in gene	ActReg chr3 #11621	1	1	0
11622	3	47,865,937	47,867,225	1,288	3	31.875	39.55	6.526	113	117	16	1	0	1	DHX30	22,182	in gene	ActReg chr3 #11622	1	1	1
11623	3	47,887,603	47,888,482	879	1	4.037	6.929	12	7	9	19	1	1	3	DHX30, MIR1226, MAP4	43643, -3003, 242727	in gene, upstream, downstream	ActReg chr3 #11623	0	0	1
11624	3	47,952,085	47,952,800	715	1	11.957	8.4	3.783	25	14	7	0	0	1	MAP4	178,327	in gene	ActReg chr3 #11624	1	0	0
11625	3	48,130,289	48,131,028	739	1	10.174	11.957	4.522	16	20	9	1	1	1	MAP4	111	in gene	ActReg chr3 #11625	0	1	0
11626	3	48,229,500	48,230,333	833	2	10.962	11.115	7.64	19	18	14	1	1	1	CDC25A	-115	upstream	ActReg chr3 #11626	1	1	0
11627	3	48,282,169	48,282,835	666	1	7.238	14.238	6.095	15	23	9	1	1	1	ZNF589	-94	upstream	ActReg chr3 #11627	0	1	0
11628	3	48,342,398	48,343,502	1,104	2	9	14.886	12.914	15	22	29	1	1	2	NME6, SPINK8	-102, 26881	upstream, downstream	ActReg chr3 #11628	0	1	1
11629	3	48,460,189	48,460,793	604	1	3.944	4.105	11.526	7	5	15	0	0	1	PLXNB1	10,969	in gene	ActReg chr3 #11629	0	0	1
11630	3	48,487,631	48,488,480	849	2	13	10.407	6.56	21	20	16	1	2	3	CCDC51, CCDC72, ATRIP	-6526, 6369, -163	upstream, downstream, upstream	ActReg chr3 #11630	1	1	0
11631	3	48,507,055	48,507,878	823	1	12.385	11.962	12.615	18	17	18	0	1	3	ATRIP, TREX1, SHISA5	19248, 237, 34195	downstream, in gene, downstream	ActReg chr3 #11631	0	0	1
11632	3	48,540,136	48,540,570	434	1	6.923	3.923	12	10	5	16	0	1	1	SHISA5	1,308	in gene	ActReg chr3 #11632	0	0	1
11633	3	48,594,051	48,594,697	646	1	7.05	8.85	10.1	17	18	14	1	1	3	PFKFB4, UCN2, COL7A1	-147, 6827, 38219	upstream, downstream, downstream	ActReg chr3 #11633	0	0	1
11634	3	48,598,322	48,602,084	3,762	4	10.814	11.873	6.922	20	21	16	0	2	3	PFKFB4, UCN2, COL7A1	-5976, 998, 32390	upstream, in gene, downstream	ActReg chr3 #11634	1	1	1
11635	3	48,608,266	48,608,764	498	1	2.214	1.111	10.8	3	2	19	0	1	3	UCN2, COL7A1, MIR711	-7314, 24078, 7895	upstream, in gene, downstream	ActReg chr3 #11635	0	0	1
11636	3	48,646,804	48,647,606	802	1	7.08	12.68	11.44	14	21	17	1	1	1	UQCRC1	-107	upstream	ActReg chr3 #11636	0	0	1
11637	3	48,672,150	48,673,583	1,433	3	13.156	13.511	9.378	23	21	20	1	1	2	SLC26A6, CELSR3	60, 27482	in gene, downstream	ActReg chr3 #11637	1	1	1
11638	3	48,698,015	48,700,041	2,026	2	11.953	16.703	9.141	26	44	14	1	1	1	CELSR3	1,320	in gene	ActReg chr3 #11638	1	1	0
11639	3	48,700,099	48,701,883	1,784	1	10.655	12.964	8.13	17	30	13	1	1	2	CELSR3, NCKIPSD	-643, 22343	upstream, downstream	ActReg chr3 #11639	0	1	0
11640	3	48,935,942	48,936,447	505	1	11.933	9.2	12.533	18	12	17	1	1	1	SLC25A20	208	in gene	ActReg chr3 #11640	0	0	1
11641	3	48,955,671	48,956,535	864	2	9.074	10.482	11	13	20	16	1	2	2	C3orf71, ARIH2	715, -178	in gene, upstream	ActReg chr3 #11641	0	1	1
11642	3	49,039,614	49,039,995	381	1	5.083	2.75	11	8	4	17	0	1	2	P4HTM, WDR6	12463, -4833	in gene, upstream	ActReg chr3 #11642	0	0	1
11643	3	49,044,490	49,045,468	978	2	9.4	12.2	11.6	22	22	18	1	1	3	P4HTM, WDR6, DALRD3	17638, 342, 13488	downstream, in gene, downstream	ActReg chr3 #11643	0	1	1
11644	3	49,053,831	49,054,486	655	1	4.95	4.7	10.55	9	10	14	0	1	7	P4HTM, WDR6, DALRD3, MIR425, NDUFAF3, MIR191, IMPDH2	26817, 9521, 4309, 3509, -3750, 3984, 12717	downstream, downstream, in gene, downstream, upstream, downstream, downstream	ActReg chr3 #11644	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11645	3	49,054,979	49,056,003	1,024	2	8.719	12.906	10.656	13	17	22	1	4	6	WDR6, DALRD3, MIR425, NDUFAF3, MIR191, IMPDH2	10854, 2976, 2176, -2417, 2651, 11384	downstream, in gene, downstream, upstream, downstream, downstream	ActReg chr3 #11645	0	1	1
11646	3	49,057,815	49,060,702	2,887	4	19.878	26.222	11.356	100	144	19	1	4	7	WDR6, DALRD3, MIR425, NDUFAF3, MIR191, IMPDH2, QRICH1	14621, -791, -1591, 1350, -1116, 7617, 72246	downstream, upstream, upstream, in gene, upstream, downstream, downstream	ActReg chr3 #11646	1	1	1
11647	3	49,062,307	49,063,131	824	1	5.52	7.96	12	9	12	16	0	3	7	WDR6, DALRD3, MIR425, NDUFAF3, MIR191, IMPDH2, QRICH1	18082, -4252, -5052, 4811, -4577, 4156, 68785	downstream, upstream, upstream, downstream, upstream, in gene, downstream	ActReg chr3 #11647	0	0	1
11648	3	49,066,465	49,067,092	627	1	8.737	12.105	15.263	13	20	25	1	1	6	DALRD3, MIR425, NDUFAF3, MIR191, IMPDH2, QRICH1	-8311, -9111, 8870, -8636, 97, 64726	upstream, upstream, downstream, upstream, in gene, downstream	ActReg chr3 #11648	0	0	1
11649	3	49,130,794	49,132,810	2,016	3	30.349	40.222	7.213	89	117	21	1	1	2	QRICH1, QARS	-298, 10569	upstream, downstream	ActReg chr3 #11649	1	1	1
11650	3	49,141,729	49,142,436	707	1	9.136	12.091	6.955	14	19	14	1	1	2	QARS, USP19	89, 16131	in gene, downstream	ActReg chr3 #11650	0	1	0
11651	3	49,157,543	49,158,546	1,003	2	8.871	13.323	12.903	13	21	26	1	1	2	USP19, LAMB2	169, 12555	in gene, downstream	ActReg chr3 #11651	0	1	1
11652	3	49,163,419	49,163,939	520	1	5.529	5.294	11.412	8	9	16	0	1	2	USP19, LAMB2	-5466, 6920	upstream, in gene	ActReg chr3 #11652	0	0	1
11653	3	49,169,889	49,171,439	1,550	1	15.354	11.979	8.729	21	25	16	0	1	1	LAMB2	-65	upstream	ActReg chr3 #11653	1	0	0
11654	3	49,203,591	49,204,476	885	1	9.889	12.111	6.96	18	23	12	1	2	2	CCDC71, KLHDC8B	-248, -4985	upstream, upstream	ActReg chr3 #11654	0	1	0
11655	3	49,313,947	49,314,790	843	1	8	10.815	7.815	12	16	11	1	2	3	C3orf62, MIR4271, USP4	140, 2815, 63168	in gene, downstream, downstream	ActReg chr3 #11655	0	1	0
11656	3	49,377,121	49,378,358	1,237	2	12.526	13.132	6.743	26	23	13	1	2	2	USP4, LOC100289130	-203, -7612	upstream, upstream	ActReg chr3 #11656	1	1	0
11657	3	49,449,536	49,450,143	607	2	11.895	6.368	8.889	20	11	17	1	2	4	RHOA, TCTA, AMT, NICN1	-313, 200, 10272, 16918	upstream, in gene, downstream, downstream	ActReg chr3 #11657	1	0	1
11658	3	49,477,348	49,477,623	275	1	2.125	2.875	14	3	4	16	0	0	0				ActReg chr3 #11658	0	0	1
11659	3	49,699,510	49,700,082	572	1	4.389	2.611	12.611	7	4	17	0	0	1	BSN	107,874	in gene	ActReg chr3 #11659	0	0	1
11660	3	49,711,556	49,712,066	510	1	9.562	9.5	12.25	15	14	18	1	1	3	BSN, APEH, MST1	119889, 376, 14385	downstream, in gene, downstream	ActReg chr3 #11660	0	0	1
11661	3	49,726,652	49,727,380	728	2	9.087	12.913	10.565	21	26	18	1	2	3	APEH, MST1, RNF123	15581, -820, 26	downstream, upstream, in gene	ActReg chr3 #11661	0	1	1
11662	3	49,738,618	49,739,535	917	1	3.069	4	11.828	8	7	17	0	0	1	RNF123	12,086	in gene	ActReg chr3 #11662	0	0	1
11663	3	49,761,011	49,762,028	1,017	1	10.344	12.688	9.031	19	22	16	1	2	4	RNF123, AMIGO3, GMPPB, IP6K1	34529, -4281, -135, 62454	downstream, upstream, upstream, downstream	ActReg chr3 #11663	0	1	0
11664	3	49,823,724	49,824,447	723	1	9.318	8.227	12.273	14	11	17	1	2	3	IP6K1, LOC100506738, CDHR4	-112, -380, 13169	upstream, upstream, downstream	ActReg chr3 #11664	0	0	1
11665	3	49,839,853	49,840,532	679	1	7.333	13.333	5.238	12	24	9	1	2	3	CDHR4, C3orf54, UBA7	-2938, -495, 11199	upstream, upstream, downstream	ActReg chr3 #11665	0	1	0
11666	3	49,841,110	49,841,616	506	1	5.312	5.562	13.25	8	9	19	1	2	3	CDHR4, C3orf54, UBA7	-4109, 676, 10028	upstream, in gene, downstream	ActReg chr3 #11666	0	0	1
11667	3	49,893,502	49,894,161	659	1	11.524	12.857	6.619	20	17	11	1	1	2	TRAIP, CAMKV	161, 13538	in gene, downstream	ActReg chr3 #11667	0	1	0
11668	3	49,904,952	49,905,729	777	2	12.96	13.833	4.952	25	28	9	0	1	1	CAMKV	2,029	in gene	ActReg chr3 #11668	1	1	0
11669	3	49,966,967	49,967,562	595	1	9.737	10.842	12.895	12	19	18	1	1	2	MON1A, RBM6	181, -10213	in gene, upstream	ActReg chr3 #11669	0	0	1
11670	3	49,977,174	49,978,131	957	2	9.567	15.667	8.033	16	25	21	1	1	2	MON1A, RBM6	-10207, 175	upstream, in gene	ActReg chr3 #11670	0	1	1
11671	3	50,214,017	50,214,435	418	1	2.667	1.692	11.308	3	3	15	0	0	2	SEMA3F, MIR566	21378, 3467	in gene, downstream	ActReg chr3 #11671	0	0	1
11672	3	50,221,639	50,222,235	596	1	4	4.389	12.278	6	8	18	0	1	2	SEMA3F, GNAT1	29089, -7106	in gene, upstream	ActReg chr3 #11672	0	0	1
11673	3	50,224,959	50,225,513	554	1	3.25	2.389	12.5	6	4	19	0	1	2	SEMA3F, GNAT1	32388, -3807	in gene, upstream	ActReg chr3 #11673	0	0	1
11674	3	50,250,100	50,250,924	824	1	3.87	6	11.538	11	11	16	0	0	1	SLC38A3	7,820	in gene	ActReg chr3 #11674	0	0	1
11675	3	50,264,297	50,265,403	1,106	2	10.559	13	6.647	27	24	12	1	0	2	SLC38A3, GNAI2	22158, -8797	downstream, upstream	ActReg chr3 #11675	1	1	0
11676	3	50,275,229	50,275,849	620	1	6.1	9.9	11.35	11	13	15	1	1	1	GNAI2	1,892	in gene	ActReg chr3 #11676	0	0	1
11677	3	50,311,110	50,311,634	524	1	5.462	5.25	13	10	10	21	1	1	2	SEMA3B, C3orf45	6332, -5146	in gene, upstream	ActReg chr3 #11677	0	0	1
11678	3	50,323,939	50,324,482	543	1	6.059	5.765	12.588	9	8	16	0	0	5	SEMA3B, C3orf45, IFRD2, HYAL3, NAT6	19170, 7692, 5816, 12689, 12502	downstream, in gene, downstream, downstream, downstream	ActReg chr3 #11678	0	0	1
11679	3	50,329,535	50,330,383	848	2	19.556	23.296	9.963	55	55	18	1	1	5	C3orf45, IFRD2, HYAL3, NAT6, HYAL1	13441, 67, 6940, 6753, 19853	downstream, in gene, downstream, downstream, downstream	ActReg chr3 #11679	1	1	0
11680	3	50,336,112	50,337,077	965	2	13.267	17.133	8.8	36	40	14	1	3	4	IFRD2, HYAL3, NAT6, HYAL1	-6568, 305, 118, 13218	upstream, in gene, in gene, downstream	ActReg chr3 #11680	1	1	0
11681	3	50,358,240	50,359,732	1,492	2	34.596	40.957	6.468	149	163	18	2	1	4	HYAL1, HYAL2, TUSC2, RASSF1	-9174, 1295, 6682, 19381	upstream, in gene, downstream, downstream	ActReg chr3 #11681	1	1	0
11682	3	50,374,164	50,375,354	1,190	2	10.081	13.162	13.351	22	23	27	1	0	4	TUSC2, RASSF1, ZMYND10, TUSC4	-9091, 3608, 8397, 13727	upstream, in gene, downstream, downstream	ActReg chr3 #11682	0	1	1
11683	3	50,387,803	50,388,970	1,167	2	13.54	15.081	8.73	31	29	14	1	3	5	RASSF1, ZMYND10, TUSC4, CYB561D2, TMEM115	-10019, -5230, 100, 89, 8553	upstream, upstream, in gene, in gene, downstream	ActReg chr3 #11683	1	1	0
11684	3	50,395,756	50,396,262	506	1	5.125	4.75	13.5	9	8	20	1	3	6	TUSC4, CYB561D2, TMEM115, CACNA2D2, LOC100506825, LOC100506802	-7523, 7712, 930, 144883, -6752, -8924	upstream, downstream, in gene, downstream, upstream, upstream	ActReg chr3 #11684	0	0	1
11685	3	50,396,669	50,397,487	818	2	13.923	14.231	6.769	23	24	9	1	3	6	TUSC4, CYB561D2, TMEM115, CACNA2D2, LOC100506825, LOC100506802	-8592, 8781, -139, 143814, -5683, -7855	upstream, downstream, upstream, downstream, upstream, upstream	ActReg chr3 #11685	1	1	0
11686	3	50,563,199	50,564,053	854	2	17.556	15.889	7	36	36	11	0	0	0				ActReg chr3 #11686	1	1	0
11687	3	50,606,518	50,607,451	933	3	10.448	14.103	12.241	24	31	22	1	2	2	C3orf18, HEMK1	1474, 75	in gene, in gene	ActReg chr3 #11687	1	1	1
11688	3	50,654,543	50,654,988	445	1	5.929	4.571	13.357	9	7	20	1	2	2	CISH, MAPKAPK3	-5503, 164	upstream, in gene	ActReg chr3 #11688	0	0	1
11689	3	50,664,611	50,665,563	952	1	8.414	11.862	5.103	14	16	11	0	0	1	MAPKAPK3	10,486	in gene	ActReg chr3 #11689	0	1	0
11690	3	51,533,275	51,533,830	555	1	9.167	11.167	8.5	14	15	14	1	1	1	VPRBP	466	in gene	ActReg chr3 #11690	0	1	0
11691	3	51,572,295	51,572,924	629	3	9	12.158	7.889	17	22	17	1	1	1	RAD54L2	-2,987	upstream	ActReg chr3 #11691	1	1	1
11692	3	51,705,253	51,705,831	578	1	9.778	11.444	10.722	14	14	14	1	1	2	RAD54L2, TEX264	129946, 320	downstream, in gene	ActReg chr3 #11692	0	0	1
11693	3	51,749,639	51,750,102	463	1	2.385	4.286	15.429	4	6	23	1	0	1	GRM2	8,789	in gene	ActReg chr3 #11693	0	0	1
11694	3	51,870,678	51,871,201	523	1	8.941	10.118	2.647	11	15	5	0	0	2	LOC100506840, IQCF3	19319, 8370	downstream, downstream	ActReg chr3 #11694	0	1	0
11695	3	51,963,290	51,964,213	923	2	11.793	17.207	3.207	26	39	9	0	0	1	RRP9	12,171	downstream	ActReg chr3 #11695	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11696	3	51,975,841	51,976,771	930	1	13.172	7.724	7.517	23	14	15	1	2	2	RRP9, PARP3	-384, -55	upstream, upstream	ActReg chr3 #11696	1	0	0
11697	3	52,016,336	52,017,661	1,325	2	15.439	11.488	5.634	25	19	14	1	1	4	ABHD14B, ABHD14A, ACY1, RPL29	-8352, 7956, -565, 12960	upstream, downstream, upstream, downstream	ActReg chr3 #11697	1	1	0
11698	3	52,029,487	52,030,281	794	2	12.2	12.52	5.72	20	22	9	1	1	2	ACY1, RPL29	12321, 74	downstream, in gene	ActReg chr3 #11698	1	1	0
11699	3	52,090,576	52,091,590	1,014	2	11.594	16.875	6.613	20	26	12	2	1	2	DUSP7, C3orf74	-622, 8045	upstream, downstream	ActReg chr3 #11699	1	1	0
11700	3	52,101,905	52,102,346	441	1	4.357	5.429	12.357	6	9	17	0	1	2	C3orf74, WDR51A	-2997, 86581	upstream, downstream	ActReg chr3 #11700	0	0	1
11701	3	52,187,956	52,189,318	1,362	2	26.333	27.767	7.651	52	76	11	1	1	1	WDR51A	69	in gene	ActReg chr3 #11701	1	1	0
11702	3	52,196,268	52,196,711	443	1	4.071	5.5	12.786	7	10	18	0	0	1	WDR51A	-7,783	upstream	ActReg chr3 #11702	0	0	1
11703	3	52,231,635	52,232,527	892	1	10.929	13.464	9.821	24	19	20	1	1	1	ALAS1	-35	upstream	ActReg chr3 #11703	0	1	0
11704	3	52,255,281	52,256,159	878	1	4.481	6.593	12.741	8	12	17	1	0	3	ALAS1, TLR9, TWF2	23604, 4459, 17463	downstream, in gene, downstream	ActReg chr3 #11704	0	0	1
11705	3	52,311,975	52,313,254	1,279	3	9.925	9.9	8.225	17	18	19	1	1	3	WDR82, MIRLET7G, GLYCTK	45, -10237, -9222	in gene, upstream, upstream	ActReg chr3 #11705	1	1	1
11706	3	52,321,541	52,322,298	757	3	11.13	10.913	10.696	22	22	20	1	1	3	WDR82, GLYCTK, MIR135A1	-9260, 83, 6405	upstream, in gene, downstream	ActReg chr3 #11706	1	1	1
11707	3	52,326,642	52,327,169	527	1	3.824	4.765	13.471	7	8	17	0	1	2	GLYCTK, MIR135A1	5069, 1419	in gene, downstream	ActReg chr3 #11707	0	0	1
11708	3	52,469,667	52,470,523	856	1	4.462	3.962	13.885	7	6	21	0	0	1	SEMA3G	8,948	in gene	ActReg chr3 #11708	0	0	1
11709	3	52,474,776	52,475,635	859	1	3	6.667	12.074	6	11	17	0	0	2	SEMA3G, TNNC1	3838, 12852	in gene, downstream	ActReg chr3 #11709	0	0	1
11710	3	52,486,623	52,487,197	574	1	5.625	5.444	12.833	10	9	18	0	2	3	SEMA3G, TNNC1, NISCH	-7867, 1147, -2614	upstream, in gene, upstream	ActReg chr3 #11710	0	0	1
11711	3	52,521,817	52,522,611	794	1	6.12	5.6	12.64	9	8	19	1	1	2	NISCH, STAB1	32690, -7142	in gene, upstream	ActReg chr3 #11711	0	0	1
11712	3	52,524,979	52,525,568	589	1	4.474	5.526	11.105	6	8	15	0	1	2	NISCH, STAB1	35749, 4083	in gene, upstream	ActReg chr3 #11712	0	0	1
11713	3	52,566,838	52,567,399	561	1	6.833	9.944	13.333	11	13	20	1	2	3	STAB1, NT5DC2, LOC440957	57762, 1975, -3503	downstream, in gene, upstream	ActReg chr3 #11713	0	0	1
11714	3	52,568,124	52,569,008	884	1	8.429	10.571	5.815	11	16	9	1	2	3	STAB1, NT5DC2, LOC440957	59210, 527, -2055	downstream, in gene, upstream	ActReg chr3 #11714	0	1	0
11715	3	52,570,191	52,571,212	1,021	2	8.062	12.156	12.812	13	21	24	1	2	3	NT5DC2, LOC440957, PBRM1	1608, 80, 149165	upstream, in gene, downstream	ActReg chr3 #11715	0	1	1
11716	3	52,643,383	52,643,829	446	1	9.071	11.214	2.333	14	16	3	0	0	1	PBRM1	76,260	in gene	ActReg chr3 #11716	0	1	0
11717	3	52,704,626	52,705,283	657	1	6.905	9.952	1.65	11	14	5	0	0	1	PBRM1	14,912	in gene	ActReg chr3 #11717	0	1	0
11718	3	52,719,738	52,720,439	701	1	8.524	12.046	7.5	16	21	17	1	5	6	PBRM1, GNL3, SNORD19, SNORD19B, SNORD69, GLT8D1	-222, 152, -3168, -4666, -6664, 19960	upstream, in gene, upstream, upstream, upstream, downstream	ActReg chr3 #11718	0	1	0
11719	3	52,738,849	52,740,590	1,741	2	11.87	12.148	6.642	23	25	16	1	2	3	GLT8D1, SPCS1, NEK4	329, -138, 65246	in gene, upstream, downstream	ActReg chr3 #11719	1	1	0
11720	3	52,804,593	52,805,446	853	2	10.889	9.519	6.333	17	19	12	1	2	2	NEK4, ITIH1	-54, -6589	upstream, upstream	ActReg chr3 #11720	1	1	0
11721	3	52,824,544	52,825,131	587	1	3.421	5.263	10.79	5	9	16	0	1	2	ITIH1, ITIH3	13229, -3947	in gene, upstream	ActReg chr3 #11721	0	0	1
11722	3	52,832,648	52,833,077	429	1	4.231	3.308	14.846	6	6	20	0	0	2	ITIH1, ITIH3	21254, 4078	downstream, in gene	ActReg chr3 #11722	0	0	1
11723	3	53,033,168	53,033,922	754	1	2.75	3.833	11.875	5	6	18	1	1	2	SFMBT1, LOC401068	46544, 484	in gene, in gene	ActReg chr3 #11723	0	0	1
11724	3	53,194,723	53,195,163	440	1	10.538	9.077	11.769	15	13	20	1	1	1	PRKCD	-280	upstream	ActReg chr3 #11724	0	0	1
11725	3	53,203,009	53,205,652	2,643	1	8.354	12.207	5.573	16	27	10	0	0	1	PRKCD	9,107	in gene	ActReg chr3 #11725	0	1	0
11726	3	53,262,522	53,263,193	671	1	7.143	6.524	11.143	9	11	14	0	0	1	TKT	27,211	in gene	ActReg chr3 #11726	0	0	1
11727	3	53,272,162	53,272,754	592	1	7.5	12.556	2.944	11	19	5	0	0	1	TKT	17,610	in gene	ActReg chr3 #11727	0	1	0
11728	3	53,381,155	53,382,153	998	3	14.935	18.355	13.742	33	42	26	1	1	1	DCP1A	0	in gene	ActReg chr3 #11728	1	1	1
11729	3	53,604,671	53,605,410	739	2	10.542	9.167	3.375	14	19	6	0	0	1	CACNA1D	76,009	in gene	ActReg chr3 #11729	1	1	0
11730	3	53,806,761	53,807,092	331	1	7.5	4.2	11.4	10	6	14	0	0	1	CACNA1D	277,895	in gene	ActReg chr3 #11730	0	0	1
11731	3	53,915,655	53,916,422	767	2	11.458	11.125	7.958	22	24	15	1	1	2	ACTR8, SELK	191, 9951	in gene, downstream	ActReg chr3 #11731	1	1	0
11732	3	53,925,415	53,926,397	982	2	12.9	9.6	5.967	27	21	11	1	1	2	ACTR8, SELK	-9677, 83	upstream, in gene	ActReg chr3 #11732	1	1	0
11733	3	54,004,524	54,005,164	640	2	10.15	11.75	5.1	22	23	9	0	0	0				ActReg chr3 #11733	1	1	0
11734	3	54,221,426	54,222,898	1,472	2	13.261	18.065	3.4	43	57	8	0	0	1	CACNA2D3	65,469	in gene	ActReg chr3 #11734	1	1	0
11735	3	54,591,835	54,592,440	605	1	9.842	11.947	1.077	16	20	2	0	0	1	CACNA2D3	435,444	in gene	ActReg chr3 #11735	0	1	0
11736	3	54,654,962	54,655,570	608	1	9.368	11.737	5.474	15	18	7	0	0	1	CACNA2D3	498,573	in gene	ActReg chr3 #11736	0	1	0
11737	3	55,201,611	55,202,470	859	1	9.259	10.667	2.417	13	15	5	0	0	0				ActReg chr3 #11737	0	1	0
11738	3	55,236,078	55,236,585	507	1	13.188	5.875	2.333	17	10	4	0	0	0				ActReg chr3 #11738	1	0	0
11739	3	55,464,929	55,465,555	626	1	6.632	11.474	2.286	11	16	4	0	0	0				ActReg chr3 #11739	0	1	0
11740	3	55,520,031	55,520,794	763	1	7.917	12.667	8.042	14	26	13	1	1	1	WNT5A	919	in gene	ActReg chr3 #11740	0	1	0
11741	3	56,528,475	56,529,238	763	2	17.333	19.083	1.917	43	49	4	0	0	0				ActReg chr3 #11741	1	1	0
11742	3	56,591,370	56,591,652	282	1	5.111	6.333	11.222	6	8	14	1	1	1	CCDC66	327	in gene	ActReg chr3 #11742	0	0	1
11743	3	56,717,049	56,717,694	645	1	9.15	11.8	5.9	12	21	8	1	1	1	C3orf63	-236	upstream	ActReg chr3 #11743	0	1	0
11744	3	56,968,369	56,968,773	404	1	3.8	2.615	10.692	6	4	16	0	0	1	ARHGEF3	144,765	in gene	ActReg chr3 #11744	0	0	1
11745	3	57,014,596	57,015,279	683	2	10.952	13.65	1.714	17	29	3	0	0	1	ARHGEF3	98,399	in gene	ActReg chr3 #11745	1	1	0
11746	3	57,051,061	57,051,817	756	1	7.5	10.333	2.737	13	13	4	0	0	1	ARHGEF3	61,897	in gene	ActReg chr3 #11746	0	1	0
11747	3	57,541,276	57,542,787	1,511	2	10.667	12.146	7.043	23	18	15	1	1	1	PDE12	50	in gene	ActReg chr3 #11747	1	1	0
11748	3	57,582,505	57,583,534	1,029	2	11.594	13.188	7.75	22	22	16	1	1	1	ARF4	196	in gene	ActReg chr3 #11748	1	1	0
11749	3	57,588,316	57,588,707	391	1	1.667	2.462	9.462	3	3	15	0	1	1	ARF4	-5,296	upstream	ActReg chr3 #11749	0	0	1
11750	3	57,741,658	57,743,092	1,434	2	8.4	12.667	7.6	15	20	16	1	2	2	LOC100287789, SLMAP	567, -799	in gene, upstream	ActReg chr3 #11750	0	1	1
11751	3	57,789,216	57,789,893	677	2	9.273	13.091	1.133	19	26	2	0	0	1	SLMAP	46,380	in gene	ActReg chr3 #11751	1	1	0
11752	3	57,791,255	57,791,933	678	2	14.667	13.095	2.188	35	27	3	0	0	1	SLMAP	48,420	in gene	ActReg chr3 #11752	1	1	0
11753	3	57,994,116	57,995,093	977	1	10.267	9.733	11.6	18	18	18	2	1	1	FLNB	477	in gene	ActReg chr3 #11753	0	0	1
11754	3	58,150,334	58,150,714	380	1	4.5	3.167	10.167	7	8	14	0	0	2	FLNB, LOC100506906	156397, 5821	in gene, in gene	ActReg chr3 #11754	0	0	1
11755	3	58,163,539	58,164,278	739	1	4.13	6.043	13.087	8	10	18	1	1	2	FLNB, LOC100506906	169781, -7563	downstream, upstream	ActReg chr3 #11755	0	0	1
11756	3	58,165,334	58,165,794	460	1	5.8	5.267	12.667	9	8	18	0	0	2	FLNB, LOC100506906	171437, -9219	downstream, upstream	ActReg chr3 #11756	0	0	1
11757	3	58,223,887	58,224,563	676	1	7.524	11.619	8.238	11	18	16	1	1	1	ABHD6	966	in gene	ActReg chr3 #11757	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11758	3	58,291,471	58,292,644	1,173	2	34.568	41.73	5.459	110	137	13	1	1	1	RPP14	85	in gene	ActReg chr3 #11758	1	1	0
11759	3	58,318,160	58,318,884	724	2	11.565	14.522	1.467	25	30	2	1	1	1	PXK	-95	upstream	ActReg chr3 #11759	1	1	0
11760	3	58,472,637	58,473,416	779	1	12.4	9.36	4.84	27	13	7	0	1	1	KCTD6	4,797	upstream	ActReg chr3 #11760	1	0	0
11761	3	58,477,383	58,477,992	609	2	7.667	9.211	3.833	17	22	7	1	1	1	KCTD6	-136	upstream	ActReg chr3 #11761	1	1	0
11762	3	58,511,864	58,513,026	1,162	2	13.46	12.351	6.189	21	24	10	0	0	1	ACOX2	10,484	in gene	ActReg chr3 #11762	1	1	0
11763	3	58,573,183	58,574,577	1,394	2	10.136	14.091	4.324	21	27	9	0	0	1	FAM107A	-10,389	upstream	ActReg chr3 #11763	1	1	0
11764	3	59,036,619	59,037,057	438	1	3.071	2.857	11.857	4	4	15	0	1	1	C3orf67	-1,123	upstream	ActReg chr3 #11764	0	0	1
11765	3	59,128,182	59,128,687	505	1	3.062	9.625	1.6	6	15	2	0	0	0				ActReg chr3 #11765	0	1	0
11766	3	59,128,968	59,129,536	568	1	4.389	9.722	2.286	8	17	4	0	0	0				ActReg chr3 #11766	0	1	0
11767	3	59,545,189	59,546,026	837	2	15.923	15.192	3.8	31	35	8	0	0	0				ActReg chr3 #11767	1	1	0
11768	3	60,262,944	60,263,546	602	1	3.895	9.947	3.5	6	17	6	0	0	1	FHIT	973,888	in gene	ActReg chr3 #11768	0	1	0
11769	3	61,301,820	61,302,128	308	1	5.7	5	9.7	10	6	12	0	0	0				ActReg chr3 #11769	0	0	1
11770	3	61,546,098	61,546,980	882	1	11.393	8.893	6.964	16	13	11	1	1	1	PTPRG	-704	upstream	ActReg chr3 #11770	1	0	0
11771	3	62,189,245	62,189,638	393	1	2.846	1.909	10.692	4	4	17	0	0	1	PTPRG	642,198	in gene	ActReg chr3 #11771	0	0	1
11772	3	62,304,171	62,305,494	1,323	2	11.341	12.829	5.824	22	22	9	1	2	2	LOC100506994, C3orf14	-210, -564	upstream, upstream	ActReg chr3 #11772	1	1	0
11773	3	62,362,403	62,363,048	645	1	2.278	1.333	11.45	4	2	18	1	1	1	FEZF2	-3,535	upstream	ActReg chr3 #11773	0	0	1
11774	3	62,514,757	62,515,370	613	1	10.79	15.263	2.944	21	31	5	0	0	1	CADPS	346,001	in gene	ActReg chr3 #11774	0	1	0
11775	3	62,573,074	62,573,764	690	1	5.409	12.318	5.8	7	19	8	0	0	1	CADPS	287,645	in gene	ActReg chr3 #11775	0	1	0
11776	3	62,589,869	62,590,523	654	1	11.3	10.3	1.917	18	15	3	0	0	1	CADPS	270,868	in gene	ActReg chr3 #11776	1	0	0
11777	3	62,859,352	62,860,021	669	1	11.714	7.714	4	16	15	7	1	1	1	CADPS	1,378	in gene	ActReg chr3 #11777	1	0	0
11778	3	62,861,572	62,862,315	743	2	12.913	12	2.478	27	26	6	0	1	1	CADPS	-879	upstream	ActReg chr3 #11778	1	1	0
11779	3	62,907,811	62,908,510	699	2	12.095	12.857	1	25	20	1	0	0	0				ActReg chr3 #11779	1	1	0
11780	3	63,053,530	63,054,462	932	2	12.069	19.586	1.857	37	48	3	0	0	0				ActReg chr3 #11780	1	1	0
11781	3	63,350,155	63,350,711	556	1	6.059	8.941	1	10	16	1	0	0	1	SYNPR	86,519	in gene	ActReg chr3 #11781	0	1	0
11782	3	63,739,100	63,739,666	566	1	8.833	9.889	2.733	14	17	4	0	0	1	LOC100130345	59,428	in gene	ActReg chr3 #11782	0	1	0
11783	3	63,795,176	63,795,880	704	1	13.364	8.136	3.364	26	11	7	0	0	2	LOC100130345, C3orf49	3283, -9513	in gene, upstream	ActReg chr3 #11783	1	0	0
11784	3	63,897,304	63,898,320	1,016	3	9.312	8.688	10.263	18	16	18	2	0	1	ATXN7	47,579	in gene	ActReg chr3 #11784	1	1	1
11785	3	63,949,958	63,950,354	396	1	8.75	10.75	1	11	15	1	0	0	1	ATXN7	99,923	in gene	ActReg chr3 #11785	0	1	0
11786	3	64,008,552	64,009,636	1,084	3	35.618	39.088	8.485	120	133	26	1	1	1	PSMD6	26	in gene	ActReg chr3 #11786	1	1	1
11787	3	64,090,063	64,090,954	891	2	11.071	12.75	5	18	22	8	0	0	1	PRICKLE2	120,623	in gene	ActReg chr3 #11787	1	1	0
11788	3	64,218,228	64,218,964	736	1	8.696	11.217	1.913	13	18	3	0	1	1	PRICKLE2	-7,465	upstream	ActReg chr3 #11788	0	1	0
11789	3	64,276,610	64,277,504	894	1	11.071	15.607	3.652	22	31	6	0	0	0				ActReg chr3 #11789	0	1	0
11790	3	64,430,489	64,430,778	289	1	4.222	2.222	9.778	7	4	13	1	0	0				ActReg chr3 #11790	0	0	1
11791	3	64,670,834	64,671,521	687	1	11.364	7	4.409	16	11	7	1	2	2	ADAMTS9, LOC100507098	2188, 631	in gene, in gene	ActReg chr3 #11791	1	0	0
11792	3	64,673,647	64,674,291	644	2	9.1	10.278	6.05	15	18	10	1	1	2	ADAMTS9, LOC100507098	-604, 3423	upstream, in gene	ActReg chr3 #11792	1	1	0
11793	3	64,973,813	64,974,440	627	2	11.25	12.3	2.895	18	20	6	0	0	0				ActReg chr3 #11793	1	1	0
11794	3	65,016,237	65,017,047	810	2	11	10.36	2.44	21	21	4	0	0	0				ActReg chr3 #11794	1	1	0
11795	3	65,949,580	65,950,261	681	1	8.762	12.333	3.562	13	17	6	0	0	2	MAGI1, LOC151877	74589, -9687	in gene, upstream	ActReg chr3 #11795	0	1	0
11796	3	65,977,712	65,978,345	633	1	6.9	10.1	1.846	12	22	3	0	0	1	MAGI1	46,481	in gene	ActReg chr3 #11796	0	1	0
11797	3	66,024,362	66,025,322	960	2	11.833	13.333	5.552	20	22	11	1	1	1	MAGI1	-333	upstream	ActReg chr3 #11797	1	1	0
11798	3	66,451,099	66,451,540	441	1	3.538	5.071	11.143	8	7	17	0	0	1	LRIG1	99,526	in gene	ActReg chr3 #11798	0	0	1
11799	3	66,551,068	66,552,009	941	1	10.233	13.8	5.033	16	27	10	1	1	1	LRIG1	-693	upstream	ActReg chr3 #11799	0	1	0
11800	3	67,068,844	67,069,736	892	2	10.464	9.25	3.107	16	17	7	0	0	1	KBTBD8	20,563	downstream	ActReg chr3 #11800	1	1	0
11801	3	67,164,071	67,164,732	661	2	18.95	17.25	1.944	41	36	3	0	0	0				ActReg chr3 #11801	1	1	0
11802	3	67,704,644	67,705,499	855	2	11.692	9.769	8.522	17	14	18	1	1	1	SUCLG2	-33	upstream	ActReg chr3 #11802	1	0	1
11803	3	68,355,705	68,356,146	441	1	9.857	7	0	18	11	0	0	0	1	FAM19A1	302,471	in gene	ActReg chr3 #11803	1	0	0
11804	3	69,062,502	69,063,300	798	1	8.6	10.56	4.875	12	14	11	1	1	2	C3orf64, TMF1	-127, 38583	upstream, downstream	ActReg chr3 #11804	0	1	0
11805	3	69,230,720	69,231,465	745	2	10.25	11.625	2.917	17	22	6	0	0	1	FRMD4B	204,338	in gene	ActReg chr3 #11805	1	1	0
11806	3	69,355,526	69,356,210	684	1	9.571	12.286	2	17	24	3	0	0	1	FRMD4B	79,562	in gene	ActReg chr3 #11806	0	1	0
11807	3	69,788,145	69,789,203	1,058	1	10.394	11.758	6.273	17	18	17	1	1	1	MITF	88	in gene	ActReg chr3 #11807	0	1	0
11808	3	70,048,361	70,049,540	1,179	1	8.811	11.757	7.103	16	23	13	0	0	0				ActReg chr3 #11808	0	1	0
11809	3	70,089,582	70,090,160	578	1	4.278	10.056	2.722	6	16	5	0	0	0				ActReg chr3 #11809	0	1	0
11810	3	70,102,266	70,102,828	562	1	12.5	7.611	2.471	20	12	4	0	0	0				ActReg chr3 #11810	1	0	0
11811	3	72,031,660	72,032,276	616	1	9.368	11.474	3.111	14	21	8	0	0	0				ActReg chr3 #11811	0	1	0
11812	3	72,173,129	72,173,746	617	1	10.053	9	1.125	19	15	2	0	0	0				ActReg chr3 #11812	1	0	0
11813	3	72,387,243	72,389,118	1,875	2	20.569	20.483	5.966	48	39	12	0	0	0				ActReg chr3 #11813	1	1	0
11814	3	72,710,119	72,710,805	686	1	12.143	4.619	1.778	16	8	2	0	0	1	LOC100506865	2,938	downstream	ActReg chr3 #11814	1	0	0
11815	3	72,897,125	72,897,863	738	1	7.783	11.87	6.652	13	22	11	1	1	1	SHQ1	104	in gene	ActReg chr3 #11815	0	1	0
11816	3	72,936,775	72,937,295	520	1	8.562	11.625	3.571	14	20	6	0	1	1	GXYLT2	-350	upstream	ActReg chr3 #11816	0	1	0
11817	3	72,987,678	72,988,095	417	1	11.308	6.846	3.615	16	9	5	0	0	1	GXYLT2	50,501	in gene	ActReg chr3 #11817	1	0	0
11818	3	73,143,037	73,143,907	870	1	8.464	10.25	3.321	13	14	6	0	0	0				ActReg chr3 #11818	0	1	0
11819	3	73,277,374	73,278,146	772	1	7.36	12.96	1.739	12	24	3	0	0	0				ActReg chr3 #11819	0	1	0
11820	3	73,432,849	73,433,511	662	1	2.789	5	11.238	8	7	15	1	0	1	PDZRN3	240,892	in gene	ActReg chr3 #11820	0	0	1
11821	3	73,629,370	73,630,005	635	1	8.65	12.9	2.105	11	26	4	0	0	1	PDZRN3	44,385	in gene	ActReg chr3 #11821	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11822	3	73,673,994	73,674,667	673	1	8.762	12.333	3.095	13	19	6	1	1	1	PDZRN3	-258	upstream	ActReg chr3 #11822	0	1	0
11823	3	75,273,389	75,274,053	664	1	10.238	12.667	3.762	16	21	8	0	0	0				ActReg chr3 #11823	0	1	0
11824	3	75,444,742	75,445,234	492	1	4	3	11.867	6	5	17	1	0	0				ActReg chr3 #11824	0	0	1
11825	3	75,481,987	75,482,563	576	1	9	12.222	2.154	16	19	4	0	0	0				ActReg chr3 #11825	0	1	0
11826	3	75,690,130	75,690,761	631	1	4.95	12.5	2.7	10	22	5	0	0	0				ActReg chr3 #11826	0	1	0
11827	3	75,695,260	75,696,125	865	1	7.333	5.185	13.148	12	12	19	0	0	0				ActReg chr3 #11827	0	0	1
11828	3	75,707,368	75,708,491	1,123	3	16.743	17.971	8.714	51	43	20	1	1	2	FRG2C, LOC100506764	-5558, -9450	upstream, upstream	ActReg chr3 #11828	1	1	1
11829	3	75,721,117	75,721,591	474	1	13.4	15	17.733	18	19	24	1	0	2	FRG2C, LOC100506764	7867, 3975	downstream, downstream	ActReg chr3 #11829	0	0	1
11830	3	78,157,559	78,157,875	316	1	2.889	2.4	11.6	4	3	14	0	0	0				ActReg chr3 #11830	0	0	1
11831	3	78,599,826	78,600,366	540	2	11.059	9.882	1	20	16	1	0	0	0				ActReg chr3 #11831	1	1	0
11832	3	79,068,024	79,069,239	1,215	3	19	21.763	9.371	55	47	19	1	0	1	ROBO1	748,428	in gene	ActReg chr3 #11832	1	1	1
11833	3	80,281,777	80,282,473	696	1	11.046	7.727	2.35	21	13	4	0	0	0				ActReg chr3 #11833	1	0	0
11834	3	80,819,681	80,820,313	632	1	7.263	13.684	5.529	12	21	9	1	0	0				ActReg chr3 #11834	0	1	0
11835	3	81,810,359	81,811,290	931	3	9.276	16.172	11.741	19	27	21	1	1	1	GBE1	126	in gene	ActReg chr3 #11835	1	1	1
11836	3	81,861,307	81,861,615	308	1	2.2	4.4	11	3	6	14	0	0	0				ActReg chr3 #11836	0	0	1
11837	3	83,273,000	83,273,735	735	1	7.739	11.652	1.647	12	18	3	0	0	0				ActReg chr3 #11837	0	1	0
11838	3	84,597,235	84,598,269	1,034	1	7.188	11.406	4	12	16	9	0	0	0				ActReg chr3 #11838	0	1	0
11839	3	85,609,423	85,609,896	473	1	7	10	1	10	17	1	0	0	1	CADM2	601,526	in gene	ActReg chr3 #11839	0	1	0
11840	3	87,382,510	87,383,052	542	1	9.059	9.176	2.471	13	18	4	0	0	0				ActReg chr3 #11840	0	1	0
11841	3	88,080,696	88,081,386	690	2	9.955	13.727	2.429	20	32	4	0	0	0				ActReg chr3 #11841	1	1	0
11842	3	88,087,532	88,088,358	826	2	10.385	14.808	2.731	19	28	4	0	0	0				ActReg chr3 #11842	1	1	0
11843	3	88,107,549	88,108,870	1,321	2	8.667	11.548	7.286	15	21	18	1	1	1	CGGBP1	-63	upstream	ActReg chr3 #11843	0	1	1
11844	3	88,198,605	88,199,585	980	3	12.516	12.29	9.935	23	22	24	1	1	2	ZNF654, C3orf38	10833, 202	downstream, in gene	ActReg chr3 #11844	1	1	1
11845	3	89,156,368	89,157,135	767	1	9.083	13.458	6.524	14	24	10	0	1	1	EPHA3	77	in gene	ActReg chr3 #11845	0	1	0
11846	3	89,163,359	89,164,182	823	1	8.115	12.154	4.231	12	20	7	1	0	1	EPHA3	7,096	in gene	ActReg chr3 #11846	0	1	0
11847	3	89,220,772	89,221,353	581	1	6.222	10	1.909	9	17	2	0	0	1	EPHA3	64,388	in gene	ActReg chr3 #11847	0	1	0
11848	3	89,731,658	89,732,199	541	1	3.353	10.765	0	7	20	0	0	0	0				ActReg chr3 #11848	0	1	0
11849	3	90,234,044	90,234,457	413	1	5.769	9.385	0	10	15	0	0	0	0				ActReg chr3 #11849	0	1	0
11850	3	93,881,404	93,881,971	567	1	8.722	10.667	2.353	13	19	4	0	0	0				ActReg chr3 #11850	0	1	0
11851	3	94,345,199	94,345,789	590	1	9.5	9.722	1.923	14	15	3	0	0	0				ActReg chr3 #11851	0	1	0
11852	3	96,532,188	96,533,753	1,565	4	9.082	10.735	9.364	17	17	19	1	1	1	EPHA6	-455	upstream	ActReg chr3 #11852	1	1	1
11853	3	97,540,767	97,541,657	890	1	6.5	10.607	8.5	9	16	13	1	1	1	CRYBG3	643	in gene	ActReg chr3 #11853	0	1	0
11854	3	97,691,031	97,691,542	511	1	6.125	11	6.111	10	14	9	1	1	1	MINA	9	in gene	ActReg chr3 #11854	0	1	0
11855	3	98,241,459	98,242,114	655	1	10.524	11.333	4.476	18	15	7	1	1	2	CLDND1, GPR15	124, -9092	in gene, upstream	ActReg chr3 #11855	1	0	0
11856	3	98,311,743	98,312,116	373	1	5.667	4.167	10.083	8	6	14	1	1	1	CPOX	526	in gene	ActReg chr3 #11856	0	0	1
11857	3	98,312,326	98,312,922	596	1	11.111	7.111	12.667	18	11	19	1	1	1	CPOX	-169	upstream	ActReg chr3 #11857	0	0	1
11858	3	98,450,952	98,451,441	489	1	9.067	4.533	11.067	13	8	15	1	1	1	ST3GAL6	-376	upstream	ActReg chr3 #11858	0	0	1
11859	3	98,488,953	98,489,670	717	1	10.13	8.522	3.043	16	14	6	0	0	1	ST3GAL6	37,739	in gene	ActReg chr3 #11859	1	0	0
11860	3	98,620,089	98,620,670	581	1	9.167	12.278	5.333	15	18	11	1	1	1	DCBLD2	154	in gene	ActReg chr3 #11860	0	1	0
11861	3	98,696,396	98,696,912	516	1	7.375	9.625	1.75	13	15	2	0	1	1	LOC100506377	-3,248	upstream	ActReg chr3 #11861	0	1	0
11862	3	98,847,822	98,848,469	647	1	6.8	10.4	3.6	13	20	6	0	0	0				ActReg chr3 #11862	0	1	0
11863	3	99,280,773	99,281,646	873	1	10.259	15.074	1.417	18	31	3	0	0	0				ActReg chr3 #11863	0	1	0
11864	3	99,536,012	99,537,026	1,014	2	10.312	14.594	4.367	15	33	11	1	1	1	C3orf26	-159	upstream	ActReg chr3 #11864	1	1	0
11865	3	99,894,361	99,895,035	674	2	9.095	11.809	1.882	17	18	3	0	0	1	C3orf26	358,020	in gene	ActReg chr3 #11865	1	1	0
11866	3	99,979,339	99,980,222	883	2	13.111	10.222	6	24	16	15	1	1	1	TBC1D23	94	in gene	ActReg chr3 #11866	1	1	0
11867	3	100,119,640	100,119,998	358	1	8.273	10.364	13.091	12	11	17	1	2	2	TOMM70A, LNP1	406, -218	in gene, upstream	ActReg chr3 #11867	0	0	1
11868	3	100,244,466	100,245,526	1,060	1	11.727	8.212	3.938	17	16	9	0	0	1	TMEM45A	33,533	in gene	ActReg chr3 #11868	1	0	0
11869	3	100,400,876	100,401,275	399	1	2.75	3.25	10.5	4	5	15	0	0	1	GPR128	72,642	in gene	ActReg chr3 #11869	0	0	1
11870	3	101,292,256	101,293,806	1,550	2	11.796	14.775	4.837	24	28	10	1	1	2	RGMTD1, PCNP	12319, -11	downstream, upstream	ActReg chr3 #11870	1	1	0
11871	3	101,394,484	101,395,121	637	1	4.95	11.55	2.8	10	16	6	1	2	3	ZBTB11, LOC100009676, RPL24	1186, -472, 10761	in gene, upstream, downstream	ActReg chr3 #11871	0	1	0
11872	3	101,497,539	101,498,879	1,340	1	8.854	11.829	6.878	15	19	13	1	1	1	FAM55C	180	in gene	ActReg chr3 #11872	0	1	0
11873	3	101,568,155	101,568,848	693	1	8.409	11.636	3.933	13	22	7	1	0	1	NFKBIZ	21,667	in gene	ActReg chr3 #11873	0	1	0
11874	3	101,689,765	101,690,222	457	1	4.143	3.214	11.357	7	5	18	0	0	1	LOC152225	30,290	in gene	ActReg chr3 #11874	0	0	1
11875	3	101,809,449	101,810,039	590	1	10.222	5.944	2.444	16	9	5	0	0	0				ActReg chr3 #11875	1	0	0
11876	3	101,875,388	101,875,958	570	1	10.556	6	1.636	17	9	2	0	0	0				ActReg chr3 #11876	1	0	0
11877	3	102,914,025	102,914,458	433	1	7.231	10.077	2	10	14	3	0	0	0				ActReg chr3 #11877	0	1	0
11878	3	104,624,918	104,625,344	426	1	3.923	6.714	8.571	6	10	16	0	0	0				ActReg chr3 #11878	0	0	1
11879	3	105,073,919	105,074,679	760	1	10.792	7.75	3.524	14	10	7	0	0	0				ActReg chr3 #11879	1	0	0
11880	3	105,086,183	105,086,780	597	1	6.667	10.889	7.278	12	17	14	1	1	1	ALCAM	768	in gene	ActReg chr3 #11880	0	1	0
11881	3	105,088,190	105,088,871	681	1	8.273	11.909	2.955	15	18	7	1	1	1	ALCAM	2,817	in gene	ActReg chr3 #11881	0	1	0
11882	3	105,587,271	105,587,833	562	1	10.765	12.588	12.647	13	18	21	1	1	1	CBLB	335	in gene	ActReg chr3 #11882	0	0	1
11883	3	105,587,946	105,588,965	1,019	1	11.406	8.219	4.276	17	16	8	1	1	1	CBLB	-568	upstream	ActReg chr3 #11883	1	0	0
11884	3	105,715,938	105,717,495	1,557	2	10.854	12.729	3.733	27	26	6	0	0	0				ActReg chr3 #11884	1	1	0
11885	3	105,867,394	105,867,658	264	1	3	2.375	11.75	4	3	14	0	0	0				ActReg chr3 #11885	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11886	3	106,147,262	106,147,825	563	1	11.167	8.778	1	20	16	1	0	0	0				ActReg chr3 #11886	1	0	0
11887	3	106,176,076	106,176,720	644	2	8.7	11.95	2.5	16	25	6	0	0	0				ActReg chr3 #11887	1	1	0
11888	3	106,362,554	106,363,038	484	1	2.267	4.6	12.733	4	9	18	0	0	0				ActReg chr3 #11888	0	0	1
11889	3	106,407,186	106,407,684	498	1	6.688	8.688	1	11	17	1	0	0	0				ActReg chr3 #11889	0	1	0
11890	3	106,484,104	106,484,568	464	1	8.214	12.429	1	13	17	1	0	0	0				ActReg chr3 #11890	0	1	0
11891	3	107,150,373	107,150,995	622	1	6.421	11.21	6.895	10	18	10	1	0	0				ActReg chr3 #11891	0	1	0
11892	3	107,809,433	107,810,449	1,016	2	8.719	12.031	6.538	20	18	16	1	1	1	CD47	-6	upstream	ActReg chr3 #11892	1	1	0
11893	3	108,139,698	108,140,251	553	2	12.706	14.706	5.286	25	25	8	0	0	1	MYH15	108,195	in gene	ActReg chr3 #11893	1	1	0
11894	3	108,308,260	108,308,936	676	1	11.476	8.571	6.048	18	15	11	1	2	2	KIAA1524, DZIP3	-107, 261	upstream, in gene	ActReg chr3 #11894	1	0	0
11895	3	109,404,014	109,404,544	530	1	10.588	9.471	3.8	14	13	6	0	0	0				ActReg chr3 #11895	1	0	0
11896	3	110,790,071	110,790,835	764	1	9.667	11.458	5.286	15	19	7	1	2	2	LOC100506555, PVRL3	-2211, -412	upstream, upstream	ActReg chr3 #11896	0	1	0
11897	3	111,070,086	111,070,584	498	1	9.667	13.2	1	17	21	1	0	0	0				ActReg chr3 #11897	0	1	0
11898	3	111,433,102	111,433,602	500	1	7.5	10.25	3.375	13	18	5	0	0	1	PLCXD2	39,829	in gene	ActReg chr3 #11898	0	1	0
11899	3	111,577,811	111,578,829	1,018	2	12.469	13.281	7.844	27	25	12	1	0	1	PHLDB2	126,993	in gene	ActReg chr3 #11899	1	1	0
11900	3	111,717,695	111,718,133	438	1	4.786	7.571	11.286	7	10	15	0	1	2	ABHD10, TAGLN3	20086, 328	downstream, in gene	ActReg chr3 #11900	0	0	1
11901	3	111,918,413	111,919,059	646	1	13.2	7.1	1.263	24	11	2	0	0	1	SLC9A10	94,338	in gene	ActReg chr3 #11901	1	0	0
11902	3	112,280,284	112,281,566	1,282	2	11.45	12.35	5.4	25	21	10	1	2	2	ATG3, SLC35A5	-440, 30	upstream, in gene	ActReg chr3 #11902	1	1	0
11903	3	112,359,873	112,360,538	665	1	9.8	13.5	2.65	16	21	4	0	1	1	CCDC80	-228	upstream	ActReg chr3 #11903	0	1	0
11904	3	112,847,176	112,847,672	496	1	10.067	6.133	1.8	19	9	2	0	0	0				ActReg chr3 #11904	1	0	0
11905	3	112,931,126	112,931,585	459	1	8.267	10.933	12.267	14	13	18	1	1	1	BOC	-20	upstream	ActReg chr3 #11905	0	0	1
11906	3	113,233,655	113,234,060	405	1	8.615	9.538	11.462	13	12	16	1	1	1	CCDC52	177	in gene	ActReg chr3 #11906	0	0	1
11907	3	113,415,509	113,416,161	652	1	13.905	10.905	5	25	23	9	1	1	2	KIAA2018, LOC100506638	-342, 20735	upstream, downstream	ActReg chr3 #11907	1	0	0
11908	3	113,464,610	113,464,914	304	1	5.333	8.889	10.889	8	18	14	1	2	2	NAA50, ATP6V1A	534, -1146	in gene, upstream	ActReg chr3 #11908	0	0	1
11909	3	113,465,783	113,466,412	629	1	10.2	6.25	7.944	20	11	12	0	2	2	NAA50, ATP6V1A	-1001, 189	upstream, in gene	ActReg chr3 #11909	1	0	0
11910	3	113,666,545	113,667,358	813	1	6	7.188	11.812	10	11	22	1	1	2	GRAMD1C, ZDHHC23	109420, 353	downstream, in gene	ActReg chr3 #11910	0	0	1
11911	3	113,775,108	113,775,910	802	2	12.8	13.32	2.13	25	22	4	1	2	2	KIAA1407, QTRTD1	-49, -102	upstream, upstream	ActReg chr3 #11911	1	1	0
11912	3	113,871,531	113,871,914	383	1	8.333	10.083	10.75	11	13	15	1	0	1	DRD3	26,177	in gene	ActReg chr3 #11912	0	0	1
11913	3	113,897,381	113,898,188	807	2	12.24	13.96	1.947	27	33	4	0	1	1	DRD3	115	in gene	ActReg chr3 #11913	1	1	0
11914	3	114,130,945	114,131,677	732	1	11.454	7	2.19	17	12	4	0	0	1	ZBTB20	734,816	in gene	ActReg chr3 #11914	1	0	0
11915	3	115,044,160	115,044,975	815	2	16.846	17.538	1	38	42	1	0	0	0				ActReg chr3 #11915	1	1	0
11916	3	115,155,276	115,156,208	932	2	12.586	17.621	2.393	24	37	5	0	0	0				ActReg chr3 #11916	1	1	0
11917	3	115,502,711	115,503,968	1,257	2	10.075	12.3	3.541	17	20	9	1	0	0				ActReg chr3 #11917	1	1	0
11918	3	115,509,417	115,510,167	750	2	12.739	17.913	2.714	28	44	6	0	0	0				ActReg chr3 #11918	1	1	0
11919	3	115,604,344	115,604,961	617	2	8.35	12.15	1.9	13	21	4	0	0	1	LSAMP	559,733	in gene	ActReg chr3 #11919	1	1	0
11920	3	115,719,142	115,719,728	586	1	13.278	9.722	3	24	14	5	0	0	1	LSAMP	444,950	in gene	ActReg chr3 #11920	1	0	0
11921	3	115,867,682	115,868,365	683	1	12.238	9.81	1.571	19	14	3	0	0	1	LSAMP	296,362	in gene	ActReg chr3 #11921	1	0	0
11922	3	116,298,622	116,299,251	629	1	7.35	9.55	1.3	13	18	2	0	0	0				ActReg chr3 #11922	0	1	0
11923	3	117,041,487	117,042,223	736	2	7.087	14.13	1.412	16	31	2	0	0	0				ActReg chr3 #11923	1	1	0
11924	3	117,340,795	117,341,454	659	1	11.191	8.476	3.267	17	12	5	0	0	0				ActReg chr3 #11924	1	0	0
11925	3	117,454,317	117,454,938	621	1	6.737	10.632	2.462	10	17	4	0	0	0				ActReg chr3 #11925	0	1	0
11926	3	117,890,419	117,890,754	335	1	4.273	4.273	9.273	5	6	13	0	0	0				ActReg chr3 #11926	0	0	1
11927	3	118,792,324	118,792,681	357	1	2.7	3.455	11.273	5	4	15	0	0	1	IGSF11	72,396	in gene	ActReg chr3 #11927	0	0	1
11928	3	119,041,503	119,042,628	1,125	2	6.778	9.611	8.647	9	18	20	1	0	1	CDGAP	28,845	in gene	ActReg chr3 #11928	0	1	1
11929	3	119,182,041	119,183,253	1,212	2	8.579	12.71	7.611	15	28	15	0	2	2	TMEM39A, KTELC1	-176, -5138	upstream, upstream	ActReg chr3 #11929	0	1	1
11930	3	119,187,621	119,188,140	519	1	8	7.812	12.062	10	11	17	1	2	2	TMEM39A, KTELC1	-5409, 95	upstream, in gene	ActReg chr3 #11930	0	0	1
11931	3	119,298,137	119,298,869	732	1	8.565	12.087	6.25	12	17	8	1	1	1	ADPRH	-20	upstream	ActReg chr3 #11931	0	1	0
11932	3	119,528,773	119,529,187	414	1	4.154	3.818	11.308	8	6	18	1	0	1	NR1I2	29,649	in gene	ActReg chr3 #11932	0	0	1
11933	3	119,812,893	119,813,456	563	1	9.722	4.375	11.278	15	11	14	1	2	2	GSK3B, LOC100506784	90, -1303	in gene, upstream	ActReg chr3 #11933	0	0	1
11934	3	119,813,830	119,814,684	854	1	10.808	8.538	11.077	16	12	16	1	2	2	GSK3B, LOC100506784	-993, -220	upstream, upstream	ActReg chr3 #11934	1	0	0
11935	3	120,004,113	120,004,524	411	1	3.769	3.308	12.385	5	5	21	1	0	0				ActReg chr3 #11935	0	0	1
11936	3	120,067,450	120,068,502	1,052	1	9.848	13.273	6.697	17	22	14	1	1	2	LRRC58, LOC100130701	210, -8689	in gene, upstream	ActReg chr3 #11936	0	1	0
11937	3	120,499,693	120,500,349	656	1	11.7	7.85	2.789	25	13	5	0	0	1	GTF2E1	38,463	in gene	ActReg chr3 #11937	1	0	0
11938	3	120,626,807	120,627,507	700	1	11.046	14.5	5.727	16	30	10	1	1	1	STXBP5L	107	in gene	ActReg chr3 #11938	0	1	0
11939	3	121,264,446	121,265,019	573	1	10.778	9.5	9.429	17	14	14	1	1	1	POLQ	121	in gene	ActReg chr3 #11939	1	0	0
11940	3	121,902,562	121,902,844	282	1	7.875	2.75	11.75	9	4	14	1	1	1	CASR	-478	upstream	ActReg chr3 #11940	0	0	1
11941	3	122,233,252	122,234,268	1,016	2	9.355	9.613	5.083	16	20	7	1	1	1	KPNA1	26	in gene	ActReg chr3 #11941	1	1	0
11942	3	122,282,545	122,283,660	815	1	6.538	7.769	11.846	10	13	18	1	2	2	PARP9, DTX3L	271, 67	in gene, in gene	ActReg chr3 #11942	0	0	1
11943	3	122,640,719	122,641,382	663	1	6.143	3.238	12.524	9	5	21	1	0	1	SEMA5B	105,526	in gene	ActReg chr3 #11943	0	0	1
11944	3	122,746,810	122,747,283	473	1	4.733	8.8	11.867	7	12	17	1	1	1	SEMA5B	-470	upstream	ActReg chr3 #11944	0	0	1
11945	3	122,785,677	122,786,612	935	2	11.69	11.31	10.586	17	16	19	1	1	1	PDIA5	288	in gene	ActReg chr3 #11945	1	0	1
11946	3	122,991,971	122,992,584	613	1	7.789	10	3.562	12	15	7	0	0	1	SEC22A	71,503	in gene	ActReg chr3 #11946	0	1	0
11947	3	123,004,908	123,006,227	1,319	2	11.659	20.146	5.805	34	41	11	0	0	1	ADCY5	161,825	in gene	ActReg chr3 #11947	1	1	0
11948	3	123,009,951	123,010,410	459	1	6.333	4.929	11.8	10	8	16	0	0	1	ADCY5	157,212	in gene	ActReg chr3 #11948	0	0	1
11949	3	123,303,449	123,304,505	1,056	1	10.091	12.212	6.667	16	16	10	2	2	2	PTPLB, LOC100506826	-53, -426	upstream, upstream	ActReg chr3 #11949	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
11950	3	123,936,033	123,937,167	1,134	2	17.971	21.029	2.697	42	52	5	0	0	1	KALRN	123,042	in gene	ActReg chr3 #11950	1	1	0
11951	3	124,147,589	124,148,438	849	1	11.308	6	2.375	22	12	5	0	0	1	KALRN	334,455	in gene	ActReg chr3 #11951	1	0	0
11952	3	124,249,065	124,249,576	511	1	8.812	12.125	2	13	19	3	0	0	1	KALRN	435,762	in gene	ActReg chr3 #11952	0	1	0
11953	3	124,249,696	124,250,188	492	1	11.812	6.188	1.545	17	9	2	0	0	1	KALRN	436,384	in gene	ActReg chr3 #11953	1	0	0
11954	3	124,448,873	124,449,732	859	2	11.667	10.63	6.852	16	21	12	1	2	4	KALRN, LOC100506841, UMPS, MIR544B	635744, 5359, 89, -1984	downstream, downstream, in gene, upstream	ActReg chr3 #11954	1	1	0
11955	3	124,531,541	124,532,643	1,102	1	6.971	11.657	4.086	11	19	7	0	0	1	ITGB5	74,052	in gene	ActReg chr3 #11955	0	1	0
11956	3	124,704,967	124,705,583	616	1	10.053	11.632	4.368	13	18	7	0	0	1	HEG1	69,527	in gene	ActReg chr3 #11956	0	1	0
11957	3	124,802,568	124,803,052	484	1	4.5	11.25	4.1	6	17	6	0	0	1	SLC12A8	128,804	in gene	ActReg chr3 #11957	0	1	0
11958	3	125,093,915	125,094,628	713	3	12.913	12.87	10.087	27	23	18	1	1	1	ZNF148	-73	upstream	ActReg chr3 #11958	1	1	1
11959	3	125,238,611	125,239,341	730	1	10.739	6.87	4.739	14	13	9	1	1	2	SNX4, OSBPL11	82, 75405	in gene, downstream	ActReg chr3 #11959	1	0	0
11960	3	125,390,434	125,391,132	698	1	4.048	2.381	10.476	9	4	18	0	0	0				ActReg chr3 #11960	0	0	1
11961	3	125,634,361	125,634,622	261	1	5.375	4.875	10.75	9	5	13	1	0	0				ActReg chr3 #11961	0	0	1
11962	3	125,694,591	125,695,034	443	1	3.786	10	3.786	5	18	6	0	0	1	ROPN1B	6,784	in gene	ActReg chr3 #11962	0	1	0
11963	3	125,898,772	125,899,316	544	1	2.214	2.941	12.765	3	5	18	1	1	1	ALDH1L1	441	in gene	ActReg chr3 #11963	0	0	1
11964	3	125,927,321	125,928,021	700	1	8.955	12.273	3.136	13	20	6	0	0	0				ActReg chr3 #11964	0	1	0
11965	3	126,074,696	126,075,695	999	1	10.452	11.839	7.29	20	19	13	1	1	2	KLF15, LOC100506907	1041, 37290	in gene, downstream	ActReg chr3 #11965	0	1	0
11966	3	126,120,502	126,120,929	427	1	1.8	3.286	11.714	3	6	15	0	0	2	LOC100506907, CCDC37	-8230, 6933	upstream, in gene	ActReg chr3 #11966	0	0	1
11967	3	126,152,599	126,153,335	736	1	1.913	5.043	11.087	4	7	16	0	0	2	CCDC37, ZXDC	39185, 41795	in gene, downstream	ActReg chr3 #11967	0	0	1
11968	3	126,245,163	126,245,961	798	1	3.458	3.48	12.16	6	5	21	0	1	2	UROC1, CHST13	-8946, 2386	upstream, in gene	ActReg chr3 #11968	0	0	1
11969	3	126,422,665	126,423,833	1,168	2	5.722	14.667	9.057	11	24	18	1	2	2	CHCHD6, LOC100132481	131, -2946	in gene, upstream	ActReg chr3 #11969	0	1	1
11970	3	126,629,777	126,630,851	1,074	2	13.412	10.265	3.824	19	17	6	0	0	1	CHCHD6	207,196	in gene	ActReg chr3 #11970	1	1	0
11971	3	126,701,151	126,701,841	690	2	12.682	10.909	10.954	22	16	18	1	1	1	PLXNA1	-5,841	upstream	ActReg chr3 #11971	1	0	1
11972	3	126,718,895	126,719,654	759	1	4.714	5.25	11.917	8	9	18	0	0	1	PLXNA1	11,837	in gene	ActReg chr3 #11972	0	0	1
11973	3	126,747,516	126,748,177	661	1	4.81	4.048	12.143	8	6	18	0	0	1	PLXNA1	40,409	in gene	ActReg chr3 #11973	0	0	1
11974	3	126,876,876	126,878,222	1,346	2	14.571	22.429	5.833	45	76	10	0	0	0				ActReg chr3 #11974	1	1	0
11975	3	126,881,659	126,882,346	687	1	7.318	11.318	2.65	12	18	4	0	0	0				ActReg chr3 #11975	0	1	0
11976	3	126,981,990	126,982,475	485	1	3.333	5.6	13.267	5	9	20	0	0	0				ActReg chr3 #11976	0	0	1
11977	3	127,023,444	127,023,888	444	1	2.571	3.571	10	5	5	17	0	0	0				ActReg chr3 #11977	0	0	1
11978	3	127,039,269	127,040,106	837	2	11.346	18.269	4	25	35	6	0	0	0				ActReg chr3 #11978	1	1	0
11979	3	127,174,573	127,175,040	467	1	6.467	8.933	12.933	10	14	23	1	0	0				ActReg chr3 #11979	0	0	1
11980	3	127,177,222	127,177,956	734	1	9.087	13.217	2.524	17	22	5	0	0	0				ActReg chr3 #11980	0	1	0
11981	3	127,262,991	127,263,516	525	1	8.188	6.812	12.875	14	10	19	0	0	0				ActReg chr3 #11981	0	0	1
11982	3	127,308,901	127,310,314	1,413	2	20.818	20.568	6.452	39	45	14	1	2	2	TPRA1, MCM2	-39, -7646	upstream, upstream	ActReg chr3 #11982	1	1	0
11983	3	127,316,500	127,317,295	795	2	7.88	12.04	5.92	18	16	11	1	2	2	TPRA1, MCM2	-7329, -356	upstream, upstream	ActReg chr3 #11983	1	1	0
11984	3	127,468,732	127,470,398	1,666	2	9.942	11.346	4.077	16	17	6	0	0	1	MGLL	72,486	in gene	ActReg chr3 #11984	1	1	0
11985	3	127,494,408	127,495,027	619	1	8.316	11.21	4.789	14	17	10	0	0	1	MGLL	47,334	in gene	ActReg chr3 #11985	0	1	0
11986	3	127,634,178	127,634,610	432	1	2.909	3.538	10.385	5	6	16	1	1	1	KBTBD12	-7,508	upstream	ActReg chr3 #11986	0	0	1
11987	3	127,770,242	127,771,225	983	2	9.433	8.067	5.267	16	18	10	1	1	1	SEC61A1	-479	upstream	ActReg chr3 #11987	1	1	0
11988	3	127,842,297	127,843,066	769	1	10.375	12.042	7.792	14	17	13	1	1	1	RUVBL1	-10	upstream	ActReg chr3 #11988	0	1	0
11989	3	127,871,975	127,872,792	817	2	11	11.76	6.56	16	21	13	1	1	1	EEFSEC	70	in gene	ActReg chr3 #11989	1	1	0
11990	3	128,129,805	128,130,249	444	1	3.5	4.071	11.071	6	6	19	0	0	1	EEFSEC	257,714	downstream	ActReg chr3 #11990	0	0	1
11991	3	128,152,148	128,152,586	438	1	3.929	3.857	12.929	6	5	20	1	0	0				ActReg chr3 #11991	0	0	1
11992	3	128,204,905	128,205,798	893	1	7.179	5.357	11.5	11	9	17	1	1	2	GATA2, LOC100506995	6679, -2601	in gene, upstream	ActReg chr3 #11992	0	0	1
11993	3	128,206,403	128,207,551	1,148	2	7.441	11.143	8.171	11	19	16	1	1	2	GATA2, LOC100506995	5053, -975	in gene, upstream	ActReg chr3 #11993	0	1	1
11994	3	128,336,037	128,337,587	1,550	2	33.083	39.521	8.167	110	116	14	1	0	1	RPN1	32,907	downstream	ActReg chr3 #11994	1	1	0
11995	3	128,369,249	128,369,932	683	3	12.048	13.286	11.143	17	19	21	1	1	1	RPN1	129	in gene	ActReg chr3 #11995	1	1	1
11996	3	128,399,254	128,400,386	1,132	1	8.917	13.222	7.057	19	24	13	1	0	0				ActReg chr3 #11996	0	1	0
11997	3	128,598,029	128,598,944	915	3	12.69	16.345	8.724	25	31	17	1	1	2	LOC653712, ACAD9	-8102, 153	upstream, in gene	ActReg chr3 #11997	1	1	1
11998	3	128,733,002	128,733,429	427	1	3.667	6.154	12.615	7	12	18	0	0	1	CCDC48	12,743	in gene	ActReg chr3 #11998	0	0	1
11999	3	128,745,687	128,746,348	661	1	12.476	8.238	3	22	12	6	1	0	1	CCDC48	25,545	in gene	ActReg chr3 #11999	1	0	0
12000	3	128,772,411	128,773,219	808	2	12.808	16.615	2.68	30	38	7	0	1	1	GP9	-6,830	upstream	ActReg chr3 #12000	1	1	0
12001	3	128,879,803	128,880,813	1,010	3	12.781	14.469	9.406	22	24	17	1	1	2	ISY1, CNBP	-279, 22502	upstream, downstream	ActReg chr3 #12001	1	1	1
12002	3	128,902,102	128,902,657	555	1	11.056	8.278	11	16	12	15	1	1	1	CNBP	431	in gene	ActReg chr3 #12002	0	0	1
12003	3	128,945,337	128,946,188	851	1	6.926	10.482	2.185	14	15	5	0	0	0				ActReg chr3 #12003	0	1	0
12004	3	128,967,949	128,968,854	905	3	11.286	12.893	10.643	19	25	18	1	1	1	COPG	-52	upstream	ActReg chr3 #12004	1	1	1
12005	3	129,034,949	129,035,872	923	1	9.571	11.31	9.828	19	19	17	1	2	2	H1FX, C3orf47	-290, 296	upstream, in gene	ActReg chr3 #12005	0	1	0
12006	3	129,075,580	129,076,096	516	1	3.154	3.125	11.353	5	8	19	0	0	0				ActReg chr3 #12006	0	0	1
12007	3	129,117,710	129,118,994	1,284	2	12.65	15.05	3.175	38	34	6	0	1	2	SNORA7B, C3orf25	-2161, 29142	upstream, downstream	ActReg chr3 #12007	1	1	0
12008	3	129,326,996	129,327,460	464	1	3.667	4.2	12.667	5	6	18	0	1	1	PLXND1	-1,646	upstream	ActReg chr3 #12008	0	0	1
12009	3	129,337,548	129,337,968	420	1	5.692	4.462	13.615	9	8	21	0	0	0				ActReg chr3 #12009	0	0	1
12010	3	129,345,883	129,346,471	588	1	7.789	11.579	8.368	11	22	12	1	0	0				ActReg chr3 #12010	0	1	0
12011	3	129,351,142	129,351,725	583	1	3.111	2.267	10.944	5	5	15	0	0	0				ActReg chr3 #12011	0	0	1
12012	3	130,533,534	130,533,916	382	1	3.667	3.167	10.5	5	7	17	0	0	0				ActReg chr3 #12012	0	0	1
12013	3	130,539,814	130,540,368	554	1	8.118	11.059	3.529	14	16	7	0	0	0				ActReg chr3 #12013	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12014	3	130,745,056	130,745,896	840	2	10.815	10.407	2.654	19	17	5	1	2	3	ATP2C1, ASTE1, NEK11	132042, 170, -218	downstream, in gene, upstream	ActReg chr3 #12014	1	1	0
12015	3	131,080,510	131,081,002	492	1	3	2.188	11.875	5	6	17	1	0	0				ActReg chr3 #12015	0	0	1
12016	3	131,100,437	131,101,206	769	1	5.708	6.708	11.333	9	10	20	1	1	1	NUDT16	306	in gene	ActReg chr3 #12016	0	0	1
12017	3	131,221,410	131,222,240	830	1	8.615	11.423	7.077	15	19	17	1	1	1	MRPL3	4	in gene	ActReg chr3 #12017	0	1	0
12018	3	131,753,612	131,754,444	832	2	9.385	10.385	6.308	24	22	13	1	1	1	CPNE4	-184	upstream	ActReg chr3 #12018	1	1	0
12019	3	132,136,183	132,136,836	653	2	11.809	7.762	9.81	20	12	15	1	1	1	DNAJC13	-44	upstream	ActReg chr3 #12019	1	0	1
12020	3	132,378,415	132,379,544	1,129	3	10.771	12.629	9.6	19	21	21	2	1	2	ACAD11, UBA5	-4, 5689	upstream, in gene	ActReg chr3 #12020	1	1	1
12021	3	133,393,192	133,393,927	735	1	4.105	2.565	10.783	7	5	17	1	0	0				ActReg chr3 #12021	0	0	1
12022	3	133,524,373	133,525,196	823	2	9.385	13.077	9.654	16	24	16	1	0	1	SRPRB	21,907	in gene	ActReg chr3 #12022	0	1	1
12023	3	133,663,528	133,664,510	982	1	6.633	12.1	4.433	12	19	8	0	0	1	SLCO2A1	84,901	in gene	ActReg chr3 #12023	0	1	0
12024	3	134,034,291	134,034,956	665	1	11.333	9.762	6.333	20	15	10	0	0	0				ActReg chr3 #12024	1	0	0
12025	3	134,089,794	134,090,354	560	1	5.882	5.471	12.647	10	8	17	0	0	1	AMOTL2	3,332	in gene	ActReg chr3 #12025	0	0	1
12026	3	134,145,978	134,146,727	749	1	14.458	12.333	2.333	27	21	4	0	1	1	LOC100507224	-4,947	upstream	ActReg chr3 #12026	1	0	0
12027	3	134,204,167	134,205,505	1,338	2	10.095	16.286	7.262	22	31	12	1	2	2	ANAPC13, CEP63	29, 261	in gene, in gene	ActReg chr3 #12027	1	1	0
12028	3	134,369,640	134,370,139	499	1	6.467	8.667	13.2	11	12	18	1	1	1	KY	-25	upstream	ActReg chr3 #12028	0	0	1
12029	3	134,513,409	134,514,680	1,271	2	12.462	8	8.282	17	12	16	1	1	1	EPHB1	-55	upstream	ActReg chr3 #12029	1	0	1
12030	3	134,635,068	134,635,760	692	1	3.905	2.273	10.682	6	5	18	0	0	1	EPHB1	121,315	in gene	ActReg chr3 #12030	0	0	1
12031	3	134,825,003	134,825,934	931	2	16.241	17.31	3.828	41	34	10	0	0	1	EPHB1	311,369	in gene	ActReg chr3 #12031	1	1	0
12032	3	134,843,650	134,844,530	880	2	11.556	12.778	4.037	23	23	10	0	0	1	EPHB1	329,991	in gene	ActReg chr3 #12032	1	1	0
12033	3	135,471,433	135,472,338	905	2	13	17.607	2.292	30	37	6	0	0	0				ActReg chr3 #12033	1	1	0
12034	3	135,683,986	135,685,333	1,347	3	9.262	9.905	6.357	19	17	11	1	1	1	PPP2R3A	144	in gene	ActReg chr3 #12034	1	1	0
12035	3	135,689,419	135,690,130	711	1	8.091	11.5	3.053	15	19	7	0	0	1	PPP2R3A	5,259	in gene	ActReg chr3 #12035	0	1	0
12036	3	135,914,042	135,914,691	649	1	8.857	12.143	6.35	15	21	11	1	1	1	MSL2	322	in gene	ActReg chr3 #12036	0	1	0
12037	3	135,914,817	135,916,108	1,291	3	11.55	12.7	7.737	22	19	19	1	1	1	MSL2	-774	upstream	ActReg chr3 #12037	1	1	1
12038	3	135,968,996	135,969,663	667	2	11.2	10.35	10.35	19	17	19	1	1	1	PCCB	162	in gene	ActReg chr3 #12038	1	0	1
12039	3	136,537,745	136,539,588	1,843	2	13.983	16.862	7.842	24	31	14	1	1	1	TMEM22	805	in gene	ActReg chr3 #12039	1	1	0
12040	3	136,580,743	136,581,683	940	2	8.621	11.103	10.345	13	19	17	1	2	3	TMEM22, LOC100507239, NCK1	43352, -311, 163	downstream, upstream, in gene	ActReg chr3 #12040	0	1	1
12041	3	137,489,669	137,490,168	499	1	4.4	5.533	12.933	6	9	19	1	1	2	SOX14, LOC100507274	6339, -3465	downstream, upstream	ActReg chr3 #12041	0	0	1
12042	3	137,833,803	137,834,737	934	2	10.517	14.034	6.345	16	22	10	1	1	2	DZIP1L, A4GNT	181, 16959	in gene, downstream	ActReg chr3 #12042	1	1	0
12043	3	137,905,923	137,907,155	1,232	1	8.105	13.184	6.421	14	22	11	1	1	1	ARMC8	391	in gene	ActReg chr3 #12043	0	1	0
12044	3	138,066,588	138,067,716	1,128	2	9.629	11.944	5.345	19	18	10	1	1	1	MRAS	527	in gene	ActReg chr3 #12044	1	1	0
12045	3	138,312,722	138,313,741	1,019	1	8.688	11.031	5.875	14	15	8	1	1	1	CEP70	-102	upstream	ActReg chr3 #12045	0	1	0
12046	3	138,327,194	138,328,010	816	1	10.059	13.423	8.13	15	23	15	1	1	1	FAIM	60	in gene	ActReg chr3 #12046	0	1	0
12047	3	138,552,358	138,553,782	1,424	2	11.159	14.296	3	23	26	7	1	0	0				ActReg chr3 #12047	1	1	0
12048	3	138,634,550	138,635,010	460	1	10	8	9.933	14	13	15	1	0	0				ActReg chr3 #12048	0	0	1
12049	3	138,669,047	138,669,558	511	1	3.812	3.6	14.688	6	9	21	1	1	2	FOXL2, C3orf72	-3320, 3226	upstream, in gene	ActReg chr3 #12049	0	0	1
12050	3	139,019,890	139,020,697	807	1	8	14.6	2.92	11	28	6	0	0	0				ActReg chr3 #12050	0	1	0
12051	3	139,048,013	139,048,584	571	1	9.222	10.333	5.944	17	19	11	0	0	0				ActReg chr3 #12051	0	1	0
12052	3	139,108,144	139,108,694	550	1	9.941	8.471	11.177	15	12	14	1	2	2	COPB2, LOC100507291	103, -238	in gene, upstream	ActReg chr3 #12052	0	0	1
12053	3	139,483,717	139,484,267	550	1	11.177	8.941	2.647	16	18	5	0	0	0				ActReg chr3 #12053	1	0	0
12054	3	139,516,391	139,517,116	725	2	12.454	13.364	1.227	24	29	2	0	0	0				ActReg chr3 #12054	1	1	0
12055	3	139,654,421	139,654,919	498	1	2.688	4.812	10.625	6	7	15	1	1	1	CLSTN2	643	in gene	ActReg chr3 #12055	0	0	1
12056	3	139,925,382	139,926,027	645	1	10.05	8.75	2.684	23	15	5	0	0	1	CLSTN2	271,677	in gene	ActReg chr3 #12056	1	0	0
12057	3	140,011,570	140,012,451	881	1	7.929	8.929	3.036	14	15	6	0	0	1	CLSTN2	357,983	in gene	ActReg chr3 #12057	0	1	0
12058	3	140,348,627	140,349,642	1,015	2	10.625	12.781	1.917	15	22	3	0	0	0				ActReg chr3 #12058	1	1	0
12059	3	140,660,463	140,660,964	501	2	10.125	8.312	8.133	13	11	13	1	1	1	SLC25A36	51	in gene	ActReg chr3 #12059	1	0	1
12060	3	140,950,151	140,950,597	446	1	10.214	11.5	10.429	15	20	15	1	1	1	ACPL2	-308	upstream	ActReg chr3 #12060	0	0	1
12061	3	140,958,925	140,959,579	654	1	6.05	10.85	2.857	10	16	4	0	0	1	ACPL2	8,570	in gene	ActReg chr3 #12061	0	1	0
12062	3	141,021,119	141,021,972	853	2	10.741	12.556	4.48	16	22	11	0	0	1	ACPL2	70,863	downstream	ActReg chr3 #12062	1	1	0
12063	3	141,030,244	141,031,097	853	1	9.115	13.692	5.538	14	24	14	1	0	0				ActReg chr3 #12063	0	1	0
12064	3	141,054,275	141,054,863	588	1	6.5	11.222	2.846	8	18	4	0	0	1	ZBTB38	11,514	in gene	ActReg chr3 #12064	0	1	0
12065	3	141,085,851	141,087,890	2,039	4	9.984	10.312	3.738	18	18	10	0	0	1	ZBTB38	43,815	in gene	ActReg chr3 #12065	1	1	0
12066	3	141,206,167	141,206,895	728	1	8.652	10.043	6.133	12	13	11	1	1	1	RASA2	605	in gene	ActReg chr3 #12066	0	1	0
12067	3	141,456,688	141,458,070	1,382	2	12.463	13.628	5.762	23	26	11	1	1	1	RNF7	328	in gene	ActReg chr3 #12067	1	1	0
12068	3	141,594,962	141,595,311	349	1	8.091	8.727	11.818	10	12	17	1	1	2	ATP1B3, LOC100507375	-334, 27436	upstream, downstream	ActReg chr3 #12068	0	0	1
12069	3	141,658,694	141,659,627	933	2	9.241	11.517	4.828	21	16	10	0	0	1	TFDP2	209,226	downstream	ActReg chr3 #12069	1	1	0
12070	3	141,867,573	141,868,536	963	2	7.833	10.333	6.367	11	14	14	1	1	2	TFDP2, GK5	332, 76395	in gene, downstream	ActReg chr3 #12070	0	1	1
12071	3	142,297,084	142,298,104	1,020	2	18.875	20.031	8.469	49	53	17	1	1	1	ATR	74	in gene	ActReg chr3 #12071	1	1	0
12072	3	142,314,698	142,315,551	853	1	11.692	13.115	4.462	17	19	10	1	1	1	PLS1	-105	upstream	ActReg chr3 #12072	0	1	0
12073	3	142,606,768	142,607,367	599	1	7.632	10.684	3.263	12	15	5	1	1	1	PCOLCE2	978	in gene	ActReg chr3 #12073	0	1	0
12074	3	142,607,374	142,607,755	381	1	9.333	8.583	12.167	13	12	19	1	1	1	PCOLCE2	481	in gene	ActReg chr3 #12074	0	0	1
12075	3	142,614,883	142,615,578	695	1	8	12.381	3.857	13	18	9	0	1	1	PCOLCE2	-7,185	upstream	ActReg chr3 #12075	0	1	0
12076	3	142,681,138	142,681,783	645	1	6.45	6.75	12.3	11	12	18	1	1	1	PAQR9	718	in gene	ActReg chr3 #12076	0	0	1
12077	3	142,695,413	142,695,880	467	1	10.8	9.733	3.077	17	14	4	0	0	0				ActReg chr3 #12077	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12078	3	142,719,653	142,721,030	1,377	2	15.233	15.465	4.721	38	42	12	1	2	2	LOC100289361, SR140	-32, -31	upstream, upstream	ActReg chr3 #12078	1	1	0
12079	3	142,840,010	142,841,134	1,124	1	6.229	7.4	12.429	14	12	21	1	1	1	CHST2	1,904	in gene	ActReg chr3 #12079	0	0	1
12080	3	143,161,304	143,161,951	647	1	6.3	12.95	2.45	10	19	4	0	0	1	SLC9A9	405,746	in gene	ActReg chr3 #12080	0	1	0
12081	3	143,405,341	143,406,050	709	2	11.435	9.857	1.182	22	16	2	0	0	1	SLC9A9	161,678	in gene	ActReg chr3 #12081	1	1	0
12082	3	143,689,620	143,690,154	534	2	10.471	9.176	7.062	15	14	11	1	1	1	C3orf58	-753	upstream	ActReg chr3 #12082	1	1	0
12083	3	143,690,600	143,692,352	1,752	4	10.036	10.382	7.145	16	19	13	1	1	1	C3orf58	836	in gene	ActReg chr3 #12083	1	1	0
12084	3	144,475,662	144,476,113	451	1	2.643	4.714	9.071	5	7	15	0	0	0				ActReg chr3 #12084	0	0	1
12085	3	145,849,706	145,850,223	517	1	5.25	10.875	1.8	7	16	2	0	0	1	PLOD2	29,318	in gene	ActReg chr3 #12085	0	1	0
12086	3	145,878,482	145,878,888	406	1	9.308	10.692	13.462	15	15	22	1	1	1	PLOD2	597	in gene	ActReg chr3 #12086	0	0	1
12087	3	145,968,296	145,968,951	655	1	6.15	10	4.889	10	19	9	1	1	1	PLSCR4	343	in gene	ActReg chr3 #12087	0	1	0
12088	3	146,186,940	146,187,437	497	1	5.071	4.875	12.688	10	6	21	1	0	1	PLSCR2	26,534	in gene	ActReg chr3 #12088	0	0	1
12089	3	146,221,500	146,222,152	652	1	11.286	9.286	2.048	18	13	4	0	0	1	PLSCR2	-8,104	upstream	ActReg chr3 #12089	1	0	0
12090	3	146,489,875	146,490,456	581	1	2.824	2.588	12.167	5	5	19	0	0	0				ActReg chr3 #12090	0	0	1
12091	3	147,111,138	147,111,813	675	1	3.19	8.667	13.667	5	16	21	1	0	1	ZIC4	12,932	in gene	ActReg chr3 #12091	0	0	1
12092	3	147,138,925	147,139,318	393	1	4.25	1.571	11.167	7	2	15	1	1	2	ZIC1, FLJ30375	11940, 1512	downstream, in gene	ActReg chr3 #12092	0	0	1
12093	3	147,987,640	147,988,122	482	1	8.067	11.6	1.714	11	14	3	0	0	0				ActReg chr3 #12093	0	1	0
12094	3	148,728,314	148,728,905	591	1	10.947	8.474	2.444	16	14	4	0	0	1	GYG1	19,414	in gene	ActReg chr3 #12094	1	0	0
12095	3	148,803,781	148,804,893	1,112	1	8.971	12.765	4.382	14	21	7	1	1	1	HLTF	4	in gene	ActReg chr3 #12095	0	1	0
12096	3	148,847,058	148,847,981	923	2	9.138	13.655	10.276	17	23	20	1	1	1	HPS3	148	in gene	ActReg chr3 #12096	0	1	1
12097	3	148,897,665	148,898,375	710	1	8.227	13.636	4.864	13	19	8	0	0	2	HPS3, CP	50649, 41812	downstream, in gene	ActReg chr3 #12097	0	1	0
12098	3	149,104,059	149,105,065	1,006	1	12.219	9.781	1.5	19	17	2	0	0	1	TM4SF1	-8,994	upstream	ActReg chr3 #12098	1	0	0
12099	3	149,375,261	149,376,290	1,029	2	12.091	9.636	9.909	16	15	15	1	0	1	WWTR1	45,285	in gene	ActReg chr3 #12099	1	0	1
12100	3	149,395,944	149,396,702	758	2	9.957	13.261	4.5	17	23	8	0	0	1	WWTR1	24,737	in gene	ActReg chr3 #12100	1	1	0
12101	3	149,469,911	149,470,591	680	3	11.381	11.714	8.429	20	21	18	1	1	2	COMMD2, C3orf16	35, 40359	in gene, downstream	ActReg chr3 #12101	1	1	1
12102	3	149,530,505	149,532,216	1,711	2	10.283	12.34	5.795	16	21	12	1	1	1	RNF13	885	in gene	ActReg chr3 #12102	1	1	0
12103	3	149,688,732	149,689,621	889	3	8.607	11.393	7.214	16	18	17	1	2	4	RNF13, PFN2, LOC646903, TMEM183B	158701, -435, 110, 11977	downstream, upstream, in gene, downstream	ActReg chr3 #12103	1	1	1
12104	3	149,812,039	149,812,703	664	1	7.6	11.55	3.9	10	19	6	0	0	0				ActReg chr3 #12104	0	1	0
12105	3	149,864,751	149,865,456	705	1	7.455	10	2.95	14	13	6	0	0	0				ActReg chr3 #12105	0	1	0
12106	3	150,125,989	150,127,347	1,358	3	11.571	10.667	8.317	17	17	16	1	1	1	TSC22D2	-120	upstream	ActReg chr3 #12106	1	1	1
12107	3	150,263,672	150,264,806	1,134	2	10.639	11.194	7.472	18	23	13	1	2	2	SERP1, EIF2A	189, -335	in gene, upstream	ActReg chr3 #12107	1	1	0
12108	3	150,320,604	150,321,831	1,227	3	11.436	13.949	12.385	22	26	28	1	1	1	SELT	151	in gene	ActReg chr3 #12108	1	1	1
12109	3	150,481,315	150,481,863	548	1	10.177	10.412	7.824	14	15	15	1	1	1	SIAH2	-326	upstream	ActReg chr3 #12109	0	1	0
12110	3	151,113,411	151,114,100	689	2	12.191	10.238	1.643	24	22	5	0	0	1	MED12L	309,079	in gene	ActReg chr3 #12110	1	1	0
12111	3	151,162,917	151,163,831	914	1	7.179	11.357	1.792	11	19	4	0	0	2	MED12L, IGSF10	358698, 13123	downstream, in gene	ActReg chr3 #12111	0	1	0
12112	3	151,693,999	151,694,515	516	1	9.812	9.125	0	16	16	0	0	0	0				ActReg chr3 #12112	1	0	0
12113	3	151,739,363	151,740,299	936	1	8.034	11.724	2.32	13	16	4	0	0	0				ActReg chr3 #12113	0	1	0
12114	3	151,935,024	151,935,559	535	1	4	6.235	10.882	6	10	15	0	0	0				ActReg chr3 #12114	0	0	1
12115	3	151,976,106	151,976,789	683	1	13.095	8	3	23	13	6	0	0	2	hCG_1806964, MBNL1	10968, -9382	downstream, upstream	ActReg chr3 #12115	1	0	0
12116	3	151,984,195	151,984,992	797	1	7.76	11.48	2.96	11	19	7	0	2	2	hCG_1806964, MBNL1	2822, -1236	in gene, upstream	ActReg chr3 #12116	0	1	0
12117	3	151,986,679	151,987,519	840	2	7.231	10.154	12.885	10	16	19	1	2	2	hCG_1806964, MBNL1	316, 1270	in gene, in gene	ActReg chr3 #12117	0	1	1
12118	3	152,339,122	152,339,585	463	1	10.533	9.133	1.429	14	12	2	0	0	0				ActReg chr3 #12118	1	0	0
12119	3	152,436,677	152,437,518	841	2	10.615	9.385	1.667	14	15	2	0	0	0				ActReg chr3 #12119	1	1	0
12120	3	152,552,711	152,553,378	667	1	8.143	12.143	7.524	12	17	13	1	1	1	P2RY1	308	in gene	ActReg chr3 #12120	0	1	0
12121	3	152,878,090	152,880,350	2,260	2	11.971	14.671	5.603	27	29	14	1	1	1	RAP2B	-809	upstream	ActReg chr3 #12121	1	1	0
12122	3	152,880,808	152,881,432	624	1	7.167	7.211	10.421	10	11	14	1	1	1	RAP2B	1,091	in gene	ActReg chr3 #12122	0	0	1
12123	3	153,066,444	153,066,835	391	1	10.833	8.917	1	15	13	1	0	0	0				ActReg chr3 #12123	1	0	0
12124	3	153,805,569	153,806,053	484	1	1.455	3.857	14.533	2	6	22	0	0	1	LOC100507524	33,188	in gene	ActReg chr3 #12124	0	0	1
12125	3	153,838,581	153,838,928	347	1	8.636	4.818	10.727	10	7	13	1	2	2	LOC100507524, SGEF	245, -395	in gene, upstream	ActReg chr3 #12125	0	0	1
12126	3	153,839,509	153,840,050	541	1	5.941	7.471	11.471	9	10	16	1	2	2	LOC100507524, SGEF	-780, 630	upstream, in gene	ActReg chr3 #12126	0	0	1
12127	3	154,138,705	154,139,389	684	2	12.619	13.714	0	28	30	0	0	0	1	GPR149	8,457	in gene	ActReg chr3 #12127	1	1	0
12128	3	154,145,517	154,145,916	399	1	3.182	9.417	11.917	8	13	14	0	1	1	GPR149	1,788	in gene	ActReg chr3 #12128	0	0	1
12129	3	154,146,661	154,147,078	417	1	5.538	5.154	12.308	8	8	19	1	1	1	GPR149	635	in gene	ActReg chr3 #12129	0	0	1
12130	3	155,462,367	155,463,090	723	2	10.261	11.391	9.043	19	16	16	1	1	1	LOC100507556	-1,213	upstream	ActReg chr3 #12130	0	1	1
12131	3	155,588,757	155,589,522	765	1	9.125	10.625	7.5	12	14	13	1	1	1	GMPS	814	in gene	ActReg chr3 #12131	0	1	0
12132	3	156,009,411	156,009,904	493	1	4.6	3.786	10	7	6	18	1	0	1	KCNAB1	171,320	in gene	ActReg chr3 #12132	0	0	1
12133	3	156,252,919	156,253,513	594	1	8.737	9.895	3	12	18	6	0	0	2	KCNAB1, SSR3	414879, 19757	in gene, downstream	ActReg chr3 #12133	0	1	0
12134	3	156,272,456	156,272,896	440	1	7.429	8.929	10.214	12	15	15	1	1	1	SSR3	297	in gene	ActReg chr3 #12134	0	0	1
12135	3	156,391,560	156,392,871	1,311	2	12.805	14.293	7.488	27	29	15	1	2	2	LOC100287227, TIPARP	1287, 10	in gene, in gene	ActReg chr3 #12135	1	1	0
12136	3	156,505,826	156,506,543	717	2	10.546	12.273	1.583	20	20	2	0	0	1	LOC730091	28,639	in gene	ActReg chr3 #12136	1	1	0
12137	3	156,533,761	156,535,241	1,480	2	11.5	13.522	3.395	23	28	7	1	1	2	LOC730091, LEKR1	322, -9595	in gene, upstream	ActReg chr3 #12137	1	1	0
12138	3	156,799,277	156,799,936	659	1	7.714	10.476	2.667	11	17	5	0	0	2	LOC339894, LOC100498859	41185, -8064	in gene, upstream	ActReg chr3 #12138	0	1	0
12139	3	156,806,619	156,807,332	713	1	8.739	13.609	8.696	14	24	14	1	1	2	LOC339894, LOC100498859	33816, -695	in gene, upstream	ActReg chr3 #12139	0	1	0
12140	3	156,845,803	156,846,562	759	1	10.25	13.125	4.583	17	25	8	0	1	1	LOC339894	-5,391	upstream	ActReg chr3 #12140	0	1	0
12141	3	156,877,623	156,878,580	957	3	15.4	14.433	13.067	35	28	22	1	1	1	CCNL1	381	in gene	ActReg chr3 #12141	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12142	3	156,892,409	156,893,325	916	2	11.034	14.414	7.931	24	28	14	1	0	0				ActReg chr3 #12142	1	1	0
12143	3	156,966,492	156,967,000	508	1	9.125	12.875	3.286	14	18	5	0	0	0				ActReg chr3 #12143	0	1	0
12144	3	157,772,849	157,773,508	659	1	10.809	10.048	2.529	21	20	4	0	0	0				ActReg chr3 #12144	1	0	0
12145	3	157,827,496	157,828,587	1,091	2	19.235	18.559	6.441	40	49	13	1	2	2	SHOX2, RSRC1	-4089, 149	upstream, in gene	ActReg chr3 #12145	1	1	0
12146	3	157,845,668	157,845,964	296	1	10.333	12.444	1	14	17	1	0	0	1	RSRC1	17,924	in gene	ActReg chr3 #12146	0	1	0
12147	3	158,288,556	158,289,173	617	1	5.789	12.421	7	9	19	10	1	1	1	MLF1	-89	upstream	ActReg chr3 #12147	0	1	0
12148	3	158,361,808	158,362,882	1,074	2	48.706	53.235	4.12	180	177	9	1	1	1	GFM1	28	in gene	ActReg chr3 #12148	1	1	0
12149	3	158,519,474	158,520,091	617	1	12.842	11.79	11.632	23	23	15	1	1	1	MFSD1	67	in gene	ActReg chr3 #12149	0	0	1
12150	3	158,800,280	158,800,771	491	1	8.688	8.375	2.312	13	14	3	0	0	1	IQCJ	13,408	in gene	ActReg chr3 #12150	0	1	0
12151	3	158,846,114	158,846,754	640	1	7.7	11.95	1.615	15	19	3	0	0	1	IQCJ	59,317	in gene	ActReg chr3 #12151	0	1	0
12152	3	158,991,261	158,991,859	598	2	11.895	10.579	1.692	25	20	2	0	1	2	IQCJ, SCHIP1	204443, 16	downstream, in gene	ActReg chr3 #12152	1	1	0
12153	3	159,482,455	159,483,829	1,374	2	11.279	11.674	5.15	20	21	17	1	0	1	SCHIP1	491,598	in gene	ActReg chr3 #12153	1	1	0
12154	3	159,778,214	159,778,723	509	1	3.875	3.231	11.062	6	5	13	0	0	0				ActReg chr3 #12154	0	0	1
12155	3	159,847,201	159,848,228	1,027	1	4.938	10.781	1.619	9	19	3	0	0	0				ActReg chr3 #12155	0	1	0
12156	3	160,097,922	160,098,567	645	1	8.25	11.75	2.5	13	19	4	0	0	1	IFT80	19,076	in gene	ActReg chr3 #12156	0	1	0
12157	3	160,117,162	160,118,331	1,169	1	7.639	12.083	4.235	18	23	8	1	4	4	IFT80, SMC4, MIR15B, MIR16-2	-426, 316, -4630, -4787	upstream, in gene, upstream, upstream	ActReg chr3 #12157	0	1	0
12158	3	160,213,761	160,214,268	507	1	2.385	10.267	4.667	4	17	7	0	1	2	LOC100507647, KPNA4	1698, 69362	in gene, downstream	ActReg chr3 #12158	0	1	0
12159	3	160,472,090	160,473,578	1,488	2	16.277	21.83	5.977	42	53	11	1	1	1	PPM1L	-1,162	upstream	ActReg chr3 #12159	1	1	0
12160	3	161,090,268	161,090,666	398	1	5.308	4.769	9.923	7	9	14	1	1	1	C3orf57	-596	upstream	ActReg chr3 #12160	0	0	1
12161	3	162,108,758	162,109,138	380	1	5.667	11.5	0	8	18	0	0	0	0				ActReg chr3 #12161	0	1	0
12162	3	162,562,206	162,562,624	418	1	4.786	4.929	10.357	6	7	16	0	0	0				ActReg chr3 #12162	0	0	1
12163	3	167,813,308	167,813,889	581	1	6.053	11	4.211	10	21	9	1	1	1	GOLIM4	-181	upstream	ActReg chr3 #12163	0	1	0
12164	3	167,967,112	167,968,195	1,083	1	7.059	10.941	3.818	10	19	11	1	1	1	C3orf50	343	in gene	ActReg chr3 #12164	0	1	0
12165	3	167,990,218	167,990,672	454	1	9.643	7.714	1.222	16	12	2	0	0	1	C3orf50	23,135	in gene	ActReg chr3 #12165	1	0	0
12166	3	169,380,901	169,381,284	383	1	3.917	4.455	10.333	6	6	17	1	1	1	MECOM	471	in gene	ActReg chr3 #12166	0	0	1
12167	3	169,939,699	169,940,409	710	2	15.591	17	2.706	32	36	5	1	1	1	PRKCI	-166	upstream	ActReg chr3 #12167	1	1	0
12168	3	170,302,253	170,302,895	642	2	11.65	12	5.053	21	20	11	1	1	1	SLC7A14	1,289	in gene	ActReg chr3 #12168	1	1	0
12169	3	170,310,519	170,310,957	438	1	8.857	10.571	4.778	12	15	6	0	1	1	SLC7A14	-6,875	upstream	ActReg chr3 #12169	0	1	0
12170	3	171,527,738	171,528,391	653	1	6.571	7.143	10.905	11	10	15	1	1	1	PLD1	209	in gene	ActReg chr3 #12170	0	0	1
12171	3	172,167,106	172,168,086	980	2	16.167	13.967	3.586	25	30	9	1	1	1	GHSR	-1,350	upstream	ActReg chr3 #12171	1	1	0
12172	3	172,428,479	172,429,271	792	2	12.24	12.56	5.04	28	23	11	1	2	2	NCEH1, LOC100505528	133, 1088	in gene, in gene	ActReg chr3 #12172	1	1	0
12173	3	172,468,200	172,468,629	429	1	10.462	5.692	2.909	16	8	4	1	1	1	ECT2	-3,885	upstream	ActReg chr3 #12173	1	0	0
12174	3	173,115,355	173,115,901	546	1	9.353	3.529	2.941	17	6	5	1	1	1	NLGN1	-616	upstream	ActReg chr3 #12174	1	0	0
12175	3	176,921,822	176,922,105	283	1	3.889	3	10	6	4	12	0	1	1	TBL1XR1	-6,915	upstream	ActReg chr3 #12175	0	0	1
12176	3	177,076,946	177,077,370	424	1	5.769	5.846	10.308	8	11	16	0	0	0				ActReg chr3 #12176	0	0	1
12177	3	177,077,483	177,078,164	681	2	12.762	8.81	4	23	16	7	0	0	0				ActReg chr3 #12177	1	1	0
12178	3	178,402,510	178,403,264	754	2	11.292	11.167	1.667	23	25	3	0	0	1	KCNMB2	148,663	in gene	ActReg chr3 #12178	1	1	0
12179	3	178,408,266	178,408,707	441	1	9	9.571	1.429	15	14	2	0	0	1	KCNMB2	154,262	in gene	ActReg chr3 #12179	0	1	0
12180	3	178,980,878	178,981,241	363	1	1	2.727	10.454	1	4	14	0	0	1	KCNMB3	3,779	in gene	ActReg chr3 #12180	0	0	1
12181	3	180,707,124	180,707,654	530	1	9.412	8.235	4.529	18	14	7	1	1	2	FXR1, DNAJC19	77155, 173	downstream, in gene	ActReg chr3 #12181	1	0	0
12182	3	181,034,408	181,034,848	440	1	10.714	6.846	1.833	14	13	2	0	0	0				ActReg chr3 #12182	1	0	0
12183	3	181,900,251	181,900,844	593	1	6.526	9.474	2.333	13	22	3	0	0	0				ActReg chr3 #12183	0	1	0
12184	3	182,816,705	182,817,620	915	1	5.071	10.893	4.154	8	17	8	1	1	1	MCCC1	203	in gene	ActReg chr3 #12184	0	1	0
12185	3	183,416,121	183,416,379	258	1	1.875	6.625	10.875	3	10	14	1	1	1	YEATS2	644	in gene	ActReg chr3 #12185	0	0	1
12186	3	183,602,391	183,603,108	717	2	10.13	11.913	5.304	19	23	11	1	1	1	PARL	-56	upstream	ActReg chr3 #12186	1	1	0
12187	3	183,852,750	183,853,562	812	2	9.88	11.52	6.957	23	14	13	1	1	1	EIF2B5	346	in gene	ActReg chr3 #12187	1	1	0
12188	3	183,892,456	183,893,036	580	1	7.833	9.778	6.722	14	17	11	1	1	2	DVL3, AP2M1	19462, 112	downstream, in gene	ActReg chr3 #12188	0	1	0
12189	3	183,950,688	183,951,176	488	1	2	3.812	10.625	3	5	17	0	1	3	VWA5B2, MIR1224, ALG3	2615, -8261, 16381	in gene, upstream, downstream	ActReg chr3 #12189	0	0	1
12190	3	183,966,340	183,967,047	707	1	11.636	9.682	6.545	22	15	12	0	2	5	VWA5B2, MIR1224, ALG3, ECE2, CAMK2N2	18376, 7500, 620, -752, 12558	downstream, downstream, in gene, upstream, downstream	ActReg chr3 #12190	1	0	0
12191	3	184,267,583	184,268,121	538	1	4.294	10.823	3	8	16	5	0	0	0				ActReg chr3 #12191	0	1	0
12192	3	184,279,361	184,279,943	582	1	5.944	9.556	4.471	10	15	9	1	1	1	EPHB3	65	in gene	ActReg chr3 #12192	0	1	0
12193	3	184,408,807	184,409,177	370	1	2.455	1.125	10.182	4	2	14	0	0	0				ActReg chr3 #12193	0	0	1
12194	3	184,893,224	184,893,726	502	1	7.333	10	2.545	9	15	4	0	0	0				ActReg chr3 #12194	0	1	0
12195	3	185,216,448	185,217,136	688	1	10.591	10.5	5.182	20	16	8	1	1	2	TMEM41A, LIPH	53, 53577	in gene, downstream	ActReg chr3 #12195	1	0	0
12196	3	185,304,130	185,304,514	384	1	8.75	9.75	11	12	14	15	1	1	1	SENP2	291	in gene	ActReg chr3 #12196	0	0	1
12197	3	185,826,731	185,827,333	602	2	11.79	10.158	2.188	21	13	4	1	1	1	ETV5	-131	upstream	ActReg chr3 #12197	1	1	0
12198	3	185,938,097	185,938,455	358	1	4.545	11	2.545	7	16	3	0	0	1	DGKG	141,747	in gene	ActReg chr3 #12198	0	1	0
12199	3	186,025,244	186,025,914	670	2	12.238	9.143	0	26	16	0	0	0	1	DGKG	54,444	in gene	ActReg chr3 #12199	1	1	0
12200	3	186,284,665	186,285,327	662	1	11.191	7.619	5.476	16	12	10	1	1	2	TBCCD1, DNAJB11	3336, -3471	in gene, upstream	ActReg chr3 #12200	1	0	0
12201	3	186,501,044	186,501,620	576	1	6.611	10.333	5.722	9	15	10	1	5	6	EIF4A2, SNORD2, SNORA81, SNORA63, SNORA4, RFC4	-29, -1253, -3132, -3756, -4070, 23152	upstream, upstream, upstream, upstream, upstream, downstream	ActReg chr3 #12201	0	1	0
12202	3	186,523,959	186,524,789	830	1	8.615	13.269	3.609	17	21	6	1	1	1	RFC4	110	in gene	ActReg chr3 #12202	0	1	0
12203	3	186,648,082	186,648,532	450	1	2.929	7.643	10.714	4	10	18	1	1	1	ST6GAL1	-8	upstream	ActReg chr3 #12203	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12204	3	187,085,372	187,085,780	408	1	2.364	3.385	10.615	4	5	17	0	1	1	RTP4	-592	upstream	ActReg chr3 #12204	0	0	1
12205	3	187,387,259	187,388,019	760	2	11.958	15.375	4.211	21	31	12	1	1	1	SST	562	in gene	ActReg chr3 #12205	1	1	0
12206	3	187,463,055	187,463,869	814	2	11.952	11	2.286	23	22	5	0	1	1	BCL6	51	in gene	ActReg chr3 #12206	1	1	0
12207	3	187,770,107	187,770,674	567	2	8	12.389	3.556	14	21	8	0	0	0				ActReg chr3 #12207	1	1	0
12208	3	190,231,164	190,231,866	702	1	6.636	10.5	4.1	11	13	11	1	1	1	IL1RAP	-325	upstream	ActReg chr3 #12208	0	1	0
12209	3	190,303,633	190,304,088	455	1	10.286	7.143	2.091	16	10	3	0	0	1	IL1RAP	72,020	in gene	ActReg chr3 #12209	1	0	0
12210	3	190,557,951	190,558,404	453	1	6.733	10.467	1	13	17	1	0	0	0				ActReg chr3 #12210	0	1	0
12211	3	191,905,349	191,905,932	583	1	5.167	10.111	0	10	17	0	0	0	1	FGF12	539,748	in gene	ActReg chr3 #12211	0	1	0
12212	3	192,675,168	192,675,732	564	1	5.5	10.222	1.882	7	15	3	0	0	0				ActReg chr3 #12212	0	1	0
12213	3	193,310,549	193,311,297	748	2	11.083	12.75	3.81	25	26	7	1	1	1	OPA1	-10	upstream	ActReg chr3 #12213	1	1	0
12214	3	193,587,042	193,587,577	535	1	11.562	9.688	6.562	15	12	10	1	0	0				ActReg chr3 #12214	1	0	0
12215	3	193,601,356	193,601,874	518	1	10.688	6.438	3.375	14	10	7	0	0	0				ActReg chr3 #12215	1	0	0
12216	3	193,721,034	193,721,852	818	2	12.92	10	6.12	20	20	10	1	1	2	LOC647323, LOC100505902	5, 67298	in gene, downstream	ActReg chr3 #12216	1	1	0
12217	3	193,852,546	193,853,204	658	1	11.45	6.45	4.3	19	11	7	1	1	1	HES1	-1,059	upstream	ActReg chr3 #12217	1	0	0
12218	3	194,392,771	194,393,588	817	2	13.52	11.56	2.8	28	20	5	1	1	1	LSG1	27	in gene	ActReg chr3 #12218	1	1	0
12219	3	194,461,371	194,461,979	608	1	7.474	9.579	3.462	12	16	6	0	0	1	LOC100507391	32,525	in gene	ActReg chr3 #12219	0	1	0
12220	3	194,500,308	194,500,666	358	1	1.4	1.545	10.909	2	2	15	0	0	1	LOC100507391	71,337	in gene	ActReg chr3 #12220	0	0	1
12221	3	194,707,152	194,707,733	581	1	9.778	6.278	2.765	15	11	5	0	0	0				ActReg chr3 #12221	1	0	0
12222	3	194,991,671	194,992,480	809	2	11.346	12.192	3.286	20	26	8	1	1	2	C3orf21, ACAP2	-180, 171742	upstream, downstream	ActReg chr3 #12222	1	1	0
12223	3	195,269,815	195,270,209	394	1	7.154	8.538	9.231	11	13	15	1	1	1	PPP1R2	212	in gene	ActReg chr3 #12223	0	0	1
12224	3	195,596,499	195,596,970	471	1	2.8	3.083	11.8	4	4	18	0	0	1	TNK2	39,146	in gene	ActReg chr3 #12224	0	0	1
12225	3	195,619,138	195,619,576	438	1	3.846	2.308	9.615	6	3	16	0	0	1	TNK2	16,523	in gene	ActReg chr3 #12225	0	0	1
12226	3	196,006,245	196,006,692	447	1	10.929	4.714	1	18	8	1	0	0	1	PCYT1A	8,116	in gene	ActReg chr3 #12226	1	0	0
12227	3	196,044,458	196,045,096	638	1	6.9	5.85	10.65	14	8	17	1	1	3	TCTEX1D2, LOC100507574, TM4SF19	582, 4658, 20481	in gene, downstream, downstream	ActReg chr3 #12227	0	0	1
12228	3	196,668,944	196,669,627	683	1	6.952	11.286	4.048	10	17	6	1	2	4	SENP5, NCBP2, LOC152217, PIGZ	74558, 179, -209, 26419	downstream, in gene, upstream, downstream	ActReg chr3 #12228	0	1	0
12229	3	196,737,791	196,738,192	401	1	2.923	5.769	11.769	5	10	17	0	0	2	MFI2, LOC100507057	18696, 8220	in gene, downstream	ActReg chr3 #12229	0	0	1
12230	3	196,743,081	196,743,386	305	1	2.333	6.667	9.889	4	11	12	0	0	1	MFI2	13,454	in gene	ActReg chr3 #12230	0	0	1
12231	3	196,755,245	196,755,831	586	1	6.222	11.5	4.333	9	18	7	1	1	1	MFI2	1,149	in gene	ActReg chr3 #12231	0	1	0
12232	3	196,758,352	196,758,893	541	1	11.941	9.176	2	21	16	4	0	1	1	MFI2	-1,935	upstream	ActReg chr3 #12232	1	0	0
12233	3	197,281,542	197,282,326	784	1	7.042	9.833	7.667	11	15	13	1	0	1	BDH1	18,260	in gene	ActReg chr3 #12233	0	1	0
12234	3	197,687,206	197,687,553	347	1	4	6.636	9.182	7	10	13	1	2	3	IQCG, RPL35A, LMLN	-493, 10327, 308	upstream, downstream, in gene	ActReg chr3 #12234	0	0	1
12235	4	52,648	55,108	2,460	3	13.714	15.649	17.636	34	35	39	1	1	1	ZNF595	651	in gene	ActReg chr4 #12235	1	1	1
12236	4	206,135	206,673	538	1	9.706	7.294	2.375	16	12	5	1	0	0				ActReg chr4 #12236	1	0	0
12237	4	330,775	331,147	372	1	6	9.25	10.583	9	14	14	1	1	1	ZNF141	-635	upstream	ActReg chr4 #12237	0	0	1
12238	4	331,703	332,067	364	1	4	10.333	12.75	6	13	20	1	1	1	ZNF141	289	in gene	ActReg chr4 #12238	0	0	1
12239	4	467,242	468,203	961	1	9.2	12.567	8.367	16	19	13	1	0	1	ZNF721	25,720	in gene	ActReg chr4 #12239	0	1	0
12240	4	492,672	493,365	693	2	11.046	11.546	8.409	25	19	13	1	2	2	ZNF721, PIGG	424, 29	in gene, in gene	ActReg chr4 #12240	1	1	0
12241	4	555,810	556,174	364	1	1.625	1	9.091	2	1	13	0	0	0				ActReg chr4 #12241	0	0	1
12242	4	575,282	575,933	651	1	6.95	10.95	3.5	10	18	6	0	0	0				ActReg chr4 #12242	0	1	0
12243	4	621,989	622,455	466	1	4.714	3.786	11.857	6	6	18	0	0	1	PDE6B	2,859	in gene	ActReg chr4 #12243	0	0	1
12244	4	622,809	623,363	554	1	3.833	4.333	11	5	6	15	0	0	1	PDE6B	3,723	in gene	ActReg chr4 #12244	0	0	1
12245	4	656,698	657,744	1,046	1	3	4.758	11.697	6	10	20	1	1	3	PDE6B, LOC100507653, ATP5I	37858, -7238, 10906	in gene, upstream, downstream	ActReg chr4 #12245	0	0	1
12246	4	659,346	659,695	349	1	1.364	4.636	11.364	3	9	15	0	0	3	PDE6B, LOC100507653, ATP5I	40157, -9537, 8607	in gene, upstream, downstream	ActReg chr4 #12246	0	0	1
12247	4	667,916	668,808	892	1	9.857	9.964	5.429	16	16	13	1	2	4	PDE6B, ATP5I, MYL5, MFSD7	48999, -235, -3349, 14611	downstream, upstream, upstream, downstream	ActReg chr4 #12247	0	1	0
12248	4	682,125	682,549	424	1	5.077	4.308	11.231	7	10	18	1	1	2	MYL5, MFSD7	10626, 636	downstream, in gene	ActReg chr4 #12248	0	0	1
12249	4	698,036	698,590	554	1	2.412	3.412	12.118	6	7	16	1	1	1	PCGF3	-1,260	upstream	ActReg chr4 #12249	0	0	1
12250	4	724,757	725,205	448	1	3.071	2.143	11.643	6	6	19	1	0	1	PCGF3	25,408	in gene	ActReg chr4 #12250	0	0	1
12251	4	774,872	775,709	837	2	8	11.039	9.923	14	18	13	1	1	2	LOC100129917, CPLX1	346, 44655	in gene, downstream	ActReg chr4 #12251	0	1	1
12252	4	775,893	776,226	333	1	8.909	8.364	12	11	12	16	1	1	2	LOC100129917, CPLX1	-423, 43886	upstream, downstream	ActReg chr4 #12252	0	0	1
12253	4	785,475	785,963	488	1	2.733	2.2	12.533	4	6	18	1	0	2	LOC100129917, CPLX1	-10083, 34226	upstream, in gene	ActReg chr4 #12253	0	0	1
12254	4	788,448	789,153	705	1	2.609	2.739	11.652	5	6	21	1	0	1	CPLX1	31,145	in gene	ActReg chr4 #12254	0	0	1
12255	4	808,276	808,734	458	1	3.857	3.5	10.429	5	6	17	0	0	1	CPLX1	11,440	in gene	ActReg chr4 #12255	0	0	1
12256	4	817,830	818,293	463	1	4.643	7.571	12.714	9	10	20	0	1	1	CPLX1	1,884	in gene	ActReg chr4 #12256	0	0	1
12257	4	866,099	866,710	611	1	3.474	6.947	12.895	7	12	18	1	0	1	GAK	59,770	in gene	ActReg chr4 #12257	0	0	1
12258	4	882,435	882,943	508	1	4.467	2.6	13.4	6	5	19	0	0	1	GAK	43,485	in gene	ActReg chr4 #12258	0	0	1
12259	4	925,533	926,263	730	1	9.609	12.957	6.435	16	19	11	1	2	2	GAK, TMEM175	276, -364	in gene, upstream	ActReg chr4 #12259	0	1	0
12260	4	958,554	959,384	830	1	4.269	5.077	13.192	10	8	18	0	0	2	TMEM175, DGKQ	32707, 8375	downstream, in gene	ActReg chr4 #12260	0	0	1
12261	4	976,268	976,890	622	1	5.211	2.421	11.632	8	4	14	0	1	3	DGKQ, SLC26A1, IDUA	-9235, 10645, -4206	upstream, in gene, upstream	ActReg chr4 #12261	0	0	1
12262	4	980,480	982,293	1,813	2	5.491	8.912	10.846	11	15	24	2	1	2	SLC26A1, IDUA	5838, 601	in gene, in gene	ActReg chr4 #12262	0	1	1
12263	4	982,705	983,691	986	1	5.452	5.129	10.387	7	9	14	1	1	2	SLC26A1, IDUA	4026, 2413	in gene, in gene	ActReg chr4 #12263	0	0	1
12264	4	984,366	985,296	930	1	4.448	7.207	15.069	7	11	22	2	1	2	SLC26A1, IDUA	2393, 4046	in gene, in gene	ActReg chr4 #12264	0	0	1
12265	4	991,634	992,293	659	1	4.619	6.095	10.143	8	12	14	1	1	2	SLC26A1, IDUA	-4739, 11178	upstream, in gene	ActReg chr4 #12265	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12266	4	1,010,786	1,011,307	521	1	2.875	5	12.438	4	9	19	0	0	1	FGFRL1	5,436	in gene	ActReg chr4 #12266	0	0	1
12267	4	1,015,920	1,016,366	446	1	4.143	3.786	12.786	5	6	18	0	0	1	FGFRL1	10,533	in gene	ActReg chr4 #12267	0	0	1
12268	4	1,020,650	1,021,235	585	1	4.765	6.889	11.278	9	10	15	1	0	1	FGFRL1	15,332	downstream	ActReg chr4 #12268	0	0	1
12269	4	1,022,329	1,023,418	1,089	1	4.706	5.324	11.265	10	9	16	1	0	1	FGFRL1	17,263	downstream	ActReg chr4 #12269	0	0	1
12270	4	1,027,474	1,028,225	751	1	2.792	5.083	11.25	6	10	17	1	0	1	FGFRL1	22,239	downstream	ActReg chr4 #12270	0	0	1
12271	4	1,029,053	1,029,744	691	1	9.045	11	13.864	17	16	22	1	0	1	FGFRL1	23,788	downstream	ActReg chr4 #12271	0	0	1
12272	4	1,030,680	1,031,369	689	1	5.636	5.455	10.954	8	8	16	0	0	1	FGFRL1	25,414	downstream	ActReg chr4 #12272	0	0	1
12273	4	1,037,083	1,037,945	862	2	14.593	14	7.037	30	27	9	0	0	0				ActReg chr4 #12273	1	1	0
12274	4	1,075,794	1,076,487	693	1	11.773	10.864	4.5	18	18	7	0	0	1	RNF212	31,442	in gene	ActReg chr4 #12274	1	0	0
12275	4	1,086,323	1,086,754	431	1	2.111	3.071	9.5	3	6	16	0	0	1	RNF212	21,044	in gene	ActReg chr4 #12275	0	0	1
12276	4	1,161,139	1,161,697	558	1	8.833	8.722	11.056	13	12	14	1	0	2	SPON2, LOC100130872-SPON2	5562, 41216	in gene, downstream	ActReg chr4 #12276	0	0	1
12277	4	1,164,417	1,164,991	574	1	5.125	3.812	12.471	7	6	19	1	1	2	SPON2, LOC100130872-SPON2	2276, 37930	in gene, downstream	ActReg chr4 #12277	0	0	1
12278	4	1,165,631	1,166,458	827	1	7.923	6.615	13	13	9	16	1	1	2	SPON2, LOC100130872-SPON2	936, 36590	in gene, in gene	ActReg chr4 #12278	0	0	1
12279	4	1,168,671	1,169,439	768	1	3.833	6.583	13.417	7	11	21	0	1	2	SPON2, LOC100130872-SPON2	-2075, 33579	upstream, in gene	ActReg chr4 #12279	0	0	1
12280	4	1,187,848	1,188,424	576	1	4.056	4.833	13.167	7	9	20	1	0	1	LOC100130872-SPON2	14,498	in gene	ActReg chr4 #12280	0	0	1
12281	4	1,198,734	1,199,143	409	1	2.923	3.769	12.077	5	6	17	0	1	3	LOC100130872-SPON2, LOC285463, CTBP1	3696, -4970, 43970	in gene, upstream, downstream	ActReg chr4 #12281	0	0	1
12282	4	1,199,723	1,200,098	375	1	3.091	3.667	12	5	6	17	0	1	3	LOC100130872-SPON2, LOC285463, CTBP1	2724, -3998, 42998	in gene, upstream, downstream	ActReg chr4 #12282	0	0	1
12283	4	1,201,731	1,202,126	395	1	3.667	3.083	12.167	5	4	19	0	2	3	LOC100130872-SPON2, LOC285463, CTBP1	706, -1980, 40980	in gene, upstream, downstream	ActReg chr4 #12283	0	0	1
12284	4	1,206,992	1,207,501	509	1	3.214	5.812	11.75	6	8	20	0	1	3	LOC100130872-SPON2, LOC285463, CTBP1	-4612, 3338, 35662	upstream, in gene, in gene	ActReg chr4 #12284	0	0	1
12285	4	1,208,046	1,208,724	678	1	3.333	4.571	13.714	4	9	21	0	1	3	LOC100130872-SPON2, LOC285463, CTBP1	-5751, 4477, 34523	upstream, in gene, in gene	ActReg chr4 #12285	0	0	1
12286	4	1,216,035	1,216,506	471	1	5.5	2.929	13.143	8	4	19	0	0	2	LOC285463, CTBP1	12362, 26638	downstream, in gene	ActReg chr4 #12286	0	0	1
12287	4	1,340,233	1,341,021	788	2	9.917	15.833	5.875	16	29	10	1	1	2	MAEA, KIAA1530	56955, -477	downstream, upstream	ActReg chr4 #12287	1	1	0
12288	4	1,368,802	1,369,373	571	1	2.529	3.118	11.294	4	6	14	0	0	1	KIAA1530	27,983	in gene	ActReg chr4 #12288	0	0	1
12289	4	1,372,333	1,373,313	980	1	2.767	4.393	11.645	5	7	15	0	0	1	KIAA1530	31,719	in gene	ActReg chr4 #12289	0	0	1
12290	4	1,374,042	1,374,594	552	1	3.389	4.778	12	6	9	14	0	0	1	KIAA1530	33,214	in gene	ActReg chr4 #12290	0	0	1
12291	4	1,395,222	1,395,983	761	1	4.208	3.75	13.208	8	7	20	0	0	2	CRIPAK, NKX1-1	10262, 4517	downstream, downstream	ActReg chr4 #12291	0	0	1
12292	4	1,403,421	1,405,819	2,398	2	20.507	27.493	5.699	91	119	11	1	1	1	NKX1-1	-4,501	upstream	ActReg chr4 #12292	1	1	0
12293	4	1,411,705	1,412,004	299	1	11.571	2	10	3	3	15	0	0	0				ActReg chr4 #12293	0	0	1
12294	4	1,505,179	1,505,836	657	1	2.524	4.048	10.238	4	6	15	1	0	0				ActReg chr4 #12294	0	0	1
12295	4	1,524,346	1,524,796	450	1	2.077	3.077	10.786	3	5	17	0	0	0				ActReg chr4 #12295	0	0	1
12296	4	1,539,385	1,539,912	527	1	2.6	2.308	13.294	5	4	22	0	0	0				ActReg chr4 #12296	0	0	1
12297	4	1,552,454	1,553,432	978	1	3.8	3.76	12.3	7	6	19	0	0	0				ActReg chr4 #12297	0	0	1
12298	4	1,554,203	1,554,769	566	1	4.867	1.615	11.389	8	3	17	1	0	0				ActReg chr4 #12298	0	0	1
12299	4	1,561,481	1,562,080	599	1	5.421	2.474	12.632	10	4	21	0	0	0				ActReg chr4 #12299	0	0	1
12300	4	1,562,185	1,562,676	491	1	7.067	7.2	12.8	10	9	19	0	0	0				ActReg chr4 #12300	0	0	1
12301	4	1,563,269	1,563,682	413	1	3.462	7.462	11.538	5	9	18	0	0	0				ActReg chr4 #12301	0	0	1
12302	4	1,565,764	1,566,300	536	1	1.25	3.25	13.562	2	6	23	0	0	1	LOC100507054	15,948	downstream	ActReg chr4 #12302	0	0	1
12303	4	1,602,262	1,602,822	560	1	3.5	5.278	11.389	5	7	15	0	0	0				ActReg chr4 #12303	0	0	1
12304	4	1,604,388	1,605,348	960	1	4.633	4.067	12.933	7	8	18	0	0	0				ActReg chr4 #12304	0	0	1
12305	4	1,605,909	1,606,516	607	1	4.579	7	12.474	11	10	17	0	0	0				ActReg chr4 #12305	0	0	1
12306	4	1,607,057	1,607,676	619	1	2.588	3.263	11.158	5	5	15	0	0	0				ActReg chr4 #12306	0	0	1
12307	4	1,612,148	1,612,575	427	1	2.182	3.077	13	4	4	18	0	0	0				ActReg chr4 #12307	0	0	1
12308	4	1,620,824	1,621,320	496	1	3.625	5	13.062	5	8	22	0	0	0				ActReg chr4 #12308	0	0	1
12309	4	1,624,568	1,625,332	764	1	3.542	3.909	12.625	7	7	18	1	0	0				ActReg chr4 #12309	0	0	1
12310	4	1,628,657	1,629,159	502	1	4.688	5.625	12.562	6	8	21	0	0	0				ActReg chr4 #12310	0	0	1
12311	4	1,630,908	1,631,271	363	1	8.417	6.75	11	20	9	16	0	0	0				ActReg chr4 #12311	0	0	1
12312	4	1,639,430	1,640,383	953	1	3.724	4.172	12.241	7	8	18	0	0	1	FAM53A	46,082	downstream	ActReg chr4 #12312	0	0	1
12313	4	1,713,927	1,715,034	1,107	2	12.706	13.823	6.083	20	19	9	1	1	3	SLBP, TMEM129, TACC3	-450, 8604, -8786	upstream, downstream, upstream	ActReg chr4 #12313	1	1	0
12314	4	1,716,012	1,716,983	971	2	17.567	18.1	4.103	50	39	6	0	2	3	SLBP, TMEM129, TACC3	-2467, 6587, -6769	upstream, downstream, upstream	ActReg chr4 #12314	1	1	0
12315	4	1,719,254	1,720,083	829	1	6.115	5.192	11.154	11	10	15	0	2	3	SLBP, TMEM129, TACC3	-5638, 3416, -3598	upstream, in gene, upstream	ActReg chr4 #12315	0	0	1
12316	4	1,747,710	1,748,460	750	1	8.375	7.875	11.833	15	15	17	0	0	1	TACC3	24,819	downstream	ActReg chr4 #12316	0	0	1
12317	4	1,753,981	1,754,481	500	1	3.75	4.5	11.5	7	7	15	0	0	1	TACC3	30,965	downstream	ActReg chr4 #12317	0	0	1
12318	4	1,763,285	1,763,738	453	1	2.556	4.231	10.571	4	6	15	0	0	0				ActReg chr4 #12318	0	0	1
12319	4	1,764,225	1,764,925	700	1	5.381	3.476	12	9	5	17	1	0	0				ActReg chr4 #12319	0	0	1
12320	4	1,778,389	1,778,967	578	1	6.167	8.278	11.5	8	14	16	0	0	0				ActReg chr4 #12320	0	0	1
12321	4	1,779,910	1,780,637	727	1	4.545	6.364	13.773	7	10	22	0	0	0				ActReg chr4 #12321	0	0	1
12322	4	1,788,281	1,789,108	827	1	3.64	1.524	11.692	9	3	20	0	1	1	FGFR3	-6,345	upstream	ActReg chr4 #12322	0	0	1
12323	4	1,794,212	1,794,708	496	1	5.8	5.4	12.533	9	8	16	1	1	1	FGFR3	-579	upstream	ActReg chr4 #12323	0	0	1
12324	4	1,797,397	1,797,821	424	1	3.538	3	10.923	8	7	13	0	1	1	FGFR3	2,570	in gene	ActReg chr4 #12324	0	0	1
12325	4	1,803,870	1,804,640	770	1	1.92	3.8	11.16	3	7	16	1	0	2	FGFR3, LETM1	9216, 53719	in gene, downstream	ActReg chr4 #12325	0	0	1
12326	4	1,810,404	1,811,379	975	1	2.867	4.167	10.367	5	7	16	0	0	2	FGFR3, LETM1	15852, 47083	downstream, downstream	ActReg chr4 #12326	0	0	1
12327	4	1,812,429	1,812,940	511	1	3.5	3.25	12.062	5	5	18	0	0	2	FGFR3, LETM1	17645, 45290	downstream, downstream	ActReg chr4 #12327	0	0	1
12328	4	1,844,646	1,845,209	563	1	3.824	3.765	10.588	6	7	15	0	0	1	LETM1	13,047	in gene	ActReg chr4 #12328	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12329	4	1,857,020	1,857,473	453	1	6	7.267	10.6	8	13	18	1	1	1	LETM1	728	in gene	ActReg chr4 #12329	0	0	1
12330	4	1,857,671	1,858,603	932	2	12.862	13.966	10.35	24	29	17	1	1	1	LETM1	-163	upstream	ActReg chr4 #12330	1	1	0
12331	4	1,871,850	1,872,401	551	1	6.353	7.353	12.882	12	12	20	1	1	1	WHSC1	-998	upstream	ActReg chr4 #12331	0	0	1
12332	4	1,985,361	1,986,249	888	1	4.357	3.929	10.821	8	6	15	0	1	4	WHSC1, SCARNA22, WHSC2, MIR943	112682, 9442, 25154, 2399	downstream, downstream, in gene, downstream	ActReg chr4 #12332	0	0	1
12333	4	1,994,148	1,994,608	460	1	2.615	3.929	12.429	5	8	17	1	1	2	WHSC2, MIR943	16581, -6174	in gene, upstream	ActReg chr4 #12333	0	0	1
12334	4	2,010,277	2,011,264	987	2	9.548	11.258	8.613	13	21	19	1	1	1	WHSC2	189	in gene	ActReg chr4 #12334	0	1	1
12335	4	2,043,048	2,043,726	678	1	8.857	9.048	14.476	14	14	22	1	1	1	C4orf48	-333	upstream	ActReg chr4 #12335	0	0	1
12336	4	2,063,705	2,064,257	552	1	3.667	4.111	10.833	7	7	15	0	1	2	NAT8L, POLN	2742, 166977	in gene, downstream	ActReg chr4 #12336	0	0	1
12337	4	2,065,261	2,065,882	621	1	3.263	4.895	12.895	5	9	20	1	0	2	NAT8L, POLN	4332, 165387	in gene, downstream	ActReg chr4 #12337	0	0	1
12338	4	2,081,898	2,082,174	276	1	2.375	1.875	13.125	3	3	15	0	0	1	POLN	148,922	in gene	ActReg chr4 #12338	0	0	1
12339	4	2,128,207	2,128,856	649	1	2.944	4.263	11.85	5	8	18	0	0	1	POLN	102,427	in gene	ActReg chr4 #12339	0	0	1
12340	4	2,243,407	2,244,178	771	2	7.25	12.875	6.875	13	21	16	1	1	2	HAUS3, MXD4	68, 19947	in gene, downstream	ActReg chr4 #12340	0	1	1
12341	4	2,248,854	2,249,349	495	1	4	2.75	12.625	7	5	20	0	1	2	HAUS3, MXD4	-5241, 14638	upstream, downstream	ActReg chr4 #12341	0	0	1
12342	4	2,252,094	2,252,534	440	1	3.357	3.714	9.571	5	5	13	0	0	2	HAUS3, MXD4	-8454, 11425	upstream, in gene	ActReg chr4 #12342	0	0	1
12343	4	2,257,748	2,258,162	414	1	1.364	4.538	11.615	2	7	15	0	0	1	MXD4	5,784	in gene	ActReg chr4 #12343	0	0	1
12344	4	2,260,712	2,261,177	465	1	4.071	4.571	11.643	6	8	19	0	0	1	MXD4	2,795	in gene	ActReg chr4 #12344	0	0	1
12345	4	2,261,299	2,261,804	505	1	4.688	7.812	12.438	6	9	17	0	1	2	MXD4, ZFYVE28	2188, 158819	in gene, downstream	ActReg chr4 #12345	0	0	1
12346	4	2,291,676	2,292,137	461	1	2.4	3.385	11.2	4	5	15	0	0	1	ZFYVE28	128,464	in gene	ActReg chr4 #12346	0	0	1
12347	4	2,293,311	2,293,928	617	1	2.95	3.895	13.2	5	6	18	0	0	1	ZFYVE28	126,751	in gene	ActReg chr4 #12347	0	0	1
12348	4	2,298,300	2,298,716	416	1	2.231	4.769	11.385	4	6	18	0	0	1	ZFYVE28	121,862	in gene	ActReg chr4 #12348	0	0	1
12349	4	2,414,978	2,415,616	638	1	5.895	9.3	4.65	13	16	7	0	1	2	ZFYVE28, LOC402160	5073, -5404	in gene, upstream	ActReg chr4 #12349	0	1	0
12350	4	2,460,596	2,461,187	591	1	3.474	2.947	10.368	8	6	16	0	0	2	LOC402160, RNF4	40190, -9904	in gene, upstream	ActReg chr4 #12350	0	0	1
12351	4	2,831,579	2,832,122	543	1	2.438	5.118	11.235	4	8	14	0	0	1	SH3BP2	37,100	in gene	ActReg chr4 #12351	0	0	1
12352	4	2,833,428	2,833,928	500	1	4.438	2.812	13.5	7	5	21	0	0	1	SH3BP2	38,928	in gene	ActReg chr4 #12352	0	0	1
12353	4	2,845,125	2,845,618	493	1	12.267	9.867	5.5	20	14	13	1	1	2	SH3BP2, ADD1	50621, -213	downstream, upstream	ActReg chr4 #12353	1	0	0
12354	4	2,932,509	2,933,460	951	1	4.9	6.467	12.5	7	12	21	1	1	4	ADD1, MFSD10, C4orf10, NOP14	87400, 3602, -4289, 32134	downstream, in gene, upstream, downstream	ActReg chr4 #12354	0	0	1
12355	4	2,935,015	2,935,740	725	1	7.727	11.409	12.318	11	16	16	1	2	4	ADD1, MFSD10, C4orf10, NOP14	89793, 1209, -1896, 29741	downstream, in gene, upstream, downstream	ActReg chr4 #12355	0	0	1
12356	4	2,936,463	2,937,064	601	2	8.316	13.421	10.368	15	21	15	1	2	4	ADD1, MFSD10, C4orf10, NOP14	91179, -177, -510, 28355	downstream, upstream, upstream, downstream	ActReg chr4 #12356	0	1	1
12357	4	2,964,411	2,965,591	1,180	2	10.324	13.135	8.486	15	23	18	1	2	2	NOP14, GRK4	117, -342	in gene, upstream	ActReg chr4 #12357	0	1	1
12358	4	3,249,400	3,250,249	849	1	2.826	6.296	11.852	5	10	16	0	1	2	HTT, C4orf44	173416, -943	downstream, upstream	ActReg chr4 #12358	0	0	1
12359	4	3,442,686	3,443,211	525	1	4.059	4.176	11.588	6	7	15	0	1	2	RGS12, HGFAC	127074, -778	downstream, upstream	ActReg chr4 #12359	0	0	1
12360	4	3,444,634	3,445,232	598	1	5.368	5.632	11.053	11	8	13	0	1	2	RGS12, HGFAC	129059, 1207	downstream, in gene	ActReg chr4 #12360	0	0	1
12361	4	3,445,245	3,445,782	537	1	9.882	6.588	14.412	14	11	19	0	1	2	RGS12, HGFAC	129639, 1787	downstream, in gene	ActReg chr4 #12361	0	0	1
12362	4	3,447,467	3,448,641	1,174	1	3.054	3.189	12.162	7	7	18	0	0	2	RGS12, HGFAC	132180, 4328	downstream, in gene	ActReg chr4 #12362	0	0	1
12363	4	3,448,660	3,449,152	492	1	5.625	4.312	10.875	8	6	17	0	0	2	RGS12, HGFAC	133032, 5180	downstream, in gene	ActReg chr4 #12363	0	0	1
12364	4	3,449,350	3,449,738	388	1	3.583	4.5	11.417	5	6	17	1	0	2	RGS12, HGFAC	133670, 5818	downstream, in gene	ActReg chr4 #12364	0	0	1
12365	4	3,450,918	3,451,445	527	1	5.562	4.688	12.188	10	8	17	0	0	2	RGS12, HGFAC	135307, 7455	downstream, in gene	ActReg chr4 #12365	0	0	1
12366	4	3,463,234	3,463,719	485	1	7.2	4.071	11.467	10	6	17	0	1	1	DOK7	-1,557	upstream	ActReg chr4 #12366	0	0	1
12367	4	3,465,510	3,466,170	660	1	3.35	2.154	13.1	7	4	18	1	1	1	DOK7	807	in gene	ActReg chr4 #12367	0	0	1
12368	4	3,478,410	3,479,337	927	1	2.828	3.724	11.621	4	6	15	0	0	1	DOK7	13,840	in gene	ActReg chr4 #12368	0	0	1
12369	4	3,486,776	3,487,445	669	1	4.619	3.2	11.571	9	6	16	0	0	1	DOK7	22,077	in gene	ActReg chr4 #12369	0	0	1
12370	4	3,487,747	3,488,335	588	1	3.059	4.222	13.611	5	8	19	0	0	1	DOK7	23,008	in gene	ActReg chr4 #12370	0	0	1
12371	4	3,503,845	3,504,409	564	1	2.467	3.706	12.118	4	7	17	0	0	2	DOK7, LRPAP1	39094, 30097	downstream, downstream	ActReg chr4 #12371	0	0	1
12372	4	3,516,204	3,516,648	444	1	5	5.714	11.286	7	6	14	1	0	1	LRPAP1	17,798	in gene	ActReg chr4 #12372	0	0	1
12373	4	3,516,674	3,517,215	541	1	7.312	6.438	12.312	11	10	16	1	0	1	LRPAP1	17,280	in gene	ActReg chr4 #12373	0	0	1
12374	4	3,518,713	3,519,841	1,128	1	3.083	4.806	11.639	5	8	16	1	0	1	LRPAP1	14,947	in gene	ActReg chr4 #12374	0	0	1
12375	4	3,582,964	3,583,609	645	1	6.3	7.65	14.95	8	11	27	0	0	0				ActReg chr4 #12375	0	0	1
12376	4	3,588,964	3,590,151	1,187	1	5.27	6.432	11.568	10	11	19	0	0	0				ActReg chr4 #12376	0	0	1
12377	4	3,598,498	3,599,131	633	1	4.158	3.579	11.474	8	6	15	0	0	0				ActReg chr4 #12377	0	0	1
12378	4	3,606,191	3,607,389	1,198	1	4.162	6.946	15.378	7	16	26	0	0	0				ActReg chr4 #12378	0	0	1
12379	4	3,633,505	3,634,315	810	1	4.24	4.12	11.72	7	7	15	0	0	1	LOC100129786	10,398	downstream	ActReg chr4 #12379	0	0	1
12380	4	3,665,526	3,666,095	569	1	1.556	2.944	11.444	3	5	17	0	0	1	LOC100133461	13,772	downstream	ActReg chr4 #12380	0	0	1
12381	4	3,691,742	3,692,229	487	1	1.583	2.357	12	3	3	17	0	0	0				ActReg chr4 #12381	0	0	1
12382	4	3,730,335	3,730,825	490	1	3.938	3.188	11.125	7	5	17	0	0	0				ActReg chr4 #12382	0	0	1
12383	4	3,745,797	3,746,399	602	1	4.857	4.833	11.556	7	8	15	0	0	0				ActReg chr4 #12383	0	0	1
12384	4	3,754,702	3,755,306	604	1	1.692	3.364	9.842	3	6	14	0	0	1	LOC100507150	10,113	downstream	ActReg chr4 #12384	0	0	1
12385	4	3,793,381	3,794,281	900	1	12.679	15.5	5.464	26	29	8	0	0	0				ActReg chr4 #12385	0	1	0
12386	4	3,799,719	3,800,139	420	1	1.917	3.167	12.923	3	5	19	0	0	0				ActReg chr4 #12386	0	0	1
12387	4	3,823,270	3,823,670	400	1	5.167	2.5	12.5	6	4	19	0	0	0				ActReg chr4 #12387	0	0	1
12388	4	3,849,994	3,850,576	582	1	2.667	2.8	10.778	4	5	14	0	0	0				ActReg chr4 #12388	0	0	1
12389	4	3,956,289	3,956,990	701	1	11	5.81	3.5	18	13	7	1	0	0				ActReg chr4 #12389	1	0	0
12390	4	4,117,059	4,117,438	379	1	2.091	3.545	10.909	3	6	14	0	0	0				ActReg chr4 #12390	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12391	4	4,249,337	4,250,399	1,062	2	9.545	11.97	6.333	17	21	13	1	2	2	TMEM128, LOC100507225	66, 2387	in gene, downstream	ActReg chr4 #12391	1	1	0
12392	4	4,387,739	4,388,285	546	1	4.235	2.8	13.353	6	4	24	1	1	1	D4S234E	29	in gene	ActReg chr4 #12392	0	0	1
12393	4	4,543,379	4,544,204	825	3	15.654	16.308	14.577	38	36	32	1	2	2	STX18, LOC100507266	-16, -67	upstream, upstream	ActReg chr4 #12393	1	1	1
12394	4	4,992,509	4,993,711	1,202	2	10.105	11.763	7.684	18	25	11	0	0	0				ActReg chr4 #12394	1	1	0
12395	4	5,039,583	5,040,161	578	1	10.316	8.158	2.684	18	13	7	0	0	0				ActReg chr4 #12395	1	0	0
12396	4	5,052,787	5,053,341	554	1	7.941	8.059	12.588	12	10	21	1	1	1	STK32B	-463	upstream	ActReg chr4 #12396	0	0	1
12397	4	5,207,834	5,208,720	886	1	12.321	8.607	2.556	19	15	4	0	0	1	STK32B	154,750	in gene	ActReg chr4 #12397	1	0	0
12398	4	5,221,687	5,222,201	514	1	9.938	13	2.929	17	25	5	0	0	1	STK32B	168,417	in gene	ActReg chr4 #12398	0	1	0
12399	4	5,339,992	5,340,608	616	2	9.2	10	2.316	16	15	4	0	0	1	STK32B	286,773	in gene	ActReg chr4 #12399	1	1	0
12400	4	5,367,264	5,367,967	703	1	9.227	12.773	2.8	18	21	5	0	0	1	STK32B	314,088	in gene	ActReg chr4 #12400	0	1	0
12401	4	5,713,865	5,714,983	1,118	1	7	11.029	3.229	11	16	5	0	2	2	EVC2, EVC	-3149, 1500	upstream, in gene	ActReg chr4 #12401	0	1	0
12402	4	5,882,559	5,883,606	1,047	1	6.182	13.97	1.852	13	32	5	0	0	2	CRMP1, LOC100507292	11703, 8876	in gene, in gene	ActReg chr4 #12402	0	1	0
12403	4	5,889,313	5,889,749	436	1	5.692	3.769	11.385	8	6	16	1	1	2	CRMP1, LOC100507292	5254, 2427	in gene, in gene	ActReg chr4 #12403	0	0	1
12404	4	6,226,834	6,227,693	859	2	12.444	9.222	4.333	28	15	6	0	0	1	LOC285484	24,803	in gene	ActReg chr4 #12404	1	1	0
12405	4	6,247,079	6,247,783	704	1	1.955	3.727	11.818	4	7	16	1	0	0				ActReg chr4 #12405	0	0	1
12406	4	6,279,343	6,279,921	578	1	2.267	3.188	12.389	4	5	19	0	0	1	WFS1	8,055	in gene	ActReg chr4 #12406	0	0	1
12407	4	6,340,204	6,340,576	372	1	5.417	4.25	10.667	8	6	16	0	0	1	PPP2R2C	133,936	in gene	ActReg chr4 #12407	0	0	1
12408	4	6,345,518	6,346,142	624	1	12.947	9.684	2.611	22	16	4	0	0	1	PPP2R2C	128,496	in gene	ActReg chr4 #12408	1	0	0
12409	4	6,364,025	6,365,166	1,141	2	12.611	17.889	4.471	32	48	10	0	0	1	PPP2R2C	109,731	in gene	ActReg chr4 #12409	1	1	0
12410	4	6,422,637	6,423,176	539	1	3.059	4.647	12.177	6	8	15	0	0	1	PPP2R2C	51,420	in gene	ActReg chr4 #12410	0	0	1
12411	4	6,479,527	6,480,146	619	1	7.211	9.842	6.579	13	15	9	0	1	1	PPP2R2C	-5,510	upstream	ActReg chr4 #12411	0	1	0
12412	4	6,576,459	6,577,418	959	2	12.233	7.267	8.133	19	10	14	1	1	1	MAN2B2	36	in gene	ActReg chr4 #12412	1	0	1
12413	4	6,641,972	6,642,338	366	1	6	7.75	11.417	10	10	17	1	1	1	MRFAP1	-290	upstream	ActReg chr4 #12413	0	0	1
12414	4	6,710,810	6,711,445	635	1	7.9	11.15	4.65	11	21	8	1	2	2	MRFAP1L1, CNO	479, -6715	in gene, upstream	ActReg chr4 #12414	0	1	0
12415	4	6,717,512	6,718,640	1,128	3	12.829	11.771	9.333	21	22	23	1	2	2	MRFAP1L1, CNO	-6470, 234	upstream, in gene	ActReg chr4 #12415	1	1	1
12416	4	6,728,560	6,729,344	784	1	3.88	11.48	6.792	6	18	14	1	0	1	CNO	11,110	downstream	ActReg chr4 #12416	0	1	0
12417	4	6,784,817	6,785,311	494	1	6.467	10.133	12.533	9	13	22	1	1	1	KIAA0232	605	in gene	ActReg chr4 #12417	0	0	1
12418	4	6,910,764	6,911,493	729	2	11.609	14.565	4.143	23	33	7	1	1	1	TBC1D14	-43	upstream	ActReg chr4 #12418	1	1	0
12419	4	6,917,831	6,918,971	1,140	2	12.914	13.429	2.735	19	28	6	0	0	1	TBC1D14	7,230	in gene	ActReg chr4 #12419	1	1	0
12420	4	6,918,975	6,919,449	474	1	8.267	4.667	11.8	11	6	19	0	0	1	TBC1D14	8,041	in gene	ActReg chr4 #12420	0	0	1
12421	4	6,988,532	6,989,544	1,012	2	16.125	12.719	4.793	27	20	12	1	0	1	TBC1D14	77,867	in gene	ActReg chr4 #12421	1	1	0
12422	4	7,069,062	7,069,978	916	1	10.357	12.143	9.679	21	19	19	1	1	2	TADA2B, GRPEL1	24364, 280	downstream, in gene	ActReg chr4 #12422	0	1	0
12423	4	7,200,386	7,201,009	623	1	3.421	2	11.632	5	5	18	0	0	1	SORCS2	6,323	in gene	ActReg chr4 #12423	0	0	1
12424	4	7,207,926	7,208,996	1,070	2	10.323	10	5.25	17	14	10	0	0	1	SORCS2	14,087	in gene	ActReg chr4 #12424	1	1	0
12425	4	7,296,973	7,297,894	921	2	11.034	6.414	9.586	20	10	20	0	0	1	SORCS2	103,059	in gene	ActReg chr4 #12425	1	0	1
12426	4	7,435,392	7,435,869	477	1	2.786	5.667	12.6	4	9	20	0	1	2	SORCS2, PSAPL1	241256, 1070	in gene, in gene	ActReg chr4 #12426	0	0	1
12427	4	7,482,684	7,483,058	374	1	4.2	2.75	12.083	8	6	15	0	0	1	SORCS2	288,497	in gene	ActReg chr4 #12427	0	0	1
12428	4	7,547,822	7,548,277	455	1	4.643	5.429	11.071	9	8	17	0	0	1	SORCS2	353,675	in gene	ActReg chr4 #12428	0	0	1
12429	4	7,651,098	7,652,058	960	1	12.433	14.5	2.536	19	27	10	0	0	1	SORCS2	457,204	in gene	ActReg chr4 #12429	0	1	0
12430	4	7,738,123	7,739,561	1,438	3	10.378	18.533	8.711	40	56	17	0	0	1	SORCS2	544,468	in gene	ActReg chr4 #12430	1	1	1
12431	4	7,940,532	7,941,648	1,116	2	12.286	15.486	6.958	22	24	13	1	1	1	AFAP1	563	in gene	ActReg chr4 #12431	1	1	0
12432	4	7,957,821	7,958,709	888	2	11.464	12.464	3.143	20	21	5	0	0	1	ABLIM2	202,294	downstream	ActReg chr4 #12432	1	1	0
12433	4	8,025,693	8,026,475	782	1	4	5.458	12.68	8	9	21	0	0	1	ABLIM2	134,475	in gene	ActReg chr4 #12433	0	0	1
12434	4	8,047,383	8,047,846	463	1	2.8	3.267	12.067	4	5	15	0	0	1	ABLIM2	112,945	in gene	ActReg chr4 #12434	0	0	1
12435	4	8,048,482	8,048,931	449	1	4.071	2.571	11.571	9	4	19	0	0	1	ABLIM2	111,853	in gene	ActReg chr4 #12435	0	0	1
12436	4	8,153,905	8,154,326	421	1	2.923	2.1	11.769	6	3	15	1	0	1	ABLIM2	6,444	in gene	ActReg chr4 #12436	0	0	1
12437	4	8,159,584	8,160,350	766	1	5.208	5.708	11.042	8	16	17	1	1	1	ABLIM2	592	in gene	ActReg chr4 #12437	0	0	1
12438	4	8,160,713	8,161,261	548	1	12.765	12.059	12.706	18	15	20	1	1	1	ABLIM2	-428	upstream	ActReg chr4 #12438	0	0	1
12439	4	8,190,432	8,190,923	491	1	5.812	5.562	12.438	10	9	20	0	0	0				ActReg chr4 #12439	0	0	1
12440	4	8,203,203	8,203,730	527	1	5.812	5.375	11.625	8	9	15	0	1	1	SH3TC1	2,406	in gene	ActReg chr4 #12440	0	0	1
12441	4	8,224,501	8,225,102	601	1	5.895	4.158	13.421	10	7	22	0	0	1	SH3TC1	23,741	in gene	ActReg chr4 #12441	0	0	1
12442	4	8,248,721	8,249,419	698	1	3.545	3.5	12.409	6	5	19	0	0	1	SH3TC1	48,010	downstream	ActReg chr4 #12442	0	0	1
12443	4	8,268,755	8,269,251	496	1	3.562	3.875	10.438	7	6	15	0	1	1	HTRA3	-2,489	upstream	ActReg chr4 #12443	0	0	1
12444	4	8,429,756	8,430,637	881	2	11.25	7.5	10.464	20	17	17	1	0	1	ACOX3	12,256	in gene	ActReg chr4 #12444	1	0	1
12445	4	8,442,089	8,442,964	875	2	10.037	10.556	7.704	16	16	15	1	2	2	ACOX3, C4orf23	-74, -6	upstream, upstream	ActReg chr4 #12445	1	1	0
12446	4	8,519,470	8,519,871	401	1	4.083	5	11.583	6	7	15	0	0	0				ActReg chr4 #12446	0	0	1
12447	4	8,540,326	8,541,075	749	1	9.478	12.217	5.043	18	19	7	0	0	0				ActReg chr4 #12447	0	1	0
12448	4	8,582,152	8,583,134	982	1	6.8	10.367	13.833	15	13	23	1	1	1	GPR78	352	in gene	ActReg chr4 #12448	0	0	1
12449	4	8,609,268	8,609,771	503	1	3.062	5.312	11.312	6	7	16	0	0	1	CPZ	15,084	in gene	ActReg chr4 #12449	0	0	1
12450	4	8,676,910	8,678,055	1,145	2	10.833	14.389	3.833	24	33	6	0	0	0				ActReg chr4 #12450	1	1	0
12451	4	8,684,281	8,684,822	541	1	3.471	2.188	14	5	4	24	0	0	0				ActReg chr4 #12451	0	0	1
12452	4	8,866,100	8,866,533	433	1	1.714	5.857	10.714	3	7	16	0	0	1	HMX1	7,227	downstream	ActReg chr4 #12452	0	0	1
12453	4	9,145,145	9,145,510	365	1	3	2.778	11.167	5	4	15	0	0	0				ActReg chr4 #12453	0	0	1
12454	4	9,783,215	9,783,890	675	1	1.647	2.455	12.524	3	4	18	1	1	1	DRD5	294	in gene	ActReg chr4 #12454	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12455	4	10,084,217	10,084,860	643	1	1.85	3.65	12.6	4	6	17	0	1	2	WDR1, MIR3138	34035, -4222	in gene, upstream	ActReg chr4 #12455	0	0	1
12456	4	10,462,655	10,463,007	352	1	4.545	8.727	9.636	6	11	15	1	1	1	ZNF518B	-3,799	upstream	ActReg chr4 #12456	0	0	1
12457	4	11,166,626	11,167,028	402	1	5.917	10.5	1	8	16	1	0	0	0				ActReg chr4 #12457	0	1	0
12458	4	11,368,883	11,369,603	720	2	10.391	11.174	1.706	19	17	3	0	2	2	MIR572, LOC643446	-1208, -1292	upstream, upstream	ActReg chr4 #12458	1	1	0
12459	4	11,545,201	11,545,795	594	1	9.316	9.895	1.769	16	18	2	0	0	0				ActReg chr4 #12459	0	1	0
12460	4	13,300,500	13,300,796	296	1	1.875	4.571	10.333	5	8	14	0	0	0				ActReg chr4 #12460	0	0	1
12461	4	13,485,821	13,486,372	551	1	11.278	11.556	10.167	19	21	13	1	1	1	RAB28	-107	upstream	ActReg chr4 #12461	0	1	0
12462	4	13,629,138	13,629,763	625	2	12.15	9.45	7.85	22	13	15	1	1	1	SOD1L	-122	upstream	ActReg chr4 #12462	1	0	1
12463	4	13,641,684	13,642,367	683	2	12.238	10.667	2.556	23	24	5	0	0	0				ActReg chr4 #12463	1	1	0
12464	4	13,655,825	13,656,485	660	1	7.714	12.524	4.722	12	22	10	0	0	0				ActReg chr4 #12464	0	1	0
12465	4	13,703,368	13,703,863	495	1	8.133	11	2.2	13	17	3	0	0	0				ActReg chr4 #12465	0	1	0
12466	4	13,908,392	13,909,531	1,139	2	14.061	17.171	2.522	43	44	6	0	0	0				ActReg chr4 #12466	1	1	0
12467	4	13,922,349	13,923,119	770	2	12.5	12.833	3.958	23	28	8	0	0	0				ActReg chr4 #12467	1	1	0
12468	4	14,197,585	14,198,319	734	2	14.217	12.913	1	28	29	1	0	0	0				ActReg chr4 #12468	1	1	0
12469	4	14,857,981	14,858,560	579	1	9.368	11.21	1	18	17	1	0	0	0				ActReg chr4 #12469	0	1	0
12470	4	15,003,260	15,005,031	1,771	2	9.5	11.143	6.727	17	21	12	1	2	2	LOC441009, CPEB2	-181, -153	upstream, upstream	ActReg chr4 #12470	1	1	0
12471	4	15,563,697	15,564,374	677	1	11.381	12.857	2.571	17	24	5	0	0	1	CC2D2A	92,546	in gene	ActReg chr4 #12471	0	1	0
12472	4	15,682,767	15,683,896	1,129	2	9.171	13.257	9.2	14	19	22	1	1	1	LOC285550	-21	upstream	ActReg chr4 #12472	0	1	1
12473	4	15,696,711	15,697,699	988	2	12.129	10.613	2.667	19	20	4	0	1	2	LOC285550, BST1	13853, -7368	downstream, upstream	ActReg chr4 #12473	1	1	0
12474	4	15,788,357	15,788,951	594	1	4.444	4.444	12.278	8	8	16	0	0	1	CD38	8,723	in gene	ActReg chr4 #12474	0	0	1
12475	4	15,922,714	15,923,559	845	2	12.518	10	3.2	23	21	6	0	0	0				ActReg chr4 #12475	1	1	0
12476	4	16,142,441	16,143,154	713	1	9.227	10.773	2.75	19	16	4	0	0	0				ActReg chr4 #12476	0	1	0
12477	4	16,574,772	16,575,347	575	1	8.778	4.278	1.273	18	8	3	0	0	1	LDB2	325,365	in gene	ActReg chr4 #12477	1	0	0
12478	4	17,513,114	17,514,285	1,171	3	11.46	15.568	6.212	24	36	19	1	2	2	QDPR, CLRN2	158, -3089	in gene, upstream	ActReg chr4 #12478	1	1	1
12479	4	17,578,396	17,578,920	524	1	8.529	9.294	12.941	12	16	23	1	1	1	LAP3	-269	upstream	ActReg chr4 #12479	0	0	1
12480	4	17,615,911	17,616,645	734	1	8.652	11.348	3.739	13	17	7	1	1	2	LAP3, MED28	37351, 5	downstream, in gene	ActReg chr4 #12480	0	1	0
12481	4	17,688,982	17,690,121	1,139	2	10.75	13.611	3.758	21	27	11	0	0	1	FAM184B	93,584	in gene	ActReg chr4 #12481	1	1	0
12482	4	17,692,245	17,693,071	826	2	12.423	14.5	3.962	24	29	7	0	0	1	FAM184B	90,477	in gene	ActReg chr4 #12482	1	1	0
12483	4	17,811,758	17,813,080	1,322	2	11.439	11.146	7.667	18	18	13	1	2	2	DCAF16, NCAPG	-38, -106	upstream, upstream	ActReg chr4 #12483	1	1	0
12484	4	18,023,331	18,024,182	851	2	12	11.231	5.154	17	22	10	1	1	1	LCORL	-273	upstream	ActReg chr4 #12484	1	1	0
12485	4	20,253,358	20,254,174	816	1	7.68	10.32	7.64	12	15	15	1	1	1	SLIT2	-1,469	upstream	ActReg chr4 #12485	0	1	0
12486	4	20,254,530	20,255,068	538	1	6.25	9.688	14	8	14	24	1	1	1	SLIT2	-436	upstream	ActReg chr4 #12486	0	0	1
12487	4	20,475,634	20,476,290	656	2	8.476	9.19	1	13	18	1	0	0	1	SLIT2	220,727	in gene	ActReg chr4 #12487	1	1	0
12488	4	20,880,266	20,881,098	832	2	16.423	13.846	3.375	38	33	4	0	0	1	KCNIP4	1,069,692	in gene	ActReg chr4 #12488	1	1	0
12489	4	21,014,693	21,015,506	813	1	8.8	11.12	1.706	15	16	3	0	0	1	KCNIP4	935,275	in gene	ActReg chr4 #12489	0	1	0
12490	4	21,889,946	21,890,560	614	1	6.05	11.3	1.222	11	16	2	0	0	1	KCNIP4	60,121	in gene	ActReg chr4 #12490	0	1	0
12491	4	21,901,967	21,902,403	436	1	8.786	3.286	1	13	5	1	0	0	1	KCNIP4	48,189	in gene	ActReg chr4 #12491	1	0	0
12492	4	22,171,901	22,172,408	507	1	10.625	7.786	1.4	16	11	2	0	0	0				ActReg chr4 #12492	1	0	0
12493	4	22,180,703	22,181,122	419	2	9.786	9.714	1.4	15	13	2	0	0	0				ActReg chr4 #12493	1	1	0
12494	4	23,325,749	23,326,567	818	1	6.692	12.577	3.923	12	20	5	0	0	0				ActReg chr4 #12494	0	1	0
12495	4	23,708,801	23,709,434	633	1	8.316	11	2.278	15	18	4	0	0	0				ActReg chr4 #12495	0	1	0
12496	4	23,729,989	23,730,619	630	2	7.526	12.368	2.833	15	22	6	0	0	0				ActReg chr4 #12496	1	1	0
12497	4	23,857,814	23,858,533	719	1	12.13	10.435	3.261	19	15	6	0	0	1	PPARGC1A	33,527	in gene	ActReg chr4 #12497	1	0	0
12498	4	23,946,966	23,947,688	722	1	9.957	5.348	0	14	9	0	0	0	0				ActReg chr4 #12498	1	0	0
12499	4	24,474,579	24,475,419	840	1	9.231	12.077	3.731	15	21	6	1	0	1	LOC729175	9,503	in gene	ActReg chr4 #12499	0	1	0
12500	4	24,585,752	24,586,513	761	1	8.167	12.333	7.875	13	18	15	1	1	1	DHX15	52	in gene	ActReg chr4 #12500	0	1	0
12501	4	24,770,656	24,772,272	1,616	1	9.196	11.902	3.562	16	20	9	0	0	0				ActReg chr4 #12501	0	1	0
12502	4	25,161,669	25,162,355	686	2	8.857	12.809	9.238	15	18	15	1	2	2	SEPSECS, LOC285540	192, -282	in gene, upstream	ActReg chr4 #12502	0	1	1
12503	4	25,174,839	25,175,672	833	1	7.269	13.769	1.733	18	25	3	0	0	1	LOC285540	12,961	in gene	ActReg chr4 #12503	0	1	0
12504	4	25,235,592	25,236,365	773	1	5.458	10.958	3.409	8	15	7	1	1	1	PI4K2B	325	in gene	ActReg chr4 #12504	0	1	0
12505	4	25,240,957	25,241,424	467	1	5.067	4.6	12.667	9	7	16	0	0	1	PI4K2B	5,537	in gene	ActReg chr4 #12505	0	0	1
12506	4	25,313,921	25,314,856	935	2	24.828	30.862	2.4	71	88	5	1	1	1	ZCCHC4	-8	upstream	ActReg chr4 #12506	1	1	0
12507	4	25,378,858	25,379,477	619	1	9.053	10.842	6.222	14	16	11	1	1	2	ZCCHC4, ANAPC4	64771, 319	downstream, in gene	ActReg chr4 #12507	0	1	0
12508	4	25,910,044	25,910,787	743	2	12.375	11.292	3.864	18	18	8	0	2	2	LOC100506024, C4orf52	-1953, -5399	upstream, upstream	ActReg chr4 #12508	1	1	0
12509	4	25,915,275	25,915,877	602	1	2.947	7.474	11.526	7	15	21	1	2	2	LOC100506024, C4orf52	-7114, -238	upstream, upstream	ActReg chr4 #12509	0	0	1
12510	4	26,060,078	26,060,652	574	1	11.778	12	3.111	19	22	5	0	0	0				ActReg chr4 #12510	0	1	0
12511	4	26,067,375	26,068,027	652	1	15.55	12.35	4.158	28	23	9	0	0	0				ActReg chr4 #12511	1	0	0
12512	4	26,198,711	26,199,412	701	1	9.5	12.682	2.667	15	19	4	0	0	0				ActReg chr4 #12512	0	1	0
12513	4	26,320,602	26,322,749	2,147	3	12.552	12.636	6.156	26	36	12	2	1	1	RBPJ	343	in gene	ActReg chr4 #12513	1	1	0
12514	4	26,585,203	26,586,135	932	2	10.759	14.069	4.296	23	26	8	1	1	1	TBC1D19	123	in gene	ActReg chr4 #12514	1	1	0
12515	4	26,858,904	26,859,810	906	2	10	12.069	4.577	16	17	10	1	2	2	LOC100506048, STIM2	2864, -2956	downstream, upstream	ActReg chr4 #12515	1	1	0
12516	4	26,861,789	26,862,374	585	1	10.579	8.632	5.895	18	12	10	1	2	2	LOC100506048, STIM2	140, -232	in gene, upstream	ActReg chr4 #12516	1	0	0
12517	4	27,156,159	27,156,779	620	1	12.85	9.15	1.529	21	15	3	0	0	0				ActReg chr4 #12517	1	0	0
12518	4	27,218,883	27,219,566	683	1	8.19	11.191	1.895	14	20	4	0	0	0				ActReg chr4 #12518	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12519	4	27,280,020	27,280,801	781	2	10.72	12.84	2.864	27	22	6	0	0	0				ActReg chr4 #12519	1	1	0
12520	4	27,351,678	27,352,362	684	2	11.182	9.545	1.385	18	15	2	0	0	0				ActReg chr4 #12520	1	1	0
12521	4	29,590,203	29,590,671	468	1	6.867	9.667	3	11	18	5	0	0	0				ActReg chr4 #12521	0	1	0
12522	4	29,719,291	29,719,787	496	1	9.75	7	1	15	12	1	0	0	0				ActReg chr4 #12522	1	0	0
12523	4	30,094,242	30,094,664	422	1	1.308	2.154	10.923	2	4	16	0	0	0				ActReg chr4 #12523	0	0	1
12524	4	30,601,785	30,602,324	539	1	5.471	8.706	1.857	10	13	2	0	0	0				ActReg chr4 #12524	0	1	0
12525	4	30,718,965	30,719,450	485	1	5.6	10.8	6.067	9	15	8	1	1	1	PCDH7	-2,830	upstream	ActReg chr4 #12525	0	1	0
12526	4	30,721,112	30,721,475	363	1	9.75	7.917	10.167	12	12	15	1	1	1	PCDH7	-744	upstream	ActReg chr4 #12526	0	0	1
12527	4	31,463,115	31,463,515	400	1	9.25	10.167	2	13	16	3	0	0	0				ActReg chr4 #12527	0	1	0
12528	4	32,011,576	32,012,238	662	1	10.619	9.381	5.19	17	13	13	0	0	0				ActReg chr4 #12528	1	0	0
12529	4	32,849,029	32,849,581	552	2	11.353	10.471	1.214	22	18	2	0	0	0				ActReg chr4 #12529	1	1	0
12530	4	35,526,653	35,527,700	1,047	2	8.576	13.091	3.207	21	26	6	0	0	0				ActReg chr4 #12530	1	1	0
12531	4	36,376,382	36,376,942	560	1	4.944	5.333	12.778	8	7	19	0	0	0				ActReg chr4 #12531	0	0	1
12532	4	36,717,960	36,719,053	1,093	2	9.147	14.029	2.241	19	29	5	0	0	0				ActReg chr4 #12532	1	1	0
12533	4	37,246,434	37,246,980	546	1	3.706	2.938	14.882	6	5	24	1	1	1	KIAA1239	17	in gene	ActReg chr4 #12533	0	0	1
12534	4	37,478,702	37,479,211	509	1	9.562	9.188	1.357	15	15	2	0	0	1	C4orf19	23,404	in gene	ActReg chr4 #12534	1	0	0
12535	4	37,630,496	37,631,084	588	1	8.632	11.21	2.933	17	23	4	0	0	1	RELL1	57,209	in gene	ActReg chr4 #12535	0	1	0
12536	4	37,649,561	37,650,295	734	1	7.364	14.478	3	14	27	5	0	0	1	RELL1	38,071	in gene	ActReg chr4 #12536	0	1	0
12537	4	37,687,336	37,688,034	698	1	8.545	12.409	2.118	13	23	4	1	1	1	RELL1	314	in gene	ActReg chr4 #12537	0	1	0
12538	4	37,731,091	37,731,626	535	1	5.176	9.941	3.5	9	16	5	0	0	0				ActReg chr4 #12538	0	1	0
12539	4	37,827,877	37,828,835	958	2	10.467	8.8	11.133	14	14	20	1	1	1	PGM2	74	in gene	ActReg chr4 #12539	1	0	1
12540	4	37,891,868	37,892,646	778	1	5.24	5.32	12.24	8	10	17	1	1	1	TBC1D1	-463	upstream	ActReg chr4 #12540	0	0	1
12541	4	38,108,139	38,108,598	459	1	4.643	2.636	12.071	9	4	17	0	0	1	TBC1D1	215,648	in gene	ActReg chr4 #12541	0	0	1
12542	4	38,189,767	38,190,199	432	1	6.308	7.538	11.923	8	13	15	0	0	0				ActReg chr4 #12542	0	0	1
12543	4	38,192,255	38,192,895	640	1	10.75	10.1	3.3	17	17	5	0	0	0				ActReg chr4 #12543	1	0	0
12544	4	38,622,275	38,622,953	678	1	7.905	11.524	1	12	17	1	0	0	1	FLJ13197	43,635	in gene	ActReg chr4 #12544	0	1	0
12545	4	38,628,475	38,628,822	347	1	2.778	4.273	11.273	4	7	16	0	0	1	FLJ13197	37,601	in gene	ActReg chr4 #12545	0	0	1
12546	4	38,753,482	38,754,167	685	1	5.833	11.714	1.5	9	19	3	0	0	0				ActReg chr4 #12546	0	1	0
12547	4	38,869,557	38,870,169	612	1	8.105	9.211	11.526	12	12	18	1	2	2	FAM114A1, MIR574	509, 210	in gene, downstream	ActReg chr4 #12547	0	0	1
12548	4	39,367,457	39,368,215	758	1	9.087	11.522	8.565	16	15	15	1	1	1	RFC1	159	in gene	ActReg chr4 #12548	0	1	0
12549	4	39,460,094	39,460,956	862	3	13.482	14.333	10.667	31	28	17	1	2	3	KLB, RPL9, LIAS	52052, 43, -140	downstream, in gene, upstream	ActReg chr4 #12549	1	1	1
12550	4	39,528,603	39,529,882	1,279	3	10.5	13.5	10.175	20	27	20	1	1	1	UGDH	-24	upstream	ActReg chr4 #12550	1	1	1
12551	4	39,640,628	39,641,541	913	1	9.483	9.517	5.793	15	14	10	1	1	1	C4orf34	-603	upstream	ActReg chr4 #12551	1	0	0
12552	4	39,771,585	39,771,983	398	1	3.5	3	12.833	5	4	19	1	0	1	UBE2K	72,120	in gene	ActReg chr4 #12552	0	0	1
12553	4	39,979,214	39,979,991	777	2	18.792	17	5.105	45	42	8	1	1	1	PDS5A	-26	upstream	ActReg chr4 #12553	1	1	0
12554	4	40,057,378	40,058,041	663	2	11.7	11.3	6	17	19	11	1	1	1	N4BP2	-815	upstream	ActReg chr4 #12554	1	1	0
12555	4	40,256,614	40,257,492	878	2	10	12.074	2.846	18	21	8	0	0	0				ActReg chr4 #12555	1	1	0
12556	4	40,631,467	40,632,068	601	1	7.737	11.158	3.632	14	18	5	1	1	1	RBM47	116	in gene	ActReg chr4 #12556	0	1	0
12557	4	40,751,702	40,752,089	387	1	2.5	2.286	11.583	4	3	17	1	1	1	NSUN7	-19	upstream	ActReg chr4 #12557	0	0	1
12558	4	40,899,417	40,900,012	595	1	10.842	12.421	1.471	21	23	2	0	0	1	APBB2	316,921	in gene	ActReg chr4 #12558	0	1	0
12559	4	40,910,793	40,911,623	830	1	10.308	8.5	5.308	17	11	9	0	0	1	APBB2	305,427	in gene	ActReg chr4 #12559	1	0	0
12560	4	41,216,220	41,216,934	714	1	10.783	13.696	5.238	14	27	10	1	1	1	APBB2	58	in gene	ActReg chr4 #12560	0	1	0
12561	4	41,218,484	41,219,047	563	1	8	10.222	6.471	15	16	11	1	1	1	APBB2	-2,130	upstream	ActReg chr4 #12561	0	1	0
12562	4	41,736,305	41,736,872	567	1	9.278	9.944	1.75	16	15	2	0	0	1	PHOX2B	14,399	downstream	ActReg chr4 #12562	1	0	0
12563	4	41,752,988	41,753,391	403	1	4.846	2.231	12.308	6	4	18	0	1	1	PHOX2B	-2,202	upstream	ActReg chr4 #12563	0	0	1
12564	4	41,882,156	41,882,548	392	1	3.75	5.167	11.083	5	5	15	1	0	0				ActReg chr4 #12564	0	0	1
12565	4	41,992,150	41,992,947	797	1	9.48	12.76	6.76	21	20	14	1	1	2	DCAF4L1, SLC30A9	8835, 25	downstream, in gene	ActReg chr4 #12565	0	1	0
12566	4	42,658,979	42,659,939	960	2	14.633	15.733	7.28	37	27	12	1	1	1	ATP8A1	-337	upstream	ActReg chr4 #12566	1	1	0
12567	4	43,341,305	43,341,879	574	1	9.722	6	1.692	15	12	3	0	0	0				ActReg chr4 #12567	1	0	0
12568	4	44,680,193	44,680,859	666	1	8.15	11.2	7.1	13	20	10	1	1	1	GUF1	93	in gene	ActReg chr4 #12568	0	1	0
12569	4	45,459,133	45,459,656	523	1	4.588	4.706	12.647	9	9	19	0	0	0				ActReg chr4 #12569	0	0	1
12570	4	45,479,384	45,479,751	367	1	3.417	4.25	12.417	5	6	18	0	0	0				ActReg chr4 #12570	0	0	1
12571	4	47,465,229	47,465,874	645	1	8.6	12.6	7.4	13	22	12	1	1	1	COMMD8	125	in gene	ActReg chr4 #12571	0	1	0
12572	4	47,839,341	47,839,701	360	1	6.636	4.818	10.546	10	7	15	1	1	3	CORIN, LOC100506842, NFXL1	538, 5268, 77112	in gene, downstream, downstream	ActReg chr4 #12572	0	0	1
12573	4	47,916,209	47,916,596	387	1	11.583	12.833	12.083	16	17	16	1	1	1	NFXL1	231	in gene	ActReg chr4 #12573	0	0	1
12574	4	48,781,072	48,782,706	1,634	2	9.471	13.157	5.585	19	20	16	1	1	1	FRYL	427	in gene	ActReg chr4 #12574	1	1	0
12575	4	48,832,630	48,833,613	983	2	11.355	12.516	8.586	18	22	12	1	1	1	OCIAD1	61	in gene	ActReg chr4 #12575	1	1	0
12576	4	52,788,976	52,789,625	649	1	4.4	10.35	2.421	11	15	4	0	0	1	DCUN1D4	80,024	downstream	ActReg chr4 #12576	0	1	0
12577	4	53,578,378	53,579,047	669	1	5.905	12.191	5.857	10	16	11	1	2	2	KIAA0114, SNORA26	91, -704	in gene, upstream	ActReg chr4 #12577	0	1	0
12578	4	53,703,968	53,704,632	664	1	13.048	10	5.111	25	16	10	0	0	0				ActReg chr4 #12578	1	0	0
12579	4	54,231,287	54,232,577	1,290	2	9.39	11.951	5.108	19	20	10	1	1	1	SCFD2	310	in gene	ActReg chr4 #12579	1	1	0
12580	4	54,243,624	54,244,482	858	2	10.185	12.482	8.519	12	18	12	1	1	1	FIP1L1	233	in gene	ActReg chr4 #12580	1	1	0
12581	4	54,373,858	54,375,016	1,158	1	6.806	11.75	1.829	12	18	3	0	0	1	LNX1	83,287	in gene	ActReg chr4 #12581	0	1	0
12582	4	54,568,710	54,569,653	943	2	10.241	12.172	5	17	19	12	0	0	1	LOC100506444	7,113	in gene	ActReg chr4 #12582	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12583	4	54,720,952	54,722,011	1,059	1	6.727	12.424	2.091	11	18	4	0	0	0				ActReg chr4 #12583	0	1	0
12584	4	54,853,964	54,854,572	608	1	9.474	6.789	4.474	18	12	9	0	0	0				ActReg chr4 #12584	1	0	0
12585	4	54,930,234	54,930,864	630	1	8.35	8.8	10.05	14	14	16	1	1	1	CHIC2	239	in gene	ActReg chr4 #12585	0	0	1
12586	4	54,957,259	54,957,545	286	1	2.778	8.556	9.556	6	13	12	0	0	1	GSX2	-8,846	upstream	ActReg chr4 #12586	0	0	1
12587	4	55,094,147	55,094,666	519	1	10.312	8.688	11.312	15	15	17	1	1	1	PDGFRA	-858	upstream	ActReg chr4 #12587	0	0	1
12588	4	55,098,264	55,098,839	575	1	3.353	5.722	11.722	5	10	16	1	0	1	PDGFRA	3,287	in gene	ActReg chr4 #12588	0	0	1
12589	4	55,099,416	55,100,302	886	1	9.321	8.321	11.857	13	12	18	1	0	1	PDGFRA	4,595	in gene	ActReg chr4 #12589	0	0	1
12590	4	55,452,369	55,453,028	659	1	10.809	10.476	1.737	16	14	3	0	0	0				ActReg chr4 #12590	1	0	0
12591	4	55,524,120	55,524,518	398	1	1.462	2.462	10.846	2	4	18	1	1	1	KIT	224	in gene	ActReg chr4 #12591	0	0	1
12592	4	55,859,621	55,859,930	309	1	2.125	5	10.222	3	7	13	0	0	0				ActReg chr4 #12592	0	0	1
12593	4	55,991,307	55,991,915	608	1	4.211	4.579	12.368	8	8	19	1	1	1	KDR	151	in gene	ActReg chr4 #12593	0	0	1
12594	4	56,261,560	56,262,542	982	2	7.161	11.387	5.967	16	22	13	1	1	2	LOC100506462, TMEM165	-10304, -39	upstream, upstream	ActReg chr4 #12594	1	1	0
12595	4	56,458,129	56,458,693	564	1	8.824	11.778	4.944	17	24	9	0	1	2	PDCL2, NMU	-32, 44054	upstream, downstream	ActReg chr4 #12595	0	1	0
12596	4	56,719,544	56,720,223	679	1	8.905	10.952	5.381	14	20	9	1	1	1	EXOC1	67	in gene	ActReg chr4 #12596	0	1	0
12597	4	56,814,589	56,815,797	1,208	1	8.789	11.395	4.848	18	19	10	1	1	1	CEP135	156	in gene	ActReg chr4 #12597	0	1	0
12598	4	56,914,660	56,915,241	581	1	8.278	11.389	2.417	11	19	4	1	0	0				ActReg chr4 #12598	0	1	0
12599	4	57,301,354	57,302,621	1,267	2	9.026	11.154	9.538	15	18	20	1	2	2	PPAT, PAICS	-142, 72	upstream, in gene	ActReg chr4 #12599	0	1	1
12600	4	57,397,621	57,398,261	640	1	8.65	11.1	1.263	15	15	2	0	1	2	ARL9, LOC100506564	26566, 1098	downstream, in gene	ActReg chr4 #12600	0	1	0
12601	4	57,774,120	57,775,062	942	2	11.207	11.103	4.741	17	18	9	1	1	1	REST	549	in gene	ActReg chr4 #12601	1	1	0
12602	4	57,775,207	57,775,757	550	1	11.706	9	4.188	16	16	5	1	1	1	REST	1,440	in gene	ActReg chr4 #12602	1	0	0
12603	4	57,843,015	57,843,632	617	1	7	7.368	14.316	11	12	21	1	2	2	C4orf14, POLR2B	503, -1786	in gene, upstream	ActReg chr4 #12603	0	0	1
12604	4	57,886,875	57,887,386	511	1	10	9.562	2.5	17	14	4	0	0	2	POLR2B, IGFBP7	42021, 89409	in gene, downstream	ActReg chr4 #12604	0	1	0
12605	4	58,029,694	58,030,747	1,053	1	10.788	7.879	7.667	17	15	14	1	0	1	LOC255130	54,292	in gene	ActReg chr4 #12605	1	0	0
12606	4	58,276,081	58,277,022	941	1	7.793	14.207	3.765	14	24	6	0	0	0				ActReg chr4 #12606	0	1	0
12607	4	60,463,639	60,464,404	765	1	7.333	11.5	1.789	11	17	6	0	0	0				ActReg chr4 #12607	0	1	0
12608	4	62,067,432	62,068,230	798	1	5.56	6.84	11.4	11	11	15	1	0	0				ActReg chr4 #12608	0	0	1
12609	4	62,068,627	62,069,143	516	1	9.125	7.562	11.188	12	11	15	1	0	0				ActReg chr4 #12609	0	0	1
12610	4	67,578,101	67,578,544	443	1	2.2	1	12.643	3	1	21	0	0	0				ActReg chr4 #12610	0	0	1
12611	4	68,148,541	68,148,835	294	1	2.9	3.4	9.6	4	5	13	0	0	0				ActReg chr4 #12611	0	0	1
12612	4	70,789,494	70,789,793	299	1	4.4	5	9.9	5	7	13	0	1	1	CSN1S1	-7,156	upstream	ActReg chr4 #12612	0	0	1
12613	4	71,553,815	71,554,485	670	1	13.381	7.19	3.095	20	10	7	1	1	1	UTP3	-46	upstream	ActReg chr4 #12613	1	0	0
12614	4	72,322,515	72,322,928	413	1	10	3.846	1.778	16	5	2	0	0	1	SLC4A4	269,718	in gene	ActReg chr4 #12614	1	0	0
12615	4	72,978,133	72,978,628	495	2	8.875	9.25	1.75	15	15	2	0	0	1	NPFFR2	80,859	in gene	ActReg chr4 #12615	1	1	0
12616	4	73,935,210	73,935,856	646	1	7	11.3	7.368	11	21	15	1	1	2	COX18, ANKRD17	-61, 188969	upstream, downstream	ActReg chr4 #12616	0	1	0
12617	4	74,570,107	74,570,692	585	1	8.632	10.947	1.889	15	17	2	0	0	0				ActReg chr4 #12617	0	1	0
12618	4	74,964,780	74,965,185	405	1	5	7.538	11.154	10	11	15	1	1	1	CXCL2	15	in gene	ActReg chr4 #12618	0	0	1
12619	4	74,974,686	74,975,711	1,025	1	7.188	12.594	1.389	11	23	3	0	0	1	CXCL2	-10,201	upstream	ActReg chr4 #12619	0	1	0
12620	4	75,023,419	75,024,026	607	2	8.105	10	7.579	14	18	15	1	1	1	MTHFD2L	-107	upstream	ActReg chr4 #12620	1	1	0
12621	4	75,607,739	75,608,287	548	1	6.882	11.529	3.765	9	19	6	0	0	0				ActReg chr4 #12621	0	1	0
12622	4	76,439,320	76,440,051	731	2	10.391	9.826	6.952	17	14	11	1	2	2	RCHY1, THAP6	-57, 31	upstream, in gene	ActReg chr4 #12622	1	1	0
12623	4	76,597,808	76,598,552	744	1	5.87	10.522	6.609	9	16	12	1	1	1	G3BP2	487	in gene	ActReg chr4 #12623	0	1	0
12624	4	77,068,964	77,069,900	936	2	9.034	9.31	4.862	20	19	9	1	1	2	NUP54, SCARB2	223, 65603	in gene, downstream	ActReg chr4 #12624	1	1	0
12625	4	77,625,330	77,625,764	434	1	4.357	10	1	5	14	1	0	0	1	SHROOM3	269,294	in gene	ActReg chr4 #12625	0	1	0
12626	4	77,817,938	77,818,289	351	1	3.364	4.545	10.546	5	7	13	1	1	1	ANKRD56	889	in gene	ActReg chr4 #12626	0	0	1
12627	4	77,997,082	77,997,601	519	1	8.412	12.353	6.294	12	18	10	1	1	1	CCNI	-216	upstream	ActReg chr4 #12627	0	1	0
12628	4	78,557,936	78,558,370	434	1	5.5	9.286	1.1	8	14	2	0	0	0				ActReg chr4 #12628	0	1	0
12629	4	81,224,004	81,224,347	343	1	1.9	3.4	11.4	4	6	15	0	0	0				ActReg chr4 #12629	0	0	1
12630	4	82,501,463	82,501,772	309	1	2.167	0	11.6	3	0	15	0	0	0				ActReg chr4 #12630	0	0	1
12631	4	82,501,797	82,502,109	312	1	1	3.111	10	1	4	13	0	0	0				ActReg chr4 #12631	0	0	1
12632	4	83,295,363	83,295,753	390	1	10.583	10.417	6.417	17	17	9	1	1	1	HNRNPD	-409	upstream	ActReg chr4 #12632	0	1	0
12633	4	83,569,196	83,569,820	624	1	10.526	5.474	3.273	16	10	5	0	0	1	SCD5	150,502	in gene	ActReg chr4 #12633	1	0	0
12634	4	83,821,721	83,822,480	759	2	10.739	13.542	5	22	29	13	1	2	3	SEC31A, LOC100499177, THAP9	-9681, -31, 263	upstream, upstream, in gene	ActReg chr4 #12634	1	1	0
12635	4	83,933,953	83,934,609	656	2	12.05	9.55	1.938	18	18	4	1	1	1	LIN54	-241	upstream	ActReg chr4 #12635	1	1	0
12636	4	83,955,797	83,956,478	681	2	13.238	14.714	5.286	27	32	9	0	1	1	COPS4	-102	upstream	ActReg chr4 #12636	1	1	0
12637	4	84,205,530	84,206,196	666	1	7.952	12.429	2.071	11	20	3	1	1	1	COQ2	204	in gene	ActReg chr4 #12637	0	1	0
12638	4	84,376,912	84,377,412	500	1	10.75	8	7.25	17	12	12	1	2	3	HELQ, MRPS18C, FAM175A	-137, 44, 29128	upstream, in gene, downstream	ActReg chr4 #12638	1	0	0
12639	4	84,405,657	84,406,183	526	1	6	9.941	1.176	9	14	2	1	1	1	FAM175A	370	in gene	ActReg chr4 #12639	0	1	0
12640	4	84,469,667	84,470,124	457	1	9.571	9.857	3.308	14	14	5	0	0	1	AGPAT9	12,242	in gene	ActReg chr4 #12640	0	1	0
12641	4	86,697,684	86,698,117	433	1	10.429	7.571	1	15	13	1	0	0	1	ARHGAP24	301,616	in gene	ActReg chr4 #12641	1	0	0
12642	4	87,927,856	87,928,684	828	2	8.269	11.5	9.038	15	18	19	1	0	1	AFF1	72,116	in gene	ActReg chr4 #12642	0	1	1
12643	4	88,343,400	88,344,085	685	2	10.048	12.286	2.474	14	22	3	1	1	1	NUDT9	7	in gene	ActReg chr4 #12643	1	1	0
12644	4	88,764,884	88,765,364	480	1	7.2	9	0	10	15	0	0	0	1	MEPE	22,561	in gene	ActReg chr4 #12644	0	1	0
12645	4	89,204,675	89,205,199	524	1	7.75	9.812	4.4	14	17	8	1	1	1	PPM1K	951	in gene	ActReg chr4 #12645	0	1	0
12646	4	89,299,923	89,300,757	834	1	10.192	9.15	5.292	15	15	10	1	1	1	HERC6	449	in gene	ActReg chr4 #12646	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GeneCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12647	4	89,444,626	89,445,049	423	1	9.308	11.769	3.923	15	15	5	1	1	1	PIGY	118	in gene	ActReg chr4 #12647	0	1	0
12648	4	89,686,882	89,687,387	505	1	10.467	13.067	1.273	20	20	2	0	0	1	FAM13A	291,189	in gene	ActReg chr4 #12648	1	0	0
12649	4	90,031,888	90,032,432	544	1	6.706	11.588	6.294	12	16	10	1	2	2	LOC731282, TIGD2	296, -1808	in gene, upstream	ActReg chr4 #12649	0	1	0
12650	4	94,755,746	94,756,083	337	1	5.1	1	10.2	7	1	15	1	0	1	ATOH1	5,836	downstream	ActReg chr4 #12650	0	0	1
12651	4	96,470,573	96,470,888	315	1	2.7	7.8	12.2	5	10	16	1	1	1	UNC5C	-369	upstream	ActReg chr4 #12651	0	0	1
12652	4	98,577,212	98,577,703	491	1	8.812	8.938	3.2	16	13	5	0	0	1	C4orf37	486,934	in gene	ActReg chr4 #12652	0	1	0
12653	4	99,182,134	99,182,441	307	1	3.6	2.8	10.4	7	5	15	1	1	1	RAP1GDS1	-240	upstream	ActReg chr4 #12653	0	0	1
12654	4	99,916,200	99,916,631	431	1	10.538	8.308	3.308	17	13	4	1	1	1	METAP1	-373	upstream	ActReg chr4 #12654	1	0	0
12655	4	100,815,175	100,815,588	413	1	5.308	10.385	2.846	8	16	4	0	1	2	MAPKSP1, DNAJB14	322, 52498	in gene, downstream	ActReg chr4 #12655	0	1	0
12656	4	103,138,982	103,139,398	416	1	9.308	9.077	1.333	15	15	2	0	0	0				ActReg chr4 #12656	1	0	0
12657	4	103,423,038	103,423,437	399	1	6.385	5.923	11.538	8	8	16	1	1	1	NFKB1	751	in gene	ActReg chr4 #12657	0	0	1
12658	4	103,563,039	103,563,500	461	1	7.333	9.333	2	11	15	3	0	0	1	MANBA	118,882	in gene	ActReg chr4 #12658	0	1	0
12659	4	103,997,713	103,998,074	361	1	6.545	7.455	12.182	9	10	17	1	1	2	NHEDC2, BDH2	277, 23131	in gene, downstream	ActReg chr4 #12659	0	0	1
12660	4	104,119,038	104,120,038	1,000	2	10.469	14.875	2.769	24	29	6	1	1	1	CENPE	28	in gene	ActReg chr4 #12660	1	1	0
12661	4	106,394,901	106,395,411	510	1	10.5	11.688	2.875	16	17	4	1	1	1	PPA2	71	in gene	ActReg chr4 #12661	0	1	0
12662	4	106,629,617	106,630,186	569	1	7.389	7.778	12.833	13	10	21	1	2	2	INTS12, GSTCD	-20, -40	upstream, upstream	ActReg chr4 #12662	0	0	1
12663	4	106,844,487	106,844,937	450	1	11	6	1.333	18	11	2	0	0	1	NPNT	28,115	in gene	ActReg chr4 #12663	1	0	0
12664	4	108,132,036	108,132,559	523	1	5.267	10.062	1	10	17	1	0	0	0				ActReg chr4 #12664	0	1	0
12665	4	108,910,757	108,911,370	613	1	8.316	11.474	2.176	13	18	4	1	1	1	HADH	193	in gene	ActReg chr4 #12665	0	1	0
12666	4	109,088,551	109,088,895	344	1	2.9	4.3	12.4	4	8	17	1	2	2	LEF1, LOC641518	1389, 42	in gene, in gene	ActReg chr4 #12666	0	0	1
12667	4	109,282,247	109,282,637	390	1	7.417	10.167	2.583	10	14	4	0	0	0				ActReg chr4 #12667	0	1	0
12668	4	109,571,424	109,572,013	589	1	6.526	11	5.947	9	16	10	1	1	1	OSTC	-23	upstream	ActReg chr4 #12668	0	1	0
12669	4	109,782,387	109,782,837	450	1	7.286	9.643	1	10	13	1	0	0	1	COL25A1	441,187	in gene	ActReg chr4 #12669	0	1	0
12670	4	109,802,392	109,802,797	405	1	10.692	5.615	3.182	16	9	5	0	0	1	COL25A1	421,205	in gene	ActReg chr4 #12670	1	0	0
12671	4	109,905,529	109,905,919	390	1	2.667	4.917	10.667	5	8	15	0	0	1	COL25A1	318,075	in gene	ActReg chr4 #12671	0	0	1
12672	4	110,331,896	110,332,419	523	1	6.294	9.294	1	10	19	1	0	0	0				ActReg chr4 #12672	0	1	0
12673	4	110,354,780	110,355,122	342	1	9.091	6.182	3.1	13	10	5	1	1	1	SEC24B	-20	upstream	ActReg chr4 #12673	1	0	0
12674	4	110,624,279	110,624,741	462	1	7.067	5.4	11.533	10	8	17	1	1	2	CASP6, PLA2G12A	119, 26732	in gene, downstream	ActReg chr4 #12674	0	0	1
12675	4	111,544,047	111,544,791	744	2	8.957	13.391	2.143	18	23	4	1	0	1	PITX2	14,089	in gene	ActReg chr4 #12675	1	1	0
12676	4	111,562,404	111,562,724	320	1	2.1	1	11	3	1	14	0	1	1	PITX2	-4,056	upstream	ActReg chr4 #12676	0	0	1
12677	4	114,613,419	114,613,966	547	1	11.118	5.353	0	16	10	0	0	0	1	CAMK2D	69,391	in gene	ActReg chr4 #12677	1	0	0
12678	4	114,693,452	114,694,030	578	1	5.222	3.333	10.056	9	5	12	0	0	0				ActReg chr4 #12678	0	0	1
12679	4	115,068,036	115,068,767	731	1	8.864	11.364	4.524	13	16	8	0	0	0				ActReg chr4 #12679	0	1	0
12680	4	115,280,971	115,281,474	503	1	4.062	9.312	3.214	6	14	5	0	0	0				ActReg chr4 #12680	0	1	0
12681	4	120,130,109	120,130,674	565	1	7.167	10.722	0	12	17	0	0	1	1	USP53	-3,391	upstream	ActReg chr4 #12681	0	1	0
12682	4	120,375,497	120,376,289	792	2	16.04	24.04	7.48	45	67	11	1	2	2	LOC100507306, LOC645513	-109, -51	upstream, upstream	ActReg chr4 #12682	1	1	0
12683	4	120,987,587	120,988,325	738	1	8.957	9.478	12.217	15	17	18	1	1	1	MAD2L1	57	in gene	ActReg chr4 #12683	0	0	1
12684	4	121,760,984	121,761,326	342	1	2.364	1.091	10.636	5	2	15	0	0	1	PRDM5	82,858	in gene	ActReg chr4 #12684	0	0	1
12685	4	122,744,791	122,745,134	343	1	11.182	12.182	10.454	17	18	15	1	1	3	EXOSC9, CCNA2, BBS7	22490, 126, 46680	downstream, in gene, downstream	ActReg chr4 #12685	0	0	1
12686	4	123,748,417	123,748,977	560	1	4.706	9.941	4.647	7	17	7	1	1	1	FGF2	834	in gene	ActReg chr4 #12686	0	1	0
12687	4	123,843,486	123,844,603	1,117	3	10.514	11.829	4.8	22	23	11	2	2	2	NUDT6, SPATA5	79, -181	in gene, upstream	ActReg chr4 #12687	1	1	0
12688	4	125,552,828	125,553,431	603	2	7.647	11.053	2	17	21	3	0	0	0				ActReg chr4 #12688	1	1	0
12689	4	126,238,575	126,239,110	535	1	8.529	10.118	9.353	14	15	13	1	1	1	FAT4	1,275	in gene	ActReg chr4 #12689	0	1	0
12690	4	127,771,246	127,771,969	723	2	11.13	9.857	1	24	24	1	0	0	0				ActReg chr4 #12690	1	1	0
12691	4	128,886,901	128,887,204	303	1	4	5.4	10.6	5	7	14	1	2	2	MFSD8, C4orf29	87, 591	in gene, in gene	ActReg chr4 #12691	0	0	1
12692	4	129,438,769	129,439,426	657	1	10	5.714	1.3	18	9	2	0	1	1	LOC100507487	2,065	in gene	ActReg chr4 #12692	1	0	0
12693	4	130,014,464	130,015,085	621	1	5.45	11.1	3.667	9	18	5	1	2	2	SCLT1, C4orf33	-10, -55	upstream, upstream	ActReg chr4 #12693	0	1	0
12694	4	135,248,121	135,248,556	435	1	5.429	9.929	2.929	10	14	4	0	0	0				ActReg chr4 #12694	0	1	0
12695	4	135,252,245	135,252,960	715	2	11.261	10.478	1.769	19	23	2	0	0	0				ActReg chr4 #12695	1	1	0
12696	4	138,974,117	138,974,599	482	1	4.067	5.2	12.733	8	7	17	0	0	0				ActReg chr4 #12696	0	0	1
12697	4	139,936,470	139,936,936	466	1	7.2	11.067	7.333	10	14	12	1	1	1	CCRN4L	-240	upstream	ActReg chr4 #12697	0	1	0
12698	4	140,222,498	140,223,052	554	1	6.529	12.294	10.647	9	21	15	1	2	2	NDUFC1, NAA15	930, 99	in gene, in gene	ActReg chr4 #12698	0	1	0
12699	4	140,477,123	140,477,708	585	2	7.278	10.667	8.056	11	16	13	1	1	1	SETD7	162	in gene	ActReg chr4 #12699	0	1	1
12700	4	141,016,979	141,017,611	632	1	11.15	5.25	2.294	17	9	5	0	0	1	MAML3	57,938	in gene	ActReg chr4 #12700	1	0	0
12701	4	141,071,920	141,072,570	650	2	9.15	10.5	8.1	12	16	12	2	0	1	MAML3	2,988	in gene	ActReg chr4 #12701	0	1	1
12702	4	141,074,877	141,075,729	852	2	8.296	10.296	4.167	17	18	8	1	1	1	MAML3	-70	upstream	ActReg chr4 #12702	1	1	0
12703	4	141,566,020	141,566,356	336	1	2.25	5.2	9.9	3	5	15	0	0	1	TBC1D9	111,283	in gene	ActReg chr4 #12703	0	0	1
12704	4	141,677,566	141,678,114	548	1	12.722	8.556	10.389	17	12	15	1	1	1	TBC1D9	-369	upstream	ActReg chr4 #12704	1	0	0
12705	4	143,484,715	143,485,346	631	2	12.05	8.5	1	21	14	1	0	0	1	INPP4B	282,574	in gene	ActReg chr4 #12705	1	1	0
12706	4	144,105,562	144,106,019	457	1	7.5	9.6	4	13	12	7	1	1	1	USP38	-280	upstream	ActReg chr4 #12706	0	1	0
12707	4	144,106,282	144,106,667	385	1	5.917	5.417	10.083	8	7	15	1	1	1	USP38	404	in gene	ActReg chr4 #12707	0	0	1
12708	4	145,935,308	145,935,597	289	1	4	1.111	9.667	7	2	12	0	0	1	ANAPC10	83,916	in gene	ActReg chr4 #12708	0	0	1
12709	4	146,101,434	146,102,077	643	1	9.25	5.65	5.8	20	11	12	1	1	1	OTUD4	-923	upstream	ActReg chr4 #12709	1	0	0
12710	4	146,540,122	146,540,607	485	1	6.333	10.667	7.667	12	16	11	1	1	1	MMAA	-176	upstream	ActReg chr4 #12710	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12711	4	146,655,720	146,656,461	741	1	7.696	9.826	3.75	13	16	7	0	0	1	C4orf51	54,734	downstream	ActReg chr4 #12711	0	1	0
12712	4	147,164,974	147,165,327	353	1	2.7	2.545	9.818	4	4	15	0	0	1	SLC10A7	277,973	downstream	ActReg chr4 #12712	0	0	1
12713	4	147,442,791	147,443,939	1,148	2	11.917	13.694	4.75	21	30	9	1	1	1	SLC10A7	-242	upstream	ActReg chr4 #12713	1	1	0
12714	4	147,467,660	147,468,033	373	1	1.5	3.167	8.917	3	4	15	0	0	0				ActReg chr4 #12714	0	0	1
12715	4	147,557,878	147,558,620	742	2	8	12.565	4	16	27	6	1	1	1	POU4F2	-1,796	upstream	ActReg chr4 #12715	1	1	0
12716	4	147,564,891	147,565,453	562	1	10.833	7	1	19	13	1	0	0	1	POU4F2	5,127	downstream	ActReg chr4 #12716	1	0	0
12717	4	148,261,314	148,261,805	491	1	11.067	6	3.067	19	9	5	0	0	0				ActReg chr4 #12717	1	0	0
12718	4	150,330,205	150,330,667	462	1	4.8	9.2	0	8	16	0	0	0	0				ActReg chr4 #12718	0	1	0
12719	4	150,999,886	151,000,222	336	1	4.2	5.2	10.4	6	7	13	1	1	1	DCLK2	-26	upstream	ActReg chr4 #12719	0	0	1
12720	4	151,422,156	151,422,509	353	1	8.091	10.546	3.182	11	16	4	0	0	1	LRBA	514,547	in gene	ActReg chr4 #12720	0	1	0
12721	4	152,020,371	152,021,141	770	1	8.417	13.792	7.375	15	27	11	1	2	2	RPS3A, SNORD73A	2, -4223	in gene, upstream	ActReg chr4 #12721	0	1	0
12722	4	152,329,736	152,330,175	439	2	11	6.154	8.308	14	10	12	1	1	1	FAM160A1	-443	upstream	ActReg chr4 #12722	1	0	1
12723	4	152,681,884	152,682,459	575	1	11.889	7.278	2.833	21	11	5	1	1	1	PET112L	4	in gene	ActReg chr4 #12723	1	0	0
12724	4	153,535,465	153,536,170	705	1	12.046	5.909	2.762	24	9	5	0	0	0				ActReg chr4 #12724	1	0	0
12725	4	153,700,905	153,701,537	632	1	12.2	9.55	2.067	20	12	3	1	2	2	TIGD4, ARFIP1	-344, 109	upstream, in gene	ActReg chr4 #12725	1	0	0
12726	4	153,904,308	153,905,498	1,190	2	13.135	17.081	1.676	22	32	3	0	0	1	FHDC1	40,768	downstream	ActReg chr4 #12726	1	1	0
12727	4	155,254,026	155,254,544	518	1	2.357	9.125	4.688	3	15	8	1	0	1	DCHS2	158,645	in gene	ActReg chr4 #12727	0	1	0
12728	4	158,141,158	158,141,906	748	1	9.565	13.609	3.13	22	26	5	1	1	1	GRIA2	-204	upstream	ActReg chr4 #12728	0	1	0
12729	4	159,015,808	159,016,297	489	1	3.375	8.25	0	5	15	0	0	0	0				ActReg chr4 #12729	0	1	0
12730	4	159,592,755	159,594,094	1,339	2	29.762	35.857	2.675	119	124	4	1	2	2	C4orf46, ETFDH	-222, 147	upstream, in gene	ActReg chr4 #12730	1	1	0
12731	4	159,644,164	159,644,844	680	1	5.667	9.905	4.056	8	14	7	1	1	1	PPID	48	in gene	ActReg chr4 #12731	0	1	0
12732	4	160,843,646	160,844,196	550	1	8.5	6.278	1	16	9	1	0	0	0				ActReg chr4 #12732	1	0	0
12733	4	163,084,866	163,085,524	658	2	11.85	13.9	4.4	22	28	9	0	1	1	FSTL5	-9	upstream	ActReg chr4 #12733	1	1	0
12734	4	164,415,379	164,416,042	663	2	7.571	11.191	7.048	14	19	13	1	1	1	C4orf43	57	in gene	ActReg chr4 #12734	1	1	0
12735	4	165,431,118	165,431,559	441	1	8.857	3.429	1.929	14	5	3	0	0	0				ActReg chr4 #12735	1	0	0
12736	4	169,194,938	169,195,425	487	1	6.733	9.562	2.438	13	16	4	0	0	1	DDX60	44,777	in gene	ActReg chr4 #12736	0	1	0
12737	4	170,744,649	170,745,455	806	2	13.24	17.16	2.417	28	43	4	0	0	0				ActReg chr4 #12737	1	1	0
12738	4	170,946,854	170,947,189	335	1	5.2	5.1	12	6	6	16	1	1	1	MFAP3L	408	in gene	ActReg chr4 #12738	0	0	1
12739	4	170,948,397	170,948,951	554	2	11.706	11.647	3	20	20	5	1	1	1	MFAP3L	-1,245	upstream	ActReg chr4 #12739	1	1	0
12740	4	171,900,064	171,900,623	559	2	9.722	9.167	2.083	18	16	3	0	0	0				ActReg chr4 #12740	1	1	0
12741	4	174,173,311	174,173,921	610	2	10.3	15.368	3.533	18	29	7	0	0	1	GALNT7	83,712	in gene	ActReg chr4 #12741	1	1	0
12742	4	174,255,334	174,256,180	846	2	10.154	13.769	8.231	15	27	13	1	1	1	HMGB2	-162	upstream	ActReg chr4 #12742	0	1	1
12743	4	174,382,126	174,382,586	460	1	5.214	9.571	2.417	7	16	3	0	0	0				ActReg chr4 #12743	0	1	0
12744	4	174,780,601	174,781,009	408	1	9.769	4.846	1	15	7	1	0	0	0				ActReg chr4 #12744	1	0	0
12745	4	175,204,820	175,205,416	596	1	8.053	11.947	3.105	15	18	5	1	2	2	FBXO8, KIAA1712	284, 290	in gene, in gene	ActReg chr4 #12745	0	1	0
12746	4	175,749,701	175,750,456	755	2	13.565	15.652	3.474	25	29	7	1	1	1	GLRA3	387	in gene	ActReg chr4 #12746	1	1	0
12747	4	175,750,589	175,750,970	381	1	10.583	4.5	3.5	13	6	5	1	1	1	GLRA3	-314	upstream	ActReg chr4 #12747	1	0	0
12748	4	177,191,766	177,192,264	498	1	8.562	10.125	3	13	16	6	0	1	1	ASB5	-1,642	upstream	ActReg chr4 #12748	0	1	0
12749	4	177,459,299	177,459,856	557	1	4.25	10.706	1.938	7	16	3	0	0	0				ActReg chr4 #12749	0	1	0
12750	4	177,713,548	177,713,815	267	1	4.375	9.875	11.25	5	13	15	1	1	1	VEGFC	214	in gene	ActReg chr4 #12750	0	0	1
12751	4	177,909,293	177,909,876	583	1	7.444	10.944	1.917	12	19	3	0	0	0				ActReg chr4 #12751	0	1	0
12752	4	178,303,100	178,303,477	377	1	4.75	5.333	12.5	6	8	17	0	0	0				ActReg chr4 #12752	0	0	1
12753	4	178,362,773	178,363,832	1,059	2	6.818	13.97	9.083	13	23	24	1	1	1	AGA	355	in gene	ActReg chr4 #12753	0	1	1
12754	4	178,365,921	178,366,432	511	1	12.125	8.688	7.062	15	12	12	0	1	1	AGA	-2,519	upstream	ActReg chr4 #12754	1	0	0
12755	4	178,457,971	178,458,403	432	1	2.143	5	9.643	3	10	16	0	0	0				ActReg chr4 #12755	0	0	1
12756	4	178,528,214	178,528,751	537	1	5.176	4.765	11.177	8	6	15	0	0	0				ActReg chr4 #12756	0	0	1
12757	4	180,016,874	180,017,489	615	2	8.947	10.842	1	17	15	1	0	0	0				ActReg chr4 #12757	1	1	0
12758	4	180,018,014	180,019,371	1,357	2	7.512	13.439	1.077	15	24	2	0	0	0				ActReg chr4 #12758	1	1	0
12759	4	180,146,592	180,148,137	1,545	2	10.878	9.735	2.467	18	18	5	0	0	0				ActReg chr4 #12759	1	1	0
12760	4	180,979,375	180,979,817	442	1	9.214	4	6.2	14	9	9	1	0	0				ActReg chr4 #12760	1	0	0
12761	4	181,463,360	181,464,072	712	2	12.609	10.261	0	27	19	0	0	0	0				ActReg chr4 #12761	1	1	0
12762	4	182,102,511	182,103,109	598	1	9.474	11.79	2.842	14	21	5	0	0	0				ActReg chr4 #12762	0	1	0
12763	4	182,609,611	182,610,436	825	1	8.5	9.962	3.792	14	16	6	0	0	0				ActReg chr4 #12763	0	1	0
12764	4	182,775,245	182,775,845	600	2	9.105	10.947	2	15	21	3	0	0	0				ActReg chr4 #12764	1	1	0
12765	4	182,871,511	182,871,990	479	1	6.933	11.667	2.923	10	18	6	0	0	0				ActReg chr4 #12765	0	1	0
12766	4	182,873,471	182,874,073	602	1	12.053	11	1	21	19	1	0	0	0				ActReg chr4 #12766	1	0	0
12767	4	183,182,556	183,183,365	809	2	11.769	18.654	2.15	29	48	4	0	0	0				ActReg chr4 #12767	1	1	0
12768	4	183,288,316	183,289,004	688	1	7.182	12.682	3.158	14	24	6	0	0	1	ODZ3	43,523	in gene	ActReg chr4 #12768	0	1	0
12769	4	183,369,120	183,370,247	1,127	1	8.25	12.972	3.306	11	21	8	1	0	1	ODZ3	124,546	in gene	ActReg chr4 #12769	0	1	0
12770	4	183,837,891	183,838,219	328	1	8.1	10.5	12.7	11	13	17	1	1	1	DCTD	575	in gene	ActReg chr4 #12770	0	0	1
12771	4	183,838,746	183,839,114	368	1	9.833	5.417	12.083	14	10	15	1	1	1	DCTD	-300	upstream	ActReg chr4 #12771	0	0	1
12772	4	183,966,163	183,966,594	431	1	2.429	3	12.357	5	5	18	0	0	0				ActReg chr4 #12772	0	0	1
12773	4	184,018,530	184,019,077	547	1	3.588	4.312	12.471	6	9	18	1	2	2	C4orf38, WWC2	1549, -1660	in gene, upstream	ActReg chr4 #12773	0	0	1
12774	4	184,019,506	184,020,588	1,082	2	14.941	10.088	4.548	32	17	11	1	2	2	C4orf38, WWC2	305, -416	in gene, upstream	ActReg chr4 #12774	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12775	4	184,263,716	184,264,153	437	1	2.538	2.846	12.231	4	4	16	0	0	0				ActReg chr4 #12775	0	0	1
12776	4	184,364,876	184,366,301	1,425	2	10.636	9.955	8.295	17	16	12	1	1	1	CDKN2AIP	-201	upstream	ActReg chr4 #12776	1	1	0
12777	4	184,425,383	184,426,238	855	3	15.885	18.192	9.577	33	40	17	1	2	2	LOC389247, ING2	-142, -410	upstream, upstream	ActReg chr4 #12777	1	1	1
12778	4	184,427,047	184,427,775	728	1	9.909	11.818	7.409	17	17	14	1	2	2	LOC389247, ING2	-1743, 1191	upstream, in gene	ActReg chr4 #12778	0	1	0
12779	4	184,580,199	184,580,644	445	1	8.286	9.5	5.786	11	13	10	1	2	2	RWDD4A, C4orf41	-90, -25	upstream, upstream	ActReg chr4 #12779	0	1	0
12780	4	184,667,471	184,667,844	373	1	5.5	3.083	10.25	8	4	15	0	0	0				ActReg chr4 #12780	0	0	1
12781	4	184,961,232	184,961,578	346	1	6.273	2.455	10.273	8	5	14	0	0	0				ActReg chr4 #12781	0	0	1
12782	4	185,339,013	185,339,524	511	1	9.875	14.188	1.1	17	24	2	0	0	1	IRF2	56,458	in gene	ActReg chr4 #12782	0	1	0
12783	4	185,395,891	185,396,688	797	1	7.8	12.36	8.76	11	19	13	1	1	1	IRF2	-563	upstream	ActReg chr4 #12783	0	1	0
12784	4	185,654,686	185,655,808	1,122	2	16.361	22.667	7.194	49	59	14	1	1	1	MLF1IP	39	in gene	ActReg chr4 #12784	1	1	0
12785	4	185,734,256	185,735,184	928	2	11.483	11.172	3.276	24	19	7	0	0	1	ACSL1	12,495	in gene	ActReg chr4 #12785	1	1	0
12786	4	185,746,157	185,746,816	659	1	6.333	12.048	4.6	9	21	9	1	1	1	ACSL1	729	in gene	ActReg chr4 #12786	0	1	0
12787	4	185,832,392	185,832,982	590	1	9.056	11.056	1.938	11	18	4	0	0	0				ActReg chr4 #12787	0	1	0
12788	4	186,063,924	186,064,694	770	1	11.542	13.333	6.826	19	20	11	1	1	1	SLC25A4	-108	upstream	ActReg chr4 #12788	0	1	0
12789	4	186,227,094	186,227,758	664	1	11.667	6.619	2.222	20	12	4	0	0	1	SNX25	96,142	in gene	ActReg chr4 #12789	1	0	0
12790	4	186,316,968	186,317,814	846	1	12	14.692	7.923	20	23	16	1	1	2	ANKRD37, UFSP2	-449, 29748	upstream, downstream	ActReg chr4 #12790	0	1	0
12791	4	186,346,634	186,347,824	1,190	2	14.243	15.811	5.784	27	33	11	1	2	2	UFSP2, C4orf47	-90, -3316	upstream, upstream	ActReg chr4 #12791	1	1	0
12792	4	186,456,163	186,456,812	649	1	11.05	6.6	4	17	11	7	1	1	1	PDLIM3	225	in gene	ActReg chr4 #12792	1	0	0
12793	4	186,494,781	186,495,428	647	1	5.238	11.762	5.81	8	23	12	0	0	0				ActReg chr4 #12793	0	1	0
12794	4	186,760,149	186,760,899	750	2	11	12.333	2.706	19	23	5	0	0	1	SORBS2	117,346	in gene	ActReg chr4 #12794	1	1	0
12795	4	186,768,379	186,769,091	712	1	12.391	5.478	3.7	27	11	6	0	0	1	SORBS2	109,135	in gene	ActReg chr4 #12795	1	0	0
12796	4	186,853,982	186,854,726	744	1	9.625	12.792	3.625	13	26	7	0	0	1	SORBS2	23,516	in gene	ActReg chr4 #12796	0	1	0
12797	4	187,111,922	187,113,739	1,817	3	10.509	12.421	9.07	17	22	19	1	1	1	CYP4V2	156	in gene	ActReg chr4 #12797	1	1	1
12798	4	187,644,155	187,644,781	626	1	7.7	10.7	6.9	11	16	16	1	1	1	FAT1	519	in gene	ActReg chr4 #12798	0	1	0
12799	4	187,646,874	187,648,317	1,443	2	7.156	11.733	7.178	12	17	19	1	1	1	FAT1	-2,608	upstream	ActReg chr4 #12799	0	1	1
12800	4	187,764,584	187,764,978	394	1	2.667	9.75	1.636	4	13	2	0	0	0				ActReg chr4 #12800	0	1	0
12801	4	187,766,176	187,766,737	561	1	11.444	9.611	3.222	22	16	6	0	0	0				ActReg chr4 #12801	1	0	0
12802	4	188,735,719	188,736,571	852	1	8.731	13.308	3.538	18	20	8	0	0	0				ActReg chr4 #12802	0	1	0
12803	4	189,333,171	189,333,460	289	1	6.333	8.111	11.111	9	10	14	0	0	0				ActReg chr4 #12803	0	0	1
12804	4	189,338,348	189,339,062	714	1	8.227	12.546	2.389	15	17	5	0	0	0				ActReg chr4 #12804	0	1	0
12805	4	189,581,877	189,582,391	514	1	8.133	11.312	2.286	10	16	3	0	0	0				ActReg chr4 #12805	0	1	0
12806	4	189,826,471	189,826,870	399	1	2.909	3.083	8.75	5	4	14	0	0	0				ActReg chr4 #12806	0	0	1
12807	4	190,600,491	190,600,927	436	1	4.538	7.462	12.769	7	11	16	0	0	0				ActReg chr4 #12807	0	0	1
12808	4	190,695,103	190,695,535	432	1	5.714	10.786	2	9	18	2	0	0	0				ActReg chr4 #12808	0	1	0
12809	4	190,861,061	190,862,597	1,536	3	13.333	16.917	9.896	23	34	24	1	1	1	FRG1	-145	upstream	ActReg chr4 #12809	1	1	1
12810	4	190,940,319	190,940,887	568	1	2.5	3.667	10.556	4	7	12	1	0	2	DUX4C, FRG2	4903, 7809	in gene, downstream	ActReg chr4 #12810	0	0	1
12811	4	190,958,718	190,959,143	425	2	12.857	8.5	1.091	23	17	2	1	0	0				ActReg chr4 #12811	1	1	0
12812	5	56,658	57,690	1,032	2	9.312	12.156	2.379	16	22	6	0	0	0				ActReg chr5 #12812	1	1	0
12813	5	139,555	140,184	629	1	4.158	3.632	11.842	8	8	17	0	1	1	PLEKHG4B	-504	upstream	ActReg chr5 #12813	0	0	1
12814	5	218,935	219,427	492	1	6.375	10.938	3.562	10	17	6	1	2	2	CCDC127, SDHA	-884, 825	upstream, in gene	ActReg chr5 #12814	0	1	0
12815	5	271,218	272,064	846	1	6.963	13.444	4.926	13	26	11	2	2	2	LOC100507671, PDCD6	-30, -95	upstream, upstream	ActReg chr5 #12815	0	1	0
12816	5	322,489	322,907	418	1	6	12.385	10.462	8	17	17	1	0	2	PDCD6, AHRR	50962, 18407	downstream, in gene	ActReg chr5 #12816	0	0	1
12817	5	372,842	373,696	854	1	8	10.518	6.074	11	16	9	1	0	1	AHRR	68,978	in gene	ActReg chr5 #12817	0	1	0
12818	5	394,788	395,286	498	1	6.667	6.467	11	9	8	16	0	0	1	AHRR	90,746	in gene	ActReg chr5 #12818	0	0	1
12819	5	398,416	399,203	787	1	9.88	6.76	8.2	16	10	11	0	0	1	AHRR	94,518	in gene	ActReg chr5 #12819	1	0	0
12820	5	416,325	416,643	318	1	4.8	8.9	11	8	10	15	0	0	1	AHRR	112,193	in gene	ActReg chr5 #12820	0	0	1
12821	5	434,516	434,973	457	1	4.429	6	13.143	8	7	19	0	0	3	AHRR, C5orf55, EXOC3	130453, 8514, -8590	in gene, downstream, upstream	ActReg chr5 #12821	0	0	1
12822	5	447,625	447,943	318	1	5.6	8.4	14.2	7	11	19	0	1	3	AHRR, C5orf55, EXOC3	143493, -4526, 4450	downstream, upstream, in gene	ActReg chr5 #12822	0	0	1
12823	5	476,547	477,031	484	1	3.133	2.467	15.133	8	4	23	1	2	4	EXOC3, LOC25845, SLC9A3, LOC100288152	33455, -3709, 47760, 647	downstream, upstream, in gene, upstream	ActReg chr5 #12823	0	0	1
12824	5	484,547	485,038	491	1	3.8	4.733	11.2	6	7	19	0	0	2	SLC9A3, LOC100288152	39757, 7356	in gene, downstream	ActReg chr5 #12824	0	0	1
12825	5	488,198	489,405	1,207	1	3.371	3.444	12.432	6	8	18	1	0	2	SLC9A3, LOC100288152	35748, 11365	in gene, downstream	ActReg chr5 #12825	0	0	1
12826	5	489,695	490,304	609	1	3.45	5.45	12.1	5	9	17	0	0	2	SLC9A3, LOC100288152	34550, 12563	in gene, downstream	ActReg chr5 #12826	0	0	1
12827	5	490,505	491,032	527	1	4.25	3	13.625	8	5	20	0	0	2	SLC9A3, LOC100288152	33781, 13332	in gene, downstream	ActReg chr5 #12827	0	0	1
12828	5	533,835	534,382	547	1	4.882	2.812	12.823	8	4	17	0	0	1	SLC9A3	-9,559	upstream	ActReg chr5 #12828	0	0	1
12829	5	537,667	538,153	486	1	1.8	3.143	13.933	3	5	21	1	0	0				ActReg chr5 #12829	0	0	1
12830	5	546,783	547,131	348	1	2.727	4.182	11.546	5	5	15	0	0	0				ActReg chr5 #12830	0	0	1
12831	5	677,813	678,172	359	1	2.875	3.182	10.273	5	4	15	1	0	1	TPPP	15,518	in gene	ActReg chr5 #12831	0	0	1
12832	5	861,351	862,061	710	1	3.444	4.909	11.273	5	8	15	0	0	1	BRD9	31,233	downstream	ActReg chr5 #12832	0	0	1
12833	5	911,965	913,154	1,189	2	14.763	15.079	3.658	36	46	7	1	0	1	TRIP13	19,590	in gene	ActReg chr5 #12833	1	1	0
12834	5	944,109	944,478	369	1	5.909	3.818	11.818	9	4	17	0	0	0				ActReg chr5 #12834	0	0	1
12835	5	952,059	952,791	732	1	2.688	3.043	11.609	5	5	18	0	0	0				ActReg chr5 #12835	0	0	1
12836	5	1,013,499	1,013,990	491	1	6.688	3.25	11.625	10	6	16	0	0	1	NKD2	4,576	in gene	ActReg chr5 #12836	0	0	1
12837	5	1,015,519	1,016,095	576	1	2.944	2.059	11.778	6	4	17	0	0	1	NKD2	6,639	in gene	ActReg chr5 #12837	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR:: 1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12838	5	1,017,154	1,017,675	521	1	3.625	4	11.625	6	7	16	0	0	1	NKD2	8,246	in gene	ActReg chr5 #12838	0	0	1
12839	5	1,056,969	1,057,321	352	1	2.7	6.545	12.818	5	9	17	0	1	2	SLC12A7, LOC100506766	55027, -1455	in gene, upstream	ActReg chr5 #12839	0	0	1
12840	5	1,100,174	1,101,666	1,492	1	3.957	2.304	12.213	11	5	21	1	0	1	SLC12A7	11,252	in gene	ActReg chr5 #12840	0	0	1
12841	5	1,122,798	1,123,311	513	1	6.312	4.625	12.875	9	7	22	0	0	0				ActReg chr5 #12841	0	0	1
12842	5	1,156,972	1,157,473	501	1	5.25	6.625	10.188	8	9	15	0	0	0				ActReg chr5 #12842	0	0	1
12843	5	1,180,089	1,180,622	533	1	6.176	4.235	12.529	9	6	17	0	0	0				ActReg chr5 #12843	0	0	1
12844	5	1,181,347	1,181,897	550	1	2.176	4.294	10.177	3	7	13	0	0	0				ActReg chr5 #12844	0	0	1
12845	5	1,183,903	1,185,098	1,195	1	5.27	4.421	10.868	10	7	18	0	0	0				ActReg chr5 #12845	0	0	1
12846	5	1,187,463	1,188,095	632	1	3.438	3.474	14.21	7	6	21	0	0	0				ActReg chr5 #12846	0	0	1
12847	5	1,200,561	1,201,062	501	1	5.812	1.75	11.625	10	2	17	0	1	1	SLC6A19	-899	upstream	ActReg chr5 #12847	0	0	1
12848	5	1,201,991	1,202,757	766	1	2.739	5.167	12.958	5	7	17	1	1	1	SLC6A19	664	in gene	ActReg chr5 #12848	0	0	1
12849	5	1,204,391	1,204,999	608	1	5.474	4.5	12.263	10	8	18	0	0	1	SLC6A19	2,985	in gene	ActReg chr5 #12849	0	0	1
12850	5	1,213,673	1,214,188	515	1	2.562	3.188	13.938	5	4	18	0	0	1	SLC6A19	12,220	in gene	ActReg chr5 #12850	0	0	1
12851	5	1,238,909	1,239,405	496	1	2.857	1.818	12.312	5	3	17	0	0	1	SLC6A18	13,687	in gene	ActReg chr5 #12851	0	0	1
12852	5	1,243,208	1,243,662	454	1	5.571	4.214	11.643	10	6	15	1	0	2	SLC6A18, TERT	17965, 51727	in gene, downstream	ActReg chr5 #12852	0	0	1
12853	5	1,244,806	1,245,463	657	1	3.85	5.65	12.85	7	9	19	0	0	2	SLC6A18, TERT	19664, 50028	in gene, downstream	ActReg chr5 #12853	0	0	1
12854	5	1,246,105	1,246,747	642	1	3.895	5.6	14.25	6	10	19	1	0	2	SLC6A18, TERT	20956, 48736	downstream, downstream	ActReg chr5 #12854	0	0	1
12855	5	1,246,792	1,247,862	1,070	2	11.242	13.576	6.939	20	27	12	1	0	2	SLC6A18, TERT	21657, 47835	downstream, downstream	ActReg chr5 #12855	1	1	0
12856	5	1,331,092	1,331,890	798	1	4.72	4.261	12.08	7	6	21	0	0	1	CLPTM1L	13,511	in gene	ActReg chr5 #12856	0	0	1
12857	5	1,347,714	1,348,094	380	1	5.273	4.818	13.182	7	6	19	0	0	1	CLPTM1L	-2,902	upstream	ActReg chr5 #12857	0	0	1
12858	5	1,358,584	1,359,094	510	1	4.375	3.846	13.5	7	6	17	0	0	1	LOC100506791	21,349	downstream	ActReg chr5 #12858	0	0	1
12859	5	1,386,260	1,386,852	592	1	2.895	7	12.421	7	11	17	1	1	2	LOC100506791, SLC6A3	-6368, 58987	upstream, downstream	ActReg chr5 #12859	0	0	1
12860	5	1,391,092	1,391,954	862	1	2.375	4.111	11.778	4	7	18	0	0	1	SLC6A3	54,020	downstream	ActReg chr5 #12860	0	0	1
12861	5	1,401,854	1,402,375	521	1	1.857	3.471	13.353	3	7	21	0	0	1	SLC6A3	43,429	in gene	ActReg chr5 #12861	0	0	1
12862	5	1,406,228	1,406,654	426	1	3.231	3.692	12.923	4	6	16	0	0	1	SLC6A3	39,102	in gene	ActReg chr5 #12862	0	0	1
12863	5	1,409,806	1,410,434	628	1	6.1	7.05	11.7	8	11	18	0	0	1	SLC6A3	35,423	in gene	ActReg chr5 #12863	0	0	1
12864	5	1,442,300	1,442,799	499	1	3.909	2.562	11.625	6	4	18	0	0	1	SLC6A3	2,994	in gene	ActReg chr5 #12864	0	0	1
12865	5	1,445,989	1,446,508	519	1	2.75	1.909	11.938	5	4	19	1	1	1	SLC6A3	-705	upstream	ActReg chr5 #12865	0	0	1
12866	5	1,466,792	1,467,409	617	1	3.474	5.158	10.947	6	8	14	1	0	1	LPCAT1	56,976	in gene	ActReg chr5 #12866	0	0	1
12867	5	1,486,958	1,487,459	501	1	5.75	7.312	10.625	9	10	13	0	0	1	LPCAT1	36,868	in gene	ActReg chr5 #12867	0	0	1
12868	5	1,524,623	1,525,026	403	1	3.308	4.846	11.846	4	7	16	1	1	1	LPCAT1	-748	upstream	ActReg chr5 #12868	0	0	1
12869	5	1,626,507	1,626,780	273	1	1.75	1	10.375	3	1	14	0	0	0				ActReg chr5 #12869	0	0	1
12870	5	1,633,891	1,634,515	624	1	6.842	11.737	6.526	12	17	9	1	0	0				ActReg chr5 #12870	0	1	0
12871	5	1,642,712	1,643,097	385	1	3.833	2	10.417	5	3	16	0	0	0				ActReg chr5 #12871	0	0	1
12872	5	1,659,890	1,660,349	459	1	1.5	5	12.071	2	8	18	0	0	0				ActReg chr5 #12872	0	0	1
12873	5	1,686,375	1,686,988	613	1	3.5	4	12.947	5	6	20	0	0	0				ActReg chr5 #12873	0	0	1
12874	5	1,703,585	1,704,181	596	1	2.111	3.778	11.667	3	5	15	0	0	1	MIR4277	5,100	downstream	ActReg chr5 #12874	0	0	1
12875	5	1,725,983	1,726,535	552	1	4.167	6.389	11.333	8	11	13	1	0	0				ActReg chr5 #12875	0	0	1
12876	5	1,730,006	1,730,494	488	1	2	2.467	12.867	5	5	21	1	0	0				ActReg chr5 #12876	0	0	1
12877	5	1,746,798	1,747,333	535	1	3.235	1	11.294	5	1	14	1	0	0				ActReg chr5 #12877	0	0	1
12878	5	1,869,318	1,869,848	530	1	2	2.5	13.188	4	5	19	0	0	1	IRX4	-13,297	downstream	ActReg chr5 #12878	0	0	1
12879	5	1,878,716	1,879,041	325	1	5.091	1.2	9.909	8	2	16	1	0	1	IRX4	4,002	in gene	ActReg chr5 #12879	0	0	1
12880	5	2,132,225	2,132,570	345	1	2.5	2.5	14.8	3	4	21	0	0	0				ActReg chr5 #12880	0	0	1
12881	5	2,335,106	2,335,450	344	1	1.889	3.8	10.5	3	5	13	0	0	0				ActReg chr5 #12881	0	0	1
12882	5	2,542,853	2,543,147	294	1	2.125	2.667	10.111	3	4	13	0	0	0				ActReg chr5 #12882	0	0	1
12883	5	2,642,995	2,643,407	412	1	1.818	2.538	11.308	3	4	15	1	0	0				ActReg chr5 #12883	0	0	1
12884	5	2,699,448	2,700,125	677	1	1.7	2	12.286	3	4	19	0	0	0				ActReg chr5 #12884	0	0	1
12885	5	2,740,198	2,740,722	524	1	2.462	3	12.625	3	5	20	1	0	1	IRX2	11,309	downstream	ActReg chr5 #12885	0	0	1
12886	5	2,749,145	2,749,729	584	1	1	4.143	12.21	1	8	18	1	2	2	IRX2, C5orf38	2332, -2825	in gene, upstream	ActReg chr5 #12886	0	0	1
12887	5	2,866,227	2,866,759	532	1	2.824	5.471	11.353	5	8	22	1	0	0				ActReg chr5 #12887	0	0	1
12888	5	2,995,728	2,996,101	373	1	2.6	1.583	10.917	4	2	17	0	0	0				ActReg chr5 #12888	0	0	1
12889	5	3,310,906	3,311,614	708	1	10.773	14.364	4.905	16	28	10	0	0	0				ActReg chr5 #12889	0	1	0
12890	5	3,320,371	3,321,094	723	1	6.696	12.174	3.565	10	21	6	0	0	0				ActReg chr5 #12890	0	1	0
12891	5	3,324,807	3,325,716	909	1	10.679	13.929	6.107	18	24	14	1	0	0				ActReg chr5 #12891	0	1	0
12892	5	3,599,558	3,599,928	370	1	1.909	3.091	10.454	2	4	14	1	0	1	IRX1	3,575	in gene	ActReg chr5 #12892	0	0	1
12893	5	3,600,160	3,600,762	602	1	1.6	4.737	10.474	3	7	16	1	0	1	IRX1	4,293	in gene	ActReg chr5 #12893	0	0	1
12894	5	4,837,667	4,837,950	283	1	1.625	3.25	11	3	6	14	0	0	0				ActReg chr5 #12894	0	0	1
12895	5	5,126,505	5,127,099	594	1	6.111	10.667	2.615	8	15	5	0	0	0				ActReg chr5 #12895	0	1	0
12896	5	5,139,300	5,139,954	654	1	3.4	7	11.75	7	12	16	1	1	1	ADAMTS16	-816	upstream	ActReg chr5 #12896	0	0	1
12897	5	5,271,408	5,271,970	562	1	5.444	11.722	4.056	13	18	7	0	0	1	ADAMTS16	131,246	in gene	ActReg chr5 #12897	0	1	0
12898	5	5,340,168	5,341,000	832	1	14.615	11.192	3.24	27	18	7	0	0	0				ActReg chr5 #12898	1	0	0
12899	5	5,421,906	5,422,955	1,049	2	13.546	12.182	8	22	25	15	1	1	1	KIAA0947	-577	upstream	ActReg chr5 #12899	1	1	0
12900	5	5,997,603	5,997,916	313	1	1.778	3.222	12	3	5	15	0	0	0				ActReg chr5 #12900	0	0	1
12901	5	6,302,580	6,303,307	727	1	5.043	9.826	2.231	10	17	4	0	0	1	FLJ33360	34,462	downstream	ActReg chr5 #12901	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12902	5	6,328,089	6,328,786	697	1	8.818	10.954	1.6	17	25	2	0	0	1	FLJ33360	8,968	in gene	ActReg chr5 #12902	0	1	0
12903	5	6,365,466	6,366,124	658	1	9.429	10.238	7.619	14	14	14	0	0	1	MED10	12,844	downstream	ActReg chr5 #12903	0	1	0
12904	5	6,377,908	6,378,710	802	1	7.68	11.76	6.652	10	18	11	1	1	1	MED10	330	in gene	ActReg chr5 #12904	0	1	0
12905	5	6,396,685	6,397,103	418	1	2.385	3.923	11.462	4	6	18	0	0	0				ActReg chr5 #12905	0	0	1
12906	5	6,633,287	6,634,041	754	1	9.783	10.522	9.739	17	16	15	1	2	2	NSUN2, SRD5A1	-191, 164	upstream, in gene	ActReg chr5 #12906	0	1	0
12907	5	6,712,111	6,713,230	1,119	2	9.4	12.286	7.548	14	23	17	1	2	2	LOC100505625, PAPD7	-4846, -2048	upstream, upstream	ActReg chr5 #12907	0	1	1
12908	5	7,868,889	7,869,517	628	2	12.1	13.95	9.25	18	25	14	1	2	3	LOC100288963, FASTKD3, MTRR	18284, -53, -14	downstream, upstream, upstream	ActReg chr5 #12908	1	1	0
12909	5	8,457,437	8,457,935	498	1	7.929	6.75	12.375	12	8	17	1	2	2	LOC729506, LOC100505738	-15, -118	upstream, upstream	ActReg chr5 #12909	0	0	1
12910	5	8,828,836	8,829,788	952	2	10.379	11.379	3.167	19	17	7	0	0	0				ActReg chr5 #12910	1	1	0
12911	5	9,244,425	9,244,984	559	1	7.706	10.177	1.714	13	14	3	0	0	1	SEMA5A	301,529	in gene	ActReg chr5 #12911	0	1	0
12912	5	9,546,392	9,546,691	299	1	2.875	2.286	9.8	5	3	13	1	3	3	SEMA5A, LOC100505806, SNORD123	-308, 139, -2398	upstream, in gene, upstream	ActReg chr5 #12912	0	0	1
12913	5	9,725,459	9,725,913	454	1	1.692	2.714	11.857	2	5	19	0	0	1	LOC285692	64,351	in gene	ActReg chr5 #12913	0	0	1
12914	5	10,065,551	10,066,109	558	1	2.529	2.235	11.765	4	4	18	0	0	0				ActReg chr5 #12914	0	0	1
12915	5	10,249,518	10,250,008	490	1	11.533	9	7.2	17	12	15	1	2	2	FAM173B, CCT5	251, -519	in gene, upstream	ActReg chr5 #12915	1	0	0
12916	5	10,250,211	10,251,176	965	1	9	10.8	8.133	14	16	14	1	2	2	FAM173B, CCT5	-679, 411	upstream, in gene	ActReg chr5 #12916	0	1	0
12917	5	10,290,120	10,290,423	303	1	4.556	1.333	10.222	6	2	13	0	0	1	CMBL	17,897	in gene	ActReg chr5 #12917	0	0	1
12918	5	10,353,177	10,353,994	817	2	9.154	13.538	11.192	15	23	18	1	1	1	6-Mar	-243	upstream	ActReg chr5 #12918	0	1	1
12919	5	10,724,819	10,725,787	968	1	7.633	10.3	4.133	14	17	8	0	0	1	DAP	36,084	in gene	ActReg chr5 #12919	0	1	0
12920	5	10,761,539	10,762,073	534	1	5	12.375	5.312	8	19	8	1	1	1	DAP	-419	upstream	ActReg chr5 #12920	0	1	0
12921	5	10,859,514	10,860,621	1,107	1	9.686	9.843	4.939	17	14	11	0	0	0				ActReg chr5 #12921	0	1	0
12922	5	11,384,531	11,385,040	509	1	1.429	2.067	11.625	2	4	21	1	0	1	CTNND2	519,325	in gene	ActReg chr5 #12922	0	0	1
12923	5	13,553,867	13,554,429	562	1	6.059	11.882	5.529	11	25	10	0	0	0				ActReg chr5 #12923	0	1	0
12924	5	13,866,970	13,867,365	395	1	7.231	9.846	1	11	16	1	0	0	1	DNAH5	77,422	in gene	ActReg chr5 #12924	0	1	0
12925	5	14,039,156	14,039,821	665	1	12.238	7.524	3.389	18	11	7	0	0	0				ActReg chr5 #12925	1	0	0
12926	5	14,144,326	14,144,780	454	1	11.286	6.857	10.786	13	11	14	1	1	1	TRIO	724	in gene	ActReg chr5 #12926	0	0	1
12927	5	14,178,448	14,179,340	892	1	5.857	12.321	2.136	9	19	4	0	0	1	TRIO	35,065	in gene	ActReg chr5 #12927	0	1	0
12928	5	14,268,229	14,269,208	979	1	8.833	10.2	3.667	19	19	7	0	0	1	TRIO	124,889	in gene	ActReg chr5 #12928	0	1	0
12929	5	14,628,296	14,628,968	672	2	10.333	13.667	1	17	28	1	0	0	0				ActReg chr5 #12929	1	1	0
12930	5	14,664,140	14,664,984	844	2	12.346	10.808	7.192	18	14	14	1	1	1	FAM105B	-221	upstream	ActReg chr5 #12930	1	1	0
12931	5	14,775,690	14,776,385	695	1	7.318	11.046	3.182	11	15	6	0	1	2	ANKH, LOC100128508	95850, 1104	in gene, in gene	ActReg chr5 #12931	0	1	0
12932	5	14,880,256	14,881,332	1,076	2	10.853	11.294	3.083	17	24	5	0	0	1	ANKH	-8,907	upstream	ActReg chr5 #12932	1	1	0
12933	5	14,937,392	14,938,009	617	1	6.842	10.368	1	12	16	1	0	0	0				ActReg chr5 #12933	0	1	0
12934	5	15,008,412	15,009,114	702	1	13.227	9.409	3.5	29	19	7	0	0	0				ActReg chr5 #12934	1	0	0
12935	5	16,178,862	16,179,318	456	2	6	11.357	8.25	10	19	14	1	2	2	MARCH11, LOC401176	807, -1257	in gene, upstream	ActReg chr5 #12935	0	1	1
12936	5	16,465,385	16,466,497	1,112	2	11.657	11.371	7.657	18	17	14	1	1	2	ZNF622, FAM134B	-47, 151177	upstream, downstream	ActReg chr5 #12936	1	1	0
12937	5	16,502,824	16,503,486	662	1	6	11	2.444	8	17	5	0	0	1	FAM134B	113,963	in gene	ActReg chr5 #12937	0	1	0
12938	5	19,045,295	19,045,696	401	1	4.231	3.846	9.154	8	5	13	0	0	0				ActReg chr5 #12938	0	0	1
12939	5	20,276,273	20,276,968	695	1	7.955	10.727	7.5	14	16	11	0	0	0				ActReg chr5 #12939	0	1	0
12940	5	20,679,063	20,679,629	566	1	7.611	10.444	1	14	19	1	0	0	0				ActReg chr5 #12940	0	1	0
12941	5	21,459,127	21,459,891	764	2	44.391	45.875	4.682	133	129	7	1	0	0				ActReg chr5 #12941	1	1	0
12942	5	21,551,954	21,552,695	741	1	7.87	12	1.9	11	19	3	0	0	0				ActReg chr5 #12942	0	1	0
12943	5	22,372,162	22,372,833	671	2	10.143	11.095	5.526	13	18	9	0	0	1	CDH12	481,234	in gene	ActReg chr5 #12943	1	1	0
12944	5	23,084,785	23,085,512	727	1	7.739	13.478	2.938	13	20	6	0	0	0				ActReg chr5 #12944	0	1	0
12945	5	25,614,554	25,614,990	436	1	2.5	4.857	9.786	5	8	17	0	0	0				ActReg chr5 #12945	0	0	1
12946	5	27,241,848	27,242,497	649	1	10.286	6.143	2.188	20	9	3	0	0	0				ActReg chr5 #12946	1	0	0
12947	5	27,439,582	27,439,872	290	1	2.5	5.571	9.6	4	6	13	0	0	0				ActReg chr5 #12947	0	0	1
12948	5	27,706,775	27,707,446	671	1	8.095	10.476	1.062	15	20	2	0	0	0				ActReg chr5 #12948	0	1	0
12949	5	28,077,693	28,078,454	761	2	8.75	8.708	9.625	13	14	17	0	0	0				ActReg chr5 #12949	0	1	1
12950	5	28,808,965	28,810,938	1,973	3	10.852	13.41	7.464	27	27	21	1	0	0				ActReg chr5 #12950	1	1	1
12951	5	30,540,266	30,540,578	312	1	2.5	1.8	10.3	3	3	14	0	0	0				ActReg chr5 #12951	0	0	1
12952	5	31,532,000	31,532,994	994	1	6.688	11.969	5.406	12	20	8	1	2	2	RNASEN, C5orf22	-215, 124	upstream, in gene	ActReg chr5 #12952	0	1	0
12953	5	32,173,831	32,174,887	1,056	1	8.394	13.121	8.654	17	24	16	1	1	1	GOLPH3	66	in gene	ActReg chr5 #12953	0	1	0
12954	5	32,390,930	32,391,571	641	1	7.1	12.15	2.111	16	20	3	0	0	2	ZFR, MIR579	53594, 3331	in gene, downstream	ActReg chr5 #12954	0	1	0
12955	5	32,712,208	32,712,729	521	1	5.062	7.125	12.375	8	11	20	1	1	1	NPR3	803	in gene	ActReg chr5 #12955	0	0	1
12956	5	32,713,924	32,714,401	477	1	5.4	5.867	11	8	9	17	1	1	1	NPR3	2,497	in gene	ActReg chr5 #12956	0	0	1
12957	5	33,049,767	33,050,528	761	1	8.208	12.958	6.125	11	23	8	0	0	0				ActReg chr5 #12957	0	1	0
12958	5	33,440,372	33,441,703	1,331	1	8.238	10.024	8.171	16	17	16	1	1	1	TARS	139	in gene	ActReg chr5 #12958	0	1	0
12959	5	33,690,884	33,691,336	452	1	7.714	10.571	0	12	17	0	0	0	1	ADAMTS12	201,014	in gene	ActReg chr5 #12959	0	1	0
12960	5	33,935,957	33,938,305	2,348	2	11.662	14.608	8.575	33	29	18	1	1	2	RXFP3, SLC45A2	640, 47649	in gene, downstream	ActReg chr5 #12960	1	1	0
12961	5	33,984,299	33,984,811	512	1	3.625	8.438	12.312	6	15	18	0	1	2	SLC45A2, AMACR	225, 23665	in gene, downstream	ActReg chr5 #12961	0	0	1
12962	5	34,001,308	34,001,838	530	1	6.176	10.823	1.5	9	15	4	0	0	1	AMACR	6,647	in gene	ActReg chr5 #12962	0	1	0
12963	5	34,007,823	34,008,517	694	2	9.864	12	9.227	13	17	14	1	1	2	AMACR, C1QTNF3	50, 35147	in gene, downstream	ActReg chr5 #12963	0	1	1
12964	5	34,047,104	34,047,781	677	1	11.273	8.909	5.056	19	13	9	0	1	1	C1QTNF3	-4,125	upstream	ActReg chr5 #12964	1	0	0
12965	5	34,053,186	34,053,847	661	1	11.9	6.8	1.833	16	12	2	0	0	1	C1QTNF3	-10,199	upstream	ActReg chr5 #12965	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
12966	5	34,839,038	34,839,764	726	1	6.565	11.13	7.609	12	19	12	1	1	2	RAI14, TTC23L	182968, 132	downstream, in gene	ActReg chr5 #12966	0	1	0
12967	5	34,914,873	34,916,231	1,358	3	10.279	15.884	7	21	34	19	1	2	2	RAD1, BRIX1	228, -268	in gene, upstream	ActReg chr5 #12967	1	1	1
12968	5	35,247,503	35,248,273	770	1	7.5	11.167	1.789	12	18	3	0	0	0				ActReg chr5 #12968	0	1	0
12969	5	35,617,433	35,618,623	1,190	2	28.514	34.838	5.486	94	96	9	1	1	1	SPEF2	39	in gene	ActReg chr5 #12969	1	1	0
12970	5	36,151,570	36,152,818	1,248	1	8.359	10.923	4.846	16	18	11	1	3	3	LMBRD2, MIR580, SKP2	-179, -4104, 5	upstream, upstream, in gene	ActReg chr5 #12970	0	1	0
12971	5	36,241,024	36,241,756	732	1	7.739	10.261	6.091	10	14	11	1	1	2	C5orf33, RANBP3L	868, 60621	in gene, downstream	ActReg chr5 #12971	0	1	0
12972	5	36,241,807	36,242,700	893	2	15.214	14.214	5.929	29	21	12	1	1	2	C5orf33, RANBP3L	5, 59758	in gene, downstream	ActReg chr5 #12972	1	1	0
12973	5	36,657,500	36,658,167	667	1	8.667	15.762	2.55	12	27	4	0	0	1	SLC1A3	51,376	in gene	ActReg chr5 #12973	0	1	0
12974	5	36,877,224	36,877,504	280	1	5.111	6.333	11.111	8	8	15	1	2	2	LOC646719, NIPBL	-568, 503	upstream, in gene	ActReg chr5 #12974	0	0	1
12975	5	37,370,861	37,371,809	948	2	11.6	14.5	3.5	22	26	7	1	1	2	NUP155, WDR70	-138, -8077	upstream, upstream	ActReg chr5 #12975	1	1	0
12976	5	37,378,865	37,379,795	930	2	43.241	50.035	4.31	160	166	9	1	1	2	NUP155, WDR70	-8133, -82	upstream, upstream	ActReg chr5 #12976	1	1	0
12977	5	37,722,929	37,723,484	555	1	11.765	6.765	3.412	20	10	5	0	0	1	WDR70	343, 794	in gene	ActReg chr5 #12977	1	0	0
12978	5	37,786,913	37,787,621	708	1	8.227	11.091	1.154	13	17	2	0	0	0				ActReg chr5 #12978	0	1	0
12979	5	37,889,674	37,890,618	944	2	11.724	13.069	2.16	18	21	4	0	0	0				ActReg chr5 #12979	1	1	0
12980	5	38,136,529	38,136,923	394	1	3.083	1.833	10.75	4	4	15	0	0	0				ActReg chr5 #12980	0	0	1
12981	5	38,601,757	38,602,450	693	2	11.364	10.318	1.333	16	20	2	0	1	2	LIFR, LOC100506495	-6596, 45239	upstream, in gene	ActReg chr5 #12981	1	1	0
12982	5	38,772,472	38,772,941	469	1	6.667	10.933	2.167	10	17	4	0	0	0				ActReg chr5 #12982	0	1	0
12983	5	38,782,952	38,783,782	830	1	7.154	11.269	2.3	13	16	4	0	0	0				ActReg chr5 #12983	0	1	0
12984	5	38,921,228	38,921,674	446	1	8.857	9.429	1.889	14	16	3	0	0	1	OSMR	75,491	in gene	ActReg chr5 #12984	0	1	0
12985	5	39,074,427	39,075,105	678	2	12.591	7.909	9.273	22	15	16	1	1	1	RICTOR	-265	upstream	ActReg chr5 #12985	1	0	1
12986	5	39,196,536	39,197,122	586	1	5.789	9.105	2.056	9	16	5	0	0	1	FYB	22,858	in gene	ActReg chr5 #12986	0	1	0
12987	5	39,399,551	39,400,118	567	1	6.5	10.611	2	11	19	3	0	0	1	DAB2	25,501	in gene	ActReg chr5 #12987	0	1	0
12988	5	39,424,903	39,425,699	796	1	9.28	12.4	5.636	16	18	8	1	1	1	DAB2	34	in gene	ActReg chr5 #12988	0	1	0
12989	5	40,410,321	40,410,921	600	1	10.79	10.368	3.5	13	16	6	0	0	0				ActReg chr5 #12989	0	1	0
12990	5	40,518,482	40,518,994	512	1	10.438	13.25	2.688	19	24	5	0	0	0				ActReg chr5 #12990	0	1	0
12991	5	40,755,069	40,756,473	1,404	2	12.659	12.796	4.143	20	18	7	1	1	2	TTC33, PRKAA1	301, 42526	in gene, downstream	ActReg chr5 #12991	1	1	0
12992	5	40,834,950	40,836,080	1,130	3	10.143	12.943	15.514	23	20	31	1	4	4	LOC100506548, RPL37, SNORD72, CARD6	-4959, -128, -2678, -5895	upstream, upstream, upstream, upstream	ActReg chr5 #12992	1	1	1
12993	5	41,095,011	41,095,400	389	1	11.083	5.083	2.625	17	7	3	0	0	0				ActReg chr5 #12993	1	0	0
12994	5	41,870,106	41,870,918	812	1	13.808	9.231	6.692	21	13	13	1	1	1	OXCT1	279	in gene	ActReg chr5 #12994	1	0	0
12995	5	41,903,788	41,904,760	972	1	11.067	9.667	8.233	16	14	18	1	1	1	C5orf51	-196	upstream	ActReg chr5 #12995	1	0	0
12996	5	41,924,931	41,926,088	1,157	2	11.833	13.861	6.444	23	29	15	1	1	2	C5orf51, FBXO4	21039, 153	downstream, in gene	ActReg chr5 #12996	1	1	0
12997	5	42,423,452	42,423,923	441	1	7.214	11.786	8.071	10	16	13	1	1	1	GHR	-324	upstream	ActReg chr5 #12997	0	1	0
12998	5	42,531,604	42,532,206	602	1	5.842	9.421	1.462	9	16	2	0	0	1	GHR	107,879	in gene	ActReg chr5 #12998	0	1	0
12999	5	42,950,512	42,951,129	617	1	10.684	6.211	3.2	17	10	5	1	0	0				ActReg chr5 #12999	1	0	0
13000	5	42,982,147	42,982,500	353	1	5.364	9	1.889	9	15	3	0	0	1	FLJ32255	11,145	downstream	ActReg chr5 #13000	0	1	0
13001	5	42,991,892	42,992,714	822	2	11.308	11.615	6.192	17	22	12	1	1	1	FLJ32255	1,165	in gene	ActReg chr5 #13001	1	1	0
13002	5	43,017,846	43,018,851	1,005	2	16	11.844	7.161	31	30	18	1	1	1	LOC648987	565	in gene	ActReg chr5 #13002	1	1	0
13003	5	43,064,599	43,065,351	752	1	13.292	9.708	4.304	24	21	8	0	2	2	hCG_2039148, LOC100506639	2098, -2153	downstream, upstream	ActReg chr5 #13003	1	0	0
13004	5	43,105,312	43,106,132	820	2	13.192	12.269	5.192	30	22	10	0	0	0				ActReg chr5 #13004	1	1	0
13005	5	43,190,870	43,191,380	510	1	8.625	11.812	2.786	13	17	4	0	1	1	MGC42105	-1,202	upstream	ActReg chr5 #13005	0	1	0
13006	5	43,191,875	43,193,226	1,351	2	8.333	11.691	8.425	11	14	15	1	1	1	MGC42105	223	in gene	ActReg chr5 #13006	0	1	1
13007	5	43,193,629	43,194,088	459	1	8.133	10.867	1	12	15	1	0	1	1	MGC42105	1,531	in gene	ActReg chr5 #13007	0	1	0
13008	5	43,396,870	43,397,414	544	1	12.471	12.823	8.176	16	20	16	1	0	1	CCL28	15,346	in gene	ActReg chr5 #13008	0	1	0
13009	5	43,483,398	43,484,533	1,135	3	10.486	15.543	8.429	16	29	20	1	1	2	C5orf28, C5orf34	27, 31222	in gene, downstream	ActReg chr5 #13009	1	1	1
13010	5	43,556,247	43,557,564	1,317	3	15.878	20.366	4.973	52	61	13	1	1	1	PAIP1	616	in gene	ActReg chr5 #13010	1	1	0
13011	5	44,808,509	44,809,949	1,440	3	16.622	16.578	8.791	39	37	26	1	2	2	LOC100506674, MRPS30	-367, 202	upstream, in gene	ActReg chr5 #13011	1	1	1
13012	5	45,694,262	45,694,972	710	2	10.727	11.364	1	18	22	1	0	1	1	HCN1	1,603	in gene	ActReg chr5 #13012	1	1	0
13013	5	49,736,916	49,737,394	478	1	13	10	12.067	22	15	20	1	1	1	EMB	79	in gene	ActReg chr5 #13013	0	0	1
13014	5	50,678,643	50,679,541	898	1	9.429	12.571	7.821	14	18	14	1	2	2	LOC642366, ISL1	396, 134	in gene, in gene	ActReg chr5 #13014	0	1	0
13015	5	52,023,466	52,023,960	494	1	10.933	4.6	4.083	20	8	7	0	0	0				ActReg chr5 #13015	1	0	0
13016	5	52,053,748	52,054,323	575	2	9.333	11.278	1.3	15	16	3	0	0	0				ActReg chr5 #13016	1	1	0
13017	5	52,083,533	52,084,430	897	1	9.893	11.214	4.8	16	19	12	1	2	2	PELO, ITGA1	207, -155	in gene, upstream	ActReg chr5 #13017	0	1	0
13018	5	52,284,631	52,286,035	1,404	1	8.614	11.046	6.61	17	20	14	1	1	1	ITGA2	177	in gene	ActReg chr5 #13018	0	1	0
13019	5	52,319,642	52,320,097	455	1	12.267	7.733	4.444	20	9	6	0	0	1	ITGA2	34,713	in gene	ActReg chr5 #13019	1	0	0
13020	5	52,405,229	52,405,931	702	1	8.727	12.727	8.045	15	20	13	1	2	2	MOCS2, LOC257396	18, -107	in gene, upstream	ActReg chr5 #13020	0	1	0
13021	5	52,777,786	52,778,108	322	1	6.7	7.4	11.5	10	11	15	1	1	1	FST	1,352	in gene	ActReg chr5 #13021	0	0	1
13022	5	53,388,679	53,389,471	792	1	9.833	12.917	2.947	16	23	7	0	0	1	ARL15	217,328	in gene	ActReg chr5 #13022	0	1	0
13023	5	53,606,238	53,607,058	820	2	12.538	10.885	7.538	18	16	11	1	1	1	ARL15	-245	upstream	ActReg chr5 #13023	1	1	0
13024	5	53,813,028	53,813,867	839	2	16.962	16.269	2.55	37	42	5	1	1	1	SNX18	-142	upstream	ActReg chr5 #13024	1	1	0
13025	5	53,953,740	53,954,150	410	1	10.077	5.769	5.308	15	9	8	0	0	0				ActReg chr5 #13025	1	0	0
13026	5	53,998,827	53,999,781	954	1	7.5	11.033	4.267	13	23	9	0	0	0				ActReg chr5 #13026	0	1	0
13027	5	54,039,440	54,040,185	745	1	3.609	10.739	1.65	5	13	2	0	0	0				ActReg chr5 #13027	0	1	0
13028	5	54,280,964	54,281,663	699	1	11.857	9.286	4.842	18	13	10	0	1	1	ESM1	101	in gene	ActReg chr5 #13028	1	0	0
13029	5	54,522,424	54,523,189	765	1	10.167	11.625	13.75	15	17	26	1	1	2	LOC345643, CCNO	337, 6702	in gene, downstream	ActReg chr5 #13029	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13030	5	54,528,101	54,529,783	1,682	2	9.808	11.039	9.1	17	16	17	2	2	2	LOC345643, CCNO	-5799, 566	upstream, in gene	ActReg chr5 #13030	0	1	1
13031	5	54,603,075	54,604,083	1,008	1	12.097	8.806	7.7	20	15	15	1	2	2	DHX29, SKIV2L2	-58, 3	upstream, in gene	ActReg chr5 #13031	1	0	0
13032	5	54,829,965	54,831,174	1,209	2	11.895	11.974	7.568	22	18	12	1	1	1	PPAP2A	304	in gene	ActReg chr5 #13032	1	1	0
13033	5	55,068,811	55,069,212	401	1	11.417	7	4	17	10	7	0	0	1	DDX4	35,166	in gene	ActReg chr5 #13033	1	0	0
13034	5	55,290,649	55,291,410	761	2	10.875	10.667	7.682	17	15	13	1	2	2	IL6ST, FLJ31104	-208, 40	upstream, in gene	ActReg chr5 #13034	1	1	0
13035	5	55,408,278	55,408,837	559	1	8.611	10.111	3	13	15	8	0	0	1	ANKRD55	120,629	in gene	ActReg chr5 #13035	0	1	0
13036	5	55,419,394	55,420,159	765	1	12.087	7.87	2.13	21	13	4	0	0	1	ANKRD55	109,410	in gene	ActReg chr5 #13036	1	0	0
13037	5	55,479,163	55,480,377	1,214	1	10.526	10.263	3.763	17	15	6	0	0	1	ANKRD55	49,416	in gene	ActReg chr5 #13037	1	0	0
13038	5	55,744,770	55,745,827	1,057	1	11.515	12.273	3.848	21	27	8	0	0	0				ActReg chr5 #13038	0	1	0
13039	5	55,794,353	55,794,879	526	1	6.571	4.188	13.125	11	8	20	0	0	0				ActReg chr5 #13039	0	0	1
13040	5	56,006,956	56,007,559	603	1	10.158	11.947	1.273	17	19	2	0	0	0				ActReg chr5 #13040	0	1	0
13041	5	56,327,836	56,328,592	756	2	16.792	13	2	36	31	4	0	0	0				ActReg chr5 #13041	1	1	0
13042	5	56,605,140	56,605,471	331	1	5.3	2.9	12.6	6	4	16	0	0	0				ActReg chr5 #13042	0	0	1
13043	5	56,682,578	56,683,171	593	1	6.263	10.158	3.632	8	15	8	0	0	0				ActReg chr5 #13043	0	1	0
13044	5	56,744,531	56,745,136	605	1	6.211	10	2	8	17	2	0	0	0				ActReg chr5 #13044	0	1	0
13045	5	57,031,062	57,031,831	769	1	11.5	10.583	2.867	17	19	6	0	0	0				ActReg chr5 #13045	0	1	0
13046	5	57,389,721	57,390,413	692	1	7.591	11.136	4.824	15	16	6	0	0	0				ActReg chr5 #13046	0	1	0
13047	5	57,610,283	57,610,871	588	1	11.111	12.944	1.4	16	22	2	0	0	0				ActReg chr5 #13047	0	1	0
13048	5	57,755,442	57,757,091	1,649	4	10.673	11.654	10.192	19	22	20	1	2	2	PLK2, LOC100289379	-353, 500	upstream, in gene	ActReg chr5 #13048	1	1	1
13049	5	57,878,433	57,879,579	1,146	2	17.971	21.314	3.057	39	45	7	1	1	1	RAB3C	67	in gene	ActReg chr5 #13049	1	1	0
13050	5	58,334,996	58,335,589	593	2	10.316	9.947	12.474	13	14	17	1	1	2	PDE4D, LOC642781	1448633, 257	in gene, in gene	ActReg chr5 #13050	1	0	1
13051	5	58,423,281	58,423,900	619	2	12.158	10.579	1.857	18	17	3	0	0	1	PDE4D	1,360,335	in gene	ActReg chr5 #13051	1	1	0
13052	5	58,489,597	58,490,240	643	1	6.667	13.667	3.85	13	23	7	0	0	1	PDE4D	1,294,007	in gene	ActReg chr5 #13052	0	1	0
13053	5	58,594,889	58,595,339	450	1	10.143	4.857	1.429	15	7	3	0	0	1	PDE4D	1,188,811	in gene	ActReg chr5 #13053	1	0	0
13054	5	59,189,275	59,190,459	1,184	2	15.243	19.838	4.343	32	44	9	1	0	1	PDE4D	594,058	in gene	ActReg chr5 #13054	1	1	0
13055	5	59,388,339	59,389,071	732	1	7.043	11.739	1.957	15	20	3	0	0	1	PDE4D	395,220	in gene	ActReg chr5 #13055	0	1	0
13056	5	59,492,098	59,492,581	483	1	9.667	8.133	4.083	14	14	6	0	0	1	PDE4D	291,586	in gene	ActReg chr5 #13056	1	0	0
13057	5	59,628,482	59,628,986	504	1	10.4	8.467	2.077	16	13	4	0	0	1	PDE4D	155,191	in gene	ActReg chr5 #13057	1	0	0
13058	5	59,995,634	59,996,758	1,124	1	7.171	12.629	6.743	14	24	14	1	1	1	DEPDC1B	-203	upstream	ActReg chr5 #13058	0	1	0
13059	5	60,457,657	60,459,129	1,472	3	12.587	11.043	7	20	17	14	1	1	2	NDUFAF2, C5orf43	217437, -91	downstream, upstream	ActReg chr5 #13059	1	1	1
13060	5	60,623,918	60,624,355	437	1	8.071	11.143	1.833	12	17	3	0	1	1	ZSWIM6	-3,964	upstream	ActReg chr5 #13060	0	1	0
13061	5	60,626,754	60,627,624	870	2	11.482	14.815	6.714	20	22	10	1	1	1	ZSWIM6	-911	upstream	ActReg chr5 #13061	1	1	0
13062	5	60,627,633	60,628,168	535	2	17.765	17.353	4.882	34	35	9	1	1	1	ZSWIM6	-200	upstream	ActReg chr5 #13062	1	1	0
13063	5	60,922,054	60,922,397	343	1	1.375	2.9	10.6	2	4	13	1	0	0				ActReg chr5 #13063	0	0	1
13064	5	60,940,838	60,941,647	809	1	13.36	7.52	1.5	20	12	2	0	0	1	FLJ37543	7,606	in gene	ActReg chr5 #13064	1	0	0
13065	5	61,699,011	61,699,939	928	2	9.179	12.345	11.077	14	16	18	1	1	2	DIMT1L, IPO11	253, -9098	in gene, upstream	ActReg chr5 #13065	0	1	1
13066	5	61,708,308	61,709,063	755	1	10.833	13.583	7.667	19	28	13	1	1	2	DIMT1L, IPO11	-8957, 112	upstream, in gene	ActReg chr5 #13066	0	1	0
13067	5	63,258,852	63,259,404	552	2	10.177	12.882	1.111	18	23	2	0	1	1	HTR1A	-1,582	upstream	ActReg chr5 #13067	1	1	0
13068	5	63,445,651	63,446,128	477	1	2.9	5	12.8	5	6	17	0	0	0				ActReg chr5 #13068	0	0	1
13069	5	63,532,369	63,532,716	347	1	1.455	1.833	9.909	2	2	14	0	0	1	RNF180	70,871	in gene	ActReg chr5 #13069	0	0	1
13070	5	64,064,011	64,065,031	1,020	2	19.438	16.5	5.031	44	35	8	1	2	2	SFRS12IP1, CWC27	-25, -234	upstream, upstream	ActReg chr5 #13070	1	1	0
13071	5	64,494,350	64,494,872	522	1	9.562	5.688	3	15	9	5	0	0	1	ADAMTS6	283,093	in gene	ActReg chr5 #13071	1	0	0
13072	5	64,858,603	64,859,505	902	1	7.5	13.857	6.964	13	24	16	1	2	2	CENPK, PPWD1	-59, -77	upstream, upstream	ActReg chr5 #13072	0	1	0
13073	5	65,017,577	65,018,002	425	1	8.538	10.538	10.308	13	16	14	1	2	2	SGTB, NLN	152, -234	in gene, upstream	ActReg chr5 #13073	0	0	1
13074	5	65,220,823	65,221,163	340	1	11	8.273	11.909	14	11	16	1	1	1	ERBB2IP	-1,391	upstream	ActReg chr5 #13074	0	0	1
13075	5	65,439,619	65,440,807	1,188	2	8.892	12.73	5.27	14	19	10	1	1	1	SFRS12	128	in gene	ActReg chr5 #13075	1	1	0
13076	5	65,528,426	65,529,169	743	1	12.261	10.87	2.81	23	18	5	0	0	1	FLJ46010	36,680	in gene	ActReg chr5 #13076	1	0	0
13077	5	66,461,771	66,462,159	388	1	3.667	5	12	8	8	16	0	0	1	MAST4	569,789	in gene	ActReg chr5 #13077	0	0	1
13078	5	67,510,833	67,512,295	1,462	1	9.087	10.891	4.643	14	17	13	1	0	0				ActReg chr5 #13078	0	1	0
13079	5	67,640,139	67,640,736	597	1	8.263	11.105	3.105	12	15	5	0	0	0				ActReg chr5 #13079	0	1	0
13080	5	67,729,869	67,730,562	693	1	10.454	14.136	8.364	16	30	13	0	0	0				ActReg chr5 #13080	0	1	0
13081	5	67,850,688	67,851,401	713	1	8.043	13.13	1.692	15	30	2	0	0	0				ActReg chr5 #13081	0	1	0
13082	5	67,979,349	67,980,003	654	1	10.429	12.714	2.524	19	24	5	0	0	0				ActReg chr5 #13082	0	1	0
13083	5	68,194,983	68,195,899	916	1	6.393	9.071	2.043	12	14	4	0	0	0				ActReg chr5 #13083	0	1	0
13084	5	68,358,934	68,359,147	213	1	1.167	1.667	10.143	2	2	12	0	0	0				ActReg chr5 #13084	0	0	1
13085	5	68,462,526	68,463,451	925	1	9.241	13.621	9.586	15	24	15	1	1	1	CCNB1	75	in gene	ActReg chr5 #13085	0	1	0
13086	5	68,484,850	68,485,875	1,025	1	6.5	11.344	4.379	12	21	8	1	1	1	CENPH	-13	upstream	ActReg chr5 #13086	0	1	0
13087	5	68,513,555	68,514,045	490	1	9.667	10.867	12.533	14	16	17	1	1	2	CENPH, MRPS36	28425, 227	downstream, in gene	ActReg chr5 #13087	0	0	1
13088	5	68,628,363	68,629,065	702	2	5.773	11.546	9.636	9	15	18	1	0	0				ActReg chr5 #13088	0	1	1
13089	5	68,630,831	68,631,082	251	1	4.875	7.5	11	11	10	13	0	0	0				ActReg chr5 #13089	0	0	1
13090	5	68,665,063	68,666,186	1,123	4	9.743	12.429	10.686	21	23	16	1	2	2	TAF9, RAD17	216, 500	in gene, in gene	ActReg chr5 #13090	1	1	1
13091	5	68,745,845	68,746,449	604	1	10.737	7	2.25	19	10	3	0	0	1	MARVELD2	35,208	downstream	ActReg chr5 #13091	1	0	0
13092	5	70,751,121	70,752,055	934	3	10.448	9.621	6.966	18	17	17	1	1	2	LOC100505674, BDP1	-9419, 146	upstream, in gene	ActReg chr5 #13092	1	1	1
13093	5	71,014,642	71,015,936	1,294	2	12.537	16.415	5.692	25	28	9	1	1	1	CARTPT	299	in gene	ActReg chr5 #13093	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13094	5	71,228,676	71,229,199	523	1	10.875	7.875	4.812	16	11	7	0	0	0				ActReg chr5 #13094	1	0	0
13095	5	71,358,637	71,359,629	992	2	12.323	12.774	1.75	25	27	3	0	0	0				ActReg chr5 #13095	1	1	0
13096	5	71,363,159	71,363,946	787	1	9.8	14.28	3.091	20	26	5	0	0	0				ActReg chr5 #13096	0	1	0
13097	5	71,402,732	71,403,209	477	1	7.533	8.133	11.933	14	11	19	1	1	1	MAP1B	-148	upstream	ActReg chr5 #13097	0	0	1
13098	5	71,403,213	71,404,097	884	2	11.714	10.214	10.286	16	14	15	1	1	1	MAP1B	537	in gene	ActReg chr5 #13098	1	0	1
13099	5	71,603,767	71,604,712	945	3	10.667	13.033	7.533	21	22	17	1	1	2	MRPS27, LOC100130998	11845, -38	in gene, upstream	ActReg chr5 #13099	1	1	1
13100	5	71,756,053	71,757,014	961	1	4.5	7.333	11.833	11	12	16	1	0	1	ZNF366	46,716	in gene	ActReg chr5 #13100	0	0	1
13101	5	71,761,285	71,762,071	786	1	11.833	9.958	1.2	17	17	2	0	0	1	ZNF366	41,571	in gene	ActReg chr5 #13101	1	0	0
13102	5	72,111,834	72,112,274	440	1	3.857	11.714	5.429	10	14	10	1	1	1	TNPO1	-364	upstream	ActReg chr5 #13102	0	1	0
13103	5	72,143,617	72,144,452	835	2	13.039	15.808	7.333	30	34	16	1	0	1	TNPO1	31,616	in gene	ActReg chr5 #13103	1	1	0
13104	5	72,250,994	72,251,942	948	1	6.8	10.433	5.8	12	18	14	1	1	1	FCHO2	-340	upstream	ActReg chr5 #13104	0	1	0
13105	5	72,511,812	72,512,584	772	2	11.708	11.792	6.708	21	18	11	1	0	0				ActReg chr5 #13105	1	1	0
13106	5	72,526,134	72,526,529	395	1	2	3.385	9.769	3	6	15	1	0	0				ActReg chr5 #13106	0	0	1
13107	5	72,606,898	72,607,867	969	1	8.567	12.067	7.833	18	16	14	0	0	0				ActReg chr5 #13107	0	1	0
13108	5	72,744,736	72,745,036	300	1	8	4.8	11.5	10	7	14	0	1	1	FOXD1	-534	upstream	ActReg chr5 #13108	0	0	1
13109	5	72,793,809	72,794,948	1,139	3	11.111	12.306	10.333	20	22	26	1	1	1	BTF3	128	in gene	ActReg chr5 #13109	1	1	1
13110	5	72,860,936	72,861,420	484	1	7.8	11.533	7.8	13	15	10	1	2	2	ANKRA2, UTP15	333, -420	in gene, upstream	ActReg chr5 #13110	0	1	0
13111	5	73,313,487	73,314,348	861	1	9.222	14	2.926	14	23	5	0	0	0				ActReg chr5 #13111	0	1	0
13112	5	73,411,993	73,412,558	565	2	10.278	9.556	1.727	21	15	3	0	0	0				ActReg chr5 #13112	1	1	0
13113	5	73,496,977	73,497,700	723	1	10.174	13.565	2.95	14	25	5	0	0	0				ActReg chr5 #13113	0	1	0
13114	5	73,936,005	73,936,523	518	1	10.812	14.188	13.375	15	19	21	1	1	1	ENC1	985	in gene	ActReg chr5 #13114	0	0	1
13115	5	74,062,501	74,063,494	993	3	21	17.29	7.452	51	49	16	1	2	3	GFM2, NSA2, FAM169A	45, -106, 99618	in gene, upstream, downstream	ActReg chr5 #13115	1	1	1
13116	5	74,161,392	74,161,665	273	1	7.222	8.889	10.222	8	10	14	1	1	1	FAM169A	1,087	in gene	ActReg chr5 #13116	0	0	1
13117	5	74,632,294	74,633,125	831	1	8.231	12.615	8.077	16	18	13	1	1	1	HMGCR	-284	upstream	ActReg chr5 #13117	0	1	0
13118	5	74,806,479	74,808,123	1,644	2	10.294	10.882	7.941	20	23	15	1	2	2	COL4A3BP, POLK	505, -356	in gene, upstream	ActReg chr5 #13118	1	1	0
13119	5	74,959,309	74,960,157	848	1	10.192	7.692	4	17	15	6	0	0	2	ANKDD1B, C5orf37	52273, 53580	in gene, downstream	ActReg chr5 #13119	1	0	0
13120	5	75,012,901	75,013,452	551	2	11	11.529	7.647	17	20	11	1	1	1	C5orf37	137	in gene	ActReg chr5 #13120	1	1	0
13121	5	75,181,622	75,182,241	619	1	10.1	10.85	2.846	14	17	4	0	0	0				ActReg chr5 #13121	0	1	0
13122	5	75,337,437	75,338,167	730	1	5.909	10.087	2.647	10	16	4	0	0	0				ActReg chr5 #13122	0	1	0
13123	5	75,399,612	75,400,491	879	2	15.393	24.643	1.381	41	65	3	0	0	1	SV2C	20,746	in gene	ActReg chr5 #13123	1	1	0
13124	5	76,086,381	76,087,040	659	1	10.619	12.524	2.167	17	24	3	0	0	0				ActReg chr5 #13124	0	1	0
13125	5	76,134,611	76,135,194	583	1	9.056	10.722	2.833	15	20	5	0	0	1	F2RL1	20,069	downstream	ActReg chr5 #13125	0	1	0
13126	5	76,169,994	76,170,461	467	1	9.643	7.571	0	16	12	0	0	0	1	S100Z	24,401	in gene	ActReg chr5 #13126	1	0	0
13127	5	76,382,498	76,383,448	950	2	11.517	12.241	5.586	18	19	11	1	3	3	ZBED3, SNORA47, LOC728723	-57, -6577, 350	in gene, upstream, in gene	ActReg chr5 #13127	1	1	0
13128	5	76,428,971	76,429,471	500	1	10.733	8.533	0	14	13	0	0	0	1	LOC728723	46,598	in gene	ActReg chr5 #13128	1	0	0
13129	5	76,463,933	76,464,837	904	1	5.655	10.414	3.64	13	18	8	0	0	0				ActReg chr5 #13129	0	1	0
13130	5	76,787,612	76,788,605	993	2	11.258	11.548	5.68	17	15	11	1	1	1	WDR41	224	in gene	ActReg chr5 #13130	1	1	0
13131	5	76,932,331	76,932,903	572	1	3.944	6.556	11.611	6	8	14	1	1	1	OTP	1,905	in gene	ActReg chr5 #13131	0	0	1
13132	5	77,189,103	77,189,776	673	2	8.952	11.571	1	18	21	1	0	0	0				ActReg chr5 #13132	1	1	0
13133	5	77,590,321	77,590,998	677	1	11.619	9.333	3.952	16	17	7	1	1	1	AP3B1	-131	upstream	ActReg chr5 #13133	1	0	0
13134	5	77,655,340	77,656,868	1,528	2	14.083	16.646	6.5	24	29	13	1	2	2	LOC728769, SCAMP1	2630, -235	in gene, upstream	ActReg chr5 #13134	1	1	0
13135	5	77,881,811	77,882,608	797	2	11.4	10.72	3.524	18	15	6	0	0	1	LHFPL2	62,439	in gene	ActReg chr5 #13135	1	1	0
13136	5	77,892,997	77,893,631	634	1	10.895	5.526	1.812	18	10	5	0	0	1	LHFPL2	51,334	in gene	ActReg chr5 #13136	1	0	0
13137	5	77,943,155	77,943,716	561	1	9.222	6.278	2	16	10	4	1	1	1	LHFPL2	1,213	in gene	ActReg chr5 #13137	1	0	0
13138	5	77,995,227	77,996,146	919	1	14.69	10.207	2.524	31	16	5	0	0	0				ActReg chr5 #13138	1	0	0
13139	5	78,641,936	78,642,847	911	2	10.786	12.393	3	22	20	6	0	0	0				ActReg chr5 #13139	1	1	0
13140	5	78,809,483	78,810,727	1,244	2	12.128	11.897	5.974	25	20	14	1	1	1	HOMER1	-405	upstream	ActReg chr5 #13140	1	1	0
13141	5	78,908,218	78,908,677	459	1	11.467	7.267	3.4	18	12	5	1	1	1	PAPD4	204	in gene	ActReg chr5 #13141	1	0	0
13142	5	79,141,170	79,141,940	770	2	10.792	13.25	2.684	18	22	5	0	0	0				ActReg chr5 #13142	1	1	0
13143	5	79,252,033	79,252,777	744	1	10.087	12	3.13	16	20	6	0	0	0				ActReg chr5 #13143	0	1	0
13144	5	79,286,576	79,287,366	790	1	8.96	9.44	12.8	14	12	23	1	1	1	MTX3	117	in gene	ActReg chr5 #13144	0	0	1
13145	5	79,421,708	79,422,276	568	1	7.222	10.556	1	10	14	1	0	0	1	SERINC5	129,906	in gene	ActReg chr5 #13145	0	1	0
13146	5	79,695,253	79,695,772	519	1	11	7.562	1	16	12	1	0	0	1	ZFYVE16	-8,326	upstream	ActReg chr5 #13146	1	0	0
13147	5	79,865,645	79,866,168	523	1	7.812	3.562	13.5	14	7	16	1	1	1	ANKRD34B	398	in gene	ActReg chr5 #13147	0	0	1
13148	5	80,528,749	80,529,136	387	1	4.083	3.583	11	5	5	13	0	1	3	RASGRF2, CKMT2, LOC100131067	272384, -197, 68446	downstream, upstream, downstream	ActReg chr5 #13148	0	0	1
13149	5	80,596,894	80,597,884	990	2	13.161	13.613	7.839	23	28	15	1	2	2	LOC100131067, ZCCHC9	-1, -13	upstream, upstream	ActReg chr5 #13149	1	1	0
13150	5	80,715,920	80,716,376	456	1	3.357	9.5	1.615	5	15	3	0	0	1	SSBP2	330,924	in gene	ActReg chr5 #13150	0	1	0
13151	5	81,046,466	81,047,631	1,165	2	12.139	12.194	6.667	21	27	12	1	1	1	SSBP2	24	in gene	ActReg chr5 #13151	1	1	0
13152	5	81,147,450	81,148,031	581	2	11.5	11.389	7	20	20	13	0	0	0				ActReg chr5 #13152	1	1	0
13153	5	81,267,647	81,268,088	441	1	7.857	9.071	6.214	11	14	10	1	1	1	ATG10	23	in gene	ActReg chr5 #13153	0	1	0
13154	5	81,570,103	81,570,781	678	1	4.238	8.81	11.809	7	13	20	0	0	1	RPS23	3,793	in gene	ActReg chr5 #13154	0	0	1
13155	5	81,573,809	81,574,540	731	2	6.652	12.652	11.87	10	21	23	1	1	1	RPS23	61	in gene	ActReg chr5 #13155	0	1	1
13156	5	82,020,132	82,020,676	544	2	10.235	10.177	2	17	19	3	0	0	0				ActReg chr5 #13156	1	1	0
13157	5	82,248,047	82,248,536	489	1	7.6	10	2.467	13	14	4	0	0	0				ActReg chr5 #13157	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13158	5	82,633,054	82,633,823	769	1	6.625	11.667	1.077	16	16	2	0	0	1	XRCC4	260,121	in gene	ActReg chr5 #13158	0	1	0
13159	5	82,769,253	82,769,811	558	1	11.235	12.529	6.294	16	23	11	1	1	1	VCAN	2,039	in gene	ActReg chr5 #13159	0	1	0
13160	5	83,267,891	83,268,555	664	1	12.905	5.15	1.933	22	10	3	0	0	1	EDIL3	412,388	in gene	ActReg chr5 #13160	1	0	0
13161	5	83,804,805	83,805,194	389	1	8	10.333	2.333	10	15	3	0	0	0				ActReg chr5 #13161	0	1	0
13162	5	86,212,665	86,213,370	705	2	11.909	12.318	3.556	21	23	8	0	0	0				ActReg chr5 #13162	1	1	0
13163	5	86,563,188	86,563,765	577	3	10.667	10.278	11.278	22	19	24	0	1	1	RASA1	-675	upstream	ActReg chr5 #13163	1	1	1
13164	5	86,563,977	86,564,743	766	1	8.167	8.75	11.25	10	15	18	1	1	1	RASA1	209	in gene	ActReg chr5 #13164	0	0	1
13165	5	86,596,496	86,597,120	624	1	8.95	7.105	1	19	14	1	0	0	1	RASA1	32,657	in gene	ActReg chr5 #13165	1	0	0
13166	5	86,708,443	86,709,342	899	2	8.214	12.107	4.037	20	17	8	1	1	1	CCNH	-56	upstream	ActReg chr5 #13166	1	1	0
13167	5	87,195,558	87,196,119	561	1	9.824	7.471	2	15	11	3	0	0	0				ActReg chr5 #13167	1	0	0
13168	5	87,436,721	87,437,534	813	2	13.08	14.8	3.4	29	31	8	1	0	0				ActReg chr5 #13168	1	1	0
13169	5	87,748,665	87,749,124	459	1	6.733	9.6	3.467	11	16	7	0	0	0				ActReg chr5 #13169	0	1	0
13170	5	87,956,672	87,957,492	820	1	6.769	13.615	7.667	13	22	14	1	0	2	LOC645323, MIR9-2	23538, 5675	in gene, downstream	ActReg chr5 #13170	0	1	0
13171	5	87,970,078	87,972,159	2,081	4	10.892	12.231	7.6	22	18	16	1	1	2	LOC645323, MIR9-2	9502, -8361	in gene, upstream	ActReg chr5 #13171	1	1	1
13172	5	87,976,090	87,976,914	824	2	9.269	8.346	6.346	13	16	12	1	0	1	LOC645323	4,118	in gene	ActReg chr5 #13172	1	1	0
13173	5	88,080,476	88,081,195	719	2	11.609	9.478	1	21	17	1	0	0	1	MEF2C	119,087	in gene	ActReg chr5 #13173	1	1	0
13174	5	89,769,734	89,770,951	1,217	3	13.29	14.158	9.842	21	24	19	1	2	2	MBLAC2, POLR3G	243, -339	in gene, upstream	ActReg chr5 #13174	1	1	1
13175	5	89,824,953	89,825,564	611	1	7.737	8.895	12.842	15	14	20	1	1	1	LYSMD3	143	in gene	ActReg chr5 #13175	0	0	1
13176	5	89,842,982	89,843,546	564	2	9.588	8.375	2.571	15	14	5	0	0	0				ActReg chr5 #13176	1	1	0
13177	5	89,854,063	89,854,998	935	2	19.724	17.552	7.92	52	42	14	1	1	1	GPR98	-87	upstream	ActReg chr5 #13177	1	1	0
13178	5	90,575,692	90,576,883	1,191	1	8.676	11.973	5.892	17	17	12	1	1	1	LOC729040	672	in gene	ActReg chr5 #13178	0	1	0
13179	5	90,678,959	90,679,740	781	1	12.583	8.458	6.417	17	13	13	0	1	2	ARRDC3, LOC100129716	-200, 3185	upstream, in gene	ActReg chr5 #13179	1	0	0
13180	5	91,144,148	91,144,849	701	1	13.046	8.818	2.111	28	16	3	0	0	0				ActReg chr5 #13180	1	0	0
13181	5	91,714,568	91,715,321	753	1	7.522	12.522	4.667	9	19	6	0	0	0				ActReg chr5 #13181	0	1	0
13182	5	92,277,543	92,277,968	425	1	3.077	2.308	11.615	5	4	20	0	0	0				ActReg chr5 #13182	0	0	1
13183	5	92,304,824	92,305,379	555	1	4.471	9.222	2.25	8	15	4	0	0	0				ActReg chr5 #13183	0	1	0
13184	5	92,414,138	92,414,767	629	2	9	11.5	1.562	18	22	3	0	0	0				ActReg chr5 #13184	1	1	0
13185	5	92,527,605	92,528,329	724	1	12.739	7.478	2.25	19	11	4	0	0	0				ActReg chr5 #13185	1	0	0
13186	5	92,915,750	92,916,446	696	1	9.333	11.381	4.952	12	20	8	1	2	2	FLJ42709, NR2F1	905, -2945	in gene, upstream	ActReg chr5 #13186	0	1	0
13187	5	92,916,913	92,917,412	499	2	17.375	17.312	4.2	33	31	8	1	2	2	FLJ42709, NR2F1	-159, -1881	upstream, upstream	ActReg chr5 #13187	1	1	0
13188	5	92,947,502	92,948,349	847	1	7.577	13.769	2.8	12	24	5	0	0	2	FAM172A, MIR2277	499479, 8569	downstream, downstream	ActReg chr5 #13188	0	1	0
13189	5	92,948,361	92,948,785	424	1	5.231	9.615	1.231	6	14	2	0	0	2	FAM172A, MIR2277	498831, 7921	downstream, downstream	ActReg chr5 #13189	0	1	0
13190	5	92,956,043	92,956,984	941	1	7.429	13.276	4.667	15	25	9	1	1	2	FAM172A, MIR2277	490891, -19	in gene, upstream	ActReg chr5 #13190	0	1	0
13191	5	92,956,991	92,957,537	546	1	8.611	11.778	6.5	15	21	11	1	1	2	FAM172A, MIR2277	490140, -770	in gene, upstream	ActReg chr5 #13191	0	1	0
13192	5	93,356,992	93,357,509	517	1	11	11.118	1.667	17	16	3	0	0	1	FAM172A	90,154	in gene	ActReg chr5 #13192	0	1	0
13193	5	93,446,937	93,447,812	875	2	9.28	11.286	7.036	17	17	11	1	1	1	FAM172A	30	in gene	ActReg chr5 #13193	1	1	0
13194	5	93,954,008	93,954,978	970	3	10.161	8.774	8.839	16	14	18	1	2	2	C5orf36, ANKRD32	-184, 102	upstream, in gene	ActReg chr5 #13194	1	1	1
13195	5	94,128,973	94,129,472	499	1	8.938	5	1.4	15	7	2	0	0	1	MCTP1	491,057	in gene	ActReg chr5 #13195	1	0	0
13196	5	94,619,506	94,619,871	365	1	5.545	7	11.091	7	9	17	1	1	1	MCTP1	591	in gene	ActReg chr5 #13196	0	0	1
13197	5	94,753,680	94,754,181	501	1	9.125	3.375	2	16	6	2	0	0	1	FAM81B	26,882	in gene	ActReg chr5 #13197	1	0	0
13198	5	94,890,339	94,891,331	992	2	16.774	15.452	8.71	33	26	16	1	2	2	TTC37, ARSK	-126, 10	upstream, in gene	ActReg chr5 #13198	1	1	0
13199	5	94,982,299	94,982,741	442	1	8.286	9.643	11.929	9	15	20	1	1	1	RFESD	39	in gene	ActReg chr5 #13199	0	0	1
13200	5	95,047,895	95,048,482	587	1	6.579	11.158	2.917	12	17	5	0	0	0				ActReg chr5 #13200	0	1	0
13201	5	95,067,225	95,067,875	650	1	6.143	12.143	6.333	11	20	14	1	1	1	RHOBTB3	700	in gene	ActReg chr5 #13201	0	1	0
13202	5	95,194,308	95,195,036	728	1	7.591	10.864	4.263	11	18	7	0	0	1	C5orf27	6,736	in gene	ActReg chr5 #13202	0	1	0
13203	5	95,719,848	95,720,518	670	1	7.714	11.762	2.421	10	19	5	0	0	1	PCSK1	48,802	downstream	ActReg chr5 #13203	0	1	0
13204	5	95,766,996	95,769,273	2,277	2	13.634	14.324	4.141	30	27	11	1	1	1	PCSK1	851	in gene	ActReg chr5 #13204	1	1	0
13205	5	95,769,527	95,770,510	983	2	18.645	24.452	2.933	46	62	6	0	1	1	PCSK1	-1,033	upstream	ActReg chr5 #13205	1	1	0
13206	5	95,819,358	95,820,191	833	2	9.115	17.615	1	20	40	1	0	0	0				ActReg chr5 #13206	1	1	0
13207	5	95,908,443	95,909,183	740	1	12.652	9.174	3.294	20	15	5	0	0	0				ActReg chr5 #13207	1	0	0
13208	5	95,997,438	95,998,169	731	1	10.348	12.478	5.19	16	20	11	1	1	1	CAST	62	in gene	ActReg chr5 #13208	0	1	0
13209	5	95,998,340	95,999,147	807	1	7.92	12.48	6.2	13	17	9	1	1	1	CAST	1,002	in gene	ActReg chr5 #13209	0	1	0
13210	5	96,038,120	96,038,715	595	1	11.556	12.556	4.611	17	17	8	1	0	1	CAST	40,676	in gene	ActReg chr5 #13210	1	0	0
13211	5	96,142,905	96,143,798	893	2	10.143	13.893	5.731	15	28	15	1	1	1	ERAP1	541	in gene	ActReg chr5 #13211	1	1	0
13212	5	96,270,376	96,272,075	1,699	2	18.358	16.226	7.208	38	30	12	1	1	1	LNPEP	-121	upstream	ActReg chr5 #13212	1	1	0
13213	5	96,518,657	96,519,542	885	2	12.815	11.185	4.375	17	17	9	1	1	1	RIOK2	-94	upstream	ActReg chr5 #13213	1	1	0
13214	5	96,636,813	96,637,085	272	1	1	1.75	10.875	1	2	13	0	0	0				ActReg chr5 #13214	0	0	1
13215	5	98,108,833	98,110,112	1,279	1	10.8	11.05	6.378	16	16	15	1	1	2	RGMB, FLJ35946	4473, -684	in gene, upstream	ActReg chr5 #13215	0	1	0
13216	5	98,264,220	98,265,600	1,380	2	10.227	10.75	8.167	17	20	15	1	2	2	CHD1, LOC100289230	-2672, 72	upstream, in gene	ActReg chr5 #13216	1	1	0
13217	5	98,652,760	98,653,361	601	1	7.158	10.053	1	11	18	1	0	0	0				ActReg chr5 #13217	0	1	0
13218	5	100,176,022	100,176,505	483	1	3.714	9.867	0	5	16	0	0	0	1	ST8SIA4	62,724	in gene	ActReg chr5 #13218	0	1	0
13219	5	100,236,007	100,237,006	999	1	5.655	11.839	4.345	10	22	10	1	1	1	ST8SIA4	2,481	in gene	ActReg chr5 #13219	0	1	0
13220	5	101,631,392	101,632,618	1,226	3	10.333	11.974	14.205	27	23	28	1	1	1	SLCO4C1	248	in gene	ActReg chr5 #13220	1	1	1
13221	5	102,170,099	102,170,746	647	1	4.1	10.75	1.647	7	18	3	0	0	0				ActReg chr5 #13221	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13222	5	102,201,414	102,202,198	784	1	10.708	8.083	6.217	16	15	12	1	1	1	PAM	279	in gene	ActReg chr5 #13222	1	0	0
13223	5	102,455,355	102,456,552	1,197	2	10.895	13.132	5.917	28	30	11	1	1	2	GIN1, PPIP5K2	-111, -9304	upstream, upstream	ActReg chr5 #13223	1	1	0
13224	5	102,898,056	102,898,514	458	1	7.857	11.286	4.571	10	18	8	0	1	1	NUDT12	205	in gene	ActReg chr5 #13224	0	1	0
13225	5	103,425,006	103,425,622	616	2	9.667	10.474	1.929	17	17	3	0	0	0				ActReg chr5 #13225	1	1	0
13226	5	103,680,756	103,681,239	483	1	4.533	10.6	2	7	14	3	0	0	0				ActReg chr5 #13226	0	1	0
13227	5	104,482,621	104,482,982	361	1	9.167	10.25	0	12	15	0	0	0	0				ActReg chr5 #13227	0	1	0
13228	5	106,724,745	106,725,320	575	1	7.944	9.278	2	13	17	4	0	0	1	EFNA5	281,564	in gene	ActReg chr5 #13228	0	1	0
13229	5	106,804,984	106,805,577	593	1	10.053	12.526	2.062	16	23	4	0	0	1	EFNA5	201,316	in gene	ActReg chr5 #13229	0	1	0
13230	5	107,006,825	107,007,286	461	1	7.786	11.643	3.571	12	14	6	1	1	1	EFNA5	-459	upstream	ActReg chr5 #13230	0	1	0
13231	5	107,007,650	107,008,316	666	1	6.2	12	4.071	9	23	7	1	1	1	EFNA5	-1,387	upstream	ActReg chr5 #13231	0	1	0
13232	5	107,008,330	107,008,818	488	1	10.133	8.933	4.308	17	14	7	1	1	1	EFNA5	-1,978	upstream	ActReg chr5 #13232	1	0	0
13233	5	107,009,049	107,009,396	347	1	4.273	6.182	10.364	6	9	14	0	1	1	EFNA5	-2,626	upstream	ActReg chr5 #13233	0	0	1
13234	5	107,054,787	107,055,320	533	1	3.5	4.125	12.125	6	8	17	0	0	0				ActReg chr5 #13234	0	0	1
13235	5	107,155,860	107,156,622	762	2	12.208	10.917	2.077	16	16	3	0	0	0				ActReg chr5 #13235	1	1	0
13236	5	107,717,191	107,717,860	669	2	9.524	10.333	11.571	13	15	19	1	1	1	FBXL17	274	in gene	ActReg chr5 #13236	0	1	1
13237	5	108,063,499	108,064,326	827	3	11.731	13.308	10.654	20	23	17	1	0	0				ActReg chr5 #13237	1	1	1
13238	5	108,084,112	108,084,649	537	1	9	5.882	12.412	15	10	23	1	1	1	FER	857	in gene	ActReg chr5 #13238	0	0	1
13239	5	109,026,251	109,026,624	373	1	6.5	4.667	10.333	9	6	15	1	1	1	MAN2A1	1,281	in gene	ActReg chr5 #13239	0	0	1
13240	5	110,074,076	110,075,154	1,078	1	7.706	11.529	8.088	15	16	17	1	1	1	SLC25A46	-139	upstream	ActReg chr5 #13240	0	1	0
13241	5	110,427,659	110,428,366	707	2	12.864	16.046	6.789	21	31	11	1	1	1	WDR36	142	in gene	ActReg chr5 #13241	1	1	0
13242	5	110,559,327	110,560,217	890	2	8.857	10.464	9.464	13	14	17	1	1	1	CAMK4	-310	upstream	ActReg chr5 #13242	0	1	1
13243	5	110,634,675	110,635,100	425	1	2.923	3.75	12.154	4	6	17	0	0	1	CAMK4	74,805	in gene	ActReg chr5 #13243	0	0	1
13244	5	110,700,461	110,701,535	1,074	2	11.788	19.576	2.125	21	42	3	0	0	1	CAMK4	140,916	in gene	ActReg chr5 #13244	1	1	0
13245	5	110,702,585	110,703,275	690	2	11.454	8.955	1.6	21	15	2	0	0	1	CAMK4	142,848	in gene	ActReg chr5 #13245	1	1	0
13246	5	110,719,337	110,719,805	468	1	7.714	10.429	3.308	12	15	4	0	0	1	CAMK4	159,489	in gene	ActReg chr5 #13246	0	1	0
13247	5	110,847,374	110,848,561	1,187	1	11.405	7.027	3.382	17	11	6	1	2	2	STARD4, LOC100505678	190, 43	in gene, in gene	ActReg chr5 #13247	1	0	0
13248	5	111,495,965	111,497,069	1,104	2	34.143	36.371	7.314	113	126	16	1	2	3	NCRNA00219, SNORA13, EPB41L4A	294, -665, 258493	in gene, upstream, downstream	ActReg chr5 #13248	1	1	0
13249	5	111,755,888	111,756,276	388	1	9.833	12.25	12.167	13	18	20	1	2	2	EPB41L4A, FLJ11235	-1072, 802	upstream, in gene	ActReg chr5 #13249	0	0	1
13250	5	111,884,193	111,884,696	503	1	11.133	5.067	1	21	9	1	0	0	0				ActReg chr5 #13250	1	0	0
13251	5	112,042,709	112,043,750	1,041	1	10.939	13.273	8.179	17	20	14	1	1	1	APC	11	in gene	ActReg chr5 #13251	0	1	0
13252	5	112,257,339	112,258,017	678	1	8.455	12.546	6.762	13	18	12	1	1	1	REEP5	353	in gene	ActReg chr5 #13252	0	1	0
13253	5	112,311,913	112,312,934	1,021	2	11.312	11.531	8.719	20	19	14	1	1	2	LOC100287967, DCP2	15515, -10	in gene, upstream	ActReg chr5 #13253	1	1	0
13254	5	112,410,709	112,411,036	327	1	5	2.444	12	6	5	17	0	0	1	MCC	413,655	in gene	ActReg chr5 #13254	0	0	1
13255	5	112,538,766	112,539,561	795	1	11.52	10.84	4.208	16	19	8	0	0	1	MCC	285,364	in gene	ActReg chr5 #13255	1	0	0
13256	5	112,771,366	112,771,868	502	1	4.933	4.267	11	8	8	16	0	1	2	MCC, TSSK1B	52910, -889	in gene, upstream	ActReg chr5 #13256	0	0	1
13257	5	112,823,376	112,824,531	1,155	3	8.694	10.333	9.278	17	18	19	1	1	1	MCC	574	in gene	ActReg chr5 #13257	1	1	1
13258	5	112,849,239	112,849,980	741	1	12.478	9.522	8.174	20	11	16	1	1	1	YTHDC2	218	in gene	ActReg chr5 #13258	1	0	0
13259	5	112,952,911	112,953,410	499	1	3.875	3.5	12.562	7	5	19	0	0	0				ActReg chr5 #13259	0	0	1
13260	5	113,088,895	113,089,244	349	1	1	2.818	8.909	1	4	12	0	0	0				ActReg chr5 #13260	0	0	1
13261	5	113,696,972	113,697,517	545	1	2.529	2.188	11.882	4	3	19	1	1	1	KCNN2	-772	upstream	ActReg chr5 #13261	0	0	1
13262	5	114,334,884	114,335,183	299	1	2.667	2	10.556	3	3	14	0	0	0				ActReg chr5 #13262	0	0	1
13263	5	114,598,198	114,598,909	711	1	9.864	11.864	10.091	14	18	15	1	1	2	PGGT1B, CCDC112	16, 33905	in gene, downstream	ActReg chr5 #13263	0	1	0
13264	5	114,790,873	114,791,803	930	2	13.241	16.724	3.655	23	33	7	0	0	0				ActReg chr5 #13264	1	1	0
13265	5	114,961,334	114,962,129	795	2	6.76	11.08	10.12	11	14	16	1	2	3	TMED7-TICAM2, LOC100505719, TMED7	145, 23889, 145	in gene, downstream, in gene	ActReg chr5 #13265	0	1	1
13266	5	115,177,022	115,177,762	740	2	11.583	14.917	5.667	28	30	8	1	2	2	ATG12, AP3S1	156, -227	in gene, upstream	ActReg chr5 #13266	1	1	0
13267	5	115,910,303	115,911,033	730	1	11.174	15.348	4.739	22	28	10	1	1	1	SEMA6A	-117	upstream	ActReg chr5 #13267	0	1	0
13268	5	116,407,945	116,408,273	328	1	4.5	4.2	10	7	6	14	0	0	0				ActReg chr5 #13268	0	0	1
13269	5	117,543,794	117,544,189	395	1	3.333	2.333	12.25	5	5	17	0	0	0				ActReg chr5 #13269	0	0	1
13270	5	117,658,163	117,658,456	293	1	4.111	2.6	9.778	6	4	12	0	0	0				ActReg chr5 #13270	0	0	1
13271	5	118,323,594	118,324,527	933	2	10.586	12.931	4.08	19	23	11	1	1	1	DTWD2	180	in gene	ActReg chr5 #13271	1	1	0
13272	5	118,603,885	118,604,416	531	1	12.059	8.294	9.412	19	11	15	1	1	1	TNFAIP8	-268	upstream	ActReg chr5 #13272	1	0	0
13273	5	118,787,991	118,788,666	675	1	8.81	9.095	14.905	16	17	27	1	1	1	HSD17B4	180	in gene	ActReg chr5 #13273	0	0	1
13274	5	119,495,664	119,496,329	665	1	10.381	6.048	2.048	22	11	4	0	0	0				ActReg chr5 #13274	1	0	0
13275	5	120,443,028	120,443,290	262	1	4.625	5.75	10.875	7	7	14	0	0	0				ActReg chr5 #13275	0	0	1
13276	5	121,297,341	121,298,035	694	2	12.046	10.591	5.75	26	18	10	1	1	1	SRFBP1	52	in gene	ActReg chr5 #13276	1	1	0
13277	5	121,602,774	121,603,290	516	1	6.438	10.188	5.062	10	15	8	0	0	0				ActReg chr5 #13277	0	1	0
13278	5	121,686,282	121,686,705	423	1	9.769	7.385	1.333	16	13	2	0	0	1	SNCAIP	38,673	in gene	ActReg chr5 #13278	1	0	0
13279	5	122,110,837	122,111,184	347	1	9.727	11.454	11	14	15	16	1	1	1	SNX2	260	in gene	ActReg chr5 #13279	0	0	1
13280	5	122,372,089	122,373,091	1,002	1	11.625	9.062	8.419	18	18	16	1	1	1	PPIC	-165	upstream	ActReg chr5 #13280	1	0	0
13281	5	122,544,897	122,545,823	926	1	12.929	8.821	4.042	23	14	6	0	0	0				ActReg chr5 #13281	1	0	0
13282	5	122,758,608	122,759,787	1,179	2	23.757	24.486	6.267	78	74	14	1	1	1	CEP120	89	in gene	ActReg chr5 #13282	1	1	0
13283	5	122,847,249	122,848,212	963	1	9.6	11.433	6.652	14	15	10	1	1	1	CSNK1G3	-63	upstream	ActReg chr5 #13283	0	1	0
13284	5	123,043,721	123,044,215	494	1	9.6	8.533	4	16	14	6	0	0	0				ActReg chr5 #13284	1	0	0
13285	5	123,088,216	123,088,682	466	1	10.467	8.6	5.267	14	13	9	0	0	0				ActReg chr5 #13285	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13286	5	123,284,759	123,285,374	615	1	4.842	5.737	12.158	7	9	18	0	0	0				ActReg chr5 #13286	0	0	1
13287	5	123,857,339	123,857,660	321	1	1.6	2	9.1	3	3	11	0	0	0				ActReg chr5 #13287	0	0	1
13288	5	123,882,208	123,882,884	676	2	11.909	11.682	2	26	26	3	0	0	0				ActReg chr5 #13288	1	1	0
13289	5	123,987,284	123,987,971	687	1	6.636	13	5.591	13	25	12	1	0	1	ZNF608	93,178	in gene	ActReg chr5 #13289	0	1	0
13290	5	123,996,964	123,997,708	744	1	10.696	5.522	1.6	14	9	3	0	0	1	ZNF608	83,469	in gene	ActReg chr5 #13290	1	0	0
13291	5	124,079,802	124,080,189	387	1	5.75	11.417	9.583	7	14	13	0	1	1	ZNF608	810	in gene	ActReg chr5 #13291	0	0	1
13292	5	124,125,553	124,127,060	1,507	1	7.872	11.255	2.487	16	20	7	0	0	0				ActReg chr5 #13292	0	1	0
13293	5	124,396,223	124,397,053	830	2	13.577	13.077	1.308	28	21	2	0	0	0				ActReg chr5 #13293	1	1	0
13294	5	124,470,302	124,470,688	386	1	7.692	10.692	1	9	16	1	0	0	0				ActReg chr5 #13294	0	1	0
13295	5	125,789,598	125,790,218	620	1	10	5.9	3.5	16	13	6	0	0	1	GRAMD3	94,120	in gene	ActReg chr5 #13295	1	0	0
13296	5	125,930,486	125,931,404	918	2	11.931	14.414	5.276	28	23	11	1	2	2	ALDH7A1, PHAX	137, -5662	in gene, upstream	ActReg chr5 #13296	1	1	0
13297	5	125,936,136	125,937,296	1,160	2	29.389	32.611	4.111	84	89	9	1	2	2	ALDH7A1, PHAX	-5634, 109	upstream, in gene	ActReg chr5 #13297	1	1	0
13298	5	126,112,052	126,112,826	774	2	12.333	10.875	5.375	21	21	9	1	1	1	LMNB1	-384	upstream	ActReg chr5 #13298	1	1	0
13299	5	126,113,183	126,114,677	1,494	1	6.511	11.511	4.872	12	16	12	1	1	1	LMNB1	1,097	in gene	ActReg chr5 #13299	0	1	0
13300	5	126,365,226	126,366,748	1,522	1	8.106	11.553	6.085	19	15	17	1	1	1	3-Mar	453	in gene	ActReg chr5 #13300	0	1	0
13301	5	127,292,925	127,293,342	417	1	10.077	10.769	3.308	15	20	4	0	0	0				ActReg chr5 #13301	0	1	0
13302	5	127,418,349	127,419,348	999	3	11.742	12.419	10.452	20	20	20	1	2	2	FLJ33630, SLC12A2	-82, -635	upstream, upstream	ActReg chr5 #13302	1	1	1
13303	5	127,420,224	127,420,600	376	1	10.333	10.5	11.583	15	14	17	1	2	2	FLJ33630, SLC12A2	-1646, 929	upstream, in gene	ActReg chr5 #13303	0	0	1
13304	5	128,005,415	128,005,842	427	1	10.769	6.154	1.25	15	8	2	0	0	0				ActReg chr5 #13304	1	0	0
13305	5	129,239,595	129,239,859	264	1	5.25	4.875	10.625	7	6	12	1	1	1	CHSY3	-796	upstream	ActReg chr5 #13305	0	0	1
13306	5	130,915,588	130,915,988	400	1	3.833	7.167	12.667	7	13	18	0	0	1	RAPGEF6	55,141	in gene	ActReg chr5 #13306	0	0	1
13307	5	130,970,306	130,971,309	1,003	2	9.129	13.806	8.484	19	23	22	1	1	2	RAPGEF6, FNIP1	122, 161949	in gene, downstream	ActReg chr5 #13307	0	1	1
13308	5	131,132,279	131,133,095	816	2	10.577	12.231	11.077	13	18	14	1	1	2	FNIP1, LOC100505572	69, 59934	in gene, downstream	ActReg chr5 #13308	0	1	1
13309	5	131,347,773	131,348,898	1,125	2	10.229	17.389	6.917	19	31	9	1	1	1	ACSL6	-986	upstream	ActReg chr5 #13309	1	1	0
13310	5	131,391,872	131,392,317	445	1	5.571	3.083	10.643	9	5	18	0	1	1	IL3	-4,253	upstream	ActReg chr5 #13310	0	0	1
13311	5	131,425,531	131,426,368	837	1	5.296	12.185	3.333	10	19	6	0	0	0				ActReg chr5 #13311	0	1	0
13312	5	131,438,472	131,439,227	755	1	5.739	11.348	4.783	9	16	9	0	0	0				ActReg chr5 #13312	0	1	0
13313	5	131,628,954	131,630,277	1,323	2	11.738	9.857	14.786	15	16	27	1	1	1	SLC22A4	-530	upstream	ActReg chr5 #13313	1	0	1
13314	5	131,725,162	131,726,182	1,020	2	11.062	11.531	4.29	16	20	9	0	0	1	SLC22A5	20,271	in gene	ActReg chr5 #13314	1	1	0
13315	5	131,825,579	131,827,110	1,531	3	9.479	12.167	8.957	20	20	18	1	1	1	IRF1	121	in gene	ActReg chr5 #13315	1	1	1
13316	5	131,832,104	131,832,807	703	1	7.591	11.954	8.136	12	18	13	1	1	1	IRF1	-5,990	upstream	ActReg chr5 #13316	0	1	0
13317	5	131,892,276	131,893,067	791	2	11.08	12.28	9.96	19	20	20	1	1	1	RAD50	55	in gene	ActReg chr5 #13317	0	1	1
13318	5	132,072,567	132,073,510	943	1	6.9	9.933	6.586	12	16	14	1	1	2	KIF3A, CCNI2	227, -10099	in gene, upstream	ActReg chr5 #13318	0	1	0
13319	5	132,201,980	132,202,855	875	2	13.143	13.179	7.964	19	20	14	1	3	4	GDF9, UQCRQ, LEAP2, AFF4	-1940, 98, -6941, 96937	upstream, in gene, upstream, downstream	ActReg chr5 #13319	1	1	0
13320	5	132,298,920	132,299,832	912	3	12.679	11.643	9.679	20	19	16	1	2	2	AFF4, LOC100506073	-22, -2098	upstream, upstream	ActReg chr5 #13320	1	1	1
13321	5	132,387,349	132,388,337	988	1	10.226	10.548	11.968	16	16	17	1	1	1	HSPA4	181	in gene	ActReg chr5 #13321	0	0	1
13322	5	132,576,044	132,576,692	648	1	11.35	13.55	5.35	20	27	8	0	0	1	FSTL4	371,855	in gene	ActReg chr5 #13322	0	1	0
13323	5	132,580,836	132,581,724	888	2	11.704	11.518	2.63	30	21	5	0	0	1	FSTL4	366,943	in gene	ActReg chr5 #13323	1	1	0
13324	5	132,582,959	132,583,676	717	1	11.046	6.182	3.412	13	10	7	0	0	1	FSTL4	364,906	in gene	ActReg chr5 #13324	1	0	0
13325	5	132,631,045	132,631,870	825	2	12.64	14.88	1.565	28	30	3	0	0	1	FSTL4	316,766	in gene	ActReg chr5 #13325	1	1	0
13326	5	132,901,585	132,902,218	633	2	9.35	11.6	2.167	16	20	3	0	0	1	FSTL4	46,322	in gene	ActReg chr5 #13326	1	1	0
13327	5	133,166,691	133,167,403	712	1	6.909	11.364	2	11	14	3	0	0	0				ActReg chr5 #13327	0	1	0
13328	5	133,339,572	133,340,264	692	1	7.545	13.136	3.5	11	19	6	1	1	1	VDAC1	515	in gene	ActReg chr5 #13328	0	1	0
13329	5	133,340,466	133,341,237	771	2	12.292	10	10.208	20	16	22	1	1	1	VDAC1	-418	upstream	ActReg chr5 #13329	1	0	1
13330	5	133,394,425	133,395,390	965	1	10.833	8.3	8	18	15	13	0	0	0				ActReg chr5 #13330	1	0	0
13331	5	133,512,226	133,513,016	790	3	12.522	14.833	11.667	20	26	17	1	1	1	SKP1	103	in gene	ActReg chr5 #13331	1	1	1
13332	5	133,561,435	133,562,540	1,105	2	10.057	9.714	7.114	19	20	13	1	1	1	PPP2CA	-37	upstream	ActReg chr5 #13332	1	1	0
13333	5	133,706,475	133,707,642	1,167	3	11.389	12	8.611	22	24	15	1	2	2	CDKL3, UBE2B	-4293, 188	upstream, in gene	ActReg chr5 #13333	1	1	1
13334	5	133,747,151	133,748,189	1,038	2	20.438	23.688	5.688	52	61	11	1	1	2	LOC100506132, CDKN2AIPNL	16239, -72	downstream, upstream	ActReg chr5 #13334	1	1	0
13335	5	133,877,198	133,877,743	545	1	7.133	12.412	3.077	12	21	6	0	0	1	PHF15	15,672	in gene	ActReg chr5 #13335	0	1	0
13336	5	134,073,767	134,075,006	1,239	2	13.895	11.21	7.605	24	29	15	1	1	1	CAMLG	180	in gene	ActReg chr5 #13336	1	1	0
13337	5	134,093,906	134,095,094	1,188	2	40.649	41.73	8.811	139	132	18	1	1	2	CAMLG, DDX46	20294, 39	downstream, in gene	ActReg chr5 #13337	1	1	0
13338	5	134,181,286	134,182,174	888	1	8.111	14.037	8.111	13	24	13	1	1	1	C5orf24	360	in gene	ActReg chr5 #13338	0	1	0
13339	5	134,210,570	134,211,353	783	1	11.125	10.417	5.833	18	14	9	1	1	1	TXNDC15	1,501	in gene	ActReg chr5 #13339	1	0	0
13340	5	134,240,191	134,240,857	666	2	9.905	10.952	3.353	15	17	6	1	1	2	TXNDC15, PCBD2	31064, -286	downstream, upstream	ActReg chr5 #13340	1	1	0
13341	5	134,362,982	134,363,897	915	1	2.679	2.72	12.071	4	8	20	1	0	1	PITX1	6,525	in gene	ActReg chr5 #13341	0	0	1
13342	5	134,364,489	134,365,075	586	1	5.278	3.312	13.222	7	8	20	1	0	1	PITX1	5,182	in gene	ActReg chr5 #13342	0	0	1
13343	5	134,366,740	134,367,196	456	1	3.643	6.071	12.429	6	9	18	1	0	1	PITX1	2,996	in gene	ActReg chr5 #13343	0	0	1
13344	5	134,374,917	134,375,202	285	1	6.111	7.111	12.778	8	9	17	1	1	1	PITX1	-5,095	upstream	ActReg chr5 #13344	0	0	1
13345	5	134,527,028	134,527,441	413	1	7.769	10.077	10.692	11	12	16	1	0	0				ActReg chr5 #13345	0	0	1
13346	5	134,543,576	134,545,055	1,479	1	8.978	11.696	3.848	16	21	7	0	0	0				ActReg chr5 #13346	0	1	0
13347	5	134,734,687	134,735,408	721	1	7.174	11.478	2.7	12	19	5	1	1	1	H2AFY	530	in gene	ActReg chr5 #13347	0	1	0
13348	5	134,871,302	134,871,852	550	1	2.588	3.235	11.941	4	6	19	1	1	1	NEUROG1	62	in gene	ActReg chr5 #13348	0	0	1
13349	5	134,914,046	134,914,745	699	1	5.409	2.8	12.364	8	5	18	1	1	1	CXCL14	574	in gene	ActReg chr5 #13349	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13350	5	135,355,982	135,356,994	1,012	2	10.188	9.75	2.5	16	20	6	0	0	1	TGFBI	-8,096	upstream	ActReg chr5 #13350	1	1	0
13351	5	135,389,187	135,389,852	665	2	12.4	12.5	3.263	20	20	7	0	0	1	TGFBI	24,935	in gene	ActReg chr5 #13351	1	1	0
13352	5	135,468,113	135,469,055	942	2	11.138	11.552	4.483	24	17	9	1	2	2	SMAD5OS, SMAD5	1995, 48	in gene, in gene	ActReg chr5 #13352	1	1	0
13353	5	135,700,658	135,701,494	836	2	15.615	17.154	1.611	35	43	3	0	1	1	TRPC7	88	in gene	ActReg chr5 #13353	1	1	0
13354	5	136,478,232	136,478,985	753	1	12.417	7.042	6.792	20	10	12	0	0	1	SPOCK1	556,410	in gene	ActReg chr5 #13354	1	0	0
13355	5	136,788,936	136,789,806	870	2	14.518	16.963	2.963	32	37	5	0	0	1	SPOCK1	45,647	in gene	ActReg chr5 #13355	1	1	0
13356	5	136,805,977	136,806,998	1,021	2	14.75	17.656	2.04	24	36	4	0	0	1	SPOCK1	28,531	in gene	ActReg chr5 #13356	1	1	0
13357	5	137,089,614	137,090,444	830	2	11.231	13.923	10.731	16	23	21	1	1	1	HNRNPA0	10	in gene	ActReg chr5 #13357	0	1	1
13358	5	137,367,997	137,368,592	595	1	5.789	11.632	9.316	10	17	14	1	2	2	FAM13B, LOC100130172	508, -188	in gene, upstream	ActReg chr5 #13358	0	1	0
13359	5	137,667,220	137,667,732	512	1	11.5	10.688	8.438	21	13	12	1	2	2	CDC25C, FAM53C	40, -5748	in gene, upstream	ActReg chr5 #13359	1	0	0
13360	5	137,672,947	137,674,322	1,375	3	44.256	55.465	10	121	164	30	1	2	2	CDC25C, FAM53C	-6118, 410	upstream, in gene	ActReg chr5 #13360	1	1	1
13361	5	137,687,808	137,689,544	1,736	3	12.527	10.546	4.615	32	31	12	1	1	2	FAM53C, KDM3B	15452, 391	downstream, in gene	ActReg chr5 #13361	1	1	0
13362	5	137,780,729	137,781,255	526	1	2.5	4.471	11.647	3	7	16	0	0	2	KDM3B, REEP2	92707, 6216	downstream, in gene	ActReg chr5 #13362	0	0	1
13363	5	137,800,077	137,801,466	1,389	3	17.209	20.093	12.907	36	43	30	1	1	1	EGR1	-410	upstream	ActReg chr5 #13363	1	1	1
13364	5	137,827,463	137,828,032	569	1	13.056	10	4.056	20	15	11	1	0	0				ActReg chr5 #13364	1	0	0
13365	5	137,878,201	137,879,625	1,424	3	11.044	14.644	9.467	18	26	25	1	1	1	ETF1	19	in gene	ActReg chr5 #13365	1	1	1
13366	5	137,910,694	137,911,654	960	3	11.867	17.533	10.933	24	31	20	1	1	1	HSPA9	144	in gene	ActReg chr5 #13366	1	1	1
13367	5	137,991,535	137,992,503	968	1	10.233	8.867	5.433	15	13	11	0	0	0				ActReg chr5 #13367	1	0	0
13368	5	137,998,154	137,999,096	942	1	10.483	11.966	4.862	22	18	10	0	0	0				ActReg chr5 #13368	0	1	0
13369	5	138,060,728	138,061,510	782	2	12.4	10.92	5.88	22	20	10	0	0	0				ActReg chr5 #13369	1	1	0
13370	5	138,609,317	138,610,303	986	1	11.767	10.2	8.567	17	16	14	1	3	3	MATR3, SNHG4, SNORA74A	369, 369, -4659	in gene, in gene, upstream	ActReg chr5 #13370	1	0	0
13371	5	138,629,321	138,630,122	801	1	7.92	7.4	15.2	13	11	24	1	0	1	MATR3	20,280	in gene	ActReg chr5 #13371	0	0	1
13372	5	138,677,174	138,678,159	985	2	10.903	11.935	11.161	15	19	23	1	1	2	MATR3, PAIP2	68225, 147	downstream, in gene	ActReg chr5 #13372	0	1	1
13373	5	138,739,405	138,740,233	828	1	12	12.077	5.5	17	20	10	1	1	3	LOC389333, SPATA24, DNAJC18	-8934, -43, 35595	upstream, upstream, downstream	ActReg chr5 #13373	0	1	0
13374	5	138,774,861	138,775,583	722	1	11.364	9.136	5.045	18	14	8	0	1	2	DNAJC18, ECSCR	-8, 9641	upstream, downstream	ActReg chr5 #13374	1	0	0
13375	5	138,897,192	138,897,896	704	1	8.773	11.182	12.864	13	19	24	1	0	0				ActReg chr5 #13375	0	0	1
13376	5	139,016,881	139,017,620	739	1	7.783	12.435	4.739	17	32	8	1	0	1	UBE2D2	76,499	downstream	ActReg chr5 #13376	0	1	0
13377	5	139,035,470	139,035,887	417	1	1.429	7	11.462	2	10	17	0	0	1	CXXC5	7,377	in gene	ActReg chr5 #13377	0	0	1
13378	5	139,038,716	139,039,156	440	1	9.357	8.214	11.786	15	10	16	0	0	1	CXXC5	10,635	in gene	ActReg chr5 #13378	0	0	1
13379	5	139,076,466	139,077,141	675	1	9.381	13.191	6.524	14	20	10	1	0	0				ActReg chr5 #13379	0	1	0
13380	5	139,127,241	139,127,788	547	1	5.235	4.059	12.059	8	5	16	1	0	0				ActReg chr5 #13380	0	0	1
13381	5	139,145,102	139,145,627	525	1	9.188	10.062	11.5	14	14	17	1	0	0				ActReg chr5 #13381	0	0	1
13382	5	139,365,062	139,365,818	756	2	10.739	11.261	2	18	17	3	0	0	1	NRG2	57,444	in gene	ActReg chr5 #13382	1	1	0
13383	5	139,422,696	139,423,589	893	2	11.321	10.321	7.321	17	19	12	1	1	1	NRG2	-258	upstream	ActReg chr5 #13383	1	1	0
13384	5	139,487,052	139,487,708	656	1	11.55	9.85	9.5	16	13	15	1	2	2	LOC100505636, PURA	770, -6328	in gene, upstream	ActReg chr5 #13384	1	0	0
13385	5	139,492,745	139,493,616	871	2	6.741	10.667	8.962	10	15	14	2	2	2	LOC100505636, PURA	-5030, -528	upstream, upstream	ActReg chr5 #13385	0	1	1
13386	5	139,493,865	139,494,798	933	2	9.897	12.414	5.5	15	22	10	1	2	2	LOC100505636, PURA	-6181, 623	upstream, in gene	ActReg chr5 #13386	1	1	0
13387	5	139,554,618	139,555,229	611	1	7.526	10.105	12.79	14	15	16	1	1	1	C5orf32	270	in gene	ActReg chr5 #13387	0	0	1
13388	5	139,601,269	139,601,944	675	1	7	10.857	1.556	13	17	2	0	0	1	C5orf32	46,953	in gene	ActReg chr5 #13388	0	1	0
13389	5	139,725,794	139,726,179	385	1	8.417	8.167	12.333	12	11	19	1	1	1	HBEGF	202	in gene	ActReg chr5 #13389	0	0	1
13390	5	139,779,971	139,782,233	2,262	2	14.9	15.471	4.486	30	34	12	1	2	2	ANKHD1-EIF4EBP3, ANKHD1	-327, -327	upstream, upstream	ActReg chr5 #13390	1	1	0
13391	5	139,943,609	139,944,661	1,052	2	12.606	18.727	6.182	33	39	12	1	3	4	SRA1, APBB3, SLC35A4, LOC100505798	-6457, 54, -285, 27542	upstream, in gene, upstream, downstream	ActReg chr5 #13391	1	1	0
13392	5	140,011,481	140,011,916	435	1	2.429	2.231	11.929	5	4	18	1	2	2	CD14, TMCO6	1588, -7314	in gene, upstream	ActReg chr5 #13392	0	0	1
13393	5	140,018,751	140,019,743	992	1	7.032	11.71	4.323	13	16	9	1	2	4	CD14, TMCO6, NDUFA2, IK	-5961, 235, 8123, -8137	upstream, in gene, downstream, upstream	ActReg chr5 #13393	0	1	0
13394	5	140,026,714	140,027,469	755	1	13.125	11.667	3.708	18	16	8	1	2	3	TMCO6, NDUFA2, IK	8079, 279, -293	downstream, in gene, upstream	ActReg chr5 #13394	1	0	0
13395	5	140,043,775	140,044,780	1,005	3	10.625	10.812	10.062	17	23	16	1	1	4	IK, WDR55, DND1, HARS	16893, -107, 8894, 26694	downstream, upstream, downstream, downstream	ActReg chr5 #13395	1	1	1
13396	5	140,070,517	140,071,486	969	1	13.167	9.267	5.467	21	16	10	1	2	3	HARS, HARS2, ZMAT2	-30, -17, -9031	upstream, upstream, upstream	ActReg chr5 #13396	1	0	0
13397	5	140,090,329	140,091,240	911	3	13.897	14.448	11.138	29	26	26	0	0	1	ZMAT2	10,752	downstream	ActReg chr5 #13397	1	1	1
13398	5	140,098,014	140,098,898	884	2	13.25	12.964	7.857	23	25	15	0	0	0				ActReg chr5 #13398	1	1	0
13399	5	140,105,259	140,106,105	846	3	13	12.846	11.476	25	25	26	0	0	0				ActReg chr5 #13399	1	1	1
13400	5	140,176,261	140,176,913	652	1	6.05	4.737	12.5	9	8	24	1	2	5	PCDHA@, PCDHA1, PCDHA2, PCDHA3, PCDHA4	10711, 10711, 2143, -4196, -10085	in gene, in gene, in gene, upstream, upstream	ActReg chr5 #13400	0	0	1
13401	5	140,215,147	140,215,498	351	1	4.364	7.455	13.364	7	11	19	1	2	9	PCDHA@, PCDHA1, PCDHA2, PCDHA3, PCDHA4, PCDHA5, PCDHA6, PCDHA7, PCDHA8	49446, 49446, 40878, 34539, 28650, 13961, 7672, 1353, -5585	in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	ActReg chr5 #13401	0	0	1
13402	5	140,305,840	140,306,637	797	1	10.96	11.96	8.48	16	18	13	1	1	15	PCDHA@, PCDHA1, PCDHA2, PCDHA3, PCDHA4, PCDHA5, PCDHA6, PCDHA7, PCDHA8, PCDHA9, PCDHA10, PCDHA11, PCDHA12, PCDHA13, PCDHAC1	140362, 140362, 131794, 125455, 119566, 104877, 98588, 92269, 85331, 78881, 70604, 58407, 51307, 44384, -64	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	ActReg chr5 #13402	0	1	0
13403	5	140,420,203	140,421,132	929	2	13.759	12.828	3.95	25	23	7	0	0	2	PCDHB@, PCDHB1	-10312, -10312	upstream, upstream	ActReg chr5 #13403	1	1	0
13404	5	140,430,886	140,431,480	594	1	5.278	12.056	4.273	9	19	7	0	2	2	PCDHB@, PCDHB1	204, 204	in gene, in gene	ActReg chr5 #13404	0	1	0
13405	5	140,473,878	140,474,559	681	1	8.286	11.809	3.143	14	19	4	0	2	3	PCDHB@, PCDHB2, PCDHB3	43239, -19, -6016	in gene, upstream, upstream	ActReg chr5 #13405	0	1	0
13406	5	140,699,873	140,700,217	344	1	11.1	7.1	12	13	10	16	1	1	1	TAF7	306	in gene	ActReg chr5 #13406	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GeneCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13407	5	140,764,169	140,764,698	529	1	3.188	4.438	12.25	4	6	17	1	3	12	PCDHGA1, PCDHGA2, PCDHGA3, PCDHGB1, PCDHGA4, PCDHGB2, PCDHGA5, PCDHGB3, PCDHGA6, PCDHGA7, PCDHGB4, PCDHGA8	54181, 46079, 40832, 34605, 29665, 24730, 20535, 14471, 10782, 1966, -3019, -7050	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream, upstream	ActReg chr5 #13407	0	0	1
13408	5	140,855,174	140,856,500	1,326	2	8.049	10.561	6.95	14	17	17	1	1	21	PCDHGA1, PCDHGA2, PCDHGA3, PCDHGB1, PCDHGA4, PCDHGB2, PCDHGA5, PCDHGB3, PCDHGA6, PCDHGA7, PCDHGB4, PCDHGA8, PCDHGB5, PCDHGA9, PCDHGB6, PCDHGA10, PCDHGB7, PCDHGA11, PCDHGA12, PCDHGC3, PCDHGC4	145585, 137483, 132236, 126009, 121069, 116134, 111939, 105875, 102186, 93370, 88385, 84354, 78142, 73317, 68067, 63094, 58555, 55300, 45679, 268, -8904	in gene, upstream	ActReg chr5 #13408	0	1	1
13409	5	140,892,966	140,893,795	829	1	7.808	10.808	5.885	12	16	10	1	0	23	PCDHGA1, PCDHGA2, PCDHGA3, PCDHGB1, PCDHGA4, PCDHGB2, PCDHGA5, PCDHGB3, PCDHGA6, PCDHGA7, PCDHGB4, PCDHGA8, PCDHGB5, PCDHGA9, PCDHGB6, PCDHGA10, PCDHGB7, PCDHGA11, PCDHGA12, PCDHGC3, PCDHGC4, PCDHGC5, DIAPH1	183128, 175026, 169779, 163552, 158612, 153677, 149482, 143418, 139729, 130913, 125928, 121897, 115685, 110860, 105610, 100637, 96098, 92843, 83222, 37811, 28639, 24572, 105242	downstream, downstream	ActReg chr5 #13409	0	1	0
13410	5	140,904,102	140,904,811	709	1	11.273	5.818	2.875	18	9	5	0	0	1	DIAPH1	94,166	in gene	ActReg chr5 #13410	1	0	0
13411	5	140,936,990	140,937,729	739	2	11.917	14.125	2.292	30	36	5	0	1	2	DIAPH1, LOC100505658	61263, -519	in gene, upstream	ActReg chr5 #13411	1	1	0
13412	5	140,943,389	140,944,307	918	2	33.586	32.207	2.077	111	92	3	0	0	2	DIAPH1, LOC100505658	54774, 5970	in gene, in gene	ActReg chr5 #13412	1	1	0
13413	5	140,998,310	140,999,170	860	2	19.741	17.556	5.308	47	43	12	1	1	2	DIAPH1, HDAC3	-118, 17683	upstream, downstream	ActReg chr5 #13413	1	1	0
13414	5	141,016,851	141,018,248	1,397	3	11.204	12.341	10.568	20	29	24	1	2	3	HDAC3, RELL2, FCHSD1	-1126, 1032, 13437	upstream, in gene, downstream	ActReg chr5 #13414	1	1	1
13415	5	141,030,788	141,031,159	371	1	8.636	6.545	11.636	13	10	16	1	1	2	FCHSD1, ARAP3	13, 30827	in gene, downstream	ActReg chr5 #13415	0	0	1
13416	5	141,037,514	141,038,211	697	2	11.546	11.954	3.381	17	23	7	0	1	2	FCHSD1, ARAP3	-6876, 23938	upstream, in gene	ActReg chr5 #13416	1	1	0
13417	5	141,061,624	141,062,391	767	1	8.125	11.792	6.375	13	18	11	0	1	1	ARAP3	-207	upstream	ActReg chr5 #13417	0	1	0
13418	5	141,071,476	141,073,252	1,776	2	16.357	18.643	6.393	42	43	11	1	0	1	ARAP3	-10,564	upstream	ActReg chr5 #13418	1	1	0
13419	5	141,075,007	141,076,589	1,582	1	9.74	10.74	4.25	16	17	8	0	0	0				ActReg chr5 #13419	0	1	0
13420	5	141,093,132	141,093,948	816	1	8.68	15.32	2.739	14	27	5	0	0	0				ActReg chr5 #13420	0	1	0
13421	5	141,113,839	141,114,991	1,152	2	14.833	17.389	3.333	35	40	7	0	0	0				ActReg chr5 #13421	1	1	0
13422	5	141,121,834	141,123,840	2,006	2	14.127	21.032	5.397	47	69	11	0	0	0				ActReg chr5 #13422	1	1	0
13423	5	141,133,244	141,134,733	1,489	2	10.128	15.213	5.143	20	30	14	1	0	0				ActReg chr5 #13423	1	1	0
13424	5	141,134,742	141,135,202	460	1	5.867	4.867	12.133	10	6	17	0	0	0				ActReg chr5 #13424	0	0	1
13425	5	141,229,499	141,230,092	593	1	10.579	7.25	7.643	16	12	16	1	0	1	PCDH1	28,149	downstream	ActReg chr5 #13425	1	0	0
13426	5	141,256,201	141,256,932	731	1	11.043	8.043	9.609	15	12	13	1	1	1	PCDH1	1,378	in gene	ActReg chr5 #13426	1	0	0
13427	5	141,258,235	141,259,140	905	1	10	13.069	9.655	16	20	13	1	1	1	PCDH1	-743	upstream	ActReg chr5 #13427	0	1	0
13428	5	141,261,975	141,263,697	1,722	2	12.778	15.759	6.407	28	32	12	1	1	1	PCDH1	-4,892	upstream	ActReg chr5 #13428	1	1	0
13429	5	141,303,085	141,303,691	606	1	7.632	9.211	12.579	12	12	22	1	1	1	KIAA0141	3	in gene	ActReg chr5 #13429	0	0	1
13430	5	141,432,907	141,433,347	440	1	9.929	10.214	1	14	15	1	0	0	0				ActReg chr5 #13430	0	1	0
13431	5	141,488,003	141,488,692	689	1	8.286	10.714	3.85	13	14	6	1	1	1	NDFIP1	23	in gene	ActReg chr5 #13431	0	1	0
13432	5	141,655,032	141,655,747	715	1	3.957	10.435	5.333	7	19	10	0	0	0				ActReg chr5 #13432	0	1	0
13433	5	141,693,627	141,694,064	437	1	6	10.714	5.714	10	15	7	0	0	1	SPRY4	10,775	in gene	ActReg chr5 #13433	0	1	0
13434	5	141,703,706	141,704,259	553	1	8.5	7.833	12.056	11	12	14	1	1	1	SPRY4	638	in gene	ActReg chr5 #13434	0	0	1
13435	5	141,704,484	141,705,150	666	1	9.9	9	11.3	14	19	16	1	1	1	SPRY4	-197	upstream	ActReg chr5 #13435	0	0	1
13436	5	141,736,279	141,736,877	598	1	9.684	10.526	7.632	13	18	15	1	0	0				ActReg chr5 #13436	0	1	0
13437	5	141,851,644	141,852,396	752	2	11.083	11.917	2.5	19	23	5	0	0	0				ActReg chr5 #13437	1	1	0
13438	5	141,854,238	141,854,820	582	1	14.579	12.526	2.625	23	19	5	0	0	0				ActReg chr5 #13438	1	0	0
13439	5	142,150,453	142,151,201	748	2	10.208	11.625	8.583	17	17	13	1	1	1	ARHGAP26	535	in gene	ActReg chr5 #13439	0	1	1
13440	5	142,201,102	142,202,209	1,107	2	12.486	14.114	2	27	33	4	0	0	1	ARHGAP26	51,363	in gene	ActReg chr5 #13440	1	1	0
13441	5	142,206,557	142,207,377	820	1	11.769	10.538	2.957	19	19	6	0	0	1	ARHGAP26	56,675	in gene	ActReg chr5 #13441	1	0	0
13442	5	142,625,238	142,626,132	894	2	14.107	10.964	2.864	25	19	7	0	0	0				ActReg chr5 #13442	1	1	0
13443	5	142,782,691	142,783,468	777	1	8.792	11.5	4.5	20	16	10	1	0	1	NR3C1	31,998	in gene	ActReg chr5 #13443	0	1	0
13444	5	142,783,579	142,784,171	592	1	8.684	10.895	3.667	14	18	5	1	0	1	NR3C1	31,202	in gene	ActReg chr5 #13444	0	1	0
13445	5	142,784,596	142,785,480	884	2	8.821	11.786	8.5	11	21	17	1	0	1	NR3C1	30,039	in gene	ActReg chr5 #13445	0	1	1
13446	5	143,897,027	143,897,326	299	1	1.889	0	8.889	2	0	12	0	0	0				ActReg chr5 #13446	0	0	1
13447	5	145,325,553	145,326,430	877	1	7.222	10.444	2.476	14	16	5	0	0	1	SH3RF2	9,865	in gene	ActReg chr5 #13447	0	1	0
13448	5	145,561,843	145,562,763	920	2	14.69	15.621	5.346	26	36	9	0	1	1	LARS	-9	upstream	ActReg chr5 #13448	1	1	0
13449	5	145,582,514	145,583,478	964	2	15.533	15.467	5.5	32	36	11	1	1	1	RBM27	-167	upstream	ActReg chr5 #13449	1	1	0
13450	5	145,719,097	145,719,980	883	1	4.571	7.464	11.214	8	10	15	1	1	1	POU4F3	951	in gene	ActReg chr5 #13450	0	0	1
13451	5	145,826,293	145,827,529	1,236	2	21.256	21.308	5.103	58	50	9	1	1	1	TCERG1	38	in gene	ActReg chr5 #13451	1	1	0
13452	5	146,204,333	146,205,229	896	2	14.321	22.393	2.625	33	59	4	0	0	1	PPP2R2B	256,252	in gene	ActReg chr5 #13452	1	1	0
13453	5	146,257,203	146,257,589	386	1	4.667	7.417	10.833	10	13	14	1	0	1	PPP2R2B	203,637	in gene	ActReg chr5 #13453	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13454	5	146,258,104	146,258,442	338	1	5.636	9.727	11.182	7	14	16	1	0	1	PPP2R2B	202,760	in gene	ActReg chr5 #13454	0	0	1
13455	5	146,888,732	146,889,743	1,011	1	9.094	11.906	6.969	15	18	13	1	0	0				ActReg chr5 #13455	0	1	0
13456	5	148,381,309	148,382,043	734	2	11	11.043	2.333	16	16	3	0	0	1	SH3TC2	61,061	in gene	ActReg chr5 #13456	1	1	0
13457	5	148,441,657	148,442,807	1,150	2	13.833	13.111	4.75	28	22	12	0	3	3	SH3TC2, MIR584, hCG_1980447	505, -260, -834	in gene, upstream, upstream	ActReg chr5 #13457	1	1	0
13458	5	148,513,440	148,514,531	1,091	1	12.257	8.343	3.714	23	14	10	0	1	1	ABLIM3	-7,069	upstream	ActReg chr5 #13458	1	0	0
13459	5	148,542,090	148,542,965	875	1	7.37	11	3.519	13	17	6	0	0	1	ABLIM3	21,473	in gene	ActReg chr5 #13459	0	1	0
13460	5	148,555,259	148,555,703	444	1	7.286	7.786	10.714	11	10	16	0	0	1	ABLIM3	34,427	in gene	ActReg chr5 #13460	0	0	1
13461	5	148,724,653	148,725,663	1,010	1	12.161	9.968	8.548	17	16	12	1	1	2	AFAP1L1, GRPEL2	73757, 181	downstream, in gene	ActReg chr5 #13461	1	0	0
13462	5	148,784,172	148,784,784	612	1	12.947	11.684	5.947	23	15	11	0	1	1	LOC728264	-1,962	upstream	ActReg chr5 #13462	1	0	0
13463	5	148,825,346	148,825,889	543	1	13.706	9.059	2.125	23	15	4	0	0	0				ActReg chr5 #13463	1	0	0
13464	5	148,835,139	148,836,154	1,015	1	12.613	9.839	3.677	22	16	8	0	0	0				ActReg chr5 #13464	1	0	0
13465	5	148,845,697	148,846,801	1,104	2	12.706	13.471	3.706	19	28	6	0	0	0				ActReg chr5 #13465	1	1	0
13466	5	148,865,552	148,866,398	846	1	9.077	10.692	3.423	17	17	5	0	0	1	CSNK1A1	65,032	downstream	ActReg chr5 #13466	0	1	0
13467	5	148,930,488	148,931,610	1,122	3	10.829	9.171	10.235	20	18	17	1	1	1	CSNK1A1	-42	upstream	ActReg chr5 #13467	1	1	1
13468	5	149,339,929	149,340,915	986	2	9.194	13.097	10.452	16	17	15	1	1	1	SLC26A2	122	in gene	ActReg chr5 #13468	0	1	1
13469	5	149,379,603	149,381,007	1,404	3	13.886	13.409	11.023	24	24	18	1	2	2	TIGD6, HMGXB3	-88, 136	upstream, in gene	ActReg chr5 #13469	1	1	1
13470	5	149,415,970	149,416,638	668	1	13.2	5.75	4.571	26	10	7	0	0	1	HMGXB3	36,135	in gene	ActReg chr5 #13470	1	0	0
13471	5	149,492,296	149,493,307	1,011	1	7.097	6.032	13.226	13	9	21	0	1	2	CSF1R, PDGFRB	134, 42621	in gene, downstream	ActReg chr5 #13471	0	0	1
13472	5	149,493,534	149,494,176	642	1	3.062	4.1	10.952	5	6	18	0	1	2	CSF1R, PDGFRB	-920, 41567	upstream, in gene	ActReg chr5 #13472	0	0	1
13473	5	149,583,461	149,583,807	346	1	4.1	2.2	13.1	6	3	18	0	0	1	SLC6A7	14,114	in gene	ActReg chr5 #13473	0	0	1
13474	5	149,643,876	149,644,492	616	1	8.947	5.053	12.947	16	12	17	0	0	1	CAMK2A	25,219	in gene	ActReg chr5 #13474	0	0	1
13475	5	149,696,392	149,697,342	950	2	12.586	12.034	3.241	27	21	5	0	0	0				ActReg chr5 #13475	1	1	0
13476	5	149,736,951	149,738,364	1,413	1	7.841	13.614	5.61	16	20	12	1	1	1	TCOF1	455	in gene	ActReg chr5 #13476	0	1	0
13477	5	149,786,133	149,786,667	534	1	2.933	7.176	12.294	6	9	19	0	0	2	TCOF1, CD74	49198, 5932	downstream, in gene	ActReg chr5 #13477	0	0	1
13478	5	149,810,576	149,810,990	414	1	6	3.455	11.231	11	5	14	0	0	0				ActReg chr5 #13478	0	0	1
13479	5	149,828,841	149,829,963	1,122	3	13.686	18.371	9.343	31	51	21	1	1	1	RPS14	-83	upstream	ActReg chr5 #13479	1	1	1
13480	5	149,880,082	149,880,928	846	1	13.518	7.963	7.37	23	13	12	0	1	1	NDST1	-7,169	upstream	ActReg chr5 #13480	1	0	0
13481	5	149,915,221	149,915,724	503	1	5.75	4.812	11.75	9	8	19	0	0	1	NDST1	27,798	in gene	ActReg chr5 #13481	0	0	1
13482	5	150,019,832	150,020,639	807	1	8.56	10.92	6.64	13	15	12	0	0	1	SYNPO	39,593	in gene	ActReg chr5 #13482	0	1	0
13483	5	150,029,740	150,030,151	411	1	3.385	5.154	13	5	8	17	0	0	1	SYNPO	49,303	in gene	ActReg chr5 #13483	0	0	1
13484	5	150,051,106	150,051,634	528	1	2.385	2.75	13.188	4	7	17	1	0	1	MYOZ3	10,966	in gene	ActReg chr5 #13484	0	0	1
13485	5	150,079,781	150,081,025	1,244	2	10.692	13.051	5.306	21	20	12	1	1	2	RBM22, DCTN4	266, 58254	in gene, downstream	ActReg chr5 #13485	1	1	0
13486	5	150,137,919	150,138,907	988	1	10.742	8.097	6.414	17	15	15	1	1	1	DCTN4	244	in gene	ActReg chr5 #13486	1	0	0
13487	5	150,180,699	150,181,257	558	1	6.667	12.222	4	11	19	9	0	0	1	C5orf62	23,470	downstream	ActReg chr5 #13487	0	1	0
13488	5	150,284,106	150,285,099	993	2	16.581	20.9	3.581	38	52	9	1	1	1	ZNF300	-57	upstream	ActReg chr5 #13488	1	1	0
13489	5	150,325,728	150,326,539	811	1	10.077	12.577	4.962	22	22	10	1	0	0				ActReg chr5 #13489	0	1	0
13490	5	150,632,446	150,633,087	641	1	9.35	11.85	7.25	19	17	11	0	1	1	GM2A	153	in gene	ActReg chr5 #13490	0	1	0
13491	5	150,826,936	150,827,709	773	2	9.583	13.625	12.625	17	21	25	1	1	1	SLC36A1	159	in gene	ActReg chr5 #13491	0	1	1
13492	5	150,910,868	150,911,338	470	1	2.533	2.267	12.533	4	3	19	1	0	1	FAT2	37,402	in gene	ActReg chr5 #13492	0	0	1
13493	5	151,062,693	151,063,106	413	1	4	5.692	10.538	6	7	14	0	0	1	SPARC	3,618	in gene	ActReg chr5 #13493	0	0	1
13494	5	151,066,226	151,066,713	487	1	6.867	8	13.8	11	11	21	0	1	1	SPARC	48	in gene	ActReg chr5 #13494	0	0	1
13495	5	151,122,204	151,122,936	732	1	12.783	6.609	3.652	21	13	6	0	0	1	ATOX1	15,640	in gene	ActReg chr5 #13495	1	0	0
13496	5	151,124,380	151,125,634	1,254	1	14.75	11.175	4.229	22	20	8	0	0	1	ATOX1	13,203	in gene	ActReg chr5 #13496	1	0	0
13497	5	151,149,894	151,150,486	592	1	5.5	4.389	11	8	8	15	1	1	1	G3BP1	-1,286	upstream	ActReg chr5 #13497	0	0	1
13498	5	151,151,096	151,151,729	633	1	11.9	7.75	7.15	19	15	14	1	1	1	G3BP1	-64	upstream	ActReg chr5 #13498	1	0	0
13499	5	151,303,896	151,305,033	1,137	2	16.25	22.306	6.028	48	67	11	1	1	1	GLRA1	-67	upstream	ActReg chr5 #13499	1	1	0
13500	5	153,418,180	153,418,855	675	1	9.81	13.143	8.45	16	25	15	1	2	2	FAM114A2, MFAP3	-20, -2	upstream, upstream	ActReg chr5 #13500	0	1	0
13501	5	153,569,564	153,570,192	628	1	10.55	9.7	9.1	17	15	14	1	1	1	GALNT10	-417	upstream	ActReg chr5 #13501	1	0	0
13502	5	153,577,488	153,578,224	736	1	9.957	11.087	5.217	15	21	9	0	0	1	GALNT10	7,561	in gene	ActReg chr5 #13502	0	1	0
13503	5	153,656,456	153,656,937	481	1	11.8	11.867	2.2	17	15	3	0	0	1	GALNT10	86,401	in gene	ActReg chr5 #13503	0	1	0
13504	5	153,824,488	153,824,819	331	1	6.2	7	10.6	9	13	12	0	1	1	SAP30L	-864	upstream	ActReg chr5 #13504	0	0	1
13505	5	153,858,808	153,859,211	403	1	1.615	5.455	12.538	4	8	18	1	1	1	HAND1	-1,185	upstream	ActReg chr5 #13505	0	0	1
13506	5	153,862,137	153,862,558	421	1	3.538	2.308	11.077	5	4	16	1	1	1	HAND1	-4,523	upstream	ActReg chr5 #13506	0	0	1
13507	5	153,884,915	153,885,381	466	1	1.538	3.214	11.8	4	5	20	0	0	0				ActReg chr5 #13507	0	0	1
13508	5	153,885,817	153,886,418	601	1	3.579	3.625	11	6	7	15	0	0	0				ActReg chr5 #13508	0	0	1
13509	5	154,134,147	154,134,820	673	2	11.524	16.333	8.824	21	29	14	1	1	2	LARP1, LOC100505847	42021, -652	in gene, upstream	ActReg chr5 #13509	1	1	0
13510	5	154,236,840	154,237,531	691	1	9.143	9.238	12.952	15	13	20	1	2	2	C5orf4, CNOT8	-6972, -1013	upstream, upstream	ActReg chr5 #13510	0	0	1
13511	5	154,237,702	154,238,501	799	2	10	11.88	5.708	23	21	11	1	2	2	C5orf4, CNOT8	-7888, -97	upstream, upstream	ActReg chr5 #13511	1	1	0
13512	5	154,317,512	154,318,214	702	2	10.136	11.682	7.273	21	23	12	1	2	2	GEMIN5, MRPL22	-87, -2770	upstream, upstream	ActReg chr5 #13512	1	1	0
13513	5	154,320,316	154,320,930	614	1	8.75	11.55	5.7	13	20	9	0	2	2	GEMIN5, MRPL22	-2847, -10	upstream, upstream	ActReg chr5 #13513	0	1	0
13514	5	154,461,905	154,462,527	622	1	8.737	11.632	2	13	21	4	0	0	0				ActReg chr5 #13514	0	1	0
13515	5	155,108,015	155,108,382	367	1	4.273	3.091	12.364	6	4	17	1	0	0				ActReg chr5 #13515	0	0	1
13516	5	157,098,185	157,098,637	452	1	6.357	7.857	11.786	11	9	15	1	2	2	LOC100289096, C5orf52	36, -150	in gene, upstream	ActReg chr5 #13516	0	0	1
13517	5	157,158,085	157,159,046	961	2	19.233	18.6	7.958	44	43	15	1	1	1	THG1L	242	in gene	ActReg chr5 #13517	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13518	5	157,170,304	157,170,987	683	1	6.636	11.318	1.647	11	15	3	1	1	2	THG1L, LSM11	12322, -110	downstream, upstream	ActReg chr5 #13518	0	1	0
13519	5	157,313,715	157,314,402	687	1	3.955	2.5	13.227	8	4	23	0	0	0				ActReg chr5 #13519	0	0	1
13520	5	157,562,499	157,563,273	774	1	7.542	12.833	3.167	12	22	5	0	0	0				ActReg chr5 #13520	0	1	0
13521	5	157,569,072	157,569,830	758	1	10.625	8.625	1.706	15	14	3	0	0	0				ActReg chr5 #13521	1	0	0
13522	5	157,817,504	157,818,117	613	1	6.5	12.2	1.167	9	23	2	0	0	0				ActReg chr5 #13522	0	1	0
13523	5	158,143,566	158,144,227	661	1	8.952	7.905	3.083	18	11	5	0	0	1	EBF1	382,892	in gene	ActReg chr5 #13523	1	0	0
13524	5	158,153,755	158,154,580	825	2	10.731	11.269	1.909	19	14	4	0	0	1	EBF1	372,621	in gene	ActReg chr5 #13524	1	1	0
13525	5	158,527,164	158,528,155	991	1	10.742	7.129	3.567	16	14	7	1	1	1	EBF1	-871	upstream	ActReg chr5 #13525	1	0	0
13526	5	158,690,164	158,690,661	497	1	8.688	11.938	11.812	14	17	19	1	1	1	UBLCP1	323	in gene	ActReg chr5 #13526	0	0	1
13527	5	159,008,748	159,009,349	601	1	10.474	10.947	3.75	16	20	6	0	0	0				ActReg chr5 #13527	0	1	0
13528	5	159,199,980	159,200,657	677	1	8.714	11.095	5.85	14	16	11	1	0	0				ActReg chr5 #13528	0	1	0
13529	5	159,329,339	159,330,207	868	2	13.852	13.593	2.545	28	21	4	0	0	0				ActReg chr5 #13529	1	1	0
13530	5	159,354,984	159,355,684	700	1	7.773	12.682	2.19	12	19	5	0	0	1	ADRA1B	11,594	in gene	ActReg chr5 #13530	0	1	0
13531	5	159,435,894	159,436,458	564	1	8.444	11.5	5.389	12	19	10	0	1	1	TTC1	-4	upstream	ActReg chr5 #13531	0	1	0
13532	5	159,545,717	159,547,022	1,305	1	8.366	11.122	4.447	14	15	11	1	1	1	PWWP2A	83	in gene	ActReg chr5 #13532	0	1	0
13533	5	159,591,901	159,592,872	971	2	10.323	11.774	5.097	20	19	9	0	0	0				ActReg chr5 #13533	1	1	0
13534	5	159,738,734	159,739,512	778	1	9.5	11.958	11.75	16	23	17	1	1	1	CCNJL	450	in gene	ActReg chr5 #13534	0	0	1
13535	5	159,848,694	159,849,272	578	1	6.778	12.056	8.278	12	18	14	1	2	2	SLU7, PTTG1	-2815, 118	upstream, in gene	ActReg chr5 #13535	0	1	0
13536	5	159,890,483	159,891,151	668	1	8	10.048	1.909	12	15	3	0	0	0				ActReg chr5 #13536	0	1	0
13537	5	159,894,803	159,895,456	653	1	8.952	10.429	6.05	17	15	13	0	1	1	MIR3142	-6,322	upstream	ActReg chr5 #13537	0	1	0
13538	5	160,593,037	160,593,506	469	1	1.462	3.933	10.8	4	6	18	0	0	0				ActReg chr5 #13538	0	0	1
13539	5	161,495,229	161,496,074	845	2	17.444	23.963	1.667	51	64	3	0	1	1	GABRG2	1,003	in gene	ActReg chr5 #13539	1	1	0
13540	5	162,886,732	162,887,227	495	1	8.667	13.4	6.867	14	17	11	1	2	2	NUDCD2, HMMR	164, -538	in gene, upstream	ActReg chr5 #13540	0	1	0
13541	5	162,932,218	162,933,226	1,008	3	10.719	14.781	7.094	24	32	17	1	1	1	MAT2B	2,491	in gene	ActReg chr5 #13541	1	1	1
13542	5	164,027,267	164,027,899	632	1	5.263	11.263	1.556	9	16	3	0	0	1	LOC100507193	303,526	in gene	ActReg chr5 #13542	0	1	0
13543	5	165,935,934	165,936,518	584	1	7.579	10.947	2.333	11	17	4	0	0	0				ActReg chr5 #13543	0	1	0
13544	5	165,989,001	165,989,826	825	2	10	14.308	1.75	19	28	2	0	0	0				ActReg chr5 #13544	1	1	0
13545	5	166,149,941	166,150,431	490	1	10.333	8.067	1.714	16	10	3	0	0	0				ActReg chr5 #13545	1	0	0
13546	5	167,913,053	167,913,944	891	2	31.286	28.25	6.652	95	76	14	1	1	1	RARS	35	in gene	ActReg chr5 #13546	1	1	0
13547	5	167,955,478	167,956,386	908	1	8.31	10.31	3.464	14	18	5	1	0	1	RARS	42,469	downstream	ActReg chr5 #13547	0	1	0
13548	5	168,006,048	168,006,346	298	1	7.7	8.3	10.7	12	10	16	1	1	1	PANK3	391	in gene	ActReg chr5 #13548	0	0	1
13549	5	168,083,210	168,083,805	595	1	7.722	11.833	2.389	10	19	4	0	0	1	SLIT3	644,626	downstream	ActReg chr5 #13549	0	1	0
13550	5	168,118,863	168,119,420	557	1	2.588	3.529	12.353	4	7	20	0	0	1	SLIT3	608,992	in gene	ActReg chr5 #13550	0	0	1
13551	5	168,601,759	168,602,479	720	2	11.826	13.87	1	24	30	1	0	0	1	SLIT3	126,014	in gene	ActReg chr5 #13551	1	1	0
13552	5	169,010,845	169,011,096	251	1	8.125	10.375	10.125	12	12	14	1	1	1	CCDC99	332	in gene	ActReg chr5 #13552	0	0	1
13553	5	169,077,649	169,078,459	810	1	11.52	6.84	1.826	15	12	3	0	0	1	DOCK2	13,803	in gene	ActReg chr5 #13553	1	0	0
13554	5	169,603,880	169,604,285	405	1	2.083	7.25	10.417	3	10	15	0	0	0				ActReg chr5 #13554	0	0	1
13555	5	169,646,422	169,647,065	643	1	11.4	8.7	2.65	19	15	4	0	0	0				ActReg chr5 #13555	1	0	0
13556	5	169,878,876	169,879,460	584	1	7	10.737	2.5	13	17	4	0	0	1	KCNIP1	98,287	in gene	ActReg chr5 #13556	0	1	0
13557	5	169,919,999	169,920,692	693	1	5	11.682	1.882	8	20	3	0	0	1	KCNIP1	139,464	in gene	ActReg chr5 #13557	0	1	0
13558	5	170,024,006	170,024,778	772	1	13.583	8.917	4.542	19	16	7	0	0	1	KCNIP1	243,511	in gene	ActReg chr5 #13558	1	0	0
13559	5	170,107,945	170,108,716	771	1	8.708	11.958	5.938	18	21	13	0	0	1	KCNIP1	327,449	in gene	ActReg chr5 #13559	0	1	0
13560	5	170,814,328	170,815,018	690	1	8.136	10.454	10.227	14	15	16	1	1	1	NPM1	-35	upstream	ActReg chr5 #13560	0	0	1
13561	5	170,855,314	170,855,563	249	1	3	7.375	12.625	4	9	15	0	0	1	FGF18	8,771	in gene	ActReg chr5 #13561	0	0	1
13562	5	171,164,553	171,164,863	310	1	2.778	1.833	12	3	3	15	0	0	0				ActReg chr5 #13562	0	0	1
13563	5	171,433,069	171,434,361	1,292	1	12.2	18.275	8.95	27	42	18	1	1	1	FBXW11	162	in gene	ActReg chr5 #13563	0	1	0
13564	5	171,614,728	171,616,086	1,358	3	10.071	11.881	8.243	17	20	16	1	2	2	STK10, EFCAB9	-61, -5769	upstream, upstream	ActReg chr5 #13564	1	1	1
13565	5	171,701,934	171,702,376	442	1	9.643	3.071	3.364	14	4	8	0	0	1	UBTD2	8,640	in gene	ActReg chr5 #13565	1	0	0
13566	5	171,969,645	171,970,254	609	1	1.4	2.474	10.316	2	4	14	0	0	0				ActReg chr5 #13566	0	0	1
13567	5	172,197,286	172,198,683	1,397	3	9.279	12.605	7.268	16	21	17	1	1	1	DUSP1	219	in gene	ActReg chr5 #13567	1	1	1
13568	5	172,385,941	172,386,902	961	2	43.067	42.467	6.9	149	141	11	3	2	3	ERGIC1, LOC100268168, RPL26L1	125198, -50, -18	downstream, upstream, upstream	ActReg chr5 #13568	1	1	0
13569	5	172,410,429	172,411,168	739	2	10.542	10.75	8.542	19	19	13	1	1	1	ATP6V0E1	35	in gene	ActReg chr5 #13569	1	1	0
13570	5	172,571,148	172,571,985	837	2	14.692	12.154	6.231	28	28	11	0	1	2	C5orf41, BNIP1	88211, 121	downstream, in gene	ActReg chr5 #13570	1	1	0
13571	5	172,661,783	172,662,952	1,169	2	8.514	10.568	6.838	15	22	13	1	1	1	NKX2-5	-52	upstream	ActReg chr5 #13571	0	1	1
13572	5	172,685,214	172,685,761	547	1	11.444	9.444	3.556	17	13	6	0	0	0				ActReg chr5 #13572	1	0	0
13573	5	172,710,641	172,711,319	678	1	4.905	11.048	5.667	9	16	10	1	0	0				ActReg chr5 #13573	0	1	0
13574	5	172,883,547	172,884,383	836	2	10.885	10.808	1.962	17	17	4	0	0	0				ActReg chr5 #13574	1	1	0
13575	5	173,043,381	173,044,154	773	2	16	13.708	3.348	45	35	6	1	1	1	SOD1	-101	upstream	ActReg chr5 #13575	1	1	0
13576	5	173,344,816	173,345,467	651	1	15.15	9.85	5.3	31	17	8	0	0	1	CPEB4	29,810	in gene	ActReg chr5 #13576	1	0	0
13577	5	173,472,383	173,473,063	680	2	15.909	13.409	2.429	32	26	4	0	1	1	HMP19	-1	upstream	ActReg chr5 #13577	1	1	0
13578	5	173,509,087	173,509,815	728	1	12	7.913	2.857	19	13	4	0	0	1	HMP19	36,727	in gene	ActReg chr5 #13578	1	0	0
13579	5	173,656,795	173,657,269	474	1	10.733	7.267	2.467	18	12	4	0	0	0				ActReg chr5 #13579	1	0	0
13580	5	174,178,599	174,178,926	327	1	7.7	2.4	10.1	11	3	14	1	0	0				ActReg chr5 #13580	0	0	1
13581	5	174,748,706	174,749,367	661	2	9.75	13.25	3.667	16	25	6	0	0	0				ActReg chr5 #13581	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13582	5	174,944,469	174,945,375	906	1	13.143	5.429	2.667	20	9	5	0	0	1	SFXN1	39,408	in gene	ActReg chr5 #13582	1	0	0
13583	5	175,058,026	175,058,599	573	1	3.944	3.722	11.944	6	6	17	0	0	0				ActReg chr5 #13583	0	0	1
13584	5	175,113,866	175,114,383	517	1	4.062	4.25	11.25	6	6	17	0	0	1	HRH2	29,084	downstream	ActReg chr5 #13584	0	0	1
13585	5	175,222,777	175,225,151	2,374	3	19.459	24.703	7.167	93	99	16	1	1	1	CPLX2	354	in gene	ActReg chr5 #13585	1	1	1
13586	5	175,238,356	175,239,068	712	1	6.611	10.227	3.136	14	16	7	0	0	1	CPLX2	15,102	in gene	ActReg chr5 #13586	0	1	0
13587	5	175,298,405	175,299,624	1,219	3	17.763	15.053	9.605	44	44	18	1	0	1	CPLX2	75,404	in gene	ActReg chr5 #13587	1	1	1
13588	5	175,619,493	175,619,909	416	1	5.462	3.385	10.385	9	5	16	0	0	1	LOC643201	6,597	in gene	ActReg chr5 #13588	0	0	1
13589	5	175,815,096	175,816,706	1,610	2	11.706	13.235	8.082	21	25	14	2	2	3	NOP16, HIGD2A, CLTB	-361, 117, 27639	upstream, in gene, downstream	ActReg chr5 #13589	1	1	0
13590	5	175,843,427	175,844,159	732	2	14.318	15.727	4.765	31	38	8	1	1	1	CLTB	-253	upstream	ActReg chr5 #13590	1	1	0
13591	5	175,874,943	175,875,663	720	1	11.652	10.391	4.316	16	14	8	1	1	1	FAF2	-53	upstream	ActReg chr5 #13591	1	0	0
13592	5	175,957,389	175,957,844	455	1	1.929	8.786	11.286	3	14	18	0	0	1	RNF44	6,805	in gene	ActReg chr5 #13592	0	0	1
13593	5	175,958,942	175,959,491	549	1	3.647	4.056	10.056	6	6	16	0	0	1	RNF44	5,205	in gene	ActReg chr5 #13593	0	0	1
13594	5	175,963,345	175,965,433	2,088	2	15.2	15.354	6.062	27	28	11	1	2	2	RNF44, CDHR2	32, -5123	in gene, upstream	ActReg chr5 #13594	1	1	0
13595	5	176,037,818	176,038,231	413	1	4.333	12.077	1.308	7	20	2	0	1	2	GPRIN1, SNCB	-893, 19533	upstream, downstream	ActReg chr5 #13595	0	1	0
13596	5	176,038,351	176,038,935	584	2	10.833	12.167	3.857	20	22	6	0	1	2	GPRIN1, SNCB	-1512, 18914	upstream, downstream	ActReg chr5 #13596	1	1	0
13597	5	176,073,844	176,074,374	530	1	8.941	8.118	11	12	12	15	1	1	2	EIF4E1B, TSPAN17	16426, -279	downstream, upstream	ActReg chr5 #13597	0	0	1
13598	5	176,103,208	176,103,826	618	1	13.053	7.105	5.421	21	13	8	0	0	0				ActReg chr5 #13598	1	0	0
13599	5	176,154,334	176,154,963	629	1	2.684	4.474	13.15	5	9	19	0	0	0				ActReg chr5 #13599	0	0	1
13600	5	176,216,705	176,217,404	699	1	11.429	6.286	3.8	22	12	11	0	0	0				ActReg chr5 #13600	1	0	0
13601	5	176,230,793	176,231,600	807	2	11.6	16.88	1.412	19	35	2	0	1	1	UNC5A	-6,364	upstream	ActReg chr5 #13601	1	1	0
13602	5	176,232,325	176,234,103	1,778	3	12.673	14.2	2.37	38	47	5	0	1	1	UNC5A	-4,346	upstream	ActReg chr5 #13602	1	1	0
13603	5	176,239,771	176,240,098	327	1	7.727	8.222	11.273	12	11	15	0	1	1	UNC5A	2,374	in gene	ActReg chr5 #13603	0	0	1
13604	5	176,249,485	176,249,949	464	1	7.214	8.143	12.643	9	14	20	0	0	1	UNC5A	12,157	in gene	ActReg chr5 #13604	0	0	1
13605	5	176,264,062	176,265,442	1,380	2	23.046	32.409	4.854	92	117	12	0	0	1	UNC5A	27,192	in gene	ActReg chr5 #13605	1	1	0
13606	5	176,277,785	176,278,234	449	1	2.25	5.5	11.786	5	8	16	0	0	1	UNC5A	40,449	in gene	ActReg chr5 #13606	0	0	1
13607	5	176,295,351	176,295,931	580	1	4.611	3.429	14.444	7	6	20	0	0	1	UNC5A	58,081	in gene	ActReg chr5 #13607	0	0	1
13608	5	176,296,213	176,296,741	528	1	1.938	3.882	12.118	4	6	16	1	0	1	UNC5A	58,917	in gene	ActReg chr5 #13608	0	0	1
13609	5	176,297,019	176,297,587	568	1	9.333	5.5	10.889	13	8	15	1	0	1	UNC5A	59,743	in gene	ActReg chr5 #13609	0	0	1
13610	5	176,304,455	176,305,096	641	1	5.65	4.55	12.45	10	8	15	1	0	2	UNC5A, HK3	67215, 21558	in gene, downstream	ActReg chr5 #13610	0	0	1
13611	5	176,305,861	176,307,365	1,504	1	3.702	4.178	11.575	7	7	18	0	0	2	UNC5A, HK3	69053, 19720	in gene, downstream	ActReg chr5 #13611	0	0	1
13612	5	176,433,384	176,434,172	788	2	11.208	12.708	7.636	16	21	11	1	1	1	UIMC1	-335	upstream	ActReg chr5 #13612	1	1	0
13613	5	176,449,370	176,449,975	605	1	10.21	12.526	11.158	19	21	15	1	1	1	ZNF346	-25	upstream	ActReg chr5 #13613	0	0	1
13614	5	176,513,920	176,514,427	507	1	8.75	9.812	10.875	13	17	14	1	1	1	FGFR4	252	in gene	ActReg chr5 #13614	0	0	1
13615	5	176,729,894	176,731,129	1,235	1	8.316	11.658	6.73	14	20	10	1	2	4	NSD1, RAB24, PRELID1, MXD3	170431, 233, -324, 5781	downstream, in gene, upstream, downstream	ActReg chr5 #13615	0	1	0
13616	5	176,734,509	176,735,325	816	1	3.12	5.56	13.2	6	9	20	1	1	4	NSD1, RAB24, PRELID1, MXD3	174837, -4173, 4082, 4375	downstream, upstream, downstream, in gene	ActReg chr5 #13616	0	0	1
13617	5	176,736,246	176,737,067	821	1	4.5	10.269	4.077	7	14	7	0	2	4	NSD1, RAB24, PRELID1, MXD3	176576, -5912, 5821, 2636	downstream, upstream, downstream, in gene	ActReg chr5 #13617	0	1	0
13618	5	176,762,530	176,762,961	431	1	3.462	3.385	12.077	7	5	16	0	0	1	LMAN2	16,140	in gene	ActReg chr5 #13618	0	0	1
13619	5	176,778,257	176,779,239	982	2	11.742	13.226	9.548	22	26	14	1	2	2	LMAN2, RGS14	137, -6096	in gene, upstream	ActReg chr5 #13619	1	1	0
13620	5	176,798,972	176,799,473	501	1	4.188	4.188	11.562	6	8	17	0	0	1	RGS14	14,378	in gene	ActReg chr5 #13620	0	0	1
13621	5	176,812,770	176,813,356	586	1	4.667	5.333	13.611	7	7	20	0	1	1	SLC34A1	1,631	in gene	ActReg chr5 #13621	0	0	1
13622	5	176,830,632	176,831,345	713	1	10.364	9.909	11.818	14	13	18	1	1	3	SLC34A1, PFN3, F12	19556, -3351, 5589	downstream, upstream, in gene	ActReg chr5 #13622	0	0	1
13623	5	176,868,388	176,868,806	418	1	3.692	4.308	11.077	7	8	18	0	1	2	GRK6, PRR7	14910, -5199	in gene, upstream	ActReg chr5 #13623	0	0	1
13624	5	176,869,127	176,869,521	394	1	4.417	5.5	12	7	10	15	0	1	2	GRK6, PRR7	15637, -4472	in gene, upstream	ActReg chr5 #13624	0	0	1
13625	5	176,874,559	176,875,986	1,427	1	11.378	8.2	5.689	16	20	12	1	1	3	GRK6, PRR7, DBN1	21585, 1476, 25422	downstream, in gene, downstream	ActReg chr5 #13625	1	0	0
13626	5	176,886,929	176,887,497	568	1	2.667	5.333	11.944	4	9	17	0	0	2	PRR7, DBN1	13417, 13481	downstream, in gene	ActReg chr5 #13626	0	0	1
13627	5	176,923,377	176,925,129	1,752	2	7.909	9.636	10.236	15	21	21	1	1	2	PDLIM7, DOK3	349, 13174	in gene, downstream	ActReg chr5 #13627	0	1	1
13628	5	176,935,095	176,935,563	468	1	3.2	5.267	12.6	6	7	17	0	1	2	DOK3, DDX41	2098, 8638	in gene, downstream	ActReg chr5 #13628	0	0	1
13629	5	176,943,302	176,944,518	1,216	3	13.579	17.895	11.105	32	40	20	1	2	3	DOK3, DDX41, FAM193B	-6483, 57, 37638	upstream, in gene, downstream	ActReg chr5 #13629	1	1	1
13630	5	176,950,836	176,951,536	700	1	3.409	4.364	14.046	5	7	19	0	1	2	DDX41, FAM193B	-7219, 30362	upstream, in gene	ActReg chr5 #13630	0	0	1
13631	5	176,972,993	176,974,015	1,022	1	10.097	12.742	3.731	17	21	6	0	0	1	FAM193B	8,044	in gene	ActReg chr5 #13631	0	1	0
13632	5	176,980,681	176,981,320	639	1	5.85	7.812	15.5	11	14	28	1	1	1	FAM193B	548	in gene	ActReg chr5 #13632	0	0	1
13633	5	177,548,544	177,549,130	586	1	3.316	3.857	13	6	7	18	0	0	2	N4BP3, RMND5B	8281, -9191	in gene, upstream	ActReg chr5 #13633	0	0	1
13634	5	177,631,173	177,631,767	594	2	8.778	12.222	12.588	14	17	22	1	1	2	HNRNPAB, AGXT2L2	-38, 28333	upstream, downstream	ActReg chr5 #13634	0	1	1
13635	5	177,633,071	177,633,648	577	1	5.611	10.944	5.833	7	16	10	0	1	2	HNRNPAB, AGXT2L2	1851, 26444	in gene, downstream	ActReg chr5 #13635	0	1	0
13636	5	177,665,876	177,666,530	654	1	2.762	4.667	11.667	5	7	16	0	1	2	AGXT2L2, COL23A1	-6400, 351353	upstream, in gene	ActReg chr5 #13636	0	0	1
13637	5	177,674,744	177,675,345	601	1	2.6	4	11.316	4	7	20	0	0	1	COL23A1	342,512	in gene	ActReg chr5 #13637	0	0	1
13638	5	177,707,230	177,707,637	407	1	4.077	5	12.154	6	9	17	0	0	1	COL23A1	310,123	in gene	ActReg chr5 #13638	0	0	1
13639	5	177,798,461	177,798,834	373	1	2.909	3.75	11.25	4	6	17	0	0	1	COL23A1	218,909	in gene	ActReg chr5 #13639	0	0	1
13640	5	177,842,644	177,843,132	488	1	3.2	2.133	12.6	5	3	18	0	0	1	COL23A1	174,668	in gene	ActReg chr5 #13640	0	0	1
13641	5	178,053,085	178,053,867	782	2	8.16	10.4	7.409	18	16	11	1	1	1	CLK4	578	in gene	ActReg chr5 #13641	1	1	0
13642	5	178,258,083	178,258,904	821	1	6.8	4.52	10.76	10	8	13	0	0	0				ActReg chr5 #13642	0	0	1
13643	5	178,286,615	178,287,249	634	1	12.05	7.95	4.5	18	11	8	1	1	1	ZNF3545	-22	upstream	ActReg chr5 #13643	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13644	5	178,322,645	178,323,137	492	2	9	10.438	9.875	12	13	15	1	1	1	ZFP2	-25	upstream	ActReg chr5 #13644	0	1	1
13645	5	178,367,575	178,367,962	387	1	6	10.5	11.833	7	14	17	1	1	2	ZFP2, ZNF454	44852, -426	downstream, upstream	ActReg chr5 #13645	0	0	1
13646	5	178,486,929	178,487,867	938	2	9.552	17.069	3.897	18	34	8	1	1	1	ZNF354C	-209	upstream	ActReg chr5 #13646	1	1	0
13647	5	178,622,487	178,622,884	397	1	3.333	5.308	10.923	5	10	17	0	1	2	ADAMTS2, LOC100507476	149746, -2003	in gene, upstream	ActReg chr5 #13647	0	0	1
13648	5	178,635,888	178,636,402	514	1	1.812	5	12.25	3	8	20	0	0	1	ADAMTS2	136,286	in gene	ActReg chr5 #13648	0	0	1
13649	5	178,639,940	178,640,376	436	1	3	2.769	11.154	6	4	18	0	0	1	ADAMTS2	132,273	in gene	ActReg chr5 #13649	0	0	1
13650	5	178,684,200	178,684,600	400	1	2.833	4.25	11.917	4	6	18	1	0	1	ADAMTS2	88,031	in gene	ActReg chr5 #13650	0	0	1
13651	5	178,718,161	178,718,542	381	1	3.083	2.583	10.833	4	4	16	0	0	1	ADAMTS2	54,080	in gene	ActReg chr5 #13651	0	0	1
13652	5	178,757,319	178,757,617	298	1	2.667	1.778	9.778	5	2	13	0	0	1	ADAMTS2	14,963	in gene	ActReg chr5 #13652	0	0	1
13653	5	178,837,919	178,838,379	460	1	2.6	5.867	11.533	5	7	17	0	0	0				ActReg chr5 #13653	0	0	1
13654	5	178,932,689	178,933,125	436	1	2.5	2.077	10.929	5	5	14	0	0	0				ActReg chr5 #13654	0	0	1
13655	5	178,986,693	178,987,189	496	1	12	12.933	11.067	20	18	16	1	0	1	RUFY1	9,370	in gene	ActReg chr5 #13655	0	0	1
13656	5	179,036,870	179,037,251	381	1	7.917	6.083	11.75	11	10	15	0	0	2	RUFY1, HNRNPH1	59489, 13662	downstream, downstream	ActReg chr5 #13656	0	0	1
13657	5	179,050,233	179,051,834	1,601	3	9	11.38	9.12	17	21	19	1	1	1	HNRNPH1	-311	upstream	ActReg chr5 #13657	0	1	1
13658	5	179,105,146	179,106,548	1,402	3	11.477	9.568	11.432	21	19	21	1	1	1	CBY3	2,128	in gene	ActReg chr5 #13658	1	0	1
13659	5	179,125,274	179,125,813	539	1	6.706	9.706	12.941	11	14	19	1	1	2	LOC729595, CANX	4345, -387	downstream, upstream	ActReg chr5 #13659	0	0	1
13660	5	179,232,202	179,232,875	673	1	5.286	9	12.905	10	12	20	1	3	4	LTC4S, MGAT4B, MIR1229, SQSTM1	11552, 1414, -7192, -850	downstream, in gene, upstream, upstream	ActReg chr5 #13660	0	0	1
13661	5	179,234,169	179,234,919	750	2	8.958	10.333	8.667	12	13	15	1	2	3	MGAT4B, MIR1229, SQSTM1	-592, -9198, 1156	upstream, upstream, in gene	ActReg chr5 #13661	0	1	1
13662	5	179,245,818	179,247,129	1,311	2	13.195	10.488	8.293	26	17	14	0	0	1	SQSTM1	13,085	in gene	ActReg chr5 #13662	1	1	0
13663	5	179,247,299	179,248,336	1,037	2	12.844	14.062	7.3	25	23	13	1	0	1	SQSTM1	14,429	in gene	ActReg chr5 #13663	1	1	0
13664	5	179,285,519	179,286,140	621	1	10.895	9.526	14.895	19	11	22	1	1	2	C5orf45, TBC1D9B	11, 49027	in gene, downstream	ActReg chr5 #13664	0	0	1
13665	5	179,305,129	179,305,575	446	1	4.214	3.643	12.286	6	6	19	0	0	1	TBC1D9B	29,504	in gene	ActReg chr5 #13665	0	0	1
13666	5	179,497,783	179,498,765	982	1	7.3	10.419	2.25	14	19	5	1	1	1	RNF130	835	in gene	ActReg chr5 #13666	0	1	0
13667	5	179,546,739	179,547,309	570	1	3.389	4.167	13.333	7	6	18	0	0	1	RASGEF1C	89,106	in gene	ActReg chr5 #13667	0	0	1
13668	5	179,606,241	179,606,712	471	1	4.857	2.714	12.286	6	4	20	0	0	1	RASGEF1C	29,654	in gene	ActReg chr5 #13668	0	0	1
13669	5	179,649,041	179,649,412	371	1	3.333	4.417	10.75	5	5	16	0	0	0				ActReg chr5 #13669	0	0	1
13670	5	179,779,467	179,780,557	1,090	2	9.853	10.941	5.909	20	20	12	1	1	1	GFPT2	303	in gene	ActReg chr5 #13670	1	1	0
13671	5	179,807,787	179,808,379	592	1	2.5	2.778	12.278	4	4	18	0	0	0				ActReg chr5 #13671	0	0	1
13672	5	179,920,943	179,921,640	697	2	10.636	16.182	3.8	25	35	6	1	1	1	CNOT6	-126	upstream	ActReg chr5 #13672	1	1	0
13673	5	180,053,410	180,053,806	396	1	3.5	3.833	12.667	5	6	16	0	0	1	FLT4	23,016	in gene	ActReg chr5 #13673	0	0	1
13674	5	180,180,283	180,181,063	780	1	4.211	1.773	12.28	8	3	22	0	0	0				ActReg chr5 #13674	0	0	1
13675	5	180,237,151	180,238,154	1,003	2	9.188	11.719	5.167	16	18	12	1	1	1	MGAT1	-515	upstream	ActReg chr5 #13675	1	1	0
13676	5	180,287,776	180,288,881	1,105	3	9.543	12.286	6.257	18	19	15	1	1	1	ZFP62	-42	upstream	ActReg chr5 #13676	1	1	1
13677	5	180,463,999	180,464,482	483	1	4	5	11.25	8	8	17	0	1	1	BTNL9	-2,985	upstream	ActReg chr5 #13677	0	0	1
13678	5	180,527,455	180,527,867	412	1	4	10.615	4.167	6	18	5	1	0	0				ActReg chr5 #13678	0	1	0
13679	5	180,596,767	180,597,269	502	2	10.188	11.375	11.938	15	20	18	1	0	0				ActReg chr5 #13679	0	1	1
13680	5	180,600,428	180,600,780	352	1	10.364	4	12.364	12	6	16	0	0	0				ActReg chr5 #13680	0	0	1
13681	5	180,614,292	180,615,083	791	2	7.72	12.48	11.44	12	19	28	0	0	1	TRIM7	17,490	downstream	ActReg chr5 #13681	0	1	1
13682	5	180,615,691	180,616,156	465	1	7.929	8.357	13.429	13	13	20	1	0	2	TRIM7, LOC100507546	16254, -9279	downstream, upstream	ActReg chr5 #13682	0	0	1
13683	5	180,618,091	180,619,174	1,083	3	11.265	14.235	8.824	23	22	17	1	1	2	TRIM7, LOC100507546	13545, -6570	downstream, upstream	ActReg chr5 #13683	1	1	1
13684	5	180,631,794	180,632,510	716	1	6.318	12.364	5.773	11	23	13	1	1	2	TRIM7, LOC100507546	25, 6950	in gene, downstream	ActReg chr5 #13684	0	1	0
13685	5	180,634,548	180,635,018	470	1	10.733	12.067	13.8	17	22	23	0	1	2	TRIM7, LOC100507546	-2606, 9581	upstream, downstream	ActReg chr5 #13685	0	0	1
13686	5	180,644,627	180,645,673	1,046	1	13.576	10.394	6.727	23	15	14	1	1	1	TRIM41	-5,156	upstream	ActReg chr5 #13686	1	0	0
13687	5	180,648,488	180,649,799	1,311	3	12.39	14.366	13.561	20	29	31	1	1	1	TRIM41	-1,163	upstream	ActReg chr5 #13687	1	1	1
13688	5	180,649,926	180,650,968	1,042	3	12.562	11.938	8.75	20	23	19	3	1	1	TRIM41	141	in gene	ActReg chr5 #13688	1	1	1
13689	5	180,670,490	180,671,278	788	2	11	8.32	10.96	19	12	20	1	5	6	TRIM41, GNB2L1, SNORD96A, LOC100289627, SNORD95, LOC100507619	20578, 22, -1995, 1919, -508, -2623	downstream, in gene, upstream, in gene, upstream, upstream	ActReg chr5 #13689	1	0	1
13690	5	180,673,395	180,674,132	737	1	9.826	7.826	12.739	18	11	16	1	4	6	GNB2L1, SNORD96A, LOC100289627, SNORD95, LOC100507619, TRIM52	-2857, -4874, 4798, -3387, 256, 14356	upstream, upstream, downstream, upstream, upstream, in gene, downstream	ActReg chr5 #13690	0	0	1
13691	5	180,687,687	180,689,213	1,526	4	12.979	10.596	11.617	26	18	20	1	2	3	LOC100507619, TRIM52, LOC100507602	14943, -331, 237	downstream, upstream, in gene	ActReg chr5 #13691	1	1	1
13692	6	292,096	292,748	652	1	8.476	11.619	4.571	15	16	8	1	1	1	DUSP22	321	in gene	ActReg chr6 #13692	0	1	0
13693	6	692,699	693,546	847	2	17.741	15.667	3.375	37	40	9	1	1	1	EXOC2	-13	upstream	ActReg chr6 #13693	1	1	0
13694	6	711,032	711,525	493	1	5.75	11.125	2.438	9	18	5	1	0	0				ActReg chr6 #13694	0	1	0
13695	6	1,335,633	1,336,081	448	1	6.429	9.357	2.333	8	15	4	0	0	0				ActReg chr6 #13695	0	1	0
13696	6	2,658,894	2,659,518	624	1	8.053	11.474	3.188	15	21	5	0	0	1	MYLK4	91,948	downstream	ActReg chr6 #13696	0	1	0
13697	6	2,763,543	2,763,987	444	1	5.286	5.214	11.571	7	8	16	0	1	1	WRNIP1	-1,901	upstream	ActReg chr6 #13697	0	0	1
13698	6	2,765,450	2,765,922	472	2	9.6	12.733	4.083	15	23	7	1	1	1	WRNIP1	20	in gene	ActReg chr6 #13698	1	1	0
13699	6	2,989,617	2,990,089	472	1	9.333	10.2	1.846	13	13	3	1	1	2	DKFZP686I15217, NQO2	1652, -10214	in gene, upstream	ActReg chr6 #13699	0	1	0
13700	6	3,069,102	3,069,564	462	1	7.571	9.857	4.286	11	12	8	1	1	1	RIPK1	-7,725	upstream	ActReg chr6 #13700	0	1	0
13701	6	3,228,017	3,228,662	645	1	2.8	5	11.5	5	9	17	1	2	2	TUBB2B, LOC100507294	-371, 180	upstream, in gene	ActReg chr6 #13701	0	0	1
13702	6	3,258,903	3,259,540	637	2	11.15	13.45	6	18	27	12	1	1	3	LOC100507294, PSMC4, SLC22A23	31062, 59, 197572	in gene, in gene, downstream	ActReg chr6 #13702	1	1	0
13703	6	3,324,249	3,325,076	827	1	7.269	10.769	3.591	12	17	6	0	0	1	SLC22A23	132,131	in gene	ActReg chr6 #13703	0	1	0
13704	6	3,808,914	3,809,510	596	1	7.895	10.842	2.933	12	19	4	0	0	0				ActReg chr6 #13704	0	1	0
13705	6	5,003,778	5,004,321	543	1	8	10.588	3.214	10	15	6	1	1	1	RPP40	222	in gene	ActReg chr6 #13705	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13706	6	5,261,285	5,261,973	688	1	5.333	10.952	9.524	8	20	13	1	2	2	LYRM4, FARS2	-457, 45	upstream, in gene	ActReg chr6 #13706	0	1	0
13707	6	7,312,986	7,313,663	677	1	7.571	11.333	6.333	14	14	11	1	1	1	SSR1	217	in gene	ActReg chr6 #13707	0	1	0
13708	6	7,542,101	7,542,436	335	1	2.727	3.273	10	4	6	13	1	2	2	LOC100505880, DSP	881, 398	in gene, in gene	ActReg chr6 #13708	0	0	1
13709	6	9,399,041	9,399,376	335	1	2.2	1	11.3	3	1	15	1	0	0				ActReg chr6 #13709	0	0	1
13710	6	10,694,641	10,695,089	448	1	10.143	7.714	6.571	14	10	10	1	2	2	C6orf52, PAK1IP1	165, -323	in gene, upstream	ActReg chr6 #13710	1	0	0
13711	6	10,722,773	10,723,549	776	2	10.333	11.25	2.6	22	21	4	1	1	1	TMEM14C	13	in gene	ActReg chr6 #13711	1	1	0
13712	6	10,747,452	10,748,116	664	2	9.667	10.238	6.95	16	19	12	1	2	2	LOC100506379, TMEM14B	112, -211	in gene, upstream	ActReg chr6 #13712	1	1	0
13713	6	10,886,828	10,887,594	766	2	14.792	14.458	3.5	36	33	8	1	2	2	GCM2, SYCP2L	-5113, 147	upstream, in gene	ActReg chr6 #13713	1	1	0
13714	6	11,093,612	11,094,416	804	2	8.08	11.4	5.083	18	17	12	1	1	2	LOC221710, HERV-FRD	-252, 18057	upstream, downstream	ActReg chr6 #13714	1	1	0
13715	6	11,143,826	11,144,425	599	2	16.474	12.158	1.778	32	27	2	0	0	1	LOC221710	49,859	downstream	ActReg chr6 #13715	1	1	0
13716	6	11,207,316	11,207,729	413	1	11.462	7.769	2.875	17	12	4	0	0	2	NEDD9, LOC100506431	175059, -7814	in gene, upstream	ActReg chr6 #13716	1	0	0
13717	6	11,402,806	11,403,097	291	1	2.444	2.667	9.556	4	4	14	0	0	0				ActReg chr6 #13717	0	0	1
13718	6	11,535,762	11,536,366	604	2	8.842	11.526	1	18	23	1	0	1	1	TMEM170B	-2,447	upstream	ActReg chr6 #13718	1	1	0
13719	6	12,441,257	12,441,763	506	1	8.188	10.938	1.077	12	20	2	0	0	0				ActReg chr6 #13719	0	1	0
13720	6	13,328,492	13,329,148	656	1	5.05	10.9	3.833	9	17	11	1	1	1	TBC1D7	-33	upstream	ActReg chr6 #13720	0	1	0
13721	6	13,574,858	13,575,125	267	1	5.375	5.625	9.75	7	9	12	1	1	1	SIRT5	199	in gene	ActReg chr6 #13721	0	0	1
13722	6	13,575,171	13,575,560	389	1	7.833	10.083	3.583	11	12	6	1	1	1	SIRT5	573	in gene	ActReg chr6 #13722	0	1	0
13723	6	13,614,726	13,616,092	1,366	2	21.262	22.619	7.244	77	76	16	1	1	3	SIRT5, NOL7, RANBP9	40617, -150, 96387	downstream, upstream, downstream	ActReg chr6 #13723	1	1	0
13724	6	13,712,228	13,712,706	478	1	9.8	8.2	2.625	17	11	3	1	1	1	RANBP9	-671	upstream	ActReg chr6 #13724	1	0	0
13725	6	14,001,583	14,002,453	870	1	11.111	6.444	2.625	17	9	5	0	0	0				ActReg chr6 #13725	1	0	0
13726	6	15,245,591	15,246,363	772	2	11.333	12.125	1.857	24	21	3	1	1	2	JARID2, LOC100506681	-550, 2910	upstream, downstream	ActReg chr6 #13726	1	1	0
13727	6	15,662,846	15,663,139	293	1	7	6.7	9	10	8	12	1	1	1	DTNBP1	297	in gene	ActReg chr6 #13727	0	0	1
13728	6	15,691,462	15,691,992	530	1	8.75	6.875	2.231	16	13	3	0	0	0				ActReg chr6 #13728	1	0	0
13729	6	16,334,829	16,335,392	563	2	10.389	10	2.357	15	18	4	0	0	1	ATXN1	426,611	in gene	ActReg chr6 #13729	1	1	0
13730	6	16,681,657	16,682,197	540	2	9.235	9.588	2.118	14	17	4	0	0	1	ATXN1	79,794	in gene	ActReg chr6 #13730	1	1	0
13731	6	16,766,392	16,766,797	405	1	9.385	4.462	0	15	6	0	0	1	1	ATXN1	-4,873	upstream	ActReg chr6 #13731	1	0	0
13732	6	17,706,862	17,707,527	665	1	7.762	12.286	4.632	16	26	8	1	1	1	NUP153	-376	upstream	ActReg chr6 #13732	0	1	0
13733	6	17,907,904	17,908,435	531	1	7.235	12.059	3.294	11	20	5	0	0	1	KIF13A	79,630	in gene	ActReg chr6 #13733	0	1	0
13734	6	18,122,580	18,123,011	431	1	9.929	7.429	1.917	14	12	3	1	1	2	NHLRC1, TPMT	56, 32579	in gene, downstream	ActReg chr6 #13734	1	0	0
13735	6	19,988,816	19,989,285	469	2	9.533	8.867	1.727	15	17	3	0	0	0				ActReg chr6 #13735	1	1	0
13736	6	20,534,365	20,534,879	514	1	10.438	6.625	2	15	10	2	0	1	1	CDKAL1	-66	upstream	ActReg chr6 #13736	1	0	0
13737	6	20,877,559	20,878,234	675	2	10.191	9.381	0	17	16	0	0	0	1	CDKAL1	343,208	in gene	ActReg chr6 #13737	1	1	0
13738	6	21,022,608	21,023,069	461	1	9.714	9.929	1.909	15	13	3	0	0	1	CDKAL1	488,150	in gene	ActReg chr6 #13738	1	0	0
13739	6	23,242,804	23,243,064	260	1	1	1	9.875	1	1	13	0	0	0				ActReg chr6 #13739	0	0	1
13740	6	24,126,905	24,127,497	592	1	6	10.737	2.929	12	17	5	0	1	1	NRSN1	787	in gene	ActReg chr6 #13740	0	1	0
13741	6	24,402,867	24,403,650	783	2	9.8	13.16	6.48	16	21	10	1	1	1	MRS2	105	in gene	ActReg chr6 #13741	1	1	0
13742	6	24,494,867	24,495,500	633	1	11.2	6.05	5	22	11	9	1	2	2	GPLD1, ALDH5A1	-5333, -14	upstream, upstream	ActReg chr6 #13742	1	0	0
13743	6	24,666,910	24,667,542	632	1	8.1	10.6	7.3	12	16	10	1	2	2	TTRAP, ACOT13	-111, -37	upstream, upstream	ActReg chr6 #13743	0	1	0
13744	6	24,775,054	24,775,839	785	1	6.917	9.667	4.087	11	13	7	1	1	1	GMNN	282	in gene	ActReg chr6 #13744	0	1	0
13745	6	25,138,459	25,138,985	526	1	7.882	9.353	2.625	11	15	4	0	0	0				ActReg chr6 #13745	0	1	0
13746	6	25,652,064	25,652,962	898	2	16.483	13.931	2.593	37	33	7	1	1	1	SCGN	84	in gene	ActReg chr6 #13746	1	1	0
13747	6	25,660,631	25,661,214	583	2	9	9.111	1.933	17	20	3	0	0	1	SCGN	8,493	in gene	ActReg chr6 #13747	1	1	0
13748	6	26,020,714	26,021,171	457	2	10.286	6	10.643	15	9	16	1	3	4	HIST1H1A, HIST1H3A, HIST1H4A, HIST1H4B	-2902, 224, -965, 6538	upstream, in gene, upstream, downstream	ActReg chr6 #13748	1	0	1
13749	6	26,031,881	26,032,369	488	1	7.2	11.667	8.2	11	14	12	1	3	4	HIST1H4A, HIST1H4B, HIST1H3B, HIST1H2AB	10218, -4645, 163, 1671	downstream, upstream, in gene, downstream	ActReg chr6 #13749	0	1	0
13750	6	26,033,254	26,033,685	431	1	2.923	10.385	5.462	6	14	9	1	3	4	HIST1H4B, HIST1H3B, HIST1H2AB, HIST1H2BB	-5989, -1181, 327, 10416	upstream, upstream, in gene, downstream	ActReg chr6 #13750	0	1	0
13751	6	26,055,934	26,056,838	904	2	5.724	7.414	11.207	12	14	18	1	1	2	HIST1H3C, HIST1H1C	10747, 313	downstream, in gene	ActReg chr6 #13751	0	1	1
13752	6	26,104,026	26,104,639	613	1	5.789	7.368	12.474	10	11	19	1	1	4	HFE, HIST1H4C, HIST1H1T, LOC100506979	16884, 171, 4032, 18902	downstream, in gene, downstream, downstream	ActReg chr6 #13752	0	0	1
13753	6	26,156,403	26,156,959	556	1	7.294	7.588	13.941	9	10	20	1	2	2	HIST1H1E, HIST1H2BD	122, -1668	in gene, upstream	ActReg chr6 #13753	0	0	1
13754	6	26,197,090	26,197,557	467	1	6.643	7.308	14.571	9	11	24	1	4	5	HIST1H4D, HIST1H3D, HIST1H2AD, HIST1H2BF, HIST1H4E	-8019, 2141, 2148, -2464, -7550	upstream, in gene, downstream, upstream, upstream	ActReg chr6 #13754	0	0	1
13755	6	26,204,847	26,205,157	310	1	10	10.1	10.3	15	14	14	1	3	4	HIST1H3D, HIST1H2AD, HIST1H2BF, HIST1H4E	-5538, -5551, 5215, 129	upstream, upstream, downstream, in gene	ActReg chr6 #13755	0	0	1
13756	6	26,220,548	26,220,963	415	1	10.231	9.385	2	15	13	2	0	2	3	HIST1H2BG, HIST1H2AE, HIST1H3E	-3883, 3607, -4628	upstream, downstream, upstream	ActReg chr6 #13756	1	0	0
13757	6	26,240,538	26,241,069	531	1	8.706	9.412	6.353	12	15	10	1	2	4	HIST1H1D, HIST1H4F, HIST1H4G, HIST1H3F	-5587, 149, 6402, 10032	upstream, in gene, downstream, downstream	ActReg chr6 #13757	0	1	0
13758	6	26,271,249	26,271,578	329	1	6.7	3.3	10.6	10	5	13	1	2	3	HIST1H3G, HIST1H2BI, LOC100507025	199, -1791, 14350	in gene, upstream, downstream	ActReg chr6 #13758	0	0	1
13759	6	26,285,224	26,285,853	629	1	8.947	10.737	6.579	13	19	9	1	2	2	LOC100507025, HIST1H4H	225, 189	in gene, in gene	ActReg chr6 #13759	0	1	0
13760	6	26,313,188	26,313,492	304	1	10.222	11.222	10.778	12	14	13	0	0	0				ActReg chr6 #13760	0	0	1
13761	6	26,522,167	26,522,714	547	1	7.765	10.235	3.706	12	16	5	1	1	1	HCG11	506	in gene	ActReg chr6 #13761	0	1	0
13762	6	26,537,557	26,538,734	1,177	2	7.27	8.649	10.568	14	16	18	1	1	2	HCG11, HMGN4	16211, -427	downstream, upstream	ActReg chr6 #13762	0	1	1
13763	6	26,554,141	26,554,698	557	1	4.889	9.333	4.722	9	16	7	0	0	1	HMGN4	15,847	downstream	ActReg chr6 #13763	0	1	0
13764	6	27,107,041	27,107,449	408	1	6	10.417	12.75	8	13	16	1	3	6	HIST1H2BJ, HIST1H2AG, HIST1H2BK, HIST1H4I, HIST1H2AH, MIR3143	-6670, 6428, 7392, 157, -7663, -8160	upstream, downstream, in gene, in gene, upstream, upstream	ActReg chr6 #13764	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13765	6	27,181,456	27,181,740	284	1	3.444	5.222	9.556	7	7	13	0	0	0				ActReg chr6 #13765	0	0	1
13766	6	27,560,386	27,560,839	453	1	10.5	8.429	6.5	15	13	11	0	0	0				ActReg chr6 #13766	1	0	0
13767	6	27,636,244	27,636,665	421	1	6	9.923	7.385	9	16	12	0	0	0				ActReg chr6 #13767	0	1	0
13768	6	27,720,902	27,721,355	453	1	4.167	10.571	3.357	6	16	5	0	0	0				ActReg chr6 #13768	0	1	0
13769	6	27,804,675	27,805,497	822	1	6.12	12.04	3.5	13	23	8	0	3	3	HIST1H4K, HIST1H2AK, HIST1H2BN	-5781, 1038, -1278	upstream, downstream, upstream	ActReg chr6 #13769	0	1	0
13770	6	27,834,723	27,835,141	418	1	1.667	2.769	11.462	4	4	15	1	2	4	HIST1H2AL, HIST1H1B, HIST1H3I, HIST1H4L	1825, 493, 5167, 6357	downstream, in gene, downstream, downstream	ActReg chr6 #13770	0	0	1
13771	6	27,860,677	27,861,420	743	1	11.522	9.565	4.826	19	15	9	2	3	3	HIST1H3J, HIST1H2AM, HIST1H2BO	-2478, -85, -155	upstream, upstream, upstream	ActReg chr6 #13771	1	0	0
13772	6	27,870,570	27,871,044	474	1	7.2	5.6	13	10	9	23	0	0	3	HIST1H2AM, HIST1H2BO, OR2B2	-9844, 9604, 9367	upstream, downstream, downstream	ActReg chr6 #13772	0	0	1
13773	6	28,048,440	28,049,033	593	1	8.579	7.789	3.895	15	12	8	0	2	3	LOC100507241, ZNF165, LOC100129195	221, 254, 56335	in gene, in gene, downstream	ActReg chr6 #13773	1	0	0
13774	6	28,092,240	28,092,848	608	1	6.211	10.105	6.158	11	18	8	0	1	2	LOC100129195, ZSCAN16	12527, 157	in gene, in gene	ActReg chr6 #13774	0	1	0
13775	6	28,109,306	28,109,997	691	2	11.364	11.682	5	19	18	8	1	2	2	LOC100129195, ZNF192	-4580, -65	upstream, upstream	ActReg chr6 #13775	1	1	0
13776	6	28,323,552	28,324,013	461	1	4.467	9.867	3.4	6	14	5	0	1	2	ZNF323, ZKSCAN3	266, 6091	in gene, in gene	ActReg chr6 #13776	0	1	0
13777	6	28,554,768	28,555,366	598	1	6.158	9.105	6	10	18	11	1	1	1	SCAND3	45	in gene	ActReg chr6 #13777	0	1	0
13778	6	28,565,106	28,565,373	267	1	2.75	8.375	9.125	4	12	13	0	0	1	SCAND3	-10,127	upstream	ActReg chr6 #13778	0	0	1
13779	6	28,574,207	28,574,753	546	1	4.333	9.556	2.308	6	15	4	0	0	0				ActReg chr6 #13779	0	1	0
13780	6	28,583,970	28,584,272	302	1	3.2	6.143	9.444	4	11	11	1	0	0				ActReg chr6 #13780	0	0	1
13781	6	28,784,881	28,785,184	303	1	9.3	4	10.4	13	6	15	0	0	0				ActReg chr6 #13781	0	0	1
13782	6	28,831,260	28,831,600	340	1	4.545	6.636	11.454	6	8	16	1	1	1	LOC401242	24	in gene	ActReg chr6 #13782	0	0	1
13783	6	28,834,197	28,834,726	529	1	8.471	9.529	4.882	9	16	9	0	1	1	LOC401242	-3,007	upstream	ActReg chr6 #13783	0	1	0
13784	6	28,949,791	28,950,171	380	1	5.583	6.083	10.417	10	8	16	0	0	0				ActReg chr6 #13784	0	0	1
13785	6	29,716,354	29,716,671	317	1	3.444	8.556	11.222	6	13	14	1	1	1	RP3-377H14.5	314	in gene	ActReg chr6 #13785	0	0	1
13786	6	29,759,792	29,760,313	521	1	9.25	7.938	3.125	14	13	5	1	0	0				ActReg chr6 #13786	1	0	0
13787	6	29,855,883	29,856,196	313	1	6.1	5.7	10.4	8	8	14	1	0	0				ActReg chr6 #13787	0	0	1
13788	6	30,180,831	30,181,246	415	1	5.923	6.538	10	8	9	16	1	1	1	TRIM26	115	in gene	ActReg chr6 #13788	0	0	1
13789	6	30,294,301	30,294,792	491	1	4.75	7.312	10.562	7	10	17	1	2	2	HCG18, TRIM39	381, -75	in gene, upstream	ActReg chr6 #13789	0	0	1
13790	6	30,294,837	30,295,229	392	1	5.5	10.583	3.727	8	16	6	1	2	2	HCG18, TRIM39	-106, 412	upstream, in gene	ActReg chr6 #13790	0	1	0
13791	6	30,345,871	30,346,516	645	2	9.25	9.25	1.917	19	15	4	0	0	0				ActReg chr6 #13791	1	1	0
13792	6	30,523,856	30,524,627	771	1	8.167	11.75	7.292	13	22	13	1	2	2	GNL1, PRR3	1130, -245	in gene, upstream	ActReg chr6 #13792	0	1	0
13793	6	30,615,063	30,615,550	487	1	5.733	7.8	12.933	8	10	19	1	1	3	C6orf134, C6orf136, DHX16	20693, 490, 25524	downstream, in gene, downstream	ActReg chr6 #13793	0	0	1
13794	6	30,640,513	30,641,236	723	2	14.773	13.273	4.4	32	30	7	1	1	2	DHX16, KIAA1949	-44, 14798	upstream, downstream	ActReg chr6 #13794	1	1	0
13795	6	30,710,541	30,710,904	363	1	6.455	9.818	12.818	10	13	17	1	2	2	FLOT1, IER3	-269, 1605	upstream, downstream	ActReg chr6 #13795	0	0	1
13796	6	30,711,869	30,712,202	333	1	6.818	6.273	10.909	13	8	14	1	2	2	FLOT1, IER3	-1582, 292	upstream, in gene	ActReg chr6 #13796	0	0	1
13797	6	30,875,346	30,876,026	680	1	9.286	14.429	7.81	17	24	13	1	2	3	DDR1, GTF2H4, VARS2	23825, -291, -6296	downstream, upstream, upstream	ActReg chr6 #13797	0	1	0
13798	6	30,881,876	30,882,673	797	1	6.08	9.6	4.957	11	13	9	1	1	2	GTF2H4, VARS2	6297, 292	downstream, in gene	ActReg chr6 #13798	0	1	0
13799	6	31,239,310	31,239,592	282	1	5.333	7	9.333	7	9	12	1	1	1	HLA-C	404	in gene	ActReg chr6 #13799	0	0	1
13800	6	31,261,020	31,261,637	617	2	7.8	11.2	1.4	15	24	2	0	0	0				ActReg chr6 #13800	1	1	0
13801	6	31,367,619	31,368,056	437	1	6	5.923	11.385	8	8	16	1	1	1	LOC100507436	276	in gene	ActReg chr6 #13801	0	0	1
13802	6	31,509,325	31,510,521	1,196	2	9.892	12	3.882	18	20	9	1	4	5	BAT1, SNORD117, SNORD84, ATP6V1G2, NFKBIL1	302, -5697, -968, 4704, -4705	in gene, upstream, upstream, downstream, upstream	ActReg chr6 #13802	1	1	0
13803	6	31,633,388	31,633,871	483	1	5.733	11	4.308	8	15	7	1	4	5	APOM, C6orf47, BAT4, CSNK2B, LY6G5B	9958, -5080, -466, -28, -5099	downstream, upstream, upstream, upstream, upstream	ActReg chr6 #13803	0	1	0
13804	6	31,707,417	31,707,971	554	1	7.444	10.556	3.944	10	15	8	1	2	3	DDAH2, CLIC1, MSH5	-9655, -3353, -31	upstream, upstream, upstream	ActReg chr6 #13804	0	1	0
13805	6	31,830,623	31,831,063	440	1	9.214	9.5	2.5	13	14	5	1	1	2	NEU1, SLC44A4	-134, 15980	upstream, downstream	ActReg chr6 #13805	0	1	0
13806	6	31,939,551	31,940,418	867	2	9.071	13.679	7.808	18	19	12	1	2	4	SKIV2L, DOM3Z, STK19, C4A	13403, 48, 1032, -9850	downstream, in gene, in gene, upstream	ActReg chr6 #13806	1	1	0
13807	6	32,024,202	32,024,455	253	1	1.375	5.375	12	3	8	15	0	0	1	TNXB	52,825	in gene	ActReg chr6 #13807	0	0	1
13808	6	32,073,122	32,073,575	453	1	4.429	10.429	1.692	7	17	3	0	0	2	TNXB, ATF6B	3805, 22682	in gene, downstream	ActReg chr6 #13808	0	1	0
13809	6	32,097,832	32,098,591	759	2	12.957	14.13	5.125	24	28	10	1	2	2	ATF6B, FKBPL	-2181, -144	upstream, upstream	ActReg chr6 #13809	1	1	0
13810	6	32,787,381	32,787,913	532	1	10.235	11.882	1.778	15	24	2	0	1	2	HLA-DOB, TAP2	-2822, 18900	upstream, downstream	ActReg chr6 #13810	0	1	0
13811	6	32,937,466	32,937,943	477	1	9.867	4	5.333	13	6	7	0	1	1	BRD2	1,267	in gene	ActReg chr6 #13811	1	0	0
13812	6	32,940,462	32,940,919	457	1	4.786	9.786	11.5	8	15	17	1	0	1	BRD2	4,253	in gene	ActReg chr6 #13812	0	0	1
13813	6	33,175,923	33,176,474	551	2	13.353	9.118	9.647	25	14	19	1	3	5	RXRB, SLC39A7, HSD17B8, MIR219-1, RING1	-7766, 7595, 3779, 586, -88	upstream, downstream, downstream, downstream, upstream	ActReg chr6 #13813	1	0	1
13814	6	33,218,470	33,218,978	508	1	9.062	3.438	5.4	15	7	8	0	0	1	VPS52	20,938	in gene	ActReg chr6 #13814	1	0	0
13815	6	33,239,484	33,240,310	826	3	10.615	7.038	6.923	17	17	14	1	3	4	VPS52, RPS18, B3GALT4, WDR46	-235, 45, -5020, 17407	upstream, in gene, upstream, downstream	ActReg chr6 #13815	1	1	1
13816	6	33,266,628	33,267,783	1,155	2	11.25	11.583	6.206	23	15	12	1	1	4	WDR46, PFDN6, RGL2, TAPBP	-9901, 9827, -29, 14959	upstream, downstream, upstream, downstream	ActReg chr6 #13816	1	1	0
13817	6	33,282,805	33,283,245	440	1	3.308	4.286	11.5	5	10	20	1	2	3	TAPBP, ZBTB22, DAXX	-861, 2694, 7768	upstream, in gene, downstream	ActReg chr6 #13817	0	0	1
13818	6	33,285,549	33,286,012	663	2	13.9	14.45	1.733	26	25	3	1	2	3	TAPBP, ZBTB22, DAXX	-3516, 39, 5113	upstream, in gene, downstream	ActReg chr6 #13818	1	1	0
13819	6	33,290,910	33,291,688	778	1	6.56	11.12	5	11	21	9	1	2	3	TAPBP, ZBTB22, DAXX	-9135, -5580, -506	upstream, upstream, upstream	ActReg chr6 #13819	0	1	0
13820	6	33,739,510	33,739,916	406	1	6.231	3.077	9.692	11	7	14	1	0	1	LEMD2	17,193	in gene	ActReg chr6 #13820	0	0	1
13821	6	33,756,722	33,757,139	417	1	10.846	8.231	1	16	12	1	1	1	2	LEMD2, MLN	-24, 14863	upstream, downstream	ActReg chr6 #13821	1	0	0
13822	6	33,780,259	33,780,880	621	2	10.474	10.895	4.889	19	23	11	0	0	1	MLN	-8,776	upstream	ActReg chr6 #13822	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13823	6	33,860,370	33,860,668	298	1	1.375	2.857	11.222	2	5	13	0	0	1	LOC100507584	4,165	in gene	ActReg chr6 #13823	0	0	1
13824	6	34,083,052	34,083,599	547	1	5.353	9.841	2.214	8	14	6	0	0	1	GRM4	18,118	in gene	ActReg chr6 #13824	0	1	0
13825	6	34,100,154	34,101,306	1,152	2	10.556	13.917	3.265	21	31	7	0	1	1	GRM4	713	in gene	ActReg chr6 #13825	1	1	0
13826	6	34,164,202	34,164,531	329	1	8.9	6.7	10.3	12	9	14	1	0	0				ActReg chr6 #13826	0	0	1
13827	6	34,216,439	34,216,888	449	1	6.286	4.714	13.571	8	8	22	1	1	2	HMGA1, C6orf1	12086, 241	downstream, in gene	ActReg chr6 #13827	0	0	1
13828	6	34,760,067	34,760,343	276	1	6.625	5	9.5	9	6	11	1	1	1	UHRF1BP1	411	in gene	ActReg chr6 #13828	0	0	1
13829	6	34,855,519	34,856,152	633	1	6.1	9.8	5.35	13	17	11	1	2	2	TAF11, ANKS1A	-16, -1203	upstream, upstream	ActReg chr6 #13829	0	1	0
13830	6	35,108,455	35,108,854	399	1	2.417	1	10.833	4	1	16	1	1	1	TCP11	533	in gene	ActReg chr6 #13830	0	0	1
13831	6	35,411,050	35,411,378	328	1	1	2	11.6	1	3	16	0	0	1	FANCE	-8,924	upstream	ActReg chr6 #13831	0	0	1
13832	6	35,435,826	35,436,465	639	2	12.65	11.05	10.177	17	14	15	1	1	3	FANCE, RPL10A, TEAD3	16007, -33, 28716	downstream, upstream, downstream	ActReg chr6 #13832	1	1	0
13833	6	35,459,263	35,459,626	363	1	1.75	3.75	10.417	3	6	13	0	0	2	TEAD3, TULP1	5417, 21203	in gene, downstream	ActReg chr6 #13833	0	0	1
13834	6	35,699,647	35,700,082	435	1	7.357	9.357	11.357	11	11	16	1	2	3	FKBP5, LOC285847, C6orf81	-3504, 4860, -4995	upstream, in gene, upstream	ActReg chr6 #13834	0	0	1
13835	6	35,754,518	35,755,153	635	1	7.25	9.05	12.2	11	14	20	1	0	3	C6orf126, C6orf127, CLPS	10443, 6004, 10267	downstream, in gene, downstream	ActReg chr6 #13835	0	0	1
13836	6	35,772,802	35,773,551	749	2	10.696	11.609	6.522	22	17	9	1	1	2	CLPS, LHFPL5	-8074, 105	upstream, in gene	ActReg chr6 #13836	1	1	0
13837	6	35,995,013	35,995,631	618	2	8.842	9.526	5.632	17	16	8	1	2	2	SLC26A8, MAPK14	-2909, -132	upstream, upstream	ActReg chr6 #13837	1	1	0
13838	6	36,237,700	36,237,975	275	1	3.25	2.875	10.125	4	3	12	0	0	1	PNPLA1	26,892	in gene	ActReg chr6 #13838	0	0	1
13839	6	36,646,416	36,646,867	451	1	7.214	9.286	12.143	9	14	18	1	1	1	CDKN1A	182	in gene	ActReg chr6 #13839	0	0	1
13840	6	36,647,822	36,648,721	899	2	8.964	10.643	5.462	22	17	10	1	1	1	CDKN1A	1,812	in gene	ActReg chr6 #13840	1	1	0
13841	6	36,807,064	36,807,383	319	1	2.5	6.5	9.2	4	9	11	1	1	2	CPNE5, LOC100127961	-3, 4986	upstream, downstream	ActReg chr6 #13841	0	0	1
13842	6	36,953,753	36,954,242	489	1	9.625	10.688	4	14	15	8	1	1	1	MTCH1	-48	upstream	ActReg chr6 #13842	0	1	0
13843	6	37,045,499	37,045,950	451	1	1.571	4.846	13.143	3	7	21	0	0	0				ActReg chr6 #13843	0	0	1
13844	6	37,321,637	37,322,096	459	1	9.571	8.429	5.143	13	11	9	1	1	1	RNF8	118	in gene	ActReg chr6 #13844	1	0	0
13845	6	37,400,847	37,401,143	296	1	10.667	9	11.889	13	12	16	1	1	1	FTSJD2	88	in gene	ActReg chr6 #13845	0	0	1
13846	6	37,493,251	37,494,070	819	2	12.32	15.72	3.238	21	28	5	0	0	0				ActReg chr6 #13846	1	1	0
13847	6	37,597,898	37,598,735	837	1	11.808	13.769	2.04	17	23	5	0	0	1	MDGA1	67,450	downstream	ActReg chr6 #13847	0	1	0
13848	6	37,786,585	37,787,600	1,015	2	10.344	14.312	7.677	17	23	12	1	1	1	ZFAND3	-215	upstream	ActReg chr6 #13848	1	1	0
13849	6	38,197,287	38,198,039	752	1	6.913	15.087	3.056	15	33	5	0	0	1	BTBD9	410,261	in gene	ActReg chr6 #13849	0	1	0
13850	6	38,325,734	38,326,262	528	1	3.562	10.062	1.455	7	14	3	0	0	1	BTBD9	281,926	in gene	ActReg chr6 #13850	0	1	0
13851	6	38,670,613	38,671,297	684	2	9.409	12.227	3.111	22	27	6	1	1	1	GLO1	-3	upstream	ActReg chr6 #13851	1	1	0
13852	6	39,056,121	39,056,571	450	1	2.308	10.214	2	4	17	3	0	0	1	GLP1R	39,789	downstream	ActReg chr6 #13852	0	1	0
13853	6	39,104,994	39,105,499	505	1	7.533	10.467	1.25	14	17	2	0	0	0				ActReg chr6 #13853	0	1	0
13854	6	39,196,810	39,197,438	628	2	8.158	9.368	11	14	17	22	1	1	1	KCNK5	127	in gene	ActReg chr6 #13854	0	1	1
13855	6	39,849,967	39,850,443	476	1	2.214	2.8	10.667	3	6	16	0	0	2	DAAM2, LOC100505635	89412, 14823	in gene, in gene	ActReg chr6 #13855	0	0	1
13856	6	40,996,018	40,996,560	542	1	4.706	5.941	10.235	10	11	13	1	0	1	UNC5CL	10,649	in gene	ActReg chr6 #13856	0	0	1
13857	6	41,068,508	41,068,959	451	1	4	3.714	11.571	7	6	18	1	0	1	NFYA	28,026	in gene	ActReg chr6 #13857	0	0	1
13858	6	41,086,833	41,087,225	392	1	9.083	10.5	1.5	14	15	2	0	0	0				ActReg chr6 #13858	0	1	0
13859	6	41,134,509	41,135,245	736	1	5	9.87	3	9	15	5	0	0	1	TREM2	-3,955	upstream	ActReg chr6 #13859	0	1	0
13860	6	41,703,104	41,703,748	644	2	14.889	11.905	2.8	31	29	6	1	1	2	TFEB, PGC	571, 11713	in gene, downstream	ActReg chr6 #13860	1	1	0
13861	6	41,754,643	41,755,628	985	2	11.935	10.774	3.387	21	22	5	1	2	4	FRS3, PRICKLE4, TOMM6, USP49	-7505, 6635, -46, 107964	upstream, downstream, upstream, downstream	ActReg chr6 #13861	1	1	0
13862	6	41,888,643	41,889,643	1,000	2	17.774	20.742	7	39	46	10	1	2	2	MED20, BYSL	-266, 178	upstream, in gene	ActReg chr6 #13862	1	1	0
13863	6	42,066,986	42,067,434	448	1	6.571	10.643	4.786	12	17	7	0	0	1	C6orf132	43,505	downstream	ActReg chr6 #13863	0	1	0
13864	6	42,092,209	42,092,546	337	1	3.455	2.2	10.454	5	3	15	0	0	1	C6orf132	18,338	in gene	ActReg chr6 #13864	0	0	1
13865	6	42,230,840	42,231,208	368	1	2.167	4.25	10.083	3	8	13	0	0	1	TRERF1	188,759	in gene	ActReg chr6 #13865	0	0	1
13866	6	42,419,388	42,419,823	435	1	11.214	7.286	3	17	12	5	1	1	1	TRERF1	178	in gene	ActReg chr6 #13866	1	0	0
13867	6	42,713,563	42,713,977	414	1	4.846	9.923	4.846	8	14	8	1	1	1	TBCC	114	in gene	ActReg chr6 #13867	0	1	0
13868	6	42,847,104	42,847,856	752	1	9.625	11.75	3.091	19	22	7	0	1	1	RPL7L1	-191	upstream	ActReg chr6 #13868	0	1	0
13869	6	42,858,505	42,858,928	423	1	10	10.077	5.692	12	12	9	1	1	2	RPL7L1, C6orf226	11045, -162	downstream, upstream	ActReg chr6 #13869	0	1	0
13870	6	42,892,968	42,893,366	398	1	3.5	5.583	10.583	6	6	15	1	1	2	PTCRA, CNPY3	9440, -3693	in gene, upstream	ActReg chr6 #13870	0	0	1
13871	6	43,149,663	43,150,178	515	1	7.882	10.118	5.8	11	17	10	1	1	2	SRF, CUL9	11000, -2	downstream, upstream	ActReg chr6 #13871	0	1	0
13872	6	43,394,844	43,395,495	651	1	14.143	4.81	4.238	23	9	9	1	1	1	ABCC10	-4,320	upstream	ActReg chr6 #13872	1	0	0
13873	6	43,476,922	43,477,527	605	1	9.263	6.579	6.421	16	12	11	1	1	4	TJAP1, C6orf154, YIPF3, POLR1C	31963, 1200, 7504, -7567	downstream, in gene, downstream, upstream	ActReg chr6 #13873	1	0	0
13874	6	43,478,122	43,478,550	428	1	7.385	10.615	10.846	10	16	14	1	2	4	TJAP1, C6orf154, YIPF3, POLR1C	33075, 88, 6392, -6455	downstream, in gene, downstream, upstream	ActReg chr6 #13874	0	0	1
13875	6	43,603,350	43,604,000	650	1	4.19	10.095	6.4	6	18	10	1	1	3	GTPBP2, MAD2L1BP, RSPH9	-6739, 6396, -9092	upstream, in gene, upstream	ActReg chr6 #13875	0	1	0
13876	6	43,607,991	43,608,427	436	1	3.571	9.714	3.429	5	14	6	0	1	2	MAD2L1BP, RSPH9	10930, -4558	in gene, upstream	ActReg chr6 #13876	0	1	0
13877	6	44,030,718	44,031,087	369	1	1.75	6.25	11.167	3	9	16	0	0	0				ActReg chr6 #13877	0	0	1
13878	6	44,095,455	44,095,764	309	1	3.5	2.7	9.5	5	6	13	1	2	2	MRPL14, TMEM63B	-418, 233	upstream, in gene	ActReg chr6 #13878	0	0	1
13879	6	44,213,939	44,215,206	1,267	2	15.1	14.975	6.35	31	31	9	1	1	3	LOC100505819, HSP90AB1, SLC35B2	7048, -277, 10711	in gene, upstream, downstream	ActReg chr6 #13879	1	1	0
13880	6	44,224,672	44,225,501	829	1	7.769	13.538	7.125	13	21	15	1	2	4	LOC100505819, HSP90AB1, SLC35B2, NFKBIE	-3466, 10237, 197, 8439	upstream, downstream, in gene, downstream	ActReg chr6 #13880	0	1	0
13881	6	44,253,178	44,254,194	1,016	2	10	11.75	3.545	20	21	6	1	0	2	TMEM151B, TCTE1	15206, 11772	downstream, in gene	ActReg chr6 #13881	1	1	0
13882	6	44,280,530	44,281,535	1,005	2	27.323	31.645	4.613	82	88	9	1	1	1	AARS2	31	in gene	ActReg chr6 #13882	1	1	0
13883	6	44,437,591	44,437,930	339	1	4.273	5.636	9.636	7	8	14	0	1	1	LOC100128935	-2,881	upstream	ActReg chr6 #13883	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13884	6	46,620,741	46,621,283	542	2	8.059	8.647	3.471	15	14	6	1	2	2	CYP39A1, SLC25A27	-489, 333	upstream, in gene	ActReg chr6 #13884	1	1	0
13885	6	47,000,832	47,001,125	293	1	3.5	5.8	9.5	4	7	12	0	0	1	GPR110	9,104	in gene	ActReg chr6 #13885	0	0	1
13886	6	47,135,918	47,136,416	498	1	9.188	8.5	2.889	16	13	4	0	0	0				ActReg chr6 #13886	1	0	0
13887	6	47,148,299	47,148,915	616	2	10.263	10.158	3.643	20	20	6	0	0	0				ActReg chr6 #13887	1	1	0
13888	6	48,396,618	48,397,111	493	1	10.733	7.467	2.2	16	11	4	0	0	0				ActReg chr6 #13888	1	0	0
13889	6	49,243,005	49,243,429	424	1	4.286	2.167	12.857	7	4	20	0	0	0				ActReg chr6 #13889	0	0	1
13890	6	49,901,189	49,901,641	452	1	2.714	4.643	11.429	5	6	21	0	0	0				ActReg chr6 #13890	0	0	1
13891	6	50,273,266	50,273,930	664	2	8.7	10.143	2	20	22	4	0	0	0				ActReg chr6 #13891	1	1	0
13892	6	50,688,222	50,688,652	430	1	6.643	9.786	1.333	9	17	2	0	0	1	TFAP2D	7,180	in gene	ActReg chr6 #13892	0	1	0
13893	6	51,263,026	51,263,706	680	1	11.905	7.524	2.059	21	14	5	0	0	0				ActReg chr6 #13893	1	0	0
13894	6	52,288,700	52,289,222	522	1	3.882	10.647	1.625	6	18	3	0	0	1	EPHC1	3,967	in gene	ActReg chr6 #13894	0	1	0
13895	6	52,859,837	52,860,196	359	1	7.917	10.583	2.667	10	14	6	1	2	3	GSTA4, RN7SK, ICK	162, -402, 66584	in gene, upstream, downstream	ActReg chr6 #13895	0	1	0
13896	6	52,929,314	52,929,977	663	2	9.9	10.2	3.111	18	21	5	1	2	2	ICK, FBXO9	-3045, -151	upstream, upstream	ActReg chr6 #13896	1	1	0
13897	6	53,213,146	53,213,885	739	1	10.87	9.087	5.435	16	15	12	1	1	1	ELOVL5	427	in gene	ActReg chr6 #13897	1	0	0
13898	6	53,223,785	53,224,873	1,088	2	12.147	11.177	7.182	21	22	11	1	0	1	ELOVL5	-10,387	upstream	ActReg chr6 #13898	1	1	0
13899	6	53,408,929	53,410,294	1,365	2	12.833	13.429	6.763	31	29	10	1	1	1	GCLC	220	in gene	ActReg chr6 #13899	1	1	0
13900	6	53,412,416	53,413,285	869	2	14.857	15.286	3.667	38	30	7	1	1	1	GCLC	-3,019	upstream	ActReg chr6 #13900	1	1	0
13901	6	53,659,304	53,660,220	916	1	5.893	10.75	3.269	9	16	6	1	1	1	LRRC1	-16	upstream	ActReg chr6 #13901	0	1	0
13902	6	53,849,074	53,849,518	444	1	9.929	10.071	2.3	13	15	3	0	0	0				ActReg chr6 #13902	0	1	0
13903	6	55,041,556	55,042,370	814	2	13.654	10.308	1.062	29	19	2	0	1	1	HCRTR2	2,892	in gene	ActReg chr6 #13903	1	1	0
13904	6	56,200,487	56,201,049	562	1	8.118	9.941	2	13	16	2	0	0	0				ActReg chr6 #13904	0	1	0
13905	6	58,287,335	58,288,168	833	2	25.654	34.875	2.32	80	107	3	1	0	0				ActReg chr6 #13905	1	1	0
13906	6	62,939,327	62,939,776	449	1	1.533	2.067	12.333	2	3	19	0	0	1	KHDRBS2	56,549	in gene	ActReg chr6 #13906	0	0	1
13907	6	62,995,867	62,996,532	665	2	13.809	12.048	5	28	21	9	1	1	1	KHDRBS2	-99	upstream	ActReg chr6 #13907	1	1	0
13908	6	64,281,569	64,282,245	676	1	15.095	10	6.438	24	14	11	1	1	1	PTP4A1	-13	upstream	ActReg chr6 #13908	1	0	0
13909	6	64,282,965	64,283,875	910	1	7.483	12.552	2.923	12	21	8	1	1	1	PTP4A1	1,500	in gene	ActReg chr6 #13909	0	1	0
13910	6	64,284,079	64,284,782	703	2	12.5	9.273	2.05	28	18	4	0	1	1	PTP4A1	2,510	in gene	ActReg chr6 #13910	1	1	0
13911	6	64,308,163	64,309,074	911	2	15.214	16.556	2.95	37	42	5	0	0	0				ActReg chr6 #13911	1	1	0
13912	6	64,345,470	64,346,423	953	3	13.767	15.567	6.615	25	31	16	1	0	0				ActReg chr6 #13912	1	1	1
13913	6	66,337,284	66,337,796	512	1	4.938	3.812	13	6	7	20	0	0	1	EYS	79,578	in gene	ActReg chr6 #13913	0	0	1
13914	6	66,470,006	66,470,717	711	2	13.091	13.046	2.429	31	31	5	0	0	0				ActReg chr6 #13914	1	1	0
13915	6	67,846,224	67,846,839	615	1	9.474	9.211	1.688	15	15	3	0	0	0				ActReg chr6 #13915	1	0	0
13916	6	68,432,622	68,433,392	770	1	4.583	3.042	13.083	7	6	18	0	0	0				ActReg chr6 #13916	0	0	1
13917	6	68,468,087	68,468,509	422	1	3.846	1.917	11.077	6	3	17	0	0	0				ActReg chr6 #13917	0	0	1
13918	6	68,535,259	68,535,586	327	1	6.727	5.455	11.546	10	7	14	0	0	0				ActReg chr6 #13918	0	0	1
13919	6	68,789,797	68,790,567	770	2	16.417	13.208	2.5	42	29	4	0	0	0				ActReg chr6 #13919	1	1	0
13920	6	69,243,139	69,243,634	495	1	1.4	4.467	12.333	3	8	20	0	0	0				ActReg chr6 #13920	0	0	1
13921	6	69,942,588	69,943,252	664	2	11.762	14.571	2.762	27	35	5	0	0	1	BAI3	597,288	in gene	ActReg chr6 #13921	1	1	0
13922	6	70,627,682	70,628,251	569	1	10.529	7.529	1.786	16	10	3	0	0	1	COL19A1	51,518	in gene	ActReg chr6 #13922	1	0	0
13923	6	71,276,618	71,276,972	354	1	8.909	7.909	10.182	12	11	15	1	1	2	FAM135A, C6orf57	155688, 170	downstream, in gene	ActReg chr6 #13923	0	0	1
13924	6	73,831,042	73,831,907	865	2	10.538	14.63	1.706	21	28	3	0	0	1	KCNQ5	499,903	in gene	ActReg chr6 #13924	1	1	0
13925	6	74,230,112	74,231,208	1,096	3	9.235	9.6	15.314	20	17	29	1	1	1	EEF1A1	95	in gene	ActReg chr6 #13925	1	1	1
13926	6	74,392,296	74,392,606	310	1	2.111	2.6	11.111	3	4	14	0	0	0				ActReg chr6 #13926	0	0	1
13927	6	74,405,322	74,406,143	821	2	8.64	9.8	3.409	13	14	5	1	2	2	LOC100506740, CD109	122, 224	in gene, in gene	ActReg chr6 #13927	1	1	0
13928	6	81,481,551	81,482,133	582	1	4.25	10.222	1.455	7	19	2	0	0	0				ActReg chr6 #13928	0	1	0
13929	6	82,462,733	82,463,397	664	1	11.429	9.762	7.19	24	13	10	1	1	1	FAM46A	-637	upstream	ActReg chr6 #13929	1	0	0
13930	6	83,902,735	83,903,214	479	1	6.933	8.133	10.933	8	11	19	1	2	2	PGM3, RWDD2A	-39, -58	upstream, upstream	ActReg chr6 #13930	0	0	1
13931	6	84,568,505	84,569,680	1,175	2	13.027	21.757	3.143	45	62	7	1	1	2	RIPPLY2, CYB5R4	6107, -278	downstream, upstream	ActReg chr6 #13931	1	1	0
13932	6	85,231,769	85,232,341	572	1	8.167	8.944	1.8	12	14	4	0	0	0				ActReg chr6 #13932	0	1	0
13933	6	85,474,181	85,474,638	457	1	5.786	10.857	5	10	16	8	1	1	1	TBX18	-510	upstream	ActReg chr6 #13933	0	1	0
13934	6	85,484,267	85,484,870	603	1	4.526	10.421	3.842	8	17	6	1	0	0				ActReg chr6 #13934	0	1	0
13935	6	86,174,358	86,174,948	590	1	8.368	10.579	2.333	13	17	4	0	0	1	NT5E	15,351	in gene	ActReg chr6 #13935	0	1	0
13936	6	86,387,858	86,389,021	1,163	4	8.083	8.333	8.8	16	18	14	1	3	3	SNHG5, SNORD50A, SNORD50B	12, -1353, -1062	in gene, upstream, upstream	ActReg chr6 #13936	1	1	1
13937	6	88,031,783	88,032,733	950	2	24.759	27.517	3	64	82	5	1	1	2	GJB7, C6orf162	6738, -48	in gene, upstream	ActReg chr6 #13937	1	1	0
13938	6	88,145,867	88,146,757	890	2	14.679	18.778	2.458	41	54	6	0	0	1	C6orf165	28,622	in gene	ActReg chr6 #13938	1	1	0
13939	6	88,182,139	88,182,921	782	2	11.64	12.64	4.92	19	20	10	1	1	2	C6orf165, SLC35A1	64840, -113	downstream, upstream	ActReg chr6 #13939	1	1	0
13940	6	88,433,045	88,433,385	340	1	10.182	4.727	2.182	16	7	4	0	0	0				ActReg chr6 #13940	1	0	0
13941	6	89,247,782	89,248,226	444	1	7.786	10.571	3.429	11	19	6	0	0	0				ActReg chr6 #13941	0	1	0
13942	6	90,012,670	90,013,086	416	1	1.308	1.846	10.538	3	2	15	0	0	1	GABRR2	12,089	in gene	ActReg chr6 #13942	0	0	1
13943	6	90,062,020	90,062,807	787	1	7.833	10.875	5.8	11	15	9	1	1	1	UBE2J1	206	in gene	ActReg chr6 #13943	0	1	0
13944	6	90,528,849	90,529,866	1,017	1	6.781	11.875	6.906	12	18	12	1	1	2	MDN1, CASP8AP2	85, -10262	in gene, upstream	ActReg chr6 #13944	0	1	0
13945	6	90,604,658	90,605,650	992	2	16.645	22	2.81	43	56	5	0	1	1	GJA10	966	in gene	ActReg chr6 #13945	1	1	0
13946	6	90,932,365	90,932,939	574	1	6.333	10.5	1	14	20	1	0	0	1	BACH2	73,975	in gene	ActReg chr6 #13946	0	1	0
13947	6	91,296,811	91,297,360	549	1	8.294	13.294	3.588	15	25	10	1	1	1	MAP3K7	-178	upstream	ActReg chr6 #13947	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
13948	6	93,550,060	93,550,530	470	1	8.8	10.533	2	14	15	2	0	0	0				ActReg chr6 #13948	0	1	0
13949	6	96,969,556	96,969,917	361	1	4.727	10.182	11	6	13	14	1	1	1	KIAA0776	34	in gene	ActReg chr6 #13949	0	0	1
13950	6	97,284,855	97,285,313	458	1	5.6	9.133	12.733	9	11	19	1	1	1	GPR63	269	in gene	ActReg chr6 #13950	0	0	1
13951	6	97,345,401	97,346,063	662	2	20.905	18.809	4.19	46	40	6	1	1	1	NDUFAF4	35	in gene	ActReg chr6 #13951	1	1	0
13952	6	99,105,524	99,106,210	686	2	11.048	7.273	1.857	21	18	2	0	0	0				ActReg chr6 #13952	1	1	0
13953	6	99,800,974	99,801,457	483	2	11.067	10.933	1.7	14	16	2	0	1	1	C6orf168	-3,684	upstream	ActReg chr6 #13953	1	1	0
13954	6	99,962,946	99,963,440	494	1	5.667	9.933	3.364	9	15	6	1	1	1	USP45	59	in gene	ActReg chr6 #13954	0	1	0
13955	6	100,036,828	100,037,239	411	1	4.462	3.385	10	7	5	15	2	0	0				ActReg chr6 #13955	0	0	1
13956	6	101,328,920	101,329,333	413	1	5	9.846	10.077	7	14	15	1	1	1	ASCC3	98	in gene	ActReg chr6 #13956	0	0	1
13957	6	101,841,166	101,841,701	535	2	10.059	11.353	3.882	20	19	6	1	1	1	GRIK2	-5,428	upstream	ActReg chr6 #13957	1	1	0
13958	6	102,062,488	102,063,098	610	1	10.316	4.316	0	17	10	0	0	0	1	GRIK2	215,932	in gene	ActReg chr6 #13958	1	0	0
13959	6	102,114,085	102,114,517	432	1	5.077	13	2.308	7	21	4	0	0	1	GRIK2	267,440	in gene	ActReg chr6 #13959	0	1	0
13960	6	105,307,275	105,307,760	485	1	7.4	10.733	2.6	15	17	7	1	1	1	HACE1	277	in gene	ActReg chr6 #13960	0	1	0
13961	6	105,335,070	105,335,645	575	1	6.889	9.944	1	13	16	1	0	0	0				ActReg chr6 #13961	0	1	0
13962	6	105,391,529	105,392,118	589	1	5.556	10.056	2.25	10	17	4	0	0	0				ActReg chr6 #13962	0	1	0
13963	6	105,850,661	105,851,651	990	2	8.645	9.355	2.273	22	14	4	1	1	2	PREP, LOC100506148	-157, 25896	upstream, downstream	ActReg chr6 #13963	1	1	0
13964	6	106,533,996	106,534,466	470	1	6.6	9.467	3.7	10	13	6	1	1	1	PRDM1	36	in gene	ActReg chr6 #13964	0	1	0
13965	6	106,773,327	106,773,765	438	1	7.929	11.429	4.214	13	13	6	1	1	1	ATG5	149	in gene	ActReg chr6 #13965	0	1	0
13966	6	106,958,403	106,958,849	446	1	7.286	12.429	4.5	12	23	7	1	1	1	AIM1	-1,104	upstream	ActReg chr6 #13966	0	1	0
13967	6	107,077,137	107,077,729	592	1	6.263	10.421	3.263	9	20	6	0	2	2	RTN4IP1, QRSL1	-60, -8	upstream, upstream	ActReg chr6 #13967	0	1	0
13968	6	107,348,924	107,349,892	968	2	20.71	26.613	2.9	57	72	6	1	1	1	C6orf203	1	in gene	ActReg chr6 #13968	1	1	0
13969	6	107,435,273	107,435,825	552	1	4.941	11.235	1.692	9	19	4	1	1	1	BEND3	87	in gene	ActReg chr6 #13969	0	1	0
13970	6	107,810,622	107,811,092	470	1	4.067	8.8	6.154	7	15	9	1	1	1	SOBP	-460	upstream	ActReg chr6 #13970	0	1	0
13971	6	108,881,568	108,881,989	421	1	8.214	4.286	10.143	11	6	16	1	1	1	FOXO3	752	in gene	ActReg chr6 #13971	0	0	1
13972	6	109,703,554	109,704,159	605	1	6.944	11.944	6.765	12	20	14	1	1	2	CD164, PPIL6	-94, 58518	upstream, downstream	ActReg chr6 #13972	0	1	0
13973	6	110,202,352	110,202,640	288	1	1.4	2.111	10.556	2	3	15	0	0	0				ActReg chr6 #13973	0	0	1
13974	6	110,299,572	110,300,207	635	2	10.1	12.65	3.35	18	22	5	1	1	1	GPR6	-409	upstream	ActReg chr6 #13974	1	1	0
13975	6	110,494,744	110,495,070	326	1	6.7	10.7	1.2	9	16	2	0	1	2	WASF1, CDC40	6300, -6717	in gene, upstream	ActReg chr6 #13975	0	1	0
13976	6	110,500,721	110,501,441	720	1	7	10.565	4.391	10	18	8	2	2	2	WASF1, CDC40	126, -543	in gene, upstream	ActReg chr6 #13976	0	1	0
13977	6	110,576,393	110,576,993	600	2	10.526	10.737	3.933	20	24	7	0	0	1	C6orf186	102,782	in gene	ActReg chr6 #13977	1	1	0
13978	6	110,868,475	110,868,998	523	1	6.133	9.059	0	9	14	0	0	0	0				ActReg chr6 #13978	0	1	0
13979	6	111,135,805	111,136,245	440	1	6.643	9	5.857	10	14	11	1	1	1	CDK19	387	in gene	ActReg chr6 #13979	0	1	0
13980	6	111,136,387	111,137,072	685	1	7.429	11.524	4.4	15	15	9	1	1	1	CDK19	-317	upstream	ActReg chr6 #13980	0	1	0
13981	6	111,303,011	111,303,695	684	1	5.05	11.095	4.333	10	16	7	1	1	1	RPF2	62	in gene	ActReg chr6 #13981	0	1	0
13982	6	111,804,331	111,804,888	557	2	10.412	8.882	6.824	14	17	14	1	2	2	REV3L, LOC643749	-195, -66	upstream, upstream	ActReg chr6 #13982	1	1	0
13983	6	112,194,500	112,194,930	430	1	5.692	6.385	12.385	8	10	19	1	1	1	FYN	-88	upstream	ActReg chr6 #13983	0	0	1
13984	6	112,364,119	112,364,626	507	2	11	9.562	1	19	15	1	0	0	0				ActReg chr6 #13984	1	1	0
13985	6	112,576,252	112,576,684	432	1	3.214	10.214	1	6	15	1	0	1	2	LAMA4, LOC100506430	-640, 18671	upstream, in gene	ActReg chr6 #13985	0	1	0
13986	6	113,768,212	113,768,551	339	1	3.75	10.454	0	6	14	0	0	0	0				ActReg chr6 #13986	0	1	0
13987	6	114,291,534	114,291,826	292	1	3.444	6.333	11.222	5	12	16	1	1	1	HDAC2	679	in gene	ActReg chr6 #13987	0	0	1
13988	6	114,291,876	114,292,850	974	2	10.333	14.067	4.931	21	25	11	1	1	1	HDAC2	-4	upstream	ActReg chr6 #13988	1	1	0
13989	6	114,664,256	114,664,572	316	1	2.6	3.5	9.4	3	5	13	1	0	0				ActReg chr6 #13989	0	0	1
13990	6	116,892,007	116,893,013	1,006	2	19.613	23.161	4.065	52	63	8	1	1	1	RWDD1	-73	upstream	ActReg chr6 #13990	1	1	0
13991	6	116,917,939	116,918,484	545	2	9.471	8.059	1	16	13	1	0	0	1	RWDD1	25,628	downstream	ActReg chr6 #13991	1	1	0
13992	6	116,989,592	116,990,008	416	1	8.385	10.385	4.273	13	13	7	0	1	1	ZUFSP	173	in gene	ActReg chr6 #13992	0	1	0
13993	6	117,001,984	117,002,449	465	1	6.533	6.2	10.067	10	7	18	1	1	1	KPNA5	-151	upstream	ActReg chr6 #13993	0	0	1
13994	6	117,694,431	117,694,766	335	1	2.111	2.636	10.727	3	4	15	0	0	1	ROS1	52,420	in gene	ActReg chr6 #13994	0	0	1
13995	6	117,996,030	117,996,846	816	2	37.962	48.846	2.48	116	137	6	1	1	1	NUS1	-179	upstream	ActReg chr6 #13995	1	1	0
13996	6	118,816,797	118,817,305	508	1	9.25	9.5	1.571	14	18	2	0	0	1	C6orf204	214,187	in gene	ActReg chr6 #13996	0	1	0
13997	6	118,971,641	118,972,307	666	1	8.095	10.905	6.714	13	16	13	1	0	1	C6orf204	59,264	in gene	ActReg chr6 #13997	0	1	0
13998	6	119,030,967	119,031,706	739	1	13.043	9.478	1.4	30	15	2	0	1	1	C6orf204	-98	upstream	ActReg chr6 #13998	1	0	0
13999	6	119,214,835	119,215,755	920	2	26.241	26.793	3.565	81	80	8	1	1	1	ASF1A	54	in gene	ActReg chr6 #13999	1	1	0
14000	6	121,655,469	121,655,964	495	1	8.133	9	7.8	10	13	13	1	1	1	C6orf170	-72	upstream	ActReg chr6 #14000	0	1	0
14001	6	125,474,713	125,475,112	399	1	9.692	8	1.846	14	12	3	1	1	1	TPD52L1	33	in gene	ActReg chr6 #14001	1	0	0
14002	6	125,622,599	125,623,339	740	1	5.783	11.087	3.35	13	17	6	1	1	1	HDDC2	313	in gene	ActReg chr6 #14002	0	1	0
14003	6	126,133,594	126,134,239	645	2	10.1	10.75	2.056	15	19	5	0	0	1	NCOA7	21,915	in gene	ActReg chr6 #14003	1	1	0
14004	6	126,277,637	126,278,294	657	2	13	13.9	5.9	28	27	9	1	1	1	HINT3	104	in gene	ActReg chr6 #14004	1	1	0
14005	6	126,860,039	126,860,638	599	1	10.5	6.889	1	20	13	1	0	0	0				ActReg chr6 #14005	1	0	0
14006	6	126,946,040	126,946,711	671	2	12.7	10.952	1.462	28	22	2	0	0	0				ActReg chr6 #14006	1	1	0
14007	6	127,587,564	127,588,530	966	1	8.7	10.433	3.5	13	17	5	1	1	1	RNF146	27	in gene	ActReg chr6 #14007	0	1	0
14008	6	127,836,993	127,838,232	1,239	2	9.5	13.105	4.515	15	20	9	1	1	1	C6orf174	2,888	in gene	ActReg chr6 #14008	1	1	0
14009	6	131,949,037	131,949,831	794	2	14.32	17.36	5.2	29	47	10	1	1	2	MED23, ENPP3	-71, -9008	upstream, upstream	ActReg chr6 #14009	1	1	0
14010	6	132,271,443	132,272,072	629	1	10.2	10.7	2.9	17	16	6	2	1	2	LOC100131774, CTGF	5127, 761	downstream, in gene	ActReg chr6 #14010	0	1	0
14011	6	133,135,076	133,135,930	854	3	19.192	15	8.192	37	32	18	1	4	4	RPS12, SNORD101, SNORD100, SNORA33	-205, -943, -2438, -2855	upstream, upstream, upstream, upstream	ActReg chr6 #14011	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14012	6	134,273,099	134,273,658	559	1	12.118	8.412	4.588	20	12	6	1	1	1	TBPL1	-923	upstream	ActReg chr6 #14012	1	0	0
14013	6	134,274,332	134,274,692	360	1	4.417	5.5	9.417	8	12	14	1	1	1	TBPL1	211	in gene	ActReg chr6 #14013	0	0	1
14014	6	134,743,834	134,744,445	611	1	10.368	7	2	16	13	2	0	0	0				ActReg chr6 #14014	1	0	0
14015	6	135,491,155	135,491,718	563	1	10.333	5.778	1	18	10	1	0	0	0				ActReg chr6 #14015	1	0	0
14016	6	135,818,460	135,819,177	717	3	8.739	10.522	7.609	18	17	14	1	2	2	AHI1, C6orf217	85, -121	in gene, upstream	ActReg chr6 #14016	1	1	1
14017	6	136,043,984	136,044,450	466	1	5.867	10.867	1	12	16	1	0	0	0				ActReg chr6 #14017	0	1	0
14018	6	136,571,166	136,571,828	662	1	7.762	12.143	4.19	12	22	6	1	1	2	FAM54A, BCLAF1	-48, 39492	upstream, downstream	ActReg chr6 #14018	0	1	0
14019	6	136,610,786	136,611,105	319	1	11.3	9	11.4	15	10	15	1	1	1	BCLAF1	44	in gene	ActReg chr6 #14019	0	0	1
14020	6	137,113,901	137,114,289	388	1	5.083	9.833	11.333	8	12	16	1	1	1	MAP3K5	-439	upstream	ActReg chr6 #14020	0	0	1
14021	6	137,540,229	137,540,852	623	1	4.944	4.579	12.21	7	13	18	1	1	1	IFNGR1	27	in gene	ActReg chr6 #14021	0	0	1
14022	6	139,309,116	139,309,559	443	1	9.929	10.357	10.071	13	15	14	1	1	1	REPS1	61	in gene	ActReg chr6 #14022	0	1	0
14023	6	139,695,510	139,696,943	1,433	2	12.622	14.133	3.872	25	31	13	1	1	1	CITED2	-441	upstream	ActReg chr6 #14023	1	1	0
14024	6	140,123,031	140,123,463	432	1	7.571	9.143	1	14	15	1	0	0	0				ActReg chr6 #14024	0	1	0
14025	6	140,364,399	140,364,997	598	1	6.889	10.316	1	13	23	1	0	0	0				ActReg chr6 #14025	0	1	0
14026	6	141,362,661	141,362,980	319	1	2.375	2.25	9.2	3	4	13	0	0	0				ActReg chr6 #14026	0	0	1
14027	6	142,467,985	142,468,766	781	2	8.917	14.292	5.833	18	25	13	1	1	1	VTA1	-35	upstream	ActReg chr6 #14027	1	1	0
14028	6	142,622,828	142,623,358	530	1	10	10.375	5.688	16	15	10	1	1	1	GPR126	37	in gene	ActReg chr6 #14028	1	0	0
14029	6	143,771,551	143,772,249	698	2	10.636	12.909	5.273	18	23	10	1	2	2	ADAT2, PEX3	-59, -18	upstream, upstream	ActReg chr6 #14029	1	1	0
14030	6	146,055,899	146,056,426	527	1	5.882	10.823	3.412	9	16	6	1	2	2	EPM2A, LOC100507557	829, 154	in gene, in gene	ActReg chr6 #14030	0	1	0
14031	6	146,349,272	146,349,930	658	2	8.095	13.619	1.75	15	29	3	0	1	1	GRM1	819	in gene	ActReg chr6 #14031	1	1	0
14032	6	148,663,581	148,664,106	525	1	4.824	8.941	1.571	8	15	3	1	1	1	SASH1	114	in gene	ActReg chr6 #14032	0	1	0
14033	6	149,256,865	149,257,231	366	1	10.091	4.091	0	15	6	0	0	0	1	UST	188,777	in gene	ActReg chr6 #14033	1	0	0
14034	6	149,333,090	149,333,654	564	2	8.882	11.177	1	17	19	1	0	0	1	UST	265,101	in gene	ActReg chr6 #14034	1	1	0
14035	6	149,638,186	149,638,697	511	1	7.812	9.375	4.083	14	18	7	1	1	1	MAP3K7IP2	-995	upstream	ActReg chr6 #14035	0	1	0
14036	6	149,866,861	149,867,586	725	2	10.174	11.609	4.435	19	22	8	1	1	1	PPIL4	-52	upstream	ActReg chr6 #14036	1	1	0
14037	6	150,070,777	150,071,272	495	1	6.5	9.5	5.188	9	14	10	1	2	2	NUP43, PCMT1	-3336, 193	upstream, in gene	ActReg chr6 #14037	0	1	0
14038	6	150,243,734	150,244,321	587	1	4.789	6.316	11.263	10	10	19	1	1	1	RAET1G	187	in gene	ActReg chr6 #14038	0	0	1
14039	6	150,378,632	150,378,944	312	1	2.3	3.1	10.2	4	5	13	1	0	1	ULBP3	11,414	downstream	ActReg chr6 #14039	0	0	1
14040	6	150,390,028	150,390,436	408	1	6.692	6	10.231	9	10	17	1	1	1	ULBP3	-30	upstream	ActReg chr6 #14040	0	0	1
14041	6	151,772,988	151,773,782	794	1	11.2	8.16	5.696	21	14	10	1	2	2	RMND1, C6orf211	-69, -37	upstream, upstream	ActReg chr6 #14041	1	0	0
14042	6	152,168,186	152,168,597	411	1	10.308	8.25	2.444	19	12	3	0	0	1	ESR1	156,760	in gene	ActReg chr6 #14042	1	0	0
14043	6	153,071,719	153,072,201	482	1	10.2	7.6	1.8	14	13	2	0	1	1	VIP	27	in gene	ActReg chr6 #14043	1	0	0
14044	6	154,360,100	154,361,204	1,104	2	18.235	26.088	3.281	45	76	6	1	0	1	OPRM1	29,016	in gene	ActReg chr6 #14044	1	1	0
14045	6	155,054,156	155,055,008	852	1	9.593	10.444	3	17	15	6	1	1	1	RBM16	70	in gene	ActReg chr6 #14045	0	1	0
14046	6	155,447,980	155,448,743	763	1	14.5	6.083	2.385	26	11	4	0	0	1	TIAM2	36,938	in gene	ActReg chr6 #14046	1	0	0
14047	6	155,492,223	155,492,728	505	1	7.062	9.938	1	11	18	1	0	0	1	TIAM2	81,052	in gene	ActReg chr6 #14047	0	1	0
14048	6	157,342,411	157,343,003	592	1	6.389	11.667	5.812	12	15	10	1	0	1	ARID1B	243,643	in gene	ActReg chr6 #14048	0	1	0
14049	6	157,469,852	157,470,285	433	1	9.929	7	3.429	13	12	6	0	0	1	ARID1B	371,004	in gene	ActReg chr6 #14049	1	0	0
14050	6	157,744,117	157,744,830	713	1	9.045	12.091	8.318	16	22	13	1	1	1	C6orf35	780	in gene	ActReg chr6 #14050	0	1	0
14051	6	157,876,784	157,877,394	610	1	7.684	9.947	3.474	12	17	7	0	0	1	ZDHHC14	74,532	in gene	ActReg chr6 #14051	0	1	0
14052	6	157,950,295	157,950,809	514	1	9.688	6.125	0	17	9	0	0	0	1	ZDHHC14	147,995	in gene	ActReg chr6 #14052	1	0	0
14053	6	158,185,337	158,186,042	705	2	9.5	11.318	2.409	14	21	3	0	0	0				ActReg chr6 #14053	1	1	0
14054	6	158,956,867	158,957,737	870	2	12.63	14.148	6.105	24	27	10	1	1	1	TMEM181	-166	upstream	ActReg chr6 #14054	1	1	0
14055	6	159,065,377	159,065,949	572	2	9.706	6.882	11.471	17	9	21	1	2	3	TMEM181, DYNLT1, SYTL3	108195, 141, -5383	downstream, in gene, upstream	ActReg chr6 #14055	1	0	1
14056	6	159,420,809	159,421,218	409	1	7.692	9.769	11.923	11	11	16	1	1	1	RSPH3	185	in gene	ActReg chr6 #14056	0	1	0
14057	6	160,113,614	160,114,328	714	1	7.409	11	3.421	12	16	6	1	1	1	SOD2	382	in gene	ActReg chr6 #14057	0	1	0
14058	6	160,114,374	160,114,753	379	1	9.583	11.5	4.545	14	19	9	1	1	1	SOD2	-210	upstream	ActReg chr6 #14058	0	1	0
14059	6	160,147,921	160,148,389	468	1	9.067	5.933	6.4	13	12	11	1	1	1	WTAP	3	in gene	ActReg chr6 #14059	1	0	0
14060	6	160,183,156	160,183,604	448	1	8.214	9.214	6.357	11	10	9	1	2	3	WTAP, LOC100129518, ACAT2	35228, -16, 391	downstream, upstream, in gene	ActReg chr6 #14060	0	1	0
14061	6	161,412,441	161,413,056	615	1	10.65	9.6	3.6	16	15	7	1	1	1	MAP3K4	-74	upstream	ActReg chr6 #14061	1	0	0
14062	6	161,458,980	161,459,502	522	1	8.625	11	0	15	19	0	0	0	1	MAP3K4	46,419	in gene	ActReg chr6 #14062	0	1	0
14063	6	163,834,223	163,834,863	640	1	10.8	10.4	2.95	16	19	5	0	1	1	QKI	-1,132	upstream	ActReg chr6 #14063	0	1	0
14064	6	164,235,546	164,236,095	549	1	6.353	9.294	1.462	11	16	2	0	0	0				ActReg chr6 #14064	0	1	0
14065	6	164,668,235	164,668,703	468	1	5.286	10.071	1.923	9	15	3	0	0	0				ActReg chr6 #14065	0	1	0
14066	6	166,076,795	166,077,098	303	1	5.1	5.6	12	7	7	17	1	1	1	PDE10A	-1,362	upstream	ActReg chr6 #14066	0	0	1
14067	6	166,308,785	166,309,482	697	2	8.818	10.954	1.867	18	22	3	0	1	1	LOC100505705	592	in gene	ActReg chr6 #14067	1	1	0
14068	6	166,400,903	166,401,751	848	2	10.423	10.231	2.769	17	15	5	1	2	2	C6orf176, LOC441177	200, 288	in gene, in gene	ActReg chr6 #14068	1	1	0
14069	6	166,795,569	166,796,235	666	1	8.619	11.762	6.476	13	16	9	1	1	1	BRP44L	584	in gene	ActReg chr6 #14069	0	1	0
14070	6	166,826,148	166,826,426	278	1	2.625	1.75	11	3	2	14	1	0	1	RPS6KA2	449,484	in gene	ActReg chr6 #14070	0	0	1
14071	6	167,412,731	167,413,144	413	1	7.385	11.923	3.75	11	19	6	1	1	1	FGFR1OP	121	in gene	ActReg chr6 #14071	0	1	0
14072	6	168,083,620	168,084,165	545	1	5.824	11.529	4.154	11	15	7	0	1	1	LOC401286	-3,989	upstream	ActReg chr6 #14072	0	1	0
14073	6	168,502,337	168,502,773	436	1	1.7	2.462	12.154	2	4	20	1	0	0				ActReg chr6 #14073	0	0	1
14074	6	168,793,899	168,794,522	623	1	1.526	3.263	9.474	2	6	13	0	0	0				ActReg chr6 #14074	0	0	1
14075	6	169,391,861	169,392,233	372	1	1.583	2.273	10.167	2	3	17	0	0	0				ActReg chr6 #14075	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14076	6	169,470,682	169,471,197	515	1	5.875	9.875	1.5	7	15	2	0	0	0				ActReg chr6 #14076	0	1	0
14077	6	169,692,532	169,692,958	426	1	6.615	10.538	1	11	14	1	0	0	0				ActReg chr6 #14077	0	1	0
14078	6	170,101,827	170,102,902	1,075	2	10.212	12.454	8.303	14	20	13	1	2	3	WDR27, C6orf120, PHF10	-205, 107, 21742	upstream, in gene, downstream	ActReg chr6 #14078	1	1	0
14079	6	170,151,521	170,152,461	940	1	5.552	10.69	6.667	13	16	16	1	2	2	TCTE3, C6orf70	-353, 270	upstream, in gene	ActReg chr6 #14079	0	1	0
14080	6	170,211,660	170,212,005	345	1	2	1.636	9.818	3	2	14	0	0	1	C6orf208	21,663	downstream	ActReg chr6 #14080	0	0	1
14081	6	170,592,745	170,593,151	406	1	3.167	2.75	10.667	4	4	15	1	0	1	DLL1	6,749	in gene	ActReg chr6 #14081	0	0	1
14082	6	170,600,588	170,600,889	301	1	2.667	3.333	11	5	5	14	1	1	1	DLL1	-1,041	upstream	ActReg chr6 #14082	0	0	1
14083	6	170,747,383	170,747,789	406	1	7.308	9.538	2.538	13	12	5	0	0	0				ActReg chr6 #14083	0	1	0
14084	6	170,863,154	170,864,000	846	2	7.741	10	3.346	15	16	7	1	2	2	PSMB1, TBP	-1160, 156	upstream, in gene	ActReg chr6 #14084	1	1	0
14085	7	82,145	82,601	456	1	2.462	5.857	12.643	5	5	18	1	0	0				ActReg chr7 #14085	0	0	1
14086	7	101,699	102,479	780	1	7.13	12.375	3.375	17	17	7	0	0	0				ActReg chr7 #14086	0	1	0
14087	7	159,622	160,126	504	1	4.429	6.133	22	7	10	40	1	0	1	LOC100507642	10,277	downstream	ActReg chr7 #14087	0	0	1
14088	7	205,690	206,577	887	1	2.607	3.357	11.643	5	5	17	1	0	1	FAM20C	13,164	in gene	ActReg chr7 #14088	0	0	1
14089	7	211,433	212,068	635	1	3.65	2.6	10.45	5	4	16	0	0	1	FAM20C	18,781	in gene	ActReg chr7 #14089	0	0	1
14090	7	301,280	301,708	428	1	1.357	3.615	10.929	2	5	16	0	1	2	FAM20C, LOC100288496	108525, -361	downstream, upstream	ActReg chr7 #14090	0	0	1
14091	7	306,159	307,506	1,347	1	3.81	4.15	11.714	8	9	17	1	0	2	FAM20C, LOC100288496	113863, 4977	downstream, downstream	ActReg chr7 #14091	0	0	1
14092	7	329,290	329,858	568	1	3.333	4.833	11.778	7	6	19	1	0	0				ActReg chr7 #14092	0	0	1
14093	7	367,223	368,024	801	1	5.84	4.04	13.52	10	8	22	0	0	0				ActReg chr7 #14093	0	0	1
14094	7	386,742	387,117	375	1	2.1	5.167	11.583	4	8	15	1	0	0				ActReg chr7 #14094	0	0	1
14095	7	416,721	417,358	637	1	2.556	2.588	10.8	5	4	16	1	1	1	LOC442497	-2,352	upstream	ActReg chr7 #14095	0	0	1
14096	7	431,305	432,005	700	1	5.955	2.909	14.046	10	4	22	0	0	1	LOC442497	12,264	downstream	ActReg chr7 #14096	0	0	1
14097	7	450,550	450,954	404	1	5.538	6	10.769	8	9	15	0	0	0				ActReg chr7 #14097	0	0	1
14098	7	455,012	455,597	585	1	5.056	7.111	13.111	9	13	20	0	0	0				ActReg chr7 #14098	0	0	1
14099	7	476,192	476,666	474	1	5.667	8.6	11.2	7	12	15	0	1	1	LOC100131372	-4,756	upstream	ActReg chr7 #14099	0	0	1
14100	7	484,456	485,098	642	1	5.1	3.5	13.1	8	5	20	0	0	0				ActReg chr7 #14100	0	0	1
14101	7	494,738	495,710	972	1	4.433	7.067	12.133	7	12	18	1	0	0				ActReg chr7 #14101	0	0	1
14102	7	501,587	502,086	499	1	2.062	3.562	10.625	5	7	16	1	0	0				ActReg chr7 #14102	0	0	1
14103	7	558,347	558,922	575	1	4.5	11.222	4.722	7	20	8	1	2	2	PDGFA, FLJ44511	847, -1394	in gene, upstream	ActReg chr7 #14103	0	1	0
14104	7	561,313	561,682	369	1	4.818	4.364	11.546	7	6	13	1	2	2	PDGFA, FLJ44511	-2016, 1469	upstream, in gene	ActReg chr7 #14104	0	0	1
14105	7	570,195	570,650	455	1	1.111	2.083	12.857	2	3	18	1	0	1	FLJ44511	10,394	downstream	ActReg chr7 #14105	0	0	1
14106	7	578,420	579,076	656	1	6.905	3.889	10.095	13	10	15	0	0	1	PRKAR1B	188,565	downstream	ActReg chr7 #14106	0	0	1
14107	7	589,421	590,028	607	1	1.722	3.789	10.737	3	6	13	1	0	1	PRKAR1B	177,589	in gene	ActReg chr7 #14107	0	0	1
14108	7	629,607	630,077	470	1	2.909	5.143	10.857	5	7	15	0	0	1	PRKAR1B	137,471	in gene	ActReg chr7 #14108	0	0	1
14109	7	633,357	633,820	463	1	5.143	5.214	13.143	7	9	18	0	0	2	PRKAR1B, LOC100505500	133725, -8894	in gene, upstream	ActReg chr7 #14109	0	0	1
14110	7	644,640	645,055	415	1	4.154	1	11.462	6	1	17	1	1	2	PRKAR1B, LOC100505500	122466, 2365	in gene, in gene	ActReg chr7 #14110	0	0	1
14111	7	655,807	656,361	554	1	4.111	3.056	10.889	7	6	20	0	0	2	PRKAR1B, LOC100505500	111229, 13602	in gene, downstream	ActReg chr7 #14111	0	0	1
14112	7	907,506	908,185	679	1	3.333	5.286	12.429	5	9	18	0	0	2	SUN1, C7orf20	52651, -8346	in gene, upstream	ActReg chr7 #14112	0	0	1
14113	7	915,582	916,525	943	2	11.367	12.633	2.609	24	23	7	1	2	3	SUN1, C7orf20, LOC100505531	60859, -138, -3533	downstream, upstream, upstream	ActReg chr7 #14113	1	1	0
14114	7	937,454	939,034	1,580	1	3.7	4.681	11.939	9	8	20	0	0	2	C7orf20, ADAP1	22053, 56045	downstream, in gene	ActReg chr7 #14114	0	0	1
14115	7	940,520	940,976	456	1	2.071	5.143	11.786	3	7	17	0	0	2	C7orf20, ADAP1	24557, 53541	downstream, in gene	ActReg chr7 #14115	0	0	1
14116	7	949,017	949,917	900	1	4.714	6.056	13.429	7	13	20	1	0	1	ADAP1	44,822	in gene	ActReg chr7 #14116	0	0	1
14117	7	959,650	960,050	400	1	3.583	3.091	11	5	5	16	2	0	1	ADAP1	34,439	in gene	ActReg chr7 #14117	0	0	1
14118	7	961,941	962,403	462	1	4.267	2.933	10.4	6	5	18	0	0	1	ADAP1	32,117	in gene	ActReg chr7 #14118	0	0	1
14119	7	965,266	965,708	442	1	7	7.286	10.5	10	10	15	0	0	1	ADAP1	28,802	in gene	ActReg chr7 #14119	0	0	1
14120	7	974,676	975,837	1,161	1	5.111	6.194	13.194	9	11	18	0	0	1	ADAP1	19,033	in gene	ActReg chr7 #14120	0	0	1
14121	7	985,579	986,073	494	1	2.667	3.133	13.467	6	4	17	1	0	1	ADAP1	8,463	in gene	ActReg chr7 #14121	0	0	1
14122	7	1,001,693	1,002,527	834	1	2.462	5.192	12.615	3	8	18	0	1	2	ADAP1, COX19	-7821, 13125	upstream, downstream	ActReg chr7 #14122	0	0	1
14123	7	1,014,489	1,015,967	1,478	3	13.109	16.717	8.239	40	43	16	1	2	2	COX19, CYP2W1	7, -7607	in gene, upstream	ActReg chr7 #14123	1	1	1
14124	7	1,059,380	1,059,909	529	1	4.412	5.941	12.353	7	8	19	1	0	2	C7orf50, MIR339	118249, 3018	in gene, downstream	ActReg chr7 #14124	0	0	1
14125	7	1,122,641	1,123,031	390	1	4.5	2	11.583	7	4	18	0	1	2	C7orf50, GPER	55057, -3607	in gene, upstream	ActReg chr7 #14125	0	0	1
14126	7	1,162,314	1,162,880	566	1	2	3.438	11.5	3	5	15	0	0	1	C7orf50	15,296	in gene	ActReg chr7 #14126	0	0	1
14127	7	1,199,454	1,200,248	794	1	10.48	9.56	5.2	15	16	7	1	1	1	ZFAND2A	4	in gene	ActReg chr7 #14127	1	0	0
14128	7	1,264,961	1,265,328	367	1	3.1	3.375	11	5	5	17	1	1	1	UNCX	-7,510	upstream	ActReg chr7 #14128	0	0	1
14129	7	1,274,382	1,274,939	557	1	3	5.235	11.941	5	9	17	1	1	1	UNCX	2,006	in gene	ActReg chr7 #14129	0	0	1
14130	7	1,282,308	1,282,900	592	1	4.222	3.389	11.222	6	7	15	1	0	1	UNCX	9,950	downstream	ActReg chr7 #14130	0	0	1
14131	7	1,293,157	1,293,881	724	1	3	3.909	9.455	5	7	16	0	0	0				ActReg chr7 #14131	0	0	1
14132	7	1,314,656	1,314,959	303	1	4.667	2.9	11.2	7	4	15	1	0	0				ActReg chr7 #14132	0	0	1
14133	7	1,315,687	1,316,021	334	1	2.4	4.2	10.9	3	5	14	1	0	0				ActReg chr7 #14133	0	0	1
14134	7	1,338,727	1,339,093	366	1	3.727	4.7	11.273	5	7	16	0	0	0				ActReg chr7 #14134	0	0	1
14135	7	1,351,599	1,352,206	607	1	4	2.632	11.316	7	4	16	1	0	0				ActReg chr7 #14135	0	0	1
14136	7	1,353,794	1,354,403	609	1	4.105	2.875	13.684	6	6	18	0	0	0				ActReg chr7 #14136	0	0	1
14137	7	1,360,779	1,361,332	553	1	1.765	2.529	10.706	3	5	16	0	0	0				ActReg chr7 #14137	0	0	1
14138	7	1,364,785	1,365,893	1,108	1	4.429	3.229	12.143	8	6	16	0	0	0				ActReg chr7 #14138	0	0	1
14139	7	1,369,465	1,369,847	382	1	1.667	4.583	12.917	5	6	17	0	0	0				ActReg chr7 #14139	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14140	7	1,380,650	1,381,244	594	1	2.938	3.333	10.889	6	7	13	0	0	0				ActReg chr7 #14140	0	0	1
14141	7	1,395,272	1,395,764	492	1	3.867	3	12.2	6	4	17	0	0	0				ActReg chr7 #14141	0	0	1
14142	7	1,397,280	1,398,096	816	1	5.208	3.28	11.192	9	6	17	0	0	0				ActReg chr7 #14142	0	0	1
14143	7	1,404,344	1,404,820	476	1	2.8	3.267	12.8	4	4	22	0	0	0				ActReg chr7 #14143	0	0	1
14144	7	1,451,869	1,452,421	552	1	7.056	5.056	13.556	11	11	20	1	0	0				ActReg chr7 #14144	0	0	1
14145	7	1,461,019	1,461,623	604	1	1.562	4.368	13.368	4	7	21	1	0	0				ActReg chr7 #14145	0	0	1
14146	7	1,469,855	1,470,365	510	1	2.375	4.688	11.625	5	8	15	0	0	1	MICALL2	28,999	downstream	ActReg chr7 #14146	0	0	1
14147	7	1,497,549	1,498,013	464	1	8.286	4.714	14	14	7	20	0	1	1	MICALL2	1,328	in gene	ActReg chr7 #14147	0	0	1
14148	7	1,498,418	1,499,097	679	2	12.095	8.762	11.952	25	12	23	1	1	1	MICALL2	352	in gene	ActReg chr7 #14148	1	0	1
14149	7	1,518,000	1,518,531	531	1	2.706	3.706	11.823	5	5	16	0	0	1	INTS1	25,753	in gene	ActReg chr7 #14149	0	0	1
14150	7	1,519,643	1,520,110	467	1	4.267	4.333	12.4	7	5	16	1	0	1	INTS1	24,142	in gene	ActReg chr7 #14150	0	0	1
14151	7	1,520,785	1,521,234	449	1	5.5	2.857	11.643	8	4	16	0	0	1	INTS1	23,009	in gene	ActReg chr7 #14151	0	0	1
14152	7	1,541,078	1,541,561	483	1	4.467	3.25	11.933	6	6	18	0	1	1	INTS1	2,699	in gene	ActReg chr7 #14152	0	0	1
14153	7	1,543,477	1,544,590	1,113	2	27.647	32.971	4.394	86	107	10	1	1	1	INTS1	-15	upstream	ActReg chr7 #14153	1	1	0
14154	7	1,551,369	1,551,815	446	1	6	3.5	12.5	10	6	17	0	1	1	INTS1	-7,574	upstream	ActReg chr7 #14154	0	0	1
14155	7	1,551,966	1,552,669	703	1	5	6.5	12.591	9	9	20	0	0	1	INTS1	-8,299	upstream	ActReg chr7 #14155	0	0	1
14156	7	1,552,686	1,553,566	880	2	7.407	10.185	12.63	11	22	21	0	0	1	INTS1	-9,108	upstream	ActReg chr7 #14156	0	1	1
14157	7	1,571,972	1,572,659	687	1	4.81	10.809	3.789	7	19	8	0	2	3	MAFK, LOC100128653, TMEM184A	1947, 2201, 23751	in gene, in gene, downstream	ActReg chr7 #14157	0	1	0
14158	7	1,573,549	1,574,121	572	1	6.556	8.389	12.722	12	12	19	0	1	3	MAFK, LOC100128653, TMEM184A	3467, 681, 22231	in gene, in gene, downstream	ActReg chr7 #14158	0	0	1
14159	7	1,578,094	1,578,767	673	1	2.714	3.381	10.952	5	6	16	0	1	3	MAFK, LOC100128653, TMEM184A	8062, -3914, 17636	in gene, upstream, downstream	ActReg chr7 #14159	0	0	1
14160	7	1,589,757	1,590,491	734	1	3	4.913	12.043	4	8	17	1	0	2	MAFK, TMEM184A	19756, 5942	downstream, in gene	ActReg chr7 #14160	0	0	1
14161	7	1,595,672	1,596,294	622	1	6.95	4.75	12.35	11	8	19	0	1	1	TMEM184A	83	in gene	ActReg chr7 #14161	0	0	1
14162	7	1,597,686	1,598,856	1,170	1	3.27	5.081	12.622	7	9	17	0	1	2	TMEM184A, PSMG3	-2205, 11397	upstream, downstream	ActReg chr7 #14162	0	0	1
14163	7	1,599,218	1,599,689	471	1	3.462	5.867	11.533	7	9	17	0	1	2	TMEM184A, PSMG3	-3387, 10215	upstream, downstream	ActReg chr7 #14163	0	0	1
14164	7	1,603,527	1,604,010	483	1	1.8	2.133	11.533	2	4	18	0	2	3	TMEM184A, PSMG3, KIAA1908	-7702, 5900, -5941	upstream, downstream, upstream	ActReg chr7 #14164	0	0	1
14165	7	1,609,264	1,610,496	1,232	2	9.128	10.564	10.103	14	21	17	1	2	2	PSMG3, KIAA1908	-212, 171	upstream, in gene	ActReg chr7 #14165	0	1	1
14166	7	1,681,650	1,682,181	531	1	2.941	3.294	11.353	4	6	14	0	0	0				ActReg chr7 #14166	0	0	1
14167	7	1,744,303	1,744,706	403	1	3.692	5.462	11.615	8	9	15	0	1	1	ELFN1	-4,294	upstream	ActReg chr7 #14167	0	0	1
14168	7	1,764,746	1,765,210	464	1	2.929	3.929	12.714	4	7	20	0	0	1	ELFN1	16,180	in gene	ActReg chr7 #14168	0	0	1
14169	7	1,780,792	1,781,216	424	1	3.714	4.5	11.786	5	8	18	0	1	2	ELFN1, LOC100505644	32206, 936	in gene, in gene	ActReg chr7 #14169	0	0	1
14170	7	1,788,756	1,789,273	517	1	2.062	4.688	13.688	5	9	22	0	1	2	ELFN1, LOC100505644	40216, -7074	downstream, upstream	ActReg chr7 #14170	0	0	1
14171	7	1,790,607	1,791,042	435	1	5.5	2.222	12.286	7	3	18	0	0	2	ELFN1, LOC100505644	42026, -8884	downstream, upstream	ActReg chr7 #14171	0	0	1
14172	7	1,797,732	1,798,124	392	1	4.583	3.917	10.333	6	6	16	0	0	0				ActReg chr7 #14172	0	0	1
14173	7	1,863,084	1,863,516	432	1	1.538	2.077	10.923	2	3	16	0	0	1	MAD1L1	409,283	in gene	ActReg chr7 #14173	0	0	1
14174	7	1,884,411	1,884,818	407	1	2.615	5.385	11.923	7	8	17	0	0	2	MAD1L1, LOC100128374	387969, 6392	in gene, in gene	ActReg chr7 #14174	0	0	1
14175	7	2,004,723	2,005,353	630	1	2.889	4.7	11.2	5	8	16	0	0	1	MAD1L1	267,545	in gene	ActReg chr7 #14175	0	0	1
14176	7	2,012,954	2,013,302	348	1	2.636	4.182	12.273	4	8	15	0	0	1	MAD1L1	259,455	in gene	ActReg chr7 #14176	0	0	1
14177	7	2,029,206	2,030,050	844	1	4.222	4.481	11.222	8	9	17	1	0	1	MAD1L1	242,955	in gene	ActReg chr7 #14177	0	0	1
14178	7	2,031,916	2,032,336	420	1	2.385	2.5	9.923	5	3	15	0	0	1	MAD1L1	240,457	in gene	ActReg chr7 #14178	0	0	1
14179	7	2,096,571	2,097,007	436	1	2.846	3.571	11.786	5	5	19	0	0	1	MAD1L1	175,794	in gene	ActReg chr7 #14179	0	0	1
14180	7	2,272,271	2,273,008	737	1	16.261	11.913	6.826	28	18	13	1	1	3	MAD1L1, FTSJ2, NUDT1	-56, 9194, -9218	upstream, downstream, upstream	ActReg chr7 #14180	1	0	0
14181	7	2,286,920	2,287,588	668	1	1.8	4.714	12.809	3	10	17	0	1	3	FTSJ2, NUDT1, SNX8	-5421, 5397, 66845	upstream, in gene, downstream	ActReg chr7 #14181	0	0	1
14182	7	2,322,765	2,323,146	381	1	4.917	5.364	10.083	6	8	14	0	0	1	SNX8	31,144	in gene	ActReg chr7 #14182	0	0	1
14183	7	2,393,342	2,394,666	1,324	2	21.881	27.143	6.69	52	59	19	1	1	1	EIF3B	-470	upstream	ActReg chr7 #14183	1	1	0
14184	7	2,457,646	2,458,089	443	1	4.571	1.929	11.714	6	3	17	0	0	1	CHST12	14,608	in gene	ActReg chr7 #14184	0	0	1
14185	7	2,490,458	2,491,033	575	1	2.889	4.944	11.556	5	8	17	0	0	1	LOC100288594	10,046	downstream	ActReg chr7 #14185	0	0	1
14186	7	2,491,164	2,491,687	523	1	9.353	10.647	14.235	15	14	22	0	0	1	LOC100288594	10,726	downstream	ActReg chr7 #14186	0	0	1
14187	7	2,509,851	2,510,266	415	1	2.538	5.077	11.308	4	7	16	0	0	0				ActReg chr7 #14187	0	0	1
14188	7	2,514,564	2,515,430	866	1	2.852	3.111	13.963	7	5	19	0	0	0				ActReg chr7 #14188	0	0	1
14189	7	2,515,693	2,516,057	364	1	4.1	2.5	13.546	6	3	21	0	0	0				ActReg chr7 #14189	0	0	1
14190	7	2,527,015	2,527,443	428	1	3.364	3.231	12.077	5	5	18	0	0	0				ActReg chr7 #14190	0	0	1
14191	7	2,537,405	2,538,006	601	1	3.632	2.667	9.684	5	6	13	0	0	0				ActReg chr7 #14191	0	0	1
14192	7	2,542,910	2,543,472	562	1	3.778	4.722	13.222	5	6	24	0	0	1	LFNG	-8,972	upstream	ActReg chr7 #14192	0	0	1
14193	7	2,548,837	2,549,671	834	1	4.346	3.808	12.346	8	7	16	0	1	1	LFNG	-2,909	upstream	ActReg chr7 #14193	0	0	1
14194	7	2,550,009	2,550,927	918	1	4.483	4.741	12.655	7	7	22	0	1	1	LFNG	-1,695	upstream	ActReg chr7 #14194	0	0	1
14195	7	2,563,879	2,565,087	1,208	1	4.919	6.757	12.351	9	11	19	1	0	1	LFNG	12,320	in gene	ActReg chr7 #14195	0	0	1
14196	7	2,594,811	2,595,440	629	3	12.35	13.1	9.3	18	20	16	1	2	2	C7orf27, IQCE	21, -3507	in gene, upstream	ActReg chr7 #14196	1	1	1
14197	7	2,598,245	2,598,942	697	2	11.333	11.762	5.769	17	26	9	1	2	2	C7orf27, IQCE	-3447, -39	upstream, upstream	ActReg chr7 #14197	1	1	0
14198	7	2,672,344	2,674,115	1,771	2	9.5	10.375	9.768	16	18	17	0	1	1	TTYH3	1,626	in gene	ActReg chr7 #14198	0	1	1
14199	7	2,679,461	2,680,439	978	1	6.567	6.933	12.5	11	10	18	0	0	1	TTYH3	8,347	in gene	ActReg chr7 #14199	0	0	1
14200	7	2,683,600	2,684,277	677	1	3.333	3.65	12.095	5	8	18	0	0	1	TTYH3	12,335	in gene	ActReg chr7 #14200	0	0	1
14201	7	2,687,079	2,687,738	659	1	2.4	3.421	11.75	5	6	15	1	0	1	TTYH3	15,805	in gene	ActReg chr7 #14201	0	0	1
14202	7	2,710,624	2,711,048	424	1	6.429	4.214	12.429	9	5	18	0	0	2	TTYH3, AMZ1	39233, -8327	downstream, upstream	ActReg chr7 #14202	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14203	7	2,719,860	2,720,629	769	1	4.167	4.174	11.292	8	10	15	0	1	1	AMZ1	1,081	in gene	ActReg chr7 #14203	0	0	1
14204	7	2,740,121	2,740,631	510	1	1.133	4.688	12.5	2	7	17	1	0	1	AMZ1	21,213	in gene	ActReg chr7 #14204	0	0	1
14205	7	2,903,107	2,903,537	430	1	12.923	10.077	11.692	16	17	16	0	0	0				ActReg chr7 #14205	0	0	1
14206	7	2,913,246	2,914,458	1,212	2	10.974	9.342	3.306	19	17	7	0	0	0				ActReg chr7 #14206	1	1	0
14207	7	2,935,697	2,936,173	476	1	3.867	5.267	11.467	6	9	15	0	0	1	CARD11	147,644	downstream	ActReg chr7 #14207	0	0	1
14208	7	2,945,644	2,946,584	940	1	2.828	5.704	12.552	6	10	21	1	0	1	CARD11	137,465	in gene	ActReg chr7 #14208	0	0	1
14209	7	2,968,329	2,968,808	479	1	4.8	3	12.667	8	5	18	1	0	1	CARD11	115,011	in gene	ActReg chr7 #14209	0	0	1
14210	7	3,000,539	3,000,967	428	1	2.286	3.786	11.357	3	5	16	0	0	1	CARD11	82,826	in gene	ActReg chr7 #14210	0	0	1
14211	7	3,067,627	3,068,136	509	2	9.688	9.438	3.923	15	17	7	0	0	1	CARD11	15,698	in gene	ActReg chr7 #14211	1	1	0
14212	7	4,248,387	4,248,948	561	1	2.824	4.529	11.059	5	6	15	0	0	1	SDK1	907,587	in gene	ActReg chr7 #14212	0	0	1
14213	7	4,265,750	4,266,190	440	1	4.214	4.462	11.714	7	8	18	0	0	1	SDK1	924,890	in gene	ActReg chr7 #14213	0	0	1
14214	7	4,509,851	4,510,411	560	1	6.389	10.167	4.167	10	15	8	0	0	0				ActReg chr7 #14214	0	1	0
14215	7	4,606,238	4,606,843	605	2	10.947	10.526	3.222	18	21	4	0	0	0				ActReg chr7 #14215	1	1	0
14216	7	4,659,929	4,660,381	452	1	5.143	9.357	6.643	8	14	10	0	0	0				ActReg chr7 #14216	0	1	0
14217	7	4,681,132	4,682,021	889	1	10.679	16.25	5.083	16	29	8	1	0	0				ActReg chr7 #14217	0	1	0
14218	7	4,814,885	4,815,554	669	2	11.619	12.286	6.286	22	19	10	1	1	2	FOXK1, KIAA0415	93289, -45	downstream, upstream	ActReg chr7 #14218	1	1	0
14219	7	4,832,219	4,832,884	665	1	3.81	4.2	13.762	6	8	21	1	0	2	KIAA0415, RADIL	17287, 90784	downstream, downstream	ActReg chr7 #14219	0	0	1
14220	7	4,856,636	4,857,233	597	1	3.5	4.579	11.947	7	9	18	1	0	1	RADIL	66,401	in gene	ActReg chr7 #14220	0	0	1
14221	7	4,859,684	4,860,724	1,040	1	3.774	3.75	13	8	6	17	0	0	1	RADIL	63,131	in gene	ActReg chr7 #14221	0	0	1
14222	7	4,918,173	4,918,507	334	1	2.909	2	11.364	6	3	16	0	0	1	RADIL	4,995	in gene	ActReg chr7 #14222	0	0	1
14223	7	4,991,395	4,992,487	1,092	2	11.912	15.235	2.792	23	30	5	0	0	1	MMD2	6,903	in gene	ActReg chr7 #14223	1	1	0
14224	7	5,002,161	5,002,750	589	1	5	2.778	11.889	7	5	16	0	1	1	MMD2	-3,611	upstream	ActReg chr7 #14224	0	0	1
14225	7	5,085,075	5,085,712	637	1	11.75	12.4	7.45	22	22	14	1	1	1	RBAK	-160	upstream	ActReg chr7 #14225	1	0	0
14226	7	5,324,141	5,324,718	577	1	5.278	8.222	12.611	9	15	20	0	1	1	SLC29A4	1,868	in gene	ActReg chr7 #14226	0	0	1
14227	7	5,337,534	5,338,092	558	1	4.111	5.167	9.944	6	8	16	0	0	2	SLC29A4, TNRC18	15252, 125364	in gene, downstream	ActReg chr7 #14227	0	0	1
14228	7	5,340,130	5,340,470	340	1	2	4.9	12.6	4	6	19	1	0	2	SLC29A4, TNRC18	17739, 122877	in gene, downstream	ActReg chr7 #14228	0	0	1
14229	7	5,342,196	5,342,624	428	1	6.143	2.786	11.714	9	5	15	2	0	2	SLC29A4, TNRC18	19849, 120767	in gene, downstream	ActReg chr7 #14229	0	0	1
14230	7	5,401,586	5,402,266	680	1	4.524	3.211	12.381	7	6	17	1	0	1	TNRC18	61,251	in gene	ActReg chr7 #14230	0	0	1
14231	7	5,459,442	5,459,930	488	1	5.067	4.867	12.2	6	7	18	1	0	2	TNRC18, LOC100129484	3491, 9264	in gene, downstream	ActReg chr7 #14231	0	0	1
14232	7	5,467,330	5,467,914	584	1	5.333	5.667	12.556	7	8	20	1	2	2	TNRC18, LOC100129484	-4445, 1328	upstream, in gene	ActReg chr7 #14232	0	0	1
14233	7	5,518,884	5,519,300	416	1	1.154	4.769	12.231	2	6	16	0	0	1	FBXL18	34,307	in gene	ActReg chr7 #14233	0	0	1
14234	7	5,527,244	5,527,689	445	1	4.929	7.071	11.857	7	11	19	0	0	2	FBXL18, MIR589	25933, 8082	in gene, downstream	ActReg chr7 #14234	0	0	1
14235	7	5,530,759	5,531,419	660	1	2.8	4.15	13.1	4	9	17	0	0	2	FBXL18, MIR589	22310, 4459	in gene, downstream	ActReg chr7 #14235	0	0	1
14236	7	5,531,681	5,532,159	478	1	2.214	2.714	11.714	3	6	17	0	0	2	FBXL18, MIR589	21479, 3628	in gene, downstream	ActReg chr7 #14236	0	0	1
14237	7	5,553,075	5,553,984	909	3	13.379	9.655	10.414	25	21	23	1	1	1	FBXL18	-130	upstream	ActReg chr7 #14237	1	1	1
14238	7	5,568,862	5,569,397	535	1	8.588	10.588	12.294	12	16	20	1	2	2	LOC100505829, ACTB	2351, 1103	in gene, in gene	ActReg chr7 #14238	0	0	1
14239	7	5,572,315	5,572,895	580	1	3.333	4.833	10.944	5	7	15	0	1	2	LOC100505829, ACTB	5827, -2373	in gene, upstream	ActReg chr7 #14239	0	0	1
14240	7	5,601,735	5,602,591	856	2	9.731	13.346	10.692	15	22	19	2	0	0				ActReg chr7 #14240	0	1	1
14241	7	5,602,887	5,603,645	758	2	7.826	11.174	11.714	14	15	21	0	0	0				ActReg chr7 #14241	0	1	1
14242	7	5,609,581	5,610,132	551	2	13.294	11.588	11.235	17	17	17	1	0	0				ActReg chr7 #14242	0	1	1
14243	7	5,632,328	5,633,825	1,497	2	8.617	11.723	10.362	14	18	16	1	1	1	FSCN1	622	in gene	ActReg chr7 #14243	0	1	1
14244	7	5,637,726	5,638,748	1,022	1	7.219	7.062	12.656	13	10	18	0	0	1	FSCN1	5,783	in gene	ActReg chr7 #14244	0	0	1
14245	7	5,642,592	5,643,243	651	1	5.857	4.667	12.762	10	7	17	1	0	1	FSCN1	10,463	in gene	ActReg chr7 #14245	0	0	1
14246	7	5,647,751	5,648,359	608	1	5	6.526	11.684	7	11	16	1	0	1	FSCN1	15,601	downstream	ActReg chr7 #14246	0	0	1
14247	7	5,820,891	5,821,971	1,080	2	7.588	12.971	7.871	15	22	16	1	1	1	RNF216	-139	upstream	ActReg chr7 #14247	0	1	1
14248	7	5,862,482	5,862,902	420	1	11.692	9.692	5.231	17	13	11	1	0	0				ActReg chr7 #14248	1	0	0
14249	7	6,048,285	6,049,254	969	1	6.129	10.871	6.387	12	20	17	1	2	2	PMS2, AIMP2	-32, -113	upstream, upstream	ActReg chr7 #14249	0	1	0
14250	7	6,120,573	6,121,455	882	2	8.786	12.536	11.25	14	21	23	1	0	0				ActReg chr7 #14250	0	1	1
14251	7	6,143,862	6,144,519	657	3	12.333	12.2	9.211	23	17	18	1	1	1	USP42	-360	upstream	ActReg chr7 #14251	1	1	1
14252	7	6,486,892	6,487,704	812	1	11.36	10.12	9.08	16	14	12	1	1	1	DAGLB	345	in gene	ActReg chr7 #14252	1	0	0
14253	7	6,550,430	6,550,899	469	1	2.462	3.133	12.6	4	4	19	0	0	1	GRID2IP	40,403	in gene	ActReg chr7 #14253	0	0	1
14254	7	6,597,038	6,597,620	582	1	4.111	3.188	11.222	7	6	15	0	1	1	GRID2IP	-6,262	upstream	ActReg chr7 #14254	0	0	1
14255	7	6,629,278	6,630,399	1,121	2	13.429	14.314	6.625	24	27	13	1	1	2	ZDHHC4, C7orf26	12773, -77	downstream, upstream	ActReg chr7 #14255	1	1	0
14256	7	6,653,374	6,654,028	654	1	3.524	3.524	11.286	5	5	15	0	1	2	C7orf26, ZNF853	23786, -1826	downstream, upstream	ActReg chr7 #14256	0	0	1
14257	7	7,222,384	7,223,046	662	1	7.714	11.809	4.381	15	18	9	1	1	1	C1GALT1	469	in gene	ActReg chr7 #14257	0	1	0
14258	7	7,261,259	7,261,855	596	1	9.722	10.222	2.7	16	15	4	0	0	1	C1GALT1	39,311	in gene	ActReg chr7 #14258	1	0	0
14259	7	7,466,828	7,467,359	531	1	10.25	6.438	1.667	15	9	2	0	0	1	COL28A1	108,367	in gene	ActReg chr7 #14259	1	0	0
14260	7	7,478,402	7,478,941	539	1	8.75	9.75	1.5	12	19	2	0	0	1	COL28A1	96,789	in gene	ActReg chr7 #14260	0	1	0
14261	7	7,802,070	7,802,472	402	1	6.462	9.769	1	10	16	1	0	0	1	tcag7.903	121,929	in gene	ActReg chr7 #14261	0	1	0
14262	7	7,835,091	7,835,643	552	1	10.471	6.588	1.6	16	9	4	0	0	1	tcag7.903	155,025	in gene	ActReg chr7 #14262	1	0	0
14263	7	8,007,957	8,008,765	808	2	8.64	11.64	8	13	16	15	1	1	2	LOC100505921, GLCCI1	-10150, -62	upstream, upstream	ActReg chr7 #14263	0	1	1
14264	7	8,473,290	8,474,320	1,030	2	9.312	10.656	3.438	17	21	11	1	1	1	NXPH1	220	in gene	ActReg chr7 #14264	1	1	0
14265	7	8,482,140	8,482,960	820	1	7.385	11.885	6.115	16	20	10	2	0	1	NXPH1	8,965	in gene	ActReg chr7 #14265	0	1	0
14266	7	10,276,879	10,277,395	516	1	5.75	9.688	1.867	10	16	3	0	0	0				ActReg chr7 #14266	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14267	7	10,979,309	10,980,428	1,119	2	13.114	14.371	6.6	24	24	12	1	1	1	NDUFA4	-55	upstream	ActReg chr7 #14267	1	1	0
14268	7	11,359,038	11,359,654	616	1	5.25	10.55	1.6	9	17	2	0	0	0				ActReg chr7 #14268	0	1	0
14269	7	12,250,330	12,251,528	1,198	2	12.132	11.553	3.211	18	19	7	1	1	1	TMEM106B	81	in gene	ActReg chr7 #14269	1	1	0
14270	7	12,443,064	12,443,753	689	1	10.818	5.636	12.864	14	10	19	1	1	1	VWDE	444	in gene	ActReg chr7 #14270	0	0	1
14271	7	12,610,396	12,610,913	517	1	3.471	8.235	14.177	7	11	22	1	1	1	SCIN	451	in gene	ActReg chr7 #14271	0	0	1
14272	7	12,726,643	12,727,482	839	2	7.538	13.077	7.25	12	19	15	1	1	1	ARL4A	581	in gene	ActReg chr7 #14272	0	1	1
14273	7	13,591,016	13,591,446	430	1	10.615	5.308	1.111	15	8	2	0	0	0				ActReg chr7 #14273	1	0	0
14274	7	13,818,337	13,819,128	791	1	8.125	12.542	2.429	15	24	5	0	0	0				ActReg chr7 #14274	0	1	0
14275	7	13,919,540	13,920,150	610	1	7.842	11.474	1.125	11	15	2	0	0	0				ActReg chr7 #14275	0	1	0
14276	7	14,272,501	14,273,136	635	1	10	7.9	1.733	17	13	3	0	0	1	DGKB	608,257	in gene	ActReg chr7 #14276	1	0	0
14277	7	15,238,153	15,238,683	530	1	9.5	10.688	1.25	16	18	2	0	0	1	TMEM195	363,222	downstream	ActReg chr7 #14277	0	1	0
14278	7	15,726,376	15,726,808	432	1	5.538	8.538	11.846	11	11	17	0	0	1	MEOX2	-284	upstream	ActReg chr7 #14278	0	0	1
14279	7	16,210,182	16,210,566	384	1	1.5	1.909	13.083	2	4	17	0	0	1	ISPD	250,573	in gene	ActReg chr7 #14279	0	0	1
14280	7	16,358,554	16,359,443	889	2	10.111	10.704	2.05	17	14	4	0	0	1	ISPD	101,934	in gene	ActReg chr7 #14280	1	1	0
14281	7	16,460,158	16,461,531	1,373	2	10.558	11.046	5.262	22	16	11	1	1	1	ISPD	103	in gene	ActReg chr7 #14281	1	1	0
14282	7	16,524,138	16,525,011	873	1	12.148	6.519	2.583	19	15	5	0	0	0				ActReg chr7 #14282	1	0	0
14283	7	16,684,760	16,686,325	1,565	3	16.674	19.674	7.878	56	48	21	2	2	2	ANKMY2, BZW2	-100, -217	upstream, upstream	ActReg chr7 #14283	1	1	1
14284	7	16,707,606	16,708,121	515	1	10.5	7.562	1.7	17	11	2	0	0	1	BZW2	22,104	in gene	ActReg chr7 #14284	1	0	0
14285	7	16,793,521	16,794,398	877	1	7.222	11.296	6.704	13	17	12	1	1	1	TSPAN13	608	in gene	ActReg chr7 #14285	0	1	0
14286	7	17,134,391	17,135,441	1,050	2	12.758	11.939	1.917	24	21	3	0	0	0				ActReg chr7 #14286	1	1	0
14287	7	17,273,445	17,273,977	532	1	5.125	10.438	1.615	7	16	2	0	0	0				ActReg chr7 #14287	0	1	0
14288	7	17,338,239	17,338,811	572	1	8.889	12	6.111	11	18	12	1	1	1	AHR	249	in gene	ActReg chr7 #14288	0	1	0
14289	7	17,411,591	17,412,277	686	1	11.905	9.316	1.059	19	17	2	0	0	0				ActReg chr7 #14289	1	0	0
14290	7	17,586,132	17,586,729	597	1	11.263	8.895	1.462	19	16	2	0	0	0				ActReg chr7 #14290	1	0	0
14291	7	17,728,927	17,729,889	962	2	11	10.774	2.136	19	18	3	0	0	0				ActReg chr7 #14291	1	1	0
14292	7	17,735,946	17,736,583	637	2	10.15	10.85	1.556	17	19	2	0	0	0				ActReg chr7 #14292	1	1	0
14293	7	17,979,188	17,980,559	1,371	1	9.605	12.419	7.122	15	20	16	1	1	1	SNX13	258	in gene	ActReg chr7 #14293	0	1	0
14294	7	18,498,353	18,498,820	467	1	8.867	9.067	2.533	14	16	6	0	0	0				ActReg chr7 #14294	0	1	0
14295	7	18,906,161	18,906,776	615	1	6.158	11.842	1.8	9	23	4	0	0	1	HDAC9	371,099	in gene	ActReg chr7 #14295	0	1	0
14296	7	19,748,247	19,749,011	764	1	9.167	12.208	6.273	16	20	12	1	2	3	TMISTNB, MIR3146, TMEM196	31, -3570, 63775	in gene, upstream, downstream	ActReg chr7 #14296	0	1	0
14297	7	19,812,035	19,813,230	1,195	2	11.351	14.676	4.865	22	21	8	1	1	1	TMEM196	-228	upstream	ActReg chr7 #14297	1	1	0
14298	7	19,997,878	19,998,399	521	1	9.875	9.562	1.909	17	14	3	0	0	0				ActReg chr7 #14298	1	0	0
14299	7	20,123,486	20,123,939	453	1	6.533	10.333	1	11	17	1	0	0	0				ActReg chr7 #14299	0	1	0
14300	7	20,198,755	20,199,336	581	1	10.778	7.778	2.333	19	15	4	0	0	1	MACC1	57,968	in gene	ActReg chr7 #14300	1	0	0
14301	7	20,258,920	20,260,159	1,239	2	13	13.368	1.44	22	22	2	0	2	2	MACC1, LOC100506098	-2526, 2339	upstream, in gene	ActReg chr7 #14301	1	1	0
14302	7	20,369,694	20,370,998	1,304	3	10.951	10.585	13.146	16	19	28	1	2	2	LOC100506130, ITGB8	1024, -379	in gene, upstream	ActReg chr7 #14302	1	1	1
14303	7	20,392,232	20,392,919	687	1	10.762	10.286	3.545	17	14	6	0	0	1	ITGB8	21,850	in gene	ActReg chr7 #14303	0	1	0
14304	7	20,636,198	20,637,444	1,246	2	10.564	11.051	3.68	20	23	7	0	0	0				ActReg chr7 #14304	1	1	0
14305	7	20,824,395	20,825,088	693	1	6.227	10.409	5.75	10	18	12	1	1	1	SP8	1,767	in gene	ActReg chr7 #14305	0	1	0
14306	7	21,806,871	21,807,353	482	1	9.8	4.214	3.133	15	7	4	0	0	1	DNAH11	224,279	in gene	ActReg chr7 #14306	1	0	0
14307	7	21,985,036	21,986,116	1,080	2	18.118	19.529	6.265	45	58	10	1	1	1	CDCA7L	-34	upstream	ActReg chr7 #14307	1	1	0
14308	7	22,122,159	22,122,799	640	1	7.75	10.35	5.4	13	15	10	1	0	0				ActReg chr7 #14308	0	1	0
14309	7	22,539,609	22,540,030	421	1	8.692	10.923	7.154	14	16	12	1	1	1	MGC87042	82	in gene	ActReg chr7 #14309	0	1	0
14310	7	22,862,101	22,862,768	667	1	8.286	11.809	5.316	14	20	9	1	1	1	TOMM7	-13	upstream	ActReg chr7 #14310	0	1	0
14311	7	22,897,912	22,899,258	1,346	2	10.786	11.548	3.317	19	21	6	0	1	1	SNORD93	2,353	downstream	ActReg chr7 #14311	1	1	0
14312	7	23,060,339	23,061,194	855	1	11	9.444	2.783	16	17	5	0	1	1	FAM126A	-6,996	upstream	ActReg chr7 #14312	1	0	0
14313	7	23,101,944	23,102,589	645	1	9.95	11.65	6.938	16	19	13	0	0	0				ActReg chr7 #14313	0	1	0
14314	7	23,145,054	23,146,016	962	2	10.613	10.581	7.452	20	17	12	1	1	2	LOC100506198, KLHL7	18864, 182	downstream, in gene	ActReg chr7 #14314	1	1	0
14315	7	23,221,099	23,222,038	939	2	13.517	13.517	5.214	24	24	12	1	1	2	KLHL7, NUPL2	76215, 122	downstream, in gene	ActReg chr7 #14315	1	1	0
14316	7	23,233,113	23,233,851	738	1	5.136	5.478	15	9	8	22	0	0	1	NUPL2	12,036	in gene	ActReg chr7 #14316	0	0	1
14317	7	23,286,556	23,287,647	1,091	1	6.412	11.353	6.618	11	18	16	1	1	1	GPNMB	785	in gene	ActReg chr7 #14317	0	1	0
14318	7	23,338,669	23,339,370	701	1	11.773	9.864	8.409	19	19	15	1	1	1	C7orf30	79	in gene	ActReg chr7 #14318	1	0	0
14319	7	23,510,763	23,511,208	445	1	11.143	7.071	4.357	16	10	7	0	1	1	IGF2BP3	-990	upstream	ActReg chr7 #14319	1	0	0
14320	7	23,513,568	23,514,613	1,045	1	9.364	11.091	8.121	17	18	16	1	1	1	IGF2BP3	-4,095	upstream	ActReg chr7 #14320	0	1	0
14321	7	23,571,212	23,571,825	613	1	7.579	10.526	10.526	12	16	13	1	1	1	TRA2A	138	in gene	ActReg chr7 #14321	0	0	1
14322	7	24,323,973	24,324,286	313	1	5.333	2.667	11.667	8	3	14	1	1	1	NPY	322	in gene	ActReg chr7 #14322	0	0	1
14323	7	24,797,173	24,797,866	693	2	9.318	9.591	6.864	17	15	12	1	1	1	DFNA5	120	in gene	ActReg chr7 #14323	1	1	0
14324	7	24,826,478	24,827,023	545	1	11.353	9.941	2.533	22	14	5	0	0	1	OSBPL3	193,010	downstream	ActReg chr7 #14324	1	0	0
14325	7	24,861,013	24,861,579	566	1	11.833	7.944	2.533	19	11	4	0	0	1	OSBPL3	158,464	in gene	ActReg chr7 #14325	1	0	0
14326	7	25,019,395	25,020,415	1,020	1	9.645	11.387	7.387	13	17	14	1	1	1	OSBPL3	-145	upstream	ActReg chr7 #14326	0	1	0
14327	7	25,164,698	25,165,628	930	2	14.586	15.138	7.345	28	25	14	1	1	2	CYCS, C7orf31	-183, 54654	upstream, downstream	ActReg chr7 #14327	1	1	0
14328	7	25,901,917	25,902,635	718	2	10.957	11.087	5.048	19	20	10	1	0	0				ActReg chr7 #14328	1	1	0
14329	7	26,240,183	26,240,506	323	1	9.6	12.8	14.1	13	17	19	1	2	2	HNRNPA2B1, CBX3	69, -755	in gene, upstream	ActReg chr7 #14329	0	0	1
14330	7	26,241,277	26,241,748	471	2	8.267	10.4	9.429	15	14	16	1	2	2	HNRNPA2B1, CBX3	-1099, 413	upstream, in gene	ActReg chr7 #14330	0	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14331	7	26,998,254	26,999,274	1,020	2	12	12.562	2.481	21	21	6	0	0	0				AdReg chr7 #14331	1	1	0
14332	7	27,088,005	27,088,327	322	1	5.2	3	10.4	7	4	15	0	0	0				AdReg chr7 #14332	0	0	1
14333	7	27,136,259	27,136,694	435	1	3.923	7.923	10.923	11	14	16	1	2	4	HOXA1, LOC100506311, HOXA2, HOXA3	-851, 492, 5918, 30163	upstream, in gene, downstream, downstream	AdReg chr7 #14333	0	0	1
14334	7	27,169,471	27,169,777	306	1	5	5.1	11.5	7	9	16	1	2	3	HOXA3, LOC285943, HOXA4	-2985, 19585, 775	upstream, downstream, in gene	AdReg chr7 #14334	0	0	1
14335	7	27,189,934	27,190,924	990	1	11.645	13.29	6.548	16	23	13	1	2	4	LOC100133311, HOXA5, HOXA6, HOXA7	10446, -7142, -3061, 5867	in gene, upstream, upstream, downstream	AdReg chr7 #14335	0	1	0
14336	7	27,213,743	27,214,375	632	1	6.4	3.5	13.1	12	7	20	1	1	4	HOXA9, MIR196B, HOXA10, HOXA11	-8910, -4877, 5817, 10776	upstream, upstream, in gene, downstream	AdReg chr7 #14336	0	0	1
14337	7	27,224,284	27,224,695	411	1	7.154	8.154	11.231	11	11	16	1	3	3	HOXA10, HOXA11, HOXA11AS	-4613, 346, -538	upstream, in gene, upstream	AdReg chr7 #14337	0	0	1
14338	7	27,238,624	27,239,193	569	1	3.562	7.778	12.333	6	14	18	1	2	3	HOXA11AS, HOXA13, NCRNA00213	13881, 817, -1148	downstream, in gene, upstream	AdReg chr7 #14338	0	0	1
14339	7	27,274,894	27,275,412	518	1	6.812	8.875	13.938	10	11	22	1	1	2	LOC100129463, EVX1	5694, -7011	downstream, downstream	AdReg chr7 #14339	0	0	1
14340	7	27,282,112	27,282,765	653	1	4.857	6.81	10.714	8	14	13	1	2	2	LOC100129463, EVX1	-1591, 274	upstream, in gene	AdReg chr7 #14340	0	0	1
14341	7	27,282,888	27,283,388	500	1	3.615	6.067	13.867	6	10	19	2	2	2	LOC100129463, EVX1	-2291, 974	upstream, in gene	AdReg chr7 #14341	0	0	1
14342	7	27,702,128	27,703,033	905	2	18.429	16.571	5.964	44	34	10	1	1	1	HIBADH	40	in gene	AdReg chr7 #14342	1	1	0
14343	7	27,779,235	27,780,203	968	1	8.2	13.4	7.767	11	24	11	1	1	1	TAX1BP1	-19	upstream	AdReg chr7 #14343	0	1	0
14344	7	28,101,798	28,102,472	674	2	11.714	10.524	5.429	18	22	9	0	0	1	JAZF1	118,302	in gene	AdReg chr7 #14344	1	1	0
14345	7	28,725,349	28,726,010	661	1	5.45	11.05	4.333	9	16	8	0	0	1	CREB5	386,739	in gene	AdReg chr7 #14345	0	1	0
14346	7	28,895,322	28,896,105	783	2	11.24	10.88	4.067	17	19	7	0	0	0				AdReg chr7 #14346	1	1	0
14347	7	28,996,203	28,997,394	1,191	1	5	3.73	14.514	10	6	20	1	1	1	TRIL	1,231	in gene	AdReg chr7 #14347	0	0	1
14348	7	29,074,801	29,075,685	884	1	8.25	14.636	1.412	14	26	2	0	0	1	CPVL	110,910	in gene	AdReg chr7 #14348	0	1	0
14349	7	29,333,238	29,333,475	237	1	0	2	11.75	0	3	15	0	0	1	CHN2	99,235	in gene	AdReg chr7 #14349	0	0	1
14350	7	29,605,691	29,606,082	391	1	4	5.462	11.692	6	8	19	1	1	1	PRR15	2,459	in gene	AdReg chr7 #14350	0	0	1
14351	7	30,028,610	30,029,222	612	1	6.632	10.421	6.867	9	14	10	1	1	1	SCRN1	989	in gene	AdReg chr7 #14351	0	1	0
14352	7	30,065,956	30,066,850	894	2	16.75	17.321	5.077	34	43	9	1	2	2	FKBP14, PLEKHA8	-135, -1885	upstream, upstream	AdReg chr7 #14352	1	1	0
14353	7	30,067,505	30,068,466	961	2	17.467	18.7	4.167	38	43	8	1	2	2	FKBP14, PLEKHA8	-1717, -303	upstream, upstream	AdReg chr7 #14353	1	1	0
14354	7	30,324,125	30,324,723	598	1	7.579	12.158	5.111	10	15	9	1	2	2	ZNRF2, MIR550-1	501, -4986	in gene, upstream	AdReg chr7 #14354	0	1	0
14355	7	30,325,402	30,325,910	508	1	8.625	10.625	5.062	14	14	9	1	2	2	ZNRF2, MIR550-1	1733, -3754	in gene, upstream	AdReg chr7 #14355	0	1	0
14356	7	30,491,660	30,492,321	661	1	3.381	3.684	12.619	10	8	18	0	0	1	NOD1	26,403	in gene	AdReg chr7 #14356	0	0	1
14357	7	30,517,924	30,518,732	808	1	8.12	10.36	4.4	11	14	7	1	1	1	NOD1	65	in gene	AdReg chr7 #14357	0	1	0
14358	7	30,590,494	30,591,030	536	1	6.882	10.588	1.727	12	16	3	0	0	1	LOC401320	26,613	in gene	AdReg chr7 #14358	0	1	0
14359	7	30,634,061	30,634,793	732	1	10	15.174	6.609	15	29	10	1	1	1	GARS	246	in gene	AdReg chr7 #14359	0	1	0
14360	7	30,688,375	30,688,867	492	1	1.438	2.8	11.25	2	5	16	0	0	1	CRHR2	33,519	downstream	AdReg chr7 #14360	0	0	1
14361	7	30,710,901	30,712,864	1,963	2	23.098	34.516	4.867	110	139	11	0	0	1	CRHR2	10,258	in gene	AdReg chr7 #14361	1	1	0
14362	7	30,756,531	30,757,133	602	1	12	11.316	3.263	21	20	5	0	0	0				AdReg chr7 #14362	1	0	0
14363	7	30,839,203	30,839,854	651	1	9.55	12.55	2.684	14	24	5	0	0	1	FAM188B	28,495	in gene	AdReg chr7 #14363	0	1	0
14364	7	31,066,759	31,067,195	436	1	1.692	3	11.538	3	6	17	0	0	0				AdReg chr7 #14364	0	0	1
14365	7	31,154,022	31,155,447	1,425	2	16.182	25.318	3	51	98	7	0	0	1	ADCYAP1R1	62,592	downstream	AdReg chr7 #14365	1	1	0
14366	7	31,900,376	31,900,989	613	1	5.158	11.947	1.786	11	24	3	0	0	1	PDE1C	437,701	in gene	AdReg chr7 #14366	0	1	0
14367	7	32,090,610	32,091,099	489	1	11.933	11.067	6.375	16	16	10	0	0	1	PDE1C	247,529	in gene	AdReg chr7 #14367	1	0	0
14368	7	32,374,586	32,375,245	659	1	7.714	10.524	2.5	14	19	3	0	0	0				AdReg chr7 #14368	0	1	0
14369	7	32,467,017	32,467,937	920	2	14.034	16.862	5.034	35	37	9	1	0	0				AdReg chr7 #14369	1	1	0
14370	7	32,529,426	32,530,419	993	2	17.806	18.355	6.621	42	49	17	1	1	2	LSM5, AVL9	4948, -5254	in gene, upstream	AdReg chr7 #14370	1	1	0
14371	7	32,931,589	32,932,037	448	1	5.214	5.929	9.357	8	8	16	1	1	1	KBTBD2	-345	upstream	AdReg chr7 #14371	0	0	1
14372	7	32,981,832	32,982,769	937	1	7.621	11.345	5.483	10	18	11	1	0	0				AdReg chr7 #14372	0	1	0
14373	7	32,996,774	32,997,839	1,065	2	12.394	12.152	3.5	17	21	8	1	1	1	FKBP9	301	in gene	AdReg chr7 #14373	1	1	0
14374	7	33,101,782	33,103,035	1,253	1	10	12.41	4.944	15	21	13	1	1	1	NT5C3	1	in gene	AdReg chr7 #14374	0	1	0
14375	7	33,147,217	33,147,768	551	1	10	8.176	3.529	16	11	6	0	1	1	RP9	1,510	in gene	AdReg chr7 #14375	1	0	0
14376	7	33,148,445	33,149,624	1,179	3	16.135	19.838	2.486	39	61	5	1	1	1	RP9	-32	upstream	AdReg chr7 #14376	1	1	0
14377	7	33,168,893	33,169,569	676	1	5.727	12.091	5.619	10	21	9	1	1	1	BBS9	79	in gene	AdReg chr7 #14377	0	1	0
14378	7	33,744,744	33,745,084	340	1	1.9	4.1	11.2	3	6	14	0	0	0				AdReg chr7 #14378	0	0	1
14379	7	34,026,398	34,027,448	1,050	2	11.152	9.909	2.179	20	27	4	0	0	1	BMPER	81,811	in gene	AdReg chr7 #14379	1	1	0
14380	7	35,043,307	35,043,887	580	1	9.167	11.444	1.944	15	19	4	0	0	1	DPY19L1	34,056	in gene	AdReg chr7 #14380	0	1	0
14381	7	35,301,241	35,301,976	735	1	2.25	5.13	11.435	4	5	17	1	0	1	TBX20	-7,897	upstream	AdReg chr7 #14381	0	0	1
14382	7	35,637,828	35,638,274	446	1	10.286	10.071	1	14	16	1	0	0	0				AdReg chr7 #14382	0	1	0
14383	7	35,733,784	35,735,245	1,461	2	12.13	13.152	8.152	26	25	16	1	1	1	HERPUD2	258	in gene	AdReg chr7 #14383	1	1	0
14384	7	35,841,244	35,841,777	533	1	6.529	11.118	5.118	11	17	9	1	1	1	7-Sep	883	in gene	AdReg chr7 #14384	0	1	0
14385	7	36,076,046	36,077,417	1,371	1	6	11.628	3.286	10	19	7	0	0	0				AdReg chr7 #14385	0	1	0
14386	7	36,154,986	36,155,685	699	1	9.545	10.864	2.938	18	23	4	0	0	0				AdReg chr7 #14386	0	1	0
14387	7	36,406,432	36,407,295	863	2	10.963	12.852	2.826	18	23	6	1	0	1	KIAA0895	22,871	in gene	AdReg chr7 #14387	1	1	0
14388	7	36,546,357	36,546,963	606	1	10.053	8.053	4.231	17	15	7	0	0	1	AOAH	217,494	downstream	AdReg chr7 #14388	1	0	0
14389	7	37,071,429	37,072,412	983	1	9.233	9.6	2.138	18	16	4	0	0	1	ELMO1	416,591	in gene	AdReg chr7 #14389	0	1	0
14390	7	37,092,140	37,092,839	699	2	8.455	13.5	2.722	19	23	4	0	0	1	ELMO1	396,022	in gene	AdReg chr7 #14390	1	1	0
14391	7	37,394,412	37,394,915	503	1	11.25	9.375	1.8	15	12	4	0	0	1	ELMO1	93,848	in gene	AdReg chr7 #14391	1	0	0
14392	7	37,487,267	37,487,791	524	1	10.312	8.625	5.812	13	12	10	1	1	1	ELMO1	982	in gene	AdReg chr7 #14392	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14393	7	37,488,284	37,488,909	625	2	6.4	10.7	9.8	11	18	16	1	1	1	ELMO1	-85	upstream	ActReg chr7 #14393	0	1	1
14394	7	39,044,879	39,045,524	645	2	9.6	8.8	1.5	19	18	3	0	0	1	POU6F2	27,592	in gene	ActReg chr7 #14394	1	1	0
14395	7	39,453,327	39,454,456	1,129	2	7.943	10.714	5.594	20	19	13	1	0	1	POU6F2	436,282	in gene	ActReg chr7 #14395	1	1	0
14396	7	39,605,655	39,606,458	803	1	9.32	13.16	4.364	12	24	7	1	1	1	C7orf36	53	in gene	ActReg chr7 #14396	0	1	0
14397	7	39,662,797	39,663,476	679	2	12.095	10	9	17	16	16	1	1	1	RALA	-26	upstream	ActReg chr7 #14397	1	0	1
14398	7	39,850,363	39,850,804	441	1	10.429	3.5	1	13	7	1	0	0	0				ActReg chr7 #14398	1	0	0
14399	7	39,989,443	39,990,451	1,008	2	9.161	9.871	10.29	20	14	19	1	1	1	CDK13	-12	upstream	ActReg chr7 #14399	1	0	1
14400	7	40,174,019	40,174,820	801	2	11.08	11.92	7.12	15	19	12	1	2	2	C7orf11, C7orf10	-168, -156	upstream, upstream	ActReg chr7 #14400	1	1	0
14401	7	40,591,097	40,591,836	739	2	9.609	10.13	3.318	18	18	5	0	0	1	C7orf10	416,891	in gene	ActReg chr7 #14401	1	1	0
14402	7	41,068,534	41,069,190	656	2	11.381	10.762	2.917	18	19	5	0	0	0				ActReg chr7 #14402	1	1	0
14403	7	41,147,121	41,147,886	765	1	8.333	12.833	3.667	16	18	8	0	0	0				ActReg chr7 #14403	0	1	0
14404	7	41,229,260	41,229,928	668	1	9.905	12	2.867	15	21	5	0	0	0				ActReg chr7 #14404	0	1	0
14405	7	41,413,728	41,414,538	810	1	6.731	11.923	2.875	9	19	6	0	0	0				ActReg chr7 #14405	0	1	0
14406	7	41,465,406	41,466,107	701	2	10.682	8.455	2	21	17	3	0	0	0				ActReg chr7 #14406	1	1	0
14407	7	42,004,508	42,005,231	723	1	4.478	3.957	12.261	9	7	17	1	0	1	GLI3	271,749	in gene	ActReg chr7 #14407	0	0	1
14408	7	42,271,739	42,272,279	540	1	9	11.588	1.091	17	18	2	0	0	1	GLI3	4,609	in gene	ActReg chr7 #14408	0	1	0
14409	7	42,927,818	42,928,487	669	1	8.238	10.095	11.667	14	14	17	0	0	0				ActReg chr7 #14409	0	0	1
14410	7	42,971,683	42,972,335	652	1	7.2	11.5	3.105	11	18	5	1	2	2	PSMA2, MRPL32	-204, 70	upstream, in gene	ActReg chr7 #14410	0	1	0
14411	7	43,057,903	43,058,541	638	1	9.8	8.3	1.632	22	12	3	0	0	0				ActReg chr7 #14411	1	0	0
14412	7	43,259,761	43,260,431	670	1	12.857	9.762	4.143	24	17	6	0	0	1	HECW1	107,898	in gene	ActReg chr7 #14412	1	0	0
14413	7	43,608,907	43,609,645	738	1	9.174	11.217	3.667	14	21	8	0	0	1	HECW1	457,078	downstream	ActReg chr7 #14413	0	1	0
14414	7	43,622,828	43,623,460	632	1	7.3	10.75	4.5	11	22	9	1	1	1	STK17A	452	in gene	ActReg chr7 #14414	0	1	0
14415	7	43,687,373	43,688,060	687	1	13.571	10.619	4.286	20	14	11	0	0	1	C7orf44	81,367	in gene	ActReg chr7 #14415	1	0	0
14416	7	43,713,950	43,714,586	636	1	7.35	11.1	1.667	16	18	2	0	0	1	C7orf44	54,815	in gene	ActReg chr7 #14416	0	1	0
14417	7	43,768,626	43,769,552	926	2	12.379	16.862	5.115	20	33	10	1	1	1	C7orf44	-6	upstream	ActReg chr7 #14417	1	1	0
14418	7	43,789,569	43,790,039	470	1	3.286	2.286	13.929	6	4	22	0	0	1	BLVRA	-8,468	upstream	ActReg chr7 #14418	0	0	1
14419	7	43,908,874	43,909,780	906	1	9.429	11.786	6.393	15	20	13	1	1	2	MRPS24, URGCP	-182, 56669	upstream, downstream	ActReg chr7 #14419	0	1	0
14420	7	43,916,857	43,917,667	810	1	3.08	6.231	13	5	10	18	0	0	2	MRPS24, URGCP	-8117, 48734	upstream, in gene	ActReg chr7 #14420	0	0	1
14421	7	43,965,557	43,966,023	466	1	9.8	9.267	5.75	16	14	9	1	2	2	URGCP, UBE2D4	206, -245	in gene, upstream	ActReg chr7 #14421	1	0	0
14422	7	44,058,411	44,059,210	799	2	42.92	51.6	4.32	134	147	9	1	0	2	SPDYE1, LOC100287164	18321, 7142	downstream, downstream	ActReg chr7 #14422	1	1	0
14423	7	44,082,530	44,082,954	424	1	10.846	9.538	1	15	17	1	0	1	2	FLJ35390, DBNL	4044, -1497	downstream, upstream	ActReg chr7 #14423	1	0	0
14424	7	44,083,786	44,084,623	837	2	10.039	9.538	8.308	18	13	16	1	1	2	FLJ35390, DBNL	5506, -35	downstream, upstream	ActReg chr7 #14424	1	0	1
14425	7	44,240,446	44,241,042	596	1	11.684	8.158	5.684	22	13	11	1	1	1	YKT6	166	in gene	ActReg chr7 #14425	1	0	0
14426	7	44,274,301	44,275,095	794	1	3.917	3.042	12.28	6	6	18	0	0	1	CAMK2B	90,532	in gene	ActReg chr7 #14426	0	0	1
14427	7	44,309,518	44,310,176	658	1	4.048	4.143	12.333	7	7	18	0	0	1	CAMK2B	55,383	in gene	ActReg chr7 #14427	0	0	1
14428	7	44,333,798	44,334,215	417	1	6.846	6.538	12.846	9	9	19	0	0	1	CAMK2B	31,224	in gene	ActReg chr7 #14428	0	0	1
14429	7	44,348,798	44,349,249	451	1	6.867	2.867	12.867	10	5	19	1	0	1	CAMK2B	16,207	in gene	ActReg chr7 #14429	0	0	1
14430	7	44,374,116	44,374,686	570	1	3.412	4.375	12.059	6	6	18	0	0	1	CAMK2B	-9,171	upstream	ActReg chr7 #14430	0	0	1
14431	7	44,530,098	44,530,599	501	1	15.25	10.938	16.5	19	19	30	1	1	1	NUDCD3	37	in gene	ActReg chr7 #14431	0	0	1
14432	7	44,613,188	44,613,959	771	2	7.917	13.292	10.75	13	23	21	1	1	2	DDX56, TMED4	564, 8254	in gene, downstream	ActReg chr7 #14432	0	1	1
14433	7	44,621,320	44,622,707	1,387	2	11.698	10.572	10.814	20	16	21	1	2	2	DDX56, TMED4	-7876, -186	upstream, upstream	ActReg chr7 #14433	1	0	1
14434	7	44,645,851	44,646,595	744	1	11.25	12.667	9.25	16	21	17	1	1	1	OGDH	102	in gene	ActReg chr7 #14434	0	1	0
14435	7	44,678,410	44,679,824	1,414	1	9.045	12.704	4.07	16	20	12	0	0	1	OGDH	32,996	in gene	ActReg chr7 #14435	0	1	0
14436	7	44,747,862	44,748,264	402	1	4.231	4.077	12.846	7	6	17	0	0	1	OGDH	101,942	in gene	ActReg chr7 #14436	0	0	1
14437	7	44,787,958	44,789,347	1,389	2	12.477	18.326	7.226	41	50	15	2	1	1	ZMIZ2	122	in gene	ActReg chr7 #14437	1	1	0
14438	7	44,835,728	44,836,599	871	1	9.852	11.556	8.222	19	15	15	1	1	1	PPIA	-78	upstream	ActReg chr7 #14438	0	1	0
14439	7	44,924,067	44,924,556	489	1	4.786	10.267	5.4	10	12	10	0	1	1	PURB	649	in gene	ActReg chr7 #14439	0	1	0
14440	7	44,925,049	44,925,802	753	1	10.792	13.042	4.85	21	22	8	0	1	1	PURB	-465	upstream	ActReg chr7 #14440	0	1	0
14441	7	45,010,175	45,010,663	488	1	2.25	3.625	12.125	3	7	17	0	0	1	MYO1G	8,285	in gene	ActReg chr7 #14441	0	0	1
14442	7	45,025,799	45,026,665	866	1	9.63	11.556	9.074	17	21	14	1	3	3	MYO1G, C7orf40, SNORA9	-7528, 27, -1123	upstream, in gene, upstream	ActReg chr7 #14442	0	1	0
14443	7	45,125,160	45,125,768	608	1	2.353	2.812	13.421	4	4	21	0	1	3	CCM2, LOC100128364, NACAD	86119, -5854, 3029	downstream, upstream, in gene	ActReg chr7 #14443	0	0	1
14444	7	45,144,771	45,145,206	435	1	7.692	5.385	12.077	9	8	15	0	3	4	TBRG4, SNORA5A, SNORA5C, SNORA5B	6329, -907, -347, 710	in gene, upstream, upstream, downstream	ActReg chr7 #14444	0	0	1
14445	7	45,150,759	45,151,823	1,064	3	10.152	16.485	9.484	18	24	18	1	4	4	TBRG4, SNORA5A, SNORA5C, SNORA5B	26, -7210, -6650, -5593	in gene, upstream, upstream, upstream	ActReg chr7 #14445	1	1	1
14446	7	45,306,773	45,307,431	658	2	11.333	14.333	1.188	28	31	2	0	0	0				ActReg chr7 #14446	1	1	0
14447	7	45,387,353	45,387,883	530	1	7.882	10.294	2	13	18	3	0	0	0				ActReg chr7 #14447	0	1	0
14448	7	45,614,977	45,615,467	490	1	3.8	3.733	14.533	6	5	24	1	1	1	ADCY1	1,097	in gene	ActReg chr7 #14448	0	0	1
14449	7	45,753,311	45,753,911	600	1	2.579	4.579	11.895	4	9	16	0	0	1	ADCY1	139,486	in gene	ActReg chr7 #14449	0	0	1
14450	7	45,808,377	45,808,923	546	2	12.823	12.823	8.75	23	23	12	1	0	0				ActReg chr7 #14450	1	1	0
14451	7	45,960,240	45,961,088	848	1	8.444	10.963	2.75	13	18	5	1	1	1	IGFBP3	207	in gene	ActReg chr7 #14451	0	1	0
14452	7	46,013,320	46,014,155	835	1	10.731	10.962	3.423	16	17	10	0	0	0				ActReg chr7 #14452	1	0	0
14453	7	46,017,535	46,018,263	728	1	9.87	12.609	5.348	15	23	11	0	0	0				ActReg chr7 #14453	0	1	0
14454	7	46,043,497	46,044,400	903	1	10.786	12	2	15	21	4	0	0	0				ActReg chr7 #14454	0	1	0
14455	7	46,046,576	46,047,178	602	1	7.789	11.579	1.154	11	17	2	0	0	0				ActReg chr7 #14455	0	1	0
14456	7	46,793,761	46,794,266	505	1	6	11.2	1	9	17	1	0	0	0				ActReg chr7 #14456	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GeneCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14457	7	46,850,485	46,851,642	1,157	2	10.583	10.833	2.6	19	18	7	0	0	0				ActReg chr7 #14457	1	1	0
14458	7	46,899,513	46,900,355	842	1	6.556	10.518	4.593	13	17	7	0	0	0				ActReg chr7 #14458	0	1	0
14459	7	47,330,921	47,331,612	691	2	11.857	9.952	1.278	19	17	3	0	0	1	TNS3	247,933	in gene	ActReg chr7 #14459	1	1	0
14460	7	47,339,970	47,340,713	743	1	12.043	11.087	5.261	19	15	8	0	0	1	TNS3	238,858	in gene	ActReg chr7 #14460	1	0	0
14461	7	47,367,054	47,367,893	839	1	8.423	12.654	6.48	15	23	14	0	0	1	TNS3	211,726	in gene	ActReg chr7 #14461	0	1	0
14462	7	47,402,136	47,403,113	977	1	8.484	12.097	2.136	16	20	3	0	0	1	TNS3	176,575	in gene	ActReg chr7 #14462	0	1	0
14463	7	47,514,467	47,515,305	838	1	14.462	13.808	5.846	26	29	10	0	0	1	TNS3	64,313	in gene	ActReg chr7 #14463	0	1	0
14464	7	47,640,004	47,640,864	860	1	11.852	9.407	2.741	19	15	5	0	0	0				ActReg chr7 #14464	1	0	0
14465	7	47,660,663	47,661,756	1,093	1	11.765	7.765	8	17	16	17	0	0	0				ActReg chr7 #14465	1	0	0
14466	7	47,826,005	47,826,638	633	1	6.95	11.9	4.438	10	19	8	0	0	2	PKD1L1, C7orf69	161716, -8568	in gene, upstream	ActReg chr7 #14466	0	1	0
14467	7	48,018,908	48,019,507	599	3	9.105	10.737	10.21	19	18	22	1	1	2	HUS1, SUN3	39, 49509	in gene, downstream	ActReg chr7 #14467	1	1	1
14468	7	48,074,876	48,076,087	1,211	2	5.289	9.632	10.658	10	15	16	1	2	2	SUN3, C7orf57	-6765, 364	upstream, in gene	ActReg chr7 #14468	0	1	1
14469	7	48,124,184	48,124,855	671	1	8.048	10.857	1.176	13	16	2	0	1	1	UPP1	-3,836	upstream	ActReg chr7 #14469	0	1	0
14470	7	48,128,168	48,128,611	443	1	10.786	8	12.143	15	13	18	2	1	1	UPP1	34	in gene	ActReg chr7 #14470	0	0	1
14471	7	48,284,229	48,284,868	639	1	7.95	12.5	1.2	14	25	2	0	0	1	ABCA13	73,491	in gene	ActReg chr7 #14471	0	1	0
14472	7	49,252,142	49,252,505	363	1	2	3.273	12.364	3	5	18	0	0	0				ActReg chr7 #14472	0	0	1
14473	7	49,493,284	49,493,583	299	1	1.111	1.2	10.778	2	2	14	0	0	0				ActReg chr7 #14473	0	0	1
14474	7	49,750,962	49,751,305	343	1	1.571	1	10.727	3	1	14	0	0	0				ActReg chr7 #14474	0	0	1
14475	7	49,813,810	49,814,199	389	1	2.083	2.5	11	3	4	15	1	1	1	VWC2	747	in gene	ActReg chr7 #14475	0	0	1
14476	7	50,342,266	50,342,680	414	1	2.846	1.4	11.231	4	2	16	0	1	1	IKZF1	-1,905	upstream	ActReg chr7 #14476	0	0	1
14477	7	50,517,662	50,518,888	1,226	3	9.103	11.538	6.897	19	22	19	1	1	2	FIGNL1, DDC	-187, 114879	upstream, downstream	ActReg chr7 #14477	1	1	1
14478	7	50,602,360	50,603,052	692	2	12.864	12.818	4.909	28	23	12	0	0	2	DDC, LOC100129427	30448, 3249	in gene, in gene	ActReg chr7 #14478	1	1	0
14479	7	50,620,217	50,621,203	986	2	13.065	16.129	3.783	36	34	8	0	0	2	DDC, LOC100129427	12444, 21253	in gene, downstream	ActReg chr7 #14479	1	1	0
14480	7	50,850,442	50,850,892	450	1	4.857	7.429	12.286	8	12	17	1	0	1	GRB10	10,492	in gene	ActReg chr7 #14480	0	0	1
14481	7	50,894,219	50,895,620	1,401	2	10.591	10.318	3.548	22	17	7	0	0	0				ActReg chr7 #14481	1	1	0
14482	7	50,919,460	50,920,451	991	1	10.452	6.935	1.935	17	12	4	0	0	0				ActReg chr7 #14482	1	0	0
14483	7	51,191,131	51,192,006	875	2	13.393	13.964	3.296	31	25	5	0	0	1	COBL	192,947	in gene	ActReg chr7 #14483	1	1	0
14484	7	51,612,898	51,613,341	443	1	10.308	6.154	3	14	8	5	0	0	0				ActReg chr7 #14484	1	0	0
14485	7	52,341,912	52,342,436	524	1	4.941	12.235	5	9	17	9	1	0	0				ActReg chr7 #14485	0	1	0
14486	7	53,103,157	53,103,844	687	1	1.909	2.955	11.091	4	5	15	1	1	1	POM121L12	151	in gene	ActReg chr7 #14486	0	0	1
14487	7	53,453,100	53,453,393	293	1	1.889	2.333	9.222	3	3	11	0	0	0				ActReg chr7 #14487	0	0	1
14488	7	53,879,358	53,879,882	524	1	7.059	12.882	5.353	10	20	10	0	1	1	FLJ45974	4	in gene	ActReg chr7 #14488	0	1	0
14489	7	54,082,859	54,083,455	596	1	6.833	12.722	1	14	25	1	0	0	0				ActReg chr7 #14489	0	1	0
14490	7	54,609,836	54,610,518	682	1	4.762	12.286	5.143	7	20	10	1	1	1	VSTM2A	158	in gene	ActReg chr7 #14490	0	1	0
14491	7	54,610,680	54,611,418	738	1	3.957	12.565	2	9	23	3	0	1	1	VSTM2A	1,030	in gene	ActReg chr7 #14491	0	1	0
14492	7	54,614,389	54,614,895	506	1	4.312	3.875	11.438	8	6	20	1	0	1	VSTM2A	4,623	in gene	ActReg chr7 #14492	0	0	1
14493	7	54,826,695	54,827,440	745	1	13.261	10.87	8.696	24	21	16	1	1	1	SEC61G	-128	upstream	ActReg chr7 #14493	1	0	0
14494	7	55,200,205	55,201,220	1,015	2	10.688	13.062	5.844	19	20	11	0	0	1	EGFR	113,987	in gene	ActReg chr7 #14494	1	1	0
14495	7	55,322,144	55,322,985	841	2	6.926	13.667	8.318	12	22	15	1	0	0				ActReg chr7 #14495	0	1	1
14496	7	55,412,012	55,412,521	509	1	1.75	5.562	14.188	3	9	22	1	0	0				ActReg chr7 #14496	0	0	1
14497	7	55,433,105	55,434,373	1,268	2	14	15.1	6.55	28	29	14	1	1	1	LANCL2	598	in gene	ActReg chr7 #14497	1	1	0
14498	7	55,517,183	55,517,568	385	1	2.462	1.455	10.077	4	3	12	1	0	0				ActReg chr7 #14498	0	0	1
14499	7	56,019,180	56,019,937	757	2	11.083	13.917	7.958	17	22	14	1	1	1	MRPS17	-53	upstream	ActReg chr7 #14499	1	1	0
14500	7	56,131,631	56,132,413	782	2	9.833	11.458	12.708	16	23	26	1	1	3	CCT6A, SNORA15, SUMF2	12644, 3859, 105	downstream, downstream, in gene	ActReg chr7 #14500	0	1	1
14501	7	56,149,477	56,149,913	436	1	4.692	5.308	12.077	6	8	18	0	0	2	SUMF2, PHKG1	17778, 10994	downstream, in gene	ActReg chr7 #14501	0	0	1
14502	7	56,173,799	56,174,547	748	1	10.304	11.826	5.87	17	19	10	1	1	2	CHCHD2, LOC389493	14, 9917	in gene, downstream	ActReg chr7 #14502	0	1	0
14503	7	56,515,481	56,516,011	530	1	7.706	10.177	9.235	11	15	14	1	0	0				ActReg chr7 #14503	0	1	0
14504	7	56,564,327	56,564,666	339	1	4.7	1.5	9.7	7	2	12	0	1	1	DKFZp434L192	580	in gene	ActReg chr7 #14504	0	0	1
14505	7	56,605,529	56,606,177	648	2	9	9.81	5.095	17	18	10	0	0	0				ActReg chr7 #14505	1	1	0
14506	7	57,440,879	57,441,290	411	1	1.875	1.167	9.769	3	2	15	0	0	0				ActReg chr7 #14506	0	0	1
14507	7	57,466,266	57,466,740	474	1	2.4	4	11.867	4	6	19	0	1	1	MIR3147	-6,228	upstream	ActReg chr7 #14507	0	0	1
14508	7	57,486,228	57,486,636	408	1	1.846	1.769	11.846	3	3	14	0	0	0				ActReg chr7 #14508	0	0	1
14509	7	57,715,093	57,715,550	457	1	5.778	3.417	10.786	9	10	16	0	0	1	LOC100287633	5,093	downstream	ActReg chr7 #14509	0	0	1
14510	7	62,518,484	62,518,773	289	1	0	2.111	10.333	0	3	13	0	0	0				ActReg chr7 #14510	0	0	1
14511	7	62,532,202	62,532,506	304	1	1	2.556	10.667	1	3	13	0	0	0				ActReg chr7 #14511	0	0	1
14512	7	62,573,779	62,574,356	577	1	2.083	5.389	10.889	4	7	15	0	0	0				ActReg chr7 #14512	0	0	1
14513	7	63,360,996	63,361,919	923	1	7.429	10.25	3.893	12	15	8	1	0	0				ActReg chr7 #14513	0	1	0
14514	7	63,386,255	63,387,422	1,167	2	11.389	13.778	5.5	23	28	10	1	0	0				ActReg chr7 #14514	1	1	0
14515	7	63,497,348	63,497,697	349	1	1.818	3.545	11.818	3	6	14	0	1	2	LOC100506050, ZNF727	-7042, -8299	upstream, upstream	ActReg chr7 #14515	0	0	1
14516	7	63,560,204	63,560,835	631	1	2.222	1.692	12.35	4	4	18	1	0	0				ActReg chr7 #14516	0	0	1
14517	7	64,299,999	64,300,258	259	1	4.222	1.571	10	6	2	13	0	0	1	ZNF138	45,357	downstream	ActReg chr7 #14517	0	0	1
14518	7	64,363,744	64,364,043	299	1	5	7.5	11.7	7	11	17	0	1	1	ZNF273	273	in gene	ActReg chr7 #14518	0	0	1
14519	7	64,699,067	64,699,895	828	1	4.737	6.423	13.192	8	12	22	1	0	0				ActReg chr7 #14519	0	0	1
14520	7	64,712,092	64,712,682	590	2	9.474	11.842	10.316	16	16	17	1	0	0				ActReg chr7 #14520	0	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14521	7	64,729,354	64,729,670	316	1	3.8	3.3	12.6	7	5	16	0	0	0				ActReg chr7 #14521	0	0	1
14522	7	64,790,610	64,791,114	504	1	10.062	6.125	1.562	16	8	3	0	0	0				ActReg chr7 #14522	1	0	0
14523	7	64,838,531	64,839,159	628	1	9.368	11	7.211	13	20	10	1	1	1	ZNF92	77	in gene	ActReg chr7 #14523	0	1	0
14524	7	65,215,327	65,216,613	1,286	2	8.146	12.732	7.171	12	21	18	1	1	1	SNORA22	-4,543	upstream	ActReg chr7 #14524	0	1	1
14525	7	65,297,114	65,297,719	605	1	11.21	9.579	3.833	24	19	6	0	1	1	DKFZp434F142	-7,782	upstream	ActReg chr7 #14525	1	0	0
14526	7	65,579,587	65,580,476	889	3	13.556	13.259	12.259	20	23	19	1	1	1	CRCP	226	in gene	ActReg chr7 #14526	1	1	1
14527	7	65,696,479	65,696,726	247	1	1.875	2.625	11.375	3	3	13	0	0	1	TPST1	26,343	in gene	ActReg chr7 #14527	0	0	1
14528	7	65,842,206	65,842,612	406	1	2.769	3.769	11.308	4	5	17	1	0	1	NCRNA00174	22,986	in gene	ActReg chr7 #14528	0	0	1
14529	7	65,958,243	65,959,268	1,025	3	10.156	11.906	10.875	19	21	21	1	1	1	LOC100289098	62	in gene	ActReg chr7 #14529	1	1	1
14530	7	66,056,670	66,057,581	911	2	7.759	12.69	11	13	24	16	1	0	0				ActReg chr7 #14530	0	1	1
14531	7	66,119,012	66,119,883	871	2	7.741	12.963	6.963	11	17	16	1	0	0				ActReg chr7 #14531	0	1	1
14532	7	66,146,695	66,147,561	866	1	9.111	11.296	9.889	16	16	15	1	0	0				ActReg chr7 #14532	0	1	0
14533	7	66,205,310	66,206,487	1,177	2	8.378	11.486	9.216	15	16	15	1	1	1	RABGEF1	255	in gene	ActReg chr7 #14533	0	1	1
14534	7	66,309,426	66,310,273	847	3	11.667	15.482	9.926	25	34	18	1	0	0				ActReg chr7 #14534	1	1	1
14535	7	66,359,464	66,360,095	631	1	9.316	11.105	3.579	19	19	6	0	0	1	LOC644794	-8,665	upstream	ActReg chr7 #14535	0	1	0
14536	7	66,367,068	66,367,406	338	1	2	4	11.909	3	5	14	1	1	1	LOC644794	-1,207	upstream	ActReg chr7 #14536	0	0	1
14537	7	66,385,654	66,386,380	726	1	15.261	10.217	5.353	28	23	11	1	1	1	C7orf42	-186	upstream	ActReg chr7 #14537	1	0	0
14538	7	66,432,054	66,432,540	486	1	3.2	5.333	11.933	6	10	18	0	0	1	C7orf42	46,094	downstream	ActReg chr7 #14538	0	0	1
14539	7	66,459,423	66,460,059	636	1	6.7	10.9	2.778	15	18	6	1	2	2	SBDS, TYW1	847, -2076	in gene, upstream	ActReg chr7 #14539	0	1	0
14540	7	66,934,953	66,935,303	350	1	1.9	2.818	10	3	4	14	0	0	0				ActReg chr7 #14540	0	0	1
14541	7	68,235,789	68,236,059	270	1	2	5.25	9.5	4	8	13	0	0	0				ActReg chr7 #14541	0	0	1
14542	7	68,552,743	68,552,918	175	1	4.4	1.8	12.2	6	2	14	0	0	0				ActReg chr7 #14542	0	0	1
14543	7	69,373,425	69,373,727	302	1	3	1	9.333	4	1	13	0	0	1	AUTS2	509,671	in gene	ActReg chr7 #14543	0	0	1
14544	7	70,650,243	70,650,498	255	1	3.5	2.25	10.25	5	3	12	0	0	1	WBSCR17	52,581	in gene	ActReg chr7 #14544	0	0	1
14545	7	72,299,819	72,300,325	506	1	8.812	10.812	8.312	11	15	11	1	1	1	TYW1B	-1,259	upstream	ActReg chr7 #14545	0	1	0
14546	7	72,395,234	72,396,105	871	1	7.481	10.37	4.667	11	15	9	1	0	1	POM121	45,733	in gene	ActReg chr7 #14546	0	1	0
14547	7	72,413,394	72,413,666	272	1	3.333	1.556	8.889	5	2	10	1	0	2	POM121, NSUN5C	63594, 11772	in gene, downstream	ActReg chr7 #14547	0	0	1
14548	7	72,847,722	72,848,233	511	1	8.688	15.938	5	16	29	7	1	1	2	FZD9, BAZ1B	-132, 88638	upstream, downstream	ActReg chr7 #14548	0	1	0
14549	7	72,936,314	72,937,338	1,024	2	11.094	13.875	5.556	19	27	9	1	1	1	BAZ1B	-211	upstream	ActReg chr7 #14549	1	1	0
14550	7	73,097,178	73,097,702	524	1	6.824	10.765	11.529	12	16	18	1	2	2	DNAJC30, WBSCR22	341, -458	in gene, upstream	ActReg chr7 #14550	0	0	1
14551	7	73,113,938	73,114,534	596	1	4.789	8.947	12	8	15	16	0	1	3	WBSCR22, STX1A, LOC100505484	16338, 19781, -4948	downstream, in gene, upstream	ActReg chr7 #14551	0	0	1
14552	7	73,129,657	73,130,631	974	2	14.258	12.613	4.323	27	26	10	0	0	2	STX1A, MIR4284	3873, 4497	in gene, downstream	ActReg chr7 #14552	1	1	0
14553	7	73,132,010	73,132,842	832	1	11.808	8.692	5.731	19	14	9	0	1	2	STX1A, MIR4284	1591, 6779	in gene, downstream	ActReg chr7 #14553	1	0	0
14554	7	73,248,951	73,249,295	344	1	6.455	6.364	11.546	9	8	15	0	1	3	CLDN4, LOC100128031, WBSCR27	3930, -2103, 7732	downstream, upstream, in gene	ActReg chr7 #14554	0	0	1
14555	7	73,255,959	73,256,381	422	1	4.692	6.308	11.846	10	9	15	0	1	3	CLDN4, LOC100128031, WBSCR27	10977, -9150, 685	downstream, upstream, in gene	ActReg chr7 #14555	0	0	1
14556	7	73,256,550	73,256,873	323	1	7.2	8.5	11.9	13	11	16	1	1	3	CLDN4, LOC100128031, WBSCR27	11518, -9691, 144	downstream, upstream, in gene	ActReg chr7 #14556	0	0	1
14557	7	73,300,681	73,301,204	523	1	3.625	2.938	12.125	5	5	19	0	0	0				ActReg chr7 #14557	0	0	1
14558	7	73,385,129	73,385,537	408	1	3.231	4.923	13.385	5	8	18	0	0	0				ActReg chr7 #14558	0	0	1
14559	7	73,387,215	73,387,961	746	1	3.826	2.545	12	8	4	20	0	0	0				ActReg chr7 #14559	0	0	1
14560	7	73,417,989	73,418,581	592	1	10.5	8.778	7	16	13	11	0	0	0				ActReg chr7 #14560	1	0	0
14561	7	73,428,010	73,428,550	540	1	3.267	7.118	13.059	8	10	17	0	0	0				ActReg chr7 #14561	0	0	1
14562	7	73,476,102	73,476,638	536	1	7.562	5.938	11	17	8	13	0	0	1	ELN	33,943	in gene	ActReg chr7 #14562	0	0	1
14563	7	73,508,535	73,509,380	845	1	10.074	6.37	8.037	12	13	11	0	0	1	LIMK1	10,801	in gene	ActReg chr7 #14563	1	0	0
14564	7	73,512,074	73,512,842	768	1	6.25	11.583	2.5	8	17	5	0	0	1	LIMK1	14,302	in gene	ActReg chr7 #14564	0	1	0
14565	7	73,634,463	73,634,896	433	1	2.786	2.571	12	4	4	17	0	0	1	LAT2	10,592	in gene	ActReg chr7 #14565	0	0	1
14566	7	73,668,277	73,669,316	1,039	3	15.212	12.061	11.156	26	22	18	1	1	1	RFC2	-58	upstream	ActReg chr7 #14566	1	1	1
14567	7	73,720,656	73,721,374	718	1	12.546	8.773	8.636	18	12	13	1	0	1	CLIP2	17,210	in gene	ActReg chr7 #14567	1	0	0
14568	7	73,752,802	73,753,401	599	1	5.167	9	11.611	9	15	14	1	0	1	CLIP2	49,296	in gene	ActReg chr7 #14568	0	0	1
14569	7	73,868,810	73,869,692	882	1	4.852	8.963	12.518	8	13	17	0	1	1	GTF2IRD1	1,131	in gene	ActReg chr7 #14569	0	0	1
14570	7	73,892,300	73,893,051	751	1	13.783	12.696	4.739	22	21	7	0	0	1	GTF2IRD1	24,555	in gene	ActReg chr7 #14570	1	0	0
14571	7	73,894,729	73,895,152	423	1	4.923	4.923	12.769	7	7	19	1	0	1	GTF2IRD1	26,820	in gene	ActReg chr7 #14571	0	0	1
14572	7	73,932,295	73,932,706	411	1	3.538	2.308	11.769	5	3	18	0	0	1	GTF2IRD1	64,380	in gene	ActReg chr7 #14572	0	0	1
14573	7	74,071,386	74,072,471	1,085	2	10	11.647	5.483	18	17	12	1	1	1	GTF2I	-102	upstream	ActReg chr7 #14573	1	1	0
14574	7	74,112,240	74,112,514	274	1	1	3	9	1	4	12	0	0	1	GTF2I	40,347	in gene	ActReg chr7 #14574	0	0	1
14575	7	74,489,195	74,489,878	683	1	7.714	11.857	6.278	13	20	10	1	1	1	WBSCR16	163	in gene	ActReg chr7 #14575	0	1	0
14576	7	75,156,835	75,157,814	979	1	7.367	12.6	6.957	15	20	13	1	0	1	HIP1	210,955	downstream	ActReg chr7 #14576	0	1	0
14577	7	75,184,872	75,185,288	416	1	2.615	2.833	11.308	4	6	15	0	0	1	HIP1	183,199	in gene	ActReg chr7 #14577	0	0	1
14578	7	75,368,448	75,369,209	761	1	12.917	8.583	6.125	23	12	11	1	1	1	HIP1	-549	upstream	ActReg chr7 #14578	1	0	0
14579	7	75,371,570	75,371,933	363	1	7.545	5.273	11.636	9	9	16	0	1	1	HIP1	-3,472	upstream	ActReg chr7 #14579	0	0	1
14580	7	75,377,223	75,377,575	352	1	4.909	1.333	9.727	11	2	13	0	0	1	HIP1	-9,120	upstream	ActReg chr7 #14580	0	0	1
14581	7	75,507,935	75,508,771	836	1	8.519	10.074	14	16	23	24	1	1	1	RHBDD2	36	in gene	ActReg chr7 #14581	0	0	1
14582	7	75,543,734	75,544,922	1,188	3	17.351	19.919	9.838	45	57	20	1	1	1	POR	-92	upstream	ActReg chr7 #14582	1	1	1
14583	7	75,613,881	75,614,381	500	1	5	3.2	11.812	7	5	17	0	0	2	POR, TMEM120A	69711, 9861	in gene, downstream	ActReg chr7 #14583	0	0	1
14584	7	75,677,039	75,677,729	690	1	8.909	11.909	5.364	12	19	10	1	2	2	STYXL1, MDH2	-63, -9	upstream, upstream	ActReg chr7 #14584	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14585	7	75,694,993	75,695,348	355	1	5.636	5.545	11.182	10	8	15	0	0	1	MDH2	17,777	in gene	AdReg chr7 #14585	0	0	1
14586	7	75,795,736	75,796,468	732	1	8.348	13.522	8.913	13	24	13	1	0	0				AdReg chr7 #14586	0	1	0
14587	7	75,830,839	75,832,055	1,216	2	9.486	13.974	4.839	27	43	13	1	1	1	SRRM3	231	in gene	AdReg chr7 #14587	1	1	0
14588	7	75,849,659	75,850,079	420	1	9.462	8.231	11.308	13	10	16	0	0	1	SRRM3	18,653	in gene	AdReg chr7 #14588	0	0	1
14589	7	75,947,519	75,947,956	437	1	6.143	8.857	12.357	9	13	16	1	0	1	YWHAG	40,605	downstream	AdReg chr7 #14589	0	0	1
14590	7	75,999,756	76,000,187	431	1	2.769	5.462	11.846	4	8	19	0	0	0				AdReg chr7 #14590	0	0	1
14591	7	76,009,176	76,009,956	780	3	12.6	11.88	9.68	27	18	18	1	0	1	SRCRB4D	29,446	downstream	AdReg chr7 #14591	1	1	1
14592	7	76,022,556	76,023,114	558	1	11.222	11.556	2.706	17	19	5	1	1	2	SRCRB4D, ZP3	16177, -4006	in gene, upstream	AdReg chr7 #14592	1	0	0
14593	7	76,132,054	76,132,454	400	1	1.4	4.538	10.538	2	7	17	0	1	2	DTX2, UPK3B	41282, -7491	in gene, upstream	AdReg chr7 #14593	0	0	1
14594	7	76,139,471	76,140,188	717	1	3.818	4.273	13.182	6	10	21	0	1	2	DTX2, UPK3B	48857, 84	downstream, in gene	AdReg chr7 #14594	0	0	1
14595	7	76,751,464	76,752,029	565	2	8.412	8.412	3.333	17	17	6	1	1	1	CCDC146	-188	upstream	AdReg chr7 #14595	1	1	0
14596	7	77,165,817	77,166,387	770	1	7.625	12.125	6.522	15	22	11	1	1	1	PTPN12	-771	upstream	AdReg chr7 #14596	0	1	0
14597	7	77,325,337	77,326,386	1,049	2	9.455	10.576	12.364	15	16	18	1	2	2	LOC100505854, RSBN1L	1096, 118	in gene, in gene	AdReg chr7 #14597	0	1	1
14598	7	77,649,023	77,649,434	411	1	7.615	6.538	9.077	13	10	16	1	0	1	MAGI2	1,433,662	in gene	AdReg chr7 #14598	0	0	1
14599	7	77,768,690	77,769,083	393	1	9.417	10	2.182	14	14	3	0	0	1	MAGI2	1,314,004	in gene	AdReg chr7 #14599	0	1	0
14600	7	77,780,583	77,781,236	653	1	7.2	11.35	2	14	19	3	0	0	1	MAGI2	1,301,981	in gene	AdReg chr7 #14600	0	1	0
14601	7	77,807,491	77,808,076	585	1	5.889	10.556	0	10	19	0	0	0	1	MAGI2	1,275,107	in gene	AdReg chr7 #14601	0	1	0
14602	7	78,250,115	78,250,810	695	2	10.667	14.048	1.812	25	29	3	0	0	1	MAGI2	832,428	in gene	AdReg chr7 #14602	1	1	0
14603	7	78,946,912	78,947,335	423	1	9.714	9.071	1	14	16	1	0	0	1	MAGI2	135,767	in gene	AdReg chr7 #14603	0	1	0
14604	7	79,081,642	79,081,946	304	1	11.444	9.333	11.556	16	14	15	1	2	2	MAGI2, LOC100505881	1096, -1514	in gene, upstream	AdReg chr7 #14604	0	0	1
14605	7	79,082,731	79,083,754	1,023	2	10.625	14.031	8.781	18	21	16	1	2	2	MAGI2, LOC100505881	-352, -66	upstream, upstream	AdReg chr7 #14605	1	1	0
14606	7	79,161,399	79,161,837	438	1	4.1	10.357	2.071	6	16	4	0	0	0				AdReg chr7 #14606	0	1	0
14607	7	79,764,258	79,764,891	633	1	9.947	11.368	6.389	14	18	10	1	1	1	GNAI1	434	in gene	AdReg chr7 #14607	0	1	0
14608	7	80,741,054	80,741,649	595	1	5.263	11.737	1.231	9	20	2	0	0	0				AdReg chr7 #14608	0	1	0
14609	7	80,820,283	80,820,753	470	1	11.533	6.8	1.889	18	9	3	0	0	0				AdReg chr7 #14609	1	0	0
14610	7	81,314,165	81,314,760	595	1	11.053	9.789	4.214	16	18	6	0	0	0				AdReg chr7 #14610	1	0	0
14611	7	81,823,427	81,823,843	416	1	4.615	10.308	1.333	10	18	2	0	0	1	CACNA2D1	249,396	in gene	AdReg chr7 #14611	0	1	0
14612	7	82,434,745	82,435,297	552	1	5.944	11	2.917	12	17	5	0	0	1	PCLO	357,176	in gene	AdReg chr7 #14612	0	1	0
14613	7	82,790,432	82,791,046	614	2	8.8	11.1	1	19	22	1	0	1	1	PCLO	1,458	in gene	AdReg chr7 #14613	1	1	0
14614	7	82,791,249	82,792,832	1,583	3	15.92	16.92	6.524	37	31	17	1	1	1	PCLO	157	in gene	AdReg chr7 #14614	1	1	1
14615	7	83,097,360	83,098,126	766	2	13.375	11.833	1	28	29	1	0	0	1	SEMA3E	180,736	in gene	AdReg chr7 #14615	1	1	0
14616	7	83,258,555	83,258,810	255	1	3.429	3.571	10.625	5	4	13	0	0	1	SEMA3E	19,797	in gene	AdReg chr7 #14616	0	0	1
14617	7	83,306,387	83,306,956	569	1	10.611	4	1.3	16	9	2	0	0	0				AdReg chr7 #14617	1	0	0
14618	7	83,866,732	83,867,392	660	1	11.429	6.667	2	22	10	4	0	0	0				AdReg chr7 #14618	1	0	0
14619	7	83,880,689	83,881,130	441	1	6.571	9.929	1.857	9	17	2	0	0	0				AdReg chr7 #14619	0	1	0
14620	7	84,815,331	84,816,365	1,034	1	9	11.531	4.806	13	15	9	1	0	0				AdReg chr7 #14620	0	1	0
14621	7	86,729,526	86,730,212	686	1	7.409	12.546	2.571	17	28	6	0	0	0				AdReg chr7 #14621	0	1	0
14622	7	86,781,200	86,782,317	1,117	1	8.914	12.086	9.829	18	21	17	1	3	3	LOC100505932, DMTP1, LOC100505951	-102, 81, -7078	upstream, in gene, upstream	AdReg chr7 #14622	0	1	0
14623	7	86,848,747	86,850,354	1,607	3	9.44	12.92	8.42	16	25	22	1	1	1	C7orf23	-519	upstream	AdReg chr7 #14623	1	1	1
14624	7	86,917,900	86,918,374	474	1	2.857	3.071	12.4	5	4	14	0	0	0				AdReg chr7 #14624	0	0	1
14625	7	86,974,262	86,975,088	826	2	10.615	11.154	8.808	13	19	14	1	2	2	TPSTG1, CROT	-133, -276	in gene, upstream	AdReg chr7 #14625	1	1	0
14626	7	87,257,128	87,257,933	805	2	10.6	10.16	6.88	19	16	17	1	1	2	ABCB1, RUNDC3B	85034, -199	in gene, upstream	AdReg chr7 #14626	1	1	0
14627	7	87,563,062	87,564,073	1,011	1	8.906	12.031	3.594	12	22	8	1	1	1	ADAM22	-135	upstream	AdReg chr7 #14627	0	1	0
14628	7	87,814,014	87,814,569	555	1	8.944	10	3.5	18	16	6	0	0	1	ADAM22	250,589	in gene	AdReg chr7 #14628	0	1	0
14629	7	87,849,115	87,849,868	753	2	11.083	16	6.792	20	31	14	1	0	1	SRI	6,817	in gene	AdReg chr7 #14629	1	1	0
14630	7	87,908,061	87,908,658	597	1	9.737	4.158	1.857	17	7	2	0	0	1	STEAP4	27,850	in gene	AdReg chr7 #14630	1	0	0
14631	7	89,975,635	89,976,388	753	3	12.375	9.417	8.542	23	16	20	1	1	1	GTPBP10	21	in gene	AdReg chr7 #14631	1	1	1
14632	7	90,394,120	90,394,610	490	1	5.133	9.6	1.75	8	14	2	0	0	1	CDK14	55,653	in gene	AdReg chr7 #14632	0	1	0
14633	7	90,893,313	90,894,101	788	1	14.375	9.417	4.667	30	14	10	1	1	1	FZD1	-76	upstream	AdReg chr7 #14633	1	0	0
14634	7	90,894,431	90,895,260	829	1	8.846	9.692	11.615	11	22	19	1	1	1	FZD1	1,062	in gene	AdReg chr7 #14634	0	0	1
14635	7	91,509,298	91,510,609	1,311	2	16.78	20.634	4.433	47	61	11	1	1	1	MTERF	63	in gene	AdReg chr7 #14635	1	1	0
14636	7	91,569,731	91,570,629	898	1	12.964	6.704	7.5	19	15	14	1	1	1	AKAP9	-9	upstream	AdReg chr7 #14636	1	0	0
14637	7	91,762,900	91,764,463	1,563	2	12.082	14.102	7.286	20	23	15	1	2	3	CYP51A1, LOC613126, LOC401387	378, 505, 30909	in gene, in gene, downstream	AdReg chr7 #14637	1	1	0
14638	7	91,808,291	91,808,689	398	1	3.818	5.917	13.583	7	9	20	1	0	1	LOC613126	45,314	in gene	AdReg chr7 #14638	0	0	1
14639	7	91,874,658	91,875,629	971	1	8.033	12.033	4.833	13	17	8	1	2	2	KRIT1, ANKIB1	271, -405	in gene, upstream	AdReg chr7 #14639	0	1	0
14640	7	92,076,668	92,077,184	516	1	9.882	10.588	10.167	14	16	16	1	1	1	GATAD1	161	in gene	AdReg chr7 #14640	0	1	0
14641	7	92,157,404	92,158,680	1,276	3	32.3	34.925	7.154	112	120	18	1	2	3	PEX1, C7orf64, MGC16142	-197, -45, -9747	upstream, upstream, upstream	AdReg chr7 #14641	1	1	1
14642	7	92,218,800	92,220,182	1,382	2	34.186	44.767	5.047	135	159	10	1	1	1	FAM133B	215	in gene	AdReg chr7 #14642	1	1	0
14643	7	92,462,217	92,462,843	626	1	11.684	10.737	5.765	18	12	9	1	0	1	CDK6	3,411	in gene	AdReg chr7 #14643	1	0	0
14644	7	92,462,983	92,463,804	821	1	6.52	10.8	6.04	10	16	11	1	1	1	CDK6	2,548	in gene	AdReg chr7 #14644	0	1	0
14645	7	92,464,712	92,465,375	663	1	10.25	9	5.9	15	13	8	1	1	1	CDK6	898	in gene	AdReg chr7 #14645	1	0	0
14646	7	92,861,112	92,861,988	876	2	10.571	14.393	4.444	23	32	10	0	2	2	HEPACAM2, CCDC132	-5768, -103	upstream, upstream	AdReg chr7 #14646	1	1	0
14647	7	93,519,713	93,520,325	612	1	5.632	10.632	7	7	17	15	1	1	1	TFPI2	46	in gene	AdReg chr7 #14647	0	1	0
14648	7	93,633,381	93,634,116	735	1	9.391	11.739	5.714	15	19	11	1	1	1	BET1	-58	upstream	AdReg chr7 #14648	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14649	7	93,730,182	93,730,503	321	1	4.2	2.8	11.1	6	4	13	0	0	0				ActReg chr7 #14649	0	0	1
14650	7	94,139,199	94,140,263	1,064	3	9.5	10.235	7	17	21	14	1	1	1	CASD1	561	in gene	ActReg chr7 #14650	1	1	1
14651	7	94,249,989	94,250,786	797	1	12.2	9.36	4.312	22	13	9	0	0	1	SGCE	35,154	in gene	ActReg chr7 #14651	1	0	0
14652	7	94,464,398	94,464,724	326	1	2.5	5.6	11.1	4	7	15	0	0	0				ActReg chr7 #14652	0	0	1
14653	7	94,536,501	94,537,184	683	2	8.909	11.318	5.105	16	24	10	1	1	1	PPP1R9A	-107	upstream	ActReg chr7 #14653	1	1	0
14654	7	94,603,038	94,603,655	617	1	9.35	11.85	3.889	15	18	8	0	0	1	PPP1R9A	66,397	in gene	ActReg chr7 #14654	0	1	0
14655	7	95,063,807	95,064,519	712	2	9.304	5.87	9.087	16	9	17	1	1	1	PON2	221	in gene	ActReg chr7 #14655	1	0	1
14656	7	95,130,729	95,131,230	501	1	10.6	6.4	1.75	14	10	2	0	0	1	ASB4	15,695	in gene	ActReg chr7 #14656	1	0	0
14657	7	95,179,101	95,179,880	779	1	9.16	10.32	3.44	14	14	6	0	0	1	LOC100506064	8,033	downstream	ActReg chr7 #14657	0	1	0
14658	7	95,858,065	95,858,467	402	1	1.545	4.818	12.077	4	10	15	0	0	2	SLC25A13, MIR591	93193, -9198	in gene, upstream	ActReg chr7 #14658	0	0	1
14659	7	95,950,783	95,951,939	1,156	3	13.784	14.243	10.135	26	27	20	1	1	1	SLC25A13	98	in gene	ActReg chr7 #14659	1	1	1
14660	7	96,338,671	96,339,390	719	1	9.909	11.682	5.273	14	17	9	1	1	1	SHFM1	173	in gene	ActReg chr7 #14660	0	1	0
14661	7	96,452,159	96,453,133	974	2	16.903	14.419	1.571	36	34	2	0	0	0				ActReg chr7 #14661	1	1	0
14662	7	96,663,664	96,664,118	454	1	3.143	2.846	12.929	4	6	18	0	0	1	DLX5	-9,748	upstream	ActReg chr7 #14662	0	0	1
14663	7	96,746,522	96,747,436	914	3	9.966	15.103	10.828	22	27	24	1	1	1	ACN9	1,074	in gene	ActReg chr7 #14663	1	1	1
14664	7	97,601,356	97,601,776	420	1	14.692	15.538	11.154	20	23	15	1	0	0				ActReg chr7 #14664	0	0	1
14665	7	97,735,825	97,736,680	855	2	9.889	11.148	6.235	16	29	13	1	1	1	LMTK2	55	in gene	ActReg chr7 #14665	1	1	0
14666	7	97,843,128	97,843,700	572	1	5.889	6	15.056	9	11	30	0	1	3	LMTK2, BHLHA15, TECPR1	107217, 1848, 38054	downstream, downstream, downstream	ActReg chr7 #14666	0	0	1
14667	7	97,846,813	97,847,625	812	1	3.538	5.462	13.308	7	9	20	0	0	3	LMTK2, BHLHA15, TECPR1	111022, 5653, 34249	downstream, downstream, in gene	ActReg chr7 #14667	0	0	1
14668	7	97,881,144	97,881,994	850	1	10.37	12.37	8.185	21	18	16	1	1	1	TECPR1	-101	upstream	ActReg chr7 #14668	0	1	0
14669	7	97,912,841	97,913,332	491	1	6.6	5.6	11.133	9	7	18	0	1	2	BRI3, BAIAP2L1	2107, 117341	in gene, downstream	ActReg chr7 #14669	0	0	1
14670	7	98,048,016	98,049,189	1,173	2	12.757	9.351	4.946	28	22	10	0	0	0				ActReg chr7 #14670	1	1	0
14671	7	98,475,963	98,477,047	1,084	2	12.088	17.5	7.033	30	39	15	1	1	2	TMEM130, TRRAP	-8832, 392	upstream, in gene	ActReg chr7 #14671	1	1	0
14672	7	98,506,999	98,507,351	352	1	3.2	2.6	10.636	5	4	15	0	0	1	TRRAP	31,062	in gene	ActReg chr7 #14672	0	0	1
14673	7	98,864,924	98,866,004	1,080	1	8.853	13.794	3.786	15	23	10	0	0	0				ActReg chr7 #14673	0	1	0
14674	7	98,923,321	98,923,859	538	1	10.471	13.941	11.353	15	21	17	1	1	1	ARPC1A	94	in gene	ActReg chr7 #14674	0	0	1
14675	7	98,971,771	98,972,425	654	1	8.667	9.762	3.95	15	14	6	1	1	2	ARPC1A, ARPC1B	48602, -231	downstream, upstream	ActReg chr7 #14675	0	1	0
14676	7	98,995,295	98,995,819	524	1	5.765	4.529	11.823	10	6	16	0	0	2	ARPC1B, PDAP1	23228, 10735	downstream, in gene	ActReg chr7 #14676	0	0	1
14677	7	99,005,558	99,006,867	1,309	2	12.439	10.854	5.805	19	29	11	1	2	3	PDAP1, BUD31, PTCD1	80, -389, 30207	in gene, upstream, downstream	ActReg chr7 #14677	1	1	0
14678	7	99,036,043	99,037,040	997	4	22.742	23.194	9.161	69	66	18	1	2	2	PTCD1, CPSF4	-122, -22	upstream, upstream	ActReg chr7 #14678	1	1	1
14679	7	99,097,455	99,098,247	792	3	10.6	12.52	8.92	18	21	19	1	2	2	ZNF394, ZKSCAN5	26, -4422	in gene, upstream	ActReg chr7 #14679	1	1	1
14680	7	99,149,334	99,150,037	703	2	11.773	13.318	6.545	29	25	10	1	2	2	C7orf38, ZNF655	72, -6360	in gene, upstream	ActReg chr7 #14680	1	1	0
14681	7	99,155,855	99,156,436	581	1	11	9.889	12.611	16	15	17	1	2	2	C7orf38, ZNF655	-6388, 100	upstream, in gene	ActReg chr7 #14681	0	0	1
14682	7	99,177,829	99,178,190	361	1	4.818	4.364	11.273	6	6	17	1	0	1	ZNF655	21,964	downstream	ActReg chr7 #14682	0	0	1
14683	7	99,213,883	99,215,162	1,279	2	20.675	26.95	5.825	54	68	14	1	1	2	LOC100506199, ZNF498	18674, -49	downstream, upstream	ActReg chr7 #14683	1	1	0
14684	7	99,457,697	99,458,317	620	1	9.789	11.158	5.588	13	17	8	0	0	2	CYP3A, CYP3A43	6166, 32371	in gene, in gene	ActReg chr7 #14684	0	1	0
14685	7	99,516,684	99,517,747	1,063	2	11.758	9.97	4.606	17	21	9	1	1	2	TRIM4, GJC3	8, 10028	in gene, downstream	ActReg chr7 #14685	1	1	0
14686	7	99,612,760	99,613,534	774	2	9.625	13.208	4.5	22	30	9	1	1	1	ZKSCAN1	-72	upstream	ActReg chr7 #14686	1	1	0
14687	7	99,647,193	99,647,789	596	1	10.474	7.684	7.579	17	14	12	0	1	1	ZSCAN21	74	in gene	ActReg chr7 #14687	1	0	0
14688	7	99,678,894	99,679,766	872	3	11.518	12.482	9.333	17	20	17	1	2	2	ZNF3, COPS6	41, -7253	in gene, upstream	ActReg chr7 #14688	1	1	1
14689	7	99,686,570	99,686,921	351	1	8.636	10.636	12.364	10	13	19	1	2	6	ZNF3, COPS6, MCM7, MIR25, MIR93, MIR106B	-7374, 162, 12682, 4521, 4725, 4952	upstream, in gene, downstream, downstream, downstream, downstream	ActReg chr7 #14689	0	0	1
14690	7	99,697,915	99,699,841	1,926	4	8.35	12.361	6.361	22	28	20	1	5	7	COPS6, MCM7, MIR25, MIR93, MIR106B, AP4M1, TAF6	12295, 549, -7612, -7408, -7181, -252, 18603	downstream, in gene, upstream, upstream, upstream, upstream, downstream	ActReg chr7 #14690	1	1	1
14691	7	99,716,577	99,717,730	1,153	2	15.444	13.917	7.389	23	26	17	0	3	3	TAF6, CNPY4, MBLAC1	328, -112, -7164	in gene, upstream, upstream	ActReg chr7 #14691	1	1	0
14692	7	99,724,321	99,725,795	1,474	3	10.891	11.587	8.826	22	17	18	1	2	3	TAF6, CNPY4, MBLAC1	-7577, 7793, 741	upstream, downstream, in gene	ActReg chr7 #14692	1	1	1
14693	7	99,964,004	99,964,569	565	1	5	3.824	9.059	10	5	12	0	1	2	PILRB, PILRA	8660, -6782	in gene, upstream	ActReg chr7 #14693	0	0	1
14694	7	100,025,572	100,027,212	1,640	3	12.784	12.137	10.608	19	18	31	1	2	3	ZCWPW1, MEPCE, C7orf47	-90, -21, 7702	upstream, upstream, downstream	ActReg chr7 #14694	1	1	1
14695	7	100,033,138	100,033,752	614	1	8.789	9	14.158	15	14	21	1	2	3	ZCWPW1, MEPCE, C7orf47	-7143, 7032, 649	upstream, downstream, in gene	ActReg chr7 #14695	0	0	1
14696	7	100,136,211	100,137,071	860	1	8.963	12	6.519	14	17	12	1	1	1	AGFG2	-193	upstream	ActReg chr7 #14696	0	1	0
14697	7	100,183,352	100,184,366	1,014	3	12.656	13.719	8.344	20	26	17	1	2	3	LRCH4, FBXO24, LOC100129845	-83, -97, 17802	upstream, upstream, downstream	ActReg chr7 #14697	1	1	1
14698	7	100,224,409	100,225,344	935	1	5.567	5.828	12.467	13	12	17	1	0	1	TFR2	14,297	in gene	ActReg chr7 #14698	0	0	1
14699	7	100,238,054	100,238,436	382	1	5.75	6.75	10.75	9	8	16	0	1	2	TFR2, ACTL6B	928, 15839	in gene, downstream	ActReg chr7 #14699	0	0	1
14700	7	100,253,642	100,254,475	833	3	8.923	9.96	7.269	19	19	16	1	1	1	ACTL6B	26	in gene	ActReg chr7 #14700	1	1	1
14701	7	100,270,915	100,271,465	550	1	11.812	14.235	6.8	21	28	10	1	1	2	GNB2, GIGYF1	-173, 15680	upstream, downstream	ActReg chr7 #14701	0	1	0
14702	7	100,275,792	100,276,350	558	1	3.765	5.765	12.059	5	10	15	0	0	2	GNB2, GIGYF1	4708, 10799	in gene, downstream	ActReg chr7 #14702	0	0	1
14703	7	100,279,300	100,280,042	742	1	6.522	7.304	11.739	14	10	16	0	0	2	GNB2, GIGYF1	8308, 7199	downstream, in gene	ActReg chr7 #14703	0	0	1
14704	7	100,302,789	100,304,462	1,673	3	9.865	10.308	9.365	16	19	20	1	1	1	POP7	-51	upstream	ActReg chr7 #14704	1	1	1
14705	7	100,434,679	100,435,420	741	1	9.174	13.087	6.857	14	24	11	1	0	1	EPHB4	-9,906	upstream	ActReg chr7 #14705	0	1	0
14706	7	100,472,136	100,473,009	873	2	7.296	13	10.111	17	20	17	1	1	3	SLC12A9, TRIP6, SRRT	22214, 7622, -129	downstream, downstream, upstream	ActReg chr7 #14706	0	1	1
14707	7	100,608,636	100,609,139	503	1	4.188	7.938	12.375	8	12	20	1	1	2	MUC3A, MUC12	61630, -4017	in gene, upstream	ActReg chr7 #14707	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14708	7	100,609,726	100,610,403	677	1	6.227	8.045	11.682	14	10	18	1	1	2	MUC3A, MUC12	62807, -2840	in gene, upstream	ActReg chr7 #14708	0	0	1
14709	7	100,612,857	100,613,414	557	1	3.389	4.111	11.556	6	7	14	0	1	2	MUC3A, MUC12	65878, 231	downstream, in gene	ActReg chr7 #14709	0	0	1
14710	7	100,701,469	100,702,071	602	2	14.21	13.421	2.353	27	26	5	0	0	1	MUC17	38,406	in gene	ActReg chr7 #14710	1	1	0
14711	7	100,743,316	100,744,230	914	1	7.103	11.931	4.571	13	18	8	0	0	1	TRIM56	14,987	downstream	ActReg chr7 #14711	0	1	0
14712	7	100,781,695	100,782,168	473	1	8.933	10.667	2.5	13	17	6	0	0	1	SERPINE1	11,552	in gene	ActReg chr7 #14712	0	1	0
14713	7	100,806,827	100,808,158	1,331	3	10.659	10.024	10.256	18	19	22	1	1	3	AP1S1, VGF, C7orf52	9806, 1360, 16065	downstream, in gene, downstream	ActReg chr7 #14713	1	1	1
14714	7	100,808,202	100,809,260	1,058	2	16.273	12.333	8.061	29	23	17	1	1	3	AP1S1, VGF, C7orf52	11045, 121, 14826	downstream, in gene, downstream	ActReg chr7 #14714	1	1	0
14715	7	100,812,308	100,813,489	1,181	1	11.973	10.162	6.405	15	17	15	0	1	3	AP1S1, VGF, C7orf52	15212, -4046, 10659	downstream, upstream, downstream	ActReg chr7 #14715	1	0	0
14716	7	100,816,293	100,817,028	735	1	7.043	10.478	9.13	12	16	14	1	1	2	VGF, C7orf52	-7808, 6897	upstream, in gene	ActReg chr7 #14716	0	1	0
14717	7	100,841,334	100,841,717	383	1	2.455	5.667	10.75	3	8	18	0	0	3	MOGAT3, DGAT2L7, PLOD3	2777, 5279, 19486	in gene, downstream, downstream	ActReg chr7 #14717	0	0	1
14718	7	100,860,661	100,861,249	588	1	9.368	10.316	12.368	12	16	24	1	2	2	PLOD3, ZNHIT1	56, -30	in gene, upstream	ActReg chr7 #14718	0	0	1
14719	7	100,887,211	100,888,717	1,506	3	11.894	11.702	9.894	24	25	20	1	2	2	CLDN15, FIS1	-5863, 407	upstream, in gene	ActReg chr7 #14719	1	1	1
14720	7	100,895,105	100,895,944	839	2	11.769	15.308	5.538	22	32	9	1	1	1	FIS1	-7,153	upstream	ActReg chr7 #14720	1	1	0
14721	7	100,951,598	100,951,962	364	1	7.455	4.727	10.091	10	6	13	0	0	2	LOC100506507, RABL5	8886, 13313	downstream, downstream	ActReg chr7 #14721	0	0	1
14722	7	101,158,003	101,158,588	585	1	4	5.312	9.889	5	8	14	0	0	1	EMID2	152,173	in gene	ActReg chr7 #14722	0	0	1
14723	7	101,190,078	101,190,534	456	1	3.357	1.455	11.2	6	4	16	0	0	1	EMID2	184,184	in gene	ActReg chr7 #14723	0	0	1
14724	7	101,202,289	101,202,759	470	1	2.8	2.6	11.133	4	5	19	0	0	2	EMID2, LOC100506527	196402, 9706	downstream, downstream	ActReg chr7 #14724	0	0	1
14725	7	101,331,499	101,331,913	414	1	6.077	7.154	11.231	9	12	16	1	0	0				ActReg chr7 #14725	0	0	1
14726	7	101,457,404	101,458,094	690	2	9.727	10.682	2.5	17	21	4	1	1	1	CUX1	-1,543	upstream	ActReg chr7 #14726	1	1	0
14727	7	101,458,413	101,458,896	483	2	11.467	11.6	9.933	17	16	14	1	1	1	CUX1	-638	upstream	ActReg chr7 #14727	1	0	1
14728	7	101,459,099	101,459,410	311	1	5.444	11.3	1	7	17	1	1	1	1	CUX1	-38	upstream	ActReg chr7 #14728	0	1	0
14729	7	101,762,306	101,762,871	565	1	8.647	10.588	3.625	12	19	5	0	0	1	CUX1	303,296	in gene	ActReg chr7 #14729	0	1	0
14730	7	101,844,534	101,845,249	715	1	3.87	4.652	11.348	6	8	16	0	0	1	CUX1	385,599	in gene	ActReg chr7 #14730	0	0	1
14731	7	101,929,228	101,929,647	419	1	4.231	6.769	11.231	8	11	17	1	2	3	CUX1, SH2B2, MIR4285	470145, 1032, -6932	downstream, in gene, upstream	ActReg chr7 #14731	0	0	1
14732	7	102,003,937	102,004,501	564	2	13.412	10.529	2.824	25	18	6	1	1	1	SPDYE6	-7,330	upstream	ActReg chr7 #14732	1	1	0
14733	7	102,036,196	102,037,267	1,071	3	11.667	13.485	9.818	25	25	20	1	1	2	PRKRIP1, MIR548O	-73, 9571	upstream, downstream	ActReg chr7 #14733	1	1	1
14734	7	102,086,708	102,087,247	539	1	4.941	6.471	12.529	7	10	23	0	0	2	ORAI2, ALKBH4	12981, 18344	in gene, downstream	ActReg chr7 #14734	0	0	1
14735	7	102,087,631	102,088,039	408	1	3.538	3.462	9.769	6	5	15	0	0	2	ORAI2, ALKBH4	13839, 17486	in gene, downstream	ActReg chr7 #14735	0	0	1
14736	7	102,092,602	102,093,184	582	1	3.632	2.533	9.105	6	5	13	0	0	2	ORAI2, ALKBH4	18897, 12428	in gene, downstream	ActReg chr7 #14736	0	0	1
14737	7	102,095,300	102,095,863	563	1	2	3.765	10.529	4	6	15	0	0	3	ORAI2, ALKBH4, LRWD1	21585, 9740, -9809	in gene, downstream, upstream	ActReg chr7 #14737	0	0	1
14738	7	102,112,913	102,113,587	674	1	4.467	4.05	11.476	7	6	15	0	0	5	ALKBH4, LRWD1, POLR2J, LOC100506726, RASA4B	-7929, 7860, 6131, 10263, 44974	upstream, in gene, downstream, downstream, downstream	ActReg chr7 #14738	0	0	1
14739	7	102,119,182	102,119,530	348	2	29	39.545	2.455	46	64	4	1	1	4	LRWD1, POLR2J, LOC100506726, RASA4B	13966, 25, 4157, 38868	downstream, in gene, downstream, downstream	ActReg chr7 #14739	1	1	0
14740	7	102,515,897	102,516,764	867	2	9.667	13.963	2.96	24	26	6	0	0	1	FBXL13	198,958	in gene	ActReg chr7 #14740	1	1	0
14741	7	102,632,016	102,632,594	578	1	10.333	8.5	1.091	18	14	2	0	0	1	FBXL13	82,983	in gene	ActReg chr7 #14741	1	0	0
14742	7	102,789,253	102,790,341	1,088	2	8.559	11.471	4.967	15	17	9	1	1	1	NAPEPLD	-228	upstream	ActReg chr7 #14742	1	1	0
14743	7	102,937,745	102,938,184	439	1	12.214	9.929	11.786	16	16	18	1	1	1	PMPCB	91	in gene	ActReg chr7 #14743	0	0	1
14744	7	102,984,795	102,985,472	677	2	10.727	12.046	6.773	20	19	12	1	2	3	DNAJC2, PSMC2, SLC26A5	187, -2956, 101491	in gene, upstream, downstream	ActReg chr7 #14744	1	1	0
14745	7	103,276,553	103,277,140	587	2	10.278	13.833	2.143	16	24	3	0	0	1	RELN	353,117	in gene	ActReg chr7 #14745	1	1	0
14746	7	103,848,046	103,848,851	805	2	10.92	12.48	5.12	23	22	9	0	1	1	ORC5L	15	in gene	ActReg chr7 #14746	1	1	0
14747	7	104,192,395	104,193,100	705	1	10.056	13.5	3.684	21	27	5	0	0	1	LHFPL3	223,643	in gene	ActReg chr7 #14747	0	1	0
14748	7	104,267,793	104,268,388	595	2	10.158	13.947	1.692	16	25	2	0	0	1	LHFPL3	298,986	in gene	ActReg chr7 #14748	1	1	0
14749	7	104,652,991	104,654,608	1,617	2	8.686	10.941	8.412	16	16	16	1	2	2	LOC100216545, MLL5	789, -838	in gene, upstream	ActReg chr7 #14749	0	1	1
14750	7	104,944,530	104,945,286	756	1	8.333	10.625	2.421	15	15	3	0	0	1	SRPK2	84,433	in gene	ActReg chr7 #14750	0	1	0
14751	7	105,172,330	105,173,112	782	2	13.917	14.125	8.25	23	31	16	1	1	2	PUS7, RINT1	-10036, 189	upstream, in gene	ActReg chr7 #14751	1	1	0
14752	7	105,415,940	105,417,096	1,156	2	10.5	13.441	1.909	28	36	4	0	0	1	ATXN7L1	100,513	in gene	ActReg chr7 #14752	1	1	0
14753	7	105,698,992	105,699,507	515	1	11.75	13.438	8.188	18	23	10	0	0	0				ActReg chr7 #14753	0	1	0
14754	7	105,752,063	105,753,353	1,290	2	9.463	9.61	3.188	18	15	6	1	1	1	SYPL1	349	in gene	ActReg chr7 #14754	1	1	0
14755	7	106,300,390	106,300,907	517	2	8.067	10.438	8.125	12	17	16	1	1	1	FLJ36031	943	in gene	ActReg chr7 #14755	0	1	1
14756	7	106,463,994	106,465,441	1,447	2	11.348	12.783	2.857	17	24	6	0	0	0				ActReg chr7 #14756	1	1	0
14757	7	106,507,948	106,508,757	809	1	2.76	4.36	14.96	5	7	27	1	1	1	PIK3CG	2,428	in gene	ActReg chr7 #14757	0	0	1
14758	7	106,968,446	106,968,995	549	1	9.167	7.222	0	17	11	0	0	0	1	COG5	256,239	in gene	ActReg chr7 #14758	1	0	0
14759	7	107,204,010	107,205,022	1,012	3	14.29	17.839	9.742	30	41	20	1	2	2	COG5, DUS4L	443, 84	in gene, in gene	ActReg chr7 #14759	1	1	1
14760	7	107,383,552	107,385,069	1,517	1	10.104	13.625	5.188	17	20	10	1	2	2	LOC100128737, CBLL1	716, 31	in gene, in gene	ActReg chr7 #14760	0	1	0
14761	7	107,988,042	107,988,571	529	1	7.312	10.25	1	14	19	1	0	0	1	NRCAM	108,535	in gene	ActReg chr7 #14761	0	1	0
14762	7	108,071,333	108,072,202	869	1	11.037	14.111	3.37	18	26	5	0	0	1	NRCAM	25,074	in gene	ActReg chr7 #14762	0	1	0
14763	7	108,082,482	108,082,934	452	1	10.286	6.071	2.286	13	10	4	0	0	1	NRCAM	14,133	in gene	ActReg chr7 #14763	1	0	0
14764	7	108,094,989	108,096,040	1,051	1	11.061	12.242	7.03	16	20	13	1	1	1	NRCAM	1,327	in gene	ActReg chr7 #14764	0	1	0
14765	7	108,096,310	108,096,687	377	1	9.417	8.75	11.333	12	14	15	1	1	1	NRCAM	343	in gene	ActReg chr7 #14765	0	0	1
14766	7	108,166,088	108,167,154	1,066	1	8.636	11.152	6.909	15	15	10	1	1	1	PNPLA8	17	in gene	ActReg chr7 #14766	0	1	0
14767	7	108,209,727	108,210,810	1,083	3	9.882	10.853	8.706	16	19	20	1	2	2	THAP5, DNAJB9	-101, -88	upstream, upstream	ActReg chr7 #14767	1	1	1
14768	7	109,996,714	109,997,261	547	1	3.529	2.471	10.353	6	4	14	0	0	0				ActReg chr7 #14768	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14769	7	111,202,068	111,202,928	860	1	10.148	7.889	4.708	16	11	10	1	1	1	IMMP2L	-151	upstream	ActReg chr7 #14769	1	0	0
14770	7	111,640,837	111,641,487	650	1	7.15	11.35	1.667	10	15	2	0	0	1	DOCK4	205,300	in gene	ActReg chr7 #14770	0	1	0
14771	7	111,846,101	111,847,121	1,020	2	11.156	11.688	6.844	19	23	14	1	2	2	DOCK4, ZNF277	-149, -32	upstream, upstream	ActReg chr7 #14771	1	1	0
14772	7	112,090,075	112,091,489	1,414	2	12.556	12.711	8.841	21	25	14	1	0	1	IFRD1	27,556	in gene	ActReg chr7 #14772	1	1	0
14773	7	112,121,758	112,122,516	758	1	10.5	5.083	1.105	16	9	2	0	1	2	IFRD1, C7orf53	58911, 1229	downstream, in gene	ActReg chr7 #14773	1	0	0
14774	7	112,124,670	112,125,196	526	1	7.059	11.471	2.5	9	17	4	0	0	2	IFRD1, C7orf53	61707, 4025	downstream, in gene	ActReg chr7 #14774	0	1	0
14775	7	112,429,747	112,430,928	1,181	2	12.649	7.432	7.757	19	12	20	1	1	1	TMEM168	141	in gene	ActReg chr7 #14775	1	0	1
14776	7	112,758,458	112,758,862	404	1	9.308	11	4.231	13	14	7	0	1	1	LOC401397	-23	upstream	ActReg chr7 #14776	0	1	0
14777	7	112,907,834	112,908,492	658	1	8.524	12.714	2.632	12	18	5	0	0	0				ActReg chr7 #14777	0	1	0
14778	7	113,233,456	113,233,730	274	1	4.778	5.857	12	6	7	17	0	0	0				ActReg chr7 #14778	0	0	1
14779	7	114,025,551	114,026,000	449	1	4.571	10.143	6.357	7	14	10	0	0	1	FOXP2	299,410	in gene	ActReg chr7 #14779	0	1	0
14780	7	114,529,603	114,530,253	650	2	11.35	11.5	2.727	27	19	4	0	0	0				ActReg chr7 #14780	1	1	0
14781	7	114,871,074	114,871,573	499	1	11.533	9.733	1	18	18	1	0	0	0				ActReg chr7 #14781	1	0	0
14782	7	114,980,914	114,981,441	527	2	9.059	8.647	1.9	19	16	3	0	0	0				ActReg chr7 #14782	1	1	0
14783	7	115,911,820	115,912,351	531	1	9.875	8.875	1.688	15	13	3	0	0	0				ActReg chr7 #14783	1	0	0
14784	7	116,166,216	116,167,119	903	2	14.714	12.607	4.857	27	19	9	1	1	1	CAV1	1,828	in gene	ActReg chr7 #14784	1	1	0
14785	7	116,216,680	116,217,660	980	2	10.133	8.9	3.5	16	16	6	0	0	0				ActReg chr7 #14785	1	1	0
14786	7	116,256,619	116,257,247	628	1	11.421	9.316	3.333	24	18	5	0	0	0				ActReg chr7 #14786	1	0	0
14787	7	116,356,558	116,357,132	574	1	14.111	11.611	2.889	24	19	6	0	0	1	MET	44,386	in gene	ActReg chr7 #14787	1	0	0
14788	7	116,416,390	116,416,805	415	1	9.846	6.154	2.923	12	10	6	0	0	1	MET	104,138	in gene	ActReg chr7 #14788	1	0	0
14789	7	116,502,560	116,502,858	298	1	8.8	12.2	11.2	13	16	15	1	1	1	CAPZA2	146	in gene	ActReg chr7 #14789	0	0	1
14790	7	116,593,984	116,594,568	584	1	9.895	9.789	1.842	15	13	3	1	3	3	ST7OT1, ST7, ST7OT4	112, 895, 323	in gene, in gene, in gene	ActReg chr7 #14790	1	0	0
14791	7	116,909,300	116,910,036	736	2	13.826	10.261	2.263	28	23	5	0	0	1	WNT2	53,675	downstream	ActReg chr7 #14791	1	1	0
14792	7	116,963,925	116,964,273	348	1	5.091	3.182	12.454	7	4	17	1	1	1	WNT2	-756	upstream	ActReg chr7 #14792	0	0	1
14793	7	117,236,226	117,236,585	359	1	4.727	3.636	11.636	7	5	19	0	0	1	CFTR	116,388	in gene	ActReg chr7 #14793	0	0	1
14794	7	119,053,645	119,054,036	391	1	1.833	3.167	10.667	3	4	14	0	0	0				ActReg chr7 #14794	0	0	1
14795	7	120,590,335	120,591,261	926	2	13.034	10.345	6.84	22	22	11	1	1	1	ING3	-19	upstream	ActReg chr7 #14795	1	1	0
14796	7	120,844,641	120,845,027	386	1	10.5	7.167	1	15	11	1	0	0	1	C7orf58	216,083	in gene	ActReg chr7 #14796	1	0	0
14797	7	121,035,882	121,036,903	1,021	2	11.875	16.719	2.679	28	41	7	1	1	1	FAM3C	30	in gene	ActReg chr7 #14797	1	1	0
14798	7	121,783,845	121,784,851	1,006	1	11.032	6.355	4.29	15	14	10	1	1	1	AASS	-4	upstream	ActReg chr7 #14798	1	0	0
14799	7	122,675,741	122,676,311	570	1	3.056	9.667	5.722	5	19	9	0	0	0				ActReg chr7 #14799	0	1	0
14800	7	123,197,473	123,198,406	933	2	15.138	13.345	3.435	29	24	7	1	1	1	NDUFA5	19	in gene	ActReg chr7 #14800	1	1	0
14801	7	123,388,542	123,389,756	1,214	3	9.974	10.974	9.943	18	19	23	1	1	1	WASL	-53	upstream	ActReg chr7 #14801	1	1	1
14802	7	123,672,509	123,673,077	568	1	10.294	11.167	6.889	14	18	16	1	1	1	TMEM229A	730	in gene	ActReg chr7 #14802	0	1	0
14803	7	124,362,880	124,363,526	646	2	8.905	9.905	1.75	18	18	2	0	0	0				ActReg chr7 #14803	1	1	0
14804	7	124,405,583	124,406,212	629	2	9.45	12.158	6.1	16	22	12	1	1	1	GPR37	-216	upstream	ActReg chr7 #14804	1	1	0
14805	7	125,203,534	125,204,510	976	2	12.036	9.667	5.034	24	15	13	0	0	0				ActReg chr7 #14805	1	1	0
14806	7	125,666,718	125,667,049	331	1	5	10.182	1	7	14	1	0	0	0				ActReg chr7 #14806	0	1	0
14807	7	125,680,492	125,680,893	401	1	4.417	5.333	11.25	8	7	15	0	0	0				ActReg chr7 #14807	0	0	1
14808	7	126,747,361	126,748,402	1,041	2	18.645	21.438	3.219	43	52	5	0	0	1	GRM8	144,547	in gene	ActReg chr7 #14808	1	1	0
14809	7	126,891,868	126,892,330	462	1	6.2	3.769	10.067	9	6	17	1	1	1	GRM8	529	in gene	ActReg chr7 #14809	0	0	1
14810	7	126,893,682	126,894,229	547	1	10.588	7.765	4.765	14	15	7	1	1	1	GRM8	-1,527	upstream	ActReg chr7 #14810	1	0	0
14811	7	127,031,954	127,032,517	563	1	8.222	10	3.375	12	14	7	1	1	1	ZNF800	532	in gene	ActReg chr7 #14811	0	1	0
14812	7	127,032,534	127,033,362	828	1	8.115	11.731	3.154	16	17	6	1	1	1	ZNF800	-181	upstream	ActReg chr7 #14812	0	1	0
14813	7	127,114,349	127,114,991	642	1	9	11.95	1.643	15	23	3	0	1	1	LOC100506682	-2,262	upstream	ActReg chr7 #14813	0	1	0
14814	7	127,291,550	127,292,296	746	2	11.917	11.25	8.667	18	15	12	1	1	1	SND1	-279	upstream	ActReg chr7 #14814	1	1	0
14815	7	127,743,482	127,743,950	468	1	1.933	2.8	12.4	3	3	19	0	0	0				ActReg chr7 #14815	0	0	1
14816	7	127,803,683	127,805,032	1,349	1	9.048	11.429	3.784	14	17	8	0	0	0				ActReg chr7 #14816	0	1	0
14817	7	127,808,248	127,809,075	827	2	8.038	12.538	13	11	21	20	1	0	0				ActReg chr7 #14817	0	1	1
14818	7	127,983,545	127,984,247	702	1	9.227	11.636	5.737	16	23	12	1	1	2	RBM28, PRRT4	66, 17843	in gene, downstream	ActReg chr7 #14818	0	1	0
14819	7	128,000,887	128,001,493	606	1	4.421	3.474	10.105	9	7	16	1	1	1	PRRT4	549	in gene	ActReg chr7 #14819	0	0	1
14820	7	128,095,539	128,096,353	814	2	9.5	12	10.308	13	16	22	1	1	1	C7orf68	62	in gene	ActReg chr7 #14820	0	1	1
14821	7	128,116,554	128,117,010	456	1	9.214	13.214	6.357	13	19	12	1	1	1	METTL2B	-1	upstream	ActReg chr7 #14821	0	1	0
14822	7	128,379,081	128,379,923	842	1	7.111	11.222	14.667	13	16	21	1	1	2	FAM71F1, CALU	24049, 146	downstream, in gene	ActReg chr7 #14822	0	0	1
14823	7	128,471,203	128,471,619	416	1	2.7	1.75	11.769	6	3	16	1	1	2	CCDC136, FLNC	39312, 928	downstream, in gene	ActReg chr7 #14823	0	0	1
14824	7	128,488,542	128,488,964	422	1	2.286	4.714	12.286	4	8	17	0	0	1	FLNC	18,270	in gene	ActReg chr7 #14824	0	0	1
14825	7	128,694,255	128,695,556	1,301	2	13.61	13.659	4.842	20	24	11	1	1	1	TNPO3	322	in gene	ActReg chr7 #14825	1	1	0
14826	7	129,251,228	129,251,744	516	1	7.824	12.412	5.176	13	20	11	1	2	2	LOC100127891, NRF1	9, -69	in gene, upstream	ActReg chr7 #14826	0	1	0
14827	7	129,402,159	129,402,556	397	1	2.25	2.909	10.5	4	4	16	1	0	2	NRF1, MIR182	150802, 7975	downstream, downstream	ActReg chr7 #14827	0	0	1
14828	7	129,420,207	129,420,785	578	1	4.056	7.278	12.278	7	11	17	1	2	3	MIR182, MIR96, MIR183	-10164, -5587, -5642	upstream, upstream, upstream	ActReg chr7 #14828	0	0	1
14829	7	129,609,577	129,610,296	719	1	5.5	11.182	4.591	11	15	7	0	0	0				ActReg chr7 #14829	0	1	0
14830	7	129,648,685	129,650,654	1,969	2	9.508	12.213	5.377	22	22	14	0	0	1	ZC3HC1	41,564	downstream	ActReg chr7 #14830	1	1	0
14831	7	129,656,804	129,657,134	330	1	1.778	2	11	3	3	15	0	0	1	ZC3HC1	34,264	downstream	ActReg chr7 #14831	0	0	1
14832	7	129,709,800	129,710,582	782	2	19.083	15.5	4	44	34	10	1	1	1	KLHDC10	-158	upstream	ActReg chr7 #14832	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14833	7	129,918,963	129,919,678	715	1	8	11.046	2.857	13	16	6	0	0	1	CPA2	12,617	in gene	AdReg chr7 #14833	0	1	0
14834	7	129,996,701	129,997,349	648	1	10.714	9.571	3.15	17	15	7	0	0	1	CPA5	12,395	in gene	AdReg chr7 #14834	1	0	0
14835	7	130,004,213	130,004,652	439	1	2.091	3	10.857	4	6	15	0	0	1	CPA5	19,802	in gene	AdReg chr7 #14835	0	0	1
14836	7	130,549,682	130,550,778	1,096	2	11.5	15.784	2.559	26	31	6	0	0	1	LOC100506860	11,751	in gene	AdReg chr7 #14836	1	1	0
14837	7	130,579,825	130,580,258	433	1	4.143	3.286	8.429	6	5	14	0	0	2	LOC100506860, hCG_2038586	41562, 18028	in gene, in gene	AdReg chr7 #14837	0	0	1
14838	7	130,645,065	130,645,664	599	1	8.842	10.316	3.467	15	17	6	0	0	1	FLJ43663	148,198	in gene	AdReg chr7 #14838	0	1	0
14839	7	130,756,804	130,757,198	394	1	14.25	9.25	2.917	22	15	5	0	0	1	FLJ43663	36,561	in gene	AdReg chr7 #14839	1	0	0
14840	7	130,873,011	130,873,856	845	1	9.37	11.259	3.083	15	16	5	0	0	1	MKLN1	78,578	in gene	AdReg chr7 #14840	0	1	0
14841	7	130,896,684	130,897,369	685	2	12.95	11.809	3.524	24	21	6	0	0	1	MKLN1	102,171	in gene	AdReg chr7 #14841	1	1	0
14842	7	131,011,946	131,013,278	1,332	2	12.829	14.341	6.707	21	30	12	1	1	2	MKLN1, LOC100506881	217757, -74	in gene, upstream	AdReg chr7 #14842	1	1	0
14843	7	131,292,220	131,293,245	1,025	2	11.438	10.406	4.094	24	19	10	0	0	0				AdReg chr7 #14843	1	1	0
14844	7	131,430,115	131,431,073	958	2	10.067	16.367	2.519	18	34	5	0	0	0				AdReg chr7 #14844	1	1	0
14845	7	131,580,314	131,581,154	840	1	8.889	11.778	1.84	15	20	4	0	0	0				AdReg chr7 #14845	0	1	0
14846	7	131,581,888	131,582,733	845	1	11.667	6.815	4.238	20	10	7	0	0	0				AdReg chr7 #14846	1	0	0
14847	7	131,977,504	131,978,114	610	1	6.1	10.25	1.75	11	17	3	0	0	1	PLXNA4	355,638	in gene	AdReg chr7 #14847	0	1	0
14848	7	132,261,100	132,261,534	434	1	1.923	2.615	10.769	5	5	17	1	0	1	PLXNA4	72,130	in gene	AdReg chr7 #14848	0	0	1
14849	7	132,468,522	132,469,140	618	1	10.158	7.421	3.444	19	14	5	0	0	1	CHCHD3	298,002	downstream	AdReg chr7 #14849	1	0	0
14850	7	132,766,527	132,767,321	794	2	9.96	11.24	4.88	18	18	8	1	1	1	CHCHD3	-91	upstream	AdReg chr7 #14850	1	1	0
14851	7	132,823,898	132,824,773	875	1	10.321	17.179	3.296	21	37	8	0	0	0				AdReg chr7 #14851	0	1	0
14852	7	133,597,834	133,598,401	567	1	9.778	10.278	1.429	15	15	2	0	0	1	EXOC4	660,294	in gene	AdReg chr7 #14852	0	1	0
14853	7	134,000,981	134,002,112	1,131	2	12.528	10.639	7.278	20	21	14	1	1	1	SLC35B4	281	in gene	AdReg chr7 #14853	1	1	0
14854	7	134,142,974	134,144,359	1,385	3	14.591	14.273	8.103	25	37	18	1	1	1	AKR1B1	222	in gene	AdReg chr7 #14854	1	1	1
14855	7	134,155,461	134,156,115	654	1	9.8	11.45	2.85	19	18	7	0	0	0				AdReg chr7 #14855	0	1	0
14856	7	134,331,162	134,332,098	936	2	19.767	21.3	3.033	56	54	5	0	1	1	BPGM	99	in gene	AdReg chr7 #14856	1	1	0
14857	7	134,832,762	134,833,197	435	1	8.071	10.357	1.182	12	15	2	0	2	2	LOC653739, TMEM140	66, 213	in gene, in gene	AdReg chr7 #14857	0	1	0
14858	7	134,854,949	134,855,883	934	2	11.103	11.931	4.786	16	19	15	1	1	2	TMEM140, C7orf49	22650, 116	downstream, in gene	AdReg chr7 #14858	1	1	0
14859	7	134,895,743	134,896,484	741	1	7.417	10.125	6.182	11	17	13	1	1	1	WDR91	203	in gene	AdReg chr7 #14859	0	1	0
14860	7	135,019,911	135,021,247	1,336	2	12.122	17.561	3.707	37	45	8	0	0	0				AdReg chr7 #14860	1	1	0
14861	7	135,126,492	135,127,044	552	1	8.944	6.556	3	16	15	6	0	0	1	CNOT4	68,107	in gene	AdReg chr7 #14861	1	0	0
14862	7	135,194,636	135,195,419	783	1	8.625	12.708	7.042	18	21	14	1	1	1	CNOT4	-152	upstream	AdReg chr7 #14862	0	1	0
14863	7	135,242,241	135,243,142	901	2	12.714	11.607	4.08	24	24	10	0	1	1	NUP205	29	in gene	AdReg chr7 #14863	1	1	0
14864	7	135,346,662	135,347,700	1,038	3	11.781	12.531	10.312	22	21	18	1	1	1	PL-5283	-40	upstream	AdReg chr7 #14864	1	1	1
14865	7	135,348,233	135,348,581	348	1	3.364	8.545	10	4	15	14	0	1	1	PL-5283	1,186	in gene	AdReg chr7 #14865	0	0	1
14866	7	135,487,401	135,488,249	848	1	8.038	11.192	3.667	17	17	6	0	0	0				AdReg chr7 #14866	0	1	0
14867	7	135,819,240	135,819,681	441	1	8.143	9.286	1.182	12	14	2	0	0	0				AdReg chr7 #14867	0	1	0
14868	7	136,541,924	136,542,898	974	2	13.033	14.967	1.364	23	44	2	0	0	0				AdReg chr7 #14868	1	1	0
14869	7	137,223,228	137,223,696	468	1	3.867	9.667	1.846	6	15	5	0	0	1	DGKI	308,147	in gene	AdReg chr7 #14869	0	1	0
14870	7	137,326,652	137,327,478	826	2	11.385	14.808	2	20	28	3	0	0	1	DGKI	204,544	in gene	AdReg chr7 #14870	1	1	0
14871	7	137,366,722	137,367,324	602	1	10.333	9.333	2.667	17	12	4	0	0	1	DGKI	164,586	in gene	AdReg chr7 #14871	1	0	0
14872	7	137,531,953	137,532,332	379	1	2.75	2.583	10.25	5	4	13	1	1	1	DGKI	-533	upstream	AdReg chr7 #14872	0	0	1
14873	7	137,663,255	137,663,819	564	1	10.167	10.833	2.733	13	15	4	0	0	1	CREB3L2	23,309	in gene	AdReg chr7 #14873	0	1	0
14874	7	138,437,059	138,437,784	725	1	12.318	10	4.6	22	19	9	0	0	1	ATP6V0A4	45,520	in gene	AdReg chr7 #14874	1	0	0
14875	7	138,440,131	138,440,978	847	1	10.5	7.615	2.6	15	14	5	0	0	1	ATP6V0A4	42,387	in gene	AdReg chr7 #14875	1	0	0
14876	7	138,549,251	138,549,942	691	1	9.952	13.381	2.381	16	23	5	0	0	1	KIAA1549	71,033	in gene	AdReg chr7 #14876	0	1	0
14877	7	138,575,479	138,576,220	741	1	10.217	12.348	4.043	17	20	8	0	0	1	KIAA1549	44,780	in gene	AdReg chr7 #14877	0	1	0
14878	7	138,666,547	138,667,008	461	1	5.667	9.533	10.733	8	13	18	1	0	0				AdReg chr7 #14878	0	0	1
14879	7	138,793,500	138,794,353	853	1	10.778	11.185	8.444	15	15	14	1	1	1	ZC3HAV1	539	in gene	AdReg chr7 #14879	0	1	0
14880	7	138,915,411	138,916,387	976	3	9.839	8.613	9.034	16	21	15	1	1	1	UBN2	-332	upstream	AdReg chr7 #14880	1	1	1
14881	7	139,024,566	139,026,467	1,901	4	12.017	12.4	9.05	28	19	22	1	1	1	C7orf55	-381	upstream	AdReg chr7 #14881	1	1	1
14882	7	139,043,696	139,045,088	1,392	1	9.682	11.432	13.159	18	26	22	1	1	1	LUC7L2	-242	upstream	AdReg chr7 #14882	0	0	1
14883	7	139,168,237	139,168,662	425	1	5.077	4.583	13.846	7	7	20	1	1	1	KLRG2	8	in gene	AdReg chr7 #14883	0	0	1
14884	7	139,365,473	139,366,026	553	1	11.588	15.118	4.118	17	28	9	0	0	0				AdReg chr7 #14884	0	1	0
14885	7	139,471,023	139,471,773	750	2	8.87	9.435	1.773	18	16	3	0	1	2	LOC100505582, TBXAS1	6295, -6649	in gene, upstream	AdReg chr7 #14885	1	1	0
14886	7	139,477,867	139,478,651	784	2	7.833	12.375	8.25	13	18	15	1	2	2	LOC100505582, TBXAS1	-566, 212	upstream, in gene	AdReg chr7 #14886	0	1	1
14887	7	139,762,579	139,763,245	666	1	4.9	10.476	3.733	9	19	6	1	1	1	PARP12	609	in gene	AdReg chr7 #14887	0	1	0
14888	7	140,103,588	140,103,989	401	1	2.083	4.75	11.5	3	7	18	0	2	2	SLC37A3, RAB19	-5477, -55	upstream, upstream	AdReg chr7 #14888	0	0	1
14889	7	140,178,792	140,179,521	729	1	6.913	10.565	6.211	13	16	13	1	1	1	MKRN1	213	in gene	AdReg chr7 #14889	0	1	0
14890	7	140,264,379	140,264,938	559	1	11.944	6.611	5.462	19	10	11	0	0	1	DENND2A	37,684	in gene	AdReg chr7 #14890	1	0	0
14891	7	140,307,134	140,307,859	725	1	10.565	10.043	4.591	15	16	8	0	1	1	DENND2A	-5,154	upstream	AdReg chr7 #14891	1	0	0
14892	7	140,339,569	140,340,374	805	1	5.958	11.52	8	9	23	14	1	0	0				AdReg chr7 #14892	0	1	0
14893	7	140,396,221	140,397,128	907	3	10	14.586	9.448	15	26	16	1	2	3	ADCK2, LOC100134713, NDUFB2	23721, 203, 193	downstream, in gene, in gene	AdReg chr7 #14893	1	1	1
14894	7	140,623,724	140,624,538	814	1	12.04	10.24	3.56	20	20	8	1	1	1	BRAF	433	in gene	AdReg chr7 #14894	1	0	0
14895	7	140,624,752	140,625,225	473	1	6.333	11.267	4.385	13	18	7	1	1	1	BRAF	-424	upstream	AdReg chr7 #14895	0	1	0
14896	7	140,714,295	140,715,254	959	2	13.533	17.033	7.133	29	35	13	1	1	1	MRPS33	7	in gene	AdReg chr7 #14896	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14897	7	140,772,064	140,773,504	1,440	2	11.587	13.109	6.065	19	25	14	1	1	1	LOC100507421	-1,040	upstream	ActReg chr7 #14897	1	1	0
14898	7	140,796,958	140,797,811	853	2	12.556	16.037	2.2	31	41	5	0	0	1	LOC100507421	23,560	in gene	ActReg chr7 #14898	1	1	0
14899	7	140,828,126	140,828,776	650	1	9.286	11.286	2	13	17	2	0	0	1	LOC100507421	54,627	in gene	ActReg chr7 #14899	0	1	0
14900	7	140,844,428	140,845,221	793	1	9.36	11.72	3.8	16	17	10	0	0	1	LOC100507421	71,000	in gene	ActReg chr7 #14900	0	1	0
14901	7	140,920,561	140,921,447	886	2	11.179	13.107	4.893	27	26	8	0	0	1	LOC100507421	147,180	in gene	ActReg chr7 #14901	1	1	0
14902	7	141,250,776	141,251,633	857	2	10.889	10.222	2.84	17	13	6	1	1	1	AGK	126	in gene	ActReg chr7 #14902	1	1	0
14903	7	141,437,544	141,438,574	1,030	2	19.938	21.75	7.25	46	60	14	1	2	3	FLJ40852, WEE2, SSBP1	-29, 29906, -117	upstream, downstream, upstream	ActReg chr7 #14903	1	1	0
14904	7	142,026,156	142,026,933	777	2	9.375	14.375	3.4	18	24	7	0	1	3	TRB@, TRBV5-1, TRBV6-1	27693, 5650, -1634	in gene, downstream, upstream	ActReg chr7 #14904	1	1	0
14905	7	142,913,166	142,913,635	469	1	4.6	10.667	3	9	19	4	0	1	1	TAS2R40	-5,772	upstream	ActReg chr7 #14905	0	1	0
14906	7	142,984,699	142,985,277	578	1	8	10.667	7.278	15	17	11	1	1	2	TMEM139, CASP2	2925, -414	in gene, upstream	ActReg chr7 #14906	0	1	0
14907	7	142,985,316	142,985,909	593	2	7.722	10.889	11.556	12	19	20	1	1	2	TMEM139, CASP2	3549, 210	downstream, in gene	ActReg chr7 #14907	0	1	1
14908	7	143,077,587	143,078,297	710	2	7.409	12.682	8.955	12	23	14	1	2	3	LOC100507507, ZYX, EPHA1	-354, -418, 28043	upstream, upstream, downstream	ActReg chr7 #14908	0	1	1
14909	7	143,598,660	143,599,288	628	1	9.474	8.579	12.263	14	13	16	1	1	1	FAM115A	198	in gene	ActReg chr7 #14909	0	0	1
14910	7	144,532,732	144,533,561	829	2	12.731	17.615	5.231	22	45	11	1	1	1	TPK1	0	in gene	ActReg chr7 #14910	1	1	0
14911	7	144,706,885	144,707,925	1,040	2	9.75	9.969	2.194	20	21	6	0	0	0				ActReg chr7 #14911	1	1	0
14912	7	144,909,013	144,909,753	740	2	10.783	15.13	1.167	24	38	2	0	0	0				ActReg chr7 #14912	1	1	0
14913	7	145,341,106	145,342,154	1,048	1	7.091	12.212	2.818	12	21	5	0	0	0				ActReg chr7 #14913	0	1	0
14914	7	145,812,511	145,814,386	1,875	2	11.373	15.576	4.981	22	39	10	1	1	1	CNTNAP2	-5	upstream	ActReg chr7 #14914	1	1	0
14915	7	147,530,451	147,530,846	395	1	4.75	10.333	2.6	7	14	7	0	0	1	CNTNAP2	1,717,195	in gene	ActReg chr7 #14915	0	1	0
14916	7	148,637,694	148,638,573	879	2	11.357	10.556	6.643	18	18	17	1	1	1	RNY5	-447	upstream	ActReg chr7 #14916	1	1	0
14917	7	148,680,467	148,680,964	497	1	11.188	10.125	6.733	17	14	14	0	1	2	RNY3, RNY1	-132, 3625	upstream, downstream	ActReg chr7 #14917	1	0	0
14918	7	148,684,013	148,684,917	904	2	12.643	9.679	4.565	19	16	11	0	1	2	RNY3, RNY1	3618, -125	downstream, upstream	ActReg chr7 #14918	1	1	0
14919	7	148,762,069	148,763,508	1,439	2	14.136	18.067	7.333	43	47	13	1	0	1	ZNF786	25,081	downstream	ActReg chr7 #14919	1	1	0
14920	7	148,787,341	148,788,488	1,147	2	7.444	12.167	7.875	12	23	17	1	1	1	ZNF786	-45	upstream	ActReg chr7 #14920	0	1	1
14921	7	148,822,814	148,824,165	1,351	3	17.372	18.605	11.954	48	43	23	1	2	2	ZNF425, ZNF398	-51, -19	upstream, upstream	ActReg chr7 #14921	1	1	1
14922	7	148,844,080	148,845,737	1,657	1	7.712	12.962	6.163	14	21	15	1	0	1	ZNF398	21,400	in gene	ActReg chr7 #14922	0	1	0
14923	7	148,892,256	148,892,966	710	2	19.652	30.091	5.81	46	70	9	1	1	1	ZNF282	34	in gene	ActReg chr7 #14923	1	1	0
14924	7	148,936,050	148,937,351	1,301	3	40.317	47.268	8.026	156	160	19	1	1	1	ZNF212	-42	upstream	ActReg chr7 #14924	1	1	1
14925	7	148,958,381	148,960,002	1,621	2	11.784	12.549	4.673	27	30	11	1	1	2	ZNF212, LOC100507573	22449, -71	downstream, upstream	ActReg chr7 #14925	1	1	0
14926	7	148,978,895	148,979,428	533	1	5.688	4.059	14.059	11	6	20	1	0	1	LOC100507573	19,899	in gene	ActReg chr7 #14926	0	0	1
14927	7	148,991,539	148,992,041	502	1	3.5	5.75	13.062	8	9	18	1	0	1	LOC100507573	32,528	in gene	ActReg chr7 #14927	0	0	1
14928	7	148,992,892	148,993,482	590	1	3.111	4.158	10.842	6	8	14	0	0	1	LOC100507573	33,925	in gene	ActReg chr7 #14928	0	0	1
14929	7	149,157,539	149,158,344	805	2	31.92	32	5.92	85	81	10	1	1	1	ZNF777	112	in gene	ActReg chr7 #14929	1	1	0
14930	7	149,321,348	149,322,446	1,098	2	37.471	36.824	3.5	120	114	7	1	0	0				ActReg chr7 #14930	1	1	0
14931	7	149,387,985	149,388,539	554	1	9.824	11.529	6.882	12	17	11	0	0	0				ActReg chr7 #14931	0	1	0
14932	7	149,397,782	149,398,158	376	1	1.5	2.917	11.5	2	5	17	0	0	0				ActReg chr7 #14932	0	0	1
14933	7	149,462,536	149,463,057	521	1	3.938	6.562	11.562	6	11	16	1	0	1	ZNF467	7,499	in gene	ActReg chr7 #14933	0	0	1
14934	7	149,499,926	149,500,291	365	1	1.333	5.333	10.5	2	8	13	0	0	1	SSPO	26,977	in gene	ActReg chr7 #14934	0	0	1
14935	7	149,506,462	149,506,803	341	1	5.545	2.455	13.091	8	3	17	0	0	1	SSPO	33,501	in gene	ActReg chr7 #14935	0	0	1
14936	7	149,524,878	149,525,317	439	1	5	2.929	12.5	7	6	17	0	0	1	SSPO	51,966	in gene	ActReg chr7 #14936	0	0	1
14937	7	149,571,020	149,571,466	446	1	10	10.357	12	12	18	19	1	2	3	ZNF862, LOC401431, ATP6V0E2	35734, -292, 1186	downstream, upstream, in gene	ActReg chr7 #14937	0	0	1
14938	7	150,065,589	150,066,911	1,322	1	5.537	11.512	4.949	10	19	10	1	1	2	REPIN1, ZNF775	371, -10156	in gene, upstream	ActReg chr7 #14938	0	1	0
14939	7	150,101,941	150,102,687	746	2	15.435	18	3.143	35	36	10	1	1	2	ZNF775, tcag7.1196	25908, -526	downstream, upstream	ActReg chr7 #14939	1	1	0
14940	7	150,498,080	150,498,694	614	1	1.778	2.85	11.65	3	6	17	1	2	2	TMEM176B, TMEM176A	61, 533	in gene, in gene	ActReg chr7 #14940	0	0	1
14941	7	150,539,122	150,539,492	370	1	3.917	5.583	9.667	7	7	15	0	0	0				ActReg chr7 #14941	0	0	1
14942	7	150,680,778	150,681,644	866	2	14.259	15.037	2.667	30	29	5	0	2	2	KCNH2, NOS3	-6197, -6933	upstream, upstream	ActReg chr7 #14942	1	1	0
14943	7	150,725,313	150,726,080	767	2	11.083	10.375	9.083	17	19	14	1	2	3	ATG9B, ABCB8, LOC100507614	-4110, 186, 5990	upstream, in gene, in gene	ActReg chr7 #14943	1	1	0
14944	7	150,736,027	150,737,371	1,344	1	7.976	11.976	8.512	14	19	14	0	1	3	ABCB8, LOC100507614, ACCN3	11189, -5013, -8906	in gene, upstream, upstream	ActReg chr7 #14944	0	1	0
14945	7	150,737,931	150,738,405	474	1	2.067	7.2	12.133	3	10	16	0	2	3	ABCB8, LOC100507614, ACCN3	12658, -6482, -7437	in gene, upstream, upstream	ActReg chr7 #14945	0	0	1
14946	7	150,745,517	150,745,948	431	1	2.538	3.923	11.692	4	6	17	1	1	3	ABCB8, ACCN3, CDK5	20222, 127, 9320	downstream, in gene, downstream	ActReg chr7 #14946	0	0	1
14947	7	150,754,744	150,755,611	867	2	12.518	13.593	7	24	28	11	1	2	4	ABCB8, ACCN3, CDK5, SLC4A2	29667, 9572, -125, -1480	downstream, downstream, upstream, upstream	ActReg chr7 #14947	1	1	0
14948	7	150,757,469	150,758,259	790	2	7.32	10.48	9.24	11	15	18	1	2	3	ACCN3, CDK5, SLC4A2	12259, -2812, 1207	downstream, upstream, in gene	ActReg chr7 #14948	0	1	1
14949	7	150,774,180	150,774,615	435	1	5.917	6.615	15.154	12	9	20	0	0	4	SLC4A2, FASTK, TMUB1, AGAP3	17740, 3554, 6223, -9429	downstream, in gene, downstream, upstream	ActReg chr7 #14949	0	0	1
14950	7	150,777,054	150,778,074	1,020	2	8.406	12.094	8.812	16	22	17	1	2	4	SLC4A2, FASTK, TMUB1, AGAP3	20907, 387, 3056, -6262	downstream, in gene, downstream, upstream	ActReg chr7 #14950	0	1	1
14951	7	150,783,993	150,784,494	501	1	6	10.312	11.125	8	16	16	1	3	3	FASTK, TMUB1, AGAP3	-6292, -3623, 417	upstream, upstream, in gene	ActReg chr7 #14951	0	0	1
14952	7	150,786,306	150,787,129	823	1	10.04	12.32	5.96	14	21	8	0	2	3	FASTK, TMUB1, AGAP3	-8766, -6097, 2891	upstream, upstream, in gene	ActReg chr7 #14952	0	1	0
14953	7	150,807,003	150,807,604	601	1	3.211	5.158	11.263	6	9	17	0	0	1	AGAP3	23,477	in gene	ActReg chr7 #14953	0	0	1
14954	7	150,822,479	150,823,009	530	1	5.765	5.765	12.529	5	9	20	1	0	1	AGAP3	38,918	in gene	ActReg chr7 #14954	0	0	1
14955	7	150,871,208	150,871,916	708	1	2.789	4.364	11.818	6	8	17	1	1	2	GBX1, ASB10	-6695, 13357	upstream, downstream	ActReg chr7 #14955	0	0	1
14956	7	150,888,826	150,889,287	461	1	3.071	1.733	11.467	5	3	17	0	1	1	ASB10	-4,137	upstream	ActReg chr7 #14956	0	0	1
14957	7	150,924,009	150,924,797	788	2	12.792	13.542	5.792	24	23	13	1	2	2	ABCF2, CHPF2	-86, -5182	upstream, upstream	ActReg chr7 #14957	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
14958	7	150,929,147	150,929,599	452	1	10.643	12.286	10.929	13	17	14	1	3	4	ABCF2, CHPF2, MIR671, SMARCD3	-5056, -212, -6134, 44858	upstream, upstream, upstream, downstream	AdReg chr7 #14958	0	0	1
14959	7	150,934,794	150,935,267	473	1	3.867	6.4	13.4	7	10	16	1	1	3	CHPF2, MIR671, SMARCD3	5445, -477, 39201	in gene, upstream, downstream	AdReg chr7 #14959	0	0	1
14960	7	150,958,663	150,959,127	464	1	3	6.214	10.929	5	9	16	0	0	1	SMARCD3	15,336	in gene	AdReg chr7 #14960	0	0	1
14961	7	151,106,812	151,107,559	747	1	2.083	3.75	11.125	3	7	15	1	3	3	WDR86, LOC100507673, LOC100131176	-61, -1127, 863	upstream, upstream, in gene	AdReg chr7 #14961	0	0	1
14962	7	151,132,645	151,133,168	523	1	2.133	2.875	13.25	4	5	18	0	0	1	CRYGN	4,193	in gene	AdReg chr7 #14962	0	0	1
14963	7	151,165,091	151,165,872	781	2	11.375	8.75	7	16	14	19	0	0	1	RHEB	51,529	in gene	AdReg chr7 #14963	1	0	1
14964	7	151,168,746	151,169,370	624	1	11.421	8.368	2.267	22	16	6	0	0	1	RHEB	47,952	in gene	AdReg chr7 #14964	1	0	0
14965	7	151,442,130	151,442,728	598	1	7.211	11.421	1.588	12	17	3	0	0	1	PRKAG2	131,887	in gene	AdReg chr7 #14965	0	1	0
14966	7	151,479,970	151,480,556	586	2	12.278	8.278	10.444	22	14	17	1	0	1	PRKAG2	94,053	in gene	AdReg chr7 #14966	1	0	1
14967	7	151,493,160	151,494,096	936	2	11.31	12.897	4.621	20	21	10	0	0	1	PRKAG2	80,688	in gene	AdReg chr7 #14967	1	1	0
14968	7	151,722,247	151,722,717	470	2	9.786	11	10.154	16	16	17	1	1	2	GALNTL5, GALNT11	69018, -296	downstream, upstream	AdReg chr7 #14968	0	1	1
14969	7	152,133,521	152,134,669	1,148	2	10.389	10.667	1.812	22	30	3	0	1	1	MLL3	-1,005	upstream	AdReg chr7 #14969	1	1	0
14970	7	152,160,878	152,162,743	1,865	2	21.086	17.828	8.018	39	32	18	1	1	1	LOC100128822	601	in gene	AdReg chr7 #14970	1	1	0
14971	7	152,217,175	152,219,811	2,636	1	9.024	13.614	6.646	19	23	12	0	0	0				AdReg chr7 #14971	0	1	0
14972	7	152,236,074	152,236,807	733	1	5.478	6	12.043	8	9	16	0	0	0				AdReg chr7 #14972	0	0	1
14973	7	152,406,613	152,407,203	590	1	10.263	8.842	2.438	16	11	4	0	0	0				AdReg chr7 #14973	1	0	0
14974	7	152,758,903	152,759,594	691	2	11.682	11.591	1.85	19	27	4	0	0	0				AdReg chr7 #14974	1	1	0
14975	7	153,752,456	153,753,043	587	1	6.647	10.222	1.5	11	18	2	0	0	1	DPP6	168,330	in gene	AdReg chr7 #14975	0	1	0
14976	7	154,794,710	154,795,629	919	2	13.923	13.31	5.28	24	27	10	1	2	2	PAXIP1, LOC202781	-487, 26	upstream, in gene	AdReg chr7 #14976	1	1	0
14977	7	154,844,487	154,845,559	1,072	2	28.849	37.576	2.897	89	110	6	0	0	0				AdReg chr7 #14977	1	1	0
14978	7	154,858,184	154,858,670	486	1	9.267	12.4	1.9	14	20	3	0	1	2	LOC100128264, HTR5A	4840, -4119	downstream, upstream	AdReg chr7 #14978	0	1	0
14979	7	154,861,136	154,862,561	1,425	2	37.133	48.178	6.156	133	194	13	2	2	2	LOC100128264, HTR5A	1419, -698	in gene, upstream	AdReg chr7 #14979	1	1	0
14980	7	154,862,720	154,863,398	678	1	8.545	10.273	6.545	14	14	14	1	2	2	LOC100128264, HTR5A	208, 513	in gene, in gene	AdReg chr7 #14980	0	1	0
14981	7	155,088,206	155,089,250	1,044	1	12.273	8.394	7.607	17	16	12	1	1	1	INSIG1	-758	upstream	AdReg chr7 #14981	1	0	0
14982	7	155,154,046	155,154,550	504	1	3.812	7.188	12.562	5	14	18	0	0	0				AdReg chr7 #14982	0	0	1
14983	7	155,164,662	155,165,140	478	1	3	5.733	11.733	5	10	17	1	0	1	LOC100286906	-9,870	upstream	AdReg chr7 #14983	0	0	1
14984	7	155,166,504	155,166,995	491	1	2.75	3.538	13.467	5	6	21	1	0	1	LOC100286906	-8,022	upstream	AdReg chr7 #14984	0	0	1
14985	7	155,215,634	155,216,025	391	1	3.364	2	12.167	6	4	16	0	0	0				AdReg chr7 #14985	0	0	1
14986	7	155,248,586	155,249,161	575	1	4.222	5.722	13.444	6	8	20	1	1	1	EN2	-1,951	upstream	AdReg chr7 #14986	0	0	1
14987	7	155,249,452	155,250,369	917	2	19.862	23.172	2.435	44	49	6	1	1	1	EN2	-914	upstream	AdReg chr7 #14987	1	1	0
14988	7	155,252,023	155,252,415	392	1	3	5.917	11.25	4	8	16	1	1	1	EN2	1,395	in gene	AdReg chr7 #14988	0	0	1
14989	7	155,436,637	155,437,996	1,359	3	10.721	8.86	4.951	19	20	10	1	2	2	LOC100506302, RBM33	-242, 113	upstream, in gene	AdReg chr7 #14989	1	1	0
14990	7	155,452,867	155,453,644	777	1	10.667	7.958	3.267	21	12	6	0	0	1	RBM33	16,052	in gene	AdReg chr7 #14990	1	0	0
14991	7	155,589,439	155,589,805	366	1	2.583	5.167	10.917	4	10	16	1	0	1	SHH	15,345	downstream	AdReg chr7 #14991	0	0	1
14992	7	155,590,068	155,590,794	726	1	2.095	5.043	13.478	4	9	18	1	0	1	SHH	14,556	downstream	AdReg chr7 #14992	0	0	1
14993	7	155,598,559	155,598,951	392	1	3	4.692	11.462	5	7	18	1	0	1	SHH	6,212	in gene	AdReg chr7 #14993	0	0	1
14994	7	155,743,655	155,744,964	1,309	2	9.488	10.902	3.659	18	16	10	0	0	0				AdReg chr7 #14994	1	1	0
14995	7	155,754,168	155,754,906	738	1	11.522	11.348	7.773	16	16	12	0	1	1	tcag7.1275	-714	upstream	AdReg chr7 #14995	0	1	0
14996	7	156,159,162	156,159,508	346	1	4.727	4	12.546	7	6	17	0	0	0				AdReg chr7 #14996	0	0	1
14997	7	156,399,885	156,400,357	472	1	2.867	4.8	9.933	6	6	16	1	1	1	LOC100506380	-1,660	upstream	AdReg chr7 #14997	0	0	1
14998	7	156,432,887	156,433,848	961	1	7.533	12.6	7.433	13	18	12	1	2	2	C7orf13, RNF32	-19, -34	upstream, upstream	AdReg chr7 #14998	0	1	0
14999	7	156,685,917	156,686,369	452	1	8.467	10.267	20.533	15	16	36	1	1	1	LMBR1	-241	upstream	AdReg chr7 #14999	0	0	1
15000	7	156,742,040	156,743,102	1,062	3	16.636	15.758	9.448	47	33	16	2	1	1	NOM1	154	in gene	AdReg chr7 #15000	1	1	1
15001	7	156,798,885	156,799,500	615	1	3.526	3.684	13.21	6	6	21	1	2	3	MNX1, LOC100506410, LOC645249	4155, 191, -4016	in gene, in gene, upstream	AdReg chr7 #15001	0	0	1
15002	7	156,801,448	156,802,229	781	1	3.833	2.792	11.333	6	5	15	2	3	3	MNX1, LOC100506410, LOC645249	1509, 2837, -1370	in gene, downstream, upstream	AdReg chr7 #15002	0	0	1
15003	7	157,074,451	157,075,125	674	1	3.857	5.714	10.857	5	8	16	0	0	0				AdReg chr7 #15003	0	0	1
15004	7	157,092,627	157,092,981	354	1	4.273	5.818	12.273	6	7	15	1	0	0				AdReg chr7 #15004	0	0	1
15005	7	157,197,505	157,198,228	723	2	11.682	11.318	5.5	18	21	9	0	0	1	DNAJB6	68,156	in gene	AdReg chr7 #15005	1	1	0
15006	7	157,216,645	157,217,052	407	1	1.7	4.333	11.917	3	8	16	1	0	1	DNAJB6	87,138	downstream	AdReg chr7 #15006	0	0	1
15007	7	157,219,138	157,219,561	423	1	2.308	4.462	12.462	3	7	17	0	0	1	DNAJB6	89,639	downstream	AdReg chr7 #15007	0	0	1
15008	7	157,357,248	157,358,252	1,004	2	13.594	16.062	4.065	27	33	8	0	0	2	PTPRN2, MIR153-2	1022732, 9364	in gene, downstream	AdReg chr7 #15008	1	1	0
15009	7	157,405,125	157,406,213	1,088	1	3.618	3.618	13.088	7	7	19	1	0	1	PTPRN2	974,813	in gene	AdReg chr7 #15009	0	0	1
15010	7	157,482,634	157,483,182	548	1	3	2.875	11.177	5	5	18	1	0	1	PTPRN2	897,574	in gene	AdReg chr7 #15010	0	0	1
15011	7	157,652,661	157,652,931	270	1	1	5.222	9.667	1	7	13	0	0	2	PTPRN2, LOC100506585	727686, 5519	in gene, in gene	AdReg chr7 #15011	0	0	1
15012	7	157,677,741	157,678,175	434	1	2.083	2.154	10.462	4	3	17	0	0	1	PTPRN2	702,524	in gene	AdReg chr7 #15012	0	0	1
15013	7	157,700,587	157,700,989	402	1	6.167	3.167	11.417	9	5	14	0	0	1	PTPRN2	679,694	in gene	AdReg chr7 #15013	0	0	1
15014	7	157,855,212	157,855,731	519	1	2.333	7.375	13	3	14	19	0	0	1	PTPRN2	525,011	in gene	AdReg chr7 #15014	0	0	1
15015	7	158,237,958	158,238,439	481	1	3	1.4	11.067	5	3	15	0	0	1	PTPRN2	142,284	in gene	AdReg chr7 #15015	0	0	1
15016	7	158,239,518	158,239,806	288	1	4.667	4.889	10.222	7	6	13	0	0	1	PTPRN2	140,820	in gene	AdReg chr7 #15016	0	0	1
15017	7	158,267,292	158,267,694	402	1	3.444	4	12	5	6	16	0	0	1	PTPRN2	112,989	in gene	AdReg chr7 #15017	0	0	1
15018	7	158,281,230	158,281,777	547	1	2.765	3.562	10.882	4	6	13	1	0	1	PTPRN2	98,979	in gene	AdReg chr7 #15018	0	0	1
15019	7	158,346,650	158,347,420	770	2	13.458	12.042	1.818	26	28	4	0	0	1	PTPRN2	33,447	in gene	AdReg chr7 #15019	1	1	0
15020	7	158,610,999	158,611,840	841	2	8.741	11.185	4.778	16	23	12	0	0	1	ESYT2	10,900	in gene	AdReg chr7 #15020	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15021	7	158,622,140	158,623,015	875	2	11.964	9.679	10.231	22	19	18	1	1	1	ESYT2	-258	upstream	ActReg chr7 #15021	1	0	1
15022	7	158,648,656	158,649,595	939	2	20.172	20.138	4.207	46	55	8	1	1	1	WDR60	-144	upstream	ActReg chr7 #15022	1	1	0
15023	7	158,822,100	158,822,696	596	1	2.312	4.684	10.158	5	8	13	0	0	2	tcag7.1307, VIPR2	21353, 115251	downstream, in gene	ActReg chr7 #15023	0	0	1
15024	7	158,823,282	158,823,842	560	1	2.944	8	12.056	5	12	20	1	0	2	tcag7.1307, VIPR2	22517, 114087	downstream, in gene	ActReg chr7 #15024	0	0	1
15025	7	158,856,561	158,857,016	455	1	1	2.273	11.357	1	3	16	1	0	1	VIPR2	80,861	in gene	ActReg chr7 #15025	0	0	1
15026	7	158,884,136	158,884,560	424	1	1.769	3.077	10.385	2	4	17	0	0	1	VIPR2	53,301	in gene	ActReg chr7 #15026	0	0	1
15027	8	1,320,423	1,320,673	250	1	2.375	2.5	10	4	3	12	0	0	0				ActReg chr8 #15027	0	0	1
15028	8	1,403,405	1,403,699	294	1	1.778	1.333	10.778	3	2	14	0	0	0				ActReg chr8 #15028	0	0	1
15029	8	1,703,509	1,704,132	623	1	6.7	10.45	2.75	12	16	5	0	0	2	LOC100507448, CLN8	8930, -8050	downstream, upstream	ActReg chr8 #15029	0	1	0
15030	8	1,711,120	1,711,511	391	1	9.833	4.727	2.875	14	7	3	1	2	2	LOC100507448, CLN8	1435, -555	in gene, upstream	ActReg chr8 #15030	1	0	0
15031	8	2,209,181	2,209,648	467	1	1.6	1.3	11.733	4	2	19	0	0	0				ActReg chr8 #15031	0	0	1
15032	8	3,040,435	3,040,747	312	1	8.1	10.8	0	11	16	0	0	0	1	CSMD1	1,811,737	in gene	ActReg chr8 #15032	0	1	0
15033	8	6,669,462	6,669,758	296	1	1	1.667	11.111	1	2	14	0	0	1	XKR5	23,556	in gene	ActReg chr8 #15033	0	0	1
15034	8	8,125,695	8,126,664	969	1	7.742	12.419	1.773	14	19	4	0	0	0				ActReg chr8 #15034	0	1	0
15035	8	8,167,944	8,168,957	1,013	2	9.871	13.065	1.059	18	19	2	0	0	1	PRAGMIN	70,807	downstream	ActReg chr8 #15035	1	1	0
15036	8	8,209,697	8,210,231	534	2	10.062	9.312	2.889	16	16	4	0	0	1	PRAGMIN	29,293	in gene	ActReg chr8 #15036	1	1	0
15037	8	9,807,193	9,807,969	776	2	13.52	17.48	2.368	33	40	6	0	0	0				ActReg chr8 #15037	1	1	0
15038	8	10,262,311	10,262,648	337	1	2.6	1.7	10.6	4	4	15	1	0	1	MSRA	350,649	in gene	ActReg chr8 #15038	0	0	1
15039	8	10,583,568	10,584,058	490	1	1.909	2.75	13.733	3	4	20	1	0	1	SOX7	4,209	in gene	ActReg chr8 #15039	0	0	1
15040	8	10,590,823	10,591,162	339	1	0	1.857	9.5	0	3	13	1	1	1	SOX7	-2,970	upstream	ActReg chr8 #15040	0	0	1
15041	8	10,697,086	10,697,569	483	1	5.467	10	7.312	9	15	11	1	1	1	PINX1	-28	upstream	ActReg chr8 #15041	0	1	0
15042	8	10,847,285	10,849,279	1,994	2	16.468	22.29	2.125	51	55	5	0	0	1	XKR6	210,593	in gene	ActReg chr8 #15042	1	1	0
15043	8	10,949,900	10,950,512	612	2	11.474	11.79	2.857	17	20	5	0	0	1	XKR6	108,669	in gene	ActReg chr8 #15043	1	1	0
15044	8	11,058,912	11,059,702	790	2	12	22.32	3.368	28	45	5	2	1	1	XKR6	-432	upstream	ActReg chr8 #15044	1	1	0
15045	8	11,141,455	11,142,301	846	2	9.346	12.346	3.095	19	17	6	1	1	1	MTMR9	-122	upstream	ActReg chr8 #15045	1	1	0
15046	8	11,324,241	11,324,876	635	1	7.55	10.8	5.55	9	15	10	1	1	1	FAM167A	-282	upstream	ActReg chr8 #15046	0	1	0
15047	8	11,339,312	11,339,741	429	1	8.154	9.846	2.308	10	16	4	0	0	0				ActReg chr8 #15047	0	1	0
15048	8	11,462,820	11,464,154	1,334	2	20.707	24.78	4.05	48	60	10	0	0	0				ActReg chr8 #15048	1	1	0
15049	8	12,417,627	12,417,982	355	1	3.8	9.636	1	6	15	1	0	0	1	LOC100506990	123,255	downstream	ActReg chr8 #15049	0	1	0
15050	8	17,013,183	17,013,711	528	1	9.294	7.059	2.333	16	13	3	1	1	1	ZDHHC2	-389	upstream	ActReg chr8 #15050	1	0	0
15051	8	17,480,655	17,481,163	508	1	9.625	6.625	2.2	15	9	3	0	0	1	PDGFRL	46,967	in gene	ActReg chr8 #15051	1	0	0
15052	8	17,779,978	17,780,635	657	2	10.6	10.25	7.05	16	14	13	1	1	1	PCM1	-60	upstream	ActReg chr8 #15052	1	1	0
15053	8	17,941,303	17,942,050	747	2	8.417	10.917	8.875	13	15	16	1	1	1	ASAH1	831	in gene	ActReg chr8 #15053	0	1	1
15054	8	18,998,664	18,999,113	449	1	6.714	10.429	1	9	15	1	0	0	0				ActReg chr8 #15054	0	1	0
15055	8	19,362,869	19,363,309	440	1	5.571	10.143	4.889	8	16	8	0	0	1	CSGALNACT1	177,172	in gene	ActReg chr8 #15055	0	1	0
15056	8	19,614,864	19,615,377	513	1	6.062	9.438	3.429	9	13	6	1	0	0				ActReg chr8 #15056	0	1	0
15057	8	19,674,488	19,675,238	750	2	11.191	13.292	3.792	24	27	7	1	1	1	INTS10	-55	upstream	ActReg chr8 #15057	1	1	0
15058	8	20,054,316	20,054,931	615	1	10.684	11.474	2.833	20	16	8	1	1	1	ATP6V1B2	-81	upstream	ActReg chr8 #15058	1	0	0
15059	8	20,107,550	20,107,816	266	1	2	1.222	9.444	3	2	12	1	0	1	LZTS1	5,120	in gene	ActReg chr8 #15059	0	0	1
15060	8	21,978,180	21,978,796	616	1	2.211	3.737	9.895	4	6	14	0	0	1	HR	10,077	in gene	ActReg chr8 #15060	0	0	1
15061	8	21,986,770	21,987,425	655	1	4.2	5.524	10.381	8	9	13	1	1	2	HR, REEP4	1468, 12351	in gene, downstream	ActReg chr8 #15061	0	0	1
15062	8	21,988,345	21,988,678	333	1	6.545	7.909	10.364	8	11	16	1	1	2	HR, REEP4	54, 10937	in gene, downstream	ActReg chr8 #15062	0	0	1
15063	8	21,999,187	21,999,854	667	2	11.381	11.809	6.75	22	19	14	1	1	2	REEP4, LGB	-72, 14824	upstream, downstream	ActReg chr8 #15063	1	1	0
15064	8	22,102,218	22,102,924	706	2	7.818	11	8.318	13	14	18	1	2	3	MIR320A, POLR3D, LOC100507071	-15, -48, 30104	upstream, upstream, downstream	ActReg chr8 #15064	0	1	1
15065	8	22,250,575	22,251,141	566	1	9.833	11.278	1.182	15	21	2	0	0	1	SLC39A14	26,096	in gene	ActReg chr8 #15065	0	1	0
15066	8	22,487,438	22,487,775	337	1	1.9	1	10.6	2	1	14	0	0	2	KIAA1967, BIN3	25461, 39055	downstream, in gene	ActReg chr8 #15066	0	0	1
15067	8	22,526,127	22,526,915	788	1	7.6	12.32	5.56	12	23	8	1	1	1	BIN3	140	in gene	ActReg chr8 #15067	0	1	0
15068	8	22,552,074	22,552,382	308	1	2.444	6	11.889	5	8	16	1	1	1	EGR3	-1,413	upstream	ActReg chr8 #15068	0	0	1
15069	8	22,602,034	22,602,815	781	1	7	10.125	4.625	10	13	8	0	0	2	PEBP4, LOC100507139	182997, -9899	in gene, upstream	ActReg chr8 #15069	0	1	0
15070	8	22,608,436	22,608,813	377	1	5.833	11.25	1.8	8	17	3	0	1	2	PEBP4, LOC100507139	176797, -3699	in gene, upstream	ActReg chr8 #15070	0	1	0
15071	8	22,635,475	22,635,858	383	1	1.286	2.75	9.5	2	4	15	0	0	1	PEBP4	149,755	in gene	ActReg chr8 #15071	0	0	1
15072	8	22,926,105	22,926,564	459	1	3.333	7.467	11.4	5	13	17	1	1	1	TNFRSF10B	366	in gene	ActReg chr8 #15072	0	0	1
15073	8	23,145,303	23,146,027	724	3	10	9.435	8.783	22	22	14	1	1	2	R3HCC1, LOXL2	53, 116057	in gene, downstream	ActReg chr8 #15073	1	1	1
15074	8	23,398,782	23,399,557	775	1	10.76	8.36	4.588	19	13	8	0	0	1	SLC25A37	12,806	in gene	ActReg chr8 #15074	1	0	0
15075	8	24,050,273	24,050,880	607	1	7.105	10.105	3.722	12	16	7	0	0	0				ActReg chr8 #15075	0	1	0
15076	8	25,045,100	25,045,751	651	1	6.7	11.6	2.167	9	18	4	0	0	1	DOCK5	3,138	in gene	ActReg chr8 #15076	0	1	0
15077	8	25,316,182	25,317,153	971	2	13.194	17.806	5.367	33	38	8	1	2	2	KCTD9, CDCA2	-683, 154	upstream, in gene	ActReg chr8 #15077	1	1	0
15078	8	26,240,177	26,240,749	572	1	11.167	10.667	7.056	17	15	12	1	1	2	PPP2R2A, BNIP3L	91456, -60	downstream, upstream	ActReg chr8 #15078	1	0	0
15079	8	26,370,091	26,370,402	311	1	3.25	1.8	10.4	5	3	14	0	1	1	PNMA2	1,237	in gene	ActReg chr8 #15079	0	0	1
15080	8	26,434,168	26,434,797	629	1	3.45	10.3	5.1	5	18	8	1	1	1	DPYSL2	-939	upstream	ActReg chr8 #15080	0	1	0
15081	8	27,695,007	27,695,590	583	2	10.21	11.316	5.667	23	20	10	1	1	1	PBK	51	in gene	ActReg chr8 #15081	1	1	0
15082	8	27,729,827	27,730,587	760	1	7.087	10.348	2.045	10	16	3	0	0	1	SCARA5	119,991	in gene	ActReg chr8 #15082	0	1	0
15083	8	28,258,463	28,259,339	876	2	9.643	10.857	3.704	17	21	8	1	0	0				ActReg chr8 #15083	1	1	0
15084	8	28,514,553	28,515,274	721	2	12.391	13.391	3.125	24	30	6	0	0	0				ActReg chr8 #15084	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15085	8	28,747,218	28,748,139	921	2	9.448	13.966	4.654	18	24	10	1	2	2	INTS9, HMBOX1	20, -233	in gene, upstream	ActReg chr8 #15085	1	1	0
15086	8	29,206,275	29,206,985	710	1	6.091	10.454	4.045	8	15	7	1	1	1	DUSP4	1,555	in gene	ActReg chr8 #15086	0	1	0
15087	8	29,370,885	29,371,335	450	1	9.5	5.286	3.923	14	13	7	0	0	0				ActReg chr8 #15087	1	0	0
15088	8	29,705,709	29,706,085	376	1	10.083	7.583	2.625	15	10	3	0	0	0				ActReg chr8 #15088	1	0	0
15089	8	29,848,424	29,848,919	495	1	10.733	6.667	1.833	15	12	2	0	0	0				ActReg chr8 #15089	1	0	0
15090	8	30,013,569	30,014,195	626	2	12.79	9.684	3.688	22	18	7	1	1	1	DCTN6	69	in gene	ActReg chr8 #15090	1	1	0
15091	8	30,670,011	30,670,726	715	2	16.826	22.714	4.308	38	52	8	1	1	1	PPP2CB	-16	upstream	ActReg chr8 #15091	1	1	0
15092	8	33,330,361	33,331,079	718	2	10	12.043	3.913	22	23	7	1	1	1	FUT10	-56	upstream	ActReg chr8 #15092	1	1	0
15093	8	33,370,466	33,371,402	936	2	21.483	19.172	4.231	51	40	7	0	2	2	C8orf41, SNORD13	-231, -59	upstream, upstream	ActReg chr8 #15093	1	1	0
15094	8	33,579,603	33,580,110	507	1	10.938	9.688	6.438	17	12	14	0	0	0				ActReg chr8 #15094	1	0	0
15095	8	37,552,923	37,553,509	586	2	10.368	11.263	1.556	21	20	4	1	1	1	ZNF703	-85	upstream	ActReg chr8 #15095	1	1	0
15096	8	37,707,128	37,707,797	669	2	8.667	9.857	4.19	17	19	6	1	1	3	GPR124, BRF2, RAB11FIP1	53061, -31, 49553	downstream, upstream, downstream	ActReg chr8 #15096	1	1	0
15097	8	37,962,656	37,963,396	740	2	12.333	13.917	5.609	22	24	9	1	1	1	ASH2L	15	in gene	ActReg chr8 #15097	1	1	0
15098	8	38,033,776	38,034,133	357	1	4.818	6.636	10.546	6	12	13	1	2	2	LSM1, BAG4	72, -152	in gene, upstream	ActReg chr8 #15098	0	0	1
15099	8	38,088,745	38,089,472	727	2	10.739	10.957	3.667	20	21	7	1	1	1	DDHD2	99	in gene	ActReg chr8 #15099	1	1	0
15100	8	38,326,896	38,326,408	512	1	7.938	10.125	4.083	11	15	6	1	1	1	FGFR1	200	in gene	ActReg chr8 #15100	0	1	0
15101	8	40,030,370	40,030,841	471	1	9.286	4.786	2.6	17	9	4	0	0	0				ActReg chr8 #15101	1	0	0
15102	8	40,977,797	40,978,430	633	2	8.789	10.474	2.545	15	16	4	0	0	0				ActReg chr8 #15102	1	1	0
15103	8	41,250,661	41,251,561	900	2	8.714	10.464	2	15	19	4	0	0	0				ActReg chr8 #15103	1	1	0
15104	8	41,575,116	41,575,783	667	1	11.571	6.714	2.545	20	11	4	0	0	1	ANK1	178,831	in gene	ActReg chr8 #15104	1	0	0
15105	8	41,753,231	41,754,016	785	2	12.84	14.24	4.13	24	26	7	1	1	1	ANK1	657	in gene	ActReg chr8 #15105	1	1	0
15106	8	42,195,720	42,196,186	466	1	10.857	5.929	6.429	15	10	9	1	1	2	IKBKB, POLB	67133, -77	downstream, upstream	ActReg chr8 #15106	1	0	0
15107	8	42,948,300	42,949,410	1,110	2	10.914	12.457	3.061	21	23	8	1	1	2	FNTA, SGK196	37413, 198	downstream, in gene	ActReg chr8 #15107	1	1	0
15108	8	48,650,936	48,651,728	792	1	6.4	11.32	5.409	9	18	10	1	1	2	KIAA0146, CEBPD	477790, -606	downstream, upstream	ActReg chr8 #15108	0	1	0
15109	8	48,872,996	48,874,080	1,084	1	10.912	15.5	4.091	23	38	9	1	2	2	PRKDC, MCM4	-795, 44	upstream, in gene	ActReg chr8 #15109	0	1	0
15110	8	48,920,655	48,921,245	590	1	12.5	13	6.778	21	19	15	1	1	1	UBE2V2	-45	upstream	ActReg chr8 #15110	1	0	0
15111	8	49,320,308	49,320,861	553	1	6.941	9.824	4.765	9	15	8	0	0	0				ActReg chr8 #15111	0	1	0
15112	8	49,426,934	49,427,295	361	1	7	8.455	14.546	10	11	23	1	0	0				ActReg chr8 #15112	0	0	1
15113	8	49,665,931	49,666,710	779	1	6.083	9.792	3.412	12	15	6	0	0	0				ActReg chr8 #15113	0	1	0
15114	8	49,812,297	49,813,011	714	2	12.091	12.364	2.682	25	23	5	0	1	1	LOC644334	-7,540	upstream	ActReg chr8 #15114	1	1	0
15115	8	49,833,637	49,834,588	951	1	5.897	10	6.103	11	15	9	0	1	2	LOC644334, SNAI2	13918, -124	downstream, upstream	ActReg chr8 #15115	0	1	0
15116	8	49,889,794	49,890,521	727	1	2.833	3.381	13.318	5	7	20	1	0	0				ActReg chr8 #15116	0	0	1
15117	8	50,630,213	50,630,523	310	1	1	1.833	11.111	1	2	15	0	0	0				ActReg chr8 #15117	0	0	1
15118	8	50,823,925	50,824,636	711	2	9.455	14.409	4.182	23	33	10	0	1	1	SNTG1	-317	upstream	ActReg chr8 #15118	1	1	0
15119	8	50,969,074	50,969,568	494	1	4.625	11.312	1.625	7	17	3	0	0	1	SNTG1	144,724	in gene	ActReg chr8 #15119	0	1	0
15120	8	51,403,941	51,404,249	308	1	4	2	8.667	6	3	11	0	0	1	SNTG1	579,498	in gene	ActReg chr8 #15120	0	0	1
15121	8	51,475,791	51,476,298	507	1	7.231	10.812	3.6	11	19	5	0	0	1	SNTG1	651,447	in gene	ActReg chr8 #15121	0	1	0
15122	8	52,183,801	52,184,208	407	1	3.231	4.077	15.385	7	6	25	0	0	0				ActReg chr8 #15122	0	0	1
15123	8	52,307,032	52,308,017	985	2	10.645	13.323	1.941	24	23	4	0	0	1	PXDNL	414,481	in gene	ActReg chr8 #15123	1	1	0
15124	8	52,811,358	52,812,673	1,315	2	8.738	10.381	7.568	14	16	20	1	2	2	PCMTD1, LOC100287313	-280, 173	upstream, in gene	ActReg chr8 #15124	0	1	1
15125	8	53,398,397	53,398,724	327	1	4.182	3.636	11.182	6	5	16	0	0	0				ActReg chr8 #15125	0	0	1
15126	8	53,448,521	53,449,118	597	1	7.111	10.056	3.125	11	19	6	0	0	1	FAM150A	29,202	in gene	ActReg chr8 #15126	0	1	0
15127	8	53,477,612	53,478,428	816	1	4.96	3.261	14.16	7	6	22	1	1	1	FAM150A	1	in gene	ActReg chr8 #15127	0	0	1
15128	8	53,625,567	53,626,219	652	1	10.333	13.048	2.524	15	21	10	1	1	1	RB1CC1	1,133	in gene	ActReg chr8 #15128	0	1	0
15129	8	53,626,990	53,627,724	734	1	7.87	11.217	7.087	11	18	12	1	1	1	RB1CC1	-331	upstream	ActReg chr8 #15129	0	1	0
15130	8	53,676,708	53,677,401	693	2	12.857	14.143	4.538	21	26	7	0	0	0				ActReg chr8 #15130	1	1	0
15131	8	53,853,570	53,853,902	332	1	8	7.5	11	9	8	16	1	1	1	NPBWR1	1,268	downstream	ActReg chr8 #15131	0	0	1
15132	8	53,866,252	53,866,858	606	1	3.368	4.158	13.053	6	6	19	0	0	0				ActReg chr8 #15132	0	0	1
15133	8	54,506,982	54,507,504	522	1	5.375	5.625	14.25	10	7	19	1	0	0				ActReg chr8 #15133	0	0	1
15134	8	54,792,356	54,794,497	2,141	5	7.851	8.687	10.716	19	18	22	1	0	1	RGS20	29,058	in gene	ActReg chr8 #15134	1	1	1
15135	8	54,794,801	54,795,306	505	1	4.062	6	11	8	10	16	1	0	1	RGS20	30,685	in gene	ActReg chr8 #15135	0	0	1
15136	8	54,934,515	54,935,358	843	2	21.269	24	3.56	63	65	8	1	1	1	TCEA1	72	in gene	ActReg chr8 #15136	1	1	0
15137	8	55,065,529	55,066,441	912	2	13.103	10.552	2.45	26	17	5	0	0	1	MRPL15	18,204	downstream	ActReg chr8 #15137	1	1	0
15138	8	55,913,723	55,914,330	607	1	10.474	7.895	2.462	19	13	4	0	0	0				ActReg chr8 #15138	1	0	0
15139	8	56,015,309	56,015,974	665	2	16.238	23.619	5.619	32	46	9	1	1	1	XKR4	624	in gene	ActReg chr8 #15139	1	1	0
15140	8	56,363,512	56,363,866	354	1	1.5	4	10.546	2	7	17	0	0	1	XKR4	348,672	in gene	ActReg chr8 #15140	0	0	1
15141	8	56,363,939	56,364,565	626	1	3.211	5.368	12.579	6	9	20	0	0	1	XKR4	349,235	in gene	ActReg chr8 #15141	0	0	1
15142	8	56,410,848	56,411,213	365	1	5.333	3.091	9.917	9	6	16	0	0	1	XKR4	396,013	in gene	ActReg chr8 #15142	0	0	1
15143	8	56,685,353	56,686,421	1,068	2	11.273	13.788	5.97	18	21	10	1	2	2	TMEM68, TGS1	-2, 96	upstream, in gene	ActReg chr8 #15143	1	1	0
15144	8	56,986,637	56,987,800	1,163	2	35.333	39.75	6.065	130	143	11	1	2	2	RPS20, SNORD54	-78, -758	upstream, upstream	ActReg chr8 #15144	1	1	0
15145	8	57,124,195	57,124,956	761	1	7.261	9.609	7.773	10	13	13	1	2	2	PLAG1, CHCHD7	-716, 260	upstream, in gene	ActReg chr8 #15145	0	1	0
15146	8	57,357,870	57,358,853	983	2	6.387	10.355	10.065	9	21	17	1	1	1	PENK	921	in gene	ActReg chr8 #15146	0	1	1
15147	8	57,802,399	57,803,062	663	1	10.619	9	3.762	20	18	7	0	0	0				ActReg chr8 #15147	1	0	0
15148	8	58,122,118	58,123,078	960	1	12.5	12.3	20.267	21	21	40	0	0	1	LOC100507651	-9,050	upstream	ActReg chr8 #15148	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15149	8	58,172,130	58,172,594	464	1	2.857	3.071	12.571	4	4	18	1	0	0				ActReg chr8 #15149	0	0	1
15150	8	58,191,619	58,191,942	323	1	2.8	2.125	10.1	4	4	14	0	1	1	C8orf71	-322	upstream	ActReg chr8 #15150	0	0	1
15151	8	58,192,013	58,192,618	605	1	2.353	3.737	9.737	4	7	13	1	1	1	C8orf71	213	in gene	ActReg chr8 #15151	0	0	1
15152	8	59,230,874	59,231,156	282	1	2.833	2.556	10.556	3	4	13	0	0	0				ActReg chr8 #15152	0	0	1
15153	8	59,323,589	59,324,436	847	1	4.462	12.346	3.769	8	18	7	1	1	1	UBXN2B	189	in gene	ActReg chr8 #15153	0	1	0
15154	8	59,465,304	59,465,999	695	1	8.409	6.591	13	14	13	18	1	1	1	SDCBP	-77	upstream	ActReg chr8 #15154	0	0	1
15155	8	59,571,210	59,572,170	960	1	8.793	10.8	4.233	18	18	10	1	1	1	NSMAF	714	in gene	ActReg chr8 #15155	0	1	0
15156	8	59,671,841	59,672,336	495	1	7.6	11.667	1	12	20	1	0	0	0				ActReg chr8 #15156	0	1	0
15157	8	59,685,022	59,685,316	294	1	2.8	2	10.8	4	4	15	0	0	0				ActReg chr8 #15157	0	0	1
15158	8	59,714,026	59,714,576	550	1	9.882	8.471	2.294	14	16	4	0	0	1	TOX	317,466	downstream	ActReg chr8 #15158	1	0	0
15159	8	60,459,446	60,459,914	468	1	1.583	2.2	11.867	3	4	19	0	0	0				ActReg chr8 #15159	0	0	1
15160	8	61,193,311	61,193,672	361	1	4.583	5.3	11.25	6	9	18	1	1	1	CA8	463	in gene	ActReg chr8 #15160	0	0	1
15161	8	61,325,971	61,326,390	419	1	11.769	9.077	5	16	12	8	0	1	1	LOC100505532	197	in gene	ActReg chr8 #15161	1	0	0
15162	8	61,328,611	61,329,335	724	1	6.045	11.046	2.579	12	18	4	0	1	1	LOC100505532	-2,596	upstream	ActReg chr8 #15162	0	1	0
15163	8	61,564,086	61,565,398	1,312	2	13.39	11.293	3.077	30	32	9	1	0	0				ActReg chr8 #15163	1	1	0
15164	8	61,626,988	61,627,282	294	1	5.778	4.875	9.333	9	8	12	1	0	1	CHD7	35,796	in gene	ActReg chr8 #15164	0	0	1
15165	8	61,863,210	61,864,139	929	2	11.517	13.931	4	22	24	9	0	0	0				ActReg chr8 #15165	1	1	0
15166	8	62,200,402	62,201,291	889	2	13.536	17.714	4.357	24	38	9	0	1	1	CLVS1	321	in gene	ActReg chr8 #15166	1	1	0
15167	8	62,408,323	62,409,303	980	2	15.867	20.5	2.708	40	43	5	0	0	2	CLVS1, ASPH	208288, 218386	in gene, downstream	ActReg chr8 #15167	1	1	0
15168	8	62,503,991	62,504,528	537	2	8.235	9.588	2.706	17	16	5	0	0	1	ASPH	122,940	in gene	ActReg chr8 #15168	1	1	0
15169	8	62,626,686	62,627,555	869	1	6.714	11.679	5.778	13	19	11	1	1	1	ASPH	79	in gene	ActReg chr8 #15169	0	1	0
15170	8	62,633,920	62,634,457	537	1	11.823	7.118	1.867	21	12	4	0	1	1	ASPH	-6,989	upstream	ActReg chr8 #15170	1	0	0
15171	8	62,672,101	62,673,305	1,204	2	11.811	11.243	4.297	19	18	8	0	0	0				ActReg chr8 #15171	1	1	0
15172	8	62,702,264	62,702,984	720	1	10.174	9.304	2.364	20	12	6	0	0	0				ActReg chr8 #15172	1	0	0
15173	8	64,080,341	64,081,613	1,272	2	6.775	11.625	7.974	11	17	18	1	1	1	YTHDF3	-144	upstream	ActReg chr8 #15173	0	1	1
15174	8	64,132,850	64,133,355	505	1	9.562	10.875	2.917	18	21	5	0	0	1	YTHDF3	51,981	downstream	ActReg chr8 #15174	0	1	0
15175	8	65,292,255	65,292,960	705	2	10.261	12.304	2.9	18	26	6	0	1	2	LOC100130155, MIR124-2	6832, 901	downstream, downstream	ActReg chr8 #15175	1	1	0
15176	8	66,064,882	66,065,592	710	2	10	10.046	1.5	15	17	2	0	0	0				ActReg chr8 #15176	1	1	0
15177	8	66,546,031	66,546,812	781	2	11.583	11.792	6.609	17	20	12	1	1	1	ARMC1	31	in gene	ActReg chr8 #15177	1	1	0
15178	8	66,753,995	66,755,063	1,068	3	10.909	10.091	7.654	19	18	17	1	1	1	PDE7A	-774	upstream	ActReg chr8 #15178	1	1	1
15179	8	66,860,730	66,861,133	403	1	10.923	11.615	5.538	15	17	8	0	0	0				ActReg chr8 #15179	0	1	0
15180	8	66,938,635	66,939,133	498	1	12.4	8.467	3.733	22	12	6	0	0	1	DNAJC5B	5,093	in gene	ActReg chr8 #15180	1	0	0
15181	8	67,024,815	67,025,966	1,151	3	12.306	13.75	9.324	18	25	24	2	0	0				ActReg chr8 #15181	1	1	1
15182	8	67,036,051	67,036,717	666	1	7.333	13.667	2.375	12	24	4	0	1	1	TRIM55	-2,894	upstream	ActReg chr8 #15182	0	1	0
15183	8	67,047,292	67,047,855	563	1	2.688	2.611	10.111	6	4	13	0	0	1	TRIM55	8,295	in gene	ActReg chr8 #15183	0	0	1
15184	8	67,089,070	67,090,644	1,574	3	17.388	18.694	9.939	53	53	19	1	1	2	TRIM55, CRH	50579, 989	downstream, in gene	ActReg chr8 #15184	1	1	1
15185	8	67,340,781	67,342,184	1,403	3	10.667	12.523	10.75	19	26	20	1	3	3	LOC100505676, RRS1, ADHFE1	-270, 219, -3236	upstream, in gene, upstream	ActReg chr8 #15185	1	1	1
15186	8	67,524,807	67,525,931	1,124	2	11.4	10.771	8.086	17	20	12	1	1	1	MYBL1	111	in gene	ActReg chr8 #15186	1	1	0
15187	8	67,578,777	67,579,973	1,196	2	13.342	13.237	5.036	22	29	9	1	1	2	VCPIP1, C8orf44	77, -9079	in gene, upstream	ActReg chr8 #15187	1	1	0
15188	8	67,624,408	67,625,027	619	1	8.333	10.4	2.471	12	19	4	1	1	1	SGK3	-174	upstream	ActReg chr8 #15188	0	1	0
15189	8	67,837,271	67,838,123	852	2	10.852	9.667	12.037	19	14	16	1	2	3	C8orf45, SNHG6, SNORD87	54713, 80, -2913	downstream, in gene, upstream	ActReg chr8 #15189	1	0	1
15190	8	67,919,515	67,920,112	597	1	8.895	11	4.684	12	20	9	0	0	1	LRRC67	20,973	in gene	ActReg chr8 #15190	0	1	0
15191	8	67,973,916	67,974,857	941	2	7.9	11.567	6.917	11	18	17	0	2	2	COPS5, CSPP1	176, -2217	in gene, upstream	ActReg chr8 #15191	0	1	1
15192	8	67,976,078	67,976,953	875	2	28.654	33.593	4.259	82	94	8	1	2	2	COPS5, CSPP1	-1953, -88	upstream, upstream	ActReg chr8 #15192	1	1	0
15193	8	67,976,993	67,977,582	589	1	3.778	9.556	6	7	18	9	1	2	2	COPS5, CSPP1	-2725, 684	upstream, in gene	ActReg chr8 #15193	0	1	0
15194	8	68,255,555	68,256,116	561	1	5.412	12.059	5.533	8	18	8	1	1	1	ARFGEF1	77	in gene	ActReg chr8 #15194	0	1	0
15195	8	70,250,220	70,250,752	532	1	3.875	5.059	9.882	6	7	14	0	0	0				ActReg chr8 #15195	0	0	1
15196	8	70,693,207	70,693,720	513	1	7.562	10.25	4.438	14	15	7	0	0	1	SLCO5A1	53,836	in gene	ActReg chr8 #15196	0	1	0
15197	8	70,744,504	70,745,171	667	1	5.762	8.19	11.762	8	12	15	1	2	2	SLCO5A1, LOC100505760	2462, -1527	in gene, upstream	ActReg chr8 #15197	0	0	1
15198	8	70,981,687	70,982,012	325	1	4.3	4.9	12.7	6	8	17	1	1	1	PRDM14	1,713	in gene	ActReg chr8 #15198	0	0	1
15199	8	70,983,030	70,983,508	478	1	3.2	2.933	12	5	5	19	1	1	1	PRDM14	293	in gene	ActReg chr8 #15199	0	0	1
15200	8	71,000,591	71,001,021	430	1	3.462	10.231	6.308	5	14	9	0	0	0				ActReg chr8 #15200	0	1	0
15201	8	71,038,892	71,039,466	574	1	4.889	10.111	3.143	7	19	5	0	0	1	NCOA2	276,841	in gene	ActReg chr8 #15201	0	1	0
15202	8	71,313,897	71,314,927	1,030	1	8.125	11.156	3.857	11	19	7	1	1	1	NCOA2	1,608	in gene	ActReg chr8 #15202	0	1	0
15203	8	71,520,150	71,521,112	962	2	23.2	24	6.31	61	66	18	1	1	1	TRAM1	63	in gene	ActReg chr8 #15203	1	1	0
15204	8	71,580,930	71,581,641	711	2	9.818	10	7.182	18	16	14	1	2	2	LACTB2, XKR9	162, -315	in gene, upstream	ActReg chr8 #15204	1	1	0
15205	8	72,111,495	72,111,816	321	1	3.6	2.7	10.5	5	4	14	0	0	1	EYA1	162,812	in gene	ActReg chr8 #15205	0	0	1
15206	8	72,177,953	72,178,697	744	2	12.478	11.826	2.429	29	25	4	0	0	1	EYA1	96,142	in gene	ActReg chr8 #15206	1	1	0
15207	8	72,703,939	72,704,510	571	1	6.471	10.941	1	9	20	1	0	0	0				ActReg chr8 #15207	0	1	0
15208	8	72,755,732	72,756,818	1,086	1	10.559	13.471	5.969	21	23	10	1	2	2	MSC, LOC100132891	456, 917	in gene, in gene	ActReg chr8 #15208	0	1	0
15209	8	74,205,443	74,206,717	1,274	2	12.128	11.077	5.256	17	21	10	1	2	2	RPL7, RDH10	-211, -1185	upstream, upstream	ActReg chr8 #15209	1	1	0
15210	8	74,207,416	74,208,080	664	1	5.095	11.476	7.474	9	16	16	1	2	2	RPL7, RDH10	-1879, 483	upstream, in gene	ActReg chr8 #15210	0	1	0
15211	8	74,371,676	74,372,476	800	1	6.92	11.4	4.72	12	16	8	0	0	1	STAU2	287,867	in gene	ActReg chr8 #15211	0	1	0
15212	8	74,432,696	74,433,272	576	1	7.056	10.222	1.714	14	17	2	0	0	1	STAU2	226,959	in gene	ActReg chr8 #15212	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15213	8	74,790,511	74,791,263	752	1	11.478	9.043	9.522	16	15	15	1	1	1	UBE2W	223	in gene	AdzReg chr8 #15213	1	0	0
15214	8	74,883,921	74,885,089	1,168	2	12.081	11.324	6.514	26	18	14	1	2	2	TCEB1, TMEM70	-159, -3872	upstream, upstream	AdzReg chr8 #15214	1	1	0
15215	8	74,888,346	74,888,712	366	1	10.5	10.167	13.583	17	14	21	1	2	2	TCEB1, TMEM70	-4183, 152	upstream, in gene	AdzReg chr8 #15215	0	0	1
15216	8	75,232,609	75,233,581	972	2	11.8	7.933	9.7	18	12	22	1	1	1	JPH1	467	in gene	AdzReg chr8 #15216	1	0	1
15217	8	75,262,295	75,263,282	987	2	13.194	25.194	4.533	34	62	7	1	1	1	GDAP1	170	in gene	AdzReg chr8 #15217	1	1	0
15218	8	75,514,118	75,514,699	581	1	10.833	3.889	2.353	17	7	4	0	1	1	FLJ39080	2,307	in gene	AdzReg chr8 #15218	1	0	0
15219	8	75,734,750	75,735,321	571	1	11.667	3.167	1.5	21	5	2	0	1	1	PI15	-1,737	upstream	AdzReg chr8 #15219	1	0	0
15220	8	75,737,273	75,737,863	590	1	5.632	9.263	1.833	10	16	3	0	1	1	PI15	796	in gene	AdzReg chr8 #15220	0	1	0
15221	8	75,988,681	75,989,154	473	2	10.2	10.6	2.714	18	18	5	0	0	0				AdzReg chr8 #15221	1	1	0
15222	8	76,696,655	76,697,106	451	1	2.929	7.071	12.214	5	10	18	0	0	0				AdzReg chr8 #15222	0	0	1
15223	8	77,599,072	77,599,987	915	2	13.828	8.448	2.385	24	20	3	0	1	2	LOC100192378, ZFHX4	-4019, 6014	upstream, in gene	AdzReg chr8 #15223	1	1	0
15224	8	79,428,049	79,429,016	967	1	9.733	15.267	3.107	23	32	7	1	1	1	PKIA	196	in gene	AdzReg chr8 #15224	0	1	0
15225	8	79,578,010	79,578,779	769	2	9.417	11.625	11	12	20	20	1	1	1	FAM164A	112	in gene	AdzReg chr8 #15225	0	1	1
15226	8	79,716,976	79,717,462	486	1	9.6	9.267	12.2	13	11	19	1	1	1	IL7	539	in gene	AdzReg chr8 #15226	0	0	1
15227	8	80,200,190	80,200,945	755	1	8.583	11.25	3.583	12	15	5	0	0	0				AdzReg chr8 #15227	0	1	0
15228	8	80,289,358	80,289,652	294	1	3.222	4.889	10	4	6	14	0	0	0				AdzReg chr8 #15228	0	0	1
15229	8	80,361,419	80,362,077	658	2	10.45	12.9	1	20	25	1	0	0	0				AdzReg chr8 #15229	1	1	0
15230	8	80,520,930	80,521,896	966	2	13.4	12.5	2	25	23	4	0	1	1	STMN2	-1,967	upstream	AdzReg chr8 #15230	1	1	0
15231	8	80,522,156	80,523,104	948	1	5.433	11.433	1.69	8	15	3	0	1	1	STMN2	-750	upstream	AdzReg chr8 #15231	0	1	0
15232	8	80,524,592	80,525,384	792	2	4.08	11.36	7.864	7	19	17	1	1	1	STMN2	1,608	in gene	AdzReg chr8 #15232	0	1	1
15233	8	80,677,336	80,678,310	974	2	7.968	14.903	6.833	17	33	13	1	2	2	HEY1, LOC100507186	2275, -2554	in gene, upstream	AdzReg chr8 #15233	1	1	0
15234	8	80,941,789	80,942,443	654	2	5.429	11.143	8.19	12	18	15	1	1	2	MRPS28, TPD52	390, 141720	in gene, downstream	AdzReg chr8 #15234	0	1	1
15235	8	81,083,183	81,083,896	713	1	6.5	12.046	4.81	8	19	13	1	1	1	TPD52	297	in gene	AdzReg chr8 #15235	0	1	0
15236	8	81,602,908	81,603,716	808	2	13.192	14.231	5.235	36	26	9	0	0	1	ZNF704	183,704	in gene	AdzReg chr8 #15236	1	1	0
15237	8	81,785,396	81,786,097	701	1	5.636	10.591	3.045	12	17	6	2	1	1	ZNF704	1,270	in gene	AdzReg chr8 #15237	0	1	0
15238	8	81,938,404	81,939,195	791	1	9.455	14.875	4.125	21	27	6	0	0	1	PAG1	85,504	in gene	AdzReg chr8 #15238	0	1	0
15239	8	82,193,051	82,193,890	839	2	8.63	10.741	7.556	15	16	15	1	1	1	FABP5	685	in gene	AdzReg chr8 #15239	0	1	1
15240	8	82,598,102	82,598,686	584	1	6	12.167	3.722	8	20	6	1	1	2	IMPA1, SLC1DA5	195, 8813	in gene, downstream	AdzReg chr8 #15240	0	1	0
15241	8	82,633,313	82,634,078	765	2	7.13	10.435	9.174	13	15	14	1	1	1	ZFAND1	-156	upstream	AdzReg chr8 #15241	0	1	1
15242	8	82,753,801	82,755,205	1,404	2	12.5	13.546	8	34	29	24	1	1	1	SNX16	18	in gene	AdzReg chr8 #15242	1	1	0
15243	8	82,771,012	82,771,544	532	1	11.688	9	1.5	16	14	2	0	0	0				AdzReg chr8 #15243	1	0	0
15244	8	84,202,627	84,203,007	380	1	4.6	4.545	11.364	7	6	14	0	0	0				AdzReg chr8 #15244	0	0	1
15245	8	85,491,306	85,491,620	314	1	3.4	3.5	9.7	5	5	12	0	0	1	RALYL	396,010	in gene	AdzReg chr8 #15245	0	0	1
15246	8	86,375,586	86,375,923	337	1	4	3.375	10.9	5	9	15	1	1	1	CA2	-377	upstream	AdzReg chr8 #15246	0	0	1
15247	8	87,317,560	87,317,994	434	2	9.643	10.857	1	17	20	1	0	0	0				AdzReg chr8 #15247	1	1	0
15248	8	87,354,106	87,354,867	761	2	13.75	12.826	4.455	27	21	10	1	1	1	WWP1	-508	upstream	AdzReg chr8 #15248	1	1	0
15249	8	88,986,281	88,986,829	548	1	6.706	10.882	1.909	11	15	3	0	0	0				AdzReg chr8 #15249	0	1	0
15250	8	88,987,185	88,987,771	586	1	7.944	11.889	1.882	13	18	5	0	0	0				AdzReg chr8 #15250	0	1	0
15251	8	89,252,021	89,252,696	675	2	13.857	9.81	1.444	26	19	3	0	0	1	MMP16	87,359	in gene	AdzReg chr8 #15251	1	1	0
15252	8	89,314,917	89,315,520	603	1	7.421	10.737	3.429	10	16	6	0	0	1	MMP16	24,499	in gene	AdzReg chr8 #15252	0	1	0
15253	8	90,623,879	90,624,514	635	1	6.05	10.85	2	10	15	2	0	0	0				AdzReg chr8 #15253	0	1	0
15254	8	90,769,715	90,770,683	968	2	9.6	12.767	8.6	18	20	14	1	1	1	RIPK2	224	in gene	AdzReg chr8 #15254	0	1	1
15255	8	90,996,006	90,997,171	1,165	2	15.528	21.389	6.424	36	52	14	1	1	1	NBN	311	in gene	AdzReg chr8 #15255	1	1	0
15256	8	91,094,662	91,095,450	788	2	14.083	17.667	4.542	31	43	8	0	1	1	CALB1	51	in gene	AdzReg chr8 #15256	1	1	0
15257	8	91,479,896	91,480,561	665	1	11.667	14.381	1.857	18	23	3	0	0	0				AdzReg chr8 #15257	0	1	0
15258	8	91,873,264	91,873,809	545	1	6.176	9.588	2.571	12	15	3	0	0	1	NECAB1	69,615	in gene	AdzReg chr8 #15258	0	1	0
15259	8	92,612,489	92,612,915	426	1	11.308	4.538	1.455	16	6	2	0	0	0				AdzReg chr8 #15259	1	0	0
15260	8	92,692,802	92,693,294	492	1	7.067	10.4	2.333	12	17	3	0	0	0				AdzReg chr8 #15260	0	1	0
15261	8	93,935,221	93,935,687	466	1	10	7.667	1	14	13	1	0	0	1	C8orf83	42,918	in gene	AdzReg chr8 #15261	1	0	0
15262	8	93,977,739	93,978,518	779	2	11.792	9.708	8.125	21	13	15	1	1	1	C8orf83	244	in gene	AdzReg chr8 #15262	1	0	1
15263	8	94,599,662	94,600,189	527	1	6.562	12.375	1.833	11	20	3	0	0	1	LOC642924	112,736	in gene	AdzReg chr8 #15263	0	1	0
15264	8	94,817,966	94,818,458	492	1	9.733	3.133	1.769	13	8	3	0	0	1	TMEM67	51,140	in gene	AdzReg chr8 #15264	1	0	0
15265	8	94,928,476	94,928,894	418	1	9.154	9.846	14.077	11	12	17	1	1	1	PDP1	-398	upstream	AdzReg chr8 #15265	0	0	1
15266	8	95,084,349	95,084,845	496	2	9.562	9.125	3.083	17	15	5	0	0	0				AdzReg chr8 #15266	1	1	0
15267	8	95,254,066	95,254,825	759	1	13.167	10.708	5.476	22	18	8	0	0	1	GEM	20,102	downstream	AdzReg chr8 #15267	1	0	0
15268	8	95,486,959	95,487,628	669	1	8.905	11.048	5.857	14	16	11	1	1	1	RAD54B	17	in gene	AdzReg chr8 #15268	0	1	0
15269	8	95,565,453	95,566,208	755	2	13.25	12.458	3.625	24	29	9	1	1	1	KIAA1429	-142	upstream	AdzReg chr8 #15269	1	1	0
15270	8	95,731,588	95,732,526	938	3	10.655	12.31	7.345	14	18	17	1	1	1	DPY19L4	-46	upstream	AdzReg chr8 #15270	1	1	1
15271	8	95,834,952	95,835,704	752	1	8.957	12.391	3.333	12	20	6	1	1	1	INTS8	-206	upstream	AdzReg chr8 #15271	0	1	0
15272	8	95,908,041	95,908,446	405	1	9.25	6.75	12.417	12	9	17	1	1	1	CCNE2	-761	upstream	AdzReg chr8 #15272	0	0	1
15273	8	95,961,700	95,962,117	417	1	5.385	2.818	11.308	7	4	18	1	1	1	TPS3INP1	-293	upstream	AdzReg chr8 #15273	0	0	1
15274	8	96,036,905	96,037,514	609	1	11.526	12.421	4.778	18	18	7	1	1	1	C8orf38	-12	upstream	AdzReg chr8 #15274	0	1	0
15275	8	96,281,004	96,282,540	1,536	2	9.062	13.625	7.625	16	22	16	1	1	1	C8orf37	-335	upstream	AdzReg chr8 #15275	1	1	0
15276	8	97,273,398	97,274,756	1,358	3	16.349	16.698	7.837	43	38	19	1	2	2	MTERFD1, PTDSS1	-281, -90	upstream, upstream	AdzReg chr8 #15276	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15277	8	97,506,773	97,507,352	579	1	4.778	9.389	11.5	8	13	14	1	1	1	SDC2	1,180	in gene	AdReg chr8 #15277	0	0	1
15278	8	97,545,984	97,546,507	523	1	2.882	4.294	12.588	5	6	18	0	0	1	SDC2	40,363	in gene	AdReg chr8 #15278	0	0	1
15279	8	98,305,781	98,306,353	572	1	7	8.889	2.385	13	15	4	0	0	0				AdReg chr8 #15279	0	1	0
15280	8	98,617,290	98,617,568	278	1	4.667	2.444	9.333	7	3	14	0	0	0				AdReg chr8 #15280	0	0	1
15281	8	98,656,131	98,656,835	704	1	10.546	11.273	9.136	15	18	15	1	1	1	MTDH	76	in gene	AdReg chr8 #15281	0	1	0
15282	8	98,787,572	98,788,071	499	1	6.375	9.75	8.062	9	15	12	1	1	1	LAPTM4B	12	in gene	AdReg chr8 #15282	0	1	0
15283	8	99,057,498	99,058,260	762	2	11.125	8.792	9.792	19	12	16	2	2	3	MATN2, RPL30, SNORA72	176568, -106, -3434	downstream, upstream, upstream	AdReg chr8 #15283	1	0	1
15284	8	99,305,939	99,306,861	922	1	8.069	10.483	3.964	14	18	8	1	1	1	NIPAL2	221	in gene	AdReg chr8 #15284	0	1	0
15285	8	99,956,193	99,957,093	900	2	12.071	11.393	6.36	18	22	9	1	1	1	OSR2	12	in gene	AdReg chr8 #15285	1	1	0
15286	8	100,024,770	100,025,813	1,043	2	11.375	10.625	10.906	18	17	23	1	1	1	VPS13B	-203	upstream	AdReg chr8 #15286	1	0	1
15287	8	100,905,453	100,906,336	883	2	9.786	10.929	7.571	18	17	13	1	1	1	COX6C	348	in gene	AdReg chr8 #15287	1	1	0
15288	8	101,118,249	101,118,513	264	1	5.125	2.857	10.875	8	5	13	1	1	1	RGS22	-37	upstream	AdReg chr8 #15288	0	0	1
15289	8	101,169,896	101,170,711	815	2	10.68	7.84	11.04	14	12	17	1	1	2	POLR2K, SPAG1	7464, 40	downstream, in gene	AdReg chr8 #15289	1	0	1
15290	8	101,321,506	101,322,418	912	2	9.393	9.643	11.571	13	14	17	1	1	1	RNF19A	365	in gene	AdReg chr8 #15290	0	1	1
15291	8	101,363,117	101,363,402	285	1	3.111	2.667	10.889	5	4	15	0	0	0				AdReg chr8 #15291	0	0	1
15292	8	101,494,420	101,495,069	649	1	6.6	12.25	3.15	15	21	4	0	0	0				AdReg chr8 #15292	0	1	0
15293	8	101,514,339	101,515,443	1,104	2	10.941	10.059	2.52	16	16	5	0	0	0				AdReg chr8 #15293	1	1	0
15294	8	101,571,498	101,572,392	894	2	13.179	12.714	8.333	28	23	17	1	1	1	ANKRD46	67	in gene	AdReg chr8 #15294	1	1	0
15295	8	101,734,507	101,735,290	783	1	7.792	12.125	2.857	11	28	6	1	1	1	PABPC1	-583	upstream	AdReg chr8 #15295	0	1	0
15296	8	101,962,694	101,963,227	533	1	12.25	8.875	7.812	20	12	12	1	1	1	YWHAZ	2,663	in gene	AdReg chr8 #15296	1	0	0
15297	8	101,963,670	101,964,642	972	2	12.548	12.839	3.935	22	18	7	1	1	1	YWHAZ	1,467	in gene	AdReg chr8 #15297	1	1	0
15298	8	101,998,408	101,999,025	617	1	10.526	10.632	2.059	16	19	4	0	0	0				AdReg chr8 #15298	0	1	0
15299	8	102,038,284	102,038,995	711	1	12.273	8.545	3.611	23	16	7	0	0	0				AdReg chr8 #15299	1	0	0
15300	8	102,075,949	102,076,498	549	1	6.471	11.706	4.235	10	16	8	0	0	1	FLJ42969	11,941	in gene	AdReg chr8 #15300	0	1	0
15301	8	102,109,717	102,111,190	1,473	1	9.935	14.587	4.69	23	23	10	0	0	0				AdReg chr8 #15301	0	1	0
15302	8	102,120,760	102,122,150	1,390	2	11.659	9.545	6.25	21	22	9	0	0	0				AdReg chr8 #15302	1	1	0
15303	8	102,138,206	102,139,438	1,232	3	12.026	11.692	8	27	21	19	1	0	0				AdReg chr8 #15303	1	1	1
15304	8	102,217,976	102,218,327	351	1	9.818	8.909	12.273	12	11	18	1	1	1	ZNF706	-191	upstream	AdReg chr8 #15304	0	0	1
15305	8	102,255,700	102,256,848	1,148	2	12.778	15.25	2.111	29	32	5	0	0	0				AdReg chr8 #15305	1	1	0
15306	8	102,892,268	102,892,687	419	1	4.769	3.333	12.385	9	6	16	0	0	1	NCALD	244,658	in gene	AdReg chr8 #15306	0	0	1
15307	8	103,024,495	103,025,217	722	1	10.696	6.957	2.1	20	11	4	0	0	1	NCALD	112,279	in gene	AdReg chr8 #15307	1	0	0
15308	8	103,187,547	103,188,355	808	1	9.062	13.375	2	15	25	3	0	0	0				AdReg chr8 #15308	0	1	0
15309	8	103,280,246	103,280,622	376	1	3.917	4.75	8.5	6	7	13	0	0	1	UBR5	144,061	in gene	AdReg chr8 #15309	0	0	1
15310	8	103,549,607	103,550,399	792	1	11.542	5.375	2.435	14	9	4	0	0	0				AdReg chr8 #15310	1	0	0
15311	8	103,580,041	103,580,612	571	1	7.444	9.778	1.706	10	18	3	0	0	1	ODF1	16,478	downstream	AdReg chr8 #15311	0	1	0
15312	8	103,768,738	103,769,416	678	1	8.095	12.333	5.143	16	23	6	0	0	0				AdReg chr8 #15312	0	1	0
15313	8	103,819,062	103,820,384	1,322	1	12.333	9.952	4.833	20	17	11	1	1	1	FLJ45248	673	in gene	AdReg chr8 #15313	1	0	0
15314	8	103,876,362	103,877,065	703	1	10.818	11.682	4.421	15	16	8	1	2	2	AZIN1, LOC100506753	-316, 148	upstream, in gene	AdReg chr8 #15314	0	1	0
15315	8	104,032,976	104,033,748	772	1	10.458	12.958	9.125	15	24	13	1	1	1	ATP6V1C1	114	in gene	AdReg chr8 #15315	0	1	0
15316	8	104,153,414	104,153,820	406	1	3.25	6.167	11.5	5	8	17	1	2	2	C8orf56, BAALC	-47, 696	upstream, in gene	AdReg chr8 #15316	0	0	1
15317	8	104,293,194	104,293,952	758	2	11.458	11.167	2.889	17	17	6	0	0	0				AdReg chr8 #15317	1	1	0
15318	8	104,311,025	104,311,848	823	1	7	11.308	3.962	14	18	8	1	1	1	FZD6	775	in gene	AdReg chr8 #15318	0	1	0
15319	8	104,360,968	104,361,984	1,016	1	10.875	7.781	3.769	19	13	7	0	0	0				AdReg chr8 #15319	1	0	0
15320	8	104,383,656	104,384,816	1,160	1	8.167	12.306	5.586	14	17	9	1	1	1	CTHRC1	450	in gene	AdReg chr8 #15320	0	1	0
15321	8	104,426,765	104,427,869	1,104	3	13.206	11.735	9.706	20	19	16	1	2	2	SLC25A32, DCAF13	151, 375	in gene, in gene	AdReg chr8 #15321	1	1	1
15322	8	104,497,669	104,498,421	752	2	13.391	15.391	2.261	23	33	4	0	0	0				AdReg chr8 #15322	1	1	0
15323	8	104,513,465	104,514,510	1,045	2	10.091	13.576	4.394	18	24	14	1	1	1	RIMS2	1,011	in gene	AdReg chr8 #15323	1	1	0
15324	8	104,992,336	104,993,231	895	1	9.786	12.893	3.071	17	26	6	0	0	1	RIMS2	479,807	in gene	AdReg chr8 #15324	0	1	0
15325	8	105,235,185	105,235,990	805	1	6.6	12.12	5.375	9	19	11	1	0	1	RIMS2	722,611	in gene	AdReg chr8 #15325	0	1	0
15326	8	105,349,064	105,349,701	637	1	13	9.65	2.053	21	15	4	0	1	1	TM7SF4	-2,672	upstream	AdReg chr8 #15326	1	0	0
15327	8	105,601,122	105,602,234	1,112	2	16.029	15.118	4.645	47	36	7	1	1	1	LRP12	-426	upstream	AdReg chr8 #15327	1	1	0
15328	8	106,331,166	106,331,563	397	1	2.923	5.25	12.077	5	10	16	1	1	1	ZFPM2	217	in gene	AdReg chr8 #15328	0	0	1
15329	8	106,331,793	106,332,148	355	1	4.364	6	11	7	8	17	1	1	1	ZFPM2	823	in gene	AdReg chr8 #15329	0	0	1
15330	8	107,072,100	107,073,104	1,004	1	8.903	13.29	1.545	18	27	3	0	0	0				AdReg chr8 #15330	0	1	0
15331	8	107,218,488	107,219,076	588	1	6.526	9.947	3.529	9	17	7	0	0	0				AdReg chr8 #15331	0	1	0
15332	8	107,257,763	107,258,455	692	2	9.762	12.048	1.733	13	20	3	0	0	0				AdReg chr8 #15332	1	1	0
15333	8	107,282,070	107,283,351	1,281	1	10.425	11.975	7.056	18	21	13	1	1	1	OXR1	237	in gene	AdReg chr8 #15333	0	1	0
15334	8	107,669,550	107,670,412	862	2	16.778	18.074	5.273	41	45	11	1	0	1	OXR1	387,508	in gene	AdReg chr8 #15334	1	1	0
15335	8	108,513,356	108,513,905	549	1	8.529	13.412	1.714	15	27	3	0	1	1	ANGPT1	-3,376	upstream	AdReg chr8 #15335	0	1	0
15336	8	109,095,690	109,096,164	474	1	5.8	4.933	11.267	14	8	16	1	1	1	RSPO2	-14	upstream	AdReg chr8 #15336	0	0	1
15337	8	109,132,276	109,133,052	776	2	13.375	10.125	1.667	23	18	2	0	0	0				AdReg chr8 #15337	1	1	0
15338	8	109,260,499	109,261,336	837	2	10.115	13.615	3.692	14	19	6	1	1	1	EIF3E	42	in gene	AdReg chr8 #15338	1	1	0
15339	8	110,345,804	110,346,826	1,022	2	12.625	16.719	8.656	26	37	14	1	2	2	NUDCD1, ENY2	35, -237	in gene, upstream	AdReg chr8 #15339	1	1	0
15340	8	110,587,135	110,587,611	476	1	2.467	5.733	10.733	6	7	18	0	0	2	EBAG9, GOLSYN	35444, 116647	downstream, in gene	AdReg chr8 #15340	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15341	8	110,698,112	110,698,804	692	2	8.955	11.136	1.75	19	22	2	0	0	1	GDLSYN	5,562	in gene	AdzReg chr8 #15341	1	1	0
15342	8	110,986,234	110,986,905	671	1	6.667	7.905	12.238	12	11	19	1	1	1	KCNV1	390	in gene	AdzReg chr8 #15342	0	0	1
15343	8	111,127,815	111,128,159	344	1	2.7	4.6	10.7	4	6	15	0	0	0				AdzReg chr8 #15343	0	0	1
15344	8	111,906,504	111,907,358	854	2	13.385	14	3.56	26	24	7	0	0	0				AdzReg chr8 #15344	1	1	0
15345	8	112,052,946	112,053,332	386	1	2.917	6.917	11.75	4	9	16	0	0	0				AdzReg chr8 #15345	0	0	1
15346	8	113,628,606	113,629,177	571	1	7.833	11.611	1.417	13	21	2	0	0	1	CSMD3	820,351	in gene	AdzReg chr8 #15346	0	1	0
15347	8	114,449,575	114,450,643	768	1	12.375	9.083	4.238	19	14	7	0	1	1	CSMD3	-1,017	upstream	AdzReg chr8 #15347	1	0	0
15348	8	116,068,105	116,068,990	885	1	11.556	8.407	1.474	19	13	3	0	0	0				AdzReg chr8 #15348	1	0	0
15349	8	116,088,676	116,089,218	542	1	10.529	6	1.636	17	10	3	0	0	0				AdzReg chr8 #15349	1	0	0
15350	8	116,660,305	116,660,961	656	1	7.762	10.952	4.611	14	21	7	1	0	1	TRPS1	20,595	in gene	AdzReg chr8 #15350	0	1	0
15351	8	116,791,399	116,792,147	748	1	9.304	10.652	4.318	19	15	7	0	0	0				AdzReg chr8 #15351	0	1	0
15352	8	117,435,797	117,436,572	775	1	8.292	10.833	2	14	15	2	0	0	0				AdzReg chr8 #15352	0	1	0
15353	8	117,778,430	117,779,278	848	1	11.482	12.185	4.63	18	23	8	1	1	1	UTP23	112	in gene	AdzReg chr8 #15353	1	0	0
15354	8	118,532,569	118,533,507	938	2	10.733	12.067	7.308	19	20	16	1	1	1	MED30	73	in gene	AdzReg chr8 #15354	1	1	0
15355	8	119,207,988	119,208,724	736	2	10.783	10.957	4.087	22	19	7	0	0	1	SAMD12	425,828	in gene	AdzReg chr8 #15355	1	1	0
15356	8	119,451,919	119,452,418	499	1	10	10.312	2	16	16	2	0	0	1	SAMD12	182,016	in gene	AdzReg chr8 #15356	1	0	0
15357	8	119,914,197	119,914,685	488	1	8	10.133	4	11	16	5	0	0	0				AdzReg chr8 #15357	0	1	0
15358	8	120,058,179	120,058,766	587	1	9.611	5.167	2.455	18	8	4	0	0	0				AdzReg chr8 #15358	1	0	0
15359	8	120,867,502	120,868,987	1,485	1	12.348	9.957	5.891	20	21	14	1	1	1	DSCC1	-74	upstream	AdzReg chr8 #15359	1	0	0
15360	8	120,885,839	120,886,725	886	1	10.964	15.357	8.786	18	28	15	1	1	1	DEPDC6	382	in gene	AdzReg chr8 #15360	0	1	0
15361	8	121,270,326	121,270,770	444	2	10.429	10	0	12	13	0	0	0	1	COL14A1	133,196	in gene	AdzReg chr8 #15361	1	1	0
15362	8	121,745,190	121,745,799	609	1	10.316	10	2.842	13	16	5	0	0	1	SNTB1	78,815	in gene	AdzReg chr8 #15362	0	1	0
15363	8	121,839,692	121,840,684	992	2	11.774	15.161	2.2	20	24	4	0	0	0				AdzReg chr8 #15363	1	1	0
15364	8	121,850,114	121,850,750	636	1	10.632	8.368	1.75	18	15	2	0	0	0				AdzReg chr8 #15364	1	0	0
15365	8	121,869,583	121,870,290	707	1	10.182	13.364	4.591	14	18	8	0	0	0				AdzReg chr8 #15365	0	1	0
15366	8	121,918,863	121,919,526	663	1	11	11.286	1.429	18	23	3	0	0	0				AdzReg chr8 #15366	0	1	0
15367	8	121,944,843	121,945,409	566	1	6	11.167	3.818	9	20	6	0	0	0				AdzReg chr8 #15367	0	1	0
15368	8	122,514,538	122,515,363	825	1	12.231	8.923	4.067	23	18	7	0	0	0				AdzReg chr8 #15368	1	0	0
15369	8	122,542,637	122,543,104	467	1	8.2	12.2	0	13	15	0	0	0	0				AdzReg chr8 #15369	0	1	0
15370	8	122,612,276	122,612,905	629	1	10.05	7.35	2	19	13	3	0	0	0				AdzReg chr8 #15370	1	0	0
15371	8	122,972,511	122,973,056	545	1	10.111	5.222	1.625	20	8	4	0	0	0				AdzReg chr8 #15371	1	0	0
15372	8	123,330,815	123,331,349	534	1	11.588	10.177	2.353	21	21	3	0	0	0				AdzReg chr8 #15372	1	0	0
15373	8	123,501,602	123,502,297	695	1	10.429	10.952	2.65	17	16	4	0	0	0				AdzReg chr8 #15373	1	0	0
15374	8	123,587,486	123,588,569	1,083	1	9.206	12.735	2.143	22	21	4	0	0	0				AdzReg chr8 #15374	0	1	0
15375	8	123,649,567	123,650,215	648	1	12.191	7.952	5.818	24	11	10	0	0	0				AdzReg chr8 #15375	1	0	0
15376	8	124,053,762	124,055,058	1,296	2	13.55	14.8	5.575	30	24	9	1	1	1	DERL1	238	in gene	AdzReg chr8 #15376	1	1	0
15377	8	124,084,682	124,085,356	674	2	8.619	10.952	10.667	12	20	19	1	1	1	WDR67	99	in gene	AdzReg chr8 #15377	0	1	1
15378	8	124,169,055	124,170,048	993	1	11.156	15.719	9.844	20	27	22	1	0	1	WDR67	84,631	downstream	AdzReg chr8 #15378	0	1	0
15379	8	124,178,601	124,179,028	427	1	1.727	2.889	11.692	3	6	17	0	0	0				AdzReg chr8 #15379	0	0	1
15380	8	124,219,701	124,220,175	474	1	3.067	1.857	11.067	5	3	18	1	1	2	FAM83A, LOC100131726	25186, -4955	in gene, upstream	AdzReg chr8 #15380	0	0	1
15381	8	124,407,862	124,409,329	1,467	3	22.022	30.196	10.174	64	101	31	1	1	1	ATAD2	110	in gene	AdzReg chr8 #15381	1	1	1
15382	8	124,553,595	124,554,266	671	1	6.524	7.095	11.524	10	10	15	1	1	1	FBXO32	-484	upstream	AdzReg chr8 #15382	0	0	1
15383	8	124,780,411	124,781,130	719	2	9.826	11.522	5.957	20	20	9	1	1	1	FAM91A1	-112	upstream	AdzReg chr8 #15383	1	1	0
15384	8	125,212,107	125,212,986	879	1	11.593	14.259	2.5	19	22	4	0	0	0				AdzReg chr8 #15384	0	1	0
15385	8	125,462,270	125,462,959	689	1	8.864	11.546	3.25	19	22	7	0	1	1	TRMT12	-434	upstream	AdzReg chr8 #15385	0	1	0
15386	8	125,486,592	125,487,331	739	1	8.667	12.75	6.591	12	23	13	1	2	2	LOC100507018, RNF139	-177, -47	upstream, upstream	AdzReg chr8 #15386	0	1	0
15387	8	125,568,353	125,568,999	646	1	3.7	6.25	11	5	10	15	0	0	2	NDUFB9, MTSS1	17333, 172054	downstream, in gene	AdzReg chr8 #15387	0	0	1
15388	8	125,763,773	125,764,444	671	1	11.619	6.571	2.111	19	11	3	0	0	0				AdzReg chr8 #15388	1	0	0
15389	8	125,784,226	125,784,828	602	1	9.889	14	2.444	15	20	5	0	0	0				AdzReg chr8 #15389	0	1	0
15390	8	125,985,177	125,986,110	933	1	9.172	12.621	5.31	21	23	11	0	1	1	ZNF572	104	in gene	AdzReg chr8 #15390	0	1	0
15391	8	126,103,621	126,104,480	859	2	5.889	11.852	10.407	10	23	18	1	2	2	KIAA0196, NSMCE2	11, -33	in gene, upstream	AdzReg chr8 #15391	0	1	1
15392	8	126,346,198	126,346,926	728	1	7.739	12.304	2.522	12	21	5	0	0	1	NSMCE2	242,479	in gene	AdzReg chr8 #15392	0	1	0
15393	8	126,408,791	126,409,410	619	1	2	2.8	9.85	3	4	14	0	0	0				AdzReg chr8 #15393	0	0	1
15394	8	126,424,158	126,425,465	1,307	2	10.049	11.049	4.22	16	20	7	0	0	0				AdzReg chr8 #15394	1	1	0
15395	8	126,425,687	126,426,262	575	1	10.111	13.444	3.722	15	23	5	0	0	0				AdzReg chr8 #15395	0	1	0
15396	8	126,442,106	126,443,152	1,046	2	9.576	13.485	5.97	19	21	11	1	1	1	TRIB1	66	in gene	AdzReg chr8 #15396	1	1	0
15397	8	126,496,499	126,497,062	563	1	8.444	10.278	1.188	12	16	2	0	0	0				AdzReg chr8 #15397	0	1	0
15398	8	126,524,973	126,525,840	867	2	11.593	13.259	5.63	24	25	9	0	0	0				AdzReg chr8 #15398	1	1	0
15399	8	126,568,201	126,569,492	1,291	1	7.725	11.025	4.079	11	17	7	0	0	0				AdzReg chr8 #15399	0	1	0
15400	8	127,509,411	127,510,136	725	2	10.727	9.636	2.722	14	16	5	0	0	0				AdzReg chr8 #15400	1	1	0
15401	8	127,512,051	127,512,862	811	1	9.04	11.76	4.68	12	17	9	0	0	0				AdzReg chr8 #15401	0	1	0
15402	8	127,559,028	127,560,064	1,036	2	12.909	11.879	3.345	19	17	5	0	0	1	FAM84B	10,920	downstream	AdzReg chr8 #15402	1	1	0
15403	8	127,568,400	127,569,723	1,323	2	12.366	13.61	6.537	20	20	16	1	1	1	FAM84B	1,405	in gene	AdzReg chr8 #15403	1	1	0
15404	8	127,570,104	127,571,170	1,066	3	16.823	15.529	9.941	40	41	20	1	1	1	FAM84B	-171	upstream	AdzReg chr8 #15404	1	1	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15405	8	127,584,131	127,584,637	506	1	11	3.867	4.333	16	8	6	0	0	0				ActReg chr8 #15405	1	0	0
15406	8	127,963,256	127,964,005	749	1	12.042	10.083	1.4	21	12	2	0	0	0				ActReg chr8 #15406	1	0	0
15407	8	128,047,844	128,048,438	594	1	9.833	11.167	2	15	19	4	0	0	0				ActReg chr8 #15407	0	1	0
15408	8	128,747,244	128,748,143	899	2	12.786	13	3.72	30	22	6	1	1	1	MYC	-622	upstream	ActReg chr8 #15408	1	1	0
15409	8	128,748,229	128,748,767	538	1	5.25	10.75	6	9	17	11	1	1	1	MYC	183	in gene	ActReg chr8 #15409	0	1	0
15410	8	128,821,787	128,822,451	664	1	9.81	9.095	3.444	15	13	6	0	0	2	PVT1, LOC100507101	15340, 15340	in gene, in gene	ActReg chr8 #15410	1	0	0
15411	8	128,843,453	128,844,789	1,336	2	9.214	11.238	3.571	20	22	9	0	0	2	PVT1, LOC100507101	37342, 37342	in gene, in gene	ActReg chr8 #15411	1	1	0
15412	8	128,863,682	128,865,233	1,551	1	9.875	13.5	4.659	19	21	10	0	0	2	PVT1, LOC100507101	57678, 57678	in gene, in gene	ActReg chr8 #15412	0	1	0
15413	8	128,871,926	128,872,602	676	1	8.238	12.809	5.667	16	20	9	0	0	2	PVT1, LOC100507101	65485, 65485	in gene, in gene	ActReg chr8 #15413	0	1	0
15414	8	128,929,787	128,930,397	610	1	9.368	10.421	6.579	14	18	9	0	0	2	PVT1, LOC100507101	123313, 123313	in gene, in gene	ActReg chr8 #15414	0	1	0
15415	8	129,157,001	129,157,808	807	2	16.72	12.88	2.417	40	28	6	0	1	1	MIR1208	-4,958	upstream	ActReg chr8 #15415	1	1	0
15416	8	129,481,748	129,482,490	742	1	10.478	8.13	1.722	17	12	3	0	0	0				ActReg chr8 #15416	1	0	0
15417	8	129,799,677	129,800,293	616	1	11.45	7.7	2.286	18	15	4	0	0	0				ActReg chr8 #15417	1	0	0
15418	8	129,970,054	129,970,677	623	1	4.316	11.474	3.25	9	22	5	0	0	0				ActReg chr8 #15418	0	1	0
15419	8	130,640,424	130,641,497	1,073	1	8.242	12.424	4.545	17	17	9	0	0	0				ActReg chr8 #15419	0	1	0
15420	8	130,719,777	130,720,925	1,148	2	10.057	8.743	3.824	16	15	8	0	0	0				ActReg chr8 #15420	1	1	0
15421	8	130,765,686	130,766,188	502	1	9.188	8.75	6.375	15	13	10	0	0	1	GSDMC	33,197	in gene	ActReg chr8 #15421	1	0	0
15422	8	130,951,944	130,952,744	800	2	12.12	12.96	6.957	20	22	11	1	1	1	FAM49B	-344	upstream	ActReg chr8 #15422	1	1	0
15423	8	131,007,240	131,008,171	931	1	7.655	10.241	3.037	12	19	6	0	0	0				ActReg chr8 #15423	0	1	0
15424	8	131,740,094	131,740,732	638	1	7.7	9.75	2.5	17	16	5	0	0	0				ActReg chr8 #15424	0	1	0
15425	8	131,820,778	131,821,479	701	1	7.727	13.091	2.273	15	21	7	0	0	1	ADCY8	231,707	in gene	ActReg chr8 #15425	0	1	0
15426	8	131,892,612	131,893,557	945	2	11.621	14.759	1.957	26	27	3	0	0	1	ADCY8	159,751	in gene	ActReg chr8 #15426	1	1	0
15427	8	132,047,418	132,047,862	444	1	9.571	4.714	1.818	14	7	3	0	0	1	ADCY8	5,195	in gene	ActReg chr8 #15427	1	0	0
15428	8	132,049,032	132,049,611	579	2	10.611	11.389	1.333	17	19	2	0	0	1	ADCY8	3,514	in gene	ActReg chr8 #15428	1	1	0
15429	8	132,052,398	132,052,818	420	1	4.077	6.077	11.692	6	11	15	1	1	1	ADCY8	227	in gene	ActReg chr8 #15429	0	0	1
15430	8	132,868,712	132,869,547	835	1	10.731	13.154	1.895	18	23	4	0	0	0				ActReg chr8 #15430	0	1	0
15431	8	133,082,567	133,083,582	1,015	2	12.871	12.613	1.591	19	23	3	0	0	1	HHLA1	34,438	in gene	ActReg chr8 #15431	1	1	0
15432	8	133,687,401	133,688,236	835	2	10.115	11.077	6.115	15	20	9	1	1	1	LRRC6	-5	upstream	ActReg chr8 #15432	1	1	0
15433	8	134,229,962	134,230,649	687	1	8.857	12.619	2.429	13	18	4	0	0	1	WISP1	26,993	in gene	ActReg chr8 #15433	0	1	0
15434	8	134,309,115	134,310,583	1,468	1	7.696	13.196	7.457	16	19	16	1	1	1	NDRG1	-302	upstream	ActReg chr8 #15434	0	1	0
15435	8	134,397,349	134,398,542	1,193	1	8.703	14.784	5.406	16	31	11	0	0	0				ActReg chr8 #15435	0	1	0
15436	8	134,403,018	134,403,666	648	1	9.4	12.7	2.429	18	24	4	0	0	0				ActReg chr8 #15436	0	1	0
15437	8	134,582,442	134,583,569	1,127	1	10.114	12.257	8.971	15	19	12	1	2	2	ST3GAL1, LOC100129104	1178, -1099	in gene, upstream	ActReg chr8 #15437	0	1	0
15438	8	134,583,996	134,584,953	957	2	5.667	10.333	7.933	12	15	18	1	2	2	ST3GAL1, LOC100129104	-291, 370	upstream, in gene	ActReg chr8 #15438	0	1	1
15439	8	135,421,320	135,422,431	1,111	2	17.941	21.912	3.219	46	55	8	0	0	0				ActReg chr8 #15439	1	1	0
15440	8	135,542,548	135,543,058	510	1	5.125	11.125	1.182	9	21	2	0	0	1	ZFAT	182,489	in gene	ActReg chr8 #15440	0	1	0
15441	8	135,752,265	135,752,917	652	1	6.15	11.55	1	10	19	1	0	0	0				ActReg chr8 #15441	0	1	0
15442	8	135,844,322	135,845,372	1,050	2	8.406	10.031	6.031	16	20	12	1	0	0				ActReg chr8 #15442	1	1	0
15443	8	135,909,410	135,910,370	960	1	11.533	11.633	3.867	18	16	7	0	0	0				ActReg chr8 #15443	1	0	0
15444	8	136,097,896	136,098,546	650	1	6.611	11.1	2.688	9	21	4	0	0	0				ActReg chr8 #15444	0	1	0
15445	8	136,201,888	136,202,597	709	2	11.348	11.043	1	20	21	1	0	0	0				ActReg chr8 #15445	1	1	0
15446	8	136,247,259	136,248,236	977	1	7.226	10.194	3.258	13	17	6	0	1	1	LOC286094	1,373	in gene	ActReg chr8 #15446	0	1	0
15447	8	136,332,477	136,333,143	666	1	9.19	11.429	2.333	13	20	3	0	0	0				ActReg chr8 #15447	0	1	0
15448	8	137,801,608	137,802,075	467	1	5.769	10.071	1	10	16	1	0	0	0				ActReg chr8 #15448	0	1	0
15449	8	138,334,234	138,334,653	419	1	9.615	9.923	1.75	14	13	3	0	0	0				ActReg chr8 #15449	0	1	0
15450	8	139,548,982	139,549,758	776	1	9.208	13.375	3.167	14	25	6	0	0	0				ActReg chr8 #15450	0	1	0
15451	8	139,653,993	139,654,776	783	2	9.792	13.917	2.053	20	29	4	0	0	1	COL22A1	271,852	in gene	ActReg chr8 #15451	1	1	0
15452	8	139,843,065	139,843,701	636	1	9.95	11.95	2.267	15	17	3	0	0	1	COL22A1	82,853	in gene	ActReg chr8 #15452	0	1	0
15453	8	139,871,752	139,872,267	515	1	3.5	2.062	10.375	5	5	14	0	0	1	COL22A1	54,227	in gene	ActReg chr8 #15453	0	0	1
15454	8	139,889,814	139,890,157	343	1	3.273	2.909	13	7	4	20	1	0	1	COL22A1	36,251	in gene	ActReg chr8 #15454	0	0	1
15455	8	139,988,070	139,988,612	542	1	8.706	6.882	1.545	16	13	2	0	0	0				ActReg chr8 #15455	1	0	0
15456	8	140,221,380	140,221,881	501	1	8.4	11.2	3.143	13	15	6	0	0	0				ActReg chr8 #15456	0	1	0
15457	8	140,227,833	140,228,538	705	2	10.409	10.227	1.923	16	16	3	0	0	0				ActReg chr8 #15457	1	1	0
15458	8	140,258,081	140,258,904	823	2	9.64	17.72	3.88	16	36	7	0	0	0				ActReg chr8 #15458	1	1	0
15459	8	140,485,730	140,486,109	379	1	2.182	1	9.818	4	1	14	0	0	0				ActReg chr8 #15459	0	0	1
15460	8	140,665,758	140,666,116	358	1	1	4.417	10.417	1	6	15	0	0	1	KCNK9	49,362	in gene	ActReg chr8 #15460	0	0	1
15461	8	140,670,781	140,671,422	641	1	10.45	12.65	4	16	25	8	0	0	1	KCNK9	44,198	in gene	ActReg chr8 #15461	0	1	0
15462	8	140,717,607	140,718,617	1,010	2	5.516	8.935	9.862	11	13	15	1	1	1	KCNK9	-2,813	upstream	ActReg chr8 #15462	0	1	1
15463	8	140,732,143	140,732,963	820	2	14.731	18.923	3	34	45	5	0	0	1	TRAPPC9	736,125	downstream	ActReg chr8 #15463	1	1	0
15464	8	140,908,680	140,909,456	776	2	10.75	14.417	4.333	23	25	8	0	0	1	TRAPPC9	559,610	in gene	ActReg chr8 #15464	1	1	0
15465	8	141,107,303	141,107,779	476	1	3.4	3.8	12.733	7	6	19	1	1	2	TRAPPC9, LOC100507278	361137, 201	in gene, in gene	ActReg chr8 #15465	0	0	1
15466	8	141,110,236	141,110,722	486	1	3.625	7.062	11.438	6	10	16	1	1	2	TRAPPC9, LOC100507278	358199, -2737	in gene, upstream	ActReg chr8 #15466	0	0	1
15467	8	141,319,220	141,320,633	1,413	2	13.477	13.046	2.359	33	34	5	0	0	1	TRAPPC9	148,752	in gene	ActReg chr8 #15467	1	1	0
15468	8	141,403,760	141,404,407	647	1	5.65	10.7	1.529	8	16	2	0	0	1	TRAPPC9	64,595	in gene	ActReg chr8 #15468	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15469	8	141,467,388	141,468,216	828	2	13.5	13.423	4.32	30	29	11	1	1	1	TRAPPC9	876	in gene	ActReg chr8 #15469	1	1	0
15470	8	141,474,004	141,475,240	1,236	2	15.641	14.359	8.436	33	25	14	1	1	1	TRAPPC9	-5,944	upstream	ActReg chr8 #15470	1	1	0
15471	8	141,520,744	141,521,369	625	1	10	11.21	7.684	14	17	13	1	1	1	CHRAC1	-345	upstream	ActReg chr8 #15471	0	1	0
15472	8	141,521,950	141,522,823	873	1	6.036	10.143	8.071	12	15	14	1	1	1	CHRAC1	985	in gene	ActReg chr8 #15472	0	1	0
15473	8	141,578,394	141,579,106	712	1	3.571	2.571	14.043	6	5	20	0	0	1	EIF2C2	66,896	in gene	ActReg chr8 #15473	0	0	1
15474	8	141,598,926	141,600,555	1,629	2	6.451	8.686	7.647	15	15	20	0	0	1	EIF2C2	45,906	in gene	ActReg chr8 #15474	0	1	1
15475	8	141,631,135	141,631,860	725	2	10.304	11.913	4.696	17	21	9	0	0	1	EIF2C2	14,149	in gene	ActReg chr8 #15475	1	1	0
15476	8	141,644,095	141,644,873	778	1	8.72	10.84	5.28	16	15	8	1	1	1	EIF2C2	1,162	in gene	ActReg chr8 #15476	0	1	0
15477	8	142,036,641	142,037,539	898	2	12.607	12.821	6.571	22	24	11	0	0	0				ActReg chr8 #15477	1	1	0
15478	8	142,045,278	142,045,952	674	1	9.364	11.091	4.045	16	21	8	0	0	0				ActReg chr8 #15478	0	1	0
15479	8	142,053,174	142,053,872	698	1	10.727	9.636	1.182	18	18	2	0	0	0				ActReg chr8 #15479	1	0	0
15480	8	142,114,624	142,114,978	354	1	3.417	3.833	10.833	5	6	17	0	0	0				ActReg chr8 #15480	0	0	1
15481	8	142,122,101	142,122,688	587	1	5.353	3.333	12.21	9	8	15	0	0	0				ActReg chr8 #15481	0	0	1
15482	8	142,137,701	142,138,327	626	1	7.789	9.842	11.316	10	12	18	1	1	1	DENND3	-706	upstream	ActReg chr8 #15482	0	0	1
15483	8	142,163,652	142,164,705	1,053	1	7.515	9.485	3.724	13	14	10	0	0	1	DENND3	25,458	in gene	ActReg chr8 #15483	0	1	0
15484	8	142,199,300	142,200,197	897	1	3.607	4.286	12.107	6	9	19	0	0	1	DENND3	61,026	in gene	ActReg chr8 #15484	0	0	1
15485	8	142,216,825	142,217,251	426	1	2.571	7.714	10.643	5	9	16	0	0	1	SLC45A4	21,635	downstream	ActReg chr8 #15485	0	0	1
15486	8	142,217,778	142,218,179	401	1	3.538	1.846	10.615	6	3	16	0	0	1	SLC45A4	20,695	downstream	ActReg chr8 #15486	0	0	1
15487	8	142,232,621	142,233,038	417	1	2.077	3.692	11.769	4	5	19	0	0	1	SLC45A4	5,844	in gene	ActReg chr8 #15487	0	0	1
15488	8	142,242,726	142,243,222	496	1	2.714	4.533	12.2	4	7	18	0	1	1	SLC45A4	-4,301	upstream	ActReg chr8 #15488	0	0	1
15489	8	142,294,864	142,295,443	579	1	3.647	6.444	12.833	8	10	18	1	0	0				ActReg chr8 #15489	0	0	1
15490	8	142,386,464	142,386,798	334	1	3.182	2	12.364	6	3	16	0	0	1	GPR20	-9,266	upstream	ActReg chr8 #15490	0	0	1
15491	8	142,406,750	142,407,467	717	1	2.636	4.565	10.174	6	8	16	0	0	0				ActReg chr8 #15491	0	0	1
15492	8	142,458,015	142,458,588	573	1	4.667	3.176	10.389	7	5	13	0	0	1	FLJ43860	59,029	in gene	ActReg chr8 #15492	0	0	1
15493	8	142,488,019	142,488,504	485	1	4.133	2.733	13.067	6	4	19	0	0	1	FLJ43860	29,069	in gene	ActReg chr8 #15493	0	0	1
15494	8	142,498,661	142,499,854	1,193	1	2.973	5.892	10.622	6	12	17	0	0	1	FLJ43860	18,073	in gene	ActReg chr8 #15494	0	0	1
15495	8	142,525,627	142,527,835	2,208	2	12.696	17.536	5.441	37	47	11	0	0	1	FLJ43860	-9,401	upstream	ActReg chr8 #15495	1	1	0
15496	8	142,576,842	142,577,947	1,105	2	12.647	16.118	7.529	22	35	12	0	0	0				ActReg chr8 #15496	1	1	0
15497	8	142,614,734	142,615,067	333	1	3.8	2.444	12	6	4	16	0	0	0				ActReg chr8 #15497	0	0	1
15498	8	142,631,264	142,632,116	852	1	2	4.185	12.037	5	9	17	0	0	0				ActReg chr8 #15498	0	0	1
15499	8	142,646,059	142,646,392	333	1	2.8	3.5	10	5	4	14	0	0	0				ActReg chr8 #15499	0	0	1
15500	8	142,659,151	142,659,617	466	1	1.875	3	12.267	2	4	18	0	0	0				ActReg chr8 #15500	0	0	1
15501	8	142,690,268	142,690,795	527	1	2.733	3.812	9.824	9	7	15	0	0	0				ActReg chr8 #15501	0	0	1
15502	8	142,725,776	142,727,004	1,228	2	18.868	23.079	3.263	45	67	6	0	0	0				ActReg chr8 #15502	1	1	0
15503	8	142,970,567	142,971,193	626	1	8.158	11.632	3.684	16	17	7	0	0	0				ActReg chr8 #15503	0	1	0
15504	8	143,055,933	143,056,539	606	1	2.533	3.917	11.053	6	6	14	0	0	0				ActReg chr8 #15504	0	0	1
15505	8	143,061,580	143,062,132	552	1	3.188	4.647	11.823	6	8	15	0	0	0				ActReg chr8 #15505	0	0	1
15506	8	143,127,948	143,128,871	923	1	2.769	4.793	12.69	4	8	21	0	0	0				ActReg chr8 #15506	0	0	1
15507	8	143,255,466	143,255,842	376	1	3.917	2.833	10.167	5	4	15	0	0	0				ActReg chr8 #15507	0	0	1
15508	8	143,263,351	143,263,950	599	1	3.895	2.526	12.526	6	5	17	0	0	0				ActReg chr8 #15508	0	0	1
15509	8	143,269,350	143,269,992	642	1	4.65	3.368	11.5	6	6	19	0	0	1	NCRNA00051	-10,046	upstream	ActReg chr8 #15509	0	0	1
15510	8	143,279,480	143,280,249	769	1	5.708	4.125	12.25	10	6	20	0	1	1	NCRNA00051	147	in gene	ActReg chr8 #15510	0	0	1
15511	8	143,298,625	143,299,306	681	1	7.429	13.905	4.9	14	24	9	0	0	2	NCRNA00051, TSNARE1	19248, 185578	downstream, in gene	ActReg chr8 #15511	0	1	0
15512	8	143,300,955	143,301,363	408	1	1	2.846	11.769	1	5	16	0	0	1	TSNARE1	183,384	in gene	ActReg chr8 #15512	0	0	1
15513	8	143,313,939	143,314,647	708	1	2.188	4.545	11.727	4	6	14	0	0	1	TSNARE1	170,250	in gene	ActReg chr8 #15513	0	0	1
15514	8	143,330,839	143,331,475	636	1	3.75	4.55	13.1	7	8	17	0	0	1	TSNARE1	153,386	in gene	ActReg chr8 #15514	0	0	1
15515	8	143,331,973	143,332,649	676	2	10.762	11.762	6.143	19	23	9	0	0	1	TSNARE1	152,232	in gene	ActReg chr8 #15515	1	1	0
15516	8	143,332,681	143,333,244	563	1	4.118	3.765	12.588	5	7	16	1	0	1	TSNARE1	151,581	in gene	ActReg chr8 #15516	0	0	1
15517	8	143,374,033	143,374,479	446	1	2.5	2.357	11.786	4	3	16	0	0	1	TSNARE1	110,287	in gene	ActReg chr8 #15517	0	0	1
15518	8	143,376,804	143,377,360	556	1	4	5.471	13.823	7	10	19	0	0	1	TSNARE1	107,461	in gene	ActReg chr8 #15518	0	0	1
15519	8	143,383,884	143,384,764	880	1	3.615	3.75	13.259	8	5	18	0	0	1	TSNARE1	100,219	in gene	ActReg chr8 #15519	0	0	1
15520	8	143,400,612	143,401,111	499	1	2	3.533	13.4	4	8	16	0	0	1	TSNARE1	83,682	in gene	ActReg chr8 #15520	0	0	1
15521	8	143,434,957	143,435,508	551	1	3.583	1.467	11.294	6	3	16	0	0	1	TSNARE1	49,311	in gene	ActReg chr8 #15521	0	0	1
15522	8	143,464,504	143,465,223	719	1	10.391	14.304	3.227	21	27	5	0	0	1	TSNARE1	19,680	in gene	ActReg chr8 #15522	0	1	0
15523	8	143,532,958	143,533,344	386	1	4.769	5	11.308	10	9	18	1	0	0				ActReg chr8 #15523	0	0	1
15524	8	143,535,490	143,535,858	368	1	1.875	4.545	11.727	3	6	15	1	0	1	BAI1	-9,703	upstream	ActReg chr8 #15524	0	0	1
15525	8	143,552,791	143,553,412	621	1	3.95	5.05	13.35	7	8	18	0	0	1	BAI1	7,724	in gene	ActReg chr8 #15525	0	0	1
15526	8	143,605,524	143,606,011	487	1	3.733	5.267	13.133	6	9	19	0	0	1	BAI1	60,390	in gene	ActReg chr8 #15526	0	0	1
15527	8	143,609,413	143,609,967	554	1	5.118	6.941	10.647	9	10	16	1	0	1	BAI1	64,313	in gene	ActReg chr8 #15527	0	0	1
15528	8	143,610,072	143,610,594	522	1	6.706	6.294	11.882	11	9	20	0	0	1	BAI1	64,956	in gene	ActReg chr8 #15528	0	0	1
15529	8	143,616,507	143,617,057	550	1	3.167	2.25	12.167	5	4	16	0	0	1	BAI1	71,405	in gene	ActReg chr8 #15529	0	0	1
15530	8	143,622,507	143,623,742	1,235	1	3.737	2.684	12.29	6	5	18	1	0	1	BAI1	77,747	in gene	ActReg chr8 #15530	0	0	1
15531	8	143,650,770	143,651,182	412	1	5.182	2.615	12.615	7	4	17	0	0	0				ActReg chr8 #15531	0	0	1
15532	8	143,655,369	143,655,818	449	1	3.571	2.857	11.643	5	5	18	0	0	0				ActReg chr8 #15532	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15533	8	143,679,920	143,680,339	419	1	4.1	4.077	11.308	5	6	16	0	0	0				ActReg chr8 #15533	0	0	1
15534	8	143,681,051	143,681,683	632	1	2.25	6.25	11.95	3	11	16	0	0	0				ActReg chr8 #15534	0	0	1
15535	8	143,692,802	143,693,404	602	1	5.444	3.833	11.889	9	6	14	0	1	1	ARC	2,730	in gene	ActReg chr8 #15535	0	0	1
15536	8	143,695,054	143,695,621	567	1	7.056	10.444	12.056	12	15	21	1	1	1	ARC	496	in gene	ActReg chr8 #15536	0	0	1
15537	8	143,700,630	143,701,010	380	1	2.333	3	12	4	5	18	0	1	1	ARC	-4,987	upstream	ActReg chr8 #15537	0	0	1
15538	8	143,702,974	143,703,588	614	1	4.5	2.5	12.6	9	5	19	0	1	1	ARC	-7,448	upstream	ActReg chr8 #15538	0	0	1
15539	8	143,715,899	143,716,553	654	1	4.429	5.5	11.286	9	9	15	0	0	0				ActReg chr8 #15539	0	0	1
15540	8	143,745,711	143,746,497	786	1	3.16	7.24	11.92	5	11	15	0	1	2	JRK, PSCA	5297, -5622	in gene, upstream	ActReg chr8 #15540	0	0	1
15541	8	143,746,817	143,747,366	549	1	4.412	4.824	11	9	7	16	0	1	2	JRK, PSCA	4310, -4635	in gene, upstream	ActReg chr8 #15541	0	0	1
15542	8	143,751,260	143,751,714	454	1	10.733	16	3.733	20	33	10	1	2	2	JRK, PSCA	-86, -239	upstream, upstream	ActReg chr8 #15542	0	1	0
15543	8	143,762,711	143,763,681	970	1	10.742	12.742	9.484	17	22	17	0	0	1	PSCA	11,470	in gene	ActReg chr8 #15543	0	1	0
15544	8	143,799,265	143,799,962	697	2	14.762	11.857	3.222	30	22	5	0	0	2	LOC100288181, C8orf55	8778, -9008	in gene, upstream	ActReg chr8 #15544	1	1	0
15545	8	143,807,662	143,808,443	781	1	8.875	7.875	13.833	13	13	21	1	2	2	LOC100288181, C8orf55	339, -569	in gene, upstream	ActReg chr8 #15545	0	0	1
15546	8	143,819,865	143,821,063	1,198	1	8.842	13	6.889	19	20	14	1	0	2	C8orf55, SLURP1	11843, 3365	downstream, downstream	ActReg chr8 #15546	0	1	0
15547	8	143,832,784	143,833,164	380	1	3.917	3.222	12.167	7	5	16	0	1	2	SLURP1, LYPD2	-9145, 978	upstream, in gene	ActReg chr8 #15547	0	0	1
15548	8	143,834,860	143,835,762	902	1	2.75	4.571	11.25	5	9	18	0	1	2	LYPD2, LYNX1	-1359, 24329	upstream, downstream	ActReg chr8 #15548	0	0	1
15549	8	143,849,804	143,850,458	654	1	3.429	4.35	11.85	5	7	17	0	0	1	LYNX1	9,509	in gene	ActReg chr8 #15549	0	0	1
15550	8	143,854,104	143,854,797	693	1	3.091	3	12.727	5	7	20	0	0	1	LYNX1	5,190	in gene	ActReg chr8 #15550	0	0	1
15551	8	143,855,182	143,855,617	435	1	3	3.714	11.5	5	6	17	0	0	1	LYNX1	4,241	in gene	ActReg chr8 #15551	0	0	1
15552	8	143,857,017	143,857,751	734	1	4.609	5.087	11.304	7	9	16	0	1	2	LYNX1, LY6D	2256, 10624	in gene, downstream	ActReg chr8 #15552	0	0	1
15553	8	143,857,864	143,858,237	373	1	2.1	6.909	12.091	3	11	16	1	1	2	LYNX1, LY6D	1590, 9958	in gene, downstream	ActReg chr8 #15553	0	0	1
15554	8	143,863,389	143,864,459	1,070	1	5	3.935	12.765	10	7	19	0	1	2	LYNX1, LY6D	-4284, 4084	upstream, downstream	ActReg chr8 #15554	0	0	1
15555	8	143,880,273	143,880,715	442	1	2.846	6.5	10.571	5	11	17	0	0	1	LOC100288207	7,064	in gene	ActReg chr8 #15555	0	0	1
15556	8	143,900,907	143,901,611	704	1	2.955	3	11.727	5	6	16	0	0	0				ActReg chr8 #15556	0	0	1
15557	8	143,915,555	143,915,967	412	1	5.917	2	12.75	8	3	16	1	1	1	GML	-456	upstream	ActReg chr8 #15557	0	0	1
15558	8	143,916,074	143,916,479	405	1	1.545	1.75	11.167	3	2	15	1	1	1	GML	59	in gene	ActReg chr8 #15558	0	0	1
15559	8	143,993,112	143,993,829	717	1	8.043	11.783	6.348	13	21	12	0	0	1	CYP11B2	5,789	in gene	ActReg chr8 #15559	0	1	0
15560	8	144,024,759	144,025,648	889	2	13.714	16.036	5.714	30	36	10	0	0	0				ActReg chr8 #15560	1	1	0
15561	8	144,052,472	144,053,278	806	1	2.826	3.2	11.76	4	5	17	0	0	0				ActReg chr8 #15561	0	0	1
15562	8	144,120,079	144,120,508	429	1	5.846	6.692	12.538	8	9	18	0	1	1	C8orf31	-386	upstream	ActReg chr8 #15562	0	0	1
15563	8	144,161,460	144,161,904	444	1	3.929	3.455	11.071	5	6	15	0	0	0				ActReg chr8 #15563	0	0	1
15564	8	144,183,001	144,183,866	865	2	11.462	13.296	7.857	23	25	16	0	0	0				ActReg chr8 #15564	1	1	0
15565	8	144,238,628	144,239,071	443	1	4.462	6.692	11.692	6	9	17	0	0	1	LY6H	3,204	downstream	ActReg chr8 #15565	0	0	1
15566	8	144,239,448	144,239,848	400	1	2.308	5	11.923	3	8	17	0	1	1	LY6H	2,405	in gene	ActReg chr8 #15566	0	0	1
15567	8	144,241,123	144,241,452	329	1	1	1	10.8	1	1	15	1	1	1	LY6H	766	in gene	ActReg chr8 #15567	0	0	1
15568	8	144,264,685	144,265,689	1,004	1	3.241	4.419	12.645	5	8	17	0	0	0				ActReg chr8 #15568	0	0	1
15569	8	144,296,683	144,296,981	298	1	4.667	5.889	12.778	10	9	16	0	1	1	GPIHBP1	1,764	in gene	ActReg chr8 #15569	0	0	1
15570	8	144,303,395	144,304,123	728	1	2.364	3.238	12.773	4	7	19	0	0	1	GPIHBP1	8,691	downstream	ActReg chr8 #15570	0	0	1
15571	8	144,317,585	144,318,524	939	1	7.379	10.69	6.276	11	15	18	0	0	0				ActReg chr8 #15571	0	1	0
15572	8	144,328,903	144,329,674	771	1	8.042	7.083	12.167	13	11	20	1	1	1	ZFP41	179	in gene	ActReg chr8 #15572	0	0	1
15573	8	144,348,923	144,349,962	1,039	2	15.273	12	4.222	30	33	7	1	1	2	ZFP41, GLI4	20333, -165	downstream, upstream	ActReg chr8 #15573	1	1	0
15574	8	144,351,997	144,353,044	1,047	1	4.697	4.531	11.424	10	10	17	0	1	3	ZFP41, GLI4, LOC100507316	23411, 2913, 11340	downstream, in gene, downstream	ActReg chr8 #15574	0	0	1
15575	8	144,357,344	144,357,765	421	1	4.5	4.231	12.286	7	8	15	0	0	2	GLI4, LOC100507316	7947, 6306	in gene, downstream	ActReg chr8 #15575	0	0	1
15576	8	144,358,316	144,358,948	632	1	5.8	6.4	11.9	8	11	18	1	0	2	GLI4, LOC100507316	9025, 5228	in gene, downstream	ActReg chr8 #15576	0	0	1
15577	8	144,359,431	144,359,902	471	1	4.286	6.071	11.571	6	9	16	0	0	2	GLI4, LOC100507316	10059, 4194	downstream, downstream	ActReg chr8 #15577	0	0	1
15578	8	144,360,512	144,361,273	761	1	8.667	9.917	13.417	13	13	21	1	0	2	GLI4, LOC100507316	11285, 2968	downstream, downstream	ActReg chr8 #15578	0	0	1
15579	8	144,362,904	144,364,553	1,649	2	32.038	34.923	4.857	133	150	11	0	1	3	GLI4, LOC100507316, ZNF696	14121, 132, -9831	downstream, in gene, upstream	ActReg chr8 #15579	1	1	0
15580	8	144,372,945	144,373,979	1,034	2	16.062	14.688	6.129	32	27	12	1	1	2	LOC100507316, ZNF696	-9602, -97	upstream, upstream	ActReg chr8 #15580	1	1	0
15581	8	144,398,960	144,399,617	657	1	2.824	4.857	10.048	6	7	14	1	0	1	TOP1MT	17,762	in gene	ActReg chr8 #15581	0	0	1
15582	8	144,416,455	144,416,802	347	1	9.455	6.545	11.909	14	9	17	1	1	1	TOP1MT	422	in gene	ActReg chr8 #15582	0	0	1
15583	8	144,457,479	144,458,220	741	1	3.652	3.619	13	7	7	21	0	1	2	C8orf51, RHPN1	-7044, 6824	upstream, in gene	ActReg chr8 #15583	0	0	1
15584	8	144,465,709	144,466,293	584	1	4.444	6.889	13.111	6	10	18	0	0	1	RHPN1	14,976	in gene	ActReg chr8 #15584	0	0	1
15585	8	144,467,029	144,467,659	630	1	7.2	12.8	12.1	13	19	17	0	0	1	RHPN1	16,319	downstream	ActReg chr8 #15585	0	0	1
15586	8	144,483,016	144,483,547	531	1	3.062	6.562	11.688	5	11	14	0	0	0				ActReg chr8 #15586	0	0	1
15587	8	144,488,679	144,489,256	577	1	3.722	4.667	12.611	6	9	21	0	0	0				ActReg chr8 #15587	0	0	1
15588	8	144,490,328	144,490,840	512	1	1	3	13	1	5	20	0	0	0				ActReg chr8 #15588	0	0	1
15589	8	144,507,489	144,507,785	296	1	4.444	4.889	10.556	9	7	13	0	0	2	LOC100507344, MAFA	3624, 4939	downstream, downstream	ActReg chr8 #15589	0	0	1
15590	8	144,523,462	144,524,184	722	1	4.955	3.227	12.454	7	6	16	0	0	1	ZC3H3	99,797	in gene	ActReg chr8 #15590	0	0	1
15591	8	144,546,893	144,547,729	836	1	2.783	2.875	13.077	5	5	21	0	0	1	ZC3H3	76,309	in gene	ActReg chr8 #15591	0	0	1
15592	8	144,593,838	144,594,393	555	1	4.882	5.353	10.941	8	10	17	0	0	1	ZC3H3	29,505	in gene	ActReg chr8 #15592	0	0	1
15593	8	144,600,282	144,600,789	507	1	4.625	3.9	10.875	8	6	14	0	0	1	ZC3H3	23,085	in gene	ActReg chr8 #15593	0	0	1
15594	8	144,623,433	144,624,157	724	1	9.364	12.409	6.682	14	28	11	1	1	1	ZC3H3	-175	upstream	ActReg chr8 #15594	0	1	0
15595	8	144,628,478	144,628,946	468	1	3.214	2.1	10.333	8	4	16	0	2	2	ZC3H3, GSDMD	-5092, -6845	upstream, upstream	ActReg chr8 #15595	0	0	1
15596	8	144,636,224	144,636,763	539	1	10.706	7.412	14.529	15	10	21	1	1	1	GSDMD	936	in gene	ActReg chr8 #15596	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15597	8	144,643,966	144,644,549	583	1	2.4	5.294	10.368	4	11	17	0	0	2	GSDMD, C8orf73	8700, 10671	in gene, downstream	ActReg chr8 #15597	0	0	1
15598	8	144,671,464	144,672,021	557	1	2.1	4.588	13	3	8	18	0	0	2	EEF1D, TIGD5	8103, -8332	in gene, upstream	ActReg chr8 #15598	0	0	1
15599	8	144,678,971	144,680,051	1,080	2	21.033	20.912	7.133	49	54	12	1	2	3	EEF1D, TIGD5, PYCRL	334, -563, 12273	in gene, upstream, downstream	ActReg chr8 #15599	1	1	0
15600	8	144,680,171	144,680,664	493	1	6.667	15.467	10	12	26	18	1	2	3	EEF1D, TIGD5, PYCRL	-572, 343, 11367	upstream, in gene, downstream	ActReg chr8 #15600	0	1	0
15601	8	144,683,460	144,683,926	466	1	3.929	4.214	12.571	7	8	15	0	1	3	EEF1D, TIGD5, PYCRL	-3848, 3619, 8091	upstream, downstream, downstream	ActReg chr8 #15601	0	0	1
15602	8	144,700,158	144,700,585	427	1	9.357	10.786	5.5	13	18	9	1	1	2	PYCRL, TSTA3	-8587, -639	upstream, upstream	ActReg chr8 #15602	0	1	0
15603	8	144,717,606	144,718,595	989	2	9.613	11.452	5.897	16	18	13	1	1	1	ZNF623	-273	upstream	ActReg chr8 #15603	1	1	0
15604	8	144,766,244	144,767,053	809	2	12.44	13.56	7.64	19	23	20	1	1	1	ZNF707	26	in gene	ActReg chr8 #15604	1	1	0
15605	8	144,803,402	144,803,844	442	1	2.5	4	12.071	5	7	17	0	0	2	MAPK15, FAM83H	5116, 12291	in gene, downstream	ActReg chr8 #15605	0	0	1
15606	8	144,804,748	144,805,107	359	1	3.636	2.909	11.909	5	5	14	0	0	2	MAPK15, FAM83H	6420, 10987	downstream, downstream	ActReg chr8 #15606	0	0	1
15607	8	144,816,121	144,816,518	397	1	5.692	3.182	11.615	10	5	19	1	2	2	FAM83H, hCG_1995004	-405, 9	upstream, in gene	ActReg chr8 #15607	0	0	1
15608	8	144,819,585	144,820,486	901	1	2.714	5.571	13.393	5	9	17	1	1	2	FAM83H, hCG_1995004	-4121, 3725	upstream, in gene	ActReg chr8 #15608	0	0	1
15609	8	144,871,545	144,872,147	602	1	2.842	3.895	11.105	4	6	15	1	0	2	LOC642574, SCRIB	18546, 25703	in gene, downstream	ActReg chr8 #15609	0	0	1
15610	8	144,873,311	144,873,884	573	1	1.833	3.222	12.722	3	6	18	0	0	2	LOC642574, SCRIB	20297, 23952	downstream, in gene	ActReg chr8 #15610	0	0	1
15611	8	144,885,964	144,886,624	660	1	4	4.429	12.238	6	8	17	1	0	2	SCRIB, MIR937	11255, 8918	in gene, downstream	ActReg chr8 #15611	0	0	1
15612	8	144,890,927	144,891,478	551	1	5.588	4.706	11.471	10	8	16	0	0	3	SCRIB, MIR937, PUF60	6347, 4010, 20335	in gene, downstream, downstream	ActReg chr8 #15612	0	0	1
15613	8	144,894,390	144,894,950	560	1	3.625	4.389	10.944	6	6	13	1	1	3	SCRIB, MIR937, PUF60	2879, 542, 16867	in gene, downstream, downstream	ActReg chr8 #15613	0	0	1
15614	8	144,895,051	144,895,480	429	1	4.692	4.077	13.692	6	7	21	1	2	3	SCRIB, MIR937, PUF60	2284, -53, 16272	in gene, upstream, downstream	ActReg chr8 #15614	0	0	1
15615	8	144,902,018	144,902,432	414	1	3.231	6.462	12.615	6	10	16	0	2	3	SCRIB, MIR937, PUF60	-4676, -7013, 9312	upstream, upstream, in gene	ActReg chr8 #15615	0	0	1
15616	8	144,911,130	144,912,022	892	1	10.071	12.786	8	16	19	14	1	1	2	PUF60, NRBP2	-39, 11570	upstream, downstream	ActReg chr8 #15616	0	1	0
15617	8	144,961,290	144,961,832	542	1	2.143	2.941	11.706	3	4	20	0	0	0				ActReg chr8 #15617	0	0	1
15618	8	144,986,854	144,987,744	890	1	5.893	4.357	10.5	8	7	15	0	0	1	PLEC1	63,614	downstream	ActReg chr8 #15618	0	0	1
15619	8	144,992,331	144,993,017	686	1	5.857	4.81	16.905	8	10	23	1	0	1	PLEC1	58,239	in gene	ActReg chr8 #15619	0	0	1
15620	8	145,001,820	145,002,316	496	1	3.938	7.062	11.312	7	9	16	1	0	1	PLEC1	48,845	in gene	ActReg chr8 #15620	0	0	1
15621	8	145,003,477	145,004,671	1,194	1	5.757	5.351	16.108	9	10	30	1	0	1	PLEC1	46,839	in gene	ActReg chr8 #15621	0	0	1
15622	8	145,005,725	145,006,240	515	1	4.125	5	12.471	7	8	22	0	0	1	PLEC1	44,931	in gene	ActReg chr8 #15622	0	0	1
15623	8	145,008,838	145,009,658	820	1	4.125	9.4	12.64	8	16	18	1	0	2	PLEC1, MIR661	41665, 10199	in gene, downstream	ActReg chr8 #15623	0	0	1
15624	8	145,010,409	145,011,319	910	1	13.893	11.071	7.25	24	16	17	0	0	2	PLEC1, MIR661	40049, 8583	in gene, downstream	ActReg chr8 #15624	1	0	0
15625	8	145,012,626	145,013,140	514	1	7.562	7.125	13.062	11	10	18	0	0	2	PLEC1, MIR661	38030, 6564	in gene, downstream	ActReg chr8 #15625	0	0	1
15626	8	145,014,755	145,015,609	854	1	7.192	9.846	11	14	17	14	0	0	2	PLEC1, MIR661	35731, 4265	in gene, downstream	ActReg chr8 #15626	0	0	1
15627	8	145,016,332	145,018,450	2,118	3	10.53	12.742	8.409	24	26	23	2	1	2	PLEC1, MIR661	33522, 2056	in gene, downstream	ActReg chr8 #15627	1	1	1
15628	8	145,018,707	145,019,375	668	1	7.143	7.714	13.429	10	10	17	1	1	2	PLEC1, MIR661	31872, 406	in gene, downstream	ActReg chr8 #15628	0	0	1
15629	8	145,019,730	145,020,548	818	1	5.615	7.346	11.923	10	10	16	0	1	2	PLEC1, MIR661	30774, -692	in gene, upstream	ActReg chr8 #15629	0	0	1
15630	8	145,021,993	145,023,349	1,356	3	12.881	12.429	10.929	22	23	17	0	1	2	PLEC1, MIR661	28242, -3224	in gene, upstream	ActReg chr8 #15630	1	1	1
15631	8	145,023,356	145,025,118	1,762	2	8.836	13.127	9.418	17	24	20	1	1	2	PLEC1, MIR661	26676, -4790	in gene, upstream	ActReg chr8 #15631	0	1	1
15632	8	145,046,163	145,047,246	1,083	1	2.71	5.618	12.235	5	10	18	1	0	2	PLEC1, PARP10	4209, 13931	in gene, downstream	ActReg chr8 #15632	0	0	1
15633	8	145,048,862	145,049,663	801	3	10.84	13.52	11.48	17	28	15	1	1	2	PLEC1, PARP10	1651, 11373	in gene, downstream	ActReg chr8 #15633	1	1	1
15634	8	145,057,131	145,057,748	617	1	5.895	6.211	10.737	9	14	13	0	2	3	PLEC1, PARP10, GRINA	-6526, 3196, -6787	upstream, in gene, upstream	ActReg chr8 #15634	0	0	1
15635	8	145,059,859	145,060,392	533	1	6.176	6.824	12	10	11	17	0	2	3	PLEC1, PARP10, GRINA	-9212, 510, -4101	upstream, in gene, upstream	ActReg chr8 #15635	0	0	1
15636	8	145,112,946	145,113,718	772	1	4.458	5.708	11.708	8	9	18	1	1	2	LOC392275, OPLAH	9309, 2252	downstream, in gene	ActReg chr8 #15636	0	0	1
15637	8	145,118,538	145,119,146	608	1	5.842	1.077	12.21	13	2	19	0	1	1	OPLAH	-3,258	upstream	ActReg chr8 #15637	0	0	1
15638	8	145,133,019	145,134,330	1,311	3	11.951	13.146	11.902	18	22	21	1	2	2	EXOSC4, GPAA1	152, -3850	in gene, upstream	ActReg chr8 #15638	1	1	1
15639	8	145,140,503	145,141,159	656	1	5	4.762	13.048	8	11	23	0	0	3	EXOSC4, GPAA1, CYC1	7309, 3307, -9129	downstream, in gene, upstream	ActReg chr8 #15639	0	0	1
15640	8	145,158,228	145,160,193	1,965	3	14.129	17.71	7.79	36	40	20	1	4	5	CYC1, LOC100507382, SHARPIN, MAF1, KIAA1875	9250, -7267, -70, -95, 3419	downstream, upstream, upstream, upstream, upstream	ActReg chr8 #15640	1	1	1
15641	8	145,162,585	145,163,293	708	1	3.312	3	11.864	6	6	17	1	2	3	SHARPIN, MAF1, KIAA1875	-3799, 3634, 310	upstream, downstream, in gene	ActReg chr8 #15641	0	0	1
15642	8	145,166,226	145,166,804	578	1	4.389	3	14.722	7	5	23	0	1	3	SHARPIN, MAF1, KIAA1875	-7375, 7210, 3886	upstream, downstream, in gene	ActReg chr8 #15642	0	0	1
15643	8	145,244,318	145,244,851	533	1	8.647	7.294	12.059	13	12	21	0	0	1	HEATR7A	41,665	in gene	ActReg chr8 #15643	0	0	1
15644	8	145,275,707	145,276,087	380	1	4.167	5.083	11.75	7	7	15	0	0	1	HEATR7A	72,978	in gene	ActReg chr8 #15644	0	0	1
15645	8	145,519,999	145,520,389	390	1	3.333	3.692	12.385	6	6	18	0	1	2	BOP1, HSF1	-5074, 4924	upstream, in gene	ActReg chr8 #15645	0	0	1
15646	8	145,534,789	145,535,311	522	1	2.375	3.688	12.188	4	5	15	0	0	2	HSF1, DGAT1	19780, 15517	in gene, downstream	ActReg chr8 #15646	0	0	1
15647	8	145,536,494	145,537,145	651	1	6.8	5.85	14.55	9	9	24	0	0	2	HSF1, DGAT1	21549, 13748	in gene, downstream	ActReg chr8 #15647	0	0	1
15648	8	145,539,846	145,540,869	1,023	1	6.25	7.125	14	9	10	21	0	0	2	HSF1, DGAT1	25087, 10210	downstream, in gene	ActReg chr8 #15648	0	0	1
15649	8	145,550,233	145,551,121	888	2	12.857	13	6.577	23	20	12	1	1	2	DGAT1, SCRT1	-110, 9266	upstream, downstream	ActReg chr8 #15649	1	1	0
15650	8	145,554,587	145,555,008	421	1	3.214	3.643	11.857	6	6	17	0	1	2	DGAT1, SCRT1	-4230, 5146	upstream, in gene	ActReg chr8 #15650	0	0	1
15651	8	145,558,535	145,560,218	1,683	1	7.962	12.788	6.692	16	18	15	1	1	2	DGAT1, SCRT1	-8809, 567	upstream, in gene	ActReg chr8 #15651	0	1	0
15652	8	145,581,118	145,581,722	604	1	7.5	8.368	12.947	12	13	18	1	3	3	C8ORFK29, FBXL6, GPR172A	-2915, 712, -805	upstream, in gene, upstream	ActReg chr8 #15652	0	0	1
15653	8	145,581,902	145,582,737	835	1	11.423	13.192	6.826	25	20	13	1	3	3	C8ORFK29, FBXL6, GPR172A	-3814, -187, 84	upstream, upstream, in gene	ActReg chr8 #15653	0	1	0
15654	8	145,597,234	145,597,928	694	1	6.455	11.454	6.455	8	16	11	1	1	1	ADCK5	-150	upstream	ActReg chr8 #15654	0	1	0
15655	8	145,620,793	145,621,577	784	1	3.72	3.64	13.8	7	6	21	1	1	4	ADCK5, CPSF1, MIR939, MIR1234	23454, 13548, -1740, 4374	downstream, in gene, upstream, downstream	ActReg chr8 #15655	0	0	1
15656	8	145,622,330	145,622,704	374	1	3.5	5.083	12.167	4	9	16	0	1	4	ADCK5, CPSF1, MIR939, MIR1234	24786, 12216, -3072, 3042	downstream, in gene, upstream, downstream	ActReg chr8 #15656	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GensCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15657	8	145,622,778	145,623,292	514	1	4.438	4.062	12.125	8	7	18	1	2	4	ADCK5, CPSF1, MIR939, MIR1234	25304, 11698, -3590, 2524	downstream, in gene, upstream, downstream	ActReg chr8 #15657	0	0	1
15658	8	145,634,958	145,635,468	510	1	7.375	8.75	10.75	13	11	16	1	1	3	CPSF1, MIR1234, SLC39A4	-480, -9654, 7060	upstream, upstream, downstream	ActReg chr8 #15658	0	0	1
15659	8	145,640,214	145,640,832	618	1	2.55	6.2	14.3	4	10	24	0	2	3	CPSF1, SLC39A4, VPS28	-5790, 1750, 13404	upstream, in gene, downstream	ActReg chr8 #15659	0	0	1
15660	8	145,649,068	145,649,623	555	1	5.647	3.812	12.941	8	9	20	1	1	3	SLC39A4, VPS28, NFKBIL2	-7072, 4582, 20467	upstream, in gene, downstream	ActReg chr8 #15660	0	0	1
15661	8	145,653,212	145,654,266	1,054	3	17.454	13.879	12.303	37	34	27	1	1	2	VPS28, NFKBIL2	188, 16073	in gene, downstream	ActReg chr8 #15661	1	1	1
15662	8	145,660,881	145,661,551	670	1	4.048	4.143	10.905	6	9	16	0	1	2	VPS28, NFKBIL2	-7289, 8596	upstream, in gene	ActReg chr8 #15662	0	0	1
15663	8	145,665,513	145,666,043	530	1	2.133	3.062	11.688	4	6	14	0	0	2	NFKBIL2, CYHR1	4034, 25253	in gene, downstream	ActReg chr8 #15663	0	0	1
15664	8	145,668,703	145,669,472	769	1	3.48	4.2	10.8	5	9	15	1	1	2	NFKBIL2, CYHR1	725, 21944	in gene, downstream	ActReg chr8 #15664	0	0	1
15665	8	145,675,795	145,676,506	711	1	5.545	4.773	12.364	8	9	15	1	1	2	NFKBIL2, CYHR1	-6338, 14881	upstream, in gene	ActReg chr8 #15665	0	0	1
15666	8	145,684,392	145,684,969	577	1	4.333	6.222	11.611	7	9	15	0	1	2	CYHR1, KIFC2	6351, -7058	in gene, upstream	ActReg chr8 #15666	0	0	1
15667	8	145,685,228	145,685,904	676	1	4.571	5.053	11.619	9	10	16	0	1	2	CYHR1, KIFC2	5465, -6172	in gene, upstream	ActReg chr8 #15667	0	0	1
15668	8	145,690,537	145,690,926	389	1	6.75	11.333	7.333	10	17	11	1	2	3	CYHR1, KIFC2, FOXH1	300, -1007, 10987	in gene, upstream, downstream	ActReg chr8 #15668	0	1	0
15669	8	145,695,054	145,695,415	361	1	5.636	4.636	11.546	8	7	17	0	1	3	CYHR1, KIFC2, FOXH1	-4203, 3496, 6484	upstream, in gene, downstream	ActReg chr8 #15669	0	0	1
15670	8	145,733,874	145,735,565	1,691	1	10.207	13.057	8.731	18	23	16	1	1	5	PPP1R16A, GPT, MFSD3, RECQL4, LRRC14	12610, 5254, 167, 8491, -8672	downstream, downstream, in gene, downstream, upstream	ActReg chr8 #15670	0	1	0
15671	8	145,737,329	145,738,680	1,351	1	4.341	7.976	13.905	10	11	19	1	1	6	PPP1R16A, GPT, MFSD3, RECQL4, LRRC14, LRRC24	15895, 8539, 3452, 5206, -5387, 14412	downstream, downstream, downstream, in gene, upstream, downstream	ActReg chr8 #15671	0	0	1
15672	8	145,747,774	145,748,205	431	1	9.429	9.643	12.214	13	18	22	1	1	5	RECQL4, LRRC14, LRRC24, C8orf82, KIAA1688	-4779, 4598, 4427, 6469, 90902	upstream, in gene, in gene, downstream, downstream	ActReg chr8 #15672	0	0	1
15673	8	145,751,547	145,752,354	807	1	4.875	8.125	10.562	7	11	16	1	2	5	RECQL4, LRRC14, LRRC24, C8orf82, KIAA1688	-8890, 8709, 316, 2358, 86791	upstream, downstream, in gene, in gene, downstream	ActReg chr8 #15673	0	0	1
15674	8	145,754,092	145,754,706	614	1	11.737	9.263	4.111	20	14	7	1	2	4	LRRC14, LRRC24, C8orf82, KIAA1688	11008, -1983, 59, 84492	downstream, upstream, in gene, downstream	ActReg chr8 #15674	1	0	0
15675	8	145,980,645	145,981,392	747	3	10.696	11	9.043	18	18	16	1	1	1	ZNF251	-48	upstream	ActReg chr8 #15675	1	1	1
15676	8	146,012,051	146,013,038	987	2	8.226	11.548	12.226	14	17	25	1	1	2	ZNF34, RPL8	181, 5261	in gene, downstream	ActReg chr8 #15676	0	1	1
15677	8	146,017,088	146,018,513	1,425	2	10.2	12.644	8.044	16	22	15	1	3	3	ZNF34, RPL8, ZNF517	-5075, 5, -6461	upstream, in gene, upstream	ActReg chr8 #15677	1	1	0
15678	8	146,052,695	146,053,397	702	2	10.4	14.682	5.5	18	27	10	1	3	3	LOC100130027, LOC100129596, ZNF7	-621, -6897, 143	upstream, upstream, in gene	ActReg chr8 #15678	1	1	0
15679	8	146,078,025	146,078,859	834	2	11.615	11.269	7.231	16	18	13	1	1	2	ZNF7, COMMD5	25539, 490	downstream, in gene	ActReg chr8 #15679	1	1	0
15680	8	146,095,261	146,095,519	258	1	3.5	5.5	10	5	10	12	0	0	1	ZNF250	31,456	downstream	ActReg chr8 #15680	0	0	1
15681	8	146,126,423	146,127,853	1,430	2	12.2	14.6	10.378	24	28	17	1	1	1	ZNF250	-292	upstream	ActReg chr8 #15681	1	1	0
15682	8	146,227,878	146,228,522	644	1	8.95	12.4	6.6	14	19	13	1	1	1	C8orf77	3	in gene	ActReg chr8 #15682	0	1	0
15683	8	146,277,748	146,278,185	437	1	8.643	12.429	6	15	21	8	1	1	1	C8orf33	142	in gene	ActReg chr8 #15683	0	1	0
15684	9	694,285	695,332	1,047	1	11.939	15.273	3.188	16	25	8	0	0	1	KANK1	190,105	in gene	ActReg chr9 #15684	0	1	0
15685	9	712,693	713,247	554	1	6.471	12.235	6.529	10	19	10	0	0	1	KANK1	208,267	in gene	ActReg chr9 #15685	0	1	0
15686	9	738,261	739,141	880	1	8	11.464	4.036	13	17	6	0	0	1	KANK1	233,998	in gene	ActReg chr9 #15686	0	1	0
15687	9	751,091	752,378	1,287	1	12.475	9.8	2.97	18	18	5	0	0	1	KANK1	247,031	downstream	ActReg chr9 #15687	1	0	0
15688	9	755,530	756,482	952	2	12.933	14.867	5	22	25	9	0	0	1	KANK1	251,303	downstream	ActReg chr9 #15688	1	1	0
15689	9	842,395	842,833	438	1	1.833	3.75	10.643	3	5	16	1	1	1	DMRT1	924	in gene	ActReg chr9 #15689	0	0	1
15690	9	969,362	969,771	409	1	5.692	2.692	10.923	7	4	15	1	1	2	DMRT1, DMRT3	127876, -7398	downstream, upstream	ActReg chr9 #15690	0	0	1
15691	9	969,834	970,320	486	1	4.667	6.6	12.733	6	10	18	1	1	2	DMRT1, DMRT3	128387, -6887	downstream, upstream	ActReg chr9 #15691	0	0	1
15692	9	970,527	971,125	598	1	4.263	8.421	14.263	7	11	23	1	1	2	DMRT1, DMRT3	129136, -6138	downstream, upstream	ActReg chr9 #15692	0	0	1
15693	9	1,045,534	1,046,011	477	1	5.4	4.533	12	7	7	19	1	1	1	DMRT2	-4,574	upstream	ActReg chr9 #15693	0	0	1
15694	9	2,014,652	2,015,748	1,096	1	9.171	11.486	5.794	15	18	14	1	1	1	SMARCA2	-142	upstream	ActReg chr9 #15694	0	1	0
15695	9	2,015,767	2,017,983	2,216	2	8.116	14.232	8.652	15	19	19	1	1	1	SMARCA2	1,533	in gene	ActReg chr9 #15695	0	1	1
15696	9	2,241,643	2,242,714	1,071	2	13.273	18.091	5.576	35	43	10	2	0	0				ActReg chr9 #15696	1	1	0
15697	9	2,260,689	2,261,295	606	1	7.105	11.105	3.632	9	18	5	0	0	0				ActReg chr9 #15697	0	1	0
15698	9	2,353,883	2,354,293	410	1	1.846	3.308	11.538	4	4	16	0	0	0				ActReg chr9 #15698	0	0	1
15699	9	2,559,407	2,560,252	845	1	9.385	12.5	3.654	14	16	7	0	0	1	FLJ35024	62,544	in gene	ActReg chr9 #15699	0	1	0
15700	9	2,574,148	2,574,608	460	1	10.5	6.429	2.769	13	9	5	0	0	1	FLJ35024	47,995	in gene	ActReg chr9 #15700	1	0	0
15701	9	2,655,212	2,656,118	906	1	8.429	12.75	2.353	13	21	5	0	0	1	VLDLR	33,872	downstream	ActReg chr9 #15701	0	1	0
15702	9	2,843,827	2,844,566	739	3	11.174	12.391	8.522	17	22	19	1	1	1	KIAA0020	-66	upstream	ActReg chr9 #15702	1	1	1
15703	9	2,933,649	2,934,462	813	1	2.56	5.045	14.16	5	9	22	1	0	0				ActReg chr9 #15703	0	0	1
15704	9	3,525,901	3,527,460	1,559	3	14.061	16.143	10.469	21	32	21	1	1	1	RFX3	-697	upstream	ActReg chr9 #15704	1	1	1
15705	9	3,862,950	3,863,675	725	1	9.318	12.364	1.923	16	16	3	0	0	1	GLIS3	456,723	in gene	ActReg chr9 #15705	0	1	0
15706	9	3,906,331	3,907,413	1,082	2	10.823	9.529	4.111	17	14	7	0	0	2	GLIS3, C9orf70	393163, 8226	in gene, downstream	ActReg chr9 #15706	1	1	0
15707	9	3,932,332	3,932,972	640	1	11.6	7.55	1.2	18	9	2	0	0	1	GLIS3	367,383	in gene	ActReg chr9 #15707	1	0	0
15708	9	3,968,754	3,969,322	568	1	10.111	12.056	2.444	18	20	4	0	0	1	GLIS3	330,997	in gene	ActReg chr9 #15708	0	1	0
15709	9	4,084,326	4,084,925	599	1	10.333	14.056	2.471	14	26	4	0	0	1	GLIS3	215,410	in gene	ActReg chr9 #15709	0	1	0
15710	9	4,238,363	4,239,059	696	1	7.955	11.5	1	16	19	1	0	0	1	GLIS3	61,324	in gene	ActReg chr9 #15710	0	1	0
15711	9	4,261,401	4,262,015	614	1	10.263	5.158	4.722	15	7	9	0	0	1	GLIS3	38,327	in gene	ActReg chr9 #15711	1	0	0
15712	9	4,290,456	4,290,910	454	1	5.571	11.429	3	8	16	5	0	1	2	GLIS3, LOC100287493	9352, -3541	in gene, upstream	ActReg chr9 #15712	0	1	0
15713	9	4,293,426	4,294,171	745	2	11.435	12.565	2.227	18	22	4	0	1	2	GLIS3, LOC100287493	6237, -426	in gene, upstream	ActReg chr9 #15713	1	1	0
15714	9	4,296,978	4,298,178	1,200	1	9.5	13.053	7.139	17	24	18	1	1	2	GLIS3, LOC100287493	2457, 3354	in gene, in gene	ActReg chr9 #15714	0	1	0
15715	9	4,298,187	4,299,426	1,239	2	10.154	11.026	8.615	19	16	14	1	1	2	GLIS3, LOC100287493	1229, 4582	in gene, in gene	ActReg chr9 #15715	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15716	9	4,299,531	4,300,298	767	1	7.917	12.5	5.917	13	25	12	1	1	2	GLIS3, LOC100287493	121, 5690	in gene, in gene	ActReg chr9 #15716	0	1	0
15717	9	4,334,291	4,334,970	679	2	11.381	10.952	7.857	15	19	12	0	0	0				ActReg chr9 #15717	1	1	0
15718	9	4,489,912	4,491,590	1,678	2	14.396	14.925	9	29	26	18	2	1	1	SLC1A1	324	in gene	ActReg chr9 #15718	1	1	0
15719	9	4,530,186	4,531,143	957	1	8.067	12.3	3.414	13	21	6	0	0	1	SLC1A1	40,237	in gene	ActReg chr9 #15719	0	1	0
15720	9	4,661,960	4,663,299	1,339	3	12.048	11.929	10.634	18	20	19	1	1	2	C9orf68, PPAPDC2	4045, 331	in gene, in gene	ActReg chr9 #15720	1	1	1
15721	9	4,666,162	4,666,690	528	1	7.938	14.353	4.294	13	23	7	0	1	2	C9orf68, PPAPDC2	248, 4128	in gene, downstream	ActReg chr9 #15721	0	1	0
15722	9	4,679,136	4,680,307	1,171	3	11.405	13.054	9.622	20	20	18	1	1	1	CDC37L1	155	in gene	ActReg chr9 #15722	1	1	1
15723	9	4,740,629	4,741,581	952	2	11.567	13.967	5.933	17	26	13	1	1	1	AK3	122	in gene	ActReg chr9 #15723	1	1	0
15724	9	4,792,235	4,793,573	1,338	1	13.524	11.476	7.19	24	17	13	1	1	1	RCL1	70	in gene	ActReg chr9 #15724	1	0	0
15725	9	4,804,040	4,805,051	1,011	1	5.774	4.806	13.419	7	8	22	1	0	1	RCL1	11,711	in gene	ActReg chr9 #15725	0	0	1
15726	9	4,984,289	4,985,652	1,363	3	16.191	14.524	8.463	27	23	20	1	1	1	JAK2	-275	upstream	ActReg chr9 #15726	1	1	1
15727	9	5,111,706	5,112,322	616	1	5.2	5.15	14.35	7	7	21	1	0	1	JAK2	126,769	in gene	ActReg chr9 #15727	0	0	1
15728	9	5,437,356	5,438,214	858	1	9.889	12.963	8.407	15	25	12	1	1	1	C9orf46	75	in gene	ActReg chr9 #15728	0	1	0
15729	9	5,440,818	5,441,609	791	1	13.08	9.16	1.947	28	19	5	0	1	2	C9orf46, CD274	-3353, -9290	upstream, upstream	ActReg chr9 #15729	1	0	0
15730	9	5,450,194	5,450,987	793	3	12	12.182	7.19	18	28	18	1	1	1	CD274	87	in gene	ActReg chr9 #15730	1	1	1
15731	9	5,628,613	5,629,011	398	1	11.583	11.333	11.667	17	15	17	1	1	1	KIAA1432	-515	upstream	ActReg chr9 #15731	0	0	1
15732	9	5,832,313	5,833,336	1,023	1	12.5	11.219	3.688	23	18	8	1	1	1	ERMP1	257	in gene	ActReg chr9 #15732	1	0	0
15733	9	6,015,159	6,016,164	1,005	1	9.594	15.25	5.962	17	28	10	0	2	2	KIAA2026, RANBP6	-7658, -21	upstream, upstream	ActReg chr9 #15733	0	1	0
15734	9	6,102,218	6,103,456	1,238	1	11.41	18.615	4.513	27	43	9	0	0	0				ActReg chr9 #15734	0	1	0
15735	9	6,364,158	6,364,808	650	1	12.095	7.524	2.5	16	13	4	0	0	0				ActReg chr9 #15735	1	0	0
15736	9	6,412,727	6,413,484	757	1	12.042	12.083	8.708	17	18	13	1	1	1	UHRF2	-46	upstream	ActReg chr9 #15736	1	0	0
15737	9	6,538,199	6,539,020	821	2	12.115	9.923	4.24	24	19	8	0	0	1	GLDC	107,083	in gene	ActReg chr9 #15737	1	1	0
15738	9	6,566,896	6,567,677	781	1	13.042	8.625	1.1	16	13	2	0	0	1	GLDC	78,406	in gene	ActReg chr9 #15738	1	0	0
15739	9	6,645,455	6,646,294	839	1	13.077	8.462	7.318	27	15	12	1	1	1	GLDC	-182	upstream	ActReg chr9 #15739	1	0	0
15740	9	6,680,624	6,681,985	1,361	3	14.209	13.256	11.302	23	24	20	1	0	0				ActReg chr9 #15740	1	1	1
15741	9	6,703,729	6,704,354	625	1	9.35	6.5	15.9	13	10	25	1	0	0				ActReg chr9 #15741	0	0	1
15742	9	6,715,910	6,716,514	604	1	9.632	9.474	12.684	17	13	17	1	1	1	KDM4C	-4,651	upstream	ActReg chr9 #15742	0	0	1
15743	9	6,756,889	6,759,230	2,341	2	14.575	11.945	9.069	27	25	19	1	0	1	KDM4C	37,196	in gene	ActReg chr9 #15743	1	1	0
15744	9	7,266,808	7,268,047	1,239	1	8.821	13.333	5.513	13	21	13	0	0	0				ActReg chr9 #15744	0	1	0
15745	9	7,319,932	7,320,714	782	2	11.28	14.24	3.739	25	25	8	0	0	0				ActReg chr9 #15745	1	1	0
15746	9	7,799,509	7,800,006	497	1	7.875	12.875	5.875	12	21	10	1	1	1	C9orf123	42	in gene	ActReg chr9 #15746	0	1	0
15747	9	7,913,173	7,913,516	343	1	2.364	2.545	10.636	4	3	16	0	0	0				ActReg chr9 #15747	0	0	1
15748	9	8,643,587	8,644,080	493	1	3.214	3.6	12.533	6	6	17	0	0	1	PTPRD	1,968,890	in gene	ActReg chr9 #15748	0	0	1
15749	9	11,064,775	11,065,453	678	2	10.714	10.762	3.188	18	16	6	0	0	0				ActReg chr9 #15749	1	1	0
15750	9	11,472,059	11,472,458	399	1	3.615	3.462	10.615	5	7	16	0	0	0				ActReg chr9 #15750	0	0	1
15751	9	11,618,141	11,618,866	725	1	2.684	5	11.87	6	9	17	1	0	0				ActReg chr9 #15751	0	0	1
15752	9	11,928,830	11,929,147	317	1	1	2.6	11	1	4	15	0	0	0				ActReg chr9 #15752	0	0	1
15753	9	12,708,513	12,709,141	628	1	7.105	11.79	1	15	17	1	0	0	2	TYRP1, LOC100506267	15441, 105545	in gene, in gene	ActReg chr9 #15753	0	1	0
15754	9	12,774,720	12,776,943	2,223	2	13.714	13.929	6.638	31	30	14	1	1	2	LOC100506267, C9orf150	38541, 819	in gene, in gene	ActReg chr9 #15754	1	1	0
15755	9	12,784,281	12,785,003	722	1	10.174	14.217	1.867	17	31	3	0	0	2	LOC100506267, C9orf150	29730, 9630	in gene, in gene	ActReg chr9 #15755	0	1	0
15756	9	12,817,404	12,818,129	725	2	10.522	11.13	6.227	18	19	14	0	1	2	LOC100506267, C9orf150	-3394, 42754	upstream, in gene	ActReg chr9 #15756	1	1	0
15757	9	12,859,337	12,860,102	765	1	11.125	8.208	2.478	14	13	4	0	0	0				ActReg chr9 #15757	1	0	0
15758	9	12,933,908	12,934,494	586	1	5.667	12.389	3.222	10	17	5	0	0	0				ActReg chr9 #15758	0	1	0
15759	9	13,082,840	13,083,328	488	1	9.562	2.8	3.571	18	5	5	0	0	0				ActReg chr9 #15759	1	0	0
15760	9	13,278,147	13,278,944	797	1	12.12	11.28	9.04	18	16	13	1	0	0				ActReg chr9 #15760	1	0	0
15761	9	13,942,596	13,943,332	736	1	9.304	13.304	1.5	17	26	3	0	0	0				ActReg chr9 #15761	0	1	0
15762	9	14,238,095	14,238,630	535	1	8.824	14.294	1.733	14	25	3	0	0	1	NFIB	160,620	in gene	ActReg chr9 #15762	0	1	0
15763	9	14,277,810	14,278,742	932	1	8.724	11.207	2.9	14	18	5	0	0	1	NFIB	120,706	in gene	ActReg chr9 #15763	0	1	0
15764	9	14,322,113	14,323,258	1,145	2	16.029	23.8	5.129	40	52	12	1	0	1	NFIB	76,297	in gene	ActReg chr9 #15764	1	1	0
15765	9	14,693,126	14,694,056	930	2	9.345	14.655	5.786	17	31	10	1	1	1	ZDHHC21	-111	upstream	ActReg chr9 #15765	1	1	0
15766	9	14,993,060	14,993,558	498	1	8.267	7.933	14.133	13	10	24	0	0	0				ActReg chr9 #15766	0	0	1
15767	9	15,306,458	15,307,033	575	1	7.5	12.389	10.333	11	16	13	1	1	1	TTC39B	613	in gene	ActReg chr9 #15767	0	0	1
15768	9	15,422,212	15,423,465	1,253	3	12.667	14.974	10.256	28	30	17	1	1	1	SNAPC3	56	in gene	ActReg chr9 #15768	1	1	1
15769	9	15,510,385	15,511,630	1,245	3	10.462	14.872	6.949	25	30	15	1	1	1	PSIP1	-4	upstream	ActReg chr9 #15769	1	1	1
15770	9	15,552,531	15,553,910	1,379	2	12.163	11.326	7.326	21	18	12	1	1	1	C9orf93	123	in gene	ActReg chr9 #15770	1	1	0
15771	9	15,697,465	15,698,136	671	1	10.524	12.667	2.556	17	21	5	0	0	1	C9orf93	144,703	in gene	ActReg chr9 #15771	0	1	0
15772	9	16,111,603	16,112,789	1,186	2	11.892	14.811	2.103	26	23	4	0	0	0				ActReg chr9 #15772	1	1	0
15773	9	16,336,840	16,338,103	1,263	2	11.436	12.231	2.171	16	18	4	0	0	0				ActReg chr9 #15773	1	1	0
15774	9	16,367,920	16,368,623	703	1	8.955	13.273	4.1	12	27	8	0	0	0				ActReg chr9 #15774	0	1	0
15775	9	16,626,436	16,627,213	777	1	12.083	8.958	3.583	21	19	6	0	0	1	BNC2	243,962	in gene	ActReg chr9 #15775	1	0	0
15776	9	16,705,159	16,705,572	413	1	7.846	8.385	11.231	10	12	17	0	0	1	BNC2	165,421	in gene	ActReg chr9 #15776	0	0	1
15777	9	16,726,657	16,727,365	708	1	10.5	12.5	4.455	17	21	8	1	0	1	BNC2	143,775	in gene	ActReg chr9 #15777	0	1	0
15778	9	16,870,388	16,871,085	697	1	11.909	9.545	6.381	17	17	11	1	1	1	BNC2	50	in gene	ActReg chr9 #15778	1	0	0
15779	9	16,963,882	16,964,676	794	1	12.76	12.48	5.76	20	20	11	0	0	0				ActReg chr9 #15779	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15780	9	17,017,812	17,018,752	940	2	17.8	20.6	4.103	42	44	7	0	0	0				ActReg chr9 #15780	1	1	0
15781	9	17,134,242	17,135,887	1,645	3	12.686	11.118	12.118	18	26	32	1	1	1	CNTLN	26	in gene	ActReg chr9 #15781	1	1	1
15782	9	17,353,776	17,354,202	426	1	3.231	1.583	12	6	2	19	0	0	1	CNTLN	218,951	in gene	ActReg chr9 #15782	0	0	1
15783	9	17,744,660	17,745,249	589	2	10.21	13.947	3.684	19	26	8	0	0	1	SH3GL2	166,001	in gene	ActReg chr9 #15783	1	1	0
15784	9	18,268,320	18,268,893	573	1	10.333	8.556	1	19	16	1	0	0	0				ActReg chr9 #15784	1	0	0
15785	9	18,315,123	18,315,622	499	1	2.688	2.812	11.438	6	6	17	0	0	0				ActReg chr9 #15785	0	0	1
15786	9	18,393,053	18,394,088	1,035	2	18.849	15.485	2.043	44	32	5	0	0	0				ActReg chr9 #15786	1	1	0
15787	9	18,459,803	18,460,498	695	1	10.727	7.591	2.667	17	14	5	0	0	0				ActReg chr9 #15787	1	0	0
15788	9	18,776,627	18,777,666	1,039	1	4.303	4.758	12.909	7	9	21	1	0	1	ADAMTSL1	303,042	in gene	ActReg chr9 #15788	0	0	1
15789	9	19,032,707	19,033,238	531	1	5.812	7.933	12.438	8	13	19	0	1	1	FAM154A	284	in gene	ActReg chr9 #15789	0	0	1
15790	9	19,048,628	19,050,235	1,607	3	11.8	14.24	9.6	21	23	17	1	1	2	RRAGA, HAUS6	59, 53471	in gene, downstream	ActReg chr9 #15790	1	1	1
15791	9	19,102,678	19,103,294	616	1	10.21	16.895	8.368	20	30	13	1	1	1	HAUS6	-84	upstream	ActReg chr9 #15791	0	1	0
15792	9	19,126,963	19,128,041	1,078	2	11.382	11.882	13.853	17	23	20	1	1	1	PLIN2	71	in gene	ActReg chr9 #15792	0	1	1
15793	9	19,128,744	19,129,198	454	1	9.071	8.214	12.286	14	10	16	0	1	1	PLIN2	-1,398	upstream	ActReg chr9 #15793	0	0	1
15794	9	19,161,514	19,162,214	700	2	14.909	14.818	2.905	29	35	5	0	0	0				ActReg chr9 #15794	1	1	0
15795	9	19,230,649	19,231,301	652	1	9.81	8.333	16.333	15	11	27	1	0	0				ActReg chr9 #15795	0	0	1
15796	9	19,231,530	19,232,477	947	1	10.276	6.172	1.704	16	10	4	0	0	0				ActReg chr9 #15796	1	0	0
15797	9	19,379,663	19,380,941	1,278	3	18.15	16.175	14.05	36	35	33	1	1	2	DENND4C, RPS6	89553, -67	downstream, upstream	ActReg chr9 #15797	1	1	1
15798	9	19,408,101	19,409,546	1,445	2	7.311	12.911	8.267	12	24	17	1	1	1	ACER2	-102	upstream	ActReg chr9 #15798	0	1	1
15799	9	19,720,151	19,720,796	645	1	6.75	10.85	1.273	15	22	2	0	0	1	SLC24A2	68,118	in gene	ActReg chr9 #15799	0	1	0
15800	9	19,748,124	19,749,077	953	2	11.867	11.133	2.966	21	18	4	0	0	1	SLC24A2	39,991	in gene	ActReg chr9 #15800	1	1	0
15801	9	19,999,335	20,000,062	727	1	12.5	11.227	1.091	22	20	2	0	0	0				ActReg chr9 #15801	1	0	0
15802	9	20,033,365	20,034,111	746	1	13.304	7.304	1.75	20	11	2	0	0	0				ActReg chr9 #15802	1	0	0
15803	9	20,289,875	20,290,303	428	1	2.846	5.769	12.308	6	8	16	0	0	0				ActReg chr9 #15803	0	0	1
15804	9	20,558,168	20,559,196	1,028	1	10.875	7.219	1.091	22	15	2	0	0	1	MLLT3	63,832	in gene	ActReg chr9 #15804	1	0	0
15805	9	20,622,097	20,623,642	1,545	2	10.25	12.875	7.646	16	20	13	0	1	1	MLLT3	-355	upstream	ActReg chr9 #15805	1	1	0
15806	9	20,683,648	20,685,001	1,353	2	11.419	10.372	7	18	22	17	1	0	1	KIAA1797	26,015	in gene	ActReg chr9 #15806	1	1	0
15807	9	21,334,603	21,335,635	1,032	1	10.406	15.375	6.844	21	26	14	1	1	1	KLHL9	310	in gene	ActReg chr9 #15807	0	1	0
15808	9	21,454,888	21,455,785	897	1	6.5	10.536	3.714	10	17	9	0	0	1	LOC554202	104,361	in gene	ActReg chr9 #15808	0	1	0
15809	9	21,505,266	21,505,941	675	2	12.191	12.809	2.632	25	27	4	0	0	2	LOC554202, MIR31	54094, 6581	in gene, downstream	ActReg chr9 #15809	1	1	0
15810	9	21,549,435	21,550,004	569	1	7.333	10.944	1.75	11	19	2	0	0	1	LOC554202	9,978	in gene	ActReg chr9 #15810	0	1	0
15811	9	21,559,303	21,559,894	591	2	8.389	11	10.278	13	16	15	1	1	1	LOC554202	99	in gene	ActReg chr9 #15811	0	1	1
15812	9	21,591,429	21,592,329	900	2	10.893	13.821	2.318	21	26	4	0	0	0				ActReg chr9 #15812	1	1	0
15813	9	21,684,714	21,685,395	681	1	13.429	10.571	3.81	23	17	7	0	0	0				ActReg chr9 #15813	1	0	0
15814	9	21,688,193	21,689,063	870	1	10.518	7.296	1.842	16	12	4	0	0	0				ActReg chr9 #15814	1	0	0
15815	9	21,695,925	21,696,718	793	1	4.28	4.76	11.56	7	10	17	1	0	0				ActReg chr9 #15815	0	0	1
15816	9	21,801,983	21,803,102	1,119	2	11.543	13.371	6.882	23	34	12	1	1	1	MTAP	-93	upstream	ActReg chr9 #15816	1	1	0
15817	9	21,836,363	21,837,242	879	1	14.296	11.259	4.259	27	18	7	0	0	1	MTAP	34,167	in gene	ActReg chr9 #15817	1	0	0
15818	9	22,147,810	22,148,682	872	1	12.037	9.593	2.538	19	19	4	0	0	0				ActReg chr9 #15818	1	0	0
15819	9	22,154,013	22,154,403	390	1	5.154	5.231	9.692	8	7	15	1	0	0				ActReg chr9 #15819	0	0	1
15820	9	22,216,710	22,217,536	826	1	8.731	12.615	3.308	14	18	7	0	0	0				ActReg chr9 #15820	0	1	0
15821	9	22,342,455	22,342,950	495	1	11.188	7.562	1.4	16	10	3	0	0	0				ActReg chr9 #15821	1	0	0
15822	9	22,446,741	22,447,265	524	1	8.824	12.823	16	15	19	28	1	1	1	DMRTA1	163	in gene	ActReg chr9 #15822	0	0	1
15823	9	23,452,144	23,452,603	459	1	3.857	2.143	12.071	6	4	18	0	0	0				ActReg chr9 #15823	0	0	1
15824	9	23,621,050	23,621,786	736	1	12.478	9.652	3.261	20	16	6	0	0	0				ActReg chr9 #15824	1	0	0
15825	9	23,824,080	23,827,014	2,934	2	15.924	20.489	4.329	50	64	11	0	1	1	ELAVL2	516	in gene	ActReg chr9 #15825	1	1	0
15826	9	23,829,340	23,830,288	948	2	14.133	10.833	3	29	19	4	0	1	1	ELAVL2	-3,751	upstream	ActReg chr9 #15826	1	1	0
15827	9	24,135,018	24,135,480	462	1	3.538	2.778	13.071	6	5	18	0	0	0				ActReg chr9 #15827	0	0	1
15828	9	25,060,868	25,061,397	529	1	2.562	3.812	10.438	4	6	17	0	0	0				ActReg chr9 #15828	0	0	1
15829	9	25,677,197	25,678,729	1,532	3	11.021	12.979	11.744	16	22	31	1	1	1	TUSC1	893	in gene	ActReg chr9 #15829	1	1	1
15830	9	25,700,958	25,701,323	365	1	2.417	10.5	5.333	4	15	9	0	0	0				ActReg chr9 #15830	0	1	0
15831	9	26,747,258	26,748,064	806	2	9.808	9.923	1.84	16	14	4	0	0	0				ActReg chr9 #15831	1	1	0
15832	9	26,748,164	26,749,113	949	1	7.966	9.828	2.273	14	16	4	0	0	0				ActReg chr9 #15832	0	1	0
15833	9	26,892,022	26,893,191	1,169	3	14.919	17.378	12.758	25	36	30	1	1	1	C9orf82	220	in gene	ActReg chr9 #15833	1	1	1
15834	9	26,946,674	26,947,889	1,215	3	15.447	18.868	9.579	24	36	21	1	2	2	PLAA, IFT74	187, 244	in gene, in gene	ActReg chr9 #15834	1	1	1
15835	9	26,955,694	26,957,039	1,345	2	10.524	12.309	4.786	20	17	12	1	0	2	PLAA, IFT74	-8898, 9329	upstream, in gene	ActReg chr9 #15835	1	1	0
15836	9	27,094,491	27,095,463	972	1	8.677	9.613	2.643	19	18	5	0	0	0				ActReg chr9 #15836	0	1	0
15837	9	27,124,900	27,126,251	1,351	2	12.833	12.548	2.548	25	33	7	0	0	1	TEK	16,428	in gene	ActReg chr9 #15837	1	1	0
15838	9	27,154,622	27,155,455	833	1	7.769	11.077	1.182	12	16	2	0	0	1	TEK	45,891	in gene	ActReg chr9 #15838	0	1	0
15839	9	27,194,276	27,195,022	746	1	9.522	14.652	3.565	22	30	7	0	0	1	TEK	85,502	in gene	ActReg chr9 #15839	0	1	0
15840	9	27,227,116	27,227,739	623	1	11.263	5.895	2.211	17	9	4	0	0	1	TEK	118,280	in gene	ActReg chr9 #15840	1	0	0
15841	9	27,572,518	27,573,421	903	2	5	9.929	9.786	11	19	17	1	1	1	C9orf72	873	in gene	ActReg chr9 #15841	0	1	1
15842	9	27,573,528	27,574,305	777	2	10	10.2	4.421	19	16	6	2	1	1	C9orf72	-74	upstream	ActReg chr9 #15842	1	1	0
15843	9	27,715,696	27,716,205	509	1	2.312	3.688	11.312	3	7	16	0	0	0				ActReg chr9 #15843	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15844	9	28,149,691	28,149,981	290	1	1	2.333	11	1	3	13	0	0	1	LINGO2	569,467	in gene	ActReg chr9 #15844	0	0	1
15845	9	29,213,424	29,214,507	1,083	1	9.529	12.853	3.788	22	21	9	1	0	0				ActReg chr9 #15845	0	1	0
15846	9	29,564,588	29,565,004	416	1	11.769	8.538	2	15	11	2	0	0	0				ActReg chr9 #15846	1	0	0
15847	9	29,810,443	29,810,788	345	1	1.636	4.545	9.909	2	7	15	0	0	0				ActReg chr9 #15847	0	0	1
15848	9	30,574,651	30,575,055	404	1	10.154	9.231	8.615	14	11	14	0	0	0				ActReg chr9 #15848	1	0	0
15849	9	31,321,226	31,321,860	634	1	2.45	2.789	11.8	8	6	16	0	0	0				ActReg chr9 #15849	0	0	1
15850	9	32,384,324	32,385,103	779	1	12.833	11.333	5.167	19	17	10	1	1	1	ACO1	112	in gene	ActReg chr9 #15850	1	0	0
15851	9	32,550,772	32,551,129	357	1	4.818	8.818	10.182	6	12	14	1	2	3	TOPORS, LOC100129250, NDUFB6	1672, -192, 22232	in gene, upstream, downstream	ActReg chr9 #15851	0	0	1
15852	9	32,552,104	32,552,740	636	2	11.4	10.8	8.25	20	19	13	1	2	3	TOPORS, LOC100129250, NDUFB6	200, 1280, 20760	in gene, in gene, downstream	ActReg chr9 #15852	1	1	0
15853	9	32,572,931	32,573,550	619	1	12.842	11.368	5.053	22	21	10	1	1	1	NDUFB6	-58	upstream	ActReg chr9 #15853	1	0	0
15854	9	32,635,857	32,636,250	393	1	2.222	3.889	10.333	3	5	18	0	1	1	TAF1L	-386	upstream	ActReg chr9 #15854	0	0	1
15855	9	33,001,171	33,001,968	797	2	11.96	9.4	10.12	20	13	17	1	1	1	APTX	57	in gene	ActReg chr9 #15855	1	0	1
15856	9	33,024,890	33,025,681	791	3	11.12	11.64	12.64	21	19	21	1	1	1	DNAJA1	76	in gene	ActReg chr9 #15856	1	1	1
15857	9	33,044,197	33,044,515	318	1	9.2	10.8	11.6	12	14	16	1	0	2	DNAJA1, SMU1	19147, 32358	downstream, in gene	ActReg chr9 #15857	0	0	1
15858	9	33,076,207	33,077,060	853	2	12.074	12.778	6.852	22	25	15	1	1	1	SMU1	81	in gene	ActReg chr9 #15858	1	1	0
15859	9	33,166,730	33,167,261	531	1	8.438	12.938	11.375	14	18	18	1	1	1	B4GALT1	361	in gene	ActReg chr9 #15859	0	0	1
15860	9	33,233,641	33,234,787	1,146	2	11.306	14.667	7.361	23	33	12	0	1	1	SPINK4	-5,982	upstream	ActReg chr9 #15860	1	1	0
15861	9	33,290,002	33,290,934	932	2	16.379	15.138	8.931	36	34	12	1	1	2	CHMP5, NFX1	25591, 50	downstream, in gene	ActReg chr9 #15861	1	1	0
15862	9	33,510,835	33,511,300	465	1	9.267	7.933	11.733	14	13	20	1	0	0				ActReg chr9 #15862	0	0	1
15863	9	33,523,297	33,524,329	1,032	2	8.875	10.375	10.062	17	19	18	1	1	1	ANKRD18B	-114	upstream	ActReg chr9 #15863	0	1	1
15864	9	34,048,513	34,049,750	1,237	2	11.053	13.184	7.211	19	25	18	1	1	1	UBAP2	-184	upstream	ActReg chr9 #15864	1	1	0
15865	9	34,126,207	34,127,097	890	1	7.167	11.393	6.821	12	14	13	1	1	1	DCAF12	119	in gene	ActReg chr9 #15865	0	1	0
15866	9	34,370,863	34,371,699	836	1	3.238	6.077	13.5	9	14	17	1	0	2	KIAA1161, C9orf24	5613, 26568	in gene, downstream	ActReg chr9 #15866	0	0	1
15867	9	34,412,825	34,413,855	1,030	2	14.5	12.156	3.259	29	30	8	0	0	1	C9orf25	45,228	in gene	ActReg chr9 #15867	1	1	0
15868	9	34,430,614	34,431,361	747	2	8.583	11.583	3.792	19	21	9	0	0	1	C9orf25	27,581	in gene	ActReg chr9 #15868	1	1	0
15869	9	34,458,272	34,458,950	678	2	14.136	10.273	4.095	38	20	8	1	2	2	C9orf25, DNAI1	-43, -200	upstream, upstream	ActReg chr9 #15869	1	1	0
15870	9	34,493,533	34,494,907	1,374	2	14.814	14.581	4.683	33	36	11	0	0	1	DNAI1	35,409	in gene	ActReg chr9 #15870	1	1	0
15871	9	34,590,982	34,591,531	549	1	2.412	5.941	11.823	5	9	18	1	1	2	CNTFR, LOC415056	-1534, 23246	upstream, downstream	ActReg chr9 #15871	0	0	1
15872	9	34,637,046	34,638,166	1,120	2	11.286	14.514	10.171	20	23	21	1	1	3	ARID3C, SIGMAR1, GALT	-9595, 162, -9029	upstream, in gene, upstream	ActReg chr9 #15872	0	1	1
15873	9	34,646,262	34,647,058	796	2	10.12	10.76	8.2	22	14	17	1	2	3	SIGMAR1, GALT, IL11RA	-8892, 25, -5522	upstream, in gene, upstream	ActReg chr9 #15873	0	1	1
15874	9	34,983,677	34,984,643	966	2	11.161	15.194	3.1	25	30	7	0	1	2	KIAA1045, DNAJB5	25968, -5565	downstream, upstream	ActReg chr9 #15874	1	1	0
15875	9	34,990,178	34,990,593	415	1	5	9.308	12.154	8	15	18	0	1	2	KIAA1045, DNAJB5	32193, 660	downstream, in gene	ActReg chr9 #15875	0	0	1
15876	9	35,071,735	35,072,876	1,141	2	11.778	9.972	7.258	20	18	16	1	1	2	VCP, FANCG	434, 7708	in gene, downstream	ActReg chr9 #15876	1	1	0
15877	9	35,079,166	35,080,210	1,044	1	8.303	12.364	7.032	12	24	16	1	2	3	VCP, FANCG, PIGO	-6949, 325, 16891	upstream, in gene, downstream	ActReg chr9 #15877	0	1	0
15878	9	35,095,957	35,096,935	978	2	15.29	13.613	6.2	30	28	11	1	1	3	PIGO, STOML2, KIAA1539	133, 6708, 19447	in gene, downstream, downstream	ActReg chr9 #15878	1	1	0
15879	9	35,102,499	35,103,521	1,022	3	10.719	12.781	9.875	23	18	19	1	2	3	PIGO, STOML2, KIAA1539	-6431, 144, 12883	upstream, in gene, downstream	ActReg chr9 #15879	1	1	1
15880	9	35,161,797	35,162,634	837	2	11.154	13.423	6.423	20	26	12	1	2	2	LOC730110, UNC13B	-52, 226	upstream, in gene	ActReg chr9 #15880	1	1	0
15881	9	35,489,795	35,491,004	1,209	1	9.486	11.568	5.514	15	16	8	1	1	1	RUSC2	392	in gene	ActReg chr9 #15881	0	1	0
15882	9	35,555,204	35,555,734	530	1	3.125	6.467	12	5	10	17	0	0	2	RUSC2, FAM166B	65462, 8427	in gene, downstream	ActReg chr9 #15882	0	0	1
15883	9	35,603,770	35,604,670	900	1	11.357	9.893	5.536	17	15	8	1	1	2	TESK1, CD72	-1061, 14204	upstream, downstream	ActReg chr9 #15883	1	0	0
15884	9	35,657,234	35,658,931	1,697	3	16.566	16.679	9.904	35	24	29	1	3	4	SIT1, RMRP, CCDC107, C9orf100	-7135, -67, -229, 7196	upstream, upstream, upstream, downstream	ActReg chr9 #15884	1	1	1
15885	9	35,690,747	35,691,219	472	1	6.2	9.067	12.467	9	11	20	1	1	3	CA9, TPM2, TLN1	17068, -930, 41409	downstream, upstream, downstream	ActReg chr9 #15885	0	0	1
15886	9	35,731,975	35,732,979	1,004	1	9.032	11.129	5.097	17	18	9	1	2	3	TLN1, CREB3, GBA2	-85, 160, 16748	upstream, in gene, downstream	ActReg chr9 #15886	0	1	0
15887	9	35,834,934	35,835,398	464	1	3.267	5.333	11.667	5	7	19	0	1	2	C9orf128, TMEM8B	-6422, 5944	upstream, in gene	ActReg chr9 #15887	0	0	1
15888	9	35,905,893	35,906,544	651	1	10.55	6.35	13.3	15	9	20	0	2	2	HRCT1, LOC158376	29, -3262	in gene, upstream	ActReg chr9 #15888	0	0	1
15889	9	35,909,787	35,910,244	457	1	6.6	3.133	12.067	8	5	17	0	1	2	HRCT1, LOC158376	3826, 535	downstream, in gene	ActReg chr9 #15889	0	0	1
15890	9	35,945,642	35,946,077	435	1	10.615	9.462	4.462	17	13	6	0	0	0				ActReg chr9 #15890	1	0	0
15891	9	36,190,818	36,191,223	405	1	9.833	11.083	12.917	12	14	18	1	1	1	CLTA	167	in gene	ActReg chr9 #15891	0	0	1
15892	9	36,258,132	36,259,241	1,109	3	17.971	15.743	7.971	46	36	16	1	0	1	GNE	18,367	in gene	ActReg chr9 #15892	1	1	1
15893	9	36,317,563	36,318,070	507	1	9.75	11.375	5.688	14	16	10	0	0	0				ActReg chr9 #15893	0	1	0
15894	9	36,327,823	36,328,471	648	1	6.7	10.95	5.35	11	18	12	0	0	1	RNF38	73,048	downstream	ActReg chr9 #15894	0	1	0
15895	9	36,400,256	36,400,717	461	1	11.2	8.333	4.733	15	11	11	1	1	1	RNF38	709	in gene	ActReg chr9 #15895	1	0	0
15896	9	36,486,758	36,487,297	539	1	5.588	12.059	8.375	11	20	15	1	0	0				ActReg chr9 #15896	0	1	0
15897	9	36,572,206	36,573,127	921	1	6.207	11.552	6.76	12	18	10	1	1	1	MELK	-239	upstream	ActReg chr9 #15897	0	1	0
15898	9	36,748,148	36,749,433	1,285	2	12.925	17.325	3.789	34	42	10	0	0	0				ActReg chr9 #15898	1	1	0
15899	9	36,772,287	36,773,206	919	2	11.966	13.655	3.13	20	21	5	0	0	0				ActReg chr9 #15899	1	1	0
15900	9	36,864,314	36,864,917	603	1	3.389	2.611	11.579	6	6	16	0	0	1	PAX5	169,861	in gene	ActReg chr9 #15900	0	0	1
15901	9	36,923,952	36,924,487	535	1	11.765	8.235	4.588	22	13	7	0	0	1	PAX5	110,257	in gene	ActReg chr9 #15901	1	0	0
15902	9	37,027,309	37,028,113	804	2	11.92	15.32	8.28	21	30	13	1	0	2	PAX5, LOC100130458	6765, -8352	in gene, upstream	ActReg chr9 #15902	1	1	0
15903	9	37,037,444	37,038,036	592	1	2.333	5.611	10.778	4	8	13	1	2	2	PAX5, LOC100130458	-3264, 1677	upstream, in gene	ActReg chr9 #15903	0	0	1
15904	9	37,422,325	37,422,955	630	2	11.8	10.8	8.25	20	17	15	1	1	1	GRHPR	-67	upstream	ActReg chr9 #15904	1	1	0
15905	9	37,464,503	37,465,385	882	1	4.885	10.071	6.321	11	14	10	1	1	1	ZBTB5	463	in gene	ActReg chr9 #15905	0	1	0
15906	9	37,592,119	37,592,954	835	1	12.308	9.231	10.217	18	14	17	1	1	1	TOMM5	100	in gene	ActReg chr9 #15906	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15907	9	37,594,495	37,595,255	760	1	3.25	9.458	3.619	7	13	7	0	1	1	TOMM5	-2,239	upstream	ActReg chr9 #15907	0	1	0
15908	9	37,784,535	37,785,597	1,062	3	10.727	13.333	6.788	20	25	16	1	2	3	RGMTD3, EXOSC3, MIR3159	31264, 1, -4387	downstream, in gene, upstream	ActReg chr9 #15908	1	1	1
15909	9	37,787,049	37,787,515	466	1	3.929	4.214	10.714	7	8	13	1	2	3	RGMTD3, EXOSC3, MIR3159	33480, -2215, -2171	downstream, upstream, upstream	ActReg chr9 #15909	0	0	1
15910	9	37,800,257	37,801,592	1,335	3	10.244	15.317	7.683	23	31	17	1	1	2	MIR3159, DCAF10	11471, 134	in gene, in gene	ActReg chr9 #15910	1	1	1
15911	9	38,005,847	38,006,229	382	1	4.5	4.583	11.417	8	6	17	0	0	1	SHB	63,172	in gene	ActReg chr9 #15911	0	0	1
15912	9	38,022,117	38,022,580	463	1	3.357	2.857	11.571	5	4	17	0	0	1	SHB	46,862	in gene	ActReg chr9 #15912	0	0	1
15913	9	38,067,396	38,068,013	617	1	7.947	9.053	11.947	11	14	19	1	1	1	SHB	1,506	in gene	ActReg chr9 #15913	0	0	1
15914	9	38,069,387	38,070,117	730	1	10.435	11.826	5.409	16	22	8	2	1	1	SHB	-542	upstream	ActReg chr9 #15914	0	1	0
15915	9	38,377,707	38,378,031	324	1	1	3.4	11.1	1	4	15	0	0	0				ActReg chr9 #15915	0	0	1
15916	9	38,487,386	38,487,769	383	1	2.75	1.909	13.5	4	3	23	1	0	0				ActReg chr9 #15916	0	0	1
15917	9	38,620,363	38,621,252	889	3	12.607	14.429	11.536	21	26	19	1	2	2	ANKRD18A, C9orf122	-447, -278	upstream, upstream	ActReg chr9 #15917	1	1	1
15918	9	44,227,312	44,227,740	428	1	7.231	10.692	5.231	11	18	9	1	0	0				ActReg chr9 #15918	0	1	0
15919	9	45,729,021	45,729,532	511	2	3.938	9.938	8.688	6	17	18	0	2	2	FAM27A, FAM27E2	2247, -4312	downstream, upstream	ActReg chr9 #15919	0	1	1
15920	9	66,454,699	66,456,092	1,393	1	9.977	13.581	19.488	18	20	41	1	2	2	LOC100287759, LOC100505956	2619, -1894	in gene, upstream	ActReg chr9 #15920	0	0	1
15921	9	66,456,944	66,457,780	836	1	6.692	11.577	12.269	10	18	22	1	2	2	LOC100287759, LOC100505956	652, 73	in gene, in gene	ActReg chr9 #15921	0	0	1
15922	9	66,457,857	66,458,751	894	2	15.889	17.148	25.846	29	36	44	1	2	2	LOC100287759, LOC100505956	-290, 1015	upstream, in gene	ActReg chr9 #15922	0	1	1
15923	9	66,520,297	66,520,616	319	1	4.3	6.7	10.9	6	10	16	0	0	2	FLJ20444, LOC100506146	33421, 33184	downstream, downstream	ActReg chr9 #15923	0	0	1
15924	9	68,408,612	68,409,207	595	1	10.278	11.389	15.167	17	21	26	1	0	0				ActReg chr9 #15924	0	0	1
15925	9	68,454,940	68,456,052	1,112	2	9.314	13.771	10.971	19	25	29	1	1	1	LOC642236	-1,121	upstream	ActReg chr9 #15925	0	1	1
15926	9	71,394,472	71,395,627	1,155	3	11.056	9.667	8.222	14	17	19	1	1	2	PIP5K1B, FAM122A	74433, 85	in gene, in gene	ActReg chr9 #15926	1	1	1
15927	9	71,795,356	71,796,058	702	1	7.045	11.136	2.864	10	22	6	0	0	1	TJP2	59,483	in gene	ActReg chr9 #15927	0	1	0
15928	9	72,287,510	72,287,844	334	1	5.545	6.727	11.909	8	10	17	1	1	1	APBA1	-402	upstream	ActReg chr9 #15928	0	0	1
15929	9	72,400,331	72,401,184	853	2	9.444	13.667	2.692	24	29	5	0	0	0				ActReg chr9 #15929	1	1	0
15930	9	72,627,896	72,628,523	627	1	4	11.1	2.45	7	20	3	0	0	0				ActReg chr9 #15930	0	1	0
15931	9	72,658,566	72,659,157	591	1	3.611	4.412	14	6	8	24	1	1	1	MAMDC2	364	in gene	ActReg chr9 #15931	0	0	1
15932	9	72,699,950	72,700,679	729	2	14.318	14.696	3.35	31	27	6	0	0	1	MAMDC2	41,817	in gene	ActReg chr9 #15932	1	1	0
15933	9	72,873,524	72,874,558	1,034	1	9.875	11.531	8.194	15	16	14	1	2	2	LOC100507299, SMC5	-259, 163	upstream, in gene	ActReg chr9 #15933	0	1	0
15934	9	73,004,384	73,005,148	764	1	8.417	12.833	1.737	11	20	4	0	0	1	KLF9	24,807	in gene	ActReg chr9 #15934	0	1	0
15935	9	73,028,624	73,029,601	977	2	17.645	14.903	5.161	40	31	11	1	1	1	KLF9	461	in gene	ActReg chr9 #15935	1	1	0
15936	9	73,033,273	73,034,800	1,527	2	14.896	13.979	6.104	28	26	10	1	1	1	KLF9	-4,463	upstream	ActReg chr9 #15936	1	1	0
15937	9	73,215,983	73,216,829	846	1	11.962	10.962	5.808	18	15	11	0	0	1	TRPM3	520,108	in gene	ActReg chr9 #15937	1	0	0
15938	9	73,517,708	73,518,199	491	1	8.333	10.533	3.267	11	15	5	0	0	1	TRPM3	218,561	in gene	ActReg chr9 #15938	0	1	0
15939	9	74,060,985	74,062,320	1,335	2	15.738	20.476	5.78	34	42	13	1	0	0				ActReg chr9 #15939	1	1	0
15940	9	74,121,659	74,122,263	604	2	10.158	11.579	0	21	25	0	0	0	0				ActReg chr9 #15940	1	1	0
15941	9	74,383,306	74,383,731	425	1	11.462	11.385	11.231	16	16	19	1	1	1	TMEM2	282	in gene	ActReg chr9 #15941	0	0	1
15942	9	74,383,921	74,384,557	636	1	9.6	11.6	8.25	14	16	14	1	1	1	TMEM2	-439	upstream	ActReg chr9 #15942	0	1	0
15943	9	74,397,697	74,398,592	895	1	11.75	15.536	5.321	22	32	11	0	0	0				ActReg chr9 #15943	0	1	0
15944	9	74,525,628	74,526,250	622	1	11.35	12.5	7.7	16	20	12	1	2	2	FAM108B1, C9orf85	209, -484	in gene, upstream	ActReg chr9 #15944	0	1	0
15945	9	74,602,291	74,603,299	1,008	2	8.875	10.312	2.556	17	21	5	0	0	0				ActReg chr9 #15945	1	1	0
15946	9	74,763,991	74,764,994	1,003	2	10.406	11.438	8.594	19	17	19	1	1	1	GDA	199	in gene	ActReg chr9 #15946	0	1	1
15947	9	74,979,724	74,980,833	1,109	2	9.229	11.286	5.771	22	19	8	1	1	1	ZFAND5	-115	upstream	ActReg chr9 #15947	1	1	0
15948	9	75,172,359	75,172,905	546	1	10.235	8.706	1.1	16	12	2	0	0	1	TMC1	35,915	in gene	ActReg chr9 #15948	1	0	0
15949	9	75,201,323	75,201,859	536	1	12.059	8.765	3.588	19	12	6	0	0	1	TMC1	64,874	in gene	ActReg chr9 #15949	1	0	0
15950	9	75,748,771	75,749,342	571	1	9.824	10.882	1.071	16	18	2	0	0	0				ActReg chr9 #15950	0	1	0
15951	9	75,834,571	75,835,686	1,115	2	9.171	12.057	1.231	19	25	2	0	0	0				ActReg chr9 #15951	1	1	0
15952	9	76,358,599	76,359,061	462	1	7.143	10.857	2.083	12	14	3	0	0	0				ActReg chr9 #15952	0	1	0
15953	9	77,567,060	77,568,113	1,053	2	9.091	10.576	6.375	15	18	11	1	1	1	C9orf40	216	in gene	ActReg chr9 #15953	1	1	0
15954	9	77,642,682	77,643,552	870	1	9.964	11.929	7.174	15	17	16	1	1	1	C9orf41	193	in gene	ActReg chr9 #15954	0	1	0
15955	9	77,702,454	77,703,157	703	2	11.476	6.955	8.818	15	11	19	1	2	2	C9orf95, OSTF1	328, -593	in gene, upstream	ActReg chr9 #15955	1	0	1
15956	9	78,505,216	78,506,362	1,146	2	8.944	11.472	7.806	16	17	14	2	1	1	PCSK5	229	in gene	ActReg chr9 #15956	0	1	1
15957	9	78,608,120	78,608,888	768	1	8.5	11.667	4.95	17	18	7	0	0	1	PCSK5	102,944	in gene	ActReg chr9 #15957	0	1	0
15958	9	78,830,857	78,831,614	757	2	10.217	14.696	2.045	20	28	3	0	0	1	PCSK5	325,675	in gene	ActReg chr9 #15958	1	1	0
15959	9	79,008,456	79,009,636	1,180	2	10.73	11.324	6.514	17	21	15	1	1	1	RFK	398	in gene	ActReg chr9 #15959	1	1	0
15960	9	79,191,102	79,191,610	508	1	9.5	7	1	14	13	1	0	0	0				ActReg chr9 #15960	1	0	0
15961	9	79,206,108	79,206,790	682	1	6.455	11.818	1.545	13	17	3	0	0	0				ActReg chr9 #15961	0	1	0
15962	9	79,302,828	79,303,572	744	1	8.217	13.826	2.55	16	22	5	0	0	1	PRUNE2	217,803	in gene	ActReg chr9 #15962	0	1	0
15963	9	79,432,993	79,433,578	585	2	11	10.111	1.688	18	16	3	0	0	1	PRUNE2	87,718	in gene	ActReg chr9 #15963	1	1	0
15964	9	79,464,862	79,465,201	339	1	2.182	2.364	9.818	4	4	14	0	0	1	PRUNE2	55,972	in gene	ActReg chr9 #15964	0	0	1
15965	9	79,520,874	79,521,868	994	2	15.581	17.806	4.935	32	37	11	1	1	1	PRUNE2	-368	upstream	ActReg chr9 #15965	1	1	0
15966	9	79,792,165	79,792,875	710	1	6.955	11.864	7.864	11	18	12	1	2	2	RP11-470P4.2, VPS13A	313, 159	in gene, in gene	ActReg chr9 #15966	0	1	0
15967	9	80,105,438	80,105,755	317	1	1.667	2.2	8.8	3	3	11	0	0	1	GNA14	157,636	in gene	ActReg chr9 #15967	0	0	1
15968	9	80,190,540	80,191,177	637	2	8.95	13.05	1	17	24	1	0	0	1	GNA14	72,374	in gene	ActReg chr9 #15968	1	1	0
15969	9	80,911,602	80,912,933	1,331	2	8.119	12.429	8.457	16	19	22	1	1	1	PSAT1	208	in gene	ActReg chr9 #15969	0	1	1
15970	9	81,167,920	81,168,734	814	1	4.92	12.6	1.3	7	19	2	0	0	0				ActReg chr9 #15970	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
15971	9	81,400,640	81,401,392	752	1	5.625	11	2.105	11	20	4	0	0	0				ActReg chr9 #15971	0	1	0
15972	9	82,186,205	82,187,085	880	1	10.929	9.714	3.885	19	19	7	1	1	1	TLE4	-233	upstream	ActReg chr9 #15972	1	0	0
15973	9	84,122,236	84,122,669	433	1	6.571	3.429	12.357	9	7	17	0	0	0				ActReg chr9 #15973	0	0	1
15974	9	84,303,696	84,304,146	450	1	8.714	7.286	15.5	11	10	24	1	1	1	TLE1	-325	upstream	ActReg chr9 #15974	0	0	1
15975	9	85,048,200	85,048,459	259	1	1	1.375	10.375	1	2	13	0	0	0				ActReg chr9 #15975	0	0	1
15976	9	85,425,918	85,426,334	416	1	10.538	6.538	2.25	14	11	4	0	0	0				ActReg chr9 #15976	1	0	0
15977	9	85,914,318	85,915,003	685	2	11.476	10.619	4.095	22	21	6	0	0	1	FRMD3	238,688	in gene	ActReg chr9 #15977	1	1	0
15978	9	86,136,223	86,136,944	721	1	8.087	10.957	1.667	16	19	3	0	0	1	FRMD3	16,765	in gene	ActReg chr9 #15978	0	1	0
15979	9	86,152,672	86,153,962	1,290	3	8.756	11.195	9.415	14	24	16	1	1	1	FRMD3	31	in gene	ActReg chr9 #15979	1	1	1
15980	9	86,571,306	86,572,043	737	2	10.348	7.565	8.609	14	12	18	1	1	1	C9orf64	-11	upstream	ActReg chr9 #15980	1	0	1
15981	9	86,594,388	86,595,361	973	2	10.194	13.419	6.968	14	20	16	1	2	3	HNRNPK, MIR7-1, RMI1	695, -10102, -763	in gene, upstream, upstream	ActReg chr9 #15981	0	1	1
15982	9	87,142,011	87,142,344	333	1	2	1.2	10.818	2	2	13	0	0	0				ActReg chr9 #15982	0	0	1
15983	9	88,555,965	88,556,400	435	1	10.929	9.357	13.214	17	12	23	1	1	1	NAA35	125	in gene	ActReg chr9 #15983	0	0	1
15984	9	88,721,787	88,722,292	505	1	12.5	9.938	0	25	14	0	0	1	1	GOLM1	-6,923	upstream	ActReg chr9 #15984	1	0	0
15985	9	88,800,059	88,801,110	1,051	1	11.061	7.848	4.5	15	13	8	0	0	0				ActReg chr9 #15985	1	0	0
15986	9	88,896,673	88,897,875	1,202	2	10.27	10.865	11.486	17	19	20	1	1	2	ISCA1, ZCCHC6	216, 72128	in gene, downstream	ActReg chr9 #15986	0	1	1
15987	9	88,968,678	88,969,765	1,087	3	15.794	12.853	8.176	32	21	16	1	1	1	ZCCHC6	181	in gene	ActReg chr9 #15987	1	1	1
15988	9	89,381,618	89,382,306	688	1	6.273	11.773	2.375	9	21	5	0	0	0				ActReg chr9 #15988	0	1	0
15989	9	89,563,175	89,563,887	712	1	8.909	11.864	4.955	17	24	10	1	2	2	GAS1, LOC100506834	-1427, 730	upstream, in gene	ActReg chr9 #15989	0	1	0
15990	9	89,813,522	89,814,002	480	1	11	6	1.375	15	9	4	0	0	0				ActReg chr9 #15990	1	0	0
15991	9	90,328,167	90,328,964	797	2	9.16	12.68	2	22	22	4	0	0	1	DAPK1	215,809	downstream	ActReg chr9 #15991	1	1	0
15992	9	90,340,437	90,341,783	1,346	1	9.048	11.762	6.31	19	18	11	1	1	1	CTSL1	136	in gene	ActReg chr9 #15992	0	1	0
15993	9	90,386,195	90,386,787	592	1	3.941	4.895	11.316	6	11	16	0	0	0				ActReg chr9 #15993	0	0	1
15994	9	90,407,489	90,408,589	1,100	2	9.529	13.823	1.8	19	28	3	0	0	0				ActReg chr9 #15994	1	1	0
15995	9	90,588,847	90,589,932	1,085	2	9.882	9.382	12.059	20	17	17	1	1	1	CDK20	306	in gene	ActReg chr9 #15995	0	1	1
15996	9	90,621,851	90,622,280	429	1	2.286	2.929	10.071	4	5	16	1	0	0				ActReg chr9 #15996	0	0	1
15997	9	90,691,200	90,691,676	476	1	5.4	10.133	9.267	9	15	11	1	0	0				ActReg chr9 #15997	0	1	0
15998	9	90,835,619	90,835,979	360	1	1.667	3.455	10.091	3	5	13	0	0	0				ActReg chr9 #15998	0	0	1
15999	9	91,002,603	91,003,070	467	1	8.429	11.786	12.571	10	16	19	1	1	1	SPIN1	-461	upstream	ActReg chr9 #15999	0	0	1
16000	9	91,794,646	91,795,561	915	2	10.552	11.759	7.448	17	16	13	0	1	1	SHC3	-1,421	upstream	ActReg chr9 #16000	1	1	0
16001	9	91,932,906	91,934,030	1,124	2	8.943	13.457	6.235	19	23	14	1	1	3	CKS2, MIR3153, SECISBP2	7355, 6328, 56	downstream, downstream, in gene	ActReg chr9 #16001	1	1	0
16002	9	92,058,294	92,058,758	464	1	5.467	6.133	12.067	9	10	16	0	0	1	SEMA4D	36,085	in gene	ActReg chr9 #16002	0	0	1
16003	9	92,134,116	92,134,753	637	1	7.85	11.35	6.45	12	19	9	0	0	0				ActReg chr9 #16003	0	1	0
16004	9	92,218,223	92,218,578	355	1	5.818	4.364	11.546	7	6	14	0	1	1	GADD45G	-1,527	upstream	ActReg chr9 #16004	0	0	1
16005	9	93,879,713	93,880,242	529	1	4.312	4.625	13.562	6	7	21	1	0	1	LOC100128909	45,563	downstream	ActReg chr9 #16005	0	0	1
16006	9	93,926,830	93,927,482	652	1	9.4	10.95	6.15	14	20	11	0	1	1	LOC100128909	-1,616	upstream	ActReg chr9 #16006	0	1	0
16007	9	93,942,894	93,943,377	483	1	2.929	2.214	11.933	5	4	19	0	0	0				ActReg chr9 #16007	0	0	1
16008	9	93,959,394	93,960,447	1,053	1	10.969	11.188	2.545	23	20	4	0	0	1	LOC100507137	12,669	downstream	ActReg chr9 #16008	0	1	0
16009	9	94,123,407	94,124,256	849	1	5.741	11.333	3.3	9	18	5	1	1	1	AUH	375	in gene	ActReg chr9 #16009	0	1	0
16010	9	94,181,430	94,182,127	697	2	11.227	10.136	2	20	17	3	0	0	1	NFIL3	4,366	in gene	ActReg chr9 #16010	1	1	0
16011	9	94,186,292	94,187,133	841	1	6.885	12.577	6.417	11	21	12	1	1	1	NFIL3	-568	upstream	ActReg chr9 #16011	0	1	0
16012	9	94,877,312	94,878,040	728	2	11.957	13.522	6.391	23	27	14	1	1	1	SPTLC1	14	in gene	ActReg chr9 #16012	1	1	0
16013	9	94,909,349	94,910,161	812	1	11.64	8.24	4.16	15	12	7	0	0	2	LOC100507197, C9orf44	6034, 6006	in gene, in gene	ActReg chr9 #16013	1	0	0
16014	9	95,055,712	95,056,454	742	2	13.25	12.917	6	29	27	9	1	2	3	IARS, SNORA84, NOL8	-45, -1208, 31793	upstream, upstream, downstream	ActReg chr9 #16014	1	1	0
16015	9	95,087,258	95,088,766	1,508	2	23.255	31.83	7.234	71	107	11	1	2	2	NOL8, CENPP	-136, 271	upstream, in gene	ActReg chr9 #16015	1	1	0
16016	9	95,287,378	95,287,989	611	1	10.21	8.789	3.615	17	13	5	0	0	2	CENPP, ECM2	199942, 10569	in gene, in gene	ActReg chr9 #16016	1	0	0
16017	9	95,400,181	95,400,605	424	1	4	4.077	13.231	8	7	18	0	0	1	IPPK	32,154	in gene	ActReg chr9 #16017	0	0	1
16018	9	95,432,037	95,432,988	951	1	9.759	14.069	8	16	22	16	1	1	1	IPPK	35	in gene	ActReg chr9 #16018	0	1	0
16019	9	95,481,324	95,481,773	449	1	5.231	4.643	11.071	7	7	14	1	0	1	BICD2	45,535	in gene	ActReg chr9 #16019	0	0	1
16020	9	95,527,000	95,528,061	1,061	2	12.242	12.454	5.5	19	25	10	1	1	1	BICD2	-447	upstream	ActReg chr9 #16020	1	1	0
16021	9	95,858,441	95,859,273	832	1	8.077	10.5	2.588	12	15	5	1	1	1	C9orf89	407	in gene	ActReg chr9 #16021	0	1	0
16022	9	95,859,634	95,860,388	754	1	6.083	11.333	4.333	11	16	10	0	1	1	C9orf89	1,561	in gene	ActReg chr9 #16022	0	1	0
16023	9	95,860,411	95,861,314	903	2	11.069	9.759	4.414	20	16	11	0	1	1	C9orf89	2,412	in gene	ActReg chr9 #16023	1	1	0
16024	9	95,926,354	95,926,958	604	1	3.889	3.579	10.684	8	7	15	0	0	0				ActReg chr9 #16024	0	0	1
16025	9	95,967,458	95,967,974	516	1	2.2	4.812	12.062	4	8	18	0	0	1	WNK2	20,504	in gene	ActReg chr9 #16025	0	0	1
16026	9	96,003,948	96,004,625	677	1	3.476	4.524	10.905	6	8	15	0	0	1	WNK2	57,074	in gene	ActReg chr9 #16026	0	0	1
16027	9	96,070,512	96,070,890	378	1	1.364	5.636	11.333	2	8	16	0	0	2	WNK2, C9orf129	123489, 37995	in gene, downstream	ActReg chr9 #16027	0	0	1
16028	9	96,328,654	96,329,188	534	1	7.647	9.706	5.294	10	14	13	1	0	2	FAM120A, PHF2	114748, -9988	downstream, upstream	ActReg chr9 #16028	0	1	0
16029	9	96,564,113	96,564,478	365	1	2.364	2.636	11.636	4	4	16	0	0	0				ActReg chr9 #16029	0	0	1
16030	9	96,572,264	96,572,639	375	1	3	1.667	10.364	4	3	14	0	0	1	MIR4291	-9,188	upstream	ActReg chr9 #16030	0	0	1
16031	9	96,658,327	96,658,773	446	1	2.429	3.071	11.714	4	5	17	0	0	0				ActReg chr9 #16031	0	0	1
16032	9	96,711,374	96,711,887	513	1	3.625	5.467	12.875	8	8	18	1	0	1	BARX1	5,978	downstream	ActReg chr9 #16032	0	0	1
16033	9	96,792,575	96,793,404	829	1	9.885	9.654	5.577	14	15	11	1	1	1	PTPDC1	-87	upstream	ActReg chr9 #16033	1	0	0
16034	9	96,928,134	96,928,891	757	1	6.545	10.522	5.762	14	16	14	1	0	2	MIRLET7A1, MIRLET7F1	-9727, -10117	upstream, upstream	ActReg chr9 #16034	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16035	9	97,021,263	97,021,994	731	1	7.043	13.435	8.087	14	23	17	1	1	1	ZNF169	50	in gene	ActReg chr9 #16035	0	1	0
16036	9	97,488,633	97,489,347	714	1	10.391	12	7.783	15	22	12	1	1	1	C9orf3	104	in gene	ActReg chr9 #16036	0	1	0
16037	9	97,545,268	97,546,101	833	2	13.615	21.538	2.385	38	52	5	0	0	1	C9orf3	56,798	in gene	ActReg chr9 #16037	1	1	0
16038	9	97,691,331	97,692,193	862	1	7.444	12	6	13	17	9	0	0	1	C9orf3	202,876	in gene	ActReg chr9 #16038	0	1	0
16039	9	98,269,148	98,270,496	1,348	2	12.302	12.698	4.829	25	21	15	1	0	1	PTCH1	9,425	in gene	ActReg chr9 #16039	1	1	0
16040	9	98,272,727	98,273,324	597	1	4.947	9.632	2.571	10	17	4	1	0	1	PTCH1	6,222	in gene	ActReg chr9 #16040	0	1	0
16041	9	98,637,093	98,638,621	1,528	4	9.723	12.064	10.915	26	24	21	1	2	2	C9orf130, C9orf102	402, -43	in gene, upstream	ActReg chr9 #16041	1	1	1
16042	9	98,764,114	98,764,405	291	1	1.5	3.333	8.778	2	4	12	0	0	0				ActReg chr9 #16042	0	0	1
16043	9	98,810,998	98,812,102	1,104	2	8.743	9.743	9.4	18	18	12	0	0	0				ActReg chr9 #16043	1	1	0
16044	9	99,019,006	99,019,434	428	1	9.857	9.071	1.786	18	13	2	0	0	1	HSD17B3	45,214	in gene	ActReg chr9 #16044	1	0	0
16045	9	99,179,306	99,179,857	551	1	11.294	7	5.588	21	9	11	1	1	1	ZNF367	1,088	in gene	ActReg chr9 #16045	1	0	0
16046	9	99,180,243	99,180,936	693	3	11.682	11.046	7.136	16	19	18	1	1	1	ZNF367	80	in gene	ActReg chr9 #16046	1	1	1
16047	9	99,328,749	99,329,529	780	1	8.75	7.417	11.583	13	14	15	1	0	1	CDC14B	52,973	in gene	ActReg chr9 #16047	0	0	1
16048	9	99,416,818	99,417,403	585	1	8.056	11.389	5	12	16	8	1	1	1	C9orf21	489	in gene	ActReg chr9 #16048	0	1	0
16049	9	99,839,637	99,839,929	292	1	1.6	2.556	11.111	2	3	14	1	0	0				ActReg chr9 #16049	0	0	1
16050	9	100,149,265	100,149,842	577	1	9.056	15.889	7.5	15	26	16	0	0	3	KIAA1529, C9orf174, hCG_2045089	148845, 79643, 9420	downstream, downstream, downstream	ActReg chr9 #16050	0	1	0
16051	9	100,151,422	100,151,833	411	1	1.833	3.308	12.615	2	5	18	0	0	1	hCG_2045089	7,346	downstream	ActReg chr9 #16051	0	0	1
16052	9	100,173,822	100,174,569	747	2	14.625	12.167	2.538	34	30	4	1	1	1	TDRD7	-107	upstream	ActReg chr9 #16052	1	1	0
16053	9	100,264,531	100,264,983	452	1	3.643	5.143	10.714	6	8	15	1	1	2	TDRD7, TMOD1	90455, 1295	downstream, in gene	ActReg chr9 #16053	0	0	1
16054	9	100,287,763	100,288,597	834	1	8.692	9.154	2.955	12	13	5	0	0	1	TMOD1	24,718	in gene	ActReg chr9 #16054	0	1	0
16055	9	100,395,281	100,396,428	1,147	2	10.806	12.556	10.667	16	18	16	1	2	2	TSTD2, NCBP1	108, 149	in gene, in gene	ActReg chr9 #16055	0	1	1
16056	9	100,458,991	100,459,792	801	3	10.2	11.76	9.8	17	19	20	1	1	1	XPA	300	in gene	ActReg chr9 #16056	1	1	1
16057	9	100,616,334	100,616,593	259	1	2.5	4.25	10.875	3	6	13	1	1	1	FOXE1	926	in gene	ActReg chr9 #16057	0	0	1
16058	9	100,617,206	100,617,594	388	1	6.667	3.25	10.917	10	4	15	1	1	1	FOXE1	1,863	in gene	ActReg chr9 #16058	0	0	1
16059	9	100,638,976	100,639,581	605	1	10.105	12	2.842	14	21	5	0	0	0				ActReg chr9 #16059	0	1	0
16060	9	100,684,202	100,685,154	952	3	17.333	19.933	8.367	36	45	17	1	1	2	C9orf156, HEMGN	174, 22456	in gene, downstream	ActReg chr9 #16060	1	1	1
16061	9	100,743,222	100,743,855	633	1	9	12.15	2.105	14	21	4	0	1	1	ANP32B	-1,951	upstream	ActReg chr9 #16061	0	1	0
16062	9	100,745,134	100,746,277	1,143	2	9.361	10.639	4.441	15	20	10	1	1	1	ANP32B	216	in gene	ActReg chr9 #16062	1	1	0
16063	9	100,746,931	100,747,337	406	1	9.769	10.692	0	13	17	0	1	1	1	ANP32B	1,645	in gene	ActReg chr9 #16063	0	1	0
16064	9	100,818,919	100,819,236	317	1	12.4	10.8	12.9	15	14	19	1	1	1	NANS	118	in gene	ActReg chr9 #16064	0	0	1
16065	9	100,880,822	100,881,583	761	1	10.333	13	6.792	18	22	12	1	1	2	TRIM14, CORO2A	286, 73754	in gene, downstream	ActReg chr9 #16065	0	1	0
16066	9	100,954,110	100,954,604	494	1	8.375	9.25	12.5	11	12	18	2	1	2	CORO2A, TBC1D2	599, 63646	in gene, downstream	ActReg chr9 #16066	0	0	1
16067	9	100,955,128	100,955,889	761	2	7.667	10.708	10.042	12	16	16	1	1	2	CORO2A, TBC1D2	-552, 62495	upstream, downstream	ActReg chr9 #16067	0	1	1
16068	9	101,017,771	101,018,500	729	2	8.957	12.043	13.348	17	26	23	1	1	1	TBC1D2	-132	upstream	ActReg chr9 #16068	0	1	1
16069	9	101,337,830	101,338,500	670	1	10.333	11.524	6.286	19	18	12	0	0	1	GABBR2	133,314	in gene	ActReg chr9 #16069	0	1	0
16070	9	101,472,317	101,473,307	990	1	7.161	13.839	4.129	14	24	9	1	1	1	GABBR2	-1,333	upstream	ActReg chr9 #16070	0	1	0
16071	9	101,983,593	101,984,676	1,083	2	11.765	14.441	6.5	18	33	12	1	2	2	ALG2, SEC61B	112, -436	in gene, upstream	ActReg chr9 #16071	1	1	0
16072	9	102,195,696	102,196,274	578	1	11.778	9	4.056	21	15	8	0	0	0				ActReg chr9 #16072	1	0	0
16073	9	102,318,975	102,319,736	761	1	6.542	10.542	2.158	10	16	4	0	0	0				ActReg chr9 #16073	0	1	0
16074	9	102,581,562	102,582,134	572	1	7.944	10.278	6.611	14	19	10	1	1	1	NR4A3	-2,289	upstream	ActReg chr9 #16074	0	1	0
16075	9	102,583,394	102,584,435	1,041	2	9	11.938	10.906	15	19	18	1	1	1	NR4A3	-223	upstream	ActReg chr9 #16075	0	1	1
16076	9	102,635,774	102,636,485	711	2	10.522	11.478	2.562	17	18	4	0	0	1	NR4A3	51,992	downstream	ActReg chr9 #16076	1	1	0
16077	9	102,668,905	102,669,537	632	1	10.35	9.35	7.85	15	12	12	1	1	1	STX17	306	in gene	ActReg chr9 #16077	1	0	0
16078	9	102,860,777	102,862,132	1,355	3	12.143	14.405	8.78	25	28	19	1	2	2	ERP44, INVS	-124, -57	upstream, upstream	ActReg chr9 #16078	1	1	1
16079	9	103,114,638	103,115,499	861	1	8.704	10.963	7.111	14	15	14	1	2	2	TEX10, LOC100507449	191, -250	in gene, upstream	ActReg chr9 #16079	0	1	0
16080	9	103,189,893	103,190,238	345	1	7.5	9.2	12.2	9	12	17	1	1	1	C9orf30	423	in gene	ActReg chr9 #16080	0	0	1
16081	9	103,191,448	103,192,090	642	1	8.35	10.8	2.45	11	14	4	0	1	1	C9orf30	2,127	in gene	ActReg chr9 #16081	0	1	0
16082	9	103,790,588	103,790,883	295	1	4	1.889	10.1	6	4	14	1	1	1	RP11-35N6.1	-296	upstream	ActReg chr9 #16082	0	0	1
16083	9	104,160,562	104,161,246	684	1	9.619	13.524	3.625	12	21	6	1	2	2	MRPL50, ZNF189	15, -259	in gene, upstream	ActReg chr9 #16083	0	1	0
16084	9	104,248,460	104,249,507	1,047	2	8.121	9.97	13.424	19	15	21	1	1	2	LOC100507465, C9orf125	17322, 492	downstream, in gene	ActReg chr9 #16084	0	1	1
16085	9	104,299,016	104,299,535	519	1	6.938	11.938	5.25	13	20	8	0	0	1	RNF20	3,142	in gene	ActReg chr9 #16085	0	1	0
16086	9	104,390,321	104,390,868	547	2	9	10	1.923	17	17	3	0	0	1	GRIN3A	110,268	in gene	ActReg chr9 #16086	1	1	0
16087	9	104,498,933	104,499,845	912	2	8.586	13.862	5.885	17	29	11	1	1	1	GRIN3A	1,473	in gene	ActReg chr9 #16087	1	1	0
16088	9	104,757,461	104,758,107	646	2	10.889	12.65	2.667	20	25	3	0	0	0				ActReg chr9 #16088	1	1	0
16089	9	105,241,479	105,241,991	512	1	7	10.562	3.769	13	16	7	0	0	0				ActReg chr9 #16089	0	1	0
16090	9	106,856,021	106,856,835	814	2	9.654	12.577	6.5	15	23	11	1	1	1	SMC2	-113	upstream	ActReg chr9 #16090	1	1	0
16091	9	106,994,788	106,995,331	543	1	6.353	10.882	1.846	9	21	3	0	0	0				ActReg chr9 #16091	0	1	0
16092	9	107,396,172	107,396,611	439	1	4.643	3	10.929	7	4	16	0	0	0				ActReg chr9 #16092	0	0	1
16093	9	107,509,535	107,510,186	651	1	6.19	10.809	7.7	11	17	15	1	1	1	NIPSNAP3A	-109	upstream	ActReg chr9 #16093	0	1	0
16094	9	107,526,116	107,526,555	439	1	9.154	9.615	11.231	12	15	14	1	1	2	NIPSNAP3A, NIPSNAP3B	16366, -116	downstream, upstream	ActReg chr9 #16094	0	0	1
16095	9	107,730,196	107,731,054	858	2	15.32	16.778	4.192	36	41	11	1	0	0				ActReg chr9 #16095	1	1	0
16096	9	108,006,354	108,007,080	726	2	8.478	12.522	7.783	14	24	18	1	1	1	SLC44A1	-212	upstream	ActReg chr9 #16096	1	1	0
16097	9	108,209,685	108,210,741	1,056	2	8.879	11.364	4.5	17	19	8	1	1	1	FSD1L	-102	upstream	ActReg chr9 #16097	1	1	0
16098	9	108,320,260	108,320,729	469	1	10.143	10.214	12.786	13	14	22	1	1	2	FSD1L, FKTN	110179, 83	downstream, in gene	ActReg chr9 #16098	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16099	9	108,874,910	108,875,310	400	1	10.692	4.833	1.9	18	9	3	0	0	0				ActReg chr9 #16099	1	0	0
16100	9	109,182,735	109,183,438	703	1	3.5	12.318	1.75	7	22	3	0	0	0				ActReg chr9 #16100	0	1	0
16101	9	109,801,684	109,802,295	611	1	12.053	5.579	1.611	20	11	3	0	0	0				ActReg chr9 #16101	1	0	0
16102	9	109,931,982	109,932,764	782	1	9.583	12.208	3.696	15	17	6	0	0	0				ActReg chr9 #16102	0	1	0
16103	9	110,045,189	110,045,855	666	1	8.9	13.7	5.211	13	23	9	1	1	1	RAD23B	-22	upstream	ActReg chr9 #16103	0	1	0
16104	9	110,045,896	110,046,498	602	1	7.316	11.105	2.895	12	19	5	1	1	1	RAD23B	653	in gene	ActReg chr9 #16104	0	1	0
16105	9	110,250,834	110,251,352	518	1	11.812	9.75	7.75	14	12	11	1	1	1	KLF4	954	in gene	ActReg chr9 #16105	1	0	0
16106	9	110,580,213	110,580,668	455	1	3.5	4.429	11.857	6	7	19	0	0	0				ActReg chr9 #16106	0	0	1
16107	9	110,803,677	110,804,484	807	1	9.038	12.115	3.769	11	20	7	0	0	0				ActReg chr9 #16107	0	1	0
16108	9	110,811,383	110,812,018	635	1	7.6	10.5	2.727	11	18	5	0	0	0				ActReg chr9 #16108	0	1	0
16109	9	110,819,581	110,820,196	615	1	10.15	9.9	1.4	19	14	2	0	0	0				ActReg chr9 #16109	1	0	0
16110	9	110,918,703	110,919,208	505	1	9.75	10	3.312	13	15	6	0	0	0				ActReg chr9 #16110	0	1	0
16111	9	111,207,810	111,208,371	561	1	11.059	9.118	3.412	16	11	6	0	0	0				ActReg chr9 #16111	1	0	0
16112	9	111,305,475	111,306,261	786	1	7.292	11.417	2.25	11	17	5	0	0	0				ActReg chr9 #16112	0	1	0
16113	9	111,313,326	111,314,185	859	1	9.481	12.185	2.783	14	18	6	0	0	0				ActReg chr9 #16113	0	1	0
16114	9	111,342,034	111,342,934	900	2	14.536	12.607	3.05	30	22	7	0	0	0				ActReg chr9 #16114	1	1	0
16115	9	111,597,524	111,598,655	1,131	2	9.943	12.286	2.321	22	20	8	0	0	0				ActReg chr9 #16115	1	1	0
16116	9	111,647,787	111,648,614	827	2	12	12.5	3.077	19	26	6	0	0	1	IKBKAP	48,408	in gene	ActReg chr9 #16116	1	1	0
16117	9	111,696,005	111,697,034	1,029	1	9.031	10.875	7.5	17	18	14	1	2	3	IKBKAP, C9orf6, CTNNAL1	89, -154, 79245	in gene, upstream, downstream	ActReg chr9 #16117	0	1	0
16118	9	111,881,411	111,882,642	1,231	1	7.526	13	4.135	12	28	12	1	1	1	C9orf5	199	in gene	ActReg chr9 #16118	0	1	0
16119	9	112,006,829	112,007,350	521	1	4.875	9.812	3.929	8	16	6	0	0	1	EPB41L4B	75,932	in gene	ActReg chr9 #16119	0	1	0
16120	9	112,082,101	112,082,567	466	1	3.733	3.667	10.667	8	5	16	1	1	1	EPB41L4B	687	in gene	ActReg chr9 #16120	0	0	1
16121	9	112,209,390	112,210,711	1,321	2	9.927	12.024	2.324	21	21	5	0	0	1	PTPN3	50,545	in gene	ActReg chr9 #16121	1	1	0
16122	9	112,231,980	112,232,868	888	2	10.393	10.964	2.25	17	16	5	0	0	1	PTPN3	28,169	in gene	ActReg chr9 #16122	1	1	0
16123	9	112,528,247	112,529,168	921	2	12.345	13.621	4.138	27	24	8	0	0	1	PALM2	125,639	in gene	ActReg chr9 #16123	1	1	0
16124	9	112,578,469	112,579,409	940	1	13.897	10.414	2.84	22	21	5	0	0	2	PALM2, PALM2-AKAP2	175871, 36362	in gene, in gene	ActReg chr9 #16124	1	0	0
16125	9	113,017,699	113,018,894	1,195	2	9.865	11.622	8.27	20	17	15	1	1	1	TXN	482	in gene	ActReg chr9 #16125	1	1	0
16126	9	113,341,203	113,341,838	635	2	11	14.15	8.75	20	26	12	1	1	1	SVEP1	640	in gene	ActReg chr9 #16126	1	1	0
16127	9	113,507,200	113,507,755	555	1	11.056	5.444	1.429	18	9	2	0	0	1	MUSK	76,426	in gene	ActReg chr9 #16127	1	0	0
16128	9	114,246,521	114,246,820	299	1	9.9	9.8	9.6	13	15	14	1	1	1	KIAA0368	355	in gene	ActReg chr9 #16128	0	0	1
16129	9	114,393,032	114,394,367	1,335	2	11.878	11.561	5.947	32	17	9	1	2	2	DNAJC25, DNAJC25-GNG10	67, 33	in gene, in gene	ActReg chr9 #16129	1	1	0
16130	9	114,505,470	114,505,976	506	1	7.438	10.938	1	13	20	1	0	0	1	C9orf84	40,056	in gene	ActReg chr9 #16130	0	1	0
16131	9	114,658,663	114,659,017	354	1	11.454	8.636	5.818	18	13	13	1	1	1	UGCG	-366	upstream	ActReg chr9 #16131	1	0	0
16132	9	115,141,553	115,142,416	863	1	7	10.704	7.556	11	18	14	1	1	1	HSDL2	-367	upstream	ActReg chr9 #16132	0	1	0
16133	9	115,479,968	115,480,599	631	1	9.35	10.85	7.789	13	17	13	1	1	1	C9orf80	104	in gene	ActReg chr9 #16133	0	1	0
16134	9	115,512,461	115,513,034	573	1	11	9.167	5.118	16	15	9	1	1	1	SNX30	-387	upstream	ActReg chr9 #16134	1	0	0
16135	9	115,513,281	115,513,876	595	1	7.235	10.167	13.667	10	14	22	1	1	1	SNX30	444	in gene	ActReg chr9 #16135	0	0	1
16136	9	115,652,220	115,652,815	595	1	3.158	2.737	13.368	6	4	19	1	1	1	SLC46A2	676	in gene	ActReg chr9 #16136	0	0	1
16137	9	115,707,876	115,708,331	455	1	5.214	2.929	10.071	8	5	15	1	0	0				ActReg chr9 #16137	0	0	1
16138	9	115,893,708	115,894,721	1,013	2	18	16.219	3.346	37	39	6	0	0	0				ActReg chr9 #16138	1	1	0
16139	9	115,983,198	115,983,884	686	1	7.091	10.818	5.727	11	21	8	1	2	2	FKBP15, SLC31A1	100, -267	in gene, upstream	ActReg chr9 #16139	0	1	0
16140	9	116,037,460	116,038,234	774	2	13.375	13.458	11.917	23	22	21	1	2	2	CDC26, PRPF4	22, -127	in gene, upstream	ActReg chr9 #16140	0	1	1
16141	9	116,102,207	116,102,995	788	1	8.84	12.36	7.32	16	23	13	1	1	2	WDR31, BSPRY	19, -9211	in gene, upstream	ActReg chr9 #16141	0	1	0
16142	9	116,172,282	116,173,245	963	2	14.267	16.433	9.067	29	33	16	1	2	3	ALAD, POLE3, C9orf43	-9145, 266, -259	upstream, in gene, upstream	ActReg chr9 #16142	1	1	0
16143	9	116,364,330	116,364,794	464	1	7.071	8.571	12	10	12	17	0	0	1	RGS3	157,551	downstream	ActReg chr9 #16143	0	0	1
16144	9	116,457,921	116,458,867	946	1	10.517	14.207	3.143	20	22	6	0	0	0				ActReg chr9 #16144	0	1	0
16145	9	116,770,708	116,771,117	409	1	3	3.231	11.154	5	5	15	0	0	1	ZNF618	132,350	in gene	ActReg chr9 #16145	0	0	1
16146	9	116,797,432	116,797,877	445	1	3.143	2.5	10.643	5	7	19	0	0	1	ZNF618	159,092	in gene	ActReg chr9 #16146	0	0	1
16147	9	116,832,801	116,833,643	842	1	3.692	5.577	12.077	7	9	16	0	0	1	AMBP	7,530	in gene	ActReg chr9 #16147	0	0	1
16148	9	116,929,973	116,930,518	545	1	2	4.5	12.647	4	8	18	1	0	1	COL27A1	12,014	in gene	ActReg chr9 #16148	0	0	1
16149	9	116,939,642	116,940,436	794	1	7.24	9.72	4.72	13	14	7	0	0	1	COL27A1	21,808	in gene	ActReg chr9 #16149	0	1	0
16150	9	116,985,632	116,986,612	980	1	9.742	5.548	3.071	17	8	8	0	0	1	COL27A1	67,891	in gene	ActReg chr9 #16150	1	0	0
16151	9	117,002,323	117,002,838	515	1	2.688	5.75	13.25	4	8	19	0	0	1	COL27A1	84,349	in gene	ActReg chr9 #16151	0	0	1
16152	9	117,018,975	117,019,593	618	1	3.55	3	11.1	5	7	16	0	0	1	COL27A1	101,053	in gene	ActReg chr9 #16152	0	0	1
16153	9	117,022,488	117,023,009	521	1	2.235	3.438	11.882	4	6	16	0	0	1	COL27A1	104,517	in gene	ActReg chr9 #16153	0	0	1
16154	9	117,023,189	117,023,492	303	1	3	4.1	11.4	5	5	15	0	0	1	COL27A1	105,109	in gene	ActReg chr9 #16154	0	0	1
16155	9	117,314,003	117,314,673	670	1	11.333	9.19	2.381	22	12	5	0	0	0				ActReg chr9 #16155	1	0	0
16156	9	117,655,966	117,656,576	610	1	8.5	10.85	2.421	11	18	5	0	1	2	LOC100505521, TNFSF8	-3276, 36499	upstream, downstream	ActReg chr9 #16156	0	1	0
16157	9	117,871,220	117,872,416	1,196	2	17.947	20.605	2.435	47	51	7	0	0	1	TNC	8,668	in gene	ActReg chr9 #16157	1	1	0
16158	9	117,880,006	117,880,813	807	1	9.04	12.04	5.76	14	18	14	0	1	1	TNC	77	in gene	ActReg chr9 #16158	0	1	0
16159	9	118,024,583	118,025,165	582	1	6.944	11.056	3.944	11	19	6	0	0	1	1-Dec	120,777	in gene	ActReg chr9 #16159	0	1	0
16160	9	118,135,296	118,136,132	836	2	11.222	8.68	2.348	19	19	6	0	0	1	1-Dec	231,617	in gene	ActReg chr9 #16160	1	1	0
16161	9	118,453,056	118,453,894	838	1	8.407	10.889	4	16	18	6	0	0	0				ActReg chr9 #16161	0	1	0
16162	9	118,706,265	118,707,436	1,171	2	9.973	11.73	2.2	19	19	5	0	0	0				ActReg chr9 #16162	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16163	9	118,863,414	118,864,249	835	1	11.538	6.885	1.895	17	10	3	0	0	0				ActReg chr9 #16163	1	0	0
16164	9	119,459,922	119,461,029	1,107	1	8.4	10.4	5.031	13	15	10	0	0	2	ASTN2, TRIM32	716842, 10894	in gene, in gene	ActReg chr9 #16164	0	1	0
16165	9	119,568,324	119,568,903	579	2	10.611	8.778	1.462	17	16	2	0	0	1	ASTN2	608,704	in gene	ActReg chr9 #16165	1	1	0
16166	9	120,176,447	120,176,757	310	1	5.7	4.4	10.6	8	6	13	1	1	1	ASTN2	715	in gene	ActReg chr9 #16166	0	0	1
16167	9	120,434,573	120,435,164	591	1	9.833	7.611	1.429	18	12	2	0	0	0				ActReg chr9 #16167	1	0	0
16168	9	120,465,707	120,466,182	475	1	10.533	8.133	2	17	10	3	0	1	1	TLR4	-516	upstream	ActReg chr9 #16168	1	0	0
16169	9	120,534,962	120,535,647	685	1	11.048	7.429	5.45	16	15	11	0	0	0				ActReg chr9 #16169	1	0	0
16170	9	120,821,558	120,822,255	697	2	13.546	12.727	1.75	26	29	2	0	0	0				ActReg chr9 #16170	1	1	0
16171	9	121,571,258	121,571,716	458	1	3.154	1.182	10.067	5	2	16	0	0	0				ActReg chr9 #16171	0	0	1
16172	9	122,132,977	122,133,533	556	1	6.353	9.647	2	9	14	3	0	1	1	DBC1	-1,516	upstream	ActReg chr9 #16172	0	1	0
16173	9	123,164,404	123,166,346	1,942	2	16.607	20.344	3.964	44	49	7	0	0	1	CDK5RAP2	177,062	in gene	ActReg chr9 #16173	1	1	0
16174	9	123,555,341	123,555,893	552	1	12.882	14.471	13	16	20	17	1	2	2	FBXW2, LOC100288842	123, -158	in gene, upstream	ActReg chr9 #16174	0	0	1
16175	9	123,604,836	123,605,821	985	2	10.567	10.267	10.333	18	18	15	1	2	2	PSMD5, LOC253039	-122, 8	upstream, in gene	ActReg chr9 #16175	1	1	0
16176	9	123,638,012	123,639,139	1,127	2	9.611	10.583	5.943	15	19	10	1	1	1	PHF19	1,031	in gene	ActReg chr9 #16176	1	1	0
16177	9	123,639,799	123,640,566	767	1	8.083	11.083	4.542	12	18	12	1	1	1	PHF19	-576	upstream	ActReg chr9 #16177	0	1	0
16178	9	123,675,322	123,676,972	1,650	2	9.885	12.808	6.519	26	27	12	0	0	1	TRAF1	15,304	in gene	ActReg chr9 #16178	1	1	0
16179	9	123,681,479	123,682,113	634	2	12.05	12.15	4.55	20	18	8	0	0	1	TRAF1	9,655	in gene	ActReg chr9 #16179	1	1	0
16180	9	123,712,823	123,713,425	602	1	6.316	12.316	1.556	10	17	2	0	0	1	C5	99,430	downstream	ActReg chr9 #16180	0	1	0
16181	9	123,836,857	123,837,807	950	2	8.7	9.967	10	14	17	21	1	0	0				ActReg chr9 #16181	0	1	1
16182	9	123,963,936	123,964,845	909	1	13.897	11.759	7.276	24	18	10	1	1	1	RAB14	-25	upstream	ActReg chr9 #16182	1	0	0
16183	9	123,996,354	123,997,466	1,112	2	9.765	12.441	3	16	17	4	0	0	0				ActReg chr9 #16183	1	1	0
16184	9	124,009,263	124,009,994	731	1	11.522	9.348	7.833	18	14	14	0	0	0				ActReg chr9 #16184	1	0	0
16185	9	124,040,715	124,041,474	759	1	11.042	10.792	5.174	18	15	10	0	0	2	GSN, LOC100128064	10714, 8025	in gene, downstream	ActReg chr9 #16185	1	0	0
16186	9	124,044,200	124,045,427	1,227	1	7.658	11.263	3.129	14	18	6	0	0	2	GSN, LOC100128064	14433, 4306	in gene, in gene	ActReg chr9 #16186	0	1	0
16187	9	124,132,226	124,134,482	2,256	3	19.457	16.929	8.441	93	65	18	1	1	1	STOM	-809	upstream	ActReg chr9 #16187	1	1	1
16188	9	124,734,569	124,735,097	528	2	10.562	11.062	3.875	20	14	7	0	0	2	TTLL11, C9orf148	121052, -8835	in gene, upstream	ActReg chr9 #16188	1	1	0
16189	9	124,854,617	124,855,971	1,354	3	11.163	15.023	7.524	25	24	15	1	1	1	TTLL11	591	in gene	ActReg chr9 #16189	1	1	1
16190	9	124,883,468	124,884,127	659	1	4.05	2.95	12.85	6	6	18	0	0	0				ActReg chr9 #16190	0	0	1
16191	9	124,893,724	124,894,454	730	1	5.217	4.545	11.391	9	10	17	0	0	0				ActReg chr9 #16191	0	0	1
16192	9	124,895,855	124,896,186	331	1	2.2	4.8	11.8	3	7	14	0	0	0				ActReg chr9 #16192	0	0	1
16193	9	125,164,627	125,165,318	691	2	10.273	9.227	4.667	19	18	9	0	0	1	PTGS1	31,743	downstream	ActReg chr9 #16193	1	1	0
16194	9	125,225,819	125,227,090	1,271	2	18.175	20.95	3.872	54	64	11	0	0	0				ActReg chr9 #16194	1	1	0
16195	9	125,667,388	125,668,115	727	3	9.043	10.87	9.087	17	17	22	1	1	2	RC3H2, ZBTB6	-189, 7858	upstream, downstream	ActReg chr9 #16195	1	1	1
16196	9	125,693,563	125,694,309	746	2	10.667	12.542	5.95	19	25	13	1	1	2	ZBTB26, RABGAP1	-157, -9352	upstream, upstream	ActReg chr9 #16196	1	1	0
16197	9	126,123,398	126,123,794	396	1	1.833	4.667	10.417	3	7	15	0	0	1	CRB2	5,148	in gene	ActReg chr9 #16197	0	0	1
16198	9	126,133,478	126,134,003	525	1	5.125	5.062	14.375	8	8	23	0	0	2	CRB2, DENND1A	15292, 558677	in gene, downstream	ActReg chr9 #16198	0	0	1
16199	9	126,689,913	126,690,849	936	2	11.367	12	1.714	19	17	3	0	1	1	DENND1A	2,036	in gene	ActReg chr9 #16199	1	1	0
16200	9	126,816,833	126,817,564	731	1	8.045	13.273	4.091	17	26	5	0	0	0				ActReg chr9 #16200	0	1	0
16201	9	126,871,284	126,873,972	2,688	2	18.548	23.833	2.506	100	119	5	0	0	0				ActReg chr9 #16201	1	1	0
16202	9	126,911,904	126,912,789	885	1	6.964	13.179	2.889	18	22	5	0	0	0				ActReg chr9 #16202	0	1	0
16203	9	127,093,720	127,094,201	481	1	3.214	4.867	11.867	6	8	18	0	0	1	NEK6	74,075	in gene	ActReg chr9 #16203	0	0	1
16204	9	127,108,636	127,109,165	529	1	5.941	4.059	11.118	11	6	17	0	1	3	NEK6, PSMB7, LOC100129034	89015, 68821, -6852	in gene, downstream, upstream	ActReg chr9 #16204	0	0	1
16205	9	127,155,085	127,155,717	632	1	12	7.35	1.75	21	10	2	0	0	1	PSMB7	22,320	in gene	ActReg chr9 #16205	1	0	0
16206	9	127,177,143	127,178,176	1,033	2	9.909	10	4.818	19	18	10	1	1	1	PSMB7	62	in gene	ActReg chr9 #16206	1	1	0
16207	9	127,230,363	127,231,020	657	1	3.524	3.905	12.143	5	7	19	0	0	1	GPR144	17,268	in gene	ActReg chr9 #16207	0	0	1
16208	9	127,241,428	127,242,050	622	1	3.526	6.7	12.9	6	9	17	0	0	2	GPR144, NR5A1	28316, 27960	downstream, downstream	ActReg chr9 #16208	0	0	1
16209	9	127,269,119	127,269,945	826	1	2.818	3.32	13.346	8	6	20	0	1	1	NR5A1	167	in gene	ActReg chr9 #16209	0	0	1
16210	9	127,532,209	127,532,709	500	1	3.75	5.312	10.312	7	7	13	1	3	3	NR6A1, LOC100505607, OLFML2A	1117, 57, -6978	in gene, in gene, upstream	ActReg chr9 #16210	0	0	1
16211	9	127,533,002	127,534,203	1,201	2	14.946	15.108	3.353	48	38	8	1	3	3	NR6A1, LOC100505607, OLFML2A	-26, 1200, -5835	upstream, in gene, upstream	ActReg chr9 #16211	1	1	0
16212	9	127,597,174	127,597,613	439	1	7.071	8.857	12.286	11	11	20	0	0	0				ActReg chr9 #16212	0	0	1
16213	9	127,602,344	127,602,880	536	1	5.824	4.941	13.294	8	7	24	0	0	0				ActReg chr9 #16213	0	0	1
16214	9	127,617,803	127,618,975	1,172	1	5.917	7.194	14.639	12	15	20	0	1	2	WDR38, RPL35	2634, 5851	in gene, downstream	ActReg chr9 #16214	0	0	1
16215	9	127,623,809	127,624,916	1,107	3	12.559	12.647	10.029	21	21	22	1	2	3	WDR38, RPL35, ARPC5L	8607, -122, -7122	downstream, upstream, upstream	ActReg chr9 #16215	1	1	1
16216	9	127,631,598	127,632,301	703	1	7.864	7.318	15.546	12	15	26	1	2	3	RPL35, ARPC5L, GOLGA1	-7709, 465, 71437	upstream, in gene, downstream	ActReg chr9 #16216	0	0	1
16217	9	127,702,966	127,704,194	1,228	2	10.256	11.436	7.718	19	17	13	1	1	2	GOLGA1, SCAI	-194, 202258	upstream, downstream	ActReg chr9 #16217	1	1	0
16218	9	127,951,329	127,952,563	1,234	3	11.368	10.737	10.368	21	20	17	1	1	1	PPP6C	272	in gene	ActReg chr9 #16218	1	1	1
16219	9	128,003,009	128,003,810	801	2	10.08	13.04	11.28	16	21	22	1	1	2	RABEPK, HSPA5	40588, 252	downstream, in gene	ActReg chr9 #16219	0	1	1
16220	9	128,023,632	128,024,816	1,184	3	9.946	10.838	7.429	18	20	18	1	1	1	GAPVD1	113	in gene	ActReg chr9 #16220	1	1	1
16221	9	128,508,139	128,509,007	868	1	7.556	9.741	6.571	12	14	12	1	2	2	LOC51145, PBX3	252, -1044	in gene, upstream	ActReg chr9 #16221	0	1	0
16222	9	128,672,673	128,673,242	569	1	6.294	10.588	2.182	11	17	3	0	0	1	PBX3	163,340	in gene	ActReg chr9 #16222	0	1	0
16223	9	128,844,067	128,845,988	1,921	2	11.083	15.783	2.879	44	50	5	0	0	0				ActReg chr9 #16223	1	1	0
16224	9	128,870,263	128,871,573	1,310	2	15.463	18.146	3.707	40	50	8	0	0	0				ActReg chr9 #16224	1	1	0
16225	9	128,985,166	128,985,747	581	1	3.176	3.389	11.167	5	6	17	2	0	0				ActReg chr9 #16225	0	0	1
16226	9	129,058,041	129,058,798	757	1	2.875	3.875	10.417	5	7	14	0	0	0				ActReg chr9 #16226	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16227	9	129,262,929	129,263,570	641	1	9.25	8.8	11.8	16	14	17	0	0	1	FAM125B	174,121	in gene	ActReg chr9 #16227	0	0	1
16228	9	129,279,016	129,279,850	834	1	8	10.692	3.2	12	16	7	0	0	1	FAM125B	190,305	downstream	ActReg chr9 #16228	0	1	0
16229	9	129,374,398	129,374,857	459	1	5.8	4.867	11.4	9	9	19	1	1	1	LMX1B	-2,095	upstream	ActReg chr9 #16229	0	0	1
16230	9	129,458,602	129,458,902	300	1	4.667	2.111	12	6	4	16	0	0	1	LMX1B	82,030	in gene	ActReg chr9 #16230	0	0	1
16231	9	129,484,461	129,484,932	471	1	3.2	7.067	12.267	5	10	20	1	0	0				ActReg chr9 #16231	0	0	1
16232	9	129,567,208	129,567,843	635	1	9.35	11.95	12	17	17	18	1	1	1	ZBTB43	240	in gene	ActReg chr9 #16232	0	0	1
16233	9	129,621,958	129,622,420	462	1	6.5	3.786	10.643	9	5	15	1	1	1	ZBTB34	-755	upstream	ActReg chr9 #16233	0	0	1
16234	9	129,811,359	129,811,912	553	1	7.722	12.444	2.154	12	25	5	0	0	1	RALGPS1	134,582	in gene	ActReg chr9 #16234	0	1	0
16235	9	129,884,255	129,885,593	1,338	2	8.833	11.714	9.357	14	19	16	0	1	2	RALGPS1, ANGPTL2	207871, 120	in gene, in gene	ActReg chr9 #16235	0	1	1
16236	9	129,986,486	129,987,063	577	1	9.056	10.5	9.222	11	14	13	1	0	1	RALGPS1	309,721	downstream	ActReg chr9 #16236	0	1	0
16237	9	130,186,509	130,187,136	627	1	8.05	12.1	9.7	11	21	15	1	1	1	ZNF79	169	in gene	ActReg chr9 #16237	0	1	0
16238	9	130,213,189	130,213,912	723	1	10.091	11.409	15.546	17	17	22	1	3	4	ZNF79, RPL12, SNORA65, LRSAM1	26897, 134, -2634, -215	downstream, in gene, upstream, upstream	ActReg chr9 #16238	0	0	1
16239	9	130,223,396	130,224,022	626	1	2.842	3	10.895	4	5	14	0	0	2	RPL12, LRSAM1	-10025, 9944	upstream, in gene	ActReg chr9 #16239	0	0	1
16240	9	130,247,818	130,248,260	442	1	3.714	2.857	10.5	7	5	16	0	0	1	LRSAM1	34,274	in gene	ActReg chr9 #16240	0	0	1
16241	9	130,321,044	130,321,834	790	1	5.28	11.64	4.125	10	20	9	0	1	2	FAM129B, LOC100506005	19829, -2498	in gene, upstream	ActReg chr9 #16241	0	1	0
16242	9	130,329,460	130,330,178	718	1	8.261	11.348	5.13	12	18	13	0	0	1	FAM129B	11,449	in gene	ActReg chr9 #16242	0	1	0
16243	9	130,330,383	130,330,937	554	1	4.824	10.882	11.588	8	16	16	1	0	1	FAM129B	10,608	in gene	ActReg chr9 #16243	0	0	1
16244	9	130,477,533	130,478,337	804	1	10.962	8.038	7.577	16	12	16	1	2	3	C9orf117, PTRH1, TTC16	8664, 1, -423	downstream, in gene, upstream	ActReg chr9 #16244	1	0	0
16245	9	130,494,277	130,494,752	475	1	3.333	5.4	12.267	5	7	17	0	0	3	TTC16, TOR2A, SH2D3C	16156, 3090, 46534	downstream, in gene, downstream	ActReg chr9 #16245	0	0	1
16246	9	130,513,592	130,514,348	756	2	11.625	14.208	4.917	17	29	8	0	0	1	SH2D3C	27,078	in gene	ActReg chr9 #16246	1	1	0
16247	9	130,578,032	130,578,515	483	1	4.077	6.467	12	6	11	16	0	1	3	FPGS, ENG, LOC100506040	13119, 38774, -72	downstream, in gene, upstream	ActReg chr9 #16247	0	0	1
16248	9	130,602,766	130,603,324	558	1	2.765	4.059	10.823	5	6	14	0	0	1	ENG	14,002	in gene	ActReg chr9 #16248	0	0	1
16249	9	130,692,584	130,693,391	807	1	9.32	6.92	15.16	12	13	25	1	1	3	PIP5KL1, DPM2, FAM102A	89, 7776, 49825	in gene, downstream, downstream	ActReg chr9 #16249	0	0	1
16250	9	130,699,510	130,700,566	1,056	1	9	11.576	6.394	13	17	12	1	2	3	PIP5KL1, DPM2, FAM102A	-6962, 725, 42774	upstream, in gene, downstream	ActReg chr9 #16250	0	1	0
16251	9	130,829,084	130,830,084	1,000	1	8.5	11.438	6.656	13	16	17	1	2	2	NAIF1, SLC25A25	15, -895	in gene, upstream	ActReg chr9 #16251	0	1	0
16252	9	130,868,829	130,869,805	976	1	3.581	3.31	10.677	8	8	16	0	0	2	SLC25A25, LOC100289019	38838, 11696	in gene, downstream	ActReg chr9 #16252	0	0	1
16253	9	130,889,617	130,891,006	1,389	3	15.442	17.861	8.368	32	33	19	1	2	3	LOC100289019, PTGES2, LOC389791	-9298, 401, -497	upstream, in gene, upstream	ActReg chr9 #16253	1	1	1
16254	9	130,952,848	130,954,441	1,593	2	16.36	19.98	6.489	59	61	14	1	0	1	CIZ1	13,018	in gene	ActReg chr9 #16254	1	1	0
16255	9	130,954,921	130,955,842	921	2	12.379	10.207	5.793	18	23	11	1	0	2	CIZ1, DNM1	11281, -10282	in gene, upstream	ActReg chr9 #16255	1	1	0
16256	9	130,966,220	130,966,744	524	1	12.125	9.188	12.25	16	11	18	1	2	2	CIZ1, DNM1	180, 819	in gene, in gene	ActReg chr9 #16256	0	0	1
16257	9	131,069,452	131,070,392	940	2	12.621	10.379	2.448	18	13	4	0	0	1	TRUB2	14,775	downstream	ActReg chr9 #16257	1	1	0
16258	9	131,084,425	131,085,524	1,099	3	15.559	16.529	12.294	32	37	22	1	2	2	TRUB2, COQ4	-277, 183	upstream, in gene	ActReg chr9 #16258	1	1	1
16259	9	131,123,938	131,124,717	779	1	7.417	8.125	12.375	11	13	18	0	0	2	SLC27A4, URM1	21488, -9271	downstream, upstream	ActReg chr9 #16259	0	0	1
16260	9	131,181,698	131,182,248	550	1	4.176	5.353	12.471	6	8	17	0	1	2	LOC100506065, CERCAM	8119, -786	in gene, upstream	ActReg chr9 #16260	0	0	1
16261	9	131,182,261	131,182,925	664	2	11.333	11.524	9.095	14	17	17	1	1	2	LOC100506065, CERCAM	8739, -166	downstream, upstream	ActReg chr9 #16261	0	1	1
16262	9	131,183,547	131,184,051	504	1	5.312	9.062	12.938	10	14	19	0	1	2	LOC100506065, CERCAM	9945, 1040	downstream, in gene	ActReg chr9 #16262	0	0	1
16263	9	131,314,237	131,314,749	512	1	4.375	7.75	12.938	7	11	23	1	1	2	GLE1, SPTAN1	47522, -373	downstream, upstream	ActReg chr9 #16263	0	0	1
16264	9	131,314,778	131,315,459	681	1	9.091	11.136	3.864	13	17	7	1	1	1	SPTAN1	252	in gene	ActReg chr9 #16264	0	1	0
16265	9	131,486,078	131,486,676	598	1	8.211	11.579	14.368	13	20	19	1	2	4	PKN3, ZDHHC12, LOC100506100, ZER1	21575, 31, -364, 47821	downstream, in gene, upstream, downstream	ActReg chr9 #16265	0	0	1
16266	9	131,533,952	131,534,839	887	3	10.5	10.25	10.643	17	22	16	1	1	1	ZER1	-197	upstream	ActReg chr9 #16266	1	1	1
16267	9	131,549,158	131,549,882	724	1	10.909	15.046	7.682	18	27	10	1	1	1	TBC1D13	10	in gene	ActReg chr9 #16267	0	1	0
16268	9	131,580,420	131,581,050	630	1	13.526	8.105	8.889	25	14	16	1	1	3	TBC1D13, ENDOG, C9orf114	31225, -44, 11350	downstream, upstream, downstream	ActReg chr9 #16268	1	0	0
16269	9	131,591,640	131,592,317	677	2	9.095	12.714	12.381	13	23	21	1	1	3	ENDOG, C9orf114, CCBL1	11199, 107, 52376	downstream, in gene, downstream	ActReg chr9 #16269	0	1	1
16270	9	131,643,716	131,644,615	899	2	21.357	20.214	4.607	48	44	10	1	2	2	CCBL1, LRRC8A	189, -226	in gene, upstream	ActReg chr9 #16270	1	1	0
16271	9	131,654,506	131,655,233	727	1	12.13	9.391	5.478	18	16	11	0	0	1	LRRC8A	10,478	in gene	ActReg chr9 #16271	1	0	0
16272	9	131,709,439	131,710,621	1,182	3	12.568	11.946	13.378	21	21	26	1	2	3	PHYHD1, DOLK, NUP188	26856, -18, 53	downstream, upstream, in gene	ActReg chr9 #16272	1	1	1
16273	9	131,798,359	131,799,373	1,014	1	8.531	12.531	6.688	18	21	15	1	1	2	SH3GLB2, FAM73B	-8287, -387	upstream, upstream	ActReg chr9 #16273	0	1	0
16274	9	131,830,248	131,830,628	380	1	1.833	4.2	11.083	3	6	17	0	0	1	FAM73B	31,185	in gene	ActReg chr9 #16274	0	0	1
16275	9	131,831,369	131,831,866	497	1	3.867	3.133	12.667	6	5	18	0	0	1	FAM73B	32,364	in gene	ActReg chr9 #16275	0	0	1
16276	9	131,842,803	131,843,734	931	1	7.655	11.69	6.103	10	17	11	1	1	2	FAM73B, DOLPP1	44015, -115	downstream, upstream	ActReg chr9 #16276	0	1	0
16277	9	131,865,118	131,865,924	806	1	4.385	5.615	12.731	8	10	17	0	1	2	CRAT, PPP2R4	7549, -7707	in gene, upstream	ActReg chr9 #16277	0	0	1
16278	9	131,888,840	131,889,717	877	1	3.565	5.074	11.741	5	11	15	0	0	1	PPP2R4	16,050	in gene	ActReg chr9 #16278	0	0	1
16279	9	131,935,617	131,936,839	1,222	1	10.026	12.605	8.026	23	19	13	1	0	1	IER5L	4,312	downstream	ActReg chr9 #16279	0	1	0
16280	9	131,964,806	131,965,532	726	1	7.182	12.773	4.773	11	19	9	1	0	0				ActReg chr9 #16280	0	1	0
16281	9	131,985,770	131,986,200	430	1	2.3	7.846	11.692	3	10	17	0	0	0				ActReg chr9 #16281	0	0	1
16282	9	132,188,355	132,188,930	575	1	3.235	3.833	10.222	5	6	13	0	0	0				ActReg chr9 #16282	0	0	1
16283	9	132,227,110	132,227,642	532	1	4.188	5	11.312	6	10	17	0	0	0				ActReg chr9 #16283	0	0	1
16284	9	132,236,115	132,237,052	937	1	4.276	10.483	4.931	8	16	10	0	0	1	LOC100506190	-9,147	upstream	ActReg chr9 #16284	0	1	0
16285	9	132,251,627	132,252,989	1,362	1	8.524	11.595	5.738	18	19	14	0	1	2	LOC100506190, LOC100128077	6578, -452	in gene, upstream	ActReg chr9 #16285	0	1	0
16286	9	132,257,966	132,259,177	1,211	1	10.21	11.737	9.974	16	15	17	1	0	2	LOC100506190, LOC100128077	12841, 5811	in gene, downstream	ActReg chr9 #16286	0	1	0
16287	9	132,275,963	132,276,526	563	1	1.611	4.5	12.611	3	7	19	0	0	1	LOC100506190	30,514	downstream	ActReg chr9 #16287	0	0	1
16288	9	132,311,775	132,312,394	619	1	4.15	5.25	10.45	8	7	14	1	0	0				ActReg chr9 #16288	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16289	9	132,331,505	132,332,307	802	1	6.92	4.96	11.48	13	7	18	1	0	0				ActReg chr9 #16289	0	0	1
16290	9	132,388,152	132,388,741	589	1	6.842	7.105	12.21	13	10	18	1	2	3	C9orf50, METTL11A, ASB6	-5391, 11, 15998	upstream, in gene, downstream	ActReg chr9 #16290	0	0	1
16291	9	132,403,448	132,405,118	1,670	2	44.038	49.615	6.019	213	204	13	1	1	2	METTL11A, ASB6	15848, 161	downstream, in gene	ActReg chr9 #16291	1	1	0
16292	9	132,449,782	132,450,245	463	1	6.8	10.067	10.933	9	13	15	0	0	1	PRRX2	22,093	in gene	ActReg chr9 #16292	0	0	1
16293	9	132,474,999	132,475,742	743	1	7.478	12.548	4.391	11	17	11	0	0	2	PRRX2, LOC100506231	47450, 5587	in gene, in gene	ActReg chr9 #16293	0	1	0
16294	9	132,498,601	132,499,013	412	1	2.692	6	12.538	4	10	17	0	0	1	PTGES	16,537	downstream	ActReg chr9 #16294	0	0	1
16295	9	132,499,578	132,500,443	565	1	6.125	5.824	11.529	10	7	16	1	0	1	PTGES	15,184	downstream	ActReg chr9 #16295	0	0	1
16296	9	132,539,188	132,539,929	741	2	11.957	13.913	6.435	19	25	14	0	0	0				ActReg chr9 #16296	1	1	0
16297	9	132,552,547	132,553,211	664	2	11.65	15.9	3.95	19	29	7	0	0	0				ActReg chr9 #16297	1	1	0
16298	9	132,565,285	132,565,731	446	1	6.214	11.357	7.214	10	20	9	1	1	2	TOR1B, TOR1A	76, 20933	in gene, downstream	ActReg chr9 #16298	0	1	0
16299	9	132,586,005	132,586,705	700	3	10.429	12.409	6.571	21	27	17	1	1	2	TOR1A, C9orf78	86, 11217	in gene, downstream	ActReg chr9 #16299	1	1	1
16300	9	132,641,503	132,642,451	948	1	2.957	2.933	10.067	5	6	14	0	0	2	USP20, FNBP1	44281, 163496	in gene, downstream	ActReg chr9 #16300	0	0	1
16301	9	132,815,969	132,816,503	534	1	12.125	11.688	14.375	18	14	20	1	1	1	GPR107	251	in gene	ActReg chr9 #16301	0	0	1
16302	9	133,060,531	133,061,876	1,345	2	13.381	16	5.119	29	40	12	0	0	1	LOC100289200	33,042	in gene	ActReg chr9 #16302	1	1	0
16303	9	133,238,038	133,238,458	420	1	4.846	1.167	11.769	6	2	17	0	0	1	HMCN2	14,859	in gene	ActReg chr9 #16303	0	0	1
16304	9	133,252,873	133,253,517	644	1	4.85	2.526	12.3	7	4	21	0	0	1	HMCN2	29,806	in gene	ActReg chr9 #16304	0	0	1
16305	9	133,258,059	133,258,596	537	1	4.294	2.438	12.412	7	4	19	0	0	1	HMCN2	34,938	in gene	ActReg chr9 #16305	0	0	1
16306	9	133,266,492	133,267,218	726	1	1.955	6.261	14.087	4	10	23	0	0	1	HMCN2	43,466	in gene	ActReg chr9 #16306	0	0	1
16307	9	133,336,783	133,337,288	505	1	7.312	5.688	10.375	12	7	14	0	0	1	ASS1	16,941	in gene	ActReg chr9 #16307	0	0	1
16308	9	133,454,624	133,455,036	412	1	3.769	7.077	12.846	7	10	21	1	2	2	LOC100272217, FUBP3	51, -130	in gene, upstream	ActReg chr9 #16308	0	0	1
16309	9	133,540,985	133,541,722	737	1	2	4.143	12.304	3	7	18	1	1	1	PRDM12	1,372	in gene	ActReg chr9 #16309	0	0	1
16310	9	133,567,722	133,568,037	315	1	8	4.6	12.9	11	5	16	0	1	2	PRDM12, EXOSC2	27898, -1279	downstream, upstream	ActReg chr9 #16310	0	0	1
16311	9	133,588,174	133,588,966	792	1	6.52	10.04	13.48	10	14	21	1	1	2	EXOSC2, ABL1	19412, -698	downstream, upstream	ActReg chr9 #16311	0	0	1
16312	9	133,641,318	133,641,923	605	1	11.684	9.105	4.737	19	15	8	0	0	1	ABL1	52,352	in gene	ActReg chr9 #16312	1	0	0
16313	9	133,709,976	133,710,625	649	1	5.81	11.048	6.15	12	17	12	1	0	1	ABL1	121,032	in gene	ActReg chr9 #16313	0	1	0
16314	9	133,794,274	133,794,717	443	1	3.077	6.308	13.923	5	10	20	1	0	1	FIBCD1	19,960	in gene	ActReg chr9 #16314	0	0	1
16315	9	133,815,401	133,816,068	667	1	5.048	5.476	13.905	8	10	21	1	1	1	FIBCD1	-1,279	upstream	ActReg chr9 #16315	0	0	1
16316	9	133,865,306	133,865,763	457	1	3.267	2.2	12.467	5	3	18	0	0	0				ActReg chr9 #16316	0	0	1
16317	9	133,884,806	133,885,287	481	1	4.067	4.143	10.733	5	7	17	1	1	1	LAMC3	542	in gene	ActReg chr9 #16317	0	0	1
16318	9	133,906,707	133,907,123	416	1	3.308	1.364	12.077	6	2	17	0	0	1	LAMC3	22,411	in gene	ActReg chr9 #16318	0	0	1
16319	9	133,952,446	133,952,884	438	1	3.643	3.833	10.357	6	6	16	0	0	1	LAMC3	68,161	in gene	ActReg chr9 #16319	0	0	1
16320	9	134,000,622	134,001,466	844	2	16.692	15.615	10.5	29	32	15	1	1	2	AIF1L, NUP214	29181, 63	downstream, in gene	ActReg chr9 #16320	1	1	0
16321	9	134,165,383	134,165,966	583	1	5.125	9.5	12.389	8	15	18	0	1	1	PPAPDC3	593	in gene	ActReg chr9 #16321	0	0	1
16322	9	134,210,119	134,210,503	384	1	2.375	5.333	10.083	3	7	15	0	0	0				ActReg chr9 #16322	0	0	1
16323	9	134,225,019	134,225,575	556	1	7.167	5.867	11.111	14	11	16	0	0	0				ActReg chr9 #16323	0	0	1
16324	9	134,248,394	134,249,323	929	2	10.552	12.379	8.154	17	20	16	1	0	0				ActReg chr9 #16324	1	1	0
16325	9	134,377,926	134,379,125	1,199	2	14.649	16.73	9.343	37	45	17	1	1	2	BAT2L1, POMT1	73048, 236	downstream, in gene	ActReg chr9 #16325	1	1	0
16326	9	134,393,991	134,394,554	563	1	4.941	6	11.647	6	9	16	0	0	2	POMT1, UCK1	15983, 12390	in gene, downstream	ActReg chr9 #16326	0	0	1
16327	9	134,408,393	134,408,814	421	1	5.846	4.692	11.308	9	8	18	0	1	2	POMT1, UCK1	30314, -1941	downstream, upstream	ActReg chr9 #16327	0	0	1
16328	9	134,649,088	134,650,607	1,519	2	9.688	13.021	7.021	22	27	12	0	0	0				ActReg chr9 #16328	1	1	0
16329	9	134,650,749	134,651,807	1,058	1	6.545	11.546	4.424	10	17	7	0	0	0				ActReg chr9 #16329	0	1	0
16330	9	134,651,816	134,652,457	641	1	8.15	13.2	4.85	14	23	8	0	0	0				ActReg chr9 #16330	0	1	0
16331	9	134,673,841	134,675,221	1,380	2	12	15.046	4.698	28	32	9	0	0	0				ActReg chr9 #16331	1	1	0
16332	9	134,712,557	134,713,320	763	1	4.125	4.917	11.333	7	10	16	0	0	0				ActReg chr9 #16332	0	0	1
16333	9	134,731,500	134,731,954	454	1	2.929	3	10.714	4	5	17	0	0	1	MED27	223,526	downstream	ActReg chr9 #16333	0	0	1
16334	9	134,835,581	134,836,963	1,382	1	7.818	10.636	2.167	15	17	6	0	0	1	MED27	118,981	in gene	ActReg chr9 #16334	0	1	0
16335	9	134,954,662	134,955,605	943	1	5.828	11	2.8	11	21	5	1	1	1	MED27	120	in gene	ActReg chr9 #16335	0	1	0
16336	9	134,989,187	134,990,212	1,025	2	10.844	14.656	2.031	29	29	4	0	0	0				ActReg chr9 #16336	1	1	0
16337	9	135,063,506	135,063,936	430	1	4	1.692	11.143	6	2	17	0	0	1	NTNG2	26,387	in gene	ActReg chr9 #16337	0	0	1
16338	9	135,069,582	135,070,194	612	1	4.5	4.474	12.632	8	7	20	0	0	1	NTNG2	32,554	in gene	ActReg chr9 #16338	0	0	1
16339	9	135,112,475	135,113,037	562	1	1.941	2.941	11.167	4	6	17	0	0	1	NTNG2	75,422	in gene	ActReg chr9 #16339	0	0	1
16340	9	135,113,935	135,114,418	483	1	3	4.067	13.533	5	6	23	0	0	1	NTNG2	76,842	in gene	ActReg chr9 #16340	0	0	1
16341	9	135,115,939	135,116,588	649	1	3.7	7.75	12.5	6	15	20	1	0	1	NTNG2	78,929	in gene	ActReg chr9 #16341	0	0	1
16342	9	135,229,917	135,230,522	605	1	13.105	8.263	5.263	20	13	9	1	1	1	SETX	153	in gene	ActReg chr9 #16342	1	0	0
16343	9	135,457,194	135,458,135	941	2	23.965	28.828	5.393	64	82	12	1	1	2	C9orf171, BARHL1	172053, -329	downstream, upstream	ActReg chr9 #16343	1	1	0
16344	9	135,544,883	135,546,195	1,312	2	9.463	12.756	8.78	13	19	22	1	2	2	DDX31, GTF3C4	249, -189	in gene, upstream	ActReg chr9 #16344	0	1	1
16345	9	135,819,523	135,820,227	704	1	8.091	9.364	11.136	12	14	16	1	1	1	TSC1	145	in gene	ActReg chr9 #16345	0	0	1
16346	9	135,859,668	135,860,141	473	1	2.111	3.467	13.067	4	5	19	0	0	1	GFI1B	5,806	in gene	ActReg chr9 #16346	0	0	1
16347	9	135,898,567	135,899,012	445	1	3.273	4.571	11.5	5	6	18	0	1	1	GTF3C5	-7,273	upstream	ActReg chr9 #16347	0	0	1
16348	9	135,906,099	135,906,753	654	1	11.762	7.905	9.667	21	15	19	1	1	1	GTF3C5	364	in gene	ActReg chr9 #16348	1	0	0
16349	9	135,995,107	135,995,334	227	1	5.286	1.5	11.143	6	3	14	0	0	1	RALGDS	29,368	in gene	ActReg chr9 #16349	0	0	1
16350	9	136,038,307	136,038,983	676	1	4.952	5.667	12.238	8	10	18	1	1	1	GBGT1	656	in gene	ActReg chr9 #16350	0	0	1
16351	9	136,132,141	136,132,772	631	1	3.2	4.85	11.55	6	8	15	0	0	1	ABO	18,174	in gene	ActReg chr9 #16351	0	0	1
16352	9	136,202,600	136,203,509	909	2	26.179	29.036	7.821	80	86	15	1	1	2	SURF6, MED22	-7, 11918	upstream, downstream	ActReg chr9 #16352	1	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16353	9	136,214,746	136,215,520	774	2	16.48	17.68	7.348	28	40	16	1	6	8	MED22, RPL7A, SNORD24, SNORD36B, SNORD36A, SNORD36C, SURF1, SURF2	-161, 64, -1118, -1816, -2178, -2568, 8228, -8288	upstream, in gene, upstream, upstream, upstream, upstream, downstream, upstream	ActReg chr9 #16353	1	1	0
16354	9	136,241,697	136,243,619	1,922	3	17.517	17.033	3.729	51	58	9	1	2	2	SURF4, C9orf96	312, -626	in gene, upstream	ActReg chr9 #16354	1	1	0
16355	9	136,265,126	136,265,723	597	1	6.556	4.944	10.778	9	8	14	0	0	2	C9orf96, REXO4	22140, 17740	in gene, downstream	ActReg chr9 #16355	0	0	1
16356	9	136,282,899	136,283,716	817	3	11	14.577	8.4	20	29	16	1	1	2	REXO4, ADAMTS13	-143, 3848	upstream, in gene	ActReg chr9 #16356	1	1	1
16357	9	136,343,502	136,344,271	769	1	6.083	6.375	11.708	10	11	17	1	1	2	C9orf7, SLC2A6	18799, 390	downstream, in gene	ActReg chr9 #16357	0	0	1
16358	9	136,350,179	136,350,597	418	1	3.846	4.846	10	6	6	13	0	1	1	SLC2A6	-6,112	upstream	ActReg chr9 #16358	0	0	1
16359	9	136,356,671	136,356,979	308	1	2.333	3.2	12.9	3	4	18	0	0	0				ActReg chr9 #16359	0	0	1
16360	9	136,358,290	136,358,974	684	1	3.762	4.619	12.476	8	7	19	0	0	0				ActReg chr9 #16360	0	0	1
16361	9	136,393,145	136,393,679	534	1	5.353	3.941	11.647	10	9	17	0	2	2	TMEM8C, ADAMTSL2	-3344, -3874	upstream, upstream	ActReg chr9 #16361	0	0	1
16362	9	136,423,845	136,424,406	561	1	7.118	9.647	2.643	13	17	8	0	0	1	ADAMTSL2	26,839	in gene	ActReg chr9 #16362	0	1	0
16363	9	136,433,649	136,434,025	376	1	4.917	7.167	12.25	9	11	19	1	0	1	ADAMTSL2	36,551	in gene	ActReg chr9 #16363	0	0	1
16364	9	136,450,460	136,451,216	756	1	4.625	2.889	14.958	7	4	22	1	1	2	ADAMTSL2, FAM163B	53552, -5493	downstream, upstream	ActReg chr9 #16364	0	0	1
16365	9	136,499,237	136,499,872	635	1	1.6	2.2	12.9	3	5	20	0	1	1	DBH	-1,931	upstream	ActReg chr9 #16365	0	0	1
16366	9	136,515,005	136,515,347	342	1	3.091	1.667	11.182	4	3	15	0	0	2	DBH, LOC100506440	13691, 7259	in gene, downstream	ActReg chr9 #16366	0	0	1
16367	9	136,524,176	136,524,689	513	1	1.5	2.6	12.438	2	6	20	0	1	3	DBH, LOC100506440, SARDH	22947, -1997, 80645	in gene, upstream, downstream	ActReg chr9 #16367	0	0	1
16368	9	136,557,773	136,558,323	550	1	3.824	4.176	11.294	7	7	18	0	0	1	SARDH	47,029	in gene	ActReg chr9 #16368	0	0	1
16369	9	136,578,155	136,578,567	412	1	1.667	2.923	11.231	3	4	17	0	0	1	SARDH	26,716	in gene	ActReg chr9 #16369	0	0	1
16370	9	136,697,982	136,698,434	452	1	1.867	2.267	10.2	3	4	15	0	0	1	VAV2	159,238	in gene	ActReg chr9 #16370	0	0	1
16371	9	136,728,391	136,728,789	398	1	1.667	3.25	11.667	2	5	16	1	0	1	VAV2	128,856	in gene	ActReg chr9 #16371	0	0	1
16372	9	136,739,174	136,740,198	1,024	1	6.375	12.5	6.188	10	20	12	0	0	1	VAV2	117,760	in gene	ActReg chr9 #16372	0	1	0
16373	9	136,748,330	136,748,904	574	1	1.875	2.471	11.889	2	4	16	0	0	2	VAV2, LOC100128155	108829, 11589	in gene, downstream	ActReg chr9 #16373	0	0	1
16374	9	136,766,385	136,766,744	359	1	3.364	3.818	11.454	5	6	15	0	1	2	VAV2, LOC100128155	90882, -6558	in gene, upstream	ActReg chr9 #16374	0	0	1
16375	9	136,771,563	136,772,139	576	1	4.889	4	10.167	7	7	13	0	0	1	VAV2	85,595	in gene	ActReg chr9 #16375	0	0	1
16376	9	136,785,150	136,785,775	625	1	3.85	5.6	12.1	8	9	15	0	0	1	VAV2	71,984	in gene	ActReg chr9 #16376	0	0	1
16377	9	136,855,948	136,856,733	785	2	8.333	11.75	6.364	16	21	11	1	1	1	VAV2	1,106	in gene	ActReg chr9 #16377	1	1	0
16378	9	136,860,305	136,860,677	372	1	4.167	6.583	10.167	7	8	17	0	1	1	VAV2	-3,045	upstream	ActReg chr9 #16378	0	0	1
16379	9	136,890,234	136,890,936	702	2	21.381	23.773	6.125	52	62	11	1	1	2	NCRNA00094, BRD3	24, 42556	in gene, downstream	ActReg chr9 #16379	1	1	0
16380	9	136,919,222	136,919,735	513	1	4.062	6.812	11.562	7	10	19	1	1	2	BRD3, LOC100130548	13663, 66	in gene, in gene	ActReg chr9 #16380	0	0	1
16381	9	136,922,902	136,923,472	570	1	3.444	3.389	11.889	8	7	17	0	0	2	BRD3, LOC100130548	9954, 3775	in gene, in gene	ActReg chr9 #16381	0	0	1
16382	9	136,926,759	136,927,543	784	1	3.042	4.042	13.042	6	8	20	0	0	2	BRD3, LOC100130548	5990, 7739	in gene, downstream	ActReg chr9 #16382	0	0	1
16383	9	136,994,391	136,994,864	473	1	4.2	2.5	12.067	6	4	19	0	1	1	WDR5	-6,583	upstream	ActReg chr9 #16383	0	0	1
16384	9	137,000,403	137,001,285	882	3	13.321	15.321	10.923	23	29	27	1	1	1	WDR5	-366	upstream	ActReg chr9 #16384	1	1	1
16385	9	137,018,699	137,019,321	622	1	3.143	1.727	13.158	5	5	19	2	0	1	WDR5	17,800	in gene	ActReg chr9 #16385	0	0	1
16386	9	137,028,081	137,028,830	749	1	4	5.091	12.304	8	10	19	1	1	2	WDR5, RNU6ATAC	27245, 1231	downstream, downstream	ActReg chr9 #16386	0	0	1
16387	9	137,029,376	137,030,784	1,408	2	12.511	12.333	6.578	22	22	13	1	1	2	WDR5, RNU6ATAC	28870, -394	downstream, upstream	ActReg chr9 #16387	1	1	0
16388	9	137,035,003	137,035,578	575	1	4.389	5.056	11.833	7	6	16	0	1	2	WDR5, RNU6ATAC	34080, -5604	downstream, upstream	ActReg chr9 #16388	0	0	1
16389	9	137,039,729	137,040,338	609	1	2.895	3.789	11.158	5	6	15	0	0	0				ActReg chr9 #16389	0	0	1
16390	9	137,105,527	137,106,227	700	1	2.667	3.176	11.546	5	5	15	0	0	0				ActReg chr9 #16390	0	0	1
16391	9	137,117,009	137,117,337	328	1	1.556	4.2	10.6	3	5	13	0	0	0				ActReg chr9 #16391	0	0	1
16392	9	137,122,866	137,123,755	889	1	2.192	2.148	11.393	6	5	21	0	0	0				ActReg chr9 #16392	0	0	1
16393	9	137,152,120	137,152,465	345	1	2.545	2.182	12	4	3	17	0	0	0				ActReg chr9 #16393	0	0	1
16394	9	137,159,150	137,159,717	567	1	3.167	3.25	10.556	5	6	16	0	0	0				ActReg chr9 #16394	0	0	1
16395	9	137,164,940	137,165,492	552	1	5.118	2.077	11.235	8	3	17	0	0	0				ActReg chr9 #16395	0	0	1
16396	9	137,207,187	137,207,687	500	1	2	1.562	11.688	3	5	15	0	0	0				ActReg chr9 #16396	0	0	1
16397	9	137,227,904	137,228,553	649	1	5.762	3.429	10.857	8	8	15	0	0	1	RXRA	9,912	in gene	ActReg chr9 #16397	0	0	1
16398	9	137,229,795	137,230,632	837	1	5.208	7.846	12.885	10	14	20	1	0	1	RXRA	11,897	in gene	ActReg chr9 #16398	0	0	1
16399	9	137,303,655	137,304,295	640	1	4.632	9.45	12.75	9	13	18	0	0	1	RXRA	85,659	in gene	ActReg chr9 #16399	0	0	1
16400	9	137,308,999	137,309,509	510	1	2.2	4.062	11.938	3	6	14	0	0	1	RXRA	90,938	in gene	ActReg chr9 #16400	0	0	1
16401	9	137,311,936	137,312,471	535	1	1.5	3.294	11.412	2	5	18	0	0	1	RXRA	93,887	in gene	ActReg chr9 #16401	0	0	1
16402	9	137,393,724	137,394,173	449	1	2.071	3.214	10.286	3	5	15	0	0	0				ActReg chr9 #16402	0	0	1
16403	9	137,428,909	137,429,360	451	1	3.538	4.786	10.714	6	6	16	0	0	1	LOC100506532	10,106	in gene	ActReg chr9 #16403	0	0	1
16404	9	137,444,921	137,445,721	800	1	2.167	4.44	11.96	5	7	18	0	0	1	LOC100506532	26,293	downstream	ActReg chr9 #16404	0	0	1
16405	9	137,521,505	137,522,074	569	1	2.643	1.588	12.706	4	3	17	0	0	0				ActReg chr9 #16405	0	0	1
16406	9	137,581,046	137,581,503	457	1	3.714	3.429	11.286	6	5	16	0	0	1	COL5A1	47,622	in gene	ActReg chr9 #16406	0	0	1
16407	9	137,590,432	137,590,959	527	1	6.118	4.706	11.765	9	7	17	0	0	1	COL5A1	57,043	in gene	ActReg chr9 #16407	0	0	1
16408	9	137,630,688	137,631,136	448	1	3.8	5.333	10.133	7	10	16	0	0	1	COL5A1	97,260	in gene	ActReg chr9 #16408	0	0	1
16409	9	137,721,128	137,721,631	503	1	1.933	4	13.533	4	6	18	0	0	2	COL5A1, LOC100506554	187727, 13154	in gene, downstream	ActReg chr9 #16409	0	0	1
16410	9	137,731,390	137,731,865	475	1	3.933	4.357	11.133	6	8	14	1	0	2	COL5A1, LOC100506554	197975, 2906	in gene, in gene	ActReg chr9 #16410	0	0	1
16411	9	137,851,193	137,851,634	441	1	2.714	1.769	11.714	4	4	15	0	0	0				ActReg chr9 #16411	0	0	1
16412	9	137,882,710	137,883,062	352	1	1.909	3.091	9.909	3	4	13	0	0	0				ActReg chr9 #16412	0	0	1
16413	9	137,969,163	137,969,815	652	1	6.7	11.45	4.1	11	18	6	0	1	1	OLFM1	2,400	in gene	ActReg chr9 #16413	0	1	0
16414	9	137,978,548	137,979,352	804	1	5	8.75	14.062	8	11	23	1	0	1	OLFM1	12,011	in gene	ActReg chr9 #16414	0	0	1
16415	9	137,982,251	137,982,942	691	1	8.857	12.381	3.238	16	22	5	0	0	1	OLFM1	15,507	in gene	ActReg chr9 #16415	0	1	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16416	9	137,989,967	137,990,811	844	2	11.192	14.231	4.231	24	29	6	0	0	1	OLFM1	23,300	in gene	ActReg chr9 #16416	1	1	0
16417	9	137,997,489	137,998,178	689	1	2.333	4.682	12	4	8	16	1	0	1	OLFM1	30,744	in gene	ActReg chr9 #16417	0	0	1
16418	9	138,048,204	138,049,016	812	2	13.44	16.12	5.28	28	32	8	0	0	0				ActReg chr9 #16418	1	1	0
16419	9	138,134,710	138,135,125	415	1	1.333	1.5	11.154	2	2	15	0	0	0				ActReg chr9 #16419	0	0	1
16420	9	138,238,345	138,238,659	314	1	3.444	2.778	10.6	5	7	17	0	0	1	C9orf62	5,401	downstream	ActReg chr9 #16420	0	0	1
16421	9	138,366,006	138,366,277	271	1	3.556	5	11	9	7	15	0	2	2	LOC100506599, KIAA0649	-2046, -5507	upstream, upstream	ActReg chr9 #16421	0	0	1
16422	9	138,366,697	138,367,327	630	2	13.947	11.421	2	33	22	3	0	2	2	LOC100506599, KIAA0649	-2917, -4636	upstream, upstream	ActReg chr9 #16422	1	1	0
16423	9	138,391,364	138,393,484	2,120	4	30.515	38.667	8.727	125	149	19	1	2	2	C9orf116, MRPS2	-663, -59	upstream, upstream	ActReg chr9 #16423	1	1	1
16424	9	138,405,148	138,405,631	483	1	3.8	7.267	12.467	5	9	15	0	0	2	MRPS2, LCN1	12906, -7897	downstream, upstream	ActReg chr9 #16424	0	0	1
16425	9	138,414,932	138,415,310	378	1	3	2.364	10.75	4	4	13	0	1	1	LCN1	1,835	in gene	ActReg chr9 #16425	0	0	1
16426	9	138,419,523	138,419,841	318	1	5.8	3.667	10	7	6	15	0	0	1	LCN1	6,396	downstream	ActReg chr9 #16426	0	0	1
16427	9	138,475,567	138,475,856	289	1	4.889	5.111	11.444	6	6	14	0	0	1	LOC100130954	8,940	in gene	ActReg chr9 #16427	0	0	1
16428	9	138,480,299	138,480,607	308	1	5.667	5.556	11.667	8	8	16	0	0	1	LOC100130954	13,682	downstream	ActReg chr9 #16428	0	0	1
16429	9	138,480,619	138,481,022	403	1	2.5	3	11	4	5	18	0	0	1	LOC100130954	14,049	downstream	ActReg chr9 #16429	0	0	1
16430	9	138,483,360	138,483,952	592	1	3.056	4.158	11.474	6	7	15	0	0	1	LOC100130954	16,885	downstream	ActReg chr9 #16430	0	0	1
16431	9	138,509,874	138,510,368	494	1	3.071	2.688	12.938	5	5	18	0	0	1	GLT6D1	21,265	downstream	ActReg chr9 #16431	0	0	1
16432	9	138,577,655	138,578,064	409	1	2.846	1.818	10.231	4	4	15	0	0	1	SOHLH1	13,515	downstream	ActReg chr9 #16432	0	0	1
16433	9	138,610,178	138,610,791	613	1	3.211	4.421	11.947	7	7	15	0	0	1	KCNT1	16,453	in gene	ActReg chr9 #16433	0	0	1
16434	9	138,611,173	138,611,807	634	1	4.105	3.167	12.368	6	5	20	0	0	1	KCNT1	17,459	in gene	ActReg chr9 #16434	0	0	1
16435	9	138,626,404	138,627,039	635	1	3.421	5.211	11.053	6	8	15	1	0	1	KCNT1	32,690	in gene	ActReg chr9 #16435	0	0	1
16436	9	138,634,110	138,634,640	530	1	2.118	3.786	10.823	4	7	15	0	0	1	KCNT1	40,344	in gene	ActReg chr9 #16436	0	0	1
16437	9	138,634,684	138,635,266	582	1	2.8	1.733	13.105	5	3	19	0	0	1	KCNT1	40,944	in gene	ActReg chr9 #16437	0	0	1
16438	9	138,636,032	138,636,882	850	1	2.654	2.84	10.333	6	5	13	1	0	1	KCNT1	42,426	in gene	ActReg chr9 #16438	0	0	1
16439	9	138,638,665	138,639,083	418	1	1.769	3.538	10.692	3	5	16	0	0	1	KCNT1	44,843	in gene	ActReg chr9 #16439	0	0	1
16440	9	138,650,972	138,651,853	881	1	3.714	4.893	13.786	6	9	19	0	0	1	KCNT1	57,381	in gene	ActReg chr9 #16440	0	0	1
16441	9	138,662,136	138,663,090	954	1	2.724	3.172	12.4	5	7	19	1	0	1	KCNT1	68,582	in gene	ActReg chr9 #16441	0	0	1
16442	9	138,664,427	138,665,198	771	1	3.87	4.292	12.333	6	6	17	0	0	1	KCNT1	70,781	in gene	ActReg chr9 #16442	0	0	1
16443	9	138,669,773	138,670,460	687	1	2.316	2.762	12.191	3	6	21	1	0	1	KCNT1	76,085	in gene	ActReg chr9 #16443	0	0	1
16444	9	138,671,917	138,672,374	457	1	7.286	4.929	12.714	11	7	17	0	0	1	KCNT1	78,114	in gene	ActReg chr9 #16444	0	0	1
16445	9	138,679,146	138,679,673	527	1	3.923	4.375	12.375	7	7	17	0	0	1	KCNT1	85,378	in gene	ActReg chr9 #16445	0	0	1
16446	9	138,680,073	138,680,777	704	1	2.6	5.545	11	4	10	17	1	0	1	KCNT1	86,384	in gene	ActReg chr9 #16446	0	0	1
16447	9	138,817,233	138,817,777	544	1	3.118	3.647	11.706	7	5	17	0	0	1	UBAC1	35,721	downstream	ActReg chr9 #16447	0	0	1
16448	9	138,822,178	138,822,563	385	1	2.833	3.917	11.833	5	7	18	0	0	1	UBAC1	30,856	downstream	ActReg chr9 #16448	0	0	1
16449	9	138,841,290	138,841,769	479	1	2.867	6.533	12.933	4	9	19	0	0	1	UBAC1	11,697	in gene	ActReg chr9 #16449	0	0	1
16450	9	138,863,629	138,864,386	757	2	14.167	16.458	5.167	32	41	10	0	0	0				ActReg chr9 #16450	1	1	0
16451	9	138,872,444	138,873,522	1,078	1	4.364	5.618	13.647	10	11	20	1	0	0				ActReg chr9 #16451	0	0	1
16452	9	138,879,631	138,880,078	447	1	2.857	2.429	12.071	5	3	20	0	0	0				ActReg chr9 #16452	0	0	1
16453	9	138,895,188	138,895,897	709	1	4.048	4.667	13.5	9	10	18	0	0	1	NACC2	91,589	downstream	ActReg chr9 #16453	0	0	1
16454	9	138,914,035	138,914,439	404	1	4.077	6	12.231	8	8	16	0	0	1	NACC2	72,894	in gene	ActReg chr9 #16454	0	0	1
16455	9	138,970,322	138,970,801	479	1	3.067	5	11.2	5	7	15	0	0	1	NACC2	16,570	in gene	ActReg chr9 #16455	0	0	1
16456	9	138,993,638	138,994,150	512	1	4.875	3.4	12.5	6	6	21	1	1	2	NACC2, LOC402382	-6763, 5771	upstream, in gene	ActReg chr9 #16456	0	0	1
16457	9	138,997,082	138,997,589	507	1	4.125	1.875	12.625	6	4	17	0	0	3	NACC2, LOC402382, C9orf69	-10204, 9212, 13396	upstream, downstream, downstream	ActReg chr9 #16457	0	0	1
16458	9	139,001,312	139,002,348	1,036	1	7.455	12.485	8.094	13	21	15	0	0	2	LOC402382, C9orf69	13707, 8901	downstream, downstream	ActReg chr9 #16458	0	1	0
16459	9	139,006,387	139,007,068	681	1	6.714	11.857	4.857	11	17	9	0	1	2	C9orf69, LOC100129999	4004, -7640	in gene, upstream	ActReg chr9 #16459	0	1	0
16460	9	139,009,907	139,011,021	1,114	1	10.529	10.514	6.16	18	23	9	1	2	2	C9orf69, LOC100129999	267, -3903	in gene, upstream	ActReg chr9 #16460	0	1	0
16461	9	139,016,423	139,016,875	452	1	7.786	6.786	11.786	10	9	19	0	2	2	C9orf69, LOC100129999	-5918, 2282	upstream, downstream	ActReg chr9 #16461	0	0	1
16462	9	139,033,931	139,034,336	405	1	4.385	5.231	10.462	6	7	16	0	0	0				ActReg chr9 #16462	0	0	1
16463	9	139,041,401	139,042,019	618	1	4.947	2.65	10.7	8	4	13	0	0	0				ActReg chr9 #16463	0	0	1
16464	9	139,065,511	139,065,906	395	1	1.571	3.25	11.917	2	5	17	0	0	0				ActReg chr9 #16464	0	0	1
16465	9	139,095,255	139,095,658	403	1	4.615	4.846	11	6	8	18	1	1	2	LHX3, QSOX2	1499, 42231	in gene, downstream	ActReg chr9 #16465	0	0	1
16466	9	139,096,241	139,096,920	679	1	7.048	7.952	14.857	14	12	24	1	1	2	LHX3, QSOX2	375, 41107	in gene, downstream	ActReg chr9 #16466	0	0	1
16467	9	139,108,572	139,109,108	536	1	2	3.176	12.059	3	5	17	0	0	1	QSOX2	28,847	in gene	ActReg chr9 #16467	0	0	1
16468	9	139,147,662	139,148,111	449	1	2.727	3.462	12	5	5	19	0	0	2	QSOX2, ESP33	-10199, 6081	upstream, downstream	ActReg chr9 #16468	0	0	1
16469	9	139,153,578	139,154,481	603	1	2.444	5.158	12.263	5	6	15	0	0	0				ActReg chr9 #16469	0	0	1
16470	9	139,166,252	139,166,774	522	1	3.75	6.812	11.625	7	9	16	0	0	0				ActReg chr9 #16470	0	0	1
16471	9	139,221,381	139,221,801	420	1	6.077	10.692	11.462	9	18	18	0	2	2	LOC26102, GPSM1	188, -341	in gene, upstream	ActReg chr9 #16471	0	0	1
16472	9	139,230,829	139,231,688	859	1	3.577	5.556	12.148	6	10	16	1	0	2	LOC26102, GPSM1	-9479, 9326	upstream, in gene	ActReg chr9 #16472	0	0	1
16473	9	139,239,300	139,240,998	1,698	1	8.151	14.415	9.132	16	23	16	1	0	1	GPSM1	18,217	in gene	ActReg chr9 #16473	0	1	0
16474	9	139,243,813	139,244,667	854	1	5.5	3.769	10.731	7	7	15	0	0	1	GPSM1	22,308	in gene	ActReg chr9 #16474	0	0	1
16475	9	139,248,815	139,249,492	677	1	3.381	3.095	11.809	7	6	18	0	0	3	GPSM1, DNLZ, CARD9	27221, 9088, 18980	in gene, downstream, downstream	ActReg chr9 #16475	0	0	1
16476	9	139,250,124	139,250,711	587	1	7.278	3.167	13.333	12	6	21	0	0	3	GPSM1, DNLZ, CARD9	28485, 7824, 17716	in gene, downstream, downstream	ActReg chr9 #16476	0	0	1
16477	9	139,264,349	139,265,268	919	1	4.36	4.815	13.31	8	9	22	1	1	3	DNLZ, CARD9, SNAPC4	-6567, 3325, 28081	upstream, in gene, downstream	ActReg chr9 #16477	0	0	1
16478	9	139,271,258	139,272,979	1,721	1	4	3.556	12.852	8	8	23	0	1	2	CARD9, SNAPC4	-3985, 20771	upstream, in gene	ActReg chr9 #16478	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16479	9	139,294,423	139,295,233	810	1	9.192	12	5.792	14	18	12	1	1	3	SNAPC4, SDCCAG3, PMPCA	-1939, 10226, -10288	upstream, downstream, upstream	ActReg chr9 #16479	0	1	0
16480	9	139,295,500	139,295,888	388	1	5.417	6.083	11.917	8	9	14	0	1	3	SNAPC4, SDCCAG3, PMPCA	-2805, 9360, -9422	upstream, downstream, upstream	ActReg chr9 #16480	0	0	1
16481	9	139,304,949	139,305,897	948	1	8.567	10.133	15.233	14	20	25	1	2	2	SDCCAG3, PMPCA	-369, 307	upstream, in gene	ActReg chr9 #16481	0	0	1
16482	9	139,312,508	139,313,024	516	1	3.882	4.765	12.765	6	7	24	1	1	2	SDCCAG3, PMPCA	-7712, 7650	upstream, in gene	ActReg chr9 #16482	0	0	1
16483	9	139,326,631	139,327,310	679	1	3.667	4.333	13.809	6	8	24	1	0	3	PMPCA, INPP5E, SEC16A	21854, 7286, 50537	downstream, in gene, downstream	ActReg chr9 #16483	0	0	1
16484	9	139,333,423	139,334,735	1,312	2	11.171	14.244	4.143	20	24	11	1	1	2	INPP5E, SEC16A	177, 43428	in gene, downstream	ActReg chr9 #16484	1	1	0
16485	9	139,349,188	139,349,741	553	1	3.375	3.412	13.059	5	8	16	1	0	1	SEC16A	28,043	in gene	ActReg chr9 #16485	0	0	1
16486	9	139,368,459	139,368,876	417	1	4.231	2.889	12.308	6	4	19	1	0	2	SEC16A, C9orf163	8840, -9280	in gene, upstream	ActReg chr9 #16486	0	0	1
16487	9	139,378,300	139,379,345	1,045	1	9.939	8.545	12.424	16	13	21	1	2	3	SEC16A, C9orf163, NOTCH1	-1315, 875, 61416	upstream, in gene, downstream	ActReg chr9 #16487	0	0	1
16488	9	139,397,705	139,398,355	650	1	3.789	4.667	11.6	7	8	15	1	0	1	NOTCH1	42,208	in gene	ActReg chr9 #16488	0	0	1
16489	9	139,399,120	139,399,668	548	1	4.941	3.706	12.941	8	6	20	1	0	1	NOTCH1	40,844	in gene	ActReg chr9 #16489	0	0	1
16490	9	139,400,772	139,401,347	575	1	4.333	3.882	11.5	7	6	16	1	0	1	NOTCH1	39,179	in gene	ActReg chr9 #16490	0	0	1
16491	9	139,415,802	139,416,292	490	1	2.429	4.062	10.75	4	7	16	0	0	1	NOTCH1	24,191	in gene	ActReg chr9 #16491	0	0	1
16492	9	139,418,076	139,418,714	638	1	7.6	6.5	11.9	13	10	17	0	0	1	NOTCH1	21,843	in gene	ActReg chr9 #16492	0	0	1
16493	9	139,422,927	139,423,567	640	1	3.158	7.25	11.4	5	11	15	0	0	1	NOTCH1	16,991	in gene	ActReg chr9 #16493	0	0	1
16494	9	139,427,791	139,428,354	563	1	2.588	4.389	10.611	5	9	14	1	0	1	NOTCH1	12,166	in gene	ActReg chr9 #16494	0	0	1
16495	9	139,458,550	139,459,753	1,203	1	4.842	4.921	12.526	10	10	21	0	0	0				ActReg chr9 #16495	0	0	1
16496	9	139,462,648	139,463,077	429	1	3.357	3.714	11.857	9	5	17	0	0	0				ActReg chr9 #16496	0	0	1
16497	9	139,470,043	139,470,395	352	1	3.364	3.455	11.818	6	5	16	0	0	0				ActReg chr9 #16497	0	0	1
16498	9	139,470,902	139,471,369	467	1	3.933	3	13.333	5	4	21	0	0	0				ActReg chr9 #16498	0	0	1
16499	9	139,493,816	139,494,399	583	1	3.556	6.778	12.056	5	9	17	0	0	0				ActReg chr9 #16499	0	0	1
16500	9	139,497,539	139,498,096	557	1	4.875	3.118	13.059	8	5	17	0	0	0				ActReg chr9 #16500	0	0	1
16501	9	139,498,459	139,498,764	305	1	2.556	3.3	12.5	5	5	17	0	0	0				ActReg chr9 #16501	0	0	1
16502	9	139,500,651	139,501,355	704	1	3.364	3.474	11.5	6	6	15	0	0	1	LOC401561	10,295	downstream	ActReg chr9 #16502	0	0	1
16503	9	139,503,965	139,504,591	626	1	2.632	4.65	14.15	5	7	20	0	0	1	LOC401561	7,020	downstream	ActReg chr9 #16503	0	0	1
16504	9	139,512,660	139,513,159	499	1	4.438	3	15.062	8	5	22	0	1	1	LOC401561	-1,611	upstream	ActReg chr9 #16504	0	0	1
16505	9	139,538,894	139,539,568	674	1	7.095	6.333	11.571	10	15	18	0	0	1	LOC100505976	15,642	downstream	ActReg chr9 #16505	0	0	1
16506	9	139,540,662	139,541,235	573	1	2.722	5.471	11.889	4	10	19	0	0	1	LOC100505976	13,925	downstream	ActReg chr9 #16506	0	0	1
16507	9	139,554,760	139,555,282	522	1	2.133	4.125	11.625	4	8	15	0	2	3	LOC100505976, EGFL7, MIR126	-148, -2356, -10033	upstream, upstream, upstream	ActReg chr9 #16507	0	0	1
16508	9	139,557,370	139,557,918	548	1	3.941	3.824	12.941	5	5	18	0	3	4	LOC100505976, EGFL7, MIR126, AGPAT2	-2771, 267, -7410, 24267	upstream, in gene, upstream, downstream	ActReg chr9 #16508	0	0	1
16509	9	139,562,807	139,563,229	422	1	2.923	3.923	12.462	4	6	17	0	1	4	LOC100505976, EGFL7, MIR126, AGPAT2	-8145, 5641, -2036, 18893	upstream, in gene, upstream, downstream	ActReg chr9 #16509	0	0	1
16510	9	139,565,148	139,565,485	337	1	7.182	6.364	13.909	12	10	22	1	1	3	EGFL7, MIR126, AGPAT2	7939, 262, 16595	in gene, downstream, downstream	ActReg chr9 #16510	0	0	1
16511	9	139,566,086	139,567,238	1,152	1	3.417	5.778	13.278	7	10	18	0	1	3	EGFL7, MIR126, AGPAT2	9285, 1608, 15249	in gene, downstream, downstream	ActReg chr9 #16511	0	0	1
16512	9	139,577,847	139,578,105	258	1	2.5	3.875	13.875	4	5	17	0	0	1	AGPAT2	3,935	in gene	ActReg chr9 #16512	0	0	1
16513	9	139,580,985	139,581,513	528	1	6.118	5.059	11.471	8	11	15	1	1	1	AGPAT2	662	in gene	ActReg chr9 #16513	0	0	1
16514	9	139,586,609	139,587,194	585	1	2	6.222	12	4	8	16	1	1	1	AGPAT2	-4,990	upstream	ActReg chr9 #16514	0	0	1
16515	9	139,607,970	139,608,800	830	1	5.308	5.346	13.346	9	9	19	0	1	1	FAM69B	1,361	in gene	ActReg chr9 #16515	0	0	1
16516	9	139,614,812	139,615,700	888	1	6.214	4.964	12.214	10	10	18	0	0	4	FAM69B, SNHG7, SNORA43, SNORA17	8232, 7380, 5433, 6075	in gene, downstream, downstream, downstream	ActReg chr9 #16516	0	0	1
16517	9	139,620,639	139,621,612	973	1	6.774	11	5.968	11	16	11	0	3	4	FAM69B, SNHG7, SNORA43, SNORA17	14101, 1511, -436, 206	downstream, in gene, upstream, downstream	ActReg chr9 #16517	0	1	0
16518	9	139,622,333	139,623,713	1,380	2	12.454	17.091	7.75	26	34	17	1	3	5	FAM69B, SNHG7, SNORA43, SNORA17, LCN10	15999, -387, -2334, -1692, 14388	downstream, upstream, upstream, upstream, downstream	ActReg chr9 #16518	1	1	0
16519	9	139,637,349	139,637,956	607	1	3.368	6.316	11.947	4	8	18	0	2	3	LCN10, LCN6, LOC100128593	-241, 5328, -2961	upstream, downstream, upstream	ActReg chr9 #16519	0	0	1
16520	9	139,694,186	139,694,606	420	1	4.769	4.308	11.462	8	5	17	1	0	4	TMEM141, KIAA1984, hCG_2022318, C9orf86	8619, 3606, 8904, -7978	downstream, in gene, downstream, upstream	ActReg chr9 #16520	0	0	1
16521	9	139,728,062	139,728,383	321	1	1.3	5.9	12.4	2	8	15	0	0	2	C9orf86, MIR4292	25848, 2813	in gene, downstream	ActReg chr9 #16521	0	0	1
16522	9	139,733,704	139,734,155	451	1	3.286	4.786	11.643	5	9	17	1	1	4	C9orf86, MIR4292, C9orf172, PHPT1	31555, 8520, -4938, -9327	in gene, downstream, upstream, upstream	ActReg chr9 #16522	0	0	1
16523	9	139,736,020	139,737,452	1,432	4	6.378	9.822	9.674	16	19	15	0	2	4	C9orf86, C9orf172, PHPT1, MAMDC4	34362, -2131, -6520, -10085	downstream, upstream, upstream, upstream	ActReg chr9 #16523	1	1	1
16524	9	139,738,336	139,738,637	301	1	2.5	4.1	12.1	4	6	18	1	2	4	C9orf86, C9orf172, PHPT1, MAMDC4	36112, -381, -4770, -8333	downstream, upstream, upstream, upstream	ActReg chr9 #16524	0	0	1
16525	9	139,742,029	139,742,853	824	2	11.577	12.462	7.885	19	21	11	1	2	4	C9orf86, C9orf172, PHPT1, MAMDC4	40067, 3574, -815, -4378	downstream, downstream, upstream, upstream	ActReg chr9 #16525	1	1	0
16526	9	139,743,414	139,744,122	708	2	17.227	13.727	4.091	33	24	8	1	2	4	C9orf86, C9orf172, PHPT1, MAMDC4	41394, 4901, 512, -3051	downstream, downstream, in gene, upstream	ActReg chr9 #16526	1	1	0
16527	9	139,746,401	139,747,150	749	1	3.391	5	14.13	6	9	19	0	1	4	C9orf172, PHPT1, MAMDC4, EDF1	7908, 3519, -44, 13963	downstream, downstream, upstream, downstream	ActReg chr9 #16527	0	0	1
16528	9	139,751,621	139,752,101	480	1	5.067	5.933	11.667	6	9	20	0	0	4	C9orf172, PHPT1, MAMDC4, EDF1	12994, 8605, 5042, 8877	downstream, downstream, in gene, downstream	ActReg chr9 #16528	0	0	1
16529	9	139,760,677	139,761,009	332	1	9.2	14.4	4	14	21	8	1	1	2	MAMDC4, EDF1	14024, -105	downstream, upstream	ActReg chr9 #16529	0	1	0
16530	9	139,776,489	139,777,395	906	1	9.75	12.679	9	15	17	18	0	1	1	TRAF2	-4,023	upstream	ActReg chr9 #16530	0	1	0
16531	9	139,796,011	139,796,864	853	2	8.296	11.667	9	14	18	16	0	0	1	TRAF2	15,472	in gene	ActReg chr9 #16531	0	1	1
16532	9	139,802,436	139,802,899	463	1	7.786	4.714	11.5	11	9	17	1	0	1	TRAF2	21,702	in gene	ActReg chr9 #16532	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Values	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16533	9	139,834,669	139,835,690	1,021	1	3.867	5.469	11.531	7	9	17	1	1	2	FBXW5, C8G	3994, -4519	in gene, upstream	ActReg chr9 #16533	0	0	1
16534	9	139,837,221	139,838,262	1,041	1	4.938	5.531	12.469	13	10	22	1	2	3	FBXW5, C8G, LCN12	1432, -1957, -9027	in gene, upstream, upstream	ActReg chr9 #16534	0	0	1
16535	9	139,838,819	139,839,546	727	2	13.046	11.591	3.769	27	23	5	1	3	3	FBXW5, C8G, LCN12	-9, -516, -7586	upstream, upstream, upstream	ActReg chr9 #16535	1	1	0
16536	9	139,841,479	139,842,190	711	1	7.227	3.227	12.682	13	5	18	0	3	3	FBXW5, C8G, LCN12	-2661, 2136, -4934	upstream, downstream, upstream	ActReg chr9 #16536	0	0	1
16537	9	139,844,339	139,845,079	740	1	7.522	11.652	8.087	11	20	10	1	2	3	FBXW5, C8G, LCN12	-5536, 5011, -2059	upstream, downstream, upstream	ActReg chr9 #16537	0	1	0
16538	9	139,847,873	139,848,630	757	1	4.391	3.739	11.565	7	6	17	0	1	3	FBXW5, C8G, LCN12	-9078, 8553, 1483	upstream, downstream, in gene	ActReg chr9 #16538	0	0	1
16539	9	139,858,778	139,859,270	492	1	4.375	6.438	11.125	8	8	17	0	0	1	LCN12	12,256	downstream	ActReg chr9 #16539	0	0	1
16540	9	139,863,277	139,863,890	613	1	6.579	4.263	13.632	13	7	23	0	0	1	PTGDS	-8,373	upstream	ActReg chr9 #16540	0	0	1
16541	9	139,864,393	139,864,953	560	1	3.529	4.529	13.823	7	7	20	0	1	1	PTGDS	-7,283	upstream	ActReg chr9 #16541	0	0	1
16542	9	139,866,537	139,867,170	633	1	3.85	4.6	11.55	6	7	14	0	1	1	PTGDS	-5,103	upstream	ActReg chr9 #16542	0	0	1
16543	9	139,891,201	139,891,724	523	1	6.562	2.625	13.125	11	3	21	0	1	3	C9orf142, CLIC3, ABCA2	4592, -438, 31912	downstream, upstream, downstream	ActReg chr9 #16543	0	0	1
16544	9	139,892,571	139,892,944	373	1	2.167	3.833	13	3	6	16	0	1	3	C9orf142, CLIC3, ABCA2	5887, -1733, 30617	downstream, upstream, downstream	ActReg chr9 #16544	0	0	1
16545	9	139,906,866	139,907,398	532	1	2.765	3.643	12.353	5	6	17	0	0	1	ABCA2	16,242	in gene	ActReg chr9 #16545	0	0	1
16546	9	139,911,993	139,912,808	815	1	4.538	4.692	10.731	8	8	17	1	0	2	ABCA2, C9orf139	10974, -9516	in gene, upstream	ActReg chr9 #16546	0	0	1
16547	9	139,914,902	139,916,491	1,589	1	3.08	4.82	12.88	6	11	22	1	1	3	ABCA2, C9orf139, FUT7	7678, -6220, 11596	in gene, upstream, downstream	ActReg chr9 #16547	0	0	1
16548	9	139,922,865	139,924,340	1,475	2	7.5	11.717	9.587	13	19	20	1	2	4	ABCA2, C9orf139, FUT7, NPDC1	-228, 1686, 3690, 17074	upstream, in gene, downstream, downstream	ActReg chr9 #16548	0	1	1
16549	9	139,925,798	139,926,371	573	1	4.444	5.222	10.611	6	9	16	1	2	4	ABCA2, C9orf139, FUT7, NPDC1	-2710, 4168, 1208, 14592	upstream, in gene, in gene, downstream	ActReg chr9 #16549	0	0	1
16550	9	139,933,986	139,934,451	465	1	4.385	2.929	12.357	6	5	18	0	1	4	C9orf139, FUT7, NPDC1, ENTPD2	12302, -6926, 6458, 14287	downstream, upstream, in gene, downstream	ActReg chr9 #16550	0	0	1
16551	9	139,935,598	139,936,441	843	1	4.231	3.462	12.808	8	6	20	0	0	4	C9orf139, FUT7, NPDC1, ENTPD2	14103, -8727, 4657, 12486	downstream, upstream, in gene, downstream	ActReg chr9 #16551	0	0	1
16552	9	139,939,649	139,940,055	406	1	1.636	11.5	11.417	3	15	17	1	1	3	C9orf139, NPDC1, ENTPD2	17936, 824, 8653	downstream, in gene, downstream	ActReg chr9 #16552	0	0	1
16553	9	139,940,433	139,941,331	898	2	10.75	10.857	12.036	18	17	16	1	1	3	C9orf139, NPDC1, ENTPD2	18966, -206, 7623	downstream, upstream, downstream	ActReg chr9 #16553	0	1	1
16554	9	139,945,385	139,946,492	1,107	1	3.25	3.516	11.588	7	7	19	0	2	2	NPDC1, ENTPD2	-5262, 2567	upstream, in gene	ActReg chr9 #16554	0	0	1
16555	9	139,957,738	139,958,995	1,257	1	3.436	6.103	13.795	8	12	20	0	0	2	ENTPD2, C9orf140	-9861, 6662	upstream, in gene	ActReg chr9 #16555	0	0	1
16556	9	139,963,361	139,963,843	482	1	6.667	5.6	11.667	12	7	18	0	1	2	C9orf140, UAP1L1	1426, -8351	in gene, upstream	ActReg chr9 #16556	0	0	1
16557	9	139,964,608	139,965,171	563	1	5.444	13.056	3.733	9	19	10	1	2	2	C9orf140, UAP1L1	139, -7064	in gene, upstream	ActReg chr9 #16557	0	1	0
16558	9	139,968,488	139,968,949	461	1	2.571	2.929	11.786	4	4	19	0	2	2	C9orf140, UAP1L1	-3690, -3235	upstream, upstream	ActReg chr9 #16558	0	0	1
16559	9	139,971,220	139,971,666	446	1	5.286	5.786	11.286	7	9	15	1	2	4	C9orf140, UAP1L1, hCG_2022304, MAN1B1	-6415, -510, 9826, -9974	upstream, upstream, downstream, upstream	ActReg chr9 #16559	0	0	1
16560	9	139,992,250	139,992,816	566	1	4.889	4.5	11.389	9	6	18	0	0	1	MAN1B1	11,116	in gene	ActReg chr9 #16560	0	0	1
16561	9	140,003,690	140,004,405	715	1	5.136	4.864	13.682	8	9	19	0	0	2	MAN1B1, DPP7	22630, 5148	downstream, downstream	ActReg chr9 #16561	0	0	1
16562	9	140,009,549	140,010,110	561	1	3.882	5.471	13.529	6	9	20	1	1	2	MAN1B1, DPP7	28412, -634	downstream, upstream	ActReg chr9 #16562	0	0	1
16563	9	140,010,227	140,010,760	533	1	5.412	4.235	13.471	10	6	23	0	1	2	MAN1B1, DPP7	29076, -1298	downstream, upstream	ActReg chr9 #16563	0	0	1
16564	9	140,043,196	140,043,641	445	1	5.071	4.857	11.214	8	7	18	1	0	1	GRIN1	9,809	in gene	ActReg chr9 #16564	0	0	1
16565	9	140,066,571	140,067,330	759	1	4.875	4	11.917	7	6	15	0	2	4	GRIN1, LRRC26, LOC100505993, ANAPC2	33341, -2459, -452, 16107	downstream, upstream, upstream, downstream	ActReg chr9 #16565	0	0	1
16566	9	140,068,334	140,069,183	849	1	5.385	3.038	11.692	8	4	20	1	2	4	GRIN1, LRRC26, LOC100505993, ANAPC2	35149, -4267, -2260, 14299	downstream, upstream, upstream, downstream	ActReg chr9 #16566	0	0	1
16567	9	140,069,609	140,070,469	860	1	8.556	7.444	12.518	16	12	15	0	2	4	GRIN1, LRRC26, LOC100505993, ANAPC2	36430, -5548, -3541, 13018	downstream, upstream, upstream, in gene	ActReg chr9 #16567	0	0	1
16568	9	140,082,438	140,084,027	1,589	4	13.857	14.102	11.326	46	29	20	1	2	3	ANAPC2, SSNA1, C9orf75	-175, 178, 11748	upstream, in gene, downstream	ActReg chr9 #16568	1	1	1
16569	9	140,099,997	140,100,485	488	1	10.938	12.25	11	19	20	20	1	3	3	C9orf75, TMEM203, NDOR1	-5261, -151, 122	upstream, upstream, in gene	ActReg chr9 #16569	0	0	1
16570	9	140,112,024	140,112,747	723	1	6.217	6.913	11.565	9	10	19	1	1	4	NDOR1, RNF208, LOC100130547, C9orf169	12266, 3390, 9880, -7259	in gene, downstream, downstream, upstream	ActReg chr9 #16570	0	0	1
16571	9	140,121,412	140,122,334	922	1	7.63	7.429	12.393	13	13	21	0	4	5	NDOR1, RNF208, LOC100130547, C9orf169, SLC34A3	21754, -6098, 392, 2229, -3336	downstream, upstream, in gene, downstream, upstream	ActReg chr9 #16571	0	0	1
16572	9	140,122,608	140,123,456	848	1	4.926	6.185	14.111	8	11	20	0	3	5	NDOR1, RNF208, LOC100130547, C9orf169, SLC34A3	22913, -7257, -767, 3388, -2177	downstream, upstream, upstream, downstream, upstream	ActReg chr9 #16572	0	0	1
16573	9	140,128,533	140,129,306	773	1	3.609	6.25	12.042	7	10	17	1	2	5	LOC100130547, C9orf169, SLC34A3, TUBB2C, FAM166A	-6654, 9275, 3710, -6792, 13303	upstream, downstream, in gene, upstream, downstream	ActReg chr9 #16573	0	0	1
16574	9	140,130,152	140,130,832	680	1	4.1	8.952	10.619	7	13	14	0	1	5	LOC100130547, C9orf169, SLC34A3, TUBB2C, FAM166A	-8227, 10848, 5283, -5219, 11730	upstream, downstream, in gene, upstream, downstream	ActReg chr9 #16574	0	0	1
16575	9	140,134,596	140,135,947	1,351	3	9.524	12.548	7.667	20	23	23	1	1	5	SLC34A3, TUBB2C, FAM166A, LOC100129722, C9orf173	10062, -440, 6951, 12678, -10459	downstream, upstream, downstream, downstream, upstream	ActReg chr9 #16575	1	1	1
16576	9	140,136,198	140,136,861	663	1	5.85	9.15	11.75	12	13	19	1	1	5	SLC34A3, TUBB2C, FAM166A, LOC100129722, C9orf173	11320, 818, 5693, 11420, -9201	downstream, in gene, downstream, downstream, upstream	ActReg chr9 #16576	0	0	1
16577	9	140,142,001	140,142,461	460	1	6.214	5.071	12.143	10	7	18	0	3	5	TUBB2C, FAM166A, LOC100129722, C9orf173, COBRA1	6520, -9, 5718, -3499, -7528	downstream, upstream, downstream, upstream, upstream	ActReg chr9 #16577	0	0	1
16578	9	140,148,781	140,149,786	1,005	2	10.452	8.194	10.52	17	15	18	1	3	4	FAM166A, LOC100129722, C9orf173, COBRA1	-7061, -1334, 3553, -476	upstream, upstream, downstream, upstream	ActReg chr9 #16578	1	0	1
16579	9	140,190,776	140,191,640	864	1	3.96	6.741	12.889	8	9	20	1	0	2	NRARP, EXD3	5495, 126506	downstream, downstream	ActReg chr9 #16579	0	0	1
16580	9	140,198,048	140,198,580	532	1	5.059	4	11.882	8	6	16	0	1	2	NRARP, EXD3	-1611, 119400	upstream, downstream	ActReg chr9 #16580	0	0	1
16581	9	140,201,490	140,201,915	425	1	3.692	5.615	12.077	6	8	17	0	1	2	NRARP, EXD3	-4999, 116012	upstream, in gene	ActReg chr9 #16581	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16582	9	140,204,004	140,204,530	526	1	1.875	2.438	11.75	5	4	16	0	1	2	NRARP, EXD3	-7564, 113447	upstream, in gene	ActReg chr9 #16582	0	0	1
16583	9	140,205,960	140,206,567	607	1	2.368	4	13.368	4	6	19	0	0	2	NRARP, EXD3	-9560, 111451	upstream, in gene	ActReg chr9 #16583	0	0	1
16584	9	140,206,786	140,207,435	649	1	2.4	4.05	13.85	4	6	25	0	0	1	EXD3	110,604	in gene	ActReg chr9 #16584	0	0	1
16585	9	140,208,179	140,208,942	763	1	2.913	4.333	13.125	5	9	20	0	0	1	EXD3	109,154	in gene	ActReg chr9 #16585	0	0	1
16586	9	140,209,364	140,209,891	527	1	3.353	3.647	14.647	5	9	22	0	0	1	EXD3	108,087	in gene	ActReg chr9 #16586	0	0	1
16587	9	140,211,099	140,211,688	589	1	3	4.474	11.632	5	8	16	1	0	1	EXD3	106,321	in gene	ActReg chr9 #16587	0	0	1
16588	9	140,214,381	140,214,740	359	1	3.182	3.909	13.364	6	5	17	0	0	1	EXD3	103,154	in gene	ActReg chr9 #16588	0	0	1
16589	9	140,216,147	140,216,836	689	1	3.579	3.048	13.046	6	4	18	1	0	1	EXD3	101,223	in gene	ActReg chr9 #16589	0	0	1
16590	9	140,218,049	140,218,525	476	1	4.429	1.923	13.571	7	3	21	1	0	1	EXD3	99,427	in gene	ActReg chr9 #16590	0	0	1
16591	9	140,222,489	140,223,085	596	1	15.316	10	2.895	37	17	6	0	0	1	EXD3	94,927	in gene	ActReg chr9 #16591	1	0	0
16592	9	140,243,601	140,244,367	766	1	2.167	3.05	12.375	5	6	18	0	0	1	EXD3	73,730	in gene	ActReg chr9 #16592	0	0	1
16593	9	140,245,454	140,246,529	1,075	1	3.412	4.735	13.147	7	10	19	0	0	1	EXD3	71,723	in gene	ActReg chr9 #16593	0	0	1
16594	9	140,248,055	140,248,479	424	1	4.692	5.385	12.385	6	8	17	1	0	1	EXD3	69,447	in gene	ActReg chr9 #16594	0	0	1
16595	9	140,263,999	140,264,501	502	1	4.357	4.875	11.312	8	9	16	0	0	1	EXD3	53,464	in gene	ActReg chr9 #16595	0	0	1
16596	9	140,268,368	140,268,937	569	1	3.2	2.278	10.333	8	3	16	1	0	1	EXD3	49,062	in gene	ActReg chr9 #16596	0	0	1
16597	9	140,284,974	140,285,620	646	1	3.25	5.15	11.95	5	10	17	0	0	1	EXD3	32,417	in gene	ActReg chr9 #16597	0	0	1
16598	9	140,288,219	140,288,623	404	1	3.231	4.5	11.308	5	6	17	0	0	1	EXD3	29,293	in gene	ActReg chr9 #16598	0	0	1
16599	9	140,325,330	140,325,809	479	1	7	4.067	11.733	9	6	17	0	0	3	EXD3, NOXA1, ENTPD8	-7855, 7722, 10332	upstream, in gene, downstream	ActReg chr9 #16599	0	0	1
16600	9	140,325,916	140,326,376	460	1	5.333	3.333	11.533	8	6	14	0	0	3	EXD3, NOXA1, ENTPD8	-8432, 8299, 9755	upstream, in gene, downstream	ActReg chr9 #16600	0	0	1
16601	9	140,326,957	140,327,360	403	1	2.385	4.769	11	4	7	18	0	0	3	EXD3, NOXA1, ENTPD8	-9444, 9311, 8743	upstream, in gene, downstream	ActReg chr9 #16601	0	0	1
16602	9	140,327,521	140,329,020	1,499	1	3.87	4.696	13.239	8	10	19	0	0	3	EXD3, NOXA1, ENTPD8	-10556, 10423, 7631	upstream, in gene, downstream	ActReg chr9 #16602	0	0	1
16603	9	140,329,943	140,330,521	578	1	3.235	4.611	12.111	5	7	18	1	0	2	NOXA1, ENTPD8	12385, 5669	downstream, in gene	ActReg chr9 #16603	0	0	1
16604	9	140,333,075	140,333,362	287	1	5	4.556	12.667	7	6	16	1	0	3	NOXA1, ENTPD8, NELF	15371, 2683, 20568	downstream, in gene, downstream	ActReg chr9 #16604	0	0	1
16605	9	140,341,476	140,341,944	468	1	5.5	7.214	12	8	9	20	0	1	2	ENTPD8, NELF	-5809, 12076	upstream, downstream	ActReg chr9 #16605	0	0	1
16606	9	140,342,757	140,343,196	439	1	1.75	2.923	13	2	4	17	0	1	2	ENTPD8, NELF	-7075, 10810	upstream, in gene	ActReg chr9 #16606	0	0	1
16607	9	140,348,836	140,349,657	821	1	5.04	3.84	11.88	8	6	18	1	0	2	NELF, PNPLA7	4540, 95740	in gene, downstream	ActReg chr9 #16607	0	0	1
16608	9	140,352,404	140,352,989	585	1	8.444	8.278	12.556	12	11	19	1	1	2	NELF, PNPLA7	1090, 92290	in gene, downstream	ActReg chr9 #16608	0	0	1
16609	9	140,391,324	140,391,834	510	1	2.5	4.25	12.5	4	8	19	0	0	1	PNPLA7	53,407	in gene	ActReg chr9 #16609	0	0	1
16610	9	140,393,969	140,394,432	463	1	4.6	1.929	11.267	6	4	17	0	0	1	PNPLA7	50,786	in gene	ActReg chr9 #16610	0	0	1
16611	9	140,409,335	140,410,227	892	1	3.714	3.522	12.714	7	7	22	0	0	1	PNPLA7	35,205	in gene	ActReg chr9 #16611	0	0	1
16612	9	140,472,837	140,473,850	1,013	2	24.194	25.806	5.935	62	76	11	1	1	2	WDR85, ZMYND19	44, 11584	in gene, downstream	ActReg chr9 #16612	1	1	0
16613	9	140,498,802	140,499,150	348	1	3.909	2.8	10.546	5	4	13	0	1	1	ARRDC1	-1,120	upstream	ActReg chr9 #16613	0	0	1
16614	9	140,507,979	140,509,375	1,396	1	6.721	8.047	12.767	14	16	20	0	0	2	ARRDC1, C9orf37	8581, 4631	in gene, downstream	ActReg chr9 #16614	0	0	1
16615	9	140,512,745	140,513,272	527	1	7.688	6.75	13.5	12	11	22	1	1	2	ARRDC1, C9orf37	12912, 300	downstream, in gene	ActReg chr9 #16615	0	0	1
16616	9	140,681,722	140,682,214	492	1	5.125	2.875	12.375	8	5	21	0	1	2	EHMT1, LOC100506062	76551, -2001	in gene, upstream	ActReg chr9 #16616	0	0	1
16617	9	140,682,562	140,682,910	348	1	4.1	3.8	11.6	5	5	15	0	1	2	EHMT1, LOC100506062	77319, -2769	in gene, upstream	ActReg chr9 #16617	0	0	1
16618	9	140,683,487	140,683,857	370	1	2.5	3.833	11.667	3	5	14	1	1	2	EHMT1, LOC100506062	78255, -3705	in gene, upstream	ActReg chr9 #16618	0	0	1
16619	9	140,711,451	140,712,019	568	1	2.059	2.062	10.389	5	4	13	0	0	1	EHMT1	106,318	in gene	ActReg chr9 #16619	0	0	1
16620	9	140,728,181	140,728,661	480	1	5.533	6.133	12	5	11	17	1	1	2	EHMT1, MIR602	123004, -4450	in gene, upstream	ActReg chr9 #16620	0	0	1
16621	9	140,777,070	140,781,076	4,006	3	12.432	14.328	16.4	38	45	27	1	0	2	LOC100133077, CACNA1B	7949, 6832	in gene, in gene	ActReg chr9 #16621	0	1	1
16622	9	140,783,021	140,785,841	2,820	3	9.705	12.25	13.591	28	37	20	0	1	2	LOC100133077, CACNA1B	2591, 12190	in gene, in gene	ActReg chr9 #16622	1	1	1
16623	9	141,014,790	141,015,514	724	1	2.444	4.091	12	5	8	18	1	0	1	CACNA1B	242,911	in gene	ActReg chr9 #16623	0	0	1
16624	X	3,615,757	3,616,325	568	1	4.667	10.444	2.889	9	16	5	0	0	1	PRKX	15,634	in gene	ActReg chrX #16624	0	1	0
16625	X	3,732,578	3,733,383	805	2	7.92	10.48	7.24	12	16	13	1	0	1	LOC389906	28,955	downstream	ActReg chrX #16625	0	1	1
16626	X	3,908,490	3,909,050	560	2	8.294	10.529	2.625	14	18	4	0	0	0				ActReg chrX #16626	1	1	0
16627	X	9,098,976	9,099,599	623	2	8.95	11.35	1	16	17	1	0	0	0				ActReg chrX #16627	1	1	0
16628	X	9,121,854	9,122,274	440	1	5.786	9.786	1.857	9	15	2	0	0	0				ActReg chrX #16628	0	1	0
16629	X	9,430,860	9,431,503	643	2	16.15	15.9	0	36	37	0	0	1	1	TBL1X	-154	upstream	ActReg chrX #16629	1	1	0
16630	X	10,602,673	10,603,112	439	1	11	5.143	1.417	16	8	2	0	0	1	MID1	248,917	in gene	ActReg chrX #16630	1	0	0
16631	X	11,775,773	11,776,175	402	1	6.273	9.308	1.909	10	12	4	1	1	1	MSL3	-304	upstream	ActReg chrX #16631	0	1	0
16632	X	12,083,196	12,083,883	687	2	15.046	15.864	3.133	36	35	6	0	0	0				ActReg chrX #16632	1	1	0
16633	X	12,566,506	12,567,324	818	2	7.6	14.68	1.941	14	28	4	0	0	1	FRMPD4	410,330	in gene	ActReg chrX #16633	1	1	0
16634	X	12,722,681	12,723,320	639	1	1.312	9.8	0	2	15	0	0	0	1	FRMPD4	566,415	in gene	ActReg chrX #16634	0	1	0
16635	X	12,738,899	12,739,839	940	2	11	18.517	2	28	41	3	0	0	1	FRMPD4	582,784	in gene	ActReg chrX #16635	1	1	0
16636	X	13,752,476	13,752,895	419	1	5.692	8.538	9.923	7	11	15	1	2	2	TRAPPC2, OFD1	69, -147	in gene, upstream	ActReg chrX #16636	0	0	1
16637	X	14,047,841	14,048,369	528	1	8.812	10.875	1.933	13	17	4	1	1	1	GEMIN8	-70	upstream	ActReg chrX #16637	0	1	0
16638	X	14,082,952	14,083,599	647	1	4.6	9.7	3.75	7	19	7	0	0	0				ActReg chrX #16638	0	1	0
16639	X	14,547,394	14,547,756	362	1	10.636	9.273	1.273	17	12	2	0	1	1	GLRA2	155	in gene	ActReg chrX #16639	1	0	0
16640	X	15,189,303	15,189,784	481	1	9.533	6.067	1	14	9	1	0	0	0				ActReg chrX #16640	1	0	0
16641	X	15,251,784	15,252,269	485	1	9.8	4.333	1	14	8	1	0	0	1	ASB9	36,563	downstream	ActReg chrX #16641	1	0	0
16642	X	15,692,758	15,693,737	979	2	9.933	10.29	4.467	14	17	7	1	0	1	TMEM27	-10,093	upstream	ActReg chrX #16642	1	1	0
16643	X	16,203,753	16,204,155	402	1	8.5	9.667	2.167	13	14	3	0	0	0				ActReg chrX #16643	0	1	0
16644	X	16,789,761	16,790,400	639	2	8.75	9.05	5	18	17	8	0	0	1	SYAP1	52,373	downstream	ActReg chrX #16644	1	1	0
16645	X	16,803,985	16,804,488	503	1	11.562	9.875	1.667	17	17	2	1	1	1	CXorf15	-319	upstream	ActReg chrX #16645	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GeneCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16646	X	18,692,831	18,693,384	553	1	6.529	6.444	11.333	11	9	23	1	1	1	RS1	-2,884	upstream	ActReg chrX #16646	0	0	1
16647	X	19,002,742	19,003,083	341	1	8.364	10.273	4.727	11	13	10	1	1	2	PHKA2, GPR64	-432, 137843	upstream, downstream	ActReg chrX #16647	0	1	0
16648	X	19,361,638	19,362,036	398	1	4.167	6.75	12.25	6	10	18	1	1	1	PDHA1	-174	upstream	ActReg chrX #16648	0	0	1
16649	X	20,532,365	20,533,104	739	2	10.261	13	2.565	22	27	5	0	0	0				ActReg chrX #16649	1	1	0
16650	X	21,392,552	21,392,874	322	1	9.2	7.3	12	12	9	16	1	1	1	CNKSR2	177	in gene	ActReg chrX #16650	0	0	1
16651	X	21,788,755	21,789,672	917	2	14.724	18.241	5.138	36	43	10	0	0	0				ActReg chrX #16651	1	1	0
16652	X	21,816,939	21,817,394	455	2	10.071	10	1.364	15	15	2	0	0	0				ActReg chrX #16652	1	1	0
16653	X	21,857,448	21,858,155	707	1	10.136	14.046	8.682	15	27	12	1	1	1	MBTPS2	145	in gene	ActReg chrX #16653	0	1	0
16654	X	22,332,543	22,333,153	610	1	11.15	9.85	2.133	18	19	3	0	0	0				ActReg chrX #16654	0	1	0
16655	X	22,760,236	22,760,682	446	1	10.071	5.429	2.455	15	8	4	0	0	0				ActReg chrX #16655	1	0	0
16656	X	23,802,949	23,803,412	463	1	1.923	9.714	2	3	13	3	0	1	1	SAT1	1,905	in gene	ActReg chrX #16656	0	1	0
16657	X	24,072,652	24,073,224	572	1	12.167	10.056	5.812	19	15	11	1	1	1	EIF2S3	-127	upstream	ActReg chrX #16657	1	0	0
16658	X	26,575,810	26,576,287	477	1	2.786	5.357	11.857	4	8	16	1	0	0				ActReg chrX #16658	0	0	1
16659	X	27,010,385	27,010,805	420	1	7.077	10	0	10	16	0	0	0	0				ActReg chrX #16659	0	1	0
16660	X	27,031,025	27,031,931	906	2	21.286	17	1.75	47	41	2	0	0	0				ActReg chrX #16660	1	1	0
16661	X	30,907,280	30,907,800	520	1	10.688	8.267	2.273	15	12	3	1	1	1	MAP3K7IP3	-29	upstream	ActReg chrX #16661	1	0	0
16662	X	37,764,991	37,765,526	535	2	9.765	10.118	7.062	16	20	12	1	0	0				ActReg chrX #16662	1	1	0
16663	X	38,186,514	38,187,295	781	2	17.792	17.208	6.375	47	41	11	1	1	1	RPGR	-116	upstream	ActReg chrX #16663	1	1	0
16664	X	38,664,060	38,664,832	772	1	6.12	10.6	6.895	12	14	10	1	0	1	MID1IP1	3,761	in gene	ActReg chrX #16664	0	1	0
16665	X	39,817,292	39,817,587	295	1	1.571	2.222	11.333	3	3	13	0	0	0				ActReg chrX #16665	0	0	1
16666	X	40,030,958	40,031,266	308	1	6.6	8.2	10.1	10	12	15	1	0	1	BCOR	5,470	in gene	ActReg chrX #16666	0	0	1
16667	X	40,034,674	40,035,792	1,118	1	7.4	11.457	8.657	13	16	15	1	1	1	BCOR	1,349	in gene	ActReg chrX #16667	0	1	0
16668	X	40,943,569	40,944,238	669	1	10.762	12.619	5.524	13	18	9	1	1	1	USP9X	-985	upstream	ActReg chrX #16668	0	1	0
16669	X	41,193,110	41,193,556	446	1	6.786	8.357	11.643	10	11	17	1	1	1	DDX3X	682	in gene	ActReg chrX #16669	0	0	1
16670	X	43,513,797	43,514,365	568	2	12.177	11.235	4.625	21	22	8	1	1	1	MAOA	-1,328	upstream	ActReg chrX #16670	1	1	0
16671	X	43,871,846	43,872,364	518	1	10.562	6.625	2.077	17	10	3	0	0	0				ActReg chrX #16671	1	0	0
16672	X	46,039,701	46,040,122	421	1	8	10.692	2.455	13	15	5	0	0	0				ActReg chrX #16672	0	1	0
16673	X	46,127,711	46,128,344	633	1	11.7	5.85	1	18	12	1	0	0	0				ActReg chrX #16673	1	0	0
16674	X	47,003,853	47,004,288	435	1	7.5	6.214	10.929	10	9	15	1	2	2	NDUFB11, RBM10	539, -561	in gene, upstream	ActReg chrX #16674	0	0	1
16675	X	47,049,782	47,050,464	682	2	13.864	16.136	5.909	32	37	9	1	1	2	RBM10, UBA1	45492, -76	downstream, upstream	ActReg chrX #16675	1	1	0
16676	X	47,052,249	47,053,416	1,167	2	12.595	11.811	3.971	21	27	10	1	1	2	RBM10, UBA1	48201, 2633	downstream, in gene	ActReg chrX #16676	1	1	0
16677	X	47,077,620	47,078,304	684	2	10.591	13.318	3.636	17	29	7	1	1	2	UBA1, CDK16	27763, 434	downstream, in gene	ActReg chrX #16677	1	1	0
16678	X	47,124,328	47,124,799	471	1	9.929	4.143	1.429	15	6	3	0	0	0				ActReg chrX #16678	1	0	0
16679	X	47,342,383	47,342,855	472	1	10.6	6.133	2.867	16	9	5	1	1	2	ZNF41, CXorf24	-274, 8653	upstream, in gene	ActReg chrX #16679	1	0	0
16680	X	47,382,605	47,383,071	466	1	10.643	5.357	3.571	19	9	6	1	0	0				ActReg chrX #16680	1	0	0
16681	X	47,441,614	47,442,036	422	2	10.154	9.385	9	13	13	15	0	1	2	SYN1, TIMP1	37431, 135	in gene, in gene	ActReg chrX #16681	1	0	1
16682	X	47,478,928	47,479,807	879	2	10.518	16.667	2.364	25	37	4	1	1	2	SYN1, CFP	-111, 10337	upstream, downstream	ActReg chrX #16682	1	1	0
16683	X	47,880,456	47,881,420	964	2	13.733	18.667	2.136	28	41	5	0	0	0				ActReg chrX #16683	1	1	0
16684	X	48,432,467	48,433,060	593	1	5.421	10.158	6.842	7	14	12	1	1	2	RBM3, LOC100506703	-73, 6787	upstream, downstream	ActReg chrX #16684	0	1	0
16685	X	48,455,679	48,456,146	467	1	11.067	6.467	3.067	17	10	4	1	1	1	WDR13	32	in gene	ActReg chrX #16685	1	0	0
16686	X	48,534,879	48,535,476	597	1	9.211	7.684	10.579	17	12	15	1	1	1	WAS	-7,009	upstream	ActReg chrX #16686	0	0	1
16687	X	48,566,339	48,566,652	313	1	1.889	2	9.778	5	3	12	0	0	1	SUV39H1	11,364	in gene	ActReg chrX #16687	0	0	1
16688	X	48,979,862	48,980,393	531	2	9.824	8.647	4.706	16	13	9	1	1	1	GPKOW	-48	upstream	ActReg chrX #16688	1	1	0
16689	X	49,022,563	49,023,176	613	1	10.79	8.211	6.105	17	13	11	1	1	3	MAGIX, PLP2, PRICKLE3	3688, -5315, 19907	in gene, upstream, downstream	ActReg chrX #16689	1	0	0
16690	X	49,056,280	49,057,002	722	2	11.304	13.783	3.864	22	27	7	1	1	2	SYP, CACNA1F	20, 33192	in gene, downstream	ActReg chrX #16690	1	1	0
16691	X	50,557,250	50,558,581	1,331	1	7	11.268	2.026	11	17	4	1	1	1	SHROOM4	-871	upstream	ActReg chrX #16691	0	1	0
16692	X	51,486,104	51,486,813	709	2	8.909	12	4.6	15	17	7	1	1	1	GSPT2	-23	upstream	ActReg chrX #16692	1	1	0
16693	X	51,545,721	51,546,197	476	1	9.2	6.933	1.667	14	13	2	0	1	1	MAGED1	-196	upstream	ActReg chrX #16693	1	0	0
16694	X	52,963,732	52,964,263	531	1	7.824	12.941	2.6	10	18	4	1	0	0				ActReg chrX #16694	0	1	0
16695	X	52,964,275	52,964,858	583	1	6.056	10.222	6	10	18	11	1	0	0				ActReg chrX #16695	0	1	0
16696	X	53,254,008	53,254,695	687	1	7.091	11.864	6.909	9	19	10	1	1	2	KDM5C, IQSEC2	253, 96171	in gene, downstream	ActReg chrX #16696	0	1	0
16697	X	53,292,675	53,293,170	495	1	7.4	11.467	3.75	13	15	6	0	0	1	IQSEC2	57,600	in gene	ActReg chrX #16697	0	1	0
16698	X	53,468,609	53,469,059	450	1	4.357	8.071	12	6	11	16	1	1	1	HSD17B10	-7,511	upstream	ActReg chrX #16698	0	0	1
16699	X	53,710,782	53,711,301	519	1	3.118	12	4.059	5	19	6	1	1	1	HUWE1	2,632	in gene	ActReg chrX #16699	0	1	0
16700	X	54,209,428	54,209,728	300	1	4.3	6.9	9.8	6	9	14	1	1	2	FAM120C, WNK3	136, 174860	in gene, downstream	ActReg chrX #16700	0	0	1
16701	X	54,466,534	54,466,972	438	1	8	11.769	5.25	12	14	9	0	1	2	TSR2, FGD1	-100, 55846	upstream, downstream	ActReg chrX #16701	0	1	0
16702	X	54,665,981	54,666,514	533	2	6.118	9.118	7.357	9	16	13	1	0	0				ActReg chrX #16702	0	1	1
16703	X	56,589,993	56,590,298	305	1	5.556	10.667	11	7	15	14	1	1	1	UBQLN2	119	in gene	ActReg chrX #16703	0	0	1
16704	X	57,021,555	57,022,011	456	1	8.286	9.786	3.929	11	13	5	1	1	1	SPIN3	205	in gene	ActReg chrX #16704	0	1	0
16705	X	63,425,421	63,426,090	669	2	12.048	11.238	6.714	22	18	11	1	1	1	FAM123B	-131	upstream	ActReg chrX #16705	1	1	0
16706	X	64,911,964	64,912,279	315	1	3.2	1	10.4	5	1	14	0	0	1	MSN	24,610	in gene	ActReg chrX #16706	0	0	1
16707	X	68,048,645	68,049,091	446	1	6.571	10.571	7.5	11	14	10	1	1	1	EFNB1	28	in gene	ActReg chrX #16707	0	1	0
16708	X	69,664,327	69,664,863	536	1	9.938	8.062	5.188	17	12	9	0	1	1	DLG3	-110	upstream	ActReg chrX #16708	1	0	0
16709	X	69,697,091	69,697,582	491	1	9.933	8	1.125	17	13	2	0	0	1	DLG3	32,631	in gene	ActReg chrX #16709	1	0	0

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16710	X	70,288,027	70,288,650	623	2	10.8	10.65	2.6	23	19	4	1	1	1	SNX12	-107	upstream	ActReg chrX #16710	1	1	0
16711	X	70,316,270	70,316,617	347	1	2.7	5.545	9.364	4	7	14	1	1	2	FOXO4, CXorf65	444, 10195	in gene, downstream	ActReg chrX #16711	0	0	1
16712	X	70,473,660	70,474,503	843	2	13.593	13.259	4.84	29	28	9	1	1	1	ZMYM3	966	in gene	ActReg chrX #16712	1	1	0
16713	X	70,752,911	70,753,294	383	1	4.75	5.333	11.75	8	6	18	1	1	1	OGT	190	in gene	ActReg chrX #16713	0	0	1
16714	X	71,130,958	71,131,286	328	1	1.7	3.3	10.4	3	5	15	1	1	1	NHSL2	184	in gene	ActReg chrX #16714	0	0	1
16715	X	71,401,236	71,401,829	593	1	7.895	11.474	2.824	12	17	6	0	1	1	PIN4	6	in gene	ActReg chrX #16715	0	1	0
16716	X	71,496,660	71,497,479	819	2	18.654	21.462	4.846	45	52	10	1	1	1	RPS4X	72	in gene	ActReg chrX #16716	1	1	0
16717	X	71,525,446	71,525,928	482	1	4.533	4	11.933	9	6	19	1	1	1	CITED1	1,350	in gene	ActReg chrX #16717	0	0	1
16718	X	71,526,583	71,527,292	709	3	10.773	12.182	7.455	22	23	12	1	1	1	CITED1	100	in gene	ActReg chrX #16718	1	1	1
16719	X	71,681,614	71,682,015	401	1	5.333	10.417	1	9	17	1	0	0	1	HDAC8	111,139	in gene	ActReg chrX #16719	0	1	0
16720	X	73,163,796	73,164,417	621	2	9.4	9.412	6.3	17	20	14	1	0	0				ActReg chrX #16720	1	1	0
16721	X	74,375,678	74,376,271	593	1	11.421	8.421	2.895	20	14	5	0	1	1	ABCB7	158	in gene	ActReg chrX #16721	1	0	0
16722	X	74,493,677	74,494,219	542	1	5.647	9.647	5.235	9	18	9	0	1	1	UPRT	54	in gene	ActReg chrX #16722	0	1	0
16723	X	77,359,530	77,359,957	427	1	10.538	8.385	5.769	14	12	8	1	1	1	PGK1	77	in gene	ActReg chrX #16723	1	0	0
16724	X	92,490,665	92,491,095	430	1	1.615	1	11.308	3	1	16	0	0	0				ActReg chrX #16724	0	0	1
16725	X	100,603,560	100,603,933	373	1	6	9.727	10.727	7	14	14	1	1	2	TIMM8A, BTK	211, 37466	in gene, downstream	ActReg chrX #16725	0	0	1
16726	X	100,645,544	100,646,305	761	2	10.875	14.708	5.625	23	30	12	1	2	3	BTK, RPL36A, GLA	-4712, -24, 17077	upstream, upstream, downstream	ActReg chrX #16726	1	1	0
16727	X	102,884,432	102,884,923	491	1	3.533	4.6	10.733	6	9	19	1	1	1	TCEAL1	1,029	in gene	ActReg chrX #16727	0	0	1
16728	X	103,401,239	103,401,954	715	2	10.391	13.727	2.261	22	32	5	1	1	2	MCART6, CXorf39	112, -9705	in gene, upstream	ActReg chrX #16728	1	1	0
16729	X	103,410,513	103,411,476	963	2	11.3	12	2.174	18	24	4	1	1	2	MCART6, CXorf39	-9286, -307	upstream, upstream	ActReg chrX #16729	1	1	0
16730	X	106,567,833	106,568,456	623	1	6.65	10.8	3.8	9	18	8	0	0	0				ActReg chrX #16730	0	1	0
16731	X	107,334,710	107,335,150	440	1	10.286	8.357	4.5	14	12	7	1	2	2	PSMD10, ATG4A	-82, -4	upstream, upstream	ActReg chrX #16731	1	0	0
16732	X	107,494,071	107,494,341	270	1	1.714	0	9.889	3	0	12	0	0	1	COL4A6	188,498	in gene	ActReg chrX #16732	0	0	1
16733	X	109,638,122	109,638,527	405	1	3.182	9.5	3.333	6	15	4	0	0	1	AMMECR1	45,137	in gene	ActReg chrX #16733	0	1	0
16734	X	115,014,565	115,014,939	374	1	6.273	3.818	11	8	6	15	0	0	0				ActReg chrX #16734	0	0	1
16735	X	117,480,002	117,480,352	350	1	5.545	4.545	10.636	8	7	15	1	1	1	WDR44	141	in gene	ActReg chrX #16735	0	0	1
16736	X	118,925,114	118,925,731	617	1	8.7	11.15	8.4	12	14	12	1	2	2	RPL39, SNORA69	184, -3975	in gene, upstream	ActReg chrX #16736	0	1	0
16737	X	119,005,438	119,006,147	709	1	6.348	10.913	3.522	11	14	6	1	2	2	RNF113A, NDUFA1	-1, 58	upstream, in gene	ActReg chrX #16737	0	1	0
16738	X	119,077,406	119,077,915	509	1	9.875	9	5.214	14	13	10	1	1	1	NKAP	75	in gene	ActReg chrX #16738	1	0	0
16739	X	119,149,800	119,150,178	378	1	3.333	3.75	9.583	5	6	15	1	0	0				ActReg chrX #16739	0	0	1
16740	X	119,763,623	119,764,141	518	1	3.188	11	3.812	6	17	6	1	1	2	MCTS1, C1GALT1C1	26138, 123	downstream, in gene	ActReg chrX #16740	0	1	0
16741	X	122,866,579	122,866,996	417	1	4.231	6.769	9.538	7	9	13	1	1	1	THOC2	117	in gene	ActReg chrX #16741	0	0	1
16742	X	128,673,979	128,674,572	593	2	15.947	13.316	2.8	34	28	5	1	1	1	OCRL	23	in gene	ActReg chrX #16742	1	1	0
16743	X	129,299,341	129,300,515	1,174	2	9.946	12.649	5.656	24	26	11	1	2	2	AIFM1, RAB33A	-67, -5845	upstream, upstream	ActReg chrX #16743	1	1	0
16744	X	129,657,875	129,658,283	408	1	4.923	3.769	10.538	8	6	16	0	0	0				ActReg chrX #16744	0	0	1
16745	X	134,049,081	134,049,485	404	1	10.077	6.846	3.231	15	16	5	1	1	1	MOSPD1	14	in gene	ActReg chrX #16745	1	0	0
16746	X	134,654,125	134,654,963	838	1	6.846	10.923	3.32	17	20	7	1	1	1	DDX26B	-11	upstream	ActReg chrX #16746	0	1	0
16747	X	134,909,298	134,909,746	448	1	7.571	9.571	3.273	9	15	6	0	0	0				ActReg chrX #16747	0	1	0
16748	X	134,975,396	134,976,025	629	1	7.211	13.053	1.889	13	23	3	0	2	2	CT45A6, SAGE1	-4466, -75	upstream, upstream	ActReg chrX #16748	0	1	0
16749	X	135,067,263	135,068,034	771	1	5.64	11.84	3.64	10	20	8	1	1	1	SLC9A6	65	in gene	ActReg chrX #16749	0	1	0
16750	X	136,520,371	136,520,595	224	1	32.571	43	58.286	43	55	76	0	0	0				ActReg chrX #16750	0	0	1
16751	X	139,521,799	139,522,121	322	1	3.2	1.2	9.2	5	2	14	1	0	0				ActReg chrX #16751	0	0	1
16752	X	140,282,830	140,283,119	289	1	2.111	4.444	9.556	3	6	12	0	0	0				ActReg chrX #16752	0	0	1
16753	X	140,846,084	140,846,672	588	1	9.389	7.167	1.643	15	12	3	0	0	0				ActReg chrX #16753	1	0	0
16754	X	142,316,454	142,316,772	318	1	2.875	2	10.9	4	3	14	0	0	0				ActReg chrX #16754	0	0	1
16755	X	144,691,322	144,691,775	453	1	10.857	1.929	1	17	4	1	0	0	0				ActReg chrX #16755	1	0	0
16756	X	149,369,101	149,369,691	590	2	11	10.667	2.176	18	16	3	0	0	0				ActReg chrX #16756	1	1	0
16757	X	150,151,319	150,151,905	586	2	13.684	13	3.737	27	28	7	1	1	1	HMGB3	-151	upstream	ActReg chrX #16757	1	1	0
16758	X	150,921,753	150,922,268	515	1	6.438	11.438	3.125	12	18	5	0	0	1	CNGA2	18,792	downstream	ActReg chrX #16758	0	1	0
16759	X	151,091,008	151,091,300	292	1	4.3	3	9.7	7	5	13	0	0	1	MAGEA4	9,793	in gene	ActReg chrX #16759	0	0	1
16760	X	151,900,667	151,900,926	259	1	1.857	5	11	3	6	14	0	3	3	LOC100130935, MAGEA12, CSAG1	-3974, 2388, -2432	upstream, in gene, upstream	ActReg chrX #16760	0	0	1
16761	X	151,999,274	151,999,708	434	1	5.692	10	1.909	10	14	5	1	2	2	CETN2, NSDHL	-190, -20	upstream, upstream	ActReg chrX #16761	0	1	0
16762	X	152,538,605	152,538,819	214	1	4.429	4.429	10.571	6	5	14	1	1	1	LOC728317	1,634	in gene	ActReg chrX #16762	0	0	1
16763	X	152,910,419	152,910,833	414	1	2.308	1.818	9.385	4	3	15	0	0	1	DUSP9	2,729	in gene	ActReg chrX #16763	0	0	1
16764	X	152,958,263	152,958,644	381	1	3.75	4	11.333	5	7	17	0	0	2	SLC6A8, BCAP31	4701, 31748	in gene, downstream	ActReg chrX #16764	0	0	1
16765	X	152,975,034	152,975,303	269	1	3.778	2	9.222	5	3	12	0	0	1	BCAP31	15,033	in gene	ActReg chrX #16765	0	0	1
16766	X	153,010,480	153,010,909	429	1	2.846	2.538	9.462	4	4	15	0	0	1	ABCD1	20,371	downstream	ActReg chrX #16766	0	0	1
16767	X	153,036,824	153,037,313	489	1	2.769	3	13.875	5	5	18	0	0	2	PLXNB3, SRPK3	7417, -9388	in gene, upstream	ActReg chrX #16767	0	0	1
16768	X	153,050,207	153,050,669	462	1	3.333	2.4	11.467	7	4	17	0	0	4	PLXNB3, SRPK3, IDH3G, SSR4	20787, 3982, 9529, -9656	downstream, in gene, downstream, upstream	ActReg chrX #16768	0	0	1
16769	X	153,140,610	153,141,378	768	2	13.125	21.417	4.292	29	46	7	0	1	1	L1CAM	405	in gene	ActReg chrX #16769	1	1	0
16770	X	153,208,200	153,208,616	416	1	1.444	3.154	10.846	3	5	16	0	1	3	NAA10, RENBP, HCFC1	-7940, 1824, 28411	upstream, in gene, downstream	ActReg chrX #16770	0	0	1
16771	X	153,220,240	153,220,759	519	1	2.154	1.933	12.312	5	3	15	1	0	1	HCFC1	16,320	in gene	ActReg chrX #16771	0	0	1
16772	X	153,236,531	153,237,124	593	1	6.158	6.947	12.474	11	9	18	1	2	4	HCFC1, TMEM187, MIR3202-1, MIR3202-2	-8, -1164, -9721, 9800	upstream, upstream, upstream, downstream	ActReg chrX #16772	0	0	1

Active Region	Chromosome	Start	End	Length	Interval Count	1_A375_pNL7_minus_lncRNA_AR::1 Avg Value	2_A375_pNL97_plus_lncRNA_AR::1 Avg Value	4_A375_EGR1::1 Avg Value	1_A375_pNL7_minus_lncRNA_AR::1 Peak Value	2_A375_pNL97_plus_lncRNA_AR::1 Peak Value	4_A375_EGR1::1 Peak Value	CGIslandCount	PromoterCount	GenesCount	Gene List	Dist to Start	Position	UCSC Link	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
16773	X	153,281,806	153,282,204	398	1	6.333	4.083	10.833	9	5	17	0	0	3	IRAK1, MIR718, MECP2	3337, 3435, 81183	in gene, downstream, downstream	ActReg chrX #16773	0	0	1
16774	X	153,599,088	153,600,001	913	3	11.207	14.552	7.586	24	27	15	1	0	2	FLNA, EMD	3462, -8053	in gene, upstream	ActReg chrX #16774	1	1	1
16775	X	153,626,290	153,626,991	701	2	9.636	12.091	6.409	16	24	9	1	3	4	LOC100507387, RPL10, SNORA70, DNASE1L1	721, 69, -1982, 13787	in gene, in gene, upstream, downstream	ActReg chrX #16775	1	1	0
16776	X	153,639,563	153,640,087	524	1	6.812	11.438	3.125	10	15	4	1	2	3	RPL10, DNASE1L1, TAZ	13254, 602, -52	downstream, in gene, upstream	ActReg chrX #16776	0	1	0
16777	X	153,692,325	153,692,892	567	1	2.143	3.909	11.588	4	5	18	1	0	1	PLXNA3	5,985	in gene	ActReg chrX #16777	0	0	1
16778	X	153,712,668	153,712,913	245	1	5.25	2.857	11.125	6	6	13	0	2	3	LAGE3, UBL4A, SLC10A3	-5194, 2142, 6212	upstream, in gene, downstream	ActReg chrX #16778	0	0	1
16779	X	154,493,388	154,494,108	720	2	7.81	11.727	2.75	17	21	5	1	1	1	RAB39B	104	in gene	ActReg chrX #16779	1	1	0
16780	X	154,841,940	154,842,419	479	1	9.267	9.933	6.333	14	14	10	1	1	1	TMLHE	443	in gene	ActReg chrX #16780	0	1	0
16781	Y	9,978,423	9,978,740	317	1	2.222	4.6	11.1	3	7	16	0	0	0				ActReg chrY #16781	0	0	1
16782	Y	9,988,039	9,988,455	416	1	4.462	5.692	15.154	7	7	24	0	0	0				ActReg chrY #16782	0	0	1
16783	Y	10,025,074	10,025,349	275	1	33.667	32	67	50	48	99	0	0	0				ActReg chrY #16783	0	0	1
16784	Y	10,029,564	10,029,867	303	1	10.8	11.5	22.1	17	17	36	0	0	0				ActReg chrY #16784	0	0	1
16785	Y	10,031,910	10,032,081	171	1	16	18.8	34.8	19	22	41	0	0	0				ActReg chrY #16785	0	0	1
16786	Y	10,037,587	10,037,979	392	3	53.818	51.333	49.917	92	94	91	0	0	0				ActReg chrY #16786	1	1	1
16787	Y	13,262,794	13,263,176	382	1	3.917	3.333	10.167	6	6	14	0	0	0				ActReg chrY #16787	0	0	1
16788	Y	21,154,733	21,155,059	326	1	1.167	2	10	2	2	14	1	1	1	CD24	-191	upstream	ActReg chrY #16788	0	0	1
16789	Y	59,008,395	59,008,616	221	1	7.714	7	14.143	10	9	17	0	0	0				ActReg chrY #16789	0	0	1

Table 12. AR and EGR1 active genes as determined via ChIP-Seq

Table 12 lists the AR and EGR1 active genes as determinied via ChIP-Seq. EGR1 ChIP-Seq was performed from A375 melanoma cells. The table also contains AR ChIP-Seq active genes (Table 9A) to enable comparative analyses.

1_A375_pNL7_minus_lncRNA_AR = AR ChIP-seq from vector control

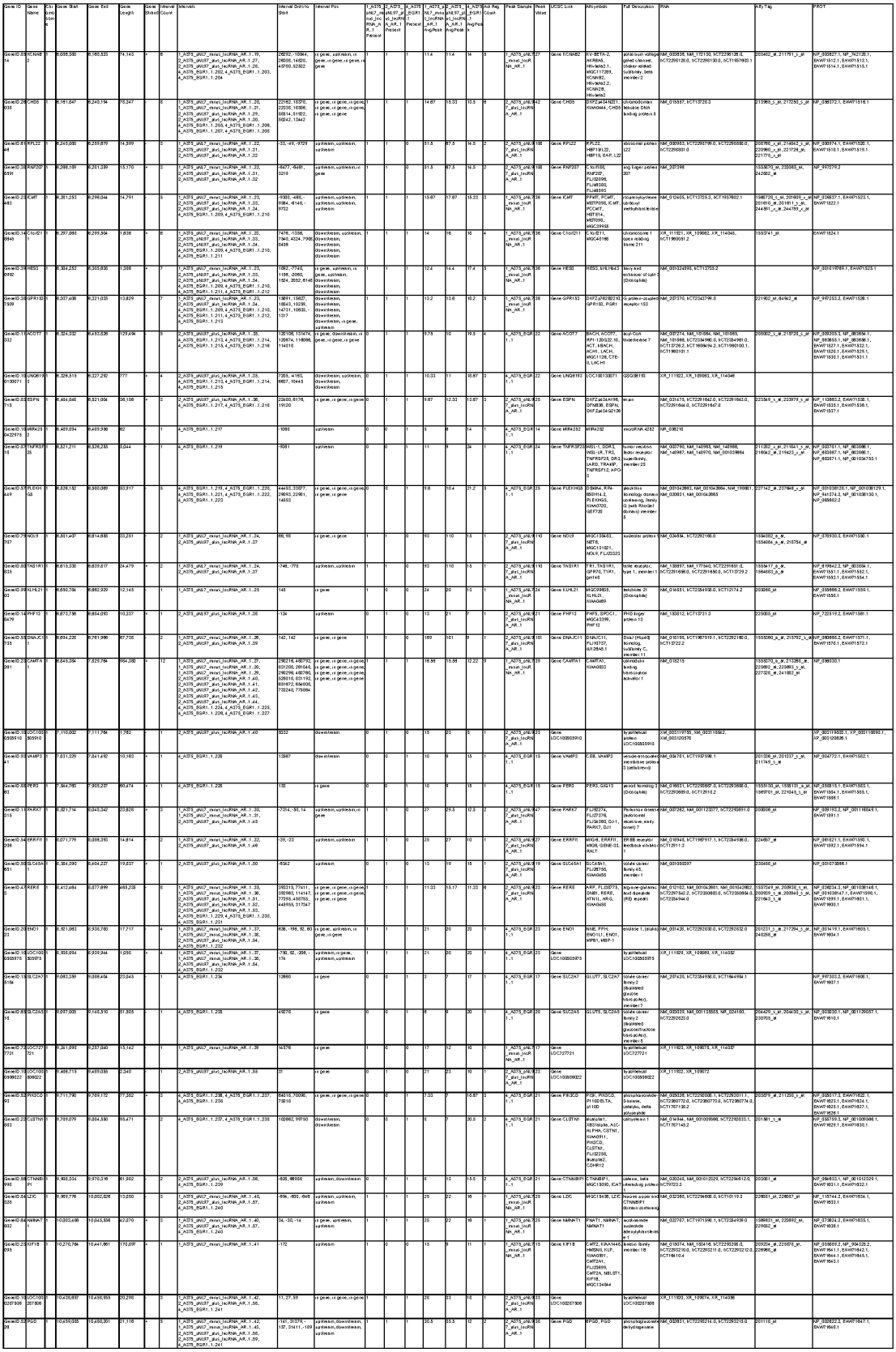
2_A375_pNL97_plus_lncRNA_AR = AR ChIP-seq from SLNCR1-expressing vector

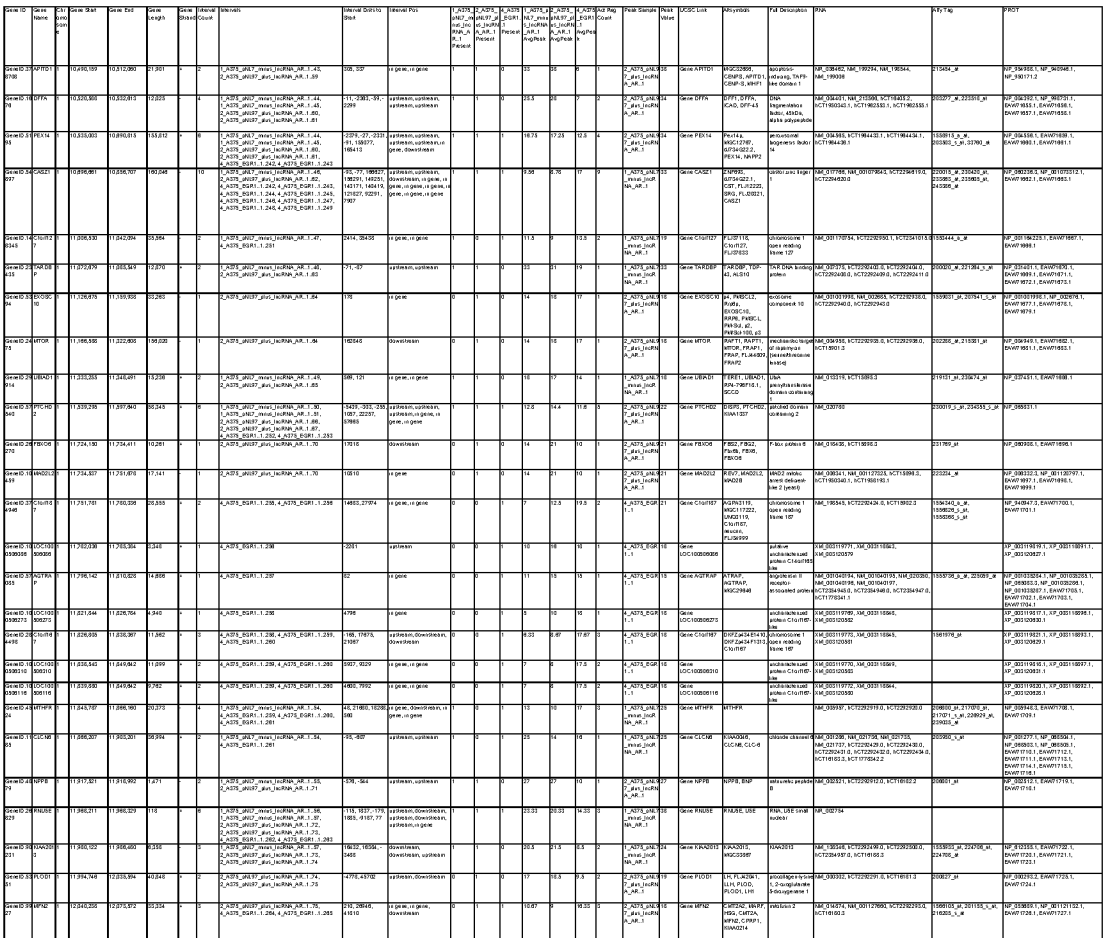
4_A375_EGR1 = EGR1 ChIP-seq

Table 12

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100288069	LOC100288069	1	700,245	714,068	13,823	-	2	1_A375_pNL7_minus_lncRNA_AR..1..0, 2_A375_pNL97_plus_lncRNA_AR..1..0	20, -44	in gene, upstream	1	1	0	25	28	14	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene LOC100288069		hypothetical LOC100288069	NR_033908		
GeneID:100287934	LOC100287934	1	721,320	722,513	1,193	+	2	1_A375_pNL7_minus_lncRNA_AR..1..0, 2_A375_pNL97_plus_lncRNA_AR..1..0	-7272, -7208	upstream, upstream	1	1	0	25	28	14	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene LOC100287934		hypothetical LOC100287934	XR_112047, XR_108279, XR_115170		
GeneID:284600	LOC284600	1	846,815	850,735	3,920	+	1	4_A375_EGR1..1..0	11793	downstream	0	0	1	7	15	15	1	4_A375_EGR1..1	15	Gene LOC284600		hypothetical LOC284600	XR_112076, XR_108282, XR_113325	1559083_x_at	
GeneID:100130417	FLJ39609	1	852,953	854,817	1,864	-	1	4_A375_EGR1..1..0	-3791	upstream	0	0	1	7	15	15	1	4_A375_EGR1..1	15	Gene FLJ39609		similar to hCG1995469	NR_026874		
GeneID:148398	SAMD11	1	861,121	879,961	18,840	+	4	4_A375_EGR1..1..0, 4_A375_EGR1..1..1, 4_A375_EGR1..1..2, 4_A375_EGR1..1..3	-2513, 11231, 14895, 17279	upstream, in gene, in gene, in gene	0	0	1	8.5	12.75	16.5	4	4_A375_EGR1..1	18	Gene SAMD11	SAMD11, MGC45873	sterile alpha motif domain containing 11	NM_152486, hCT2341076.0	1560477_a_at	NP_689699.2, EAW56307.1
GeneID:26155	NOC2L	1	879,583	894,679	15,096	-	8	2_A375_pNL97_plus_lncRNA_AR..1..1, 2_A375_pNL97_plus_lncRNA_AR..1..2, 4_A375_EGR1..1..1, 4_A375_EGR1..1..2, 4_A375_EGR1..1..3, 4_A375_EGR1..1..4, 4_A375_EGR1..1..5, 4_A375_EGR1..1..6	55, -1241, 22327, 18863, 16279, -2281, -4633, -7209	in gene, upstream, downstream, downstream, downstream, upstream, upstream, upstream	0	1	1	11.75	14.25	17.14	8	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene NOC2L	FLJ35172, NET7, NET15, NIR, NOC2L, DKFZp564C186	nucleolar complex associated 2 homolog (S. cerevisiae)	NM_015658, hCT2275821.0, hCT2275823.0, hCT2275826.0	1559139_at, 202115_s_at	NP_056473.2, EAW56304.1, EAW56305.1, EAW56306.1
GeneID:339451	KLHL17	1	895,967	901,095	5,128	+	5	2_A375_pNL97_plus_lncRNA_AR..1..1, 2_A375_pNL97_plus_lncRNA_AR..1..2, 4_A375_EGR1..1..4, 4_A375_EGR1..1..5, 4_A375_EGR1..1..6	-1343, -47, 993, 3345, 5921	upstream, upstream, in gene, in gene, downstream	0	1	1	13.4	15.6	17.25	5	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene KLHL17	KLHL17, RP11-54O7.6	kelch-like 17 (Drosophila)	NM_198317, hCT1954985.2, hCT22913.4, hCT2341075.0, hCT2353011.0	1555850_at, 229792_at	NP_938073.1, EAW56300.1, EAW56301.1, EAW56302.1, EAW56303.1
GeneID:84069	PLEKHN1	1	901,877	910,488	8,611	+	7	2_A375_pNL97_plus_lncRNA_AR..1..1, 2_A375_pNL97_plus_lncRNA_AR..1..2, 4_A375_EGR1..1..4, 4_A375_EGR1..1..5, 4_A375_EGR1..1..6, 4_A375_EGR1..1..7, 4_A375_EGR1..1..8	-7253, -5957, -4917, -2565, 11, 9739, 11979	upstream, upstream, upstream, upstream, in gene, downstream, downstream	0	1	1	11.43	13.57	17	7	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene PLEKHN1	DKFZp434H2010, MGC120616, MGC120613, PLEKHN1, RP11-54O7.7	pleckstrin homology domain containing, family N member 1	NM_032129, NM_001160184, hCT22914.2	224125_at	NP_115505.2, NP_001153656.1, EAW56299.1
GeneID:84808	C1orf170	1	910,579	917,473	6,894	-	3	4_A375_EGR1..1..6, 4_A375_EGR1..1..7, 4_A375_EGR1..1..8	15585, 5657, 3617	downstream, in gene, in gene	0	0	1	9	11	16.67	3	4_A375_EGR1..1	23	Gene C1orf170	C1orf170, RP11-54O7.8, MGC13275, FLJ92510	chromosome 1 open reading frame 170	NR_027693	224501_at	
GeneID:57801	HES4	1	934,342	935,552	1,210	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1, 2_A375_pNL97_plus_lncRNA_AR..1..3, 4_A375_EGR1..1..9	-560, -608, -3472	upstream, upstream, upstream	1	1	1	15	14.5	12	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene HES4	bHLHb42, HES4	hairy and enhancer of split 4 (Drosophila)	NM_021170, NM_001142467, hCT1809955.2	227347_x_at	NP_066993.1, NP_001135939.1, EAW56296.1
GeneID:9636	ISG15	1	948,847	949,920	1,073	+	1	4_A375_EGR1..1..9	-9623	upstream	0	0	1	7	7	15	1	4_A375_EGR1..1	15	Gene ISG15	UCRP, IP17, hUCRP, IFI15, ISG15, G1P2	ISG15 ubiquitin-like modifier	NM_005101, hCT1809958.1	205483_s_at	NP_005092.1, EAW56295.1
GeneID:375790	AGRN	1	955,503	991,492	35,989	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2, 2_A375_pNL97_plus_lncRNA_AR..1..4, 4_A375_EGR1..1..10, 4_A375_EGR1..1..11, 4_A375_EGR1..1..12, 4_A375_EGR1..1..13	39473, 39457, 27302, 31409, 33841, 43985	downstream, downstream, in gene, in gene, in gene, downstream	1	1	1	11.4	12.4	17.2	5	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene AGRN	FLJ45064, AGRN	agrin	NM_198576, hCT1809981.2	212283_at, 212285_s_at, 217410_at, 217419_x_at	NP_940978.2, EAW56293.1
GeneID:401934	LOC401934	1	1,007,126	1,009,687	2,561	-	1	4_A375_EGR1..1..13	10199	downstream	0	0	1	15	16	17	1	4_A375_EGR1..1	17	Gene LOC401934		hypothetical LOC401934	XM_002345348, XM_002342025, XM_002346363		XP_002345387.1, XP_002342066.1, XP_002346404.1
GeneID:54991	C1orf159	1	1,017,198	1,051,736	34,538	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3, 2_A375_pNL97_plus_lncRNA_AR..1..5, 4_A375_EGR1..1..14, 4_A375_EGR1..1..15	120, 136, 30200, -6248	in gene, in gene, in gene, upstream	1	1	1	12	13.67	13	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene C1orf159	FLJ38119, FLJ20584, C1orf159, FLJ21143	chromosome 1 open reading frame 159	NM_017891, hCT1809957.2, hCT1954984.1, hCT1954988.1, hCT2275800.0	219337_at	NP_060361.4, EAW56288.1, EAW56289.1, EAW56290.1, EAW56291.1
GeneID:406984	MIR200B	1	1,102,484	1,102,578	94	+	5	2_A375_pNL97_plus_lncRNA_AR..1..6, 4_A375_EGR1..1..19, 4_A375_EGR1..1..20, 4_A375_EGR1..1..21, 4_A375_EGR1..1..22	-8984, -9001, -8466, -1972, 556	upstream, upstream, upstream, upstream, downstream	0	1	1	8.33	9.67	19.33	3	4_A375_EGR1..1	24	Gene MIR200B	MIR200B, MIRN200B	microRNA 200b	NR_029639		
GeneID:406983	MIR200A	1	1,103,243	1,103,332	89	+	5	2_A375_pNL97_plus_lncRNA_AR..1..6, 4_A375_EGR1..1..19, 4_A375_EGR1..1..20, 4_A375_EGR1..1..21, 4_A375_EGR1..1..22	-9723, -9760, -9227, -2731, -203	upstream, upstream, upstream, upstream, upstream	0	1	1	8.33	9.67	19.33	3	4_A375_EGR1..1	24	Gene MIR200A	MIRN200A, MIR200A	microRNA 200a	NR_029834		
GeneID:554210	MIR429	1	1,104,385	1,104,467	82	+	3	4_A375_EGR1..1..21, 4_A375_EGR1..1..22, 4_A375_EGR1..1..23	-3873, -1345, 9963	upstream, upstream, downstream	0	0	1	5.67	8.33	16.67	3	4_A375_EGR1..1	22	Gene MIR429	hsa-mir-429, MIR429, MIRN429	microRNA 429	NR_029957		
GeneID:100506376	LOC100506376	1	1,108,436	1,114,935	6,499	-	5	4_A375_EGR1..1..21, 4_A375_EGR1..1..22, 4_A375_EGR1..1..23, 4_A375_EGR1..1..24, 4_A375_EGR1..1..25	14423, 11895, 567, -849, -5705	downstream, downstream, in gene, upstream, upstream	0	0	1	4.8	6.6	18.6	5	4_A375_EGR1..1	22	Gene LOC100506376		hypothetical protein LOC100506376	XM_003119803, XM_003118493, XM_003120337		XP_003119851.1, XP_003118541.1, XP_003120385.1
GeneID:254173	TTLL10	1	1,109,286	1,133,313	24,027	+	6	4_A375_EGR1..1..21, 4_A375_EGR1..1..22, 4_A375_EGR1..1..23, 4_A375_EGR1..1..24, 4_A375_EGR1..1..25, 4_A375_EGR1..1..26	-8774, -6246, 5082, 6298, 11354, 30234	upstream, upstream, in gene, in gene, in gene, downstream	0	0	1	4.67	7.5	18.83	6	4_A375_EGR1..1	22	Gene TTLL10	TTLL10, FLJ38119, FLJ42131, TTLL5	tubulin tyrosine ligase-like family, member 10	NM_153254, NM_001130045, hCT11506.4, hCT1840872.2	1552418_at, 1552419_s_at, 236418_at	NP_694986.2, NP_001123517.1, EAW56285.1, EAW56286.1
GeneID:8784	TNFRSF18	1	1,138,888	1,142,089	3,201	-	4	4_A375_EGR1..1..26, 4_A375_EGR1..1..27, 4_A375_EGR1..1..28, 4_A375_EGR1..1..29	2569, -4103, -5399, -9639	in gene, upstream, upstream, upstream	0	0	1	5.75	8.5	17.25	4	4_A375_EGR1..1	19	Gene TNFRSF18	AITR, GITR, TNFRSF18, GITRD	tumor necrosis factor receptor superfamily, member 18	NM_004195, NM_148901, NM_148902, hCT11492.3, hCT1965824.1, hCT2275787.0	223851_s_at, 224553_s_at	NP_004186.1, NP_683699.1, NP_683700.1, EAW56282.1, EAW56283.1, EAW56284.1
GeneID:7293	TNFRSF4	1	1,146,706	1,149,512	2,806	-	6	4_A375_EGR1..1..26, 4_A375_EGR1..1..27, 4_A375_EGR1..1..28, 4_A375_EGR1..1..29, 4_A375_EGR1..1..30, 4_A375_EGR1..1..31	9992, 3320, 2024, -2216, -3672, -8184	downstream, downstream, in gene, upstream, upstream, upstream	0	0	1	5.5	7.67	17	6	4_A375_EGR1..1	19	Gene TNFRSF4	TXGP1L, ACT35, TNFRSF4, OX40, CD134	tumor necrosis factor receptor superfamily, member 4	NM_003327, hCT1647620.3, hCT1954939.0, hCT1954940.1, hCT2352999.0	208023_at, 214228_x_at	NP_003318.1, EAW56281.1, EAW56278.1, EAW56279.1, EAW56280.1
GeneID:51150	SDF4	1	1,152,288	1,167,447	15,159	-	7	2_A375_pNL97_plus_lncRNA_AR..1..7, 4_A375_EGR1..1..27, 4_A375_EGR1..1..28, 4_A375_EGR1..1..29, 4_A375_EGR1..1..30, 4_A375_EGR1..1..31, 4_A375_EGR1..1..32	-6313, 21255, 19959, 15719, 14263, 9751, -7666	upstream, downstream, downstream, downstream, in gene, in gene, upstream	0	1	1	7.71	9	17	7	4_A375_EGR1..1	22	Gene SDF4	Cab45, SDF4	stromal cell derived factor 4	NM_016176, NM_016547, hCT10259.3, hCT1954881.1, hCT1954882.1, hCT1954883.1, hCT1954884.1, hCT1954885.1, hCT2275778.0	217855_x_at, 221972_s_at, 224472_x_at, 232032_x_at	NP_057260.2, NP_057631.1, EAW56272.1, EAW56275.1, EAW56276.1, EAW56277.1, EAW56271.1, EAW56273.1, EAW56274.1
GeneID:126792	B3GALT6	1	1,167,629	1,170,421	2,792	+	3	2_A375_pNL97_plus_lncRNA_AR..1..7, 4_A375_EGR1..1..31, 4_A375_EGR1..1..32	6131, -9933, 7466	downstream, upstream, downstream	0	1	1	9.33	11.67	17	3	4_A375_EGR1..1	22	Gene B3GALT6	B3GALT6, beta3GalT6	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6	NM_080605, hCT1642223.3	1553959_a_at, 225733_at, 226427_s_at	NP_542172.2, EAW56269.1
GeneID:388581	FAM132A	1	1,177,833	1,182,102	4,269	-	3	2_A375_pNL97_plus_lncRNA_AR..1..7, 4_A375_EGR1..1..32, 4_A375_EGR1..1..33	8342, 6987, -826	downstream, downstream, upstream	0	1	1	10	12.67	18.33	3	4_A375_EGR1..1	22	Gene FAM132A	MGC105127, C1QTNF12, FAM132A, C1QDC2	family with sequence similarity 132, member A	NM_001014980	243292_at	NP_001014980.1
GeneID:118424	UBE2J2	1	1,189,292	1,209,234	19,942	-	4	4_A375_EGR1..1..33, 4_A375_EGR1..1..34, 4_A375_EGR1..1..35, 4_A375_EGR1..1..36	26306, 1074, -654, -8590	downstream, in gene, upstream, upstream	0	0	1	8.25	11.5	19	4	4_A375_EGR1..1	23	Gene UBE2J2	PRO2121, UBE2J2, NCUBE2, NCUBE-2	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)	NM_058167, NM_194315, NM_194457, NM_194458, hCT11499.4, hCT1954908.2, hCT1954909.2, hCT1965628.2, hCT1965627.2, hCT1965626.2, hCT1965630.2, hCT1965632.2, hCT2343765.0, hCT2352995.0, hCT2352996.0, hCT2352997.0, hCT2352998.0	224347_x_at, 225209_s_at, 226704_at	NP_477515.2, NP_919296.1, NP_919439.1, NP_919440.1, EAW56260.1, EAW56265.1, EAW56255.1, EAW56256.1, EAW56257.1, EAW56258.1, EAW56259.1, EAW56261.1, EAW56262.1, EAW56263.1, EAW56264.1, EAW56266.1, EAW56267.1
GeneID:6339	SCNN1D	1	1,217,489	1,227,409	9,920	+	8	1_A375_pNL7_minus_lncRNA_AR..1..4, 2_A375_pNL97_plus_lncRNA_AR..1..8, 4_A375_EGR1..1..34, 4_A375_EGR1..1..35, 4_A375_EGR1..1..36, 4_A375_EGR1..1..37, 4_A375_EGR1..1..38, 4_A375_EGR1..1..39	17071, 17071, -9329, -7601, 335, 3791, 5007, 17607	downstream, downstream, upstream, upstream, in gene, in gene, in gene, downstream	1	1	1	10.67	13.33	19.33	6	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SCNN1D	MGC149711, SCNN1D, SCNED, dNaCh, MGC149710, ENaCd, ENaCdelta	sodium channel, nonvoltage-gated 1, delta	NM_002978, NM_001130413, hCT1954887.1, hCT1954888.1, hCT1954889.1, hCT1954890.0	208456_at	NP_002969.2, NP_001123885.1, EAW56251.1, EAW56252.1, EAW56253.1, EAW56254.1
GeneID:116983	ACAP3	1	1,227,764	1,243,269	15,505	-	9	1_A375_pNL7_minus_lncRNA_AR..1..4, 1_A375_pNL7_minus_lncRNA_AR..1..5, 2_A375_pNL97_plus_lncRNA_AR..1..8, 2_A375_pNL97_plus_lncRNA_AR..1..9, 4_A375_EGR1..1..36, 4_A375_EGR1..1..37, 4_A375_EGR1..1..38, 4_A375_EGR1..1..39, 4_A375_EGR1..1..40	8709, -331, 8709, -443, 25445, 21989, 20773, 8173, 2369	in gene, upstream, in gene, upstream, downstream, downstream, downstream, in gene, in gene	1	1	1	12.83	15.17	17.83	6	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene ACAP3	ACAP3, KIAA1716, CENTB5	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3	NM_030649, hCT2275759.0, hCT2275761.0, hCT2275762.0, hCT2275763.0, hCT2275764.0	225529_at, 225542_at	NP_085152.2, EAW56246.1, EAW56247.1, EAW56248.1, EAW56249.1, EAW56250.1
GeneID:126789	PUSL1	1	1,243,994	1,247,057	3,063	+	6	1_A375_pNL7_minus_lncRNA_AR..1..4, 1_A375_pNL7_minus_lncRNA_AR..1..5, 2_A375_pNL97_plus_lncRNA_AR..1..8, 2_A375_pNL97_plus_lncRNA_AR..1..9, 4_A375_EGR1..1..39, 4_A375_EGR1..1..40	-9434, -394, -9434, -282, -8898, -3114	upstream, upstream, upstream, upstream, upstream, upstream	1	1	1	18	21	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene PUSL1	FLJ90811, PUSL1	pseudouridylate synthase-like 1	NM_153339, hCT11500.4	228733_at	NP_699170.1, EAW56245.1
GeneID:54973	CPSF3L	1	1,246,965	1,260,046	13,081	-	7	1_A375_pNL7_minus_lncRNA_AR..1..5, 2_A375_pNL97_plus_lncRNA_AR..1..9, 4_A375_EGR1..1..40, 4_A375_EGR1..1..41, 4_A375_EGR1..1..42, 4_A375_EGR1..1..43, 4_A375_EGR1..1..44	16446, 16334, 19166, -3922, -8914, -8154, -8999	downstream, downstream, downstream, upstream, upstream, upstream, upstream	1	1	1	11.67	13.17	17	6	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene CPSF3L	RC-68, RC68, FLJ20542, INTS11, FLJ13294, INT11, CPSF73L, CPSF3L	cleavage and polyadenylation specific factor 3-like	NM_017871, hCT11501.2, hCT1954913.1, hCT1954914.1, hCT1954916.1, hCT1954920.1, hCT1966942.1, hCT1966943.1, hCT2353001.0, hCT2353002.0, hCT2353003.0, hCT2353004.0, hCT2353005.0, hCT2353006.0	217994_x_at, 224312_x_at, 232437_at, 233583_s_at, 233625_x_at	NP_060341.2, EAW56234.1, EAW56232.1, EAW56235.1, EAW56236.1, EAW56242.1, EAW56233.1, EAW56237.1, EAW56238.1, EAW56239.1, EAW56240.1, EAW56241.1, EAW56243.1, EAW56244.1
GeneID:80772	GLTPD1	1	1,260,143	1,264,276	4,133	+	5	4_A375_EGR1..1..41, 4_A375_EGR1..1..42, 4_A375_EGR1..1..43, 4_A375_EGR1..1..44, 4_A375_EGR1..1..45	3825, 6617, 8057, 8902, 13873	in gene, downstream, downstream, downstream, downstream	0	0	1	10	10.4	17.6	5	4_A375_EGR1..1	20	Gene GLTPD1	MGC10334, GLTPD1	glycolipid transfer protein domain containing 1	NM_001029885, hCT11498.4, hCT1969070.2		NP_001025056.1, EAW56230.1, EAW56231.1
GeneID:83756	TAS1R3	1	1,266,726	1,269,844	3,118	+	5	4_A375_EGR1..1..41, 4_A375_EGR1..1..42, 4_A375_EGR1..1..43, 4_A375_EGR1..1..44, 4_A375_EGR1..1..45	-2756, 234, 1474, 2319, 7290	upstream, in gene, in gene, in gene, downstream	0	0	1	10	10.4	17.6	5	4_A375_EGR1..1	20	Gene TAS1R3	TAS1R3, T1R3	taste receptor, type 1, member 3	NM_152228		NP_689414.1
GeneID:1855	DVL1	1	1,270,658	1,284,492	13,834	-	5	4_A375_EGR1..1..41, 4_A375_EGR1..1..42, 4_A375_EGR1..1..43, 4_A375_EGR1..1..44, 4_A375_EGR1..1..45	20524, 17532, 16292, 15447, 10476	downstream, downstream, downstream, downstream, in gene	0	0	1	10	10.4	17.6	5	4_A375_EGR1..1	20	Gene DVL1	DVL, MGC54245, DVL1L1, DVL1	dishevelled, dsh homolog 1 (Drosophila)	NM_004421, hCT11491.3, hCT1954892.1, hCT2352993.0, hCT2352994.0	203230_at	NP_004412.2, EAW56227.1, EAW56224.1, EAW56225.1, EAW56226.1
GeneID:100506404	LOC100506404	1	1,303,575	1,322,851	19,276	+	5	1_A375_pNL7_minus_lncRNA_AR..1..6, 2_A375_pNL97_plus_lncRNA_AR..1..10, 4_A375_EGR1..1..46, 4_A375_EGR1..1..47, 4_A375_EGR1..1..48	7061, 7049, 2761, 6409, 7049	in gene, in gene, in gene, in gene, in gene	1	1	1	28	27.5	19	2	2_A375_pNL97_plus_lncRNA_AR..1	49	Gene LOC100506404		hypothetical LOC100506404	XR_112082, XR_108283		
GeneID:54998	AURKAIP1	1	1,309,110	1,310,818	1,708	-	5	1_A375_pNL7_minus_lncRNA_AR..1..6, 2_A375_pNL97_plus_lncRNA_AR..1..10, 4_A375_EGR1..1..46, 4_A375_EGR1..1..47, 4_A375_EGR1..1..48	162, 194, 4482, 834, 194	in gene, in gene, downstream, in gene, in gene	1	1	1	28	27.5	19	2	2_A375_pNL97_plus_lncRNA_AR..1	49	Gene AURKAIP1	FLJ20608, AKIP, AURKAIP1, AIP	aurora kinase A interacting protein 1	NM_017900, NM_001127229, NM_001127230, hCT11495.3, hCT1954898.0	218580_x_at, 225552_x_at, 227546_x_at, 228800_x_at	NP_060370.1, NP_001120701.1, NP_001120702.1, EAW56218.1, EAW56219.1
GeneID:81669	CCNL2	1	1,321,091	1,334,718	13,627	-	4	1_A375_pNL7_minus_lncRNA_AR..1..6, 2_A375_pNL97_plus_lncRNA_AR..1..10, 2_A375_pNL97_plus_lncRNA_AR..1..11, 2_A375_pNL97_plus_lncRNA_AR..1..12	24062, 24094, -130, -8066	downstream, downstream, upstream, upstream	1	1	0	24.67	32	15	3	2_A375_pNL97_plus_lncRNA_AR..1	49	Gene CCNL2	HLA-ISO, ANIA-6B, CCNM, SB138, PCEE, DKFZp761A1210, HCLA-ISO, DKFZp762O195, CCNL2	cyclin L2	NM_030937, NM_001039577, hCT11502.3, hCT1809975.2, hCT1954921.1, hCT1954922.1, hCT1954923.1, hCT2275738.0, hCT2275739.0	225555_x_at	NP_112199.2, NP_001034666.1, EAW56212.1, EAW56213.1, EAW56215.1, EAW56217.1, EAW56211.1, EAW56214.1, EAW56216.1
GeneID:148413	LOC148413	1	1,334,910	1,337,426	2,516	+	2	2_A375_pNL97_plus_lncRNA_AR..1..11, 2_A375_pNL97_plus_lncRNA_AR..1..12	-62, 7674	upstream, downstream	0	1	0	14	23.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene LOC148413		hypothetical LOC148413	NR_015434	225920_at, 225934_at	
GeneID:55052	MRPL20	1	1,337,276	1,342,693	5,417	-	2	2_A375_pNL97_plus_lncRNA_AR..1..11, 2_A375_pNL97_plus_lncRNA_AR..1..12	7645, -91	downstream, upstream	0	1	0	14	23.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene MRPL20	MGC74465, MRP-L20, MGC4779, L20mt, MRPL20	mitochondrial ribosomal protein L20	NM_017971, hCT11496.3, hCT1954901.1, hCT1954902.1	220526_s_at, 220527_at, 224803_s_at	NP_060441.2, EAW56206.1, EAW56207.1, EAW56208.1
GeneID:441869	HCG_20426	1	1,353,800	1,356,650	2,850	-	2	4_A375_EGR1..1..49, 4_A375_EGR1..1..50	1754, -9302	in gene, upstream	0	0	1	6.5	6.5	16	2	4_A375_EGR1..1	17	Gene HCG_20426	LOC441869	hypothetical protein LOC441869	NM_001145210, NR_026671	1556181_at, 1556182_x_at	NP_001138682.1
GeneID:643965	TMEM88B	1	1,361,508	1,363,167	1,659	+	5	4_A375_EGR1..1..49, 4_A375_EGR1..1..50, 4_A375_EGR1..1..51, 4_A375_EGR1..1..52, 4_A375_EGR1..1..53	-6612, 4444, 5626, 10300, 11356	upstream, downstream, downstream, downstream, downstream	0	0	1	6.8	7.6	16.6	5	4_A375_EGR1..1	19	Gene TMEM88B	TMEM88B	transmembrane protein 88B	NM_001146685		NP_001140157.1
GeneID:100288271	LOC100288271	1	1,365,912	1,369,900	3,988	-	6	4_A375_EGR1..1..50, 4_A375_EGR1..1..51, 4_A375_EGR1..1..52, 4_A375_EGR1..1..53, 4_A375_EGR1..1..54, 4_A375_EGR1..1..55	3948, 2764, -1908, -2984, -4660, -7220	in gene, in gene, upstream, upstream, upstream, upstream	0	0	1	6.33	8.5	17.5	6	4_A375_EGR1..1	20	Gene LOC100288271		hypothetical LOC100288271	XR_112083, XR_112084, XR_108284, XR_108285, XR_113329		
GeneID:84656	VWA1	1	1,370,903	1,378,262	7,359	+	6	4_A375_EGR1..1..50, 4_A375_EGR1..1..51, 4_A375_EGR1..1..52, 4_A375_EGR1..1..53, 4_A375_EGR1..1..54, 4_A375_EGR1..1..55	-4951, -3767, 905, 1981, 3657, 6217	upstream, upstream, in gene, in gene, in gene, in gene	0	0	1	6.33	8.5	17.5	6	4_A375_EGR1..1	20	Gene VWA1	VWA1, DKFZp761O051, FLJ22215, WARP	von Willebrand factor A domain containing 1	NM_022834, NM_199121, hCT2276501.0, hCT2276503.0, hCT2276504.0, hCT2353007.0, hCT2353008.0	218731_s_at, 228851_at	NP_073745.2, NP_954572.2, EAW56197.1, EAW56199.1, EAW56200.1, EAW56201.1, EAW56198.1
GeneID:219293	ATAD3C	1	1,385,069	1,405,538	20,469	+	5	2_A375_pNL97_plus_lncRNA_AR..1..13, 4_A375_EGR1..1..55, 4_A375_EGR1..1..56, 4_A375_EGR1..1..57, 4_A375_EGR1..1..58	21971, -7949, 6131, 10814, 13203	downstream, upstream, in gene, in gene, in gene	0	1	1	7	10.6	16.2	5	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ATAD3C	FLJ34599, ATAD3C, FLJ37163	ATPase family, AAA domain containing 3C	NM_001039211	240210_at	NP_001034300.2
GeneID:83858	ATAD3B	1	1,407,164	1,431,582	24,418	+	3	2_A375_pNL97_plus_lncRNA_AR..1..13, 4_A375_EGR1..1..58, 4_A375_EGR1..1..59	-124, -8892, 23820	upstream, upstream, in gene	0	1	1	9.33	13.67	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ATAD3B	KIAA1273, AAA-TOB3, ATAD3B, TOB3	ATPase family, AAA domain containing 3B	NM_031921, hCT2276508.1, hCT2276509.1, hCT2276510.1	223617_x_at, 227237_x_at, 233091_at	NP_114127.3, EAW56192.1, EAW56193.1, EAW56194.1
GeneID:55210	ATAD3A	1	1,447,523	1,470,067	22,544	+	7	1_A375_pNL7_minus_lncRNA_AR..1..7, 2_A375_pNL97_plus_lncRNA_AR..1..14, 4_A375_EGR1..1..60, 4_A375_EGR1..1..61, 4_A375_EGR1..1..62, 4_A375_EGR1..1..63, 4_A375_EGR1..1..64	-67, -35, -195, 22701, 24125, 29117, 30341	upstream, upstream, upstream, downstream, downstream, downstream, downstream	1	1	1	10.2	10	17.8	5	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene ATAD3A	FLJ35514, ATAD3A, FLJ10709	ATPase family, AAA domain containing 3A	NM_018188, NM_001170535, NM_001170536, hCT1809953.2, hCT1982112.1, hCT1982113.1, hCT1982114.1, hCT2352989.0, hCT2352990.0	219068_x_at, 227700_x_at	NP_060658.3, NP_001164006.1, NP_001164007.1, EAW56186.1, EAW56187.1, EAW56189.1, EAW56188.1, EAW56190.1, EAW56191.1
GeneID:339453	C1orf70	1	1,470,158	1,475,740	5,582	-	4	4_A375_EGR1..1..61, 4_A375_EGR1..1..62, 4_A375_EGR1..1..63, 4_A375_EGR1..1..64	5516, 4092, -900, -2124	in gene, in gene, upstream, upstream	0	0	1	7.75	8.25	17.75	4	4_A375_EGR1..1	22	Gene C1orf70	C1orf70	chromosome 1 open reading frame 70	NM_001114748		NP_001108220.1
GeneID:29101	SSU72	1	1,477,053	1,510,262	33,209	-	8	1_A375_pNL7_minus_lncRNA_AR..1..8, 2_A375_pNL97_plus_lncRNA_AR..1..15, 4_A375_EGR1..1..61, 4_A375_EGR1..1..62, 4_A375_EGR1..1..63, 4_A375_EGR1..1..64, 4_A375_EGR1..1..65, 4_A375_EGR1..1..66	-108, -42, 40036, 38814, 33622, 32398, 19590, -138	upstream, upstream, downstream, downstream, downstream, in gene, in gene, upstream	1	1	1	10.17	10.5	18.33	6	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SSU72	PNAS-120, FLJ13048, SSU72, HSPC182	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	NM_014188, hCT10254.2, hCT2275838.0	223051_at, 223052_x_at, 223053_x_at, 226229_s_at, 227244_s_at, 229329_s_at, 229330_at	NP_054907.1, EAW56183.1, EAW56182.1
GeneID:643988	LOC643988	1	1,533,388	1,535,470	2,082	-	1	4_A375_EGR1..1..67	-1554	upstream	0	0	1	5	9	17	1	4_A375_EGR1..1	17	Gene LOC643988		hypothetical LOC643988	XR_108286	227185_at	
GeneID:142678	MIB2	1	1,550,795	1,565,990	15,195	+	1	4_A375_EGR1..1..68	13109	in gene	0	0	1	8	11	18	1	4_A375_EGR1..1	18	Gene MIB2	FLJ39787, ZZANK1, FLJ20648, FLJ41406, ZZZ5, MIB2	mindbomb homolog 2 (Drosophila)	NM_080875, NM_001170686, NM_001170687, NM_001170688, NM_001170689, NR_033183, hCT2336669.0, hCT2336670.0, hCT2353014.0, hCT2353015.0, hCT2353016.0, hCT2353017.0	226644_at, 226281_at, 241377_s_at, 241378_at, 241541_at	NP_543151.2, NP_001164157.1, NP_001164158.1, NP_001164159.1, NP_001164160.1, EAW56179.1, EAW56174.1, EAW56175.1, EAW56176.1, EAW56177.1, EAW56178.1
GeneID:8510	MMP23B	1	1,567,560	1,570,030	2,470	+	1	4_A375_EGR1..1..68	-3656	upstream	0	0	1	8	11	18	1	4_A375_EGR1..1	18	Gene MMP23B	MMP22, MIFR, MMP23A, MMP23B, MIFR-1	matrix metallopeptidase 23B	NM_006983	207118_s_at	NP_008914.1

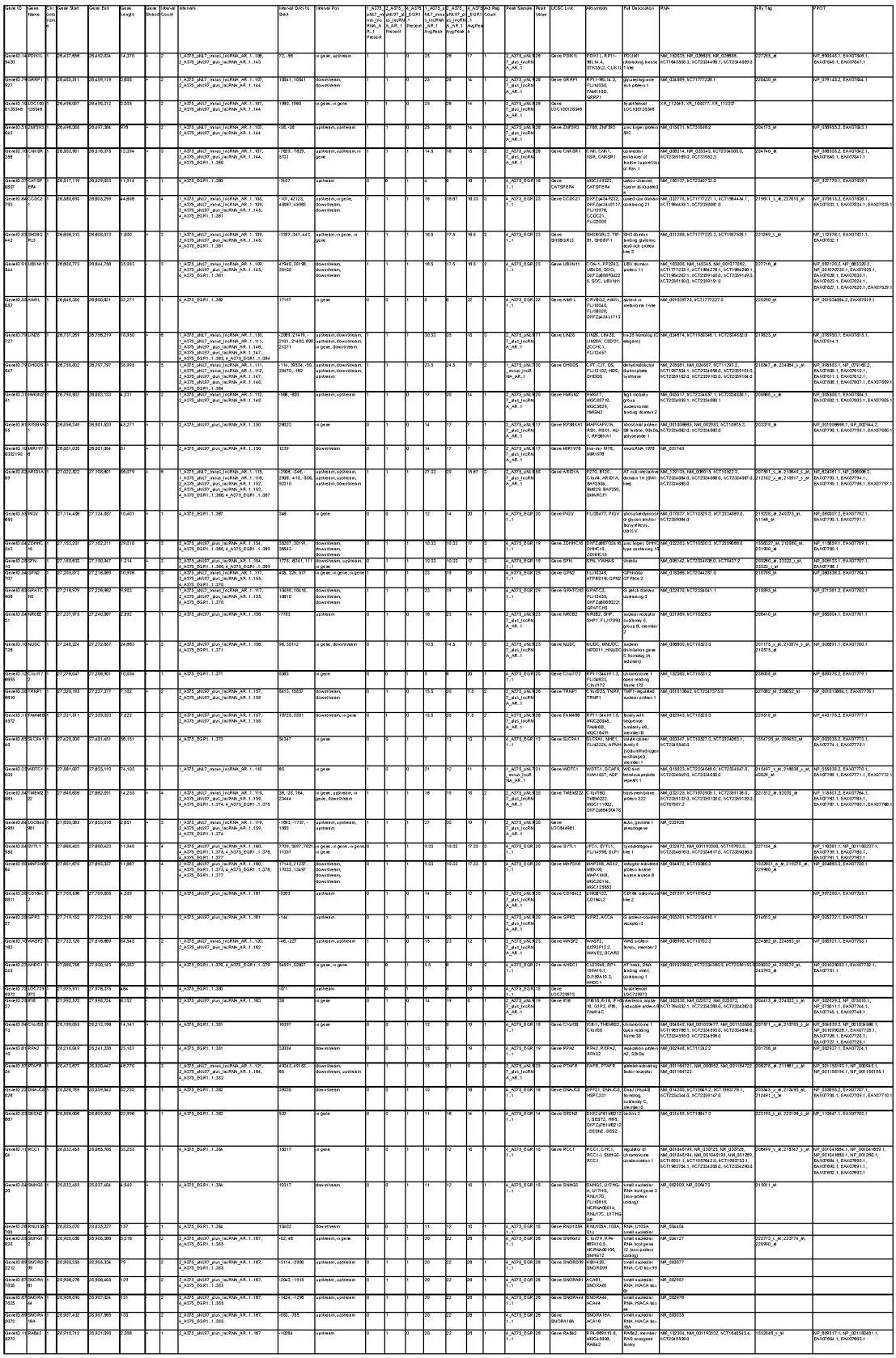
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:984	CDK11B	1	1,571,100	1,590,473	19,373	-	3	1_A375_pNL7_minus_lncRNA_AR..1..9, 2_A375_pNL97_plus_lncRNA_AR..1..16, 4_A375_EGR1..1..66	-23, -135, 26569	upstream, upstream, downstream	1	1	1	13	14	15	2	4_A375_EGR1..1	18	Gene CDK11B	CDC2L1, FLJ59152, CDC2L2, p58CDC2L1, p58, CDK11-p58, p58CLK-1, PK58, CDK11B, CDK11, CLK-1, CDK11-p110, CDK11-p46	cyclin-dependent kinase 11B	NM_033486, NM_033487, NM_033488, NM_033489, NM_033492, NM_033493, hCT2340548.0, hCT2340549.0, hCT2340550.0, hCT2340551.0	211289_x_at	NP_277021.1, NP_277022.1, NP_277023.1, NP_277024.1, NP_277027.1, NP_277028.1, EAW56170.1, EAW56171.1, EAW56172.1, EAW56173.1
GeneID:728661	RP11-345P4.4	1	1,592,939	1,624,243	31,304	-	5	1_A375_pNL7_minus_lncRNA_AR..1..9, 1_A375_pNL7_minus_lncRNA_AR..1..10, 2_A375_pNL97_plus_lncRNA_AR..1..16, 2_A375_pNL97_plus_lncRNA_AR..1..17, 4_A375_EGR1..1..69	33747, -349, 33835, -237, 5523	downstream, upstream, downstream, upstream, in gene	1	1	1	15.67	17	13	3	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene RP11-345P4.4	SLC35E2B, MGC117254, KIAA0447, DKFZp564C093, MGC104754, DKFZp666M0669, FLJ43631, SLC35E2, LOC728661	similar to solute carrier family 35, member E2	NM_001110781	217122_s_at	NP_001104251.1
GeneID:728642	CDK11A	1	1,634,169	1,655,791	21,622	-	2	1_A375_pNL7_minus_lncRNA_AR..1..10, 2_A375_pNL97_plus_lncRNA_AR..1..17	31199, 31311	downstream, downstream	1	1	0	23	27	7	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene CDK11A	MGC131975, CDK11A, p58GTA, CDC2L2, PITSLRE, CDK11-p58, CDC2L3, CDK11-p110, CDK11-p46	cyclin-dependent kinase 11A	NM_033529, NM_024011	207428_x_at, 210474_s_at, 212401_s_at, 215329_s_at	NP_277071.2, NP_076916.2
GeneID:2782	GNB1	1	1,716,729	1,822,495	105,766	-	1	4_A375_EGR1..1..70	-577	upstream	0	0	1	7	9	16	1	4_A375_EGR1..1	16	Gene GNB1	GNB1		NM_002074, hCT14577.3, hCT2336557.0, hCT2336559.0, hCT2336560.0	1570108_at, 200744_s_at, 200745_s_at, 200746_s_at	NP_002065.1, EAW56150.1, EAW56147.1, EAW56148.1, EAW56149.1
GeneID:163688	CALML6	1	1,846,266	1,848,733	2,467	+	3	4_A375_EGR1..1..71, 4_A375_EGR1..1..72, 4_A375_EGR1..1..73	1019, 3762, 5403	in gene, downstream, downstream	0	0	1	7.33	8	16.67	3	4_A375_EGR1..1	20	Gene CALML6	CAGLP, CALML6	calmodulin-like 6	NM_138705, hCT14572.3, hCT2336624.0, hCT2352991.0	1552402_at	NP_619650.2, EAW56144.1, EAW56145.1, EAW56146.1
GeneID:339456	TMEM52	1	1,849,029	1,850,740	1,711	-	3	4_A375_EGR1..1..71, 4_A375_EGR1..1..72, 4_A375_EGR1..1..73	3455, 692, -929	downstream, in gene, upstream	0	0	1	7.33	8	16.67	3	4_A375_EGR1..1	20	Gene TMEM52	TMEM52	transmembrane protein 52	NM_178545, hCT14574.3, hCT2352992.0	230467_at	NP_848640.1, EAW56142.1, EAW56143.1
GeneID:85452	KIAA1751	1	1,884,752	1,935,276	50,524	-	2	4_A375_EGR1..1..74, 4_A375_EGR1..1..75	34924, 33324	in gene, in gene	0	0	1	6.5	7	17	2	4_A375_EGR1..1	17	Gene KIAA1751	FLJ45476, RP1-140A9.6, KIAA1751	KIAA1751	NM_001080484	216781_at, 216807_at	NP_001073953.1
GeneID:2563	GABRD	1	1,950,768	1,962,192	11,424	+	2	4_A375_EGR1..1..76, 4_A375_EGR1..1..77	2416, 8824	in gene, in gene	0	0	1	4.5	10	20	2	4_A375_EGR1..1	20	Gene GABRD	MGC45284, EIG10, GABRD, EJM7, GEFSP5	gamma-aminobutyric acid (GABA) A receptor, delta	NM_000815, hCT2336629.0	208457_at, 230255_at	NP_000806.2, EAW56137.1
GeneID:5590	PRKCZ	1	1,981,909	2,116,834	134,925	+	9	1_A375_pNL7_minus_lncRNA_AR..1..11, 1_A375_pNL7_minus_lncRNA_AR..1..12, 2_A375_pNL97_plus_lncRNA_AR..1..18, 4_A375_EGR1..1..78, 4_A375_EGR1..1..79, 4_A375_EGR1..1..80, 4_A375_EGR1..1..81, 4_A375_EGR1..1..82, 4_A375_EGR1..1..83	84619, 139371, 85611, -597, 25291, 83195, 118763, 128571, 129611	in gene, downstream, in gene, upstream, in gene, in gene, in gene, in gene, in gene	1	1	1	9.5	10.5	16.83	8	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PRKCZ	PRKCZ, PKC2, PKC-ZETA	protein kinase C, zeta	NM_002744, NM_001033581, NM_001033582, hCT15713.3, hCT2345155.0	1569748_at, 202178_at, 220846_s_at	NP_002735.3, NP_001028753.1, NP_001028754.1, EAW56130.1, EAW56131.1
GeneID:100506504	LOC100506504	1	2,113,246	2,115,492	2,246	-	3	1_A375_pNL7_minus_lncRNA_AR..1..12, 4_A375_EGR1..1..82, 4_A375_EGR1..1..83	-5786, 5012, 3972	upstream, downstream, downstream	1	0	1	9	8	16.67	3	4_A375_EGR1..1	23	Gene LOC100506504		hypothetical protein LOC100506504	XM_003119801, XM_003118494, XM_003120338		XP_003119849.1, XP_003118542.1, XP_003120386.1
GeneID:199990	C1orf86	1	2,115,899	2,139,172	23,273	-	8	1_A375_pNL7_minus_lncRNA_AR..1..12, 4_A375_EGR1..1..82, 4_A375_EGR1..1..83, 4_A375_EGR1..1..84, 4_A375_EGR1..1..85, 4_A375_EGR1..1..86, 4_A375_EGR1..1..87, 4_A375_EGR1..1..88	17892, 28692, 27852, 4724, 3844, 1796, -252, -7004	in gene, downstream, downstream, in gene, in gene, in gene, upstream, upstream	1	0	1	9.38	9.75	17.63	8	4_A375_EGR1..1	23	Gene C1orf86	FP7162, C1orf86, FLJ31031, MGC120153	chromosome 1 open reading frame 86	NM_182533, NM_001146310, hCT1809286.4, hCT2336603.2, hCT2343773.1, hCT2344478.1, hCT2350220.0	1556309_s_at, 1556544_at, 1562875_at, 229113_s_at, 230649_at, 236498_s_at, 236499_at, 236584_at	NP_872339.2, NP_001139782.1, EAW56125.1, EAW56127.1, EAW56128.1, EAW56129.1, EAW56126.1
GeneID:100128003	LOC100128003	1	2,120,482	2,125,024	4,542	-	4	1_A375_pNL7_minus_lncRNA_AR..1..12, 4_A375_EGR1..1..82, 4_A375_EGR1..1..83, 4_A375_EGR1..1..84	3744, 14544, 13504, -9424	in gene, downstream, downstream, upstream	1	0	1	9.5	7.5	18.25	4	4_A375_EGR1..1	23	Gene LOC100128003	FLJ43456, FLJ30256, FLJ46660	hypothetical LOC100128003	NR_024445		
GeneID:6497	SKI	1	2,160,134	2,241,652	81,518	+	7	1_A375_pNL7_minus_lncRNA_AR..1..13, 4_A375_EGR1..1..89, 4_A375_EGR1..1..90, 4_A375_EGR1..1..91, 4_A375_EGR1..1..92, 4_A375_EGR1..1..93, 4_A375_EGR1..1..94	2522, -1862, 39290, 42378, 64122, 84314, 89114	in gene, upstream, in gene, in gene, in gene, downstream, downstream	1	0	1	8.71	8	17	7	4_A375_EGR1..1	24	Gene SKI	SKI, SKV	v-ski sarcoma viral oncogene homolog (avian)	NM_003036, hCT14250.3, hCT1965410.1	204270_at	NP_003027.1, EAW56117.1, EAW56118.1
GeneID:79906	MORN1	1	2,252,696	2,322,993	70,297	-	13	4_A375_EGR1..1..93, 4_A375_EGR1..1..94, 4_A375_EGR1..1..95, 4_A375_EGR1..1..96, 4_A375_EGR1..1..97, 4_A375_EGR1..1..98, 4_A375_EGR1..1..99, 4_A375_EGR1..1..100, 4_A375_EGR1..1..101, 4_A375_EGR1..1..102, 4_A375_EGR1..1..103, 4_A375_EGR1..1..104, 4_A375_EGR1..1..105	78545, 73745, 70609, 67761, 63521, 62417, 58257, 55217, 50945, 47281, 46001, 9510, 8817	downstream, downstream, downstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	7.39	8.54	17.31	13	4_A375_EGR1..1	23	Gene MORN1	FLJ13941, MORN1	MORN repeat containing 1	NM_024848, hCT15721.3	1554268_at, 1563666_at, 219852_s_at, 222933_at	NP_079124.1, EAW56115.1
GeneID:11079	RER1	1	2,323,214	2,336,883	13,669	+	3	2_A375_pNL97_plus_lncRNA_AR..1..19, 4_A375_EGR1..1..104, 4_A375_EGR1..1..105	21250, -9731, -9038	downstream, upstream, upstream	0	1	1	10.67	13.67	16	3	4_A375_EGR1..1	16	Gene RER1	RER1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	NM_007033, hCT15722.4, hCT2336643.1, hCT2336644.1, hCT2336645.1, hCT2336646.1, hCT2345156.0	202296_s_at, 202297_s_at, 213296_at	NP_008964.3, EAW56109.1, EAW56110.1, EAW56112.1, EAW56113.1, EAW56114.1, EAW56111.1
GeneID:5192	PEX10	1	2,336,241	2,344,010	7,769	-	3	2_A375_pNL97_plus_lncRNA_AR..1..19, 4_A375_EGR1..1..106, 4_A375_EGR1..1..107	-454, -3838, -6358	upstream, upstream, upstream	0	1	1	9	11.33	17.33	3	4_A375_EGR1..1	20	Gene PEX10	MGC1998, NALD, RNF69, PEX10	peroxisomal biogenesis factor 10	NM_002617, NM_153818, hCT1809271.3, hCT1981950.1, hCT1981951.1, hCT2353009.0	206351_s_at, 206352_s_at	NP_002608.1, NP_722540.1, EAW56105.1, EAW56106.1, EAW56107.1, EAW56108.1
GeneID:9651	PLCH2	1	2,407,754	2,436,964	29,210	+	13	4_A375_EGR1..1..116, 4_A375_EGR1..1..117, 4_A375_EGR1..1..118, 4_A375_EGR1..1..119, 4_A375_EGR1..1..120, 4_A375_EGR1..1..121, 4_A375_EGR1..1..122, 4_A375_EGR1..1..123, 4_A375_EGR1..1..124, 4_A375_EGR1..1..125, 4_A375_EGR1..1..126, 4_A375_EGR1..1..127, 4_A375_EGR1..1..128	-10090, -9450, -3850, -2154, -282, 2134, 3590, 10662, 14646, 26654, 28262, 33782, 34756	upstream, upstream, upstream, upstream, upstream, in gene, in gene, in gene, in gene, in gene, in gene, downstream, downstream	0	0	1	6.46	7.46	16.08	13	4_A375_EGR1..1	23	Gene PLCH2	PLCL4, PLCH2, PLC-eta2, PLCeta2	phospholipase C, eta 2	NM_014638, hCT2336652.2, hCT2336655.1, hCT2336656.1, hCT2349659.0	206080_at	NP_055453.2, EAW56104.1, EAW56101.1, EAW56102.1, EAW56103.1
GeneID:55229	PANK4	1	2,439,975	2,458,035	18,060	-	9	1_A375_pNL7_minus_lncRNA_AR..1..14, 2_A375_pNL97_plus_lncRNA_AR..1..20, 4_A375_EGR1..1..125, 4_A375_EGR1..1..126, 4_A375_EGR1..1..127, 4_A375_EGR1..1..128, 4_A375_EGR1..1..129, 4_A375_EGR1..1..130, 4_A375_EGR1..1..131	419, 19, 23427, 22019, 16499, 15523, 7875, 691, -6477	in gene, in gene, downstream, downstream, in gene, in gene, in gene, in gene, upstream	1	1	1	10.71	10.29	17.43	7	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene PANK4	FLJ10782, PANK4, DKFZp547M242	pantothenate kinase 4	NM_018216, hCT15719.3, hCT2336585.0, hCT2336586.0	218771_at	NP_060686.1, EAW56097.1, EAW56098.1, EAW56099.1
GeneID:388585	HES5	1	2,460,184	2,461,684	1,500	-	5	1_A375_pNL7_minus_lncRNA_AR..1..14, 2_A375_pNL97_plus_lncRNA_AR..1..20, 4_A375_EGR1..1..129, 4_A375_EGR1..1..130, 4_A375_EGR1..1..131	4068, 3668, 11524, 4340, -2628	downstream, downstream, downstream, downstream, upstream	1	1	1	16.67	17.33	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene HES5	HES5, bHLHb38	hairy and enhancer of split 5 (Drosophila)	NM_001010926, hCT1965454.1	239230_at	NP_001010926.1, EAW56096.1
GeneID:115110	LOC115110	1	2,481,359	2,484,284	2,925	-	4	4_A375_EGR1..1..132, 4_A375_EGR1..1..133, 4_A375_EGR1..1..134, 4_A375_EGR1..1..135	10801, 7260, 6268, -4836	downstream, downstream, downstream, upstream	0	0	1	6.5	8.75	17.25	4	4_A375_EGR1..1	19	Gene LOC115110	DKFZp762D186, FLJ46690	hypothetical LOC115110	NR_026927	232190_x_at, 233562_at, 233960_s_at	
GeneID:100133445	LOC100133445	1	2,487,566	2,488,448	882	-	2	4_A375_EGR1..1..134, 4_A375_EGR1..1..135	10432, -872	downstream, upstream	0	0	1	6.5	9	18.5	2	4_A375_EGR1..1	19	Gene LOC100133445	FLJ46690	hypothetical LOC100133445	XR_112079, XR_108288, XR_113327		
GeneID:8764	TNFRSF14	1	2,487,805	2,495,268	7,463	+	3	4_A375_EGR1..1..134, 4_A375_EGR1..1..135, 4_A375_EGR1..1..136	-9789, 1315, 12899	upstream, in gene, downstream	0	0	1	5.33	7	16.67	3	4_A375_EGR1..1	19	Gene TNFRSF14	TNFRSF14, HVEA, LIGHTR, ATAR, HVEM, TR2	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	NM_003820, hCT15715.3, hCT1957716.1, hCT1957717.1, hCT1965450.1, hCT1965451.1, hCT1965452.1	209354_at	NP_003811.2, EAW56092.1, EAW56090.1, EAW56091.1, EAW56093.1, EAW56094.1, EAW56089.1
GeneID:100506589	LOC100506589	1	2,497,974	2,515,972	17,998	+	2	4_A375_EGR1..1..135, 4_A375_EGR1..1..136	-6654, 2730	upstream, in gene	0	0	1	3.5	4.5	15.5	2	4_A375_EGR1..1	16	Gene LOC100506589		hypothetical LOC100506589	XR_112080, XR_108289, XR_113328		
GeneID:127281	C1orf93	1	2,518,249	2,522,902	4,653	+	2	4_A375_EGR1..1..137, 4_A375_EGR1..1..138	8999, 10263	downstream, downstream	0	0	1	6	5	17	2	4_A375_EGR1..1	17	Gene C1orf93	C1orf93, DKFZp547M123, MGC26818, RP3-395M20.10	chromosome 1 open reading frame 93	NM_152371, hCT15723.5, hCT2349868.0, hCT2349869.0, hCT2353018.0, hCT2353019.0, hCT2353020.0	231835_at	NP_689584.1, EAW56087.1, EAW56083.1, EAW56084.1, EAW56085.1, EAW56088.1, EAW56086.1
GeneID:79258	MMEL1	1	2,522,081	2,564,481	42,400	-	3	1_A375_pNL7_minus_lncRNA_AR..1..15, 4_A375_EGR1..1..137, 4_A375_EGR1..1..138	-9759, 37233, 35969	upstream, in gene, in gene	1	0	1	10	7.67	16.67	3	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene MMEL1	NL2, MGC119456, NEP2, SEP, NEPII, MMEL2, MGC119455, MMEL1, MGC119454, NL1	membrane metallo-endopeptidase-like 1	NM_033467, hCT15720.4, hCT2336578.0, hCT2336579.0	1552930_at	NP_258428.2, EAW56080.1, EAW56081.1, EAW56082.1
GeneID:100287898	LOC100287898	1	2,572,807	2,706,230	133,423	-	3	1_A375_pNL7_minus_lncRNA_AR..1..15, 4_A375_EGR1..1..139, 4_A375_EGR1..1..140	131990, 130262, 11606	in gene, in gene, in gene	1	0	1	8.67	7	16.67	3	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100287898	TTC34		XM_002342015, XM_003119811, XM_003120448		XP_002342056.1, XP_003119859.1, XP_003120496.1
GeneID:140625	ACTRT2	1	2,938,046	2,939,467	1,421	+	2	4_A375_EGR1..1..155, 4_A375_EGR1..1..156	-8542, 6602	upstream, downstream	0	0	1	4.5	8	15.5	2	4_A375_EGR1..1	16	Gene ACTRT2	HARPM2, ARPT2, Arp-T2, ARPM2, FLJ25424, ACTRT2	actin-related protein T2	NM_080431	237360_at	NP_536356.3
GeneID:440556	FLJ42875	1	2,976,181	2,984,289	8,108	-	1	4_A375_EGR1..1..157	-202	upstream	0	0	1	5	3	14	1	4_A375_EGR1..1	14	Gene FLJ42875	DKFZp761G0122, MGC35434	hypothetical LOC440556	NR_015440, NR_024371	231275_at, 236360_at, 237108_x_at, 242269_at	
GeneID:63976	PRDM16	1	2,985,742	3,355,185	369,443	+	14	4_A375_EGR1..1..157, 4_A375_EGR1..1..158, 4_A375_EGR1..1..159, 4_A375_EGR1..1..160, 4_A375_EGR1..1..161, 4_A375_EGR1..1..162, 4_A375_EGR1..1..163, 4_A375_EGR1..1..164, 4_A375_EGR1..1..165, 4_A375_EGR1..1..166, 4_A375_EGR1..1..167, 4_A375_EGR1..1..168, 4_A375_EGR1..1..169, 4_A375_EGR1..1..170	-1251, 27458, 36210, 46346, 172594, 178274, 194162, 210226, 215906, 243058, 303954, 322842, 343538, 359410	upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	4.86	5.79	16.79	14	4_A375_EGR1..1	24	Gene PRDM16	MEL1, MGC166915, PRDM16, KIAA1675, PFM13	PR domain containing 16	NM_199454, NM_022114, hCT2291466.0, hCT2291468.0, hCT1641960.3	220928_s_at, 232424_at	NP_955533.2, NP_071397.3, EAW71449.1, EAW71450.1, EAW71451.1
GeneID:27237	ARHGEF16	1	3,371,147	3,397,677	26,530	+	4	4_A375_EGR1..1..171, 4_A375_EGR1..1..172, 4_A375_EGR1..1..173, 4_A375_EGR1..1..174	8653, 13792, 17557, 18837	in gene, in gene, in gene, in gene	0	0	1	7.25	8	19	4	4_A375_EGR1..1	22	Gene ARHGEF16	GEF16, NBR, ARHGEF16	Rho guanine exchange factor (GEF) 16	NM_014448, hCT1640305.2, hCT1950384.1	206009_s_at	NP_055263.2, EAW71452.1, EAW71453.1
GeneID:1953	MEGF6	1	3,404,506	3,528,059	123,553	-	14	4_A375_EGR1..1..175, 4_A375_EGR1..1..176, 4_A375_EGR1..1..177, 4_A375_EGR1..1..178, 4_A375_EGR1..1..179, 4_A375_EGR1..1..180, 4_A375_EGR1..1..181, 4_A375_EGR1..1..182, 4_A375_EGR1..1..183, 4_A375_EGR1..1..184, 4_A375_EGR1..1..185, 4_A375_EGR1..1..186, 4_A375_EGR1..1..187, 4_A375_EGR1..1..188	114379, 108827, 102523, 101467, 100763, 100027, 92187, 90299, 62907, 57995, 53979, 33659, 27463, 13051	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	7.14	8.36	16.64	14	4_A375_EGR1..1	22	Gene MEGF6	MEGF6, KIAA0815, EGFL3	multiple EGF-like-domains 6	NM_001409	213942_at, 226869_at	NP_001400.3
GeneID:693135	MIR551A	1	3,477,259	3,477,354	95	-	2	4_A375_EGR1..1..184, 4_A375_EGR1..1..185	7290, 3274	downstream, downstream	0	0	1	6	5.5	17	2	4_A375_EGR1..1	19	Gene MIR551A	MIRN551A, MIR551A	microRNA 551a	NR_030277		
GeneID:49856	WDR8	1	3,547,331	3,566,671	19,340	-	1	4_A375_EGR1..1..189	-1630	upstream	0	0	1	4	8	17	1	4_A375_EGR1..1	17	Gene WDR8	MGC99569, FLJ20430, WRAP73, WDR8	WD repeat containing, antisense to TP73	NM_017818, hCT2291841.0, hCT11155.3, hCT1962894.1	219322_s_at, 236381_s_at, 236382_at	NP_060288.3, EAW71461.1, EAW71459.1, EAW71460.1
GeneID:7161	TP73	1	3,569,129	3,650,467	81,338	+	7	4_A375_EGR1..1..189, 4_A375_EGR1..1..190, 4_A375_EGR1..1..191, 4_A375_EGR1..1..192, 4_A375_EGR1..1..193, 4_A375_EGR1..1..194, 4_A375_EGR1..1..195	-828, 22199, 33719, 37847, 65623, 74967, 76247	upstream, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	5	8.14	17	7	4_A375_EGR1..1	21	Gene TP73	P73, TP73	tumor protein p73	NM_005427, NM_001126240, NM_001126241, NM_001126242, hCT2291498.0, hCT2291500.0, hCT2291505.0, hCT10153.3, hCT1950406.1, hCT1950407.1	1554379_a_at, 220804_s_at, 232546_at	NP_005418.1, NP_001119712.1, NP_001119713.1, NP_001119714.1, EAW71464.1, EAW71467.1, EAW71463.1, EAW71465.1, EAW71466.1, EAW71468.1
GeneID:100506635	LOC100506635	1	3,591,416	3,591,970	554	-	1	4_A375_EGR1..1..190	642	downstream	0	0	1	4	5	21	1	4_A375_EGR1..1	21	Gene LOC100506635		hypothetical protein LOC100506635	XM_003118495, XM_003120577		XP_003118543.1, XP_003120625.1
GeneID:57212	KIAA0495	1	3,652,548	3,663,937	11,389	-	2	4_A375_EGR1..1..194, 4_A375_EGR1..1..195	19841, 16561	downstream, downstream	0	0	1	5	7	17.5	2	4_A375_EGR1..1	18	Gene KIAA0495	PDAM, KIAA0495, MGC138189	KIAA0495	NR_033708, NR_033709, NR_033710, NR_033711, NR_033712, hCT2291836.0, hCT2291837.0, hCT2291838.0, hCT2354937.0	1569502_s_at, 213339_at, 213340_s_at	EAW71471.1, EAW71474.1, EAW71472.1, EAW71473.1
GeneID:57470	LRRC47	1	3,696,784	3,713,068	16,284	-	2	1_A375_pNL7_minus_lncRNA_AR..1..16, 2_A375_pNL97_plus_lncRNA_AR..1..21	12, 12	in gene, in gene	1	1	0	19	20	5	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LRRC47	LRRC47, KIAA1185	leucine rich repeat containing 47	NM_020710, hCT2291873.0, hCT11152.3	212904_at	NP_065761.1, EAW71479.1, EAW71478.1
GeneID:9731	KIAA0562	1	3,728,645	3,773,797	45,152	-	2	1_A375_pNL7_minus_lncRNA_AR..1..17, 4_A375_EGR1..1..196	101, 29	in gene, in gene	1	0	1	16	13	15	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene KIAA0562	KIAA0562, GlyBP	KIAA0562	NM_014704, hCT1967675.1, hCT2291868.0, hCT2291869.0, hCT11151.4	204074_s_at, 204075_s_at, 243696_at	NP_055519.1, EAW71481.1, EAW71482.1, EAW71483.1, EAW71484.1
GeneID:1677	DFFB	1	3,773,845	3,801,993	28,148	+	2	1_A375_pNL7_minus_lncRNA_AR..1..17, 4_A375_EGR1..1..196	-149, -77	upstream, upstream	1	0	1	16	13	15	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene DFFB	DFF-40, DFF40, DFF2, DFFB, CAD, CPAN	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	NM_004402, hCT22751.3, hCT2291526.0, hCT2291529.0, hCT2291531.0, hCT2354959.0, hCT1950426.1, hCT1950427.1	206752_s_at	NP_004393.1, EAW71486.1, EAW71487.1, EAW71488.1, EAW71489.1, EAW71490.1, EAW71485.1, EAW71491.1
GeneID:339448	C1orf174	1	3,805,697	3,816,857	11,160	-	2	2_A375_pNL97_plus_lncRNA_AR..1..22, 4_A375_EGR1..1..197	-807, -3431	upstream, upstream	0	1	1	7.5	13	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C1orf174	C1orf174, RP13-531C17.2	chromosome 1 open reading frame 174	NM_207356, hCT2354933.0, hCT1782202.2	222000_at, 238010_at	NP_997239.2, EAW71493.1, EAW71492.1
GeneID:100133612	LOC100133612	1	3,816,968	3,832,011	15,043	+	3	2_A375_pNL97_plus_lncRNA_AR..1..22, 4_A375_EGR1..1..197, 4_A375_EGR1..1..198	696, 3320, 14006	in gene, in gene, in gene	0	1	1	6.33	10.67	14.67	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100133612	FLJ26663	similar to hCG1815312	NR_024455		
GeneID:55966	AJAP1	1	4,715,105	4,843,851	128,746	+	2	4_A375_EGR1..1..200, 4_A375_EGR1..1..201	4799, 72170	in gene, in gene	0	0	1	6	5	15	2	4_A375_EGR1..1	17	Gene AJAP1	SHREW1, SHREW-1, AJAP1, MOT8, RP3-426F10.1	adherens junctions associated protein 1	NM_001042478, NM_018836, hCT5750.3	206460_at, 215789_s_at, 215790_at	NP_001035943.1, NP_061324.1, EAW71504.1
GeneID:261734	NPHP4	1	5,922,870	6,052,531	129,661	-	2	1_A375_pNL7_minus_lncRNA_AR..1..18, 2_A375_pNL97_plus_lncRNA_AR..1..26	-45, 355	upstream, in gene	1	1	0	23	36	7	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene NPHP4	KIAA0673, SLSN4, POC10, FLJ46306, NPHP4	nephronophthisis 4	NM_015102, hCT2296807.0, hCT2354934.0, hCT2354935.0, hCT2354936.0, hCT13736.2	213471_at, 216344_at	NP_055917.1, EAW71511.1, EAW71507.1, EAW71508.1, EAW71509.1, EAW71510.1



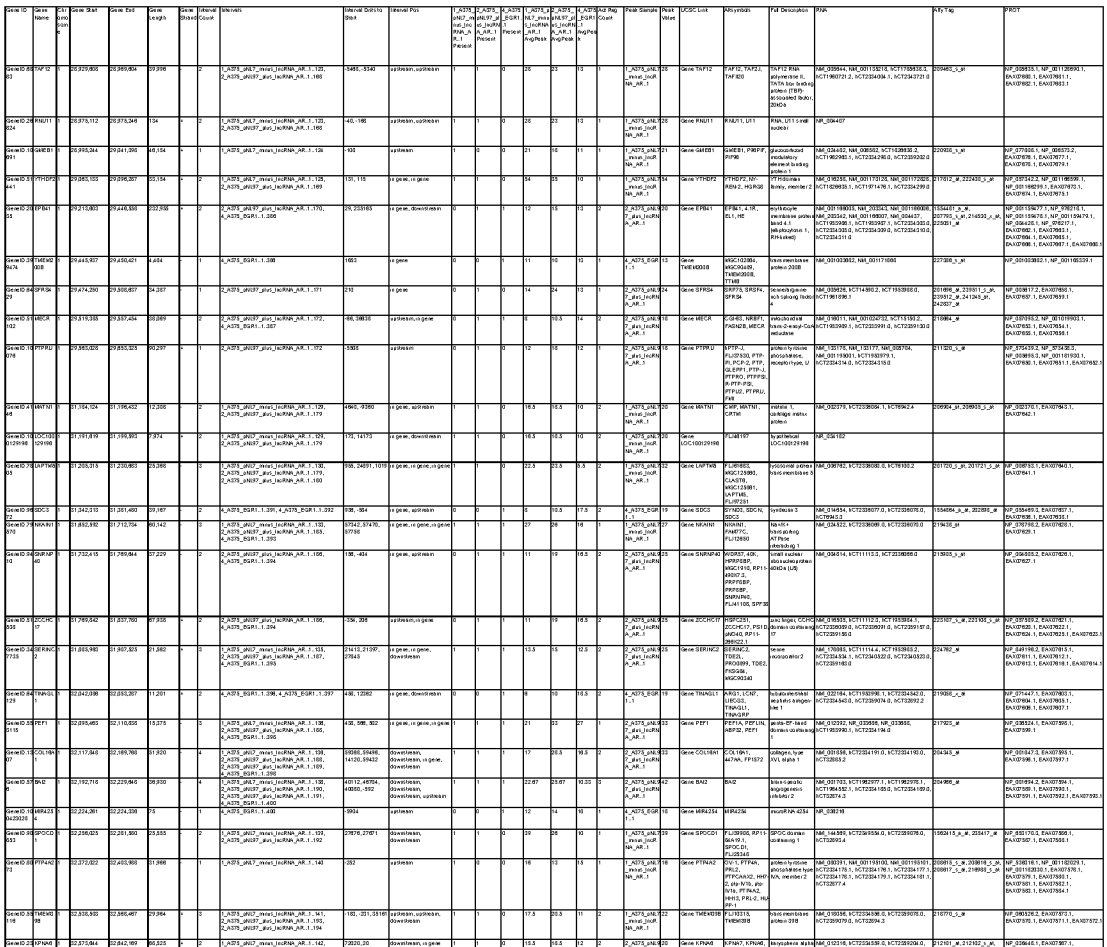


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:27129	HSPB7	1	16,340,523	16,345,285	4,762	-	1	4_A375_EGR1..1..281	-6363	upstream	0	0	1	4	6	17	1	4_A375_EGR1..1	17	Gene HSPB7	cvHSP, DKFZp779D0968, HSPB7, FLJ32733	heat shock 27kDa protein family, member 7 (cardiovascular)	NM_014424, hCT14613.3, hCT2296331.1, hCT2352488.0	218934_s_at, 235682_s_at	NP_055239.1, EAW51761.1, EAW51760.1, EAW51762.1
GeneID:1187	CLCNKA	1	16,348,486	16,360,545	12,059	+	2	4_A375_EGR1..1..281, 4_A375_EGR1..1..282	3162, 7546	in gene, in gene	0	0	1	7	7.5	16	2	4_A375_EGR1..1	17	Gene CLCNKA	hClC-Ka, CLCK1, MGC61490, ClC-K1, CLCNKA	chloride channel Ka	NM_004070, NM_001042704, hCT1808938.2	207047_s_at	NP_004061.3, NP_001036169.1, EAW51763.1
GeneID:348487	FAM131C	1	16,384,264	16,400,127	15,863	-	2	1_A375_pNL7_minus_lncRNA_AR..1..61, 2_A375_pNL97_plus_lncRNA_AR..1..84	-2433, -3233	upstream, upstream	1	1	0	19	22	10	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene FAM131C	C1orf117, RP11-5P18.9, FAM131C, FLJ36766	family with sequence similarity 131, member C	NM_182623, hCT15638.3, hCT2296328.0	235455_at	NP_872429.2, EAW51768.1, EAW51767.1
GeneID:1969	EPHA2	1	16,450,832	16,482,582	31,750	-	9	1_A375_pNL7_minus_lncRNA_AR..1..62, 1_A375_pNL7_minus_lncRNA_AR..1..63, 4_A375_EGR1..1..283, 4_A375_EGR1..1..284, 4_A375_EGR1..1..285, 4_A375_EGR1..1..286, 4_A375_EGR1..1..287, 4_A375_EGR1..1..288, 4_A375_EGR1..1..289	33078, 54, 22870, 17974, 15702, 11734, 982, 502, -1130	downstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	1	0	1	11.75	10.75	16.5	8	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene EPHA2	ARCC2, EPHA2, ECK	EPH receptor A2	NM_004431, hCT15631.2, hCT2296325.0	203499_at	NP_004422.2, EAW51769.1, EAW51770.1
GeneID:100506484	LOC100506484	1	16,481,730	16,483,824	2,094	+	4	1_A375_pNL7_minus_lncRNA_AR..1..63, 4_A375_EGR1..1..287, 4_A375_EGR1..1..288, 4_A375_EGR1..1..289	798, -130, 350, 1982	in gene, upstream, in gene, in gene	1	0	1	11	12	17.67	3	4_A375_EGR1..1	20	Gene LOC100506484		hypothetical LOC100506484	XR_108384		
GeneID:128272	ARHGEF19	1	16,524,599	16,539,104	14,505	-	2	4_A375_EGR1..1..290, 4_A375_EGR1..1..291	3616, 2240	in gene, in gene	0	0	1	7.5	6.5	17	2	4_A375_EGR1..1	19	Gene ARHGEF19	ARHGEF19, FLJ33962, WGEF, RP4-733M16.1	Rho guanine nucleotide exchange factor (GEF) 19	NM_153213, hCT15634.4	226857_at	NP_694945.2, EAW51771.1
GeneID:79363	C1orf89	1	16,558,182	16,563,659	5,477	-	1	4_A375_EGR1..1..292	5643	downstream	0	0	1	5	7	15	1	4_A375_EGR1..1	15	Gene C1orf89	MGC10731, C1orf89, RSG1, RP4-733M16.4	REM2 and RAB-like small GTPase 1	NM_030907, hCT15636.3	220963_s_at	NP_112169.2, EAW51773.1
GeneID:54455	FBXO42	1	16,576,559	16,678,948	102,389	-	3	1_A375_pNL7_minus_lncRNA_AR..1..64, 2_A375_pNL97_plus_lncRNA_AR..1..86, 4_A375_EGR1..1..293	-204, 228, 100	upstream, in gene, in gene	1	1	1	24	15	17	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene FBXO42	JFK, FBXO42, Fbx42, KIAA1332	F-box protein 42	NM_018994, hCT15635.3, hCT2296319.0	1559566_at, 221812_at, 221813_at, 47773_at	NP_061867.1, EAW51774.1, EAW51775.1
GeneID:26099	C1orf144	1	16,693,583	16,724,640	31,057	+	2	1_A375_pNL7_minus_lncRNA_AR..1..65, 2_A375_pNL97_plus_lncRNA_AR..1..87	337, 305	in gene, in gene	1	1	0	36	37	13	1	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene C1orf144	C1orf144, DKFZp566C0424, MGC70432	chromosome 1 open reading frame 144	NM_015609, NM_001114600, hCT2295884.1	212003_at, 212004_at	NP_056424.1, NP_001108072.1, EAW51777.1
GeneID:374955	SPATA21	1	16,725,138	16,763,919	38,781	-	2	1_A375_pNL7_minus_lncRNA_AR..1..66, 2_A375_pNL97_plus_lncRNA_AR..1..88	-3217, -3185	upstream, upstream	1	1	0	36	39	16	1	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene SPATA21	spergen-2, spergen2, MGC27074, SPATA21	spermatogenesis associated 21	NM_198546, hCT1642372.2	1570241_at, 1570242_x_at	NP_940948.1, EAW51779.1
GeneID:55707	NECAP2	1	16,767,167	16,786,585	19,418	+	2	1_A375_pNL7_minus_lncRNA_AR..1..66, 2_A375_pNL97_plus_lncRNA_AR..1..88	-31, -63	upstream, upstream	1	1	0	36	39	16	1	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene NECAP2	NECAP2, FLJ10420	NECAP endocytosis associated 2	NM_001145277, NM_001145278, NM_018090, hCT15640.4, hCT1961738.1, hCT1961739.1, hCT1961740.1, hCT1961742.1	220731_s_at	NP_001138749.1, NP_001138750.1, NP_060560.1, EAW51780.1, EAW51783.1, EAW51784.1, EAW51781.1, EAW51782.1
GeneID:55672	NBPF1	1	16,890,412	16,939,982	49,570	-	2	2_A375_pNL97_plus_lncRNA_AR..1..89, 4_A375_EGR1..1..294	78, -146	in gene, upstream	0	1	1	53	59	43	1	2_A375_pNL97_plus_lncRNA_AR..1	59	Gene NBPF1	NBG, AB14, AB13, AB23, AD2, KIAA1693, FLJ20719, NBPF, NBPF1	neuroblastoma breakpoint family, member 1	NM_017940	230712_at	NP_060410.2
GeneID:100506687	LOC100506687	1	17,215,034	17,216,161	1,127	-	3	2_A375_pNL97_plus_lncRNA_AR..1..92, 4_A375_EGR1..1..304, 4_A375_EGR1..1..305	-6591, -6495, -6911	upstream, upstream, upstream	0	1	1	10	16.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100506687		hypothetical LOC100506687	XR_108385		
GeneID:26870	RNU1-2	1	17,222,475	17,222,638	163	+	6	1_A375_pNL7_minus_lncRNA_AR..1..69, 2_A375_pNL97_plus_lncRNA_AR..1..92, 2_A375_pNL97_plus_lncRNA_AR..1..93, 4_A375_EGR1..1..304, 4_A375_EGR1..1..305, 4_A375_EGR1..1..306	9077, 277, 9109, 181, 597, 9173	downstream, downstream, downstream, downstream, downstream, downstream	1	1	1	38	49.67	19	3	2_A375_pNL97_plus_lncRNA_AR..1	112	Gene RNU1-2	RNU1C2, U1C21, U1C1, RNU1C1, RNU1-2	RNA, U1 small nuclear 2	NR_004427		
GeneID:9696	CROCC	1	17,248,445	17,299,474	51,029	+	7	1_A375_pNL7_minus_lncRNA_AR..1..70, 2_A375_pNL97_plus_lncRNA_AR..1..94, 4_A375_EGR1..1..307, 4_A375_EGR1..1..308, 4_A375_EGR1..1..309, 4_A375_EGR1..1..310, 4_A375_EGR1..1..311	-8289, -7813, -8264, 3907, 16451, 24899, 26531	upstream, upstream, upstream, in gene, in gene, in gene, in gene	1	1	1	11.8	13.8	22	5	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene CROCC	CROCC, ROLT, KIAA0445	ciliary rootlet coiled-coil, rootletin	NM_014675, hCT2253457.0, hCT2253458.0, hCT2253459.0, hCT2253460.0	206274_s_at, 216419_at	NP_055490.3, EAW94814.1, EAW94815.1, EAW94816.1, EAW94817.1
GeneID:23400	ATP13A2	1	17,312,453	17,338,423	25,970	-	1	4_A375_EGR1..1..312	6563	in gene	0	0	1	10	6	17	1	4_A375_EGR1..1	17	Gene ATP13A2	ATP13A2, FLJ26510, KRPPD, PARK9, HSA9947	ATPase type 13A2	NM_022089, NM_001141973, NM_001141974, hCT16252.3, hCT1961480.1, hCT2255236.0, hCT2357813.0	218608_at	NP_071372.1, NP_001135445.1, NP_001135446.1, EAW94824.1, EAW94826.1, EAW94827.1, EAW94825.1
GeneID:11240	PADI2	1	17,393,256	17,445,948	52,692	-	1	4_A375_EGR1..1..313	273	in gene	0	0	1	7	7	17	1	4_A375_EGR1..1	17	Gene PADI2	PADI2, PDI2, PAD2, PAD-H19, KIAA0994	peptidyl arginine deiminase, type II	NM_007365, hCT16254.3, hCT2255233.0	1554384_at, 1554385_a_at, 209791_at	NP_031391.2, EAW94831.1, EAW94830.1
GeneID:400743	LOC400743	1	17,520,821	17,521,393	572	+	1	4_A375_EGR1..1..315	-8955	upstream	0	0	1	5	10	14	1	4_A375_EGR1..1	14	Gene LOC400743	FLJ45933	FLJ45933 protein	XR_108386		
GeneID:51702	PADI3	1	17,575,593	17,610,728	35,135	+	1	2_A375_pNL97_plus_lncRNA_AR..1..95	44919	downstream	0	1	0	12	16	7	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene PADI3	MGC126308, PAD3, PADI3, PDI3, MGC126307	peptidyl arginine deiminase, type III	NM_016233, hCT16248.2	220779_at	NP_057317.2, EAW94834.1
GeneID:23569	PADI4	1	17,634,690	17,690,495	55,805	+	1	4_A375_EGR1..1..316	33982	in gene	0	0	1	10	6	16	1	4_A375_EGR1..1	16	Gene PADI4	PDI5, PADI4, PDI4, PADI5, PAD4, PAD	peptidyl arginine deiminase, type IV	NM_012387, hCT16249.2, hCT2253466.0	211412_at, 211413_s_at, 220001_at	NP_036519.2, EAW94835.1, EAW94836.1
GeneID:55920	RCC2	1	17,733,251	17,766,220	32,969	-	2	2_A375_pNL97_plus_lncRNA_AR..1..96, 4_A375_EGR1..1..317	124, 22412	in gene, in gene	0	1	1	9	13.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene RCC2	DKFZp762N0610, KIAA1470, RCC2, TD-60	regulator of chromosome condensation 2	NM_018715, NM_001136204, hCT16253.3, hCT2255232.1	224578_at	NP_061185.1, NP_001129676.1, EAW94838.1, EAW94839.1
GeneID:55160	ARHGEF10L	1	17,866,330	18,024,370	158,040	+	3	1_A375_pNL7_minus_lncRNA_AR..1..71, 4_A375_EGR1..1..319, 4_A375_EGR1..1..320	5798, 98774, 137206	in gene, in gene, in gene	1	0	1	10	6.67	12	3	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ARHGEF10L	GrinchGEF, ARHGEF10L, FLJ10521, RP11-473A10.1, KIAA1626	Rho guanine nucleotide exchange factor (GEF) 10-like	NM_018125, NM_001011722, hCT1955046.1, hCT2253470.0, hCT2253471.0, hCT2253474.0, hCT2253475.0	1570511_at, 221656_s_at	NP_060595.3, NP_001011722.2, EAW94840.1, EAW94841.1, EAW94842.1, EAW94843.1, EAW94844.1
GeneID:81569	ACTL8	1	18,149,477	18,153,558	4,081	+	2	1_A375_pNL7_minus_lncRNA_AR..1..72, 2_A375_pNL97_plus_lncRNA_AR..1..97	8611, 8611	downstream, downstream	1	1	0	28	32	2	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene ACTL8	ACTL8, CT57	actin-like 8	NM_030812, hCT16251.3	214957_at	NP_110439.2, EAW94846.1
GeneID:84966	IGSF21	1	18,434,240	18,704,979	270,739	+	1	4_A375_EGR1..1..321	3275	in gene	0	0	1	5	6	15	1	4_A375_EGR1..1	15	Gene IGSF21	IGSF21, MGC15730, FLJ41177	immunoglobin superfamily, member 21	NM_032880, hCT16235.3	227154_at	NP_116269.3, EAW94848.1
GeneID:5081	PAX7	1	18,957,500	19,075,360	117,860	+	1	4_A375_EGR1..1..322	74132	in gene	0	0	1	5	6	15	1	4_A375_EGR1..1	15	Gene PAX7	FLJ37460, PAX7B, HUP1, PAX7, RMS2	paired box 7	NM_001135254, NM_013945, NM_002584, hCT1686498.2, hCT1955042.0, hCT2252879.0, hCT2252881.0	208080_at	NP_001128726.1, NP_039236.1, NP_002575.1, EAW94854.1, EAW94855.1, EAW94856.1, EAW94853.1
GeneID:8659	ALDH4A1	1	19,197,924	19,229,293	31,369	-	1	1_A375_pNL7_minus_lncRNA_AR..1..74	77	in gene	1	0	0	21	14	8	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ALDH4A1	ALDH4, P5CDh, DKFZp779M035, ALDH4A1, P5CD	aldehyde dehydrogenase 4 family, member A1	NM_003748, NM_170726, NM_001161504, hCT16232.3, hCT1955043.1, hCT2252965.0	203722_at, 211552_s_at	NP_003739.2, NP_733844.1, NP_001154976.1, EAW94858.1, EAW94859.1, EAW94860.1
GeneID:100302278	MIR1290	1	19,223,565	19,223,642	77	-	1	1_A375_pNL7_minus_lncRNA_AR..1..74	-5574	upstream	1	0	0	21	14	8	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene MIR1290	MIRN1290, hsa-mir-1290, MIR1290	microRNA 1290	NR_031622		
GeneID:126917	IFFO2	1	19,230,774	19,282,826	52,052	-	5	1_A375_pNL7_minus_lncRNA_AR..1..74, 1_A375_pNL7_minus_lncRNA_AR..1..75, 2_A375_pNL97_plus_lncRNA_AR..1..99, 2_A375_pNL97_plus_lncRNA_AR..1..100, 2_A375_pNL97_plus_lncRNA_AR..1..101	53810, 23722, 29941, 23628, 1050	downstream, in gene, in gene, in gene, in gene	1	1	0	16	17.25	11.25	4	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene IFFO2	IFFO2	intermediate filament family orphan 2	NM_001136265	225615_at	NP_001129737.1
GeneID:23352	UBR4	1	19,401,000	19,536,746	135,746	-	2	1_A375_pNL7_minus_lncRNA_AR..1..76, 2_A375_pNL97_plus_lncRNA_AR..1..102	-102, -214	upstream, upstream	1	1	0	28	19	6	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene UBR4	KIAA0462, FLJ41863, KIAA1307, ZUBR1, p600, UBR4, RBAF600	ubiquitin protein ligase E3 component n-recognin 4	NM_020765, hCT2256791.0, hCT2256792.0, hCT2256793.0, hCT2256794.0, hCT2256795.0, hCT2357800.0	1563113_at, 211950_at, 215636_at, 231889_at, 232907_at	NP_065816.2, EAW94865.1, EAW94864.1, EAW94866.1, EAW94867.1, EAW94868.1, EAW94869.1
GeneID:23065	KIAA0090	1	19,544,584	19,578,046	33,462	-	5	1_A375_pNL7_minus_lncRNA_AR..1..76, 1_A375_pNL7_minus_lncRNA_AR..1..77, 2_A375_pNL97_plus_lncRNA_AR..1..102, 2_A375_pNL97_plus_lncRNA_AR..1..103, 4_A375_EGR1..1..323	41198, -162, 41086, -66, -34	downstream, upstream, downstream, upstream, upstream	1	1	1	32	27.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene KIAA0090	RP1-43E13.1, KIAA0090	KIAA0090	NM_015047, hCT1955051.1, hCT2357808.0, hCT32353.3	1558186_s_at, 212394_at, 212395_s_at, 212396_s_at, 215991_s_at	NP_055862.1, EAW94872.1, EAW94870.1, EAW94871.1
GeneID:51154	MRTO4	1	19,578,075	19,586,622	8,547	+	3	1_A375_pNL7_minus_lncRNA_AR..1..77, 2_A375_pNL97_plus_lncRNA_AR..1..103, 4_A375_EGR1..1..323	133, 37, 5	in gene, in gene, in gene	1	1	1	36	36	17	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene MRTO4	MRT4, dJ657E11.4, MRTO4, C1orf33	mRNA turnover 4 homolog (S. cerevisiae)	NM_016183, hCT1955050.1, hCT1986273.1, hCT32350.3	220668_s_at, 235763_at	NP_057267.2, EAW94873.1, EAW94874.1, EAW94875.1
GeneID:54898	PQLC2	1	19,638,740	19,655,794	17,054	+	1	4_A375_EGR1..1..324	15084	in gene	0	0	1	6	5	15	1	4_A375_EGR1..1	15	Gene PQLC2	FLJ26665, FLJ20320, FLJ26661, FLJ23906, PQLC2	PQ loop repeat containing 2	NM_001040125, NM_001040126, NM_017765, hCT1955052.1, hCT2357807.0, hCT2357808.0, hCT2357809.0, hCT2357810.0, hCT32354.3	1555781_at, 1555783_x_at, 220453_at	NP_001035214.1, NP_001035215.1, NP_060235.2, EAW94882.1, EAW94883.1, EAW94886.1, EAW94884.1, EAW94885.1, EAW94887.1
GeneID:3362	HTR6	1	19,991,780	20,006,055	14,275	+	2	1_A375_pNL7_minus_lncRNA_AR..1..78, 2_A375_pNL97_plus_lncRNA_AR..1..104	11324, 11372	in gene, in gene	1	1	0	39	50	10	1	2_A375_pNL97_plus_lncRNA_AR..1	50	Gene HTR6	HTR6, 5-HT6R, 5-HT6	5-hydroxytryptamine (serotonin) receptor 6	NM_000871, hCT29015.2	1552857_a_at, 206944_at	NP_000862.1, EAW94896.1
GeneID:255104	TMCO4	1	20,008,706	20,126,410	117,704	-	2	1_A375_pNL7_minus_lncRNA_AR..1..78, 2_A375_pNL97_plus_lncRNA_AR..1..104	123306, 123258	downstream, downstream	1	1	0	39	50	10	1	2_A375_pNL97_plus_lncRNA_AR..1	50	Gene TMCO4	TMCO4, DKFZp686C23231, RP5-1056L3.6	transmembrane and coiled-coil domains 4	NM_181719, hCT1955765.1, hCT2258747.0, hCT2258749.0, hCT2357818.0, hCT2357819.0, hCT2357820.0, hCT29016.3	1560292_a_at, 227007_at	NP_859070.3, EAW94899.1, EAW94897.1, EAW94898.1, EAW94900.1, EAW94901.1, EAW94902.1, EAW94903.1
GeneID:127731	VWA5B1	1	20,617,412	20,681,387	63,975	+	2	1_A375_pNL7_minus_lncRNA_AR..1..79, 2_A375_pNL97_plus_lncRNA_AR..1..105	68220, 67998	downstream, downstream	1	1	0	24	13	5	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene VWA5B1	FLJ32784, FLJ43845, VWA5B1	von Willebrand factor A domain containing 5B1	NM_001039500	1552853_at, 1552854_a_at	NP_001034589.2
GeneID:339505	LOC339505	1	20,666,294	20,755,287	88,993	-	5	1_A375_pNL7_minus_lncRNA_AR..1..79, 1_A375_pNL7_minus_lncRNA_AR..1..80, 2_A375_pNL97_plus_lncRNA_AR..1..105, 2_A375_pNL97_plus_lncRNA_AR..1..106, 2_A375_pNL97_plus_lncRNA_AR..1..107	69855, 57207, 69879, 57207, 17282	downstream, in gene, downstream, in gene, in gene	1	1	0	24	24.33	6.33	3	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene LOC339505		hypothetical LOC339505	NR_033867	1557373_at	
GeneID:55450	CAMK2N1	1	20,808,884	20,812,728	3,844	-	2	2_A375_pNL97_plus_lncRNA_AR..1..108, 4_A375_EGR1..1..325	-8456, -464	upstream, upstream	0	1	1	13.5	15	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CAMK2N1	RP11-401M16.1, CAMK2N1, MGC22256, PRO1489	calcium/calmodulin-dependent protein kinase II inhibitor 1	NM_018584, hCT1955770.2, hCT29420.4	218309_at, 228302_x_at, 229163_at	NP_061054.2, EAW94924.1, EAW94923.1
GeneID:79594	MUL1	1	20,825,941	20,834,674	8,733	-	4	1_A375_pNL7_minus_lncRNA_AR..1..81, 2_A375_pNL97_plus_lncRNA_AR..1..108, 2_A375_pNL97_plus_lncRNA_AR..1..109, 4_A375_EGR1..1..326	82, 13490, 146, 2	in gene, downstream, in gene, in gene	1	1	1	19	18.5	11	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene MUL1	MAPL, RNF218, MULAN, C1orf166, FLJ12875, MUL1, RP11-401M16.2, GIDE	mitochondrial E3 ubiquitin ligase 1	NM_024544, hCT2258548.0, hCT2258550.0, hCT2357795.0, hCT29419.2	218246_at	NP_078820.2, EAW94928.1, EAW94926.1, EAW94927.1, EAW94929.1
GeneID:978	CDA	1	20,915,444	20,945,401	29,957	+	1	4_A375_EGR1..1..327	5004	in gene	0	0	1	3	5	16	1	4_A375_EGR1..1	16	Gene CDA	CDD, CDA	cytidine deaminase	NM_001785, hCT1961488.1, hCT2357815.0, hCT28924.3	205627_at	NP_001776.1, EAW94931.1, EAW94932.1, EAW94933.1
GeneID:65018	PINK1	1	20,959,948	20,978,004	18,056	+	1	2_A375_pNL97_plus_lncRNA_AR..1..110	27748	downstream	0	1	0	14	15	13	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene PINK1	FLJ27236, PARK6, BRPK, PINK1	PTEN induced putative kinase 1	NM_032409, hCT2357824.0, hCT30119.3	209018_s_at, 209019_s_at	NP_115785.1, EAW94934.1, EAW94935.1
GeneID:1650	DDOST	1	20,978,260	20,988,037	9,777	-	1	2_A375_pNL97_plus_lncRNA_AR..1..110	341	in gene	0	1	0	14	15	13	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene DDOST	AGER1, DDOST, AGE-R1, MGC2191, OST48, OKSW-cl.45, WBP1, OST, OKSWcl45, KIAA0115	dolichyl-diphosphooligosaccharide--protein glycosyltransferase	NM_005216, hCT1955779.1, hCT1955780.1, hCT1955781.1, hCT2258547.0, hCT30117.3	208674_x_at, 208675_s_at	NP_005207.2, EAW94937.1, EAW94936.1, EAW94938.1, EAW94939.1, EAW94940.1
GeneID:57576	KIF17	1	20,990,507	21,044,317	53,810	-	1	2_A375_pNL97_plus_lncRNA_AR..1..110	56821	downstream	0	1	0	14	15	13	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene KIF17	KIF3X, KIAA1405, KIF17B, KIF17	kinesin family member 17	NM_020816, NM_001122819, hCT1955782.1, hCT2258539.0, hCT2258541.0, hCT2258542.0, hCT2357823.0, hCT30118.3	222144_at	NP_065867.2, NP_001116291.1, EAW94941.1, EAW94942.1, EAW94944.1, EAW94946.1, EAW94943.1, EAW94945.1
GeneID:50809	HP1BP3	1	21,069,171	21,113,181	44,010	-	1	1_A375_pNL7_minus_lncRNA_AR..1..82	221	in gene	1	0	0	21	17	9	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene HP1BP3	HP1BP3, MGC43701	heterochromatin protein 1, binding protein 3	NM_016287, hCT2258531.0, hCT2258534.0, hCT2258535.0, hCT30116.2	1554251_at, 220633_s_at, 224591_at, 224592_x_at, 229204_at	NP_057371.2, EAW94953.1, EAW94950.1, EAW94951.1, EAW94952.1
GeneID:8672	EIF4G3	1	21,132,972	21,503,340	370,368	-	1	4_A375_EGR1..1..328	141038	in gene	0	0	1	5	12	16	1	4_A375_EGR1..1	16	Gene EIF4G3	eIF4GII, eIF-4G 3, eIF4G 3, EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	NM_003760, hCT1955725.1, hCT2258522.0, hCT2258525.0	1554309_at, 1554310_a_at, 201935_s_at, 201936_s_at	NP_003751.2, EAW94955.1, EAW94954.1, EAW94956.1
GeneID:1889	ECE1	1	21,543,740	21,672,034	128,294	-	1	2_A375_pNL97_plus_lncRNA_AR..1..111	83882	in gene	0	1	0	12	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ECE1	ECE, ECE1	endothelin converting enzyme 1	NM_001397, NM_001113347, NM_001113348, NM_001113349, hCT1688617.1, hCT1955776.0, hCT1955777.1, hCT1955778.1, hCT2254416.0, hCT2254420.0, hCT2254422.0, hCT2254423.0, hCT2254425.0, hCT2254426.0	201749_at, 201750_s_at	NP_001388.1, NP_001106818.1, NP_001106819.1, NP_001106820.1, EAW94958.1, EAW94963.1, EAW94957.1, EAW94959.1, EAW94960.1, EAW94961.1, EAW94962.1, EAW94964.1, EAW94965.1, EAW94966.1
GeneID:100506824	LOC100506824	1	21,592,575	21,593,744	1,169	+	1	2_A375_pNL97_plus_lncRNA_AR..1..111	-4223	upstream	0	1	0	12	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100506824		hypothetical LOC100506824	XR_112046, XR_108370, XR_115632		
GeneID:84224	NBPF3	1	21,766,631	21,811,393	44,762	+	2	1_A375_pNL7_minus_lncRNA_AR..1..83, 2_A375_pNL97_plus_lncRNA_AR..1..112	13993, 13961	in gene, in gene	1	1	0	16	14	3	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene NBPF3	AE2, DKFZp434D177, NBPF3	neuroblastoma breakpoint family, member 3	NM_032264, hCT1955783.1, hCT2253622.0, hCT2253623.0	1556825_s_at, 223638_at	NP_115640.1, EAW94973.1, EAW94971.1, EAW94972.1

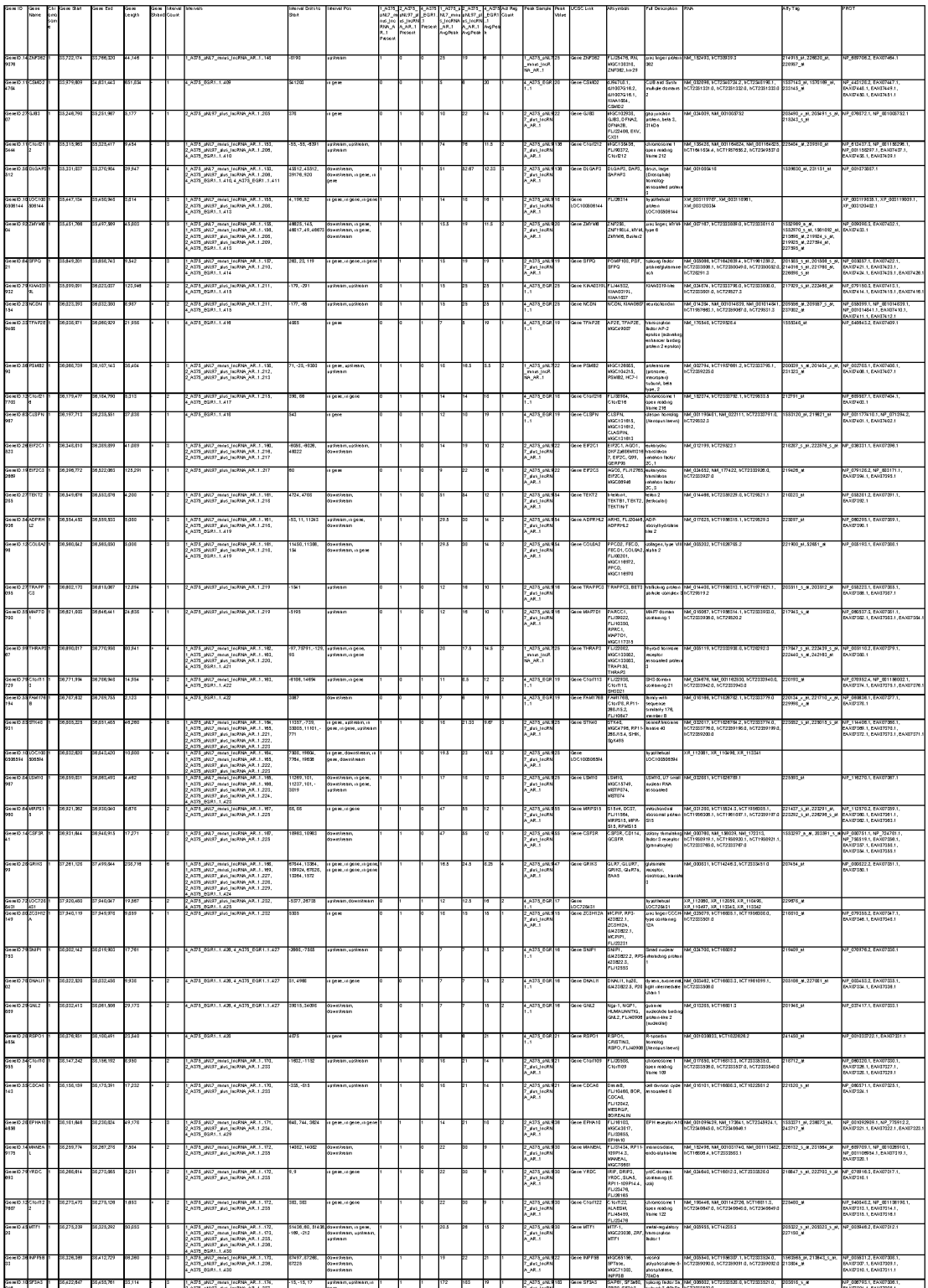
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.249	ALPL	1	21,835,858	21,904,905	69,047	+	1	4_A375_EGR1..1..329	350	in gene	0	0	1	5	5	14	1	4_A375_EGR1..1	14	Gene ALPL	HOPS, AP-TNAP, ALPL, MGC167935, TNAP, FLJ40094, MGC161443, APTNAP, TNSALP, FLJ93059	alkaline phosphatase, liver/bone/kidney	NM_000478, NM_001127501, NM_001177520, hCT1777409.1, hCT1955775.1, hCT2253629.0, hCT30114.3	1557924_s_at, 215783_s_at	NP_000469.3, NP_001120973.2, NP_001170991.1, EAW94975.1, EAW94976.1, EAW94977.1, EAW94974.1
GeneID.5909	RAP1GAP	1	21,922,708	21,995,856	73,148	-	6	1_A375_pNL7_minus_lncRNA_AR..1..84, 1_A375_pNL7_minus_lncRNA_AR..1..85, 2_A375_pNL97_plus_lncRNA_AR..1..113, 2_A375_pNL97_plus_lncRNA_AR..1..114, 4_A375_EGR1..1..330, 4_A375_EGR1..1..331	21298, 10048, 21328, 10084, 60976, 752	in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	16	18.25	14.5	4	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene RAP1GAP	RAP1GAP, RAPGAP, RAP1GAP1, RAP1GA1, KIAA0474, RAP1GAPII	RAP1 GTPase activating protein	NM_001145657, NM_001145658, NM_002885, hCT1848939.2, hCT2254405.1, hCT2254407.1, hCT2254408.1, hCT2254409.1, hCT2254410.1, hCT2357818.0, hCT28819.4	203911_at, 210618_at	NP_001139129.1, NP_001139130.1, NP_002876.2, EAW94979.1, EAW94980.1, EAW94986.1, EAW94981.1, EAW94982.1, EAW94983.1, EAW94984.1, EAW94985.1
GeneID.84196	USP48	1	22,004,791	22,109,688	104,897	-	4	1_A375_pNL7_minus_lncRNA_AR..1..86, 1_A375_pNL7_minus_lncRNA_AR..1..87, 2_A375_pNL97_plus_lncRNA_AR..1..115, 4_A375_EGR1..1..331	76520, 120, 152, 114584	in gene, in gene, in gene, downstream	1	1	1	16.33	15.33	10.67	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene USP48	USP31, MGC14879, RAP1GA1, DKFZp762M1713, USP48, MGC132556	ubiquitin specific peptidase 48	NM_032236, NM_001032730, hCT1955736.1, hCT2254397.0, hCT2254398.0, hCT2254402.0, hCT2254403.0, hCT2254404.0	220078_at, 220079_s_at, 225925_s_at, 229812_at, 232621_at	NP_115612.4, NP_001027902.1, EAW94987.1, EAW94990.1, EAW94991.1, EAW94992.1, EAW94988.1, EAW94989.1
GeneID.3339	HSPG2	1	22,148,737	22,222,804	74,067	-	2	4_A375_EGR1..1..332, 4_A375_EGR1..1..333	44828, 35972	in gene, in gene	0	0	1	6	5	16.5	2	4_A375_EGR1..1	17	Gene HSPG2	SJS, SJS1, PRCAN, SJA, PLC, HSPG2	heparan sulfate proteoglycan 2	NM_005529, hCT2254394.0, hCT2254395.0, hCT2254396.0, hCT2357822.0	201654_s_at, 201655_s_at	NP_005520.4, EAW94995.1, EAW94994.1, EAW94996.1, EAW94997.1
GeneID.29092	HSPC157	1	22,351,707	22,357,716	6,009	+	1	2_A375_pNL97_plus_lncRNA_AR..1..117	-187	upstream	0	1	0	18	17	9	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene HSPC157		hypothetical LOC29092	NR_023918, NR_023919	219885_at	
GeneID.54361	WNT4	1	22,443,798	22,469,519	25,721	-	1	4_A375_EGR1..1..334	9215	in gene	0	0	1	4	4	13	1	4_A375_EGR1..1	13	Gene WNT4	SERKAL, WNT-4, WNT4	wingless-type MMTV integration site family, member 4	NM_030761, hCT31223.2	1556689_a_at, 208606_s_at	NP_110388.2, EAW95010.1
GeneID.9923	ZBTB40	1	22,778,344	22,857,650	79,306	+	2	2_A375_pNL97_plus_lncRNA_AR..1..118, 4_A375_EGR1..1..336	504, 24	in gene, in gene	0	1	1	12	16	15	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ZBTB40	ZNF923, MGC133098, KIAA0478, ZBTB40	zinc finger and BTB domain containing 40	NM_014870, NM_001083621, hCT1957953.1, hCT1957954.1	1559726_at, 203956_s_at, 203959_s_at	NP_055685.3, NP_001077090.1, EAW95011.1, EAW95012.1
GeneID.2046	EPHA8	1	22,890,004	22,930,087	40,083	+	2	1_A375_pNL7_minus_lncRNA_AR..1..90, 2_A375_pNL97_plus_lncRNA_AR..1..119	46140, 46108	downstream, downstream	1	1	0	72	79	7	1	2_A375_pNL97_plus_lncRNA_AR..1	79	Gene EPHA8	EK3, EEK, EPHA8, HEK3, KIAA1459	EPH receptor A8	NM_001006943, NM_020526, hCT31226.3	1554069_at, 231796_at	NP_001006944.1, NP_065387.1, EAW95013.1
GeneID.2048	EPHB2	1	23,037,331	23,241,823	204,492	+	1	4_A375_EGR1..1..337	2797	in gene	0	0	1	8	8	17	1	4_A375_EGR1..1	17	Gene EPHB2	Tyro5, EPHB2, EK5, PCBC, CAPB, EPHT3, ERK, Hek5, MGC87492, DRT	EPH receptor B2	NM_017449, NM_004442, hCT1955735.1, hCT2254224.0, hCT2254225.0, hCT2254226.0, hCT2254227.0	209588_at, 209589_s_at, 210651_s_at, 211165_x_at	NP_059145.2, NP_004433.2, EAW95022.1, EAW95023.1, EAW95024.1, EAW95025.1, EAW95026.1
GeneID.729059	LOC729059	1	23,337,327	23,342,343	5,016	-	2	1_A375_pNL7_minus_lncRNA_AR..1..91, 2_A375_pNL97_plus_lncRNA_AR..1..120	-3385, -3529	upstream, upstream	1	1	0	22	23	9	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC729059		hypothetical LOC729059	XR_112037, XR_108371, XR_115633	231551_at	
GeneID.23028	KDM1A	1	23,345,941	23,410,184	64,243	+	2	1_A375_pNL7_minus_lncRNA_AR..1..91, 2_A375_pNL97_plus_lncRNA_AR..1..120	-213, -69	upstream, upstream	1	1	0	22	23	9	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene KDM1A	KIAA0601, BHC110, KDM1A, LSD1, AOF2, KDM1	lysine (K)-specific demethylase 1A	NM_015013, NM_001009999, hCT1955774.1, hCT2254191.0, hCT30093.2	1555897_at, 212348_s_at, 236652_at	NP_055828.2, NP_001009999.1, EAW95031.1, EAW95032.1, EAW95033.1
GeneID.10236	HNRNPR	1	23,636,276	23,670,853	34,577	-	1	2_A375_pNL97_plus_lncRNA_AR..1..121	-347	upstream	0	1	0	14	19	3	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene HNRNPR	HNRPR, hnRNP R, FLJ25714, HNRNPR, hnRNP R	heterogeneous nuclear ribonucleoprotein R	NM_005826, NM_001102397, NM_001102398, NM_001102399, hCT1955785.1, hCT1955786.1, hCT30153.3	208765_s_at, 208766_s_at, 232004_at	NP_005817.1, NP_001095867.1, NP_001095868.1, NP_001095869.1, EAW95040.1, EAW95042.1, EAW95041.1
GeneID.80818	ZNF436	1	23,685,941	23,698,357	10,416	-	3	1_A375_pNL7_minus_lncRNA_AR..1..92, 2_A375_pNL97_plus_lncRNA_AR..1..122, 4_A375_EGR1..1..339	869, -7403, 997	in gene, upstream, in gene	1	1	1	18.5	19	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ZNF436	ZNF, ZNF436, Zfp46, KIAA1710	zinc finger protein 436	NM_001077195, NM_030634, hCT1955772.2, hCT2349678.0, hCT30089.4	226113_at, 226114_at	NP_001070663.1, NP_085137.1, EAW95043.1, EAW95044.1, EAW95045.1
GeneID.148898	C1orf213	1	23,695,464	23,698,332	2,868	+	3	1_A375_pNL7_minus_lncRNA_AR..1..92, 2_A375_pNL97_plus_lncRNA_AR..1..122, 4_A375_EGR1..1..339	24, 8298, -104	in gene, downstream, upstream	1	1	1	18.5	19	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene C1orf213	C1orf213, FLJ90508	chromosome 1 open reading frame 213	NR_033890, NR_033891, hCT2254703.0	229086_at	EAW95046.1
GeneID.6920	TCEA3	1	23,707,555	23,751,261	43,706	-	1	2_A375_pNL97_plus_lncRNA_AR..1..122	47501	downstream	0	1	0	17	20	9	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TCEA3	TFIIS, TCEA3, TFIIS.H	transcription elongation factor A (SII), 3	NM_003196, hCT1955773.1, hCT30092.3	226388_at, 241976_at	NP_003187.1, EAW95048.1, EAW95049.1
GeneID.1870	E2F2	1	23,832,922	23,857,713	24,791	-	3	2_A375_pNL97_plus_lncRNA_AR..1..123, 2_A375_pNL97_plus_lncRNA_AR..1..124, 4_A375_EGR1..1..340	-223, -8623, 465	upstream, upstream, in gene	0	1	1	13	18	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene E2F2	E2F-2, E2F2	E2F transcription factor 2	NM_004091, hCT2256361.0, hCT2350460.0, hCT2350461.0, hCT28817.3	207042_at, 228361_at, 235582_at	NP_004082.1, EAW95057.1, EAW95055.1, EAW95056.1, EAW95058.1
GeneID.729856	LOC729856	1	23,997,268	23,997,735	467	+	2	1_A375_pNL7_minus_lncRNA_AR..1..93, 2_A375_pNL97_plus_lncRNA_AR..1..125	2444, 2508	downstream, downstream	1	1	0	32	36	4	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene LOC729856		elongation factor 1 alpha-like	XM_001130168, XM_001131535, XM_001715076		XP_001130168.2, XP_001131535.2, XP_001715130.2
GeneID.6135	RPL11	1	24,018,294	24,022,915	4,621	+	2	2_A375_pNL97_plus_lncRNA_AR..1..126, 4_A375_EGR1..1..341	10, 10	in gene, in gene	0	1	1	19	25	20	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene RPL11	L11, DBA7, GIG34, RPL11	ribosomal protein L11	NM_000975, hCT1777320.1, hCT1955732.1	200010_at	NP_000966.2, EAW95066.1, EAW95067.1
GeneID.6924	TCEB3	1	24,069,856	24,088,549	18,693	+	1	2_A375_pNL97_plus_lncRNA_AR..1..127	96	in gene	0	1	0	16	23	12	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TCEB3	SIII, FLJ36760, FLJ42849, TCEB3, EloA, SIII p110, TCEB3A	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	NM_003198, hCT2254721.0, hCT28784.3	1570625_at, 1570627_at, 202818_s_at, 202819_s_at	NP_003189.2, EAW95070.1, EAW95071.1
GeneID.11313	LYPLA2	1	24,117,646	24,122,029	4,383	+	2	1_A375_pNL7_minus_lncRNA_AR..1..94, 2_A375_pNL97_plus_lncRNA_AR..1..128	8722, 9634	downstream, downstream	1	1	0	20	32	17	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene LYPLA2	APT-2, LYPLA2, DJ886K2.4	lysophospholipase II	NM_007260, hCT2254733.0, hCT2254734.0, hCT2254736.0, hCT2254737.0, hCT2254739.0, hCT2254740.0	202292_x_at, 215568_x_at	NP_009191.1, EAW95077.1, EAW95078.1, EAW95079.1, EAW95080.1, EAW95081.1, EAW95082.1
GeneID.2582	GALE	1	24,122,089	24,127,294	5,205	-	2	1_A375_pNL7_minus_lncRNA_AR..1..94, 2_A375_pNL97_plus_lncRNA_AR..1..128	926, 14	in gene, in gene	1	1	0	20	32	17	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene GALE	FLJ95174, FLJ97302, SDR1E1, GALE	UDP-galactose-4-epimerase	NM_001008216, NM_000403, NM_001127621, hCT1955752.1, hCT1955753.1, hCT1955754.1, hCT1955755.1, hCT2256363.0, hCT2256364.0, hCT2256367.0, hCT2256370.0, hCT2256371.0, hCT2256373.0, hCT28915.3	1557649_at, 1557651_x_at, 202528_at	NP_001008217.1, NP_000394.2, NP_001121093.1, EAW95083.1, EAW95085.1, EAW95092.1, EAW95084.1, EAW95086.1, EAW95087.1, EAW95088.1, EAW95089.1, EAW95090.1, EAW95091.1, EAW95093.1
GeneID.3155	HMGCL	1	24,128,367	24,151,949	23,582	-	3	1_A375_pNL7_minus_lncRNA_AR..1..94, 2_A375_pNL97_plus_lncRNA_AR..1..128, 4_A375_EGR1..1..342	25581, 24669, 205	downstream, downstream, in gene	1	1	1	19	25.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene HMGCL	HL, HMGCL	3-hydroxymethyl-3-methylglutaryl-CoA lyase	NM_000191, NM_001166059, hCT1955761.1, hCT1955764.1, hCT2357617.0, hCT28917.2	202772_at	NP_000182.2, NP_001159531.1, EAW95094.1, EAW95095.1, EAW95096.1, EAW95097.1
GeneID.55629	PNRC2	1	24,286,301	24,289,952	3,651	+	1	4_A375_EGR1..1..343	-141	upstream	0	0	1	14	13	18	1	4_A375_EGR1..1	18	Gene PNRC2	FLJ20312, MGC99541, PNRC2	proline-rich nuclear receptor coactivator 2	NM_017761, hCT1777123.2, hCT1955726.1	217779_s_at, 222406_s_at	NP_060231.1, EAW95101.1, EAW95102.1
GeneID.10772	SFRS13A	1	24,292,935	24,306,953	14,018	-	4	1_A375_pNL7_minus_lncRNA_AR..1..95, 2_A375_pNL97_plus_lncRNA_AR..1..129, 4_A375_EGR1..1..343, 4_A375_EGR1..1..344	329, 137, 20793, 185	in gene, in gene, downstream, in gene	1	1	1	18.5	20.5	19.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene SFRS13A	SRrp40, SRp38, FLJ43846, SFRS13A, TASR1, NSSR, TASR2, FUSIP2, DKFZp686H0644, FLJ30749, SRSF10, FUSIP1, SFRS13, TASR	serine/arginine-rich splicing factor 10	NM_001191005, NM_001191006, NM_001191007, NM_001191009, NM_006625, NM_054016, NR_034035, hCT2256349.0, hCT2256351.0, hCT2256352.0, hCT2256354.0, hCT2357605.0	204299_at, 206095_s_at, 210178_x_at, 213594_x_at	NP_001177934.1, NP_001177935.1, NP_473357.1, NP_006616.1, NP_001177936.1, NP_001177938.1, EAW95103.1, EAW95104.1, EAW95105.1, EAW95106.1, EAW95107.1
GeneID.127294	MYOM3	1	24,382,531	24,438,665	56,134	-	1	2_A375_pNL97_plus_lncRNA_AR..1..130	60585	downstream	0	1	0	16	15	1	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene MYOM3	FLJ35961, MYOM3, MGC71463, RP11-293P20.1	myomesin family, member 3	NM_152372, hCT1955728.2, hCT2256346.0, hCT2357798.0	230284_at, 238124_at	NP_689585.3, EAW95108.1, EAW95109.1, EAW95110.1
GeneID.163702	IL28RA	1	24,480,647	24,513,751	33,104	-	1	4_A375_EGR1..1..345	30135	in gene	0	0	1	5	5	17	1	4_A375_EGR1..1	17	Gene IL28RA	IFNLR, IFNLR1, IL-28R1, CRF2/12, LICR2, IL28RA	interleukin 28 receptor, alpha (interferon, lambda receptor)	NM_170743, NM_173064, NM_173065, hCT2256344.0, hCT2341114.0, hCT2341115.0, hCT2341116.0, hCT2341117.0, hCT2357814.0	1555499_a_at, 244261_at	NP_734464.1, NP_775087.1, NP_775088.1, EAW95113.1, EAW95115.1, EAW95117.1, EAW95114.1, EAW95116.1, EAW95118.1
GeneID.57822	GRHL3	1	24,645,812	24,690,972	45,160	+	2	1_A375_pNL7_minus_lncRNA_AR..1..97, 2_A375_pNL97_plus_lncRNA_AR..1..132	46188, 46060	downstream, downstream	1	1	0	22	19	7	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene GRHL3	GRHL3, SOM, TFCP2L4, MGC46624	grainyhead-like 3 (Drosophila)	NM_021180, NM_198173, NM_198174, NM_001195010, hCT1813422.3, hCT2348170.1, hCT2348171.0, hCT2348172.0	232116_at	NP_067003.2, NP_937816.1, NP_937817.3, NP_001181939.1, EAW95120.1, EAW95121.1, EAW95122.1, EAW95123.1
GeneID.90529	C1orf201	1	24,683,489	24,727,949	44,460	-	2	1_A375_pNL7_minus_lncRNA_AR..1..97, 2_A375_pNL97_plus_lncRNA_AR..1..132	35949, 36077	in gene, in gene	1	1	0	22	19	7	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene C1orf201	FLJ33340, C1orf201	chromosome 1 open reading frame 201	NM_178122, hCT11082.2, hCT1955745.1, hCT2256340.0, hCT2256341.0, hCT2357811.0, hCT2357812.0	227694_at, 233693_at	NP_835223.1, EAW95125.1, EAW95124.1, EAW95126.1, EAW95128.1, EAW95129.1, EAW95127.1
GeneID.57185	NIPAL3	1	24,742,245	24,799,473	57,228	+	4	1_A375_pNL7_minus_lncRNA_AR..1..98, 2_A375_pNL97_plus_lncRNA_AR..1..133, 4_A375_EGR1..1..346, 4_A375_EGR1..1..347	-69, -165, -2245, 40491	upstream, upstream, upstream, in gene	1	1	1	12	15.67	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene NIPAL3	DKFZp686E22155, DJ462O23.2, NIPAL3, NPAL3	NIPA-like domain containing 3	NM_020448, hCT11081.3	210287_at, 214579_at, 225875_s_at, 225876_at, 229735_s_at	NP_065181.1, EAW95130.1
GeneID.25932	CLIC4	1	25,071,760	25,170,815	99,055	+	2	4_A375_EGR1..1..348, 4_A375_EGR1..1..349	240, 103024	in gene, downstream	0	0	1	11.5	15	19	2	4_A375_EGR1..1	20	Gene CLIC4	CLIC4, huH1, MTCLIC, H1, p64H1, DKFZp566G223, FLJ38640, CLIC4L	chloride intracellular channel 4	NM_013943, hCT15161.3, hCT2253300.0, hCT2253301.0, hCT2253303.0, hCT2253304.0	201559_s_at, 201560_at, 221881_s_at	NP_039234.1, EAW95146.1, EAW95142.1, EAW95143.1, EAW95144.1, EAW95145.1
GeneID.864	RUNX3	1	25,226,002	25,291,501	65,499	-	3	1_A375_pNL7_minus_lncRNA_AR..1..99, 2_A375_pNL97_plus_lncRNA_AR..1..134, 4_A375_EGR1..1..350	15437, 5165, 35693	in gene, in gene, in gene	1	1	1	14.33	16.67	12.67	3	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene RUNX3	AML2, RUNX3, MGC16070, CBFA3, FLJ34510, PEBP2aC	runt-related transcription factor 3	NM_001031680, NM_004350, hCT1955718.1, hCT1955719.1, hCT2254122.0	204197_s_at, 204198_s_at, 234926_x_at	NP_001026850.1, NP_004341.1, EAW95147.1, EAW95148.1, EAW95149.1
GeneID.57035	C1orf63	1	25,568,740	25,573,985	5,245	-	4	2_A375_pNL97_plus_lncRNA_AR..1..137, 2_A375_pNL97_plus_lncRNA_AR..1..138, 4_A375_EGR1..1..353, 4_A375_EGR1..1..354	665, 84, 225, -479	in gene, in gene, in gene, upstream	0	1	1	13.5	18.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene C1orf63	RP3-465N24.4, DJ465N24.2.1, C1orf63, NPD014	chromosome 1 open reading frame 63	NM_020317, hCT2254136.0, hCT2254137.0, hCT2254138.0, hCT2254139.0, hCT2357821.0	209006_s_at, 209007_s_at	NP_064713.3, EAW95159.1, EAW95157.1, EAW95158.1, EAW95160.1, EAW95161.1
GeneID.6007	RHD	1	25,598,981	25,656,936	57,955	+	1	4_A375_EGR1..1..355	65867	downstream	0	0	1	13	9	13	1	4_A375_EGR1..1	13	Gene RHD	RhDCw, RHXIII, RhK562-II, RH, MGC165007, RHD, RHDVA(TT), CD240D, RhPI, RHCED, RHPII, RhII, Rh4, DIIIc, RHDel, RH30	Rh blood group, D antigen	NM_016124, NM_001127691	210429_at, 210430_x_at, 210586_x_at	NP_057208.2, NP_001121163.1
GeneID.23585	TMEM50A	1	25,664,811	25,688,852	24,041	+	1	4_A375_EGR1..1..355	37	in gene	0	0	1	13	9	13	1	4_A375_EGR1..1	13	Gene TMEM50A	IFNRC, SMP1, TMEM50A, RP11-335G20.3	transmembrane protein 50A	NM_014313, hCT1955746.1, hCT2254135.0	217766_s_at, 222401_s_at	NP_055128.1, EAW95169.1, EAW95168.1
GeneID.26119	LDLRAP1	1	25,870,076	25,895,377	25,301	+	2	1_A375_pNL7_minus_lncRNA_AR..1..101, 2_A375_pNL97_plus_lncRNA_AR..1..139	26372, 25412	downstream, downstream	1	1	0	15	20	14	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LDLRAP1	MGC34705, ARH, FHCB1, DKFZp586D0624, FHCB2, LDLRAP1, ARH1, ARH2	low density lipoprotein receptor adaptor protein 1	NM_015627, hCT1777234.2, hCT2334511.1, hCT2334512.1, hCT2334514.0	221790_s_at, 57082_at	NP_056442.2, EAX07873.1, EAX07872.1, EAX07874.1, EAX07875.1
GeneID.57134	MAN1C1	1	25,943,959	26,111,258	167,299	+	1	4_A375_EGR1..1..356	-1143	upstream	0	0	1	8	11	16	1	4_A375_EGR1..1	16	Gene MAN1C1	MAN1C1, MAN1C, pp6318, HMIC, MAN1A3	mannosidase, alpha, class 1C, member 1	NM_020379, hCT14859.2, hCT1967795.1	214180_at, 218918_at	NP_065112.1, EAX07870.1, EAX07871.1
GeneID.57190	SEPN1	1	26,126,667	26,144,713	18,046	+	2	1_A375_pNL7_minus_lncRNA_AR..1..102, 4_A375_EGR1..1..357	19669, 20021	downstream, downstream	1	0	1	17	16	17	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene SEPN1	SELN, RSMD1, FLJ24021, MDRS1, SEPN1, RSS	selenoprotein N, 1	NM_020451, NM_206926	224659_at	NP_065184.2, NP_996809.1
GeneID.56181	FAM54B	1	26,146,397	26,159,433	13,036	+	2	1_A375_pNL7_minus_lncRNA_AR..1..102, 4_A375_EGR1..1..357	-61, 291	upstream, in gene	1	0	1	17	16	17	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene FAM54B	MST116, HYST1888, MSTP116, FAM54B	family with sequence similarity 54, member B	NM_019557, NM_001099625, NM_001099626, NM_001099627	224280_s_at	NP_062457.3, NP_001093095.1, NP_001093096.1, NP_001093097.1
GeneID.648471	LOC646471	1	26,146,445	26,150,097	3,652	-	2	1_A375_pNL7_minus_lncRNA_AR..1..102, 4_A375_EGR1..1..357	3761, 3409	downstream, in gene	1	0	1	17	16	17	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene LOC646471		hypothetical LOC646471	NR_024498		
GeneID.3925	STMN1	1	26,210,677	26,233,368	22,691	-	2	4_A375_EGR1..1..358, 4_A375_EGR1..1..359	13224, 1000	in gene, in gene	0	0	1	7	7.5	14	2	4_A375_EGR1..1	16	Gene STMN1	C1orf215, MGC138870, Lag, SMN, PR22, STMN1, OP18, LAP18, PP17, MGC138869, PP19, FLJ32206	stathmin 1	NM_005563, NM_203399, NM_203401, NM_001145454, hCT14857.2, hCT1967793.2, hCT1967794.2, hCT2351956.0, hCT2351957.0, hCT2351958.0, hCT2351959.0	200783_s_at, 217714_x_at	NP_005554.1, NP_981944.1, NP_001138926.1, NP_981946.1, EAX07855.1, EAX07856.1, EAX07854.1, EAX07857.1, EAX07858.1, EAX07859.1, EAX07860.1
GeneID.5051	PAFAH2	1	26,286,258	26,324,648	38,390	-	2	1_A375_pNL7_minus_lncRNA_AR..1..103, 2_A375_pNL97_plus_lncRNA_AR..1..140	-24, -56	upstream, upstream	1	1	0	26	30	8	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene PAFAH2	FLJ26025, PAFAH2, HSD-PLA2	platelet-activating factor acetylhydrolase 2, 40kDa	NM_000437, hCT14856.2, hCT2359170.0	205232_s_at, 205233_s_at	NP_000428.2, EAX07852.1, EAX07853.1
GeneID.2134	EXTL1	1	26,348,271	26,362,955	14,684	+	4	1_A375_pNL7_minus_lncRNA_AR..1..104, 1_A375_pNL7_minus_lncRNA_AR..1..105, 2_A375_pNL97_plus_lncRNA_AR..1..141, 2_A375_pNL97_plus_lncRNA_AR..1..142	7165, 13617, 7121, 13617	in gene, in gene, in gene, in gene	1	1	0	25.5	24	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene EXTL1	MGC70794, EXTL1, EXTL	exostoses (multiple)-like 1	NM_004455, hCT13943.2	206329_at	NP_004446.2, EAX07851.1
GeneID.7780	SLC30A2	1	26,364,514	26,372,604	8,090	-	4	1_A375_pNL7_minus_lncRNA_AR..1..104, 1_A375_pNL7_minus_lncRNA_AR..1..105, 2_A375_pNL97_plus_lncRNA_AR..1..141, 2_A375_pNL97_plus_lncRNA_AR..1..142	17148, 10716, 17212, 10716	downstream, downstream, downstream, downstream	1	1	0	25.5	24	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene SLC30A2	ZNT2, FLJ36708, SLC30A2, ZnT-2, PP12488, MGC11303	solute carrier family 30 (zinc transporter), member 2	NM_001004434, NM_032513, hCT1641076.2, hCT2334144.0	224485_s_at, 230084_at	NP_001004434.1, NP_115902.1, EAX07849.1, EAX07850.1

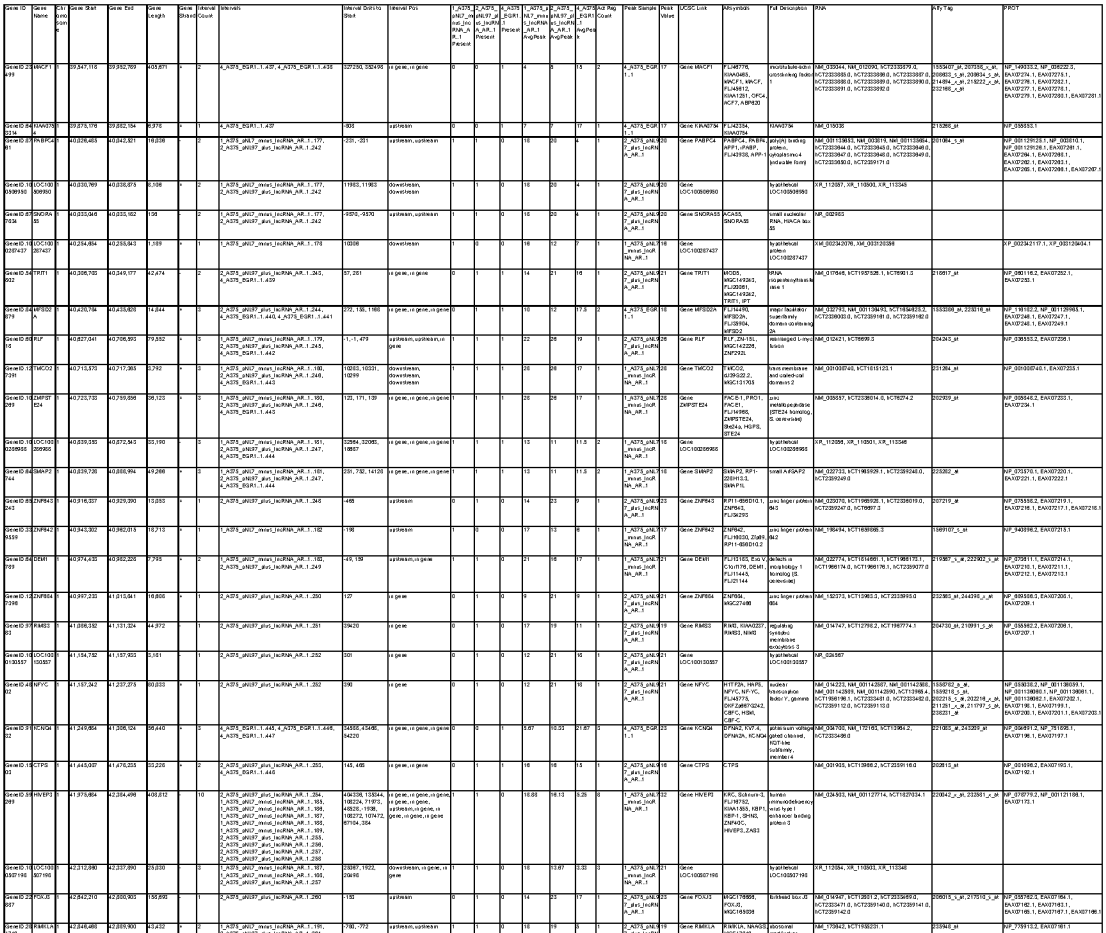


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_uNG7_myNG7_all_lncRNA_AR_1 Percent	2_A375_2_A375_myNG7_all_lncRNA_AR_1 Percent	3_A375_EGFR_1 Percent	1_A375_2_A375_NG7_mycNG7_all_lncRNA_AR_1 Avg Peak	2_A375_2_A375_myNG7_all_lncRNA_AR_1 Avg Peak	3_A375_EGFR_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:14436	PDIR1L	1	28,237,856	28,432,554	14,376	+	2	1_A375_uNG7_myncl_lncRNA_AR_1:.199, 2_A375_uNG7_glun_lncRNA_AR_1:.143	72; -56	sr:gene, upstream	1	1	0	25	26	17	1	2_A375_uNG7_glun_lncRNA_AR_1	26	Gene PDIR1L	PDIR1, RP11-961I4.4, ST43312, CL1K1L1	PDIA6I disulfide isomerase like	NM_152535, NR_039955, NR_039956, NCT19433990.3, NCT23244961, NCT23440899.0	227253_at	NP_690345.1, EAX07648.1, EAX07645.1, EAX07647.1
GeneID:27827	GRRP1	1	28,455,511	28,455,119	2,808	+	2	1_A375_uNG7_myncl_lncRNA_AR_1:.197, 2_A375_uNG7_glun_lncRNA_AR_1:.144	10641, 10561	downstream, downstream	1	1	0	25	26	14	1	2_A375_uNG7_glun_lncRNA_AR_1	26	Gene GRRP1	KPI1-961I4.5, FLJ14550, PAR1/2D, GRRP1	glycoprotein rich protein 1	NM_024595, NCT17772281.1	220430_at	NP_37914.5.2, EAX07644.1
GeneID:10128348	LOC10012834	1	28,456,007	28,456,312	2,305	-	2	1_A375_uNG7_myncl_lncRNA_AR_1:.197, 2_A375_uNG7_glun_lncRNA_AR_1:.144	1960, 1960	sr:gene, sr:gene	1	1	0	25	26	14	1	2_A375_uNG7_glun_lncRNA_AR_1	26	Gene LOC100128348	LOC100128348	hypothetical LOC100128348	XR_112949, XR_109277, XR_111537		
GeneID:84202	ZNF593	1	28,456,355	28,457,364	976	+	2	1_A375_uNG7_myncl_lncRNA_AR_1:.197, 2_A375_uNG7_glun_lncRNA_AR_1:.144	56; -56	upstream, upstream	1	1	0	25	26	14	1	2_A375_uNG7_glun_lncRNA_AR_1	26	Gene ZNF593	ZT68, ZNF593	zinc finger protein 593	NM_015071, NCT19164.2	224179_at	NP_599155.2, EAX07643.1
GeneID:10296	CNKSR1	1	28,503,561	28,616,373	12,334	+	3	1_A375_uNG7_myncl_lncRNA_AR_1:.197, 2_A375_uNG7_glun_lncRNA_AR_1:.144, 3_A375_EGR1_1:.265	-74829, -7629, 8721	upstream, upstream, sr:gene	1	1	1	14.3	16	13	2	2_A375_uNG7_glun_lncRNA_AR_1	26	Gene CNKSR1	CNK, CNK1, KSR, CNKSR1	connector enhancer of kinase suppressor of Ras 1	NM_006314, NR_023345, NCT23345003.0, NCT23591869.0, NCT31932.3	224740_at	NP_89635.2, EAX07642.1, EAX07641.1
GeneID:27837	CATSPER4	1	28,517,119	28,529,053	11,914	+	1	3_A375_EGR1_1:.390	-7637	upstream	0	0	1	4	8	16	1	3_A375_EGR1_1	16	Gene CATSPER4	WDC149223, CATSPER4	cation channel, sperm associated 4	NM_198137, NCT23467.0		NP_937770.1, EAX07629.1
GeneID:84202	CCDC21	1	28,560,680	28,605,299	44,808	+	4	1_A375_uNG7_myncl_lncRNA_AR_1:.193, 2_A375_uNG7_myncl_lncRNA_AR_1:.173, 3_A375_uNG7_glun_lncRNA_AR_1:.143, 4_A375_EGR1_1:.381	-103, 42133, 43697, 43998	upstream, sr:gene, downstream, downstream	1	1	1	16	16.67	16.33	3	4_A375_EGR1_1	23	Gene CCDC21	DKFZp434P232, DKFZp434J0117, FLJ13976, CCDC21, FLJ12000	coiled-coil domain containing 21	NM_032776, NCT17772201.1, NCT19644541.1, NCT19644541.1, NCT23393081.0	219911_s_at, 227618_at	NP_079115.2, EAX07639.1, EAX07639.1, EAX07634.1, EAX07633.1
GeneID:84422	SHSBGR3	1	28,696,210	28,806,013	1,800	+	3	1_A375_uNG7_myncl_lncRNA_AR_1:.197, 2_A375_uNG7_glun_lncRNA_AR_1:.143, 3_A375_EGR1_1:.381	-397, 347,443	upstream, sr:gene, sr gene	1	1	1	16.3	17.5	16.5	2	3_A375_EGR1_1	23	Gene SHSBGR3	SHSBGR3, TIP81, SHSBP1	SH3 domain binding glutamic acid-rich protein like 3	NM_031298, NCT17772222.2, NCT19976281.1	221269_s_at	NP_112376.1, EAX07631.1, EAX07632.1
GeneID:11844	UBXN11	1	28,806,773	28,844,756	35,983	-	3	1_A375_uNG7_myncl_lncRNA_AR_1:.199, 2_A375_uNG7_glun_lncRNA_AR_1:.145, 3_A375_EGR1_1:.381	41940, 56196, 59100	downstream, downstream, downstream, downstream	1	1	1	16.3	17.5	16.5	2	3_A375_EGR1_1	23	Gene UBXN11	CGI-1, FP12243, UBXD5, SOCL, DKFZp686H0421, SOC, UBXN11	UBX domain protein 11	NM_183008, NM_145543, NM_020377282, NCT17772351.1, NCT19642761.0, NCT19642392.1, NCT19642392.2, NCT23591845.0, NCT23591951.0, NCT23591951.0	227716_at	NP_89210.2, NP_683320.2, NP_001070700.1, EAX07625.1, EAX07624.1, EAX07623.1, EAX07624.1, EAX07622.1, EAX07623.1, EAX07629.1
GeneID:83461	AIM1L	1	28,845,330	28,860,821	22,271	-	1	4_A375_EGR1_1:.382	17197	sr:gene	0	0	1	8	8	22	1	4_A375_EGR1_1	22	Gene AIM1L	CRYBG2, AIM1L	beaded sr melanosome l-like	NM_001037735, NCT17772227.0	230290_at	NP_001034864.2, EAX07619.1
GeneID:79727	LIN28	1	28,737,269	28,756,219	18,950	+	6	1_A375_uNG7_myncl_lncRNA_AR_1:.110, 2_A375_uNG7_myncl_lncRNA_AR_1:.111, 3_A375_uNG7_glun_lncRNA_AR_1:.148, 4_A375_uNG7_glun_lncRNA_AR_1:.147, 5_A375_EGR1_1:.365, 4_A375_EGR1_1:.364	-2385, 21419, 2161, 21403, 699, 21371	upstream, downstream, upstream, downstream, sr:gene, downstream	1	1	1	30.33	35	15	3	2_A375_uNG7_glun_lncRNA_AR_1	71	Gene LIN28	LIN28, LIN-28, LIN28A, CSDD1, ZCCHC1, FLJ10497	lin-28 homolog (C elegans)	NM_024674, NCT19905846.1, NCT23346952.0	219623_at	NP_078950.1, EAX07615.1, EAX07614.1
GeneID:79478	DHDDS	1	28,756,902	28,797,797	35,995	+	5	1_A375_uNG7_myncl_lncRNA_AR_1:.111, 2_A375_uNG7_myncl_lncRNA_AR_1:.112, 3_A375_uNG7_glun_lncRNA_AR_1:.147, 4_A375_uNG7_glun_lncRNA_AR_1:.146, 5_A375_EGR1_1:.384	-114, 39354, -50, 39470, -162	upstream, downstream, upstream, downstream, upstream	1	1	1	23.5	24.5	17	2	1_A375_uNG7_glun_lncRNA_AR_1	30	Gene DHDDS	CPT, CIT, DS, FLJ13102, HDS, DHDDS	dehydrodolichyl diphosphate synthase	NM_033551, NM_024657, NCT11293.2, NCT19735A.1, NCT23345810, NCT23591931.0, NCT23591932.0, NCT23591931.0, NCT23591934.0	216547_at, 224084_s_at	NP_996523.1, NP_079182.2, EAX07606.1, EAX07610.1, EAX07611.1, EAX07612.1, EAX07608.1, EAX07607.1, EAX07609.1
GeneID:51180	HRN3N2	1	28,795,902	28,803,103	4,231	+	2	1_A375_uNG7_myncl_lncRNA_AR_1:.112, 2_A375_uNG7_glun_lncRNA_AR_1:.142	-988, -803	upstream, upstream	1	1	0	17	20	14	1	2_A375_uNG7_glun_lncRNA_AR_1	30	Gene HRN3N2	HRN37, MGC26716, MGC9828, HRN3N2	high mobility group nucleosomal binding domain 2	NM_055317, NCT23345851.1, NCT23345861.1, NCT23345991.1, NCT23345991.1	209860_s_at	NP_059005.1, EAX07604.1, EAX07602.1, EAX07603.1
GeneID:91768	RFS6HA1	1	28,836,249	28,901,820	43,271	+	1	2_A375_uNG7_glun_lncRNA_AR_1:.150	29823	sr:gene	0	0	1	14	17	7	1	2_A375_uNG7_glun_lncRNA_AR_1	17	Gene RFS6HA1	MAPKAPK1N, RSKL, RSY1, HU1, RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	NM_031389893, NM_002953, NCT19973.3, NCT23345982.0, NCT23345983.0	202219_at	NP_001038984.1, NP_002944.2, EAX07796.1, EAX07799.1, EAX07800.1
GeneID:10839797	MIR1976	1	28,861,035	28,861,064	31	+	1	2_A375_uNG7_glun_lncRNA_AR_1:.150	1239	downstream	0	0	1	14	17	7	1	2_A375_uNG7_glun_lncRNA_AR_1	17	Gene MIR1976	hsa-mir-1976, MIR1976	microRNA 1976	NR_031740		
GeneID:83439	ARID1A	1	27,022,922	27,105,801	89,279	+	6	1_A375_uNG7_myncl_lncRNA_AR_1:.115, 2_A375_uNG7_myncl_lncRNA_AR_1:.118, 3_A375_uNG7_glun_lncRNA_AR_1:.152, 4_A375_uNG7_glun_lncRNA_AR_1:.153, 5_A375_EGR1_1:.366, 4_A375_EGR1_1:.397	-2906, -346, -2906, -410, -566, 92110	upstream, upstream, downstream, upstream, upstream, downstream	1	1	1	27.33	29	15.67	2	2_A375_uNG7_glun_lncRNA_AR_1	56	Gene ARID1A	P270, B120, OSIN, ARID1A, BAF250a, BAF250, MRD14, BAF250, SWI/SNF	AT rich interactive domain 1A (SWI-like)	NM_139135, NM_006015, NCT03223.3, NCT23345961.0, NCT23345961.0, NCT23345972.0, NCT23345961.0	235951_s_at, 219549_s_at, 212152_x_at, 219917_s_at	NP_824381.1, NP_006456.3, EAX07795.1, EAX07794.1, EAX07796.1, EAX07798.1, EAX07797.1
GeneID:23750	SFN	1	27,589,835	27,592,947	1,314	+	2	2_A375_uNG7_glun_lncRNA_AR_1:.154, 3_A375_EGR1_1:.265, 4_A375_EGR1_1:.269	1775, 4241, 111	downstream, upstream, sr:gene	0	1	1	10.33	10.33	17	3	4_A375_EGR1_1	19	Gene SFN	SFN, YWHAS	stratifin	NM_006142, NCT23345830.0, NCT9437.2	205360_at, 33320_r_at, 33325_r_at	NP_006130.1, EAX07787.1, EAX07788.1
GeneID:54674	GPN2	1	27,205,973	27,216,999	10,996	-	3	1_A375_uNG7_myncl_lncRNA_AR_1:.117, 2_A375_uNG7_glun_lncRNA_AR_1:.155, 3_A375_EGR1_1:.370	408, 325, 517	sr:gene, sr:gene, sr:gene	1	1	1	23	19	29	1	3_A375_EGR1_1	29	Gene GPN2	FLJ10349, MTB018, GPN2	GPN-loop GTPase 2	NM_015986, NCT23344287.0	219799_at	NP_3965136.3, EAX07764.1
GeneID:84328	GPATC1	1	27,216,979	27,226,962	9,983	+	3	2_A375_uNG7_myncl_lncRNA_AR_1:.117, 3_A375_uNG7_glun_lncRNA_AR_1:.155, 4_A375_EGR1_1:.370	10618, 10418, 10810	downstream, downstream, downstream, downstream	1	1	1	23	19	29	1	3_A375_EGR1_1	29	Gene GPATCH8	GPATC3, FLJ12455, DKFZp686B0223, GPATCH8	G patch domain containing 8	NM_020370, NCT23345841.1	218985_at	NP_079381.2, EAX07763.1
GeneID:54478	NR0B2	1	27,237,973	27,240,987	2,992	-	1	2_A375_uNG7_glun_lncRNA_AR_1:.156	-7753	upstream	0	0	1	16	23	14	1	2_A375_uNG7_glun_lncRNA_AR_1	23	Gene NR0B2	NR0B2, SHP, SHP1, FLJ10799	nuclear receptor subfamily 0, group B, member 2	NM_021969, NCT10526.3	206410_at	NP_066564.1, EAX07761.1
GeneID:10163725	NUDC	1	27,245,224	27,272,957	24,865	+	2	2_A375_uNG7_glun_lncRNA_AR_1:.156, 3_A375_EGR1_1:.371	96, 30112	sr:gene, downstream	0	1	1	16.5	14.5	17	2	2_A375_uNG7_glun_lncRNA_AR_1	23	Gene NUDC	NUDC, MNUDC, NPD011, HNUDC	nuclear distribution gene C homolog (A. nidulans)	NM_006600, NCT10523.3	201175_x_at, 210574_s_at, 210575_at	NP_006581.1, EAX07760.1
GeneID:10270997	C1orf172	1	27,276,047	27,288,901	10,834	-	1	4_A375_EGR1_1:.371	6383	sr:gene	0	0	1	8	8	30	1	4_A375_EGR1_1	20	Gene C1orf172	KPI1-344H13.3, FLJ34833, C1orf172	chromosome 1 open reading frame 172	NM_182395, NCT10331.2	236068_at	NP_899378.2, EAX07779.1
GeneID:55150	TRNP1	1	27,320,155	27,327,277	7,182	+	2	2_A375_uNG7_glun_lncRNA_AR_1:.157, 3_A375_uNG7_glun_lncRNA_AR_1:.156	6413, 15657	downstream, downstream	0	1	0	15.5	20	7.5	2	2_A375_uNG7_glun_lncRNA_AR_1	28	Gene TRNP1	C1orf223, TNRP, TRNP1	TMPP-regulated nuclear protein 1	NM_031013842, NCT23273.0	227802_at, 239052_at	NP_00013864.1, EAX07776.1
GeneID:11572	FAM48B1	1	27,331,811	27,339,333	7,522	-	2	2_A375_uNG7_glun_lncRNA_AR_1:.157, 3_A375_uNG7_glun_lncRNA_AR_1:.156	10723, 3301	downstream, sr:gene	0	1	0	15.5	20	7.5	2	2_A375_uNG7_glun_lncRNA_AR_1	28	Gene FAM48B	KPI1-344H13.6, MGC20045, FAM48B, MGC18491	family with sequence similarity 48, member B	NM_032943, NCT10323.3	225916_at	NP_443179.2, EAX07777.1
GeneID:84988	SLC9A1	1	27,425,900	27,451,451	56,151	-	1	4_A375_EGR1_1:.370	56347	sr:gene	0	0	1	7	10	10	1	4_A375_EGR1_1	13	Gene SLC9A1	SLC9A1, NHE1, FLJ42224, APNH	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1	NM_003047, NCT10327.2, NCT23345851.1, NCT23459465.0	1554720_at, 209455_at	NP_3850358.2, EAX07773.1, EAX07774.1, EAX07775.1
GeneID:23075	WDTC1	1	27,561,007	27,655,110	74,103	+	1	1_A375_uNG7_myncl_lncRNA_AR_1:.118	65	sr:gene	1	0	0	21	12	11	1	1_A375_uNG7_glun_lncRNA_AR_1	21	Gene WDTC1	WDTC1, DCAF9, HAN1027, ADP	WD and tetratricopeptide repeats 1	NM_015033, NCT23345680.0, NCT23345847.0, NCT23345849.0, NCT23345850.0	215467_s_at, 219039_s_at, 60029_at	NP_3855830.2, EAX07770.1, EAX07780.1, EAX07771.1, EAX07772.1
GeneID:64744	TMEM220	1	27,845,838	27,862,891	14,255	+	4	1_A375_uNG7_myncl_lncRNA_AR_1:.119, 2_A375_uNG7_glun_lncRNA_AR_1:.159, 3_A375_EGR1_1:.374, 4_A375_EGR1_1:.375	36, -26, 164, 23444	sr:gene, upstream, sr gene, downstream	1	1	1	16	19	16	2	2_A375_uNG7_glun_lncRNA_AR_1	30	Gene TMEM220	C1orf160, TMEM220, MGC111002, DKFZp664D070	transmembrane protein 220	NM_022123, NCT10109.1, NCT23591138.0, NCT23591120.0, NCT23591139.0, NCT9597.2	221312_at, 32076_at	NP_115951.2, EAX07784.1, EAX07785.1, EAX07786.1, EAX07787.1
GeneID:84988	LOC284881	1	27,850,365	27,853,016	2,651	+	3	1_A375_uNG7_myncl_lncRNA_AR_1:.119, 2_A375_uNG7_glun_lncRNA_AR_1:.159, 3_A375_EGR1_1:.374	-1893, -1757, -1083	upstream, upstream, upstream	1	1	1	27	30	19	1	3_A375_EGR1_1	30	Gene LOC284881		actin, gamma 1 pseudogene	NR_033926		
GeneID:23768	PTK6	1	27,992,972	27,998,704	5,733	+	1	2_A375_uNG7_glun_lncRNA_AR_1:.163	98	sr:gene	0	0	1	14	19	8	1	2_A375_uNG7_glun_lncRNA_AR_1	24	Gene PTK6	PTK6, BRK, SRMS, HYB, GIP3, IFIB, PTK6	protein tyrosine kinase 6	NM_005038, NM_032672, NM_032673, NCT17864532.1, NCT23343960.0, NCT23343982.0	203419_at, 224323_s_at	NP_3852250.3, NP_0010821, NP_573811.1, EAX07744.1, EAX07745.1, EAX07746.1
GeneID:84335	CTDSP2	1	28,199,055	28,212,196	14,141	+	1	4_A375_EGR1_1:.381	49397	sr:gene	0	0	1	13	9	19	1	4_A375_EGR1_1	19	Gene CTDSP2	KIAA1651, THEMIS2, CTDSP2	KIAA1651 protein	NM_005447, NM_001039477, NM_001105508, NCT19637981.1, NCT23345932.0, NCT23345940.0, NCT23345960.0	227571_x_at, 213165_s_at	NP_3945292.2, NP_001034998.1, NP_001039026.1, EAX07725.1, EAX07726.1, EAX07727.1, EAX07729.1
GeneID:8431	RPA2	1	28,216,049	28,241,208	25,160	-	1	4_A375_EGR1_1:.381	32664	downstream	0	0	1	13	9	19	1	4_A375_EGR1_1	19	Gene RPA2	RPA2, REPA2, RPA32	replication protein A2, 32kDa	NM_002946, NCT11262.2	201756_at	NP_002927.1, EAX07724.1
GeneID:55107	PPAPR	1	28,472,877	28,520,447	48,570	-	3	1_A375_uNG7_myncl_lncRNA_AR_1:.121, 2_A375_uNG7_glun_lncRNA_AR_1:.164, 4_A375_EGR1_1:.382	49543, 49182, 65	downstream, downstream, upstream	1	1	1	15	21	9	2	4_A375_EGR1_1	33	Gene PPAPR	PAPR, PPAPR	platelet-activating factor receptor	NM_001164721, NM_000952, NM_001164722, NM_001164723	206276_at, 211081_s_at	NP_001158193.1, NP_000943.1, NP_001158194.1, NP_001158195.1
GeneID:23293	DNAJC8	1	28,526,769	28,535,842	22,793	+	1	4_A375_EGR1_1:.382	39630	downstream	0	0	1	10	7	18	1	4_A375_EGR1_1	18	Gene DNAJC8	SPF31, DNAJC8	DnaJ (Hsp40) homolog, subfamily C, member 8	NM_014380, NCT10947.2, NCT19837761.1, NCT23234344.0, NCT23591147.0	203553_s_at, 213249_at, 212491_s_at	NP_3836552.2, EAX07707.1, EAX07708.1, EAX07709.1, EAX07710.1
GeneID:83881	SESN2	1	28,556,956	28,569,002	22,996	+	1	4_A375_EGR1_1:.383	522	sr:gene	0	0	1	11	16	14	1	4_A375_EGR1_1	14	Gene SESN2	DKFZp761H022, SESN2, HI95, DKFZp761H0222, SESN2, SES2	sestrin 2	NM_031459, NCT19847.3	223189_s_at, 223198_s_at	NP_115947.1, EAX07702.1
GeneID:11843	RCC1	1	28,632,455	28,665,700	33,255	+	1	4_A375_EGR1_1:.384	13017	sr:gene	0	0	1	11	12	16	1	4_A375_EGR1_1	16	Gene RCC1	RCC1, CHC1, RCC1-L, SNHG3	regulator of chromosome condensation 1	NM_001048199, NR_033725, NR_033726, NM_001048194, NM_001048195, NM_001269, NCT19851.1, NCT19378A2.0, NCT19837A2.0, NCT19837A.1, NCT23345810.0, NCT23345240.0	200489_s_at, 213747_s_at	NP_001034664.1, NP_001041655.1, NP_001041655.1, NP_001260.1, EAX07694.1, EAX07693.1, EAX07696.1, EAX07691.1, EAX07692.1, EAX07693.1
GeneID:84773	SNHG3	1	28,632,455	28,637,404	4,949	+	1	4_A375_EGR1_1:.384	13017	downstream	0	0	1	11	12	16	1	4_A375_EGR1_1	16	Gene SNHG3	SNHG3, U17HG, U17HG, FAM, FAM70, FLJ38819, NCRNA00014, RNA70, U17HG	small nucleolar RNA host gene 3 (non-protein coding)	NR_002909, NR_033673	213011_at	
GeneID:26987	RNU105A	1	28,633,070	28,633,227	157	+	1	4_A375_EGR1_1:.384	10622	downstream	0	0	1	11	12	16	1	4_A375_EGR1_1	16	Gene RNU105A	RNU105A, U105A, Stu	RNA, U105A small nucleolar	NR_004404		
GeneID:85027	SNHG12	1	28,905,930	28,906,366	2,316	+	2	2_A375_uNG7_glun_lncRNA_AR_1:.167, 4_A375_EGR1_1:.365	-62, 45	upstream, sr:gene	0	1	1	20	22	26	1	4_A375_EGR1_1	28	Gene SNHG12	C1orf29, RPN-MB110.3, NCRNA00100, SNHG12	small nucleolar RNA host gene 12 (non-protein coding)	NM_026127	223773_s_at, 223774_at, 220960_at	
GeneID:26993	SNORD99	1	28,905,258	28,905,334	79	-	2	2_A375_uNG7_glun_lncRNA_AR_1:.167, 3_A375_EGR1_1:.365	-3114, -2998	upstream, upstream	0	1	1	20	22	26	1	4_A375_EGR1_1	28	Gene SNORD99	RBM20, SNORD99	small nucleolar RNA, C/D box 99	NR_003277		
GeneID:26976	SNORA91	1	28,906,276	28,906,403	129	-	2	2_A375_uNG7_glun_lncRNA_AR_1:.167, 3_A375_EGR1_1:.365	-2943, -1915	upstream, upstream	0	1	1	20	22	26	1	4_A375_EGR1_1	28	Gene SNORA91	ACA61, SNORA91	small nucleolar RNA, H/ACA box 91	NR_002967		
GeneID:26976	SNORA44	1	28,906,936	28,907,024	151	-	2	2_A375_uNG7_glun_lncRNA_AR_1:.167, 3_A375_EGR1_1:.365	-1424, -1298	upstream, upstream	0	1	1	20	22	26	1	4_A375_EGR1_1	28	Gene SNORA44	SNORA44, ACA44	small nucleolar RNA, H/ACA box 44	NR_002976		
GeneID:26976	SNORA16A	1	28,907,432	28,907,583	153	-	2	2_A375_uNG7_glun_lncRNA_AR_1:.167, 3_A375_EGR1_1:.365	-883, -755	upstream, upstream	0	1	1	20	22	26	1	4_A375_EGR1_1	28	Gene SNORA16A	SNORA16A, ACA16	small nucleolar RNA, H/ACA box 16A	NR_003053		
GeneID:5870	RAB42	1	28,916,712	28,921,066	2,356	+	1	2_A375_uNG7_glun_lncRNA_AR_1:.167	-10264	upstream	0	1	0	20	22	26	1	2_A375_uNG7_glun_lncRNA_AR_1	26	Gene RAB42	KIAA1509, MGC45598, Rab42	RAB42, member RAS oncogene family	NM_152304, NM_001193532, NCT19405A.4, NCT23459380.0	1553648_s_at	NP_689517.1, NP_001180481.1, EAX07694.1, EAX07693.1



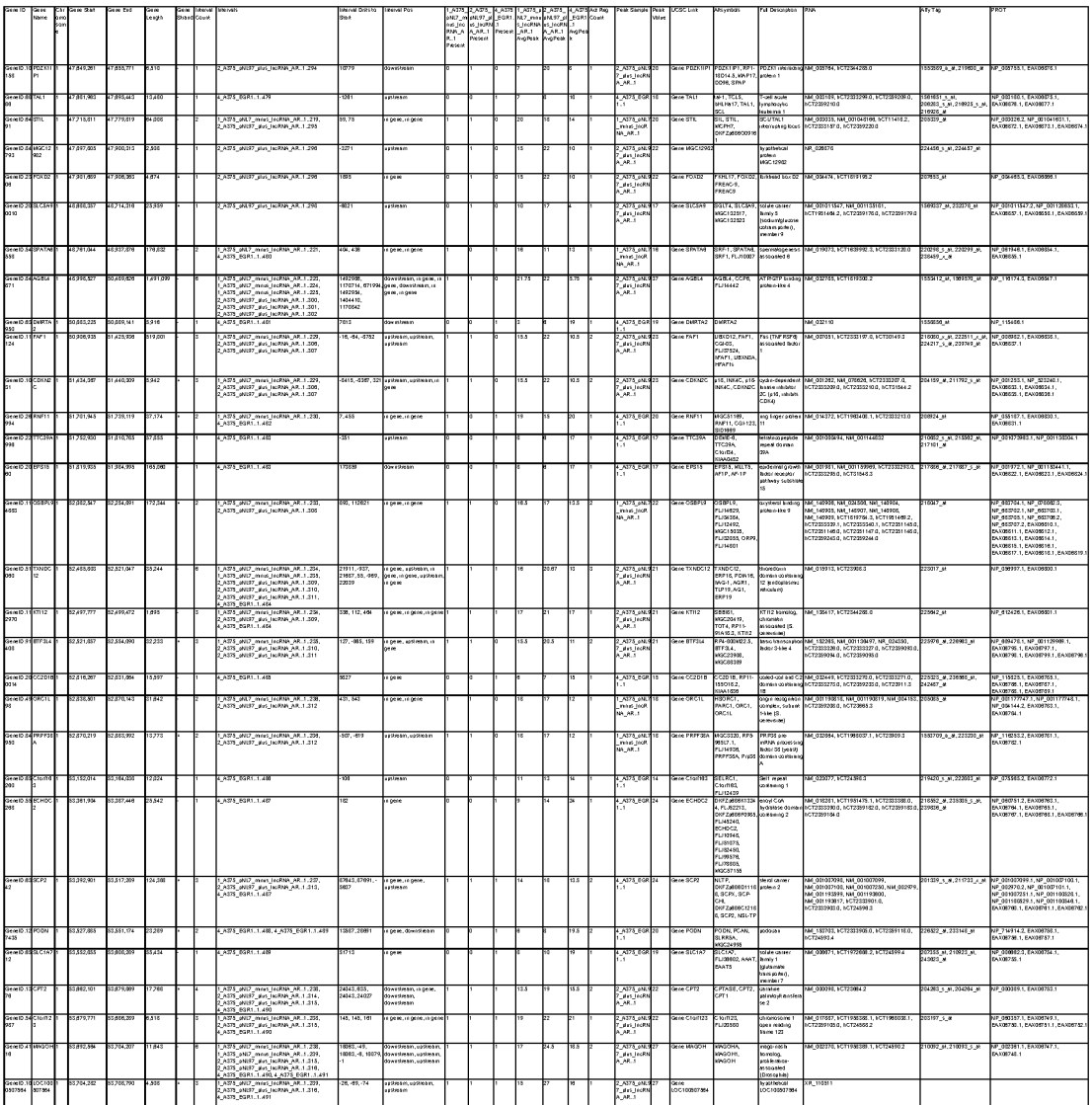
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	f_A375_2_A375_shN7_invitro_lncRNA_AR_1 Percent	f_A375_2_A375_shN7_shRNA_AR_1 Percent	f_A375_shN7_invitro_lncRNA_AR_1 Avg Peak	f_A375_shN7_shRNA_AR_1 Avg Peak	f_A375_EGR1_shRNA_AR_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:85033	TAF12	1	28,229,805	28,269,904	39,996	-	2	1_A375_shN7_invitro_lncRNA_AR_1:129, 2_A375_shN37_plus_lncRNA_AR_1:166	5485, -5340	upstream, upstream	1	1	0	26	23	13	1	1_A375_shN7_invitro_lncRNA_AR_1	326	Gene TAF12	TAF12, TAF12...	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa	NM_029544, NM_001132515, XM_011539335.2, XM_011540272.2, XM_017234084.1, XM_017234721.0	29485_s_at	NP_083523.1, NP_001126890.1, EAX07695.1, EAX07697.1...
GeneID:26191	RNU11	1	28,979,112	28,979,348	154	+	2	1_A375_shN7_invitro_lncRNA_AR_1:123, 2_A375_shN37_plus_lncRNA_AR_1:165	-46, -186	upstream, upstream	1	1	0	26	23	13	1	1_A375_shN7_invitro_lncRNA_AR_1	726	Gene RNU11	RNU11, U11	RNA, U11 small nuclear	NR_004407		
GeneID:10240	GABDB1	1	28,993,244	29,041,396	48,154	+	1	1_A375_shN7_invitro_lncRNA_AR_1:126	-100	upstream	1	0	0	21	16	11	1	1_A375_shN7_invitro_lncRNA_AR_1	721	GABDB1, PRPF, PRP8	gluconolactonase (pregluconolactonase) 1, TATA box binding protein 1	NM_024402, NM_006562, XM_017163938.2, XM_017162983.1, XM_017234290.0, XM_017235292.0	220935_s_at	NP_077005.1, NP_006570.2, EAX07676.1, EAX07677.1...
GeneID:53347	YTHDF2	1	29,060,103	29,096,367	36,264	+	2	1_A375_shN7_invitro_lncRNA_AR_1:125, 2_A375_shN37_plus_lncRNA_AR_1:169	131, 115	up gene, up gene	1	1	0	54	55	10	1	1_A375_shN7_invitro_lncRNA_AR_1	554	YTHDF2	YTHDF2, hYT-RNA2, HGRG8	YT521-B (human homolog, member 2	NM_016560, NM_001170126, NM_001170125, XM_017219623.1, XM_017219478.1, XM_017234299.0	217812_at, 222430_s_at	NP_057344.2, NP_001166599.1, NP_001166291.1, EAX07673.1...
GeneID:26270	EPB41	1	29,210,803	29,446,559	232,836	+	2	2_A375_shN37_plus_lncRNA_AR_1:170, 3_A375_DGR1:1.288	26, 233163	up gene, downstream	0	1	1	12	15	13	2	2_A375_shN37_plus_lncRNA_AR_1	620	Gene EPB41	EPB41, 4.1R, EL1, HE	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	NM_001199035, NM_203343, NM_001166006, NM_203342, NM_001166007, NM_004437, NM_001166008, XM_017219005.1, XM_017219007.1, XM_017234330.0, XM_017234331.0, XM_017234310.0	1554451_a_at, 227765_s_at, 229831_at, 214532_x_at, 229811_at	NP_001159777.1, NP_976316.1, NP_001159778.1, NP_001159779.1, NP_004428.1, NP_976317.1...
GeneID:84570	TMEM216	1	29,445,927	29,450,421	4,494	-	1	4_A375_DGR1:1.288	1663	up gene	0	0	1	11	10	10	1	4_A375_DGR1	13	Gene TMEM2038	MGC103866, MGC36409, TMEM2038, TTI38	trans-membrane protein 2038	NM_001033602, NM_001171690	227366_s_at	NP_001030812.1, NP_001165539.1
GeneID:84269	SPRSH	1	29,474,290	29,505,837	34,267	-	1	2_A375_shN37_plus_lncRNA_AR_1:171	210	up gene	0	1	0	14	24	13	1	2_A375_shN37_plus_lncRNA_AR_1	624	Gene SPRS4	SPRY3, SRSF4, SPRS4	sprouty homolog 4 (Drosophila)	NM_030628, XM_017439012.2, XM_017439950.0, XM_017451996.1	231696_at, 239311_s_at, 239312_at, 241043_at, 242027_at	NP_369117.2, EAX07666.1, EAX07667.1, EAX07669.1...
GeneID:51102	MECR	1	29,519,355	29,537,434	38,080	-	2	2_A375_shN37_plus_lncRNA_AR_1:172, 4_A375_DGR1:1.287	-66, 39838	upstream, up gene	0	1	1	8	10.5	14	2	2_A375_shN37_plus_lncRNA_AR_1	616	Gene MECR	C-SH3, NRBP1, PNDM28, MECR	mitochondrial trans-2-enoyl-CoA reductase	NM_016011, NM_001024732, XM_017431962.2, XM_017432989.1, XM_017433190.2	218864_at	NP_057093.2, NP_001019903.1, EAX07655.1, EAX07656.1...
GeneID:10376	PTPRU	1	29,565,026	29,653,323	90,297	+	1	2_A375_shN37_plus_lncRNA_AR_1:172	5305	upstream	0	1	0	12	15	12	1	2_A375_shN37_plus_lncRNA_AR_1	616	Gene PTPRU	SPTP-1, FLJ37530, PTP-Pi, PCP-2, PTP-Q, EPTP1, PTP-U, PTPRO, PTPRQ, R-PTP-PSI, PTPU2, PTPRU, PHI	protein tyrosine phosphatase, receptor type, U	NM_133176, NM_130177, NM_005704, NM_001198931, XM_017433979.1, XM_017434314.0, XM_017434315.0	211320_s_at	NP_579439.2, NP_570438.2, NP_005695.2, NP_001181931.1, EAX07666.1, EAX07651.1, EAX07652.1...
GeneID:84164	MINT	1	31,164,124	31,196,422	32,298	-	2	1_A375_shN7_invitro_lncRNA_AR_1:129, 2_A375_shN37_plus_lncRNA_AR_1:179	4965, 9380	up gene, upstream	1	1	0	16.5	16.5	10	2	1_A375_shN7_invitro_lncRNA_AR_1	620	Gene MINT1	C-MP, MINT1, CAT1d	intima 1, (s-fringe intra-) protein	NM_032779, XM_017439056.1, XM_017439424.1	209804_at, 209805_s_at	NP_116167.2, EAX07642.1
GeneID:10129198	LOC10012919	1	31,191,819	31,199,993	7,974	+	2	1_A375_shN7_invitro_lncRNA_AR_1:129, 2_A375_shN37_plus_lncRNA_AR_1:179	170, 14173	up gene, downstream	1	1	0	16.5	16.5	10	2	1_A375_shN7_invitro_lncRNA_AR_1	620	Gene LOC100129198	FLJ46197	hypothetical LOC100129198	NR_026102		
GeneID:57678	LNPTM2	1	31,205,313	31,230,863	25,550	-	0	1_A375_shN7_invitro_lncRNA_AR_1:130, 2_A375_shN37_plus_lncRNA_AR_1:179, 3_A375_shN37_plus_lncRNA_AR_1:100	938, 24891, 1019	up gene, up gene, up gene	1	1	0	22.5	22.5	6.5	2	1_A375_shN7_invitro_lncRNA_AR_1	622	Gene LNPTM2	FLJ46965, MGC129980, CLN7B, MGC129981, LAPTM5, FLJ46231	lysosomal pathway transmembrane 5	NM_030762, XM_017439082.0, XM_017439122.0	231702_s_at, 231721_s_at	NP_004748.1, EAX07640.1, EAX07641.1
GeneID:9469	SDC3	1	31,342,510	31,391,400	39,167	-	2	4_A375_DGR1:1.291, 4_A375_EGR1:1.292	938, -964	up gene, upstream	0	0	1	0	10.5	17.5	2	4_A375_EGR1	19	Gene SDC3	SYND3, SDC3N, SDC3	syndecan 3	NM_014654, XM_017235077.0, XM_017235078.0, XM_017234.2	1554064_a_at, 202260_at	NP_055469.3, EAX07637.1, EAX07638.1, EAX07639.1...
GeneID:79370	NKAIN1	1	31,892,592	31,912,704	20,142	-	3	1_A375_shN7_invitro_lncRNA_AR_1:132, 2_A375_shN37_plus_lncRNA_AR_1:165, 3_A375_DGR1:1.293	57542, 37470, 57795	up gene, up gene, up gene	1	1	1	27	26	16	1	1_A375_shN7_invitro_lncRNA_AR_1	627	Gene NKAIN1	NKAIN1, FAM77C, FLJ12690	Na/K+ transporting ATPase interacting 1	NM_024522, XM_017238068.0, XM_017238070.0	219438_at	NP_078792.2, EAX07625.1, EAX07626.1
GeneID:94274	SNRNP40	1	31,732,415	31,769,844	37,229	-	2	2_A375_shN37_plus_lncRNA_AR_1:166, 3_A375_DGR1:1.294	198, -404	up gene, upstream	0	1	1	11	19	16.5	2	2_A375_shN37_plus_lncRNA_AR_1	625	Gene SNRNP40	WDR57, 40K, HPRP40B, MGC1916, RP11-465O7.2, PRPF40B, PRP40B, SNRNP40, FLJ41105, SPF30	small nuclear ribonucleoprotein 40kDa (U5)	NM_004614, XM_017111153.2, XM_017236666.0	213503_s_at	NP_004605.2, EAX07626.1, EAX07627.1
GeneID:57535	ZCCHC17	1	31,769,542	31,837,760	67,936	+	2	2_A375_shN37_plus_lncRNA_AR_1:166, 4_A375_DGR1:1.294	-359, 206	upstream, up gene	0	1	1	11	19	16.5	2	2_A375_shN37_plus_lncRNA_AR_1	625	Gene ZCCHC17	HSPC251, ZCCHC17, PSI:Hs1p3_HUMAN, RP11-286O22.1	zinc finger, CCHC domain containing 17	NM_016535, XM_017111123, XM_017235564.1, XM_017236009.0, XM_017235011.0, XM_017235180.0	223107_s_at, 223108_s_at	NP_057619.2, EAX07621.1, EAX07622.1, EAX07623.1, EAX07624.1...
GeneID:7735	SERINC2	1	31,833,983	31,907,823	31,362	+	3	1_A375_shN37_plus_lncRNA_AR_1:133, 2_A375_shN37_plus_lncRNA_AR_1:167, 3_A375_DGR1:1.295	21413, 21297, 27845	up gene, up gene, downstream	1	1	1	13.5	15	12.5	2	2_A375_shN37_plus_lncRNA_AR_1	623	Gene SERINC2	SERINC2, TDE2L, PRO36891, TDE2, FKSG58, MGC90240	serine incorporator 2	NM_178865, XM_017111114, XM_017235932.1, XM_017234334.1, XM_017234332.0, XM_017234333.0, XM_017235180.0	224762_at	NP_849192.2, EAX07615.1, EAX07611.1, EAX07612.1, EAX07613.1, EAX07614.1...
GeneID:84679	TINAGL1	1	32,042,089	32,053,267	11,201	+	2	4_A375_DGR1:1.296, 4_A375_EGR1:1.297	438, 12282	up gene, downstream	0	0	1	8	10	10.5	2	4_A375_EGR1	19	Gene TINAGL1	ARG1, LCAT, LEG22, TINAGL1, TINAGRP	tubulointerstitial nephritis antigen-like 1	NM_022164, XM_017183998.1, XM_017234542.0, XM_017235434.0, XM_017235974.1, XM_017235972.2	219066_x_at	NP_071407.1, EAX07603.1, EAX07604.1, EAX07605.1...
GeneID:55276	PEF1	1	32,095,465	32,110,656	15,375	-	3	3_A375_shN7_invitro_lncRNA_AR_1:136, 4_A375_shN37_plus_lncRNA_AR_1:165, 5_A375_DGR1:1.296	435, 566, 502	up gene, up gene, up gene	1	1	1	21	33	27	1	2_A375_shN37_plus_lncRNA_AR_1	623	Gene PEF1	PEF1A, PEF1N, dbPEF2, PEF1	penta-EF-hand domain containing 1	NM_012392, NR_033656, NR_033655, XM_017183992.1, XM_017235194.2	217923_at	NP_036524.1, EAX07595.1, EAX07596.1
GeneID:1307	COL19A1	1	32,117,848	32,169,766	51,920	+	4	1_A375_shN7_invitro_lncRNA_AR_1:139, 2_A375_shN37_plus_lncRNA_AR_1:168, 3_A375_shN37_plus_lncRNA_AR_1:189, 4_A375_DGR1:1.295	69086, 69496, 14120, 59422	downstream, downstream, downstream, up gene, downstream	1	1	1	17	26.5	19.5	2	2_A375_shN37_plus_lncRNA_AR_1	623	Gene COL19A1	COL19A1, bA74A.1, FP1572	collagen, type XIX, alpha 1	NM_001858, XM_017234191.0, XM_017234193.0, XM_017235853.2	204345_at	NP_001844.3, EAX07593.1, EAX07596.1, EAX07597.1...
GeneID:5378	BAZ2	1	32,192,715	32,229,845	36,930	+	4	1_A375_shN7_invitro_lncRNA_AR_1:138, 2_A375_shN37_plus_lncRNA_AR_1:190, 3_A375_shN37_plus_lncRNA_AR_1:191, 4_A375_DGR1:1.400	4012, 45704, 40050, -592	downstream, downstream, downstream, upstream	1	1	1	22.67	25.67	10.33	3	2_A375_shN37_plus_lncRNA_AR_1	642	Gene BAZ2	BAZ2	bromodomain adjacent to zinc finger domain, 2B	NM_001753, XM_017183977.1, XM_017183978.1, XM_017184552.1, XM_017234183.0, XM_017234189.0, XM_017235674.0	204966_at	NP_001744.2, EAX07594.1, EAX07595.1, EAX07596.1, EAX07597.1...
GeneID:10168	MRPA23	1	32,224,261	32,224,339	79	+	1	4_A375_DGR1:1.400	-5934	upstream	0	0	1	12	14	10	1	4_A375_DGR1	10	Gene MRPA23	MRPA23a	mitoriboRAN 4234	NR_038218		
GeneID:9650	SPOCD1	1	32,256,025	32,281,360	25,335	-	2	1_A375_shN37_invitro_lncRNA_AR_1:133, 2_A375_shN37_plus_lncRNA_AR_1:192	27678, 27651	downstream, downstream	1	1	0	29	26	16	1	1_A375_shN7_invitro_lncRNA_AR_1	639	Gene SPOCD1	FLJ39000, RP11-89A19.1, SPOCD1, CXorf40	SPOC domain containing 1	NM_144589, XM_017236559.0, XM_017236976.0, XM_017236.4	1563415_a_at, 235417_at	NP_653170.2, EAX07668.1, EAX07687.1, EAX07688.1...
GeneID:5794	PTPN21	1	32,272,022	32,403,968	31,946	-	1	1_A375_shN7_invitro_lncRNA_AR_1:140	282	upstream	1	0	0	16	13	13	1	1_A375_shN7_invitro_lncRNA_AR_1	618	Gene PTPN21	DVU-1, PTPAN, PRL2, PTPCAN32, HM-2_chr N1b, pTPN32, N1s, PTPN2, HH15, PRL-2, HU-PP-1	protein tyrosine phosphatase type, non-receptor type, 21	NM_080391, NM_001193100, NM_001193101, XM_017234179.1, XM_017234177.1, XM_017234178.1, XM_017234179.1, XM_017234181.1, XM_017235077.4	208951_s_at, 208950_s_at, 208952_x_at, 208953_s_at	NP_536216.1, NP_001182029.1, NP_001182030.1, EAX07578.1, EAX07580.1, EAX07581.1, EAX07582.1, EAX07584.1...
GeneID:3387	TMEM238	1	32,335,933	32,365,467	29,564	+	3	1_A375_shN37_invitro_lncRNA_AR_1:141, 2_A375_shN37_plus_lncRNA_AR_1:193, 3_A375_shN37_plus_lncRNA_AR_1:194	-183, -231, 33161	upstream, upstream, downstream	1	1	1	17.3	20.3	11	2	2_A375_shN37_plus_lncRNA_AR_1	622	Gene TMEM238	FLJ43115, TMEM238	trans-membrane protein 238	NM_178036, XM_017234.586.0, XM_017235976.0, XM_017235979.0, XM_017235934.2	219770_s_at	NP_840126.2, EAX07572.1, EAX07573.1, EAX07574.1, EAX07575.1...
GeneID:2335	KPNA6	1	32,373,844	32,642,169	268,325	+	2	2_A375_shN37_plus_lncRNA_AR_1:142, 3_A375_shN37_plus_lncRNA_AR_1:194	73220, 20	downstream, up gene	1	1	0	13.5	16.5	12	2	2_A375_shN37_plus_lncRNA_AR_1	620	Gene KPNA6	KPNA7, KPNA6, FLJ11249, IPOA7, MGC17416	karyopherin alpha 6 (importin alpha 7)	NM_013316, XM_017235439.0, XM_017235934.0, XM_017235.2	212161_at, 212162_x_at, 212163_at, 226976_at	NP_036445.1, EAX07567.1, EAX07568.1, EAX07569.1...
GeneID:2770	TXLNA	1	32,845,343	32,880,899	35,541	+	3	1_A375_shN37_invitro_lncRNA_AR_1:142, 2_A375_shN37_plus_lncRNA_AR_1:195, 3_A375_shN37_plus_lncRNA_AR_1:401	519, 23743, 23657	up gene, downstream, downstream	1	2	1	16.3	18	24.3	2	4_A375_EGR1	31	Gene TXLNA	MGC11693, TXLNA, TXLNA, bA234.A11.6, dJ1, MGC116871, RP4-622L9.4	fibrinogen-like	NM_175932, XC7234972.0, XC7234972.0	1561358_at, 212050_at, 231169_at, 240729_at	NP_787945.1, EAX07566.1, EAX07566.1
GeneID:7960	CCDC28B	1	32,886,282	32,870,991	4,709	-	2	1_A375_shN37_invitro_lncRNA_AR_1:143, 4_A375_DGR1:1.401	4808, 9030	downstream, downstream	1	0	1	15	15	31	1	4_A375_EGR1	31	Gene CCDC28B	CCDC28B, MGC13031, MGC16441, RP4-622L9.5	coiled-coil domain containing 28B	NM_032498, XM_017183994.1, XC7233196.0	219583_at, 227972_s_at	NP_377272.2, EAX07565.1, EAX07564.1
GeneID:5381	IQCC	1	32,871,208	32,874,366	3,052	+	2	1_A375_shN37_invitro_lncRNA_AR_1:142, 4_A375_DGR1:1.401	-145, -4	upstream, upstream	1	0	1	15	15	31	1	4_A375_EGR1	31	Gene IQCC	FLJ10347, MGC102334.1, RP4-622L9.6, IQCC	IQ motif containing C	NM_018134, NM_001169342, XC7233966.2	208650_at	NP_060604.2, NP_001133514.1, EAX07562.1
GeneID:1478	DCDC2B	1	32,874,493	32,881,797	7,312	+	2	1_A375_shN37_invitro_lncRNA_AR_1:143, 4_A375_DGR1:1.401	-3907, -3482	upstream, upstream	1	0	1	15	15	31	1	4_A375_EGR1	31	Gene DCDC2B	DCDC2B	doublecortin domain containing 2B	NM_001079834	233916_at	NP_001072934.1
GeneID:8307	LOC100130	1	32,874,870	32,881,555	6,686	-	2	1_A375_shN37_invitro_lncRNA_AR_1:143, 4_A375_DGR1:1.401	9970, 9626	downstream, downstream	1	0	1	15	15	31	1	4_A375_EGR1	31	Gene LOC100507457		hypothetical LOC100507457	XR_110301, XR_110303		
GeneID:3866	C1orf91	1	32,881,795	32,887,928	6,134	-	1	1_A375_shN7_invitro_lncRNA_AR_1:143	10035	downstream	1	0	0	15	15	31	1	4_A375_EGR1	31	Gene C1orf91	KIAA1646, C1orf91, MGC13137, RP4-622L9.7, RP4-622L9, TMEM234, PRO1935, FLJ90779	ubiquitin-like with PHD and ring finger domains 1	NM_019116, XC7183997.1, XC7234175.0, XC7235237.0, XC7235923.0, XC7235923.0	223866_s_at, 223876_at, 234095_s_at	NP_061991.2, EAX07557.1, EAX07558.1, EAX07559.1, EAX07560.1...
GeneID:8670	EIF3I	1	32,887,971	32,897,305	9,334	+	2	1_A375_shN37_plus_lncRNA_AR_1:144, 2_A375_shN37_plus_lncRNA_AR_1:195	13817, 13949	downstream, downstream	1	1	0	20	16	16	1	1_A375_shN37_plus_lncRNA_AR_1	620	Gene EIF3I	EIF3S2, EIF3, TRIP1, EIF3S2, MTG16-2, MTG-16, WAIT-2, TRIP-1	eukaryotic translation initiation factor 3, subunit I	NM_003757, XC7183992.1, XC7182976.2, XC7182990.2	200756_at	NP_003746.1, EAX07555.1, EAX07552.1, EAX07553.1, EAX07554.1...
GeneID:8477	FAM167B	1	32,712,818	32,714,461	1,643	+	1	4_A375_DGR1:1.402	3384	downstream	0	0	1	7	11	22	1	4_A375_EGR1	22	Gene FAM167B	MGC10820, FAM167B, C1orf60	family with sequence similarity 167, member B	NM_032846, XC7234988.0, XC7182996.2	223837_at	NP_116372.2, EAX07547.1, EAX07548.1
GeneID:3932	LCK	1	32,716,540	32,751,766	34,926	+	5	2_A375_shN37_plus_lncRNA_AR_1:196, 3_A375_DGR1:1.402, 4_A375_EGR1:1.403	4084, -166, 41030	downstream, upstream, downstream	0	0	1	12	13.5	21	2	4_A375_EGR1	22	Gene LCK	LSK, p56lck, pMGC, LCK, YT16	lymphocyte-specific protein tyrosine kinase	NM_005356, NM_001042771, XC7193995.1, XC7234.571.0, XC7234.573.0, XC7234.574.0, XC7235051.3	204890_s_at, 204891_s_at	NP_005347.5, NP_001030238.1, EAX07542.1, EAX07544.1, EAX07545.1, EAX07546.1...
GeneID:3014	HDAC1	1	32,737,705	32,799,324	41,619	+	3	2_A375_shN37_plus_lncRNA_AR_1:196, 3_A375_DGR1:1.403, 4_A375_EGR1:1.404	196, 132, 48004	up gene, up gene, downstream	0	1	1	14	14.3	16.5	2	2_A375_shN37_plus_lncRNA_AR_1	620	Gene HDAC1	HDAC1, GON-10, SNT2a6SH1220, RPD3, RPD3L1, HD1	histone deacetylase 1	NM_004964, XC7234.570.0, XC7182982.3	230209_at	NP_004.553.2, EAX07541.1, EAX07540.1
GeneID:8554	MARCKS	1	32,799,440	32,801,854	2,394	+	1	4_A375_DGR1:1.404	1676	upstream	0	0	1	11	9	17	1	4_A375_EGR1	17	Gene MARCKS1	MLP1, FLJ41.4.1R, MACMARCKS, MARCKS1, MRP, MLP	MARCKS-like 1	NM_023009, XC7182996.1, XC7181.6892.1, XC7234.182.0	200944_at	NP_375335.1, EAX07537.1, EAX07538.1, EAX07539.1
GeneID:1005	LOC100130071	1	32,826,071	32,827,944	973	-	1	2_A375_shN37_plus_lncRNA_AR_1:197	10372	downstream	1	0	0	13	20	15	1	2_A375_shN37_plus_lncRNA_AR_1	620	Gene LOC100129071		hypothetical LOC100130071	NR_001167678		NP_001161148.1
GeneID:5330	BSDC1	1	32,830,764	32,860,992	29,956	+	1	2_A375_shN37_plus_lncRNA_AR_1:198	294	up gene	0	1	0	15	20	11	1	2_A375_shN37_plus_lncRNA_AR_1	620	Gene BSDC1	DKFZp686B0310, BSDC1, FLJ10278	BSD domain containing 1	NM_018045, NM_001143993, NM_001143989, NM_001143990, XC7196622.1, XC7197.1330.1, XC7197.1331.1, XC7239093.0, XC7239092.0, XC7239.3	1559771_at, 218804_at, 222350_s_at	NP_060115.3, NP_001137093.1, NP_001137091.1, NP_001137092.1, EAX07526.1, EAX07529.1...
GeneID:5351	KIAA1522	1	33,207,512	33,240,871	33,359	+	1	4_A375_DGR1:1.408	29104	up gene	0	0	0	8	9	24	1	4_A375_DGR1	24	Gene KIAA1522	KIAA1522		NM_020955, XC7196.14.25.3, XC7234.722.0	224748_at	NP_065998.2, EAX07509.1, EAX07510.1
GeneID:8565	YARS	1	33,240,540	33,265,853	42,793	-	4	1_A375_shN37_invitro_lncRNA_AR_1:145, 2_A375_shN37_plus_lncRNA_AR_1:199, 3_A375_shN37_plus_lncRNA_AR_1:405, 4_A375_EGR1:1.408	657, 657, 43817, 788	up gene, up gene, downstream, up gene	1	1	1	37	37.5	30.5	2	2_A375_shN37_plus_lncRNA_AR_1	638	Gene YARS	YTS, YRS, YARS, CMTDC, TYRAS	tyrosyl-tRNA synthetase	NM_003680, XC7234127.0, XC7234134.0, XC7235413.0	213245_s_at, 235765_at	NP_003671.1, EAX07511.1, EAX07508.1, EAX07507.1
GeneID:7864	S100PBP	1	33,283,176	33,224,478	41,303	+	3	2_A375_shN37_invitro_lncRNA_AR_1:143, 3_A375_shN37_plus_lncRNA_AR_1:199, 4_A375_DGR1:1.408	-200, -300, -312	upstream, upstream, upstream	1	1	1	66	68	17	1	4_A375_EGR1	18	Gene S100PBP	S100PBP, FLJ12855, S100PBPR, DKFZp761G2325	S100P binding protein	NM_022753, NM_001017436, XC7233726.0, XC7234727.0, XC7235940.2	216370_s_at, 222810_at	NP_073590.2, NP_001070436.1, EAX07501.1, EAX07502.1...
GeneID:3315	HPCA	1	33,332,096	33,360,347	6,149	+	1	4_A375_DGR1:1.407	-399	upstream	0	0	1	9	8	19	1	4_A375_EGR1	19	Gene HPCA	HPCA, BDR2	hippocalcin	NM_002142, XC7234729.0, XC7234730.0, XC7234722.0, XC7234733.0, XC7234734.0	205434_at	NP_002134.2, EAX07494.1, EAX07495.1, EAX07496.1, EAX07497.1, EAX07498.1
GeneID:1563	TMEM45B	1	33,360,196	33,366,953	6,757	-	1	4_A375_DGR1:1.407	13241	downstream	0	0	1	9	8	19	1	4_A375_EGR1	19	Gene TMEM45A	MGC10137, CAC1, BCJP, CAC-1, TMEM45A	trans-membrane protein 34	NM_033554, XC7233126.0, XC7235026.0	223336_at	NP_277036.1, EAX07492.1, EAX07493.1
GeneID:5744	RNF199	1	33,402,030	33,430,268	28,238	+	1	2_A375_shN37_plus_lncRNA_AR_1:200	6342	upstream	0	1	0	9	17	8	1	2_A375_shN37_plus_lncRNA_AR_1	617	Gene RNF199	ERGC3, RNF199, FLJ90003, SKUAH	exp ingor protein 199	NM_183241, NM_001127581, XC7239216.0, XC7235217.0, XC7239.43.2	213035_at, 36596_at	NP_899172.2, NP_001120023.1, EAX07488.1, EAX07489.1, EAX07491.1
GeneID:3431	ADC	1	33,546,714	33,555,953	29,281	+	4	1_A375_shN37_invitro_lncRNA_AR_1:148, 2_A375_shN37_plus_lncRNA_AR_1:201, 3_A375_shN37_plus_lncRNA_AR_1:202, 4_A375_DGR1:1.408	48048, 16598, 48048, 104	downstream, up gene, downstream, up gene	1	1	1	37.67	40.33	11.67	3	2_A375_shN37_plus_lncRNA_AR_1	614	Gene ADC	AZ2, ODC11, ADCA1, ADC, ODC-y	arginine decarboxylase	NM_052998, XC7193.4.021.1, XC7234739.0, XC7234741.0, XC7234742.0, XC7234743.0, XC7234747.0, XC7239170.0, XC7239173.0, XC7239174.0, XC7239176.0, XC7239176.0, XC7239177.0, XC7239.27.3	1554393_a_at, 209300_at	NP_437214.1, EAX07481.1, EAX07482.1, EAX07483.1, EAX07484.1, EAX07485.1, EAX07486.1, EAX07487.1, EAX07488.1, EAX07472.1, EAX07473.1, EAX07474.1, EAX07476.1, EAX07477.1, EAX07478.1, EAX07479.1, EAX07480.1, EAX07482.1
GeneID:8355	TRIM62	1	33,811,003	33,847,871	36,868	-	1	2_A375_shN37_plus_lncRNA_AR_1:203	29639	up gene	0	1	0	14	15	9	1	2_A375_shN37_plus_lncRNA_AR_1	615	Gene TRIM62	FLJ10799, FLJ16555, TRIM62, DKFZp	tripartite motif-containing 62	NM_016207, XC7234112.0, XC7234113.0, XC7236036.3	219272_at, 236563_at, 56338_at	NP_057291.2, EAX07465.1, EAX07466.1, EAX07467.1

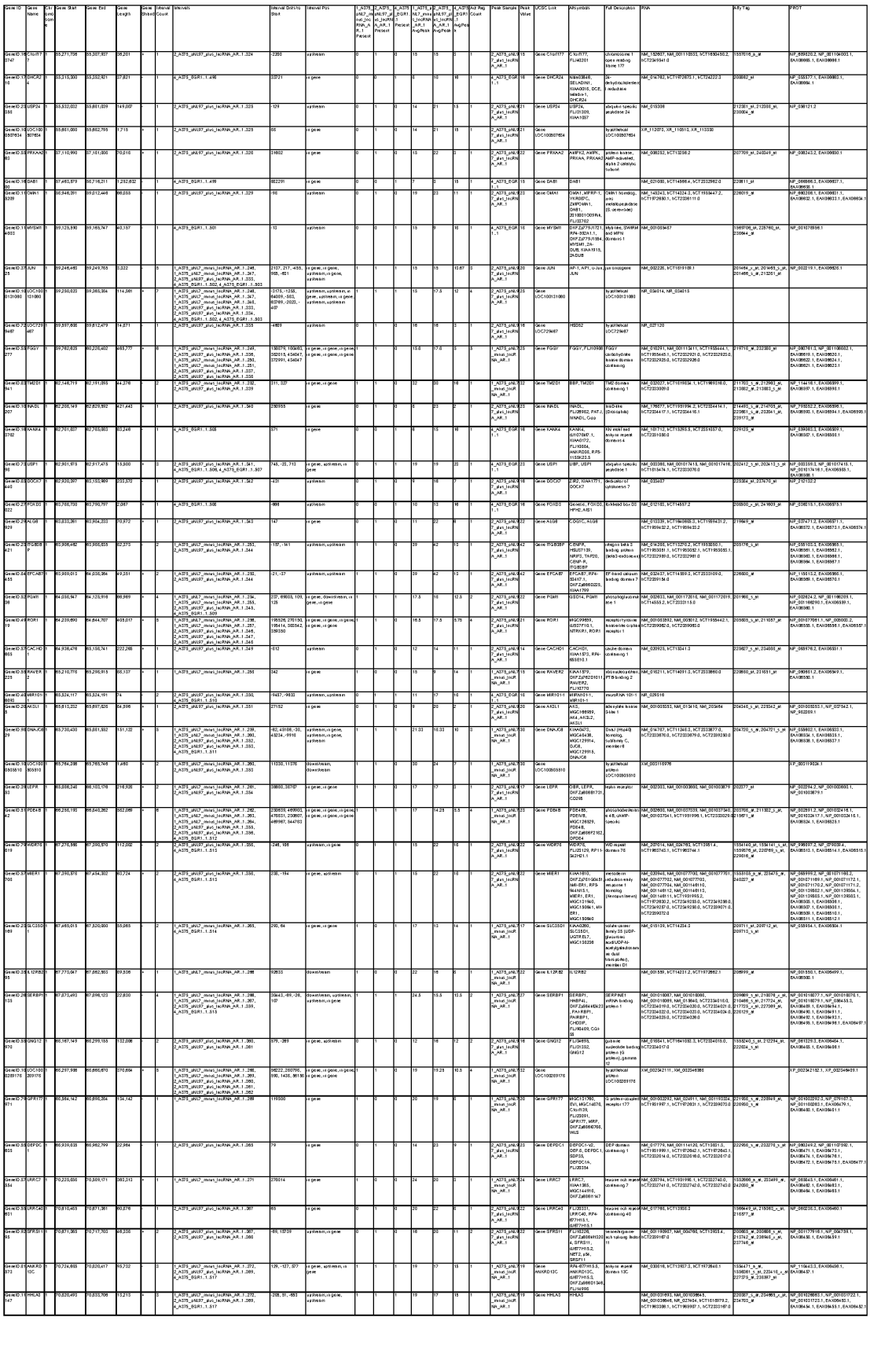




Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_DMSO_vs_ALK_1_Percent	2_A375_DMSO_vs_ALK_1_Percent	4_A375_EGFR_1_Percent	1_A375_plncRNA_ALK_1_Avg Peak	2_A375_plncRNA_ALK_1_Avg Peak	4_A375_EGFR_1_Avg Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
GeneID:2318	MKCF1	1	39,547,115	39,552,769	5655	+	2	4_A375_EGR1_1.437:4_A375_EGR1_1.438	229250, 552495	sr:gene,sr:gene	0	0	1	4	6	15	2	4_A375_EGR1_1.1	17	Gene MKCF1	FLI46778, KIAA0483, MKCF1, sMKCF, FLI46812, KIAA1291, OFCA, KCF7, MPH20	microtubule-actin crosslinking factor	NM_033044, NM_012093, XC72333579.3, XC72333580.0, XC72333581.0, XC72333582.0, XC72333583.0, XC72333584.0, XC72333585.0, XC72333586.0, XC72333587.0, XC72333588.0, XC72333589.0, XC72333590.0, XC72333591.0, XC72333592.0	1553407_at_207355_x_at, 209803_s_at_209804_x_at, EAX72724.1, EAX07019.1, EAX72726.1, EAX07282.1, 214894_x_at_213222_x_at, EAX72727.1, EAX07019.1, EAX72728.1, EAX07286.1, EAX07281.1	NP_149353.2, NP_006222.3, EAX72724.1, EAX07019.1, EAX72726.1, EAX07282.1, EAX72727.1, EAX07019.1, EAX72728.1, EAX07286.1, EAX07281.1
GeneID:84	RAW3760	1	39,675,176	39,682,184	6976	+	1	4_A375_EGR1_1.439	-908	upstream	0	0	1	7	7	17	1	4_A375_EGR1_1.1	17	Gene RAW3794	FLI42354, RAW3794	RAW3794	NM_019035	213260_at	NP_835553.1
GeneID:87	PABPC4	1	40,036,453	40,042,321	18,008	-	2	1_A375_plnX7_mrna1_lncRNA_AR_1.177:2_A375_plnX7_gtuc_lncRNA_AR_1.242	-231, -231	upstream, upstream	1	1	0	16	20	4	1	2_A375_plnX7_gtuc_lncRNA_AR_1	20	Gene PABPC4	PABPC4, PABP4, APP1, iPABP, FLI42535, hPP1	polyA(+) binding protein, cytoplasmic-4 (inducible form)	NM_001136553, NM_003819, NM_001135984, XC72333944.0, XC72333945.0, XC72333946.0, XC72333947.0, XC72333948.0, XC72333949.0, XC72335930.0, XC72335171.0	201984_s_at	NP_001129125.1, NP_003810.1, NP_001129126.1, EAX07281.1, EAX72784.1, EAX07283.1, EAX72785.1, EAX07283.1, EAX72787.1
GeneID:10	LOC1003	0	40,039,769	40,039,873	5,105	+	2	1_A375_plnX7_mrna1_lncRNA_AR_1.177:2_A375_plnX7_gtuc_lncRNA_AR_1.242	11993, 11963	downstream, downstream	1	1	0	16	20	4	1	2_A375_plnX7_gtuc_lncRNA_AR_1	20	Gene LOC100809950	hypothetical LOC100809950	XR_112387, XR_110900, XR_113345		
GeneID:87	SNORA5	5	40,032,045	40,033,162	1118	+	2	1_A375_plnX7_mrna1_lncRNA_AR_1.177:2_A375_plnX7_gtuc_lncRNA_AR_1.242	-8972, -8930	upstream, upstream	1	1	0	16	20	4	1	2_A375_plnX7_gtuc_lncRNA_AR_1	20	Gene SNORA55	RCA55, SNORA55	small nucleolar RNA, H/ACA box 55	NR_002953		
GeneID:10	LOC1003	0	40,264,854	40,265,943	1,089	+	1	1_A375_plnX7_mrna1_lncRNA_AR_1.178	10308	downstream	1	0	0	16	12	7	1	1_A375_plnX7_lncRNA_AR_1	16	Gene LOC100287427	hypothetical protein LOC100287427	XM_002342076, XM_002312598		XP_002342117.1, XP_002129434.1
GeneID:54	TRIT1	1	40,306,765	40,349,177	42,474	-	2	2_A375_plnX7_gtuc_lncRNA_AR_1.243:2_A375_EGR1_1.439	57, 261	sr:gene,sr:gene	0	1	1	14	21	16	1	2_A375_plnX7_gtuc_lncRNA_AR_1	21	Gene TRIT1	MOD5, MGC142263, FLJ20081, MGC142262, TRIT1, IPT	tRNA isopentenyltransferase 1	NM_017646, XC71957526.1, XC78901.3	219917_at	NP_060116.2, EAX07252.1, EAX07253.1
GeneID:64	HIP55[2	A	40,429,784	40,435,805	14,844	+	3	2_A375_plnX7_gtuc_lncRNA_AR_1.244:4_A375_EGR1_1.440:4_A375_EGR1_1.441	272, 136, 1186	sr:gene,sr:gene,sr:gene	0	1	1	10	12	17.5	2	4_A375_EGR1_1.1	18	Gene HIP55[A	FLI46746, HIP55[2A, FLJ39164, HIP55[2	integrin facilitator superfamily domain-containing 2A	NM_032793, NM_001139419, XC71834823.2, XC72336933.0, XC72359181.0, XC72359182.0	1553599_at, 223018_at	NP_116162.2, NP_001129553.1, EAX07246.1, EAX07247.1, EAX07248.1, EAX07249.1
GeneID:85	RLF	1	40,627,241	40,706,591	79,350	+	3	1_A375_plnX7_mrna1_lncRNA_AR_1.179:2_A375_plnX7_gtuc_lncRNA_AR_1.245:3_A375_EGR1_1.442	-1, -1, 479	upstream, upstream, sr:gene	1	1	1	22	26	19	1	2_A375_plnX7_gtuc_lncRNA_AR_1	20	Gene RLF	RLF_ZN151, MGC142226, ZNF925	rearranged L-myc fusion	NM_012421, XC78699.3	204243_at	NP_036353.2, EAX07256.1
GeneID:12	TMCO2	1	40,712,370	40,717,393	5,792	+	3	2_A375_plnX7_mrna1_lncRNA_AR_1.180:2_A375_plnX7_gtuc_lncRNA_AR_1.246:2_A375_EGR1_1.443	10233, 10331, 10299	downstream, downstream, downstream	1	1	1	26	26	17	1	1_A375_plnX7_lncRNA_AR_1	26	Gene TMCO2	TMCO2, dJ392G22.2, MGC131703	transmembrane and coiled-coil domains 2	NM_031300[40], XC71815123.1	231264_at	NP_001030740.1, EAX07255.1
GeneID:10	ZMPST	1	40,723,730	40,739,696	36,123	+	3	1_A375_plnX7_mrna1_lncRNA_AR_1.180:2_A375_plnX7_gtuc_lncRNA_AR_1.246:2_A375_EGR1_1.443	123, 171, 139	sr:gene,sr:gene,sr:gene	1	1	1	26	26	17	1	1_A375_plnX7_lncRNA_AR_1	26	Gene ZMPSTE24	FACE1, FRO1, FACE1, FLI14965, ZMPSTE24, Ste24a, HGPS, STE24	zinc metalloproteidase (STE24 homolog, S. cerevisiae)	NM_005857, XC72336014.0, XC78274.2	202939_at	NP_005846.2, EAX07253.1, EAX07254.1
GeneID:10	LOC1003	0	40,839,555	40,872,943	33,190	-	3	1_A375_plnX7_mrna1_lncRNA_AR_1.181:2_A375_plnX7_gtuc_lncRNA_AR_1.247:2_A375_EGR1_1.444	52564, 32085, 19857	sr:gene,sr:gene,sr:gene	1	1	1	13	11	11.5	2	1_A375_plnX7_lncRNA_AR_1	16	Gene LOC100259955	hypothetical LOC100259955	CR_112056, XR_110501, XR_113346		
GeneID:84	SWAP72	1	40,839,730	40,868,994	29,265	+	3	1_A375_plnX7_mrna1_lncRNA_AR_1.181:2_A375_plnX7_gtuc_lncRNA_AR_1.247:2_A375_EGR1_1.444	291, 732, 14120	sr:gene,sr:gene,sr:gene	1	1	1	13	11	11.5	2	1_A375_plnX7_lncRNA_AR_1	16	Gene SWAP2	SWAP2, RP1-89B10.1, SWAP1L	small ArfGAP2	NM_032733, XC71969926.1, XC72359246.0, XC72359249.0	223262_at	NP_076370.1, EAX07220.1, EAX07221.1, EAX07222.1
GeneID:86	ZNF643	1	40,916,337	40,929,390	13,053	+	1	2_A375_plnX7_gtuc_lncRNA_AR_1.245	-466	upstream	0	0	1	14	23	9	1	2_A375_plnX7_gtuc_lncRNA_AR_1	23	Gene ZNF643	RP11-89B10.1, ZNF643, FLI56293	zinc finger protein 643	NM_022078, XC71969928.1, XC72359010.0, XC72359247.0, XC76977.3	220719_at	NP_075355.2, EAX07219.1, EAX72716.1, EAX07217.1, EAX72718.1
GeneID:33	ZNF842	1	40,943,302	40,962,013	18,713	+	1	1_A375_plnX7_mrna1_lncRNA_AR_1.182	-196	upstream	1	0	0	17	13	8	1	1_A375_plnX7_lncRNA_AR_1	17	Gene ZNF842	ZNF842, FLI16030, ZNF842, RP11-466D10.2	zinc finger protein 842	NM_178494, XC71839588.3	1569107_i_at	NP_840358.2, EAX07215.1
GeneID:84	DENR	1	40,974,435	40,992,225	17,791	+	2	1_A375_plnX7_mrna1_lncRNA_AR_1.183:2_A375_plnX7_gtuc_lncRNA_AR_1.249	-49, 139	upstream, sr:gene	1	1	0	21	16	17	1	1_A375_plnX7_mrna1_lncRNA_AR_1	21	Gene DENR	FLI15165, Eca V-like, C1orf178, DENR, FLI11445, FLI21144	defects in initiation/biology 1 homolog (S. cerevisiae)	NM_032774, XC71814681.1, XC71969751.1, XC71969774.3, XC72359377.0	210587_s_at_223902_s_at	NP_075811.1, EAX07214.1, EAX07215.1, EAX07211.1, EAX07212.1, EAX07213.1
GeneID:12	ZNF664	1	40,997,233	41,010,041	16,808	+	1	2_A375_plnX7_gtuc_lncRNA_AR_1.250	127	sr:gene	0	1	0	9	21	9	1	2_A375_plnX7_gtuc_lncRNA_AR_1	21	Gene ZNF664	ZNF664, MGC27486	zinc finger protein 664	NM_152373, XC71839612, XC72359955.0	232365_at_244356_x_at	NP_689566.2, EAX07205.1, EAX07206.1
GeneID:37	RIMS3	1	41,086,332	41,131,324	44,972	-	1	2_A375_plnX7_gtuc_lncRNA_AR_1.251	59420	sr:gene	0	1	0	17	19	11	1	2_A375_plnX7_gtuc_lncRNA_AR_1	19	Gene RIMS3	RIMS3, KIAA0237, RIMS3_NH2	regulating synaptic membrane exocytosis 3	NM_014747, XC71827662.2, XC71967774.1	204720_at_210991_i_at	NP_055562.2, EAX07209.1, EAX72297.1
GeneID:10	LOC1003	1	41,154,752	41,157,903	3,151	-	1	2_A375_plnX7_gtuc_lncRNA_AR_1.252	320	sr:gene	0	1	0	12	21	16	1	2_A375_plnX7_gtuc_lncRNA_AR_1	21	Gene LOC100130357	hypothetical LOC100130357	NR_026357		
GeneID:48	NFYC	1	41,157,242	41,237,373	80,131	+	1	2_A375_plnX7_gtuc_lncRNA_AR_1.252	190	sr:gene	0	1	0	12	21	16	1	2_A375_plnX7_gtuc_lncRNA_AR_1	21	Gene NFYC	HTF3A, HAP5, NFYC, NF-YC, CBF-C, DKFZp667G2420, CBFC, HSM, CBFC	nuclear transcription factor-Y, gamma	NM_014223, NM_001142697, NM_001142698, NM_001142699, NM_001142700, NM_001142701, XC71988143.1, XC71988196.1, XC72359412.0, XC72359112.0, XC72359113.0	1555762_s_at, 1559210_i_at, 1559210_i_at_202215_s_at_202216_x_at_211231_x_at_211797_i_at, 226201_at	NP_853639.2, NP_001138699.1, NP_001138698.1, NP_001138700.1, NP_001138701.1, NP_001138702.1, EAX07260.1, EAX07261.1, EAX07262.1, EAX07263.1
GeneID:91	KCNQ4	1	41,249,864	41,306,124	56,260	+	3	1_A375_plnX7_mrna1_lncRNA_AR_1.446:4_A375_EGR1_1.446:4_A375_EGR1_1.447	54555, 45486, 54220	sr:gene,sr:gene,sr:gene	0	0	1	5.67	10.33	21.67	3	4_A375_EGR1_1.1	23	Gene KCNQ4	DFNA2, KV7.4, DFNA2A, KCNQ4	potassium voltage-gated channel, KQT-like subfamily, member 4	NM_004700, NM_172163, XC71839612.2, XC72334980.0	221805_at_243209_at	NP_004691.2, NP_751896.1, EAX07196.1, EAX07197.1
GeneID:13	CTPS	1	41,445,097	41,476,255	33,226	+	2	2_A375_plnX7_gtuc_lncRNA_AR_1.253:2_A375_EGR1_1.448	145, 495	sr:gene,sr:gene	0	1	1	16	16	15	1	2_A375_plnX7_gtuc_lncRNA_AR_1	16	Gene CTPS	CTPS	hypothetical LOC100130357	NM_001905, XC71839862.2, XC72359116.0	202613_at	NP_001896.2, EAX07193.1, EAX72180.1
GeneID:39	HIVEP3	1	41,975,864	42,264,499	288,812	-	10	2_A375_plnX7_gtuc_lncRNA_AR_1.254:2_A375_plnX7_mrna1_lncRNA_AR_1.163:1_A375_plnX7_mrna1_lncRNA_AR_1.169:1_A375_plnX7_mrna1_lncRNA_AR_1.167:1_A375_plnX7_mrna1_lncRNA_AR_1.168:1_A375_plnX7_mrna1_lncRNA_AR_1.169:1_A375_plnX7_mrna1_lncRNA_AR_1.255:1_A375_plnX7_mrna1_lncRNA_AR_1.256:1_A375_plnX7_mrna1_lncRNA_AR_1.257:1_A375_plnX7_mrna1_lncRNA_AR_1.258	49639, 153844, 188224, 71973, 48826, 1936, 188272, 107472, 67104, 264	sr:gene,sr:gene,sr:gene,sr:gene,sr:gene,sr:gene,sr:gene	1	1	0	16.69	16.13	5.25	6	1_A375_plnX7_lncRNA_AR_1	32	Gene HIVEP3	KRC, Schnurri-3, FLI16752, KIAA1555, KRC1, HIVEP3, ZNF40C, HIVEP3_ZAS3	human immunodeficiency virus type I enhancer binding protein 3	NM_024503, NM_001127714, XC71827034.1, XC72359422.0	1555762_s_at, 1559210_i_at, 1559210_i_at_202215_s_at_202216_x_at_211231_x_at_211797_i_at, 226201_at	NP_073730.2, NP_001121189.1, EAX07192.1
GeneID:10	LOC1003	1	42,312,890	42,337,890	25,000	+	3	1_A375_plnX7_mrna1_lncRNA_AR_1.187:1_A375_plnX7_mrna1_lncRNA_AR_1.193:1_A375_plnX7_mrna1_lncRNA_AR_1.257	23087, 1922, 20490	downstream, sr:gene, sr:gene	1	1	0	16	13.67	3.33	1	1_A375_plnX7_lncRNA_AR_1	21	Gene LOC100507166	hypothetical LOC100507166	XR_112084, XR_110903, XR_113346		
GeneID:22	FOXJ2	1	42,842,210	42,850,903	158,693	+	1	2_A375_plnX7_gtuc_lncRNA_AR_1.260	-153	upstream	0	1	0	14	23	17	1	2_A375_plnX7_gtuc_lncRNA_AR_1	23	Gene FOXJ2	MGC179995, FOXJ2, MGC179995	forkhead box J2	NM_012367, XC71839512.2, XC72335497.0, XC72335471.0, XC72359140.0, XC72359142.0	206015_s_at_215010_s_at	NP_036762.1, EAX07164.1, EAX07165.1, EAX07166.1, EAX07167.1, EAX07168.1
GeneID:28	RMRL1	1	42,846,468	42,849,900	43,432	+	2	1_A375_plnX7_gtuc_lncRNA_AR_1.191:2_A375_plnX7_gtuc_lncRNA_AR_1.261	-780, -772	upstream, upstream	1	1	0	16	19	9	1	2_A375_plnX7_gtuc_lncRNA_AR_1	19	Gene RMRL1A	RMRL1A, NANOS2, MGC47819, FNM92A	abnormal oncofibrosis ankle-1 ankle family member A	NM_173842, XC71839231.1	233948_at	NP_776113.2, EAX07161.1
GeneID:84	ZMYND1	2	42,896,030	42,921,908	25,878	-	2	2_A375_plnX7_gtuc_lncRNA_AR_1.262:2_A375_EGR1_1.449	-302, -302	upstream, upstream	0	1	1	14	22	22	1	2_A375_plnX7_gtuc_lncRNA_AR_1	22	Gene ZMYND12	DHFZ-ah342k23.3, ZMYND12	zinc finger, MYND type containing 12	NM_032237, NM_001146192, XC71439[3.3, XC71965146.1	223608_at	NP_115933.3, NP_001139664.1, EAX07189.1, EAX07190.1
GeneID:79	PPCS	1	42,922,175	42,926,956	3,910	+	2	2_A375_plnX7_gtuc_lncRNA_AR_1.262:2_A375_EGR1_1.449	67, 67	sr:gene,sr:gene	0	1	1	14	22	22	1	2_A375_plnX7_gtuc_lncRNA_AR_1	22	Gene PPCS	MGC117387, PPCS, MGC139220, FLI11535	phosphopantothenoylcysteine synthetase	NM_024564, NM_001077417, XC72346268.0	218241_at	NP_078940.2, NP_001070915.1, EAX07195.1
GeneID:10	LOC1003	1	42,930,937	42,939,800	10,131	+	2	2_A375_plnX7_gtuc_lncRNA_AR_1.262:2_A375_EGR1_1.449	-6717, -6717	upstream, upstream	0	1	1	14	22	22	1	2_A375_plnX7_gtuc_lncRNA_AR_1	22	Gene LOC100507214	hypothetical LOC100507214	XR_112083, XR_110904, XR_113349		
GeneID:23	CCDC3	1	43,000,980	43,120,355	119,375	+	4	1_A375_plnX7_mrna1_lncRNA_AR_1.192:1_A375_plnX7_mrna1_lncRNA_AR_1.193:2_A375_plnX7_gtuc_lncRNA_AR_1.265:1_A375_EGR1_1.450	-4764, 123445, 125852, 122725	upstream, downstream, downstream, downstream	1	1	1	24.5	22.5	11	2	1_A375_plnX7_mrna1_lncRNA_AR_1	29	Gene CCDC30	PTD01, CCDC30, FLI30772, PTD001	coiled-coil domain containing 30	NM_031030[30]	221101_at_230977_at	NP_001074116.1
GeneID:10	PPH	1	43,124,046	43,142,429	18,383	+	3	1_A375_plnX7_mrna1_lncRNA_AR_1.192:2_A375_plnX7_gtuc_lncRNA_AR_1.265:2_A375_EGR1_1.450	-45, 144, 242	upstream,sr:gene,sr:gene	1	1	1	20	22	20	1	2_A375_plnX7_gtuc_lncRNA_AR_1	22	Gene PPIH	USH-CYP, MGC3016, SnuCyp-20, CYP-20, PPIH, CYPH	ataxia/polyvalent vaccine H	NM_006347, XC71839212.2, XC71962548.1, XC71963347.1, XC71963348.1, XC71963349.1, XC71967680.1	204228_at, 238142_at	NP_006338.1, EAX07182.1, EAX07183.1, EAX07184.1, EAX07185.1, EAX07186.1, EAX72154.1
GeneID:10	CLDN19	1	43,195,764	43,205,923	7,161	-	1	1_A375_plnX7_mrna1_lncRNA_AR_1.451	37	sr:gene	0	0	1	2	7	16	1	1_A375_plnX7_lncRNA_AR_1	16	Gene CLDN19	CLDN19	claudin 19	NM_148960, NM_001122593, NM_001165117, XC71427[0.4, XC72344[4.0	1552553_at, 1554594_s_at, 1554603_at	NP_683763.2, NP_001116697.1, NP_001172646.1, EAX07145.1, EAX72147.1
GeneID:84	LEPRE1	1	43,212,006	43,232,755	20,749	-	2	2_A375_EGR1_1.451:4_A375_EGR1_1.452	29887, -173	downstream, upstream	0	0	1	10	12.5	23	2	4_A375_EGR1_1.1	30	Gene LEPRE1	LEPRE1, OGN1, MGC113724, FLI30553	leucine proline-enriched proteoglycan (leprecan) 1	NM_022356, NM_001142699, XC71427[0.3, XC71965372.1, XC71965373.1, XC71965374.1, XC71965375.1, XC71965376.1, XC71965377.1, XC71965380.0	220760_s_at	NP_071753.3, NP_001139761.1, EAX07142.1, EAX07143.1, EAX07144.1, EAX07145.1
GeneID:79	ChiaSD	1	43,232,916	43,241,416	8,502	+	1	2_A375_EGR1_1.452	12	sr:gene	0	0	1	16	16	30	1	4_A375_EGR1_1.1	30	Gene ChiaSD	MGC9353, ChiaSD	chitotriosidase-1 spare-making bone 50	NM_024097, XC71427[2.3, XC71965366.2, XC72359142.0, XC72359146.0	219406_at_62212_at	NP_077052.2, EAX07141.1, EAX07139.1, EAX07140.1
GeneID:11	ERWP	1	43,262,776	43,310,660	27,884	+	1	2_A375_plnX7_gtuc_lncRNA_AR_1.264	29552	downstream	0	1	0	14	17	13	1	2_A375_plnX7_lncRNA_AR_1	17	Gene ERWNP	MGC116912, MGC116910, SC-PRO381, MGC116910, KIAA1851, ERWNP	SCY1-like 3 (S. cerevisiae)-like protein	NM_018336, NM_001017922, XC72335512.0, XC72359099.0, XC72359100.0	219903_at	NP_060788.2, NP_001017922.1, EAX07130.1, EAX07131.1, EAX07132.1, EAX07133.1
GeneID:83	ZNF691	1	43,312,260	43,316,145	3,886	+	1	2_A375_plnX7_gtuc_lncRNA_AR_1.264	-152	upstream	0	1	0	14	17	13	1	2_A375_plnX7_lncRNA_AR_1	17	Gene ZNF691	ZfpR91, ZNF691, RP11-342M1.8	zinc finger protein 691	NM_015911	232763_s_at	NP_056795.1
GeneID:89	SLC2A11	1	43,291,049	43,324,947	33,899	-	3	1_A375_plnX7_mrna1_lncRNA_AR_1.196:2_A375_plnX7_gtuc_lncRNA_AR_1.266:2_A375_EGR1_1.455	142, 111, 34850	sr:gene,sr:gene,downstream	1	1	1	16	16.5	15.5	2	4_A375_EGR1_1.1	30	Gene SLC2A11	MGC141899, MGC141893, GLT1H, PEG, GLUT11, GLUT11S, GYT1T, SLC2A11, GLUT	solute carrier family 2 (facilitated glucose transporter), member 11	NM_030815, NM_001017922, XC71839513.1, XC72359212.0, XC72359099.0, XC72359100.0	203249_at, 203250_s_at	NP_085118.2, EAX07124.1, EAX72122.1
GeneID:44	FLJ22223	1	43,374,730	43,449,029	74,299	+	2	1_A375_plnX7_mrna1_lncRNA_AR_1.194:2_A375_plnX7_gtuc_lncRNA_AR_1.268	-16, 16	upstream,sr:gene	1	1	0	14	20	11	1	2_A375_plnX7_lncRNA_AR_1	20	Gene FLJ22224	hypothetical LOC440894	NR_033967	1559852_at	
GeneID:43	MPL	1	43,803,475	43,820,155	16,680	+	1	2_A375_plnX7_gtuc_lncRNA_AR_1.267	11565	sr:gene	0	1	0	11	20	12	1	2_A375_plnX7_gtuc_lncRNA_AR_1	20	Gene MPL	CD110, TPOR, c-MPL, MPLV, MPL	myeloproliferative leukemia virus oncogene	NM_005373, XC71429[6.2, XC72335849.0, XC72335850.0	207350_at_211903_s_at, 211904_s_at	NP_005364.1, EAX07103.1, EAX07104.1, EAX07105.1
GeneID:99	CDC20	1	43,824,826	43,828,674	4,248	+	2	2_A375_plnX7_gtuc_lncRNA_AR_1.267:2_A375_EGR1_1.456	-5988, 6235	upstream, downstream	0	1	1	13.5	19.5	13.5	2	2_A375_plnX7_gtuc_lncRNA_AR_1	20	Gene CDC20	CDC20, CDC20A, bA276H15.5, p55CDC, MGC102824	cell division cycle 20, homolog (S. cerevisiae)	NM_001255, XC71429[6.3, XC71965860.0	202870_s_at	NP_001246.2, EAX07101.1, EAX07102.1
GeneID:84	ELOVL1	1	43,829,072	43,833,899	4,827	-	1	4_A375_EGR1_1.456	638	sr:gene	0	0	1	16	19	19	1	4_A375_EGR1_1.1	19	Gene ELOVL1	ELOVL1, CGI-65	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	NM_022821, XC72347[9.0	219029_at_87163_at	NP_073732.1, EAX07100.1
GeneID:10	MED6	1	43,849,966	43,858,463	8,498	-	3	1_A375_plnX7_mrna1_lncRNA_AR_1.195:2_A375_plnX7_gtuc_lncRNA_AR_1.265:1_A375_EGR1_1.455	55, 165, -261	sr:gene, upstream, upstream	1	1	1	17	24	20	1	2_A375_plnX7_lncRNA_AR_1	24	Gene MED6	MGC17544, MED6, HRC32, MGC19541	mediator complex subunit 6	NM_052877, NM_201542, XC72335596.0	213126_at, 213127_s_at, 213896_s_at	NP_443109.2, NP_963838.2, EAX07099.1
GeneID:14	Cfap54	1	43,855,356	43,872,365	17,009	+	3	1_A375_plnX7_mrna1_lncRNA_AR_1.195:2_A375_plnX7_gtuc_lncRNA_AR_1.265:1_A375_EGR1_1.455	-132, 92, 108	upstream, sr:gene, sr:gene	1	1	1	17	24	20	1	2_A375_plnX7_lncRNA_AR_1	24	Gene Cfap54	FLJ35032, C1orf64, SZT2A	chromosome 1 open reading frame 64	NM_031013981	1569709_at	NP_001129779.1
GeneID:23	RAW3467	1	43,886,797	43,916,304	29,507	+	1	4_A375_EGR1_1.458	20831	sr:gene	0	0	1	5	9	15	1	4_A375_EGR1_1.1	15	Gene RAW3467	FLJ30455, SZT2, FLJ34233, RAW3467, SZT2B, KP11-3688I3.3, FLJ10357	RAW3467	NM_015284	220900_at_219364_s_at	NP_056099.2
GeneID:23	HIY1	1	43,916,639	43,919,960	3,338	-	1	4_A375_EGR1_1.458	2352	sr:gene	0	0	1	5	9	15	1	4_A375_EGR1_1.1	15	Gene HIY1	MGC20787, HIY1, HT038	hydroxyproline isomerase (putative)	NM_031199982, NM_031207, XC71982951.1, XC71983700.1, XC72335493.0, XC72335532.0, XC72335533.0	221435_s_at_223822_s_at, 222705_s_at	NP_001177899.1, NP_112454.3, EAX07096.1, EAX07097.1, EAX07094.1, EAX07092.1, EAX07093.1
GeneID:57	PTPRF	1	43,996,547	44,089,343	92,796	+	3	1_A375_plnX7_mrna1_lncRNA_AR_1.196:2_A375_plnX7_gtuc_lncRNA_AR_1.269:1_A375_EGR1_1.457	-7323, -7339, 69161	upstream, upstream, sr:gene	1	1	1	17	20	9.5	2	1_A375_plnX7_lncRNA_AR_1	20	Gene PTPRF	FLJ43982, FLJ42335, PTPRF, LAR, FLJ43997	protein tyrosine phosphatase, receptor type, F	NM_130440, NM_002840, XC71833122.2, XC72333981.0, XC72333982.0, XC72333983.0	209655_s_at_209656_x_at, 209657_s_at_213996_at	NP_569727.2, NP_002831.2, EAX07086.1, EAX07087.1, EAX07088.1, EAX07089.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:8487	ST3GAL3	1	44,173,218	44,396,831	223,613	+	4	1_A375_pNL7_minus_lncRNA_AR..1..197, 1_A375_pNL7_minus_lncRNA_AR..1..198, 2_A375_pNL97_plus_lncRNA_AR..1..270, 2_A375_pNL97_plus_lncRNA_AR..1..271	127070, 222206, 127262, 128302	in gene, in gene, in gene, in gene	1	1	0	22.5	20	5.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene ST3GAL3	ST3GalIII, ST3N, ST3GAL3, ST3GALII, SIAT6	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	NM_006279, NM_174964, NM_174965, NM_174966, NM_174967, NM_174969, NM_174970, NM_174968, NM_174971, NM_174963, hCT16326.3, hCT2333700.0, hCT2333703.0	1555171_at, 1555181_a_at, 1555676_at, 1555702_a_at, 1555703_at, 225905_s_at, 231659_at	NP_006270.1, NP_777624.1, NP_777625.1, NP_777626.1, NP_777627.1, NP_777629.1, NP_777630.1, NP_777628.2, NP_777631.2, NP_777623.2, EAX07082.1, EAX07083.1, EAX07084.1
GeneID:9048	ARTN	1	44,398,992	44,402,912	3,920	+	4	1_A375_pNL7_minus_lncRNA_AR..1..198, 1_A375_pNL7_minus_lncRNA_AR..1..199, 2_A375_pNL97_plus_lncRNA_AR..1..272, 4_A375_EGR1..1..458	-3588, 13424, 13424, 13380	upstream, downstream, downstream, downstream	1	1	1	24.5	23.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene ARTN	ARTN, EVN, ENOVIN, NBN	artemin	NM_057090, NM_057091, NM_001136215, hCT16325.2, hCT1963729.1, hCT1963730.0, hCT1963731.0, hCT2333704.0, hCT2333705.0, hCT2333707.0, hCT2333712.0	207675_x_at, 210237_at, 216052_x_at	NP_476431.2, NP_476432.2, NP_001129687.1, EAX07074.1, EAX07077.1, EAX07078.1, EAX07075.1, EAX07076.1, EAX07079.1, EAX07080.1, EAX07081.1
GeneID:9670	IPO13	1	44,412,478	44,433,694	21,216	+	4	1_A375_pNL7_minus_lncRNA_AR..1..199, 1_A375_pNL7_minus_lncRNA_AR..1..200, 2_A375_pNL97_plus_lncRNA_AR..1..272, 4_A375_EGR1..1..458	-82, 21730, -82, -128	upstream, downstream, upstream, upstream	1	1	1	24.5	21	11	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene IPO13	IPO13, KIAA0724, RANBP13, IMP13, KAP13, LGL2	importin 13	NM_014652, hCT16322.2, hCT2333714.0	203546_at	NP_055467.3, EAX07072.1, EAX07073.1
GeneID:1802	DPH2	1	44,435,653	44,439,043	3,390	+	2	1_A375_pNL7_minus_lncRNA_AR..1..200, 4_A375_EGR1..1..459	-1445, 11355	upstream, downstream	1	0	1	16	11.5	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene DPH2	DPH2, DPH2L2	DPH2 homolog (S. cerevisiae)	NM_001039589, NM_001384, hCT16323.2, hCT2359106.0	204514_at	NP_001034678.1, NP_001375.2, EAX07070.1, EAX07071.1
GeneID:533	ATP6V0B	1	44,440,602	44,443,972	3,370	+	2	1_A375_pNL7_minus_lncRNA_AR..1..200, 4_A375_EGR1..1..459	-8394, 6406	upstream, downstream	1	0	1	16	11.5	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene ATP6V0B	HATPL, ATP6V0B, VMA16, ATP6F	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	NM_001039457, NM_004047, hCT16324.2, hCT1963712.1, hCT2359110.0, hCT2359111.0	200078_s_at	NP_001034546.1, NP_004038.1, EAX07066.1, EAX07067.1, EAX07068.1, EAX07069.1
GeneID:8704	B4GALT2	1	44,444,866	44,456,840	11,974	+	1	4_A375_EGR1..1..459	2142	in gene	0	0	1	8	8	20	1	4_A375_EGR1..1	20	Gene B4GALT2	beta4Gal-T2, B4Gal-T2, B4Gal-T3, B4GALT2	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	NM_003780, NM_001005417, hCT1963303.1, hCT2333720.0, hCT2333722.0, hCT2333723.0	209413_at	NP_003771.1, NP_001005417.1, EAX07062.1, EAX07063.1, EAX07064.1, EAX07065.1
GeneID:6536	SLC6A9	1	44,462,155	44,497,134	34,979	-	2	2_A375_pNL97_plus_lncRNA_AR..1..273, 4_A375_EGR1..1..460	830, 7054	in gene, in gene	0	1	1	9	14	16.5	2	4_A375_EGR1..1	19	Gene SLC6A9	GLYT1, DKFZp547A1118, SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	NM_008934, NM_201649, NM_001024845, hCT16326.2, hCT1953759.1, hCT2333436.0, hCT2359188.0	207043_s_at	NP_008865.2, NP_964012.2, NP_001020016.1, EAX07054.1, EAX07055.1, EAX07057.1, EAX07056.1
GeneID:55929	DMAP1	1	44,679,125	44,686,351	7,226	+	1	1_A375_pNL7_minus_lncRNA_AR..1..201	-5	upstream	1	0	0	30	25	14	1	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene DMAP1	FLJ11543, DMAP1, DKFZp686L09142, SWC4, KIAA1425, DNMAP1, DNMTAP1, MEAF2, EAF2	DNA methyltransferase 1 associated protein 1	NM_019100, NM_001034023, NM_001034024, hCT16329.3, hCT1966158.1, hCT1966162.1, hCT1966165.1, hCT2359190.0, hCT2359191.0	224163_s_at	NP_061973.1, NP_001029195.1, NP_001029196.1, EAX07046.1, EAX07048.1, EAX07049.1, EAX07047.1, EAX07050.1, EAX07051.1
GeneID:79033	ERI3	1	44,686,742	44,820,939	134,197	-	3	1_A375_pNL7_minus_lncRNA_AR..1..201, 1_A375_pNL7_minus_lncRNA_AR..1..202, 4_A375_EGR1..1..461	141619, 27435, 115499	downstream, in gene, in gene	1	0	1	18.33	15	12	3	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene ERI3	MGC2683, FLJ22943, PRNPIP, PINT1, ERI3	ERI1 exoribonuclease family member 3	NM_024066, hCT16331.2, hCT2333427.0, hCT2333429.0, hCT2359198.0	208973_at	NP_076971.1, EAX07043.1, EAX07042.1, EAX07044.1, EAX07045.1
GeneID:55182	RNF220	1	44,870,960	45,117,396	246,436	+	3	1_A375_pNL7_minus_lncRNA_AR..1..203, 2_A375_pNL97_plus_lncRNA_AR..1..274, 4_A375_EGR1..1..462	126912, 126960, 226480	in gene, in gene, in gene	1	1	1	22	22.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene RNF220	FLJ10597, RNF220, C1orf164	ring finger protein 220	NM_018150	219988_s_at	NP_060620.2
GeneID:339541	C1orf228	1	45,140,394	45,191,263	50,869	+	5	1_A375_pNL7_minus_lncRNA_AR..1..204, 1_A375_pNL7_minus_lncRNA_AR..1..205, 2_A375_pNL97_plus_lncRNA_AR..1..275, 2_A375_pNL97_plus_lncRNA_AR..1..276, 4_A375_EGR1..1..463	47266, 56566, 47446, 56582, 46966	in gene, downstream, in gene, downstream, in gene	1	1	1	24	30.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene C1orf228	p40, NCRNA00082, MGC33556, C1orf228	chromosome 1 open reading frame 228	NM_001145636, hCT13275.3, hCT2359131.0	238365_s_at, 238366_at, 238367_s_at, 239644_x_at, 242520_s_at	NP_001139108.1, EAX07026.1, EAX07027.1
GeneID:26830	RNU5D	1	45,196,741	45,196,840	99	-	6	1_A375_pNL7_minus_lncRNA_AR..1..204, 1_A375_pNL7_minus_lncRNA_AR..1..205, 2_A375_pNL97_plus_lncRNA_AR..1..275, 2_A375_pNL97_plus_lncRNA_AR..1..276, 4_A375_EGR1..1..463, 4_A375_EGR1..1..464	9160, -120, 9000, -136, 9480, -7446	downstream, upstream, downstream, upstream, downstream, upstream	1	1	1	17.67	24	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene RNU5D	U5DS, RNU5D, U5DL	RNA, U5D small nuclear	NR_002755		
GeneID:11004	KIF2C	1	45,205,490	45,233,439	27,949	+	6	1_A375_pNL7_minus_lncRNA_AR..1..205, 1_A375_pNL7_minus_lncRNA_AR..1..206, 2_A375_pNL97_plus_lncRNA_AR..1..276, 2_A375_pNL97_plus_lncRNA_AR..1..277, 4_A375_EGR1..1..464, 4_A375_EGR1..1..465	-8530, 35596, -8514, 35614, -1202, 35790	upstream, downstream, upstream, downstream, upstream, downstream	1	1	1	16.33	23	17.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene KIF2C	KNSL6, KIF2C, MCAK	kinesin family member 2C	NM_006845, hCT1814606.3	209408_at, 211519_s_at	NP_006836.2, EAX07025.1
GeneID:6202	RPS8	1	45,241,246	45,244,412	3,166	+	3	1_A375_pNL7_minus_lncRNA_AR..1..206, 2_A375_pNL97_plus_lncRNA_AR..1..277, 4_A375_EGR1..1..465	-158, -142, 34	upstream, upstream, in gene	1	1	1	23	24	24	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene RPS8	RPS8, S8		NM_001012, hCT2333698.0, hCT2333697.0	200858_s_at	NP_001003.1, EAX07024.1, EAX07023.1
GeneID:26811	SNORD55	1	45,241,537	45,241,610	73	+	3	1_A375_pNL7_minus_lncRNA_AR..1..206, 2_A375_pNL97_plus_lncRNA_AR..1..277, 4_A375_EGR1..1..465	-449, -433, -257	upstream, upstream, upstream	1	1	1	23	24	24	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SNORD55	SNORD55, RNU39, U39, U55, RNU55, SNORD39	small nucleolar RNA, C/D box 55	NR_000015		
GeneID:94161	SNORD46	1	45,242,164	45,242,261	97	+	3	1_A375_pNL7_minus_lncRNA_AR..1..206, 2_A375_pNL97_plus_lncRNA_AR..1..277, 4_A375_EGR1..1..465	-1076, -1060, -884	upstream, upstream, upstream	1	1	1	23	24	24	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SNORD46	U46, RNU46, SNORD46, U40, RNU40	small nucleolar RNA, C/D box 46	NR_000024		
GeneID:94162	SNORD38A	1	45,243,514	45,243,584	70	+	3	1_A375_pNL7_minus_lncRNA_AR..1..206, 2_A375_pNL97_plus_lncRNA_AR..1..277, 4_A375_EGR1..1..465	-2426, -2410, -2234	upstream, upstream, upstream	1	1	1	23	24	24	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SNORD38A	RNU38A, SNORD38A, U38A	small nucleolar RNA, C/D box 38A	NR_001456		
GeneID:94163	SNORD38B	1	45,244,062	45,244,130	68	+	3	1_A375_pNL7_minus_lncRNA_AR..1..206, 2_A375_pNL97_plus_lncRNA_AR..1..277, 4_A375_EGR1..1..465	-2974, -2958, -2782	upstream, upstream	1	1	1	23	24	24	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SNORD38B	U38B, SNORD38B, RNU38B	small nucleolar RNA, C/D box 38B	NR_001457		
GeneID:266675	BEST4	1	45,249,257	45,253,426	4,169	-	3	1_A375_pNL7_minus_lncRNA_AR..1..206, 2_A375_pNL97_plus_lncRNA_AR..1..277, 4_A375_EGR1..1..465	12338, 12322, 12146	downstream, downstream, downstream	1	1	1	23	24	24	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene BEST4	BEST4, VMD2L2, MGC126872	bestrophin 4	NM_153274, hCT2341150.0	1552296_at	NP_695006.1, EAX07022.1
GeneID:1263	PLK3	1	45,266,036	45,271,867	5,831	+	1	4_A375_EGR1..1..466	398	in gene	0	0	1	10	9	16	1	4_A375_EGR1..1	16	Gene PLK3	CNK, FNK, PLK3, PRK	polo-like kinase 3 (Drosophila)	NM_004073, hCT9662.3	204958_at, 215462_at, 229825_at	NP_004064.2, EAX07021.1
GeneID:343521	TCTEX1D4	1	45,271,580	45,272,957	1,377	-	1	4_A375_EGR1..1..466	6525	downstream	0	0	1	10	9	16	1	4_A375_EGR1..1	16	Gene TCTEX1D4	TCTEX1D4		NM_001013632		NP_001013654.1
GeneID:149478	BTBD19	1	45,274,154	45,279,801	5,647	+	4	1_A375_pNL7_minus_lncRNA_AR..1..207, 2_A375_pNL97_plus_lncRNA_AR..1..278, 4_A375_EGR1..1..466, 4_A375_EGR1..1..467	11606, 11606, -7722, 14337	downstream, downstream, upstream, downstream	1	1	1	16.33	17.33	14	3	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene BTBD19	BTBD19	BTB (POZ) domain containing 19	NM_001136537	1557049_at, 236102_s_at	NP_001130009.1
GeneID:8643	PTCH2	1	45,285,516	45,308,616	23,100	-	3	1_A375_pNL7_minus_lncRNA_AR..1..207, 2_A375_pNL97_plus_lncRNA_AR..1..278, 4_A375_EGR1..1..467	22856, 22856, 20125	in gene, in gene, in gene	1	1	1	19.5	21.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene PTCH2	PTCH2, PTC2	patched homolog 2 (Drosophila)	NM_003738, NM_001166292, hCT9661.3	221292_at	NP_003729.3, NP_001159764.1, EAX07017.1
GeneID:8891	EIF2B3	1	45,316,194	45,452,361	136,167	-	2	1_A375_pNL7_minus_lncRNA_AR..1..208, 2_A375_pNL97_plus_lncRNA_AR..1..279	9, 73	in gene, in gene	1	1	0	47	57	10	1	2_A375_pNL97_plus_lncRNA_AR..1	57	Gene EIF2B3	EIF-2B, EIF2Bgamma, EIF2B3	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	NM_020365, NM_001166588, hCT2333987.0, hCT2333988.0, hCT2359221.0, hCT2359222.0, hCT2359223.0, hCT9665.3	218466_at	NP_065098.1, NP_001160060.1, EAX07011.1, EAX07012.1, EAX07013.1, EAX07016.1, EAX07014.1, EAX07015.1
GeneID:79654	HECTD3	1	45,468,220	45,477,027	8,807	-	2	1_A375_pNL7_minus_lncRNA_AR..1..209, 2_A375_pNL97_plus_lncRNA_AR..1..280	-733, -701	upstream, upstream	1	1	0	46	43	10	1	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene HECTD3	MGC161630, RP11-69J16.1, FLJ31963, HECTD3, FLJ21156	HECT domain containing 3	NM_024602, hCT1815098.1, hCT2333985.0	218632_at	NP_078878.3, EAX07009.1, EAX07010.1
GeneID:7389	UROD	1	45,477,805	45,481,341	3,536	+	2	1_A375_pNL7_minus_lncRNA_AR..1..209, 2_A375_pNL97_plus_lncRNA_AR..1..280	-45, -77	upstream, upstream	1	1	0	46	43	10	1	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene UROD	PCT, UROD	uroporphyrinogen decarboxylase	NM_000374, NR_036510, hCT2359226.0, hCT6898.2	208970_s_at, 208971_at, 222074_at	NP_000365.3, EAX07008.1, EAX07007.1
GeneID:57643	ZSWIM5	1	45,482,074	45,672,250	190,176	-	2	1_A375_pNL7_minus_lncRNA_AR..1..209, 2_A375_pNL97_plus_lncRNA_AR..1..280	194490, 194522	downstream, downstream	1	1	0	46	43	10	1	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene ZSWIM5	KIAA1511, ZSWIM5	zinc finger, SWIM-type containing 5	NM_020883	232336_at	NP_065934.1
GeneID:400752	hCG_1820661	1	45,769,582	45,771,291	1,709	+	1	4_A375_EGR1..1..468	82	in gene	0	0	1	16	22	21	1	4_A375_EGR1..1	21	Gene hCG_1820661	LOC400752	hypothetical LOC400752	NR_024270	1564697_a_at	
GeneID:84842	HPDL	1	45,792,545	45,794,347	1,802	+	1	2_A375_pNL97_plus_lncRNA_AR..1..281	479	in gene	0	1	0	8	22	15	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene HPDL	MGC15668, HPDL, RP4-534D1.1, GLOXD1, 4-HPPD-L	4-hydroxyphenylpyruvate dioxygenase-like	NM_032756, hCT1633603.1	229332_at	NP_116145.1, EAX07002.1
GeneID:4595	MUTYH	1	45,794,914	45,806,142	11,228	-	1	2_A375_pNL97_plus_lncRNA_AR..1..281	13116	downstream	0	1	0	8	22	15	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MUTYH	MYH, MGC4416, CYP2C, MUTYH	mutY homolog (E. coli)	NM_012222, NM_001048171, NM_001048172, NM_001048173, NM_001048174, NM_001128425, hCT1818872.3, hCT1966772.1, hCT2359120.0, hCT2359121.0, hCT2359122.0, hCT2359123.0, hCT2359124.0, hCT2359125.0, hCT2359126.0, hCT2359127.0, hCT2359128.0	207727_s_at	NP_036354.1, NP_001041636.1, NP_001041637.1, NP_001041638.1, NP_001041639.1, NP_001121897.1, EAX06991.1, EAX06992.1, EAX06993.1, EAX06994.1, EAX06995.1, EAX06996.1, EAX06997.1, EAX07001.1, EAX06998.1, EAX06999.1, EAX07000.1
GeneID:10420	TESK2	1	45,809,555	45,956,840	147,285	-	3	1_A375_pNL7_minus_lncRNA_AR..1..210, 2_A375_pNL97_plus_lncRNA_AR..1..282, 4_A375_EGR1..1..469	-8952, -9016, 104	upstream, upstream, in gene	1	1	1	21.5	23	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene TESK2	TESK2		NM_007170, hCT2333975.0, hCT2333976.0, hCT2333977.0, hCT2333978.0	205486_at	NP_009101.2, EAX06989.1, EAX06986.1, EAX06987.1, EAX06988.1
GeneID:126661	CCDC163P	1	45,959,598	45,965,751	6,153	-	3	1_A375_pNL7_minus_lncRNA_AR..1..210, 2_A375_pNL97_plus_lncRNA_AR..1..282, 4_A375_EGR1..1..469	-41, -105, 9015	upstream, upstream, downstream	1	1	1	21.5	23	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene CCDC163P	C1orf231, CCDC163P	coiled-coil domain containing 163, pseudogene	NR_033296, NR_033297, NR_033298	1559003_a_at, 236900_x_at	
GeneID:25974	MMACHC	1	45,965,856	45,976,739	10,883	+	3	1_A375_pNL7_minus_lncRNA_AR..1..210, 2_A375_pNL97_plus_lncRNA_AR..1..282, 4_A375_EGR1..1..469	-64, 0, -9120	upstream, in gene, upstream	1	1	1	21.5	23	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene MMACHC	DKFZp564I122, MMACHC, cblC, FLJ25671, RP11-291L19.3	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	NM_015506, hCT1818880.1	211774_s_at	NP_056321.2, EAX06983.1
GeneID:5052	PRDX1	1	45,976,707	45,987,609	10,902	-	2	2_A375_pNL97_plus_lncRNA_AR..1..283, 4_A375_EGR1..1..470	25, 137	in gene, in gene	0	1	1	17	25	22	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene PRDX1	PAGB, PRXI, PRDX1, PRX1, MSP23, TDPX2, NKEFA, PAGA, PAG	peroxiredoxin 1	NM_181696, NM_181697, NM_002574, hCT1818878.2, hCT1982879.1, hCT1982880.1, hCT1966792.1, hCT2333968.0, hCT2333971.0, hCT2359180.0, hCT2359181.0	208680_at	NP_859047.1, NP_859048.1, NP_002565.1, EAX06979.1, EAX06980.1, EAX06982.1, EAX06975.1, EAX06976.1, EAX06977.1, EAX06978.1, EAX06981.1
GeneID:4678	NASP	1	46,049,717	46,084,567	34,850	+	3	1_A375_pNL7_minus_lncRNA_AR..1..211, 2_A375_pNL97_plus_lncRNA_AR..1..284, 4_A375_EGR1..1..471	-117, -85, 139	upstream, upstream, in gene	1	1	1	28	18	17	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene NASP	PRO1999, MGC20372, MGC2297, DKFZp547F162, FLJ31599, MGC19722, FLJ35510, NASP, FLB7527	nuclear autoantigenic sperm protein (histone-binding)	NM_002482, NM_152298, hCT1963738.1, hCT2334446.0, hCT2334448.0, hCT2334450.0, hCT2359216.0, hCT32147.3	201969_at, 201970_s_at, 242918_at	NP_002473.2, NP_689511.2, EAX06964.1, EAX06965.1, EAX06966.1, EAX06969.1, EAX06967.1, EAX06968.1
GeneID:60313	GPBP1L1	1	46,092,976	46,152,302	59,326	-	4	1_A375_pNL7_minus_lncRNA_AR..1..212, 2_A375_pNL97_plus_lncRNA_AR..1..285, 2_A375_pNL97_plus_lncRNA_AR..1..286, 4_A375_EGR1..1..472	-786, 94, -1490, -50	upstream, in gene, upstream, upstream	1	1	1	15	19	12	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene GPBP1L1	RP11-767N6.1, GPBP1L1, SP192	GC-rich promoter binding protein 1-like 1	NM_021639, hCT2333960.0, hCT2333961.0, hCT2333962.0, hCT2333963.0, hCT2333964.0	1569320_at, 217877_s_at, 222452_s_at	NP_067652.1, EAX06958.1, EAX06956.1, EAX06957.1, EAX06959.1, EAX06960.1
GeneID:51249	TMEM69	1	46,153,847	46,160,108	6,261	+	4	1_A375_pNL7_minus_lncRNA_AR..1..212, 2_A375_pNL97_plus_lncRNA_AR..1..285, 2_A375_pNL97_plus_lncRNA_AR..1..286, 4_A375_EGR1..1..472	-759, -1639, -55, -1495	upstream, upstream, upstream, upstream	1	1	1	15	19	12	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TMEM69	MGC104183, C1orf154, RP11-767N6.4, FLJ21029, TMEM69	transmembrane protein 69	NM_016486, hCT2334451.0, hCT2334452.0	223335_at	NP_057570.2, EAX06954.1, EAX06953.1
GeneID:3652	IPP	1	46,159,996	46,216,485	56,489	-	6	1_A375_pNL7_minus_lncRNA_AR..1..212, 2_A375_pNL97_plus_lncRNA_AR..1..285, 2_A375_pNL97_plus_lncRNA_AR..1..286, 2_A375_pNL97_plus_lncRNA_AR..1..287, 4_A375_EGR1..1..472, 4_A375_EGR1..1..473	63397, 64277, 62693, 261, 64133, 5	downstream, downstream, downstream, in gene, downstream, in gene	1	1	1	15.33	19	15.33	3	4_A375_EGR1..1	22	Gene IPP	KLHL27, IPP	intracisternal A particle-promoted polypeptide	NM_005897, NM_001145349, hCT1644595.3, hCT2333958.0, hCT2333959.0	1554739_at, 1554740_a_at, 219843_at, 241393_at	NP_005888.1, NP_001138821.1, EAX06950.1, EAX06951.1, EAX06952.1
GeneID:8503	PIK3R3	1	46,505,812	46,598,708	92,896	-	4	1_A375_pNL7_minus_lncRNA_AR..1..213, 2_A375_pNL97_plus_lncRNA_AR..1..288, 2_A375_pNL97_plus_lncRNA_AR..1..289, 4_A375_EGR1..1..474	180, 244, -1868, 580	in gene, in gene, upstream, in gene	1	1	1	25	29	9	2	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene PIK3R3	FLJ41892, DKFZp686P05226, p55, PIK3R3, p55-GAMMA	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_003629, NM_001114172, hCT1819329.2, hCT1981473.1, hCT2333951.0, hCT2333952.0, hCT2359213.0	202743_at, 211580_s_at	NP_003620.3, NP_001107644.1, EAX06944.1, EAX06945.1, EAX06946.1, EAX06947.1, EAX06943.1
GeneID:55624	POMGNT1	1	46,654,353	46,685,977	31,624	-	2	4_A375_EGR1..1..475, 4_A375_EGR1..1..476	22073, 16985	in gene, in gene	0	0	1	12.5	13	18	2	4_A375_EGR1..1	20	Gene POMGNT1	MGAT1.2, FLJ20277, DKFZp761B182, MDDGC3, POMGNT1, MEB, GNTI.2, MDDGB3, MDDGA3	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	NM_017739, NR_024332, hCT13194.3, hCT2333947.0, hCT2333948.0, hCT2333949.0, hCT2359098.0	217944_at, 233636_s_at, 233639_at	NP_060209.3, EAX06935.1, EAX06932.1, EAX06933.1, EAX06934.1, EAX06936.1
GeneID:541468	C1orf190	1	46,669,006	46,686,928	17,922	+	2	4_A375_EGR1..1..475, 4_A375_EGR1..1..476	-5102, -14	upstream, upstream	0	0	1	12.5	13	18	2	4_A375_EGR1..1	20	Gene C1orf190	C1orf190, FLJ25163	chromosome 1 open reading frame 190	NM_001013615, hCT1642489.2	235214_at	NP_001013633.1, EAX06931.1
GeneID:8438	RAD54L	1	46,713,367	46,744,145	30,778	+	2	1_A375_pNL7_minus_lncRNA_AR..1..214, 2_A375_pNL97_plus_lncRNA_AR..1..290	-7, 9	upstream, in gene	1	1	0	29	36	10	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene RAD54L	hHR54, hRAD54, RAD54A, HR54, RAD54L	RAD54-like (S. cerevisiae)	NM_003579, NM_001142548, hCT13183.2, hCT2333345.0	204558_at	NP_003570.2, NP_001136020.1, EAX06929.1, EAX06930.1
GeneID:10489	LRRC41	1	46,744,072	46,769,038	24,966	-	3	1_A375_pNL7_minus_lncRNA_AR..1..215, 1_A375_pNL7_minus_lncRNA_AR..1..216, 2_A375_pNL97_plus_lncRNA_AR..1..291	846, -210, 1390	in gene, upstream, in gene	1	1	0	19.5	19.5	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LRRC41	MUF1, PP7759, RP4-636H5.2, LRRC41, MGC126571, MGC126573	leucine rich repeat containing 41	NM_006369, hCT2333318.0, hCT2333320.0	1555831_s_at, 1556983_at, 201932_at, 215785_at	NP_006360.3, EAX06926.1, EAX06927.1
GeneID:7388	UQCRH	1	46,769,380	46,782,448	13,068	+	3	1_A375_pNL7_minus_lncRNA_AR..1..215, 1_A375_pNL7_minus_lncRNA_AR..1..216, 2_A375_pNL97_plus_lncRNA_AR..1..291	-1186, -132, -1732	upstream, upstream, upstream	1	1	0	19.5	19.5	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene UQCRH	QCR6, UQCR8, UQCRH, MGC111572	ubiquinol-cytochrome c reductase hinge protein	NM_006004, hCT13184.2, hCT1963362.1, hCT1963363.1, hCT2333348.0, hCT2333351.0	202233_s_at	NP_005995.2, EAX06924.1, EAX06922.1, EAX06923.1, EAX06925.1, EAX06926.1
GeneID:9813	KIAA0494	1	47,140,831	47,184,736	43,905	-	2	1_A375_pNL7_minus_lncRNA_AR..1..217, 2_A375_pNL97_plus_lncRNA_AR..1..292	-128, -144	upstream, upstream	1	1	0	45	41	9	1	1_A375_pNL7_minus_lncRNA_AR..1	45	Gene KIAA0494	KIAA0494, RP11-8J9.3	KIAA0494	NM_014774, hCT1819315.1, hCT2333304.1	1559022_at, 201775_s_at, 201776_s_at, 201777_s_at, 201778_s_at	NP_055589.1, EAX06894.1, EAX06893.1

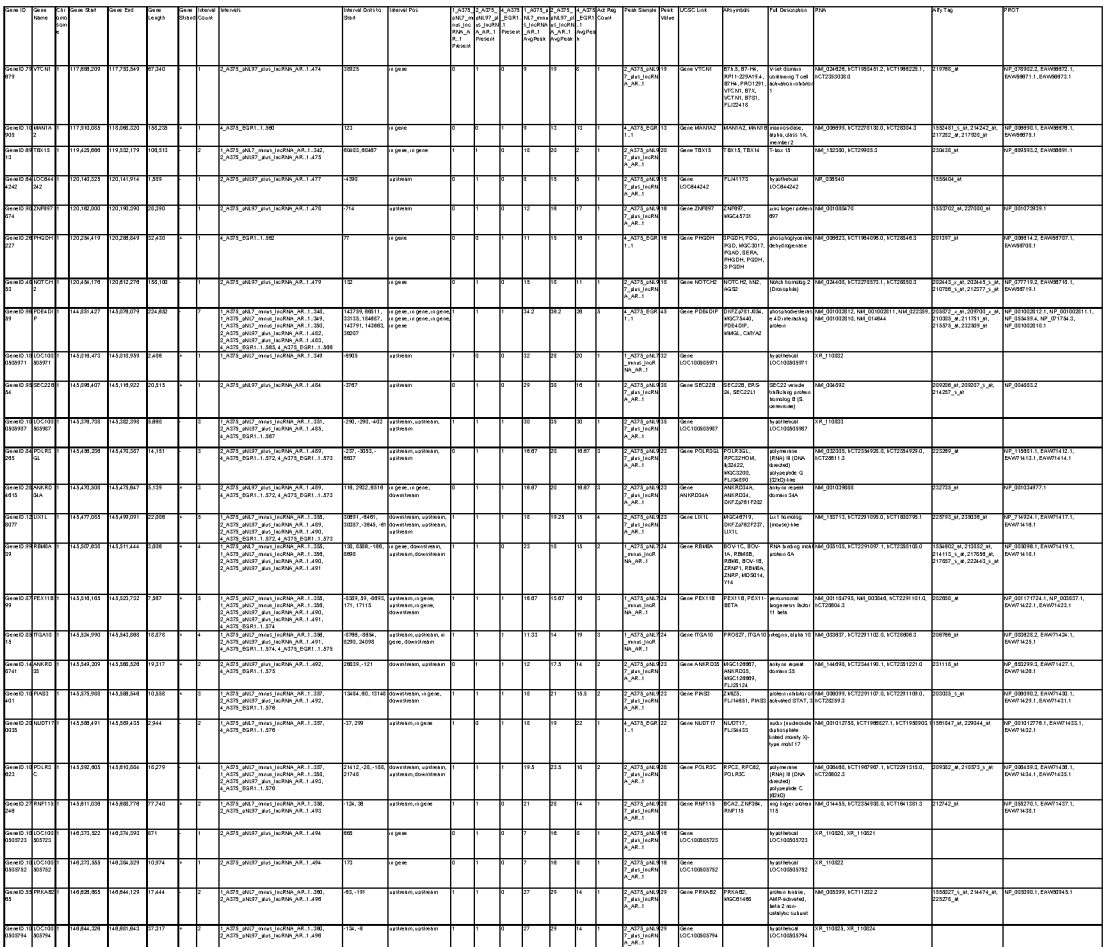




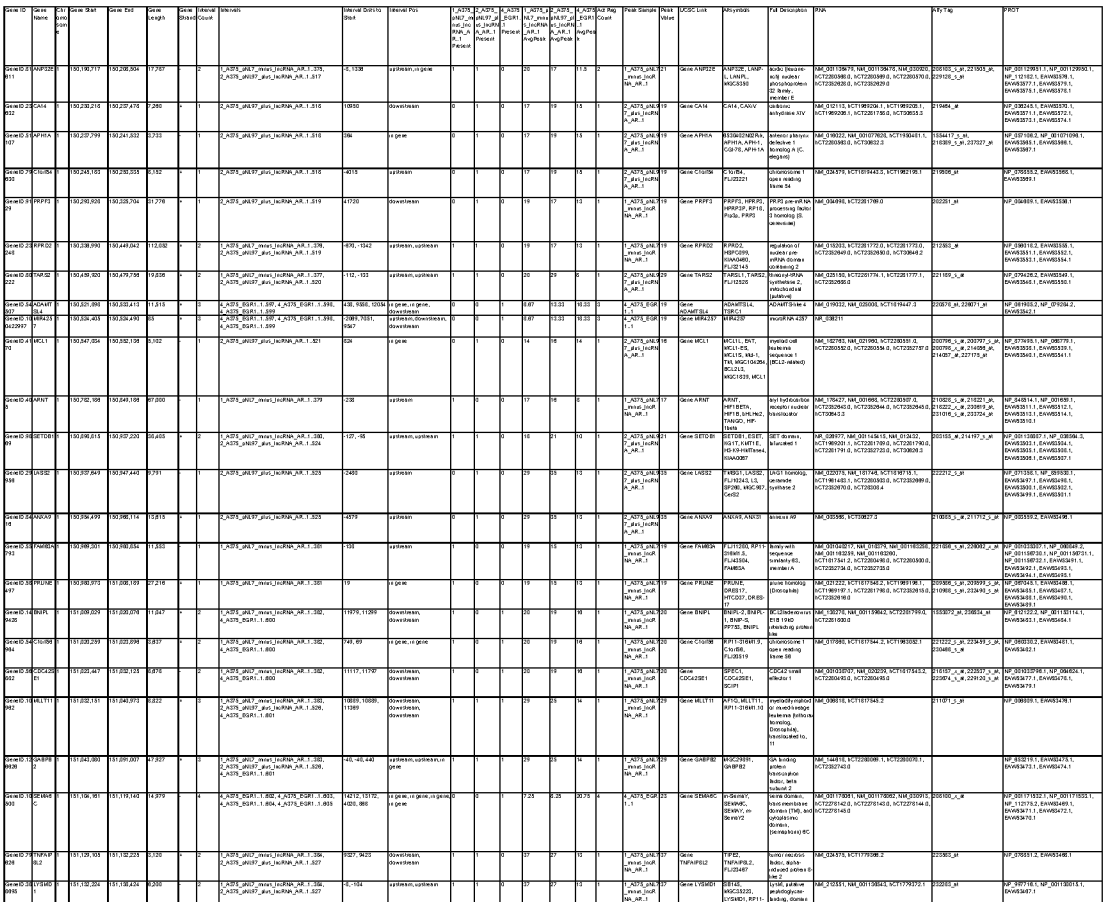
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.1491	CTH	1	70,876,901	70,905,534	28,633	+	1	2_A375_pNL97_plus_lncRNA_AR..1..370	-53	upstream	0	1	0	14	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CTH	MGC9471, CTH	cystathionase (cystathionine gamma-lyase)	NM_001190463, NM_001902, NM_153742, hCT12775.3, hCT1962917.1	206085_s_at, 217127_at	NP_001177392.1, NP_001893.2, NP_714964.2, EAX06450.1, EAX06451.1
GeneID.9406	ZRANB2	1	71,526,974	71,546,972	17,998	-	2	1_A375_pNL7_minus_lncRNA_AR..1..273, 2_A375_pNL97_plus_lncRNA_AR..1..371	60, 92	in gene, in gene	1	1	0	32	30	6	1	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene ZRANB2	ZIS, ZIS2, DKFZp686J1831, FLJ41119, ZIS1, ZNF265, ZRANB2, DKFZp686N09117	zinc finger, RAN-binding domain containing 2	NM_005455, NM_203350, hCT1644643.3, hCT1615428.1, hCT1956911.1, hCT2333052.0	223016_x_at, 223716_s_at, 241345_at	NP_005446.2, NP_976225.1, EAX06432.1, EAX06433.1, EAX06434.1, EAX06435.1
GeneID.257194	NEGR1	1	71,868,625	72,748,277	879,652	-	1	1_A375_pNL7_minus_lncRNA_AR..1..274	-1067	upstream	1	0	0	16	15	13	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene NEGR1	DMML2433, Ntra, KILON, IGLON4, MGC46680, NEGR1	neuronal growth regulator 1	NM_173808, hCT1640140.4, hCT2347990.0, hCT2347991.0	1553194_at, 229461_x_at, 239548_at, 243357_at	NP_776169.2, EAX06429.1, EAX06428.1, EAX06430.1
GeneID.51086	TNNI3K	1	74,663,947	75,010,108	346,161	+	2	1_A375_pNL7_minus_lncRNA_AR..1..275, 2_A375_pNL97_plus_lncRNA_AR..1..372	304373, 304373	in gene, in gene	1	1	0	43	62	2	1	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene TNNI3K	TNNI3K, MGC33828, CARK, MGC142099	TNNI3 interacting kinase	NM_015978, NM_001112808, hCT2332706.0	220415_at	NP_057062.1, NP_001106279.1, EAX06415.1
GeneID.34	ACADM	1	76,190,043	76,229,355	39,312	+	2	2_A375_pNL97_plus_lncRNA_AR..1..374, 4_A375_EGR1..1..518	229, 277	in gene, in gene	0	1	1	15	17	17	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ACADM	FLJ18227, FLJ99884, ACAD1, MCADH, FLJ93013, MCAD, ACADM	acyl-CoA dehydrogenase, C-4 to C-12 straight chain	NM_000016, NM_001127328, hCT14015.3, hCT1962228.1, hCT2359207.0	202502_at	NP_000007.1, NP_001120800.1, EAX06399.1, EAX06400.1, EAX06401.1
GeneID.5876	RABGGTB	1	76,251,888	76,260,764	8,876	+	2	2_A375_pNL97_plus_lncRNA_AR..1..375, 4_A375_EGR1..1..519	50, 10898	in gene, downstream	0	1	1	6.5	13	17	2	4_A375_EGR1..1	18	Gene RABGGTB	GGTB, RABGGTB	Rab geranylgeranyltransferase, beta subunit	NM_004582, hCT13954.3, hCT1969200.1, hCT2332711.0, hCT2359245.0, hCT2359246.0	209180_at, 209181_s_at, 213704_at	NP_004573.2, EAX06395.1, EAX06394.1, EAX06396.1, EAX06397.1, EAX06398.1
GeneID.692085	SNORD45C	1	76,252,757	76,252,834	77	+	2	2_A375_pNL97_plus_lncRNA_AR..1..375, 4_A375_EGR1..1..519	-821, 10027	upstream, downstream	0	1	1	6.5	13	17	2	4_A375_EGR1..1	18	Gene SNORD45C	SNORD45C, U45C	small nucleolar RNA, C/D box 45C	NR_003042		
GeneID.26805	SNORD45A	1	76,253,574	76,253,657	83	+	2	2_A375_pNL97_plus_lncRNA_AR..1..375, 4_A375_EGR1..1..519	-1638, 9210	upstream, downstream	0	1	1	6.5	13	17	2	4_A375_EGR1..1	18	Gene SNORD45A	U45a, SNORD45A, RNU45A	small nucleolar RNA, C/D box 45A	NR_002749		
GeneID.26804	SNORD45B	1	76,255,162	76,255,232	70	+	2	2_A375_pNL97_plus_lncRNA_AR..1..375, 4_A375_EGR1..1..519	-3226, 7622	upstream, downstream	0	1	1	6.5	13	17	2	4_A375_EGR1..1	18	Gene SNORD45B	U45b, RNU45B, SNORD45B	small nucleolar RNA, C/D box 45B	NR_002746		
GeneID.4438	MSH4	1	76,262,630	76,378,923	116,293	+	1	4_A375_EGR1..1..519	154	in gene	0	0	1	4	10	18	1	4_A375_EGR1..1	18	Gene MSH4	MSH4		NM_002440, hCT13953.3, hCT2332713.0	210533_at	NP_002431.2, EAX06392.1, EAX06393.1
GeneID.81849	ST6GALNAC5	1	77,333,186	77,529,737	196,551	+	3	1_A375_pNL7_minus_lncRNA_AR..1..276, 2_A375_pNL97_plus_lncRNA_AR..1..376, 2_A375_pNL97_plus_lncRNA_AR..1..377	172478, 990, 169214	in gene, in gene, in gene	1	1	0	16.67	18	7	3	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene ST6GALNAC5	ST6GALNAC5, SIAT7E, ST6GalNAcV, MGC3184	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	NM_030965, hCT1957977.1	1562753_at, 220979_s_at, 230462_at	NP_112227.1, EAX06386.1
GeneID.10026	PIGK	1	77,554,666	77,685,132	130,466	-	1	2_A375_pNL97_plus_lncRNA_AR..1..378	108	in gene	0	1	0	12	21	12	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PIGK	PIGK, GPI8, MGC22559	phosphatidylinositol glycan anchor biosynthesis, class K	NM_005482, hCT13908.3, hCT1969199.1, hCT2332697.0, hCT2359232.0	1555394_at, 209707_at, 227639_at	NP_005473.1, EAX06380.1, EAX06381.1, EAX06382.1, EAX06383.1
GeneID.26009	ZZZ3	1	78,030,190	78,148,343	118,153	-	2	2_A375_pNL97_plus_lncRNA_AR..1..379, 2_A375_pNL97_plus_lncRNA_AR..1..380	23, -841	in gene, upstream	0	1	0	13	16.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ZZZ3	FLJ10362, ATAC1, DKFZp564I052, DKFZp313N0119, ZZZ3	zinc finger, ZZ-type containing 3	NM_015534, hCT2332693.0, hCT2332694.0, hCT2332695.0, hCT2359087.0, hCT2359088.0	212693_at, 229325_at	NP_056349.1, EAX06373.1, EAX06372.1, EAX06374.1, EAX06375.1, EAX06376.1
GeneID.374986	FAM73A	1	78,245,309	78,344,077	98,768	+	1	1_A375_pNL7_minus_lncRNA_AR..1..277	17219	in gene	1	0	0	13	9	3	1	1_A375_pNL7_minus_lncRNA_AR..1	13	Gene FAM73A	DKFZp686M07168, FLJ35093, FAM73A	family with sequence similarity 73, member A	NM_198549, hCT2348843.0	235125_x_at, 243042_at	NP_940951.1, EAX06384.1
GeneID.11080	DNAJB4	1	78,470,636	78,482,998	12,362	+	1	2_A375_pNL97_plus_lncRNA_AR..1..381	-346	upstream	0	1	0	13	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene DNAJB4	DNAJB4, HLJ1, DNAJW, DjB4	DnaJ (Hsp40) homolog, subfamily B, member 4	NM_007034, hCT2332683.1, hCT2332684.0	203810_at, 203811_s_at	NP_008965.2, EAX06355.1, EAX06354.1
GeneID.23266	LPHN2	1	82,266,082	82,458,107	192,025	+	2	2_A375_pNL97_plus_lncRNA_AR..1..384, 2_A375_pNL97_plus_lncRNA_AR..1..385	974, 120014	in gene, in gene	0	1	0	11.5	17	5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LPHN2	LPHN2, CL2, LPHH1, CIRL2, LEC1	latrophilin 2	NM_012302, hCT1950476.1, hCT2332929.0, hCT2332930.0, hCT2332931.0, hCT2332932.0, hCT2332933.0, hCT2332934.0, hCT2332935.0, hCT2332937.0, hCT2332938.0, hCT2332939.0, hCT2332941.0, hCT2332942.0, hCT2332943.0, hCT2332944.0, hCT2332945.0, hCT2332946.0, hCT233	206953_s_at	NP_036434.1, EAX06333.1, EAX06321.1, EAX06322.1, EAX06323.1, EAX06335.1, EAX06324.1, EAX06325.1, EAX06326.1, EAX06327.1, EAX06328.1, EAX06329.1, EAX06334.1, EAX06337.1, EAX06330.1, EAX06331.1, EAX06332.1, EAX06336.1, EAX06338.1, EAX06339.1, EAX06340.1, EA
GeneID.79739	TTLL7	1	84,335,057	84,464,833	129,776	-	2	1_A375_pNL7_minus_lncRNA_AR..1..279, 2_A375_pNL97_plus_lncRNA_AR..1..386	33, -63	in gene, upstream	1	1	0	16	20	6	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TTLL7	FLJ36855, FLJ23033, TTLL7, RP5-836J3.2	tubulin tyrosine ligase-like family, member 7	NM_024686, hCT1953615.1, hCT1953616.1	219882_at	NP_078962.4, EAW73251.1, EAW73252.1
GeneID.80135	RPF1	1	84,944,920	84,964,033	19,113	+	1	2_A375_pNL97_plus_lncRNA_AR..1..387	-164	upstream	0	1	0	13	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene RPF1	RPF1, RP11-118B23.1, FLJ12475, BXDC5, DKFZp761M0215, DKFZp761G0415	ribosome production factor 1 homolog (S. cerevisiae)	NM_025065, hCT16212.2	218462_at, 234243_at, 234244_at	NP_079341.2, EAW73237.1
GeneID.148423	C1orf52	1	85,715,636	85,725,355	9,719	-	1	4_A375_EGR1..1..522	171	in gene	0	0	1	10	6	15	1	4_A375_EGR1..1	15	Gene C1orf52	RP11-234D19.1, FLJ44982, gm117, C1orf52	chromosome 1 open reading frame 52	NM_198077, NR_024113, hCT15992.3	228135_at, 239038_at	NP_932343.1, EAW73209.1
GeneID.8915	BCL10	1	85,731,459	85,742,587	11,128	-	2	4_A375_EGR1..1..522, 4_A375_EGR1..1..523	17403, -7029	downstream, upstream	0	0	1	7.5	5.5	14.5	2	4_A375_EGR1..1	15	Gene BCL10	CIPER, CLAP, c-E10, BCL10, mE10, CARMEN	B-cell CLL/lymphoma 10	NM_003921	1557257_at, 1557258_a_at, 205263_at	NP_003912.1
GeneID.646626	LOC646626	1	85,742,123	85,743,771	1,648	+	1	4_A375_EGR1..1..523	7493	downstream	0	0	1	5	3	14	1	4_A375_EGR1..1	14	Gene LOC646626		hypothetical LOC646626	XM_001715407, XM_933761, XM_942822	244619_at	XP_001715459.1, XP_938874.1, XP_947915.1
GeneID.23576	DDAH1	1	85,784,166	86,044,046	259,878	-	3	1_A375_pNL7_minus_lncRNA_AR..1..280, 2_A375_pNL97_plus_lncRNA_AR..1..388, 4_A375_EGR1..1..524	57198, 57102, 1710	in gene, in gene, in gene	1	1	1	15	19	12	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene DDAH1	FLJ25539, DDAH, FLJ21264, DDAH1	dimethylarginine dimethylaminohydrolase 1	NM_012137, NM_001134445, hCT2328980.2, hCT2328981.1, hCT2340528.1, hCT2350179.0	1553565_s_at, 209094_at, 229456_s_at, 243711_at	NP_036269.1, NP_001127917.1, EAW73199.1, EAW73200.1, EAW73201.1, EAW73202.1
GeneID.3491	CYR61	1	86,046,444	86,049,650	3,206	+	1	4_A375_EGR1..1..524	-4108	upstream	0	0	1	6	10	14	1	4_A375_EGR1..1	14	Gene CYR61	CYR61, IGFBP10, CCN1, GIG1	cysteine-rich, angiogenic inducer, 61	NM_001554, hCT14759.2, hCT1969149.1, hCT2329002.0	201289_at, 210764_s_at	NP_001545.2, EAW73196.1, EAW73197.1, EAW73198.1
GeneID.57489	ODF2L	1	86,812,507	86,862,025	49,518	-	1	4_A375_EGR1..1..525	409	in gene	0	0	1	9	13	14	1	4_A375_EGR1..1	14	Gene ODF2L	dJ977L11.1, MGC111080, RP5-977L11.1, ODF2L, KIAA1229	outer dense fiber of sperm tails 2-like	NM_001007022, NM_001184765, NM_001184766, NM_020729, hCT16361.3, hCT1953661.1, hCT2328717.0, hCT2328719.0, hCT2355121.0	228577_x_at, 230926_s_at, 231909_x_at	NP_001007023.2, NP_001171694.1, NP_001171695.1, NP_065780.2, EAW73188.1, EAW73192.1, EAW73189.1, EAW73190.1, EAW73191.1
GeneID.1179	CLCA1	1	86,934,526	86,965,977	31,451	+	2	1_A375_pNL7_minus_lncRNA_AR..1..281, 2_A375_pNL97_plus_lncRNA_AR..1..389	18466, 18210	in gene, in gene	1	1	0	16	16	3	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CLCA1	CLCRG1, hCaCC-1, CaCC-1, GOB5, FLJ95147, CACC1, hCLCA1, CACC, CLCA1	chloride channel accessory 1	NM_001285, hCT16357.2	210107_at	NP_001276.2, EAW73186.1
GeneID.9403	15-Sep	1	87,328,128	87,380,107	51,979	-	1	2_A375_pNL97_plus_lncRNA_AR..1..390	315	in gene	0	1	0	9	13	4	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene SEP15		15 kDa selenoprotein	NM_004261, NM_203341, hCT16354.3, hCT1953622.2, hCT1953623.1, hCT1969175.1, hCT2355122.0	200902_at	NP_004252.2, NP_976086.1, EAW73176.1, EAW73177.1, EAW73178.1, EAW73180.1, EAW73179.1
GeneID.9653	HS2ST1	1	87,380,335	87,575,681	195,346	+	1	2_A375_pNL97_plus_lncRNA_AR..1..390	-543	upstream	0	1	0	9	13	4	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene HS2ST1	MGC131986, KIAA0448, dJ604K5.2, FLJ11317, HS2ST1	heparan sulfate 2-O-sulfotransferase 1	NM_012262, NM_001134492, hCT1959963.1, hCT1959964.1, hCT2328970.0, hCT2328972.0	203283_s_at, 203284_s_at, 203285_s_at, 230465_at	NP_036394.1, NP_001127964.1, EAW73170.1, EAW73171.1, EAW73172.1, EAW73173.1
GeneID.5586	PKN2	1	89,149,922	89,301,938	152,016	+	1	2_A375_pNL97_plus_lncRNA_AR..1..392	-74	upstream	0	1	0	8	14	6	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene PKN2	PRKCL2, Pak-2, PRK2, MGC150606, PAK2, PKN2, PRO2042, MGC71074	protein kinase N2	NM_006256, hCT14845.3, hCT2328928.0, hCT2328930.0, hCT2328931.0, hCT2355130.0	210989_at, 212628_at, 212629_s_at, 230400_s_at	NP_006247.1, EAW73161.1, EAW73162.1, EAW73163.1, EAW73164.1, EAW73165.1
GeneID.2959	GTF2B	1	89,318,321	89,357,301	38,980	-	2	2_A375_pNL97_plus_lncRNA_AR..1..393, 4_A375_EGR1..1..526	53, 181	in gene, in gene	0	1	1	16	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene GTF2B	TF2B, TFIIB, GTF2B	general transcription factor IIB	NM_001514, hCT15997.2, hCT1969170.1	208066_s_at	NP_001505.1, EAW73159.1, EAW73160.1
GeneID.56267	CCBL2	1	89,401,456	89,458,643	57,187	-	1	2_A375_pNL97_plus_lncRNA_AR..1..394	427	in gene	0	1	0	8	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CCBL2	DKFZp547N1117, KAT3, MGC9398, CCBL2, RP4-531M19.2, DKFZp667D0223, KATIII	cysteine conjugate-beta lyase 2	NM_001008662, NM_001008661	209472_at, 227748_at	NP_001008662.1, NP_001008661.1
GeneID.494115	RBMXL1	1	89,445,139	89,458,643	13,504	-	1	2_A375_pNL97_plus_lncRNA_AR..1..394	427	in gene	0	1	0	8	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene RBMXL1	FLJ32614, DKFZp547N1117, RBMXL1, RBMI, DKFZp667D0223	RNA binding motif protein, X-linked-like 1	NM_019610, NM_001162536		NP_062556.2, NP_001156008.1
GeneID.284695	ZNF326	1	90,460,678	90,494,094	33,416	+	2	1_A375_pNL7_minus_lncRNA_AR..1..282, 2_A375_pNL97_plus_lncRNA_AR..1..395	90, 26	in gene, in gene	1	1	0	18	15	5	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ZNF326	FLJ20403, MGC81591, ZNF326, ZAN75, dJ871E2.1, Zfp326	zinc finger protein 326	NM_182976, NM_182975, hCT13957.3, hCT1952358.1, hCT2328538.0, hCT2355147.0	227680_at, 234093_at, 241720_at	NP_892021.1, NP_892020.1, EAW73125.1, EAW73126.1, EAW73127.1, EAW73128.1
GeneID.84146	ZNF644	1	91,380,855	91,487,671	106,816	-	1	4_A375_EGR1..1..527	167	in gene	0	0	1	10	13	17	1	4_A375_EGR1..1	17	Gene ZNF644	ZNF644, MGC60165, Zep-2, MGC70410, KIAA1221, BM-005	zinc finger protein 644	NM_032186, NM_201269, NM_016620, hCT14328.3	1553725_s_at, 222580_at, 229684_s_at	NP_115562.3, NP_958357.1, NP_057704.2, EAW73118.1
GeneID.100505857	LOC100505857	1	91,485,753	91,487,282	1,529	-	1	4_A375_EGR1..1..527	-222	upstream	0	0	1	10	13	17	1	4_A375_EGR1..1	17	Gene LOC100505857		hypothetical LOC100505857	XR_110475		
GeneID.164045	HFM1	1	91,726,323	91,870,426	144,103	-	2	1_A375_pNL7_minus_lncRNA_AR..1..283, 2_A375_pNL97_plus_lncRNA_AR..1..396	122, 90	in gene, in gene	1	1	0	21	22	6	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene HFM1	helicase, MGC163397, FLJ39011, SEC63D1, Si-11-6, FLJ36760, RP11-539G11.1, MER3, Si-11, HFM1	HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)	NM_001017975, hCT2328398.0	1564285_at, 241469_at	NP_001017975.3, EAW73116.1
GeneID.7049	TGFBR3	1	92,145,900	92,351,787	205,887	-	2	2_A375_pNL97_plus_lncRNA_AR..1..397, 2_A375_pNL97_plus_lncRNA_AR..1..398	58539, 587	in gene, in gene	0	1	0	11.5	18	5.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene TGFBR3	betaglycan, BGCAN, TGFBR3	transforming growth factor, beta receptor III	NM_003243, hCT12604.3, hCT2328511.0	204731_at	NP_003234.2, EAW73113.1, EAW73112.1
GeneID.646617	LOC646617	1	92,540,093	92,540,968	875	-	1	2_A375_pNL97_plus_lncRNA_AR..1..399	-5176	upstream	0	1	0	10	14	9	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene LOC646617		SET nuclear oncogene pseudogene			
GeneID.284697	BTBD8	1	92,545,862	92,613,397	67,535	+	1	2_A375_pNL97_plus_lncRNA_AR..1..399	282	in gene	0	1	0	10	14	9	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene BTBD8	BTBD8		NM_183242, hCT1657708.5, hCT1812995.3, hCT2355139.0	1569693_at	NP_899065.2, EAW73104.1, EAW73102.1, EAW73103.1
GeneID.11146	GLMN	1	92,711,955	92,764,566	52,611	-	3	1_A375_pNL7_minus_lncRNA_AR..1..284, 2_A375_pNL97_plus_lncRNA_AR..1..400, 4_A375_EGR1..1..528	310, 182, 134	in gene, in gene, in gene	1	1	1	15	17	14	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene GLMN	FAP68, GLMN, GVM, GLML, VMGLOM, FAP, FAP48, FKBPAP	glomulin, FKBP associated protein	NM_053274, hCT13989.3, hCT1952356.1	207153_s_at, 236924_at, 237386_at	NP_444504.1, EAW73097.1, EAW73098.1
GeneID.79871	RPAP2	1	92,764,522	92,853,732	89,210	+	3	1_A375_pNL7_minus_lncRNA_AR..1..284, 2_A375_pNL97_plus_lncRNA_AR..1..400, 4_A375_EGR1..1..528	-266, -138, -90	upstream, upstream, upstream	1	1	1	15	17	14	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene RPAP2	C1orf82, RPAP2, FLJ13150	RNA polymerase II associated protein 2	NM_024813, hCT13995.3, hCT2355109.0	219504_s_at, 222893_s_at	NP_079089.2, EAW73095.1, EAW73096.1
GeneID.6125	RPL5	1	93,297,594	93,307,481	9,887	+	2	1_A375_pNL7_minus_lncRNA_AR..1..285, 2_A375_pNL97_plus_lncRNA_AR..1..401	-90, -90	upstream, upstream	1	1	0	156	156	13	1	2_A375_pNL97_plus_lncRNA_AR..1	156	Gene RPL5	L5, MGC117339, DBA6, MSTP030, RPL5	ribosomal protein L5	NM_000969, hCT2329247.0, hCT2329248.0, hCT2355116.0	1556498_at, 200937_s_at, 213080_x_at, 213689_x_at	NP_000960.2, EAW73088.1, EAW73087.1, EAW73089.1
GeneID.6083	SNORD21	1	93,302,846	93,302,940	94	+	2	1_A375_pNL7_minus_lncRNA_AR..1..285, 2_A375_pNL97_plus_lncRNA_AR..1..401	-5342, -5342	upstream, upstream	1	1	0	156	156	13	1	2_A375_pNL97_plus_lncRNA_AR..1	156	Gene SNORD21	SNORD21, U21, RNU21	small nucleolar RNA, C/D box 21	NR_000006		
GeneID.26782	SNORA66	1	93,306,276	93,306,408	132	+	2	1_A375_pNL7_minus_lncRNA_AR..1..285, 2_A375_pNL97_plus_lncRNA_AR..1..401	-8772, -8772	upstream, upstream	1	1	0	156	156	13	1	2_A375_pNL97_plus_lncRNA_AR..1	156	Gene SNORA66	RNU66, SNORA66, U66	small nucleolar RNA, H/ACA box 66	NR_002444	210035_s_at	
GeneID.388650	FAM69A	1	93,307,721	93,427,079	119,358	-	2	1_A375_pNL7_minus_lncRNA_AR..1..285, 2_A375_pNL97_plus_lncRNA_AR..1..401	129575, 129575	downstream, downstream	1	1	0	156	156	13	1	2_A375_pNL97_plus_lncRNA_AR..1	156	Gene FAM69A	FLJ23493, FAM69A	family with sequence similarity 69, member A	NM_001006605, hCT13993.2	216044_x_at	NP_001006606.2, EAW73086.1
GeneID.22823	MTF2	1	93,544,792	93,604,638	59,846	+	1	2_A375_pNL97_plus_lncRNA_AR..1..402	-66	upstream	0	1	0	13	23	6	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MTF2	PCL2, RP5-976O13.1, dJ976O13.2, MTF2, M96	metal response element binding transcription factor 2	NM_007358, NM_001164391, NM_001164392, NM_001164393, hCT23129.3, hCT2355144.0, hCT2355145.0	203345_s_at, 203346_s_at, 203347_s_at, 209705_at	NP_031384.1, NP_001157863.1, NP_001157864.1, NP_001157865.1, EAW73084.1, EAW73085.1, EAW73083.1

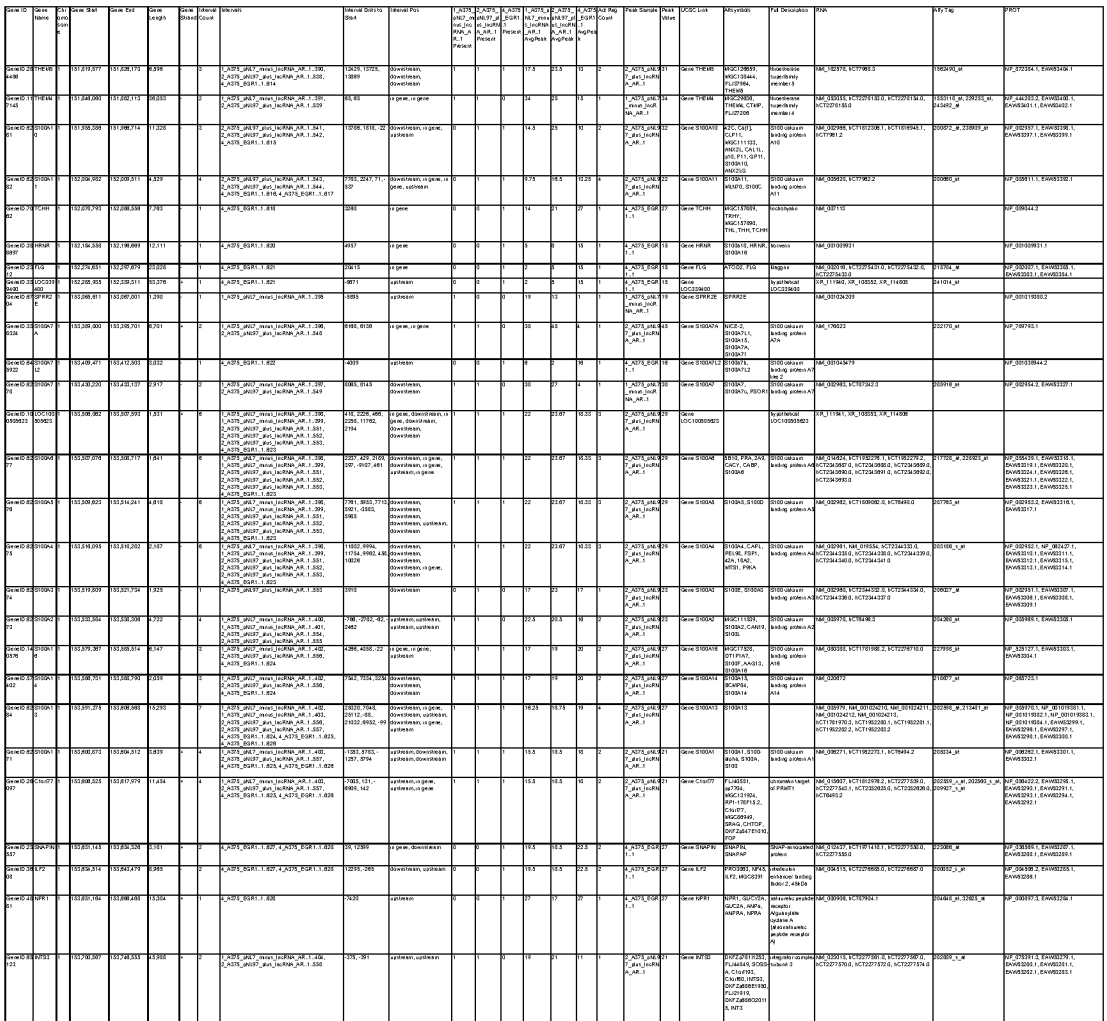
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:50999	TMED5	1	93,615,299	93,646,246	30,947	-	2	1_A375_pNL7_minus_lncRNA_AR..1..286, 2_A375_pNL97_plus_lncRNA_AR..1..403	150, 134	in gene, in gene	1	1	0	21	21	9	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene TMED5	TMED5, DKFZp781B2248, CGI-100	transmembrane emp24 protein transport domain containing 5	NM_016040, NR_030761, NM_001167830, hCT22667.3, hCT2329069.0	1556613_at, 1556614_s_at, 202194_at, 202195_s_at, 239263_at, 242263_at	NP_057124.3, NP_001161302.1, EAW73081.1, EAW73082.1
GeneID:343099	CCDC18	1	93,645,920	93,744,270	98,350	+	2	1_A375_pNL7_minus_lncRNA_AR..1..286, 2_A375_pNL97_plus_lncRNA_AR..1..403	176, 192	in gene, in gene	1	1	0	21	21	9	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene CCDC18	CCDC18, RP4-717I23.1, NY-SAR-41, dJ717I23.1	coiled-coil domain containing 18	NM_206886, hCT2329251.0, hCT2329252.0, hCT2329253.0	228022_at, 232362_at, 236665_at	NP_996769.2, EAW73080.1, EAW73078.1, EAW73079.1
GeneID:8412	BCAR3	1	94,027,348	94,147,385	120,037	-	2	1_A375_pNL7_minus_lncRNA_AR..1..287, 1_A375_pNL7_minus_lncRNA_AR..1..288	75769, 1113	in gene, in gene	1	0	0	16.5	13	6.5	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene BCAR3	SH2D3B, BCAR3, KIAA0554, NSP2	breast cancer anti-estrogen resistance 3	NM_003567, hCT2329063.1, hCT2329064.1, hCT2329065.1, hCT2329066.1	204032_at	NP_003558.1, EAW73067.1, EAW73065.1, EAW73066.1, EAW73068.1
GeneID:100129046	LOC100129046	1	94,057,525	94,065,587	8,062	+	1	1_A375_pNL7_minus_lncRNA_AR..1..287	14091	downstream	1	0	0	18	14	5	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100129046		hypothetical LOC100129046	NR_034091		
GeneID:100126348	MIR760	1	94,312,388	94,312,467	79	+	1	4_A375_EGR1..1..529	716	downstream	0	0	1	14	13	23	1	4_A375_EGR1..1	23	Gene MIR760	MIRN760, hsa-mir-760, MIR760	microRNA 760	NR_030621		
GeneID:100505940	LOC100505940	1	94,713,414	94,800,404	86,990	+	2	1_A375_pNL7_minus_lncRNA_AR..1..289, 2_A375_pNL97_plus_lncRNA_AR..1..404	77890, 78010	in gene, in gene	1	1	0	17	14	1	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene LOC100505940		hypothetical LOC100505940	XR_112091, XR_110477, XR_113517		
GeneID:199857	ALG14	1	95,446,279	95,536,507	90,228	-	1	2_A375_pNL97_plus_lncRNA_AR..1..406	-5	upstream	0	1	0	20	21	12	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ALG14	MGC19780, ALG14	asparagine-linked glycosylation 14 homolog (S. cerevisiae)	NM_144988, hCT1952372.1, hCT23098.2	1553954_at	NP_659425.1, EAW73026.1, EAW73027.1
GeneID:1806	DPYD	1	97,543,299	98,386,615	843,316	-	3	1_A375_pNL7_minus_lncRNA_AR..1..294, 2_A375_pNL97_plus_lncRNA_AR..1..409, 4_A375_EGR1..1..530	231, 343, 231	in gene, in gene, in gene	1	1	1	22	20	30	1	4_A375_EGR1..1	30	Gene DPYD	MGC132008, DPYD, DHP, MGC70799, DHPDHASE, DPD	dihydropyrimidine dehydrogenase	NM_000110, NM_001160301, hCT1952369.1, hCT2326187.0	1554534_at, 1554536_at, 204646_at	NP_000101.2, NP_001153773.1, EAW73002.1, EAW73003.1
GeneID:400765	FLJ35409	1	98,508,712	98,511,014	2,302	-	4	1_A375_pNL7_minus_lncRNA_AR..1..295, 2_A375_pNL97_plus_lncRNA_AR..1..410, 2_A375_pNL97_plus_lncRNA_AR..1..411, 2_A375_pNL97_plus_lncRNA_AR..1..412	-2906, 102, -970, 2906	upstream, in gene, upstream, upstream	1	1	0	19.67	31.33	8.33	3	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene FLJ35409		FLJ35409 protein	XR_112090, XR_110478, XR_113505	1559504_at, 1559506_x_at	
GeneID:406928	MIR137	1	98,511,626	98,511,727	101	-	4	1_A375_pNL7_minus_lncRNA_AR..1..295, 2_A375_pNL97_plus_lncRNA_AR..1..410, 2_A375_pNL97_plus_lncRNA_AR..1..411, 2_A375_pNL97_plus_lncRNA_AR..1..412	-2193, 615, -257, 2193	upstream, downstream, upstream, upstream	1	1	0	19.67	31.33	8.33	3	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene MIR137	MIR137, MIRN137	microRNA 137	NR_029679		
GeneID:54873	PALMD	1	100,111,431	100,160,097	48,666	+	1	2_A375_pNL97_plus_lncRNA_AR..1..415	36881	in gene	0	1	0	11	14	2	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene PALMD	C1orf11, FLJ20271, PALMD, PALML	palmdelphin	NM_017734, hCT23067.3, hCT2355148.0	218736_s_at, 222725_s_at, 232187_at	NP_060204.1, EAW72990.1, EAW72989.1
GeneID:178	AGL	1	100,315,640	100,389,579	73,939	+	3	1_A375_pNL7_minus_lncRNA_AR..1..296, 2_A375_pNL97_plus_lncRNA_AR..1..416, 4_A375_EGR1..1..531	-56, 72, -120	upstream, in gene, upstream	1	1	1	15	22	23	1	4_A375_EGR1..1	23	Gene AGL	GDE, AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase	NM_000028, NM_000645, NM_000643, NM_000646, NM_000644, NM_000642, hCT1814575.1, hCT22678.2, hCT23064.2, hCT23065.2, hCT2328473.0, hCT2328477.0, hCT2328478.0, hCT2328479.0	203566_s_at	NP_000019.2, NP_000636.2, NP_000634.2, NP_000637.2, NP_000635.2, NP_000633.2, EAW72980.1, EAW72981.1, EAW72982.1, EAW72983.1, EAW72984.1, EAW72985.1, EAW72986.1, EAW72987.1
GeneID:730081	LOC730081	1	100,433,942	100,435,838	1,896	-	1	2_A375_pNL97_plus_lncRNA_AR..1..417	382	in gene	0	1	0	23	33	15	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene LOC730081		hypothetical LOC730081	XR_112089, XR_110479, XR_113508		
GeneID:23443	SLC35A3	1	100,435,540	100,489,006	53,466	+	1	2_A375_pNL97_plus_lncRNA_AR..1..417	-84	upstream	0	1	0	23	33	15	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene SLC35A3	SLC35A3, DKFZp781P1297	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3	NM_012243, hCT22676.2, hCT2328480.0, hCT2328481.0	206770_s_at, 209865_at, 226894_at	NP_036375.1, EAW72978.1, EAW72977.1, EAW72979.1
GeneID:64645	HIAT1	1	100,503,789	100,548,933	45,144	+	3	1_A375_pNL7_minus_lncRNA_AR..1..297, 2_A375_pNL97_plus_lncRNA_AR..1..418, 4_A375_EGR1..1..532	-120, -237, 115	upstream, upstream, in gene	1	1	1	19	28	18	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene HIAT1	HIAT1, DKFZp564L0864	hippocampus abundant transcript 1	NM_033055, hCT23019.2	225222_at	NP_149044.2, EAW72976.1
GeneID:163786	SASS6	1	100,549,100	100,598,511	49,411	-	2	1_A375_pNL7_minus_lncRNA_AR..1..298, 2_A375_pNL97_plus_lncRNA_AR..1..419	-161, 31	upstream, in gene	1	1	0	17	26	8	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene SASS6	SAS-6, SAS6, MGC119440, FLJ22097, SASS6	spindle assembly 6 homolog (C. elegans)	NM_194292, hCT2328214.0, hCT2328215.0	231895_at	NP_919268.1, EAW72974.1, EAW72975.1
GeneID:54462	CCDC76	1	100,598,708	100,616,054	17,346	+	2	1_A375_pNL7_minus_lncRNA_AR..1..298, 2_A375_pNL97_plus_lncRNA_AR..1..419	-34, -226	upstream, upstream	1	1	0	17	26	8	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene CCDC76	FLJ11219, FLJ10287, CCDC76	coiled-coil domain containing 76	NM_019083, hCT23017.3, hCT2328485.0, hCT2328486.0, hCT2355134.0	219130_at, 232489_at	NP_061956.2, EAW72971.1, EAW72970.1, EAW72972.1, EAW72973.1
GeneID:8556	CDC14A	1	100,818,023	100,985,833	167,810	+	2	1_A375_pNL7_minus_lncRNA_AR..1..299, 2_A375_pNL97_plus_lncRNA_AR..1..420	169, 345	in gene, in gene	1	1	0	19	17	13	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene CDC14A	hCDC14, CDC14A, cdc14	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	NM_033312, NM_003672, NM_033313, hCT1967649.1, hCT2328492.0, hCT2328493.0, hCT2355140.0, hCT24042.3	205288_at, 210440_s_at, 210441_at, 210742_at, 210743_s_at	NP_201569.1, NP_003663.2, NP_201570.1, EAW72958.1, EAW72960.1, EAW72957.1, EAW72959.1
GeneID:2135	EXTL2	1	101,337,941	101,360,418	22,477	-	1	4_A375_EGR1..1..533	-990	upstream	0	0	1	9	10	14	1	4_A375_EGR1..1	14	Gene EXTL2	EXTL2, EXTR2	exostoses (multiple)-like 2	NM_001033025, NM_001439, hCT1967645.1, hCT2355149.0, hCT24040.4	209537_at	NP_001028197.1, NP_001430.1, EAW72946.1, EAW72947.1, EAW72948.1
GeneID:148867	SLC30A7	1	101,361,632	101,447,311	85,679	+	1	4_A375_EGR1..1..533	-224	upstream	0	0	1	9	10	14	1	4_A375_EGR1..1	14	Gene SLC30A7	SLC30A7, ZnTL2, ZnT-7, ZNT7, DKFZp686M0368	solute carrier family 30 (zinc transporter), member 7	NM_133496, NM_001144884, hCT2328319.0, hCT2328320.0	226217_at, 226601_at, 239598_at, 240277_at	NP_598003.2, NP_001138356.1, EAW72942.1, EAW72943.1
GeneID:51611	DPH5	1	101,455,179	101,491,362	36,183	-	1	2_A375_pNL97_plus_lncRNA_AR..1..422	-254	upstream	0	1	0	16	18	16	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene DPH5	HSPC143, NPD015, AD-018, CGI-30, MGC61450, DPH5	DPH5 homolog (S. cerevisiae)	NM_015958, NM_001077395, NM_001077394, hCT1962725.2, hCT1962726.1, hCT1962728.2, hCT1962729.2, hCT1967646.2, hCT2328227.1, hCT2355150.0, hCT2355151.0, hCT2355152.0, hCT24041.4	219590_x_at, 222360_at, 223671_x_at, 224060_s_at, 224198_x_at	NP_057042.2, NP_001070863.1, NP_001070862.1, EAW72935.1, EAW72938.1, EAW72940.1, EAW72932.1, EAW72933.1, EAW72934.1, EAW72936.1, EAW72937.1, EAW72939.1, EAW72941.1
GeneID:100506051	LOC100506051	1	101,491,434	101,546,991	55,557	+	1	2_A375_pNL97_plus_lncRNA_AR..1..422	182	in gene	0	1	0	16	18	16	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100506051		hypothetical LOC100506051	XR_110482		
GeneID:118427	OLFM3	1	102,268,127	102,462,790	194,663	-	3	1_A375_pNL7_minus_lncRNA_AR..1..302, 2_A375_pNL97_plus_lncRNA_AR..1..423, 2_A375_pNL97_plus_lncRNA_AR..1..424	230, 91910, 230	in gene, in gene, in gene	1	1	0	23.5	35	4.5	2	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene OLFM3	NOELIN3_V6, NOELIN3_V2, NOELIN3_V1, NOELIN3_V3, OPTIMEDIN, NOELIN3_V5, NOELIN3_V4, OLFM3, NOELIN3, NOE3	olfactomedin 3	NM_058170, hCT2328217.0, hCT2328219.0, hCT24249.2	1554524_a_at, 1554526_at	NP_477518.2, EAW72922.1, EAW72921.1, EAW72923.1
GeneID:55170	PRMT6	1	107,599,267	107,601,916	2,649	+	3	1_A375_pNL7_minus_lncRNA_AR..1..305, 2_A375_pNL97_plus_lncRNA_AR..1..426, 4_A375_EGR1..1..535	109, 317, -51	in gene, in gene, upstream	1	1	1	16	25	16	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene PRMT6	PRMT6, FLJ10559, FLJ51477, HRMT1L6	protein arginine methyltransferase 6	NM_018137, hCT1644369.3	223275_at	NP_060607.2, EAW51248.1
GeneID:22854	NTNG1	1	107,682,629	108,024,475	341,846	+	2	1_A375_pNL7_minus_lncRNA_AR..1..306, 2_A375_pNL97_plus_lncRNA_AR..1..427	-4389, -4341	upstream, upstream	1	1	0	22	26	3	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene NTNG1	KIAA0976, NTNG1, Lmnt1	netrin G1	NM_014917, NM_001113226, NM_001113228, hCT1951529.1, hCT2294772.0	206713_at, 236088_at	NP_055732.2, NP_001106697.1, NP_001106699.1, EAW51249.1, EAW51250.1
GeneID:29957	SLC25A24	1	108,677,445	108,742,974	65,529	-	1	2_A375_pNL97_plus_lncRNA_AR..1..430	-514	upstream	0	1	0	14	19	13	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SLC25A24	SCAMC-1, DKFZp586G0123, SLC25A24, APC1	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	NM_213651, NM_013386, hCT2294436.0, hCT2352452.0	1569121_at, 204342_at, 244481_at	NP_998816.1, NP_037518.3, EAW51254.1, EAW51255.1
GeneID:163479	FNDC7	1	109,255,556	109,285,371	29,815	+	1	4_A375_EGR1..1..536	33652	downstream	0	0	1	15	15	19	1	4_A375_EGR1..1	19	Gene FNDC7	MGC163293, FNDC7, FLJ35838, RP11-293A10.2	fibronectin type III domain containing 7	NM_001144937, hCT2344193.0	240837_at	NP_001138409.1, EAW56329.1
GeneID:6814	STXBP3	1	109,289,285	109,352,148	62,863	+	1	4_A375_EGR1..1..536	123	in gene	0	0	1	15	15	19	1	4_A375_EGR1..1	19	Gene STXBP3	STXBP3, MUNC18-3, MUNC18C, PSP, UNC-18C	syntaxin binding protein 3	NM_007269, hCT1809934.2, hCT2279231.0, hCT2279232.0	1560486_at, 203310_at	NP_009200.2, EAW56331.1, EAW56330.1, EAW56332.1
GeneID:29899	GPSM2	1	109,419,603	109,473,044	53,441	+	2	1_A375_pNL7_minus_lncRNA_AR..1..307, 2_A375_pNL97_plus_lncRNA_AR..1..431	13, -83	in gene, upstream	1	1	0	18	15	10	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene GPSM2	LGN, Pins, PINS, GPSM2, DFNB82	G-protein signaling modulator 2	NM_013296, hCT1960757.2, hCT2279235.1, hCT2279237.1, hCT2279238.1, hCT31165.4	205240_at, 221922_at	NP_037428.3, EAW56340.1, EAW56341.1, EAW56342.1, EAW56343.1, EAW56344.1
GeneID:22911	WDR47	1	109,512,836	109,584,850	72,014	-	2	1_A375_pNL7_minus_lncRNA_AR..1..308, 4_A375_EGR1..1..537	242, 514	in gene, in gene	1	0	1	17	16	23	1	4_A375_EGR1..1	23	Gene WDR47	KIAA0893, FLJ90135, WDR47	WD repeat domain 47	NM_014969, NM_001142550, NM_001142551, hCT2353084.0, hCT29400.2	203655_at	NP_055784.3, NP_001136022.1, NP_001136023.1, EAW56350.1, EAW56351.1
GeneID:6884	TAF13	1	109,606,998	109,618,624	11,626	-	2	1_A375_pNL7_minus_lncRNA_AR..1..309, 2_A375_pNL97_plus_lncRNA_AR..1..432	-80, 32	upstream, in gene	1	1	0	17	21	8	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TAF13	TAF13, TAFII18, MGC22425, TAF2K	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	NM_005645, hCT2297496.0, hCT29999.2	205966_at	NP_005636.1, EAW56354.1, EAW56355.1
GeneID:56900	TMEM167B	1	109,633,403	109,639,554	6,151	+	4	1_A375_pNL7_minus_lncRNA_AR..1..310, 1_A375_pNL7_minus_lncRNA_AR..1..311, 2_A375_pNL97_plus_lncRNA_AR..1..433, 2_A375_pNL97_plus_lncRNA_AR..1..434	-75, 9253, -91, 9285	upstream, downstream, upstream, downstream	1	1	0	52.5	54.5	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	66	Gene TMEM167B	AD-020, FLJ90710, C1orf119, TMEM167B	transmembrane protein 167B	NM_020141, hCT2279245.0, hCT31169.3	222495_at	NP_064526.1, EAW56357.1, EAW56356.1
GeneID:677768	SCARNA2	1	109,642,815	109,643,234	419	+	4	1_A375_pNL7_minus_lncRNA_AR..1..310, 1_A375_pNL7_minus_lncRNA_AR..1..311, 2_A375_pNL97_plus_lncRNA_AR..1..433, 2_A375_pNL97_plus_lncRNA_AR..1..434	-9487, -159, -9503, -127	upstream, upstream, upstream, upstream	1	1	0	52.5	54.5	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	66	Gene SCARNA2	SCARNA2, HBII-382, mgU2-25/61	small Cajal body-specific RNA 2	NR_003023	237137_at	
GeneID:127003	C1orf194	1	109,646,573	109,656,479	7,906	-	2	1_A375_pNL7_minus_lncRNA_AR..1..311, 2_A375_pNL97_plus_lncRNA_AR..1..434	13823, 13791	downstream, downstream	1	1	0	39	45	15	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene C1orf194	C1orf194	chromosome 1 open reading frame 194	NM_001122961	231044_at	NP_001116433.1
GeneID:6301	SARS	1	109,756,515	109,780,804	24,289	+	1	4_A375_EGR1..1..538	26941	downstream	0	0	1	17	16	17	1	4_A375_EGR1..1	17	Gene SARS	SARS, SERRS, SERS, FLJ36399	seryl-tRNA synthetase	NM_006513, NR_034072, NR_034073, hCT1966407.1, hCT1966408.1, hCT1966409.2, hCT2279254.1, hCT2353056.0, hCT2353057.0, hCT31166.4	200802_at, 237689_at	NP_006504.2, EAW56368.1, EAW56365.1, EAW56366.1, EAW56370.1, EAW56371.1, EAW56367.1, EAW56369.1
GeneID:1952	CELSR2	1	109,792,641	109,818,378	25,737	+	3	4_A375_EGR1..1..538, 4_A375_EGR1..1..539, 4_A375_EGR1..1..540	-9185, 351, 5535	upstream, in gene, in gene	0	0	1	9.67	10.33	18	3	4_A375_EGR1..1	21	Gene CELSR2	CDHF10, Flamingo1, FLJ45845, FLJ34118, FLJ45143, EGFL2, MEGF3, CELSR2, KIAA0279, FLJ42737	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	NM_001408, hCT2279248.0	204029_at, 36499_at	NP_001399.1, EAW56372.1
GeneID:343263	MYBPHL	1	109,834,987	109,849,863	14,876	-	1	2_A375_pNL97_plus_lncRNA_AR..1..435	7215	in gene	0	1	0	17	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MYBPHL	MYBPHL	myosin binding protein H-like	NM_001010985, hCT2353061.0, hCT31170.2		NP_001010985.2, EAW56379.1, EAW56378.1
GeneID:6272	SORT1	1	109,852,192	109,940,563	88,371	-	1	2_A375_pNL97_plus_lncRNA_AR..1..435	98115	downstream	0	1	0	17	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SORT1	LDLCQ6, NT3, Gp95, SORT1	sortilin 1	NM_002959, hCT31181.3	212797_at, 212807_s_at, 224818_at	NP_002950.3, EAW56380.1
GeneID:284612	SYPL2	1	110,009,100	110,024,764	15,664	+	4	1_A375_pNL7_minus_lncRNA_AR..1..312, 1_A375_pNL7_minus_lncRNA_AR..1..313, 1_A375_pNL7_minus_lncRNA_AR..1..314, 2_A375_pNL97_plus_lncRNA_AR..1..436	-55, 16980, 17826, 17780	upstream, downstream, downstream, downstream	1	1	0	42.5	49	12	2	2_A375_pNL97_plus_lncRNA_AR..1	84	Gene SYPL2	MG29, SYPL2	synaptophysin-like 2	NM_001040709, hCT2279442.0	230811_at	NP_001035799.1, EAW56385.1
GeneID:127002	ATXN7L2	1	110,026,561	110,035,426	8,865	+	6	1_A375_pNL7_minus_lncRNA_AR..1..313, 1_A375_pNL7_minus_lncRNA_AR..1..314, 1_A375_pNL7_minus_lncRNA_AR..1..315, 2_A375_pNL97_plus_lncRNA_AR..1..436, 2_A375_pNL97_plus_lncRNA_AR..1..437, 4_A375_EGR1..1..541	-461, 367, 10111, 319, 10143, 10239	upstream, in gene, downstream, in gene, downstream, downstream	1	1	1	66.5	79.5	16	2	2_A375_pNL97_plus_lncRNA_AR..1	84	Gene ATXN7L2	MGC46534, ATXN7L2, FLJ00361	ataxin 7-like 2	NM_153340	230036_at	NP_699171.3
GeneID:284613	CYB561D1	1	110,036,658	110,043,063	6,405	+	5	1_A375_pNL7_minus_lncRNA_AR..1..314, 1_A375_pNL7_minus_lncRNA_AR..1..315, 2_A375_pNL97_plus_lncRNA_AR..1..436, 2_A375_pNL97_plus_lncRNA_AR..1..437, 4_A375_EGR1..1..541	-9730, 14, -9778, 46, 142	upstream, in gene, upstream, in gene, in gene	1	1	1	66.5	79.5	16	2	2_A375_pNL97_plus_lncRNA_AR..1	84	Gene CYB561D1	CYB561D1, FLJ44753, FLJ39035, MGC138204	cytochrome b-561 domain containing 1	NM_182580, NM_001134400, NM_001134402, NM_001134403, NM_001134404		NP_872386.1, NP_001127872.1, NP_001127874.1, NP_001127875.1, NP_001127876.1
GeneID:2780	GNAT2	1	110,145,889	110,155,705	9,816	-	1	4_A375_EGR1..1..542	-7111	upstream	0	0	1	12	17	16	1	4_A375_EGR1..1	16	Gene GNAT2	GNAT2, ACHM4, GNATC	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2	NM_005272, hCT2279814.0, hCT31511.2	210604_at	NP_005263.1, EAW56394.1, EAW56395.1
GeneID:271	AMPD2	1	110,162,459	110,174,677	12,218	+	1	4_A375_EGR1..1..542	357	in gene	0	0	1	12	17	16	1	4_A375_EGR1..1	16	Gene AMPD2	AMPD2		NM_203404, NM_139156, NM_004037, hCT1966411.1, hCT2279454.0, hCT2279455.0, hCT2279456.0, hCT2279458.0, hCT31499.2	212360_at	NP_981949.1, NP_631895.1, NP_004028.3, EAW56399.1, EAW56400.1, EAW56401.1, EAW56396.1, EAW56397.1, EAW56398.1
GeneID:100506210	LOC100506210	1	110,250,714	110,252,912	2,198	+	1	4_A375_EGR1..1..543	4214	downstream	0	0	1	6	5	17	1	4_A375_EGR1..1	17	Gene LOC100506210		hypothetical protein LOC100506210	XM_003119806, XM_003118962, XM_003120449		XP_003119854.1, XP_003119010.1, XP_003120497.1
GeneID:2949	GSTM5	1	110,254,864	110,260,890	6,026	+	1	4_A375_EGR1..1..543	64	in gene	0	0	1	6	5	17	1	4_A375_EGR1..1	17	Gene GSTM5	GSTM5-5, GTM5, GSTM5	glutathione S-transferase mu 5	NM_000851, hCT2353024.0, hCT31498.3	205752_s_at	NP_000842.2, EAW56407.1, EAW56408.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.10768	AHCYL1	1	110,527,308	110,566,364	39,056	+	2	1_A375_pNL7_minus_lncRNA_AR..1..317, 2_A375_pNL97_plus_lncRNA_AR..1..439	295, -44	in gene, upstream	1	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene AHCYL1	PRO0233, IRBIT, DCAL, XPVKONA, AHCYL1	adenosylhomocysteinase-like 1	NM_006621, hCT1960758.1, hCT2279405.0, hCT2279408.0, hCT2279409.0, hCT2279410.0, hCT31502.3	200848_at, 200849_s_at, 200850_s_at, 207464_at	NP_006612.2, EAW56423.1, EAW56422.1, EAW56424.1, EAW56425.1, EAW56426.1, EAW56427.1
GeneID.388662	SLC8A17	1	110,693,132	110,744,824	51,692	+	2	1_A375_pNL7_minus_lncRNA_AR..1..318, 2_A375_pNL97_plus_lncRNA_AR..1..440	5604, 5604	in gene, in gene	1	1	0	21	24	4	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SLC8A17	NTT4, SLC8A17	solute carrier family 6, member 17	NM_001010898, hCT31513.3	229925_at, 233287_at	NP_001010898.1, EAW56432.1
GeneID.64783	RBM15	1	110,881,945	110,889,303	7,358	+	3	1_A375_pNL7_minus_lncRNA_AR..1..319, 2_A375_pNL97_plus_lncRNA_AR..1..441, 2_A375_pNL97_plus_lncRNA_AR..1..442	-425, -713, 2071	upstream, upstream, in gene	1	1	0	19.5	17	10	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene RBM15	FLJ21943, OTT1, MGC119584, SPEN, RBM15, OTT, FLJ12479	RNA binding motif protein 15	NM_022768, hCT1642035.3, hCT2279432.0, hCT2279434.0	1555760_a_at, 1555761_x_at, 1555762_s_at, 219286_s_at, 228455_at, 232971_at	NP_073605.4, EAW56438.1, EAW56439.1, EAW56440.1
GeneID.10542	HBXIP	1	110,943,875	110,950,546	6,671	-	1	2_A375_pNL97_plus_lncRNA_AR..1..443	308	in gene	0	1	0	14	28	13	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene HBXIP	XIP, HBXIP, MGC71071	hepatitis B virus x interacting protein	NM_006402, hCT31507.3	202299_s_at, 202300_at	NP_006393.2, EAW56447.1
GeneID.3738	KCNA3	1	111,214,310	111,217,655	3,345	-	1	4_A375_EGR1..1..545	655	in gene	0	0	1	3	5	17	1	4_A375_EGR1..1	17	Gene KCNA3	HLK3, HUKIII, MK3, HGK5, KCNA3, PCN3, HPCN3, KV1.3	potassium voltage-gated channel, shaker-related subfamily, member 3	NM_002232	207237_at	NP_002223.3
GeneID.55791	C1orf103	1	111,489,812	111,506,566	16,754	-	1	2_A375_pNL97_plus_lncRNA_AR..1..447	-346	upstream	0	1	0	13	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene C1orf103	RIF1, FLJ11269, LRIF1, C1orf103, RP11-96K19.1	chromosome 1 open reading frame 103	NM_018372, NM_001006945, hCT2278599.1, hCT31239.4	220235_s_at	NP_060842.3, NP_001008946.1, EAW56460.1, EAW56461.1
GeneID.128338	DRAM2	1	111,659,954	111,682,838	22,884	-	1	2_A375_pNL97_plus_lncRNA_AR..1..448	-410	upstream	0	1	0	13	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene DRAM2	RP5-1180E21.1, MGC54289, TMEM77, DRAM2, WWFQ154, PRO180	DNA-damage regulated autophagy modulator 2	NM_178454, hCT2353067.0, hCT2353068.0, hCT2353069.0, hCT2353070.0, hCT31243.3	225228_at, 225230_at	NP_848549.3, EAW56466.1, EAW56464.1, EAW56465.1, EAW56466.1, EAW56467.1
GeneID.10390	CEPT1	1	111,682,249	111,727,724	45,475	+	1	2_A375_pNL97_plus_lncRNA_AR..1..446	999	in gene	0	1	0	13	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CEPT1	MGC45223, CEPT1, DKFZp313G0615	choline/ethanolamine phosphotransferase 1	NM_001007794, NM_006090, hCT2278193.0, hCT2278197.0, hCT2278201.0, hCT31234.3	1561864_at, 219375_at	NP_001007795.1, NP_006081.1, EAW56469.1, EAW56470.1, EAW56471.1, EAW56472.1
GeneID.55924	C1orf183	1	112,264,686	112,298,419	33,733	-	3	1_A375_pNL7_minus_lncRNA_AR..1..323, 2_A375_pNL97_plus_lncRNA_AR..1..449, 4_A375_EGR1..1..546	51, 275, 16499	in gene, in gene, in gene	1	1	1	16.5	18	15	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene C1orf183	C1orf183, FLJ31105	chromosome 1 open reading frame 183	NM_019099, NM_198926, hCT2278297.0, hCT31333.3	220476_s_at, 229382_at, 229808_at, 241809_at	NP_061972.1, NP_945120.1, EAW56504.1, EAW56505.1
GeneID.100506343	LOC100506343	1	112,282,463	112,290,420	7,957	+	3	1_A375_pNL7_minus_lncRNA_AR..1..323, 2_A375_pNL97_plus_lncRNA_AR..1..449, 4_A375_EGR1..1..546	15905, 15661, -543	downstream, downstream, upstream	1	1	1	16.5	18	15	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene LOC100506343		hypothetical LOC100506343	XR_112100, XR_110466, XR_113706		
GeneID.11218	DDX20	1	112,298,190	112,310,199	12,009	+	2	1_A375_pNL7_minus_lncRNA_AR..1..323, 2_A375_pNL97_plus_lncRNA_AR..1..449	178, -46	in gene, upstream	1	1	0	25	23	13	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene DDX20	DKFZp434H052, GEMIN3, DP103, DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	NM_007204, hCT2277978.1, hCT31332.3	223331_s_at, 224315_at	NP_009135.4, EAW56507.1, EAW56508.1
GeneID.3752	KCND3	1	112,318,454	112,531,777	213,323	-	3	1_A375_pNL7_minus_lncRNA_AR..1..324, 2_A375_pNL97_plus_lncRNA_AR..1..450, 2_A375_pNL97_plus_lncRNA_AR..1..451	155633, 155617, 124161	in gene, in gene, in gene	1	1	0	23	27.5	5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene KCND3	KSHIVB, KCND3, MGC142035, KCND3L, MGC142037, KV4.3, KCND3S	potassium voltage-gated channel, Shal-related subfamily, member 3	NM_004980, NM_172198, hCT2278294.0, hCT2353022.0, hCT31335.2	211301_at, 211827_s_at	NP_004971.2, NP_751948.1, EAW56510.1, EAW56511.1, EAW56512.1
GeneID.55917	CTTNBP2NL	1	112,938,800	113,003,786	64,986	+	1	4_A375_EGR1..1..547	-9624	upstream	0	0	1	7	8	17	1	4_A375_EGR1..1	17	Gene CTTNBP2NL	FLJ13278, CTTNBP2NL, DKFZp547A023	CTTNBP2 N-terminal like	NM_018704, hCT2277965.0, hCT2277966.0, hCT31340.2	214731_at, 226000_at, 231822_at, 239525_at, 240868_at	NP_061174.1, EAW56516.1, EAW56515.1, EAW56517.1
GeneID.54879	ST7L	1	113,066,140	113,162,040	95,900	-	2	1_A375_pNL7_minus_lncRNA_AR..1..327, 2_A375_pNL97_plus_lncRNA_AR..1..454	-264, 259	upstream, in gene	1	1	0	20	18	13	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ST7L	ST7R, FAM4B, ST7L, FLJ20284, STLR, FLJ11657	suppression of tumorigenicity 7 like	NM_017744, NM_138727, NM_138728, NM_138729, hCT2278286.0, hCT2278288.0, hCT2278289.0, hCT2278291.0, hCT29705.3	1552738_a_at, 1552739_s_at, 219984_at, 230079_at, 233141_s_at, 236123_at	NP_060214.2, NP_620055.1, NP_620056.1, NP_620057.1, EAW56520.1, EAW56521.1, EAW56522.1, EAW56523.1, EAW56524.1
GeneID.829	CAPZA1	1	113,162,075	113,214,241	52,166	+	4	1_A375_pNL7_minus_lncRNA_AR..1..327, 2_A375_pNL97_plus_lncRNA_AR..1..454, 2_A375_pNL97_plus_lncRNA_AR..1..455, 4_A375_EGR1..1..548	229, -294, 55349, 55509	in gene, upstream, downstream, downstream	1	1	1	16.5	20.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CAPZA1	CAPPA1, CAPZA1, CAPZ, CAZ1	capping protein (actin filament) muscle Z-line, alpha 1	NM_006135, hCT2277974.0, hCT2353046.0, hCT29707.3	208374_s_at, 217392_at, 241275_at	NP_006126.1, EAW56525.1, EAW56526.1, EAW56527.1
GeneID.4343	MOV10	1	113,217,048	113,243,368	26,320	+	5	1_A375_pNL7_minus_lncRNA_AR..1..328, 2_A375_pNL97_plus_lncRNA_AR..1..455, 2_A375_pNL97_plus_lncRNA_AR..1..456, 4_A375_EGR1..1..548, 4_A375_EGR1..1..549	30296, 376, 30392, 536, 32456	downstream, in gene, downstream, in gene, downstream	1	1	1	13.67	16.33	15	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MOV10	FLJ32791, MOV10, DKFZp667O1423, gb110, KIAA1631, fSAP113	Mov10, Moloney leukemia virus 10, homolog (mouse)	NM_020963, NM_001130079, hCT2278397.0, hCT2278399.0, hCT2278400.0, hCT29706.3	223849_s_at, 233917_s_at	NP_066014.1, NP_001123551.1, EAW56528.1, EAW56529.1, EAW56530.1, EAW56531.1
GeneID.389	RHOC	1	113,243,749	113,250,025	6,276	-	3	1_A375_pNL7_minus_lncRNA_AR..1..328, 2_A375_pNL97_plus_lncRNA_AR..1..456, 4_A375_EGR1..1..549	2681, 2585, 521	in gene, in gene, in gene	1	1	1	14	13	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene RHOC	ARHC, MGC61427, MGC1448, RHOC, ARH9, RHOH9, H9	ras homolog gene family, member C	NM_001042678, NM_175744, NM_001042679	200885_at, 235742_at	NP_001036143.1, NP_786886.1, NP_001036144.1
GeneID.333926	PPM1J	1	113,252,616	113,257,950	5,334	-	3	1_A375_pNL7_minus_lncRNA_AR..1..328, 2_A375_pNL97_plus_lncRNA_AR..1..456, 4_A375_EGR1..1..549	10606, 10510, 8446	downstream, downstream, downstream	1	1	1	14	13	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene PPM1J	PPM1J, PPP2CZ, DKFZp434P1514, MGC90149, PP2Czeta, MGC19531, PP2CZ, FLJ35951	protein phosphatase 1J (PP2C domain containing)	NM_005167	229484_at	NP_005158.5
GeneID.128322	LOC128322	1	113,290,717	113,291,097	380	+	1	4_A375_EGR1..1..550	-4413	upstream	0	0	1	4	4	15	1	4_A375_EGR1..1	15	Gene LOC128322		nuclear transport factor 2-like	XM_001716411, XM_060943, XM_938602		XP_001716463.1, XP_060943.1, XP_943695.1
GeneID.6566	SLC16A1	1	113,454,469	113,498,975	44,506	-	2	1_A375_pNL7_minus_lncRNA_AR..1..329, 2_A375_pNL97_plus_lncRNA_AR..1..457	271, 287	in gene, in gene	1	1	0	21	30	25	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SLC16A1	MCT1, SLC16A1, MGC44475, HHF7, MCT, FLJ36745	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	NM_003051, NM_001166496, hCT2278772.0, hCT2353023.0, hCT28668.4	1557918_s_at, 202234_s_at, 202235_at, 202236_s_at, 209900_s_at	NP_003042.3, NP_001159968.1, EAW56551.1, EAW56552.1, EAW56553.1
GeneID.100506392	LOC100506392	1	113,499,020	113,511,609	12,589	+	2	1_A375_pNL7_minus_lncRNA_AR..1..329, 2_A375_pNL97_plus_lncRNA_AR..1..457	-316, -332	upstream, upstream	1	1	0	21	30	25	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene LOC100506392		hypothetical LOC100506392	XR_110490		
GeneID.9860	LRIG2	1	113,615,831	113,667,342	51,511	+	2	1_A375_pNL7_minus_lncRNA_AR..1..330, 2_A375_pNL97_plus_lncRNA_AR..1..458	169, 169	in gene, in gene	1	1	0	25	40	15	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene LRIG2	KIAA0806, LIG2, DKFZp451C181, LRIG2	leucine-rich repeats and immunoglobulin-like domains 2	NM_014813, hCT2278413.0, hCT28309.2	205953_at, 242164_s_at, 242165_at	NP_055628.1, EAW56556.1, EAW56557.1
GeneID.260425	MAGI3	1	113,933,475	114,228,545	295,070	+	1	2_A375_pNL97_plus_lncRNA_AR..1..459	66173	in gene	0	1	0	12	14	3	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene MAGI3	RP4-730K3.1, MAGI3, MAGI-3, dJ730K3.2, MGC163281	membrane associated guanylate kinase, WW and PDZ domain containing 3	NM_152900, NM_001142782, hCT2349961.0, hCT2349962.0, hCT2349963.0, hCT2353065.0, hCT2353066.0	224307_x_at, 226770_at	NP_690864.2, NP_001136254.1, EAW56559.1, EAW56560.1, EAW56562.1, EAW56563.1, EAW56561.1
GeneID.10745	PHTF1	1	114,239,824	114,301,777	61,953	-	2	2_A375_pNL97_plus_lncRNA_AR..1..460, 4_A375_EGR1..1..551	-90, -303	upstream, upstream	0	1	1	14	14	15	1	4_A375_EGR1..1	15	Gene PHTF1	PHTF, PHTF1	putative homeodomain transcription factor 1	NM_006608, hCT2278582.0, hCT2278583.0, hCT2278584.0, hCT29880.2	205702_at, 210191_s_at, 215285_s_at, 235844_at	NP_006599.2, EAW56567.1, EAW56566.1, EAW56568.1, EAW56569.1
GeneID.54665	RSBN1	1	114,304,454	114,355,070	50,616	-	2	2_A375_pNL97_plus_lncRNA_AR..1..460, 4_A375_EGR1..1..551	53203, 52990	downstream, downstream	0	1	1	14	14	15	1	4_A375_EGR1..1	15	Gene RSBN1	DKFZp761E21150, RP11-324J2.1, ROSBIN, RSBN1	round spermatid basic protein 1	NM_018364, hCT2278559.0, hCT2353047.0, hCT29884.3	213694_at, 222788_s_at, 222789_at, 222790_s_at, 222791_at	NP_060834.2, EAW56572.1, EAW56570.1, EAW56571.1
GeneID.100287722	LOC100287722	1	114,399,257	114,443,859	44,602	+	2	1_A375_pNL7_minus_lncRNA_AR..1..331, 2_A375_pNL97_plus_lncRNA_AR..1..461	46847, 46847	downstream, downstream	1	1	0	33	29	8	1	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene LOC100287722		hypothetical LOC100287722	XR_112103, XR_110491, XR_113711		
GeneID.10717	AP4B1	1	114,437,677	114,447,741	10,064	-	2	1_A375_pNL7_minus_lncRNA_AR..1..331, 2_A375_pNL97_plus_lncRNA_AR..1..461	-163, -163	upstream, upstream	1	1	0	33	29	8	1	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene AP4B1	BETA-4, AP4B1	adaptor-related protein complex 4, beta 1 subunit	NM_006594	231714_s_at, 231962_at, 236221_at	NP_006585.2
GeneID.64858	DCLRE1B	1	114,447,915	114,456,708	8,793	+	2	1_A375_pNL7_minus_lncRNA_AR..1..331, 2_A375_pNL97_plus_lncRNA_AR..1..461	-11, -11	upstream, upstream	1	1	0	33	29	8	1	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene DCLRE1B	APOLLO, DCLRE1B, FLJ13998, SNM1B, FLJ12810, SNMIB, DKFZp686C24167	DNA cross-link repair 1B	NM_022836, hCT2353030.0, hCT29881.3	219490_s_at, 222889_at	NP_073747.1, EAW56583.1, EAW56582.1
GeneID.204851	HIPK1	1	114,471,996	114,520,422	48,426	+	2	1_A375_pNL7_minus_lncRNA_AR..1..332, 2_A375_pNL97_plus_lncRNA_AR..1..462	146, 164	in gene, in gene	1	1	0	30	21	13	1	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene HIPK1	KIAA0630, Nbak2, Myak, HIPK1, MGC33446, MGC33548, MGC26642	homeodomain interacting protein kinase 1	NM_152696, NM_198268, NM_198269, NM_181358, hCT2278086.0, hCT2278087.0, hCT2278088.0, hCT2278089.0, hCT2278090.0, hCT2353051.0, hCT2353052.0, hCT2353053.0, hCT29887.3	1552515_at, 1552516_a_at, 212291_at, 212293_at	NP_689909.2, NP_938009.1, NP_938010.1, NP_852003.1, EAW56587.1, EAW56591.1, EAW56585.1, EAW56586.1, EAW56588.1, EAW56589.1, EAW56590.1, EAW56592.1, EAW56593.1
GeneID.148281	SYT6	1	114,631,914	114,696,472	64,558	-	2	1_A375_pNL7_minus_lncRNA_AR..1..333, 2_A375_pNL97_plus_lncRNA_AR..1..463	39872, 23304	in gene, in gene	1	1	0	13.5	14.5	9	2	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene SYT6	SYT6		NM_205848, hCT2353054.0, hCT2353055.0, hCT29889.3	244227_at	NP_995320.1, EAW56596.1, EAW56597.1, EAW56598.1
GeneID.51592	TRIM33	1	114,935,399	115,053,781	118,382	-	1	4_A375_EGR1..1..552	645	in gene	0	0	1	11	10	24	1	4_A375_EGR1..1	24	Gene TRIM33	TIFGAMMA, FLJ32925, TRIM33, RFG7, TF1G, ECTO, PTC7, TIF1G, TIF1GAMMA	tripartite motif containing 33	NM_015906, NM_033020, hCT2278545.0, hCT2278547.0, hCT28306.3	210266_s_at, 212435_at, 212436_at, 214815_at	NP_056990.3, NP_148980.2, EAW56599.1, EAW56600.1, EAW56601.1
GeneID.7812	CSDE1	1	115,259,537	115,300,671	41,134	-	1	2_A375_pNL97_plus_lncRNA_AR..1..465	255	in gene	0	1	0	14	19	18	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CSDE1	UNR, CSDE1, DKFZp779J1455, D1S155E, RP5-1000E10.3, DKFZp779B0247, FLJ26882	cold shock domain containing E1, RNA-binding	NM_007158, NM_001007553, NM_001130523, hCT2278801.0, hCT2278803.0, hCT2278804.0, hCT2278805.0, hCT2278807.0, hCT2278809.0, hCT2353028.0, hCT29899.3	202646_s_at, 219939_s_at, 222975_s_at	NP_009089.4, NP_001007554.1, NP_001123995.1, EAW56613.1, EAW56614.1, EAW56615.1, EAW56612.1, EAW56616.1, EAW56617.1, EAW56618.1, EAW56619.1
GeneID.80143	SIKE1	1	115,312,100	115,323,308	11,208	-	1	1_A375_pNL7_minus_lncRNA_AR..1..334	140	in gene	1	0	0	24	14	15	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene SIKE1	DKFZp686A0768, SIKE, SIKE1, FLJ21168	suppressor of IKBKE 1	NM_025073, NM_001102396, hCT29702.3	204665_at, 204666_s_at, 221705_s_at	NP_079349.2, NP_001095866.1, EAW56620.1
GeneID.4803	NGF	1	115,828,537	115,880,857	52,320	-	2	1_A375_pNL7_minus_lncRNA_AR..1..336, 4_A375_EGR1..1..553	37857, 537	in gene, in gene	1	0	1	14.5	11	10.5	2	4_A375_EGR1..1	18	Gene NGF	NGFB, MGC161426, HSAN5, MGC161428, Beta-NGF, NGF	nerve growth factor (beta polypeptide)	NM_002506, hCT28307.2	206814_at	NP_002497.2, EAW56629.1
GeneID.100506434	LOC100506434	1	115,876,436	115,878,915	2,479	-	1	4_A375_EGR1..1..553	-1405	upstream	0	0	1	12	10	18	1	4_A375_EGR1..1	18	Gene LOC100506434		hypothetical protein LOC100506434	XM_003118984		XP_003119012.1
GeneID.81839	VANGL1	1	116,184,574	116,240,845	56,271	+	1	4_A375_EGR1..1..555	29826	in gene	0	0	1	10	8	17	1	4_A375_EGR1..1	17	Gene VANGL1	VANGL1, KITENIN, LPP2, STB2, MGC5336, STBM2	vang-like 1 (van gogh, Drosophila)	NM_138959, NM_001172411, NM_001172412, hCT2353034.0, hCT2353035.0, hCT29182.3	219330_at, 229134_at, 229492_at, 229997_at	NP_620409.1, NP_001165882.1, NP_001165883.1, EAW56630.1, EAW56631.1, EAW56632.1
GeneID.845	CASQ2	1	116,242,624	116,311,426	68,802	-	2	1_A375_pNL7_minus_lncRNA_AR..1..337, 1_A375_pNL7_minus_lncRNA_AR..1..338	41122, 40546	in gene, in gene	1	0	0	18	11.5	3	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene CASQ2	PDIB2, FLJ93514, FLJ26321, CASQ2	calsequestrin 2 (cardiac muscle)	NM_001232, hCT2278816.0, hCT2278817.0	207317_s_at	NP_001223.2, EAW56635.1, EAW56636.1
GeneID.126868	C1orf161	1	116,654,376	116,677,861	23,485	+	1	2_A375_pNL97_plus_lncRNA_AR..1..466	11320	in gene	0	1	0	7	18	2	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene C1orf161	MAB21L3, FLJ38716, RP5-1185H19.1, C1orf161	chromosome 1 open reading frame 161	NM_152367, hCT2278531.1, hCT2344824.0	1553333_at	NP_689580.2, EAW56643.1, EAW56642.1
GeneID.476	ATP1A1	1	116,915,795	116,947,396	31,601	+	2	4_A375_EGR1..1..557, 4_A375_EGR1..1..558	-51, 797	upstream, in gene	0	0	1	13.5	11	19.5	2	4_A375_EGR1..1	23	Gene ATP1A1	ATP1A1, MGC3285, MGC51750	ATPase, Na+/K+ transporting, alpha 1 polypeptide	NM_000701, NM_001160233, NM_001160234, hCT1983402.1, hCT1983403.1, hCT1983404.1, hCT2278534.0, hCT29179.3	220948_s_at	NP_000692.2, NP_001153705.1, NP_001153706.1, EAW56645.1, EAW56646.1, EAW56647.1, EAW56644.1, EAW56648.1
GeneID.100506459	LOC100506459	1	117,035,638	117,041,834	6,196	-	2	1_A375_pNL7_minus_lncRNA_AR..1..339, 2_A375_pNL97_plus_lncRNA_AR..1..471	-5526, -10070	upstream, upstream	1	1	0	15	15.5	5	2	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene LOC100506459		hypothetical LOC100506459	XR_112104, XR_110492, XR_113712		
GeneID.965	CD58	1	117,057,156	117,113,715	56,559	-	3	1_A375_pNL7_minus_lncRNA_AR..1..339, 2_A375_pNL97_plus_lncRNA_AR..1..471, 2_A375_pNL97_plus_lncRNA_AR..1..472	66355, 61811, 99	downstream, downstream, in gene	1	1	0	14.33	17	6.67	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CD58	FLJ23181, CD58, FLJ43722, LFA3, LFA-3	CD58 molecule	NM_001144822, NM_001779, NR_026665, hCT1981678.1, hCT2282188.0, hCT2282190.0, hCT2353063.0, hCT28305.3	205173_x_at, 211744_s_at, 216322_at, 216942_s_at, 222061_at	NP_001138294.1, NP_001770.1, EAW56652.1, EAW56654.1, EAW56655.1, EAW56656.1, EAW56653.1
GeneID.3321	IGSF3	1	117,117,031	117,210,314	93,283	-	1	2_A375_pNL97_plus_lncRNA_AR..1..472	96698	downstream	0	1	0	13	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene IGSF3	EWI-3, MGC117164, V8, IGSF3	immunoglobulin superfamily, member 3	NM_001542, NM_001007237, hCT2282183.0, hCT2282185.0, hCT2282186.0	1552672_a_at, 1556162_at, 1556163_a_at, 202421_at	NP_001533.2, NP_001007238.1, EAW56657.1, EAW56658.1, EAW56659.1
GeneID.914	CD2	1	117,297,086	117,311,851	14,765	+	1	2_A375_pNL97_plus_lncRNA_AR..1..473	23458	downstream	0	1	0	6	18	2	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CD2	SRBC, T11, FLJ46032, CD2	CD2 molecule	NM_001767, hCT30312.3	205831_at	NP_001758.2, EAW56661.1
GeneID.80263	TRIM45	1	117,653,677	117,664,411	10,734	-	1	4_A375_EGR1..1..559	-165	upstream	0	0	1	10	13	18	1	4_A375_EGR1..1	18	Gene TRIM45	FLJ13181, TRIM45, RNF99	tripartite motif containing 45	NM_025188, NM_001145635, hCT2353039.0, hCT30313.3	219923_at, 242056_at	NP_079464.2, NP_001139107.1, EAW56668.1, EAW56669.1
GeneID.100506478	LOC100506478	1	117,671,466	117,682,904	11,438	+	1	4_A375_EGR1..1..559	-6690	upstream	0	0	1	10	13	18	1	4_A375_EGR1..1	18	Gene LOC100506478		hypothetical LOC100506478	XR_112105, XR_110493, XR_113713		



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_2_A375_3_A375_4_A375_4_A375_ Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:7790	VTCN1	1	117,698,209	117,730,549	97,340	-	1	2_A375_shU97_plus_lacRNA_NR_1.474	39825	sv gene	0	1	0	9	19	8	1	2_A375_shU97_plus_lacRNA_NR_1	19	Gene VTCN1	B7H3, B7-H4, RP11-239A7.4, B7h4, PRO1291, VTCN1, B7X, VCTN1, B7S1, FLJ22416	V-set domain containing T cell activation inhibitor 1	NM_024626, ICT01904512, ICT01966226.1, ICT2309030.0	219782_at	NP_378922.2, EAW68872.1, EAW68871.1, EAW68873.1
GeneID:10	MAN1A2	1	117,910,053	118,098,320	188,268	+	1	4_A375_DGR1...1.590	123	sv gene	0	0	1	9	13	10	1	4_A375_DGR1	13	Gene MAN1A2	MAN1A2, MAN1B	mannosidase, alpha, class 1A, member 2	NM_006699, ICT02701800.0, ICT02834.3	1552481_s_at, 214242_at, 217202_at, 217203_at	NP_006690.1, EAW68676.1, EAW68675.1
GeneID:69	TBX15	1	119,428,666	119,532,179	106,512	-	2	1_A375_shU7_minus_lacRNA_NR_1...242, 2_A375_shU97_plus_lacRNA_NR_1.475	69403, 60487	sv gene, sv gene	1	1	0	16	20	2	1	2_A375_shU97_plus_lacRNA_NR_1	20	Gene TBX15	TBX15, TBX14	T-box 15	NM_152380, ICT29605.0	230036_at	NP_689595.2, EAW68691.1
GeneID:64	LOC644	1	120,140,325	120,141,914	1,589	-	1	2_A375_shU97_plus_lacRNA_NR_1.477	-4390	upstream	0	1	0	6	15	8	1	2_A375_shU97_plus_lacRNA_NR_1	15	Gene LOC644242	FLJ41175	hypothetical LOC644242	NR_038540	1559604_at	
GeneID:69	ZNF697	1	120,182,000	120,190,290	20,350	-	1	2_A375_shU97_plus_lacRNA_NR_1.476	-714	upstream	0	1	0	12	16	17	1	2_A375_shU97_plus_lacRNA_NR_1	16	Gene ZNF697	ZNF697, MGC45731	zinc finger protein 697	NM_031305, 670	1553702_at, 227000_at	NP_001073939.1
GeneID:26	PHGDH	1	120,294,419	120,298,549	22,430	+	1	4_A375_DGR1...582	77	sv gene	0	2	1	11	15	16	1	4_A375_DGR1	16	Gene PHGDH	3PGDH, PDG, PGD, MGC3017, PHAD, 3SRA, PHGDH, PGDH, 3-PGDH	phosphoglycerate dehydrogenase	NM_006623, ICT01964090.0, ICT02648.3	201397_at	NP_006614.2, EAW68707.1, EAW68708.1
GeneID:46	NOTCH2	1	120,456,176	120,612,276	156,100	-	1	2_A375_shU97_plus_lacRNA_NR_1.479	132	sv gene	0	1	0	15	16	11	1	2_A375_shU97_plus_lacRNA_NR_1	16	Gene NOTCH2	NOTCH2, hN2, AGS2	Notch homolog 2 (Drosophila)	NM_024408, ICT02705571.1, ICT02650.3	202443_x_at, 202443_s_at, 210755_s_at, 212277_s_at	NP_077719.2, EAW68716.1, EAW68719.1
GeneID:99	PDE4DIP	1	144,839,427	145,078,079	234,652	-	7	1_A375_shU7_minus_lacRNA_NR_1...340, 1_A375_shU7_minus_lacRNA_NR_1...349, 1_A375_shU7_minus_lacRNA_NR_1...350, 2_A375_shU97_plus_lacRNA_NR_1.462, 2_A375_shU97_plus_lacRNA_NR_1.463, 4_A375_DGR1...585, 4_A375_DGR1...588	142709, 69811, 22135, 104807, 14791, 143983, 39207	sv gene, sv gene, sv gene, sv gene, sv gene, sv gene, sv gene	1	1	1	34.2	38.2	39	1	4_A375_DGR1	1...1	48	Gene PDE4DIP	DKFZp781J05, MGC75440, PDE4DIP, MMGL, CMYA5	phosphodiesterase 4D interacting protein	NM_001032132, NM_001003811, NM_032399, NM_001032810, NM_014644	205972_x_at, 207930_x_at, 210303_at, 211751_at, 215379_at, 232382_at	NP_001028123.1, NP_001003811.1, NP_115574.3, NP_001028110.1
GeneID:10	LOC1003	1	145,016,473	145,016,593	2,458	+	1	2_A375_shU7_minus_lacRNA_NR_1.349	-6905	upstream	1	0	0	22	26	20	1	1_A375_shU7_minus_lacRNA_NR_1	32	Gene LOC100505971	hypothetical LOC100505971	XR_110822		
GeneID:39	SEC22B	1	145,096,407	145,116,922	20,515	+	1	2_A375_shU97_plus_lacRNA_NR_1.464	-3767	upstream	0	1	0	29	30	16	1	2_A375_shU97_plus_lacRNA_NR_1	16	Gene SEC22B	SEC22B, ERS-dp, SEC2251	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	NM_004892	209206_at, 209207_s_at, 214257_s_at	NP_004883.2
GeneID:10	LOC1003	1	145,276,703	145,282,399	5,696	-	3	1_A375_shU7_minus_lacRNA_NR_1.336, 2_A375_shU97_plus_lacRNA_NR_1.465, 4_A375_DGR1...587	-290, -293, -402	upstream, upstream, upstream	1	1	1	30	35	30	1	2_A375_shU97_plus_lacRNA_NR_1	30	Gene LOC100505967	hypothetical LOC100505967	XR_110853		
GeneID:54	POLR3	1	145,498,356	145,579,597	81,151	-	3	2_A375_shU97_plus_lacRNA_NR_1.469, 4_A375_DGR1...572, 4_A375_DGR1...573	-237, -3055, -6657	upstream, upstream, upstream	0	1	1	16.67	20	16.67	0	2_A375_shU97_plus_lacRNA_NR_1	20	Gene POLR3GL	POLR3GL, RPC32/HOM, MGC4276, MGC3200, FLJ36200	polymerase (RNA) III (DNA directed) polypeptide G (32kD) like	NM_032335, ICT02547628.0, ICT02549290.0, ICT02811.3	223289_at	NP_115681.1, EAW70412.1, EAW70413.1, EAW70414.1
GeneID:23	ANKRD	1	145,479,305	145,479,647	6,339	+	3	2_A375_shU97_plus_lacRNA_NR_1.469, 4_A375_DGR1...572, 4_A375_DGR1...573	118, 2902, 6518	sv gene, sv gene, downstream	0	1	1	16.67	20	16.67	0	2_A375_shU97_plus_lacRNA_NR_1	20	Gene ANKRD34A	ANKRD34A, ANKRD34, DKFZp761F232	ankyrin repeat domain 34A	NM_031039656	232703_at	NP_001034977.1
GeneID:13	LOC1311	1	145,477,055	145,499,091	22,036	+	5	1_A375_shU7_minus_lacRNA_NR_1...339, 2_A375_shU97_plus_lacRNA_NR_1.469, 2_A375_shU97_plus_lacRNA_NR_1.490, 4_A375_DGR1...572, 4_A375_DGR1...573	20891, -6481, 20357, -3845, -6657	downstream, upstream, downstream, upstream, upstream	1	1	1	16	19.25	15	4	2_A375_shU97_plus_lacRNA_NR_1	23	Gene LOC13...	MGC45719, DKFZp761F231, LY3.1	Ly1 homolog (mouse)-like	NM_152713, ICT02591095.0, ICT1820796.1	223793_at, 223936_at	NP_719424.1, EAW70417.1, EAW70418.1
GeneID:99	RBM6A	1	145,507,833	145,511,444	3,608	+	4	1_A375_shU7_minus_lacRNA_NR_1...338, 1_A375_shU7_minus_lacRNA_NR_1...339, 2_A375_shU97_plus_lacRNA_NR_1.490, 2_A375_shU97_plus_lacRNA_NR_1.491,	136, 6368, -166, 6856	sv gene, downstream, upstream, downstream	1	1	0	23	16	13	2	1_A375_shU7_minus_lacRNA_NR_1	24	Gene RBM6A	BOV-TC, BOV-1A, RBM6B, RBM6, ZNRP1, RBM6A, ZNRP, HEXIM1, Y14	RNA binding motif protein 6A	NM_033103, ICT02591097.1, ICT02550108.0	1558602_at, 210552_at, 214113_s_at, 217038_at, 217087_x_at, 232443_s_at	NP_005768.1, EAW70416.1, EAW70416.1
GeneID:67	PEX11B	1	145,516,165	145,523,732	7,567	+	5	1_A375_shU7_minus_lacRNA_NR_1...332, 1_A375_shU7_minus_lacRNA_NR_1...339, 2_A375_shU97_plus_lacRNA_NR_1.490, 2_A375_shU97_plus_lacRNA_NR_1.491, 4_A375_DGR1...574	-6385.99, -6993, 171, 17113	upstream, sv gene, upstream, sv gene, downstream	1	1	1	16.67	15.67	16	3	1_A375_shU7_minus_lacRNA_NR_1	24	Gene PEX11B	PEX11B, PEX11 BETA	peroxisomal biogenesis factor 11 beta	NM_001164795, NM_003846, ICT02591011.0, ICT2809.0	202656_at	NP_001157724.1, NP_003837.1, EAW74422.1, EAW74423.1
GeneID:83	ITGA10	1	145,524,990	145,542,866	16,876	+	4	1_A375_shU7_minus_lacRNA_NR_1.336, 2_A375_shU97_plus_lacRNA_NR_1.491, 4_A375_DGR1...574, 4_A375_DGR1...575	-6766, -6934, 6290, 24098	sv/flank, sv/flank, sv gene, downstream	1	1	1	11.33	14	19	3	1_A375_shU7_minus_lacRNA_NR_1	24	Gene ITGA10	FROG27, ITGA10	integrin, alpha 10	NM_003637, ICT02591102.0, ICT2809.0	206566_at	NP_003628.2, EAW71424.1, EAW71425.1
GeneID:14	ANKRD	1	145,549,209	145,560,326	10,217	+	2	2_A375_shU97_plus_lacRNA_NR_1.492, 4_A375_DGR1...573	20839, -121	downstream, upstream	0	1	1	12	17.5	14	2	2_A375_shU97_plus_lacRNA_NR_1	23	Gene ANKRD28	MGC129897, ANKRD28, MGC129899, FLJ25124	ankyrin repeat domain 28	NM_144590, ICT02441961.1, ICT02551221.0	231116_at	NP_653293.2, EAW71427.1, EAW71428.1
GeneID:10	PIAS3	1	145,579,668	145,588,348	10,336	+	3	1_A375_shU7_minus_lacRNA_NR_1.337, 2_A375_shU97_plus_lacRNA_NR_1.492, 4_A375_DGR1...576	13484, 60, 12140	downstream, sv gene, downstream	1	1	1	16	21	15.5	2	2_A375_shU97_plus_lacRNA_NR_1	23	Gene PIAS3	ZMIS3, FLJ44851, PIAS3	protein inhibitor of activated STAT, 3	NM_0399[illegible], ICT02591107.0, ICT02591109.0, ICT02839.2	2003[illegible]_s_at	NP_0399[illegible].2, EAW71438.1, EAW71439.1, EAW71440.1
GeneID:29	NUDT17	1	145,586,491	145,589,435	2,944	-	2	1_A375_shU7_minus_lacRNA_NR_1.337, 4_A375_DGR1...576	-27, 299	upstream, sv gene	1	0	1	16	19	22	1	4_A375_DGR1	22	Gene NUDT17	NUDT17, FLJ94433	nudix (nucleoside diphosphate linked moiety X)-type motif 17	NM_031127756, ICT19986227.1, ICT1993901.1	1561647_at, 229044_at	NP_031127761.1, EAW71433.1, EAW71432.1
GeneID:10	POLR2	1	145,592,903	145,610,664	18,279	+	4	1_A375_shU7_minus_lacRNA_NR_1.337, 1_A375_shU7_minus_lacRNA_NR_1.338, 2_A375_shU97_plus_lacRNA_NR_1.493, 4_A375_DGR1...576	21612, -26, -166, 21748	downstream, upstream, upstream, downstream	1	1	1	19.3	23.5	18	2	2_A375_shU97_plus_lacRNA_NR_1	26	Gene POLR3C	RPC3, RPC62, POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	NM_006385, ICT1967987.1, ICT2291515.0, ICT2809[illegible].2	209302_at, 210573_s_at	NP_006376.3, EAW71436.1, EAW71434.1, EAW71435.1
GeneID:27	RNF115	1	145,611,036	145,660,776	77,740	+	2	2_A375_shU7_minus_lacRNA_NR_1.338, 2_A375_shU97_plus_lacRNA_NR_1.493	-13K, 39	upstream, sv gene	1	1	0	21	26	14	1	2_A375_shU97_plus_lacRNA_NR_1	26	Gene RNF115	BCA2, ZNF364, RNF115	ring finger protein 115	NM_0144[illegible], ICT02547[illegible].0, ICT1641301.3	212742_at	NP_[illegible]2761.1, EAW71437.1, EAW71438.1
GeneID:10	LOC1003	1	146,270,522	146,274,200	671	-	1	2_A375_shU97_plus_lacRNA_NR_1.494	665	sv gene	0	1	0	7	16	8	1	2_A375_shU97_plus_lacRNA_NR_1	16	Gene LOC100505723	hypothetical LOC100505723	XR_110820, XR_110821		
GeneID:10	LOC1003	1	146,270,555	146,284,329	10,974	+	1	2_A375_shU97_plus_lacRNA_NR_1.494	172	sv gene	0	1	0	7	16	8	1	2_A375_shU97_plus_lacRNA_NR_1	16	Gene LOC100505752	hypothetical LOC100505752	XR_110822		
GeneID:55	PRKAB2	1	146,626,955	146,644,129	17,444	-	2	1_A375_shU7_minus_lacRNA_NR_1.340, 2_A375_shU97_plus_lacRNA_NR_1.496	-65, -191	upstream, upstream	1	1	0	27	29	14	1	2_A375_shU97_plus_lacRNA_NR_1	29	Gene PRKAB2	PRKAB2, MGC61496	protein kinase, AMP-activated, beta 2 non-catalytic subunit	NM_005399, ICT11232.2	1555827_s_at, 214474_at, 225276_at	NP_003390.1, EAW69394.1
GeneID:10	LOC1003	1	146,644,328	146,651,643	97,317	+	2	1_A375_shU7_minus_lacRNA_NR_1.340, 2_A375_shU97_plus_lacRNA_NR_1.496	-13K, -6	upstream, upstream	1	1	0	27	29	14	1	2_A375_shU97_plus_lacRNA_NR_1	29	Gene LOC100505794	hypothetical LOC100505794	XR_110823, XR_110824		
GeneID:23	FAM35	1	146,659,064	146,697,230	41,246	-	1	2_A375_shU97_plus_lacRNA_NR_1.497	238	sv gene	0	1	0	10	14	12	1	2_A375_shU97_plus_lacRNA_NR_1	14	Gene FAM35	FAM35		NM_031449, NM_001144829, NM_001144830, ICT02549270.0, ICT02549351.0, ICT02549340.1, ICT02549341.0, ICT02636150.0	1559662_at, 205776_at, 210300_s_at, 240422_at	NP_001438322, NP_001138301.1, NP_001138302.1, EAW69340.1, EAW69341.1, EAW69342.1, EAW69339.1, EAW69342.1
GeneID:89	KIAA0513	1	146,714,291	146,787,443	83,152	+	2	1_A375_shU7_minus_lacRNA_NR_1.340, 2_A375_shU97_plus_lacRNA_NR_1.498	-51, 13	upstream, sv gene	1	1	0	21	24	16	1	2_A375_shU97_plus_lacRNA_NR_1	24	Gene CHD11	ALC1, CHD11, Chromodomain Helicase DNA binding protein 1-like	chromodomain helicase DNA binding protein 1-like	NM_015736, ICT02555992.0, ICT02555590.0, ICT2335594.0	1558660_s_at, 207845_s_at, 212539_at, 230070_at, 244948_at	NP_056273.3, EAW69238.1, EAW69237.1, EAW69238.1
GeneID:89	BCL9	1	147,013,182	147,090,017	84,835	+	3	1_A375_shU7_minus_lacRNA_NR_1.340, 2_A375_shU97_plus_lacRNA_NR_1.498, 2_A375_shU97_plus_lacRNA_NR_1.500	58226, -6910, 59784	sv gene, upstream, sv gene	1	1	0	16	25	10.5	2	2_A375_shU97_plus_lacRNA_NR_1	27	Gene BCL9	BCL9, LGS, MGC131991	B-cell CLL/lymphoma 9	NM_004326, ICT02555596.0, ICT02885.3	204129_at	NP_004317.2, EAW69322.1, EAW69323.1
GeneID:55	ACP6	1	147,119,165	147,142,634	23,469	-	3	1_A375_shU7_minus_lacRNA_NR_1.339, 2_A375_shU97_plus_lacRNA_NR_1.501, 2_A375_shU97_plus_lacRNA_NR_1.502	-36, -54, -6422	upstream, upstream, upstream	1	1	0	19.5	20.5	10	2	2_A375_shU97_plus_lacRNA_NR_1	25	Gene ACP6	ACP6, ACP-L1, PACPL1, LHAP-6, lysophosphatase	acid phosphatase 6, lysophosphatidic	NM_018581, ICT02702.0	218765_at	NP_061145.3, EAW69301.1
GeneID:27	GJA5	1	147,238,332	147,243,484	17,152	-	2	1_A375_shU7_minus_lacRNA_NR_1.338, 2_A375_shU97_plus_lacRNA_NR_1.502	22536, 12908	Downstream, Downstream	1	1	0	39	41	9	1	2_A375_shU97_plus_lacRNA_NR_1	41	Gene GJA5	GJA5, CX40, MGC11168	gap junction protein, alpha 5, 40kDa	NM_005266, NM_181703, ICT2259932.0, ICT1809004.2	214466_at, 228791_at	NP_005257.2, NP_859094.1, EAW69225.1, EAW69230.1
GeneID:28	NBPF14	1	146,600,842	146,625,565	22,206	-	3	1_A375_shU7_minus_lacRNA_NR_1.338, 2_A375_shU97_plus_lacRNA_NR_1.500, 4_A375_DGR1...581	23512, 23126, 23512	Downstream, Downstream, Downstream	1	1	1	20	24	20	1	4_A375_DGR1	33	Gene NBPF14	FLJ38532, FLJ45370, DJ535E19.C1.1, NBPF14, NBPF	neuroblastoma breakpoint family, member 14	NM_015563		NP_056186.1
GeneID:10	LOC1003	1	146,630,249	146,631,181	110,932	-	2	1_A375_shU7_minus_lacRNA_NR_1.339, 4_A375_DGR1...582	119661, 119613	Downstream, Downstream	1	1	1	19	12	39	1	4_A375_DGR1	28	Gene LOC100216142	neuroblastoma breakpoint family, member	XR_110792		
GeneID:28	NBPF15	1	146,630,166	146,696,267	66,079	+	2	2_A375_shU97_plus_lacRNA_NR_1.507, 4_A375_DGR1...583	-1432, -1696	upstream, upstream	0	1	1	21.5	25.5	17.5	2	2_A375_shU97_plus_lacRNA_NR_1	36	Gene NBPF15	AB14, FLJ10350, NBPF15, MGC8902, FLJ98648	neuroblastoma breakpoint family, member 15	NM_173630, NM_001170733	213912_s_at	NP_775900.2, NP_001158236.1
GeneID:84	FLJ37965	1	146,694,456	146,696,310	1,854	+	2	4_A375_DGR1...588, 4_A375_DGR1...589	10164, -9976	upstream, upstream	0	0	1	7	8	20	2	4_A375_DGR1	27	Gene FLJ37965	hypothetical LOC643911	XR_110843	1558879_at	
GeneID:28	RNF13	1	149,234,888	149,234,221	183	-	3	1_A375_shU7_minus_lacRNA_NR_1.339, 2_A375_shU97_plus_lacRNA_NR_1.511, 4_A375_DGR1...590	688, 206, 517	Downstream, Downstream, Downstream	1	1	1	49	62	62	1	4_A375_DGR1	62	Gene RNF13	RNF13, UTF13, RNF(P1, RNF(P1, UTP13, UP-13	RING FINGER protein 13	NM_007282, ICT02555950.0, ICT02555590.0, ICT2335594.0	1558660_s_at, 207845_s_at, 212539_at, 230070_at, 244948_at	NP_009113.1, EAW69227.1, EAW69228.1
GeneID:28	LOC2833	1	149,279,478	149,291,742	12,266	+	2	4_A375_DGR1...591, 4_A375_DGR1...592	15100, 19122	Downstream, Downstream	0	0	2	11	15	17.5	2	4_A375_DGR1	28	Gene LOC283892	FLJ31550, LOC283892	hypothetical LOC283892	NM_207022	233163_s_at	
GeneID:64	RFFL	1	149,308,909	149,312,134	7,245	+	1	4_A375_DGR1...592	14348	Downstream	0	0	1	16	19	20	1	4_A375_DGR1	20	Gene RFFL	RFFL, RNF(P1-403)12.9	ring finger protein (C3H2C3 type) like	NM_133342		
GeneID:84	LOC2844	1	149,675,680	149,679,929	749	+	1	4_A375_DGR1...592	6384	Downstream	0	0	1	14	11	30	1	4_A375_DGR1	30	Gene LOC644634	hypothetical LOC644634	LRP8B protein ENSP00000351[illegible]	NM_001135539		NP_001135539.1
GeneID:83	HIST2H	1	149,836,010	149,838,232	2,222	-	5	1_A375_shU7_minus_lacRNA_NR_1.331, 2_A375_shU97_plus_lacRNA_NR_1.512, 2_A375_shU97_plus_lacRNA_NR_1.513, 4_A375_DGR1...594, 4_A375_DGR1...595	-138, -360, -1096, 622, -360	upstream, upstream, upstream, sv gene, upstream	1	1	1	16.5	20	36	2	4_A375_DGR1	36	Gene HIST2H2BE	MGC119004, MGC129776, HIST2H2BE, HDB(L103, HDB-1, HDB, MGC119002, HDB(FG, GL103, MGC129703, HDBG	histone cluster 2, H2be	NM_003528	202708_s_at	NP_003519.1
GeneID:83	HIST2H	1	149,838,323	149,838,961	639	-	5	1_A375_shU7_minus_lacRNA_NR_1.331, 2_A375_shU97_plus_lacRNA_NR_1.512, 2_A375_shU97_plus_lacRNA_NR_1.513, 4_A375_DGR1...594, 4_A375_DGR1...595	-197, 87, 932, 925, 87	upstream, sv gene, downstream, upstream, sv gene	1	1	1	16.5	20	36	2	4_A375_DGR1	36	Gene HIST2H2AC	2DHQ, H2AFQ, HSH-GL103, HIST2H2AC, MGC74490, H2A	histone cluster 2, H2ac	NM_003517, ICT2216892.0		NP_003508.1, EAW69364.1
GeneID:83	HIST2H	1	149,839,019	149,839,466	447	-	5	1_A375_shU7_minus_lacRNA_NR_1.331, 2_A375_shU97_plus_lacRNA_NR_1.512, 2_A375_shU97_plus_lacRNA_NR_1.513, 4_A375_DGR1...594, 4_A375_DGR1...595	1086, 674, 1086, 674	upstream, sv gene, downstream, downstream	1	1	1	16.5	20	36	2	4_A375_DGR1	36	Gene HIST2H2AB	HIST2H2AB		NM_175065, ICT02216891.1		NP_780235.1, EAW69360.1
GeneID:10	LOC1003	1	149,870,539	149,896,907	22,371	+	3	1_A375_shU7_minus_lacRNA_NR_1.332, 2_A375_shU97_plus_lacRNA_NR_1.514, 4_A375_DGR1...596	28655, 28272, 28144	downstream, downstream, downstream	1	1	1	23	16	22	1	1_A375_shU7_minus_lacRNA_NR_1	23	Gene LOC100507840	hypothetical LOC100507840	XR_111184, XR_108548, XR_114799		
GeneID:99	SV2A	1	149,876,970	149,889,434	14,464	-	3	1_A375_shU7_minus_lacRNA_NR_1.332, 2_A375_shU97_plus_lacRNA_NR_1.514, 4_A375_DGR1...596	-10052, -10074, 10248	upstream, upstream, downstream	1	1	1	23	16	22	1	1_A375_shU7_minus_lacRNA_NR_1	23	Gene SV2A	SV2, SV2A, KIAA0736	synaptic vesicle glycoprotein 2A	NM_014849, ICT01694222.2, ICT2216830.0, ICT2329824.0	202369_at	NP_055994.3, EAW65196.1, EAW63917.1, EAW63916.1
GeneID:10	SF3B4	1	149,898,211	149,899,702	6,491	-	3	1_A375_shU7_minus_lacRNA_NR_1.332, 2_A375_shU97_plus_lacRNA_NR_1.514, 4_A375_DGR1...596	-66, -106, 22	sv gene, upstream, sv gene	1	1	1	23	16	22	1	1_A375_shU7_minus_lacRNA_NR_1	23	Gene SF3B4	SAP49, PHS49, MGC10036, SF3B4, SF3b49	splicing factor 3b, subunit 4, 49kDa	NM_005850, ICT02512.3	209344_s_at	NP_005841.1, EAW63916.1
GeneID:10	MTMR11	1	149,930,543	149,932,791	6,249	+	4	1_A375_shU7_minus_lacRNA_NR_1.332, 2_A375_shU97_plus_lacRNA_NR_1.514, 2_A375_shU97_plus_lacRNA_NR_1.515, 4_A375_DGR1...596	9175, 8953, 2345, 9111	downstream, downstream, downstream, downstream	1	1	1	19	16	18	2	1_A375_shU7_minus_lacRNA_NR_1	23	Gene MTMR11	CMA, MTMR11, RP11-212A13.1	myotubularin related protein 11	NM_181873, NM_001143932, ICT01924051.1, ICT2216877.0, ICT2329297.0, ICT2329298.0, ICT2329990.0, ICT2329930.0, ICT2809.2	1559834_s_at, 202078_s_at	NP_[illegible]2.1, NP_001139034.1, EAW63900.1, EAW63903.1, EAW63902.1, EAW63901.1, EAW63911.1, EAW63902.1, EAW63904.1
GeneID:56	OTUD7B	1	149,912,251	149,932,696	20,455	-	3	1_A375_shU7_minus_lacRNA_NR_1.332, 2_A375_shU7_minus_lacRNA_NR_1.374, 2_A375_shU97_plus_lacRNA_NR_1.515	3965, 30, 11550	sv gene, sv gene, downstream	1	1	0	22	19.67	30.33	3	1_A375_shU7_minus_lacRNA_NR_1	26	Gene OTUD7B	OTUD7B, CEZANNE, ZA20D1	OTU domain containing 7B	NM_032333, ICT01969221.1, ICT2216997.0	1558139_s_at, 220031_at, 227426_at, 229455_at, 229964_at	NP_[illegible]4.2, EAW63557.1, EAW63558.1
GeneID:11	VPS45	1	150,039,542	150,117,005	76,163	+	1	2_A375_shU97_plus_lacRNA_NR_1.516	242	sv gene	0	1	0	17	27	12	1	2_A375_shU97_plus_lacRNA_NR_1	27	Gene VPS45	VPS45A, VPS45, HIVPS45, dJ542K, VPS45, VPS45B, VPS45A, H1	vacuolar protein sorting 45 homolog (S. cerevisiae)	NM_007259, ICT02701400.0, ICT02654.2	207967_at, 209260_at	NP_009190.2, EAW65564.1, EAW63565.1





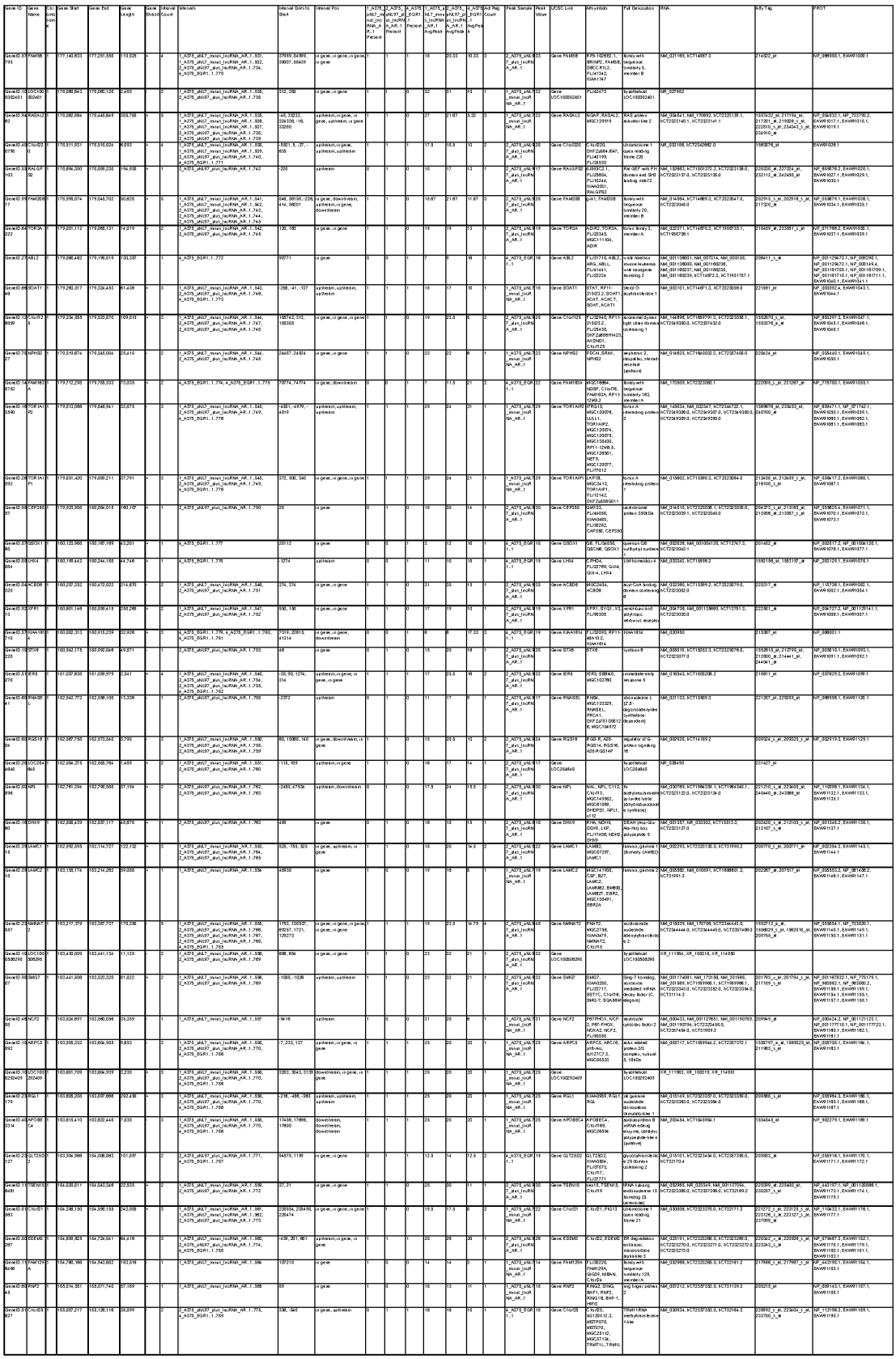
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:3570	IL6R	1	154,377,669	154,440,188	62,519	+	3	2_A375_pNL97_plus_lncRNA_AR..1..567, 4_A375_EGR1..1..638, 4_A375_EGR1..1..639	1115, 91, 29435	in gene, in gene, in gene	0	1	1	13	11.67	16.67	3	4_A375_EGR1..1	18	Gene IL6R	IL-6R-1, CD126, MGC104991, IL6RA, IL-6R-alpha, IL6R	interleukin 6 receptor	NM_181359, NM_000565, hCT1950712.1, hCT2280196.0, hCT2352647.0	205945_at, 217489_s_at, 226333_at	NP_852004.1, NP_000556.1, EAW53199.1, EAW53200.1, EAW53201.1
GeneID:55585	UBE2Q1	1	154,521,051	154,531,120	10,069	-	4	1_A375_pNL7_minus_lncRNA_AR..1..409, 1_A375_pNL7_minus_lncRNA_AR..1..410, 2_A375_pNL97_plus_lncRNA_AR..1..568, 2_A375_pNL97_plus_lncRNA_AR..1..569	-258, -9298, -304, -9298	upstream, upstream, upstream, upstream	1	1	0	27	31	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene UBE2Q1	UBE2Q1, PRO3094, UBE2Q, GTAP, NICE-5	ubiquitin-conjugating enzyme E2Q family member 1	NM_017582, hCT22719.2	217978_s_at, 222480_at, 231818_s_at	NP_060052.3, EAW53193.1
GeneID:1141	CHRNB2	1	154,540,257	154,552,354	12,097	+	4	1_A375_pNL7_minus_lncRNA_AR..1..409, 1_A375_pNL7_minus_lncRNA_AR..1..410, 2_A375_pNL97_plus_lncRNA_AR..1..568, 2_A375_pNL97_plus_lncRNA_AR..1..569	-8881, 159, -8833, 159	upstream, in gene, upstream, in gene	1	1	0	27	31	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene CHRNB2	CHRNB2, nAChRB2, EFNL3	cholinergic receptor, nicotinic, beta 2 (neuronal)	NM_000748, hCT9794.3	206635_at, 241389_at	NP_000739.1, EAW53192.1
GeneID:103	ADAR	1	154,554,533	154,600,456	45,923	-	3	2_A375_pNL97_plus_lncRNA_AR..1..570, 2_A375_pNL97_plus_lncRNA_AR..1..571, 4_A375_EGR1..1..640	19880, 166, 72	in gene, in gene, in gene	0	1	1	16.5	18.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ADAR	DSRAD, DRADA, K88dsRBP, P136, IFI4, G1P1, p136, K88DSRBP, ADAR, DSH, ADAR1, IFI-4	adenosine deaminase, RNA-specific	NM_001111, NM_001025107, NM_015840, NM_015841, NM_001193495, hCT1962263.1, hCT2278463.0, hCT2278464.0, hCT2278465.0, hCT2278467.0, hCT2278469.0, hCT2352674.0, hCT9875.2	201786_s_at	NP_001102.2, NP_001020278.1, NP_056655.2, NP_056656.2, NP_001180424.1, EAW53189.1, EAW53183.1, EAW53184.1, EAW53185.1, EAW53186.1, EAW53187.1, EAW53188.1, EAW53190.1
GeneID:3782	KCNN3	1	154,679,902	154,842,754	162,852	-	3	4_A375_EGR1..1..641, 4_A375_EGR1..1..642, 4_A375_EGR1..1..643	128130, 55662, 23282	in gene, in gene, in gene	0	0	1	7.67	8	15.67	3	4_A375_EGR1..1	17	Gene KCNN3	KCNN3, KCa2.3, SK3, SKCA3, hSK3	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	NM_170782, NM_002249, hCT11092.2, hCT2278482.0, hCT2352720.0, hCT2352721.0	205902_at, 205903_s_at	NP_740752.1, NP_002240.3, EAW53179.1, EAW53180.1, EAW53181.1, EAW53182.1
GeneID:10654	PMVK	1	154,897,208	154,909,484	12,276	-	2	1_A375_pNL7_minus_lncRNA_AR..1..411, 2_A375_pNL97_plus_lncRNA_AR..1..572	172, 124	in gene, in gene	1	1	0	40	41	16	1	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene PMVK	PMVK, HUMPMKI, PMKA, PMKASE, PMK	phosphomevalonate kinase	NM_006556, hCT1777356.2, hCT1984606.1	203515_s_at	NP_006547.1, EAW53177.1, EAW53178.1
GeneID:57326	PBXIP1	1	154,916,556	154,928,567	12,011	-	5	1_A375_pNL7_minus_lncRNA_AR..1..411, 1_A375_pNL7_minus_lncRNA_AR..1..412, 2_A375_pNL97_plus_lncRNA_AR..1..572, 2_A375_pNL97_plus_lncRNA_AR..1..573, 4_A375_EGR1..1..644	19255, -5769, 19207, -5769, -5609	downstream, upstream, downstream, upstream, upstream	1	1	1	33.5	39.5	20.5	2	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene PBXIP1	HPIP, PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	NM_020524, hCT2278476.1, hCT2278478.0, hCT2352750.0	207838_x_at, 212259_s_at, 214176_s_at, 214177_s_at	NP_065385.2, EAW53174.1, EAW53175.1, EAW53176.1
GeneID:90780	PYGO2	1	154,929,502	154,934,258	4,756	-	5	1_A375_pNL7_minus_lncRNA_AR..1..412, 2_A375_pNL97_plus_lncRNA_AR..1..573, 2_A375_pNL97_plus_lncRNA_AR..1..574, 4_A375_EGR1..1..644, 4_A375_EGR1..1..645	-78, -78, -9582, 82, -7118	upstream, upstream, upstream, in gene, upstream	1	1	1	18	24.67	21.33	3	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene PYGO2	1190004M21Rik, FLJ33226, PYGO2	pygopus homolog 2 (Drosophila)	NM_138300, hCT2344269.0, hCT2344270.0	225370_at, 239666_at	NP_612157.1, EAW53172.1, EAW53173.1
GeneID:6464	SHC1	1	154,934,774	154,946,959	12,185	-	6	1_A375_pNL7_minus_lncRNA_AR..1..412, 2_A375_pNL97_plus_lncRNA_AR..1..573, 2_A375_pNL97_plus_lncRNA_AR..1..574, 2_A375_pNL97_plus_lncRNA_AR..1..575, 4_A375_EGR1..1..644, 4_A375_EGR1..1..645	12623, 12623, 3119, -8721, 12783, 5583	downstream, downstream, in gene, upstream, downstream, in gene	1	1	1	16.5	27.5	18.25	4	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene SHC1	SHC1, SHCA, FLJ26504, SHC	SHC (Src homology 2 domain containing) transforming protein 1	NM_003029, NM_183001, NM_001130040, NM_001130041, hCT2278470.1, hCT2278473.1, hCT2278477.0, hCT2352636.0, hCT2352637.0	201469_s_at, 214853_s_at	NP_003020.2, NP_892113.4, NP_001123512.1, NP_001123513.1, EAW53168.1, EAW53170.1, EAW53167.1, EAW53169.1, EAW53171.1
GeneID:1163	CKS1B	1	154,947,118	154,951,725	4,607	+	3	2_A375_pNL97_plus_lncRNA_AR..1..574, 2_A375_pNL97_plus_lncRNA_AR..1..575, 4_A375_EGR1..1..645	-3278, 8582, -5742	upstream, downstream, upstream	0	1	1	15.67	24	16	3	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene CKS1B	PNAS-16, CKS1B, CKS1, PNAS-18, ckshs1	CDC28 protein kinase regulatory subunit 1B	NM_001826, NR_024163, hCT1777359.3, hCT1963031.2, hCT2351530.0, hCT2351531.0, hCT2351532.0, hCT2351533.0, hCT2351534.0	201897_s_at	NP_001817.1, EAW53165.1, EAW53160.1, EAW53161.1, EAW53164.1, EAW53166.1, EAW53162.1, EAW53163.1
GeneID:100423020	MIR4258	1	154,948,169	154,948,259	90	+	3	2_A375_pNL97_plus_lncRNA_AR..1..574, 2_A375_pNL97_plus_lncRNA_AR..1..575, 4_A375_EGR1..1..645	-4329, 7511, -6793	upstream, downstream, upstream	0	1	1	15.67	24	16	3	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene MIR4258	MIR4258	microRNA 4258	NR_036212		
GeneID:80308	FLAD1	1	154,955,770	154,965,587	9,817	+	5	1_A375_pNL7_minus_lncRNA_AR..1..413, 1_A375_pNL7_minus_lncRNA_AR..1..414, 2_A375_pNL97_plus_lncRNA_AR..1..575, 2_A375_pNL97_plus_lncRNA_AR..1..576, 4_A375_EGR1..1..646	17702, 16668, -90, 17638, 17990	downstream, downstream, upstream, downstream, downstream	1	1	1	28	33.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene FLAD1	FAD1, MGC31803, FADS, FLAD1, RP11-307C12.7, MGC40255, PP591	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	NM_001184891, NM_001184892, NM_025207, NM_201398, hCT11091.2, hCT1953595.1, hCT1953596.1, hCT1953598.1, hCT2352696.0, hCT2352697.0, hCT2352698.0	205661_s_at, 212541_at	NP_001171820.1, NP_001171821.1, NP_079483.3, NP_958800.1, EAW53154.1, EAW53155.1, EAW53153.1, EAW53156.1, EAW53157.1, EAW53158.1, EAW53159.1
GeneID:55891	LENEP	1	154,968,062	154,968,791	729	+	6	1_A375_pNL7_minus_lncRNA_AR..1..413, 1_A375_pNL7_minus_lncRNA_AR..1..414, 1_A375_pNL7_minus_lncRNA_AR..1..415, 2_A375_pNL97_plus_lncRNA_AR..1..576, 4_A375_EGR1..1..646, 4_A375_EGR1..1..647	7410, 8594, 10514, 7346, 7698, 10162	downstream, downstream, downstream, downstream, downstream, downstream	1	1	1	28	25	22.5	2	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene LENEP	LENEP, LEP503	lens epithelial protein	NM_018655, hCT1783402.1	221115_s_at	NP_061125.1, EAW53152.1
GeneID:51043	ZBTB7B	1	154,975,112	154,990,999	15,887	+	8	1_A375_pNL7_minus_lncRNA_AR..1..413, 1_A375_pNL7_minus_lncRNA_AR..1..414, 1_A375_pNL7_minus_lncRNA_AR..1..415, 2_A375_pNL97_plus_lncRNA_AR..1..576, 4_A375_EGR1..1..646, 4_A375_EGR1..1..647, 4_A375_EGR1..1..648, 4_A375_EGR1..1..649	-1640, -456, 1464, -1704, -1352, 1112, 9048, 15096	upstream, upstream, in gene, upstream, upstream, in gene, in gene, in gene	1	1	1	21	20.5	21.75	4	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene ZBTB7B	ZNF857B, THPOK, ZFP67, ZBTB15, ZBTB7B, c-Krox, hcKrox, DKFZp686G01254	zinc finger and BTB domain containing 7B	NM_015872, hCT2280155.0, hCT2280156.0, hCT2280157.0	205853_at, 235145_at	NP_056956.2, EAW53150.1, EAW53149.1, EAW53151.1
GeneID:127579	DCST2	1	154,991,003	155,006,257	15,254	-	2	4_A375_EGR1..1..648, 4_A375_EGR1..1..649	22097, 16049	downstream, downstream	0	0	1	14	16	21	2	4_A375_EGR1..1	22	Gene DCST2	DCST2, FLJ32934	DC-STAMP domain containing 2	NM_144622, hCT2278524.1, hCT2278525.1, hCT2349468.0	242968_at	NP_653223.2, EAW53148.1, EAW53146.1, EAW53147.1
GeneID:149095	DCST1	1	155,006,300	155,023,406	17,106	+	6	1_A375_pNL7_minus_lncRNA_AR..1..416, 4_A375_EGR1..1..650, 4_A375_EGR1..1..651, 4_A375_EGR1..1..652, 4_A375_EGR1..1..653, 4_A375_EGR1..1..654	17044, 15001, 17092, 17935, 24132, 26372	in gene, in gene, in gene, downstream, downstream, downstream	1	0	1	15	13.2	18.6	5	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene DCST1	FLJ32785, RP11-307C12.10, DCST1	DC-STAMP domain containing 1	NM_152494, NM_001143687	1553680_at	NP_689707.2, NP_001137159.1
GeneID:100505666	LOC100505666	1	155,017,667	155,036,419	18,752	-	8	1_A375_pNL7_minus_lncRNA_AR..1..416, 2_A375_pNL97_plus_lncRNA_AR..1..577, 4_A375_EGR1..1..650, 4_A375_EGR1..1..651, 4_A375_EGR1..1..652, 4_A375_EGR1..1..653, 4_A375_EGR1..1..654, 4_A375_EGR1..1..655	13075, 195, 15118, 13027, 12184, 5987, 3747, 1651	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	13.71	14.29	18.29	7	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene LOC100505666		hypothetical LOC100505666	XR_111946, XR_111947, XR_108354, XR_108356, XR_108355, XR_114611, XR_114613, XR_114612		
GeneID:8751	ADAM15	1	155,023,762	155,035,252	11,490	+	8	1_A375_pNL7_minus_lncRNA_AR..1..416, 2_A375_pNL97_plus_lncRNA_AR..1..577, 4_A375_EGR1..1..650, 4_A375_EGR1..1..651, 4_A375_EGR1..1..652, 4_A375_EGR1..1..653, 4_A375_EGR1..1..654, 4_A375_EGR1..1..655	-418, 12462, -2461, -370, 473, 6670, 8910, 11006	upstream, downstream, upstream, upstream, in gene, in gene, in gene, in gene	1	1	1	13.71	14.29	18.29	7	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene ADAM15	MDC15, ADAM15	ADAM metallopeptidase domain 15	NM_003815, NM_207191, NM_207194, NM_207195, NM_207196, NM_207197	1555898_a_at, 217007_s_at	NP_003806.3, NP_997074.1, NP_997077.1, NP_997078.1, NP_997079.1, NP_997080.1
GeneID:1945	EFNA4	1	155,036,213	155,042,029	5,816	+	4	2_A375_pNL97_plus_lncRNA_AR..1..577, 4_A375_EGR1..1..653, 4_A375_EGR1..1..654, 4_A375_EGR1..1..655	11, -5781, -3541, 1445	in gene, upstream, upstream, upstream	0	1	1	10	13	19.25	4	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene EFNA4	EFNA4, FLJ57652, EPLG4, MGC125826, EFL4, LERK4	ephrin-A4	NM_005227, NM_182689, NM_182690, hCT11095.2, hCT2280163.0, hCT2352737.0	205107_s_at	NP_005218.1, NP_872631.1, NP_872632.2, EAW53138.1, EAW53139.1, EAW53140.1
GeneID:1944	EFNA3	1	155,051,348	155,060,014	8,666	+	5	4_A375_EGR1..1..656, 4_A375_EGR1..1..657, 4_A375_EGR1..1..658, 4_A375_EGR1..1..659, 4_A375_EGR1..1..660	1228, 5724, 6958, 12908, 14844	in gene, in gene, in gene, downstream, downstream	0	0	1	10	13.6	16	5	4_A375_EGR1..1	21	Gene EFNA3	EFL2, Ehk1-L, LERK3, EPLG3, EFNA3	ephrin-A3	NM_004952, hCT11094.3, hCT1953801.1	210132_at	NP_004943.1, EAW53137.1, EAW53136.1
GeneID:1942	EFNA1	1	155,100,349	155,107,386	7,037	+	8	1_A375_pNL7_minus_lncRNA_AR..1..417, 2_A375_pNL97_plus_lncRNA_AR..1..578, 2_A375_pNL97_plus_lncRNA_AR..1..579, 2_A375_pNL97_plus_lncRNA_AR..1..580, 4_A375_EGR1..1..661, 4_A375_EGR1..1..662, 4_A375_EGR1..1..663, 4_A375_EGR1..1..664	1251, -477, 6195, 12739, -1373, 2307, 7331, 7939	in gene, upstream, downstream, downstream, upstream, in gene, downstream, downstream	1	1	1	17.25	19.5	18.25	4	4_A375_EGR1..1	24	Gene EFNA1	TNFAIP4, EFNA1, ECKLG, B61, EFL1, EPLG1, LERK1	ephrin-A1	NM_182685, NM_004428, hCT1783408.2, hCT2280166.0, hCT2280167.0, hCT2280168.0, hCT2352708.0	202023_at	NP_872626.1, NP_004419.2, EAW53131.1, EAW53132.1, EAW53133.1, EAW53134.1, EAW53135.1
GeneID:55974	RAG1AP1	1	155,108,288	155,111,334	3,046	+	8	1_A375_pNL7_minus_lncRNA_AR..1..417, 2_A375_pNL97_plus_lncRNA_AR..1..578, 2_A375_pNL97_plus_lncRNA_AR..1..579, 2_A375_pNL97_plus_lncRNA_AR..1..580, 4_A375_EGR1..1..661, 4_A375_EGR1..1..662, 4_A375_EGR1..1..663, 4_A375_EGR1..1..664	-6668, -6416, 258, 4600, -9312, -5632, -606, 0	upstream, upstream, in gene, downstream, upstream, upstream, upstream, in gene	1	1	1	17.25	19.5	18.25	4	4_A375_EGR1..1	24	Gene RAG1AP1	HsSWEET1, RAG1AP1, SLC50A1, SWEET1, slv, SCP	recombination activating gene 1 activating protein 1	NM_018845, NM_001122837, NM_001122839, hCT1950804.1, hCT2280170.0, hCT2280173.0, hCT90560.3	219125_s_at	NP_061333.2, NP_001116309.1, NP_001116311.1, EAW53127.1, EAW53128.1, EAW53129.1, EAW53130.1
GeneID:54344	DPM3	1	155,112,367	155,112,996	629	+	5	2_A375_pNL97_plus_lncRNA_AR..1..579, 2_A375_pNL97_plus_lncRNA_AR..1..580, 4_A375_EGR1..1..662, 4_A375_EGR1..1..663, 4_A375_EGR1..1..664	4452, -92, 10340, 5316, 4708	downstream, upstream, downstream, downstream, downstream	0	1	1	17.67	18.33	17.33	3	4_A375_EGR1..1	24	Gene DPM3	MGC125904, DPM3, MGC34275, CDG1O, MGC125905	dolichyl-phosphate mannosyltransferase polypeptide 3	NM_018973, NM_153741, hCT1640883.3, hCT1953578.1	219373_at	NP_061846.2, NP_714963.1, EAW53125.1, EAW53126.1
GeneID:200185	KRTCAP2	1	155,141,884	155,145,804	3,920	-	2	1_A375_pNL7_minus_lncRNA_AR..1..418, 2_A375_pNL97_plus_lncRNA_AR..1..581	-52, -20	upstream, upstream	1	1	0	156	142	16	1	1_A375_pNL7_minus_lncRNA_AR..1	156	Gene KRTCAP2	KCP2, KRTCAP2	keratinocyte associated protein 2	NM_173852	224885_s_at	NP_776251.1
GeneID:80128	TRIM46	1	155,146,360	155,157,445	11,085	+	5	1_A375_pNL7_minus_lncRNA_AR..1..418, 1_A375_pNL7_minus_lncRNA_AR..1..419, 2_A375_pNL97_plus_lncRNA_AR..1..581, 2_A375_pNL97_plus_lncRNA_AR..1..582, 4_A375_EGR1..1..665	-504, 17944, -536, 18440, 10120	upstream, downstream, upstream, downstream, in gene	1	1	1	60.67	57.33	17.67	3	1_A375_pNL7_minus_lncRNA_AR..1	156	Gene TRIM46	TRIM46, TRIFIC, FLJ23229, GENEY	tripartite motif containing 46	NM_025058, hCT2278820.0, hCT2278821.0, hCT2278822.0, hCT2352717.0	220909_at, 238147_at	NP_079334.3, EAW53123.1, EAW53120.1, EAW53121.1, EAW53122.1
GeneID:4582	MUC1	1	155,158,300	155,162,700	4,400	-	3	1_A375_pNL7_minus_lncRNA_AR..1..419, 2_A375_pNL97_plus_lncRNA_AR..1..582, 4_A375_EGR1..1..665	-1604, -2100, 6220	upstream, upstream, downstream	1	1	1	13	15	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MUC1	H23AG, PEMT, PEM, MUC1, EMA, CD227, PUM, KL-6, MAM6	mucin 1, cell surface associated	NM_002456, NM_001018016, NM_001018017, NM_001044390, NM_001044391, NM_001044392, NM_001044393	207847_s_at, 211695_x_at, 213693_s_at	NP_002447.4, NP_001018016.1, NP_001037855.1, NP_001037856.1, NP_001037857.1, NP_001018017.1, NP_001037858.1
GeneID:693235	MIR92B	1	155,164,968	155,165,063	95	+	3	1_A375_pNL7_minus_lncRNA_AR..1..419, 2_A375_pNL97_plus_lncRNA_AR..1..582, 4_A375_EGR1..1..665	-664, -168, -8468	upstream, upstream, upstream	1	1	1	13	15	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MIR92B	MIRN92B, hsa-mir-92b, MIR92B	microRNA 92b	NR_030281		
GeneID:7059	THBS3	1	155,165,379	155,177,690	12,311	-	4	1_A375_pNL7_minus_lncRNA_AR..1..419, 2_A375_pNL97_plus_lncRNA_AR..1..582, 4_A375_EGR1..1..665, 4_A375_EGR1..1..666	13386, 12890, 21210, -1094	downstream, downstream, downstream, upstream	1	1	1	13.67	14	17.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene THBS3	MGC119565, MGC119564, TSP3, THBS3	thrombospondin 3	NM_007112, hCT1954408.1, hCT7162.2	209561_at	NP_009043.1, EAW53109.1, EAW53110.1
GeneID:100129268	LOC100129268	1	155,170,593	155,175,575	4,982	+	3	1_A375_pNL7_minus_lncRNA_AR..1..419, 2_A375_pNL97_plus_lncRNA_AR..1..582, 4_A375_EGR1..1..666	-6289, -5793, 8191	upstream, upstream, downstream	1	1	1	17.5	16.5	16	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100129268		hypothetical LOC100129268	XR_111944, XR_111943, XR_111945, XR_108358, XR_108357, XR_114615, XR_114614		
GeneID:4580	MTX1	1	155,178,490	155,183,625	5,135	+	1	4_A375_EGR1..1..666	294	in gene	0	0	1	15	12	17	1	4_A375_EGR1..1	17	Gene MTX1	MTX1, MTXN, MTX	metaxin 1	NM_198883, NM_002455, hCT2278824.1, hCT2278825.1, hCT2278827.1, hCT2352738.0	210386_s_at	NP_942584.1, NP_002446.2, EAW53105.1, EAW53106.1, EAW53107.1, EAW53108.1
GeneID:2629	GBA	1	155,204,239	155,214,653	10,414	-	6	1_A375_pNL7_minus_lncRNA_AR..1..420, 2_A375_pNL97_plus_lncRNA_AR..1..583, 2_A375_pNL97_plus_lncRNA_AR..1..584, 2_A375_pNL97_plus_lncRNA_AR..1..585, 4_A375_EGR1..1..667, 4_A375_EGR1..1..668	29, 17789, -35, -5891, 29, -5795	in gene, downstream, upstream, upstream, in gene, upstream	1	1	1	17.67	23.67	22.33	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene GBA	GBA1, GBA, GLUC, GCB	glucosidase, beta, acid	NM_001005742, NM_001005741, NM_000157, NM_001171811, NM_001171812, hCT2277266.1, hCT2277267.2, hCT2277268.2, hCT2352748.0	209093_s_at, 210589_s_at, 216400_at	NP_001005742.1, NP_001005741.1, NP_000148.2, NP_001165282.1, NP_001165283.1, EAW53101.1, EAW53100.1, EAW53102.1, EAW53103.1
GeneID:10712	FAM189B	1	155,216,996	155,225,274	8,278	-	7	1_A375_pNL7_minus_lncRNA_AR..1..420, 2_A375_pNL97_plus_lncRNA_AR..1..584, 2_A375_pNL97_plus_lncRNA_AR..1..585, 2_A375_pNL97_plus_lncRNA_AR..1..586, 4_A375_EGR1..1..667, 4_A375_EGR1..1..668, 4_A375_EGR1..1..669	10650, 10568, 4730, -6654, 10650, 4826, -6	downstream, downstream, in gene, upstream, downstream, in gene, upstream	1	1	1	17.5	24.25	21.75	4	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene FAM189B	FAM189B, COTE1, C1orf2	family with sequence similarity 189, member B	NM_006589, NM_198264, hCT1954396.1, hCT1954397.1, hCT2352633.0, hCT2352634.0, hCT2352635.0, hCT7149.2	1555515_a_at, 203550_s_at	NP_006580.2, NP_937995.1, EAW53094.1, EAW53095.1, EAW53097.1, EAW53099.1, EAW53096.1, EAW53098.1
GeneID:10067	SCAMP3	1	155,225,770	155,232,195	6,425	-	4	2_A375_pNL97_plus_lncRNA_AR..1..585, 2_A375_pNL97_plus_lncRNA_AR..1..586, 4_A375_EGR1..1..668, 4_A375_EGR1..1..669	11651, 67, 11747, 6915	downstream, in gene, downstream, downstream	0	1	1	15.67	23	20.33	3	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SCAMP3	SCAMP3, C1orf3	secretory carrier membrane protein 3	NM_005698, NM_052837, hCT1963120.1, hCT1963122.1, hCT1963123.1, hCT1963124.1	201771_at	NP_005689.2, NP_443069.1, EAW53090.1, EAW53091.1, EAW53092.1, EAW53093.1
GeneID:1196	CLK2	1	155,232,659	155,243,281	10,622	-	4	2_A375_pNL97_plus_lncRNA_AR..1..586, 2_A375_pNL97_plus_lncRNA_AR..1..587, 4_A375_EGR1..1..669, 4_A375_EGR1..1..670	11153, -4143, 18001, -4239	downstream, upstream, downstream, upstream	0	1	1	16	22.67	21.33	3	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene CLK2	CLK2, hCLK2, MGC61500	CDC-like kinase 2	NM_003993, hCT2277258.0, hCT7150.2, hCT7151.2	203229_s_at	NP_003984.2, EAW53089.1, EAW53087.1, EAW53088.1
GeneID:57657	HCN3	1	155,247,374	155,259,638	12,264	+	2	2_A375_pNL97_plus_lncRNA_AR..1..587, 4_A375_EGR1..1..670	50, 146	in gene, in gene	0	1	1	15	21	24	1	4_A375_EGR1..1	24	Gene HCN3	KIAA1535, HCN3, MGC131493	hyperpolarization activated cyclic nucleotide-gated potassium channel 3	NM_020897, hCT2278829.1, hCT2278830.1, hCT2278831.1, hCT2352638.0, hCT2352639.0, hCT7160.3	228741_s_at	NP_065948.1, EAW53082.1, EAW53081.1, EAW53083.1, EAW53084.1, EAW53085.1, EAW53086.1
GeneID:5313	PKLR	1	155,259,084	155,271,225	12,141	-	2	1_A375_pNL7_minus_lncRNA_AR..1..421, 2_A375_pNL97_plus_lncRNA_AR..1..588	-7399, -7367	upstream, upstream	1	1	0	22	27	14	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene PKLR	PKLR, PKR, PKL, PKRL, PK1, RPK	pyruvate kinase, liver and RBC	NM_000298, NM_181871, hCT1954411.2, hCT7165.3	207858_s_at, 210451_at	NP_000289.1, NP_870986.1, EAW53079.1, EAW53080.1
GeneID:2224	FDPS	1	155,278,539	155,290,457	11,918	+	5	1_A375_pNL7_minus_lncRNA_AR..1..421, 2_A375_pNL97_plus_lncRNA_AR..1..588, 2_A375_pNL97_plus_lncRNA_AR..1..589, 4_A375_EGR1..1..671, 4_A375_EGR1..1..672	85, 53, 15957, 12293, 18165	in gene, in gene, downstream, downstream, downstream	1	1	1	13.25	17.5	17.25	4	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene FDPS	FPPS, FDPS, FPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)	NM_002004, NM_001135821, NM_001135822, hCT2278837.0, hCT2278838.1, hCT2278840.1, hCT2352749.0	201275_at	NP_001995.1, NP_001129293.1, NP_001129294.1, EAW53075.1, EAW53076.1, EAW53078.1, EAW53077.1
GeneID:284618	C1orf104	1	155,290,251	155,293,938	3,687	-	3	2_A375_pNL97_plus_lncRNA_AR..1..589, 4_A375_EGR1..1..671, 4_A375_EGR1..1..672	-558, 3106, -2766	upstream, in gene, upstream	0	1	1	10.33	14.33	18.33	3	4_A375_EGR1..1	21	Gene C1orf104	C1orf104, FLJ35976, RP11-21N7.3	chromosome 1 open reading frame 104	NM_001039517	1552862_at	NP_001034606.1
GeneID:23623	RUSC1	1	155,290,640	155,300,909	10,269	+	3	2_A375_pNL97_plus_lncRNA_AR..1..589, 4_A375_EGR1..1..671, 4_A375_EGR1..1..672	3856, 192, 6084	in gene, in gene, in gene	0	1	1	10.33	14.33	18.33	3	4_A375_EGR1..1	21	Gene RUSC1	DKFZp761A1822, NESCA, RUSC1	RUN and SH3 domain containing 1	NM_014328, NM_001105203, NM_001105204, NM_001105205, hCT2278834.1, hCT2278835.1, hCT2278836.1, hCT2344271.0	206949_s_at	NP_055143.2, NP_001098673.1, NP_001098674.1, NP_001098675.1, EAW53070.1, EAW53071.1, EAW53069.1, EAW53072.1
GeneID:55870	ASH1L	1	155,305,052	155,532,324	227,272	-	3	1_A375_pNL7_minus_lncRNA_AR..1..422, 2_A375_pNL97_plus_lncRNA_AR..1..590, 4_A375_EGR1..1..672	-572, -540, 235620	upstream, upstream, downstream	1	1	1	26	29.5	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene ASH1L	KMT2H, ASH1, FLJ10504, ASH1L1, ASH1L, KIAA1420	ash1 (absent, small, or homeotic)-like (Drosophila)	NM_018489, hCT7156.3	218554_s_at, 222667_s_at, 226447_at	NP_060959.2, EAW53066.1
GeneID:645676	LOC645676	1	155,531,772	155,533,735	1,963	+	2	1_A375_pNL7_minus_lncRNA_AR..1..422, 2_A375_pNL97_plus_lncRNA_AR..1..590	1124, 1092	in gene, in gene	1	1	0	46	46	14	1	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene LOC645676	FLJ44595	hypothetical LOC645676	NR_027023	1554057_at	
GeneID:55249	YY1AP1	1	155,629,233	155,658,791	29,558	-	3	1_A375_pNL7_minus_lncRNA_AR..1..423, 2_A375_pNL97_plus_lncRNA_AR..1..591, 4_A375_EGR1..1..673	71, 71, 583	in gene, in gene, in gene	1	1	1	53	70	27	1	2_A375_pNL97_plus_lncRNA_AR..1	70	Gene YY1AP1	YY1AP1, FLJ13914, YAP, HCCA2, HCCA1, FLJ10875, YY1AP	YY1 associated protein 1	NM_139118, NM_139119, hCT2277245.0, hCT2277246.0, hCT2277247.0, hCT2352711.0, hCT2352712.0, hCT2352713.0, hCT2352714.0, hCT2352715.0, hCT2352716.0	217836_s_at, 227608_at, 232516_x_at	NP_620829.1, NP_620830.1, EAW53052.1, EAW53056.1, EAW53058.1, EAW53060.1, EAW53053.1, EAW53054.1, EAW53055.1, EAW53057.1, EAW53059.1
GeneID:7818	DAP3	1	155,658,874	155,708,320	49,446	+	4	1_A375_pNL7_minus_lncRNA_AR..1..423, 2_A375_pNL97_plus_lncRNA_AR..1..591, 2_A375_pNL97_plus_lncRNA_AR..1..592, 4_A375_EGR1..1..673	-154, -154, 56466, -666	upstream, upstream, downstream, upstream	1	1	1	35	47.5	22	2	2_A375_pNL97_plus_lncRNA_AR..1	70	Gene DAP3	DAP-3, MRP-S29, FLJ12817, bMRP-10, DKFZp686G12159, MRPS29, DAP3, MGC126058, MGC126059	death associated protein 3	NM_033657, NM_004632, hCT1954429.1, hCT1966078.1, hCT1966079.1, hCT1966080.1, hCT1966081.1, hCT1966082.1, hCT2278846.0, hCT2278848.0, hCT8225.3	208822_s_at	NP_387506.1, NP_004623.1, EAW53043.1, EAW53048.1, EAW53049.1, EAW53051.1, EAW53044.1, EAW53045.1, EAW53046.1, EAW53047.1, EAW53050.1
GeneID:100505728	LOC100505728	1	155,714,903	155,715,773	870	-	1	2_A375_pNL97_plus_lncRNA_AR..1..592	413	in gene	0	1	0	17	25	17	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC100505728		hypothetical LOC100505728	XR_111942, XR_108359, XR_114616		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:54856	GON4L	1	155,719,510	155,826,972	107,462	-	4	1_A375_pNL7_minus_lncRNA_AR..1..424, 2_A375_pNL97_plus_lncRNA_AR..1..592, 2_A375_pNL97_plus_lncRNA_AR..1..593, 2_A375_pNL97_plus_lncRNA_AR..1..594	-132, 111612, -68, -3236	upstream, downstream, upstream, upstream	1	1	0	26.67	37.67	18.33	3	2_A375_pNL97_plus_lncRNA_AR..1	66	Gene GON4L	RP11-101O6.1, MGC138817, GON4L, GON-4, RP11-243J16.4, FLJ20203, MGC138818, GON4, KIAA1606, FLJ12923, FLJ23040, DKFZp761I241	gon-4-like (C. elegans)	NM_001037533, NM_032292, hCT2349480.0, hCT2349481.0, hCT2349482.0, hCT2349483.0, hCT2349484.0, hCT2349485.0, hCT2352622.0, hCT2352623.0	1555913_at, 218873_at, 219846_at, 223555_at	NP_001032622.1, NP_115668.4, EAW53029.1, EAW53030.1, EAW53031.1, EAW53035.1, EAW53032.1, EAW53033.1, EAW53034.1, EAW53036.1
GeneID:23208	SYT11	1	155,829,260	155,854,990	25,730	+	3	1_A375_pNL7_minus_lncRNA_AR..1..424, 2_A375_pNL97_plus_lncRNA_AR..1..593, 2_A375_pNL97_plus_lncRNA_AR..1..594	-2156, -2220, 948	upstream, upstream, in gene	1	1	0	31.5	44	16	2	2_A375_pNL97_plus_lncRNA_AR..1	66	Gene SYT11	MGC17226, SYT12, MGC10881, KIAA0080, DKFZp761D015, SYT11	synaptotagmin XI	NM_152280, hCT2278860.0, hCT8241.3	209197_at, 209198_s_at	NP_689493.3, EAW53026.1, EAW53025.1
GeneID:22889	KIAA0907	1	155,882,836	155,904,188	21,352	-	4	1_A375_pNL7_minus_lncRNA_AR..1..425, 2_A375_pNL97_plus_lncRNA_AR..1..595, 4_A375_EGR1..1..674, 4_A375_EGR1..1..675	28, 44, 156, -8020	in gene, in gene, in gene, upstream	1	1	1	21.5	21	19.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene KIAA0907	KIAA0907, BLOM7, RP11-336K24.1	KIAA0907	NM_014949, hCT1954423.2, hCT2351511.0, hCT8219.3	202220_at, 230028_at	NP_055764.2, EAW53023.1, EAW53021.1, EAW53022.1
GeneID:677771	SCARNA4	1	155,895,749	155,895,877	128	-	3	1_A375_pNL7_minus_lncRNA_AR..1..425, 2_A375_pNL97_plus_lncRNA_AR..1..595, 4_A375_EGR1..1..674	-8283, -8267, -8155	upstream, upstream, upstream	1	1	1	27	28	16	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene SCARNA4	ACA26, SCARNA4	small Cajal body-specific RNA 4	NR_003005		
GeneID:339403	RXFP4	1	155,911,480	155,912,625	1,145	+	5	1_A375_pNL7_minus_lncRNA_AR..1..425, 2_A375_pNL97_plus_lncRNA_AR..1..595, 4_A375_EGR1..1..674, 4_A375_EGR1..1..675, 4_A375_EGR1..1..676	-7320, -7336, -7448, 728, 9336	upstream, upstream, upstream, in gene, downstream	1	1	1	17.67	18	19	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene RXFP4	MGC126556, GPCR142, RLN3R2, RXFP4, RXFPR4, GPR100, MGC126558	relaxin/insulin-like family peptide receptor 4	NM_181885, hCT2351614.0		NP_871001.1, EAW53020.1
GeneID:9181	ARHGEF2	1	155,916,630	155,948,336	31,706	-	4	1_A375_pNL7_minus_lncRNA_AR..1..426, 4_A375_EGR1..1..675, 4_A375_EGR1..1..676, 4_A375_EGR1..1..677	7856, 36128, 27520, 12240	in gene, downstream, in gene, in gene	1	0	1	13.75	13.5	16.5	4	4_A375_EGR1..1	21	Gene ARHGEF2	GEFH1, DKFZp547P1516, ARHGEF2, DKFZp547L106, P40, FLJ45440, GEF-H1, GEF, LFP40, KIAA0651	Rho/Rac guanine nucleotide exchange factor (GEF) 2	NM_004723, NM_001162383, NM_001162384, hCT2277223.1, hCT2277224.1, hCT2277225.1, hCT2277226.1, hCT2277227.1, hCT2351567.0, hCT2351566.0	1554783_s_at, 207629_s_at, 209435_s_at, 235595_at	NP_004714.2, NP_001155855.1, NP_001155856.1, EAW53014.1, EAW53015.1, EAW53016.1, EAW53012.1, EAW53013.1, EAW53017.1, EAW53018.1
GeneID:56893	UBQLN4	1	156,005,092	156,023,516	18,424	-	3	1_A375_pNL7_minus_lncRNA_AR..1..427, 2_A375_pNL97_plus_lncRNA_AR..1..596, 4_A375_EGR1..1..678	-964, -1028, -1168	upstream, upstream, upstream	1	1	1	26	30	19	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene UBQLN4	CIP75, UBQLN4, UBIN, A1U, C1orf6	ubiquilin 4	NM_020131, hCT1954431.1, hCT2277217.0, hCT2277218.0, hCT2277219.0, hCT2352651.0	222252_x_at, 224513_s_at	NP_064516.2, EAW53005.1, EAW53006.1, EAW53007.1, EAW53008.1, EAW53009.1
GeneID:28956	ROBLD3	1	156,024,517	156,028,301	3,784	+	3	1_A375_pNL7_minus_lncRNA_AR..1..427, 2_A375_pNL97_plus_lncRNA_AR..1..596, 4_A375_EGR1..1..678	-37, 27, 187	upstream, in gene, in gene	1	1	1	26	30	19	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene ROBLD3	ROBLD3, Ragulator2, MAPKSP1AP, ENDAP, LAMTOR2, HSPC003, p14, MAPBPIP	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	NM_014017, NM_001145264, hCT1963147.1	218291_at	NP_054736.1, NP_001138736.1, EAW53004.1
GeneID:57111	RAB25	1	156,030,966	156,040,295	9,329	+	4	1_A375_pNL7_minus_lncRNA_AR..1..427, 2_A375_pNL97_plus_lncRNA_AR..1..596, 4_A375_EGR1..1..678, 4_A375_EGR1..1..679	-6486, -6422, -6282, 15402	upstream, upstream, upstream, downstream	1	1	1	19	20	19.5	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene RAB25	RAB25, CATX-8, RAB11C	RAB25, member RAS oncogene family	NM_020387, hCT8238.2	218186_at	NP_065120.2, EAW53003.1
GeneID:92312	MEX3A	1	156,041,804	156,051,789	9,985	-	1	4_A375_EGR1..1..679	5421	in gene	0	0	1	12	10	20	1	4_A375_EGR1..1	20	Gene MEX3A	RKHD4, MEX-3A, MEX3A	mex-3 homolog A (C. elegans)	NM_001093725	226346_at, 227512_at, 236665_at	NP_001087194.1
GeneID:4000	LMNA	1	156,084,461	156,109,878	25,417	+	8	1_A375_pNL7_minus_lncRNA_AR..1..428, 1_A375_pNL7_minus_lncRNA_AR..1..429, 2_A375_pNL97_plus_lncRNA_AR..1..597, 2_A375_pNL97_plus_lncRNA_AR..1..598, 2_A375_pNL97_plus_lncRNA_AR..1..599, 2_A375_pNL97_plus_lncRNA_AR..1..600, 4_A375_EGR1..1..680, 4_A375_EGR1..1..681	-365, 12419, -9357, 451, 8051, 12595, 20435, 21427	upstream, in gene, upstream, in gene, in gene, in gene, in gene, in gene	1	1	1	16.5	16.17	14.83	6	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene LMNA	IDC, FPL, LMNA, LMNL1, LGMD1B, LMNC, PRO1, LFP, CMT2B1, EMD2, FPLD, LMN1, HGPS, LDP1, CMD1A, CDDC, CDCD1	lamin A/C	NM_005572, NM_170707, NM_170708, hCT2278868.0, hCT2278869.0, hCT2278870.0, hCT2278871.0, hCT2278873.0	1554600_s_at, 203411_s_at, 212086_x_at, 212089_at, 214213_x_at	NP_005563.1, NP_733821.1, NP_733822.1, EAW52996.1, EAW52997.1, EAW52998.1, EAW52999.1, EAW53000.1
GeneID:9673	SLC25A44	1	156,163,730	156,182,587	18,857	+	1	2_A375_pNL97_plus_lncRNA_AR..1..601	302	in gene	0	1	0	12	20	13	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SLC25A44	RP11-54H19.3, FLJ90431, SLC25A44, KIAA0446	solute carrier family 25, member 44	NM_014655, hCT1963145.2	212663_at, 32091_at	NP_055470.1, EAW52991.1
GeneID:11243	PMF1	1	156,182,784	156,209,833	27,049	+	1	4_A375_EGR1..1..682	31275	downstream	0	0	1	6	12	21	1	4_A375_EGR1..1	21	Gene PMF1	PMF1	polyamine-modulated factor 1	NM_007221	202337_at	NP_009152.2
GeneID:632	BGLAP	1	156,211,951	156,213,112	1,161	+	1	4_A375_EGR1..1..682	2106	downstream	0	0	1	6	12	21	1	4_A375_EGR1..1	21	Gene BGLAP	OC, BGLAP, BGP, PMF1	bone gamma-carboxyglutamate (gla) protein	NM_199173	206956_at	NP_954642.1
GeneID:79957	PAQR6	1	156,213,207	156,217,843	4,636	-	1	4_A375_EGR1..1..682	3784	in gene	0	0	1	6	12	21	1	4_A375_EGR1..1	21	Gene PAQR6	FLJ22672, PAQR6	progestin and adipoQ receptor family member VI	NM_024897, NM_198406, hCT1954436.1, hCT1954437.1, hCT2281937.0, hCT2349482.0, hCT2352656.0, hCT2352657.0, hCT2352658.0, hCT2352659.0, hCT2352660.0, hCT8233.3	219236_at	NP_079173.2, NP_940798.1, EAW52975.1, EAW52978.1, EAW52982.1, EAW52984.1, EAW52976.1, EAW52977.1, EAW52979.1, EAW52980.1, EAW52981.1, EAW52983.1
GeneID:23381	SMG5	1	156,219,015	156,252,820	33,805	-	2	2_A375_pNL97_plus_lncRNA_AR..1..602, 4_A375_EGR1..1..682	21772, 36561	in gene, downstream	0	1	1	12	17.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene SMG5	LPTS-RP1, RP11-54H19.7, FLJ12287, LPTSRP1, SMG-5, EST1B, FLJ34864, SMG5, KIAA1089	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	NM_015327, hCT2281930.0, hCT8240.3	212147_at, 34868_at	NP_056142.2, EAW52973.1, EAW52974.1
GeneID:7203	CCT3	1	156,278,752	156,308,195	29,443	-	1	2_A375_pNL97_plus_lncRNA_AR..1..603	-285	upstream	0	1	0	18	20	6	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CCT3	TRIC5, PIG48, CCT-gamma, TCP-1-gamma, CCT3, CCTG	chaperonin containing TCP1, subunit 3 (gamma)	NM_001008800, NM_005998, hCT8218.3	200910_at	NP_001008800.1, NP_005989.3, EAW52987.1
GeneID:100505747	LOC100505747	1	156,305,717	156,307,029	1,312	-	1	2_A375_pNL97_plus_lncRNA_AR..1..603	-1451	upstream	0	1	0	18	20	6	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100505747		hypothetical LOC100505747	XR_111956, XR_108360, XR_114617		
GeneID:128229	C1orf182	1	156,307,105	156,316,786	9,681	+	1	2_A375_pNL97_plus_lncRNA_AR..1..603	1375	in gene	0	1	0	18	20	6	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C1orf182	RP11-443G18.5, C1orf182, MGC26877, SSTK-IP	chromosome 1 open reading frame 182	NM_144627, hCT2282110.0, hCT2352709.0, hCT2352710.0	230608_at	NP_653228.1, EAW52964.1, EAW52965.1, EAW52966.1
GeneID:57127	RHBG	1	156,339,003	156,355,011	16,008	+	2	4_A375_EGR1..1..683, 4_A375_EGR1..1..684	7925, 16677	in gene, downstream	0	0	1	6.5	11.5	23.5	2	4_A375_EGR1..1	28	Gene RHBG	RHBG, SLC42A2	Rh family, B glycoprotein (gene/pseudogene)	NM_020407, NR_026549, hCT2352661.0, hCT2352662.0, hCT2352663.0, hCT2352664.0, hCT8236.3	220510_at	NP_065140.3, EAW52962.1, EAW52959.1, EAW52960.1, EAW52961.1, EAW52963.1
GeneID:10485	C1orf61	1	156,374,055	156,399,184	25,129	-	4	1_A375_pNL7_minus_lncRNA_AR..1..430, 2_A375_pNL97_plus_lncRNA_AR..1..604, 2_A375_pNL97_plus_lncRNA_AR..1..605, 4_A375_EGR1..1..685	7664, 14752, 7728, 7760	in gene, in gene, in gene, in gene	1	1	1	23.5	23.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene C1orf61	FLJ38303, C1orf61, CROC4	chromosome 1 open reading frame 61	NM_006365, hCT8215.1	1559402_a_at, 1570451_at, 205103_at, 222301_at	NP_006356.1, EAW52956.1
GeneID:100505765	LOC100505765	1	156,379,749	156,382,685	2,936		4	1_A375_pNL7_minus_lncRNA_AR..1..430, 2_A375_pNL97_plus_lncRNA_AR..1..604, 2_A375_pNL97_plus_lncRNA_AR..1..605, 4_A375_EGR1..1..685	-8835, -1747, -8771, -8739	upstream, upstream, upstream, upstream	1	1	1	23.5	23.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene LOC100505765		hypothetical LOC100505765	XR_111955, XR_108361, XR_114616		
GeneID:407046	MIR9-1	1	156,390,133	156,390,221	88		4	1_A375_pNL7_minus_lncRNA_AR..1..430, 2_A375_pNL97_plus_lncRNA_AR..1..604, 2_A375_pNL97_plus_lncRNA_AR..1..605, 4_A375_EGR1..1..685	-1299, 5789, -1235, -1203	upstream, downstream, upstream, upstream	1	1	1	23.5	23.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene MIR9-1	MIR9-1, MIRN9-1, hsa-mir-9-1, miRNA9-1	microRNA 9-1	NR_029691		
GeneID:4209	MEF2D	1	156,433,519	156,470,529	37,010		9	1_A375_pNL7_minus_lncRNA_AR..1..431, 1_A375_pNL7_minus_lncRNA_AR..1..432, 1_A375_pNL7_minus_lncRNA_AR..1..433, 2_A375_pNL97_plus_lncRNA_AR..1..606, 2_A375_pNL97_plus_lncRNA_AR..1..607, 2_A375_pNL97_plus_lncRNA_AR..1..608, 2_A375_pNL97_plus_lncRNA_AR..1..609, 4_A375_EGR1..1..686, 4_A375_EGR1..1..687	44065, -783, -4607, 43793, -351, -2751, -4767, 32669, -4159	downstream, upstream, upstream, downstream, upstream, upstream, upstream, in gene, upstream	1	1	1	27.4	29.8	18.2	5	1_A375_pNL7_minus_lncRNA_AR..1	52	Gene MEF2D	DKFZp686I1536, MEF2D	myocyte enhancer factor 2D	NM_005920, hCT2281908.0, hCT2281910.0, hCT2281912.0, hCT2281913.0, hCT2281915.0	203003_at, 203004_s_at, 225641_at	NP_005911.1, EAW52949.1, EAW52948.1, EAW52950.1, EAW52951.1, EAW52952.1
GeneID:128239	IQGAP3	1	156,495,197	156,542,396	47,199		1	2_A375_pNL97_plus_lncRNA_AR..1..610	20868	in gene	0	1	0	22	29	12	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene IQGAP3	MGC1947, IQGAP3, MGC10170, MGC10831	IQ motif containing GTPase activating protein 3	NM_178229, hCT1954441.2, hCT2349469.0, hCT2352702.0	1569061_at, 1569062_s_at, 229538_s_at, 241939_at	NP_839943.2, EAW52946.1, EAW52945.1, EAW52947.1
GeneID:164118	TTC24	1	156,549,519	156,556,562	7,043	+	1	4_A375_EGR1..1..688	12257	downstream	0	0	1	22	19	19	1	4_A375_EGR1..1	19	Gene TTC24	FLJ20249, TTC24	tetratricopeptide repeat domain 24	NM_001105669		NP_001099139.2
GeneID:128240	APOA1BP	1	156,561,558	156,564,091	2,533	+	4	1_A375_pNL7_minus_lncRNA_AR..1..434, 2_A375_pNL97_plus_lncRNA_AR..1..611, 4_A375_EGR1..1..688, 4_A375_EGR1..1..689	10410, 9898, 218, 9610	downstream, downstream, in gene, downstream	1	1	1	16.5	19.5	19	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene APOA1BP	APOA1BP, MGC119143, AIBP, MGC119145, MGC119144, YJEFN1	apolipoprotein A-I binding protein	NM_144772, hCT2349461.0, hCT2352652.0, hCT8231.2	225427_s_at	NP_658985.2, EAW52941.1, EAW52942.1, EAW52943.1
GeneID:54865	GPATCH4	1	156,564,279	156,571,270	6,991	-	4	1_A375_pNL7_minus_lncRNA_AR..1..434, 2_A375_pNL97_plus_lncRNA_AR..1..611, 4_A375_EGR1..1..688, 4_A375_EGR1..1..689	-698, -186, 9494, 102	upstream, upstream, downstream, in gene	1	1	1	16.5	19.5	19	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene GPATCH4	GPATCH4, GPATC4	G patch domain containing 4	NM_182679, NM_015590, hCT2281898.0, hCT2281899.0, hCT2352732.0, hCT2352733.0	220596_at, 221733_s_at, 224632_at, 224633_s_at, 224634_at	NP_872620.1, NP_056405.2, EAW52935.1, EAW52936.1, EAW52937.1, EAW52938.1
GeneID:60484	HAPLN2	1	156,589,086	156,595,517	6,431	+	1	4_A375_EGR1..1..690	4706	in gene	0	0	1	13	21	19	1	4_A375_EGR1..1	19	Gene HAPLN2	BRAL1, HAPLN2	hyaluronan and proteoglycan link protein 2	NM_021817, hCT1645004.3, hCT2282117.0	220142_at	NP_068589.1, EAW52933.1, EAW52934.1
GeneID:63827	BCAN	1	156,611,740	156,629,320	17,580	+	7	1_A375_pNL7_minus_lncRNA_AR..1..435, 1_A375_pNL7_minus_lncRNA_AR..1..436, 2_A375_pNL97_plus_lncRNA_AR..1..612, 2_A375_pNL97_plus_lncRNA_AR..1..613, 2_A375_pNL97_plus_lncRNA_AR..1..614, 4_A375_EGR1..1..691, 4_A375_EGR1..1..692	18500, 19524, 10212, 18438, 20164, 356, 5604	downstream, downstream, in gene, downstream, downstream, in gene, in gene	1	1	1	18.4	21.8	17.8	5	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene BCAN	BCAN, CSPG7, BEHAB, MGC13038	brevican	NM_198427, NM_021948, hCT1967465.1, hCT2282120.0, hCT2282123.0, hCT2282124.0, hCT8230.3	219107_at, 221623_at, 223632_s_at, 223633_s_at, 242643_at, 91920_at	NP_940819.1, NP_068767.3, EAW52927.1, EAW52928.1, EAW52929.1, EAW52931.1, EAW52930.1
GeneID:10763	NES	1	156,638,555	156,647,189	8,634	-	5	1_A375_pNL7_minus_lncRNA_AR..1..435, 1_A375_pNL7_minus_lncRNA_AR..1..436, 2_A375_pNL97_plus_lncRNA_AR..1..613, 2_A375_pNL97_plus_lncRNA_AR..1..614, 2_A375_pNL97_plus_lncRNA_AR..1..615	16949, 15925, 17013, 15285, 181	downstream, downstream, downstream, downstream, in gene	1	1	0	22	27	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene NES	Nbla00170, NES, FLJ21841	nestin	NM_006617, hCT2281890.0, hCT2281892.0, hCT2281894.0, hCT2352695.0	218678_at, 229346_at	NP_006608.1, EAW52923.1, EAW52924.1, EAW52925.1, EAW52926.1
GeneID:1382	CRABP2	1	156,669,403	156,675,375	5,972	-	2	4_A375_EGR1..1..693, 4_A375_EGR1..1..694	335, -545	in gene, upstream	0	0	1	13.5	13.5	17	2	4_A375_EGR1..1	19	Gene CRABP2	CRABP2, RBP6, CRABP-II	cellular retinoic acid binding protein 2	NM_001878, hCT2281887.0, hCT2281888.0	202575_at	NP_001869.1, EAW52922.1, EAW52921.1
GeneID:81875	ISG20L2	1	156,692,413	156,697,705	5,292	-	2	1_A375_pNL7_minus_lncRNA_AR..1..437, 2_A375_pNL97_plus_lncRNA_AR..1..616	-919, -887	upstream, upstream	1	1	0	33	31	15	1	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene ISG20L2	FLJ12671, ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	NM_030980, hCT1813894.2, hCT2281884.0	208114_s_at, 212768_s_at, 216502_at, 233728_at	NP_112242.1, EAW52919.1, EAW52920.1
GeneID:51093	C1orf66	1	156,698,263	156,706,752	8,489	+	4	1_A375_pNL7_minus_lncRNA_AR..1..437, 1_A375_pNL7_minus_lncRNA_AR..1..438, 2_A375_pNL97_plus_lncRNA_AR..1..616, 2_A375_pNL97_plus_lncRNA_AR..1..617	361, 12745, 329, 12553	in gene, downstream, in gene, downstream	1	1	0	34.5	28.5	16	2	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene C1orf66	CGI-41, C1orf66, RRNAD1	chromosome 1 open reading frame 66	NM_015997, NM_001142560, hCT2282127.0, hCT2282128.0, hCT2282129.0, hCT2352627.0	218914_at	NP_057081.3, NP_001136032.1, EAW52915.1, EAW52916.1, EAW52917.1, EAW52918.1
GeneID:79590	MRPL24	1	156,707,094	156,710,923	3,829	-	5	1_A375_pNL7_minus_lncRNA_AR..1..437, 1_A375_pNL7_minus_lncRNA_AR..1..438, 2_A375_pNL97_plus_lncRNA_AR..1..616, 2_A375_pNL97_plus_lncRNA_AR..1..617, 2_A375_pNL97_plus_lncRNA_AR..1..618	12299, -85, 12331, 107, -7681	downstream, upstream, downstream, in gene, upstream	1	1	0	28	25.67	15	3	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene MRPL24	MRPL24, FLJ20917, MGC9831, MGC22737, MRP-L24, MRP-L18, L24mt	mitochondrial ribosomal protein L24	NM_145729, NM_024540, hCT1813895.1, hCT1966613.1	218270_at	NP_663781.1, NP_078816.2, EAW52913.1, EAW52914.1
GeneID:3068	HDGF	1	156,711,899	156,722,240	10,341	-	5	1_A375_pNL7_minus_lncRNA_AR..1..438, 1_A375_pNL7_minus_lncRNA_AR..1..439, 2_A375_pNL97_plus_lncRNA_AR..1..617, 2_A375_pNL97_plus_lncRNA_AR..1..618, 2_A375_pNL97_plus_lncRNA_AR..1..619	11232, 560, 11424, 3456, 576	downstream, in gene, downstream, in gene, in gene	1	1	0	43	42.33	14	3	2_A375_pNL97_plus_lncRNA_AR..1	61	Gene HDGF	HDGF, FLJ96580, HMG1L2, DKFZp686J1764	hepatoma-derived growth factor (high-mobility group protein 1-like)	NM_004494, NM_001126050, NM_001126051, hCT1813898.1, hCT2281879.0, hCT2352690.0	200896_x_at, 216484_x_at	NP_004485.1, NP_001119522.1, NP_001119523.1, EAW52910.1, EAW52911.1, EAW52912.1
GeneID:5546	PRCC	1	156,737,274	156,770,609	33,335	+	3	1_A375_pNL7_minus_lncRNA_AR..1..440, 2_A375_pNL97_plus_lncRNA_AR..1..620, 4_A375_EGR1..1..695	-234, -154, 134	upstream, upstream, in gene	1	1	1	41	45	15	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene PRCC	RCCP1, MGC17178, TPRC, MGC4723, PRCC	papillary renal cell carcinoma (translocation-associated)	NM_005973, hCT1967979.1, hCT31083.2	208938_at	NP_005964.3, EAW52909.1, EAW52908.1
GeneID:4914	NTRK1	1	156,785,542	156,851,642	66,100	+	2	4_A375_EGR1..1..696, 4_A375_EGR1..1..697	29370, 58234	in gene, in gene	0	0	1	7	8	19.5	2	4_A375_EGR1..1	23	Gene NTRK1	TRKA, p140-TrkA, NTRK1, DKFZp781I14186, Trk-A, TRK1, TRK, MTC	neurotrophic tyrosine kinase, receptor, type 1	NM_001007792, NM_002529, NM_001012331, hCT2282133.0, hCT2352646.0, hCT31074.3	208605_s_at	NP_001007793.1, NP_002520.2, NP_001012331.1, EAW52900.1, EAW52901.1, EAW52902.1
GeneID:3645	INSRR	1	156,810,865	156,828,866	18,001	-	1	4_A375_EGR1..1..698	13754	in gene	0	0	1	7	7	23	1	4_A375_EGR1..1	23	Gene INSRR	INSRR, IRR	insulin receptor-related receptor	NM_014215, hCT2281875.0, hCT31077.1	215776_at	NP_055030.1, EAW52903.1, EAW52904.1
GeneID:375033	PEAR1	1	156,863,523	156,886,226	22,703	+	3	4_A375_EGR1..1..698, 4_A375_EGR1..1..699, 4_A375_EGR1..1..700	-632, 15053, 27161	upstream, in gene, downstream	0	0	1	8.33	8.33	19.33	3	4_A375_EGR1..1	22	Gene PEAR1	FLJ00193, JEDI, PEAR1, MEGF12	platelet endothelial aggregation receptor 1	NM_001080471	228618_at	NP_001073940.1
GeneID:149499	C1orf92	1	156,890,424	156,902,880	12,456	+	2	4_A375_EGR1..1..700, 4_A375_EGR1..1..701	280, 6952	in gene, in gene	0	0	1	10.5	12.5	20.5	2	4_A375_EGR1..1	22	Gene C1orf92	FLJ77598, C1orf92, RP11-356J7.1, MGC45468, LRRC71, FLJ32884	chromosome 1 open reading frame 92	NM_144702, hCT2349493.0, hCT2352691.0, hCT2352692.0, hCT31082.4	237251_at	NP_653303.2, EAW52897.1, EAW52895.1, EAW52896.1, EAW52898.1
GeneID:9826	ARHGEF11	1	156,904,632	157,015,162	110,530	-	2	2_A375_pNL97_plus_lncRNA_AR..1..621, 4_A375_EGR1..1..701	98610, 117786	in gene, downstream	0	1	1	15	18	13.5	2	4_A375_EGR1..1	19	Gene ARHGEF11	GTRAP48, PDZ-RHOGEF, ARHGEF11, DKFZp667F1223, KIAA0380	Rho guanine nucleotide exchange factor (GEF) 11	NM_014784, NM_198236, hCT2281871.0, hCT2352704.0, hCT29445.3	202913_at, 202914_s_at, 238730_at	NP_055599.1, NP_937879.1, EAW52892.1, EAW52893.1, EAW52894.1
GeneID:768220	MIR765	1	156,905,923	156,906,036	113	-	2	2_A375_pNL97_plus_lncRNA_AR..1..621, 4_A375_EGR1..1..701	-10316, 8660	upstream, downstream	0	1	1	15	18	13.5	2	4_A375_EGR1..1	19	Gene MIR765	MIRN765, MIR765, hsa-mir-765	microRNA 765	NR_030527		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:2117	ETV3	1	157,094,459	157,108,383	13,924	-	3	1_A375_pNL7_minus_lncRNA_AR..1..441, 2_A375_pNL97_plus_lncRNA_AR..1..622, 4_A375_EGR1..1..702	-273, 95, 639	upstream, in gene, in gene	1	1	1	20	24	18	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ETV3	PE-1, PE1, METS, bA110J1.4, FLJ79173, ETV3	ets variant 3	NM_005240, NM_001145312, hCT2281667.1, hCT31078.3	1552423_at, 214460_at	NP_005231.1, NP_001138784.1, EAW52888.1, EAW52889.1
GeneID:55243	KIRREL	1	157,963,063	158,065,846	102,783	+	2	1_A375_pNL7_minus_lncRNA_AR..1..442, 4_A375_EGR1..1..704	44745, 75849	in gene, in gene	1	0	1	14.5	10.5	12	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene KIRREL	MGC129543, MGC129542, NEPH1, FLJ10845, KIRREL	kin of IRRE like (Drosophila)	NM_018240, hCT2275271.0, hCT2275272.0, hCT31205.3	220825_s_at, 225303_at, 232467_at	NP_060710.3, EAW52853.1, EAW52854.1, EAW52855.1
GeneID:100505785	LOC100505785	1	157,995,345	158,001,611	6,266	+	1	1_A375_pNL7_minus_lncRNA_AR..1..442	12463	downstream	1	0	0	27	15	6	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene LOC100505785		hypothetical LOC100505785	XR_108382		
GeneID:646266	hCG_1654703	1	158,101,834	158,110,430	8,596	-	2	2_A375_pNL97_plus_lncRNA_AR..1..623, 2_A375_pNL97_plus_lncRNA_AR..1..624	-4642, -5698	upstream, upstream	0	1	0	16	21.5	7	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene hCG_1654703	LOC646266	hCG1654703	NR_033946	1566745_at, 1566746_a_at	
GeneID:912	CD1D	1	158,149,737	158,158,217	8,480	+	2	2_A375_pNL97_plus_lncRNA_AR..1..625, 4_A375_EGR1..1..705	1111, 1373	in gene, in gene	0	1	1	15	20	19	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CD1D	R3, CD1A, CD1D, MGC34622	CD1d molecule	NM_001766, hCT2275255.0, hCT2275257.0, hCT31197.2	205789_at	NP_001757.1, EAW52847.1, EAW52848.1, EAW52849.1
GeneID:3428	IFI16	1	158,979,682	159,024,945	45,263	+	2	1_A375_pNL7_minus_lncRNA_AR..1..443, 2_A375_pNL97_plus_lncRNA_AR..1..626	-10050, -10018	upstream, upstream	1	1	0	16	22	6	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene IFI16	IFI16, MGC9466, PYHIN2, IFNGIP1	interferon, gamma-inducible protein 16	NM_005531, hCT2275171.1, hCT2275172.0, hCT2275173.0, hCT2275174.1, hCT2275176.1, hCT2275177.1, hCT2352642.0	206332_s_at, 208965_s_at, 208966_x_at	NP_005522.2, EAW52799.1, EAW52797.1, EAW52800.1, EAW52801.1, EAW52803.1, EAW52798.1, EAW52802.1
GeneID:9447	AIM2	1	159,032,275	159,046,647	14,372	-	1	2_A375_pNL97_plus_lncRNA_AR..1..627	-521	upstream	0	1	0	14	24	7	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene AIM2	PYHIN4, AIM2	absent in melanoma 2	NM_004833, hCT1644666.1	206513_at	NP_004824.1, EAW52795.1
GeneID:57863	CADM3	1	159,141,377	159,172,932	31,555	+	6	1_A375_pNL7_minus_lncRNA_AR..1..445, 1_A375_pNL7_minus_lncRNA_AR..1..446, 2_A375_pNL97_plus_lncRNA_AR..1..629, 2_A375_pNL97_plus_lncRNA_AR..1..630, 4_A375_EGR1..1..706, 4_A375_EGR1..1..707	4111, 5855, 4159, 5855, -385, 30559	in gene, in gene, in gene, in gene, upstream, in gene	1	1	1	32	31.75	10.25	4	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene CADM3	IGSF4B, NECL1, TSLL1, Necl-1, synCAM3, BIgR, FLJ10698, CADM3	cell adhesion molecule 3	NM_021189, NM_001127173, hCT1967975.1, hCT2275181.0, hCT30662.3	211677_x_at, 213946_x_at, 216835_at, 221921_s_at	NP_067012.1, NP_001120645.1, EAW52792.1, EAW52793.1, EAW52794.1
GeneID:100131825	LOC100131825	1	159,165,775	159,172,194	6,419	-	1	4_A375_EGR1..1..707	256	in gene	0	0	1	5	6	14	1	4_A375_EGR1..1	14	Gene LOC100131825		hypothetical LOC100131825	XR_111952, XR_108290, XR_114821		
GeneID:2532	DARC	1	159,174,510	159,176,290	1,780	+	1	4_A375_EGR1..1..707	-2574	upstream	0	0	1	5	6	14	1	4_A375_EGR1..1	14	Gene DARC	Dfy, GPD, CD234, CCBP1, FY, WBCQ1, GpFy, DARC	Duffy blood group, chemokine receptor	NM_002036, NM_001122951	208335_s_at	NP_002027.2, NP_001116423.1
GeneID:54935	DUSP23	1	159,750,759	159,752,333	1,574	+	1	4_A375_EGR1..1..709	121	in gene	0	0	1	19	23	22	1	4_A375_EGR1..1	22	Gene DUSP23	FLJ20442, VHZ, LDP-3, DUSP25, RP11-190A12.1, DUSP23, MOSP	dual specificity phosphatase 23	NM_017823, hCT1805295.1	223402_at	NP_060293.2, EAW52775.1
GeneID:343413	FCRL6	1	159,772,173	159,786,047	13,874	+	2	1_A375_pNL7_minus_lncRNA_AR..1..447, 2_A375_pNL97_plus_lncRNA_AR..1..631	2787, 2771	in gene, in gene	1	1	0	20	25	6	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene FCRL6	FcRH6, FCRL6, FLJ16056	Fc receptor-like 6	NM_001004310		NP_001004310.2
GeneID:284677	C1orf204	1	159,804,264	159,825,137	20,873	-	1	4_A375_EGR1..1..710	209	in gene	0	0	1	16	12	21	1	4_A375_EGR1..1	21	Gene C1orf204	FLJ20442, FLJ39167, C1orf204	chromosome 1 open reading frame 204	NM_001134233	1556633_at	NP_001127705.1
GeneID:391123	VSIG8	1	159,824,106	159,832,447	8,341	-	1	4_A375_EGR1..1..710	7519	in gene	0	0	1	16	12	21	1	4_A375_EGR1..1	21	Gene VSIG8	VSIG8	V-set and immunoglobulin domain containing 8	NM_001013661		NP_001013683.1
GeneID:8407	TAGLN2	1	159,887,903	159,895,284	7,381	-	4	1_A375_pNL7_minus_lncRNA_AR..1..448, 2_A375_pNL97_plus_lncRNA_AR..1..632, 2_A375_pNL97_plus_lncRNA_AR..1..633, 4_A375_EGR1..1..711	-108, 14980, -124, 532	upstream, downstream, upstream, in gene	1	1	1	22	25	16.5	2	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene TAGLN2	TAGLN2, HA1756, KIAA0120	transgelin 2	NM_003564, hCT1967976.1, hCT1967977.1, hCT2352718.0, hCT2352719.0, hCT30982.2	200916_at, 210978_s_at	NP_003555.1, EAW52762.1, EAW52759.1, EAW52760.1, EAW52761.1, EAW52763.1
GeneID:57549	IGSF9	1	159,898,829	159,915,386	16,557	-	3	1_A375_pNL7_minus_lncRNA_AR..1..448, 2_A375_pNL97_plus_lncRNA_AR..1..633, 4_A375_EGR1..1..711	19994, 19978, 20834	downstream, downstream, downstream	1	1	1	33	33	26	1	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene IGSF9	Nrt1, KIAA1355, IGSF9, FP18798, IGSF9A	immunoglobulin superfamily, member 9	NM_020789, NM_001135050, hCT2352744.0, hCT2352745.0, hCT30988.3	229276_at	NP_065840.2, NP_001128522.1, EAW52756.1, EAW52757.1, EAW52758.1
GeneID:93183	PIGM	1	159,997,462	160,001,783	4,321	-	2	1_A375_pNL7_minus_lncRNA_AR..1..449, 2_A375_pNL97_plus_lncRNA_AR..1..634	-9, 55	upstream, in gene	1	1	0	23	25	12	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene PIGM	MGC29896, PIGM, GPI-MT-I	phosphatidylinositol glycan anchor biosynthesis, class M	NM_145167, hCT1831298.2, hCT2349468.0	223470_at, 235168_at, 236622_at	NP_660150.1, EAW52752.1, EAW52751.1
GeneID:3766	KCNJ10	1	160,007,257	160,040,051	32,794	-	3	1_A375_pNL7_minus_lncRNA_AR..1..449, 2_A375_pNL97_plus_lncRNA_AR..1..634, 4_A375_EGR1..1..712	38259, 38323, 8051	downstream, downstream, in gene	1	1	1	15	16.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene KCNJ10	SESAME, KIR1.2, KCNJ10, BIRK-10, KIR4.1, KCNJ13-PEN	potassium inwardly-rectifying channel, subfamily J, member 10	NM_002241, hCT2275629.0, hCT2349492.0, hCT30985.4	206692_at, 226581_at	NP_002232.2, EAW52750.1, EAW52748.1, EAW52749.1
GeneID:3765	KCNJ9	1	160,051,360	160,059,212	7,852	+	2	4_A375_EGR1..1..713, 4_A375_EGR1..1..714	2976, 16928	in gene, downstream	0	0	1	6.5	15	16	2	4_A375_EGR1..1	16	Gene KCNJ9	KCNJ9, GIRK3, KIR3.3	potassium inwardly-rectifying channel, subfamily J, member 9	NM_004983, hCT30987.2	207527_at	NP_004974.2, EAW52747.1
GeneID:93185	IGSF8	1	160,061,130	160,068,408	7,278	-	2	4_A375_EGR1..1..713, 4_A375_EGR1..1..714	14072, 120	downstream, in gene	0	0	1	6.5	15	16	2	4_A375_EGR1..1	16	Gene IGSF8	CD81P3, CD316, EWI2, EWI-2, KGSF8, PGRL, LIR-D1, KCT-4	immunoglobulin superfamily, member 8	NM_052868, hCT2275625.0, hCT2275626.0, hCT2275628.0, hCT30994.3	225025_at	NP_443100.1, EAW52744.1, EAW52743.1, EAW52745.1, EAW52746.1
GeneID:844	CASQ1	1	160,160,285	160,171,676	11,391	+	1	2_A375_pNL97_plus_lncRNA_AR..1..635	15363	downstream	0	1	0	14	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CASQ1	PDIB1, CASQ, CASQ1	calsequestrin 1 (fast-twitch, skeletal muscle)	NM_001231, hCT30991.3	219645_at	NP_001222.3, EAW52738.1
GeneID:8682	PEA15	1	160,175,125	160,185,162	10,037	+	1	2_A375_pNL97_plus_lncRNA_AR..1..635	523	in gene	0	1	0	14	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PEA15	MAT1, PED, HMAT1, HUMMAT1H, PEA15, MAT1H, PEA-15	phosphoprotein enriched in astrocytes 15	NM_003768, hCT1967978.1, hCT2352724.0, hCT30984.2	200787_s_at, 200788_s_at	NP_003759.1, EAW52734.1, EAW52733.1, EAW52735.1
GeneID:50717	DCAF8	1	160,185,505	160,232,350	46,845	-	4	1_A375_pNL7_minus_lncRNA_AR..1..450, 2_A375_pNL97_plus_lncRNA_AR..1..635, 2_A375_pNL97_plus_lncRNA_AR..1..636, 4_A375_EGR1..1..715	126, 56702, 158, 126	in gene, downstream, in gene, in gene	1	1	1	16	20	24.5	2	4_A375_EGR1..1	31	Gene DCAF8	DCAF8, H326, WDR42A, MGC117276, MGC118891, FLJ35657, MGC99840, DKFZp781G1096	DDB1 and CUL4 associated factor 8	NM_015726, NR_028103, NR_028104, NR_028105, NR_028106, hCT2275656.0, hCT2275657.0, hCT30990.3	1554049_s_at, 202249_s_at, 202250_s_at, 216855_s_at, 232339_at, 233637_at, 236340_at, 243318_at	NP_056541.2, EAW52732.1, EAW52730.1, EAW52731.1
GeneID:100287049	LOC100287049	1	160,222,704	160,232,568	9,864	+	3	1_A375_pNL7_minus_lncRNA_AR..1..450, 2_A375_pNL97_plus_lncRNA_AR..1..636, 4_A375_EGR1..1..715	9520, 9488, 9520	in gene, in gene, in gene	1	1	1	22	20	31	1	4_A375_EGR1..1	31	Gene LOC100287049		hypothetical LOC100287049	XM_002342146, XM_003119757, XM_003120798		XP_002342187.1, XP_003119805.1, XP_003120846.1
GeneID:100505665	LOC100505665	1	160,231,518	160,232,567	1,049	+	3	1_A375_pNL7_minus_lncRNA_AR..1..450, 2_A375_pNL97_plus_lncRNA_AR..1..636, 4_A375_EGR1..1..715	706, 674, 706	in gene, in gene, in gene	1	1	1	22	20	31	1	4_A375_EGR1..1	31	Gene LOC100505665		hypothetical LOC100505665	XR_108292		
GeneID:5824	PEX19	1	160,246,599	160,254,941	8,342	-	2	1_A375_pNL7_minus_lncRNA_AR..1..451, 2_A375_pNL97_plus_lncRNA_AR..1..637	29, 61	in gene, in gene	1	1	0	23	26	15	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene PEX19	PXMP1, HK33, FLJ55298, PEX19, D1S2223E, PMPI, PXF, PMP1	peroxisomal biogenesis factor 19	NM_002857, NM_001193644, NR_036492, NR_036493, hCT2275653.0, hCT2352722.0, hCT30983.3	201706_s_at, 201707_at	NP_002848.1, NP_001180573.1, EAW52727.1, EAW52728.1, EAW52729.1
GeneID:1314	COPA	1	160,258,377	160,313,354	54,977	-	2	1_A375_pNL7_minus_lncRNA_AR..1..451, 2_A375_pNL97_plus_lncRNA_AR..1..637	56442, 56474	downstream, downstream	1	1	0	23	26	15	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene COPA	FLJ26320, HEP-COP, COPA	coatomer protein complex, subunit alpha	NM_004371, NM_001098398, hCT2275651.0, hCT2352619.0, hCT30995.3	1559662_at, 208684_at, 214336_s_at, 214337_at	NP_004362.2, NP_001091868.1, EAW52723.1, EAW52724.1, EAW52725.1
GeneID:57216	VANGL2	1	160,370,364	160,398,468	28,104	+	1	4_A375_EGR1..1..716	-252	upstream	0	0	1	7	9	16	1	4_A375_EGR1..1	16	Gene VANGL2	LPP1, MGC119403, KIAA1215, VANGL2, STBM1, STBM, LTAP, STB1, MGC119404	vang-like 2 (van gogh, Drosophila)	NM_020335, hCT11938.4, hCT2276699.1	226029_at	NP_065068.1, EAW52718.1, EAW52717.1
GeneID:4063	LY9	1	160,765,928	160,798,045	32,117	+	2	1_A375_pNL7_minus_lncRNA_AR..1..452, 2_A375_pNL97_plus_lncRNA_AR..1..638	30232, 30264	in gene, in gene	1	1	0	24	25	4	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LY9	hly9, SLAMF3, mLY9, CD229, LY9	lymphocyte antigen 9	NM_002348, NM_001033667, hCT16994.2, hCT2276631.0, hCT2276632.0, hCT2352663.0, hCT2352664.0, hCT2352665.0, hCT2352666.0	210370_s_at, 215967_s_at, 231124_x_at	NP_002339.2, NP_001028839.1, EAW52696.1, EAW52698.1, EAW52699.1, EAW52700.1, EAW52695.1, EAW52697.1, EAW52701.1
GeneID:51744	CD244	1	160,799,950	160,832,692	32,742	-	2	1_A375_pNL7_minus_lncRNA_AR..1..452, 2_A375_pNL97_plus_lncRNA_AR..1..638	36532, 36500	downstream, downstream	1	1	0	24	25	4	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene CD244	NAIL, Nmrk, 2B4, NKR2B4, SLAMF4, CD244	CD244 molecule, natural killer cell receptor 2B4	NM_016382, NM_001166663, NM_001166664, hCT11929.3, hCT2275511.0, hCT2275513.0, hCT2352669.0	220307_at, 234320_at	NP_057466.1, NP_001160135.1, NP_001160136.1, EAW52691.1, EAW52692.1, EAW52693.1, EAW52694.1
GeneID:100131187	TSTD1	1	161,007,421	161,008,774	1,353	-	1	4_A375_EGR1..1..717	150	in gene	0	0	1	9	6	16	1	4_A375_EGR1..1	16	Gene TSTD1	KAT, TSTD1	thiosulfate sulfurtransferase (rhodanese)-like domain containing 1	NM_001113205, NM_001113206, NM_001113207		NP_001106676.1, NP_001106677.1, NP_001106678.1
GeneID:7391	USF1	1	161,009,041	161,015,757	6,716	-	2	4_A375_EGR1..1..717, 4_A375_EGR1..1..718	7133, -3491	downstream, upstream	0	0	1	8.5	7.5	17	2	4_A375_EGR1..1	18	Gene USF1	UEF, MLTF, bHLHb11, HYPLIP1, FCHL1, FCHL, MLTFI, USF1	upstream transcription factor 1	NM_007122, NM_207005, hCT11926.2, hCT1967894.1	231766_at	NP_009053.1, NP_996888.1, EAW52675.1, EAW52676.1
GeneID:257106	ARHGAP30	1	161,016,732	161,039,760	23,028	-	2	4_A375_EGR1..1..717, 4_A375_EGR1..1..718	31136, 20512	downstream, in gene	0	0	1	8.5	7.5	17	2	4_A375_EGR1..1	18	Gene ARHGAP30	FLJ00267, ARHGAP30, FLJ44128	Rho GTPase activating protein 30	NM_181720, NM_001025598, hCT2275497.1, hCT2275498.1, hCT2349476.0, hCT2349477.0, hCT2349478.0, hCT2352738.0, hCT2352739.0, hCT2352740.0	226219_at, 241346_at	NP_859071.2, NP_001020769.1, EAW52669.1, EAW52671.1, EAW52672.1, EAW52673.1, EAW52667.1, EAW52668.1, EAW52670.1, EAW52674.1
GeneID:5202	PFDN2	1	161,070,346	161,087,866	17,520	-	4	1_A375_pNL7_minus_lncRNA_AR..1..453, 2_A375_pNL97_plus_lncRNA_AR..1..639, 4_A375_EGR1..1..719, 4_A375_EGR1..1..720	106, 140, 56, -6326	in gene, in gene, in gene, upstream	1	1	1	15	12.5	20.5	2	4_A375_EGR1..1	24	Gene PFDN2	PFDN2, PFD2	prefoldin subunit 2	NM_012394, hCT2275494.0	218336_at	NP_036526.2, EAW52658.1
GeneID:4817	NIT1	1	161,087,882	161,095,235	7,373	+	6	1_A375_pNL7_minus_lncRNA_AR..1..453, 1_A375_pNL7_minus_lncRNA_AR..1..454, 2_A375_pNL97_plus_lncRNA_AR..1..639, 2_A375_pNL97_plus_lncRNA_AR..1..640, 4_A375_EGR1..1..719, 4_A375_EGR1..1..720	-102, 14794, -138, 14842, -54, 6330	upstream, downstream, upstream, downstream, upstream, in gene	1	1	1	19.67	17	16.67	3	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene NIT1	NIT1, MGC57670	nitrilase 1	NM_001185092, NM_001185093, NM_001185094, NM_005600, hCT10942.3, hCT1950447.1, hCT2276584.0, hCT2276586.0	202891_at, 241395_at	NP_001172021.1, NP_001172022.1, NP_005591.1, NP_001172023.1, EAW52654.1, EAW52656.1, EAW52655.1, EAW52657.1
GeneID:9191	DEDD	1	161,090,767	161,102,478	11,711	-	6	1_A375_pNL7_minus_lncRNA_AR..1..453, 1_A375_pNL7_minus_lncRNA_AR..1..454, 2_A375_pNL97_plus_lncRNA_AR..1..639, 2_A375_pNL97_plus_lncRNA_AR..1..640, 4_A375_EGR1..1..719, 4_A375_EGR1..1..720	14718, -178, 14752, -226, 14670, 6286	downstream, upstream, downstream, upstream, downstream, in gene	1	1	1	19.67	17	16.67	3	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene DEDD	FLDED1, DEDD, DEDD1, CASP8IP1, DEFT, KE05	death effector domain containing	NM_032998, NM_001039711, NM_001039712, hCT11927.3, hCT1967911.1, hCT2275488.0, hCT2275489.0, hCT2275490.0, hCT2275491.0	202480_s_at, 211255_x_at, 215156_s_at	NP_127491.1, NP_001034800.1, NP_001034801.1, EAW52648.1, EAW52650.1, EAW52652.1, EAW52649.1, EAW52651.1, EAW52653.1
GeneID:51506	UFC1	1	161,123,534	161,128,646	5,112	+	8	1_A375_pNL7_minus_lncRNA_AR..1..455, 1_A375_pNL7_minus_lncRNA_AR..1..456, 2_A375_pNL97_plus_lncRNA_AR..1..641, 2_A375_pNL97_plus_lncRNA_AR..1..642, 2_A375_pNL97_plus_lncRNA_AR..1..643, 4_A375_EGR1..1..721, 4_A375_EGR1..1..722, 4_A375_EGR1..1..723	5554, 12594, 370, 5618, 12562, 322, 5610, 7282	downstream, downstream, in gene, downstream, downstream, in gene, downstream, downstream	1	1	1	25.75	28.75	16.5	4	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene UFC1	UFC1, HSPC155	ubiquitin-fold modifier conjugating enzyme 1	NM_016406, hCT2276588.2, hCT2349467.0	217797_at	NP_057490.2, EAW52646.1, EAW52647.1
GeneID:27005	USP21	1	161,129,254	161,135,516	6,262	+	8	1_A375_pNL7_minus_lncRNA_AR..1..455, 1_A375_pNL7_minus_lncRNA_AR..1..456, 2_A375_pNL97_plus_lncRNA_AR..1..641, 2_A375_pNL97_plus_lncRNA_AR..1..642, 2_A375_pNL97_plus_lncRNA_AR..1..643, 4_A375_EGR1..1..721, 4_A375_EGR1..1..722, 4_A375_EGR1..1..723	-166, 6874, -5350, -102, 6842, -5398, 90, 1562	upstream, downstream, upstream, upstream, downstream, upstream, in gene, in gene	1	1	1	25.75	28.75	16.5	4	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene USP21	USP21, USP23, USP16, MGC3394	ubiquitin specific peptidase 21	NM_012475, NM_001014443, hCT1804993.2, hCT2276594.0, hCT2276595.0, hCT2276596.1	218367_x_at, 232219_x_at, 234735_s_at	NP_036607.3, NP_001014443.1, EAW52642.1, EAW52643.1, EAW52644.1, EAW52645.1
GeneID:5498	PPOX	1	161,136,181	161,141,010	4,829	+	6	1_A375_pNL7_minus_lncRNA_AR..1..455, 1_A375_pNL7_minus_lncRNA_AR..1..456, 2_A375_pNL97_plus_lncRNA_AR..1..642, 2_A375_pNL97_plus_lncRNA_AR..1..643, 4_A375_EGR1..1..722, 4_A375_EGR1..1..723	-7093, -53, -7029, -85, -6837, -5365	upstream, upstream, upstream, upstream, upstream, upstream	1	1	1	26.33	30	16	3	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene PPOX	MGC8485, V290M, PPOX, PPO, VP	protoporphyrinogen oxidase	NM_000309, NM_001122764, hCT1804992.2, hCT1950444.1, hCT1966607.1, hCT2276597.0, hCT2276598.0, hCT2276599.0, hCT2352675.0	204768_s_at, 238117_at, 238118_s_at	NP_000300.1, NP_001116236.1, EAW52636.1, EAW52637.1, EAW52638.1, EAW52641.1, EAW52635.1, EAW52639.1, EAW52640.1
GeneID:8703	B4GALT3	1	161,141,101	161,147,314	6,213	-	3	1_A375_pNL7_minus_lncRNA_AR..1..456, 2_A375_pNL97_plus_lncRNA_AR..1..643, 4_A375_EGR1..1..723	11186, 11218, 16498	downstream, downstream, downstream	1	1	1	33.5	37	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene B4GALT3	beta4Gal-T3, B4GALT3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	NM_003779, hCT1805014.2, hCT2275484.1, hCT2275485.0, hCT2343741.0, hCT2343742.0, hCT2352620.0, hCT2352621.0	210243_s_at, 238312_s_at	NP_003770.1, EAW52628.1, EAW52629.1, EAW52630.1, EAW52631.1, EAW52633.1, EAW52632.1, EAW52634.1
GeneID:9507	ADAMTS4	1	161,159,538	161,168,845	9,307	-	4	2_A375_pNL97_plus_lncRNA_AR..1..644, 4_A375_EGR1..1..724, 4_A375_EGR1..1..725, 4_A375_EGR1..1..726	-3379, 8077, 5325, 749	upstream, in gene, in gene, in gene	0	1	1	11	14.25	17.5	4	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ADAMTS4	KIAA0688, ADAMTS-2, ADAMTS4, ADMP-1, ADAMTS-4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	NM_005099, hCT8887.3	1555380_at	NP_005090.3, EAW52627.1
GeneID:4720	NDUFS2	1	161,169,105	161,184,185	15,080	+	4	2_A375_pNL97_plus_lncRNA_AR..1..644, 4_A375_EGR1..1..724, 4_A375_EGR1..1..725, 4_A375_EGR1..1..726	3119, -8337, -5585, -1009	in gene, upstream, upstream, upstream	0	1	1	11	14.25	17.5	4	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene NDUFS2	CI-49, NDUFS2		NM_004550, NM_001166159, hCT2276604.0, hCT8911.4	201966_at	NP_004541.1, NP_001159631.1, EAW52625.1, EAW52626.1
GeneID:2207	FCER1G	1	161,185,087	161,189,038	3,951	+	1	2_A375_pNL97_plus_lncRNA_AR..1..645	10849	downstream	0	1	0	13	19	15	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene FCER1G	FCRG, FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	NM_004106, hCT2276607.0, hCT2276608.0	1554899_s_at, 204232_at	NP_004097.1, EAW52623.1, EAW52624.1
GeneID:336	APOA2	1	161,192,083	161,193,418	1,335	-	1	2_A375_pNL97_plus_lncRNA_AR..1..645	-2518	upstream	0	1	0	13	19	15	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene APOA2	ApoA-II, APOA2, apoAII, Apo-AII		NM_001643, hCT2275480.1, hCT2343743.0, hCT2345694.0, hCT2345696.0, hCT2345697.0	219465_at, 219466_s_at	NP_001634.1, EAW52622.1, EAW52618.1, EAW52619.1, EAW52620.1, EAW52621.1
GeneID:84134	TOMM40L	1	161,195,833	161,200,408	4,575	+	1	2_A375_pNL97_plus_lncRNA_AR..1..645	103	in gene	0	1	0	13	19	15	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TOMM40L	TOMM40B, FLJ12770, RP11-297K8.10, TOMM40L	translocase of outer mitochondrial membrane 40 homolog (yeast)-like	NM_032174, hCT2276609.0, hCT2344327.0, hCT2344328.0, hCT2344329.0, hCT2344330.0, hCT2344331.0, hCT2352707.0	226059_at	NP_115550.2, EAW52611.1, EAW52613.1, EAW52614.1, EAW52615.1, EAW52617.1, EAW52612.1, EAW52616.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9970	NR1I3	1	161,199,456	161,208,000	8,544	-	1	2_A375_pNL97_plus_lncRNA_AR..1..645	12064	downstream	0	1	0	13	19	15	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene NR1I3	MGC97144, MGC97209, NR1I3, CAR, MB67, MGC150433, CAR1	nuclear receptor subfamily 1, group I, member 3	NM_001077469, NM_005122, NM_001077470, NM_001077471, NM_001077472, NM_001077473, NM_001077474, NM_001077475, NM_001077476, NM_001077478, NM_001077477, NM_001077479, NM_001077480, NM_001077481, NM_001077482, hCT1805016.1, hCT2352640.0, hCT2352641.0	1570166_at, 207007_at	NP_001070937.1, NP_005113.1, NP_001070938.1, NP_001070939.1, NP_001070940.1, NP_001070941.1, NP_001070942.1, NP_001070943.1, NP_001070944.1, NP_001070946.1, NP_001070945.1, NP_001070947.1, NP_001070948.1, NP_001070949.1, NP_001070950.1, EAW52608.1, EAW526
GeneID:100505703	LOC100505703	1	161,369,199	161,392,630	23,431	+	9	1_A375_pNL7_minus_lncRNA_AR..1..458, 1_A375_pNL7_minus_lncRNA_AR..1..459, 1_A375_pNL7_minus_lncRNA_AR..1..460, 2_A375_pNL97_plus_lncRNA_AR..1..647, 2_A375_pNL97_plus_lncRNA_AR..1..648, 2_A375_pNL97_plus_lncRNA_AR..1..649, 2_A375_pNL97_plus_lncRNA_AR..1..650, 4_A375_EGR1..1..727, 4_A375_EGR1..1..726	-9039, 401, 22737, -9615, -8991, 401, 22641, 401, 22673	upstream, in gene, in gene, upstream, upstream, in gene, in gene, in gene, in gene	1	1	1	19.67	23.33	19.33	3	4_A375_EGR1..1	27	Gene LOC100505703		hypothetical LOC100505703	XR_108294, XR_114625		
GeneID:2212	FCGR2A	1	161,475,205	161,489,360	14,155	+	2	2_A375_pNL97_plus_lncRNA_AR..1..652, 4_A375_EGR1..1..730	-6565, 16443	upstream, downstream	0	1	1	17	16	12.5	2	4_A375_EGR1..1	24	Gene FCGR2A	CDw32, FCGR2A1, FCGR2A, CD32, MGC30032, FCG2, IGFR2, FCGR2, CD32A, MGC23887, FcGR	Fc fragment of IgG, low affinity IIa, receptor (CD32)	NM_021642, NM_001136219	1565673_at, 1565674_at, 203561_at	NP_067674.2, NP_001129691.1
GeneID:3310	HSPA6	1	161,494,036	161,496,687	2,651	+	4	2_A375_pNL97_plus_lncRNA_AR..1..653, 4_A375_EGR1..1..730, 4_A375_EGR1..1..731, 4_A375_EGR1..1..732	6760, -366, 6140, 6880	downstream, upstream, downstream, downstream	0	1	1	13.33	12.33	19.33	3	4_A375_EGR1..1	24	Gene HSPA6	HSPA6		NM_002155	117_at, 213418_at	NP_002146.2
GeneID:2214	FCGR3A	1	161,511,549	161,520,413	8,864	-	3	1_A375_pNL7_minus_lncRNA_AR..1..461, 2_A375_pNL97_plus_lncRNA_AR..1..654, 4_A375_EGR1..1..733	10301, 10349, 10349	downstream, downstream, downstream	1	1	1	25	33	22	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene FCGR3A	FCG3, FCGR3, IGFR3, FCR-10, FCRIII, FCGR3A, CD16, FCRIIIA, CD16A, FCGRIII	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	NM_000569, NM_001127592, NM_001127593, NM_001127595, NM_001127596	204006_s_at	NP_000560.5, NP_001121064.1, NP_001121065.1, NP_001121067.1, NP_001121068.1
GeneID:84824	FCRLA	1	161,676,762	161,684,142	7,380	+	2	1_A375_pNL7_minus_lncRNA_AR..1..462, 2_A375_pNL97_plus_lncRNA_AR..1..655	15174, 15158	downstream, downstream	1	1	0	32	34	12	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene FCRLA	FCRX, FCRLe, FCRLc2, FREB, FCRLA, FCRL, FCRLd, FCRLM1, FCRL1, FCRLb, RP11-474I16.5, MGC4595, FCRLc1, FCRLX	Fc receptor-like A	NM_032738, NM_001184866, NM_001184867, NM_001184870, NM_001184871, NM_001184872, NM_001184873, hCT1641704.2, hCT1951537.1, hCT1960931.1, hCT1960932.1, hCT1960933.1, hCT2357410.0, hCT2357411.0	235372_at, 235400_at, 235401_s_at	NP_116127.3, NP_001171795.1, NP_001171796.1, NP_001171799.1, NP_001171800.1, NP_001171801.1, NP_001171802.1, EAW90683.1, EAW90684.1, EAW90685.1, EAW90686.1, EAW90687.1, EAW90688.1, EAW90689.1
GeneID:127943	FCRLB	1	161,692,457	161,697,933	5,476	+	6	1_A375_pNL7_minus_lncRNA_AR..1..462, 1_A375_pNL7_minus_lncRNA_AR..1..463, 1_A375_pNL7_minus_lncRNA_AR..1..464, 2_A375_pNL97_plus_lncRNA_AR..1..655, 2_A375_pNL97_plus_lncRNA_AR..1..656, 4_A375_EGR1..1..734	-521, 3959, 7671, -537, 3663, 4247	upstream, in gene, downstream, upstream, in gene, in gene	1	1	1	26.67	24	13	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene FCRLB	FCRLM2, FCRLB, FCRL2, RP11-474I16.6, FCRLY, FREB-2, FcRY, FLJ31052	Fc receptor-like B	NM_001002901, hCT1642726.2, hCT2357414.0	238452_at	NP_001002901.1, EAW90690.1, EAW90691.1
GeneID:11266	DUSP12	1	161,719,581	161,726,952	7,371	+	5	1_A375_pNL7_minus_lncRNA_AR..1..465, 1_A375_pNL7_minus_lncRNA_AR..1..466, 2_A375_pNL97_plus_lncRNA_AR..1..657, 2_A375_pNL97_plus_lncRNA_AR..1..658, 4_A375_EGR1..1..735	-29, 16547, -61, 16547, 99	upstream, downstream, upstream, downstream, in gene	1	1	1	26	25	17.5	2	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene DUSP12	DUSP12, YVH1, DUSP1	dual specificity phosphatase 12	NM_007240, hCT6660.3	218576_s_at	NP_009171.1, EAW90692.1
GeneID:22926	ATF6	1	161,736,084	161,928,852	192,768	+	2	1_A375_pNL7_minus_lncRNA_AR..1..466, 2_A375_pNL97_plus_lncRNA_AR..1..656	44, 44	in gene, in gene	1	1	0	21	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ATF6	ATF6, ATF6A	activating transcription factor 6	NM_007348, hCT6676.2	203952_at, 217550_at, 231927_at	NP_031374.2, EAW90694.1
GeneID:25903	OLFML2B	1	161,952,982	161,993,844	40,862	-	2	2_A375_pNL97_plus_lncRNA_AR..1..659, 4_A375_EGR1..1..736	20460, 50636	in gene, downstream	0	1	1	10.5	14	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene OLFML2B	RP11-227F8.1, MGC51337, OLFML2B	olfactomedin-like 2B	NM_015441, hCT1806448.1, hCT2323229.0, hCT6681.2	213125_at	NP_056256.1, EAW90696.1, EAW90697.1, EAW90698.1
GeneID:9722	NOS1AP	1	162,039,581	162,339,813	300,232	+	2	1_A375_pNL7_minus_lncRNA_AR..1..467, 2_A375_pNL97_plus_lncRNA_AR..1..661	240739, 240771	in gene, in gene	1	1	0	30	33	5	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene NOS1AP	6330408P19Rik, NOS1AP, MGC138500, CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	NM_001126060, NM_014697, NM_001164757, hCT6684.3	1563512_at, 215153_at	NP_001119532.2, NP_055512.1, NP_001158229.1, EAW90700.1
GeneID:117157	SH2D1B	1	162,365,056	162,381,926	16,872	-	1	1_A375_pNL7_minus_lncRNA_AR..1..468	7144	in gene	1	0	0	19	12	7	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene SH2D1B	SH2D1B, EAT2	SH2 domain containing 1B	NM_053282, hCT1642725.3, hCT1984702.2, hCT2344789.0	1553176_at, 1553177_at	NP_444512.2, EAW90703.1, EAW90704.1, EAW90705.1
GeneID:127933	UHMK1	1	162,466,964	162,499,419	32,455	+	3	1_A375_pNL7_minus_lncRNA_AR..1..469, 2_A375_pNL97_plus_lncRNA_AR..1..662, 4_A375_EGR1..1..737	812, 748, 844	in gene, in gene, in gene	1	1	1	21	28	17	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene UHMK1	FLJ23015, UHMK1, KIS, DKFZp434C1613, KIST	U2AF homology motif (UHM) kinase 1	NM_001184763, NM_144624, NM_175866, hCT2323214.1, hCT2323215.1, hCT2349335.0, hCT6682.4	1552856_s_at, 227740_at, 235003_at	NP_001171692.1, NP_653225.2, NP_787062.1, EAW90706.1, EAW90707.1, EAW90708.1, EAW90709.1
GeneID:6675	UAP1	1	162,531,296	162,569,633	38,337	+	4	1_A375_pNL7_minus_lncRNA_AR..1..470, 2_A375_pNL97_plus_lncRNA_AR..1..663, 2_A375_pNL97_plus_lncRNA_AR..1..664, 4_A375_EGR1..1..738	448, 400, 44208, -224	in gene, in gene, downstream, upstream	1	1	1	16.5	22	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene UAP1	AGX, UAP1, SPAG2, AGX2, AGX1	UDP-N-acteylglucosamine pyrophosphorylase 1	NM_003115, hCT1951536.1, hCT2323216.0, hCT6679.3	209340_at	NP_003106.3, EAW90712.1, EAW90710.1, EAW90711.1
GeneID:4921	DDR2	1	162,602,228	162,750,255	148,027	+	1	2_A375_pNL97_plus_lncRNA_AR..1..665	540	in gene	0	1	0	16	17	5	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene DDR2	TKT, TYRO10, MIG20a, DDR2, NTRKR3	discoidin domain receptor tyrosine kinase 2	NM_006182, NM_001014796, hCT2357443.0, hCT5716.3	205168_at, 225442_at, 227561_at, 235631_at	NP_006173.2, NP_001014796.1, EAW90713.1, EAW90714.1
GeneID:83540	NUF2	1	163,291,723	163,325,553	33,830	+	2	1_A375_pNL7_minus_lncRNA_AR..1..472, 2_A375_pNL97_plus_lncRNA_AR..1..667	-43, 21	upstream, in gene	1	1	0	51	66	18	1	2_A375_pNL97_plus_lncRNA_AR..1	66	Gene NUF2	NUF2R, CT106, NUF2, CDCA1	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	NM_031423, NM_145697, hCT1957725.1, hCT2357422.0, hCT6216.2	223381_at	NP_113611.2, NP_663735.2, EAW90735.1, EAW90736.1, EAW90737.1
GeneID:5087	PBX1	1	164,528,802	164,821,045	292,243	+	2	1_A375_pNL7_minus_lncRNA_AR..1..473, 4_A375_EGR1..1..742	-634, 44670	upstream, in gene	1	0	1	10.5	10	10	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene PBX1	MGC126627, DKFZp686B09108, PBX1	pre-B-cell leukemia homeobox 1	NM_002585, hCT14111.3, hCT1951556.2, hCT2326852.0, hCT2326854.1	205253_at, 212148_at, 212151_at	NP_002576.1, EAW90740.1, EAW90738.1, EAW90739.1, EAW90741.1
GeneID:400794	LOC400794	1	165,446,079	165,551,341	105,262	-	2	1_A375_pNL7_minus_lncRNA_AR..1..474, 2_A375_pNL97_plus_lncRNA_AR..1..669	42605, 42637	in gene, in gene	1	1	0	20	21	5	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC400794		hypothetical LOC400794	NR_026744	1556801_at, 1557761_s_at, 1561693_at	
GeneID:440699	LRRC52	1	165,513,478	165,533,185	19,707	+	2	1_A375_pNL7_minus_lncRNA_AR..1..474, 2_A375_pNL97_plus_lncRNA_AR..1..669	-4742, -4774	upstream, upstream	1	1	0	20	21	5	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LRRC52	LRRC52, FLJ25811	leucine rich repeat containing 52	NM_001005214	1556484_at	NP_001005214.2
GeneID:4259	MGST3	1	165,600,450	165,624,857	24,407	+	3	1_A375_pNL7_minus_lncRNA_AR..1..475, 2_A375_pNL97_plus_lncRNA_AR..1..670, 4_A375_EGR1..1..743	-290, 174, -354	upstream, in gene, upstream	1	1	1	23	20	17	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene MGST3	MGST3, GST-III	microsomal glutathione S-transferase 3	NM_004528, hCT1808738.3, hCT1951549.2, hCT2345060.0, hCT2345061.0, hCT2345062.0, hCT2357427.0	201403_s_at, 244122_at	NP_004519.1, EAW90756.1, EAW90752.1, EAW90753.1, EAW90755.1, EAW90757.1, EAW90754.1
GeneID:223	ALDH9A1	1	165,631,449	165,667,900	36,451	-	1	1_A375_pNL7_minus_lncRNA_AR..1..476	177	in gene	1	0	0	19	19	18	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene ALDH9A1	E3, TMABADH, ALDH9A1, ALDH9, ALDH4, ALDH7	aldehyde dehydrogenase 9 family, member A1	NM_000696, hCT12638.3	201612_at	NP_000687.3, EAW90758.1
GeneID:54499	TMCO1	1	165,693,528	165,738,135	44,607	-	2	1_A375_pNL7_minus_lncRNA_AR..1..477, 2_A375_pNL97_plus_lncRNA_AR..1..671	87, -105	in gene, upstream	1	1	0	27	21	13	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene TMCO1	RP11-466F5.7, PNAS-136, TMCC4, PCIA3, TMCO1, HP10122	transmembrane and coiled-coil domains 1	NM_019026, hCT1804924.3, hCT2345057.0, hCT2345058.0, hCT2345059.0	208715_at, 208716_s_at, 210766_x_at, 211098_x_at	NP_061899.1, EAW90763.1, EAW90762.1, EAW90764.1, EAW90765.1
GeneID:100147773	LOC100147773	1	165,738,166	165,744,844	6,678	+	2	1_A375_pNL7_minus_lncRNA_AR..1..477, 2_A375_pNL97_plus_lncRNA_AR..1..671	-118, 74	upstream, in gene	1	1	0	27	21	13	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene LOC100147773	FLJ42974	hypothetical LOC100147773	XR_111961, XR_108300, XR_114979		
GeneID:7371	UCK2	1	165,796,890	165,877,343	80,453	+	1	1_A375_pNL7_minus_lncRNA_AR..1..478	731	in gene	1	0	0	15	13	8	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene UCK2	TSA903, DKFZp686M04245, UCK2, UMPK, UK	uridine-cytidine kinase 2	NM_012474, hCT13781.2, hCT1951554.1, hCT1951555.1	209825_s_at	NP_036606.2, EAW90766.1, EAW90767.1, EAW90769.1
GeneID:149297	FAM78B	1	166,039,256	166,135,958	96,702	-	4	1_A375_pNL7_minus_lncRNA_AR..1..480, 1_A375_pNL7_minus_lncRNA_AR..1..481, 2_A375_pNL97_plus_lncRNA_AR..1..672, 2_A375_pNL97_plus_lncRNA_AR..1..673	-634, -4234, -618, -4170	upstream, upstream, upstream, upstream	1	1	0	19	21	5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene FAM78B	MGC131653, FAM78B	family with sequence similarity 78, member B	NM_001017961, hCT1951557.1	1558113_at	NP_001017961.1, EAW90771.1
GeneID:57645	POGK	1	166,808,724	166,823,709	14,985	+	1	2_A375_pNL97_plus_lncRNA_AR..1..674	-308	upstream	0	1	0	17	24	9	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene POGK	LST003, KRBOX2, BASS2, KIAA1513, POGK, KIAA15131	pogo transposable element with KRAB domain	NM_017542, hCT2322790.0, hCT2322791.0, hCT2322793.0	218229_s_at, 222564_at	NP_060012.3, EAW90777.1, EAW90775.1, EAW90776.1
GeneID:117143	TADA1	1	166,825,747	166,845,654	19,907	-	3	1_A375_pNL7_minus_lncRNA_AR..1..482, 2_A375_pNL97_plus_lncRNA_AR..1..675, 4_A375_EGR1..1..749	54, 38, 630	in gene, in gene, in gene	1	1	1	38	35	17	1	1_A375_pNL7_minus_lncRNA_AR..1	38	Gene TADA1	hADA1, ADA1, HFI1, RP1-9E21.4, TADA1L, TADA1, STAF42	transcriptional adaptor 1	NM_053053, hCT29232.3	1559289_at, 225455_at	NP_444281.1, EAW90778.1
GeneID:387597	ILDR2	1	166,887,996	166,944,561	56,565	-	2	1_A375_pNL7_minus_lncRNA_AR..1..483, 2_A375_pNL97_plus_lncRNA_AR..1..676	22737, 22737	in gene, in gene	1	1	0	23	22	2	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene ILDR2	ILDR2, dJ782G3.1, RP4-782G3.2, C1orf32	immunoglobulin-like domain containing receptor 2	NM_199351, hCT29230.3		NP_955383.1, EAW90779.1
GeneID:92235	DUSP27	1	167,064,087	167,098,402	34,315	+	2	2_A375_pNL97_plus_lncRNA_AR..1..677, 4_A375_EGR1..1..750	41545, 26585	downstream, in gene	0	1	1	14	18	11	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene DUSP27	DUSP27		NM_001080426	232252_at	NP_001073895.1
GeneID:5451	POU2F1	1	167,190,143	167,385,342	195,199	+	5	1_A375_pNL7_minus_lncRNA_AR..1..485, 1_A375_pNL7_minus_lncRNA_AR..1..486, 2_A375_pNL97_plus_lncRNA_AR..1..679, 2_A375_pNL97_plus_lncRNA_AR..1..680, 4_A375_EGR1..1..751	161, 1345, -266, 1521, -596	in gene, in gene, upstream, in gene, upstream	1	1	1	24.5	18	12	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene POU2F1	POU2F1, FLJ42836, OCT1, OTF1	POU class 2 homeobox 1	NM_002697, hCT1951562.1, hCT2324115.0, hCT29227.3	206789_s_at	NP_002688.2, EAW90787.1, EAW90786.1, EAW90788.1
GeneID:919	CD247	1	167,399,877	167,487,847	87,970	-	2	2_A375_pNL97_plus_lncRNA_AR..1..681, 4_A375_EGR1..1..752	903, 79223	in gene, in gene	0	1	1	14.5	15.5	14	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CD247	T3Z, CD247, CD3H, CD3Q, CD3-ZETA, TCRZ, CD3Z	CD247 molecule	NM_198053, NM_000734, hCT1807549.2, hCT1982038.1, hCT2357440.0	210031_at	NP_932170.1, NP_000725.1, EAW90790.1, EAW90791.1, EAW90792.1
GeneID:8804	CREG1	1	167,510,250	167,523,056	12,806	-	2	1_A375_pNL7_minus_lncRNA_AR..1..487, 2_A375_pNL97_plus_lncRNA_AR..1..682	320, -10032	in gene, upstream	1	1	0	19	20	7	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CREG1	CREG, CREG1	cellular repressor of E1A-stimulated genes 1	NM_003851, hCT2324200.0, hCT32589.3	201200_at	NP_003842.1, EAW90794.1, EAW90795.1
GeneID:92241	RCSD1	1	167,599,474	167,675,486	76,012	+	4	1_A375_pNL7_minus_lncRNA_AR..1..488, 2_A375_pNL97_plus_lncRNA_AR..1..683, 4_A375_EGR1..1..753, 4_A375_EGR1..1..754	84430, 84386, 84362, 85294	downstream, downstream, downstream, downstream	1	1	1	31	39	21	1	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene RCSD1	MK2S4, MGC126611, MGC21654, CAPZIP, RCSD1, MGC126585	RCSD domain containing 1	NM_052862, hCT2324121.1, hCT2324122.1, hCT2349443.0, hCT33673.4	225763_at	NP_443094.3, EAW90799.1, EAW90796.1, EAW90797.1, EAW90798.1
GeneID:9019	MPZL1	1	167,691,167	167,761,156	69,989	+	5	1_A375_pNL7_minus_lncRNA_AR..1..488, 2_A375_pNL97_plus_lncRNA_AR..1..683, 2_A375_pNL97_plus_lncRNA_AR..1..684, 4_A375_EGR1..1..753, 4_A375_EGR1..1..754	-7283, -7347, 45, -7331, -8419	upstream, upstream, in gene, upstream, upstream	1	1	1	23.5	32.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene MPZL1	FLJ21047, PZR, PZRa, PZRb, MPZL1, MPZL1b, PZR1b	myelin protein zero-like 1	NM_003953, NM_024569, NM_001146191, hCT1982098.1, hCT1982099.1, hCT2324127.0, hCT33667.3	201874_at, 201875_s_at, 210087_s_at, 210210_at, 210594_x_at	NP_003944.1, NP_078845.3, NP_001139663.1, EAW90800.1, EAW90801.1, EAW90802.1, EAW90803.1
GeneID:25874	BRP44	1	167,887,310	167,906,278	18,968	-	4	1_A375_pNL7_minus_lncRNA_AR..1..489, 2_A375_pNL97_plus_lncRNA_AR..1..685, 4_A375_EGR1..1..755, 4_A375_EGR1..1..756	-378, 1126, 1062, 70	upstream, in gene, in gene, in gene	1	1	1	16	21	30	1	4_A375_EGR1..1	30	Gene BRP44	MGC125753, MGC125752, DKFZp564B167, BRP44	brain protein 44	NM_015415, NM_001143674, NR_026550, hCT2324191.0, hCT2324192.0, hCT2357430.0, hCT2357431.0	202427_s_at, 227669_at	NP_056230.1, NP_001137146.1, EAW90813.1, EAW90814.1, EAW90815.1, EAW90816.1
GeneID:55827	DCAF6	1	167,905,908	168,045,081	139,173	+	4	1_A375_pNL7_minus_lncRNA_AR..1..489, 2_A375_pNL97_plus_lncRNA_AR..1..685, 4_A375_EGR1..1..755, 4_A375_EGR1..1..756	748, -756, -692, 300	in gene, upstream, upstream, in gene	1	1	1	16	21	30	1	4_A375_EGR1..1	30	Gene DCAF6	1200006M05Rik, FLJ23798, MSTP055, ARCAP, IQWD1, DCAF6, PC326, NRIP	DDB1 and CUL4 associated factor 6	NM_018442, NM_001017977, hCT2324129.0, hCT2324130.0, hCT2324131.0, hCT2324132.0, hCT2324133.0	217908_s_at, 232349_x_at, 241209_at	NP_060912.2, NP_001017977.1, EAW90808.1, EAW90809.1, EAW90811.1, EAW90812.1, EAW90810.1
GeneID:23432	GPR161	1	168,053,997	168,105,624	51,627	-	1	4_A375_EGR1..1..757	-666	upstream	0	0	1	12	16	17	1	4_A375_EGR1..1	17	Gene GPR161	GPR161, RE2, FLJ33952	G protein-coupled receptor 161	NM_153832, hCT1951606.1, hCT1951607.1	206971_at, 206972_s_at, 214104_at, 230369_at, 232350_x_at, 235961_at	NP_722561.1, EAW90819.1, EAW90818.1
GeneID:261726	TIPRL	1	168,148,171	168,171,352	23,181	+	1	2_A375_pNL97_plus_lncRNA_AR..1..686	245	in gene	0	1	0	13	23	21	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TIPRL	dJ69E11.3, MGC3794, TIP, TIP41, TIPRL	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	NM_152902, NM_001031800, hCT2357379.0, hCT33676.2	1553677_a_at, 1554351_a_at, 214773_x_at, 226619_x_at	NP_690866.1, NP_001026970.1, EAW90820.1, EAW90821.1
GeneID:375035	SFT2D2	1	168,195,255	168,212,088	16,833	+	2	2_A375_pNL97_plus_lncRNA_AR..1..687, 4_A375_EGR1..1..758	11145, 329	in gene, in gene	0	1	1	17.5	19	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SFT2D2	dJ747L4.C1.2, FLJ34085, SFT2D2, UNQ512	SFT2 domain containing 2	NM_199344, hCT33671.3	214838_at	NP_955376.1, EAW90822.1
GeneID:9095	TBX19	1	168,250,278	168,283,664	33,386	+	1	2_A375_pNL97_plus_lncRNA_AR..1..688	40058	downstream	0	1	0	15	18	4	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TBX19	FLJ34543, dJ747L4.1, TBS19, FLJ34085, TBX19, FLJ26302, TPIT	T-box 19	NM_005149, hCT33670.2	208638_at	NP_005140.1, EAW90824.1
GeneID:1805	DPT	1	168,664,695	168,698,442	33,747	-	3	1_A375_pNL7_minus_lncRNA_AR..1..493, 1_A375_pNL7_minus_lncRNA_AR..1..494, 2_A375_pNL97_plus_lncRNA_AR..1..689	19978, 9626, 9782	in gene, in gene, in gene	1	1	0	21	18	8.5	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene DPT	TRAMP, DPT	dermatopontin	NM_001937, hCT29035.3	207977_s_at, 213068_at, 213071_at	NP_001928.2, EAW90830.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Positions	1_A375_2_A375_3_A375_4_A375_5_A375_6_A375_7_A375_8_A375_9_A375_10_A375_Add Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:48 1	ATP1B1	1	169,078,947	169,101,990	23,043	+	3	2_A375_uhi37_dist_lncRNA_AR_1.690,2_A375_uhi37_dist_lncRNA_AR_1.691,2_A375_uhi37_dist_lncRNA_AR_1.692	-385, 161, 9481	upstream, cis gene, cis gene	0 1 0 17 21.33 9.97 3	2_A375_uhi37_dist_lncRNA_AR_1	Gene ATP1B1	UCSC Link	ATP1B1, ATP1B	ATPase, Na+/K+ transporting, beta 1 polypeptide	NM_001677, XM_011519591.1, XM_017029032.2	201242_s_at, 201243_s_at	NP_001668.1, EAW49033.1, EAW49032.1
GeneID:29 9522	NME7	1	169,101,769	169,207,108	205,417	-	5	1_A375_uhi37_mixed_lncRNA_AR_1.498,1_A375_uhi37_mixed_lncRNA_AR_1.499,2_A375_uhi37_dist_lncRNA_AR_1.693	29450, 55745, 58714	cis gene, cis gene, cis gene	1 1 0 33 4.5 5.5 2	2_A375_uhi37_dist_lncRNA_AR_1	Gene NME7	UCSC Link	bnd25-HT, FLJ21194, MND2H7, NME7	actin-related protein 1 homolog B, centractin beta (yeast), centrosomal protein of 225 kDa, centrosomal protein of 240 kDa, centrosomal protein of 240 kDa isoform 1, centrosomal protein of 240 kDa isoform 2, centrosomal protein of 240 kDa isoform 3, centrosomal protein of 240 kDa isoform 4, centrosomal protein of 240 kDa isoform 5, centrosomal protein of 240 kDa isoform 6, centrosomal protein of 240 kDa isoform 7, centrosomal protein of 240 kDa isoform 8, centrosomal protein of 240 kDa isoform 9, centrosomal protein of 240 kDa isoform 10, centrosomal protein of 240 kDa isoform 11, centrosomal protein of 240 kDa isoform 12, centrosomal protein of 240 kDa isoform 13, centrosomal 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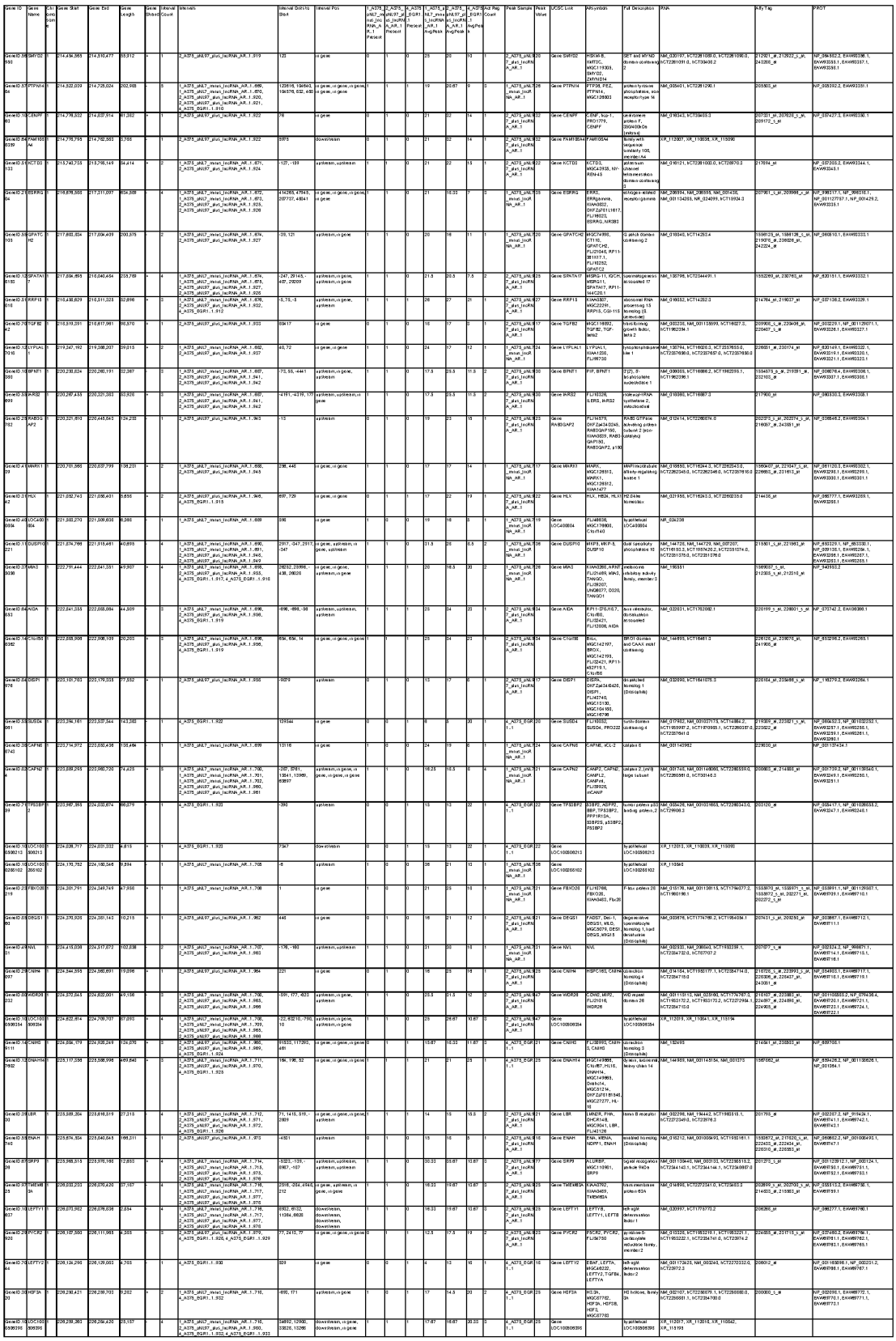


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_shN7_mrna_lncRNA_R_1 Percent	2_A375_shN7_gRNA_lncRNA_R_1 Percent	3_A375_shN7_gRNA_lncRNA_R_1 Percent	1_A375_shN7_mrna_lncRNA_R_1 Avg Peak	2_A375_shN7_gRNA_lncRNA_R_1 Avg Peak	3_A375_shN7_gRNA_lncRNA_R_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:3577955	FAM58B	1	177,140,655	177,231,535	110,825	+	4	1_A375_shN7_mrnaL_lncRNA_R_1:535, 1_A375_shN7_mrnaL_lncRNA_R_1:822, 2_A375_shN7_gRNaL_lncRNA_R_1:754, 4_A375_DSR1_1:770	57959, 64999, 68007, 68439	sr:gene, sr:gene_vs:gene, sr:gene	1	1	1	16	20.93	16.33	3	2_A375_shN7_gRNA_lncRNA_R_1	93	LOC100240401	FAM58B	RP5-1026B2.1, BRWD2, ENSE00001908302, DBCC R1L2, FLJ41342, SWA1947	Bromodomain and WD repeat-containing protein 2	NM_031165, XCT145873	214622_at		NP_599035.1, EAW91009.1
GeneID:1024401	LOC100240401	1	179,080,843	179,080,130	2,685	-	2	1_A375_shN7_mrnaL_lncRNA_R_1:535, 2_A375_shN7_gRNaL_lncRNA_R_1:755	312, 280	sr:gene, sr:gene	1	1	0	32	51	10	1	1_A375_shN7_mrnaL_lncRNA_R_1	52	Gene LOC100240401	FLJ42475	hypothetical LOC100240401	NR_029862			
GeneID:84633	RASAL2	1	179,080,894	179,448,849	368,788	+	5	1_A375_shN7_mrnaL_lncRNA_R_1:535, 1_A375_shN7_mrnaL_lncRNA_R_1:536, 1_A375_shN7_mrnaL_lncRNA_R_1:537, 2_A375_shN7_gRNaL_lncRNA_R_1:755, 2_A375_shN7_gRNaL_lncRNA_R_1:759	+45, 33232, 224336, +16, 33260	sp:Hsa:sn_vs:gene, sr:gene, sp:Hsa:sn_vs:gene	1	1	0	27	21.67	5.33	1	1_A375_shN7_mrnaL_lncRNA_R_1	52	Gene RASAL2	NGAP, RASAL3, WGC129919	RAS protein activator like 2	NM_004841, NM_170692, XCT223139.1, XCT223140.1, XCT223141.1	1557432_at, 217714_at, 217201_at_219926_s_at, 223910_s_at_224343_s_at, 234910_at	NP_004832.1, NP_733762.2, EAW91017.1, EAW91016.1, EAW91019.1
GeneID:4439	CTC1	17	176,811,951	176,816,024	8,093	+	4	1_A375_shN7_mrnaL_lncRNA_R_1:536, 1_A375_shN7_mrnaL_lncRNA_R_1:537, 2_A375_shN7_gRNaL_lncRNA_R_1:740, 4_A375_DSR1_1:771	-5321.5, -27, -825	sp:Hsa:sn_vs:gene, sp:Hsa:sn_vs:gene	1	1	1	17.5	16.5	10	2	2_A375_shN7_gRNA_lncRNA_R_1	20	Gene Ctc1p220	C17orf220, DKFZp564J047, FLJ40199, FLJ58930	Uncharacterized conserved protein, localized to telomeres	NM_025156, XCT252982.0	1563076_at	EAW91026.1
GeneID:5887	RALGPS2	1	176,894,200	176,899,235	194,936	+	1	2_A375_shN7_gRNaL_lncRNA_R_1:742	-205	sp:Hsa:sn	0	1	0	10	17	13	1	2_A375_shN7_gRNA_lncRNA_R_1	17	Gene RALGPS2	D1053G21.1, FLJ38504, FLJ40244, SWA4231, RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	NM_152483, XCT150137.2, XCT223138.0, XCT223137.0, XCT223139.0	2203356_at_227204_at, 232112_at_242456_at	NP_689768.3, EAW91026.1, EAW91027.1, EAW91029.1, EAW91030.1
GeneID:3917	FAM20B	1	179,998,074	179,845,702	90,629	+	5	1_A375_shN7_mrnaL_lncRNA_R_1:540, 1_A375_shN7_mrnaL_lncRNA_R_1:541, 2_A375_shN7_gRNaL_lncRNA_R_1:742, 2_A375_shN7_gRNaL_lncRNA_R_1:744, 2_A375_shN7_gRNaL_lncRNA_R_1:745	648, 59166, -226, +44, 98201	sr:gene, down:intron, sp:Hsa:sn:gene, down:intron	1	1	0	10.67	21.67	11.67	3	2_A375_shN7_gRNA_lncRNA_R_1	28	Gene FAM20B	glycosaminoglycan xylosylkinase, FAM20B	Family with sequence similarity 20, member B	NM_014864, XCT148893.2, XCT223947.0, XCT223946.0	202915_s_at_202918_s_at, 217282_at	NP_055978.1, EAW91038.1, EAW91034.1, EAW91035.1
GeneID:8477	TORSA	1	179,230,112	179,085,151	14,819	-	2	1_A375_shN7_mrnaL_lncRNA_R_1:542, 2_A375_shN7_gRNaL_lncRNA_R_1:745	130, 150	sr:gene, sr:gene	1	1	0	19	19	13	1	2_A375_shN7_gRNA_lncRNA_R_1	19	Gene TORSA	AAA2, TORSA, FLJ22345, WGC111164, ADIR	torsin family 3, member A	NM_022371, XCT148702.2, XCT155735.1, XCT155736.1	215459_at, 233581_s_at	NP_071766.2, EAW91038.1, EAW91037.1, EAW91039.1
GeneID:25	ABL2	1	179,098,482	179,196,819	130,337	+	1	4_A375_DSR1_1:772	19771	sr:gene	0	0	1	7	9	16	1	4_A375_DSR1_1	16	Gene ABL2	FLJ20715, ABL2, ARG, ABLL, FLJ41441, FLJ22224	v-abl Abelson murine leukemia viral oncogene homolog 2	NM_001136001, NM_007314, NM_009168, NM_001136002, NM_001168236, NM_001168237, NM_001168238, NM_001168239, XCT148722.2, XCT153757.1	208411_s_at	NP_001126773.1, NP_009298.1, NP_001126772.1, NP_001161709.1, NP_001161710.1, NP_001161711.1, EAW91040.1, EAW91041.1
GeneID:8869	SOAT1	1	179,282,017	179,324,433	91,416	+	3	1_A375_shN7_mrnaL_lncRNA_R_1:543, 2_A375_shN7_gRNaL_lncRNA_R_1:748, 4_A375_DSR1_1:773	-299, -41, -137	sp:Hsa:sn, sp:Hsa:sn	1	1	1	16	17	16	1	1_A375_shN7_mrnaL_lncRNA_R_1	16	Gene SOAT1	STAT, RP11-215D22.2, SOAT1, ACAT, SOAT_ACAT1	sterol O-acyltransferase 1	NM_003101, XCT149713.2, XCT223936.0	221981_at	NP_003092.4, EAW91043.1, EAW91044.1
GeneID:1202	TOR3A	1	179,259,555	179,322,670	189,015	+	3	1_A375_shN7_mrnaL_lncRNA_R_1:544, 2_A375_shN7_gRNaL_lncRNA_R_1:747, 2_A375_shN7_gRNaL_lncRNA_R_1:746	188742, 512, 185305	sr:gene, sr:gene, sr:gene	1	1	0	19	23.5	8	2	2_A375_shN7_gRNA_lncRNA_R_1	23	Gene Ctc1p125	FLJ22410, RP11-213D22.2, FLJ39435, DKFZp686H1423, MGC9401, C1orf125	torsin family 3, member A	NM_148398, XCT155770.1, XCT223936.1, XCT223937.0	1553870_s_at, 1553276_a_at	NP_683297.3, EAW91047.1, EAW91045.1, EAW91046.1, EAW91048.1
GeneID:2746	NPHS2	1	179,319,874	179,345,064	25,410	-	2	1_A375_shN7_mrnaL_lncRNA_R_1:544, 2_A375_shN7_gRNaL_lncRNA_R_1:748	24457, 24924	sr:gene, sr:gene	1	1	0	23	22	16	1	1_A375_shN7_mrnaL_lncRNA_R_1	23	Gene NPHS2	PODN, STRN1, NPHS2	podocin 2, stomatin, stomatin-related (podocyt	NM_014513, XCT156503.2, XCT237458.0	229624_at	NP_055340.1, EAW91049.1, EAW91050.1
GeneID:1427	FAM183A	1	179,712,295	179,788,333	77,039	+	2	4_A375_DSR1_1:774, 4_A375_DSR1_1:775	70774, 74774	sr:gene, down:intron	0	0	1	7	11.5	21	2	4_A375_DSR1_1	22	Gene FAM183A	MGC19994, MDSP, C1orf76, FAM183A, RP11-124I8.2	family with sequence similarity 183, member A	NM_175309, XCT223066.1	222093_s_at, 231297_at	NP_787703.1, EAW91055.1
GeneID:1539	TORIAIP2	1	179,813,999	179,848,941	35,075	-	3	1_A375_shN7_mrnaL_lncRNA_R_1:545, 2_A375_shN7_gRNaL_lncRNA_R_1:749, 4_A375_DSR1_1:776	-4581, -4979, -4019	sp:Hsa:sn, sp:Hsa:sn, sp:Hsa:sn	1	1	1	29	24	21	1	1_A375_shN7_mrnaL_lncRNA_R_1	29	Gene TORIAIP2	PRO3215, WGC130074, LULL1, TORIAIP2, WGC130074, WGC130073, WGC129493, RP11-124I8.3, WGC129561, MPL1, WGC130077, FLJ37612	torsin A interacting protein 2	NM_145334, NM_022547, XCT224972.1, XCT224973.1, XCT224974.1, XCT224975.1, XCT224976.1, XCT224977.1, XCT224978.1, XCT224979.1, XCT224980.0, XCT224981.0, XCT224982.0, XCT224983.0, XCT224984.0, XCT224985.0, XCT224986.0, XCT224987.0, XCT224988.0, XCT224989.0, XCT224990.0	1569078_at, 233655_at, 1569078_at, 233655_at	NP_839711.3, NP_071742.1, EAW91058.1, EAW91059.1, EAW91060.1, EAW91061.1, EAW91062.1, EAW91063.1, EAW91062.1
GeneID:2497	TORIAIP1	1	179,831,420	179,889,211	57,791	+	3	1_A375_shN7_mrnaL_lncRNA_R_1:545, 2_A375_shN7_gRNaL_lncRNA_R_1:749, 4_A375_DSR1_1:776	-372, 600, 540	sp:Hsa:sn_vs:gene, sp:Hsa:sn_vs:gene	1	1	1	29	24	21	1	1_A375_shN7_mrnaL_lncRNA_R_1	29	Gene TORIAIP1	LAP1B, MGC9413, TORIAIP1, FLJ13142, DKFZp686G011	torsin A interacting protein 1	NM_015932, XCT153863.2, XCT223934.0	213488_at, 213489_s_at, 218160_s_at	NP_056717.2, EAW91066.1, EAW91067.1
GeneID:9859	CEP350	1	179,920,935	180,056,015	160,107	+	1	2_A375_shN7_gRNaL_lncRNA_R_1:750	26	sp:Hsa:sn	0	1	0	16	30	14	1	2_A375_shN7_gRNA_lncRNA_R_1	30	Gene CEP350	CAP350, FLJ44055, KIAA0465, FLJ38262, CAP350, CEP350	centrosomal protein 350kDa	NM_014810, XCT223936.1, XCT223938.0, XCT223939.1, XCT223940.0	204375_s_at, 213163_at, 213164_at, 213165_at_213957_s_at	NP_055635.4, EAW91071.1, EAW91070.1, EAW91072.1, EAW91073.1
GeneID:3778	QSOX1	1	180,120,966	180,187,169	66,203	+	1	4_A375_DSR1_1:777	28512	sp:Hsa:sn	0	0	1	3	12	16	1	4_A375_DSR1_1	16	Gene QSOX1	QSI, FLJ45656, QSCN6, QSCN1	quiescin Q6 sulfhydryl oxidase 1	NM_002826, NM_001004128, XCT153767.3, XCT223942.1	201462_at	NP_002817.2, NP_001004128.1, EAW91076.1, EAW91077.1
GeneID:3995	LRH4	1	180,199,442	180,244,166	44,748	+	1	4_A375_DSR1_1:778	-1274	sp:Hsa:sn	0	0	1	11	10	15	1	4_A375_DSR1_1	15	Gene LRH4	C1R4L, FLJ22769, Golv, Golv4, LRH4	LIM homeobox 4	NM_033340, XCT153898.2	1553156_at, 1553157_at	NP_620129.1, EAW91078.1
GeneID:6442	ACBD6	1	180,257,332	180,272,022	214,870	-	2	1_A375_shN7_mrnaL_lncRNA_R_1:546, 2_A375_shN7_gRNaL_lncRNA_R_1:751	374, 374	sp:Hsa:sn, sr:gene	1	1	0	31	35	15	1	2_A375_shN7_gRNA_lncRNA_R_1	35	Gene ACBD6	MGC3454, ACBD6	acyl-CoA binding domain containing 6	NM_032390, XCT153892.7, XCT223970.0, XCT223969.0	225317_at	NP_115738.1, EAW91082.1, EAW91083.1, EAW91084.1
GeneID:5324	XPR1	1	180,601,148	180,639,415	258,269	+	2	1_A375_shN7_mrnaL_lncRNA_R_1:547, 2_A375_shN7_gRNaL_lncRNA_R_1:752	930, 150	sr:gene, sr:gene	1	1	0	17	19	10	1	2_A375_shN7_gRNA_lncRNA_R_1	19	Gene XPR1	XPR1, SYG1, XI, HSPC159	xenotropic and polytropic retrovirus receptor	NM_004736, NM_001135999, XCT137513.3, XCT223933.0	222361_at	NP_004727.2, NP_001129741.1, EAW91085.1, EAW91087.1
GeneID:5511	KIAA1810	1	180,682,313	180,915,239	232,926	+	3	4_A375_DSR1_1:779, 4_A375_DSR1_1:780, 4_A375_DSR1_1:781	7019, 32615, 45114	sp:Hsa:sn:gene, sp:Hsa:sn:gene	0	0	1	8	17.33	1	4	4_A375_DSR1_1	19	Gene KIAA1614	FLJ35393, RP11-484N13.2, KIAA1614	KIAA1614	NM_020950	213387_at	NP_066031.1
GeneID:1057	CITED2	6	180,842,175	180,992,648	49,831	-	1	2_A375_shN7_gRNaL_lncRNA_R_1:753	445	sp:Hsa:sn	0	0	1	15	20	16	1	2_A375_shN7_gRNA_lncRNA_R_1	20	Gene CITED2	CITED2	cytokine-6	NM_006079, XCT152822.3, XCT223976.0, XCT223977.0	1552816_at, 212799_at, 212800_at_214441_at, 244041_at	NP_006070.1, EAW91092.1, EAW91091.1, EAW91092.1
GeneID:3161	ER3	1	181,037,835	181,039,979	2,341	+	4	1_A375_shN7_mrnaL_lncRNA_R_1:548, 1_A375_shN7_mrnaL_lncRNA_R_1:754, 2_A375_shN7_gRNaL_lncRNA_R_1:755, 4_A375_DSR1_1:782	-35, 90, 1274, 214	sp:Hsa:sn, sp:Hsa:sn, sp:Hsa:sn	1	1	1	17	23.5	16	2	2_A375_shN7_gRNA_lncRNA_R_1	23	Gene IER3	IER3, IEX1, GRINI, WGC102760	immediate early response 3	NM_016545, XCT153820.2	210611_at	NP_057629.2, EAW91099.1
GeneID:8601	RNASEL	1	182,542,772	182,596,105	53,334	-	1	2_A375_shN7_gRNaL_lncRNA_R_1:755	2372	sp:Hsa:sn	0	1	0	11	17	9	1	2_A375_shN7_gRNA_lncRNA_R_1	17	Gene RNASEL	RNS6, MGC133329, RNASEL, PRCA1, DKFZp781D0812 6, MGC139172	ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	NM_021133, XCT153879.3	221287_at, 221283_at	NP_066956.1, EAW91126.1
GeneID:8865	RGS16	1	182,587,754	182,593,545	5,792	-	3	1_A375_shN7_mrnaL_lncRNA_R_1:550, 1_A375_shN7_mrnaL_lncRNA_R_1:755, 2_A375_shN7_gRNaL_lncRNA_R_1:759	60, 15060, 140	sr:gene, down:intron, sr:gene	1	1	0	15	20.5	10	2	2_A375_shN7_gRNA_lncRNA_R_1	24	Gene RGS16	RGS16, AZ5-RGS14, RGS16, AZ5-RGS14P	regulator of G-protein signaling 16	NM_002929, XCT141892.2	209324_s_at_209323_s_at	NP_002918.3, EAW91129.1
GeneID:2381	LOC284440	1	182,594,273	182,598,764	1,439	-	2	1_A375_shN7_mrnaL_lncRNA_R_1:551, 2_A375_shN7_gRNaL_lncRNA_R_1:760	-113, 109	sp:Hsa:sn, sp:Hsa:sn	1	1	0	16	17	14	1	2_A375_shN7_gRNA_lncRNA_R_1	17	Gene LOC284840	LOC284840	hypothetical LOC284840	NR_038490	231427_at	
GeneID:3852	NR1	1	182,781,294	182,798,566	97,184	+	2	2_A375_shN7_gRNaL_lncRNA_R_1:762, 2_A375_shN7_gRNaL_lncRNA_R_1:763	-2455, 47554	sp:Hsa:sn, down:intron	0	1	0	17.5	24	15.5	2	2_A375_shN7_gRNA_lncRNA_R_1	30	Gene NR1	NAC, NPL, C1r12, C1r1r12, MGC141962, MGC61989, DKFZP, NPL1, C1r12	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	NM_020765, XCT199239.1, XCT199454.1, XCT223122.0, XCT223124.0	221210_s_at_223403_at, 240440_at_243088_at	NP_065797.1, EAW91134.1, EAW91132.1, EAW91133.1, EAW91135.1
GeneID:1810	DHX9	1	182,808,439	182,837,117	48,678	+	1	2_A375_shN7_gRNaL_lncRNA_R_1:765	458	sp:Hsa:sn	0	1	0	16	16	15	1	2_A375_shN7_gRNA_lncRNA_R_1	16	Gene DHX9	RHA, NDH1, DDX9, LKP, FLJ17406, NDH2	DEAH (Asp-Glu-Ala-His) box polypeptide 9	NM_001357, NR_033332, XCT155513.3, XCT223127.0	202423_s_at_212103_s_at, 212107_s_at	NP_001348.2, EAW91135.1, EAW91137.1
GeneID:2719	UAMC1	1	182,992,993	183,114,727	122,132	+	3	1_A375_shN7_mrnaL_lncRNA_R_1:552, 2_A375_shN7_gRNaL_lncRNA_R_1:764, 2_A375_shN7_gRNaL_lncRNA_R_1:765	525, -753, 323	sp:Hsa:sn, sp:Hsa:sn, sp:Hsa:sn	1	1	0	16	20	14.5	2	2_A375_shN7_gRNA_lncRNA_R_1	22	Gene UAMC1	LAMB2, WGC62729, UAMC1	laminin, gamma 1 (formerly LAMB2)	NM_032293, XCT222138.0, XCT151992.2	200770_s_at, 200771_at	NP_002284.3, EAW91143.1, EAW91144.1
GeneID:3918	LAMC2	1	183,135,174	183,214,282	79,065	+	1	4_A375_shN7_mrnaL_lncRNA_R_1:556	48856	sp:Hsa:sn	1	0	0	19	16	8	1	1_A375_shN7_mrnaL_lncRNA_R_1	19	Gene LAMC2	MGC141956, LAMB2T, CSF, B27, LAMC2, LAMB2, EMBG, LAMB2T, EBR2, MGC135491, EBR2A	laminin, gamma 2	NM_005562, NM_018891, XCT156955.2, XCT151991.2	202267_at_202737_at	NP_005553.3, NP_061982.2, EAW91148.1, EAW91147.1
GeneID:2338	NARPAT2	1	183,217,379	183,267,727	170,356	-	5	1_A375_shN7_mrnaL_lncRNA_R_1:556, 1_A375_shN7_mrnaL_lncRNA_R_1:769, 2_A375_shN7_gRNaL_lncRNA_R_1:767, 2_A375_shN7_gRNaL_lncRNA_R_1:768, 2_A375_shN7_gRNaL_lncRNA_R_1:769	1783, 135537, 99537, 1721, 129273	sp:Hsa:sn, sr:gene, sr:gene, sp:Hsa:sn, sr:gene, sr:gene	1	1	1	19	23.5	14.75	4	2_A375_shN7_gRNA_lncRNA_R_1	46	Gene NARPAT2	PWT2, WGC2798, KIAA0470, NARPAT2, C1r1r13	acidic nuclear receptor phosphoprotein 32 family, member B, pseudogene 2	NM_019232, NM_178708, XCT224444.0, XCT224444.0, XCT224445.0, XCT237439.0	1552712_s_at, 1568029_at, 1562699_at, 209759_at	NP_061985.2, EAW91149.1, EAW91150.1, EAW91151.1
GeneID:1005	LOC100506290	1	183,430,009	183,441,154	11,325	-	2	1_A375_shN7_mrnaL_lncRNA_R_1:556, 2_A375_shN7_gRNaL_lncRNA_R_1:769	666, 654	sp:Hsa:sn, sr:gene	1	1	0	23	32	21	1	2_A375_shN7_gRNA_lncRNA_R_1	32	Gene LOC100506290	LOC100506290	hypothetical LOC100506290	XR_111954, XR_108316, XR_114950		
GeneID:3983	SIAT7	1	183,441,509	183,523,328	81,822	+	2	1_A375_shN7_mrnaL_lncRNA_R_1:556, 2_A375_shN7_gRNaL_lncRNA_R_1:769	-1056, -1028	sp:Hsa:sn, sp:Hsa:sn	1	1	0	23	32	21	1	2_A375_shN7_gRNA_lncRNA_R_1	32	Gene SIAT7	SIAT7, WGC2250, FLJ37171, EST1C, C1orf84, SIAT-7, SIAT7_MOUSE	Sialyltransferase 7 (beta-galactoside alpha-2,3-sialyltransferase) D, isoform	NM_031174, NM_173136, NM_201566, NM_201569, XCT169966.1, XCT169968.1, XCT223534.0, XCT223536.0, XCT111114.2	201793_x_at, 201794_s_at, 201795_at, 217169_s_at	NP_001167622.1, NP_775179.1, NP_983982.1, NP_983982.2, EAW91156.1, EAW91154.1, EAW91155.1, EAW91157.1, EAW91158.1
GeneID:4481	NCF2	1	183,824,897	183,890,036	65,139	-	1	1_A375_shN7_mrnaL_lncRNA_R_1:557	-9418	sp:Hsa:sn	1	0	0	31	20	8	1	1_A375_shN7_mrnaL_lncRNA_R_1	31	Gene NCF2	P67PHOX, NCF2, NCF2_MEF-PHOX, NOXA2, NCF2, FLJ39255	neutrophil cytosolic factor 2	NM_000433, NM_001127651, NM_001190769, NM_001190770, XCT225449.0, XCT225449.0, XCT151969.3	209949_at	NP_000424.2, NP_001121123.1, NP_001177715.1, NP_001177725.1, EAW91160.1, EAW91161.1, EAW91162.1, EAW91163.1
GeneID:1048	ARPC3	1	183,848,332	183,859,565	9,833	-	3	1_A375_shN7_mrnaL_lncRNA_R_1:557, 2_A375_shN7_gRNaL_lncRNA_R_1:770, 4_A375_DSR1_1:798	-7, 233, 137	sp:Hsa:sn, sr:gene, sr:gene	1	1	1	25	20	20	1	1_A375_shN7_mrnaL_lncRNA_R_1	25	Gene ARPC3	ARPC3, ARC16, p16-Arc, dJ1127C7.3, MGC68522	actin related protein 2/3 complex, subunit 3, 16kDa	NM_005717, XCT156994.2, XCT237372.1	1568797_a_at, 1569225_at, 211963_s_at	NP_005706.1, EAW91166.1, EAW91163.1
GeneID:1024439	LOC100240409	1	183,851,709	183,864,929	8,230	+	3	1_A375_shN7_mrnaL_lncRNA_R_1:556, 2_A375_shN7_gRNaL_lncRNA_R_1:770, 4_A375_DSR1_1:798	3283, 3043, 3139	down:intron, sr:gene, sr:gene	1	1	1	25	20	20	1	1_A375_shN7_mrnaL_lncRNA_R_1	25	Gene LOC100240409	LOC100240409	hypothetical LOC100240409	XR_111963, XR_108319, XR_114951		
GeneID:2317	RGL1	1	183,868,205	183,897,886	292,436	+	3	1_A375_shN7_mrnaL_lncRNA_R_1:556, 2_A375_shN7_gRNaL_lncRNA_R_1:770, 4_A375_DSR1_1:798	-218, -456, -580	sp:Hsa:sn, sp:Hsa:sn, sp:Hsa:sn	1	1	1	25	20	20	1	1_A375_shN7_mrnaL_lncRNA_R_1	25	Gene RGL1	KIAA0269, RGL1, RGL	ral guanine nucleotide dissociation stimulator-like 1	NM_015149, XCT223535.0, XCT223535.0, XCT223536.0	209365_s_at	NP_055964.3, EAW91166.1, EAW91165.1, EAW91167.1
GeneID:4035	APOBEC4	1	183,919,410	183,922,448	7,038	-	3	1_A375_shN7_mrnaL_lncRNA_R_1:556, 2_A375_shN7_gRNaL_lncRNA_R_1:770, 4_A375_DSR1_1:798	17456, 17696, 17650	Downstream, Downstream, Downstream	1	1	1	25	20	20	1	1_A375_shN7_mrnaL_lncRNA_R_1	25	Gene APOBEC4	APOBEC4, C1orf85, MGC26594	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 4 (putative)	NM_203454, XCT156599.1	1554543_at	NP_982279.1, EAW91169.1
GeneID:2297	GLT25D2	1	183,954,988	184,009,693	101,697	-	2	1_A375_shN7_mrnaL_lncRNA_R_1:771, 4_A375_DSR1_1:797	94573, 1199	sr:gene, sr:gene	0	1	1	12.5	14	12.5	2	4_A375_DSR1_1	19	Gene GLT25D2	GLT25D2, WGA09A, FLJ20773, C1orf17, FLJ37771	glycosyltransferase 25 family member 2	NM_016101, XCT223434.0, XCT237396.0, XCT221764.0	209883_at	NP_057185.1, EAW91170.1, EAW91171.1, EAW91172.1
GeneID:1178	TSEN15	1	184,030,811	184,043,348	22,538	+	2	1_A375_shN7_mrnaL_lncRNA_R_1:556, 2_A375_shN7_gRNaL_lncRNA_R_1:772	37, 21	sr:gene, sr:gene	1	1	0	25	30	11	1	2_A375_shN7_gRNA_lncRNA_R_1	30	Gene TSEN15	tsn15, TSEN15, C1orf19	tRNA splicing endonuclease 15 homolog (S. cerevisiae)	NM_032460, NR_023376, NM_001127054, NM_001190769, XCT223395.0, XCT223396.0, XCT221692.2	225399_at_225400_at, 225327_s_at	NP_001177.1, EAW91173.1, EAW91174.1, EAW91175.1
GeneID:6101	Ctc1p21	1	184,398,190	184,398,153	242,006	+	3	1_A375_shN7_mrnaL_lncRNA_R_1:561, 2_A375_shN7_gRNaL_lncRNA_R_1:962, 2_A375_shN7_gRNaL_lncRNA_R_1:773	228584, 228496, 228474	sp:Hsa:sn, sr:gene, sr:gene, sr:gene	1	1	0	19.5	17.5	8	2	1_A375_shN7_mrnaL_lncRNA_R_1	22	Gene Ctc1p21	C1orf21, FKS13	chromosome 1 open reading frame 21	NM_030936, XCT223376.0, XCT223771.3	221272_s_at_223125_s_at, 223126_s_at_223127_s_at, 223699_at	NP_112197.3, EAW91178.1, EAW91177.1
GeneID:8324	EDEM3	1	184,859,923	184,729,041	99,216	-	3	1_A375_shN7_mrnaL_lncRNA_R_1:562, 2_A375_shN7_gRNaL_lncRNA_R_1:774, 4_A375_DSR1_1:799	-439, 261, 661	sp:Hsa:sn, sp:Hsa:sn, sr:gene	1	1	1	20	26	20	1	2_A375_shN7_gRNA_lncRNA_R_1	26	Gene EDEM3	C1orf22, EDEM3	ER degradation enhancer, mannosidase alpha-like 3	NM_025191, XCT223529.0, XCT223529.0, XCT223530.0, XCT223270.0, XCT223271.0, XCT223272.0, XCT223273.0	220342_s_at_220926_s_at, 223343_s_at	NP_079497.3, EAW91182.1, EAW91176.1, EAW91179.1, EAW91180.1, EAW91181.1, EAW91183.1
GeneID:1517	FAM129A	1	184,790,166	184,843,662	163,516	+	1	2_A375_shN7_mrnaL_lncRNA_R_1:564	107218	sr:gene	0	0	1	14	14	3	1	2_A375_shN7_gRNA_lncRNA_R_1	14	Gene FAM129A	FLJ38220, FAM129A, GOS28, NIBAN, C1orf24	family with sequence similarity 129, member A	NM_052988, XCT223228.0, XCT221661.2	217668_s_at, 217667_s_at	NP_443165.1, EAW91184.1, EAW91185.1
GeneID:8878	RNP2	1	185,014,551	185,071,740	57,189	+	1	1_A375_shN7_mrnaL_lncRNA_R_1:565	69	sr:gene	0	0	1	16	13	11	1	1_A375_shN7_mrnaL_lncRNA_R_1	16	Gene RNP2	RNA2, SYAP, BNP1, RNP2, RNG18, BNP-1, RP10	ring finger protein 2	NM_007212, XCT223573.0, XCT151393.3	205215_at	NP_009143.1, EAW91187.1, EAW91188.1
GeneID:8167	Ctc1p33	1	185,097,217	185,136,118	38,899	-	2	2_A375_shN7_gRNaL_lncRNA_R_1:775, 4_A375_DSR1_1:799	336, -343	sr:gene, sp:Hsa:sn	0	1	1	16	16	16	1	2_A375_shN7_gRNA_lncRNA_R_1	16	Gene Ctc1p33	C1orf33, MGC20012.3, MSTP070, MSTP070, MGC23112, MGC37139, TRMT11L, TRMT11	TRMT11 tRNA methyltransferase-like	NM_030934, XCT223373.0, XCT221664.3	220992_s_at_223434_s_at, 223350_s_at	NP_112186.3, EAW91189.1, EAW91190.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.54823	C1orf26	1	185,126,192	185,260,913	134,721	+	2	2_A375_pNL97_plus_lncRNA_AR..1..775, 4_A375_EGR1..1..789	-432, 464	upstream, in gene	0	1	1	16	16	18	1	4_A375_EGR1..1	18	Gene C1orf26	C1orf26, HsSwt1, FLJ35944, SWT1, FLJ20121	SWT1 RNA endoribonuclease homolog (S. cerevisiae)	NM_017673, NM_001105518, hCT1951760.1	223546_at	NP_060143.4, NP_001098988.1, EAW91191.1
GeneID.10625	IVNS1ABP	1	185,265,520	185,286,461	20,941	-	1	2_A375_pNL97_plus_lncRNA_AR..1..776	141	in gene	0	1	0	15	24	16	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene IVNS1ABP	NS1-BP, NS1BP, KIAA0850, FLJ10962, FLJ35593, FLJ38593, FLARA3, IVNS1ABP, HSPC068, FLJ10411, ND1, DKFZp686K06216, KLHL39, NS-1, FLJ10069	influenza virus NS1A binding protein	NM_006469, hCT2357351.0, hCT31138.3	201362_at, 201363_s_at, 206245_s_at, 239152_at, 244235_at	NP_006460.2, EAW91193.1, EAW91194.1
GeneID.83872	HMCN1	1	185,703,683	186,160,085	456,402	+	5	2_A375_pNL97_plus_lncRNA_AR..1..780, 2_A375_pNL97_plus_lncRNA_AR..1..781, 1_A375_pNL7_minus_lncRNA_AR..1..569, 1_A375_pNL7_minus_lncRNA_AR..1..570, 2_A375_pNL97_plus_lncRNA_AR..1..782	-99, 55933, 448797, 453501, 453677	upstream, in gene, in gene, in gene, in gene	1	1	0	18.25	22.5	8.5	4	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene HMCN1	FIBL6, ARMD1, FIBL-6, FBLN6, HMCN1	hemicentin 1	NM_031935, hCT2323083.0, hCT2323085.0, hCT2323086.0	235944_at	NP_114141.2, EAW91198.1, EAW91199.1, EAW91200.1
GeneID.7175	TPR	1	186,280,784	186,344,457	63,673	-	2	1_A375_pNL7_minus_lncRNA_AR..1..573, 2_A375_pNL97_plus_lncRNA_AR..1..784	-343, -183	upstream, upstream	1	1	0	35	23	17	1	1_A375_pNL7_minus_lncRNA_AR..1	35	Gene TPR	TPR		NM_003292, hCT2323236.0, hCT2323239.0, hCT2357439.0, hCT32452.3	1557227_s_at, 201730_s_at, 201731_s_at, 215220_s_at, 228709_at	NP_003283.2, EAW91204.1, EAW91203.1, EAW91205.1, EAW91206.1
GeneID.54953	C1orf27	1	186,344,890	186,390,503	45,613	+	2	1_A375_pNL7_minus_lncRNA_AR..1..573, 2_A375_pNL97_plus_lncRNA_AR..1..784	-90, -250	upstream, upstream	1	1	0	35	23	17	1	1_A375_pNL7_minus_lncRNA_AR..1	35	Gene C1orf27	ODR4, odr-4, FLJ20505, TTG1, C1orf27	chromosome 1 open reading frame 27	NM_017847, NM_001164245, NM_001164246, hCT2323094.0, hCT2323095.0, hCT32454.3	218721_s_at, 222720_x_at	NP_060317.3, NP_001157717.1, NP_001157718.1, EAW91207.1, EAW91208.1, EAW91209.1
GeneID.5743	PTGS2	1	186,640,944	186,649,559	8,615	-	1	2_A375_pNL97_plus_lncRNA_AR..1..786	-361	upstream	0	1	0	12	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene PTGS2	COX-2, PGHS-2, hCox-2, PTGS2, GRIPGHS, PHS-2, PGG/HS, COX2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	NM_000963, hCT31137.3	1554997_a_at, 204748_at	NP_000954.1, EAW91216.1
GeneID.440704	LOC440704	1	190,760,636	190,770,786	10,150	+	1	4_A375_EGR1..1..791	-9342	upstream	0	0	1	5	6	16	1	4_A375_EGR1..1	16	Gene LOC440704		hypothetical LOC440704	NR_033922	1562556_at	
GeneID.5997	RGS2	1	192,778,169	192,781,407	3,238	+	1	2_A375_pNL97_plus_lncRNA_AR..1..792	55	in gene	0	1	0	20	20	12	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene RGS2	RGS2, G0S8	regulator of G-protein signaling 2, 24kDa	NM_002923, hCT2323326.0, hCT31156.3	202388_at	NP_002914.1, EAW91231.1, EAW91232.1
GeneID.51377	UCHL5	1	192,984,899	193,028,521	43,622	-	3	1_A375_pNL7_minus_lncRNA_AR..1..583, 2_A375_pNL97_plus_lncRNA_AR..1..793, 4_A375_EGR1..1..792	-23, 9, -279	upstream, in gene, upstream	1	1	1	34	35	24	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene UCHL5	UCH37, CGI-70, INO80R, UCHL5	ubiquitin carboxyl-terminal hydrolase L5	NM_015984, hCT1796536.1, hCT1813150.1, hCT1814584.1, hCT2357420.0, hCT2357421.0, hCT32322.2	1570145_at, 219960_s_at, 220083_x_at	NP_057068.1, EAW91238.1, EAW91234.1, EAW91235.1, EAW91236.1, EAW91237.1, EAW91233.1
GeneID.6738	TROVE2	1	193,028,552	193,060,907	32,355	+	3	1_A375_pNL7_minus_lncRNA_AR..1..583, 2_A375_pNL97_plus_lncRNA_AR..1..793, 4_A375_EGR1..1..792	-8, -40, 248	upstream, upstream, in gene	1	1	1	34	35	24	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene TROVE2	SSA2, RORNP, RO60, TROVE2	TROVE domain family, member 2	NM_001042369, NM_001042370, NM_001173524, NM_001173525, NM_004600, NR_033393, hCT2323332.1, hCT2323333.1, hCT2349435.0, hCT2349436.0, hCT2349437.0, hCT2349438.0, hCT2349439.0, hCT2349440.0, hCT32323.4	207520_at, 210438_x_at, 212839_s_at, 212852_s_at, 213027_at	NP_001035828.1, NP_001035829.2, NP_004591.2, NP_001166995.1, NP_001166996.1, EAW91240.1, EAW91239.1, EAW91241.1, EAW91242.1, EAW91243.1, EAW91244.1, EAW91245.1, EAW91246.1, EAW91247.1
GeneID.51022	GLRX2	1	193,065,600	193,075,244	9,644	-	2	2_A375_pNL97_plus_lncRNA_AR..1..794, 4_A375_EGR1..1..793	892, 876	in gene, in gene	0	1	1	15	20	18	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene GLRX2	GLRX2, bA101E13.1, GRX2	glutaredoxin 2	NM_016066, NM_197962, hCT2323424.0, hCT32324.2	219933_at	NP_057150.2, NP_932066.1, EAW91248.1, EAW91249.1
GeneID.79577	CDC73	1	193,091,088	193,223,945	132,857	+	4	1_A375_pNL7_minus_lncRNA_AR..1..584, 2_A375_pNL97_plus_lncRNA_AR..1..795, 4_A375_EGR1..1..794, 4_A375_EGR1..1..795	112, 48, -96, 119872	in gene, in gene, upstream, in gene	1	1	1	16	17.5	21.5	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene CDC73	C1orf28, FLJ23316, HRPT2, HYX, HPTJT, CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	NM_024529, hCT32327.3	218578_at	NP_078805.3, EAW91250.1
GeneID.343450	KCNT2	1	196,194,913	196,577,499	382,586	-	2	1_A375_pNL7_minus_lncRNA_AR..1..588, 2_A375_pNL97_plus_lncRNA_AR..1..797	-709, -357	upstream, upstream	1	1	0	21	21	19	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene KCNT2	MGC119610, KCNT2, KCa4.2, MGC119613, SLO2.1, SLICK, MGC119611, MGC119612	potassium channel, subfamily T, member 2	NM_198503, hCT1951764.2, hCT2323329.1	234103_at, 244455_at	NP_940905.2, EAW91256.1, EAW91255.1
GeneID.3080	CFHR2	1	196,912,934	196,928,356	15,422	+	1	4_A375_EGR1..1..799	-9766	upstream	0	0	1	6	11	22	1	4_A375_EGR1..1	22	Gene CFHR2	FHR2, CFHR2, HFL3, CFHL2	complement factor H-related 2	NM_005666, hCT32137.2	206910_x_at	NP_005657.1, EAW91267.1
GeneID.259266	ASPM	1	197,053,257	197,115,824	62,567	-	2	1_A375_pNL7_minus_lncRNA_AR..1..589, 2_A375_pNL97_plus_lncRNA_AR..1..798	46, -46	in gene, upstream	1	1	0	26	26	14	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ASPM	FLJ43117, FLJ10549, Calmbp1, FLJ10517, MCPH5, ASP, DKFZp686N06164, ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	NM_018136, hCT2344429.0, hCT2344431.0, hCT2344432.0, hCT2357375.0, hCT2357376.0	219918_s_at, 232238_at, 239002_at	NP_060606.3, EAW91272.1, EAW91270.1, EAW91271.1, EAW91273.1, EAW91274.1
GeneID.360023	ZBTB41	1	197,122,814	197,169,672	46,858	-	3	1_A375_pNL7_minus_lncRNA_AR..1..589, 2_A375_pNL97_plus_lncRNA_AR..1..798, 2_A375_pNL97_plus_lncRNA_AR..1..799	53896, 53600, -1016	downstream, downstream, upstream	1	1	0	21.5	32.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene ZBTB41	FRBZ1, ZBTB41, DKFZp686C06120, RP11-469L3.1, FLJ36199, ZNF924	zinc finger and BTB domain containing 41	NM_194314, hCT2323576.0	226962_at	NP_919290.2, EAW91275.1
GeneID.388722	C1orf53	1	197,871,682	197,876,497	4,815	+	3	1_A375_pNL7_minus_lncRNA_AR..1..590, 2_A375_pNL97_plus_lncRNA_AR..1..800, 4_A375_EGR1..1..800	254, 126, 9102	in gene, in gene, downstream	1	1	1	23	25	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene C1orf53	C1orf53	chromosome 1 open reading frame 53	NM_001024594, hCT1796690.2	1556507_at, 1556508_a_at	NP_001019765.1, EAW91286.1
GeneID.56956	LHX9	1	197,881,635	197,899,273	17,638	+	4	1_A375_pNL7_minus_lncRNA_AR..1..590, 2_A375_pNL97_plus_lncRNA_AR..1..800, 4_A375_EGR1..1..800, 4_A375_EGR1..1..801	-9699, -9827, -851, 5341	upstream, upstream, upstream, in gene	1	1	1	19.67	22	17.33	3	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene LHX9	LHX9		NM_020204, NM_001014434, hCT2323689.1, hCT2323690.1, hCT2349432.0, hCT2349433.0, hCT2349434.0, hCT32141.3	1560253_at, 1562738_at, 1565406_a_at, 1565407_at	NP_064589.2, NP_001014434.1, EAW91287.1, EAW91288.1, EAW91290.1, EAW91292.1, EAW91289.1, EAW91291.1
GeneID.140609	NEK7	1	198,126,108	198,291,550	165,442	+	2	2_A375_pNL97_plus_lncRNA_AR..1..803, 4_A375_EGR1..1..802	464, 564	in gene, in gene	0	1	1	10	17	18	1	4_A375_EGR1..1	18	Gene NEK7	NEK7		NM_133494, hCT2323693.0, hCT2323694.0, hCT2323695.0, hCT32030.3	212530_at	NP_598001.1, EAW91293.1, EAW91294.1, EAW91295.1, EAW91296.1
GeneID.5788	PTPRC	1	198,608,137	198,726,545	118,408	+	1	2_A375_pNL97_plus_lncRNA_AR..1..805	74423	in gene	0	1	0	6	16	3	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene PTPRC	LY5, CD45, T200, B220, GP180, CD45R, LCA, PTPRC	protein tyrosine phosphatase, receptor type, C	NM_080921, NM_080923, NM_002838, hCT1951768.0, hCT1958680.1, hCT2323697.0, hCT2323700.0	1552480_s_at, 1569830_at, 207238_s_at, 212587_s_at, 212588_at	NP_563578.1, NP_563580.1, NP_002829.2, EAW91300.1, EAW91301.1, EAW91303.1, EAW91302.1
GeneID.2494	NR5A2	1	199,996,770	200,146,552	149,782	+	4	1_A375_pNL7_minus_lncRNA_AR..1..594, 2_A375_pNL97_plus_lncRNA_AR..1..807, 2_A375_pNL97_plus_lncRNA_AR..1..808, 4_A375_EGR1..1..803	47966, 11649, 152636, 120510	in gene, in gene, downstream, in gene	1	1	1	14.25	13.75	9	4	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene NR5A2	FTZ-F1beta, FTF, NR5A2, hB1F, LRH-1, hB1F-2, LRH1, CPF, B1F2, B1F, FTZ-F1	nuclear receptor subfamily 5, group A, member 2	NM_003822, NM_205860, hCT10323.3, hCT1951270.1, hCT2323911.0, hCT2323912.0	1560469_at, 208337_s_at, 208343_s_at, 210174_at	NP_003813.1, NP_995582.1, EAW91305.1, EAW91306.1, EAW91307.1, EAW91308.1
GeneID.9928	KIF14	1	200,520,625	200,589,862	69,237	-	2	1_A375_pNL7_minus_lncRNA_AR..1..595, 2_A375_pNL97_plus_lncRNA_AR..1..809	6, -90	in gene, upstream	1	1	0	24	21	14	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene KIF14	MGC142302, KIAA0042, KIF14	kinesin family member 14	NM_014875, hCT1953663.1, hCT2324103.0, hCT2324104.0	206364_at, 236641_at	NP_055690.1, EAW91315.1, EAW91316.1, EAW91317.1
GeneID.83479	DDX59	1	200,613,165	200,639,126	25,961	-	3	1_A375_pNL7_minus_lncRNA_AR..1..596, 2_A375_pNL97_plus_lncRNA_AR..1..810, 4_A375_EGR1..1..804	196, 246, 246	in gene, in gene, in gene	1	1	1	26	32	21	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene DDX59	ZNHIT5, DDX59, DKFZp564B1023	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	NM_001031725, hCT1953662.1, hCT2324101.0	223862_x_at, 228385_at, 228386_s_at	NP_001026895.2, EAW91318.1, EAW91319.1
GeneID.23271	CAMSAP1L1	1	200,708,686	200,829,832	121,146	+	2	2_A375_pNL97_plus_lncRNA_AR..1..811, 4_A375_EGR1..1..805	-236, -462	upstream, upstream	0	1	1	13	25	19	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene CAMSAP1L1	KIAA1078, MGC150681, MGC150680, CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	NM_203459, hCT1953665.2, hCT2340421.0	212763_at, 212765_at, 217198_s_at	NP_982284.1, EAW91321.1, EAW91320.1
GeneID.2848	GPR25	1	200,842,166	200,843,251	1,085	+	1	2_A375_pNL97_plus_lncRNA_AR..1..812	7498	downstream	0	1	0	18	24	6	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene GPR25	GPR25	G protein-coupled receptor 25	NM_005298, hCT1808659.0	221363_x_at	NP_005289.2, EAW91322.1
GeneID.55765	C1orf106	1	200,860,639	200,884,864	24,225	+	4	1_A375_pNL7_minus_lncRNA_AR..1..597, 2_A375_pNL97_plus_lncRNA_AR..1..813, 4_A375_EGR1..1..806, 4_A375_EGR1..1..807	-159, -127, -287, 24737	upstream, upstream, upstream, downstream	1	1	1	18	21.5	18.5	2	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene C1orf106	FLJ10901, C1orf106, MGC125608	chromosome 1 open reading frame 106	NM_018265, NM_001142569, hCT2323623.0	219010_at	NP_060735.2, NP_001136041.1, EAW91323.1
GeneID.847215	C1orf81	1	200,886,588	200,935,792	49,204	+	2	4_A375_EGR1..1..807, 4_A375_EGR1..1..808	-1212, 54356	upstream, downstream	0	0	1	6	8	19.5	2	4_A375_EGR1..1	22	Gene C1orf81	C1orf81	chromosome 1 open reading frame 81	XR_111999, XR_108341, XR_114932		
GeneID.23046	KIF21B	1	200,938,520	200,992,828	54,308	-	3	4_A375_EGR1..1..808, 4_A375_EGR1..1..809, 4_A375_EGR1..1..810	51684, 41095, 23292	in gene, in gene, in gene	0	0	1	6	9	19	3	4_A375_EGR1..1	22	Gene KIF21B	FLJ16314, KIF21B	kinesin family member 21B	NM_017596	204411_at	NP_060066.2
GeneID.779	CACNA1S	1	201,008,640	201,081,694	73,054	-	4	4_A375_EGR1..1..811, 4_A375_EGR1..1..812, 4_A375_EGR1..1..813, 4_A375_EGR1..1..814	63918, 50398, 40990, -2893	in gene, in gene, in gene, upstream	0	0	1	8.75	9	19.5	4	4_A375_EGR1..1	25	Gene CACNA1S	CACNL1A3, HOKPP, HOKPP1, CCHL1A3, MHS5, TTPP1, CACNA1S, hypoPP, Cav1.1	calcium channel, voltage-dependent, L type, alpha 1S subunit	NM_000069, hCT2326831.0, hCT2357390.0, hCT8739.2	217515_s_at	NP_000060.2, EAW91333.1, EAW91334.1, EAW91335.1
GeneID.647219	ASCL5	1	201,083,633	201,099,369	15,736	-	1	4_A375_EGR1..1..814	14762	in gene	0	0	1	9	9	25	1	4_A375_EGR1..1	25	Gene ASCL5	ASCL5, bHLHa47	achaete-scute complex homolog 5 (Drosophila)	XM_001718227, XM_001719321, XM_940986		XP_001718279.2, XP_001719373.2, XP_946059.4
GeneID.91156	IGFN1	1	201,159,953	201,198,080	38,127	+	3	1_A375_pNL7_minus_lncRNA_AR..1..598, 2_A375_pNL97_plus_lncRNA_AR..1..814, 4_A375_EGR1..1..815	39215, 39359, 25727	downstream, downstream, in gene	1	1	1	11.5	11.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene IGFN1	IGFN1, DKFZp434B1231, EEF1A2BP1	immunoglobulin-like and fibronectin type III domain containing 1	NM_001164586, hCT2323632.1, hCT2323634.1, hCT2349361.0	1563098_at, 229275_at	NP_001158058.1, EAW91349.1, EAW91347.1, EAW91348.1
GeneID.5317	PKP1	1	201,252,580	201,302,121	49,541	+	4	1_A375_pNL7_minus_lncRNA_AR..1..599, 4_A375_EGR1..1..818, 4_A375_EGR1..1..819, 4_A375_EGR1..1..820	27452, -8399, 28, 41868	in gene, upstream, in gene, in gene	1	0	1	14.5	11.5	20	4	4_A375_EGR1..1	26	Gene PKP1	MGC138829, PKP1, B6P	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	NM_000299, NM_001005337, hCT2323638.0, hCT2323639.0, hCT8732.3	205724_at, 221854_at	NP_000290.2, NP_001005337.1, EAW91350.1, EAW91351.1, EAW91352.1
GeneID.7139	TNNT2	1	201,328,142	201,346,805	18,663	-	1	4_A375_EGR1..1..821	13029	in gene	0	0	1	4	6	25	1	4_A375_EGR1..1	25	Gene TNNT2	cTnT, MGC3889, TnTC, CMH2, LVNC6, RCM3, TNNT2, CMPD2	troponin T type 2 (cardiac)	NM_000364, NM_001001430, NM_001001431, NM_001001432, hCT1641354.3, hCT1954459.1, hCT1954460.1, hCT1954461.1, hCT1954462.1, hCT2326807.0, hCT2326808.0, hCT2326810.0, hCT2357437.0, hCT2357438.0	1563855_at, 215389_s_at	NP_000355.2, NP_001001430.1, NP_001001431.1, NP_001001432.1, EAW91358.1, EAW91359.1, EAW91353.1, EAW91354.1, EAW91355.1, EAW91356.1, EAW91357.1, EAW91360.1, EAW91361.1, EAW91362.1
GeneID.23612	PHLDA3	1	201,434,622	201,438,299	3,677	-	3	1_A375_pNL7_minus_lncRNA_AR..1..600, 2_A375_pNL97_plus_lncRNA_AR..1..816, 2_A375_pNL97_plus_lncRNA_AR..1..817	7099, 7131, -293	downstream, downstream, upstream	1	1	0	24.5	21	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene PHLDA3	TIH1, PHLDA3	pleckstrin homology-like domain, family A, member 3	NM_012396, hCT8731.2	218634_at	NP_036528.1, EAW91369.1
GeneID.1465	CSRP1	1	201,452,658	201,476,387	23,729	-	7	1_A375_pNL7_minus_lncRNA_AR..1..601, 1_A375_pNL7_minus_lncRNA_AR..1..602, 2_A375_pNL97_plus_lncRNA_AR..1..818, 2_A375_pNL97_plus_lncRNA_AR..1..819, 4_A375_EGR1..1..822, 4_A375_EGR1..1..823, 4_A375_EGR1..1..824	17891, 163, 17891, 227, 25955, 12659, 419	in gene, in gene, in gene, in gene, downstream, in gene, in gene	1	1	1	16.25	16.5	17.75	4	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene CSRP1	CRP, CSRP1, CYRP, CSRP, D1S181E, DKFZp686M148, CRP1	cysteine and glycine-rich protein 1	NM_004078, NM_001193570, NM_001193571, NM_001193572, hCT2357354.0, hCT8730.3	200621_at	NP_004069.1, NP_001180499.1, NP_001180500.1, NP_001180501.1, EAW91370.1, EAW91371.1
GeneID.100506590	LOC100506590	1	201,474,793	201,475,173	380	-	3	1_A375_pNL7_minus_lncRNA_AR..1..602, 2_A375_pNL97_plus_lncRNA_AR..1..819, 4_A375_EGR1..1..824	-1051, -987, -795	upstream, upstream, upstream	1	1	1	23	21	19	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene LOC100506590		hypothetical protein LOC100506590	XM_003118499		XP_003118547.1
GeneID.89796	NAV1	1	201,617,450	201,796,102	178,652	+	4	1_A375_pNL7_minus_lncRNA_AR..1..605, 2_A375_pNL97_plus_lncRNA_AR..1..823, 2_A375_pNL97_plus_lncRNA_AR..1..824, 2_A375_pNL97_plus_lncRNA_AR..1..825	180790, 582, 65190, 180726	downstream, in gene, in gene, downstream	1	1	0	32.33	40.67	11.67	3	2_A375_pNL97_plus_lncRNA_AR..1	78	Gene NAV1	STEERIN1, DKFZp781D0314, FLJ12560, POMFIL3, FLJ14203, NAV1, KIAA1151, UNC53H1, MGC14961	neuron navigator 1	NM_020443, NM_001167738, hCT2323648.1, hCT2323650.1, hCT2323653.1	224770_s_at, 224771_at, 224772_at, 224773_at, 224774_s_at, 233567_at, 233670_at	NP_065176.3, NP_001161210.1, EAW91372.1, EAW91373.1, EAW91374.1
GeneID.55705	IPO9	1	201,798,288	201,853,422	55,134	+	2	1_A375_pNL7_minus_lncRNA_AR..1..605, 2_A375_pNL97_plus_lncRNA_AR..1..825	-48, -112	upstream, upstream	1	1	0	72	78	16	1	2_A375_pNL97_plus_lncRNA_AR..1	78	Gene IPO9	FLJ10402, DKFZp761M1547, Imp9, IPO9	importin 9	NM_018085, hCT2323619.1, hCT2323620.1, hCT2357429.0	213785_at, 217685_at, 242581_at, 244703_x_at	NP_060555.2, EAW91376.1, EAW91375.1, EAW91377.1
GeneID.149345	SHISA4	1	201,857,797	201,861,715	3,918	+	1	4_A375_EGR1..1..825	8347	downstream	0	0	1	9	13	19	1	4_A375_EGR1..1	19	Gene SHISA4	MGC102893, SHISA4, MGC129812, FLJ18233, C1orf40, TMEM58, MGC129813	shisa homolog 4 (Xenopus laevis)	NR_030775, NM_198149, hCT1642348.3, hCT1966355.1	226674_at	NP_937792.2, EAW91378.1, EAW91379.1
GeneID.25802	LMOD1	1	201,865,584	201,915,716	50,132	-	4	1_A375_pNL7_minus_lncRNA_AR..1..606, 2_A375_pNL97_plus_lncRNA_AR..1..826, 4_A375_EGR1..1..825, 4_A375_EGR1..1..826	-8732, -8764, 49572, -8668	upstream, upstream, in gene, upstream	1	1	1	16	17	21	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene LMOD1	FLJ55689, 64kD, D1, SM-LMOD, 1D, LMOD1	leiomodin 1 (smooth muscle)	NM_012134, hCT2326767.0, hCT6263.3	203766_s_at, 211562_s_at	NP_036266.2, EAW91380.1, EAW91381.1
GeneID.10440	TIMM17A	1	201,924,619	201,939,789	15,170	+	3	1_A375_pNL7_minus_lncRNA_AR..1..606, 2_A375_pNL97_plus_lncRNA_AR..1..826, 4_A375_EGR1..1..826	-171, -139, -235	upstream, upstream, upstream	1	1	1	23	21	23	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene TIMM17A	TIMM17A, TIM17, TIM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	NM_006335, hCT1953674.1, hCT1953675.1, hCT8728.2	201821_s_at, 201822_at, 215168_at, 215171_s_at	NP_006326.1, EAW91383.1, EAW91384.1, EAW91385.1
GeneID.6051	RNPEP	1	201,951,766	201,975,275	23,509	+	3	2_A375_pNL97_plus_lncRNA_AR..1..827, 4_A375_EGR1..1..827, 4_A375_EGR1..1..828	330, 28437, 30570	in gene, downstream, downstream	0	1	1	11.67	14	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RNPEP	RNPEP, DKFZp547H084	arginyl aminopeptidase (aminopeptidase B)	NM_020216, hCT1647188.2, hCT2357409.0	208270_s_at	NP_064601.3, EAW91386.1, EAW91387.1

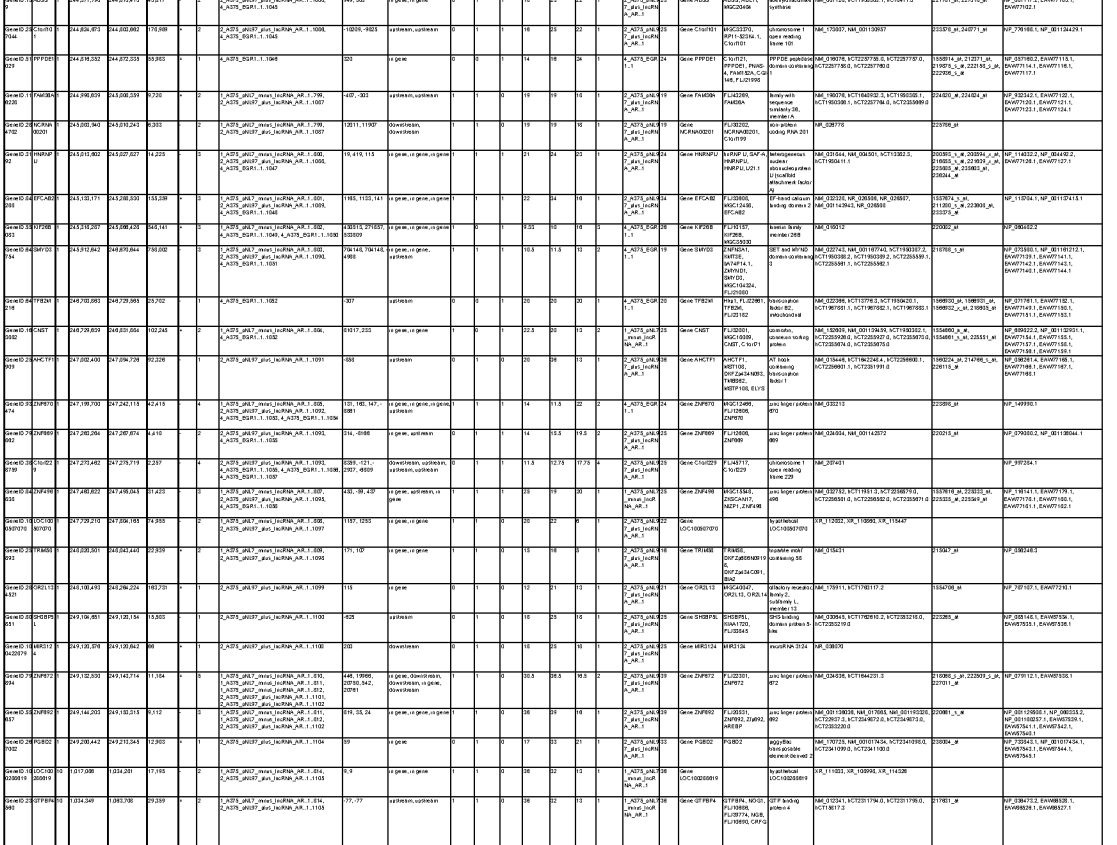
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.100289488	LOC100289488	1	201,969,179	201,979,238	10,059	-	3	4_A375_EGR1..1..827, 4_A375_EGR1..1..828, 4_A375_EGR1..1..829	-965, -3098, -8090	upstream, upstream, upstream	0	0	1	7.33	11.33	16.67	3	4_A375_EGR1..1	18	Gene LOC100289488		hypothetical LOC100289488	XR_108327		
GeneID.1999	ELF3	1	201,979,690	201,988,316	8,626	+	3	4_A375_EGR1..1..827, 4_A375_EGR1..1..828, 4_A375_EGR1..1..829	513, 2646, 7636	in gene, in gene, downstream	0	0	1	7.33	11.33	16.67	3	4_A375_EGR1..1	18	Gene ELF3	ESE-1, EPR-1, ERT, ESX, ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	NM_001114309, NM_004433, hCT1953704.1, hCT1953705.1, hCT2357435.0, hCT86011.2	201510_at, 210827_s_at, 229842_at	NP_001107781.1, NP_004424.3, EAW91388.1, EAW91389.1, EAW91390.1, EAW91391.1
GeneID.9283	GPR37L1	1	202,092,029	202,098,834	6,805	+	2	4_A375_EGR1..1..830, 4_A375_EGR1..1..831	179, 5475	in gene, in gene	0	0	1	7	8.5	19.5	2	4_A375_EGR1..1	20	Gene GPR37L1	ET(B)R-LP-2, GPR37L1, ETBR-LP-2	G protein-coupled receptor 37 like 1	NM_004767	207055_at	NP_004758.3
GeneID.127829	ARL8A	1	202,101,977	202,113,866	11,889	-	2	4_A375_EGR1..1..830, 4_A375_EGR1..1..831	21658, 16362	downstream, downstream	0	0	1	7	8.5	19.5	2	4_A375_EGR1..1	20	Gene ARL8A	ARL8A, GIE2, FLJ45195, ARL10B	ADP-ribosylation factor-like 8A	NM_138795, hCT1808722.1, hCT1966365.1, hCT2326765.0, hCT2357366.0, hCT2357367.0	1556155_at, 225347_at	NP_620150.1, EAW91397.1, EAW91395.1, EAW91396.1, EAW91398.1, EAW91399.1
GeneID.29089	UBE2T	1	202,300,785	202,311,094	10,309	-	3	1_A375_pNL7_minus_lncRNA_AR..1..607, 1_A375_pNL7_minus_lncRNA_AR..1..608, 2_A375_pNL97_plus_lncRNA_AR..1..828	6, -7306, -10	in gene, upstream, upstream	1	1	0	18	20.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene UBE2T	UBE2T, PIG50, HSPC150	ubiquitin-conjugating enzyme E2T (putative)	NM_014176, hCT2326750.0, hCT2326751.0, hCT2326752.0, hCT2326753.0, hCT2326754.0	223229_at	NP_054895.1, EAW91414.1, EAW91411.1, EAW91412.1, EAW91413.1, EAW91415.1
GeneID.4660	PPP1R12B	1	202,317,830	202,557,697	239,867	+	4	1_A375_pNL7_minus_lncRNA_AR..1..607, 1_A375_pNL7_minus_lncRNA_AR..1..608, 2_A375_pNL97_plus_lncRNA_AR..1..828, 4_A375_EGR1..1..833	-6742, 570, -6726, 40954	upstream, in gene, upstream, in gene	1	1	1	13.33	14.67	13	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene PPP1R12B	FLJ40942, MYPT2, MGC87886, MGC131980, PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	NM_002481, NM_032103, NM_032104, NM_001167857, NM_001167858, hCT2326724.0, hCT2326725.0, hCT2326726.0, hCT2326727.0, hCT2326728.0, hCT2326729.0, hCT2326730.0, hCT2326731.0, hCT2326732.0, hCT2326733.0	1555444_a_at, 1557553_at, 201957_at, 201958_s_at	NP_002472.2, NP_115286.1, NP_115287.1, NP_001161329.1, NP_001161330.1, EAW91416.1, EAW91417.1, EAW91418.1, EAW91419.1, EAW91420.1, EAW91421.1, EAW91422.1, EAW91423.1, EAW91424.1, EAW91425.1
GeneID.127833	SYT2	1	202,559,724	202,679,551	119,827	-	8	1_A375_pNL7_minus_lncRNA_AR..1..609, 1_A375_pNL7_minus_lncRNA_AR..1..610, 2_A375_pNL97_plus_lncRNA_AR..1..829, 2_A375_pNL97_plus_lncRNA_AR..1..830, 2_A375_pNL97_plus_lncRNA_AR..1..831, 4_A375_EGR1..1..834, 4_A375_EGR1..1..835, 4_A375_EGR1..1..836	53071, 17279, 53231, 29706, 17263, 97247, 66319, 511	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	19.67	20.83	12.17	8	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene SYT2	FLJ42519, SYT2, SytII	synaptotagmin II	NM_177402, NM_001136504, hCT22973.4, hCT2349408.0		NP_796376.2, NP_001129976.1, EAW91429.1, EAW91430.1
GeneID.10765	KDM5B	1	202,696,532	202,777,549	81,017	-	5	1_A375_pNL7_minus_lncRNA_AR..1..611, 2_A375_pNL97_plus_lncRNA_AR..1..832, 2_A375_pNL97_plus_lncRNA_AR..1..833, 4_A375_EGR1..1..837, 4_A375_EGR1..1..838	-2419, 93, -2403, 1293, -2579	upstream, in gene, upstream, in gene, upstream	1	1	1	17.33	19	19.67	3	4_A375_EGR1..1	25	Gene KDM5B	FLJ10538, PLU1, KDM5B, CT31, FLJ12459, PUT1, JARID1B, FLJ23670, FLJ12491, RBBP2H1A, PLU-1, FLJ16281	lysine (K)-specific demethylase 5B	NM_006618, hCT2326742.0, hCT2326743.0, hCT2326744.0, hCT2357373.0	201547_at, 201548_s_at, 201549_x_at, 211202_s_at	NP_006609.3, EAW91433.1, EAW91432.1, EAW91434.1, EAW91435.1
GeneID.100506696	LOC100506696	1	202,760,074	202,761,040	966	+	5	1_A375_pNL7_minus_lncRNA_AR..1..611, 2_A375_pNL97_plus_lncRNA_AR..1..832, 2_A375_pNL97_plus_lncRNA_AR..1..833, 4_A375_EGR1..1..837, 4_A375_EGR1..1..838	-106, -2818, -122, -3618, 54	upstream, upstream, upstream, upstream, in gene	1	1	1	17.33	19	19.67	3	4_A375_EGR1..1	25	Gene LOC100506696		hypothetical LOC100506696	XR_111976, XR_111975, XR_108330, XR_108329, XR_114965, XR_114964		
GeneID.641515	LOC641515	1	202,789,385	202,798,353	8,968	+	3	1_A375_pNL7_minus_lncRNA_AR..1..611, 2_A375_pNL97_plus_lncRNA_AR..1..833, 4_A375_EGR1..1..838	-9417, -9433, -9257	upstream, upstream, upstream	1	1	1	23	22	25	1	4_A375_EGR1..1	25	Gene LOC641515		hypothetical LOC641515	XR_108331, XR_114966		
GeneID.59349	KLHL12	1	202,860,230	202,896,371	36,141	-	2	2_A375_pNL97_plus_lncRNA_AR..1..834, 4_A375_EGR1..1..840	-81, 63	upstream, in gene	0	1	1	16	21	23	1	4_A375_EGR1..1	23	Gene KLHL12	C3IP1, KLHL12, DKIR, FLJ27152	kelch-like 12 (Drosophila)	NM_021633, hCT1642356.3, hCT2324000.0, hCT2324001.0, hCT2324002.0, hCT2357416.0	219931_s_at, 225068_at	NP_067646.1, EAW91445.1, EAW91444.1, EAW91446.1, EAW91447.1, EAW91448.1
GeneID.51094	ADIPOR1	1	202,909,960	202,927,700	17,740	-	2	2_A375_pNL97_plus_lncRNA_AR..1..835, 4_A375_EGR1..1..841	340, 692	in gene, in gene	0	1	1	15	21	18	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ADIPOR1	ACDCR1, CGI45, CGI-45, FLJ25385, ADIPOR1, FLJ42464, TESBP1A, PAQR1	adiponectin receptor 1	NM_015999, NM_001127687, hCT1788471.2, hCT1953672.1	217748_at	NP_057083.2, NP_001121159.1, EAW91449.1, EAW91450.1
GeneID.51706	CYB5R1	1	202,931,001	202,936,404	5,403	-	2	2_A375_pNL97_plus_lncRNA_AR..1..835, 4_A375_EGR1..1..841	9044, 9396	downstream, downstream	0	1	1	15	21	18	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CYB5R1	B5R1, NQO3A2, B5R.1, CYB5R1, humb5R2	cytochrome b5 reductase 1	NM_016243, hCT1968419.1, hCT2323994.0, hCT2323997.0, hCT87610.2	1560043_at, 202263_at	NP_057327.2, EAW91454.1, EAW91451.1, EAW91452.1, EAW91453.1
GeneID.92703	TMEM183A	1	202,976,534	202,993,197	16,663	+	2	2_A375_pNL97_plus_lncRNA_AR..1..836, 4_A375_EGR1..1..842	-166, 19306	upstream, downstream	0	1	1	18	15.5	17.5	2	4_A375_EGR1..1	22	Gene TMEM183A	TMEM183A, C1orf37	transmembrane protein 183A	NM_138391, hCT2323770.0, hCT2323771.0, hCT2357365.0	212164_at	NP_612400.3, EAW91456.1, EAW91457.1, EAW91458.1
GeneID.100507405	LOC100507405	1	203,005,844	203,015,635	9,791	+	2	4_A375_EGR1..1..842, 4_A375_EGR1..1..843	-10004, 11713	upstream, downstream	0	0	1	11	14	16	2	4_A375_EGR1..1	22	Gene LOC100507405		lipin-alpha-1-like	XM_003119788, XM_003118503, XM_003120639		XP_003119816.1, XP_003118551.1, XP_003120687.1
GeneID.8497	PPFIA4	1	203,020,311	203,047,864	27,553	+	3	4_A375_EGR1..1..843, 4_A375_EGR1..1..844, 4_A375_EGR1..1..845	-2754, 8057, 33449	upstream, in gene, downstream	0	0	1	11	10.67	15.33	3	4_A375_EGR1..1	17	Gene PPFIA4	PPFIA4		NM_015053, hCT2323772.0, hCT2323773.0, hCT2323774.0, hCT2323775.0	214978_s_at	NP_055868.1, EAW91462.1, EAW91459.1, EAW91460.1, EAW91461.1
GeneID.4656	MYOG	1	203,052,257	203,055,377	3,120	-	1	4_A375_EGR1..1..845	1617	in gene	0	0	1	9	9	17	1	4_A375_EGR1..1	17	Gene MYOG	MYOGENIN, bHLHc3, MYOG, MYF4	myogenin (myogenic factor 4)	NM_002479, hCT15441.2, hCT2323990.0	207282_s_at	NP_002470.2, EAW91463.1, EAW91464.1
GeneID.134	ADORA1	1	203,096,836	203,136,533	39,697	+	2	2_A375_pNL97_plus_lncRNA_AR..1..837, 4_A375_EGR1..1..846	506, 636	in gene, in gene	0	1	1	16	21	20	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ADORA1	RDC7, ADORA1	adenosine A1 receptor	NM_001048230, NM_000674, hCT14222.2	205481_at, 216220_s_at	NP_001041695.1, NP_000665.1, EAW91465.1
GeneID.100506775	LOC100506775	1	203,256,280	203,257,926	1,646	+	1	2_A375_pNL97_plus_lncRNA_AR..1..838	-6164	upstream	0	1	0	13	20	13	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100506775		hypothetical LOC100506775	XR_111974, XR_108333, XR_108332, XR_114967		
GeneID.730227	LOC730227	1	203,267,866	203,274,453	6,587	-	1	4_A375_EGR1..1..847	-555	upstream	0	0	1	13	19	21	1	4_A375_EGR1..1	21	Gene LOC730227		hypothetical LOC730227	NR_034150, NR_034151	215756_at	
GeneID.7832	BTG2	1	203,274,664	203,278,730	4,066	+	1	4_A375_EGR1..1..847	344	in gene	0	0	1	13	19	21	1	4_A375_EGR1..1	21	Gene BTG2	TIS21, BTG2, MGC126063, MGC126064, PC3	BTG family, member 2	NM_006763, hCT1641050.1, hCT2323779.0	201235_s_at, 201236_s_at	NP_006754.1, EAW91476.1, EAW91475.1
GeneID.5549	PRELP	1	203,444,863	203,460,460	15,597	+	2	1_A375_pNL7_minus_lncRNA_AR..1..613, 4_A375_EGR1..1..851	11965, 11917	in gene, in gene	1	0	1	17	15	23	1	4_A375_EGR1..1	23	Gene PRELP	MST161, SLRR2A, MSTP161, PRELP, MGC45323	proline/arginine-rich end leucine-rich repeat protein	NM_002725, NM_201348, hCT15444.2	204223_at, 228224_at, 37022_at	NP_002716.1, NP_958505.1, EAW91481.1
GeneID.26254	OPTC	1	203,463,271	203,478,077	14,806	+	2	1_A375_pNL7_minus_lncRNA_AR..1..613, 4_A375_EGR1..1..851	-8423, -8471	upstream, upstream	1	0	1	17	15	23	1	4_A375_EGR1..1	23	Gene OPTC	OPT, OPTC	opticin	NM_014359, hCT15445.2	223884_at	NP_055174.1, EAW91482.1
GeneID.9877	ZC3H11A	1	203,764,751	203,823,256	58,505	+	4	1_A375_pNL7_minus_lncRNA_AR..1..617, 2_A375_pNL97_plus_lncRNA_AR..1..842, 4_A375_EGR1..1..852, 4_A375_EGR1..1..853	65873, 65989, 8241, 66113	downstream, downstream, in gene, downstream	1	1	1	20.5	27	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene ZC3H11A	ZC3H11A, DKFZp781G2455, DKFZp686D03108, ZC3HDC11A, DKFZp686F14109, KIAA0663	zinc finger CCCH-type containing 11A	NM_014827, hCT1817001.1, hCT2323762.0	1565667_a_at, 205787_x_at, 205788_s_at	NP_055642.3, EAW91492.1, EAW91493.1
GeneID.100381270	ZBED6	1	203,766,651	203,769,590	2,939	+	1	4_A375_EGR1..1..852	6341	downstream	0	0	1	6	6	16	1	4_A375_EGR1..1	16	Gene ZBED6	ZBED6, MGR		NM_001174108		NP_001167579.1
GeneID.6635	SNRPE	1	203,830,740	203,840,280	9,540	+	3	1_A375_pNL7_minus_lncRNA_AR..1..617, 2_A375_pNL97_plus_lncRNA_AR..1..842, 4_A375_EGR1..1..853	-116, -20, 124	upstream, upstream, in gene	1	1	1	35	46	15	1	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene SNRPE	SME, Sm-E, SNRPE, B-raf	small nuclear ribonucleoprotein polypeptide E	NM_003094, hCT2323766.1, hCT2323767.1	203316_s_at, 231112_at	NP_003085.1, EAW91494.1, EAW91495.1
GeneID.9580	SOX13	1	204,042,246	204,096,871	54,625	+	6	1_A375_pNL7_minus_lncRNA_AR..1..618, 2_A375_pNL97_plus_lncRNA_AR..1..843, 4_A375_EGR1..1..854, 4_A375_EGR1..1..855, 4_A375_EGR1..1..856, 4_A375_EGR1..1..857	762, 966, -550, 50090, 53114, 57062	in gene, in gene, upstream, in gene, in gene, downstream	1	1	1	11.8	10.2	17	5	4_A375_EGR1..1	20	Gene SOX13	MGC117216, Sox-13, SOX13, ICA12	SRY (sex determining region Y)-box 13	NM_005686, hCT2357395.0, hCT5725.3	1569111_at, 209736_at, 38918_at	NP_005677.2, EAW91499.1, EAW91500.1
GeneID.55224	ETNK2	1	204,100,190	204,121,307	21,117	-	3	4_A375_EGR1..1..855, 4_A375_EGR1..1..856, 4_A375_EGR1..1..857	28971, 25947, 21979	downstream, downstream, downstream	0	0	1	11.67	9.33	18	3	4_A375_EGR1..1	20	Gene ETNK2	HMFT1716, EKI2, ETNK2, FLJ10761	ethanolamine kinase 2	NM_018208, hCT2324696.0, hCT2324698.0, hCT2357394.0, hCT7451.2	219268_at	NP_060678.2, EAW91504.1, EAW91501.1, EAW91502.1, EAW91503.1
GeneID.127841	LOC127841	1	204,337,558	204,338,847	1,289	-	1	4_A375_EGR1..1..858	-7937	upstream	0	0	1	16	12	21	1	4_A375_EGR1..1	21	Gene LOC127841		hypothetical LOC127841	NR_027022	1565554_at, 1565556_at	
GeneID.84919	PPP1R15B	1	204,372,492	204,380,944	8,452	-	2	2_A375_pNL97_plus_lncRNA_AR..1..844, 4_A375_EGR1..1..859	-5712, 126	upstream, in gene	0	1	1	14	17	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PPP1R15B	CREP, FLJ14744, PPP1R15B	protein phosphatase 1, regulatory (inhibitor) subunit 15B	NM_032833, hCT1816155.2	224692_at	NP_116222.3, EAW91511.1
GeneID.5287	PIK3C2B	1	204,391,758	204,459,474	67,716	-	1	2_A375_pNL97_plus_lncRNA_AR..1..844	72618	downstream	0	1	0	13	17	9	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PIK3C2B	PIK3C2B, DKFZp686G16234, C2-PI3K	phosphoinositide-3-kinase, class 2, beta polypeptide	NM_002646, hCT2324704.0, hCT7448.2	204484_at	NP_002637.3, EAW91513.1, EAW91514.1
GeneID.4194	MDM4	1	204,485,511	204,527,248	41,737	+	3	1_A375_pNL7_minus_lncRNA_AR..1..619, 1_A375_pNL7_minus_lncRNA_AR..1..620, 4_A375_EGR1..1..860	-9319, 121, -9831	upstream, in gene, upstream	1	0	1	23.5	17.5	21.5	2	4_A375_EGR1..1	26	Gene MDM4	MGC132766, DKFZp781B1423, HDMX, MDMX, MRP1, MDM4	Mdm4 p53 binding protein homolog (mouse)	NM_002393, NR_024171, hCT2324145.0, hCT7450.3	205655_at, 235589_s_at, 236814_at, 241876_at	NP_002384.2, EAW91515.1, EAW91516.1
GeneID.10446	LRRN2	1	204,586,301	204,654,597	68,296	-	5	1_A375_pNL7_minus_lncRNA_AR..1..621, 2_A375_pNL97_plus_lncRNA_AR..1..845, 4_A375_EGR1..1..861, 4_A375_EGR1..1..862, 4_A375_EGR1..1..863	37829, 37733, 66917, 46565, 613	in gene, in gene, in gene, in gene, in gene	1	1	1	22.25	27.25	16.75	4	2_A375_pNL97_plus_lncRNA_AR..1	61	Gene LRRN2	LRRN5, GAC1, LRANK1, LRRN2, FIGLER7	leucine rich repeat neuronal 2	NM_006338, NM_201630, hCT2324701.0, hCT2357360.0, hCT7444.1	205154_at, 216164_at, 216167_at	NP_006329.2, NP_963924.1, EAW91520.1, EAW91521.1, EAW91522.1
GeneID.100506655	LOC100506655	1	204,595,903	204,598,845	2,942	+	2	4_A375_EGR1..1..861, 4_A375_EGR1..1..862	-8223, 12129	upstream, downstream	0	0	1	6.5	9	16.5	2	4_A375_EGR1..1	20	Gene LOC100506655		hypothetical LOC100506655	XR_111971, XR_108336, XR_114971		
GeneID.23114	NFASC	1	204,797,782	204,991,950	194,168	+	4	1_A375_pNL7_minus_lncRNA_AR..1..622, 2_A375_pNL97_plus_lncRNA_AR..1..847, 2_A375_pNL97_plus_lncRNA_AR..1..848, 4_A375_EGR1..1..864	9034, 8954, 161450, 118058	in gene, in gene, in gene, in gene	1	1	1	17	21.33	14	3	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene NFASC	DKFZp686P2250, KIAA0756, NF, NRCAML, FLJ46866, NFASC	neurofascin homolog (chicken)	NM_001005389, NM_015090, NM_001005388, NM_001160331, NM_001160332, NM_001160333	213438_at, 214799_at, 230242_at, 243645_at	NP_001005389.2, NP_055905.2, NP_001005388.2, NP_001153803.1, NP_001153804.1, NP_001153805.1
GeneID.5929	RBBP5	1	205,055,270	205,091,150	35,880	-	2	1_A375_pNL7_minus_lncRNA_AR..1..623, 2_A375_pNL97_plus_lncRNA_AR..1..849	-194, -242	upstream, upstream	1	1	0	49	50	13	1	2_A375_pNL97_plus_lncRNA_AR..1	50	Gene RBBP5	RBBP5, SWD1, RBQ3	retinoblastoma binding protein 5	NM_005057, NM_001193272, NM_001193273, hCT1966342.2, hCT2324522.0, hCT2357361.0, hCT7446.3	205169_at	NP_005048.2, NP_001180201.1, NP_001180202.1, EAW91536.1, EAW91537.1, EAW91538.1, EAW91539.1
GeneID.25778	DSTYK	1	205,111,631	205,180,727	69,096	-	3	1_A375_pNL7_minus_lncRNA_AR..1..624, 2_A375_pNL97_plus_lncRNA_AR..1..850, 4_A375_EGR1..1..865	407, -73, 106	in gene, upstream, in gene	1	1	1	18	26	22	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene DSTYK	RIP5, HDCMD38P, DustyPK, DSTYK, KIAA0472, RIPK5	dual serine/threonine and tyrosine protein kinase	NM_015375, NM_199462, hCT2324517.0, hCT2324518.0, hCT2324519.0, hCT2324520.0, hCT2324521.0	211514_at, 211515_s_at, 214663_at, 229017_s_at	NP_056190.1, NP_955749.1, EAW91540.1, EAW91541.1, EAW91542.1, EAW91544.1, EAW91543.1
GeneID.9911	TMCC2	1	205,197,038	205,242,471	45,433	+	1	2_A375_pNL97_plus_lncRNA_AR..1..851	30930	in gene	0	1	0	16	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TMCC2	FLJ38497, TMCC2, HUCEP11, KIAA0481	transmembrane and coiled-coil domain family 2	NM_014858, hCT1954451.1, hCT1954452.1, hCT2323816.0, hCT8014.3	1555503_a_at, 213096_at	NP_055673.2, EAW91545.1, EAW91546.1, EAW91547.1, EAW91548.1
GeneID.100506871	LOC100506871	1	205,236,636	205,236,992	356	+	1	2_A375_pNL97_plus_lncRNA_AR..1..851	-8666	upstream	0	1	0	16	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100506871		hypothetical protein LOC100506871	XM_003119760, XM_003118502, XM_003120647		XP_003119808.1, XP_003118550.1, XP_003120695.1
GeneID.55220	KLHDC8A	1	205,305,648	205,326,039	20,391	-	1	4_A375_EGR1..1..867	18615	in gene	0	0	1	6	7	18	1	4_A375_EGR1..1	18	Gene KLHDC8A	FLJ10748, KLHDC8A	kelch domain containing 8A	NM_018203, hCT1816972.1, hCT2324515.0, hCT2357380.0, hCT8012.3	219331_s_at, 222671_at	NP_060673.1, EAW91550.1, EAW91551.1, EAW91552.1, EAW91553.1
GeneID.100506918	LOC100506918	1	205,404,013	205,425,214	21,201	-	6	1_A375_pNL7_minus_lncRNA_AR..1..626, 1_A375_pNL7_minus_lncRNA_AR..1..627, 2_A375_pNL97_plus_lncRNA_AR..1..853, 2_A375_pNL97_plus_lncRNA_AR..1..854, 4_A375_EGR1..1..868, 4_A375_EGR1..1..869	6798, -3010, -2016, -3106, 15646, 266	in gene, upstream, upstream, upstream, in gene, in gene	1	1	1	17.5	21.5	13	4	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene LOC100506918		hypothetical LOC100506918	XR_111966, XR_108337, XR_114972		
GeneID.442891	MIR135B	1	205,417,430	205,417,526	96	-	5	1_A375_pNL7_minus_lncRNA_AR..1..626, 1_A375_pNL7_minus_lncRNA_AR..1..627, 2_A375_pNL97_plus_lncRNA_AR..1..853, 4_A375_EGR1..1..868, 4_A375_EGR1..1..869	-890, -10698, -9706, 7958, -7402	upstream, upstream, upstream, downstream, upstream	1	1	1	17.5	21.5	13	4	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene MIR135B	MIRN135B, MIR135B	microRNA 135b	NR_029893		
GeneID.284577	LOC284577	1	205,425,045	205,438,152	13,107	+	5	1_A375_pNL7_minus_lncRNA_AR..1..626, 1_A375_pNL7_minus_lncRNA_AR..1..627, 2_A375_pNL97_plus_lncRNA_AR..1..853, 2_A375_pNL97_plus_lncRNA_AR..1..854, 4_A375_EGR1..1..869	-6629, 3179, 2187, 3275, -117	upstream, in gene, in gene, in gene, upstream	1	1	1	20.67	25.67	11.33	3	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene LOC284577		hypothetical LOC284577	XR_111970, XR_108339, XR_114974		
GeneID.5129	CDK18	1	205,473,684	205,501,921	28,237	+	2	4_A375_EGR1..1..870, 4_A375_EGR1..1..871	21580, 24364	in gene, in gene	0	0	1	11.5	13.5	21.5	2	4_A375_EGR1..1	24	Gene CDK18	PCTAIRE, PCTK3, PCTAIRE3, CDK18	cyclin-dependent kinase 18	NM_002596, NM_212502, NM_212503, hCT1954454.2, hCT1954455.2, hCT2351133.0, hCT8018.4	214797_s_at	NP_002587.2, NP_997667.1, NP_997668.1, EAW91559.1, EAW91560.1, EAW91562.1, EAW91561.1
GeneID.148808	MFSD4	1	205,538,112	205,572,046	33,934	+	1	4_A375_EGR1..1..872	1088	in gene	0	0	1	10	12	15	1	4_A375_EGR1..1	15	Gene MFSD4	FLJ34577, FLJ45392, FLJ25004, DKFZp564C1416, MFSD4, DKFZp761N1114, UNQ3064	major facilitator superfamily domain containing 4	NM_181644, hCT1954457.1, hCT1954458.1, hCT2323793.0, hCT2323794.0, hCT2323797.0, hCT8019.3	229254_at, 238682_at, 239304_at, 242372_s_at	NP_857595.3, EAW91566.1, EAW91564.1, EAW91565.1, EAW91567.1, EAW91569.1, EAW91568.1
GeneID.2005	ELK4	1	205,585,235	205,602,000	16,765	-	3	1_A375_pNL7_minus_lncRNA_AR..1..628, 2_A375_pNL97_plus_lncRNA_AR..1..855, 4_A375_EGR1..1..873	848, 816, 784	in gene, in gene, in gene	1	1	1	32	38	18	1	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene ELK4	SAP1, ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	NM_001973, NM_021795, hCT1787065.1, hCT2324504.0, hCT2324506.0, hCT2324507.0, hCT9947.2	205994_at, 208919_at, 230549_at	NP_001964.2, NP_068567.1, EAW91570.1, EAW91571.1, EAW91572.1, EAW91574.1, EAW91573.1
GeneID.85414	SLC45A3	1	205,626,981	205,649,630	22,649	-	2	4_A375_EGR1..1..874, 4_A375_EGR1..1..875	18716, -370	in gene, upstream	0	0	1	8	8	17	2	4_A375_EGR1..1	20	Gene SLC45A3	PCANAP6, PCANAP2, PCANAP8, SLC45A3, IPCA-6, IPCA-2, PRST, IPCA6, IPCA-8	solute carrier family 45, member 3	NM_033102, hCT10222.2, hCT2324502.0, hCT2324503.0	228696_at, 238499_at	NP_149093.1, EAW91576.1, EAW91575.1, EAW91577.1
GeneID.64710	NUCKS1	1	205,681,947	205,719,361	37,414	-	2	2_A375_pNL97_plus_lncRNA_AR..1..856, 4_A375_EGR1..1..876	-31, 649	upstream, in gene	0	1	1	11.5	16.5	20	2	4_A375_EGR1..1	26	Gene NUCKS1	FLJ32016, FLJ21480, FLJ38536, NUCKS, JC7, NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	NM_022731, hCT2324499.0, hCT2324500.0	217802_s_at, 222027_at, 222424_s_at, 226880_at, 229353_s_at	NP_073568.2, EAW91578.1, EAW91579.1
GeneID.8934	RAB7L1	1	205,737,114	205,744,610	7,496	-	2	1_A375_pNL7_minus_lncRNA_AR..1..629, 2_A375_pNL97_plus_lncRNA_AR..1..857	34, 34	in gene, in gene	1	1	0	29	28	9	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene RAB7L1	DKFZp686P1051, RAB7L1, RAB7L	RAB7, member RAS oncogene family-like 1	NM_003929, NM_001135662, NM_001135663, NM_001135664, hCT1817029.1, hCT2324498.0	218699_at, 218700_s_at, 243777_at	NP_003920.1, NP_001129134.1, NP_001129135.1, NP_001129136.1, EAW91580.1, EAW91581.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:254428	SLC41A1	1	205,758,221	205,782,161	23,940	-	2	2_A375_pNL97_plus_lncRNA_AR..1..858, 4_A375_EGR1..1..877	-399, 7377	upstream, in gene	0	1	1	11	19	15	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene SLC41A1	SLC41A1, MgtE	solute carrier family 41, member 1	NM_173854, hCT10220.2, hCT2357425.0	225570_at	NP_776253.3, EAW91583.1, EAW91582.1
GeneID:100131354	LOC100131354	1	205,781,868	205,784,368	2,500	+	2	2_A375_pNL97_plus_lncRNA_AR..1..858, 4_A375_EGR1..1..877	692, -7084	in gene, upstream	0	1	1	11	19	15	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC100131354		hypothetical LOC100131354	XM_001719408		XP_001719458.1
GeneID:115019	SLC26A9	1	205,882,176	205,912,588	30,412	-	2	1_A375_pNL7_minus_lncRNA_AR..1..630, 2_A375_pNL97_plus_lncRNA_AR..1..859	9484, 9452	in gene, in gene	1	1	0	22	24	8	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SLC26A9	SLC26A9		NM_134325, NM_052934, hCT1959430.1, hCT2324493.0	242271_at	NP_599152.2, NP_443166.1, EAW91587.1, EAW91588.1
GeneID:100505650	LOC100505650	1	206,279,146	206,288,199	9,053	-	1	2_A375_pNL97_plus_lncRNA_AR..1..860	12375	downstream	0	1	0	9	17	7	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC100505650		hypothetical LOC100505650	XR_112000, XR_112002, XR_112001, XR_110787, XR_110789, XR_110788, XR_114976, XR_114978, XR_114977		
GeneID:23380	SRGAP2	1	206,516,196	206,637,783	121,587	+	2	1_A375_pNL7_minus_lncRNA_AR..1..631, 2_A375_pNL97_plus_lncRNA_AR..1..861	127548, 127516	downstream, downstream	1	1	0	25	27	15	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SRGAP2	FNBP2, ARHGAP34, SRGAP2, SRGAP3, KIAA0456	SLIT-ROBO Rho GTPase activating protein 2	NM_001042758, NM_015326, NM_001170637, hCT1957107.1	1556202_at, 1556203_a_at, 213329_at, 227649_s_at	NP_001036223.1, NP_056141.2, NP_001164108.1, EAW93550.1
GeneID:9641	IKBKE	1	206,643,586	206,670,223	26,637	+	2	1_A375_pNL7_minus_lncRNA_AR..1..631, 2_A375_pNL97_plus_lncRNA_AR..1..861	156, 126	in gene, in gene	1	1	0	25	27	15	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene IKBKE	IKBKE, MGC125295, IKK-i, KIAA0151, IKKE, MGC125297, IKKI, MGC125294, IKK-E	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	NM_001193321, NM_014002, NM_001193322, hCT2282271.0, hCT2357632.0, hCT28260.2	204549_at, 214398_s_at	NP_001180250.1, NP_054721.1, NP_001180251.1, EAW93547.1, EAW93548.1, EAW93549.1
GeneID:1939	LGTN	1	206,764,974	206,785,904	20,930	-	3	1_A375_pNL7_minus_lncRNA_AR..1..632, 2_A375_pNL97_plus_lncRNA_AR..1..862, 4_A375_EGR1..1..878	126, 16, 176	in gene, in gene, in gene	1	1	1	51	53	16	1	2_A375_pNL97_plus_lncRNA_AR..1	53	Gene LGTN	EIF2D, LGTN, HCA56	eukaryotic translation initiation factor 2D	NM_006893, hCT2281782.0, hCT2281783.0, hCT2281784.0, hCT2281785.0, hCT2281786.0	218253_s_at	NP_008824.2, EAW93537.1, EAW93538.1, EAW93536.1, EAW93539.1, EAW93540.1
GeneID:8444	DYRK3	1	206,808,681	206,822,542	13,861	+	2	2_A375_pNL97_plus_lncRNA_AR..1..863, 4_A375_EGR1..1..879	-33, -161	upstream, upstream	0	1	1	24	22	34	1	4_A375_EGR1..1	34	Gene DYRK3	hYAK3-2, REDK, DYRK5, DYRK3, RED	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	NM_003582, NM_001004023, hCT1962300.1, hCT2357653.0, hCT2357654.0	1560785_at, 210151_s_at	NP_003573.2, NP_001004023.1, EAW93533.1, EAW93534.1, EAW93535.1
GeneID:9261	MAPKAPK2	1	206,858,289	206,907,626	49,337	+	3	2_A375_pNL97_plus_lncRNA_AR..1..864, 4_A375_EGR1..1..880, 4_A375_EGR1..1..881	-273, 1359, 44591	upstream, in gene, in gene	0	1	1	9.67	14.33	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MAPKAPK2	MK2, MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	NM_004759, NM_032960, hCT13298.4, hCT1950045.2, hCT2282279.1, hCT2282280.1, hCT2282282.1, hCT2282283.1, hCT2282285.1, hCT2282288.1	201460_at, 201461_s_at, 215050_x_at	NP_004750.1, NP_116584.2, EAW93525.1, EAW93527.1, EAW93529.1, EAW93532.1, EAW93526.1, EAW93528.1, EAW93530.1, EAW93531.1
GeneID:11009	IL24	1	207,070,788	207,077,484	6,696	+	3	1_A375_pNL7_minus_lncRNA_AR..1..633, 2_A375_pNL97_plus_lncRNA_AR..1..865, 2_A375_pNL97_plus_lncRNA_AR..1..866	-7236, -6900, -6436	upstream, upstream, upstream	1	1	0	19	18	7	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene IL24	ST16, FISP, MOB5, MDA7, IL24, Mob-5, mda-7, IL10B, C49A, IL-24	interleukin 24	NM_001185156, NM_001185157, NM_001185158, NM_006850, hCT13292.2, hCT2357631.0	206569_at	NP_001172085.1, NP_001172086.1, NP_006841.1, NP_001172087.1, EAW93518.1, EAW93519.1
GeneID:5284	PIGR	1	207,101,867	207,119,811	17,944	-	1	4_A375_EGR1..1..882	10851	in gene	0	0	1	9	7	16	1	4_A375_EGR1..1	16	Gene PIGR	MGC125362, FLJ22667, PIGR, MGC125361	polymeric immunoglobulin receptor	NM_002644, hCT1640781.3, hCT2281675.1	204213_at, 226147_s_at, 229659_s_at	NP_002635.2, EAW93516.1, EAW93515.1
GeneID:79098	C1orf116	1	207,191,866	207,206,101	14,235	-	1	2_A375_pNL97_plus_lncRNA_AR..1..867	11189	in gene	0	1	0	14	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene C1orf116	MGC2742, FLJ36507, SARG, DKFZp666H2010, C1orf116, MGC4309	chromosome 1 open reading frame 116	NM_023938, NM_001083924, hCT13300.2	219476_at, 219856_at, 226885_at	NP_076427.2, NP_001077393.1, EAW93511.1
GeneID:55432	YOD1	1	207,217,194	207,224,422	7,228	-	2	2_A375_pNL97_plus_lncRNA_AR..1..868, 4_A375_EGR1..1..883	-2234, -2202	upstream, upstream	0	1	1	14	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene YOD1	YOD1, OTUD2, DKFZp451J1719, DUBA8, PRO0907	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)	NM_018566, hCT1828362.0	215150_at, 227309_at	NP_061036.3, EAW93509.1
GeneID:5208	PFKFB2	1	207,226,620	207,254,368	27,748	+	2	2_A375_pNL97_plus_lncRNA_AR..1..868, 4_A375_EGR1..1..883	36, 4	in gene, in gene	0	1	1	14	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PFKFB2	PFKFB2, PFK-2/FBPase-2, DKFZp781D2217, MGC138310, MGC138308	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	NM_006212, NM_001018053, hCT1850212.1, hCT1953706.1	207931_s_at, 209992_at, 226733_at, 238450_at	NP_006203.2, NP_001018063.1, EAW93507.1, EAW93508.1
GeneID:100129101	LOC100129101	1	207,303,594	207,495,474	191,880	-	4	1_A375_pNL7_minus_lncRNA_AR..1..634, 2_A375_pNL97_plus_lncRNA_AR..1..869, 2_A375_pNL97_plus_lncRNA_AR..1..870, 4_A375_EGR1..1..884	116662, 116666, 103058, 125842	in gene, in gene, in gene, in gene	1	1	1	11.33	14.67	7	3	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100129101		hypothetical LOC100129101	XM_001721125, XM_001716664, XM_001715999		XP_001721177.1, XP_001716716.1, XP_001716051.1
GeneID:1380	CR2	1	207,627,645	207,663,240	35,595	+	1	4_A375_EGR1..1..885	35	in gene	0	0	1	6	12	16	1	4_A375_EGR1..1	16	Gene CR2	SLEB9, CD21, C3DR, CR2	complement component (3d/Epstein Barr virus) receptor 2	NM_001006658, NM_001877, hCT2282683.0, hCT2282699.0, hCT2357626.0	205544_s_at	NP_001006659.1, NP_001868.2, EAW93461.1, EAW93462.1, EAW93463.1
GeneID:5362	PLXNA2	1	208,195,587	208,417,665	222,078	-	4	1_A375_pNL7_minus_lncRNA_AR..1..635, 2_A375_pNL97_plus_lncRNA_AR..1..871, 2_A375_pNL97_plus_lncRNA_AR..1..872, 4_A375_EGR1..1..886	138289, 138001, 59809, 213329	in gene, in gene, in gene, in gene	1	1	1	14.33	13	11.33	3	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene PLXNA2	FLJ30634, KIAA0463, FLJ11751, PLXN2, OCT, PLXNA2	plexin A2	NM_025179, hCT2281607.1	207290_at, 213030_s_at, 227032_at	NP_079455.3, EAW93457.1
GeneID:3914	LAMB3	1	209,788,215	209,825,820	37,605	-	2	1_A375_pNL7_minus_lncRNA_AR..1..640, 2_A375_pNL97_plus_lncRNA_AR..1..882	1036, -772	in gene, upstream	1	1	0	20	21.5	6	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene LAMB3	LAM5, BM600-125KDA, FLJ99565, LAMB3, LAMNB1	laminin, beta 3	NM_000228, NM_001017402, NM_001127641, hCT12368.3, hCT2357619.0	209270_at	NP_000219.2, NP_001017402.1, NP_001121113.1, EAW93448.1, EAW93449.1
GeneID:80342	TRAF3IP3	1	209,929,394	209,955,668	26,274	+	1	4_A375_EGR1..1..888	27830	downstream	0	0	1	7	10	16	1	4_A375_EGR1..1	16	Gene TRAF3IP3	MGC163289, T3JAM, FLJ44151, DJ434O14.3, TRAF3IP3, MGC117354	TRAF3 interacting protein 3	NM_025228, hCT13578.3, hCT1970979.1, hCT2357637.0, hCT2357638.0	205604_s_at, 213888_s_at, 215275_at, 231932_at, 240265_at	NP_079504.2, EAW93442.1, EAW93441.1, EAW93443.1, EAW93444.1
GeneID:148304	C1orf74	1	209,955,662	209,957,890	2,228	-	1	4_A375_EGR1..1..888	666	in gene	0	0	1	7	10	16	1	4_A375_EGR1..1	16	Gene C1orf74	FLJ25078, C1orf74	chromosome 1 open reading frame 74	NM_152485, hCT1821674.1	229933_at	NP_689698.1, EAW93440.1
GeneID:3664	IRF6	1	209,961,262	209,979,479	18,217	-	2	4_A375_EGR1..1..888, 4_A375_EGR1..1..889	22455, 23	downstream, in gene	0	0	1	9	10.5	16.5	2	4_A375_EGR1..1	17	Gene IRF6	PIT, LPS, OFC6, IRF6, VWS, PPS, VWS1	interferon regulatory factor 6	NM_006147, hCT1963171.1, hCT2281572.0	1552477_a_at, 1552478_a_at, 202597_at	NP_006138.1, EAW93438.1, EAW93439.1
GeneID:27042	C1orf107	1	210,001,312	210,030,910	29,598	+	3	1_A375_pNL7_minus_lncRNA_AR..1..641, 2_A375_pNL97_plus_lncRNA_AR..1..883, 2_A375_pNL97_plus_lncRNA_AR..1..884	12098, 32, 12320	in gene, in gene, in gene	1	1	0	19	25.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene C1orf107	C1orf107, DIEXF, DEF, FLJ41660, DJ434O14.5, DKFZp686E19106, MGC29875, FLJ12704	chromosome 1 open reading frame 107	NM_014388, hCT13572.1	204699_s_at, 204700_x_at, 214193_s_at, 220251_at	NP_055203.4, EAW93437.1
GeneID:255928	SYT14	1	210,111,538	210,337,636	226,098	+	9	1_A375_pNL7_minus_lncRNA_AR..1..643, 1_A375_pNL7_minus_lncRNA_AR..1..644, 1_A375_pNL7_minus_lncRNA_AR..1..645, 2_A375_pNL97_plus_lncRNA_AR..1..887, 2_A375_pNL97_plus_lncRNA_AR..1..888, 2_A375_pNL97_plus_lncRNA_AR..1..889, 2_A375_pNL97_plus_lncRNA_AR..1..890, 4_A375_EGR1..1..890, 4_A375_EGR1..1..891	-434, 136942, 194542, -402, 110, 136942, 191822, 40558, 47710	upstream, in gene, in gene, upstream, in gene, in gene, in gene, in gene, in gene	1	1	1	19.17	20.5	9.67	6	2_A375_pNL97_plus_lncRNA_AR..1	53	Gene SYT14	MGC163195, sytXIV, FLJ34198, SYT14	synaptotagmin XIV	NM_153262, NM_001146261, NM_001146262, NM_001146264, NR_027458, NR_027459, hCT2344307.1, hCT2357629.0	1553854_at	NP_694994.2, NP_001139733.1, NP_001139734.1, NP_001139736.1, EAW93434.1, EAW93435.1
GeneID:574036	C1orf133	1	210,404,804	210,407,466	2,662	-	2	1_A375_pNL7_minus_lncRNA_AR..1..647, 4_A375_EGR1..1..892	821, 662	in gene, in gene	1	0	1	17	19	15	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene C1orf133	C1orf133	chromosome 1 open reading frame 133	NR_024337	230121_at	
GeneID:56256	SERTAD4	1	210,406,195	210,416,460	10,265	+	2	1_A375_pNL7_minus_lncRNA_AR..1..647, 4_A375_EGR1..1..892	450, 589	in gene, in gene	1	0	1	17	19	15	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene SERTAD4	DJ667H12.2, SERTAD4	SERTA domain containing 4	NM_019605, hCT13577.3, hCT2281445.0, hCT2281447.0	229674_at, 230660_at	NP_062551.1, EAW93433.1, EAW93431.1, EAW93432.1
GeneID:55733	HHAT	1	210,501,596	210,849,638	348,042	+	7	1_A375_pNL7_minus_lncRNA_AR..1..649, 1_A375_pNL7_minus_lncRNA_AR..1..650, 1_A375_pNL7_minus_lncRNA_AR..1..651, 2_A375_pNL97_plus_lncRNA_AR..1..893, 2_A375_pNL97_plus_lncRNA_AR..1..894, 2_A375_pNL97_plus_lncRNA_AR..1..895, 4_A375_EGR1..1..894	46148, 110740, 270100, 46116, 65572, 269732, 1044	in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	21.6	23.2	10.8	5	1_A375_pNL7_minus_lncRNA_AR..1	35	Gene HHAT	FLJ34867, SKI1, FLJ10724, HHAT, MART2, Skn	hedgehog acyltransferase	NM_001122834, NM_018194, NM_001170564, NM_001170580, NM_001170587, NM_001170588, hCT1952965.1, hCT2281448.0, hCT2281449.0, hCT2281451.0, hCT2357624.0	219687_at	NP_001116306.1, NP_060664.2, NP_001164035.1, NP_001164051.1, NP_001164058.1, NP_001164059.1, EAW93426.1, EAW93427.1, EAW93428.1, EAW93429.1, EAW93430.1
GeneID:3756	KCNH1	1	210,851,657	211,307,457	455,800	-	4	1_A375_pNL7_minus_lncRNA_AR..1..652, 2_A375_pNL97_plus_lncRNA_AR..1..896, 2_A375_pNL97_plus_lncRNA_AR..1..897, 2_A375_pNL97_plus_lncRNA_AR..1..898	407313, 407285, 394305, -170	in gene, in gene, in gene, upstream	1	1	0	18.33	23.67	5	3	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene KCNH1	h-eag, KCNH1, Kv10.1, EAG1, EAG, MGC142269	potassium voltage-gated channel, subfamily H (eag-related), member 1	NM_172362, NM_002238, hCT1952974.1, hCT2357628.0	207635_s_at	NP_758872.1, NP_002229.1, EAW93424.1, EAW93425.1
GeneID:55758	RCOR3	1	211,432,708	211,489,727	57,019	+	3	1_A375_pNL7_minus_lncRNA_AR..1..653, 1_A375_pNL7_minus_lncRNA_AR..1..654, 2_A375_pNL97_plus_lncRNA_AR..1..899	-548, 1052, -372	upstream, in gene, upstream	1	1	0	19	17	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RCOR3	FLJ10876, RCOR3, RP11-318L16.1, FLJ16298	REST corepressor 3	NM_018254, NM_001136223, NM_001136225, NM_001136224, hCT1821419.1	218344_s_at, 222605_at, 241433_at	NP_060724.1, NP_001129695.1, NP_001129697.1, NP_001129696.2, EAW93423.1
GeneID:7779	SLC30A1	1	211,748,381	211,752,099	3,718	-	3	2_A375_pNL97_plus_lncRNA_AR..1..900, 4_A375_EGR1..1..895, 4_A375_EGR1..1..896	323, 403, -397	in gene, in gene, upstream	0	1	1	15	21	20	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SLC30A1	ZNT1, ZRC1, SLC30A1	solute carrier family 30 (zinc transporter), member 1	NM_021194, hCT15373.2	212907_at, 228181_at, 242716_at	NP_067017.2, EAW93412.1
GeneID:4751	NEK2	1	211,836,122	211,848,967	12,845	-	1	2_A375_pNL97_plus_lncRNA_AR..1..902	39	in gene	0	1	0	21	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene NEK2	NLK1, HsPK21, NEK2A, NEK2	NIMA (never in mitosis gene a)-related kinase 2	NM_002497, hCT14581.2, hCT2266442.0	204641_at, 211080_s_at	NP_002488.1, EAW93411.1, EAW93410.1
GeneID:9926	LPGAT1	1	211,916,799	212,004,114	87,315	-	1	1_A375_pNL7_minus_lncRNA_AR..1..656	94866	downstream	1	0	0	20	13	7	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LPGAT1	FAM34A, FAM34A1, LPGAT1, NET8	lysophosphatidylglycerol acyltransferase 1	NM_014873, hCT1963874.1, hCT2266440.0	1555058_a_at, 202651_at	NP_055688.1, EAW93408.1, EAW93407.1
GeneID:25896	INTS7	1	212,114,698	212,208,884	94,186	-	3	1_A375_pNL7_minus_lncRNA_AR..1..657, 2_A375_pNL97_plus_lncRNA_AR..1..903, 2_A375_pNL97_plus_lncRNA_AR..1..904	4436, 4436, -236	in gene, in gene, upstream	1	1	0	24.5	26.5	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene INTS7	DKFZp434B168, INT7, INTS7, C1orf73	integrator complex subunit 7	NM_015434, hCT2266435.0, hCT2266436.0, hCT2266437.0, hCT2266438.0, hCT2357633.0, hCT2357634.0, hCT2357635.0	1570173_at, 218783_at, 222250_s_at	NP_056249.1, EAW93405.1, EAW93400.1, EAW93401.1, EAW93404.1, EAW93406.1, EAW93402.1, EAW93403.1
GeneID:51514	DTL	1	212,208,919	212,278,187	69,268	+	3	1_A375_pNL7_minus_lncRNA_AR..1..657, 2_A375_pNL97_plus_lncRNA_AR..1..903, 2_A375_pNL97_plus_lncRNA_AR..1..904	-4471, -4471, 201	upstream, upstream, in gene	1	1	0	24.5	26.5	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene DTL	DTL, L2DTL, RAMP, DCAF2, CDT2	denticleless homolog (Drosophila)	NM_016448, hCT1963889.1, hCT2287655.0, hCT2287659.0, hCT2287660.0	218585_s_at, 222680_s_at	NP_057532.2, EAW93396.1, EAW93395.1, EAW93397.1, EAW93398.1
GeneID:5525	PPP2R5A	1	212,458,879	212,535,205	76,326	+	4	1_A375_pNL7_minus_lncRNA_AR..1..658, 2_A375_pNL97_plus_lncRNA_AR..1..905, 4_A375_EGR1..1..898, 4_A375_EGR1..1..899	97, 1, -479, 669	in gene, in gene, upstream, in gene	1	1	1	30	33	20	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene PPP2R5A	MGC131915, PPP2R5A, PR61A, B56A	protein phosphatase 2, regulatory subunit B', alpha	NM_006243, hCT2281700.0, hCT28968.2	202186_x_at, 202187_s_at	NP_006234.1, EAW93392.1, EAW93393.1
GeneID:467	ATF3	1	212,738,697	212,794,117	55,420	+	6	1_A375_pNL7_minus_lncRNA_AR..1..662, 2_A375_pNL97_plus_lncRNA_AR..1..909, 2_A375_pNL97_plus_lncRNA_AR..1..910, 4_A375_EGR1..1..901, 4_A375_EGR1..1..902, 4_A375_EGR1..1..903	43383, -6217, 43383, 41847, 42711, 44327	in gene, upstream, in gene, in gene, in gene, in gene	1	1	1	14.5	17.25	15.75	4	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene ATF3	ATF3, FLJ41705		NM_001674, NM_001040619, NM_001030287, hCT1983209.1, hCT1983210.1, hCT2281705.0, hCT2281709.0, hCT30442.3, hCT30443.3	1554420_at, 1554980_a_at, 202672_s_at	NP_001665.1, NP_001035709.1, NP_001025458.1, EAW93383.1, EAW93387.1, EAW93388.1, EAW93384.1, EAW93385.1, EAW93386.1
GeneID:55509	BATF3	1	212,859,759	212,873,327	13,568	-	1	4_A375_EGR1..1..904	-209	upstream	0	0	1	17	15	24	1	4_A375_EGR1..1	24	Gene BATF3	FLJ37535, JUNDM1, BATF3, FLJ38352, SNFT, JDP1	basic leucine zipper transcription factor, ATF-like 3	NM_018664, hCT30451.1	220358_at	NP_061134.1, EAW93381.1
GeneID:25936	NSL1	1	212,899,495	212,965,139	65,644	-	4	1_A375_pNL7_minus_lncRNA_AR..1..664, 2_A375_pNL97_plus_lncRNA_AR..1..911, 4_A375_EGR1..1..905, 4_A375_EGR1..1..906	35, 51, 31091, -77	in gene, in gene, in gene, upstream	1	1	1	18	17.5	21	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene NSL1	DC8, NSL1, C1orf48, MIS14, DKFZp566O1646	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	NM_015471, NM_001042549, hCT2281499.0, hCT30449.2	209484_s_at, 230592_at, 235799_at	NP_056286.3, NP_001036014.1, EAW93379.1, EAW93380.1
GeneID:128387	TATDN3	1	212,965,170	212,990,167	24,997	+	3	1_A375_pNL7_minus_lncRNA_AR..1..664, 2_A375_pNL97_plus_lncRNA_AR..1..911, 4_A375_EGR1..1..906	-86, -82, 46	upstream, upstream, in gene	1	1	1	28	28	23	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene TATDN3	TATDN3, MGC142198	TatD DNase domain containing 3	NM_001042552, NM_001042553, NM_001146169, NM_001146170, NM_001146171	228687_at, 235089_at	NP_001036017.1, NP_001036018.1, NP_001139641.1, NP_001139642.1, NP_001139643.1
GeneID:149643	C1orf227	1	213,003,483	213,020,991	17,508	-	1	2_A375_pNL97_plus_lncRNA_AR..1..912	-10849	upstream	0	1	0	14	22	32	1	4_A375_EGR1..1	32	Gene C1orf227	C1orf227	chromosome 1 open reading frame 227	NM_001024601, hCT2343106.0	1559390_a_at	NP_001019772.1, EAW93375.1
GeneID:642946	LQK1	1	213,029,946	213,031,480	1,534	-	2	2_A375_pNL97_plus_lncRNA_AR..1..912, 4_A375_EGR1..1..907	-160, -552	upstream, upstream	0	1	1	14	22	32	1	4_A375_EGR1..1	32	Gene LQK1	NCRNA00292, LQK1	non-protein coding RNA 292	NR_027265, NR_027266	235126_at	
GeneID:28982	FLVCR1	1	213,031,597	213,070,197	38,600	+	2	2_A375_pNL97_plus_lncRNA_AR..1..912, 4_A375_EGR1..1..907	43, 435	in gene, in gene	0	1	1	14	22	32	1	4_A375_EGR1..1	32	Gene FLVCR1	FLJ33420, AXPC1, FLVCR1, PCA, PCARP, FLVCR, MFSD7B	feline leukemia virus subgroup C cellular receptor 1	NM_014053, hCT30445.3	222906_at	NP_054772.1, EAW93374.1
GeneID:79805	VASH2	1	213,123,887	213,164,927	41,040	+	1	4_A375_EGR1..1..908	26225	in gene	0	0	1	6	11	16	1	4_A375_EGR1..1	16	Gene VASH2	VASH2, FLJ12505, RP11-275G3.1	vasohibin 2	NM_024749, NM_001136474, NM_001136475, hCT2281716.0, hCT2357623.0, hCT28967.2	1555092_at, 219740_at	NP_079025.2, NP_001129946.1, NP_001129947.1, EAW93371.1, EAW93372.1, EAW93373.1
GeneID:90806	ANGEL2	1	213,165,524	213,189,168	23,644	-	1	2_A375_pNL97_plus_lncRNA_AR..1..914	46	in gene	0	1	0	16	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ANGEL2	ANGEL2, KIAA0759L, FLJ12793	angel homolog 2 (Drosophila)	NM_144567, hCT2281495.0, hCT2281496.0, hCT2357620.0, hCT2357621.0, hCT2357622.0, hCT30892.2	217630_at, 221825_at, 221826_at	NP_653168.2, EAW93365.1, EAW93366.1, EAW93367.1, EAW93368.1, EAW93369.1, EAW93370.1
GeneID:26750	RPS6KC1	1	213,224,588	213,446,808	222,220	+	1	2_A375_pNL97_plus_lncRNA_AR..1..915	-166	upstream	0	1	0	23	28	16	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene RPS6KC1	RPS6KC1, humS6PKh1, RPK118	ribosomal protein S6 kinase, 52kDa, polypeptide 1	NM_012424, NM_001136138, hCT1642735.3, hCT1967498.1, hCT2281720.0	218909_at	NP_036556.2, NP_001129610.1, EAW93362.1, EAW93363.1, EAW93364.1
GeneID:100505832	LOC100505832	1	213,991,095	214,139,608	148,513	-	1	1_A375_pNL7_minus_lncRNA_AR..1..667	-7046	upstream	1	0	0	20	14	5	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LOC100505832		hypothetical LOC100505832	XR_112008, XR_110635, XR_115089		
GeneID:5629	PROX1	1	214,161,860	214,209,766	47,906	+	1	4_A375_EGR1..1..909	-5124	upstream	0	0	1	7	12	21	1	4_A375_EGR1..1	21	Gene PROX1	PROX1		NM_002763, hCT2281067.0, hCT30407.3	207401_at, 228656_at	NP_002754.2, EAW93359.1, EAW93360.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:84746	ACBD3	1	226,332,380	226,374,423	42,043	-	3	1_A375_pNL7_minus_lncRNA_AR..1..720, 2_A375_pNL97_plus_lncRNA_AR..1..981, 4_A375_EGR1..1..935	-9, -73, -41	upstream, upstream, upstream	1	1	1	16	16	17	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene ACBD3	GOLPH1, PAP7, GCP60, ACBD3, GOCAP1	acyl-CoA binding domain containing 3	NM_022735, hCT1775776.0, hCT2282177.0	202323_s_at, 202324_s_at	NP_073572.2, EAW69776.1, EAW69775.1
GeneID:286826	LIN9	1	226,418,861	226,497,198	78,337	-	2	1_A375_pNL7_minus_lncRNA_AR..1..721, 2_A375_pNL97_plus_lncRNA_AR..1..982	414, 398	in gene, in gene	1	1	0	21	33	10	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene LIN9	BARPsv, TGS, Lin-9, LIN9, BARA, TGS1	lin-9 homolog (C. elegans)	NM_173083, hCT2349292.0, hCT2349293.0, hCT2354717.0	1552771_a_at, 230365_at, 235039_x_at	NP_775106.2, EAW69781.1, EAW69780.1, EAW69782.1
GeneID:142	PARP1	1	226,548,392	226,595,801	47,409	-	2	1_A375_pNL7_minus_lncRNA_AR..1..722, 2_A375_pNL97_plus_lncRNA_AR..1..983	121, 164	in gene, in gene	1	1	0	19	17	8	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene PARP1	PARP, pADPRT-1, ADPRT, PARP-1, PPOL, PARP1, ADPRT 1, ADPRT1	poly (ADP-ribose) polymerase 1	NM_001618, hCT2282172.0, hCT2282173.0, hCT5787.3	208644_at	NP_001609.2, EAW69783.1, EAW69784.1, EAW69785.1
GeneID:375057	C1orf95	1	226,736,501	226,793,303	56,802	+	1	4_A375_EGR1..1..936	53547	in gene	0	0	1	12	10	20	1	4_A375_EGR1..1	20	Gene C1orf95	C1orf95, DKFZp761P211	chromosome 1 open reading frame 95	NM_001003665	213925_at, 232104_at	NP_001003665.1
GeneID:3707	ITPKB	1	226,819,391	226,926,876	107,485	-	1	2_A375_pNL97_plus_lncRNA_AR..1..984	35604	in gene	0	1	0	18	25	12	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene ITPKB	ITPKB, IP3K-B, IP3K, IP3KB, IP3-3KB, PIG37	inositol 1,4,5-trisphosphate 3-kinase B	NM_002221, hCT2282166.0	1554306_at, 203723_at, 232499_at, 232526_at, 235213_at	NP_002212.3, EAW69793.1
GeneID:56997	CABC1	1	227,127,938	227,175,246	47,308	+	9	1_A375_pNL7_minus_lncRNA_AR..1..724, 1_A375_pNL7_minus_lncRNA_AR..1..725, 2_A375_pNL97_plus_lncRNA_AR..1..985, 4_A375_EGR1..1..937, 4_A375_EGR1..1..938, 4_A375_EGR1..1..939, 4_A375_EGR1..1..940, 4_A375_EGR1..1..941, 4_A375_EGR1..1..942	-9058, -370, -386, -482, 286, 24766, 34174, 39102, 40636	upstream, upstream, upstream, upstream, in gene, in gene, in gene, in gene, in gene	1	1	1	10.67	13	16.5	6	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene CABC1	MGC4849, COQ8, CABC1, ARCA2, SCAR9, ADCK3	aarF domain containing kinase 3	NM_020247, hCT1778120.1, hCT1953180.1, hCT1953181.1, hCT1953182.1, hCT1953183.1	218168_s_at, 222542_x_at	NP_064632.2, EAW69801.1, EAW69802.1, EAW69803.1, EAW69804.1, EAW69805.1
GeneID:8476	CDC42BPA	1	227,177,566	227,505,826	328,260	-	2	4_A375_EGR1..1..942, 4_A375_EGR1..1..943	337250, -156	downstream, upstream	0	0	1	10	15	20.5	2	4_A375_EGR1..1	24	Gene CDC42BPA	CDC42BPA, FLJ23347, MRCKA, PK428, DKFZp686L1738, KIAA0451, DKFZp686P1738, MRCK	CDC42 binding protein kinase alpha (DMPK-like)	NM_003607, NM_014826, hCT2349294.0, hCT2349295.0, hCT2354718.0, hCT2354719.0	203794_at, 213595_s_at, 214464_at, 215296_at, 240735_at	NP_003598.2, NP_055641.3, EAW69806.1, EAW69807.1, EAW69808.1, EAW69809.1
GeneID:339500	ZNF678	1	227,751,220	227,850,164	98,944	+	2	2_A375_pNL97_plus_lncRNA_AR..1..989, 4_A375_EGR1..1..945	244, -2004	in gene, upstream	0	1	1	10	12	14	2	4_A375_EGR1..1	16	Gene ZNF678	MGC15634, MGC42493, FLJ18355, ZNF678, FLJ22822	zinc finger protein 678	NM_178549, NR_033184, hCT2354701.0, hCT33518.4	1554922_at, 232028_at, 242923_at	NP_848644.2, EAW69813.1, EAW69812.1
GeneID:100130093	LOC100130093	1	227,916,240	227,922,078	5,838	+	5	1_A375_pNL7_minus_lncRNA_AR..1..726, 2_A375_pNL97_plus_lncRNA_AR..1..990, 4_A375_EGR1..1..946, 4_A375_EGR1..1..947, 4_A375_EGR1..1..948	6736, 6768, 347, 6704, 12928	downstream, downstream, in gene, downstream, downstream	1	1	1	14.67	17.67	20.67	3	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene LOC100130093		hypothetical LOC100130093	NR_024485, NR_024486		
GeneID:85094	JMJD4	1	227,918,890	227,923,112	4,222	-	5	1_A375_pNL7_minus_lncRNA_AR..1..726, 2_A375_pNL97_plus_lncRNA_AR..1..990, 4_A375_EGR1..1..946, 4_A375_EGR1..1..947, 4_A375_EGR1..1..948	136, 104, 6525, 168, -6056	in gene, in gene, downstream, in gene, upstream	1	1	1	14.67	17.67	20.67	3	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene JMJD4	MGC129898, JMJD4, FLJ12517	jumonji domain containing 4	NM_023007, NM_001161465, hCT1953247.1, hCT33524.3	218560_s_at, 222671_s_at	NP_075383.2, NP_001154937.1, EAW69818.1, EAW69819.1
GeneID:116841	SNAP47	1	227,922,897	227,968,932	46,235	+	9	1_A375_pNL7_minus_lncRNA_AR..1..726, 2_A375_pNL97_plus_lncRNA_AR..1..990, 4_A375_EGR1..1..946, 4_A375_EGR1..1..947, 4_A375_EGR1..1..948, 4_A375_EGR1..1..949, 4_A375_EGR1..1..950, 4_A375_EGR1..1..951, 4_A375_EGR1..1..952	279, 311, -8110, 247, 6471, 28623, 46375, 53015, 53655	in gene, in gene, upstream, in gene, in gene, in gene, downstream, downstream, downstream	1	1	1	11.14	13.43	20.86	7	4_A375_EGR1..1	29	Gene SNAP47	HEL170, DKFZp686M10160, FLJ12517, C1orf142, SVAP1, SNAP47, SNAP-47	synaptosomal-associated protein, 47kDa	NM_053052, hCT1953253.1, hCT33525.3	225244_at, 230610_at	NP_444280.2, EAW69816.1, EAW69817.1
GeneID:7483	WNT9A	1	228,109,165	228,135,676	26,511	-	6	1_A375_pNL7_minus_lncRNA_AR..1..729, 2_A375_pNL97_plus_lncRNA_AR..1..991, 4_A375_EGR1..1..955, 4_A375_EGR1..1..956, 4_A375_EGR1..1..957, 4_A375_EGR1..1..958	13116, 13100, 26428, 24327, 22812, -793	in gene, in gene, in gene, in gene, in gene, upstream	1	1	1	12.2	11.4	17.2	5	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene WNT9A	MGC138165, WNT9A, WNT14, MGC141991	wingless-type MMTV integration site family, member 9A	NM_003395, hCT33515.3	1553045_at, 230643_at	NP_003386.1, EAW69821.1
GeneID:646262	LOC646262	1	228,163,473	228,165,863	2,390	-	1	4_A375_EGR1..1..959	6963	downstream	0	0	1	2	2	12	1	4_A375_EGR1..1	12	Gene LOC646262		capicua homolog (Drosophila) pseudogene			
GeneID:89780	WNT3A	1	228,194,752	228,248,961	54,209	+	3	4_A375_EGR1..1..960, 4_A375_EGR1..1..961, 4_A375_EGR1..1..962	32000, 51840, 57920	in gene, in gene, downstream	0	0	1	5.33	10	18.33	3	4_A375_EGR1..1	24	Gene WNT3A	MGC119419, WNT3A, MGC119420, MGC119418	wingless-type MMTV integration site family, member 3A	NM_033131, hCT33528.2		NP_149122.1, EAW69829.1
GeneID:100506571	LOC100506571	1	228,261,610	228,264,251	2,641	-	3	2_A375_pNL97_plus_lncRNA_AR..1..992, 4_A375_EGR1..1..962, 4_A375_EGR1..1..963	-5917, 11579, -6693	upstream, downstream, upstream	0	1	1	13	14.5	21	2	4_A375_EGR1..1	24	Gene LOC100506571		hypothetical protein LOC100506571	XM_003119777, XM_003119160, XM_003120910		XP_003119825.1, XP_003119208.1, XP_003120958.1
GeneID:375	ARF1	1	228,270,361	228,286,913	16,552	+	10	1_A375_pNL7_minus_lncRNA_AR..1..730, 2_A375_pNL97_plus_lncRNA_AR..1..992, 2_A375_pNL97_plus_lncRNA_AR..1..993, 2_A375_pNL97_plus_lncRNA_AR..1..994, 4_A375_EGR1..1..963, 4_A375_EGR1..1..964, 4_A375_EGR1..1..965, 4_A375_EGR1..1..966, 4_A375_EGR1..1..967, 4_A375_EGR1..1..968	26599, -193, 20815, 26599, 583, 14327, 16135, 19927, 23463, 26695	downstream, upstream, downstream, downstream, in gene, in gene, in gene, downstream, downstream, downstream	1	1	1	14.57	17.43	17.86	7	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene ARF1	ARF1	ADP-ribosylation factor 1	NM_001658, NM_001024226, NM_001024227, NM_001024228, hCT1686515.0, hCT1686516.0, hCT1777164.1, hCT1953232.1, hCT2354728.0, hCT2354729.0	1565651_at, 200065_s_at, 208750_s_at, 232175_at, 244504_x_at	NP_001649.1, NP_001019397.1, NP_001019398.1, NP_001019399.1, EAW69832.1, EAW69834.1, EAW69831.1, EAW69833.1, EAW69835.1, EAW69836.1
GeneID:79169	C1orf35	1	228,288,428	228,291,022	2,594	-	8	1_A375_pNL7_minus_lncRNA_AR..1..730, 2_A375_pNL97_plus_lncRNA_AR..1..993, 2_A375_pNL97_plus_lncRNA_AR..1..994, 4_A375_EGR1..1..964, 4_A375_EGR1..1..965, 4_A375_EGR1..1..966, 4_A375_EGR1..1..967, 4_A375_EGR1..1..968	-5936, 46, -5936, 6334, 4526, 734, 2802, -6034	upstream, in gene, upstream, downstream, downstream, in gene, upstream, upstream	1	1	1	13.67	17.17	17.83	6	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene C1orf35	MGC4174, MMTAG2, hMMTAG2, C1orf35	chromosome 1 open reading frame 35	NM_024319, hCT1953255.1, hCT2354726.0, hCT2354727.0	219063_at	NP_077295.1, EAW69838.1, EAW69837.1, EAW69839.1
GeneID:100506628	LOC100506628	1	228,291,253	228,304,782	13,529	-	8	1_A375_pNL7_minus_lncRNA_AR..1..730, 2_A375_pNL97_plus_lncRNA_AR..1..993, 2_A375_pNL97_plus_lncRNA_AR..1..994, 4_A375_EGR1..1..964, 4_A375_EGR1..1..965, 4_A375_EGR1..1..966, 4_A375_EGR1..1..967, 4_A375_EGR1..1..968	7822, 13806, 7822, 20094, 18286, 14494, 10956, 7726	in gene, downstream, in gene, downstream, downstream, downstream, in gene, in gene	1	1	1	13.67	17.17	17.83	6	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene LOC100506628		hypothetical LOC100506628	XR_112020, XR_110847, XR_115199		
GeneID:128308	MRPL55	1	228,294,380	228,297,013	2,633	-	8	1_A375_pNL7_minus_lncRNA_AR..1..730, 2_A375_pNL97_plus_lncRNA_AR..1..993, 2_A375_pNL97_plus_lncRNA_AR..1..994, 4_A375_EGR1..1..964, 4_A375_EGR1..1..965, 4_A375_EGR1..1..966, 4_A375_EGR1..1..967, 4_A375_EGR1..1..968	53, 8037, 53, 12325, 10517, 6725, 3189, -43	in gene, downstream, in gene, downstream, downstream, downstream, downstream, upstream	1	1	1	13.67	17.17	17.83	6	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene MRPL55	MRPL55, L55mt, AAVG5835, MGC61802, MRP-L55, PRO19675, DKFZp686D1387	mitochondrial ribosomal protein L55	NM_181463, NM_181454, NM_181455, NM_181456, NM_181462, NM_181464, NM_181465, NM_181441, hCT1953244.1, hCT2354703.0, hCT2354704.0, hCT2354705.0, hCT2354706.0, hCT2354707.0, hCT2354708.0, hCT2354709.0, hCT2354710.0, hCT2354711.0	225719_s_at, 227024_s_at	NP_852128.1, NP_852119.1, NP_852127.2, NP_852120.1, NP_852121.1, NP_852129.1, NP_852106.1, NP_852130.1, EAW69840.1, EAW69841.1, EAW69842.1, EAW69843.1, EAW69844.1, EAW69845.1, EAW69846.1, EAW69847.1, EAW69848.1, EAW69849.1
GeneID:2987	GUK1	1	228,327,929	228,336,656	8,727	+	4	1_A375_pNL7_minus_lncRNA_AR..1..731, 4_A375_EGR1..1..969, 4_A375_EGR1..1..970, 4_A375_EGR1..1..971	-249, 359, 9959, 16871	upstream, in gene, downstream, downstream	1	0	1	13.33	14.67	18	3	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene GUK1	FLJ42686, GUK1, FLJ43710, GMK	guanylate kinase 1	NM_000858, NM_001159390, NM_001159391, hCT2259103.1, hCT2259104.0, hCT2259107.1, hCT2259110.1, hCT2259113.1, hCT2340512.0, hCT2340513.0, hCT2350107.0, hCT2350108.0	200075_s_at, 213621_s_at	NP_000849.1, NP_001152862.1, NP_001152863.1, EAW69854.1, EAW69856.1, EAW69859.1, EAW69851.1, EAW69852.1, EAW69853.1, EAW69855.1, EAW69857.1, EAW69858.1
GeneID:57165	GJC2	1	228,337,553	228,347,527	9,974	+	7	1_A375_pNL7_minus_lncRNA_AR..1..731, 1_A375_pNL7_minus_lncRNA_AR..1..732, 2_A375_pNL97_plus_lncRNA_AR..1..995, 4_A375_EGR1..1..969, 4_A375_EGR1..1..970, 4_A375_EGR1..1..971, 4_A375_EGR1..1..972	-9673, 15935, 15919, -9265, 335, 7247, 13551	upstream, downstream, downstream, upstream, in gene, in gene, downstream	1	1	1	20.8	24	17	5	2_A375_pNL97_plus_lncRNA_AR..1	65	Gene GJC2	GJA12, PMLDAR, CX46.6, MGC105119, LMPH1C, HLD2, SPG44, GJC2, Cx47	gap junction protein, gamma 2, 47kDa	NM_020435, hCT2259108.0	207025_at, 214302_x_at	NP_065168.2, EAW69860.1
GeneID:100506642	LOC100506642	1	228,351,795	228,352,549	754	-	4	1_A375_pNL7_minus_lncRNA_AR..1..732, 2_A375_pNL97_plus_lncRNA_AR..1..995, 4_A375_EGR1..1..971, 4_A375_EGR1..1..972	-939, -923, 7749, 1445	upstream, upstream, downstream, downstream	1	1	1	23	27.67	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	65	Gene LOC100506642		hypothetical LOC100506642	XR_110848		
GeneID:200205	C1orf69	1	228,353,429	228,369,958	16,529	+	4	1_A375_pNL7_minus_lncRNA_AR..1..732, 2_A375_pNL97_plus_lncRNA_AR..1..995, 4_A375_EGR1..1..971, 4_A375_EGR1..1..972	59, 43, -8629, -2325	in gene, in gene, upstream, upstream	1	1	1	23	27.67	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	65	Gene C1orf69	FLJ13849, C1orf69, IBA57, FLJ12734	IBA57, non-sulfur cluster assembly homolog (S. cerevisiae)	NM_001010867, hCT2348727.0	1558898_at, 215490_at, 231983_at, 236629_at	NP_001010867.1, EAW69862.1
GeneID:84033	OBSCN	1	228,395,861	228,566,575	170,714	+	13	4_A375_EGR1..1..973, 4_A375_EGR1..1..974, 4_A375_EGR1..1..975, 4_A375_EGR1..1..976, 4_A375_EGR1..1..977, 4_A375_EGR1..1..978, 4_A375_EGR1..1..979, 4_A375_EGR1..1..980, 4_A375_EGR1..1..981, 4_A375_EGR1..1..982, 4_A375_EGR1..1..983, 4_A375_EGR1..1..984, 4_A375_EGR1..1..985	1051, 48779, 69019, 72091, 75211, 98571, 108587, 128283, 132663, 143083, 152427, 167371, 168987	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	6.69	8.15	19.31	13	4_A375_EGR1..1	27	Gene OBSCN	FLJ14124, MGC120411, MGC120409, UNC89, DKFZp666E245, MGC120412, ARHGEF30, OBSCN, MGC138590, KIAA1556, MGC120410, KIAA1639	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	NM_052843, NM_001098623, hCT2344869.0, hCT2354712.0	220427_at, 229854_at	NP_443075.2, NP_001092093.1, EAW69866.1, EAW69867.1
GeneID:92815	HIST3H2A	1	228,645,065	228,645,560	495	-	2	1_A375_pNL7_minus_lncRNA_AR..1..733, 2_A375_pNL97_plus_lncRNA_AR..1..996	-72, -660	upstream, upstream	1	1	0	28	27	14	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene HIST3H2A	HIST3H2A, MGC3165	histone cluster 3, H2a	NM_033445	221582_at, 231661_x_at	NP_254280.1
GeneID:128312	HIST3H2BB	1	228,645,808	228,646,259	451	+	2	1_A375_pNL7_minus_lncRNA_AR..1..733, 2_A375_pNL97_plus_lncRNA_AR..1..996	-176, 432	upstream, in gene	1	1	0	28	27	14	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene HIST3H2BB	HIST3H2BB		NM_175055		NP_778225.1
GeneID:149603	RNF187	1	228,675,068	228,683,889	8,821	+	3	1_A375_pNL7_minus_lncRNA_AR..1..734, 2_A375_pNL97_plus_lncRNA_AR..1..997, 2_A375_pNL97_plus_lncRNA_AR..1..998	-166, -252, 13732	upstream, upstream, downstream	1	1	0	40	51.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	64	Gene RNF187	RNF187, RACO1	ring finger protein 187	NM_001010858	1569294_at, 212155_at, 228470_at, 229207_x_at, 230682_at	NP_001010858.2
GeneID:100129094	LOC100129094	1	228,696,347	228,699,658	3,311	-	1	2_A375_pNL97_plus_lncRNA_AR..1..998	10656	downstream	0	1	0	14	19	10	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100129094		similar to hCG2038765	XM_001722254, XM_001722031, XM_001721663		XP_001722306.1, XP_001722083.1, XP_001721935.1
GeneID:100169751	RN5S1	1	228,746,013	228,746,133	120	-	1	4_A375_EGR1..1..987	3093	downstream	0	0	1	5	6	17	1	4_A375_EGR1..1	17	Gene RN5S1	RN5S1	RNA, 5S ribosomal 1	NR_023363		
GeneID:100169753	RN5S2	1	228,748,254	228,748,374	120	-	1	4_A375_EGR1..1..987	5334	downstream	0	0	1	5	6	17	1	4_A375_EGR1..1	17	Gene RN5S2	RN5S2	RNA, 5S ribosomal 2	NR_023364		
GeneID:100169754	RN5S3	1	228,750,495	228,750,615	120	-	1	4_A375_EGR1..1..987	7575	downstream	0	0	1	5	6	17	1	4_A375_EGR1..1	17	Gene RN5S3	RN5S3	RNA, 5S ribosomal 3	NR_023365		
GeneID:100169755	RN5S4	1	228,752,736	228,752,856	120	-	1	4_A375_EGR1..1..987	9816	downstream	0	0	1	5	6	17	1	4_A375_EGR1..1	17	Gene RN5S4	RN5S4	RNA, 5S ribosomal 4	NR_023366		
GeneID:100169759	RN5S8	1	228,761,654	228,761,774	120	-	1	4_A375_EGR1..1..988	-9506	upstream	0	0	1	10	6	15	1	4_A375_EGR1..1	15	Gene RN5S8	RN5S8	RNA, 5S ribosomal 8	NR_023370		
GeneID:100169760	RN5S9	1	228,763,893	228,764,013	120	-	1	4_A375_EGR1..1..988	-7267	upstream	0	0	1	10	6	15	1	4_A375_EGR1..1	15	Gene RN5S9	RN5S9	RNA, 5S ribosomal 9	NR_023371		
GeneID:100169761	RN5S10	1	228,766,135	228,766,255	120	-	1	4_A375_EGR1..1..988	-5025	upstream	0	0	1	10	6	15	1	4_A375_EGR1..1	15	Gene RN5S10	RN5S10	RNA, 5S ribosomal 10	NR_023372		
GeneID:100169762	RN5S11	1	228,768,376	228,768,496	120	-	1	4_A375_EGR1..1..988	-2784	upstream	0	0	1	10	6	15	1	4_A375_EGR1..1	15	Gene RN5S11	RN5S11	RNA, 5S ribosomal 11	NR_023373		
GeneID:100169763	RN5S12	1	228,770,616	228,770,736	120	-	1	4_A375_EGR1..1..988	-544	upstream	0	0	1	10	6	15	1	4_A375_EGR1..1	15	Gene RN5S12	RN5S12	RNA, 5S ribosomal 12	NR_023374		
GeneID:100169764	RN5S13	1	228,772,841	228,772,961	120	-	3	1_A375_pNL7_minus_lncRNA_AR..1..735, 2_A375_pNL97_plus_lncRNA_AR..1..999, 4_A375_EGR1..1..988	-9631, -9615, 1661	upstream, upstream, downstream	1	1	1	15.5	14.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RN5S13	RN5S13	RNA, 5S ribosomal 13	NR_023375		
GeneID:100169765	RN5S14	1	228,775,082	228,775,202	120	-	5	1_A375_pNL7_minus_lncRNA_AR..1..735, 1_A375_pNL7_minus_lncRNA_AR..1..736, 2_A375_pNL97_plus_lncRNA_AR..1..999, 2_A375_pNL97_plus_lncRNA_AR..1..1000, 4_A375_EGR1..1..988	-7390, -6638, -7374, -6316, 3922	upstream, upstream, upstream, upstream, downstream	1	1	1	15.5	14.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RN5S14	RN5S14	RNA, 5S ribosomal 14	NR_023376		
GeneID:100169766	RN5S15	1	228,777,313	228,777,433	120	-	5	1_A375_pNL7_minus_lncRNA_AR..1..735, 1_A375_pNL7_minus_lncRNA_AR..1..736, 2_A375_pNL97_plus_lncRNA_AR..1..999, 2_A375_pNL97_plus_lncRNA_AR..1..1000, 4_A375_EGR1..1..988	-5159, -8407, -5143, -8087, 6153	upstream, upstream, upstream, upstream, downstream	1	1	1	15.5	14.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RN5S15	RN5S15	RNA, 5S ribosomal 15	NR_023377		
GeneID:100169767	RN5S16	1	228,779,554	228,779,674	120	-	5	1_A375_pNL7_minus_lncRNA_AR..1..735, 1_A375_pNL7_minus_lncRNA_AR..1..736, 2_A375_pNL97_plus_lncRNA_AR..1..999, 2_A375_pNL97_plus_lncRNA_AR..1..1000, 4_A375_EGR1..1..988	-2918, -4166, -2902, -3846, 8394	upstream, upstream, upstream, upstream, downstream	1	1	1	15.5	14.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RN5S16	RN5S16	RNA, 5S ribosomal 16	NR_023378		
GeneID:100169768	RN5S17	1	228,781,785	228,781,905	120	-	4	1_A375_pNL7_minus_lncRNA_AR..1..735, 1_A375_pNL7_minus_lncRNA_AR..1..736, 2_A375_pNL97_plus_lncRNA_AR..1..999, 2_A375_pNL97_plus_lncRNA_AR..1..1000	-687, -1935, -671, -1615	upstream, upstream, upstream, upstream	1	1	0	21	23	16	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RN5S17	RN5S17	RNA, 5S ribosomal 17	NR_023379		
GeneID:58480	RHOU	1	228,870,869	228,882,411	11,542	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1001	11	in gene	0	1	0	17	20	12	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene RHOU	RHOU, DJ646B12.2, WRCH1, hG28K, ARHU, CDC42L1, FLJ10616, DJ646B12.2	ras homolog gene family, member U	NM_021205, hCT2259083.0, hCT5894.3	223168_at, 223169_s_at	NP_067028.1, EAW69865.1, EAW69866.1
GeneID:5867	RAB4A	1	229,406,879	229,440,518	33,639	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1006	-95	upstream	0	1	0	11	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene RAB4A	RAB4, HRES-1/RAB4, RAB4A	RAB4A, member RAS oncogene family	NM_004578, hCT1950474.1, hCT1966889.0, hCT1966890.1, hCT2258183.1, hCT2258185.1, hCT2258188.0, hCT2354745.0	203581_at, 203582_s_at	NP_004569.2, EAW69891.1, EAW69889.1, EAW69892.1, EAW69893.1, EAW69894.1, EAW69890.1, EAW69895.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.128731	C1orf98	1	229,456,752	229,478,688	21,936	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1007	128	in gene	0	1	0	18	22	19	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene C1orf98	C1orf98, FLJ41471, FLJ37298	chromosome 1 open reading frame 98	NM_145257, hCT1645411.3	1553897_at, 1553898_a_at, 1555145_at, 225904_at	NP_660300.3, EAW69897.1
GeneID.58	ACTA1	1	229,566,992	229,569,843	2,851	-	4	1_A375_pNL7_minus_lncRNA_AR..1..740, 4_A375_EGR1..1..991, 4_A375_EGR1..1..992, 4_A375_EGR1..1..993	3251, 1795, 1059, 51	downstream, in gene, in gene, in gene	1	0	1	12	13.25	18.75	4	4_A375_EGR1..1	23	Gene ACTA1	ASMA, CFTD1, ACTA, CFTD, ACTA1, NEM2, NEM1, MPFD, NEM3, CFTDM	actin, alpha 1, skeletal muscle	NM_001100, hCT6537.3	203872_at	NP_001091.1, EAW69898.1
GeneID.55746	NUP133	1	229,577,044	229,644,088	67,044	-	5	2_A375_pNL97_plus_lncRNA_AR..1..1008, 4_A375_EGR1..1..991, 4_A375_EGR1..1..992, 4_A375_EGR1..1..993, 4_A375_EGR1..1..994	-72, 76040, 75304, 74298, 24	upstream, downstream, downstream, downstream, in gene	0	1	1	11.75	15.25	22.5	4	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene NUP133	NUP133, hNUP133, MGC21133, FLJ10814	nucleoporin 133kDa	NM_018230, hCT2259099.0, hCT2259101.0	202184_s_at, 233420_at, 233421_s_at	NP_060700.2, EAW69899.1, EAW69900.1
GeneID.23456	ABCB10	1	229,652,329	229,694,442	42,113	-	5	1_A375_pNL7_minus_lncRNA_AR..1..741, 2_A375_pNL97_plus_lncRNA_AR..1..1008, 2_A375_pNL97_plus_lncRNA_AR..1..1009, 4_A375_EGR1..1..994, 4_A375_EGR1..1..995	-408, 50282, -438, 50378, -374	upstream, downstream, upstream, downstream, upstream	1	1	1	25.5	35	23.5	2	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene ABCB10	MTABC2, EST20237, ABCB10, M-ABC2	ATP-binding cassette, sub-family B (MDR/TAP), member 10	NM_012089, hCT6540.3	223320_s_at	NP_036221.2, EAW69901.1
GeneID.27097	TAF5L	1	229,728,856	229,761,794	32,938	-	3	1_A375_pNL7_minus_lncRNA_AR..1..742, 2_A375_pNL97_plus_lncRNA_AR..1..1010, 4_A375_EGR1..1..996	-142, -158, -334	upstream, upstream, upstream	1	1	1	33	37	19	1	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene TAF5L	PAF65B, TAF5L	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	NM_014409, NM_001025247, hCT2343350.0, hCT6536.4	1554415_at, 213654_at	NP_055224.1, NP_001020418.1, EAW69902.1, EAW69903.1
GeneID.9816	URB2	1	229,761,981	229,795,946	33,965	+	5	1_A375_pNL7_minus_lncRNA_AR..1..742, 1_A375_pNL7_minus_lncRNA_AR..1..743, 2_A375_pNL97_plus_lncRNA_AR..1..1010, 2_A375_pNL97_plus_lncRNA_AR..1..1011, 4_A375_EGR1..1..996	-45, 38115, -29, 38147, 147	upstream, downstream, upstream, downstream, in gene	1	1	1	35	36	15	2	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene URB2	NPA2, KIAA0133, URB2, MGC138837, NET10, MGC138838	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	NM_014777, hCT2258193.0, hCT5783.3	205284_at	NP_055592.2, EAW69904.1, EAW69905.1
GeneID.2590	GALNT2	1	230,202,956	230,417,875	214,919	+	2	1_A375_pNL7_minus_lncRNA_AR..1..745, 2_A375_pNL97_plus_lncRNA_AR..1..1012	6500, 37760	in gene, in gene	1	1	0	15.5	17.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene GALNT2	GALNT2, GalNAc-T2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	NM_004481, hCT2258198.0, hCT2258197.0, hCT2258199.0, hCT6957.3	217787_s_at, 217788_s_at, 223991_s_at, 239930_at	NP_004472.1, EAW69909.1, EAW69908.1, EAW69910.1, EAW69911.1
GeneID.79805	PGBD5	1	230,457,392	230,513,391	55,999	-	2	4_A375_EGR1..1..997, 4_A375_EGR1..1..998	44847, 40399	in gene, in gene	0	0	1	8.5	8.5	17.5	2	4_A375_EGR1..1	19	Gene PGBD5	DKFZp761A0620, PGBD5, FLJ11413	piggyBac transposable element derived 5	NM_024554, hCT2349316.0	219225_at	NP_078830.3, EAW69912.1
GeneID.22796	COG2	1	230,778,202	230,829,731	51,529	+	3	1_A375_pNL7_minus_lncRNA_AR..1..747, 2_A375_pNL97_plus_lncRNA_AR..1..1016, 4_A375_EGR1..1..1001	-58, -58, 61510	upstream, upstream, downstream	1	1	1	130.5	123	16	2	1_A375_pNL7_minus_lncRNA_AR..1	253	Gene COG2	COG2, LDLC	component of oligomeric golgi complex 2	NM_007357, NM_001145036, hCT2354740.0, hCT6956.3	203073_at, 243608_at	NP_031383.1, NP_001138508.1, EAW69915.1, EAW69916.1
GeneID.183	AGT	1	230,838,269	230,850,336	12,067	-	1	4_A375_EGR1..1..1001	10624	in gene	0	0	1	8	9	16	1	4_A375_EGR1..1	16	Gene AGT	ANHU, FLJ92595, AGT, SERPINA8, FLJ97926	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	NM_000029, hCT2260859.0, hCT5782.2	202834_at	NP_000020.1, EAW69919.1, EAW69918.1
GeneID.84886	C1orf198	1	230,972,865	231,005,335	32,470	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1017, 2_A375_pNL97_plus_lncRNA_AR..1..1018	12311, 10647	in gene, in gene	0	1	0	14.5	20.5	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene C1orf198	C1orf198, FLJ38847, FLJ14525, MGC10710, DKFZp667D152, FLJ16283	chromosome 1 open reading frame 198	NM_032800, NM_001136494, NM_001136495, hCT1950063.0, hCT1966867.1, hCT1966868.0, hCT2354742.0, hCT2354743.0	223063_at	NP_116189.1, NP_001129966.1, NP_001129967.1, EAW69923.1, EAW69924.1, EAW69925.1, EAW69926.1, EAW69927.1
GeneID.79573	TTC13	1	231,041,987	231,114,818	72,831	-	3	1_A375_pNL7_minus_lncRNA_AR..1..748, 2_A375_pNL97_plus_lncRNA_AR..1..1019, 4_A375_EGR1..1..1002	-86, -134, -166	upstream, upstream, upstream	1	1	1	30	29	19	1	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene TTC13	FLJ22584, TTC13	tetratricopeptide repeat domain 13	NM_001122835, NM_024525, hCT1957671.1, hCT1957672.1, hCT2260850.0, hCT2260853.0, hCT2260854.0	219481_at	NP_001116307.2, NP_078801.3, EAW69929.1, EAW69930.1, EAW69931.1, EAW69932.1, EAW69933.1
GeneID.84801	ARV1	1	231,114,823	231,136,479	21,656	+	3	1_A375_pNL7_minus_lncRNA_AR..1..748, 2_A375_pNL97_plus_lncRNA_AR..1..1019, 4_A375_EGR1..1..1002	-119, -71, -39	upstream, upstream, upstream	1	1	1	30	29	19	1	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene ARV1	ARV1		NM_022786, hCT1965283.2, hCT1965285.2, hCT2343339.0, hCT2343340.0, hCT2343341.0, hCT2343342.0, hCT2343343.0, hCT5695.4	223223_at, 236140_at	NP_073623.1, EAW69935.1, EAW69934.1, EAW69936.1, EAW69937.1, EAW69938.1, EAW69939.1, EAW69940.1, EAW69941.1
GeneID.440730	TRIM67	1	231,296,874	231,357,314	58,840	+	5	1_A375_pNL7_minus_lncRNA_AR..1..751, 1_A375_pNL7_minus_lncRNA_AR..1..752, 2_A375_pNL97_plus_lncRNA_AR..1..1021, 4_A375_EGR1..1..1003, 4_A375_EGR1..1..1004	-338, 48686, -530, -1936, -39	upstream, in gene, upstream, upstream, upstream	1	1	1	17	19.67	17.33	3	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene TRIM67	TRIM67, TNL, FLJ44831	tripartite motif containing 67	NM_001004342, hCT5934.3	233357_at	NP_001004342.3, EAW69946.1
GeneID.126061	C1orf131	1	231,359,509	231,376,924	17,415	-	1	4_A375_EGR1..1..1005	-292	upstream	0	0	1	17	17	20	1	4_A375_EGR1..1	20	Gene C1orf131	C1orf131, DKFZp547B1713	chromosome 1 open reading frame 131	NM_152379, hCT2344786.0, hCT2344787.0, hCT2354720.0, hCT2354721.0, hCT5936.3	226242_at	NP_689592.2, EAW69949.1, EAW69948.1, EAW69950.1, EAW69951.1, EAW69952.1
GeneID.8443	GNPAT	1	231,376,919	231,413,719	36,800	+	1	4_A375_EGR1..1..1005	297	in gene	0	0	1	17	17	20	1	4_A375_EGR1..1	20	Gene GNPAT	GNPAT, DAP-AT, DHAPAT, DAPAT	glyceronephosphate O-acyltransferase	NM_014236, hCT5710.3	201958_s_at	NP_055051.1, EAW69953.1
GeneID.149371	EXOC8	1	231,468,482	231,473,578	5,096	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1022, 4_A375_EGR1..1..1006	-22, -70	upstream, upstream	0	1	1	28	28	20	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene EXOC8	EXOC8, SEC84, EXO84, Exo84p	exocyst complex component 8	NM_175876, hCT1644409.3	227577_at	NP_787072.2, EAW69955.1
GeneID.83932	C1orf124	1	231,473,682	231,489,989	16,307	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1022, 4_A375_EGR1..1..1006	-82, -34	upstream, upstream	0	1	1	28	28	20	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene C1orf124	C1orf124, PRO4323, dJ876B10.3, DDDL1880, DKFZp547N043	chromosome 1 open reading frame 124	NM_032018, NM_001010984, hCT2258033.0, hCT2258034.0, hCT5935.3	223511_at	NP_114407.3, NP_001010984.1, EAW69956.1, EAW69957.1, EAW69958.1
GeneID.100303453	TSNAX-DISC1	1	231,664,399	232,177,018	512,619	+	5	1_A375_pNL7_minus_lncRNA_AR..1..754, 2_A375_pNL97_plus_lncRNA_AR..1..1023, 2_A375_pNL97_plus_lncRNA_AR..1..1024, 4_A375_EGR1..1..1009, 4_A375_EGR1..1..1010	-63, -143, 516449, 1, 96353	upstream, upstream, downstream, in gene, in gene	1	1	1	18	22.67	15	3	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene TSNAX-DISC1		TSNAX-DISC1 gene	NR_028393, NR_028394, NR_028395, NR_028397, NR_028399, NR_028400, NR_028396, NR_028398		
GeneID.7257	TSNAX	1	231,664,399	231,702,270	37,871	+	3	1_A375_pNL7_minus_lncRNA_AR..1..754, 2_A375_pNL97_plus_lncRNA_AR..1..1023, 4_A375_EGR1..1..1009	-63, -143, 1	upstream, upstream, in gene	1	1	1	25	38	16	1	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene TSNAX	TRAX, DISC1, TSNAX	translin-associated factor X	NM_005999, hCT1966849.1, hCT2258035.0, hCT2354735.0, hCT5712.3	203983_at	NP_005990.1, EAW69962.1, EAW69961.1, EAW69963.1, EAW69964.1
GeneID.27185	DISC1	1	231,762,561	232,177,018	414,457	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1024, 4_A375_EGR1..1..1010	420287, 191	downstream, in gene	0	1	1	14.5	15	14.5	2	4_A375_EGR1..1	25	Gene DISC1	KIAA0457, SCZD9, FLJ25311, FLJ41105, DISC1, FLJ13381, FLJ21640, C1orf136	disrupted in schizophrenia 1	NM_018662, NM_001012957, NM_001012958, NM_001012959, NM_001164550, NM_001164551, NM_001164552, NM_001164553, NM_001164554, NM_001164555, NM_001164556, NM_001164537, NM_001164538, NM_001164539, NM_001164540, NM_001164541, NM_001164542, NM_001164544, NM_001	207759_s_at	NP_061132.2, NP_001012975.1, NP_001158022.1, NP_001158023.1, NP_001012976.1, NP_001012977.1, NP_001158024.1, NP_001158025.1, NP_001158026.1, NP_001158027.1, NP_001158028.1, NP_001158009.1, NP_001158010.1, NP_001158011.1, NP_001158012.1, NP_001158013.1, NP
GeneID.84284	C1orf57	1	233,086,370	233,114,219	27,849	+	1	1_A375_pNL7_minus_lncRNA_AR..1..756	-162	upstream	1	0	0	18	14	16	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene C1orf57	RP4-678E16.2, MGC13186, C1orf57, NTPCR, FLJ11383, HCR-NTPase	chromosome 1 open reading frame 57	NM_032324, hCT1950062.1, hCT1966852.1, hCT2349028.0, hCT2349029.0, hCT2354724.0	223272_s_at, 226613_at	NP_115700.1, EAW69979.1, EAW69976.1, EAW69977.1, EAW69978.1, EAW69980.1
GeneID.80003	PCNXL2	1	233,119,882	233,431,459	311,577	-	3	1_A375_pNL7_minus_lncRNA_AR..1..757, 2_A375_pNL97_plus_lncRNA_AR..1..1030, 4_A375_EGR1..1..1013	182563, 182339, 304635	in gene, in gene, in gene	1	1	1	19	16.5	10.5	2	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene PCNXL2	KIAA0435, FLJ11383, PCNXL2	pecanex-like 2 (Drosophila)	NM_014801, hCT2349270.0, hCT2349271.0, hCT2349272.0, hCT2349273.0, hCT2349274.0	1554256_a_at, 205689_at, 220481_at, 39850_s_at	NP_055616.3, EAW69985.1, EAW69982.1, EAW69983.1, EAW69984.1, EAW69986.1
GeneID.84451	KIAA1804	1	233,463,514	233,520,894	57,380	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1031	598	in gene	0	1	0	11	14	2	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene KIAA1804	MLK4, dJ862P8.3, RP5-862P8.2	mixed lineage kinase 4	NM_032435, hCT2349315.0, hCT2354733.0	228565_at	NP_115811.2, EAW69988.1, EAW69987.1
GeneID.146641	SLC35F3	1	234,040,679	234,460,262	419,583	+	5	1_A375_pNL7_minus_lncRNA_AR..1..759, 2_A375_pNL97_plus_lncRNA_AR..1..1033, 2_A375_pNL97_plus_lncRNA_AR..1..1034, 2_A375_pNL97_plus_lncRNA_AR..1..1035, 4_A375_EGR1..1..1014	313289, 86657, 281401, 309209, 745	in gene, in gene, in gene, in gene, in gene	1	1	1	13.8	16.4	10.2	5	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SLC35F3	SLC35F3, FLJ37712	solute carrier family 35, member F3	NM_173508, hCT1950028.1	229065_at, 231520_at	NP_775779.1, EAW69991.1
GeneID.100506776	LOC100506776	1	234,508,553	234,509,379	826	+	3	1_A375_pNL7_minus_lncRNA_AR..1..760, 2_A375_pNL97_plus_lncRNA_AR..1..1036, 4_A375_EGR1..1..1015	35, 3, -13	in gene, in gene, upstream	1	1	1	36	28	24	1	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene LOC100506776		hypothetical LOC100506776	XR_110850		
GeneID.388753	C1orf31	1	234,509,429	234,519,791	10,362	+	3	1_A375_pNL7_minus_lncRNA_AR..1..760, 2_A375_pNL97_plus_lncRNA_AR..1..1036, 4_A375_EGR1..1..1015	-85, -53, -37	upstream, upstream, upstream	1	1	1	36	28	24	1	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene C1orf31	C1orf31	chromosome 1 open reading frame 31	NM_001012985, hCT1763140.1	225638_at	NP_001013003.1, EAW69992.1
GeneID.100506795	LOC100506795	1	234,863,837	234,867,525	3,688	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1037	3557	in gene	0	1	0	9	16	4	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100506795		hypothetical LOC100506795	XR_112026, XR_110851, XR_115203		
GeneID.100506810	LOC100506810	1	234,859,789	234,867,390	7,601	+	1	1_A375_pNL7_minus_lncRNA_AR..1..762	-1005	upstream	1	0	0	16	13	6	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene LOC100506810		hypothetical LOC100506810	XR_112022, XR_110852, XR_115204		
GeneID.9804	TOMM20	1	235,272,656	235,292,256	19,600	-	4	1_A375_pNL7_minus_lncRNA_AR..1..766, 2_A375_pNL97_plus_lncRNA_AR..1..1043, 4_A375_EGR1..1..1019, 4_A375_EGR1..1..1020	320, 192, 20976, 288	in gene, in gene, downstream, in gene	1	1	1	17	20.5	22	2	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene TOMM20	TOM20, MOM19, TOMM20, MAS20, MGC117367, KIAA0016	translocase of outer mitochondrial membrane 20 homolog (yeast)	NM_014765, hCT1950454.2, hCT2260513.0	200662_s_at, 212773_s_at	NP_055580.1, EAW70003.1, EAW70004.1
GeneID.677802	SNORA14B	1	235,291,118	235,291,252	134	-	3	1_A375_pNL7_minus_lncRNA_AR..1..766, 2_A375_pNL97_plus_lncRNA_AR..1..1043, 4_A375_EGR1..1..1020	-684, -812, -716	upstream, upstream, upstream	1	1	1	25	31	28	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene SNORA14B	SNORA14B, ACA14b	small nucleolar RNA, H/ACA box 14B	NR_002956		
GeneID.23029	RBM34	1	235,294,498	235,324,571	30,073	-	4	1_A375_pNL7_minus_lncRNA_AR..1..766, 2_A375_pNL97_plus_lncRNA_AR..1..1043, 2_A375_pNL97_plus_lncRNA_AR..1..1044, 4_A375_EGR1..1..1020	32835, 32507, -101, 32603	downstream, downstream, upstream, downstream	1	1	1	22	29	19	2	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene RBM34	RBM34, KIAA0117	RNA binding motif protein 34	NM_015014, NM_001161533, NR_027762, hCT10389.3, hCT1962913.1, hCT1962914.2	212591_at, 214942_at, 214943_s_at	NP_055829.2, NP_001155005.1, EAW70005.1, EAW70006.1, EAW70007.1
GeneID.51742	ARID4B	1	235,330,210	235,491,532	161,322	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1044, 2_A375_pNL97_plus_lncRNA_AR..1..1045	168860, -724	downstream, upstream	0	1	0	17.5	23.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene ARID4B	BCAA, RBP1L1, ARID4B, RBBP1L1, MGC163290, BRCAA1, DKFZp313M2420, SAP180	AT rich interactive domain 4B (RBP1-like)	NM_016374, NM_031371, hCT10388.3, hCT2260503.0, hCT2260505.0, hCT2260506.0, hCT2260507.0, hCT2260508.0, hCT2260509.0, hCT2354723.0	221230_s_at, 223111_x_at, 224322_at, 235959_at	NP_057458.4, NP_112739.2, EAW70008.1, EAW70009.1, EAW70012.1, EAW70013.1, EAW70010.1, EAW70011.1, EAW70014.1, EAW70015.1
GeneID.9453	GGPS1	1	235,491,753	235,507,847	16,094	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1045	503	in gene	0	1	0	16	20	17	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene GGPS1	GGPPS, GGPS1, GGPPS1	geranylgeranyl diphosphate synthase 1	NM_001037277, NM_004837, hCT10132.4, hCT1962910.1, hCT1962911.1, hCT1962912.1, hCT2354722.0	202321_at, 202322_s_at	NP_001032354.1, NP_004828.1, EAW70016.1, EAW70017.1, EAW70018.1, EAW70020.1, EAW70019.1
GeneID.6905	TBCE	1	235,530,728	235,612,280	81,552	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1046	248	in gene	0	1	0	20	17	16	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TBCE	KCS, pac2, HRD, TBCE, KCS1	tubulin folding cofactor E	NM_003193, NM_001079515, hCT14874.3, hCT1958367.1, hCT1958368.1, hCT1958369.1, hCT2354734.0	203714_s_at, 203715_at	NP_003184.1, NP_001072983.1, EAW70021.1, EAW70023.1, EAW70024.1, EAW70025.1, EAW70022.1
GeneID.148789	B3GALNT2	1	235,610,533	235,667,781	57,248	-	4	1_A375_pNL7_minus_lncRNA_AR..1..769, 2_A375_pNL97_plus_lncRNA_AR..1..1047, 4_A375_EGR1..1..1021, 4_A375_EGR1..1..1022	-363, -219, -187, -5371	upstream, upstream, upstream, upstream	1	1	1	17	16	18	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene B3GALNT2	B3GALNT2, MGC39558, B3GalNAc-T2	beta-1,3-N-acetylgalactosaminyltransferase 2	NM_152490, hCT14875.2, hCT2260502.0, hCT2354738.0	1553891_at, 1561714_a_at, 1562391_at, 226233_at	NP_689703.1, EAW70026.1, EAW70027.1, EAW70028.1
GeneID.2786	GNG4	1	235,710,985	235,814,054	103,069	-	4	1_A375_pNL7_minus_lncRNA_AR..1..770, 2_A375_pNL97_plus_lncRNA_AR..1..1048, 4_A375_EGR1..1..1023, 4_A375_EGR1..1..1024	8390, 8390, 55953, 14246	in gene, in gene, in gene, in gene	1	1	1	12.33	15.33	18	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene GNG4	DKFZp547K1018, FLJ34187, GNG4, FLJ23803	guanine nucleotide binding protein (G protein), gamma 4	NM_001098721, NM_004485, NM_001098722, hCT14567.2, hCT1950456.1	1555765_a_at, 205184_at	NP_001092191.1, NP_004476.1, NP_001092192.1, EAW70030.1, EAW70031.1
GeneID.1130	LYST	1	235,824,343	236,030,220	205,877	-	3	1_A375_pNL7_minus_lncRNA_AR..1..771, 2_A375_pNL97_plus_lncRNA_AR..1..1049, 4_A375_EGR1..1..1025	-306, -340, 476	upstream, upstream, in gene	1	1	1	19	16	20	1	4_A375_EGR1..1	20	Gene LYST	CHS1, CHS, LYST	lysosomal trafficking regulator	NM_000081, hCT16583.2, hCT2259865.0, hCT2259867.0, hCT2259868.0, hCT2259870.0	1562511_at, 203518_at, 210943_s_at, 215415_s_at	NP_000072.2, EAW70038.1, EAW70034.1, EAW70035.1, EAW70036.1, EAW70037.1
GeneID.4811	NID1	1	236,139,130	236,228,481	89,351	-	5	1_A375_pNL7_minus_lncRNA_AR..1..773, 2_A375_pNL97_plus_lncRNA_AR..1..1052, 2_A375_pNL97_plus_lncRNA_AR..1..1053, 2_A375_pNL97_plus_lncRNA_AR..1..1054, 4_A375_EGR1..1..1026	65865, 65281, 39142, 161, 71585	in gene, in gene, in gene, in gene, in gene	1	1	1	15.5	17.75	14.25	4	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene NID1	NID, NID1	nidogen 1	NM_002508, hCT16582.3, hCT2259863.0, hCT2354737.0	1561062_at, 202007_at, 202008_s_at	NP_002499.2, EAW70039.1, EAW70040.1, EAW70041.1
GeneID.56605	ERO1LB	1	236,378,422	236,445,339	66,917	-	3	1_A375_pNL7_minus_lncRNA_AR..1..774, 2_A375_pNL97_plus_lncRNA_AR..1..1056, 4_A375_EGR1..1..1027	-5029, -5093, 187	upstream, upstream, in gene	1	1	1	13	19	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ERO1LB	DKFZp779I0141, ERO1LB, DKFZp779C1042, FLJ11003	ERO1-like beta (S. cerevisiae)	NM_019891, hCT1950453.1, hCT2259657.0	220012_at, 231944_at	NP_063944.3, EAW70045.1, EAW70046.1
GeneID.3964	LGALS8	1	236,681,565	236,712,996	31,431	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1057, 4_A375_EGR1..1..1028	5663, 5763	in gene, in gene	0	1	1	15	27	31	1	4_A375_EGR1..1	31	Gene LGALS8	Gal-8, PCTA-1, Po66-CBP, LGALS8, PCTA1	lectin, galactoside-binding, soluble, 8	NM_006499, NM_201543, NM_201544, NM_201545, hCT14554.4, hCT1966007.1, hCT1966008.1, hCT2261463.0, hCT2354702.0	208933_s_at, 208934_s_at, 208935_s_at, 208936_x_at, 210731_s_at, 210732_s_at	NP_006490.3, NP_963837.1, NP_963838.1, NP_963839.1, EAW70053.1, EAW70055.1, EAW70054.1, EAW70056.1, EAW70057.1
GeneID.100287902	LOC100287902	1	236,686,369	236,687,808	1,439	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1057, 4_A375_EGR1..1..1028	560, 460	in gene, in gene	0	1	1	15	27	31	1	4_A375_EGR1..1	31	Gene LOC100287902		hypothetical LOC100287902	NR_034040		
GeneID.88	ACTN2	1	236,849,770	236,927,556	77,786	+	1	1_A375_pNL7_minus_lncRNA_AR..1..775	60534	in gene	1	0	0	21	15	7	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ACTN2	ACTN2, CMD1AA	actinin, alpha 2	NM_001103, hCT1950460.1, hCT1966228.1	203861_s_at, 203862_s_at, 203863_at, 203864_s_at	NP_001094.1, EAW70064.1, EAW70065.1
GeneID.4548	MTR	1	236,958,561	237,067,261	108,700	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1058, 4_A375_EGR1..1..1029	75, 279	in gene, in gene	0	1	1	16	18	17	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MTR	MS, FLJ45386, MTR, cblG, FLJ43216, FLJ33168	5-methyltetrahydrofolate-homocysteine methyltransferase	NM_000254, hCT1950459.1, hCT2354736.0	203774_at	NP_000245.2, EAW70066.1, EAW70067.1
GeneID.6262	RYR2	1	237,205,702	237,997,288	791,586	+	4	1_A375_pNL7_minus_lncRNA_AR..1..776, 2_A375_pNL97_plus_lncRNA_AR..1..1059, 2_A375_pNL97_plus_lncRNA_AR..1..1060, 4_A375_EGR1..1..1030	717114, 717210, 740634, 162570	in gene, in gene, in gene, in gene	1	1	1	17.33	16	10	3	1_A375_pNL7_minus_lncRNA_AR..1	35	Gene RYR2	ARVD2, ARVC2, VTSIP, RYR2	ryanodine receptor 2 (cardiac)	NM_001035, hCT15967.3, hCT2261478.0, hCT2261480.0	207557_s_at, 214044_at	NP_001026.2, EAW70069.1, EAW70070.1, EAW70071.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:80760	ITIH5	10	7,601,232	7,708,961	107,729	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1117	16765	in gene	0	1	0	14	15	3	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene ITIH5	pp14776, ITIH5, MGC10848, DKFZp686F0145	inter-alpha (globulin) inhibitor H5	NM_001001851, NM_030569, NM_032817, hCT2311517.1, hCT2311519.1, hCT2311520.1, hCT2356772.0, hCT1951856.1	1553243_at, 219064_at	NP_001001851.1, NP_085046.4, NP_116206.3, EAW86379.1, EAW86380.1, EAW86383.1, EAW86381.1, EAW86382.1
GeneID:83860	TAF3	10	7,860,873	8,056,714	196,041	+	2	1_A375_pNL7_minus_lncRNA_AR..1..823, 2_A375_pNL97_plus_lncRNA_AR..1..1116	-225, -246	upstream, upstream	1	1	0	29	23	11	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene TAF3	TAFII140, TAFII-140, TAF140, TAF3, MGC25063	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa	NM_031923	235119_at, 235154_at	NP_114129.1
GeneID:26019	UPF2	10	11,962,021	12,085,023	123,002	-	2	1_A375_pNL7_minus_lncRNA_AR..1..824, 2_A375_pNL97_plus_lncRNA_AR..1..1119	15, -33	in gene, upstream	1	1	0	20	19	7	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene UPF2	HUPF2, RENT2, smg-3, DKFZp434D222, MGC138834, UPF2, MGC138835, KIAA1408	UPF2 regulator of nonsense transcripts homolog (yeast)	NM_015542, NM_080599, hCT2311377.0, hCT2311379.0, hCT2311381.0, hCT2311384.0, hCT2356801.0, hCT16007.3	203519_s_at	NP_056357.1, NP_542166.1, EAW86328.1, EAW86329.1, EAW86331.1, EAW86333.1, EAW86330.1, EAW86332.1
GeneID:55388	MCM10	10	13,203,554	13,253,104	49,550	+	2	1_A375_pNL7_minus_lncRNA_AR..1..825, 2_A375_pNL97_plus_lncRNA_AR..1..1120	-130, -66	upstream, upstream	1	1	0	27	18	6	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene MCM10	PRO2249, MCM10, DNA43, CNA43, MGC126776	minichromosome maintenance complex component 10	NM_018518, NM_182751, hCT2311373.0, hCT32044.3	220651_s_at, 222962_s_at, 223570_at	NP_060988.3, NP_877428.1, EAW86297.1, EAW86298.1
GeneID:22929	SEPHS1	10	13,360,080	13,390,280	30,200	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1121	-88	upstream	0	1	0	10	15	14	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene SEPHS1	SELD, SPS, MGC4980, SPS1, SEPHS1	selenophosphate synthetase 1	NM_012247, hCT2311246.0, hCT2311247.0, hCT2311248.0, hCT2311249.0, hCT2311250.0	208939_at, 208940_at, 208941_s_at	NP_036379.2, EAW86293.1, EAW86289.1, EAW86290.1, EAW86291.1, EAW86292.1
GeneID:8559	PRPF18	10	13,828,939	13,872,868	43,929	+	2	1_A375_pNL7_minus_lncRNA_AR..1..826, 2_A375_pNL97_plus_lncRNA_AR..1..1123	-75, -27	upstream, upstream	1	1	0	58	69	9	1	2_A375_pNL97_plus_lncRNA_AR..1	69	Gene PRPF18	PRP18, PRPF18, hPrp18, FLJ10210	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	NM_003675, hCT1967848.2, hCT2350297.0, hCT2350298.0, hCT31034.3	221546_at, 221547_at, 223665_s_at, 232473_at	NP_003666.1, EAW86280.1, EAW86281.1, EAW86282.1, EAW86283.1
GeneID:55691	FRMD4A	10	13,685,706	14,372,866	687,160	-	5	1_A375_pNL7_minus_lncRNA_AR..1..827, 1_A375_pNL7_minus_lncRNA_AR..1..828, 2_A375_pNL97_plus_lncRNA_AR..1..1124, 2_A375_pNL97_plus_lncRNA_AR..1..1125, 2_A375_pNL97_plus_lncRNA_AR..1..1126	178946, 85714, 617826, 337506, 85762	in gene, in gene, in gene, in gene, in gene	1	1	0	14.25	15.5	3	4	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene FRMD4A	KIAA1294, bA295P9.4, FRMD4, FLJ10210, FRMD4A	FERM domain containing 4A	NM_018027, hCT2311237.0, hCT2356813.0, hCT1952487.1	1554033_at, 1554034_a_at, 1560031_at, 208475_at, 208476_s_at, 225163_at, 225167_at, 225168_at	NP_060497.3, EAW86276.1, EAW86275.1, EAW86277.1
GeneID:441549	CDNF	10	14,861,251	14,879,983	18,732	-	1	4_A375_EGR1..1..1063	-1041	upstream	0	0	1	6	7	19	1	4_A375_EGR1..1	19	Gene CDNF	ARMETL1, CDNF	cerebral dopamine neurotrophic factor	NM_001029954, hCT2340537.0, hCT2340538.0, hCT2340539.0, hCT16692.3	1566896_at	NP_001025125.2, EAW86266.1, EAW86263.1, EAW86264.1, EAW86265.1
GeneID:51182	HSPA14	10	14,880,261	14,913,740	33,479	+	1	4_A375_EGR1..1..1063	783	in gene	0	0	1	6	7	19	1	4_A375_EGR1..1	19	Gene HSPA14	HSP70-4, MGC131990, HSPA14, HSP70L1	heat shock 70kDa protein 14	NM_016299, hCT2312265.1, hCT2343731.0, hCT2343732.0, hCT2343733.0, hCT16695.3	219212_at, 226887_at, 227650_at	NP_057383.2, EAW86261.1, EAW86258.1, EAW86259.1, EAW86260.1, EAW86262.1
GeneID:80013	FAM188A	10	15,820,175	15,902,519	82,344	-	2	1_A375_pNL7_minus_lncRNA_AR..1..830, 2_A375_pNL97_plus_lncRNA_AR..1..1127	-73, -9	upstream, upstream	1	1	0	13	14	3	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene FAM188A	my042, C10orf97, RP11-394I23.1, DERP5, FLJ13397, FAM188A, CARP, MST126, MSTP126	family with sequence similarity 188, member A	NM_024948, hCT2311201.0, hCT15276.3	1554509_a_at, 218297_at	NP_079224.1, EAW86233.1, EAW86234.1
GeneID:6251	RSU1	10	16,632,615	16,859,453	226,838	-	1	1_A375_pNL7_minus_lncRNA_AR..1..831	205065	in gene	1	0	0	15	14	2	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene RSU1	RSP-1, FLJ31034, RSU1	Ras suppressor protein 1	NM_152724, NM_012425, hCT2311535.0, hCT2311537.0, hCT2356799.0	1560937_at, 1569543_at, 201980_s_at, 215618_at, 230490_x_at	NP_689937.2, NP_036557.1, EAW86222.1, EAW86223.1, EAW86224.1
GeneID:8029	CUBN	10	16,865,965	17,171,816	305,851	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1128	15848	in gene	0	1	0	7	15	2	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene CUBN	CUBN, FLJ90747, gp280, MGA1, IFCR, FLJ90055	cubilin (intrinsic factor-cobalamin receptor)	NM_001081, hCT1821868.2	206775_at	NP_001072.2, EAW86221.1
GeneID:1787	TRDMT1	10	17,184,982	17,244,070	59,088	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1129, 4_A375_EGR1..1..1064	614, 550	in gene, in gene	0	1	1	15	14	17	1	4_A375_EGR1..1	17	Gene TRDMT1	RNMT1, MHSAIIP, TRDMT1, PuMet, DNMT2, DMNT2, PUMET, M.HsaIIP	tRNA aspartic acid methyltransferase 1	NM_004412	206308_at, 232121_at	NP_004403.1
GeneID:100507347	LOC100507347	10	17,256,245	17,268,897	12,652	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1130, 4_A375_EGR1..1..1065	-2495, -2479	upstream, upstream	0	1	1	11	20	22	1	4_A375_EGR1..1	22	Gene LOC100507347		hypothetical LOC100507347	XR_111052, XR_109013, XR_114342		
GeneID:7431	VIM	10	17,270,258	17,279,592	9,334	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1130, 2_A375_pNL97_plus_lncRNA_AR..1..1131, 4_A375_EGR1..1..1065	1134, 10478, 1118	in gene, downstream, in gene	0	1	1	9.5	17.5	14	2	4_A375_EGR1..1	22	Gene VIM	VIM, FLJ36605	vimentin	NM_003380, hCT13718.2, hCT1964478.1	1555938_x_at, 201426_s_at	NP_003371.2, EAW86215.1, EAW86216.1
GeneID:338596	ST8SIA6	10	17,362,676	17,496,254	133,578	-	1	4_A375_EGR1..1..1066	446	in gene	0	0	1	7	7	16	1	4_A375_EGR1..1	16	Gene ST8SIA6	SIAT8F, ST8SIA6, SIA8F, ST8SIA-VI	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	NM_001004470		NP_001004470.1
GeneID:8027	STAM	10	17,686,124	17,757,907	71,783	+	2	1_A375_pNL7_minus_lncRNA_AR..1..832, 2_A375_pNL97_plus_lncRNA_AR..1..1132	-44, -44	upstream, upstream	1	1	0	18	22	11	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene STAM	STAM1, STAM, DKFZp686J2352	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	NM_003473, hCT2356797.0, hCT12506.2, hCT1964292.1	203544_s_at	NP_003464.1, EAW86208.1, EAW86207.1, EAW86209.1
GeneID:387640	C10orf140	10	21,802,407	21,814,611	12,204	-	1	1_A375_pNL7_minus_lncRNA_AR..1..833	-141	upstream	1	0	0	14	13	6	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene C10orf140	FLJ45187, C10orf140, DKFZp761J229, DLN-1	chromosome 10 open reading frame 140	NM_207371, hCT2360305.0	1559265_at, 1559266_s_at	NP_997254.3, EAW86167.1
GeneID:8028	MLLT10	10	21,823,102	22,032,554	209,452	+	1	1_A375_pNL7_minus_lncRNA_AR..1..833	-8350	upstream	1	0	0	14	13	6	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene MLLT10	DKFZp686E10210, MLLT10, MGC75086, AF10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	NM_004641, hCT1967491.1, hCT2311272.0, hCT2311273.0, hCT2311275.0, hCT1964505.1	1563321_s_at, 205408_at, 216480_x_at, 216503_s_at, 216506_x_at, 216509_x_at, 225992_at, 230122_at, 238257_at	NP_004632.1, EAW86163.1, EAW86161.1, EAW86162.1, EAW86164.1, EAW86165.1
GeneID:100499489	LOC100499489	10	22,724,354	22,726,858	2,504	-	1	4_A375_EGR1..1..1068	746	in gene	0	0	1	9	12	15	1	4_A375_EGR1..1	15	Gene LOC100499489		hypothetical LOC100499489	NR_036533		
GeneID:100289455	LOC100289455	10	22,726,015	22,727,388	1,373	+	1	4_A375_EGR1..1..1068	97	in gene	0	0	1	9	12	15	1	4_A375_EGR1..1	15	Gene LOC100289455		hypothetical LOC100289455	XR_111046, XR_109016, XR_114347		
GeneID:56243	KIAA1217	10	23,983,675	24,836,772	853,097	+	4	1_A375_pNL7_minus_lncRNA_AR..1..835, 2_A375_pNL97_plus_lncRNA_AR..1..1133, 2_A375_pNL97_plus_lncRNA_AR..1..1134, 4_A375_EGR1..1..1069	95557, 95541, 131893, 641141	in gene, in gene, in gene, in gene	1	1	1	19.33	20.33	5.67	3	1_A375_pNL7_minus_lncRNA_AR..1	41	Gene KIAA1217	SKT, DKFZp761L0424, MGC31990, KIAA1217	KIAA1217	NM_001098500, NM_001098501, NM_019590, hCT2348746.0, hCT2348747.0, hCT2356803.0	1554438_at, 1560115_a_at, 1562988_at, 231807_at, 232046_at, 232762_at	NP_001091970.1, NP_001091971.1, NP_062536.2, EAW86123.1, EAW86124.1, EAW86125.1
GeneID:100128811	LOC100128811	10	25,447,001	25,465,205	18,204	-	4	1_A375_pNL7_minus_lncRNA_AR..1..836, 1_A375_pNL7_minus_lncRNA_AR..1..837, 2_A375_pNL97_plus_lncRNA_AR..1..1135, 2_A375_pNL97_plus_lncRNA_AR..1..1136	1621, 357, 1621, 501	in gene, in gene, in gene, in gene	1	1	0	29	35	16	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene LOC100128811		hypothetical LOC100128811	NR_027333		
GeneID:57512	GPR158	10	25,464,290	25,891,156	426,866	+	4	1_A375_pNL7_minus_lncRNA_AR..1..836, 1_A375_pNL7_minus_lncRNA_AR..1..837, 2_A375_pNL97_plus_lncRNA_AR..1..1135, 2_A375_pNL97_plus_lncRNA_AR..1..1136	-706, 558, -706, 414	upstream, in gene, upstream, in gene	1	1	0	29	35	16	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene GPR158	GPR158, FLJ37601, RP11-59G22.1, KIAA1136	G protein-coupled receptor 158	NM_020752	232195_at	NP_065803.2
GeneID:53904	MYO3A	10	26,223,002	26,501,465	278,463	+	1	4_A375_EGR1..1..1070	263494	downstream	0	0	1	3	1	16	1	4_A375_EGR1..1	16	Gene MYO3A	MYO3A, DFNB30	myosin IIIA	NM_017433, hCT15737.3	1569186_at, 221400_at, 244384_at	NP_059129.3, EAW86105.1
GeneID:2572	GAD2	10	26,505,236	26,593,491	88,255	+	1	4_A375_EGR1..1..1070	1260	in gene	0	0	1	3	1	16	1	4_A375_EGR1..1	16	Gene GAD2	GAD65, GAD2, MGC161605, MGC161607	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	NM_000818, NM_001134366, hCT2310957.0, hCT2356808.0, hCT14541.3, hCT1964380.1	1566801_at, 206780_at, 211284_at, 216651_s_at, 243285_at	NP_000809.1, NP_001127838.1, EAW86101.1, EAW86102.1, EAW86103.1, EAW86104.1
GeneID:10006	ABI1	10	27,035,525	27,150,016	114,491	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1137, 4_A375_EGR1..1..1071	240, 446	in gene, in gene	0	1	1	9	16	14	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ABI1	SSH3BP1, E3B1, NAP1BP, SSH3BP, ABI1, ABI-1	abl-interactor 1	NM_001012750, NM_001012751, NM_001012752, NM_001178116, NM_001178119, NM_001178120, NM_001178121, NM_001178122, NM_001178123, NM_001178124, NM_001178125, NM_005470, hCT2311440.0, hCT2311441.0, hCT2311443.0, hCT2311444.0, hCT2311445.0, hCT2356812.0, hCT163	1559890_a_at, 209027_s_at, 209028_s_at	NP_001012768.1, NP_001012769.1, NP_001012770.1, NP_001171587.1, NP_001171590.1, NP_001171591.1, NP_005461.2, NP_001171592.1, NP_001171593.1, NP_001171594.1, NP_001171595.1, NP_001171596.1, EAW86077.1, EAW86078.1, EAW86079.1, EAW86080.1, EAW86081.1, EAW860
GeneID:10730	YME1L1	10	27,399,383	27,443,321	43,938	-	1	1_A375_pNL7_minus_lncRNA_AR..1..838	-71	upstream	1	0	0	13	11	10	1	1_A375_pNL7_minus_lncRNA_AR..1	13	Gene YME1L1	PAMP, MEG4, FTSH, YME1L, YME1L1	YME1-like 1 (S. cerevisiae)	NM_014263, NM_139312, hCT16385.3, hCT1962986.1, hCT1962987.1, hCT1962988.1, hCT1962989.1	201351_s_at, 201352_at, 216304_x_at, 232216_at	NP_055078.1, NP_647473.1, EAW86068.1, EAW86069.1, EAW86071.1, EAW86072.1, EAW86070.1
GeneID:84930	MASTL	10	27,443,753	27,475,848	32,095	+	1	1_A375_pNL7_minus_lncRNA_AR..1..838	-361	upstream	1	0	0	13	11	10	1	1_A375_pNL7_minus_lncRNA_AR..1	13	Gene MASTL	GWL, RP11-85G18.2, FLJ14813, THC2, MASTL, GREATWALL	microtubule associated serine/threonine kinase-like	NM_001172303, NM_032844, NM_001172304, hCT2311496.0, hCT2311498.0, hCT2356780.0, hCT16387.2	228468_at	NP_001165774.1, NP_116233.2, NP_001165775.1, EAW86064.1, EAW86065.1, EAW86066.1, EAW86067.1
GeneID:100288039	LOC100288039	10	27,551,925	27,602,834	50,909	+	1	4_A375_EGR1..1..1073	-10161	upstream	0	0	1	11	13	12	1	4_A375_EGR1..1	12	Gene LOC100288039		armadillo repeat-containing protein 4-like	XM_002342965		XP_002343006.1
GeneID:22931	RAB18	10	27,793,249	27,829,099	35,850	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1138	-33	upstream	0	1	0	12	23	12	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RAB18	RAB18LI1, RAB18	RAB18, member RAS oncogene family	NM_021252, hCT2311501.0, hCT15904.3	223336_s_at, 224377_s_at, 224787_s_at, 229398_at	NP_067075.1, EAW86055.1, EAW86054.1
GeneID:220929	ZNF438	10	31,133,563	31,320,866	187,303	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1141	98	in gene	0	1	0	9	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ZNF438	bA330O11.1, ZNF438, MGC126671, FLJ32761	zinc finger protein 438	NM_182755, NM_001143766, NM_001143767, NM_001143768, NM_001143769, NM_001143770, NM_001143771, NR_026560, hCT2356816.0, hCT1822494.2, hCT1984410.1, hCT1984411.1	229743_at, 244752_at	NP_877432.1, NP_001137238.1, NP_001137239.1, NP_001137240.1, NP_001137241.1, NP_001137242.1, NP_001137243.1, EAW85995.1, EAW85996.1, EAW85997.1, EAW85998.1
GeneID:100507663	LOC100507663	10	31,310,000	31,311,746	1,746	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1141	-9022	upstream	0	1	0	9	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100507663		hypothetical protein LOC100507663	XM_003119464, XM_003118621, XM_003120653		XP_003119512.1, XP_003118669.1, XP_003120701.1
GeneID:80314	EPC1	10	32,557,859	32,636,113	78,254	-	1	1_A375_pNL7_minus_lncRNA_AR..1..840	945	in gene	1	0	0	13	9	5	1	1_A375_pNL7_minus_lncRNA_AR..1	13	Gene EPC1	Epl1, EPC1, DKFZp781P2312	enhancer of polycomb homolog 1 (Drosophila)	NM_025209, hCT2310903.0, hCT2310904.0, hCT2356814.0, hCT2356815.0	223875_s_at, 225417_at, 234989_s_at, 238633_at	NP_079485.1, EAW85972.1, EAW85973.1, EAW85974.1, EAW85975.1
GeneID:8829	NRP1	10	33,466,419	33,623,833	157,414	-	1	4_A375_EGR1..1..1076	-407	upstream	0	0	1	12	10	16	1	4_A375_EGR1..1	16	Gene NRP1	VEGF165R, DKFZp686A03134, BDCA4, NP1, CD304, DKFZp781F1414, NRP1, NRP	neuropilin 1	NM_003873, NM_001024628, NM_001024629, hCT2311143.0, hCT2311147.0, hCT10139.3, hCT1966627.1	1561365_at, 210510_s_at, 210615_at, 212298_at	NP_003864.4, NP_001019799.1, NP_001019800.1, EAW85942.1, EAW85943.1, EAW85944.1, EAW85945.1
GeneID:56288	PARD3	10	34,398,488	35,104,253	705,765	-	3	1_A375_pNL7_minus_lncRNA_AR..1..841, 2_A375_pNL97_plus_lncRNA_AR..1..1143, 2_A375_pNL97_plus_lncRNA_AR..1..1144	579613, 579597, 104765	in gene, in gene, in gene	1	1	0	13	21	2.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene PARD3	SE2-5LT1, ASIP, Bazooka, SE2-5L16, PAR3, SE2-5T2, FLJ21015, PARD3A, PARD3, Baz, PAR3alpha	par-3 partitioning defective 3 homolog (C. elegans)	NM_001184785, NM_001184786, NM_001184787, NM_001184788, NM_001184789, NM_001184790, NM_001184791, NM_001184792, NM_001184793, NM_001184794, NM_019619, hCT2356794.0, hCT12502.3, hCT1955362.1	210094_s_at, 221280_s_at, 221526_x_at, 221527_s_at	NP_001171714.1, NP_001171715.1, NP_001171716.1, NP_001171717.1, NP_001171718.1, NP_001171719.1, NP_062565.2, NP_001171720.1, NP_001171721.1, NP_001171722.1, NP_001171723.1, EAW85932.1, EAW85933.1, EAW85934.1
GeneID:8453	CUL2	10	35,298,798	35,379,294	80,496	-	2	1_A375_pNL7_minus_lncRNA_AR..1..842, 2_A375_pNL97_plus_lncRNA_AR..1..1145	-194, -162	upstream, upstream	1	1	0	40	32	5	1	1_A375_pNL7_minus_lncRNA_AR..1	40	Gene CUL2	MGC131970, CUL2	cullin 2	NM_003591	203078_at, 203079_s_at	NP_003582.2
GeneID:8325	FZD8	10	35,927,177	35,930,362	3,185	-	2	1_A375_pNL7_minus_lncRNA_AR..1..843, 2_A375_pNL97_plus_lncRNA_AR..1..1146	-1036, -950	upstream, upstream	1	1	0	15	15	5	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene FZD8	FZD8, hFZ8, FZ-8	frizzled homolog 8 (Drosophila)	NM_031866, hCT16417.2	216587_s_at, 224325_at, 227405_s_at	NP_114072.1, EAW85909.1
GeneID:7581	ZNF33A	10	38,299,578	38,348,995	49,417	+	1	4_A375_EGR1..1..1077	390	in gene	0	0	1	9	15	17	1	4_A375_EGR1..1	17	Gene ZNF33A	FLJ23404, KOX5, ZNF33A, ZZAPK, NF11A, KIAA0065, KOX2, ZNF11A, ZNF33, ZNF11, KOX31	zinc finger protein 33A	NM_006974, NM_006954, hCT2311132.1, hCT2311133.1, hCT2349098.0, hCT2349099.0, hCT2349100.0, hCT2349101.0, hCT2349102.0	224276_at, 231684_at, 232673_at	NP_008905.1, NP_008885.1, EAW85888.1, EAW85889.1, EAW85893.1, EAW85894.1, EAW85890.1, EAW85891.1, EAW85892.1
GeneID:100505906	LOC100505906	10	43,247,312	43,265,069	17,757	+	1	4_A375_EGR1..1..1078	2672	in gene	0	0	1	3	8	24	1	4_A375_EGR1..1	24	Gene LOC100505906		hypothetical protein LOC100505906	XM_003118994, XM_003120655		XP_003119042.1, XP_003120703.1
GeneID:9790	BMS1	10	43,277,954	43,330,385	52,431	+	2	1_A375_pNL7_minus_lncRNA_AR..1..844, 2_A375_pNL97_plus_lncRNA_AR..1..1147	268, 238	in gene, in gene	1	1	0	16	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene BMS1	BMS1L, BMS1, KIAA0187	BMS1 homolog, ribosome assembly protein (yeast)	NM_014753, hCT2294229.0, hCT2294231.0, hCT2294232.0	203082_at	NP_055568.3, EAW86572.1, EAW86571.1, EAW86573.1
GeneID:5979	RET	10	43,572,517	43,625,799	53,282	+	1	4_A375_EGR1..1..1080	-4869	upstream	0	0	1	4	3	15	1	4_A375_EGR1..1	15	Gene RET	RET, RET-ELE1, CDHF12, PTC, MTC1, CDHR16, MEN2B, RET51, MEN2A, HSCR1	ret proto-oncogene	NM_020975, NM_020630, hCT2294252.0, hCT2294254.0, hCT2356837.0, hCT2356838.0, hCT2356839.0, hCT1808965.2, hCT1808966.1, hCT1981730.1, hCT1986712.1	205879_x_at, 211421_s_at, 215771_x_at	NP_066124.1, NP_065681.1, EAW86581.1, EAW86582.1, EAW86583.1, EAW86584.1, EAW86576.1, EAW86577.1, EAW86578.1, EAW86579.1, EAW86580.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.3185	HNRNPF	10	43,881,065	43,904,896	23,831	-	1	4_A375_EGR1..1..1082	11832	in gene	0	0	1	10	8	16	1	4_A375_EGR1..1	16	Gene HNRNPF	mcs94-1, MGC110997, OK/SW-cl.23, HNRNPF, HNRPF	heterogeneous nuclear ribonucleoprotein F	NM_001098208, NM_004966, NM_001098207, NM_001098205, NM_001098204, NM_001098206, hCT2356826.0, hCT2356827.0, hCT2356828.0, hCT1808961.3, hCT1966541.1	201376_s_at	NP_001091678.1, NP_004957.1, NP_001091677.1, NP_001091675.1, NP_001091674.1, NP_001091676.1, EAW86595.1, EAW86596.1, EAW86597.1, EAW86598.1, EAW86599.1
GeneID.220992	ZNF485	10	44,101,855	44,113,352	11,497	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1150, 4_A375_EGR1..1..1083	33, 353	in gene, in gene	0	1	1	11	16	15	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ZNF485	ZNF485		NM_145312, hCT2294206.2, hCT1778958.3	1552427_at	NP_660355.2, EAW86606.1, EAW86605.1
GeneID.7580	ZNF32	10	44,139,307	44,144,326	5,019	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1151	-10	upstream	0	1	0	9	16	3	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ZNF32	KOX30, ZNF32	zinc finger protein 32	NM_006973, NM_001005368, hCT2356831.0, hCT1787013.3, hCT1965682.1	209538_at	NP_008904.1, NP_001005368.1, EAW86609.1, EAW86610.1, EAW86611.1
GeneID.100130539	LOC100130539	10	44,788,204	44,790,179	1,975	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1152	8584	downstream	0	1	0	7	16	4	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100130539		hypothetical protein LOC100130539	XM_001724322, XM_001716390		XP_001724374.2, XP_001716442.2
GeneID.100507539	LOC100507539	10	46,951,472	46,966,835	15,363	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1154, 4_A375_EGR1..1..1085	-16, 18808	upstream, downstream	0	1	1	10	13.5	11.5	2	4_A375_EGR1..1	19	Gene LOC100507539		hypothetical LOC100507539	XR_110467		
GeneID.83849	SYT15	10	46,955,444	46,970,601	15,157	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1154, 4_A375_EGR1..1..1085	19145, 521	downstream, in gene	0	1	1	10	13.5	11.5	2	4_A375_EGR1..1	19	Gene SYT15	SYT15, CHR10SYT, sytXV	synaptotagmin XV	NM_031912, NM_181519, hCT1773017.3	1560878_at, 1560879_a_at	NP_114118.2, NP_852660.1, EAW54662.1
GeneID.9721	GPRIN2	10	46,993,546	47,000,568	7,022	+	1	4_A375_EGR1..1..1086	5606	in gene	0	0	1	10	8	19	1	4_A375_EGR1..1	19	Gene GPRIN2	GRIN2, GPRIN2, KIAA0514, MGC15171	G protein regulated inducer of neurite outgrowth 2	NM_014696	1554541_a_at, 206747_at	NP_055511.2
GeneID.57705	WDFY4	10	49,893,518	50,191,001	297,483	+	1	4_A375_EGR1..1..1089	60434	in gene	0	0	1	3	5	15	1	4_A375_EGR1..1	15	Gene WDFY4	KIAA1607, MGC45899, C10orf64, FLJ17416, WDFY4, MGC40604, FLJ38288, FLJ45748	WDFY family member 4	NM_020945	229597_s_at	NP_065996.1
GeneID.644168	DRGX	10	50,574,161	50,599,907	25,746	-	2	1_A375_pNL7_minus_lncRNA_AR..1..848, 2_A375_pNL97_plus_lncRNA_AR..1..1156	-6269, -6301	upstream, upstream	1	1	0	21	17	9	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene DRGX	PRRXL1, DRG11, DRGX	dorsal root ganglia homeobox	NM_001080520		NP_001073989.1
GeneID.1103	CHAT	10	50,817,141	50,873,150	56,009	+	2	1_A375_pNL7_minus_lncRNA_AR..1..849, 2_A375_pNL97_plus_lncRNA_AR..1..1157	-1973, -1909	upstream, upstream	1	1	0	26	27	8	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene CHAT	CMS1A, CHAT, CHOACTASE, CMS1A2	choline acetyltransferase	NM_020984, NM_020549, NM_020985, NM_020986, NM_001142929, NM_001142933, NM_001142934, hCT2277816.0, hCT2277817.0, hCT2277818.0, hCT2277819.0, hCT2277821.0, hCT2349376.0, hCT2349377.0	221197_s_at	NP_066264.3, NP_065574.3, NP_066265.3, NP_066266.3, NP_001136401.1, NP_001136405.1, NP_001136406.1, EAW93086.1, EAW93087.1, EAW93088.1, EAW93089.1, EAW93090.1, EAW93091.1, EAW93092.1
GeneID.6572	SLC18A3	10	50,818,347	50,820,766	2,419	+	2	1_A375_pNL7_minus_lncRNA_AR..1..849, 2_A375_pNL97_plus_lncRNA_AR..1..1157	-3179, -3115	upstream, upstream	1	1	0	26	27	8	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SLC18A3	MGC12716, SLC18A3, VACHT	solute carrier family 18 (vesicular acetylcholine), member 3	NM_003055, hCT23548.3	207150_at	NP_003046.2, EAW93093.1
GeneID.282966	C10orf53	10	50,887,684	50,916,956	29,272	+	1	4_A375_EGR1..1..1090	-4	upstream	0	0	1	9	8	17	1	4_A375_EGR1..1	17	Gene C10orf53	C10orf53, FLJ60598	chromosome 10 open reading frame 53	NM_182554, NM_001042427, hCT2277820.1, hCT2344966.0, hCT2349391.0	1555051_at, 239998_at	NP_872360.2, NP_001035892.1, EAW93083.1, EAW93084.1, EAW93085.1
GeneID.55753	OGDHL	10	50,942,687	50,970,425	27,738	-	1	1_A375_pNL7_minus_lncRNA_AR..1..850	-71	upstream	1	0	0	15	15	4	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene OGDHL	OGDHL		NM_018245, NM_001143996, NM_001143997, hCT2277591.0, hCT23932.3, hCT1966504.1	219277_s_at	NP_060715.2, NP_001137468.1, NP_001137469.1, EAW93080.1, EAW93081.1, EAW93082.1
GeneID.653252	TIMM23B	10	51,371,379	51,734,610	363,231	+	1	4_A375_EGR1..1..1091	200957	in gene	0	0	1	13	9	15	1	4_A375_EGR1..1	15	Gene TIMM23B	TIMM23B, bA592B15.7	translocase of inner mitochondrial membrane 23 homolog B (yeast)	XM_003118952, XM_003118954, XM_003118953		XP_003119000.1, XP_003119002.1, XP_003119001.1
GeneID.4477	MSMB	10	51,549,553	51,562,595	13,042	+	1	4_A375_EGR1..1..1091	22763	downstream	0	0	1	13	9	15	1	4_A375_EGR1..1	15	Gene MSMB	PSP57, IGBF, PN44, PSP94, PSP, PSP-94, MSP, MSPB, PRPS, HPC13, MSMB	microseminoprotein, beta-	NM_002443, NM_138634, hCT2256409.0, hCT2256410.0, hCT2256412.0	207430_s_at, 210297_s_at	NP_002434.1, NP_619540.1, EAW53863.1, EAW53864.1, EAW53865.1
GeneID.8031	NCOA4	10	51,565,108	51,590,734	25,626	+	1	4_A375_EGR1..1..1091	7226	in gene	0	0	1	13	9	15	1	4_A375_EGR1..1	15	Gene NCOA4	DKFZp762E1112, PTC3, NCOA4, ELE1, RFG, ARA70	nuclear receptor coactivator 4	NM_001145260, NM_001145261, NM_001145262, NM_001145263, NM_005437, hCT2256413.0, hCT2256414.0, hCT2256416.0, hCT2256417.0	210774_s_at	NP_001138732.1, NP_001138733.1, NP_005428.1, NP_001138734.1, NP_001138735.1, EAW53866.1, EAW53867.1, EAW53868.1, EAW53869.1
GeneID.259230	SGMS1	10	52,065,345	52,383,737	318,392	-	3	1_A375_pNL7_minus_lncRNA_AR..1..851, 1_A375_pNL7_minus_lncRNA_AR..1..852, 2_A375_pNL97_plus_lncRNA_AR..1..1158	153, -679, -695	in gene, upstream, upstream	1	1	0	19	20.5	6	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SGMS1	SGMS1, MOB1, TMEM23, hmob33, SMS1, MGC17342, MOB	sphingomyelin synthase 1	NM_147156, hCT2340901.0, hCT23547.4, hCT1658438.4, hCT1950129.1	212989_at	NP_671512.1, EAW80431.1, EAW80429.1, EAW80430.1, EAW80432.1
GeneID.5592	PRKG1	10	52,750,945	54,055,274	1,304,329	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1159	842015	in gene	0	1	0	12	20	2	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PRKG1	PGK, CGKI, cGKI-alpha, cGKI-BETA, DKFZp686K042, PRKG1B, PRKG1, FLJ36117, MGC71944, PRKGR1B, PKG	protein kinase, cGMP-dependent, type I	NM_001098512, NM_006258, hCT2350053.0, hCT2350054.0	207119_at, 211380_s_at	NP_001091982.1, NP_006249.1, EAW54140.1, EAW54141.1
GeneID.7019	TFAM	10	60,145,176	60,155,897	10,721	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1162, 4_A375_EGR1..1..1092	72, -8	in gene, upstream	0	1	1	8	19	17	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TFAM	TFAM, TCF6L2, TCF6, MTTF1, TCF6L1, mtTFA, TCF6L3	transcription factor A, mitochondrial	NM_003201, hCT2322020.0, hCT2322021.0, hCT31464.2, hCT1686512.1, hCT1957619.1	203176_s_at, 203177_x_at, 208541_x_at	NP_003192.1, EAW54172.1, EAW54171.1, EAW54173.1, EAW54174.1, EAW54175.1
GeneID.84457	PHYHIPL	10	60,936,348	61,007,534	71,186	+	1	4_A375_EGR1..1..1094	420	in gene	0	0	1	6	4	17	1	4_A375_EGR1..1	17	Gene PHYHIPL	PHYHIPL, KIAA1796	phytanoyl-CoA 2-hydroxylase interacting protein-like	NM_032439, NM_001143774, hCT2352836.0, hCT2352837.0, hCT32398.2	226623_at	NP_115815.2, NP_001137246.1, EAW54184.1, EAW54185.1, EAW54186.1
GeneID.8030	CCDC6	10	61,548,521	61,666,818	118,297	-	3	1_A375_pNL7_minus_lncRNA_AR..1..854, 2_A375_pNL97_plus_lncRNA_AR..1..1163, 4_A375_EGR1..1..1095	482, 482, 1314	in gene, in gene, in gene	1	1	1	49.5	51.5	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	98	Gene CCDC6	FLJ32286, H4, PTC, TPC, CCDC6, TST1, D10S170	coiled-coil domain containing 6	NM_005436, hCT2322339.0, hCT2322340.0	204716_at, 225010_at	NP_005427.2, EAW54196.1, EAW54197.1
GeneID.219623	TMEM26	10	63,166,401	63,213,208	46,807	-	1	4_A375_EGR1..1..1096	408	in gene	0	0	1	3	2	14	1	4_A375_EGR1..1	14	Gene TMEM26	DKFZp686D0912 8, MGC35010, TMEM26	transmembrane protein 26	NM_178505, hCT2321991.1, hCT1643216.3	1555025_at	NP_848600.2, EAW54220.1, EAW54219.1
GeneID.84890	ADO	10	64,564,516	64,568,239	3,723	+	1	1_A375_pNL7_minus_lncRNA_AR..1..856	-324	upstream	1	0	0	15	7	2	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene ADO	DKFZp564C046, ADO, FLJ14547, C10orf22	2-aminoethanethiol (cysteamine) dioxygenase	NM_032804, hCT2322461.0, hCT2322463.0, hCT1641864.3	212500_at, 212502_at, 229409_s_at	NP_116193.2, EAW54237.1, EAW54235.1, EAW54236.1
GeneID.1959	EGR2	10	64,571,756	64,578,927	7,171	-	1	1_A375_pNL7_minus_lncRNA_AR..1..856	14735	downstream	1	0	0	15	7	2	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene EGR2	KROX20, AT591, FLJ14547, CMT4E, DKFZp686J1957, CMT1D, EGR2	early growth response 2	NM_000399, NM_001136177, NM_001136178, NM_001136179, hCT2352833.0, hCT31468.1	205249_at	NP_000390.2, NP_001129649.1, NP_001129650.1, NP_001129651.1, EAW54238.1, EAW54239.1
GeneID.221035	REEP3	10	65,281,123	65,384,883	103,760	+	1	4_A375_EGR1..1..1097	285	in gene	0	0	1	5	12	14	1	4_A375_EGR1..1	14	Gene REEP3	REEP3, MGC87479, C10orf74	receptor accessory protein 3	NM_001001330, hCT1957625.1	225785_at, 235016_at	NP_001001330.1, EAW54246.1
GeneID.23411	SIRT1	10	69,644,427	69,678,147	33,720	+	1	4_A375_EGR1..1..1099	-123	upstream	0	0	1	11	12	22	1	4_A375_EGR1..1	22	Gene SIRT1	SIR2L1, SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	NM_012238, NM_001142498, hCT2322197.0, hCT23494.2	218878_s_at	NP_036370.2, NP_001135970.1, EAW54258.1, EAW54259.1
GeneID.84665	MYPN	10	69,869,250	69,971,774	102,524	+	2	1_A375_pNL7_minus_lncRNA_AR..1..858, 1_A375_pNL7_minus_lncRNA_AR..1..859	26974, 44288	in gene, in gene	1	0	0	19	9	2	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene MYPN	MYOP, MYPN	myopalladin	NM_032578, hCT2322199.0, hCT24046.3	235387_at	NP_115967.2, EAW54268.1, EAW54267.1
GeneID.55680	RUFY2	10	70,103,275	70,167,051	63,776	-	2	1_A375_pNL7_minus_lncRNA_AR..1..860, 2_A375_pNL97_plus_lncRNA_AR..1..1167	107, 107	in gene, in gene	1	1	0	29	28	9	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene RUFY2	ZFYVE13, FLJ10063, RABIP4R, KIAA1537, RUFY2	RUN and FYVE domain containing 2	NM_001042417, NM_017987, hCT2322274.0, hCT2322278.0, hCT2352816.0, hCT2352817.0, hCT1958442.1, hCT1958443.1	1554133_at, 1569630_a_at, 219957_at, 233191_at, 233192_s_at, 235345_at, 238550_at	NP_001035882.1, NP_060457.4, EAW54291.1, EAW54292.1, EAW54293.1, EAW54294.1, EAW54290.1, EAW54295.1
GeneID.1763	DNA2	10	70,173,821	70,231,879	58,058	-	3	1_A375_pNL7_minus_lncRNA_AR..1..860, 2_A375_pNL97_plus_lncRNA_AR..1..1167, 4_A375_EGR1..1..1100	64935, 64935, 359	downstream, downstream, in gene	1	1	1	19	15.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene DNA2	DNA2L, MGC133297, DNA2, KIAA0083, FLJ10063	DNA replication helicase 2 homolog (yeast)	NM_001080449	213647_at	NP_001073918.1
GeneID.80312	TET1	10	70,320,117	70,454,239	134,122	+	2	1_A375_pNL7_minus_lncRNA_AR..1..861, 4_A375_EGR1..1..1101	171, -5	in gene, upstream	1	0	1	14	12	15	1	4_A375_EGR1..1	15	Gene TET1	FLJ10839, KIAA1676, CXXC6, FLJ41442, LCX, bA119F7.1, TET1	tet oncogene 1	NM_030625, hCT2348108.0	228906_at	NP_085128.2, EAW54299.1
GeneID.79009	DDX50	10	70,661,034	70,706,603	45,569	+	2	1_A375_pNL7_minus_lncRNA_AR..1..862, 2_A375_pNL97_plus_lncRNA_AR..1..1168	54742, 54774	downstream, downstream	1	1	0	19	18	13	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene DDX50	DDX50, GUB, GU2, MGC3199, RH-II/GuB	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	NM_024045, hCT10434.2	1566814_at, 1566815_a_at, 221699_s_at	NP_076950.1, EAW54304.1
GeneID.9188	DDX21	10	70,715,892	70,744,279	28,387	+	3	1_A375_pNL7_minus_lncRNA_AR..1..862, 2_A375_pNL97_plus_lncRNA_AR..1..1168, 2_A375_pNL97_plus_lncRNA_AR..1..1169	-116, -84, 32620	upstream, upstream, downstream	1	1	0	14	17.5	8.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene DDX21	RH-II/GU, DDX21, GURDB, GUA, DKFZp686F2117 2, RH-II/GuA	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	NM_004728, hCT2322659.1, hCT2350250.0, hCT9884.3	208152_s_at, 224654_at	NP_004719.2, EAW54307.1, EAW54305.1, EAW54306.1
GeneID.100507126	LOC100507126	10	70,744,076	70,762,819	18,743	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1169	14307	in gene	0	1	0	9	17	4	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC100507126		hypothetical LOC100507126	XR_111072, XR_110410, XR_114373		
GeneID.26128	KIAA1279	10	70,748,477	70,776,739	28,262	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1169	35	in gene	0	1	0	9	17	4	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene KIAA1279	KBP, DKFZp586B0923, TTC20, KIAA1279	KIAA1279	NM_015634, hCT9885.2	212453_at	NP_056449.1, EAW54308.1
GeneID.9559	VPS26A	10	70,883,908	70,932,617	48,709	+	1	1_A375_pNL7_minus_lncRNA_AR..1..863	56028	downstream	1	0	0	24	20	14	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene VPS26A	PEP8A, VPS26A, HB58, FLJ12930, VPS26, Hbeta58	vacuolar protein sorting 26 homolog A (S. pombe)	NM_004896, NM_001035260, hCT2322666.0, hCT16384.3, hCT1961896.1	201807_at, 243316_x_at	NP_004887.2, NP_001030337.1, EAW54311.1, EAW54312.1, EAW54313.1
GeneID.6832	SUPV3L1	10	70,939,993	70,968,849	28,856	+	1	1_A375_pNL7_minus_lncRNA_AR..1..863	-57	upstream	1	0	0	24	20	14	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene SUPV3L1	SUPV3L1, SUV3	suppressor of var1, 3-like 1 (S. cerevisiae)	NM_003171, hCT2322671.0, hCT16382.3	212894_at	NP_003162.2, EAW54314.1, EAW54315.1
GeneID.23555	TSPAN15	10	71,211,226	71,267,423	56,197	+	2	4_A375_EGR1..1..1102, 4_A375_EGR1..1..1103	41542, 54726	in gene, in gene	0	0	1	4	8	13	2	4_A375_EGR1..1	13	Gene TSPAN15	NET7, 2700063A19Rik, TSPAN15, TM4SF15, NET-7	tetraspanin 15	NM_012339, hCT2352838.0, hCT14177.2	218693_at	NP_036471.1, EAW54327.1, EAW54326.1
GeneID.50674	NEUROG3	10	71,331,791	71,333,210	1,419	-	2	1_A375_pNL7_minus_lncRNA_AR..1..864, 2_A375_pNL97_plus_lncRNA_AR..1..1170	5498, 5514	downstream, downstream	1	1	0	21	16	6	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene NEUROG3	ngn3, NEUROG3, Atoh5, Math4B, bHLHa7	neurogenin 3	NM_020999, hCT1826614.0	207965_at	NP_066279.2, EAW54328.1
GeneID.1305	COL13A1	10	71,561,644	71,718,904	157,260	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1171	67748	in gene	0	1	0	10	16	2	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene COL13A1	COL13A1, FLJ42485, COLXIIIA1	collagen, type XIII, alpha 1	NM_001130103, NM_080798, NM_080800, NM_080801, NM_080802, NM_080805, hCT2322618.0, hCT2322619.0, hCT2322620.0, hCT2322621.0, hCT2322622.0, hCT2322623.0, hCT2322624.0, hCT2322625.0, hCT2322626.0, hCT2322627.0, hCT2322628.0, hCT2322629.0, hCT2322630.0, hCT2	208535_x_at, 211343_s_at, 211809_x_at	NP_001123575.1, NP_542988.3, NP_542990.3, NP_542991.3, NP_542992.3, NP_542995.3, EAW54334.1, EAW54335.1, EAW54336.1, EAW54342.1, EAW54343.1, EAW54344.1, EAW54345.1, EAW54346.1, EAW54333.1, EAW54337.1, EAW54338.1, EAW54339.1, EAW54340.1, EAW54341.1, EAW543
GeneID.8879	SGPL1	10	72,575,704	72,640,946	65,242	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1172	520	in gene	0	1	0	6	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SGPL1	SPL, KIAA1252, SGPL1, FLJ13811	sphingosine-1-phosphate lyase 1	NM_003901, hCT14890.3	208381_s_at, 212321_at, 212322_at	NP_003892.2, EAW54414.1
GeneID.64072	CDH23	10	73,156,691	73,575,704	419,013	+	2	1_A375_pNL7_minus_lncRNA_AR..1..865, 2_A375_pNL97_plus_lncRNA_AR..1..1173	398509, 398477	in gene, in gene	1	1	0	32	42	9	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene CDH23	KIAA1774, DKFZp434P2350, CDHR23, FLJ00233, KIAA1812, FLJ36499, MGC102761, USH1D, CDH23	cadherin-related 23	NM_022124, NM_052836, NM_001171930, NM_001171931, NM_001171932, NM_001171933, NM_001171934, NM_001171935, NM_001171936, hCT2322700.0, hCT2322701.0, hCT2322702.0, hCT2322703.0, hCT2322704.0, hCT2322705.0, hCT2322706.0	1552436_a_at, 224527_at, 232845_at, 232846_s_at	NP_071407.4, NP_443068.1, NP_001165401.1, NP_001165402.1, NP_001165403.1, NP_001165404.1, NP_001165405.1, NP_001165406.1, NP_001165407.1, EAW54426.1, EAW54427.1, EAW54428.1, EAW54429.1, EAW54430.1, EAW54431.1, EAW54432.1
GeneID.5660	PSAP	10	73,576,055	73,611,082	35,027	-	2	1_A375_pNL7_minus_lncRNA_AR..1..866, 2_A375_pNL97_plus_lncRNA_AR..1..1174	-9190, -9334	upstream, upstream	1	1	0	15	15	3	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene PSAP	FLJ00245, SAP1, MGC110993, PSAP, GLBA	prosaposin	NM_001042465, NM_002778, NM_001042466, hCT2322980.0, hCT2352843.0, hCT1826905.2	200866_s_at, 200871_s_at	NP_001035930.1, NP_002769.1, NP_001035931.1, EAW54436.1, EAW54437.1, EAW54438.1
GeneID.54541	DDIT4	10	74,033,677	74,035,797	2,120	+	4	2_A375_pNL97_plus_lncRNA_AR..1..1175, 4_A375_EGR1..1..1105, 4_A375_EGR1..1..1106, 4_A375_EGR1..1..1107	19, -365, -13, 2355	in gene, upstream, upstream, downstream	0	1	1	9.5	12.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene DDIT4	REDD-1, Dig2, RP11-442H21.1, DDIT4, REDD1, FLJ20500	DNA-damage-inducible transcript 4	NM_019058, hCT2322317.0, hCT2322318.0	202887_s_at	NP_061931.1, EAW54452.1, EAW54453.1

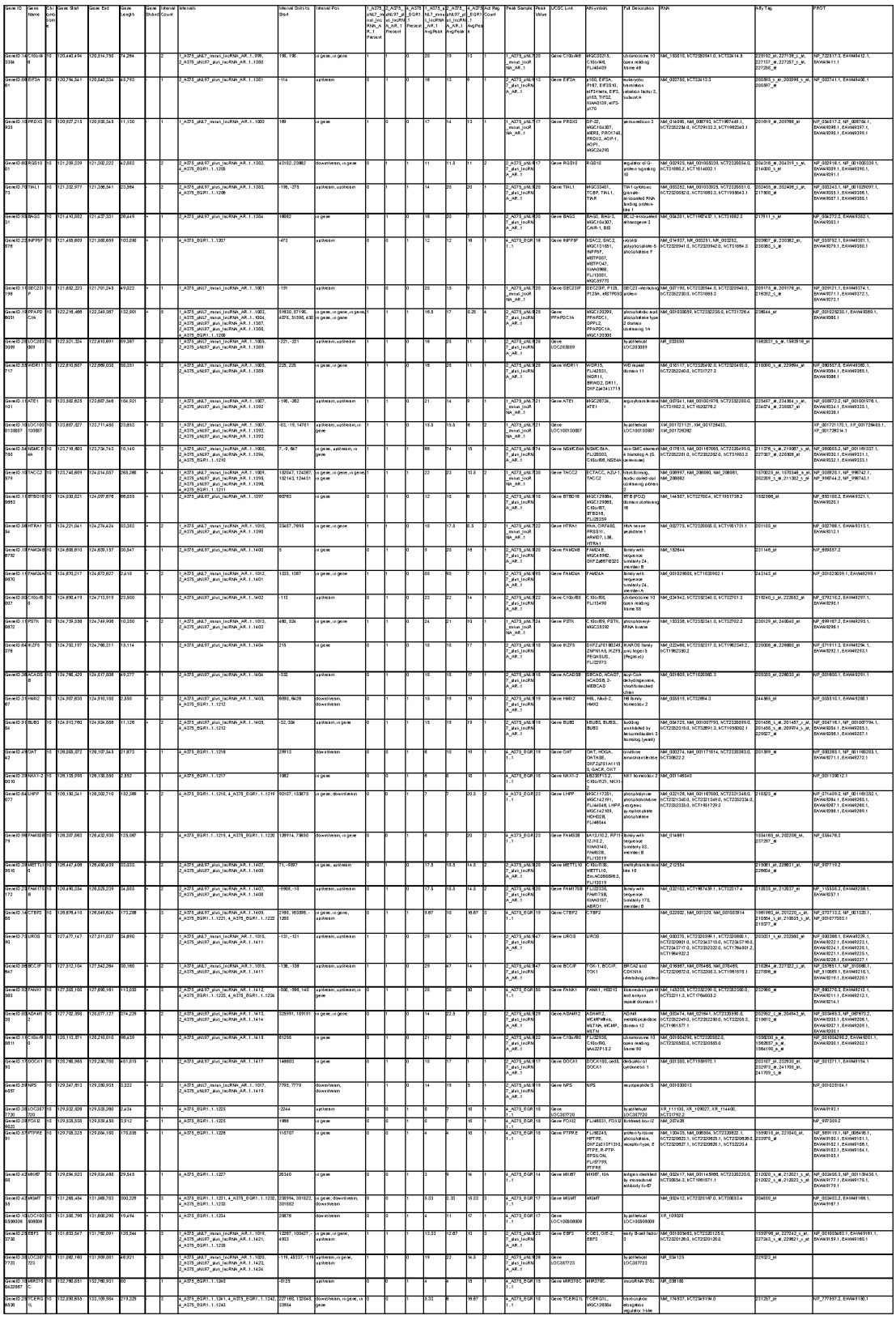
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Exon Count	Intervals	Intervals Distribution	Interval Positions	1_A375_2_A375_uNG7_myUG7_plus_lncRNA_R_1 Present	2_A375_2_A375_uNG7_plus_lncRNA_R_1 Present	3_A375_EGFR_1 Present	1_A375_plus_NG7_myUG7_plus_lncRNA_R_1 Avg Reads	2_A375_plus_NG7_myUG7_plus_lncRNA_R_1 Avg Reads	3_A375_EGFR_1 Avg Reads	Adj Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
GeneID:3467166	DNAJB12	10	74,092,565	74,114,907	22,319	+	2	1_A375_uNG7_myUG7_plus_lncRNA_R_1_696, 2_A375_uNG7_plus_lncRNA_R_1_1178	299, 235	sr:gene, sr:gene	1	1	0	17	16	10	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	DNAJB12	DNAJB12, DNAJ (Hsp40) homolog, subfamily B, member 12	Dnaj (Hsp40) homolog, subfamily B, member 12	NM_001037762, NM_017606, NC_T2223550.0, NC_T2223599.0, NC_T2229247.0	2023893_at, 2023898_at, 2023897_s_at, 214339_at	NP_001032762.2, NP_060096.3, EAW64434.1, EAW64435.1, EAW64436.1
GeneID:3467233	PAPH1	10	74,266,973	74,356,702	89,727	-	2	1_A375_uNG7_myUG7_minus_lncRNA_R_1_686, 2_A375_uNG7_plus_lncRNA_R_1_1177	26, -20	sr:gene, upstream	1	1	0	25	28	14	1	2_A375_uNG7_plus_lncRNA_R_1	0.6	PAPH1	PAPH, PAPH1	acid phosphatase, 5-like	NM_001017992, NM_001142355, NM_001142356, NM_030917, NC_T2223245.0, NC_T2223549.0, NC_T2229212.0, NC_T1219244.3	207343_s_at	NP_001017992.1, NP_001138007.1, NP_001138008.1, NP_030902.2, EAW64455.1, EAW64456.1, EAW64457.1, EAW64458.1
GeneID:3467319	ECD	10	74,894,262	74,927,850	33,571	-	1	1_A375_uNG7_minus_lncRNA_R_1_689	61	sr:gene	1	0	0	16	14	12	1	1_A375_uNG7_minus_lncRNA_R_1	1.6	ECD	DCR2, HSD11, ECD	ecdysteroidesis homolog (Drosophila)	NM_007265, NM_001135752, NM_001135753, NM_020233, NC_T2223545.0, NC_T2229253.0, NC_T1203313.3	2020312_at	NP_009196.1, NP_001129224.1, NP_001129225.1, EAW64477.1, EAW64478.1
GeneID:3467982	FAM149B1	10	74,927,877	75,001,909	74,032	+	1	2_A375_uNG7_plus_lncRNA_R_1_699	-65	upstream	1	0	0	16	14	12	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	FAM149B1	FAM149B1, FAM149B1	family with sequence similarity 149, member B1	NM_175348	1560753_at, 215456_at, 215483_s_at, 213096_s_at, 235859_at	NP_775483.1
GeneID:3468133	ANXA11	10	75,135,169	75,172,541	37,372	-	1	a_A375_EGR1_1.1109	203	sr:gene	0	0	1	14	10	10	1	a_A375_EGR1_1.1	1.6	ANXA11	ANX11, ANXA11, SNX, SYNEXIN	annexin A11	NM_001136, NM_004039, NC_T2223534.2, NC_T1219233.2	201386_s_at, 209860_s_at	NP_001147.1, NP_004029.1, EAW64493.1, EAW64494.1
GeneID:3468490	ZMYND17	10	75,183,337	75,190,319	6,982	-	1	a_A375_EGR1_1.1109	19827	downstream	0	0	1	14	10	10	1	a_A375_EGR1_1.1	1.6	ZMYND17	FLJ10163, ZMYND17	zinc finger, MYND domain containing 17	NM_031024.3, NC_T1760680.1	1417_at	NP_001019764.1, EAW64495.1
GeneID:3468232	PPP3CB	10	75,196,955	75,235,702	39,219	-	2	1_A375_uNG7_minus_lncRNA_R_1_1176, 2_A375_uNG7_plus_lncRNA_R_1_1110	-99, 422	upstream, sr:gene	0	1	1	9.5	11	12.5	2	2_A375_uNG7_plus_lncRNA_R_1	1.7	PPP3CB	CAN2, CALNB2, PP2Bbeta, PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	NM_021132, NM_001142353, NM_001142354, NC_T2223539.0, NC_T2223579.0, NC_T2223633.0, NC_T9391.2, NC_T1953001.1	202432_at, 209517_at	NP_066955.1, NP_001138023.1, NP_001138024.1, EAW64497.1, EAW64498.1, EAW64500.1, EAW64501.1, EAW64498.1
GeneID:3468322	LOC100289187, LOC100507259	10	75,255,510	75,256,414	904	+	2	2_A375_uNG7_plus_lncRNA_R_1_1176, 2_A375_uNG7_plus_lncRNA_R_1_1110	580, -155	sr:gene, upstream	0	1	1	9.5	11	12.5	2	2_A375_uNG7_plus_lncRNA_R_1	1.7	Gene LOC100507259		hypothetical LOC100507259	XR_110417, XR_114350		
GeneID:3468198	USP54	10	75,257,256	75,335,403	78,137	-	2	2_A375_uNG7_plus_lncRNA_R_1_1175, 2_A375_uNG7_plus_lncRNA_R_1_1110	79661, 80072	downstream, downstream	0	1	1	9.3	11	12.3	2	2_A375_uNG7_plus_lncRNA_R_1	1.7	Gene USP54	C10orf29, bA137J10.3, bA137J10.4, FLJ37310, USP54	ubiquitin specific peptidase 54	NM_152586, NC_T2223525.1, NC_T1787639.4, NC_T1787570.4	227224_at, 230322_at	NP_689799.3, EAW64509.1, EAW64502.1, EAW64503.1
GeneID:3468322	ADK	10	75,310,965	75,469,060	558,096	+	1	2_A375_uNG7_plus_lncRNA_R_1_1160	25699	sr:gene	0	0	1	13	16	14	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene ADK	AK, ADK	adenosine kinase	NM_001123, NM_006721, NC_T2223553.2, NC_T2223594.2	204119_s_at, 204120_s_at	NP_001114.3, NP_006712.2, EAW64553.1, EAW64555.1
GeneID:3468322	MYST4	10	76,356,279	76,772,409	209,290	+	2	2_A375_uNG7_plus_lncRNA_R_1_671, 2_A375_uNG7_plus_lncRNA_R_1_1161	-11, -139	upstream, upstream	1	1	0	13	16	2	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene MYST4	FLJ90333, qkf, bA198, MORF, KIAA0383, MOZ4, MOZ2, DKFZp313G016 (pentagl	MYST histone acetyltransferase (monocytic leukemia) 4	NM_012330, NC_T2223600.0, NC_T2224599.0, NC_T1950422.1	1562239_at, 213574_s_at, 213575_at, 213462_s_at, 213462_x_at, 214486_x_at	NP_036462.2, EAW64599.1, EAW64577.1, EAW64578.1, EAW64580.1
GeneID:3468322	DUSP13	10	76,834,160	76,886,970	14,760	-	1	a_A375_EGR1_1.1111	1139	sr:gene	0	0	1	3	12	10	1	a_A375_EGR1_1.1	1.6	Gene DUSP13	MDSP, DUSP13A, DUSP13B, DUSP13, FLJ35405, BED.P, TMDP, SKRPA	dual specificity phosphatase 13	NM_001007721, NM_001007722, NM_001007723, NM_013994, NC_T2223623.0, NC_T1950618.1, NC_T1950417.1	219983_at	NP_001007721.1, NP_001007723.1, NP_001007724.1, NP_037443.3, EAW64581.1, EAW64584.1, EAW64582.1, EAW64583.1
GeneID:3468322	SNMDE	10	76,871,393	76,941,861	70,468	+	1	a_A375_EGR1_1.1111	3553	upstream	0	0	1	3	12	10	1	a_A375_EGR1_1.1	1.6	Gene SAMD8	SMD1, FLJ25932, SAMD8	sterile alpha motif domain containing 8	NM_001174136, NM_144990, NC_T2223697.1, NC_T2223930.0, NC_T2229961.0, NC_T1951183.3	242082_at	NP_001167671.1, NP_653261.1, EAW64585.1, EAW64586.1, EAW64587.1, EAW64588.1
GeneID:3468322	VDAC2	10	76,969,912	76,991,206	21,294	+	3	1_A375_uNG7_minus_lncRNA_R_1_672, 2_A375_uNG7_plus_lncRNA_R_1_1162, 2_A375_uNG7_plus_lncRNA_R_1_1112	593, 392, 25403	sr:gene, sr:gene, downstream	1	1	1	21.5	17	15.3	2	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene VDAC2	POR, FLJ23841, VDAC2	voltage-dependent anion channel 2	NM_001145153, NM_001145423, NM_003373, NC_T2223673, NC_T2223931.0, NC_T2229655.0, NC_T1950284.1, NC_T1950283.2, NC_T1950424.1, NC_T1950425.1	211662_s_at	NP_001137172.1, NP_001137173.1, NP_003363.2, EAW64571.1, EAW64572.1, EAW64573.1, EAW64589.1, EAW64570.1, EAW64574.1
GeneID:3468322	COMTD1	10	76,993,729	76,999,770	6,041	-	1	a_A375_EGR1_1.1112	436	sr:gene	0	0	1	7	8	15	1	a_A375_EGR1_1.1	1.6	Gene COMTD1	COMTD1, FLJ23941	catechol-O-methyltransferase domain containing	NM_144589, NC_T1950362, NC_T1950423.1	226870_at	NP_653160.2, EAW64576.1, EAW64578.1
GeneID:3468322	ZNF503	10	77,157,802	77,161,915	3,911	-	3	1_A375_uNG7_plus_lncRNA_R_1_1163, 2_A375_uNG7_plus_lncRNA_R_1_1156, 2_A375_uNG7_plus_lncRNA_R_1_1163	-102, -563, -1543	upstream, upstream, upstream	0	1	0	10	17.67	7	0	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene ZNF503	ZNF503, FLJ43745, NOL2-503	zinc finger protein 503	NM_032772, NC_T2223842.0, NC_T1950019.1, NC_T1950020.0	227195_at, 230864_at, 232178_at	NP_116181.2, EAW64560.1, EAW64579.1, EAW64561.1
GeneID:3468322	C10orf11	10	77,181,298	77,185,740	7,454	+	3	1_A375_uNG7_plus_lncRNA_R_1_1183, 2_A375_uNG7_plus_lncRNA_R_1_1164, 2_A375_uNG7_plus_lncRNA_R_1_1165	330, 610, 1770	sr:gene, sr:gene, sr:gene	1	1	0	10	17.67	7	3	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene C10orf11	FLJ90096, C10orf11, KCAN/DN243	chromosome 10 open reading frame 11	NR_026421, NM_024232		
GeneID:3468322	C10orf11	10	77,342,519	78,217,100	774,811	+	1	1_A375_uNG7_minus_lncRNA_R_1_673	-9175	upstream	1	0	0	17	11	5	1	1_A375_uNG7_minus_lncRNA_R_1	1.7	Gene C10orf11	C10orf11, C10orf11	chromosome 10 open reading frame 11	NM_020324, NC_T2345278.0, NC_T2345277.0, NC_T1950044	223703_at, 244168_at	NP_064515.1, EAW64598.1, EAW64565.1, EAW64567.1
GeneID:3468322	KCNAW1	10	78,829,539	79,297,877	468,218	+	12	1_A375_uNG7_minus_lncRNA_R_1_674, 1_A375_uNG7_minus_lncRNA_R_1_675, 1_A375_uNG7_minus_lncRNA_R_1_676, 1_A375_uNG7_minus_lncRNA_R_1_677, 1_A375_uNG7_minus_lncRNA_R_1_678, 1_A375_uNG7_minus_lncRNA_R_1_679, 2_A375_uNG7_plus_lncRNA_R_1_1158, 2_A375_uNG7_plus_lncRNA_R_1_1159, 2_A375_uNG7_plus_lncRNA_R_1_1160, 2_A375_uNG7_plus_lncRNA_R_1_1189, 2_A375_uNG7_plus_lncRNA_R_1_1190, 2_A375_uNG7_plus_lncRNA_R_1_1113	209207, 208853, 245001, 131753, 186007, 84886, 340381, 309209, 244989, 121823, 126509, 121663	sr:gene, sr:gene, sr:gene, sr:gene, sr:gene, sr:gene, sr:gene, sr:gene, sr:gene, sr:gene, sr:gene, sr:gene	1	1	1	10.22	19.11	6.33	9	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene KCNAW1	SLO, kiaA, KIAA1083, SHOCA, mSLO1, BKTM, SLO1, bK268A15.1, hCa1.1, SLO-ALPHA, DKFZp686K1427, KCA66M	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	NM_020347, NM_001012497, NM_001161382, NM_001161383, NC_T2232401.1, NC_T2232405.1, NC_T2232630.0, NC_T1940644, NC_T1963772.2, NC_T1963774.2	214101_s_at, 221303_s_at, 221844_s_at, 229614_at	NP_065233.2, NP_001012797.1, NP_001154824.1, NP_001154825.1, EAW64611.1, EAW64612.1, EAW64613.1, EAW64614.1, EAW64615.1, EAW64616.1
GeneID:3468322	DGS1	10	79,350,349	79,806,345	455,796	-	3	1_A375_uNG7_minus_lncRNA_R_1_681, 2_A375_uNG7_plus_lncRNA_R_1_1192, 2_A375_uNG7_plus_lncRNA_R_1_1114	77200, 77324, 682	sr:gene, sr:gene, sr:gene	1	1	1	14.3	17	17	2	1_A375_EGR1_1.1	2.2	Gene DGS1	KIAA0365, P-DGS, DGS, DGS1, P-DG, PDG	ditch, large homolog 5 (Drosophila)	NM_014977, NC_T2223730.0, NC_T2223816.0, NC_T2229702, NC_T1219236.2	231661_s_at, 219499_at	NP_054735.3, EAW64608.1, EAW64611.1, EAW64612.1
GeneID:3468322	LOC100289292	10	79,806,970	79,809,903	2,933	+	1	a_A375_EGR1_1.1114	674	upstream	0	0	1	9	9.5	22	1	a_A375_EGR1_1.1	1.6	Gene LOC100289292		hypothetical LOC100289292	NR_024563		
GeneID:3468322	POLR3A	10	79,734,907	79,769,266	34,291	-	5	1_A375_uNG7_minus_lncRNA_R_1_682, 2_A375_uNG7_plus_lncRNA_R_1_1193, 2_A375_uNG7_plus_lncRNA_R_1_1115	16, 16, -4270	sr:gene, sr:gene, upstream	1	1	1	19.3	19.5	16.5	2	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene POLR3A	RPC155, RPC1, POLR3A, hRPC155	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	NM_007055, NC_T1955.3	1564318_at, 227672_at, 231862_at	NP_009186.2, EAW64617.1
GeneID:3468322	RPS24	10	79,793,516	79,816,971	23,455	+	3	2_A375_uNG7_minus_lncRNA_R_1_682, 2_A375_uNG7_plus_lncRNA_R_1_1193, 2_A375_uNG7_plus_lncRNA_R_1_1115	-4235, -4236, 50	upstream, upstream, sr:gene	1	1	1	19.3	19.5	16.5	2	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene RPS24	EBS.3, RPS24, DKFZp686N1506	eyes absent homolog 324	NM_001142593, NM_001142592, NM_001142555, NM_033022, NM_001026, NM_001142554, NC_T2224249.0, NC_T2232452.0, NC_T2232459.0, NC_T2232494.0, NC_T2232496.0, NC_T2232497.0, NC_T2232498.0, NC_T1219727.2, NC_T1950418.1, NC_T1950419.1	1559570_at, 200891_s_at	NP_001129583.1, NP_001138754.1, NP_149852.1, NP_001139797.1, NP_001139798.1, NP_001139799.1, EAW64618.1, EAW64619.1, EAW64620.1, EAW64621.1, EAW64622.1, EAW64623.1, EAW64624.1, EAW64627.1, EAW64624.1, EAW64625.1
GeneID:3468322	LOC100507960	10	80,008,248	80,012,402	4,398	+	1	2_A375_uNG7_plus_lncRNA_R_1_1194	7866	downstream	0	1	0	16	21	8	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene LOC100132967	FLJ32712	hypothetical LOC100132967	XR_111879, XR_110434, XR_114387		
GeneID:3468322	LOC283850	10	80,703,685	80,827,305	124,122	-	4	1_A375_uNG7_minus_lncRNA_R_1_668, 2_A375_uNG7_plus_lncRNA_R_1_1196, 2_A375_uNG7_plus_lncRNA_R_1_1197, 2_A375_uNG7_plus_lncRNA_R_1_1117	94223, 93992, 27, -3979	sr:gene, sr:gene, upstream, upstream	1	1	1	15	17	9	3	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene LOC283850	MGC125551, FLJ44222	hypothetical LOC283850	NR_015429, NR_024229, NR_024451	1565745_s_at	
GeneID:3468322	ZMIZ1	10	80,826,792	81,076,265	247,490	+	8	2_A375_uNG7_plus_lncRNA_R_1_1197, 2_A375_uNG7_plus_lncRNA_R_1_1198, 2_A375_uNG7_plus_lncRNA_R_1_1199, 2_A375_uNG7_plus_lncRNA_R_1_1117, 2_A375_uNG7_minus_lncRNA_R_1_666, 2_A375_uNG7_plus_lncRNA_R_1_1200, 4_A375_EGR1_1.1116, 4_A375_EGR1_1.1119, 4_A375_EGR1_1.1120	-1980, 12938, 69200, 1992, 230264, 252200, 213446, 224643, 220545	upstream,sr:gene, sr:gene, sr:gene, downstream, sr:gene, sr:gene, sr:gene	1	1	1	13.5	15.66	10.5	8	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene ZMIZ1	KIAA1224, ZMIZ1, EMP10, Dyrk1b, EWA1224, TRAFP16, Rek17, Wiz, FLJ10341	zinc finger, MIZ-type containing 1	NM_020338, NC_T2232399.0, NC_T2232402.0, NC_T2232403.0, NC_T2232649.0, NC_T1940769.0, NC_T1950421.1	212124_at, 232369_at, 233982_at	NP_065071.1, EAW64640.1, EAW64641.1, EAW64642.1, EAW64643.1, EAW64644.1, EAW64645.1, EAW64646.1
GeneID:3468322	PPF	10	81,107,230	81,115,090	7,870	+	1	2_A375_uNG7_plus_lncRNA_R_1_1201	-52	upstream	0	1	0	12	17	7	1	2_A375_uNG7_plus_lncRNA_R_1	1.7	Gene PRF	CYP2, PPF, MGC117307, CyP-D, FLJ40798	peptidylprolyl isomerase F	NM_005729, NC_T2232408.0, NC_T2232436.0, NC_T2232410.0, NC_T1970.1	201429_at, 201430_s_at	NP_005720.1, EAW64648.1, EAW64647.1, EAW64648.1
GeneID:3468322	ZCCHC24	10	81,142,081	81,203,353	60,302	-	3	1_A375_uNG7_minus_lncRNA_R_1_687, 1_A375_uNG7_minus_lncRNA_R_1_688, 2_A375_uNG7_plus_lncRNA_R_1_1121	7447, -249, 6871	sr:gene, upstream, sr:gene	1	0	1	17.33	14.67	12.67	3	1_A375_uNG7_minus_lncRNA_R_1	1.6	Gene ZCCHC24	ZCCHC24, C10orf56, FLJ40756	zinc finger, CCHC domain containing 24	NM_152387, NC_T2232474.0, NC_T1140777.2	212419_at, 212423_at	NP_689156.2, EAW64650.1, EAW64649.1
GeneID:3468322	LOC100289974	10	81,884,454	81,891,557	29,003	+	2	1_A375_uNG7_minus_lncRNA_R_1_689, 2_A375_uNG7_plus_lncRNA_R_1_1202	242, -110	sr:gene, upstream	1	1	0	16	26	12	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene LOC100289974	MGC50059, FLJ97799	BMS1 homolog, ribosome assembly protein (yeast) pseudogene	NR_033837		
GeneID:3468322	LOC219347	10	81,833,939	81,838,949	52,960	-	1	1_A375_uNG7_minus_lncRNA_R_1_690	337	sr:gene	1	0	0	16	12	13	1	1_A375_uNG7_minus_lncRNA_R_1	1.6	Gene LOC219347	FLJ98693, FLJ98692, FLJ17203, FLJ17224	hypothetical LOC219347	NM_027429, NR_027426, NR_027430, NR_027432, NR_027431	232294_at	
GeneID:3468322	C10orf87	10	81,838,436	81,852,307	13,881	+	1	1_A375_uNG7_minus_lncRNA_R_1_690	188	sr:gene	1	0	0	16	12	13	1	1_A375_uNG7_minus_lncRNA_R_1	1.6	Gene C10orf87	bA368J7.8, FLJ13265, C10orf87	chromosome 10 open reading frame 87	NM_025135, NC_T1980108.1, NC_T1950108.1, NC_T2235021.0, NC_T2235022.0, NC_T2235023.0, NC_T2235024.0	218574_s_at, 222643_s_at	NP_079411.2, EAW64643.1, EAW64610.1, EAW64609.1, EAW64611.1, EAW64612.1, EAW64613.1, EAW64614.1, EAW64615.1
GeneID:3468322	PLAC9	10	81,892,286	81,904,764	12,326	+	1	2_A375_uNG7_plus_lncRNA_R_1_1203	5280	upstream	0	1	0	10	15	7	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene PLAC9	MGC104710, PLAC9	placenta-specific 9	NM_001012973, NC_T2234439.0, NC_T2234438.0, NC_T1953.2	227419_x_at	NP_001012991.1, EAW64406.1, EAW64407.1
GeneID:3468322	ANXA11	10	81,914,860	81,965,326	50,466	-	1	2_A375_uNG7_plus_lncRNA_R_1_1204	-50	upstream	0	1	0	14	16	8	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene ANXA11	ANX11, ANXA11, CAP50	annexin A11	NM_001157, NM_145868, NM_145869, NC_T2227399.0, NC_T2227897.0, NC_T2229619.0, NC_T2229619.0, NC_T2229907.0, NC_T2235619.0, NC_T2235620.2	208200_s_at, 214703_s_at	NP_001146.1, NP_665876.1, NP_665877.1, EAW64399.1, EAW64400.1, EAW64403.1, EAW64401.1, EAW64402.1, EAW64404.1
GeneID:3468322	LOC439990	10	81,967,479	81,979,413	11,934	-	1	2_A375_uNG7_plus_lncRNA_R_1_1204	-2071	upstream	0	1	0	14	16	8	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene LOC439990		hypothetical LOC439990	XR_111892, XR_110436, XR_114392	1569022_at	
GeneID:3468322	C10orf89	10	82,368,242	82,392,793	24,311	+	1	a_A375_EGR1_1.1122	434	sr:gene	0	0	1	13	11	19	1	a_A375_EGR1_1.1	1.6	Gene C10orf89	FLJ12539, MGC4245, C10orf89, FLJ14952, FLJ44312	chromosome 10 open reading frame 89	NM_022333, NR_024372	224429_at, 228533_at, 232682_x_at	NP_071929.3
GeneID:3468322	TSPAN14	10	82,214,536	82,282,291	68,255	+	1	a_A375_EGR1_1.1123	79894	downstream	0	2	1	8	9	14	1	a_A375_EGR1_1.1	1.6	Gene TSPAN14	TSPAN14, MGC11332, THASP14, DC-TMP2	tetraspanin 14	NM_030927, NM_001128929, NC_T1970751.1, NC_T1970753.1, NC_T1970704.1, NC_T2236019.0, NC_T2236020.0, NC_T1140644	221822_s_at, 223314_at	NP_112189.2, NP_001127751.1, EAW66334.1, EAW66335.1, EAW66336.1, EAW66337.1, EAW66338.1
GeneID:3468322	SHD04B1	10	82,297,855	82,406,316	108,836	+	1	a_A375_EGR1_1.1123	-9026	upstream	0	0	1	8	9	14	1	a_A375_EGR1_1.1	1.6	Gene SHD04B	FLJ41864, SHD04B	SH2 domain containing 4B	NM_207372, NM_001143719	1563849_at	NP_997355.2, NP_001139199.1
GeneID:3468322	NRG3	10	83,033,070	84,746,653	1,111,583	+	3	1_A375_uNG7_minus_lncRNA_R_1_691, 2_A375_uNG7_plus_lncRNA_R_1_1203, 2_A375_uNG7_plus_lncRNA_R_1_1138	103166, 103199, 482	sr:gene, sr:gene, sr:gene	1	1	1	13	13.5	11.5	2	2_A375_uNG7_plus_lncRNA_R_1	1.7	Gene NRG3	pro-NRG3, NRG3, NRG3	neuregulin 3	NM_001010848, NM_001165972, NM_001165973, NC_T2240337.3	229233_at	NP_001010848.2, NP_001159444.1, NP_001159445.1, EAW66374.1
GeneID:3468322	GHITM	10	83,899,185	83,913,311	14,126	+	2	2_A375_uNG7_plus_lncRNA_R_1_1207, 2_A375_uNG7_plus_lncRNA_R_1_1208	271, 17503	sr:gene, downstream	0	1	0	13.5	16	7	2	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene GHITM	PTD012, MyD11, HSPC252, MIC31, DERP2, GHITM, TMBIM3, FLJ20854, DKFZp686C0246	growth hormone inducible transmembrane protein	NM_014294, NC_T2270508.0, NC_T2270509.0, NC_T2235612.0, NC_T1910113.3	1554610_s_at, 209248_s_at	NP_055029.2, EAW66369.1, EAW66367.1, EAW66366.1, EAW66370.1
GeneID:3468322	LOC100289292	10	83,935,736	83,934,413	14,879	+	2	2_A375_uNG7_minus_lncRNA_R_1_692, 2_A375_uNG7_plus_lncRNA_R_1_1209	11824, 11590	sr:gene, sr:gene	1	1	0	53	56	8	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene LOC170425		hypothetical LOC170425	XR_111891, XR_110435, XR_114388	1569021_at	
GeneID:3468322	GRID1	10	87,359,312	88,126,250	766,938	+	3	2_A375_uNG7_plus_lncRNA_R_1_1210, 2_A375_uNG7_plus_lncRNA_R_1_1211, 2_A375_uNG7_plus_lncRNA_R_1_1212	49874, 167762, 59626	sr:gene, sr:gene, sr:gene	0	1	0	16	17.67	7.67	0	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene GRID1	GRID1, KIAA1226	glutamate receptor, ionotropic, delta 1	NM_017551, NC_T2270570.1, NC_T2270574.0, NC_T2345032.0, NC_T1963696.2	1555067_at, 1555068_s_at	NP_060021.1, EAW66330.1, EAW66329.1, EAW66340.1, EAW66341.1
GeneID:3468322	VAPA1	10	88,199,013	88,201,341	2,328	+	1	2_A375_uNG7_plus_lncRNA_R_1_693	69	sr:gene	1	0	0	16	21	9	1	1_A375_uNG7_plus_lncRNA_R_1	1.6	Gene VAPA1	KIAA0261, FOE, VAPA1, VAPA	vesicle associated membrane protein-associated protein A	NM_015943, NC_T2270571.0, NC_T2345038.0, NC_T2345027.0, NC_T1140542.2	1554447_s_at, 212284_s_at, 212287_at, 212288_at	NP_056831.1, EAW66333.1, EAW66334.1, EAW66336.1, EAW66337.1
GeneID:3468322	BMPR1A	10	88,316,196	88,864,945	565,549	+	1	1_A375_uNG7_minus_lncRNA_R_1_694	-451	upstream	1	0	0	15	11	12	1	1_A375_uNG7_minus_lncRNA_R_1	1.6	Gene BMPR1A	CD292, Wp23bet, ALK3, ACVRL03, BKR3, BMPR1A	bone morphogenetic protein receptor, type IA	NM_004329, NC_T2275472.0	204632_s_at, 213978_at	NP_004320.2, EAW66320.1
GeneID:3468322	MMP22	10	88,693,297	88,717,423	22,126	-	1	a_A375_EGR1_1.1132	11249	sr:gene	0	0	1	7	8	17	1	a_A375_EGR1_1.1	1.7	Gene MMP22	EndoGlyc-1, MMP22, FLJ10465, EMILINE	multimerin 2	NM_024758, NC_T1143723.3	219931_s_at, 223622_s_at, 235262_at	NP_079022.2, EAW66319.1
GeneID:3468322	SNCG	10	88,716,286	88,720,817	4,729	+	1	2_A375_uNG7_plus_lncRNA_R_1_1214	12976	downstream	0	1	0	16	27	11	1	2_A375_uNG7_plus_lncRNA_R_1	1.7	Gene SNCG	BCSG1, SNCG, BR	synuclein, gamma (breast cancer-specific protein 1)	NM_003087, NC_T2275470.0, NC_T2275475.0, NC_T1140662.3, NC_T1963640.1	208694_at, 209927_at	NP_003078.2, EAW66317.1, EAW66318.1, EAW66316.1
GeneID:3468322	LOC100289292	10	88,725,495	88,731,366	5,870	-	1	2_A375_uNG7_plus_lncRNA_R_1_1214	-196	upstream	0	1	0	16	27	11	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene LOC100132992		hypothetical LOC100132992	XR_111894, XR_110439, XR_114391		
GeneID:3468322	C10orf116	10	88,726,165	88,730,998	4,776	+	1	2_A375_uNG7_plus_lncRNA_R_1_1214	3076	downstream	0	1	0	16	27	11	1	2_A375_uNG7_plus_lncRNA_R_1	1.6	Gene C10orf116	APAF, C10orf116	chromosome 10 open reading frame 116	NM_006529	200971_s_at	NP_006520.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.119385	AGAP11	10	88,730,498	88,769,960	39,462	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1214	768	in gene	0	1	0	16	27	11	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene AGAP11	AGAP11, KIAA1975	ankyrin repeat and GTPase domain Arf GTPase activating protein 11	NM_133447	1557360_at, 1557362_x_at	NP_597704.1
GeneID.2746	GLUD1	10	88,809,959	88,854,776	44,817	-	6	1_A375_pNL7_minus_lncRNA_AR..1..895, 1_A375_pNL7_minus_lncRNA_AR..1..896, 2_A375_pNL97_plus_lncRNA_AR..1..1215, 2_A375_pNL97_plus_lncRNA_AR..1..1216, 4_A375_EGR1..1..1133, 4_A375_EGR1..1..1134	216, -584, 200, -632, 216, -344	in gene, upstream, in gene, upstream, in gene, upstream	1	1	1	16.5	17	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene GLUD1	GLUD1, GDH1, MGC132003, GLUD, GDH	glutamate dehydrogenase 1	NM_005271, hCT2273052.1, hCT2273053.1, hCT2273055.1, hCT2273057.1, hCT2356025.0	200946_x_at, 200947_s_at, 244802_at	NP_005262.1, EAW80301.1, EAW80300.1, EAW80302.1, EAW80303.1, EAW80304.1
GeneID.54537	FAM35A	10	88,854,953	88,951,222	96,269	+	6	1_A375_pNL7_minus_lncRNA_AR..1..895, 1_A375_pNL7_minus_lncRNA_AR..1..896, 2_A375_pNL97_plus_lncRNA_AR..1..1215, 2_A375_pNL97_plus_lncRNA_AR..1..1216, 4_A375_EGR1..1..1133, 4_A375_EGR1..1..1134	-393, 407, -377, 455, -393, 167	upstream, in gene, upstream, in gene, upstream, in gene	1	1	1	16.5	17	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene FAM35A	bA163M19.1, FAM35A, FAM35A1, MGC5560	family with sequence similarity 35, member A	NM_019054, hCT2329308.0, hCT2329309.0	220547_s_at	NP_061927.2, EAW81363.1, EAW81364.1
GeneID.9562	MINPP1	10	89,264,223	89,313,218	48,995	+	2	1_A375_pNL7_minus_lncRNA_AR..1..897, 2_A375_pNL97_plus_lncRNA_AR..1..1217	398, 513	in gene, in gene	1	1	0	18	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MINPP1	MINPP2, HIPER1, MIPP, MINPP1, DKFZp564L2016	multiple inositol polyphosphate histidine phosphatase, 1	NM_001178117, NM_001178118, NM_004897, hCT2322243.0, hCT2322244.0	209585_s_at	NP_001171588.1, NP_001171589.1, NP_004888.2, EAW50165.1, EAW50166.1
GeneID.9060	PAPSS2	10	89,419,476	89,507,462	87,986	+	2	1_A375_pNL7_minus_lncRNA_AR..1..899, 4_A375_EGR1..1..1135	11980, 238	in gene, in gene	1	0	1	13.5	14	13.5	2	4_A375_EGR1..1	22	Gene PAPSS2	ATPSK2, PAPSS2, SK2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	NM_004670, NM_001015880, hCT2322247.0, hCT2322248.0, hCT14438.3	203058_s_at, 203059_s_at, 203060_s_at	NP_004661.2, NP_001015880.1, EAW50181.1, EAW50182.1, EAW50183.1
GeneID.84896	ATAD1	10	89,512,875	89,577,917	65,042	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1220	-195	upstream	0	1	0	15	17	15	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ATAD1	FLJ14600, FNP001, ATAD1, AFDC1	ATPase family, AAA domain containing 1	NM_032810, hCT2321838.1, hCT14439.3, hCT1957990.1, hCT1957991.1	224850_at	NP_116199.2, EAW50178.1, EAW50177.1, EAW50179.1, EAW50180.1
GeneID.100144748	KILLIN	10	89,618,918	89,623,194	4,276	-	2	1_A375_pNL7_minus_lncRNA_AR..1..900, 2_A375_pNL97_plus_lncRNA_AR..1..1222	250, -150	in gene, upstream	1	1	0	20	19	13	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene KILLIN	KILLIN, KLLN	killin protein	NM_001126049		NP_001119521.1
GeneID.5728	PTEN	10	89,623,195	89,728,532	105,337	+	2	1_A375_pNL7_minus_lncRNA_AR..1..900, 2_A375_pNL97_plus_lncRNA_AR..1..1222	-251, 149	upstream, in gene	1	1	0	20	19	13	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene PTEN	BZS, MHAM, 10q23del, MMAC1, PTEN1, GLM2, MGC11227, DEC, PTEN, TEP1	phosphatase and tensin homolog	NM_000314, hCT2322251.1, hCT2322253.1, hCT2352333.0, hCT1775388.2	204053_x_at, 204054_at, 211711_s_at, 222176_at, 225363_at, 227469_at, 233254_x_at, 233314_at, 242622_x_at	NP_000305.3, EAW50173.1, EAW50172.1, EAW50174.1, EAW50175.1
GeneID.55328	RNLS	10	90,033,621	90,343,082	309,461	-	3	1_A375_pNL7_minus_lncRNA_AR..1..902, 2_A375_pNL97_plus_lncRNA_AR..1..1223, 4_A375_EGR1..1..1136	108490, 197450, 74	in gene, in gene, in gene	1	1	1	9.33	10	9.67	3	4_A375_EGR1..1	17	Gene RNLS	RENALASE, C10orf59, FLJ11218, RNLS	renalase, FAD-dependent amine oxidase	NM_001031709, NM_018363, hCT2321715.0, hCT2321716.0, hCT2321719.0, hCT2352292.0, hCT1950707.1	220584_at, 223824_at	NP_001026879.2, NP_060833.1, EAW50167.1, EAW50169.1, EAW50170.1, EAW50171.1, EAW50168.1
GeneID.142910	LIPJ	10	90,346,519	90,366,733	20,214	+	1	4_A375_EGR1..1..1136	-3511	upstream	0	0	1	8	5	17	1	4_A375_EGR1..1	17	Gene LIPJ	LIPJ, LIPL1, bA425M17.2, FLJ11218	lipase, family member J	NM_001010939, hCT2352325.0, hCT1820084.2	1569571_at, 1569873_at, 1569874_s_at	NP_001010939.2, EAW50165.1, EAW50166.1
GeneID.643414	LIPK	10	90,484,301	90,512,513	28,212	+	1	4_A375_EGR1..1..1137	3859	in gene	0	0	1	9	11	15	1	4_A375_EGR1..1	15	Gene LIPK	bA180O14.2, LIPK, LIPL2	lipase, family member K	NM_001080518		NP_001073987.1
GeneID.57559	STAMBPL1	10	90,640,028	90,683,244	43,216	+	3	1_A375_pNL7_minus_lncRNA_AR..1..903, 2_A375_pNL97_plus_lncRNA_AR..1..1224, 4_A375_EGR1..1..1138	566, 278, 282	in gene, in gene, in gene	1	1	1	21	21	18	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene STAMBPL1	ALMalpha, KIAA1373, AMSH-LP, STAMBPL1, FLJ31524, bA399O19.2, AMSH-FP	STAM binding protein-like 1	NM_020799, hCT2321818.0, hCT2321819.1, hCT2321820.1	220603_at, 227606_s_at, 227607_at, 231891_at	NP_065850.1, EAW50156.1, EAW50157.1, EAW50158.1
GeneID.100507575	LOC100507575	10	91,094,411	91,102,416	8,005	-	2	1_A375_pNL7_minus_lncRNA_AR..1..904, 2_A375_pNL97_plus_lncRNA_AR..1..1225	-9744, -9744	upstream, upstream	1	1	0	25	33	2	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene LOC100507575		hypothetical LOC100507575	XR_110434		
GeneID.24138	IFIT5	10	91,174,325	91,180,759	6,434	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1226	555	in gene	0	1	0	15	22	12	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene IFIT5	FLJ53857, FLJ92676, RI58, IFIT5	interferon-induced protein with tetratricopeptide repeats 5	NM_012420, hCT15690.2	203595_s_at, 203596_s_at	NP_036552.1, EAW50135.1
GeneID.387700	SLC16A12	10	91,190,051	91,295,313	105,262	-	1	4_A375_EGR1..1..1139	193	in gene	0	0	1	4	4	16	1	4_A375_EGR1..1	16	Gene SLC16A12	MCT12, SLC16A12, CJMG, DKFZp686E168	solute carrier family 16, member 12 (monocarboxylic acid transporter 12)	NM_213606, hCT1643480.3		NP_998771.3, EAW50134.1
GeneID.53354	PANK1	10	91,342,749	91,405,215	62,466	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1227	767	in gene	0	1	0	13	17	9	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PANK1	PANK1a, PANK1, PANK1b, PANK, MGC24596	pantothenate kinase 1	NM_138316, NM_148977, NM_148978, hCT2321552.0, hCT2321553.0, hCT2352251.0, hCT15893.3	226649_at	NP_612189.2, NP_683878.1, NP_683879.1, EAW50130.1, EAW50132.1, EAW50133.1, EAW50131.1
GeneID.9585	KIF20B	10	91,461,367	91,534,700	73,333	+	2	1_A375_pNL7_minus_lncRNA_AR..1..905, 2_A375_pNL97_plus_lncRNA_AR..1..1228	73, 9	in gene, in gene	1	1	0	25	29	10	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene KIF20B	KRMP1, KIF20B, MPP1, MPHOSPH1, DKFZp434P0810, MPP-1, DKFZp434B0435, CT90	kinesin family member 20B	NM_016195, hCT2321614.0, hCT2321616.0, hCT14656.3	205235_s_at	NP_057279.2, EAW50126.1, EAW50127.1, EAW50128.1
GeneID.3363	HTR7	10	92,500,575	92,617,671	117,096	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1233	82471	in gene	0	1	0	12	21	4	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene HTR7	5-HT7, HTR7	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	NM_000872, NM_019859, NM_019860, hCT2321442.1, hCT2321444.1, hCT1826965.3	216098_s_at	NP_000863.1, NP_062873.1, NP_062874.1, EAW50118.1, EAW50119.1, EAW50120.1
GeneID.10556	RPP30	10	92,631,709	92,668,312	36,603	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1234	35	in gene	0	1	0	19	20	17	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene RPP30	TSG15, RPP30, FLJ36491	ribonuclease P/MRP 30kDa subunit	NM_006413, NM_001104546	203436_at	NP_006404.1, NP_001098016.1
GeneID.100188947	LOC100188947	10	93,066,719	93,299,337	232,618	-	2	1_A375_pNL7_minus_lncRNA_AR..1..907, 2_A375_pNL97_plus_lncRNA_AR..1..1237	129684, 27721	in gene, in gene	1	1	0	11	17	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100188947		hypothetical LOC100188947	NR_024467		
GeneID.143279	HECTD2	10	93,170,096	93,274,520	104,424	+	2	1_A375_pNL7_minus_lncRNA_AR..1..907, 2_A375_pNL97_plus_lncRNA_AR..1..1237	-443, 101520	upstream, in gene	1	1	0	11	17	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene HECTD2	HECTD2, FLJ16050	HECT domain containing 2	NM_173497, NM_182765, hCT2348089.1, hCT2351051.0, hCT2352328.0	1565899_at, 227566_at, 238603_at	NP_775768.2, NP_877497.2, EAW50109.1, EAW50110.1, EAW50111.1
GeneID.143282	FGFBP3	10	93,666,345	93,669,258	2,913	-	2	1_A375_pNL7_minus_lncRNA_AR..1..908, 2_A375_pNL97_plus_lncRNA_AR..1..1241	566, 566	in gene, in gene	1	1	0	79	85	13	1	2_A375_pNL97_plus_lncRNA_AR..1	85	Gene FGFBP3	MGC39320, FGFBP3, C10orf13, FGF-BP3	fibroblast growth factor binding protein 3	NM_152429, hCT1819921.2	238453_at	NP_689642.3, EAW50104.1
GeneID.9044	BTAF1	10	93,683,736	93,790,082	106,346	+	1	1_A375_pNL7_minus_lncRNA_AR..1..909	-120	upstream	1	0	0	22	21	9	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene BTAF1	TAF(II)170, BTAF1, TAFII170, MOT1, TAF172, MGC138406, KIAA0940	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)	NM_003972, hCT2352266.0, hCT10355.3	209430_at	NP_003963.1, EAW50103.1, EAW50102.1
GeneID.22849	CPEB3	10	93,808,397	94,050,875	242,478	-	2	1_A375_pNL7_minus_lncRNA_AR..1..910, 2_A375_pNL97_plus_lncRNA_AR..1..1242	-101, 91	upstream, in gene	1	1	0	24	21	12	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene CPEB3	CPEB3		NM_001178137, NM_014912, hCT2352361.0, hCT11393.3	1555250_a_at, 205773_at, 243651_at	NP_001171608.1, NP_055727.3, EAW50097.1, EAW50098.1
GeneID.54708	5-Mar	10	94,050,920	94,113,721	62,801	+	2	1_A375_pNL7_minus_lncRNA_AR..1..910, 2_A375_pNL97_plus_lncRNA_AR..1..1242	56, -136	in gene, upstream	1	1	0	24	21	12	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene MARCH5	FLJ20445, RNF153, MITOL, MARCH5, MARCH-V	membrane-associated ring finger (C3HC4) 5	NM_017824, hCT2321931.0, hCT2321933.0, hCT11398.3	218582_at, 226394_at	NP_060294.1, EAW50096.1, EAW50094.1, EAW50095.1
GeneID.3832	KIF11	10	94,352,825	94,415,152	62,327	+	2	1_A375_pNL7_minus_lncRNA_AR..1..913, 2_A375_pNL97_plus_lncRNA_AR..1..1245	-1401, -1417	upstream, upstream	1	1	0	17	15	15	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene KIF11	TRIP5, KNSL1, KIF11, HKSP, EG5	kinesin family member 11	NM_004523, hCT201239.3	204444_at	NP_004514.2, EAW50089.1
GeneID.3087	HHEX	10	94,449,681	94,455,408	5,727	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1246	271	in gene	0	1	0	10	17	14	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene HHEX	HOX11L-PEN, PRH, HMPH, PRHX, HEX, HHEX	hematopoietically expressed homeobox	NM_002729, hCT2321540.0, hCT1820031.1	204689_at, 215933_s_at	NP_002720.1, EAW50086.1, EAW50087.1
GeneID.54536	EXOC6	10	94,594,470	94,819,251	224,781	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1247	57766	in gene	0	1	0	12	23	5	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene EXOC6	EXOC6, SEC15L3, SEC15L, DKFZp761I2124, FLJ1125, Sec15p, FLJ11251, MGC33397, SEC15L1, EXOC6A, SEC15	exocyst complex component 6	NM_001013848, NM_019053, hCT2321542.0, hCT2321544.0, hCT2352263.0, hCT2352264.0, hCT30768.3	226259_at, 232599_at, 233924_s_at	NP_001013870.1, NP_061926.3, EAW50082.1, EAW50083.1, EAW50084.1, EAW50085.1, EAW50086.1
GeneID.26509	MYOF	10	95,066,186	95,242,074	175,888	-	2	1_A375_pNL7_minus_lncRNA_AR..1..915, 2_A375_pNL97_plus_lncRNA_AR..1..1249	-118, -70	upstream, upstream	1	1	0	28	30	10	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene MYOF	FLJ90777, MYOF, FER1L3, FLJ36571	myoferlin	NM_013451, NM_133337, hCT2321494.0, hCT2352269.0, hCT2352270.0, hCT30781.3	201798_s_at, 211864_s_at, 217518_at	NP_038479.1, NP_579899.1, EAW50073.1, EAW50074.1, EAW50075.1, EAW50076.1
GeneID.55165	CEP55	10	95,256,369	95,288,849	32,480	+	2	1_A375_pNL7_minus_lncRNA_AR..1..916, 2_A375_pNL97_plus_lncRNA_AR..1..1250	79, 15	in gene, in gene	1	1	0	19	22	7	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CEP55	C10orf3, CEP55, URCC6, FLJ10540, CT111	centrosomal protein 55kDa	NM_018131, NM_001127182, hCT2352272.0, hCT30784.3	218542_at	NP_060601.3, NP_001120654.1, EAW50071.1, EAW50072.1
GeneID.118924	C10orf4	10	95,427,640	95,462,329	34,689	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1251	-39	upstream	0	1	0	24	28	17	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene C10orf4	F26C11.1-like, FRA10A, FRA10AC1, C10orf4	chromosome 10 open reading frame 4	NM_145246, hCT2321383.1, hCT2349230.0, hCT2352288.0, hCT2352289.0, hCT2352290.0, hCT2352291.0, hCT30789.4	226398_s_at, 236596_at	NP_660289.2, EAW50056.1, EAW50055.1, EAW50057.1, EAW50058.1, EAW50060.1, EAW50059.1, EAW50061.1
GeneID.9211	LGI1	10	95,517,566	95,557,916	40,350	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1252	-5737	upstream	0	1	0	15	19	1	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LGI1	IB1099, ETL1, EPITEMPIN, LGI1, EPT	leucine-rich, glioma inactivated 1	NM_005097, hCT2322063.0, hCT2322064.0, hCT2322065.0	206349_at	NP_005088.1, EAW50051.1, EAW50052.1, EAW50053.1
GeneID.159371	TMEM20	10	95,653,730	95,662,491	8,761	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1253	-146	upstream	0	1	0	16	21	7	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TMEM20	C10orf80, FLJ33990, TMEM20	transmembrane protein 20	NM_153226, NM_001134658, hCT2344324.0, hCT2344325.0, hCT1646014.4, hCT1827097.3	231012_at, 239265_at	NP_694958.1, NP_001128130.1, EAW50046.1, EAW50047.1, EAW50048.1, EAW50049.1
GeneID.51196	PLCE1	10	95,753,746	96,088,149	334,403	+	6	1_A375_pNL7_minus_lncRNA_AR..1..917, 1_A375_pNL7_minus_lncRNA_AR..1..918, 2_A375_pNL97_plus_lncRNA_AR..1..1254, 2_A375_pNL97_plus_lncRNA_AR..1..1255, 2_A375_pNL97_plus_lncRNA_AR..1..1256, 2_A375_pNL97_plus_lncRNA_AR..1..1257	-1778, 72574, -1938, 72622, 121998, 230846	upstream, in gene, upstream, in gene, in gene, in gene	1	1	0	23.5	34.75	4.25	4	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene PLCE1	KIAA1516, NPHS3, PLCE, MGC167842, PLCE1, PPLC, FLJ23659	phospholipase C, epsilon 1	NM_016341, NM_001165979, hCT2322071.0, hCT1813992.1	1566739_at, 1566740_at, 205111_s_at, 205112_at, 214159_at, 239904_at	NP_057425.3, NP_001159451.1, EAW50042.1, EAW50043.1
GeneID.64318	NOC3L	10	96,092,989	96,122,683	29,694	-	2	1_A375_pNL7_minus_lncRNA_AR..1..919, 2_A375_pNL97_plus_lncRNA_AR..1..1258	27, 123	in gene, in gene	1	1	0	25	18	13	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene NOC3L	FLJ12820, FAD24, AD24, C10orf117, NOC3L	nucleolar complex associated 3 homolog (S. cerevisiae)	NM_022451, hCT30416.3	218889_at	NP_071896.8, EAW50041.1
GeneID.23232	TBC1D12	10	96,162,186	96,296,089	133,903	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1259	143510	downstream	0	1	0	13	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TBC1D12	TBC1D12, FLJ12820, KIAA0608, FLJ10339	TBC1 domain family, member 12	NM_015188	1557609_s_at, 221858_at	NP_056003.1
GeneID.3070	HELLS	10	96,305,574	96,361,856	56,282	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1259	122	in gene	0	1	0	13	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene HELLS	SMARCA6, LSH, Nbla10143, FLJ10339, PASG, HELLS	helicase, lymphoid specific	NM_018063, hCT2322073.0, hCT2322074.0, hCT2322076.0, hCT2352259.0, hCT2352260.0, hCT2352261.0, hCT2352262.0, hCT2352263.0, hCT2352264.0, hCT2352265.0, hCT2352266.0, hCT2352267.0, hCT30418.3	220085_at, 223556_at, 234040_at	NP_060533.2, EAW50038.1, EAW50026.1, EAW50027.1, EAW50034.1, EAW50037.1, EAW50028.1, EAW50029.1, EAW50030.1, EAW50031.1, EAW50032.1, EAW50033.1, EAW50035.1, EAW50036.1
GeneID.142827	C10orf129	10	96,953,957	96,988,686	34,729	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1260, 4_A375_EGR1..1..1141	-10421, 36643	upstream, downstream	0	1	1	13.5	17.5	14	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene C10orf129	ACSM6, C10orf129, bA310E22.3	chromosome 10 open reading frame 129	NM_207321, hCT1833044.2		NP_997204.2, EAW50014.1
GeneID.9124	PDLIM1	10	96,997,329	97,050,781	53,452	-	1	4_A375_EGR1..1..1141	59981	downstream	0	0	1	5	9	16	1	4_A375_EGR1..1	16	Gene PDLIM1	hCLIM1, CLP36, CLP-36, CLIM1, PDLIM1	PDZ and LIM domain 1	NM_020992, hCT30743.4, hCT1951260.2, hCT1962343.1, hCT1962344.1	208690_s_at	NP_066272.1, EAW50009.1, EAW50010.1, EAW50011.1, EAW50012.1
GeneID.10580	SORBS1	10	97,071,530	97,321,171	249,641	-	3	1_A375_pNL7_minus_lncRNA_AR..1..921, 1_A375_pNL7_minus_lncRNA_AR..1..922, 2_A375_pNL97_plus_lncRNA_AR..1..1261	169315, 167091, 169315	in gene, in gene, in gene	1	1	0	20.5	22	2	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene SORBS1	KIAA1296, SORBS1, DKFZp451C066, FLAF2, SH3D5, SH3P12, DKFZp586P1422, R85FL, SORB1, CAP, FLJ12406	sorbin and SH3 domain containing 1	NM_006434, NM_015385, NM_001034954, NM_001034955, NM_001034956, NM_024991, NM_001034957, hCT2323641.0, hCT2323644.0, hCT2323646.0, hCT2323649.0, hCT2323651.0, hCT2323654.0, hCT2323657.0, hCT2323659.0, hCT30741.2, hCT1820018.1, hCT1820019.1	211705_s_at, 211819_s_at, 218087_s_at, 222513_s_at	NP_006425.2, NP_056200.1, NP_001030126.1, NP_001030127.1, NP_001030128.1, NP_079267.1, NP_001030129.1, EAW49998.1, EAW49999.1, EAW50000.1, EAW50001.1, EAW50002.1, EAW50003.1, EAW50004.1, EAW50005.1, EAW50006.1, EAW50007.1, EAW50008.1
GeneID.5832	ALDH18A1	10	97,365,686	97,416,567	50,881	-	1	1_A375_pNL7_minus_lncRNA_AR..1..923	183	in gene	1	0	0	22	15	14	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene ALDH18A1	PYCS, MGC117316, P5CS, ALDH18A1, GSAS	aldehyde dehydrogenase 18 family, member A1	NM_002860, NM_001017423, hCT2323635.0, hCT2323637.0, hCT2352239.0, hCT29199.3	217791_s_at, 222416_at	NP_002851.2, NP_001017423.1, EAW49994.1, EAW49995.1, EAW49996.1, EAW49997.1
GeneID.26123	TCTN3	10	97,423,153	97,453,900	30,747	-	4	1_A375_pNL7_minus_lncRNA_AR..1..923, 1_A375_pNL7_minus_lncRNA_AR..1..924, 2_A375_pNL97_plus_lncRNA_AR..1..1262, 4_A375_EGR1..1..1142	37516, 172, 172, 284	downstream, in gene, in gene, in gene	1	1	1	19.5	18	14	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene TCTN3	C10orf61, TCTN3, DKFZp564D116, TECT3	tectonic family member 3	NM_015631, NM_001143973, hCT30742.3	212121_at, 212123_at	NP_056446.4, NP_001137445.1, EAW49993.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.100127869	C10orf131	10	97,867,722	97,898,415	30,693	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1263	-202	upstream	0	1	0	16	21	16	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene C10orf131	bA690P14.3, C10orf131, FLJ10895	chromosome 10 open reading frame 131	NM_001130446		NP_001123918.2
GeneID.728556	LOC728556	10	97,760,957	97,849,953	88,996	-	4	1_A375_pNL7_minus_lncRNA_AR..1..925, 1_A375_pNL7_minus_lncRNA_AR..1..926, 2_A375_pNL97_plus_lncRNA_AR..1..1264, 2_A375_pNL97_plus_lncRNA_AR..1..1265	45905, -127, 46657, 33	in gene, upstream, in gene, in gene	1	1	0	18.33	17.67	11	3	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene LOC728556	FLJ34077, MGC10764	hypothetical LOC728556	XR_111097, XR_110439, XR_114413		
GeneID.54619	CCNJ	10	97,803,159	97,820,627	17,468	+	2	1_A375_pNL7_minus_lncRNA_AR..1..925, 2_A375_pNL97_plus_lncRNA_AR..1..1264	889, 137	in gene, in gene	1	1	0	15	13.5	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene CCNJ	CCNJ, bA690P14.1	cyclin J	NM_019084, NM_001134375, NM_001134376, hCT2321580.0	219470_x_at, 222868_at, 229091_s_at	NP_061957.2, NP_001127847.1, NP_001127848.1, EAW49984.1
GeneID.9849	ZNF518A	10	97,889,472	97,923,517	34,045	+	3	1_A375_pNL7_minus_lncRNA_AR..1..927, 2_A375_pNL97_plus_lncRNA_AR..1..1266, 4_A375_EGR1..1..1143	192, 256, 224	in gene, in gene, in gene	1	1	1	19	31	20	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene ZNF518A	MGC125710, ZNF518, MGC125707, ZNF518A, DKFZp781O2147	zinc finger protein 518A	NM_014803, hCT2321584.0	204291_at, 215644_at, 244132_x_at	NP_055618.2, EAW49983.1
GeneID.7093	TLL2	10	98,124,383	98,273,683	149,320	-	3	1_A375_pNL7_minus_lncRNA_AR..1..928, 2_A375_pNL97_plus_lncRNA_AR..1..1267, 2_A375_pNL97_plus_lncRNA_AR..1..1268	17619, 17491, 115	in gene, in gene, in gene	1	1	0	19.5	31.5	8	2	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene TLL2	MGC133313, TLL2, KIAA0932, MGC133312	tolloid-like 2	NM_012465, hCT2349223.0, hCT14422.4	206027_s_at, 215008_at, 215643_s_at	NP_036597.1, EAW49976.1, EAW49975.1
GeneID.56889	TM9SF3	10	98,277,867	98,346,809	68,942	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1266	73241	downstream	0	1	0	14	16	12	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene TM9SF3	TM9SF3, RP11-34E5.1, EP70-P-iso, SMBP	transmembrane 9 superfamily member 3	NM_020123, hCT2321396.0, hCT2321399.0, hCT16908.3	217758_s_at, 222399_s_at, 228610_at, 239626_x_at	NP_064508.3, EAW49974.1, EAW49972.1, EAW49973.1
GeneID.118788	PIK3AP1	10	98,353,069	98,480,279	127,210	-	1	4_A375_EGR1..1..1144	311	in gene	0	0	1	6	7	18	1	4_A375_EGR1..1	18	Gene PIK3AP1	PIK3AP1, RP11-34E5.3, BCAP	phosphoinositide-3-kinase adaptor protein 1	NM_152309, hCT2352364.0, hCT1640813.3	1554508_at, 226459_at	NP_689522.2, EAW49968.1, EAW49969.1
GeneID.6585	SLIT1	10	98,757,795	98,945,683	187,888	-	3	2_A375_pNL97_plus_lncRNA_AR..1..1269, 4_A375_EGR1..1..1145, 4_A375_EGR1..1..1146	104063, 16051, -589	in gene, in gene, upstream	0	1	1	9	13.67	12	3	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SLIT1	SLIL1, SLIT1, MEGF4, Slit-1, MGC164811, SLIT3, SLIT-1	slit homolog 1 (Drosophila)	NM_003061, hCT2322084.1, hCT2322088.1, hCT2340271.0, hCT16912.4	1557815_a_at, 206221_s_at, 213601_at	NP_003052.2, EAW49956.1, EAW49957.1, EAW49958.1, EAW49959.1
GeneID.10023	FRAT1	10	99,079,022	99,081,672	2,650	+	2	1_A375_pNL7_minus_lncRNA_AR..1..929, 2_A375_pNL97_plus_lncRNA_AR..1..1270	-110, -142	upstream, upstream	1	1	0	25	20	7	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene FRAT1	FRAT1, FLJ97193	frequently rearranged in advanced T-cell lymphomas	NM_005479, hCT2322413.1, hCT14420.3	219889_at	NP_005470.2, EAW49951.1, EAW49950.1
GeneID.23401	FRAT2	10	99,092,254	99,094,458	2,204	-	3	1_A375_pNL7_minus_lncRNA_AR..1..930, 2_A375_pNL97_plus_lncRNA_AR..1..1271, 2_A375_pNL97_plus_lncRNA_AR..1..1272	-150, 826, -134	upstream, in gene, upstream	1	1	0	17.5	18.5	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene FRAT2	FRAT2, MGC10562	frequently rearranged in advanced T-cell lymphomas 2	NM_012083, hCT1830634.2	209864_at	NP_036215.1, EAW49949.1
GeneID.5223	PGAM1	10	99,186,027	99,193,198	7,171	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1273	5	in gene	0	1	0	11	19	9	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PGAM1	PGAMA, PGAM1, PGAM-B	phosphoglycerate mutase 1 (brain)	NM_002629, hCT1967408.1, hCT2322418.0, hCT2322421.0, hCT2322422.0, hCT2322423.0, hCT2322425.0, hCT2352271.0, hCT1827142.2	200886_s_at	NP_002620.1, EAW49938.1, EAW49939.1, EAW49941.1, EAW49942.1, EAW49943.1, EAW49937.1, EAW49940.1, EAW49944.1
GeneID.51013	EXOSC1	10	99,195,686	99,205,788	10,102	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1273	19736	downstream	0	1	0	11	19	9	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene EXOSC1	EXOSC1, SKI4, Csl4p, Ski4p, CGI-108, CSL4, hCsl4p, p13	exosome component 1	NM_016046, hCT16904.3	1559044_at, 218369_s_at, 222609_s_at	NP_057130.1, EAW49936.1
GeneID.64210	MMS19	10	99,218,081	99,258,366	40,285	-	1	1_A375_pNL7_minus_lncRNA_AR..1..931	565	in gene	1	0	0	14	19	16	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene MMS19	FLJ34167, hMMS19, MGC99604, MMS19, MET18, MMS19L, FLJ95146	MMS19 nucleotide excision repair homolog (S. cerevisiae)	NM_022362, hCT2322103.0, hCT2322104.0, hCT2322105.0, hCT2322106.0, hCT2322107.0, hCT2352311.0, hCT2352312.0, hCT16910.3	202167_s_at	NP_071757.4, EAW49922.1, EAW49921.1, EAW49925.1, EAW49926.1, EAW49927.1, EAW49923.1, EAW49924.1, EAW49928.1
GeneID.80019	UBTD1	10	99,258,788	99,330,980	72,192	+	5	1_A375_pNL7_minus_lncRNA_AR..1..931, 1_A375_pNL7_minus_lncRNA_AR..1..932, 2_A375_pNL97_plus_lncRNA_AR..1..1274, 2_A375_pNL97_plus_lncRNA_AR..1..1275, 4_A375_EGR1..1..1148	-987, 44048, 43848, 44176, 73848	upstream, in gene, in gene, in gene, downstream	1	1	1	13.67	18.67	14	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene UBTD1	UBTD1, FLJ11807	ubiquitin domain containing 1	NM_024954, hCT2322437.0, hCT2322440.0, hCT1641198.2	219172_at	NP_079230.1, EAW49920.1, EAW49918.1, EAW49919.1
GeneID.26287	ANKRD2	10	99,332,256	99,343,641	11,385	+	1	4_A375_EGR1..1..1148	160	in gene	0	0	1	9	16	17	1	4_A375_EGR1..1	17	Gene ANKRD2	MGC104314, ANKRD2, ARPP	ankyrin repeat domain 2 (stretch responsive muscle)	NM_020349, NM_001129981, hCT2322443.0, hCT16263.3	221232_s_at	NP_065082.2, NP_001123453.1, EAW49916.1, EAW49917.1
GeneID.60370	AVPI1	10	99,437,181	99,447,015	9,834	-	3	1_A375_pNL7_minus_lncRNA_AR..1..933, 2_A375_pNL97_plus_lncRNA_AR..1..1276, 4_A375_EGR1..1..1149	-217, -249, 7	upstream, upstream, in gene	1	1	1	22	21	21	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene AVPI1	VIP32, RP11-548K23.7, PP5395, VIT32, AVPI1	arginine vasopressin-induced 1	NM_021732, hCT2341102.0, hCT1642887.3	218631_at	NP_068378.2, EAW49905.1, EAW49904.1
GeneID.83742	MARVELD1	10	99,473,465	99,477,909	4,444	+	2	1_A375_pNL7_minus_lncRNA_AR..1..934, 2_A375_pNL97_plus_lncRNA_AR..1..1277	13223, 423	downstream, in gene	1	1	0	15.5	16	14	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MARVELD1	FLJ22343, MARVELD1, MARVD1, MGC4415, bA548K23.8, GB14, FLJ23440, RP11-548K23.8, MRVLDC1	MARVEL domain containing 1	NM_031484, hCT1642888.3	223095_at, 234917_at	NP_113672.1, EAW49903.1
GeneID.100270710	LOC100270710	10	99,477,217	99,493,298	16,081	-	4	1_A375_pNL7_minus_lncRNA_AR..1..934, 1_A375_pNL7_minus_lncRNA_AR..1..935, 2_A375_pNL97_plus_lncRNA_AR..1..1277, 2_A375_pNL97_plus_lncRNA_AR..1..1278	6610, -3758, 19410, -3470	in gene, upstream, downstream, upstream	1	1	0	15.67	16.67	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100270710		hypothetical LOC100270710	NR_026754		
GeneID.118813	ZFYVE27	10	99,496,878	99,520,664	23,786	+	3	1_A375_pNL7_minus_lncRNA_AR..1..934, 1_A375_pNL7_minus_lncRNA_AR..1..935, 2_A375_pNL97_plus_lncRNA_AR..1..1278	-10190, 178, -110	upstream, in gene, upstream	1	1	0	17	15	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ZFYVE27	RP11-459F3.2, ZFYVE27, PROTRUDIN, SPG33	zinc finger, FYVE domain containing 27	NM_001002261, NM_001002262, NM_001174119, NM_001174120, NM_001174121, NM_001174122, NM_144588, hCT2322453.0, hCT2352274.0, hCT2352275.0, hCT2352276.0, hCT2352277.0, hCT2352278.0, hCT2352279.0, hCT16265.2	225218_at	NP_001002261.1, NP_001002262.1, NP_001167590.1, NP_001167591.1, NP_001167592.1, NP_001167593.1, NP_653189.3, EAW49895.1, EAW49896.1, EAW49897.1, EAW49898.1, EAW49899.1, EAW49900.1, EAW49901.1, EAW49902.1
GeneID.100505561	LOC100505561	10	99,588,235	99,609,555	21,320	-	2	1_A375_pNL7_minus_lncRNA_AR..1..936, 2_A375_pNL97_plus_lncRNA_AR..1..1280	6435, 6371	in gene, in gene	1	1	0	26	26	4	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene LOC100505561		hypothetical LOC100505561	XR_110441		
GeneID.401647	GOLGA7B	10	99,609,996	99,627,782	17,786	+	3	1_A375_pNL7_minus_lncRNA_AR..1..936, 2_A375_pNL97_plus_lncRNA_AR..1..1280, 2_A375_pNL97_plus_lncRNA_AR..1..1281	-6676, -6612, 11252	upstream, upstream, in gene	1	1	0	20.5	25.5	5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene GOLGA7B	bA459F3.4, bA451M19.3, C10orf132, GOLGA7B, MGC131701, C10orf133	golgi autoantigen, golgin subfamily a, 7B	NM_001010917, hCT16266.3	228066_at	NP_001010917.1, EAW49893.1
GeneID.55118	CRTAC1	10	99,624,758	99,790,585	165,827	-	7	1_A375_pNL7_minus_lncRNA_AR..1..937, 2_A375_pNL97_plus_lncRNA_AR..1..1281, 2_A375_pNL97_plus_lncRNA_AR..1..1282, 2_A375_pNL97_plus_lncRNA_AR..1..1283, 2_A375_pNL97_plus_lncRNA_AR..1..1284, 4_A375_EGR1..1..1151, 4_A375_EGR1..1..1152	148153, 169337, 148153, 141081, 38777, 139193, 1017	in gene, downstream, in gene, in gene, in gene, in gene, in gene	1	1	1	14.5	19.33	10.67	6	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene CRTAC1	FLJ10320, CRTAC1, CEP-68, ASPIC1	cartilage acidic protein 1	NM_018058, hCT2322092.0, hCT2322093.0, hCT16260.3	1555958_at, 221204_s_at	NP_060528.3, EAW49892.1, EAW49890.1, EAW49891.1
GeneID.100128300	LOC100128300	10	99,827,889	99,831,335	3,446	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1281	-6641	upstream	0	1	0	15	23	6	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100128300		hypothetical LOC100128300	XR_111108, XR_110442, XR_114417		
GeneID.27291	C10orf28	10	99,894,381	100,004,654	110,273	+	3	1_A375_pNL7_minus_lncRNA_AR..1..940, 2_A375_pNL97_plus_lncRNA_AR..1..1287, 2_A375_pNL97_plus_lncRNA_AR..1..1288	115, 30, 112531	in gene, in gene, downstream	1	1	0	14.5	15	6.5	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene C10orf28	C10orf28, GIDRP86, FLJ25458, GIDRP88, FLJ37160, PSORT	chromosome 10 open reading frame 28	NM_014472, hCT2349214.0, hCT2349215.0, hCT2349216.0	210455_at, 228374_at	NP_055287.4, EAW49889.1, EAW49887.1, EAW49888.1
GeneID.84171	LOXL4	10	100,007,443	100,028,007	20,564	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1288, 2_A375_pNL97_plus_lncRNA_AR..1..1289	21095, -1465	downstream, upstream	0	1	0	13	17.5	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOXL4	FLJ21889, LOXL4, LOXC	lysyl oxidase-like 4	NM_032211, hCT16279.4	1570219_at, 227145_at	NP_115587.6, EAW49886.1
GeneID.3257	HPS1	10	100,175,956	100,206,704	30,748	-	1	4_A375_EGR1..1..1153	17136	in gene	0	0	1	6	6	19	1	4_A375_EGR1..1	19	Gene HPS1	HPS, HPS1, MGC5277	Hermansky-Pudlak syndrome 1	NM_182639, NM_000195, hCT2321277.0, hCT2321278.0, hCT2321279.0, hCT2321281.0, hCT2321283.0, hCT1960709.1, hCT1960710.1	203308_x_at, 203309_s_at, 210112_at, 239382_at	NP_872577.1, NP_000186.2, EAW49877.1, EAW49881.1, EAW49882.1, EAW49883.1, EAW49878.1, EAW49879.1, EAW49880.1
GeneID.60495	HPSE2	10	100,216,834	100,995,632	778,798	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1292	747104	in gene	0	1	0	12	23	3	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene HPSE2	FLJ11684, MGC133234, HPSE2, UFS, HPA2, FLJ44022, HPR2	heparanase 2	NM_021828, NM_001166244, NM_001166245, NM_001166246, hCT2344370.0, hCT2344371.0, hCT2344372.0	220927_s_at	NP_068600.4, NP_001159716.1, NP_001159717.1, NP_001159718.1, EAW49873.1, EAW49874.1, EAW49872.1
GeneID.159296	NKX2-3	10	101,292,690	101,296,281	3,591	+	1	4_A375_EGR1..1..1154	1998	in gene	0	0	1	3	6	18	1	4_A375_EGR1..1	18	Gene NKX2-3	NKX2.3, CSX3, NKX2-3, NKX2C, NK2.3, NKX4-3	NK2 transcription factor related, locus 3 (Drosophila)	NM_145285, hCT9466.4	1553808_a_at	NP_660328.2, EAW49867.1
GeneID.81894	SLC25A28	10	101,370,275	101,380,221	9,946	-	2	1_A375_pNL7_minus_lncRNA_AR..1..942, 4_A375_EGR1..1..1155	-1027, -963	upstream, upstream	1	0	1	26	19	28	1	4_A375_EGR1..1	28	Gene SLC25A28	NPD016, MFRN2, MRS4L, SLC25A28, DKFZp547C109, MRS3/4	solute carrier family 25, member 28	NM_031212, hCT2321465.0, hCT9464.3, hCT1962278.1, hCT1962279.1	221432_s_at, 223192_at	NP_112489.3, EAW49864.1, EAW49863.1, EAW49865.1, EAW49866.1
GeneID.57089	ENTPD7	10	101,419,263	101,471,002	51,739	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1293	-223	upstream	0	1	0	16	22	9	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ENTPD7	ENTPD7, DKFZp667O124, FLJ30978, LALP1, FLJ31630, MGC141913, FLJ95384, FLJ41522, RP11-483F11.1	ectonucleoside triphosphate diphosphohydrolase 7	NM_020354, hCT2321563.0, hCT2352247.0, hCT9467.3	220153_at	NP_065087.1, EAW49862.1, EAW49860.1, EAW49861.1
GeneID.10613	ERLIN1	10	101,909,847	101,945,814	35,967	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1294	86	in gene	0	1	0	14	23	14	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ERLIN1	KE04, KEO4, C10orf69, ERLIN1, SPFH1, Erlin-1	ER lipid raft associated 1	NM_006459, NM_001100626, hCT2321455.0, hCT9419.3	202441_at, 202444_s_at	NP_006450.2, NP_001094096.1, EAW49846.1, EAW49847.1
GeneID.1147	CHUK	10	101,948,124	101,989,344	41,220	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1294	43816	downstream	0	1	0	14	23	14	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CHUK	IKK1, IKBKA, CHUK, NFKBIKA, IKK-alpha, IKKA, TCF16	conserved helix-loop-helix ubiquitous kinase	NM_001278, hCT10466.3	209666_s_at	NP_001269.3, EAW49845.1
GeneID.55280	CWF19L1	10	101,992,055	102,027,437	35,382	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1295	45	in gene	0	1	0	16	35	11	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene CWF19L1	CWF19L1, FLJ10996	CWF19-like 1, cell cycle control (S. pombe)	NM_018294, hCT1967371.1, hCT1967372.1, hCT2352357.0, hCT2352358.0, hCT2352359.0, hCT2352360.0, hCT10485.3	218787_x_at, 229036_at, 233568_x_at	NP_060764.3, EAW49844.1, EAW49839.1, EAW49841.1, EAW49842.1, EAW49843.1, EAW49838.1, EAW49840.1
GeneID.282991	BLOC1S2	10	102,033,713	102,046,439	12,726	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1295, 4_A375_EGR1..1..1156	19047, 71	downstream, in gene	0	1	1	16	24.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene BLOC1S2	BLOS2, BLOC1S2, MGC10120, RP11-316M21.4, FLJ30135	biogenesis of lysosomal organelles complex-1, subunit 2	NM_173809, NM_001001342, hCT2350919.0, hCT2350920.0, hCT10487.5	225049_at	NP_776170.2, NP_001001342.1, EAW49835.1, EAW49836.1, EAW49837.1
GeneID.9033	PKD2L1	10	102,047,903	102,090,243	42,340	-	3	2_A375_pNL97_plus_lncRNA_AR..1..1296, 4_A375_EGR1..1..1156, 4_A375_EGR1..1..1157	5187, 43875, -8797	in gene, downstream, upstream	0	1	1	15	15	13	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene PKD2L1	PCL, PKDL, PKD2L1, TRPP3, PKD2L	polycystic kidney disease 2-like 1	NM_016112, hCT2321447.0, hCT10483.2	221061_at	NP_057196.2, EAW49834.1, EAW49833.1
GeneID.6319	SCD	10	102,106,772	102,124,588	17,816	+	3	1_A375_pNL7_minus_lncRNA_AR..1..943, 2_A375_pNL97_plus_lncRNA_AR..1..1297, 4_A375_EGR1..1..1157	236, 300, -7732	in gene, in gene, upstream	1	1	1	15	16	13	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SCD	FADS5, SCDOS, SCD, MSTP008, SCD1	stearoyl-CoA desaturase (delta-9-desaturase)	NM_005063, hCT2322391.0, hCT2322393.0, hCT2322394.0, hCT10484.3	200831_s_at, 200832_s_at, 211162_x_at, 211708_s_at	NP_005054.3, EAW49827.1, EAW49828.1, EAW49829.1, EAW49830.1
GeneID.25956	SEC31B	10	102,246,403	102,279,595	33,192	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1298	13035	in gene	0	1	0	9	25	2	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene SEC31B	SEC31L2, DKFZp434M183, SEC31B-1, SEC31B	SEC31 homolog B (S. cerevisiae)	NM_015490, hCT2321308.0, hCT2352224.0, hCT2352225.0, hCT1951248.0	209689_at	NP_056305.1, EAW49821.1, EAW49822.1, EAW49823.1, EAW49824.1
GeneID.4714	NDUFB8	10	102,283,497	102,289,636	6,139	-	2	1_A375_pNL7_minus_lncRNA_AR..1..944, 2_A375_pNL97_plus_lncRNA_AR..1..1299	-5946, -5916	upstream, upstream	1	1	0	34	48	11	1	2_A375_pNL97_plus_lncRNA_AR..1	48	Gene NDUFB8	CI-ASHI, ASHI, NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	NM_005004, hCT15775.3, hCT1957994.0	201226_at, 201227_s_at, 214241_at	NP_004995.1, EAW49820.1, EAW49819.1
GeneID.55662	HIF1AN	10	102,295,641	102,313,681	18,040	+	2	1_A375_pNL7_minus_lncRNA_AR..1..944, 2_A375_pNL97_plus_lncRNA_AR..1..1299	-57, -89	upstream, upstream	1	1	0	34	48	11	1	2_A375_pNL97_plus_lncRNA_AR..1	48	Gene HIF1AN	FIH1, DKFZp762F1811, FLJ20615, FLJ22027, HIF1AN	hypoxia inducible factor 1, alpha subunit inhibitor	NM_017902, hCT2322358.0, hCT15783.3	218525_s_at, 59999_at	NP_060372.2, EAW49818.1, EAW49817.1
GeneID.5076	PAX2	10	102,505,468	102,589,698	84,230	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1301	81316	in gene	0	1	0	14	18	18	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PAX2	PAX2		NM_003990, NM_003988, NM_003987, NM_000278, NM_003989, hCT1967382.1, hCT1967383.1, hCT2322363.0, hCT2322364.0, hCT2322366.0, hCT15776.2, hCT15777.2, hCT1962304.1	206228_at, 206229_x_at	NP_003981.2, NP_003979.2, NP_003978.2, NP_000269.2, NP_003980.2, EAW49816.1, EAW49809.1, EAW49810.1, EAW49811.1, EAW49812.1, EAW49813.1, EAW49814.1, EAW49815.1
GeneID.55719	FAM178A	10	102,672,326	102,724,891	52,565	+	1	4_A375_EGR1..1..1158	696	in gene	0	0	1	13	12	17	1	4_A375_EGR1..1	17	Gene FAM178A	C10orf6, FAM178A, MGC90157	family with sequence similarity 178, member A	NM_018121, NM_001136123, NR_024245, hCT2344373.0, hCT2344374.0, hCT2344375.0, hCT2352316.0	1553909_x_at, 203461_at, 203462_at, 235590_at	NP_060591.3, NP_001129595.1, EAW49805.1, EAW49806.1, EAW49807.1, EAW49808.1
GeneID.57715	SEMA4G	10	102,732,286	102,745,372	13,086	+	2	1_A375_pNL7_minus_lncRNA_AR..1..946, 2_A375_pNL97_plus_lncRNA_AR..1..1302	14914, 14850	downstream, downstream	1	1	0	18	22	16	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SEMA4G	SEMA4G, MGC102867, KIAA1619, FLJ20590	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	NM_017893, hCT2322374.0, hCT2322375.0, hCT2352326.0, hCT15787.3	203483_at, 219194_at	NP_060363.2, EAW49802.1, EAW49801.1, EAW49803.1, EAW49804.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.84545	MRPL43	10	102,737,579	102,747,272	9,693	-	2	1_A375_pNL7_minus_lncRNA_AR..1..946, 2_A375_pNL97_plus_lncRNA_AR..1..1302	72, 136	in gene, in gene	1	1	0	16	22	16	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MRPL43	bMRP36a, MRPL43, MGC48892, MGC17989	mitochondrial ribosomal protein L43	NM_032112, NM_176793, NM_176794, NM_176792, hCT2321301.0, hCT2352355.0, hCT2352356.0, hCT15789.1, hCT1951249.1, hCT1951250.1	224332_s_at, 230026_at, 230027_s_at	NP_115488.2, NP_789763.1, NP_789762.1, NP_789764.1, EAW49796.1, EAW49797.1, EAW49795.1, EAW49798.1, EAW49799.1, EAW49800.1
GeneID.56652	C10orf2	10	102,747,293	102,754,158	6,865	+	3	1_A375_pNL7_minus_lncRNA_AR..1..946, 2_A375_pNL97_plus_lncRNA_AR..1..1302, 2_A375_pNL97_plus_lncRNA_AR..1..1303	-93, -157, 11235	upstream, upstream, downstream	1	1	0	16	20	14	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene C10orf2	C10orf2, ATXN8, FLJ21832, PEOA3, IOSCA, MTDPS7, TWINL, PEO, PEO1, SANDO, SCA8	chromosome 10 open reading frame 2	NM_021830, NM_001163812, NM_001163813, NM_001163814, hCT2352324.0, hCT15786.3	218590_at	NP_068602.2, NP_001157284.1, NP_001157285.1, NP_001157286.1, EAW49793.1, EAW49794.1
GeneID.84445	LZTS2	10	102,756,965	102,767,590	10,625	+	5	1_A375_pNL7_minus_lncRNA_AR..1..946, 2_A375_pNL97_plus_lncRNA_AR..1..1302, 2_A375_pNL97_plus_lncRNA_AR..1..1303, 2_A375_pNL97_plus_lncRNA_AR..1..1304, 4_A375_EGR1..1..1159	-9765, -9829, 1563, 11611, 9787	upstream, upstream, in gene, downstream, in gene	1	1	1	13.5	17.25	14.75	4	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LZTS2	LAPSER1, KIAA1813, LZTS2	leucine zipper, putative tumor suppressor 2	NM_032429, hCT2322379.0, hCT2352327.0, hCT15788.3	1555881_s_at, 224473_x_at, 225013_at, 232129_s_at	NP_115805.1, EAW49792.1, EAW49790.1, EAW49791.1
GeneID.79955	PDZD7	10	102,777,089	102,790,879	13,790	-	2	1_A375_pNL7_minus_lncRNA_AR..1..947, 2_A375_pNL97_plus_lncRNA_AR..1..1304	-1633, 22303	upstream, downstream	1	1	0	16.5	19	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene PDZD7	PDZD7, PDZK7	PDZ domain containing 7	NM_024895, hCT15790.3	220555_s_at	NP_079171.1, EAW49788.1
GeneID.81855	SFXN3	10	102,790,996	102,800,998	10,002	+	1	1_A375_pNL7_minus_lncRNA_AR..1..947	1516	in gene	1	0	0	22	19	14	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene SFXN3	SFXN3, BA108L7.2, SFXN3	sideroflexin 3	NM_030971, hCT2322381.0	1559993_at, 217226_s_at, 220974_x_at	NP_112233.2, EAW49787.1
GeneID.81621	KAZALD1	10	102,820,999	102,825,351	4,352	+	2	4_A375_EGR1..1..1160, 4_A375_EGR1..1..1161	121, 5209	in gene, downstream	0	0	1	14.5	13.5	21	2	4_A375_EGR1..1	24	Gene KAZALD1	IGFBP-rP10, FKSG28, BONO1, FKSG40, KAZALD1, FLJ24094	Kazal-type serine peptidase inhibitor domain 1	NM_030929, hCT2322383.0, hCT2322384.0, hCT2322385.0, hCT2322386.0	1568598_at, 217511_at, 221000_s_at	NP_112191.2, EAW49782.1, EAW49783.1, EAW49784.1, EAW49785.1
GeneID.100505670	LOC100505670	10	102,826,056	102,827,888	1,832	+	2	4_A375_EGR1..1..1160, 4_A375_EGR1..1..1161	-4936, 152	upstream, in gene	0	0	1	14.5	13.5	21	2	4_A375_EGR1..1	24	Gene LOC100505670		hypothetical LOC100505670	XR_111127, XR_110446, XR_114421		
GeneID.100038246	TLX1NB	10	102,849,078	102,890,903	41,825	-	4	1_A375_pNL7_minus_lncRNA_AR..1..948, 1_A375_pNL7_minus_lncRNA_AR..1..949, 2_A375_pNL97_plus_lncRNA_AR..1..1305, 2_A375_pNL97_plus_lncRNA_AR..1..1306	49975, 45047, 50039, 45111	downstream, downstream, downstream, downstream	1	1	0	19.5	24	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene TLX1NB	TDI, TLX1NB, APT-B7, TD1	TLX1 neighbor	NM_001085398		NP_001078867.1
GeneID.8945	BTRC	10	103,113,825	103,317,070	203,245	+	6	1_A375_pNL7_minus_lncRNA_AR..1..950, 1_A375_pNL7_minus_lncRNA_AR..1..951, 2_A375_pNL97_plus_lncRNA_AR..1..1307, 2_A375_pNL97_plus_lncRNA_AR..1..1308, 4_A375_EGR1..1..1162, 4_A375_EGR1..1..1163	-145, 10799, -177, 10763, 10799, 212363	upstream, in gene, upstream, in gene, in gene, downstream	1	1	1	17	22.33	22.67	3	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene BTRC	betaTrCP, FBXW1, FWD1, BETA-TRCP, bTrCP1, FBW1A, FBXW1A, bTrCP, BTRC, MGC4643	beta-transducin repeat containing	NM_033637, NM_003939, hCT2322298.1, hCT2322297.1, hCT2322299.1, hCT2352363.0, hCT1951242.1	1563620_at, 204901_at, 216091_s_at, 222374_at, 224471_s_at	NP_378663.1, NP_003930.1, EAW49770.1, EAW49771.1, EAW49773.1, EAW49774.1, EAW49772.1
GeneID.6468	FBXW4	10	103,370,421	103,454,743	84,322	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1309	663	in gene	0	1	0	15	18	10	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene FBXW4	SHSF3, FBWD4, DAC, SHFM3, FBXW4, FBW4	F-box and WD repeat domain containing 4	NM_022039, hCT2321971.1, hCT2348003.0, hCT1814001.2	221519_at	NP_071322.1, EAW49751.1, EAW49752.1, EAW49753.1
GeneID.2253	FGF8	10	103,529,887	103,535,759	5,872	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1310, 4_A375_EGR1..1..1164	-7601, -7025	upstream, upstream	0	1	1	18	19	19	1	4_A375_EGR1..1	19	Gene FGF8	AIGF, HBGF-8, FGF8, MGC149376, KAL6	fibroblast growth factor 8 (androgen-induced)	NM_006119, NM_033163, NM_033164, NM_033165, hCT1967402.1, hCT2321966.0, hCT2321968.0, hCT2352298.0, hCT16758.3	208449_s_at	NP_006110.1, NP_149353.1, NP_149354.1, NP_149355.1, EAW49746.1, EAW49749.1, EAW49747.1, EAW49748.1, EAW49750.1
GeneID.10360	NPM3	10	103,541,082	103,543,170	2,088	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1310, 4_A375_EGR1..1..1164	-190, 386	upstream, in gene	0	1	1	18	19	19	1	4_A375_EGR1..1	19	Gene NPM3	PORMIN, TMEM123, NPM3	nucleophosmin/nucleoplasmin 3	NM_006993, hCT16757.3	205129_at	NP_008924.1, EAW49745.1
GeneID.10724	MGEA5	10	103,544,200	103,578,222	34,022	-	4	1_A375_pNL7_minus_lncRNA_AR..1..952, 2_A375_pNL97_plus_lncRNA_AR..1..1310, 2_A375_pNL97_plus_lncRNA_AR..1..1311, 4_A375_EGR1..1..1164	-82, 34862, -178, 35436	upstream, downstream, upstream, downstream	1	1	1	26	26	14	2	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene MGEA5	OGA, NCOAT, FLJ11229, KIAA0679, MGEA5, MEA5, FLJ23355	meningioma expressed antigen 5 (hyaluronidase)	NM_012215, NM_001142434, hCT2321962.0, hCT2321964.0, hCT2352323.0, hCT16770.3	200898_s_at, 200899_s_at, 214972_at, 223494_at, 235868_at	NP_036347.1, NP_001135906.1, EAW49741.1, EAW49742.1, EAW49743.1, EAW49744.1
GeneID.100289509	LOC100289509	10	103,578,825	103,588,646	9,821	+	3	1_A375_pNL7_minus_lncRNA_AR..1..952, 2_A375_pNL97_plus_lncRNA_AR..1..1311, 4_A375_EGR1..1..1165	-521, -425, 11895	upstream, upstream, downstream	1	1	1	23	29	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene LOC100289509		hypothetical LOC100289509	XR_111126, XR_110447, XR_114422		
GeneID.30819	KCNIP2	10	103,585,731	103,603,677	17,946	-	5	1_A375_pNL7_minus_lncRNA_AR..1..952, 1_A375_pNL7_minus_lncRNA_AR..1..953, 2_A375_pNL97_plus_lncRNA_AR..1..1311, 2_A375_pNL97_plus_lncRNA_AR..1..1312, 4_A375_EGR1..1..1165	25373, 2557, 25277, 2557, 12957	downstream, in gene, downstream, in gene, in gene	1	1	1	27.67	36.33	14.67	3	2_A375_pNL97_plus_lncRNA_AR..1	51	Gene KCNIP2	MGC17241, KCHIP2, KCNIP2, DKFZp566L1246	Kv channel interacting protein 2	NM_173192, NM_173195, NM_173194, NM_173197, NM_173191, NM_014591, NM_173193, hCT2321950.0, hCT2321952.0, hCT2321953.0, hCT2321955.0, hCT2321956.0, hCT2321957.0, hCT2321958.0, hCT16759.3, hCT1951251.2, hCT1951252.2, hCT1951253.2	1555230_a_at, 221321_s_at, 223727_at, 224528_s_at	NP_775284.1, NP_775287.1, NP_055406.2, NP_775283.1, NP_775286.1, NP_775289.1, NP_775285.1, EAW49730.1, EAW49731.1, EAW49732.1, EAW49733.1, EAW49734.1, EAW49735.1, EAW49740.1, EAW49736.1, EAW49737.1, EAW49738.1, EAW49739.1
GeneID.79591	C10orf76	10	103,605,356	103,815,932	210,576	-	5	1_A375_pNL7_minus_lncRNA_AR..1..953, 1_A375_pNL7_minus_lncRNA_AR..1..954, 2_A375_pNL97_plus_lncRNA_AR..1..1312, 2_A375_pNL97_plus_lncRNA_AR..1..1313, 2_A375_pNL97_plus_lncRNA_AR..1..1314	214812, 26, 214812, -4, -9092	downstream, in gene, downstream, upstream, upstream	1	1	0	26	34.67	10.67	3	2_A375_pNL97_plus_lncRNA_AR..1	51	Gene C10orf76	FLJ13114, MGC125927, C10orf76	chromosome 10 open reading frame 76	NM_024541, hCT2321946.0, hCT2321948.0, hCT1951256.1	1568733_at, 218891_at, 55662_at	NP_078817.2, EAW49728.1, EAW49727.1, EAW49729.1
GeneID.79803	HPS6	10	103,825,147	103,827,793	2,646	+	3	1_A375_pNL7_minus_lncRNA_AR..1..954, 2_A375_pNL97_plus_lncRNA_AR..1..1313, 2_A375_pNL97_plus_lncRNA_AR..1..1314	-9243, -9211, -123	upstream, upstream, upstream	1	1	0	23.5	26.5	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene HPS6	FLJ22501, HPS6, MGC20522, RP11-302K17.1	Hermansky-Pudlak syndrome 6	NM_024747, hCT2322308.0, hCT2322307.0	219052_at, 230371_at	NP_079023.2, EAW49725.1, EAW49726.1
GeneID.23082	PPRC1	10	103,892,787	103,910,090	17,303	+	4	1_A375_pNL7_minus_lncRNA_AR..1..955, 2_A375_pNL97_plus_lncRNA_AR..1..1315, 2_A375_pNL97_plus_lncRNA_AR..1..1316, 4_A375_EGR1..1..1166	-147, -115, 19117, 221	upstream, upstream, downstream, in gene	1	1	1	27.5	28	16	2	1_A375_pNL7_minus_lncRNA_AR..1	38	Gene PPRC1	MGC74642, PPRC1, PRC, RP11-302K17.6, KIAA0595	peroxisome proliferator-activated receptor gamma, coactivator-related 1	NM_015062, hCT2322309.0, hCT2352320.0, hCT16766.3	203737_s_at	NP_055877.3, EAW49719.1, EAW49720.1, EAW49721.1
GeneID.9221	NOLC1	10	103,911,933	103,923,627	11,694	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1316	-29	upstream	0	1	0	17	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NOLC1	NOPP130, KIAA0035, NOPP140, NOLC1, NS5ATP13, P130	nucleolar and coiled-body phosphoprotein 1	NM_004741, hCT1967404.1, hCT1967405.1, hCT2352302.0, hCT2352303.0, hCT2352304.0, hCT16761.3	205895_s_at, 211949_s_at, 211951_at	NP_004732.2, EAW49715.1, EAW49713.1, EAW49716.1, EAW49717.1, EAW49718.1, EAW49714.1
GeneID.83401	ELOVL3	10	103,986,143	103,989,346	3,203	+	1	4_A375_EGR1..1..1167	3969	downstream	0	0	1	16	19	17	1	4_A375_EGR1..1	17	Gene ELOVL3	CIG-30, ELOVL3, CIG30, MGC21435	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	NM_152310, hCT16767.2	234513_at	NP_689523.1, EAW49711.1
GeneID.5309	PITX3	10	103,989,946	104,001,231	11,285	-	3	1_A375_pNL7_minus_lncRNA_AR..1..956, 4_A375_EGR1..1..1167, 4_A375_EGR1..1..1168	-4081, 11119, 495	upstream, in gene, in gene	1	0	1	14.33	13	18.33	3	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene PITX3	MGC12766, PTX3, PITX3, CTPP4	paired-like homeodomain 3	NM_005029, hCT2321942.0, hCT16763.3	208277_at	NP_005020.1, EAW49709.1, EAW49710.1
GeneID.8729	GBF1	10	104,005,309	104,142,649	137,340	+	3	1_A375_pNL7_minus_lncRNA_AR..1..956, 2_A375_pNL97_plus_lncRNA_AR..1..1317, 4_A375_EGR1..1..1168	3, 116291, -4573	in gene, in gene, upstream	1	1	1	13	12.67	11.33	3	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene GBF1	KIAA0248, FLJ21283, MGC134878, ARF1GEF, MGC134877, FLJ21500, GBF1	golgi brefeldin A resistant guanine nucleotide exchange factor 1	NM_004193, hCT2344326.1	201439_at	NP_004184.1, EAW49707.1
GeneID.4791	NFKB2	10	104,154,229	104,162,281	8,052	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1318	-85	upstream	0	1	0	16	21	14	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NFKB2	NFKB2, p52, LYT10, LYT-10	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NM_002502, NM_001077494, NM_001077493, hCT2322137.0, hCT2322138.0, hCT2322139.0, hCT2322140.0, hCT2352307.0, hCT1686444.2, hCT1820469.1	207535_s_at, 209636_at, 211524_at	NP_002493.3, NP_001070962.1, NP_001070961.1, EAW49701.1, EAW49702.1, EAW49704.1, EAW49700.1, EAW49703.1, EAW49705.1, EAW49706.1
GeneID.5662	PSD	10	104,162,376	104,178,901	16,525	-	4	1_A375_pNL7_minus_lncRNA_AR..1..957, 2_A375_pNL97_plus_lncRNA_AR..1..1318, 2_A375_pNL97_plus_lncRNA_AR..1..1319, 2_A375_pNL97_plus_lncRNA_AR..1..1320	-1667, 24757, -603, -1667	upstream, downstream, upstream, upstream	1	1	0	26	32.67	12.67	3	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene PSD	TYL, KIAA2011, PSD1, PSD	pleckstrin and Sec7 domain containing	NM_002779, hCT2321910.0, hCT2321911.0, hCT16771.3	208102_s_at	NP_002770.3, EAW49693.1, EAW49694.1, EAW49695.1
GeneID.79176	FBXL15	10	104,179,571	104,182,893	3,322	+	5	1_A375_pNL7_minus_lncRNA_AR..1..957, 1_A375_pNL7_minus_lncRNA_AR..1..958, 2_A375_pNL97_plus_lncRNA_AR..1..1319, 2_A375_pNL97_plus_lncRNA_AR..1..1320, 2_A375_pNL97_plus_lncRNA_AR..1..1321	1197, 12877, -87, 1197, 12781	in gene, downstream, upstream, in gene, downstream	1	1	0	29.67	34.33	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene FBXL15	FLJ16137, Fbl15, FBXO37, FBXL15, MGC11279, JET, PSD	F-box and leucine-rich repeat protein 15	NM_024326, hCT16772.3	218938_at	NP_077302.3, EAW49699.1
GeneID.100288939	LOC100288939	10	104,181,242	104,182,893	1,651	-	5	1_A375_pNL7_minus_lncRNA_AR..1..957, 1_A375_pNL7_minus_lncRNA_AR..1..958, 2_A375_pNL97_plus_lncRNA_AR..1..1319, 2_A375_pNL97_plus_lncRNA_AR..1..1320, 2_A375_pNL97_plus_lncRNA_AR..1..1321	2125, -9555, 3389, 2125, -9459	downstream, upstream, downstream, downstream, upstream	1	1	0	29.67	34.33	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene LOC100288939		hypothetical protein LOC100288939	XM_003119474, XM_002343013, XM_003120659		XP_003119522.1, XP_002343054.1, XP_003120707.1
GeneID.79004	CUEDC2	10	104,183,002	104,192,423	9,421	-	5	1_A375_pNL7_minus_lncRNA_AR..1..957, 1_A375_pNL7_minus_lncRNA_AR..1..958, 2_A375_pNL97_plus_lncRNA_AR..1..1319, 2_A375_pNL97_plus_lncRNA_AR..1..1320, 2_A375_pNL97_plus_lncRNA_AR..1..1321	11655, -25, 12919, 11655, 71	downstream, upstream, downstream, downstream, in gene	1	1	0	29.67	34.33	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene CUEDC2	CUEDC2, MGC2491, C10orf66, bA18I14.5	CUE domain containing 2	NM_024040, hCT2321907.0, hCT2321908.0, hCT16773.3	218097_s_at	NP_076945.2, EAW49698.1, EAW49696.1, EAW49697.1
GeneID.574447	MIR146B	10	104,196,269	104,196,341	72	+	2	1_A375_pNL7_minus_lncRNA_AR..1..958, 2_A375_pNL97_plus_lncRNA_AR..1..1321	-3821, -3917	upstream, upstream	1	1	0	21	26	13	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene MIR146B	MIRN146B, miRNA146B, MIR146B	microRNA 146b	NR_030169		
GeneID.10121	ACTR1A	10	104,238,986	104,262,512	23,526	-	2	1_A375_pNL7_minus_lncRNA_AR..1..959, 2_A375_pNL97_plus_lncRNA_AR..1..1322	-1136, -112	upstream, upstream	1	1	0	21.5	18	9	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene ACTR1A	CTRN1, ACTR1A, ARP1, FLJ52800, FLJ55002, FLJ52695	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	NM_005736, hCT2321901.1, hCT2321902.1, hCT2340897.0, hCT14106.2	200720_s_at, 200721_s_at, 236713_at	NP_005727.1, EAW49686.1, EAW49685.1, EAW49687.1, EAW49688.1
GeneID.51684	SUFU	10	104,263,719	104,393,214	129,495	+	2	1_A375_pNL7_minus_lncRNA_AR..1..959, 2_A375_pNL97_plus_lncRNA_AR..1..1322	-71, -1095	upstream, upstream	1	1	0	21.5	18	9	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene SUFU	PRO1280, SUFUXL, SUFUH, SUFU	suppressor of fused homolog (Drosophila)	NM_001178133, NM_016169, hCT2322155.0, hCT2322156.0, hCT2322157.0, hCT2352308.0	222749_at, 224201_s_at, 224202_at, 224203_at	NP_001171604.1, NP_057253.2, EAW49681.1, EAW49682.1, EAW49683.1, EAW49684.1
GeneID.81603	TRIM8	10	104,404,252	104,418,076	13,824	+	2	1_A375_pNL7_minus_lncRNA_AR..1..960, 4_A375_EGR1..1..1169	1506, 21556	in gene, downstream	1	0	1	13	12.5	13	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene TRIM8	RNF27, TRIM8, GERP	tripartite motif containing 8	NM_030912, hCT2322159.0, hCT13880.2	221012_s_at, 223131_s_at, 223132_s_at, 226015_s_at	NP_112174.2, EAW49679.1, EAW49680.1
GeneID.403	ARL3	10	104,433,488	104,474,190	40,702	-	4	2_A375_pNL97_plus_lncRNA_AR..1..1323, 4_A375_EGR1..1..1169, 4_A375_EGR1..1..1170, 4_A375_EGR1..1..1171	462, 48382, 44766, -274	in gene, downstream, downstream, upstream	0	1	1	8.33	11	17.33	3	4_A375_EGR1..1	18	Gene ARL3	ARL3, ARFL3	ADP-ribosylation factor-like 3	NM_004311, hCT13675.1	1566590_at, 202641_at, 213433_at	NP_004302.1, EAW49678.1
GeneID.118980	SFXN2	10	104,474,298	104,498,946	24,648	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1323, 4_A375_EGR1..1..1171	-570, 166	upstream, in gene	0	1	1	13	15	18	1	4_A375_EGR1..1	18	Gene SFXN2	SFXN2	sideroflexin 2	NM_178858, hCT2322162.1, hCT2349219.0, hCT13881.4	227560_at	NP_849189.1, EAW49676.1, EAW49675.1, EAW49677.1
GeneID.119032	C10orf32	10	104,613,967	104,624,718	10,751	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1324	209	in gene	0	1	0	15	34	9	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene C10orf32	FLJ40752, MGC27171, C10orf32, DKFZp686B2219, RP11-753C18.6	chromosome 10 open reading frame 32	NM_144591, NM_001136200	225334_at	NP_653192.2, NP_001129672.1
GeneID.22978	NT5C2	10	104,845,940	104,953,056	107,116	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1325	336	in gene	0	1	0	12	15	9	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene NT5C2	NT5C2, cN-II, PNT5, NT5B, GMP	5'-nucleotidase, cytosolic II	NM_012229, NM_001134373, hCT2321894.0, hCT12939.3	209155_s_at, 241776_at	NP_036361.1, NP_001127845.1, EAW49656.1, EAW49657.1
GeneID.729020	hCG_2024410	10	105,005,644	105,007,773	2,129	+	1	1_A375_pNL7_minus_lncRNA_AR..1..961	-4252	upstream	1	0	0	16	13	8	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene hCG_2024410	LOC729020	rcRPE	NM_001143909		NP_001137381.1
GeneID.9118	INA	10	105,036,920	105,050,106	13,186	+	4	1_A375_pNL7_minus_lncRNA_AR..1..962, 1_A375_pNL7_minus_lncRNA_AR..1..963, 2_A375_pNL97_plus_lncRNA_AR..1..1327, 2_A375_pNL97_plus_lncRNA_AR..1..1328	-3992, 1736, -3992, 1768	upstream, in gene, upstream, in gene	1	1	0	31	39.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene INA	NF-66, MGC12702, FLJ57501, FLJ18662, TXBP-1, INA, NEF5	internexin neuronal intermediate filament protein, alpha	NM_032727, hCT2322182.0, hCT15249.2	204465_s_at	NP_116116.1, EAW49653.1, EAW49654.1
GeneID.84108	PCGF6	10	105,062,553	105,110,891	48,338	-	3	1_A375_pNL7_minus_lncRNA_AR..1..964, 2_A375_pNL97_plus_lncRNA_AR..1..1329, 4_A375_EGR1..1..1172	459, 43, 59	in gene, in gene, in gene	1	1	1	16	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PCGF6	PCGF6, MGC17541, RNF134, MBLR, MGC15678	polycomb group ring finger 6	NM_032154, NM_001011663, hCT1967341.1, hCT2321887.0, hCT2321889.0, hCT2352365.0, hCT2352366.0, hCT1951243.1	224326_s_at	NP_115530.2, NP_001011663.1, EAW49648.1, EAW49649.1, EAW49650.1, EAW49652.1, EAW49647.1, EAW49651.1
GeneID.6877	TAF5	10	105,127,724	105,148,822	21,098	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1330, 4_A375_EGR1..1..1173, 4_A375_EGR1..1..1174	148, 28828, 29884	in gene, downstream, downstream	0	1	1	10	15.33	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TAF5	TAF5, TAF2D, TAFII100	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	NM_006951, hCT2352226.0, hCT15246.3	1553526_a_at, 210053_at	NP_008882.2, EAW49646.1, EAW49645.1
GeneID.84833	USMG5	10	105,148,814	105,156,223	7,409	-	2	4_A375_EGR1..1..1173, 4_A375_EGR1..1..1174	-129, -1185	upstream, upstream	0	0	1	7.5	13.5	17	2	4_A375_EGR1..1	19	Gene USMG5	MGC14697, DKFZp566D211, USMG5, DAPIT, bA792D24.4, HCVFTP2	up-regulated during skeletal muscle growth 5 homolog (mouse)	NM_032747, hCT1961328.1, hCT1961329.1, hCT1984740.1	225413_at	NP_116136.1, EAW49643.1, EAW49642.1, EAW49644.1
GeneID.100302174	MIR1307	10	105,154,010	105,154,158	148	-	2	4_A375_EGR1..1..1173, 4_A375_EGR1..1..1174	-2194, -3250	upstream, upstream	0	0	1	7.5	13.5	17	2	4_A375_EGR1..1	19	Gene MIR1307	MIRN1307, MIR1307, hsa-mir-1307	microRNA 1307	NR_031707		
GeneID.22984	PDCD11	10	105,156,412	105,206,019	49,607	+	3	4_A375_EGR1..1..1173, 4_A375_EGR1..1..1174, 4_A375_EGR1..1..1175	-60, 996, 55364	upstream, in gene, downstream	0	0	1	9.33	13	19	3	4_A375_EGR1..1	23	Gene PDCD11	PDCD11, ALG-4, NFBP, ALG4, RRP5, KIAA0185	programmed cell death 11	NM_014976, hCT2321765.0, hCT15251.3, hCT1951246.1	212422_at, 212424_at	NP_055791.1, EAW49641.1, EAW49639.1, EAW49640.1
GeneID.51063	CALHM2	10	105,206,543	105,212,162	5,619	-	1	4_A375_EGR1..1..1175	386	in gene	0	0	1	13	12	23	1	4_A375_EGR1..1	23	Gene CALHM2	FAM26B, CALHM2	calcium homeostasis modulator 2	NM_015916, NR_024552, hCT1967384.1, hCT1967385.1, hCT2321428.0, hCT2321430.0, hCT2352227.0, hCT15248.4	221585_s_at, 57715_at	NP_057000.2, EAW49638.1, EAW49633.1, EAW49635.1, EAW49637.1, EAW49636.1, EAW49634.1
GeneID.100505820	LOC100505820	10	105,212,603	105,222,452	9,849	+	1	4_A375_EGR1..1..1175	-827	upstream	0	0	1	13	12	23	1	4_A375_EGR1..1	23	Gene LOC100505820		hypothetical LOC100505820	XR_111121, XR_110451, XR_114426		

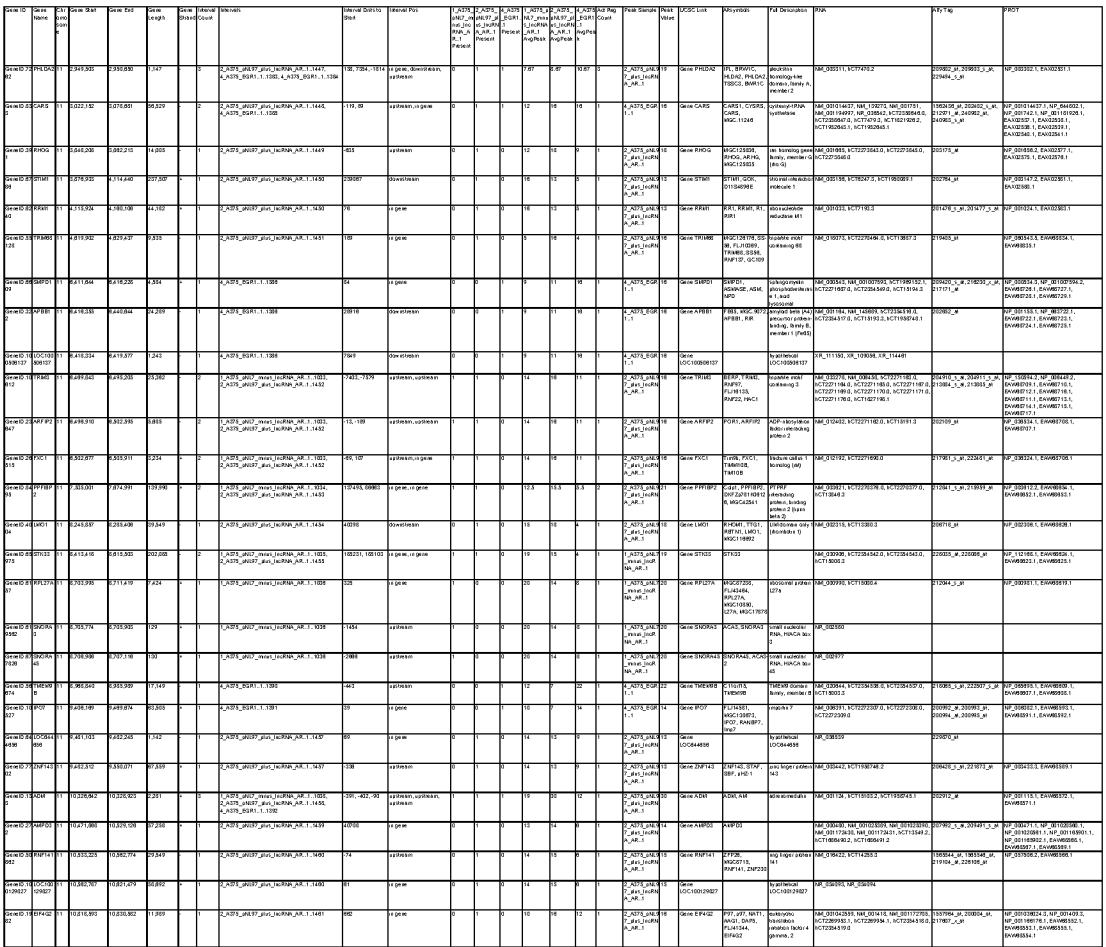
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	AltSymbols	Full Description	RNA	Affy Tag	PROT
GeneID.255022	CALHM1	10	105,213,144	105,218,648	5,504	-	1	4_A375_EGR1..1..1175	6672	downstream	0	0	1	13	12	23	1	4_A375_EGR1..1	23	Gene CALHM1	CALHM1, FAM26C, MGC39617, MGC39514	calcium homeostasis modulator 1	NM_001001412, hCT2321427.1	1554367_at	NP_001001412.3, EAW49632.1
GeneID.9148	NEURL	10	105,253,735	105,352,309	98,574	+	1	4_A375_EGR1..1..1176	62057	in gene	0	0	1	8	8	18	1	4_A375_EGR1..1	18	Gene NEURL	bA416N2.1, NEURL, neu, neu-1, RNF67, NEURL1	neuralized homolog (Drosophila)	NM_004210, hCT2321769.0, hCT2321772.0, hCT15247.3	204888_s_at, 204889_s_at	NP_004201.3, EAW49628.1, EAW49629.1, EAW49630.1
GeneID.9644	SH3PXD2A	10	105,353,784	105,615,164	261,380	-	12	1_A375_pNL7_minus_lncRNA_AR..1..965, 1_A375_pNL7_minus_lncRNA_AR..1..966, 1_A375_pNL7_minus_lncRNA_AR..1..967, 2_A375_pNL97_plus_lncRNA_AR..1..1331, 2_A375_pNL97_plus_lncRNA_AR..1..1332, 2_A375_pNL97_plus_lncRNA_AR..1..1333, 2_A375_pNL97_plus_lncRNA_AR..1..1334, 2_A375_pNL97_plus_lncRNA_AR..1..1335, 4_A375_EGR1..1..1177, 4_A375_EGR1..1..1178, 4_A375_EGR1..1..1179, 4_A375_EGR1..1..1180	194908, 108188, 27116, 194812, 108060, 54444, 26556, -6372, 242492, 195036, 98705, 56732	in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream, in gene, in gene, in gene, in gene	1	1	1	15.25	15.75	13.5	8	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SH3PXD2A	SH3MD1, FISH, SH3PXD2A, TSK5	SH3 and PX domains 2A	NM_014631, hCT2321414.0, hCT2321415.0, hCT2321416.0, hCT1951241.1	207661_s_at, 213252_at, 224817_at	NP_055446.2, EAW49625.1, EAW49622.1, EAW49623.1, EAW49624.1
GeneID.100505839	LOC100505839	10	105,506,537	105,515,167	8,630	+	3	1_A375_pNL7_minus_lncRNA_AR..1..968, 2_A375_pNL97_plus_lncRNA_AR..1..1332, 4_A375_EGR1..1..1179	439, 567, 9922	in gene, in gene, downstream	1	1	1	15.5	17	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LOC100505839		hypothetical LOC100505839	XR_110452		
GeneID.79991	OBFC1	10	105,637,316	105,678,045	40,729	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1336	22461	in gene	0	1	0	12	20	3	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene OBFC1	STN1, bA541N10.2, RPA-32, AAF-44, OBFC1, RP11-541N10.2, AAF44, FLJ22559	oligonucleotide/oligosaccharide-binding fold containing 1	NM_024928, hCT15252.3, hCT1957992.1	219100_at	NP_079204.2, EAW49620.1, EAW49619.1
GeneID.119392	C10orf78	10	105,881,816	105,886,143	4,327	+	1	1_A375_pNL7_minus_lncRNA_AR..1..969	-246	upstream	1	0	0	17	13	9	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene C10orf78	MEIR5, bA373N18.1, MEI5, FLJ41960, C10orf78	MEI5 meiotic recombination protein homolog (S. cerevisiae)	NM_145247, NM_001002759, hCT1647813.3, hCT1951235.1	236027_at, 238794_at	NP_660290.3, NP_001002759.1, EAW49610.1, EAW49611.1
GeneID.80217	C10orf79	10	105,889,646	105,992,120	102,474	-	2	1_A375_pNL7_minus_lncRNA_AR..1..969, 2_A375_pNL97_plus_lncRNA_AR..1..1337	110552, 152	downstream, in gene	1	1	0	14	18	10	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene C10orf79	bA373N18.2, FLJ22944, C10orf79, FLJ38006, WDR96	WD repeat domain 96	NM_025145, hCT2349220.1, hCT2349221.0, hCT2349222.1, hCT14247.4, hCT1961047.2	220919_s_at, 224251_at, 231084_at, 243896_at	NP_079421.5, EAW49608.1, EAW49605.1, EAW49606.1, EAW49607.1, EAW49609.1
GeneID.9446	GSTO1	10	106,013,952	106,027,222	13,270	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1338, 4_A375_EGR1..1..1182	512, 752	in gene, in gene	0	1	1	15	15	16	1	4_A375_EGR1..1	16	Gene GSTO1	DKFZp686H13163, GSTTLp28, GSTO1, P28	glutathione S-transferase omega 1	NM_001191002, NM_001191003, NM_004832, hCT12937.3, hCT1962309.1, hCT1962310.0, hCT1962311.0	1557915_s_at, 201470_at	NP_001177931.1, NP_001177932.1, NP_004823.1, EAW49601.1, EAW49602.1, EAW49604.1, EAW49603.1
GeneID.119391	GSTO2	10	106,028,631	106,059,176	30,545	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1339	31721	downstream	0	1	0	16	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene GSTO2	bA127L20.1, GSTO2	glutathione S-transferase omega 2	NM_183239, NM_001191013, NM_001191014, NM_001191015, hCT1960706.2, hCT1964896.1, hCT1964897.1	227163_at	NP_899062.1, NP_001177942.1, NP_001177943.1, NP_001177944.1, EAW49598.1, EAW49600.1, EAW49599.1
GeneID.85450	ITPRIP	10	106,071,899	106,093,663	21,764	-	4	1_A375_pNL7_minus_lncRNA_AR..1..970, 1_A375_pNL7_minus_lncRNA_AR..1..971, 2_A375_pNL97_plus_lncRNA_AR..1..1340, 2_A375_pNL97_plus_lncRNA_AR..1..1341	4415, -4769, 4415, -4769	in gene, upstream, in gene, upstream	1	1	0	39	36.5	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene ITPRIP	DANGER, KIAA1754, bA127L20.2, ITPRIP, bA127L20	inositol 1,4,5-triphosphate receptor interacting protein	NM_033397, hCT1657457.3, hCT1952594.1	225582_at	NP_203755.1, EAW49597.1, EAW49596.1
GeneID.100505856	LOC100505856	10	106,083,122	106,086,762	3,640	+	2	1_A375_pNL7_minus_lncRNA_AR..1..970, 2_A375_pNL97_plus_lncRNA_AR..1..1340	6126, 6126	downstream, downstream	1	1	0	26	21	7	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene LOC100505856		hypothetical LOC100505856	XR_111119, XR_110453, XR_114428		
GeneID.22986	SORCS3	10	106,400,859	107,024,993	624,134	+	4	1_A375_pNL7_minus_lncRNA_AR..1..972, 1_A375_pNL7_minus_lncRNA_AR..1..973, 2_A375_pNL97_plus_lncRNA_AR..1..1343, 4_A375_EGR1..1..1183	183493, 296829, 183461, -627	in gene, in gene, in gene, upstream	1	1	1	28.33	35.33	9	3	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene SORCS3	SORCS3, SORCS	sortilin-related VPS10 domain containing receptor 3	NM_014978, hCT2344376.2, hCT2351174.0	215522_at	NP_055793.1, EAW49590.1, EAW49589.1
GeneID.120	ADD3	10	111,765,726	111,895,323	129,597	+	4	1_A375_pNL7_minus_lncRNA_AR..1..974, 2_A375_pNL97_plus_lncRNA_AR..1..1346, 2_A375_pNL97_plus_lncRNA_AR..1..1347, 4_A375_EGR1..1..1186	1394, 1442, 71042, 2274	in gene, in gene, in gene, in gene	1	1	1	11	15.33	12	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ADD3	ADDL, ADD3	adducin 3 (gamma)	NM_016824, NM_001121, NM_019903, hCT2321217.0, hCT2321219.0, hCT2321221.0, hCT1984113.1	201034_at, 201752_s_at, 201753_s_at, 205882_x_at	NP_058432.1, NP_001112.2, NP_063968.1, EAW49571.1, EAW49572.1, EAW49574.1, EAW49573.1
GeneID.4601	MXI1	10	111,967,363	112,047,123	79,760	+	2	1_A375_pNL7_minus_lncRNA_AR..1..975, 2_A375_pNL97_plus_lncRNA_AR..1..1348	-67, 3117	upstream, in gene	1	1	0	18	15	10	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene MXI1	bHLHc11, MXI1, MXD2, MGC43220, MXI, MAD2	MAX interactor 1	NM_130439, NM_005962, NM_001008541, hCT2321200.0, hCT2321201.0, hCT2321203.0, hCT2321204.0, hCT1951738.1, hCT1951739.1	202364_at	NP_569157.2, NP_005953.4, NP_001008541.1, EAW49565.1, EAW49567.1, EAW49568.1, EAW49566.1, EAW49569.1, EAW49570.1
GeneID.1847	DUSP5	10	112,257,625	112,271,302	13,677	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1351, 2_A375_pNL97_plus_lncRNA_AR..1..1352	-217, 791	upstream, in gene	0	1	0	10.5	16.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene DUSP5	DUSP5, HVH3, DUSP	dual specificity phosphatase 5	NM_004419, hCT2321209.0, hCT1951740.1	209457_at	NP_004410.3, EAW49560.1, EAW49559.1
GeneID.9126	SMC3	10	112,327,449	112,364,392	36,943	+	2	1_A375_pNL7_minus_lncRNA_AR..1..979, 2_A375_pNL97_plus_lncRNA_AR..1..1355	-217, -153	upstream, upstream	1	1	0	40	43	15	1	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene SMC3	HCAP, BAM, SMC3, CSPG6, SMC3L1, CDLS3, BMH	structural maintenance of chromosomes 3	NM_005445, hCT2321211.0, hCT2321212.0	1558925_at, 209257_s_at, 209258_s_at, 209259_s_at	NP_005436.1, EAW49558.1, EAW49557.1
GeneID.282996	RBM20	10	112,404,155	112,599,227	195,072	+	4	1_A375_pNL7_minus_lncRNA_AR..1..980, 1_A375_pNL7_minus_lncRNA_AR..1..981, 2_A375_pNL97_plus_lncRNA_AR..1..1356, 2_A375_pNL97_plus_lncRNA_AR..1..1357	28101, 130032, 28133, 129973	in gene, in gene, in gene, in gene	1	1	0	20.5	22	7	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene RBM20	RBM20		NM_001134363	236783_at	NP_001127835.1
GeneID.92482	NCRNA00081	10	112,658,488	112,679,124	20,636	-	3	1_A375_pNL7_minus_lncRNA_AR..1..982, 2_A375_pNL97_plus_lncRNA_AR..1..1358, 4_A375_EGR1..1..1188	100, 116, 644	in gene, in gene, in gene	1	1	1	23	27	15	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene NCRNA00081	bA348N5.3, BBIP10, BBIP1, NCRNA00081	BBSome interacting protein 1	NR_024141	213220_at, 213224_s_at, 226993_s_at, 232665_at, 232910_at, 236043_at, 239684_at	
GeneID.8036	SHOC2	10	112,679,301	112,773,425	94,124	+	3	1_A375_pNL7_minus_lncRNA_AR..1..982, 2_A375_pNL97_plus_lncRNA_AR..1..1358, 4_A375_EGR1..1..1188	-277, -293, -821	upstream, upstream, upstream	1	1	1	23	27	15	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SHOC2	SUR8, SIAA0862, KIAA0862, SOC-2, FLJ80412, SOC2, SHOC2, SUR-8	soc-2 suppressor of clear homolog (C. elegans)	NM_007373, hCT2352294.0, hCT31986.3, hCT1962345.0	202777_at	NP_031399.2, EAW49550.1, EAW49548.1, EAW49549.1
GeneID.57678	GPAM	10	113,909,622	113,943,525	33,903	-	2	1_A375_pNL7_minus_lncRNA_AR..1..985, 2_A375_pNL97_plus_lncRNA_AR..1..1361	-91, -59	upstream, upstream	1	1	0	21	26	12	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene GPAM	RP11-426E5.2, KIAA1560, GPAM, GPAT1, MGC26846, GPAT	glycerol-3-phosphate acyltransferase, mitochondrial	NM_020918, hCT2352255.0, hCT2352256.0, hCT32243.3	225420_at, 225424_at	NP_065969.3, EAW49544.1, EAW49543.1, EAW49545.1
GeneID.84429	ZDHHC6	10	114,190,058	114,206,672	16,614	-	3	1_A375_pNL7_minus_lncRNA_AR..1..986, 2_A375_pNL97_plus_lncRNA_AR..1..1362, 4_A375_EGR1..1..1189	-126, 64, -37	upstream, in gene, upstream	1	1	1	19	17	23	1	4_A375_EGR1..1	23	Gene ZDHHC6	ZNF376, ZDHHC6, FLJ21952	zinc finger, DHHC-type containing 6	NM_022494, hCT2320967.0, hCT2352257.0, hCT2352258.0, hCT32244.3, hCT1958000.1, hCT1958001.1	218249_at	NP_071939.1, EAW49526.1, EAW49528.1, EAW49529.1, EAW49530.1, EAW49531.1, EAW49527.1
GeneID.143187	VTI1A	10	114,206,756	114,578,503	371,747	+	4	1_A375_pNL7_minus_lncRNA_AR..1..986, 1_A375_pNL7_minus_lncRNA_AR..1..987, 2_A375_pNL97_plus_lncRNA_AR..1..1362, 4_A375_EGR1..1..1189	44, 187260, -148, -47	in gene, in gene, upstream, upstream	1	1	1	17.5	12.5	13.5	2	4_A375_EGR1..1	23	Gene VTI1A	Vti1-rp2, VTI1A, MVti1	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	NM_145206, hCT2349196.0, hCT1951726.1	1552536_at, 235034_at, 235923_at, 236649_at, 242356_at	NP_660207.2, EAW49525.1, EAW49524.1
GeneID.100422909	MIR4295	10	114,393,929	114,394,013	84	+	1	1_A375_pNL7_minus_lncRNA_AR..1..987	87	downstream	1	0	0	16	8	4	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene MIR4295	MIR4295	microRNA 4295	NR_036177		
GeneID.6934	TCF7L2	10	114,710,009	114,927,437	217,428	+	3	1_A375_pNL7_minus_lncRNA_AR..1..988, 2_A375_pNL97_plus_lncRNA_AR..1..1363, 2_A375_pNL97_plus_lncRNA_AR..1..1364	41991, 9255, 41991	in gene, in gene, in gene	1	1	0	17.5	18	7.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene TCF7L2	TCF4, TCF-4, TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	NM_001146283, NM_001146284, NM_001146285, NM_001146286, NM_030756, NM_001146274, hCT2322954.0, hCT2322955.0, hCT2322956.0, hCT2322957.0, hCT2322958.0, hCT2322959.0, hCT2322960.0, hCT2322961.0, hCT2322963.0, hCT2352336.0, hCT2352337.0, hCT32266.3	212759_s_at, 212761_at, 212762_s_at, 216035_x_at, 216037_x_at, 216511_s_at, 236094_at	NP_001139755.1, NP_001139756.1, NP_110383.2, NP_001139757.1, NP_001139758.1, NP_001139746.1, EAW49506.1, EAW49507.1, EAW49508.1, EAW49509.1, EAW49510.1, EAW49511.1, EAW49513.1, EAW49516.1, EAW49512.1, EAW49514.1, EAW49515.1, EAW49517.1
GeneID.840	CASP7	10	115,438,935	115,490,664	51,729	+	3	1_A375_pNL7_minus_lncRNA_AR..1..990, 2_A375_pNL97_plus_lncRNA_AR..1..1366, 4_A375_EGR1..1..1190	521, 137, 121	in gene, in gene, in gene	1	1	1	17	24	18	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CASP7	CMH-1, CASP7, MCH3, ICE-LAP3	caspase 7, apoptosis-related cysteine peptidase	NM_033340, NM_001227, NM_033339, NM_033338, hCT2322972.0, hCT2352293.0, hCT1820339.2, hCT1957988.1, hCT1962044.1	207181_s_at	NP_203126.1, NP_001218.1, NP_203124.1, NP_203125.1, EAW49495.1, EAW49496.1, EAW49494.1, EAW49497.1, EAW49498.1
GeneID.9937	DCLRE1A	10	115,594,484	115,613,859	19,375	-	2	1_A375_pNL7_minus_lncRNA_AR..1..991, 2_A375_pNL97_plus_lncRNA_AR..1..1367	-205, -893	upstream, upstream	1	1	0	14.5	16	10	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene DCLRE1A	SNM1, KIAA0086, PSO2, SNM1A, DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)	NM_014881, hCT2320951.0, hCT32263.2	209604_at	NP_055696.3, EAW49489.1, EAW49490.1
GeneID.374354	NHLRC2	10	115,614,391	115,672,265	57,874	+	2	1_A375_pNL7_minus_lncRNA_AR..1..991, 2_A375_pNL97_plus_lncRNA_AR..1..1367	-327, 381	upstream, in gene	1	1	0	14.5	16	10	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene NHLRC2	FLJ20147, FLJ33312, NHLRC2, DKFZp779F115, FLJ25621, MGC45492	NHL repeat containing 2	NM_198514, hCT2352329.0, hCT32264.2	219353_at, 235356_at, 236185_at, 244320_at	NP_940916.2, EAW49488.1, EAW49487.1
GeneID.55088	C10orf118	10	115,881,974	115,934,364	52,390	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1368	604	in gene	0	1	0	15	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C10orf118	MGC118918, C10orf118, FLJ35301, MGC129699, FLJ10166	chromosome 10 open reading frame 118	NM_018017	219644_at, 227701_at, 229399_at	NP_060487.2
GeneID.100302224	MIR2110	10	115,933,864	115,933,938	74	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1368	178	downstream	0	1	0	15	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MIR2110	MIR2110, hsa-mir-2110	microRNA 2110	NR_031747		
GeneID.56165	TDRD1	10	115,939,029	115,992,063	53,034	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1368, 4_A375_EGR1..1..1192	-5269, 60663	upstream, downstream	0	1	1	9	12.5	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TDRD1	CT41.1, FLJ21082, TDRD1	tudor domain containing 1	NM_198795, hCT2321168.1, hCT2321169.1, hCT2343998.1, hCT2352301.0, hCT32213.4	221018_s_at	NP_942090.1, EAW49477.1, EAW49476.1, EAW49478.1, EAW49479.1, EAW49480.1
GeneID.340706	VWA2	10	115,999,018	116,049,751	50,733	+	1	4_A375_EGR1..1..1192	694	in gene	0	0	1	3	5	19	1	4_A375_EGR1..1	19	Gene VWA2	NET42, AMACO, MGC157755, CCSP-2, VWA2	von Willebrand factor A domain containing 2	NM_198496, hCT31090.2		NP_940898.1, EAW49475.1
GeneID.84632	AFAP1L2	10	116,054,583	116,164,515	109,932	-	5	1_A375_pNL7_minus_lncRNA_AR..1..992, 2_A375_pNL97_plus_lncRNA_AR..1..1369, 2_A375_pNL97_plus_lncRNA_AR..1..1370, 4_A375_EGR1..1..1193, 4_A375_EGR1..1..1194	58947, 15187, 9571, 58771, 419	in gene, in gene, in gene, in gene, in gene	1	1	1	15	14.5	11.25	4	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene AFAP1L2	FLJ14564, AFAP1L2, XB130, KIAA1914	actin filament associated protein 1-like 2	NM_032550, NM_001001936, hCT2321075.1, hCT2349237.0, hCT2352305.0, hCT2352306.0, hCT32214.2	226829_at	NP_115939.1, NP_001001936.1, EAW49470.1, EAW49472.1, EAW49473.1, EAW49474.1, EAW49471.1
GeneID.142940	TRUB1	10	116,697,952	116,737,439	39,487	+	1	1_A375_pNL7_minus_lncRNA_AR..1..993	32	in gene	1	0	0	16	19	5	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene TRUB1	TRUB1, PUS4	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	NM_139169, hCT32217.3	226339_at, 235447_at, 236020_s_at, 241605_at, 241606_s_at	NP_631908.1, EAW49463.1
GeneID.26033	ATRNL1	10	116,853,124	117,708,496	855,372	+	1	4_A375_EGR1..1..1195	523164	in gene	0	0	1	4	4	15	1	4_A375_EGR1..1	15	Gene ATRNL1	ATRNL1, FLJ45344, ALP, bA338L11.1, KIAA0534, bA454H24.1	attractin-like 1	NM_207303, hCT2321029.0, hCT2352319.0, hCT31089.3	1569796_s_at, 213744_at, 213745_at	NP_997186.1, EAW49460.1, EAW49459.1, EAW49461.1
GeneID.2674	GFRA1	10	117,816,436	118,033,126	216,690	-	2	1_A375_pNL7_minus_lncRNA_AR..1..994, 4_A375_EGR1..1..1196	89734, 109786	in gene, in gene	1	0	1	13	10.5	11	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene GFRA1	MGC23045, TRNR1, FLJ10561, GFR-ALPHA-1, DKFZp313E1012, RET1L, FLJ31546, GFRA1, GDNFRA, DKFZp686J0156, GDNFR, RETL1	GDNF family receptor alpha 1	NM_005264, NM_145793, NM_001145453, hCT2320985.0, hCT2352362.0, hCT32231.2	205696_s_at	NP_005255.1, NP_665736.1, NP_001138925.1, EAW49456.1, EAW49457.1, EAW49458.1
GeneID.5407	PNLIPRP1	10	118,350,490	118,368,666	18,196	+	1	4_A375_EGR1..1..1197	18742	downstream	0	0	1	4	10	14	1	4_A375_EGR1..1	14	Gene PNLIPRP1	PNLIPRP1, PLRP1	pancreatic lipase-related protein 1	NM_006229, hCT2321035.0, hCT32229.3	206694_at, 210722_at	NP_006220.1, EAW49450.1, EAW49449.1
GeneID.259217	HSPA12A	10	118,430,703	118,502,085	71,382	-	1	4_A375_EGR1..1..1198	805	in gene	0	0	1	10	5	14	1	4_A375_EGR1..1	14	Gene HSPA12A	KIAA0417, HSPA12A, FLJ13874	heat shock 70kDa protein 12A	NM_025015	214434_at, 220763_at	NP_079291.2
GeneID.57698	KIAA1598	10	118,644,306	118,765,088	120,782	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1371	533	in gene	0	1	0	16	15	8	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene KIAA1598	SHOOTIN1, shootin-1, KIAA1598, MGC40476, DKFZp686A0439	KIAA1598	NM_001127211, NM_018330, hCT2321181.1, hCT2321182.1, hCT2321183.0, hCT2321184.1, hCT2352367.0	221802_s_at	NP_001120683.1, NP_060800.2, EAW49434.1, EAW49435.1, EAW49436.1, EAW49438.1, EAW49437.1
GeneID.11023	VAX1	10	118,888,032	118,897,812	9,780	-	1	4_A375_EGR1..1..1199	-2812	upstream	0	0	1	4	8	15	1	4_A375_EGR1..1	15	Gene VAX1	MGC126745, VAX1, MGC126743	ventral anterior homeobox 1	NM_199131, NM_001112704, hCT2350718.0, hCT32183.4		NP_954582.1, NP_001106175.1, EAW49432.1, EAW49433.1
GeneID.338567	KCNK18	10	118,957,000	118,969,810	12,810	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1372, 4_A375_EGR1..1..1201, 4_A375_EGR1..1..1202	19384, 19208, 20040	downstream, downstream, downstream	0	1	1	13	14.5	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene KCNK18	KCNK18, TRESK, TRESK-2, TRIK, MGR13, TRESK2, K2p18.1	potassium channel, subfamily K, member 18	NM_181840		NP_862823.1
GeneID.118987	PDZD8	10	119,042,806	119,134,937	92,331	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1373	-263	upstream	0	1	0	16	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PDZD8	FLJ25412, PDZK8, PDZD8, FLJ34427, bA129M16.2	PDZ domain containing 8	NM_173791, hCT32179.3	225629_at, 225630_at	NP_776152.1, EAW49427.1
GeneID.2834	PRLHR	10	120,352,916	120,355,160	2,244	-	4	1_A375_pNL7_minus_lncRNA_AR..1..998, 2_A375_pNL97_plus_lncRNA_AR..1..1378, 2_A375_pNL97_plus_lncRNA_AR..1..1379, 4_A375_EGR1..1..1203	856, 824, -584, -298	in gene, in gene, upstream, upstream	1	1	1	21	24	18	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PRLHR	GPR10, MGC126541, PrRPR, PRLHR, GR3, MGC126539	prolactin releasing hormone receptor	NM_004248, hCT2321565.0, hCT32412.2	231805_at	NP_004239.1, EAW49413.1, EAW49414.1



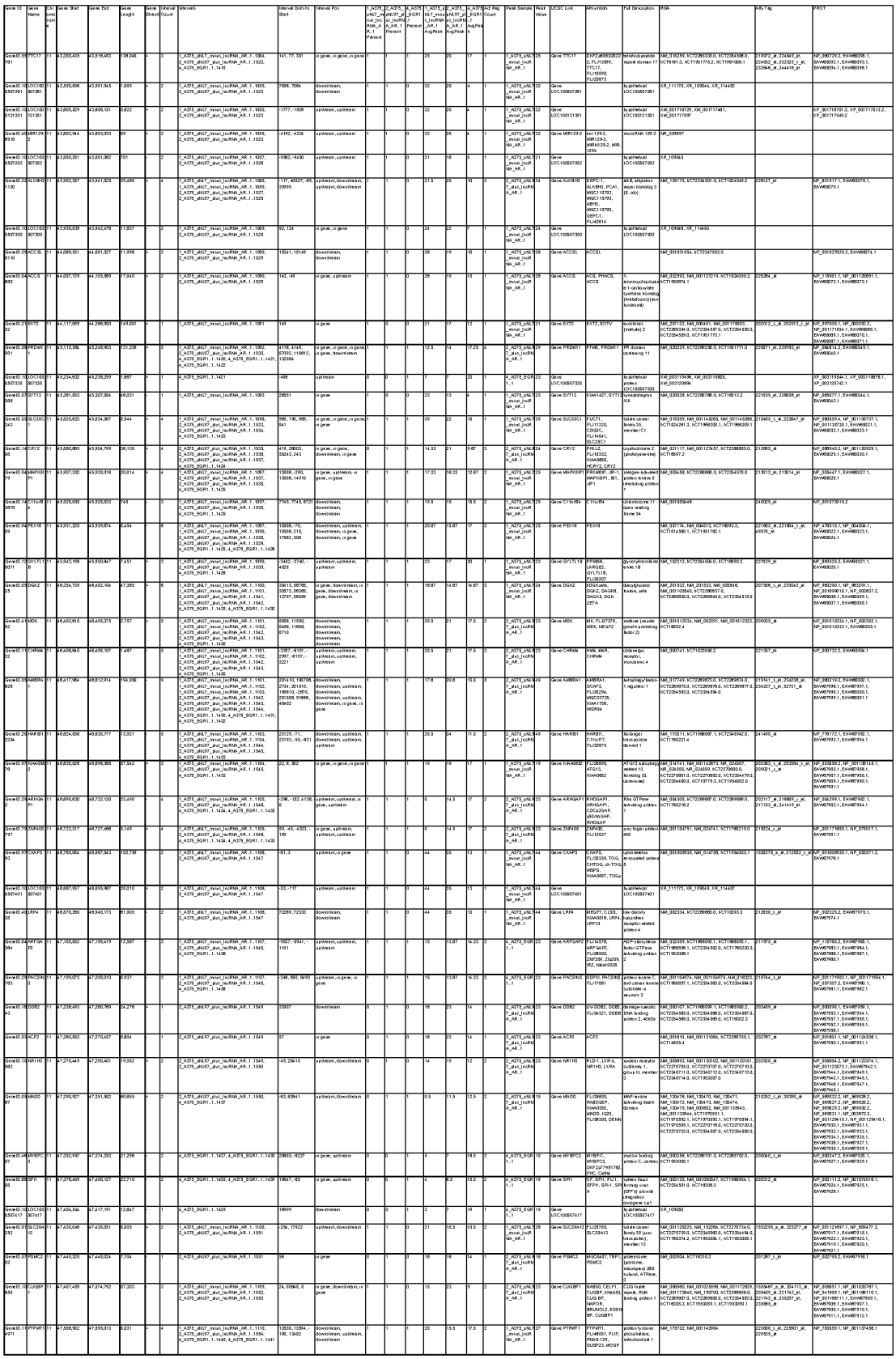
Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_uNU7_...R_1 Percent	2_A375_2_A375_uNU7_...R_1 Percent	3_A375_2_A375_uNU7_...R_1 Percent	1_A375_2_A375_NU7_mimic_lncRNA_AR_1 Avg Peak	2_A375_2_A375_uNU7_...R_1 Avg Peak	3_A375_2_A375_uNU7_...R_1 Avg Peak	Add Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:10 03394	C10orf6 9	10	120,449,494	120,514,758	74,264	-	2	1_A375_uNU7_mimic_lncRNA_AR_1...999, 2_A375_uNU7_plus_lncRNA_AR_1...1000	166, 195	vs gene, cr gene	1	1	0	20	19	13	1	1_A375_uNU7_...R_1	320	Gene C10orf6	MGC33213, C10orf6, FLJ46409	chromosome 10 open reading frame 69	NM_152510, NCT03609411, NCT02611435	229192_at, 227735_s_at, 227737_at, 227737_s_at, 227356_at	NP_725517.3, ENSP00432 12.1, ENSN0411.1
GeneID:88 81	EIF5A	19	50,276,341	50,540,334	43,793	-	1	2_A375_uNU7_plus_lncRNA_AR_1...1351	-114	upstream	0	1	0	16	13	8	1	2_A375_uNU7_plus_lncRNA_AR_1	913	Gene EIF5A	eIF5, EIF5A, PHT, EIF5D1, MTGF4/eIF5, EIF5, dt55, TIP32, SMAP038, eIF5, p70	eukaryotic translation initiation factor 5, subunit A	NM_020756, NCT02613513	200805_s_at, 200896_s_at, 200897_at	NP_0007411.1, ENSP44498.1
GeneID:10 915	PRDX2	19	20,937,215	20,938,545	11,330	-	1	1_A375_uNU7_minus_lncRNA_AR_1...1000	169	vs gene	1	0	0	17	14	10	1	1_A375_uNU7_...R_1	17	Gene PRDX2	SP-22, NKEFB, AOE37, HBP23, PRDX2, ACP-1, hOPI, MGC24293	peroxiredoxin 2	NM_016082, NM_008793, NCT01967491, NCT02622543.0, NCT01933.0, NCT01962543.1	200169_at, 200768_at	NP_056517.2, NP_008784.1, ENSN0398.1, ENSN0397.1, ENSN0398.1, ENSN0399.1
GeneID:88 01	RGS10	10	121,299,339	121,302,222	42,883	-	2	2_A375_uNU7_plus_lncRNA_AR_1...1302, 4_A375_DGR1...1205	42102, 23982	downstream, vs gene	0	1	1	11	11.3	11	2	2_A375_uNU7_...R_1	617	Gene RGS10	RGS10	regulator of G-protein signaling 10	NM_003925, NM_001003329, NCT02300454.0, NCT01662.2, NCT1614002.1	204316_at, 204319_s_at, 214690_s_at	NP_002916.1, NP_001003239.1, ENSN0399.1, ENSN0390.1, ENSN0391.1
GeneID:70 72	TIAL1	10	121,332,977	121,396,541	63,564	-	2	2_A375_uNU7_plus_lncRNA_AR_1...1303, 4_A375_DGR1...1206	-195, -215	upstream, upstream	0	1	1	14	20	20	1	2_A375_uNU7_...R_1	620	Gene TIAL1	MGC23401, TCBP, TIAL1, TIAR	TIA1 cytotoxic granule-associated RNA binding protein-like 1	NM_022332, NM_001033910, NCT02300510.0, NCT02305612.0, NCT01663.3, NCT01958421.1	202405_at, 202406_s_at, 217502_at	NP_0022431.1, NP_001029097.1, ENSN0355.1, ENSN0356.1, ENSN0357.1, ENSN0358.1
GeneID:88 31	BAG3	10	121,419,662	121,437,351	26,419	+	1	2_A375_uNU7_plus_lncRNA_AR_1...1304	18662	vs gene	0	1	0	16	20	7	1	2_A375_uNU7_...R_1	620	Gene BAG3	BAG3, BAG-3, MGC104307, CAIR-1, BIS	BC-2-associated athanogene 3	NM_004281, NCT01974151.1, NCT01662.3	217911_s_at	NP_004272.2, ENSN0352.1, ENSN0353.1
GeneID:23 876	INPP5F	10	121,499,609	121,598,699	103,090	+	1	4_A375_DGR1...1337	-473	upstream	0	0	1	12	12	18	1	4_A375_DGR1...1	16	Gene INPP5F	SAC2, SAC-2, MGC131881, INPP5F, MSTP027, MSTP047, KIAA0986, FLJ13581, MGC99779	suppressor of G-protein signaling 10	NM_014937, NR_002331, NR_002332, NCT02209412.0, NCT01664.3	230907_at, 230382_at, 230383_s_at	NP_0358921, ENSP43501.1, ENSN0279.1, ENSN0350.1
GeneID:11 9833	SEC23IP	11	121,892,203	121,701,243	49,022	+	1	1_A375_uNU7_minus_lncRNA_AR_1...1001	-191	upstream	0	0	0	20	15	9	1	1_A375_uNU7_...R_1	620	Gene SEC23IP	SEC23IP, P125, MSTP053	SEC23 interacting protein	NM_007166, NCT02305944.0, NCT02305945.0, NCT02302300.0, NCT01665.3	220179_at, 220178_at, 218392_s_at	NP_0095211.1, ENSP44374.1, ENSN0272.1, ENSN0273.1, ENSN0272.1, ENSN0273.1
GeneID:19 4631	PPAPD C1A	19	122,218,466	122,249,587	132,901	+	5	1_A375_uNU7_minus_lncRNA_AR_1...1003, 2_A375_uNU7_minus_lncRNA_AR_1...1004, 3_A375_uNU7_plus_lncRNA_AR_1...1307, 4_A375_uNU7_plus_lncRNA_AR_1...1306, 5_A375_DGR1...1208	51830, 57196, 4078, 51995, 430	vs gene, cr gene, vs gene, vs gene, cr gene	1	1	1	16.5	17	6.25	4	Gene PPAPD C1A	623	Gene PPAPD C1A	MGC102299, PPAPDC1, DPPL2, PPAPDC1A, MGC125300	phosphatidic acid phosphatase type 2 domain containing 1A	NM_031030.0, NCT02302250.0, NCT01726.4	238644_at	NP_0010230.1, ENSP43691.1, ENSN0355.1
GeneID:88 3089	LOC283 089	10	122,321,324	122,810,991	89,387	-	2	2_A375_uNU7_minus_lncRNA_AR_1...1005, 2_A375_uNU7_plus_lncRNA_AR_1...1309	-221, -221	upstream, upstream	0	1	0	16	26	11	1	2_A375_uNU7_...R_1	626	Gene LOC283089	hypothetical LOC283089	NR_033590	1562831_s_at, 1563916_at	
GeneID:88 717	WDR11	10	122,810,607	122,889,035	80,351	+	2	2_A375_uNU7_minus_lncRNA_AR_1...1005, 2_A375_uNU7_plus_lncRNA_AR_1...1309	225, 225	vs gene, cr gene	1	1	0	16	26	11	1	2_A375_uNU7_...R_1	626	Gene WDR11	WDR15, FLJ42531, WDR11, BRWD2, DR11, DKFZp434J1715	WD repeat domain 11	NM_018117, NCT02304162.0, NCT02304163.0, NCT02302440.0, NCT01727.3	210393_s_at, 229864_at	NP_5965973, ENSP43981.1, ENSN0354.1, ENSN0355.1, ENSN0356.1
GeneID:10 101	ATE1	10	123,502,823	123,607,348	104,521	-	2	1_A375_uNU7_minus_lncRNA_AR_1...1007, 2_A375_uNU7_plus_lncRNA_AR_1...1312	-192, -262	upstream, upstream	0	1	0	21	14	9	1	1_A375_uNU7_...R_1	621	Gene ATE1	MGC26724, ATE1	arg-tRNA-protein transferase 1	NM_007041, NM_001001976, NCT02302300.0, NCT01662.3, NCT1602762.2	223467_at, 234364_s_at, 234474_at, 235687_at	NP_0095722.2, NP_001001976.1, ENSN0334.1, ENSN0335.1, ENSN0336.1
GeneID:10 0133887	LOC100 130887	10	123,607,827	123,711,480	23,653	+	3	1_A375_uNU7_minus_lncRNA_AR_1...1007, 2_A375_uNU7_plus_lncRNA_AR_1...1312, 3_A375_uNU7_plus_lncRNA_AR_1...1313	-63, -19, 14761	upstream, upstream, vs gene	1	1	0	15.5	15.5	8	2	1_A375_uNU7_...R_1	621	Gene LOC100130887	hypothetical LOC100130887	XM_001721131, XM_001726433, XM_001726282	XP_0017211.70.1, XP_0017284.51.1, XP_0017281.4.1
GeneID:54 782	NSMCE 1	10	123,716,803	123,736,743	19,140	-	5	1_A375_uNU7_minus_lncRNA_AR_1...1003, 2_A375_uNU7_plus_lncRNA_AR_1...1314, 4_A375_DGR1...1210	7, -9, 567	vs gene, upstream, vs gene	1	1	1	66	74	15	1	2_A375_uNU7_...R_1	674	Gene NSMCE4A	NSMCE4A, bA388N3.3, C10orf56, NSE4A	non-SMC element 4 homolog A (S. cerevisiae)	NM_017615, NM_001167665, NCT02304190.0, NCT02302301.0, NCT02302302.0, NCT01663.3	211376_s_at, 219087_s_at, 227387_at, 232826_at	NP_0600853.2, NP_001161327.1, ENSN0331.1, ENSN0332.1, ENSN0333.1
GeneID:10 979	TACC2	10	123,748,899	124,014,097	265,198	+	4	1_A375_uNU7_minus_lncRNA_AR_1...1009, 2_A375_uNU7_plus_lncRNA_AR_1...1315, 3_A375_uNU7_plus_lncRNA_AR_1...1316, 4_A375_DGR1...1211	132047, 124087, 132143, 124431	vs gene, cr gene, vs gene, vs gene	1	1	1	22	23	13.5	2	1_A375_uNU7_...R_1	630	Gene TACC2	ECTACC, AZU-1, TACC2	transforming, acidic coiled-coil containing protein 2	NM_006997, NM_206860, NM_206861, NM_206862	1570033_at, 1570348_s_at, 202260.5_s_at, 211382.2_s_at	NP_0088261, NP_9967421, NP_9967442, NP_9967421
GeneID:11 9955	BTBD16	10	124,830,821	124,897,876	99,055	+	1	2_A375_uNU7_plus_lncRNA_AR_1...1317	60763	vs gene	0	1	0	12	16	8	1	2_A375_uNU7_...R_1	616	Gene BTBD16	MGC129984, MGC129985, C10orf67, BTBD16, FLJ25339	BTB (POZ) domain containing 16	NM_144,557, NCT02700.4, NCT1951736.2	1552566_at	NP_6551062, ENSP43321.1, ENSN0320.1
GeneID:88 54	HTRA1	10	124,220,641	124,274,424	53,283	+	2	1_A375_uNU7_minus_lncRNA_AR_1...1010, 2_A375_uNU7_plus_lncRNA_AR_1...1318	33457, 7693	vs gene, cr gene	1	1	0	16	17.5	8.5	2	2_A375_uNU7_...R_1	622	Gene HTRA1	HtrA, CARAS0, PRSS11, HTRA1, IGFBP7	HtrA serine peptidase 1	NM_002773, NCT02300508.0, NCT1951731.1	201185_at	NP_0027661, ENSP43113.1, ENSN0312.1
GeneID:19 8782	FAM24B	19	124,808,810	124,839,137	30,347	-	1	2_A375_uNU7_plus_lncRNA_AR_1...1400	5	vs gene	0	1	0	9	20	16	1	2_A375_uNU7_...R_1	620	Gene FAM24B	FAM24, MGC43992, DKFZp667G023	family with sequence similarity 24, member B	NM_152644	2331146_at	NP_6895572
GeneID:11 9970	FAM20A	17	124,870,217	124,872,627	2,410	+	2	1_A375_uNU7_minus_lncRNA_AR_1...1012, 2_A375_uNU7_plus_lncRNA_AR_1...1401	1325, 1287	vs gene, cr gene	1	1	0	66	95	7	1	2_A375_uNU7_...R_1	695	Gene FAM20A	FAM20A	family with sequence similarity 24, member A	NM_001029860, NCT1629662.1	243143_at	NP_0010239.91.1, EWN49299.1
GeneID:88 097	C10orf88	10	124,890,419	124,712,019	23,600	-	1	2_A375_uNU7_plus_lncRNA_AR_1...1402	-112	upstream	0	0	1	23	22	14	1	2_A375_uNU7_...R_1	622	Gene C10orf88	C.10orf88, FLJ13490	chromosome 10 open reading frame 88	NM_024942, NCT2552340.0, NCT02701.3	219240_s_at, 222832_at	NP_0791162, ENSP43297.1, ENSN0295.1
GeneID:11 9972	PSTK	10	124,739,556	124,749,908	10,350	+	2	1_A375_uNU7_minus_lncRNA_AR_1...1013, 2_A375_uNU7_plus_lncRNA_AR_1...1403	-680, 524	vs gene, cr gene	1	1	0	24	21	10	1	1_A375_uNU7_...R_1	624	Gene PSTK	C.10orf69, PSTK, MGC33392	phosphoseryl-tRNA kinase	NM_153338, NCT2552341.0, NCT02702.2	230129_at, 240040_at	NP_6991572, ENSP43293.1, ENSN0296.1
GeneID:84 376	RZF5	10	124,793,197	124,798,311	18,114	-	1	2_A375_uNU7_plus_lncRNA_AR_1...1404	215	vs gene	0	1	0	16	16	17	1	2_A375_uNU7_...R_1	616	Gene RZF5	DKFZp761B224, DKFZp761K215, FLJ43/SUS, FLJ22572	RAP/S family zinc finger 5 (Reg(e)ulin)	NM_022498, NCT2552317.0, NCT1962546.2, NCT1962390.2	220099_at, 229680_at	NP_3791113, ENSN0291.1, ENSN0292.1, ENSN0293.1
GeneID:38 0	ACADSB	10	124,798,429	124,817,006	49,377	+	1	2_A375_uNU7_plus_lncRNA_AR_1...1405	-332	upstream	0	1	0	16	16	17	1	2_A375_uNU7_...R_1	616	Gene ACADSB	SBCAD, ACAD7, ACADSB, 2-MEBCAD	acyl-CoA dehydrogenase, short/branched chain	NM_001609, NCT1629585.3	205355_at, 229830_at	NP_0010001, ENSN0291.1
GeneID:31 97	HHIP2	10	124,907,830	124,910,168	2,350	+	2	2_A375_uNU7_plus_lncRNA_AR_1...1406, 4_A375_DGR1...1212	6080, 6428	downstream, downstream	0	1	1	15	19	19	1	2_A375_uNU7_...R_1	619	Gene HHIP2	HHIL, hhip2-2, HHIP2	HH interacting protein 2	NM_0335119, NCT02284.3	2443869_at	NP_0355101, ENSN0238.1
GeneID:54 64	BUB3	10	124,910,760	124,929,686	11,126	+	2	2_A375_uNU7_plus_lncRNA_AR_1...1408, 4_A375_DGR1...1212	-32, 356	upstream, vs gene	0	1	1	15	19	19	1	2_A375_uNU7_...R_1	619	Gene BUB3	BUB3, BUB3L, BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	NM_004725, NM_001007791, NCT02300990.0, NCT02301150.0, NCT02991.2, NCT01550002.1	201456_s_at, 201457_s_at, 201458_s_at, 209974_s_at, 229977_at	NP_0047161, NP_001007794.1, ENSN0354.1, ENSN0355.1, ENSN0356.1, ENSN0357.1
GeneID:49 42	GNT	19	126,858,972	126,107,343	51,873	-	1	4_A375_DGR1...1218	29813	downstream	0	0	1	8	10	19	1	4_A375_EGR1...1	19	Gene GNT	GNT, HOGA, GNTASE, DKFZp761A115, GACR, GNT	acetylserotonin O-methyltransferase	NM_000274, NM_001171874, NCT2303093.0, NCT03622.2	231899_at	NP_0002651, NP_0011682.51, ENSP43271.1, ENSP43272.1
GeneID:39 0010	NKX1-2	10	126,128,990	126,130,590	2,552	-	1	4_A375_DGR1...1217	1062	vs gene	0	0	1	6	6	16	1	4_A375_EGR1...1	16	Gene NKX1-2	HEX3/PEX12, C10orf121, NKX1	NK1 homeobox 2	NM_0311465.60		NP_0011361.2.1
GeneID:84 077	LHPP	10	126,180,341	126,202,710	152,288	+	2	4_A375_DGR1...1216, 4_A375_EGR1...1219	69107, 153875	vs gene, downstream	0	0	1	7	7	20.5	2	4_A375_EGR1...1	23	Gene LHPP	MGC117251, MGC142191, FLJ44648, LHPP, MGC142189, HDHD6, FLJ46944	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	NM_022126, NM_001167690, NCT2312465.0, NCT2312466.0, NCT2312349.0, NCT2322330.0, NCT1961729.2	216523_at	NP_0744093, NP_0011615.32.1, ENSN0284.1, ENSN0285.1, ENSN0286.1, ENSN0288.1, ENSN0289.1
GeneID:98 79	FAM53B	10	126,207,883	126,432,930	123,047	-	2	4_A375_DGR1...1219, 4_A375_EGR1...1220	128914, 79850	downstream, vs gene	0	0	1	8	7	20	2	4_A375_EGR1...1	23	Gene FAM53B	bA112J10.2, RP11-112J10.2, KIAA0140, FAM53B, FLJ13019	family with sequence similarity 53, member B	NM_014981	1554165_at, 202206_at, 237267_at	NP_0554763
GeneID:39 9616	METTL10	10	126,447,406	126,482,439	35,033	-	2	2_A375_uNU7_plus_lncRNA_AR_1...1407, 2_A375_uNU7_plus_lncRNA_AR_1...1408	71, -9587	vs gene, upstream	0	1	0	17.5	16.5	14.5	2	2_A375_uNU7_...R_1	620	Gene METTL10	C.10orf38, METTL10, Em:AC005899.2, FLJ13219	methyltransferase like 10	NM_213554	215081_at, 229831_at, 229834_at	NP_9977192
GeneID:23 172	FAM178B	10	126,490,334	126,525,229	34,895	+	2	2_A375_uNU7_plus_lncRNA_AR_1...1407, 2_A375_uNU7_plus_lncRNA_AR_1...1408	-19908, -18	upstream, upstream	0	1	0	17.5	16.5	14.5	2	2_A375_uNU7_...R_1	620	Gene FAM178B	FLJ22155, FAM178B, KIAA0107, MERO1	family with sequence similarity 178, member B	NM_032182, NCT01674381.1, NCT02317.4	213539_at, 213837_at	NP_1153583, ENSP43298.1, ENSN0327.1
GeneID:14 55	CTBP2	10	126,676,416	126,849,624	173,208	-	3	2_A375_uNU7_plus_lncRNA_AR_1...1409, 4_A375_DGR1...1221, 4_A375_DGR1...1222	2165, 163086, - 1255	vs gene, cr gene, upstream	0	1	1	9.67	10	16.67	3	4_A375_EGR1...1	19	Gene CTBP2	CTBP2		NM_022802, NM_001129, NM_001083914	1561962_at, 201202_s_at, 210954_s_at, 210955_s_at, 211577_s_at	NP_0775113, NP_001120.1, NP_0010775.01.1
GeneID:70 90	UROS	10	127,477,147	127,511,027	34,890	-	2	1_A375_uNU7_minus_lncRNA_AR_1...1015, 2_A375_uNU7_plus_lncRNA_AR_1...1411	-131, -131	upstream, upstream	1	1	0	29	47	14	1	2_A375_uNU7_...R_1	647	Gene UROS	UROS		NM_000376, NCT2303096.1, NCT2303097.0, NCT2347310.0, NCT2347311.0, NCT2347186.0, NCT2347170.0, NCT2322322.0, NCT1764691.2, NCT1964122.2	200931_s_at, 232990_at	NP_0003661, ENSP43229.1, ENSP43222.1, ENSP43223.1, ENSP43224.1, ENSP43225.1, ENSP43226.1, ENSP43227.1, ENSP43228.1, ENSP43227.1
GeneID:88 647	BCCIP	19	127,312,104	127,342,264	30,160	+	2	1_A375_uNU7_minus_lncRNA_AR_1...1015, 2_A375_uNU7_plus_lncRNA_AR_1...1411	-136, -156	upstream, upstream	1	1	0	29	47	14	1	2_A375_uNU7_...R_1	647	Gene BCCIP	TOK1, BCCIP, TOK1	BRCA2 and CDKN1A interacting protein	NM_016567, NM_078466, NM_078469, NCT2306722.0, NCT2306.3, NCT1961676.1	213284_at, 227322_s_at, 227896_at	NP_1578511, NP_5109671, NP_5109681, ENSP43161.1, ENSP43162.1, ENSP43163.1, ENSP43164.1, ENSP43165.1
GeneID:88 565	FAN1	15	127,668,108	127,696,161	113,053	+	5	2_A375_uNU7_plus_lncRNA_AR_1...1412, 4_A375_DGR1...1223, 4_A375_DGR1...1224	-590, -599, 140	upstream, upstream, vs gene	0	1	1	26	26	50	1	4_A375_EGR1...1	50	Gene FAN1	FAN1, HSD13	Fanconi-associated nuclease 1 homolog (S. pombe)	NM_145235, NCT2302296.0, NCT2302298.0, NCT02211.3, NCT1964605.2	232468_at	NP_8927673, ENSP43212.1, ENSP43213.1, ENSP43214.1
GeneID:83 33	ADAM12	10	127,782,890	128,077,127	294,229	-	2	2_A375_uNU7_plus_lncRNA_AR_1...1413, 2_A375_uNU7_plus_lncRNA_AR_1...1414	5239991, 169191	vs gene, vs gene	0	1	0	14	22.5	7	2	2_A375_uNU7_...R_1	629	Gene ADAM12	KIAA0582, MCAMP/Mltns, MLTNA, MCAMP, MLTN	ADAM metallopeptidase domain 12	NM_003474, NM_021641, NCT2329190.0, NCT2322449.0, NCT2322360.0, NCT02205.3, NCT1961377.1	202952_s_at, 214943_at, 215813_s_at	NP_0034653, NP_0976572, ENSP43203.1, ENSN0339.1, ENSN0337.1, ENSN0339.1, ENSN0338.1
GeneID:11 9911	C10orf9 0	10	128,110,871	128,210,010	99,139	+	1	2_A375_uNU7_plus_lncRNA_AR_1...1415	61256	vs gene	0	1	0	21	22	8	1	2_A375_uNU7_...R_1	622	Gene C10orf90	FLJ22355, C10orf90, bA422P11.2	chromosome 10 open reading frame 90	NM_001012294, NCT2329553.0, NCT2329555.0	1558090_s_at, 1563837_s_at, 1564196_s_at	NP_0010022.62, ENSN0301.1, ENSN0302.1, ENSN0302.1
GeneID:10 93	DOCK1	10	128,786,965	129,230,760	461,815	+	1	2_A375_uNU7_plus_lncRNA_AR_1...1417	148603	vs gene	0	1	0	16	17	7	1	2_A375_uNU7_...R_1	617	Gene DOCK1	DOCK180, ced-5, DOCK1	dedicator of cytokinesis 1	NM_001380, NCT1939972.1	200787_s_at, 232830_at, 232831_at, 241782_at, 241789_s_at	NP_0012711, ENSN4119.4.1
GeneID:58 4557	NPS	19	129,247,813	129,250,935	3,222	+	2	1_A375_uNU7_minus_lncRNA_AR_1...1017, 2_A375_uNU7_plus_lncRNA_AR_1...1419	7765, 7779	downstream, downstream	1	1	0	14	19	5	1	2_A375_uNU7_...R_1	619	Gene NPS	NPS	neuropeptide S	NM_031030.2	1554165_at, 202206_at, 237267_at	NP_0012251.64.1
GeneID:38 7730	LOC387 720	10	129,832,928	129,838,280	5,434	-	1	4_A375_DGR1...1225	-2244	upstream	0	0	1	8	7	16	1	4_A375_EGR1...1	16	Gene LOC387720		hypothetical LOC387720	XR_111130, XR_109027, XR_114430, NCT01792.2		ENSN0193.1
GeneID:39 5522	FOXI2	10	129,838,535	129,839,450	5,912	+	1	4_A375_DGR1...1225	1966	vs gene	0	0	1	8	7	16	1	4_A375_EGR1...1	16	Gene FOXI2	FLJ46631, FOXI2	forkhead box I2	NM_207436		NP_9973092
GeneID:37 91	PTPRE	10	129,708,323	129,896,160	176,838	+	1	4_A375_DGR1...1226	116707	vs gene	0	0	1	4	4	16	1	4_A375_EGR1...1	16	Gene PTPRE	FLJ39245, HPTPE, DKFZp81SP1310, PTPRE, R-PTP-EPSILON, FLJ97709, PTPRE	protein tyrosine phosphatase, receptor type, E	NM_130435, NM_006504, NCT2329822.1, NCT2329823.1, NCT2329835.1, NCT2329836.0, NCT2329827.1, NCT2329826.1, NCT2322.4	1559815_at, 221540_at, 223976_at	NP_1395151, NP_0064951, ENSN0351.1, ENSN0352.1, ENSN0353.1, ENSN0354.1, ENSN0355.1, ENSN0356.1, ENSN0357.1
GeneID:42 6597	MKI67	10	129,954,923	129,984,466	29,543	-	1	4_A375_DGR1...1227	26340	vs gene	0	0	1	3	9	14	1	4_A375_EGR1...1	14	Gene MKI67	MKI67, NIA	antigen identified by monoclonal antibody Ki-67	NM_002417, NM_001145966, NCT2329220.0, NCT2329.2, NCT1961671.1	212020_s_at, 212021_s_at, 212022_s_at, 212023_s_at	NP_0026031, NP_0011394.51, ENSN0177.1, ENSN0176.1, ENSN0178.1
GeneID:42 53	MGMT	10	131,265,434	131,368,703	300,329	+	3	2_A375_DGR1...1231, 4_A375_EGR1...1232, 4_A375_DGR1...1233	238194, 301622, 201602	vs gene, downstream, downstream	0	0	1	5.33	3.33	13.33	3	4_A375_EGR1...1	17	Gene MGMT	MGMT		NM_002412, NCT2320187.0, NCT300832.4	204489_at	NP_0024332, ENSN4166.1, ENSN4167.1
GeneID:10 1509008	LOC100 509008	10	131,598,799	131,600,290	19,494	+	1	4_A375_DGR1...1234	20878	downstream	0	0	1	4	11	17	1	4_A375_EGR1...1	17	Gene LOC100509008		hypothetical LOC100509008	XR_109303		
GeneID:23 5735	EBF3	10	131,830,547	131,792,091	235,544	-	5	1_A375_uNU7_minus_lncRNA_AR_1...1019, 2_A375_uNU7_plus_lncRNA_AR_1...1421, 4_A375_DGR1...1228	12697, 100427, - 4803	vs gene, cr gene, upstream	1	1	1	13.33	12.67	10	3	2_A375_uNU7_...R_1	623	Gene EBF3	COE3, COE-2, EBF3	early B-cell factor 3	NM_0010035.63, NCT2320125.5, NCT2320126.0, NCT2320126.2	1559795_at, 227242_s_at, 227243_s_at, 229621_s_at	NP_0010035.63.1, ENSN0181.1, ENSN0183.1, ENSN0183.1
GeneID:38 7723	LOC387 723	10	131,882,160	131,909,051	48,921	-	5	1_A375_uNU7_minus_lncRNA_AR_1...1020, 2_A375_uNU7_plus_lncRNA_AR_1...1423, 4_A375_DGR1...1424	-119, 45333, -119	upstream, vs gene, upstream	1	1	0	19	22	14.5	2	2_A375_uNU7_...R_1	628	Gene LOC387723		hypothetical LOC387723	NR_024123	229923_at	
GeneID:10 0422687	MIR370 7C	10	132,780,551	132,780,931	380	-	1	4_A375_DGR1...1362	-6125	upstream	0	0	1	4	8	15	1	4_A375_EGR1...1	15	Gene MIR370C	MIR370C	microRNA 370c	NR_030180		
GeneID:23 8939	TCERG1L	10	132,890,655	133,109,954	219,229	-	3	4_A375_DGR1...1241, 4_A375_EGR1...1242, 4_A375_DGR1...1243	22166, 132644, 23864	downstream, vs gene, vs gene	0	0	1	5.33	8	16.67	3	4_A375_EGR1...1	16	Gene TCERG1L	TCERG1L, MGC19884	transcription elongation regulator 1-like	NM_174937, NCT2349194.0	2312.97_at	NP_7779972, ENSP44190.1

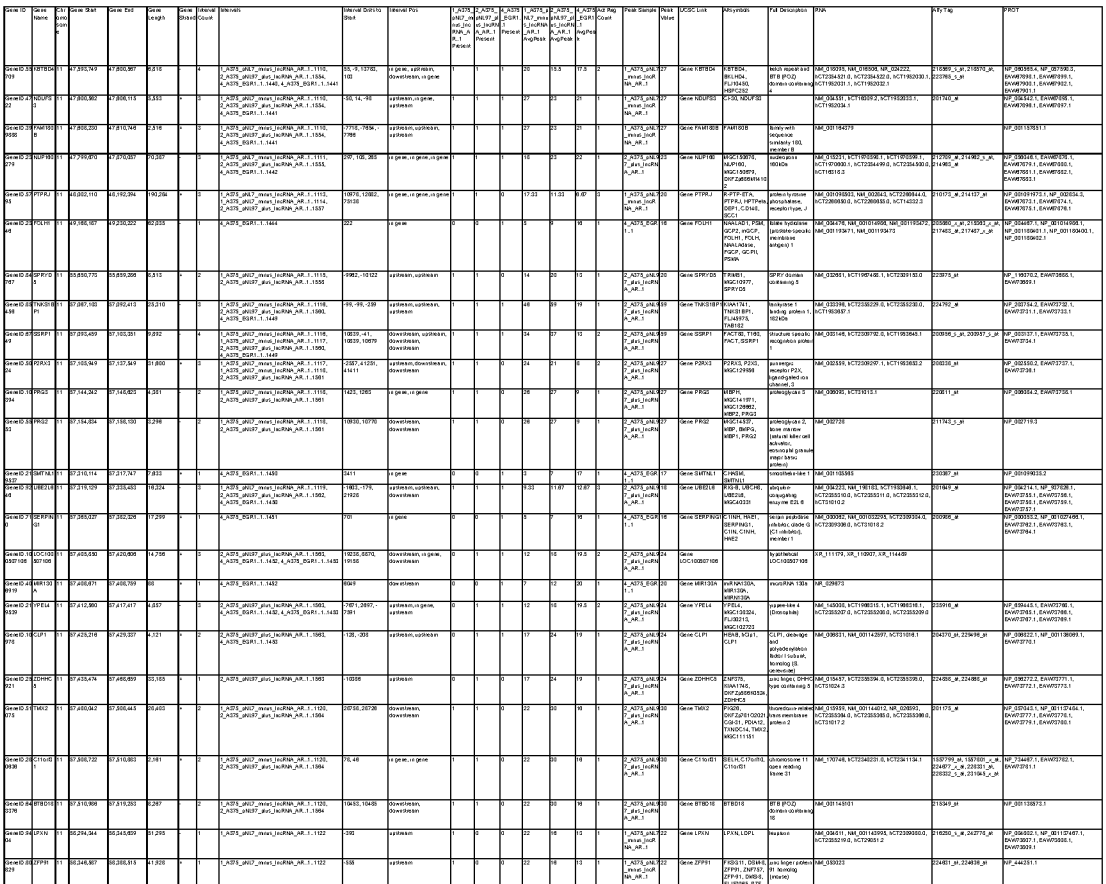
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:282973	JAKMIP3	10	133,918,313	133,998,313	80,000	+	4	4_A375_EGR1..1..1244, 4_A375_EGR1..1..1245, 4_A375_EGR1..1..1246, 4_A375_EGR1..1..1247	16151, 28279, 63767, 64247	in gene, in gene, in gene, in gene	0	0	1	7.25	7	18.25	4	4_A375_EGR1..1	22	Gene JAKMIP3	bA140A10.5, C10orf39, FLJ41432, C10orf14, JAKMIP3, Jamp3, NECC2, FLJ37657	Janus kinase and microtubule interacting protein 3	NM_001105521, hCT1767489.2	233078_at	NP_001098991.1, EAW49141.1
GeneID:10570	DPYSL4	10	134,000,414	134,019,280	18,866	+	3	4_A375_EGR1..1..1248, 4_A375_EGR1..1..1249, 4_A375_EGR1..1..1250	10002, 16610, 21154	in gene, in gene, downstream	0	0	1	7.33	7	16.67	3	4_A375_EGR1..1	21	Gene DPYSL4	CRMP3, DRP-4, DPYSL4, ULIP4	dihydropyrimidinase-like 4	NM_006426, hCT2320097.0, hCT2320098.0, hCT2320099.0, hCT2320100.0, hCT2320101.0, hCT2320102.0, hCT2320103.0, hCT2320104.0	205492_s_at, 205493_s_at, 214301_s_at	NP_006417.2, EAW49133.1, EAW49131.1, EAW49135.1, EAW49136.1, EAW49137.1, EAW49132.1, EAW49134.1, EAW49138.1
GeneID:282974	STK32C	10	134,020,996	134,121,477	100,481	-	5	4_A375_EGR1..1..1249, 4_A375_EGR1..1..1250, 4_A375_EGR1..1..1251, 4_A375_EGR1..1..1252, 4_A375_EGR1..1..1253	104453, 99909, 84101, 81265, 901	downstream, in gene, in gene, in gene, in gene	0	0	1	9	8.2	18	5	4_A375_EGR1..1	21	Gene STK32C	PKE, RP11-140A10.1, YANK3, STK32C, MGC23665	serine/threonine kinase 32C	NM_173575, hCT2320010.1, hCT2320011.1, hCT2320012.1, hCT2344964.0	227634_at, 230934_at	NP_775846.2, EAW49127.1, EAW49126.1, EAW49128.1, EAW49129.1
GeneID:100506057	LOC100506057	10	134,137,643	134,145,373	7,730	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1022, 2_A375_pNL97_plus_lncRNA_AR..1..1427, 2_A375_pNL97_plus_lncRNA_AR..1..1428, 4_A375_EGR1..1..1254	-275, 11528, -344, -275	upstream, downstream, upstream, upstream	1	1	1	12.5	20	14	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100506057		hypothetical LOC100506057	XR_111132, XR_111131, XR_109031, XR_109030, XR_114404, XR_114403		
GeneID:80313	LRRC27	10	134,145,614	134,195,010	49,396	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1022, 2_A375_pNL97_plus_lncRNA_AR..1..1428, 4_A375_EGR1..1..1254, 4_A375_EGR1..1..1255	34, 103, 34, 57063	in gene, in gene, in gene, downstream	1	1	1	10.5	16	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LRRC27	LRRC27	leucine rich repeat containing 27	NM_030626, NM_001143757, NM_001143758, NM_001143759, NR_026559, hCT2352285.0, hCT2352286.0, hCT2352287.0, hCT1787490.2	1558483_at, 1558484_s_at, 228686_at	NP_085129.1, NP_001137229.1, NP_001137230.1, NP_001137231.1, EAW49122.1, EAW49124.1, EAW49121.1, EAW49123.1
GeneID:170394	PWWP2B	10	134,210,702	134,231,363	20,661	+	5	4_A375_EGR1..1..1255, 4_A375_EGR1..1..1256, 4_A375_EGR1..1..1257, 4_A375_EGR1..1..1258, 4_A375_EGR1..1..1259	-8025, 2866, 11666, 12210, 20226	upstream, in gene, in gene, in gene, in gene	0	0	1	5.8	7.2	16.6	5	4_A375_EGR1..1	18	Gene PWWP2B	FLJ39621, PWWP2B, PWWP2, pp8607, RP11-273H7.1, FLJ46823, bA432J24.1	PWWP domain containing 2B	NM_001099637, NM_138499, hCT1957391.1	227999_at, 238046_x_at, 238051_x_at	NP_001092107.1, NP_612508.3, EAW49120.1
GeneID:170393	C10orf91	10	134,258,714	134,261,825	3,111	+	6	4_A375_EGR1..1..1260, 4_A375_EGR1..1..1261, 4_A375_EGR1..1..1262, 4_A375_EGR1..1..1263, 4_A375_EGR1..1..1264, 4_A375_EGR1..1..1265	-6426, 918, 5926, 6662, 10436, 12676	upstream, in gene, downstream, downstream, downstream, downstream	0	0	1	5.83	7.83	17	6	4_A375_EGR1..1	20	Gene C10orf91	C10orf91, RP11-432J24.4, bA432J24.4	chromosome 10 open reading frame 91	NM_173541, hCT2349207.0, hCT2349206.0	1553660_at	NP_775812.1, EAW49119.1, EAW49118.1
GeneID:3632	INPP5A	10	134,351,353	134,596,984	245,631	+	7	2_A375_pNL97_plus_lncRNA_AR..1..1429, 4_A375_EGR1..1..1272, 4_A375_EGR1..1..1273, 4_A375_EGR1..1..1274, 4_A375_EGR1..1..1275, 4_A375_EGR1..1..1276, 4_A375_EGR1..1..1277	255015, 106364, 116295, 191031, 196439, 222551, 255591	downstream, in gene, in gene, in gene, in gene, in gene, downstream	0	1	1	6.83	10.67	16.67	6	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene INPP5A	INPP5A, MGC116949, DKFZp434A1721, 5PTASE, MGC116947	inositol polyphosphate-5-phosphatase, 40kDa	NM_005539, hCT2289563.0, hCT2289566.0	1554757_a_at, 203006_at	NP_005530.3, EAW61306.1, EAW61307.1
GeneID:84504	NKX6-2	10	134,598,320	134,599,537	1,217	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1429, 4_A375_EGR1..1..1277	-6631, -7407	upstream, upstream	0	1	1	12	25	14	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene NKX6-2	NKX6B, NKX6-2, NKX6.2, GTX, MGC126684	NK6 homeobox 2	NM_177400, hCT1780459.2	235632_at	NP_796374.1, EAW61308.1
GeneID:54777	C10orf92	10	134,621,896	134,674,391	52,495	-	10	4_A375_EGR1..1..1278, 4_A375_EGR1..1..1279, 4_A375_EGR1..1..1280, 4_A375_EGR1..1..1281, 4_A375_EGR1..1..1282, 4_A375_EGR1..1..1283, 4_A375_EGR1..1..1284, 4_A375_EGR1..1..1285, 4_A375_EGR1..1..1286, 4_A375_EGR1..1..1287	48615, 33527, 25943, 24567, 11607, 10951, 9719, -1129, -6921, -8377	in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream, upstream, upstream	0	0	1	5.9	5.7	16.9	10	4_A375_EGR1..1	21	Gene C10orf92	DKFZp434A1721, bB137A17.2, bA288G11.4, bA288G11.5, C10orf124, C10orf123, C10orf92, FLJ46273	chromosome 10 open reading frame 92	XM_003119476, XM_003118625, XM_003120662, hCT9236.2	220539_at	XP_003119526.1, XP_003118673.1, XP_003120710.1, EAW61309.1
GeneID:100506209	LOC100506209	10	134,679,424	134,740,999	61,575	-	11	4_A375_EGR1..1..1285, 4_A375_EGR1..1..1286, 4_A375_EGR1..1..1287, 4_A375_EGR1..1..1288, 4_A375_EGR1..1..1289, 4_A375_EGR1..1..1290, 4_A375_EGR1..1..1291, 4_A375_EGR1..1..1292, 4_A375_EGR1..1..1293, 4_A375_EGR1..1..1294, 4_A375_EGR1..1..1295	65479, 59667, 58231, 46012, 21276, 16327, 13511, 10167, 7575, 6119, -985	downstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	0	0	1	5.36	5	16.27	11	4_A375_EGR1..1	21	Gene LOC100506209	DKFZp434A1721	TPR repeat-containing protein C10orf93-like	XM_003119477, XM_003118626		XP_003119525.1, XP_003118674.1
GeneID:255352	C10orf93	10	134,742,689	134,756,089	13,400	-	3	4_A375_EGR1..1..1293, 4_A375_EGR1..1..1294, 4_A375_EGR1..1..1295	22665, 21209, 14105	downstream, downstream, downstream	0	0	1	6	6	17	3	4_A375_EGR1..1	18	Gene C10orf93	C10orf93, bB137A17.3, RP13-137A17.3	chromosome 10 open reading frame 93	NM_173572, hCT2290172.0	1552964_at, 1555573_at	NP_775843.3, EAW61310.1
GeneID:100289424	LOC100289424	10	134,777,219	134,778,763	1,564	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1023, 2_A375_pNL97_plus_lncRNA_AR..1..1430, 4_A375_EGR1..1..1296	-305, -369, -6513	upstream, upstream, upstream	1	1	1	14	13	13	2	4_A375_EGR1..1	21	Gene LOC100289424	FLJ52635	hypothetical LOC100289424	XR_111133, XR_109032, XR_114446		
GeneID:399829	LOC399829	10	134,779,038	134,790,001	10,963	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1023, 2_A375_pNL97_plus_lncRNA_AR..1..1430, 4_A375_EGR1..1..1296, 4_A375_EGR1..1..1297, 4_A375_EGR1..1..1298	50, 114, 8258, 16994, 19674	in gene, in gene, in gene, downstream, downstream	1	1	1	10	10.75	14.75	4	4_A375_EGR1..1	21	Gene LOC399829		hypothetical LOC399829	XR_111134, XR_109033, XR_114445		
GeneID:100128127	LOC100128127	10	134,899,473	134,900,137	664	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1431, 4_A375_EGR1..1..1301	8553, 6345	downstream, downstream	0	1	1	16	16	17	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100128127		hypothetical LOC100128127			
GeneID:84435	GPR123	10	134,901,409	134,945,179	43,770	+	6	2_A375_pNL97_plus_lncRNA_AR..1..1431, 4_A375_EGR1..1..1301, 4_A375_EGR1..1..1302, 4_A375_EGR1..1..1303, 4_A375_EGR1..1..1304, 4_A375_EGR1..1..1305	-7825, -7617, 9343, 25599, 51987, 53839	upstream, upstream, in gene, in gene, downstream, downstream	0	1	1	8.4	8.4	16.6	5	4_A375_EGR1..1	19	Gene GPR123	FLJ37356, GPR123, FLJ25875	G protein-coupled receptor 123	NM_001083909, hCT2348920.0, hCT2353675.0	239221_at	NP_001077378.1, EAW61312.1, EAW61313.1
GeneID:85442	KNDC1	10	134,973,971	135,039,916	65,945	+	10	4_A375_EGR1..1..1306, 4_A375_EGR1..1..1307, 4_A375_EGR1..1..1308, 4_A375_EGR1..1..1309, 4_A375_EGR1..1..1310, 4_A375_EGR1..1..1311, 4_A375_EGR1..1..1312, 4_A375_EGR1..1..1313, 4_A375_EGR1..1..1314, 4_A375_EGR1..1..1315	-1331, 761, 6941, 25949, 37165, 37933, 39865, 41357, 52509, 65690	upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	6.2	6.1	17.2	10	4_A375_EGR1..1	21	Gene KNDC1	C10orf23, FLJ16067, RASGEF2, KNDC1, bB439H18.3	kinase non-catalytic C-lobe domain (KIND) containing 1	NM_152643	230359_at, 230556_at, 233146_at	NP_689856.6
GeneID:8433	UTF1	10	135,043,778	135,045,062	1,284	+	1	4_A375_EGR1..1..1315	-3917	upstream	0	0	1	4	4	13	1	4_A375_EGR1..1	13	Gene UTF1	UTF1	undifferentiated embryonic cell transcription factor 1	NM_003577, hCT1786196.1	208275_x_at	NP_003568.2, EAW61322.1
GeneID:27287	VENTX	10	135,051,408	135,055,433	4,025	+	1	4_A375_EGR1..1..1316	10606	downstream	0	0	1	4	7	21	1	4_A375_EGR1..1	21	Gene VENTX	MGC119911, VENTX2, NA88A, MGC119910, VENTX, HPX42B	VENT homeobox homolog (Xenopus laevis)	NM_014468, hCT1786197.2	207376_at	NP_055283.1, EAW61323.1
GeneID:574448	MIR202	10	135,061,015	135,061,124	109	-	1	4_A375_EGR1..1..1316	-892	upstream	0	0	1	4	7	21	1	4_A375_EGR1..1	21	Gene MIR202	MIR202, hsa-mir-202, MIRN202	microRNA 202	NR_030170		
GeneID:101	ADAM8	10	135,075,920	135,090,407	14,487	-	3	2_A375_pNL97_plus_lncRNA_AR..1..1432, 4_A375_EGR1..1..1317, 4_A375_EGR1..1..1318	-2073, 18215, -905	upstream, downstream, upstream	0	1	1	14	20	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene ADAM8	CD156, ADAM8, MS2, MGC134985	ADAM metallopeptidase domain 8	NM_001109, NM_001164489, NM_001164490, hCT2353662.0, hCT1812473.1	205179_s_at, 205180_s_at	NP_001100.3, NP_001157961.1, NP_001157962.1, EAW61325.1, EAW61326.1
GeneID:100506167	LOC100506167	10	135,077,563	135,095,026	17,463	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1432, 4_A375_EGR1..1..1317, 4_A375_EGR1..1..1318	14917, -5371, 13749	in gene, upstream, in gene	0	1	1	14	20	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC100506167		hypothetical LOC100506167	XR_111137, XR_111135, XR_111136, XR_109036, XR_109034, XR_109035, XR_114444, XR_114442, XR_114443		
GeneID:10844	TUBGCP2	10	135,093,138	135,122,644	29,506	-	5	2_A375_pNL97_plus_lncRNA_AR..1..1432, 2_A375_pNL97_plus_lncRNA_AR..1..1433, 4_A375_EGR1..1..1318, 4_A375_EGR1..1..1319, 4_A375_EGR1..1..1320	30164, 15732, 31332, 13124, -9740	downstream, in gene, downstream, in gene, upstream	0	1	1	13.5	14.5	16.75	4	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene TUBGCP2	Spc97p, GCP2, TUBGCP2, SPBC97, MGC138162	tubulin, gamma complex associated protein 2	NM_006659, hCT2290208.0, hCT2290213.0	202476_s_at, 202477_s_at, 213563_s_at	NP_006650.1, EAW61328.1, EAW61327.1
GeneID:118472	ZNF511	10	135,122,423	135,126,666	4,243	+	1	4_A375_EGR1..1..1320	9961	downstream	0	0	1	14	10	19	1	4_A375_EGR1..1	19	Gene ZNF511	MGC30008, ZNF511	zinc finger protein 511	NM_145806, hCT10201.3, hCT1959553.1, hCT1959554.1, hCT1959555.1	225307_at	NP_665805.2, EAW61332.1, EAW61330.1, EAW61331.1, EAW61333.1
GeneID:50632	CALY	10	135,138,928	135,150,475	11,547	-	2	4_A375_EGR1..1..1320, 4_A375_EGR1..1..1321	16091, 1099	downstream, in gene	0	0	1	11	9	16	2	4_A375_EGR1..1	19	Gene CALY	CALY, DRD1IP, NSG3	calcyon neuron-specific vesicular protein	NM_015722, hCT10202.2, hCT1962284.1	219896_at	NP_056537.1, EAW61334.1, EAW61335.1
GeneID:118471	PRAP1	10	135,160,844	135,166,187	5,343	+	4	4_A375_EGR1..1..1322, 4_A375_EGR1..1..1323, 4_A375_EGR1..1..1324, 4_A375_EGR1..1..1325	4276, 5012, 10004, 11156	in gene, in gene, downstream, downstream	0	0	1	7	8.5	18.5	4	4_A375_EGR1..1	23	Gene PRAP1	UPA, RP11-122K13.6, PRAP1, MGC126792, PRO1195	proline-rich acidic protein 1	NM_001145201, NM_145202, hCT10216.3	243669_s_at	NP_001138673.1, NP_660203.3, EAW61336.1
GeneID:282969	C10orf125	10	135,168,658	135,171,529	2,871	-	4	4_A375_EGR1..1..1322, 4_A375_EGR1..1..1323, 4_A375_EGR1..1..1324, 4_A375_EGR1..1..1325	8409, 5873, 661, -471	downstream, downstream, in gene, upstream	0	0	1	7	8.5	18.5	4	4_A375_EGR1..1	23	Gene C10orf125	FUCU, FLJ26016, C10orf125, MGC149256	chromosome 10 open reading frame 125	NM_001098483, NM_198472, hCT10217.2, hCT1808712.0	230259_at	NP_001091953.1, NP_940874.2, EAW61337.1, EAW61338.1
GeneID:1892	ECHS1	10	135,175,987	135,186,908	10,921	-	5	4_A375_EGR1..1..1323, 4_A375_EGR1..1..1324, 4_A375_EGR1..1..1325, 4_A375_EGR1..1..1326, 4_A375_EGR1..1..1327	21052, 16060, 14908, -3476, -5236	downstream, downstream, downstream, upstream, upstream	0	0	1	7.8	9	19	5	4_A375_EGR1..1	23	Gene ECHS1	ECHS1, SCEH	enoyl CoA hydratase, short chain, 1, mitochondrial	NM_004092, hCT9992.2	201135_at	NP_004083.3, EAW61339.1
GeneID:196743	PAOX	10	135,192,741	135,205,198	12,457	+	5	2_A375_pNL97_plus_lncRNA_AR..1..1434, 4_A375_EGR1..1..1326, 4_A375_EGR1..1..1327, 4_A375_EGR1..1..1328, 4_A375_EGR1..1..1329	15099, -2357, -597, 12475, 15067	downstream, upstream, upstream, downstream, downstream	0	1	1	8.25	11.25	16.75	4	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PAOX	PAO, MGC45464, PAOX, DKFZp434J245	polyamine oxidase (exo-N4-amino)	NM_207127, NM_207128, NM_152911, hCT2353676.0, hCT2353677.0, hCT2353678.0, hCT2353679.0, hCT2353680.0, hCT2353681.0, hCT10214.3, hCT1816950.1	221941_at, 50400_at	NP_997010.1, NP_997011.1, NP_690875.1, EAW61341.1, EAW61342.1, EAW61346.1, EAW61340.1, EAW61343.1, EAW61344.1, EAW61345.1, EAW61347.1
GeneID:92170	MTG1	10	135,207,621	135,234,174	26,553	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1434, 4_A375_EGR1..1..1328, 4_A375_EGR1..1..1329	219, -2405, 187	in gene, upstream, in gene	0	1	1	6.5	13	15	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MTG1	GTP, MTG1, GTPBP7, RP11-108K14.2	mitochondrial GTPase 1 homolog (S. cerevisiae)	NM_138384, hCT1950227.2, hCT1950228.2	212767_at	NP_612393.2, EAW61348.1, EAW61349.1
GeneID:1571	CYP2E1	10	135,340,867	135,352,620	11,753	+	1	4_A375_EGR1..1..1332	1213	in gene	0	0	1	6	6	18	1	4_A375_EGR1..1	18	Gene CYP2E1	CYP2E, CYP2E1, P450-J, CPE1, P450C2E	cytochrome P450, family 2, subfamily E, polypeptide 1	NM_000773, hCT2343614.0, hCT9986.4	1431_at, 209975_at, 209976_s_at, 222100_at	NP_000764.1, EAW61356.1, EAW61357.1
GeneID:147199	SCGB1C1	11	193,080	194,573	1,493	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1024, 2_A375_pNL97_plus_lncRNA_AR..1..1435, 4_A375_EGR1..1..1333, 4_A375_EGR1..1..1334	-3112, -3416, -3320, 2152	upstream, upstream, upstream, downstream	1	1	1	19.5	20.5	31.5	2	4_A375_EGR1..1	47	Gene SCGB1C1	SCGB1C1, RYD5	secretoglobin, family 1C, member 1	NM_145651, hCT1779488.2	1552449_a_at	NP_663626.2, EAW90678.1
GeneID:113746	ODF3	11	196,761	200,258	3,497	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1024, 2_A375_pNL97_plus_lncRNA_AR..1..1435, 4_A375_EGR1..1..1333, 4_A375_EGR1..1..1334	-6793, -7097, -7001, -1529	upstream, upstream, upstream, upstream	1	1	1	19.5	20.5	31.5	2	4_A375_EGR1..1	47	Gene ODF3	hSHIPPO, SHIPPO1, CT135, ODF3, TISP50	outer dense fiber of sperm tails 3	NM_053280, hCT1779281.2	1553051_s_at, 233795_at	NP_444510.2, EAW61249.1
GeneID:51272	BET1L	11	202,924	207,422	4,498	-	1	4_A375_EGR1..1..1334	12190	downstream	0	0	1	8	11	16	1	4_A375_EGR1..1	16	Gene BET1L	BET1L, HSPC197, GS15, BET1L1, GOLIM3	blocked early in transport 1 homolog (S. cerevisiae)-like	NM_016526, NM_001098787, hCT2348980.0, hCT2348981.0	220470_at, 223023_at	NP_057610.2, NP_001092257.1, EAW61247.1, EAW61248.1
GeneID:171389	NLRP6	11	278,570	285,304	6,734	+	1	4_A375_EGR1..1..1335	11510	downstream	0	0	1	5	7	15	1	4_A375_EGR1..1	15	Gene NLRP6	CLR11.4, PAN3, NALP6, NLRP6, PYPAF5	NLR family, pyrin domain containing 6	NM_138329, hCT29047.2	1552932_at	NP_612202.1, EAW61233.1
GeneID:80162	ATHL1	11	289,138	295,688	6,550	+	1	4_A375_EGR1..1..1335	942	in gene	0	0	1	5	7	15	1	4_A375_EGR1..1	15	Gene ATHL1	MGC129859, MGC129858, ATHL1, FLJ22635	ATH1, acid trehalase-like 1 (yeast)	NM_025092, hCT2258002.1, hCT2258003.1, hCT2258004.1, hCT2258005.1, hCT2258006.1, hCT2258007.1, hCT2258008.1, hCT2258009.1, hCT2353666.0, hCT2353667.0	219359_at	NP_079368.3, EAW61229.1, EAW61223.1, EAW61225.1, EAW61230.1, EAW61231.1, EAW61224.1, EAW61226.1, EAW61227.1, EAW61228.1, EAW61232.1
GeneID:387733	IFITM5	11	298,203	299,526	1,323	-	1	4_A375_EGR1..1..1335	9446	downstream	0	0	1	5	7	15	1	4_A375_EGR1..1	15	Gene IFITM5	fragilis4, Hrmp1, IFITM5, BRIL	interferon induced transmembrane protein 5	NM_001025295, hCT29049.2		NP_001020466.1, EAW61222.1
GeneID:338707	B4GALNT4	11	369,795	382,117	12,322	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1025, 2_A375_pNL97_plus_lncRNA_AR..1..1436	-5187, -5219	upstream, upstream	1	1	0	43	43	12	1	1_A375_pNL7_minus_lncRNA_AR..1	43	Gene B4GALNT4	B4GALNT4, FLJ25045	beta-1,4-N-acetyl-galactosaminyl transferase 4	NM_178537, hCT2272428.0	238060_s_at, 238080_at	NP_848632.2, EAX02321.1
GeneID:11187	PKP3	11	394,217	404,908	10,691	+	1	4_A375_EGR1..1..1337	2660	in gene	0	0	1	9	8	12	1	4_A375_EGR1..1	12	Gene PKP3	PKP3	plakophilin 3	NM_007183, hCT2272434.0, hCT1955891.1	209872_s_at, 209873_s_at	NP_009114.1, EAX02323.1, EAX02322.1
GeneID:59307	SIGIRR	11	405,716	417,397	11,681	-	1	4_A375_EGR1..1..1337	20320	downstream	0	0	1	9	8	12	1	4_A375_EGR1..1	12	Gene SIGIRR	MGC110992, SIGIRR, TIR8	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	NM_021805, NM_001135053, NM_001135054, hCT10145.4	218921_at, 52940_at	NP_068577.2, NP_001128525.1, NP_001128526.1, EAX02324.1
GeneID:338440	ANO9	11	417,930	442,011	24,081	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1026, 2_A375_pNL97_plus_lncRNA_AR..1..1437, 2_A375_pNL97_plus_lncRNA_AR..1..1438	-6261, -6437, -6309	upstream, upstream, upstream	1	1	0	16.5	23.5	7	2	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene ANO9	PIG5, TMEM16J, ANO9, TP53I5	anoctamin 9	NM_001012302, hCT2274619.0	227393_at	NP_001012302.2, EAX02326.1
GeneID:81490	PTDSS2	11	450,280	491,387	41,107	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1026, 2_A375_pNL97_plus_lncRNA_AR..1..1437, 2_A375_pNL97_plus_lncRNA_AR..1..1438, 4_A375_EGR1..1..1338	-8, -1632, 40, 50264	upstream, upstream, in gene, downstream	1	1	1	12	19	9.33	3	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene PTDSS2	PTDSS2, FLJ46373, PSS2	phosphatidylserine synthase 2	NM_030783, hCT9680.3, hCT1957141.1, hCT1957142.1	221005_s_at	NP_110410.1, EAX02327.1, EAX02328.1, EAX02329.1
GeneID:6050	RNH1	11	494,512	507,273	12,761	-	1	4_A375_EGR1..1..1338	6729	in gene	0	0	1	3	10	14	1	4_A375_EGR1..1	14	Gene RNH1	MGC4569, MGC18200, RNH, RAI, RNH1, MGC54054	ribonuclease/angiogenin inhibitor 1	NM_203384, NM_002939, NM_203386, NM_203389, NM_203387, NM_203388, NM_203383, NM_203385, hCT2274613.0, hCT2358666.0, hCT2358667.0, hCT9679.3, hCT1952216.1, hCT1952218.1, hCT1952219.1	1555529_at, 206050_s_at	NP_976318.1, NP_002930.2, NP_976322.1, NP_976323.1, NP_976321.1, NP_976320.1, NP_976317.1, NP_976319.1, EAX02330.1, EAX02331.1, EAX02332.1, EAX02333.1, EAX02334.1, EAX02335.1, EAX02336.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:3265	HRAS	11	532,242	535,550	3,308	-	3	2_A375_pNL97_plus_lncRNA_AR..1..1439, 4_A375_EGR1..1..1339, 4_A375_EGR1..1..1340	-1662, 734, -1554	upstream, in gene, upstream	0	1	1	9.5	14	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene HRAS	C-H-RAS, CTLO, HAMSV, RASH1, C-HA-RAS1, C-BAS/HAS, H-RASIDX, N-RAS, K-RAS, HRAS, HRAS1	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	NM_005343, NM_176795, NM_001130442, hCT2274723.0, hCT2274724.0, hCT9678.3, hCT1952214.0, hCT1952215.1	212983_at	NP_005334.1, NP_789765.1, NP_001123914.1, EAX02337.1, EAX02339.1, EAX02341.1, EAX02338.1, EAX02340.1
GeneID:115399	LRRC56	11	537,522	554,916	17,394	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1439, 4_A375_EGR1..1..1339, 4_A375_EGR1..1..1340	-290, -2706, -418	upstream, upstream, upstream	0	1	1	9.5	14	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LRRC56	DKFZp761L1518, FLJ00101, LRRC56	leucine rich repeat containing 56	NM_198075, hCT2272450.0, hCT2272455.0, hCT2272459.0	232554_at	NP_932341.1, EAX02343.1, EAX02342.1, EAX02344.1
GeneID:100506211	LOC100506211	11	565,657	568,420	2,763	-	1	4_A375_EGR1..1..1341	-7324	upstream	0	0	1	8	13	17	1	4_A375_EGR1..1	17	Gene LOC100506211	MIR210HG	hypothetical LOC100506211	XR_111141, XR_111142, XR_111143, XR_109058, XR_109059, XR_109060, XR_114449, XR_114450, XR_114451		
GeneID:406992	MIR210	11	568,089	568,198	109	-	1	4_A375_EGR1..1..1341	-7546	upstream	0	0	1	8	13	17	1	4_A375_EGR1..1	17	Gene MIR210	MIRN210, MIR210, mir-210	microRNA 210	NR_029623		
GeneID:143666	LOC143666	11	573,808	575,885	2,077	-	1	4_A375_EGR1..1..1341	141	in gene	0	0	1	8	13	17	1	4_A375_EGR1..1	17	Gene LOC143666		hypothetical LOC143666	NR_026967		
GeneID:57661	PHRF1	11	576,483	612,222	35,739	+	2	4_A375_EGR1..1..1341, 4_A375_EGR1..1..1342	-739, 21501	upstream, in gene	0	0	1	7	10	15	2	4_A375_EGR1..1	17	Gene PHRF1	RNF221, PHRF1, KIAA1542	PHD and ring finger domains 1	NM_020901, hCT2358665.0, hCT9675.2	234952_s_at, 237379_at	NP_065952.2, EAX02353.1, EAX02354.1
GeneID:10522	DEAF1	11	644,225	695,740	51,515	-	2	4_A375_EGR1..1..1343, 4_A375_EGR1..1..1344	35004, -7316	in gene, upstream	0	0	1	6.5	7.5	14.5	2	4_A375_EGR1..1	15	Gene DEAF1	NUDR, ZMYND5, DEAF1, SPN	deformed epidermal autoregulatory factor 1 (Drosophila)	NM_021008, hCT1952186.1, hCT1952187.1	209407_s_at, 230059_at	NP_066288.2, EAX02371.1, EAX02370.1
GeneID:283232	TMEM80	11	695,616	704,129	8,513	+	1	4_A375_EGR1..1..1344	7440	in gene	0	0	1	10	10	15	1	4_A375_EGR1..1	15	Gene TMEM80	FLJ55823, FLJ38216, TMEM80	transmembrane protein 80	NM_174940, NM_001042463, hCT2348898.0, hCT1817095.3	221951_at, 65630_at	NP_777600.2, NP_001035928.1, EAX02372.1, EAX02373.1
GeneID:64787	EPS8L2	11	706,120	727,727	21,607	+	1	4_A375_EGR1..1..1344	-3064	upstream	0	0	1	10	10	15	1	4_A375_EGR1..1	15	Gene EPS8L2	FLJ22171, MGC126530, FLJ21935, FLJ16738, MGC3088, EPS8R2, EPS8L2	EPS8-like 2	NM_022772, hCT2272475.0, hCT1817090.2	218180_s_at, 222546_s_at, 229020_x_at	NP_073609.2, EAX02376.1, EAX02375.1
GeneID:51286	CEND1	11	787,110	790,126	3,016	-	1	4_A375_EGR1..1..1345	-4594	upstream	0	0	1	5	8	15	1	4_A375_EGR1..1	15	Gene CEND1	MGC34328, CEND1, FLJ90066, BM88	cell cycle exit and neuronal differentiation 1	NM_016564	219591_at	NP_057648.2
GeneID:79751	SLC25A22	11	790,475	798,269	7,794	-	4	4_A375_EGR1..1..1345, 4_A375_EGR1..1..1346, 4_A375_EGR1..1..1347, 4_A375_EGR1..1..1348	3549, -2478, -4499, -7267	in gene, upstream, upstream, upstream	0	0	1	6.5	5.25	14.5	4	4_A375_EGR1..1	17	Gene SLC25A22	EIEE3, GC1, FLJ13044, SLC25A22, NET44	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	NM_024698, NM_001191060, NM_001191061, hCT2274655.1, hCT2274656.1, hCT2274657.1, hCT2274658.1, hCT2351651.0	218725_at	NP_078974.1, NP_001177989.1, NP_001177990.1, EAX02388.1, EAX02387.1, EAX02386.1, EAX02385.1, EAX02389.1
GeneID:55367	LRDD	11	799,179	805,250	6,071	-	7	1_A375_pNL7_minus_lncRNA_AR..1..1027, 2_A375_pNL97_plus_lncRNA_AR..1..1440, 4_A375_EGR1..1..1345, 4_A375_EGR1..1..1346, 4_A375_EGR1..1..1347, 4_A375_EGR1..1..1348, 4_A375_EGR1..1..1349	-4414, -4208, 10530, 4503, 2482, -286, -4670	upstream, upstream, downstream, in gene, in gene, upstream, upstream	1	1	1	8.8	7.6	14.4	5	4_A375_EGR1..1	17	Gene LRDD	MGC16925, DKFZp434D229, PIDD, LRDD	leucine-rich repeats and death domain containing	NM_145886, NM_145887, hCT2358651.0, hCT2358652.0, hCT1960612.1	221640_s_at	NP_665893.2, NP_665894.2, EAX02390.1, EAX02391.1, EAX02392.1
GeneID:6181	RPLP2	11	809,936	812,876	2,940	+	6	1_A375_pNL7_minus_lncRNA_AR..1..1027, 2_A375_pNL97_plus_lncRNA_AR..1..1440, 4_A375_EGR1..1..1346, 4_A375_EGR1..1..1347, 4_A375_EGR1..1..1348, 4_A375_EGR1..1..1349	-272, -480, -9189, -7166, -4400, -16	upstream, upstream, upstream, upstream, upstream, upstream	1	1	1	9.5	8	14.25	4	4_A375_EGR1..1	17	Gene RPLP2	MGC71408, RPLP2, RPP2, D11S2243E, LP2, P2	ribosomal protein, large, P2	NM_001004, hCT1817072.2, hCT1952178.1	200908_s_at, 200909_s_at, 217670_at	NP_000995.1, EAX02393.1, EAX02394.1
GeneID:619565	SNORA52	11	811,681	811,814	133	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1027, 2_A375_pNL97_plus_lncRNA_AR..1..1440, 4_A375_EGR1..1..1347, 4_A375_EGR1..1..1348, 4_A375_EGR1..1..1349	-2017, -2225, -8913, -6145, -1761	upstream, upstream, upstream, upstream, upstream	1	1	1	11	9.67	15	3	4_A375_EGR1..1	17	Gene SNORA52	ACA52, SNORA52	small nucleolar RNA, H/ACA box 52	NR_002585		
GeneID:57104	PNPLA2	11	818,901	825,573	6,672	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1027, 1_A375_pNL7_minus_lncRNA_AR..1..1028, 2_A375_pNL97_plus_lncRNA_AR..1..1440, 4_A375_EGR1..1..1349	-9237, 16267, -9445, -8981	upstream, downstream, upstream, upstream	1	1	1	18	16	11	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene PNPLA2	DKFZp667M109, TTS-2.2, 1110001C14Rik, PEDF-R, TTS2, PNPLA2, ATGL, DESNUTRIN, FP17548	patatin-like phospholipase domain containing 2	NM_020376, hCT2341012.1, hCT2344480.1	212705_x_at, 213862_at, 39854_r_at	NP_065109.1, EAX02396.1, EAX02395.1
GeneID:283229	EFCAB4A	11	827,585	831,991	4,406	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1028, 4_A375_EGR1..1..1350, 4_A375_EGR1..1..1351	7583, 9599, 13940	downstream, downstream, downstream	1	0	1	12	9.67	13.67	3	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene EFCAB4A	FLJ46033, MGC88858, MGC45840, EFCAB4A	EF-hand calcium binding domain 4A	NM_173584, hCT2341000.1, hCT2348907.0, hCT2348906.0	227429_at	NP_775855.3, EAX02398.1, EAX02397.1, EAX02399.1
GeneID:977	CD151	11	832,952	838,835	5,883	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1028, 1_A375_pNL7_minus_lncRNA_AR..1..1029, 2_A375_pNL97_plus_lncRNA_AR..1..1441, 4_A375_EGR1..1..1350, 4_A375_EGR1..1..1351	2216, 9768, 9736, 4232, 8573	in gene, downstream, downstream, in gene, downstream	1	1	1	22.75	20.75	10.5	4	1_A375_pNL7_minus_lncRNA_AR..1	55	Gene CD151	RAPH, GP27, SFA1, PETA-3, TSPAN24, MER2, CD151	CD151 molecule (Raph blood group)	NM_004357, NM_139030, NM_139029, NM_001039490, hCT2272465.1, hCT2272466.0, hCT2272467.1, hCT2272468.1, hCT2272490.1, hCT2358635.0, hCT2358636.0, hCT2358637.0	204306_s_at	NP_004348.2, NP_620599.1, NP_620598.1, NP_001034579.1, EAX02401.1, EAX02402.1, EAX02400.1, EAX02403.1, EAX02404.1, EAX02405.1, EAX02406.1, EAX02407.1
GeneID:5441	POLR2L	11	839,721	842,529	2,808	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1028, 1_A375_pNL7_minus_lncRNA_AR..1..1029, 2_A375_pNL97_plus_lncRNA_AR..1..1441, 4_A375_EGR1..1..1350, 4_A375_EGR1..1..1351	7381, -191, -159, 5345, 1004	downstream, upstream, upstream, downstream, in gene	1	1	1	22.75	20.75	10.5	4	1_A375_pNL7_minus_lncRNA_AR..1	55	Gene POLR2L	RPB10, RPB10beta, RBP10, POLR2L, hsRPB10b, RPABC5, RPB7.6, hRPB7.6	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	NM_021128, hCT1817075.2	202586_at, 211730_s_at	NP_066951.1, EAX02408.1
GeneID:7106	TSPAN4	11	842,824	867,116	24,292	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1028, 1_A375_pNL7_minus_lncRNA_AR..1..1029, 2_A375_pNL97_plus_lncRNA_AR..1..1441, 4_A375_EGR1..1..1350, 4_A375_EGR1..1..1351	-7656, -104, -136, -5640, -1299	upstream, upstream, upstream, upstream, upstream	1	1	1	22.75	20.75	10.5	4	1_A375_pNL7_minus_lncRNA_AR..1	55	Gene TSPAN4	TSPAN4, TETRASPAN, NAG-2, NAG2, TM4SF7, TSPAN-4	tetraspanin 4	NM_003271, NM_001025234, NM_001025235, NM_001025236, NM_001025237, NM_001025238, NM_001025239, hCT2272492.0, hCT2272493.0, hCT2272495.0	209263_x_at, 209264_s_at	NP_003262.1, NP_001020405.1, NP_001020406.1, NP_001020407.1, NP_001020408.1, NP_001020409.1, NP_001020410.1, EAX02409.1, EAX02410.1, EAX02411.1
GeneID:4583	MUC2	11	1,074,875	1,104,417	29,542	+	2	4_A375_EGR1..1..1352, 4_A375_EGR1..1..1353	5265, 10853	in gene, in gene	0	0	1	4.5	4.5	16.5	2	4_A375_EGR1..1	21	Gene MUC2	MUC2, MLP, SMUC	mucin 2, oligomeric mucus/gel-forming	NM_002457, hCT2272501.0, hCT1817080.2	204673_at	NP_002448.2, EAX02422.1, EAX02421.1
GeneID:727897	MUC5B	11	1,244,295	1,283,406	39,111	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1442	2121	in gene	0	1	0	10	15	11	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene MUC5B	MUC5B, MUC5, MUC9, MG1	mucin 5B, oligomeric mucus/gel-forming	NM_002458	213432_at, 222268_x_at	NP_002449.2
GeneID:54472	TOLLIP	11	1,295,598	1,330,892	35,294	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1030	-180	upstream	1	0	0	14	15	15	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene TOLLIP	TOLLIP, FLJ33531, IL-1RAcPIP	toll interacting protein	NM_019009, hCT2358641.0, hCT31638.3, hCT1952268.1	217930_s_at, 222469_s_at, 233881_s_at	NP_061882.2, EAX02435.1, EAX02433.1, EAX02434.1
GeneID:255512	LOC255512	11	1,330,938	1,331,937	999	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1030	134	in gene	1	0	0	14	15	15	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene LOC255512		hypothetical LOC255512	NR_029409	1555865_at	
GeneID:9024	BRSK2	11	1,411,129	1,483,332	72,203	+	2	4_A375_EGR1..1..1356, 4_A375_EGR1..1..1357	6695, 23695	in gene, in gene	0	0	1	3.5	5	15	2	4_A375_EGR1..1	18	Gene BRSK2	FLJ41362, STK29, BRSK2, PEN11B, SAD1, C11orf7	BR serine/threonine kinase 2	NM_003957, hCT2358668.0, hCT2358669.0, hCT2358670.0, hCT2358671.0, hCT87665.3, hCT1817087.1, hCT1952183.1, hCT1952184.1, hCT1952185.1	215010_s_at, 223715_at	NP_003948.2, EAX02436.1, EAX02440.1, EAX02441.1, EAX02442.1, EAX02443.1, EAX02437.1, EAX02438.1, EAX02439.1, EAX02444.1
GeneID:1850	DUSP8	11	1,575,281	1,593,150	17,869	-	1	4_A375_EGR1..1..1358	-1906	upstream	0	0	1	4	4	13	1	4_A375_EGR1..1	13	Gene DUSP8	FLJ42958, HVH-5, C11orf81, FLJ42478, HB5, DUSP8, HVH8	dual specificity phosphatase 8	NM_004420, hCT2276368.0, hCT1823204.2	206374_at	NP_004411.2, EAX02452.1, EAX02451.1
GeneID:338651	LOC338651	11	1,593,971	1,620,414	26,443	+	1	4_A375_EGR1..1..1358	1065	in gene	0	0	1	4	4	13	1	4_A375_EGR1..1	13	Gene LOC338651	FLJ30579	hypothetical LOC338651	NR_021489	1566219_at	
GeneID:402778	LOC402778	11	1,756,030	1,769,349	13,319	-	2	4_A375_EGR1..1..1359, 4_A375_EGR1..1..1360	341, -3179	in gene, upstream	0	0	1	6.5	8	14.5	2	4_A375_EGR1..1	16	Gene LOC402778	FLJ78511, FLJ12231	CD225 family protein FLJ76511	NM_001170820	1564573_at	NP_001164291.1
GeneID:1509	CTSD	11	1,773,985	1,785,222	11,237	-	3	4_A375_EGR1..1..1359, 4_A375_EGR1..1..1360, 4_A375_EGR1..1..1361	16214, 12694, 2822	downstream, downstream, in gene	0	0	1	6.33	7	15.67	3	4_A375_EGR1..1	18	Gene CTSD	CTSD, MGC2311, CLN10, CPSD	cathepsin D	NM_001909, hCT2358634.0, hCT41148.3, hCT1952271.1	200766_at, 227863_at, 227866_at	NP_001900.1, EAX02463.1, EAX02461.1, EAX02462.1
GeneID:90019	SYT8	11	1,855,674	1,858,750	3,076	+	2	4_A375_EGR1..1..1362, 4_A375_EGR1..1..1363	-8410, -1662	upstream, upstream	0	0	1	7.5	7.5	16.5	2	4_A375_EGR1..1	16	Gene SYT8	SYT8, DKFZp434K0322	synaptotagmin VIII	NM_138567, hCT2358657.0, hCT6515.3	232602_at	NP_612634.3, EAX02466.1, EAX02465.1
GeneID:7136	TNNI2	11	1,860,233	1,862,910	2,677	+	1	4_A375_EGR1..1..1363	-6441	upstream	0	0	1	7	10	15	1	4_A375_EGR1..1	15	Gene TNNI2	DA2B, FSSV, AMCD2B, fsTnI, TNNI2	troponin I type 2 (skeletal, fast)	NM_001145829, NM_003282, NM_001145841, hCT2271460.1, hCT2348092.0, hCT6508.3	206393_at	NP_001139301.1, NP_003273.1, NP_001139313.1, EAX02467.1, EAX02468.1, EAX02469.1
GeneID:4046	LSP1	11	1,874,200	1,913,493	39,293	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1443, 4_A375_EGR1..1..1364	10440, 29192	in gene, in gene	0	1	1	7	10.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LSP1	LSP1, pp52, WP34	lymphocyte-specific protein 1	NM_002339, NM_001013253, NM_001013254, NM_001013255, hCT2271483.0, hCT2271484.0	203523_at	NP_002330.1, NP_001013271.1, NP_001013272.1, NP_001013273.1, EAX02470.1, EAX02471.1
GeneID:100423021	MIR4298	11	1,880,694	1,880,766	72	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1443	-3874	upstream	0	1	0	10	18	9	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MIR4298	MIR4298	microRNA 4298	NR_036185		
GeneID:7140	TNNT3	11	1,940,799	1,959,936	19,137	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1031, 2_A375_pNL97_plus_lncRNA_AR..1..1444	27793, 27809	downstream, downstream	1	1	0	33	51	8	1	2_A375_pNL97_plus_lncRNA_AR..1	51	Gene TNNT3	DKFZp779M2348, TNNT3, TNTF	troponin T type 3 (skeletal, fast)	NM_001042782, NM_006757, NM_001042780, NM_001042781, hCT1952151.1	1569986_x_at, 205693_at	NP_001036247.1, NP_006748.1, NP_001036245.1, NP_001036246.1, EAW50569.1
GeneID:6150	MRPL23	11	1,968,502	1,977,839	9,337	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1031, 2_A375_pNL97_plus_lncRNA_AR..1..1444, 4_A375_EGR1..1..1365	90, 106, 9674	in gene, in gene, downstream	1	1	1	17.5	27	11	2	2_A375_pNL97_plus_lncRNA_AR..1	51	Gene MRPL23	RPL23, RPL23L, FLJ45387, L23MRP, MRPL23	mitochondrial ribosomal protein L23	NM_021134, hCT2271488.0, hCT2271489.0	1562392_at, 213897_s_at	NP_066957.3, EAX02472.1, EAX02473.1
GeneID:723961	INS-IGF2	11	2,150,350	2,182,439	32,089	-	3	4_A375_EGR1..1..1367, 4_A375_EGR1..1..1368, 4_A375_EGR1..1..1369	-1789, -3321, -4825	upstream, upstream, upstream	0	0	1	4.33	4.33	15.67	3	4_A375_EGR1..1	16	Gene INS-IGF2	INSIGF	INS-IGF2 readthrough	NM_001042376, NR_003512		NP_001035835.1
GeneID:3630	INS	11	2,181,009	2,182,439	1,430	-	3	4_A375_EGR1..1..1367, 4_A375_EGR1..1..1368, 4_A375_EGR1..1..1369	-1789, -3321, -4825	upstream, upstream, upstream	0	0	1	4.33	4.33	15.67	3	4_A375_EGR1..1	16	Gene INS	MODY10, IRDN, IDDM2, INS, ILPR	insulin	NM_000207, NM_001185097, NM_001185098, hCT2276399.0, hCT6504.3	206598_at	NP_000198.1, NP_001172026.1, NP_001172027.1, EAX02488.1, EAX02489.1
GeneID:7054	TH	11	2,185,159	2,193,035	7,876	-	3	4_A375_EGR1..1..1367, 4_A375_EGR1..1..1368, 4_A375_EGR1..1..1369	8827, 7275, 5771	downstream, in gene, in gene	0	0	1	4.33	4.33	15.67	3	4_A375_EGR1..1	16	Gene TH	TYH, DYT14, TH, DYT5b	tyrosine hydroxylase	NM_199292, NM_000360, NM_199293, hCT6509.2, hCT1952152.1, hCT1952153.1, hCT1952154.1, hCT1952155.2	208291_s_at	NP_954986.2, NP_000351.2, NP_954987.2, EAX02490.1, EAX02491.1, EAX02493.1, EAX02492.1, EAX02494.1
GeneID:975	CD81	11	2,398,547	2,418,649	20,102	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1032, 2_A375_pNL97_plus_lncRNA_AR..1..1445, 4_A375_EGR1..1..1370	23277, 23277, 29829	downstream, downstream, downstream	1	1	1	12.5	10	16	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene CD81	CD81, CVID6, TSPAN28, S5.7, TAPA1	CD81 molecule	NM_004356, hCT6502.2, hCT1952146.1	200675_at	NP_004347.1, EAX02507.1, EAX02508.1
GeneID:10078	TSSC4	11	2,423,523	2,425,106	1,583	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1032, 2_A375_pNL97_plus_lncRNA_AR..1..1445, 4_A375_EGR1..1..1370	-1699, -1699, 4653	upstream, upstream, downstream	1	1	1	12.5	10	16	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene TSSC4	TSSC4		NM_005706, hCT5693.3, hCT1952140.1, hCT1952141.0, hCT1952142.1	218612_s_at	NP_005697.2, EAX02513.1, EAX02510.1, EAX02511.1, EAX02512.1
GeneID:29850	TRPM5	11	2,425,745	2,444,275	18,530	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1032, 2_A375_pNL97_plus_lncRNA_AR..1..1445, 4_A375_EGR1..1..1370	22451, 22451, 16099	downstream, downstream, in gene	1	1	1	12.5	10	16	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene TRPM5	TRPM5, LTRPC5, MTR1	transient receptor potential cation channel, subfamily M, member 5	NM_014555, hCT2276356.0, hCT2358654.0, hCT7476.2	223935_at	NP_055370.1, EAX02515.1, EAX02514.1, EAX02516.1
GeneID:3784	KCNQ1	11	2,466,221	2,870,340	404,119	+	11	4_A375_EGR1..1..1371, 4_A375_EGR1..1..1372, 4_A375_EGR1..1..1373, 4_A375_EGR1..1..1374, 4_A375_EGR1..1..1375, 4_A375_EGR1..1..1376, 4_A375_EGR1..1..1377, 4_A375_EGR1..1..1378, 4_A375_EGR1..1..1379, 4_A375_EGR1..1..1380, 4_A375_EGR1..1..1381	20947, 70995, 86451, 90803, 95011, 254803, 344675, 356755, 375971, 396819, 400926	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	5	6.36	16	11	4_A375_EGR1..1	19	Gene KCNQ1	WRS, RWS, ATFB3, LQT1, Kv7.1, Kv1.9, LQT, FLJ26167, KCNA9, ATFB1, SQT2, KCNQ1, KCNA8, JLNS1, KVLQT1	potassium voltage-gated channel, KQT-like subfamily, member 1	NM_181798, NM_000218, hCT2271528.0, hCT2358639.0, hCT2358640.0, hCT1821917.1, hCT1952192.0	204486_at, 204487_s_at, 211217_s_at	NP_861463.1, NP_000209.2, EAX02517.1, EAX02518.1, EAX02519.1, EAX02521.1, EAX02520.1
GeneID:10984	KCNQ1OT1	11	2,661,768	2,721,228	59,460	-	1	4_A375_EGR1..1..1376	204	in gene	0	0	1	9	10	19	1	4_A375_EGR1..1	19	Gene KCNQ1OT1	KvDMR1, KvLQT1-AS, LIT1, KCNQ10T1, FLJ41078, NCRNA00012, KCNQ1OT1	KCNQ1 overlapping transcript 1 (non-protein coding)	NR_002728	237249_at, 243428_at, 243435_at, 244727_at	
GeneID:1028	CDKN1C	11	2,904,448	2,906,995	2,547	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1446, 4_A375_EGR1..1..1382	531, 243	in gene, in gene	0	1	1	10	15	15	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene CDKN1C	KIP2, WBS, CDKN1C, BWS, p57, BWCR	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	NM_000076, NM_001122630, NM_001122631, hCT1821915.1, hCT1952649.1	213182_x_at, 213183_s_at, 213348_at, 216894_x_at, 219533_at, 219534_x_at	NP_000067.1, NP_001116102.1, NP_001116103.1, EAX02524.1, EAX02525.1
GeneID:5003	SLC22A18AS	11	2,909,327	2,925,175	15,848	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1446, 4_A375_EGR1..1..1382	18711, 18423	downstream, downstream	0	1	1	10	15	15	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene SLC22A18AS	SLC22A18AS, SLC22A1LS, BWR1B, BWSCR1B, ORCTL2S, p27-BWR1B	solute carrier family 22 (organic cation transporter), member 18 antisense	NM_007105, hCT7473.2, hCT1952637.0	206097_at	NP_009036.2, EAX02527.1, EAX02526.1
GeneID:5002	SLC22A18	11	2,920,951	2,946,476	25,525	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1447, 4_A375_EGR1..1..1383, 4_A375_EGR1..1..1384	29561, 22345, 31513	downstream, in gene, downstream	0	1	1	7.67	8.67	10.67	3	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SLC22A18	BWSCR1A, IMPT1, TSSC5, SLC22A1L, p45-BWR1A, BWR1A, ITM, ORCTL2, SLC22A18, DKFZp667A184, HET	solute carrier family 22, member 18	NM_183233, NM_002555, hCT2358645.0, hCT7471.2, hCT1952636.1	204981_at	NP_899056.2, NP_002546.3, EAX02528.1, EAX02529.1, EAX02530.1



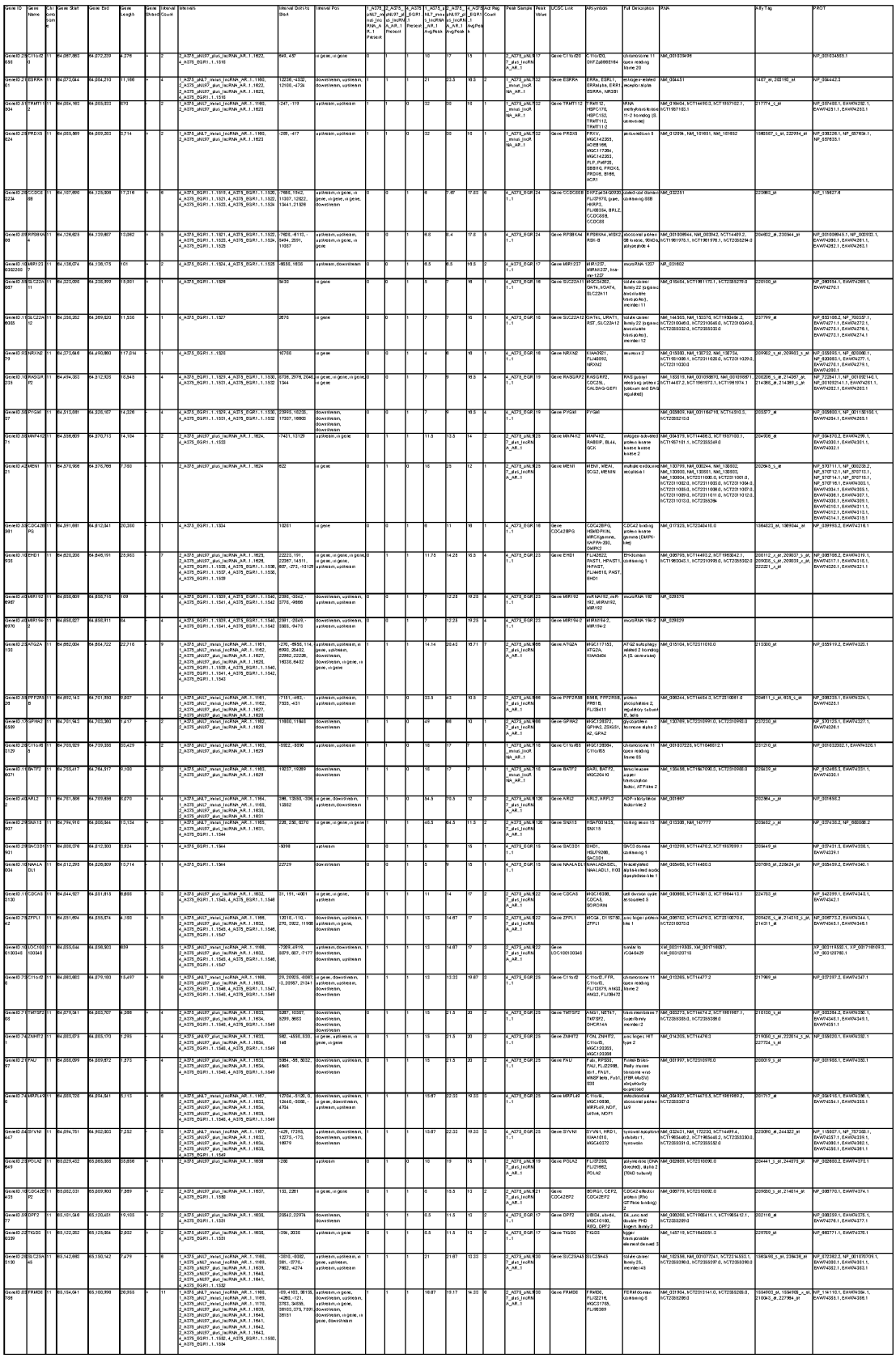
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.89797	NAV2	11	19,372,271	20,143,147	770,876	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1050, 2_A375_pNL97_plus_lncRNA_AR..1..1472, 2_A375_pNL97_plus_lncRNA_AR..1..1473	568737, 568721, 761921	in gene, in gene, in gene	1	1	0	14	17	5.5	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene NAV2	FLJ77876, NAV2, UNC53H2, FLJ23707, HELAD1, KIAA1419, RAINB1, STEERIN2, FLJ10633, POMFIL2, FLJ11030	neuron navigator 2	NM_145117, NM_182964, NM_001111018, NM_001111019, hCT2270156.1, hCT2270157.1, hCT2270160.1, hCT2270161.1, hCT2270162.1, hCT2348690.0	1556606_at, 1567357_at, 1567358_at, 218330_s_at, 222599_s_at, 239141_at	NP_660093.2, NP_892009.3, NP_001104488.1, NP_001104489.1, EAW68345.1, EAW68348.1, EAW68343.1, EAW68344.1, EAW68346.1, EAW68347.1
GeneID.120237	DBX1	11	20,177,760	20,181,870	4,110	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1051, 2_A375_pNL97_plus_lncRNA_AR..1..1474	1486, 1454	in gene, in gene	1	1	0	28	37	8	1	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene DBX1	DBX1		NM_001029865, hCT5910.1		NP_001025036.1, EAW68342.1
GeneID.9152	SLC6A5	11	20,620,946	20,676,610	55,664	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1475	494	in gene	0	1	0	15	29	3	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene SLC6A5	SLC6A5, GLYT-2, GLYT2, NET1	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	NM_004211, hCT14449.3	210810_s_at	NP_004202.2, EAW68330.1
GeneID.203859	ANO5	11	22,214,722	22,304,913	90,191	+	1	4_A375_EGR1..1..1399	-418	upstream	0	0	1	8	8	17	1	4_A375_EGR1..1	17	Gene ANO5	TMEM16E, LGMD2L, GDD1, ANO5	anoctamin 5	NM_213599, NM_001142649, hCT1823568.2	229313_at	NP_998764.1, NP_001136121.1, EAW68325.1
GeneID.57084	SLC17A6	11	22,359,667	22,401,049	41,382	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1476	-371	upstream	0	1	0	12	30	5	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SLC17A6	SLC17A6, VGLUT2, DNPI	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	NM_020346, hCT23663.3	220551_at	NP_065079.1, EAW68324.1
GeneID.627	BDNF	11	27,676,440	27,743,605	67,165	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1052, 1_A375_pNL7_minus_lncRNA_AR..1..1053, 1_A375_pNL7_minus_lncRNA_AR..1..1054, 2_A375_pNL97_plus_lncRNA_AR..1..1478, 2_A375_pNL97_plus_lncRNA_AR..1..1479, 2_A375_pNL97_plus_lncRNA_AR..1..1480	2645, 1541, -443, 2709, 1429, 485	in gene, in gene, upstream, in gene, in gene, in gene	1	1	0	18.5	21.25	6.5	4	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene BDNF	MGC34632, BDNF	brain-derived neurotrophic factor	NM_170731, NM_170732, NM_170733, NM_001709, NM_170734, NM_170735, NM_001143805, NM_001143806, NM_001143807, NM_001143808, NM_001143809, NM_001143810, NM_001143811, NM_001143812, NM_001143813, NM_001143814, NM_001143816, hCT2269104.1, hCT2269107.1, hCT2346	206382_s_at, 239367_at	NP_733927.1, NP_733928.1, NP_733929.1, NP_733930.1, NP_733931.1, NP_001700.2, NP_001137277.1, NP_001137278.1, NP_001137279.1, NP_001137280.1, NP_001137281.1, NP_001137282.1, NP_001137283.1, NP_001137284.1, NP_001137285.1, NP_001137286.1, NP_001137288.1, E
GeneID.81930	KIF18A	11	28,042,163	28,129,746	87,583	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1482	-156	upstream	0	1	0	8	14	6	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene KIF18A	DKFZp434G2226, KIF18A, MS-KIF18A	kinesin family member 18A	NM_031217, hCT18535.3	221258_s_at	NP_112494.3, EAW68271.1
GeneID.198074	METT5D1	11	28,129,798	28,355,054	225,256	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1482	106	in gene	0	1	0	8	14	6	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene METT5D1	FLJ33979, METTL15, METT5D1	methyltransferase 5 domain containing 1	NM_152636, NM_001113528, hCT2269228.1, hCT2269230.1, hCT2349306.0, hCT2354573.0	1562830_at, 1565698_at, 1565900_at, 236773_at, 242247_at	NP_689849.2, NP_001107000.1, EAW68266.1, EAW68267.1, EAW68268.1, EAW68269.1
GeneID.341019	DCDC1	11	31,284,171	31,391,321	107,150	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1485	-87	upstream	0	1	0	11	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene DCDC1	DCDC1, FLJ44076	doublecortin domain containing 1	NM_181807, hCT1646343.3		NP_861523.2, EAW68246.1
GeneID.120526	DNAJC24	11	31,391,377	31,454,382	63,005	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1485	31	in gene	0	1	0	11	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene DNAJC24	ZCSL3, DPH4, DNAJC24, JJJ3	DnaJ (Hsp40) homolog, subfamily C, member 24	NM_181706, hCT2348798.0, hCT2348799.0, hCT2348800.0, hCT2348886.0, hCT2348887.0, hCT2348888.0, hCT18998.5	1570048_at, 213853_at, 242562_at	NP_859057.4, EAW68247.1, EAW68241.1, EAW68242.1, EAW68243.1, EAW68246.1, EAW68244.1, EAW68245.1
GeneID.5954	RCN1	11	32,112,477	32,127,272	14,795	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1058	-2781	upstream	1	0	0	17	13	7	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene RCN1	FLJ55835, RCN1, RCAL, PIG20, RCN, FLJ37041	reticulocalbin 1, EF-hand calcium binding domain	NM_002901, hCT2266696.0, hCT18996.3	201063_at	NP_002892.1, EAW68226.1, EAW68227.1
GeneID.7490	WT1	11	32,409,325	32,457,087	47,762	-	1	4_A375_EGR1..1..1402	799	in gene	0	0	1	13	13	17	1	4_A375_EGR1..1	17	Gene WT1	WT33, GUD, WT1, WIT-2, AWT1, WAGR, NPHS4	Wilms tumor 1	NM_000378, NM_024424, NM_024425, NM_024426, hCT1969179.1, hCT1969180.0, hCT2354584.0, hCT2354585.0, hCT2354586.0, hCT1823775.1, hCT18460.2	206067_s_at, 216953_s_at	NP_000369.3, NP_077742.2, NP_077743.2, NP_077744.3, EAW68220.1, EAW68226.1, EAW68221.1, EAW68222.1, EAW68223.1, EAW68224.1, EAW68225.1
GeneID.51352	WIT1	11	32,457,285	32,461,636	4,351	+	1	4_A375_EGR1..1..1402	-997	upstream	0	0	1	13	13	17	1	4_A375_EGR1..1	17	Gene WIT1	MGC120207, dJ74J1.1, WT1-AS, WIT-1, WT1AS, MGC120209, WIT1, WT1-AS1, MGC120208	WT1 antisense RNA (non-protein coding)	NR_023920	206954_at	
GeneID.79832	QSER1	11	32,914,792	33,001,816	87,024	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1060, 4_A375_EGR1..1..1403, 4_A375_EGR1..1..1404	-744, -4808, 216	upstream, upstream, in gene	1	0	1	13	8.33	11.33	3	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene QSER1	FLJ21924, QSER1	glutamine and serine rich 1	NM_001076786, hCT1823778.3	219705_at, 226265_at, 229862_at, 244563_at	NP_001070254.1, EAW68214.1
GeneID.91614	DEPDC7	11	33,037,410	33,055,128	17,718	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1061, 1_A375_pNL7_minus_lncRNA_AR..1..1062, 2_A375_pNL97_plus_lncRNA_AR..1..1488, 2_A375_pNL97_plus_lncRNA_AR..1..1489, 4_A375_EGR1..1..1405	-98, 23606, 30, 23516, -66	upstream, downstream, in gene, downstream, upstream	1	1	1	19.5	23.5	18	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene DEPDC7	DEPDC7, TR2, dJ85M6.4	DEP domain containing 7	NM_001077242, NM_139160, hCT2336460.0, hCT18458.2	228293_at	NP_001070710.1, NP_631899.2, EAW68212.1, EAW68213.1
GeneID.55346	TCP11L1	11	33,060,963	33,095,109	34,146	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1062, 2_A375_pNL97_plus_lncRNA_AR..1..1489	253, -35	in gene, upstream	1	1	0	19	28	13	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene TCP11L1	dJ85M6.3, FLJ11336, FLJ11386, TCP11L1	t-complex 11 (mouse)-like 1	NM_001145541, NM_018393, hCT2336461.0, hCT2336462.0, hCT2336463.0, hCT2336464.0, hCT2336465.0, hCT18459.1	205796_at, 205797_s_at, 233472_at	NP_001139013.1, NP_060863.3, EAW68205.1, EAW68206.1, EAW68208.1, EAW68210.1, EAW68207.1, EAW68209.1
GeneID.10114	HIPK3	11	33,279,168	33,375,939	96,771	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1490	-64	upstream	0	1	0	15	17	13	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene HIPK3	YAK1, FIST3, DYRK6, PKY, HIPK3	homeodomain interacting protein kinase 3	NM_005734, NM_001048200, hCT2336446.0, hCT2336447.0	207764_s_at, 210148_at, 213697_at, 226297_at	NP_005725.3, NP_001041665.1, EAW68198.1, EAW68199.1
GeneID.25758	C11orf41	11	33,563,877	33,695,648	131,771	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1064, 1_A375_pNL7_minus_lncRNA_AR..1..1065, 2_A375_pNL97_plus_lncRNA_AR..1..1491, 2_A375_pNL97_plus_lncRNA_AR..1..1492, 2_A375_pNL97_plus_lncRNA_AR..1..1493	91463, 128763, 91208, 128371, 140395	in gene, in gene, in gene, in gene, downstream	1	1	0	14.33	15.33	5.33	3	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C11orf41	C11orf69, FLJ36966, G2, MGC34830, C11orf41	chromosome 11 open reading frame 41	NM_012194	214772_at, 244584_at	NP_036326.2
GeneID.966	CD59	11	33,724,556	33,758,025	33,469	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1066, 1_A375_pNL7_minus_lncRNA_AR..1..1067, 2_A375_pNL97_plus_lncRNA_AR..1..1494, 4_A375_EGR1..1..1406	13756, -455, 14025, 121	in gene, upstream, in gene, in gene	1	1	1	15.5	16.5	12.5	2	4_A375_EGR1..1	19	Gene CD59	MIRL, MACIF, MGC2354, CD59, HRF-20, MIN2, MEM43, MIC11, MIN1, EJ30, MIN3, EL32, G344, 1F5, FLJ92039, MSK21, 16.3A5, EJ16, HRF20, p18-20, FLJ38134, MAC-IP	CD59 molecule, complement regulatory protein	NM_001127223, NM_203330, NM_203329, NM_001127225, NM_203331, NM_000611, NM_001127226, NM_001127227, hCT2336233.0, hCT2336234.0	200983_x_at, 200984_s_at, 200985_s_at, 212463_at, 228748_at	NP_001120695.1, NP_976075.1, NP_000602.1, NP_001120697.1, NP_976076.1, NP_976074.1, NP_001120698.1, NP_001120699.1, EAW68192.1, EAW68193.1
GeneID.26273	FBXO3	11	33,762,490	33,796,071	33,581	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1067, 4_A375_EGR1..1..1406, 4_A375_EGR1..1..1407	37591, 36167, 327	downstream, downstream, in gene	1	0	1	13	12	22.5	2	4_A375_EGR1..1	26	Gene FBXO3	FBA, FBX3, DKFZp564B092, FBXO3	F-box protein 3	NM_033406, NM_012175, hCT1969181.1, hCT2336229.0, hCT2354546.0, hCT2354547.0, hCT2354548.0, hCT18706.3	218432_at, 229955_at, 232615_at, 232651_at, 236686_at, 242791_at	NP_208385.1, NP_036307.2, EAW68187.1, EAW68188.1, EAW68189.1, EAW68190.1, EAW68186.1, EAW68191.1
GeneID.100507109	LOC100507109	11	33,797,734	33,801,299	3,565	+	1	4_A375_EGR1..1..1407	-1990	upstream	0	0	1	9	8	26	1	4_A375_EGR1..1	26	Gene LOC100507109		hypothetical LOC100507109	XR_111158, XR_109037, XR_114475		
GeneID.4076	CAPRIN1	11	34,073,230	34,124,157	50,927	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1069, 2_A375_pNL97_plus_lncRNA_AR..1..1497, 2_A375_pNL97_plus_lncRNA_AR..1..1498	82, -78, 53938	in gene, upstream, downstream	1	1	0	23	26.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene CAPRIN1	RNG105, CAPRIN1, M11S1, GPIP137, caprin-1, p137GPI, GPIAP1	cell cycle associated protein 1	NM_005898, NM_203364, hCT2268993.0, hCT2268994.0, hCT2354576.0, hCT2354577.0, hCT18711.3	200722_s_at, 200723_s_at, 225340_s_at, 226265_at, 226289_at, 226990_at, 243370_at	NP_005889.3, NP_976240.1, EAW68176.1, EAW68177.1, EAW68178.1, EAW68180.1, EAW68179.1
GeneID.55226	NAT10	11	34,127,111	34,168,458	41,347	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1498	57	in gene	0	1	0	24	34	11	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene NAT10	KIAA1709, NET43, DKFZp434C116, ALP, FLJ10774, FLJ23850, FLJ12179, NAT10	N-acetyltransferase 10 (GCN5-related)	NM_024662, NM_001144030, hCT2268997.0, hCT18707.3	217684_at	NP_078938.2, NP_001137502.1, EAW68174.1, EAW68175.1
GeneID.25841	ABTB2	11	34,172,534	34,379,555	207,021	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1070, 1_A375_pNL7_minus_lncRNA_AR..1..1071, 2_A375_pNL97_plus_lncRNA_AR..1..1499, 2_A375_pNL97_plus_lncRNA_AR..1..1500, 2_A375_pNL97_plus_lncRNA_AR..1..1501, 2_A375_pNL97_plus_lncRNA_AR..1..1502	26499, 18595, 142915, 106659, 55411, -1053	in gene, in gene, in gene, in gene, in gene, upstream	1	1	0	16.67	17.17	6.83	6	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene ABTB2	ABTB2, DKFZp586C1619	ankyrin repeat and BTB (POZ) domain containing 2	NM_145804, hCT2354561.0, hCT1951779.1	213497_at, 232624_at	NP_665803.2, EAW68172.1, EAW68173.1
GeneID.847	CAT	11	34,460,472	34,493,607	33,135	+	1	4_A375_EGR1..1..1408	120	in gene	0	0	1	14	14	23	1	4_A375_EGR1..1	23	Gene CAT	MGC138424, CAT, MGC138422	catalase	NM_001752, hCT2269001.0, hCT17632.3	201432_at, 211922_s_at, 215573_at, 238383_at	NP_001743.1, EAW68170.1, EAW68171.1
GeneID.26298	EHF	11	34,642,588	34,684,835	42,247	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1073, 1_A375_pNL7_minus_lncRNA_AR..1..1074, 2_A375_pNL97_plus_lncRNA_AR..1..1504	33092, 33956, 33316	in gene, in gene, in gene	1	1	0	18	24	5	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene EHF	EHF, ESE3, ESEJ	ets homologous factor	NM_012153, hCT1969193.1, hCT19736.3, hCT2269004.0, hCT2354555.0, hCT2354556.0	219850_s_at, 222932_at, 224189_x_at, 225645_at, 232360_at, 232361_s_at, 241397_at	NP_036285.2, EAW68162.1, EAW68163.1, EAW68164.1, EAW68165.1, EAW68166.1
GeneID.51074	APIP	11	34,903,842	34,937,939	34,097	-	1	4_A375_EGR1..1..1409	-301	upstream	0	0	1	16	11	18	1	4_A375_EGR1..1	18	Gene APIP	APIP2, CGI29, MMRP19, dJ179L10.2, APIP, CGI-29	APAF1 interacting protein	NM_015957, hCT1823868.2	218698_at, 232630_at	NP_057041.2, EAW68161.1
GeneID.8050	PDHX	11	34,937,677	35,017,675	79,998	+	1	4_A375_EGR1..1..1409	563	in gene	0	0	1	16	11	18	1	4_A375_EGR1..1	18	Gene PDHX	PDX1, PDHX, E3BP, proX, DLDBP, OPDX	pyruvate dehydrogenase complex, component X	NM_003477, NM_001135024, NM_001166158, hCT2297693.0, hCT2297694.0, hCT2354498.0	203067_at	NP_003468.2, NP_001128496.1, NP_001159630.1, EAW68158.1, EAW68159.1, EAW68160.1
GeneID.100507144	LOC100507144	11	35,154,197	35,159,574	5,377	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1506, 4_A375_EGR1..1..1410	-1226, -1098	upstream, upstream	0	1	1	15	25	23	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC100507144		hypothetical LOC100507144	XR_111155, XR_109039, XR_114478		
GeneID.960	CD44	11	35,160,417	35,253,949	93,532	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1075, 2_A375_pNL97_plus_lncRNA_AR..1..1506, 2_A375_pNL97_plus_lncRNA_AR..1..1507, 4_A375_EGR1..1..1410	28031, 383, 28095, 255	in gene, in gene, in gene, in gene	1	1	1	18	24	15	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene CD44	MIC4, ECMR-III, Pgp1, MUTCH-I, HCELL, MC56, CSPG8, IN, MDU3, CD44, CDW44, LHR, MGC10468, MDU2	CD44 molecule (Indian blood group)	NM_000610, NM_001001389, NM_001001390, NM_001001391, NM_001001392, hCT2297697.0, hCT2297698.0, hCT2297699.0, hCT2297700.0, hCT2297701.0, hCT2297702.0, hCT2297703.0, hCT2297704.0, hCT2297705.0, hCT2354552.0, hCT2354553.0, hCT1951772.1	1557905_s_at, 1565868_at, 204489_s_at, 204490_s_at, 209835_x_at, 210916_s_at, 212014_x_at, 212063_at, 216056_at, 217523_at, 234411_x_at, 234418_x_at	NP_000601.3, NP_001001389.1, NP_001001390.1, NP_001001391.1, NP_001001392.1, EAW68152.1, EAW68144.1, EAW68145.1, EAW68146.1, EAW68147.1, EAW68148.1, EAW68149.1, EAW68150.1, EAW68151.1, EAW68153.1, EAW68154.1, EAW68155.1
GeneID.25891	PAMR1	11	35,453,374	35,547,176	93,802	-	1	4_A375_EGR1..1..1411	93704	in gene	0	0	1	5	8	15	1	4_A375_EGR1..1	15	Gene PAMR1	DKFZP586H2123, PAMR1, RAMP, FP938	peptidase domain containing associated with muscle regeneration 1	NM_015430, NM_001001991, hCT1951780.1	213661_at	NP_056245.2, NP_001001991.1, EAW68140.1
GeneID.24147	FJX1	11	35,639,735	35,642,421	2,686	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1076, 2_A375_pNL97_plus_lncRNA_AR..1..1508	1113, 1449	in gene, in gene	1	1	0	19	20	15	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene FJX1	FLJ22416, FLJ25593, FJX1	four jointed box 1 (Drosophila)	NM_014344, hCT19093.2	219522_at	NP_055159.2, EAW68138.1
GeneID.54765	TRIM44	11	35,684,353	35,830,930	146,577	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1077, 2_A375_pNL97_plus_lncRNA_AR..1..1509, 2_A375_pNL97_plus_lncRNA_AR..1..1510	63327, 47, 63359	in gene, in gene, in gene	1	1	0	29	29.5	9	2	1_A375_pNL7_minus_lncRNA_AR..1	41	Gene TRIM44	DIPB, TRIM44, HSA249128, MGC3490, MC7	tripartite motif containing 44	NM_017583, hCT2297711.0, hCT2297712.0, hCT19094.3	217759_at, 217760_at	NP_060053.2, EAW68134.1, EAW68133.1, EAW68135.1
GeneID.143458	LDLRAD3	11	35,965,612	36,252,841	287,229	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1078, 2_A375_pNL97_plus_lncRNA_AR..1..1511, 2_A375_pNL97_plus_lncRNA_AR..1..1512, 2_A375_pNL97_plus_lncRNA_AR..1..1513	205780, 47700, 58356, 205812	in gene, in gene, in gene, in gene	1	1	0	19	21.33	5.33	3	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene LDLRAD3	LDLRAD3	low density lipoprotein receptor class A domain containing 3	NM_174902, hCT2268389.1, hCT2348868.0, hCT2348869.0	234985_at, 244338_at	NP_777562.1, EAW68127.1, EAW68125.1, EAW68126.1
GeneID.29099	COMMD9	11	36,293,842	36,310,999	17,157	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1514	-73	upstream	0	1	0	16	20	7	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene COMMD9	COMMD9, HSPC166, FLJ31106	COMM domain containing 9	NM_014186, NM_001101653, hCT2354527.0, hCT17639.2, hCT1814572.1	218072_at	NP_054905.2, NP_001095123.1, EAW68128.1, EAW68129.1, EAW68130.1
GeneID.79899	PRR5L	11	36,317,725	36,486,754	169,029	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1514, 2_A375_pNL97_plus_lncRNA_AR..1..1515	-8653, 135715	upstream, in gene	0	1	0	16	20	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PRR5L	PROTOR2, FLJ22630, MGC16218, FLJ14213, PRR5L	proline rich 5 like	NM_024841, NM_001160167, NM_001160168, NM_001160169, hCT1823920.2, hCT1958672.1	1555488_a_at, 219363_at, 233119_at, 233379_at	NP_079117.3, NP_001153639.1, NP_001153640.1, NP_001153641.1, EAW68123.1, EAW68124.1
GeneID.7189	TRAF6	11	36,510,723	36,531,822	21,099	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1079, 2_A375_pNL97_plus_lncRNA_AR..1..1516, 4_A375_EGR1..1..1412	78, 46, 238	in gene, in gene, in gene	1	1	1	63	93	22	1	2_A375_pNL97_plus_lncRNA_AR..1	93	Gene TRAF6	RNF85, TRAF6, MGC:3310	TNF receptor-associated factor 6	NM_004620, NM_145803, hCT2268155.0, hCT2268156.0, hCT2268158.0, hCT2354539.0	205558_at	NP_004611.1, NP_665802.1, EAW68119.1, EAW68120.1, EAW68121.1, EAW68122.1
GeneID.5897	RAG2	11	36,613,493	36,619,829	6,336	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1080, 2_A375_pNL97_plus_lncRNA_AR..1..1517	3785, 3925	in gene, in gene	1	1	0	18	19	8	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene RAG2	RAG-2, RAG2	recombination activating gene 2	NM_000536, NR_033666, hCT1643134.1	215117_at	NP_000527.2, EAW68117.1
GeneID.119710	C11orf74	11	36,616,093	36,680,817	64,724	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1080, 2_A375_pNL97_plus_lncRNA_AR..1..1517	-29, -169	upstream, upstream	1	1	0	18	19	8	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C11orf74	C11orf74, FLJ38678	chromosome 11 open reading frame 74	NM_138787, hCT1969187.1, hCT1969189.1, hCT2354524.0, hCT2354525.0, hCT19032.2	228249_at	NP_620142.2, EAW68114.1, EAW68112.1, EAW68113.1, EAW68115.1, EAW68116.1
GeneID.100507187	LOC100507187	11	40,669,774	41,481,768	811,994	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1082	582760	in gene	1	0	0	20	10	4	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LOC100507187		hypothetical LOC100507187	XR_109041		
GeneID.8539	API5	11	43,333,505	43,366,080	32,575	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1083, 2_A375_pNL97_plus_lncRNA_AR..1..1521, 4_A375_EGR1..1..1417	-1, -33, 95	upstream, upstream, in gene	1	1	1	103	128	14	1	2_A375_pNL97_plus_lncRNA_AR..1	128	Gene API5	API5, AAC-11, AAC11	apoptosis inhibitor 5	NR_024625, NM_006595, NM_001142930, NM_001142931, hCT2268328.0, hCT2268329.0	201686_x_at, 201687_s_at, 214959_s_at, 214960_at, 233078_at	NP_006586.1, NP_001136402.1, NP_001136403.1, EAW68098.1, EAW68099.1



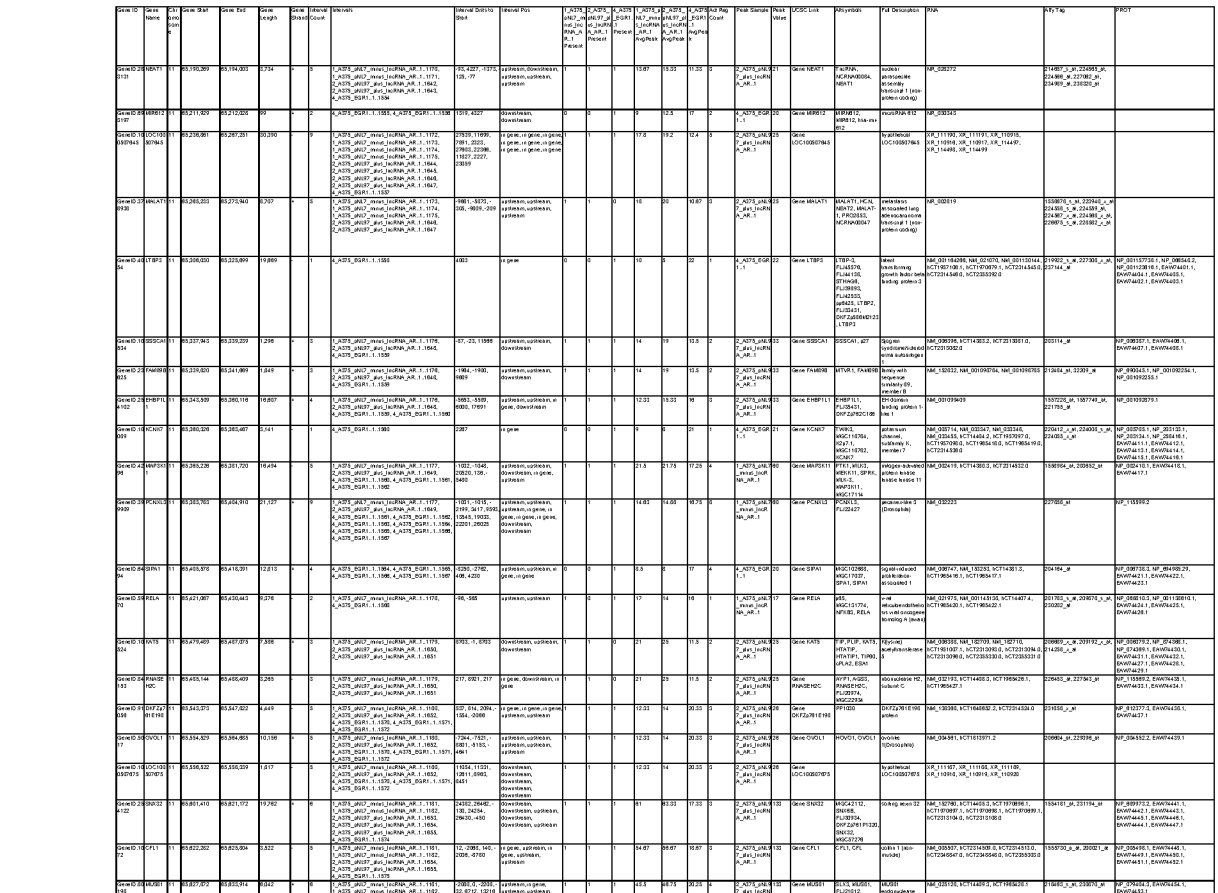


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:54949	SDHAF2	11	61,197,597	61,214,239	16,642	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1132, 2_A375_pNL97_plus_lncRNA_AR..1..1579, 4_A375_EGR1..1..1463	-189, -253, 163	upstream, upstream, in gene	1	1	1	17	18	16	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SDHAF2	SDH5, PGL2, FLJ20487, SDHAF2, C11orf79	succinate dehydrogenase complex assembly factor 2	NM_017841	223046_at	NP_060311.1
GeneID:390205	LRRC10B	11	61,276,272	61,278,490	2,218	+	2	4_A375_EGR1..1..1464, 4_A375_EGR1..1..1465	-400, 7760	upstream, downstream	0	0	1	6.5	7	20	2	4_A375_EGR1..1	21	Gene LRRC10B	LRRC10B		NM_001145077		NP_001138549.1
GeneID:9066	SYT7	11	61,282,785	61,348,298	65,513	-	10	1_A375_pNL7_minus_lncRNA_AR..1..1133, 1_A375_pNL7_minus_lncRNA_AR..1..1134, 1_A375_pNL7_minus_lncRNA_AR..1..1135, 2_A375_pNL97_plus_lncRNA_AR..1..1580, 2_A375_pNL97_plus_lncRNA_AR..1..1581, 2_A375_pNL97_plus_lncRNA_AR..1..1582, 4_A375_EGR1..1..1464, 4_A375_EGR1..1..1465, 4_A375_EGR1..1..1466, 4_A375_EGR1..1..1467	35336, 13482, -726, 35354, 13482, -662, 72426, 64266, 13466, -7266	in gene, in gene, upstream, in gene, in gene, upstream, downstream, in gene, in gene, upstream	1	1	1	26.33	27.17	16.17	6	2_A375_pNL97_plus_lncRNA_AR..1	69	Gene SYT7	SYT-VII, MGC150517, SYT7, IPCA-7, PCANAP7	synaptotagmin VII	NM_004200, hCT2311622.0, hCT2311623.0, hCT2311624.0, hCT2311625.0, hCT32130.3	1559392_s_at, 1559956_at, 226167_at, 232025_at	NP_004191.2, EAW73953.1, EAW73954.1, EAW73955.1, EAW73956.1, EAW73957.1
GeneID:747	DAGLA	11	61,447,910	61,514,473	66,563	+	1	4_A375_EGR1..1..1466	69674	downstream	0	0	1	12	8	16	1	4_A375_EGR1..1	16	Gene DAGLA	DAGLA, DAGLALPHA, C11orf11, NSDDR, DAGL(ALPHA)	diacylglycerol lipase, alpha	NM_006133, hCT2310303.0, hCT2310304.0, hCT2310305.0, hCT32133.3	214128_at	NP_006124.1, EAW73959.1, EAW73960.1, EAW73961.1, EAW73962.1
GeneID:745	C11orf9	11	61,520,121	61,555,989	35,868	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1136, 2_A375_pNL97_plus_lncRNA_AR..1..1583, 4_A375_EGR1..1..1468, 4_A375_EGR1..1..1469, 4_A375_EGR1..1..1470	40103, 40119, -2537, 16871, 40359	downstream, downstream, upstream, in gene, downstream	1	1	1	16.33	15.67	17.33	3	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene C11orf9	MGC10781, Ndt80, MRF, KIAA0954, C11orf9	chromosome 11 open reading frame 9	NM_001127392, NM_013279, hCT2310307.0, hCT2310308.0, hCT2310310.0, hCT2310311.0, hCT2310314.0, hCT2355288.0	204073_s_at, 217462_at, 217463_s_at	NP_001120864.1, NP_037411.1, EAW73963.1, EAW73964.1, EAW73965.1, EAW73966.1, EAW73966.1, EAW73967.1
GeneID:26070	DKFZP434K028	11	61,521,501	61,525,136	3,635	-	1	4_A375_EGR1..1..1468	7552	downstream	0	0	1	12	8	16	1	4_A375_EGR1..1	16	Gene DKFZP434K028	MGC34024	hypothetical LOC26070	NR_026682	1554880_at, 234356_at	
GeneID:100507462	LOC100507462	11	61,534,400	61,534,987	587	+	1	4_A375_EGR1..1..1469	2592	downstream	0	0	1	6	3	22	1	4_A375_EGR1..1	22	Gene LOC100507462		hypothetical protein LOC100507462	XM_003119501, XM_003119184, XM_003120703		XP_003119549.1, XP_003119232.1, XP_003120751.1
GeneID:746	C11orf10	11	61,556,602	61,560,085	3,483	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1136, 2_A375_pNL97_plus_lncRNA_AR..1..1583, 4_A375_EGR1..1..1470	-139, -155, -395	upstream, upstream, upstream	1	1	1	31	36	14	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene C11orf10	C11orf10	chromosome 11 open reading frame 10	NM_014206, hCT2311615.0, hCT32117.1	218213_s_at	NP_055021.1, EAW73971.1, EAW73970.1
GeneID:693196	MIR611	11	61,559,967	61,560,033	66	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1136, 2_A375_pNL97_plus_lncRNA_AR..1..1583, 4_A375_EGR1..1..1470	-191, -207, -447	upstream, upstream, upstream	1	1	1	31	36	14	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene MIR611	MIR611, MIRN611, hsa-mir-611	microRNA 611	NR_030342		
GeneID:2237	FEN1	11	61,560,150	61,564,710	4,560	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1136, 2_A375_pNL97_plus_lncRNA_AR..1..1583, 4_A375_EGR1..1..1470	74, 90, 330	in gene, in gene, in gene	1	1	1	31	36	14	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene FEN1	FEN1, MF1, FEN-1, RAD2	flap structure-specific endonuclease 1	NM_004111, hCT32115.2	204767_s_at, 204768_s_at	NP_004102.1, EAW73972.1
GeneID:3992	FADS1	11	61,567,097	61,584,529	17,432	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1136, 1_A375_pNL7_minus_lncRNA_AR..1..1137, 2_A375_pNL97_plus_lncRNA_AR..1..1583, 2_A375_pNL97_plus_lncRNA_AR..1..1584, 4_A375_EGR1..1..1470, 4_A375_EGR1..1..1471	24305, 81, 24289, 113, 24049, 1569	downstream, in gene, downstream, in gene, downstream, in gene	1	1	1	20.33	21	14	3	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene FADS1	FADS6, FADSD5, FADS1, D5D, LLCDL1, FLJ90273, FLJ38956, TU12	fatty acid desaturase 1	NM_013402, hCT2311614.0	208962_s_at, 208963_x_at, 208964_s_at	NP_037534.3, EAW73973.1
GeneID:100302263	MIR1908	11	61,582,633	61,582,712	79	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1137, 2_A375_pNL97_plus_lncRNA_AR..1..1584, 4_A375_EGR1..1..1471	-1736, -1704, -248	upstream, upstream, upstream	1	1	1	15	13.5	14	2	4_A375_EGR1..1	18	Gene MIR1908	MIR1908, hsa-mir-1908, MIRN1908	microRNA 1908	NR_031729		
GeneID:9415	FADS2	11	61,595,713	61,634,825	39,112	+	2	4_A375_EGR1..1..1472, 4_A375_EGR1..1..1473	14415, 34511	in gene, in gene	0	0	1	3	5	15.5	2	4_A375_EGR1..1	16	Gene FADS2	DES6, FADSD6, LLCDL2, SLL0262, TU13, FADS2, D6D	fatty acid desaturase 2	NM_004265, hCT2310309.0, hCT2310312.1	202218_s_at, 243953_at	NP_004256.1, EAW73974.1, EAW73975.1
GeneID:3995	FADS3	11	61,640,998	61,659,006	18,008	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1138, 1_A375_pNL7_minus_lncRNA_AR..1..1139, 2_A375_pNL97_plus_lncRNA_AR..1..1585, 2_A375_pNL97_plus_lncRNA_AR..1..1586	542, -5658, 670, -5586	in gene, upstream, in gene, upstream	1	1	0	20	17	13	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene FADS3	FADS3, LLCDL3, CYB5RP	fatty acid desaturase 3	NM_021727, hCT2311608.0, hCT2311609.0, hCT32119.2	204257_at, 216080_s_at	NP_068373.1, EAW73976.1, EAW73977.1, EAW73978.1
GeneID:5866	RAB3IL1	11	61,664,773	61,684,997	20,224	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1138, 1_A375_pNL7_minus_lncRNA_AR..1..1139, 2_A375_pNL97_plus_lncRNA_AR..1..1585, 2_A375_pNL97_plus_lncRNA_AR..1..1586	26533, 20133, 26661, 20405	downstream, in gene, downstream, downstream	1	1	0	20	17	13	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene RAB3IL1	RAB3IL1, GRAB	RAB3A interacting protein (rabin3)-like 1	NM_013401, hCT1668451.1, hCT1769079.1, hCT2355359.0	219579_at	NP_037533.2, EAW73981.1, EAW73979.1, EAW73980.1
GeneID:7439	BEST1	11	61,717,356	61,731,935	14,579	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1140, 2_A375_pNL97_plus_lncRNA_AR..1..1587	17700, 18324	downstream, downstream	1	1	0	17	16	16	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene BEST1	TU15B, RP50, BMD, BEST, BEST1, ARB, VMD2	bestrophin 1	NM_004183, NM_001139443, hCT1964651.1, hCT2310320.0, hCT2310321.0, hCT2355361.0, hCT2355362.0, hCT2355363.0, hCT32112.2	1554442_at, 1554443_s_at, 207671_s_at	NP_004174.1, NP_001132915.1, EAW73982.1, EAW73985.1, EAW73986.1, EAW73987.1, EAW73983.1, EAW73984.1, EAW73988.1
GeneID:2495	FTH1	11	61,731,757	61,735,132	3,375	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1140, 2_A375_pNL97_plus_lncRNA_AR..1..1587	76, -546	in gene, upstream	1	1	0	17	16	16	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene FTH1	FTH1, PLIF, MGC104426, FTH, PIG15, FTHL6, FHC	ferritin, heavy polypeptide 1	NM_002032, hCT1814821.1, hCT2311605.1, hCT2345283.0, hCT2345284.0, hCT2345285.0, hCT2345286.0, hCT2345287.0, hCT2345288.0, hCT2345289.0, hCT2345290.0, hCT2345291.0, hCT2345292.0, hCT2349787.0	200748_s_at, 214211_at	NP_002023.2, EAW73998.1, EAW73989.1, EAW73991.1, EAW73995.1, EAW73996.1, EAW73990.1, EAW73992.1, EAW73993.1, EAW73994.1, EAW73997.1, EAW73999.1, EAW74000.1, EAW74001.1
GeneID:3619	INCENP	11	61,891,445	61,920,635	29,190	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1141, 4_A375_EGR1..1..1474, 4_A375_EGR1..1..1475	11, 6091, 17035	in gene, in gene, in gene	1	0	1	10	11.33	15.67	3	4_A375_EGR1..1	16	Gene INCENP	INCENP, MGC111393, FLJ31633	inner centromere protein antigens 135/155kDa	NM_001040694, NM_020238, hCT2310324.0, hCT2310325.0, hCT2310326.0	219769_at, 242787_at	NP_001035784.1, NP_064623.2, EAW74003.1, EAW74004.1, EAW74005.1
GeneID:10647	SCGB1D2	11	62,009,724	62,012,280	2,556	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1142, 2_A375_pNL97_plus_lncRNA_AR..1..1590	3300, 3204	downstream, downstream	1	1	0	23	23	9	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene SCGB1D2	LIPB, LPHB, SCGB1D2	secretoglobin, family 1D, member 2	NM_006551, hCT31098.2	206799_at	NP_006542.1, EAW74009.1
GeneID:80150	ASRGL1	11	62,104,774	62,160,887	56,113	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1591	186	in gene	0	1	0	11	23	14	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ASRGL1	FLJ22316, CRASH, ALP, ALP1, ASRGL1	asparaginase like 1	NM_025080, NM_001083926, hCT1769088.1, hCT1958529.1, hCT2309592.0, hCT2309595.0, hCT2355221.0, hCT2355222.0	218857_s_at, 222764_at	NP_079356.3, NP_001077395.1, EAW74012.1, EAW74013.1, EAW74016.1, EAW74017.1, EAW74014.1, EAW74015.1
GeneID:79026	AHNAK	11	62,201,016	62,314,332	113,316	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1143, 2_A375_pNL97_plus_lncRNA_AR..1..1592, 4_A375_EGR1..1..1476, 4_A375_EGR1..1..1477	-6548, 63420, 1287, -596	upstream, in gene, in gene, upstream	1	1	1	12.75	14.25	15	4	4_A375_EGR1..1	21	Gene AHNAK	AHNAK, AHNAKRS, MGC5395	AHNAK nucleoprotein	NM_024060, NM_001620, hCT1769091.1	1563580_at, 211986_at, 220016_at, 235281_x_at, 236855_at	NP_076965.2, NP_001611.1, EAW74019.1
GeneID:1937	EEF1G	11	62,327,073	62,341,460	14,387	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1143, 4_A375_EGR1..1..1476	20580, -746	downstream, upstream	1	0	1	14	11	15	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene EEF1G	GIG35, EF1G, EEF1G	eukaryotic translation elongation factor 1 gamma	NM_001404, hCT2315306.1, hCT2315307.1, hCT2315310.1, hCT2315311.1, hCT2315313.1, hCT2355304.0	200689_x_at, 211345_x_at, 211927_x_at	NP_001395.1, EAW74023.1, EAW74024.1, EAW74026.1, EAW74027.1, EAW74028.1, EAW74025.1
GeneID:64852	TUT1	11	62,342,517	62,359,109	16,592	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1144, 2_A375_pNL97_plus_lncRNA_AR..1..1593, 2_A375_pNL97_plus_lncRNA_AR..1..1594, 4_A375_EGR1..1..1478	-75, -27, -10043, 16901	upstream, upstream, upstream, downstream	1	1	1	28	20	14.33	3	1_A375_pNL7_minus_lncRNA_AR..1	60	Gene TUT1	FLJ22347, MGC149809, STARPAP, FLJ22267, RBM21, TUT1, PAPD2, FLJ21850, TUTase, MGC131987	terminal uridylyl transferase 1, U6 snRNA-specific	NM_022830, hCT2315309.1	218965_s_at	NP_073741.2, EAW74029.1
GeneID:9219	MTA2	11	62,360,675	62,369,303	8,628	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1144, 2_A375_pNL97_plus_lncRNA_AR..1..1593, 2_A375_pNL97_plus_lncRNA_AR..1..1594	10119, 10167, 151	downstream, downstream, in gene	1	1	0	36.5	26.5	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	60	Gene MTA2	MTA1L1, DKFZp686F2281, MTA2, PID	metastasis associated 1 family, member 2	NM_004739, hCT11461.3, hCT2315304.0	203444_s_at	NP_004730.2, EAW74032.1, EAW74031.1
GeneID:256364	EML3	11	62,369,691	62,380,237	10,546	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1144, 2_A375_pNL97_plus_lncRNA_AR..1..1594, 2_A375_pNL97_plus_lncRNA_AR..1..1595	21053, 11085, -9331	downstream, downstream, upstream	1	1	0	28.33	24	13	3	1_A375_pNL7_minus_lncRNA_AR..1	60	Gene EML3	FLJ35827, MGC111422, ELP95, EML3	echinoderm microtubule associated protein like 3	NM_153265, hCT11467.2, hCT1965771.1, hCT1965772.1, hCT2315299.0, hCT2315300.0, hCT2315302.0, hCT2355382.0, hCT2355383.0	203442_x_at, 203443_at, 212989_x_at	NP_694997.2, EAW74033.1, EAW74034.1, EAW74036.1, EAW74038.1, EAW74040.1, EAW74035.1, EAW74037.1, EAW74039.1
GeneID:6094	ROM1	11	62,380,213	62,382,592	2,379	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1595	9355	downstream	0	1	0	12	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ROM1	ROM, ROSP1, ROM1, RP7, TSPAN23	retinal outer segment membrane protein 1	NM_000327, hCT2309600.0	205606_at	NP_000318.1, EAW74041.1
GeneID:26229	B3GAT3	11	62,382,766	62,389,446	6,680	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1595	-120	upstream	0	1	0	12	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene B3GAT3	B3GAT3, GLCATI	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	NM_012200, hCT2315298.1, hCT2355278.0, hCT7047.4	203452_at, 35179_at	NP_036332.2, EAW74043.1, EAW74042.1, EAW74044.1
GeneID:23193	GANAB	11	62,392,298	62,414,104	21,806	-	3	2_A375_pNL97_plus_lncRNA_AR..1..1595, 2_A375_pNL97_plus_lncRNA_AR..1..1596, 4_A375_EGR1..1..1479	24536, 24, 136	downstream, in gene, in gene	0	1	1	13.5	18	14	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene GANAB	G2AN, KIAA0088, GLUII, GANAB	glucosidase, alpha, neutral AB	NM_198334, NM_198335, hCT11462.4, hCT1961126.2, hCT1961127.3, hCT1967467.2, hCT2355374.0, hCT2355375.0	211934_x_at, 214626_s_at	NP_938148.1, NP_938149.2, EAW74045.1, EAW74046.1, EAW74047.1, EAW74050.1, EAW74048.1, EAW74049.1
GeneID:80789	INTS5	11	62,414,320	62,420,774	6,454	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1596, 4_A375_EGR1..1..1479	6694, 6606	downstream, downstream	0	1	1	15	17	16	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene INTS5	INT5, INTS5, KIAA1698	integrator complex subunit 5	NM_030628, hCT2315291.1	221818_at, 53968_at	NP_085131.1, EAW74051.1
GeneID:79081	C11orf48	11	62,430,289	62,439,241	8,952	-	8	1_A375_pNL7_minus_lncRNA_AR..1..1145, 1_A375_pNL7_minus_lncRNA_AR..1..1146, 2_A375_pNL97_plus_lncRNA_AR..1..1597, 2_A375_pNL97_plus_lncRNA_AR..1..1598, 2_A375_pNL97_plus_lncRNA_AR..1..1599, 4_A375_EGR1..1..1480, 4_A375_EGR1..1..1481, 4_A375_EGR1..1..1482	6937, -279, 6537, 5417, -7, 6441, -391, -7063	in gene, upstream, in gene, in gene, upstream, in gene, upstream, upstream	1	1	1	17.33	18	22.67	3	4_A375_EGR1..1	32	Gene C11orf48	MGC2477, C11orf48	chromosome 11 open reading frame 48	NM_024099, hCT1772911.3, hCT1953710.1, hCT2345225.0, hCT2345226.0, hCT2345227.0, hCT2345228.0, hCT2355284.0	221637_s_at	NP_077004.2, EAW74058.1, EAW74053.1, EAW74054.1, EAW74055.1, EAW74056.1, EAW74052.1, EAW74057.1
GeneID:751071	METTL12	11	62,432,779	62,434,923	2,144	+	7	1_A375_pNL7_minus_lncRNA_AR..1..1145, 1_A375_pNL7_minus_lncRNA_AR..1..1146, 2_A375_pNL97_plus_lncRNA_AR..1..1597, 2_A375_pNL97_plus_lncRNA_AR..1..1598, 2_A375_pNL97_plus_lncRNA_AR..1..1599, 4_A375_EGR1..1..1480, 4_A375_EGR1..1..1481	-475, 6741, -75, 1045, 6469, 21, 6853	upstream, downstream, upstream, in gene, downstream, in gene, downstream	1	1	1	16.5	16.5	25.5	2	4_A375_EGR1..1	32	Gene METTL12	METTL12		NM_001043229	236680_at, 239316_at	NP_001036694.1
GeneID:692158	SNORA57	11	62,432,894	62,433,042	148	+	7	1_A375_pNL7_minus_lncRNA_AR..1..1145, 1_A375_pNL7_minus_lncRNA_AR..1..1146, 2_A375_pNL97_plus_lncRNA_AR..1..1597, 2_A375_pNL97_plus_lncRNA_AR..1..1598, 2_A375_pNL97_plus_lncRNA_AR..1..1599, 4_A375_EGR1..1..1480, 4_A375_EGR1..1..1481	-590, 6626, -190, 930, 6354, -94, 6738	upstream, downstream, upstream, downstream, downstream, upstream, downstream	1	1	1	16.5	16.5	25.5	2	4_A375_EGR1..1	32	Gene SNORA57	U99, SNORA57	small nucleolar RNA, H/ACA box 57	NR_004390		
GeneID:790955	C11orf83	11	62,439,126	62,439,852	726	+	8	1_A375_pNL7_minus_lncRNA_AR..1..1145, 1_A375_pNL7_minus_lncRNA_AR..1..1146, 2_A375_pNL97_plus_lncRNA_AR..1..1597, 2_A375_pNL97_plus_lncRNA_AR..1..1598, 2_A375_pNL97_plus_lncRNA_AR..1..1599, 4_A375_EGR1..1..1480, 4_A375_EGR1..1..1481, 4_A375_EGR1..1..1482	-6822, 394, -6422, -5302, 122, -6326, 506, 7176	upstream, in gene, upstream, upstream, in gene, upstream, in gene, downstream	1	1	1	17.33	18	22.67	3	4_A375_EGR1..1	32	Gene C11orf83	C11orf83, UNQ655, CCDS41658.1, MGC87549	chromosome 11 open reading frame 83	NM_001085372	229099_at	NP_001078841.1
GeneID:51035	UBXN1	11	62,443,972	62,446,527	2,555	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1146, 2_A375_pNL97_plus_lncRNA_AR..1..1598, 2_A375_pNL97_plus_lncRNA_AR..1..1599, 4_A375_EGR1..1..1481, 4_A375_EGR1..1..1482	7007, 12703, 7279, 6895, 223	downstream, downstream, downstream, downstream, in gene	1	1	1	17.33	18	22.67	3	4_A375_EGR1..1	32	Gene UBXN1	2B28, SAKS1, UBXN1, UBXD10	UBX domain protein 1	NM_015853, hCT1960780.1, hCT2315286.0, hCT2315287.0, hCT2315288.0, hCT2355314.0, hCT2355315.0, hCT2355316.0	201871_s_at, 210623_at	NP_056937.2, EAW74067.1, EAW74063.1, EAW74064.1, EAW74065.1, EAW74066.1, EAW74061.1, EAW74062.1
GeneID:221091	LRRN4CL	11	62,453,874	62,457,200	3,326	-	1	4_A375_EGR1..1..1482	10696	downstream	0	0	1	15	17	17	1	4_A375_EGR1..1	17	Gene LRRN4CL	MGC61707, LRRN4CL	LRRN4 C-terminal like	NM_203422	1556427_s_at	NP_981967.1
GeneID:26580	BSCL2	11	62,457,747	62,477,046	19,299	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1147, 2_A375_pNL97_plus_lncRNA_AR..1..1600	-170, -106	upstream, upstream	1	1	0	17	14	15	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene BSCL2	MGC4694, FLJ16651, BSCL2, HMN5, GNG3LG, SPG17	Berardinelli-Seip congenital lipodystrophy 2 (seipin)	NM_032667, NM_001130702, NM_001122955		NP_116056.3, NP_001124174.1, NP_001116427.1
GeneID:2785	GNG3	11	62,475,114	62,476,678	1,564	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1147, 2_A375_pNL97_plus_lncRNA_AR..1..1600	2102, 2038	downstream, downstream	1	1	0	17	14	15	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene GNG3	GNG3		NM_012202, hCT1772903.1	222005_s_at	NP_036334.1, EAW74082.1
GeneID:221092	HNRNPUL2	11	62,482,220	62,494,821	12,601	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1147, 2_A375_pNL97_plus_lncRNA_AR..1..1600, 2_A375_pNL97_plus_lncRNA_AR..1..1601, 2_A375_pNL97_plus_lncRNA_AR..1..1602, 4_A375_EGR1..1..1483	17605, 17669, 605, -198, -59	downstream, downstream, in gene, upstream, upstream	1	1	1	14	16.67	13	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene HNRNPUL2	HNRNPUL2, DKFZp762N1910, HNRPUL2	heterogeneous nuclear ribonucleoprotein U-like 2	NM_001079559	222284_at, 66053_at	NP_001073027.1
GeneID:283237	TTC9C	11	62,495,952	62,506,108	10,156	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1601, 2_A375_pNL97_plus_lncRNA_AR..1..1602, 4_A375_EGR1..1..1483	-1936, -933, -1072	upstream, upstream, upstream	0	1	1	12.5	18	12	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TTC9C	MGC29649, TTC9C	tetratricopeptide repeat domain 9C	NM_173810, hCT2309604.0, hCT2355256.0	1569189_at, 226175_at	NP_776171.1, EAW74086.1, EAW74087.1
GeneID:5438	POLR2G	11	62,529,011	62,534,187	5,176	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1148, 2_A375_pNL97_plus_lncRNA_AR..1..1603	9656, 10077	downstream, downstream	1	1	0	16	21	11	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene POLR2G	MGC138387, RPB19, hRPB19, hsRPB7, RPB7, POLR2G, MGC138389	polymerase (RNA) II (DNA directed) polypeptide G	NM_002696, hCT2309605.0, hCT2309606.0, hCT2355259.0	202306_at	NP_002687.1, EAW74091.1, EAW74090.1, EAW74092.1
GeneID:10629	TAF6L	11	62,538,875	62,554,814	15,939	+	7	1_A375_pNL7_minus_lncRNA_AR..1..1148, 1_A375_pNL7_minus_lncRNA_AR..1..1149, 1_A375_pNL7_minus_lncRNA_AR..1..1150, 2_A375_pNL97_plus_lncRNA_AR..1..1603, 2_A375_pNL97_plus_lncRNA_AR..1..1604, 2_A375_pNL97_plus_lncRNA_AR..1..1605, 4_A375_EGR1..1..1484	-206, 16133, 20421, 213, 15861, 20453, 20613	upstream, downstream, downstream, in gene, in gene, downstream, downstream	1	1	1	16.33	23.33	15.67	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene TAF6L	PAF65A, FLJ11136, MGC4288, TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	NM_006473, hCT2309607.1, hCT2309608.1, hCT2309609.1, hCT2344938.0	213209_at, 213210_at, 213211_s_at, 222053_at, 230049_at	NP_006464.1, EAW74094.1, EAW74093.1, EAW74095.1, EAW74096.1
GeneID:374395	TMEM179B	11	62,554,874	62,557,872	2,998	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1149, 1_A375_pNL7_minus_lncRNA_AR..1..1150, 2_A375_pNL97_plus_lncRNA_AR..1..1604, 2_A375_pNL97_plus_lncRNA_AR..1..1605, 4_A375_EGR1..1..1484	134, 4422, -138, 4454, 4614	in gene, downstream, upstream, downstream, downstream	1	1	1	19.5	24.5	18	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene TMEM179B	TMEM179B	transmembrane protein 179B	NM_199337, hCT2309610.0, hCT2309612.0, hCT2309614.0	228089_x_at	NP_955369.1, EAW74098.1, EAW74099.1, EAW74100.1
GeneID:79064	TMEM223	11	62,557,787	62,559,486	1,699	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1149, 1_A375_pNL7_minus_lncRNA_AR..1..1150, 2_A375_pNL97_plus_lncRNA_AR..1..1604, 2_A375_pNL97_plus_lncRNA_AR..1..1605, 4_A375_EGR1..1..1484	4478, 190, 4750, 158, -2	downstream, in gene, downstream, in gene, upstream	1	1	1	19.5	24.5	18	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene TMEM223	TMEM223, MGC3196	transmembrane protein 223	NM_001080501	220934_s_at, 236981_at	NP_001073970.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:10482	NXF1	11	82,559,598	82,572,984	13,386	-	8	1_A375_pNL7_minus_lncRNA_AR..1..1149, 1_A375_pNL7_minus_lncRNA_AR..1..1150, 1_A375_pNL7_minus_lncRNA_AR..1..1151, 2_A375_pNL97_plus_lncRNA_AR..1..1604, 2_A375_pNL97_plus_lncRNA_AR..1..1605, 2_A375_pNL97_plus_lncRNA_AR..1..1606, 4_A375_EGR1..1..1464, 4_A375_EGR1..1..1465	17956, 13668, 100, 18228, 13636, 52, 13476, 4	downstream, downstream, in gene, downstream, downstream, in gene, downstream, in gene	1	1	1	22.33	23.33	19.33	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene NXF1	NXF1, MEX67, DKFZp667O0311, TAP	nuclear RNA export factor 1	NM_001081491, NM_006362, hCT2315263.1, hCT2315264.1, hCT2315265.1, hCT2315266.1, hCT2344940.0	208922_s_at	NP_001074960.1, NP_006353.2, EAW74103.1, EAW74104.1, EAW74106.1, EAW74107.1, EAW74105.1
GeneID:6811	STX5	11	82,574,389	82,599,580	25,191	-	11	1_A375_pNL7_minus_lncRNA_AR..1..1151, 1_A375_pNL7_minus_lncRNA_AR..1..1152, 1_A375_pNL7_minus_lncRNA_AR..1..1153, 1_A375_pNL7_minus_lncRNA_AR..1..1154, 2_A375_pNL97_plus_lncRNA_AR..1..1606, 2_A375_pNL97_plus_lncRNA_AR..1..1607, 2_A375_pNL97_plus_lncRNA_AR..1..1608, 2_A375_pNL97_plus_lncRNA_AR..1..1609, 4_A375_EGR1..1..1465, 4_A375_EGR1..1..1466, 4_A375_EGR1..1..1467	26698, 552, -152, -9668, 26646, 584, -7331, -9668, 26600, -7272, -9640	downstream, in gene, upstream, upstream, downstream, in gene, upstream, upstream, downstream, upstream, upstream	1	1	1	31.5	31.5	28.75	4	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene STX5	SED5, STX5, STX5A	syntaxin 5	NM_003164, hCT1772907.1, hCT2315259.1, hCT2315260.1	203330_s_at	NP_003155.2, EAW74110.1, EAW74108.1, EAW74109.1
GeneID:54663	WDR74	11	82,600,383	82,607,628	7,245	-	8	1_A375_pNL7_minus_lncRNA_AR..1..1152, 1_A375_pNL7_minus_lncRNA_AR..1..1153, 1_A375_pNL7_minus_lncRNA_AR..1..1154, 2_A375_pNL97_plus_lncRNA_AR..1..1607, 2_A375_pNL97_plus_lncRNA_AR..1..1608, 2_A375_pNL97_plus_lncRNA_AR..1..1609, 4_A375_EGR1..1..1466, 4_A375_EGR1..1..1467	8620, 7916, -1620, 8652, 737, -1620, 798, -1572	downstream, downstream, upstream, downstream, in gene, upstream, in gene, upstream	1	1	1	32.67	35	31	3	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene WDR74	WDR74, FLJ21730, FLJ10439	WD repeat domain 74	NM_018093, hCT1784638.2, hCT2340857.0	218278_at, 221712_s_at	NP_060563.2, EAW74111.1, EAW74112.1
GeneID:26855	RNU2-2	11	82,609,098	82,609,233	137	-	8	1_A375_pNL7_minus_lncRNA_AR..1..1152, 1_A375_pNL7_minus_lncRNA_AR..1..1153, 1_A375_pNL7_minus_lncRNA_AR..1..1154, 2_A375_pNL97_plus_lncRNA_AR..1..1607, 2_A375_pNL97_plus_lncRNA_AR..1..1608, 2_A375_pNL97_plus_lncRNA_AR..1..1609, 4_A375_EGR1..1..1466, 4_A375_EGR1..1..1467	10225, 9521, -15, 10257, 2342, -15, 2401, 33	downstream, downstream, upstream, downstream, downstream, upstream, downstream, in gene	1	1	1	32.67	35	31	3	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene RNU2-2	U2, RNU2B, RNU2-2	RNA, U2 small nuclear 2	NR_002761		
GeneID:23642	SNHG1	11	82,619,480	82,623,380	3,900	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1154, 2_A375_pNL97_plus_lncRNA_AR..1..1609, 2_A375_pNL97_plus_lncRNA_AR..1..1610, 4_A375_EGR1..1..1467	14112, 14112, -224, 14160	downstream, downstream, upstream, downstream	1	1	1	38.5	42	38.5	2	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene SNHG1	NCRNA00057, U22HG, SNHG1, UHG	small nucleolar RNA host gene 1 (non-protein coding)	NR_003098	224610_at	
GeneID:9304	SNORD22	11	82,620,382	82,620,507	125	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1610	-3077	upstream	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SNORD22	U22, RNU22, SNORD22	small nucleolar RNA, C/D box 22	NR_000008		
GeneID:9298	SNORD31	11	82,620,798	82,620,885	87	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1610	-2719	upstream	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SNORD31	SNORD31, RNU31, U31	small nucleolar RNA, C/D box 31	NR_002560		
GeneID:9299	SNORD30	11	82,621,135	82,621,204	69	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1610	-2380	upstream	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SNORD30	SNORD30, RNU30, U30	small nucleolar RNA, C/D box 30	NR_002561		
GeneID:9297	SNORD29	11	82,621,376	82,621,440	64	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1610	-2144	upstream	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SNORD29	U29, RNU29, SNORD29	small nucleolar RNA, C/D box 29	NR_002559		
GeneID:9300	SNORD28	11	82,622,093	82,622,167	74	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1610	-1417	upstream	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SNORD28	SNORD28, U28, RNU28	small nucleolar RNA, C/D box 28	NR_002562		
GeneID:9301	SNORD27	11	82,622,484	82,622,555	71	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1610	-1029	upstream	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SNORD27	RNU27, U27, SNORD27	small nucleolar RNA, C/D box 27	NR_002563		
GeneID:9302	SNORD26	11	82,622,764	82,622,838	74	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1610	-746	upstream	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SNORD26	U26, SNORD26, RNU26	small nucleolar RNA, C/D box 26	NR_002564		
GeneID:9303	SNORD25	11	82,623,037	82,623,103	66	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1610	-481	upstream	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SNORD25	SNORD25, U25, RNU25	small nucleolar RNA, C/D box 25	NR_002565		
GeneID:6520	SLC3A2	11	82,623,518	82,656,353	32,835	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1155, 2_A375_pNL97_plus_lncRNA_AR..1..1610, 2_A375_pNL97_plus_lncRNA_AR..1..1611, 4_A375_EGR1..1..1468	25282, 66, 25314, 24941	in gene, in gene, in gene, in gene	1	1	1	25	34.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	48	Gene SLC3A2	4F2, 4T2HC, NACAE, MDU1, CD98, 4F2HC, CD98HC, SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	NM_001012661, NM_001012662, NM_001012663, NM_001012664, NM_001013251, NM_002394, hCT2309580.0, hCT2309581.0, hCT2309582.0, hCT2309583.0, hCT2355337.0, hCT2355338.0	200924_s_at	NP_001012679.1, NP_001012680.1, NP_001012681.1, NP_001012682.1, NP_001013269.1, NP_002385.3, EAW74118.1, EAW74119.1, EAW74120.1, EAW74121.1, EAW74122.1, EAW74123.1
GeneID:1128	CHRM1	11	82,676,151	82,689,012	12,861	-	1	4_A375_EGR1..1..1469	-5516	upstream	0	0	1	4	2	16	1	4_A375_EGR1..1	16	Gene CHRM1	M1R, HM1, CHRM1, MGC30125, M1	cholinergic receptor, muscarinic 1	NM_000738, hCT2315251.0, hCT2315252.0, hCT2315254.0	231783_at	NP_000729.2, EAW74124.1, EAW74125.1, EAW74126.1
GeneID:9356	SLC22A6	11	82,744,069	82,752,469	8,400	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1156, 2_A375_pNL97_plus_lncRNA_AR..1..1612	4693, 4725	in gene, in gene	1	1	0	24	19	6	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene SLC22A6	FLJ55736, SLC22A6, MGC45260, HOAT1, ROAT1, PAHT, OAT1	solute carrier family 22 (organic anion transporter), member 6	NM_004790, NM_153276, NM_153277, NM_153278, hCT12402.2, hCT2315246.0, hCT2315247.0, hCT2315248.0	210343_s_at, 216599_x_at	NP_004781.2, NP_695008.1, NP_695009.1, NP_695010.1, EAW74130.1, EAW74131.1, EAW74129.1, EAW74132.1
GeneID:54979	HRASLS2	11	83,320,242	83,330,855	10,613	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1613	-4004	upstream	0	1	0	14	15	2	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene HRASLS2	PLA1/2-2, FLJ20556, HRASLS2	HRAS-like suppressor 2	NM_017878, hCT1641002.1	216759_at, 216760_at, 221122_at	NP_060348.1, EAW74157.1
GeneID:11145	PLA2G16	11	83,341,934	83,381,941	40,007	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1613	47082	downstream	0	1	0	14	15	2	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene PLA2G16	MGC118754, HRASLS3, HREV107-3, PLA2G16, AdPLA, H-REV107-1, HREV107	phospholipase A2, group XVI	NM_007069, NM_001128203, hCT2310772.0, hCT2310773.0, hCT2355212.0	209581_at, 235110_at	NP_009000.2, NP_001121675.1, EAW74158.1, EAW74159.1, EAW74160.1
GeneID:25923	ATL3	11	83,396,437	83,439,083	42,646	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1157, 2_A375_pNL97_plus_lncRNA_AR..1..1614	-53, 11	upstream, in gene	1	1	0	27	18	11	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene ATL3	DKFZp564J0863, ATL3	atlastin GTPase 3	NM_015459, hCT2310774.1, hCT2310775.1, hCT2355297.0	223452_s_at, 223453_s_at	NP_056274.3, EAW74163.1, EAW74161.1, EAW74162.1
GeneID:10313	RTN3	11	83,448,922	83,527,363	78,441	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1157, 2_A375_pNL97_plus_lncRNA_AR..1..1614, 2_A375_pNL97_plus_lncRNA_AR..1..1615	-9786, -9650, 518	upstream, upstream, in gene	1	1	0	18.5	18.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene RTN3	ASYIP, NSPLII, RTN3-A1, HAP, RTN3, NSPL2	reticulon 3	NM_201429, NM_201430, NM_201428, NM_006054, hCT1814006.2, hCT2310251.0, hCT2310252.0, hCT2355355.0, hCT2355356.0, hCT2355357.0, hCT2355358.0	219549_s_at, 224564_s_at	NP_958832.1, NP_958833.1, NP_006045.1, NP_958831.1, EAW74167.1, EAW74169.1, EAW74164.1, EAW74165.1, EAW74166.1, EAW74168.1, EAW74170.1
GeneID:144097	C11orf84	11	83,580,923	83,595,190	14,267	+	1	4_A375_EGR1..1..1490	389	in gene	0	0	1	12	12	16	1	4_A375_EGR1..1	16	Gene C11orf84	DKFZp762N0114, C11orf84	chromosome 11 open reading frame 84	NM_138471, hCT1814018.2	227292_at	NP_612480.1, EAW74172.1
GeneID:2011	MARK2	11	83,606,400	83,678,492	72,092	+	3	4_A375_EGR1..1..1491, 4_A375_EGR1..1..1492, 4_A375_EGR1..1..1493	77832, 80816, 81592	downstream, downstream, downstream	0	0	1	6.33	8.33	17.33	3	4_A375_EGR1..1	19	Gene MARK2	Par1b, MARK2, MGC99619, EMK1, EMK-1, PAR-1	MAP/microtubule affinity-regulating kinase 2	NM_017490, NM_004954, NM_001039469, NM_001163296, NM_001163297, hCT12454.3, hCT1686304.3, hCT1950044.1, hCT2310256.0, hCT2310257.0, hCT2310260.0, hCT2355377.0	203942_s_at, 211062_x_at	NP_059672.2, NP_004945.4, NP_001034558.2, NP_001156768.1, NP_001156769.1, EAW74174.1, EAW74175.1, EAW74176.1, EAW74177.1, EAW74178.1, EAW74179.1, EAW74180.1
GeneID:283248	RCOR2	11	83,678,693	83,684,316	5,623	-	3	4_A375_EGR1..1..1491, 4_A375_EGR1..1..1492, 4_A375_EGR1..1..1493	284, -2900, -3676	in gene, upstream, upstream	0	0	1	6.33	8.33	17.33	3	4_A375_EGR1..1	19	Gene RCOR2	RCOR2	REST corepressor 2	NM_173587, hCT12458.3, hCT2310765.0	236030_at	NP_775858.2, EAW74181.1, EAW74182.1
GeneID:79829	NAA40	11	83,708,442	83,724,458	16,016	+	1	4_A375_EGR1..1..1494	22350	downstream	0	0	1	10	10	14	1	4_A375_EGR1..1	14	Gene NAA40	FLJ13848, NAT11, PATT1, NAA40	N(alpha)-acetyltransferase 40, NatD catalytic subunit, homolog (S. cerevisiae)	NM_024771, hCT12463.3, hCT2310267.0, hCT2355217.0	218734_at	NP_079047.2, EAW74183.1, EAW74184.1, EAW74185.1
GeneID:1351	COX8A	11	83,742,079	83,744,015	1,936	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1158, 2_A375_pNL97_plus_lncRNA_AR..1..1616, 2_A375_pNL97_plus_lncRNA_AR..1..1617, 4_A375_EGR1..1..1495	11937, 33, 11905, 11937	downstream, in gene, downstream, downstream	1	1	1	15.5	21.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene COX8A	COX8L, COX8-2, COX, COX8, VIII-L, VIII, COX8A	cytochrome c oxidase subunit 8A (ubiquitous)	NM_004074, hCT18291.3	201119_s_at	NP_004065.1, EAW74186.1
GeneID:55611	OTUB1	11	83,753,325	83,765,892	12,567	+	6	1_A375_pNL7_minus_lncRNA_AR..1..1158, 2_A375_pNL97_plus_lncRNA_AR..1..1617, 2_A375_pNL97_plus_lncRNA_AR..1..1618, 4_A375_EGR1..1..1495, 4_A375_EGR1..1..1496, 4_A375_EGR1..1..1497	891, 659, 22771, 891, 18035, 22043	in gene, in gene, downstream, in gene, downstream, downstream	1	1	1	9.75	12.5	16.25	4	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene OTUB1	FLJ20113, OTB1, OTUB1, MGC111158, MGC4584, OTU1, HSPC263, FLJ40710	OTU domain, ubiquitin aldehyde binding 1	NM_017670, NR_003089, hCT1965468.1, hCT2355298.0, hCT2355299.0, hCT2355300.0, hCT2355301.0	201245_s_at, 201246_s_at, 38710_at	NP_060140.2, EAW74189.1, EAW74187.1, EAW74188.1, EAW74190.1, EAW74191.1
GeneID:28992	MACROD1	11	83,766,030	83,933,585	167,555	-	11	2_A375_pNL97_plus_lncRNA_AR..1..1618, 4_A375_EGR1..1..1496, 4_A375_EGR1..1..1497, 4_A375_EGR1..1..1498, 4_A375_EGR1..1..1499, 4_A375_EGR1..1..1500, 4_A375_EGR1..1..1501, 4_A375_EGR1..1..1502, 4_A375_EGR1..1..1503, 4_A375_EGR1..1..1504, 4_A375_EGR1..1..1505	157489, 162225, 158217, 147869, 143809, 138865, 131441, 126945, 83345, 14929, 12860	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	1	1	6	8.64	16.64	11	4_A375_EGR1..1	21	Gene MACROD1	LRP16, MACROD1	MACRO domain containing 1	NM_014067, hCT12453.3, hCT1957095.1	1559731_x_at, 219188_s_at	NP_054786.2, EAW74193.1, EAW74192.1
GeneID:10963	STIP1	11	83,953,587	83,972,020	18,433	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1619, 4_A375_EGR1..1..1506, 4_A375_EGR1..1..1507	-579, -891, 21149	upstream, upstream, downstream	0	1	1	9.5	14	16	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene STIP1	HOP, P60, STIP1, STI1L, IEF-SSP-3521, STI1	stress-induced-phosphoprotein 1	NM_006819, hCT12456.3, hCT2310214.0, hCT2355381.0	212009_s_at, 213330_s_at	NP_006810.1, EAW74196.1, EAW74197.1, EAW74198.1
GeneID:83706	FERMT3	11	83,974,152	83,991,363	17,211	+	3	4_A375_EGR1..1..1507, 4_A375_EGR1..1..1508, 4_A375_EGR1..1..1509	584, 14168, 19976	in gene, in gene, downstream	0	0	1	13	10.33	18.67	3	4_A375_EGR1..1	25	Gene FERMT3	URP2SF, URP2, MIG-2, UNC112C, KIND3, MIG2B, FERMT3, MGC10966	fermitin family homolog 3 (Drosophila)	NM_178443, NM_031471, hCT1951005.1, hCT2310216.0	223303_at	NP_848537.1, NP_113659.3, EAW74199.1, EAW74200.1
GeneID:83707	TRPT1	11	83,991,271	83,993,726	2,455	-	2	4_A375_EGR1..1..1508, 4_A375_EGR1..1..1509	5406, -402	downstream, upstream	0	0	1	15	11.5	20.5	2	4_A375_EGR1..1	25	Gene TRPT1	TRPT1, MGC11134	tRNA phosphotransferase 1	NM_001160389, NM_001033678, NM_001160390, NM_031472, NM_001160392, NM_001160393, hCT1965375.1, hCT1965376.1, hCT1965379.1	223436_s_at	NP_001153861.1, NP_001028850.2, NP_113660.1, NP_001153862.1, NP_001153864.1, NP_001153865.1, EAW74201.1, EAW74202.1, EAW74203.1
GeneID:84304	NUDT22	11	83,993,736	83,997,486	3,750	+	2	4_A375_EGR1..1..1508, 4_A375_EGR1..1..1509	-5418, 390	upstream, in gene	0	0	1	15	11.5	20.5	2	4_A375_EGR1..1	25	Gene NUDT22	NUDT22, MGC13045	nudix (nucleoside diphosphate linked moiety X)-type motif 22	NM_032344, NM_001128613, NM_001128612, hCT2343805.0, hCT2343807.0, hCT2343809.0, hCT2343811.0, hCT2343813.0, hCT2343814.0, hCT2343815.0, hCT2343817.0	1556848_at, 224484_s_at	NP_115720.1, NP_001122085.1, NP_001122084.1, EAW74204.1, EAW74207.1, EAW74210.1, EAW74205.1, EAW74206.1, EAW74208.1, EAW74209.1, EAW74211.1
GeneID:3338	DNAJC4	11	83,997,753	84,001,753	4,000	+	4	4_A375_EGR1..1..1508, 4_A375_EGR1..1..1509, 4_A375_EGR1..1..1510, 4_A375_EGR1..1..1511	-9433, -3625, 10567, 11431	upstream, upstream, downstream, downstream	0	0	1	13.25	11.5	22.25	4	4_A375_EGR1..1	27	Gene DNAJC4	MCG18, HSPF2, MGC57189, DNAJC4, MGC19482, MGC71863, DANJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	NM_005528, hCT2343804.0, hCT2343806.0, hCT2343808.0, hCT2343810.0, hCT2343812.0, hCT2343816.0, hCT2343818.0, hCT2343819.0, hCT2343820.0	206781_at, 206782_s_at, 213919_at, 223371_s_at, 223372_at, 226622_s_at	NP_005519.2, EAW74212.1, EAW74215.1, EAW74216.1, EAW74217.1, EAW74218.1, EAW74213.1, EAW74214.1, EAW74219.1, EAW74220.1
GeneID:7423	VEGFB	11	84,002,266	84,006,259	3,993	+	6	1_A375_pNL7_minus_lncRNA_AR..1..1159, 2_A375_pNL97_plus_lncRNA_AR..1..1620, 4_A375_EGR1..1..1509, 4_A375_EGR1..1..1510, 4_A375_EGR1..1..1511, 4_A375_EGR1..1..1512	11142, 12598, -8136, 6054, 6918, 11270	downstream, downstream, upstream, downstream, downstream, downstream	1	1	1	15.2	15.2	19.2	5	4_A375_EGR1..1	27	Gene VEGFB	VEGFL, VEGFB, VRF	vascular endothelial growth factor B	NM_003377, hCT12451.5, hCT1954867.2, hCT1957094.3	203683_s_at	NP_003368.1, EAW74222.1, EAW74221.1, EAW74223.1
GeneID:2286	FKBP2	11	84,008,413	84,011,607	3,194	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1159, 2_A375_pNL97_plus_lncRNA_AR..1..1620, 4_A375_EGR1..1..1510, 4_A375_EGR1..1..1511, 4_A375_EGR1..1..1512	4995, 6451, -93, 771, 5123	downstream, downstream, upstream, in gene, downstream	1	1	1	14.75	15.5	20	4	4_A375_EGR1..1	27	Gene FKBP2	PPIase, FKBP-13, FKBP2	FK506 binding protein 2, 13kDa	NM_004470, NM_057092, NM_001135208, hCT12452.3, hCT1961959.1	203391_at	NP_004461.2, NP_476433.1, NP_001128680.1, EAW74224.1, EAW74225.1
GeneID:26472	PPP1R14B	11	84,011,951	84,014,413	2,462	-	7	1_A375_pNL7_minus_lncRNA_AR..1..1159, 2_A375_pNL97_plus_lncRNA_AR..1..1620, 4_A375_EGR1..1..1510, 4_A375_EGR1..1..1511, 4_A375_EGR1..1..1512, 4_A375_EGR1..1..1513, 4_A375_EGR1..1..1514	1005, -451, 6093, 5229, 877, -7827, -9251	in gene, upstream, downstream, downstream, in gene, upstream, upstream	1	1	1	12.5	12.17	19.17	6	4_A375_EGR1..1	27	Gene PPP1R14B	PPP1R14B, PHI-1, PLCB3N, PNG, SOM172	protein phosphatase 1, regulatory (inhibitor) subunit 14B	NM_138689, hCT2310784.0, hCT2310786.0	212680_x_at, 226138_s_at, 230374_at	NP_619634.1, EAW74226.1, EAW74227.1
GeneID:100507590	LOC100507590	11	84,014,611	84,015,679	1,068	+	7	1_A375_pNL7_minus_lncRNA_AR..1..1159, 2_A375_pNL97_plus_lncRNA_AR..1..1620, 4_A375_EGR1..1..1510, 4_A375_EGR1..1..1511, 4_A375_EGR1..1..1512, 4_A375_EGR1..1..1513, 4_A375_EGR1..1..1514	-1203, 253, -6291, -5427, -1075, 7629, 9053	upstream, in gene, upstream, upstream, upstream, downstream, downstream	1	1	1	12.5	12.17	19.17	6	4_A375_EGR1..1	27	Gene LOC100507590		hypothetical LOC100507590	XR_110912		
GeneID:5331	PLCB3	11	84,018,995	84,036,924	17,929	+	9	1_A375_pNL7_minus_lncRNA_AR..1..1159, 2_A375_pNL97_plus_lncRNA_AR..1..1620, 2_A375_pNL97_plus_lncRNA_AR..1..1621, 4_A375_EGR1..1..1511, 4_A375_EGR1..1..1512, 4_A375_EGR1..1..1513, 4_A375_EGR1..1..1514, 4_A375_EGR1..1..1515, 4_A375_EGR1..1..1516	-5587, -4131, 18477, -9811, -5459, 3245, 4669, 12013, 12653	upstream, upstream, downstream, upstream, upstream, in gene, in gene, in gene, in gene	1	1	1	12.38	11.88	19.75	8	4_A375_EGR1..1	27	Gene PLCB3	FLJ37084, PLCB3	phospholipase C, beta 3 (phosphatidylinositol-specific)	NM_000932, NM_001184883, hCT12464.4, hCT2355216.0	213384_x_at	NP_000923.1, NP_001171812.1, EAW74230.1, EAW74231.1
GeneID:572	BAD	11	84,037,300	84,052,176	14,876	-	4	2_A375_pNL97_plus_lncRNA_AR..1..1621, 4_A375_EGR1..1..1515, 4_A375_EGR1..1..1516, 4_A375_EGR1..1..1517	14704, 21168, 20528, -3600	in gene, downstream, downstream, upstream	0	1	1	9.5	10.5	20.25	4	4_A375_EGR1..1	27	Gene BAD	BAD, BCL2L8, BBC2	BCL2-associated agonist of cell death	NM_004322, NM_032989, hCT12460.2, hCT2311041.0, hCT2311042.0, hCT2355215.0	1861_at, 209364_at, 232680_at	NP_004313.1, NP_116784.1, EAW74233.1, EAW74234.1, EAW74235.1, EAW74236.1
GeneID:56834	GPR137	11	84,051,811	84,056,972	5,161	+	1	4_A375_EGR1..1..1517	3965	in gene	0	0	1	3	7	17	1	4_A375_EGR1..1	17	Gene GPR137	C11orf4, GPR137, GPR137A, TM7SF1L1	G protein-coupled receptor 137	NM_001170726, NM_001170881, NM_020155, NM_001170880, NM_001177358, hCT14504.3, hCT2310011.0, hCT2310013.0, hCT2310014.0	219430_at, 221966_at, 43934_at	NP_001164197.1, NP_001164352.1, NP_064540.3, NP_001164351.1, NP_001170829.1, EAW74240.1, EAW74237.1, EAW74238.1, EAW74239.1
GeneID:50801	KCNK4	11	84,058,793	84,067,503	8,710	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1622, 4_A375_EGR1..1..1517, 4_A375_EGR1..1..1518	9719, -3017, 9527	downstream, upstream, downstream	0	1	1	6.5	12	16	2	4_A375_EGR1..1	17	Gene KCNK4	KCNK4, TRAAK1, K2p4.1	potassium channel, subfamily K, member 4	NM_033310	224552_s_at	NP_201567.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_3_A375_4_A375_5_A375_6_A375_7_A375_8_A375_9_A375_10_A375_Adj Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
GeneID:23 5501	C11orf20	11	64,267,955	64,272,259	4,376	+	2	2_A375_shl37_plus_lncRNA_hR_1.1622, 2_A375_DGR1_1.1616	649, 457	+z gene, +z gene	0	1	1	10	17	13	1	2_A375_shl37_plus_lncRNA_hR_1.1	17	Gene C11orf20	C11orf20, DKFZp686E164	chromosome 11 open reading frame 20	NM_001079596			XP_005245655.1
GeneID:23 01	ESRRA	11	64,273,044	64,284,210	11,166	+	4	1_A375_shl37_minus_lncRNA_hR_1.1160, 2_A375_shl37_plus_lncRNA_hR_1.1622, 2_A375_shl37_plus_lncRNA_hR_1.1623, 2_A375_DGR1_1.1616	12036, -4532, 12160, -4724	Downstream, upstream, Downstream, upstream	1	1	1	21	23.5	16.5	2	2_A375_shl37_plus_lncRNA_hR_1.1	32	Gene ESRRA	ERRa, ESRL1, ERRA#alpha, ERR1, ESRRA, NR1B1	estrogen-related receptor alpha	NM_004451	1487_at, 202180_at	NP_004442.3
GeneID:23 504	TRMT112	11	64,284,165	64,285,053	870	-	2	2_A375_shl37_minus_lncRNA_hR_1.1160, 2_A375_shl37_plus_lncRNA_hR_1.1623	-247, -119	upstream, upstream	1	1	0	32	30	19	1	1_A375_shl37_minus_lncRNA_hR_1.1	32	Gene TRMT112	TRM112, HSPC170, HSPC152, TRMT112, TRMT11-2	RNA methyltransferase 11-2 homolog (S. cerevisiae)	NM_016404, NCT1444903, NCT19370221,	217794_s_at	NP_057488.1, ENSP00000362252.1, ENAH4293.1, ENAH4293.1
GeneID:23 624	PRDX5	11	64,285,369	64,289,283	3,714	+	2	1_A375_shl37_minus_lncRNA_hR_1.1160, 2_A375_shl37_plus_lncRNA_hR_1.1623	-289, -417	upstream, upstream	1	1	0	32	30	16	1	1_A375_shl37_minus_lncRNA_hR_1.1	32	Gene PRDX5	PRXV, MSC142355, HOS8166, MGC117354, MGC142203, PLP, PMP20, SBBI10, PRDX5, PRO08, 8196, ACR1	peroxiredoxin 5	NM_012094, NM_181651, NM_181652	1560367_s_at, 222994_at	NP_036226.1, NP_857634.1, NP_857635.1
GeneID:23 3234	CCDC88	11	64,107,690	64,125,008	17,318	+	8	4_A375_DGR1_1.1519, 4_A375_DGR1_1.1520, 4_A375_DGR1_1.1521, 4_A375_DGR1_1.1522, 4_A375_DGR1_1.1523, 4_A375_DGR1_1.1524, 4_A375_DGR1_1.1525	-7885, 1942, 11307, 12022, 13441, 21328	upstream, +z gene, +z gene, +z gene, +z gene, +z gene, Downstream	0	2	1	8	7.67	17.83	6	4_A375_DGR1_1.1	24	Gene CCDC88B	DKFZp434G0923, FLJ12970, girdin, HKRP1, FLJ40394, GIRLZ, CCDC88B, CCDC88	coiled-coil domain containing 88B	NM_032251	229983_at	NP_115627.6
GeneID:23 06	RPS6KA1	11	64,126,625	64,139,667	13,042	+	5	4_A375_DGR1_1.1521, 4_A375_DGR1_1.1522, 4_A375_DGR1_1.1523, 4_A375_DGR1_1.1524, 4_A375_DGR1_1.1525	-7926, -6113, -5494, 2691, 11557	upstream, upstream, upstream, upstream, gene, +z gene	0	3	1	8.6	8.4	17.6	5	4_A375_DGR1_1.1	24	Gene RPS6KA1	RPS6KA, MSK2	ribosomal protein S6 kinase, 90kDa, polypeptide 4	NM_001006944, NM_002952, NCT14449 2, NCT19619705.1, NCT19619706.1, NCT20352394.0	204622_x_at, 230544_at	NP_001006945.1, NP_002933.1, ENAH4266.1, ENAH4266.1, ENAH4282.1, ENAH4282.1
GeneID:10 0302260	MIR1237	11	64,136,074	64,136,175	101	+	2	4_A375_DGR1_1.1524, 4_A375_DGR1_1.1525	-9536, 1635	upstream, downstream	0	2	1	8.5	9.5	18.5	2	4_A375_DGR1_1.1	17	Gene MIR1237	MIR1237, miRNA1237, hsa-mir-1237	microRNA 1237	NR_031602		
GeneID:23 597	SLC22A11	11	64,325,095	64,336,999	15,901	+	1	4_A375_DGR1_1.1526	5630	+z gene	0	2	1	5	7	16	1	4_A375_DGR1_1.1	16	Gene SLC22A11	MGC54352, OAT4, hOAT4, SLC22A11	solute carrier family 22 (organic anion/cation transporter), member 11	NM_194454, NCT19611172.1, NCT20352570.0	220100_at	NP_390754.1, ENAH4299.1, ENAH4276.1
GeneID:10 6005	SLC22A12	11	64,356,202	64,369,620	11,836	+	1	4_A375_DGR1_1.1527	2676	+z gene	0	2	1	7	7	16	1	4_A375_DGR1_1.1	16	Gene SLC22A12	OAT4L1, URAT1, RST, SLC22A12	solute carrier family 22 (organic anion/cation transporter), member 12	NM_144583, NM_153370, NCT19390658.2, NCT20350482.0, NCT20350483.0, NCT20350490.0, NCT20353312.0, NCT20353313.0	227799_at	NP_653106.2, NP_700357.1, ENAH4271.1, ENAH4272.1, ENAH4275.1, ENAH4276.1, ENAH4273.1, ENAH4274.1
GeneID:23 79	NRXN2	11	64,373,848	64,490,860	117,014	+	1	4_A375_DGR1_1.1528	93768	+z gene	0	2	1	4	9	18	1	4_A375_DGR1_1.1	16	Gene NRXN2	KIAA0921, FLJ40392, MRXN2	neurexin 2	NM_015080, NM_138732, NM_138734, NCT19610061.1, NCT20110300.0, NCT20110301.0, NCT20110302.0	209982_s_at, 209983_s_at	NP_055895.1, NP_620080.1, NP_620081.1, ENAH4277.1, ENAH4278.1, ENAH4279.1, ENAH4280.1
GeneID:10 235	RASGRP2	11	64,494,353	64,512,926	18,345	+	4	4_A375_DGR1_1.1529, 4_A375_DGR1_1.1530, 4_A375_DGR1_1.1531, 4_A375_DGR1_1.1532	6758, 2976, 3046	+z gene, +z gene, +z gene, +z gene	0	3	1	7	9	18.5	4	4_A375_DGR1_1.1	19	Gene RASGRP2	RASGRP2, CDC25L, CALDAG-GEFI	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	NM_153619, NM_001099570, NM_001099571, NM_001114457.2, NCT19619731.1, NCT19619741.1	206256_s_at, 214297_s_at, 214386_at, 214389_s_at	NP_722541.1, NP_001092143.1, NP_001092141.1, ENAH4281.1, ENAH4282.1, ENAH4283.1
GeneID:23 37	PYGM	11	64,513,691	64,526,167	14,328	+	4	4_A375_DGR1_1.1529, 4_A375_DGR1_1.1530, 4_A375_DGR1_1.1531, 4_A375_DGR1_1.1532	23893, 16235, 17507, 16693	Downstream, Downstream, Downstream, Downstream	0	3	1	7	9	18.5	4	4_A375_DGR1_1.1	19	Gene PYGM	PYGM		NM_005609, NM_001162718, NCT14393.3, NCT20352150	203377_at	NP_005600.1, NP_001148190.1, ENAH4284.1, ENAH4285.1
GeneID:23 71	MAP4K2	11	64,536,609	64,570,713	14,104	-	2	2_A375_shl37_plus_lncRNA_hR_1.1624, 4_A375_DGR1_1.1533	-7431, 13129	upstream, +z gene	0	1	1	11.5	13.5	14	2	2_A375_shl37_plus_lncRNA_hR_1.3	23	Gene MAP4K2	MAP4K2, RAB8IP, BL44, GCK	mitogen-activated protein kinase kinase kinase kinase 2	NM_004579, NCT14449.2, NCT19701001.1, NCT19701011.1, NCT20353249.0	204038_at	NP_004570.2, ENAH4286.1, ENAH4301.1, ENAH4302.1
GeneID:23 06	MENH	11	64,570,906	64,576,766	5,860	-	1	2_A375_shl37_plus_lncRNA_hR_1.1624	622	+z gene	0	1	0	16	25	12	1	2_A375_shl37_plus_lncRNA_hR_1	23	Gene MENH	MENH, MENI, SCG2, MENIN	multiple endocrine neoplasia I	NM_130799, NM_000244, NM_130802, NM_130800, NM_130801, NM_130803, NM_130804, NCT20110300.0, NCT20110301.0, NCT20110302.0, NCT20110303.0, NCT20110304.0, NCT20110305.0, NCT20110306.0, NCT20110307.0, NCT20110308.0, NCT20110310.0, NCT20110312.0, NCT20353294	202945_s_at	NP_570711.1, NP_000235.2, NP_570712.1, NP_570713.1, NP_570714.1, NP_570715.1, NP_570716.1, ENAH4303.1, ENAH4304.1, ENAH4305.1, ENAH4306.1, ENAH4307.1, ENAH4308.1, ENAH4309.1, ENAH4310.1, ENAH4311.1, ENAH4312.1, ENAH4313.1, ENAH4314.1, ENAH4315.1
GeneID:23 561	CDC42BPG	11	64,591,691	64,612,941	20,250	-	1	4_A375_DGR1_1.1534	10251	+z gene	0	0	1	8	11	18	1	4_A375_DGR1_1.1	16	Gene CDC42BPG	CDC42BPG, HSKID-PK1N, MRCKgamma, DKFPn-200, DMPK2	CDC42 binding protein kinase gamma (DMPK-like)	NM_017533, NCT20340418.0	1564023_at, 1569044_at	NP_059993.2, ENAH4318.1
GeneID:10 938	EHD1	11	64,620,205	64,646,191	25,985	-	7	2_A375_shl37_plus_lncRNA_hR_1.1623, 2_A375_shl37_plus_lncRNA_hR_1.1626, 2_A375_DGR1_1.1535, 4_A375_DGR1_1.1535, 4_A375_DGR1_1.1537, 4_A375_DGR1_1.1538	22223, 191, 22397, 14311, 697, -275, -1619	+z gene, +z gene, +z gene, +z gene, +z gene, upstream, upstream	0	1	1	11.75	14.25	16.5	4	4_A375_DGR1_1.1	23	Gene EHD1	FLJ42622, PAST1, HPAST1, HPAST, FLJ44618, PAST, EHD1	EH-domain containing 1	NM_006795, NCT14449.2, NCT19830421, NCT19830431, NCT20350952.0, NCT20355392.0	200112_x_at, 203037_s_at, 203038_s_at, 203039_x_at, 222221_x_at	NP_006786.2, ENAH4319.1, ENAH4317.1, ENAH4316.1, ENAH4320.1, ENAH4321.1
GeneID:40 6947	MIR192	11	64,650,609	64,650,716	109	-	4	4_A375_DGR1_1.1535, 4_A375_DGR1_1.1536, 4_A375_DGR1_1.1537, 4_A375_DGR1_1.1538, 4_A375_DGR1_1.1539, 4_A375_DGR1_1.1540, 4_A375_DGR1_1.1541, 4_A375_DGR1_1.1542	2385, -3042, -3776, -4668	Downstream, upstream, upstream, upstream	0	3	1	7	12.25	19.25	4	4_A375_DGR1_1.1	23	Gene MIR192	miR-NAT62, miR-192, MIRN192, MIR192	microRNA 192	NR_029576		
GeneID:40 9970	MIR194-2	11	64,650,827	64,650,911	84	-	4	4_A375_DGR1_1.1535, 4_A375_DGR1_1.1536, 4_A375_DGR1_1.1537, 4_A375_DGR1_1.1538, 4_A375_DGR1_1.1539, 4_A375_DGR1_1.1540, 4_A375_DGR1_1.1541, 4_A375_DGR1_1.1542	2381, -2849, -3363, -4472	Downstream, upstream, upstream, upstream	0	3	1	7	12.25	19.25	4	4_A375_DGR1_1.1	23	Gene MIR194-2	MIRNA194-2, MIR194-2	microRNA 194-2	NR_029829		
GeneID:23 150	ATG2A	11	64,662,004	64,684,722	22,718	-	9	1_A375_shl37_minus_lncRNA_hR_1.1161, 1_A375_shl37_minus_lncRNA_hR_1.1162, 2_A375_shl37_plus_lncRNA_hR_1.1627, 2_A375_shl37_plus_lncRNA_hR_1.1628, 2_A375_shl37_plus_lncRNA_hR_1.1629, 4_A375_DGR1_1.1535, 4_A375_DGR1_1.1540, 4_A375_DGR1_1.1541, 4_A375_DGR1_1.1542, 4_A375_DGR1_1.1543	279, -6553, 114, 6992, 35422, 22982, 22226, 16336, 6402	upstream, upstream, antisense, exon, upstream, Downstream, Downstream, gene, +z gene, +z gene	1	1	1	14.14	20.43	16.71	7	2_A375_shl37_plus_lncRNA_hR_1.3	66	Gene ATG2A	MGC117151, ATG2A, SWAP404	ATG2 autophagy related 2 homolog A (S. cerevisiae)	NM_015104, NCT20110310.0	213300_at	NP_055910.2, ENAH4322.1
GeneID:23 06	PPP2R5B	11	64,692,143	64,701,950	9,807	+	4	1_A375_shl37_minus_lncRNA_hR_1.1161, 1_A375_shl37_minus_lncRNA_hR_1.1162, 2_A375_shl37_plus_lncRNA_hR_1.1627, 2_A375_shl37_plus_lncRNA_hR_1.1628, 2_A375_shl37_plus_lncRNA_hR_1.1629	-7191, -483, -7935, -431	upstream, upstream, upstream, upstream	1	1	0	33.5	43	10.5	2	2_A375_shl37_plus_lncRNA_hR_1.3	66	Gene PPP2R5B	B56B, PPP2R5B, PR61B, FLJ35411	protein phosphatase 2, regulatory subunit B, beta	NM_006244, NCT14464.3, NCT20100810.0	204811_s_at, 653_s_at	NP_006235.1, ENAH4324.1, ENAH4323.1
GeneID:10 9309	GPHN2	11	64,701,943	64,703,390	1,417	-	2	2_A375_shl37_plus_lncRNA_hR_1.1628, 2_A375_shl37_plus_lncRNA_hR_1.1629	11800, 11948	Downstream, Downstream	1	1	0	49	66	10	1	2_A375_shl37_plus_lncRNA_hR_1.3	66	Gene GPHN2	MGC126872, GPHN2_ISS03, 42, GPA2	glycerophine homolog alpha 2	NM_130789, NCT20100910.0, NCT20100920.0	237230_at	NP_570125.1, ENAH4327.1, ENAH4328.1
GeneID:23 5129	C11orf85	11	64,709,329	64,729,356	20,029	-	2	2_A375_shl37_plus_lncRNA_hR_1.1628, 2_A375_shl37_plus_lncRNA_hR_1.1629	-5922, -5690	upstream, upstream	1	1	0	16	17	7	1	1_A375_shl37_minus_lncRNA_hR_1.1	16	Gene C11orf85	MGC126894, C11orf85	chromosome 11 open reading frame 85	NM_031037229, NCT14465612.1	231210_at	NP_001032922.1, ENAH4329.1
GeneID:10 9371	BATF2	11	64,735,417	64,764,517	29,100	-	2	2_A375_shl37_plus_lncRNA_hR_1.1628, 2_A375_shl37_plus_lncRNA_hR_1.1629	19037, 19289	Downstream, Downstream	1	1	0	16	17	7	1	1_A375_shl37_minus_lncRNA_hR_1.1	16	Gene BATF2	SKAP3, BATF2, MGC20410	basic leucine zipper transcription factor, ATF-like 2	NM_138456, NCT19709636, NCT20100980.0	228459_at	NP_619485.3, ENAH4331.1, ENAH4330.1
GeneID:40 2	ARL2	11	64,761,906	64,769,656	8,070	+	4	1_A375_shl37_minus_lncRNA_hR_1.1164, 1_A375_shl37_minus_lncRNA_hR_1.1165, 2_A375_shl37_plus_lncRNA_hR_1.1630, 2_A375_shl37_plus_lncRNA_hR_1.1631	398, 13503, -306, 12662	+z gene, Downstream, upstream, Downstream	1	1	0	54.5	70.5	12	2	2_A375_shl37_plus_lncRNA_hR_1.3	120	Gene ARL2	ARL2, ARP1.2	ADP-ribosylation factor-like 2	NM_001667	202964_s_at	NP_001658.2
GeneID:29 707	SNX15	11	64,794,910	64,806,044	11,134	+	5	2_A375_shl37_minus_lncRNA_hR_1.1165, 2_A375_shl37_plus_lncRNA_hR_1.1631, 2_A375_DGR1_1.1644	236, 256, 6370	+z gene, +z gene, +z gene	1	1	1	46.5	64.5	11.5	2	2_A375_shl37_plus_lncRNA_hR_1.3	100	Gene SNX15	HSA7001435, SNX15	sorting nexin 15	NM_013338, NM_147777	205402_s_at	NP_037430.2, NP_680088.2
GeneID:29 041	SACS	11	64,806,378	64,812,300	5,924	+	1	4_A375_DGR1_1.1644	9098	upstream	0	0	1	5	9	15	1	4_A375_DGR1_1.1	15	Gene SACS	SHD1, HSJ1P0298, SACS01	SHC3 domain containing 1	NM_012299, NCT14476.2, NCT19370991.1	209449_at	NP_037431.3, ENAH4338.1, ENAH4339.1
GeneID:10 004	NAALAD	11	64,812,355	64,826,009	13,714	-	1	4_A375_DGR1_1.1644	22729	downstream	0	0	1	5	9	15	1	4_A375_DGR1_1.1	15	Gene NAALADL1	NAALADASE1, NAALADL1, I100	N-acetylated alpha-linked acidic dipeptidase-like 1	NM_020145, NCT14480.3	207809_at, 229624_at	NP_064519.2, ENAH4340.1
GeneID:10 3130	CDCA5	11	64,844,927	64,851,815	6,888	-	3	2_A375_shl37_plus_lncRNA_hR_1.1633, 4_A375_DGR1_1.1545, 4_A375_DGR1_1.1546	-31, 191, -4061	+z gene, +z gene, upstream	0	1	1	11	14	17	2	2_A375_shl37_plus_lncRNA_hR_1.3	82	Gene CDCA5	MGC16039, CDCA5, SORORIN	sell division cycle associated 5	NM_080668, NCT14361.3, NCT19844.13	224763_at	NP_542399.1, ENAH4343.1, ENAH4342.1
GeneID:74 62	ZFP1	11	64,851,894	64,855,874	4,180	+	5	1_A375_shl37_minus_lncRNA_hR_1.1166, 2_A375_shl37_plus_lncRNA_hR_1.1632, 4_A375_DGR1_1.1545, 4_A375_DGR1_1.1546, 4_A375_DGR1_1.1547	13016, -110, 270, 3922, 11998	Downstream, upstream, upstream, gene, Downstream	1	1	1	13	14.67	17	3	2_A375_shl37_plus_lncRNA_hR_1.3	82	Gene ZFP1	MGC4, D15750, ZFP1	zinc finger protein homolog 1	NM_007152, NCT14479.2, NCT21100700.0, NCT21100710.0	209426_s_at, 214310_s_at, 214311_at	NP_009073.2, ENAH4344.1, ENAH4345.1, ENAH4346.1
GeneID:10 0130348	LOC100130348	11	64,855,944	64,856,903	959	-	5	1_A375_shl37_minus_lncRNA_hR_1.1166, 2_A375_shl37_plus_lncRNA_hR_1.1632, 4_A375_DGR1_1.1545, 4_A375_DGR1_1.1546, 4_A375_DGR1_1.1547	-7309, 4916, 6974, 807, -7177	upstream, downstream, Downstream, Downstream, upstream	1	1	1	13	14.67	17	3	2_A375_shl37_plus_lncRNA_hR_1.3	82	Gene LOC100130348		hypothetical LOC100130348	XM_002117935, XM_001716007, XM_001707710		XP_002117981.1, XP_001716093.2, XP_001707792.1
GeneID:73 8	C11orf2	11	64,860,863	64,879,160	18,297	+	6	1_A375_shl37_minus_lncRNA_hR_1.1166, 2_A375_shl37_plus_lncRNA_hR_1.1633, 4_A375_DGR1_1.1546, 4_A375_DGR1_1.1547, 4_A375_DGR1_1.1548, 4_A375_DGR1_1.1549	26, 20923, -6967, -3, 20567, 21341	+z gene, Downstream, upstream, upstream, Downstream, Downstream	1	1	1	13	13.33	19.67	3	2_A375_shl37_plus_lncRNA_hR_1.3	25	Gene C11orf2	C11orf2, FFR, C11orf2, FLJ13279, ANG2, ANG2, FLJ39472	chromosome 11 open reading frame 2	NM_012366, NCT14477.2	217989_at	NP_037197.2, ENAH4347.1
GeneID:73 06	TMTSF2	11	64,879,341	64,883,767	4,398	+	4	2_A375_shl37_plus_lncRNA_hR_1.1633, 2_A375_shl37_plus_lncRNA_hR_1.1634, 4_A375_DGR1_1.1546, 4_A375_DGR1_1.1547, 4_A375_DGR1_1.1548, 4_A375_DGR1_1.1549	5267, 10307, 5259, 9663	Downstream, Downstream, Downstream, Downstream, Downstream, Downstream	1	1	1	15	21.5	20	2	2_A375_shl37_plus_lncRNA_hR_1.3	25	Gene TMTSF2	KIAA1, NET47, TMTSF2, DHCR14A	trans-membrane 7 superfamily member 2	NM_022272, NCT14474.2, NCT19819871.1, NCT20353305.0, NCT20353306.0	213150_s_at	NP_071355.2, ENAH4348.1, ENAH4349.1, ENAH4350.1
GeneID:74 1	ZNHIT2	11	64,883,878	64,885,170	1,293	+	4	1_A375_shl37_minus_lncRNA_hR_1.1166, 2_A375_shl37_plus_lncRNA_hR_1.1634, 4_A375_DGR1_1.1546, 4_A375_DGR1_1.1549	640, -4886, 930, 148	Downstream, upstream, +z gene, +z gene	1	1	1	15	21.5	20	2	2_A375_shl37_plus_lncRNA_hR_1.3	25	Gene ZNHIT2	FOXL, ZNHIT2, C11orf8, MGC120265, MGC120266	zinc finger, HIT type 2	NM_014355, NCT14478.3	217690_s_at, 222614_s_at, 227734_s_at	NP_055220.1, ENAH4352.1
GeneID:21 77	FAU	11	64,886,699	64,889,872	3,173	+	4	2_A375_shl37_plus_lncRNA_hR_1.1633, 2_A375_shl37_plus_lncRNA_hR_1.1634, 4_A375_DGR1_1.1546, 4_A375_DGR1_1.1549	3284, -56, 3032, 4965	Downstream, upstream, Downstream, Downstream	1	1	1	15	21.5	20	2	4_A375_DGR1_1.1	25	Gene FAU	Fau, RPS30, FAU, FLJ22598, ki-1, FAUT, HNSP beta, Fau1, S30	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed	NM_001997, NCT21009916.0	200019_s_at	NP_001988.1, ENAH4353.1
GeneID:74 6	MRPL49	11	64,889,726	64,894,541	5,115	+	6	1_A375_shl37_minus_lncRNA_hR_1.1167, 2_A375_shl37_plus_lncRNA_hR_1.1633, 2_A375_shl37_plus_lncRNA_hR_1.1634, 2_A375_shl37_plus_lncRNA_hR_1.1635, 4_A375_DGR1_1.1546, 4_A375_DGR1_1.1549	12764, -5126, 0, 12645, -5095, -, 4764	Downstream, upstream, +z gene, downstream, upstream, upstream	1	1	1	15.67	22.33	19.33	3	4_A375_DGR1_1.1	25	Gene MRPL49	C11orf6, mitochondrial ribosomal protein L49	mitochondrial ribosomal protein L49	NM_030927, NCT14475.3, NCT19819892.1, NCT20353307.0	201717_at	NP_056716.1, ENAH4358.1, ENAH4354.1, ENAH4355.1
GeneID:64 647	SYVN1	11	64,894,751	64,902,003	7,252	-	5	1_A375_shl37_minus_lncRNA_hR_1.1167, 2_A375_shl37_plus_lncRNA_hR_1.1633, 2_A375_shl37_plus_lncRNA_hR_1.1634, 2_A375_shl37_plus_lncRNA_hR_1.1635, 2_A375_shl37_plus_lncRNA_hR_1.1636	-429, 17350, 12275, -173, 18679	upstream, Downstream, Downstream, upstream, Downstream	1	1	1	15.67	22.33	19.33	3	4_A375_DGR1_1.1	25	Gene SYVN1	SYVN1, HRD1, HRD1L, MGC40372	synovial apoptosis inhibitor 1, synoviolin	NM_032431, NM_152293, NCT14499.4, NCT19834482.3, NCT19834483.2, NCT20353310.0, NCT20353311.0, NCT20353312.0	223060_at, 244322_at	NP_115937.1, NP_757358.1, ENAH4357.1, ENAH4359.1, ENAH4360.1, ENAH4362.1, ENAH4361.1
GeneID:23 649	POLA2	11	65,029,422	65,060,955	35,534	+	1	4_A375_DGR1_1.1636	280	upstream	0	0	1	0	10	19	1	4_A375_DGR1_1.1	19	Gene POLA2	FLJ21393, FLJ21662, POLA2	polymerase (DNA directed), alpha 2 (70 kD subunit)	NM_002689, NCT21009.0	204441_s_at, 244573_at	NP_002680.2, ENAH4370.1
GeneID:10 635	CDC42EP2	11	65,082,331	65,089,900	7,569	+	2	2_A375_shl37_plus_lncRNA_hR_1.1637, 4_A375_DGR1_1.1550	135, 2281	+z gene, +z gene	0	1	1	8	13.5	13	2	2_A375_shl37_plus_lncRNA_hR_1.3	21	Gene CDC42EP2	BORG1, CEP2, CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2	NM_006779, NCT21009.0	209920_s_at, 214014_at	NP_006770.1, ENAH4374.1
GeneID:54 77	DPF2	11	65,101,348	65,120,451	19,103	+	2	2_A375_shl37_plus_lncRNA_hR_1.1638, 4_A375_DGR1_1.1551	20842, 22974	Downstream, Downstream	0	1	1	8.5	11.5	13	2	4_A375_DGR1_1.1	17	Gene DPF2	UBI04, ubi-ki4, MGC10180, REQ, DPF2	D4, zinc and double PHD fingers, family 2	NM_006268, NCT19854.11, NCT19854.12, NCT20352269.0	202216_at	NP_006259.1, ENAH4376.1, ENAH4377.1
GeneID:22 9339	TIGD5	11	65,122,262	65,125,954	3,692	+	2	2_A375_shl37_plus_lncRNA_hR_1.1638, 4_A375_DGR1_1.1551	-356, 3036	Downstream, upstream, gene	0	1	1	8.5	11.5	13	2	4_A375_DGR1_1.1	17	Gene TIGD5	TIGD5	hypothetical protein LOC79719	NM_145719, NCT21643051.5	229769_at	NP_665771.1, ENAH4378.1
GeneID:28 3130	SLC35A5	11	65,142,680	65,150,142	7,479	-	6	1_A375_shl37_minus_lncRNA_hR_1.1168, 2_A375_shl37_plus_lncRNA_hR_1.1638, 2_A375_shl37_plus_lncRNA_hR_1.1639, 2_A375_shl37_plus_lncRNA_hR_1.1640, 2_A375_shl37_plus_lncRNA_hR_1.1641, 4_A375_DGR1_1.1552	-3910, -9302, 591, -3776, 7862, 4274	upstream, upstream, gene, upstream, upstream, Downstream	1	1	1	21	21.67	13.33	3	2_A375_shl37_plus_lncRNA_hR_1.3	30	Gene SLC35A5	SLC35A5	solute carrier family 35, member A5	NM_152386, NM_001077241, NCT21143353.1, NCT20353395.0, NCT20353397.0, NCT20353398.0	1563490_s_at, 239638_at	NP_972362.2, NP_001070791.1, ENAH4380.1, ENAH4381.1, ENAH4382.1
GeneID:83 709	FRMD6	11	65,154,041	65,193,998	39,958	+	11	1_A375_shl37_minus_lncRNA_hR_1.1168, 1_A375_shl37_minus_lncRNA_hR_1.1169, 1_A375_shl37_minus_lncRNA_hR_1.1170, 2_A375_shl37_plus_lncRNA_hR_1.1639, 2_A375_shl37_plus_lncRNA_hR_1.1640, 2_A375_shl37_plus_lncRNA_hR_1.1641, 2_A375_shl37_plus_lncRNA_hR_1.1642, 2_A375_shl37_plus_lncRNA_hR_1.1643, 4_A375_DGR1_1.1552, 4_A375_DGR1_1.1553, 4_A375_DGR1_1.1554	69, 4183, 38128, 4280, -121, 5763, 34536, 36103, 375, 7391, 39151	upstream, gene, Downstream, upstream, upstream, gene, upstream, Downstream, Downstream, +z gene, +z gene, Downstream	1	1	1	16.67	19.17	14.33	6	2_A375_shl37_plus_lncRNA_hR_1.3	30	Gene FRMD6	FRMD6, FLJ22216, MGC21753, FLJ90369	FERM domain containing 6	NM_031904, NCT21031411.0, NCT21032508.0,	1554602_at, 1554609_x_at	NP_114110.1, ENAH4384.1, ENAH4385.1, ENAH4386.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Positions	T_A375_pAU7_mut_lncRNA_AR_1 Percent	A_A375_pAU7_mut_lncRNA_AR_1 Percent	A_A375_pAU7_mut_lncRNA_AR_1 Percent	T_A375_pAU7_mut_lncRNA_AR_1 Avg Peak	T_A375_pAU7_mut_lncRNA_AR_1 Avg Peak	A_A375_pAU7_mut_lncRNA_AR_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:2313121	NEAT1	11	65,190,269	65,194,003	3734	+	5	1_A375_pAU7_mut_lncRNA_AR_1.1170,1_A375_pAU7_mut_lncRNA_AR_1.1171,1_A375_pAU37_dut_lncRNA_AR_1.1642,2_A375_pAU37_dut_lncRNA_AR_1.1643,2_A375_pAU37_dut_lncRNA_AR_1.1644	-93, 4227, -1373, 125, -77	upstream, downstream, upstream, upstream, upstream							2	2_A375_pAU37_dut_lncRNA_AR_1			NEAT1, lncRNA, NCRNA00094, NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	NR_028272	2145857_s_at:224593_at, 2243866_a_at:227382_at, 2234869_a_at:230320_at	
GeneID:89	MIR612	11	65,211,929	65,212,026	98	+	2	A_A375_DGR1_1.1555,A_A375_DGR1_1.1556	1319, 4227	downstream, downstream	0	0	1	9	12.5	17	2	A_A375_DGR1_1.1	20	Gene MIR612	MIR612, hsa-mir-612	microRNA 612	NR_030345		
GeneID:10	LOC100	11	65,236,981	65,267,351	30,370	-	9	1_A375_pAU7_mut_lncRNA_AR_1.1172,1_A375_pAU7_mut_lncRNA_AR_1.1173,1_A375_pAU7_mut_lncRNA_AR_1.1174,1_A375_pAU7_mut_lncRNA_AR_1.1175,2_A375_pAU37_dut_lncRNA_AR_1.1644,2_A375_pAU37_dut_lncRNA_AR_1.1645,2_A375_pAU37_dut_lncRNA_AR_1.1646,2_A375_pAU37_dut_lncRNA_AR_1.1647,2_A375_pAU37_dut_lncRNA_AR_1.1650	27939, 11699, 7981, 2223, 27603, 22386, 11627, 2227, 23859	upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream							1	2_A375_pAU37_dut_lncRNA_AR_1		Gene LOC100507845		hypothetical LOC100507845	XR_111190, XR_111191, XR_110918, XR_110919, XR_110917, XR_114497, XR_114498, XR_114499		
GeneID:27	MALAT1	11	65,265,233	65,272,940	7,707	+	5	1_A375_pAU7_mut_lncRNA_AR_1.1173,1_A375_pAU7_mut_lncRNA_AR_1.1174,1_A375_pAU7_mut_lncRNA_AR_1.1175,2_A375_pAU37_dut_lncRNA_AR_1.1648,2_A375_pAU37_dut_lncRNA_AR_1.1647	-9881, -5870, 305, -9809, -209	upstream, upstream, upstream, upstream, upstream							2	2_A375_pAU37_dut_lncRNA_AR_1		Gene MALAT1	MALAT1, HCN, NEAT2, MALAT-1, PRO2853, NCRNA00047	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	NR_002819	1559870_s_at:222948_x_at, 2243866_s_at:224599_at, 2243867_x_at:234861_x_at, 2298975_s_at:229362_x_at	
GeneID:40	LTBP3	11	65,306,030	65,325,899	19,869	-	1	A_A375_DGR1_1.1556	4003	upstream	0	0	1	10	9	22	1	A_A375_DGR1_1.1	22	Gene LTBP3	LTBP-3, FLJ45579, FLJ46139, FLJ46268, FLJ39093, FLJ42333, pdf425, LTBP2, FLJ35431, DKFZp686H0123, LTBP3	latent transforming growth factor beta binding protein 3	NM_001164286, NM_021070, NM_001130144, NCT01827189.1, NCT01979679.1, NCT02145465.0, NCT02539292.0	219922_s_at:227302_at, 2211238:16.1, EAW74481.1, EAW74483.1, EAW74485.1, EAW74482.1, EAW74483.1	227144_at	NP_001157730.1, NP_066543.2, NP_001129816.1, EAW74481.1, EAW74483.1, EAW74485.1, EAW74482.1, EAW74483.1
GeneID:10	SSSCA1	11	65,237,943	65,239,239	1,296	+	3	1_A375_pAU7_mut_lncRNA_AR_1.1176,2_A375_pAU37_dut_lncRNA_AR_1.1645,2_A375_pAU37_dut_lncRNA_AR_1.1638	-67, -23, 11566	upstream, upstream, downstream							2	2_A375_pAU37_dut_lncRNA_AR_1		Gene SSSCA1	SSSCA1, p27	Sjogren syndrome/scleroderma autoantigen 1	NM_006396, NCT14383.2, NCT21338.0, NCT21338.2	203114_at	NP_006387.1, EAW74486.1, EAW74487.1, EAW74488.1
GeneID:22	FAM89B	11	65,239,920	65,241,869	1,949	+	3	1_A375_pAU7_mut_lncRNA_AR_1.1176,2_A375_pAU37_dut_lncRNA_AR_1.1645,2_A375_pAU37_dut_lncRNA_AR_1.1638	-1864, -1900, 9969	upstream, upstream, downstream							2	2_A375_pAU37_dut_lncRNA_AR_1		Gene FAM89B	MTVR1, FAM89B	leucy-rich repeat(in FLII) interacting protein 3	NM_152632, NM_001097604, NM_001097605	213464_at, 32309_a_at	NP_690045.1, NP_001092234.1, NP_001092235.1
GeneID:23	EHBP1L1	11	65,243,539	65,280,116	36,607	+	4	1_A375_pAU7_mut_lncRNA_AR_1.1176,2_A375_pAU37_dut_lncRNA_AR_1.1645,2_A375_pAU37_dut_lncRNA_AR_1.1639,4_A375_DGR1_1.1560	3663, 5599, 6005, 17951	upstream, upstream, upstream, upstream							2	2_A375_pAU37_dut_lncRNA_AR_1		Gene EHBP1L1	EHBP1L1, FLJ34511, DKFZp762C186	EH domain binding protein 1-like 1	NM_001079949	1557225_at, 1557749_at, 221783_at	NP_001073279.1
GeneID:10	KCNK7	11	65,280,326	65,285,467	5,141	-	1	A_A375_DGR1_1.1560	2267	upstream	0	0	1	9	8	21	1	A_A375_DGR1_1.1	21	Gene KCNK7	TWIK2, MGC102764, 62a1, MGC102762, KCNK7	potassium channel, subfamily K, member 7	NM_033714, NM_033347, NM_033348, NM_033345, NCT14484.2, NCT16376970.2, NCT16376971.0, NCT16534160.0, NCT19654190.0, NCT21413390.0	220412_x_at:224008_s_at, 224283_x_at	NP_033720.1, NP_203132.1, NP_203134.1, NP_203136.1, EAW74411.1, EAW74412.1, EAW74413.1, EAW74414.1, EAW74415.1, EAW74416.1
GeneID:42	MAP3K11	11	65,365,236	65,381,720	16,484	-	5	1_A375_pAU7_mut_lncRNA_AR_1.1177,2_A375_pAU37_dut_lncRNA_AR_1.1649,2_A375_pAU37_dut_lncRNA_AR_1.1586,4_A375_DGR1_1.1580,4_A375_DGR1_1.1582	-1022, -1045, 20820, 126, -5400	upstream, upstream, downstream, upstream, upstream							1	1_A375_pAU37_dut_lncRNA_AR_1		Gene MAP3K11	PTK1, MLK3, MEKK11, SPRK, MLK-3, MAP3K11, MGC71714	mitogen-activated protein kinase kinase kinase 11	NM_002419, NCT14383.2, NCT21145322.0	1568964_at, 203952_at	NP_002410.1, EAW74418.1, EAW74417.1
GeneID:39	PCNXL3	11	65,385,765	65,494,910	21,127	+	6	1_A375_pAU7_mut_lncRNA_AR_1.1177,2_A375_pAU37_dut_lncRNA_AR_1.1649,4_A375_DGR1_1.1581,4_A375_DGR1_1.1582,4_A375_DGR1_1.1583,4_A375_DGR1_1.1584,4_A375_DGR1_1.1585,4_A375_DGR1_1.1587	-1081, -1515, 2199, 3417, 5599, 13845, 19035, 22201, 26025	upstream, upstream, upstream, upstream, upstream, upstream, upstream							1	1_A375_pAU37_dut_lncRNA_AR_1		Gene PCNXL3	PCNXL3, FLJ22427	pecanex-like 3 (Drosophila)	NM_032223	227856_at	NP_115599.2
GeneID:84	SIPA1	11	65,493,976	65,416,391	12,515	+	4	A_A375_DGR1_1.1564,A_A375_DGR1_1.1565,A_A375_DGR1_1.1566,A_A375_DGR1_1.1567	6290, -2782, 499, 4200	upstream, upstream, upstream, upstream	0	0	1	8.5	8	17	4	A_A375_DGR1_1.1	20	Gene SIPA1	MGC102669, MGC119237, SPA1, SIPA1	signal-induced proliferation-associated 1	NM_006747, NM_153253, NCT14381.3, NCT19654181.1, NCT19654197.1	204164_at	NP_006738.3, NP_694599.29, EAW74422.1, EAW74423.1
GeneID:58	RELA	11	65,621,087	65,630,443	9,276	-	2	1_A375_pAU7_mut_lncRNA_AR_1.1178,1_A375_pAU7_mut_lncRNA_AR_1.1598	-196, -565	upstream, upstream	1	0	1	17	14	18	1	1_A375_pAU37_dut_lncRNA_AR_1	17	Gene RELA	p65, MGC131774, NFKB3, RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	NM_021975, NM_001145138, NCT14407.4, NCT19654301.1, NCT19654321.1	201783_s_at:203676_s_at	NP_068810.3, NP_001138010.1, EAW74434.1, EAW74435.1, EAW74438.1
GeneID:10	KAT5	11	65,479,469	65,487,873	7,998	+	3	1_A375_pAU7_mut_lncRNA_AR_1.1179,2_A375_pAU37_dut_lncRNA_AR_1.1650,2_A375_pAU37_dut_lncRNA_AR_1.1651	6563, -1, 6763	downstream, upstream, downstream	1	1	1	0	21	25	11.5	2	2_A375_pAU37_dut_lncRNA_AR_1	23	Gene KAT5	EP, PLIP, KAT5, HTATIP, HTATIP1, TIP60, cPLIP, ESA1	Tip(-like) acetyltransferase 1	NM_006388, NM_182709, NM_182710, NCT19810071.1, NCT20139363.0, NCT21339439.0, NCT21339960.0, NCT20833303.0, NCT20833331.0	208955_x_at:209192_x_at, 214358_x_at	NP_006379.2, NP_874386.1, NP_874387.1, EAW74430.1, EAW74431.1, EAW74432.1, EAW74427.1, EAW74428.1, EAW74429.1
GeneID:84	RANGE	11	65,493,144	65,495,409	2,265	-	3	1_A375_pAU7_mut_lncRNA_AR_1.1179,2_A375_pAU37_dut_lncRNA_AR_1.1650,2_A375_pAU37_dut_lncRNA_AR_1.1651	217, 6921, 217	upstream, downstream, upstream	1	1	0	21	25	11.5	2	2_A375_pAU37_dut_lncRNA_AR_1	23	Gene RANGEHDC	RAN, member RAS oncogene family, RANGEHDC, FLJ20774, MGC22394	ADP-ribosylarginine HydrolaseLike 2	NM_032193, NCT14408.2, NCT19654261.1, NCT19654271.1	226453_at, 227943_at	NP_115568.2, EAW74439.1, EAW74433.1, EAW74434.1
GeneID:91	DHFZp781	11	65,543,373	65,547,822	4,449	-	5	1_A375_pAU7_mut_lncRNA_AR_1.1180,2_A375_pAU37_dut_lncRNA_AR_1.1652,2_A375_pAU37_dut_lncRNA_AR_1.1575,4_A375_DGR1_1.1571,4_A375_DGR1_1.1572	527, 614, 2094, 5981, -5155, 4961	upstream, upstream, upstream, upstream, upstream	1	1	1	12.33	14	30.33	3	2_A375_pAU37_dut_lncRNA_AR_1	26	Gene DHFZp781E196	RP1030	DHFZp781E196 protein	NM_152360, NCT16406832.2, NCT23145424.0	231656_s_at	NP_612377.3, EAW74436.1, EAW74437.1
GeneID:30	OVOL1	11	65,554,329	65,564,865	10,536	+	5	1_A375_pAU7_mut_lncRNA_AR_1.1180,2_A375_pAU37_dut_lncRNA_AR_1.1652,2_A375_pAU37_dut_lncRNA_AR_1.1575,4_A375_DGR1_1.1571,4_A375_DGR1_1.1572	7264, -7531, 6981, -9155, 4961	upstream, upstream, upstream, upstream, upstream	1	1	1	12.33	14	30.33	3	2_A375_pAU37_dut_lncRNA_AR_1	26	Gene OVOL1	HOVO1, OVOL1	ovo-like 1(Drosophila)	NM_004561, NCT16131971.2	209804_at, 229298_at	NP_004552.2, EAW74439.1
GeneID:10	LOC100	11	65,556,532	65,556,339	1,817	+	5	1_A375_pAU7_mut_lncRNA_AR_1.1180,2_A375_pAU37_dut_lncRNA_AR_1.1652,2_A375_pAU37_dut_lncRNA_AR_1.1575,4_A375_DGR1_1.1571,4_A375_DGR1_1.1572	11554, 11531, 10511, 8983, 6451	upstream, upstream, upstream, downstream, downstream	1	1	1	12.33	14	30.33	3	2_A375_pAU37_dut_lncRNA_AR_1	26	Gene LOC100507845		hypothetical LOC100507845	XR_111197, XR_111198, XR_111199, XR_110918, XR_110919, XR_110920		
GeneID:23	SNX22	11	65,661,410	65,821,172	19,762	+	6	1_A375_pAU7_mut_lncRNA_AR_1.1181,2_A375_pAU37_dut_lncRNA_AR_1.1652,2_A375_pAU37_dut_lncRNA_AR_1.1653,2_A375_pAU37_dut_lncRNA_AR_1.1654,2_A375_pAU37_dut_lncRNA_AR_1.1655,2_A375_pAU37_dut_lncRNA_AR_1.1574	24302, 28442, 135, 24254, 29630, 440	downstream, downstream, upstream, downstream, upstream, upstream	1	1	1	81	83.33	17.33	3	2_A375_pAU37_dut_lncRNA_AR_1	23	Gene SNX22	MGC42112, SNX6B, DKFZp781P1320, SNX22, MGC37278	sorting nexin 22	NM_152780, NCT14403.3, NCT19709816.1, NCT19709971.1, NCT19709991.1, NCT23131040.0, NCT23131060.0	1554161_at, 231194_at	NP_689973.2, EAW74441.1, EAW74442.1, EAW74443.1, EAW74445.1, EAW74446.1, EAW74444.1, EAW74447.1
GeneID:10	CFL1	11	65,822,262	65,825,904	3,822	-	5	1_A375_pAU7_mut_lncRNA_AR_1.1181,1_A375_pAU7_mut_lncRNA_AR_1.1654,2_A375_pAU37_dut_lncRNA_AR_1.1654,2_A375_pAU37_dut_lncRNA_AR_1.1655,2_A375_pAU37_dut_lncRNA_AR_1.1575	12, -2365, 143, 2205, -6760	upstream, upstream, upstream, upstream	1	1	1	54.67	66.67	10.67	3	2_A375_pAU37_dut_lncRNA_AR_1	23	Gene CFL1	CFL1, CFL	cofilin 1 (non-muscle)	NM_005507, NCT23145081.0, NCT23145113.0, NCT23645467.0, NCT23645643.0, NCT23653303.0	1555730_a_at, 200021_at	NP_005487.1, EAW74448.1, EAW74449.1, EAW74450.1, EAW74451.1, EAW74452.1
GeneID:89	MUSK1	11	65,877,872	65,933,914	56,042	+	8	1_A375_pAU7_mut_lncRNA_AR_1.1181,2_A375_pAU37_dut_lncRNA_AR_1.1652,2_A375_pAU37_dut_lncRNA_AR_1.1653,2_A375_pAU37_dut_lncRNA_AR_1.1654,2_A375_pAU37_dut_lncRNA_AR_1.1655,2_A375_pAU37_dut_lncRNA_AR_1.1656,2_A375_pAU37_dut_lncRNA_AR_1.1578	-2980, 0, -2030, 22, 6712, 13216	upstream, upstream, upstream, upstream, downstream, downstream	1	1	1	45.5	66.75	30.25	4	2_A375_pAU37_dut_lncRNA_AR_1	23	Gene MUSK1	SLK3, MUSK1, FLJ23212, FLJ44872	MUSK muscle,excitation, (S.cerevisiae)	NM_005138, NCT14489.3, NCT19656261.1	216483_s_at, 203870_at	NP_005128.2, EAW74454.1, EAW74453.1
GeneID:33	EFEMP2	11	65,933,912	65,940,340	6,428	-	7	1_A375_pAU7_mut_lncRNA_AR_1.1181,2_A375_pAU37_dut_lncRNA_AR_1.1652,2_A375_pAU37_dut_lncRNA_AR_1.1654,2_A375_pAU37_dut_lncRNA_AR_1.1655,2_A375_pAU37_dut_lncRNA_AR_1.1576,4_A375_DGR1_1.1576,4_A375_DGR1_1.1577	14548, 12488, 14676, 12500, 8598, 7445, 10220	upstream, upstream, upstream, downstream, upstream, upstream	1	1	1	30.6	31.6	30.2	3	2_A375_pAU37_dut_lncRNA_AR_1	23	Gene EFEMP2	FBLN4, UPH1, MBP1, EFEMP2	EGF containing fibulin-like extracellular matrix protein 2	NM_016938, NCT23145111.0, NCT23145310.0, NCT23145190.0, NCT23145320.0, NCT23535340.0, NCT23535460.0, NCT23535470.0, NCT23535540.0	206560_s_at, 209358_s_at	NP_058634.3, EAW74439.1, EAW74455.1, EAW74456.1, EAW74457.1, EAW74458.1, EAW74437.1, EAW74459.1
GeneID:16	CTSW	11	65,947,264	65,951,212	3,926	+	8	1_A375_pAU7_mut_lncRNA_AR_1.1183,1_A375_pAU7_mut_lncRNA_AR_1.1184,2_A375_pAU37_dut_lncRNA_AR_1.1656,2_A375_pAU37_dut_lncRNA_AR_1.1657,2_A375_pAU37_dut_lncRNA_AR_1.1578,4_A375_DGR1_1.1577,4_A375_DGR1_1.1579	6862, 11052, 3864, 11054, 8196, 3276, 9682, 11724	downstream, downstream, downstream, downstream, upstream, downstream, downstream	1	1	1	16.25	19.75	22	4	2_A375_pAU37_dut_lncRNA_AR_1	27	Gene CTSW	CTSW, LYPN	cathepsin W	NM_001335, NCT14392.2, NCT21131212.0	214480_at	NP_001326.2, EAW74439.1, EAW74463.1
GeneID:91	FIBP	11	65,951,211	65,956,010	4,799	-	10	1_A375_pAU7_mut_lncRNA_AR_1.1183,1_A375_pAU7_mut_lncRNA_AR_1.1184,2_A375_pAU37_dut_lncRNA_AR_1.1656,2_A375_pAU37_dut_lncRNA_AR_1.1657,4_A375_DGR1_1.1578,4_A375_DGR1_1.1577,4_A375_DGR1_1.1579,4_A375_DGR1_1.1580	74, -2328, 122, 2280, 14922, 9430, 74, -2916, 9760, -6356	upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream	1	1	1	16	19.67	30.83	6	2_A375_pAU37_dut_lncRNA_AR_1	27	Gene FIBP	FGFBP, FIBP-1, FIBP	fibroblast growth factor (acidic) binding protein	NM_004214, NM_176097, NCT14393.4, NCT19619851.1, NCT19619941.1	202041_s_at	NP_004205.2, NP_942600.1, EAW74459.1, EAW74460.1, EAW74461.1
GeneID:10	CCDC88	11	65,957,573	65,959,108	1,231	+	11	1_A375_pAU7_mut_lncRNA_AR_1.1183,1_A375_pAU7_mut_lncRNA_AR_1.1184,2_A375_pAU37_dut_lncRNA_AR_1.1656,2_A375_pAU37_dut_lncRNA_AR_1.1657,2_A375_pAU37_dut_lncRNA_AR_1.1658,2_A375_pAU37_dut_lncRNA_AR_1.1577,4_A375_DGR1_1.1578,4_A375_DGR1_1.1579,4_A375_DGR1_1.1580,4_A375_DGR1_1.1581,4_A375_DGR1_1.1582	-1929, 451, -1967, 450, 9773, 7215, -1928, 1153, 3665, 6430, 9284	upstream, upstream, downstream, upstream, upstream, upstream, upstream, upstream, upstream	1	1	1	15.33	16	19.83	6	2_A375_pAU37_dut_lncRNA_AR_1	27	Gene CCDC88B	CCDC88B, DIP4	coiled-coil domain containing 88B	NM_032940, NCT14388.2	204859_at, 204810_s_at, 212260_at	NP_116329.2, EAW74446.1
GeneID:84	POSL1	11	65,959,992	65,967,997	8,005	+	12	1_A375_pAU7_mut_lncRNA_AR_1.1183,1_A375_pAU7_mut_lncRNA_AR_1.1184,2_A375_pAU37_dut_lncRNA_AR_1.1656,2_A375_pAU37_dut_lncRNA_AR_1.1657,2_A375_pAU37_dut_lncRNA_AR_1.1658,2_A375_pAU37_dut_lncRNA_AR_1.1659,2_A375_pAU37_dut_lncRNA_AR_1.1660,2_A375_pAU37_dut_lncRNA_AR_1.1577,4_A375_DGR1_1.1578,4_A375_DGR1_1.1579,4_A375_DGR1_1.1580,4_A375_DGR1_1.1581,4_A375_DGR1_1.1582	12691, 9991, 2883, 12109, 9829, 949, 17429, 12691, 5999, 8237, 3829, 733	downstream, downstream, upstream, downstream, upstream, downstream, upstream, downstream, upstream	1	1	1	13.71	17.42	19.29	7	2_A375_pAU37_dut_lncRNA_AR_1	27	Gene POSL1	PAN, PRAF, POSL1, bb1	POSH-like adaptor 1	NM_038438, NCT23145081.0	224420_at	NP_056251.1, EAW74449.1
GeneID:83	C11orf8	11	65,984,281	65,988,831	2,230	+	9	1_A375_pAU7_mut_lncRNA_AR_1.1185,2_A375_pAU37_dut_lncRNA_AR_1.1661,2_A375_pAU37_dut_lncRNA_AR_1.1659,2_A375_pAU37_dut_lncRNA_AR_1.1660,2_A375_pAU37_dut_lncRNA_AR_1.1582,4_A375_DGR1_1.1556,4_A375_DGR1_1.1588,4_A375_DGR1_1.1587	3171, -333, 3073, -317, 6223, 7331, 1274, -1501, -1823	downstream, upstream, downstream, upstream, downstream, upstream, upstream	1	1	1	26.57	28.43	15.14	7	2_A375_pAU37_dut_lncRNA_AR_1	13	Gene C11orf66	RI-EGI, FB29, C11orf66	ribonuclease/angiogenin inhibitor 1 pseudogene 66	NM_031480, NM_001113853, NCT19403418.0, NCT23145020.0	221324_at	NP_113638.2, NP_001129107.1, EAW74470.1, EAW74471.1
GeneID:10	DRAP1	11	65,988,726	65,989,945	2,220	+	9	1_A375_pAU7_mut_lncRNA_AR_1.1185,1_A375_pAU7_mut_lncRNA_AR_1.1186,2_A375_pAU37_dut_lncRNA_AR_1.1659,2_A375_pAU37_dut_lncRNA_AR_1.1660,2_A375_pAU37_dut_lncRNA_AR_1.1582,4_A375_DGR1_1.1556,4_A375_DGR1_1.1588,4_A375_DGR1_1.1587	-3366, 93, -3272, 125, -5320, -7325, -1376, 1304, 9432	upstream, upstream, upstream, upstream, upstream, upstream, upstream	1	1	1	26.57	28.43	15.14	7	2_A375_pAU37_dut_lncRNA_AR_1	13	Gene DRAP1	DRAP1, NC2-alpha	DR1-associated protein 1 (negative cofactor 2 alpha)	NM_006642, NCT14392.2	202258_at, 230160_x_at	NP_006633.2, EAW74472.1
GeneID:28	TSGA10	11	65,715,115	65,727,454	14,319	+	5	1_A375_pAU7_mut_lncRNA_AR_1.1185,2_A375_pAU37_dut_lncRNA_AR_1.1661,2_A375_pAU37_dut_lncRNA_AR_1.1586	18621, 16037, 1859	downstream, downstream, upstream	1	1	1	56.5	50	13.5	2	1_A375_pAU37_dut_lncRNA_AR_1	25	Gene TSGA10IP	FLJ32550, MGC129465, TSGA10IP, FAM161C, MGC129465, MGC129466	testis specific, 10 interacting protein	NM_152782, NCT23131116.0	1553652_at	NP_689975.2, EAW74479.1
GeneID:89	SART1	11	65,729,160	65,747,807	18,647	+	2	1_A375_pAU7_mut_lncRNA_AR_1.1185,2_A375_pAU37_dut_lncRNA_AR_1.1661	-24, -8	upstream, upstream	1	1	0	105	98	11	1	1_A375_pAU37_dut_lncRNA_AR_1	25	Gene SART1	MGC2030, Sart98, SMNRP110, SART1, Ant1, SART1.99, HOM61	squamous cell carcinoma antigen recognized by T cells	NM_005146, NCT14413.2, NCT23131116.0	200081_at	NP_005137.1, EAW74475.1, EAW74474.1
GeneID:64	EIF1AD	11	65,764,017	65,769,876	5,861	-	2	1_A375_pAU7_mut_lncRNA_AR_1.1189,2_A375_pAU37_dut_lncRNA_AR_1.1662	-162, -33	upstream, upstream	1	1	0	30	27	14	1	1_A375_pAU37_dut_lncRNA_AR_1	30	Gene EIF1AD	MGC11102, EIF1AD, bagosin	eukaryotic translation initiation factor 1A domain containing	NM_032325, NCT14412.3, NCT23144971.1, NCT23144991.1, NCT23145001.1, NCT23614080.0	223982_s_at, 223077_at	NP_115701.2, EAW74479.1, EAW74476.1, EAW74480.1, EAW74481.1, EAW74482.1
GeneID:56	BNIP1	11	65,769,930	65,777,617	7,687	+	2	1_A375_pAU7_mut_lncRNA_AR_1.1189,2_A375_pAU37_dut_lncRNA_AR_1.1662	210, 61	upstream, upstream	1	1	0	30	27	14	1	1_A375_pAU37_dut_lncRNA_AR_1	30	Gene BNIP1	BNIP, BNIP1, MGC11181, BCRP1, DKFZp564	Bcl-2/adenovirus E1B 19kDa interacting protein 1	NM_033995, NM_001143955, NCT14393.4, NCT23131191.1, NCT23131211.1, NCT23131232.1	210125_s_at	NP_035151.1, NP_001129437.1, EAW74483.1, EAW74484.1, EAW74485.1, EAW74486.1
GeneID:14	CSTB	11	65,779,482	65,780,978	1,514	+	2	1_A375_pAU7_mut_lncRNA_AR_1.1189,2_A375_pAU37_dut_lncRNA_AR_1.1662	-9702, -9551	upstream, upstream	1	1	0	30	27	14	1	1_A375_pAU37_dut_lncRNA_AR_1	30	Gene CSTB	CSTB		NM_000100, NM_001130691, NCT14393.4, NCT23131211.1, NCT23131232.1	200838_at, 231240_at	NP_000091.1, EAW74487.1
GeneID:10	CATSPER1	11	65,784,233	65,793,968	9,735	+	1	A_A375_DGR1_1.1569	1369	upstream	0	0	1	3	8	16	1	A_A375_DGR1_1.1	16	Gene CATSPER1	MGC33390, CATSPER1, CATSPER, MGC33338	calcium channel, sperm associated 1	NM_053054, NCT14414.2, NCT23144960.0	1552233_at	NP_444282.2, EAW74488.1, EAW74489.1
GeneID:89	GALSYT1	11	65,806,238	65,816,851	9,615	-	2	1_A375_pAU7_mut_lncRNA_AR_1.1190,2_A375_pAU37_dut_lncRNA_AR_1.1663	-3125, -3349	upstream, upstream	1	1	0	25	20	14	1	1_A375_pAU37_dut_lncRNA_AR_1	25	Gene GALSYT2	GALSYT2, GALSYT2, MGC142112, MGC142114, GALSYT-2	galactose-3-O-sulfotransferase 2	NM_020390, NCT14389.4	1552297_at	NP_149025.1, EAW74490.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.10992	SF3B2	11	65,819,816	65,836,382	16,566	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1190, 2_A375_pNL97_plus_lncRNA_AR..1..1663	-40, 164	upstream, in gene	1	1	0	25	20	14	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene SF3B2	SF3b1, SF3B145, SF3B2, SAP145, SF3b150, Cus1	splicing factor 3b, subunit 2, 145kDa	NM_006842, hCT14395.3, hCT2350265.0, hCT2350266.0, hCT2350267.0, hCT2350268.0, hCT2350269.0, hCT2350270.0, hCT2350271.0, hCT2350272.0, hCT2350273.0, hCT2350274.0	1558230_at, 200619_at	NP_006833.2, EAW74492.1, EAW74493.1, EAW74496.1, EAW74499.1, EAW74500.1, EAW74491.1, EAW74494.1, EAW74495.1, EAW74497.1, EAW74498.1, EAW74501.1
GeneID.64837	KLC2	11	66,024,765	66,035,332	10,567	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1664, 2_A375_pNL97_plus_lncRNA_AR..1..1665, 4_A375_EGR1..1..1590	463, 10461, 619	in gene, in gene, in gene	0	1	1	15.5	17	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene KLC2	KLC2, FLJ12387	kinesin light chain 2	NM_022822, NM_001134774, NM_001134775, NM_001134776, hCT2350675.0	218906_x_at	NP_073733.1, NP_001128246.1, NP_001128247.1, NP_001128248.1, EAW74507.1
GeneID.81876	RAB1B	11	66,036,056	66,044,963	8,907	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1664, 2_A375_pNL97_plus_lncRNA_AR..1..1665, 4_A375_EGR1..1..1591	-10808, -830, 14024	upstream, upstream, downstream	0	1	1	13.67	16.33	17.33	3	4_A375_EGR1..1	21	Gene RAB1B	RAB1B		NM_030981	220984_s_at	NP_112243.1
GeneID.254263	CNIH2	11	66,045,696	66,051,683	5,987	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1191, 2_A375_pNL97_plus_lncRNA_AR..1..1665, 2_A375_pNL97_plus_lncRNA_AR..1..1666, 4_A375_EGR1..1..1591	11424, -10470, 11648, 4364	downstream, upstream, downstream, in gene	1	1	1	16.67	18	16	3	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene CNIH2	CNIH2, Cnil, MGC50896, CNIH-2	cornichon homolog 2 (Drosophila)	NM_182553, hCT2350674.0	230070_at	NP_872359.1, EAW74508.1
GeneID.10897	YIF1A	11	66,052,051	66,056,638	4,587	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1191, 2_A375_pNL97_plus_lncRNA_AR..1..1666, 4_A375_EGR1..1..1591	-482, -708, 6556	upstream, upstream, downstream	1	1	1	18	19.5	16.5	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene YIF1A	YIF1P, 54TM, FinGER7, YIF1A, YIF1	Yip1 interacting factor homolog A (S. cerevisiae)	NM_020470, hCT2314492.0	202418_at	NP_065203.2, EAW74509.1
GeneID.256472	TMEM151A	11	66,059,373	66,064,135	4,762	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1191, 2_A375_pNL97_plus_lncRNA_AR..1..1666, 4_A375_EGR1..1..1591	-2253, -2029, -9293	upstream, upstream, upstream	1	1	1	18	19.5	16.5	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene TMEM151A	TMEM151, MGC33486, TMEM151A	transmembrane protein 151A	NM_153266, hCT11363.3	235614_at	NP_694998.1, EAW74510.1
GeneID.9610	RIN1	11	66,099,542	66,104,000	4,458	-	7	1_A375_pNL7_minus_lncRNA_AR..1..1192, 1_A375_pNL7_minus_lncRNA_AR..1..1193, 2_A375_pNL97_plus_lncRNA_AR..1..1667, 4_A375_EGR1..1..1592, 4_A375_EGR1..1..1593, 4_A375_EGR1..1..1594, 4_A375_EGR1..1..1595	-64, -6352, -96, 898, -896, -6526, 10616	upstream, upstream, upstream, in gene, upstream, upstream, upstream	1	1	1	20.5	21.25	16.75	4	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene RIN1	RIN1		NM_004292, hCT11362.2	205211_s_at	NP_004283.2, EAW74512.1
GeneID.25855	BRMS1	11	66,104,804	66,112,582	7,778	-	9	1_A375_pNL7_minus_lncRNA_AR..1..1192, 1_A375_pNL7_minus_lncRNA_AR..1..1193, 1_A375_pNL7_minus_lncRNA_AR..1..1194, 2_A375_pNL97_plus_lncRNA_AR..1..1667, 4_A375_EGR1..1..1592, 4_A375_EGR1..1..1593, 4_A375_EGR1..1..1594, 4_A375_EGR1..1..1595, 4_A375_EGR1..1..1596	8518, 230, -2970, 8466, 9476, 7668, 54, -2234, -3002	downstream, in gene, upstream, downstream, downstream, in gene, in gene, upstream, upstream	1	1	1	20.6	19.8	17.6	5	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene BRMS1	DKFZp564A063, BRMS1	breast cancer metastasis suppressor 1	NM_015399, NM_001024957, hCT11365.4, hCT1984667.1, hCT1984668.1, hCT1984669.1	215631_s_at	NP_056214.1, NP_001020128.1, EAW74513.1, EAW74514.1, EAW74515.1, EAW74516.1
GeneID.11041	B3GNT1	11	66,112,843	66,115,161	2,318	-	9	1_A375_pNL7_minus_lncRNA_AR..1..1192, 1_A375_pNL7_minus_lncRNA_AR..1..1193, 1_A375_pNL7_minus_lncRNA_AR..1..1194, 2_A375_pNL97_plus_lncRNA_AR..1..1667, 4_A375_EGR1..1..1592, 4_A375_EGR1..1..1593, 4_A375_EGR1..1..1594, 4_A375_EGR1..1..1595, 4_A375_EGR1..1..1596	11097, 2609, -391, 11065, 12057, 10265, 2633, 345, -423	downstream, downstream, upstream, downstream, downstream, downstream, downstream, in gene, upstream	1	1	1	20.6	19.8	17.6	5	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene B3GNT1	iGNT, B3GNT1, iGAT, BETA3GNTI, B3GNT6, B3GN-T1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	NM_006876, hCT11247.3, hCT2310830.0	203188_at, 228203_at	NP_006867.1, EAW74517.1, EAW74518.1
GeneID.3177	SLC29A2	11	66,129,992	66,139,291	9,299	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1668	571	in gene	0	1	0	14	17	18	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene SLC29A2	DER12, ENT2, SLC29A2, HNP36	solute carrier family 29 (nucleoside transporters), member 2	NM_001532, hCT11384.3, hCT2310825.0, hCT2310828.0, hCT2310829.0	1553540_a_at, 1560082_at, 1560149_at, 1560151_x_at, 204717_s_at	NP_001523.2, EAW74519.1, EAW74520.1, EAW74521.1, EAW74522.1
GeneID.100505504	LOC100505504	11	66,176,665	66,184,608	7,943	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1195, 1_A375_pNL7_minus_lncRNA_AR..1..1196, 1_A375_pNL7_minus_lncRNA_AR..1..1197, 2_A375_pNL97_plus_lncRNA_AR..1..1669, 4_A375_EGR1..1..1597	-313, 9871, 12567, 12583, 12103	upstream, downstream, downstream, downstream, downstream	1	1	1	125.5	140	14	2	2_A375_pNL97_plus_lncRNA_AR..1	262	Gene LOC100505504		hypothetical LOC100505504	XR_110921		
GeneID.266743	NPAS4	11	66,188,475	66,194,177	5,702	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1196, 1_A375_pNL7_minus_lncRNA_AR..1..1197, 2_A375_pNL97_plus_lncRNA_AR..1..1669, 4_A375_EGR1..1..1597	-2139, 757, 773, 293	upstream, in gene, in gene, in gene	1	1	1	235	262	16	1	2_A375_pNL97_plus_lncRNA_AR..1	262	Gene NPAS4	Le-PAS, NPAS4, NXF, bHLHe79, PASD10	neuronal PAS domain protein 4	NM_178864, hCT1813988.2	1554299_at, 240794_at	NP_849195.2, EAW74525.1
GeneID.65003	MRPL11	11	66,202,550	66,206,310	3,760	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1198, 2_A375_pNL97_plus_lncRNA_AR..1..1670, 2_A375_pNL97_plus_lncRNA_AR..1..1671	-122, -154, -4922	upstream, upstream, upstream	1	1	0	23.5	21.5	11	2	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene MRPL11	L11MT, CGI-113, MRPL11, MRP-L11, MGC111024	mitochondrial ribosomal protein L11	NM_016050, NM_170738, NM_170739, hCT2310821.0, hCT2310822.0, hCT2310823.0, hCT2310824.0, hCT2355292.0, hCT2355293.0	219162_s_at	NP_057134.1, NP_733934.1, NP_733935.1, EAW74526.1, EAW74529.1, EAW74530.1, EAW74527.1, EAW74528.1, EAW74531.1
GeneID.246330	PELI3	11	66,234,336	66,244,808	10,472	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1199, 2_A375_pNL97_plus_lncRNA_AR..1..1672, 4_A375_EGR1..1..1598	13728, 13584, 9248	downstream, downstream, in gene	1	1	1	19.5	18.5	16.5	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene PELI3	MGC35521, PELI3	pellino homolog 3 (Drosophila)	NM_145065, NM_001098510, hCT11745.4, hCT2310136.1, hCT2310138.1, hCT2310142.1, hCT2350698.0	235431_s_at, 244214_at	NP_659502.2, NP_001091980.1, EAW74532.1, EAW74533.1, EAW74534.1, EAW74536.1, EAW74535.1
GeneID.100505554	LOC100505554	11	66,244,817	66,247,706	2,889	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1199, 2_A375_pNL97_plus_lncRNA_AR..1..1672, 4_A375_EGR1..1..1598	-358, -214, 4122	upstream, upstream, downstream	1	1	1	19.5	18.5	16.5	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene LOC100505554		hypothetical LOC100505554	XR_111186, XR_110922, XR_114501		
GeneID.10072	DPP3	11	66,247,880	66,277,130	29,250	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1199, 2_A375_pNL97_plus_lncRNA_AR..1..1672, 4_A375_EGR1..1..1598	184, 40, -4298	in gene, in gene, upstream	1	1	1	19.5	18.5	16.5	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene DPP3	FLJ11387, FLJ22331, DPPIII, DPP3	dipeptidyl-peptidase 3	NM_005700, NM_130443	218567_x_at, 232510_s_at	NP_005691.2, NP_569710.2
GeneID.254359	ZDHHC24	11	66,306,735	66,313,671	6,936	-	1	4_A375_EGR1..1..1599	-857	upstream	0	0	1	4	8	19	1	4_A375_EGR1..1	19	Gene ZDHHC24	ZDHHC24		NM_207340, hCT11744.2	205834_x_at, 227549_x_at, 232091_s_at	NP_997223.1, EAW74545.1
GeneID.89	ACTN3	11	66,314,391	66,330,797	16,406	+	1	4_A375_EGR1..1..1599	137	in gene	0	0	1	4	8	19	1	4_A375_EGR1..1	19	Gene ACTN3	MGC117005, MGC117002, ACTN3	actinin, alpha 3	NM_001104, hCT11741.3	206891_at	NP_001095.1, EAW74546.1
GeneID.10432	RBM14	11	66,384,053	66,397,405	13,352	+	1	4_A375_EGR1..1..1600	43	in gene	0	0	1	12	16	19	1	4_A375_EGR1..1	19	Gene RBM14	RBM14, TMEM137, MGC31756, SIP, SYTIP1, MGC15912, COAA, DKFZp779J0927, PSP2	RNA binding motif protein 14	NM_006328, hCT11219.4, hCT1981280.1	1555639_a_at, 204178_s_at	NP_006319.1, EAW74552.1, EAW74553.1
GeneID.83759	RBM4B	11	66,432,469	66,445,275	12,806	-	1	4_A375_EGR1..1..1601	-133	upstream	0	0	1	14	14	23	1	4_A375_EGR1..1	23	Gene RBM4B	RBM4B, RBM4L, RBM30, MGC10871, ZCCHC15, ZCRB3B	RNA binding motif protein 4B	NM_031492, hCT1641439.3	209497_s_at	NP_113680.1, EAW74558.1
GeneID.6712	SPTBN2	11	66,452,720	66,488,870	36,150	-	1	4_A375_EGR1..1..1601	43462	downstream	0	0	1	14	14	23	1	4_A375_EGR1..1	23	Gene SPTBN2	GTRAP41, SCA5, SPTBN2	spectrin, beta, non-erythrocytic 2	NM_006946, hCT1984044.1, hCT1984045.1, hCT2310610.0	205155_s_at	NP_008877.1, EAW74561.1, EAW74559.1, EAW74560.1
GeneID.79703	C11orf80	11	66,512,207	66,610,967	98,760	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1673	17565	in gene	0	1	0	11	16	5	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C11orf80	C11orf80, FLJ22531	chromosome 11 open reading frame 80	NM_024650, hCT2310175.0, hCT2310176.0	204922_at, 236593_at	NP_078926.3, EAW74562.1, EAW74563.1
GeneID.9986	RCE1	11	66,610,883	66,614,003	3,120	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1200, 2_A375_pNL97_plus_lncRNA_AR..1..1674	13117, 12989	downstream, downstream	1	1	0	19	16	12	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene RCE1	RCE1B, FACE2, RCE1A, RCE1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	NM_005133, NM_001032279, hCT2310178.0, hCT2310179.0, hCT2310180.0	205332_at, 205333_s_at	NP_005124.1, NP_001027450.1, EAW74565.1, EAW74566.1, EAW74567.1
GeneID.5091	PC	11	66,615,997	66,725,847	109,850	-	8	1_A375_pNL7_minus_lncRNA_AR..1..1200, 1_A375_pNL7_minus_lncRNA_AR..1..1201, 2_A375_pNL97_plus_lncRNA_AR..1..1674, 2_A375_pNL97_plus_lncRNA_AR..1..1675, 2_A375_pNL97_plus_lncRNA_AR..1..1676, 4_A375_EGR1..1..1602, 4_A375_EGR1..1..1603, 4_A375_EGR1..1..1604	101847, 66039, 101975, 66007, 119, 100332, 98711, 97223	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	18	20.5	14.17	6	2_A375_pNL97_plus_lncRNA_AR..1	57	Gene PC	PC, PCB	pyruvate carboxylase	NM_022172, NM_000920, NM_001040716, hCT1966921.1, hCT1966922.0, hCT1966923.1, hCT2310598.0, hCT2310603.0	204476_s_at	NP_071504.2, NP_000911.2, NP_001035806.1, EAW74568.1, EAW74570.1, EAW74572.1, EAW74569.1, EAW74571.1
GeneID.78999	LRFN4	11	66,624,876	66,627,946	3,070	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1200, 2_A375_pNL97_plus_lncRNA_AR..1..1674, 4_A375_EGR1..1..1602, 4_A375_EGR1..1..1603, 4_A375_EGR1..1..1604	-876, -1004, 639, 2280, 3746	upstream, upstream, in gene, in gene, downstream	1	1	1	12.75	11	16.75	4	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene LRFN4	SALM3., MGC3103, FIGLER6, SALM3, LRFN4	leucine rich repeat and fibronectin type III domain containing 4	NM_024036, hCT11699.3, hCT2310182.0	219491_at	NP_076941.2, EAW74573.1, EAW74574.1
GeneID.254439	C11orf86	11	66,742,754	66,744,479	1,725	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1677	-4386	upstream	0	1	0	22	25	4	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene C11orf86	FLJ22675, C11orf86	chromosome 11 open reading frame 86	NM_001136485	233938_at	NP_001129957.1
GeneID.156	ADRBK1	11	67,033,905	67,054,029	20,124	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1678, 4_A375_EGR1..1..1605, 4_A375_EGR1..1..1606	22319, 15364, 16463	downstream, in gene, in gene	0	1	1	7.67	10	15	3	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ADRBK1	BARK1, FLJ16718, BETA-ARK1, GRK2, ADRBK1	adrenergic, beta, receptor kinase 1	NM_001619, hCT11218.3, hCT2310192.0	201401_s_at, 201402_at, 38447_at	NP_001610.2, EAW74581.1, EAW74582.1
GeneID.338692	ANKRD13D	11	67,056,762	67,069,955	13,193	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1202, 2_A375_pNL97_plus_lncRNA_AR..1..1678, 2_A375_pNL97_plus_lncRNA_AR..1..1679, 4_A375_EGR1..1..1605, 4_A375_EGR1..1..1606	14358, -538, 14276, -7493, -6394	downstream, upstream, downstream, upstream, upstream	1	1	1	12.5	15.5	13.75	4	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene ANKRD13D	MGC50828, ANKRD13D	ankyrin repeat domain 13 family, member D	NM_207354, NR_030767, hCT12149.3, hCT2310197.0, hCT2355317.0, hCT2355318.0	226205_at, 244756_at	NP_997237.2, EAW74586.1, EAW74583.1, EAW74584.1, EAW74585.1
GeneID.54961	SSH3	11	67,070,919	67,080,078	9,159	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1202, 2_A375_pNL97_plus_lncRNA_AR..1..1679, 4_A375_EGR1..1..1607	201, 121, 13981	in gene, in gene, downstream	1	1	1	21.5	23	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene SSH3	SSH3L, FLJ42240, SSH3, FLJ20515, FLJ10928	slingshot homolog 3 (Drosophila)	NM_017857, hCT12147.3, hCT1950482.1, hCT2310200.0, hCT2310201.0, hCT2310202.0, hCT2310203.0, hCT2310205.0, hCT2355307.0, hCT2355308.0, hCT2355309.0	219241_x_at, 219919_s_at, 51192_at	NP_060327.3, EAW74593.1, EAW74587.1, EAW74588.1, EAW74591.1, EAW74594.1, EAW74589.1, EAW74590.1, EAW74592.1, EAW74595.1, EAW74596.1
GeneID.100130987	LOC100130987	11	67,085,310	67,159,156	73,846	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1203, 2_A375_pNL97_plus_lncRNA_AR..1..1680, 2_A375_pNL97_plus_lncRNA_AR..1..1681, 4_A375_EGR1..1..1607, 4_A375_EGR1..1..1608	56418, 56482, 73970, -430, 47554	in gene, in gene, downstream, upstream, in gene	1	1	1	13.5	16	15.25	4	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100130987	FLJ36636	similar to hCG1815675	NR_024469		
GeneID.23529	CLCF1	11	67,131,639	67,141,648	10,009	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1203, 2_A375_pNL97_plus_lncRNA_AR..1..1680, 4_A375_EGR1..1..1608	-60, -144, 6764	upstream, upstream, in gene	1	1	1	11.5	14.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CLCF1	CISS2, CLCF1, NNT1, CLC, BSF-3, NNT-1, NR6, BSF3	cardiotrophin-like cytokine factor 1	NM_013246, NM_001166212, hCT12133.4, hCT1981288.1	219500_at	NP_037378.1, NP_001159684.1, EAW74601.1, EAW74602.1
GeneID.5883	RAD9A	11	67,159,423	67,165,883	6,460	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1681	-143	upstream	0	1	0	15	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RAD9A	RAD9A, RAD9	RAD9 homolog A (S. pombe)	NM_004584, hCT12135.4, hCT1985341.1, hCT1985342.1	1562022_s_at, 204828_at	NP_004575.1, EAW74605.1, EAW74604.1, EAW74606.1
GeneID.5499	PPP1CA	11	67,165,652	67,169,376	3,724	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1681	10098	downstream	0	1	0	15	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PPP1CA	PP1alpha, MGC15877, PP-1A, PPP1CA, PPP1A, MGC1674	protein phosphatase 1, catalytic subunit, alpha isoform	NM_002708, NM_206873, NM_001008709, hCT12142.4, hCT1985352.1, hCT1985354.1, hCT2355267.0	200846_s_at	NP_002699.1, NP_996756.1, NP_001008709.1, EAW74608.1, EAW74609.1, EAW74610.1, EAW74607.1
GeneID.374403	TBC1D10C	11	67,171,412	67,177,560	6,148	+	1	4_A375_EGR1..1..1609	14906	downstream	0	0	1	6	8	18	1	4_A375_EGR1..1	18	Gene TBC1D10C	FLJ00332, CARABIN, MGC46488, TBC1D10C	TBC1 domain family, member 10C	NM_198517, hCT1985358.1, hCT1985357.0, hCT1985360.0, hCT2355326.0, hCT2355327.0	228256_at	NP_940919.1, EAW74614.1, EAW74611.1, EAW74612.1, EAW74613.1, EAW74615.1
GeneID.57571	ATPGD1	11	67,183,149	67,193,078	9,929	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1682, 4_A375_EGR1..1..1609	12787, 3171	downstream, in gene	0	1	1	9.5	17.5	16	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene ATPGD1	CARNS1, ATPGD1, KIAA1394	ATP-grasp domain containing 1	NM_020811, NM_001166222	228984_at	NP_065862.1, NP_001159694.1
GeneID.6199	RPS6KB2	11	67,195,935	67,202,879	6,944	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1682, 4_A375_EGR1..1..1609	1, -9615	in gene, upstream	0	1	1	9.5	17.5	16	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene RPS6KB2	P70-beta-1, S6K-beta2, p70S6Kb, STK14B, KLS, P70-beta, SRK, S6K2, RPS6KB2, P70-beta-2, p70(S6K)-beta	ribosomal protein S6 kinase, 70kDa, polypeptide 2	NM_003952, hCT12140.3, hCT1981292.1, hCT2310427.0, hCT2310430.0	203777_s_at	NP_003943.2, EAW74620.1, EAW74618.1, EAW74619.1, EAW74621.1
GeneID.5790	PTPRCAP	11	67,202,981	67,205,153	2,172	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1682	9217	downstream	0	1	0	13	29	14	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene PTPRCAP	MGC138602, PTPRCAP, MGC138603, CD45-AP, LPAP	protein tyrosine phosphatase, receptor type, C-associated protein	NM_005608, hCT2312505.1	204960_at	NP_005599.1, EAW74622.1
GeneID.57175	CORO1B	11	67,205,518	67,211,263	5,745	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1682	15327	downstream	0	1	0	13	29	14	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene CORO1B	DKFZp762I166, CORONIN-2, CORO1B	coronin, actin binding protein, 1B	NM_020441, NM_001018070, hCT2312503.0, hCT2312508.0, hCT2312509.0, hCT2355339.0	221754_s_at, 64486_at	NP_065174.1, NP_001018080.1, EAW74623.1, EAW74624.1, EAW74625.1, EAW74626.1
GeneID.57010	CABP4	11	67,222,818	67,229,245	6,427	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1204, 2_A375_pNL97_plus_lncRNA_AR..1..1683	14046, 14014	downstream, downstream	1	1	0	25	29	16	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene CABP4	CABP4, CSNB2B	calcium binding protein 4	NM_145200, hCT1639891.4, hCT2310432.1, hCT2310434.1, hCT2310435.1	1552890_a_at, 1554201_at, 1554202_x_at	NP_660201.1, EAW74628.1, EAW74627.1, EAW74629.1, EAW74630.1
GeneID.80194	TMEM134	11	67,231,819	67,236,731	4,912	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1204, 2_A375_pNL97_plus_lncRNA_AR..1..1683	-133, -101	upstream, upstream	1	1	0	25	29	16	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene TMEM134	TMEM134, FLJ21749, MGC149891	transmembrane protein 134	NM_025124, NM_001078651, NM_001078650, hCT1965516.1, hCT1965518.1, hCT1965521.1, hCT2355368.0, hCT2355369.0, hCT2355370.0	1558712_at, 218531_at, 233018_at	NP_079400.1, NP_001072119.1, NP_001072118.1, EAW74632.1, EAW74633.1, EAW74634.1, EAW74631.1, EAW74635.1, EAW74636.1
GeneID.9049	AIP	11	67,250,505	67,258,579	8,074	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1684	295	in gene	0	1	0	20	15	11	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene AIP	SMTPHN, XAP2, FKBP16, AIP, FKBP37, ARA9	aryl hydrocarbon receptor interacting protein	NM_003977, hCT12139.2	201761_s_at, 201762_s_at	NP_003968.2, EAW74637.1
GeneID.9600	PITPNM1	11	67,259,239	67,272,843	13,604	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1205, 2_A375_pNL97_plus_lncRNA_AR..1..1684, 2_A375_pNL97_plus_lncRNA_AR..1..1685	-3253, 22043, -2549	upstream, downstream, upstream	1	1	0	20.5	15.5	12	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene PITPNM1	PITPNM1, Rd9, NIR2, PITPNM, DRES9, RDGB, RDGBA1, RDGBA, RDGB1, FLJ44997	phosphatidylinositol transfer protein, membrane-associated 1	NM_004910, NM_001130848, hCT12137.4, hCT1965344.1, hCT1965345.1, hCT2312499.0, hCT2355251.0, hCT2355252.0	203826_s_at	NP_004901.2, NP_001124320.1, EAW74638.1, EAW74639.1, EAW74642.1, EAW74643.1, EAW74640.1, EAW74641.1
GeneID.10263	CDK2AP2	11	67,273,968	67,276,102	2,134	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1205, 2_A375_pNL97_plus_lncRNA_AR..1..1685, 4_A375_EGR1..1..1610	6, 710, -8018	in gene, in gene, upstream	1	1	1	14	11	14	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene CDK2AP2	FLJ10636, CDK2AP2, DOC-1R, p14	cyclin-dependent kinase 2 associated protein 2	NM_005851, hCT12138.2	203252_at	NP_005842.1, EAW74644.1
GeneID.51475	CABP2	11	67,286,418	67,290,899	4,481	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1205, 4_A375_EGR1..1..1610	14803, 6779	downstream, downstream	1	0	1	14	11	14	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene CABP2	CABP2	calcium binding protein 2	NM_016366, NM_031204, hCT12144.2, hCT1984057.0, hCT2355272.0	207745_at	NP_057450.2, NP_112481.2, EAW74645.1, EAW74646.1, EAW74647.1

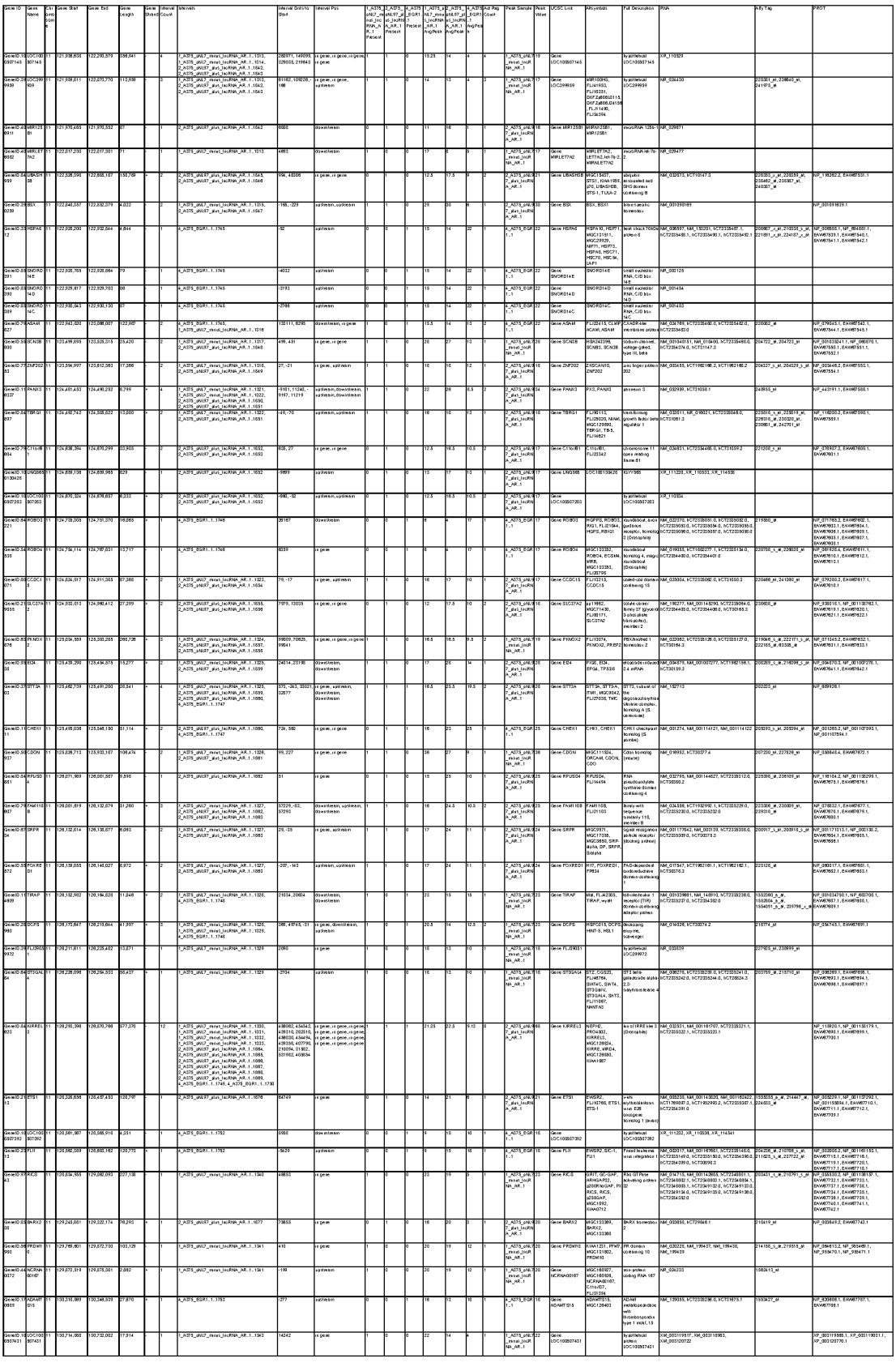
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_uNG7_myLNG7_plus_lncRNA_AR_1 Percent	2_A375_uNG7_plus_lncRNA_AR_1 Percent	4_A375_EGR1_lncRNA_AR_1 Percent	1_A375_plus_lncRNA_AR_1 AvgRank	2_A375_plus_lncRNA_AR_1 AvgRank	4_A375_EGR1_lncRNA_AR_1 AvgRank	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:19 3909621	LOC100 383621	11	87,270,251	87,274,177	3,926	-	2	2_A375_uNG7_plus_lncRNA_AR_1.1699, 4_A375_EGR1_1.1611	1191, -1934	upstream, upstream	0	1	1	13.5	16	15.5	2	2_A375_uNG7_plus_lncRNA_AR_1	926	Gene LOC100383621	MGC129825, C11orf72, MGC129824, FLJ90234	chromosome 11 open reading frame 72	XM_003119592, XM_003119787, XM_003120707		XP_003119592.1, XP_003119835.1, XP_003120708.1
GeneID:47 23	NDUFV1	11	87,274,323	87,295,012	20,689	+	2	2_A375_uNG7_plus_lncRNA_AR_1.1699, 4_A375_EGR1_1.1611	45, 9208	vs gene, downstream	0	1	1	13.5	16	15.5	2	2_A375_uNG7_plus_lncRNA_AR_1	926	Gene NDUFV1	Cr3/II, NDUFV1, FLJ90339, CI51KD, UQOR	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	NM_007103, NM_001169102, NCT12143.3, NCT19640331.1, NCT19640341.1, NCT19640351.1, NCT23104452.0	208714_at_227793_at	NP_009094.2, NP_001158574.1, EAW74852.1, EAW74854.1, EAW74855.1, EAW74856.1, EAW74853.1
GeneID:28 4332	NUDT6	11	87,393,409	87,397,401	3,992	-	2	4_A375_EGR1_1.1612, 4_A375_EGR1_1.1613	428, -4193	vs gene, upstream	0	0	1	16.5	16	16.5	2	4_A375_EGR1_1	919	Gene NUDT6	FLJ41567, NUDT6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	NM_181843, NCT19653941.1, NCT23553721.0		NP_853528.1, EAW74890.1, EAW74891.1
GeneID:54 7585	TBX19	11	87,396,774	87,407,851	11,077	-	2	4_A375_EGR1_1.1612, 4_A375_EGR1_1.1613	10653, -72	downstream, upstream	0	0	1	16.5	16	16.5	2	4_A375_EGR1_1	919	Gene TBX19	TBX19, TBX13, TBX7	T-box 19	NM_033995, NCT12134.4	207689_at_222277_at	NP_036995.2, EAW74882.1
GeneID:81 703	ACY3	11	87,410,026	87,416,100	6,074	-	1	4_A375_EGR1_1.1613	11026	downstream	0	0	1	19	14	19	1	4_A375_EGR1_1	919	Gene ACY3	ACY-3, MGC97440, ACY3, HCdR1	aminoacylase 3 (provisional)	NM_030830, NCT12150.3, NCT23125351.0	1534974_at, 233451_at	NP_542385.1, EAW74883.1, EAW74884.1
GeneID:22 0	ALDH18A1	11	87,429,833	87,445,963	16,032	-	2	4_A375_EGR1_1.1614, 4_A375_EGR1_1.1615	10813, 14853	vs gene, vs gene	0	0	1	7.5	8.5	17.5	2	4_A375_EGR1_1	920	Gene ALDH18A1	ALDH6, ALDH18	aldehyde dehydrogenase 18 family, member A1	NM_002860, NM_001021813, NCT12143.3	208451_s_at_209242_s_at	NP_001028682.1, NP_001028709.1, EAW74893.1
GeneID:19 0132261	LOC100 132261	11	87,722,753	87,723,540	788	-	1	2_A375_uNG7_plus_lncRNA_AR_1.1697	146	vs gene	0	1	0	8	13	11	1	2_A375_uNG7_plus_lncRNA_AR_1	913	Gene LOC100132261		hypothetical LOC100132261			
GeneID:81 822	UNC93B1	11	87,756,875	87,771,993	15,119	-	2	2_A375_uNG7_plus_lncRNA_AR_1.1695, 4_A375_EGR1_1.1617	-5951, 673	upstream, vs gene	0	1	1	9.5	15	13	2	2_A375_uNG7_plus_lncRNA_AR_1	922	Gene UNC93B1	UNC93, MGC129817, Unc-93B1, UNC-93B1, UNC93B	unc-93 homolog B1 (C. elegans)	NM_030930, NCT23125351.0, NCT23125352.0	220950_s_at_220951_s_at	NP_112192.2, EAW74877.1, EAW74878.1
GeneID:22 1	ALDH3B1	11	87,776,046	87,795,743	20,895	+	7	2_A375_uNG7_plus_lncRNA_AR_1.1695, 2_A375_uNG7_plus_lncRNA_AR_1.1696, 4_A375_EGR1_1.1617, 4_A375_EGR1_1.1618, 4_A375_EGR1_1.1619, 4_A375_EGR1_1.1620, 4_A375_EGR1_1.1621	1808, 19832, 8220, 16400, 24484, 29380, 33044	vs gene, vs gene, upstream, vs gene, downstream, downstream, downstream, downstream	0	1	1	11.14	12	13.43	7	2_A375_uNG7_plus_lncRNA_AR_1	922	Gene ALDH3B1	ALDH, ALDH3B1, FLJ28433, ALDH7, FLJ36710	aldehyde dehydrogenase 3 family, member B1	NM_000694, NM_001003910, NM_001161472, NCT11522.2, NCT23104332.0, NCT23104340.0, NCT23053710.0, NCT23053724.0	1565731_at_203840_at, 211084_s_at	NP_000685.1, NP_001025161.1, NP_001154445.1, EAW74876.1, EAW74880.1, EAW74881.1, EAW74878.1, EAW74882.1, EAW74883.1
GeneID:47 28	NDUFS1	11	87,795,094	87,894,114	99,020	+	4	2_A375_uNG7_plus_lncRNA_AR_1.1699, 4_A375_EGR1_1.1619, 4_A375_EGR1_1.1620, 4_A375_EGR1_1.1621	-2424, 2420, 3284, 8106	upstream, vs gene, vs gene, downstream	0	1	1	12.25	11.25	13.25	4	2_A375_uNG7_plus_lncRNA_AR_1	920	Gene NDUFS1	CI-75kD, NDUFS1, TYKY, Cr-2ck	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	NM_004494, NCT11233.7, NCT18127.1, NCT23104360.0, NCT23053270.0	202169_s_at_203190_at, 232169_x_at	NP_003437.1, EAW74888.1, EAW74889.1, EAW74887.1, EAW74890.1
GeneID:10 512	TCIRG1	11	87,896,465	87,916,366	19,901	-	3	4_A375_EGR1_1.1619, 4_A375_EGR1_1.1620, 4_A375_EGR1_1.1621	-5971, -5075, -291	upstream, upstream, upstream	0	0	1	8.33	8.33	19.67	3	4_A375_EGR1_1	919	Gene TCIRG1	a3, OPTB1, OC116, Vph1, Ac116, OC-116kDa, TIRC7, Bt-/, ATP6N1C, ATP6V0A3, TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	NM_006019, NM_006053, NCT16985.2, NCT23104491.0, NCT23104582.0, NCT23104583.0	204156_s_at	NP_006010.2, NP_006044.1, EAW74859.1, EAW74860.1, EAW74861.1, EAW74857.1, EAW74858.1, EAW74863.1
GeneID:51 111	SUV420H1	11	87,923,597	87,960,764	37,277	+	4	1_A375_uNG7_minus_lncRNA_AR_1.1398, 2_A375_uNG7_plus_lncRNA_AR_1.1699, 4_A375_EGR1_1.1622, 4_A375_EGR1_1.1623	-1490, -464, -346, 1712	upstream, upstream, upstream, upstream	1	1	1	15.5	21	19.5	2	2_A375_uNG7_plus_lncRNA_AR_1	927	Gene SUV420H1	KMT5B, CGI-85, SUV420H1, MGC21189, MGC118906, MGC702, MGC118907, CGI-85	suppressor of variegation 4-20 homolog 1 (Drosophila)	NM_017635, NM_016028, NCT19540.1, NCT19550.1, NCT23125351.0, NCT23125354.0, NCT23125250	219292_s_at_222598_at, 222750_at_242845_at	NP_060100.3, NP_057122.3, EAW74897.1, EAW74898.1, EAW74900.1, EAW74701.1, EAW74899.1
GeneID:23 636	C11orf24	11	88,226,693	88,239,489	12,796	-	1	2_A375_uNG7_plus_lncRNA_AR_1.1691	-278	upstream	0	1	0	14	20	15	1	2_A375_uNG7_plus_lncRNA_AR_1	920	Gene C11orf24	C11orf24, DKFZp434K1315	chromosome 11 open reading frame 24	NM_022335, NCT16327.2, NCT23125155.0, NCT23552650	218299_at_52198_at	NP_071723.1, EAW74792.1, EAW74703.1, EAW74704.1
GeneID:49 41	LRP5	11	68,030,105	68,218,743	188,638	+	3	4_A375_EGR1_1.1624, 4_A375_EGR1_1.1625, 4_A375_EGR1_1.1626	139324, 154066, 194644	vs gene, vs gene, vs gene	0	0	1	8.33	9.67	10.33	3	4_A375_EGR1_1	919	Gene LRP5	LRP5, HBCH2, LR3, OPPG, EVR4, LRP7, OPTA1, HBM, BMND1, EVR1, OPG	low density lipoprotein receptor-related protein 5	NM_002335, NCT16866.2, NCT23104497.0, NCT23104498.0	209468_at_229891_at	EAW74706.1, EAW74705.1
GeneID:59 291	SAPS2	11	86,235,166	86,362,902	154,816	+	1	4_A375_EGR1_1.1627	-555	upstream	0	0	1	17	16	24	1	4_A375_EGR1_1	924	Gene SAPS2	C11orf25, DKFZp762E1510, DKFZp761D230, PPP6R2, MGC123711, SWA1/SIT4, DKFZp761E2319, MGC123712, SAPLa, FLJ43895, SAPL, PP6R3, SAPS2, FLJ11030	SAPS domain family, member 2	NM_015512, NM_001164160, NM_001164161, NM_001164162, NM_001164163, NM_001164164, NCT16226.2, NCT23104760.0, NCT23104761.0, NCT23104772.0, NCT23104773.0, NCT23104774.0	217000_s_at_223497_s_at, 223312_at	NP_056702.2, NP_001157652.1, NP_001157653.1, NP_001157654.1, NP_001157655.1, NP_001157656.1, EAW74709.1, EAW74708.1, EAW74710.1, EAW74711.1, EAW74712.1
GeneID:21 9427	MRPL21	11	86,830,746	86,871,303	12,557	-	3	1_A375_uNG7_minus_lncRNA_AR_1.1397, 2_A375_uNG7_plus_lncRNA_AR_1.1699, 2_A375_uNG7_plus_lncRNA_AR_1.1626	-25, 29, -121	upstream, vs gene, upstream	1	1	1	27	31	29	1	2_A375_uNG7_plus_lncRNA_AR_1	931	Gene MRPL21	L21mt, MGC62012, MRPL21, MRP-L21	mitochondrial ribosomal protein L21	NM_181914, NM_181915, NCT18315.3, NCT23125351.0, NCT23554031.0, NCT23554032.0	225315_at	NP_852478.1, NP_852479.1, EAW74724.1, EAW74725.1, EAW74727.1, EAW74726.1, EAW74728.1
GeneID:38 08	IGHMBP2	11	68,871,319	68,908,099	36,780	+	3	1_A375_uNG7_minus_lncRNA_AR_1.1397, 2_A375_uNG7_plus_lncRNA_AR_1.1693, 2_A375_uNG7_plus_lncRNA_AR_1.1626	-5, -53, 105	vs gene, upstream, vs gene	1	1	1	27	31	27	1	2_A375_uNG7_plus_lncRNA_AR_1	931	Gene IGHMBP2	IGHMBP2, FLJ36235, SMUBP2, SMUBP, SMUBP-2, HCSA, HMN6, FLJ41171, CATF1	immunoglobulin mu binding protein 2	NM_002180, NCT16316.2	213960_s_at_31981_at	NP_002171.2, EAW74729.1
GeneID:11 8535	MRGPRF	11	86,771,882	86,780,850	8,968	-	1	4_A375_EGR1_1.1629	2062	vs gene	0	0	1	7	7	10	1	4_A375_EGR1_1	919	Gene MRGPRF	PCTA, DKFZp686B2122, FLJ40111, MRGPRF, GPR186, GPR140, FLJ90534, FLJ40990, MRGF, FLJ35714, MGC21627	MAS-related GPR, member F	NM_001098615, NM_145015		NP_660349.1, NP_689432.2
GeneID:26 579	MYEOV	11	69,361,632	69,384,764	23,132	+	2	1_A375_uNG7_minus_lncRNA_AR_1.1395, 1_A375_uNG7_minus_lncRNA_AR_1.1209	-4302, -7706	downstream, downstream	1	1	0	26	19.5	10	2	1_A375_uNG7_minus_lncRNA_AR_1	930	Gene MYEOV	OCIM, MYEOV	myeloma overexpressed (in a subset of t(11;14) positive multiple myeloma)	NM_138788, NCT19727.1, NCT23552096.0	227342_s_at_227343_at	NP_620123.2, EAW74741.1, EAW74740.1
GeneID:19 0609834	LOC100 609834	11	69,246,439	69,244,369	2,070	-	2	2_A375_uNG7_plus_lncRNA_AR_1.1693, 4_A375_EGR1_1.1634	-6987, -9480	upstream, upstream	0	1	1	10.5	16.5	13	2	4_A375_EGR1_1	920	Gene LOC100609834		hypothetical LOC100609834	XR_111194, XR_110008, XR_114592		
GeneID:59 5	CCND1	11	69,455,875	69,469,342	13,468	+	2	4_A375_EGR1_1.1639, 4_A375_EGR1_1.1640	2963, 7699	vs gene, vs gene	0	0	1	10.5	10.5	17.5	2	4_A375_EGR1_1	919	Gene CCND1	PRAD1, BCL1, D11S287, CCND1, D11S287E	cyclin D1	NM_053056, NCT18098.0, NCT23098581, NCT23493024.0	208712_s_at_208712_at	NP_444284.1, EAW74748.1, EAW74749.1, EAW74748.1, EAW74747.1
GeneID:22 3064	GRAOV1	11	69,490,331	69,490,965	634	-	2	2_A375_uNG7_plus_lncRNA_AR_1.1699, 2_A375_uNG7_plus_lncRNA_AR_1.1651	197, 117	vs gene, vs gene	0	1	1	26	26	17	1	2_A375_uNG7_plus_lncRNA_AR_1	928	Gene GRAOV1	FADS1, GRAOV1	cold shock domain protein 1	NM_198431, NCT19137.2, NCT23552193.0	228878_at_243511_at	NP_705152.1, EAW74749.1, EAW74750.1
GeneID:23 9	FGF4	11	69,587,797	69,590,171	2,374	-	1	4_A375_EGR1_1.1662	1275	vs gene	0	0	1	5	8	22	1	4_A375_EGR1_1	922	Gene FGF4	HST-1, HSTF1, HBGF-4, FGF4, HST, KFGF, Hst-1/KS3	fibroblast growth factor 4	NM_002007, NCT19002.3	1552662_a_at_206163_at	NP_002006.1, EAW74752.1
GeneID:23 48	FGF3	11	69,824,798	69,834,162	9,365	-	1	4_A375_EGR1_1.1664	1424	vs gene	0	0	1	7	13	21	1	4_A375_EGR1_1	921	Gene FGF3	FGF3, INT2, HBGF-3	fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog)	NM_005247, NCT19133.2, NCT23099972.0	214371_at	NP_005238.1, EAW74753.1, EAW74754.1
GeneID:55 107	ANO1	11	69,924,455	70,035,651	111,243	+	2	1_A375_uNG7_minus_lncRNA_AR_1.1212, 2_A375_uNG7_plus_lncRNA_AR_1.1697	61696, 61756	vs gene, vs gene	1	1	0	16	15	10	1	1_A375_uNG7_minus_lncRNA_AR_1	916	Gene ANO1	DRACV2, ANO1, TAOS2, FLJ10261, TMEM16A, DOG1	anoctamin 1, calcium activated chloride channel	NM_018043, NM_033911, NCT16225.3, TAOS2, FLJ10261, TMEM16A, DOG1	1553269_a_at_216834_at	NP_060115.5, EAW74736.1, EAW74737.1, EAW74739.1
GeneID:37 72	FADD	11	70,045,269	70,053,908	8,639	+	1	4_A375_EGR1_1.1648	253	vs gene	0	0	1	11	12	18	1	4_A375_EGR1_1	919	Gene FADD	GIG3, MGC9328, MORT1, FADD	Fas (TNFRSF6)-associated via death domain	NM_003824, NCT16474.10.3, NCT23099980.0, NCT23099981.0	202539_s_at	NP_003815.1, EAW74760.1, EAW74761.1, EAW74762.1
GeneID:29 17	CTTN	11	70,244,612	70,262,690	35,078	+	2	4_A375_EGR1_1.1647, 4_A375_EGR1_1.1648	824, 252	upstream, vs gene	0	0	1	15	15	16	2	4_A375_EGR1_1	919	Gene CTTN	FLJ39439, CTTN, EMS1	cortactin	NM_005231, NM_001184740, NM_138565, NCT14570.2, NCT23098730.0, NCT23098753.0, NCT23553542.0, NCT23553543.0	1565727_at_203282_at, 214075_at_214074_s_at, 214762_at_227473_at	NP_005222.2, NP_001171669.1, NP_612832.1, EAW74767.1, EAW74766.1, EAW74765.1, EAW74768.1, EAW74769.1
GeneID:23 941	SHANK2	11	70,212,961	70,333,906	120,947	-	13	1_A375_uNG7_minus_lncRNA_AR_1.1214, 2_A375_uNG7_plus_lncRNA_AR_1.1699, 2_A375_uNG7_plus_lncRNA_AR_1.1645, 4_A375_EGR1_1.1630, 4_A375_EGR1_1.1631, 4_A375_EGR1_1.1632, 4_A375_EGR1_1.1633, 4_A375_EGR1_1.1634, 4_A375_EGR1_1.1635, 4_A375_EGR1_1.1636, 4_A375_EGR1_1.1637, 4_A375_EGR1_1.1638, 4_A375_EGR1_1.1639	43166, 439232, 61156, 63185, 68416, 69131, 84120, 88956, 402899, 426560, 580712, 121664, 118400	vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene	1	1	1	10.92	13.75	16.33	12	2_A375_uNG7_plus_lncRNA_AR_1	931	Gene SHANK2	CORTBP1, KIAA0419, SHANK2, SPANK-3, CTTNBP1, SHANK	SH3 and multiple ankyrin repeat domains 2	NM_012309, NM_133266, NCT23441.20.0, NCT23441290.0, NCT23441310.0, NCT23441330.0, NCT23441340.0, NCT23441350.0, NCT23441360.0, NCT23553400.0	1564277_at_213057_at, 213385_at_213826_at, 213830_s_at_236861_at	NP_036417.2, NP_073572.2, EAW74771.1, EAW74772.1, EAW74773.1, EAW74776.1, EAW74775.1, EAW74774.1, EAW74776.1, EAW74777.1, EAW74778.1, EAW74779.1
GeneID:55 199	FAM69C	11	71,490,937	71,512,200	10,725	+	1	4_A375_EGR1_1.1662	0	vs gene	0	0	1	9	9	10	1	4_A375_EGR1_1	913	Gene FAM69C	FLJ21199, FLJ10661, MGC41599, FAM69C	family with sequence similarity 69, member C	NM_152483, NM_018172, NM_020199655, NCT23099932.1, NCT23099933.1, NCT23099934.1, NCT23099935.1, NCT23099936.1, NCT23412290.0, NCT23412300.0, NCT23553220.0	220393_at	NP_689776.1, NP_060422.2, NP_001093123.1, EAW74795.1, EAW74791.1, EAW74793.1, EAW74798.1, EAW74797.1, EAW74796.1, EAW74801.1, EAW74802.1
GeneID:55 298	RNF121	11	71,839,765	71,908,643	68,878	+	2	1_A375_uNG7_minus_lncRNA_AR_1.1215, 2_A375_uNG7_plus_lncRNA_AR_1.1701	138, 232	vs gene, vs gene	1	1	0	20	20	11	1	1_A375_uNG7_minus_lncRNA_AR_1	920	Gene RNF121	RNF121, FLJ10299	ring finger protein 121	NM_016320, NR_024147, NR_024148, NCT19224.20.1, NCT19224.21, NCT19224.22.1, NCT23553510.0, NCT23553534.0	219021_at	NP_057190.2, EAW74809.1, EAW74808.1, EAW74810.1, EAW74811.1
GeneID:49 28	NUMA1	11	71,712,911	71,791,873	77,962	+	4	1_A375_uNG7_minus_lncRNA_AR_1.1218, 2_A375_uNG7_plus_lncRNA_AR_1.1702, 2_A375_uNG7_plus_lncRNA_AR_1.1703, 2_A375_uNG7_plus_lncRNA_AR_1.1695	28837, 38786, -597, 67221	vs gene, vs gene, upstream, vs gene	1	1	0	15.67	16.33	12.33	3	1_A375_uNG7_minus_lncRNA_AR_1	931	Gene NUMA1	NUMA, NUMA1	nuclear mitotic apparatus protein 1	NM_006185, NCT23104192.0, NCT23104360.0, NCT23104746.0, NCT23104760.0, NCT23104770.0, NCT23104963.0, NCT23105900.0, NCT23552760.0, NCT23553291.0	1554863_s_at, 200747_s_at_214230_at, 214231_s_at	NP_006167.2, EAW74827.1, EAW74823.1, EAW74822.1, EAW74821.1, EAW74826.1, EAW74824.1, EAW74825.1, EAW74828.1, EAW74829.1, EAW74830.1, EAW74831.1
GeneID:10 0422953	MIR3185	11	71,783,274	71,783,348	74	-	1	2_A375_uNG7_plus_lncRNA_AR_1.1703	-5912	upstream	0	1	0	9	15	12	1	2_A375_uNG7_plus_lncRNA_AR_1	915	Gene MIR3185	MIR3185	microRNA 3185	NR_036132		
GeneID:23 074	LRTOMT	11	71,791,392	71,821,926	30,535	+	2	2_A375_uNG7_plus_lncRNA_AR_1.1703, 4_A375_EGR1_1.1636	576, 23776	vs gene, vs gene	0	1	1	8	13.5	16	2	4_A375_EGR1_1	920	Gene LRTOMT	LRTOMT1, DFNB85, LRRC51, UNQ3072, FLJ22451, COMT2, LRTOMT	weaver, neutrophil-specific antigen homolog	NM_145309, NM_001143007, NR_026059, NCT14503.7, NCT23104320, NCT23104331, NCT23104332, NCT23104333, NCT23104334, NCT23104335, NCT23553332.0	1569802_at_229517_at	NP_660352.1, NP_001138779.1, NP_001138780.1, NP_001138781.1, NP_001138782.1, NP_001138783.1, EAW74832.1, EAW74833.1, EAW74834.1
GeneID:23 934	C11orf59	11	71,808,356	71,814,453	6,098	-	1	4_A375_EGR1_1.1634	272	vs gene	0	0	1	7	16	20	1	4_A375_EGR1_1	920	Gene C11orf59	p18, PDRO, LAMTOR1, FLJ30525, Rgp1-like, Pdrg, C11orf59	chromosome 11 open reading frame 59	NM_017427, NCT14343.2, NCT23553267.0	223609_at	NP_060277.1, EAW74837.1, EAW74838.1
GeneID:23 906	C11orf67	11	71,820,603	71,823,822	3,219	-	1	4_A375_EGR1_1.1634	9962	downstream	0	0	1	7	16	20	1	4_A375_EGR1_1	920	Gene C11orf67	C11orf67, DKFZp564H082, HSPC203	chromosome 11 open reading frame 67	NM_194342, NCT14343.7, NCT19374.12.0, NCT19374.13.1, NCT23104360.0, NCT23104365.0	234218_at	NP_919423.1, EAW74841.1, EAW74839.1, EAW74840.1, EAW74843.1, EAW74842.1
GeneID:23 50	FOLR2	11	71,827,819	71,832,994	5,176	+	2	1_A375_uNG7_minus_lncRNA_AR_1.1217, 2_A375_uNG7_plus_lncRNA_AR_1.1704	6489, 6455	downstream, downstream	1	1	0	25	24	18	1	1_A375_uNG7_minus_lncRNA_AR_1	925	Gene FOLR2	FOLR2, BETA-HFR, FR-PS, FR-BETA, FBXPL-1	folate receptor 2 (fetal)	NM_000803, NM_001113834, NM_001113835, NM_001113836, NCT11570.2	204979_s_at_229619_at	NP_000794.3, NP_001107596.1, NP_001107597.1, NP_001107598.1, NP_001107599.1
GeneID:38 08	INPP1	11	71,935,502	71,950,101	14,599	+	2	2_A375_uNG7_minus_lncRNA_AR_1.1217, 2_A375_uNG7_plus_lncRNA_AR_1.1704	1394, -1576	upstream, upstream	1	1	0	25	24	18	1	1_A375_uNG7_minus_lncRNA_AR_1	923	Gene INPP1	INPP1, SHIP2	inositol polyphosphate phosphatase-like 1	NM_001567, NCT14337.2, NCT23097657.0	201995_s_at	NP_001556.3, EAW74553.1, EAW74554.1
GeneID:49 1	PHOX2A	11	71,950,121	71,955,320	5,199	-	1	4_A375_EGR1_1.1668	-9026	upstream	0	0	1	8	7	10	1	4_A375_EGR1_1	918	Gene PHOX2A	ARIX(B), PHOX2A, ARIX, PMX2A, NCAM2, MGC32227, CPEN42	paired-like homeobox 2a	NM_005169, NCT14341.3	214809_at	NP_005150.2, EAW74556.1
GeneID:23 077	LOC220 077	11	71,960,456	71,962,352	1,896	-	1	4_A375_EGR1_1.1668	1184	vs gene	0	0	1	8	7	10	1	4_A375_EGR1_1	918	Gene LOC220077		dedicator of cytokinesis 1 pseudogene		216393_at_216393_at	

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:81570	CLPB	11	72,003,469	72,145,568	142,099	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1218, 2_A375_pNL97_plus_lncRNA_AR..1..1705, 4_A375_EGR1..1..1667	-32, -64, 53280	upstream, upstream, in gene	1	1	1	14.5	14	13	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene CLPB	CLPB, SKD3, FLJ13152, HSP78	ClpB caseinolytic peptidase B homolog (E. coli)	NM_030813, hCT15212.2, hCT1952436.1, hCT2310117.0	221845_s_at, 224510_s_at	NP_110440.1, EAW74860.1, EAW74858.1, EAW74859.1
GeneID:5138	PDE2A	11	72,287,185	72,385,494	98,309	-	3	2_A375_pNL97_plus_lncRNA_AR..1..1706, 4_A375_EGR1..1..1668, 4_A375_EGR1..1..1669	-2570, 45254, -2794	upstream, in gene, upstream	0	1	1	12.5	17	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene PDE2A	PDE2A, PDE2A1, PED2A4	phosphodiesterase 2A, cGMP-stimulated	NM_002599, NM_001143839, NR_026572, NM_001146209, hCT1952437.1, hCT2310110.0	204134_at	NP_002590.1, NP_001137311.1, NP_001139681.1, EAW74861.1, EAW74862.1
GeneID:116985	ARAP1	11	72,396,114	72,463,434	67,320	-	3	2_A375_pNL97_plus_lncRNA_AR..1..1706, 4_A375_EGR1..1..1669, 4_A375_EGR1..1..1670	75370, 75146, 35562	downstream, downstream, in gene	0	1	1	9.5	17.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene ARAP1	KIAA0782, CENTD2, ARAP1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1	NM_001040118, NM_015242, NM_001135190, hCT15211.2, hCT2310105.0, hCT2310107.0, hCT2310108.0	212516_at, 242039_at, 34206_at	NP_001035207.1, NP_056057.2, NP_001128662.1, EAW74863.1, EAW74864.1, EAW74865.1, EAW74866.1
GeneID:10809	STARD10	11	72,465,774	72,504,750	38,976	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1707	-336	upstream	0	1	0	17	23	16	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene STARD10	NY-CO-28, STARD10, SDCCAG28, CGI-52, PCTP2, MGC14401	StAR-related lipid transfer (START) domain containing 10	NM_006645, hCT15215.3, hCT1957419.1, hCT1960860.1, hCT1960861.1, hCT2310098.0, hCT2310099.0	223103_at, 232322_x_at, 238911_at	NP_006636.2, EAW74868.1, EAW74867.1, EAW74869.1, EAW74870.1, EAW74871.1, EAW74872.1
GeneID:89849	ATG16L2	11	72,525,451	72,540,680	15,229	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1219, 2_A375_pNL97_plus_lncRNA_AR..1..1708	-235, -219	upstream, upstream	1	1	0	28	23	13	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene ATG16L2	FLJ00012, WDR80, ATG16L2, ATG16B	ATG16 autophagy related 16-like 2 (S. cerevisiae)	NM_033388, hCT15216.3, hCT2309769.0, hCT2309771.0, hCT2309772.0, hCT2355270.0, hCT2355271.0	225863_at, 229389_at	NP_203746.1, EAW74874.1, EAW74875.1, EAW74876.1, EAW74878.1, EAW74879.1, EAW74877.1
GeneID:9873	FCHSD2	11	72,547,790	72,853,143	305,353	-	1	4_A375_EGR1..1..1671	151	in gene	0	0	1	8	12	20	1	4_A375_EGR1..1	20	Gene FCHSD2	NWK, KIAA0769, SH3MD3, FCHSD2	FCH and double SH3 domains 2	NM_014824, hCT1952427.1, hCT2310095.0	1554360_at, 203620_s_at	NP_055639.2, EAW74880.1, EAW74881.1
GeneID:9828	ARHGEF17	11	73,019,663	73,080,425	60,762	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1709	68497	downstream	0	1	0	15	21	6	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ARHGEF17	KIAA0337, p164-RhoGEF, ARHGEF17, FLJ90019, TEM4, P164RHOGEF	Rho guanine nucleotide exchange factor (GEF) 17	NM_014786, hCT13876.2	203756_at	NP_055601.2, EAW74891.1
GeneID:84957	RELT	11	73,087,405	73,108,519	21,114	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1709, 4_A375_EGR1..1..1672, 4_A375_EGR1..1..1673	755, 8819, 18099	in gene, in gene, in gene	0	1	1	9	12	13.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RELT	RELT, TNFRSF19L, FLJ14993	RELT tumor necrosis factor receptor	NM_032871, NM_152222, hCT14437.3, hCT1952434.1, hCT1952435.1, hCT2309933.0, hCT2309934.0, hCT2309938.0, hCT2355214.0	227060_at	NP_116260.2, NP_689408.1, EAW74892.1, EAW74893.1, EAW74894.1, EAW74898.1, EAW74895.1, EAW74896.1, EAW74897.1
GeneID:23201	FAM168A	11	73,117,028	73,309,228	192,200	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1220, 2_A375_pNL97_plus_lncRNA_AR..1..1710	-292, -164	upstream, upstream	1	1	0	16	20	11	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene FAM168A	FAM168A, KIAA0280, TCRP1	family with sequence similarity 168, member A	NM_015159	212357_at, 36612_at	NP_055974.1
GeneID:51642	MRPL48	11	73,498,917	73,575,656	76,739	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1221, 1_A375_pNL7_minus_lncRNA_AR..1..1222, 2_A375_pNL97_plus_lncRNA_AR..1..1711, 2_A375_pNL97_plus_lncRNA_AR..1..1712	-8165, 91, -8261, 91	upstream, in gene, upstream, in gene	1	1	0	20.5	22.5	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene MRPL48	FLJ17047, L48MT, MRPL48, MGC13323, HSPC290, MRP-L48, FLJ99260, CGI-118	mitochondrial ribosomal protein L48	NM_016055, hCT18476.2	218281_at	NP_057139.1, EAW74913.1
GeneID:51287	CHCHD8	11	73,583,712	73,587,890	4,178	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1713	82	in gene	0	1	0	14	17	12	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene CHCHD8	E2IG2, MGC117206, CHCHD8, DKFZp762H1711	coiled-coil-helix-coiled-coil-helix domain containing 8	NM_016565, hCT18473.2, hCT1956000.0, hCT2316379.0	220647_s_at	NP_057649.2, EAW74915.1, EAW74914.1, EAW74916.1
GeneID:80227	PAAF1	11	73,588,033	73,638,779	50,746	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1713	-225	upstream	0	1	0	14	17	12	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PAAF1	Rpn14, WDR71, FLJ11848, PAAF, PAAF1	proteasomal ATPase-associated factor 1	NM_025155, hCT2309949.0, hCT2355210.0, hCT2355211.0	1568702_a_at, 218957_s_at	NP_079431.1, EAW74918.1, EAW74917.1, EAW74919.1
GeneID:7351	UCP2	11	73,685,716	73,693,889	8,173	-	1	4_A375_EGR1..1..1674	-735	upstream	0	0	1	12	13	16	1	4_A375_EGR1..1	16	Gene UCP2	SLC25A8, BMIQ4, UCPH, UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	NM_003355, hCT18468.3, hCT2316378.0	208997_s_at, 208998_at	NP_003346.2, EAW74923.1, EAW74924.1
GeneID:26005	C2CD3	11	73,745,480	73,882,064	136,584	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1223, 2_A375_pNL97_plus_lncRNA_AR..1..1714, 2_A375_pNL97_plus_lncRNA_AR..1..1715	-304, 133520, -368	upstream, in gene, upstream	1	1	0	16	24	7	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene C2CD3	DKFZp586P0123, FLJ34770, C2CD3	C2 calcium-dependent domain containing 3	NM_015531	1558756_at, 213199_at, 231708_at, 36552_at	NP_056346.3
GeneID:51400	PPME1	11	73,882,366	73,965,746	83,380	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1223, 2_A375_pNL97_plus_lncRNA_AR..1..1715	0, 64	in gene, in gene	1	1	0	19	24	12	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PPME1	PME-1, FLJ22226, PPME1	protein phosphatase methylesterase 1	NM_016147, hCT17598.3	217841_s_at, 49077_at	NP_057231.1, EAW74932.1
GeneID:283208	P4HA3	11	73,977,702	74,022,699	44,997	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1716	34635	in gene	0	1	0	8	16	5	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene P4HA3	P4HA3		NM_182904, hCT18477.3, hCT2355260.0, hCT2355261.0	1560715_at, 228703_at	NP_878907.1, EAW74934.1, EAW74935.1, EAW74936.1
GeneID:283209	PGM2L1	11	74,041,361	74,109,502	68,141	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1224	-462	upstream	1	0	0	23	19	14	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene PGM2L1	PGM2L1, FLJ32029, BM32A	phosphoglucomutase 2-like 1	NM_173582, hCT18470.4	1569448_at, 229256_at, 229553_at, 235149_at, 238417_at	NP_775853.2, EAW74937.1
GeneID:387787	LIPT2	11	74,202,923	74,204,755	1,832	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1226, 2_A375_pNL97_plus_lncRNA_AR..1..1718	131, 147	in gene, in gene	1	1	0	19	19	10	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene LIPT2	LIPT2		NM_001144869		NP_001138341.1
GeneID:100287896	LOC100287896	11	74,204,465	74,209,267	4,802	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1226, 2_A375_pNL97_plus_lncRNA_AR..1..1718	139, 123	in gene, in gene	1	1	0	19	19	10	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene LOC100287896		hypothetical protein LOC100287896	XM_002343118, XM_003119510, XM_003120706		XP_002343159.1, XP_003119558.1, XP_003120758.1
GeneID:254225	RNF169	11	74,459,913	74,553,458	93,545	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1227, 1_A375_pNL7_minus_lncRNA_AR..1..1228, 2_A375_pNL97_plus_lncRNA_AR..1..1719, 2_A375_pNL97_plus_lncRNA_AR..1..1720, 4_A375_EGR1..1..1675	-73, 5927, -73, 101111, 823	upstream, in gene, upstream, downstream, in gene	1	1	1	19.25	19	10	4	1_A375_pNL7_minus_lncRNA_AR..1	41	Gene RNF169	KIAA1991, RNF169	ring finger protein 169	NM_001098638	226739_at	NP_001092108.1
GeneID:143570	XRRA1	11	74,551,955	74,660,232	108,277	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1720, 2_A375_pNL97_plus_lncRNA_AR..1..1721	99208, 24	in gene, in gene	0	1	0	11.5	23	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene XRRA1	XRRA1	X-ray radiation resistance associated 1	NM_182969	230557_at, 237666_at	NP_892014.1
GeneID:9789	SPCS2	11	74,660,292	74,690,076	29,784	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1721	-84	upstream	0	1	0	11	28	13	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene SPCS2	MGC117366, SPCS2, KIAA0102	signal peptidase complex subunit 2 homolog (S. cerevisiae)	NM_014752, hCT1971010.1	201240_s_at	NP_055567.2, EAW74952.1
GeneID:11309	SLCO2B1	11	74,862,040	74,917,445	55,405	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1229, 2_A375_pNL97_plus_lncRNA_AR..1..1722, 4_A375_EGR1..1..1676	63560, 63592, 42440	downstream, downstream, in gene	1	1	1	36	33.5	12	2	1_A375_pNL7_minus_lncRNA_AR..1	66	Gene SLCO2B1	OATP-B, OATPB, SLCO2B1, DKFZp686E0517, OATP2B1, SLC21A9, KIAA0880	solute carrier organic anion transporter family, member 2B1	NM_007256, NM_001145211, NM_001145212, hCT16542.2, hCT2309843.0, hCT2309844.0	203472_s_at, 203473_at, 211557_x_at	NP_009187.1, NP_001138683.1, NP_001138684.1, EAW74956.1, EAW74957.1, EAW74958.1
GeneID:100507050	LOC100507050	11	74,951,422	74,953,243	1,821	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1230, 2_A375_pNL97_plus_lncRNA_AR..1..1723	-6462, -6462	upstream, upstream	1	1	0	32	40	8	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene LOC100507050		hypothetical protein LOC100507050	XM_003119180, XM_003120716		XP_003119228.1, XP_003120764.1
GeneID:6188	RPS3	11	75,110,562	75,116,733	6,171	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1231, 2_A375_pNL97_plus_lncRNA_AR..1..1724, 4_A375_EGR1..1..1677, 4_A375_EGR1..1..1678	30, 158, -9106, 128	in gene, in gene, upstream, in gene	1	1	1	12	12.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene RPS3	RPS3, FLJ26283, S3, MGC87870, FLJ27450	ribosomal protein S3	NM_001005, hCT2310640.0	208692_at	NP_000996.2, EAW74963.1
GeneID:6079	SNORD15A	11	75,111,435	75,111,582	147	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1231, 2_A375_pNL97_plus_lncRNA_AR..1..1724, 4_A375_EGR1..1..1677, 4_A375_EGR1..1..1678	-843, -715, -9979, -747	upstream, upstream, upstream, upstream	1	1	1	12	12.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SNORD15A	SNORD15A, U15A, SNORNA, RNU15A	small nucleolar RNA, C/D box 15A	NR_000005		
GeneID:114599	SNORD15B	11	75,115,465	75,115,610	145	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1231, 2_A375_pNL97_plus_lncRNA_AR..1..1724, 4_A375_EGR1..1..1678	-4873, -4745, -4777	upstream, upstream, upstream	1	1	1	18	20	19	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SNORD15B	RNU15B, U15B, SNORD15B	small nucleolar RNA, C/D box 15B	NR_000025		
GeneID:871	SERPINH1	11	75,273,170	75,283,846	10,676	+	1	4_A375_EGR1..1..1679	174	in gene	0	0	1	8	12	17	1	4_A375_EGR1..1	17	Gene SERPINH1	AsTP3, SERPINH1, HSP47, RA-A47, SERPINH2, CBP2, PPROM, CBP1, PIG14, gp46	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	NM_001235, hCT19003.2, hCT1970990.2, hCT1970991.2, hCT2310645.1, hCT2343821.0, hCT2355255.0	207714_s_at	NP_001226.2, EAW74977.1, EAW74974.1, EAW74975.1, EAW74976.1, EAW74978.1, EAW74979.1
GeneID:84649	DGAT2	11	75,479,778	75,512,579	32,801	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1232, 2_A375_pNL97_plus_lncRNA_AR..1..1726, 4_A375_EGR1..1..1680	-114, -162, -322	upstream, upstream, upstream	1	1	1	27	28	19	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene DGAT2	DKFZp686A15125, GS1999FULL, DGAT2, HMFN1045	diacylglycerol O-acyltransferase homolog 2 (mouse)	NM_032564, hCT19005.3, hCT2310649.0	224327_s_at, 226064_s_at	NP_115953.2, EAW74984.1, EAW74985.1
GeneID:100506113	LOC100506113	11	75,524,424	75,525,842	1,418	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1727	226	in gene	0	1	0	13	20	11	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100506113		hypothetical LOC100506113	XR_111204, XR_110693, XR_114507		
GeneID:7405	UVRAG	11	75,526,212	75,855,282	329,070	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1727, 2_A375_pNL97_plus_lncRNA_AR..1..1728	-596, 338556	upstream, downstream	0	1	0	13.5	19.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene UVRAG	UVRAG, p63, DHTX, VPS38	UV radiation resistance associated gene	NM_003369, hCT19008.3, hCT2310651.0	203241_at	NP_003360.2, EAW74986.1, EAW74987.1
GeneID:7481	WNT11	11	75,897,370	75,917,574	20,204	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1233, 2_A375_pNL97_plus_lncRNA_AR..1..1729, 4_A375_EGR1..1..1682	-2618, -2554, 358	upstream, upstream, in gene	1	1	1	12.5	14	14	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene WNT11	MGC141946, HWNT11, MGC141948, WNT11	wingless-type MMTV integration site family, member 11	NM_004626, hCT19002.1, hCT1971015.1	206737_at	NP_004617.2, EAW74989.1, EAW74988.1
GeneID:5612	PRKRIR	11	76,061,004	76,091,880	30,876	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1235, 2_A375_pNL97_plus_lncRNA_AR..1..1731, 2_A375_pNL97_plus_lncRNA_AR..1..1732	-248, 248, -248	upstream, in gene, upstream	1	1	0	93	101	15	1	2_A375_pNL97_plus_lncRNA_AR..1	101	Gene PRKRIR	MGC102750, DAP4, PRKRIR, P52rIPK, THAP0	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	NM_004705, hCT2310834.0, hCT2310835.0, hCT2310837.0	209323_at	NP_004696.2, EAW74993.1, EAW74991.1, EAW74992.1
GeneID:100506127	LOC100506127	11	76,092,360	76,119,176	26,816	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1235, 2_A375_pNL97_plus_lncRNA_AR..1..1731, 2_A375_pNL97_plus_lncRNA_AR..1..1732	-232, -728, -232	upstream, upstream, upstream	1	1	0	93	101	15	1	2_A375_pNL97_plus_lncRNA_AR..1	101	Gene LOC100506127	FLJ43633, FLJ37770	putative uncharacterized protein FLJ37770-like	XM_003119509, XM_003119508, XM_003119507, XM_003119174, XM_003119173, XM_003119172, XM_003120711, XM_003120710, XM_003120709		XP_003119557.1, XP_003119556.1, XP_003119555.1, XP_003119222.1, XP_003119221.1, XP_003119220.1, XP_003120759.1, XP_003120758.1, XP_003120757.1
GeneID:56946	C11orf30	11	76,156,069	76,262,589	106,520	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1733	-208	upstream	0	1	0	20	19	9	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C11orf30	EMSY, GL002, C11orf30, FLJ90741	chromosome 11 open reading frame 30	NM_020193, hCT2312764.0, hCT2312765.0, hCT2312766.0, hCT2312767.0, hCT2312769.0	1569349_at, 219012_s_at, 222806_s_at, 222807_at, 234689_x_at, 242847_at	NP_064578.2, EAW74998.1, EAW74996.1, EAW74997.1, EAW74999.1, EAW75000.1
GeneID:726	CAPN5	11	76,777,992	76,837,201	59,209	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1736, 4_A375_EGR1..1..1686, 4_A375_EGR1..1..1687	6632, 6840, 26328	in gene, in gene, in gene	0	1	1	9	12	17.5	2	4_A375_EGR1..1	20	Gene CAPN5	nCL-3, FLJ46245, CAPN5, HTRA3	calpain 5	NM_004055, hCT2312787.1, hCT2351381.0, hCT33143.3	205166_at, 226292_at	NP_004046.2, EAW75015.1, EAW75014.1, EAW75016.1
GeneID:4975	OMP	11	76,813,886	76,814,377	491	+	1	4_A375_EGR1..1..1687	-9566	upstream	0	0	1	7	8	20	1	4_A375_EGR1..1	20	Gene OMP	OMP	olfactory marker protein	NM_006189, hCT1642242.0	221361_at	NP_006180.1, EAW75017.1
GeneID:5058	PAK1	11	77,033,060	77,185,108	152,048	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1739	-396	upstream	0	1	0	17	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PAK1	MGC130001, MGC130000, PAKalpha, PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	NM_002576, NM_001128620, hCT1954872.1, hCT2313054.0, hCT2313056.0, hCT33146.3	1565772_at, 209615_s_at, 226507_at, 230100_x_at	NP_002567.3, NP_001122092.1, EAW75026.1, EAW75027.1, EAW75028.1, EAW75029.1
GeneID:282679	AQP11	11	77,300,680	77,321,401	20,721	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1740	-136	upstream	0	1	0	9	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene AQP11	AQP11, AQPX1	aquaporin 11	NM_173039, hCT2309957.1, hCT2355277.0	229526_at	NP_766627.1, EAW75031.1, EAW75030.1
GeneID:1207	CLNS1A	11	77,327,196	77,348,851	21,655	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1237, 2_A375_pNL97_plus_lncRNA_AR..1..1741	-29, 19	upstream, in gene	1	1	0	17	22	13	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CLNS1A	CLNS1A, CLNS1B, CLCI, ICln	chloride channel, nucleotide-sensitive, 1A	NM_001293, hCT18250.3	209143_s_at	NP_001284.1, EAW75032.1
GeneID:51773	RSF1	11	77,377,274	77,531,880	154,606	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1238, 2_A375_pNL97_plus_lncRNA_AR..1..1742	1266, 1364	in gene, in gene	1	1	0	16	16	4	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene RSF1	RSF1, HBXAP, XAP8, RSF-1, p325	remodeling and spacing factor 1	NM_016578, hCT2344677.0, hCT2344678.0, hCT2344680.0	218166_s_at, 222540_s_at, 222541_at, 223618_s_at	NP_057662.3, EAW75033.1, EAW75034.1, EAW75035.1
GeneID:28971	C11orf67	11	77,532,208	77,583,398	51,190	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1238, 2_A375_pNL97_plus_lncRNA_AR..1..1742	-1616, -1712	upstream, upstream	1	1	0	16	16	4	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C11orf67	PTD015, CK067, FLJ21035, C11orf67, MGC3367	chromosome 11 open reading frame 67	NM_024684, hCT18251.2, hCT2309959.0, hCT2309960.0, hCT2309961.0	220266_at, 221599_at, 221600_s_at	NP_078960.1, EAW75036.1, EAW75037.1, EAW75038.1, EAW75039.1
GeneID:92105	INTS4	11	77,589,766	77,705,717	115,951	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1239, 2_A375_pNL97_plus_lncRNA_AR..1..1743	-331, -139	upstream, upstream	1	1	0	18	25	10	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene INTS4	MGC16733, INTS4, MST093, INT4	integrator complex subunit 4	NM_033547	1553870_at, 1569253_at, 1569254_s_at, 225169_at, 233193_x_at	NP_291025.3
GeneID:79053	ALG8	11	77,811,988	77,850,699	38,711	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1744, 4_A375_EGR1..1..1688	-53, 107	upstream, in gene	0	1	1	16	22	16	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ALG8	CDG1H, ALG8, MGC2840	asparagine-linked glycosylation 8, alpha-1,3-glucosyltransferase homolog (S. cerevisiae)	NM_024079, NM_001007027, hCT1969009.1, hCT2310401.0, hCT2310403.0, hCT2355341.0	203545_at	NP_076984.2, NP_001007028.1, EAW75048.1, EAW75049.1, EAW75050.1, EAW75051.1
GeneID:283219	KCTD21	11	77,882,298	77,899,664	17,366	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1240, 2_A375_pNL97_plus_lncRNA_AR..1..1745	-144, -112	upstream, upstream	1	1	0	47	67	15	1	2_A375_pNL97_plus_lncRNA_AR..1	67	Gene KCTD21	KCTD21	potassium channel tetramerisation domain containing 21	NM_001029859, hCT1644284.2, hCT2310399.0	229873_at	NP_001025030.1, EAW75054.1, EAW75053.1

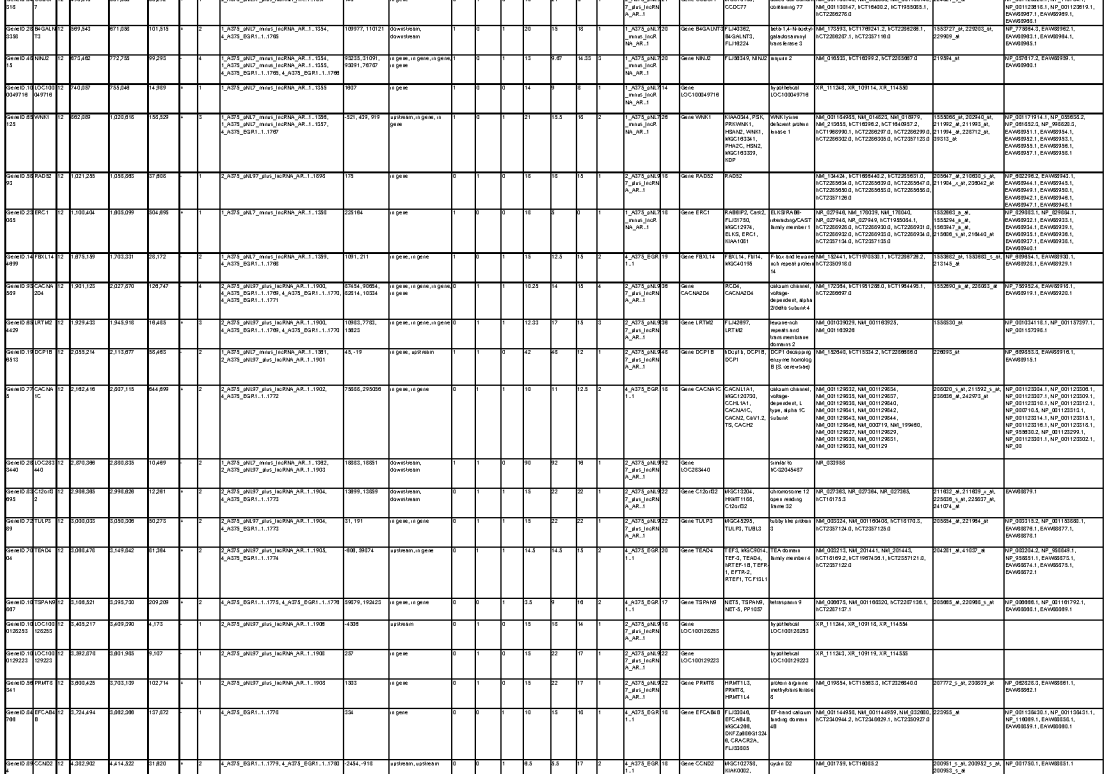
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:57558	USP35	11	77,899,856	77,925,757	25,899	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1240, 2_A375_pNL97_plus_lncRNA_AR..1..1745	-50, -82	upstream, upstream	1	1	0	47	87	15	1	2_A375_pNL97_plus_lncRNA_AR..1	87	Gene USP35	USP35		NM_020798	229198_at	NP_065849.1
GeneID:79731	NARS2	11	78,147,016	78,285,909	138,893	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1746	101	in gene	0	1	0	14	17	13	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene NARS2	FLJ23441, SLM5, NARS2	asparaginyl-tRNA synthetase 2, mitochondrial (putative)	NM_024678, NR_027479, hCT17605.3, hCT2310394.0, hCT2310396.0	219217_at	NP_078954.4, EAW75062.1, EAW75061.1, EAW75063.1
GeneID:26011	ODZ4	11	78,364,328	79,151,695	787,367	-	1	4_A375_EGR1..1..1690	319	in gene	0	0	1	4	8	16	1	4_A375_EGR1..1	16	Gene ODZ4	TNM4, Ten-M4, Doc4, ODZ4, FLJ99165	odz, odd Oz/ten-m homolog 4 (Drosophila)	NM_001098816	213273_at	NP_001092286.2
GeneID:27314	RAB30	11	82,692,476	82,782,884	90,408	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1747	-26	upstream	0	1	0	15	23	10	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RAB30	RAB30	RAB30, member RAS oncogene family	NM_014488, hCT18425.3, hCT2310547.0, hCT2310548.0, hCT2310549.0	206530_at, 227642_at, 228003_at	NP_055303.2, EAW75080.1, EAW75078.1, EAW75079.1, EAW75081.1
GeneID:100506233	LOC100506233	11	82,783,119	82,785,008	1,889	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1747	-207	upstream	0	1	0	15	23	10	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100506233		hypothetical LOC100506233	XR_111200, XR_111201, XR_110898, XR_110897, XR_114510, XR_114511		
GeneID:100506259	LOC100506259	11	82,789,752	82,790,924	1,172	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1747	8012	downstream	0	1	0	15	23	10	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100506259		hypothetical LOC100506259	XR_111199, XR_110898, XR_114512		
GeneID:51585	PCF11	11	82,868,137	82,896,836	28,699	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1241, 2_A375_pNL97_plus_lncRNA_AR..1..1746	37623, 37303	downstream, downstream	1	1	0	18	17	11	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene PCF11	KIAA0824, PCF11	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)	NM_015885, hCT17809.2, hCT2310335.0	203378_at, 227822_at	NP_056969.2, EAW75083.1, EAW75084.1
GeneID:100506282	LOC100506282	11	82,902,887	82,904,704	1,817	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1241, 2_A375_pNL97_plus_lncRNA_AR..1..1746	-1056, -736	upstream, upstream	1	1	0	18	17	11	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100506282		hypothetical LOC100506282	XR_110899		
GeneID:338699	ANKRD42	11	82,905,291	82,960,013	54,722	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1241, 2_A375_pNL97_plus_lncRNA_AR..1..1746	469, 149	in gene, in gene	1	1	0	18	17	11	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ANKRD42	SARP, ANKRD42, FLJ37874	ankyrin repeat domain 42	NM_182603, hCT1644122.2, hCT2355231.0	232600_at, 243151_at	NP_872409.2, EAW75086.1, EAW75087.1
GeneID:60492	CCDC90B	11	82,972,506	82,997,377	24,871	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1242, 2_A375_pNL97_plus_lncRNA_AR..1..1749, 4_A375_EGR1..1..1691	-127, -127, 97	upstream, upstream, in gene	1	1	1	58	76	18	1	2_A375_pNL97_plus_lncRNA_AR..1	76	Gene CCDC90B	MGC104239, MDS025, MDS011, CCDC90B	coiled-coil domain containing 90B	NM_021825, hCT18468.3, hCT1964122.1, hCT2355324.0, hCT2355325.0	1568834_s_at, 218288_s_at, 222577_at	NP_068597.2, EAW75090.1, EAW75088.1, EAW75089.1, EAW75091.1
GeneID:1740	DLG2	11	83,166,055	85,338,314	2,172,259	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1243, 1_A375_pNL7_minus_lncRNA_AR..1..1244, 4_A375_EGR1..1..1692, 4_A375_EGR1..1..1693	912842, -1302, 1318698, 425994	in gene, upstream, in gene, in gene	1	0	1	13	9	11.25	4	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene DLG2	PSD93, PSD-93, MGC131811, DKFZp781D1854, FLJ37266, DLG2, DKFZp781E0954	discs, large homolog 2 (Drosophila)	NM_001142702, NM_001364, NM_001142699, NM_001142700, hCT18487.4, hCT2310272.1, hCT2310538.1	208253_at, 228973_at	NP_001136174.1, NP_001355.2, NP_001136171.1, NP_001136172.1, EAW75093.1, EAW75094.1, EAW75095.1
GeneID:55863	TMEM126B	11	85,339,622	85,347,583	7,961	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1244	-8	upstream	1	0	0	19	13	10	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene TMEM126B	MGC111203, HT007, TMEM126B	transmembrane protein 126B	NM_018480, NM_001193537, NM_001193538, NR_036485, hCT1641097.3, hCT1962027.0, hCT2310346.0, hCT2310347.0, hCT2355404.0, hCT2355405.0	1554537_at, 221622_s_at	NP_060950.3, NP_001180466.1, NP_001180467.1, EAW75099.1, EAW75100.1, EAW75101.1, EAW75096.1, EAW75097.1, EAW75098.1
GeneID:84233	TMEM126A	11	85,358,963	85,367,597	8,634	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1750, 4_A375_EGR1..1..1694	-99, 17037	upstream, downstream	0	1	1	14.5	16	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TMEM126A	OPA7, DKFZp586C1924, TMEM126A	transmembrane protein 126A	NM_032273, hCT18815.3	223334_at	NP_115649.1, EAW75102.1
GeneID:58487	CREBZF	11	85,368,608	85,376,182	7,574	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1750, 4_A375_EGR1..1..1694	17318, 182	downstream, in gene	0	1	1	14.5	16	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CREBZF	ZF, FLJ94018, SMILE, CREBZF	CREB/ATF bZIP transcription factor	NM_001039618, NR_028024, NR_028025, NR_028026, NR_028027, hCT1641684.2	202977_s_at, 202978_s_at, 202979_s_at, 213584_s_at, 225594_at, 225595_at	NP_001034707.1, EAW75103.1
GeneID:54843	SYTL2	11	85,405,284	85,522,178	116,914	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1245, 2_A375_pNL97_plus_lncRNA_AR..1..1751	91949, 91988	in gene, in gene	1	1	0	24	28	3	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene SYTL2	SGA72M, FLJ45597, EXO4, MGC102768, FLJ34802, KIAA1597, SLP2, SLP2A, FLJ42764, CHR11SYT, SYTL2, FLJ21219	synaptotagmin-like 2	NM_032379, NM_206927, NM_206928, NM_206929, NM_206930, NM_001162951, NM_001162952, NM_001162953, NM_032943, hCT18812.3, hCT2310576.0, hCT2310577.0, hCT2310578.0, hCT2310580.0, hCT2310581.0, hCT2310582.0	220613_s_at, 225496_s_at, 232914_s_at	NP_115755.2, NP_996810.1, NP_001156423.1, NP_996811.1, NP_996812.1, NP_996813.1, NP_116561.1, NP_001156424.1, NP_001156425.1, EAW75107.1, EAW75108.1, EAW75109.1, EAW75110.1, EAW75111.1, EAW75112.1, EAW75113.1
GeneID:100506308	LOC100506308	11	85,563,600	85,565,986	2,386	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1752	130	in gene	0	1	0	10	22	7	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100506308		hypothetical protein LOC100506308	XM_003119508, XM_003119175, XM_003120712		XP_003119554.1, XP_003119223.1, XP_003120760.1
GeneID:220047	CCDC83	11	85,566,144	85,631,051	64,907	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1246, 2_A375_pNL97_plus_lncRNA_AR..1..1752	35120, -288	in gene, upstream	1	1	0	13.5	16.5	5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CCDC83	FLJ42119, HSD9, MGC34732, CCDC83	coiled-coil domain containing 83	NM_173556, hCT1641883.4, hCT2355323.0	237160_at	NP_775827.2, EAW75114.1, EAW75115.1
GeneID:8301	PICALM	11	85,668,485	85,780,108	111,623	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1247	12	in gene	1	0	0	19	11	11	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene PICALM	PICALM, CALM, CLTH, LAP	phosphatidylinositol binding clathrin assembly protein	NM_007166, NM_001008660, hCT1767873.2, hCT1767874.2, hCT1767875.2, hCT1964108.1, hCT2310563.0, hCT2310564.0, hCT2310566.0, hCT2310567.0, hCT2310568.0, hCT2310570.0, hCT2355378.0	203134_at, 212508_at, 212511_at, 215236_s_at, 215832_x_at	NP_009097.2, NP_001008660.1, EAW75124.1, EAW75125.1, EAW75126.1, EAW75128.1, EAW75118.1, EAW75119.1, EAW75120.1, EAW75121.1, EAW75122.1, EAW75123.1, EAW75127.1
GeneID:8726	EED	11	85,955,815	85,989,781	33,966	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1249, 2_A375_pNL97_plus_lncRNA_AR..1..1754	121, -135	in gene, upstream	1	1	0	17	29	10	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene EED	WAIT1, HEED, EED	embryonic ectoderm development	NM_003797, NM_152991, hCT18942.3, hCT2355265.0, hCT2355266.0	209572_s_at, 210656_at	NP_003788.2, NP_694536.1, EAW75129.1, EAW75130.1, EAW75131.1
GeneID:51501	C11orf73	11	86,013,253	86,056,985	43,732	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1250	-65	upstream	1	0	0	25	20	8	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene C11orf73	HSPC179, C11orf73, FLJ43020, HSPC138, L7RN6	chromosome 11 open reading frame 73	NM_016401, NR_024596, NR_024597, NR_024598, hCT2310361.0, hCT2310362.0, hCT2310363.0, hCT2355227.0, hCT2355228.0	219979_s_at, 230326_s_at	NP_057485.2, EAW75133.1, EAW75134.1, EAW75135.1, EAW75136.1, EAW75137.1
GeneID:10873	ME3	11	86,152,150	86,383,678	231,528	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1251, 1_A375_pNL7_minus_lncRNA_AR..1..1252, 2_A375_pNL97_plus_lncRNA_AR..1..1755, 2_A375_pNL97_plus_lncRNA_AR..1..1756, 2_A375_pNL97_plus_lncRNA_AR..1..1757, 4_A375_EGR1..1..1695	39646, 606, 212542, 39774, 329, 446	in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	17.33	17	10.33	3	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene ME3	ME3, FLJ34862	malic enzyme 3, NADP(+)-dependent, mitochondrial	NM_006680, NM_001014811, NM_001161586, hCT18939.3, hCT2310557.0, hCT2310559.0, hCT2310561.0, hCT2310562.0	204663_at, 231295_at	NP_006671.2, NP_001014811.1, NP_001155058.1, EAW75138.1, EAW75139.1, EAW75141.1, EAW75140.1, EAW75142.1
GeneID:100506368	LOC100506368	11	86,666,663	86,711,992	45,329	+	1	4_A375_EGR1..1..1696	39545	in gene	0	0	1	6	4	14	1	4_A375_EGR1..1	14	Gene LOC100506368		hypothetical LOC100506368	XR_110901, XR_114515		
GeneID:1075	CTSC	11	88,026,760	88,070,941	44,181	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1759, 4_A375_EGR1..1..1698	29, 221	in gene, in gene	0	1	1	15	20	18	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CTSC	CTSC, HMS, JP, PALS, DPPI, CPPI, PLS, JPD, DPP1	cathepsin C	NM_148170, NM_001114173, NM_001814, hCT11863.1, hCT2353414.0	201487_at, 225646_at, 225647_s_at, 231234_at	NP_680475.1, NP_001107645.1, NP_001805.3, EAW59363.1, EAW59364.1
GeneID:2915	GRM5	11	88,237,744	88,796,816	559,072	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1254, 2_A375_pNL97_plus_lncRNA_AR..1..1760, 2_A375_pNL97_plus_lncRNA_AR..1..1761	359024, 367760, 353936	in gene, in gene, in gene	1	1	0	16.33	20	3.67	3	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene GRM5	MGLUR5, GPRC1E, GRM5, mGlu5	glutamate receptor, metabotropic 5	NM_000842, NM_001143831, hCT2348982.0, hCT2348983.0	1565389_s_at, 207235_s_at, 214217_at	NP_000833.1, NP_001137303.1, EAW59358.1, EAW59359.1
GeneID:7299	TYR	11	88,911,040	89,028,927	117,887	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1255	-9344	upstream	1	0	0	19	13	5	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene TYR	OCAIA, TYR, OCA1A, CMM8, SHEP3	tyrosinase (oculocutaneous albinism IA)	NM_000372, hCT10762.4, hCT2258943.1	1555504_at, 1555505_a_at, 206630_at	NP_000363.1, EAW59356.1, EAW59357.1
GeneID:26973	CHORDC1	11	89,933,597	89,956,532	22,935	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1762	308	in gene	0	1	0	13	16	9	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CHORDC1	FLJ37289, CHP1, CHORDC1	cysteine and histidine-rich domain (CHORD) containing 1	NM_012124, NM_001144073, hCT2334896.0, hCT2334897.0, hCT2334898.0, hCT2334899.0, hCT2354466.0	218566_s_at, 239436_at	NP_036256.2, NP_001137545.1, EAW66867.1, EAW66869.1, EAW66870.1, EAW66871.1, EAW66866.1
GeneID:120103	SLC36A4	11	92,880,850	92,931,095	50,245	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1763	311	in gene	0	1	0	13	19	8	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SLC36A4	PAT4, FLJ38932, SLC36A4	solute carrier family 36 (proton/amino acid symporter), member 4	NM_152313, hCT1786097.2, hCT2354455.0, hCT2354456.0	234978_at	NP_689526.2, EAW66895.1, EAW66896.1, EAW66897.1
GeneID:56935	C11orf75	11	93,211,638	93,276,546	64,908	-	1	4_A375_EGR1..1..1701	62018	in gene	0	0	1	3	8	20	1	4_A375_EGR1..1	20	Gene C11orf75	FN5, C11orf75	chromosome 11 open reading frame 75	NM_020179, hCT1643893.2, hCT1950672.1, hCT1981467.1, hCT2334479.0, hCT2354460.0	219606_s_at	NP_064564.1, EAW66905.1, EAW66901.1, EAW66902.1, EAW66903.1, EAW66904.1
GeneID:85459	KIAA1731	11	93,394,816	93,463,522	68,706	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1764	320	in gene	0	1	0	15	20	12	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene KIAA1731	KIAA1731, FLJ40913	KIAA1731	NM_033395	1565629_at, 1569302_at, 215018_at, 229878_at	NP_203753.1
GeneID:692075	SNORD6	11	93,464,669	93,464,739	70	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1765, 4_A375_EGR1..1..1702	-9917, -9965	upstream, upstream	0	1	1	10	16	19	1	4_A375_EGR1..1	19	Gene SNORD6	SNORD6, mgh28S-2412	small nucleolar RNA, C/D box 6	NR_003036		
GeneID:677792	SNORA1	11	93,465,170	93,465,299	129	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1765, 4_A375_EGR1..1..1702	-9357, -9405	upstream, upstream	0	1	1	10	16	19	1	4_A375_EGR1..1	19	Gene SNORA1	SNORA1, ACA1	small nucleolar RNA, H/ACA box 1	NR_003026		
GeneID:654320	SNORA8	11	93,465,527	93,465,665	138	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1765, 4_A375_EGR1..1..1702	-8991, -9039	upstream, upstream	0	1	1	10	16	19	1	4_A375_EGR1..1	19	Gene SNORA8	SNORA8, ACA8	small nucleolar RNA, H/ACA box 8	NR_002920		
GeneID:692072	SNORD5	11	93,466,394	93,466,466	72	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1765, 4_A375_EGR1..1..1702	-8190, -8238	upstream, upstream	0	1	1	10	16	19	1	4_A375_EGR1..1	19	Gene SNORD5	SNORD5, mgh28S-2410	small nucleolar RNA, C/D box 5	NR_003033		
GeneID:677805	SNORA18	11	93,466,632	93,466,763	131	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1765, 4_A375_EGR1..1..1702	-7893, -7941	upstream, upstream	0	1	1	10	16	19	1	4_A375_EGR1..1	19	Gene SNORA18	ACA18, SNORA18	small nucleolar RNA, H/ACA box 18	NR_002959		
GeneID:100302240	MIR1304	11	93,466,840	93,466,930	90	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1765, 4_A375_EGR1..1..1702	-7726, -7774	upstream, upstream	0	1	1	10	16	19	1	4_A375_EGR1..1	19	Gene MIR1304	MIRN1304, MIR1304, hsa-mir-1304	microRNA 1304	NR_031639		
GeneID:677822	SNORA40	11	93,468,276	93,468,402	126	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1765, 4_A375_EGR1..1..1702	-6254, -6302	upstream, upstream	0	1	1	10	16	19	1	4_A375_EGR1..1	19	Gene SNORA40	ACA40, SNORA40	small nucleolar RNA, H/ACA box 40	NR_002973		
GeneID:79101	TAF1D	11	93,469,095	93,474,703	5,608	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1765, 4_A375_EGR1..1..1702	47, -1	in gene, upstream	0	1	1	10	16	19	1	4_A375_EGR1..1	19	Gene TAF1D	TAF1D, MGC5306, JOSD3, TAF(I)41, RAFI41	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	NM_024116, hCT2334474.0, hCT2334476.0, hCT2334477.0	218750_at, 221580_s_at, 222728_s_at	NP_077021.1, EAW66912.1, EAW66913.1, EAW66914.1
GeneID:28970	C11orf54	11	93,474,793	93,496,247	21,454	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1765, 4_A375_EGR1..1..1702	-137, -89	upstream, upstream	0	1	1	10	16	19	1	4_A375_EGR1..1	19	Gene C11orf54	PTD012, C11orf54	chromosome 11 open reading frame 54	NM_014039, hCT10870.3, hCT1965782.1, hCT2334391.0, hCT2334392.0, hCT2354464.0	1559623_at, 223268_at, 229851_s_at	NP_054758.2, EAW66915.1, EAW66916.1, EAW66917.1, EAW66918.1, EAW66919.1
GeneID:9440	MED17	11	93,517,405	93,546,496	29,091	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1766	547	in gene	0	1	0	13	17	15	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene MED17	CRSP77, DRIP80, TRAP80, MED17, CRSP6, FLJ10812	mediator complex subunit 17	NM_004268, hCT12014.3, hCT2334393.0	221517_s_at, 223115_at, 232483_at	NP_004259.3, EAW66920.1, EAW66921.1
GeneID:154810	AMOTL1	11	94,501,508	94,609,918	108,410	+	6	1_A375_pNL7_minus_lncRNA_AR..1..1256, 1_A375_pNL7_minus_lncRNA_AR..1..1257, 1_A375_pNL7_minus_lncRNA_AR..1..1258, 1_A375_pNL7_minus_lncRNA_AR..1..1259, 2_A375_pNL97_plus_lncRNA_AR..1..1767, 2_A375_pNL97_plus_lncRNA_AR..1..1768	-84, 22556, 34492, 112028, -164, 112028	upstream, in gene, in gene, downstream, upstream, downstream	1	1	0	36.25	34.25	6.25	4	1_A375_pNL7_minus_lncRNA_AR..1	74	Gene AMOTL1	JEAP, AMOTL1	angiomotin like 1	NM_130847, hCT12565.3, hCT2334682.1, hCT2354397.0	225450_at, 225459_at, 228840_at, 235277_at	NP_570899.1, EAW66945.1, EAW66943.1, EAW66944.1
GeneID:10929	SFRS2B	11	94,800,056	94,804,388	4,332	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1769	275	in gene	0	1	0	14	19	8	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SFRS2B	SRSF8, SRP46, SFRS2B	serine/arginine-rich splicing factor 8	NM_032102, hCT1812374.1, hCT1813985.1, hCT2334671.0	213152_s_at, 214789_x_at, 228760_at, 229471_s_at, 236929_at	NP_115285.1, EAW66954.1, EAW66955.1, EAW66956.1
GeneID:23052	ENDOD1	11	94,822,974	94,865,815	42,841	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1770, 4_A375_EGR1..1..1703	43330, -270	downstream, upstream	0	1	1	6	15	10	2	4_A375_EGR1..1	18	Gene ENDOD1	KIAA0830, MGC86092, ENDOD1	endonuclease domain containing 1	NM_015036	212570_at, 212573_at	NP_055851.1
GeneID:143684	FAM76B	11	95,502,106	95,522,954	20,848	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1771	-150	upstream	0	1	0	18	26	17	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene FAM76B	MGC33371, FAM76B	family with sequence similarity 76, member B	NM_144664, hCT12543.3, hCT2354386.0, hCT2354387.0	1553749_at, 1553750_a_at, 226753_at, 232046_at	NP_653265.3, EAW66964.1, EAW66962.1, EAW66963.1
GeneID:9702	CEP57	11	95,523,642	95,565,854	42,212	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1771	-538	upstream	0	1	0	18	26	17	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene CEP57	KIAA0092, PIG8, TSP57, CEP57	centrosomal protein 57kDa	NM_014679, hCT12544.3, hCT1965785.1, hCT2334325.0, hCT2334326.0, hCT2354388.0, hCT2354389.0	203491_s_at, 203492_x_at, 203493_s_at, 203494_s_at, 209882_s_at	NP_055494.2, EAW66968.1, EAW66965.1, EAW66966.1, EAW66969.1, EAW66970.1, EAW66967.1
GeneID:8898	MTMR2	11	95,566,044	95,657,371	91,327	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1263, 2_A375_pNL97_plus_lncRNA_AR..1..1772	203, 155	in gene, in gene	1	1	0	22	33	13	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene MTMR2	CMT4B1, CMT4B, MTMR2, KIAA1073	myotubularin related protein 2	NR_023356, NM_016156, NM_201278, NM_201281, hCT12542.3, hCT2354383.0, hCT2354384.0, hCT2354385.0	203211_s_at, 203212_s_at, 214649_s_at	NP_057240.3, NP_958435.1, NP_958436.1, EAW66972.1, EAW66973.1, EAW66974.1, EAW66971.1
GeneID:84441	MAML2	11	95,711,440	96,076,344	364,904	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1264, 2_A375_pNL97_plus_lncRNA_AR..1..1773, 2_A375_pNL97_plus_lncRNA_AR..1..1774, 1_A375_pNL7_minus_lncRNA_AR..1..1265	328688, 220312, 186776, 1526	in gene, in gene, in gene, in gene	1	1	0	15.25	17	7.5	4	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene MAML2	MAML2, MAM3, KIAA1819, MGC176701, MAM-3, MAM2, MLL-MAML2, DKFZp686N0150	mastermind-like 2 (Drosophila)	NM_032427, hCT2348993.0	235108_at, 235457_at	NP_115803.1, EAW66975.1
GeneID:100422991	MIR1260B	11	96,074,602	96,074,690	88	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1265	214	downstream	1	0	0	16	16	13	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene MIR1260B	MIR1260B	microRNA 1260b	NR_038125		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:7225	TRPC6	11	101,322,295	101,454,659	132,364	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1775	141998	downstream	0	1	0	9	14	2	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene TRPC6	FLJ14863, FSGS2, TRP6, FLJ11098, TRPC6	transient receptor potential cation channel, subfamily C, member 6	NM_004621, hCT2335292.0, hCT2335293.0, hCT32167.2	206528_at, 217287_s_at	NP_004612.2, EAW67004.1, EAW67003.1, EAW67005.1
GeneID:10413	YAP1	11	101,981,192	102,104,154	122,962	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1776	-72	upstream	0	1	0	12	16	4	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene YAP1	YKI, YAP2, YAP1, YAP65, YAP	Yes-associated protein 1	NM_001130145, NM_006106, NM_001195044, NM_001195045, hCT1957216.1, hCT2354472.0, hCT2354473.0, hCT2354474.0, hCT32749.2	213342_at, 224894_at, 224895_at	NP_001123617.1, NP_006097.2, NP_001181973.1, NP_001181974.1, EAW67012.1, EAW67013.1, EAW67011.1, EAW67014.1, EAW67015.1
GeneID:330	BIRC3	11	102,188,194	102,208,465	20,271	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1777, 4_A375_EGR1..1..1709	29790, 29790	downstream, downstream	0	1	1	13	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene BIRC3	CIAP2, HIAP1, AIP1, RNF49, c-IAP2, API2, HAIP1, BIRC3, MIHC, MALT2	baculoviral IAP repeat containing 3	NM_001165, NM_182962, hCT32748.3	210538_s_at	NP_001156.1, NP_892007.1, EAW67017.1
GeneID:329	BIRC2	11	102,217,966	102,249,401	31,435	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1777, 4_A375_EGR1..1..1709	18, 18	in gene, in gene	0	1	1	13	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene BIRC2	Hiap-2, cIAP1, RNF48, API1, BIRC2, HIAP2, c-IAP1, MIHB	baculoviral IAP repeat containing 2	NM_001166, hCT2334466.0	202076_at	NP_001157.1, EAW67018.1
GeneID:114908	TMEM123	11	102,267,056	102,323,775	56,719	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1267, 2_A375_pNL97_plus_lncRNA_AR..1..1778	383, 447	in gene, in gene	1	1	0	16	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene TMEM123	KCT3, PORMIN, PORIMIN, TMEM123	transmembrane protein 123	NM_052932, hCT2335287.0, hCT2354475.0, hCT32750.2	211967_at	NP_443164.2, EAW67019.1, EAW67020.1, EAW67021.1
GeneID:727869	LOC727869	11	102,323,650	102,332,769	9,119	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1267, 2_A375_pNL97_plus_lncRNA_AR..1..1778	-258, -322	upstream, upstream	1	1	0	16	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC727869		hypothetical LOC727869	XR_111211, XR_110515, XR_114519	239241_at	
GeneID:9313	MMP20	11	102,447,566	102,496,063	48,497	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1268	32191	in gene	1	0	0	16	9	4	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene MMP20	AI2A2, MMP20, MMP-20	matrix metallopeptidase 20	NM_004771, hCT32746.2	207599_at	NP_004762.2, EAW67024.1
GeneID:100288077	LOC100288077	11	102,654,407	102,707,497	53,090	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1269	59897	downstream	1	0	0	19	6	5	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene LOC100288077		hypothetical LOC100288077	XR_111210, XR_110516, XR_114520		
GeneID:4314	MMP3	11	102,706,528	102,714,342	7,814	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1269	36	in gene	1	0	0	19	6	5	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene MMP3	MGC126104, MGC126102, MGC126103, SL-1, CHDS6, STMY1, STR1, MMP-3, MMP3, STMY	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	NM_002422, hCT32744.3	205828_at	NP_002413.1, EAW67032.1
GeneID:79659	DYNC2H1	11	102,980,160	103,350,591	370,431	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1779	0	in gene	0	1	0	13	17	7	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene DYNC2H1	FLJ11756, DNCH2, ATD3, DHC2, DHC1b, hdhc11, DYNC2H1, DYH1B	dynein, cytoplasmic 2, heavy chain 1	NM_001080463, NM_001377	1561939_at, 1565149_at, 219489_at	NP_001073932.1, NP_001368.2
GeneID:2893	GRIA4	11	105,480,800	105,852,819	372,019	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1271, 2_A375_pNL97_plus_lncRNA_AR..1..1782, 2_A375_pNL97_plus_lncRNA_AR..1..1783	63200, 63200, 109504	in gene, in gene, in gene	1	1	0	16	19.5	3.5	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene GRIA4	GRIA4, GluA4, GLUR4C, GLURD, GLUR4	glutamate receptor, ionotrophic, AMPA 4	NM_001077244, NM_000829, NM_001077243, NM_001112812, hCT2334764.0, hCT2334766.0, hCT2334767.0, hCT2334768.0	1569176_at, 208464_at, 236883_x_at	NP_001070712.1, NP_000820.3, NP_001070711.2, NP_001106283.1, EAW67067.1, EAW67069.1, EAW67066.1, EAW67068.1
GeneID:84437	KIAA1826	11	105,878,629	105,892,954	14,325	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1784, 4_A375_EGR1..1..1710	108, 154	in gene, in gene	0	1	1	14	18	15	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene KIAA1826	KIAA1826		NM_032424, hCT31789.2	223799_at, 227418_at	NP_115800.1, EAW67071.1
GeneID:2977	GUCY1A2	11	106,557,910	106,889,171	331,261	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1272, 2_A375_pNL97_plus_lncRNA_AR..1..1785	-781, -813	upstream, upstream	1	1	0	22	44	11	1	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene GUCY1A2	GUC1A2, GC-SA2, GUCY1A2	guanylate cyclase 1, soluble, alpha 2	NM_000855, hCT31787.3	206927_s_at	NP_000846.1, EAW67081.1
GeneID:91801	ALKBH8	11	107,373,453	107,436,461	63,008	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1273, 2_A375_pNL97_plus_lncRNA_AR..1..1786	2701, 333	in gene, in gene	1	1	0	16.5	13.5	4.5	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ALKBH8	FLJ38204, ABH8, MGC10235, ALKBH8	alkB, alkylation repair homolog 8 (E. coli)	NM_138775, hCT2334823.1, hCT2354414.0, hCT31960.4	235610_at, 235713_at	NP_620130.2, EAW67088.1, EAW67089.1, EAW67090.1
GeneID:6588	SLN	11	107,578,101	107,582,787	4,686	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1787	12483	downstream	0	1	0	13	16	4	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SLN	SLN, MGC12301, MGC125855, MGC125854	sarcolipin	NM_003063, hCT30582.1	205374_at	NP_003054.1, EAW67094.1
GeneID:54733	SLC35F2	11	107,661,717	107,729,914	68,197	-	1	4_A375_EGR1..1..1711	602	in gene	0	0	1	6	11	14	1	4_A375_EGR1..1	14	Gene SLC35F2	FLJ13018, DKFZp667H1615, SLC35F2, HSNOV1	solute carrier family 35, member F2	NM_017515, hCT1964850.1, hCT2334818.0, hCT2354410.0, hCT2354411.0, hCT31957.2	218826_at	NP_059985.2, EAW67098.1, EAW67095.1, EAW67096.1, EAW67097.1, EAW67099.1
GeneID:54734	RAB39	11	107,799,277	107,834,208	34,931	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1788	115	in gene	0	1	0	6	14	13	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene RAB39	RAB39		NM_017516, hCT1640103.2	1554800_at	NP_059986.1, EAW67100.1
GeneID:4863	NPAT	11	108,028,117	108,093,365	65,248	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1789, 4_A375_EGR1..1..1712	-491, -507	upstream, upstream	0	1	1	9	15	18	1	4_A375_EGR1..1	18	Gene NPAT	p220, NPAT, E14/NPAT, E14	nuclear protein, ataxia-telangiectasia locus	NM_002519, hCT2334906.0, hCT30750.3	209798_at, 211584_s_at, 211585_at	NP_002510.2, EAW67107.1, EAW67108.1
GeneID:472	ATM	11	108,093,559	108,239,826	146,267	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1789, 4_A375_EGR1..1..1712	297, 313	in gene, in gene	0	1	1	9	15	18	1	4_A375_EGR1..1	18	Gene ATM	ATM, TELO1, DKFZp781A0353, AT1, ATDC, ATE, TEL1, ATC, ATD, ATA, MGC74674	ataxia telangiectasia mutated	NM_000051, hCT2334886.1, hCT2334888.1, hCT2334889.1, hCT2334890.1, hCT2334891.1, hCT2354367.0, hCT2354368.0, hCT29277.5	1553387_at, 1554631_at, 1570352_at, 210858_x_at, 212672_at	NP_000042.3, EAW67111.1, EAW67108.1, EAW67109.1, EAW67110.1, EAW67112.1, EAW67113.1, EAW67114.1, EAW67115.1
GeneID:23086	EXPH5	11	108,378,158	108,464,374	86,216	-	1	4_A375_EGR1..1..1713	662	in gene	0	0	1	4	7	14	1	4_A375_EGR1..1	14	Gene EXPH5	MGC133291, DKFZp586F1223, MGC134967, SLAC2-B, SLAC2B, DKFZp781H0795, EXPH5, KIAA0624	exophilin 5	NM_015065, NM_001144763, NM_001144765, hCT30752.2	214734_at, 215226_at	NP_055880.2, NP_001138235.1, NP_001138237.1, EAW67121.1
GeneID:5450	POU2AF1	11	111,222,980	111,250,157	27,177	-	1	4_A375_EGR1..1..1714	-3	upstream	0	0	1	3	7	14	1	4_A375_EGR1..1	14	Gene POU2AF1	POU2AF1, BOB1, OBF1, OCAB, OBF-1	POU class 2 associating factor 1	NM_006235, hCT30726.2	1569675_at, 205267_at	NP_006226.2, EAW67137.1
GeneID:644277	LOC644277	11	111,299,223	111,327,330	28,107	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1275	18217	in gene	1	0	0	17	5	5	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene LOC644277		hypothetical LOC644277	XR_110541, XR_114547		
GeneID:5519	PPP2R1B	11	111,597,632	111,637,169	39,537	-	1	4_A375_EGR1..1..1715	337	in gene	0	0	1	7	10	14	1	4_A375_EGR1..1	14	Gene PPP2R1B	PR65B, PPP2R1B, MGC26454, PP2A-Abeta	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	NM_181699, NM_002716, NM_001177562, NM_001177563, NM_181700, hCT2335632.0, hCT30727.3	202883_s_at, 202884_s_at, 202885_s_at, 202886_s_at, 222351_at	NP_859050.1, NP_002707.3, NP_001171033.1, NP_001171034.1, NP_859051.1, EAW67151.1, EAW67150.1
GeneID:79796	ALG9	11	111,652,919	111,742,305	89,386	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1276, 2_A375_pNL97_plus_lncRNA_AR..1..1792	-7583, -7199	upstream, upstream	1	1	0	18	15	6	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ALG9	DIBD1, DKFZp586M2420, FLJ21845, CDG1L, LOH11CR1J, ALG9	asparagine-linked glycosylation 9, alpha-1,2-mannosyltransferase homolog (S. cerevisiae)	NM_024740, NM_001077690, NM_001077692, NM_001077691, hCT2335626.0, hCT2335627.0, hCT2335628.0, hCT2335629.0, hCT2335630.0, hCT2354430.0, hCT2354431.0, hCT2354432.0	219374_s_at, 228817_at	NP_079016.2, NP_001071158.1, NP_001071160.1, NP_001071159.1, EAW67152.1, EAW67156.1, EAW67153.1, EAW67154.1, EAW67155.1, EAW67157.1, EAW67158.1, EAW67159.1
GeneID:91893	FDXACB1	11	111,744,780	111,750,153	5,373	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1276, 2_A375_pNL97_plus_lncRNA_AR..1..1792	265, 649	in gene, in gene	1	1	0	18	15	6	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene FDXACB1	FDXACB1		NM_138378	229989_at	NP_612387.1
GeneID:64776	C11orf1	11	111,749,946	111,754,796	4,850	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1276, 2_A375_pNL97_plus_lncRNA_AR..1..1792	-60, -444	upstream, upstream	1	1	0	18	15	6	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene C11orf1	FLJ23499, C11orf1	chromosome 11 open reading frame 1	NM_022761, hCT30724.2	218925_s_at, 222765_x_at, 231530_s_at, 231538_at	NP_073598.1, EAW67160.1
GeneID:4684	NCAM1	11	112,831,995	113,149,158	317,163	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1794	37	in gene	0	1	0	6	16	7	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene NCAM1	NCAM1, NCAM, MSK39, CD56	neural cell adhesion molecule 1	NM_000615, NM_001076682, NM_181351, hCT2334944.1, hCT2334945.1, hCT2334946.1, hCT2334947.1, hCT2334948.1, hCT2334950.1, hCT2354470.0, hCT2354471.0	1562999_at, 209968_s_at, 212843_at, 214952_at, 217359_s_at, 227394_at, 229799_s_at, 231532_at	NP_000606.3, NP_001070150.1, NP_851996.2, EAW67201.1, EAW67203.1, EAW67207.1, EAW67202.1, EAW67204.1, EAW67205.1, EAW67206.1, EAW67208.1
GeneID:54970	TTC12	11	113,185,251	113,237,114	51,863	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1795	301	in gene	0	1	0	11	21	5	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TTC12	TTC12, FLJ20535, FLJ13859, TPARM	tetratricopeptide repeat domain 12	NM_017868, hCT2349002.0, hCT2349003.0, hCT2349004.0, hCT2354427.0, hCT2354428.0	1554531_at, 215598_at, 219587_at, 244571_s_at	NP_060338.3, EAW67214.1, EAW67210.1, EAW67211.1, EAW67212.1, EAW67213.1
GeneID:1813	DRD2	11	113,280,317	113,346,001	65,684	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1278, 1_A375_pNL7_minus_lncRNA_AR..1..1279, 2_A375_pNL97_plus_lncRNA_AR..1..1796, 2_A375_pNL97_plus_lncRNA_AR..1..1797, 2_A375_pNL97_plus_lncRNA_AR..1..1798	27073, 649, 26913, 26993, 649	in gene, in gene, in gene, in gene, in gene	1	1	0	33.33	37	9.67	3	2_A375_pNL97_plus_lncRNA_AR..1	74	Gene DRD2	D2DR, DRD2, D2R	dopamine receptor D2	NM_000795, NM_016574, hCT1768544.2, hCT2334985.0, hCT2334986.0, hCT2334987.0, hCT2334990.0, hCT2334991.0, hCT30845.3	206590_x_at, 211624_s_at, 216924_s_at, 216938_x_at	NP_000786.1, NP_057658.2, EAW67219.1, EAW67222.1, EAW67224.1, EAW67225.1, EAW67220.1, EAW67221.1, EAW67223.1
GeneID:100422855	MIR4301	11	113,320,745	113,320,810	65	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1278, 2_A375_pNL97_plus_lncRNA_AR..1..1796, 2_A375_pNL97_plus_lncRNA_AR..1..1797	1682, 3722, 1802	downstream, downstream, downstream	1	1	0	20.5	18.5	6.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene MIR4301	MIR4301	microRNA 4301	NR_036183		
GeneID:9183	ZW10	11	113,603,909	113,644,425	40,516	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1280, 2_A375_pNL97_plus_lncRNA_AR..1..1801	-119, -71	upstream, upstream	1	1	0	32	29	6	1	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene ZW10	ZW10, KNTC1AP, MGC149821, HZW10	ZW10, kinetochore associated, homolog (Drosophila)	NM_004724, hCT30844.2	204612_at	NP_004715.1, EAW67229.1
GeneID:644672	CLDN25	11	113,650,518	113,651,207	689	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1280, 2_A375_pNL97_plus_lncRNA_AR..1..1801	-5974, -6022	upstream, upstream	1	1	0	32	29	6	1	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene CLDN25	CLDN25		NM_001101389		NP_001094859.1
GeneID:3359	HTR3A	11	113,845,797	113,861,035	15,238	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1281, 2_A375_pNL97_plus_lncRNA_AR..1..1802	16251, 16251	downstream, downstream	1	1	0	32	39	5	1	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene HTR3A	5HT3R, HTR3, 5-HT3R, HTR3A, 5-HT3A, 5-HT-3	5-hydroxytryptamine (serotonin) receptor 3A	NM_000869, NM_213621, NM_001161772, hCT1971536.1, hCT1971538.1, hCT2354467.0, hCT30842.3	216615_s_at, 217002_s_at	NP_000860.2, NP_998786.2, NP_001155244.1, EAW67237.1, EAW67238.1, EAW67239.1, EAW67240.1
GeneID:4837	NNMT	11	114,166,535	114,183,238	16,703	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1803	-679	upstream	0	1	0	9	14	7	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene NNMT	NNMT	nicotinamide N-methyltransferase	NM_006169, hCT2334917.0, hCT30808.3	202237_at, 202238_s_at, 231559_at	NP_006160.1, EAW67244.1, EAW67243.1
GeneID:100506941	LOC100506941	11	114,167,095	114,168,862	1,767	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1803	3006	downstream	0	1	0	9	14	7	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene LOC100506941		hypothetical LOC100506941	XR_111222, XR_110521, XR_114526		
GeneID:54494	C11orf71	11	114,262,170	114,271,139	8,969	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1805	3	in gene	0	1	0	14	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene C11orf71	FLJ20010, C11orf71	chromosome 11 open reading frame 71	NM_019021, hCT2334993.0	218789_s_at, 222743_s_at	NP_061894.2, EAW67245.1
GeneID:10179	RBM7	11	114,271,384	114,279,635	8,251	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1805	-246	upstream	0	1	0	14	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RBM7	RBM7, FLJ11153	RNA binding motif protein 7	NM_016090, hCT2334918.0, hCT2354369.0, hCT2354370.0	218379_at, 235045_at	NP_057174.1, EAW67247.1, EAW67246.1, EAW67248.1
GeneID:25996	REXO2	11	114,310,108	114,321,001	10,893	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1282, 2_A375_pNL97_plus_lncRNA_AR..1..1806	100, 36	in gene, in gene	1	1	0	22	32	9	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene REXO2	SFN, REXO2, RFN, DKFZp566E144, REX2, CGI-114, MGC111570	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	NM_015523, hCT2334919.0, hCT29253.2	218194_at, 223989_s_at, 239616_at	NP_056338.2, EAW67249.1, EAW67250.1
GeneID:23705	CADM1	11	115,044,345	115,375,241	330,896	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1283, 1_A375_pNL7_minus_lncRNA_AR..1..1284, 1_A375_pNL7_minus_lncRNA_AR..1..1285, 2_A375_pNL97_plus_lncRNA_AR..1..1807, 2_A375_pNL97_plus_lncRNA_AR..1..1808, 2_A375_pNL97_plus_lncRNA_AR..1..1809	281961, 3865, 116, 203257, 1385, 297	in gene, in gene, in gene, in gene, in gene, in gene	1	1	0	13	13.2	6	5	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene CADM1	MGC51880, sTSLC-1, Necl-2, sgIGSF, RA175, ST17, CADM1, IGSF4A, DKFZp686F1789, NECL2, MGC149785, SYNCAM, synCAM1, IGSF4, TSLC1, BL2	cell adhesion molecule 1	NM_014333, NM_001098517, hCT2334938.0, hCT2354364.0, hCT2354365.0, hCT2354366.0, hCT29243.2	209030_s_at, 209031_at, 209032_s_at, 232787_at, 244345_at	NP_055148.3, NP_001091987.1, EAW67258.1, EAW67257.1, EAW67256.1, EAW67260.1, EAW67259.1
GeneID:345	APOC3	11	116,700,624	116,703,787	3,163	+	1	4_A375_EGR1..1..1724	6000	downstream	0	0	1	6	6	18	1	4_A375_EGR1..1	18	Gene APOC3	APOCIII, MGC150353, APOC3	apolipoprotein C-III	NM_000040, hCT2335395.0, hCT32604.1	205820_s_at, 231587_at	NP_000031.1, EAW67272.1, EAW67273.1
GeneID:335	APOA1	11	116,706,469	116,708,338	1,869	-	1	4_A375_EGR1..1..1724	1714	in gene	0	0	1	6	6	18	1	4_A375_EGR1..1	18	Gene APOA1	MGC117399, APOA1	apolipoprotein A-I	NM_000039, hCT1955712.1, hCT2335729.0, hCT2354349.0, hCT32602.2	204450_x_at, 217073_x_at, 231694_at	NP_000030.1, EAW67274.1, EAW67275.1, EAW67276.1, EAW67277.1
GeneID:23387	SIK3	11	116,714,118	116,968,993	254,875	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1289, 1_A375_pNL7_minus_lncRNA_AR..1..1290, 4_A375_EGR1..1..1724	71201, 25441, 262369	in gene, in gene, downstream	1	0	1	14.33	10.33	7.67	3	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene SIK3	FLJ12240, L19, KIAA0999, SIK3, QSK	SIK family kinase 3	NM_025164, hCT2335724.0, hCT32605.3	1554929_at, 1563455_at, 204155_s_at, 204156_at, 204157_s_at, 213034_at	NP_079440.2, EAW67278.1, EAW67279.1
GeneID:5049	PAFAH1B2	11	117,015,000	117,047,810	32,810	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1291, 2_A375_pNL97_plus_lncRNA_AR..1..1812, 4_A375_EGR1..1..1725	34472, 34440, 34984	downstream, downstream, downstream	1	1	1	61	69	24	1	2_A375_pNL97_plus_lncRNA_AR..1	69	Gene PAFAH1B2	PAFAH1B2		NM_001184746, NM_001184747, NM_001184748, NM_002572, hCT1966836.1, hCT30521.3	1569431_at, 210160_at, 224777_s_at	NP_001171675.1, NP_001171676.1, NP_002563.1, NP_001171677.1, EAW67281.1, EAW67282.1
GeneID:51092	SIDT2	11	117,049,939	117,066,161	16,222	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1291, 2_A375_pNL97_plus_lncRNA_AR..1..1812, 4_A375_EGR1..1..1725	-467, -499, 45	upstream, upstream, in gene	1	1	1	61	69	24	1	2_A375_pNL97_plus_lncRNA_AR..1	69	Gene SIDT2	FLJ90656, CGI-40, DKFZp686L17253, SIDT2	SID1 transmembrane family, member 2	NM_001040455, hCT2335404.1, hCT2335406.0, hCT2335407.0, hCT2344518.0, hCT2344519.0, hCT2344520.0, hCT2344521.0, hCT2344522.0, hCT2344523.0, hCT2344524.0, hCT2344525.0, hCT2344526.0, hCT2344527.0, hCT2354466.0	218765_at, 56256_at	NP_001035545.1, EAW67294.1, EAW67283.1, EAW67284.1, EAW67285.1, EAW67291.1, EAW67286.1, EAW67287.1, EAW67288.1, EAW67289.1, EAW67290.1, EAW67292.1, EAW67293.1, EAW67296.1, EAW67295.1
GeneID:9159	PCSK7	11	117,075,768	117,102,811	27,023	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1292, 2_A375_pNL97_plus_lncRNA_AR..1..1813	-357, -357	upstream, upstream	1	1	0	53	54	7	1	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene PCSK7	SPC7, LPC, PC8, FLJ23503, PCSK7, FLJ45329, PC7	proprotein convertase subtilisin/kexin type 7	NM_004716, hCT2335716.0, hCT2335718.0, hCT2335719.0	203118_at, 232521_at	NP_004707.2, EAW67304.1, EAW67303.1, EAW67305.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:257160	RNF214	11	117,103,404	117,156,404	53,000	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1292, 2_A375_pNL97_plus_lncRNA_AR..1..1813	-236, -236	upstream, upstream	1	1	0	53	54	7	1	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene RNF214	DKFZp547C195, RNF214	ring finger protein 214	NM_207343, NM_001077239, hCT2354345.0, hCT29566.2	227114_at	NP_997226.2, NP_001070707.1, EAW67306.1, EAW67307.1
GeneID:23621	BACE1	11	117,156,414	117,186,972	30,558	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1293, 2_A375_pNL97_plus_lncRNA_AR..1..1814, 4_A375_EGR1..1..1726	-47, -100, -100	upstream, upstream, upstream	1	1	1	21	20	13	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene BACE1	BACE1, HSPC104, ASP2, BACE, FLJ90568, KIAA1149	beta-site APP-cleaving enzyme 1	NM_012104, NM_138971, NM_138972, NM_138973, hCT1966055.1, hCT2335710.0, hCT2335711.0, hCT2335712.0, hCT2335713.0, hCT2335715.0, hCT2354435.0, hCT2354436.0, hCT2354437.0, hCT29178.3	217904_s_at, 222462_s_at, 222463_s_at, 224335_s_at	NP_036236.1, NP_620427.1, NP_620428.1, NP_620429.1, EAW67312.1, EAW67313.1, EAW67308.1, EAW67309.1, EAW67310.1, EAW67311.1, EAW67314.1, EAW67315.1, EAW67316.1, EAW67317.1
GeneID:22897	CEP164	11	117,198,571	117,283,982	85,411	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1815	277	in gene	0	1	0	10	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CEP164	KIAA1052, FLJ54767, CEP164	centrosomal protein 164kDa	NM_014956, hCT1950917.1, hCT2335415.0, hCT2335416.0, hCT2354457.0	1558953_s_at, 204250_s_at, 204251_s_at	NP_055771.4, EAW67321.1, EAW67318.1, EAW67319.1, EAW67320.1
GeneID:100129201	LOC100129201	11	117,206,917	117,207,347	430	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1815	8499	downstream	0	1	0	10	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100129201		hypothetical protein LOC100129201	XM_001725443, XM_003118961, XM_003120720		XP_001725495.1, XP_003119029.1, XP_003120768.1
GeneID:57453	DSCAML1	11	117,298,489	117,667,976	369,487	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1294, 2_A375_pNL97_plus_lncRNA_AR..1..1816, 4_A375_EGR1..1..1727, 4_A375_EGR1..1..1728, 4_A375_EGR1..1..1729	199976, 199944, 338520, 271352, 48298	in gene, in gene, in gene, in gene, in gene	1	1	1	7	7.75	13.5	4	4_A375_EGR1..1	17	Gene DSCAML1	DSCAML1, KIAA1132	Down syndrome cell adhesion molecule like 1	NM_020693, hCT1950931.0, hCT2354456.0	232059_at, 234908_s_at	NP_065744.2, EAW67323.1, EAW67322.1
GeneID:916	CD3E	11	118,175,295	118,186,890	11,595	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1817	12225	downstream	0	1	0	16	19	7	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CD3E	CD3E, TCRE, T3E, FLJ18683	CD3e molecule, epsilon (CD3-TCR complex)	NM_000733, hCT1963416.1, hCT1963417.1, hCT1963418.1, hCT2335746.0, hCT32417.3	205456_at	NP_000724.1, EAW67361.1, EAW67360.1, EAW67362.1, EAW67363.1, EAW67364.1
GeneID:917	CD3G	11	118,215,059	118,224,497	9,438	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1818	15117	downstream	0	1	0	11	30	11	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene CD3G	MGC138597, CD3-GAMMA, CD3G, FLJ17620, T3G, FLJ17664, FLJ94613, FLJ79544	CD3g molecule, gamma (CD3-TCR complex)	NM_000073, hCT1647007.3	206804_at	NP_000064.1, EAW67366.1
GeneID:9354	UBE4A	11	118,230,302	118,269,926	39,624	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1295, 2_A375_pNL97_plus_lncRNA_AR..1..1818, 2_A375_pNL97_plus_lncRNA_AR..1..1819	41954, -126, 42082	downstream, upstream, downstream	1	1	0	14	23	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene UBE4A	UFD2, E4, UBOX2, UBE4A, MGC133315, KIAA0126	ubiquitination factor E4A (UFD2 homolog, yeast)	NM_004788	202036_at	NP_004779.2
GeneID:10632	ATP5L	11	118,272,104	118,280,562	8,458	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1295, 2_A375_pNL97_plus_lncRNA_AR..1..1819	152, 280	in gene, in gene	1	1	0	17	16	14	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ATP5L	ATP5JG, ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	NM_006476, NR_033759	207573_x_at, 208745_at, 208746_x_at, 210453_x_at	NP_006467.4
GeneID:84798	MGC13053	11	118,303,856	118,305,921	2,065	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1296, 2_A375_pNL97_plus_lncRNA_AR..1..1820, 2_A375_pNL97_plus_lncRNA_AR..1..1821	-1119, 365, -1071	upstream, in gene, upstream	1	1	0	22	24.5	11	2	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene MGC13053		hypothetical MGC13053	XR_111217, XR_110526, XR_114531	211775_x_at	
GeneID:4297	MLL	11	118,307,205	118,395,936	88,731	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1296, 2_A375_pNL97_plus_lncRNA_AR..1..1820, 2_A375_pNL97_plus_lncRNA_AR..1..1821, 4_A375_EGR1..1..1730	-165, -1669, -213, 97863	upstream, upstream, upstream, downstream	1	1	1	18.67	19.67	13	3	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene MLL	FLJ11783, CXXC7, KMT2A, MLL/GAS7, HTRX1, MLL, TRX1, TET1-MLL, ALL-1, MLL1A, HRX	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	NM_005933, hCT1956297.2, hCT1956298.2, hCT2335761.1, hCT2335764.1, hCT30555.4	1559856_s_at, 1565436_s_at, 212076_at, 212078_s_at, 212079_s_at, 212080_at, 216624_s_at, 226981_at, 244110_at	NP_005924.2, EAW67383.1, EAW67380.1, EAW67381.1, EAW67382.1, EAW67384.1
GeneID:143941	TTC36	11	118,398,210	118,401,740	3,530	+	1	4_A375_EGR1..1..1730	6676	downstream	0	0	1	12	10	17	1	4_A375_EGR1..1	17	Gene TTC36	HBP21, TTC36	tetratricopeptide repeat domain 36	NM_001080441	237350_at	NP_001073910.1
GeneID:84866	TMEM25	11	118,401,803	118,417,313	15,510	+	1	4_A375_EGR1..1..1730	3285	in gene	0	0	1	12	10	17	1	4_A375_EGR1..1	17	Gene TMEM25	TMEM25, FLJ14399	transmembrane protein 25	NM_001144034, NM_001144036, NM_001144037, NM_001144038, NM_032780, NM_001144035, hCT1950930.1, hCT2335768.0, hCT2335769.0, hCT2335770.0, hCT2354423.0, hCT31481.3	226647_at, 238514_at	NP_001137506.1, NP_001137508.1, NP_001137509.1, NP_001137510.1, NP_001137507.1, NP_116169.2, EAW67388.1, EAW67389.1, EAW67390.1, EAW67391.1, EAW67392.1, EAW67393.1
GeneID:56912	C11orf60	11	118,415,243	118,436,791	21,548	-	1	4_A375_EGR1..1..1730	31703	downstream	0	0	1	12	10	17	1	4_A375_EGR1..1	17	Gene C11orf60	C11orf2, FLJ21827, IFT46, C11orf60	chromosome 11 open reading frame 60	NM_020153, NM_001168618, hCT2335913.0, hCT2335914.0, hCT31478.4	218483_s_at	NP_064538.3, NP_001162089.1, EAW67394.1, EAW67395.1, EAW67396.1
GeneID:372	ARCN1	11	118,443,102	118,473,748	30,646	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1297, 2_A375_pNL97_plus_lncRNA_AR..1..1822, 4_A375_EGR1..1..1731	36194, 36366, 36301	downstream, downstream, downstream	1	1	1	26	17	19	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene ARCN1	ARCN1, COPD	archain 1	NM_001655, NM_001142281, hCT2335772.0, hCT2354412.0, hCT31474.3	201176_s_at	NP_001646.2, NP_001135753.1, EAW67397.1, EAW67398.1, EAW67399.1
GeneID:23187	PHLDB1	11	118,477,213	118,528,741	51,528	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1297, 2_A375_pNL97_plus_lncRNA_AR..1..1822, 4_A375_EGR1..1..1731	2083, 2275, 2190	in gene, in gene, in gene	1	1	1	26	17	19	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene PHLDB1	MGC111531, FLJ00141, DKFZp686H039, DKFZp686O24210, LL5A, FLJ90266, PHLDB1, KIAA0638	pleckstrin homology-like domain, family B, member 1	NM_015157, NM_001144758, NM_001144759, hCT1950929.1, hCT2335775.0, hCT2354415.0, hCT2354416.0, hCT2354417.0, hCT2354418.0, hCT2354419.0, hCT31479.2	212134_at, 216019_x_at, 216102_at	NP_055972.1, NP_001138230.1, NP_001138231.1, EAW67401.1, EAW67406.1, EAW67407.1, EAW67400.1, EAW67402.1, EAW67403.1, EAW67404.1, EAW67405.1
GeneID:1656	DDX6	11	118,618,472	118,661,972	43,500	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1823	-140	upstream	0	1	0	10	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene DDX6	HLR2, RCK, P54, FLJ36338, DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	NM_004397, hCT2335907.0, hCT29866.3	204909_at	NP_004388.2, EAW67413.1, EAW67412.1
GeneID:643	CXCR5	11	118,754,541	118,766,971	12,430	+	1	4_A375_EGR1..1..1732	18323	downstream	0	0	1	2	7	17	1	4_A375_EGR1..1	17	Gene CXCR5	BLR1, CXCR5, MGC117347, MDR15, CD185	chemokine (C-X-C motif) receptor 5	NM_032966, NM_001716, hCT2335890.0, hCT29183.3	206126_at, 216734_s_at	NP_116743.1, NP_001707.1, EAW67415.1, EAW67416.1
GeneID:283149	BCL9L	11	118,766,849	118,781,613	14,764	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1824, 4_A375_EGR1..1..1732	-9075, 6749	upstream, in gene	0	1	1	10.5	14.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene BCL9L	DLNB11, BCL9L, BCL9-2	B-cell CLL/lymphoma 9-like	NM_182557	227616_at, 228065_at	NP_872363.1
GeneID:7379	UPK2	11	118,827,008	118,829,269	2,261	+	1	4_A375_EGR1..1..1734	766	in gene	0	0	1	10	7	17	1	4_A375_EGR1..1	17	Gene UPK2	MGC138598, UP2, UPII, UPK2	uroplakin 2	NM_006760	207862_at	NP_006751.1
GeneID:338657	CCDC84	11	118,868,652	118,886,455	17,803	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1827, 4_A375_EGR1..1..1735	-372, 20860	upstream, downstream	0	1	1	14	15.5	20	2	4_A375_EGR1..1	26	Gene CCDC84	CCDC84, DLNB14	coiled-coil domain containing 84	NM_198489, hCT2335891.0, hCT2335892.0, hCT2354440.0	227206_at	NP_940891.1, EAW67424.1, EAW67422.1, EAW67423.1
GeneID:6230	RPS25	11	118,886,422	118,889,057	2,635	-	1	4_A375_EGR1..1..1735	-655	upstream	0	0	1	14	14	26	1	4_A375_EGR1..1	26	Gene RPS25	S25, RPS25	ribosomal protein S25	NM_001028, hCT1966833.1, hCT29862.3	200091_s_at	NP_001019.1, EAW67425.1, EAW67426.1
GeneID:51399	TRAPPC4	11	118,889,241	118,894,384	5,143	+	1	4_A375_EGR1..1..1735	471	in gene	0	0	1	14	14	26	1	4_A375_EGR1..1	26	Gene TRAPPC4	HSPC172, PTD009, CGI-104, TRS23, SYNBINDIN, SBDN, TRAPPC4	trafficking protein particle complex 4	NM_016146	217958_at, 217959_s_at, 234456_at	NP_057230.1
GeneID:2542	SLC37A4	11	118,895,061	118,901,616	6,555	-	1	4_A375_EGR1..1..1735	11904	downstream	0	0	1	14	14	26	1	4_A375_EGR1..1	26	Gene SLC37A4	MGC15729, G6PT1, GSD1d, G6PT2, TRG19, G6PT3, GSD1b, PRO0685, SLC37A4, GSD1c	solute carrier family 37 (glucose-6-phosphate transporter), member 4	NM_001164277, NM_001164278, NM_001164279, NM_001467, NM_001164280, hCT1950921.1, hCT1950922.1, hCT1958397.1, hCT2335966.0, hCT2335968.0, hCT2335969.0, hCT2335971.0, hCT29880.3	202830_s_at, 217289_s_at	NP_001157749.1, NP_001157750.1, NP_001157751.1, NP_001157752.1, NP_001458.1, EAW67434.1, EAW67432.1, EAW67433.1, EAW67435.1, EAW67436.1, EAW67437.1, EAW67438.1, EAW67439.1
GeneID:55823	VPS11	11	118,938,493	118,952,688	14,195	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1302, 2_A375_pNL97_plus_lncRNA_AR..1..1828, 4_A375_EGR1..1..1736	17059, 35, 63	downstream, in gene, in gene	1	1	1	17	20	13	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene VPS11	END1, hVPS11, VPS11, RNF108, PEP5	vacuolar protein sorting 11 homolog (S. cerevisiae)	NM_021729, hCT2335700.0, hCT2335701.0, hCT30850.4	203292_s_at	NP_068375.3, EAW67444.1, EAW67445.1, EAW67446.1
GeneID:3145	HMBS	11	118,955,587	118,964,259	8,672	+	7	1_A375_pNL7_minus_lncRNA_AR..1..1302, 1_A375_pNL7_minus_lncRNA_AR..1..1303, 1_A375_pNL7_minus_lncRNA_AR..1..1304, 2_A375_pNL97_plus_lncRNA_AR..1..1829, 2_A375_pNL97_plus_lncRNA_AR..1..1830, 4_A375_EGR1..1..1737, 4_A375_EGR1..1..1738	-35, 10525, 17149, 10397, 17065, 9533, 10493	upstream, downstream, downstream, downstream, downstream, downstream, downstream	1	1	1	19.25	19.5	15.75	4	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene HMBS	PBG-D, PBGD, HMBS, PORC, UPS	hydroxymethylbilane synthase	NM_000190, NM_001024382, hCT1950927.1, hCT2354408.0, hCT2354409.0, hCT30849.2	203040_s_at	NP_000181.2, NP_001019553.1, EAW67447.1, EAW67448.1, EAW67449.1, EAW67450.1
GeneID:3014	H2AFX	11	118,964,584	118,966,177	1,593	-	7	1_A375_pNL7_minus_lncRNA_AR..1..1302, 1_A375_pNL7_minus_lncRNA_AR..1..1303, 1_A375_pNL7_minus_lncRNA_AR..1..1304, 2_A375_pNL97_plus_lncRNA_AR..1..1829, 2_A375_pNL97_plus_lncRNA_AR..1..1830, 4_A375_EGR1..1..1737, 4_A375_EGR1..1..1738	10625, 65, -8559, 193, -8495, 1057, 97	downstream, in gene, upstream, in gene, upstream, in gene, in gene	1	1	1	19.25	19.5	15.75	4	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene H2AFX	H2A/X, H2AX, H2A.X, H2AFX	H2A histone family, member X	NM_002105, hCT30847.3	205436_s_at, 212524_x_at, 212525_s_at, 213344_s_at	NP_002096.1, EAW67451.1
GeneID:1798	DPAGT1	11	118,967,213	118,972,785	5,572	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1303, 1_A375_pNL7_minus_lncRNA_AR..1..1304, 2_A375_pNL97_plus_lncRNA_AR..1..1829, 2_A375_pNL97_plus_lncRNA_AR..1..1830, 4_A375_EGR1..1..1737, 4_A375_EGR1..1..1738	6673, 49, 6801, 113, 7665, 6705	downstream, in gene, downstream, in gene, downstream, downstream	1	1	1	19.67	20	17.67	3	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene DPAGT1	UGAT, ALG7, DPAGT2, DGPT, D11S366, DPAGT1, CDG-Ij, CDG1J, DPAGT, G1PT, GPT, UAGT	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	NM_001382, hCT1950923.1, hCT1958405.1, hCT2335959.0, hCT30848.3	209509_s_at	NP_001373.2, EAW67455.1, EAW67452.1, EAW67453.1, EAW67454.1
GeneID:9854	C2CD2L	11	118,978,093	118,987,827	9,734	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1304, 2_A375_pNL97_plus_lncRNA_AR..1..1830	-5357, -5421	upstream, upstream	1	1	0	19	25	11	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene C2CD2L	DLNB23, KIAA0285, TMEM24, C2CD2L	C2CD2-like	NM_014807, hCT1950915.1, hCT1950916.1, hCT2335660.0, hCT2335663.0	204757_s_at, 204758_s_at	NP_055622.3, EAW67457.1, EAW67456.1, EAW67458.1, EAW67459.1
GeneID:867	CBL	11	119,076,990	119,178,859	101,869	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1305, 2_A375_pNL97_plus_lncRNA_AR..1..1831, 4_A375_EGR1..1..1739	12386, 12402, 110658	in gene, in gene, downstream	1	1	1	14	15	11.5	2	4_A375_EGR1..1	18	Gene CBL	RNF55, C-CBL, CBL2, CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	NM_005188, hCT6270.2	206607_at, 225231_at, 225234_at, 229010_at, 243475_at	NP_005179.2, EAW67476.1
GeneID:4162	MCAM	11	119,179,234	119,187,840	8,606	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1306, 4_A375_EGR1..1..1739	-4192, 192	upstream, in gene	1	0	1	15	14.5	13.5	2	4_A375_EGR1..1	18	Gene MCAM	CD146, MCAM, MUC18	melanoma cell adhesion molecule	NM_006500, hCT2335950.0, hCT6271.2	203625_x_at, 209086_x_at, 209087_x_at, 210869_s_at, 211042_x_at, 211340_s_at	NP_006491.2, EAW67478.1, EAW67477.1
GeneID:79102	RNF26	11	119,205,237	119,208,022	2,785	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1832, 4_A375_EGR1..1..1740	-181, 235	upstream, in gene	0	1	1	15	17	20	1	4_A375_EGR1..1	20	Gene RNF26	MGC2642, RNF26	ring finger protein 26	NM_032015, hCT1646848.2	224338_s_at, 224947_at	NP_114404.1, EAW67479.1
GeneID:83552	MFRP	11	119,209,652	119,217,383	7,731	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1832, 4_A375_EGR1..1..1740	12327, 11911	downstream, downstream	0	1	1	15	17	20	1	4_A375_EGR1..1	20	Gene MFRP	MFRP, RD6, FLJ30570, MGC32938, DKFZp586B0621, NNO2, MCOP5	membrane frizzled-related protein	NM_031433, hCT1769106.2	224286_at	NP_113621.1, EAW67483.1
GeneID:114902	C1QTNF5	11	119,209,652	119,217,383	7,731	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1832, 4_A375_EGR1..1..1740	12327, 11911	downstream, downstream	0	1	1	15	17	20	1	4_A375_EGR1..1	20	Gene C1QTNF5	FLJ30570, DKFZp586B0621, C1QTNF5, CTRP5, LORD	C1q and tumor necrosis factor related protein 5	NM_015645, hCT2335949.0, hCT6272.3	223499_at	NP_056460.1, EAW67482.1, EAW67481.1
GeneID:100499227	LOC100499227	11	119,252,486	119,369,944	117,458	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1307, 2_A375_pNL97_plus_lncRNA_AR..1..1833	112120, 112088	in gene, in gene	1	1	0	51	60	8	1	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene LOC100499227		hypothetical LOC100499227	NR_034160		
GeneID:5818	PVRL1	11	119,508,608	119,599,435	90,827	-	2	2_A375_pNL97_plus_lncRNA_AR..1..1836, 4_A375_EGR1..1..1741	-861, 94155	upstream, downstream	0	1	1	9.5	13.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PVRL1	OFC7, SK-12, PRR1, CD111, PRR, HVEC, PVRR, MGC142031, nectin-1, CLPED1, MGC16207, PVRL1, HIgR, PVRR1, ED4	poliovirus receptor-related 1 (herpesvirus entry mediator C)	NM_203285, NM_203286, NM_002855, hCT1963555.1, hCT1963556.1, hCT2335981.0	208455_at, 211845_at, 211846_s_at, 225211_at	NP_976030.1, NP_976031.1, NP_002846.3, EAW67492.1, EAW67493.1, EAW67494.1
GeneID:100507077	LOC100507077	11	119,810,421	119,817,424	7,003	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1836	-10325	upstream	0	1	0	14	24	10	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LOC100507077		hypothetical LOC100507077	XR_110527		
GeneID:220323	OAF	11	120,081,747	120,100,650	18,903	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1310, 2_A375_pNL97_plus_lncRNA_AR..1..1838, 2_A375_pNL97_plus_lncRNA_AR..1..1839	-147, 429, 7266	upstream, in gene, in gene	1	1	0	22.5	19.5	10	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene OAF	NS5ATP13TP2, MGC52117, OAF	OAF homolog (Drosophila)	NM_178507, hCT2335030.1	1553569_at, 1553570_x_at	NP_848602.1, EAW67502.1
GeneID:25833	POU2F3	11	120,110,951	120,190,653	79,702	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1311, 2_A375_pNL97_plus_lncRNA_AR..1..1840, 4_A375_EGR1..1..1742	65033, 65017, 65049	downstream, downstream, in gene	1	1	1	22	25	11	2	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene POU2F3	MGC126698, Epoc-1, Skn-1a, FLJ40063, OCT11, POU2F3, PLA-1	POU class 2 homeobox 3	NM_014352, hCT1952991.1	207109_at, 215355_at	NP_055167.2, EAW67503.1
GeneID:219902	TMEM136	11	120,196,016	120,201,347	5,331	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1311, 2_A375_pNL97_plus_lncRNA_AR..1..1840	-32, -48	upstream, upstream	1	1	0	37	45	8	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene TMEM136	TMEM136, MGC17839	transmembrane protein 136	NM_174926, hCT2354393.0, hCT7376.2	1554076_s_at, 230166_at, 238497_at	NP_777586.1, EAW67505.1, EAW67506.1
GeneID:23365	ARHGEF12	11	120,207,946	120,360,645	152,699	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1312	95094	in gene	1	0	0	18	8	3	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ARHGEF12	LARG, ARHGEF12, PRO2792, KIAA0382, DKFZp686O2372	Rho guanine nucleotide exchange factor (GEF) 12	NM_015313, hCT2335035.0, hCT2335036.0, hCT5981.3	1559833_at, 1566093_at, 1570471_at, 201333_s_at, 201334_s_at, 201335_s_at, 210741_at, 233620_at, 233621_s_at, 234129_at, 234541_s_at, 234542_at, 234544_at	NP_056128.1, EAW67509.1, EAW67508.1, EAW67510.1
GeneID:219899	TBCEL	11	120,894,803	120,980,356	85,553	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1841	58765	in gene	0	1	0	10	20	2	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TBCEL	EI, TBCEL, LRRC35, FLJ14177, MGC10233	tubulin folding cofactor E-like	NM_152715, NM_001130047, hCT1952987.1, hCT2354434.0, hCT7277.2	231997_at	NP_689928.3, NP_001123519.1, EAW67513.1, EAW67514.1, EAW67515.1



Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Start	Interval Pos	1_AS75_2_AS75_2_AS75_3_AS75_4_AS75_4_AS75_Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
Gene ID:10 3907149	LOC100 907149	11	121,938,695	122,270,579	356,941	-	4	1_AS75_gAL7_mrna1_lncRNA_AR...1313, 1_AS75_gAL7_mrna1_lncRNA_AR...1314, 2_AS75_gAL007_glut_lncRNA_AR...1642, 2_AS75_gAL007_glut_lncRNA_AR...1643	280971, 146099, 229039, 219643	cr gene, cr gene, cr gene, cr gene	1	1	0	13.25	14	4	4	1_AS75_gAL719_mrna1_lncRNA_AR...1	Gene LOC100907149			lysyl-tRNA synthetase-like	XR_110329		
Gene ID:39 9939	LOC399 939	11	121,938,911	122,052,270	113,359	-	3	1_AS75_gAL7_mrna1_lncRNA_AR...1313, 2_AS75_gAL007_glut_lncRNA_AR...1642, 2_AS75_gAL007_glut_lncRNA_AR...1643	91182, 109236, 188	cr gene, cr gene, upstream	1	1	0	14	13	4	3	1_AS75_gAL717_mrna1_lncRNA_AR...1	Gene LOC399939	MIR100HG, FLJ41933, FLJ43331, DKFZp686G0115, DKFZp686J04156, FLJ21490, FLJ39784	lysyl-tRNA synthetase-like	NR_024430	223091_at, 239640_at, 241979_at	
Gene ID:49 6911	MIR125 B1	11	121,970,453	121,970,552	97	-	1	2_AS75_gAL007_glut_lncRNA_AR...1642	6900	downstream	0	1	0	11	10	1	1	2_AS75_gAL618_glut_lncRNA_AR...1	Gene MIR125B1	MIRN125B1, MIR125B1	microRNA 125b-1	NR_029871		
Gene ID:49 8882	MIRLET7 FA2	11	122,017,230	122,017,301	71	-	1	1_AS75_gAL7_mrna1_lncRNA_AR...1313	4483	downstream	0	0	0	17	9	5	1	1_AS75_gAL517_mrna1_lncRNA_AR...1	Gene MIRLET7A2	MIRLET7A2, LET7A2, let-7a-2, LET7A2, let-7a-2, MIRNLET7A2	microRNA let-7a-2	NR_029477		
Gene ID:54 959	UBASH 3B	11	122,529,295	122,602,187	165,893	+	2	2_AS75_gAL007_glut_lncRNA_AR...1643, 2_AS75_gAL007_glut_lncRNA_AR...1648	994, 48898	cr gene, cr gene	0	1	0	12.5	17.5	9	2	2_AS75_gAL601_glut_lncRNA_AR...1	Gene UBASH3B	MGC154077, STS1, KIAA1959, p70, UBASH3B, STS-1, TULA-2	ubiquitin associated and SH3 domain containing B	NM_032872, NT_010473	235353_s_at, 235359_at, 235462_at, 235507_at, 240307_at	NP_116222.2, EAW58535.1
Gene ID:39 8239	BSX	11	122,648,337	122,652,379	4,022	-	2	1_AS75_gAL7_mrna1_lncRNA_AR...1315, 2_AS75_gAL007_glut_lncRNA_AR...1647	-168, -229	upstream, upstream	1	1	0	29	30	8	1	2_AS75_gAL630_glut_lncRNA_AR...1	Gene BSX	BSX, BSX1	brain-specific homeobox	NM_001078189		NP_001071657.1
Gene ID:55 12	HSPA8	11	122,926,200	122,932,644	6,844	-	1	1_AS75_BGR1...1765	-52	upstream	0	0	1	15	14	22	1	1_AS75_BGR1...1	Gene HSPA8	HSP74 kD, HSP71, HSC71/3151, HSC/P9229, NIP71, HSP72, HSPA10, HSC71, HSC70, HSC54, LAP1	heat shock 70kDa protein 8	NM_006597, NM_153201, NT_033541, NT_033968, NT_167190, NT_167191, NT_167192, NT_167193, NT_167194, NT_167195, NT_167196, NT_167197, NT_167198, NT_167199, NT_167200, NT_167201, NT_167202, NT_167203, NT_167204, NT_167205, NT_167206, NT_167207, NT_167208, NT_167209, NT_167210, NT_167211, NT_167212, NT_167213, NT_167214, NT_167215, NT_167216, NT_167217, NT_167218, NT_167219, NT_167220, NT_167221, NT_167222, NT_167223, NT_167224, NT_167225, NT_167226, NT_167227, NT_167228, NT_167229, NT_167230, NT_167231, NT_167232, NT_167233, NT_167234, NT_167235, NT_167236, NT_167237, NT_167238, NT_167239, NT_167240, NT_167241, NT_167242, NT_167243, NT_167244, NT_167245, NT_167246, NT_167247, NT_167248, NT_167249, NT_167250, NT_167251, NT_167252, NT_167253, 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Gene ID:49 6911	MIR125 B1	11	121,970,453	121,970,552	97	-	1	2_AS75_gAL007_glut_lncRNA_AR...1642	6900	downstream	0	1	0	11	10	1	1	2_AS75_gAL618_glut_lncRNA_AR...1	Gene MIR125B1	MIRN125B1, MIR125B1	microRNA 125b-1	NR_029871		
Gene ID:49 8882	MIRLET7 FA2	11	122,017,230	122,017,301	71	-	1	1_AS75_gAL7_mrna1_lncRNA_AR...1313	4483	downstream	0	0	0	17	9	5	1	1_AS75_gAL517_mrna1_lncRNA_AR...1	Gene MIRLET7A2	MIRLET7A2, LET7A2, let-7a-2, LET7A2, let-7a-2, MIRNLET7A2	microRNA let-7a-2	NR_029477		
Gene ID:54 959	UBASH 3B	11	122,529,295	122,602,187	165,893	+	2	2_AS75_gAL007_glut_lncRNA_AR...1643, 2_AS75_gAL007_glut_lncRNA_AR...1648	994, 48898	cr gene, cr gene	0	1	0	12.5	17.5	9	2	2_AS75_gAL601_glut_lncRNA_AR...1	Gene UBASH3B	MGC154077, STS1, KIAA1959, p70, UBASH3B, STS-1, TULA-2	ubiquitin associated and SH3 domain containing B	NM_032872, NT_010473	235353_s_at, 235359_at, 235462_at, 235507_at, 240307_at	NP_116222.2, EAW58535.1
Gene ID:39 8239	BSX	11	122,648,337	122,652,379	4,022	-	2	1_AS75_gAL7_mrna1_lncRNA_AR...1315, 2_AS75_gAL007_glut_lncRNA_AR...1647	-168, -229	upstream, upstream	1	1	0	29	30	8	1	2_AS75_gAL630_glut_lncRNA_AR...1	Gene BSX	BSX, BSX1	brain-specific homeobox	NM_001078189		NP_001071657.1
Gene ID:55 12	HSPA8	11	122,926,200	122,932,644	6,844	-	1	1_AS75_BGR1...1765	-52	upstream	0	0	1	15	14	22	1	1_AS75_BGR1...1	Gene HSPA8	HSP74 kD, HSP71, HSC71/3151, HSC/P9229, NIP71, HSP72, HSPA10, HSC71, HSC70, HSC54, LAP1	heat shock 70kDa protein 8	NM_006597, NM_153201, NT_033541, NT_033968, NT_167190, NT_167191, NT_167192, NT_167193, NT_167194, NT_167195, NT_167196, NT_167197, NT_167198, NT_167199, NT_167200, NT_167201, NT_167202, NT_167203, NT_167204, NT_167205, NT_167206, NT_167207, NT_167208, NT_167209, NT_167210, NT_167211, NT_167212, NT_167213, NT_167214, NT_167215, NT_167216, NT_167217, NT_167218, NT_167219, NT_167220, NT_167221, NT_167222, NT_167223, NT_167224, NT_167225, NT_167226, NT_167227, NT_167228, NT_167229, NT_167230, NT_167231, NT_167232, NT_167233, NT_167234, NT_167235, NT_167236, NT_167237, NT_167238, NT_167239, NT_167240, NT_167241, NT_167242, NT_167243, NT_167244, NT_167245, NT_167246, NT_167247, NT_167248, NT_167249, NT_167250, NT_167251, NT_167252, NT_167253, 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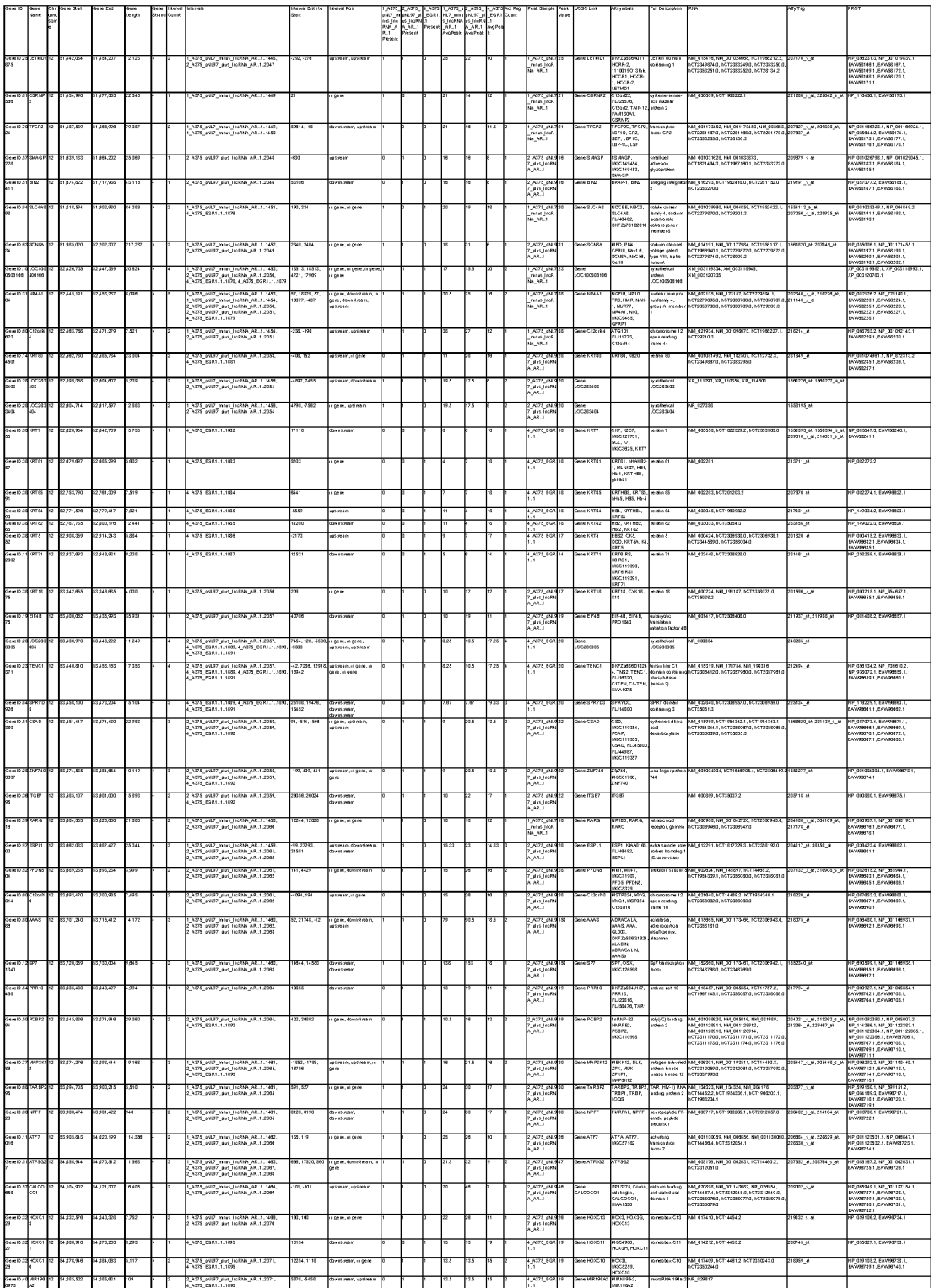


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_3_A375_4_A375_1_A375_2_A375_3_A375_4_A375 Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alu Tag	PROT
GeneID:49155	LTBP3	11	64,493,537	64,500,734	7,377	+	1	2_A375_shU7_plus_lncRNA_NR_1:1914	115	cv gene	0 1 0 16 20 15 1	2_A375_shU7_plus_lncRNA_NR_1	20	Gene LTBP3	LTBP, TGFB2-BP, TNF-R-III, TNFRSF5, TNFR-RI, LTBP-3, CD16, TNFCR, D1S2870	prometrotoxin beta receptor (TNFR-I superfamily, member 5)	NM_002342, XCT13627.2, XCT1907587.1	203605_at, 232619_s_at, 243400_s_at	NP_002333.1, EAW66600.1, EAW66602.1
GeneID:53875	TAPBPL	12	6,361,177	6,371,485	10,311	+	1	4_A375_EGR1_1:1764	16399	downstream	0 0 1 15 21 17 1	4_A375_EGR1_1.1	17	Gene TAPBPL	TAPBPL, TAPBP-R, FLJ10142	TAP binding protein-like	NM_019009, XCT2292997.1, XCT2292998.1, XCT2292999.1	219748_at, 219747_s_at	NP_890478.1, EAW66796.1, EAW66797.1, EAW66799.1
GeneID:66	VAMP1	12	6,371,403	6,379,643	8,440	-	2	4_A375_EGR1_1:1764, 4_A375_EGR1_1:1765	67, -7101	cv gene, upstream	0 0 1 10 12.5 17 2	4_A375_EGR1_1.1	17	Gene VAMP1	SYB1, DKFZp686H0211, VAMP1, VAMP-1	vesicle-associated membrane protein 1 (synaptobrevin 1)	NM_014232, NM_014231, NM_199245, XCT13431.1, XCT1907089.1, XCT1907089.2, XCT2295540.0, XCT2297090.0	207100_s_at, 207101_at, 210226_at	NP_055036.1, NP_055046.1, NP_954745.1, EAW66793.1, EAW66796.1, EAW66797.1, EAW66794.1
GeneID:39	NCAPG2	12	6,803,295	6,841,132	37,834	+	5	1_A375_shU7_minus_lncRNA_NR_1:1394, 2_A375_shU7_plus_lncRNA_NR_1:1915, 2_A375_shU7_plus_lncRNA_NR_1:1916, 4_A375_EGR1_1:1788, 4_A375_EGR1_1:1797	40807, 40446, 40242, 40130, 40054	Downstream, Downstream, Downstream, Downstream, Downstream	1 1 1 13.33 21.33 16.33 3	2_A375_shU7_plus_lncRNA_NR_1	28	Gene NCAPG2	CAP-D2, bMAG190, CAPG1, NCAPD2, hCAP-D2	non-SMC condensin I complex, subunit D2	NM_014865, XCT1542973, XCT2293855.0, XCT2297090.0	201774_s_at	NP_055850.3, EAW66788.1, EAW66789.1, EAW66790.1
GeneID:28	GAPDH	12	6,643,837	6,647,336	3,879	+	5	1_A375_shU7_minus_lncRNA_NR_1:1394, 2_A375_shU7_plus_lncRNA_NR_1:1915, 2_A375_shU7_plus_lncRNA_NR_1:1916, 4_A375_EGR1_1:1788, 4_A375_EGR1_1:1797	-182, 67, 3383, 599, 5465	upstream, cv gene, cv gene, cv gene, Downstream	1 1 1 13.33 21.33 16.33 3	2_A375_shU7_plus_lncRNA_NR_1	28	Gene GAPDH	MGC88868, GAPDH, G3PD, GAPD	glyceraldehyde-3-phosphate dehydrogenase	NM_002046, XCT2292608.0, XCT2297101.0	212581_x_at, 213453_x_at, 217398_x_at, APPX-HUMGAPDHN031#F_0_at, APPX-HUMGAPDHN031#F_5_at, APPX-HUMGAPDHN031#F_M_at	NP_002037.2, EAW66767.1, EAW66768.1, EAW66769.1
GeneID:23	IFFO1	12	6,845,894	6,865,249	19,355	-	5	1_A375_shU7_minus_lncRNA_NR_1:1394, 2_A375_shU7_plus_lncRNA_NR_1:1915, 2_A375_shU7_plus_lncRNA_NR_1:1916, 4_A375_EGR1_1:1788, 4_A375_EGR1_1:1797	21944, 21935, 18209, 21201, 18037	Downstream, Downstream, Downstream, Downstream, cv gene	1 1 1 13.33 21.33 16.33 3	2_A375_shU7_plus_lncRNA_NR_1	28	Gene IFFO1	MGC117389, IFFO, DKFZp686E223, HOMTES-103, IFFO1, FLJ20703	intermediate filament family orphan 1	NM_019379, NM_001159437, NM_030750, NR_038467, XCT13932.2, XCT2296997.0, XCT2297090.0, XCT2295570.0, XCT2295574.0	209721_s_at, 39332_at	NP_001034769.1, NP_001180358.1, NP_542756.2, EAW66781.1, EAW66782.1, EAW66783.1, EAW66782.1, EAW66783.1
GeneID:48	NOP2	12	6,866,037	6,877,480	11,443	-	1	4_A375_EGR1_1:1788	51	cv gene	0 0 1 11 15 21 1	4_A375_EGR1_1.1	21	Gene NOP2	MGC117354, NOP120, NOP2, MGC149287, p120, MGC149285, NOL1, NSUN1	NOP2 nucleolar protein homolog (yeast)	NM_006178, NM_001032714, XCT2295365.0	214427_at	NP_006169.2, NP_001028056.1, EAW66769.1
GeneID:16	CHD4	12	6,879,246	6,718,551	37,305	-	2	4_A375_EGR1_1:1788, 4_A375_EGR1_1:1789	59122, 151	Downstream, cv gene	0 0 1 12 14.5 19.5 2	4_A375_EGR1_1.1	21	Gene CHD4	Mi2-BETA, CHD4, mi-2b, DKFZp686D0916	chromodomain helicase DNA binding protein 4	NM_001273, XCT2295992.0, XCT2296998.0, XCT2299097.0	1569419_at, 201162_s_at, 201163_s_at, 201164_s_at	NP_001264.2, EAW66779.1, EAW66777.1, EAW66778.1
GeneID:37	LPAR3	12	6,720,001	6,743,297	17,296	-	1	4_A375_EGR1_1:1793	19357	cv gene	0 0 1 8 9 25 1	4_A375_EGR1_1.1	23	Gene LPAR3	LPA3, LPAR3, HYQ_010, GPR32, GPR35	lysophosphatidic acid receptor 3	NM_012400, NM_001142991, XCT2299777.1, XCT2344452.0	230252_at, 231760_at	NP_036533.1, NP_001139433.1, EAW66775.1, EAW66776.1
GeneID:51	ING4	12	6,759,704	6,772,306	12,604	-	2	1_A375_shU7_minus_lncRNA_NR_1:1385, 2_A375_shU7_plus_lncRNA_NR_1:1917	-126, -220	upstream, upstream	1 0 0 19 19 0 1	1_A375_shU7_minus_lncRNA_NR_1	19	Gene ING4	ING4, p29ING4, my038, MGC13357	inhibitor of growth family, member 4	NM_001127552, NM_016162, NM_001127563, XCT2295365.0, XCT2297090.0, XCT2297091.0, XCT2297092.0, XCT2297093.0, XCT2297094.0, XCT2297095.0, XCT2297096.0, XCT2297097.0, XCT2297098.0, XCT2297099.0, XCT2297100.0, XCT2297101.0	216224_at, 46828_at	NP_001121624.1, NP_057248.2, NP_001121553.1, NP_001121555.1, NP_001121557.1, NP_001121558.1, EAW66762.1, EAW66763.1, EAW66764.1, EAW66765.1, EAW66766.1, EAW66767.1, EAW66768.1, EAW66770.1, EAW66771.1, EAW66772.1, EAW66773.1
GeneID:15	ZNF384	12	6,775,845	6,795,676	20,832	-	4	1_A375_shU7_minus_lncRNA_NR_1:1385, 2_A375_shU7_minus_lncRNA_NR_1:1385, 2_A375_shU7_plus_lncRNA_NR_1:1917, 2_A375_shU7_plus_lncRNA_NR_1:1918	28844, -76, 28140, 212	Downstream, upstream, Downstream, cv gene	1 1 0 19.5 16.5 6 2	2_A375_shU7_plus_lncRNA_NR_1	20	Gene ZNF384	CHAF1A, TNRC1, ZNF384, NP_ERDA2, FLJ39143, CHAF1, NM74, CZ	zinc finger protein 384	NM_130479, NM_001029916, NM_001033917, NM_001029916, NM_001029919, NM_001029920, NM_001133734, XCT13082.3, XCT1894390.3, XCT2296982.0, XCT2296986.0, XCT2297100.0, XCT2297110.0	212389_at	NP_877753.2, NP_001029053.1, NP_001029056.1, NP_001033071.1, NP_001033068.1, NP_001033069.1, NP_001129236.1, EAW66763.1, EAW66766.1, EAW66767.1, EAW66768.1, EAW66769.1, EAW66770.1, EAW66771.1, EAW66772.1, EAW66773.1
GeneID:19	C12orf53	12	6,802,937	6,809,812	6,855	-	2	1_A375_shU7_minus_lncRNA_NR_1:1386, 2_A375_shU7_plus_lncRNA_NR_1:1916	11060, 11546	Downstream, Downstream	1 1 0 20 16 6 1	1_A375_shU7_minus_lncRNA_NR_1	20	Gene C12orf53	C12orf53, DKFZp547D220, RHAP	chromosome 12 open reading frame 53	NM_153503, XCT17074.4, XCT2241534.0, XCT2401135.0, XCT2401136.0, XCT2401138.0	1553666_at, 229165_at	NP_710152.1, EAW66731.1, EAW66732.1, EAW66733.1, EAW66734.1
GeneID:30	COPS7A	12	6,833,190	6,841,041	7,851	+	2	1_A375_shU7_minus_lncRNA_NR_1:1387, 2_A375_shU7_plus_lncRNA_NR_1:1919	148, 226	cv gene, cv gene	1 1 0 33 30 16 1	1_A375_shU7_minus_lncRNA_NR_1	33	Gene COPS7A	COPS7A, CSN7A, MGC110077	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	NM_001164795, NM_016319, NM_001164803, NM_001164794, XCT19874.0, XCT2297090.0, XCT2297091.0, XCT2297092.0, XCT2297093.0, XCT2297101.0	209079_at	NP_001157667.1, NP_057403.1, NP_001157669.1, NP_001157668.1, EAW66745.1, EAW66747.1, EAW66748.1, EAW66749.1
GeneID:59	MLF2	12	6,837,156	6,862,836	9,476	-	1	2_A375_shU7_plus_lncRNA_NR_1:1920	238	cv gene	0 0 1 17 16 17 1	2_A375_shU7_plus_lncRNA_NR_1	18	Gene MLF2	NTNM, MLF2	myeloid leukemia factor 2	NM_005439, NR_038581, XCT17082.2, XCT2295990.0	209045_at	NP_005430.1, EAW66742.1, EAW66744.1
GeneID:60	CD4	12	6,846,836	6,923,976	31,205	+	2	1_A375_shU7_minus_lncRNA_NR_1:1386, 2_A375_shU7_plus_lncRNA_NR_1:1921	39656, 39570	Downstream, Downstream	1 1 0 20 16 15 1	1_A375_shU7_minus_lncRNA_NR_1	20	Gene CD4	CD4mut, CD4	CD4 molecule	NM_000616, NM_001195014, NM_001199035, NM_001199036, XCT19.4, XCT2295365.0, XCT2297090.0, XCT2297091.0, XCT2297092.0, XCT2297093.0, XCT2297094.0, XCT2297095.0, XCT2297096.0, XCT2297097.0, XCT2297098.0, XCT2297099.0, XCT2297100.0, XCT2297101.0	203537_at, 216424_at	NP_000597.1, NP_001181943.1, NP_001181944.1, NP_001181945.1, NP_001181946.1, EAW66735.1, EAW66739.1
GeneID:27	GPR162	12	6,930,983	6,938,583	8,820	+	2	1_A375_shU7_minus_lncRNA_NR_1:1388, 2_A375_shU7_plus_lncRNA_NR_1:1921	7981, 7245	Downstream, Downstream	1 1 0 20 16 15 1	1_A375_shU7_minus_lncRNA_NR_1	20	Gene GPR162	FLJ78937, n-2, GRCA, GPR162	G protein-coupled receptor 162	NM_194449, NM_019558, XCT2285598.1, XCT2285614.0, XCT2285616.0	230606_s_at	NP_382094.1, NP_061822.1, EAW66735.1, EAW66736.1, EAW66737.1
GeneID:10	LEPREL1	12	6,957,372	6,969,016	11,645	+	3	1_A375_shU7_minus_lncRNA_NR_1:1966, 2_A375_shU7_plus_lncRNA_NR_1:1921, 4_A375_EGR1_1:1791	1052, 658, 12730	cv gene, cv gene, Downstream	1 1 1 15 11 17 2	2_A375_shU7_minus_lncRNA_NR_1	20	Gene LEPREL1	RSAH7926, GRCB, P3H3, LEPREL2	leprecan-like 2	NM_018192, XCT2285580.1, XCT2297130.0, XCT2297131.0, XCT2297132.0	204954_at	NP_055777.2, EAW66731.1, EAW66732.1, EAW66733.1, EAW66734.1
GeneID:27	GNB3	12	6,949,375	6,958,537	7,162	+	3	1_A375_shU7_minus_lncRNA_NR_1:1389, 2_A375_shU7_plus_lncRNA_NR_1:1922, 4_A375_EGR1_1:1791	12359, 12299, 697	Downstream, Downstream, cv gene	1 1 1 20.5 26 14.5 2	2_A375_shU7_plus_lncRNA_NR_1	24	Gene GNB3	GNB3		NM_002075, XCT17983.2	206947_at	NP_002084.1, EAW66730.1
GeneID:83	CDCA3	12	6,957,972	6,960,436	2,464	-	3	1_A375_shU7_minus_lncRNA_NR_1:1389, 2_A375_shU7_plus_lncRNA_NR_1:1922, 4_A375_EGR1_1:1791	-1205, -1256, 10164	upstream, upstream,	1 1 1 20.5 26 14.5 2	2_A375_shU7_plus_lncRNA_NR_1	24	Gene CDCA3	GRCC5, CDCA3, FBXO32, TOME-1, MGC13057	cell division cycle associated 3	NM_031299, XCT19702.2, XCT1934389.1	221436_s_at, 222027_at	NP_112561.1, EAW66729.1, EAW66728.1
GeneID:89	USP3	12	6,961,283	6,973,796	14,311	+	4	1_A375_shU7_minus_lncRNA_NR_1:1389, 2_A375_shU7_minus_lncRNA_NR_1:1922, 2_A375_shU7_plus_lncRNA_NR_1:1922, 4_A375_EGR1_1:1792	379, 379, 21677, 13631	cv gene, cv gene, Downstream, Downstream,	1 1 1 20.67 26.33 15 3	2_A375_shU7_plus_lncRNA_NR_1	24	Gene USP3	SNT1, USP3	ubiquitin specific peptidase 3 (ubiquitin-specific protease 3)	NM_030441, NM_001079538, XCT17982.2, XCT19874.0, XCT2295322.0, XCT2307106.0	208031_s_at	NP_030472.2, NP_001070006.1, NP_001070007.1, EAW66734.1, EAW66735.1, EAW66727.1, EAW66727.1
GeneID:71	TPI1	12	6,976,594	6,990,110	13,516	+	2	2_A375_shU7_plus_lncRNA_NR_1:1922, 4_A375_EGR1_1:1792	6525, 152	Downstream, cv gene	0 0 1 13.5 16.5 17.5 2	2_A375_shU7_plus_lncRNA_NR_1	21	Gene TPI1	TPI, MGC88105, TPI1	triosephosphate isomerase 1	NM_000365, NM_001159357, NR_027453, XCT17994.4, XCT19874.29.1, XCT19874.30.1	200027_s_at, 210039_s_at, 213011_s_at	NP_000356.1, NP_001137791.1, EAW66721.1, EAW66722.1, EAW66723.1
GeneID:44	SPSB2	12	6,990,099	6,992,331	2,232	-	2	2_A375_shU7_plus_lncRNA_NR_1:1921, 4_A375_EGR1_1:1792	-291, 3765	upstream, Downstream	0 0 1 13.5 16.5 17.5 2	2_A375_shU7_plus_lncRNA_NR_1	21	Gene SPSB2	hucAry/ankyrin repeat/b-domain and SOCS box-containing 2	NM_001146816, NM_032641, XCT17983.3, XCT2295940.0	223360_at	NP_001139288.1, NP_116030.1, EAW66719.1, EAW66720.1
GeneID:16	ATN1	12	7,033,826	7,051,494	17,668	+	6	1_A375_shU7_minus_lncRNA_NR_1:1371, 1_A375_shU7_minus_lncRNA_NR_1:1372, 1_A375_shU7_minus_lncRNA_NR_1:1923, 2_A375_shU7_plus_lncRNA_NR_1:1926, 4_A375_EGR1_1:1795, 4_A375_EGR1_1:1796	13670, 20186, 13670, 20086, 13648, 19716	upstream, downstream, cv gene, downstream, cv gene, downstream,	1 1 1 65 65.5 21.5 2	2_A375_shU7_minus_lncRNA_NR_1	11	Gene ATN1	B37, D12S755E, HRS, ATN1, DRPLA, MOD	atrophin 1	NM_001940, NM_001007026, XCT17994.2, XCT2295482.0, XCT2295494.0	1553734_s_at, 230077_at, 211076_s_at, 229265_s_at, 40489_at	NP_001931.2, NP_001007027.1, EAW66706.1, EAW66707.1, EAW66708.1
GeneID:19	RNU7-1	12	7,082,979	7,083,041	62	+	6	1_A375_shU7_minus_lncRNA_NR_1:1371, 1_A375_shU7_minus_lncRNA_NR_1:1372, 1_A375_shU7_minus_lncRNA_NR_1:1923, 2_A375_shU7_plus_lncRNA_NR_1:1926, 4_A375_EGR1_1:1795, 4_A375_EGR1_1:1796	5983, 5113, -9983, 723, -9907, 388	upstream, Downstream, upstream, Downstream, upstream, Downstream	1 1 1 65 65.5 21.5 2	2_A375_shU7_plus_lncRNA_NR_1	11	Gene RNU7	RNU7-1, U7.1, RNU7	RNA, U7 small nuclear 1	NR_023317		
GeneID:11	C12orf57	12	7,083,203	7,088,165	7,962	+	6	1_A375_shU7_minus_lncRNA_NR_1:1371, 1_A375_shU7_minus_lncRNA_NR_1:1372, 1_A375_shU7_minus_lncRNA_NR_1:1923, 2_A375_shU7_plus_lncRNA_NR_1:1926, 4_A375_EGR1_1:1795, 4_A375_EGR1_1:1796	5907, 599, 9907, 805, -6131, 141	upstream, cv gene, upstream, cv gene, upstream, cv gene	1 1 1 65 65.5 21.5 2	2_A375_shU7_plus_lncRNA_NR_1	11	Gene C12orf57	FLJ17350, GRCC10, C12orf57	chromosome 12 open reading frame 57	NM_138425, XCT19874.32.1	224719_s_at	NP_612434.1, EAW66708.1
GeneID:57	PTPN6	12	7,055,740	7,070,479	14,739	+	12	1_A375_shU7_minus_lncRNA_NR_1:1371, 1_A375_shU7_minus_lncRNA_NR_1:1372, 1_A375_shU7_minus_lncRNA_NR_1:1373, 1_A375_shU7_minus_lncRNA_NR_1:1374, 2_A375_shU7_plus_lncRNA_NR_1:1923, 2_A375_shU7_plus_lncRNA_NR_1:1926, 2_A375_shU7_plus_lncRNA_NR_1:1927, 2_A375_shU7_plus_lncRNA_NR_1:1928, 4_A375_EGR1_1:1795, 4_A375_EGR1_1:1796, 4_A375_EGR1_1:1797	-5444, -7140, 14654, 24180, 5444, -2026, 14620, 23992, 6865, -2396, 21186, 24094	upstream, upstream, Downstream, upstream, upstream, Downstream, upstream, Downstream, upstream, Downstream, Downstream, Downstream	1 1 1 38.6 36 30.6 5	2_A375_shU7_plus_lncRNA_NR_1	11	Gene PTPN6	SHP-1L, SH-PTP1, SHP-1, HCPH, HCP, PTP-1C, SHP1, HPTP1C, PTPN6	protein tyrosine phosphatase, non-receptor type 6	NM_080548, NM_002831, NM_080549, XCT17993.2, XCT2296497.0, XCT2296499.0, XCT2296547.0, XCT2296547.1	209967_s_at	NP_536358.1, NP_002822.2, NP_536359.1, EAW66700.1, EAW66701.1, EAW66703.1, EAW66702.1, EAW66704.1
GeneID:49	LOC100507944	12	7,072,409	7,073,610	1,201	+	6	1_A375_shU7_minus_lncRNA_NR_1:1373, 1_A375_shU7_minus_lncRNA_NR_1:1374, 1_A375_shU7_minus_lncRNA_NR_1:1927, 2_A375_shU7_plus_lncRNA_NR_1:1928, 4_A375_EGR1_1:1796, 4_A375_EGR1_1:1797	-1765, 7511, 1965, 7324, 4515, 7415	upstream, Downstream, upstream, Downstream, upstream, Downstream	1 1 1 17.67 16.33 20.33 3	4_A375_EGR1_1.1	28	Gene LOC100507944		hypothetical LOC100507944	XR_111251, XR_109127, XR_114394		
GeneID:40	MIR200C	12	7,072,982	7,073,029	47	+	6	1_A375_shU7_minus_lncRNA_NR_1:1373, 1_A375_shU7_minus_lncRNA_NR_1:1374, 1_A375_shU7_minus_lncRNA_NR_1:1927, 2_A375_shU7_plus_lncRNA_NR_1:1928, 4_A375_EGR1_1:1796, 4_A375_EGR1_1:1797	-2235, 7055, -2332, 6671, 4086, 6962	upstream, Downstream, upstream, Downstream, upstream, Downstream,	1 1 1 17.67 16.33 20.33 3	4_A375_EGR1_1.1	28	Gene MIR200C	MIRN200C, MIR200C	microRNA 200c	NR_029779		
GeneID:49	MIR141	12	7,073,280	7,073,334	54	+	6	1_A375_shU7_minus_lncRNA_NR_1:1373, 1_A375_shU7_minus_lncRNA_NR_1:1374, 1_A375_shU7_minus_lncRNA_NR_1:1927, 2_A375_shU7_plus_lncRNA_NR_1:1928, 4_A375_EGR1_1:1796, 4_A375_EGR1_1:1797	-2808, 6660, 2700, 6673, 3956, 6864	upstream, Downstream, upstream, Downstream, Downstream, Downstream	1 1 1 17.67 16.33 20.33 3	4_A375_EGR1_1.1	28	Gene MIR141	MIRN141, MIR141	microRNA 141	NR_029682		
GeneID:19	PHB2	12	7,074,315	7,079,918	5,603	+	6	1_A375_shU7_minus_lncRNA_NR_1:1373, 1_A375_shU7_minus_lncRNA_NR_1:1374, 1_A375_shU7_minus_lncRNA_NR_1:1927, 2_A375_shU7_plus_lncRNA_NR_1:1928, 4_A375_EGR1_1:1796, 4_A375_EGR1_1:1797	6262, -4, 5396, 183, 2966, 92	Downstream, upstream, Downstream, cv gene, cv gene, cv gene	1 1 1 17.67 16.33 20.33 3	4_A375_EGR1_1.1	28	Gene PHB2	B27, REA, BAP, Hap37, BCAP37, PHB2, MGC117395, PNAS-141	prohibitin 2	NM_007270, NM_001144831, XCT17987.3	201569_at	NP_009204.1, NP_001138393.1, EAW66699.1
GeneID:87	SCAFN12	12	7,076,930	7,078,799	289	-	6	1_A375_shU7_minus_lncRNA_NR_1:1373, 1_A375_shU7_minus_lncRNA_NR_1:1374, 1_A375_shU7_minus_lncRNA_NR_1:1927, 2_A375_shU7_plus_lncRNA_NR_1:1928, 4_A375_EGR1_1:1796, 4_A375_EGR1_1:1797	6143, -2151, 6231, -2364, 189, -3355	Downstream, upstream, Downstream, upstream, upstream	1 1 1 17.67 16.33 20.33 3	4_A375_EGR1_1.1	28	Gene SCAFN12	SCAFN12, UBY	small Cajal body-specific RNA 12	NR_033010		
GeneID:10	EMG1	12	7,079,944	7,085,165	5,221	+	6	1_A375_shU7_minus_lncRNA_NR_1:1373, 1_A375_shU7_minus_lncRNA_NR_1:1374, 1_A375_shU7_minus_lncRNA_NR_1:1927, 2_A375_shU7_plus_lncRNA_NR_1:1928, 4_A375_EGR1_1:1796, 4_A375_EGR1_1:1797	-5020, -24, -9356, -211, -3018, -120	upstream, Downstream, upstream, Downstream, upstream, upstream	1 1 1 17.67 16.33 20.33 3	4_A375_EGR1_1.1	28	Gene EMG1	EMG1, NEP1, MRT52, C2F, Gnu21, BWCN5	EMG1 nucleolar 18S rRNA methyltransferase homolog (S. cerevisiae)	NM_006331, XCT17994.4, XCT19874.35.2, XCT2349137.0, XCT2349138.0, XCT2349139.0	209232_at	NP_006322.4, EAW66696.1, EAW66694.1, EAW66695.1, EAW66697.1, EAW66696.1
GeneID:16	LPCAT3	12	7,085,347	7,133,642	48,296	+	4	1_A375_shU7_minus_lncRNA_NR_1:1374, 2_A375_shU7_plus_lncRNA_NR_1:1926, 4_A375_EGR1_1:1796, 4_A375_EGR1_1:1797	43822, 46169, 44814, 46016	Downstream, Downstream, Downstream, Downstream,	1 1 1 14 13.5 20.5 2	4_A375_EGR1_1.1	28	Gene LPCAT3	LPLAT 5, MBOAT5, LPCAT, DACT3, lenny, LPCAT3, C2F, LPSAT	lysophosphatidylcholine acyltransferase 3	NM_033189, XCT19703.2, XCT19543571.1, XCT2295922.0	202763_at, 213915_at	NP_058705.4, EAW66692.1, EAW66693.1
GeneID:51	C1R	12	7,247,148	7,261,899	14,752	-	1	4_A375_EGR1_1:1797	613	cv gene	0 0 1 9 11 18 1	4_A375_EGR1_1.1	18	Gene C1R	C1-LP, C1R1, C1R-LP, C1R, C1qrs	complement component 1, r subcomponent	NM_019346, XCT17072.2, XCT2298119.0	218803_at, 213645_s_at	NP_037403.2, EAW66666.1, EAW66669.1
GeneID:25	UNQ2500	12	7,260,904	7,274,447	13,543	+	1	2_A375_shU7_plus_lncRNA_NR_1:1927	152	cv gene	0 0 1 9 11 18 1	2_A375_shU7_plus_lncRNA_NR_1	18	Gene UNQ2500	LOC283314, MART2595	hypothetical LOC283314	NR_038947	1560320_s_at, 1564224_s_at	
GeneID:38	PEX5	12	7,341,799	7,371,170	29,411	+	3	1_A375_shU7_minus_lncRNA_NR_1:1375, 2_A375_shU7_plus_lncRNA_NR_1:1929, 2_A375_shU7_plus_lncRNA_NR_1:1930	550, 389, 33	cv gene, cv gene, cv gene	1 1 1 25 29 19 3	2_A375_shU7_plus_lncRNA_NR_1	29	Gene PEX5	PTS1R, PEX5, PEX5L, PXR-1, FLJ39146, PTS1-BP	peroxisomal biogenesis factor 5	NM_000319, NM_001131023, NM_001131024, NM_001131025, NM_001174122, XCT19754.2, XCT2295459.0, XCT2295470.0, XCT2295494.0, XCT2295495.0	205344_at, 215481_s_at	NP_000310.2, NP_001124496.1, NP_001124497.1, NP_001124498.1, EAW66673.1, EAW66670.1, EAW66671.1, EAW66672.1, EAW66673.1, EAW66674.1
GeneID:23	CD163L1	12	7,307,396	7,336,749	29,353	+	1	2_A375_shU7_plus_lncRNA_NR_1:1930	74803	cv gene	0 0 1 11 17 6 1	2_A375_shU7_plus_lncRNA_NR_1	17	Gene CD163L1	CD163L, CD163L1, M160	CD163 molecule like 1	NM_174941, XCT19274.2, XCT2337093.0	223653_at	NP_777601.2, EAW66667.1, EAW66668.1
GeneID:33	FOXJ2	12	6,165,339	6,200,116	22,239	+	2	1_A375_shU7_minus_lncRNA_NR_1:1376, 2_A375_shU7_plus_lncRNA_NR_1:1932, 2_A375_shU7_plus_lncRNA_NR_1:1933	-5947, -5947, -200	upstream, upstream, upstream,	1 1 0 16 20.5 6 2	2_A375_shU7_plus_lncRNA_NR_1	23	Gene FOXJ2	FOXJ2, FHX	forkhead box J2	NM_014168, XCT13717.2, XCT2323430.0	1553353_at, 202734_at	NP_055556.1, EAW66642.1, EAW66643.1
GeneID:28	NECAP1	12	6,234,907	6,250,375	15,468	+	2	1_A375_shU7_minus_lncRNA_NR_1:1377, 2_A375_shU7_plus_lncRNA_NR_1:1934	-119, -119	upstream, upstream	1 1 0 24 25 10 1	2_A375_shU7_plus_lncRNA_NR_1	23	Gene NECAP1	NECAP1, DKFZp686H183, MGC131900	NECAP endocytosis associated 1	NM_015939, NR_024298, XCT13312.2, XCT1907332.1, XCT2323424.0, XCT2377105.0	209300_s_at	NP_056124.2, EAW66638.1, EAW66639.1, EAW66637.1, EAW66639.1
GeneID:19	PHC1	12	6,987,316	9,094,085	28,747	+	3	1_A375_shU7_minus_lncRNA_NR_1:1378, 2_A375_shU7_plus_lncRNA_NR_1:1935, 2_A375_shU7_plus_lncRNA_NR_1:1936	33572, 23356, 33540	Downstream, Downstream, Downstream	1 1 0 13 15.5 11 2	1_A375_shU7_plus_lncRNA_NR_1	21	Gene PHC1	RPH1, EDR1, PHC1, RAE28	polyhomeotic homolog 1 (Drosophila)	NM_004426, XCT2295095.1, XCT2295096.1	223856_at	NP_004417.2, EAW66600.1, EAW66601.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.4074	M6PR	12	9,092,984	9,102,252	9,268	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1378, 2_A375_pNL97_plus_lncRNA_AR..1..1935, 2_A375_pNL97_plus_lncRNA_AR..1..1936	-436, 11580, -404	upstream, downstream, upstream	1	1	0	13	15.5	11	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene M6PR	CD-MPR, MPR46, FLJ32994, SMPR, M6PR	mannose-6-phosphate receptor (cation dependent)	NM_002355, hCT16338.4, hCT1961746.2, hCT1961747.2, hCT1961749.2	200900_s_at, 200901_s_at	NP_002346.1, EAW88596.1, EAW88598.1, EAW88597.1, EAW88599.1
GeneID.253128	C12orf33	12	9,208,185	9,217,888	9,461	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1379, 4_A375_EGR1..1..1801	674, -1356	in gene, upstream	1	0	1	11.5	8.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene C12orf33	FLJ41814, C12orf33, MGC40170	chromosome 12 open reading frame 33	NR_034140	1555040_at	
GeneID.144571	LOC144571	12	9,217,773	9,220,651	2,878	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1379, 4_A375_EGR1..1..1801	-761, 1251	upstream, in gene	1	0	1	11.5	8.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene LOC144571		hypothetical LOC144571	NR_026971	1564139_at	
GeneID.2	A2M	12	9,220,304	9,268,558	48,254	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1379, 4_A375_EGR1..1..1801	51566, 49534	downstream, downstream	1	0	1	11.5	8.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene A2M	DKFZp779B086, CPAMD5, S863-7, FWP007, A2M	alpha-2-macroglobulin	NM_000014, hCT16340.4	1556450_at, 217757_at	NP_000005.2, EAW88590.1
GeneID.4973	OLR1	12	10,310,899	10,324,790	13,891	-	1	4_A375_EGR1..1..1803	18550	downstream	0	0	1	10	16	15	1	4_A375_EGR1..1	15	Gene OLR1	LOX1, CLEC8A, SLOX1, SCARE1, LOXIN, OLR1	oxidized low density lipoprotein (lectin-like) receptor 1	NM_002543, NM_001172632, NM_001172633, hCT1950874.0, hCT1962901.1, hCT2298726.0, hCT29382.2	210004_at	NP_002534.1, NP_001166103.1, NP_001166104.1, EAW96157.1, EAW96158.1, EAW96159.1, EAW96156.1
GeneID.55110	MAGOHB	12	10,758,794	10,766,183	9,389	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1381, 2_A375_pNL97_plus_lncRNA_AR..1..1938	71, 39	in gene, in gene	1	1	0	23	29	11	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene MAGOHB	MGN2, magoh, MAGOHB, FLJ10292, mago	mago-nashi homolog B (Drosophila)	NM_018048, hCT1812470.2, hCT1950856.1, hCT2349784.0, hCT2349785.0	218894_s_at, 222776_at, 241806_at	NP_060518.1, EAW96198.1, EAW96196.1, EAW96197.1, EAW96199.1
GeneID.55359	STYK1	12	10,771,538	10,826,891	55,353	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1381, 2_A375_pNL97_plus_lncRNA_AR..1..1938	60779, 60747	downstream, downstream	1	1	0	23	29	11	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene STYK1	DKFZp761P1010, STYK1, SuRTK106, NOK	serine/threonine/tyrosine kinase 1	NM_018423, hCT16559.1	220030_at, 221696_s_at	NP_060893.2, EAW96200.1
GeneID.8531	CSDA	12	10,851,676	10,875,953	24,277	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1382, 2_A375_pNL97_plus_lncRNA_AR..1..1939, 4_A375_EGR1..1..1804	1073, 673, 657	in gene, in gene, in gene	1	1	1	26	16	21	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene CSDA	CSDA, DBPA, ZONAB, CSDA1	cold shock domain protein A	NM_003651, NM_001145426, hCT1815415.1, hCT18561.3, hCT1950865.1, hCT2298187.0, hCT2298188.0	201160_s_at, 201161_s_at, 213319_s_at, 228634_s_at	NP_003642.3, NP_001138898.1, EAW96201.1, EAW96202.1, EAW96204.1, EAW96205.1, EAW96203.1
GeneID.100506226	LOC100506226	12	10,902,833	10,930,043	27,210	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1383	-161	upstream	1	0	0	15	12	2	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene LOC100506226		hypothetical LOC100506226	XR_111272, XR_111271, XR_109085, XR_109084, XR_114569, XR_114568		
GeneID.11272	PRR4	12	10,998,448	11,324,213	325,765	-	1	4_A375_EGR1..1..1805	53	in gene	0	0	1	13	14	15	1	4_A375_EGR1..1	15	Gene PRR4	DKFZp779L1763, FLJ18757, PRR4, PROL4, LPRP	proline rich 4 (lacrimal)	NM_001098538, NM_007244, hCT2350238.0	204919_at	NP_001092008.1, NP_009175.2, EAW96213.1
GeneID.5554	PRH1	12	11,033,560	11,324,210	290,650	-	1	4_A375_EGR1..1..1805	50	in gene	0	0	1	13	14	15	1	4_A375_EGR1..1	15	Gene PRH1	PA, PRH1, MGC74958, Pa	proline-rich protein HaeIII subfamily 1	NM_006250, hCT2298206.2, hCT2344974.1, hCT2344975.1, hCT2344976.1	205272_s_at	NP_006241.2, EAW96215.1, EAW96214.1, EAW96216.1, EAW96217.1
GeneID.2120	ETV6	12	11,802,788	12,048,336	245,548	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1385, 2_A375_pNL97_plus_lncRNA_AR..1..1941, 2_A375_pNL97_plus_lncRNA_AR..1..1942	-868, -804, 70108	upstream, upstream, in gene	1	1	0	15	17.5	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ETV6	TEL/ABL, TEL, ETV6	ets variant 6	NM_001987, hCT18464.3	205585_at, 225764_at, 235056_at, 239740_at	NP_001978.1, EAW96240.1
GeneID.4040	LRP6	12	12,268,959	12,419,811	150,852	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1387, 2_A375_pNL97_plus_lncRNA_AR..1..1944, 4_A375_EGR1..1..1806	-221, -285, -253	upstream, upstream, upstream	1	1	1	20	25	26	1	4_A375_EGR1..1	26	Gene LRP6	FLJ90421, LRP6, FLJ90062, ADCAD2	low density lipoprotein receptor-related protein 6	NM_002336, hCT17703.3	205606_at, 225745_at, 34697_at	NP_002327.2, EAW96253.1
GeneID.54682	MANSC1	12	12,482,218	12,503,169	20,951	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1388, 4_A375_EGR1..1..1809	-6879, -7263	upstream, upstream	1	0	1	26	18	17	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene MANSC1	MANSC1, 9130403P13Rik, LOH12CR3, FLJ10298	MANSC domain containing 1	NM_018050, hCT1643554.3, hCT1950843.1	220945_x_at	NP_060520.2, EAW96254.1, EAW96255.1
GeneID.503693	LOH12CR2	12	12,508,342	12,510,001	1,659	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1388, 4_A375_EGR1..1..1809	-47, -431	upstream, upstream	1	0	1	26	18	17	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene LOH12CR2	LOH2CR12, LOH12CR2	loss of heterozygosity, 12, chromosomal region 2	NR_024061	236311_at	
GeneID.118426	LOH12CR1	12	12,510,020	12,619,836	109,816	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1388, 2_A375_pNL97_plus_lncRNA_AR..1..1945, 4_A375_EGR1..1..1809	28, 41468, 412	in gene, in gene, in gene	1	1	1	19	17.5	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene LOH12CR1	LOH1CR12, LOH12CR1	loss of heterozygosity, 12, chromosomal region 1	NM_058169, hCT18841.4, hCT1951414.2, hCT2349803.0, hCT2357938.0	227723_at	NP_477517.1, EAW96257.1, EAW96258.1, EAW96259.1, EAW96260.1
GeneID.1389	CREBL2	12	12,764,831	12,798,041	33,210	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1389	-95	upstream	1	0	0	21	14	12	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene CREBL2	MGC117311, MGC138362, CREBL2	cAMP responsive element binding protein-like 2	NM_001310, hCT18833.3, hCT1951411.1, hCT2298173.0	201988_s_at, 201989_s_at, 201990_s_at	NP_001301.1, EAW96269.1, EAW96268.1, EAW96270.1
GeneID.2842	GPR19	12	12,813,995	12,849,121	35,126	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1390, 2_A375_pNL97_plus_lncRNA_AR..1..1946	11457, 11281	in gene, in gene	1	1	0	21	27	4	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene GPR19	GPR19		NM_006143	207183_at	NP_006134.1
GeneID.1027	CDKN1B	12	12,870,302	12,875,305	5,003	+	6	1_A375_pNL7_minus_lncRNA_AR..1..1391, 1_A375_pNL7_minus_lncRNA_AR..1..1392, 1_A375_pNL7_minus_lncRNA_AR..1..1393, 2_A375_pNL97_plus_lncRNA_AR..1..1947, 2_A375_pNL97_plus_lncRNA_AR..1..1948, 4_A375_EGR1..1..1810	2, 8034, 9378, -158, 8098, 7554	in gene, downstream, downstream, upstream, downstream, downstream	1	1	1	18	19	9.67	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CDKN1B	KIP1, CDKN1B, CDKN4, MEN4, P27KIP1, MEN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	NM_004064, hCT18834.2, hCT1951412.1	209112_at	NP_004055.1, EAW96275.1, EAW96276.1
GeneID.81575	APOLD1	12	12,878,851	12,944,400	65,549	+	6	1_A375_pNL7_minus_lncRNA_AR..1..1391, 1_A375_pNL7_minus_lncRNA_AR..1..1392, 1_A375_pNL7_minus_lncRNA_AR..1..1393, 2_A375_pNL97_plus_lncRNA_AR..1..1947, 2_A375_pNL97_plus_lncRNA_AR..1..1948, 4_A375_EGR1..1..1810	-8547, -515, 829, 8707, -451, -995	upstream, upstream, in gene, upstream, upstream, upstream	1	1	1	18	19	9.67	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene APOLD1	DKFZp434F0318, FLJ25138, VERGE, APOLD1, FLJ95166	apolipoprotein L domain containing 1	NM_030817, NM_001130415	221031_s_at	NP_110444.3, NP_001123887.1
GeneID.9052	GPRC5A	12	13,043,956	13,066,600	22,644	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1394, 2_A375_pNL97_plus_lncRNA_AR..1..1949, 2_A375_pNL97_plus_lncRNA_AR..1..1950, 4_A375_EGR1..1..1811	76, -9332, 556, 572	in gene, upstream, in gene, in gene	1	1	1	15	18.5	14	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene GPRC5A	RAI3, GPCR5A, GPRC5A, RAIG1	G protein-coupled receptor, family C, group 5, member A	NM_003979, hCT18835.3	203108_at	NP_003970.1, EAW96289.1
GeneID.50865	HEBP1	12	13,127,798	13,153,243	25,445	-	1	4_A375_EGR1..1..1812	-165	upstream	0	0	1	16	17	12	1	4_A375_EGR1..1	12	Gene HEBP1	HEBP, HEBP1, HBP	heme binding protein 1	NM_015987, hCT18836.4, hCT2299032.0	218450_at	NP_057071.2, EAW96295.1, EAW96296.1
GeneID.57613	KIAA1467	12	13,197,315	13,236,383	39,068	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1395, 2_A375_pNL97_plus_lncRNA_AR..1..1951	-99, 141	upstream, in gene	1	1	0	20	24	16	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene KIAA1467	DKFZp761O012, KIAA1467	KIAA1467	NM_020853, hCT19368.2	1559302_at, 213232_at, 213234_at	NP_065904.1, EAW96298.1
GeneID.83445	GSG1	12	13,237,042	13,256,619	19,577	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1952	1483	in gene	0	1	0	19	26	7	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene GSG1	MGC111023, GSG1, MGC3146	germ cell associated 1	NM_031289, NM_153823, NM_001080554, NM_001080555, hCT19369.3, hCT1951415.1, hCT2299029.0, hCT2357939.0, hCT2357940.0	221252_s_at, 241553_at	NP_112579.2, NP_722545.2, NP_001074023.1, NP_001074024.1, EAW96299.1, EAW96300.1, EAW96301.1, EAW96302.1, EAW96303.1
GeneID.2904	GRIN2B	12	13,714,410	14,133,022	418,612	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1396, 2_A375_pNL97_plus_lncRNA_AR..1..1953	252094, 252446	in gene, in gene	1	1	0	16	16	0	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene GRIN2B	NR2B, MGC142178, NMDAR2B, GRIN2B, hNR3, MGC142180	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	NM_000834, hCT1951423.0	210411_s_at, 210412_at	NP_000825.2, EAW96311.1
GeneID.121504	HIST4H4	12	14,923,654	14,924,065	411	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1398, 2_A375_pNL97_plus_lncRNA_AR..1..1955	161, 209	in gene, in gene	1	1	0	22	17	13	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene HIST4H4	HIST1H4D, HIST1H4H, HIST1H4E, HIST1H4B, HIST2H4A, HIST2H4B, HIST1H4A, HIST1H4L, HIST1H4J, H4/p, MGC24116, HIST1H4C, HIST4H4, HIST1H4I, HIST1H4F, HIST1H4K	histone cluster 4, H4	NM_175054		NP_778224.1
GeneID.55766	H2AFJ	12	14,927,270	14,930,936	3,666	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1398, 2_A375_pNL97_plus_lncRNA_AR..1..1955	-3386, -3414	upstream, upstream	1	1	0	22	17	13	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene H2AFJ	FLJ52230, H2AJ, H2AFJ, MGC921, FLJ10903	H2A histone family, member J	NM_177925, NR_027716, hCT1639889.4, hCT2350491.0	220936_s_at, 224301_x_at, 225245_x_at, 226213_at	NP_808760.1, EAW96327.1, EAW96326.1
GeneID.5800	PTPRO	12	15,475,487	15,750,335	274,848	+	1	4_A375_EGR1..1..1813	161	in gene	0	0	1	7	8	16	1	4_A375_EGR1..1	16	Gene PTPRO	PTP-U2, PTP-oc, GLEPP1, PTPRO, PTPU2	protein tyrosine phosphatase, receptor type, O	NM_002848, NM_030667, NM_030668, NM_030669, NM_030670, NM_030671, hCT16291.2, hCT1813194.1, hCT1813196.2, hCT2298358.1, hCT2298359.1, hCT2298365.1	1554199_at, 208121_s_at	NP_002839.1, NP_109592.1, NP_109593.1, NP_109594.1, NP_109595.1, NP_109596.1, EAW96348.1, EAW96349.1, EAW96350.1, EAW96351.1, EAW96352.1, EAW96353.1
GeneID.2059	EPS8	12	15,773,075	15,942,510	169,435	-	6	2_A375_pNL97_plus_lncRNA_AR..1..1957, 2_A375_pNL97_plus_lncRNA_AR..1..1958, 2_A375_pNL97_plus_lncRNA_AR..1..1959, 2_A375_pNL97_plus_lncRNA_AR..1..1960, 4_A375_EGR1..1..1814, 4_A375_EGR1..1..1815	101088, 88142, 31518, -88, 462, -114	in gene, in gene, in gene, upstream, in gene, upstream	0	1	1	12.75	17.75	7.25	4	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene EPS8	EPS8	epidermal growth factor receptor pathway substrate 8	NM_004447, hCT1951425.2, hCT2357930.0	202609_at	NP_004438.3, EAW96354.1, EAW96355.1
GeneID.11171	STRAP	12	16,035,288	16,056,412	21,124	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1399, 2_A375_pNL97_plus_lncRNA_AR..1..1961, 4_A375_EGR1..1..1816	-88, 328, -58	upstream, in gene, upstream	1	1	1	20	16	16	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene STRAP	STRAP, PT-WD, MAWD, UNRIP	serine/threonine kinase receptor associated protein	NM_007178, hCT16290.3	1558002_at, 200870_at	NP_009109.3, EAW96356.1
GeneID.89869	PLCZ1	12	18,836,116	18,890,918	54,802	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1962	14054	in gene	0	1	0	11	17	3	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PLCZ1	PLCzeta, PLCZ1, MGC149685, NYD-SP27	phospholipase C, zeta 1	NM_033123, hCT15321.3, hCT1951397.1, hCT1971450.1	231425_at	NP_149114.2, EAW96389.1, EAW96388.1, EAW96390.1
GeneID.121536	AEBP2	12	19,592,608	19,675,173	82,565	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1963, 4_A375_EGR1..1..1818, 4_A375_EGR1..1..1819	224, -32, 1024	in gene, upstream, in gene	0	1	1	7.5	12	16	2	4_A375_EGR1..1	16	Gene AEBP2	AEBP2, MGC17922	AE binding protein 2	NM_153207, NM_001114176, hCT1951424.2, hCT2298434.1, hCT2344967.0	225689_at, 235184_at	NP_694939.2, NP_001107648.1, EAW96398.1, EAW96399.1, EAW96400.1
GeneID.100506393	LOC100506393	12	20,167,619	20,251,802	84,183	+	1	4_A375_EGR1..1..1820	87581	downstream	0	0	1	4	6	15	1	4_A375_EGR1..1	15	Gene LOC100506393		hypothetical protein LOC100506393	XM_003118646		XP_003118694.1
GeneID.6579	SLCO1A2	12	21,417,534	21,548,371	130,837	-	1	4_A375_EGR1..1..1821	34243	in gene	0	0	1	3	2	14	1	4_A375_EGR1..1	14	Gene SLCO1A2	SLCO1A2, OATP1A2, OATP, SLC21A3, OATP-A	solute carrier organic anion transporter family, member 1A2	NM_134431, NM_021094, hCT16171.3, hCT2298869.0, hCT2298871.0, hCT2298872.0	207308_at, 211480_s_at, 211481_at	NP_602307.1, NP_066580.1, EAW96422.1, EAW96423.1, EAW96424.1, EAW96425.1
GeneID.3945	LDHB	12	21,788,275	21,810,789	22,514	-	1	4_A375_EGR1..1..1822	165	in gene	0	0	1	17	13	15	1	4_A375_EGR1..1	15	Gene LDHB	LDHB, LDH-H, TRG-5	lactate dehydrogenase B	NM_001174097, NM_002300, hCT15908.3, hCT2298874.0	201030_x_at, 213564_x_at	NP_001167568.1, NP_002291.1, EAW96448.1, EAW96449.1
GeneID.55907	CMAS	12	22,199,159	22,218,602	19,443	+	1	4_A375_EGR1..1..1823	201	in gene	0	0	1	8	10	16	1	4_A375_EGR1..1	16	Gene CMAS	CMAS		NM_018686, hCT15909.3, hCT2298825.0, hCT2357923.0	218111_s_at, 241065_x_at	NP_061156.1, EAW96464.1, EAW96465.1, EAW96466.1
GeneID.6489	ST8SIA1	12	22,346,325	22,487,648	141,323	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1403	-1104	upstream	1	0	0	16	11	3	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene ST8SIA1	SIAT8A, SIAT8, ST8SiaI, ST8SIA1, GD3S	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	NM_003034, hCT15908.3, hCT2298835.0, hCT2357914.0, hCT2357915.0	1569788_at, 210073_at	NP_003025.1, EAW96468.1, EAW96469.1, EAW96470.1, EAW96471.1
GeneID.9847	KIAA0528	12	22,601,517	22,697,452	95,935	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1404, 2_A375_pNL97_plus_lncRNA_AR..1..1966	-20, -20	upstream, upstream	1	1	0	28	35	13	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene KIAA0528	DKFZp779N2044, KIAA0528	KIAA0528	NM_014802, hCT15907.2, hCT2298832.0, hCT2298833.0, hCT2357919.0	212943_at	NP_055617.1, EAW96474.1, EAW96473.1, EAW96475.1, EAW96476.1
GeneID.55500	ETNK1	12	22,778,076	22,843,608	65,532	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1969	198	in gene	0	1	0	15	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ETNK1	EKI1, Nbla10396, EKI, ETNK1, EKI 1	ethanolamine kinase 1	NM_018638, NM_001039481, hCT13824.3, hCT1987884.1, hCT2357934.0	219017_at, 222262_s_at, 224453_s_at, 224454_at, 225290_at, 226432_at, 231576_at	NP_061108.2, NP_001034570.1, EAW96478.1, EAW96479.1, EAW96480.1
GeneID.6660	SOX5	12	23,685,231	24,715,380	1,030,149	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1971	611508	in gene	0	1	0	18	20	3	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SOX5	L-SOX5, MGC35153, SOX5	SRY (sex determining region Y)-box 5	NM_178010, NM_006940, NM_152989, hCT1951385.2, hCT2298450.1, hCT2298451.1, hCT2349788.0, hCT2349789.0, hCT2349790.0, hCT2357933.0	1569836_at, 207336_at, 235285_at	NP_821078.1, NP_008871.3, NP_694534.1, EAW96486.1, EAW96488.1, EAW96491.1, EAW96487.1, EAW96489.1, EAW96490.1, EAW96492.1
GeneID.3845	KRAS	12	25,358,180	25,403,854	45,674	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1405, 2_A375_pNL97_plus_lncRNA_AR..1..1973	-402, -466	upstream, upstream	1	1	0	22	22	8	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene KRAS	K-RAS4A, KRAS, C-K-RAS, Ki-RAS, KRAS1, K-RAS4B, NS3, KRAS2, NS, K-RAS2B, RASK2, K-RAS2A	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	NM_004985, NM_033360, hCT1965959.1, hCT2300689.0, hCT2300691.0, hCT5752.3	1559203_s_at, 1559204_x_at, 204009_s_at, 204010_s_at, 214352_s_at	NP_004976.2, NP_203524.1, EAW96511.1, EAW96512.1, EAW96513.1, EAW96514.1
GeneID.160492	IFLTD1	12	25,629,016	25,801,488	172,472	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1975	181440	downstream	0	1	0	12	18	4	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene IFLTD1	IFLTD1, FLJ36004, Pas1c1	intermediate filament tail domain containing 1	NM_152590, NM_001145727, NM_001145728, NM_001145729, NR_027298, hCT1650229.4, hCT2349782.0, hCT2349783.0	1552665_a_at	NP_689803.2, NP_001139199.1, NP_001139200.1, NP_001139201.1, EAW96516.1, EAW96518.1, EAW96517.1
GeneID.11228	RASSF8	12	26,126,688	26,232,825	106,137	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1407	36704	in gene	1	0	0	18	9	2	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene RASSF8	RASSF8, DKFZp434O0227, FLJ11542, HOJ1, C12orf2	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	NM_007211, NM_001164746, NM_001164747, NM_001164748, hCT1951417.2, hCT2299045.1, hCT2299047.1, hCT29271.4	207754_at, 225946_at, 235996_at	NP_009142.2, NP_001158218.1, NP_001158219.1, NP_001158220.1, EAW96522.1, EAW96524.1, EAW96523.1, EAW96525.1
GeneID.100506529	LOC100506529	12	26,164,711	26,173,442	8,731	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1407	-1319	upstream	1	0	0	18	9	2	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100506529		hypothetical LOC100506529	XR_111285, XR_109094, XR_114579		
GeneID.79365	BHLHE41	12	26,272,959	26,278,003	5,044	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1976	-1517	upstream	0	1	0	14	15	6	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene BHLHE41	BHLHE41, SHARP1, BHLHB3, DEC2, SHARP-1	basic helix-loop-helix family, member e41	NM_030762, hCT2298768.0, hCT29273.3	221530_s_at, 223185_s_at, 231242_at, 231243_s_at	NP_110389.1, EAW96528.1, EAW96527.1
GeneID.3709	ITPR2	12	26,488,285	26,986,131	497,846	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1409, 2_A375_pNL97_plus_lncRNA_AR..1..1979	141523, 579	in gene, in gene	1	1	0	17	16	4.5	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ITPR2	ITPR2, IP3R2	inositol 1,4,5-triphosphate receptor, type 2	NM_002223, hCT2298779.1, hCT2298780.1	202660_at, 202661_at, 202662_s_at, 211360_s_at	NP_002214.2, EAW96534.1, EAW96535.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:55726	C12orf11	12	27,058,112	27,091,254	33,142	-	1	4_A375_EGR1..1..1825	-122	upstream	0	0	1	13	22	17	1	4_A375_EGR1..1	17	Gene C12orf11	C12orf11, NET48, FLJ10637, FLJ10630	chromosome 12 open reading frame 11	NM_018164, hCT2296777.0, hCT29586.2	221652_s_at	NP_060634.2, EAW96538.1, EAW96539.1
GeneID:26127	FGFR1OP2	12	27,091,305	27,119,581	28,276	+	1	4_A375_EGR1..1..1825	71	in gene	0	0	1	13	22	17	1	4_A375_EGR1..1	17	Gene FGFR1OP2	FGFR1OP2, DKFZp586C1423, WIT3.0, FLJ37569, HSPC123-like, DKFZp564O1863	FGFR1 oncogene partner 2	NM_015633, NM_001171887, NM_001171888, hCT1951416.1, hCT29588.2	1556282_at, 1556283_s_at, 223262_s_at, 223263_s_at, 233898_s_at, 236808_at, 243619_at	NP_056448.1, NP_001165358.1, NP_001165359.1, EAW96540.1, EAW96541.1
GeneID:51768	TM7SF3	12	27,124,503	27,167,339	42,836	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1980	-8325	upstream	0	1	0	10	17	10	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TM7SF3	TM7SF3		NM_016551, hCT29587.3	1563898_at, 217974_at, 222477_s_at, 226478_at	NP_057635.1, EAW96542.1
GeneID:9412	MED21	12	27,175,483	27,182,682	7,199	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1980	181	in gene	0	1	0	10	17	10	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene MED21	SRB7, MED21, SURB7	mediator complex subunit 21	NM_004264, hCT2298552.0, hCT2298553.0, hCT2298554.0, hCT2298555.0	209362_at, 209363_s_at	NP_004255.2, EAW96546.1, EAW96544.1, EAW96545.1, EAW96547.1
GeneID:23012	STK38L	12	27,397,078	27,478,892	81,814	+	2	2_A375_pNL97_plus_lncRNA_AR..1..1981, 2_A375_pNL97_plus_lncRNA_AR..1..1982	-54, 634	upstream, in gene	0	1	0	9	21.5	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene STK38L	NDR2, KIAA0965, STK38L	serine/threonine kinase 38 like	NM_015000, hCT2299822.0, hCT2357943.0, hCT30012.2	212565_at, 212572_at	NP_055815.1, EAW96551.1, EAW96549.1, EAW96550.1
GeneID:60488	MRPS35	12	27,863,706	27,909,237	45,531	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1410, 2_A375_pNL97_plus_lncRNA_AR..1..1983	102, 102	in gene, in gene	1	1	0	28	25	13	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene MRPS35	MDS023, MRPS35, MRPS28, MGC104278, MRP-S28, HDCMD11P, DKFZp762P093	mitochondrial ribosomal protein S35	NM_001190864, NM_021821, hCT2357942.0, hCT30011.3	217942_at	NP_001177793.1, NP_068593.2, EAW96567.1, EAW96568.1
GeneID:83857	TMTC1	12	29,653,746	29,937,692	283,946	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1412, 1_A375_pNL7_minus_lncRNA_AR..1..1413, 2_A375_pNL97_plus_lncRNA_AR..1..1988, 2_A375_pNL97_plus_lncRNA_AR..1..1989, 4_A375_EGR1..1..1828	143580, 43036, 143708, 43004, 1308	in gene, in gene, in gene, in gene, in gene	1	1	1	16.33	17.67	8.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TMTC1	FLJ41625, ARG99, OLF, TMTC1A, TMTC1, FLJ31400	transmembrane and tetratricopeptide repeat containing 1	NM_001193451, NM_175861	224397_s_at, 226322_at, 226931_at, 244506_at	NP_001180380.1, NP_787057.2
GeneID:100287314	LOC100287314	12	30,947,977	30,955,645	7,668	+	3	2_A375_pNL97_plus_lncRNA_AR..1..1990, 2_A375_pNL97_plus_lncRNA_AR..1..1991, 4_A375_EGR1..1..1829	631, 2023, 951	in gene, in gene, in gene	0	1	1	12.5	19	15	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100287314		hypothetical LOC100287314	XR_111267, XR_109096, XR_114561		
GeneID:441631	TSPAN11	12	31,079,838	31,149,537	69,699	+	1	2_A375_pNL97_plus_lncRNA_AR..1..1992	228	in gene	0	1	0	10	18	10	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TSPAN11	TSPAN11, VSSW1971	tetraspanin 11	NM_001080509	227610_at	NP_001073978.1
GeneID:1663	DDX11	12	31,226,779	31,257,725	30,946	+	1	4_A375_EGR1..1..1830	10608	in gene	0	0	1	1	6	11	1	4_A375_EGR1..1	11	Gene DDX11	MGC133249, CHLR1, DDX11, MGC9335, CHL1, KRG2	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	NM_030653, NM_004399, NM_152438, hCT2289403.1, hCT2289405.1, hCT2289407.1, hCT2289411.1, hCT2350467.0, hCT2350468.0, hCT2350469.0, hCT2350471.0	213378_s_at, 232616_s_at	NP_085911.2, NP_004390.3, NP_689651.1, EAW88580.1, EAW88582.1, EAW88583.1, EAW88576.1, EAW88577.1, EAW88578.1, EAW88579.1, EAW88581.1
GeneID:144203	OVOS2	12	31,267,684	31,359,088	91,404	-	1	4_A375_EGR1..1..1831	86896	in gene	0	0	1	6	10	18	1	4_A375_EGR1..1	18	Gene OVOS2	DKFZp686C0336	ovostatin 2	XM_003120218, XM_002343151	228245_s_at	XP_003120266.1, XP_002343192.1
GeneID:58516	FAM60A	12	31,433,518	31,479,159	45,641	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1415, 2_A375_pNL97_plus_lncRNA_AR..1..1993, 2_A375_pNL97_plus_lncRNA_AR..1..1994, 4_A375_EGR1..1..1832	1159, 1159, 135, 1143	in gene, in gene, in gene, in gene	1	1	1	13.5	15.5	18	2	4_A375_EGR1..1	20	Gene FAM60A	L4, FAM60A, C12orf14, TERA	family with sequence similarity 60, member A	NM_021238, NM_001135811, NM_001135812, hCT2289014.0, hCT2289016.0, hCT2289017.0, hCT2289018.0, hCT2289020.0, hCT2289022.0, hCT2289023.0	220147_s_at	NP_067061.1, NP_001129283.1, NP_001129284.1, EAW88561.1, EAW88562.1, EAW88567.1, EAW88563.1, EAW88564.1, EAW88565.1, EAW88566.1
GeneID:79857	FLJ13224	12	31,477,250	31,478,879	1,629	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1415, 2_A375_pNL97_plus_lncRNA_AR..1..1993, 2_A375_pNL97_plus_lncRNA_AR..1..1994, 4_A375_EGR1..1..1832	750, 750, 1774, 766	in gene, in gene, downstream, in gene	1	1	1	13.5	15.5	18	2	4_A375_EGR1..1	20	Gene FLJ13224		hypothetical LOC79857	NR_026606	220211_at	
GeneID:254013	C12orf72	12	31,800,094	31,822,016	21,922	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1416, 2_A375_pNL97_plus_lncRNA_AR..1..1995	12096, 12194	in gene, in gene	1	1	0	50	51	10	1	2_A375_pNL97_plus_lncRNA_AR..1	51	Gene C12orf72	C12orf72, METTL20, MGC50559	chromosome 12 open reading frame 72	NM_173602, NM_001135863, NM_001135864, hCT2349176.0, hCT2349177.0, hCT2349178.0, hCT30426.4	1554582_a_at, 1554583_a_at, 1563474_at, 1563475_s_at, 1569792_a_at	NP_776163.1, NP_001129335.1, NP_001129336.1, EAW88545.1, EAW88546.1, EAW88547.1, EAW88548.1
GeneID:196394	AMN1	12	31,824,071	31,882,108	58,037	-	1	2_A375_pNL97_plus_lncRNA_AR..1..1996	124	in gene	0	1	0	19	23	6	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene AMN1	AMN1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	NM_001113402, NR_004854, hCT1950877.2, hCT2357117.0	226258_at	NP_001106873.1, EAW88544.1, EAW88543.1
GeneID:55196	C12orf35	12	32,112,353	32,146,041	33,688	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1418, 2_A375_pNL97_plus_lncRNA_AR..1..1997	-113, -97	upstream, upstream	1	1	0	17	22	10	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene C12orf35	FLJ20696, C12orf35, FLJ10652	chromosome 12 open reading frame 35	NM_018169, hCT1950844.1, hCT1950845.1	218614_at, 227152_at	NP_060639.3, EAW88536.1, EAW88537.1
GeneID:636	BICD1	12	32,260,185	32,531,141	270,956	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1420, 2_A375_pNL97_plus_lncRNA_AR..1..2000	-345, -25	upstream, upstream	1	1	0	19	18	11	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene BICD1	BICD, BICD1	bicaudal D homolog 1 (Drosophila)	NM_001714, NM_001003398, hCT2284941.0, hCT2284944.0, hCT31230.2	1554020_at, 1556051_a_at, 204741_at, 214806_at, 228691_at	NP_001705.2, NP_001003398.1, EAW88532.1, EAW88533.1, EAW88534.1
GeneID:10059	DNM1L	12	32,832,137	32,898,584	66,447	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1421, 1_A375_pNL7_minus_lncRNA_AR..1..1422, 2_A375_pNL97_plus_lncRNA_AR..1..2002	-41, 76839, 2	upstream, downstream, in gene	1	1	0	20	17	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene DNM1L	DNM1L, FLJ41912, DYMPLE, DVLP, DRP1, DYNIV-11, HDYNIV, DLP1, VPS1	dynamin 1-like	NM_012062, NM_012063, NM_005690, hCT1950884.2, hCT1950885.2, hCT1950886.2, hCT2284632.0, hCT2284634.0, hCT2284635.0, hCT2284636.0, hCT2284637.0, hCT2284638.0	203105_s_at, 226154_at, 237797_at	NP_036192.2, NP_036193.2, NP_005681.2, EAW88523.1, EAW88525.1, EAW88526.1, EAW88519.1, EAW88520.1, EAW88521.1, EAW88522.1, EAW88524.1, EAW88527.1
GeneID:51067	YARS2	12	32,899,459	32,908,874	9,415	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1422	-102	upstream	1	0	0	21	14	18	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene YARS2	CGI-04, mt-TyrRS, MLASA2, YARS2, MT-TYRRS, FLJ13995, TYRRS	tyrosyl-tRNA synthetase 2, mitochondrial	NM_001040436, hCT2284347.0, hCT2284348.0	218470_at	NP_001035526.1, EAW88517.1, EAW88518.1
GeneID:341359	SYT10	12	33,528,348	33,592,754	64,406	-	1	4_A375_EGR1..1..1835	546	in gene	0	0	1	5	10	18	1	4_A375_EGR1..1	18	Gene SYT10	SYT10, MGC119437, MGC119438	synaptotagmin X	NM_198992, hCT30097.3		NP_945343.1, EAW88510.1
GeneID:84920	ALG10	12	34,175,216	34,181,237	6,021	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2003	144	in gene	0	1	0	14	19	7	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ALG10	ALG10, KCR1, FLJ14751, DIE2	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog (S. pombe)	NM_032834, hCT1828583.2	1552304_at, 1552306_at	NP_116223.3, EAW88508.1
GeneID:144245	ALG10B	12	38,710,557	38,723,528	12,971	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1423, 2_A375_pNL97_plus_lncRNA_AR..1..2004, 4_A375_EGR1..1..1837	-77, -61, -13	upstream, upstream, upstream	1	1	1	18	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ALG10B	ALG10, KCR1, ALG10B	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog B (yeast)	NM_001013620, hCT1768333.1		NP_001013642.1, EAW57795.1
GeneID:144402	CPNE8	12	39,046,002	39,299,420	253,418	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1425, 2_A375_pNL97_plus_lncRNA_AR..1..2006	-276, -356	upstream, upstream	1	1	0	19	20	11	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CPNE8	MGC129845, CPNE8, MGC129846	copine VIII	NM_153634, hCT2353256.0, hCT29499.2	228365_at, 241706_at, 243727_at	NP_705898.1, EAW57799.1, EAW57798.1
GeneID:55605	KIF21A	12	39,687,030	39,837,192	150,162	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2007	200	in gene	0	1	0	14	17	10	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene KIF21A	KIF21A, CFEOM, FEOM1, KIAA1708, CFEOM3B, CFEOM1, FEOM3A, DKFZp779C159, FLJ20052, FEOM	kinesin family member 21A	NM_001173463, NM_001173464, NM_001173465, NM_017641, hCT1950723.1, hCT2279134.0, hCT2279136.0, hCT2279137.0, hCT30434.3	226003_at, 231875_at	NP_001166934.1, NP_001166935.1, NP_060111.2, NP_001166936.1, EAW57803.1, EAW57805.1, EAW57802.1, EAW57804.1, EAW57806.1
GeneID:114134	SLC2A13	12	40,148,823	40,499,661	350,838	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2008	86717	in gene	0	1	0	12	24	1	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SLC2A13	HMIT, MGC48624, SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	NM_052885, hCT29500.3	1552694_at, 1552695_a_at, 227176_at, 234286_at, 234561_at	NP_443117.3, EAW57611.1
GeneID:283464	GXYLT1	12	42,475,647	42,538,673	63,026	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2009	241	in gene	0	1	0	12	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene GXYLT1	GLT8D3, GXYLT1, FLJ43151	glucoside xylosyltransferase 1	NM_001099650, NM_173601	226686_at, 232021_at	NP_001093120.1, NP_775872.1
GeneID:10138	YAF2	12	42,550,908	42,632,154	81,246	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1426	890	in gene	1	0	0	17	13	6	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene YAF2	MGC41856, DKFZp779H1820, YAF2	YY1 associated factor 2	NM_001190977, NM_001190979, NM_001190980, NM_005748, NR_034000, hCT2279386.2, hCT2279387.2, hCT2345213.1, hCT2349845.0, hCT2349846.0, hCT2353290.0, hCT2353291.0	206238_s_at, 244763_at	NP_001177906.1, NP_001177908.1, NP_005739.2, NP_001177909.1, EAW57834.1, EAW57839.1, EAW57835.1, EAW57836.1, EAW57837.1, EAW57838.1, EAW57840.1
GeneID:144165	PRICKLE1	12	42,852,140	42,983,572	131,432	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1427, 2_A375_pNL97_plus_lncRNA_AR..1..2010, 4_A375_EGR1..1..1838	466, 596, 660	in gene, in gene, in gene	1	1	1	30	35	17	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene PRICKLE1	EPM1B, RILP, FLJ31937, PRICKLE1, MGC138903, FLJ31627, MGC138902	prickle homolog 1 (Drosophila)	NM_153026, NM_001144881, NM_001144882, NM_001144883, hCT2353294.0, hCT30697.3	226065_at, 226069_at, 230708_at, 232811_x_at	NP_694571.2, NP_001138353.1, NP_001138354.1, NP_001138355.1, EAW57854.1, EAW57855.1
GeneID:83448	PUS7L	12	44,122,410	44,152,596	30,186	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2012	-44	upstream	0	1	0	12	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PUS7L	DKFZp434G1415, PUS7L, FLJ40012, DKFZp781B2388, FLJ34711	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	NM_001098614, NM_031292, NM_001098615, hCT30749.3	221025_x_at, 229751_s_at	NP_001092084.1, NP_112582.3, NP_001092085.1, EAW57868.1
GeneID:51135	IRAK4	12	44,152,747	44,183,346	30,599	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2012	-107	upstream	0	1	0	12	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene IRAK4	IRAK4, NY-REN-64, IPD1, REN64	interleukin-1 receptor-associated kinase 4	NM_001114182, NM_016123, NM_001145256, NM_001145257, NM_001145258, hCT30745.3	219618_at	NP_001107654.1, NP_057207.2, NP_001138728.1, NP_001138729.1, NP_001138730.1, EAW57867.1
GeneID:84216	TMEM117	12	44,229,962	44,783,541	553,579	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2013	133910	in gene	0	1	0	14	18	5	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TMEM117	DKFZp434K2435, TMEM117	transmembrane protein 117	NM_032256, hCT2279098.0, hCT2279100.0	223594_at	NP_115632.1, EAW57871.1, EAW57872.1
GeneID:4753	NELL2	12	44,902,058	45,307,711	405,653	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2014	37151	in gene	0	1	0	12	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene NELL2	NELL2, NRP2	NEL-like 2 (chicken)	NM_006159, NM_001145107, NM_001145108, NM_001145109, NM_001145110, hCT1967268.0, hCT2353304.0, hCT29542.3	203413_at	NP_006150.1, NP_001138579.1, NP_001138580.1, NP_001138581.1, NP_001138582.1, EAW57873.1, EAW57874.1, EAW57875.1
GeneID:51054	PLEKHA9	12	45,566,847	45,609,789	42,942	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1429, 1_A375_pNL7_minus_lncRNA_AR..1..1430, 2_A375_pNL97_plus_lncRNA_AR..1..2015, 4_A375_EGR1..1..1840	61, -643, 61, -67	in gene, upstream, in gene, upstream	1	1	1	21	13.5	13	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene PLEKHA9	PLEKHA9, FLJ14156, PLEKHA8P1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 9	NM_015899, hCT1957982.1, hCT1982253.1, hCT31116.3	220157_x_at	NP_056983.1, EAW57878.1, EAW57879.1, EAW57880.1
GeneID:196527	ANO6	12	45,609,770	45,834,187	224,417	+	7	1_A375_pNL7_minus_lncRNA_AR..1..1429, 1_A375_pNL7_minus_lncRNA_AR..1..1430, 1_A375_pNL7_minus_lncRNA_AR..1..1431, 2_A375_pNL97_plus_lncRNA_AR..1..2015, 2_A375_pNL97_plus_lncRNA_AR..1..2016, 2_A375_pNL97_plus_lncRNA_AR..1..2017, 4_A375_EGR1..1..1840	-42, 662, 199622, -42, 199574, 223190, 86	upstream, in gene, in gene, upstream, in gene, in gene, in gene	1	1	1	22.75	18.75	9	4	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene ANO6	ANO6, MGC104751, TMEM16F	anoctamin 6	NM_001025356, NM_001142678, NM_001142679, NM_001142680	224906_at, 240947_at	NP_001020527.2, NP_001136150.1, NP_001136151.1, NP_001136152.1
GeneID:400027	LOC400027	12	46,119,503	46,121,704	2,201	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2018, 2_A375_pNL97_plus_lncRNA_AR..1..2019	216, -1032	in gene, upstream	0	1	0	18	23.5	8	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene LOC400027		hypothetical LOC400027	NR_026406	226413_at, 238916_at	
GeneID:196528	ARID2	12	46,123,620	46,301,819	178,199	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2018, 2_A375_pNL97_plus_lncRNA_AR..1..2019	-2132, -884	upstream, upstream	0	1	0	18	23.5	8	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene ARID2	DKFZp779P0222, p200, BAF200, ARID2, DKFZp686G052, FLJ30619, KIAA1557	AT rich interactive domain 2 (ARID, RFX-like)	NM_152641, hCT2280140.1, hCT2280141.1, hCT2280142.1, hCT2280143.1	1553349_at, 225486_at, 225490_at, 231090_s_at	NP_689854.2, EAW57888.1, EAW57889.1, EAW57890.1, EAW57891.1
GeneID:9169	SFRS2IP	12	46,312,914	46,384,401	71,487	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1433, 1_A375_pNL7_minus_lncRNA_AR..1..1434, 2_A375_pNL97_plus_lncRNA_AR..1..2020, 2_A375_pNL97_plus_lncRNA_AR..1..2021	-143, -1295, 50873, -175	upstream, upstream, in gene, upstream	1	1	0	20.33	17.33	10	3	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene SFRS2IP	SRRP129, CASP11, SCAF11, SRSF2IP, SIP1, SFRS2IP	SR-related CTD-associated factor 11	NM_004719, hCT2295747.0, hCT2353305.0, hCT29543.3	206989_s_at, 209376_x_at, 213850_s_at, 225336_at, 232597_x_at, 235579_at	NP_004710.2, EAW57893.1, EAW57892.1, EAW57894.1
GeneID:81539	SLC38A1	12	46,576,838	46,663,208	86,370	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2022	616	in gene	0	1	0	19	23	14	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene SLC38A1	SAT1, NAT2, SNAT1, ATA1, SLC38A1	solute carrier family 38, member 1	NM_030674, NM_001077484, hCT2295745.1, hCT2295746.1, hCT2353288.0, hCT2353289.0, hCT30763.5	218237_s_at, 224579_at, 224580_at, 236857_at	NP_109599.3, NP_001070952.1, EAW57895.1, EAW57896.1, EAW57897.1, EAW57898.1, EAW57899.1
GeneID:54407	SLC38A2	12	46,751,971	46,766,845	14,874	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2023	149	in gene	0	1	0	9	18	17	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SLC38A2	KIAA1382, ATA2, SAT2, SLC38A2, SNAT2, PRO1068	solute carrier family 38, member 2	NM_018976, hCT1950270.1, hCT2295742.0, hCT30761.3	218041_x_at, 220924_s_at, 222982_x_at	NP_061849.2, EAW57900.1, EAW57901.1, EAW57902.1
GeneID:100288798	LOC100288798	12	46,761,530	47,268,854	487,324	+	6	1_A375_pNL7_minus_lncRNA_AR..1..1435, 1_A375_pNL7_minus_lncRNA_AR..1..1436, 2_A375_pNL97_plus_lncRNA_AR..1..2024, 2_A375_pNL97_plus_lncRNA_AR..1..2025, 2_A375_pNL97_plus_lncRNA_AR..1..2026, 4_A375_EGR1..1..1843	-3686, 162150, -3634, 136502, 162150, 443542	upstream, in gene, upstream, in gene, in gene, in gene	1	1	1	15.25	20	10.5	4	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene LOC100288798		hypothetical LOC100288798	XR_111276, XR_110375, XR_114587		
GeneID:55089	SLC38A4	12	47,158,544	47,219,780	61,236	-	1	4_A375_EGR1..1..1843	-5292	upstream	0	0	1	4	10	12	1	4_A375_EGR1..1	12	Gene SLC38A4	MGC126876, SLC38A4, NAT3, PAAT, FLJ10191, ATA3	solute carrier family 38, member 4	NM_018018, NM_001143824, hCT18391.2, hCT1950266.1, hCT2295737.0, hCT2353302.0	1555345_at, 220786_s_at	NP_060488.2, NP_001137296.1, EAW57917.1, EAW57918.1, EAW57919.1, EAW57920.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:347902	AMIGO2	12	47,469,490	47,473,734	4,244	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2027	-8063	upstream	0	1	0	12	15	2	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene AMIGO2	ALI1, AMIGO2, DEGA	adhesion molecule with Ig-like domain 2	NM_181847, NM_001143668, hCT1640762.3, hCT2279774.1	222108_at	NP_862830.1, NP_001137140.1, EAW57923.1, EAW57924.1
GeneID:79657	RPAP3	12	48,055,715	48,099,844	44,129	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2028	132	in gene	0	1	0	16	21	11	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RPAP3	RPAP3, FLJ21908	RNA polymerase II associated protein 3	NM_024604, NM_001146075, NM_001146076, hCT18654.3, hCT2353263.0	1557984_s_at, 218842_at	NP_078880.2, NP_001139547.1, NP_001139548.1, EAW57937.1, EAW57938.1
GeneID:8909	P11	12	48,103,517	48,119,355	15,838	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2028, 4_A375_EGR1..1..1844	19843, -10229	downstream, upstream	0	1	1	10	13.5	14	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene P11	PP11, PRSS26, MGC133268, P11, ENDOU	26 serine protease	NM_006025, NM_001172439, NM_001172440, hCT17663.1, hCT2353281.0	206605_at	NP_006016.1, NP_001165910.1, NP_001165911.1, EAW57940.1, EAW57941.1
GeneID:10411	RAPGEF3	12	48,128,453	48,152,889	24,436	-	3	4_A375_EGR1..1..1844, 4_A375_EGR1..1..1845, 4_A375_EGR1..1..1846	23305, 22201, 18249	in gene, in gene, in gene	0	0	1	8	7	20	3	4_A375_EGR1..1	23	Gene RAPGEF3	HSU79275, MGC21410, bcm910, EPAC, EPAC1, RAPGEF3, CAMP-GEFI	Rap guanine nucleotide exchange factor (GEF) 3	NM_001098531, NM_006105, NM_001098532, hCT18846.3, hCT1962243.1, hCT2353306.0, hCT2353307.0, hCT2353308.0, hCT2353309.0	210051_at	NP_001092001.1, NP_006096.2, NP_001092002.1, EAW57944.1, EAW57945.1, EAW57948.1, EAW57946.1, EAW57947.1, EAW57949.1
GeneID:79022	TMEM106C	12	48,357,330	48,362,661	5,331	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2029	78	in gene	0	1	0	10	25	12	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene TMEM106C	MGC111210, MGC5576, TMEM106C	transmembrane protein 106C	NM_024056, NM_001143841, NM_001143842, NM_001143843, hCT18651.3	201764_at, 239631_at	NP_076961.1, NP_001137313.1, NP_001137314.1, NP_001137315.1, EAW57965.1
GeneID:1280	COL2A1	12	48,366,748	48,398,285	31,537	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2029	40677	downstream	0	1	0	10	25	12	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene COL2A1	AOM, SEDC, ANFH, COL2A1, COL11A3, MGC131516	collagen, type II, alpha 1	NM_033150, NM_001844, hCT18846.3, hCT1952863.1, hCT2282152.0, hCT2282153.0, hCT2282155.0	213492_at, 217404_s_at	NP_149162.2, NP_001835.3, EAW57966.1, EAW57967.1, EAW57969.1, EAW57970.1, EAW57968.1
GeneID:29843	SENP1	12	48,436,757	48,499,641	62,884	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2030, 4_A375_EGR1..1..1847, 4_A375_EGR1..1..1848	-455, 70265, -103	upstream, downstream, upstream	0	1	1	15	16	17.5	2	4_A375_EGR1..1	19	Gene SENP1	SuPr2, SENP1	SUMO1/sentrin specific peptidase 1	NM_014554, hCT1967259.1, hCT2282147.0	1552812_a_at, 226619_at	NP_055369.1, EAW57971.1, EAW57972.1
GeneID:5213	PFKM	12	48,499,656	48,540,187	40,531	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2030, 4_A375_EGR1..1..1848	440, 86	in gene, in gene	0	1	1	19	19	19	1	4_A375_EGR1..1	19	Gene PFKM	PFKX, PFK1, PFKA, PFKM, PFK-1, MGC8699, GSD7	phosphofructokinase, muscle	NM_001166686, NM_000289, NM_001166687, NM_001166688, hCT2280085.0, hCT2280087.0, hCT2280088.0	210976_s_at	NP_001160158.1, NP_000280.1, NP_001160159.1, NP_001160160.1, EAW57973.1, EAW57974.1, EAW57975.1
GeneID:643162	DKFZP779L1853	12	48,592,146	48,595,814	3,668	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2031	-370	upstream	0	1	0	13	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene DKFZP779L1853	FLJ43957	hypothetical LOC643162	XR_111277, XR_110335, XR_114568		
GeneID:121275	OR10AD1	12	48,596,122	48,597,075	953	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2031	5299	downstream	0	1	0	13	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene OR10AD1	OR10AD1P, OR12-1, OR10AD1	olfactory receptor, family 10, subfamily AD, member 1	NM_001004134, hCT1813563.3		NP_001004134.1, EAW57976.1
GeneID:341568	OR8S1	12	48,919,415	48,921,886	2,471	+	1	4_A375_EGR1..1..1849	-5063	upstream	0	0	1	1	5	13	1	4_A375_EGR1..1	13	Gene OR8S1	OR8S1	olfactory receptor, family 8, subfamily S, member 1	NM_001005203		NP_001005203.2
GeneID:54934	C12orf41	12	49,046,994	49,076,035	29,041	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1437, 2_A375_pNL97_plus_lncRNA_AR..1..2032, 4_A375_EGR1..1..1850	131, 99, 51	in gene, in gene, in gene	1	1	1	16	19	21	1	4_A375_EGR1..1	21	Gene C12orf41	FLJ20436, FLJ12670, C12orf41	chromosome 12 open reading frame 41	NM_017822, hCT18086.2, hCT1958549.0, hCT1958550.0, hCT2282177.0, hCT2282178.0, hCT2282180.0	221821_s_at	NP_060292.3, EAW57995.1, EAW57991.1, EAW57993.1, EAW57994.1, EAW57996.1, EAW57992.1
GeneID:144438	LOC144438	12	49,082,245	49,086,229	3,984	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1437, 2_A375_pNL97_plus_lncRNA_AR..1..2032, 4_A375_EGR1..1..1850	10325, 10293, 10245	downstream, downstream, downstream	1	1	1	16	19	21	1	4_A375_EGR1..1	21	Gene LOC144438		hypothetical LOC144438	NR_024266	225493_at	
GeneID:904	CCNT1	12	49,086,752	49,110,781	24,029	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2033, 4_A375_EGR1..1..1851	173, 109	in gene, in gene	0	1	1	18	19	22	1	4_A375_EGR1..1	22	Gene CCNT1	HIVE1, CYCT1, CCNT, CCNT1	cyclin T1	NM_001240, hCT1814192.2	206967_at	NP_001231.2, EAW57998.1
GeneID:255411	LOC255411	12	49,121,218	49,159,569	38,351	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2033	-10610	upstream	0	1	0	18	19	22	1	4_A375_EGR1..1	22	Gene LOC255411	FLJ27495	hypothetical LOC255411	NR_029448, NR_029449	1560619_at	
GeneID:9416	DDX23	12	49,223,539	49,245,957	22,418	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1438, 2_A375_pNL97_plus_lncRNA_AR..1..2034	-43, -107	upstream, upstream	1	1	0	25	25	9	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene DDX23	PRPF28, DDX23, U5-100K, MGC8416, prp28, U5-100KD	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	NM_004818, hCT17659.3, hCT2282165.1, hCT2282166.1, hCT2350368.0, hCT2350369.0, hCT2350370.0, hCT2350371.0, hCT2350372.0	201440_at, 40465_at	NP_004809.2, EAW58015.1, EAW58010.1, EAW58012.1, EAW58013.1, EAW58017.1, EAW58011.1, EAW58014.1, EAW58016.1
GeneID:27289	RND1	12	49,250,916	49,259,653	8,737	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1438, 2_A375_pNL97_plus_lncRNA_AR..1..2034	13853, 13569	downstream, downstream	1	1	0	25	25	9	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene RND1	RHOS, ARHS, RHO6, RND1, FLJ42294	Rho family GTPase 1	NM_014470, hCT2282164.0	210056_at	NP_055285.1, EAW58019.1
GeneID:85478	CCDC65	12	49,297,893	49,315,359	17,466	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1439, 2_A375_pNL97_plus_lncRNA_AR..1..2035	-89, 27	upstream, in gene	1	1	0	22	23	4	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CCDC65	FLJ25663, NYD-SP28, FLJ35732, CCDC65	coiled-coil domain containing 65	NM_033124, hCT1802281.1, hCT2280111.1	1552320_a_at, 1552321_a_at, 1561523_at	NP_149115.2, EAW58020.1, EAW58021.1
GeneID:377	ARF3	12	49,329,992	49,351,252	21,260	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1440, 2_A375_pNL97_plus_lncRNA_AR..1..2036, 4_A375_EGR1..1..1852	36, -44, 212	in gene, upstream, in gene	1	1	1	21	22	15	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ARF3	ARF3	ADP-ribosylation factor 3	NM_001659, hCT1962255.1, hCT2353264.0, hCT31648.2	200011_s_at, 200734_s_at, 211622_s_at	NP_001650.1, EAW58027.1, EAW58025.1, EAW58026.1
GeneID:7480	WNT10B	12	49,359,123	49,365,641	6,518	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1440, 2_A375_pNL97_plus_lncRNA_AR..1..2036, 4_A375_EGR1..1..1852, 4_A375_EGR1..1..1853, 4_A375_EGR1..1..1854, 4_A375_EGR1..1..1855	14425, 14345, 14601, 1465, -375, -6711	downstream, downstream, downstream, in gene, upstream, upstream	1	1	1	10.75	13.5	16.25	4	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene WNT10B	WNT-12, SHFM6, WNT10B	wingless-type MMTV integration site family, member 10B	NM_003394, hCT2282156.0, hCT32764.2	206213_at	NP_003385.2, EAW58029.1, EAW58028.1
GeneID:7471	WNT1	12	49,372,236	49,376,396	4,160	+	3	4_A375_EGR1..1..1853, 4_A375_EGR1..1..1854, 4_A375_EGR1..1..1855	-8080, -6220, 116	upstream, upstream, in gene	0	0	1	7.33	10.67	16.67	3	4_A375_EGR1..1	18	Gene WNT1	WNT1, INT1	wingless-type MMTV integration site family, member 1	NM_005430, hCT32787.2	208570_at	NP_005421.1, EAW58030.1
GeneID:8085	MLL2	12	49,412,758	49,449,107	36,349	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1441, 2_A375_pNL97_plus_lncRNA_AR..1..2037, 4_A375_EGR1..1..1856	-5581, -5613, -5325	upstream, upstream, upstream	1	1	1	37	35	15	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene MLL2	KMT2D, KMS, MLL4, CAGL114, ALR, TNRC21, MLL2, AAD10, KMT2B	myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482, hCT2300492.0, hCT2300493.0, hCT32763.3	211790_s_at, 227527_at, 227528_s_at, 231974_at	NP_003473.3, EAW58035.1, EAW58034.1, EAW58036.1
GeneID:121268	RHEBL1	12	49,458,468	49,463,775	5,307	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1441, 2_A375_pNL97_plus_lncRNA_AR..1..2037, 4_A375_EGR1..1..1856	9067, 9055, 9343	downstream, downstream, downstream	1	1	1	37	35	15	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene RHEBL1	FLJ25797, RHEBL1, MGC34869, RHEBL1c	Ras homolog enriched in brain like 1	NM_144593, hCT2353293.0, hCT32776.3	1553713_a_at, 1570253_a_at	NP_653194.1, EAW58037.1, EAW58038.1
GeneID:50846	DHH	12	49,483,204	49,488,602	5,398	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2038	2618	in gene	0	1	0	9	20	11	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene DHH	DHH, MGC35145, HHG-3	desert hedgehog homolog (Drosophila)	NM_021044, hCT32771.4	1552730_at	NP_066382.1, EAW58039.1
GeneID:55716	LMBR1L	12	49,490,922	49,504,680	13,758	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2038, 2_A375_pNL97_plus_lncRNA_AR..1..2039	18698, 8	downstream, in gene	0	1	0	12	19	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LMBR1L	FLJ36251, LMBR1L, KIAA1174, LIMR, FLJ10494	limb region 1 homolog (mouse)-like	NM_018113, hCT2300483.0, hCT2300484.0, hCT2300485.0, hCT2300486.0, hCT2300487.0, hCT2300488.0, hCT2353266.0, hCT2353267.0	220036_s_at	NP_060583.2, EAW58040.1, EAW58041.1, EAW58044.1, EAW58046.1, EAW58047.1, EAW58042.1, EAW58043.1, EAW58045.1
GeneID:100288366	LOC100288366	12	49,514,157	49,527,171	13,014	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1442, 2_A375_pNL97_plus_lncRNA_AR..1..2039, 4_A375_EGR1..1..1857	10003, -9485, 10667	in gene, upstream, in gene	1	1	1	15.5	15	16.5	2	4_A375_EGR1..1	21	Gene LOC100288366		hypothetical LOC100288366	XR_111281, XR_111280, XR_110343, XR_110342, XR_110341, XR_114591		
GeneID:10376	TUBA1B	12	49,521,565	49,525,304	3,739	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1442, 4_A375_EGR1..1..1857	1144, 280	in gene, in gene	1	0	1	16	12	21	1	4_A375_EGR1..1	21	Gene TUBA1B	K-ALPHA-1, TUBA1B	tubulin, alpha 1b	NM_006082, hCT2300480.1, hCT2300482.1	1565668_at, 201090_x_at, 211058_x_at, 211072_x_at, 212639_x_at, 213646_x_at	NP_006073.2, EAW58048.1, EAW58049.1
GeneID:100289104	LOC100289104	12	49,551,351	49,583,095	31,744	+	1	4_A375_EGR1..1..1858	31145	in gene	0	0	1	12	11	19	1	4_A375_EGR1..1	19	Gene LOC100289104		hypothetical LOC100289104	XR_110346, XR_110345, XR_110347, XR_110344, XR_110348		
GeneID:7846	TUBA1A	12	49,578,582	49,582,861	4,279	-	1	4_A375_EGR1..1..1858	365	in gene	0	0	1	12	11	19	1	4_A375_EGR1..1	19	Gene TUBA1A	B-ALPHA-1, TUBA1A, LIS3, TUBA3, FLJ25113	tubulin, alpha 1a	NM_006009, hCT2300477.1, hCT2300478.1, hCT2300479.1, hCT2300481.1	209118_s_at	NP_006000.2, EAW58052.1, EAW58053.1, EAW58054.1, EAW58055.1
GeneID:100293982	LOC100293982	12	49,626,573	49,658,539	31,966	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1443, 1_A375_pNL7_minus_lncRNA_AR..1..1444, 2_A375_pNL97_plus_lncRNA_AR..1..2040, 4_A375_EGR1..1..1859	30187, -893, -805, -437	in gene, upstream, upstream, upstream	1	1	1	18.5	16.5	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LOC100293982		hypothetical LOC100293982	XR_111287, XR_110349, XR_114597		
GeneID:84790	TUBA1C	12	49,658,865	49,667,113	8,248	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1444, 2_A375_pNL97_plus_lncRNA_AR..1..2040, 4_A375_EGR1..1..1859	367, 479, 111	in gene, in gene, in gene	1	1	1	17	19	20	1	4_A375_EGR1..1	20	Gene TUBA1C	MGC16851, MGC14580, TUBA1C, bcm948, TUBA6	tubulin, alpha 1c	NM_032704, hCT1814177.2	209251_x_at, 211750_x_at	NP_116093.1, EAW58057.1
GeneID:5630	PRPH	12	49,688,909	49,692,481	3,572	+	1	4_A375_EGR1..1..1860	1875	in gene	0	0	1	9	10	19	1	4_A375_EGR1..1	19	Gene PRPH	NEF4, PRPH1, PRPH	peripherin	NM_006262, hCT2281663.0, hCT2353248.0	213847_at	NP_006253.2, EAW58060.1, EAW58061.1
GeneID:10024	TROAP	12	49,716,971	49,725,514	8,543	+	4	2_A375_pNL97_plus_lncRNA_AR..1..2041, 4_A375_EGR1..1..1861, 4_A375_EGR1..1..1862, 4_A375_EGR1..1..1863	133, 13749, 16133, 18581	in gene, downstream, downstream, downstream	0	1	1	9	10	15.75	4	4_A375_EGR1..1	19	Gene TROAP	TROAP, TASTIN	trophinin associated protein (tastin)	NM_005480, NM_001100620, hCT2281684.1, hCT2345215.0, hCT32773.2	1566596_a_at, 204649_at	NP_005471.3, NP_001094090.1, EAW58062.1, EAW58063.1, EAW58064.1
GeneID:338761	C1QL4	12	49,726,200	49,730,971	4,771	-	5	2_A375_pNL97_plus_lncRNA_AR..1..2041, 2_A375_pNL97_plus_lncRNA_AR..1..2042, 4_A375_EGR1..1..1861, 4_A375_EGR1..1..1862, 4_A375_EGR1..1..1863	13867, -9693, 251, -2133, -4581	downstream, upstream, in gene, upstream, upstream	0	1	1	10	11.8	15.2	5	4_A375_EGR1..1	19	Gene C1QL4	C1QL4, C1QTNF11, MGC131708	complement component 1, q subcomponent-like 4	NM_001008223, hCT32768.2		NP_001008224.1, EAW58065.1
GeneID:79962	DNAJC22	12	49,741,041	49,745,897	4,856	+	5	2_A375_pNL97_plus_lncRNA_AR..1..2042, 4_A375_EGR1..1..1861, 4_A375_EGR1..1..1862, 4_A375_EGR1..1..1863, 4_A375_EGR1..1..1864	-177, -10321, -7937, -5489, 2083	upstream, upstream, upstream, upstream, in gene	0	1	1	9.4	9.8	16	5	4_A375_EGR1..1	19	Gene DNAJC22	wus, FLJ13236, DNAJC22	DnaJ (Hsp40) homolog, subfamily C, member 22	NM_024902, hCT2281646.1, hCT32769.4	220441_at, 244193_at	NP_079178.2, EAW58067.1, EAW58066.1
GeneID:65244	SPATS2	12	49,760,688	49,921,207	160,519	+	2	4_A375_EGR1..1..1865, 4_A375_EGR1..1..1866	592, 66526	in gene, in gene	0	0	1	5.5	4.5	16.5	2	4_A375_EGR1..1	18	Gene SPATS2	SPATS2, NBla00526, SCR59, SPATA10, P59SCR, FLJ13117	spermatogenesis associated, serine-rich 2	NM_023071, hCT2281660.0, hCT2281662.0, hCT2345304.0, hCT2353278.0	1570130_at, 218324_s_at, 222593_s_at, 222594_s_at	NP_075559.2, EAW58070.1, EAW58068.1, EAW58069.1, EAW58071.1
GeneID:23416	KCNH3	12	49,932,940	49,952,077	19,137	+	4	2_A375_pNL97_plus_lncRNA_AR..1..2043, 4_A375_EGR1..1..1867, 4_A375_EGR1..1..1868, 4_A375_EGR1..1..1869	26809, 626, 18484, 26684	downstream, in gene, in gene, downstream	0	1	1	8	11.67	17.33	3	4_A375_EGR1..1	20	Gene KCNH3	KIAA1282, ELK2, KCNH3, BEC1, Kv12.2	potassium voltage-gated channel, subfamily H (eag-related), member 3	NM_012284, hCT11280.4, hCT1967221.1	223726_at	NP_036416.1, EAW58073.1, EAW58074.1
GeneID:10445	MCRS1	12	49,952,085	49,961,911	9,826	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2043, 4_A375_EGR1..1..1868, 4_A375_EGR1..1..1869	162, 10487, 67	in gene, downstream, in gene	0	1	1	8	12	18.5	2	4_A375_EGR1..1	20	Gene MCRS1	ICP22BP, INO80Q, P78, MSP58, MCRS1, MCRS2	microspherule protein 1	NM_006337, NM_001012300, hCT11275.4, hCT1957258.1, hCT1967219.1, hCT2300468.0, hCT2300469.0, hCT2300472.0	202556_s_at	NP_006328.2, NP_001012300.1, EAW58075.1, EAW58076.1, EAW58078.1, EAW58080.1, EAW58077.1, EAW58079.1
GeneID:7009	TMBIM6	12	50,135,293	50,158,717	23,424	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2044	35	in gene	0	1	0	17	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TMBIM6	TEGT, TMBIM6, BI-1, BAXI1	transmembrane BAX inhibitor motif containing 6	NM_001098576, NM_003217, hCT11274.3, hCT1967217.1, hCT2281655.0, hCT2281659.0, hCT2281661.0	200803_s_at, 200804_at	NP_001092046.1, NP_003208.2, EAW58089.1, EAW58090.1, EAW58091.1, EAW58092.1, EAW58093.1
GeneID:57701	NCKAP5L	12	50,184,929	50,222,208	37,279	-	3	4_A375_EGR1..1..1870, 4_A375_EGR1..1..1871, 4_A375_EGR1..1..1872	36592, 31536, 672	in gene, in gene, in gene	0	0	1	3.67	7.67	17.33	3	4_A375_EGR1..1	20	Gene NCKAP5L	FP1193, NCKAP5L, KIAA1602, FLJ36581, MGC129883	NCK-associated protein 5-like	NM_001037806	231865_at	NP_001032895.2
GeneID:100288644	LOC100288644	12	50,222,326	50,234,937	12,611	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1445, 2_A375_pNL97_plus_lncRNA_AR..1..2045, 4_A375_EGR1..1..1872	14698, 14186, -790	downstream, downstream, upstream	1	1	1	11	16	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100288644	FLJ30580	hypothetical LOC100288644	NR_027499, NR_027500, NR_027501		
GeneID:144233	BCDIN3D	12	50,229,826	50,236,912	7,086	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1445, 2_A375_pNL97_plus_lncRNA_AR..1..2045, 4_A375_EGR1..1..1872	-112, 400, 15376	upstream, in gene, downstream	1	1	1	11	16	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene BCDIN3D	BCDIN3D		NM_181708, hCT2300459.0	234979_at	NP_859059.1, EAW58101.1
GeneID:359	AQP2	12	50,344,524	50,352,664	8,140	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1446	16788	downstream	1	0	0	20	16	15	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene AQP2	MGC34501, AQP2, AQP-CD, WCH-CD	aquaporin 2 (collecting duct)	NM_000486, hCT11270.4	206672_at, 236630_at, 240285_at	NP_000477.1, EAW58109.1
GeneID:362	AQP5	12	50,355,279	50,359,461	4,182	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1446	6033	downstream	1	0	0	20	16	15	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene AQP5	AQP5		NM_001651, hCT1640307.3	213611_at	NP_001642.1, EAW58110.1
GeneID:363	AQP6	12	50,366,620	50,370,922	4,302	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1446	-5308	upstream	1	0	0	20	16	15	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene AQP6	KID, AQP2L, AQP6	aquaporin 6, kidney specific	NM_001652	208435_s_at, 216219_at	NP_001643.2
GeneID:41	ACCN2	12	50,451,487	50,477,394	25,907	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2046	-735	upstream	0	1	0	11	18	10	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ACCN2	BNaC2, ASIC, ASIC1, ASIC1A, hBNaC2, ACCN2	amiloride-sensitive cation channel 2, neuronal	NM_001095, NM_020039, hCT1950344.1, hCT2282327.0, hCT2353254.0, hCT9538.3	205156_s_at, 37953_s_at	NP_001086.2, NP_064423.2, EAW58116.1, EAW58117.1, EAW58118.1, EAW58119.1
GeneID:2819	GPD1	12	50,497,801	50,505,096	7,295	+	1	4_A375_EGR1..1..1874	8295	downstream	0	0	1	21	15	22	1	4_A375_EGR1..1	22	Gene GPD1	GPD1, FLJ26652	glycerol-3-phosphate dehydrogenase 1 (soluble)	NM_005276, hCT11272.3, hCT2282336.0	1563034_at, 1563035_x_at, 204997_at, 213706_at	NP_005267.2, EAW58129.1, EAW58128.1
GeneID:84987	C12orf62	12	50,505,900	50,514,234	8,334	+	1	4_A375_EGR1..1..1874	198	in gene	0	0	1	21	15	22	1	4_A375_EGR1..1	22	Gene C12orf62	C12orf62, MGC14288	chromosome 12 open reading frame 62	NM_032901, hCT1813091.2	225772_s_at	NP_116290.1, EAW58130.1
GeneID:57609	DIP2B	12	50,898,788	51,142,450	243,662	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1447	16	in gene	1	0	0	16	15	7	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene DIP2B	MGC104005, DIP2B, KIAA1463	DIP2 disco-interacting protein 2 homolog B (Drosophila)	NM_173602, hCT2282345.1, hCT2282348.1	1553271_at, 224872_at, 242970_at	NP_775873.2, EAW58149.1, EAW58150.1
GeneID:4891	SLC11A2	12	51,373,566	51,422,058	48,492	-	1	4_A375_EGR1..1..1875	1802	in gene	0	0	1	12	12	20	1	4_A375_EGR1..1	20	Gene SLC11A2	SLC11A2, NRAMP2, DMT1, DCT1, FLJ37416	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	NM_000617, NM_001174125, NM_001174126, NM_001174127, NM_001174128, NM_001174129, NM_001174130, NR_033421, NR_033422, hCT1968223.1, hCT1968224.1, hCT2282608.0, hCT2353257.0, hCT2353258.0, hCT2353259.0, hCT28138.3	203123_s_at, 203124_s_at, 203125_x_at, 210047_at, 237108_at	NP_000608.1, NP_001167596.1, NP_001167597.1, NP_001167598.1, NP_001167599.1, NP_001167600.1, NP_001167601.1, EAW58159.1, EAW58160.1, EAW58161.1, EAW58162.1, EAW58163.1, EAW58164.1, EAW58165.1



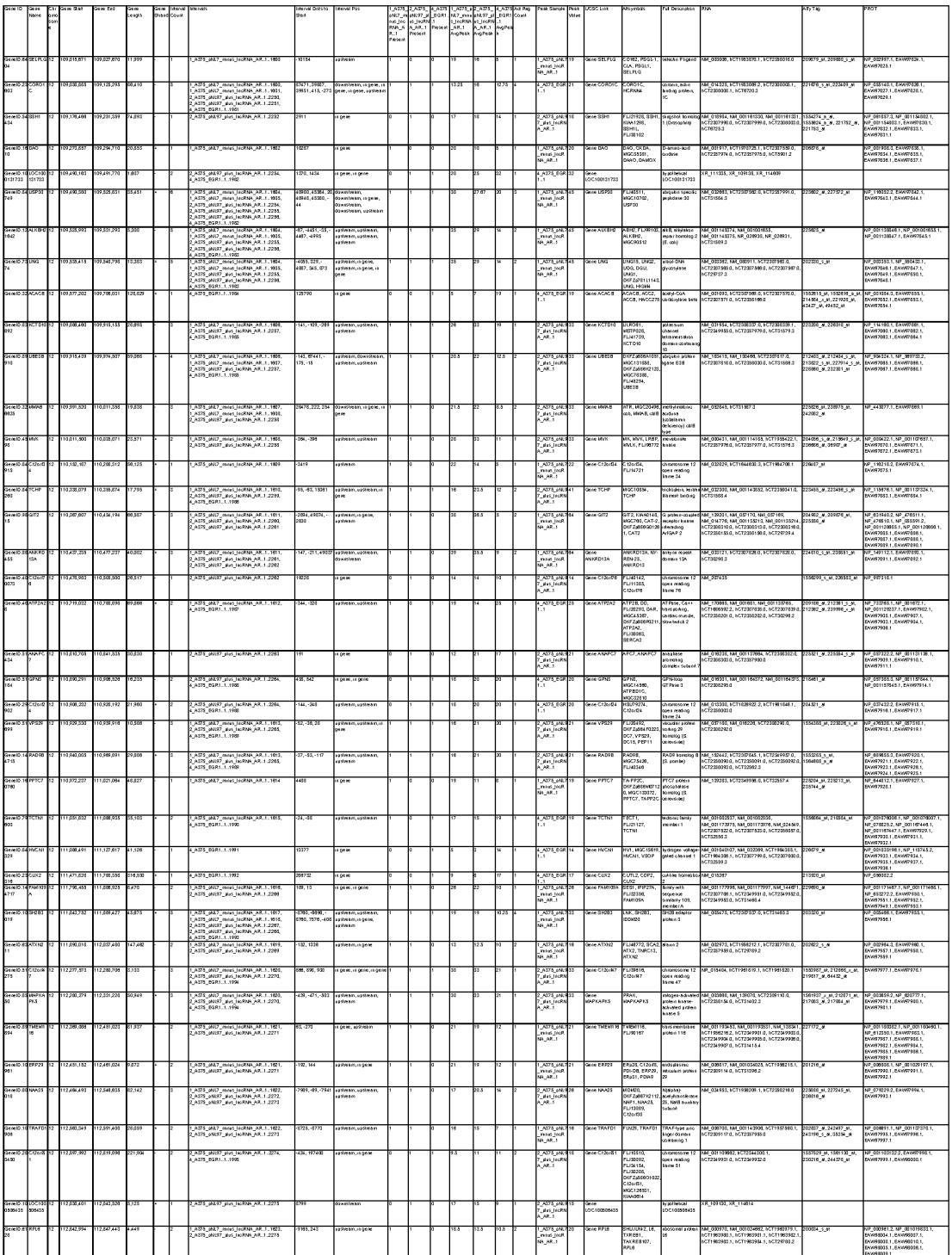
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:3221	HOXC4	12	54,410,642	54,449,814	39,172	+	3	2_A375_pNL97_plus_lncRNA_AR..1..2072, 2_A375_pNL97_plus_lncRNA_AR..1..2073, 4_A375_EGR1..1..1898	1454, 16534, 16686	in gene, in gene, in gene	0	1	1	9	22	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene HOXC4	HOX3, HOXC4, HOX3E, cp19	homeobox C4	NM_153633, NM_014620	206194_at	NP_705897.1, NP_055435.2
GeneID:693200	MIR615	12	54,427,734	54,427,829	95	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2073, 4_A375_EGR1..1..1898	-556, -406	upstream, upstream	0	1	1	7	16	19	1	4_A375_EGR1..1	19	Gene MIR615	MIR615, hsa-mir-615, MIRN615	microRNA 615	NR_030753		
GeneID:440101	FLJ12825	12	54,452,038	54,516,018	63,980	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2074	67946	downstream	0	1	0	11	15	12	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene FLJ12825	FLJ31855	hypothetical LOC440101	NR_026655	1557296_at, 233006_at	
GeneID:400043	LOC400043	12	54,519,855	54,528,627	8,772	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2074	129	in gene	0	1	0	11	15	12	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LOC400043		hypothetical LOC400043	NR_026656	226582_at	
GeneID:23468	CBX5	12	54,624,730	54,673,915	49,185	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1467, 4_A375_EGR1..1..1897	-645, -613	upstream, upstream	1	0	1	21	18	18	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene CBX5	HP1A, CBX5, HP1	chromobox homolog 5	NM_012117, NM_001127321, NM_001127322, hCT2312030.0, hCT2312031.0, hCT2312032.0	209715_at, 242089_at	NP_036249.1, NP_001120793.1, NP_001120794.1, EAW96758.1, EAW96759.1, EAW96760.1
GeneID:3178	HNRNPA1	12	54,674,488	54,679,030	4,542	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1467, 4_A375_EGR1..1..1897	72, 40	in gene, in gene	1	0	1	21	18	18	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene HNRNPA1	HNRNPA1, hnRNP-A1, hnRNP A1, HNRPA1L3, HNRPA1, MGC102835	heterogeneous nuclear ribonucleoprotein A1	NM_002136, NM_031157, hCT2311219.0, hCT2311220.0, hCT2311222.0, hCT2311223.0, hCT2311224.0, hCT2311225.0, hCT2311226.0, hCT2311227.0, hCT2311228.0, hCT2311229.0	200016_x_at, 214280_x_at	NP_002127.1, NP_112420.1, EAW96761.1, EAW96762.1, EAW96763.1, EAW96770.1, EAW96764.1, EAW96765.1, EAW96766.1, EAW96767.1, EAW96768.1, EAW96769.1
GeneID:100506653	LOC100506653	12	54,679,687	54,680,871	1,184	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1467, 4_A375_EGR1..1..1897	-5127, -5159	upstream, upstream	1	0	1	21	18	18	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene LOC100506653		hypothetical LOC100506653	XR_111294, XR_110355, XR_114638		
GeneID:22818	COPZ1	12	54,718,911	54,745,633	26,722	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2076	35609	downstream	0	1	0	15	20	8	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene COPZ1	COPZ1, zeta1-COP, CGI-120, COPZ	coatomer protein complex, subunit zeta 1	NM_016057, hCT2311230.0, hCT2311231.0	217726_at, 222386_s_at	NP_057141.1, EAW96775.1, EAW96774.1
GeneID:53831	GPR84	12	54,756,229	54,758,270	2,041	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2076	3550	downstream	0	1	0	15	20	8	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene GPR84	EX33, GPCR4, GPR84	G protein-coupled receptor 84	NM_020370, hCT1821539.1	223767_at	NP_065103.1, EAW96776.1
GeneID:25946	ZNF385A	12	54,762,920	54,785,083	22,163	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2076	30363	downstream	0	1	0	15	20	8	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ZNF385A	ZFP385, ZNF385A, HZF, RZF, DKFZp586G1122, ZNF385	zinc finger protein 385A	NM_015481, NM_001130967, NM_001130968, hCT2312024.0, hCT2358156.0, hCT28589.3	226111_s_at	NP_056296.1, NP_001124439.1, NP_001124440.1, EAW96777.1, EAW96778.1, EAW96779.1
GeneID:3678	ITGA5	12	54,789,045	54,813,050	24,005	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2077	-9350	upstream	0	1	0	9	16	7	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ITGA5	FNRA, VLA5A, ITGA5, CD49e	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	NM_002205, hCT13032.3, hCT2306158.0, hCT2306160.0	201389_at	NP_002196.2, EAW96780.1, EAW96781.1, EAW96782.1
GeneID:121355	GTSF1	12	54,849,736	54,867,386	17,650	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1468, 4_A375_EGR1..1..1898	26, 56	in gene, in gene	1	0	1	17	13	19	1	4_A375_EGR1..1	19	Gene GTSF1	GTSF1, FLJ32942, FAM112B	gametocyte specific factor 1	NM_144594, hCT1821543.1, hCT2358047.0, hCT2358048.0	227711_at	NP_653195.2, EAW96785.1, EAW96783.1, EAW96784.1
GeneID:3071	NCKAP1L	12	54,891,495	54,936,899	45,404	+	1	4_A375_EGR1..1..1899	51993	downstream	0	0	1	12	10	20	1	4_A375_EGR1..1	20	Gene NCKAP1L	HEM1, NCKAP1L	NCK-associated protein 1-like	NM_005337, NM_001184976, hCT13028.3, hCT2308009.0	209734_at	NP_005328.2, NP_001171905.1, EAW96786.1, EAW96787.1
GeneID:5153	PDE1B	12	54,943,177	54,973,023	29,846	+	1	4_A375_EGR1..1..1899	311	in gene	0	0	1	12	10	20	1	4_A375_EGR1..1	20	Gene PDE1B	PDE1B1, PDES1B, PDE1B	phosphodiesterase 1B, calmodulin-dependent	NM_001165975, NM_000924, hCT2308010.0, hCT2308011.0, hCT2308013.0, hCT2308014.0	208444_at	NP_001159447.1, NP_000915.1, EAW96788.1, EAW96789.1, EAW96790.1, EAW96791.1
GeneID:5502	PPP1R1A	12	54,973,024	54,982,443	9,419	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2078	-4661	upstream	0	1	0	11	21	4	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PPP1R1A	I1, PPP1R1A, IPP1		NM_006741, hCT13029.2	205478_at, 235129_at	NP_006732.3, EAW96792.1
GeneID:58158	NEUROD4	12	55,413,729	55,423,801	10,072	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1470, 2_A375_pNL97_plus_lncRNA_AR..1..2079	47, -1	in gene, upstream	1	1	0	33	31	5	1	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene NEUROD4	ATH3, NEUROD4, bHLHa4, Atoh3, ATH-3, MATH-3	neurogenic differentiation 4	NM_021191, hCT1642784.1	221318_at	NP_067014.2, EAW96803.1
GeneID:403282	OR6C65	12	55,794,313	55,795,251	938	+	1	4_A375_EGR1..1..1900	-7945	upstream	0	0	1	6	7	16	1	4_A375_EGR1..1	16	Gene OR6C65	OR6C65	olfactory receptor, family 6, subfamily C, member 65	NM_001005518, hCT2351487.0		NP_001005518.1, EAW96810.1
GeneID:3679	ITGA7	12	56,078,352	56,106,089	27,737	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1471, 2_A375_pNL97_plus_lncRNA_AR..1..2080, 2_A375_pNL97_plus_lncRNA_AR..1..2081	-8972, -3703, -9047	upstream, upstream, upstream	1	1	0	17.5	20	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ITGA7	ITGA7, FLJ25220	integrin, alpha 7	NM_002206, NM_001144996, NM_001144997, hCT11825.3, hCT1967150.1, hCT1967151.1, hCT2308937.0, hCT2308938.0	209663_s_at, 216331_at	NP_002197.2, NP_001138468.1, NP_001138469.1, EAW96819.1, EAW96820.1, EAW96821.1, EAW96822.1, EAW96823.1
GeneID:2647	BLOC1S1	12	56,109,820	56,113,487	3,667	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1471, 1_A375_pNL7_minus_lncRNA_AR..1..1472, 2_A375_pNL97_plus_lncRNA_AR..1..2080, 2_A375_pNL97_plus_lncRNA_AR..1..2081, 4_A375_EGR1..1..1901	5241, 12292, -26, 5316, 13220	downstream, downstream, upstream, downstream, downstream	1	1	1	17	18.25	12	4	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene BLOC1S1	MGC87455, MICoA, RT14, BLOS1, FLJ97089, GCN5L1, FLJ39337, BLOC1S1	biogenesis of lysosomal organelles complex-1, subunit 1	NM_001487, hCT11824.2	202592_at	NP_001478.1, EAW96824.1
GeneID:5959	RDH5	12	56,114,151	56,118,526	4,375	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1471, 1_A375_pNL7_minus_lncRNA_AR..1..1472, 2_A375_pNL97_plus_lncRNA_AR..1..2080, 2_A375_pNL97_plus_lncRNA_AR..1..2081, 4_A375_EGR1..1..1901	910, 7981, -4359, 985, 6889	in gene, downstream, upstream, in gene, downstream	1	1	1	17	18.25	12	4	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RDH5	RDH5, SDR9C5, RDH1, FLJ97089, FLJ39337, HSD17B9	retinol dehydrogenase 5 (11-cis/9-cis)	NM_002905, hCT11826.2, hCT2307639.0	210106_at, 236291_at	NP_002896.2, EAW96826.1, EAW96825.1
GeneID:967	CD63	12	56,119,230	56,122,910	3,680	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1471, 1_A375_pNL7_minus_lncRNA_AR..1..1472, 2_A375_pNL97_plus_lncRNA_AR..1..2080, 2_A375_pNL97_plus_lncRNA_AR..1..2081, 4_A375_EGR1..1..1901	7649, 798, 13118, 7774, -130	downstream, in gene, downstream, downstream, upstream	1	1	1	17	18.25	12	4	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CD63	MLA1, OMA81H, ME491, LAMP-3, TSPAN30, CD63	CD63 molecule	NM_001780, NM_001040034, hCT11823.2, hCT1823138.1, hCT1967164.1	200663_at	NP_001771.1, NP_001035123.1, EAW96827.1, EAW96828.1, EAW96829.1
GeneID:100506701	LOC100506701	12	56,122,888	56,124,636	1,748	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1471, 1_A375_pNL7_minus_lncRNA_AR..1..1472, 2_A375_pNL97_plus_lncRNA_AR..1..2081, 4_A375_EGR1..1..1901	-7827, -776, -7752, 152	upstream, upstream, upstream, in gene	1	1	1	17.33	17.33	12.33	3	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene LOC100506701		hypothetical LOC100506701	XR_111297, XR_110356, XR_114641		
GeneID:29095	ORMDL2	12	56,211,806	56,214,959	3,153	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1473, 2_A375_pNL97_plus_lncRNA_AR..1..2082, 4_A375_EGR1..1..1902	11714, 11536, 11575	downstream, downstream, downstream	1	1	1	20	18	18	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ORMDL2	adoplin-2, ORMDL2, HSPC160, MSTP095, MST095	ORM1-like 2 (S. cerevisiae)	NM_014182, hCT1823151.2	218556_at	NP_054901.1, EAW96840.1
GeneID:85406	DNAJC14	12	56,214,744	56,223,420	8,676	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1473, 2_A375_pNL97_plus_lncRNA_AR..1..2082, 4_A375_EGR1..1..1902, 4_A375_EGR1..1..1903	-100, 76, 39, -3780	upstream, in gene, in gene, upstream	1	1	1	13	15	17	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene DNAJC14	DRIP78, DNAJC14, DNAJ, LIP6, HDJ3	DnaJ (Hsp40) homolog, subfamily C, member 14	NM_032364	223420_at	NP_115740.5
GeneID:440104	LOC440104	12	56,223,392	56,230,030	6,638	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1473, 2_A375_pNL97_plus_lncRNA_AR..1..2082, 4_A375_EGR1..1..1902, 4_A375_EGR1..1..1903	128, -48, -11, 3608	in gene, upstream, upstream, in gene	1	1	1	13	15	17	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LOC440104		1110012D08Rik pseudogene	NR_036476, NR_036477, NR_036478, NR_036479	1557124_at, 227106_at	
GeneID:4327	MMP19	12	56,229,214	56,236,735	7,521	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1473, 2_A375_pNL97_plus_lncRNA_AR..1..2082, 4_A375_EGR1..1..1902, 4_A375_EGR1..1..1903	13215, 13391, 13354, 9535	downstream, downstream, downstream, downstream	1	1	1	13	15	17	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene MMP19	RASI-1, MMP19, MMP18	matrix metallopeptidase 19	NM_002429, hCT2340218.1, hCT2340219.1	204574_s_at	NP_002420.1, EAW96844.1, EAW96845.1
GeneID:84305	WIBG	12	56,295,197	56,321,697	26,500	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1474, 4_A375_EGR1..1..1904	461, -4363	in gene, upstream	1	0	1	15.5	10	12	2	4_A375_EGR1..1	19	Gene WIBG	PYM, MGC13064, WIBG	within bgcn homolog (Drosophila)	NM_032345, NM_001143853, hCT1647266.2, hCT1955008.1	1569428_at, 224465_s_at, 242304_at	NP_115721.1, NP_001137325.1, EAW96847.1, EAW96846.1
GeneID:1606	DGKA	12	56,324,946	56,347,807	22,861	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1474, 4_A375_EGR1..1..1904	-3730, 1134	upstream, in gene	1	0	1	15.5	10	12	2	4_A375_EGR1..1	19	Gene DGKA	MGC42356, DAGK1, DAGK, DGKA, MGC12821, DGK-alpha	diacylglycerol kinase, alpha 80kDa	NM_001345, NM_201444, NM_201445, NM_201554, hCT1955019.1, hCT2307646.0, hCT2307647.0	203385_at, 211272_s_at	NP_001336.2, NP_958852.1, NP_958853.1, NP_963848.1, EAW96849.1, EAW96850.1, EAW96851.1
GeneID:6490	SILV	12	56,347,889	56,359,826	11,937	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1475	-7854	upstream	1	0	0	28	19	17	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene SILV	SIL, SI, PMEL, SILV, gp100, ME20, D12S53E, PMEL17	premelanosome protein	NM_006928, hCT16120.3, hCT1955018.0, hCT2308919.0, hCT2308921.0	209848_s_at	NP_008859.1, EAW96852.1, EAW96853.1, EAW96854.1, EAW96855.1
GeneID:1017	CDK2	12	56,360,556	56,366,568	6,012	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1475	7124	downstream	1	0	0	28	19	17	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene CDK2	p33(CDK2), CDK2	cyclin-dependent kinase 2	NM_052827, NM_001798, hCT16113.3, hCT1955017.1, hCT2307649.0, hCT2307651.0, hCT2307652.0	204252_at, 211803_at, 211804_s_at	NP_439892.2, NP_001789.2, EAW96856.1, EAW96857.1, EAW96858.1, EAW96860.1, EAW96859.1
GeneID:5869	RAB5B	12	56,367,662	56,388,490	20,828	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1475	-182	upstream	1	0	0	28	19	17	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene RAB5B	RAB5B	RAB5B, member RAS oncogene family	NM_002868, hCT2307654.0, hCT2307655.0, hCT2307657.0	201276_at	NP_002859.1, EAW96862.1, EAW96863.1, EAW96864.1
GeneID:100131294	LOC100131294	12	56,373,755	56,374,851	1,096	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1475	7171	downstream	1	0	0	28	19	17	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene LOC100131294		RAB13, member RAS oncogene family pseudogene			
GeneID:6821	SUOX	12	56,391,043	56,399,309	8,266	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1476, 2_A375_pNL97_plus_lncRNA_AR..1..2083	10013, 10013	downstream, downstream	1	1	0	23	22	9	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene SUOX	SUOX	sulfite oxidase	NM_000456, NM_001032386, NM_001032387, hCT16111.2, hCT1955016.1, hCT2307658.0, hCT2307659.0, hCT2358212.0	1553030_a_at, 204067_at	NP_000447.2, NP_001027558.1, NP_001027559.1, EAW96867.1, EAW96869.1, EAW96870.1, EAW96868.1, EAW96871.1
GeneID:64375	IKZF4	12	56,414,689	56,432,219	17,530	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1477, 2_A375_pNL97_plus_lncRNA_AR..1..2084, 4_A375_EGR1..1..1905	21023, 20991, 21119	downstream, downstream, downstream	1	1	1	21	23	15	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene IKZF4	ZNFN1A4, EOS, IKZF4, KIAA1782	IKAROS family zinc finger 4 (Eos)	NM_022465, hCT16119.4, hCT2307662.1, hCT2349797.0	208472_at, 226759_at, 226781_at, 229752_at	NP_071910.3, EAW96874.1, EAW96872.1, EAW96873.1
GeneID:6231	RPS26	12	56,435,686	56,438,007	2,321	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1477, 2_A375_pNL97_plus_lncRNA_AR..1..2084, 4_A375_EGR1..1..1905	26, -6, 122	in gene, upstream, in gene	1	1	1	21	23	15	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RPS26	DBA10, MGC104292, S26, RPS26	ribosomal protein S26	NM_001029, hCT2307668.0, hCT2307670.0, hCT2307671.0	217753_s_at	NP_001020.2, EAW96876.1, EAW96877.1, EAW96878.1
GeneID:2065	ERBB3	12	56,473,892	56,497,128	23,236	+	3	2_A375_pNL97_plus_lncRNA_AR..1..2085, 2_A375_pNL97_plus_lncRNA_AR..1..2086, 2_A375_pNL97_plus_lncRNA_AR..1..2087	-604, 924, 24346	upstream, in gene, downstream	0	1	0	16	21.33	15	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene ERBB3	ERBB3, MDA-BF-1, c-erbB-3, c-erbB3, erbB3-S, MGC88033, HER3, p45-sErbB3, p85-sErbB3, p180-ErbB3, ErbB-3, LCCS2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	NM_001982, NM_001005915, hCT16108.2, hCT2307676.0, hCT2307678.0, hCT2307680.0, hCT2307681.0	1563252_at, 1563253_s_at, 202454_s_at, 215638_at, 226213_at	NP_001973.2, NP_001005915.1, EAW96879.1, EAW96880.1, EAW96881.1, EAW96883.1, EAW96882.1
GeneID:5036	PA2G4	12	56,498,103	56,507,694	9,591	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1478, 2_A375_pNL97_plus_lncRNA_AR..1..2087, 2_A375_pNL97_plus_lncRNA_AR..1..2088, 4_A375_EGR1..1..1906	13929, 137, 13977, 13945	downstream, in gene, downstream, downstream	1	1	1	21.5	25.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene PA2G4	PA2G4, p38-2G4, EBP1, HG4-1	proliferation-associated 2G4, 38kDa	NM_006191, hCT2307665.0, hCT2307667.0	208676_s_at, 214794_at	NP_006182.2, EAW96884.1, EAW96885.1
GeneID:6171	RPL41	12	56,510,374	56,511,616	1,242	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1478, 2_A375_pNL97_plus_lncRNA_AR..1..2088, 4_A375_EGR1..1..1906	1656, 1706, 1674	downstream, downstream, downstream	1	1	1	22	23	20	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RPL41	RPL41, L41		NM_021104, NM_001035267, hCT2307669.1, hCT2348770.0	201492_s_at	NP_066927.1, NP_001030344.1, EAW96886.1, EAW96887.1
GeneID:84872	ZC3H10	12	56,512,030	56,516,276	4,246	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1478, 2_A375_pNL97_plus_lncRNA_AR..1..2088, 4_A375_EGR1..1..1906	2, 50, 16	in gene, in gene, in gene	1	1	1	22	23	20	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ZC3H10	FLJ14451, ZC3H10, ZC3HDC10	zinc finger CCCH-type containing 10	NM_032786, hCT1823165.2, hCT2307691.2	227430_at	NP_116175.1, EAW96888.1, EAW96889.1
GeneID:23344	ESYT1	12	56,521,966	56,538,460	16,474	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1478, 1_A375_pNL7_minus_lncRNA_AR..1..1479, 2_A375_pNL97_plus_lncRNA_AR..1..2088, 2_A375_pNL97_plus_lncRNA_AR..1..2089, 4_A375_EGR1..1..1906	-9954, 24302, -9906, 24318, -9938	upstream, downstream, upstream, downstream, upstream	1	1	1	21.5	21.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ESYT1	KIAA0747, MBC2, ESYT1, FAM62A	extended synaptotagmin-like protein 1	NM_001184796, NM_015292, hCT16123.2, hCT2307695.0, hCT2307696.0, hCT2307697.0	208858_s_at, 244234_at	NP_001171725.1, NP_056107.1, EAW96890.1, EAW96891.1, EAW96892.1, EAW96893.1
GeneID:140465	MYL6B	12	56,546,335	56,551,771	5,436	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1479, 2_A375_pNL97_plus_lncRNA_AR..1..2089	-47, -31	upstream, upstream	1	1	0	21	20	8	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene MYL6B	MLC1SA, MYL6B	myosin, light chain 6B, alkali, smooth muscle and non-muscle	NM_002475, hCT2307700.1, hCT2307702.1, hCT2307704.1, hCT2358106.0, hCT2358107.0	204173_at	NP_002466.1, EAW96894.1, EAW96895.1, EAW96896.1, EAW96897.1, EAW96898.1
GeneID:4637	MYL6	12	56,552,100	56,555,386	3,286	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1479, 2_A375_pNL97_plus_lncRNA_AR..1..2089	-5812, -5796	upstream, upstream	1	1	0	21	20	8	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene MYL6	MLC3SM, LC17A, ESMLC, LC17B, MLC3NM, MYL6, MLC1SM, LC17-GI, LC17-NM	myosin, light chain 6, alkali, smooth muscle and non-muscle	NM_021019, NM_079423, hCT2307699.1, hCT2307701.1, hCT2307703.1, hCT2307705.1, hCT2307706.1, hCT2307707.1, hCT2344311.0	212082_s_at, 214002_at	NP_066299.2, NP_524147.2, EAW96899.1, EAW96900.1, EAW96901.1, EAW96904.1, EAW96902.1, EAW96903.1, EAW96905.1
GeneID:6601	SMARCC2	12	56,555,636	56,583,351	27,715	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1479, 2_A375_pNL97_plus_lncRNA_AR..1..2089, 2_A375_pNL97_plus_lncRNA_AR..1..2090	37063, 37047, -185	downstream, downstream, upstream	1	1	0	18.5	23	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene SMARCC2	Rsc8, CRACC2, BAF170, SMARCC2, DKFZp313D0832	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	NM_001130420, NM_003075, NM_139067, hCT16125.3, hCT2308912.0, hCT2308914.0	1561973_at, 201320_at, 201321_s_at	NP_001123892.1, NP_003066.2, NP_620706.1, EAW96906.1, EAW96907.1, EAW96908.1
GeneID:10193	RNF41	12	56,598,285	56,615,735	17,450	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1480, 2_A375_pNL97_plus_lncRNA_AR..1..2091	-2345, -2409	upstream, upstream	1	1	0	33	42	9	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene RNF41	MGC45228, NRDP1, RNF41, SBBI03	ring finger protein 41	NM_005785, NM_194358, NM_194359, hCT16105.4, hCT2308909.1, hCT2308910.1	201961_s_at, 201962_s_at	NP_005776.1, NP_919339.1, NP_919340.1, EAW96909.1, EAW96910.1, EAW96911.1
GeneID:79035	OBFC2B	12	56,618,125	56,623,638	5,513	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1480, 2_A375_pNL97_plus_lncRNA_AR..1..2091	-45, 19	upstream, in gene	1	1	0	33	42	9	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene OBFC2B	hSSB1, SSB1, MGC2731, OBFC2B, SOSS-B1	oligonucleotide/oligosaccharide-binding fold containing 2B	NM_024068, hCT16129.3, hCT2307709.1, hCT2350545.0, hCT2350546.0	218903_s_at	NP_076973.1, EAW96912.1, EAW96913.1, EAW96914.1, EAW96915.1
GeneID:283375	SLC39A5	12	56,623,820	56,631,630	7,810	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1480, 2_A375_pNL97_plus_lncRNA_AR..1..2091	-5740, -5676	upstream, upstream	1	1	0	33	42	9	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene SLC39A5	LZT-Hs7, SLC39A5, MGC34778, ZIP5	solute carrier family 39 (metal ion transporter), member 5	NM_173596, NM_001135195, hCT16131.3, hCT2307710.1, hCT2307711.1	1552281_at, 231667_at	NP_775867.2, NP_001128667.1, EAW96916.1, EAW96917.1, EAW96918.1
GeneID:283373	ANKRD52	12	56,631,591	56,652,143	20,552	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2092, 2_A375_pNL97_plus_lncRNA_AR..1..2093	-209, -8561	upstream, upstream	0	1	0	12.5	15	10	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ANKRD52	ANKRD33, FLJ34236, ANKRD52	ankyrin repeat domain 52	NM_173595	226257_at	NP_775866.2
GeneID:93058	COQ10A	12	56,660,642	56,664,750	4,108	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2092, 2_A375_pNL97_plus_lncRNA_AR..1..2093	-8290, 62	upstream, in gene	0	1	0	12.5	15	10	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene COQ10A	COQ10A, FLJ32452	coenzyme Q10 homolog A (S. cerevisiae)	NM_144576, NM_001099337, hCT16128.4, hCT2307715.1, hCT2307716.1	225747_at	NP_653177.3, NP_001092807.1, EAW96920.1, EAW96921.1, EAW96922.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	AltSymbols	Full Description	RNA	Affy Tag	PROT
GeneID:1431	CS	12	56,665,483	56,694,175	28,692	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2093	33471	downstream	0	1	0	12	14	11	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene CS	CS	citrate synthase	NM_004077, hCT2308904.0, hCT2308905.0	208660_at	NP_004068.2, EAW96923.1, EAW96924.1
GeneID:10330	CNPY2	12	56,704,212	56,710,128	5,916	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2094, 4_A375_EGR1..1..1907	144, 98	in gene, in gene	0	1	1	14	19	19	1	4_A375_EGR1..1	19	Gene CNPY2	CNPY2, ZSIG9, TMEM4, HP10390, MSAP	canopy 2 homolog (zebrafish)	NM_001190991, NM_014255, hCT2308895.2, hCT2349793.0, hCT2349794.0	1557798_at, 202857_at, 209796_s_at, 209797_at	NP_001177920.1, NP_055070.1, EAW96925.1, EAW96926.1, EAW96927.1
GeneID:9924	PAN2	12	56,710,007	56,727,837	17,830	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2094, 4_A375_EGR1..1..1907	17853, 17805	downstream, in gene	0	1	1	14	19	19	1	4_A375_EGR1..1	19	Gene PAN2	KIAA0710, PAN2, USP52, FLJ39360	PAN2 poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	NM_014871, NM_001166279, NM_001127460, hCT2308894.1, hCT2308898.1, hCT2308901.1, hCT2358058.0, hCT2358059.0	203117_s_at	NP_055686.3, NP_001159751.1, NP_001120932.1, EAW96928.1, EAW96930.1, EAW96931.1, EAW96929.1, EAW96932.1
GeneID:283377	SPRYD4	12	56,862,301	56,864,769	2,468	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1461, 2_A375_pNL97_plus_lncRNA_AR..1..2095	67, 63	in gene, in gene	1	1	0	45	42	13	1	1_A375_pNL7_minus_lncRNA_AR..1	45	Gene SPRYD4	DKFZp686N0877, SPRYD4	SPRY domain containing 4	NM_207344, hCT16124.2	225616_at	NP_997227.1, EAW96941.1
GeneID:27165	GLS2	12	56,864,736	56,882,181	17,445	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1461, 2_A375_pNL97_plus_lncRNA_AR..1..2095, 4_A375_EGR1..1..1906	19613, 19797, -251	downstream, downstream, upstream	1	1	1	26.5	26.5	15	2	1_A375_pNL7_minus_lncRNA_AR..1	45	Gene GLS2	MGC71567, GLS2, LGA, hLGA, GLS, GA	glutaminase 2 (liver, mitochondrial)	NM_013267, hCT16103.2, hCT2308884.0, hCT2358164.0, hCT2358165.0	1564705_at, 1564706_s_at, 1564707_x_at, 205531_s_at	NP_037399.2, EAW96943.1, EAW96942.1, EAW96944.1, EAW96945.1
GeneID:5939	RBMS2	12	56,915,609	56,989,980	74,371	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1462	57479	in gene	1	0	0	15	11	4	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene RBMS2	FLJ39093, FLJ43262, FLJ40023, RBMS2, SCR3	RNA binding motif, single stranded interacting protein 2	NM_002898, hCT1955009.1, hCT2307728.0	205228_at, 34187_at	NP_002889.1, EAW96947.1, EAW96948.1
GeneID:11176	BAZ2A	12	56,989,380	57,030,163	40,783	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1463, 1_A375_pNL7_minus_lncRNA_AR..1..1464, 2_A375_pNL97_plus_lncRNA_AR..1..2096, 2_A375_pNL97_plus_lncRNA_AR..1..2097, 2_A375_pNL97_plus_lncRNA_AR..1..2098, 4_A375_EGR1..1..1909	5939, 1235, 5971, 1235, -9645, 5987	in gene, in gene, in gene, in gene, upstream, in gene	1	1	1	31.33	36	12	3	2_A375_pNL97_plus_lncRNA_AR..1	66	Gene BAZ2A	FLJ13768, FLJ45876, BAZ2A, DKFZp781B109, FLJ13780, KIAA0314, TIP5, WALp3	bromodomain adjacent to zinc finger domain, 2A	NM_013449, hCT16115.4, hCT2308879.0, hCT2308881.0	201353_s_at, 201354_s_at, 201355_s_at, 215437_x_at	NP_038477.2, EAW96949.1, EAW96950.1, EAW96951.1
GeneID:506	ATP5B	12	57,031,959	57,039,852	7,893	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1463, 1_A375_pNL7_minus_lncRNA_AR..1..1464, 2_A375_pNL97_plus_lncRNA_AR..1..2096, 2_A375_pNL97_plus_lncRNA_AR..1..2097, 2_A375_pNL97_plus_lncRNA_AR..1..2098, 4_A375_EGR1..1..1909	15626, 10924, 15660, 10924, 44, 15676	downstream, downstream, downstream, downstream, in gene, downstream	1	1	1	31.33	36	12	3	2_A375_pNL97_plus_lncRNA_AR..1	66	Gene ATP5B	ATPMB, ATP5B, MGC5231, ATPSB	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	NM_001686, hCT16121.3	201322_at	NP_001677.2, EAW96952.1
GeneID:692090	SNORD59B	12	57,037,464	57,037,538	74	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1464, 2_A375_pNL97_plus_lncRNA_AR..1..2097, 2_A375_pNL97_plus_lncRNA_AR..1..2098	8610, 8610, -2270	downstream, downstream, upstream	1	1	0	21	23	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene SNORD59B	SNORD59B, U59B	small nucleolar RNA, C/D box 59B	NR_003046		
GeneID:26789	SNORD59A	12	57,038,811	57,038,885	74	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1464, 2_A375_pNL97_plus_lncRNA_AR..1..2097, 2_A375_pNL97_plus_lncRNA_AR..1..2098	9957, 9957, -923	downstream, downstream, upstream	1	1	0	21	23	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene SNORD59A	SNORD59A, RNU59, U59	small nucleolar RNA, C/D box 59A	NR_002737		
GeneID:10728	PTGES3	12	57,057,125	57,082,078	24,953	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1465, 2_A375_pNL97_plus_lncRNA_AR..1..2099, 4_A375_EGR1..1..1910	190, 254, -2	in gene, in gene, upstream	1	1	1	17	19	15	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PTGES3	P23, TEBP, cPGES, PTGES3	prostaglandin E synthase 3 (cytosolic)	NM_006601, hCT2309388.0, hCT2309389.0, hCT2309390.0, hCT2309391.0, hCT2358182.0, hCT2358183.0	200627_at	NP_006592.3, EAW96958.1, EAW96953.1, EAW96954.1, EAW96955.1, EAW96957.1, EAW96956.1
GeneID:4666	NACA	12	57,106,211	57,119,326	13,115	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2100	254	in gene	0	1	0	16	24	13	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene NACA	HSD48, NACA, NACA1, MGC117224	nascent polypeptide-associated complex alpha subunit	NM_005594, NM_001113201, NM_001113202, NM_001113203	200735_x_at, 208635_x_at	NP_005585.1, NP_001106672.1, NP_001106673.1, NP_001106674.1
GeneID:5557	PRIM1	12	57,125,384	57,146,146	20,762	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2100	27074	downstream	0	1	0	16	24	13	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PRIM1	p49, PRIM1, MGC12308	primase, DNA, polypeptide 1 (49kDa)	NM_000946	205053_at	NP_000937.1
GeneID:4640	MYO1A	12	57,422,301	57,443,893	21,592	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2101	229	in gene	0	1	0	17	18	4	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MYO1A	DFNA48, MYHL, MYO1A, MIHC, BBMI	myosin IA	NM_005379, hCT2309372.1, hCT2309373.0, hCT2309375.1	211916_s_at	NP_005370.1, EAW96983.1, EAW96981.1, EAW96982.1
GeneID:23306	TMEM194A	12	57,449,426	57,472,574	23,148	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2101, 2_A375_pNL97_plus_lncRNA_AR..1..2102, 4_A375_EGR1..1..1911	28910, -9762, -8866	downstream, upstream, upstream	0	1	1	17	19	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TMEM194A	TMEM194, KIAA0286, DKFZp686N1766, TMEM194A	transmembrane protein 194A	NM_015257, NM_001130963, hCT2348776.0, hCT2348777.0, hCT32503.4	212619_at, 212621_at	NP_056072.2, NP_001124435.1, EAW96984.1, EAW96985.1, EAW96986.1
GeneID:4665	NAB2	12	57,482,677	57,489,259	6,582	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2102, 4_A375_EGR1..1..1911	-341, -1237	upstream, upstream	0	1	1	17	20	17	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene NAB2	MADER, NAB2, MGC75085	NGFI-A binding protein 2 (EGR1 binding protein 2)	NM_005967, hCT2308501.0, hCT2308505.0, hCT32497.3	212803_at, 216017_s_at	NP_005958.1, EAW96987.1, EAW96988.1, EAW96989.1
GeneID:6778	STAT6	12	57,489,187	57,505,196	16,009	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2102, 4_A375_EGR1..1..1911	22860, 23756	downstream, downstream	0	1	1	17	20	17	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene STAT6	STAT6C, STAT6B, D12S1644, STAT6, IL-4-STAT	signal transducer and activator of transcription 6, interleukin-4 induced	NM_001178078, NM_001178079, NM_001178080, NM_001178081, NM_003153, NR_033659	201331_s_at, 201332_s_at	NP_001171549.1, NP_001171550.1, NP_003144.3, NP_001171551.1, NP_001171552.1
GeneID:4035	LRP1	12	57,522,282	57,607,142	84,860	+	1	4_A375_EGR1..1..1912	47366	in gene	0	0	1	5	6	16	1	4_A375_EGR1..1	16	Gene LRP1	IGFBP3R, CD91, FLJ16451, MGC88725, APOER, APR, TGFBR5, LRP1, LRP, A2MR	low density lipoprotein receptor-related protein 1	NM_002332, hCT1817524.2, hCT2308512.0	1555353_at, 1569042_at, 200784_s_at, 200785_s_at	NP_002323.2, EAW96991.1, EAW96990.1
GeneID:6472	SHMT2	12	57,623,356	57,628,718	5,362	+	6	1_A375_pNL7_minus_lncRNA_AR..1..1486, 1_A375_pNL7_minus_lncRNA_AR..1..1487, 2_A375_pNL97_plus_lncRNA_AR..1..2103, 2_A375_pNL97_plus_lncRNA_AR..1..2104, 4_A375_EGR1..1..1913, 4_A375_EGR1..1..1914	9700, 13252, 9652, 13252, 10532, 11012	downstream, downstream, downstream, downstream, downstream, downstream	1	1	1	33.75	31.5	15.5	4	1_A375_pNL7_minus_lncRNA_AR..1	66	Gene SHMT2	GLYA, SHMT, SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	NM_005412, NM_001166356, NM_001166357, NM_001166358, NM_001166359, NR_029415, NR_029416, NR_029417, hCT1817523.0, hCT1955024.1, hCT2308515.0, hCT2358159.0, hCT2358160.0, hCT2358161.0, hCT2358162.0, hCT2358163.0, hCT32501.2	214095_at, 214096_s_at, 214437_s_at	NP_005403.2, NP_001159828.1, NP_001159829.1, NP_001159830.1, NP_001159831.1, EAW96993.1, EAW96994.1, EAW96995.1, EAW96996.1, EAW96997.1, EAW96998.1, EAW96999.1, EAW97000.1, EAW97001.1
GeneID:56901	NDUFA4L2	12	57,628,686	57,634,545	5,859	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1486, 1_A375_pNL7_minus_lncRNA_AR..1..1487, 2_A375_pNL97_plus_lncRNA_AR..1..2103, 2_A375_pNL97_plus_lncRNA_AR..1..2104, 4_A375_EGR1..1..1913, 4_A375_EGR1..1..1914	1489, -2063, 1537, -2063, 657, 177	in gene, upstream, in gene, upstream, in gene, in gene	1	1	1	33.75	31.5	15.5	4	1_A375_pNL7_minus_lncRNA_AR..1	66	Gene NDUFA4L2	NUOMS, NDUFA4L2, FLJ26118	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	NM_020142, hCT2309362.0, hCT32506.2	218484_at	NP_064527.1, EAW97002.1, EAW97003.1
GeneID:246329	STAC3	12	57,637,242	57,644,969	7,727	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1486, 1_A375_pNL7_minus_lncRNA_AR..1..1487, 2_A375_pNL97_plus_lncRNA_AR..1..2103, 2_A375_pNL97_plus_lncRNA_AR..1..2104, 4_A375_EGR1..1..1913, 4_A375_EGR1..1..1914	11913, 8361, 11961, 8361, 11081, 10601	downstream, downstream, downstream, downstream, downstream, downstream	1	1	1	33.75	31.5	15.5	4	1_A375_pNL7_minus_lncRNA_AR..1	66	Gene STAC3	STAC3, MGC2793	SH3 and cysteine rich domain 3	NM_145064, hCT2309361.0, hCT2358167.0, hCT2358166.0, hCT32507.3	230652_at	NP_659501.1, EAW97005.1, EAW97004.1, EAW97006.1, EAW97007.1
GeneID:3626	INHBC	12	57,828,543	57,844,609	16,066	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1488, 2_A375_pNL97_plus_lncRNA_AR..1..2105, 4_A375_EGR1..1..1915, 4_A375_EGR1..1..1916	24961, 24961, 21697, 26225	downstream, downstream, downstream, downstream	1	1	1	12	13.67	14.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene INHBC	INHBC, IHBC	inhibin, beta C	NM_005538, hCT1961147.1	207687_at, 207688_s_at	NP_005529.1, EAW97011.1
GeneID:83729	INHBE	12	57,849,096	57,851,791	2,695	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1488, 2_A375_pNL97_plus_lncRNA_AR..1..2105, 4_A375_EGR1..1..1915, 4_A375_EGR1..1..1916	4408, 4408, 1144, 5672	downstream, downstream, in gene, downstream	1	1	1	12	13.67	14.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene INHBE	MGC4638, INHBE	inhibin, beta E	NM_031479, hCT1961148.1	210587_at	NP_113667.1, EAW97012.1
GeneID:2735	GLI1	12	57,853,918	57,866,051	12,133	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1488, 2_A375_pNL97_plus_lncRNA_AR..1..2105, 4_A375_EGR1..1..1915, 4_A375_EGR1..1..1916	-414, -414, -3678, 850	upstream, upstream, upstream, in gene	1	1	1	12	13.67	14.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene GLI1	GLI1, GLI	GLI family zinc finger 1	NM_005269, NM_001160045, NM_001167609, hCT2308523.0	206646_at	NP_005260.1, NP_001153517.1, NP_001161081.1, EAW97013.1
GeneID:64333	ARHGAP9	12	57,866,038	57,873,633	7,595	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1489, 2_A375_pNL97_plus_lncRNA_AR..1..2106	-8095, -8127	upstream, upstream	1	1	0	16	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ARHGAP9	FLJ16525, RGL1, 10C, ARHGAP9, MGC1295	Rho GTPase activating protein 9	NM_032496, NM_001080156, NM_001080157, hCT2309354.0, hCT2309355.0, hCT2309356.0, hCT2358108.0, hCT30920.4	224451_x_at, 226908_s_at, 232543_x_at	NP_115885.2, NP_001073625.1, NP_001073626.1, EAW97014.1, EAW97015.1, EAW97018.1, EAW97016.1, EAW97017.1
GeneID:4141	MARS	12	57,881,851	57,910,433	28,582	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1489, 2_A375_pNL97_plus_lncRNA_AR..1..2106, 2_A375_pNL97_plus_lncRNA_AR..1..2107	-123, -91, 32117	upstream, upstream, downstream	1	1	0	13	17	12	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene MARS	FLJ35667, MARS, MRS, MTRNS, METRS	methionyl-tRNA synthetase	NM_004990, hCT2344312.1, hCT2344313.1	201475_x_at, 213671_s_at, 213672_at	NP_004981.2, EAW97019.1, EAW97020.1
GeneID:1649	DDIT3	12	57,910,371	57,914,300	3,929	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2107	332	in gene	0	1	0	10	17	13	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene DDIT3	CHOP10, CHOP, CHOP-10, CEBPZ, MGC4154, DDIT3, GADD153	DNA-damage-inducible transcript 3	NM_001195053, NM_001195054, NM_001195055, NM_001195056, NM_004083, NM_001195057, hCT1955021.1, hCT1955022.1, hCT30913.3	209383_at	NP_001181982.1, NP_001181983.1, NP_004074.2, NP_001181984.1, NP_001181985.1, NP_001181986.1, EAW97021.1, EAW97022.1, EAW97023.1
GeneID:693201	MIR616	12	57,912,946	57,913,042	96	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2107	-926	upstream	0	1	0	10	17	13	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene MIR616	MIR616, hsa-mir-616, MIRN616	microRNA 616	NR_030346		
GeneID:114785	MBD6	12	57,916,659	57,923,931	7,272	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2107	-2691	upstream	0	1	0	10	17	13	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene MBD6	KIAA1887, MBD6	methyl-CpG binding domain protein 6	NM_052897, hCT2308524.1, hCT2308525.1, hCT2308526.1	214384_s_at, 226078_s_at, 227832_at, 227833_s_at	NP_443129.3, EAW97024.1, EAW97025.1, EAW97026.1
GeneID:10540	DCTN2	12	57,924,094	57,940,978	16,884	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2107	27010	downstream	0	1	0	10	17	13	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene DCTN2	DYNAMITIN, RBP50, DCTN2, DCTN50	dynactin 2 (p50)	NM_006400, hCT2309348.0, hCT2309349.0, hCT2309350.0	200932_s_at, 232505_at	NP_006391.1, EAW97028.1, EAW97027.1, EAW97029.1
GeneID:115557	GEFT	12	58,003,963	58,011,026	7,063	+	1	4_A375_EGR1..1..1917	10597	downstream	0	0	1	6	6	16	1	4_A375_EGR1..1	16	Gene GEFT	p63RhoGEF, ARHGEF25, GEFT	Rho guanine nucleotide exchange factor (GEF) 25	NM_182947, NM_001111270	227427_at	NP_891992.2, NP_001104740.1
GeneID:65012	SLC26A10	12	58,013,693	58,019,934	6,241	+	1	4_A375_EGR1..1..1917	867	in gene	0	0	1	6	6	16	1	4_A375_EGR1..1	16	Gene SLC26A10	SLC26A10, FLJ32654	solute carrier family 26, member 10	NM_133489	214951_at	NP_597996.2
GeneID:2583	B4GALNT1	12	58,019,551	58,026,985	7,434	-	1	4_A375_EGR1..1..1917	12425	downstream	0	0	1	6	6	16	1	4_A375_EGR1..1	16	Gene B4GALNT1	GALGT, B4GALNT1, GALNACT	beta-1,4-N-acetyl-galactosaminyl transferase 1	NM_001478, hCT2309341.0, hCT30910.2	1555385_at, 206435_at	NP_001469.1, EAW97042.1, EAW97043.1
GeneID:10956	OS9	12	58,087,738	58,115,340	27,602	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1490, 2_A375_pNL97_plus_lncRNA_AR..1..2108, 4_A375_EGR1..1..1918, 4_A375_EGR1..1..1919	32550, 33403, 32342, 33126	downstream, downstream, downstream, downstream	1	1	1	17	13	18	1	4_A375_EGR1..1	18	Gene OS9	OS-9, ERLEC2, OS9	osteosarcoma amplified 9, endoplasmic reticulum lectin	NM_006812, NM_001017956, NM_001017957, NM_001017958, hCT2358203.0, hCT2358204.0, hCT2358205.0, hCT31404.3	200714_x_at, 215399_s_at	NP_006803.1, NP_001017956.1, NP_001017957.1, NP_001017958.1, EAW97044.1, EAW97047.1, EAW97045.1, EAW97046.1
GeneID:116986	AGAP2	12	58,118,994	58,135,940	16,946	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1490, 1_A375_pNL7_minus_lncRNA_AR..1..1491, 2_A375_pNL97_plus_lncRNA_AR..1..2108, 4_A375_EGR1..1..1918, 4_A375_EGR1..1..1919, 4_A375_EGR1..1..1920	15852, -2398, 14799, 15860, 15076, 4484	in gene, upstream, in gene, in gene, in gene, in gene	1	1	1	15.67	14.33	17.67	3	4_A375_EGR1..1	28	Gene AGAP2	KIAA0167, AGAP2, FLJ16430, GGAP2, PIKE, CENTG1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	NM_014770, NM_001122772, hCT1971571.1, hCT2308333.0, hCT2308334.0, hCT31393.3	206152_at, 215080_s_at	NP_055585.1, NP_001116244.1, EAW97048.1, EAW97049.1, EAW97050.1, EAW97051.1
GeneID:100130776	hCG_2014417	12	58,120,023	58,122,139	2,116	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1490, 2_A375_pNL97_plus_lncRNA_AR..1..2108, 4_A375_EGR1..1..1918, 4_A375_EGR1..1..1919, 4_A375_EGR1..1..1920	265, 1118, 57, 841, 11433	in gene, in gene, in gene, in gene, downstream	1	1	1	14.5	12.5	23	2	4_A375_EGR1..1	28	Gene hCG_2014417	LOC100130776	hypothetical LOC100130776	NR_027032		
GeneID:8302	TSPAN31	12	58,138,784	58,142,026	3,242	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1491, 4_A375_EGR1..1..1920	-446, -7326	upstream, upstream	1	0	1	15	15	17.5	2	4_A375_EGR1..1	28	Gene TSPAN31	TSPAN31, SAS	tetraspanin 31	NM_005981, hCT2308078.1, hCT2308079.1, hCT2341417.0, hCT31394.4	203226_s_at, 203227_s_at	NP_005972.1, EAW97054.1, EAW97055.1, EAW97056.1, EAW97057.1
GeneID:1019	CDK4	12	58,142,003	58,146,164	4,161	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1491	7826	downstream	1	0	0	18	18	7	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene CDK4	PSK-J3, MGC14458, CMM3, CDK4	cyclin-dependent kinase 4	NM_000075, hCT1971572.1, hCT2308328.0, hCT2308330.0, hCT2308331.0, hCT31395.2	202246_s_at	NP_000066.1, EAW97059.1, EAW97058.1, EAW97060.1, EAW97061.1, EAW97062.1
GeneID:92979	9-Mar	12	58,148,900	58,153,689	4,789	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1491, 2_A375_pNL97_plus_lncRNA_AR..1..2109	-10584, 11676	upstream, downstream	1	1	0	16	21	11	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene MARCH9	FLJ38578, RNF179, MARCH-IX, MARCH9	membrane-associated ring finger (C3HC4) 9	NM_138396, hCT2308085.0, hCT2358185.0, hCT31403.1	226454_at, 230001_at	NP_612405.2, EAW97065.1, EAW97063.1, EAW97064.1
GeneID:1594	CYP27B1	12	58,156,117	58,160,976	4,859	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1492, 2_A375_pNL97_plus_lncRNA_AR..1..2109, 2_A375_pNL97_plus_lncRNA_AR..1..2110, 4_A375_EGR1..1..1921, 4_A375_EGR1..1..1922	-4976, 400, -4944, -4816, -5616	upstream, in gene, upstream, upstream, upstream	1	1	1	21	32.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene CYP27B1	PDDR, CYP27B, VDD1, VDDRI, CYP27B1, P450c1, VDR, CP2B, VDDR, CYP1, CYP1alpha	cytochrome P450, family 27, subfamily B, polypeptide 1	NM_000785	205676_at	NP_000776.1
GeneID:4234	METTL1	12	58,162,351	58,165,914	3,563	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1492, 2_A375_pNL97_plus_lncRNA_AR..1..2109, 2_A375_pNL97_plus_lncRNA_AR..1..2110, 4_A375_EGR1..1..1921, 4_A375_EGR1..1..1922	-38, 5336, -6, 122, -678	upstream, downstream, upstream, in gene, upstream	1	1	1	21	32.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene METTL1	C12orf1, FLJ95748, METTL1, YDL201w, TRM8	methyltransferase like 1	NM_005371, NM_023033	204027_s_at	NP_005362.3, NP_075422.3
GeneID:25895	FAM119B	12	58,166,383	58,176,324	9,941	+	7	1_A375_pNL7_minus_lncRNA_AR..1..1492, 1_A375_pNL7_minus_lncRNA_AR..1..1493, 2_A375_pNL97_plus_lncRNA_AR..1..2109, 2_A375_pNL97_plus_lncRNA_AR..1..2110, 2_A375_pNL97_plus_lncRNA_AR..1..2111, 4_A375_EGR1..1..1921, 4_A375_EGR1..1..1922	-431, 10129, -5807, -463, 10129, -591, 209	upstream, downstream, upstream, upstream, downstream, upstream, in gene	1	1	1	62	71.67	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	150	Gene FAM119B	DKFZp586D0919, FAM119B, METTL21B	family with sequence similarity 119, member B	NM_015433, NM_206914, hCT2308087.1, hCT2308090.1, hCT31400.4	213681_s_at	NP_056248.2, NP_996797.1, EAW97072.1, EAW97073.1, EAW97074.1
GeneID:10102	TSFM	12	58,176,528	58,196,639	20,111	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1493, 2_A375_pNL97_plus_lncRNA_AR..1..2110, 2_A375_pNL97_plus_lncRNA_AR..1..2111, 4_A375_EGR1..1..1922	-16, -10608, -16, -9936	upstream, upstream, upstream, upstream	1	1	1	66	95.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	150	Gene TSFM	EFTS, COXPD3, EF-TS, EF-Tsmt, TSFM, EFTSMT	Ts translation elongation factor, mitochondrial	NM_001172695, NM_001172696, NM_001172697, NM_005726, hCT1971573.1, hCT2308094.1, hCT2358184.0, hCT31398.3	212656_at, 214331_at, 214332_s_at	NP_001166166.1, NP_001166167.1, NP_005717.3, NP_001166168.1, EAW97077.1, EAW97078.1, EAW97075.1, EAW97076.1
GeneID:10106	CTDSP2	12	58,213,710	58,240,747	27,037	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1494, 4_A375_EGR1..1..1923	923, 779	in gene, in gene	1	0	1	17	14	22	1	4_A375_EGR1..1	22	Gene CTDSP2	OS4, PSR2, SCP2, CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	NM_005730, hCT1962527.1, hCT1971574.1, hCT1971575.1, hCT2308312.0, hCT2308314.0, hCT2308317.0, hCT2358209.0, hCT2358210.0, hCT31406.4	203445_s_at, 208735_s_at	NP_005721.3, EAW97088.1, EAW97082.1, EAW97083.1, EAW97087.1, EAW97089.1, EAW97081.1, EAW97084.1, EAW97085.1, EAW97086.1
GeneID:100506805	LOC100506805	12	58,230,876	58,237,544	6,668	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1494, 4_A375_EGR1..1..1923	8948, 9092	downstream, downstream	1	0	1	17	14	22	1	4_A375_EGR1..1	22	Gene LOC100506805		hypothetical LOC100506805	XR_110363		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100289282	LOC100289282	12	58,273,046	58,273,873	827	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2112	9626	downstream	0	1	0	13	21	6	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100289282		hypothetical protein LOC100289282	XM_002343174, XM_003120739		XP_002343215.1, XP_003120787.1
GeneID:100289313	LOC100289313	12	58,289,528	58,299,028	9,500	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2112	16356	downstream	0	1	0	13	21	6	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100289313		hypothetical LOC100289313	XR_111317, XR_110384, XR_114646		
GeneID:100506844	LOC100506844	12	58,325,232	58,329,947	4,715	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1495	-5081	upstream	1	0	0	17	12	10	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene LOC100506844		hypothetical LOC100506844	XR_111314, XR_111316, XR_111315, XR_110365, XR_110366, XR_114647, XR_114648, XR_114649		
GeneID:91419	XRCC6BP1	12	58,335,445	58,351,052	15,607	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1495	-437	upstream	1	0	0	17	12	10	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene XRCC6BP1	MGC134818, XRCC6BP1, KUB3, MGC134817	XRCC6 binding protein 1	NM_033276, hCT1816507.2	1554349_at, 227678_at	NP_150592.1, EAW97091.1
GeneID:121227	LRIG3	12	59,265,937	59,314,262	48,325	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1499, 4_A375_EGR1..1..1924	70, -42	in gene, upstream	1	0	1	17	9	17	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene LRIG3	LRIG3, FLJ90440, KIAA3016, FLJ26573, LIG3	leucine-rich repeats and immunoglobulin-like domains 3	NM_153377, NM_001136051, hCT2356180.0, hCT30356.2	226908_at	NP_700356.2, NP_001129523.1, EAW97094.1, EAW97095.1
GeneID:9958	USP15	12	62,654,187	62,799,898	145,711	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1502, 2_A375_pNL97_plus_lncRNA_AR..1..2117, 4_A375_EGR1..1..1925	-139, -171, 161	upstream, upstream, in gene	1	1	1	166	173	16	1	2_A375_pNL97_plus_lncRNA_AR..1	173	Gene USP15	UNPH4, MGC131982, MGC149838, KIAA0529, USP15, MGC74854	ubiquitin specific peptidase 15	NM_006313, hCT1821360.2, hCT2306163.0, hCT2306164.0	209475_at, 210681_s_at, 231990_at	NP_006304.1, EAW97104.1, EAW97105.1, EAW97106.1
GeneID:23041	MON2	12	62,860,597	62,991,363	130,766	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1503, 2_A375_pNL97_plus_lncRNA_AR..1..2118, 4_A375_EGR1..1..1926, 4_A375_EGR1..1..1927	136491, 135863, 135627, 136663	downstream, downstream, downstream, downstream	1	1	1	21	22	18	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MON2	MGC35493, MON2, KIAA1040	MON2 homolog (S. cerevisiae)	NM_015026	212754_s_at, 212755_at	NP_055841.2
GeneID:283416	C12orf61	12	62,995,531	62,997,214	1,683	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1503, 2_A375_pNL97_plus_lncRNA_AR..1..2118, 4_A375_EGR1..1..1926, 4_A375_EGR1..1..1927	126, 734, 990, -66	in gene, in gene, in gene, upstream	1	1	1	21	22	18	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene C12orf61	FLJ25590, C12orf61	chromosome 12 open reading frame 61	NM_175895, hCT2306301.1	1557312_at	NP_787091.1, EAW97110.1
GeneID:406891	MIRLET7I	12	62,997,466	62,997,549	83	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1503, 2_A375_pNL97_plus_lncRNA_AR..1..2118, 4_A375_EGR1..1..1926, 4_A375_EGR1..1..1927	-378, -986, -1242, -186	upstream, upstream, upstream, upstream	1	1	1	21	22	18	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MIRLET7I	MIRLET7I, hsa-let-7i, LET7I, MIRNLET7I	microRNA let-7i	NR_029661		
GeneID:57460	PPM1H	12	63,037,762	63,328,665	290,903	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1504, 1_A375_pNL7_minus_lncRNA_AR..1..1505, 2_A375_pNL97_plus_lncRNA_AR..1..2120, 2_A375_pNL97_plus_lncRNA_AR..1..2121, 2_A375_pNL97_plus_lncRNA_AR..1..2122	202665, 150873, 209833, 148697, 441	in gene, in gene, in gene, in gene, in gene	1	1	0	17.2	18.2	9.4	5	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene PPM1H	NERPP-2C, KIAA1157, FLJ13253, ARHCL1, PPM1H, URCC2	protein phosphatase 1H (PP2C domain containing)	NM_020700	1558654_at, 212686_at, 233911_s_at	NP_065751.1
GeneID:10329	TMEM5	12	64,173,637	64,202,887	29,250	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2123, 4_A375_EGR1..1..1929	123, 395	in gene, in gene	0	1	1	13	22	15	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene TMEM5	TMEM5, HP10481	transmembrane protein 5	NM_014254, hCT2356177.0, hCT23756.2	204807_at, 204808_s_at	NP_055069.1, EAW97120.1, EAW97121.1
GeneID:57522	SRGAP1	12	64,238,541	64,541,613	303,072	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1506, 2_A375_pNL97_plus_lncRNA_AR..1..2124	-717, -717	upstream, upstream	1	1	0	23	14	14	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene SRGAP1	FLJ22166, SRGAP1, ARHGAP13, KIAA1304	SLIT-ROBO Rho GTPase activating protein 1	NM_020762, hCT1960834.1, hCT2306181.0	1554473_at, 1569269_s_at, 233888_s_at	NP_065813.1, EAW97122.1, EAW97123.1
GeneID:144577	C12orf66	12	64,586,419	64,616,076	29,657	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1507	-244	upstream	1	0	0	25	18	12	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene C12orf66	C12orf66, FLJ32549	chromosome 12 open reading frame 66	NM_152440, hCT23965.2	1554067_at, 1554068_s_at, 235026_at	NP_689653.3, EAW97124.1
GeneID:11260	XPOT	12	64,798,233	64,842,464	44,231	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1508, 2_A375_pNL97_plus_lncRNA_AR..1..2125	47943, 231	downstream, in gene	1	1	0	14.5	16	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene XPOT	XPO3, XPOT	exportin, tRNA (nuclear export receptor for tRNAs)	NM_007235, hCT2306512.0, hCT2306513.0, hCT2306514.0, hCT2306515.0, hCT2306516.0	212160_at	NP_009166.2, EAW97132.1, EAW97128.1, EAW97129.1, EAW97130.1, EAW97131.1
GeneID:29110	TBK1	12	64,845,937	64,895,891	49,954	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1508	239	in gene	1	0	0	17	16	14	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene TBK1	T2K, FLJ11330, NAK, TBK1	TANK-binding kinase 1	NM_013254, hCT31928.3	1554391_at, 218520_at	NP_037386.1, EAW97133.1
GeneID:23329	TBC1D30	12	65,174,589	65,272,411	97,822	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1509, 1_A375_pNL7_minus_lncRNA_AR..1..1510, 2_A375_pNL97_plus_lncRNA_AR..1..2126, 4_A375_EGR1..1..1930	40547, 45635, 45651, 44419	in gene, in gene, in gene, in gene	1	1	1	21	17.67	7.33	3	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene TBC1D30	KIAA0984, TBC1D30	TBC1 domain family, member 30	XM_003119536, XM_003119539, XM_003119538, XM_001716833, XM_003119537, XM_003118950, XM_003118948, XM_003118951, XM_037557, XM_003118949, XM_003120747, XM_003120745, XM_003120746, XM_939476, XM_003120748	213912_at, 213913_s_at, 215186_at	XP_003119584.1, XP_003119587.1, XP_001716885.2, XP_003119586.1, XP_003119585.1, XP_003118998.1, XP_037557.5, XP_944569.2, XP_003118996.1, XP_003118999.1, XP_003118997.1, XP_003120795.1, XP_003120793.1, XP_003120796.1, XP_003120794.1
GeneID:11197	WIF1	12	65,444,404	65,515,346	70,942	-	1	4_A375_EGR1..1..1931	322	in gene	0	0	1	4	10	15	1	4_A375_EGR1..1	15	Gene WIF1	WIF-1, WIF1	WNT inhibitory factor 1	NM_007191, hCT13843.3, hCT2348029.0	204712_at	NP_009122.2, EAW97146.1, EAW97147.1
GeneID:100507065	LOC100507065	12	65,860,597	66,036,152	175,555	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1511	-8952	upstream	1	0	0	16	14	3	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene LOC100507065		hypothetical LOC100507065	XR_111309, XR_111311, XR_111310, XR_110370, XR_110369, XR_110371, XR_114653, XR_114652, XR_114654		
GeneID:8091	HMGA2	12	66,218,240	66,360,071	141,831	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1513, 2_A375_pNL97_plus_lncRNA_AR..1..2127, 2_A375_pNL97_plus_lncRNA_AR..1..2128, 4_A375_EGR1..1..1932	-400, -672, 128, 1376	upstream, upstream, in gene, in gene	1	1	1	14.5	19	15	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene HMGA2	BABL, HMGI-C, HMGA2, HMGIC, LIPO, STQTL9	high mobility group AT-hook 2	NM_003483, NM_003484, hCT1963920.1	1558682_at, 1558683_a_at, 1559891_at, 1561633_at, 1567223_at, 1567224_at, 1568286_at, 1568287_at, 208025_s_at	NP_003474.1, NP_003475.1, EAW97152.1
GeneID:51643	TMBIM4	12	66,530,717	66,563,807	33,090	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1514, 2_A375_pNL97_plus_lncRNA_AR..1..2129	31, 127	in gene, in gene	1	1	0	26	29	13	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene TMBIM4	S1R, GAAP, TMBIM4, ZPRO, LFG4, CGI-119	transmembrane BAX inhibitor motif containing 4	NM_016056, hCT1951633.1, hCT2306664.0, hCT2356016.0, hCT2356017.0, hCT7747.3	219206_x_at, 222645_x_at, 223892_s_at	NP_057140.2, EAW97158.1, EAW97159.1, EAW97160.1, EAW97161.1, EAW97162.1
GeneID:92797	HELB	12	66,696,356	66,731,958	35,602	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2130	-52	upstream	0	1	0	8	20	6	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene HELB	HELB		NM_033647, hCT1813162.1, hCT1813163.1, hCT2357966.0	1552787_at, 1552788_a_at, 1570200_at	NP_387467.2, EAW97165.1, EAW97166.1, EAW97167.1
GeneID:23426	GRIP1	12	66,741,211	67,072,925	331,714	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1515, 2_A375_pNL97_plus_lncRNA_AR..1..2131	45293, 45245	in gene, in gene	1	1	0	16	20	3	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene GRIP1	GRIP, GRIP1	glutamate receptor interacting protein 1	NM_001178074, NM_021150	214018_at	NP_001171545.1, NP_066973.2
GeneID:55832	CAND1	12	67,663,061	67,708,388	45,327	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1517, 2_A375_pNL97_plus_lncRNA_AR..1..2134	139, 203	in gene, in gene	1	1	0	24	23	17	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene CAND1	FLJ10929, KIAA0829, CAND1, FLJ38691, FLJ10114, FLJ90441, TIP120A, TIP120, DKFZp434M1414	cullin-associated and neddylation-dissociated 1	NM_018448, hCT2306402.0, hCT7623.3	207483_s_at, 208838_at, 208839_s_at, 239771_at	NP_060918.2, EAW97171.1, EAW97172.1
GeneID:100507250	LOC100507250	12	69,068,151	69,080,583	12,432	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1519, 2_A375_pNL97_plus_lncRNA_AR..1..2137	-153, -121	upstream, upstream	1	1	0	25	29	12	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene LOC100507250		hypothetical LOC100507250	XR_111306, XR_110376, XR_114658		
GeneID:57122	NUP107	12	69,080,731	69,136,473	55,742	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1519, 2_A375_pNL97_plus_lncRNA_AR..1..2137	5, -27	in gene, upstream	1	1	0	25	29	12	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene NUP107	NUP84, NUP107	nucleoporin 107kDa	NM_020401, hCT12522.2, hCT1957147.1	218768_at	NP_065134.1, EAW97194.1, EAW97195.1
GeneID:4069	LYZ	12	69,742,134	69,748,013	5,879	+	1	4_A375_EGR1..1..1933	11402	downstream	0	0	1	17	14	18	1	4_A375_EGR1..1	18	Gene LYZ	LZM, LYZ	lysozyme (renal amyloidosis)	NM_000239, hCT15579.3, hCT1951650.1, hCT2307032.0	1555745_a_at, 213975_s_at	NP_000230.1, EAW97220.1, EAW97221.1, EAW97222.1
GeneID:100507298	LOC100507298	12	69,747,201	69,758,078	10,877	-	1	4_A375_EGR1..1..1933	4542	in gene	0	0	1	17	14	18	1	4_A375_EGR1..1	18	Gene LOC100507298		hypothetical LOC100507298	XR_110377		
GeneID:8089	YEATS4	12	69,753,532	69,784,576	31,044	+	1	4_A375_EGR1..1..1933	4	in gene	0	0	1	17	14	18	1	4_A375_EGR1..1	18	Gene YEATS4	YAF9, 4930573H17Rik, YEATS4, NUBI-1, GAS41, B230215M10Rik	YEATS domain containing 4	NM_006530, hCT15578.3, hCT2356144.0	218911_at	NP_006521.1, EAW97223.1, EAW97224.1
GeneID:10818	FRS2	12	69,864,129	69,973,562	109,433	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2138	115263	downstream	0	1	0	13	22	15	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene FRS2	SNT1, FRS2A, FRS2, SNT-1, FRS2alpha, SNT	fibroblast growth factor receptor substrate 2	NM_006654, NM_001042555, hCT1951647.1, hCT2307038.0, hCT2307039.0	221308_at, 226045_at, 236486_at	NP_006645.3, NP_001036020.1, EAW97225.1, EAW97226.1, EAW97227.1
GeneID:10576	CCT2	12	69,979,208	69,995,357	16,149	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2138	184	in gene	0	1	0	13	22	15	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CCT2	TCP-1-beta, CCT2, 99D8.1, CCT-beta, MGC142074, CCTB, PRO1633, MGC142076	chaperonin containing TCP1, subunit 2 (beta)	NM_006431, hCT15577.3, hCT1951646.1, hCT2306490.0	201946_s_at, 201947_s_at	NP_006422.1, EAW97229.1, EAW97228.1, EAW97230.1
GeneID:117177	RAB3IP	12	70,132,631	70,216,984	84,353	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1520	83241	in gene	1	0	0	17	12	5	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene RAB3IP	RABIN3, FLJ14660, FLJ22548, RAB3IP, MGC71495	RAB3A interacting protein (rabin3)	NM_175624, NM_175623, NM_001024647, NM_175625, NM_022456, hCT15582.3, hCT1951655.1, hCT2306494.0, hCT2356147.0, hCT2356148.0, hCT2356149.0	1565799_at, 1565800_x_at, 223471_at, 228432_at, 231399_at, 238526_at, 238653_at	NP_783323.1, NP_783322.1, NP_071901.2, NP_783324.1, NP_001019818.1, EAW97237.1, EAW97238.1, EAW97239.1, EAW97240.1, EAW97241.1, EAW97242.1
GeneID:196446	C12orf28	12	70,219,298	70,352,504	133,206	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1520	-3426	upstream	1	0	0	17	12	5	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene C12orf28	FLJ25056, C12orf15, MGC126689, bcm1377, C12orf28	chromosome 12 open reading frame 28	XM_001718058, XM_001718908, XM_001716650, hCT1640476.3	1556267_at	XP_001718110.2, XP_001718960.1, XP_001716702.2, EAW97243.1
GeneID:100507317	LOC100507317	12	70,636,086	70,637,114	1,028	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2140, 4_A375_EGR1..1..1934	410, 122	in gene, in gene	0	1	1	12	19	19	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100507317		hypothetical LOC100507317	XR_111305, XR_110378, XR_114659		
GeneID:4848	CNOT2	12	70,636,777	70,748,773	111,996	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2140, 4_A375_EGR1..1..1934	-73, 215	upstream, in gene	0	1	1	12	19	19	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CNOT2	NOT2, FLJ26456, CDC36, NOT2H, CNOT2, HSPC131	CCR4-NOT transcription complex, subunit 2	NM_014515, hCT16289.3, hCT1951656.1, hCT1951657.1, hCT1951658.1, hCT2356215.0	217798_at, 222181_at, 222182_s_at, 233054_at	NP_055330.1, EAW97249.1, EAW97245.1, EAW97246.1, EAW97247.1, EAW97248.1
GeneID:5787	PTPRB	12	70,910,630	71,031,219	120,589	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2141	27379	in gene	0	1	0	13	19	7	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PTPRB	HPTP-BETA, PTPB, R-PTP-BETA, DKFZp686E2262, HPTPB, PTPRB, MGC142023, FLJ44133, DKFZp686H15164, VEPTP, MGC59935	protein tyrosine phosphatase, receptor type, B	NM_002837, NM_001109754, hCT16271.3, hCT1951659.2	1560105_at, 205846_at, 230250_at	NP_002828.3, NP_001103224.1, EAW97253.1, EAW97254.1
GeneID:5801	PTPRR	12	71,031,862	71,314,584	282,722	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1521, 2_A375_pNL97_plus_lncRNA_AR..1..2142	1027, 888	in gene, in gene	1	1	0	16	17	9	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PTPRR	PCPTP1, PTPRQ, MGC131968, PTPBR7, FLJ34328, DKFZp781C1038, PTP-SL, MGC148170, EC-PTP, PTPRR	protein tyrosine phosphatase, receptor type, R	NM_002849, NM_130846, hCT16535.3, hCT1957864.1	206084_at, 210675_s_at	NP_002840.1, NP_570897.1, EAW97255.1, EAW97256.1
GeneID:8549	LGR5	12	71,833,813	71,978,622	144,809	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2143	43	in gene	0	1	0	18	20	8	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LGR5	GRP49, GPR67, HG38, LGR5, FEX, GPR49, MGC117008	leucine-rich repeat containing G protein-coupled receptor 5	NM_003667, hCT14876.3, hCT2358225.0	210393_at, 213880_at	NP_003658.1, EAW97259.1, EAW97258.1
GeneID:196441	ZFC3H1	12	72,003,379	72,057,749	54,370	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1522	501	in gene	1	0	0	17	17	15	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ZFC3H1	MGC90200, PSRC2, MGC23401, DKFZp686A0722, CCDC131, ZFC3H1, KIAA0546	zinc finger, C3H1-type containing	NM_144982, hCT16538.4, hCT2306448.1, hCT2306450.1, hCT2349799.0, hCT2356169.0	1553736_at, 213065_at	NP_659419.3, EAW97261.1, EAW97260.1, EAW97262.1, EAW97263.1, EAW97264.1
GeneID:83591	THAP2	12	72,057,784	72,074,419	16,635	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1522, 2_A375_pNL97_plus_lncRNA_AR..1..2144	-536, 22152	upstream, downstream	1	1	0	15.5	19	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene THAP2	DKFZp564I0422, THAP2	THAP domain containing, apoptosis associated protein 2	NM_031435, hCT16534.2	223566_at, 230380_at	NP_113623.1, EAW97265.1
GeneID:55266	TMEM19	12	72,079,878	72,097,840	17,962	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2144	58	in gene	0	1	0	14	21	12	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TMEM19	FLJ10936, TMEM19	transmembrane protein 19	NM_018279, hCT1812612.2, hCT1951636.1, hCT1951637.1, hCT2306530.0	219941_at, 226880_at, 229126_at, 230676_s_at	NP_060749.2, EAW97269.1, EAW97266.1, EAW97267.1, EAW97268.1
GeneID:121278	TPH2	12	72,332,626	72,426,221	93,595	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1523, 1_A375_pNL7_minus_lncRNA_AR..1..1524, 2_A375_pNL97_plus_lncRNA_AR..1..2145, 2_A375_pNL97_plus_lncRNA_AR..1..2146	46, 42510, 30, 42494	in gene, in gene, in gene, in gene	1	1	0	23.5	24.5	4.5	2	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene TPH2	ADHD7, MGC138872, NTPH, TPH2, MGC138871, FLJ37295	tryptophan hydroxylase 2	NM_173353, hCT16299.4, hCT2349798.0, hCT2358055.0	1555332_at	NP_775489.2, EAW97278.1, EAW97277.1, EAW97279.1
GeneID:283392	LOC283392	12	72,847,267	72,867,269	20,002	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2147	601	in gene	0	1	0	21	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC283392		hypothetical LOC283392	NR_026836, NR_026837		
GeneID:29953	TRHDE	12	72,666,529	73,059,422	392,893	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2147	159	in gene	0	1	0	21	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TRHDE	TRH-DE, TRHDE, PAP-II, FLJ22381, PGPEP2	thyrotropin-releasing hormone degrading enzyme	NM_013381, hCT14873.2	1560897_at, 1560898_a_at, 219937_at	NP_037513.1, EAW97281.1
GeneID:100507377	LOC100507377	12	74,526,953	74,686,411	159,458	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2149	-133	upstream	0	1	0	12	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100507377		hypothetical protein LOC100507377	XM_003118937		XP_003118985.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:552889	LOC552889	12	74,931,551	74,935,232	3,681	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1525, 4_A375_EGR1..1..1935	81, 129	in gene, in gene	1	0	1	15	12	18	1	4_A375_EGR1..1	18	Gene LOC552889	FLJ32060, MGC17298, ATXN7L3B	ataxin 7-like 3B	NM_001136262	212113_at, 212114_at	NP_001129734.1
GeneID:3747	KCNC2	12	75,433,898	75,603,511	169,615	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1526, 2_A375_pNL97_plus_lncRNA_AR..1..2150, 2_A375_pNL97_plus_lncRNA_AR..1..2151	31527, 31511, 39	in gene, in gene, in gene	1	1	0	16	18	5.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene KCNC2	KCNC2, KV3.2, MGC138198	potassium voltage gated channel, Shaw-related subfamily, member 2	NM_139137, NM_139136, NM_153748, hCT2306868.0, hCT2306869.0, hCT2306870.0, hCT2306871.0, hCT2357970.0, hCT2357971.0, hCT2357972.0, hCT2357973.0	222289_at, 240614_at	NP_631875.1, NP_631874.1, NP_715624.1, EAW97287.1, EAW97288.1, EAW97292.1, EAW97289.1, EAW97290.1, EAW97291.1, EAW97293.1, EAW97294.1
GeneID:84898	CAPS2	12	75,669,759	75,723,836	54,077	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1527, 2_A375_pNL97_plus_lncRNA_AR..1..2152, 2_A375_pNL97_plus_lncRNA_AR..1..2153	-198, -228, -4724	upstream, upstream, upstream	1	1	0	21.5	26	11	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene CAPS2	FLJ34520, CAPS2, UG0636c06	calcyphosine 2	NM_032606, hCT2347673.1, hCT2349895.0, hCT2349896.0, hCT2349897.0, hCT2349898.0	1560458_s_at, 224370_s_at	NP_115995.2, EAW97296.1, EAW97297.1, EAW97298.1, EAW97299.1, EAW97300.1
GeneID:256710	GLIPR1L1	12	75,728,463	75,764,170	35,707	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1527, 2_A375_pNL97_plus_lncRNA_AR..1..2152, 2_A375_pNL97_plus_lncRNA_AR..1..2153	-4431, -4399, 97	upstream, upstream, in gene	1	1	0	21.5	26	11	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene GLIPR1L1	PRO7434, MGC26856, GLIPR1L1, ALKN2972	GLI pathogenesis-related 1 like 1	NM_152779, hCT1656549.2, hCT1966187.1	238298_at	NP_689992.1, EAW97301.1, EAW97302.1
GeneID:144321	GLIPR1L2	12	75,784,889	75,817,820	32,931	+	1	4_A375_EGR1..1..1936	37847	downstream	0	0	1	3	5	12	1	4_A375_EGR1..1	12	Gene GLIPR1L2	MGC39497, GLIPR1L2	GLI pathogenesis-related 1 like 2	NM_152436, hCT1812525.2, hCT2349786.0, hCT2358146.0		NP_689649.1, EAW97304.1, EAW97303.1, EAW97305.1
GeneID:11010	GLIPR1	12	75,874,513	75,895,716	21,203	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1528, 2_A375_pNL97_plus_lncRNA_AR..1..2154	30927, 30911	downstream, downstream	1	1	0	24	21	5	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene GLIPR1	RTVP1, GLIPR1, CRISP7, GLIPR	GLI pathogenesis-related 1	NM_006851, hCT17644.4, hCT2306701.1, hCT2306702.1	204221_x_at, 204222_s_at, 214085_x_at, 226136_at, 226142_at	NP_006842.2, EAW97308.1, EAW97306.1, EAW97307.1
GeneID:11103	KRR1	12	75,891,419	75,905,418	13,999	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1528, 2_A375_pNL97_plus_lncRNA_AR..1..2154	-22, -6	upstream, upstream	1	1	0	24	21	5	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene KRR1	HRB2, RIP-1, KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	NM_007043, hCT19040.4	203202_at, 203203_s_at, 232441_at, 235038_at	NP_008974.5, EAW97309.1
GeneID:100289143	LOC100289143	12	76,332,785	76,371,830	39,045	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1529, 1_A375_pNL7_minus_lncRNA_AR..1..1530	-5681, 5647	upstream, in gene	1	0	0	20	11	3.5	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LOC100289143		similar to nucleolar protein family A, member 3	XM_002343200, XM_003120750		XP_002343241.1, XP_003120798.1
GeneID:22822	PHLDA1	12	76,419,227	76,425,556	6,329	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1531, 1_A375_pNL7_minus_lncRNA_AR..1..1532, 2_A375_pNL97_plus_lncRNA_AR..1..2156, 2_A375_pNL97_plus_lncRNA_AR..1..2157, 4_A375_EGR1..1..1937	11220, 164, 180, -780, -204	downstream, in gene, in gene, upstream, upstream	1	1	1	17.5	19	12.5	2	4_A375_EGR1..1	20	Gene PHLDA1	TDAG51, PHRIP, PHLDA1, DT1P1B11, MGC131738	pleckstrin homology-like domain, family A, member 1	NM_007350, hCT17650.3, hCT2307103.0	217998_at	NP_031376.3, EAW97313.1, EAW97312.1
GeneID:114882	OSBPL8	12	76,745,577	76,953,589	208,012	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2159, 4_A375_EGR1..1..1938	117, -155	in gene, upstream	0	1	1	15	15	15	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene OSBPL8	MGC133203, MSTP120, OSBPL8, DKFZp686A11164, OSBP10, MST120, ORP8, MGC126578	oxysterol binding protein-like 8	NM_020841, NM_001003712, hCT18565.3, hCT1951665.1, hCT2307087.0, hCT2358062.0	212582_at, 212585_at, 226986_at	NP_065892.1, NP_001003712.1, EAW97324.1, EAW97325.1, EAW97326.1, EAW97327.1
GeneID:1466	CSRP2	12	77,252,496	77,272,799	20,303	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2161	-257	upstream	0	1	0	10	17	12	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene CSRP2	LMO5, SmLIM, CSRP2, CRP2	cysteine and glycine-rich protein 2	NM_001321, hCT18389.2, hCT1961392.1	207030_s_at, 211126_s_at	NP_001312.1, EAW97336.1, EAW97337.1
GeneID:89795	NAV3	12	78,225,069	78,606,790	381,721	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2164	16755	in gene	0	1	0	10	16	2	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene NAV3	NAV3, POMFIL1, unc53H3, KIAA0938, STEERIN3	neuron navigator 3	NM_014903, hCT2344319.0, hCT2344320.0	1552658_a_at, 204823_at, 216486_at, 216632_at	NP_055718.4, EAW97342.1, EAW97341.1
GeneID:4659	PPP1R12A	12	80,167,343	80,329,235	161,892	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1534, 2_A375_pNL97_plus_lncRNA_AR..1..2165, 4_A375_EGR1..1..1941	403, 275, 307	in gene, in gene, in gene	1	1	1	24	32	16	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene PPP1R12A	MGC133042, PPP1R12A, MBS, MYPT1	protein phosphatase 1, regulatory (inhibitor) subunit 12A	NM_002480, NM_001143885, NM_001143886, hCT1951671.1, hCT1951672.1, hCT1951673.1, hCT2358043.0, hCT2358044.0, hCT2358045.0	201602_s_at, 201603_at, 201604_s_at	NP_002471.1, NP_001137357.1, NP_001137358.1, EAW97351.1, EAW97353.1, EAW97354.1, EAW97352.1, EAW97355.1, EAW97356.1
GeneID:29080	CCDC59	12	82,746,083	82,752,584	6,501	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1536, 2_A375_pNL97_plus_lncRNA_AR..1..2166	328, 328	in gene, in gene	1	1	0	125	107	11	1	1_A375_pNL7_minus_lncRNA_AR..1	125	Gene CCDC59	HSPC128, TAP26, DKFZp686K1021, BR22, CCDC59, FLJ10294	coiled-coil domain containing 59	NM_014167, NR_033192, hCT14843.3, hCT2358141.0	218936_s_at, 222792_s_at	NP_054886.2, EAW97380.1, EAW97379.1
GeneID:84190	C12orf26	12	82,752,276	82,873,018	120,742	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1536, 2_A375_pNL97_plus_lncRNA_AR..1..2166, 4_A375_EGR1..1..1942	-20, -20, 114956	upstream, upstream, in gene	1	1	1	67	56	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	125	Gene C12orf26	C12orf26, FLJ22789	chromosome 12 open reading frame 26	NM_032230, hCT1971605.1, hCT1971606.1	229018_at	NP_115606.2, EAW97381.1, EAW97382.1
GeneID:160335	TMTC2	12	83,080,934	83,528,065	447,131	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2167, 4_A375_EGR1..1..1943	508, 41690	in gene, in gene	0	1	1	10	10.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene TMTC2	DKFZp762A217, TMTC2	transmembrane and tetratricopeptide repeat containing 2	NM_152588, hCT1768129.4, hCT2350663.0	228574_at, 235775_at	NP_689801.1, EAW97384.1, EAW97385.1
GeneID:55117	SLC6A15	12	85,253,267	85,306,606	53,339	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1537, 1_A375_pNL7_minus_lncRNA_AR..1..1538, 2_A375_pNL97_plus_lncRNA_AR..1..2168, 4_A375_EGR1..1..1944	1102, -18, 76, 14	in gene, upstream, in gene, in gene	1	1	1	19	27	21	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SLC6A15	V7-3, SBAT1, NTT73, FLJ10316, MGC87066, DKFZp761I0921, hv7-3, SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	NM_182767, NM_018057, NM_001146335, hCT17662.3, hCT2306905.0, hCT2306907.0	206376_at, 232283_at, 239352_at, 240419_at	NP_877499.1, NP_060527.2, NP_001139807.1, EAW97388.1, EAW97389.1, EAW97390.1
GeneID:144448	TSPAN19	12	85,408,094	85,430,055	21,961	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1539	19887	in gene	1	0	0	22	19	1	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene TSPAN19	FLJ44351, TSPAN19	tetraspanin 19	NM_001100917		NP_001094387.1
GeneID:84125	LRRIQ1	12	85,430,099	85,638,883	208,784	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1540, 2_A375_pNL97_plus_lncRNA_AR..1..2169	56589, 56653	in gene, in gene	1	1	0	21	25	4	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LRRIQ1	FLJ12303, LRRIQ1	leucine-rich repeats and IQ motif containing 1	NM_032165, NM_001079910, hCT18716.3, hCT2306897.1, hCT2306900.1, hCT2349942.0	223817_at	NP_115541.3, NP_001073379.1, EAW97393.1, EAW97394.1, EAW97395.1, EAW97396.1
GeneID:8092	ALX1	12	85,674,036	85,695,562	21,526	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1541, 2_A375_pNL97_plus_lncRNA_AR..1..2170	428, 238	in gene, in gene	1	1	0	24	25	14	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene ALX1	ALX1, CART1, FND3	ALX homeobox 1	NM_006982, hCT17665.3	206837_at	NP_008913.2, EAW97398.1
GeneID:160419	C12orf50	12	88,373,816	88,423,176	49,360	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1543, 2_A375_pNL97_plus_lncRNA_AR..1..2174	-6216, -6232	upstream, upstream	1	1	0	23	20	9	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene C12orf50	C12orf50, FLJ35821	chromosome 12 open reading frame 50	NM_152589, hCT1644321.3, hCT2349889.0, hCT2349890.0	238219_at	NP_689802.1, EAW97406.1, EAW97407.1, EAW97408.1
GeneID:91298	C12orf29	12	88,429,268	88,443,937	14,669	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1543, 2_A375_pNL97_plus_lncRNA_AR..1..2174	124, 140	in gene, in gene	1	1	0	23	20	9	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene C12orf29	FLJ38158, DKFZp686L04169, DKFZp434N2030, MGC102978, DKFZp313K0438, C12orf29	chromosome 12 open reading frame 29	NM_001009894, hCT1967601.2, hCT2346772.0, hCT2346773.0, hCT2346774.0	213701_at, 228376_at	NP_001009894.2, EAW97412.1, EAW97409.1, EAW97410.1, EAW97411.1
GeneID:80184	CEP290	12	88,442,790	88,535,993	93,203	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2175	41	in gene	0	1	0	16	26	8	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene CEP290	BBS14, LCA10, FLJ21979, JBTS6, rd16, SLSN6, 3H11Ag, CEP290, MKS4, JBTS5, CT87, POC3, FLJ13615, NPHP6, KIAA0373	centrosomal protein 290kDa	NM_025114, hCT18446.3, hCT2307123.0	1558650_at, 205250_s_at, 221663_s_at	NP_079390.3, EAW97413.1, EAW97414.1
GeneID:160418	TMTC3	12	88,536,073	88,593,664	57,591	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2175	-121	upstream	0	1	0	16	26	8	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene TMTC3	FLJ90492, SMILE, TMTC3, DKFZp686O22167, DKFZp686M1969, DKFZp686C0968, DKFZp686O2342	transmembrane and tetratricopeptide repeat containing 3	NM_181783, hCT18444.4	1560017_at, 226800_at, 226804_at	NP_861448.2, EAW97415.1
GeneID:4254	KITLG	12	88,886,570	88,974,250	87,680	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1547	-118	upstream	1	0	0	14	8	11	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene KITLG	Kitl, KITLG, SF, KL-1, SCF, MGF, SHEP7, FPH2, DKFZp686F2250	KIT ligand	NM_000899, NM_003994, hCT18442.3, hCT18443.3, hCT2307114.0, hCT2307116.0	207029_at, 211124_s_at, 226534_at	NP_000890.1, NP_003985.2, EAW97416.1, EAW97417.1, EAW97418.1, EAW97419.1
GeneID:1848	DUSP6	12	89,741,837	89,746,296	4,459	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1550, 1_A375_pNL7_minus_lncRNA_AR..1..1551, 2_A375_pNL97_plus_lncRNA_AR..1..2181, 2_A375_pNL97_plus_lncRNA_AR..1..2182, 4_A375_EGR1..1..1945	648, -298, 1668, 778, -1640	in gene, upstream, in gene, in gene, upstream	1	1	1	15.75	15.75	14.5	4	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene DUSP6	DUSP6, MKP3, PYST1	dual specificity phosphatase 6	NM_001946, NM_022652, hCT17735.3, hCT2307454.0, hCT2307456.0	208891_at, 208892_s_at, 208893_s_at	NP_001937.2, NP_073143.2, EAW97422.1, EAW97423.1, EAW97424.1
GeneID:282809	WDR51B	12	89,813,501	89,919,777	106,276	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1553, 1_A375_pNL7_minus_lncRNA_AR..1..1554, 2_A375_pNL97_plus_lncRNA_AR..1..2184	85889, -95, -127	in gene, upstream, upstream	1	1	0	59.5	52	10.5	2	1_A375_pNL7_minus_lncRNA_AR..1	101	Gene WDR51B	PIX1, FLJ41111, WDR51B, POC1B, FLJ14923	POC1 centriolar protein homolog B (Chlamydomonas)	NM_172240, hCT18747.3, hCT2358198.0, hCT2358199.0	226263_at	NP_758440.1, EAW97426.1, EAW97425.1, EAW97427.1
GeneID:8693	GALNT4	12	89,913,189	89,918,535	5,346	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1554, 2_A375_pNL97_plus_lncRNA_AR..1..2184	-1337, -1369	upstream, upstream	1	1	0	101	90	15	1	1_A375_pNL7_minus_lncRNA_AR..1	101	Gene GALNT4	GALNACT4, GALNT4, FLJ93314, GALNAC-T4, GalNAcT4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)	NM_003774, hCT1805815.2	220442_at, 231632_at	NP_003765.2, EAW97428.1
GeneID:338758	LOC338758	12	90,102,732	90,105,729	2,997	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1555, 2_A375_pNL97_plus_lncRNA_AR..1..2185, 2_A375_pNL97_plus_lncRNA_AR..1..2186, 4_A375_EGR1..1..1948	858, -1276, 838, -652	in gene, upstream, in gene, upstream	1	1	1	10.67	15	18	3	4_A375_EGR1..1	23	Gene LOC338758		hypothetical LOC338758	NR_026136	238893_at	
GeneID:694	BTG1	12	92,534,054	92,539,673	5,619	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1558, 1_A375_pNL7_minus_lncRNA_AR..1..1559, 2_A375_pNL97_plus_lncRNA_AR..1..2189	8457, -519, 153	downstream, upstream, in gene	1	1	0	16.5	15.5	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene BTG1	BTG1		NM_001731, hCT12274.3, hCT2307173.0	1559975_at, 200920_s_at, 200921_s_at	NP_001722.1, EAW97467.1, EAW97466.1
GeneID:8411	EEA1	12	93,166,285	93,323,107	156,822	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2195, 4_A375_EGR1..1..1949	-253, -285	upstream, upstream	0	1	1	11	18	19	1	4_A375_EGR1..1	19	Gene EEA1	ZFYVE2, MST105, MSTP105, EEA1	early endosome antigen 1	NM_003566, hCT11229.5, hCT2307219.1	204840_s_at, 204841_s_at, 225865_at	NP_003557.2, EAW97471.1, EAW97472.1
GeneID:11163	NUDT4	12	93,771,701	93,797,024	25,323	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1563, 2_A375_pNL97_plus_lncRNA_AR..1..2196	10075, -389	in gene, upstream	1	1	0	13.5	23	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene NUDT4	HDCMB47P, DIPP2beta, DIPP2alpha, KIAA0487, NUDT4, DKFZp686I1281, DIPP2	nudix (nucleoside diphosphate linked moiety X)-type motif 4	NM_019094, NM_199040, hCT2307198.0, hCT2307199.0, hCT2307200.0, hCT2307201.0, hCT2307202.0	212181_s_at, 212183_at	NP_061967.3, NP_950241.1, EAW97476.1, EAW97477.1, EAW97478.1, EAW97479.1, EAW97475.1
GeneID:28977	MRPL42	12	93,861,270	93,896,432	35,162	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2197	170	in gene	0	1	0	16	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MRPL42	MRPL31, MRP-L31, L31MT, S32MT, MRPL42, MRPS32, L42MT, HSPC204, RPML31, PTD007	mitochondrial ribosomal protein L42	NM_014050, NM_172177, NM_172178, hCT1647261.3, hCT1951360.1, hCT1951361.1, hCT2307203.0, hCT2307207.0, hCT2358118.0, hCT2358119.0	217919_s_at, 222466_s_at	NP_054769.1, NP_751917.1, NP_751918.1, EAW97483.1, EAW97485.1, EAW97486.1, EAW97484.1, EAW97487.1, EAW97488.1, EAW97489.1
GeneID:144481	LOC144481	12	93,959,404	93,965,978	6,574	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1564, 2_A375_pNL97_plus_lncRNA_AR..1..2198, 4_A375_EGR1..1..1950	1786, 1349, 1468	in gene, in gene, in gene	1	1	1	29	23	17	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene LOC144481		hypothetical protein LOC144481	XM_003118939, XM_003118940, XM_003120753, XM_003120754	1559315_s_at	XP_003118987.1, XP_003118988.1, XP_003120801.1, XP_003120802.1
GeneID:8835	SOCS2	12	93,963,598	93,969,978	6,380	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1564, 2_A375_pNL97_plus_lncRNA_AR..1..2198, 4_A375_EGR1..1..1950	594, 1031, 914	in gene, in gene, in gene	1	1	1	29	23	17	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene SOCS2	SOCS2, SSI-2, SSI2, Cish2, CIS2, STATI2, SOCS-2	suppressor of cytokine signaling 2	NM_003877, hCT2307208.0, hCT31344.2	203372_s_at, 203373_at	NP_003868.1, EAW97492.1, EAW97493.1
GeneID:8738	CRADD	12	94,071,151	94,244,532	173,381	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1565, 2_A375_pNL97_plus_lncRNA_AR..1..2199, 2_A375_pNL97_plus_lncRNA_AR..1..2200	369, 529, 141713	in gene, in gene, in gene	1	1	0	16	17	4.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CRADD	MGC9163, RAIDD, CRADD	CASP2 and RIPK1 domain containing adaptor with death domain	NM_003805, hCT31343.3	209833_at	NP_003796.1, EAW97497.1
GeneID:10154	PLXNC1	12	94,542,499	94,699,225	156,726	+	2	4_A375_EGR1..1..1951, 4_A375_EGR1..1..1952	-7715, 973	upstream, in gene	0	0	1	7.5	8	17	2	4_A375_EGR1..1	19	Gene PLXNC1	CD232, PLXN-C1, PLXNC1, VESPR	plexin C1	NM_005761, hCT2307212.0	206470_at, 206471_s_at, 213241_at, 235328_at	NP_005752.1, EAW97500.1
GeneID:51134	CCDC41	12	94,702,056	94,853,764	151,708	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1567, 2_A375_pNL97_plus_lncRNA_AR..1..2202	180, 196	in gene, in gene	1	1	0	22	20	11	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene CCDC41	CCDC41, MGC149726, NY-REN-58	coiled-coil domain containing 41	NM_001042399, NM_016122, hCT2307261.0, hCT2307263.0, hCT2307264.0, hCT2358214.0, hCT31346.3	219644_at, 239282_at	NP_001035858.1, NP_057206.2, EAW97501.1, EAW97502.1, EAW97504.1, EAW97505.1, EAW97503.1
GeneID:144486	LOC144486	12	94,853,779	94,856,346	2,567	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1567, 2_A375_pNL97_plus_lncRNA_AR..1..2202	-195, -211	upstream, upstream	1	1	0	22	20	11	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene LOC144486		hypothetical LOC144486	NR_027035	237021_at	
GeneID:57458	TMCC3	12	94,960,900	95,044,324	83,424	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1568, 1_A375_pNL7_minus_lncRNA_AR..1..1569, 2_A375_pNL97_plus_lncRNA_AR..1..2203	34132, 5700, 34532	in gene, in gene, in gene	1	1	0	17.5	15.5	5.5	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene TMCC3	KIAA1145, TMCC3	transmembrane and coiled-coil domain family 3	NM_020698, hCT2307256.0, hCT2307257.0, hCT9981.3	226489_at	NP_065749.2, EAW97512.1, EAW97510.1, EAW97511.1
GeneID:55967	NDUFA12	12	95,365,109	95,397,511	32,402	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1570, 2_A375_pNL97_plus_lncRNA_AR..1..2204	39, 60	in gene, in gene	1	1	0	35	19	7	1	1_A375_pNL7_minus_lncRNA_AR..1	35	Gene NDUFA12	B17.2, DAP13, NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	NM_018838, hCT1829952.2, hCT2307253.0	223244_s_at	NP_061326.1, EAW97515.1, EAW97516.1
GeneID:7181	NR2C1	12	95,414,057	95,467,404	53,347	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1571, 2_A375_pNL97_plus_lncRNA_AR..1..2205	-4, -52	upstream, upstream	1	1	0	35	37	13	1	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene NR2C1	NR2C1, TR2	nuclear receptor subfamily 2, group C, member 1	NM_001032287, NM_003297, NM_001127362, hCT1686317.2, hCT2358060.0, hCT2358061.0, hCT9229.2	204791_at, 210530_s_at, 210531_at	NP_001027458.1, NP_003288.2, NP_001120834.1, EAW97517.1, EAW97518.1, EAW97520.1, EAW97519.1

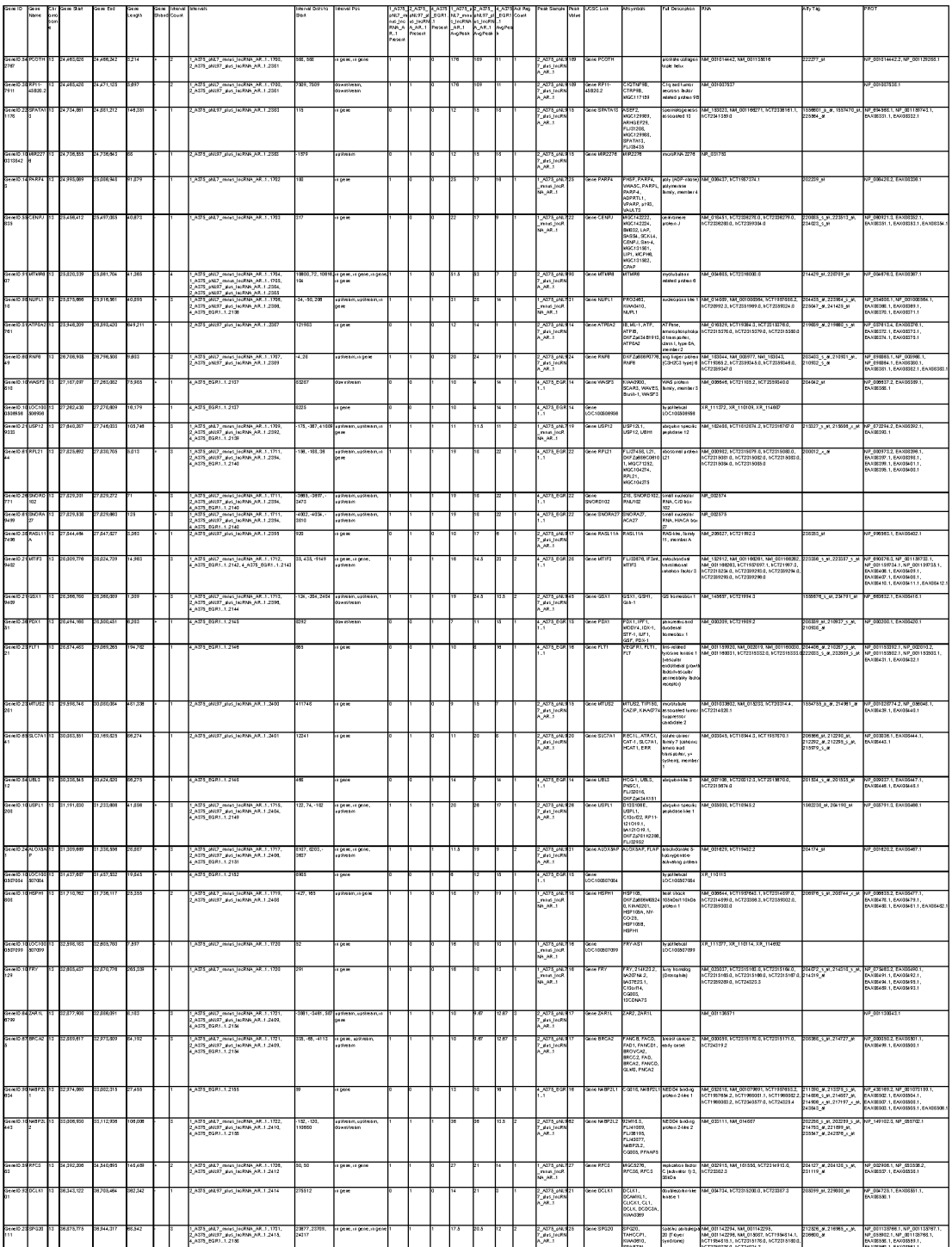
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.55785	FGD6	12	95,470,525	95,611,240	140,715	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1571, 1_A375_pNL7_minus_lncRNA_AR..1..1572, 2_A375_pNL97_plus_lncRNA_AR..1..2205, 2_A375_pNL97_plus_lncRNA_AR..1..2206	143632, -868, 143784, -288	downstream, upstream, downstream, upstream	1	1	0	26	26.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene FGD6	FGD6, ZFYVE24	FYVE, RhoGEF and PH domain containing 6	NM_018351, hCT24308.3	1555136_at, 1555137_a_at, 219901_at	NP_060821.3, EAW97521.1
GeneID.55591	VEZT	12	95,611,522	95,696,566	85,044	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1572, 2_A375_pNL97_plus_lncRNA_AR..1..2206	606, 6	in gene, in gene	1	1	0	17	16	17	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene VEZT	VEZATIN, VEZT, DKFZp761C241	vezatin, adherens junctions transmembrane protein	NM_017599, hCT1951860.2, hCT2307163.1, hCT2307164.1, hCT2307166.1, hCT2307167.1, hCT2307169.1, hCT2358035.0, hCT2358036.0, hCT2358037.0, hCT2358038.0, hCT2358039.0, hCT2358040.0, hCT24309.4	207263_x_at, 223089_at, 223090_x_at, 223875_s_at	NP_060069.3, EAW97525.1, EAW97526.1, EAW97527.1, EAW97530.1, EAW97533.1, EAW97524.1, EAW97528.1, EAW97529.1, EAW97531.1, EAW97532.1, EAW97534.1, EAW97535.1, EAW97536.1
GeneID.10988	METAP2	12	95,867,822	95,909,615	41,793	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1574, 2_A375_pNL97_plus_lncRNA_AR..1..2208	-14, 16	upstream, in gene	1	1	0	26	35	12	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene METAP2	METAP2, MNPEP, MAP2, p67eIF2, p67	methionyl aminopeptidase 2	NM_006838, hCT2307236.0, hCT2358206.0, hCT2358207.0	209861_s_at, 213899_at, 227993_at	NP_006829.1, EAW97537.1, EAW97538.1, EAW97539.1
GeneID.59277	NTN4	12	96,051,583	96,184,536	132,953	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1575	-660	upstream	1	0	0	16	10	6	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene NTN4	PRO3091, FLJ23180, NTN4	netrin 4	NM_021229, hCT1963698.1, hCT2358024.0	223315_at	NP_067052.2, EAW97544.1, EAW97545.1
GeneID.120935	CCDC38	12	96,260,626	96,336,428	75,802	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1576	64660	in gene	1	0	0	14	8	1	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene CCDC38	CCDC38, FLJ40089	coiled-coil domain containing 38	NM_182496, hCT2343967.0, hCT24311.3	1557620_a_at	NP_872302.2, EAW97551.1, EAW97550.1
GeneID.4048	LTA4H	12	96,394,611	96,429,365	34,754	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1577, 2_A375_pNL97_plus_lncRNA_AR..1..2209, 4_A375_EGR1..1..1953	-43, 5, -459	upstream, in gene, upstream	1	1	1	23	26	20	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene LTA4H	LTA4H		NM_000895, hCT1951930.1, hCT1951932.1, hCT2307318.0, hCT2307320.0	208771_s_at	NP_000886.1, EAW97560.1, EAW97557.1, EAW97558.1, EAW97559.1
GeneID.5128	CDK17	12	96,672,039	96,794,366	122,327	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2211, 4_A375_EGR1..1..1955	1118, 942	in gene, in gene	0	1	1	15	16	21	1	4_A375_EGR1..1	21	Gene CDK17	CDK17, PCTK2, PCTAIRE2	cyclin-dependent kinase 17	NM_001170464, NM_002595, hCT2307330.0, hCT2307331.0, hCT2358070.0, hCT24315.3	206474_at, 221918_at	NP_001163935.1, NP_002586.2, EAW97566.1, EAW97567.1, EAW97568.1, EAW97569.1
GeneID.374467	C12orf63	12	97,041,753	97,159,048	117,295	+	1	4_A375_EGR1..1..1956	28903	in gene	0	0	1	2	3	14	1	4_A375_EGR1..1	14	Gene C12orf63	FLJ44112, C12orf63	chromosome 12 open reading frame 63	XM_003119541, XM_003118942, XM_003120736, hCT2307133.0		XP_003119589.1, XP_003118990.1, XP_003120784.1, EAW97575.1
GeneID.121441	NEDD1	12	97,301,001	97,347,469	46,468	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1578, 2_A375_pNL97_plus_lncRNA_AR..1..2212	55, 167	in gene, in gene	1	1	0	16	15	16	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene NEDD1	GCP-WD, NEDD1, TUBGCP7, FLJ35902	neural precursor cell expressed, developmentally down-regulated 1	NM_001135175, NM_152905, NM_001135176, NM_001135177, hCT2307136.0, hCT2358071.0, hCT2358072.0, hCT24316.3	1552417_a_at, 1560116_a_at, 234984_at	NP_001128647.1, NP_690869.1, NP_001128648.1, NP_001128649.1, EAW97578.1, EAW97579.1, EAW97577.1, EAW97580.1
GeneID.643770	LOC643770	12	98,879,322	98,897,627	18,305	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1580, 2_A375_pNL97_plus_lncRNA_AR..1..2216, 4_A375_EGR1..1..1957	411, 443, -53	in gene, in gene, upstream	1	1	1	26	18	26	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene LOC643770		hypothetical LOC643770	XR_111325, XR_110331, XR_114602		
GeneID.100128191	LOC100128191	12	98,906,751	98,910,004	3,253	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1580, 2_A375_pNL97_plus_lncRNA_AR..1..2216, 2_A375_pNL97_plus_lncRNA_AR..1..2217, 4_A375_EGR1..1..1957, 4_A375_EGR1..1..1958	12766, 12620, 276, 12324, 420	downstream, downstream, in gene, downstream, in gene	1	1	1	21	17.5	21.5	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene LOC100128191		hypothetical LOC100128191	NR_027157		
GeneID.7112	TMPO	12	98,909,351	98,944,157	34,806	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2217, 4_A375_EGR1..1..1958	377, 233	in gene, in gene	0	1	1	16	17	17	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TMPO	LEMD4, TMPO, MGC61508, PRO0868, TP, LAP2, CMD1T	thymopoietin	NM_001032283, NM_001032284, NM_003276, hCT2307591.0, hCT2307592.0, hCT2307593.0, hCT2358189.0, hCT2358190.0, hCT2358191.0	203432_at, 209753_s_at, 209754_s_at, 224944_at	NP_001027454.1, NP_001027455.1, NP_003267.1, EAW97590.1, EAW97591.1, EAW97594.1, EAW97589.1, EAW97592.1, EAW97593.1
GeneID.5250	SLC25A3	12	98,987,403	98,995,778	8,375	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1581	5	in gene	1	0	0	24	21	16	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene SLC25A3	SLC25A3, OK/SW-cl.48, PHC	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	NM_213611, NM_002635, NM_005888, hCT1952509.1, hCT1952510.1, hCT1958300.1, hCT1981345.1, hCT1965545.1, hCT2307595.0	200030_s_at	NP_998776.1, NP_002626.1, NP_005879.1, EAW97595.1, EAW97598.1, EAW97599.1, EAW97596.1, EAW97597.1, EAW97600.1
GeneID.677832	SNORA53	12	98,993,413	98,993,662	249	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1581	-6005	upstream	1	0	0	24	21	16	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene SNORA53	SNORA53, ACA53	small nucleolar RNA, H/ACA box 53	NR_003015		
GeneID.121457	IKBIP	12	99,007,162	99,038,569	31,407	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1582, 2_A375_pNL97_plus_lncRNA_AR..1..2218, 4_A375_EGR1..1..1959	-179, -323, -771	upstream, upstream, upstream	1	1	1	15	15	16	1	4_A375_EGR1..1	16	Gene IKBIP	FLJ31051, IKIP, IKBIP	IKBKB interacting protein	NM_201613, NM_201612, NM_153687, hCT2307751.0, hCT27953.2	227295_at, 235202_x_at, 236249_at	NP_963907.1, NP_963906.1, NP_710154.1, EAW97601.1, EAW97602.1
GeneID.317	APAF1	12	99,039,078	99,129,211	90,133	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1582, 2_A375_pNL97_plus_lncRNA_AR..1..2218, 4_A375_EGR1..1..1959, 4_A375_EGR1..1..1960	-310, -166, 282, 33242	upstream, upstream, in gene, in gene	1	1	1	10.5	10.5	16	2	4_A375_EGR1..1	16	Gene APAF1	APAF1, APAF-1, CED4, DKFZp781B1145	apoptotic peptidase activating factor 1	NM_181861, NM_181868, NM_181869, NM_001160, NM_013229, hCT2307601.0, hCT2307602.0, hCT2307604.0, hCT2307606.0, hCT2307607.0, hCT2357967.0, hCT2357968.0, hCT27948.2, hCT27949.2	204859_s_at, 211553_x_at, 211554_s_at	NP_863651.1, NP_863658.1, NP_001151.1, NP_037361.1, NP_863659.1, EAW97610.1, EAW97603.1, EAW97604.1, EAW97605.1, EAW97606.1, EAW97607.1, EAW97608.1, EAW97609.1, EAW97611.1
GeneID.56899	ANKS1B	12	99,129,071	100,378,432	1,249,361	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1583, 2_A375_pNL97_plus_lncRNA_AR..1..2219, 2_A375_pNL97_plus_lncRNA_AR..1..2220, 4_A375_EGR1..1..1961	529136, 1170272, 1087504, -446	in gene, in gene, in gene, upstream	1	1	1	10	11.25	6.25	4	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ANKS1B	MGC26087, AIDA1, EB-1, EB1, ANKS1B, ANKS2, AIDA, cajalin-2	ankyrin repeat and sterile alpha motif domain containing 1B	NM_152788, NM_181670, NM_020140	219989_s_at, 227439_at, 227440_at, 227441_s_at, 240292_x_at	NP_690001.3, NP_858058.2, NP_064525.1
GeneID.23074	UHRF1BP1L	12	100,430,863	100,536,642	105,779	-	1	4_A375_EGR1..1..1962	226	in gene	0	0	1	7	11	16	1	4_A375_EGR1..1	16	Gene UHRF1BP1L	KIAA0701, UHRF1BP1L	UHRF1 binding protein 1-like	NM_015054, NM_001006947, hCT12896.4, hCT1953877.1	1554291_at, 1554292_a_at, 213118_at, 213120_at	NP_055869.1, NP_001006948.1, EAW97619.1, EAW97620.1
GeneID.9971	NR1H4	12	100,867,879	100,957,843	89,964	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1584, 2_A375_pNL97_plus_lncRNA_AR..1..2221, 2_A375_pNL97_plus_lncRNA_AR..1..2222	65505, 65537, 100097	in gene, in gene, downstream	1	1	0	22.5	24.5	6.5	2	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene NR1H4	FXR, RIP14, MGC163445, BAR, HRR-1, HRR1, NR1H4	nuclear receptor subfamily 1, group H, member 4	NM_005123, hCT11975.2, hCT2307277.0, hCT2358104.0	1554375_a_at, 206340_at, 243800_at	NP_005114.1, EAW97638.1, EAW97639.1, EAW97640.1
GeneID.283431	GAS2L3	12	100,967,489	101,018,690	51,201	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2222	267	in gene	0	1	0	14	20	11	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene GAS2L3	GAS2L3		NM_174942, hCT12898.3, hCT2349938.0, hCT2349939.0, hCT2349940.0	235709_at, 238756_at	NP_777602.1, EAW97642.1, EAW97641.1, EAW97643.1, EAW97644.1
GeneID.121601	ANO4	12	101,188,374	101,522,419	334,045	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1586, 2_A375_pNL97_plus_lncRNA_AR..1..2224, 4_A375_EGR1..1..1963	31930, 31898, 232906	in gene, in gene, in gene	1	1	1	11.5	10.5	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene ANO4	TMEM16D, MGC130026, FLJ35277, ANO4, FLJ34272, FLJ34221	anoctamin 4	NM_178826, hCT1645123.3, hCT1958540.2, hCT2345377.1	229749_at, 236420_s_at, 239883_s_at	NP_849148.2, EAW97645.1, EAW97646.1, EAW97647.1
GeneID.27340	UTP20	12	101,673,905	101,780,397	106,492	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1587	19983	in gene	1	0	0	14	9	2	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene UTP20	DRIM, UTP20	UTP20, small subunit (SSU) processome component, homolog (yeast)	NM_014503, hCT12933.3, hCT2307229.0, hCT2307231.0, hCT2307232.0, hCT2307233.0	209725_at	NP_055318.2, EAW97654.1, EAW97652.1, EAW97653.1, EAW97655.1, EAW97656.1
GeneID.400	ARL1	12	101,786,914	101,801,572	14,658	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2225	-12	upstream	0	1	0	11	16	14	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ARL1	ARFL1, ARL1	ADP-ribosylation factor-like 1	NM_001177, hCT1820920.1, hCT1957557.1, hCT1960841.1, hCT1981824.1	201657_at, 201658_at, 201659_s_at	NP_001168.1, EAW97657.1, EAW97658.1, EAW97659.1, EAW97660.1
GeneID.56994	CHPT1	12	102,091,417	102,122,846	31,429	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2226	711	in gene	0	1	0	15	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CHPT1	CPT, CPT1, CHPT1	choline phosphotransferase 1	NM_020244, hCT12934.2, hCT1953881.1, hCT1953882.1, hCT2358137.0, hCT2358138.0	1559739_at, 221675_s_at, 230384_at	NP_064629.2, EAW97675.1, EAW97673.1, EAW97674.1, EAW97676.1, EAW97677.1
GeneID.55332	DRAM1	12	102,271,105	102,317,401	46,296	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2227, 4_A375_EGR1..1..1964	255, -148	in gene, upstream	0	1	1	16	16	15	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene DRAM1	DRAM, FLJ11259, DRAM1	DNA-damage regulated autophagy modulator 1	NM_018370, hCT2307389.0, hCT2307390.0	218627_at, 241992_at	NP_060840.2, EAW97686.1, EAW97685.1
GeneID.79023	NUP37	12	102,467,970	102,512,361	44,391	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2229	-1431	upstream	0	1	0	16	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NUP37	NUP37, FLJ22618, MGC5585, p37	nucleoporin 37kDa	NM_024057, hCT12966.1, hCT1953887.1	218622_at	NP_076962.2, EAW97689.1, EAW97688.1
GeneID.55010	C12orf48	12	102,513,956	102,591,298	77,342	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2229	-164	upstream	0	1	0	16	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene C12orf48	FLJ20641, AROM, PARPBP, C12orf48	chromosome 12 open reading frame 48	NM_017915, hCT1820890.1, hCT2307392.0, hCT2358150.0	220060_s_at, 224147_at, 227928_at	NP_060385.3, EAW97690.1, EAW97691.1, EAW97692.1
GeneID.429	ASCL1	12	103,351,452	103,354,294	2,842	+	1	4_A375_EGR1..1..1965	1026	in gene	0	0	1	4	10	16	1	4_A375_EGR1..1	16	Gene ASCL1	HASH1, MASH1, ASH1, ASCL1, bHLHa46	achaete-scute complex homolog 1 (Drosophila)	NM_004316, hCT12965.2	209985_s_at, 209987_s_at, 209988_s_at, 213768_s_at	NP_004307.2, EAW97703.1
GeneID.374470	C12orf42	12	103,695,733	103,889,749	194,016	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2230	21	in gene	0	1	0	7	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C12orf42	MGC43592, MGC57409, C12orf42, FLJ25323	chromosome 12 open reading frame 42	NM_001099336, NM_198521, hCT2340694.0, hCT2340695.0, hCT2340696.0, hCT2340697.0, hCT2340698.0, hCT2340699.0	1561376_at, 239977_at	NP_001092806.1, NP_940923.2, EAW97704.1, EAW97706.1, EAW97707.1, EAW97709.1, EAW97705.1, EAW97708.1
GeneID.51559	NT5DC3	12	104,166,081	104,234,975	68,894	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1591	38975	in gene	1	0	0	16	16	7	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene NT5DC3	FLJ11266, GNN, TU12B1-TY, TU12B1TY, NT5DC3	5'-nucleotidase domain containing 3	NM_001031701, hCT1960352.1, hCT2307434.0, hCT2307435.0, hCT2307436.0	218786_at, 234737_at	NP_001026871.1, EAW97718.1, EAW97715.1, EAW97716.1, EAW97717.1
GeneID.7184	HSP90B1	12	104,324,189	104,341,703	17,514	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1592, 2_A375_pNL97_plus_lncRNA_AR..1..2232	26819, 26891	downstream, downstream	1	1	0	23	26	15	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene HSP90B1	GRP94, GP96, ECGP, TRA1, HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	NM_003299, hCT12957.2, hCT2344666.0	200598_s_at, 200599_s_at, 216449_x_at, 216450_x_at	NP_003290.1, EAW97724.1, EAW97723.1
GeneID.728568	C12orf73	12	104,343,980	104,350,993	7,013	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1592, 1_A375_pNL7_minus_lncRNA_AR..1..1593, 2_A375_pNL97_plus_lncRNA_AR..1..2232, 2_A375_pNL97_plus_lncRNA_AR..1..2233, 4_A375_EGR1..1..1966	-15, -8815, 113, -8591, -8527	upstream, upstream, in gene, upstream, upstream	1	1	1	23.5	31.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene C12orf73	C12orf73, DKFZp547P055, FLJ13975	chromosome 12 open reading frame 73	NM_001135570	226927_at, 226943_at	NP_001129042.1
GeneID.6996	TDG	12	104,359,593	104,382,656	23,063	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1592, 1_A375_pNL7_minus_lncRNA_AR..1..1593, 2_A375_pNL97_plus_lncRNA_AR..1..2232, 2_A375_pNL97_plus_lncRNA_AR..1..2233, 4_A375_EGR1..1..1966	-8585, 215, -8713, -9, -73	upstream, in gene, upstream, upstream, upstream	1	1	1	23.5	31.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene TDG	TDG		NM_003211, hCT2307503.1, hCT2307505.1, hCT2358224.0	203743_s_at	NP_003202.3, EAW97727.1, EAW97728.1, EAW97729.1
GeneID.29915	HCFC2	12	104,458,236	104,500,302	42,066	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2234	100	in gene	0	1	0	13	22	16	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene HCFC2	HCFC2, HCF2, HCF-2, FLJ94012	host cell factor C2	NM_013320, hCT11979.2, hCT2358109.0	219484_at	NP_037452.1, EAW97737.1, EAW97736.1
GeneID.7296	TXNRD1	12	104,609,559	104,744,062	134,503	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2235, 2_A375_pNL97_plus_lncRNA_AR..1..2236	71081, 73033	in gene, in gene	0	1	0	10	19	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TXNRD1	GRIM-12, TR1, TR, TRXR1, TXNRD1, MGC9145, TXNR	thioredoxin reductase 1	NM_182729, NM_182742, NM_182743, NM_003330, NM_001093771, hCT1957554.2, hCT2307512.0, hCT2357954.0	201266_at	NP_877393.1, NP_877419.1, NP_003321.3, NP_001087240.1, NP_877420.1, EAW97743.1, EAW97744.1, EAW97745.1
GeneID.50515	CHST11	12	104,850,692	105,155,792	305,100	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1594, 2_A375_pNL97_plus_lncRNA_AR..1..2237, 4_A375_EGR1..1..1967, 4_A375_EGR1..1..1968	-116, -132, 1164, 262760	upstream, upstream, in gene, in gene	1	1	1	10	12.67	16	3	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CHST11	DKFZp667A035, CHST11, C4ST1, C4ST, C4ST-1, HSA269537, FLJ41682	carbohydrate (chondroitin 4) sulfotransferase 11	NM_001173982, NM_018413, hCT2307515.1, hCT2307516.1, hCT2351951.0	219634_at, 226368_at, 226372_at	NP_001167453.1, NP_060883.1, EAW97748.1, EAW97749.1, EAW97750.1
GeneID.23325	KIAA1033	12	105,501,492	105,562,908	61,416	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2238	44	in gene	0	1	0	20	24	16	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene KIAA1033	KIAA1033		NM_015275, hCT1953867.1, hCT2358170.0, hCT2358171.0, hCT6531.3	212794_s_at, 212795_at, 215936_s_at	NP_056090.1, EAW97761.1, EAW97758.1, EAW97759.1, EAW97760.1
GeneID.255394	TCP11L2	12	106,696,581	106,740,793	44,212	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1595, 2_A375_pNL97_plus_lncRNA_AR..1..2240, 4_A375_EGR1..1..1969	-197, -229, 283	upstream, upstream, in gene	1	1	1	28	30	16	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene TCP11L2	TCP11L2, MGC40368	t-complex 11 (mouse)-like 2	NM_152772, hCT1958539.2, hCT2349908.0, hCT2349909.0, hCT2349910.0, hCT2349911.0, hCT2349912.0	1553861_at, 1559413_at, 1565000_a_at, 1565525_a_at, 1565527_x_at, 1569206_at, 1569207_s_at, 244249_at	NP_689985.1, EAW97778.1, EAW97774.1, EAW97776.1, EAW97777.1, EAW97779.1, EAW97775.1
GeneID.55703	POLR3B	12	106,751,436	106,903,976	152,540	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2241, 4_A375_EGR1..1..1970	20, 340	in gene, in gene	0	1	1	20	20	22	1	4_A375_EGR1..1	22	Gene POLR3B	POLR3B, DKFZp686B10117, FLJ10388, RPC2, C128	polymerase (RNA) III (DNA directed) polypeptide B	NM_018082, NM_001160708, hCT1958538.1, hCT2307477.0	1556803_at, 1556804_s_at, 219459_at	NP_060552.4, NP_001154180.1, EAW97780.1, EAW97781.1
GeneID.100287944	LOC100287944	12	106,889,736	107,168,696	278,960	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1596, 2_A375_pNL97_plus_lncRNA_AR..1..2242, 4_A375_EGR1..1..1971	760, 660, 280	in gene, in gene, in gene	1	1	1	23	22	14	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene LOC100287944		hypothetical protein LOC100287944	XM_002343163		XP_002343224.1
GeneID.55188	RIC8B	12	107,168,399	107,283,094	114,695	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1596, 2_A375_pNL97_plus_lncRNA_AR..1..2242, 4_A375_EGR1..1..1971	-463, -363, 17	upstream, upstream, in gene	1	1	1	23	22	14	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene RIC8B	FLJ10620, MGC39476, RIC8, RIC8B, hSyn	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	NM_018157, hCT2307484.0, hCT2358208.0, hCT7135.2	219446_at, 229637_at	NP_060627.2, EAW97785.1, EAW97786.1, EAW97787.1
GeneID.90488	C12orf23	12	107,349,544	107,367,813	18,269	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2243, 4_A375_EGR1..1..1972	184, -808	in gene, upstream	0	1	1	9	11	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene C12orf23	FLJ11721, MGC17943, C12orf23, FLJ13959	chromosome 12 open reading frame 23	NM_152261, hCT2307465.0, hCT7550.3	224759_s_at	NP_689474.1, EAW97790.1, EAW97791.1
GeneID.1407	CRY1	12	107,385,142	107,487,598	102,456	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2244, 4_A375_EGR1..1..1973	52, -62	in gene, upstream	0	1	1	11	16	13	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CRY1	PHLL1, CRY1	cryptochrome 1 (photolyase-like)	NM_004075, hCT1953871.1, hCT2307573.0, hCT2307575.0	209674_at	NP_004066.1, EAW97796.1, EAW97795.1, EAW97797.1
GeneID.11137	PWP1	12	108,079,590	108,106,257	26,667	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2245, 4_A375_EGR1..1..1974	26, -6	in gene, upstream	0	1	1	15	16	19	1	4_A375_EGR1..1	19	Gene PWP1	IEF-SSP-9502, PWP1	PWP1 homolog (S. cerevisiae)	NM_007062, hCT2307409.0, hCT7547.1	201606_s_at, 201607_at, 201608_s_at	NP_008993.1, EAW97803.1, EAW97802.1
GeneID.9671	WSCD2	12	108,523,511	108,644,314	120,803	+	6	1_A375_pNL7_minus_lncRNA_AR..1..1597, 1_A375_pNL7_minus_lncRNA_AR..1..1598, 2_A375_pNL97_plus_lncRNA_AR..1..2247, 2_A375_pNL97_plus_lncRNA_AR..1..2248, 2_A375_pNL97_plus_lncRNA_AR..1..2249, 4_A375_EGR1..1..1976	84665, 98921, 84841, 84937, 99273, 73	in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	10.75	17	9.25	4	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene WSCD2	WSCD2, MGC117165, KIAA0789	WSC domain containing 2	NM_014653, hCT2307398.0, hCT2307399.0, hCT2307400.0	207637_at, 229032_at	NP_055468.2, EAW97807.1, EAW97808.1, EAW97809.1
GeneID.9733	SART3	12	108,915,991	108,955,165	39,174	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1599, 4_A375_EGR1..1..1980	413, 317	in gene, in gene	1	0	1	22	18	16	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene SART3	DSAP1, SART3, KIAA0156, P100, p110, RP11-13G14, p110(nrb), TIP110, MGC138188	squamous cell carcinoma antigen recognized by T cells 3	NM_014706, hCT2358025.0, hCT6722.3	1554276_at, 200069_at, 209127_s_at, 209128_s_at	NP_055521.1, EAW97816.1, EAW97817.1
GeneID.23479	ISCU	12	108,956,294	108,963,160	6,866	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1599, 4_A375_EGR1..1..1980	-1542, -1446	upstream, upstream	1	0	1	22	18	16	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene ISCU	NIFU, 2310020H20Rik, MGC74517, hnifU, NIFUN, ISCU, HML, ISU2	iron-sulfur cluster scaffold homolog (E. coli)	NM_014301, NM_213595, hCT2307549.0, hCT2358084.0, hCT2358085.0, hCT2358086.0, hCT6727.2	209075_s_at	NP_055116.1, NP_998760.1, EAW97818.1, EAW97819.1, EAW97820.1, EAW97822.1, EAW97821.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.115811	IQCD	12	113,833,246	113,858,880	25,634	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1627, 2_A375_pNL97_plus_lncRNA_AR..1..2279, 4_A375_EGR1..1..1999	35466, 35468, 35616	downstream, downstream, downstream	1	1	1	29	26	16	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene IQCD	4933433C09Rik, IQCD	IQ motif containing D	NM_138451, hCT1956206.1, hCT2307980.0, hCT2307982.0	1552540_s_at	NP_612460.1, EAW98044.1, EAW98043.1, EAW98045.1
GeneID.80024	SLC24A6	12	113,736,571	113,772,925	36,354	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1628	-211	upstream	1	0	0	19	16	4	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene SLC24A6	SLC24A6, FLJ22233, NCLX, NCKX6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	NM_024959, hCT2307974.0, hCT2307975.0, hCT2307977.0, hCT31635.3	218749_s_at, 222727_s_at	NP_079235.2, EAW98049.1, EAW98048.1, EAW98050.1, EAW98051.1
GeneID.196463	PLBD2	12	113,796,371	113,827,458	31,087	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1629, 2_A375_pNL97_plus_lncRNA_AR..1..2280	98, 109	in gene, in gene	1	1	0	24	22	12	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene PLBD2	P76, PLBD2	phospholipase B domain containing 2	NM_001159727, NM_173542, hCT2358193.0, hCT31634.3	228845_at	NP_001153199.1, NP_775813.2, EAW98052.1, EAW98053.1
GeneID.113675	SDSL	12	113,860,216	113,876,081	15,865	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1630	-152	upstream	1	0	0	24	17	14	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene SDSL	SDH 2, TDH, SDS-RS1, SDSL	serine dehydratase-like	NM_138432, hCT2307682.0, hCT2307683.0, hCT31633.1	228274_at	NP_612441.1, EAW98057.1, EAW98058.1, EAW98059.1
GeneID.64211	LHX5	12	113,900,694	113,909,877	9,183	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1631, 2_A375_pNL97_plus_lncRNA_AR..1..2281, 4_A375_EGR1..1..2000, 4_A375_EGR1..1..2001	-8187, -8171, 4117, 677	upstream, upstream, in gene, in gene	1	1	1	11.67	14.67	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LHX5	MGC129689, LHX5	LIM homeobox 5	NM_022363, hCT31631.1	208333_at	NP_071758.1, EAW98060.1
GeneID.100506452	LOC100506452	12	113,909,808	113,918,286	8,478	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1631, 2_A375_pNL97_plus_lncRNA_AR..1..2281, 4_A375_EGR1..1..2000, 4_A375_EGR1..1..2001	8256, 8240, -4048, -608	in gene, in gene, upstream, upstream	1	1	1	11.67	14.67	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC100506452		hypothetical LOC100506452	XR_111339, XR_109131, XR_114615		
GeneID.9904	RBM19	12	114,254,543	114,404,176	149,633	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2283	-16	upstream	0	1	0	16	17	9	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene RBM19	RBM19, KIAA0682, DKFZp586F1023	RNA binding motif protein 19	NM_016196, NM_001146698, NM_001146699, hCT31594.2, hCT31595.2	205115_s_at, 206019_at	NP_057280.2, NP_001140170.1, NP_001140171.1, EAW98062.1, EAW98063.1
GeneID.6926	TBX3	12	115,108,059	115,121,969	13,910	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2284, 4_A375_EGR1..1..2004	-111, 18145	upstream, downstream	0	1	1	9.5	9.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TBX3	TBX3, UMS, TBX3-ISO, XHL	T-box 3	NM_005996, NM_016569, hCT1956047.0, hCT1959659.1, hCT2307500.0, hCT2307501.0, hCT2358073.0, hCT31596.2	219682_s_at, 222917_s_at, 225544_at, 228344_s_at, 229565_x_at, 229576_s_at, 243234_at	NP_005987.3, NP_057653.3, EAW98069.1, EAW98070.1, EAW98072.1, EAW98073.1, EAW98071.1, EAW98074.1
GeneID.79794	C12orf49	12	117,153,596	117,175,843	22,247	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2293	-125	upstream	0	1	0	23	34	7	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene C12orf49	C12orf49, FLJ21415	chromosome 12 open reading frame 49	NM_024738, hCT1956214.1, hCT30979.2	218687_s_at, 222767_s_at	NP_079014.1, EAW98088.1, EAW98089.1
GeneID.84900	RNFT2	12	117,176,096	117,291,436	115,340	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1635, 2_A375_pNL97_plus_lncRNA_AR..1..2293, 2_A375_pNL97_plus_lncRNA_AR..1..2294, 2_A375_pNL97_plus_lncRNA_AR..1..2295, 2_A375_pNL97_plus_lncRNA_AR..1..2296	120032, -126, 75285, 81200, 119920	downstream, upstream, in gene, in gene, downstream	1	1	0	17.5	23.25	6.25	4	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene RNFT2	RNFT2, TMEM118, FLJ14627	ring finger protein, transmembrane 2	NM_032814, NM_001109903, hCT1820423.3, hCT2307626.0, hCT2358053.0	1553209_at, 221908_at, 221909_at	NP_116203.2, NP_001103373.1, EAW98090.1, EAW98091.1, EAW98092.1
GeneID.8739	HRK	12	117,299,027	117,319,232	20,205	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1635, 2_A375_pNL97_plus_lncRNA_AR..1..2296	23104, 23216	downstream, downstream	1	1	0	20	21	4	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene HRK	DP5, HRK, HARAKIRI	harakiri, BCL2 interacting protein (contains only BH3 domain)	NM_003806, hCT29775.2	206684_s_at, 206665_at	NP_003797.1, EAW98093.1
GeneID.26259	FBXW8	12	117,348,761	117,468,953	120,192	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2297	5927	in gene	0	1	0	11	16	2	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene FBXW8	FBW6, FBXW6, FBW8, FBXO29, FBXW8, FBX29, MGC33534	F-box and WD repeat domain containing 8	NM_012174, NM_153348, hCT2307629.0, hCT2307630.0, hCT2358124.0, hCT31608.3	231863_at	NP_036306.1, NP_699179.2, EAW98094.1, EAW98095.1, EAW98096.1, EAW98097.1
GeneID.54997	TESC	12	117,476,728	117,537,251	60,523	-	2	4_A375_EGR1..1..2005, 4_A375_EGR1..1..2006	883, 499	in gene, in gene	0	0	1	10.5	14	14.5	2	4_A375_EGR1..1	17	Gene TESC	TESC, CHP3, TSC, FLJ20607	tescalcin	NM_017899, NM_001168325, NR_031766, hCT1956207.1, hCT2307779.0, hCT2358194.0, hCT2358195.0	218872_at, 240553_at	NP_060369.3, NP_001161797.1, EAW98098.1, EAW98099.1, EAW98100.1, EAW98101.1
GeneID.100506570	LOC100506570	12	118,570,053	118,583,387	13,334	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1637, 2_A375_pNL97_plus_lncRNA_AR..1..2298	8795, 9419	in gene, in gene	1	1	0	15	18	15	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100506570		hypothetical LOC100506570	XR_111344, XR_109137, XR_109138, XR_114620		
GeneID.5037	PEBP1	12	118,573,870	118,583,390	9,520	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1637, 2_A375_pNL97_plus_lncRNA_AR..1..2298	722, 98	in gene, in gene	1	1	0	15	18	15	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PEBP1	PEBP, PBP, RKIP, HCNP, PEBP1	phosphatidylethanolamine binding protein 1	NM_002567, hCT2309027.0, hCT2309028.0	205353_s_at, 210825_s_at, 211941_s_at	NP_002558.1, EAW98122.1, EAW98123.1
GeneID.51347	TAOK3	12	118,587,606	118,810,750	223,144	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1638, 2_A375_pNL97_plus_lncRNA_AR..1..2299, 2_A375_pNL97_plus_lncRNA_AR..1..2300	-130, -130, -3554	upstream, upstream, upstream	1	1	0	29	23	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene TAOK3	FLJ31808, JIK, DPK, MAP3K18, DKFZp666H245, TAOK3	TAO kinase 3	NM_016281, hCT1615220.1, hCT1957568.1	220761_s_at, 221508_at	NP_057365.3, EAW98124.1, EAW98125.1
GeneID.64426	SUDS3	12	118,814,358	118,855,840	41,482	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1638, 2_A375_pNL97_plus_lncRNA_AR..1..2299, 2_A375_pNL97_plus_lncRNA_AR..1..2300	-3476, -3476, -54	upstream, upstream, upstream	1	1	0	29	23	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene SUDS3	SAP45, SUDS3, MGC104711, FLJ00052, SDS3	suppressor of defective silencing 3 homolog (S. cerevisiae)	NM_022491, hCT1956213.1, hCT2309040.0, hCT2309043.0, hCT2358054.0, hCT30906.3	224974_at, 233841_s_at	NP_071936.2, EAW98137.1, EAW98138.1, EAW98139.1, EAW98140.1, EAW98141.1
GeneID.84530	SRRM4	12	119,419,396	119,600,857	181,461	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1639, 2_A375_pNL97_plus_lncRNA_AR..1..2301	79708, 79772	in gene, in gene	1	1	0	28	36	6	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene SRRM4	nSR100, SRRM4, MGC176729, MU-MB-2.76, KIAA1853	serine/arginine repetitive matrix 4	NM_194286, hCT16345.3	230010_at, 236151_at, 237626_at	NP_919262.2, EAW98142.1
GeneID.11113	CIT	12	120,123,598	120,315,092	191,494	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2302	212	in gene	0	1	0	15	23	15	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CIT	CIT, CRIK, KIAA0949, STK21	citron (rho-interacting, serine/threonine kinase 21)	NM_007174, hCT18924.4, hCT2349943.0, hCT2349944.0, hCT2349945.0	212801_at, 242872_at	NP_009105.1, EAW98155.1, EAW98156.1, EAW98157.1, EAW98158.1
GeneID.92558	CCDC64	12	120,427,648	120,532,299	104,651	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1640, 1_A375_pNL7_minus_lncRNA_AR..1..1641, 1_A375_pNL7_minus_lncRNA_AR..1..1642, 2_A375_pNL97_plus_lncRNA_AR..1..2303, 2_A375_pNL97_plus_lncRNA_AR..1..2304	-336, 352, 97120, 126, 97131	upstream, in gene, in gene, in gene, in gene	1	1	0	16.67	17.33	6.67	3	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene CCDC64	H_267D11.1, CCDC64, FLJ26450, BICDR-1	coiled-coil domain containing 64	NM_207311, hCT2307915.0, hCT2307916.0, hCT2307917.0, hCT2358058.0	215015_at, 226320_x_at	NP_997194.2, EAW98160.1, EAW98159.1, EAW98161.1, EAW98162.1
GeneID.11021	RAB35	12	120,532,899	120,554,643	21,744	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1642, 2_A375_pNL97_plus_lncRNA_AR..1..2304	29875, 29864	downstream, downstream	1	1	0	21	16	7	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene RAB35	RAB1C, RAY, H-ray, RAB35	RAB35, member RAS oncogene family	NM_001167606, NM_006861, hCT2308872.0, hCT2358001.0, hCT2358002.0	205461_at, 221619_at, 225620_at	NP_001161078.1, NP_006852.1, EAW98163.1, EAW98164.1, EAW98165.1
GeneID.10985	GCN1L1	12	120,565,014	120,632,513	67,499	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1643, 1_A375_pNL7_minus_lncRNA_AR..1..1644, 2_A375_pNL97_plus_lncRNA_AR..1..2305, 2_A375_pNL97_plus_lncRNA_AR..1..2306, 4_A375_EGR1..1..2008, 4_A375_EGR1..1..2009	1, -6559, 65, -6559, 145, -6303	in gene, upstream, in gene, upstream, in gene, upstream	1	1	1	113.5	121	22	2	2_A375_pNL97_plus_lncRNA_AR..1	217	Gene GCN1L1	PRIC295, GCN1L, GCN1, KIAA0219, GCN1L1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	NM_006836, hCT18923.3, hCT2308865.0, hCT2308866.0	212139_at, 216232_s_at	NP_006827.1, EAW98169.1, EAW98167.1, EAW98166.1
GeneID.6175	RPLP0	12	120,634,503	120,639,014	4,511	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1643, 1_A375_pNL7_minus_lncRNA_AR..1..1644, 2_A375_pNL97_plus_lncRNA_AR..1..2305, 2_A375_pNL97_plus_lncRNA_AR..1..2306, 4_A375_EGR1..1..2008, 4_A375_EGR1..1..2009	6502, -58, 6566, -58, 6646, 198	downstream, upstream, downstream, upstream, downstream, in gene	1	1	1	113.5	121	22	2	2_A375_pNL97_plus_lncRNA_AR..1	217	Gene RPLP0	MGC111226, PRLP0, LP0, L10E, RPLP0, P0, RPP0, MGC88175	ribosomal protein, large, P0	NM_053275, NM_001002, hCT2308860.1, hCT2308861.0, hCT2308862.1, hCT2308863.1, hCT2358000.1	201033_x_at, 208856_x_at, 211720_x_at, 211972_x_at	NP_444505.1, NP_000993.1, EAW98170.1, EAW98171.1, EAW98173.1, EAW98174.1, EAW98172.1
GeneID.100506649	LOC100506649	12	120,639,111	120,651,201	12,090	+	7	1_A375_pNL7_minus_lncRNA_AR..1..1643, 1_A375_pNL7_minus_lncRNA_AR..1..1644, 2_A375_pNL97_plus_lncRNA_AR..1..2305, 2_A375_pNL97_plus_lncRNA_AR..1..2306, 4_A375_EGR1..1..2008, 4_A375_EGR1..1..2009, 4_A375_EGR1..1..2010	-6599, -39, -6663, -39, -6743, -295, 13545	upstream, upstream, upstream, upstream, upstream, upstream, downstream	1	1	1	77	82.33	20.33	3	2_A375_pNL97_plus_lncRNA_AR..1	217	Gene LOC100506649		hypothetical LOC100506649	XR_111345, XR_111346, XR_109139, XR_109140, XR_114621, XR_114622		
GeneID.5829	PXN	12	120,648,250	120,703,563	55,313	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1644, 1_A375_pNL7_minus_lncRNA_AR..1..1645, 1_A375_pNL7_minus_lncRNA_AR..1..1646, 2_A375_pNL97_plus_lncRNA_AR..1..2306, 4_A375_EGR1..1..2009, 4_A375_EGR1..1..2010	64491, 33979, -213, 64491, 64747, 50907	downstream, in gene, upstream, downstream, downstream, in gene	1	1	1	59.5	61	16.75	4	2_A375_pNL97_plus_lncRNA_AR..1	217	Gene PXN	FLJ16691, PXN	paxillin	NM_001080855, NM_002859, NM_025157, hCT18914.3, hCT1955415.2, hCT2308854.1, hCT2308857.1, hCT2308856.1	201087_at, 211823_s_at	NP_001074324.1, NP_002850.2, NP_079433.3, EAW98175.1, EAW98177.1, EAW98178.1, EAW98176.1, EAW98179.1
GeneID.26834	RNU4-2	12	120,729,566	120,729,706	140	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1647, 1_A375_pNL7_minus_lncRNA_AR..1..1648, 2_A375_pNL97_plus_lncRNA_AR..1..2307, 4_A375_EGR1..1..2012, 4_A375_EGR1..1..2013	-54, -1366, -102, 10, -998	upstream, upstream, upstream, in gene, upstream	1	1	1	46	56	20	1	2_A375_pNL97_plus_lncRNA_AR..1	56	Gene RNU4-2	RNU4C, RNU4-1B, U4A, U4b, RNU4B1, U4c, RNU4-2	RNA, U4 small nuclear 2	NR_003137		
GeneID.26835	RNU4-1	12	120,730,897	120,731,040	143	-	7	1_A375_pNL7_minus_lncRNA_AR..1..1647, 1_A375_pNL7_minus_lncRNA_AR..1..1648, 1_A375_pNL7_minus_lncRNA_AR..1..1649, 2_A375_pNL97_plus_lncRNA_AR..1..2307, 2_A375_pNL97_plus_lncRNA_AR..1..2308, 4_A375_EGR1..1..2012, 4_A375_EGR1..1..2013	1280, -32, -9120, 1232, -9152, 1344, 336	downstream, upstream, upstream, downstream, upstream, downstream, downstream	1	1	1	37	41.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	56	Gene RNU4-1	U4BL, U4, RNU4-1, RNU4A, RNU4B2	RNA, U4 small nuclear 1	NR_003925		
GeneID.23409	SIRT4	12	120,740,124	120,751,045	10,921	+	6	1_A375_pNL7_minus_lncRNA_AR..1..1647, 1_A375_pNL7_minus_lncRNA_AR..1..1648, 1_A375_pNL7_minus_lncRNA_AR..1..1649, 2_A375_pNL97_plus_lncRNA_AR..1..2307, 2_A375_pNL97_plus_lncRNA_AR..1..2308, 4_A375_EGR1..1..2013	-10364, -9052, 36, -10316, 68, -9420	upstream, upstream, in gene, upstream, in gene, upstream	1	1	1	37	41.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	56	Gene SIRT4	MGC130047, SIR2L4, MGC130046, SIRT4, MGC57437	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	NM_012240, hCT18916.2, hCT2308058.0	220047_at, 222248_s_at	NP_036372.1, EAW98182.1, EAW98183.1
GeneID.4440	MSI1	12	120,779,133	120,806,958	27,825	-	1	4_A375_EGR1..1..2014	21902	in gene	0	0	1	6	6	17	1	4_A375_EGR1..1	17	Gene MSI1	MSI1		NM_002442, hCT18926.3, hCT2349946.0, hCT2349947.0	206333_at	NP_002433.1, EAW98186.1, EAW98185.1, EAW98187.1
GeneID.1337	COX6A1	12	120,875,904	120,878,532	2,628	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1650, 2_A375_pNL97_plus_lncRNA_AR..1..2309, 4_A375_EGR1..1..2015	8304, 8352, 8496	downstream, downstream, downstream	1	1	1	20	28	18	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene COX6A1	COX6AL, COX6A1, MGC104500, COX6A	cytochrome c oxidase subunit VIa polypeptide 1	NM_004373, hCT1816775.1, hCT2308018.0	200925_at, 224344_at, 234876_at	NP_004364.2, EAW98190.1, EAW98191.1
GeneID.51499	TRIAP1	12	120,881,764	120,884,215	2,451	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1650, 2_A375_pNL97_plus_lncRNA_AR..1..2309, 4_A375_EGR1..1..2015	7, -41, -185	in gene, upstream, upstream	1	1	1	20	28	18	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene TRIAP1	WF-1, P53CSV, TRIAP1, HSPC132	TP53 regulated inhibitor of apoptosis 1	NM_016399, hCT17663.1	218403_at	NP_057483.1, EAW98192.1
GeneID.283459	GATC	12	120,884,241	120,901,556	17,315	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1650, 1_A375_pNL7_minus_lncRNA_AR..1..1651, 2_A375_pNL97_plus_lncRNA_AR..1..2309, 2_A375_pNL97_plus_lncRNA_AR..1..2310, 4_A375_EGR1..1..2015	-33, 23343, 15, 23423, 159	upstream, downstream, in gene, downstream, in gene	1	1	1	23.5	30	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene GATC	FLJ37000, GATC, 15E1.2, MGC129938	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)	NM_176818, NR_033684, hCT18921.2	214711_at	NP_789788.1, EAW98193.1
GeneID.8683	SFRS9	12	120,899,471	120,907,558	8,087	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1651, 2_A375_pNL97_plus_lncRNA_AR..1..2310	-26, -108	upstream, upstream	1	1	0	27	32	11	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene SFRS9	SFRS9, SRp30c, SRSF9	serine/arginine-rich splicing factor 9	NM_003769, hCT18913.2	200044_at, 201698_s_at, 225430_at	NP_003760.1, EAW98194.1
GeneID.8655	DYNLL1	12	120,907,660	120,936,298	28,638	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1651, 2_A375_pNL97_plus_lncRNA_AR..1..2310, 2_A375_pNL97_plus_lncRNA_AR..1..2311	-76, 4, 26644	upstream, in gene, in gene	1	1	0	20.5	24.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene DYNLL1	DYNLL1, LC8, DNCLC1, DNCL1, PIN, DLC1, LC8a, MGC126138, DLC8, MGC126137, hdlc1	dynein, light chain, LC8-type 1	NM_001037494, NM_001037495, NM_003746, hCT18909.1, hCT2308021.0, hCT2308022.0	200703_at	NP_001032583.1, NP_001032584.1, NP_003737.1, EAW98195.1, EAW98196.1, EAW98197.1
GeneID.100506668	LOC100506668	12	120,925,095	120,933,743	8,648	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2311	-561	upstream	0	1	0	14	17	13	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC100506668		hypothetical LOC100506668	XR_111348, XR_111347, XR_109142, XR_109141, XR_114624, XR_114623		
GeneID.84274	COQ5	12	120,941,082	120,966,964	25,882	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2311, 2_A375_pNL97_plus_lncRNA_AR..1..2312, 2_A375_pNL97_plus_lncRNA_AR..1..2313	32860, 100, -5372	downstream, in gene, upstream	0	1	0	14.67	17	9.67	3	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene COQ5	MGC4767, MGC104303, COQ5	coenzyme Q5 homolog, methyltransferase (S. cerevisiae)	NM_032314, hCT1816781.2, hCT18920.2	223114_at	NP_115690.3, EAW98199.1, EAW98198.1
GeneID.9921	RNF10	12	120,972,132	121,015,397	43,265	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2312, 2_A375_pNL97_plus_lncRNA_AR..1..2313	-5266, 204	upstream, in gene	0	1	0	15	17	8	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene RNF10	RIE2, MGC126758, RNF10, KIAA0262, MGC126764	ring finger protein 10	NM_014868, hCT18912.2, hCT2308024.0, hCT2308025.0, hCT2357989.0, hCT2357990.0	207801_s_at, 208832_at	NP_055683.3, EAW98201.1, EAW98200.1, EAW98202.1, EAW98203.1, EAW98204.1
GeneID.9761	MLEC	12	121,124,949	121,139,667	14,718	+	1	4_A375_EGR1..1..2016	-309	upstream	0	0	1	16	12	16	1	4_A375_EGR1..1	16	Gene MLEC	MLEC, KIAA0152	malectin	NM_014730, hCT1816776.1, hCT1955412.1, hCT2308034.0	200616_s_at, 200617_at	NP_055545.1, EAW98212.1, EAW98213.1, EAW98214.1
GeneID.35	ACADS	12	121,163,571	121,177,811	14,240	+	1	4_A375_EGR1..1..2017	13741	in gene	0	0	1	6	6	17	1	4_A375_EGR1..1	17	Gene ACADS	SCAD, ACAD3, ACADS	acyl-CoA dehydrogenase, C-2 to C-3 short chain	NM_000017, hCT18498.2	202366_at	NP_000008.1, EAW98218.1
GeneID.121665	UNQ1887	12	121,201,035	121,342,151	141,116	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1652, 2_A375_pNL97_plus_lncRNA_AR..1..2314, 2_A375_pNL97_plus_lncRNA_AR..1..2315	-3321, -121, -2873	upstream, upstream, upstream	1	1	0	13.5	20	6	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene UNQ1887	MGC126676, PRO4332, SPPL3, DKFZp586C1324, MGC126674, PSL4, IMP2, MGC90402, MDHV1887	signal peptide peptidase 3	NM_139015, hCT1816783.4, hCT1966205.2, hCT1966206.2, hCT2351276.0	1554564_a_at, 1554565_x_at, 1566696_at, 1566697_at, 224638_at, 224639_at, 224640_at	NP_620584.2, EAW98220.1, EAW98221.1, EAW98222.1, EAW98223.1
GeneID.8638	OASL	12	121,458,095	121,476,780	18,685	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1653, 2_A375_pNL97_plus_lncRNA_AR..1..2316	-116, -180	upstream, upstream	1	1	0	53	35	11	1	1_A375_pNL7_minus_lncRNA_AR..1	53	Gene OASL	OASL, p59OASL, TRIP14	2'-5'-oligoadenylate synthetase-like	NM_198213, NM_003733, hCT18501.2, hCT1955413.1, hCT2309628.0, hCT2309629.0	205660_at, 210797_s_at	NP_937856.1, NP_003724.1, EAW98235.1, EAW98236.1, EAW98237.1, EAW98238.1
GeneID.10645	CAMKK2	12	121,675,495	121,736,111	60,616	-	2	4_A375_EGR1..1..2018, 4_A375_EGR1..1..2019	24111, 1903	in gene, in gene	0	0	1	8.5	9.5	17.5	2	4_A375_EGR1..1	21	Gene CAMKK2	KIAA0787, CAMKK, MGC15254, CAMKK2, CAMKKB	calcium/calmodulin-dependent protein kinase kinase 2, beta	NM_006549, NM_153499, NM_153500, NM_172216, NM_172226, NM_172214, NM_172215, hCT18503.2, hCT2309611.0, hCT2309613.0, hCT2309615.0, hCT2309616.0, hCT2309618.0, hCT2309619.0, hCT2358112.0, hCT2358113.0, hCT2358114.0, hCT2358115.0, hCT2358116.0	207359_at, 210787_s_at, 212252_at, 213812_s_at	NP_006540.3, NP_705719.2, NP_705720.1, NP_757363.1, NP_757365.1, NP_757380.1, NP_757364.1, EAW98247.1, EAW98248.1, EAW98249.1, EAW98250.1, EAW98251.1, EAW98252.1, EAW98255.1, EAW98253.1, EAW98254.1, EAW98256.1, EAW98257.1, EAW98258.1
GeneID.51433	ANAPC5	12	121,746,048	121,792,012	45,964	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1654, 2_A375_pNL97_plus_lncRNA_AR..1..2317	1676, 1676	in gene, in gene	1	1	0	24	20	10	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene ANAPC5	APC5, ANAPC5	anaphase promoting complex subunit 5	NM_016237, NM_001137559, hCT17651.4, hCT2345157.1, hCT2358219.0	200098_s_at, 208721_s_at, 208722_s_at, 211036_x_at, 239651_at	NP_057321.2, NP_001131031.1, EAW98259.1, EAW98260.1, EAW98261.1

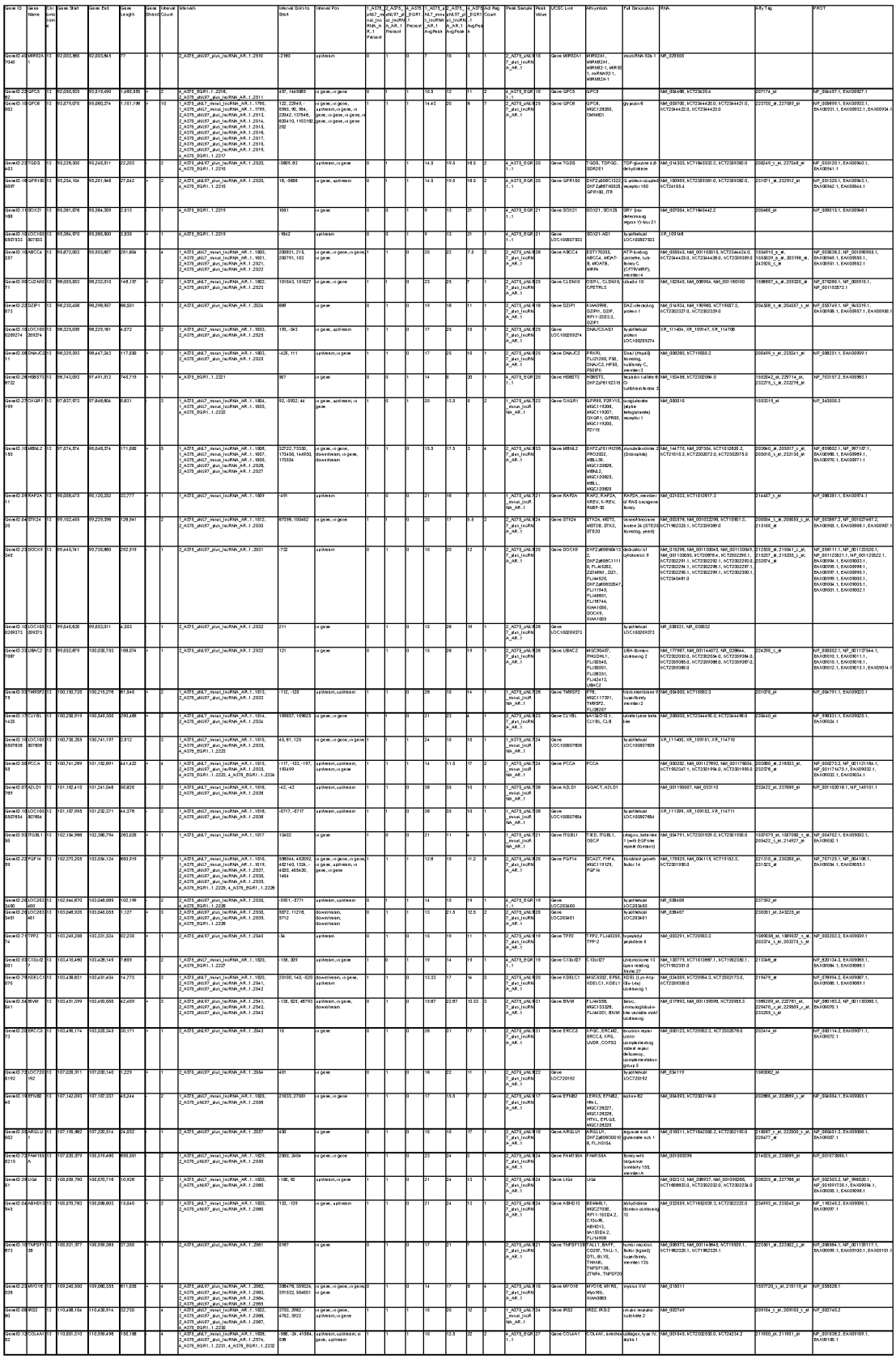
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.80196	RNF34	12	121,837,902	121,862,155	24,253	+	1	4_A375_EGR1..1..2020	-5710	upstream	0	0	1	5	6	12	1	4_A375_EGR1..1	12	Gene RNF34	RIF, RFI, RNF34, RIFF, hRFI, CARP1, FLJ21786, CARP-1	ring finger protein 34	NM_025126, NM_194271, hCT18502.3, hCT2309331.0, hCT2356111.0	219035_s_at, 229655_at, 238288_at	NP_079402.2, NP_919247.1, EAW98262.1, EAW98263.1, EAW98264.1
GeneID.84678	KDM2B	12	121,866,899	122,018,920	152,021	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1655, 2_A375_pNL97_plus_lncRNA_AR..1..2318, 4_A375_EGR1..1..2021	113672, 113960, 113176	in gene, in gene, in gene	1	1	1	25	21	15	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene KDM2B	JHDM1B, CXXC2, PCCX2, FBXL10, KDM2B, Fbl10	lysine (K)-specific demethylase 2B	NM_001005366, NM_032590, hCT18499.3, hCT2309709.0, hCT2309710.0	226215_s_at	NP_001005366.1, NP_115979.3, EAW98266.1, EAW98267.1, EAW98268.1
GeneID.54509	RHOF	12	122,215,860	122,231,594	15,934	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1656, 2_A375_pNL97_plus_lncRNA_AR..1..2319, 2_A375_pNL97_plus_lncRNA_AR..1..2320, 4_A375_EGR1..1..2022	-3542, -406, -4454, -406	upstream, upstream, upstream, upstream	1	1	1	16.67	15.33	14.67	3	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene RHOF	RIF, FLJ20247, ARHF, RHOF	ras homolog gene family, member F (in filopodia)	NM_019034, hCT10568.2, hCT2309705.0	1554538_at, 1554539_a_at, 219045_at, 219154_at, 222812_s_at, 236667_at	NP_061907.2, EAW98278.1, EAW98279.1
GeneID.338799	LOC338799	12	122,233,173	122,241,390	8,217	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1656, 2_A375_pNL97_plus_lncRNA_AR..1..2319, 2_A375_pNL97_plus_lncRNA_AR..1..2320, 4_A375_EGR1..1..2022, 4_A375_EGR1..1..2023	6254, 9390, 5342, 9390, -8962	in gene, downstream, in gene, downstream, upstream	1	1	1	16.5	14.25	15.5	4	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene LOC338799	FLJ37163	hypothetical LOC338799	NR_002809	1558042_s_at, 226369_at	
GeneID.23067	SETD1B	12	122,242,638	122,270,562	27,924	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1656, 2_A375_pNL97_plus_lncRNA_AR..1..2320, 4_A375_EGR1..1..2023	-7502, -6590, 7714	upstream, upstream, in gene	1	1	1	15	13.67	13	3	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene SETD1B	KMT2G, KIAA1076, FLJ20803, SETD1B, Set1B	SET domain containing 1B	NM_015048	213153_at	NP_055863.1
GeneID.3242	HPD	12	122,277,433	122,326,517	49,084	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1657, 2_A375_pNL97_plus_lncRNA_AR..1..2321	53, -107	in gene, upstream	1	1	0	28	21	7	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene HPD	4-HPPD, HPD, PPD, GLOD3, HPPDASE, 4HPPD	4-hydroxyphenylpyruvate dioxygenase	NM_002150, NM_001171993, hCT1957563.2, hCT9657.2	206024_at	NP_002141.1, NP_001165464.1, EAW98291.1, EAW98292.1
GeneID.5715	PSMD9	12	122,326,646	122,355,771	29,125	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1657, 2_A375_pNL97_plus_lncRNA_AR..1..2321	-182, -22	upstream, upstream	1	1	0	28	21	7	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene PSMD9	PSMD9, MGC8644, Rpn4, p27	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	NM_002813, hCT2309314.0, hCT2309315.0, hCT2309316.0, hCT2356019.0, hCT2356020.0	207805_s_at, 209334_s_at	NP_002804.2, EAW98295.1, EAW98293.1, EAW98294.1, EAW98296.1, EAW98297.1
GeneID.100506691	LOC100506691	12	122,505,987	122,506,870	883	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2322	10429	downstream	0	1	0	17	23	3	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100506691		hypothetical LOC100506691	XR_109143		
GeneID.22877	MLXIP	12	122,516,760	122,517,172	412	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2322	-344	upstream	0	1	0	17	23	3	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MLXIP	MONDOA, bHLHe36, MIR, MLXIP, KIAA0867	MLX interacting protein	NM_014938, hCT1957558.2, hCT2309320.1, hCT2309321.1	1554886_a_at, 202519_at, 211789_s_at, 225157_at	NP_055753.3, EAW98304.1, EAW98305.1, EAW98306.1
GeneID.56616	DIABLO	12	122,692,209	122,712,068	19,859	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1658, 4_A375_EGR1..1..2024	1556, 1572	in gene, in gene	1	0	1	19	14	17	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene DIABLO	FLJ10537, FLJ25049, SMAC, DIABLO, DIABLO-S, SMAC3	diablo homolog (Drosophila)	NM_019887, NM_138929, NR_024600, NR_024601	219350_s_at	NP_063940.1, NP_620307.1
GeneID.65082	VPS33A	12	122,716,094	122,751,068	34,974	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1658, 1_A375_pNL7_minus_lncRNA_AR..1..1659, 2_A375_pNL97_plus_lncRNA_AR..1..2323, 4_A375_EGR1..1..2024, 4_A375_EGR1..1..2025	40556, -4, 124, 40572, 444	downstream, upstream, in gene, downstream, in gene	1	1	1	23.5	20.5	17.5	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene VPS33A	FLJ23187, FLJ22395, VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	NM_022916	204590_x_at, 244400_at	NP_075067.2
GeneID.6249	CLIP1	12	122,755,981	122,907,116	151,135	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1659, 2_A375_pNL97_plus_lncRNA_AR..1..2323, 4_A375_EGR1..1..2025	156044, 156172, 156492	downstream, downstream, downstream	1	1	1	28	27	18	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene CLIP1	CLIP-170, MGC131604, RSN, CLIP170, CLIP, CLIP1, CYLN1	CAP-GLY domain containing linker protein 1	NM_002956, NM_198240, hCT2309714.0, hCT2309715.0, hCT2309716.0, hCT2309718.0	1556924_s_at, 1566012_at, 201975_at, 210716_s_at, 240444_x_at	NP_002947.1, NP_937883.1, EAW98320.1, EAW98321.1, EAW98322.1, EAW98323.1
GeneID.8562	DENR	12	123,237,371	123,255,953	18,582	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2324, 4_A375_EGR1..1..2026	5, -27	in gene, upstream	0	1	1	15	18	28	1	4_A375_EGR1..1	28	Gene DENR	DRP1, DRP, SMAP-3, DENR	density-regulated protein	NM_003677, hCT2349948.0, hCT2349949.0, hCT2356050.0, hCT2356051.0, hCT2356052.0, hCT24384.4	221509_at, 231896_s_at, 234347_s_at, 234915_s_at	NP_003668.2, EAW98341.1, EAW98339.1, EAW98340.1, EAW98342.1, EAW98343.1, EAW98338.1
GeneID.9026	HIP1R	12	123,320,039	123,347,507	27,468	+	2	4_A375_EGR1..1..2027, 4_A375_EGR1..1..2028	19897, 24025	in gene, in gene	0	0	1	8.5	5.5	17	2	4_A375_EGR1..1	17	Gene HIP1R	KIAA0655, ILWEQ, FLJ27022, HIP12, HIP3, MGC47513, HIP1R, FLJ14000	huntingtin interacting protein 1 related	NM_003959, hCT1821119.2, hCT24376.3	209559_at	NP_003950.1, EAW98346.1, EAW98347.1
GeneID.79720	VPS37B	12	123,349,875	123,380,712	30,837	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1660, 2_A375_pNL97_plus_lncRNA_AR..1..2325, 4_A375_EGR1..1..2027, 4_A375_EGR1..1..2028	-24, -88, 40776, 36848	upstream, upstream, downstream, downstream	1	1	1	14.67	14	15	3	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene VPS37B	VPS37B, FLJ12750	vacuolar protein sorting 37 homolog B (S. cerevisiae)	NM_024667, hCT1963699.1, hCT1963700.1, hCT2309220.0, hCT24379.2	221704_s_at	NP_078943.1, EAW98348.1, EAW98349.1, EAW98350.1, EAW98351.1
GeneID.23457	ABCB9	12	123,413,539	123,459,752	46,213	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1661, 1_A375_pNL7_minus_lncRNA_AR..1..1662, 2_A375_pNL97_plus_lncRNA_AR..1..2326, 2_A375_pNL97_plus_lncRNA_AR..1..2327, 4_A375_EGR1..1..2029, 4_A375_EGR1..1..2030	30376, 477, 30600, 456, -4952, -6744	in gene, in gene, in gene, in gene, upstream, upstream	1	1	1	19.75	20	12.5	4	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene ABCB9	ABCB9, hABCB9, KIAA1520, TAPL, EST122234	ATP-binding cassette, sub-family B (MDR/TAP), member 9	NM_203444, NM_019625, NM_019624, hCT1821103.3, hCT2309208.1, hCT2309209.1, hCT2309210.0, hCT2309211.0, hCT2309212.1, hCT2309214.1, hCT2343838.0, hCT2343839.0, hCT2356049.0, hCT24383.4	1555323_at, 207321_s_at, 214209_s_at	NP_982269.1, NP_062571.1, NP_062570.1, EAW98353.1, EAW98354.1, EAW98356.1, EAW98355.1, EAW98358.1, EAW98357.1, EAW98359.1, EAW98360.1, EAW98361.1, EAW98362.1, EAW98363.1
GeneID.79676	OGFOD2	12	123,459,354	123,464,588	5,234	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1662, 2_A375_pNL97_plus_lncRNA_AR..1..2327, 4_A375_EGR1..1..2029, 4_A375_EGR1..1..2030	-79, -58, 5350, 7142	upstream, upstream, downstream, downstream	1	1	1	16.67	19.67	14	3	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene OGFOD2	OGFOD2, DKFZp686H15154, MGC120434, FLJ13491, MGC120436, FLJ37501	2-oxoglutarate and iron-dependent oxygenase domain containing 2	NM_024623, hCT2308155.0, hCT2356008.0, hCT2356009.0, hCT2356010.0, hCT2356011.0, hCT2356012.0, hCT2356013.0, hCT2356014.0, hCT24381.2	219245_s_at, 219246_s_at, 44617_at	NP_078899.1, EAW98367.1, EAW98364.1, EAW98365.1, EAW98371.1, EAW98372.1, EAW98366.1, EAW98368.1, EAW98369.1, EAW98370.1
GeneID.51329	ARL6IP4	12	123,464,880	123,467,460	2,580	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1662, 2_A375_pNL97_plus_lncRNA_AR..1..2327, 4_A375_EGR1..1..2029, 4_A375_EGR1..1..2030	-5605, -5584, -176, 1616	upstream, upstream, upstream, in gene	1	1	1	16.67	19.67	14	3	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene ARL6IP4	SRp37, SFRS20, SRp25, SR-25, ARL6IP4, MGC814	ADP-ribosylation-like factor 6 interacting protein 4	NM_001002252, NM_016638, NM_001002251, NM_018694, hCT1821108.2, hCT2308128.0, hCT2308129.0, hCT2308130.0, hCT2308131.0, hCT2308132.0, hCT2308134.0, hCT2308135.0, hCT2357994.0, hCT24373.2	218216_x_at, 220597_s_at	NP_001002252.1, NP_057722.2, NP_001002251.1, NP_061164.2, EAW98378.1, EAW98381.1, EAW98373.1, EAW98374.1, EAW98375.1, EAW98376.1, EAW98377.1, EAW98379.1, EAW98380.1, EAW98382.1
GeneID.57605	PITPNM2	12	123,468,027	123,594,975	126,948	-	7	1_A375_pNL7_minus_lncRNA_AR..1..1662, 1_A375_pNL7_minus_lncRNA_AR..1..1663, 2_A375_pNL97_plus_lncRNA_AR..1..2327, 2_A375_pNL97_plus_lncRNA_AR..1..2328, 2_A375_pNL97_plus_lncRNA_AR..1..2329, 4_A375_EGR1..1..2029, 4_A375_EGR1..1..2030	135700, 20575, 135679, 24511, 20703, 130271, 126479	downstream, in gene, downstream, in gene, in gene, downstream, downstream	1	1	1	18	19	11	5	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene PITPNM2	PITPNM2, RDGBA2, KIAA1457, RDGB2, NIR3	phosphatidylinositol transfer protein, membrane-associated 2	NM_020845, hCT2309204.0, hCT2309205.0, hCT2309206.0, hCT24380.3	1552923_a_at, 1552924_a_at, 232950_s_at	NP_065896.1, EAW98386.1, EAW98383.1, EAW98384.1, EAW98385.1
GeneID.100507091	LOC100507091	12	123,565,931	123,569,291	3,360	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1663, 2_A375_pNL97_plus_lncRNA_AR..1..2328, 2_A375_pNL97_plus_lncRNA_AR..1..2329	8469, 4533, 8341	downstream, downstream, downstream	1	1	0	17	18	6.5	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene LOC100507091		hypothetical LOC100507091	XR_111356, XR_109101, XR_114628		
GeneID.10198	MPHOSPH9	12	123,640,946	123,706,441	65,495	-	1	4_A375_EGR1..1..2031	71593	downstream	0	0	1	6	9	18	1	4_A375_EGR1..1	18	Gene MPHOSPH9	MPP9, MPP-9, FLJ12954, MPHOSPH9, DKFZp434J034	M-phase phosphoprotein 9	NM_022782, hCT2309197.1, hCT2309198.2, hCT2309199.1, hCT2309200.1, hCT2309201.1, hCT2309202.1, hCT2357969.0	1558369_at, 206205_at, 215731_s_at, 221965_at, 237156_s_at	NP_073619.2, EAW98394.1, EAW98388.1, EAW98389.1, EAW98391.1, EAW98392.1, EAW98390.1, EAW98393.1
GeneID.91574	C12orf65	12	123,717,844	123,742,506	24,662	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1665, 2_A375_pNL97_plus_lncRNA_AR..1..2330, 4_A375_EGR1..1..2032, 4_A375_EGR1..1..2033, 4_A375_EGR1..1..2034	-212, -297, -356, 428, 33516	upstream, upstream, upstream, in gene, downstream	1	1	1	14.67	15.67	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene C12orf65	FLJ38663, C12orf65, COXPD7	chromosome 12 open reading frame 65	NM_001143905, NM_152269, NM_001194995, hCT2308139.0, hCT2308140.0	223476_s_at, 223477_s_at, 232650_at	NP_001137377.1, NP_689482.1, NP_001181924.1, EAW98395.1, EAW98396.1
GeneID.8099	CDK2AP1	12	123,745,538	123,756,687	11,149	-	2	4_A375_EGR1..1..2034, 4_A375_EGR1..1..2035	5327, 3535	in gene, in gene	0	0	1	9	9.5	18	2	4_A375_EGR1..1	18	Gene CDK2AP1	ST19, p12DOC-1, doc-1, CDK2AP1, DOC1, DORC1	cyclin-dependent kinase 2 associated protein 1	NM_004642, hCT2309193.0, hCT2309194.0, hCT2309195.0	201938_at	NP_004633.1, EAW98398.1, EAW98399.1, EAW98400.1
GeneID.196383	RILPL2	12	123,899,936	123,921,264	21,328	-	1	4_A375_EGR1..1..2036	366	in gene	0	0	1	14	11	16	1	4_A375_EGR1..1	16	Gene RILPL2	RILPL2, FLJ32372, MGC7036, FLJ30380	Rab interacting lysosomal protein-like 2	NM_145058, hCT85197.3	227983_at	NP_659495.1, EAW98411.1
GeneID.10959	TMED2	12	124,069,076	124,082,888	13,812	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1666, 1_A375_pNL7_minus_lncRNA_AR..1..1667, 2_A375_pNL97_plus_lncRNA_AR..1..2331, 2_A375_pNL97_plus_lncRNA_AR..1..2332, 4_A375_EGR1..1..2037	-84, 17420, -20, 17452, 17516	upstream, downstream, upstream, downstream, downstream	1	1	1	30.5	35	19	2	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene TMED2	FLJ21323, RNP24, P24A, TMED2	transmembrane emp24 domain trafficking protein 2	NM_006815, hCT1781766.2, hCT2336930.0	200087_s_at, 204426_at, 204427_s_at	NP_006806.1, EAW98417.1, EAW98418.1
GeneID.100507130	LOC100507130	12	124,082,395	124,100,564	18,169	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1667, 2_A375_pNL97_plus_lncRNA_AR..1..2332, 4_A375_EGR1..1..2037	14068, 14036, 13972	in gene, in gene, in gene	1	1	1	28	25	28	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene LOC100507130		hypothetical LOC100507130	XR_109103, XR_114630		
GeneID.57696	DDX55	12	124,086,672	124,105,482	18,810	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1667, 2_A375_pNL97_plus_lncRNA_AR..1..2332, 4_A375_EGR1..1..2037	-176, -144, -80	upstream, upstream, upstream	1	1	1	28	25	28	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene DDX55	MGC33209, KIAA1595, DDX55, FLJ16577	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	NM_020936, hCT2336931.0, hCT2336932.0, hCT2336933.0, hCT2356152.0, hCT2356153.0	231843_at	NP_065987.1, EAW98422.1, EAW98419.1, EAW98420.1, EAW98421.1, EAW98423.1
GeneID.1967	EIF2B1	12	124,105,570	124,118,323	12,753	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1668, 2_A375_pNL97_plus_lncRNA_AR..1..2333	147, 147	in gene, in gene	1	1	0	21	32	13	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene EIF2B1	MGC125868, EIF2B1, MGC117409, EIF2BA, MGC125869, EIF2B	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa	NM_001414, hCT1625252.2, hCT1966872.1	201632_at	NP_001405.1, EAW98425.1, EAW98424.1
GeneID.2967	GTF2H3	12	124,118,361	124,145,334	26,953	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1668, 2_A375_pNL97_plus_lncRNA_AR..1..2333	-205, -205	upstream, upstream	1	1	0	21	32	13	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene GTF2H3	GTF2H3, TFB4, BTF2, TFIIH	general transcription factor IIH, polypeptide 3, 34kDa	NM_001516, hCT2336938.0, hCT2336937.0, hCT2336939.0, hCT2336940.0	222104_x_at	NP_001507.2, EAW98426.1, EAW98427.1, EAW98428.1, EAW98429.1
GeneID.79867	TCTN2	12	124,155,660	124,192,948	37,288	+	1	4_A375_EGR1..1..2038	-12	upstream	0	0	1	9	13	16	1	4_A375_EGR1..1	16	Gene TCTN2	C12orf38, TCTN2, MKS8, TECT2, FLJ12975	tectonic family member 2	NM_024809, NM_001143850	208438_x_at, 239928_at	NP_079085.2, NP_001137322.1
GeneID.144347	FAM101A	12	124,773,710	124,800,566	26,856	+	3	2_A375_pNL97_plus_lncRNA_AR..1..2335, 4_A375_EGR1..1..2039, 4_A375_EGR1..1..2040	642, 18162, 19762	in gene, in gene, in gene	0	1	1	7.33	13	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene FAM101A	FAM101A, FLJ44614	family with sequence similarity 101, member A	NM_181709, hCT16429.3	227320_at	NP_859060.3, EAW98447.1
GeneID.9612	NCOR2	12	124,808,961	125,052,010	243,049	-	12	1_A375_pNL7_minus_lncRNA_AR..1..1669, 2_A375_pNL97_plus_lncRNA_AR..1..2336, 2_A375_pNL97_plus_lncRNA_AR..1..2337, 4_A375_EGR1..1..2041, 4_A375_EGR1..1..2042, 4_A375_EGR1..1..2043, 4_A375_EGR1..1..2044, 4_A375_EGR1..1..2045, 4_A375_EGR1..1..2046, 4_A375_EGR1..1..2047, 4_A375_EGR1..1..2048, 4_A375_EGR1..1..2049	-374, 714, -342, 232266, 225578, 207530, 203338, 170746, 161706, 86106, 66858, 25322	upstream, in gene, upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	8.82	11.73	15.64	11	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene NCOR2	TRAC-1, SMRTE, FLJ25011, CTG26, NCOR2, SMRTE-tau, SMRT, TNRC14, TRAC1	nuclear receptor co-repressor 2	NM_001077261, NM_006312, hCT16428.3, hCT1962322.1, hCT1962323.1, hCT2336974.0, hCT2336976.0, hCT2336977.0	207760_s_at, 208868_s_at, 208869_s_at, 215205_x_at	NP_001070729.1, NP_006303.3, EAW98448.1, EAW98449.1, EAW98452.1, EAW98453.1, EAW98450.1, EAW98451.1
GeneID.100288312	LOC100288312	12	125,394,083	125,397,359	3,276	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1671, 1_A375_pNL7_minus_lncRNA_AR..1..1672, 2_A375_pNL97_plus_lncRNA_AR..1..2341, 4_A375_EGR1..1..2052, 4_A375_EGR1..1..2053	5245, 7773, 5341, 5181, 12253	downstream, downstream, downstream, downstream, downstream	1	1	1	29	25	16	3	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene LOC100288312		hypothetical LOC100288312	XR_109105, XR_109104		
GeneID.7316	UBC	12	125,396,192	125,399,577	3,385	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1671, 1_A375_pNL7_minus_lncRNA_AR..1..1672, 2_A375_pNL97_plus_lncRNA_AR..1..2341, 4_A375_EGR1..1..2052, 4_A375_EGR1..1..2053	249, -2279, 153, 313, -6759	in gene, upstream, in gene, in gene, upstream	1	1	1	29	25	16	3	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene UBC	UBC, HMG20	ubiquitin C	NM_021009, hCT1782398.3, hCT2308461.1, hCT2308464.1, hCT2343716.0	208980_s_at, 211296_x_at	NP_066289.2, EAW98463.1, EAW98464.1, EAW98465.1, EAW98466.1
GeneID.57647	DHX37	12	125,431,372	125,473,667	42,295	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1674, 4_A375_EGR1..1..2055, 4_A375_EGR1..1..2056	48227, 49427, 36891	downstream, downstream, in gene	1	0	1	17	13	19.67	3	4_A375_EGR1..1	25	Gene DHX37	MGC2695, DHX37, DDX37, FLJ41974, MGC46245, KIAA1517, MGC4322	DEAH (Asp-Glu-Ala-His) box polypeptide 37	NM_032656, hCT1955088.1, hCT2308448.0, hCT2308451.0	223384_s_at, 223385_at	NP_116045.2, EAW98468.1, EAW98467.1, EAW98469.1
GeneID.114795	TMEM132B	12	125,811,162	126,143,589	332,427	+	1	4_A375_EGR1..1..2057	23558	in gene	0	0	1	2	3	15	1	4_A375_EGR1..1	15	Gene TMEM132B	KIAA1906, TMEM132B, KIAA1786	transmembrane protein 132B	NM_052907, hCT1645157.3, hCT2348822.1, hCT24056.5	1563468_at, 236824_at	NP_443139.2, EAW98476.1, EAW98477.1, EAW98478.1
GeneID.144423	GLT1D1	12	129,338,081	129,469,509	131,428	+	1	4_A375_EGR1..1..2058	116511	in gene	0	0	1	2	6	16	1	4_A375_EGR1..1	16	Gene GLT1D1	FLJ31978, GLT1D1	glycosyltransferase 1 domain containing 1	NM_144669, hCT1645058.2, hCT2357958.0	229770_at	NP_653270.1, EAW98496.1, EAW98497.1
GeneID.121256	TMEM132D	12	129,556,271	130,388,212	831,941	-	1	4_A375_EGR1..1..2059	532	in gene	0	0	1	2	3	15	1	4_A375_EGR1..1	15	Gene TMEM132D	TMEM132D, MOLT, MGC138771, KIAA1944, MGC138770	transmembrane protein 132D	NM_133448, hCT2308078.0	236377_at	NP_597705.2, EAW98500.1
GeneID.440119	FLJ31485	12	130,636,138	130,646,223	10,085	-	2	4_A375_EGR1..1..2060, 4_A375_EGR1..1..2061	719, -3505	in gene, upstream	0	0	1	2	3.5	13	2	4_A375_EGR1..1	13	Gene FLJ31485	FLJ41644, FLJ31719	hypothetical LOC440119	NR_033834	239569_at, 243351_at	
GeneID.11211	FZD10	12	130,647,032	130,650,285	3,253	+	2	4_A375_EGR1..1..2060, 4_A375_EGR1..1..2061	-1526, 2696	upstream, in gene	0	0	1	2	3.5	13	2	4_A375_EGR1..1	13	Gene FZD10	CD350, hFz10, FZD10, Fz10, FzE7, FZ-10	frizzled homolog 10 (Drosophila)	NM_007197, hCT12466.3	219764_at	NP_009128.1, EAW98507.1
GeneID.5901	RAN	12	131,356,617	131,360,826	4,209	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2349	-489	upstream	0	1	0	11	15	13	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene RAN	TC4, Gsp1, ARA24, RAN	RAN, member RAS oncogene family	NM_006325, hCT1782813.3, hCT2308101.1, hCT2308103.1	200749_at, 200750_s_at	NP_006316.1, EAW98516.1, EAW98515.1, EAW98517.1
GeneID.283383	GPR133	12	131,438,452	131,626,010	187,558	+	7	1_A375_pNL7_minus_lncRNA_AR..1..1681, 2_A375_pNL97_plus_lncRNA_AR..1..2350, 2_A375_pNL97_plus_lncRNA_AR..1..2351, 4_A375_EGR1..1..2062, 4_A375_EGR1..1..2063, 4_A375_EGR1..1..2064, 4_A375_EGR1..1..2065	90924, 29996, 91180, 151724, 177356, 184652, 185036	in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	9.17	12	14.17	6	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene GPR133	GPR133, MGC138512, MGC138514, FLJ16770, PGR25, DKFZp434B1272	G protein-coupled receptor 133	NM_198827	232267_at	NP_942122.2
GeneID.100128640	LOC100128640	12	131,472,857	131,474,573	1,716	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2350	6125	downstream	0	1	0	12	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100128640		hypothetical LOC100128640	XR_111360, XR_109110, XR_114635		
GeneID.338797	LOC338797	12	131,850,570	131,851,069	499	+	1	4_A375_EGR1..1..2067	2806	downstream	0	0	1	6	4	16	1	4_A375_EGR1..1	16	Gene LOC338797		hypothetical LOC338797	XR_111362, XR_109112, XR_114636		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Starts	Interval Ends	1_A375_2_A375_uNG7_myUG7_all_lncRNA_lncRNA_R_1 Percent	2_A375_2_A375_NG7_myUG7_all_lncRNA_lncRNA_R_1 Percent	4_A375_2_A375_EGR1_lncRNA_R_1 Percent	1_A375_2_A375_NG7_myUG7_all_lncRNA_lncRNA_R_1 Avg Reads	2_A375_2_A375_UG7_myUG7_all_lncRNA_lncRNA_R_1 Avg Reads	4_A375_2_A375_EGR1_lncRNA_R_1 Avg Reads	Ad Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:84	SFRS8	12	132,199,655	132,256,202	56,547	+	7	1_A375_uNG7_myuni_lncRNA_NR_1:1663, 1_A375_uNG7_myuni_lncRNA_NR_1:1664, 1_A375_uNG7_dlucl_lncRNA_NR_1:2353, 1_A375_uNG7_dlucl_lncRNA_NR_1:2354, 2_A375_uNG7_dlucl_lncRNA_NR_1:2355, 2_A375_EGR1_1:2076, 4_A375_EGR1_1:2071	147, 12741, 19, 7310:2, 74351, 8951, 76372	12741, 19, 7310:2, 74351, 8951, 76372	splicesom, cg gene, splicesom, u gene, splicesom, u gene	1	1	1	13.2	16	10	5	2_A375_uNG7_dlucl_lncRNA_NR_1	0.26	SFRS8	SRAP, SFRS8, SFSRAP, WGC167082	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	NM_004592, XCT1936001.1, XCT2352211.0	202773_s_at, 202774_s_at, 202775_s_at, 243078_at	NP_004583.2, EAW66326.1, EAW66327.1
GeneID:45	MMP17	12	132,312,941	132,338,316	25,376	+	3	1_A375_uNG7_dlucl_lncRNA_NR_1:1665, 2_A375_uNG7_dlucl_lncRNA_NR_1:2356, 4_A375_EGR1_1:2072	-109, -125, 24082	splicesom, upstream, downstream	1	1	1	22	17	9.5	2	1_A375_uNG7_dlucl_lncRNA_NR_1	0.33	MMP17	MMP17, MT4-MMP	matrix metallopeptidase 17 (membrane-inserted)	NM_016155, XCT227922.0	236224_s_at	NP_057239.4, EAW66328.1
GeneID:84	ULK1	12	132,379,279	132,407,707	28,428	+	5	4_A375_EGR1_1:2074, 4_A375_EGR1_1:2075, 4_A375_EGR1_1:2076, 4_A375_EGR1_1:2077, 4_A375_EGR1_1:2078	1073, 7473, 21009, 23121, 23673	sr gene, cr gene, us gene, downstream	0	0	1	9.4	8.2	10	5	4_A375_EGR1_1.1	0.24	ULK1	Unc51.1, FLJ38455, ULK1, ATG1A, FLJ44673, UNC51.ATG1	unc-51-like kinase 1 (C. elegans)	NM_003565, XCT1782678.2	330333_at	NP_003564.1, EAW66329.1
GeneID:83	FUS1	12	132,413,743	132,428,408	14,666	+	1	4_A375_EGR1_1:2079	1007	sr gene	0	0	1	12	8	24	1	4_A375_EGR1_1.1	0.24	FUS1	MGC11286, FUS1, HNASH1	phosphoacetylsphingosine synthase 1	NM_001030019, NM_025013, NM_001030020, XCT1782762.2, XCT2350187.0, XCT2350188.0, XCT2350190.0	2116870_at	NP_001030191.1, NP_079491.2, NP_001030020.1, EAW66330.1, EAW66331.1, EAW66332.1, EAW66332.1
GeneID:37	EPS00	12	132,436,555	132,568,005	130,497	+	1	4_A375_EGR1_1:2080	113626	sr gene	0	0	1	5	6	17	1	4_A375_EGR1_1.1	0.17	EPS00	EPS00, EPS00L1, EPS00L2, DKFZp434Q225, PK56, FLJ42015, FLJ45115	EPS15 (c-ab) binding protein p00	NM_015039, XCT2351177.0, XCT2350116.0, XCT2350119.0	212379_at, 212380_s_at, 230826_at, 230829_s_at	NP_359824.2, EAW66333.1, EAW66334.1, EAW66336.1
GeneID:31	DDX51	12	132,821,139	132,838,590	17,741	-	5	1_A375_uNG7_dlucl_lncRNA_NR_1:1668, 1_A375_uNG7_dlucl_lncRNA_NR_1:2357, 4_A375_EGR1_1:2080, 4_A375_EGR1_1:2081, 4_A375_EGR1_1:2082	-112, -32, 10256, 2976, -3152	splicesom, upstream, downstream, u gene, upstream	1	1	1	10.75	12.5	16.5	4	2_A375_uNG7_dlucl_lncRNA_NR_1	0.27	DDX51	DKFZp686N2051, DDX51, MGC42195	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	NM_170696, XCT57975.3	1554653_at, 214968_at, 229462_at	NP_775738.2, EAW66343.1
GeneID:79	NOCA1	12	132,838,993	132,839,168	7,993	+	4	1_A375_uNG7_myuni_lncRNA_NR_1:1669, 2_A375_uNG7_dlucl_lncRNA_NR_1:2357, 4_A375_EGR1_1:2081, 4_A375_EGR1_1:2082	-1, -91, -3189, 3029	splicesom, upstream, upstream, sr gene	1	1	1	12.33	13.67	18.33	3	2_A375_uNG7_dlucl_lncRNA_NR_1	0.27	NOCA1, MGC3182, NIST49, NOC4	eukaryotic complex associated 4 homolog (S. cerevisiae)	NM_030776, XCT1967481.1, XCT60123.2	2188661_at	NP_079983.1, EAW66344.1, EAW66344.1
GeneID:53	GALNT9	12	132,850,917	132,890,573	39,656	+	6	4_A375_EGR1_1:2085, 4_A375_EGR1_1:2087, 4_A375_EGR1_1:2088, 4_A375_EGR1_1:2089, 4_A375_EGR1_1:2090, 4_A375_EGR1_1:2092	9581, 71409, 78935, 85407, 41661, 10529, 289, -8079	splicesom, sr gene, u gene, cr gene, u gene, cr gene, upstream	0	0	1	8.13	8.5	10.83	6	4_A375_EGR1_1.1	0.23	GALNT9	GALNAC-T9, GALNT9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 (GalNAc-T9)	NM_021539, NM_001128256	229451_at	NP_596350.2, NP_001118706.1
GeneID:10	LOC1002	12	132,859,977	132,887,498	5,529	+	1	4_A375_EGR1_1:2090	12247	downstream	0	0	1	8	10	17	1	4_A375_EGR1_1.1	0.17	Gene LOC100130235		hypothetical LOC100130235	NR_024365		
GeneID:10	LOC1002	12	132,859,022	132,938,810	1,866	+	3	4_A375_EGR1_1:2102, 4_A375_EGR1_1:2103, 4_A375_EGR1_1:2104	-7454, -4510, 7168	splicesom, upstream, downstream	0	0	1	8.67	7	16	3	4_A375_EGR1_1.1	0.20	Gene LOC100509976		hypothetical protein LOC100509976	XR_111383, XR_110102, XR_114872		
GeneID:57	FBXL51	12	132,897,157	133,161,774	64,617	+	9	4_A375_EGR1_1:2105, 4_A375_EGR1_1:2106, 4_A375_EGR1_1:2107, 4_A375_EGR1_1:2108, 4_A375_EGR1_1:2109, 4_A375_EGR1_1:2110, 4_A375_EGR1_1:2111, 4_A375_EGR1_1:2112, 4_A375_EGR1_1:2114	5211, 7891, 9520, 18619, 16155, 29845, 59851, 72860, 93179	sr gene, cr gene, us gene, sr gene, cr gene, us gene, downstream	0	0	1	6.33	5.89	17.56	9	4_A375_EGR1_1.1	0.26	Gene FBXL51	KIAA1545, FBXL51	F-box-like 1	NM_031142641	225703_at, 225704_at	NP_001139115.1
GeneID:10	LOC1002	12	132,898,205	133,097,454	1,276	+	3	4_A375_EGR1_1:2105, 4_A375_EGR1_1:2109, 4_A375_EGR1_1:2110	-9725, -2432, -596	splicesom, upstream, upstream	0	0	1	9	7	16	3	4_A375_EGR1_1.1	0.19	Gene LOC100509998		hypothetical protein LOC100509998	XM_003116935		XP_003116983.1
GeneID:10	LOC1002	12	133,127,764	133,131,333	3,749	+	2	4_A375_EGR1_1:2112, 4_A375_EGR1_1:2113	-778, 12933	splicesom, downstream	0	0	1	5	4.5	13.5	2	4_A375_EGR1_1.1	0.18	Gene LOC100507023		hypothetical protein LOC100507023	XM_003119585, XM_003119586, XM_003120787		XP_003119633.1, XP_003120933.1
GeneID:10	LOC1002	12	133,179,754	133,198,560	7,249	-	1	4_A375_EGR1_1:2115	8650	sr gene	0	0	1	8	10	22	1	4_A375_EGR1_1.1	0.22	Gene LOC100507035		arachidonate 5-lipoxygenase-activating protein LOC643774-like	XM_003119548, XM_003119565, XM_003119587, XM_003119588, XM_003120790, XM_003120799		XP_003119581.1, XP_003119582.1, XP_003119583.1, XP_003119584.1, XP_003120907.1
GeneID:54	POLE	12	133,200,343	133,280,943	80,597	+	2	1_A375_uNG7_myuni_lncRNA_NR_1:1667, 2_A375_uNG7_dlucl_lncRNA_NR_1:2358	-55, -138	splicesom, upstream	1	1	0	34	26	1	1	1_A375_uNG7_myuni_lncRNA_NR_1	0.34	Gene POLE	DKFZp434P222, FLJ27434, POLE, POLE1	polymerase (DNA directed), epsilon	NM_006231, XCT1993438.1, XCT2355109.0, XCT2355110.0, XCT2355112.0, XCT2352577.0	1561940_at, 218026_s_at	NP_006222.2, EAW66336.1, EAW66337.1, EAW66338.1, EAW66339.1, EAW66332.1
GeneID:56	PXMP2	12	133,256,192	133,281,577	17,385	+	5	1_A375_uNG7_myuni_lncRNA_NR_1:1667, 1_A375_uNG7_myuni_lncRNA_NR_1:1668, 1_A375_uNG7_dlucl_lncRNA_NR_1:2355, 1_A375_uNG7_dlucl_lncRNA_NR_1:2359, 4_A375_EGR1_1:2116	-102, 22372, -112, 23656, 23500	splicesom, downstream, splicesom, downstream, downstream	1	1	1	25	23	9.5	2	1_A375_uNG7_dlucl_lncRNA_NR_1	0.34	Gene PXMP2	PXMP2, FLJ39322, PMP22	peroxisomal membrane protein 2, 22kDa	NM_018663, XCT1627542.2, XCT2352248.0	210976_s_at	NP_061133.1, EAW66326.1, EAW66429.1
GeneID:19	PSAN8	12	133,287,293	133,299,223	11,930	+	3	1_A375_uNG7_myuni_lncRNA_NR_1:1668, 1_A375_uNG7_dlucl_lncRNA_NR_1:2359, 4_A375_EGR1_1:2118	-129, -113, -431	splicesom, splicesom, upstream	1	1	1	16	16	16	1	4_A375_EGR1_1.1	0.16	Gene PSAN8	MGC43332, PSAN8, BXLB(HS)	phosphoglycerate mutase family member 3	NM_031178843, NM_001170844, NM_133570.3, XCT1627346.4, XCT2350916.0, XCT2352917.0	1553837_at, 1559842_at	NP_001164314.1, NP_001164315.1, NP_612642.2, EAW66325.1, EAW66326.1, EAW66327.1
GeneID:23	ANKLE2	12	133,332,254	133,338,451	99,197	+	1	1_A375_uNG7_myuni_lncRNA_NR_1:1669	-461	upstream	1	2	0	16	11	10	1	1_A375_uNG7_dlucl_lncRNA_NR_1	0.16	Gene ANKLE2	LEM27, KIAA0862, FLJ90152, ANKLE2, FLJ22350	ankyrin repeat and LEM domain containing 2	NM_015114	212200_at, 212201_at, 212982_x_at	NP_056929.1
GeneID:20	GOLGA3	12	133,343,453	133,408,426	99,931	-	5	1_A375_uNG7_myuni_lncRNA_NR_1:1670, 1_A375_uNG7_dlucl_lncRNA_NR_1:2360, 4_A375_EGR1_1:2117, 4_A375_EGR1_1:2118, 4_A375_EGR1_1:2119	66514, -110, 44893, 39730, 33042	downstream, upstream, sr gene, u gene, cr gene, u gene	1	1	1	9.8	10.6	13.8	5	2_A375_uNG7_dlucl_lncRNA_NR_1	0.24	Gene GOLGA3	GOLGA3, MEA-2 GCP170	golgi autoantigen, golgin subfamily a, 3	NM_005895, NM_001172537, XCT1932512.2, XCT2355104.0, XCT2352571.0, XCT2352572.0	1554667_at, 202108_at, 229643_at	NP_005886.2, NP_001166002.1, EAW64817.1, EAW64818.1, EAW64819.1, EAW64820.1
GeneID:33	CHPF	12	133,418,956	133,464,204	47,249	-	2	1_A375_uNG7_myuni_lncRNA_NR_1:1671, 2_A375_uNG7_dlucl_lncRNA_NR_1:2361	-299, -340	splicesom, upstream	1	1	0	17	14	10	1	1_A375_uNG7_myuni_lncRNA_NR_1	0.17	Gene CHPF	FLJ10799, CHPF, MGC13348, RHP198, FLJ38629, RHP198	chondroitin sulfate N-acetylgalactosaminyltransferase 1	NM_001161544, NM_001161545, NM_001161546, NM_001161547, XCT1932334.4, XCT1998977.1, XCT2350919.0, XCT2350101.0, XCT2352986.0, XCT2352987.0, XCT2352988.0	2108824_at, 223561_s_at	NP_001154016.1, NP_001154017.1, NP_001154018.1, NP_060892.2, NP_001154019.1, EAW64810.1, EAW64809.1, EAW64811.1, EAW64812.1, EAW64813.1, EAW64814.1, EAW64815.1
GeneID:19	ZNF803	12	133,490,919	133,532,992	64,073	+	1	2_A375_uNG7_dlucl_lncRNA_NR_1:2362	60	sr gene	0	0	1	9	27	7	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.27	Gene ZNF803	DKFZp686B223, ZNF803, DKFZp434B016, FLJ16520, FLJ41957	zinc finger protein 803	NM_152232, NM_001164713		NP_689391.1, NP_001158187.1
GeneID:74	ZNF26	12	133,580,056	133,589,153	29,097	+	1	2_A375_uNG7_dlucl_lncRNA_NR_1:2363	-96	upstream	0	0	1	15	21	12	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.21	Gene ZNF26	ZNF26, FLJ20753, KOX20	zinc finger protein 26	NM_018991, XCT1993436.1, XCT2356036.0	1555323_s_at, 219593_at	NP_061857.2, EAW66503.1, EAW64934.1
GeneID:76	ZNF140	12	133,607,057	133,656,280	27,223	+	2	1_A375_uNG7_myuni_lncRNA_NR_1:1681, 2_A375_uNG7_dlucl_lncRNA_NR_1:2364	-45, 526	splicesom, sr gene	1	1	0	20	24	15	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.24	Gene ZNF140	ZNF140, HPZ-3P	zinc finger protein 140	NM_003445, XCT133322.3, XCT1997170.1, XCT2352670.0, XCT2352674.0, XCT2352678.0	204322_at, 233581_at	NP_003434.2, EAW66799.1, EAW64794.1, EAW64795.1, EAW64796.1, EAW64798.1
GeneID:44	SCG_10	12	133,696,870	133,707,039	10,169	-	1	4_A375_EGR1_1:2120	275	sr gene	0	0	1	11	13	21	1	4_A375_EGR1_1.1	0.21	Gene SCG_10/SCG2	ZNF691, LOC440122	SCG10-like 137	XR_111384, XR_110103, XR_114870	1566283_at	
GeneID:79	ZNF12	12	133,707,214	133,736,551	29,337	+	1	4_A375_EGR1_1:2120	-459	upstream	0	0	1	11	13	21	1	4_A375_EGR1_1.1	0.21	Gene ZNF12	ZNF12, KOX1	zinc finger protein 12	NM_018394, XCT1624009.2, XCT2355976.0, XCT2355979.0	214350_s_at, 229545_at, 233366_at	NP_060864.2, EAW66790.1, EAW64792.1
GeneID:10	ZNF265	12	133,737,993	133,762,856	23,703	+	1	2_A375_uNG7_dlucl_lncRNA_NR_1:2365	21	sr gene	0	0	1	10	13	11	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.23	Gene ZNF265	HZF2, ZNF265, MGC126495	zinc finger protein 265	NM_005815, NM_152643, NM_001165833, NM_001165855, NM_001165856, NM_001165857, NM_001165851, NM_001165852, NM_001165854, XCT1627972.3, XCT2352676.0, XCT2352679.0, XCT2352680.0	1553795_at, 1553796_at, 1553797_at, 209959_at, 230020_at	NP_005806.1, NP_689422.2, NP_001159355.1, NP_001159357.1, NP_001159358.1, NP_001159359.1, NP_001159353.1, NP_001159354.1, EAW64788.1, EAW64789.1, EAW64787.1, EAW64788.1, EAW64793.1
GeneID:10	TUBA3C	12	133,747,916	133,753,956	6,020	-	1	4_A375_EGR1_1:2122	-56	upstream	0	2	1	9	8	17	1	4_A375_EGR1_1.1	0.17	Gene TUBA3C	TUBA2, TUBA3D, TUBA3C, bA459E5.3	tubulin, alpha 3c	NM_006001, XCT1810853.2, XCT2218241.1	210827_x_at	NP_006182.2, EAW66211.1, EAW66210.1
GeneID:54	MPHOS	13	20,207,788	20,247,899	39,811	+	1	2_A375_uNG7_dlucl_lncRNA_NR_1:2367	788	sr gene	0	0	1	12	15	11	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.15	Gene MPHOSPH8	MPHOSPH8, TRAG, HSMPP8, MGC13271, mpp8	M-phase phosphoprotein 8	NM_017930, XCT1612642.2, XCT2314338.0, XCT2329290.0	221771_s_at, 223941_at, 227026_at, 240942_at	NP_060400.2, EAW66200.1, EAW66201.1, EAW66229.1
GeneID:58	PSPC1	13	20,244,696	20,337,863	108,167	-	1	2_A375_uNG7_dlucl_lncRNA_NR_1:2366	-69	upstream	0	1	0	9	15	6	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.16	Gene PSPC1	PSPC1, PSP1, MGC14925, DKFZp686B447	paraspeckle component 1	NM_001042414, NR_002272, XCT2314782.1, XCT2314783.1, XCT2314789.1	218371_s_at, 222981_s_at, 223612_at, 230924_at, 239724_s_at	NP_001033879.1, EAW66234.1, EAW66232.1, EAW66233.1
GeneID:82	ZMYM5	13	20,297,826	20,437,776	140,152	-	5	1_A375_uNG7_myuni_lncRNA_NR_1:1682, 1_A375_uNG7_dlucl_lncRNA_NR_1:2369, 4_A375_EGR1_1:2125	-50, -50, 112	splicesom, upstream, cr gene	1	1	1	29	34	18	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.34	Gene ZMYM5	ZNF237, MYM, ZNF237A, ZMYM5, ZNF198.1	zinc finger, MYM type 5	NM_001039535, NM_001039849, NM_001143854, XCT2314795.0, XCT2314770.0, XCT2314771.0, XCT2314775.0, XCT2314774.0, XCT2314776.0, XCT2314778.0	206852_at, 206744_s_at, 215842_x_at, 233820_s_at	NP_001034733.1, NP_001034735.1, EAW66230.1, EAW66231.1, EAW66240.1, EAW66241.1, EAW66238.1, EAW66239.1, EAW66241.1
GeneID:48	LOC4301	13	20,437,134	20,439,190	2,056	+	3	1_A375_uNG7_myuni_lncRNA_NR_1:1683, 2_A375_uNG7_dlucl_lncRNA_NR_1:2369, 4_A375_EGR1_1:2126	732, 732, 840	splicesom, sr gene, cr gene, us gene	1	1	1	29	34	18	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.34	Gene LOC430099		hypothetical LOC430099	XR_110102	2330136_at	
GeneID:77	ZMYM2	13	20,532,510	20,665,966	133,156	+	1	2_A375_uNG7_dlucl_lncRNA_NR_1:2370	-998	upstream	0	0	1	15	15	12	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.15	Gene ZMYM2	ZNF198, SCLL, MYM, ZMYM2, RAMP, FIM	zinc finger, MYM type 2	NM_001100994, NM_001100995, NM_020453, XCT1932334.3, XCT2314790.0, XCT2329322.0, XCT2329323.0	202775_s_at, 210281_s_at, 210282_at	NP_001170693.1, NP_001170694.1, NP_003444.1, NP_852072.1, EAW62440.1, EAW62441.1, EAW62442.1, EAW62443.1, EAW62447.1, EAW62448.1
GeneID:27	GJA3	13	20,712,394	20,725,163	22,769	-	1	1_A375_uNG7_myuni_lncRNA_NR_1:1683	-401	upstream	1	2	0	19	11	10	1	1_A375_uNG7_myuni_lncRNA_NR_1	0.19	Gene GJA3	CZP3, GJA3, CX46	gap junction protein, alpha 3, 46kDa	NM_021954, XCT1573.1	206560_s_at, 233672_at	NP_068773.2, EAW66251.1
GeneID:53	CRYL1	13	20,977,809	21,100,012	122,208	-	2	2_A375_uNG7_dlucl_lncRNA_NR_1:2371, 2_A375_uNG7_dlucl_lncRNA_NR_1:2372	108740, -484	sr gene, upstream	0	1	0	15	17.5	8.5	2	2_A375_uNG7_dlucl_lncRNA_NR_1	0.16	Gene CRYL1	lambda-CRY, MGC14925, CRYL1, DKFZp686E1926, GS41	crystallin, lambda 1	NM_013974, XCT1574.3, XCT1618114.1, XCT2314783.0, XCT2314785.0, XCT2314786.0, XCT2314790.0, XCT2314740.0	2207833_s_at	NP_039258.2, EAW66260.1, EAW66261.1, EAW66262.1, EAW66263.1, EAW66264.1
GeneID:22	NBAT2	13	21,203,072	21,246,057	44,984	-	5	1_A375_uNG7_myuni_lncRNA_NR_1:1684, 2_A375_uNG7_dlucl_lncRNA_NR_1:2373, 4_A375_EGR1_1:2128	249, -71, 23	sr gene, splicesom, cr gene	1	1	1	16	16	20	1	4_A375_EGR1_1.1	0.20	Gene NBAT2	NBAT2, ESP13	N(6)-adenosine-specific DNA methyltransferase 2 (putative)	NM_174933, XCT1618116.2, XCT1998358.1, XCT2352564.4, XCT2359115.0	2227054_at	NP_777555.1, EAW63279.1, EAW63277.1, EAW63276.1, EAW66260.1
GeneID:84	XPO4	13	21,251,466	21,476,913	139,448	+	3	1_A375_uNG7_myuni_lncRNA_NR_1:1684, 2_A375_uNG7_dlucl_lncRNA_NR_1:2373, 4_A375_EGR1_1:2129	139103, 132053, 126661	downstream, downstream, downstream	1	1	1	16	16	20	1	4_A375_EGR1_1.1	0.20	Gene XPO4	XPO4, IPAK1735, FLJ13049	exportin 4	NM_022459, XCT1612978.3, XCT2352538.0, XCT2352539.0	2116479_s_at, 222849_at	NP_071903.4, EAW63262.1, EAW63263.1
GeneID:24	LATS2	13	21,347,175	21,835,702	488,547	+	3	1_A375_uNG7_myuni_lncRNA_NR_1:1685, 2_A375_uNG7_myuni_lncRNA_NR_1:1686, 2_A375_uNG7_dlucl_lncRNA_NR_1:2374	1168, 138, 74	sr gene, cr gene, us gene	1	1	1	17	13.5	7	2	1_A375_uNG7_myuni_lncRNA_NR_1	0.16	Gene LATS2	FLJ10181, LATS2, KPM	LATS, large tumor suppressor, homolog 2 (Drosophila)	NM_014572, XCT1612979.2, XCT2314839.0	2039779_s_at, 231993_s_at, 231994_at, 237013_at, 239346_at	NP_055387.2, EAW63287.1, EAW63288.1
GeneID:22	SIX3	13	21,727,704	21,760,741	33,037	-	3	1_A375_uNG7_myuni_lncRNA_NR_1:1687, 2_A375_uNG7_dlucl_lncRNA_NR_1:2375, 4_A375_EGR1_1:2127	101, 291, -75	sr gene, cr gene, splicesom	1	1	1	27	29	27	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.29	Gene SIX3	SIX3, MGC4833	sine oculis homeobox homolog 3 (Drosophila), R-HPX	NM_145091, NM_001159017, XCT1990390.2, XCT2359383.0, XCT2314852.1	2271163_at	NP_659456.4, NP_001159489.1, EAW62795.1, EAW62794.1, EAW66266.1
GeneID:79	MRPS2	13	21,760,972	21,783,223	22,551	+	3	1_A375_uNG7_myuni_lncRNA_NR_1:1687, 2_A375_uNG7_dlucl_lncRNA_NR_1:2375, 4_A375_EGR1_1:2127	186, 108, 444	sr gene, cr gene, us gene	1	1	1	27	29	27	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.29	Gene MRPS2	bMRP65, MRP65, MGC3243	mitochondrial ribosomal protein S2	NM_002preliminary, XCT1618118.1, XCT2314419.0	2043955_s_at, 2043957_x_at, 224333_s_at	NP_079931.1, EAW66266.1, EAW66267.1
GeneID:40	LOC4300	13	21,872,342	21,879,657	7,315	+	2	1_A375_uNG7_myuni_lncRNA_NR_1:1693, 2_A375_uNG7_dlucl_lncRNA_NR_1:2376	-150, -150	splicesom, upstream	1	1	0	141	160	13	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.19	Gene LOC430794		hypothetical LOC430794	XR_111387, XR_110104, XR_114892	236837_x_at, 242760_at	
GeneID:10	LOC1002	13	21,877,310	21,922,990	45,330	-	3	1_A375_uNG7_myuni_lncRNA_NR_1:1693, 2_A375_uNG7_dlucl_lncRNA_NR_1:2376, 4_A375_EGR1_1:2128	59865, 50995, 27932	downstream, downstream, sr gene	1	1	1	72.5	62	15.5	2	4_A375_EGR1_1.1	0.19	Gene LOC100509910		hypothetical LOC100509910	XR_111393, XR_111395, XR_110125, XR_110124, XR_114893, XR_114561		
GeneID:22	EPHA1	13	22,066,926	22,176,355	111,327	-	1	2_A375_uNG7_dlucl_lncRNA_NR_1:2377	115	sr gene	0	0	0	14	16	12	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.16	Gene EPHA1	1110005O20Rik, EPHA1, DKFZp5610, FLJ34555	EF-hand domain family, member A1	NM_152726, XCT2222553.0, XCT2359087.0	212410_at	NP_609139.1, EAW63313.1, EAW63312.1
GeneID:10	LOC1002	13	22,764,424	22,830,965	66,241	+	1	4_A375_EGR1_1:2129	42326	sr gene	0	0	1	5	5	14	1	4_A375_EGR1_1.1	0.14	Gene LOC100509822		hypothetical LOC100509822	XR_111386, XR_110103, XR_114883		
GeneID:26	SACS	13	23,902,963	24,007,541	104,578	-	2	1_A375_uNG7_myuni_lncRNA_NR_1:1695, 1_A375_uNG7_dlucl_lncRNA_NR_1:2134	-93, 181	splicesom, upstream	1	1	0	17	15	17	1	1_A375_uNG7_myuni_lncRNA_NR_1	0.17	Gene SACS	SACS, ARSACS, DNAJC29, DKFZp686B1516	spastic ataxia of Charlevoix-Saguenay (sacsin)	NM_014363, XCT1993126.1	213262_at	NP_055178.3, EAW66323.1
GeneID:10	LOC1002	13	23,993,110	24,003,006	9,896	+	2	1_A375_uNG7_myuni_lncRNA_NR_1:1699, 1_A375_uNG7_dlucl_lncRNA_NR_1:2136	14626, 14570	downstream, downstream	1	1	1	17	15	17	1	1_A375_uNG7_myuni_lncRNA_NR_1	0.17	Gene LOC100509860	SNCS-AS1	SNCS antisense RNA 1 (non-protein coding)	XR_110106		
GeneID:10	LOC1002	13	24,045,651	24,051,803	17,932	+	1	2_A375_uNG7_dlucl_lncRNA_NR_1:2378	-2145	upstream	0	1	0	8	19	8	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.19	Gene LOC100509867		hypothetical LOC100509867	XR_111372, XR_110107, XR_114868		
GeneID:55	TNFRSF1	13	24,144,723	24,230,252	103,530	+	2	2_A375_uNG7_dlucl_lncRNA_NR_1:2379, 4_A375_EGR1_1:2130	-279, 6973	splicesom, cr gene	0	1	0	12	19	8	2	2_A375_uNG7_dlucl_lncRNA_NR_1	0.23	Gene TNFRSF19	TEFA, TNFRSF19, TRADE, TAJ-alpha, TROY-alpha, necrotic lesions, necrotic lesions 19	tumor necrosis factor receptor superfamily, member 19	NM_018647, NM_148957, XCT1533013.3, XCT2314686.0, XCT2314687.0	223527_at, 224393_s_at, 227812_at	NP_981117.2, NP_061980.1, EAW63225.1, EAW63226.1, EAW63227.1
GeneID:23	MFEP	13	24,394,326	24,465,567	137,239	-	2	1_A375_uNG7_myuni_lncRNA_NR_1:1700, 2_A375_uNG7_dlucl_lncRNA_NR_1:2381	-39, -29	splicesom, upstream	1	1	0	176	169	11	1	2_A375_uNG7_dlucl_lncRNA_NR_1	0.19	Gene MFEP	MEP, MFEP, HMIP	mitochondrial ribonucleoside peptidase	NM_033932, XCT1563442, XCT2314777.0	204355_at, 36830_at	NP_339932.2, EAW63321.1, EAW63320.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:341640	FREM2	13	39,261,173	39,461,268	200,095	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2421	201515	downstream	0	1	0	12	17	3	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene FREM2	DKFZp781I048, FREM2, DKFZp686J0811, KIAA1074	FRAS1 related extracellular matrix protein 2	NM_207361, hCT1819474.2, hCT2315014.0	230964_at	NP_997244.3, EAX08607.1, EAX08608.1
GeneID:80209	C13orf23	13	39,584,002	39,612,252	28,250	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1735, 2_A375_pNL97_plus_lncRNA_AR..1..2422	140, 124	in gene, in gene	1	1	0	32	42	12	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene C13orf23	C13orf23, bA50D16.2, FLJ23780, FLJ12661	chromosome 13 open reading frame 23	NM_025138, NM_170719, hCT1819469.2, hCT1954778.1	218420_s_at, 225687_at	NP_079414.3, NP_733837.2, EAX08610.1, EAX08611.1
GeneID:387921	NHLRC3	13	39,612,455	39,624,246	11,791	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1735, 2_A375_pNL97_plus_lncRNA_AR..1..2422	-343, -327	upstream, upstream	1	1	0	32	42	12	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene NHLRC3	NHLRC3, DKFZp313M1221, DKFZp686E1140	NHL repeat containing 3	NM_001012754, NM_001017370, hCT1642582.2, hCT1954774.1, hCT2359308.0, hCT2359309.0	227040_at, 236953_s_at, 239314_at	NP_001012772.1, NP_001017370.1, EAX08612.1, EAX08613.1, EAX08614.1, EAX08615.1
GeneID:646982	LOC646982	13	40,921,269	41,055,143	133,874	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1737, 1_A375_pNL7_minus_lncRNA_AR..1..1738, 2_A375_pNL97_plus_lncRNA_AR..1..2426	78471, 27111, 27207	in gene, in gene, in gene	1	1	0	17.5	10.5	2.5	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC646982	FLJ21437, TTL	tubulin tyrosine ligase	NR_024505, NR_024506, NR_024507	1554927_at, 1555264_a_at, 233432_at	
GeneID:2308	FOXO1	13	41,129,801	41,240,734	110,933	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1739, 2_A375_pNL97_plus_lncRNA_AR..1..2427	1214, 1678	in gene, in gene	1	1	0	16	22	7	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene FOXO1	FKHR, FOXO1, FKH1, FOXO1A	forkhead box O1	NM_002015, hCT23372.2	202723_s_at, 202724_s_at, 228484_s_at	NP_002006.2, EAX08627.1
GeneID:10240	MRPS31	13	41,303,432	41,345,347	41,915	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1740, 2_A375_pNL97_plus_lncRNA_AR..1..2428, 4_A375_EGR1..1..2160	19, 35, -61	in gene, in gene, upstream	1	1	1	25	25	25	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene MRPS31	MRPS31, IMOGN38, S31mt, MRP-S31	mitochondrial ribosomal protein S31	NM_005830, hCT23954.2	212603_at, 212604_at, 243821_at	NP_005821.2, EAX08629.1
GeneID:1997	ELF1	13	41,506,055	41,593,508	87,453	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2429, 4_A375_EGR1..1..2161	97508, 97540	downstream, downstream	0	1	1	17	18	15	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ELF1	ELF1		NM_001145353, NM_172373, hCT2315465.0, hCT23960.3	212418_at, 212420_at	NP_001138825.1, NP_758961.1, EAX08640.1, EAX08641.1
GeneID:11193	WBP4	13	41,635,697	41,658,139	22,442	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1741, 2_A375_pNL97_plus_lncRNA_AR..1..2430, 4_A375_EGR1..1..2162, 4_A375_EGR1..1..2163	-765, -17, -721, 143	upstream, upstream, upstream, in gene	1	1	1	29	24	19	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene WBP4	WBP4, MGC117310, FBP21	WW domain binding protein 4 (formin binding protein 21)	NM_007187, hCT2315159.0, hCT23953.3	203597_s_at, 203598_s_at, 203599_s_at	NP_009118.1, EAX08643.1, EAX08644.1
GeneID:89890	KBTBD6	13	41,701,709	41,706,936	5,227	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2431, 4_A375_EGR1..1..2164	24, 216	in gene, in gene	0	1	1	25	27	12	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene KBTBD6	FLJ36260, DKFZp547E1912, KBTBD6, DKFZp547M073	kelch repeat and BTB (POZ) domain containing 6	NM_152903	1553111_a_at, 226479_at	NP_690867.3
GeneID:84078	KBTBD7	13	41,765,711	41,768,702	2,991	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1742, 2_A375_pNL97_plus_lncRNA_AR..1..2432	-18, -2	upstream, upstream	1	1	0	18	28	11	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene KBTBD7	KBTBD7, DKFZp434E2318	kelch repeat and BTB (POZ) domain containing 7	NM_032138, hCT1644424.3	223412_at	NP_115514.2, EAX08647.1
GeneID:79612	NAA16	13	41,885,341	41,951,166	65,825	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1743, 2_A375_pNL97_plus_lncRNA_AR..1..2433, 4_A375_EGR1..1..2165	-141, -29, 259	upstream, upstream, in gene	1	1	1	21	17	21	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene NAA16	MGC40612, NAA16, DKFZp686O08147, NARG1L	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	NM_018527, NM_024561, NM_001110798, hCT2315204.0, hCT2315206.1, hCT2315207.0, hCT2315208.1, hCT2315209.1, hCT2315211.0, hCT2359339.0	1555450_a_at, 219378_at	NP_060997.2, NP_078837.3, NP_001104268.1, EAX08654.1, EAX08657.1, EAX08658.1, EAX08655.1, EAX08656.1, EAX08659.1, EAX08660.1
GeneID:28984	C13orf15	13	42,031,542	42,045,013	13,471	+	1	4_A375_EGR1..1..2166	-214	upstream	0	0	1	9	12	22	1	4_A375_EGR1..1	22	Gene C13orf15	C13orf15, RGC-32, bA157L14.2, MGC87338, KIAA0564, RGC32	chromosome 13 open reading frame 15	NM_014059, hCT1954803.1, hCT23377.3	218723_s_at, 228193_s_at, 239827_at	NP_054778.2, EAX08664.1, EAX08663.1
GeneID:23078	KIAA0564	13	42,140,961	42,535,221	394,260	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2434	-139	upstream	0	1	0	16	16	17	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene KIAA0564	FLJ21779, KIAA0564	KIAA0564	NM_015058, NM_001009814, hCT2315440.0, hCT2315442.0, hCT24029.3	212946_at, 214231_s_at	NP_055873.1, NP_001009814.1, EAX08665.1, EAX08666.1, EAX08667.1
GeneID:100507240	LOC100507240	13	42,535,305	42,555,701	20,396	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2434	55	in gene	0	1	0	16	16	17	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100507240		hypothetical LOC100507240	XR_111385, XR_110117, XR_114695		
GeneID:160851	DGKH	13	42,622,889	42,803,888	180,999	+	2	4_A375_EGR1..1..2167, 4_A375_EGR1..1..2168	-7561, 631	upstream, in gene	0	0	1	11.5	14	15.5	2	4_A375_EGR1..1	16	Gene DGKH	DGKH, DGKeta, DKFZp761I1510	diacylglycerol kinase, eta	NM_152910, NM_178009, hCT2315220.1, hCT2315221.1, hCT2359350.0, hCT2359351.0, hCT24028.4	1553300_a_at	NP_690874.2, NP_821077.1, EAX08671.1, EAX08672.1, EAX08673.1, EAX08675.1, EAX08674.1
GeneID:94240	EPSTI1	13	43,462,122	43,566,377	104,255	-	1	4_A375_EGR1..1..2170	137	in gene	0	0	1	7	8	18	1	4_A375_EGR1..1	18	Gene EPSTI1	EPSTI1, BRESI1, MGC29634	epithelial stromal interaction 1 (breast)	NM_001002264, NM_033255, hCT2315626.0, hCT2315627.0, hCT2359319.0	227609_at, 235276_at	NP_001002264.1, NP_150280.1, EAX08684.1, EAX08685.1, EAX08686.1
GeneID:29103	DNAJC15	13	43,597,362	43,683,306	85,944	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2436	35086	in gene	0	1	0	14	13	5	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene DNAJC15	DNAJC15, MCJ, DNAJD1, HSD18	DnaJ (Hsp40) homolog, subfamily C, member 15	NM_013238, hCT23358.3	218435_at, 227606_at	NP_037370.2, EAX08688.1
GeneID:160857	CCDC122	13	44,410,488	44,453,826	43,338	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1744, 4_A375_EGR1..1..2171	546, 578	in gene, in gene	1	0	1	15	15	18	1	4_A375_EGR1..1	18	Gene CCDC122	CCDC122, FLJ31846	coiled-coil domain containing 122	NM_144974, hCT2315859.1, hCT2315862.1, hCT2344949.0, hCT23992.3		NP_659411.2, EAX08697.1, EAX08698.1, EAX08699.1, EAX08700.1
GeneID:144811	C13orf31	13	44,453,420	44,468,068	14,648	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1744, 4_A375_EGR1..1..2171	-140, -172	upstream, upstream	1	0	1	15	15	18	1	4_A375_EGR1..1	18	Gene C13orf31	C13orf31, DKFZp686D11119, FLJ38725	chromosome 13 open reading frame 31	NM_153218, NM_001128303, hCT23991.4	1553141_at, 1553142_at, 228937_at	NP_694950.2, NP_001121775.1, EAX08701.1
GeneID:100507253	LOC100507253	13	44,716,464	44,728,215	11,751	+	3	2_A375_pNL97_plus_lncRNA_AR..1..2438, 2_A375_pNL97_plus_lncRNA_AR..1..2439, 4_A375_EGR1..1..2172	-9424, 17520, -432	upstream, downstream, upstream	0	1	1	15.33	21	8.33	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC100507253		hypothetical LOC100507253	XR_111384, XR_110116, XR_114696		
GeneID:8848	TSC22D1	13	45,007,655	45,150,701	143,046	-	1	4_A375_EGR1..1..2173	-1523	upstream	0	0	1	9	13	22	1	4_A375_EGR1..1	22	Gene TSC22D1	TSC22, RP11-269C23.2, TSC22D1, TGFB1I4, MGC17597, DKFZp686O19206	TSC22 domain family, member 1	NM_006022, NM_183422, hCT1954802.1, hCT23380.2	215111_s_at, 235315_at, 243133_at	NP_006013.1, NP_904358.2, EAX08710.1, EAX08711.1
GeneID:641467	LOC641467	13	45,150,029	45,154,568	4,539	+	1	4_A375_EGR1..1..2173	2195	in gene	0	0	1	9	13	22	1	4_A375_EGR1..1	22	Gene LOC641467		hypothetical LOC641467	XR_111383, XR_110119, XR_114697	229990_at, 237745_at	
GeneID:26747	NUFIP1	13	45,513,384	45,563,613	50,229	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1747, 2_A375_pNL97_plus_lncRNA_AR..1..2443, 4_A375_EGR1..1..2176	93, -131, -163	in gene, upstream, upstream	1	1	1	18	18	22	1	4_A375_EGR1..1	22	Gene NUFIP1	NUFIP1, bA540M5.1, NUFIP	nuclear fragile X mental retardation protein interacting protein 1	NM_012345, hCT1819653.2	205134_s_at, 205135_s_at, 205136_s_at	NP_036477.2, EAX08719.1
GeneID:55425	KIAA1704	13	45,563,687	45,602,405	38,718	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1747, 2_A375_pNL97_plus_lncRNA_AR..1..2443, 4_A375_EGR1..1..2176	-167, 57, 89	upstream, in gene, in gene	1	1	1	18	18	22	1	4_A375_EGR1..1	22	Gene KIAA1704	KIAA1704, RP11-245H20.2, AD029, bA245H20.2, LSR7	KIAA1704	NM_018559, hCT1810480.0, hCT2315559.0, hCT2359314.0, hCT23985.3	220171_x_at, 223606_x_at, 226429_at, 229076_s_at, 229891_x_at	NP_061029.2, EAX08722.1, EAX08720.1, EAX08721.1, EAX08723.1
GeneID:100287603	LOC100287603	13	45,911,001	45,916,722	5,721	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1748, 2_A375_pNL97_plus_lncRNA_AR..1..2444, 4_A375_EGR1..1..2177	4359, 4375, 4391	in gene, in gene, in gene	1	1	1	18	26	21	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene LOC100287603		hypothetical LOC100287603	XR_111380, XR_111381, XR_110120, XR_110121, XR_114699, XR_114700		
GeneID:7178	TPT1	13	45,911,304	45,915,297	3,993	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1748, 2_A375_pNL97_plus_lncRNA_AR..1..2444, 4_A375_EGR1..1..2177	-63, -79, -95	upstream, upstream, upstream	1	1	1	18	26	21	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene TPT1	TCTP, HRF, p02, TPT1, FLJ27337	tumor protein, translationally-controlled 1	NM_003295, hCT1808839.1, hCT1817189.1, hCT1817190.1, hCT1817192.1, hCT23983.2	211943_x_at, 212284_x_at, 212869_x_at, 214327_x_at, 216520_s_at	NP_003286.1, EAX08735.1, EAX08731.1, EAX08732.1, EAX08733.1, EAX08734.1
GeneID:677814	SNORA31	13	45,911,615	45,911,744	129	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1748, 2_A375_pNL97_plus_lncRNA_AR..1..2444, 4_A375_EGR1..1..2177	-3616, -3632, -3648	upstream, upstream, upstream	1	1	1	18	26	21	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene SNORA31	SNORA31, ACA31	small nucleolar RNA, H/ACA box 31	NR_002967		
GeneID:100190939	LOC100190939	13	45,915,480	45,965,618	50,138	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1748, 2_A375_pNL97_plus_lncRNA_AR..1..2444, 4_A375_EGR1..1..2177	-120, -104, -88	upstream, upstream, upstream	1	1	1	18	26	21	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene LOC100190939	FLJ42341, FLJ45662	hypothetical LOC100190939	NR_024458		
GeneID:253512	SLC25A30	13	45,967,451	45,992,516	25,065	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2445	580	in gene	0	1	0	13	20	15	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SLC25A30	KMCP1, SLC25A30	solute carrier family 25, member 30	NM_001010875, hCT1961241.1	216712_at, 216721_at, 226782_at, 236171_at	NP_001010875.1, EAX08739.1
GeneID:100507293	LOC100507293	13	45,991,959	45,994,506	2,547	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2445	-23	upstream	0	1	0	13	20	15	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100507293		hypothetical protein LOC100507293	XM_003119553, XM_003118892, XM_003120768		XP_003119601.1, XP_003118940.1, XP_003120816.1
GeneID:83548	COG3	13	46,039,071	46,110,760	71,689	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2446	513	in gene	0	1	0	16	20	13	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene COG3	SEC34, COG3	component of oligomeric golgi complex 3	NM_031431, hCT20445.3, hCT2315569.0, hCT2359320.0	1554339_a_at, 223450_s_at	NP_113619.1, EAX08741.1, EAX08742.1, EAX08743.1
GeneID:23091	ZC3H13	13	46,536,314	46,626,894	90,580	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2447	46	in gene	0	1	0	14	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ZC3H13	DKFZp434D1812, ZC3H13, KIAA0853, FLJ35669	zinc finger CCCH-type containing 13	NM_015070, hCT1968082.1, hCT20446.3, hCT2315904.0	209651_at, 212402_at, 227536_at	NP_055885.3, EAX08750.1, EAX08751.1, EAX08752.1
GeneID:1361	CPB2	13	46,627,322	46,679,211	51,889	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2447	52363	downstream	0	1	0	14	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CPB2	TAFI, PCPB, CPB2, CPU	carboxypeptidase B2 (plasma)	NM_016413, NM_001872, hCT20442.3, hCT20443.3	206651_s_at	NP_057497.3, NP_001863.2, EAX08754.1, EAX08755.1
GeneID:23143	LRCH1	13	47,127,296	47,327,176	199,880	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1749	720	in gene	1	0	0	20	13	12	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LRCH1	KIAA1016, FLJ41660, NP81, LRCH1, CHDC1	leucine-rich repeats and calponin homology (CH) domain containing 1	NM_015116, NM_001164211, NM_001164213, hCT2346439.0	214936_at, 235012_at	NP_055931.1, NP_001157683.1, NP_001157685.1, EAX08766.1
GeneID:2098	ESD	13	47,345,391	47,371,367	25,976	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2448, 4_A375_EGR1..1..2178	563, 455	in gene, in gene	0	1	1	12	13	18	1	4_A375_EGR1..1	18	Gene ESD	FGH, FLJ11763, ESD	esterase D/formylglutathione hydrolase	NM_001984, hCT1966004.1, hCT1966005.1, hCT21159.3	209009_at, 215095_at, 215096_s_at, 228162_at, 240808_at	NP_001975.1, EAX08767.1, EAX08768.1, EAX08769.1
GeneID:8803	SUCLA2	13	48,516,791	48,575,462	58,671	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2450, 4_A375_EGR1..1..2179	-202, 54	upstream, in gene	0	1	1	13	17	17	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene SUCLA2	A-BETA, SCS-betaA, MTDPS5, SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	NM_003850, hCT1954797.2, hCT1954798.2, hCT21925.2, hCT2345207.0	202930_s_at	NP_003841.1, EAX08776.1, EAX08775.1, EAX08777.1, EAX08778.1
GeneID:55270	NUDT15	13	48,611,703	48,621,282	9,579	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1751, 2_A375_pNL97_plus_lncRNA_AR..1..2451	9, 105	in gene, in gene	1	1	0	26	26	23	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene NUDT15	RP11-90M2.1, MTH2, NUDT15, FLJ10956, MGC104352	nudix (nucleoside diphosphate linked moiety X)-type motif 15	NM_018283, hCT1641093.2	219347_at	NP_060753.1, EAX08782.1
GeneID:29079	MED4	13	48,650,092	48,669,240	19,148	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1752, 2_A375_pNL97_plus_lncRNA_AR..1..2452	-8, -72	upstream, upstream	1	1	0	63	99	15	1	2_A375_pNL97_plus_lncRNA_AR..1	99	Gene MED4	RP11-90M2.2, MED4, FLJ10956, HSPC126, DRIP36, VDRIP, TRAP36	mediator complex subunit 4	NM_014166, hCT19494.3, hCT1954790.1, hCT1966243.1, hCT2359356.0	217843_s_at, 222438_at	NP_054885.1, EAX08785.1, EAX08783.1, EAX08784.1, EAX08786.1
GeneID:5925	RB1	13	48,877,883	49,056,026	178,143	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1754	143013	in gene	1	0	0	15	9	2	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene RB1	OSRC, RB, p105-Rb, pRb, RB1, pp110	retinoblastoma 1	NM_000321, hCT21924.2, hCT2315956.0	203132_at, 211540_s_at	NP_000312.2, EAX08793.1, EAX08794.1
GeneID:10161	LPAR6	13	48,985,181	49,018,840	33,659	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1754	-2056	upstream	1	0	0	15	9	2	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene LPAR6	MGC120358, P2RY5, ARWH1, LPAR6, P2Y5, LAH3	lysophosphatidic acid receptor 6	NM_005767, NM_001162497, NM_001162498	1557763_at, 218589_at	NP_005758.2, NP_001155969.1, NP_001155970.1
GeneID:1102	RCBTB2	13	49,063,099	49,107,316	44,217	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1755, 4_A375_EGR1..1..2180	404, 532	in gene, in gene	1	0	1	18	17	25	1	4_A375_EGR1..1	25	Gene RCBTB2	RCBTB2, CHC1L	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	NM_001268, hCT21215.4, hCT2316212.0	1561585_at, 204759_at	NP_001259.1, EAX08800.1, EAX08799.1
GeneID:22862	FNDC3A	13	49,550,048	49,783,915	233,867	+	1	4_A375_EGR1..1..2181	384	in gene	0	0	1	16	13	24	1	4_A375_EGR1..1	24	Gene FNDC3A	FLJ31509, KIAA0970, FNDC3, FNDC3A, bA203I16.5, bA203I16.1, HUGO	fibronectin type III domain containing 3A	NM_001079673, NM_014923, hCT1953965.0, hCT2315967.0, hCT2315968.0, hCT2315969.0, hCT2315970.0, hCT2359298.0, hCT2359299.0, hCT2359300.0	202304_at, 215910_s_at, 238961_s_at, 241611_s_at	NP_001073141.1, NP_055738.3, EAX08803.1, EAX08805.1, EAX08808.1, EAX08809.1, EAX08804.1, EAX08807.1, EAX08806.1, EAX08810.1
GeneID:81617	CAB39L	13	49,882,786	50,018,221	135,435	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2455	45	in gene	0	1	0	17	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CAB39L	MO2L, bA103J18.3, FLJ12577, RP11-103J18.3, MO25-BETA, CAB39L	calcium binding protein 39-like	NM_001079670, NM_030925, hCT21213.3, hCT2315871.0, hCT2315872.0, hCT2315875.0	221003_s_at, 225914_s_at, 225915_at	NP_001073138.1, NP_112187.2, EAX08820.1, EAX08821.1, EAX08822.1, EAX08823.1
GeneID:83852	SETDB2	13	50,018,429	50,069,139	50,710	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2455, 2_A375_pNL97_plus_lncRNA_AR..1..2456	-253, 52035	upstream, downstream	0	1	0	14.5	18.5	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SETDB2	DKFZp586I0123, C13orf4, SETDB2, CLLD8, DKFZp761J1217, KMT1F, CLLL8	SET domain, bifurcated 2	NM_031915, NM_001160308, hCT20485.3, hCT2359355.0, hCT2359358.0	1564970_at, 1564972_x_at, 235338_s_at, 235339_at, 238731_at	NP_114121.2, NP_001153780.1, EAX08824.1, EAX08825.1, EAX08826.1
GeneID:51131	PHF11	13	50,069,801	50,103,117	33,316	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2456	663	in gene	0	1	0	12	19	8	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PHF11	PHF11, NY-REN-34, APY, NYREN34, IGEL, BCAP, IGHER, IGER	PHD finger protein 11	NM_001040443, NM_001040444, hCT1954791.1, hCT1954792.1	221816_s_at, 242060_x_at	NP_001035533.1, NP_001035534.1, EAX08827.1, EAX08828.1
GeneID:55213	RCBTB1	13	50,106,082	50,159,719	53,637	-	1	4_A375_EGR1..1..2182	16103	in gene	0	0	1	8	4	13	1	4_A375_EGR1..1	13	Gene RCBTB1	MGC33184, GLP, RP11-185C18.1, CLLD7, CLLL7, RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	NM_018191, hCT20486.3	1554934_at, 218352_at, 237417_at	NP_060661.3, EAX08829.1
GeneID:3839	KPNA3	13	50,273,443	50,367,057	93,614	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1757, 2_A375_pNL97_plus_lncRNA_AR..1..2457	113, 145	in gene, in gene	1	1	0	27	28	11	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene KPNA3	SRP1, KPNA3, hSRP1, SRP1gamma, IPOA4, SRP4	karyopherin alpha 3 (importin alpha 4)	NM_002267, hCT2315856.0, hCT2315857.0, hCT2315858.0	221502_at, 221503_s_at	NP_002258.2, EAX08838.1, EAX08837.1, EAX08839.1

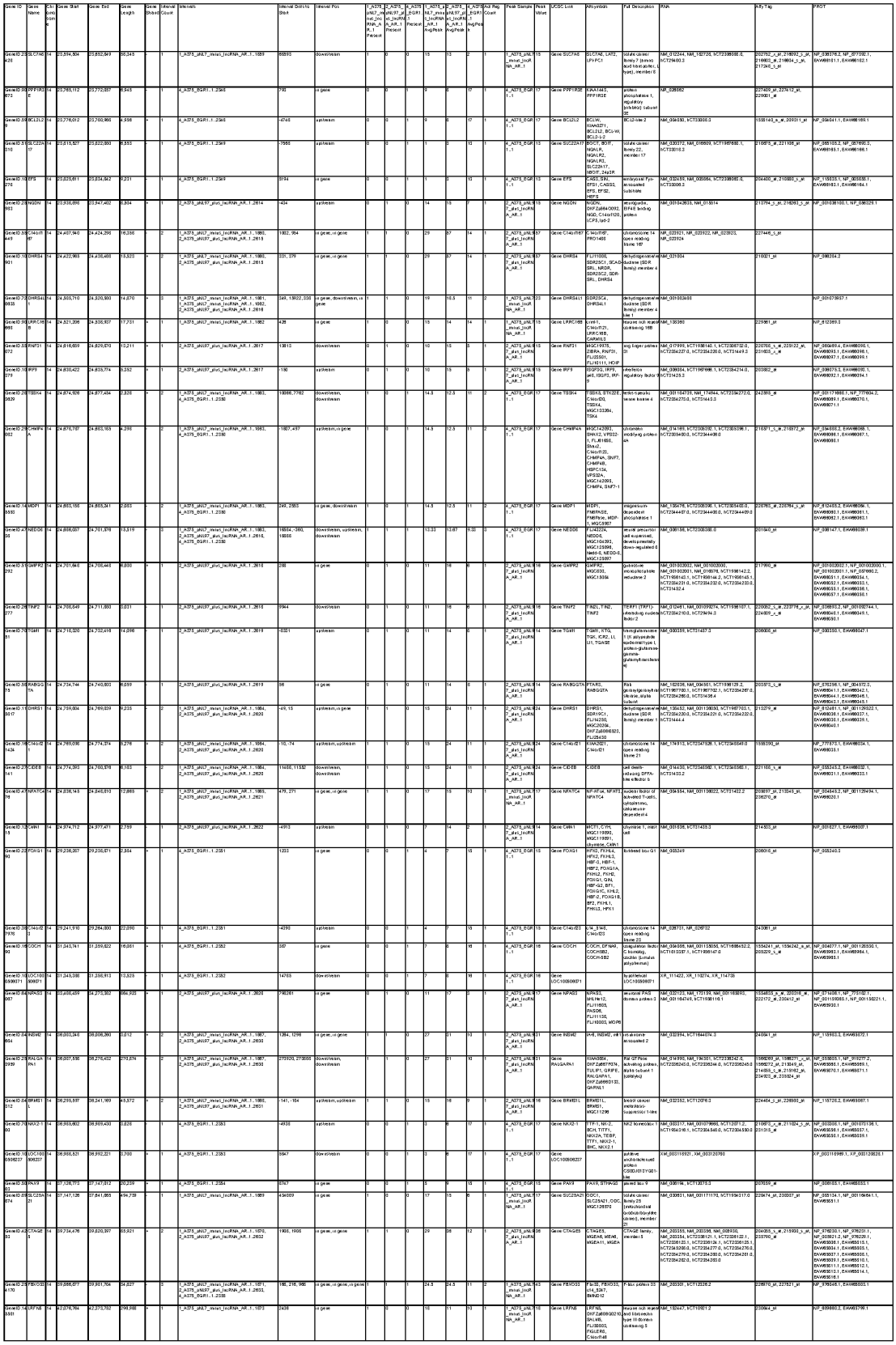
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.57213	C13orf1	13	50,486,842	50,510,626	23,784	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1758, 2_A375_pNL97_plus_lncRNA_AR..1..2458	194, 162	in gene, in gene	1	1	0	47	75	13	1	2_A375_pNL97_plus_lncRNA_AR..1	75	Gene C13orf1	CLLD6, C13orf1	chromosome 13 open reading frame 1	NM_020456, NM_001127482, NR_023351, hCT1966248.1, hCT1966249.1, hCT2315850.0, hCT2315852.0	214668_at, 230151_at	NP_065189.1, NP_001120954.1, EAX08840.1, EAX08841.1, EAX08842.1, EAX08843.1
GeneID.8847	DLEU2	13	50,556,688	50,699,677	142,989	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1759, 2_A375_pNL97_plus_lncRNA_AR..1..2459, 2_A375_pNL97_plus_lncRNA_AR..1..2460	853, 1437, 701	in gene, in gene, in gene	1	1	0	15	29	15	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene DLEU2	DLEU2, RFP2OS, BCMSUN, MGC88287, MIR15AHG, NCRNA00022, TRIM13OS, 1B4, DLB2, LEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	NR_002612	1556820_a_at, 1556821_x_at, 1563229_at, 1564443_at, 1569600_at, 216870_x_at, 239936_at, 242854_x_at	
GeneID.79621	RNASEH2B	13	51,483,892	51,544,596	60,704	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2463	266	in gene	0	1	0	11	20	15	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene RNASEH2B	FLJ11712, DLEU8, AGS2, RNASEH2B	ribonuclease H2, subunit B	NM_024570, NM_001142279, hCT1954794.1, hCT19861.2	215040_at, 219056_at, 229210_at, 233156_at	NP_078846.2, NP_001135751.1, EAX08863.1, EAX08864.1
GeneID.647166	LOC647166	13	51,658,287	51,723,129	64,842	-	1	4_A375_EGR1..1..2183	345	in gene	0	0	1	3	7	15	1	4_A375_EGR1..1	15	Gene LOC647166	DKFZp434L0514	hypothetical protein LOC647166	XM_930192		XP_935285.2
GeneID.26512	INTS6	13	51,935,701	52,027,275	91,574	-	1	4_A375_EGR1..1..2184	187	in gene	0	0	1	13	10	17	1	4_A375_EGR1..1	17	Gene INTS6	DDX26A, DBI-1, INT6, Notchl2, DKFZp434B105, DICE1, INTS6, HDB, DDX26	integrator complex subunit 6	NM_012141, NM_001039937, NM_001039938, hCT20283.2, hCT2315827.0, hCT2315829.0, hCT2350286.0, hCT2350287.0, hCT2350288.0, hCT2350289.0, hCT2350290.0, hCT2350291.0	1568695_s_at, 218619_at, 222239_s_at, 235283_at	NP_036273.1, NP_001035026.1, NP_001035027.1, EAX08876.1, EAX08877.1, EAX08881.1, EAX08873.1, EAX08874.1, EAX08875.1, EAX08878.1, EAX08879.1, EAX08880.1
GeneID.100507398	LOC100507398	13	52,027,477	52,028,852	1,375	+	1	4_A375_EGR1..1..2184	-389	upstream	0	0	1	13	10	17	1	4_A375_EGR1..1	17	Gene LOC100507398		hypothetical LOC100507398	XR_111386, XR_110124, XR_114676		
GeneID.79758	DHRS12	13	52,342,131	52,378,293	36,162	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2464, 2_A375_pNL97_plus_lncRNA_AR..1..2465	389, -91	in gene, upstream	0	1	0	12.5	17.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene DHRS12	DHRS12, SDR40C1, FLJ13639	dehydrogenase/reductase (SDR family) member 12	NM_024705, NM_001031719, hCT1954795.0, hCT1954796.1, hCT1966247.0, hCT20284.1, hCT2359343.0, hCT2359344.0	204800_s_at, 204801_s_at, 231345_s_at	NP_078981.1, NP_001026889.1, EAX08884.1, EAX08885.1, EAX08888.1, EAX08889.1, EAX08886.1, EAX08887.1
GeneID.100507413	LOC100507413	13	52,377,733	52,387,356	9,623	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2464, 2_A375_pNL97_plus_lncRNA_AR..1..2465	171, 651	in gene, in gene	0	1	0	12.5	17.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100507413		hypothetical LOC100507413	XR_111387, XR_110125, XR_114677		
GeneID.283521	RP11-327P2.4	13	52,387,463	52,419,266	31,803	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2464, 2_A375_pNL97_plus_lncRNA_AR..1..2465	41382, 40902	downstream, downstream	0	1	0	12.5	17.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene RP11-327P2.4	FLJ37307, NCRNA00282	hypothetical LOC283521	NR_027047, NR_027048	1557465_at	
GeneID.341676	NEK5	13	52,638,898	52,703,214	64,316	-	1	4_A375_EGR1..1..2185	302	in gene	0	0	1	7	8	16	1	4_A375_EGR1..1	16	Gene NEK5	NEK5, MGC75495	NIMA (never in mitosis gene a)-related kinase 5	NM_199289		NP_954983.1
GeneID.4752	NEK3	13	52,706,779	52,733,996	27,217	-	1	4_A375_EGR1..1..2185	31084	downstream	0	0	1	7	8	16	1	4_A375_EGR1..1	16	Gene NEK3	HSPK36, NEK3, MGC29949	NIMA (never in mitosis gene a)-related kinase 3	NM_001146099, NR_027415, hCT20280.3, hCT2359328.0, hCT2359329.0, hCT2359330.0, hCT2359331.0	211089_s_at, 213116_at	NP_001139571.1, EAX08907.1, EAX08905.1, EAX08906.1, EAX08908.1, EAX08909.1
GeneID.51028	VPS36	13	52,986,737	53,024,763	38,026	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1760, 2_A375_pNL97_plus_lncRNA_AR..1..2466, 2_A375_pNL97_plus_lncRNA_AR..1..2467	443, 251, -4869	in gene, in gene, upstream	1	1	0	15	17.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene VPS36	EAP45, CGI-145, C13orf9, DKFZp781E0871, VPS36	vacuolar protein sorting 36 homolog (S. cerevisiae)	NM_016075	222478_at, 240086_at	NP_057159.2
GeneID.26586	CKAP2	13	53,029,495	53,050,763	21,268	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1760, 2_A375_pNL97_plus_lncRNA_AR..1..2466, 2_A375_pNL97_plus_lncRNA_AR..1..2467	-5175, -4983, 137	upstream, upstream, in gene	1	1	0	15	17.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CKAP2	se20-10, DKFZp686L1238, LB1, FLJ10749, TMAP, CKAP2	cytoskeleton associated protein 2	NM_001098525, NM_018204, hCT1950508.1, hCT2251744.0	234784_x_at	NP_001091995.1, NP_060674.3, EAW55889.1, EAW55890.1
GeneID.144983	HNRNPA1L2	13	53,191,605	53,217,919	26,314	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1761, 2_A375_pNL97_plus_lncRNA_AR..1..2468, 2_A375_pNL97_plus_lncRNA_AR..1..2469	35275, 43, 35323	downstream, in gene, downstream	1	1	0	17.5	29.5	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene HNRNPA1L2	HNRNPA1L2, MGC102957	heterogeneous nuclear ribonucleoprotein A1-like 2	NM_001011724, NM_001011725, hCT2254988.0, hCT2254989.0, hCT2254990.0	238698_at	NP_001011724.1, NP_001011725.1, EAW52040.1, EAW52041.1, EAW52042.1
GeneID.10910	SUGT1	13	53,226,831	53,262,433	35,602	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1761, 2_A375_pNL97_plus_lncRNA_AR..1..2469	49, 97	in gene, in gene	1	1	0	24	36	12	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene SUGT1	SGT1, SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	NM_006704, NM_001130912, hCT1967573.1, hCT20731.3, hCT2254995.0, hCT2352518.0	234686_at	NP_006695.1, NP_001124384.1, EAW52043.1, EAW52044.1, EAW52045.1, EAW52046.1
GeneID.5100	PCDH8	13	53,418,109	53,422,774	4,665	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1762, 2_A375_pNL97_plus_lncRNA_AR..1..2470	-2197, -2108	upstream, upstream	1	1	0	15	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PCDH8	ARCADLIN, PCDH8, PAPC	protocadherin 8	NM_002590, NM_032949, hCT18843.4, hCT1968177.1, hCT2255127.0	206935_at	NP_002581.2, NP_116567.1, EAW52049.1, EAW52050.1, EAW52051.1
GeneID.81624	DIAPH3	13	60,239,717	60,738,119	498,402	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2471	71	in gene	0	1	0	18	27	9	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene DIAPH3	NSDAN, DRF3, diap3, mDia2, AUNA1, DIAPH3, AN, FLJ34705, DKFZp686A13178, DKFZp434C0931	diaphanous homolog 3 (Drosophila)	NM_030932, NM_001042517, hCT2254691.0, hCT2254692.0, hCT2254694.0, hCT2254695.1, hCT2254696.0, hCT2254697.0	220997_s_at, 229097_at, 232596_at	NP_112194.2, NP_001035982.1, EAW52069.1, EAW52070.1, EAW52072.1, EAW52074.1, EAW52071.1, EAW52073.1
GeneID.5101	PCDH9	13	66,876,966	67,804,468	927,502	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1767, 2_A375_pNL97_plus_lncRNA_AR..1..2476	-140, -266	upstream, upstream	1	1	0	21	18	7	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene PCDH9	PCDH9		NM_020403, NM_203487, hCT2325676.0	219737_s_at, 219738_s_at	NP_065136.1, NP_982354.1, EAW80499.1
GeneID.730236	LOC730236	13	67,804,715	67,805,815	1,100	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1767, 2_A375_pNL97_plus_lncRNA_AR..1..2476	-107, 21	upstream, in gene	1	1	0	21	18	7	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene LOC730236		hypothetical LOC730236	XM_001715647, XM_001133153, XM_001714412	241471_at	XP_001715699.1, XP_001133153.1, XP_001714464.1
GeneID.440145	C13orf37	13	73,282,495	73,301,938	19,443	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1769, 2_A375_pNL97_plus_lncRNA_AR..1..2479, 4_A375_EGR1..1..2202	18, 2, 402	in gene, in gene, in gene	1	1	1	31	30	19	1	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene C13orf37	MOZART1, MZT1, MGC150539, C13orf37, FLJ21869	chromosome 13 open reading frame 37	NM_001071775	225578_at, 226530_at	NP_001065243.1
GeneID.79866	C13orf34	13	73,302,042	73,330,328	28,286	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1769, 2_A375_pNL97_plus_lncRNA_AR..1..2479, 4_A375_EGR1..1..2202	-122, -106, -506	upstream, upstream, upstream	1	1	1	31	30	19	1	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene C13orf34	C13orf34, BORA, FLJ22624	chromosome 13 open reading frame 34	NM_024808, hCT1819879.2, hCT1953045.1	219544_at	NP_079084.2, EAW80514.1, EAW80515.1
GeneID.11278	KLF12	13	74,260,149	74,708,066	447,917	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2480, 2_A375_pNL97_plus_lncRNA_AR..1..2481	-30, -2142	upstream, upstream	0	1	0	14	15	10	2	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene KLF12	HSPC122, KLF12, AP2REP, AP-2rep	Kruppel-like factor 12	NM_007249, hCT1960115.1, hCT23987.3	206965_at, 206966_s_at, 208467_at, 214276_at, 227281_at, 229681_at, 238940_at, 239019_at	NP_009180.3, EAW80529.1, EAW80528.1
GeneID.9882	TBC1D4	13	75,858,809	76,056,250	197,441	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2483	-356	upstream	0	1	0	16	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TBC1D4	TBC1D4, AS160, DKFZp779C0666	TBC1 domain family, member 4	NM_014832, hCT19319.3, hCT1956914.1, hCT2326169.0	203386_at, 203387_s_at	NP_055647.2, EAW80538.1, EAW80536.1, EAW80537.1
GeneID.170622	COMMD6	13	76,099,350	76,111,991	12,641	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1772, 2_A375_pNL97_plus_lncRNA_AR..1..2484, 4_A375_EGR1..1..2203	-105, -169, 19197	upstream, upstream, downstream	1	1	1	14	18.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene COMMD6	Acrg, COMMD6	COMM domain containing 6	NM_203495, NM_203497, hCT1640004.3, hCT1965964.1, hCT1965965.1	225312_at, 240030_at	NP_987091.1, NP_987093.1, EAW80539.1, EAW80540.1, EAW80541.1
GeneID.7347	UCHL3	13	76,123,927	76,180,069	56,142	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1773, 2_A375_pNL97_plus_lncRNA_AR..1..2485	-215, -236	upstream, upstream	1	1	0	22	22	12	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene UCHL3	UCH-L3, UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	NM_006002, hCT1968021.1, hCT20736.3, hCT2325769.0, hCT2325770.0, hCT2325771.0, hCT2325772.0	204616_at	NP_005993.1, EAW80546.1, EAW80542.1, EAW80543.1, EAW80544.1, EAW80547.1, EAW80545.1
GeneID.4008	LMO7	13	76,194,570	76,434,006	239,436	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1774, 4_A375_EGR1..1..2204	16276, 16134	in gene, in gene	1	0	1	22	11	17	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene LMO7	FBXO20, KIAA0858, LOMP, FBX20, LMO7	LIM domain 7	NM_005358, NM_015842, hCT2325775.0, hCT2325778.0, hCT2325782.0, hCT2325784.0, hCT2325785.0, hCT2325787.0, hCT2325788.0	1556377_s_at, 202674_s_at, 241140_at, 242722_at	NP_005349.3, NP_056667.2, EAW80550.1, EAW80552.1, EAW80554.1, EAW80555.1, EAW80549.1, EAW80551.1, EAW80553.1
GeneID.1203	CLN5	13	77,566,059	77,576,652	10,593	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2488	261	in gene	0	1	0	17	18	16	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CLN5	FLJ90628, CLN5, NCL	ceroid-lipofuscinosis, neuronal 5	NM_006493, hCT19323.2, hCT2325868.0	204084_s_at, 204085_s_at, 214252_s_at	NP_006484.1, EAW80562.1, EAW80561.1
GeneID.23077	MYCBP2	13	77,618,792	77,901,177	282,385	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1775, 2_A375_pNL97_plus_lncRNA_AR..1..2489, 2_A375_pNL97_plus_lncRNA_AR..1..2490	-2295, -135, -2247	upstream, upstream, upstream	1	1	0	18.5	24.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene MYCBP2	PAM, DKFZp686M08244, MYCBP2, FLJ21646, FLJ10106, FLJ21597, FLJ13826, KIAA0916	MYC binding protein 2	NM_015057, hCT1953047.0, hCT2325946.0, hCT2325948.0, hCT2325949.0	1557370_s_at, 201959_s_at, 201960_s_at	NP_055872.4, EAW80565.1, EAW80564.1, EAW80566.1, EAW80567.1
GeneID.100505518	LOC100505518	13	78,393,072	78,482,818	89,746	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1776, 1_A375_pNL7_minus_lncRNA_AR..1..1777	35086, 99684	in gene, downstream	1	0	0	18	12	3	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100505518		hypothetical LOC100505518	XR_110130		
GeneID.1910	EDNRB	13	78,469,616	78,492,966	23,350	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1777	230	in gene	1	0	0	18	12	5	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene EDNRB	HSCR, ETRB, WS4A, ETB, HSCR2, ABCDS, ETBR, EDNRB	endothelin receptor type B	NM_003991, NM_000115, NM_001122659, hCT2325937.0, hCT2325938.0, hCT2325939.0, hCT2325940.0, hCT2325941.0, hCT2325942.0	204271_s_at, 204273_at, 206701_x_at	NP_003982.1, NP_000106.1, NP_001116131.1, EAW80573.1, EAW80574.1, EAW80575.1, EAW80576.1, EAW80577.1, EAW80578.1
GeneID.64062	RBM26	13	79,894,089	79,979,923	85,834	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2492	-637	upstream	0	1	0	13	19	13	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene RBM26	FLJ20957, PRO1777, ZC3H17, C13orf10, MGC133295, RBM26, SE70-2, RP11-255E21.1, ARRS2, MGC133296	RNA binding motif protein 26	NM_022118, hCT1960102.1, hCT2326781.0, hCT2326782.0, hCT2326785.0	215847_at, 215751_at, 218422_s_at, 220509_at, 222626_at, 227355_at, 229433_at	NP_071401.3, EAW80593.1, EAW80591.1, EAW80592.1, EAW80594.1
GeneID.100505538	LOC100505538	13	79,980,483	79,998,471	17,988	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2492	77	in gene	0	1	0	13	19	13	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100505538	RBM26-AS1	hypothetical LOC100505538	XR_111394, XR_110131, XR_114702		
GeneID.10253	SPRY2	13	80,910,111	80,915,086	4,975	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2495, 4_A375_EGR1..1..2205, 4_A375_EGR1..1..2206	-2290, 430, -274	upstream, in gene, upstream	0	1	1	12	14	17	3	4_A375_EGR1..1	29	Gene SPRY2	SPRY2, hSPRY2, MGC23039	sprouty homolog 2 (Drosophila)	NM_005842, hCT23425.3	204011_at	NP_005833.1, EAW80601.1
GeneID.114798	SLITRK1	13	84,451,343	84,456,528	5,185	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1788, 2_A375_pNL97_plus_lncRNA_AR..1..2497, 2_A375_pNL97_plus_lncRNA_AR..1..2498	256, 2416, 366	in gene, in gene, in gene	1	1	0	25.5	35.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	50	Gene SLITRK1	TTM, LRRC12, KIAA1910, SLITRK1, RP11-395N17.1, FLJ54428, KIAA0918	SLIT and NTRK-like family, member 1	NM_052910, hCT1647464.1	236734_at	NP_443142.1, EAW80606.1
GeneID.642345	hCG_1795283	13	88,096,242	88,323,218	226,976	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1791, 2_A375_pNL97_plus_lncRNA_AR..1..2506, 2_A375_pNL97_plus_lncRNA_AR..1..2507, 4_A375_EGR1..1..2213	172098, 172050, -302, 109277	in gene, in gene, upstream, in gene	1	1	1	15.67	19.33	8.33	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene hCG_1795283	LOC642345	hCG1818123	NR_033629	232848_at	
GeneID.26050	SLITRK5	13	88,324,870	88,331,871	7,001	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2507	-1350	upstream	0	1	0	23	28	11	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene SLITRK5	bA364G4.2, SLITRK5, LRRC11, FLJ56374, KIAA0918	SLIT and NTRK-like family, member 5	NM_015567	214930_at	NP_056382.1
GeneID.407975	MIR17HG	13	92,000,074	92,006,829	6,755	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2510	1334	in gene	0	1	0	7	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MIR17HG	FLJ14178, MGC126270, MIHG1, NCRNA00048, miR-17-92, MIRHG1, MIRH1, C13orf25, MIR17HG	MIR17 host gene (non-protein coding)	NR_027349, NR_027350	232291_at, 233636_at	
GeneID.406952	MIR17	13	92,002,859	92,002,942	83	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2510	-1451	upstream	0	1	0	7	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MIR17	miRNA17, MIR17, MIRN91, miR17-3p, MIR91, hsa-mir-17, MIRN17, miR-17, miRNA91, MIR17-5p	microRNA 17	NR_029487		
GeneID.406953	MIR18A	13	92,003,005	92,003,075	70	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2510	-1597	upstream	0	1	0	7	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MIR18A	MIRN18, MIR18A, MIRN18A, hsa-mir-18a, miR-18, MIR18, miRNA18A, hsa-mir-18	microRNA 18a	NR_029488		
GeneID.406979	MIR19A	13	92,003,145	92,003,226	81	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2510	-1737	upstream	0	1	0	7	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MIR19A	miR-19a, hsa-mir-19a, MIRN19A, miRNA19A, MIR19A	microRNA 19a	NR_029489		
GeneID.406982	MIR20A	13	92,003,319	92,003,389	70	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2510	-1911	upstream	0	1	0	7	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MIR20A	miRNA20A, MIR20, hsa-mir-20a, hsa-mir-20, MIR20A, MIRN20A, MIRN20, miR-20	microRNA 20a	NR_029492		
GeneID.406980	MIR19B1	13	92,003,446	92,003,532	86	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2510	-2036	upstream	0	1	0	7	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MIR19B1	MIRN19B1, MIR19B1, miR-19b-1, miRNA19B1	microRNA 19b-1	NR_029490		



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_2_A375_3_A375_4_A375_4_A375_Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene ID:4911946	MIR92A1	13	92,203,966	92,203,943	77	+	1	2_A375_uhi37_plus_lncRNA_AR_1.2310	-2186	upstream	0 1 0 7 16 8 1	2_A375_uhi37_plus_lncRNA_AR_1	16	Gene MIR92A1	MIR92A1, MIR92A1-1, MIR92A1-2, MIR92-1, miRNA92-1, MIR92A-1	microRNA 92a-1	NR_029500		
Gene ID:5262	GPC5	13	92,930,955	93,316,490	385,535	+	2	4_A375_EGR1_2.2216, 2_A375_uhi37_plus_lncRNA_AR_1.2311	497, 1445085	sr gene, rr gene	0 1 1 10.5 12 11 2	4_A375_EGR1_1.1	12	Gene GPC5	GPC5		NM_004466, XCT236250.4	207174_at	NP_004457.1, EAW50927.1
Gene ID:10262	GPC6	13	93,879,976	95,080,274	1,181,196	+	10	1_A375_uhi37_minus_lncRNA_AR_1.1795, 1_A375_uhi37_minus_lncRNA_AR_1.1799, 1_A375_uhi37_plus_lncRNA_AR_1.2313, 2_A375_uhi37_plus_lncRNA_AR_1.2314, 2_A375_uhi37_plus_lncRNA_AR_1.2315, 2_A375_uhi37_plus_lncRNA_AR_1.2316, 2_A375_uhi37_plus_lncRNA_AR_1.2317, 2_A375_uhi37_plus_lncRNA_AR_1.2318, 2_A375_uhi37_plus_lncRNA_AR_1.2319, 4_A375_EGR1_1.2217	122, 22949 - 6960, 90, 954, 22842, 107545, 828410, 1103182	sr gene, rr gene, upstream,sr gene, rr gene,intergene, rr gene, rr gene	1 1 1 14.43 20 8 7	2_A375_uhi37_plus_lncRNA_AR_1	25	Gene GPC6	GPC6, MGC126295, OMIM21	glypican 6	NM_005708, XCT234442.0, XCT234421.0, XCT234422.0, XCT234423.0	223700_at, 227089_at	NP_005699.1, EAW50933.1, EAW50931.1, EAW50932.1, EAW50934.1
Gene ID:23753	GDS	13	93,226,398	93,246,911	22,203	-	2	4_A375_uhi37_plus_lncRNA_AR_1.2320, 4_A375_EGR1_1.2218	-5809, 83	upstream, rr gene	0 1 1 14.5 19.5 16.5 2	4_A375_EGR1_1.1	20	Gene TGDS	TGDS, TDPGD, SDR2E1	TDP-glucose 4,6-dehydratase	NM_014305, XCT164553.3, XCT2291080.0	209249_s_at, 227048_at	NP_055120.1, EAX09940.1, EAX09941.1
Gene ID:10497	GPR160	13	93,254,104	93,281,948	27,842	+	2	4_A375_uhi37_plus_lncRNA_AR_1.2320, 4_A375_EGR1_1.2219	16, 5858	rr gene, upstream	0 1 1 14.5 19.5 16.5 2	4_A375_EGR1_1.1	20	Gene GPR160	DKFZp686C15222, DKFZp686Y16023, GPR160, ITR	G protein-coupled receptor 160	NM_139393, XCT2291081.0, XCT2291082.0, XCT241163.4	231071_at, 232912_at	NP_631920.1, EAW50943.1, EAW50942.1, EAW50944.1
Gene ID:10197	SOX21	13	95,361,076	95,364,309	3,233	-	1	4_A375_EGR1_1.2219	1061	rr gene	0 0 1 9 13 21 1	4_A375_EGR1_1.1	21	Gene SOX21	SOX21, SOX2B	SRY (sex determining region Y)-box 21	NM_007084, XCT1964542.2	205486_at	NP_009115.1, EAW50948.1
Gene ID:10197	LOC100507533	13	95,364,970	95,366,500	2,530	+	1	4_A375_EGR1_1.2219	-1642	upstream	0 2 1 9 13 21 1	4_A375_EGR1_1.1	21	Gene LOC100507533	SOX21-AS1	hypothetical LOC100507533	XR_109168		
Gene ID:10257	ABCC4	13	95,872,883	95,933,887	061,004	+	4	1_A375_uhi37_minus_lncRNA_AR_1.1800, 1_A375_uhi37_minus_lncRNA_AR_1.1801, 1_A375_uhi37_plus_lncRNA_AR_1.2321, 2_A375_uhi37_plus_lncRNA_AR_1.2322	2008831, 215, 2007791, 103	sr gene,rr gene,rr gene,rr gene	1 1 1 0 20 22 7.5 2	2_A375_uhi37_plus_lncRNA_AR_1	26	Gene ABCC4	EST170201, ABCC4, MOAT-B, MOATB, MRP4	ATP-binding cassette, sub-B, MDR/TAP, member 4	NM_005845, NM_001105515, XCT2344424.0, XCT2344425.0, XCT2344426.0, XCT2394439.0	1554810_s_at, 1553839_s_at, 203166_at, 243826_s_at	NP_005836.2, NP_001096953.1, EAW50945.1, EAW50946.1, EAW50947.1, EAW50932.1
Gene ID:11571	C13ORF18	13	96,065,655	96,232,010	166,157	+	2	1_A375_uhi37_minus_lncRNA_AR_1.1802, 2_A375_uhi37_plus_lncRNA_AR_1.2323	101645, 101627	sr gene, rr gene	1 1 1 0 23 25 7 1	2_A375_uhi37_plus_lncRNA_AR_1	25	Gene C13ORF18	DKFLp, C13ORF18, CPETRL3	chromosome 13 open reading frame 18	NM_182545, NM_006964, NM_001166100	1559667_s_at, 205526_at	NP_876895.1, NP_008915.1, NP_001153272.1
Gene ID:23373	DZIP1	13	96,230,436	96,296,957	66,521	-	1	2_A375_uhi37_plus_lncRNA_AR_1.2324	699	sr gene	0 1 0 19 18 11 1	2_A375_uhi37_plus_lncRNA_AR_1	26	Gene DZIP1	KIAA0990, DZIP1, DZIP, RP11-218I3.3, DZIP1	DAZ interacting protein 1	NM_014934, NM_180990, XCT19857.3, XCT2302127.0, XCT2302129.0	204506_s_at, 204537_s_at	NP_057475.1, NP_945319.1, EAW50936.1, EAW50937.1, EAW50938.1
Gene ID:10199	LOC100287274	13	96,235,089	96,239,161	4,072	-	2	1_A375_uhi37_minus_lncRNA_AR_1.1803, 2_A375_uhi37_plus_lncRNA_AR_1.2325	190, -943	sr gene, upstream	1 1 1 0 17 25 10 1	2_A375_uhi37_plus_lncRNA_AR_1	25	Gene LOC100287274	DKFZp686I15217	hypothetical protein LOC100287274	XR_111404, XR_109147, XR_114708		
Gene ID:11111	DNAJC13	3	96,239,393	96,447,343	117,830	+	2	1_A375_uhi37_minus_lncRNA_AR_1.1803, 2_A375_uhi37_plus_lncRNA_AR_1.2325	-428, 111	upstream,rr gene	1 1 1 0 17 25 10 1	2_A375_uhi37_plus_lncRNA_AR_1	25	Gene DNAJC13	FLJ21250, FSI, DNAJC13, HP30, RSHP1	DnaJ (Hsp40) homolog, subfamily C, member 13	NM_015268, XCT2302084.0	203489_s_at, 233541_at	NP_056351.1, EAW50939.1
Gene ID:29788	HSBP1L1	13	96,743,693	97,491,812	748,719	+	1	4_A375_EGR1_1.2221	907	sr gene	0 0 1 14 9 30 1	4_A375_EGR1_1.1	20	Gene HSBP1L1	HSBP1L1, DKFZp761E1215	HSBP1-like 1	NM_138436, XCT2302084.0	1552842_at, 229714_at, 232275_s_at, 232276_at	NP_722572.2, EAW50962.1
Gene ID:27199	CXXGR1	13	97,837,972	97,846,804	8,831	-	3	1_A375_uhi37_minus_lncRNA_AR_1.1804, 1_A375_uhi37_minus_lncRNA_AR_1.1805, 1_A375_EGR1_1.2222	92, -6922, 44	sr gene, upstream, rr gene	1 0 1 0 20 12.5 6 2	1_A375_uhi37_minus_lncRNA_NA_AR_1	23	Gene CXXGR1	GPR99, PZR1/3, MGC119206, MGC119207, CXXGR1, GPR99, MGC119205, PZY15	G protein-coupled receptor 99	NM_020518	1553219_at	NP_543008.2
Gene ID:10150	MBNL2	13	97,874,574	98,046,574	171,800	+	5	1_A375_uhi37_minus_lncRNA_AR_1.1806, 1_A375_uhi37_minus_lncRNA_AR_1.1807, 1_A375_uhi37_minus_lncRNA_AR_1.1808, 1_A375_uhi37_plus_lncRNA_AR_1.2326, 2_A375_uhi37_plus_lncRNA_AR_1.2327	32722, 75530, 175456, 144900, 172554	sr gene, rr gene, downstream, sr gene, downstream	1 1 1 0 15.5 17.5 5 4	2_A375_uhi37_plus_lncRNA_AR_1	23	Gene MBNL2	DKFZp761H1206, MBLL39, MGC126808, MBNL2, MGC126805, MBLL, MGC126806	muscleblind-like (Drosophila)	2 NM_144776, NM_207304, XCT1612620.2, XCT2161.0, XCT2302072.0, XCT2302073.0	225962_at, 235017_s_at, 235018_s_at, 232126_at	NP_659032.1, NP_997107.1, EAW50965.1, EAW50966.1, EAW50967.1, EAW50971.1
Gene ID:11111	RAPSA	13	98,066,475	98,120,252	53,777	+	1	1_A375_uhi37_minus_lncRNA_AR_1.1809	-491	upstream	1 0 0 21 16 7 1	1_A375_uhi37_plus_lncRNA_AR_1	21	Gene RAPSA	RAPS2, RAPSA, MREV, K-REV, RABT-32	RAPSA, member of RAS oncogene family	NM_021033, XCT1612617.3	214487_s_at	NP_066391.1, EAW50974.1
Gene ID:26119	EIF5A2	3	99,102,455	99,229,399	126,941	-	2	2_A375_uhi37_plus_lncRNA_AR_1.1812, 2_A375_uhi37_plus_lncRNA_AR_1.2330	69396, 100452	sr gene, rr gene	1 1 0 20 17 8.5 2	2_A375_uhi37_plus_lncRNA_AR_1	24	Gene STK24	STK24, MST3, MST38, STK3, STE20	serine/threonine kinase 24 (STE20 homolog, yeast)	NM_003576, NM_001033294, XCT189013.3, XCT189220.1, XCT2303986.0	205954_s_at, 209853_s_at, 231666_at	NP_003567.2, NP_001027497.2, EAW50968.1, EAW50969.1, EAW50970.1
Gene ID:23545	DOCK9	13	99,445,741	99,735,990	292,919	-	1	2_A375_uhi37_plus_lncRNA_AR_1.2331	-732	upstream	0 1 0 10 20 12 1	2_A375_uhi37_plus_lncRNA_AR_1	20	Gene DOCK9	DKFZp686H04153, DKFZp686C11176, FLJ43282, DZIMN1, ZIZ1, FLJ44335, DKFZp686I02047, FLJ11945, FLJ45611, FLJ18744, KIAA1268, DOCK9, KIAA1083	dedicator of cytokinesis 9	NM_015296, NM_001130945, NM_001130946, NM_001130950, XCT209764.1, XCT2302282.1, XCT2302283.0, XCT2302284.1, XCT2302285.0, XCT2302286.1, XCT2302287.1, XCT2302288.1, XCT2302289.1, XCT2302290.1, XCT2340481.0	212535_at, 212591_s_at, 212537_at, 215256_s_at, 232274_at	NP_056111.1, NP_001120520.1, NP_001120521.1, NP_001123522.1, EAW50994.1, EAW50953.1, EAW50995.1, EAW50996.1, EAW50997.1, EAW50998.1, EAW50999.1, EAW51000.1, EAW51001.1, EAW51002.1
Gene ID:10197	LOC100287273	13	99,646,635	99,653,011	6,353	-	1	2_A375_uhi37_plus_lncRNA_AR_1.2332	211	sr gene	0 1 0 15 26 19 1	2_A375_uhi37_plus_lncRNA_AR_1	26	Gene LOC100287273		hypothetical LOC100287273	NR_038551, NR_038552		
Gene ID:7997	UBAC2	13	99,852,879	100,038,793	186,074	+	1	2_A375_uhi37_plus_lncRNA_AR_1.2332	121	sr gene	0 1 0 15 26 19 1	2_A375_uhi37_plus_lncRNA_AR_1	26	Gene UBAC2	MGC90407, PHG-DHL1, FLJ39343, FLJ38001, FLJ38331, FLJ42413, UBAC2	UBA domain containing 2	NM_177967, NM_001144072, NR_029844, XCT2302083.0, XCT2302084.0, XCT2339394.0, XCT2339395.0, XCT2339396.0, XCT2339397.0, XCT2339580.0	224256_s_at	NP_808852.1, NP_001137944.1, EAW50916.1, EAW50911.1, EAW50918.1, EAW50919.1, EAW50912.1, EAW50913.1, EAW50914.1
Gene ID:7979	TMPSF2	13	100,182,725	100,213,276	61,345	+	2	2_A375_uhi37_plus_lncRNA_AR_1.1813, 2_A375_uhi37_plus_lncRNA_AR_1.2331	-112, -126	upstream, upstream	1 1 0 26 16 14 1	1_A375_uhi37_plus_lncRNA_NA_AR_1	28	Gene TMPSF2	PTS	transmembrane 9 superfamily member 2	NM_004503, XCT165802.3	201076_at	NP_004791.1, EAW50923.1
Gene ID:1435	CLYBL	13	100,238,919	100,349,200	360,489	+	2	2_A375_uhi37_plus_lncRNA_AR_1.1814, 2_A375_uhi37_plus_lncRNA_AR_1.2334	108657, 109823	sr gene, rr gene	1 1 1 0 21 23 4 1	2_A375_uhi37_plus_lncRNA_AR_1	23	Gene CLYBL	KIAA1616.1, CLYBL, CLIB	citrate lyase beta like	NM_206900, XCT2344456.0, XCT2344457.0	235440_at	NP_996331.1, EAW50923.1, EAW50924.1
Gene ID:5978	LOC100507838	13	100,738,355	100,741,197	2,912	-	3	1_A375_uhi37_minus_lncRNA_AR_1.1815, 2_A375_uhi37_plus_lncRNA_AR_1.2333, 2_A375_EGR1_1.2220	45, 81, 125	sr gene, rr gene, sr gene	1 1 1 1 24 16 10 1	1_A375_uhi37_plus_lncRNA_NA_AR_1	24	Gene LOC100507838		hypothetical LOC100507838	XR_111403, XR_109151, XR_114710		
Gene ID:95	PCCA	13	100,741,299	101,102,691	441,432	+	4	2_A375_uhi37_plus_lncRNA_AR_1.1815, 2_A375_uhi37_plus_lncRNA_AR_1.2333, 4_A375_EGR1_1.2220, 4_A375_EGR1_1.2226	-117, -123, -197, 160499	upstream, upstream, upstream, sr gene	1 1 1 0 14 11.5 17 2	1_A375_uhi37_plus_lncRNA_NA_AR_1	24	Gene PCCA	PCCA		NM_000282, NM_001127692, NM_001178034, XCT1902547.1, XCT2301914.0, XCT2301915.0	202980_at, 216833_at, 232276_at	NP_000272.2, NP_001121164.1, NP_001174251.1, EAW50932.1, EAW50933.1, EAW50934.1
Gene ID:7769	AZLD1	13	101,182,418	101,241,048	58,826	-	2	2_A375_uhi37_plus_lncRNA_AR_1.1816, 2_A375_uhi37_plus_lncRNA_AR_1.2336	-42, -42	upstream, upstream	1 1 0 36 35 10 1	4_A375_uhi37_minus_lncRNA_NA_AR_1	36	Gene AZLD1	SGACT, AZLD1		NM_001199097, NM_022110	223422_at, 237689_at	NP_001182161.1, NP_149101.1
Gene ID:5978	LOC100507854	13	101,187,995	101,232,371	44,376	-	2	2_A375_uhi37_minus_lncRNA_AR_1.1816, 2_A375_uhi37_plus_lncRNA_AR_1.2336	-5717, -5717	upstream, upstream	1 1 0 36 35 10 1	1_A375_uhi37_plus_lncRNA_NA_AR_1	36	Gene LOC100507854		hypothetical LOC100507854	XR_111399, XR_109152, XR_114711		
Gene ID:96	ITGB1	13	102,104,998	102,280,794	283,828	+	1	1_A375_uhi37_minus_lncRNA_AR_1.1817	13402	sr gene	1 1 0 21 11 4 1	1_A375_uhi37_plus_lncRNA_NA_AR_1	21	Gene ITGB1	FIBD, ITGB1, CD29	integrin, beta-like 1 (with EGF-like repeat domains)	NM_004791, XCT2301929.0, XCT2301930.0	1557074_at, 1557080_s_at, 209422_s_at, 214027_at	NP_004782.1, EAW50953.1, EAW50952.1
Gene ID:99	FGF14	13	102,370,205	103,096,124	960,919	-	7	1_A375_uhi37_minus_lncRNA_AR_1.1818, 1_A375_uhi37_minus_lncRNA_AR_1.1819, 2_A375_uhi37_plus_lncRNA_AR_1.2337, 2_A375_uhi37_plus_lncRNA_AR_1.2338, 2_A375_uhi37_plus_lncRNA_AR_1.2339, 4_A375_EGR1_1.2225, 4_A375_EGR1_1.2228	539044, 452092, 452140, 1124, 4020, 465420, 1464	sr gene, rr gene, rr gene, upstream, rr gene, upstream, rr gene, rr gene	1 1 1 1 12.6 15 11.2 5	2_A375_uhi37_plus_lncRNA_AR_1	25	Gene FGF14	SCA27, FHF4, MGC119129, FGF14	fibroblast growth factor 14	NM_175929, NM_004115, XCT191552.5, XCT2301936.0	221310_at, 230266_at, 231822_at	NP_787125.1, NP_004108.1, EAW50934.1
Gene ID:5481	LOC283531	13	102,944,870	103,048,069	102,199	+	2	2_A375_uhi37_plus_lncRNA_AR_1.2335, 4_A375_EGR1_1.2228	-5921, -5771	upstream, upstream	0 0 1 14 9.5 19 1	4_A375_EGR1_1.1	19	Gene LOC283531		hypothetical LOC283531	NR_038455	237392_at	
Gene ID:5481	LOC283531	13	103,048,926	103,048,055	1,127	+	3	2_A375_uhi37_plus_lncRNA_AR_1.2335, 2_A375_uhi37_plus_lncRNA_AR_1.2339, 2_A375_EGR1_1.2228	5872, 11218, 5712	downstream, downstream, downstream	0 1 1 10 21.5 12.5 2	2_A375_uhi37_plus_lncRNA_AR_1	25	Gene LOC283531		hypothetical LOC283531	NR_038457	230031_at, 243229_at	
Gene ID:7170	TPP2	13	103,249,266	103,331,524	82,258	+	1	2_A375_uhi37_plus_lncRNA_AR_1.2340	-54	upstream	0 1 0 15 19 11 1	2_A375_uhi37_plus_lncRNA_AR_1	19	Gene TPP2	TPP2, FLJ40315	tripeptidyl peptidase II	NM_003291, XCT20903.0	1569036_at, 1569037_s_at, 203274_s_at, 203275_s_at	NP_003282.2, EAW50959.1
Gene ID:7174	ERCC5	13	103,498,174	103,538,345	39,171	+	1	2_A375_uhi37_plus_lncRNA_AR_1.2343	18	sr gene	0 1 0 26 31 17 1	2_A375_uhi37_plus_lncRNA_AR_1	31	Gene ERCC5	XPGC, ERCM2, ERCC5, XPG, DKFZp686D08222	excision repair cross-complementing rodent repair deficiency, complementation group 5	NM_000123, XCT20952.3, XCT2302076.0	202214_at	NP_000114.2, EAW50971.1, EAW50972.1
Gene ID:7170	KDELC1	13	103,438,831	103,451,404	14,773	-	3	1_A375_uhi37_minus_lncRNA_AR_1.1820, 2_A375_uhi37_plus_lncRNA_AR_1.2341, 2_A375_uhi37_plus_lncRNA_AR_1.2342	23100, 141, -620	downstream, sr gene, upstream	1 1 0 13.33 17 14 3	2_A375_uhi37_plus_lncRNA_AR_1	20	Gene KDELC1	MGC3202, ERS1, KDELC1, KDEL1	KDEL (Lys-Asp-Glu-Leu) containing 1	NM_030915, XCT20954.3, XCT2302770.0, XCT2309380.0	219479_at	NP_076994.2, EAW50971.1, EAW50968.1, EAW50969.1
Gene ID:5611	BIVM	13	103,451,599	103,492,695	42,469	+	5	2_A375_uhi37_plus_lncRNA_AR_1.2341, 2_A375_uhi37_plus_lncRNA_AR_1.2342, 2_A375_uhi37_plus_lncRNA_AR_1.2343	-139, 623, 46795	upstream,sr gene, downstream	0 1 0 13.67 22.67 13.33 2	2_A375_uhi37_plus_lncRNA_AR_1	24	Gene BIVM	FLJ44356, MGC133326, FLJ44351, BIVM	basic, immunoglobulin-like variable motif containing	NM_017922, NM_001159299, XCT20953.3	1565229_at, 222761_at, 229475_s_at, 229559_s_at, 233255_s_at	NP_060183.2, NP_001153060.1, EAW50970.1
Gene ID:2078	ERCC5	13	103,498,174	103,538,345	39,171	+	1	2_A375_uhi37_plus_lncRNA_AR_1.2343	18	sr gene	0 1 0 26 31 17 1	2_A375_uhi37_plus_lncRNA_AR_1	31	Gene ERCC5	XPGC, ERCM2, ERCC5, XPG, DKFZp686D08222	excision repair cross-complementing rodent repair deficiency, complementation group 5	NM_000123, XCT20952.3, XCT2302076.0	202214_at	NP_000114.2, EAW50971.1, EAW50972.1
Gene ID:5162	LOC729151	13	107,028,911	107,030,140	1,229	+	1	2_A375_uhi37_plus_lncRNA_AR_1.2344	401	sr gene	0 1 0 16 22 11 1	2_A375_uhi37_plus_lncRNA_AR_1	22	Gene LOC729152		hypothetical LOC729152	NR_034119	1563062_at	
Gene ID:4649	EPHB2	13	107,142,093	107,187,337	45,244	-	2	2_A375_uhi37_plus_lncRNA_AR_1.1820, 2_A375_uhi37_plus_lncRNA_AR_1.2339	21033, 27051	sr gene, rr gene	1 1 0 17 15.5 7 2	2_A375_uhi37_plus_lncRNA_AR_1	17	Gene EPHB2	LERK5, EPHB2, Hek5, MGC126227, MGC126228, HTK5, EPLG5, MGC126225	eph-like tyrosine kinase 5	NM_004093, XCT2302194.0	202865_at, 202869_s_at	NP_004084.1, EAW50955.1
Gene ID:5322	ARGLU1	13	107,198,992	107,230,314	34,552	+	1	2_A375_uhi37_plus_lncRNA_AR_1.2337	430	sr gene	0 1 0 16 16 10 1	2_A375_uhi37_plus_lncRNA_AR_1	16	Gene ARGLU1	ARGLU1, DKFZp686D00039, FLJ10154	arginine and glutamate rich 1	NM_015011, XCT1662588.2, XCT2302170.0	218087_s_at, 223509_s_at	NP_055811.2, EAW50951.1, EAW50967.1, EAW50971.1
Gene ID:3218	FAM155A	13	107,838,979	108,378,490	999,511	+	2	2_A375_uhi37_plus_lncRNA_AR_1.1829, 2_A375_uhi37_plus_lncRNA_AR_1.2355	2805, 2404	sr gene, rr gene	1 1 0 23 24 8 1	2_A375_uhi37_plus_lncRNA_AR_1	24	Gene FAM155A	FAM155A	Binary with sequence similarity 155, member A	NM_031930	214529_at, 233969_at	NP_001073895.1
Gene ID:61	UGA	13	108,639,790	108,679,716	39,926	-	2	1_A375_uhi37_minus_lncRNA_AR_1.1832, 2_A375_uhi37_plus_lncRNA_AR_1.2360	-100, 92	upstream, rr gene	1 1 0 21 24 13 1	2_A375_uhi37_plus_lncRNA_AR_1	24	Gene UGA	UGA		NM_032112, NM_206937, NM_001039266, NCT16666310.0, XCT2302232.0, XCT2302234.0	206235_at, 227766_at	NP_932333.2, NP_996820.1, NP_001017120.1, EAW50934.1, EAW50936.1, EAW50961.1
Gene ID:9443	ABHD10	13	108,679,783	108,698,603	18,840	+	2	1_A375_uhi37_minus_lncRNA_AR_1.1833, 2_A375_uhi37_plus_lncRNA_AR_1.2360	133, -139	sr gene, upstream	1 1 0 21 24 13 1	2_A375_uhi37_plus_lncRNA_AR_1	24	Gene ABHD10	BEM46L1, MGC27659, RP11-183D4.2, C13orf6, ABHD10, bA183D4.2, FLJ14356	alpha/beta hydrolase domain containing 10	NM_032259, XCT1662039.3, XCT2302228.0	224893_at, 233849_at	NP_115634.2, EAW50961.1, EAW50967.1
Gene ID:8772	TNFSF13B	13	109,521,977	109,539,365	37,388	+	1	2_A375_uhi37_plus_lncRNA_AR_1.2361	6167	sr gene	0 1 0 17 21 7 1	2_A375_uhi37_plus_lncRNA_AR_1	21	Gene TNFSF13B	TALL1, BAFF, CD257, TALL-1, bB71-93.1, TNFSF20, TNFSF13B, ZTNF4, TNFSF20	tumor necrosis factor (ligand) superfamily, member 13b	NM_006573, NM_001146943, XCT19597.1, XCT1662320.1, XCT1662321.1	223301_at, 223302_s_at	NP_006564.1, NP_001128117.1, EAW50961.1, EAW50963.1, EAW50967.1
Gene ID:228	MYO1E	13	109,248,500	109,680,555	611,055	+	4	2_A375_uhi37_plus_lncRNA_AR_1.2362, 2_A375_uhi37_plus_lncRNA_AR_1.2363, 2_A375_uhi37_plus_lncRNA_AR_1.2364, 2_A375_uhi37_plus_lncRNA_AR_1.2365	338476, 339324, 339832, 554601	sr gene, rr gene, rr gene, rr gene	1 0 1 0 14 17 8 4	2_A375_uhi37_plus_lncRNA_AR_1	16	Gene MYO1E	MYO1E, MYR2, Myo16b, KIAA0663	myosin IE	NM_004998, XCT20955.3	1557720_s_at, 218119_at	NP_005518.1
Gene ID:90	IRS2	13	110,486,164	110,498,914	12,750	-	4	1_A375_uhi37_minus_lncRNA_AR_1.1822, 2_A375_uhi37_plus_lncRNA_AR_1.2366, 2_A375_uhi37_plus_lncRNA_AR_1.2367, 4_A375_EGR1_1.2230	2733, 3962, -4762, 3922	sr gene, rr gene, upstream,sr gene	1 1 1 16 20 12 2	1_A375_uhi37_plus_lncRNA_NA_AR_1	24	Gene IRS2	IRS2, IRS-2	insulin receptor substrate 2	NM_003749	209184_s_at, 209185_s_at	NP_003740.2
Gene ID:1302	COL4A1	13	110,801,310	110,939,496	138,186	-	4	1_A375_uhi37_minus_lncRNA_AR_1.1826, 2_A375_uhi37_plus_lncRNA_AR_1.2374, 4_A375_EGR1_1.2231, 4_A375_EGR1_1.2232	-596, -34, 41064, 836	upstream, upstream, intergene, upstream	1 1 1 0 12.5 22 2	4_A375_EGR1_1.1	27	Gene COL4A1	COL4A1, arresten	collagen, type IV, alpha 1	NM_001845, XCT2302530.0, XCT24254.2	211980_at, 217891_at	NP_001836.2, EAW50961.1, EAW50967.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:1284	COL4A2	13	110,959,631	111,165,374	205,743	+	9	1_A375_pNL7_minus_lncRNA_AR..1..1836, 1_A375_pNL7_minus_lncRNA_AR..1..1837, 2_A375_pNL97_plus_lncRNA_AR..1..2574, 2_A375_pNL97_plus_lncRNA_AR..1..2575, 4_A375_EGR1..1..2232, 1_A375_pNL7_minus_lncRNA_AR..1..1838, 2_A375_pNL97_plus_lncRNA_AR..1..2576, 4_A375_EGR1..1..2233, 4_A375_EGR1..1..2234	433, 12641, -111, 12417, 721, 192465, 192353, 108321, 198289	in gene, in gene, upstream, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	17	16.4	15.8	5	4_A375_EGR1..1	27	Gene COL4A2	FLJ22259, DKFZp686I14213, COL4A2	collagen, type IV, alpha 2	NM_001846, hCT2359360.0, hCT24235.3	211964_at, 211966_at	NP_001837.2, EAX09112.1, EAX09111.1
GeneID:55647	RAB20	13	111,175,413	111,214,071	38,658	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2577, 4_A375_EGR1..1..2235	407, 35927	in gene, in gene	0	1	1	9.5	15.5	19	2	4_A375_EGR1..1	20	Gene RAB20	FLJ20429, RAB20	RAB20, member RAS oncogene family	NM_017817, hCT24236.2	219622_at, 237373_at	NP_060287.1, EAX09113.1
GeneID:55739	CARKD	13	111,268,008	111,292,343	24,335	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1839, 2_A375_pNL97_plus_lncRNA_AR..1..2578, 4_A375_EGR1..1..2236, 4_A375_EGR1..1..2237, 4_A375_EGR1..1..2238	-166, 376, -456, 10360, 27000	upstream, in gene, upstream, in gene, downstream	1	1	1	11	12.33	18	3	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene CARKD	FLJ10769, LP3298, FLJ52550, FLJ34548, CARKD	carbohydrate kinase domain containing	NM_018210, hCT1962332.1, hCT1962333.1, hCT1962334.1, hCT1962335.0, hCT1962336.1, hCT1962337.1, hCT1967445.1, hCT2302674.0, hCT2359371.0, hCT2359372.0, hCT2359373.0, hCT23741.2	217940_s_at	NP_060680.2, EAX09118.1, EAX09114.1, EAX09119.1, EAX09120.1, EAX09124.1, EAX09115.1, EAX09116.1, EAX09117.1, EAX09121.1, EAX09122.1, EAX09123.1, EAX09125.1
GeneID:79587	CARS2	13	111,293,757	111,358,480	64,723	-	5	2_A375_pNL97_plus_lncRNA_AR..1..2579, 2_A375_pNL97_plus_lncRNA_AR..1..2580, 4_A375_EGR1..1..2238, 4_A375_EGR1..1..2239, 4_A375_EGR1..1..2240	-6980, -9128, 63472, -6544, -9284	upstream, upstream, in gene, upstream, upstream	0	1	1	13.33	14.67	21	3	4_A375_EGR1..1	26	Gene CARS2	FLJ42514, FLJ12118, CARS2, DKFZp667A2315, DKFZp686G08243	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	NM_024537, hCT1952868.2	218153_at, 231023_at	NP_078813.1, EAX09126.1
GeneID:3621	ING1	13	111,365,083	111,373,421	8,338	+	4	2_A375_pNL97_plus_lncRNA_AR..1..2579, 2_A375_pNL97_plus_lncRNA_AR..1..2580, 4_A375_EGR1..1..2239, 4_A375_EGR1..1..2240	357, 2525, -59, 2661	in gene, in gene, upstream, in gene	0	1	1	17	16.5	22.5	2	4_A375_EGR1..1	26	Gene ING1	p47, ING1, p47ING1a, p33ING1b, p33ING1, p33, p24ING1c	inhibitor of growth family, member 1	NM_005537, NM_198217, NM_198218, NM_198219, hCT1813462.1, hCT1952880.1, hCT1952881.1, hCT2302687.0, hCT2359365.0	1557179_s_at, 208415_x_at, 209808_x_at, 210350_x_at, 237555_at, 244617_at	NP_005528.3, NP_937860.1, NP_937861.1, NP_937862.1, EAX09127.1, EAX09129.1, EAX09128.1, EAX09130.1, EAX09131.1
GeneID:283487	C13orf29	13	111,516,334	111,522,655	6,321	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2581	-65	upstream	0	1	0	23	26	10	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene C13orf29	FLJ97904, C13orf29	chromosome 13 open reading frame 29	NR_027701		
GeneID:55608	ANKRD10	13	111,530,887	111,567,416	36,529	-	4	2_A375_pNL97_plus_lncRNA_AR..1..2581, 2_A375_pNL97_plus_lncRNA_AR..1..2582, 4_A375_EGR1..1..2243, 4_A375_EGR1..1..2244	44696, 184, 312, -660	downstream, in gene, in gene, upstream	0	1	1	20.5	26	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ANKRD10	DKFZp686B07190, ANKRD10, FLJ20093	ankyrin repeat domain 10	NM_017664, hCT1644830.2, hCT2302868.0, hCT2302870.0	218093_s_at, 223251_s_at, 226663_at, 227280_at, 239116_at, 241414_at	NP_060134.2, EAX09134.1, EAX09135.1, EAX09136.1
GeneID:100505512	LOC100505512	13	111,597,823	111,623,935	26,112	-	2	4_A375_EGR1..1..2245, 4_A375_EGR1..1..2246	17951, 16511	in gene, in gene	0	0	1	10	15	15	2	4_A375_EGR1..1	16	Gene LOC100505512		hypothetical LOC100505512	XR_111396, XR_109156, XR_114715		
GeneID:8874	ARHGEF7	13	111,767,624	111,958,081	190,457	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1840, 2_A375_pNL97_plus_lncRNA_AR..1..2583, 4_A375_EGR1..1..2248, 4_A375_EGR1..1..2249	38200, 38392, -600, 38120	in gene, in gene, upstream, in gene	1	1	1	20	19.5	21	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene ARHGEF7	KIAA0412, P85COOL1, PAK3, COOL1, KIAA0142, DKFZp686C12170, Nbla10314, P85, P50, COOL-1, P85SPR, P50BP, DKFZp761K1021, PIXB, ARHGEF7, BETA-PIX	Rho guanine nucleotide exchange factor (GEF) 7	NM_003899, NM_145735, NM_001113511, NM_001113512, NM_001113513, hCT1952882.2, hCT2302697.1, hCT2302699.1, hCT2302700.1, hCT2302701.1, hCT2350672.0, hCT2350673.0, hCT2359381.0	1562270_at, 1562271_x_at, 202547_s_at, 202548_s_at, 229642_at, 235412_at, 239397_at, 242999_at	NP_003890.1, NP_663788.1, NP_001106983.1, NP_001106984.1, NP_001106985.1, EAX09144.1, EAX09142.1, EAX09143.1, EAX09145.1, EAX09146.1, EAX09147.1, EAX09148.1, EAX09149.1
GeneID:100505533	LOC100505533	13	111,800,544	111,805,924	5,380	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1840, 2_A375_pNL97_plus_lncRNA_AR..1..2583, 4_A375_EGR1..1..2249	100, -92, 180	in gene, upstream, in gene	1	1	1	27	30	27	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene LOC100505533		hypothetical LOC100505533	XR_111395, XR_109157, XR_114716		
GeneID:6656	SOX1	13	112,721,913	112,726,020	4,107	+	1	4_A375_EGR1..1..2263	-9177	upstream	0	0	1	3	5	18	1	4_A375_EGR1..1	18	Gene SOX1	SOX1		NM_005986, hCT1640565.3	208533_at, 230962_at, 237472_at	NP_005977.2, EAX09158.1
GeneID:10426	TUBGCP3	13	113,139,328	113,242,481	103,153	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1841, 2_A375_pNL97_plus_lncRNA_AR..1..2584, 4_A375_EGR1..1..2268	505, 625, -127	in gene, in gene, upstream	1	1	1	16	22	19	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene TUBGCP3	Spc98p, SPBC98, TUBGCP3, GCP3	tubulin, gamma complex associated protein 3	NM_006322, hCT18496.2, hCT2304169.0, hCT2304171.0, hCT2304172.0	1554086_at, 203690_at, 215739_s_at	NP_006313.1, EAX09164.1, EAX09163.1, EAX09165.1, EAX09166.1
GeneID:23250	ATP11A	13	113,344,643	113,541,482	196,839	+	3	4_A375_EGR1..1..2269, 4_A375_EGR1..1..2270, 4_A375_EGR1..1..2271	142189, 186477, 196877	in gene, in gene, downstream	0	0	1	5.33	6.33	17.33	3	4_A375_EGR1..1	19	Gene ATP11A	ATP11A, ATPIS, ATPIH	ATPase, class VI, type 11A	NM_032189, NM_015205, hCT2303898.0	213582_at, 215842_s_at, 216486_s_at, 230875_s_at, 241603_at, 241604_at	NP_115565.3, NP_056020.2, EAX09171.1
GeneID:100506063	LOC100506063	13	113,548,736	113,612,478	63,742	+	2	4_A375_EGR1..1..2271, 4_A375_EGR1..1..2272	-5216, 40000	upstream, in gene	0	0	1	5	8	22	2	4_A375_EGR1..1	25	Gene LOC100506063		hypothetical LOC100506063	XR_111408, XR_110307, XR_114720		
GeneID:100289410	LOC100289410	13	113,621,798	113,622,952	1,154	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2585	-152	upstream	0	1	0	9	23	17	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100289410	MCF2L-AS1	MCF2L antisense RNA 1 (non-protein coding)	NR_034002		
GeneID:23263	MCF2L	13	113,622,757	113,752,862	130,105	+	19	2_A375_pNL97_plus_lncRNA_AR..1..2585, 2_A375_pNL97_plus_lncRNA_AR..1..2586, 4_A375_EGR1..1..2273, 4_A375_EGR1..1..2274, 4_A375_EGR1..1..2275, 4_A375_EGR1..1..2276, 4_A375_EGR1..1..2277, 4_A375_EGR1..1..2278, 4_A375_EGR1..1..2279, 4_A375_EGR1..1..2280, 4_A375_EGR1..1..2281, 4_A375_EGR1..1..2282, 4_A375_EGR1..1..2283, 4_A375_EGR1..1..2284, 4_A375_EGR1..1..2285, 4_A375_EGR1..1..2286, 4_A375_EGR1..1..2287, 4_A375_EGR1..1..2288, 4_A375_EGR1..1..2289	347, 98411, 25915, 26475, 37707, 42251, 45755, 53691, 65435, 73723, 74663, 79323, 87547, 97499, 98715, 105767, 109211, 110203, 138427	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, downstream	0	1	1	6.9	9.64	19.74	19	4_A375_EGR1..1	26	Gene MCF2L	FLJ12122, ARHGEF14, KIAA0362, OST, DBS, MCF2L	MCF.2 cell line derived transforming sequence-like	NM_024979, NM_001112732, hCT1813208.1, hCT19026.3, hCT2302466.1, hCT2340540.0, hCT2340541.0, hCT2359370.0	1552743_at, 1559427_at, 1563608_at, 1563609_a_at, 212935_at, 220464_at, 239636_at, 35147_at	NP_079255.3, NP_001106203.1, EAX09175.1, EAX09176.1, EAX09177.1, EAX09179.1, EAX09178.1, EAX09180.1
GeneID:2155	F7	13	113,760,105	113,774,995	14,890	+	4	4_A375_EGR1..1..2289, 4_A375_EGR1..1..2290, 4_A375_EGR1..1..2291, 4_A375_EGR1..1..2292	1079, 9943, 15959, 24311	in gene, in gene, downstream, downstream	0	0	1	6.5	7.75	20.25	4	4_A375_EGR1..1	26	Gene F7	F7		NM_000131, NM_019616, hCT1813209.2, hCT19021.3	207300_s_at, 237414_at	NP_000122.1, NP_062562.1, EAX09182.1, EAX09183.1
GeneID:2159	F10	13	113,777,113	113,803,843	26,730	+	4	4_A375_EGR1..1..2290, 4_A375_EGR1..1..2291, 4_A375_EGR1..1..2292, 4_A375_EGR1..1..2293	-7065, -1049, 7303, 21522	upstream, upstream, in gene, in gene	0	0	1	7.25	8.5	20.25	4	4_A375_EGR1..1	26	Gene F10	F10, FX, FXA	coagulation factor X	NM_000504, hCT19022.3, hCT2359382.0	205620_at	NP_000495.1, EAX09184.1, EAX09185.1
GeneID:55795	PCID2	13	113,831,925	113,863,029	31,104	-	6	1_A375_pNL7_minus_lncRNA_AR..1..1842, 2_A375_pNL97_plus_lncRNA_AR..1..2587, 2_A375_pNL97_plus_lncRNA_AR..1..2588, 2_A375_pNL97_plus_lncRNA_AR..1..2589, 4_A375_EGR1..1..2294, 4_A375_EGR1..1..2295	53, 21349, 20341, 117, 23813, 21	in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	18.25	19.75	15	4	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene PCID2	MGC16774, DKFZp686C20226, FLJ11305, F10, PCID2, FLJ99362	PCI domain containing 2	NM_018386, NM_001127202, NM_001127203, hCT19028.2, hCT1967441.1, hCT1967442.1, hCT1967443.1, hCT2302798.0, hCT2302799.0, hCT2359374.0, hCT2359375.0, hCT2359376.0, hCT2359377.0, hCT2359378.0	219940_s_at, 225149_at	NP_060856.2, NP_001120674.1, NP_001120675.1, EAX09189.1, EAX09192.1, EAX09196.1, EAX09190.1, EAX09191.1, EAX09193.1, EAX09194.1, EAX09195.1, EAX09197.1, EAX09198.1, EAX09199.1
GeneID:100506079	LOC100506079	13	113,842,110	113,843,310	1,200	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2587, 2_A375_pNL97_plus_lncRNA_AR..1..2588, 4_A375_EGR1..1..2294	1630, 622, 4094	downstream, in gene, downstream	0	1	1	13.33	16.67	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100506079		hypothetical protein LOC100506079	XM_003119561, XM_003118933, XM_003120774		XP_003119609.1, XP_003118981.1, XP_003120822.1
GeneID:8451	CUL4A	13	113,863,086	113,919,392	56,306	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1842, 2_A375_pNL97_plus_lncRNA_AR..1..2589, 4_A375_EGR1..1..2295	-110, -174, -76	upstream, upstream, upstream	1	1	1	33	29	23	1	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene CUL4A	CUL4A		NM_003589, NM_001008895, hCT19027.1	201423_s_at, 201424_s_at, 227757_at, 232466_at, 242194_at	NP_003580.1, NP_001008895.1, EAX09201.1
GeneID:3916	LAMP1	13	113,951,469	113,977,741	26,272	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1843, 2_A375_pNL97_plus_lncRNA_AR..1..2590, 4_A375_EGR1..1..2296	-77, -77, -461	upstream, upstream, upstream	1	1	1	37	36	20	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene LAMP1	LGP120, LAMPA, CD107a, LAMP1	lysosomal-associated membrane protein 1	NM_005561, hCT19023.2, hCT2302484.0	201551_s_at, 201552_at, 201553_s_at, 213728_at	NP_005552.3, EAX09203.1, EAX09202.1
GeneID:79774	GRTP1	13	113,978,505	114,018,463	39,958	-	2	4_A375_EGR1..1..2297, 4_A375_EGR1..1..2298	13023, -2273	in gene, upstream	0	0	1	6	8.5	17	2	4_A375_EGR1..1	19	Gene GRTP1	MGC138330, FLJ22474, MGC138328, GRTP1, TBC1D6	growth hormone regulated TBC protein 1	NM_024719, hCT19025.3, hCT2302789.0, hCT2302791.0	206712_at, 229377_at	NP_078995.2, EAX09204.1, EAX09205.1, EAX09206.1
GeneID:113622	ADPRHL1	13	114,076,260	114,107,839	31,579	-	6	4_A375_EGR1..1..2302, 4_A375_EGR1..1..2303, 4_A375_EGR1..1..2304, 4_A375_EGR1..1..2305, 4_A375_EGR1..1..2306, 4_A375_EGR1..1..2307	41535, 40159, 39439, 30591, 20351, 6111	downstream, downstream, downstream, in gene, in gene, in gene	0	0	1	10.33	8.5	19.33	6	4_A375_EGR1..1	22	Gene ADPRHL1	ADPRHL1, ARH2	ADP-ribosylhydrolase like 1	NM_199162, NM_138430, hCT18462.2, hCT1967439.1	1553163_at, 238054_at	NP_954631.1, NP_612439.2, EAX09208.1, EAX09209.1
GeneID:55208	DCUN1D2	13	114,110,134	114,145,023	34,889	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1845, 2_A375_pNL97_plus_lncRNA_AR..1..2593	-225, -289	upstream, upstream	1	1	0	22	38	7	1	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene DCUN1D2	FLJ20092, C13orf17, FLJ10704, DCUN1D2	DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)	NM_001014283, hCT18419.3, hCT1967438.1	219116_s_at	NP_001014305.1, EAX09210.1, EAX09211.1
GeneID:55002	TMCO3	13	114,145,308	114,204,544	59,236	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1845, 2_A375_pNL97_plus_lncRNA_AR..1..2593, 4_A375_EGR1..1..2308	-60, 4, 55876	upstream, in gene, in gene	1	1	1	16	22.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene TMCO3	C13orf11, FLJ20623, TMCO3	transmembrane and coiled-coil domains 3	NM_017905, hCT18461.3, hCT1952885.1, hCT2302429.0, hCT2302430.0	220240_s_at, 220241_at, 226050_at, 230317_x_at	NP_060375.4, EAX09212.1, EAX09213.1, EAX09214.1, EAX09215.1
GeneID:7027	TFDP1	13	114,239,003	114,295,788	56,785	+	1	4_A375_EGR1..1..2309	23445	in gene	0	0	1	7	7	20	1	4_A375_EGR1..1	20	Gene TFDP1	DRTF1, DP1, Dp-1, TFDP1	transcription factor Dp-1	NM_007111, NR_026580, hCT2302434.0, hCT2302435.0, hCT2302436.0, hCT2302437.0	204147_s_at, 212330_at, 242538_at, 242939_at	NP_009042.1, EAX09217.1, EAX09216.1, EAX09218.1, EAX09219.1
GeneID:496	ATP4B	13	114,303,119	114,312,513	9,394	-	3	4_A375_EGR1..1..2310, 4_A375_EGR1..1..2311, 4_A375_EGR1..1..2312	2145, -255, -9695	in gene, upstream, upstream	0	0	1	6	12	21	3	4_A375_EGR1..1	24	Gene ATP4B	ATP4B, ATP6B	ATPase, H+/K+ exchanging, beta polypeptide	NM_000705, hCT2349660.0, hCT9948.3	1563405_at, 1563407_x_at, 207546_at	NP_000696.1, EAX09220.1, EAX09221.1
GeneID:6011	GRK1	13	114,321,594	114,325,992	4,398	+	6	4_A375_EGR1..1..2311, 4_A375_EGR1..1..2312, 4_A375_EGR1..1..2313, 4_A375_EGR1..1..2314, 4_A375_EGR1..1..2315, 4_A375_EGR1..1..2316	-8826, 614, 2365, 1730, 4258, 11490	upstream, in gene, in gene, in gene, in gene, in gene	0	0	1	6.83	11.5	19.83	6	4_A375_EGR1..1	25	Gene GRK1	GPRK1, GRK1, RHOK, RK	G protein-coupled receptor kinase 1	NM_002929, hCT9702.3	208041_at	NP_002920.1, EAX09222.1
GeneID:100130386	LOC100130386	13	114,451,484	114,454,062	2,578	-	1	4_A375_EGR1..1..2317	3246	downstream	0	0	1	7	5	15	1	4_A375_EGR1..1	15	Gene LOC100130386	FLJ32873	hypothetical LOC100130386	NR_026084		
GeneID:348013	FAM70B	13	114,462,216	114,514,899	52,683	+	10	1_A375_pNL7_minus_lncRNA_AR..1..1846, 1_A375_pNL7_minus_lncRNA_AR..1..1847, 2_A375_pNL97_plus_lncRNA_AR..1..2594, 2_A375_pNL97_plus_lncRNA_AR..1..2595, 4_A375_EGR1..1..2318, 4_A375_EGR1..1..2319, 4_A375_EGR1..1..2320, 4_A375_EGR1..1..2321, 4_A375_EGR1..1..2322, 4_A375_EGR1..1..2323	26120, 61912, 26056, 62744, 16312, 41496, 47928, 51656, 61576, 63040	in gene, downstream, in gene, downstream, in gene, in gene, in gene, in gene, downstream, downstream	1	1	1	13.5	14.67	19	6	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene FAM70B	FAM70B, MGC20579, RP11-199F6.1, FLJ57936	family with sequence similarity 70, member B	NM_182614, hCT2302442.0	238226_at	NP_872420.1, EAX09225.1
GeneID:2621	GAS6	13	114,523,522	114,567,046	43,524	-	9	1_A375_pNL7_minus_lncRNA_AR..1..1847, 1_A375_pNL7_minus_lncRNA_AR..1..1848, 2_A375_pNL97_plus_lncRNA_AR..1..2595, 4_A375_EGR1..1..2321, 4_A375_EGR1..1..2322, 4_A375_EGR1..1..2323, 4_A375_EGR1..1..2324, 4_A375_EGR1..1..2325, 4_A375_EGR1..1..2326	42916, 26134, 42086, 53174, 43254, 41790, 24038, 20518, -10266	in gene, in gene, in gene, downstream, in gene, in gene, in gene, in gene, upstream	1	1	1	12.17	13	16.5	6	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene GAS6	AXSF, FLJ34709, GAS6, DKFZp666G247, AXLLG	growth arrest-specific 6	NM_000820, NM_001143945, NM_001143946, hCT1951843.2	1598_g_at, 202177_at	NP_000811.1, NP_001137417.1, NP_001137418.1, EAX09226.1
GeneID:650669	FLJ41484	13	114,545,293	114,548,734	3,441	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1848, 4_A375_EGR1..1..2324, 4_A375_EGR1..1..2325	-4361, -2265, 1235	upstream, upstream, in gene	1	0	1	12.33	11.33	15	3	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene FLJ41484	FLJ35543	hypothetical LOC650669	XR_110591, XR_114722	238097_at, 238127_at	
GeneID:100506394	LOC100506394	13	114,567,150	114,569,805	2,655	+	1	4_A375_EGR1..1..2326	10162	downstream	0	0	1	6	12	15	1	4_A375_EGR1..1	15	Gene LOC100506394		hypothetical LOC100506394	XR_110592, XR_114723		
GeneID:643365	FLJ44054	13	114,588,610	114,628,485	39,875	+	4	4_A375_EGR1..1..2326, 4_A375_EGR1..1..2327, 4_A375_EGR1..1..2328, 4_A375_EGR1..1..2329	-9296, -6162, 430, 33866	upstream, upstream, in gene, in gene	0	0	1	7.5	8.75	17.5	4	4_A375_EGR1..1	20	Gene FLJ44054		hypothetical LOC643365	NR_024609	1570447_at	
GeneID:22821	RASA3	13	114,747,194	114,898,095	150,901	-	12	1_A375_pNL7_minus_lncRNA_AR..1..1849, 1_A375_pNL7_minus_lncRNA_AR..1..1850, 2_A375_pNL97_plus_lncRNA_AR..1..2596, 2_A375_pNL97_plus_lncRNA_AR..1..2597, 2_A375_pNL97_plus_lncRNA_AR..1..2598, 4_A375_EGR1..1..2330, 4_A375_EGR1..1..2331, 4_A375_EGR1..1..2332, 4_A375_EGR1..1..2333, 4_A375_EGR1..1..2334, 4_A375_EGR1..1..2335, 4_A375_EGR1..1..2336	66991, 3535, 67667, 3551, 719, 154751, 153087, 102575, 76511, 65662, 3791, 1391	in gene, in gene, in gene, in gene, in gene, downstream, downstream, in gene, in gene, in gene, in gene, in gene	1	1	1	13.71	15	17.86	7	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene RASA3	MGC47588, GAPIII, GAP1IP4BP, MGC46517, RASA3	RAS p21 protein activator 3	NM_007368, hCT11220.3, hCT1812383.2, hCT2302747.0	206220_s_at, 206221_at, 225562_at	NP_031394.2, EAX09233.1, EAX09232.1, EAX09234.1
GeneID:8881	CDC16	13	115,000,362	115,038,150	37,788	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1851, 2_A375_pNL97_plus_lncRNA_AR..1..2599, 2_A375_pNL97_plus_lncRNA_AR..1..2600, 4_A375_EGR1..1..2337, 4_A375_EGR1..1..2338	214, -106, 48356, 46870, 47238	in gene, upstream, downstream, downstream, downstream	1	1	1	20.67	15.67	14.33	3	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene CDC16	ANAPC6, APC6, CDC16, CUT9	cell division cycle 16 homolog (S. cerevisiae)	NM_001078645, NM_003903, hCT2302319.0, hCT2302320.0, hCT2302321.0, hCT2302322.0, hCT2302323.0, hCT2302324.0, hCT2302325.0, hCT2359383.0, hCT2359384.0	202717_s_at, 209658_at, 209659_s_at	NP_001072113.1, NP_003894.3, EAX09237.1, EAX09240.1, EAX09241.1, EAX09244.1, EAX09238.1, EAX09239.1, EAX09242.1, EAX09243.1, EAX09245.1
GeneID:65110	UPF3A	13	115,047,078	115,071,283	24,205	+	4	2_A375_pNL97_plus_lncRNA_AR..1..2600, 2_A375_pNL97_plus_lncRNA_AR..1..2601, 4_A375_EGR1..1..2337, 4_A375_EGR1..1..2338	-356, 32746, 154, 522	upstream, downstream, in gene, in gene	0	1	1	19	18	17.67	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene UPF3A	UPF3A, HUPF3A, FLJ35267, RENT3A, FLJ57970, UPF3	UPF3 regulator of nonsense transcripts homolog A (yeast)	NM_023011, NM_080687, hCT2302312.0, hCT2302313.0, hCT2302314.0, hCT2302315.0, hCT2359379.0, hCT2359380.0	206958_s_at, 206959_s_at, 214323_s_at, 217596_at	NP_075387.1, NP_542418.1, EAX09247.1, EAX09248.1, EAX09249.1, EAX09252.1, EAX09250.1, EAX09251.1

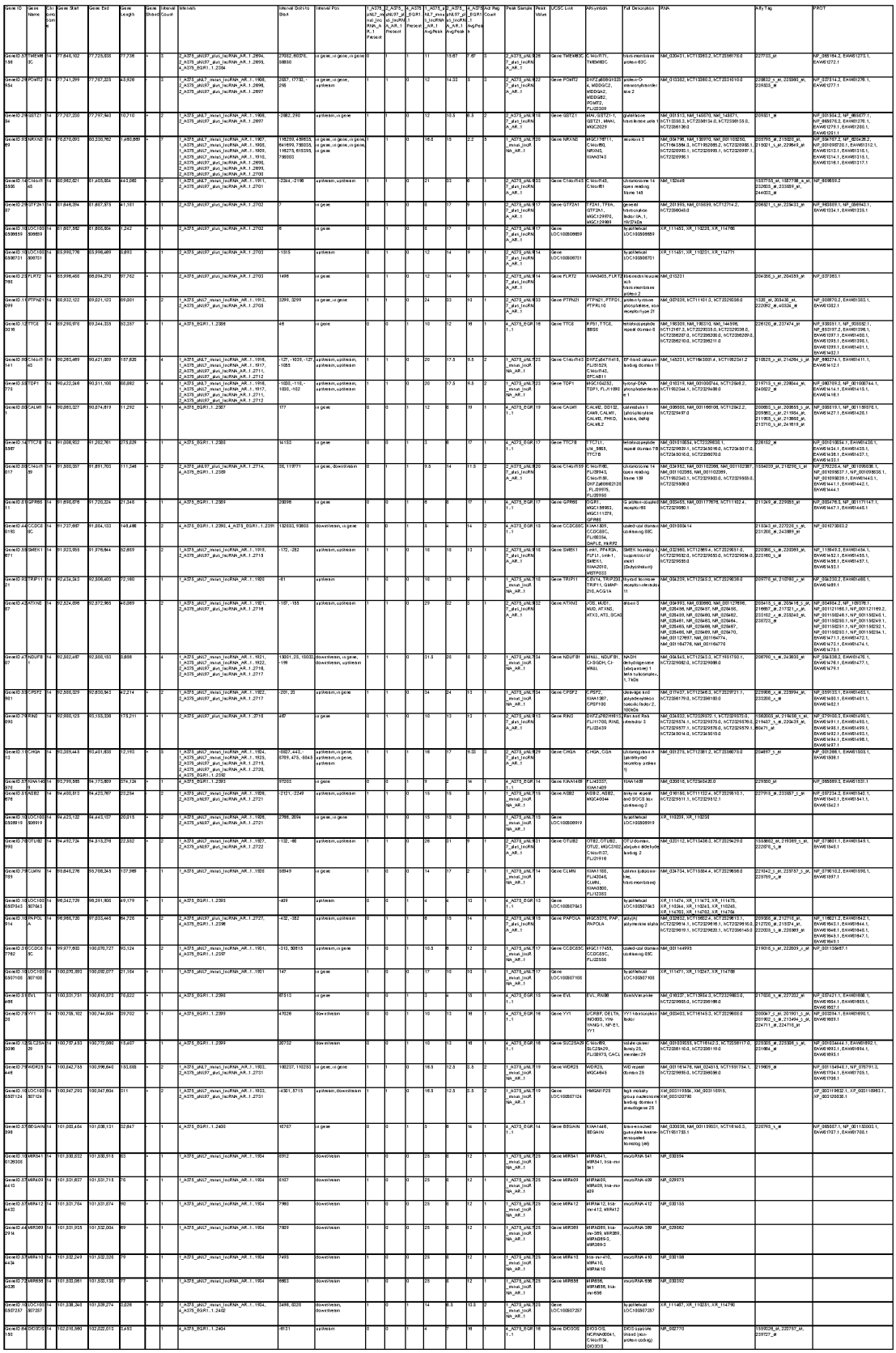
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.283489	ZNF828	13	115,079,965	115,092,803	12,838	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2601	-141	upstream	0	1	0	19	28	17	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene ZNF828	KIAA1802, C13orf8, FLJ90413, CAMP, ZNF828	zinc finger protein 828	NM_032436, NM_001164144, NM_001164145, hCT1648208.2, hCT2302316.0	228194_at	NP_115812.1, NP_001157616.1, NP_001157617.1, EAX09253.1, EAX09254.1
GeneID.91875	TTC5	14	20,757,290	20,774,153	16,863	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1852, 2_A375_pNL97_plus_lncRNA_AR..1..2603	41, 73	in gene, in gene	1	1	0	28	43	7	1	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene TTC5	Strap, TTC5	tetratricopeptide repeat domain 5	NM_138376, hCT2354235.0, hCT2354236.0, hCT31744.3	228557_at	NP_612385.2, EAW66480.1, EAW66481.1, EAW66482.1
GeneID.57820	CCNB1IP1	14	20,779,529	20,801,457	21,928	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1852, 1_A375_pNL7_minus_lncRNA_AR..1..1853, 2_A375_pNL97_plus_lncRNA_AR..1..2603, 4_A375_EGR1..1..2339	27345, -10111, 27377, -9967	downstream, upstream, downstream, upstream	1	1	1	28.5	31.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene CCNB1IP1	CCNB1IP1, HEI10, C14orf18	cyclin B1 interacting protein 1	NM_182849, NM_182851, NM_021178, NM_182852, hCT2304866.0	217988_at	NP_878269.1, NP_878271.1, NP_067001.3, NP_878272.1, EAW66479.1
GeneID.85495	RPPH1	14	20,811,230	20,811,570	340	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1853, 4_A375_EGR1..1..2339	2, 146	in gene, in gene	1	0	1	27	20	27	1	4_A375_EGR1..1	27	Gene RPPH1	RPPH1, H1RNA	ribonuclease P RNA component H1	NR_002312	1558684_at	
GeneID.10038	PARP2	14	20,811,773	20,826,063	14,290	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1853, 4_A375_EGR1..1..2339	-205, -349	upstream, upstream	1	0	1	27	20	27	1	4_A375_EGR1..1	27	Gene PARP2	pADPRT-2, ADPRTL3, PARP-2, PARP2, ADPRTL2, ADPRT2	poly (ADP-ribose) polymerase 2	NM_005484, NM_001042618, hCT1967705.1, hCT2354230.0, hCT31740.3	204752_x_at, 214086_s_at, 215773_x_at	NP_005475.2, NP_001036083.1, EAW66476.1, EAW66477.1, EAW66478.1
GeneID.90809	TMEM55B	14	20,926,012	20,929,837	3,825	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2604	-8123	upstream	0	1	0	12	20	11	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TMEM55B	TMEM55B, C14orf9, DKFZp434M0519, MGC26684	transmembrane protein 55B	NM_144568, NM_001100814, hCT2304861.0, hCT2354234.0, hCT31742.2	225287_s_at	NP_653169.2, NP_001094284.1, EAW66460.1, EAW66461.1, EAW66462.1
GeneID.4860	PNP	14	20,937,538	20,946,165	8,627	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2604	222	in gene	0	1	0	12	20	11	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PNP	PRO1837, MGC117396, PNP, NP, MGC125915, FLJ97312, PUNP, FLJ94043, MGC125916, FLJ97288	purine nucleoside phosphorylase	NM_000270, hCT1957485.1, hCT31733.2	201695_s_at	NP_000261.2, EAW66458.1, EAW66459.1
GeneID.341799	OR6S1	14	21,108,855	21,109,850	995	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2605	9530	downstream	0	1	0	10	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene OR6S1	OR6S1, OR6S1Q, OR14-37	olfactory receptor, family 6, subfamily S, member 1	NM_001001968, hCT1646048.4		NP_001001968.1, EAW66452.1
GeneID.283	ANG	14	21,152,336	21,162,345	10,009	+	1	4_A375_EGR1..1..2342	-1136	upstream	0	0	1	13	11	17	1	4_A375_EGR1..1	17	Gene ANG	MGC71966, MGC22466, ALS9, ANG, RNASE4, RNASE5, HEL168	angiogenin, ribonuclease, RNase A family, 5	NM_001145, NM_001097577	205141_at	NP_001136.1, NP_001091046.1
GeneID.6038	RNASE4	14	21,152,372	21,168,758	16,386	+	1	4_A375_EGR1..1..2342	-1172	upstream	0	0	1	13	11	17	1	4_A375_EGR1..1	17	Gene RNASE4	RNS4, RNASE4, MGC9306	ribonuclease, RNase A family, 4	NM_194431, NM_002937	205158_at, 213397_x_at	NP_919412.1, NP_002928.1
GeneID.51222	ZNF219	14	21,558,205	21,572,863	14,658	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1854, 2_A375_pNL97_plus_lncRNA_AR..1..2607	831, 767	in gene, in gene	1	1	0	27	30	9	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene ZNF219	ZNF219, ZFP219	zinc finger protein 219	NM_016423, NM_001101672, NM_001102454, hCT1817685.3, hCT2306355.1, hCT2306356.1, hCT32491.4	219314_s_at, 222864_s_at	NP_057507.2, NP_001095142.1, NP_001095924.1, EAW66404.1, EAW66405.1, EAW66406.1, EAW66407.1
GeneID.643382	C14orf176	14	21,567,096	21,571,863	4,767	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1854, 2_A375_pNL97_plus_lncRNA_AR..1..2607	4936, 5000	downstream, downstream	1	1	0	27	30	9	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene C14orf176	C14orf95, NCRNA00220, C14orf176		NM_001146683	1558594_at	NP_001140155.1
GeneID.84932	RAB2B	14	21,927,179	21,945,132	17,953	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1855, 2_A375_pNL97_plus_lncRNA_AR..1..2608, 2_A375_pNL97_plus_lncRNA_AR..1..2609	-180, 20831, -164	upstream, downstream, upstream	1	1	0	34.5	49.5	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	77	Gene RAB2B	FLJ14824, RAB2B	RAB2B, member RAS oncogene family	NM_032846, NR_028074, NM_001163380, hCT1957515.1, hCT1957516.1, hCT32494.2	225074_at	NP_116235.2, NP_001156852.1, EAW66382.1, EAW66383.1, EAW66384.1
GeneID.9878	TOX4	14	21,945,335	21,967,319	21,984	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1855, 2_A375_pNL97_plus_lncRNA_AR..1..2609	-23, -39	upstream, upstream	1	1	0	54	77	7	1	2_A375_pNL97_plus_lncRNA_AR..1	77	Gene TOX4	C14orf92, LCP1, MIG7, TOX4, KIAA0737	TOX high mobility group box family member 4	NM_014828, hCT2306576.0, hCT2354238.0	201683_x_at, 201684_s_at, 201685_s_at, 232097_at	NP_055643.1, EAW66380.1, EAW66381.1
GeneID.56339	METTL3	14	21,966,282	21,979,457	13,175	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1856, 2_A375_pNL97_plus_lncRNA_AR..1..2610	-63, -111	upstream, upstream	1	1	0	26	33	7	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene METTL3	IME4, MGC4336, METTL3, M6A, Spo8, MT-A70	methyltransferase like 3	NM_019852, hCT2306341.0	209265_s_at, 213653_at, 242111_at	NP_062826.2, EAW66379.1
GeneID.6297	SALL2	14	21,989,231	22,005,337	16,106	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1856, 2_A375_pNL97_plus_lncRNA_AR..1..2610	25817, 25769	downstream, downstream	1	1	0	26	33	7	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene SALL2	FLJ10414, HSAL2, ZNF795, p150(Sal2), Sal-2, SALL2, FLJ55746, KIAA0360	sal-like 2 (Drosophila)	NM_005407, hCT1817677.2, hCT1957461.1	213283_s_at	NP_005398.1, EAW66376.1, EAW66377.1
GeneID.6955	TRA@	14	22,090,057	23,021,075	931,018	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	916023	in gene	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRA@	MGC71411, TCRA, MGC22624, TRA@, FLJ22602, TCRD, TRA, MGC117436, MGC23964	T cell receptor alpha locus		216191_s_at, 217143_s_at	
GeneID.28738	TRAJ17	14	22,995,812	22,995,874	62	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	10268	downstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ17	TRAJ17	T cell receptor alpha joining 17			
GeneID.28739	TRAJ16	14	22,997,487	22,997,546	59	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	8593	downstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ16	TRAJ16	T cell receptor alpha joining 16			
GeneID.28740	TRAJ15	14	22,998,580	22,998,641	61	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	7500	downstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ15	TRAJ15	T cell receptor alpha joining 15			
GeneID.28741	TRAJ14	14	22,999,278	22,999,329	51	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	6802	downstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ14	TRAJ14	T cell receptor alpha joining 14			
GeneID.28742	TRAJ13	14	23,000,026	23,000,088	62	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	6054	downstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ13	TRAJ13	T cell receptor alpha joining 13			
GeneID.28743	TRAJ12	14	23,000,889	23,000,948	59	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	5191	downstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ12	TRAJ12	T cell receptor alpha joining 12			
GeneID.28744	TRAJ11	14	23,001,452	23,001,511	59	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	4628	downstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ11	TRAJ11	T cell receptor alpha joining 11			
GeneID.28745	TRAJ10	14	23,002,445	23,002,508	63	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	3635	downstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ10	TRAJ10	T cell receptor alpha joining 10			
GeneID.28746	TRAJ9	14	23,004,502	23,004,562	60	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	1578	downstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ9	TRAJ9	T cell receptor alpha joining 9			
GeneID.28747	TRAJ8	14	23,005,092	23,005,151	59	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	988	downstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ8	TRAJ8	T cell receptor alpha joining 8			
GeneID.28748	TRAJ7	14	23,006,567	23,006,625	58	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	-487	upstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ7	TRAJ7	T cell receptor alpha joining 7			
GeneID.28749	TRAJ6	14	23,008,016	23,008,077	61	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	-1936	upstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ6	TRAJ6	T cell receptor alpha joining 6			
GeneID.28750	TRAJ5	14	23,009,190	23,009,249	59	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	-3110	upstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ5	TRAJ5	T cell receptor alpha joining 5			
GeneID.28751	TRAJ4	14	23,011,142	23,011,204	62	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	-5062	upstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ4	TRAJ4	T cell receptor alpha joining 4			
GeneID.28752	TRAJ3	14	23,012,122	23,012,183	61	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	-6042	upstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ3	TRAJ3	T cell receptor alpha joining 3			
GeneID.28753	TRAJ2	14	23,013,015	23,013,080	65	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	-6935	upstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ2	TRAJ2	T cell receptor alpha joining 2 (non-functional)			
GeneID.28754	TRAJ1	14	23,013,981	23,014,042	61	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2611	-7901	upstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRAJ1	TRAJ1	T cell receptor alpha joining 1 (non-functional)			
GeneID.122704	MRPL52	14	23,299,092	23,304,246	5,154	+	1	4_A375_EGR1..1..2343	156	in gene	0	0	1	6	11	15	1	4_A375_EGR1..1	15	Gene MRPL52	MRPL52		NM_178336, NM_180982, NM_181304, NM_181305, NM_181306, NM_181307, hCT1956191.2, hCT2348966.0, hCT2348967.0, hCT2350548.0, hCT2350549.0, hCT2350550.0, hCT2350551.0	221997_s_at, 226241_s_at	NP_848026.1, NP_851313.1, NP_851821.1, NP_851822.1, NP_851823.1, NP_851824.1, EAW66238.1, EAW66239.1, EAW66240.1, EAW66241.1, EAW66242.1, EAW66243.1, EAW66244.1
GeneID.4323	MMP14	14	23,305,793	23,316,803	11,010	+	2	4_A375_EGR1..1..2343, 4_A375_EGR1..1..2344	-6545, 9439	upstream, in gene	0	0	1	5.5	9	14.5	2	4_A375_EGR1..1	15	Gene MMP14	MT1-MMP, MTMMP1, MMP14, MMP-X1	matrix metallopeptidase 14 (membrane-inserted)	NM_004995, hCT2305589.0, hCT33250.3	160020_at, 202827_s_at, 202828_s_at, 217279_x_at	NP_004986.1, EAW66236.1, EAW66237.1
GeneID.26020	LRP10	14	23,340,960	23,347,293	6,333	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1857, 2_A375_pNL97_plus_lncRNA_AR..1..2612	15680, 15680	downstream, downstream	1	1	0	28	24	5	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene LRP10	MST087, MGC142274, MSTP087, DKFZp564C1940, MGC142276, LRP9, MGC8675, LRP10	low density lipoprotein receptor-related protein 10	NM_014045, hCT1956187.1, hCT2305592.0, hCT2305594.0, hCT33259.3	201412_at, 231881_at	NP_054764.2, EAW66235.1, EAW66232.1, EAW66233.1, EAW66234.1
GeneID.161253	REM2	14	23,352,432	23,356,889	4,457	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1857, 2_A375_pNL97_plus_lncRNA_AR..1..2612	4208, 4208	in gene, in gene	1	1	0	28	24	5	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene REM2	FLJ38964, REM2	RAS (RAD and GEM)-like GTP binding 2	NM_173527, hCT33263.3	235699_at	NP_775798.2, EAW66231.1
GeneID.100505758	LOC100505758	14	23,388,509	23,392,616	4,107	+	1	4_A375_EGR1..1..2345	10467	downstream	0	0	1	18	11	22	1	4_A375_EGR1..1	22	Gene LOC100505758		hypothetical LOC100505758	XR_111413, XR_110265, XR_114726		
GeneID.10419	PRMT5	14	23,389,733	23,398,661	8,928	-	1	4_A375_EGR1..1..2345	-315	upstream	0	0	1	18	11	22	1	4_A375_EGR1..1	22	Gene PRMT5	JBP1, HRMT1L5, SKB1Hs, PRMT5, IBP72, SKB1	protein arginine methyltransferase 5	NM_001039619, NM_006109, hCT1956168.0, hCT1956169.1, hCT2354264.0, hCT2354265.0, hCT33252.3	1564520_s_at, 1564521_x_at, 217786_at	NP_001034708.1, NP_006100.2, EAW66217.1, EAW66219.1, EAW66220.1, EAW66221.1, EAW66218.1
GeneID.84962	JUB	14	23,440,409	23,451,851	11,442	-	1	4_A375_EGR1..1..2346	1099	in gene	0	0	1	6	8	16	1	4_A375_EGR1..1	16	Gene JUB	Ajuba, MGC15563, JUB	jub, ajuba homolog (Xenopus laevis)	NM_032876, NM_198086, hCT2305107.0, hCT33025.3	1553764_a_at, 225806_at, 225807_at, 243446_at	NP_116265.1, NP_932352.1, EAW66204.1, EAW66205.1
GeneID.60686	C14orf93	14	23,456,110	23,479,360	23,250	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1858, 2_A375_pNL97_plus_lncRNA_AR..1..2613, 4_A375_EGR1..1..2346	3006, 3040, 28606	in gene, in gene, downstream	1	1	1	12.5	15.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene C14orf93	C14orf93, FLJ12154	chromosome 14 open reading frame 93	NM_021944, NM_001130706, NM_001130708, hCT2305098.0, hCT2305099.0, hCT2305101.0, hCT2305102.0, hCT2305103.0, hCT2354299.0, hCT2354300.0, hCT2354301.0	219009_at	NP_068763.2, NP_001124178.1, NP_001124180.1, EAW66196.1, EAW66197.1, EAW66200.1, EAW66198.1, EAW66199.1, EAW66201.1, EAW66202.1, EAW66203.1
GeneID.22985	ACIN1	14	23,527,773	23,564,823	37,050	-	1	4_A375_EGR1..1..2347	727	in gene	0	0	1	9	11	13	1	4_A375_EGR1..1	13	Gene ACIN1	KIAA0670, ACINUS, ACIN1, ACN, ISAP152, DKFZp667N107	apoptotic chromatin condensation inducer 1	NM_014977, NM_001164814, NM_001164815, NM_001164816, NM_001164817, hCT2305147.0, hCT2305149.0, hCT33003.2	201715_s_at	NP_055792.1, NP_001158286.1, NP_001158287.1, NP_001158288.1, NP_001158289.1, EAW66188.1, EAW66186.1, EAW66187.1
GeneID.55017	C14orf119	14	23,564,788	23,569,665	4,877	+	1	4_A375_EGR1..1..2347	-692	upstream	0	0	1	9	11	13	1	4_A375_EGR1..1	13	Gene C14orf119	FLJ21141, FLJ20671, C14orf119, MGC74723	chromosome 14 open reading frame 119	NM_017924, hCT33004.3	223080_at	NP_060394.1, EAW66185.1
GeneID.100128908	LOC100128908	14	23,569,631	23,574,171	4,540	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1859, 4_A375_EGR1..1..2347	-10085, 10075	upstream, downstream	1	0	1	12	12	7.5	2	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene LOC100128908		hypothetical LOC100128908	XR_111414, XR_110266, XR_114727		
GeneID.1053	CEBPE	14	23,586,515	23,588,474	1,959	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1859	4218	downstream	1	0	0	15	13	2	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene CEBPE	CEBPE, C/EBP-epsilon, CRP1	CCAAT/enhancer binding protein (C/EBP), epsilon	NM_001805, hCT33023.3	214523_at	NP_001796.2, EAW66183.1



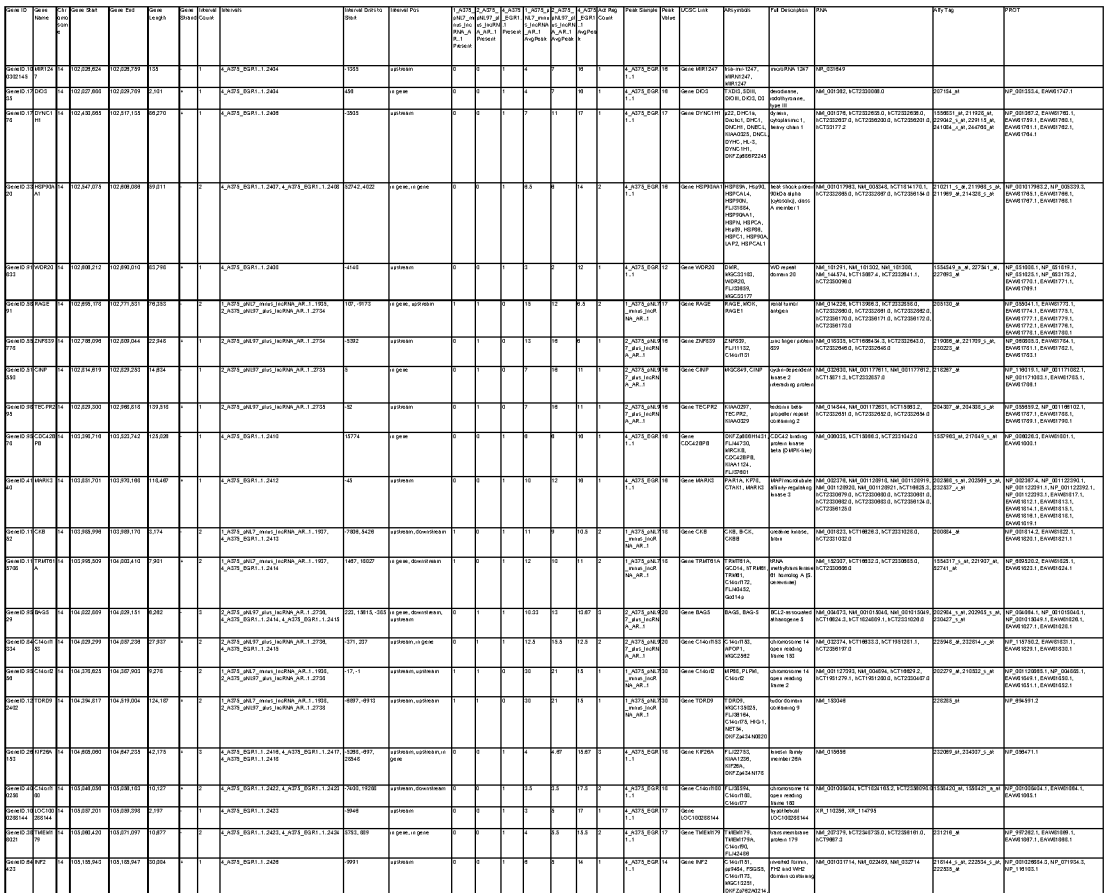
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_unN7_minus_lncRNA_AR_1 Percent	2_A375_2_A375_unN7_plus_lncRNA_AR_1 Percent	4_A375_EGR1_SGR1_lncRNA_AR_1 Percent	1_A375_plus_unN7_minus_lncRNA_AR_1 AvgPeak	2_A375_plus_unN7_plus_lncRNA_AR_1 AvgPeak	4_A375_EGR1_SGR1_lncRNA AvgPeak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:23526	SLC7A6	14	23,594,804	23,632,549	37,745	-	1	1_A375_unN7_minus_lncRNA_AR_1	69893	downstream	1	0	0	15	13	2	1	1_A375_unN7_minus_lncRNA_AR_1	15	Gene SLC7A6	SLC7A6, LAT2, LPI-PC1	solute carrier family 7 (amino acid transporter), type), member 6	NM_012244, NM_182728, XC723599358.0, XC729483.3	2327S2_x_at, 219092_x_at, 219882_at, 219894_x_at, 217245_x_at	NP_036376.2, NP_877292.1, EAW66811.1, EAW66812.1
GeneID:55873	PPP1R32	14	23,765,112	23,772,257	6,946	+	1	4_A375_EGR1_1.2Se6	792	in gene	0	0	1	9	8	17	1	4_A375_EGR1_1	17	Gene PPP1R32	RNA1483, PPP1R3E	protein phosphatase 1, regulatory (inhibitor) subunit 35	NR_026852	227489_at, 227612_at, 229001_at	
GeneID:596	BCL2L2	14	23,776,012	23,790,966	4,956	+	1	4_A375_EGR1_1.2Se6	-4748	upstream	0	0	1	9	8	17	1	4_A375_EGR1_1	17	Gene BCL2L2	BCLW, BWA271, BCL2L2, BCL-W, BCL2-L-2	BCL2-like 2	NM_004050, XC733000.3	1559140_a_at, 209311_at	NP_004041.1, EAW66169.1
GeneID:5310	SLC22A17	14	23,815,527	23,822,060	6,533	-	1	4_A375_EGR1_1.2Se9	-7566	upstream	0	0	1	1	0	10	1	4_A375_EGR1_1	13	Gene SLC22A17	BOCT, BOIT, NGAL/R, NGAL/R2, NGALR2, SLC22A17, SBOIT, Zsig28	solute carrier family 22, member 17	NM_020372, NM_016609, XC719958580.1, XC730018.3	210679_at, 221198_at	NP_065103.2, NP_057692.2, EAW66163.1, EAW66166.1
GeneID:1839	EFS	14	23,825,811	23,834,542	8,731	-	1	4_A375_EGR1_1.2Se9	5764	in gene	0	0	1	1	0	10	1	4_A375_EGR1_1	13	Gene EFS	CASS, SIN, EFS1, CAS03, EFS, EFS2, HEF3	embryonal Fyn-associated substrate	NM_032459, NM_020594, XC723599580.3, XC730009.2	204400_at, 210550_x_at	NP_115025.1, NP_065535.1, EAW66163.1, EAW66164.1
GeneID:2357	NIN2GN	14	23,836,896	23,947,402	6,804	+	1	1_A375_unN7_plus_lncRNA_AR_1	-454	upstream	0	1	0	14	15	7	1	2_A375_unN7_plus_lncRNA_AR_1	15	Gene NIN2GN	NIN2GN, DKFZp564O092, NAG, C14orf120, ICP5, bpt-2	ninein-like, eIF4E binding protein	NM_031042839, NM_015814	213784_x_at, 214693_x_at	NP_001038100.1, NP_056529.1
GeneID:5993	C14orf167	14	24,407,940	24,424,298	16,358	-	2	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	1002, 954	in gene; nr gene	1	1	0	29	57	14	1	2_A375_unN7_plus_lncRNA_AR_1	57	Gene C14orf167	C14orf167, PRO1485	chromosome 14 open reading frame 167	NR_023921, NR_023922, NR_023923, AB_023524	227448_s_at	
GeneID:1012	DHRS4	14	24,422,965	24,436,488	13,523	+	2	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	331, 379	in gene; nr gene	1	1	0	29	57	14	1	2_A375_unN7_plus_lncRNA_AR_1	57	Gene DHRS4	FLJ11000, SDR2C1, SCAD-SRL, NRDR, SDR2C2, SDR-SRL, DHRS4	dehydrogenase/reductase (SDR family) member 4	NM_021004	218021_at	NP_066284.2
GeneID:7203	DHRS411	14	24,503,710	24,520,993	14,270	+	2	1_A375_unN7_minus_lncRNA_AR_1, 1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	249, 13922, 238	in gene; downstream, in gene	1	1	0	19	10.5	11	2	1_A375_unN7_plus_lncRNA_AR_1	23	Gene DHRS411	SDR2C4, DHRS4L1	dehydrogenase/reductase (SDR family) member 4 like 1	NM_001032406		NP_001073837.1
GeneID:9901	LRRC16B	14	24,521,206	24,539,937	17,731	+	1	1_A375_unN7_minus_lncRNA_AR_1	428	in gene	1	0	0	15	14	14	1	1_A375_unN7_minus_lncRNA_AR_1	15	Gene LRRC16B	LIV41, C14orf121, LRRC16B, CARMIL3	leucine rich repeat containing 16B	NM_130390	229981_at	NP_612389.3
GeneID:5872	RNF31	14	24,816,659	24,829,870	13,211	+	1	2_A375_unN7_plus_lncRNA_AR_1	13813	downstream	0	1	0	10	15	5	1	2_A375_unN7_plus_lncRNA_AR_1	15	Gene RNF31	MGC19979, ZIBRA, RNF31, FLJ23501, FLJ45111, HOIP	ring finger protein 31	NM_017999, XC719698140.1, XC723697320.0, XC729432720.0, XC729432350.0, XC731449.2	220765_s_at, 223122_at, 223123_x_at	NP_060469.4, EAW66096.1, EAW66098.1, EAW66099.1, EAW66097.1, EAW66099.1
GeneID:1058	IRF9	14	24,830,422	24,835,774	5,352	+	1	2_A375_unN7_plus_lncRNA_AR_1	-190	upstream	0	1	0	10	15	5	1	2_A375_unN7_plus_lncRNA_AR_1	15	Gene IRF9	ISGF3G, IRF9, p48, ISGF3, IRF-9	interferon regulatory factor 9	NM_006084, XC719676981.1, XC729432741.0, XC731423.3	203882_at	NP_006073.3, EAW66092.1, EAW66093.1, EAW66094.1
GeneID:2887	TSSK4	14	24,874,926	24,877,484	2,559	+	2	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	10088, 7702	downstream, downstream	1	0	1	14.3	12.5	11	2	1_A375_unN7_plus_lncRNA_AR_1	17	Gene TSSK4	TSSK5, STK22F, C14orf20, TSSK4, MGC132284, TSK4	testis-specific kinase 4	NM_001164726, NM_178944, XC723562772.0, XC729427.0, XC731443.3	242369_at	NP_001158198.1, NP_777604.2, EAW66090.1, EAW66092.1, EAW66070.1, EAW66071.1
GeneID:2902	CNNM4	14	24,876,787	24,893,163	16,376	-	2	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	1807, 497	upstream, in gene	1	0	1	14.3	12.5	11	2	1_A375_unN7_plus_lncRNA_AR_1	17	Gene CNNM4	MGC142293, DKFZp313E1235, CNNM4, VPS22, UNQ1886, DKFZp434L1235, C14orf23, CNNM4A, SNF7, CNNM4B, HSPC134, VPS22A, MGC142293, CNNM4, SNF7-1	cyclin-dependent kinase 5	NM_020184, XC723393700.1, XC723393961.1, XC729364060.0, XC729444060.0	219571_s_at, 219572_at	NP_034355.2, EAW66086.1, EAW66088.1, EAW66087.1, EAW66085.1
GeneID:1424	MDP1	14	24,893,156	24,895,341	2,185	-	2	1_A375_unN7_minus_lncRNA_AR_1, 1_A375_unN7_plus_lncRNA_AR_1	249, 2353	in gene; downstream	1	0	1	14.3	12.5	11	2	1_A375_unN7_plus_lncRNA_AR_1	17	Gene MDP1	MDP1, PMEPA5E, PMEPAse, MDP-1, MGC9367	magnesium-dependent phosphatase 1	NM_139276, XC723393961.1, XC723545410.0, XC729444070.0, XC729444060.0, XC729444070.0	220765_at, 220764_s_at	NP_612453.2, EAW66096.1, EAW66098.1, EAW66091.1, EAW66092.1, EAW66082.1
GeneID:4760	NEDD8	14	24,896,037	24,701,978	15,819	-	3	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1, A375_EGR1_1.2Se6	18864, -580, 18858	downstream, upstream, downstream	1	1	1	13.33	13.67	8.33	3	4_A375_EGR1_1	17	Gene NEDD8	FLJ43224, MDGA, MGC104391, MGC115598, Nedd-8, NEDD-8, MGC133997	ninein (GSK3B interacting protein)	NM_006156, XC723393961.1, XC723544420.0, XC729444070.0	201640_at	NP_006147.1, EAW66089.1
GeneID:5192	GWPR2	14	24,701,848	24,705,448	3,600	+	1	1_A375_unN7_plus_lncRNA_AR_1, 2010	288	in gene	0	0	1	11	16	8	1	2_A375_unN7_plus_lncRNA_AR_1	16	Gene GWPR2	GWPR2, MGC630, MGC15998	g protein-coupled receptor for motility 2 pseudogene 2	NM_001002002, NM_001002000, NM_001002001, NM_015976, XC719961422.2, XC719961421.0, XC719961442.2, XC719961451.1, XC723442310.0, XC723423220.0, XC723423232.0, XC723423310.0, XC723432.4	217990_at	NP_001002002.1, NP_001002000.1, NP_001002001.1, NP_057992.2, EAW66143.1, EAW66152.1, EAW66153.1, EAW66156.1, EAW66155.1, EAW66157.1, EAW66158.1
GeneID:2677	TINF2	14	24,705,649	24,711,950	6,031	-	1	1_A375_unN7_plus_lncRNA_AR_1, 2010	9944	downstream	0	1	0	11	16	8	1	2_A375_unN7_plus_lncRNA_AR_1	16	Gene TINF2	TIN2L, TIN2, TINF2	TERF1 (TRF1)-interacting nuclear factor 2	NM_012461, NM_001099274, XC719961071.1, XC723542150.0, XC729434.2	220082_s_at, 223778_x_at	NP_036612.2, NP_001027744.1, EAW66045.1, EAW66049.1, EAW66050.1
GeneID:7014	TG4R1	14	24,716,520	24,732,418	14,899	+	1	2_A375_unN7_plus_lncRNA_AR_1, 2019	-5321	upstream	0	1	0	11	14	8	1	2_A375_unN7_plus_lncRNA_AR_1	14	Gene TG4R1	TG4R, R-TG, TGR, ICRC, LI1, TGA2E	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)	NM_000359, XC731457.3	206606_at	NP_000350.1, EAW66047.1
GeneID:5873	RABGGTA	14	24,734,744	24,740,903	6,159	-	1	2_A375_unN7_plus_lncRNA_AR_1, 2019	56	in gene	0	1	0	11	14	8	1	2_A375_unN7_plus_lncRNA_AR_1	14	Gene RABGGTA	PTAR2, RABGGTA	Rab geranylgeranyltransferase, alpha subunit	NM_182936, NM_004581, XC719961291.2, XC719977001.1, XC719977021.1, XC723542670.0, XC723542680.0, XC731458.4	205572_s_at	NP_878296.1, NP_004572.2, EAW66041.1, EAW66042.1, EAW66044.1, EAW66045.1, EAW66043.1, EAW66045.1
GeneID:1610	DHRS1	14	24,759,804	24,769,039	9,235	-	2	1_A375_unN7_minus_lncRNA_AR_1, 1_A375_unN7_plus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	-49, 15	upstream, in gene	1	1	0	15	24	11	1	2_A375_unN7_plus_lncRNA_AR_1	24	Gene DHRS1	DHRS1, SDR31X1, FLJ14230, MGC20356, DKFZp686I0323, FLJ25439	dehydrogenase/reductase (SDR family) member 1	NM_138432, NM_001136030, XC719977031.1, XC729432300.0, XC729432431.0, XC729432320.0, XC731444.4	213279_at	NP_612481.1, NP_001129322.1, EAW66030.1, EAW66031.1, EAW66032.1, EAW66033.1, EAW66040.1
GeneID:1436	C14orf2	14	24,769,936	24,774,374	4,278	+	1	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	-10, -74	upstream, upstream	1	1	0	15	24	11	1	2_A375_unN7_plus_lncRNA_AR_1	24	Gene C14orf2	EVAN2/3?, C14orf2	chromosome 14 open reading frame 2	NM_174913, XC723479281.1, XC723485840.0	1558390_at	NP_777973.1, EAW66054.1, EAW66055.1
GeneID:2512	CDEB	14	24,774,393	24,780,978	6,585	-	2	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	11488, 11532	downstream, downstream	1	1	0	15	24	11	1	2_A375_unN7_plus_lncRNA_AR_1	24	Gene CDEB	CDEB	cell death-inducing DFFA-like effector b	NM_014430, XC723485580.1, XC723485580.1, XC731433.2	221165_s_at	NP_055213.3, EAW66032.1, EAW66033.1
GeneID:4775	NFATC4	14	24,836,143	24,846,610	12,868	+	2	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	479, 271	in gene; nr gene	1	1	0	17	15	10	1	1_A375_unN7_plus_lncRNA_AR_1	17	Gene NFATC4	NFAT4c, NFATC, activated B-cells, cytoplasmic, calcineurin-dependent 4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	NM_004554, NM_001136022, XC731422.2	208897_at, 213543_at, 208210_at	NP_004545.2, NP_001129494.1, EAW66020.1
GeneID:1315	C4W1	14	24,974,712	24,977,471	2,759	-	1	2_A375_unN7_plus_lncRNA_AR_1, 2022	-4913	upstream	0	1	0	7	14	2	1	2_A375_unN7_plus_lncRNA_AR_1	14	Gene C4W1	MCF7, CYH, MGC119890, MGC119891, dityrosine_C4W1	dityrosine 1, matrix cell	NM_031936, XC731433.3	214833_at	NP_001027.1, EAW66007.1
GeneID:2250	FOXG1	14	29,236,267	29,238,671	2,404	+	1	4_A375_EGR1_1.2Se1	1253	in gene	0	0	1	4	7	15	1	4_A375_EGR1_1	15	Gene FOXG1	BF1/2, FKH14, HFK2, FKH-2, HBF-2, HBF-1, HBF2, FOXG1A, FKH12, FKH5, FOXG1, QIN, HBF-22, BF1, FOXG1C, KIH-2, HBF-2, FOXG1-B, BF2, FKH-1, FKH12, HFK1	forkhead box G1	NM_005249	206016_at	NP_005240.3
GeneID:7976	C14orf2	14	29,241,910	29,264,300	22,391	+	1	4_A375_EGR1_1.2Se1	-4290	upstream	0	0	1	4	7	15	1	4_A375_EGR1_1	15	Gene C14orf2	C14_3.1e3, C14orf2	chromosome 14 open reading frame 23	NR_028731, NR_029132	243081_at	
GeneID:90	COCH	14	31,243,741	31,359,622	16,081	+	1	4_A375_EGR1_1.2Se2	287	in gene	0	0	1	7	8	16	1	4_A375_EGR1_1	16	Gene COCH	COCH, DFNB9, COCH1B2, COCH-SB2	coagulation factor C homolog, cochlin (Limulus polyphemus)	NM_004086, NM_001135055, XC719984512.2, XC719985187.1, XC719985187.2	1554241_at, 1554242_s_at, 205225_s_at	NP_004077.1, NP_001128593.1, EAW66063.1, EAW66064.1, EAW66065.1
GeneID:1005	LOC10050	14	31,345,388	31,358,913	13,525	-	1	4_A375_EGR1_1.2Se2	14765	downstream	0	1	0	7	8	16	1	4_A375_EGR1_1	16	Gene LOC100509071	hypothetical LOC100509071	XR_111423, XR_110274, XR_114735		
GeneID:8042	NPAS3	14	33,206,459	34,273,362	994,928	+	1	2_A375_unN7_plus_lncRNA_AR_1, 2020	796261	in gene	0	1	0	11	17	5	1	2_A375_unN7_plus_lncRNA_AR_1	17	Gene NPAS3	NPAS3, bHLHe12, FLJ11605, PASD6, FLJ11135, FLJ45003, MOPE	neuronal PAS domain protein 3	NM_022123, NM_173159, NM_001163910, NM_001164749, XC719981116.1	1554683_s_at, 205016_at, 222072_at, 230412_at	NP_071406.1, NP_775182.1, NP_001150985.1, NP_001150221.1, EAW66930.1
GeneID:8664	INSM2	14	38,003,348	38,006,360	3,012	+	2	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	1364, 1298	in gene; nr gene	1	1	0	27	31	10	1	2_A375_unN7_plus_lncRNA_AR_1	31	Gene INSM2	IA-4, INSM2, dkfz	insulinoma-associated 2	NM_032894, XC719840774.3	240941_at	NP_116783.2, EAW66972.1
GeneID:2939	RALGAPA1	14	58,007,595	58,276,452	270,874	-	2	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	270900, 270555	downstream, downstream	1	1	0	27	31	10	1	2_A375_unN7_plus_lncRNA_AR_1	31	Gene RALGAPA1	KIAA0864, DKFZp667F074, TULIP1, GRP8, RALGAPA1, DKFZp686I0135, GAPA1	Ral GTPase activating protein, alpha subunit 1 (catalytic)	NM_014990, NM_139031, XC723634242.0, XC723635420.0, XC723635445.0, NM_001164749, XC719981116.1	1556269_at, 1556271_x_at, 1556272_at, 213845_at, 214555_s_at, 213162_at, 234302_x_at, 233524_at	NP_055805.1, NP_612777.2, EAW65998.1, EAW65999.1, EAW66701.1, EAW66971.1
GeneID:5845	BRMS1L	14	58,295,977	58,341,169	45,372	+	2	1_A375_unN7_minus_lncRNA_AR_1, 2_A375_unN7_plus_lncRNA_AR_1	-141, 154	upstream, upstream	1	1	0	15	16	9	1	2_A375_unN7_plus_lncRNA_AR_1	16	Gene BRMS1L	BRMS1, BRMS1, MGC11296	breast cancer metastasis-suppressor 1-like	NM_032332, XC713276.3	224454_s_at, 226593_at	NP_115726.2, EAW65967.1
GeneID:7705	NKX2-1	14	36,993,802	36,999,430	5,628	-	1	4_A375_EGR1_1.2Se3	-4936	upstream	0	0	1	3	8	17	1	4_A375_EGR1_1	17	Gene NKX2-1	TTF-1, NK-2, BCH, TITF1, TTF1, NKX2-1, BHC, NKX2.1	NK2 homeobox 1	NM_003317, NM_001079668, XC712971.2, XC719541615.1, XC723434560.0, XC723434590.0	210972_x_at, 211324_s_at, 231315_at	NP_003308.1, NP_001070139.1, EAW66566.1, EAW66567.1, EAW66568.1, EAW66569.1
GeneID:1002	LOC10050	14	38,966,521	38,992,221	25,700	+	1	4_A375_EGR1_1.2Se3	5967	downstream	0	0	1	3	8	17	1	4_A375_EGR1_1	17	Gene LOC100506227	pulmonary surfactant-associated protein C-like	XM_003119991, XM_003120760		XP_003119999.1, XP_003120826.1
GeneID:5077	PAX9	14	37,126,773	37,147,912	20,239	+	1	4_A375_EGR1_1.2Se4	6747	in gene	0	0	1	5	9	15	1	4_A375_EGR1_1	15	Gene PAX9	PAX9, STHAG3	paired box 9	NM_006194, XC712070.3	207559_at	NP_006185.1, EAW66553.1
GeneID:8997	SLC25A21	14	37,147,126	37,841,993	694,739	-	1	1_A375_unN7_minus_lncRNA_AR_1, 1869	45469	in gene	1	0	0	17	15	9	1	1_A375_unN7_minus_lncRNA_AR_1	17	Gene SLC25A21	ODC1, SLC25A21, ODC, MGC126570	solute carrier family 25 (mitochondrial carrier; oxodicarboxylate carrier), member 21	NM_030631, NM_001171170, XC719543117.0	229274_at, 233037_at	NP_085134.1, NP_001164841.1, EAW66551.1
GeneID:4263	CTAGE5	14	39,734,476	39,820,207	85,921	+	2	1_A375_unN7_minus_lncRNA_AR_1, 1870, 2_A375_unN7_plus_lncRNA_AR_1, 2832	1905, 1905	in gene; nr gene	1	1	0	29	38	12	1	2_A375_unN7_plus_lncRNA_AR_1	38	Gene CTAGE5	CTAGE5, KIAA0846, MEM2, MGEA11, MGEA	CTAGE family, member 5	NM_203353, NM_203358, NM_005930, NM_203354, XC723581121.1, XC723581121.2, XC723581123.1, XC723581125.1, XC723633080.0, XC723634277.0, XC723634279.0, XC723642792.0, XC723642802.0, XC723642804.0, XC723642822.0, XC723642832.0	204053_x_at, 215902_s_at, 233760_at	NP_976230.1, NP_976231.1, NP_005910.2, NP_976229.1, EAW65908.1, EAW65910.1, EAW65909.1, EAW65905.1, EAW65907.1, EAW65906.1, EAW65910.1, EAW65911.1, EAW65912.1, EAW65914.1, EAW65916.1
GeneID:2516	FBXO33	14	39,866,977	39,901,764	34,827	-	2	1_A375_unN7_minus_lncRNA_AR_1, 1871, 2_A375_unN7_plus_lncRNA_AR_1, 2832, A375_EGR1_1.2Se6	186, 216, 990	in gene; nr gene, in gene	1	1	1	24.5	24.5	11	2	1_A375_unN7_plus_lncRNA_AR_1	43	Gene FBXO33	FBX33, FBXO33, bA4_G3K7, Bdt9D12	F-box protein 33	NM_033391, XC712526.2	229870_at, 227521_at	NP_976241.1, EAW65905.1
GeneID:1459	LRFN5	14	42,076,764	42,373,702	296,938	+	1	1_A375_unN7_minus_lncRNA_AR_1, 1871	2436	in gene	1	0	0	16	11	10	1	1_A375_unN7_minus_lncRNA_AR_1	16	Gene LRFN5	LRFN5, DKFZp686G0216, SALM5, FLJ38003, FIGLER5, C14orf148	leucine rich repeat and fibronectin type III domain containing 5	NM_152447, XC710921.2	230844_at	NP_689660.2, EAW65796.1

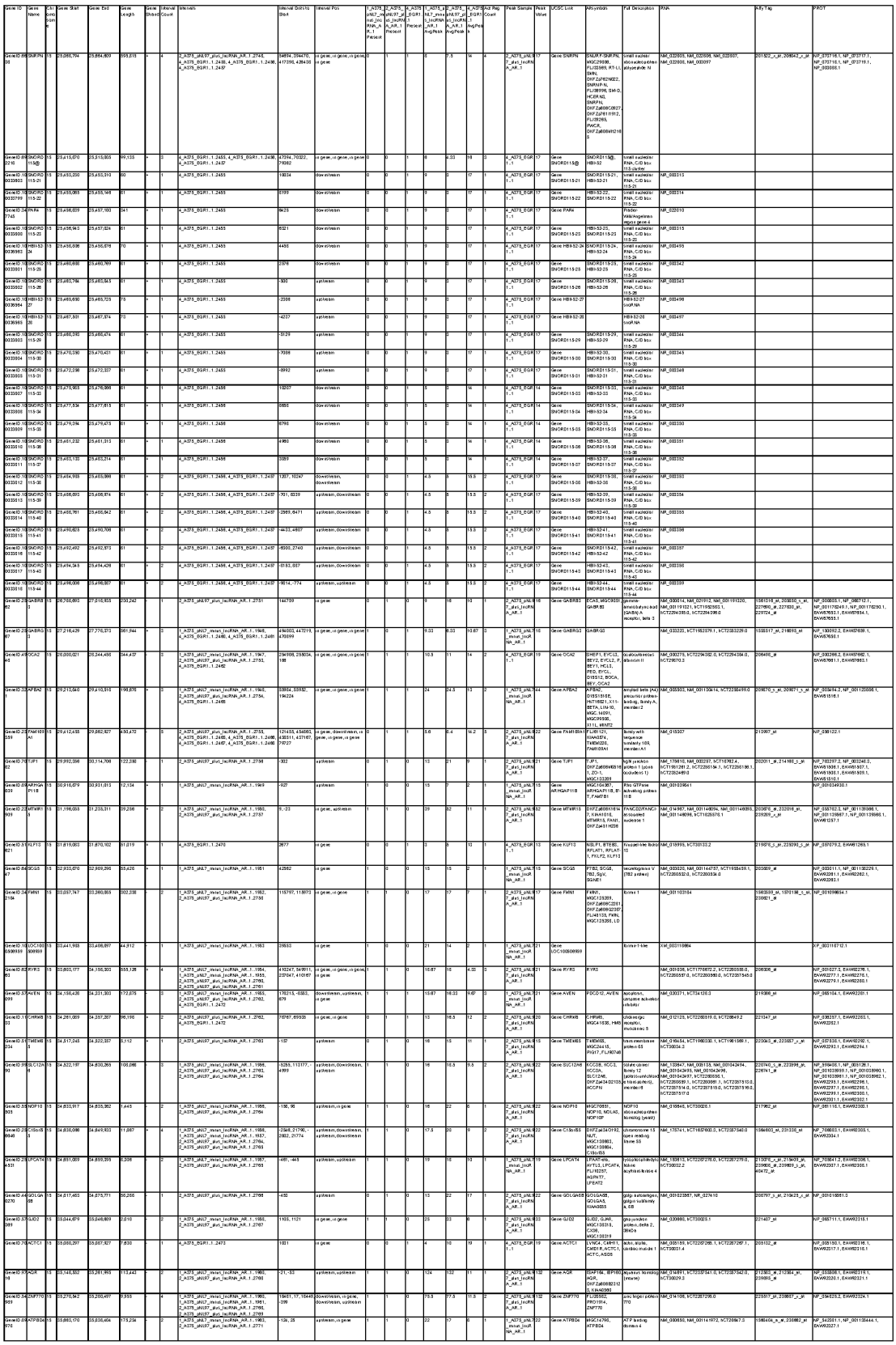
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:2287	FKBP3	14	45,584,802	45,603,732	18,930	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1874, 2_A375_pNL97_plus_lncRNA_AR..1..2635	212, 148	in gene, in gene	1	1	0	36	49	5	1	2_A375_pNL97_plus_lncRNA_AR..1	49	Gene FKBP3	FKBP-25, PPIase, FKBP3	FK506 binding protein 3, 25kDa	NM_002013, hCT10936.3	218003_s_at, 222485_at	NP_002004.1, EAW65765.1
GeneID:57697	FANCM	14	45,605,136	45,670,093	64,957	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1874, 2_A375_pNL97_plus_lncRNA_AR..1..2635	-1616, -1552	upstream, upstream	1	1	0	36	49	5	1	2_A375_pNL97_plus_lncRNA_AR..1	49	Gene FANCM	MGC176453, FAAP250, FANCM, KIAA1596	Fanconi anemia, complementation group M	NM_020937, hCT11959.5, hCT1814116.2, hCT2304216.2, hCT2344020.2	1554277_s_at, 231971_at, 234733_s_at, 242711_x_at	NP_065988.1, EAW65781.1, EAW65782.1, EAW65783.1, EAW65784.1
GeneID:55320	C14orf106	14	45,672,393	45,722,605	50,212	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1875, 2_A375_pNL97_plus_lncRNA_AR..1..2636	-19, 13	upstream, in gene	1	1	0	22	21	7	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene C14orf106	KIAA1903, HSA242977, MI18BP1, MIS18BP1, KNL2, FLJ11186, C14orf106	MIS18 binding protein 1	NM_018353, hCT1955699.0, hCT2304130.0, hCT2304131.0, hCT2354259.0	208500_s_at, 226830_at, 241816_at, 244173_at	NP_060823.3, EAW65780.1, EAW65777.1, EAW65778.1, EAW65779.1
GeneID:6235	RPS29	14	50,044,039	50,053,094	9,055	-	1	4_A375_EGR1..1..2356	-166	upstream	0	0	1	9	10	18	1	4_A375_EGR1..1	18	Gene RPS29	S29, RPS29	ribosomal protein S29	NM_001030001, NM_001032, hCT11223.2, hCT1955698.1	201094_at	NP_001025172.1, NP_001023.1, EAW65765.1, EAW65766.1
GeneID:6029	RN7SL1	14	50,053,298	50,053,596	298	+	1	4_A375_EGR1..1..2356	-18	upstream	0	0	1	9	10	18	1	4_A375_EGR1..1	18	Gene RN7SL1	RNSRP1, RN7SL1, 7SL, 7L1a, RN7SL	RNA, 7SL, cytoplasmic 1	NR_002715		
GeneID:122769	PPIL5	14	50,065,415	50,081,390	15,975	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2639, 4_A375_EGR1..1..2357	185, 289	in gene, in gene	0	1	1	19	29	19	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene PPIL5	MGC20689, LRR-1, LRR1, PPIL5, 4-1BBLRR	leucine rich repeat protein 1	NM_152329, NM_203467, hCT1640170.4, hCT2350057.0, hCT2354254.0, hCT2354255.0	235113_at, 242154_x_at	NP_689542.2, NP_982292.1, EAW65761.1, EAW65762.1, EAW65763.1, EAW65764.1
GeneID:55172	C14orf104	14	50,091,892	50,101,948	10,056	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1877	1148	in gene	1	0	0	16	11	13	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene C14orf104	C14orf104, FLJ10563, KTU, CILD10	chromosome 14 open reading frame 104	NM_001083908, NM_018139, hCT11224.3, hCT2304126.0, hCT2304127.0	219166_at	NP_001077377.1, NP_060609.2, EAW65755.1, EAW65756.1, EAW65757.1
GeneID:5427	POLE2	14	50,110,278	50,154,935	44,657	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1877, 2_A375_pNL97_plus_lncRNA_AR..1..2640	54135, -4673	downstream, upstream	1	1	0	15	16.5	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene POLE2	POLE2, DPE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	NM_002692, hCT11222.3	205909_at	NP_002683.2, EAW65754.1
GeneID:122773	KLHDC1	14	50,159,823	50,219,870	60,047	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2640	-15	upstream	0	1	0	14	22	4	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene KLHDC1	MGC126646, MST025, MGC126644, KLHDC1	kelch domain containing 1	NM_172193, hCT1814272.2, hCT2348530.0	1552733_at, 1564272_a_at, 1564273_at	NP_751943.1, EAW65753.1, EAW65752.1
GeneID:23588	KLHDC2	14	50,234,787	50,249,856	15,069	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1878, 2_A375_pNL97_plus_lncRNA_AR..1..2641	-67, -35	upstream, upstream	1	1	0	37	36	5	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene KLHDC2	HCLP-1, LCP, KLHDC2	kelch domain containing 2	NM_014315, hCT2304671.0, hCT2354284.0	217906_at	NP_055130.1, EAW65749.1, EAW65750.1
GeneID:9147	SDCCAG1	14	50,250,532	50,319,539	69,007	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1879	-13	upstream	1	0	0	20	9	7	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene SDCCAG1	NY-CO-1, NEMF, FLJ10051, SDCCAG1	nuclear export mediator factor	NM_004713, hCT2304117.0, hCT2304118.0, hCT2304119.0, hCT2304120.0, hCT2304121.0, hCT2304122.0, hCT2304123.0	1557950_at, 1558675_s_at, 1569594_a_at, 218649_x_at	NP_004704.2, EAW65745.1, EAW65741.1, EAW65742.1, EAW65743.1, EAW65744.1, EAW65746.1, EAW65747.1
GeneID:378708	RN7SL2	14	50,329,289	50,329,587	298	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1879	10015	downstream	1	0	0	20	9	7	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene RN7SL2	7L30.1, RNSRP2, 7SL1c, 7L1C, RN7SL2	RNA, 7SL, cytoplasmic 2	NR_027260		
GeneID:382	ARF6	14	50,359,736	50,363,772	4,036	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2642, 4_A375_EGR1..1..2358	-40, 56	upstream, in gene	0	1	1	14	15	15	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene ARF6	ARF6, DKFZp564M0264	ADP-ribosylation factor 6	NM_001663, hCT2304674.0	203311_s_at, 203312_x_at, 214182_at, 224788_at	NP_001654.1, EAW65740.1
GeneID:283551	C14orf182	14	50,448,430	50,474,238	25,808	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2643	4158	in gene	0	1	0	13	14	12	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene C14orf182	C14orf182, MGC149108	chromosome 14 open reading frame 182	NM_001012706, hCT1649904.3	1569274_at, 237460_x_at, 239777_at	NP_001012724.1, EAW65736.1
GeneID:100506463	LOC100506463	14	50,469,934	50,470,644	710	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2643	564	in gene	0	1	0	13	14	12	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene LOC100506463		hypothetical protein LOC100506463	XM_003118922		XP_003118970.1
GeneID:79944	L2HGDH	14	50,709,152	50,778,947	69,795	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1880, 2_A375_pNL97_plus_lncRNA_AR..1..2644	163, 195	in gene, in gene	1	1	0	26	30	11	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene L2HGDH	C14orf160, FLJ12618, L2HGDH, DURANIN	L-2-hydroxyglutarate dehydrogenase	NM_024884, hCT13116.2	220089_at, 224459_at, 224460_s_at	NP_079160.1, EAW65725.1
GeneID:27109	ATP5S	14	50,779,047	50,792,960	13,913	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1880, 2_A375_pNL97_plus_lncRNA_AR..1..2644	-263, -295	upstream, upstream	1	1	0	26	30	11	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene ATP5S	HSU79253, ATPW, ATP5S	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	NM_001003803, NM_001003805, NM_015684, NR_033761, hCT2304677.0, hCT2304678.0, hCT2304679.0, hCT2304681.0, hCT2304682.0, hCT2354289.0	1554177_a_at, 206992_s_at, 206993_at, 213995_at, 237400_at, 238799_at	NP_001003803.1, NP_001003805.1, NP_056499.2, EAW65719.1, EAW65721.1, EAW65723.1, EAW65718.1, EAW65720.1, EAW65722.1
GeneID:114088	TRIM9	14	51,441,979	51,562,422	120,443	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2645	630	in gene	0	1	0	15	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TRIM9	SPRING, RNF91, TRIM9, KIAA0282	tripartite motif containing 9	NM_015163, NM_052978, hCT12040.3, hCT1824815.2, hCT2304362.0, hCT2304363.0, hCT2304364.0	209859_at, 230280_at	NP_055978.4, NP_443210.1, EAW65660.1, EAW65661.1, EAW65662.1, EAW65663.1, EAW65664.1
GeneID:100506566	LOC100506566	14	51,555,675	51,558,006	2,331	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2645	6117	downstream	0	1	0	15	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100506566		hypothetical LOC100506566	XR_110293, XR_114748		
GeneID:22795	NID2	14	52,471,520	52,535,946	64,426	-	1	4_A375_EGR1..1..2359	282	in gene	0	0	1	7	7	20	1	4_A375_EGR1..1	20	Gene NID2	NID2		NM_007361, hCT12044.2	204114_at	NP_031387.3, EAW65656.1
GeneID:10979	FERMT2	14	53,323,989	53,417,815	93,826	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1881	-10121	upstream	1	0	0	17	9	3	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene FERMT2	mig-2, UNC112, MIG2, PLEKHC1, FERMT2, FLJ34213, KIND2, UNC112B, FLJ44462, DKFZp686G11125	fermitin family homolog 2 (Drosophila)	NM_006832, NM_001134999, NM_001135000, hCT12050.3, hCT2328365.0, hCT2356204.0	209209_s_at, 209210_s_at, 214212_x_at	NP_006823.1, NP_001128471.1, NP_001128472.1, EAW80618.1, EAW80619.1, EAW80620.1
GeneID:2764	GMFB	14	54,941,209	54,955,744	14,535	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2651	128	in gene	0	1	0	19	14	4	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene GMFB	GMFB, GMF	glia maturation factor, beta	NM_004124, hCT13714.2, hCT1808788.1	202543_s_at, 202544_at	NP_004115.1, EAW80638.1, EAW80639.1
GeneID:23034	SAMD4A	14	55,034,637	55,260,033	225,396	+	1	4_A375_EGR1..1..2360	-2701	upstream	0	0	1	10	9	17	1	4_A375_EGR1..1	17	Gene SAMD4A	SAMD4A, KIAA1053, Smaug1, SMGA, SMG, DKFZp434H0350, hSmaug1, DKFZp686A1532, Smaug, SAMD4	sterile alpha motif domain containing 4A	NM_015589, NM_001161576, NM_001161577, hCT2328277.0, hCT2328278.0, hCT2328279.0	212845_at, 215120_s_at, 215495_s_at, 215496_at	NP_056404.3, NP_001155048.1, NP_001155049.1, EAW80644.1, EAW80645.1, EAW80646.1
GeneID:11169	WDHD1	14	55,405,656	55,493,819	88,163	-	1	4_A375_EGR1..1..2361	-37	upstream	0	0	1	8	10	24	1	4_A375_EGR1..1	24	Gene WDHD1	CHTF4, CTF4, WDHD1, AND-1	WD repeat and HMG-box DNA binding protein 1	NM_001008396, NM_007086, hCT2326557.0	204727_at, 204728_s_at, 216228_s_at	NP_001008397.1, NP_009017.1, EAW80654.1
GeneID:122809	SOCS4	14	55,493,844	55,516,207	22,363	+	1	4_A375_EGR1..1..2361	12	in gene	0	0	1	8	10	24	1	4_A375_EGR1..1	24	Gene SOCS4	SOCS7, DKFZp686J1586, SOCS4	suppressor of cytokine signaling 4	NM_080867, NM_199421	1552792_at, 226178_at	NP_543143.1, NP_955453.1
GeneID:100129075	C14orf33	14	56,042,875	56,046,810	3,935	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1882, 2_A375_pNL97_plus_lncRNA_AR..1..2653	42, 74	in gene, in gene	1	1	0	17	17	5	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene C14orf33	C14orf33	chromosome 14 open reading frame 33	NR_027123		
GeneID:3895	KTN1	14	56,046,925	56,151,302	104,377	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1882, 2_A375_pNL97_plus_lncRNA_AR..1..2653	-157, -189	upstream, upstream	1	1	0	17	17	5	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene KTN1	MU-RMS-40.19, KIAA0004, KTN1, KNT, MGC133337, CG1	kinectin 1 (kinesin receptor)	NM_001079521, NM_182926, NM_001079522, NM_004986, hCT13213.3, hCT1817059.1, hCT1817060.1, hCT2356149.0, hCT2356150.0	200914_x_at, 200915_x_at, 214709_s_at	NP_001072989.1, NP_891556.1, NP_001072990.1, NP_004977.2, EAW80663.1, EAW80665.1, EAW80661.1, EAW80662.1, EAW80664.1
GeneID:645687	C14orf34	14	56,247,853	56,263,392	15,539	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2654	-6560	upstream	0	1	0	9	17	1	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene C14orf34	C14orf34	chromosome 14 open reading frame 34	NR_026796, NR_026797		
GeneID:54916	C14orf101	14	57,046,511	57,116,233	69,722	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1883, 2_A375_pNL97_plus_lncRNA_AR..1..2655	-207, -175	upstream, upstream	1	1	0	67	73	4	1	2_A375_pNL97_plus_lncRNA_AR..1	73	Gene C14orf101	FLJ20392, C14orf101	chromosome 14 open reading frame 101	NM_017799, hCT23717.3	219757_s_at, 225675_at	NP_060269.3, EAW80691.1
GeneID:5015	OTX2	14	57,267,425	57,277,184	9,759	-	1	4_A375_EGR1..1..2362	12336	downstream	0	0	1	1	4	14	1	4_A375_EGR1..1	14	Gene OTX2	OTX2, MGC45000, MCOPS5	orthodenticle homeobox 2	NM_021728, NM_172337, hCT1966401.1, hCT23719.3	231731_at, 242128_at	NP_068374.1, NP_758840.1, EAW80692.1, EAW80693.1
GeneID:55860	ACTR10	14	58,666,833	58,702,354	35,521	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1884, 2_A375_pNL97_plus_lncRNA_AR..1..2656	-193, -177	upstream, upstream	1	1	0	14	21	7	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ACTR10	ACTR11, ACTR10, HARP11, Arp11	actin-related protein 10 homolog (S. cerevisiae)	NM_018477, hCT13324.2	222230_s_at	NP_060947.1, EAW80714.1
GeneID:23002	DAAM1	14	59,655,399	59,836,471	181,072	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2657	33017	in gene	0	1	0	7	16	5	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene DAAM1	KIAA0666, FLJ41657, DAAM1	dishevelled associated activator of morphogenesis 1	NM_014992, hCT13093.3, hCT1817057.1, hCT1817058.1	216060_s_at, 232552_at, 244062_at	NP_055807.1, EAW80748.1, EAW80747.1, EAW80749.1
GeneID:112849	C14orf149	14	59,939,406	59,951,073	11,667	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2658	353	in gene	0	1	0	15	20	15	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C14orf149	FLJ25436, C14orf149	chromosome 14 open reading frame 149	NM_144581, hCT13094.3	227699_at	NP_653182.1, EAW80752.1
GeneID:51528	JKAMP	14	59,951,161	59,972,081	20,920	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2658	-441	upstream	0	1	0	15	20	15	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene JKAMP	HSPC213, CDA06, C14orf100, HSPC327, JKAMP, JAMP	JNK1/MAPK8-associated membrane protein	NM_016475, NM_001098625, hCT12068.2, hCT1817036.1, hCT1817037.1, hCT2356099.0, hCT2356100.0, hCT2356101.0	223215_s_at, 223547_at	NP_057559.2, NP_001092095.1, EAW80753.1, EAW80755.1, EAW80757.1, EAW80758.1, EAW80754.1, EAW80756.1
GeneID:6252	RTN1	14	60,062,694	60,337,557	274,863	-	1	4_A375_EGR1..1..2363	51109	in gene	0	0	1	5	1	13	1	4_A375_EGR1..1	13	Gene RTN1	NSP, RTN1, MGC133250	reticulon 1	NM_021136, NM_206852, NM_206857, hCT1824916.2, hCT1955157.1, hCT1955158.1	203485_at, 210222_s_at	NP_066959.1, NP_996734.1, NP_996739.1, EAW80762.1, EAW80763.1, EAW80764.1
GeneID:64430	C14orf135	14	60,558,629	60,601,532	42,903	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2659	155	in gene	0	1	0	13	20	8	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C14orf135	FLJ38170, FBP2, FLJ12799, C14orf135	chromosome 14 open reading frame 135	NM_022495, hCT2329468.0	1566971_at, 219972_s_at, 235187_s_at	NP_071940.4, EAW80768.1
GeneID:317761	C14orf39	14	60,902,674	60,952,764	50,090	-	1	4_A375_EGR1..1..2364	252	in gene	0	0	1	6	10	18	1	4_A375_EGR1..1	18	Gene C14orf39	MGC149706, Six6os1, C14orf39	chromosome 14 open reading frame 39	NM_174978, hCT1955155.2, hCT2356147.0	1561985_at	NP_777638.2, EAW80760.1, EAW80761.1
GeneID:6495	SIX1	14	61,111,417	61,116,155	4,738	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1885, 2_A375_pNL97_plus_lncRNA_AR..1..2660	155, -6021	in gene, upstream	1	1	0	15	12.5	7.5	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene SIX1	TIP39, DFNA23, SIX1, BOS3	SIX homeobox 1	NM_005982, hCT13013.2, hCT1966378.1	205817_at, 228347_at, 230911_at	NP_005973.1, EAW80785.1, EAW80784.1
GeneID:5583	PRKCH	14	61,788,515	62,017,698	229,183	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1886, 2_A375_pNL97_plus_lncRNA_AR..1..2662	34333, 232237	in gene, downstream	1	1	0	19.5	12.5	3	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene PRKCH	nPKC-eta, PRKCL, MGC26269, PKC-L, PKCL, MGC5363, PRKCH	protein kinase C, eta	NM_006255, hCT13455.2, hCT2336287.0, hCT2356076.0	206099_at, 218764_at	NP_006246.2, EAW80801.1, EAW80800.1, EAW80802.1
GeneID:400221	FLJ22447	14	62,037,314	62,121,431	84,117	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1887, 2_A375_pNL97_plus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..2664	91681, -7618, 91998	downstream, upstream, downstream	1	1	0	16.5	21.5	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene FLJ22447		hypothetical LOC400221	XR_111431, XR_110296, XR_114752		
GeneID:3091	HIF1A	14	62,162,119	62,214,977	52,858	+	1	4_A375_EGR1..1..2365	409	in gene	0	0	1	11	12	22	1	4_A375_EGR1..1	22	Gene HIF1A	HIF1-ALPHA, HIF1, MOP1, HIF-1alpha, HIF1A, bHLHe78, PASD8	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	NM_001530, NM_181054, hCT12285.3, hCT1817046.1, hCT2356054.0, hCT2356055.0	200989_at	NP_001521.1, NP_851397.1, EAW80806.1, EAW80807.1, EAW80808.1, EAW80809.1
GeneID:646113	FLJ43390	14	62,584,075	62,595,132	11,057	+	1	4_A375_EGR1..1..2367	197	in gene	0	0	1	3	7	14	1	4_A375_EGR1..1	14	Gene FLJ43390	FLJ37214, FLJ39142, FLJ16510	hypothetical LOC646113	NR_015358	231186_at, 236902_at	
GeneID:112840	WDR89	14	64,063,757	64,108,591	44,834	-	1	4_A375_EGR1..1..2368	46628	downstream	0	0	1	3	5	12	1	4_A375_EGR1..1	12	Gene WDR89	MSTP050, MGC9907, C14orf150, WDR89	WD repeat domain 89	NM_080666, NM_001008726, hCT1641590.2, hCT2329183.0	235025_at, 238650_x_at, 244036_at	NP_542397.1, NP_001008726.1, EAW80831.1, EAW80832.1
GeneID:2100	ESR2	14	64,693,751	64,805,268	111,517	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2666, 4_A375_EGR1..1..2369	-508, 100	upstream, in gene	0	1	1	7.5	12	10.5	2	4_A375_EGR1..1	16	Gene ESR2	ESR-BETA, ESRB, ER-BETA, Erb, NR3A2, ESTRB, ESR2	estrogen receptor 2 (ER beta)	NM_001437, NM_001040275, NM_001040276, hCT12536.1, hCT1955174.1, hCT1955175.1, hCT2329191.0, hCT2329192.0, hCT2329193.0, hCT2329194.0, hCT2329196.0, hCT2329197.0, hCT2356052.0	1569554_at, 210780_at, 211117_x_at, 211118_x_at, 211119_at, 211120_x_at	NP_001428.1, NP_001035365.1, NP_001035366.1, EAW80847.1, EAW80850.1, EAW80854.1, EAW80845.1, EAW80846.1, EAW80848.1, EAW80849.1, EAW80851.1, EAW80852.1, EAW80853.1
GeneID:441687	LOC441687	14	64,812,191	64,814,329	2,138	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2666, 4_A375_EGR1..1..2369	8553, 9161	downstream, downstream	0	1	1	7.5	12	10.5	2	4_A375_EGR1..1	16	Gene LOC441687	TEX21P	testis expressed 21, pseudogene	NR_033777		
GeneID:7597	ZBTB25	14	64,953,555	64,970,554	16,999	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2667	-358	upstream	0	1	0	14	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ZBTB25	C14orf51, KUP, ZBTB25, ZNF46	zinc finger and BTB domain containing 25	NM_006977, hCT1817107.1, hCT1817108.1, hCT2328858.0	214482_at	NP_008908.2, EAW80860.1, EAW80859.1, EAW80861.1
GeneID:22890	ZBTB1	14	64,971,292	65,000,408	29,116	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2667	-380	upstream	0	1	0	14	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ZBTB1	ZNF909, ZBTB1, KIAA0997	zinc finger and BTB domain containing 1	NM_014950, NM_001123329, hCT32946.1	1557036_at, 205092_x_at, 213376_at	NP_055765.2, NP_001116801.1, EAW80863.1
GeneID:26030	PLEKHG3	14	65,171,193	65,211,060	39,867	+	1	4_A375_EGR1..1..2370	36639	in gene	0	0	1	3	4	15	1	4_A375_EGR1..1	15	Gene PLEKHG3	MGC156300, KIAA0599, ARHGEF43, PLEKHG3, MGC156299	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	NM_015549, hCT2326627.0, hCT2326628.0, hCT2326629.0, hCT2326630.0, hCT2326631.0	212821_at, 212823_s_at, 217044_s_at	NP_056364.1, EAW80873.1, EAW80869.1, EAW80870.1, EAW80871.1, EAW80872.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.6710	SPTB	14	65,213,001	65,289,866	76,865	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2668, 4_A375_EGR1..1..2370	16442, 61834	in gene, downstream	0	1	1	5.5	10	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SPTB	SPTB, HS2, HSPTB1, SPH2, EL3	spectrin, beta, erythrocytic	NM_001024858, NM_000347, hCT2328845.0, hCT2328846.0, hCT2328847.0, hCT2328848.0, hCT2328849.0, hCT2328851.0, hCT2356102.0, hCT32944.3	208416_s_at, 214145_s_at	NP_001020029.1, NP_000338.3, EAW80875.1, EAW80876.1, EAW80877.1, EAW80882.1, EAW80878.1, EAW80879.1, EAW80880.1, EAW80881.1
GeneID.2342	FNTB	14	65,453,507	65,529,370	75,863	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2669	253	in gene	0	1	0	13	18	9	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene FNTB	FNTB, MGC31935, FPTB	farnesyltransferase, CAAX box, beta	NM_002028, hCT32951.2	1568865_at, 1773_at, 204764_at, 225851_at, 233263_at	NP_002019.1, EAW80897.1
GeneID.440184	C14orf53	14	66,953,109	66,965,271	12,162	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1888, 2_A375_pNL97_plus_lncRNA_AR..1..2670	21536, 21536	downstream, downstream	1	1	0	17	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C14orf53	MGC88374, NCRNA00238, C14orf53	chromosome 14 open reading frame 53	NR_024338, NR_024339, hCT2330219.0, hCT2356196.0	237205_at	EAW80922.1, EAW80921.1
GeneID.10243	GPHN	14	66,974,125	67,648,525	674,400	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1888, 2_A375_pNL97_plus_lncRNA_AR..1..2670	520, 520	in gene, in gene	1	1	0	17	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene GPHN	KIAA1385, GPHN, GPHRYN, GPH, GEPH	gephyrin	NM_020806, NM_001024218, hCT11848.4, hCT1955809.2, hCT2330221.1, hCT2351227.0	220773_s_at, 223319_at, 234941_s_at	NP_065857.1, NP_001019389.1, EAW80923.1, EAW80924.1, EAW80925.1, EAW80926.1
GeneID.64398	MPP5	14	67,708,021	67,802,536	94,515	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2671	383	in gene	0	1	0	10	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MPP5	PALS1, FLJ12615, MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	NM_022474, hCT13005.3	219321_at, 226092_at, 235884_at	NP_071919.2, EAW80930.1
GeneID.51382	ATP6V1D	14	67,804,589	67,826,591	22,002	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1889, 2_A375_pNL97_plus_lncRNA_AR..1..2672	-225, -257	upstream, upstream	1	1	0	86	71	9	1	1_A375_pNL7_minus_lncRNA_AR..1	86	Gene ATP6V1D	VATD, ATP6M, VMA8, ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	NM_015994, hCT13001.3, hCT2330332.0	208898_at, 208899_x_at, 214923_at	NP_057078.1, EAW80931.1, EAW80932.1
GeneID.1965	EIF2S1	14	67,827,034	67,853,233	26,199	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1889, 2_A375_pNL97_plus_lncRNA_AR..1..2672	-218, -186	upstream, upstream	1	1	0	86	71	9	1	1_A375_pNL7_minus_lncRNA_AR..1	86	Gene EIF2S1	EIF-2, EIF-2alpha, EIF2S1, EIF-2A, EIF2A, EIF2	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	NM_004094, hCT13002.3, hCT2330218.0	201142_at, 201143_s_at, 201144_s_at	NP_004085.1, EAW80934.1, EAW80933.1
GeneID.26499	PLEK2	14	67,853,700	67,878,826	25,126	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2673	-2356	upstream	0	1	0	12	17	5	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PLEK2	PLEK2		NM_016445, hCT13006.3	218644_at	NP_057529.1, EAW80935.1
GeneID.57475	PLEKHH1	14	68,000,008	68,056,255	56,247	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2674	-138	upstream	0	1	0	7	15	6	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene PLEKHH1	PLEKHH1		NM_020715, hCT13009.4	225726_s_at, 225727_at	NP_065766.1, EAW80940.1
GeneID.10490	VTI1B	14	68,117,866	68,141,602	23,736	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1890, 2_A375_pNL97_plus_lncRNA_AR..1..2675	162, 98	in gene, in gene	1	1	0	20	28	11	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene VTI1B	VTI1, VTI1B, VTI1-LIKE, VTI2, VTI1L	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	NM_006370, hCT2328910.0, hCT2328911.0, hCT2328912.0	209452_s_at, 225926_at, 225928_at	NP_006361.1, EAW80947.1, EAW80945.1, EAW80946.1
GeneID.51109	RDH11	14	68,143,517	68,162,510	18,993	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1890, 2_A375_pNL97_plus_lncRNA_AR..1..2675	21070, 21006	downstream, downstream	1	1	0	20	28	11	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene RDH11	FLJ32633, ARSDR1, CGI82, RALR1, MDT1, PSDR1, SDR7C1, RDH11, HCBP12, SCALD	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	NM_016026, hCT12999.3, hCT2328908.0, hCT2356193.0	217042_at, 217775_s_at, 217776_at, 232359_at	NP_057110.3, EAW80949.1, EAW80948.1, EAW80950.1
GeneID.145226	RDH12	14	68,168,603	68,201,168	32,565	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1891, 2_A375_pNL97_plus_lncRNA_AR..1..2676	37413, 37429	downstream, downstream	1	1	0	18	14	1	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene RDH12	RDH12, LCA13, FLJ30273, SDR7C2, LCA3	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	NM_152443, hCT1955810.1	242998_at	NP_689656.2, EAW80951.1
GeneID.23503	ZFYVE26	14	68,213,237	68,283,306	70,069	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1891, 2_A375_pNL97_plus_lncRNA_AR..1..2676	77290, 77274	downstream, downstream	1	1	0	18	14	1	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ZFYVE26	DKFZp686F19106, SPG15, DKFZp781H1112, ZFYVE26, KIAA0321	zinc finger, FYVE domain containing 26	NM_015346, hCT13008.3, hCT13007.4, hCT2328905.1, hCT2328906.1, hCT2356057.0	213073_at, 37943_at	NP_056161.2, EAW80954.1, EAW80952.1, EAW80953.1, EAW80955.1, EAW80956.1
GeneID.5890	RAD51L1	14	68,286,496	69,062,738	776,242	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2677, 2_A375_pNL97_plus_lncRNA_AR..1..2678	356144, 726704	in gene, in gene	0	1	0	8.5	15.5	2.5	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene RAD51L1	RAD51L1, RAD51B, MGC34245, hREC2, REC2, R51H2	RAD51-like 1 (S. cerevisiae)	NM_002877, NM_133509, NM_133510, hCT2340268.0, hCT2340269.0, hCT2340270.0	1554496_at, 210255_at, 216880_at	NP_002868.1, NP_598193.2, NP_598194.1, EAW80957.1, EAW80958.1, EAW80959.1
GeneID.87	ACTN1	14	69,340,840	69,446,083	105,243	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2679, 4_A375_EGR1..1..2372	28003, 36131	in gene, in gene	0	1	1	6	11.5	12	2	4_A375_EGR1..1	16	Gene ACTN1	FLJ40884, ACTN1, FLJ54432	actinin, alpha 1	NM_001102, NM_001130004, NM_001130005, hCT13336.3, hCT2329780.0, hCT2329782.0, hCT2329785.0, hCT2356040.0, hCT2356041.0	208636_at, 208637_x_at, 211160_x_at, 237401_at	NP_001093.1, NP_001123476.1, NP_001123477.1, EAW80973.1, EAW80975.1, EAW80976.1, EAW80971.1, EAW80972.1, EAW80974.1
GeneID.55218	EXD2	14	69,658,194	69,710,737	52,543	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1892, 2_A375_pNL97_plus_lncRNA_AR..1..2680	14, 62	in gene, in gene	1	1	0	15	17	6	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene EXD2	EXDL2, C14orf114, EXD2, FLJ10738, DKFZp781A0133, DKFZp781L15100	exonuclease 3'-5' domain containing 2	NM_018199, NM_001193360, NM_001193361, NM_001193362, NM_001193363, NR_034164, NR_034165, hCT13338.2, hCT2329384.0	1555806_a_at, 218383_at	NP_060669.1, NP_001180289.1, NP_001180290.1, NP_001180291.1, NP_001180292.1, EAW80984.1, EAW80985.1
GeneID.100289511	LOC100289511	14	70,233,000	70,234,430	1,430	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1893	734	in gene	1	0	0	15	9	13	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene LOC100289511		hypothetical LOC100289511	NR_029378		
GeneID.6430	SFRS5	14	70,233,829	70,238,722	4,893	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1893	-133	upstream	1	0	0	15	9	13	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene SFRS5	SFRS5, SRP40, SRSF5, HRS	serine/arginine-rich splicing factor 5	NM_001039465, NM_006925, hCT13058.3, hCT1955068.1, hCT2328888.0, hCT2328889.0, hCT2356103.0, hCT2356104.0, hCT2356105.0, hCT2356106.0, hCT2356107.0	203380_x_at, 210077_s_at, 212266_s_at	NP_001034554.1, NP_006856.2, EAW81002.1, EAW81003.1, EAW81004.1, EAW81008.1, EAW81005.1, EAW81006.1, EAW81007.1, EAW81009.1, EAW81010.1
GeneID.6554	SLC10A1	14	70,242,552	70,264,006	21,454	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1893	30310	downstream	1	0	0	15	9	13	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene SLC10A1	SLC10A1, NTCP	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	NM_003049, hCT13056.2	207185_at	NP_003040.1, EAW81011.1
GeneID.64093	SMOC1	14	70,346,143	70,499,083	152,940	+	1	4_A375_EGR1..1..2373	-47	upstream	0	0	1	4	5	11	1	4_A375_EGR1..1	11	Gene SMOC1	SMOC1		NM_022137, NM_001034852, hCT13084.3, hCT2328890.0, hCT2328892.0, hCT2356148.0	222783_s_at, 222784_at	NP_071420.1, NP_001030024.1, EAW81013.1, EAW81014.1, EAW81015.1, EAW81016.1
GeneID.6547	SLC8A3	14	70,510,934	70,655,787	144,853	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2681	135851	in gene	0	1	0	12	18	3	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SLC8A3	NCX3, SLC8A3	solute carrier family 8 (sodium/calcium exchanger), member 3	NM_058240, NM_182932, NM_182936, NM_033262, NM_183002, NM_001130417, hCT2328950.1, hCT2328951.1, hCT2328952.1, hCT2328953.1, hCT2348842.0, hCT2348843.0, hCT2348844.0, hCT2348845.0, hCT2348846.0	1562403_a_at, 1568559_a_at	NP_489479.1, NP_891977.1, NP_150287.1, NP_001123889.1, NP_891981.1, NP_892114.1, EAW81018.1, EAW81019.1, EAW81020.1, EAW81021.1, EAW81022.1, EAW81023.1, EAW81024.1, EAW81026.1, EAW81025.1
GeneID.51241	COX16	14	70,791,798	70,826,444	34,646	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1894, 2_A375_pNL97_plus_lncRNA_AR..1..2682	28, 60	in gene, in gene	1	1	0	17	20	7	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene COX16	HSPC203, C14orf112, COX16	COX16 cytochrome c oxidase assembly homolog (S. cerevisiae)	NM_016468, hCT1824658.1	217645_at, 223191_at	NP_057552.1, EAW81031.1
GeneID.55333	SYNJ2BP	14	70,833,213	70,883,807	50,594	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1894, 2_A375_pNL97_plus_lncRNA_AR..1..2682	57391, 57423	downstream, downstream	1	1	0	17	20	7	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SYNJ2BP	FLJ11271, ARIP2, SYNJ2BP, OMP25, FLJ41973	synaptojanin 2 binding protein	NM_018373, hCT2328946.0, hCT2328947.0	219156_at, 235722_at	NP_060843.2, EAW81032.1, EAW81033.1
GeneID.53349	ZFYVE1	14	73,436,159	73,493,920	57,761	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1896	-84	upstream	1	0	0	18	15	4	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ZFYVE1	ZFYVE1, DFCP1, KIAA1589, TAFF1, ZNFN2A1	zinc finger, FYVE domain containing 1	NM_178441, NM_021260, hCT12611.3, hCT2356069.0	223387_at, 223388_s_at	NP_848535.1, NP_067083.1, EAW81064.1, EAW81065.1
GeneID.399671	HEATR4	14	73,945,192	74,025,651	80,459	-	2	4_A375_EGR1..1..2374, 4_A375_EGR1..1..2375	67939, -7725	in gene, upstream	0	0	1	6.5	7.5	15	2	4_A375_EGR1..1	16	Gene HEATR4	MGC48595, HEATR4	HEAT repeat containing 4	NM_203309, hCT2340941.0, hCT2340942.0	1560727_at	NP_976054.1, EAW81117.1, EAW81116.1
GeneID.79697	C14orf169	14	73,957,644	73,960,105	2,461	+	1	4_A375_EGR1..1..2374	66	in gene	0	0	1	6	10	16	1	4_A375_EGR1..1	16	Gene C14orf169	C14orf169, MAPJD, NO66, FLJ21802	chromosome 14 open reading frame 169	NM_024644	219526_at	NP_078920.2
GeneID.10965	ACOT2	14	74,035,772	74,042,359	6,587	+	1	4_A375_EGR1..1..2375	-2396	upstream	0	0	1	7	5	14	1	4_A375_EGR1..1	14	Gene ACOT2	PTE2A, CTE1A, ACOT2, ZAP128, PTE2, MTE1	acyl-CoA thioesterase 2	NM_006821	202982_s_at	NP_006812.3
GeneID.641372	ACOT6	14	74,083,548	74,086,592	3,044	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1897	-4156	upstream	1	0	0	18	10	6	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ACOT6	ACOT6, c14_5530, C14orf42, MGC161656, MGC161658	acyl-CoA thioesterase 6	NM_001037162, hCT12811.2	241949_at	NP_001032239.1, EAW81122.1
GeneID.145482	PTGR2	14	74,318,534	74,352,168	33,634	+	1	4_A375_EGR1..1..2376	35130	downstream	0	0	1	6	12	14	1	4_A375_EGR1..1	14	Gene PTGR2	FLJ99229, ZADH1, PGR2, DKFZp686P10120, PTGR2, FLJ39091	prostaglandin reductase 2	NM_152444, NM_001146154, NM_001146155, hCT12810.3, hCT2356142.0, hCT2356143.0, hCT2356144.0	230774_at	NP_689657.1, NP_001139626.1, NP_001139627.1, EAW81132.1, EAW81134.1, EAW81135.1, EAW81133.1
GeneID.57862	ZNF410	14	74,353,586	74,398,803	45,217	+	1	4_A375_EGR1..1..2376	78	in gene	0	0	1	6	12	14	1	4_A375_EGR1..1	14	Gene ZNF410	ZNF410, APA1, APA-1	zinc finger protein 410	NM_021188, hCT12818.3, hCT1953561.1, hCT2329898.0, hCT2329899.0, hCT2329900.0, hCT2329901.0, hCT2356188.0, hCT2356189.0	202010_s_at, 209944_at	NP_067011.1, EAW81137.1, EAW81136.1, EAW81138.1, EAW81142.1, EAW81143.1, EAW81139.1, EAW81140.1, EAW81141.1
GeneID.145483	FAM161B	14	74,400,705	74,416,835	16,130	-	1	4_A375_EGR1..1..2377	3075	in gene	0	0	1	2	2	16	1	4_A375_EGR1..1	16	Gene FAM161B	c14_5547, FLJ31697, C14orf44, FAM161B	family with sequence similarity 161, member B	NM_152445, hCT2332127.0, hCT2332128.0	242808_x_at	NP_689658.1, EAW81144.1, EAW81145.1
GeneID.51004	COQ6	14	74,416,643	74,429,815	13,172	+	1	4_A375_EGR1..1..2377	-2863	upstream	0	0	1	2	2	16	1	4_A375_EGR1..1	16	Gene COQ6	COQ6, CGI-10	coenzyme Q6 homolog, monooxygenase (S. cerevisiae)	NM_182476, NM_182480, hCT12808.3, hCT2356140.0, hCT2356141.0	218760_at	NP_872282.1, NP_872286.1, EAW81146.1, EAW81147.1, EAW81148.1
GeneID.338917	VSX2	14	74,706,175	74,729,441	23,266	+	1	4_A375_EGR1..1..2378	1665	in gene	0	0	1	6	10	19	1	4_A375_EGR1..1	19	Gene VSX2	RET1, MCOPCB3, HOX10, CHX10, VSX2, MCOP2	visual system homeobox 2	NM_182894, hCT12821.2, hCT2329014.0		NP_878314.1, EAW81164.1, EAW81163.1
GeneID.5826	ABCD4	14	74,751,980	74,769,767	17,787	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1898, 2_A375_pNL97_plus_lncRNA_AR..1..2685, 4_A375_EGR1..1..2379	39, 7, 215	in gene, in gene, in gene	1	1	1	21	15	16	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ABCD4	P70R, P79R, ABCD4, PMP69, ABC41, EST352188, PXMP1L	ATP-binding cassette, sub-family D (ALD), member 4	NR_003256, NM_005050, hCT12806.2, hCT1963603.1, hCT1963604.1, hCT1963605.1, hCT2329272.0, hCT2329276.0, hCT2329277.0, hCT2329278.0	203981_s_at, 203982_s_at	NP_005041.1, EAW81167.1, EAW81165.1, EAW81166.1, EAW81168.1, EAW81169.1, EAW81170.1, EAW81171.1, EAW81172.1
GeneID.84656	TMEM90A	14	74,872,598	74,892,805	20,209	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1899	213	in gene	1	0	0	14	12	4	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene TMEM90A	TMEM90A, IFITMD4, CAPUCIN	transmembrane protein 90A	NM_001105579	237053_at	NP_001099049.1
GeneID.4053	LTBP2	14	74,964,886	75,079,034	114,148	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2686	-7556	upstream	0	1	0	13	15	9	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LTBP2	LTBP2, C14orf141, GLC3D, LTBP3, MSTP031	latent transforming growth factor beta binding protein 2	NM_000428, hCT1952868.1, hCT2329307.1	204682_at, 223690_at	NP_000419.1, EAW81182.1, EAW81183.1
GeneID.1743	DLST	14	75,348,594	75,370,450	21,856	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1900, 2_A375_pNL97_plus_lncRNA_AR..1..2687	-82, -98	upstream, upstream	1	1	0	19	16	11	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene DLST	DLTS, DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	NM_001933, NR_033814, hCT13453.3, hCT2329029.0, hCT2356058.0, hCT2356059.0	215210_s_at	NP_001924.2, EAW81202.1, EAW81199.1, EAW81200.1, EAW81201.1
GeneID.2353	FOS	14	75,745,481	75,748,937	3,456	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1902, 2_A375_pNL97_plus_lncRNA_AR..1..2689, 4_A375_EGR1..1..2380	-121, -57, 247	upstream, upstream, in gene	1	1	1	23	29	18	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene FOS	FOS, AP-1, C-FOS	FBJ murine osteosarcoma viral oncogene homolog	NM_005252, hCT13449.3, hCT2329124.0, hCT2329126.0	209189_at	NP_005243.1, EAW81228.1, EAW81227.1, EAW81229.1
GeneID.100287415	LOC100287415	14	75,745,527	75,746,831	1,304	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1902, 2_A375_pNL97_plus_lncRNA_AR..1..2689, 4_A375_EGR1..1..2380	1471, 1407, 1103	downstream, downstream, in gene	1	1	1	23	29	18	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene LOC100287415		hypothetical LOC100287415	XR_111456, XR_110225, XR_114765		
GeneID.10538	BATF	14	75,988,784	76,013,335	24,551	+	1	4_A375_EGR1..1..2381	24256	in gene	0	0	1	6	4	15	1	4_A375_EGR1..1	15	Gene BATF	B-ATF, SFA-2, SFA2, BATF1, BATF	basic leucine zipper transcription factor, ATF-like	NM_006399, hCT11572.1	205965_at	NP_006390.1, EAW81234.1
GeneID.7043	TGFB3	14	76,424,442	76,448,092	23,650	-	1	1_A375_pNL7_minus_lncRNA_AR..1..1903	-4036	upstream	1	0	0	16	13	6	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene TGFB3	FLJ16571, ARVD, TGFB3, TGF-beta3	transforming growth factor, beta 3	NM_003239, hCT11568.3	1555540_at, 209747_at	NP_003230.1, EAW81249.1
GeneID.112752	C14orf179	14	76,452,096	76,550,092	97,996	+	1	1_A375_pNL7_minus_lncRNA_AR..1..1903	32	in gene	1	0	0	16	13	6	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene C14orf179	MGC16028, IFT43, C14orf179, FLJ32173	chromosome 14 open reading frame 179	NM_052873, NM_001102564	1566899_at, 226195_at, 226196_s_at	NP_443105.2, NP_001096034.1
GeneID.145497	C14orf166B	14	77,292,725	77,336,645	43,920	+	1	4_A375_EGR1..1..2382	47035	downstream	0	0	1	6	4	14	1	4_A375_EGR1..1	14	Gene C14orf166B	C14orf166B	chromosome 14 open reading frame 166B	NM_194287, hCT12334.3	233941_at, 234453_s_at	NP_919263.2, EAW81265.1
GeneID.64207	C14orf4	14	77,490,886	77,495,034	4,148	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2692, 4_A375_EGR1..1..2383	-4294, 2159	upstream, in gene	0	1	1	9.5	15.5	10	2	4_A375_EGR1..1	15	Gene C14orf4	EAP1, KIAA1865, C14orf4, IRF2BPL	chromosome 14 open reading frame 4	NM_024496	223474_at	NP_078772.1
GeneID.283576	ZDHHC22	14	77,597,613	77,608,134	10,521	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1905, 2_A375_pNL97_plus_lncRNA_AR..1..2693	7878, 7942	in gene, in gene	1	1	0	39	53	10	1	2_A375_pNL97_plus_lncRNA_AR..1	53	Gene ZDHHC22	ZDHHC22, C14orf59	zinc finger, DHHC-type containing 22	NM_174976	229805_at, 229875_at	NP_777636.2

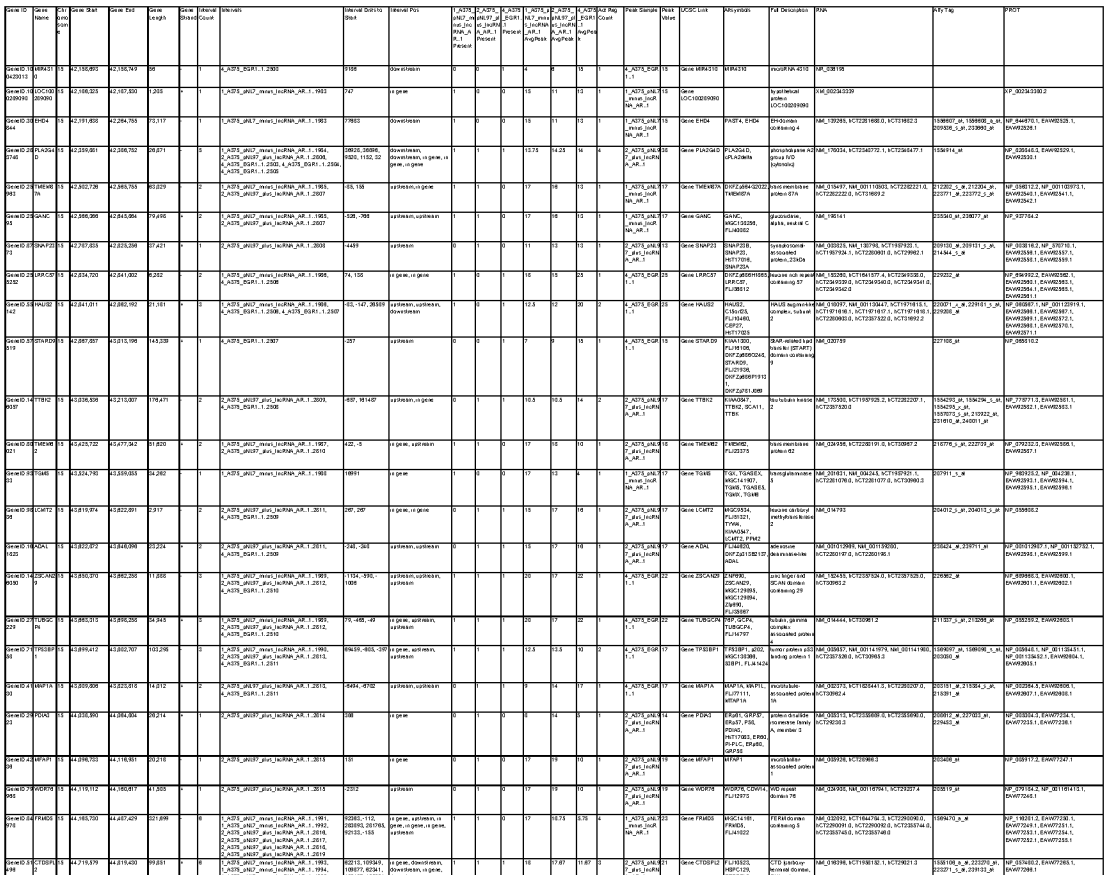


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_uhl27_wt_A375_gt1_lncRNA_A_R_1 Percent	2_A375_uhl27_wt_A375_gt1_lncRNA_1 Percent	3_A375_1_A375_uhl27_wt_A375_gt1_lncRNA_1 Avg Reads	4_A375_2_A375_uhl27_wt_A375_gt1_lncRNA_1 Avg Reads	5_A375_1_A375_uhl27_wt_A375_gt1_lncRNA_1 Avg Peak	Adj Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	FPKT
GeneID:3571MEM196	MEM3C	14	77,845,102	77,725,655	77,726	+	3	2_A375_uhl37_plus_lncRNA_AR_1.2694, 2_A375_uhl37_plus_lncRNA_AR_1.2693, 2_A375_EGR1_1.2394	27552, 60376, 59850	sr:gene, sr:gene, sr:gene	0	1	1	11	13.67	7.67	3	2_A375_uhl.628_plus_lncRNA_AR_1	Gene:TMEM3C	C14orf171, TMEM83C	transmembrane protein 83C	NM_030431, XCT132852.2, XCT215817.0	227733_at	NP_085184.2, EWK61272.1, EWK61272.1
GeneID:28:PCMT1934	PCMT2	12	77,741,299	77,707,323	43,976	-	3	1_A375_uhl37_minus_lncRNA_AR_1.1908, 2_A375_uhl37_plus_lncRNA_AR_1.2696, 2_A375_uhl37_plus_lncRNA_AR_1.2697	2687, 17732, -295	sr:gene, sr:gene, upstream	1	1	0	12	14.33	5	3	2_A375_uhl.632_plus_lncRNA_AR_1	Gene:PCMT2	EHTP,dj869d13.05, protein-O-isoaspartate(D-aspartate) O-methyltransferase 2	NM_013302, XCT132852.2, XCT231610.0	23:9832_s_at, 225992_at, 225933_at	NP_037514.2, EWK61276.1, EWK61277.1
GeneID:29:GSTZ154	GSTZ1	14	77,707,200	77,707,943	10,710	+	2	1_A375_uhl37_minus_lncRNA_AR_1.1908, 2_A375_uhl37_plus_lncRNA_AR_1.2697	-2982, 2490	upstream, sr:gene	1	1	0	12	10.5	8.5	2	2_A375_uhl.616_plus_lncRNA_AR_1	Gene:GSTZ1	MAA, GSTZ1-1, GSTZ1, MAAI, MGC20279	glutathione transferase zeta 1	NM_001310, NM_145870, NM_145871, XCT132852.2, XCT230134.0, XCT230135.0, XCT236139.0	209581_at	NP_001304.2, NP_665877.1, NP_665878.2, EWK61278.1, EWK61279.1, EWK61280.1, EWK61281.1
GeneID:30:NRXN39	NRXN2	14	78,070,993	80,030,762	1,959,969	+	7	1_A375_uhl37_minus_lncRNA_AR_1.1907, 1_A375_uhl37_minus_lncRNA_AR_1.1906, 1_A375_uhl37_minus_lncRNA_AR_1.1905, 1_A375_uhl37_minus_lncRNA_AR_1.1910, 2_A375_uhl37_plus_lncRNA_AR_1.2695, 2_A375_uhl37_plus_lncRNA_AR_1.2699, 2_A375_uhl37_plus_lncRNA_AR_1.2700	116259, 458653, 64169, 786033, 18275, 615395, 786033	sr:gene, sr:gene, sr:gene, sr:gene, sr:gene, sr:gene, sr:gene	1	1	0	16.5	15	2.2	5	1_A375_uhl.620_minus_lncRNA_AR_1	Gene:NRXN2	MGC174971, C14orf60, MRXN2, RAMP743	neurexin 2	NM_004796, NM_138910, NM_001135230, XCT154599.3, XCT192695.2, XCT232995.1, XCT232995.2, XCT232997.1, XCT232998.1	203765_at, 215020_at, 219221_s_at, 223649_at	NP_004787.2, NP_612438.2, NP_001295120.1, EWK65312.1, EWK65316.1, EWK65314.1, EWK65315.1, EWK65316.1, EWK65317.1
GeneID:31:MC14orf145	MC14orf145	14	80,982,821	81,005,964	443,080	-	2	1_A375_uhl37_minus_lncRNA_AR_1.1911, 2_A375_uhl37_plus_lncRNA_AR_1.2701	-2364, -2196	upstream, upstream	1	1	0	21	23	8	1	2_A375_uhl.633_plus_lncRNA_AR_1	Gene:C14orf145	C14orf145, C14orf81	chromosome 14 open reading frame 145	NM_152448	1557:53_at, 1557:78_s_at, 222853_s_at, 222329_at, 244023_at	NP_689619.2
GeneID:29:GTF2H257	GTF2H1	11	61,846,994	61,867,974	41,181	+	1	2_A375_uhl37_plus_lncRNA_AR_1.2702	7	sr:gene	0	1	0	8	8	7	1	2_A375_uhl.617_plus_lncRNA_AR_1	Gene:GTF2H1	TFIH1, TFIIH, GTF2H1, MGC129701, MGC129699	general transcription factor IIH, 1, 62kDa	NM_001995, NM_016089, XCT127A.2, XCT236943.0	208521_s_at, 223433_at	NP_983999.1, NP_057442.1, EWK61334.1, EWK61335.1
GeneID:18:LOC10395859	LOC100395859	14	61,867,982	61,868,804	1,242	+	1	2_A375_uhl37_plus_lncRNA_AR_1.2702	6	sr:gene	0	1	0	8	7	6	1	2_A375_uhl.617_plus_lncRNA_AR_1	Gene:LOC100395859	hypothetical LOC100395859	XR_111453, XR_110228, XR_114786		
GeneID:18:LOC10395972	LOC100395972	14	63,990,179	63,990,489	6,893	-	1	2_A375_uhl37_plus_lncRNA_AR_1.2703	-1515	upstream	0	1	0	12	14	6	1	2_A375_uhl.614_plus_lncRNA_AR_1	Gene:LOC100396731	hypothetical LOC100396731	XR_111451, XR_110231, XR_114771		
GeneID:23:FLRT2765	FLRT2	14	65,996,466	66,004,370	97,762	+	1	2_A375_uhl37_plus_lncRNA_AR_1.2702	1496	sr:gene	0	1	0	12	14	9	1	2_A375_uhl.614_plus_lncRNA_AR_1	Gene:FLRT2	KIAA0465, FLRT2	Fibronectin leucine rich transmembrane protein 2	NM_013231	204356_s_at, 204359_at	NP_037385.1
GeneID:19:PTPN21699	PTPN21	14	66,832,122	69,021,123	69,001	-	2	1_A375_uhl37_minus_lncRNA_AR_1.1913, 2_A375_uhl37_plus_lncRNA_AR_1.2703	2399, 2299	sr:gene, sr:gene	1	1	0	24	33	10	1	2_A375_uhl.633_plus_lncRNA_AR_1	Gene:PTPN21	PTPN21, PTPD1, PTPRL10	protein tyrosine phosphatase, non-receptor type 21	NM_007039, XCT111012.2, XCT232958.0	1326_at, 209436_at, 222092_at, 40526_at	NP_008970.2, EWK61302.1, EWK61302.1
GeneID:12:TTC8936	TTC8	14	69,290,976	69,344,355	53,337	+	1	4_A375_EGR1_1.2396	446	sr:gene	0	0	1	10	12	10	1	4_A375_EGR1_1.1	Gene:TTC8	PJR1, TTC8, BBS8	tetratricopeptide repeat domain 8	NM_198309, NM_198310, NM_144596, XCT121672.3, XCT232933.0, XCT232939.0, XCT236207.0, XCT236236.0, XCT236239.0, XCT236240.0, XCT236211.0	226120_at, 237474_at	NP_938051.1, NP_938052.1, NP_938197.2, EWK61395.1, EWK61397.1, EWK61400.1, EWK61393.1, EWK61395.1, EWK61399.1, EWK61401.1, EWK61402.1
GeneID:30:C14orf141	C14orf140	14	90,265,469	90,421,059	157,820	-	4	1_A375_uhl37_minus_lncRNA_AR_1.1916, 1_A375_uhl37_minus_lncRNA_AR_1.1917, 2_A375_uhl37_plus_lncRNA_AR_1.2711, 2_A375_uhl37_plus_lncRNA_AR_1.2712	-127, -1035, -127, -1053	upstream, upstream, upstream, upstream	1	1	0	20	17.5	6.5	2	1_A375_uhl.623_minus_lncRNA_AR_1	Gene:C14orf145	DKFZp547H145, FLJ35329, C14orf145, EFCAB11	EF-hand calcium binding domain 14	NM_145231, XCT196300.4, XCT192541.2	210525_s_at, 214264_s_at	NP_660274.1, EWK61411.1, EWK61412.1
GeneID:33:TDP1775	TDP1	14	90,422,248	90,511,106	88,862	+	4	1_A375_uhl37_minus_lncRNA_AR_1.1918, 1_A375_uhl37_minus_lncRNA_AR_1.1917, 2_A375_uhl37_plus_lncRNA_AR_1.2711, 2_A375_uhl37_plus_lncRNA_AR_1.2712	-1031, -116, -1031, -102	upstream, upstream, upstream, upstream	1	1	0	20	17.5	6.5	2	1_A375_uhl.623_plus_lncRNA_AR_1	Gene:TDP1	MGC104252, TDP1, FLJ11090	tyrosyl-DNA phosphodiesterase 1	NM_018319, NM_001008744, XCT126A.2, XCT192344.1, XCT232949.0	219715_s_at, 239044_at, 240822_at	NP_060789.2, NP_001008744.1, EWK61414.1, EWK61415.1, EWK61416.1
GeneID:35:CALM1	CALM1	14	90,985,327	90,974,419	11,292	+	1	4_A375_EGR1_1.2397	177	sr:gene	0	0	1	12	15	19	1	4_A375_EGR1_1.1	Gene:CALM1	CALM2, DD132, CAM1, CALM1, CALM3, PHKD, CALML2	calmodulin 1 (phosphorylase kinase, delta)	NM_006888, NM_001199106, XCT129A.2, XCT229497.0	200883_s_at, 200884_s_at, 200885_s_at, 211956_at, 211955_s_at, 213710_s_at, 241819_at	NP_006879.2, NP_001186035.1, NP_001186036.1, EWK61421.1, EWK61420.1
GeneID:14:TTC7B557	TTC7B	14	91,896,902	91,892,761	273,629	-	1	4_A375_EGR1_1.2398	14153	sr:gene	0	0	1	3	8	17	1	4_A375_EGR1_1.1	Gene:TTC7B	TTC7J1, chk_5953, TTC7B	tetratricopeptide repeat domain 7B	NM_001010834, XCT232965.1, XCT232969.1, XCT236150.0, XCT236151.0, XCT236156.0, XCT236157.0, XCT236160.0	226152_at	NP_001010834.1, EWK61435.1, EWK61434.1, EWK61433.1, EWK61436.1, EWK61437.1, EWK61438.1
GeneID:35:C14orf159117	C14orf159	14	91,930,357	91,891,703	111,248	-	2	2_A375_uhl37_plus_lncRNA_AR_1.2714, 4_A375_EGR1_1.2399	35, 119771	sr:gene, downstream	0	1	1	9.5	14	11.5	2	2_A375_uhl.639_plus_lncRNA_AR_1	Gene:C14orf159	C14orf159, FLJ39143, C14orf181, DKFZp686I02126, FLJ39975, FLJ39990	chromosome 14 open reading frame 159	NM_194332, NM_001102396, NM_001102397, XCT154599.3, XCT192695.2, XCT232995.1, XCT232995.2, XCT232997.1, XCT232998.1	1554039_at, 218295_s_at, 218296_at	NP_919228.4, NP_001096838.1, NP_001093537.1, NP_001093539.1, EWK61439.1, EWK61440.1, EWK61441.1, EWK61442.1, EWK61443.1, EWK61444.1
GeneID:35:GPR66111	GPR66	14	91,896,976	91,720,224	21,345	-	1	4_A375_EGR1_1.2399	29056	sr:gene	0	0	1	8	8	17	1	4_A375_EGR1_1.1	Gene:GPR66	GPCR97, MGC159563, MGC111379, GPR66	G protein-coupled receptor 66	NM_005455, NM_001177674, XCT110.2.4, XCT229580.1	211249_at, 229583_at	NP_005464.1, NP_001171147.1, EWK61447.1, EWK61446.1
GeneID:43:CCDC8397	CCDC8	14	91,737,987	91,894,103	149,488	+	2	4_A375_EGR1_1.2399, 4_A375_EGR1_1.2398	152653, 93855	downstream, sr:gene	0	0	1	3	9	14	2	4_A375_EGR1_1.1	Gene:CCDC85C	KIAA1825, CCDC85C, FLJ90334, DKFLE, PARP2	coiled-coil domain containing 85C	NM_001039414	213343_at, 227228_s_at, 231266_at, 243889_at	NP_001307883.2
GeneID:33:SMEK1871	SMEK1	14	91,923,955	91,976,944	52,809	-	2	1_A375_uhl37_minus_lncRNA_AR_1.1919, 2_A375_uhl37_plus_lncRNA_AR_1.2715	-172, -252	upstream, upstream	1	1	0	16	16	13	1	2_A375_uhl.616_plus_lncRNA_AR_1	Gene:SMEK1	SMEK, PPA1R3A, PP1F1, shk-1, SMEK1, KIAA2010, MSTP033	SMEK homolog 1, suppressor of clr1 (Dictyostelium)	NM_032460, XCT129B9.4, XCT229531.0, XCT229532.0, XCT229533.0, XCT229534.0, XCT229535.0	223285_s_at, 223286_s_at, 223560_s_at	NP_115943.2, EWK61434.1, EWK61432.1, EWK61435.1, EWK61436.1, EWK61437.1, EWK61432.1
GeneID:35:TRIP11121	TRIP11	14	92,434,343	92,506,403	72,160	-	1	1_A375_uhl37_minus_lncRNA_AR_1.1920	-81	upstream	1	0	0	16	13	9	1	1_A375_uhl.618_minus_lncRNA_AR_1	Gene:TRIP11	CEV14, TRIP230, TRIP11, GMAP-210, ACG1a	thyroid hormone receptor interactor 11	NM_004239, XCT125A3.3, XCT229536.0	209719_at, 210580_x_at	NP_004230.2, EWK61466.1, EWK61469.1
GeneID:43:ATXN287	ATXN2	12	92,524,896	92,572,965	48,069	-	2	1_A375_uhl37_minus_lncRNA_AR_1.1921, 2_A375_uhl37_plus_lncRNA_AR_1.2716	-187, -153	upstream, upstream	1	1	0	29	32	0	1	2_A375_uhl.632_plus_lncRNA_AR_1	Gene:ATXN2	CGI, MJD1, ataxin-2, ATX2, ATX2_SCA2	ataxin 2	NM_002973, NM_030666, NM_001127696, NM_025496, NR_029457, NR_029466, NM_025462, NR_029461, NR_029465, NR_029464, NR_029463, NR_029466, NR_029467, NR_029468, NR_029469, NR_029470, NM_001127697, NM_001164774, NM_001164776, NM_001164778, NM_001164779	205413_s_at, 205416_s_at, 216987_at, 217221_s_at, 233162_s_at, 233240_at, 238723_at	NP_002964.2, NP_1063761, NP_001121166.1, NP_001121169.2, NP_001118246.1, NP_001118247.1, NP_001118250.1, NP_001118249.1, NP_001118251.1, NP_001118252.1, NP_001118253.1, NP_001118254.1, EWK61470.1, EWK61472.1, EWK61473.1, EWK61474.1, EWK61475.1
GeneID:43:NDUFB837	NDUFB1	14	92,562,487	92,566,153	3,666	+	4	1_A375_uhl37_minus_lncRNA_AR_1.1921, 1_A375_uhl37_minus_lncRNA_AR_1.1922, 2_A375_uhl37_plus_lncRNA_AR_1.2716, 2_A375_uhl37_plus_lncRNA_AR_1.2717	13001, 23, 1003, -199	downstream, sr:gene, downstream, upstream	1	1	0	31.3	26	6	2	1_A375_uhl.634_plus_lncRNA_AR_1	Gene:NDUFB1	MNLL, NDUFB1, CI-SGDH, CI-MNLL	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7.5kDa	NM_004.543, XCT125A3.3, XCT150.150.1, XCT229582.0, XCT229588.0	208760_s_at, 243932_at	NP_004538.2, EWK61478.1, EWK61478.1, EWK61477.1, EWK61478.1
GeneID:33:CPSF2981	CPSF2	14	92,566,329	92,600,943	42,214	+	2	2_A375_uhl37_plus_lncRNA_AR_1.1922, 2_A375_uhl37_plus_lncRNA_AR_1.2717	-201, 22	upstream, sr:gene	1	1	0	34	24	13	1	2_A375_uhl.634_plus_lncRNA_AR_1	Gene:CPSF2	CPSF2, KIAA1307, FLJ39721, CPSF100	cleavage and polyadenylation specific factor 2, 100kDa	NM_031437, XCT125A6.3, XCT229721.1, XCT236179.0, XCT236180.0	229966_s_at, 229994_at, 233205_s_at	NP_539133.1, EWK61483.1, EWK61483.1, EWK61482.1
GeneID:29:RIN2690	RIN2	14	92,960,023	93,165,359	175,211	+	1	2_A375_uhl37_plus_lncRNA_AR_1.2718	440	sr:gene	0	0	1	10	13	13	1	2_A375_uhl.613_plus_lncRNA_AR_1	Gene:RIN2	DKFZp434H168, FLJ11700, RIN2, FLJ22439	Ras and Rab interactor 2	NM_018932, XCT232932.1, XCT232933.0, XCT232974.1, XCT232975.0, XCT232976.0, XCT232979.1, XCT234504.0, XCT234505.0	1563003_at, 219498_s_at, 219499_at, 239439_at, 85471_at	NP_076938.3, EWK61490.1, EWK61491.1, EWK61493.1, EWK61495.1, EWK61499.1, EWK61492.1, EWK61493.1, EWK61495.1, EWK61497.1
GeneID:19:CHGA13	CHGA	14	93,389,443	93,401,808	12,193	+	5	1_A375_uhl37_minus_lncRNA_AR_1.1924, 1_A375_uhl37_minus_lncRNA_AR_1.1923, 2_A375_uhl37_plus_lncRNA_AR_1.2719, 2_A375_uhl37_plus_lncRNA_AR_1.2720, 2_A375_EGR1_1.2395	-6837, 443, -6769, 479, -6643	upstream, sr:gene, upstream, sr:gene, upstream	1	1	0	16	17	6.33	3	2_A375_uhl.629_plus_lncRNA_AR_1	Gene:CHGA	CHGA, CGA	chromogranin A (parathyroid secretory protein 1)	NM_001275, XCT123B1.2, XCT236073.0	204697_s_at	NP_001266.1, EWK61503.1, EWK61508.1
GeneID:37:KIAA1409576	KIAA1409	14	93,799,585	94,175,869	376,126	+	1	4_A375_EGR1_1.2393	97253	sr:gene	0	0	1	9	9	14	1	4_A375_EGR1_1.1	Gene:KIAA1409	FLJ43237, KIAA1409	KIAA1409	NM_020515, XCT236042.0	220930_at	NP_065569.3, EWK61531.1
GeneID:31:ASB2878	ASB2	14	94,490,513	94,423,767	23,254	-	2	1_A375_uhl37_minus_lncRNA_AR_1.1926, 2_A375_uhl37_plus_lncRNA_AR_1.2721	-2121, -2249	upstream, upstream	1	1	0	15	15	5	1	1_A375_uhl.615_minus_lncRNA_AR_1	Gene:ASB2	KIAA0262, ASB2, MGC40344	ankyrin repeat and SOCS box-containing 2	NM_016120, XCT111.2.4, XCT229610.1, XCT229511.1, XCT229512.1	227715_s_at, 233357_s_at	NP_057204.2, EWK61543.1, EWK61541.1, EWK61542.1
GeneID:18:LOC10395919	LOC100395919	14	94,425,132	94,443,157	20,015	+	2	2_A375_uhl37_plus_lncRNA_AR_1.1926, 2_A375_uhl37_plus_lncRNA_AR_1.2721	2768, 2894	sr:gene, sr:gene	1	1	0	15	15	5	1	2_A375_uhl.615_plus_lncRNA_AR_1	Gene:LOC100395919	hypothetical LOC100395919	XR_110229, XR_110233		
GeneID:29:OTUB2990	OTUB2	14	94,492,734	94,515,378	22,932	-	2	1_A375_uhl37_minus_lncRNA_AR_1.1927, 2_A375_uhl37_plus_lncRNA_AR_1.2722	-132, -98	upstream, upstream	1	1	0	26	31	9	1	2_A375_uhl.611_plus_lncRNA_AR_1	Gene:OTUB2	OTUB2, OTUD7, OTUD, MGC31102, C14orf137, FLJ21910	OTU domain, ubiquitin aldehyde binding 2	NM_032112, XCT134B3.3, XCT229429.0	1553662_at, 219369_s_at	NP_079011.1, EWK61549.1, EWK61548.1
GeneID:29:CLMN765	CLMN	14	95,648,276	95,766,343	137,049	-	1	1_A375_uhl37_minus_lncRNA_AR_1.1928	58849	sr:gene	1	0	0	14	17	2	1	1_A375_uhl.614_minus_lncRNA_AR_1	Gene:CLMN	KIAA1185, FLJ43845, CLMN, RAM2900, FLJ12383	calmin (calponin-like, transmembrane)	NM_024734, XCT153B4.4, XCT229586.0	221042_s_at, 229797_s_at, 229792_x_at	NP_079010.2, EWK61596.1, EWK61597.1
GeneID:18:LOC10357043	LOC100357043	14	95,842,729	96,291,905	49,179	+	1	4_A375_EGR1_1.2395	-409	upstream	0	0	1	4	9	10	1	4_A375_EGR1_1.1	Gene:LOC100357043	hypothetical LOC100357043	XR_111474, XR_111473, XR_111475, XR_110244, XR_110243, XR_110245, XR_111.763, XR_114252, XR_114.764	209295_at, 212715_at, 212720_at, 212721_at, 222035_s_at, 223961_at	NP_116221.2, EWK65842.1, EWK65843.1, EWK65844.1, EWK65845.1, EWK65846.1, EWK65847.1, EWK65849.1
GeneID:19:RNPC1314	RNPC1A	14	96,966,730	97,033,446	84,726	+	2	2_A375_uhl37_plus_lncRNA_AR_1.2727, 4_A375_EGR1_1.2396	-452, -352	upstream, upstream	1	0	1	8	15	14	1	2_A375_uhl.615_plus_lncRNA_AR_1	Gene:PAPOLA	MGC3276, PAP, PAPOLA	poly(A) polymerase alpha	NM_020832, XCT156B2.2, XCT229615.1, XCT229614.1, XCT229616.1, XCT229615.2, XCT229616.0, XCT229617.0, XCT229618.0, XCT229619.1, XCT229620.1, XCT229621.1, XCT229622.1	209295_at, 212715_at, 212720_at, 212721_at, 222035_s_at, 223961_at	NP_116221.2, EWK65842.1, EWK65843.1, EWK65844.1, EWK65845.1, EWK65846.1, EWK65847.1, EWK65849.1
GeneID:35:CCDC827762	CCDC85C	14	99,977,605	100,070,727	93,124	-	2	1_A375_uhl37_minus_lncRNA_AR_1.1931, 1_A375_EGR1_1.2397	-310, 30815	upstream, sr:gene	1	0	1	10.5	8	12	2	1_A375_uhl.617_minus_lncRNA_AR_1	Gene:CCDC85C	MGC117455, CCDC85C, FLJ22550	coiled-coil domain containing 85C	NM_01144995	219016_s_at, 222829_s_at	NP_001139687.1
GeneID:18:LOC10357108	LOC100357108	14	100,070,693	100,092,077	21,164	+	1	1_A375_uhl37_minus_lncRNA_AR_1.1931	147	sr:gene	1	0	0	17	10	10	1	1_A375_uhl.617_minus_lncRNA_AR_1	Gene:LOC100357108	hypothetical LOC100357108	XR_111471, XR_110247, XR_114788		
GeneID:35:EVL	EVL	14	100,091,751	100,091,973	76,822	+	1	4_A375_EGR1_1.2398	95510	sr:gene	0	0	1	3	8	15	1	4_A375_EGR1_1.1	Gene:EVL	EVL, RN186	Ena/VASP-like	NM_016337, XCT139B4.3, XCT229583.0, XCT229585.0, XCT229586.0	217036_s_at, 227222_at	NP_057421.1, EWK61588.1, EWK61584.1, EWK61585.1, EWK61587.1
GeneID:37:YY126	YY1	14	100,708,102	100,744,004	59,702	+	1	4_A375_EGR1_1.2399	47026	downstream	0	0	1	10	13	16	1	4_A375_EGR1_1.1	Gene:YY1	UCABF, DELTA, INO80D, YY1, YRAG-1, NF-E1, YY1	YY1 transcription factor	NM_003403, XCT161A3.3, XCT229680.0	200047_s_at, 201901_s_at, 201902_s_at, 213494_s_at, 224711_at, 224716_at	NP_003394.1, EWK65890.1, EWK65891.1
GeneID:12:SLC25A3996	SLC25A29	14	100,797,453	100,772,800	25,007	-	1	4_A375_EGR1_1.2399	20732	downstream	0	0	1	10	13	16	1	4_A375_EGR1_1.1	Gene:SLC25A29	C14orf80, SLC25A29, FLJ39573, CACL	calcium binder family 25, member 29	NM_031213.5, XCT161A2.3, XCT236117.0, XCT236119.0	223355_at, 223356_s_at, 231484_at	NP_001034444.1, EWK65892.1, EWK65893.1, EWK65894.1, EWK65895.1
GeneID:29:WDR23446	WDR23	14	100,842,733	100,996,840	153,688	+	2	1_A375_uhl37_minus_lncRNA_AR_1.1933, 2_A375_uhl37_plus_lncRNA_AR_1.2731	100237, 116293	sr:gene, sr:gene	1	1	0	16.5	12.5	5.5	2	1_A375_uhl.619_minus_lncRNA_AR_1	Gene:WDR23	WDR23, MGC4645	WD repeat domain 23	NM_031164.5, XCT161A6.3, XCT193784.1, XCT229955.0, XCT229956.0	219689_at	NP_001154948.1, NP_076791.3, EWK65704.1, EWK65705.1, EWK65706.1
GeneID:10:LOC10057124	LOC100057124	14	100,847,293	100,847,904	611	+	2	1_A375_uhl37_minus_lncRNA_AR_1.1933, 2_A375_uhl37_plus_lncRNA_AR_1.2731	-4931, 5715	upstream, downstream	1	1	0	16.5	12.5	5.5	2	1_A375_uhl.619_minus_lncRNA_AR_1	Gene:LOC100057124	RNGNT F25	high mobility group nucleosomal binding domain 1 pseudogene 25	NM_001319559, NM_033116915, NM_001120790	NM_001319821, XP_005119963.1, XP_005120030.1	
GeneID:37:BEGAN598	BEGAIN	14	101,002,464	101,038,151	35,847	-	1	4_A375_EGR1_1.2400	16767	sr:gene	0	0	1	3	9	14	1	4_A375_EGR1_1.1	Gene:BEGAIN	KIAA1445, BEGAIN	brain-enriched guanylate kinase-associated homolog (rat)	NM_020038, NM_001135931, XCT161A5.3, XCT193733.1	220763_s_at	NP_064033.1, NP_001130003.1, EWK61707.1, EWK61708.1
GeneID:10:MIR9412128308	MIR9412	14	101,030,932	101,030,915	93	+	1	2_A375_uhl37_minus_lncRNA_AR_1.1934	6912	downstream	1	0	0	25	8	12	1	2_A375_uhl.625_minus_lncRNA_AR_1	Gene:MIR941	MIR941, MIR941, hsa-mir-941	microRNA 941	NM_033194		
GeneID:37:MIR4091441	MIR4091	14	101,030,837	101,030,715	76	+	1	2_A375_uhl37_minus_lncRNA_AR_1.1934	6797	downstream	1	0	0	25	8	12	1	2_A375_uhl.625_minus_lncRNA_AR_1	Gene:MIR409	MIR4091, MIR409, hsa-mir-409	microRNA 409	NM_029975		
GeneID:37:MIR4124433	MIR412	14	101,030,784	101,031,074	90	+	1	2_A375_uhl37_minus_lncRNA_AR_1.1934	7960	downstream	1	0	0	25	8	12	1	2_A375_uhl.625_minus_lncRNA_AR_1	Gene:MIR412	MIR412, hsa-mir-412, MIR412	microRNA 412	NM_059133		
GeneID:44:MIR5992914	MIR5992	14	101,030,955	101,032,004	997	+	1	1_A375_uhl37_minus_lncRNA_AR_1.1934	7829	downstream	1	0	0	25	8	12	1	1_A375_uhl.625_minus_lncRNA_AR_1	Gene:MIR5992	MIR5992, hsa-mir-5992, MIR5992-2, MIR5992-3	microRNA 5992	NM_029862		
GeneID:37:MIR4410434	MIR4410	14	101,032,249	101,032,328	79	+	1	4_A375_EGR1_1.2401	7485	downstream	1	0	0	25	8	12	1	4_A375_EGR1_1.1	Gene:MIR410	MIR410, hsa-mir-410, MIR410, MIR1610	microRNA 410	NM_033188		
GeneID:37:MIR6958438	MIR6958	14	101,032,061	101,032,195	97	+	1	4_A375_EGR1_1.2401	6963	downstream	1	0	0	25	8	12	1	4_A375_EGR1_1.1	Gene:MIR6958	MIR6958, MIR6958, hsa-mir-6958	microRNA 6958	NM_032392		
GeneID:18:LOC10357257	LOC100357257	14	101,038,365	101,039,274	1,029	+	2	1_A375_uhl37_minus_lncRNA_AR_1.1934, 4_A375_EGR1_1.2402	5498, 6026	downstream, downstream	1	0	0	14	8.5	10.5	2	1_A375_uhl.625_minus_lncRNA_AR_1	Gene:LOC100357257	hypothetical LOC100357257	XR_111467, XR_110231, XR_114790		
GeneID:64:DKFZP5631502	DKFZP5631502	14	102,019,360	102,022,013	2,653	-	1	4_A375_EGR1_1.2404	6131	upstream	0	0	1	4	7	18	1	4_A375_EGR1_1.1	Gene:DKFZP5631502	DKFZp5631502, MGC129.00, NCRNA00041, C14orf134, DKFZP5631502	DKFZ supported cloned (pro-pollen-coding)	NM_152710	1559230_at, 222757_at, 239727_at	

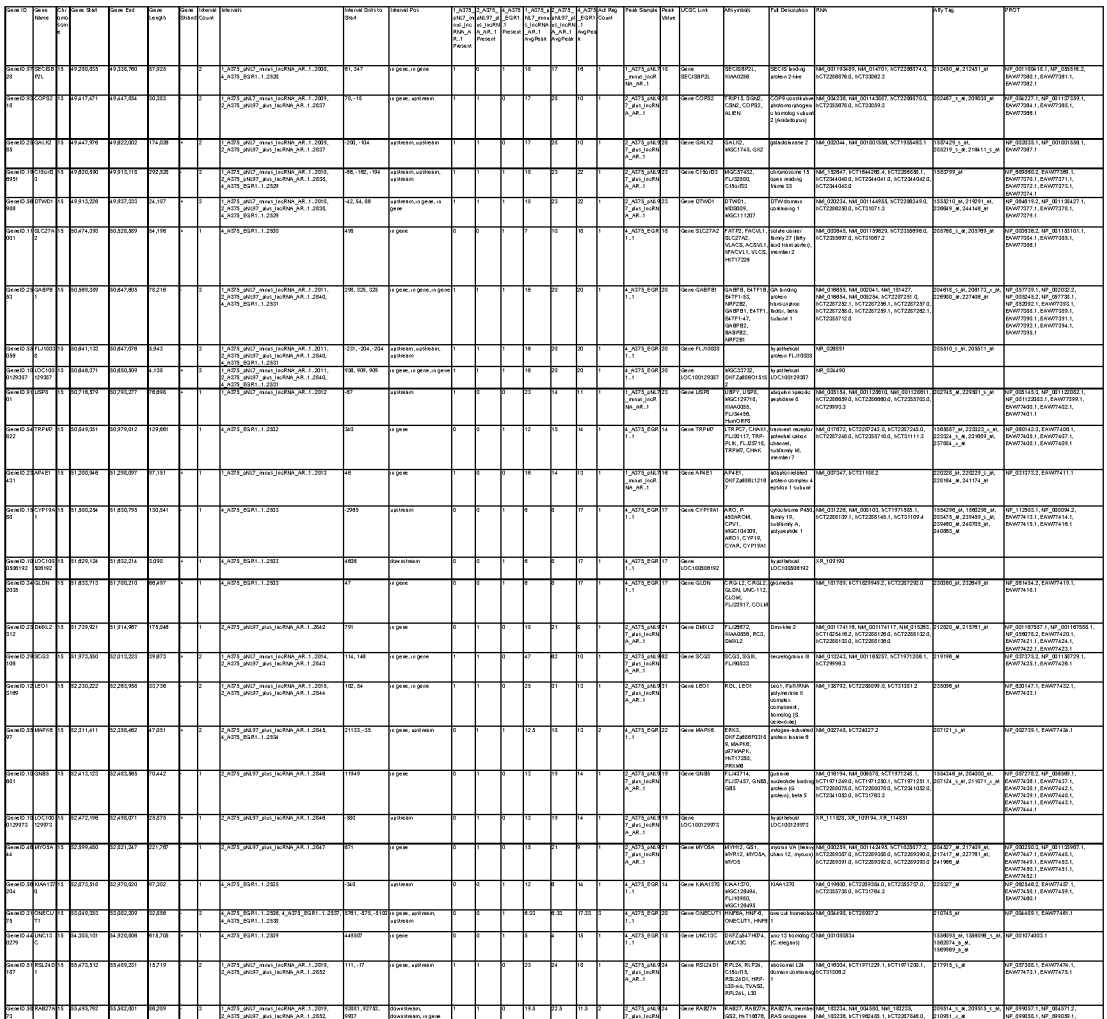


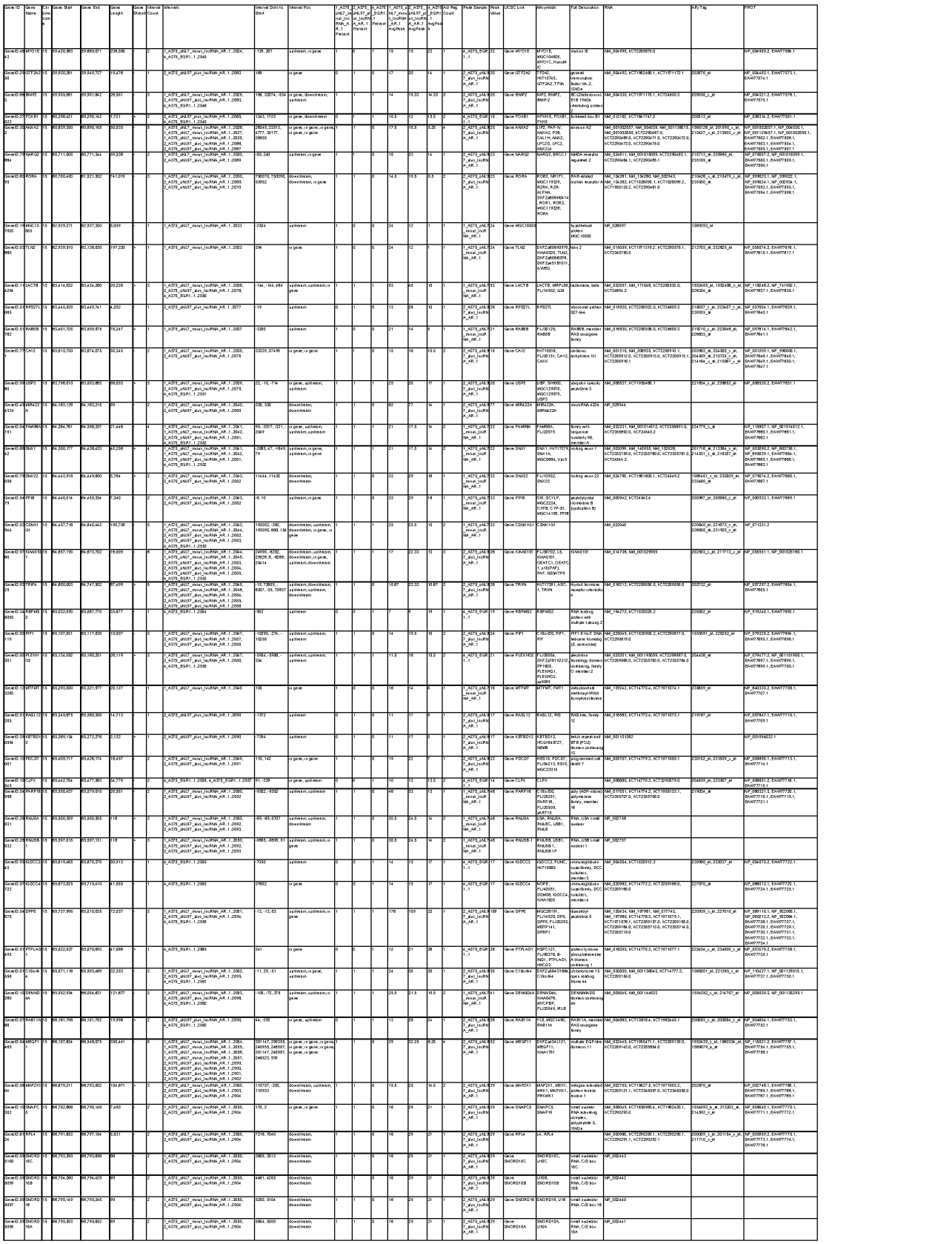


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.100507466	LOC100507466	15	35,836,396	36,151,202	312,806	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1963, 2_A375_pNL97_plus_lncRNA_AR..1.2771, 2_A375_pNL97_plus_lncRNA_AR..1.2772	132, -17, 192324	in gene, upstream, in gene	1	1	0	16.5	19.5	5	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene LOC100507466		hypothetical LOC100507466	XR_111502, XR_109173, XR_114838		
GeneID.84529	C15orf41	15	36,871,812	37,102,449	230,637	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1965, 2_A375_pNL97_plus_lncRNA_AR..1.2774	-372, -306	upstream, upstream	1	1	0	16	25	6	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene C15orf41	C15orf41, MGC11326, FLJ22851, HH114	chromosome 15 open reading frame 41	NM_032499, NM_001130010, hCT1825490.2, hCT2279691.0, hCT2357566.0	224486_s_at, 232506_s_at, 232507_at	NP_115888.1, NP_001123482.1, EAW92336.1, EAW92337.1, EAW92338.1
GeneID.161742	SPRED1	15	38,545,052	38,649,450	104,398	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1967, 2_A375_pNL97_plus_lncRNA_AR..1.2776, 4_A375_EGR1..1.2474	-604, -780, -412	upstream, upstream, upstream	1	1	1	15	16	16	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SPRED1	SPRED1, FLJ33903, NFLS	sprouty-related, EVH1 domain containing 1	NM_152594, hCT28837.3	226837_at, 235074_at, 244439_at	NP_689807.1, EAW92368.1
GeneID.283742	FAM98B	15	38,746,326	38,777,063	30,735	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1968, 2_A375_pNL97_plus_lncRNA_AR..1.2777, 4_A375_EGR1..1.2475	72, 40, 24	in gene, in gene, in gene	1	1	1	29	31	18	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene FAM98B	FAM98B, FLJ38426	family with sequence similarity 98, member B	NM_173611, NM_001042429, hCT2349414.0, hCT2349415.0, hCT29547.4	1553825_at, 1564637_a_at, 225068_at	NP_775882.2, NP_001035894.1, EAW92369.1, EAW92370.1, EAW92371.1
GeneID.7057	THBS1	15	39,873,280	39,889,668	16,388	+	5	1_A375_pNL7_minus_lncRNA_AR..1..1972, 2_A375_pNL97_plus_lncRNA_AR..1.2785, 2_A375_pNL97_plus_lncRNA_AR..1.2786, 4_A375_EGR1..1.2476, 4_A375_EGR1..1.2477	2976, 0, 2976, 48, 1392	in gene, in gene, in gene, in gene, in gene	1	1	1	18.33	19.33	17	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene THBS1	TSP, THBS, THBS1, TSP-1, TSP1, THBS-1	thrombospondin 1	NM_003246, hCT1826182.4, hCT1972728.2, hCT2279831.1	201107_s_at, 201108_s_at, 201109_s_at, 201110_s_at, 215775_at, 235086_at, 239336_at	NP_003237.2, EAW92379.1, EAW92380.1, EAW92381.1
GeneID.161835	FSIP1	15	39,892,232	40,075,039	182,807	-	5	1_A375_pNL7_minus_lncRNA_AR..1..1973, 2_A375_pNL97_plus_lncRNA_AR..1.2787, 2_A375_pNL97_plus_lncRNA_AR..1.2788, 4_A375_EGR1..1.2478, 4_A375_EGR1..1.2479	5119, 5119, 74, 136927, -1	in gene, in gene, in gene, in gene, upstream	1	1	1	12.33	15	14.67	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene FSIP1	FSIP1, HSD10, FLJ35989	fibrous sheath interacting protein 1	NM_152597, hCT2351064.0, hCT2357546.0, hCT29942.4	1553822_a_at	NP_689810.3, EAW92382.1, EAW92383.1, EAW92384.1
GeneID.11245	GPR176	15	40,092,931	40,213,093	120,162	-	1	2_A375_pNL97_plus_lncRNA_AR..1.2789	485	in gene	0	1	0	14	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene GPR176	GPR176, GPR, Gm1012	G protein-coupled receptor 176	NM_007223, hCT2279967.0, hCT28636.2	206673_at, 227846_at	NP_009154.1, EAW92385.1, EAW92386.1
GeneID.100505534	LOC100505534	15	40,213,211	40,217,100	3,889	+	1	2_A375_pNL97_plus_lncRNA_AR..1.2789	-603	upstream	0	1	0	14	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100505534		hypothetical LOC100505534	XR_109178, XR_114839		
GeneID.440275	EIF2AK4	15	40,226,347	40,327,797	101,450	+	2	2_A375_pNL97_plus_lncRNA_AR..1.2790, 2_A375_pNL97_plus_lncRNA_AR..1.2791	42581, 105141	in gene, downstream	0	1	0	15	16	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene EIF2AK4	KIAA1338, GCN2, EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	NM_001013703, hCT29941.4	225164_s_at, 237145_at	NP_001013725.2, EAW92388.1
GeneID.6727	SRP14	15	40,327,891	40,331,389	3,498	-	1	2_A375_pNL97_plus_lncRNA_AR..1.2791	-99	upstream	0	1	0	17	17	10	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene SRP14	MGC14326, ALURBP, SRP14	signal recognition particle 14kDa (homologous Alu RNA binding protein)	NM_003134, hCT2281965.0, hCT2281966.0	200007_at	NP_003125.3, EAW92390.1, EAW92391.1
GeneID.100131089	LOC100131089	15	40,331,512	40,359,491	27,979	+	1	2_A375_pNL97_plus_lncRNA_AR..1.2791	-24	upstream	0	1	0	17	17	10	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC100131089		hypothetical LOC100131089	XR_111499, XR_109179, XR_114840		
GeneID.90427	BMF	15	40,380,091	40,401,075	20,984	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1974, 2_A375_pNL97_plus_lncRNA_AR..1.2792, 2_A375_pNL97_plus_lncRNA_AR..1.2793	-141, 9907, -141	upstream, in gene, upstream	1	1	0	29	24.5	6	2	1_A375_pNL7_minus_lncRNA_AR..1	38	Gene BMF	FLJ00065, BMF	Bcl2 modifying factor	NM_001003940, NM_033503, NM_001003942, NM_001003943, hCT29940.3	226530_at	NP_001003940.1, NP_277038.1, NP_001003942.1, NP_001003943.1, EAW92393.1
GeneID.701	BUB1B	15	40,453,210	40,513,337	60,127	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1975, 2_A375_pNL97_plus_lncRNA_AR..1.2794	102, 70	in gene, in gene	1	1	0	34	42	12	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene BUB1B	BUB1beta, BUB1B, Bub1A, BUBR1, SSK1, MAD3L, hBUBR1	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	NM_001211, hCT30203.2	203755_at	NP_001202.4, EAW92394.1
GeneID.56924	PAK6	15	40,509,629	40,569,688	60,059	+	2	2_A375_pNL97_plus_lncRNA_AR..1.2795, 4_A375_EGR1..1.2480	65027, 49123	downstream, in gene	0	1	1	9.5	16	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PAK6	PAK5, PAK6	p21 protein (Cdc42/Rac)-activated kinase 6	NM_020168, NM_001128628, NM_001128629, hCT2281190.0, hCT2281192.0, hCT2281193.0, hCT2281194.0, hCT2281195.0, hCT2357550.0, hCT30204.2	1555310_a_at, 219461_at	NP_064553.1, NP_001122100.1, NP_001122101.1, EAW92398.1, EAW92399.1, EAW92400.1, EAW92395.1, EAW92397.1, EAW92398.1, EAW92401.1
GeneID.100131244	LOC100131244	15	40,573,645	40,574,787	1,142	-	1	2_A375_pNL97_plus_lncRNA_AR..1.2795	131	in gene	0	1	0	9	21	6	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100131244		hypothetical protein LOC100131244	NM_001190479		NP_001177408.1
GeneID.5330	PLCB2	15	40,580,098	40,600,174	20,076	-	1	2_A375_pNL97_plus_lncRNA_AR..1.2795	25518	downstream	0	1	0	9	21	6	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PLCB2	FLJ38135, PLCB2	phospholipase C, beta 2	NM_004573, hCT2281960.1, hCT2281962.1	204046_at, 210388_at	NP_004564.2, EAW92403.1, EAW92402.1
GeneID.100505573	LOC100505573	15	40,617,183	40,618,916	1,733	+	3	1_A375_pNL7_minus_lncRNA_AR..1..1976, 2_A375_pNL97_plus_lncRNA_AR..1.2796, 4_A375_EGR1..1.2481	-1503, -1503, 10433	upstream, upstream, downstream	1	1	1	56.5	66	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	126	Gene LOC100505573		hypothetical LOC100505573	XR_111498, XR_109180, XR_114841		
GeneID.388115	C15orf52	15	40,623,653	40,633,168	9,515	-	4	1_A375_pNL7_minus_lncRNA_AR..1..1976, 2_A375_pNL97_plus_lncRNA_AR..1.2796, 4_A375_EGR1..1.2481, 4_A375_EGR1..1.2482	17466, 17466, 5552, 3248	downstream, downstream, in gene, in gene	1	1	1	42.67	47.33	15.67	3	2_A375_pNL97_plus_lncRNA_AR..1	126	Gene C15orf52	C15orf52, DKFZp686N1466, FLJ43339	chromosome 15 open reading frame 52	NM_207380, hCT1825772.2, hCT2281958.1	227272_at	NP_997263.2, EAW92405.1, EAW92404.1
GeneID.85455	DISP2	15	40,650,434	40,663,256	12,822	+	3	4_A375_EGR1..1.2483, 4_A375_EGR1..1.2484, 4_A375_EGR1..1.2485	9139, 10494, 11070	in gene, in gene, in gene	0	0	1	6.33	6	16.67	3	4_A375_EGR1..1	17	Gene DISP2	HsT16908, DKFZp547N223, DISP2, DISPB, KIAA1742	dispatched homolog 2 (Drosophila)	NM_033510, hCT1647526.4, hCT2343633.0	229579_s_at	NP_277045.1, EAW92407.1, EAW92406.1
GeneID.22893	BAHD1	15	40,733,411	40,760,441	27,030	+	2	4_A375_EGR1..1.2486, 4_A375_EGR1..1.2487	-1187, 18365	upstream, in gene	0	0	1	8.5	8.5	18	2	4_A375_EGR1..1	18	Gene BAHD1	BAHD1, KIAA0945	bromo adjacent homology domain containing 1	NM_014952, hCT2281208.0, hCT2357534.0, hCT30199.2	203051_at	NP_055767.3, EAW92417.1, EAW92416.1, EAW92418.1
GeneID.90416	C15orf57	15	40,845,298	40,857,252	11,954	-	1	4_A375_EGR1..1.2488	-4450	upstream	0	0	1	18	19	19	1	4_A375_EGR1..1	19	Gene C15orf57	FLJ25915, C15orf57, CCDC32, MGC20481	chromosome 15 open reading frame 57	NM_052849, NM_001080792, NM_001080791, hCT2281949.1, hCT2281951.1, hCT2340341.0, hCT2340342.0, hCT2340343.0, hCT2340344.0, hCT2340345.0, hCT2340346.0	1556848_at, 1560814_a_at, 225397_at	NP_443081.1, NP_001074261.1, NP_001074260.1, EAW92422.1, EAW92426.1, EAW92427.1, EAW92420.1, EAW92421.1, EAW92423.1, EAW92424.1, EAW92425.1
GeneID.27079	RPUSD2	15	40,861,537	40,866,661	5,124	+	1	4_A375_EGR1..1.2488	165	in gene	0	0	1	18	19	19	1	4_A375_EGR1..1	19	Gene RPUSD2	FLJ31409, C18B11, RPUSD2, C15orf19	RNA pseudouridylate synthase domain containing 2	NM_152260, hCT30208.2	221940_at	NP_689473.1, EAW92428.1
GeneID.57082	CASC5	15	40,886,447	40,954,881	68,434	+	2	2_A375_pNL97_plus_lncRNA_AR..1.2797, 4_A375_EGR1..1.2489	-335, -367	upstream, upstream	0	1	1	19	21	21	1	4_A375_EGR1..1	21	Gene CASC5	hSpc105, AF15Q14, CT29, hKNL-1, D40, KNL1, KIAA1570, CASC5	cancer susceptibility candidate 5	NM_144508, NM_170589, hCT2281210.0, hCT2281211.0	1552680_a_at, 1552682_a_at, 220247_at, 228323_at	NP_653091.2, NP_733468.2, EAW92429.1, EAW92430.1
GeneID.55177	FAM82A2	15	41,028,086	41,047,458	19,372	-	2	2_A375_pNL97_plus_lncRNA_AR..1.2798, 4_A375_EGR1..1.2490	98, -8942	in gene, upstream	0	1	1	14	17	18	2	4_A375_EGR1..1	20	Gene FAM82A2	FAM82A2, RMD3, FLJ10579, ptpip51, FAM82C, hRMD-3	family with sequence similarity 82, member A2	NM_018145, hCT2281945.0, hCT2281946.0, hCT2357563.0, hCT2357564.0, hCT2357565.0, hCT30215.2	218126_at	NP_060615.1, EAW92441.1, EAW92437.1, EAW92438.1, EAW92439.1, EAW92440.1, EAW92436.1
GeneID.2644	GCHFR	15	41,056,285	41,059,911	3,626	+	2	2_A375_pNL97_plus_lncRNA_AR..1.2798, 4_A375_EGR1..1.2490	-8925, 115	upstream, in gene	0	1	1	14	17	18	2	4_A375_EGR1..1	20	Gene GCHFR	MGC138467, HsT16933, GCHFR, MGC138469, GFRP, P35	GTP cyclohydrolase I feedback regulator	NM_005258, hCT1957207.1, hCT30213.2	204867_at	NP_005249.1, EAW92442.1, EAW92443.1
GeneID.55192	DNAJC17	15	41,060,067	41,099,676	39,609	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1977, 2_A375_pNL97_plus_lncRNA_AR..1.2799, 4_A375_EGR1..1.2490	-36, -100, 43276	upstream, upstream, downstream	1	1	1	19	19.5	16	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene DNAJC17	DNAJC17, FLJ10634	DnaJ (Hsp40) homolog, subfamily C, member 17	NM_018163, hCT2357538.0, hCT30216.2	219861_at	NP_060633.1, EAW92444.1, EAW92445.1
GeneID.643338	C15orf62	15	41,062,159	41,064,647	2,488	+	1	4_A375_EGR1..1.2490	-5759	upstream	0	0	1	17	19	20	1	4_A375_EGR1..1	20	Gene C15orf62	C15orf62		NM_001130448	1569064_at, 1569065_s_at	NP_001123920.1
GeneID.84936	ZFYVE19	15	41,099,274	41,106,767	7,493	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1977, 2_A375_pNL97_plus_lncRNA_AR..1.2799	438, 502	in gene, in gene	1	1	0	21	20	12	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ZFYVE19	MPFYVE, FLJ14840, ZFYVE19	zinc finger, FYVE domain containing 19	NM_001077268, hCT2281220.0, hCT2349423.0, hCT2349424.0, hCT2349425.0, hCT2349426.0, hCT2349427.0, hCT2349428.0, hCT2357561.0, hCT30214.3	225643_at	NP_001070736.1, EAW92454.1, EAW92447.1, EAW92448.1, EAW92449.1, EAW92451.1, EAW92450.1, EAW92452.1, EAW92453.1, EAW92455.1
GeneID.54866	PPP1R14D	15	41,107,643	41,120,907	13,264	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1977, 2_A375_pNL97_plus_lncRNA_AR..1.2799	21195, 21131	downstream, downstream	1	1	0	21	20	12	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene PPP1R14D	FLJ20251, PPP1R14D, GBPI1, CPI17-like, MGC119014, MGC119016, GBPI-1	protein phosphatase 1, regulatory (inhibitor) subunit 14D	NM_017726, NM_001130143, hCT30210.2	220082_at	NP_060196.1, NP_001123615.1, EAW92456.1
GeneID.57617	VPS18	15	41,186,628	41,196,173	9,545	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1978, 4_A375_EGR1..1.2491, 4_A375_EGR1..1.2492, 4_A375_EGR1..1.2493	44, -148, 12300, 12844	in gene, upstream, downstream, downstream	1	0	1	12.33	11	17.67	3	4_A375_EGR1..1	20	Gene VPS18	KIAA1475, PEP3, VPS18	vacuolar protein sorting 18 homolog (S. cerevisiae)	NM_020857, hCT2281224.0, hCT2281225.0, hCT2281226.0, hCT2357560.0, hCT30205.2	1552276_a_at, 223346_at	NP_065908.1, EAW92461.1, EAW92462.1, EAW92463.1, EAW92464.1, EAW92465.1
GeneID.100505662	LOC100505662	15	41,199,009	41,201,765	2,756	+	2	4_A375_EGR1..1.2492, 4_A375_EGR1..1.2493	-81, 463	upstream, in gene	0	0	1	10	10.5	18	2	4_A375_EGR1..1	20	Gene LOC100505662		hypothetical LOC100505662	XR_109184		
GeneID.54567	DLL4	15	41,221,531	41,231,258	9,727	+	1	4_A375_EGR1..1.2494	69	in gene	0	0	1	11	10	18	1	4_A375_EGR1..1	18	Gene DLL4	DLL4, hdelta2, MGC126344	delta-like 4 (Drosophila)	NM_019074, hCT30211.3	223525_at	NP_061947.1, EAW92466.1
GeneID.54617	INO80	15	41,271,078	41,408,340	137,262	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1979, 2_A375_pNL97_plus_lncRNA_AR..1.2800	-268, -236	upstream, upstream	1	1	0	77	104	10	1	2_A375_pNL97_plus_lncRNA_AR..1	104	Gene INO80	hINO80, INOC1, INO80A, INO80	INO80 homolog (S. cerevisiae)	NM_017553, hCT2281712.0, hCT2281717.0, hCT2357533.0, hCT30206.3	225357_s_at, 229358_x_at	NP_060023.1, EAW92468.1, EAW92469.1, EAW92470.1, EAW92471.1
GeneID.161829	EXD1	15	41,474,926	41,522,895	47,969	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1980, 2_A375_pNL97_plus_lncRNA_AR..1.2801	-305, -273	upstream, upstream	1	1	0	47	55	13	1	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene EXD1	EXD1, MGC33637, EXDL1	exonuclease 3'-5' domain containing 1	NM_152596, hCT1971918.2	1553907_a_at	NP_689809.2, EAW92473.1
GeneID.11261	CHP	15	41,523,437	41,574,085	50,648	+	4	1_A375_pNL7_minus_lncRNA_AR..1..1980, 2_A375_pNL97_plus_lncRNA_AR..1.2801, 2_A375_pNL97_plus_lncRNA_AR..1.2802, 4_A375_EGR1..1.2495	-237, -269, 52755, 52755	upstream, upstream, downstream, downstream	1	1	1	32.5	36	15	2	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene CHP	SLC9A1BP	calcium binding protein P22	NM_007236, hCT2281014.0, hCT2281015.0, hCT2281016.0, hCT2281017.0	207993_s_at, 214665_s_at	NP_009167.1, EAW92474.1, EAW92475.1, EAW92476.1, EAW92477.1
GeneID.729082	LOC729082	15	41,576,201	41,591,795	15,594	+	2	2_A375_pNL97_plus_lncRNA_AR..1.2802, 4_A375_EGR1..1.2495	-9, -9	upstream, upstream	0	1	1	18	17	17	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC729082		hypothetical LOC729082	NR_026757		
GeneID.11339	OIP5	15	41,601,466	41,624,819	23,353	-	2	1_A375_pNL7_minus_lncRNA_AR..1..1981, 2_A375_pNL97_plus_lncRNA_AR..1.2803	243, 259	in gene, in gene	1	1	0	22	21	14	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene OIP5	MIS18B, CT86, hMIS18beta, LINT25, OIP5, MIS18beta, 5730547N13Rik	Opa interacting protein 5	NM_007280, hCT1642461.1, hCT2281708.0	213599_at	NP_009211.1, EAW92481.1, EAW92480.1
GeneID.51203	NUSAP1	15	41,624,926	41,673,248	48,322	+	2	1_A375_pNL7_minus_lncRNA_AR..1..1981, 2_A375_pNL97_plus_lncRNA_AR..1.2803	-350, -386	upstream, upstream	1	1	0	22	21	14	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene NUSAP1	PRO0310p1, LNP, Q0310, FLJ13421, ANKT, SAPL, BM037, NUSAP1, NUSAP	nucleolar and spindle associated protein 1	NM_016454, NM_016359, NM_001129897, hCT2281019.0, hCT2281021.0, hCT2357530.0, hCT2357531.0, hCT30538.3	218039_at, 219978_s_at	NP_060924.4, NP_057443.2, NP_001123369.1, EAW92482.1, EAW92484.1, EAW92485.1, EAW92483.1, EAW92486.1
GeneID.51103	NDUFAF1	15	41,679,551	41,694,642	15,091	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1982, 2_A375_pNL97_plus_lncRNA_AR..1.2804, 4_A375_EGR1..1.2496	-30, 50, 50	upstream, in gene, in gene	1	1	1	18	19	21	1	4_A375_EGR1..1	21	Gene NDUFAF1	CGI65, CIA30, NDUFAF1, CGI-65	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	NM_016013, hCT1825835.2, hCT2281704.0, hCT2281705.0	204125_at	NP_057097.2, EAW92487.1, EAW92488.1, EAW92489.1
GeneID.23168	RTF1	15	41,709,302	41,775,761	66,459	+	1	4_A375_EGR1..1.2497	410	in gene	0	0	1	14	12	19	1	4_A375_EGR1..1	19	Gene RTF1	KIAA0252, RTF1, CDG1N, GTL7	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	NM_015138, hCT2281023.0, hCT2357527.0, hCT30543.3	212301_at, 212302_at, 230832_at	NP_055953.3, EAW92491.1, EAW92490.1, EAW92492.1
GeneID.3706	ITPKA	15	41,786,122	41,795,747	9,625	+	1	4_A375_EGR1..1.2498	9238	in gene	0	0	1	5	9	18	1	4_A375_EGR1..1	18	Gene ITPKA	IP3KA, ITPKA, IP3-3KA	inositol 1,4,5-trisphosphate 3-kinase A	NM_002220, hCT30539.2	205874_at	NP_002211.1, EAW92493.1
GeneID.4058	LTK	15	41,795,840	41,806,085	10,245	-	1	4_A375_EGR1..1.2498	10725	downstream	0	0	1	5	9	18	1	4_A375_EGR1..1	18	Gene LTK	TYK1, LTK	leukocyte receptor tyrosine kinase	NM_206961, NM_002344, NM_001135685, hCT1957920.1, hCT2281697.0, hCT2281698.0, hCT2281701.0, hCT2281702.0, hCT2281703.0, hCT2357523.0, hCT30541.3	207106_s_at, 217184_s_at	NP_996844.1, NP_002335.2, NP_001129157.1, EAW92494.1, EAW92499.1, EAW92501.1, EAW92495.1, EAW92496.1, EAW92497.1, EAW92498.1, EAW92500.1
GeneID.26015	RPAP1	15	41,809,374	41,836,464	27,090	-	1	4_A375_EGR1..1.2499	60	in gene	0	0	1	16	16	23	1	4_A375_EGR1..1	23	Gene RPAP1	RPAP1, DKFZp727M111, KIAA1403, FLJ12732, MGC858	RNA polymerase II associated protein 1	NM_015540, hCT2281693.0, hCT2281694.0, hCT2281696.0, hCT30542.1	218441_s_at	NP_056355.2, EAW92505.1, EAW92502.1, EAW92503.1, EAW92504.1
GeneID.7301	TYRO3	15	41,851,220	41,871,536	20,316	+	1	2_A375_pNL97_plus_lncRNA_AR..1.2805	26346	downstream	0	1	0	8	17	8	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TYRO3	FLJ16467, Dtk, BYK, TYRO3, RSE, Sky, Tif, Brt	TYRO3 protein tyrosine kinase	NM_006293, hCT2281030.0, hCT2281032.0, hCT28884.3	211431_s_at, 211432_s_at	NP_006284.2, EAW92507.1, EAW92506.1, EAW92508.1
GeneID.8681	JMJD7-PLA2G4B	15	42,120,283	42,140,346	20,063	+	1	4_A375_EGR1..1.2500	29280	downstream	0	0	1	4	6	15	1	4_A375_EGR1..1	15	Gene JMJD7-PLA2G4B	PLA2G4B, HsT16992, cPLA2-beta, JMJD7-PLA2G4B	JMJD7-PLA2G4B readthrough	NM_005090, NR_015346, hCT2281042.0, hCT2281043.0, hCT28960.2	219095_at, 222256_s_at, 60528_at	NP_005081.1, EAW92522.1, EAW92520.1, EAW92521.1
GeneID.100137049	PLA2G4B	15	42,131,011	42,140,346	9,335	+	1	4_A375_EGR1..1.2500	18552	downstream	0	0	1	4	6	15	1	4_A375_EGR1..1	15	Gene PLA2G4B	FLJ53173, FLJ17693, DKFZp686N12131, PLA2G4B, FLJ42498, HsT16992, cPLA2-beta	phospholipase A2, group IVB (cytosolic)	NM_001114633		NP_001108105.1
GeneID.51332	SPTBN5	15	42,140,344	42,186,275	45,931	-	3	1_A375_pNL7_minus_lncRNA_AR..1..1983, 4_A375_EGR1..1.2500, 4_A375_EGR1..1.2501	-797, 36712, 15635	upstream, in gene, in gene	1	0	1	8	6.67	15.33	3	4_A375_EGR1..1	18	Gene SPTBN5	HUSPECV, BSPECV, SPTBN5, HUBSPECV	spectrin, beta, non-erythrocytic 5	NM_016642, hCT29402.3	220087_at, 237097_at	NP_057726.3, EAW92523.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Start	Interval Pos	n7_A375_DMSO_lncRNA_AR_1 Percent	n8_A375_DMSO_lncRNA_AR_1 Percent	n9_A375_DMSO_lncRNA_AR_1 Percent	n7_A375_plus_lncRNA_AR_1 Avg Peak	n8_A375_plus_lncRNA_AR_1 Avg Peak	n9_A375_plus_lncRNA_AR_1 Avg Peak	Add Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:10 04943113	MIR431 0	19	42,195,695	42,195,749	55	-	1	4_A375_EGR1.1.2900	9155	downstream	0	0	1	4	8	15	1	4_A375_EGR1.1.1	15	Gene MIR4310	MIR4310	microRNA 4310	NR_036195		
GeneID:10 52939360	LOC1002 29093	19	42,196,325	42,197,930	1,606	+	1	1_A375_shN7_mrna1_lncRNA_AR_1.1903	747	in gene	1	0	0	15	11	13	1	1_A375_shN7_mrna1_lncRNA_AR_1.1	15	Gene LOC100293060		hypothetical protein LOC100293060	XM_00234339		XP_00234339.2
GeneID:10 6644	EHD4	19	42,191,606	42,264,755	73,117	-	1	1_A375_shN7_mrna1_lncRNA_AR_1.1903	77803	downstream	1	0	0	15	11	13	1	1_A375_shN7_mrna1_lncRNA_AR_1	15	Gene EHD4	PAST4, EHD4	EH-domain containing 4	NM_139265, NC_000019.10, NC_018922.2	1536607_at, 1536608_s_at, 209326_s_at, 213993_at	NP_644670.1, ENSP00325.1, ENSP00326.1
GeneID:10 3740	PLA2G4D	19	42,259,661	42,266,752	29,671	-	5	1_A375_shN7_mrna1_lncRNA_AR_1.1904, 2_A375_shN7_dlur1_lncRNA_AR_1.2006, 3_A375_EGR1.1.2503, 4_A375_EGR1.1.2556, 5_A375_EGR1.1.2595	28926, 28998, 29305, 1152, 32	downstream, downstream, downstream, in gene, in gene, in gene	1	1	1	13.75	14.25	16	4	2_A375_shN7_dlur1_lncRNA_AR_1	15	Gene PLA2G4D	PLA2G4D, cPLA2delta	phospholipase A2, group IVD (cytosolic)	NM_178034, NC_000007.12, NC_018654.77.1	1554914_at	NP_620540.3, ENSP00329.1, ENSP00330.1
GeneID:10 983	TMEM87 A	19	42,302,728	42,365,753	63,029	-	2	1_A375_shN7_mrna1_lncRNA_AR_1.1903, 2_A375_shN7_dlur1_lncRNA_AR_1.2007	-53, 158	upstream,in gene	1	1	0	17	16	13	1	1_A375_shN7_mrna1_lncRNA_AR_1	17	Gene TMEM87A	DKFZp686H22022, TMEM87A	transmembrane protein 87A	NM_018477, NM_001115003, NC_018922.2, NC_000019.10, NC_018922.2	212202_s_at, 212204_at, 223771_at, 223772_s_at	NP_060127.2, NP_001102073.1, ENSP00340.1, ENSP00342.1, ENSP00342.2
GeneID:10 95	GANC	19	42,366,266	42,845,994	79,496	+	2	1_A375_shN7_mrna1_lncRNA_AR_1.1905, 2_A375_shN7_dlur1_lncRNA_AR_1.2007	-526, -766	upstream,upstream	1	1	0	17	16	13	1	1_A375_shN7_mrna1_lncRNA_AR_1	17	Gene GANC	GANC, MGC150295, FLJ40002	glucosidase, alpha, neutral C	NM_176141	233340_at, 239077_at	NP_927764.2
GeneID:10 73	SNAP23	15	42,767,655	42,825,298	57,421	+	1	2_A375_shN7_dlur1_lncRNA_AR_1.2030	-4439	upstream	0	0	1	11	13	13	1	2_A375_shN7_dlur1_lncRNA_AR_1	13	Gene SNAP23	SNAP23B, SNAP23, HST17018, SNAP23A	synaptosomal-associated protein, 23kDa	NM_003825, NM_130795, NC_018927.2, NC_000015.9, NC_018927.2	209120_at, 209121_s_at, 214344_s_at	NP_003816.2, NP_570716.1, ENSP00358.1, ENSP00357.1, ENSP00359.1
GeneID:10 9232	LRRC37	19	42,834,720	42,841,802	8,282	-	2	1_A375_shN7_mrna1_lncRNA_AR_1.1908, 2_A375_shN7_dlur1_lncRNA_AR_1.2036	74, 156	in gene,in gene	1	0	1	16	15	25	1	1_A375_shN7_mrna1_lncRNA_AR_1	25	Gene LRRC37	DKFZp686H15053, LRRC37, FLJ35512	leucine rich repeat containing 37	NM_152260, NC_018927.2, NC_000019.10, NC_018927.2	1554292_at, 1554294_s_at, 1557073_s_at, 213122_at, 231810_at, 243091_at	NP_689473.1, ENSP00365.1, ENSP00364.1, ENSP00366.1, ENSP00361.1
GeneID:10 142	HAUS2	19	42,841,011	42,882,192	41,181	+	3	1_A375_shN7_mrna1_lncRNA_AR_1.1908, 2_A375_EGR1.1.2598, 3_A375_EGR1.1.2597	-83, -147, 38569	upstream, upstream, downstream	1	1	1	12.3	12	20	2	2_A375_shN7_dlur1_lncRNA_AR_1.1	25	Gene HAUS2	HAUS2, dkfzp434j0213, FLJ10460, CEP27, HST17025	HAUS augmin-like complex, subunit 2	NM_018097, NM_001139447, NC_018927.2, NC_000019.10, NC_018927.2	220071_x_at, 221951_s_at, 223020_at	NP_060667.1, NP_001129119.1, ENSP00366.1, ENSP00367.1, ENSP00372.1, ENSP00368.1, ENSP00370.1, ENSP00371.1
GeneID:10 519	STARD9	15	42,957,357	43,013,196	143,239	+	1	1_A375_EGR1.1.2927	-257	upstream	0	0	1	7	9	15	1	1_A375_EGR1.1.1	15	Gene STARD9	KIAA1000, FLJ16105, DKFZp686P0243, STARD9, FLJ21936, DKFZp686P0191, DKFZp781J089	START-related lipid transfer (START) domain containing 9	NM_020759	227168_at	NP_065810.2
GeneID:10 9537	TTBK2	15	43,036,936	43,210,007	173,471	-	2	2_A375_shN7_dlur1_lncRNA_AR_1.2009, 3_A375_EGR1.1.2598	-697, 161487	upstream,in gene	0	1	1	10.5	10.5	14	2	2_A375_shN7_dlur1_lncRNA_AR_1	17	Gene TTBK2	KIAA0847, TTBK2, SCA11, TTBK	tau tubulin kinase 2	NM_173500, NC_018927.2, NC_000015.9, NC_018927.2	1554293_at, 1554294_s_at, 1554295_x_at, 1557073_s_at, 213122_at, 231810_at, 243091_at	NP_775711.3, ENSP00351.1, ENSP00353.1
GeneID:10 221	TMEM82	15	43,425,722	43,477,342	51,620	+	2	1_A375_shN7_mrna1_lncRNA_AR_1.1907, 2_A375_shN7_dlur1_lncRNA_AR_1.2010	422, -5	in gene, upstream	1	1	0	17	16	10	1	2_A375_shN7_dlur1_lncRNA_AR_1	16	Gene TMEM82	TMEM82, FLJ23379	transmembrane protein 82	NM_024958, NC_000019.10, NC_018927.2	218776_s_at, 222739_at	NP_079232.2, ENSP00368.1, ENSP00367.1
GeneID:10 53	TGM5	15	43,524,790	43,559,055	34,266	-	1	1_A375_shN7_mrna1_lncRNA_AR_1.1908	18891	in gene	1	0	0	17	13	4	1	1_A375_shN7_dlur1_lncRNA_AR_1	17	Gene TGM5	TGM, TGASE3, MGC141907, TGM5, TGASE5, TGM5, TGM6	transglutaminase 5	NM_201631, NM_004245, NC_018927.2, NC_000019.10, NC_018927.2, NC_000019.10	207911_s_at	NP_958823.2, NP_004238.1, ENSP00361.1, ENSP00364.1, ENSP00365.1, ENSP00366.1
GeneID:10 96	LCAT12	15	43,819,974	43,822,891	2,917	-	2	2_A375_shN7_dlur1_lncRNA_AR_1.2011, 4_A375_EGR1.1.2508	287, 287	in gene,in gene	0	1	1	15	17	16	1	2_A375_shN7_dlur1_lncRNA_AR_1	17	Gene LCAT12	MGC29534, FLJ35231, TYKI, KIAA0347, LCAT12, FPM2	lecithin cholesterol methyltransferase 2	NM_014793	204012_s_at, 204013_s_at	NP_055608.2
GeneID:10 1625	ADAL	15	43,822,872	43,846,098	23,224	+	2	2_A375_shN7_dlur1_lncRNA_AR_1.2011, 4_A375_EGR1.1.2508	-248, -368	upstream, upstream	0	1	1	15	17	16	1	2_A375_shN7_dlur1_lncRNA_AR_1	17	Gene ADAL	FLJ44870, DKFZp781B2102, ADAL	adenosine deaminase-like	NM_031312999, NM_001139200, NC_018927.2, NC_000019.10, NC_018927.2	235424_at, 239711_at	NP_001129727.1, NP_001127523.1, ENSP00345.1, ENSP00399.1
GeneID:10 6030	ZSCAN29	15	43,850,370	43,862,350	11,980	-	3	1_A375_shN7_mrna1_lncRNA_AR_1.1909, 2_A375_shN7_dlur1_lncRNA_AR_1.2012, 3_A375_EGR1.1.2510	-1134, -990, -1006	upstream, upstream, upstream	1	1	1	20	17	22	1	1_A375_EGR1.1.1	22	Gene ZSCAN29	ZNF690, ZSCAN29, MGC129995, MGC129994, ZNF90, FLJ20087	zinc finger and SCAN domain containing 29	NM_152435, NC_018927.2, NC_000019.10, NC_018927.2, NC_000019.9	236962_at	NP_689485.3, ENSP00360.1, ENSP00362.1
GeneID:10 229	TUBGCP4	15	43,865,513	43,890,356	24,843	+	5	1_A375_shN7_mrna1_lncRNA_AR_1.1909, 2_A375_shN7_dlur1_lncRNA_AR_1.2012, 4_A375_EGR1.1.2510	376, 458, -49	in gene, upstream, upstream	1	1	1	20	17	22	1	4_A375_EGR1.1.1	22	Gene TUBGCP4	WP-CCR4, TUBGCP4, FLJ10797	tubulin, gamma complex associated protein 4	NM_014444, NC_018927.2	211337_s_at, 212296_at	NP_036219.2, ENSP00353.1
GeneID:10 56	TPST2IP	15	43,899,412	43,902,707	103,296	+	3	1_A375_shN7_mrna1_lncRNA_AR_1.1910, 2_A375_shN7_dlur1_lncRNA_AR_1.2013, 3_A375_EGR1.1.2511	69439, -803, -297	in gene, upstream, upstream	1	1	1	12.5	13.5	10	2	4_A375_EGR1.1.1	17	Gene TPST2IP1	TPST2IP1, dj302l7.1, MGC130399, SSFP1, FLJ41424	Golgi phosphoprotein 3 (coat protein) binding protein 1	NM_030937, NM_001147979, NM_001141960, NC_018927.2, NC_000019.10	1569097_at, 1569098_s_at, 203369_at	NP_038845.1, NP_001139431.1, NP_001139432.1, ENSP00364.1, ENSP00363.1
GeneID:10 30	MAP1A	15	43,909,906	43,922,916	14,012	-	2	2_A375_shN7_dlur1_lncRNA_AR_1.2013, 4_A375_EGR1.1.2511	-9494, -9702	upstream, upstream	0	1	1	9	14	17	1	4_A375_EGR1.1.1	17	Gene MAP1A	MAP1A, KIAP1, FLJ70111, MTAP1A	microtubule-associated protein 1A	NM_002373, NC_018927.2, NC_000015.9, NC_018927.2	200181_at, 213364_s_at, 213391_at	NP_002364.3, ENSP00366.1, ENSP00367.1, ENSP00368.1
GeneID:10 23	PDIA3	15	44,035,906	44,064,904	28,214	+	1	2_A375_shN7_dlur1_lncRNA_AR_1.2014	598	in gene	0	1	0	8	14	8	1	2_A375_shN7_dlur1_lncRNA_AR_1	14	Gene PDIA3	ERp61, GRP58, ERp57, PSB, PDIA3, HST17083, ERBP, PI-PLC, ERp60, GRP58	protein disulfide isomerase family A, member 3	NM_005313, NC_018927.2, NC_000019.10, NC_018927.2, NC_000019.9	200972_at, 227053_at, 229403_at	NP_005304.3, ENSP00354.1, ENSP00355.1, ENSP00356.1, ENSP00357.1, ENSP00358.1
GeneID:10 38	MPAP1	19	44,096,783	44,116,951	20,218	-	1	2_A375_shN7_dlur1_lncRNA_AR_1.2015	151	in gene	0	1	0	17	16	10	1	2_A375_shN7_dlur1_lncRNA_AR_1	19	Gene MPAP1	MPAP1	myosin phosphatase Rho interacting protein	NM_030928, NC_018966.3	225408_at	NP_056917.2, ENSP00347.1
GeneID:10 966	WDR76	15	44,119,112	44,160,817	41,305	+	1	2_A375_shN7_dlur1_lncRNA_AR_1.2015	-2332	upstream	0	1	0	17	16	10	1	2_A375_shN7_dlur1_lncRNA_AR_1	19	Gene WDR76	WDR76, CDW14, FLJ12973	WD repeat domain 76	NM_024902, NM_001167941, NC_018927.2	223819_at	NP_079184.2, NP_001161412.1, ENSP00346.1
GeneID:10 976	FRMD8	15	44,163,720	44,487,429	321,698	-	8	1_A375_shN7_mrna1_lncRNA_AR_1.1911, 1_A375_shN7_mrna2_lncRNA_AR_1.1912, 1_A375_shN7_mrna3_lncRNA_AR_1.2016, 1_A375_shN7_mrna4_lncRNA_AR_1.2017, 1_A375_shN7_mrna5_lncRNA_AR_1.2018, 1_A375_shN7_mrna6_lncRNA_AR_1.2019	62263, -112, 268993, 281765, 62132, -183	in gene, upstream, in gene, in gene, upstream	1	1	0	17	10.75	3.75	4	1_A375_shN7_mrna1_lncRNA_AR_1	23	Gene FRMD8	MGC14199, FRMD8, FLJ41022	FERM domain containing 8	NM_032932, NC_018947.9, NC_018927.2, NC_000019.10, NC_018927.2, NC_000019.10, NC_018927.2, NC_000019.9	1569470_s_at	NP_116301.2, ENSP00338.1, ENSP00339.1, ENSP00341.1, ENSP00342.1, ENSP00343.1, ENSP00340.1, ENSP00342.2, ENSP00343.2
GeneID:10 498	CTDSPL2	15	44,719,579	44,819,430	99,851	+	6	1_A375_shN7_mrna1_lncRNA_AR_1.1913, 2_A375_shN7_mrna2_lncRNA_AR_1.1914, 3_A375_shN7_mrna3_lncRNA_AR_1.1915, 4_A375_shN7_mrna4_lncRNA_AR_1.2020, 5_A375_shN7_mrna5_lncRNA_AR_1.2021, 6_A375_EGR1.1.2512	62213, 109349, 108977, 62341, 108197, 109221	in gene, downstream, downstream, in gene, downstream, downstream	1	1	1	16	17.67	11.67	3	2_A375_shN7_dlur1_lncRNA_AR_1	21	Gene CTDSPL2	FLJ10323, HSPC129, CTDSPL2, HSPC056	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	NM_016396, NC_018966.3, NC_018927.2	1568106_s_at, 222270_at, 223271_s_at, 239133_at	NP_057493.2, ENSP00365.1, ENSP00366.1
GeneID:10 5212	LOC8435 12	19	44,826,783	44,829,121	2,418	-	5	1_A375_shN7_mrna1_lncRNA_AR_1.1916, 2_A375_shN7_mrna2_lncRNA_AR_1.1917, 3_A375_shN7_dlur1_lncRNA_AR_1.2021, 4_A375_shN7_dlur1_lncRNA_AR_1.2022, 5_A375_EGR1.1.2512	180, -335, 365, -719, 321	in gene, upstream, in gene, upstream, in gene	1	1	1	16	16	15	2	1_A375_shN7_mrna1_lncRNA_AR_1	20	Gene LOC8435 12		hypothetical LOC84312	BC 054170, NR_034171		
GeneID:10 89	EIF3J	15	44,829,266	44,835,001	29,735	+	5	2_A375_shN7_dlur1_lncRNA_AR_1.2021, 3_A375_shN7_mrna3_lncRNA_AR_1.1918, 4_A375_shN7_mrna4_lncRNA_AR_1.1919, 5_A375_shN7_dlur1_lncRNA_AR_1.2022, 6_A375_EGR1.1.2513	-338, 193, -332, 576, -466	upstream,in gene, upstream,in gene, upstream	0	1	1	16	16	15	2	2_A375_shN7_dlur1_lncRNA_AR_1	20	Gene EIF3J	MTF3-p35, EIF3J, MTF3-delta, EIF3S1	eukaryotic translation initiation factor 3, subunit J	NM_003756, NC_018912.2, NC_018927.2, NC_000019.10, NC_018927.2	200284_s_at, 200903_s_at	NP_003740.2, ENSP00286.1, ENSP00289.1, ENSP00287.1, ENSP00288.1, ENSP00287.2, ENSP00287.1
GeneID:10 203	SPG11	15	44,854,894	44,935,878	100,982	-	2	1_A375_shN7_dlur1_lncRNA_AR_1.2023, 2_A375_EGR1.1.2513	132, 64	in gene,in gene	0	1	1	16	23	16	1	2_A375_shN7_dlur1_lncRNA_AR_1	23	Gene SPG11	SPG11, DKFZp762B1512, FLJ25416, KIAA1840	spastic paraplegia 11 (autosomal recessive)	NM_025137, NM_001159227, NC_018927.2, NC_000019.10, NC_018927.2	1559727_at, 203512_at, 232403_at, 241920_x_at	NP_079413.3, NP_001139099.1, ENSP00372.1, ENSP00373.1
GeneID:10 7135	PATL2	19	44,937,800	44,949,656	11,856	-	2	1_A375_shN7_dlur1_lncRNA_AR_1.2023, 2_A375_EGR1.1.2513	13042, 13294	downstream, downstream	0	1	1	16	23	16	1	2_A375_shN7_dlur1_lncRNA_AR_1	23	Gene PATL2	PATL2, PATL2, MPATH-8	protein associated with topoisomerase II homolog 2 (yeast)	NM_001145312	230763_at	NP_001138834.1
GeneID:10 9845	B2M	15	45,003,665	45,010,357	6,672	+	5	1_A375_shN7_mrna1_lncRNA_AR_1.1998, 2_A375_shN7_dlur1_lncRNA_AR_1.2024, 4_A375_EGR1.1.2514	91, -5, -101	in gene, upstream, upstream	1	1	1	19	25	15	1	2_A375_shN7_dlur1_lncRNA_AR_1	25	Gene B2M	B2M		NM_004048, NC_018927.2, NC_000015.9, NC_018927.2	201891_s_at, 216251_s_at, 232011_at	NP_004039.1, ENSP00277.1, ENSP00278.1, ENSP00278.2
GeneID:10 9948	C15orf39	15	45,248,900	45,271,421	22,521	+	1	4_A375_EGR1.1.2515	28	in gene	0	0	1	3	9	10	1	4_A375_EGR1.1.1	10	Gene C15orf39	MGC33951, C15orf39	chromosome 15 open reading frame 39	NM_152445, NC_018935.2	224976_at	NP_689681.1, ENSP00281.1
GeneID:10 52	SORD	15	45,315,302	45,347,267	31,965	+	1	4_A375_EGR1.1.2516	154	in gene	0	0	1	10	16	16	1	4_A375_EGR1.1.1	16	Gene SORD	SORD1, SORD	sorbitol dehydrogenase	NM_003104, NR_034039, NC_018936.1, NC_000015.10	201983_at	NP_003093.2, ENSP00282.1, ENSP00284.1
GeneID:10 998	DUOX2	15	45,364,052	45,406,359	21,307	-	1	4_A375_EGR1.1.2517	-3931	upstream	0	0	1	8	8	15	1	4_A375_EGR1.1.1	15	Gene DUOX2	LNOX2, THOX2, TDH6, P138-TDH, DUOX2, TDH2	dual oxidase 2	NM_014080, NC_018947.9	219727_at	NP_054799.4, ENSP00272.1
GeneID:10 3733	DUOXA 2	15	45,406,825	45,410,304	3,791	+	1	4_A375_EGR1.1.2517	2857	in gene	0	0	1	8	8	15	1	4_A375_EGR1.1.1	15	Gene DUOXA2	bMRP/NOH36, DUOXA2, TDH5	dual oxidase maturation factor 2	NM_207581, NC_018924.9	230915_at	NP_997484.2, ENSP00281.1
GeneID:10 527	DUOXA 1	15	45,409,955	45,422,257	12,272	-	1	4_A375_EGR1.1.2517	12897	downstream	0	0	1	8	8	15	1	4_A375_EGR1.1.1	15	Gene DUOXA1	NIP, mol, NUMBP, DUOXA1, FLJ25334	dual oxidase maturation factor 1	NM_144565, NC_018911.8, NC_018911.7, NC_000015.9, NC_018911.8	1554843_s_at, 1554844_x_at	NP_653166.2, ENSP00272.1, ENSP00273.1, ENSP00273.2, ENSP00273.3, ENSP00273.4
GeneID:10 925	SHF	15	45,549,412	45,593,373	53,961	-	6	1_A375_shN7_mrna1_lncRNA_AR_1.1999, 2_A375_shN7_mrna2_lncRNA_AR_1.2000, 3_A375_shN7_dlur1_lncRNA_AR_1.2026, 4_A375_shN7_dlur1_lncRNA_AR_1.2027, 5_A375_EGR1.1.2516, 6_A375_EGR1.1.2519, 7_A375_EGR1.1.2520, 8_A375_EGR1.1.2521	2443, 701, 2493, 735, 21403, 3439, 797, -19	in gene, in gene, in gene, in gene, in gene, upstream	1	1	1	16.33	16	20	3	4_A375_EGR1.1.1	28	Gene SHF	SHF, MGC126860, MGC126862	Src homology 2 domain-containing transforming protein D	NM_138356, NC_018966.3, NC_018966.0, NC_018966.3, NC_000019.10	1559727_at, 203512_at, 232403_at, 241920_x_at	NP_619633.3, ENSP00330.1, ENSP00331.1, ENSP00332.1, ENSP00333.1, ENSP00334.1, ENSP00335.1, ENSP00336.1
GeneID:10 329	SPATA31	15	45,894,519	45,910,817	16,299	+	2	1_A375_shN7_dlur1_lncRNA_AR_1.2031, 2_A375_EGR1.1.2522	-109, 28155	upstream, downstream	0	0	1	17.5	14	17.5	2	2_A375_shN7_dlur1_lncRNA_AR_1	32	Gene SPATA31	FLJ12259, SPATA31, MGC5347	spermatogenesis associated family 31	NM_024093, NR_027635, NC_018947.9, NC_000019.9	219894_at, 219893_at, 222183_s_at	NP_076988.2, ENSP00310.1, ENSP00311.1
GeneID:10 619	C15orf48	15	45,722,785	45,725,947	3,163	+	1	4_A375_EGR1.1.2522	-109	upstream	0	0	1	10	9	16	1	4_A375_EGR1.1.1	16	Gene C15orf48	C15orf48, NMES1, FONF-11, FLJ20845, MGC22329	chromosome 15 open reading frame 48	NM_197955, NR_028412, NC_018947.9, NC_000019.10	225464_at	NP_932348.1, NP_115788.1, ENSP00312.1, ENSP00313.1
GeneID:10 6128011	MIR147 8	19	45,725,248	45,725,327	79	-	1	4_A375_EGR1.1.2522	-3624	upstream	0	0	1	10	9	16	1	4_A375_EGR1.1.1	16	Gene MIR147 8	MIR147B, MIRN147B	microRNA 147b	NR_036199		
GeneID:10 255	PLD5	19	45,879,417	45,901,909	22,492	+	2	2_A375_shN7_dlur1_lncRNA_AR_1.2032, 3_A375_shN7_dlur1_lncRNA_AR_1.2029	100, 190	in gene,in gene	1	1	0	26	26	15	1	2_A375_shN7_dlur1_lncRNA_AR_1	26	Gene PLD5	PA, PLD5, PHLUD	aldolase homolog (mouse)	NM_012395	222826_at, 224853_at, 224852_at	NP_036528.1
GeneID:10 9697	CTXN2	15	45,885,997	45,893,951	12,954	+	2	2_A375_shN7_dlur1_lncRNA_AR_1.2033, 3_A375_shN7_dlur1_lncRNA_AR_1.2030	-997, -999	upstream, upstream	1	1	0	32	35	8	1	2_A375_shN7_dlur1_lncRNA_AR_1	35	Gene CTXN2	CTXN2, DKFZp781K0440	cortexin 2	NM_031143666		NP_001139140.1
GeneID:10 56	DUT	15	45,825,621	45,835,970	11,349	+	4	1_A375_shN7_mrna1_lncRNA_AR_1.2034, 2_A375_shN7_mrna2_lncRNA_AR_1.2035, 3_A375_shN7_dlur1_lncRNA_AR_1.2031, 4_A375_EGR1.1.2526	-5, 783, 833, -37	upstream, in gene, in gene, upstream	1	1	1	17	30	16	1	2_A375_shN7_dlur1_lncRNA_AR_1	30	Gene DUT	FLJ20922, DUT, dUTPase	deoxyuridine triphosphatase	NM_001025245, NM_001948, NM_001025249, NC_018927.2, NC_000019.10, NC_018927.2	200953_at, 200958_s_at, 200952_s_at	NP_001020519.1, NP_001939.1, NP_001020525.1, ENSP00349.1, ENSP00349.2, ENSP00352.1, ENSP00352.2, ENSP00351.1
GeneID:10 00	FBN1	15	45,700,503	45,837,363	297,482	-	3	1_A375_shN7_mrna1_lncRNA_AR_1.2035, 2_A375_shN7_dlur1_lncRNA_AR_1.2032, 3_A375_shN7_dlur1_lncRNA_AR_1.2033	211669, 209841, 241	in gene, in gene, in gene	1	1	1	10.67	13.33	7.33	3	1_A375_shN7_mrna1_lncRNA_AR_1	15	Gene FBN1	FBN1, MFS2, FBN, MFS1, WMS, SGS1, FBN1, OCTD	fibrillin 1	NM_000138, NC_018939.9, NC_018927.2	202463_s_at, 202798_s_at, 233316_at	NP_000129.3, ENSP00354.1, ENSP00355.1, ENSP00356.1, ENSP00357.1, ENSP00358.1, ENSP00359.1, ENSP00360.1, ENSP00361.1, ENSP00362.1, ENSP00363.1
GeneID:10 5536159	LOC1003 09939	19	45,935,634	45,944,213	8,579	+	1	2_A375_shN7_dlur1_lncRNA_AR_1.2033	-1110	upstream	0	1	0	8	16	10	1	2_A375_shN7_dlur1_lncRNA_AR_1	16	Gene LOC1003 09939		hypothetical LOC100309939	XR_109197		
GeneID:10 995	CEP152	15	43,930,103	43,993,343	63,240	-	1	4_A375_EGR1.1.2527	271	in gene	0	0	1	11	13	16	1	4_A375_EGR1.1.1	16	Gene CEP152	FLJ21094, MCPH4, CEP152, KIAA0912	centrosomal protein 152kDa	NM_014985, NM_001194994, NC_018961.2	213070_s_at, 213602_at, 235535_at, 239413_at	NP_058000.2, NP_001101027.1, ENSP00355.1
GeneID:10 5508104	LOC1003 06104	19	45,992,695	45,994,106	1,211	+	1	4_A375_EGR1.1.2527	177	in gene	0	0	1	11	13	16	1	4_A375_EGR1.1.1	16	Gene LOC1003 06104		hypothetical LOC100306104	XR_109192		
GeneID:10 9894	SHC4	15	49,115,934	49,253,941	139,707	-	3	2_A375_shN7_dlur1_lncRNA_AR_1.2034, 3_A375_shN7_dlur1_lncRNA_AR_1.2033, 4_A375_shN7_dlur1_lncRNA_AR_1.2036	136469, 65935, 53877	in gene, in gene, in gene	0	1	1	10.67	19	10	3	2_A375_shN7_dlur1_lncRNA_AR_1	23	Gene SHC4	Rai.P, SHC.D, SHC4, MGC34023	SHC (Src homology 2 domain containing) family, member 4	NM_203349	235338_at, 235236_at	NP_976224.3
GeneID:10 741	EID1	19	49,170,230	49,172,360	2,030	+	1	2_A375_shN7_dlur1_lncRNA_AR_1.2035	48	in gene	0	1	0	13	25	14	1	2_A375_shN7_dlur1_lncRNA_AR_1	23	Gene EID1	KIAA1911, EP300-interacting inhibitor of differentiation 1	EP300-interacting inhibitor of differentiation 1	NM_014335, NC_018966.2	209969_s_at, 209970_x_at, 211896_at	NP_055150.1, ENSP00337.1

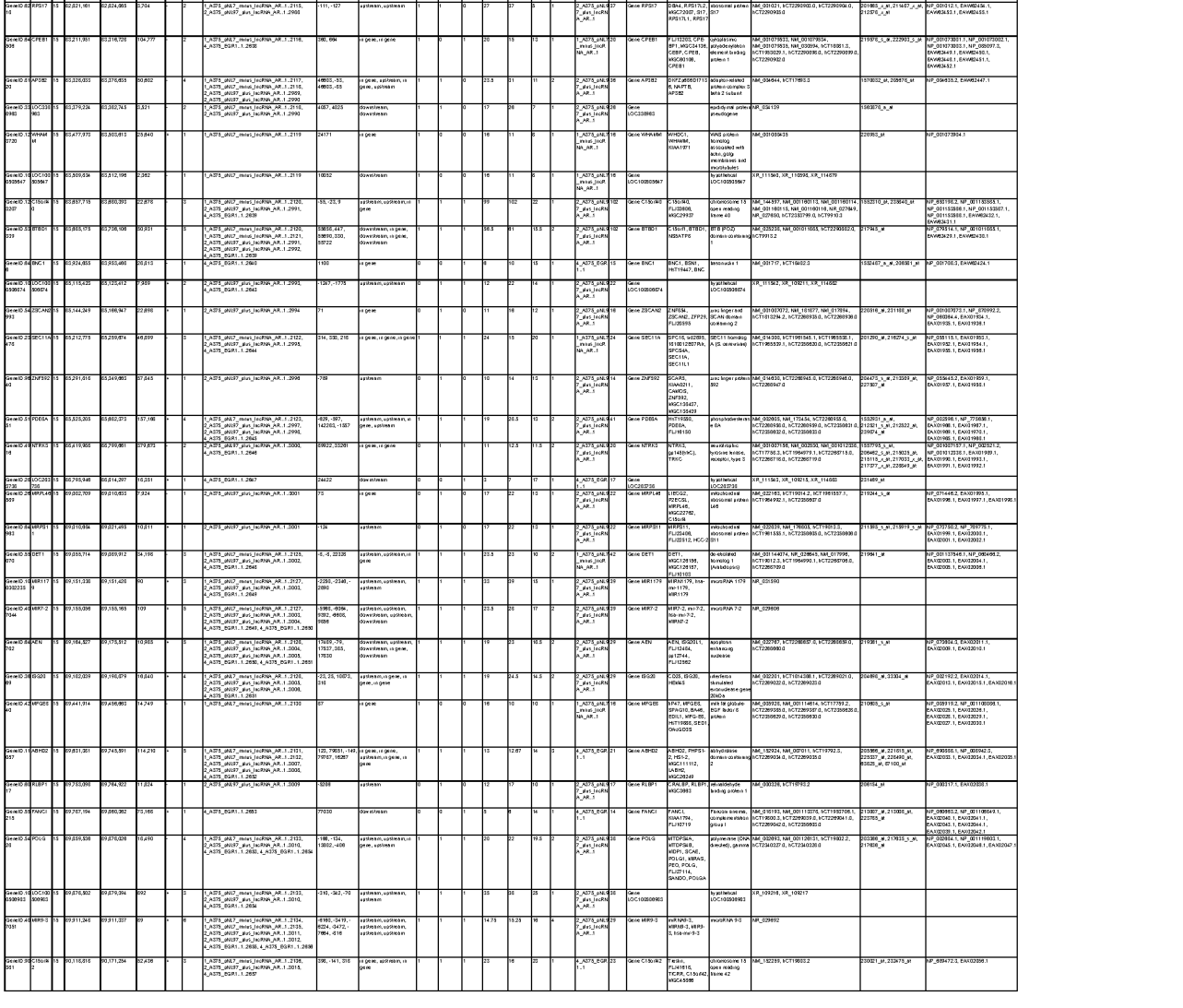


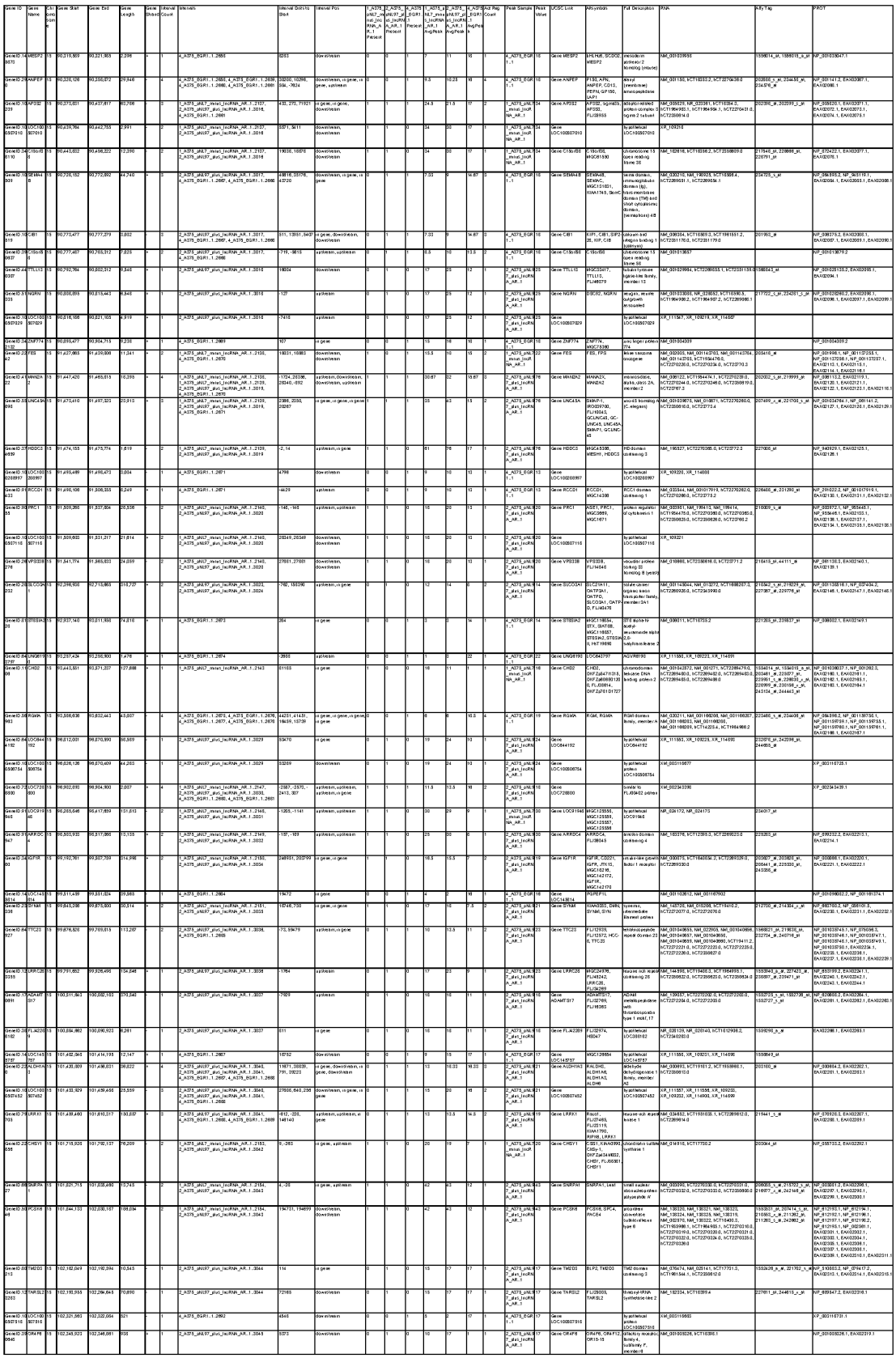


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_DMSO_NA7_mock_72hr_rep_Incr_RNA_AR_1 Percent	2_A375_DMSO_NA7_mock_72hr_rep_lncRNA_AR_1 Percent	3_A375_DMSO_NA7_mock_72hr_rep_lncRNA_AR_1 Percent	4_A375_DMSO_NA7_mock_72hr_rep_lncRNA_AR_1 Avg Peak	5_A375_DMSO_NA7_mock_72hr_rep_lncRNA_AR_1 Avg Peak	6_A375_EGFR_NA7_mock_72hr_rep_lncRNA_AR_1 Avg Peak	Ab2 Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
GeneID:4914403	MYO1E	15	59,426,965	59,865,971	439,006	-	2	1_A375_uNA7_mrna1_lncRNA_AR_1:-2024, a_A375_EGR1_1.2540	-129, 207	upstream, cis gene	1	0	1	15	15	22	1	a_A375_EGR1_1.1	22	Gene MYO1E	MYO1E, MGC104403, MYO1C, Hanc64c	myosin IE	NM_004998, XCT2205975.0		XP_004993.2, EAW77596.1
GeneID:2842873	ZNF342	13	99,930,261	99,946,707	16,476	-	1	2_A375_uNA7_mrna1_lncRNA_AR_1:2093	189	cis gene	0	1	0	17	20	14	1	2_A375_uNA7_mrna1_lncRNA_AR_1	20	Gene ZFP342	ZFP342, HHTEM3, ZFTF2H2, TFPA	general transcription factor IIA, 2, 12kDa	NM_034492, XCT1992488.1, XCT1951752.1	202870_at	NP_034493.1, EAW77573.1, EAW77874.1
GeneID:8997	BNIP2	15	59,933,061	59,961,842	28,781	-	3	1_A375_uNA7_mrna1_lncRNA_AR_1:2025, 2_A375_uNA7_dup1_lncRNA_AR_1:2093, a_A375_EGR1_1.2548	196, 32874, -534	cis gene, downstream, upstream	1	1	1	14	13.33	14.33	3	2_A375_uNA7_dup1_lncRNA_AR_1	20	Gene BNIP2	BNIP2, BNIP2, BNIP-2	BCL2/adenovirus E1B 19kDa interacting protein	NM_004330, XCT1911176.1, XCT4500.3	209395_s_at	NP_004321.2, EAW77576.1, EAW77878.1
GeneID:2958322	FOXB1	15	60,298,421	60,299,142	1,721	+	2	2_A375_uNA7_dup1_lncRNA_AR_1:2093, a_A375_EGR1_1.2548	1363, 1723	cis gene, downstream	0	1	1	10.5	12	13.5	2	a_A375_EGR1_1.1	16	Gene FOXB1	FOXB1-5, FOXB1, FKH5	forkhead box B1	NM_012182, XCT1861747.2	206815_at	NP_036114.2, EAW77581.1
GeneID:3382	ANXA2	15	60,839,350	60,890,165	50,815	-	5	1_A375_uNA7_mrna1_lncRNA_AR_1:2025, 1_A375_uNA7_dup1_lncRNA_AR_1:2027, 1_A375_uNA7_dup2_lncRNA_AR_1:2030, 2_A375_uNA7_dup1_lncRNA_AR_1:2096, 2_A375_uNA7_dup2_lncRNA_AR_1:2097	28548, 23513, 4777, 30177, 28505	cis gene, cis gene, cis gene, cis gene, cis gene	1	1	0	17.5	16.5	5.25	4	a_A375_EGR1_1.1	25	Gene ANXA2	ANX2, ANX2P, ANXA2, P36, CAL1H, ANX2, LPC2D, LPC2, ANX2L4	annexin A2	NM_001002857, NM_004039, NM_001136015, NM_001002856, XCT2290467.0, XCT2290469.0, XCT2290471.0, XCT2290472.0, XCT2290473.0, XCT2290476.0	201590_x_at, 201590_x_at, 210427_x_at, 213503_x_at	NP_001002857.1, NP_004030.1, NP_001002855.1, EAW77582.1, EAW77585.1, EAW77883.1, EAW77884.1, EAW77885.1, EAW77887.1
GeneID:7864	NAR02	13	80,711,808	80,771,344	59,536	-	2	1_A375_uNA7_mrna1_lncRNA_AR_1:2030, 2_A375_uNA7_dup1_lncRNA_AR_1:2099	-59, 240	upstream, cis gene	1	1	0	16	23	14	1	2_A375_uNA7_dup1_lncRNA_AR_1	23	Gene NAR02	NAR02, BRCC1	NARA recently regulated 2	NM_139311, NM_001018009, XCT2290483.1, XCT2290484.3, XCT2290485.1	218715_at, 228990_at, 229189_at	NP_976057.2, NP_001018099.1, EAW77585.1, EAW77909.1, EAW77910.1
GeneID:6095	RORA	15	60,700,450	61,321,902	741,019	-	3	1_A375_uNA7_mrna1_lncRNA_AR_1:2030, 1_A375_uNA7_dup1_lncRNA_AR_1:2099, 1_A375_uNA7_dup2_lncRNA_AR_1:2070	780976, 750096, 53962	downstream, downstream, cis gene	1	1	0	14.5	19.5	8.5	2	2_A375_uNA7_dup1_lncRNA_AR_1	23	Gene RORA	RORA, NR1F1, MGC119329, RZRA, RZR-ALPHA, DKFZp686H0514, ROR1, ROR2, MGC119326, RORA	RAR-related orphan receptor A	NM_134261, NM_134260, NM_002943, NM_134262, XCT1926699.1, XCT1926699.2, XCT1926120.2, XCT2290481.0	210426_x_at, 210479_s_at, 229580_at	NP_599021.1, NP_599022.1, NP_599024.1, NP_002934.1, EAW77912.1, EAW77915.1, EAW77894.1, EAW77896.1
GeneID:1970302	MGC16903	15	62,929,371	62,937,390	8,019	-	1	1_A375_uNA7_mrna1_lncRNA_AR_1:2033	-2324	upstream	1	0	0	24	12	1	1	1_A375_uNA7_mrna1_lncRNA_AR_1	24	Gene MGC16903		hypothetical protein MGC16903	NR_026997	1569292_at	
GeneID:6957	TLN2	15	62,939,510	63,136,630	197,120	+	1	1_A375_uNA7_mrna1_lncRNA_AR_1:2033	594	cis gene	1	0	0	24	12	1	1	1_A375_uNA7_mrna1_lncRNA_AR_1	24	Gene TLN2	DKFZp686I09379, talin 2, bA440G20.1, TLN2, DKFZp686I09379, DKFZp451B031, TLN2G	talin 2	NM_015059, XCT1911319.2, XCT2290578.1, XCT2407830.0	212763_at, 232629_at	NP_055874.2, EAW77618.1, EAW77619.1, EAW77617.1
GeneID:1963	LACTB	15	63,414,032	63,434,260	20,228	+	3	1_A375_uNA7_mrna1_lncRNA_AR_1:2026, 2_A375_uNA7_dup1_lncRNA_AR_1:2076, a_A375_EGR1_1.2530	-144, -164, 454	upstream, upstream, cis gene	1	1	1	33	40	16	1	a_A375_uNA7_mrna1_lncRNA_AR_1	33	Gene LACTB	LACTB, MRPL58, FLJ41602, G2A	lactamase, beta	NM_032037, NM_171846, XCT2265533.0, XCT24894.3	1553455_at, 1552498_s_at, 226254_at	NP_115624.2, NP_741982.1, EAW77627.1, EAW77630.1
GeneID:3163	RPS27L	15	63,445,929	63,449,741	4,292	-	1	2_A375_uNA7_dup1_lncRNA_AR_1:2077	-19	upstream	0	1	0	13	26	10	1	2_A375_uNA7_dup1_lncRNA_AR_1	26	Gene RPS27L	RPS27L	ribosomal protein S27-like	NM_015920, XCT2285932.0, XCT24869.3	218937_s_at, 223437_s_at, 230553_at	NP_057004.1, EAW77629.1, EAW77640.1
GeneID:5762	RABEB	15	65,451,726	65,559,975	76,247	+	1	1_A375_uNA7_mrna1_lncRNA_AR_1:2027	-3200	upstream	1	0	0	21	14	5	1	1_A375_uNA7_mrna1_lncRNA_AR_1	21	Gene RABEB	FLJ35125, RABEB	RABEB, member RAS oncogene family	NM_016530, XCT2285536.0, XCT24868.0	219210_s_at, 223546_at, 229852_at	NP_057614.1, EAW77642.1, EAW77641.1
GeneID:7705	CA12	15	63,815,700	63,874,075	58,245	-	2	2_A375_uNA7_dup1_lncRNA_AR_1:2078, 2_A375_uNA7_dup2_lncRNA_AR_1:2078	53339, 57499	cis gene, cis gene	1	1	0	15	16	10.5	2	2_A375_uNA7_dup1_lncRNA_AR_1	16	Gene CA12	HT16918, FLJ35151, CA12, CAXII	carbonic anhydrase XII	NM_001218, NM_206925, XCT2289140.1, XCT2289910.0, XCT2289915.1, XCT2289916.1	202963_at, 204508_s_at, 204509_at, 210735_s_at, 214164_x_at, 215387_s_at	NP_001209.1, NP_996908.1, EAW77648.1, EAW77649.1, EAW77650.1, EAW77647.1
GeneID:9901	USP3	15	63,796,610	63,855,965	59,355	+	3	1_A375_uNA7_mrna1_lncRNA_AR_1:2029, 1_A375_uNA7_dup1_lncRNA_AR_1:2079, a_A375_EGR1_1.2551	-22, -10, -716	cis gene, upstream, upstream	1	1	1	25	25	17	1	2_A375_uNA7_dup1_lncRNA_AR_1	25	Gene USP3	USP, SHH30, MGC129078, MGC129079, USP3	ubiquitin specific peptidase 3	NM_006537, XCT1938498.1	221884_s_at, 229852_at	NP_006528.2, EAW77651.1
GeneID:4345	MRPL23	13	64,165,129	64,165,218	89	-	2	2_A375_uNA7_mrna1_lncRNA_AR_1:2040, 2_A375_uNA7_dup1_lncRNA_AR_1:2050	338, 338	downstream, downstream	1	1	0	62	77	14	1	2_A375_uNA7_dup1_lncRNA_AR_1	77	Gene MRPL23A	MRPL23A, MRNA22A	mitochondrial L23a	NR_029944		
GeneID:5441	FAM190A	13	64,364,761	64,398,307	21,546	-	4	1_A375_uNA7_mrna1_lncRNA_AR_1:2041, 1_A375_uNA7_mrna2_lncRNA_AR_1:2042, 1_A375_uNA7_dup1_lncRNA_AR_1:2051, a_A375_EGR1_1.2552	65, -2017, -221, -20419	cis gene, upstream, upstream, upstream	1	1	1	21	17.5	14	2	1_A375_uNA7_mrna1_lncRNA_AR_1	22	Gene FAM98A	FAM98A, FLJ22575	family with sequence similarity 98, member A	NM_032231, NM_001014812, XCT2336991.0, XCT2336992.0, XCT24548.2	224791_s_at	NP_115977.1, NP_001014812.1, EAW77660.1, EAW77661.1, EAW77662.1
GeneID:8861	SNX1	15	64,398,077	64,436,403	40,326	+	4	1_A375_uNA7_mrna1_lncRNA_AR_1:2041, 1_A375_uNA7_mrna2_lncRNA_AR_1:2042, 1_A375_uNA7_dup1_lncRNA_AR_1:2051, a_A375_EGR1_1.2552	-2083, 47, -1849, 279	upstream, cis gene, upstream, cis gene	1	1	1	21	17.5	14	2	1_A375_uNA7_mrna1_lncRNA_AR_1	22	Gene SNX1	SNX1, HHT17370, SNX1A, MGC26564, Vps5	sorting nexin 1	NM_003099, NM_148953, NM_152426, XCT2337970.0, XCT2337971.0, XCT2337972.0, XCT24544.2	201716_at, 213384_x_at, 214321_s_at, 216357_at	NP_003090.2, NP_683736.1, EAW77664.1, EAW77665.1, EAW77666.1, EAW77663.1
GeneID:7693	SNX22	15	64,443,916	64,449,800	5,784	+	2	1_A375_uNA7_dup1_lncRNA_AR_1:2043, 2_A375_uNA7_dup1_lncRNA_AR_1:2052	11444, 11436	downstream, downstream	1	1	0	33	29	16	1	2_A375_uNA7_dup1_lncRNA_AR_1	29	Gene SNX22	FLJ12592, SNX22	sorting nexin 22	NM_024796, XCT1961605.1, XCT24549.2	1569451_s_at, 233695_at, 233460_at	NP_079074.2, EAW77666.1, EAW77667.1
GeneID:5464	PPIB	15	64,446,034	64,455,354	7,340	-	2	1_A375_uNA7_dup1_lncRNA_AR_1:2043, 2_A375_uNA7_dup1_lncRNA_AR_1:2052	-8, 10	upstream, cis gene	1	1	0	33	29	16	1	2_A375_uNA7_dup1_lncRNA_AR_1	33	Gene PPIB	CYP, SCYLP, MGC2234, CYPB, CYP-S1, MGC14199, PPIB	peptidylprolyl isomerase B (cyclophilin B)	NM_000942, XCT24343.4	200967_at, 200968_s_at	NP_000933.1, EAW77669.1
GeneID:8353	CSNK1G1	15	64,457,716	64,648,442	190,726	-	5	1_A375_uNA7_mrna1_lncRNA_AR_1:2043, 1_A375_uNA7_mrna2_lncRNA_AR_1:2044, 1_A375_uNA7_dup1_lncRNA_AR_1:2052, 1_A375_uNA7_dup2_lncRNA_AR_1:2053, a_A375_EGR1_1.2553	193002, -292, 190396, 689, 1	downstream, upstream, downstream, cis gene, cis gene	1	1	1	25	25.5	15	2	1_A375_uNA7_mrna1_lncRNA_AR_1	33	Gene CSNK1G1	CSNK1G1		NM_022048	220940_at, 221473_s_at, 229883_at, 231302_s_at	NP_071331.2
GeneID:8971	RANBP10	13	64,837,193	64,870,702	33,509	-	6	1_A375_uNA7_mrna1_lncRNA_AR_1:2044, 1_A375_uNA7_mrna2_lncRNA_AR_1:2045, 2_A375_uNA7_dup1_lncRNA_AR_1:2053, 2_A375_uNA7_dup2_lncRNA_AR_1:2054, 2_A375_uNA7_dup3_lncRNA_AR_1:2055, a_A375_EGR1_1.2553	24956, -8252, 23826.6, -8266, 23414	downstream, upstream, downstream, cis gene, upstream, downstream	1	1	1	17	22.33	13	3	2_A375_uNA7_dup1_lncRNA_AR_1	28	Gene RANBP10	FLJ38702, LS, RANO101, DEATC1, DEATC1, U(IUPAF), RNF, NEMP79	RANO101	NM_014758, NM_001029909	202503_s_at, 217013_x_at	NP_055551.1, NP_001025160.1
GeneID:5587	TRPV4	15	64,900,003	64,747,922	97,499	+	5	1_A375_uNA7_mrna1_lncRNA_AR_1:2045, 1_A375_uNA7_mrna2_lncRNA_AR_1:2046, 2_A375_uNA7_dup1_lncRNA_AR_1:2054, 2_A375_uNA7_dup2_lncRNA_AR_1:2055, a_A375_EGR1_1.2554	-19, 72855, -6307, -35, 72857	upstream, downstream, upstream, upstream, downstream	1	1	0	10.67	22.33	10.67	3	2_A375_uNA7_dup1_lncRNA_AR_1	26	Gene TRPV4	H17739.1, ASO1, TRPV4	thyroid hormone receptor interactor 4	NM_016112, XCT2289536.0, XCT2289539.0	202332_at	NP_057207.2, EAW77654.1, EAW77655.1
GeneID:5464	RBP4BP	13	65,032,030	65,087,770	55,877	-	1	1_A375_EGR1_1.2564	-982	upstream	0	0	1	7	9	19	1	a_A375_EGR1_1.1	19	Gene RBP4B2	RBP4B2	RNA binding protein with multiple splicing 2	NM_194272, XCT1626828.2	220802_at	NP_919245.1, EAW77680.1
GeneID:5588	PIP1	19	65,107,851	65,117,855	10,007	-	3	1_A375_uNA7_mrna1_lncRNA_AR_1:2047, 1_A375_uNA7_dup1_lncRNA_AR_1:2057, 1_A375_uNA7_dup2_lncRNA_AR_1:2058	-10295, -274, -10256	upstream, upstream, upstream	1	1	0	14	19.5	10	2	2_A375_uNA7_dup1_lncRNA_AR_1	24	Gene PIP1	C19orf20, PIP1, PIP	PIP1 5-to-3' DNA tetrose kinase homolog (S. cerevisiae)	NM_020045, XCT1625908.2, XCT2290617.0, XCT2290619.0	1555891_at, 228252_at	NP_064630.1, EAW77693.1, EAW77696.1
GeneID:8001	PLEKHG2	19	65,134,092	65,180,201	46,110	+	3	1_A375_uNA7_mrna1_lncRNA_AR_1:2047, 2_A375_uNA7_dup1_lncRNA_AR_1:2058, a_A375_EGR1_1.2555	-9984, -9999, -234	upstream, upstream, upstream	1	1	1	11.5	16	15.5	2	a_A375_EGR1_1.1	21	Gene PLEKHG2	FLJ38664, DKFZp761K2312, PLEKHG2, FLJ21910, FLJ21912, pp5969	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	NM_023001, NM_001159359, XCT2289987.0, XCT2289988.0, XCT2337810.0, XCT2337934.0	204439_at, 223307_at	NP_374272.2, NP_001150163.1, EAW77697.1, EAW77698.1, EAW77699.1, EAW77700.1
GeneID:1328281	MTFMT	15	65,210,830	65,221,977	26,127	-	1	1_A375_uNA7_mrna1_lncRNA_AR_1:2048	108	cis gene	1	0	0	16	14	8	1	1_A375_uNA7_dup1_lncRNA_AR_1	16	Gene MTFMT	MTFMT, FMT1	mitochondrial methionyl-tRNA formyltransferase	NM_139242, XCT1477.4, XCT1971074.1	213669_at	NP_640338.2, EAW77708.1, EAW77707.1
GeneID:5893	RASL12	13	65,345,875	65,360,366	14,715	-	1	2_A375_uNA7_dup1_lncRNA_AR_1:2090	-1372	upstream	0	1	0	11	17	8	1	2_A375_uNA7_dup1_lncRNA_AR_1	17	Gene RASL12	RASL12, RIS	RAS-like, family 12	NM_016583, XCT1477.4, XCT1971075.1	219187_at	NP_057947.1, EAW77710.1, EAW77709.1
GeneID:3994	KBTBD13	13	65,389,134	65,272,278	3,122	+	1	2_A375_uNA7_dup1_lncRNA_AR_1:2090	-7394	upstream	0	1	0	11	17	8	1	2_A375_uNA7_dup1_lncRNA_AR_1	17	Gene KBTBD13	KBTBD13, HCGIH4727, MDHB	kelch repeat and BTB (POZ) domain containing 13	NM_031101592		NP_001094322.1
GeneID:5501	PDCD7	15	65,409,717	65,426,174	16,457	-	2	1_A375_uNA7_mrna1_lncRNA_AR_1:2049, 1_A375_uNA7_dup1_lncRNA_AR_1:2091	-110, -142	cis gene, cis gene	1	0	1	19	22	7	1	2_A375_uNA7_dup1_lncRNA_AR_1	22	Gene PDCD7	HBS1L, PDCD7, FLJ34213, ES15, MGC22515	programmed cell death 7	NM_033107, XCT1477.3, XCT1971060.1	230162_at, 231939_x_at	NP_036956.1, EAW77715.1, EAW77714.1
GeneID:1045	CLPX	15	65,442,764	65,477,983	34,779	-	2	a_A375_EGR1_1.2558, a_A375_EGR1_1.2559	91, -229	cis gene, upstream	0	0	1	10	12	13.5	2	a_A375_EGR1_1.1	14	Gene CLPX	CLPX		NM_006660, XCT1477.2, XCT2290879.0	204809_at, 223307_at	NP_006651.2, EAW77718.1, EAW77715.1
GeneID:5464	PARP16	15	65,530,457	65,579,016	48,560	-	2	1_A375_uNA7_dup1_lncRNA_AR_1:2060, 2_A375_uNA7_dup1_lncRNA_AR_1:2092	-9302, -9302	upstream, upstream	1	1	0	46	93	13	1	1_A375_uNA7_mrna1_lncRNA_AR_1	46	Gene PARP16	C15orf29, FLJ25251, PARP16, FLJ25309, pART13	poly (ADP-ribose) polymerase family, member 16	NM_078151, XCT1477.2, XCT1958133.1, XCT2357072.0, XCT2357076.0	219264_at	NP_060223.1, EAW77720.1, EAW77718.1, EAW77719.1, EAW77721.1
GeneID:2831	RNU5A-1	15	65,566,309	65,566,903	118	+	3	1_A375_uNA7_dup1_lncRNA_AR_1:2060, 2_A375_uNA7_dup1_lncRNA_AR_1:2092, 2_A375_uNA7_dup2_lncRNA_AR_1:2093	-69, -69, 6707	upstream, upstream, downstream	1	1	0	30.5	24.5	14	2	2_A375_uNA7_dup1_lncRNA_AR_1	34	Gene RNU5A	U5A, RNU5A-1, RNU5C, U5B1, RNU5	RNA, U5A small nuclear 1	NR_002756		
GeneID:2832	RNU5B-1	15	65,597,015	65,597,151	116	+	3	1_A375_uNA7_dup1_lncRNA_AR_1:2060, 2_A375_uNA7_dup1_lncRNA_AR_1:2092, 2_A375_uNA7_dup2_lncRNA_AR_1:2093	-3693, -3693, 61	upstream, upstream, cis gene	1	1	0	30.5	24.5	14	2	2_A375_uNA7_dup1_lncRNA_AR_1	34	Gene RNU5B-1	RNU5B, U5B1, RNU5B-1, RNU5B-1P	RNA, U5B small nuclear 1	NR_002757		
GeneID:8509	KIDCC4	13	65,816,483	65,870,376	53,913	-	1	a_A375_EGR1_1.2566	-7030	upstream	0	0	1	14	15	17	1	a_A375_EGR1_1.1	17	Gene KIDCC4	KIDCC4, FLN4C, HSTI6080	immunoglobulin superfamily, DCC subclass, member 4	NM_194564, XCT1626912.2	230960_at, 233037_at	NP_954733.2, EAW77722.1
GeneID:8509	KIDCC4	13	65,870,623	65,715,410	41,365	-	1	a_A375_EGR1_1.2566	37662	cis gene	0	0	1	14	15	17	1	a_A375_EGR1_1.1	17	Gene KIDCC4	KIDCC4, MCPE, FLJ42031, DO4456, KIDCC4, RIAA1828	immunoglobulin superfamily, DCC subclass, member 4	NM_033092, XCT1477.2, XCT2289566.0, XCT2289568.0	227870_at	NP_990113.1, EAW77721.1, EAW77724.1, EAW77723.1
GeneID:5464	DPP8	15	65,737,956	65,810,853	72,897	-	5	1_A375_uNA7_mrna1_lncRNA_AR_1:2061, 1_A375_uNA7_dup1_lncRNA_AR_1:2094, a_A375_EGR1_1.2559	-13, -13, 93	upstream, upstream, cis gene	1	1	1	176	169	23	1	2_A375_uNA7_dup1_lncRNA_AR_1	169	Gene DPP8	MGC26119, FLJ14935, DP8, DPP8, FLJ35201, MSTP141, DPRP1	dipeptidyl-peptidase 8	NM_130434, NM_197961, NM_017745, NM_197962, XCT1477.6, XCT1971073.1, XCT1971076.1, XCT2357157.0, XCT2357158.0, XCT2357159.0, XCT2357160.0, XCT2357161.0, XCT2357162.0, XCT2357163.0, XCT2357164.0, XCT2357165.0	220929_s_at, 227016_at	NP_997195.1, NP_997196.1, NP_997197.1, NP_060152.2, NP_997198.1, EAW77725.1, EAW77727.1, EAW77726.1, EAW77728.1, EAW77729.1, EAW77730.1, EAW77731.1, EAW77732.1, EAW77733.1, EAW77734.1
GeneID:3319	PTPLAD1	15	65,822,027	65,870,893	47,866	+	1	a_A375_EGR1_1.2560	341	cis gene	0	0	1	12	21	28	1	a_A375_EGR1_1.1	28	Gene PTPLAD1	HSPC121, FLJ90376, 8-Mar-1, PTPLAD1, HSPC122	protein tyrosine phosphatase-like A domain containing 1	NM_018395, XCT1477.2, XCT1971077.1	222454_at, 234002_at	NP_060865.2, EAW77736.1, EAW77735.1
GeneID:8109	C15orf44	15	65,871,116	65,903,469	32,353	-	3	1_A375_uNA7_mrna1_lncRNA_AR_1:2062, 1_A375_uNA7_dup1_lncRNA_AR_1:2095, 1_A375_uNA7_dup2_lncRNA_AR_1:2096	-11, 29, -51	upstream, cis gene, upstream	1	1	1	24	36	30	1	2_A375_uNA7_dup1_lncRNA_AR_1	36	Gene C15orf44	DKFZp564O1864, C15orf44	chromosome 15 open reading frame 44	NM_030930, NM_001136043, XCT1477.3, XCT2289138.0	1569801_at, 221283_s_at	NP_110427.1, NP_001129515.1, EAW77737.1, EAW77738.1
GeneID:1082	DENND4A	15	65,952,954	66,054,851	101,877	-	3	1_A375_uNA7_dup1_lncRNA_AR_1:2063, 2_A375_uNA7_dup1_lncRNA_AR_1:2096, a_A375_EGR1_1.2562	-105, -70, 375	upstream, upstream, cis gene	1	1	1	25.5	21.5	19.5	2	1_A375_uNA7_mrna1_lncRNA_AR_1	41	Gene DENND4A	DENND4A, bA440N3, KIAA0476, MNTCPBP, FLJ23545, IRLB	DENN/MADD domain containing 4A	NM_005848, NM_001144523	1554352_s_at, 214767_at	NP_005839.3, NP_001132295.1
GeneID:8108	RAB11A	15	66,081,768	66,161,762	79,995	+	2	2_A375_uNA7_dup1_lncRNA_AR_1:2096, a_A375_EGR1_1.2563	44, -282	cis gene, upstream	0	1	0	13	26	24	1	2_A375_uNA7_dup1_lncRNA_AR_1	26	Gene RAB11A	FLB, MGC14380, RAB11A	RAB11A, member RAS oncogene family	NM_004663, XCT1961814, XCT1962448.1	203883_s_at, 203884_s_at	NP_004654.1, EAW77753.1, EAW77752.1
GeneID:5464	MEQP1	15	66,167,854	66,346,073	550,441	-	6	1_A375_uNA7_mrna1_lncRNA_AR_1:2064, 1_A375_uNA7_mrna2_lncRNA_AR_1:2065, 1_A375_uNA7_mrna3_lncRNA_AR_1:2066, 1_A375_uNA7_dup1_lncRNA_AR_1:2097, 1_A375_uNA7_dup2_lncRNA_AR_1:2098, 2_A375_uNA7_dup1_lncRNA_AR_1:2099, 2_A375_uNA7_dup2_lncRNA_AR_1:2100, 2_A375_uNA7_dup3_lncRNA_AR_1:2101, 2_A375_uNA7_dup4_lncRNA_AR_1:2102	200147, 295555, 245955, 245957, 200147, 245957, 245823, 939	upstream, cis gene, cis gene, upstream, cis gene, cis gene, cis gene	1	1	0	29	32.33	6.25	4	2_A375_uNA7_dup1_lncRNA_AR_1	32	Gene MEQP1	DKFZp434J121, MEQP11, RIAA1761	multiple EGF-like domains 11	NM_032445, XCT1953471.1, XCT2291813.0, XCT2293143.0, XCT2355854.0	1553439_s_at, 1560136_at, 1568079_a_at	NP_115531.2, EAW77737.1, EAW77734.1, EAW77735.1, EAW77736.1
GeneID:5662	MAP2K1	15	66,679,211	66,763,862	104,671	+	3	1_A375_uNA7_mrna1_lncRNA_AR_1:2066, 2_A375_uNA7_dup1_lncRNA_AR_1:2100, 2_A375_uNA7_dup2_lncRNA_AR_1:2104	110797, -220, 15933	downstream, upstream, downstream	1	1	1	15.5	25	14.5	2	2_A375_uNA7_dup1_lncRNA_AR_1	29	Gene MAP2K1	MAP2K1, MEK1, MKK1, PRKMK1	mitogen-activated protein kinase kinase 1	NM_002755, XCT1962733.3, XCT1971053.2, XCT2291121.1, XCT2293572.0, XCT2345936.0	202076_at	NP_002746.1, EAW77756.1, EAW77755.1, EAW77757.1, EAW77758.1
GeneID:5610	SNAPC4	15	66,762,866	66,790,148	27,283	-	2	1_A375_uNA7_dup1_lncRNA_AR_1:2100, a_A375_EGR1_1.2564	176, 2	cis gene, cis gene	1	0	0	16	29	21	1	2_A375_uNA7_dup1_lncRNA_AR_1	29	Gene SNAPC4	SNAPC4, SNAP19	small nuclear RNA activating complex, polypeptide 4, 190kDa	NM_003081, XCT1630985.4, XCT1962420.1, XCT2292250.0	1554093_s_at, 213283_at, 214392_s_at	NP_003140.1, EAW77770.1, EAW77771.1, EAW77772.1
GeneID:8766	RPL4	15	66,791,853	66,797,164	5,331	-	2	1_A375_uNA7_mrna1_lncRNA_AR_1:2065, 2_A375_uNA7_dup1_lncRNA_AR_1:2104	7218, 7040	downstream, downstream	1	1	0	16	29	21	1	2_A375_uNA7_dup1_lncRNA_AR_1	29	Gene RPL4	L4, RPL4		NM_000968, XCT2292038.1, XCT2292039.1, XCT2292041.1, XCT2292292.1	200809_s_at, 201154_x_at, 201155_s_at	NP_000959.2, EAW77773.1, EAW77774.1, EAW77776.1
GeneID:5109	SNORD16C	15	66,792,990	66,792,858	68	-	2	1_A375_uNA7_mrna1_lncRNA_AR_1:2065, 2_A375_uNA7_dup1_lncRNA_AR_1:2104	5983, 5812	downstream, downstream	1	1	0	16	29	21	1	2_A375_uNA7_dup1_lncRNA_AR_1	29	Gene SNORD16C	SNORD16C, U16C	small nucleolar RNA, C/D box 16C	NR_002443		
GeneID:6099	SNORD16B	15	66,794,360	66,794,429	69	-	2	1_A375_uNA7_mrna1_lncRNA_AR_1:2065, 2_A375_uNA7_dup1_lncRNA_AR_1:2104	4481, 4265	downstream, downstream	1	1	0	16	29	21	1	2_A375_uNA7_dup1_lncRNA_AR_1	29	Gene SNORD16B	SNORD16B, U16B	small nucleolar RNA, C/D box 16B	NR_002442		
GeneID:6097	SNORD16	15	66,793,149	66,793,345	99	-	2	1_A375_uNA7_mrna1_lncRNA_AR_1:2065, 2_A375_uNA7_dup1_lncRNA_AR_1:2104	5283, 5104	downstream, downstream	1	1	0	16	29	21	1	2_A375_uNA7_dup1_lncRNA_AR_1	29	Gene SNORD16	SNORD16, U16	small nucleolar RNA, C/D box 16	NR_002440		
GeneID:6096	SNORD16A	15	66,793,583	66,793,682	99	-	2	1_A375_uNA7_mrna1_lncRNA_AR_1:2065, 2_A375_uNA7_dup1_lncRNA_AR_1:2104	5984, 5806	downstream, downstream	1	1	0	16	29	21	1	2_A375_uNA7_dup1_lncRNA_AR_1	29	Gene SNORD16A	SNORD16A, U16A	small nucleolar RNA, C/D box 16A	NR_002441		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.55055	ZWILCH	15	66,797,431	66,841,823	44,392	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2058, 2_A375_pNL97_plus_lncRNA_AR..1..2904	-7463, -7287	upstream, upstream	1	1	0	16	29	21	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene ZWILCH	KNTC1AP, ZWILCH, MGC111034, FLJ10036, FLJ16343, hZwilch	Zwilch, kinetochore associated, homolog (Drosophila)	NR_003105, NM_017975, hCT1961597.2, hCT2289123.0, hCT2289124.0	218349_s_at, 222606_at	NP_060445.3, EAW77777.1, EAW77778.1, EAW77779.1
GeneID.4091	SMAD6	15	66,994,674	67,074,338	79,664	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2059, 2_A375_pNL97_plus_lncRNA_AR..1..2906, 2_A375_pNL97_plus_lncRNA_AR..1..2907, 4_A375_EGR1..1..2565, 4_A375_EGR1..1..2566	-466, -690, 63633, -16, 67150	upstream, upstream, in gene, upstream, in gene	1	1	1	13.67	14.67	11.33	3	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene SMAD6	MADH6, SMAD6, HsT17432, MADH7	SMAD family member 6	NM_001142861, NR_027654, NM_005585, hCT1955464.1, hCT2289131.0, hCT2355772.0	207069_s_at, 209886_s_at, 209887_at, 213565_s_at	NP_001136333.1, NP_005576.3, EAW77784.1, EAW77785.1, EAW77786.1
GeneID.4088	SMAD3	15	67,358,195	67,487,533	129,338	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2061, 4_A375_EGR1..1..2567	25533, 118765	in gene, in gene	1	0	1	12	13.5	12	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene SMAD3	MGC60396, HsT17436, DKFZp686J10186, MADH3, SMAD3, DKFZp586N0721, JV15-2, HSPC193	SMAD family member 3	NM_005902, NM_001145102, NM_001145103, NM_001145104, hCT13618.3, hCT2289154.0, hCT2355738.0	205396_at, 205397_x_at, 205398_s_at, 218284_at	NP_005893.1, NP_001138574.1, NP_001138575.1, NP_001138576.1, EAW77789.1, EAW77790.1, EAW77788.1
GeneID.79719	AAGAB	15	67,493,366	67,547,074	53,708	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2062, 2_A375_pNL97_plus_lncRNA_AR..1..2909	2, -82	in gene, upstream	1	1	0	31	36	15	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene AAGAB	p34, AAGAB, DKFZp686G08119, DKFZp667D2317, FLJ11506	alpha- and gamma-adaptin binding protein	NM_024666, hCT15087.4, hCT2355724.0	202851_at, 202852_s_at, 243284_at	NP_078942.3, EAW77793.1, EAW77792.1
GeneID.84799	IQCH	15	67,547,138	67,794,142	247,004	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2062, 2_A375_pNL97_plus_lncRNA_AR..1..2909	-66, -2	upstream, upstream	1	1	0	31	36	15	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene IQCH	NYDSP5, FLJ12476, IQCH, DKFZp434F2114	IQ motif containing H	NM_022784, NM_001031715, hCT1660332.3, hCT2289167.0, hCT2355747.0, hCT2355748.0	1569610_at, 1569611_a_at, 220361_at, 224165_s_at, 239812_s_at, 239813_at	NP_073621.2, NP_001026885.1, EAW77794.1, EAW77795.1, EAW77796.1, EAW77797.1
GeneID.100506686	LOC100506686	15	67,695,950	67,814,182	118,232	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2063	934	in gene	1	0	0	15	6	7	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene LOC100506686		hypothetical LOC100506686	XR_111515, XR_111514, XR_109209, XR_109208, XR_114665, XR_114664		
GeneID.145853	C15orf61	15	67,813,522	67,819,641	6,119	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2063	-274	upstream	1	0	0	15	6	7	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene C15orf61	C15orf61, FLJ59587	chromosome 15 open reading frame 61	NM_001143936	229742_at	NP_001137408.1
GeneID.5607	MAP2K5	15	67,835,021	68,099,452	264,431	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2064	-109	upstream	1	0	0	14	11	13	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene MAP2K5	HsT17454, MAP2K5, PRKMK5, MAPKK5, MEK5	mitogen-activated protein kinase kinase 5	NM_002757, NM_145160, hCT1955465.1, hCT2290250.0, hCT2290251.0, hCT2290252.0	204756_at, 210482_x_at, 211370_s_at, 211371_at, 216435_at, 216765_at	NP_002748.1, NP_660143.1, EAW77799.1, EAW77800.1, EAW77801.1, EAW77802.1
GeneID.390598	LBXCOR1	15	68,117,941	68,126,174	8,233	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2910, 2_A375_pNL97_plus_lncRNA_AR..1..2911	-4405, 14827	upstream, downstream	0	1	0	16	22.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LBXCOR1	FUSSEL15, LBXCOR1, SKOR1, CORL1	Lbxcor1 homolog (mouse)	NM_001031807		NP_001026977.1
GeneID.26827	RNU6-1	15	68,132,278	68,132,383	105	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2911	-365	upstream	0	1	0	17	22	13	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene RNU6-1	RNU6-1, U6, RNU6A, RNU6	RNA, U6 small nuclear 1	NR_004394		
GeneID.10116	FEM1B	15	68,570,141	68,583,640	13,499	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2065, 2_A375_pNL97_plus_lncRNA_AR..1..2912	-157, -173	upstream, upstream	1	1	0	27	32	14	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene FEM1B	FEM1B, FIAA, DKFZp451E0710, F1A-ALPHA	fem-1 homolog b (C. elegans)	NM_015322, hCT13617.3, hCT2290262.0	212367_at, 212373_at, 212374_at	NP_056137.1, EAW77818.1, EAW77819.1
GeneID.22801	ITGA11	15	68,594,042	68,724,492	130,450	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2066, 4_A375_EGR1..1..2569	59548, 115946	in gene, in gene	1	0	1	11.5	7	14	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ITGA11	HsT18964, ITGA11	integrin, alpha 11	NM_001004439, hCT14921.3, hCT2290466.0	1554819_a_at, 222899_at	NP_001004439.1, EAW77821.1, EAW77820.1
GeneID.283673	TMEM84	15	69,373,190	69,388,164	14,974	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2914	-6449	upstream	0	1	0	14	21	7	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TMEM84	MGC126845, FLJ33768, MGC126843, NCRNA00277, TMEM84	non-protein coding RNA 277	NR_026949, hCT2341183.0, hCT2341184.0, hCT2341185.0	240912_x_at	EAW77833.1, EAW77835.1, EAW77834.1
GeneID.26035	GLCE	15	69,452,973	69,564,544	111,571	+	1	4_A375_EGR1..1..2572	19	in gene	0	0	1	10	11	14	1	4_A375_EGR1..1	14	Gene GLCE	HSEPI, GLCE, KIAA0836	glucuronic acid epimerase	NM_015554, hCT13620.3	213552_at	NP_056369.1, EAW77837.1
GeneID.54852	PAQR5	15	69,591,294	69,699,976	108,682	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2915	115234	downstream	0	1	0	14	25	10	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene PAQR5	MPRG, PAQR5, FLJ20190	progestin and adipoQ receptor family member V	NM_001104554, NM_017705, hCT2288960.0, hCT31031.3	220333_at, 242871_at	NP_001098024.1, NP_060175.3, EAW77838.1, EAW77839.1
GeneID.145694	LOC145694	15	69,689,243	69,707,368	18,125	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2915	640	in gene	0	1	0	14	25	10	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC145694		hypothetical LOC145694	XR_111513, XR_109210, XR_114666	243822_at	
GeneID.9493	KIF23	15	69,706,686	69,740,764	34,078	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2067, 2_A375_pNL97_plus_lncRNA_AR..1..2915, 2_A375_pNL97_plus_lncRNA_AR..1..2916, 4_A375_EGR1..1..2573	36592, -160, 36824, 36496	downstream, upstream, downstream, downstream	1	1	1	16.5	26.5	19.5	2	4_A375_EGR1..1	29	Gene KIF23	MKLP-1, KNSL5, MKLP1, CHO1, KIF23	kinesin family member 23	NM_004856, NM_138555, hCT2288962.0, hCT31032.3	204709_s_at, 244427_at	NP_004847.2, NP_612565.1, EAW77841.1, EAW77842.1
GeneID.6176	RPLP1	15	69,745,159	69,747,884	2,725	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2067, 2_A375_pNL97_plus_lncRNA_AR..1..2916, 4_A375_EGR1..1..2573	121, 153, 25	in gene, in gene, in gene	1	1	1	19	26	29	1	4_A375_EGR1..1	29	Gene RPLP1	RPLP1, MGC5215, LP1, RPP1, P1, FLJ27448	ribosomal protein, large, P1	NM_001003, NM_213725, hCT1971216.1, hCT2355773.0, hCT30044.3	200763_s_at, 244191_at	NP_000994.1, NP_998890.1, EAW77843.1, EAW77844.1, EAW77845.1
GeneID.7090	TLE3	15	70,340,543	70,390,256	49,713	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2920	366	in gene	0	1	0	12	17	7	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TLE3	KIAA1547, HsT18976, ESG, GRG3, FLJ39460, TLE3, ESG3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	NM_005078, NM_020908, NM_001105192, hCT2288619.0, hCT2288620.0, hCT2288623.0, hCT30041.3	206472_s_at, 212769_at, 212770_at, 226340_at	NP_005069.2, NP_065959.1, NP_001098662.1, EAW77848.1, EAW77849.1, EAW77850.1, EAW77851.1
GeneID.55323	LARP6	15	71,123,689	71,146,498	22,809	-	1	4_A375_EGR1..1..2576	-5742	upstream	0	0	1	4	10	19	1	4_A375_EGR1..1	19	Gene LARP6	FLJ11196, ACHN, LARP6	La ribonucleoprotein domain family, member 6	NM_197958, NM_018357, hCT2355701.0, hCT31906.2	218651_s_at, 236565_s_at	NP_932062.1, NP_060827.2, EAW77860.1, EAW77861.1
GeneID.56906	THAP10	15	71,173,681	71,184,753	11,072	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2077	-463	upstream	1	0	0	16	20	12	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene THAP10	THAP10	THAP domain containing 10	NM_020147, hCT31903.3	219596_at	NP_064532.1, EAW77863.1
GeneID.54839	LRRC49	15	71,184,987	71,342,436	157,449	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2077	229	in gene	1	0	0	16	20	12	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene LRRC49	LRRC49, FLJ20156	leucine rich repeat containing 49	NM_017691, hCT2355693.0, hCT2355694.0, hCT2355695.0, hCT31904.2	219338_s_at	NP_060161.2, EAW77865.1, EAW77864.1, EAW77866.1, EAW77867.1
GeneID.79875	THSD4	15	71,433,788	72,075,722	641,934	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2926	154052	in gene	0	1	0	12	21	5	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene THSD4	FVSY9334, PRO34005, FLJ13710, ADAMTSL6, THSD4	thrombospondin, type I, domain containing 4	NM_024817, hCT1955476.1, hCT2290602.0, hCT2290605.0	219153_s_at, 222835_at, 226506_at, 234323_at	NP_079093.2, EAW77874.1, EAW77873.1, EAW77875.1
GeneID.5315	PKM2	15	72,491,370	72,523,684	32,314	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2078, 2_A375_pNL97_plus_lncRNA_AR..1..2927, 4_A375_EGR1..1..2577	164, 356, 226	in gene, in gene, in gene	1	1	1	17	17	24	1	4_A375_EGR1..1	24	Gene PKM2	TCB, PKM, THBP1, PK3, MGC3932, PKM2, OIP3, CTHBP	pyruvate kinase, muscle	NM_002654, NM_182470, NM_182471, hCT2291824.0, hCT2291825.0, hCT2291827.0, hCT2291828.0, hCT2291829.0, hCT2291830.0, hCT2355762.0	201251_at	NP_002645.3, NP_872270.1, NP_872271.1, EAW77884.1, EAW77885.1, EAW77887.1, EAW77886.1, EAW77888.1, EAW77889.1, EAW77890.1
GeneID.56965	PARP6	15	72,533,522	72,563,628	30,106	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2078, 1_A375_pNL7_minus_lncRNA_AR..1..2079, 2_A375_pNL97_plus_lncRNA_AR..1..2927, 2_A375_pNL97_plus_lncRNA_AR..1..2928, 4_A375_EGR1..1..2577, 4_A375_EGR1..1..2578	40108, -1568, 40300, -1556, 40172, -1012	downstream, upstream, downstream, upstream, downstream, upstream	1	1	1	67.5	89.5	20.5	2	2_A375_pNL97_plus_lncRNA_AR..1	122	Gene PARP6	pART17, MGC131971, PARP6	poly (ADP-ribose) polymerase family, member 6	NM_020214, hCT1951320.1, hCT2291808.0, hCT2291813.0, hCT2291815.0, hCT2291816.0, hCT2291818.0, hCT2291819.0, hCT2291820.0, hCT31723.3	219639_x_at, 232683_s_at, 234710_s_at	NP_064599.2, EAW77891.1, EAW77892.1, EAW77893.1, EAW77894.1, EAW77899.1, EAW77895.1, EAW77896.1, EAW77897.1, EAW77898.1
GeneID.60677	BRUNOL6	15	72,577,068	72,612,525	35,457	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2080, 1_A375_pNL7_minus_lncRNA_AR..1..2081, 2_A375_pNL97_plus_lncRNA_AR..1..2929	445, -211, 397	in gene, upstream, in gene	1	1	0	26	27	12	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene BRUNOL6	BRUNOL6, CELF6	CUGBP, Elav-like family member 6	NM_052840, NM_001172684, NM_001172685, hCT2355688.0, hCT31720.3	227775_at	NP_443072.3, NP_001166155.1, NP_001166156.1, EAW77900.1, EAW77901.1
GeneID.3073	HEXA	15	72,635,778	72,668,520	32,742	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2082, 2_A375_pNL97_plus_lncRNA_AR..1..2930	104, 104	in gene, in gene	1	1	0	26	29	12	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene HEXA	MGC99608, HEXA, TSD	hexosaminidase A (alpha polypeptide)	NM_000520, hCT31718.4	1556426_at, 201765_s_at, 215155_at	NP_000511.2, EAW77902.1
GeneID.80072	C15orf34	15	72,668,454	72,671,129	2,675	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2082, 2_A375_pNL97_plus_lncRNA_AR..1..2930	-36, -36	upstream, upstream	1	1	0	26	29	12	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene C15orf34	FLJ13315, C15orf34	chromosome 15 open reading frame 34	NR_027262, hCT1826479.3	220718_at	EAW77903.1
GeneID.25820	ARIH1	15	72,766,667	72,878,896	112,229	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2931, 2_A375_pNL97_plus_lncRNA_AR..1..2932	-139, 725	upstream, in gene	0	1	0	12	23	15	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ARIH1	HARI, UBCH7BP, FLJ20329, ARI, ARIH1, DKFZp686O13120, FLJ93116, HHARI	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	NM_005744, hCT2290634.0, hCT30037.3	201876_at, 201879_at, 201680_at, 201881_s_at	NP_005735.2, EAW77908.1, EAW77907.1
GeneID.585	BBS4	15	72,978,526	73,030,817	52,291	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2933	162	in gene	0	1	0	15	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene BBS4	BBS4	Bardet-Biedl syndrome 4	NM_033028, hCT1958156.1, hCT31722.3	212744_at, 212745_s_at	NP_149017.2, EAW77913.1, EAW77912.1
GeneID.83440	ADPGK	15	73,043,708	73,076,126	32,418	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2083, 2_A375_pNL97_plus_lncRNA_AR..1..2934	94, 14	in gene, in gene	1	1	0	25	31	14	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene ADPGK	ADP-GK, DKFZp434B195, ADPGK, 2610017G09Rik	ADP-dependent glucokinase	NM_031284, NR_023318, NR_023319, hCT1826480.4, hCT1962439.1, hCT1962441.1, hCT2355728.0, hCT2355729.0, hCT2355730.0, hCT2355731.0, hCT2355732.0	220980_s_at, 224455_s_at	NP_112574.3, EAW77914.1, EAW77917.1, EAW77919.1, EAW77920.1, EAW77921.1, EAW77915.1, EAW77916.1, EAW77918.1
GeneID.4756	NEO1	15	73,344,825	73,597,547	252,722	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2935	-441	upstream	0	1	0	6	19	9	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene NEO1	HsT17534, NEO1, IGDCC2, DKFZp547B146, DKFZp547A066, NGN	neogenin 1	NM_002499, NM_001172624, NM_001172623, hCT2289444.0, hCT2289445.0	204321_at, 225270_at, 229877_at	NP_002490.2, NP_001166095.1, NP_001166094.1, EAW77923.1, EAW77924.1
GeneID.10021	HCN4	15	73,612,200	73,661,605	49,405	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2084, 2_A375_pNL97_plus_lncRNA_AR..1..2936, 4_A375_EGR1..1..2579	22389, 22389, 29877	in gene, in gene, in gene	1	1	1	12	20.5	14	2	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene HCN4	HCN4, SSS2	hyperpolarization activated cyclic nucleotide-gated potassium channel 4	NM_005477, hCT32091.3	206946_at	NP_005468.1, EAW77925.1
GeneID.27020	NPTN	15	73,852,344	73,925,753	73,409	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2937	601	in gene	0	1	0	7	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene NPTN	DKFZp686L2477, MGC102805, GP65, np55, SDFR1, np65, NPTN, GP55, SDR1	neuroplastin	NM_012428, NM_017455, NM_001161363, NM_001161364, hCT1971214.1, hCT32089.3, hCT32090.3	202228_s_at	NP_036560.1, NP_059429.1, NP_001154835.1, NP_001154836.1, EAW77930.1, EAW77932.1, EAW77931.1
GeneID.161514	TBC1D21	15	74,165,968	74,181,555	15,587	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2940	24379	downstream	0	1	0	16	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TBC1D21	TBC1D21, MGC34741	TBC1 domain family, member 21	NM_153356, hCT2355708.0, hCT32096.3	231475_at	NP_699187.1, EAW77936.1, EAW77937.1
GeneID.9399	STOML1	15	74,275,560	74,284,635	9,075	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2087, 2_A375_pNL97_plus_lncRNA_AR..1..2941	-101, -101	upstream, upstream	1	1	0	108	111	7	1	2_A375_pNL97_plus_lncRNA_AR..1	111	Gene STOML1	STOML1, hUNC-24, SLP-1, STORP, FLJ36370	stomatin (EPB72)-like 1	NM_004809, hCT1963258.1, hCT1963259.1, hCT1971254.1, hCT2355698.0, hCT2355699.0, hCT32087.2	1556320_at, 204701_s_at, 33736_at	NP_004800.2, EAW77944.1, EAW77940.1, EAW77941.1, EAW77942.1, EAW77945.1, EAW77943.1
GeneID.5371	PML	15	74,287,014	74,340,160	53,146	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2087, 2_A375_pNL97_plus_lncRNA_AR..1..2941, 4_A375_EGR1..1..2581, 4_A375_EGR1..1..2582	-2278, -2278, 37978, 50138	upstream, upstream, in gene, in gene	1	1	1	42.33	42.33	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	111	Gene PML	TRIM19, RNF71, PML, MYL, PP8675	promyelocytic leukemia	NM_033238, NM_033249, NM_033246, NM_002675, NM_033247, NM_033239, NM_033240, NM_033250, NM_033244, hCT1962499.3, hCT1971444.1	206503_x_at, 209640_at, 210362_x_at, 211013_x_at, 211588_s_at, 211589_at, 235508_at, 239582_at	NP_150241.2, NP_150252.1, NP_150242.1, NP_150249.1, NP_002666.1, NP_150250.2, NP_150247.2, NP_150243.2, NP_150253.2, EAW77946.1, EAW77947.1
GeneID.283731	LOC283731	15	74,418,714	74,421,619	2,905	-	3	4_A375_EGR1..1..2583, 4_A375_EGR1..1..2584, 4_A375_EGR1..1..2585	1043, -3629, -4421	in gene, upstream, upstream	0	0	1	7.33	10.33	17.67	3	4_A375_EGR1..1	21	Gene LOC283731		hypothetical LOC283731	NR_027073	1560723_at	
GeneID.57611	ISLR2	15	74,421,715	74,429,143	7,428	+	3	4_A375_EGR1..1..2583, 4_A375_EGR1..1..2584, 4_A375_EGR1..1..2585	-1139, 3533, 4325	upstream, in gene, in gene	0	0	1	7.33	10.33	17.67	3	4_A375_EGR1..1	21	Gene ISLR2	ISLR2, KIAA1465	immunoglobulin superfamily containing leucine rich repeat 2	NM_001130136, NM_020851, NM_001130137, NM_001130138, hCT1774546.2, hCT1955657.1, hCT2292056.0	232208_at	NP_001123608.1, NP_065902.1, NP_001123609.1, NP_001123610.1, EAW99359.1, EAW99361.1, EAW99360.1
GeneID.3671	ISLR	15	74,466,087	74,469,212	3,125	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2942	5945	downstream	0	1	0	18	23	12	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ISLR	ISLR, MGC102816, HsT17563	immunoglobulin superfamily containing leucine rich repeat	NM_005545, NM_201526, hCT1777105.2, hCT2348894.0	207191_s_at	NP_005536.1, NP_958934.1, EAW99357.1, EAW99358.1
GeneID.64220	STRA6	15	74,471,807	74,501,371	29,564	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2942, 2_A375_pNL97_plus_lncRNA_AR..1..2943, 4_A375_EGR1..1..2586	29339, 6059, 18075	in gene, in gene, in gene	0	1	1	12	16	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene STRA6	FLJ12541, PP14296, STRA6, MCOPS9	stimulated by retinoic acid gene 6 homolog (mouse)	NM_022369, NM_001142617, NM_001142618, NM_001142619, NM_001142620, hCT2291065.0, hCT2291067.0, hCT2291068.0, hCT2358319.0	1569334_at, 1569335_a_at, 221701_s_at	NP_071764.3, NP_001136089.1, NP_001136090.1, NP_001136091.1, NP_001136092.1, EAW99356.1, EAW99353.1, EAW99354.1, EAW99355.1
GeneID.80125	CCDC33	15	74,528,667	74,628,482	99,815	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2088, 1_A375_pNL7_minus_lncRNA_AR..1..2089, 2_A375_pNL97_plus_lncRNA_AR..1..2944, 2_A375_pNL97_plus_lncRNA_AR..1..2945, 4_A375_EGR1..1..2587, 4_A375_EGR1..1..2588	28917, 55333, 28669, 55461, 78597, 103205	in gene, in gene, in gene, in gene, in gene, downstream	1	1	1	18.5	22	13.25	4	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene CCDC33	FLJ23168, MGC34145, FLJ32855, CCDC33, CT61	coiled-coil domain containing 33	NM_182791, NM_025055, hCT2292067.0, hCT2292068.0, hCT2292071.0, hCT2358299.0, hCT32080.2	1563090_at, 220908_at	NP_877592.2, NP_079331.3, EAW99343.1, EAW99344.1, EAW99345.1, EAW99346.1, EAW99347.1
GeneID.1583	CYP11A1	15	74,630,103	74,660,081	29,978	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2946, 4_A375_EGR1..1..2588, 4_A375_EGR1..1..2589	-6143, 28209, -6319	upstream, in gene, upstream	0	1	1	8	10	15.5	2	4_A375_EGR1..1	18	Gene CYP11A1	CYP11A, P450SCC, CYP11A1	cytochrome P450, family 11, subfamily A, polypeptide 1	NM_000781, NM_001099773, hCT2291083.1, hCT32075.3	204309_at	NP_000772.2, NP_001093243.1, EAW99341.1, EAW99342.1
GeneID.729739	LOC729739	15	74,646,797	74,656,961	10,164	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2946, 4_A375_EGR1..1..2589	19427, 19603	downstream, downstream	0	1	1	8	14	16	1	4_A375_EGR1..1	16	Gene LOC729739		hypothetical LOC729739	XR_111533, XR_109164, XR_114671		
GeneID.8482	SEMA7A	15	74,701,630	74,726,299	24,669	-	1	4_A375_EGR1..1..2590	23435	in gene	0	0	1	7	8	15	1	4_A375_EGR1..1	15	Gene SEMA7A	JMH, CDw108, MGC126696, SEMAK1, H-Sema-L, SEMAL, SEMA7A, H-SEMA-K1, MGC126692, CD108	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	NM_003612, NM_001146029, NM_001146030, hCT32073.3	210063_at	NP_003603.1, NP_001139501.1, NP_001139502.1, EAW99340.1

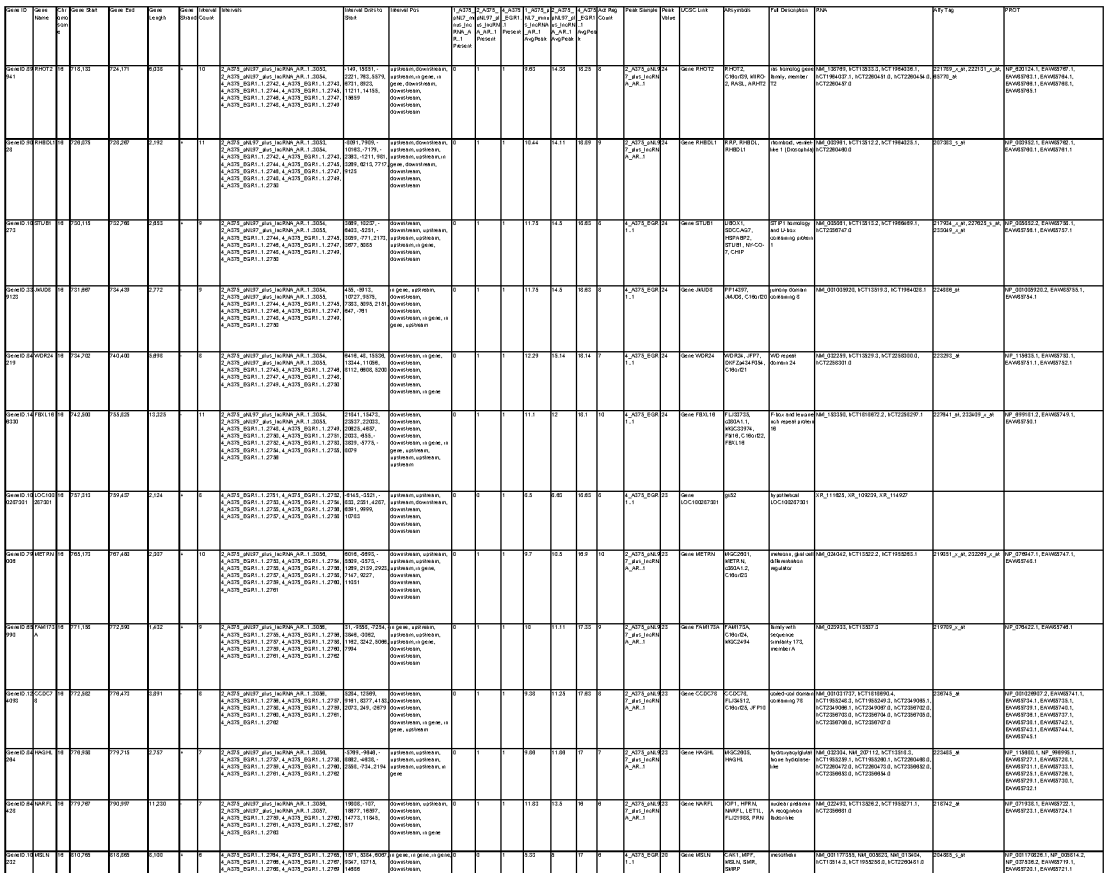
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:10620	ARID3B	15	74,833,548	74,890,472	56,924	+	2	4_A375_EGR1..1..2591, 4_A375_EGR1..1..2592	5092, 56604	in gene, downstream	0	0	1	13.5	13	19	2	4_A375_EGR1..1	19	Gene ARID3B	BDP, ARID3B, DRIL2	AT rich interactive domain 3B (BRIGHT-like)	NM_006465, hCT2358296.0, hCT32072.2	218964_at	NP_006456.1, EAW99326.1, EAW99327.1
GeneID:1198	CLK3	15	74,900,713	74,922,542	21,829	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2090, 4_A375_EGR1..1..2592	7351, -6361	in gene, upstream	1	0	1	15	13.5	16	2	4_A375_EGR1..1	19	Gene CLK3	PHCLK3, CLK3, PHCLK3/152, FLJ22858	CDC-like kinase 3	NM_003992, NM_001130028, hCT1777101.1, hCT1952449.0, hCT1952450.0, hCT1952451.1, hCT1952452.0, hCT1952453.1	202140_s_at	NP_003983.2, NP_001123500.1, EAW99320.1, EAW99321.1, EAW99322.1, EAW99323.1, EAW99324.1, EAW99325.1
GeneID:80153	EDC3	15	74,922,899	74,988,386	65,487	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2091	66	in gene	1	0	0	26	15	14	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene EDC3	FLJ31777, FLJ21128, YJEFN2, YJDC, LSM16, EDC3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	NM_025083, NM_001142443, NM_001142444, hCT2291067.0, hCT2291068.0, hCT2291069.0, hCT2358317.0	219207_at, 226042_at	NP_079359.2, NP_001135915.1, NP_001135916.1, EAW99316.1, EAW99317.1, EAW99319.1, EAW99318.1
GeneID:1543	CYP1A1	15	75,011,883	75,017,877	5,994	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2947, 2_A375_pNL97_plus_lncRNA_AR..1..2948, 4_A375_EGR1..1..2593	1461, -1099, -411	in gene, upstream, upstream	0	1	1	14.5	23	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene CYP1A1	AHRR, P450DX, CYP1A1, AHH, CP11, P450-C, CYP1, P1-450	cytochrome P450, family 1, subfamily A, polypeptide 1	NM_000499, hCT2343624.0, hCT29989.4	205749_at	NP_000490.1, EAW99315.1, EAW99314.1
GeneID:594855	CPLX3	15	75,118,951	75,124,136	5,185	+	1	4_A375_EGR1..1..2594	12857	downstream	0	0	1	7	5	16	1	4_A375_EGR1..1	16	Gene CPLX3	CPLX3, FLJ00250, CPX-III, CPXIII, DKFZp434E1719, FLJ00167, FLJ13993, NBla11589	complexin 3	NM_001030005, hCT2292101.0, hCT32078.2	219775_s_at	NP_001025176.1, EAW99307.1, EAW99306.1
GeneID:25989	ULK3	15	75,128,459	75,135,552	7,093	-	2	4_A375_EGR1..1..2594, 4_A375_EGR1..1..2595	3744, -256	in gene, upstream	0	0	1	10.5	9.5	19.5	2	4_A375_EGR1..1	23	Gene ULK3	DKFZp434C131, ULK3, FLJ90566	unc-51-like kinase 3 (C. elegans)	NM_001099436	225087_at	NP_001092906.1
GeneID:10066	SCAMP2	15	75,137,197	75,165,670	28,473	-	2	4_A375_EGR1..1..2594, 4_A375_EGR1..1..2595	33882, 29882	downstream, downstream	0	0	1	10.5	9.5	19.5	2	4_A375_EGR1..1	23	Gene SCAMP2	SCAMP2	secretory carrier membrane protein 2	NM_005697, hCT2358295.0, hCT32071.3	218143_s_at, 224921_at	NP_005688.2, EAW99299.1, EAW99300.1
GeneID:4351	MPI	15	75,182,410	75,190,565	8,155	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2092, 1_A375_pNL7_minus_lncRNA_AR..1..2093, 2_A375_pNL97_plus_lncRNA_AR..1..2949, 4_A375_EGR1..1..2596	-10, 17161, 16962, 66	upstream, downstream, downstream, in gene	1	1	1	17.5	18.5	17	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene MPI	MPI, PMI, PMI1, CDG1B, FLJ39201	mannose phosphate isomerase	NM_002435, hCT2294520.0, hCT2294522.0, hCT2294523.0, hCT2294526.0	202472_at, 230524_at	NP_002426.1, EAW99295.1, EAW99296.1, EAW99297.1, EAW99298.1
GeneID:57184	C15orf17	15	75,192,328	75,199,462	7,134	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2092, 1_A375_pNL7_minus_lncRNA_AR..1..2093, 2_A375_pNL97_plus_lncRNA_AR..1..2949, 4_A375_EGR1..1..2596	17062, -109, 70, 16966	downstream, upstream, in gene, downstream	1	1	1	17.5	18.5	17	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene C15orf17	FLJ00005, C15orf17	chromosome 15 open reading frame 17	NM_020447, hCT1777494.2, hCT1953012.2, hCT2346818.0, hCT2346819.0, hCT2346820.0, hCT2358290.0	224798_s_at, 224804_s_at, 224805_s_at	NP_065180.1, EAW99291.1, EAW99289.1, EAW99292.1, EAW99293.1, EAW99294.1, EAW99290.1
GeneID:9377	COX5A	15	75,212,616	75,230,495	17,879	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2094, 2_A375_pNL97_plus_lncRNA_AR..1..2950	148, 31	in gene, in gene	1	1	0	20	19	14	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene COX5A	VA, COX, COX-VA, COX5A	cytochrome c oxidase subunit Va	NM_004255, hCT2292220.0, hCT2292221.0	203663_s_at, 217451_at, 229426_at	NP_004246.2, EAW99287.1, EAW99288.1
GeneID:54913	RPP25	15	75,247,443	75,249,775	2,332	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2095, 2_A375_pNL97_plus_lncRNA_AR..1..2951, 4_A375_EGR1..1..2597, 4_A375_EGR1..1..2598	-113, 847, 1119, -1745	upstream, in gene, in gene, upstream	1	1	1	12.5	11.5	18.5	2	4_A375_EGR1..1	21	Gene RPP25	FLJ20374, RPP25	ribonuclease P/MRP 25kDa subunit	NM_017793, hCT1643355.3, hCT2292218.0	219143_s_at, 223415_at	NP_060263.2, EAW99285.1, EAW99286.1
GeneID:192683	SCAMP5	15	75,287,876	75,313,836	25,960	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2097, 2_A375_pNL97_plus_lncRNA_AR..1..2953, 2_A375_pNL97_plus_lncRNA_AR..1..2954, 4_A375_EGR1..1..2599, 4_A375_EGR1..1..2600	-180, -198, 28124, 2238, 28124	upstream, upstream, downstream, in gene, downstream	1	1	1	12.67	16.67	14.67	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SCAMP5	DKFZp686L1799, MGC24969, SCAMP5	secretory carrier membrane protein 5	NM_001178111, NM_001178112, NM_138967, NR_033660, hCT13184.2, hCT2294530.0, hCT2294532.0, hCT2358320.0, hCT2358321.0, hCT2358322.0, hCT2358323.0, hCT2358324.0	212699_at, 234586_at	NP_001171582.1, NP_001171583.1, NP_620417.1, EAW99277.1, EAW99278.1, EAW99279.1, EAW99280.1, EAW99281.1, EAW99282.1, EAW99283.1, EAW99284.1
GeneID:60490	PPCDC	15	75,315,927	75,343,067	27,140	+	3	2_A375_pNL97_plus_lncRNA_AR..1..2954, 2_A375_pNL97_plus_lncRNA_AR..1..2955, 4_A375_EGR1..1..2600	73, 20137, 73	in gene, in gene, in gene	0	1	1	15	20	13	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PPCDC	MDS018, FLJ14585, PPCDC	phosphopantothenoylcysteine decarboxylase	NM_021823, hCT13010.3, hCT1961703.1	219066_at	NP_068595.3, EAW99276.1, EAW99275.1
GeneID:56905	C15orf39	15	75,494,221	75,504,510	10,289	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2957	147	in gene	0	1	0	13	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C15orf39	FLJ46337, C15orf39, DKFZp434H132, MGC117209	chromosome 15 open reading frame 39	NM_015492, hCT2294539.0, hCT2294540.0	204494_s_at, 204495_s_at, 215087_at	NP_056307.2, EAW99272.1, EAW99273.1
GeneID:54939	COMMD4	15	75,628,374	75,632,614	4,240	+	2	4_A375_EGR1..1..2603, 4_A375_EGR1..1..2604	122, 12818	in gene, downstream	0	0	1	8.5	14.5	17	2	4_A375_EGR1..1	18	Gene COMMD4	FLJ20452, COMMD4	COMM domain containing 4	NM_017828, hCT2294551.0, hCT2294552.0, hCT2294554.0	208441_s_at, 209132_s_at, 209133_s_at	NP_060298.2, EAW99262.1, EAW99261.1, EAW99263.1
GeneID:79661	NEIL1	15	75,639,331	75,647,588	8,257	+	1	4_A375_EGR1..1..2604	1661	in gene	0	0	1	7	14	18	1	4_A375_EGR1..1	18	Gene NEIL1	FLJ22402, hFPG1, FPG1, NEIL1, NEI1	nei endonuclease VIII-like 1 (E. coli)	NM_024608, hCT1777482.3, hCT1962650.1, hCT1962651.1, hCT1962653.1, hCT2358313.0, hCT2358314.0	219396_s_at, 241477_at	NP_078884.2, EAW99255.1, EAW99256.1, EAW99257.1, EAW99258.1, EAW99260.1, EAW99259.1
GeneID:693216	MIR631	15	75,645,952	75,646,026	74	-	1	4_A375_EGR1..1..2604	5034	downstream	0	0	1	7	14	18	1	4_A375_EGR1..1	18	Gene MIR631	MIRN631, hsa-mir-631, MIR631	microRNA 631	NR_030360		
GeneID:4123	MAN2C1	15	75,648,133	75,660,941	12,808	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2958, 4_A375_EGR1..1..2604, 4_A375_EGR1..1..2605	621, 19949, 45	in gene, downstream, in gene	0	1	1	13.5	18	22	2	4_A375_EGR1..1	26	Gene MAN2C1	MAN2C1, MANA6, MANA, MGC87979, MANA1, DKFZp686E23167	mannosidase, alpha, class 2C, member 1	NM_006715, hCT1777488.2, hCT1962646.1, hCT2358312.0	203668_at, 238069_at, 238230_x_at	NP_006706.2, EAW99254.1, EAW99252.1, EAW99253.1
GeneID:25942	SIN3A	15	75,661,720	75,748,124	86,404	-	3	2_A375_pNL97_plus_lncRNA_AR..1..2958, 4_A375_EGR1..1..2605, 4_A375_EGR1..1..2606	87804, 87228, 252	downstream, downstream, in gene	0	1	1	13.5	14.5	25	2	4_A375_EGR1..1	26	Gene SIN3A	SIN3A, FLJ90319, DKFZp434K2235, KIAA0700	SIN3 homolog A, transcription regulator (yeast)	NM_001145357, NM_001145358, NM_015477, hCT2292207.0, hCT2292208.1, hCT2292209.1	225135_at, 236189_at	NP_001138829.1, NP_001138830.1, NP_056292.1, EAW99249.1, EAW99250.1, EAW99251.1
GeneID:10073	SNUPN	15	75,890,424	75,918,719	28,295	-	2	2_A375_pNL97_plus_lncRNA_AR..1..2959, 4_A375_EGR1..1..2607	735, 863	in gene, in gene	0	1	1	11	25	16	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene SNUPN	Snurportin1, SNUPN, RNUT1, KPNBL	snurportin 1	NM_005701, NM_001042581, NM_001042588, hCT2292202.0, hCT2292203.0	207438_s_at	NP_005692.1, NP_001036046.1, NP_001036053.1, EAW99245.1, EAW99246.1
GeneID:55272	IMP3	15	75,931,426	75,932,664	1,238	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2098, 4_A375_EGR1..1..2608	456, -232	in gene, upstream	1	0	1	18	19	14	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene IMP3	MRPS4, BRMS2, C15orf12, DKFZp586L0118, FLJ10968, IMP3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	NM_018285	221688_s_at	NP_060755.1
GeneID:257364	SNX33	15	75,941,346	75,950,966	9,620	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2098, 4_A375_EGR1..1..2608	-9140, -8452	upstream, upstream	1	0	1	18	19	14	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene SNX33	SNX33, SNX30, MGC32065, SH3PXD3C, SH3PX3	sorting nexin 33	NM_153271, hCT1786890.1	227151_at	NP_695003.1, EAW99243.1
GeneID:1464	CSPG4	15	75,966,663	76,005,189	38,526	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2099, 1_A375_pNL7_minus_lncRNA_AR..1..2100, 2_A375_pNL97_plus_lncRNA_AR..1..2960, 2_A375_pNL97_plus_lncRNA_AR..1..2961, 2_A375_pNL97_plus_lncRNA_AR..1..2962, 4_A375_EGR1..1..2609, 4_A375_EGR1..1..2610	16437, -731, 17525, 15781, -747, 30101, 3317	in gene, upstream, in gene, in gene, upstream, in gene, in gene	1	1	1	12.4	15.4	12.6	5	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CSPG4	CSPG4, HMW-MAA, MCSPG, MCSP, MSK16, NG2, MEL-CSPG	chondroitin sulfate proteoglycan 4	NM_001897, hCT1777484.2, hCT2292200.0	204736_s_at, 214297_at	NP_001888.2, EAW99239.1, EAW99240.1
GeneID:161753	ODF3L1	15	76,016,319	76,020,027	3,708	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2962	-10363	upstream	0	1	0	18	24	9	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ODF3L1	ODF3L1, MGC48988	outer dense fiber of sperm tails 3-like 1	NM_175881, hCT1777492.1	236245_at	NP_787077.1, EAW99238.1
GeneID:92912	UBE2Q2	15	76,135,622	76,193,388	57,766	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2101, 2_A375_pNL97_plus_lncRNA_AR..1..2963, 4_A375_EGR1..1..2612	48778, 60666, 60538	in gene, downstream, downstream	1	1	1	16.5	15	10.5	2	4_A375_EGR1..1	20	Gene UBE2Q2	UBE2Q2, DKFZp762C143	ubiquitin-conjugating enzyme E2Q family member 2	NM_173469, NM_001145335, hCT2294568.0, hCT2294569.0	224747_at	NP_775740.1, NP_001138807.1, EAW99233.1, EAW99234.1
GeneID:26263	FBXO22	15	76,196,200	76,226,944	30,744	+	2	2_A375_pNL97_plus_lncRNA_AR..1..2963, 4_A375_EGR1..1..2612	66, -40	in gene, upstream	0	1	1	18	18	20	1	4_A375_EGR1..1	20	Gene FBXO22	FISTC1, FLJ13986, MGC31799, FBX22, FBXO22	F-box protein 22	NM_012170, NM_147188, hCT1961788.2, hCT1961787.2, hCT2358315.0, hCT29550.4	219638_at, 225734_at, 225736_at, 225737_s_at	NP_036302.1, NP_671717.1, EAW99229.1, EAW99230.1, EAW99231.1, EAW99232.1
GeneID:145957	NRG4	15	76,234,314	76,304,785	70,471	-	1	4_A375_EGR1..1..2613	35281	in gene	0	0	1	4	5	14	1	4_A375_EGR1..1	14	Gene NRG4	NRG4, HRG4, DKFZp779N0541, DKFZp779N1944	neuregulin 4	NM_138573, hCT1953661.2, hCT2346912.0	242426_at	NP_612640.1, EAW99226.1, EAW99227.1
GeneID:2108	ETFA	15	76,508,628	76,603,810	95,182	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2102, 2_A375_pNL97_plus_lncRNA_AR..1..2964, 4_A375_EGR1..1..2614	226, 226, 96	in gene, in gene, in gene	1	1	1	16	19	22	1	4_A375_EGR1..1	22	Gene ETFA	GA2, EMA, MADD, ETFA	electron-transfer-flavoprotein, alpha polypeptide	NM_000126, NM_001127716, hCT1961602.1, hCT30665.2	201931_at	NP_000117.1, NP_001121188.1, EAW99221.1, EAW99222.1
GeneID:64843	ISL2	15	76,629,147	76,634,816	5,669	+	1	4_A375_EGR1..1..2615	3045	in gene	0	0	1	4	12	20	1	4_A375_EGR1..1	20	Gene ISL2	FLJ10160, ISL2	ISL LIM homeobox 2	NM_145805, hCT32063.3	232352_at	NP_665804.1, EAW99220.1
GeneID:49855	SCAPER	15	76,640,526	77,176,217	535,691	-	1	4_A375_EGR1..1..2615	544025	downstream	0	0	1	4	12	20	1	4_A375_EGR1..1	20	Gene SCAPER	MSTP063, KIAA1454, ZNF291, SCAPER, FLJ31533, FLJ31953, FLJ46212, Zfp291	S-phase cyclin A-associated protein in the ER	NM_020843, NM_001145923, hCT2290916.0, hCT2290919.0, hCT32064.4	209741_x_at, 215848_at, 216399_s_at	NP_065894.2, NP_001139395.1, EAW99217.1, EAW99218.1, EAW99219.1
GeneID:5955	RCN2	15	77,223,962	77,242,601	18,639	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2103, 2_A375_pNL97_plus_lncRNA_AR..1..2965	23270, 23318	downstream, downstream	1	1	0	17	14	3	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene RCN2	ERC-55, RCN2, E6BP, TCBP49, ERC55	reticulocalbin 2, EF-hand calcium binding domain	NM_002902, hCT32061.2	201485_s_at, 201486_at	NP_002893.1, EAW99216.1
GeneID:100506704	LOC100506704	15	77,241,494	77,247,823	6,329	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2103, 2_A375_pNL97_plus_lncRNA_AR..1..2965	591, 543	in gene, in gene	1	1	0	17	14	3	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene LOC100506704		hypothetical LOC100506704	XR_111535, XR_109166, XR_114870		
GeneID:9051	PSTPIP1	15	77,287,465	77,329,671	42,206	+	1	4_A375_EGR1..1..2617	40439	in gene	0	0	1	6	14	16	1	4_A375_EGR1..1	16	Gene PSTPIP1	H-PIP, CD2BP1, CD2BP1S, PSTPIP, PSTPIP1, PAPAS, CD2BP1L	proline-serine-threonine phosphatase interacting protein 1	NM_003978, hCT1961811.1, hCT1967867.1, hCT32066.2	211178_s_at	NP_003969.2, EAW99215.1, EAW99213.1, EAW99214.1
GeneID:10099	TSPAN3	15	77,336,359	77,363,570	27,211	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2104, 2_A375_pNL97_plus_lncRNA_AR..1..2966, 4_A375_EGR1..1..2617	18, 18, 35666	in gene, in gene, downstream	1	1	1	15.5	16.5	9	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene TSPAN3	TM4-A, TSPAN-3, TSPAN3, TM4SF8	tetraspanin 3	NM_005724, NM_198902, NM_001168412, hCT2290907.1, hCT2290908.0, hCT32062.3	200972_at, 200973_s_at	NP_005715.1, NP_944492.1, NP_001161884.1, EAW99209.1, EAW99210.1, EAW99211.1
GeneID:10363	HMG20A	15	77,713,243	77,777,945	64,702	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2967	-907	upstream	0	1	0	4	17	3	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene HMG20A	HMG20A, HMGXB1, FLJ10739, HMGX1	high mobility group 20A	NM_018200, hCT1769190.1, hCT1953852.1, hCT2358308.0	218152_at	NP_060670.1, EAW99201.1, EAW99202.1, EAW99203.1
GeneID:84894	LINGO1	15	77,905,369	77,924,709	19,340	-	2	4_A375_EGR1..1..2619, 4_A375_EGR1..1..2620	17957, 16261	in gene, in gene	0	0	1	7.5	8	15.5	2	4_A375_EGR1..1	16	Gene LINGO1	LRRN6A, LINGO1, LERN1, UNQ201, FLJ14594, MGC17422	leucine rich repeat and Ig domain containing 1	NM_032808, hCT1645503.2, hCT2292560.0, hCT2292562.0, hCT2292563.0	227933_at	NP_116197.4, EAW99195.1, EAW99196.1, EAW99197.1, EAW99198.1
GeneID:91450	LOC91450	15	78,285,575	78,286,567	992	-	1	4_A375_EGR1..1..2623	5767	downstream	0	0	1	5	10	17	1	4_A375_EGR1..1	17	Gene LOC91450		hypothetical LOC91450	NR_026998	233418_at	
GeneID:23102	TBC1D2B	15	78,287,327	78,369,994	82,667	-	1	4_A375_EGR1..1..2623	89194	downstream	0	0	1	5	10	17	1	4_A375_EGR1..1	17	Gene TBC1D2B	KIAA1055, FLJ20166, TBC1D2B	TBC1 domain family, member 2B	NM_015079, NM_144572, hCT2344950.0, hCT2358309.0, hCT30181.3	212796_s_at, 215640_at, 215951_at, 230377_s_at	NP_055894.6, NP_653173.1, EAW99188.1, EAW99189.1, EAW99190.1
GeneID:3419	IDH3A	15	78,441,719	78,462,884	21,165	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2970	137	in gene	0	1	0	16	26	13	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene IDH3A	IDH3A		NM_005530, hCT2293520.0, hCT29234.3	202069_s_at, 202070_s_at	NP_005521.1, EAW99181.1, EAW99182.1
GeneID:80349	WDR61	15	78,575,577	78,591,940	16,363	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2107	68	in gene	1	0	0	15	14	9	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene WDR61	WDR61, SKI8, REC14	WD repeat domain 61	NM_025234, hCT2292529.0, hCT2292530.0, hCT2292532.0	215156_at, 221531_at, 221532_s_at, 232075_at, 237208_at	NP_079510.1, EAW99175.1, EAW99173.1, EAW99174.1
GeneID:3658	IREB2	15	78,730,518	78,793,798	63,280	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2108, 2_A375_pNL97_plus_lncRNA_AR..1..2971, 4_A375_EGR1..1..2624, 4_A375_EGR1..1..2625	-294, -278, -118, 69738	upstream, upstream, upstream, downstream	1	1	1	13.5	15	23.5	2	4_A375_EGR1..1	28	Gene IREB2	IREB2, ACO3, FLJ23381, IRP2, IRP2AD	iron-responsive element binding protein 2	NM_004136, hCT2292060.0, hCT2292062.0, hCT30184.3	1555476_at, 214666_x_at, 225892_at	NP_004127.1, EAW99170.1, EAW99169.1, EAW99171.1
GeneID:123688	AGPHD1	15	78,799,906	78,829,715	29,809	+	1	4_A375_EGR1..1..2625	350	in gene	0	0	1	10	11	19	1	4_A375_EGR1..1	19	Gene AGPHD1	AGPHD1	aminoglycoside phosphotransferase domain containing 1	NM_001013619, NM_001083612, hCT2358297.0, hCT30186.2	236150_at	NP_001013641.2, NP_001077081.1, EAW99167.1, EAW99166.1
GeneID:1136	CHRNA3	15	78,885,394	78,913,637	28,243	-	1	4_A375_EGR1..1..2626	933	in gene	0	0	1	4	3	17	1	4_A375_EGR1..1	17	Gene CHRNA3	NACHRA3, PAOD2, MGC104879, CHRNA3, LNCR2	cholinergic receptor, nicotinic, alpha 3	NM_000743, NM_001166694, hCT1769482.1, hCT1954748.1, hCT2290933.0, hCT2290934.0	210221_at, 211587_x_at, 211772_x_at	NP_000734.2, NP_001160166.1, EAW99156.1, EAW99157.1, EAW99158.1, EAW99159.1
GeneID:1143	CHRNB4	15	78,916,636	78,933,587	16,951	-	2	4_A375_EGR1..1..2626, 4_A375_EGR1..1..2627	20663, 307	downstream, in gene	0	0	1	5	5	18.5	2	4_A375_EGR1..1	20	Gene CHRNB4	CHRNB4		NM_000750	207516_at	NP_000741.1
GeneID:11173	ADAMTS7	15	79,051,545	79,103,773	52,228	-	2	4_A375_EGR1..1..2628, 4_A375_EGR1..1..2629	39997, 33277	in gene, in gene	0	0	1	5	6.5	12.5	2	4_A375_EGR1..1	14	Gene ADAMTS7	DKFZp434H204, ADAMTS-7, ADAMTS7, ADAM-TS 7, ADAM-TS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	NM_014272, hCT1640704.3, hCT2290940.0, hCT2290941.0, hCT2358316.0	220705_s_at, 220706_at, 226911_at	NP_055087.2, EAW99151.1, EAW99148.1, EAW99149.1, EAW99150.1
GeneID:5923	RASGRF1	15	79,252,289	79,383,215	130,926	-	1	4_A375_EGR1..1..2630	92615	in gene	0	0	1	7	5	17	1	4_A375_EGR1..1	17	Gene RASGRF1	GNRP, GRF55, CDC25L, RASGRF1, PP13187, CDC25, GRF1, H-GRF55	Ras protein-specific guanine nucleotide-releasing factor 1	NM_153815, NM_002891, NM_001145648, hCT14839.3, hCT2358310.0	1554992_at, 210550_s_at, 215688_at	NP_722522.1, NP_002882.3, NP_001139120.1, EAW99141.1, EAW99142.1
GeneID:729911	LOC729911	15	79,484,049	79,579,362	95,313	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2972	3266	in gene	0	1	0	21	25	7	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC729911		hypothetical LOC729911	XM_001130803, XM_001134184, XM_001719915		XP_001130803.2, XP_001134184.2, XP_001719967.2
GeneID:100506846	LOC100506846	15	79,505,439	79,576,156	70,717	-	1	2_A375_pNL97_plus_lncRNA_AR..1..2972	60	in gene	0	1	0	21	25	7	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC100506846		hypothetical protein LOC100506846	XM_003119613, XM_003118682, XM_003120615		XP_003119661.1, XP_003118710.1, XP_003120663.1
GeneID:390616	ANKRD34C	15	79,575,146	79,590,581	15,435	+	1	2_A375_pNL97_plus_lncRNA_AR..1..2972	950	in gene	0	1	0	21	25	7	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene ANKRD34C	FLJ45093, ANKRD34C, FLJ33346	ankyrin repeat domain 34C	NM_001146341	216073_at	NP_001139813.1



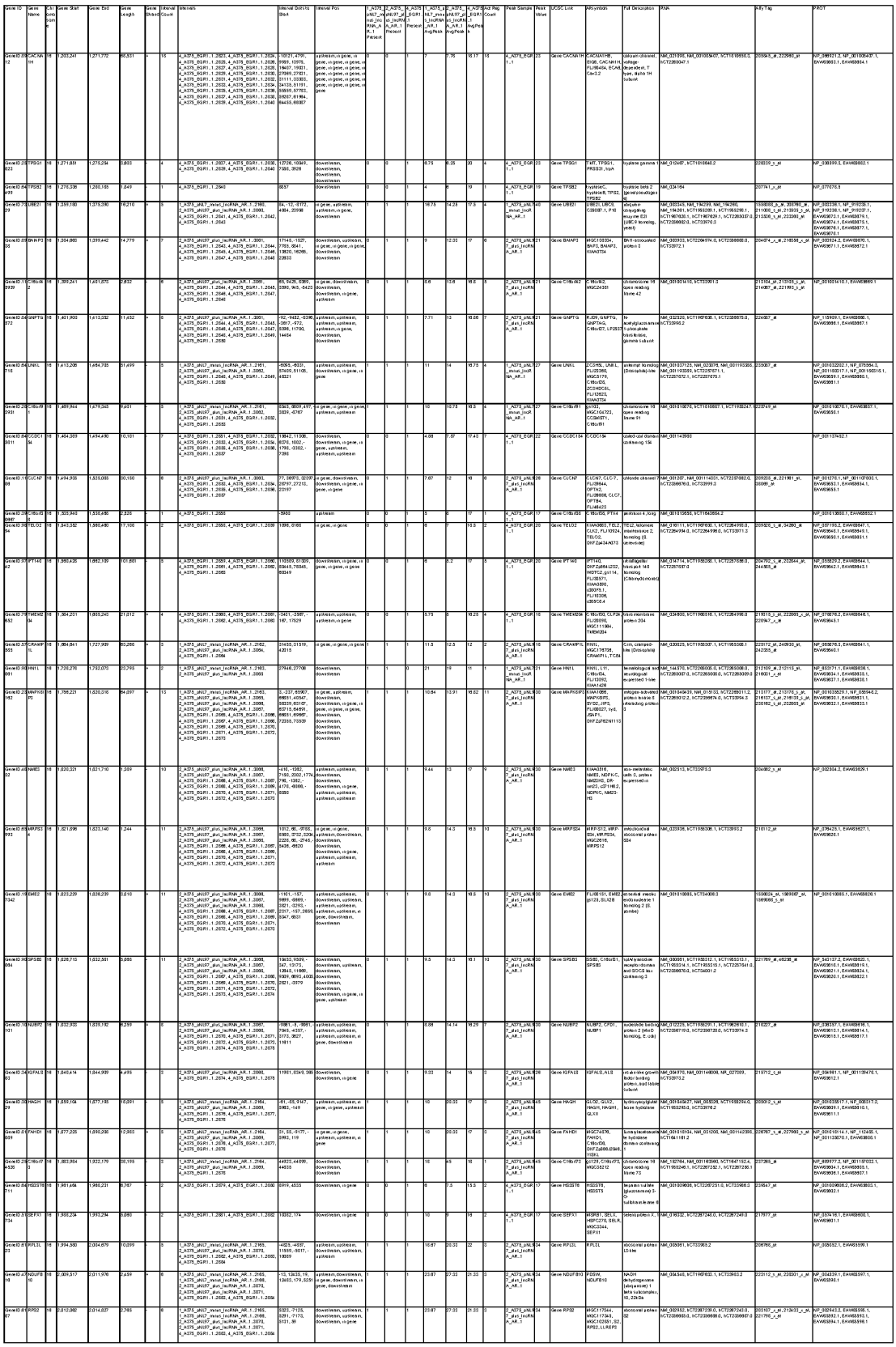


Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_uNG7_myNUT_jet_lncRNA_R_1 Percent	2_A375_2_A375_uNG7_myNUT_jet_lncRNA_R_1 Percent	3_A375_2_A375_uNG7_myNUT_jet_lncRNA_R_1 Percent	1_A375_jet_NUT_myc_lncRNA_R_1 Avg Peak	2_A375_jet_uNUT_myc_lncRNA_R_1 Avg Peak	3_A375_jet_EGFR1_lncRNA_R_1 Avg Peak	Ad Tag Count	Peak Sample	Peak Values	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:145675	MRSP2	13	50,319,569	50,321,965	2,396	+	1	4_A375_EGFR1..1.2665	2665	downstream	0	0	1	7	11	16	1	4_A375_EGFR1..1.1	16	Gene MRSP2	bHLHd8, SCDC, MRSP2	microRNA (pri-miRNA) 2 homolog (mouse)	NM_031079936	1598614_st_1598616_s_at	NP_001030247.1
GeneID:284 80	ANPEP	15	90,226,126	90,235,072	29,946	-	4	4_A375_EGFR1..1.2666, 4_A375_EGFR1..1.2669, 4_A375_EGFR1..1.2666, 4_A375_EGFR1..1.2661	50200, 10296, 556, -7624	downstream, upstream, gene, upstream	0	0	1	9.5	10.25	16	4	4_A375_EGFR1..1.1	16	Gene ANPEP	P130, APN, ANPEP, CD13, PEPN, GP150, GATP	alanyl (membrane) aminopeptidase	NM_031150, XCT182532.2, XCT227436.0	2628566_s_at, 2344.99_at, 234576_at	NP_001141.2, EAX02907.1, EAX02906.1
GeneID:189 239	AP1S2	19	50,373,831	50,437,817	63,756	-	3	1_A375_uNG7_myc1_lncRNA_NR_1.2137, 2_A375_uNG7_dup1_lncRNA_NR_1.2016, 3_A375_EGFR1..1.2661	482, 272, 71921	upstream, gene, downstream	1	1	1	24.5	21.5	77	2	1_A375_uNG7_myc1_lncRNA_NR_1.2137	34	Gene AP1S2	AP1S2, bg:mb23, AP1S2, FLJ38153	adaptin-related protein complex 1 sigma 2 subunit	NM_003529, NR_023391, XCT161284.3, XCT196493.1, XCT196494.1, XCT227431.0, XCT239894.0	332390_at, 202259_s_at	NP_003520.1, EAX03011.1, EAX03072.1, EAX03073.1, EAX03074.1, EAX03075.1
GeneID:102 724010	LOC102 507010	13	50,439,764	50,442,755	2,991	-	2	1_A375_uNG7_myc1_lncRNA_NR_1.2137, 2_A375_uNG7_dup1_lncRNA_NR_1.2016	5371, 5411	downstream, downstream	1	1	0	34	30	77	1	1_A375_uNG7_myc1_lncRNA_NR_1.2137	34	Gene LOC102507010	hypothetical LOC102507010	XR_109216			
GeneID:340 8110	C13orf33	13	50,443,822	50,454,222	10,400	-	2	1_A375_uNG7_myc1_lncRNA_NR_1.2137, 2_A375_uNG7_dup1_lncRNA_NR_1.2016	19038, 15578	downstream, downstream	1	1	0	34	30	77	1	1_A375_uNG7_myc1_lncRNA_NR_1.2137	34	Gene C13orf33	C13orf33, MGC851890	cytochrome 13 open reading frame 33	NM_152618, XCT183182.2, XCT235870.0	1215449_at, 229899_at, 229791_at	NP_872422.1, EAX02977.1, EAX02976.1
GeneID:102 509	SEMA4B	15	90,729,152	90,772,892	43,740	+	3	2_A375_uNG7_plus_lncRNA_NR_1.2017, 3_A375_EGFR1..1.2660, 4_A375_EGFR1..1.2666	49018, 35176, 43720	downstream, upstream, gene, upstream	0	1	1	7.33	9	14.67	3	4_A375_EGFR1..1.1	16	Gene SEMA4B	SEMA4B, SEMAC, MGC131051, MGC131053, KIAA1745, Sema	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	NM_020210, NM_198923, XCT183884.4, XCT236931.1, XCT236934.1	234725_s_at	NP_066559.2, NP_945187.1, EAX03054.1, EAX03055.1, EAX03056.1
GeneID:102 724010	CBS	15	90,772,477	90,777,279	2,802	-	3	2_A375_uNG7_plus_lncRNA_NR_1.2017, 3_A375_EGFR1..1.2660, 4_A375_EGFR1..1.2666	511, 13891, 8457	upstream, downstream, downstream	0	1	1	7.33	9	14.67	3	4_A375_EGFR1..1.1	16	Gene CBS	KYP1, CBS1, SPD, SB, KIP, CBS	cystathionine beta-synthase (serine)	NM_000354, XCT183813.2, XCT196151.2, XCT231179.0, XCT231179.2	201663_at	NP_000070.2, EAX02880.1, EAX02881.1, EAX02880.2
GeneID:284 8837	C15orf58	15	90,777,487	90,785,312	7,826	+	2	2_A375_uNG7_plus_lncRNA_NR_1.2017, 4_A375_EGFR1..1.2666	-719, -9618	upstream, upstream	0	1	1	8.5	10	13.5	2	4_A375_EGFR1..1.1	16	Gene C15orf58	C15orf58	chromosome 15 open reading frame 58	NM_031013837		NP_001138792.2
GeneID:144 5337	TTLL13	19	50,792,764	50,802,312	9,548	+	1	2_A375_uNG7_plus_lncRNA_NR_1.2018	18004	downstream	0	1	0	17	25	12	1	2_A375_uNG7_plus_lncRNA_NR_1	25	Gene TTLL13	MGC33417, TTLL13, FLJ46079	tubulin tyrosine ligase-like family, member 13	NM_031229984, XCT226855.1, XCT233159.0, XCT233159.1	1566643_at	NP_001253153.2, EAX02958.1, EAX02958.2, EAX02958.3, EAX02958.4
GeneID:317 335	NGRN	13	50,806,815	50,815,443	8,648	+	1	2_A375_uNG7_plus_lncRNA_NR_1.2018	-127	upstream	0	1	0	17	25	12	1	2_A375_uNG7_plus_lncRNA_NR_1	25	Gene NGRN	D3S92, NGRN	myelin, neuritin and growth associated	NM_031033005, NR_023932, XCT165785.5, XCT164398.2, XCT164397.2, XCT229896.1	2177722_s_at, 224261_s_at	NP_001029860.2, EAX02936.1, EAX02936.2, EAX02936.3, EAX02936.4, EAX02936.5
GeneID:102 507029	LOC102 507029	13	50,816,168	50,821,103	4,919	+	1	2_A375_uNG7_plus_lncRNA_NR_1.2018	-7416	upstream	0	1	0	17	25	12	1	2_A375_uNG7_plus_lncRNA_NR_1	25	Gene LOC102507029	hypothetical LOC102507029	XR_111567, XR_109279, XR_114557			
GeneID:542 2132	ZNF774	13	50,819,477	50,834,715	15,239	+	1	2_A375_uNG7_plus_lncRNA_NR_1.2018	107	up gene	0	1	0	15	16	16	1	2_A375_uNG7_plus_lncRNA_NR_1	25	Gene ZNF774	ZNF774, MGC73380	zinc finger protein 774	NM_031034309		NP_001034309.2
GeneID:233 42	FES	15	91,427,965	91,439,006	11,041	+	2	1_A375_uNG7_myc1_lncRNA_NR_1.2135, 4_A375_EGFR1..1.2670	18031, 16983	downstream, downstream	1	2	1	15.5	10	15	2	2_A375_uNG7_myc1_lncRNA_NR_1	22	Gene FES	FES, FPS	feline sarcoma oncogene	NM_002005, NM_001147701, NM_001147704, NM_001147705, XCT179547.6, XCT179547.7, XCT179547.8, XCT227030.0, XCT227034.0, XCT227701.3	205416_at	NP_001998.1, NP_001137253.1, NP_001137266.1, NP_001137267.1, EAX02115.1, EAX02115.2, EAX02115.3, EAX02116.1, EAX02116.2
GeneID:414 22	MANZA2	13	91,447,420	91,469,815	16,395	+	4	1_A375_uNG7_myc1_lncRNA_NR_1.2135, 1_A375_uNG7_myc1_lncRNA_NR_1.2139, 2_A375_uNG7_dup1_lncRNA_NR_1.2019, 4_A375_EGFR1..1.2670	-1724, 28596, 28540, -692	upstream, downstream, downstream, upstream	1	1	1	30.67	32	15.67	3	2_A375_uNG7_plus_lncRNA_NR_1	25	Gene MANDA2	MANDA2X, MANDA2	intersectin/dock, alpha/beta/gamma 2A, member 2	NM_0981122, XCT179447.1, XCT227023.0, XCT227024.0, XCT227024.1, XCT227024.2, XCT227025.0, XCT227026.0, XCT227027.2	2020822_s_at, 219999_at	NP_001138112.1, EAX02119.1, EAX02120.1, EAX02121.1, EAX02122.1, EAX02123.1, EAX02123.2, EAX02116.3
GeneID:389 696	UNC4A5	13	91,473,410	91,497,323	23,913	+	3	1_A375_uNG7_myc1_lncRNA_NR_1.2135, 2_A375_uNG7_dup1_lncRNA_NR_1.2019, 3_A375_EGFR1..1.2671	28596, 2550, 20267	downstream, downstream, downstream	1	1	1	30	32	13	2	2_A375_uNG7_plus_lncRNA_NR_1	25	Gene UNC4A5A	SWAP-1, IROG9700, FLJ45943, GCUNC45, GC-UNC45, UNC45A, SWAP1, GCUNC-45	unc-45 homolog A (C. elegans)	NM_031039878, NM_019871, XCT227029.0, XCT227029.2, XCT235916.0, XCT2773.4	2027499_x_at, 227102_s_at	NP_001034764.1, NP_061141.2, EAX02127.1, EAX02126.1, EAX02129.0
GeneID:375 4659	HDDC3	15	91,474,155	91,475,774	1,619	-	2	1_A375_uNG7_myc1_lncRNA_NR_1.2135, 2_A375_uNG7_dup1_lncRNA_NR_1.2019	-2,14	upstream, upstream	1	1	0	61	56	17	1	2_A375_uNG7_plus_lncRNA_NR_1	25	Gene HDDC3	MGC45398, MESH1, HDDC3	HD domain containing 3	NM_198327, XCT227035.0, XCT227272.3	227005_at	NP_940929.1, EAX02125.1, EAX02126.1
GeneID:101 2939897	LOC100 2939897	13	91,476,489	91,476,473	2,034	-	1	4_A375_EGFR1..1.2671	4766	downstream	0	0	1	9	10	13	1	4_A375_EGFR1..1.1	13	Gene LOC102602997	hypothetical LOC102602997	XR_109220, XR_114699			
GeneID:514 433	RCCD1	13	91,476,106	91,506,355	30,249	+	1	4_A375_EGFR1..1.2671	-4629	upstream	0	0	1	9	10	13	1	4_A375_EGFR1..1.1	13	Gene RCCD1	RCCD1, MGC14388	RCC1 domain containing 1	NM_033544, NM_001017919, XCT2302482.0, XCT2302486.0, XCT237.5.2	228468_at, 231260_at	NP_290222.2, NP_001017919.1, EAX02132.1, EAX02131.1, EAX02132.2
GeneID:350 55	PRC1	15	91,509,266	91,537,304	28,038	-	2	1_A375_uNG7_myc1_lncRNA_NR_1.2140, 2_A375_uNG7_dup1_lncRNA_NR_1.2020	-142, -165	upstream, upstream	1	1	0	16	20	13	1	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene PRC1	ASE1, PRC1, MGC29951, MGC1671	protein regulator of cytokinesis 1	NM_003981, NM_199413, NM_199414, XCT179547.5, XCT2302482.0, XCT2302486.0, XCT2302487.0, XCT2302488.0, XCT237.5.2	218009_s_at	NP_003972.3, NP_955402.1, NP_955401.1, EAX02102.1, EAX02136.1, EAX02137.1, EAX02138.1, EAX02135.1, EAX02136.2
GeneID:102 5527116	LOC102 507116	13	91,509,933	91,531,217	21,814	+	2	1_A375_uNG7_myc1_lncRNA_NR_1.2140, 2_A375_uNG7_dup1_lncRNA_NR_1.2020	28249, 28249	downstream, downstream	1	1	0	16	20	13	1	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene LOC102507116	hypothetical LOC102507116	XR_109221			
GeneID:284 278	VPS33B	15	91,541,774	91,565,833	24,059	-	2	1_A375_uNG7_myc1_lncRNA_NR_1.2140, 2_A375_uNG7_dup1_lncRNA_NR_1.2020	27681, 27681	downstream, downstream	1	1	0	16	20	13	1	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene VPS33B	VPS33B, FLJ14946	vacuolar protein sorting 33 homolog B (yeast)	NM_0189986, XCT2389816.0, XCT227712.2, XCT227712.3	218419_at, 44111_s_at	NP_061136.3, EAX02140.1, EAX02139.1
GeneID:283 232	SLCO3A1	15	92,298,936	92,715,965	316,727	+	2	2_A375_uNG7_plus_lncRNA_NR_1.2022, 2_A375_uNG7_dup1_lncRNA_NR_1.2024	2782, 159296	upstream, upstream	0	0	1	12	14	8	2	2_A375_uNG7_plus_lncRNA_NR_1	14	Gene SLCO3A1	SLCO3A1, OATP3A1, OATP3, SLCO3A1, OATP-D, FLJ40476	solute carrier organic anion transporter family, member 3A1	NM_031143044, NM_013272, XCT189837.1, XCT2895920.0, XCT234399.0	210522_s_at, 210529_at, 227387_at, 229778_at	NP_001138616.1, NP_037404.2, EAX02146.1, EAX02147.1, EAX02146.2
GeneID:830 09	STBSN2	15	92,937,140	93,011,998	74,858	+	1	4_A375_EGFR1..1.2673	384	up gene	0	0	1	3	9	14	1	4_A375_EGFR1..1.1	14	Gene STBSN2	MGC118554, STX, SNT8B, MGC118557, STBSN2, STBSN2-IS, HsT19690	STI1 dutch-hx suhm-wasmuede stable STBSN2-STBSN2-IS, tally/toxicil-beta 2	NM_999011, XCT187.0.2	221269_at, 235937_at	NP_999002.1, EAX02149.1
GeneID:844 2197	LNGR1	15	93,237,424	93,239,900	1,476	+	1	4_A375_EGFR1..1.2674	-2656	upstream	0	0	1	1	3	22	1	4_A375_EGFR1..1.1	22	Gene LNGR1	LOC643797	NGVR4R30	XR_111350, XR_109223, XR_114691		
GeneID:176 08	CHD2	15	93,443,551	93,571,207	127,656	+	1	1_A375_uNG7_myc1_lncRNA_NR_1.2143	61163	up gene	1	2	0	16	11	1	1	1_A375_uNG7_myc1_lncRNA_NR_1	16	Gene CHD2	CHD2, DHF2A47131.3, DHF2A69801.3, FLJ30894, DHF2A101727	chromodomain helicase DNA binding protein 2	NM_031428372, NM_001271, XCT2289479.0, XCT2289480.0, XCT2289482.0, XCT2289483.0, XCT2289484.0, XCT2289485.0, XCT2289486.0	1554614_at, 1554615_s_at, 1554616_at, 233977_at, 239951_x_at, 239953_at, 239956_x_at, 243154_at, 244442_at	NP_001030837.1, NP_001262.3, EAX02180.1, EAX02181.1, EAX02182.1, EAX02183.1, EAX02183.2, EAX02184.1
GeneID:389 983	RGMA	15	93,566,936	93,622,443	43,507	-	4	4_A375_EGFR1..1.2675, 4_A375_EGFR1..1.2676, 4_A375_EGFR1..1.2677, 4_A375_EGFR1..1.2678	44251, 41431, 18459, 15739	up gene, up gene, up gene, up gene	0	0	1	8	9	16.5	4	4_A375_EGFR1..1.1	19	Gene RGMA	RGM, RGMA	RGM domain family, member A	NM_020311, NM_001166200, NM_001166207, NM_001166208, NM_001166209, XCT142254.4, XCT189419.2	1234560_s_at, 234009_at	NP_064595.2, NP_001159730.1, NP_001159731.1, NP_001159740.1, NP_001159741.1, EAX02198.1, EAX02198.2
GeneID:644 4192	LOC644 192	15	93,612,931	93,670,950	56,020	-	1	2_A375_uNG7_plus_lncRNA_NR_1.2029	53470	up gene	0	1	0	19	24	10	1	2_A375_uNG7_plus_lncRNA_NR_1	24	Gene LOC644192	hypothetical LOC644192	XR_111353, XR_109223, XR_114692	232976_at, 242298_at, 244693_at	
GeneID:102 5506754	LOC102 506754	13	98,628,126	98,670,409	44,283	+	1	2_A375_uNG7_plus_lncRNA_NR_1.2029	53209	downstream	0	1	0	19	24	10	1	2_A375_uNG7_plus_lncRNA_NR_1	24	Gene LOC102506754	hypothetical protein LOC102506754	XM_002310677		XP_002310725.1
GeneID:729 5930	LOC729 800	15	99,902,930	99,904,900	2,007	+	4	1_A375_uNG7_myc1_lncRNA_NR_1.2147, 2_A375_uNG7_dup1_lncRNA_NR_1.2030, 4_A375_EGFR1..1.2680, 4_A375_EGFR1..1.2681	-2387, -2370, -2413, 307	upstream, upstream, upstream, up gene	1	1	1	11.5	13.5	16	2	4_A375_EGFR1..1.1	16	Gene LOC729800	hypothetical LOC729800	lysine-rich FLJ00402 protein	NM_002343196		XP_002343419.1
GeneID:919 945	LOC919 945	15	99,065,645	99,417,859	351,812	-	2	1_A375_uNG7_myc1_lncRNA_NR_1.2145, 2_A375_uNG7_dup1_lncRNA_NR_1.2031	-1205, -1141	upstream, upstream	1	1	0	30	29	9	1	1_A375_uNG7_myc1_lncRNA_NR_1	30	Gene LOC919945	MGC125555, MGC125559, MGC125557, MGC125558	hypothetical LOC91945	NM_026172, NR_024173	234017_at	
GeneID:511 947	ARRDC4	15	99,563,935	99,577,966	13,135	+	2	1_A375_uNG7_myc1_lncRNA_NR_1.2145, 2_A375_uNG7_dup1_lncRNA_NR_1.2032	-197, -169	upstream, upstream	1	1	0	25	30	8	1	2_A375_uNG7_plus_lncRNA_NR_1	30	Gene ARRDC4	ARRDC4, FLJ90643	arrestin domain containing 4	NM_183376, XCT123953.2, XCT2695222.0	225283_at	NP_899232.2, EAX02151.1, EAX02154.1
GeneID:344 90	IGFBP7	15	99,192,761	99,207,709	314,996	+	2	2_A375_uNG7_plus_lncRNA_NR_1.2150, 2_A375_uNG7_plus_lncRNA_NR_1.3056	248951, 263799	up gene, up gene	1	1	0	16.5	15.5	7	2	2_A375_uNG7_plus_lncRNA_NR_1	19	Gene IGFBP7	IGFBP, CSF3, MAC425, IGFBP-rP1, MGC142168, MGC142172, IGFBP, MGC142170	insulin-like growth factor binding protein 7	NM_0909775, XCT184005.2, XCT2895230.0	203927_at, 203928_at, 205641_at, 225302_at, 243295_at	NP_3096981, EAX02201.1, EAX02221.1, EAX02222.1
GeneID:144 5514	LOC144 514	13	99,311,439	99,331,924	39,985	-	1	4_A375_EGFR1..1.2684	19472	up gene	0	0	1	4	9	16	1	4_A375_EGFR1..1.1	16	Gene LOC144514	PNPEP1L		NM_0313082.2, NM_0311697.1		NP_001309082.2, NP_001159374.1
GeneID:253 339	SYNM	15	99,845,230	99,875,900	30,514	+	2	1_A375_uNG7_myc1_lncRNA_NR_1.2151, 2_A375_uNG7_dup1_lncRNA_NR_1.3033	19048, 700	up gene, up gene	1	1	0	17	16	7.5	2	2_A375_uNG7_plus_lncRNA_NR_1	21	Gene SYNM	SYNM253, DKFZp313H1621, SYNM, SYN	synemin, intermediate filament protein	NM_145735, NR_015259, XCT19410.2, XCT2270077.0, XCT2270076.0	212720_at, 214304_s_at	NP_6977052, NP_0961103, EAX02231.1, EAX02232.2
GeneID:644 927	TTC23	13	99,876,926	99,769,815	113,297	-	2	2_A375_uNG7_plus_lncRNA_NR_1.3036, 4_A375_EGFR1..1.2688	-73, 89479	upstream, up gene	0	1	1	10	13.5	11	2	2_A375_uNG7_plus_lncRNA_NR_1	23	Gene TTC23	FLJ12709, FLJ12972, HCC-9, TTC23	tetratricopeptide repeat domain 23	NM_031049655, NM_022903, NM_031040866, NM_031040657, NM_001040655, NM_031040659, NM_001040660, XCT19411.2, XCT2272231.0, XCT2272232.0, XCT2272233.0, XCT2272236.0, XCT2389827.0	1569221_at, 219936_at, 232754_at, 240758_at	NP_0010397433.1, NP_076398.3, NP_0010397441.1, NP_0010397442.1, NP_0010397443.1, NP_0010397450.1, EAX02234.1, EAX02235.1, EAX02236.1, EAX02237.1, EAX02238.1, EAX02239.1
GeneID:153 5350	LRRC28	15	99,791,852	99,826,498	134,646	+	1	2_A375_uNG7_plus_lncRNA_NR_1.3056	1764	upstream	0	1	0	17	23	9	1	2_A375_uNG7_plus_lncRNA_NR_1	23	Gene LRRC28	MGC24979, FLJ45342, LRRC28, FLJ52319, KIAA1790, RPRB, LRRX1	leucine rich repeat containing 28	NM_144795, XCT19408.3, XCT1864993.1, XCT2895922.0, XCT2895923.0, XCT2895924.0	1553940_s_at, 227423_at, 235897_at, 239471_at	NP_8537192, EAX02241.1, EAX02240.1, EAX02243.1, EAX02243.2, EAX02244.1
GeneID:135 6091	ADAMTS 17	15	100,511,563	100,592,103	370,540	+	1	2_A375_uNG7_plus_lncRNA_NR_1.3037	-7929	upstream	0	1	0	16	16	11	1	2_A375_uNG7_plus_lncRNA_NR_1	16	Gene ADAMTS17	ADAMTS17, FLJ32765, FLJ16363	ADAM metallopeptidase with thrombospondin type 1 motif, 17	NM_139057, XCT227220.0, XCT227220.0, XCT227230.0, XCT227230.1	1552723_s_at, 1552726_at, 1552727_s_at	NP_6208853, EAX02264.1, EAX02261.1, EAX02263.1, EAX02263.2
GeneID:388 3182	FLJ42393	15	100,594,992	100,690,923	95,931	-	1	2_A375_uNG7_plus_lncRNA_NR_1.3037	611	up gene	0	1	0	16	16	11	1	2_A375_uNG7_plus_lncRNA_NR_1	16	Gene FLJ42393	FLJ42974, HB047	hypothetical LOC388182	NR_026109, NR_026140, XCT1812936.2, XCT2340200.0	1559290_s_at	EAX02266.1, EAX02265.1
GeneID:144 5737	LOC145 737	13	101,402,945	101,414,195	12,147	+	1	4_A375_EGFR1..1.2687	18752	downstream	0	0	1	9	15	17	1	4_A375_EGFR1..1.1	17	Gene LOC145737	MGC126884	hypothetical LOC145737	XR_111555, XR_109251, XR_114696	1559849_at	
GeneID:284 0	ALDH1A3	15	101,430,009	101,498,831	68,822	+	4	2_A375_uNG7_plus_lncRNA_NR_1.3040, 2_A375_uNG7_plus_lncRNA_NR_1.3041, 2_A375_uNG7_plus_lncRNA_NR_1.3041, 4_A375_EGFR1..1.2688	19877, 35839, 791, 39223	up gene, downstream, up gene, downstream	1	1	1	15	16.33	16.33	3	2_A375_uNG7_plus_lncRNA_NR_1	21	Gene ALDH1A3	RALDH3, ALDH1A3, ALDH6	retinal dehydrogenase 1 family, member A3	NM_000693, XCT191612.2, XCT1938866.1, XCT2389810.0	203180_at	NP_000684.2, EAX02282.1, EAX02281.1, EAX02283.1
GeneID:102 5507452	LOC102 507452	13	101,433,929	101,439,455	25,559	-	3	2_A375_uNG7_plus_lncRNA_NR_1.3040, 2_A375_uNG7_plus_lncRNA_NR_1.3041, 2_A375_uNG7_plus_lncRNA_NR_1.3041, 4_A375_EGFR1..1.2688	27668, 640, 256	downstream, up gene, up gene	0	1	0	15	20	16	2	2_A375_uNG7_plus_lncRNA_NR_1	21	Gene LOC102507452	hypothetical LOC102507452	XR_111557, XR_111556, XR_109233, XR_109222, XR_114693, XR_114699			
GeneID:791 705	LRRX1	13	101,439,490	101,610,217	170,727	-	3	2_A375_uNG7_plus_lncRNA_NR_1.3041, 4_A375_EGFR1..1.2688, 4_A375_EGFR1..1.2689	-612, -220, 148140	upstream, upstream, up gene	1	1	1	13	13.5	14.5	2	2_A375_uNG7_plus_lncRNA_NR_1	19	Gene LRRX1	Rax/rl, FLJ27465, FLJ32119, KIAA1790, RPRB, LRRX1	leucine rich repeat homeobox 1	NM_024432, XCT19316.1, XCT2289612.0, XCT2289614.0	219441_x_at	NP_0769216, EAX02307.1, EAX02288.1, EAX02289.1
GeneID:228 936	CHSY1	15	101,718,926	101,792,137	78,209	-	2	1_A375_uNG7_myc1_lncRNA_NR_1.2153, 2_A375_uNG7_plus_lncRNA_NR_1.3042	9, -265	up gene, upstream	1	1	0	20	19	7	1	1_A375_uNG7_myc1_lncRNA_NR_1	20	Gene CHSY1	CSS1, KIAA0990, CSGy-1, DHF2a84M022, CHSY, FLJ66361, CHSY1	chondroitin sulfate synthase 1	NM_014918, XCT177750.2	203044_at	NP_5577332, EAX02292.1
GeneID:888 27	SNRPA1	15	101,821,715	101,838,490	16,775	-	2	1_A375_uNG7_myc1_lncRNA_NR_1.2154, 2_A375_uNG7_plus_lncRNA_NR_1.3043	4, -28	up gene, upstream	1	1	0	42	43	12	1	2_A375_uNG7_plus_lncRNA_NR_1	43	Gene SNRPA1	SNRPA1, Lsm1	small nuclear ribonucleoprotein polypeptide A'	NM_0030992, XCT227033.0, XCT227033.1, XCT227033.2, XCT227033.3, XCT227033.4, XCT2389809.0	209365_s_at, 213702_s_at, 214307_x_at, 214308_s_at, 242148_at	NP_0030831.2, EAX02296.1, EAX02297.1, EAX02298.1, EAX02299.1, EAX02300.1
GeneID:368 48	PCSK9	15	101,844,193	102,030,187	185,994	-	2	1_A375_uNG7_myc1_lncRNA_NR_1.2154, 2_A375_uNG7_plus_lncRNA_NR_1.3043	194731, 194699	downstream, downstream	1	1	0	42	43	12	1	2_A375_uNG7_plus_lncRNA_NR_1	43	Gene PCSK9	PCSK9, SPC4, PCSK4	proprotein convertase subtilisin/kexin type 9	NM_174936, NM_174922, XCT184003.2, XCT2302482.0, XCT2302486.0, XCT2302487.0, XCT2302488.0, XCT237.5.2	1553931_at, 207614_1_s_at, 213052_x_at, 213052_x_at, 213812_s_at, 213812_s_at, 242982_at	NP_8121931, NP_8121941, NP_8121921, NP_9121961, NP_8121971, NP_8121962, NP_8121951, NP_0025911, EAX02302.1, EAX02303.1, EAX02304.1, EAX02306.1, EAX02307.1, EAX02308.1, EAX02309.1, EAX02310.1, EAX02311.1
GeneID:667 213	TMED3	13	102,182,049	102,192,594	10,545	-	1	2_A375_uNG7_plus_lncRNA_NR_1.3044	114	up gene	0	1	0	15	17	17	1	2_A375_uNG7_plus_lncRNA_NR_1	17	Gene TMED3	ELP2, TMED2	TMED domain containing 3	NM_0766744, NM_020141, XCT17751.3, XCT1901844.1, XCT2289812.0	1553429_s_at, 221762_s_at	NP_9100853.2, NP_0764722, EAX02312.1, EAX02314.1, EAX02315.2
GeneID:127 3283	TARSL2	13	102,193,353	102,256,843	70,890	-	1	2_A375_uNG7_plus_lncRNA_NR_1.3044	72169	up gene	0	1	0	15	17	17	1	2_A375_uNG7_plus_lncRNA_NR_1	17	Gene TARSL2	FLJ20503, TARSL2	threonyl-tRNA synthetase-like 2	NM_182334, XCT183894	227611_at, 244615_s_at	NP_8935472, EAX02318.1
GeneID:102 5507516	LOC102 507516	13	102,231,583	102,232,054	471	-	1	4_A375_EGFR1..1.2692	4545	downstream	0	0	1	5	9	17	1	4_A375_EGFR1..1.1	17	Gene LOC102507516	hypothetical protein LOC102507516	NM_0011169935			XP_0031167301
GeneID:394 0640	CRAFB	15	102,249,923	102,346,661	956	+	1	2_A375_uNG7_plus_lncRNA_NR_1.3045	5273	downstream	0	1	0	10	17	1	1	2_A375_uNG7_plus_lncRNA_NR_1	17	Gene CRAFB	CRAFB, CRAF12, CR15-19	olfactory receptor, family 4, subfamily F, member B	NM_0010035226, XCT19395.1		NP_0010035226.1, EAX02319.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:390649	OR4F15	15	102,358,390	102,359,328	938	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3045	-7094	upstream	0	1	0	10	17	1	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene OR4F15	OR4F15		NM_001001674, hCT2345750.1		NP_001001674.1, EAX02320.1
GeneID:51728	POLR3K	16	96,979	103,632	6,653	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3046, 4_A375_EGR1..1..2693	80, -8496	in gene, upstream	0	1	1	11.5	14	13	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene POLR3K	hRPC11, RPC11, C11-RNP3, RPC12.5, POLR3K, RPC10, My010, C11	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa	NM_016310, hCT1826347.2	218866_s_at, 222766_at	NP_057394.2, EAW85879.1
GeneID:79622	SNRNP25	16	103,829	107,669	3,840	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3046, 4_A375_EGR1..1..2693, 4_A375_EGR1..1..2694	-277, 8299, 11115	upstream, downstream, downstream	0	1	1	10	13	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SNRNP25	FLJ22940, SNRNP25, C16orf33	small nuclear ribonucleoprotein 25kDa (U11/U12)	NM_024571, hCT1783566.2, hCT1958665.1	218493_at	NP_078847.1, EAW85878.1, EAW85877.1
GeneID:64285	RHBDF1	16	108,058	122,629	14,571	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2155, 2_A375_pNL97_plus_lncRNA_AR..1..3046, 2_A375_pNL97_plus_lncRNA_AR..1..3047, 4_A375_EGR1..1..2693, 4_A375_EGR1..1..2694, 4_A375_EGR1..1..2695, 4_A375_EGR1..1..2696	4101, 19077, -187, 10501, 7665, -5200, -7403	in gene, downstream, upstream, in gene, in gene, upstream, upstream	1	1	1	11.71	14.43	14	7	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene RHBDF1	gene-89, RHBDF1, Dist1, hDist1, FLJ22357, C16orf8, gene-90, EGFR-RS, FLJ2235	rhomboid 5 homolog 1 (Drosophila)	NM_022450, hCT1783567.2, hCT1953824.1, hCT2258266.0, hCT2356763.0	218686_s_at, 222711_s_at	NP_071895.3, EAW85876.1, EAW85873.1, EAW85874.1, EAW85875.1
GeneID:4350	MPG	16	127,018	135,845	8,827	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2155, 2_A375_pNL97_plus_lncRNA_AR..1..3047, 4_A375_EGR1..1..2695, 4_A375_EGR1..1..2696	-8490, -4202, 811, 3014	upstream, upstream, in gene, in gene	1	1	1	13	15.5	13.75	4	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MPG	AAG, Mid1, MDG, anpg, ADPG, PIG16, APNG, CRA36.1, PIG11, MPG	N-methylpurine-DNA glycosylase	NM_001015052, NM_002434, NM_001015054, hCT1953839.2, hCT1966700.1, hCT1966701.1	203686_at	NP_001015052.1, NP_002425.2, NP_001015054.1, EAW85870.1, EAW85871.1, EAW85872.1
GeneID:8131	C16orf35	16	135,800	188,672	52,872	-	2	4_A375_EGR1..1..2695, 4_A375_EGR1..1..2696	60843, 58640	downstream, downstream	0	0	1	11	10.5	17	2	4_A375_EGR1..1	18	Gene C16orf35	RMD11, CGTHBA, HS-40, NPR3, NPRL3, C16orf35, MARE	chromosome 16 open reading frame 35	NM_001039476, NM_001077350	203269_s_at, 210872_s_at, 214273_x_at	NP_001034565.1, NP_001070818.1
GeneID:55692	LUC7L	16	238,970	279,449	40,479	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2156, 2_A375_pNL97_plus_lncRNA_AR..1..3048	57, 73	in gene, in gene	1	1	0	19	24	15	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LUC7L	LUC7L, Luc7, LUC7B1, FLJ10231, LUC7-LIKE, SR+89, hLuc7B1	LUC7-like (S. cerevisiae)	NM_201412, NM_018032, hCT1966703.1, hCT1966706.2, hCT2349137.0, hCT2349138.0, hCT2349139.0, hCT2349140.0, hCT2349141.0, hCT2349142.0, hCT2356655.0, hCT2356656.0, hCT2356657.0	1557066_at, 1557067_s_at, 220143_x_at, 223295_s_at, 223546_x_at	NP_958815.1, NP_060502.1, EAW85853.1, EAW85854.1, EAW85859.1, EAW85860.1, EAW85850.1, EAW85851.1, EAW85852.1, EAW85855.1, EAW85856.1, EAW85857.1, EAW85858.1
GeneID:100129478	LOC100129478	16	280,529	281,471	942	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2156, 2_A375_pNL97_plus_lncRNA_AR..1..3048	-1137, -1153	upstream, upstream	1	1	0	19	24	15	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LOC100129478		hypothetical LOC100129478	XM_001719774, XM_001721251, XM_001723250		XP_001719826.1, XP_001721303.1, XP_001723302.1
GeneID:83986	ITFG3	16	284,801	316,119	31,318	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2156, 2_A375_pNL97_plus_lncRNA_AR..1..3048, 4_A375_EGR1..1..2697, 4_A375_EGR1..1..2698, 4_A375_EGR1..1..2699	-5409, -5425, 34639, 38863, 39839	upstream, upstream, downstream, downstream, downstream	1	1	1	9.5	10	16.5	4	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ITFG3	C16orf9, gs19, ITFG3, FLJ32603, DKFZp761D0211	integrin alpha FG-GAP repeat containing 3	NM_032039, hCT2260382.0, hCT2260384.0, hCT2260385.0, hCT2260387.0, hCT2260388.0, hCT2260389.0	224749_at	NP_114428.1, EAW85844.1, EAW85845.1, EAW85847.1, EAW85848.1, EAW85849.1, EAW85846.1
GeneID:8786	RGS11	16	318,310	325,914	7,604	-	4	4_A375_EGR1..1..2697, 4_A375_EGR1..1..2698, 4_A375_EGR1..1..2699, 4_A375_EGR1..1..2700	6474, 2250, 1274, -5382	in gene, in gene, in gene, upstream	0	0	1	7	5.5	18.25	4	4_A375_EGR1..1	22	Gene RGS11	RGS11, RS11	regulator of G-protein signaling 11	NM_003834, NM_183337, hCT2258242.0, hCT2258243.0, hCT2258244.0, hCT2348346.0, hCT2356759.0	1554643_at, 206107_at, 211872_s_at	NP_003825.1, NP_899180.1, EAW85839.1, EAW85841.1, EAW85842.1, EAW85843.1, EAW85840.1
GeneID:398	ARHGDIG	16	330,606	333,003	2,397	+	3	4_A375_EGR1..1..2698, 4_A375_EGR1..1..2699, 4_A375_EGR1..1..2700	-6942, -5966, 690	upstream, upstream, in gene	0	0	1	6.67	5	18	3	4_A375_EGR1..1	22	Gene ARHGDIG	ARHGDIG, RHOGDI-3	Rho GDP dissociation inhibitor (GDI) gamma	NM_001176	206868_s_at	NP_001167.2
GeneID:64714	PDIA2	16	333,118	337,209	4,091	+	3	4_A375_EGR1..1..2698, 4_A375_EGR1..1..2699, 4_A375_EGR1..1..2700	-9454, -8478, -1822	upstream, upstream, upstream	0	0	1	6.67	5	18	3	4_A375_EGR1..1	22	Gene PDIA2	PDI, PDIR, PDA2, PDIA2, PDIP	protein disulfide isomerase family A, member 2	NM_006849	206691_s_at, 206869_at, 216127_at	NP_006840.2
GeneID:8312	AXIN1	16	337,440	402,464	65,024	-	7	2_A375_pNL97_plus_lncRNA_AR..1..3049, 4_A375_EGR1..1..2700, 4_A375_EGR1..1..2701, 4_A375_EGR1..1..2702, 4_A375_EGR1..1..2703, 4_A375_EGR1..1..2704, 4_A375_EGR1..1..2705	25024, 71166, 48112, 11696, -2460, -6666, -9536	in gene, downstream, in gene, in gene, upstream, upstream, upstream	0	1	1	9.43	11.29	19	7	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene AXIN1	AXIN, AXIN1, MGC52315	axin 1	NM_181050, NM_003502, hCT2258222.0, hCT2258225.1	212849_at	NP_851393.1, NP_003493.1, EAW85835.1, EAW85836.1
GeneID:10573	MRPL28	16	417,396	420,540	3,144	-	5	4_A375_EGR1..1..2704, 4_A375_EGR1..1..2705, 4_A375_EGR1..1..2706, 4_A375_EGR1..1..2707, 4_A375_EGR1..1..2708	11366, 8540, 5644, -5412, -7044	downstream, downstream, downstream, upstream, upstream	0	0	1	9.8	11	19.4	5	4_A375_EGR1..1	25	Gene MRPL28	p15, MRPL28, MAAT1, MGC8499	mitochondrial ribosomal protein L28	NM_006428, hCT1783565.4, hCT1965912.2, hCT1965913.2, hCT2343719.0, hCT2343720.0, hCT2356733.0, hCT2356734.0, hCT2356735.0	204599_s_at	NP_006419.2, EAW85829.1, EAW85827.1, EAW85830.1, EAW85832.1, EAW85834.1, EAW85828.1, EAW85831.1, EAW85833.1
GeneID:58986	TMEM8A	16	420,776	431,950	11,174	-	5	4_A375_EGR1..1..2705, 4_A375_EGR1..1..2706, 4_A375_EGR1..1..2707, 4_A375_EGR1..1..2708, 4_A375_EGR1..1..2709	19950, 17054, 5998, 4366, 526	downstream, downstream, in gene, in gene, in gene	0	0	1	9.2	11.6	18	5	4_A375_EGR1..1	25	Gene TMEM8A	TMEM8, M83, TMEM6, TMEM8A	transmembrane protein 8A	NM_021259, hCT2256322.0, hCT2256323.0, hCT2356716.0	221882_s_at, 222716_at	NP_067082.2, EAW85825.1, EAW85823.1, EAW85824.1
GeneID:100134366	LOC100134366	16	432,241	442,960	10,719	+	3	4_A375_EGR1..1..2707, 4_A375_EGR1..1..2708, 4_A375_EGR1..1..2709	-6289, -4657, -617	upstream, upstream, upstream	0	0	1	6	10	15.33	3	4_A375_EGR1..1	17	Gene LOC100134366		similar to hCG1644121	NR_024453		
GeneID:9727	RAB11FIP3	16	475,868	572,481	96,613	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2157, 1_A375_pNL7_minus_lncRNA_AR..1..2156, 2_A375_pNL97_plus_lncRNA_AR..1..3050, 2_A375_pNL97_plus_lncRNA_AR..1..3051, 4_A375_EGR1..1..2710, 4_A375_EGR1..1..2711, 4_A375_EGR1..1..2712, 4_A375_EGR1..1..2713	-420, 101868, 101612, 102972, 940, 32540, 57004, 102684	upstream, downstream, downstream, downstream, in gene, in gene, in gene, downstream	1	1	1	12.67	13.5	15.67	6	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene RAB11FIP3	KIAA0665, RAB11FIP3, Rab11-FIP3	RAB11 family interacting protein 3 (class II)	NM_014700, NM_001142272, hCT2260403.0, hCT2260404.0, hCT2260405.0, hCT2260406.0, hCT2260407.0, hCT2260408.0	203933_at, 214999_s_at, 228613_at	NP_055515.1, NP_001135744.1, EAW85805.1, EAW85807.1, EAW85809.1, EAW85810.1, EAW85806.1, EAW85808.1
GeneID:84493	C16orf10	16	576,847	577,407	560	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2156, 2_A375_pNL97_plus_lncRNA_AR..1..3050, 2_A375_pNL97_plus_lncRNA_AR..1..3051, 4_A375_EGR1..1..2713, 4_A375_EGR1..1..2714, 4_A375_EGR1..1..2715, 4_A375_EGR1..1..2716	-129, 127, -1233, 945, -7937, -9345, -10273	upstream, in gene, upstream, upstream, upstream, upstream, upstream	1	1	1	11.6	13.6	15.6	5	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene C16orf10	NCRNA00235, C16orf10	non-protein coding RNA 235	NR_024121		
GeneID:6650	SOLH	16	577,856	604,636	26,780	+	18	1_A375_pNL7_minus_lncRNA_AR..1..2156, 2_A375_pNL97_plus_lncRNA_AR..1..3050, 2_A375_pNL97_plus_lncRNA_AR..1..3051, 4_A375_EGR1..1..2713, 4_A375_EGR1..1..2714, 4_A375_EGR1..1..2715, 4_A375_EGR1..1..2716, 4_A375_EGR1..1..2717, 4_A375_EGR1..1..2718, 4_A375_EGR1..1..2719, 4_A375_EGR1..1..2720, 4_A375_EGR1..1..2721, 4_A375_EGR1..1..2722, 4_A375_EGR1..1..2723, 4_A375_EGR1..1..2724, 4_A375_EGR1..1..2725, 4_A375_EGR1..1..2726, 4_A375_EGR1..1..2727	-320, -576, 784, 496, 7466, 8696, 9624, 13120, 21166, 21776, 24046, 26432, 28266, 28684, 31066, 31964, 33246, 35966	upstream, upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, downstream, downstream, downstream, downstream, downstream, downstream	1	1	1	8	8.69	17.44	16	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SOLH	CAPN15, SOLH, MGC131491	small optic lobes homolog (Drosophila)	NM_005632, hCT13508.3	204275_at, 230295_at	NP_005623.1, EAW85803.1
GeneID:100507047	LOC100507047	16	588,950	589,861	911	+	7	2_A375_pNL97_plus_lncRNA_AR..1..3051, 4_A375_EGR1..1..2714, 4_A375_EGR1..1..2715, 4_A375_EGR1..1..2716, 4_A375_EGR1..1..2717, 4_A375_EGR1..1..2718, 4_A375_EGR1..1..2719	-10310, -3606, -2196, -1270, 2026, 10074, 10662	upstream, upstream, upstream, upstream, downstream, downstream, downstream	0	1	1	8.29	9.57	17.57	7	4_A375_EGR1..1	23	Gene LOC100507047		hypothetical LOC100507047	XR_109234		
GeneID:100423037	MIR3176	16	593,277	593,366	89	+	7	4_A375_EGR1..1..2714, 4_A375_EGR1..1..2715, 4_A375_EGR1..1..2716, 4_A375_EGR1..1..2717, 4_A375_EGR1..1..2718, 4_A375_EGR1..1..2719, 4_A375_EGR1..1..2720	-7933, -6525, -5597, -2301, 5747, 6355, 8627	upstream, upstream, upstream, upstream, downstream, downstream, downstream	0	0	1	7.86	8.14	17.71	7	4_A375_EGR1..1	23	Gene MIR3176	MIR3176	microRNA 3176	NR_036137		
GeneID:146325	C16orf11	16	610,422	615,529	5,107	+	11	4_A375_EGR1..1..2720, 4_A375_EGR1..1..2721, 4_A375_EGR1..1..2722, 4_A375_EGR1..1..2723, 4_A375_EGR1..1..2724, 4_A375_EGR1..1..2725, 4_A375_EGR1..1..2726, 4_A375_EGR1..1..2727, 4_A375_EGR1..1..2728, 4_A375_EGR1..1..2729, 4_A375_EGR1..1..2730	-8518, -6134, -4278, -3702, -1478, -582, 662, 3402, 4874, 5674, 7626	upstream, upstream, upstream, upstream, upstream, upstream, in gene, in gene, in gene, downstream, downstream	0	0	1	5.91	6.55	17.82	11	4_A375_EGR1..1	20	Gene C16orf11	C16orf11	chromosome 16 open reading frame 11	NM_145270, hCT1956050.2	1553626_a_at	NP_660313.1, EAW85802.1
GeneID:283948	NHLRC4	16	617,032	619,495	2,463	+	8	4_A375_EGR1..1..2724, 4_A375_EGR1..1..2725, 4_A375_EGR1..1..2726, 4_A375_EGR1..1..2727, 4_A375_EGR1..1..2728, 4_A375_EGR1..1..2729, 4_A375_EGR1..1..2730, 4_A375_EGR1..1..2731	-8066, -7192, -5926, -3208, -1736, -936, 1016, 11416	upstream, upstream, upstream, upstream, upstream, upstream, in gene, downstream	0	0	1	5.88	6	18.25	8	4_A375_EGR1..1	20	Gene NHLRC4	FLJ36208, NHLRC4	NHL repeat containing 4	NM_176677, hCT2349179.0	1558431_at	NP_788850.1, EAW85801.1
GeneID:9091	PIGQ	16	620,004	634,109	14,105	+	11	4_A375_EGR1..1..2725, 4_A375_EGR1..1..2726, 4_A375_EGR1..1..2727, 4_A375_EGR1..1..2728, 4_A375_EGR1..1..2729, 4_A375_EGR1..1..2730, 4_A375_EGR1..1..2731, 4_A375_EGR1..1..2732, 4_A375_EGR1..1..2733, 4_A375_EGR1..1..2734, 4_A375_EGR1..1..2735	-10164, -8900, -6180, -4708, -3908, -1956, 8444, 10364, 12966, 13960, 22684	upstream, upstream, upstream, upstream, upstream, upstream, in gene, in gene, in gene, in gene, downstream	0	0	1	6.64	5.55	17.55	11	4_A375_EGR1..1	20	Gene PIGQ	PIGQ, GPI1, hGPI1, c407A10.1, MGC12693	phosphatidylinositol glycan anchor biosynthesis, class Q	NM_004204, NM_148920, hCT13511.3, hCT1984023.1, hCT1984024.1, hCT2260419.0, hCT2260422.0, hCT2260423.0	1555359_at, 204144_s_at	NP_004195.2, NP_683721.1, EAW85795.1, EAW85796.1, EAW85797.1, EAW85799.1, EAW85798.1, EAW85800.1
GeneID:57799	RAB40C	16	639,357	679,273	39,916	+	11	1_A375_pNL7_minus_lncRNA_AR..1..2159, 2_A375_pNL97_plus_lncRNA_AR..1..3052, 4_A375_EGR1..1..2732, 4_A375_EGR1..1..2733, 4_A375_EGR1..1..2734, 4_A375_EGR1..1..2735, 4_A375_EGR1..1..2736, 4_A375_EGR1..1..2737, 4_A375_EGR1..1..2738, 4_A375_EGR1..1..2739, 4_A375_EGR1..1..2740	47075, 47075, -8989, -6365, -5373, 3331, 24003, 36995, 41923, 47459, 48483	downstream, downstream, upstream, upstream, upstream, in gene, in gene, in gene, downstream, downstream, downstream	1	1	1	11.22	10.67	18.89	9	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene RAB40C	RARL, RASL8C, RAB40C	RAB40C, member RAS oncogene family	NM_021168, NM_001172663, NM_001172664, NM_001172665, NM_001172666, hCT13524.3, hCT1984032.1, hCT1984033.1, hCT1984034.1	1569398_at, 213466_at, 227289_s_at, 227898_s_at	NP_066991.3, NP_001166134.1, NP_001166135.1, NP_001166136.1, NP_001166137.1, EAW85791.1, EAW85792.1, EAW85793.1, EAW85794.1
GeneID:117166	WFIKKN1	16	681,012	684,116	3,104	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2159, 2_A375_pNL97_plus_lncRNA_AR..1..3052, 4_A375_EGR1..1..2737, 4_A375_EGR1..1..2738, 4_A375_EGR1..1..2739, 4_A375_EGR1..1..2740, 4_A375_EGR1..1..2741	5420, 5420, -4660, 266, 5604, 6828, 10604	downstream, downstream, upstream, in gene, downstream, downstream, downstream	1	1	1	15	16.8	21.4	5	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene WFIKKN1	C16orf12, RJD2, WFIKKN1, WFIKKN, MGC126651, MGC126655	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1	NM_053284, hCT1658065.1	1552811_at	NP_444514.1, EAW85790.1
GeneID:84326	C16orf13	16	684,429	686,347	1,918	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2159, 2_A375_pNL97_plus_lncRNA_AR..1..3052, 4_A375_EGR1..1..2737, 4_A375_EGR1..1..2738, 4_A375_EGR1..1..2739, 4_A375_EGR1..1..2740, 4_A375_EGR1..1..2741	-85, -85, 9995, 5067, -469, -1493, -5269	upstream, upstream, downstream, downstream, upstream, upstream, upstream	1	1	1	15	16.8	21.4	5	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene C16orf13	C16orf13, JFP2, MGC13114	chromosome 16 open reading frame 13	NM_032366, NM_001040160, NM_001040161, NM_001040162, NM_001040165, hCT13538.3, hCT1956057.1, hCT1956060.1, hCT1966476.1, hCT2356727.0, hCT2356728.0	1554466_a_at, 227378_x_at, 227380_x_at, 228114_x_at, 228118_x_at, 230851_x_at	NP_115742.3, NP_001035250.1, NP_001035251.1, NP_001035252.1, NP_001035255.1, EAW85785.1, EAW85784.1, EAW85786.1, EAW85787.1, EAW85788.1, EAW85789.1
GeneID:100287175	LOC100287175	16	686,817	688,620	1,803	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2159, 2_A375_pNL97_plus_lncRNA_AR..1..3052, 4_A375_EGR1..1..2738, 4_A375_EGR1..1..2739, 4_A375_EGR1..1..2740, 4_A375_EGR1..1..2741	-365, -365, -5537, -1, 1023, 4799	upstream, upstream, upstream, upstream, in gene, downstream	1	1	1	16.75	19	22	4	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene LOC100287175		hypothetical LOC100287175	XR_111626, XR_109236, XR_114925		
GeneID:100130285	LOC100130285	16	691,039	691,735	696	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2159, 2_A375_pNL97_plus_lncRNA_AR..1..3052, 4_A375_EGR1..1..2738, 4_A375_EGR1..1..2739, 4_A375_EGR1..1..2740, 4_A375_EGR1..1..2741	5303, 5303, 10455, 4919, 3895, 119	downstream, downstream, downstream, downstream, downstream, in gene	1	1	1	16.75	19	22	4	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene LOC100130285	FLJ40285	hypothetical LOC100130285	XR_109235, XR_114924		
GeneID:84331	FAM195A	16	691,849	698,474	6,625	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2159, 2_A375_pNL97_plus_lncRNA_AR..1..3052, 4_A375_EGR1..1..2739, 4_A375_EGR1..1..2740, 4_A375_EGR1..1..2741	-5417, -5417, -5033, -4009, -233	upstream, upstream, upstream, upstream, upstream	1	1	1	20.33	23.33	23.67	3	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene FAM195A	C16orf14, MGC104301, FAM195A, c349E10.1, MGC15416	family with sequence similarity 195, member A	NM_138418, hCT13534.3, hCT1984039.1, hCT1966470.1, hCT2345138.0	1553715_s_at, 225661_at, 231516_at	NP_612427.2, EAW85781.1, EAW85779.1, EAW85780.1, EAW85782.1
GeneID:100507146	LOC100507146	16	698,473	699,029	556	-	1	4_A375_EGR1..1..2741	7413	downstream	0	0	1	13	13	20	1	4_A375_EGR1..1	20	Gene LOC100507146		hypothetical LOC100507146	XR_109237		
GeneID:197335	WDR90	16	699,363	717,829	18,466	+	7	2_A375_pNL97_plus_lncRNA_AR..1..3053, 4_A375_EGR1..1..2741, 4_A375_EGR1..1..2742, 4_A375_EGR1..1..2743, 4_A375_EGR1..1..2744, 4_A375_EGR1..1..2745, 4_A375_EGR1..1..2746	18621, -7747, 16549, 19533, 24349, 25501, 27693	downstream, upstream, in gene, downstream, downstream, downstream, downstream	0	1	1	8.67	12.83	18.83	6	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene WDR90	FLJ36483, C16orf16, KIAA1924, C16orf19, WDR90, C16orf15, C16orf18, FLJ44660, C16orf17	WD repeat domain 90	NM_145294	227894_at, 236049_at, 242211_x_at	NP_660337.3
GeneID:100507167	LOC100507167	16	713,960	715,807	1,847	+	5	2_A375_pNL97_plus_lncRNA_AR..1..3053, 4_A375_EGR1..1..2742, 4_A375_EGR1..1..2743, 4_A375_EGR1..1..2744, 4_A375_EGR1..1..2745	4024, 1952, 4936, 9752, 10904	downstream, downstream, downstream, downstream, downstream	0	1	1	8.5	13.5	18.5	4	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LOC100507167		hypothetical LOC100507167	XR_109238		



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_pNU27_vs_pNU27_all_lncRNA_IR_1 Percent	2_A375_pNU27_all_lncRNA_IR_1 Present	3_A375_EGFR_1 Present	1_A375_pNU27_all_lncRNA_IR_1 Avg Peak	2_A375_pNU27_all_lncRNA_IR_1 Avg Peak	3_A375_EGFR_1 Avg Peak	Add Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:39941	RHOT2	19	710,153	724,171	14,018	+	10	2_A375_pNU27_plus_lncRNA_IR_1..3053,2_A375_pNU27_plus_lncRNA_IR_1..3054,2_A375_EGFR_1..2742,4_A375_EGFR_1..2742,1_A375_EGFR_1..2744,4_A375_EGFR_1..2745,1_A375_EGFR_1..2746,4_A375_EGFR_1..2747,1_A375_EGFR_1..2749	149,15551,-2251,782,5979,6701,8923,1211,14155,19659	upstream,downstream,upstream,gene,overlaps,downstream,downstream,downstream,downstream,downstream	0	1	1	9.83	14.56	16.25	6	2_A375_pNU27_T_plus_lncRNA_AR_1	24	Gene RHOT2	RHOT2, C16orf28, MIRO-2, RASL, ARHT2	rab homolog gene family, member T2	NM_130789,NCT03333,NCT1964036.1,NCT1964037.1,NCT2260431.0,NCT2260434.0,NCT2260435.0	55770_at	NP_570124.1, EAW65797.1, EAW65783.1, EAW65784.1, EAW65785.1, EAW65786.1, EAW65787.1, EAW65783.1
GeneID:39942	RHBDL1	19	736,076	739,260	3,185	+	11	2_A375_pNU27_plus_lncRNA_IR_1..3053,2_A375_pNU27_plus_lncRNA_IR_1..3054,2_A375_EGFR_1..2742,4_A375_EGFR_1..2742,1_A375_EGFR_1..2744,4_A375_EGFR_1..2745,1_A375_EGFR_1..2746,4_A375_EGFR_1..2747,1_A375_EGFR_1..2749,4_A375_EGFR_1..2750	-6991,7909,-10163,-7179,-2361,-1211,9915,3269,6213,7705,9125	upstream,downstream,upstream,upstream,upstream,upstream,upstream,gene,downstream,downstream,downstream,downstream,downstream,downstream	0	1	1	10.44	14.11	16.89	9	2_A375_pNU27_T_plus_lncRNA_AR_1	24	Gene RHBDL1	RHP, RHBDL1, RHBD11	rhomboid, veinlet-like 1 (Drosophila)	NM_032991,NCT15212.2,NCT1964023.1,NCT2260440.0	537353_s_at	NP_597992.1, EAW65792.1, EAW65793.1, EAW65791.1
GeneID:10073	ITGB1BP2	19	750,115	752,786	2,653	+	9	2_A375_pNU27_plus_lncRNA_IR_1..3054,2_A375_pNU27_plus_lncRNA_IR_1..3055,1_A375_EGFR_1..2744,4_A375_EGFR_1..2745,1_A375_EGFR_1..2746,4_A375_EGFR_1..2747,1_A375_EGFR_1..2749,4_A375_EGFR_1..2750	3989,5227,-6403,-8251,2695,-771,2175,3677,-5055	downstream,downstream,upstream,upstream,upstream,upstream,gene,downstream,downstream	0	1	1	11.75	14.5	16.85	6	4_A375_EGFR_1..1	24	Gene ITGB1	ITGB1, CD29, FNRB, MDF2, MSK12	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	NM_205581,NCT15212.2,NCT1966499.1,NCT2260747.0	217904_x_at,217925_s_at,233698_x_at	NP_205552.2, EAW65798.1, EAW65795.1, EAW65797.1
GeneID:33	JAUD1	19	751,897	754,439	2,772	-	9	2_A375_pNU27_plus_lncRNA_IR_1..3054,2_A375_pNU27_plus_lncRNA_IR_1..3055,1_A375_EGFR_1..2744,4_A375_EGFR_1..2745,1_A375_EGFR_1..2746,4_A375_EGFR_1..2747,1_A375_EGFR_1..2749,4_A375_EGFR_1..2750	436,-1813,10727,3575,7283,3099,2151,647,-761	u gene, upstream, downstream, downstream, downstream, downstream, u gene, u gene, upstream	0	1	1	11.75	14.3	16.83	8	4_A375_EGFR_1..1	24	Gene JAUD1	PF14297, zf-AD, C19orf29	zinc-ribbon domain containing 5	NM_031009920,NCT15319.3,NCT1964026.1	224699_at	NP_001009220.2, EAW65793.1, EAW65794.1
GeneID:64219	WDR24	19	734,702	743,448	8,746	-	8	2_A375_pNU27_plus_lncRNA_IR_1..3054,2_A375_pNU27_plus_lncRNA_IR_1..3055,1_A375_EGFR_1..2744,4_A375_EGFR_1..2745,1_A375_EGFR_1..2746,4_A375_EGFR_1..2747,4_A375_EGFR_1..2748,4_A375_EGFR_1..2750	6416,48,15539,12844,11086,6112,4605,5208	downstream,u gene,downstream,downstream,downstream,downstream,u gene	0	1	1	12.29	13.14	16.14	7	4_A375_EGFR_1..1	24	Gene WDR24	WDR24, JFP7, DKFZp434P094, C16orf21	WD repeat domain 24	NM_032305,NCT13829.3,NCT2260300.0,NCT2260301.0	223280_at	NP_115835.1, EAW65783.1, EAW65782.1
GeneID:14930	FBXL16	19	742,008	755,826	13,819	-	11	2_A375_pNU27_plus_lncRNA_IR_1..3054,2_A375_pNU27_plus_lncRNA_IR_1..3055,1_A375_EGFR_1..2744,4_A375_EGFR_1..2745,1_A375_EGFR_1..2746,4_A375_EGFR_1..2747,1_A375_EGFR_1..2749,4_A375_EGFR_1..2750,1_A375_EGFR_1..2752,4_A375_EGFR_1..2753,4_A375_EGFR_1..2758	21841,15473,20577,22033,20623,4857,2203,-935,3939,-5775,-5079	downstream,downstream,downstream,downstream,downstream,downstream,u gene,downstream,upstream,upstream,upstream,upstream	0	1	1	11.1	12	16.1	10	4_A375_EGFR_1..1	24	Gene FBXL16	FLJ32733, cl00041.1, MGC23376, FB16_C19orf22, FBL16	F-box and leucine-rich repeat protein 16	NM_182350,NCT01869722.0,NCT2262297.1	227841_at,233699_x_at	NP_899031.2, EAW65749.1, EAW65750.1
GeneID:10267331	LOC100287301	19	737,313	739,437	2,124	+	6	4_A375_EGFR_1..2751,4_A375_EGFR_1..2752,4_A375_EGFR_1..2753,4_A375_EGFR_1..2756,4_A375_EGFR_1..2758,4_A375_EGFR_1..2760,4_A375_EGFR_1..2761	-6165,-5321,-633,2351,4267,6581,9955,10163	upstream,upstream,upstream,downstream,downstream,downstream,downstream,downstream	0	0	1	8.3	8.83	16.83	6	4_A375_EGFR_1..1	23	Gene LOC100287301	ps32	hypothetical LOC100287301	XR_111823,XR_109239,XR_114927		
GeneID:79158	METRNL	19	765,173	767,480	2,307	+	10	2_A375_pNU27_plus_lncRNA_IR_1..3056,2_A375_EGFR_1..2753,4_A375_EGFR_1..2756,4_A375_EGFR_1..2758,4_A375_EGFR_1..2759,4_A375_EGFR_1..2760,4_A375_EGFR_1..2761	6016,-6693,-3305,-5575,1269,2139,2922,2167,9227,11251	downstream,upstream,upstream,upstream,upstream,u gene,downstream,downstream,downstream,downstream	0	1	1	9.7	10.5	16.9	10	2_A375_pNU27_T_plus_lncRNA_AR_1	23	Gene METRNL	MGC2651, METRNL, cl00A12, C19orf23	meteorin, glial cell differentiation regulator	NM_024042,NCT13522.2,NCT1955263.1	219551_x_at,232269_x_at	NP_076947.1, EAW65747.1, EAW65745.1
GeneID:85995	FAM175A	19	771,156	772,590	1,432	+	6	2_A375_pNU27_plus_lncRNA_IR_1..3056,4_A375_EGFR_1..2756,4_A375_EGFR_1..2758,4_A375_EGFR_1..2759,4_A375_EGFR_1..2760,4_A375_EGFR_1..2761	51,-1555,-7254,5949,-3562,1182,3242,5096,7994	u gene, upstream, downstream, upstream, u gene, downstream, downstream, downstream, downstream	0	1	1	10	11.11	17.33	9	2_A375_pNU27_T_plus_lncRNA_AR_1	23	Gene FAM175A	FAM175A, C19orf24, MGC24494	family with sequence similarity 175, member A	NM_032933,NCT15337.0	219709_x_at	NP_376422.1, EAW65748.1
GeneID:12560	CCDC78	19	772,982	778,470	5,891	+	6	2_A375_pNU27_plus_lncRNA_IR_1..3056,2_A375_EGFR_1..2756,4_A375_EGFR_1..2758,4_A375_EGFR_1..2759,4_A375_EGFR_1..2760,4_A375_EGFR_1..2761,4_A375_EGFR_1..2762	6264,12569,9191,8277,4150,2013,349,-2679	downstream,downstream,downstream,downstream,downstream,u gene, u gene, upstream	0	1	1	9.38	11.29	17.83	6	2_A375_pNU27_T_plus_lncRNA_AR_1	23	Gene CCDC78	CCDC78, PLK/S12, C19orf25, cFP10	coiled-coil domain containing 78	NM_031031737,NCT15169914,NCT15163542.2,NCT1963249.2,NCT2260983.1,NCT2260984.1,NCT2260985.1,NCT2260986.1,NCT2260987.0,NCT2260988.0,NCT2260989.0,NCT2260990.0,NCT2260991.0,NCT2260992.0,NCT2260993.0,NCT2260994.0,NCT2260995.0,NCT2260996.0,NCT2260997.0	239749_at	NP_001029937.2, EAW65741.1, EAW65742.1, EAW65735.1, EAW65740.1, EAW65737.1, EAW65730.1, EAW65742.1, EAW65744.1, EAW65743.1
GeneID:64284	HKSHL	19	779,598	779,715	2,737	+	7	2_A375_pNU27_plus_lncRNA_IR_1..3056,1_A375_EGFR_1..2754,4_A375_EGFR_1..2756,4_A375_EGFR_1..2758,4_A375_EGFR_1..2760,4_A375_EGFR_1..2761,4_A375_EGFR_1..2762	-5781,-9848,-8982,-4835,2360,-734,2194	downstream,upstream,upstream,upstream,upstream,upstream,u gene	0	0	1	9.89	11.89	17	7	2_A375_pNU27_T_plus_lncRNA_AR_1	23	Gene HKSHL	MGC2655, HKSHL	hydroxykynureninase like, hydrolase-like	NM_032334, NM_207112, NCT13512.3,NCT15532.1,NCT1963280.1,NCT2260948.0,NCT2260972.0,NCT2260973.0,NCT2260974.0,NCT2260975.0,NCT2260976.0,NCT2260977.0,NCT2260978.0,NCT2260979.0,NCT2260980.0,NCT2260981.0,NCT2260982.0,NCT2260983.0,NCT2260984.0	223483_at	NP_115850.1, NP_996992.1, EAW65727.1, EAW65728.1, EAW65731.1, EAW65733.1, EAW65728.1, EAW65729.1, EAW65730.1, EAW65722.1
GeneID:64284	NAKPL1	19	779,797	790,997	11,200	-	7	2_A375_pNU27_plus_lncRNA_IR_1..3056,2_A375_pNU27_plus_lncRNA_IR_1..3057,4_A375_EGFR_1..2756,4_A375_EGFR_1..2760,4_A375_EGFR_1..2761,4_A375_EGFR_1..2762,4_A375_EGFR_1..2763	19005,-107,18877,16897,14772,11648,517	downstream,upstream,downstream,downstream,downstream,downstream,u gene	0	0	1	11.83	13.5	18	6	2_A375_pNU27_T_plus_lncRNA_AR_1	23	Gene NAKPL1	IOP1, HPRN, NAKPL1, LET1L, FLJ21900, PRN	isodecyl protonex A receptors, fodorin-like	NM_032443,NCT15326.2,NCT1955271.1,NCT2259981.0	219742_at	NP_071735.1, EAW65722.1, EAW65724.1
GeneID:10168	MSLN	19	810,768	815,668	4,900	+	8	4_A375_EGFR_1..2764,4_A375_EGFR_1..2765,4_A375_EGFR_1..2766,4_A375_EGFR_1..2767,4_A375_EGFR_1..2768,4_A375_EGFR_1..2769	1871,3354,-6087,u gene, u gene, u gene	u gene, u gene, u gene, u gene	0	0	1	5.33	6	17	6	4_A375_EGFR_1..1	20	Gene MSLN	C-kit1, MPF, MSLN, SMR, SMRP	mesothelin	NM_001177355, NM_003823, NM_013404, NCT13514.3, NCT15532.0, NCT2260461.0	204583_s_at	NP_037178.2, NP_620014.2, NP_037536.2, EAW65719.1, EAW65720.1, EAW65721.1
GeneID:44832	MSLNL	19	819,435	832,826	13,391	-	9	2_A375_pNU27_plus_lncRNA_IR_1..3056,2_A375_EGFR_1..2764,4_A375_EGFR_1..2765,4_A375_EGFR_1..2766,4_A375_EGFR_1..2767,4_A375_EGFR_1..2768,4_A375_EGFR_1..2769,4_A375_EGFR_1..2770,4_A375_EGFR_1..2771	-5794,20590,16777,16094,12614,8446,7475,-416,-1922	upstream,downstream,upstream,downstream,u gene, u gene, upstream, upstream	0	1	1	7.33	8.11	16.78	9	2_A375_pNU27_T_plus_lncRNA_AR_1	26	Gene MSLNL	C19orf57, MPF1, MSLNL	mesothelin-like	NM_031025190,NCT1964917.1,NCT2262286.0,NCT2262287.0		NP_001020611.2, EAW65715.1, EAW65716.1, EAW65717.1
GeneID:79158982	MIR6852	19	820,155	820,277	94	+	6	4_A375_EGFR_1..2764,4_A375_EGFR_1..2765,4_A375_EGFR_1..2766,4_A375_EGFR_1..2767,4_A375_EGFR_1..2768,4_A375_EGFR_1..2769	-7567,-4939,-3281,-71,4297,6265	upstream,upstream,upstream,upstream,downstream	0	0	1	5.33	6	17	6	4_A375_EGFR_1..1	20	Gene MIR6852	MIR6852, bta-mir-882, MIR6852	microRNA 6852	NM_032354		
GeneID:11000	RPUSD1	19	834,976	838,283	3,469	-	8	2_A375_pNU27_plus_lncRNA_IR_1..3056,2_A375_EGFR_1..2765,4_A375_EGFR_1..2770,4_A375_EGFR_1..2771,4_A375_EGFR_1..2772,4_A375_EGFR_1..2773	-329,12932,5029,3055,-5805,-7665	upstream,downstream,downstream,downstream,upstream,upstream	0	1	1	6.67	11.33	16	6	2_A375_pNU27_T_plus_lncRNA_AR_1	26	Gene RPUSD1	C19orf60, MGC19580, RLUC1, RPUSD1	RNA pseudouridylate synthase domain containing 1	NM_058192,NCT2262262.0,NCT2262263.0,NCT2262264.0,NCT2262265.0	226976_at	NP_476372.1, EAW65718.1, EAW65712.1, EAW65713.1, EAW65714.1
GeneID:85922	CHTF18	19	838,822	845,074	6,252	+	9	2_A375_pNU27_plus_lncRNA_IR_1..3056,1_A375_EGFR_1..2771,4_A375_EGFR_1..2772,4_A375_EGFR_1..2773,4_A375_EGFR_1..2774,4_A375_EGFR_1..2775,4_A375_EGFR_1..2776,4_A375_EGFR_1..2777	96,-5210,-7774,5370,7426,10754,11748,12930,16982	u gene, upstream, upstream, u gene, u gene, downstream, downstream	0	1	1	7.78	11.11	17.56	9	2_A375_pNU27_T_plus_lncRNA_AR_1	26	Gene CHTF18	C3D1D2.2, CHTF18, C19L12, RLAB1, C3D1D2.4, CI18, C3D1D2.3, C19orf61	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	NM_022092,NCT2260402.0,NCT2260404.0,NCT2260405.0,NCT2260406.0,NCT2260407.0,NCT2260408.0,NCT2260409.0,NCT2260410.0,NCT2260411.0,NCT2260412.0	226969_s_at	NP_071375.1, EAW65708.1, EAW65704.1, EAW65706.1, EAW65710.1, EAW65711.1, EAW65708.1, EAW65709.1, EAW65710.1
GeneID:57784	GNG13	19	843,041	850,731	7,690	+	7	2_A375_pNU27_plus_lncRNA_IR_1..3056,1_A375_EGFR_1..2773,4_A375_EGFR_1..2774,4_A375_EGFR_1..2775,4_A375_EGFR_1..2776,4_A375_EGFR_1..2777	12613,8541,4853,1557,383,819,-4551	downstream,downstream,downstream,u gene, u gene, upstream, upstream	0	1	1	7	11.89	17.43	7	2_A375_pNU27_T_plus_lncRNA_AR_1	26	Gene GNG13	GNG13, hG-25, Gigyanin g13	guanine nucleotide binding protein (G protein), gamma 13	NM_019541,NCT15541.2,NCT2258200.0	220806_x_at	NP_062525.1, EAW65702.1, EAW65703.1
GeneID:38199	PRR25	19	855,443	863,881	8,438	+	8	4_A375_EGFR_1..2773,4_A375_EGFR_1..2774,4_A375_EGFR_1..2775,4_A375_EGFR_1..2776,4_A375_EGFR_1..2777,4_A375_EGFR_1..2778	-4393,-6997,-5975,-3891,1413,1810	upstream,upstream,upstream,upstream,u gene, downstream	0	0	1	5.67	6.83	16.67	8	4_A375_EGFR_1..1	21	Gene PRR25	pp84, PRR25	proline rich 25	NM_031013938		NP_001013980.1
GeneID:84419	LMF1	19	1,001,834	1,031,310	127,884	+	14	2_A375_pNU27_plus_lncRNA_IR_1..3059,2_A375_EGFR_1..2781,4_A375_EGFR_1..2783,4_A375_EGFR_1..2784,4_A375_EGFR_1..2785,4_A375_EGFR_1..2786,4_A375_EGFR_1..2787,4_A375_EGFR_1..2788,4_A375_EGFR_1..2789,4_A375_EGFR_1..2790,4_A375_EGFR_1..2791,4_A375_EGFR_1..2792	10822,13690,129396,12564,112668,112190,101606,71626,83422,-2138,-2194,-4334,6750,-7768	u gene, downstream, upstream, u gene, u gene, u gene, u gene, u gene, upstream, upstream, upstream, upstream	0	1	1	8.07	8.93	18	14	4_A375_EGFR_1..1	23	Gene LMF1	FKBN112A, FKBN112, LMF1, C16orf28, FLJ22322, FLJ12681, dadFKBP39, cFP11	lipase maturation factor 1	NM_022773, NR_033845, NR_033848, NM_206442, NCT13827.0, NCT2257824.0, NCT2257825.0, NCT2257827.0, NCT2259894.0	1569043_s_at, 219155_s_at,219139_s_at, 242303_at,48142_at	NP_073610.2, EAW65697.1, EAW65698.1, EAW65699.1, EAW65700.1
GeneID:30312	SOX8	19	1,031,936	1,036,979	5,771	+	8	4_A375_EGFR_1..2781,4_A375_EGFR_1..2782,4_A375_EGFR_1..2783,4_A375_EGFR_1..2784,4_A375_EGFR_1..2785,4_A375_EGFR_1..2786,4_A375_EGFR_1..2787,4_A375_EGFR_1..2788	1965,2704,4094,4345,7298	u gene, u gene, u gene, downstream, downstream, downstream, downstream, downstream	0	0	1	8	8.6	18.6	5	4_A375_EGFR_1..1	20	Gene SOX8	MGC24437, SOX8	SRY (sex determining region Y)-box 8	NM_014587,NCT13829.3,NCT2260329.0	236113_s_at	NP_055402.2, EAW65691.1, EAW65692.1
GeneID:54480	LOC148336	19	1,114,091	1,138,751	14,660	-	10	2_A375_pNU27_plus_lncRNA_IR_1..3060,2_A375_EGFR_1..2809,4_A375_EGFR_1..2810,4_A375_EGFR_1..2811,4_A375_EGFR_1..2812,4_A375_EGFR_1..2813,4_A375_EGFR_1..2814,4_A375_EGFR_1..2815,4_A375_EGFR_1..2816	23883,22776,21883,12185,6861,91,-405,1233,-5175,-4057	downstream,downstream,downstream,downstream,u gene, u gene, upstream, upstream, upstream, upstream	0	0	1	8.1	8.5	18.3	10	4_A375_EGFR_1..1	16	Gene LOC148336	FLJ32252	hypothetical LOC148336	NR_027242,NCT2345930.1,NCT2347031.1	1557148_x_at	EAW65695.1, EAW65696.1
GeneID:85477	SSTR5	19	1,122,796	1,131,434	8,639	+	8	4_A375_EGFR_1..2810,4_A375_EGFR_1..2811,4_A375_EGFR_1..2812,4_A375_EGFR_1..2813,4_A375_EGFR_1..2814,4_A375_EGFR_1..2815,4_A375_EGFR_1..2816,4_A375_EGFR_1..2817	4190,-3719,3554,8203,7390,9165,10012,10276	upstream, upstream, u gene, u gene, u gene, upstream, upstream, upstream	0	0	1	8	8.25	18.25	8	4_A375_EGFR_1..1	16	Gene SSTR5	SSTR5, SS-3-R		NM_001053, NM_001172690, NCT1842821.1	214553_at	NP_001044.1, NP_001166031.1, EAW65697.1
GeneID:39843	C1QTNF8	19	1,138,228	1,148,244	10,016	-	8	4_A375_EGFR_1..2812,4_A375_EGFR_1..2813,4_A375_EGFR_1..2814,4_A375_EGFR_1..2815,4_A375_EGFR_1..2816,4_A375_EGFR_1..2817,4_A375_EGFR_1..2818,4_A375_EGFR_1..2819	17654,17108,16160,14340,13476,8212,936,-7229	downstream,upstream,upstream,upstream,upstream,upstream,u gene, u gene, upstream	0	0	1	8.88	8.75	18.63	8	4_A375_EGFR_1..1	19	Gene C1QTNF8	C1QTNF8, C1QTNF5, UNQ6529	C1q and tumor necrosis factor related protein 8	NM_207419, NCT1647130.0		NP_997302.2, EAW65698.1
GeneID:10183	GSS	19	1,148,811	1,160,895	12,084	+	4	4_A375_EGFR_1..2817,4_A375_EGFR_1..2818,4_A375_EGFR_1..2819,4_A375_EGFR_1..2820	20883,13496,7212,3743	downstream, u gene, u gene, u gene	0	0	1	7.5	7.25	17.5	4	4_A375_EGFR_1..1	19	Gene GSS		hypothetical LOC100126765	XR_111823, XR_109243, XR_114902		

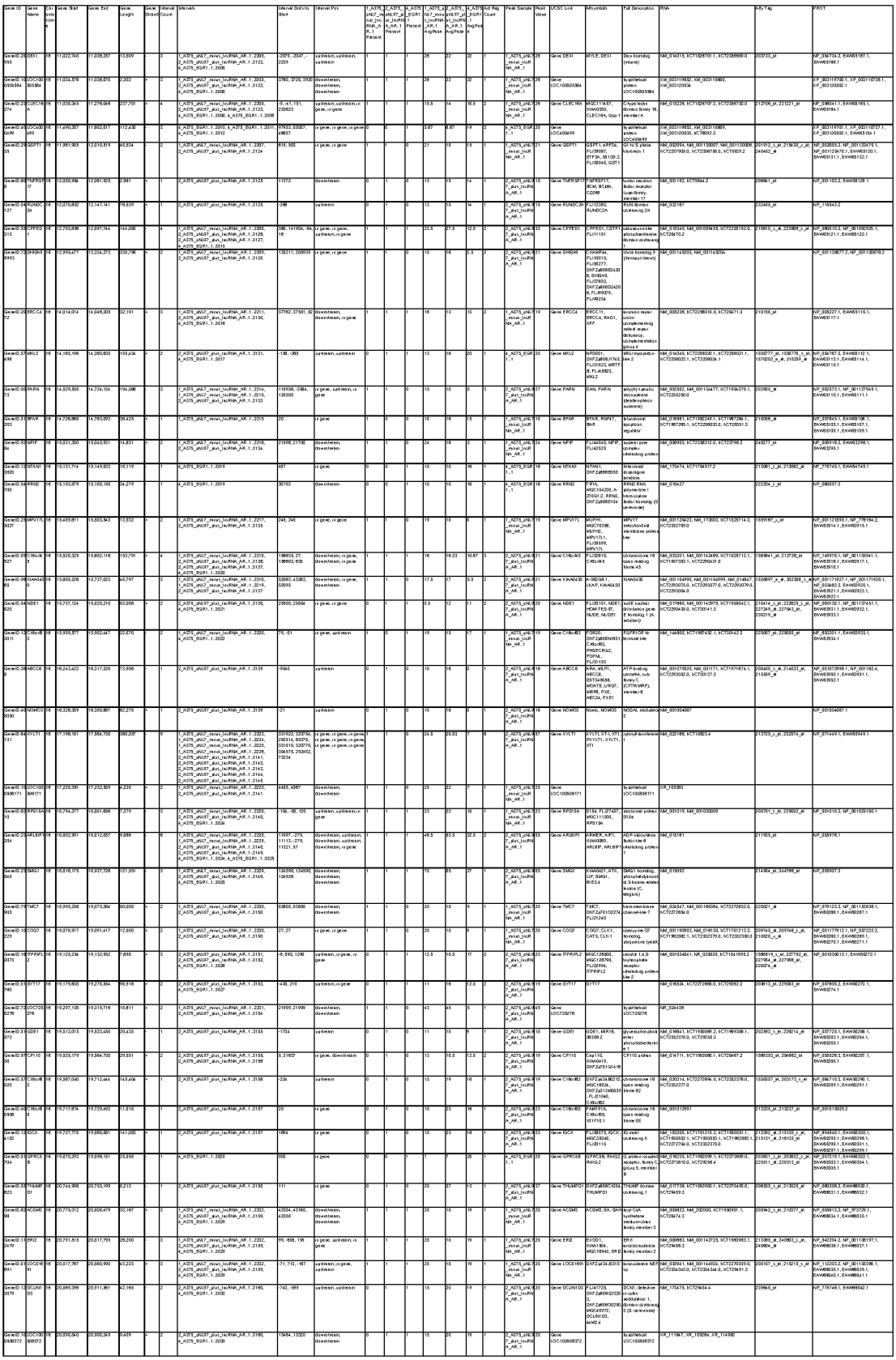


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_shN7_wtA375_shN7_incRNA_AR_1 Present	2_A375_shN7_wtA375_shN7_incRNA_AR_1 Present	3_A375_shN7_incRNA_AR_1 Present	1_A375_shN7_incRNA_AR_1 Avg Peak	2_A375_shN7_incRNA_AR_1 Avg Peak	3_A375_shN7_incRNA_AR_1 Avg Peak	Add Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:2312	CACNA1H	16	1,203,241	1,271,792	68,551	+	16	4_A375_EGFR1.1.2823, 4_A375_EGFR1.1.2838, 4_A375_EGFR1.1.2839, 4_A375_EGFR1.1.2838, 4_A375_EGFR1.1.2837, 4_A375_EGFR1.1.2839, 4_A375_EGFR1.1.2838, 4_A375_EGFR1.1.2831, 4_A375_EGFR1.1.2832, 4_A375_EGFR1.1.2834, 4_A375_EGFR1.1.2839, 4_A375_EGFR1.1.2838, 4_A375_EGFR1.1.2837, 4_A375_EGFR1.1.2838, 4_A375_EGFR1.1.2839, 4_A375_EGFR1.1.2840	10121, 4791, 9991, 13976, 19607, 19031, 27589, 27321, 31111, 33303, 34135, 51191, 56859, 57781, 59267, 61994, 64455, 66367	upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	7	7.76	16.17	18	4_A375_EGFR1..1	23	Gene:CACNA1H	CACNA1H, Gm38, CACHA1H, FLJ46454, ECA6, Cav3.2	calcium channel, voltage-dependent, T type, alpha 1H subunit	NM_021098, NM_001003407, NC_000016.9, NC_018930.2	2359615_at_222990_at	NP_066921.2, NP_001003407.1, EAW66633.1, EAW66664.1
GeneID:8420	TPSG1	16	1,271,631	1,278,234	6,603	+	4	4_A375_EGFR1.1.2837, 4_A375_EGFR1.1.2838, 4_A375_EGFR1.1.2839, 4_A375_EGFR1.1.2840	12726, 19349, 7886, 3926	Downstream, Downstream, Downstream, Downstream	0	0	1	8.75	8.35	20	4	4_A375_EGFR1..1	23	Gene:TPSG1	TAT, TPSG1, PRSS31, tryA	tryptase gamma 1	NM_012467, NC_000016.9	233039_s_at	NP_036590.3, EAW66662.1
GeneID:8420	TPSB2	16	1,276,026	1,290,165	14,140	+	1	4_A375_EGFR1.1.2840	9837	Downstream	0	0	1	4	8	19	1	4_A375_EGFR1..1	19	Gene:TPSB2	tryptase beta 2 (gene/pseudogene), TPSB2	tryptase beta 2	NM_024164	207741_x_at	NP_077076.3
GeneID:7320	UBE2I	19	3,991,180	4,078,290	87,110	+	5	1_A375_shN7_incrRNA_AR_1.2160, 2_A375_shU87_plus_IncRNA_AR_1.2090, 3_A375_shU87_plus_IncRNA_AR_1.2091, 4_A375_EGFR1.1.2641, 4_A375_EGFR1.1.2642, 4_A375_EGFR1.1.2643	64, -12, -8772, 4084, 23998	up gene, upstream, upstream, up gene, downstream	1	1	1	16.73	14.25	17.8	4	1_A375_shN7_incrRNA_AR_1.2160	Gene:UBE2I	UBE2I, UBC9, C358B7.1, P18	ubiquitin conjugating enzyme E2I (UBC9 homolog, yeast)	NM_003345, NM_194259, NM_194260, NC_000019.9, NC_018941.5, NT_011362.9, NT_167190.1, NC_000019.10, NT_011362.10, NT_167190.2, NC_018941.6	1555668_a_at_206760_at, 211006_s_at_213033_s_at, 213306_s_at_213393_at	NP_003336.1, NP_919238.1, NP_919239.1, NP_919237.1, EAW66673.1, EAW66674.1, EAW66674.1, EAW66675.1, EAW66676.1, EAW66677.1, EAW66678.1
GeneID:8947	BNIP3	19	1,354,660	1,359,442	14,779	+	7	2_A375_shU87_plus_IncRNA_AR_1.3061, 3_A375_shU87_plus_IncRNA_AR_1.2643, 4_A375_EGFR1.1.2644, 4_A375_EGFR1.1.2645, 4_A375_EGFR1.1.2646, 4_A375_EGFR1.1.2647, 4_A375_EGFR1.1.2648	17143, -1527, 7753, 9541, 13635, 16285, 22833	Downstream, upstream, up gene, in gene, up gene, Downstream, Downstream	0	1	1	9	12.33	17	6	2_A375_shU87_plus_IncRNA_AR_1	21	Gene:BNIP3	BNIP3, BNIP3, BNIP3, bcl2/adenovirus E1B 19kDa interacting protein 3	BCL2/adenovirus E1B 19kDa interacting protein 3	NM_004331, NC_000019.9, NC_018941.5, NT_011362.9	204974_s_at_216536_x_at	NP_004324.2, EAW66670.1, EAW66671.1, EAW66672.1
GeneID:1151	C16orf86	16	1,399,241	1,401,675	2,432	-	6	2_A375_shU87_plus_IncRNA_AR_1.3061, 3_A375_shU87_plus_IncRNA_AR_1.2644, 4_A375_EGFR1.1.2645, 4_A375_EGFR1.1.2646, 4_A375_EGFR1.1.2647, 4_A375_EGFR1.1.2648	65, 9426, 9369, 5360, 905, -5425	up gene, downstream, Downstream, Downstream, up gene, upstream	0	1	1	8.6	13.6	16.6	5	2_A375_shU87_plus_IncRNA_AR_1	21	Gene:C16orf62	C16orf62, MGC24281	chromosome 16 open reading frame 42	NM_001031410, NC_000016.9	215104_at_213053_x_at, 214087_at_221952_x_at	NP_001031410.1, EAW66669.1
GeneID:5472	GNPTG	16	1,491,900	1,513,352	11,452	+	5	2_A375_shU87_plus_IncRNA_AR_1.3061, 3_A375_shU87_plus_IncRNA_AR_1.2644, 4_A375_EGFR1.1.2644, 4_A375_EGFR1.1.2645, 4_A375_EGFR1.1.2646, 4_A375_EGFR1.1.2647, 4_A375_EGFR1.1.2648, 4_A375_EGFR1.1.2649, 4_A375_EGFR1.1.2650	-92, -9452, -9396, 3917, -972, 5388, 11793, 14454	upstream, upstream, upstream, upstream, in gene, Downstream, Downstream	0	1	1	7.71	13	16.66	7	2_A375_shU87_plus_IncRNA_AR_1	21	Gene:GNPTG	N-ACETYLGLUCOSAMINE-1-PHOSPHOTRANSFERASE, GAMMA SUBUNIT, LPSS1	N-acetylglucosamine-1-phosphate transferase, gamma subunit	NM_032520, NC_000016.9, NT_187633.1, NC_018930.2	224587_at	NP_115925.1, EAW66666.1, EAW66666.1, EAW66667.1
GeneID:8461	UNK1	16	1,413,206	1,484,705	51,499	-	5	1_A375_shU87_mrwt_IncRNA_AR_1.2161, 2_A375_shU87_plus_IncRNA_AR_1.2092, 3_A375_shU87_plus_IncRNA_AR_1.2644, 4_A375_EGFR1.1.2650	-6905, -6931, 57609, 51105, 46821	upstream, upstream, Downstream, in gene, in gene	1	1	1	11	14	16.75	4	1_A375_shU87_mrwt_IncRNA_AR_1	27	Gene:UNK1	ZCCHC5, UNK1, FLJ22360, MGC31179, C16orf26, ZCCHC5OL, FLJ12623, SHA0704	zinc-finger homology (Drosophila)-like 1	NM_031377.25, NM_027976, NM_001119366, NC_000016.9, NT_187633.1, NC_018930.2	235087_at	NP_001032222.1, NP_079564.3, NP_001103171.1, NP_001103170.1, EAW66665.1, EAW66665.1, EAW66666.1
GeneID:2306	C16orf86	19	1,489,944	1,479,548	9,651	-	5	1_A375_shU87_mrwt_IncRNA_AR_1.2161, 2_A375_shU87_plus_IncRNA_AR_1.2092, 3_A375_shU87_plus_IncRNA_AR_1.2643, 4_A375_EGFR1.1.2631, 4_A375_EGFR1.1.2632, 4_A375_EGFR1.1.2633	6343, 6809, 497, 3324, -6767	up gene, in gene, up gene, upstream, upstream	1	1	1	10	10.75	16.5	4	1_A375_shU87_plus_IncRNA_AR_1	27	Gene:C16orf61	gm101, MGC10272, CCDC97, C16orf61	chromosome 16 open reading frame 61	NM_001010976, NC_018930.2, NT_187633.1, NC_000016.9	1233749_at	NP_001010976.1, EAW66667.1, EAW66668.1
GeneID:8441	CCDC1 54	19	1,484,309	1,494,490	10,181	-	7	4_A375_EGFR1.1.2631, 4_A375_EGFR1.1.2632, 4_A375_EGFR1.1.2633, 4_A375_EGFR1.1.2634, 4_A375_EGFR1.1.2635, 4_A375_EGFR1.1.2636, 4_A375_EGFR1.1.2637	11842, 11396, 8016, 1602, -1766, -3162, -7286	Downstream, Downstream, up gene, in gene, upstream, upstream	0	0	1	4.66	7.97	17.43	7	4_A375_EGFR1.1.2631	22	Gene:CCDC154	CCDC154	coiled-coil domain containing 154	NM_001142998		NP_001136432.1
GeneID:1115	CLCN7	16	1,974,935	1,931,085	50,150	+	8	2_A375_shU87_plus_IncRNA_AR_1.3061, 3_A375_shU87_plus_IncRNA_AR_1.2633, 4_A375_EGFR1.1.2634, 4_A375_EGFR1.1.2635, 4_A375_EGFR1.1.2636, 4_A375_EGFR1.1.2637	77, 38972, 32397, 29797, 27213, 23197	up gene, downstream, Downstream, in gene, in gene, in gene, in gene	0	1	1	7.67	12	18	6	2_A375_shU87_plus_IncRNA_AR_1	28	Gene:CLCN7	CLCN7, CLC-7, FLJ39844, OPTA2, FLJ39898, CLC7, OPTB4, FLJ46423	chloride channel 7	NM_001287, NM_001114331, NC_018930.2, NT_187633.1, NC_000016.9, NT_011362.9	209223_at_221981_at, 209389_at	NP_001278.1, NP_001107603.1, EAW66653.1, EAW66654.1, EAW66655.1
GeneID:2306	C16orf62	19	1,503,940	1,506,490	2,550	+	1	4_A375_EGFR1.1.2635	-3900	upstream	0	0	1	5	8	17	1	4_A375_EGFR1.1.2635	17	Gene:C16orf62	C16orf62, PTX4	pentraxin 4, long	NM_001013693, NC_018930.2		NP_001013693.1, EAW66652.1
GeneID:8847	TEC02	19	1,943,252	1,949,490	17,105	+	2	4_A375_EGFR1.1.2638, 4_A375_EGFR1.1.2639	1084, 8166	up gene, in gene	0	0	1	8	7	10.5	2	4_A375_EGFR1.1.2638	20	Gene:TEC02	KIAA0663, TEL2, CLK2, FLJ10924, TEL/2, DKFZp434A073	TEL2, telomere maintenance 2, TEL/2, DKFZp434A073	NM_016111, NC_018930.2, NT_187633.1, NC_000016.9	220928_s_at, 54392_at	NP_057195.2, EAW66647.1, EAW66648.1, EAW66649.1, EAW66650.1, EAW66651.1
GeneID:3577	PTT4G	19	1,960,426	1,962,109	101,661	-	5	2_A375_shU87_plus_IncRNA_AR_1.3061, 3_A375_shU87_plus_IncRNA_AR_1.2644, 4_A375_EGFR1.1.2639, 4_A375_EGFR1.1.2640, 4_A375_EGFR1.1.2641, 4_A375_EGFR1.1.2642, 4_A375_EGFR1.1.2643	113359, 61359, 59645, 56045, 50249	Downstream, in gene, in gene, in gene, in gene	0	0	1	6	8.2	17	5	4_A375_EGFR1.1.2639	20	Gene:PTT4G	PTT4G, DKFZp564J232, HGTC2, ptt14, FLJ39371, KIAA0350, UBXD13, FLJ10306, UBXD4	ubiquitin regulatory X (UBX) domain protein 4	NM_014714, NC_018930.2, NT_187633.1, NC_000016.9	204792_s_at_223644_at, 244565_at	NP_055530.2, EAW66644.1, EAW66645.1, EAW66646.1, EAW66651.1
GeneID:8523	TMEM2 04	19	1,964,251	1,969,245	21,212	+	4	2_A375_shU87_plus_IncRNA_AR_1.3061, 4_A375_EGFR1.1.2640	-3431, -2987, 187, 17529	upstream, upstream, upstream, up gene	0	0	1	5.75	9	16.25	4	4_A375_EGFR1.1.2640	16	Gene:TMEM204	C16orf51, CLP36, FLJ30999, MGC111984, TMEM204	transmembrane protein 204	NM_024930, NC_018930.2, NT_187633.1, NC_000016.9	219115_s_at_222993_s_at, 220947_s_at	NP_079178.2, EAW66640.1, EAW66641.1, EAW66642.1
GeneID:5552	CRAMP1L	19	1,984,841	1,727,999	60,266	+	5	2_A375_shU87_plus_IncRNA_AR_1.3062, 3_A375_shU87_plus_IncRNA_AR_1.2644, 4_A375_EGFR1.1.2641	31455, 31519, 42015	up gene, in gene, up gene	1	1	1	11.5	12.5	12	2	2_A375_shU87_plus_IncRNA_AR_1	16	Gene:CRAMP1L	RNTL, MGC118758, CRAMP1L, TCEN	Crm, cramped-like (Drosophila)	NM_020625, NC_018930.2, NT_187633.1, NC_000016.9	220172_at_240930_at, 242325_at	NP_065676.3, EAW66641.1, EAW66642.1
GeneID:8611	HNT1	19	1,720,276	1,752,075	33,765	+	2	1_A375_shU87_mrwt_IncRNA_AR_1.2163, 2_A375_shU87_plus_IncRNA_AR_1.3063	27948, 27708	Downstream, Downstream, in gene	1	1	0	21	19	11	1	1_A375_shU87_mrwt_IncRNA_AR_1	21	Gene:HNT1	HNT1, L11, C16orf34, FLJ13092, KIAA1429	hemitriad protein homolog (S. cerevisiae) 1-like	NM_144570, NC_018930.2, NT_187633.1, NC_000016.9, NT_187633.2, NC_018930.3	212109_at_212115_at, 216031_s_at	NP_653211.1, EAW66638.1, EAW66639.1, EAW66640.1, EAW66638.1, EAW66639.1, EAW66640.1, EAW66638.1
GeneID:2356	MAP4K3	19	1,756,221	1,820,516	64,297	+	13	2_A375_shU87_mrwt_IncRNA_AR_1.2163, 2_A375_shU87_plus_IncRNA_AR_1.3063, 3_A375_shU87_plus_IncRNA_AR_1.3066, 3_A375_shU87_plus_IncRNA_AR_1.3067, 4_A375_EGFR1.1.2635, 4_A375_EGFR1.1.2636, 4_A375_EGFR1.1.2637, 4_A375_EGFR1.1.2638, 4_A375_EGFR1.1.2639, 4_A375_EGFR1.1.2640, 4_A375_EGFR1.1.2641, 4_A375_EGFR1.1.2642, 4_A375_EGFR1.1.2643	2, -227, 65907, 66031, 40547, 58035, 63187, 62715, 64491, 66031, 65997, 72359, 73539	up gene, upstream, Downstream, Downstream, up gene, in gene, in gene, Downstream, Downstream, Downstream, Downstream, Downstream, Downstream	1	1	1	10.64	13.91	18.62	11	2_A375_shU87_plus_IncRNA_AR_1	30	Gene:MAP4K3	KIAA1059, MAP4K3P2, DKFZp686I2232, FLJ00027, lyd, SKY1, DKFZp762N1113	mitogen-activated protein kinase kinase kinase kinase 3	NM_031494.39, NM_031103, NC_018930.2, NT_187633.1, NC_000016.9, NT_187633.2, NC_018930.3	210177_at_213776_s_at, 216137_s_at_216139_s_at, 230182_s_at_233055_at	NP_001035297.1, NP_036945.2, EAW66630.1, EAW66631.1, EAW66632.1, EAW66633.1
GeneID:4869	NME3	19	1,820,321	1,821,710	1,389	-	10	2_A375_shU87_plus_IncRNA_AR_1.3066, 3_A375_shU87_plus_IncRNA_AR_1.3067, 4_A375_EGFR1.1.2635, 4_A375_EGFR1.1.2636, 4_A375_EGFR1.1.2637, 4_A375_EGFR1.1.2638, 4_A375_EGFR1.1.2639, 4_A375_EGFR1.1.2640, 4_A375_EGFR1.1.2641, 4_A375_EGFR1.1.2642, 4_A375_EGFR1.1.2643	-418, -1282, 7150, 2332, 1774, 796, -1062, -4176, -6566, 6080	upstream, upstream, Downstream, Downstream, in gene, upstream, upstream, upstream, upstream	0	1	1	9.44	13	17	9	2_A375_shU87_plus_IncRNA_AR_1	30	Gene:NME3	KIAA0318, NM23, NDPK-C, NM23H3, DR-nm23, c21rf62, NDPKC, NME3-HS	non-metastatic cells 3, protein expressed in	NM_002513, NC_018930.2	204862_s_at	NP_002504.2, EAW65829.1
GeneID:8561	MRPS34	19	1,821,896	1,823,140	1,244	-	11	2_A375_shU87_plus_IncRNA_AR_1.3066, 2_A375_shU87_plus_IncRNA_AR_1.3067, 3_A375_shU87_plus_IncRNA_AR_1.3065, 3_A375_shU87_plus_IncRNA_AR_1.3066, 4_A375_EGFR1.1.2635, 4_A375_EGFR1.1.2636, 4_A375_EGFR1.1.2637, 4_A375_EGFR1.1.2638, 4_A375_EGFR1.1.2639, 4_A375_EGFR1.1.2640, 4_A375_EGFR1.1.2641, 4_A375_EGFR1.1.2642, 4_A375_EGFR1.1.2643	1012, 66, -1656, 6365, 3732, 3204, 2235, 65, -2745, 3435, -6820	up gene, in gene, upstream, Downstream, Downstream, Downstream, in gene, upstream, upstream, upstream	0	1	1	9.6	14.3	18.5	10	2_A375_shU87_plus_IncRNA_AR_1	30	Gene:MRPS34	MRPS12, MRP-S34, MRPS34, MGC20516, MRPS12	mitochondrial ribosomal protein S34	NM_023936, NC_018930.2, NT_187633.1, NC_000019.9	218112_at	NP_076425.1, EAW65827.1, EAW65828.1
GeneID:1161	EME2	19	1,823,229	1,836,239	13,010	+	11	2_A375_shU87_plus_IncRNA_AR_1.3066, 2_A375_shU87_plus_IncRNA_AR_1.3067, 3_A375_shU87_plus_IncRNA_AR_1.3065, 3_A375_shU87_plus_IncRNA_AR_1.3066, 4_A375_EGFR1.1.2635, 4_A375_EGFR1.1.2636, 4_A375_EGFR1.1.2637, 4_A375_EGFR1.1.2638, 4_A375_EGFR1.1.2639, 4_A375_EGFR1.1.2640, 4_A375_EGFR1.1.2641, 4_A375_EGFR1.1.2642, 4_A375_EGFR1.1.2643	1101, -157, 5869, -5865, 3921, -2293, 2217, -197, 2659, 5347, 6531	upstream, upstream, Downstream, Downstream, upstream, upstream, upstream, upstream, in gene, Downstream, Downstream	0	1	1	9.8	14.3	18.5	10	2_A375_shU87_plus_IncRNA_AR_1	30	Gene:EME2	FLJ30151, EME2, dJ223L10.2, KIAA1008	essential meiotic endonuclease 1 homolog 2 (S. pombe)	NM_001010865, NC_018930.2	1559624_at, 1561687_at, 1569680_s_at	NP_001010865.1, EAW66636.1
GeneID:9662	SPSB3	16	1,826,715	1,832,591	5,876	-	11	2_A375_shU87_plus_IncRNA_AR_1.3066, 2_A375_shU87_plus_IncRNA_AR_1.3067, 3_A375_shU87_plus_IncRNA_AR_1.3065, 3_A375_shU87_plus_IncRNA_AR_1.3066, 4_A375_EGFR1.1.2635, 4_A375_EGFR1.1.2636, 4_A375_EGFR1.1.2637, 4_A375_EGFR1.1.2638, 4_A375_EGFR1.1.2639, 4_A375_EGFR1.1.2640, 4_A375_EGFR1.1.2641, 4_A375_EGFR1.1.2642, 4_A375_EGFR1.1.2643	10650, 9509, 7471, 12845, 11989, 9809, 8055, 4309, 2921, -2979	Downstream, Downstream, Downstream, Downstream, Downstream, Downstream, Downstream, Downstream, Downstream, in gene, upstream	0	1	1	9.5	14.3	18.1	10	2_A375_shU87_plus_IncRNA_AR_1	30	Gene:SPSB3	SSB3, C16orf31, SPSB3	ssB/Ayesodcas repeats-containing SOCS box-containing 3	NM_080861, NC_018930.2, NT_187633.1, NC_000016.9, NT_187633.2, NC_018930.3	221769_at_46238_at	NP_542127.2, EAW65822.1, EAW65823.1, EAW65824.1, EAW65825.1, EAW65822.1, EAW65823.1
GeneID:1010	NUBP2	19	1,832,935	1,839,192	6,259	+	8	2_A375_shU87_plus_IncRNA_AR_1.3067, 2_A375_shU87_plus_IncRNA_AR_1.3068, 3_A375_shU87_plus_IncRNA_AR_1.3067, 3_A375_shU87_plus_IncRNA_AR_1.3068, 4_A375_EGFR1.1.2641, 4_A375_EGFR1.1.2642, 4_A375_EGFR1.1.2643, 4_A375_EGFR1.1.2644, 4_A375_EGFR1.1.2645	9981, -3, -9991, 7063, -4257, 5373, 3627, 11811	upstream, upstream, upstream, upstream, upstream, upstream, upstream, in gene, Downstream	0	1	1	8.66	14.14	16.29	7	2_A375_shU87_plus_IncRNA_AR_1	30	Gene:NUBP2	NUBP2, CFD1, NUBP1	nucleotide binding protein 2 (MinD homolog, E. coli)	NM_012225, NC_018930.2, NT_187633.1, NC_000019.9, NT_187633.2, NC_018930.3	210227_at	NP_036357.1, EAW65818.1, EAW65819.1, EAW65820.1, EAW65821.1, EAW65817.1
GeneID:3430	IGFALS	16	1,840,414	1,844,909	4,495	-	3	2_A375_shU87_plus_IncRNA_AR_1.3066, 3_A375_shU87_plus_IncRNA_AR_1.2674, 4_A375_EGFR1.1.2675	11961, 8349, 986	Downstream, Downstream, Downstream	0	1	1	9.33	14	15	3	2_A375_shU87_plus_IncRNA_AR_1	28	Gene:IGFALS	IGFALS, ALS	acid labile subunit	NM_004970, NM_001146808, NR_027089, NC_018930.2	219712_s_at	NP_004961.1, NP_001138478.1, EAW66612.1
GeneID:3800	RAGH	19	1,899,104	1,877,785	19,091	-	5	2_A375_shU87_mrwt_IncRNA_AR_1.2164, 2_A375_shU87_plus_IncRNA_AR_1.3069, 3_A375_shU87_plus_IncRNA_AR_1.2676, 4_A375_EGFR1.1.2677, 4_A375_EGFR1.1.2678	-81, -65, 9167, 5962, -149	upstream, upstream, in gene, upstream	1	1	1	10	20.33	17	5	2_A375_shU87_plus_IncRNA_AR_1	43	Gene:RAGH	GLO2, GLX2, RAGH, RAGHL, GLO2	hydroxyacylglutathione hydrolase	NM_031494.27, NM_003626, NC_018930.2, NT_187633.1, NC_000019.9, NT_011362.9	205012_s_at	NP_003617.2, EAW65809.1, EAW65810.1, EAW65811.1
GeneID:8510	FAHD1	19	1,877,225	1,890,206	12,982	+	5	2_A375_shU87_mrwt_IncRNA_AR_1.2164, 2_A375_shU87_plus_IncRNA_AR_1.3069, 3_A375_shU87_plus_IncRNA_AR_1.2676, 4_A375_EGFR1.1.2677, 4_A375_EGFR1.1.2678	31, 55, -9177, -5962, 119	in gene, in gene, upstream, upstream, in gene	1	1	1	10	20.33	17	5	2_A375_shU87_plus_IncRNA_AR_1	43	Gene:FAHD1	MGC74370, FAHD1, C16orf26, DKFZp686J0944, YHBX	fumarylacetoacetate hydrolase domain containing 1	NM_031510.04, NM_031200, NM_001142366, NC_018930.2, NT_187633.1	220767_s_at_227992_s_at	NP_001101614.1, NP_112458.1, NP_001138730.1, EAW65805.1
GeneID:2306	C16orf13	19	1,883,994	1,922,179	55,186	-	3	2_A375_shU87_mrwt_IncRNA_AR_1.2164, 2_A375_shU87_plus_IncRNA_AR_1.3069, 3_A375_shU87_plus_IncRNA_AR_1.2676	44823, 44099, 44033	Downstream, Downstream, Downstream	1	1	1	16	45	16	1	2_A375_shU87_plus_IncRNA_AR_1	43	Gene:C16orf13	gm129, C16orf13, MGC33212	chromosome 16 open reading frame 13	NM_152784, NM_001163980, NT_187633.1, NC_000016.9, NT_187633.2, NC_018930.3	237263_at	NP_689777.2, NP_001157022.1, EAW65804.1, EAW65805.1, EAW65806.1, EAW65807.1
GeneID:8420	HS3ST3B1	19	1,961,494	1,966,231	4,737	+	2	2_A375_shU87_plus_IncRNA_AR_1.2674, 4_A375_EGFR1.1.2680	6919, 4555	Downstream, in gene	0	0	1	8	7.5	15.5	2	4_A375_EGFR1.1.1	17	Gene:HS3ST6	HS3ST6, HS3ST3	heparan sulfate (glucosamine) 3-O-sulfotransferase 6	NM_001029906, NC_018930.2, NT_187633.1, NC_000016.9, NT_187633.2	239547_at	NP_001029906.2, EAW65803.1, EAW65802.1
GeneID:5310	SEPX1	19	1,968,234	1,993,234	0,990	+	2	4_A375_EGFR1.1.2681, 4_A375_EGFR1.1.2682	10002, 174	Downstream, in gene	0	0	1	10	9	19	2	4_A375_EGFR1.1.1	17	Gene:SEPX1	MSRB1, SELX, HSPC270, SELR, MGC3344, SEPX1	selenoprotein X, 1	NM_019232, NC_018930.2, NT_187633.1, NC_000016.9, NT_187633.2	217977_at	NP_057316.1, EAW65800.1, EAW65801.1
GeneID:8572	RPL3L	19	1,974,300	2,004,879	30,579	-	5	2_A375_shU87_mrwt_IncRNA_AR_1.2165, 2_A375_shU87_plus_IncRNA_AR_1.3070, 3_A375_shU87_plus_IncRNA_AR_1.2682, 4_A375_EGFR1.1.2683, 4_A375_EGFR1.1.2684	4825, -4837, 1350, -5017, 10089	upstream, upstream, upstream, upstream, upstream	1	1	1	16.67	20.33	22	5	2_A375_shU87_plus_IncRNA_AR_1	34	Gene:RPL3L	RPL3L	ribosomal protein L3-like	NM_005061, NC_018930.2	206768_at	NP_005052.1, EAW65799.1
GeneID:4724	NDUFB10	19	2,009,317	2,011,976	2,439	+	6	2_A375_shU87_mrwt_IncRNA_AR_1.2165, 3_A375_shU87_plus_IncRNA_AR_1.3070, 4_A375_EGFR1.1.2684, 4_A375_EGFR1.1.2685, 4_A375_EGFR1.1.2686, 4_A375_EGFR1.1.2687	+15, 12635, 19, 12635, 179, 5231	upstream, Downstream, in gene, Downstream, in gene, Downstream	1	1	1	23.67	27.33	21.33	3	2_A375_shU87_plus_IncRNA_AR_1	34	Gene:NDUFB10	PDSW, NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	NM_004548, NC_018930.2, NT_187633.1, NC_000016.9, NT_187633.2	223212_s_at_228301_x_at	NP_004539.1, EAW65797.1, EAW65798.1
GeneID:8740	RPS2	19	2,012,092	2,014,827	2,735	-	6	2_A375_shU87_mrwt_IncRNA_AR_1.2165, 2_A375_shU87_plus_IncRNA_AR_1.3070, 3_A375_shU87_plus_IncRNA_AR_1.3070, 3_A375_shU87_plus_IncRNA_AR_1.3071, 4_A375_EGFR1.1.2683, 4_A375_EGFR1.1.2684	5323, -7123, 5291, -7173, 5121, 39	Downstream, upstream, Downstream, Downstream, in gene	1	1	1	23.67	27.33	21.33	3	2_A375_shU87_plus_IncRNA_AR_1	34	Gene:RPS2	MGC117344, MGC117343, MGC102581, S2, RPS2, LLRep3	ribosomal protein S2	NM_002952, NC_018930.2, NT_187633.1, NC_000019.9, NT_187633.2, NC_018930.3	200107_x_at_212433_x_at, 221760_x_at	NP_002943.2, EAW65808.1, EAW65809.1, EAW65994.1, EAW65996.1

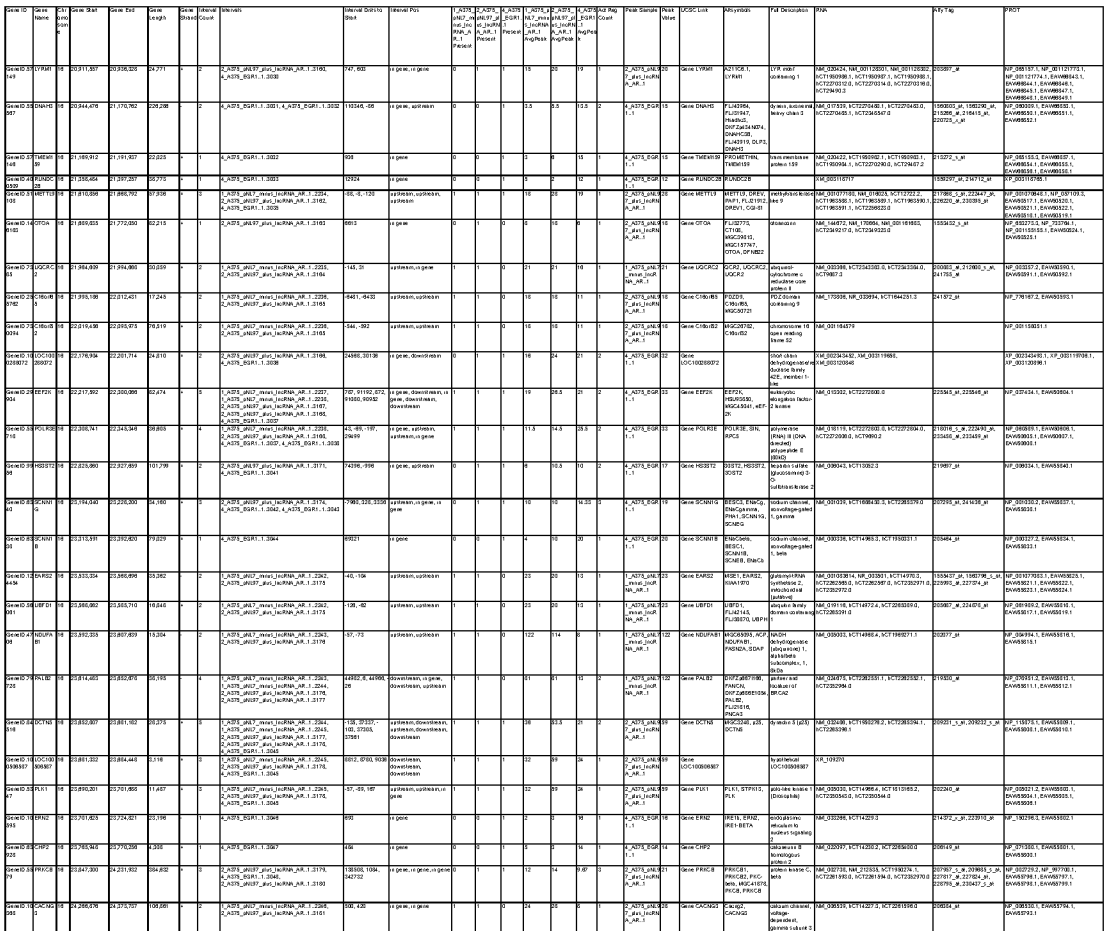
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.574042	SNORA10	16	2,012,335	2,012,467	132	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2165, 1_A375_pNL7_minus_lncRNA_AR..1..2166, 2_A375_pNL97_plus_lncRNA_AR..1..3070, 2_A375_pNL97_plus_lncRNA_AR..1..3071, 4_A375_EGR1..1..2883, 4_A375_EGR1..1..2884	2983, -9485, 2931, -9533, 2771, -2301	downstream, upstream, downstream, upstream, downstream, upstream	1	1	1	23.67	27.33	21.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene SNORA10	ACA10, SNORA10	small nucleolar RNA, H/ACA box 10	NR_002327		
GeneID.26784	SNORA64	16	2,012,974	2,013,107	133	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2165, 1_A375_pNL7_minus_lncRNA_AR..1..2166, 2_A375_pNL97_plus_lncRNA_AR..1..3070, 2_A375_pNL97_plus_lncRNA_AR..1..3071, 4_A375_EGR1..1..2883, 4_A375_EGR1..1..2884	3603, -8845, 3571, -8893, 3411, -1661	downstream, upstream, downstream, upstream, downstream, upstream	1	1	1	23.67	27.33	21.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene SNORA64	SNORA64, U64, RNU64	small nucleolar RNA, H/ACA box 64	NR_002326		
GeneID.735301	SNHG9	16	2,014,997	2,015,505	508	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2165, 1_A375_pNL7_minus_lncRNA_AR..1..2166, 2_A375_pNL97_plus_lncRNA_AR..1..3070, 2_A375_pNL97_plus_lncRNA_AR..1..3071, 4_A375_EGR1..1..2883, 4_A375_EGR1..1..2884	-5493, 6955, -5461, 7003, -5301, -229	upstream, downstream, upstream, downstream, upstream, upstream	1	1	1	23.67	27.33	21.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene SNHG9	SNHG9, NCRNA00082, DKFZp686N08141	small nucleolar RNA host gene 9 (non-protein coding)	NR_003142	228645_at	
GeneID.677844	SNORA78	16	2,015,185	2,015,311	126	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2165, 1_A375_pNL7_minus_lncRNA_AR..1..2166, 2_A375_pNL97_plus_lncRNA_AR..1..3070, 2_A375_pNL97_plus_lncRNA_AR..1..3071, 4_A375_EGR1..1..2883, 4_A375_EGR1..1..2884	-5681, 6767, -5649, 6815, -5489, -417	upstream, downstream, upstream, downstream, upstream, upstream	1	1	1	23.67	27.33	21.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene SNORA78	ACA64, SNORA78	small nucleolar RNA, H/ACA box 78	NR_003020	1558954_at	
GeneID.146310	RNF151	16	2,016,875	2,018,976	2,101	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2165, 1_A375_pNL7_minus_lncRNA_AR..1..2166, 2_A375_pNL97_plus_lncRNA_AR..1..3070, 2_A375_pNL97_plus_lncRNA_AR..1..3071, 4_A375_EGR1..1..2883, 4_A375_EGR1..1..2884, 4_A375_EGR1..1..2885, 4_A375_EGR1..1..2886	-7371, 5077, -7339, 5125, -7179, -2107, 11013, 11989	upstream, downstream, upstream, downstream, upstream, upstream, downstream, downstream	1	1	1	17.8	19.4	19.8	5	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene RNF151	RNF151, MGC129921	ring finger protein 151	NM_174903	236689_at	NP_777563.2
GeneID.10607	TBL3	16	2,022,064	2,028,751	6,687	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2166, 2_A375_pNL97_plus_lncRNA_AR..1..3071, 2_A375_pNL97_plus_lncRNA_AR..1..3072, 4_A375_EGR1..1..2884, 4_A375_EGR1..1..2885, 4_A375_EGR1..1..2886, 4_A375_EGR1..1..2887	-112, -84, 11696, 7296, 5824, 6800, 8048	upstream, upstream, downstream, upstream, in gene, downstream, downstream	1	1	1	15	15.5	19.67	6	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene TBL3	SAZD, TBL3	transducin (beta)-like 3	NM_006453, hCT2271015.0, hCT2271016.0, hCT2271017.0, hCT2356729.0, hCT33982.3	209820_s_at	NP_006444.2, EAW85588.1, EAW85585.1, EAW85587.1, EAW85586.1, EAW85589.1
GeneID.124056	NOXO1	16	2,028,918	2,031,440	2,522	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2166, 2_A375_pNL97_plus_lncRNA_AR..1..3071, 2_A375_pNL97_plus_lncRNA_AR..1..3072, 4_A375_EGR1..1..2885, 4_A375_EGR1..1..2886, 4_A375_EGR1..1..2887, 4_A375_EGR1..1..2888	9468, 9440, -2320, 3552, 2576, 1328, -9312	downstream, downstream, upstream, downstream, downstream, in gene, upstream	1	1	1	13.17	14.5	18	6	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene NOXO1	MGC20258, P41NOXA, SH3PXD5, SNX28, P41NOXC, P41NOX, NOXO1, P41NOXB	NADPH oxidase organizer 1	NM_144603, NM_172167, NM_172168, hCT2356699.0, hCT2356700.0, hCT2356701.0, hCT34005.3	235329_at	NP_653204.1, NP_751907.1, NP_751908.1, EAW85581.1, EAW85582.1, EAW85583.1, EAW85584.1
GeneID.2671	GFER	16	2,034,150	2,037,749	3,599	+	5	2_A375_pNL97_plus_lncRNA_AR..1..3072, 4_A375_EGR1..1..2885, 4_A375_EGR1..1..2886, 4_A375_EGR1..1..2887, 4_A375_EGR1..1..2888	-390, -8262, -5286, -4038, 6602	upstream, upstream, upstream, upstream, downstream	0	1	1	10.2	11	18.8	5	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene GFER	HSS, GFER, HPO1, HPO2, ALR, HERV1, HPO, ERV1	growth factor, augmenter of liver regeneration	NM_005262, hCT1955298.1, hCT2271018.0, hCT33977.3	204659_s_at, 204660_at	NP_005253.3, EAW85579.1, EAW85578.1, EAW85580.1
GeneID.9143	SYNGR3	16	2,039,968	2,044,276	4,308	+	5	2_A375_pNL97_plus_lncRNA_AR..1..3072, 4_A375_EGR1..1..2887, 4_A375_EGR1..1..2888, 4_A375_EGR1..1..2889, 4_A375_EGR1..1..2890	-6208, -9858, 784, 9344, 14528	upstream, upstream, in gene, downstream, downstream	0	1	1	10.2	11.4	18.8	5	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SYNGR3	MGC20003, SYNGR3, MGC.20003	synaptogyrin 3	NM_004209, hCT2271021.0	205691_at	NP_004200.2, EAW85577.1
GeneID.90850	ZNF598	16	2,047,768	2,059,763	11,995	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3073, 4_A375_EGR1..1..2888, 4_A375_EGR1..1..2889, 4_A375_EGR1..1..2890	-237, 19011, 10451, 5267	upstream, downstream, in gene, in gene	0	1	1	10.75	13.5	18.25	4	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene ZNF598	DKFZp762F135, ZNF598, FLJ00086	zinc finger protein 598	NM_178167, hCT2287214.0, hCT2287216.0, hCT2287219.0, hCT2287220.0, hCT2356756.0, hCT2356757.0, hCT33989.3	225104_at, 232387_x_at	NP_835461.1, EAW85573.1, EAW85569.1, EAW85570.1, EAW85572.1, EAW85574.1, EAW85571.1, EAW85575.1
GeneID.283869	NPW	16	2,069,521	2,070,756	1,235	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2167, 2_A375_pNL97_plus_lncRNA_AR..1..3073, 4_A375_EGR1..1..2891	3687, -9521, 5775	downstream, upstream, downstream	1	1	1	14.33	16.67	15.67	3	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene NPW	L8, L8C, PPNPW, NPW, PPL8	neuropeptide W	NM_001099456	243110_x_at	NP_001092926.2
GeneID.9351	SLC9A3R2	16	2,076,888	2,089,027	12,139	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2167, 1_A375_pNL7_minus_lncRNA_AR..1..2168, 2_A375_pNL97_plus_lncRNA_AR..1..3074, 2_A375_pNL97_plus_lncRNA_AR..1..3075, 4_A375_EGR1..1..2891, 4_A375_EGR1..1..2892, 4_A375_EGR1..1..2893	-3480, 20984, 6776, 20856, -1592, 6440, 6840	upstream, downstream, in gene, downstream, upstream, in gene, in gene	1	1	1	13.8	13.2	15.4	5	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene SLC9A3R2	NHERF2, SIP-1, TKA-1, NHE3RF2, SLC9A3R2, E3KARP, OCTS2, SIP1, NHERF-2, MGC104639	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	NM_004785, NM_001130012, hCT1967631.1, hCT2271025.0, hCT2356724.0, hCT33980.2	209830_s_at	NP_004776.3, NP_001123484.1, EAW85563.1, EAW85564.1, EAW85565.1, EAW85566.1
GeneID.4913	NTHL1	16	2,089,816	2,097,867	8,051	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2168, 2_A375_pNL97_plus_lncRNA_AR..1..3074, 2_A375_pNL97_plus_lncRNA_AR..1..3075, 4_A375_EGR1..1..2892, 4_A375_EGR1..1..2893	-5, 14203, 123, 14539, 12139	upstream, downstream, in gene, downstream, downstream	1	1	1	14.67	14.33	15.33	3	4_A375_EGR1..1	18	Gene NTHL1	OCTS3, NTH1, NTHL1	nth endonuclease III-like 1 (E. coli)	NM_002528, hCT2287211.0	209731_at	NP_002519.1, EAW85562.1
GeneID.7249	TSC2	16	2,097,990	2,138,713	40,723	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2168, 2_A375_pNL97_plus_lncRNA_AR..1..3075, 4_A375_EGR1..1..2894, 4_A375_EGR1..1..2895, 4_A375_EGR1..1..2896, 4_A375_EGR1..1..2897, 4_A375_EGR1..1..2898, 4_A375_EGR1..1..2899	-118, -246, 13802, 25530, 26234, 28730, 43896, 45466	upstream, upstream, in gene, in gene, in gene, in gene, downstream, downstream	1	1	1	8.71	9.14	19	7	4_A375_EGR1..1	26	Gene TSC2	TSC4, TSC2, FLJ43106, LAM	tuberous sclerosis 2	NM_001077183, NM_000548, NM_001114382, hCT2271028.0, hCT2271029.0, hCT2271030.0, hCT2271032.0, hCT2271033.0	215624_at, 215735_s_at	NP_001070651.1, NP_000539.2, NP_001107854.1, EAW85557.1, EAW85558.1, EAW85560.1, EAW85556.1, EAW85559.1
GeneID.5310	PKD1	16	2,138,711	2,185,899	47,188	-	3	4_A375_EGR1..1..2898, 4_A375_EGR1..1..2899, 4_A375_EGR1..1..2900	44011, 42443, 20155	in gene, in gene, in gene	0	0	1	5.33	6	19.33	3	4_A375_EGR1..1	26	Gene PKD1	PBP, Pc-1, TRPP1, PKD1	polycystic kidney disease 1 (autosomal dominant)	NM_001009944, NM_000296, hCT2287202.1, hCT2287204.1, hCT2287205.0	202327_s_at, 202328_s_at, 216949_s_at	NP_001009944.2, NP_000287.3, EAW85553.1, EAW85554.1, EAW85555.1
GeneID.100188847	MIR1225	16	2,140,196	2,140,285	89	-	2	4_A375_EGR1..1..2898, 4_A375_EGR1..1..2899	-1603, -3171	upstream, upstream	0	0	1	6.5	7.5	23	2	4_A375_EGR1..1	26	Gene MIR1225	MIR1225, MIRN1225	microRNA 1225	NR_030646		
GeneID.100287400	LOC100287400	16	2,155,539	2,156,193	654	+	1	4_A375_EGR1..1..2900	10205	downstream	0	0	1	3	3	12	1	4_A375_EGR1..1	12	Gene LOC100287400		hypothetical protein LOC100287400	XM_003119641, XM_002343408		XP_003119689.1, XP_002343449.1
GeneID.25837	RAB26	16	2,198,651	2,204,141	5,490	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3076, 4_A375_EGR1..1..2901, 4_A375_EGR1..1..2902, 4_A375_EGR1..1..2903	4165, 6613, 11157, 15013	in gene, downstream, downstream, downstream	0	1	1	11.25	16	19.25	4	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene RAB26	V46133, RAB26	RAB26, member RAS oncogene family	NM_014353, hCT1955279.1, hCT1955280.0, hCT2271036.0	219562_at, 50965_at	NP_055168.2, EAW85550.1, EAW85551.1, EAW85552.1
GeneID.100507303	LOC100507303	16	2,204,803	2,205,359	556	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3076, 4_A375_EGR1..1..2901, 4_A375_EGR1..1..2902, 4_A375_EGR1..1..2903	2543, 95, -4449, -8305	downstream, in gene, upstream, upstream	0	1	1	11.25	16	19.25	4	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene LOC100507303		hypothetical LOC100507303	XR_111621, XR_109242, XR_114905		
GeneID.26788	SNORD60	16	2,205,024	2,205,106	82	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3076, 4_A375_EGR1..1..2901, 4_A375_EGR1..1..2902, 4_A375_EGR1..1..2903	2290, -158, -4702, -8558	downstream, upstream, upstream, upstream	0	1	1	11.25	16	19.25	4	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene SNORD60	U60, RNU60, SNORD60	small nucleolar RNA, C/D box 60	NR_002736		
GeneID.84231	TRAF7	16	2,205,799	2,228,130	22,331	+	7	2_A375_pNL97_plus_lncRNA_AR..1..3076, 4_A375_EGR1..1..2901, 4_A375_EGR1..1..2902, 4_A375_EGR1..1..2903, 4_A375_EGR1..1..2904, 4_A375_EGR1..1..2905, 4_A375_EGR1..1..2906	-2983, -535, 4009, 7865, 12041, 15545, 31097	upstream, upstream, in gene, in gene, in gene, in gene, downstream	0	1	1	9.71	12	18.86	7	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene TRAF7	RNF119, RFWD1, DKFZp586I021, TRAF7, MGC7807	TNF receptor-associated factor 7	NM_032271, hCT2271043.0, hCT2271045.0, hCT2271047.0, hCT32300.3	223029_s_at, 223030_at, 223031_s_at	NP_115647.2, EAW85546.1, EAW85547.1, EAW85548.1, EAW85549.1
GeneID.57524	CASKIN1	16	2,227,184	2,246,465	19,281	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2169, 2_A375_pNL97_plus_lncRNA_AR..1..3077, 4_A375_EGR1..1..2904, 4_A375_EGR1..1..2905, 4_A375_EGR1..1..2906, 4_A375_EGR1..1..2907	-9055, -9071, 28825, 25121, 9589, 5537	upstream, upstream, downstream, downstream, in gene, in gene	1	1	1	14.4	13.2	19.4	5	1_A375_pNL7_minus_lncRNA_AR..1	43	Gene CASKIN1	CASKIN1, ANKS5A	CASK interacting protein 1	NM_020764, hCT2287197.0, hCT2287198.0, hCT32298.3	1552689_at, 1569737_a_at, 239169_at	NP_065815.1, EAW85545.1, EAW85543.1, EAW85544.1
GeneID.64223	MLST8	16	2,255,450	2,259,416	3,966	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2169, 2_A375_pNL97_plus_lncRNA_AR..1..3077, 2_A375_pNL97_plus_lncRNA_AR..1..3078, 4_A375_EGR1..1..2908, 4_A375_EGR1..1..2909	70, 86, 9942, 1590, 4518	in gene, in gene, downstream, in gene, downstream	1	1	1	17.25	18.75	18.25	4	1_A375_pNL7_minus_lncRNA_AR..1	43	Gene MLST8	GBL, GbetaL, MGC111011, POP3, LST8, WAT1, MLST8	MTOR associated protein, LST8 homolog (S. cerevisiae)	NM_022372, hCT1955287.1, hCT1966526.1, hCT1966527.1, hCT1966528.1, hCT2271048.0, hCT32301.2	220587_s_at	NP_071767.3, EAW85537.1, EAW85538.1, EAW85539.1, EAW85540.1, EAW85541.1, EAW85542.1
GeneID.283870	C16orf79	16	2,259,254	2,261,011	1,757	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2169, 2_A375_pNL97_plus_lncRNA_AR..1..3077, 2_A375_pNL97_plus_lncRNA_AR..1..3078, 4_A375_EGR1..1..2908, 4_A375_EGR1..1..2909	5491, 5475, -4361, 3971, 1043	downstream, downstream, upstream, downstream, in gene	1	1	1	17.25	18.75	18.25	4	1_A375_pNL7_minus_lncRNA_AR..1	43	Gene C16orf79	C16orf79, MGC21830	chromosome 16 open reading frame 79	NM_182563, hCT1959616.1, hCT2287192.0	1553990_at	NP_872369.1, EAW85535.1, EAW85536.1
GeneID.283871	PGP	16	2,261,603	2,264,822	3,219	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2169, 2_A375_pNL97_plus_lncRNA_AR..1..3077, 2_A375_pNL97_plus_lncRNA_AR..1..3078, 4_A375_EGR1..1..2908, 4_A375_EGR1..1..2909	9302, 9286, -570, 7782, 4854	downstream, downstream, upstream, downstream, downstream	1	1	1	17.25	18.75	18.25	4	1_A375_pNL7_minus_lncRNA_AR..1	43	Gene PGP	PGP, MGC4692	phosphoglycolate phosphatase	NM_001042371	218410_s_at, 222622_at	NP_001035830.1
GeneID.1877	E4F1	16	2,273,567	2,285,743	12,176	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3078, 4_A375_EGR1..1..2910	-8175, 12929	upstream, downstream	0	1	1	8.5	10.5	14	2	4_A375_EGR1..1	18	Gene E4F1	E4F, E4F1, MGC99614	E4F transcription factor 1	NM_004424, hCT2271058.1, hCT2271059.1, hCT2271060.1	218524_at	NP_004415.2, EAW85531.1, EAW85532.1, EAW85533.1
GeneID.1775	DNASE1L2	16	2,286,468	2,288,712	2,244	+	1	4_A375_EGR1..1..2910	26	in gene	0	0	1	6	7	18	1	4_A375_EGR1..1	18	Gene DNASE1L2	DNAS1L2, DNASE1L2	deoxyribonuclease I-like 2	NM_001374, hCT2271055.1, hCT2271057.1, hCT2271056.1, hCT2356745.0	207192_at	NP_001365.1, EAW85526.1, EAW85527.1, EAW85528.1, EAW85529.1
GeneID.1632	DCI	16	2,289,873	2,301,602	11,729	-	1	4_A375_EGR1..1..2910	15106	downstream	0	0	1	6	7	18	1	4_A375_EGR1..1	18	Gene DCI	ECI1, DCI	enoyl-CoA delta isomerase 1	NM_001178029, NM_001919, hCT1955286.1, hCT2356721.0, hCT32297.2	209759_s_at	NP_001171500.1, NP_001910.2, EAW85523.1, EAW85524.1, EAW85525.1
GeneID.10921	RNPS1	16	2,303,121	2,318,114	14,993	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2170, 2_A375_pNL97_plus_lncRNA_AR..1..3079, 4_A375_EGR1..1..2911, 4_A375_EGR1..1..2912, 4_A375_EGR1..1..2913	-190, -94, 130, -734, -8302	upstream, upstream, in gene, upstream, upstream	1	1	1	24	24	18	2	1_A375_pNL7_minus_lncRNA_AR..1	43	Gene RNPS1	RNPS1, MGC117332, E5.1	RNA binding protein S1, serine-rich domain	NM_080594, NM_006711, hCT2287173.0, hCT2287174.0, hCT2287175.0, hCT2287177.0, hCT2287178.0, hCT2287180.0, hCT2287181.0	200060_s_at, 207939_x_at	NP_542161.1, NP_006702.1, EAW85516.1, EAW85517.1, EAW85520.1, EAW85522.1, EAW85518.1, EAW85519.1, EAW85521.1
GeneID.100126328	MIR940	16	2,321,748	2,321,841	93	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2170, 2_A375_pNL97_plus_lncRNA_AR..1..3079, 4_A375_EGR1..1..2911, 4_A375_EGR1..1..2912, 4_A375_EGR1..1..2913	-3444, -3540, -3784, -2900, 4668	upstream, upstream, upstream, upstream, downstream	1	1	1	24	24	18	2	1_A375_pNL7_minus_lncRNA_AR..1	43	Gene MIR940	hsa-mir-940, MIRN940, MIR940	microRNA 940	NR_030636		
GeneID.21	ABCA3	16	2,325,879	2,390,747	64,868	-	9	1_A375_pNL7_minus_lncRNA_AR..1..2170, 2_A375_pNL97_plus_lncRNA_AR..1..3079, 2_A375_pNL97_plus_lncRNA_AR..1..3080, 4_A375_EGR1..1..2911, 4_A375_EGR1..1..2912, 4_A375_EGR1..1..2913, 4_A375_EGR1..1..2914, 4_A375_EGR1..1..2915, 4_A375_EGR1..1..2916	72443, 72539, -293, 72763, 71899, 64331, 55771, 54331, 31963	downstream, downstream, upstream, downstream, downstream, in gene, in gene, in gene, in gene	1	1	1	14	13.33	15.33	6	1_A375_pNL7_minus_lncRNA_AR..1	43	Gene ABCA3	ABC-C, MGC72201, ABCA3, ABC3, EST111653, MGC166979, SMDP3, LBM180	ATP-binding cassette, sub-family A (ABC1), member 3	NM_001089, hCT32291.3	204343_at	NP_001080.2, EAW85515.1
GeneID.899	CCNF	16	2,479,395	2,508,859	29,464	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3081, 4_A375_EGR1..1..2917, 4_A375_EGR1..1..2918, 4_A375_EGR1..1..2919	38853, -323, 31141, 31933	downstream, upstream, downstream, downstream	0	1	1	9	11.25	18.25	4	4_A375_EGR1..1	24	Gene CCNF	CCNF, FBXO1, FBX1	cyclin F	NM_001761, hCT1955250.2	204826_at, 204827_s_at	NP_001752.2, EAW85510.1
GeneID.80178	C16orf59	16	2,510,115	2,514,964	4,849	+	6	2_A375_pNL97_plus_lncRNA_AR..1..3081, 2_A375_pNL97_plus_lncRNA_AR..1..3082, 4_A375_EGR1..1..2918, 4_A375_EGR1..1..2919, 4_A375_EGR1..1..2920, 4_A375_EGR1..1..2921	7933, 14109, 421, 1213, 9149, 13245	downstream, downstream, in gene, in gene, downstream, downstream	0	1	1	10.33	12.33	15.17	6	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene C16orf59	FLJ13909, C16orf59	chromosome 16 open reading frame 59	NM_025108, hCT1955276.1, hCT1955277.1, hCT2271066.0, hCT2356651.0, hCT24217.3	219556_at	NP_079384.2, EAW85505.1, EAW85506.1, EAW85507.1, EAW85508.1, EAW85509.1
GeneID.4917	NTN3	16	2,521,500	2,524,146	2,646	+	5	2_A375_pNL97_plus_lncRNA_AR..1..3081, 2_A375_pNL97_plus_lncRNA_AR..1..3082, 4_A375_EGR1..1..2919, 4_A375_EGR1..1..2920, 4_A375_EGR1..1..2921	-3452, 2724, -10172, -2236, 1680	upstream, downstream, upstream, upstream, in gene	0	1	1	10.6	12.8	14.8	5	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NTN3	NTN3, NTN2L	netrin 3	NM_006181, hCT24156.3	207840_x_at, 211635_x_at, 211640_x_at	NP_006172.1, EAW85504.1
GeneID.57465	TBC1D24	16	2,525,147	2,553,499	28,352	+	6	2_A375_pNL97_plus_lncRNA_AR..1..3081, 2_A375_pNL97_plus_lncRNA_AR..1..3082, 4_A375_EGR1..1..2920, 4_A375_EGR1..1..2921, 4_A375_EGR1..1..2922, 4_A375_EGR1..1..2923	-7099, -923, -5683, -1787, 21264, 26837	upstream, upstream, upstream, upstream, in gene, in gene	0	1	1	11.67	11.83	15	6	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TBC1D24	MGC102885, FIME, TBC1D24, KIAA1171	TBC1 domain family, member 24	NM_020705	227632_at, 227908_at	NP_065756.1
GeneID.527	ATP6V0C	16	2,563,953	2,570,219	6,266	+	2	4_A375_EGR1..1..2924, 4_A375_EGR1..1..2925	6943, 13903	downstream, downstream	0	0	1	8.5	11	18	2	4_A375_EGR1..1	19	Gene ATP6V0C	Vma3, ATP6L, ATP6C, VPPC, VATL, ATPL, ATP6V0C	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	NM_001694, hCT1819508.2	200954_at, 36994_at	NP_001685.1, EAW85501.1
GeneID.51005	AMDHD2	16	2,570,363	2,580,955	10,592	+	3	4_A375_EGR1..1..2924, 4_A375_EGR1..1..2925, 4_A375_EGR1..1..2926	533, 7493, 11429	in gene, in gene, downstream	0	0	1	10.33	13.33	19	3	4_A375_EGR1..1	21	Gene AMDHD2	CGI-14, AMDHD2	amidohydrolase domain containing 2	NM_001145815, NM_015944, hCT1955241.1, hCT1955242.1, hCT5633.3	219082_at	NP_001139287.1, NP_057028.2, EAW85498.1, EAW85499.1, EAW85500.1
GeneID.752014	CEMP1	16	2,580,036	2,594,077	14,041	-	3	4_A375_EGR1..1..2924, 4_A375_EGR1..1..2925, 4_A375_EGR1..1..2926	23181, 16221, 12285	downstream, downstream, in gene	0	0	1	10.33	13.33	19	3	4_A375_EGR1..1	21	Gene CEMP1	CP-23, CEMP1, CP23	cementum protein 1	NM_001048212	222009_at, 227841_at	NP_001041677.1
GeneID.100422974	MIR3178	16	2,581,923	2,582,006	83	-	2	4_A375_EGR1..1..2925, 4_A375_EGR1..1..2926	4150, 214	downstream, downstream	0	0	1	11.5	17.5	20	2	4_A375_EGR1..1	21	Gene MIR3178	MIR3178	microRNA 3178	NR_036139		
GeneID.5170	PDPK1	16	2,587,970	2,653,189	65,219	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2171, 2_A375_pNL97_plus_lncRNA_AR..1..3083, 4_A375_EGR1..1..2925, 4_A375_EGR1..1..2926, 4_A375_EGR1..1..2927	65406, 65534, -10114, -6178, 65550	downstream, downstream, upstream, upstream, downstream	1	1	1	13.33	19.67	19.67	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PDPK1	MGC35290, PDPK1, MGC20087, PRO0461, PDK1	3-phosphoinositide dependent protein kinase-1	NM_031268, NM_002613, hCT6648.4	204524_at, 224986_s_at, 32029_at	NP_112558.2, NP_002604.1, EAW85495.1
GeneID.652276	PRO0461	16	2,653,385	2,680,495	27,110	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2171, 2_A375_pNL97_plus_lncRNA_AR..1..3083, 4_A375_EGR1..1..2927	-9, 119, 135	upstream, in gene, in gene	1	1	1	17	24	19	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PRO0461	FLJ39075, MGC74552, MGC121033, MGC138157, LOC652276	hypothetical LOC652276	NR_015441		
GeneID.100507321	LOC100507321	16	2,711,150	2,723,440	12,290	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2172, 2_A375_pNL97_plus_lncRNA_AR..1..3084	-9008, -9008	upstream, upstream	1	1	0	23	20	13	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene LOC100507321		hypothetical LOC100507321	XR_111635, XR_109243, XR_114906		
GeneID.54442	KCTD5	16	2,732,495	2,759,031	26,536	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2172, 2_A375_pNL97_plus_lncRNA_AR..1..3084, 4_A375_EGR1..1..2928, 4_A375_EGR1..1..2929	-47, -47, 16289, 33265	upstream, upstream, in gene, downstream	1	1	1	15	14.67	16.33	3	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene KCTD5	KCTD5, FLJ20040	potassium channel tetramerisation domain containing 5	NM_018992, hCT1955805.1, hCT1955806.1, hCT2270987.0, hCT2270989.0	218474_s_at, 222645_s_at, 229837_s_at	NP_061865.1, EAW85490.1, EAW85488.1, EAW85489.1, EAW85491.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:83886	PRSS27	16	2,762,423	2,770,552	8,129	-	1	4_A375_EGR1..1..2929	4792	in gene	0	0	1	15	16	21	1	4_A375_EGR1..1	21	Gene PRSS27	PRSS27, CAPH2, MPN	protease, serine 27	NM_031948, hCT1817765.2, hCT2356712.0	232074_at	NP_114154.1, EAW85485.1, EAW85486.1
GeneID:100128786	LOC100128786	16	2,787,077	2,802,601	15,524	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2173, 2_A375_pNL97_plus_lncRNA_AR..1..3085, 4_A375_EGR1..1..2930, 4_A375_EGR1..1..2931	233, 201, 15113, 201	in gene, in gene, in gene, in gene	1	1	1	13	12.5	17	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene LOC100128786	FLJ25760, FLJ31501	hypothetical LOC100128786	NR_027274, NR_027275		
GeneID:23524	SRRM2	16	2,802,330	2,821,413	19,083	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2173, 2_A375_pNL97_plus_lncRNA_AR..1..3085, 4_A375_EGR1..1..2931	38, 70, 70	in gene, in gene, in gene	1	1	1	22	21	17	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene SRRM2	DKFZp686O15166, CWF21, DKFZp667L0421, SRL300, MGC40295, Cwc21, SRm300, 300-KD, KIAA0324, SRRM2, FLJ22250, FLJ21926	serine/arginine repetitive matrix 2	NM_016333, hCT1955800.1, hCT2270991.0, hCT2270992.0, hCT2270994.0, hCT2270995.0, hCT2270997.0, hCT6641.1	1554871_a_at, 207435_s_at, 208610_s_at, 216629_at	NP_057417.3, EAW85480.1, EAW85477.1, EAW85479.1, EAW85481.1, EAW85483.1, EAW85478.1, EAW85482.1
GeneID:64063	PRSS22	16	2,902,728	2,908,171	5,443	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2174, 1_A375_pNL7_minus_lncRNA_AR..1..2175, 2_A375_pNL97_plus_lncRNA_AR..1..3086, 2_A375_pNL97_plus_lncRNA_AR..1..3087, 4_A375_EGR1..1..2932, 4_A375_EGR1..1..2933, 4_A375_EGR1..1..2934	-3029, -10149, -3125, -10089, 4843, -1589, -10069	upstream, upstream, upstream, upstream, in gene, upstream, upstream	1	1	1	12.25	16.75	17.25	4	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene PRSS22	PRSS22, BSSP-4, hBSSP-4, MGC9599, SP001LA	protease, serine, 22	NM_022119, hCT1827694.2	205847_at	NP_071402.1, EAW85456.1
GeneID:114984	FLYWCH2	16	2,933,196	2,949,383	16,187	+	3	4_A375_EGR1..1..2935, 4_A375_EGR1..1..2936, 4_A375_EGR1..1..2937	196, 13684, 22100	in gene, in gene, downstream	0	0	1	9	10.33	20	3	4_A375_EGR1..1	23	Gene FLYWCH2	FLYWCH2	FLYWCH family member 2	NM_138439, NM_001142499, NM_001142500, hCT1817782.1	226079_at	NP_612448.1, NP_001135971.1, NP_001135972.1, EAW85455.1
GeneID:84256	FLYWCH1	16	2,961,980	3,001,209	39,229	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2176, 2_A375_pNL97_plus_lncRNA_AR..1..3088, 4_A375_EGR1..1..2937, 4_A375_EGR1..1..2938, 4_A375_EGR1..1..2939	-156, -124, -6684, 17844, 41692	upstream, upstream, upstream, in gene, downstream	1	1	1	11	11.75	16.25	4	4_A375_EGR1..1	23	Gene FLYWCH1	FLYWCH1	FLYWCH-type zinc finger 1	NM_032296, NM_020912, hCT2258617.0, hCT2258620.0, hCT2258621.0, hCT2258622.0, hCT6650.3	223950_s_at, 225952_at, 234106_s_at	NP_115672.2, NP_065963.1, EAW85450.1, EAW85452.1, EAW85453.1, EAW85454.1, EAW85451.1
GeneID:79412	KREMEN2	16	3,014,217	3,018,381	4,164	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2177, 2_A375_pNL97_plus_lncRNA_AR..1..3089, 4_A375_EGR1..1..2940, 4_A375_EGR1..1..2941, 4_A375_EGR1..1..2942, 4_A375_EGR1..1..2943, 4_A375_EGR1..1..2944	4663, 4855, -233, 4631, 5740, 6871, 10071	downstream, downstream, upstream, downstream, downstream, downstream, downstream	1	1	1	13.4	15	18.4	5	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene KREMEN2	KRM2, MGC16709, MGC10791, KREMEN2	kringle containing transmembrane protein 2	NM_024507, NM_172229, hCT2258623.0, hCT2258624.0, hCT2356738.0, hCT2356739.0, hCT6651.3	219692_at	NP_078783.1, NP_757384.1, EAW85445.1, EAW85446.1, EAW85447.1, EAW85449.1, EAW85448.1
GeneID:124222	PAQR4	16	3,019,342	3,023,485	4,143	+	10	1_A375_pNL7_minus_lncRNA_AR..1..2177, 2_A375_pNL97_plus_lncRNA_AR..1..3089, 2_A375_pNL97_plus_lncRNA_AR..1..3090, 4_A375_EGR1..1..2940, 4_A375_EGR1..1..2941, 4_A375_EGR1..1..2942, 4_A375_EGR1..1..2943, 4_A375_EGR1..1..2944, 4_A375_EGR1..1..2945, 4_A375_EGR1..1..2946	-462, -270, 11298, -5356, -494, 615, 3746, 4946, 10258, 11378	upstream, upstream, downstream, upstream, upstream, in gene, in gene, downstream, downstream, downstream	1	1	1	11.57	14.71	18.29	7	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene PAQR4	FLJ30002, PAQR4	progestin and adipoQ receptor family member IV	NM_152341, hCT1817749.2, hCT2258626.0, hCT2258628.0, hCT2356670.0	212858_at	NP_689554.2, EAW85441.1, EAW85442.1, EAW85443.1, EAW85444.1
GeneID:9088	PKMYT1	16	3,022,792	3,030,474	7,682	-	12	1_A375_pNL7_minus_lncRNA_AR..1..2177, 2_A375_pNL97_plus_lncRNA_AR..1..3089, 2_A375_pNL97_plus_lncRNA_AR..1..3090, 4_A375_EGR1..1..2940, 4_A375_EGR1..1..2941, 4_A375_EGR1..1..2942, 4_A375_EGR1..1..2943, 4_A375_EGR1..1..2944, 4_A375_EGR1..1..2945, 4_A375_EGR1..1..2946, 4_A375_EGR1..1..2947, 4_A375_EGR1..1..2948	11594, 11402, -166, 16490, 11626, 10517, 7366, 6186, 874, -246, -5622, -7766	downstream, downstream, upstream, downstream, downstream, downstream, in gene, in gene, in gene, upstream, upstream, upstream	1	1	1	10.44	13.22	18.11	9	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene PKMYT1	PKMYT1, DKFZp547K1610, MYT1, FLJ20093	protein kinase, membrane associated tyrosine/threonine 1	NM_182687, NM_004203, hCT2257534.0, hCT6639.3	204267_x_at	NP_872629.1, NP_004194.3, EAW85439.1, EAW85440.1
GeneID:283875	LOC283875	16	3,039,055	3,044,510	5,455	+	6	2_A375_pNL97_plus_lncRNA_AR..1..3090, 4_A375_EGR1..1..2945, 4_A375_EGR1..1..2946, 4_A375_EGR1..1..2947, 4_A375_EGR1..1..2948, 4_A375_EGR1..1..2949	-8415, -9455, -8335, -2959, -815, 11729	upstream, upstream, upstream, upstream, upstream, downstream	0	1	1	6.8	9.6	18	5	4_A375_EGR1..1	19	Gene LOC283875	FLJ46402	hypothetical LOC283875	NR_033661	1564122_at	
GeneID:100507378	LOC100507378	16	3,051,301	3,052,017	716	+	2	4_A375_EGR1..1..2949, 4_A375_EGR1..1..2950	-517, 6379	upstream, downstream	0	0	1	7	5	19	2	4_A375_EGR1..1	19	Gene LOC100507378		hypothetical LOC100507378	XR_109244		
GeneID:9080	CLDN9	16	3,062,457	3,064,506	2,049	+	10	1_A375_pNL7_minus_lncRNA_AR..1..2178, 1_A375_pNL7_minus_lncRNA_AR..1..2179, 1_A375_pNL7_minus_lncRNA_AR..1..2180, 2_A375_pNL97_plus_lncRNA_AR..1..3091, 2_A375_pNL97_plus_lncRNA_AR..1..3092, 4_A375_EGR1..1..2950, 4_A375_EGR1..1..2951, 4_A375_EGR1..1..2952, 4_A375_EGR1..1..2953, 4_A375_EGR1..1..2954	8455, 9807, 11783, 8903, 11815, -4777, 1095, 5831, 8439, 11207	downstream, downstream, downstream, downstream, downstream, upstream, in gene, downstream, downstream, downstream	1	1	1	13.4	11.8	17.8	5	4_A375_EGR1..1	22	Gene CLDN9	CLDN9	claudin 9	NM_020982	214635_at	NP_066192.1
GeneID:9074	CLDN6	16	3,064,713	3,068,188	3,475	-	11	1_A375_pNL7_minus_lncRNA_AR..1..2178, 1_A375_pNL7_minus_lncRNA_AR..1..2179, 1_A375_pNL7_minus_lncRNA_AR..1..2180, 2_A375_pNL97_plus_lncRNA_AR..1..3091, 2_A375_pNL97_plus_lncRNA_AR..1..3092, 4_A375_EGR1..1..2950, 4_A375_EGR1..1..2951, 4_A375_EGR1..1..2952, 4_A375_EGR1..1..2953, 4_A375_EGR1..1..2954, 4_A375_EGR1..1..2955	-2724, -3876, -6052, -3172, -6084, 10508, 4636, -100, -2708, -5476, -9348	upstream, upstream, upstream, upstream, upstream, downstream, downstream, upstream, upstream, upstream, upstream	1	1	1	12.67	10.67	18.17	6	4_A375_EGR1..1	22	Gene CLDN6	CLDN6		NM_021195, hCT1640118.2, hCT2257532.0	206474_at, 237610_at	NP_067018.2, EAW85431.1, EAW85432.1
GeneID:51330	TNFRSF12A	16	3,070,313	3,072,384	2,071	+	11	1_A375_pNL7_minus_lncRNA_AR..1..2178, 1_A375_pNL7_minus_lncRNA_AR..1..2179, 1_A375_pNL7_minus_lncRNA_AR..1..2180, 2_A375_pNL97_plus_lncRNA_AR..1..3091, 2_A375_pNL97_plus_lncRNA_AR..1..3092, 4_A375_EGR1..1..2951, 4_A375_EGR1..1..2952, 4_A375_EGR1..1..2953, 4_A375_EGR1..1..2954, 4_A375_EGR1..1..2955, 4_A375_EGR1..1..2956	599, 1751, 3927, 1047, 3959, -6761, -2025, 583, 3351, 7223, 11223	in gene, in gene, downstream, in gene, downstream, upstream, upstream, in gene, downstream, downstream, downstream	1	1	1	12.83	11	17.67	6	4_A375_EGR1..1	22	Gene TNFRSF12A	TWEAKR, CD266, TNFRSF12A, FN14	tumor necrosis factor receptor superfamily, member 12A	NM_016639, hCT1955801.1, hCT2258638.0, hCT6652.2	218368_s_at	NP_057723.1, EAW85429.1, EAW85428.1, EAW85430.1
GeneID:54985	HCFC1R1	16	3,072,626	3,074,287	1,661	-	11	1_A375_pNL7_minus_lncRNA_AR..1..2178, 1_A375_pNL7_minus_lncRNA_AR..1..2179, 1_A375_pNL7_minus_lncRNA_AR..1..2180, 2_A375_pNL97_plus_lncRNA_AR..1..3091, 2_A375_pNL97_plus_lncRNA_AR..1..3092, 4_A375_EGR1..1..2951, 4_A375_EGR1..1..2952, 4_A375_EGR1..1..2953, 4_A375_EGR1..1..2954, 4_A375_EGR1..1..2955, 4_A375_EGR1..1..2956	3375, 2223, 47, 2927, 15, 10735, 5999, 3391, 623, -3249, -7249	downstream, downstream, in gene, downstream, in gene, downstream, downstream, downstream, in gene, upstream, upstream	1	1	1	12.83	11	17.67	6	4_A375_EGR1..1	22	Gene HCFC1R1	HPIP, MGC70711, HCFC1R1, FLJ20568, MGC99622	host cell factor C1 regulator 1 (XPO1 dependent)	NM_001002017, NM_001002018, NM_017885, hCT1955802.1, hCT2356740.0, hCT2356741.0, hCT6654.3	218537_at, 45714_at	NP_001002017.1, NP_001002018.1, NP_060355.1, EAW85424.1, EAW85426.1, EAW85427.1, EAW85425.1
GeneID:79228	THOC6	16	3,074,032	3,077,756	3,724	-	11	1_A375_pNL7_minus_lncRNA_AR..1..2178, 1_A375_pNL7_minus_lncRNA_AR..1..2179, 1_A375_pNL7_minus_lncRNA_AR..1..2180, 2_A375_pNL97_plus_lncRNA_AR..1..3091, 2_A375_pNL97_plus_lncRNA_AR..1..3092, 4_A375_EGR1..1..2951, 4_A375_EGR1..1..2952, 4_A375_EGR1..1..2953, 4_A375_EGR1..1..2954, 4_A375_EGR1..1..2955, 4_A375_EGR1..1..2956	-3120, -1968, 206, -2672, 240, -10460, -5744, -3136, -368, 3504, 7504	upstream, upstream, in gene, upstream, in gene, upstream, upstream, upstream, upstream, in gene, downstream	1	1	1	12.83	11	17.67	6	4_A375_EGR1..1	22	Gene THOC6	MGC2655, THOC6, WDR58, fSAP35	THO complex 6 homolog (Drosophila)	NM_024339, NM_001142350, hCT1956544.1, hCT2356752.0, hCT6655.3	218648_at	NP_077315.2, NP_001135822.1, EAW85421.1, EAW85422.1, EAW85423.1
GeneID:146439	CCDC64B	16	3,077,866	3,085,542	7,674	-	10	1_A375_pNL7_minus_lncRNA_AR..1..2178, 1_A375_pNL7_minus_lncRNA_AR..1..2179, 1_A375_pNL7_minus_lncRNA_AR..1..2180, 2_A375_pNL97_plus_lncRNA_AR..1..3091, 2_A375_pNL97_plus_lncRNA_AR..1..3092, 4_A375_EGR1..1..2952, 4_A375_EGR1..1..2953, 4_A375_EGR1..1..2954, 4_A375_EGR1..1..2955, 4_A375_EGR1..1..2956	14630, 13478, 11302, 14182, 11270, 17254, 14646, 11878, 8006, 4006	downstream, downstream, downstream, downstream, downstream, downstream, downstream, downstream, downstream, in gene	1	1	1	13.2	11.4	17.6	5	4_A375_EGR1..1	22	Gene CCDC64B	CCDC64B, BICDR-2, MGC158089	coiled-coil domain containing 64B	NM_001103175	235095_at	NP_001096645.1
GeneID:100128770	LOC100128770	16	3,082,482	3,089,134	6,652	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2180, 2_A375_pNL97_plus_lncRNA_AR..1..3092, 4_A375_EGR1..1..2954, 4_A375_EGR1..1..2955, 4_A375_EGR1..1..2956, 4_A375_EGR1..1..2957	-8242, -8210, -8818, -4946, -946, 13806	upstream, upstream, upstream, upstream, upstream, downstream	1	1	1	12.25	11.5	16.75	4	4_A375_EGR1..1	22	Gene LOC100128770		hypothetical LOC100128770	XR_111634, XR_109245, XR_114906		
GeneID:64386	MMP25	16	3,096,682	3,110,727	14,045	+	1	4_A375_EGR1..1..2957	-394	upstream	0	0	1	11	13	17	1	4_A375_EGR1..1	17	Gene MMP25	MMP20, MMPL1, MT-MMP 6, MMP-25, MT-MMP6, MT6-MMP, MMP25, MT6MMP, MMP20A, MTMMP6	matrix metallopeptidase 25	NM_022468	207289_at, 207890_s_at	NP_071913.1
GeneID:100507419	LOC100507419	16	3,103,355	3,109,364	6,009	-	1	4_A375_EGR1..1..2957	13076	downstream	0	0	1	11	13	17	1	4_A375_EGR1..1	17	Gene LOC100507419		hypothetical protein LOC100507419	XM_003119649, XM_003118684, XM_003120630		XP_003119697.1, XP_003118732.1, XP_003120678.1
GeneID:81854	MGC3771	16	3,160,461	3,165,599	5,138	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2181, 2_A375_pNL97_plus_lncRNA_AR..1..3093, 2_A375_pNL97_plus_lncRNA_AR..1..3094	-9153, 9183, -9137	upstream, downstream, upstream	1	1	0	18	18	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene MGC3771	MGC1912	hypothetical LOC81854	NR_024166, NR_024167	208136_s_at	
GeneID:7755	ZNF205	16	3,162,563	3,170,518	7,955	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2181, 2_A375_pNL97_plus_lncRNA_AR..1..3093, 2_A375_pNL97_plus_lncRNA_AR..1..3094	12189, -6147, 12173	downstream, upstream, downstream	1	1	0	18	18	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene ZNF205	Zfp13, ZNF205, ZNF210	zinc finger protein 205	NM_003456, NM_001042428, hCT2258656.1, hCT2258657.1, hCT2258659.1, hCT2258664.1, hCT2343789.0, hCT2356683.0	206416_at	NP_003447.2, NP_001035893.1, EAW85396.1, EAW85397.1, EAW85399.1, EAW85400.1, EAW85398.1, EAW85401.1
GeneID:100507458	LOC100507458	16	3,181,669	3,184,878	3,209	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2181, 2_A375_pNL97_plus_lncRNA_AR..1..3094, 4_A375_EGR1..1..2958	10126, 10142, -9149	downstream, downstream, upstream	1	1	1	17	13.5	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene LOC100507458		hypothetical LOC100507458	XR_111636, XR_111637, XR_109246, XR_109247, XR_114909, XR_114910		
GeneID:7760	ZNF213	16	3,185,057	3,192,805	7,748	+	9	1_A375_pNL7_minus_lncRNA_AR..1..2181, 1_A375_pNL7_minus_lncRNA_AR..1..2182, 2_A375_pNL97_plus_lncRNA_AR..1..3094, 2_A375_pNL97_plus_lncRNA_AR..1..3095, 2_A375_pNL97_plus_lncRNA_AR..1..3096, 4_A375_EGR1..1..2958, 4_A375_EGR1..1..2959, 4_A375_EGR1..1..2960, 4_A375_EGR1..1..2961	-10305, 15626, -10321, 15903, 17791, 8970, 10367, 15679, 17623	upstream, downstream, upstream, downstream, downstream, downstream, downstream, downstream, downstream	1	1	1	15.6	13.2	18.6	5	4_A375_EGR1..1	28	Gene ZNF213	ZKSCAN21, CR53, ZNF213	zinc finger protein 213	NM_004220, NM_001134655, hCT2258662.1, hCT2258663.1	227207_x_at	NP_004211.1, NP_001128127.1, EAW85393.1, EAW85394.1
GeneID:7752	ZNF200	16	3,272,325	3,285,457	13,132	-	1	4_A375_EGR1..1..2966	369	in gene	0	0	1	12	14	16	1	4_A375_EGR1..1	16	Gene ZNF200	ZNF200, MGC45293	zinc finger protein 200	NM_003454, NM_198087, NM_198088, NM_001145446, NM_001145447, NM_001145448, hCT1962212.1, hCT2356713.0, hCT2356714.0, hCT2356715.0, hCT2356716.0, hCT7675.3	207338_s_at, 214706_at	NP_003445.2, NP_932353.1, NP_001138918.1, NP_001138919.1, NP_001138920.1, NP_932354.1, EAW85384.1, EAW85385.1, EAW85386.1, EAW85387.1, EAW85388.1, EAW85389.1
GeneID:4210	MEFV	16	3,292,028	3,306,627	14,599	-	2	4_A375_EGR1..1..2966, 4_A375_EGR1..1..2967	21539, -7709	downstream, upstream	0	0	1	13	15.5	20	2	4_A375_EGR1..1	24	Gene MEFV	MEFV, MEF, FMF, MGC126586, MGC126560, TRIM20	Mediterranean fever	NM_000243, hCT2257563.0, hCT7667.3	208262_x_at	NP_000234.1, EAW85382.1, EAW85383.1
GeneID:283876	FLJ39639	16	3,313,768	3,317,567	3,799	+	1	4_A375_EGR1..1..2967	566	in gene	0	0	1	14	17	24	1	4_A375_EGR1..1	24	Gene FLJ39639		hypothetical protein FLJ39639	NR_033904	243547_at	
GeneID:91151	TIGD7	16	3,348,832	3,351,400	2,568	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2184, 2_A375_pNL97_plus_lncRNA_AR..1..3097, 4_A375_EGR1..1..2968	-4024, -4168, -4472	upstream, upstream, upstream	1	1	1	18	17	15	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene TIGD7	TIGD7, Sancho, FLJ99447, FLJ98002	tigger transposable element derived 7	NM_033208	224365_s_at, 232089_at, 238793_at	NP_149985.2
GeneID:7627	ZNF75A	16	3,355,433	3,368,576	13,143	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2184, 2_A375_pNL97_plus_lncRNA_AR..1..3097, 4_A375_EGR1..1..2968	-9, 135, 439	upstream, in gene, in gene	1	1	1	18	17	15	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ZNF75A	FLJ31529, ZNF75A, MGC59959	zinc finger protein 75a	NM_153028, hCT1964160.1, hCT1964161.1, hCT2356671.0, hCT2356672.0	227670_at, 239204_at, 242633_x_at	NP_694573.1, EAW85377.1, EAW85374.1, EAW85375.1, EAW85376.1
GeneID:4993	OR2C1	16	3,405,889	3,406,924	1,035	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3098	9247	downstream	0	1	0	13	15	13	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene OR2C1	OLFmf3, MGC163200, OR2C1, OR2C2P, MGC95444	olfactory receptor, family 2, subfamily C, member 1	NM_012368, hCT1647368.1	221460_at	NP_036500.2, EAW85373.1
GeneID:100463285	MTRNR2L4	16	3,421,053	3,422,283	1,230	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3098	7147	downstream	0	1	0	13	15	13	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene MTRNR2L4	HN4, MTRNR2L4	MT-RNR2-like 4	NM_001190476		NP_001177405.1
GeneID:54925	ZNF434	16	3,432,085	3,451,025	18,940	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2185, 2_A375_pNL97_plus_lncRNA_AR..1..3099, 4_A375_EGR1..1..2969	-111, -207, 61	upstream, upstream, in gene	1	1	1	27	30	22	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene ZNF434	FLJ31901, MGC4179, ZNF434, FLJ20417	zinc finger protein 434	NM_017610, hCT2257554.0, hCT2257557.0, hCT2257558.0, hCT7668.3	218937_at, 220292_at	NP_060280.2, EAW85369.1, EAW85370.1, EAW85371.1, EAW85372.1
GeneID:7727	ZNF174	16	3,451,190	3,459,364	8,174	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2185, 2_A375_pNL97_plus_lncRNA_AR..1..3099, 4_A375_EGR1..1..2969	-54, 42, -246	upstream, in gene, upstream	1	1	1	27	30	22	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene ZNF174	ZNF174, ZSCAN8	zinc finger protein 174	NM_003450, NM_001032292, hCT7676.2	205252_at, 210290_at, 210291_s_at	NP_003441.1, NP_001027463.1, EAW85366.1
GeneID:79903	NAT15	16	3,493,668	3,536,963	43,295	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2186, 2_A375_pNL97_plus_lncRNA_AR..1..3100	14172, 14220	in gene, in gene	1	1	0	17	19	17	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene NAT15	FLJ14154, NAT15, FLJ11693	N-acetyltransferase 15 (GCN5-related, putative)	NM_001083600, NM_001083601, NM_024845	218661_at, 45526_g_at	NP_001077069.1, NP_001077070.1, NP_079121.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.846174	C16orf90	16	3,543,484	3,545,421	1,937	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2187, 2_A375_pNL97_plus_lncRNA_AR..1..3101	-5459, -5395	upstream, upstream	1	1	0	24	24	12	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene C16orf90	C16orf90	chromosome 16 open reading frame 90	NM_001080524		NP_001073993.1
GeneID.23059	CLUAP1	16	3,550,963	3,587,669	36,706	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2187, 2_A375_pNL97_plus_lncRNA_AR..1..3101	-83, -147	upstream, upstream	1	1	0	24	24	12	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CLUAP1	KIAA0643, FAP22, FLJ13297, CLUAP1	clusterin associated protein 1	NM_024793, NM_015041, hCT1957525.1, hCT2258661.0, hCT7661.1	204576_s_at, 204577_s_at	NP_079069.1, NP_055856.1, EAW85352.1, EAW85353.1, EAW85354.1
GeneID.197358	NLRC3	16	3,589,033	3,627,392	38,359	-	2	4_A375_EGR1..1..2970, 4_A375_EGR1..1..2971	27056, 15344	in gene, in gene	0	0	1	5.5	4	15.5	2	4_A375_EGR1..1	17	Gene NLRC3	CLR16.2, NOD3, NLRC3, FLJ00348	NLR family, CARD domain containing 3	NM_178844, hCT2340982.1, hCT2340983.1, hCT2343393.0, hCT2356673.0	238295_s_at	NP_849172.2, EAW85350.1, EAW85348.1, EAW85349.1, EAW85351.1
GeneID.84464	BTBD12	16	3,631,182	3,661,585	30,403	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2188, 4_A375_EGR1..1..2972, 4_A375_EGR1..1..2973	177, 15185, 337	in gene, in gene, in gene	1	0	1	10.5	9.5	18.5	2	4_A375_EGR1..1	19	Gene BTBD12	FANCP, MUS312, KIAA1987, SLX4, BTBD12, KIAA1784	BTB (POZ) domain containing 12	NM_032444, hCT2257548.1, hCT2257549.1, hCT2257550.1	232147_at, 239687_at	NP_115820.2, EAW85345.1, EAW85346.1, EAW85347.1
GeneID.1773	DNASE1	16	3,702,940	3,708,098	5,158	+	1	4_A375_EGR1..1..2974	-636	upstream	0	0	1	7	5	18	1	4_A375_EGR1..1	18	Gene DNASE1	FLJ44902, DNASE1, DNL1, FLJ38093, DKFZp686H0155, DRNI	deoxyribonuclease I	NM_005223, hCT2258692.0, hCT7673.3	1557189_at, 1558548_at, 210165_at, 228929_at, 240144_at, 241854_at, 243127_x_at	NP_005214.2, EAW85343.1, EAW85344.1
GeneID.10131	TRAP1	16	3,708,038	3,767,598	59,560	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3102, 4_A375_EGR1..1..2974	-82, 65294	upstream, downstream	0	1	1	11	12.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TRAP1	HSP75, TRAP1, HSP90L	TNF receptor-associated protein 1	NM_016292, hCT2257545.1, hCT2343698.0, hCT2343699.0, hCT2356711.0, hCT7672.4	201391_at, 239622_at	NP_057376.2, EAW85338.1, EAW85339.1, EAW85340.1, EAW85341.1, EAW85342.1
GeneID.1387	CREBBP	16	3,775,055	3,930,121	155,066	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2189, 2_A375_pNL97_plus_lncRNA_AR..1..3102, 4_A375_EGR1..1..2975	569, 162441, -1191	in gene, downstream, upstream	1	1	1	13.33	15.33	14.33	3	4_A375_EGR1..1	21	Gene CREBBP	CBP, CREBBP, RSTS, KAT3A	CREB binding protein	NM_001079846, NM_004380, hCT2257541.0, hCT2257543.0, hCT2356708.0, hCT5653.2	202160_at, 211808_s_at, 228177_at, 235856_at	NP_001073315.1, NP_004371.2, EAW85334.1, EAW85335.1, EAW85336.1, EAW85337.1
GeneID.8345	SRL	16	4,239,375	4,292,081	52,706	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2190, 2_A375_pNL97_plus_lncRNA_AR..1..3103	58214, 58353	downstream, downstream	1	1	0	17	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SRL	SRL	sarcalumenin	NM_001098814	235718_at	NP_001092284.1
GeneID.100507501	LOC100507501	16	4,295,826	4,303,790	7,964	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3104, 4_A375_EGR1..1..2976	-274, 206	upstream, in gene	0	1	1	14	18	18	1	4_A375_EGR1..1	18	Gene LOC100507501		hypothetical LOC100507501	XR_111629, XR_109248, XR_114911		
GeneID.7023	TFAP4	16	4,307,187	4,323,001	15,814	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3104, 2_A375_pNL97_plus_lncRNA_AR..1..3105, 4_A375_EGR1..1..2976	18937, 1129, 19417	downstream, in gene, downstream	0	1	1	15.5	21.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene TFAP4	AP-4, TFAP4, bHLHc41	transcription factor AP-4 (activating enhancer binding protein 4)	NM_003223, hCT2259305.0, hCT2259306.0, hCT2259307.0	205688_at	NP_003214.1, EAW85320.1, EAW85321.1, EAW85322.1
GeneID.84662	GLIS2	16	4,382,225	4,389,598	7,373	+	1	4_A375_EGR1..1..2979	11247	downstream	0	0	1	10	7	17	1	4_A375_EGR1..1	17	Gene GLIS2	NKL, NPHP7, GLIS2, FLJ38247	GLIS family zinc finger 2	NM_032575, hCT2260967.0, hCT6190.2	223378_at	NP_115964.2, EAW85318.1, EAW85317.1
GeneID.51025	Magmas	16	4,390,252	4,401,300	11,048	-	1	4_A375_EGR1..1..2979	7828	in gene	0	0	1	10	7	17	1	4_A375_EGR1..1	17	Gene Magmas	CGI-136, Tim16, MAGMAS, TIMM16, TIM16, Magmas, PAM16	mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction	NM_016069	218969_at	NP_057153.8
GeneID.79585	CORO7	16	4,404,543	4,466,639	62,096	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2191, 2_A375_pNL97_plus_lncRNA_AR..1..3106, 4_A375_EGR1..1..2980, 4_A375_EGR1..1..2981, 4_A375_EGR1..1..2982, 4_A375_EGR1..1..2983	-9281, -9009, 54959, 41743, 24911, 13903	upstream, upstream, in gene, in gene, in gene, in gene	1	1	1	10	10.2	16.4	5	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene CORO7	CORO7, FLJ22021, POD1, FLJ44166, CRN7, 0610011B16Rik	coronin 7	NM_024535	219040_at	NP_078811.3
GeneID.114990	VASN	16	4,421,849	4,433,529	11,680	+	3	4_A375_EGR1..1..2980, 4_A375_EGR1..1..2981, 4_A375_EGR1..1..2982	-10169, 3047, 19879	upstream, in gene, downstream	0	0	1	4.33	5.67	16	3	4_A375_EGR1..1	17	Gene VASN	VASN, SLITL2	vasorin	NM_138440, hCT1658711.2	225867_at	NP_612449.2, EAW85311.1
GeneID.9093	DNAJA3	16	4,475,856	4,506,778	30,918	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2191, 2_A375_pNL97_plus_lncRNA_AR..1..3106	62, -210	in gene, upstream	1	1	0	26	23	16	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene DNAJA3	FLJ45758, DNAJA3, TID1, hTid-1	DnaJ (Hsp40) homolog, subfamily A, member 3	NM_005147, NM_001135110, hCT2260972.0, hCT2260973.0, hCT6186.2	1554078_s_at, 205963_s_at	NP_005138.3, NP_001128582.1, EAW85303.1, EAW85304.1, EAW85305.1
GeneID.57407	NMRAL1	16	4,511,695	4,524,896	13,201	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2192, 4_A375_EGR1..1..2984	-1040, -1656	upstream, upstream	1	0	1	14	15	18	1	4_A375_EGR1..1	18	Gene NMRAL1	FLJ25918, NMRAL1, HSCARG, SDR48A1	NmrA-like family domain containing 1	NM_020677, hCT2259293.0, hCT2259294.0	223208_s_at, 231271_x_at	NP_065728.1, EAW85301.1, EAW85302.1
GeneID.3163	HMOX2	16	4,524,719	4,560,348	35,629	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2192, 4_A375_EGR1..1..2984	1217, 2033	in gene, in gene	1	0	1	14	15	18	1	4_A375_EGR1..1	18	Gene HMOX2	HO-2, HMOX2	heme oxygenase (decycling) 2	NM_002134, NM_001127204, NM_001127205, NM_001127206, hCT2260976.0, hCT2260979.0	218120_s_at, 218121_at	NP_002125.3, NP_001120676.1, NP_001120677.1, NP_001120678.1, EAW85299.1, EAW85300.1
GeneID.29965	C16orf5	16	4,560,676	4,588,816	28,140	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3107	48	in gene	0	1	0	13	22	11	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene C16orf5	I1, C16orf5, CDIP	chromosome 16 open reading frame 5	NM_013399, hCT1958264.1, hCT1958265.1, hCT2356659.0, hCT2356660.0, hCT2356661.0, hCT2356662.0, hCT2356663.0, hCT6194.3	218183_at, 223980_s_at	NP_037531.2, EAW85294.1, EAW85291.1, EAW85292.1, EAW85296.1, EAW85298.1, EAW85293.1, EAW85295.1, EAW85297.1
GeneID.124402	FAM100A	16	4,656,883	4,664,927	8,044	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2193, 1_A375_pNL7_minus_lncRNA_AR..1..2194, 1_A375_pNL7_minus_lncRNA_AR..1..2195, 2_A375_pNL97_plus_lncRNA_AR..1..3108, 2_A375_pNL97_plus_lncRNA_AR..1..3109, 4_A375_EGR1..1..2985, 4_A375_EGR1..1..2986	143, -1121, -9697, -65, -9681, 959, -593	in gene, upstream, upstream, upstream, upstream, in gene, upstream	1	1	1	17	18.67	15.67	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene FAM100A	PP11303, FAM100A, FLJ31223, FLJ32185	family with sequence similarity 100, member A	NM_145253, hCT2343671.0, hCT2343672.0, hCT2343673.0, hCT2343674.0, hCT6208.3	1558975_at, 1558976_x_at, 225674_at	NP_660296.1, EAW85287.1, EAW85284.1, EAW85285.1, EAW85286.1, EAW85288.1
GeneID.23295	MGRN1	16	4,674,826	4,740,975	66,149	+	10	1_A375_pNL7_minus_lncRNA_AR..1..2193, 1_A375_pNL7_minus_lncRNA_AR..1..2194, 1_A375_pNL7_minus_lncRNA_AR..1..2195, 2_A375_pNL97_plus_lncRNA_AR..1..3108, 2_A375_pNL97_plus_lncRNA_AR..1..3109, 4_A375_EGR1..1..2986, 4_A375_EGR1..1..2987, 4_A375_EGR1..1..2988, 4_A375_EGR1..1..2989, 4_A375_EGR1..1..2990	-10042, -8776, -202, -9834, -218, 9308, 58150, 66934, 68582, 73462	upstream, upstream, upstream, upstream, in gene, downstream, downstream, downstream	1	1	1	10.83	13	16.17	6	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MGRN1	KIAA0544, MGRN1, RNF156	mahogunin, ring finger 1	NM_015246, NM_001142289, NM_001142290, NM_001142291, hCT2260984.0, hCT2260985.0, hCT2356668.0, hCT6198.2	212576_at	NP_056061.1, NP_001135761.1, NP_001135762.1, NP_001135763.1, EAW85279.1, EAW85280.1, EAW85281.1, EAW85282.1
GeneID.100507570	LOC100507570	16	4,684,326	4,690,624	6,298	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2195, 2_A375_pNL97_plus_lncRNA_AR..1..3109	16000, 16016	downstream, downstream	1	1	0	16	23	10	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100507570		hypothetical LOC100507570	XR_111630, XR_109249, XR_114912		
GeneID.84309	NUDT16L1	16	4,743,694	4,745,860	2,166	+	4	4_A375_EGR1..1..2988, 4_A375_EGR1..1..2989, 4_A375_EGR1..1..2990, 4_A375_EGR1..1..2991	-1934, -266, 4594, 6504	upstream, upstream, downstream, downstream	0	0	1	7	8.25	16.75	4	4_A375_EGR1..1	19	Gene NUDT16L1	NUDT16L1, SDOS, MGC11275	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	NM_032349, NM_001193452, hCT1958267.1, hCT6197.3	224477_s_at	NP_115725.1, NP_001180381.1, EAW85277.1, EAW85278.1
GeneID.124401	ANKS3	16	4,746,513	4,784,163	37,650	-	6	2_A375_pNL97_plus_lncRNA_AR..1..3110, 4_A375_EGR1..1..2988, 4_A375_EGR1..1..2989, 4_A375_EGR1..1..2990, 4_A375_EGR1..1..2991, 4_A375_EGR1..1..2992	3, 42403, 40755, 35675, 31985, -8989	in gene, downstream, downstream, in gene, in gene, upstream	0	1	1	7.33	9.17	15.5	6	4_A375_EGR1..1	19	Gene ANKS3	KIAA1977, FLJ32767, FLJ32345, ANKS3	ankyrin repeat and sterile alpha motif domain containing 3	NM_133450, hCT2259279.1, hCT2259280.1, hCT2343669.0, hCT2343670.0, hCT2356692.0, hCT2356693.0, hCT6204.3	227303_at	NP_597707.1, EAW85275.1, EAW85269.1, EAW85270.1, EAW85273.1, EAW85274.1, EAW85271.1, EAW85272.1
GeneID.146562	C16orf71	16	4,784,289	4,799,397	15,108	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3110, 4_A375_EGR1..1..2992	-129, 8863	upstream, in gene	0	1	1	8	11	13	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene C16orf71	DKFZp686H2240, FLJ43261, C16orf71	chromosome 16 open reading frame 71	NM_139170, hCT2356694.0, hCT6205.2	222089_s_at	NP_631909.2, EAW85266.1, EAW85267.1
GeneID.26048	ZNF500	16	4,800,815	4,817,166	16,351	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2196, 2_A375_pNL97_plus_lncRNA_AR..1..3111, 4_A375_EGR1..1..2992	14, -114, 24014	in gene, upstream, downstream	1	1	1	14.5	15.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ZNF500	ZKSCAN18, ZNF500	zinc finger protein 500	NM_021646, hCT6191.3	213639_s_at, 213641_at, 41113_at	NP_067678.1, EAW85268.1
GeneID.124404	12-Sep	16	4,827,670	4,838,399	10,729	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3111	21119	downstream	0	1	0	26	26	16	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene SEPT12	SEPT12, FLJ25410	septin 12	NM_144605, NM_001154458, hCT2356658.0, hCT6192.2	230947_at	NP_653206.2, NP_001147930.1, EAW85264.1, EAW85265.1
GeneID.84656	GLYR1	16	4,853,204	4,897,303	44,099	-	1	4_A375_EGR1..1..2993	423	in gene	0	0	1	12	7	19	1	4_A375_EGR1..1	19	Gene GLYR1	N-PAC, BM045, NP60, HIBDL, GLYR1	glyoxylate reductase 1 homolog (Arabidopsis)	NM_032569, hCT1955058.2, hCT2259272.0, hCT2259274.1, hCT2259275.0, hCT2356690.0, hCT2356691.0, hCT6201.3	218508_x_at, 221628_s_at, 222115_x_at, 222852_s_at	NP_115958.2, EAW85255.1, EAW85251.1, EAW85252.1, EAW85253.1, EAW85254.1, EAW85256.1, EAW85257.1
GeneID.29855	UBN1	16	4,897,912	4,932,363	34,451	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2197, 2_A375_pNL97_plus_lncRNA_AR..1..3112, 4_A375_EGR1..1..2993	12104, 12136, -1032	in gene, in gene, upstream	1	1	1	15	15.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene UBN1	VT4, VT, UBN1	ubinuclein 1	NM_016936, NM_001079514, hCT2356751.0, hCT6189.3	207253_s_at, 209088_s_at	NP_058632.2, NP_001072982.1, EAW85249.1, EAW85250.1
GeneID.5493	PPL	16	4,932,506	4,987,136	54,626	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2198, 2_A375_pNL97_plus_lncRNA_AR..1..3113, 2_A375_pNL97_plus_lncRNA_AR..1..3114, 4_A375_EGR1..1..2994, 4_A375_EGR1..1..2995	-8704, -6206, -7776, 43744, 18400	upstream, upstream, upstream, in gene, in gene	1	1	1	12.6	10.6	12.6	5	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene PPL	KIAA0568, PPL, MGC134672	periplakin	NM_002705, hCT6199.3	203407_at	NP_002696.3, EAW85246.1
GeneID.9717	SEC14L5	16	5,008,318	5,089,156	80,838	+	2	4_A375_EGR1..1..2996, 4_A375_EGR1..1..2997	434, 67234	in gene, downstream	0	0	1	7.5	8.5	18	2	4_A375_EGR1..1	19	Gene SEC14L5	SEC14L5, KIAA0420, PRELID4B	SEC14-like 5 (S. cerevisiae)	NM_014692	210169_at	NP_055507.1
GeneID.51172	NAGPA	16	5,074,845	5,083,942	9,097	-	1	4_A375_EGR1..1..2997	8390	in gene	0	0	1	4	3	19	1	4_A375_EGR1..1	19	Gene NAGPA	NAGPA, UCE, APAA	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	NM_016256, hCT1826808.1, hCT2356696.0	205090_s_at	NP_057340.2, EAW85245.1, EAW85246.1
GeneID.100507589	LOC100507589	16	5,083,703	5,094,000	10,297	+	1	4_A375_EGR1..1..2997	-8151	upstream	0	0	1	4	3	19	1	4_A375_EGR1..1	19	Gene LOC100507589	FLJ30660	hypothetical LOC100507589	XR_109250		
GeneID.56052	ALG1	16	5,121,810	5,137,380	15,570	+	1	4_A375_EGR1..1..2998	5614	in gene	0	0	1	2	4	17	1	4_A375_EGR1..1	17	Gene ALG1	ALG1, HMT1, HMT-1, HMAT1, CDG1K	asparagine-linked glycosylation 1, beta-1,4-mannosyltransferase homolog (S. cerevisiae)	NM_019109, hCT2260995.0, hCT2260996.0	223355_at	NP_061982.3, EAW85241.1, EAW85240.1
GeneID.196483	FAM86A	16	5,134,301	5,147,789	13,488	-	1	4_A375_EGR1..1..2998	20365	downstream	0	0	1	2	4	17	1	4_A375_EGR1..1	17	Gene FAM86A	FAM86A, MGC19636, SB153	family with sequence similarity 86, member A	NM_201400, NM_201598, hCT1962510.1, hCT2259250.0, hCT2259252.0, hCT2259255.0, hCT2259257.0, hCT2259259.0, hCT2259261.0, hCT2259262.0, hCT2356764.0, hCT2356765.0, hCT2356766.0		NP_958802.1, NP_963892.1, EAW85229.1, EAW85230.1, EAW85237.1, EAW85238.1, EAW85231.1, EAW85232.1, EAW85233.1, EAW85234.1, EAW85235.1, EAW85236.1, EAW85239.1
GeneID.54715	A2BP1	16	6,069,132	7,763,340	1,694,208	+	1	4_A375_EGR1..1..2999	1415060	in gene	0	0	1	1	3	14	1	4_A375_EGR1..1	14	Gene A2BP1	FOX1, HRNBP1, A2BP1, RBFOX1, FOX-1	RNA binding protein, fox-1 homolog (C. elegans) 1	NM_018723, NM_145891, NM_145892, NM_145893, NM_001142333, NM_001142334, hCT1955054.1, hCT2259778.0, hCT2259779.0, hCT2259781.0, hCT2259784.0	1553422_s_at, 221217_s_at, 235070_at	NP_061193.2, NP_665898.1, NP_665899.1, NP_665900.1, NP_001135805.1, NP_001135806.1, EAW85216.1, EAW85217.1, EAW85218.1, EAW85219.1, EAW85220.1
GeneID.79091	C16orf68	16	8,715,527	8,740,079	24,552	+	1	4_A375_EGR1..1..3000	89	in gene	0	0	1	12	12	18	1	4_A375_EGR1..1	18	Gene C16orf68	MGC2654, C16orf68, METTL22, FLJ12433	chromosome 16 open reading frame 68	NM_024109, hCT2258460.1, hCT2258464.1, hCT2344097.0	218945_at, 233742_at	NP_077014.2, EAW85211.1, EAW85210.1, EAW85212.1
GeneID.25880	TMEM186	16	8,889,037	8,891,505	2,468	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3118	-79	upstream	0	1	0	18	27	8	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene TMEM186	C16orf51, TMEM186, DKFZp564K2062	transmembrane protein 186	NM_015421, hCT2258054.0, hCT5661.3	204676_at	NP_056236.2, EAW85205.1, EAW85206.1
GeneID.5373	PMM2	16	8,891,670	8,943,194	51,524	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3118	-86	upstream	0	1	0	18	27	8	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene PMM2	PMM2, CDG1a, PMM 2, CDG1, CDGS	phosphomannomutase 2	NM_000303, hCT1955056.2, hCT2356722.0, hCT2356723.0, hCT6423.3	203201_at	NP_000294.1, EAW85203.1, EAW85200.1, EAW85201.1, EAW85202.1
GeneID.23589	CARHSP1	16	8,946,802	8,962,863	16,061	-	2	4_A375_EGR1..1..3001, 4_A375_EGR1..1..3002	4367, 2223	in gene, in gene	0	0	1	8.5	9	15	2	4_A375_EGR1..1	16	Gene CARHSP1	MGC111446, CSDC1, CRHSP-24, CARHSP1	calcium regulated heat stable protein 1, 24kDa	NM_001042476, NM_014316, hCT2256042.0, hCT2256043.0, hCT2256045.0, hCT6426.3	1566134_at, 1566135_at, 218384_at, 224910_at	NP_001035941.1, NP_055131.2, EAW85196.1, EAW85197.1, EAW85198.1, EAW85199.1
GeneID.100507655	LOC100507655	16	8,955,847	8,957,794	1,947	-	2	4_A375_EGR1..1..3001, 4_A375_EGR1..1..3002	-702, -2846	upstream, upstream	0	0	1	8.5	9	15	2	4_A375_EGR1..1	16	Gene LOC100507655		hypothetical protein LOC100507655	XM_003118687		XP_003118735.1
GeneID.7874	USP7	16	8,985,951	9,057,341	71,390	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2202, 2_A375_pNL97_plus_lncRNA_AR..1..3119	31453, 31533	in gene, in gene	1	1	0	24	20	8	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene USP7	TEF1, USP7, HAUSP	ubiquitin specific peptidase 7 (herpes virus-associated)	NM_003470, hCT1955061.1, hCT2356748.0	201498_at, 201499_s_at, 222032_s_at, 230987_s_at	NP_003461.2, EAW85194.1, EAW85195.1
GeneID.2903	GRIN2A	16	9,847,265	10,276,611	429,346	-	1	4_A375_EGR1..1..3003	995	in gene	0	0	1	13	13	18	1	4_A375_EGR1..1	18	Gene GRIN2A	NR2A, GRIN2A, NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	NM_000833, NM_001134407, NM_001134408, hCT1686556.1	206534_at	NP_000824.1, NP_001127879.1, NP_001127880.1, EAW85187.1
GeneID.2013	EMP2	16	10,622,279	10,674,539	52,260	-	1	4_A375_EGR1..1..3004	21611	in gene	0	0	1	14	10	18	1	4_A375_EGR1..1	18	Gene EMP2	MGC9056, XMP, EMP2	epithelial membrane protein 2	NM_001424, hCT2256117.0, hCT2256118.0, hCT5665.3	204975_at, 225078_at, 225079_at, 236500_at	NP_001415.1, EAW85180.1, EAW85181.1, EAW85182.1
GeneID.146279	TEKT5	16	10,721,361	10,788,802	67,441	-	1	4_A375_EGR1..1..3005	41666	in gene	0	0	1	8	12	16	1	4_A375_EGR1..1	16	Gene TEKT5	MGC163210, TEKT5, MGC163208, FLJ32871	tektin 5	NM_144674, hCT5661.3	1553468_at, 1553469_a_at	NP_653275.1, EAW85179.1
GeneID.4682	NUBP1	16	10,837,698	10,863,208	25,510	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3120, 4_A375_EGR1..1..3006	46, 24702	in gene, in gene	0	1	1	10	16	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene NUBP1	MGC130052, MGC130053, NBP, NBP1, NUBP1, MGC117406	nucleotide binding protein 1 (MinD homolog, E. coli)	NM_002484, hCT2257489.0	203978_at	NP_002475.2, EAW85178.1
GeneID.780776	FAM18A	16	10,860,533	10,912,621	52,088	-	2	4_A375_EGR1..1..3006, 4_A375_EGR1..1..3007	50221, -9139	in gene, upstream	0	0	1	6	8.5	18	2	4_A375_EGR1..1	23	Gene FAM18A	YDR084C, FAM18A	family with sequence similarity 18, member A	NM_001079512	1560638_at	NP_001072980.1
GeneID.4261	CIITA	16	10,971,055	11,018,840	47,785	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2203, 1_A375_pNL7_minus_lncRNA_AR..1..2204, 2_A375_pNL97_plus_lncRNA_AR..1..3121	1420, 18129, 1937	in gene, in gene, in gene	1	1	0	16	17	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CIITA	C2TA, CIITAIV, CIITA, MHC2TA, NLRA	class II, major histocompatibility complex, transactivator	NM_000246, hCT1954361.1, hCT2257491.0, hCT2257492.0, hCT2257494.0, hCT2257495.0, hCT2257497.0, hCT6089.3	205101_at, 210925_at, 211884_s_at	NP_000237.2, EAW85168.1, EAW85169.1, EAW85170.1, EAW85173.1, EAW85174.1, EAW85171.1, EAW85172.1

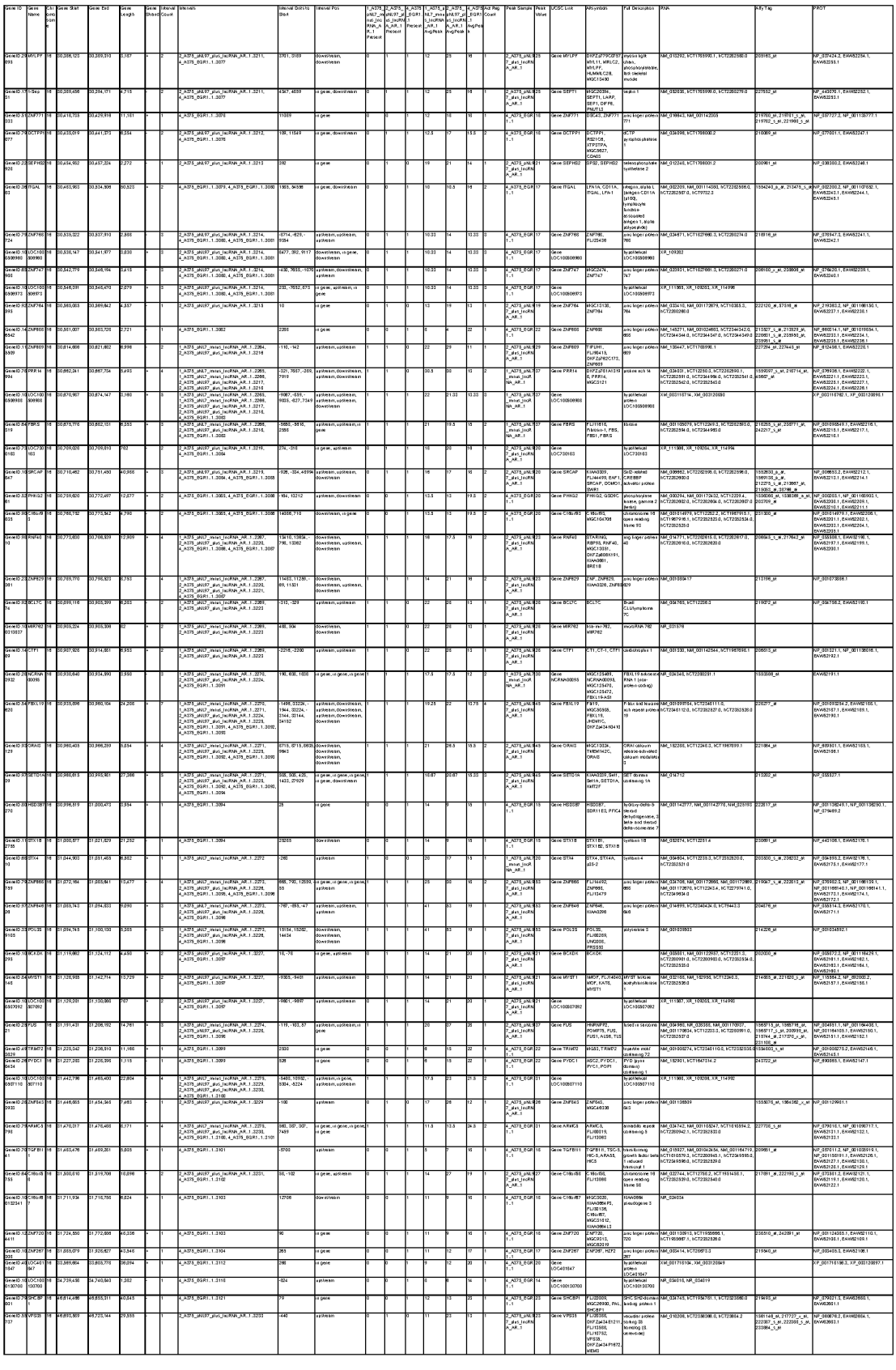


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_pfa27_neg_RNA_R_1 Percent	2_A375_pfa27_neg_RNA_R_1 Percent	4_A375_pfa27_neg_RNA_R_1 Percent	1_A375_pfa27_neg_lncRNA_RNA_R_1 Avg Reads	2_A375_pfa27_neg_lncRNA_RNA_R_1 Avg Reads	4_A375_pfa27_neg_lncRNA_RNA_R_1 Avg Reads	Ad Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:2835	DEX1	16	11,222,745	11,235,257	12,509	-	3	1_A375_pfa27_minus_lncRNA_RR_1.1.2355, 2_A375_pfa27_plus_lncRNA_RR_1.1.3122, 4_A375_RGR1_1.3006	-2979, -2947, -2239	upstream, upstream, upstream	1	1	1	26	22	22	1	1_A375_pfa27_minus_lncRNA_RR_1.1	26	Gene DEX1	MYLE, DEX1	Dbx homolog (mouse)	NM_014015, XCT1526701.1, XCT2356680.0	2035122_at		NP_054734.2, EAW65187.1, EAW65188.1
GeneID:1615	LOC100383864	16	11,234,376	11,235,016	2,352	+	3	1_A375_pfa27_minus_lncRNA_RR_1.1.2355, 2_A375_pfa27_plus_lncRNA_RR_1.1.3122, 4_A375_RGR1_1.3006	3785, 3126, 3930	downstream, downstream, downstream	1	1	1	26	22	22	1	1_A375_pfa27_minus_lncRNA_RR_1.1	26	Gene LOC100383864		hypothetical protein LOC100383864	XM_003119692, XM_003316865, XM_003120934			XP_003119740.1, XP_003119738.1, XP_003120982.1
GeneID:2350	CLEC16A	16	11,235,343	11,276,948	237,701	+	4	1_A375_pfa27_minus_lncRNA_RR_1.1.2355, 2_A375_pfa27_plus_lncRNA_RR_1.1.3122, 3_A375_RGR1_1.3009, 4_A375_RGR1_1.3009	-9, -41, 151, 2338523	upstream, upstream, upstream, gene, up gene	1	1	1	15.5	14	16.5	2	1_A375_pfa27_minus_lncRNA_RR_1.1	29	Gene CLEC16A	MGC114437, KIAA0350, CLEC16A, Gap1	C-type lectin domain family 16, member A	NM_015226, XCT1526707.3, XCT2356730.0	2127698_at, 231221_at		NP_056211.1, EAW65165.1, EAW65164.1
GeneID:4891	LOC400499	09	11,490,987	11,802,517	312,530	+	3	4_A375_RGR1_1.3002, 4_A375_RGR1_1.3011, 4_A375_RGR1_1.3012	97653, 69057, 48857	up gene, up gene, up gene	0	0	1	5.67	6.67	7.5	3	4_A375_RGR1_1.1	20	Gene LOC400499		hypothetical protein LOC400499	XM_003119692, XM_003316865, XM_003120935, XCT932.3			XP_003119740.1, XP_003119737.1, XP_003120983.1, EAW65154.1
GeneID:2599	QSPT1	19	11,961,965	12,010,519	48,554	-	2	1_A375_pfa27_minus_lncRNA_RR_1.2207, 2_A375_pfa27_plus_lncRNA_RR_1.3124	615, 500	up gene, up gene	1	1	0	21	16	15	1	1_A375_pfa27_minus_lncRNA_RR_1.1	21	Gene QSPT1	QSPT1, HPR3A, FLJ39951, ETF3h, 3610B.2, FLJ38044, QSPT	QI 1c S plasia inducible 1	NM_002994, NM_001135007, NM_001135008, XCT2357999.0, XCT2357982.0, XCT932.2	201912_s_at, 215435_x_at, 243462_at		NP_002985.2, NP_001125479.1, NP_001125480.1, EAW65130.1, EAW65132.1
GeneID:8878	TNFRSF17	16	12,255,956	12,261,925	2,981	+	1	2_A375_pfa27_plus_lncRNA_RR_1.3125	11372	downstream	0	1	0	13	15	14	1	2_A375_pfa27_plus_lncRNA_RR_1.1	15	Gene TNFRSF17	TNFRSF17, BCMA, CD269	tumor necrosis factor receptor superfamily, member 17	NM_001192, XCT5844.2	209561_at		NP_001183.2, EAW65129.1
GeneID:6447	RUNDC2A	16	12,270,692	12,747,141	76,839	+	1	2_A375_pfa27_plus_lncRNA_RR_1.3133	-298	upstream	0	1	0	13	15	14	1	2_A375_pfa27_plus_lncRNA_RR_1.1	15	Gene RUNDC2A	RUNDC2A	RUN domain containing 2A	NM_032167	232469_at		NP_115543.2
GeneID:5562	CPPED1	16	12,753,698	12,897,744	144,088	+	4	1_A375_pfa27_minus_lncRNA_RR_1.2205, 2_A375_pfa27_plus_lncRNA_RR_1.3126, 3_A375_pfa27_plus_lncRNA_RR_1.3127, 4_A375_RGR1_1.3015	586, 141904, -64, 16	up gene, up gene, upstream, up gene	1	1	1	22.5	27.5	12.5	2	2_A375_pfa27_plus_lncRNA_RR_1.1	33	Gene CPPED1	CPPED1, CSPP1, FLJ11151	calcineurin-like phosphoesterase domain containing	NM_015452, NM_001099455, XCT2351902.0, XCT2354702.2	219610_s_at, 222868_s_at		NP_056512.2, NP_001092925.1, EAW65121.1, EAW65122.1
GeneID:7203	SHISA9	16	12,956,477	13,034,373	555,756	+	2	2_A375_pfa27_plus_lncRNA_RR_1.3129, 2_A375_pfa27_plus_lncRNA_RR_1.3130	135211, 203809	up gene, up gene	1	1	0	15	16	8.5	2	2_A375_pfa27_plus_lncRNA_RR_1.1	21	Gene SHISA9	CKAMP44, FLJ10315, FLJ38277, DKFZp686D24208, SHISA9, FLJ25553, DKFZp686D24208, FLJ40629, FLJ40634	cornichon homolog 4 (Drosophila)	NM_001145535, NM_001145534			NP_001138772.2, NP_001138678.2
GeneID:2072	ERCC4	16	14,014,014	14,046,205	32,191	+	3	1_A375_pfa27_minus_lncRNA_RR_1.2211, 2_A375_pfa27_plus_lncRNA_RR_1.3130, 4_A375_RGR1_1.3016	37762, 37551, 62	downstream, downstream, up gene	1	1	1	16	13	13	2	1_A375_pfa27_minus_lncRNA_RR_1.1	19	Gene ERCC4	ERCC4, RAD1, XPF	excision repair cross-complementing rodent repair deficiency, complementation group 4	NM_005236, XCT2356016.0, XCT2357713.0	210155_at		NP_005227.1, EAW65116.1, EAW65117.1
GeneID:3776	MIIG2	19	14,165,166	14,360,650	195,484	+	2	2_A375_pfa27_plus_lncRNA_RR_1.3131, 4_A375_RGR1_1.3017	-166, -360	upstream, upstream	0	1	1	13	16	20	1	4_A375_RGR1_1.1	20	Gene MIIG2	NPD001, DKFZp686J1745, FLJ10523, MRTF-B, FLJ45803, MKL2	myocardin-like protein 2	NM_014048, XCT2356020.1, XCT2356021.1, XCT2356023.1, XCT2356024.1	1555777_at, 1556776_s_at, 1570202_a_at, 216269_at		NP_054767.2, EAW65112.1, EAW65114.1, EAW65115.1
GeneID:5548	PARN	16	14,325,555	14,724,124	194,598	-	3	1_A375_pfa27_minus_lncRNA_RR_1.2214, 1_A375_pfa27_minus_lncRNA_RR_1.2215, 2_A375_pfa27_plus_lncRNA_RR_1.3133	118998, -2984, 126308	up gene, upstream, up gene	1	1	0	15	16	8	0	2_A375_pfa27_plus_lncRNA_RR_1.1	27	Gene PARN	DAN, PARN	poly(A)-specific ribonuclease (deadenylation nuclease)	NM_002582, NM_001134477, XCT1934276.1, XCT2353290.0	232369_at		NP_002572.1, NP_001127949.1, EAW65110.1, EAW65111.1
GeneID:5513	BPAR	19	14,726,865	14,763,093	36,229	+	1	1_A375_pfa27_minus_lncRNA_RR_1.2215	20	up gene	1	0	0	16	16	15	1	1_A375_pfa27_minus_lncRNA_RR_1.1	16	Gene BPAR	BPAR, RNF47, BkA	bifunctional apoptosis regulator	NM_016581, XCT1982491.1, XCT1982594.1, XCT1982595.1, XCT2356032.0, XCT2353113	210056_at		NP_057945.1, EAW65106.1, EAW65105.1, EAW65107.1, EAW65108.1, EAW65109.1
GeneID:5547	NPIP	19	13,951,300	13,954,551	14,851	+	2	1_A375_pfa27_minus_lncRNA_RR_1.2216, 2_A375_pfa27_plus_lncRNA_RR_1.3134	-3196, 21708	downstream, downstream	1	1	0	24	18	8	1	1_A375_pfa27_minus_lncRNA_RR_1.1	24	Gene NPIP	FLJ44545, NPIP, FLJ42525	nuclear pore complex interacting protein	NM_030935, XCT2356012.0, XCT2356163.3	244077_at		NP_008178.2, EAW65296.1, EAW65293.1
GeneID:1328	NTAN1	19	13,931,714	13,949,693	18,119	-	1	4_A375_RGR1_1.3019	457	up gene	0	0	1	10	10	10	1	4_A375_RGR1_1.1	10	Gene NTAN1	NTAN1, DKFZp686B0336	N-terminal asparagine amidase	NM_175474, XCT1794317.2	212081_s_at, 213062_at		NP_775745.1, EAW65479.1
GeneID:5447	RRN3	16	15,183,879	15,186,198	54,279	-	1	4_A375_RGR1_1.3019	38762	downstream	0	0	1	10	10	10	1	4_A375_RGR1_1.1	10	Gene RRN3	TIF1A, MGC104235_A, ZTG31.2, RRN3, DKFZp686E15140	RRN3 RNA polymerase I transcription factor homolog (S cerevisiae)	NM_016427	222284_s_at		NP_390977.3
GeneID:2316	MPV17L	19	15,459,811	15,503,543	13,912	+	2	1_A375_pfa27_minus_lncRNA_RR_1.2217, 2_A375_pfa27_plus_lncRNA_RR_1.3135	246, 248	up gene, up gene	1	1	0	19	16	8	1	1_A375_pfa27_minus_lncRNA_RR_1.1	19	Gene MPV17L	MLITH3, MGC70396, MLITH2, MPV17L1, FLJ39599, MPV17L	MPV17 mitochondrial membrane protein like	NM_001129823, NM_172803, XCT1825714.3, XCT2357787.0	1559187_x_at		NP_001121695.1, NP_776164.2, EAW69314.1, EAW69315.1
GeneID:5567	C19orf8	19	15,526,325	15,662,116	193,791	+	4	1_A375_pfa27_minus_lncRNA_RR_1.2218, 2_A375_pfa27_plus_lncRNA_RR_1.3136, 3_A375_pfa27_plus_lncRNA_RR_1.3137, 4_A375_RGR1_1.3020	136655, 27, 136503, 605	downstream, up gene, downstream, up gene	1	1	1	16	16.33	10.67	3	2_A375_pfa27_plus_lncRNA_RR_1.1	21	Gene C19orf8	FLJ32618, C19orf8	chromosome 19 open reading frame 49	NM_032301, NM_001142499, XCT1825712.1, XCT1977353.1, XCT2356431.0	1565641_at, 212736_at		NP_149976.1, NP_001135941.1, EAW69318.1, EAW69317.1, EAW69319.1
GeneID:8660	KIAA0430	19	15,855,226	15,877,823	45,797	-	3	1_A375_pfa27_minus_lncRNA_RR_1.2218, 1_A375_pfa27_minus_lncRNA_RR_1.2219, 4_A375_RGR1_1.3021	53583, 43283, 32893	downstream, up gene, downstream	1	1	0	17.5	17	5.5	2	2_A375_pfa27_plus_lncRNA_RR_1.1	21	Gene KIAA0430	K-SRGR1, LKAP, KIAA0430	KIAA0430	NM_015459, NM_001164099, NM_014847, XCT2293070.0, XCT2293077.0, XCT2293079.0, XCT2293094.0	1558897_a_at, 202388_s_at		NP_001137977.1, NP_001171925.1, NP_055652.2, EAW69201.1, EAW69202.1, EAW69203.1
GeneID:5434	NDE1	19	15,737,124	15,820,210	83,086	+	2	2_A375_pfa27_plus_lncRNA_RR_1.3135, 4_A375_RGR1_1.3021	29650, 29894	up gene, up gene	0	1	1	8.5	12	11	2	2_A375_pfa27_plus_lncRNA_RR_1.1	20	Gene NDE1	FLJ30101, NDE1, HOM-TES-97, MUDE, MuDE1	nudE nuclear distribution gene E homolog 1 (A. nidulans)	NM_017668, NM_001143979, XCT1935542.1, XCT2290436.0, XCT3014.3	219414_s_at, 223023_s_at, 227249_at, 227943_at, 230215_at		NP_060138.1, NP_001129431.1, EAW69311.1, EAW69312.1, EAW69313.1
GeneID:1253	C19orf8	19	15,956,977	15,962,447	22,270	+	2	1_A375_pfa27_minus_lncRNA_RR_1.2220, 4_A375_RGR1_1.3022	-76, -61	up gene, upstream	1	0	1	19	15	17	1	1_A375_pfa27_minus_lncRNA_RR_1.1	19	Gene C19orf8	FSHR1, OIP-1e	FSHR1/OIP-1e	NM_144600, XCT1987452.1, XCT3001423	223087_at, 223088_at		NP_653201.1, EAW69305.1, EAW69304.1
GeneID:3864	ABCC8	11	18,243,422	18,317,328	73,906	-	1	2_A375_pfa27_plus_lncRNA_RR_1.3139	-1945	upstream	0	1	0	10	16	9	1	2_A375_pfa27_plus_lncRNA_RR_1.1	16	Gene ABCC8	ABA, HRLP1, ABCC8, SUR, SUR1, MGC3496, HI036, URQ7, WBRR, PXE, ABC34, PXE1	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	NM_001287126, NM_001171, XCT1971674.1, XCT2353832.0, XCT3013.3	206450_s_at, 214033_at, 215839_at		NP_001274055.1, NP_001161.2, EAW69393.1, EAW69391.1, EAW69392.1
GeneID:1004	NOMO3	16	16,226,389	16,286,997	60,276	+	1	2_A375_pfa27_plus_lncRNA_RR_1.3139	-21	upstream	0	1	0	10	16	8	1	2_A375_pfa27_plus_lncRNA_RR_1.1	16	Gene NOMO3	Nomo, NOMO2	NODAL modulator 3	NM_001034087			NP_001034087.1
GeneID:8521	XYLT1	16	17,196,161	17,364,766	568,605	+	9	1_A375_pfa27_minus_lncRNA_RR_1.2223, 1_A375_pfa27_minus_lncRNA_RR_1.2224, 1_A375_pfa27_minus_lncRNA_RR_1.2225, 1_A375_pfa27_minus_lncRNA_RR_1.2226, 2_A375_pfa27_plus_lncRNA_RR_1.3141, 2_A375_pfa27_plus_lncRNA_RR_1.3142, 2_A375_pfa27_plus_lncRNA_RR_1.3143, 2_A375_pfa27_plus_lncRNA_RR_1.3144, 2_A375_pfa27_plus_lncRNA_RR_1.3145	201502, 329754, 29214, 85276, 231610, 329770, 29476, 293402, 79234	up gene, up gene, up gene, up gene, up gene, up gene, up gene	1	1	0	24.5	26.83	7	6	2_A375_pfa27_plus_lncRNA_RR_1.1	27	Gene XYLT1	XYLT1, XYLT, XT1, XYLT1, XYLT1, XT1	xylosyltransferase I	NM_022166, XCT1982254	213725_s_at, 222574_at		NP_071449.1, EAW69349.1
GeneID:1001	LOC100383171	19	17,226,391	17,232,569	6,235	+	2	2_A375_pfa27_plus_lncRNA_RR_1.3141	4455, 4587	downstream, downstream	1	1	0	25	22	7	1	2_A375_pfa27_plus_lncRNA_RR_1.1	25	Gene LOC100383171		hypothetical LOC100383171	XR_109385			
GeneID:8231	RPS15A	16	18,794,277	18,801,898	7,379	-	3	1_A375_pfa27_minus_lncRNA_RR_1.2225, 2_A375_pfa27_plus_lncRNA_RR_1.3145, 4_A375_RGR1_1.3024	-106, -80, 120	upstream, upstream, up gene	1	1	1	23	22	16	1	2_A375_pfa27_plus_lncRNA_RR_1.1	23	Gene RPS15A	S15A, FLJ27457, MGC111393, RPS15A	ribosomal protein S15a	NM_001019, NM_001030009	200781_s_at, 224692_at		NP_001010.2, NP_001025180.1
GeneID:2354	ARL6IP1	16	18,802,991	18,812,857	9,866	+	6	1_A375_pfa27_minus_lncRNA_RR_1.2225, 1_A375_pfa27_minus_lncRNA_RR_1.2226, 2_A375_pfa27_plus_lncRNA_RR_1.3146, 2_A375_pfa27_plus_lncRNA_RR_1.3147, 2_A375_pfa27_plus_lncRNA_RR_1.3148, 2_A375_pfa27_plus_lncRNA_RR_1.3149, 4_A375_RGR1_1.3025, 4_A375_RGR1_1.3026	11097, -279, 11115, -279, 11221, 57	downstream, upstream, downstream, upstream, downstream, up gene	1	1	1	46.5	53.5	52.5	2	2_A375_pfa27_plus_lncRNA_RR_1.1	35	Gene ARL6IP1	ARMER, AIP1, SWAP70, ARL6IP, ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	NM_015161	211933_at		NP_055976.1
GeneID:2353	SMG1	16	18,816,173	18,937,728	121,556	+	5	1_A375_pfa27_minus_lncRNA_RR_1.2225, 1_A375_pfa27_minus_lncRNA_RR_1.2226, 4_A375_RGR1_1.3025	126590, 124590, 33026	downstream, downstream, downstream	1	1	1	70	85	29	1	2_A375_pfa27_plus_lncRNA_RR_1.1	35	Gene SMG1	KIAA0421, ATX, LIP, SMG1, SMG1	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	NM_015092	214964_at, 244798_at		NP_055907.3
GeneID:7467	TMC7	16	18,995,256	19,075,364	80,005	+	2	2_A375_pfa27_plus_lncRNA_RR_1.3150, 2_A375_pfa27_plus_lncRNA_RR_1.3151	63856, 63656	downstream, downstream	1	1	0	20	16	9	1	2_A375_pfa27_plus_lncRNA_RR_1.1	20	Gene TMC7	TMC7, DKFZp761Q223, FLJ21240	transmembrane channel-like 7	NM_024547, NM_001163094, XCT2270852.0, XCT2272884.0	220021_at		NP_079123.3, NP_001130636.1, EAW69288.1, EAW69287.1
GeneID:1674	COQ7	16	19,076,917	19,091,417	12,500	+	2	2_A375_pfa27_plus_lncRNA_RR_1.3150, 2_A375_pfa27_plus_lncRNA_RR_1.3151	27, 27	up gene, up gene	1	1	0	20	16	9	1	2_A375_pfa27_plus_lncRNA_RR_1.1	20	Gene COQ7	COQ7, CLK1, CAT5, CLK-1	coenzyme Q7 homolog, ubiquinone (yeast)	NM_001166903, NM_016135, XCT1972113.3, XCT1962982.1, XCT2352393.0, XCT2352377.0	209743_at, 209748_s_at, 210070_s_at		NP_001159772.1, NP_057222.2, EAW69280.1, EAW69269.1, EAW69270.1, EAW69271.1
GeneID:1677	TFRP1L2	19	19,125,254	19,132,952	7,699	+	3	2_A375_pfa27_plus_lncRNA_RR_1.3151, 2_A375_pfa27_plus_lncRNA_RR_1.3152, 2_A375_pfa27_plus_lncRNA_RR_1.3026	-6, 690, 1296	upstream, up gene, up gene	0	1	1	12.5	10.5	17	2	2_A375_pfa27_plus_lncRNA_RR_1.1	23	Gene TFRP1L2	MGC126890, MGC126791, FLJ20164, TFRP1L2	vacuolar H+-translocating ATPase 116kDa isoform 1	NM_031354.1, NR_023028, XCT1841693.2	1568810_s_at, 227792_at, 227954_at, 227998_at, 230274_at		NP_001030113.1, EAW69272.1
GeneID:8317	SYT17	19	19,179,838	19,278,554	98,716	+	2	2_A375_pfa27_plus_lncRNA_RR_1.3153, 2_A375_pfa27_plus_lncRNA_RR_1.3027	-438, 316	upstream, up gene	0	1	1	11	16	12.5	2	2_A375_pfa27_plus_lncRNA_RR_1.1	19	Gene SYT17	SYT17		NM_018834, XCT2372668.0, XCT2362682.3	209613_at, 229083_at		NP_061374.1, EAW69270.1, EAW69274.1
GeneID:2278	LOC728276	19	19,297,105	19,315,716	18,611	+	2	2_A375_pfa27_plus_lncRNA_RR_1.3154, 2_A375_pfa27_plus_lncRNA_RR_1.3155	21999, 21999	downstream, downstream	1	1	0	4.5	6.5	5	1	2_A375_pfa27_plus_lncRNA_RR_1.1	45	Gene LOC728276		hypothetical LOC728276	NR_024436			
GeneID:5733	QDER1	19	19,510,015	19,533,450	20,435	-	1	2_A375_pfa27_plus_lncRNA_RR_1.3155	-1734	upstream	0	1	0	11	16	9	1	2_A375_pfa27_plus_lncRNA_RR_1.1	16	Gene QDE1	QDE1, HRH16, 3B3B2	glycerophosphodiester phosphodiesterase 1	NM_018941, XCT1993088.2, XCT1995096.1, XCT2352760.0, XCT2352583.3	232853_s_at, 239214_at		NP_061314.2, EAW69238.1, EAW69239.1
GeneID:5720	CPT1B	19	19,535,179	19,564,700	29,551	+	2	2_A375_pfa27_plus_lncRNA_RR_1.3155, 2_A375_pfa27_plus_lncRNA_RR_1.3156	5, 31657	up gene, downstream	0	1	0	15	16.5	12.5	2	2_A375_pfa27_plus_lncRNA_RR_1.1	19	Gene CPT1B	Cpg110, KIAA0419, DKFZp761G146	CPT1B protein	NM_014717, XCT1995096.1, XCT2364672.2	1565353_at, 236462_at		NP_055526.3, EAW69237.1, EAW69238.1
GeneID:2737	C19orf8	19	19,567,040	19,712,444	143,404	+	1	2_A375_pfa27_plus_lncRNA_RR_1.3156	-236	upstream	0	1	0	15	19	16	1	2_A375_pfa27_plus_lncRNA_RR_1.1	19	Gene C19orf8	DKFZp434B0210, MGC19828, DKFZp761H0531, FLJ21040, C19orf8 2	chromosome 19 open reading frame 62	NM_030314, XCT2372769.0, XCT2352378.0, XCT2352377.0	1555837_at, 203173_s_at		NP_084710.3, EAW69290.1, EAW69291.1
GeneID:4048	C19orf8	19	19,717,674	19,729,492	11,819	+	1	2_A375_pfa27_plus_lncRNA_RR_1.3157	20	up gene	0	1	0	10	23	16	1	2_A375_pfa27_plus_lncRNA_RR_1.1	23	Gene C19orf8	FAM197A, C19orf8, 1511F10.1	chromosome 19 open reading frame 68	NM_031012991	213229_at, 213237_at		NP_001013009.2
GeneID:1232	IQCG	19	19,727,778	19,800,981	141,693	+	1	2_A375_pfa27_plus_lncRNA_RR_1.3157	1884	up gene	0	1	0	10	23	16	1	2_A375_pfa27_plus_lncRNA_RR_1.1	23	Gene IQCG	FLJ38575, IQCG, MGC33540, FLJ30115	IQ motif containing G	NM_152330, XCT1972215.2, XCT1995091.1, XCT1995092.1, XCT1995093.1, XCT1962982.1, XCT2272764.0, XCT2352375.0	213392_at, 213193_x_at, 213191_at, 218133_at, 218134_s_at		NP_689745.1, EAW69300.1, EAW69298.1, EAW69299.1, EAW69301.1, EAW69302.1, EAW69298.1
GeneID:3704	GPRC5B	16	19,870,293	19,896,151	25,858	+	1	2_A375_pfa27_plus_lncRNA_RR_1.3158	950	up gene	0	1	0	7	7	5	1	4_A375_RGR1_1.1	26	Gene GPRC5B	GPRC5B, RAI3 2	G protein-coupled receptor, family C, group 5, member B	NM_016235, XCT1962999.1, XCT2319609.0, XCT2352369.2	230801_s_at, 230802_at, 230803_at, 230804_at, 230805_at		NP_057915.1, EAW69302.1, EAW69303.1, EAW69304.1, EAW69305.1
GeneID:8233	THUMPD1	19	20,744,906	20,763,199	18,293	-	1	2_A375_pfa27_plus_lncRNA_RR_1.3158	111	up gene	0	1	0	20	27	13	1	2_A375_pfa27_plus_lncRNA_RR_1.1	27	Gene THUMPD1	DKFZp686C1053, THUMPD1	THUMP domain containing 1	NM_017735, XCT1982068.1, XCT2270495.0, XCT2363.2	206555_s_at, 213023_at		NP_060206.2, EAW69330.1, EAW69331.1, EAW69332.1
GeneID:8324	ACSM3	16	20,779,312	20,806,479	28,167	+	3	1_A375_pfa27_minus_lncRNA_RR_1.2222, 2_A375_pfa27_plus_lncRNA_RR_1.3159, 4_A375_RGR1_1.3029	42554, 43166, 42556	downstream, downstream, downstream	1	1	1	28	16	19	1	1_A375_pfa27_minus_lncRNA_RR_1.1	28	Gene ACSM3	ACSM3, SA, SLC27A3	acyl-CoA synthetase medium-chain family member 3	NM_005622, NM_202000, XCT1930781.1, XCT3474.3	203942_s_at, 218277_at		NP_005613.2, NP_973729.1, EAW69334.1, EAW69333.1
GeneID:1178	ERI2	19	20,791,913	20,817,795	26,200	-	3	1_A375_pfa27_minus_lncRNA_RR_1.2222, 2_A375_pfa27_plus_lncRNA_RR_1.3159, 4_A375_RGR1_1.3029	99, 488, 196	up gene, upstream, up gene	1	1	1	28	16	19	1	1_A375_pfa27_minus_lncRNA_RR_1.1	28	Gene ERI2	EXOD1, KIAA1804, MGC16942, ERI2	ERI1 exoribonuclease family member 2	NM_030963, NM_001142723, XCT1982982.1, XCT2349.2	213393_at, 240803_s_at, 240804_at		NP_542394.2, NP_001136797.1, EAW69336.1, EAW69337.1
GeneID:6911	LOC389191	19	20,817,767	20,860,990	43,223	+	3	1_A375_pfa27_minus_lncRNA_RR_1.2222, 2_A375_pfa27_plus_lncRNA_RR_1.3159, 4_A375_RGR1_1.3029	-71, 713, -167	upstream, up gene, upstream	1	1	1	26	16	19	1	1_A375_pfa27_minus_lncRNA_RR_1.1	26	Gene LOC389191	DKFZp434J0315	ribonuclease NET1	NM_033041, NM_001142824, XCT2370359.0, XCT2354340.0, XCT2354344.0, XCT2349.1	230107_s_at, 213215_s_at		NP_112203.2, NP_001139396.1, EAW69335.1, EAW69340.1, EAW69341.1
GeneID:5579	DCUN1D3	13	20,869,398	20,911,961	42,163	-	2	2_A375_pfa27_plus_lncRNA_RR_1.3160, 4_A375_RGR1_1.3030	-742, -899	upstream, upstream	0	1	1	15	20	19	1	2_A375_pfa27_plus_lncRNA_RR_1.1	20	Gene DCUN1D3	FLJ41725, DKFZp686G2220, MGC40372, DCUN1D3, 4eMG4	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)	NM_173475, XCT2349.4	239948_at		NP_775746.1, EAW69342.1
GeneID:1001	LOC100383872	19	20,896,940	20,905,349	8,409	+	2	2_A375_pfa27_plus_lncRNA_RR_1.3160, 2_A375_pfa27_plus_lncRNA_RR_1.3030	13484, 13320	downstream, downstream	1	1	1	15	20	19	1	2_A375_pfa27_plus_lncRNA_RR_1.1	20	Gene LOC100383872		hypothetical LOC100383872	XR_111967, XR_109284, XR_114980			



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	A375_DMSO_miRNA7_miRNA_AR_1 Percent	A375_DMSO_miRNA7_plus_lncRNA_AR_1 Percent	A375_DMSO_NA7_minus_lncRNA_AR_1 Avg Reads	A375_plus_lncRNA_AR_1 Avg Reads	A375_plus_EGFR_lncRNA_AR_1 Avg Reads	Ad Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
Gene ID-3511491	LYRM1	19	20,311,837	20,336,326	24,771	+	2	2_A375_uNA7_plus_lncRNA_AR_1..3160, 4_A375_EGR1..1.3032	747, 600	+z gene, +z gene	0	1	1	15	20	19	1	2_A375_uNA7_plus_lncRNA_AR_1	20	Gene LYRM1	A2116.1, LYRM1	LYR motif containing 1	NM_020424, NM_001128501, NM_001128502, NCT01609881, NCT01609971, NCT01609881, NCT02701012.0, NCT02703314.0, NCT02701969.0, NCT2940.2	220697_at	NP_065157.1, NP_001121773.1, NP_001121774.1, EAW98543.1, EAW98544.1, EAW98546.1, EAW98547.1, EAW98548.1, EAW98549.1
Gene ID-3511497	DNAH5	19	20,944,476	21,170,762	226,286	+	2	4_A375_EGR1..1..3031, 4_A375_EGR1..1.3032	193345, -66	+z gene, upstream	0	0	1	3.5	5.5	10.5	2	4_A375_EGR1..1	15	Gene DNAH5	FLJ43964, FLJ51947, Hsadb2, DHF2a1b.M24, DNAHC5B, FLJ43919, DLP2, DNAH2	dynein, axonemal, heavy chain 5	NM_017539, NCT02704581, NCT02704503.0, NCT02704515.1, NCT2345547.0	11560603_at, 11560790_at, 11560791_at, 215875_at, 216415_at, 220725_x_at	220725_x_at	NP_060039.1, EAW98553.1, EAW98552.1, EAW98551.1, EAW98552.1
Gene ID-3511498	TMEM189	19	21,169,912	21,191,937	22,025	+	1	4_A375_EGR1..1..3032	998	+z gene	0	0	1	3	8	15	1	4_A375_EGR1..1..1	15	Gene TMEM189	PRO9677, TMEM189, TMEM189	transmembrane protein 189	NM_020422, NCT01609821, NCT01609831, NCT01609941.1, NCT2270210.0, NCT2346472.0	212272_x_at	212272_x_at	NP_065155.3, EAW98537.1, EAW98535.1, EAW98536.1, EAW98538.1
Gene ID-4301939	RUNDC3B	19	21,356,464	21,397,257	56,775	+	1	4_A375_EGR1..1..3033	12924	+z gene	0	0	1	5	2	12	1	4_A375_EGR1..1..1	12	Gene RUNDC3B	RUNDC2B		NM_203116717	1580297_at, 214712_at	1580297_at, 214712_at	XP_005116768.1
Gene ID-3511505	METTL9	19	21,810,696	21,866,792	97,936	+	3	1_A375_uNA7_minus_lncRNA_AR_1..2324, 2_A375_uNA37_plus_lncRNA_AR_1..3162, 4_A375_EGR1..1.3028	68, -8, -120	+z gene, upstream, upstream, upstream	1	1	1	16	28	19	1	2_A375_uNA16_plus_lncRNA_AR_1	20	Gene METTL9	METTL9, DFEV, RMT1, PL-DYRK2, DREV1, CGI-91	methyltransferase like 9	NM_031077103, NM_018023, NCT12222.2, NCT1963580.1, NCT1963591.1, NCT1963590.1, NCT1963591.1, NCT2256623.0	217886_s_at, 222447_at, 222620_at, 233093_at	222620_at, 233093_at	NP_001078483.1, NP_037109.3, EAW98517.1, EAW98520.1, EAW98521.1, EAW98522.1, EAW98518.1, EAW98519.1
Gene ID-3511506	OTOA	19	21,869,825	21,972,850	102,215	+	1	2_A375_uNA37_plus_lncRNA_AR_1..3163	6863	+z gene	0	0	1	0	6	16	1	2_A375_uNA16_plus_lncRNA_AR_1	6	Gene OTOA	FLJ22773, CT100, MGC29610, MGC137767, OTOA, DFNB22	otoancorin	NM_144672, NM_170994, NM_001161665, NCT2439270.0, NCT2347022.0	1553422_s_at	1553422_s_at	NP_653273.3, NP_733796.1, NP_001155155.1, EAW98524.1, EAW98523.1
Gene ID-7521683	UQCRC2	19	21,984,809	21,994,966	20,089	+	2	1_A375_uNA7_minus_lncRNA_AR_1..2233, 2_A375_uNA37_plus_lncRNA_AR_1..3164	-145, 31	+z intron, +z gene	1	1	0	21	21	16	1	1_A375_uNA37_minus_lncRNA_AR_1	21	Gene UQCRC2	QCR2, UQCRC2, UQCR2	ubiquinol-cytochrome c reductase core protein II	NM_003366, NCT2343355.0, NCT2343364.0, NCT9967.3	200955_at, 212660_s_at, 241753_at	200955_at, 212660_s_at, 241753_at	NP_003357.2, EAW93990.1, EAW93991.1, EAW93992.1
Gene ID-2387682	C19orf18	19	21,999,198	22,012,451	17,245	-	2	1_A375_uNA7_minus_lncRNA_AR_1..2229, 2_A375_uNA37_plus_lncRNA_AR_1..3165	-6461, -6433	+z intron, upstream	1	1	0	16	16	11	1	2_A375_uNA16_plus_lncRNA_AR_1	16	Gene C19orf18	PSD29, C19orf18, MGC30721	PDZ domain containing 9	NM_170936, NR_033994, NCT1644231.3	241972_at	241972_at	NP_776187.2, EAW93995.1
Gene ID-2387694	C19orf18	19	22,019,438	22,093,973	76,519	+	2	1_A375_uNA7_minus_lncRNA_AR_1..2228, 2_A375_uNA37_plus_lncRNA_AR_1..3165	-544, -592	+z intron, upstream	1	1	0	16	16	11	1	2_A375_uNA16_plus_lncRNA_AR_1	16	Gene C19orf18	MGC26752, C19orf18	ubiquinone 10 kDa core binding frame 52	NM_031184579			NP_001159251.1
Gene ID-1012683972	LOC103091	19	22,776,994	22,781,714	54,310	+	2	2_A375_uNA37_plus_lncRNA_AR_1..3166, 4_A375_EGR1..1.3038	24466, 30138	+z gene, downstream	0	0	1	16	24	21	2	4_A375_EGR1..1	22	Gene LOC102693972		chon ulcon dichydrogenase(ubiquinone) flavoprotein 2, mitochondrial	XM_002343432, XM_003119668, XM_003120046			XP_002343478.1, XP_003119716.1, XP_003120396.1
Gene ID-2387704	EEF2K	19	22,217,992	22,300,066	82,074	+	5	1_A375_uNA37_minus_lncRNA_AR_1..2227, 1_A375_uNA7_minus_lncRNA_AR_1..2235, 1_A375_uNA37_plus_lncRNA_AR_1..3167, 2_A375_uNA37_plus_lncRNA_AR_1..3166, 4_A375_EGR1..1.3027	797, 91192, 672, 91802, 90952	+z gene, downstream, +z gene, downstream, downstream	1	1	1	19	26.5	21	2	4_A375_EGR1..1	23	Gene EEF2K	EEF2K, HSA35350, MGC43584, eEF-2 kinase	eukaryotic elongation factor-2 kinase	NM_013302, NCT2270500.0	225545_at, 235545_at	225545_at, 235545_at	NP_037434.1, EAW93804.1
Gene ID-5981715	POLR3E	19	22,308,741	22,345,348	36,608	+	4	1_A375_uNA7_minus_lncRNA_AR_1..2230, 1_A375_uNA37_plus_lncRNA_AR_1..3166, 4_A375_EGR1..1.3029, 4_A375_EGR1..1.3030	43, -69, -197, -29699	+z gene, upstream, upstream, +z gene	1	1	1	11.3	14.3	25.5	2	4_A375_EGR1..1	33	Gene POLR3E	POLR3E, SIN, RPC3	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	NM_018119, NCT02720500.0, NCT2270204.0, NCT2720900.0, NCT9900.2	219016_s_at, 222491_at, 233485_at, 233485_at	219016_s_at, 222491_at, 233485_at, 233485_at	NP_060089.1, EAW98908.1, EAW98909.1, EAW98907.1, EAW98908.1
Gene ID-3981698	HSD17B7	19	22,825,960	22,827,697	101,799	+	2	2_A375_uNA37_plus_lncRNA_AR_1..3171, 4_A375_EGR1..1.3041	74396, -998	+z gene, upstream	0	1	1	8	10.5	10	2	4_A375_EGR1..1	17	Gene HSD17B7	3DST2, HSD17B7, 3DST2	keratan sulfate Gal-6 sulfotransferase 2	NM_006543, NCT03082.3	219697_at		NP_006534.1, EAW93940.1
Gene ID-8503743	SCN4N1B	19	23,194,630	23,220,300	34,180	+	3	2_A375_uNA37_plus_lncRNA_AR_1..3174, 4_A375_EGR1..1.3042, 4_A375_EGR1..1.3043	27982, 328, 3356	+z intron, +z gene, +z gene	0	1	1	10	10	14.33	3	4_A375_EGR1..1	19	Gene SCN4N1B	BESC4, ENaCg, SCNN1G, PHA1, SCNN1G, SCNEG	sodium channel, nonvoltage-gated 1, gamma	NM_001039, NCT16984030.5, NCT2855799.0	220295_at, 241436_at	220295_at, 241436_at	NP_001033.2, EAW95837.1, EAW95839.1
Gene ID-8503744	SCN4N1B	19	23,210,191	23,292,620	79,029	+	1	4_A375_EGR1..1..3044	69021	+z gene	0	0	1	4	10	20	1	4_A375_EGR1..1..1	20	Gene SCN4N1B	BESC1, SCN4N1B, SCN4B, ENaCb	sodium channel, nonvoltage-gated 1, beta	NM_050336, NCT14963.2, NCT1550331.1	205464_at	205464_at	NP_050127.2, EAW95834.1, EAW95833.1
Gene ID-1245436	EARS2	19	23,333,354	23,366,896	33,262	-	2	1_A375_uNA37_minus_lncRNA_AR_1..2242, 2_A375_uNA37_plus_lncRNA_AR_1..3175	-45, -156	+z intron, upstream	1	1	0	23	20	13	1	1_A375_uNA37_minus_lncRNA_AR_1	23	Gene EARS2	MGE1, EARS2, IGHA1970	glutamyl-tRNA synthetase 2, mitochondrial (putative)	NM_031603814, NR_033301, NCT14970.3, NCT22623950.0, NCT22629870.0, NCT2352971.0, NCT2352972.0	1555437_at, 1560796_s_at, 223903_at, 223724_at	223903_at, 223724_at	NP_001078933.1, EAW95825.1, EAW95821.1, EAW95822.1, EAW95823.1, EAW95824.1
Gene ID-5461061	UBFD1	19	23,366,992	23,393,710	16,845	+	2	1_A375_uNA7_minus_lncRNA_AR_1..2242, 2_A375_uNA37_plus_lncRNA_AR_1..3175	-126, -82	+z intron, upstream	1	1	0	23	20	13	1	1_A375_uNA37_minus_lncRNA_AR_1	23	Gene UBFD1	UBFD1, FLJ42143, FLJ38370, UBFM	ubiquitin-like fold domain containing	NM_019116, NCT14972.4, NCT2265309.0, NCT2265291.0	209867_at, 224059_at	209867_at, 224059_at	NP_061989.2, EAW95819.1, EAW95818.1, EAW95817.1, EAW95819.1
Gene ID-4709106	NDUFA11	19	23,392,223	23,407,829	15,304	-	2	1_A375_uNA7_minus_lncRNA_AR_1..2243, 2_A375_uNA37_plus_lncRNA_AR_1..3176	-57, -73	+z intron, upstream	1	1	0	122	114	6	1	1_A375_uNA37_minus_lncRNA_AR_1	122	Gene NDUFA11	MGC45929, NCF1, NDUFA11, FKSNZA, SDAF1	NADH dehydrogenase (ubiquinone) 1 alpha/beta subcomplex, 1, 8kDa	NM_030933, NCT14966.4, NCT1995271.1	203277_at	203277_at	NP_036794.1, EAW95816.1, EAW95815.1
Gene ID-7961726	PALB2	19	23,814,483	23,832,616	18,133	+	4	1_A375_uNA7_minus_lncRNA_AR_1..2243, 1_A375_uNA37_minus_lncRNA_AR_1..2244, 2_A375_uNA37_plus_lncRNA_AR_1..3176, 2_A375_uNA37_plus_lncRNA_AR_1..3177	44402.8, 44966, 26	+downstream, +z gene, downstream, upstream	1	1	0	61	61	13	2	1_A375_uNA37_minus_lncRNA_AR_1	122	Gene PALB2	DKFZp686T16B, FANCN, DKFZp686E15064, PALB2, FLJ22516, PNCA3	partner and localizer of BRCA2	NM_024675, NCT2263531.1, NCT2263532.1, NCT2529964.0	219320_at	219320_at	NP_078951.2, EAW95813.1, EAW95812.1, EAW95811.1, EAW95812.1
Gene ID-6418	DCTN3	19	23,832,907	23,861,162	28,275	+	5	1_A375_uNA7_minus_lncRNA_AR_1..2244, 1_A375_uNA37_minus_lncRNA_AR_1..2245, 2_A375_uNA37_plus_lncRNA_AR_1..3177, 2_A375_uNA37_plus_lncRNA_AR_1..3178, 4_A375_EGR1..1.3045	-139, -37337, -160, -37505, 37561	+z intron, downstream, +z intron, downstream, downstream	1	1	1	36	53.5	21	2	2_A375_uNA16_plus_lncRNA_AR_1	59	Gene DCTN3	MGC3246, p25, DCTN3	dynactin 3 (p25)	NM_032486, NCT16802.8, NCT2265294.1, NCT2265296.1	209211_x_at, 209232_x_at	209211_x_at, 209232_x_at	NP_115973.1, EAW95809.1, EAW95810.1
Gene ID-1012683987	LOC100	19	23,861,332	23,864,448	3,116	+	3	1_A375_uNA37_minus_lncRNA_AR_1..2245, 2_A375_uNA37_plus_lncRNA_AR_1..3178, 4_A375_EGR1..1.3046	6912, 6793, 9036	+downstream, downstream, downstream, downstream	1	1	1	32	99	34	1	2_A375_uNA16_plus_lncRNA_AR_1	59	Gene LOC100093687		hypothetical LOC100093687	XR_109270			
Gene ID-5301	PLK1	19	23,890,201	23,901,866	11,457	+	5	1_A375_uNA37_minus_lncRNA_AR_1..2245, 1_A375_uNA37_plus_lncRNA_AR_1..3179, 4_A375_EGR1..1.3048	-57, -69, 167	+z intron, upstream, +z gene	1	1	1	32	99	34	1	2_A375_uNA16_plus_lncRNA_AR_1	59	Gene PLK1	PLK1, STPK12, PLK	polo-like kinase 1 (Drosophila)	NM_005030, NCT14969.4, NCT16131652.2, NCT2350543.0, NCT2350544.0	202240_at	202240_at	NP_005021.2, EAW95802.1, EAW95804.1, EAW95805.1, EAW95806.1
Gene ID-5981	ERN2	19	23,701,823	23,724,821	23,196	-	1	4_A375_EGR1..1..3046	6160	+z gene	0	0	1	2	0	16	1	4_A375_EGR1..1..1	16	Gene ERN2	IRE1b, ERN2, IRE1-BETA	endoplasmic reticulum to nucleus signaling 2	NM_033266, NCT14229.3	214172_x_at, 223910_at		NP_130296.1, EAW95802.1
Gene ID-8503	CHP2	19	23,765,445	23,770,258	4,368	+	1	4_A375_EGR1..1..3047	4758	+z gene	0	0	1	5	3	14	1	4_A375_EGR1..1..1	14	Gene CHP2		calcineurin B homologous protein 2	NM_022097, NCT14230.2, NCT2265600.0	208149_at		NP_071333.1, EAW95801.1, EAW95800.1
Gene ID-5981	PRKCB	19	23,847,300	24,231,802	384,502	+	3	1_A375_uNA37_plus_lncRNA_AR_1..3179, 1_A375_uNA37_plus_lncRNA_AR_1..3180, 2_A375_uNA37_plus_lncRNA_AR_1..3180	138505, 1094, 342722	+z intron, +z gene, +z gene	1	1	1	12	14	9.67	1	2_A375_uNA16_plus_lncRNA_AR_1	21	Gene PRKCB	PRKCB1, PRKCB2, PKCbeta, MGC45931, PKCB, PRKCB	protein kinase C, beta	NM_002738, NR_012533, NCT19302.4, NCT2261950.0, NCT2261954.0, NCT2352970.0	207857_s_at, 209683_s_at, 227017_at, 227824_at, 235758_at, 235872_at	207857_s_at, 209683_s_at, 227017_at, 227824_at, 235758_at, 235872_at	NP_002729.2, NP_997700.1, EAW95796.1, EAW95797.1, EAW95798.1, EAW95799.1
Gene ID-1012683995	CACNG5	19	24,266,076	24,275,707	109,091	+	2	1_A375_uNA37_plus_lncRNA_AR_1..3181, 2_A375_uNA37_plus_lncRNA_AR_1..3181	500, 430	+z gene, +z gene	1	1	0	24	26	8	1	2_A375_uNA16_plus_lncRNA_AR_1	26	Gene CACNG5	Cacng5, CACNG5	calcium channel, voltage-dependent, gamma subunit 5	NM_006535, NCT14277.3, NCT2261916.0	206054_at		NP_006535.1, EAW95794.1, EAW95792.1
Gene ID-3981	RBBP8	19	24,330,908	24,364,164	33,276	+	1	2_A375_uNA37_plus_lncRNA_AR_1..3182	-232	+z intron	0	0	0	19	23	9	1	2_A375_uNA16_plus_lncRNA_AR_1	23	Gene RBBP8	P270R, DKFZp686P08082, CtIP, RBBP8, RACT, RBQ-1, DKFZp781B2423, MRE80	retinoblastoma binding protein 8	NM_006719, NM_016703, NM_032628, NCT23810631.1, NCT23409064.0, NCT23409065.0, NCT23529852.0	1552229_at, 205078_s_at, 212761_at, 212763_at, 235862_s_at, 235874_at, 235944_at	205078_s_at, 212761_at, 212763_at, 235862_s_at, 235874_at, 235944_at	NP_008812.2, NP_001170.1, NP_116115.2, EAW95769.1, EAW95770.1, EAW95771.1, EAW95792.1, EAW95790.1
Gene ID-5311	FLJ43298	19	24,872,743	24,892,363	19,840	-	2	1_A375_uNA37_minus_lncRNA_AR_1..2247, 2_A375_uNA37_plus_lncRNA_AR_1..3183	-1919, 1455	+z gene, +z gene	1	1	0	21	24	5	1	2_A375_uNA16_plus_lncRNA_AR_1	24	Gene FLJ43298		hypothetical LOC440911	XR_111852, XR_109271, XR_114993			
Gene ID-3227	TNRC6A	19	24,741,049	24,837,545	96,497	+	1	2_A375_uNA37_plus_lncRNA_AR_1..3184	-266	+z intron	0	0	0	16	17	7	1	2_A375_uNA16_plus_lncRNA_AR_1	17	Gene TNRC6A	KIAA1460, CAGH26, FLJ20543, TNRC6, GW1, TNRC6A, MGC73356, DKFZp686I0117, GW182	trinucleotide repeat containing 6A	NM_014494, NCT23444850.0, NCT23444870.0, NCT23444871.0, NCT23444872.0, NCT23444874.0	1553548_a_at, 224764_at, 224765_s_at, 233938_at, 234754_s_at, 243934_at	224765_s_at, 234754_s_at, 243934_at	NP_055733.2, EAW95765.1, EAW95763.1, EAW95764.1, EAW95766.1, EAW95767.1
Gene ID-1155594	SLC5A11	19	24,837,582	24,932,944	95,392	+	2	1_A375_uNA37_minus_lncRNA_AR_1..2248, 2_A375_uNA37_plus_lncRNA_AR_1..3185	12554, 12538	+z gene, +z gene	1	1	0	25	29	8	1	2_A375_uNA16_plus_lncRNA_AR_1	29	Gene SLC5A11	SMT2, SMLT8, RNST1, RST1, SLC5A11	solute carrier family 5 (sodium/glucose cotransporter), member 11	NM_052944, NCT14141.3	237254_at		NP_443176.2, EAW95760.1
Gene ID-3511	ARHGAP17	19	24,930,710	24,936,913	93,965	+	1	4_A375_EGR1..1..3050	-223	+z intron	0	0	1	7	11	19	1	4_A375_EGR1..1..1	19	Gene ARHGAP17	FLJ21587, FP4354, MRGX, KIAA1717, MADRIN, RICH1, DKFZp686A14382, MSTP110, MSTP035, MGC67855, WBP15, FLJ43266, MSTP095, RICH1B, MSTP096, MSTP110	Rho GTPase activating protein 17	NM_031936834, NM_015854, NCT19302.5, NCT2529969.0	1552229_at, 205078_s_at, 212761_at, 212763_at, 235862_s_at, 235874_at, 235944_at	205078_s_at	NP_001036810.1, NP_056924.4, EAW95776.1, EAW95779.1
Gene ID-3227	ZNRF3-KIAA0	19	24,947,322	25,060,855	31,333	-	1	1_A375_uNA37_minus_lncRNA_AR_1..2250	-107	+z intron	1	0	0	16	11	7	1	1_A375_uNA16_plus_lncRNA_AR_1	18	Gene ZNRF3-KIAA0	ZNRF3, FLJ23199, ZNRF3-KIAA0, ZSCAN31,	zinc finger and RING finger with KRAB and SCAN domains 2	NM_031012951, NCT16124981.1	223819_at		NP_001012999.2, EAW93766.1
Gene ID-3511	JMJD5	19	27,214,307	27,230,909	16,262	+	2	1_A375_uNA37_plus_lncRNA_AR_1..2251, 2_A375_uNA37_plus_lncRNA_AR_1..3187	97, 9	+z gene, +z gene	1	1	0	46	83	12	1	2_A375_uNA16_plus_lncRNA_AR_1	83	Gene JMJD5	JMJD5, FLJ12796	jumonji domain containing 5	NM_1537773, NM_001143542, NCT13742.2	223870_at, 237229_at	223870_at, 237229_at	NP_079049.2, NP_001128030.1, EAW93759.1
Gene ID-1155	NSMCE1	19	27,236,315	27,260,113	43,798	-	2	1_A375_uNA37_minus_lncRNA_AR_1..2169, 4_A375_EGR1..1.3051	-271, -47	+z intron, upstream	0	1	1	14	16	13	1	2_A375_uNA16_plus_lncRNA_AR_1	16	Gene NSMCE1	NSE1, NSMCE1	non-SMC element 1 homolog (S. cerevisiae)	NM_1455302, NCT19143.2, NCT16560830.1, NCT23529901.0, NCT23529911.0, NCT23529920.0	224868_at		NP_001137.2, EAW93757.1, EAW93754.1, EAW93755.1, EAW93756.1
Gene ID-3512	FLJ21409	19	27,260,167	27,299,979	39,808	+	2	2_A375_uNA37_plus_lncRNA_AR_1..3188, 4_A375_EGR1..1.3051	217, -7	+z gene, upstream	0	1	1	14	16	13	1	2_A375_uNA16_plus_lncRNA_AR_1	16	Gene FLJ21409		hypothetical LOC439912	XR_111854, XR_109274, XR_114998		234218_at, 234827_at	
Gene ID-8515	EZR	19	27,413,465	27,485,365	49,900	+	1	4_A375_EGR1..1..3052	30107	+z gene	0	0	1	12	14	15	1	4_A375_EGR1..1..1	15	Gene EZR	VIL2, EZR, MSC10397	villoferlin 21 receptor	NM_131078, NM_021799, NM_1053779, NCT22553153.0, NCT22529483.0, NCT22529986.0, NCT6469.3	210921_at, 221855_s_at	210921_at, 221855_s_at	NP_551984.1, NP_003370.1, NP_551985.4, EAW93748.1, EAW93747.1, EAW93749.1, EAW93745.1
Gene ID-2387	KIAA0368	19	27,561,466	27,791,892	230,224	+	1	1_A375_uNA7_minus_lncRNA_AR_1..2252	179998	+z gene	1	0	0	23	16	15	1	1_A375_uNA37_minus_lncRNA_AR_1	23	Gene KIAA0368	KIAA0368		NM_0153282, NCT19168694.1	213169_at		NP_056117.2, EAW93743.1
Gene ID-8395	GSG1L	19	27,795,650	28,074,850	279,200	+	5	1_A375_uNA37_minus_lncRNA_AR_1..2253, 2_A375_uNA37_plus_lncRNA_AR_1..3189, 4_A375_EGR1..1.3053	2481356, 295742, 222694	+z gene, +z gene, +z gene	1	1	1	17	31	11.5	2	2_A375_uNA16_plus_lncRNA_AR_1	55	Gene GSG1L	PRO19551, GSG1L, MGC19379	GSG1-like	NM_2011097653, NM_144973, NCT22593372.0, NCT22529979.0, NCT6411.3	238761_at		NP_001102333.1, NP_653276.1, EAW93745.1, EAW93741.1, EAW93742.1
Gene ID-1012683987	LOC100	19	28,296,208	28,303,363	7,779	-	1	4_A375_EGR1..1..3053	-9127	+z intron	0	0	1	2	9	17	1	4_A375_EGR1..1..1	17	Gene LOC100093703		hypothetical LOC100093703	XR_109276			
Gene ID-5595	SBK1	19	28,303,940	28,335,700	31,330	+	2	1_A375_uNA37_minus_lncRNA_AR_1..2254, 2_A375_uNA37_plus_lncRNA_AR_1..3190, 4_A375_EGR1..1.3055	11726, 11765, 6812	+z gene, +z gene, +z gene	1	1	1	12.5	16.5	13	2	4_A375_EGR1..1	26	Gene SBK1	SBK1, Sbk	SH3-binding domain kinase 1	NM_031024401, NCT16694.4	226545_at, 226549_at		NP_001018721.1, EAW93733.1
Gene ID-1012683991	CLN3	19	28,466,900	28,503,623	19,023	-	1	4_A375_uNA37_plus_lncRNA_AR_1..3191	191	+z gene	0	1	0	17	22	10	1	2_A375_uNA16_plus_lncRNA_AR_1	22	Gene CLN3	BTS, JNCL, CLN3, MGC102849	battenin, lysosomal/endosomal membrane transmembrane protein, ceroid-lipofuscinosis, neuronal 3	NM_031043432, NM_000086, NCT17834653.2, NCT19077441.1, NCT19077421.1, NCT19077451.1, NCT19077441.1, NCT19077461.1, NCT22723220.0, NCT22723240.0, NCT22723260.0, NCT22723270.0, NCT22723280.0, NCT22723220.0, NCT22723240.0, NCT22723260.0, NCT22723270.0, NCT22723280.0, NCT227	209279_s_at, 218599_x_at	209279_s_at, 218599_x_at	NP_001034077.1, NP_000077.1, EAW93261.1, EAW93263.1, EAW93259.1, EAW93260.1, EAW93264.1, EAW93265.1, EAW93266.1, EAW93267.1, EAW93268.1, EAW93269.1, EAW93266.1, EAW93261.1, EAW93262.1, EAW93263.1, EAW93264.1, EAW93265.1, EAW93267.1
Gene ID-3511	APOBEC4	19	28,803,993	28,810,302	4,309	+	1	2_A375_uNA37_plus_lncRNA_AR_1..3191	-2521	+z intron	0	1	0	17	22	10	1	2_A375_uNA16_plus_lncRNA_AR_1	22	Gene APOBEC4	APOB100R, APOBR, APOB48R	apolipoprotein B receptor	NM_0199942, NCT16234561.1, NCT22533090.0, NCT22733100.0	220023_at		NP_001138.2, EAW93256.1, EAW93276.1, EAW93260.1
Gene ID-2467776	ILF3	19	28,810,663	28,816,155	7,472	-	1	2_A375_uNA37_plus_lncRNA_AR_1..3191	14863	+downstream	0	1	0	17	22	10	1	2_A375_uNA16_plus_lncRNA_AR_1	22	Gene ILF3	ILF3, ILG3, IL-2, NF45, ILF3/DR, NF90, MGC71973	interleukin 27	NM_1496391, NCT16496819.3	1552993_at		NP_990834.2, EAW92277.1

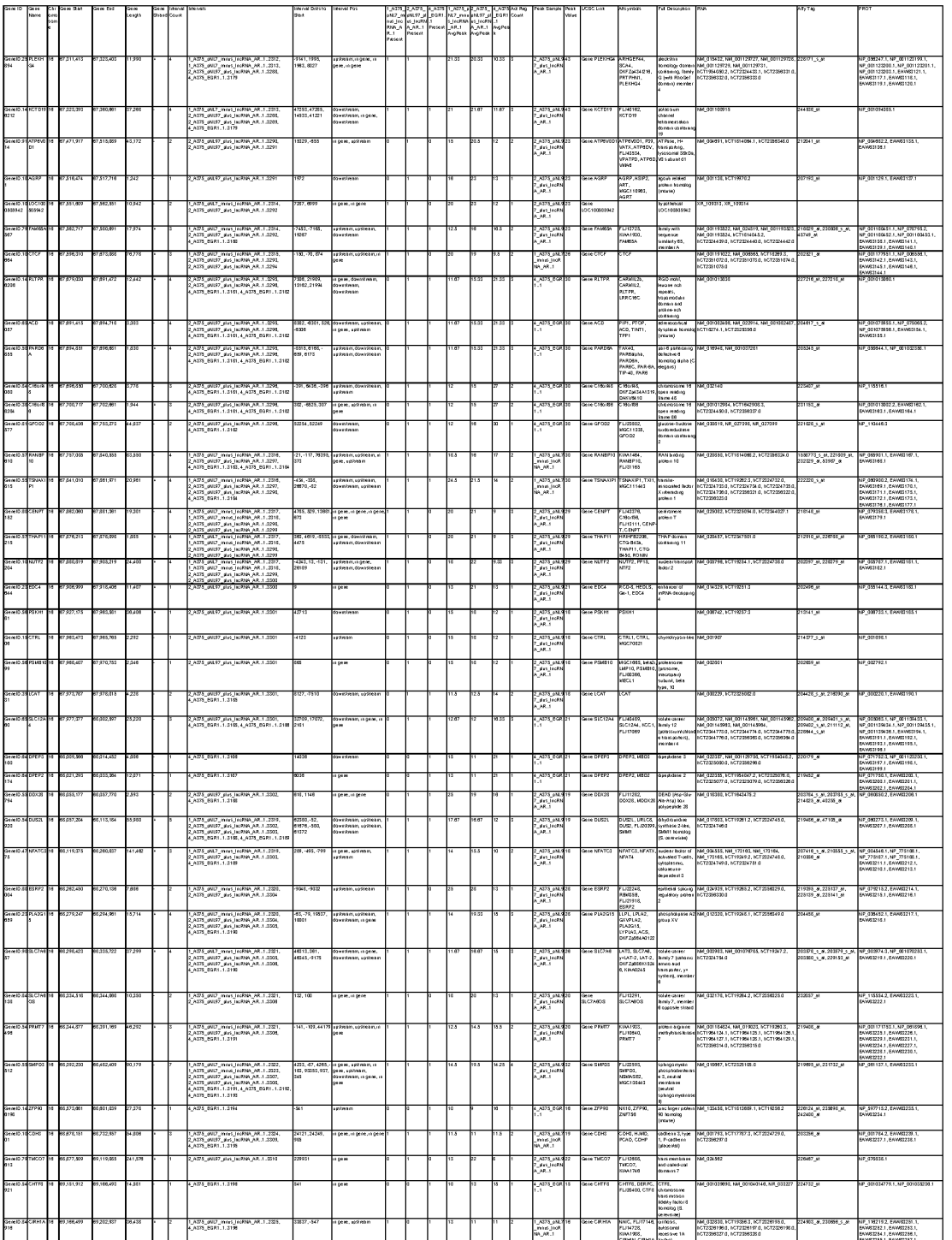
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_antiG7_eGFP_antisense_lncRNA_R1_1 Present	2_A375_2_A375_antiG7_eGFP_antisense_lncRNA_R1_2 Present	3_A375_1_A375_NG7_eGFP_antisense_lncRNA_R1_3 Present	1_A375_1_A375_NG7_eGFP_antisense_lncRNA_R1_1 Avg Peak	2_A375_2_A375_NG7_eGFP_antisense_lncRNA_R1_2 Avg Peak	3_A375_1_A375_NG7_eGFP_antisense_lncRNA_R1_3 Avg Peak	Ad Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:11273	ATXN2L	16	28,234,414	28,245,555	11,144	+	6	1_A375_ctrl7_minus_lncRNA_R1_1:2253, 2_A375_ctrl37_plus_lncRNA_R1_1:3192, 2_A375_ctrl37_plus_lncRNA_R1_1:3193, 2_A375_ctrl37_plus_lncRNA_R1_1:3194, 2_A375_ctrl37_plus_lncRNA_R1_1:3196, 4_A375_EGR1_1:3097	2(652, 430, 1089, 2)346, 382, 12469	5(overdrawn, upstream, in gene, downstream, upstream,in gene				14.75	20	17.25	4	2_A375_ctrl37_plus_lncRNA_R1_1	0		SCA2, ATXN2L, ATXN2L, A2LG, ATXP	Ataxin 2-like	NM_148714, NM_007243, NM_148414, NM_148415, NM_148416, NCT11959510.2, NCT11959397.1, NCT22071880.0, NCT22071910.0, NCT22071952.0, NCT22071960.0, NCT22071990.0, NCT22072300.0, NCT22072511.0, NCT22073212.0	2318806_s_at_207795_s_at	NP_997765.1, NP_009178.2, NP_997765.1, NP_997701.1, NP_997701.1, NP_997762.1, EAW61994.1, EAW61995.1, EAW61996.1, EAW61997.1, EAW61998.1, EAW61999.1, EAW61990.1, EAW61991.1, EAW61992.1, EAW61993.1, EAW61994.1, EAW61995.1, EAW61996.1
GeneID:23724	TUFM	16	28,853,702	28,857,729	4,027	+	3	1_A375_ctrl7_minus_lncRNA_R1_1:2253, 2_A375_ctrl37_plus_lncRNA_R1_1:3194, 4_A375_EGR1_1:3097	33, -31, 10849	3(overdrawn, upstream, downstream				15.5	20.5	17	2	2_A375_ctrl37_plus_lncRNA_R1_1	0		Tu translation elongation factor, mitochondrial	Tu translation elongation factor, mitochondrial	NM_003321, NCT11955516.1, NCT11957071.1	201113_at_233192_at	NP_003312.2, EAW65997.1, EAW61998.1
GeneID:23970	SH3BP1	19	49,275,976	49,305,554	10,458	+	2	1_A375_ctrl37_plus_lncRNA_R1_1:3193, 4_A375_EGR1_1:3098	-186, 18428	upstream, downstream	0	1		12.5	12.5	18.5	2	2_A375_ctrl37_plus_lncRNA_R1_1	0		SH3BP1, PSH, DKFZp547G110, SH3D1, bMAR299	SH3B adaptor protein 1	NM_001145812, NM_015023, NM_001145795, 2)NM_001145796, NM_001142797, NCT11955309.1, NCT11955510.0, NCT22072420.0, NCT22072960.0, NCT22073299.0, NCT22073901.0	209322_s_at_40149_at	NP_001139284.1, NP_056018.2, NP_001139285.1, NP_001139286.1, EAW62000.1, EAW62001.1, EAW62002.1, EAW62003.1, EAW62004.1, EAW62005.1
GeneID:498	ATP2A1	16	28,889,809	28,918,830	29,021	+	3	1_A375_EGR1_1:3088, 4_A375_EGR1_1:3099, 4_A375_EGR1_1:3098	1863, 28191, 27835	in gene, downstream, downstream	0	0	1	8.67	8.33	19.33	3	4_A375_EGR1_1.1	20	Gene ATP2A1	ATP2A1, SERCA1, ATP2A	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	NM_004320, NM_170201, NCT9780.4	203444_at_233893_at	NP_004311.1, NP_775292.1, EAW62008.1
GeneID:102809392	LOC102809392	16	28,890,279	28,891,241	962	+	1	4_A375_EGR1_1:3098	-261	upstream	0	0	1	10	8	19	1	4_A375_EGR1_1.1	19	Gene LOC102809392	hypothetical LOC102809392	NR_109276		
GeneID:7678	RABEP2	16	28,916,742	28,936,822	20,080	+	3	1_A375_EGR1_1:3099, 4_A375_EGR1_1:3098, 4_A375_EGR1_1:3097	20832, 19186, 332	in gene, in gene, upstream	0	0	1	7	7.67	19	3	4_A375_EGR1_1.1	20	Gene RABEP2	RABEP2, FRA, FLJ22262	rabaptin, RAB GTPase binding effector protein 2	NM_024816, NCT22072470.0	219097_at, 74864_s_at, 77990_i_at	NP_079092.2, EAW62007.1
GeneID:955	CD19	16	28,945,260	28,950,865	5,606	+	1	4_A375_EGR1_1:3091	-8596	upstream	0	0	1	11	8	18	1	4_A375_EGR1_1.1	16	Gene CD19	MGC12552, CD19, CVID3, B4	CD19 molecule	NM_001178099, NM_001770, NCT19950551, NCT19970551.1, NCT19970582.2, NCT19714162.1, NCT22031502, NCT19514.2	208356_x_at	NP_001761.3, EAW62009.1, EAW62009.1, EAW62010.1, EAW62010.1, EAW62012.1
GeneID:9641	NFATC2IP	16	28,962,518	28,977,768	15,486	+	1	2_A375_ctrl37_plus_lncRNA_R1_1:3196	23764	downstream	0	0	1	22	22	12	1	2_A375_ctrl37_plus_lncRNA_R1_1	32	Gene NFATC2IP	FLJ14859, MGC126790, MGC126787, MP45, ESC2, RAD60, NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcium-dependent 2 interacting protein	NM_032815, NCT22071482.0, NCT22071488.0	213898_at, 213899_at, 217376_at, 217377_s_at, 229323_at, 235152_at	NP_115924.2, EAW65014.1, EAW62015.1
GeneID:8135	SPNS1	16	28,968,098	28,993,999	9,773	+	1	2_A375_ctrl37_plus_lncRNA_R1_1:3198	18	in gene	0	1	0	22	22	12	1	2_A375_ctrl37_plus_lncRNA_R1_1	32	Gene SPNS1	SPNS, SPNS1, UNC, PTD038, SPNS1, HSpns1, vrs, FLJ35388	sprinter homolog 1 (Drosophila)	NM_032035, NM_001143445, NM_001142449, 2)NM_001142450, NM_001142451, NCT22071981.1, NCT22072170.1, NCT22071750.1, NCT22072177.1, NCT22072179.1, NCT22023153.0, NCT22023154.0	223073_at	NP_114427.1, NP_001128930.1, NP_001128922.1, NP_001128923.1, EAW62020.1, EAW62021.1, EAW62016.1, EAW62017.1, EAW62018.1, EAW62019.1, EAW62020.1, EAW62022.1, EAW62023.1
GeneID:231	LAT	16	28,996,147	29,002,104	5,957	+	1	2_A375_ctrl37_plus_lncRNA_R1_1:3199	-10035	upstream	0	0	1	22	22	12	1	2_A375_ctrl37_plus_lncRNA_R1_1	32	Gene LAT	LAT, pp28, LAT1	linker for activation of T cells	NM_014387, NM_001014957, NM_001014958, 2)NM_001014959, NCT22071713.0, NCT22071761.1, NCT22071800.1, NCT22071801.1, NCT22071820.0, NCT23443972, NCT23443980.0, NCT23023150.0	209561_s_at_210003_at	NP_338032.1, NP_001014957.1, NP_001014959.2, NP_001014958.1, EAW62024.1, EAW62027.1, EAW62025.1, EAW62026.1, EAW62028.1, EAW62029.1, EAW62030.1, EAW62031.1
GeneID:8832	ZG16	16	29,789,961	29,791,940	2,279	+	5	1_A375_ctrl37_minus_lncRNA_R1_1:2257, 2_A375_ctrl37_plus_lncRNA_R1_1:3199, 4_A375_EGR1_1:3092	12559, 12039, 1355	downstream, downstream, downstream, downstream	1	1	1	16	19	24	1	4_A375_EGR1_1.1	24	Gene ZG16	ZG16P, ZG16, MGC34829, FLJ90278, ZG16, MGC142371, MGC163997, NS318	zymogen granule protein 16 homolog (rat)	NM_152336		NP_689511.1
GeneID:3832	KIF22	16	29,802,086	29,816,708	14,846	+	6	1_A375_ctrl7_minus_lncRNA_R1_1:2257, 1_A375_ctrl37_minus_lncRNA_R1_1:2256, 1_A375_ctrl37_minus_lncRNA_R1_1:2255, 2_A375_ctrl37_plus_lncRNA_R1_1:3199, 2_A375_ctrl37_plus_lncRNA_R1_1:3200, 2_A375_ctrl37_plus_lncRNA_R1_1:3201, 2_A375_ctrl37_plus_lncRNA_R1_1:3202, 4_A375_EGR1_1:3092, 4_A375_EGR1_1:3096	-139, 15715, 486, 14710, 17142, 21142, 42, 14742	upstream, downstream, upstream, downstream, downstream, upstream, downstream, downstream	1	1	1	17	16.2	19.6	5	4_A375_EGR1_1.1	24	Gene KIF22	KID, A-229A12, OBP-1, KIF22, OBP1, OBP2, KNSL4	kinesin family member 22	NM_007317, NCT22044972.0, NCT22044976.0, NCT22044977.0, NCT22044978.0, NCT22044980.0, NCT22044982.0	202163_s_at_218993_s_at	NP_213358.1, EAW69308.1, EAW69309.1, EAW69307.1, EAW69310.1, EAW69311.1, EAW69306.1
GeneID:41	MAZ	16	29,817,555	29,822,504	4,949	+	6	1_A375_ctrl7_minus_lncRNA_R1_1:2256, 1_A375_ctrl37_minus_lncRNA_R1_1:2255, 2_A375_ctrl37_plus_lncRNA_R1_1:3201, 2_A375_ctrl37_plus_lncRNA_R1_1:3202, 2_A375_ctrl37_plus_lncRNA_R1_1:3203, 4_A375_EGR1_1:3095	3321, -1007, 1343, 3343, 5586, -1055	in gene, upstream, in gene, downstream, downstream, upstream	1	1	1	17.2	16.2	12.6	5	2_A375_ctrl37_plus_lncRNA_R1_1	21	Gene MAZ	SAP1, PUR1, ZNF801, ZF87, MAZ, SAP-5, Pur-1, SAP-2, ZiF87	MYC-associated zinc finger protein (purine-binding transcription factor)	NM_001042539, NM_002383, NCT22080311.0, NCT23449702.0, NCT23449703.0, NCT23449710.0, NCT23449811.0, NCT23449812.0, NCT23449894.0, NCT23449895.0, NCT23449901.0, NCT23449907.0	207824_s_at_213364_x_at, 235795_x_at_239807_s_at	NP_001139554.1, NP_002374.2, EAW69303.1, EAW69304.1, EAW69301.1, EAW69302.1, EAW69314.1, EAW69297.1, EAW69298.1, EAW69299.1, EAW69300.1, EAW69312.1
GeneID:11276	PRR12	19	29,222,409	29,227,202	4,793	+	6	1_A375_ctrl7_minus_lncRNA_R1_1:2256, 1_A375_ctrl37_plus_lncRNA_R1_1:3200, 2_A375_ctrl37_plus_lncRNA_R1_1:3201, 2_A375_ctrl37_plus_lncRNA_R1_1:3202, 2_A375_ctrl37_plus_lncRNA_R1_1:3203, 4_A375_EGR1_1:3095	-1603, -9541, 4203, -309, 4513, -6609	upstream, upstream, upstream, upstream, downstream, upstream	1	1	1	17.2	16.2	12.6	5	2_A375_ctrl37_plus_lncRNA_R1_1	21	Gene PRR12	PRR12, DKFZp547J199, FLJ25313, PTH2D1	proline rich transmembrane protein 2	NM_145239, NCT22080642.1, NCT22080644.1, NCT22080837.1, NCT22081972.0	227192_at	NP_940932.2, EAW69300.1, EAW69301.1, EAW69302.1
GeneID:7647	PHC1/SCR3	12	29,227,826	29,233,016	5,208	+	4	1_A375_ctrl37_plus_lncRNA_R1_1:2255, 2_A375_ctrl37_plus_lncRNA_R1_1:3201, 2_A375_ctrl37_plus_lncRNA_R1_1:3202, 2_A375_ctrl37_plus_lncRNA_R1_1:3203	5192, -5325, 4325, -104	upstream, upstream, upstream, upstream	1	1	0	17	17.5	12	4	2_A375_ctrl37_plus_lncRNA_R1_1	20	Gene C1QL/B3	C1QL/B3, PA1, SHSL, MGC14858, FLJ22459	complement component 1, q subcomponent like 3	NM_024418, NCT22080830.0	210300_at	NP_076782.1, EAW79189.1
GeneID:9961	MVP	19	29,831,767	29,859,341	27,574	+	4	1_A375_ctrl37_plus_lncRNA_R1_1:2253, 2_A375_ctrl37_plus_lncRNA_R1_1:3202, 2_A375_ctrl37_plus_lncRNA_R1_1:3203, 4_A375_EGR1_1:3094	-10011, -8567, 4363, 24357	upstream, upstream, upstream,in gene	1	1	1	14.75	14	13	4	4_A375_EGR1_1.1	20	Gene MVP	MVP, LRP, VAULT1	major vault protein	NM_017458, NM_005115, NCT22080839.1, NCT22080940.1, NCT22080943.1, NCT22080945.1, NCT22080952.1, NCT22080955.1, NCT23442322.0, NCT23443303.0, NCT23539901.0	202160_s_at_213076_at	NP_059447.2, NP_005106.2, EAW79078.1, EAW79093.1, EAW79094.1, EAW79095.1, EAW79096.1, EAW79083.1, EAW79084.1, EAW79085.1, EAW79086.1, EAW79087.1
GeneID:1062	CDIPT	19	29,869,976	29,874,976	4,999	-	2	1_A375_ctrl7_minus_lncRNA_R1_1:2259, 2_A375_ctrl37_plus_lncRNA_R1_1:3204	-142, -256	upstream, upstream	1	1	0	61	76	10	1	2_A375_ctrl37_plus_lncRNA_R1_1	16	Gene CDIPT	PIS, CDIPT, MGC1326, PIS1	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	NM_006119, NCT12119.4, NCT19618932.1, NCT23559974.0	201283_s_at	NP_006110.1, EAW79976.1, EAW79977.1, EAW79976.1
GeneID:4435	LOC44056	19	29,875,004	29,879,074	4,070	+	5	1_A375_ctrl7_minus_lncRNA_R1_1:2255, 2_A375_ctrl37_plus_lncRNA_R1_1:3204, 4_A375_EGR1_1:3095	-256, -155, 13570	upstream, upstream, downstream	1	1	1	33	60	54	2	2_A375_ctrl37_plus_lncRNA_R1_1	16	Gene LOC440356	FLJ27521	hypothetical LOC440356	NR_015396, NR_026370	240537_s_at	
GeneID:2663	SEZ6L2	16	29,882,400	29,910,900	28,500	-	5	1_A375_ctrl7_minus_lncRNA_R1_1:2259, 2_A375_ctrl37_plus_lncRNA_R1_1:3204, 2_A375_ctrl37_plus_lncRNA_R1_1:3205, 4_A375_EGR1_1:3095, 4_A375_EGR1_1:3096	23850, 23784, 844, 23504, -2357	upstream, upstream, in gene, upstream	1	1	1	21.75	22.25	13.25	4	2_A375_ctrl37_plus_lncRNA_R1_1	16	Gene SEZ6L2	SEZ6L2, FLJ16317, PSH	seizure related 6 homolog (mouse)-like 2	NM_032410, NM_201573, NM_001114999, 2)NM_001114998, NCT11958244.3	219720_s_at_223436_at, 223327_s_at_239404_x_at, 239406_x_at	NP_115804.1, NP_963998.2, NP_963997.1, NP_001107872.1, NP_001107872.1
GeneID:2592	ASPHD1	16	29,912,147	29,917,377	5,230	+	2	2_A375_ctrl37_plus_lncRNA_R1_1:3205, 4_A375_EGR1_1:3096	722, 643	upstream,in gene	0	1		10.5	16.5	12.5	2	2_A375_ctrl37_plus_lncRNA_R1_1	21	Gene ASPHD1	ASPHD1	aspartate beta-hydroxylase domain containing 1	NM_181718, NCT03259836.3, NCT23559962.0	1553997_s_at_214993_at	NP_859059.2, EAW79972.1, EAW79971.1
GeneID:8318	TACK2	19	29,935,222	29,935,861	10,339	+	3	1_A375_EGR1_1:3089, 1_A375_ctrl7_minus_lncRNA_R1_1:2260, 2_A375_ctrl37_plus_lncRNA_R1_1:3207	14074, 22202, 22426	in gene, downstream, downstream	1	1	1	13	12	18	2	1_A375_ctrl7_minus_lncRNA_R1_1	21	Gene TACK2	PSK, KAA0651, PSK1-BETA, TAK1, MMP3317, TACK2, PSK1, TAK2	TAO kinase 2	NM_004782, NM_016151, NCT19939139.1, NCT22080700.0, NCT9408.2	204077_x_at_204078_s_at, 204698_s_at	NP_004773.1, NP_057228.2, EAW79983.1, EAW79984.1, EAW79985.1
GeneID:8494	HIRIP3	19	30,004,311	30,007,412	3,101	+	4	1_A375_EGR1_1:3086, 1_A375_ctrl7_minus_lncRNA_R1_1:2260, 2_A375_ctrl37_plus_lncRNA_R1_1:3209, 2_A375_ctrl37_plus_lncRNA_R1_1:3207, 4_A375_EGR1_1:3089	6116, -12, -236, 7740	downstream, upstream, upstream, upstream	1	1	1	10.67	10	16	3	1_A375_ctrl7_minus_lncRNA_R1_1	21	Gene HIRIP3	HIRIP3	HIRA interacting protein 3	NM_003609, NCT22079997.0, NCT19289.3	204504_s_at_223697_at	NP_003600.2, EAW79960.1, EAW79961.1
GeneID:2863	INO80E	16	30,007,551	30,017,112	9,561	+	4	1_A375_EGR1_1:3085, 1_A375_ctrl7_minus_lncRNA_R1_1:2260, 2_A375_ctrl37_plus_lncRNA_R1_1:3209, 2_A375_ctrl37_plus_lncRNA_R1_1:3208	-5255, -167, 117, 7621	upstream, upstream, in gene, in gene	1	1	1	10.67	10	16	3	1_A375_ctrl7_minus_lncRNA_R1_1	21	Gene INO80E	INO80E, FLJ30379, CCDC51, DKFZp761E1116, FLJ90652	INO80 complex subunit E	NM_175918, NCT11959230.3, NCT22080674.1, NCT22081260.0, NCT22080976.0, NCT22081277.0, NCT22080978.0, NCT22080979.0	227268_at	NP_795355.1, EAW79950.1, EAW79954.1, EAW79955.1, EAW79956.1, EAW79957.1, EAW79951.1, EAW79952.1, EAW79953.1
GeneID:6450	DOC2A	16	30,016,833	30,022,401	5,568	+	3	1_A375_ctrl37_plus_lncRNA_R1_1:3208, 2_A375_ctrl37_plus_lncRNA_R1_1:3207, 4_A375_EGR1_1:3088	14877, 14783, 7249	downstream, downstream, downstream	1	1	1	13.5	12	19	2	2_A375_ctrl37_plus_lncRNA_R1_1	21	Gene DOC2A	Doc2, DOC2A		NM_003586, NCT19892434.4, NCT19895836.2, NCT19895312.2, NCT22079897.1, NCT22079898.1, NCT22079899.1, NCT23441213.0, NCT23441214.0, NCT23441215.0	203744_at	NP_003577.2, EAW79946.1, EAW79947.1, EAW79948.1, EAW79949.1, EAW79944.1, EAW79945.1, EAW79946.1, EAW79947.1, EAW79948.1, EAW79950.1
GeneID:8878	TAC1/SCR2	19	30,034,935	30,036,023	1,088	+	1	4_A375_EGR1_1:3090	2102	downstream	0	0	1	9	8	16	1	4_A375_EGR1_1.1	16	Gene C1QL/B2	MGC125422, FLJ25404, C1QL/B2	complement component 1, q subcomponent like 2	NM_031929, NM_001109890	1557162_at	NP_001103291.1, NP_001103150.1
GeneID:8339	FAM57B	19	30,035,745	30,042,169	6,424	+	1	4_A375_EGR1_1:3070	5426	in gene	0	0	1	9	8	16	1	4_A375_EGR1_1.1	16	Gene FAM57B	FP1165, FAM57B, DKFZp434D117	family with sequence similarity 57, member B	NM_201476, NCT19392421.2, NCT19574381.1, NCT22078907.0	227761_s_at	NP_115986.2, EAW79937.1, EAW79938.1, EAW79939.1
GeneID:22	ALDOA	16	30,064,491	30,081,705	17,244	+	3	1_A375_ctrl37_plus_lncRNA_R1_1:2261, 2_A375_ctrl37_plus_lncRNA_R1_1:3209, 2_A375_ctrl37_plus_lncRNA_R1_1:3210	12149, 12117, 10825	in gene, in gene, in gene	1	1	1	16	14	12.5	2	2_A375_ctrl37_plus_lncRNA_R1_1	24	Gene ALDOA	ALDA, DKFZp779F, ALDOA, MGC117392, MGC12432, GSD12	aldolase A, fructose-bisphosphate	NM_000034, NM_184041, NM_184043, NM_001127617, NCT19910702.2, NCT19910711.1, NCT22080982.0, NCT22080988.0	200965_s_at_214957_s_at, 200966_x_at	NP_000025.1, NP_909030.1, NP_909031.1, NP_001121615.1, NP_000022.2, EAW79923.1, EAW79926.1, EAW79934.1, EAW79933.1
GeneID:5230	PFKL	19	30,087,365	30,096,893	9,528	+	3	1_A375_ctrl37_plus_lncRNA_R1_1:2262, 2_A375_ctrl37_plus_lncRNA_R1_1:3209, 2_A375_ctrl37_plus_lncRNA_R1_1:3212	18843, 15975, 13216	downstream, downstream, downstream	1	1	1	20	33	19	1	2_A375_ctrl37_plus_lncRNA_R1_1	21	Gene PFKL	PFKL, PFK, PFHD, PFRK, PFK, PFKN	platelet phosphofructokinase 4, formerly, 1), catalytic subunit	NM_002720, NCT19892281.3, NCT19574382.2, NCT19668455.0, NCT19668547.1	208602_at	NP_002711.1, EAW79928.1, EAW79929.1, EAW79930.1, EAW79931.1
GeneID:8611	TBX6	16	30,097,114	30,103,303	6,191	+	4	1_A375_ctrl37_plus_lncRNA_R1_1:2262, 2_A375_ctrl37_plus_lncRNA_R1_1:3209, 4_A375_EGR1_1:3072, 4_A375_EGR1_1:3073	123, -155, 934, 4701	upstream, upstream, in gene, upstream	1	1	1	15.5	22.5	16.5	2	2_A375_ctrl37_plus_lncRNA_R1_1	23	Gene TBX6	DFNB97, TBX6	T-box 6	NM_004608, NCT19892271.1, NCT22078564.0	207684_at_215122_at	NP_004599.2, EAW79927.1, EAW79927.1
GeneID:8355	YPEL5	16	30,103,655	30,107,557	3,902	+	4	1_A375_ctrl37_plus_lncRNA_R1_1:2262, 2_A375_ctrl37_plus_lncRNA_R1_1:3209, 4_A375_EGR1_1:3072, 4_A375_EGR1_1:3073	4205, 4177, 4036, 299	downstream, downstream, downstream, upstream	1	1	1	15.5	22.5	16.5	2	2_A375_ctrl37_plus_lncRNA_R1_1	23	Gene YPEL5	MGC10350, YPEL5	yippee-like 5 (Drosophila)	NM_031477, NM_001145524, NCT19892443.5, NCT19574382.3, NCT19655481.1, NCT22023171.0	223179_at_232207_s_at	NP_113665.3, NP_001139996.1, EAW79922.1, EAW79923.1, EAW79924.1, EAW79925.1
GeneID:3271621	LOC102721621	16	30,103,685	30,123,828	20,781	+	5	1_A375_ctrl37_plus_lncRNA_R1_1:2262, 2_A375_ctrl37_plus_lncRNA_R1_1:3209, 2_A375_ctrl37_plus_lncRNA_R1_1:3210, 4_A375_EGR1_1:3072, 4_A375_EGR1_1:3073, 4_A375_EGR1_1:3074	-1727, -1705, 3384, 3571, 20539	upstream, upstream, downstream, downstream, upstream	1	1	1	12.67	17.67	17	3	2_A375_ctrl37_plus_lncRNA_R1_1	23	Gene LOC102721621	LOC102721621	hypothetical LOC102721621	NR_027051		
GeneID:3509614	LOC102509914	16	30,107,751	30,116,541	8,790	+	4	1_A375_ctrl37_plus_lncRNA_R1_1:2262, 2_A375_ctrl37_plus_lncRNA_R1_1:3209, 4_A375_EGR1_1:3072, 4_A375_EGR1_1:3073	4423, -4391, 8283, 165	upstream, upstream, upstream,in gene	1	1	1	15.5	22.5	16.5	2	2_A375_ctrl37_plus_lncRNA_R1_1	23	Gene LOC102509914	LOC102509914	hypothetical LOC102509914	NR_109351		
GeneID:793	GDPD3	16	30,116,101	30,124,876	8,747	-	2	1_A375_EGR1_1:3073, 4_A375_EGR1_1:3074	18842, -6948	downstream, upstream	0	0	1	7.5	10	17.5	2	4_A375_EGR1_1.1	16	Gene GDPD3	MGC4171, FLJ25803, GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	NM_024307, NCT22078721.1, NCT22078751.1, NCT22078771.1	219722_s_at	NP_077283.2, EAW79918.1, EAW79919.1, EAW79920.1
GeneID:8338	MAPK3	16	30,125,426	30,134,800	9,254	+	1	4_A375_EGR1_1:3074	908	in gene	0	0	1	7	8	16	1	4_A375_EGR1_1.1	16	Gene MAPK3	P44MAPK, MAPK3, ERK1, HUMERK1A, HS44KDAP, P44ERK1, MGC20180, PRKM3	mitogen-activated protein kinase 3	NM_001040056, NM_002746, NM_001109891, 2)NM_001109892, NCT22078701.1, NCT22078871.1, NCT22078703.1, NCT22078760.0, NCT22078783.1, NCT22078970.0	212046_x_at	NP_001035145.1, NP_002737.2, NP_001103891.1, EAW79912.1, EAW79914.1, EAW79915.1, EAW79913.1, EAW79916.1, EAW79917.1
GeneID:1781	CORO1A	16	30,194,751	30,200,397	5,646	+	1	4_A375_EGR1_1:3075	4821	in gene	0	0	1	7	8	16	1	4_A375_EGR1_1.1	16	Gene CORO1A	p57kDa, actin-binding protein, 58,	NM_007074, NM_001193333, NM_007074, 2)NM_001193333, NCT19894312.1, NCT19895442.2, NCT22047203.0, NCT23473734.0, NCT23473734.0, NCT23539700.0	209083_at	NP_009005.1, NP_001180262.1, NP_009005.1, NP_001180262.1, EAW79936.1, EAW79935.1, EAW79937.1, EAW79939.1, EAW79938.1
GeneID:6500	BOLA2B	16	30,204,256	30,205,627	1,371	+	1	4_A375_EGR1_1:3075	8075	downstream	0	0	1	7	8	16	1	4_A375_EGR1_1.1	16	Gene BOLA2B	BOLA2B, BOLA2		NM_031039182		NP_001034271.1
GeneID:5930	GIYD1	16	30,205,217	30,208,882	3,665	+	1	4_A375_EGR1_1:3075	9665	upstream	0	0	1	7	8	16	1	4_A375_EGR1_1.1	16	Gene GIYD1	GIYD1, SLX1A, GIYD2, SLX1B	SLX1 structure-specific endonuclease subunit homolog A (S. cerevisiae)	NM_031014999, NM_001015000	218317_s_at	NP_001014999.1, NP_001015000.1
GeneID:1161	SULT1A3/4	16	30,205,745	30,215,650	9,907	+	1	4_A375_EGR1_1:3075	-8191	upstream	0	0	1	7	8	16	1	4_A375_EGR1_1.1	16	Gene SULT1A3	ST1A3, TS1ST, MSTD1467, SULT1A4, SULT1A3, TS1ST, HMSTS, STM, TLPST, M-PST	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3	NM_053196, NM_177532		NP_001157.1, NP_808228.1
GeneID:1795	CD2BP2	16	30,282,857	30,286,862	4,005	-	3	1_A375_ctrl37_minus_lncRNA_R1_1:2263, 2_A375_ctrl37_plus_lncRNA_R1_1:3210, 4_A375_EGR1_1:3076	-420, -262, 4152	upstream, upstream, upstream	1	1		14	12	17	2	2_A375_ctrl37_plus_lncRNA_R1_1	20	Gene CD2BP2	PWR16, LIN1, CD2BP2-LIS-SDN, Sin40	CD2 (cytoplasmic) tail binding protein 2	NM_006110, NM_034485, NCT22080381.1, NCT22080382.1	202256_at_202257_s_at	NP_006101.1, EAW62190.1, EAW62189.1
GeneID:6000	TBC1D10B	16	30,286,422	30,291,822	15,400	-	5	1_A375_ctrl7_minus_lncRNA_R1_1:2263, 1_A375_ctrl37_minus_lncRNA_R1_1:2262, 2_A375_ctrl37_plus_lncRNA_R1_1:3210, 2_A375_ctrl37_plus_lncRNA_R1_1:3211, 4_A375_EGR1_1:3076, 4_A375_EGR1_1:3077	14418, 14376, 6302, 10735, 7790	downstream, downstream, upstream, in gene, upstream	1	1		13.33	16.33	19.67	3	2_A375_ctrl37_plus_lncRNA_R1_1	23	Gene TBC1D10B	TBC1D10B, FP2451, DKFZp434P176	TBC1 domain family, member 10B	NM_015327, NCT22052051.1, NCT22052052.1, NCT23523222.0	220947_s_at	NP_056142.2, EAW62236.1, EAW62237.1



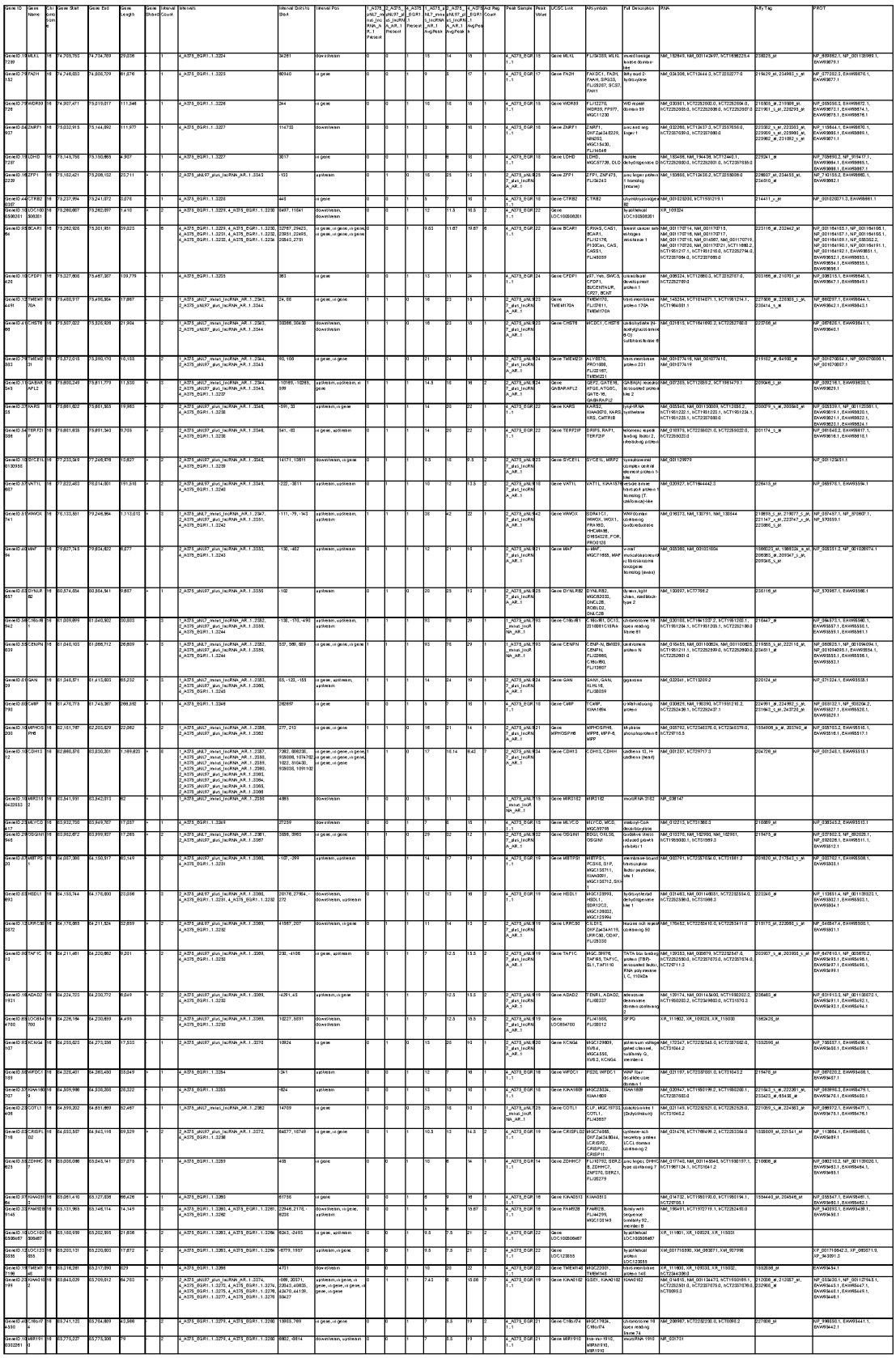
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_pfd27_MyLFP_pos_incRNA_R_1 Percent	2_A375_pfd27_plus_lncRNA_R_1 Percent	4_A375_EGR1_pfd27_plus_lncRNA_R_1 Percent	1_A375_pfd27_MyLFP_pos_incRNA_R_1 AvgRank	2_A375_pfd27_plus_lncRNA_R_1 AvgRank	4_A375_EGR1_pfd27_plus_lncRNA_R_1 AvgRank	Ad Tag Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:29	MYLPF	19	35,395,123	35,399,310	4,187	+	2	2_A375_pfd27_plus_lncRNA_R_1...3211, A_A375_EGR1...3077	3761, 3169	downstream, downstream	0	1	1	12	25	16	1	2_A375_pfd27_plus_lncRNA_R_1	23	Gene MYLPF	DKFZp779C0783	myosin light chain, phosphorylatable, fast skeletal muscle	NM_013292, XCT1765990.1, hCT2262592.0	2301/63_at	NP_037424.2, EAW62254.1, EAW62253.1
GeneID:151	Sep-11	19	35,399,456	35,294,971	4,715	+	2	2_A375_pfd27_plus_lncRNA_R_1...3211, A_A375_EGR1...3077	4367, 4839	sr gene, downstream	0	1	1	12	25	16	1	2_A375_pfd27_plus_lncRNA_R_1	23	Gene SEPT1	SEPT1	septin 1	NM_052838, XCT1765990.0, hCT2262579.0	227552_at	NP_443570.1, EAW62252.1, EAW62253.1
GeneID:33	ZNF771	19	35,416,703	35,420,918	11,181	+	1	A_A375_EGR1...3076	11859	sr gene	0	0	1	12	16	16	1	A_A375_EGR1	16	Gene ZNF771	ZNF43, ZKP771	zinc finger protein 771	NM_178843, NM_001142355	219760_at, 219761_s_at, 219762_s_at, 221986_s_at	NP_997727.2, NP_001138777.1
GeneID:79	DCTPP1	19	35,835,019	35,841,375	6,354	+	2	2_A375_pfd27_plus_lncRNA_R_1...3212, A_A375_EGR1...3076	108, 11549	sr gene, downstream	0	1	1	12.5	17	13.5	2	A_A375_EGR1	16	Gene DCTPP1	DCTPP1, PIG016, ITPTPA, MGC3627, CGI63	dCTP pyrophosphatase 1	NM_030906, XCT1768000.2	219089_at	NP_377931.1, EAW62247.1
GeneID:23	SEPHS2	19	35,854,592	35,857,224	2,272	-	1	2_A375_pfd27_plus_lncRNA_R_1...3213	592	sr gene	0	1	0	19	21	14	1	2_A375_pfd27_plus_lncRNA_R_1	21	Gene SEPHS2	SPS2, SEPHS2	selenophosphate synthetase 2	NM_012248, XCT1768001.2	202961_at	NP_036350.2, EAW62248.1
GeneID:38	ITGAL	16	30,483,903	30,534,306	50,403	+	2	A_A375_EGR1...3079, A_A375_EGR1...3080	1903, 34598	sr gene, downstream	0	0	1	10	10.5	16	2	A_A375_EGR1	17	Gene ITGAL	ITGAL, CD11A, ITGAL, LFA-1	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	NM_002209, NM_001114380, XCT2023086.0, hCT2023597.0, hCT9772.3	1554240_a_at, 213479_s_at	NP_002200.2, NP_001107582.1, EAW62243.1, EAW62244.1, EAW62245.1
GeneID:78	ZNF766	16	30,533,322	30,537,910	2,588	-	2	2_A375_pfd27_plus_lncRNA_R_1...3214, A_A375_EGR1...3080, A_A375_EGR1...3081	-5774, -925, -1084	upstream, upstream, upstream	0	1	1	10.33	14	13.33	3	A_A375_EGR1	17	Gene ZNF766	ZNF766, FLJ25439	zinc finger protein 766	NM_024671, XCT1627660.3, hCT2260274.0	218918_at	NP_079047.3, EAW62241.1, EAW62242.1
GeneID:16	LOC100390980	19	30,536,147	30,541,977	5,830	+	3	2_A375_pfd27_plus_lncRNA_R_1...3214, A_A375_EGR1...3080, A_A375_EGR1...3081	3477, 392, 9117	downstream, sr gene, downstream	0	1	1	10.33	14	13.33	3	A_A375_EGR1	17	Gene LOC100390980		hypothetical LOC100390980	XR_109302		
GeneID:83	ZNF747	16	30,542,779	30,546,194	3,415	-	3	2_A375_pfd27_plus_lncRNA_R_1...3214, A_A375_EGR1...3080, A_A375_EGR1...3081	-439, 7655, -1679	upstream, downstream, upstream	0	1	1	10.33	14	13.33	3	A_A375_EGR1	17	Gene ZNF747	MGC2474, ZNF747	zinc finger protein 747	NM_032391, XCT1627681.0, hCT2262271.0	208160_s_at, 233908_at	NP_079620.1, EAW62239.1, EAW62240.1
GeneID:10	LOC100390973	19	30,546,591	30,546,870	2,279	+	3	2_A375_pfd27_plus_lncRNA_R_1...3214, A_A375_EGR1...3080, A_A375_EGR1...3081	232, -7652, 875	sr gene, upstream, sr gene	0	1	1	10.33	14	13.33	3	A_A375_EGR1	17	Gene LOC100390973		hypothetical LOC100390973	XR_111983, XR_109303, XR_114996		
GeneID:83	ZNF764	16	30,565,655	30,569,842	4,187	-	1	2_A375_pfd27_plus_lncRNA_R_1...3215	10	sr gene	0	0	1	13	19	13	1	2_A375_pfd27_plus_lncRNA_R_1	19	Gene ZNF764	MGC13130, ZNF764	zinc finger protein 764	NM_032410, NM_001173979, hCT10353.3, hCT2262280.0	222120_at, 57318_at	NP_115983.2, NP_001186130.1, EAW62237.1, EAW62238.1
GeneID:14	ZNF865	19	30,661,007	30,663,728	2,721	-	1	A_A375_EGR1...3082	2266	sr gene	0	0	1	6	8	22	1	A_A375_EGR1	22	Gene ZNF865	ZNF865	zinc finger protein 865	NM_145271, NM_001024853, hCT2344342.0, hCT2344344.0, hCT2344547.0, hCT2344549.0	210527_s_at, 213529_at, 229951_s_at, 235950_at, 235951_s_at	NP_660614.1, NP_001018554.1, EAW62233.1, EAW62234.1, EAW62235.1, EAW62236.1
GeneID:11	ZNF869	19	30,814,866	30,821,862	6,996	-	2	1_A375_pfd27_minus1_lncRNA_R_1...2284, 2_A375_pfd27_plus_lncRNA_R_1...3216	-110, -142	upstream, upstream	1	1	0	22	29	11	1	2_A375_pfd27_plus_lncRNA_R_1	29	Gene ZNF869	FLJ41941, DKFZp686C17125, ZNF869	zinc finger protein 869	NM_138447, XCT1768998.1	237284_at, 237445_at	NP_612458.1, EAW62226.1
GeneID:76	PRR14	19	30,862,241	30,867,704	5,463	+	4	1_A375_pfd27_minus1_lncRNA_R_1...2285, 2_A375_pfd27_minus1_lncRNA_R_1...2286, 2_A375_pfd27_plus_lncRNA_R_1...3217, 2_A375_pfd27_plus_lncRNA_R_1...3218, A_A375_EGR1...3083	-321, 7657, -269, 7919	upstream, downstream, upstream, downstream	1	1	0	30.5	30	15	2	1_A375_pfd27_minus1_lncRNA_R_1	27	Gene PRR14	DKFZp761A1339, PRR14, MGC5121	proline rich 14	NM_024031, XCT12350.0, hCT2262590.1, hCT2262591.0, hCT2262596.0, hCT2262597.0, hCT2262545.0, hCT2262545.0	1559097_s_at, 219714_at, 41667_at	NP_076936.1, EAW62222.1, EAW62223.1, EAW62225.1, EAW62227.1, EAW62228.1, EAW62229.1
GeneID:10	LOC100390995	19	30,870,167	30,874,147	3,980	+	5	1_A375_pfd27_minus1_lncRNA_R_1...2285, 1_A375_pfd27_minus1_lncRNA_R_1...2286, 2_A375_pfd27_plus_lncRNA_R_1...3217, 2_A375_pfd27_plus_lncRNA_R_1...3218, A_A375_EGR1...3083	-1987, -935, -1023, -837, 7341	upstream, upstream, upstream, upstream, upstream	1	1	1	22	21.33	13.33	3	1_A375_pfd27_minus1_lncRNA_R_1	27	Gene LOC100390995		hypothetical protein LOC100390995	XM_003116734, XM_003120850		XP_003116782.1, XP_003120998.1
GeneID:84	FBXL5	19	30,873,776	30,882,151	8,376	+	3	1_A375_pfd27_minus1_lncRNA_R_1...2286, 2_A375_pfd27_plus_lncRNA_R_1...3218, A_A375_EGR1...3083	-5883, -5810, 2084	upstream, upstream, sr gene	0	1	1	21	19.5	15	2	2_A375_pfd27_plus_lncRNA_R_1	27	Gene FBXL5	FLJ11616, Fbxlos-1, FBS, FBS1, FBXL5	f-box and leucine-rich repeat protein 5	NM_012300, XCT12347.0, hCT2262593.0, hCT2262594.0, hCT2344965.0	212255_s_at, 232771_at, 242217_s_at	NP_036930.4, EAW62216.1, EAW62217.1, EAW62218.1
GeneID:73	LOC728323	19	30,709,626	30,709,810	762	-	2	2_A375_pfd27_plus_lncRNA_R_1...3219, A_A375_EGR1...3084	274, -318	sr gene, upstream	0	1	1	16	20	16	1	2_A375_pfd27_plus_lncRNA_R_1	20	Gene LOC728323		hypothetical protein LOC728323	XR_111989, XR_109204, XR_114994		
GeneID:10	SRCAP	16	30,710,462	30,781,450	70,988	+	3	2_A375_pfd27_plus_lncRNA_R_1...3219, A_A375_EGR1...3084, A_A375_EGR1...3085	-626, -334, 46994	upstream, upstream, downstream	0	1	1	16	17	16	2	2_A375_pfd27_plus_lncRNA_R_1	20	Gene SRCAP	KIAA0269, FLJ44499, EAF1, SRCAP, DOMO1, Snf2l	Snf2-related CBP activator protein	NM_006662, XCT2025995.0, hCT2262596.0, hCT2262600.0	1552600_s_at, 1565120_s_at, 212275_s_at, 213997_at, 215050_s_at, 33798_s_at	NP_008553.2, EAW62212.1, EAW62213.1, EAW62214.1
GeneID:52	PHKG2	16	30,799,820	30,822,497	12,677	+	2	A_A375_EGR1...3085, A_A375_EGR1...3086	-954, 12212	upstream, downstream	0	0	1	13.5	13	19.5	2	A_A375_EGR1	20	Gene PHKG2	PHKG2, GSD6C	phosphorylase kinase, gamma 2 (testis)	NM_006284, NM_001173432, XCT12229.4, hCT2262582.0, hCT2262584.0, hCT2262587.0	1558060_at, 1558089_s_at, 202769_at	NP_002053.1, NP_001160901.1, EAW62205.1, EAW62210.1, EAW62211.1
GeneID:55	C16orf59	16	30,795,782	30,797,542	1,760	-	2	A_A375_EGR1...3085, A_A375_EGR1...3086	14008, 710	downstream, sr gene	0	0	1	13.5	13	19.5	2	A_A375_EGR1	20	Gene C16orf59	C16orf59, MGC104708	chromosome 16 open reading frame 59	NM_001014979, XCT12252.2, XCT1997915.1, hCT1997916.1, hCT2252523.0, hCT2252534.0, hCT2252535.0	231350_at	NP_001014979.1, EAW62205.1, EAW62206.1, EAW62207.1, EAW62202.1, EAW62203.1, EAW62204.1, EAW62253.1
GeneID:99	RNF43	17	30,772,830	30,788,829	12,999	+	4	1_A375_pfd27_minus1_lncRNA_R_1...2287, 2_A375_pfd27_plus_lncRNA_R_1...3220, A_A375_EGR1...3086, A_A375_EGR1...3087	13410, 13834, -796, 13282	downstream, downstream, upstream, downstream	1	1	1	16	17.5	19	2	2_A375_pfd27_plus_lncRNA_R_1	23	Gene RNF43	STARING, RBP59, RNF43, MGC13091, DKFZp686X01, KIAA0851, BR018	ring finger protein 43	NM_017763, XCT2026815.0, hCT2262617.0, hCT2262618.0, hCT2262620.0	1558549_s_at, 217642_at	NP_065696.1, EAW62196.1, EAW62197.1, EAW62199.1, EAW62200.1
GeneID:23	ZNF829	19	30,789,770	30,795,823	6,053	-	4	1_A375_pfd27_minus1_lncRNA_R_1...2287, 2_A375_pfd27_plus_lncRNA_R_1...3220, A_A375_EGR1...3086, A_A375_EGR1...3087	11453, 11295, 89, 11331	downstream, downstream, downstream, downstream	1	1	1	14	21	16	2	2_A375_pfd27_plus_lncRNA_R_1	23	Gene ZNF829	ZNF_ZNF829, KIAA0328, ZNF829	zinc finger protein	NM_031035417	213198_at	NP_031073898.1
GeneID:83	BCL7C	16	30,899,116	30,903,399	4,283	-	2	2_A375_pfd27_plus_lncRNA_R_1...3220, 2_A375_pfd27_plus_lncRNA_R_1...3221	-312, -329	upstream, upstream	1	1	0	22	26	13	1	2_A375_pfd27_plus_lncRNA_R_1	26	Gene BCL7C	BCL7C	Bcl-7 C-Ulysinalone 7C	NM_004765, XCT12258.3	210972_at	NP_004758.2, EAW62190.1
GeneID:11	MIR762	19	30,903,224	30,903,308	82	+	2	2_A375_pfd27_plus_lncRNA_R_1...3219, 2_A375_pfd27_plus_lncRNA_R_1...3223	455, 934	downstream, downstream	0	0	1	22	26	13	1	2_A375_pfd27_plus_lncRNA_R_1	26	Gene MIR762	hsa-mir-762, MIR762	microRNA 762	NR_031976		
GeneID:14	CTF1	19	30,907,926	30,914,361	6,435	+	2	2_A375_pfd27_plus_lncRNA_R_1...3220, 2_A375_pfd27_plus_lncRNA_R_1...3221	-2216, -2290	upstream, upstream	0	0	1	22	26	13	1	2_A375_pfd27_plus_lncRNA_R_1	26	Gene CTF1	CTF1, CT-1, CTF1	cardiotrophin 1	NM_001330, NM_001142344, hCT1997895.1	206513_at	NP_001321.1, NP_001139018.1, EAW62192.1
GeneID:28	NCRNA00093	19	30,930,840	30,934,990	4,950	-	2	2_A375_pfd27_plus_lncRNA_R_1...3220, 2_A375_pfd27_plus_lncRNA_R_1...3224, A_A375_EGR1...3091	190, 630, 1838	sr gene, sr gene, sr gene	1	1	1	17.5	17.5	12	2	A_A375_pfd27_plus_lncRNA_R_1	30	Gene NCRNA00093	MGC113489, NCRNA00093, MGC113470, MGC125472, FBL119-AS1	FBJ-19 antisense RNA 1 (zinc-finger-containing)	NR_026348, XCT2392231.1	1553599_at	EAW62191.1
GeneID:54	FBXL19	19	30,935,896	30,960,104	24,208	+	7	1_A375_pfd27_minus1_lncRNA_R_1...2292, 1_A375_pfd27_minus1_lncRNA_R_1...2293, 1_A375_pfd27_minus1_lncRNA_R_1...2294, 2_A375_pfd27_plus_lncRNA_R_1...3225, 2_A375_pfd27_plus_lncRNA_R_1...3226, A_A375_EGR1...3091, A_A375_EGR1...3092	-1498, 33226, -1964, 33224, -2144, 32144, 34152	upstream, downstream, upstream, downstream, upstream, downstream, downstream	1	1	1	19.25	22	13.75	4	A_A375_EGR1	45	Gene FBXL19	F-box and leucine-rich repeat protein 19	NM_031309754, XCT2345111.0, hCT2345112.0, hCT2323237.0, hCT2323238.0	226277_at	NP_001091254.2, EAW62165.1, EAW62166.1, EAW62169.1, EAW62160.1
GeneID:83	ORAI3	19	30,960,403	30,966,359	5,634	+	4	1_A375_pfd27_minus1_lncRNA_R_1...2291, 2_A375_pfd27_plus_lncRNA_R_1...3225, 2_A375_pfd27_plus_lncRNA_R_1...3226, A_A375_EGR1...3092, A_A375_EGR1...3093	5715, 9115, 6639, 996.5	downstream, downstream, downstream, downstream, downstream	1	1	1	21	26.5	15.5	2	2_A375_pfd27_plus_lncRNA_R_1	45	Gene ORAI3	MGC13024, TMEM142C, ORAI3	ORAI calcium release-activated calcium modulator 3	NM_152288, XCT12246.0, hCT1997899.1	221984_at	NP_689501.1, EAW62163.1, EAW62166.1
GeneID:97	SETD1A	19	30,966,815	30,993,961	27,266	+	5	2_A375_pfd27_plus_lncRNA_R_1...3225, 2_A375_pfd27_plus_lncRNA_R_1...3226, 2_A375_pfd27_plus_lncRNA_R_1...3227, A_A375_EGR1...3092, A_A375_EGR1...3094	556, 936, 426, 1433, 27929	sr gene, sr gene, sr gene, sr gene, downstream	1	1	1	16.67	20.67	13.33	3	A_A375_EGR1	45	Gene SETD1A	KIAA0220, Set1, Setd1a, SETD1A, hSET2F	SET domain containing 1A	NM_014712	213202_at	NP_055127.1
GeneID:69	HSD3B7	19	30,996,519	31,000,473	3,954	+	1	A_A375_EGR1...3094	25	sr gene	0	0	1	14	9	15	1	A_A375_EGR1	15	Gene HSD3B7	HSD3B7, SDR11E3, PFKA	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	NM_031427?7, NM_001142772, NM_025192	222817_at	NP_001138249.1, NP_001139250.1, NP_079489.2
GeneID:11	SYT18	19	31,000,577	31,021,629	21,052	+	1	A_A375_EGR1...3094	23253	downstream	0	0	1	14	9	15	1	A_A375_EGR1	15	Gene SYT18	SYT18?, SYT18Z, SYT18	synotagmin 18	NM_052974, XCT12251.4	230981_at	NP_443106.1, EAW62176.1
GeneID:68	STX4	16	31,044,903	31,051,468	6,552	+	1	2_A375_pfd27_minus1_lncRNA_R_1...2272	2182	upstream	1	1	0	20	17	15	1	1_A375_pfd27_minus1_lncRNA_R_1	20	Gene STX4	STX4, STX4A, p35-2	syntaxin 4	NM_004604, XCT12235.3, hCT2352020.0, hCT2352021.0	203310_s_at, 238222_at	NP_004595.2, EAW62178.1, EAW62177.1
GeneID:79	ZNF865	19	31,072,164	31,083,941	10,477	+	4	2_A375_pfd27_plus_lncRNA_R_1...3225, 2_A375_pfd27_plus_lncRNA_R_1...3226, 2_A375_pfd27_plus_lncRNA_R_1...3227, A_A375_EGR1...3094, A_A375_EGR1...3095	666, 792, 12259, 53	sr gene, sr gene, sr gene, upstream	1	1	1	25	30	16	2	A_A375_EGR1	53	Gene ZNF865	FLJ14492, ZNF865, FLJ13479	zinc finger protein 865	NM_031305, NM_001172866, NM_001172867, NM_001172870, hCT12343.4, hCT2279741.0, hCT2419634.0	219047_s_at, 223513_at	NP_076992.2, NP_001158133.1, NP_001158140.1, NP_001158141.1, EAW62172.1, EAW62174.1, EAW62172.1
GeneID:39	ZNF648	19	31,085,743	31,094,823	9,080	+	3	2_A375_pfd27_plus_lncRNA_R_1...3227, 2_A375_pfd27_plus_lncRNA_R_1...3228, A_A375_EGR1...3096	-787, -893, 47	upstream, upstream, upstream	1	1	1	41	53	19	1	2_A375_pfd27_plus_lncRNA_R_1	53	Gene ZNF648	ZNF648, KIAA0298	zinc finger protein 648	NM_014999, XCT23404.0, hCT1442.3	204476_at	NP_055714.3, EAW62170.1, EAW62171.1
GeneID:33	POLS	19	31,094,743	31,100,100	5,358	+	3	2_A375_pfd27_plus_lncRNA_R_1...3227, 2_A375_pfd27_plus_lncRNA_R_1...3228, A_A375_EGR1...3096	19154, 13282, 14434	downstream, downstream, downstream	1	1	1	41	53	19	1	2_A375_pfd27_plus_lncRNA_R_1	53	Gene POLS	POLS5, FLJ38205, UNQ205, PRO535	polymerase S	NM_031035932	214226_at	NP_031034592.1
GeneID:19	BCAS4	20	31,116,862	31,124,112	7,250	+	2	2_A375_pfd27_plus_lncRNA_R_1...3227, A_A375_EGR1...3097	116, 76	sr gene, upstream	0	1	1	14	21	20	1	2_A375_pfd27_plus_lncRNA_R_1	21	Gene BCAS4	BCAS4		NM_030851, NM_001122897, XCT12311.3, hCT2260991.0, hCT2260993.0, hCT2323534.0, hCT2323535.0	202020_at	NP_036772.2, NP_001116429.1, EAW62161.1, EAW62162.1, EAW62163.1, EAW62164.1, EAW62182.1
GeneID:54	MYST1	16	31,126,935	31,142,714	15,779	+	2	2_A375_pfd27_plus_lncRNA_R_1...3227, A_A375_EGR1...3097	-9165, -9481	upstream, upstream	0	1	1	14	21	20	1	2_A375_pfd27_plus_lncRNA_R_1	21	Gene MYST1	MOF, FLJ14240, KAT8	MYST histone acetyltransferase 1	NM_032188, NM_182958, XCT12363.3, hCT2323539.0	214883_at, 221823_s_at	NP_115584.2, NP_872300.2, EAW62157.1, EAW62158.1
GeneID:10	LOC100390992	19	31,129,281	31,130,986	1,707	-	2	2_A375_pfd27_plus_lncRNA_R_1...3227, A_A375_EGR1...3097	-9901, -9997	upstream, upstream	0	1	1	14	21	20	1	2_A375_pfd27_plus_lncRNA_R_1	21	Gene LOC100390992		hypothetical LOC100390992	XR_111987, XR_109203, XR_114992		
GeneID:23	PLIS	19	31,191,431	31,206,192	14,761	+	3	2_A375_pfd27_plus_lncRNA_R_1...3224, 2_A375_pfd27_plus_lncRNA_R_1...3228, A_A375_EGR1...3096	-119, -103, 97	upstream, upstream, sr gene	1	1	1	20	27	20	1	2_A375_pfd27_plus_lncRNA_R_1	27	Gene PLIS	HRIHFB2, POHP75, PLIS, FLIS1, ALI56, TLS	lissencephaly 1 interacting protein 1	NM_004986, NM_033358, NM_001170377, NM_001170834, XCT12233.3, hCT2260991.0, hCT2323537.0	1565713_at, 1565716_at, 1565717_at, 209593_at, 211764_s_at, 213702_x_at, 231166_at	NP_004977.1, NP_001154493.1, NP_001154505.1, EAW62180.1, EAW62181.1, EAW62182.1
GeneID:49	TRMT2A	19	31,225,342	31,236,910	11,568	+	1	A_A375_EGR1...3099	2330	sr gene	0	0	1	8	15	22	1	A_A375_EGR1	22	Gene TRMT2A	MGS1, TRMT2	transfer RNA methyltransferase 2 homolog (S. cerevisiae)	NM_001002274, XCT23451110.0, hCT2323536.0, hCT2323537.0	1554603_s_at	NP_001002743.2, EAW62145.1, EAW62145.1
GeneID:26	PYDC1	19	31,227,265	31,229,996	1,315	+	1	A_A375_EGR1...3099	526	sr gene	0	0	1	8	15	22	1	A_A375_EGR1	22	Gene PYDC1	MGC2, PYDC1, PYC1, PGP1	PYD (pyrin and DCC domain) containing 1	NM_152901, XCT1647314.2	243722_at	NP_690865.1, EAW62147.1
GeneID:10	LOC100390995	19	31,442,796	31,493,400	22,604	+	4	1_A375_pfd27_minus1_lncRNA_R_1...2295, 2_A375_pfd27_plus_lncRNA_R_1...3229, 2_A375_pfd27_plus_lncRNA_R_1...3230, 2_A375_pfd27_plus_lncRNA_R_1...3231, A_A375_EGR1...3100	-9485, 10592, -9304, -5224	upstream, sr gene, upstream, upstream	1	1	1	17.5	23	23.5	2	A_A375_EGR1	31	Gene LOC100390995		hypothetical LOC100390995	XR_111985, XR_109206, XR_114992		
GeneID:26	ZNF843	19	31,449,955	31,454,345	7,493	-	1	2_A375_pfd27_plus_lncRNA_R_1...3229	-100	upstream	0	0	1	17	26	12	1	2_A375_pfd27_plus_lncRNA_R_1	26	Gene ZNF843	ZNF843, MGC40338	zinc finger protein 843	NM_031136939	1553070_at, 1564382_x_at	NP_001129691.1
GeneID:79	ARMC3	19	31,470,317	31,478,468	8,171	+	4	1_A375_pfd27_minus1_lncRNA_R_1...2295, 2_A375_pfd27_plus_lncRNA_R_1...3230, A_A375_EGR1...3100, 4_A375_EGR1...3101	946, 587, 937, 7459	sr gene, sr gene, sr gene, sr gene	1	1	1	11.5	13.5	24.5	2	A_A375_EGR1	31	Gene ARMC3	ARMC3, FLJ90019, FLJ10965	armadillo repeat containing 3	NM_024742, NM_001103247, XCT10394.2, hCT2260942.1, hCT2323533.0	227758_s_at	NP_079016.1, NP_001097717.1, EAW62131.1, EAW62132.1, EAW62133.1
GeneID:30	TGFBI	5	31,483,476	31,489,261	5,803	+	1	A_A375_EGR1...3101	-5705	upstream	0	0	1	5	7	16	1	A_A375_EGR1	16	Gene TGFBI	TGFBI, TGC-5, BIGH3, RE-S, ARAS5, MCD	transforming growth factor beta 1 induced transcript 1	NM_000327, NM_001043434, NM_001164719, hCT10579.2, hCT2260945.1, hCT2345955.0, hCT2345960.0, hCT2323529.0	203851_at	NP_000318.2, NP_001035910.1, NP_001158191.1, EAW62125.1, EAW62126.1, EAW62127.1, EAW62128.1
GeneID:84	C16orf58	16	31,500,610	31,519,708	19,098	-	2	2_A375_pfd27_plus_lncRNA_R_1...3231, A_A375_EGR1...3102	585, -102	sr gene, upstream	0	1	1	14	27	19	1	2_A375_pfd27_plus_lncRNA_R_1	27	Gene C16orf58	C16orf58, FLJ13986	chromosome 16 open reading frame 58	NM_032742, XCT12362.2, hCT1651456.1, hCT2323539.0, hCT2323540.0	217891_at, 222190_s_at	NP_076351.2, EAW62121.1, EAW62119.1, EAW62120.1, EAW62122.1
GeneID:10	LOC100390997	19	31,711,934	31,716,756	4,824	+	1	A_A375_EGR1...3103	12706	downstream	0	0	1	11	9	16	1	A_A375_EGR1	16	Gene C16orf87	MGC3030, KIAA0894-PS, FLJ35155, C16orf87, MGC31612, KIAA0894-L2	KIAA0894 pseudogene 2	NR_024054		
GeneID:12	ZNF720	19	31,724,550	31,772,668	48,038	+	1	A_A375_EGR1...3103	90	sr gene	0	0	1	11	9	16	1	A_A375_EGR1	16	Gene ZNF720	ZNF720, MGC39315, MGC26319	zinc finger protein 720	NM_031339?3, XCT10366?5.1, XCT1650?7.1, hCT2323536.0	235510_at, 242091_at	NP_001124355.1, EAW62110.1, EAW62109.1, EAW62109.1
GeneID:10	ZNF287	19	31,855,079	31,928,827	43,348	+	1	A_A375_EGR1...3104	283	sr gene	0	0	1	11	12	17	1	A_A375_EGR1	17	Gene ZNF287	ZNF287, HZF2	zinc finger protein 287	NM_032414, XCT2067.3	219940_at	NP_115803.3, EAW62108.1
GeneID:40	LOC401547	19	33,869,864	33,869,778	86,914	+	1	A_A375_EGR1...3112	286	sr gene	0	0	1	9	12	20	1	A_A375_EGR1	20	Gene LOC401547		hypothetical protein LOC401547	XM_001716194, XM_003120849		XP_001716196.3, XP_003120997.1
GeneID:10	LOC100390700	19	34,239,436	34,240,840	1,352	-	1	A_A375_EGR1...3116	-824	upstream	0	0	1	8	8	14	1	A_A375_EGR1	14	Gene LOC100390700		hypothetical protein LOC100390700	NR_026010, NR_034019		
GeneID:79	SHCBP1	16	46,814,486	46,855,311	40,825	-	1	A_A375_EGR1...3121	79	sr gene	0	0	1	12	13	25	1	A_A375_EGR1	25	Gene SHCBP1	FLJ23300, MGC29930, PAL, SHCBP1	SHC SH2-domain binding protein 1	NM_024745, XCT1654?01.1, hCT2323580.0	219489_at	NP_079021.2, EAW62660.1, EAW62661.1
GeneID:55	VPS35	16	46,855,369	46,925,144	69,855	+	1	2_A375_pfd27_plus_lncRNA_R_1...3233	-445	upstream	0	1	0	11	23	13	1	2_A375_pfd27_plus_lncRNA_R_1	23	Gene VPS35	FLJ25355, DKFZp434E121, FLJ10355, FLJ10762, VPS35, DKFZp434P167, MEM3	vacuolar protein sorting 35 (yeast)	NM_018206, XCT23360.0, hCT23864.2	1561148_at, 217727_x_at, 222307_s_at, 222308_s_at, 224384_s_at	NP_060676.2, EAW62664.1, EAW62663.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:23594	ORC6L	16	46,723,558	46,732,306	8,748	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3233	26	in gene	0	1	0	11	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ORC6L	ORC6, ORC6L	origin recognition complex, subunit 6	NM_014321, hCT2323677.0, hCT23557.2	219105_x_at	NP_055136.1, EAW82686.1, EAW82685.1
GeneID:84706	GPT2	16	46,918,306	46,965,201	46,893	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2277, 2_A375_pNL97_plus_lncRNA_AR..1..3235	-356, -212	upstream, upstream	1	1	0	16	23	16	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene GPT2	ALT2, GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	NM_133443, NM_001142466, hCT14429.2, hCT1954784.1, hCT2356338.0	224839_s_at	NP_597700.1, NP_001135938.1, EAW82690.1, EAW82691.1, EAW82692.1
GeneID:81533	ITFG1	16	47,189,297	47,495,018	305,721	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3236	-66	upstream	0	1	0	13	15	11	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene ITFG1	CDA08, TIP, ITFG1	integrin alpha FG-GAP repeat containing 1	NM_030790, hCT1953950.1, hCT2323638.0	1558151_at, 221449_s_at, 239044_at	NP_110417.2, EAW82698.1, EAW82699.1
GeneID:5257	PHKB	16	47,495,210	47,735,434	240,224	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3236	-106	upstream	0	1	0	13	15	11	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene PHKB	DKFZp781E15103, FLJ41698, PHKB	phosphorylase kinase, beta	NM_000293, NM_001031835, hCT14783.2, hCT2323663.0	202738_s_at, 202739_s_at, 242246_at	NP_000284.1, NP_001027005.1, EAW82700.1, EAW82701.1
GeneID:94160	ABCC12	16	48,116,884	48,180,681	63,797	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2280, 2_A375_pNL97_plus_lncRNA_AR..1..3239, 2_A375_pNL97_plus_lncRNA_AR..1..3240, 4_A375_EGR1..1..3126	19625, 64969, 23465, 31289	in gene, downstream, in gene, in gene	1	1	1	14.75	17	12.5	4	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene ABCC12	MRP9, MGC27071, ABCC12	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	NM_033226, hCT1954616.1, hCT1971679.0, hCT1971680.1, hCT2323933.0, hCT2356367.0, hCT2356368.0, hCT2356369.0, hCT2356370.0, hCT2356371.0, hCT2356372.0	1552590_a_at, 1553410_a_at	NP_150229.2, EAW82710.1, EAW82705.1, EAW82711.1, EAW82712.1, EAW82714.1, EAW82706.1, EAW82707.1, EAW82708.1, EAW82709.1, EAW82713.1
GeneID:85320	ABCC11	16	48,200,822	48,269,088	68,266	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2281, 2_A375_pNL97_plus_lncRNA_AR..1..3241	-9184, -9184	upstream, upstream	1	1	0	23	29	11	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene ABCC11	MRP8, WW, EWWD, ABCC11	ATP-binding cassette, sub-family C (CFTR/MRP), member 11	NM_033151, NM_032583, NM_145186, hCT1954776.1, hCT1954777.0, hCT2323924.0, hCT2323925.0, hCT2323926.0, hCT2323927.0, hCT2356359.0, hCT2356360.0	1554911_at, 224146_s_at	NP_149163.2, NP_115972.2, NP_660187.1, EAW82716.1, EAW82720.1, EAW82721.1, EAW82715.1, EAW82717.1, EAW82718.1, EAW82719.1, EAW82722.1
GeneID:83752	LONP2	16	48,278,211	48,387,407	109,196	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2281, 2_A375_pNL97_plus_lncRNA_AR..1..3241	61, 61	in gene, in gene	1	1	0	23	29	11	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene LONP2	LONP2, MGC4840, LONPL, LONP	lon peptidase 2, peroxisomal	NM_031490, hCT14766.3, hCT2323568.1, hCT2356362.0	221833_at, 221834_at, 223098_s_at, 223099_s_at, 229663_at	NP_113678.2, EAW82724.1, EAW82723.1, EAW82725.1
GeneID:23090	ZNF423	16	49,524,521	49,860,918	336,397	-	3	4_A375_EGR1..1..3127, 4_A375_EGR1..1..3128, 4_A375_EGR1..1..3129	225302, 195286, 9050	in gene, in gene, upstream	0	0	1	3.33	5	15.67	3	4_A375_EGR1..1	17	Gene ZNF423	OAZ, Zfp104, Roaz, MGC138520, ZFP423, KIAA0760, Ebfaz, ZNF423, MGC138522	zinc finger protein 423	NM_015069, hCT1953959.2	214761_at	NP_055884.2, EAW82735.1
GeneID:255919	TMEM188	16	50,059,189	50,070,999	11,810	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2284, 2_A375_pNL97_plus_lncRNA_AR..1..3246	-213, -161	upstream, upstream	1	1	0	69	66	13	1	1_A375_pNL7_minus_lncRNA_AR..1	69	Gene TMEM188	TMEM188, FLJ38101, DKFZp313D2416, TMP125, C16orf69	transmembrane protein 188	NM_153261, hCT1953966.2, hCT2344801.0, hCT2344802.0, hCT2356310.0	235812_at	NP_694993.2, EAW82739.1, EAW82738.1, EAW82740.1, EAW82741.1
GeneID:100505486	LOC100505486	16	50,134,250	50,186,967	52,717	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2285, 2_A375_pNL97_plus_lncRNA_AR..1..3247	87, 119	in gene, in gene	1	1	0	18	17	10	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100505486		hypothetical LOC100505486	XR_109296, XR_109295		
GeneID:64282	PAPD5	16	50,186,829	50,269,221	82,392	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2285, 2_A375_pNL97_plus_lncRNA_AR..1..3247	51, 19	in gene, in gene	1	1	0	18	17	10	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene PAPD5	FLJ40270, TRF4-2, PAPD5	PAP associated domain containing 5	NM_001040284, NM_001040285, hCT16012.3, hCT2323958.0, hCT2323960.0, hCT2323962.0	226643_s_at, 229043_at	NP_001035374.2, NP_001035375.2, EAW82747.1, EAW82748.1, EAW82749.1, EAW82750.1
GeneID:113	ADCY7	16	50,321,823	50,352,043	30,220	+	2	4_A375_EGR1..1..3132, 4_A375_EGR1..1..3133	3960, 9669	in gene, in gene	0	0	1	8	8	17	2	4_A375_EGR1..1	20	Gene ADCY7	KIAA0037, ADCY7, FLJ36387, AC7	adenylate cyclase 7	NM_001114, hCT16015.4, hCT1953963.1, hCT2343774.0	1554627_a_at, 203741_s_at	NP_001105.1, EAW82755.1, EAW82753.1, EAW82754.1
GeneID:85407	NKD1	16	50,582,241	50,668,641	86,400	+	1	4_A375_EGR1..1..3134	663	in gene	0	0	1	8	8	16	1	4_A375_EGR1..1	16	Gene NKD1	Naked1, NKD1	naked cuticle homolog 1 (Drosophila)	NM_033119, hCT15425.3	1553115_at	NP_149110.1, EAW82761.1
GeneID:1540	CYLD	16	50,775,961	50,835,846	59,885	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3248	64467	downstream	0	1	0	14	17	4	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene CYLD	FLJ31664, KIAA0849, TEM, MFT1, CDMT, USPL2, MFT, FLJ78684, EAC, FLJ20180, CYLD, CYLD1, SBS, HSPC057, CYLDI	cylindromatosis (turban tumor syndrome)	NM_015247, NM_001042355, NM_001042412, hCT1953955.1, hCT2323945.0, hCT2323946.0, hCT2323948.0, hCT2356304.0, hCT2356305.0	213295_at, 214272_at, 221903_s_at, 221905_at, 222142_at, 39582_at, 60084_at	NP_056062.1, NP_001035814.1, NP_001035877.1, EAW82768.1, EAW82769.1, EAW82773.1, EAW82770.1, EAW82771.1, EAW82772.1
GeneID:27324	TOX3	16	52,471,918	52,581,714	109,796	-	1	4_A375_EGR1..1..3135	67666	in gene	0	0	1	6	5	14	1	4_A375_EGR1..1	14	Gene TOX3	TOX3, TNRC9, CAGF9	TOX high mobility group box family member 3	NM_001080430, NM_001146188	214774_x_at, 215108_x_at, 216623_x_at, 230745_s_at	NP_001073899.2, NP_001139660.1
GeneID:80205	CHD9	16	53,088,945	53,361,414	272,469	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2288, 2_A375_pNL97_plus_lncRNA_AR..1..3252, 2_A375_pNL97_plus_lncRNA_AR..1..3253, 2_A375_pNL97_plus_lncRNA_AR..1..3254, 4_A375_EGR1..1..3138	44047, -177, 75807, 76847, -241	in gene, upstream, in gene, in gene, upstream	1	1	1	13.5	17.25	11.25	4	4_A375_EGR1..1	22	Gene CHD9	KISH2, CHD9, AD013, PRIC320, CReMM	chromodomain helicase DNA binding protein 9	NM_025134, hCT2324359.0, hCT2324360.0, hCT2324361.1, hCT2324363.0, hCT2324364.0, hCT2324367.1	212615_at, 212616_at, 220586_at, 229586_at, 235388_at, 239654_at, 240387_at, 243680_at	NP_079410.4, EAW82793.1, EAW82794.1, EAW82795.1, EAW82796.1, EAW82797.1, EAW82798.1
GeneID:643802	LOC643802	16	53,404,183	53,404,901	718	-	1	4_A375_EGR1..1..3139	-2715	upstream	0	0	1	5	6	17	1	4_A375_EGR1..1	17	Gene LOC643802		similar to M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	XM_001716660, XM_001719265, XM_001716409		XP_001716912.2, XP_001719317.2, XP_001716461.2
GeneID:5934	RBL2	16	53,468,351	53,525,560	57,209	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2289, 2_A375_pNL97_plus_lncRNA_AR..1..3255	33, 321	in gene, in gene	1	1	0	22	18	13	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene RBL2	RBL2, FLJ26459, Rb2, P130	retinoblastoma-like 2 (p130)	NM_005611, hCT2324373.0, hCT2324374.0	212331_at, 212332_at	NP_005602.3, EAW82801.1, EAW82802.1
GeneID:64400	AKTIP	16	53,525,192	53,537,170	11,978	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2290	-382	upstream	1	0	0	16	18	14	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene AKTIP	FTS, FT1, AKTIP	AKT interacting protein	NM_022476, NM_001012398, hCT2324415.0, hCT2324416.0, hCT2324417.0, hCT2324418.0, hCT2324419.0, hCT2324420.0, hCT2356380.0	218373_at, 223894_s_at	NP_071921.1, NP_001012398.1, EAW82805.1, EAW82807.1, EAW82808.1, EAW82809.1, EAW82803.1, EAW82804.1, EAW82806.1
GeneID:23322	RPGRIP1L	16	53,633,818	53,737,771	103,953	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3256	-37	upstream	0	1	0	17	23	11	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RPGRIP1L	JBTS7, CORS3, MKS5, NPHP8, KIAA1005, RPGRIP1L, FTM, DKFZp686C0668	RPGRIP1-like	NM_015272, NM_001127897, hCT14561.2	213959_s_at	NP_056087.2, NP_001121369.1, EAW82810.1
GeneID:79068	FTO	16	53,737,875	54,148,379	410,504	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3256, 1_A375_pNL7_minus_lncRNA_AR..1..2291, 2_A375_pNL97_plus_lncRNA_AR..1..3257	-67, 376665, 376665	upstream, in gene, in gene	1	1	0	17	20.5	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene FTO	FTO, KIAA1752, MGC5149	fat mass and obesity associated	NM_001080432	209702_at	NP_001073901.1
GeneID:79191	IRX3	16	54,317,212	54,320,378	3,166	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2292, 2_A375_pNL97_plus_lncRNA_AR..1..3258, 4_A375_EGR1..1..3140	-726, 626, -742	upstream, in gene, upstream	1	1	1	12.5	13	13	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene IRX3	IRX3, IRX-1, FLJ99187, IRXB1	iroquois homeobox 3	NM_024336, hCT14563.4, hCT2346062.0	229638_at	NP_077312.2, EAW82815.1, EAW82814.1
GeneID:4313	MMP2	16	55,513,081	55,540,586	27,505	+	1	4_A375_EGR1..1..3142	423	in gene	0	0	1	7	14	20	1	4_A375_EGR1..1	20	Gene MMP2	MMP-II, CLG4, CLG4A, TBE-1, MONA, MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	NM_004530, NM_001127891, hCT15262.3, hCT1953066.1, hCT1953067.1, hCT1953068.0, hCT1953069.1	1566677_at, 1566678_at, 201069_at	NP_004521.1, NP_001121363.1, EAW82824.1, EAW82825.1, EAW82826.1, EAW82828.1, EAW82827.1
GeneID:54947	LPCAT2	16	55,542,913	55,620,582	77,669	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2293	30111	in gene	1	0	0	18	5	0	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LPCAT2	DKFZp686H22112, LysoPAFAT, AYTL1, LPCAT2, FLJ20481	lysophosphatidylcholine acyltransferase 2	NM_017839, hCT1780935.2	222833_at, 227889_at, 229791_at, 239598_s_at	NP_060309.2, EAW82829.1
GeneID:2775	GNAO1	16	56,225,251	56,391,356	166,105	+	2	4_A375_EGR1..1..3143, 4_A375_EGR1..1..3144	159218, 162205	in gene, in gene	0	0	1	3.5	7	17.5	2	4_A375_EGR1..1	22	Gene GNAO1	G-ALPHA-o, GNAO, DKFZp686O0962, GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	NM_020988, NM_138736, hCT15260.3, hCT1954528.1	204762_s_at, 204763_s_at, 215912_at, 231951_at	NP_066268.1, NP_620073.2, EAW82849.1, EAW82850.1
GeneID:267	AMFR	16	56,395,364	56,459,444	64,080	-	1	4_A375_EGR1..1..3144	71988	downstream	0	0	1	5	9	22	1	4_A375_EGR1..1	22	Gene AMFR	RNF45, GP78, AMFR	autocrine motility factor receptor	NM_001144	202203_s_at, 202204_s_at	NP_001135.3
GeneID:11051	NUDT21	16	56,463,048	56,485,261	22,213	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3262	65	in gene	0	1	0	14	14	15	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene NUDT21	CPSF5, DKFZp686H1588, CFIM25, NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	NM_007006, hCT15025.3, hCT2324618.0	202697_at, 213461_at, 224830_at	NP_008937.1, EAW82859.1, EAW82860.1
GeneID:55239	OGFOD1	16	56,485,424	56,511,407	25,983	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3262	-246	upstream	0	1	0	14	14	15	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene OGFOD1	TPA1, OGFOD1, FLJ10826, KIAA1612	2-oxoglutarate and iron-dependent oxygenase domain containing 1	NM_018233, hCT15023.3, hCT2324045.0	221090_s_at, 225106_s_at, 225110_at, 241739_at	NP_060703.3, EAW82861.1, EAW82862.1
GeneID:583	BBS2	16	56,518,259	56,554,008	35,749	-	1	4_A375_EGR1..1..3145	424	in gene	0	0	1	14	13	16	1	4_A375_EGR1..1	16	Gene BBS2	MGC20703, BBS2, BBS	Bardet-Biedl syndrome 2	NM_031885, hCT1962505.1, hCT1962506.1	223227_at	NP_114091.3, EAW82864.1, EAW82863.1
GeneID:4504	MT3	16	56,623,267	56,625,000	1,733	+	1	4_A375_EGR1..1..3146	349	in gene	0	0	1	11	10	17	1	4_A375_EGR1..1	17	Gene MT3	MT3, GIF, GIFB, GRIF	metallothionein 3	NM_005954, hCT15015.3, hCT1828894.3, hCT2344692.0	205970_at	NP_005945.1, EAW82866.1, EAW82867.1, EAW82868.1
GeneID:4502	MT2A	16	56,642,478	56,643,409	931	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3263, 2_A375_pNL97_plus_lncRNA_AR..1..3264	-1198, -14	upstream, upstream	0	1	0	13.5	20.5	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene MT2A	MT2, MT2A	metallothionein 2A	NM_005953, hCT2324056.0, hCT2345305.1	212185_x_at	NP_005944.1, EAW82869.1, EAW82870.1
GeneID:4489	MT1A	16	56,672,578	56,673,999	1,421	+	1	4_A375_EGR1..1..3147	9374	downstream	0	0	1	4	4	22	1	4_A375_EGR1..1	22	Gene MT1A	MT1A, MT1, MT1S, MGC32848, MTC	metallothionein 1A	NM_005946		NP_005937.2
GeneID:4490	MT1B	16	56,685,811	56,687,116	1,305	+	2	4_A375_EGR1..1..3147, 4_A375_EGR1..1..3148	-3859, 11181	upstream, downstream	0	0	1	2.5	4.5	18.5	2	4_A375_EGR1..1	22	Gene MT1B	MT1B, MTP, MT1Q, MT1	metallothionein 1B	NM_005947, hCT1828695.2		NP_005938.1, EAW82880.1
GeneID:4494	MT1F	16	56,691,855	56,693,215	1,360	+	2	4_A375_EGR1..1..3147, 4_A375_EGR1..1..3148	-9903, 5137	upstream, downstream	0	0	1	2.5	4.5	18.5	2	4_A375_EGR1..1	22	Gene MT1F	MT1F, MT1, MGC32732	metallothionein 1F	NM_005949, hCT1828424.2	213629_x_at, 217165_x_at	NP_005940.1, EAW82881.1
GeneID:4495	MT1G	16	56,700,653	56,701,977	1,324	-	1	4_A375_EGR1..1..3148	4985	downstream	0	0	1	1	5	15	1	4_A375_EGR1..1	15	Gene MT1G	MT1, MT1G, MT1K, MGC12386	metallothionein 1G	NM_005950, hCT15016.2, hCT1961614.1	204745_x_at, 210472_at	NP_005941.1, EAW82883.1, EAW82882.1
GeneID:4496	MT1H	16	56,703,726	56,705,041	1,315	+	1	4_A375_EGR1..1..3148	-6734	upstream	0	0	1	1	5	15	1	4_A375_EGR1..1	15	Gene MT1H	MT1H, MT1, MGC70702	metallothionein 1H	NM_005951, hCT2324066.0	206461_x_at	NP_005942.1, EAW82884.1
GeneID:100505742	LOC100505742	16	56,743,137	56,763,980	20,843	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2295, 4_A375_EGR1..1..3149	-244, -148	upstream, upstream	1	0	1	18	14	18	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100505742		hypothetical LOC100505742	XR_109305		
GeneID:9688	NUP93	16	56,764,017	56,878,877	114,860	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2295, 4_A375_EGR1..1..3149	207, 111	in gene, in gene	1	0	1	18	14	18	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene NUP93	NUP93, MGC21106, KIAA0095	nucleoporin 93kDa	NM_014669, hCT15014.3	202188_at	NP_055484.3, EAW82887.1
GeneID:9709	HERPUD1	16	56,965,748	56,977,793	12,045	+	1	4_A375_EGR1..1..3150	422	in gene	0	0	1	16	22	17	1	4_A375_EGR1..1	17	Gene HERPUD1	KIAA0025, Mif1, HERP, HERPUD1, SUP	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	NM_014685, NM_001010989, NM_001010990, hCT15021.2, hCT1954522.1, hCT2356365.0	217168_s_at	NP_055500.1, NP_001010989.1, NP_001010990.1, EAW82892.1, EAW82893.1, EAW82894.1
GeneID:84166	NLRC5	16	57,023,410	57,117,436	94,026	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2296	11134	in gene	1	0	0	21	11	17	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene NLRC5	CLR16.1, NLRC5, NOD4, NOD27, FLJ21709, FLJ39711	NLR family, CARD domain containing 5	NM_032206, hCT15019.3, hCT2324079.0, hCT2324082.0, hCT2324083.0, hCT2324084.0	226474_at	NP_115582.3, EAW82902.1, EAW82898.1, EAW82899.1, EAW82900.1, EAW82901.1
GeneID:89970	RSPRY1	16	57,220,241	57,272,950	52,709	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2297, 2_A375_pNL97_plus_lncRNA_AR..1..3265	58575, 58607	downstream, downstream	1	1	0	29	25	14	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene RSPRY1	RSPRY1, KIAA1972	ring finger and SPRY domain containing 1	NM_133368, hCT15020.3, hCT2356361.0, hCT2356362.0	225770_at, 225773_at, 225774_at	NP_588609.1, EAW82911.1, EAW82909.1, EAW82910.1
GeneID:23568	ARL2BP	16	57,279,038	57,287,545	8,507	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2297, 2_A375_pNL97_plus_lncRNA_AR..1..3265	-222, -190	upstream, upstream	1	1	0	29	25	14	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene ARL2BP	BART1, ARL2BP, BART	ADP-ribosylation factor-like 2 binding protein	NM_012106, hCT15011.2, hCT1961615.1	202091_at, 202092_s_at	NP_036238.1, EAW82913.1, EAW82914.1
GeneID:6367	CCL22	16	57,392,695	57,400,102	7,407	+	1	4_A375_EGR1..1..3152	13705	downstream	0	0	1	12	10	18	1	4_A375_EGR1..1	18	Gene CCL22	MDC, A-152E5.1, SCYA22, STCP-1, ABCD-1, CCL22, MGC34554, DC/B-CK	chemokine (C-C motif) ligand 22	NM_002990, hCT7517.2	207861_at	NP_002981.2, EAW82918.1
GeneID:6376	CX3CL1	16	57,406,414	57,418,956	12,542	+	1	4_A375_EGR1..1..3152	-14	upstream	0	0	1	12	10	18	1	4_A375_EGR1..1	18	Gene CX3CL1	NTN, NTT, SCYD1, neurotactin, CXC3, CX3CL1, fractalkine, C3Xkine, ABCD-3, CXC3C	chemokine (C-X3-C motif) ligand 1	NM_002996, hCT6126.2	203687_at, 823_at	NP_002987.1, EAW82919.1
GeneID:57019	CIAPIN1	16	57,462,086	57,481,369	19,283	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2298, 2_A375_pNL97_plus_lncRNA_AR..1..3267	-39, -215	upstream, upstream	1	1	0	20	17	14	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene CIAPIN1	PRO0915, Anamorsin, 2810413N20Rik, DRE2, CIAPIN1	cytokine induced apoptosis inhibitor 1	NM_020313, hCT1960342.1, hCT1960343.1, hCT7536.2	208424_s_at, 208968_s_at	NP_064709.2, EAW82922.1, EAW82923.1, EAW82924.1

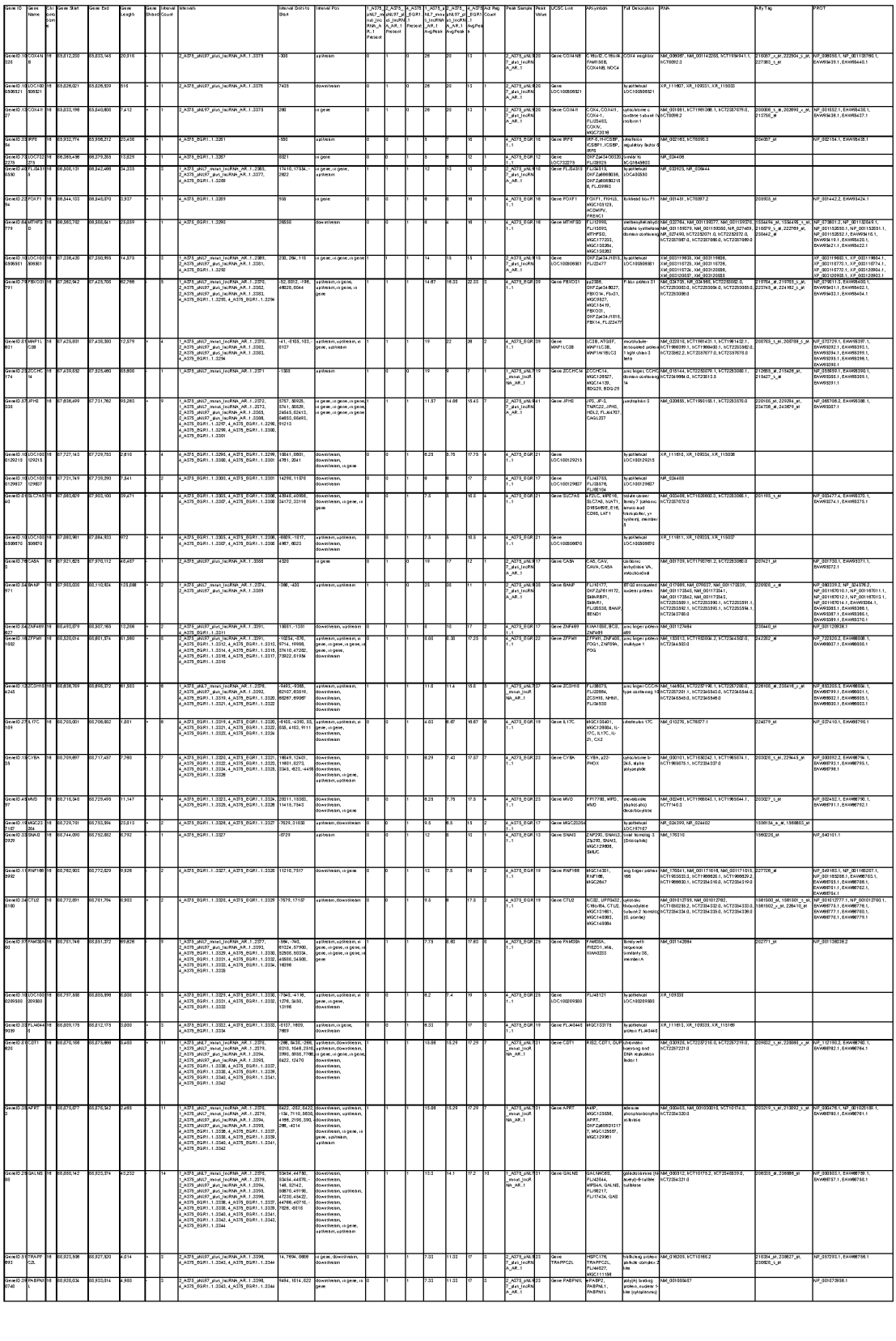
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.57017	COQ9	16	57,481,349	57,495,187	13,838	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2298, 1_A375_pNL7_minus_lncRNA_AR..1..2299, 2_A375_pNL97_plus_lncRNA_AR..1..3267, 2_A375_pNL97_plus_lncRNA_AR..1..3268, 4_A375_EGR1..1..3153	59, 15163, 235, 15211, 15259	in gene, downstream, in gene, downstream, downstream	1	1	1	46	48.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene COQ9	COQ9, DKFZp434K046, C16orf49	coenzyme Q9 homolog (S. cerevisiae)	NM_020312	212226_s_at, 235622_at	NP_064708.1
GeneID.5432	POLR2C	16	57,496,551	57,505,921	9,370	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2299, 2_A375_pNL97_plus_lncRNA_AR..1..3268, 4_A375_EGR1..1..3153	-39, 9, 57	upstream, in gene, in gene	1	1	1	72	80	20	1	2_A375_pNL97_plus_lncRNA_AR..1	80	Gene POLR2C	RPB31, hsRPB3, hRPB33, RPB3, POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	NM_032940	208996_s_at, 214263_x_at, 216282_x_at	NP_116558.1
GeneID.55715	DOK4	16	57,505,870	57,520,385	14,515	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2299, 2_A375_pNL97_plus_lncRNA_AR..1..3268, 4_A375_EGR1..1..3153	23873, 23825, 23777	downstream, downstream, downstream	1	1	1	72	80	20	1	2_A375_pNL97_plus_lncRNA_AR..1	80	Gene DOK4	FLJ10488, DOK4	docking protein 4	NM_018110, hCT1960339.1, hCT1960340.1, hCT7527.2	207747_s_at, 209690_s_at, 209691_s_at	NP_060580.2, EAW82933.1, EAW82932.1, EAW82934.1
GeneID.9289	GPR56	16	57,653,910	57,698,944	45,034	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2300, 2_A375_pNL97_plus_lncRNA_AR..1..3269, 4_A375_EGR1..1..3154, 4_A375_EGR1..1..3155	14186, 3738, -3542, 8536	in gene, in gene, upstream, in gene	1	1	1	14.5	15.75	12.25	4	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene GPR56	BFPP, GPR56, TM7XN1, TM7LN4, DKFZp781L1398	G protein-coupled receptor 56	NM_005682, NM_201524, NM_201525, NM_001145770, NM_001145771, NM_001145772, NM_001145773, NM_001145774, hCT1953763.2, hCT1960337.2, hCT2324578.1, hCT2351963.0, hCT2351964.0, hCT2351965.0, hCT7520.3	206582_s_at, 212070_at	NP_005673.3, NP_958932.1, NP_001139242.1, NP_001139243.1, NP_001139244.1, NP_958933.1, NP_001139245.1, NP_001139246.1, EAW82939.1, EAW82940.1, EAW82941.1, EAW82942.1, EAW82943.1, EAW82944.1, EAW82945.1
GeneID.10300	KATNB1	16	57,769,660	57,791,162	21,502	+	1	4_A375_EGR1..1..3156	27060	downstream	0	0	1	8	7	18	1	4_A375_EGR1..1	18	Gene KATNB1	KAT, KATNB1	katanin p80 (WD repeat containing) subunit B 1	NM_005886, hCT1808831.1, hCT2324590.0, hCT7526.3	203162_s_at, 203163_at, 229077_at	NP_005877.2, EAW82951.1, EAW82950.1, EAW82952.1
GeneID.3801	KIFC3	16	57,792,129	57,836,439	44,310	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3270, 4_A375_EGR1..1..3156, 4_A375_EGR1..1..3157	-297, 39719, 26775	upstream, in gene, in gene	0	1	1	9.67	14.33	15	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene KIFC3	KIFC3, FLJ34694, DKFZp686D23201	kinesin family member C3	NM_005550, NM_001130099, NM_001130100, hCT1953760.1, hCT1953776.1, hCT2356296.0, hCT7529.3	209681_at	NP_005541.3, NP_001123571.1, NP_001123572.1, EAW82953.1, EAW82954.1, EAW82955.1, EAW82956.1
GeneID.388282	LOC388282	16	57,844,549	57,850,831	6,282	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3270	-7613	upstream	0	1	0	16	24	10	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LOC388282		hypothetical LOC388282	XR_111562, XR_109306, XR_115276		
GeneID.79650	C16orf57	16	58,035,305	58,055,522	20,217	+	1	4_A375_EGR1..1..3158	25615	downstream	0	0	1	14	16	18	1	4_A375_EGR1..1	18	Gene C16orf57	PN, HVSL1, C16orf57, FLJ13154	chromosome 16 open reading frame 57	NM_024598, hCT1953777.1, hCT1953780.1, hCT7531.1	1554016_a_at, 1554119_at, 218060_s_at	NP_078874.2, EAW82962.1, EAW82963.1, EAW82964.1
GeneID.4324	MMP15	16	58,059,282	58,080,805	21,523	+	1	4_A375_EGR1..1..3158	1836	in gene	0	0	1	14	16	18	1	4_A375_EGR1..1	18	Gene MMP15	SMCP-2, MMP15, MTMMP2, MT2-MMP	matrix metallopeptidase 15 (membrane-inserted)	NM_002428, hCT2324601.0, hCT7522.1	203365_s_at, 243683_at	NP_002419.1, EAW82966.1, EAW82965.1
GeneID.29105	C16orf80	16	58,147,498	58,163,298	15,800	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3271	-85	upstream	0	1	0	15	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene C16orf80	GTL3, EVORF, ISAP23, C16orf80	chromosome 16 open reading frame 80	NM_013242, hCT7523.1	217957_at	NP_037374.1, EAW82967.1
GeneID.1459	CSNK2A2	16	58,191,811	58,231,782	39,971	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2301, 2_A375_pNL97_plus_lncRNA_AR..1..3272	-250, -234	upstream, upstream	1	1	0	26	28	9	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene CSNK2A2	CSNK2A2, CK2A2, FLJ43934, CSNK2A1	casein kinase 2, alpha prime polypeptide	NM_001896, hCT7524.2	203575_at, 224922_at	NP_001887.1, EAW82969.1
GeneID.64785	GINS3	16	58,426,298	58,440,048	13,750	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2302, 2_A375_pNL97_plus_lncRNA_AR..1..3273	70, 70	in gene, in gene	1	1	0	51	74	16	1	2_A375_pNL97_plus_lncRNA_AR..1	74	Gene GINS3	FLJ13912, PSF3, GINS3	GINS complex subunit 3 (Psf3 homolog)	NM_022770, NM_001126129, NM_001126130, hCT1953764.1, hCT1953765.1, hCT2323890.0, hCT8127.3	218719_s_at, 45633_at	NP_073607.2, NP_001119601.1, NP_001119602.1, EAW82973.1, EAW82975.1, EAW82976.1, EAW82974.1
GeneID.85009	NDRG4	16	58,497,549	58,547,523	49,974	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3274, 4_A375_EGR1..1..3160, 4_A375_EGR1..1..3161	51923, 37683, 51603	downstream, in gene, downstream	0	1	1	12.5	16	18	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene NDRG4	SMAP-8, KIAA1180, DKFZp686I1615, NDRG4, FLJ30586, FLJ42011, MGC19632	NDRG family member 4	NM_020465, NM_001130487, NM_022910, hCT1953766.1, hCT1953767.1, hCT6989.3	209159_s_at	NP_065198.1, NP_001123959.1, NP_075061.1, EAW82977.1, EAW82978.1, EAW82979.1
GeneID.100505804	LOC100505804	16	58,534,047	58,536,141	2,094	+	1	4_A375_EGR1..1..3160	1185	in gene	0	0	1	8	10	19	1	4_A375_EGR1..1	19	Gene LOC100505804		hypothetical LOC100505804	XR_109308		
GeneID.79918	SETD6	16	58,549,383	58,554,431	5,048	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3274, 4_A375_EGR1..1..3161	89, -231	in gene, upstream	0	1	1	17	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SETD6	FLJ21148, SETD6	SET domain containing 6	NM_024860, NM_001160305, hCT1971593.1, hCT1971594.0	1554555_a_at, 219751_at	NP_079136.2, NP_001153777.1, EAW82980.1, EAW82981.1
GeneID.23019	CNOT1	16	58,553,855	58,663,750	109,895	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3274, 4_A375_EGR1..1..3161	114278, 114598	downstream, downstream	0	1	1	17	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CNOT1	CNOT1, NOT1H, KIAA1007, FLJ36492, CDC39, NOT1, AD-005, FLJ90644, DKFZp686B0722, DKFZp686O166	CCR4-NOT transcription complex, subunit 1	NM_016284, NM_206999	1554052_at, 200860_s_at, 200861_at	NP_057368.3, NP_996882.1
GeneID.55238	SLC38A7	16	58,700,298	58,718,674	18,376	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2303	82	in gene	1	0	0	18	19	9	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene SLC38A7	SLC38A7, FLJ10815, FLJ12724	solute carrier family 38, member 7	NM_018231, hCT1952985.1, hCT1952988.1, hCT6988.2	218727_at, 222215_at, 56821_at	NP_060701.1, EAW82986.1, EAW82985.1, EAW82987.1
GeneID.2806	GOT2	16	58,741,035	58,768,246	27,211	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2304, 2_A375_pNL97_plus_lncRNA_AR..1..3275	86, -10	in gene, upstream	1	1	0	53	56	12	1	2_A375_pNL97_plus_lncRNA_AR..1	56	Gene GOT2	FLJ40994, KATIV, GOT2, mitAAT, KAT4	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	NM_002080, hCT2324016.0, hCT6113.2	200708_at	NP_002071.2, EAW82989.1, EAW82988.1
GeneID.1009	CDH11	16	64,980,683	65,155,919	175,236	-	1	4_A375_EGR1..1..3164	117231	in gene	0	0	1	4	5	17	1	4_A375_EGR1..1	17	Gene CDH11	OB, CAD11, CDHOB, CDH11, OSF-4	cadherin 11, type 2, OB-cadherin (osteoblast)	NM_001797, hCT17767.4, hCT1955855.2, hCT2324091.0	207172_s_at, 207173_x_at, 239789_at	NP_001788.2, EAW83002.1, EAW83000.1, EAW83001.1
GeneID.283867	LOC283867	16	65,318,402	65,610,203	291,801	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3276	162939	in gene	0	1	0	16	21	10	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC283867		hypothetical LOC283867	NR_027755	231518_at	
GeneID.1003	CDH5	16	66,400,525	66,438,689	38,164	+	1	4_A375_EGR1..1..3165	-5581	upstream	0	0	1	9	8	16	1	4_A375_EGR1..1	16	Gene CDH5	FLJ17376, CDH5, CD144, 7B4	cadherin 5, type 2 (vascular endothelium)	NM_001795, hCT17766.3	204677_at	NP_001786.2, EAW83009.1
GeneID.7084	TK2	16	66,541,906	66,584,315	42,409	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2309, 2_A375_pNL97_plus_lncRNA_AR..1..3281	-2245, 379	upstream, in gene	1	1	0	18.5	22.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TK2	TK2, MTDPS2, MTTK		NM_004614, NM_001172643, NM_001172644, NM_001172645, hCT1640853.2, hCT2324178.0, hCT2324179.1, hCT2324181.0, hCT2356320.0	204227_s_at, 204276_at, 204277_s_at, 230313_at, 240300_at	NP_004605.4, NP_001166114.1, NP_001166115.1, NP_001166116.1, EAW83014.1, EAW83016.1, EAW83013.1, EAW83015.1, EAW83017.1
GeneID.51192	CKLF	16	66,586,466	66,600,154	13,688	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2309, 2_A375_pNL97_plus_lncRNA_AR..1..3281	94, -2530	in gene, upstream	1	1	0	18.5	22.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CKLF	CKLF3, CKLF4, CKLF1, C32, CKLF2, UCK-1, CKLF, HSPC224	chemokine-like factor	NM_016951, NM_016326, NM_181640, NM_181641, NM_001040138, hCT1954049.1, hCT19980.2, hCT2324167.0, hCT2324169.0	219161_s_at, 221058_s_at, 223451_s_at	NP_058647.1, NP_057410.1, NP_857591.1, NP_857592.1, NP_001035228.1, EAW83019.1, EAW83020.1, EAW83021.1, EAW83022.1
GeneID.123920	CMTM3	16	66,638,202	66,647,795	9,593	+	1	4_A375_EGR1..1..3166	1478	in gene	0	0	1	9	10	18	1	4_A375_EGR1..1	18	Gene CMTM3	CKLFSF3, BNAS2, FLJ31762, CMTM3, MGC51958	CKLF-like MARVEL transmembrane domain containing 3	NM_144601, NM_181553, NM_181554, NM_001048251, hCT20001.2, hCT2356350.0, hCT2356351.0, hCT2356352.0, hCT2356353.0	1555704_at, 1555705_a_at, 224733_at	NP_653202.1, NP_853531.1, NP_001041716.1, NP_853532.1, EAW83031.1, EAW83033.1, EAW83032.1, EAW83034.1, EAW83035.1
GeneID.146223	CMTM4	16	66,648,653	66,730,610	81,957	-	2	4_A375_EGR1..1..3166, 4_A375_EGR1..1..3167	90930, 706	downstream, in gene	0	0	1	9	8.5	17.5	2	4_A375_EGR1..1	18	Gene CMTM4	CMTM4, CKLFSF4	CKLF-like MARVEL transmembrane domain containing 4	NM_178818, NM_181521, hCT19998.3, hCT2324187.0	1554677_s_at, 224998_at, 225009_at	NP_848933.1, NP_852662.1, EAW83036.1, EAW83037.1
GeneID.283847	CCDC79	16	66,788,879	66,835,523	46,644	-	1	4_A375_EGR1..1..3168	99	in gene	0	0	1	6	8	15	1	4_A375_EGR1..1	15	Gene CCDC79	FLJ35894, CCDC79	coiled-coil domain containing 79	NM_001136505	1553451_at	NP_001129977.1
GeneID.8883	NAE1	16	66,836,781	66,864,879	28,098	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2310, 4_A375_EGR1..1..3168	127, 29455	in gene, downstream	1	0	1	11	9.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene NAE1	A-116A10.1, HPP1, ula-1, APPBP1, NAE1	NEDD8 activating enzyme E1 subunit 1	NM_003905, NM_001018159, NM_001018160, hCT1813484.1, hCT2325347.0	202266_s_at	NP_003896.1, NP_001018169.1, NP_001018170.1, EAW83042.1, EAW83043.1
GeneID.57546	PDP2	16	66,914,436	66,921,855	7,419	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2311, 2_A375_pNL97_plus_lncRNA_AR..1..3282, 4_A375_EGR1..1..3169	-7225, 124, 17	upstream, in gene, in gene	1	1	1	18.5	21.5	14	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene PDP2	PPM2C2, KIAA1348, PDP2	pyruvate dehyrogenase phosphatase catalytic subunit 2	NM_020786	232681_at	NP_065837.1
GeneID.100505926	LOC100505926	16	66,922,667	66,924,184	1,517	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3282, 4_A375_EGR1..1..3169	-8107, -8214	upstream, upstream	0	1	1	18	26	15	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene LOC100505926		hypothetical LOC100505926	XR_109312		
GeneID.1014	CDH16	16	66,942,025	66,952,766	10,741	-	1	4_A375_EGR1..1..3170	-3138	upstream	0	0	1	3	11	20	1	4_A375_EGR1..1	20	Gene CDH16	CDH16		NM_004062, hCT19976.2, hCT2356343.0, hCT2356344.0	206517_at	NP_004053.1, EAW83052.1, EAW83050.1, EAW83051.1
GeneID.6236	RRAD	16	66,955,582	66,959,439	3,857	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3283, 4_A375_EGR1..1..3170, 4_A375_EGR1..1..3171	-9169, 3535, -9025	upstream, in gene, upstream	0	1	1	10.5	15	19	2	4_A375_EGR1..1	20	Gene RRAD	RAD1, RAD, REM3, RRAD	Ras-related associated with diabetes	NM_004165, NM_001128850, hCT19975.2, hCT2325343.0, hCT2356308.0	204802_at, 204803_s_at, 231100_at	NP_004156.1, NP_001122322.1, EAW83053.1, EAW83054.1, EAW83055.1
GeneID.51647	FAM96B	16	66,965,958	66,968,320	2,362	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3283, 4_A375_EGR1..1..3170, 4_A375_EGR1..1..3171	-288, 12416, -144	upstream, downstream, upstream	0	1	1	10.5	15	19	2	4_A375_EGR1..1	20	Gene FAM96B	FAM96B, CGI-128	family with sequence similarity 96, member B	NM_016062, NR_024525, hCT19979.3	218074_at	NP_057146.1, EAW83056.1
GeneID.8824	CES2	16	66,968,347	66,978,999	10,652	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3283, 4_A375_EGR1..1..3171	261, 117	in gene, in gene	0	1	1	18	19	18	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CES2	CES2A1, iCE, CES2, CE-2, PCE-2	carboxylesterase 2 (intestine, liver)	NM_003869, NM_198061, hCT19977.2, hCT2324460.0, hCT2324462.0	209667_at, 209668_x_at, 213509_x_at	NP_003860.2, NP_932327.1, EAW83057.1, EAW83058.1, EAW83059.1
GeneID.23491	CES3	16	66,995,132	67,009,052	13,920	+	1	4_A375_EGR1..1..3172	18132	downstream	0	0	1	6	7	14	1	4_A375_EGR1..1	14	Gene CES3	ES31, CES3, FLJ21736	carboxylesterase 3	NM_001185176, NM_001185177, NM_024922	220335_x_at, 234006_s_at	NP_001172105.1, NP_001172106.1, NP_079198.2
GeneID.283848	CES8	16	67,022,492	67,043,661	21,169	+	1	4_A375_EGR1..1..3172	-9226	upstream	0	0	1	6	7	14	1	4_A375_EGR1..1	14	Gene CES8	CES8, CES8, FLJ37464, FLJ37002, CES4A	carboxylesterase 4A	NM_001190201, NM_001190202, NM_173815, hCT1814072.1	228903_at	NP_001177130.1, NP_001177131.1, NP_776176.4, EAW83065.1
GeneID.80262	C16orf70	16	67,143,915	67,182,442	38,527	+	1	4_A375_EGR1..1..3173	32501	in gene	0	0	1	4	6	15	1	4_A375_EGR1..1	15	Gene C16orf70	LIN10, C16orf6, FLJ12076, C16orf70	chromosome 16 open reading frame 70	NM_025187, hCT1963177.1, hCT19995.3, hCT2324470.0, hCT2324472.0, hCT2324473.0, hCT2324474.0, hCT2356313.0	220601_at, 223440_at	NP_079463.2, EAW83078.1, EAW83072.1, EAW83074.1, EAW83075.1, EAW83077.1, EAW83073.1, EAW83076.1
GeneID.84752	B3GNT9	16	67,182,005	67,184,902	2,897	-	2	4_A375_EGR1..1..3173, 4_A375_EGR1..1..3174	8486, -9706	downstream, upstream	0	0	1	8.5	7.5	15.5	2	4_A375_EGR1..1	16	Gene B3GNT9	MGC4655, B3GNT9	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	NM_033309, hCT1645487.3	226058_at	NP_171608.2, EAW83079.1
GeneID.8717	TRADD	16	67,188,088	67,193,812	5,724	-	1	4_A375_EGR1..1..3174	-796	upstream	0	0	1	13	9	16	1	4_A375_EGR1..1	16	Gene TRADD	MGC11078, Hs.89862, TRADD	TNFRSF1A-associated via death domain	NM_003789, hCT20000.3	1729_at, 205641_s_at, 213443_at	NP_003780.1, EAW83081.1
GeneID.55336	FBXL8	16	67,193,891	67,198,077	4,186	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3284, 4_A375_EGR1..1..3174	14269, 717	downstream, in gene	0	1	1	15	17.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene FBXL8	MGC19959, FBL8, FLJ11278, FBXL8	F-box and leucine-rich repeat protein 8	NM_018378	220080_at	NP_060848.2
GeneID.3299	HSF4	16	67,197,288	67,203,848	6,560	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3284, 4_A375_EGR1..1..3174, 4_A375_EGR1..1..3175	10872, -2680, 11640	downstream, upstream, downstream	0	1	1	11.67	15	16	3	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene HSF4	HSF4, CTM	heat shock transcription factor 4	NM_001538, NM_001040667	210977_s_at	NP_001529.2, NP_001035757.1
GeneID.8996	NOL3	16	67,204,405	67,209,643	5,238	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3284, 2_A375_pNL97_plus_lncRNA_AR..1..3285, 4_A375_EGR1..1..3174, 4_A375_EGR1..1..3175	3755, 15051, -9797, 4523	in gene, downstream, upstream, in gene	0	1	1	13.5	17.5	15	4	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene NOL3	CARD2, NOL3, MYP, NOP, ARC, FLJ35304, MYC, NOP30	nucleolar protein 3 (apoptosis repressor with CARD domain)	NM_001185057, NM_001185058, NM_003946, hCT1988495.2, hCT2324468.1, hCT2345279.0	1558738_at, 221566_s_at, 221567_at, 59625_at	NP_001171986.1, NP_001171987.1, NP_003937.1, EAW83087.1, EAW83088.1, EAW83089.1
GeneID.653319	KIAA0895L	16	67,209,505	67,217,883	8,378	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3284, 2_A375_pNL97_plus_lncRNA_AR..1..3285, 2_A375_pNL97_plus_lncRNA_AR..1..3286, 4_A375_EGR1..1..3175	9723, -1573, -8005, 8955	downstream, upstream, upstream, downstream	0	1	1	14	21.25	13.5	4	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene KIAA0895L	KIAA0895L	KIAA0895-like	NM_001040715	1558041_a_at	NP_001035805.1
GeneID.283849	EXOC3L	16	67,218,282	67,224,107	5,825	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3284, 2_A375_pNL97_plus_lncRNA_AR..1..3285, 2_A375_pNL97_plus_lncRNA_AR..1..3286, 4_A375_EGR1..1..3175	15947, 4651, -1781, 15179	downstream, in gene, upstream, downstream	0	1	1	14	21.25	13.5	4	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene EXOC3L	EXOC3L1, FLJ35587, FLJ35539, MGC88052, EXOC3L	exocyst complex component 3-like	NM_178516	1554937_x_at, 1559272_at	NP_848611.2
GeneID.1874	E2F4	16	67,226,068	67,232,821	6,753	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3285, 2_A375_pNL97_plus_lncRNA_AR..1..3286	-6612, -160	upstream, upstream	0	1	0	17	24.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene E2F4	E2F-4, E2F4	E2F transcription factor 4, p107/p130-binding	NM_001950, hCT2324482.1, hCT2324484.1, hCT2356345.0	202248_at, 38707_r_at	NP_001941.2, EAW83094.1, EAW83095.1, EAW83096.1
GeneID.79767	ELMO3	16	67,233,028	67,237,927	4,899	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3286	-7140	upstream	0	1	0	15	24	10	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ELMO3	CED-12, ELMO-3, ELMO3, FLJ13824, CED12	engulfment and cell motility 3	NM_024712, hCT2324483.0, hCT2324485.1	219411_at	NP_078988.2, EAW83097.1, EAW83098.1
GeneID.442901	MIR328	16	67,236,224	67,236,298	74	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3286	10410	downstream	0	1	0	15	24	10	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene MIR328	MIRN328, hsa-mir-328, MIR328	microRNA 328	NR_029887		
GeneID.26231	LRRC29	16	67,241,042	67,260,901	19,859	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3287, 4_A375_EGR1..1..3176, 4_A375_EGR1..1..3177	-155, -379, -3547	upstream, upstream, upstream	0	1	1	11	20.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene LRRC29	FBL9, LRRC29, FBXL9	leucine rich repeat containing 29	NM_012163, NM_001004055, hCT19991.3, hCT2325332.0, hCT2325333.0, hCT2356307.0, hCT2356308.0, hCT2356309.0	232545_at	NP_036295.1, NP_001004055.1, EAW83099.1, EAW83100.1, EAW83102.1, EAW83104.1, EAW83101.1, EAW83103.1
GeneID.29100	TMEM208	16	67,261,016	67,263,182	2,166	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3287, 4_A375_EGR1..1..3176, 4_A375_EGR1..1..3177	40, 264, 3432	in gene, in gene, downstream	0	1	1	11	20.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene TMEM208	HSPC171, TMEM208	transmembrane protein 208	NM_014187, hCT19989.3, hCT2324426.0, hCT2356301.0, hCT2356302.0	221597_s_at	NP_054906.2, EAW83108.1, EAW83105.1, EAW83106.1, EAW83107.1
GeneID.29109	FHOD1	16	67,263,292	67,281,425	18,133	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3287, 4_A375_EGR1..1..3176, 4_A375_EGR1..1..3177, 4_A375_EGR1..1..3178	20369, 20145, 16977, 1329	downstream, downstream, in gene, in gene	0	1	1	12	18.33	18.33	3	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene FHOD1	FHOD1, FHOS	formin homology 2 domain containing 1	NM_013241, hCT19972.2, hCT2345052.0, hCT2345053.0, hCT2345054.0, hCT2345055.0	218530_at	NP_037373.2, EAW83112.1, EAW83109.1, EAW83110.1, EAW83111.1, EAW83113.1
GeneID.6553	SLC9A5	16	67,282,855	67,306,094	23,239	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2312, 1_A375_pNL7_minus_lncRNA_AR..1..2313, 2_A375_pNL97_plus_lncRNA_AR..1..3288, 4_A375_EGR1..1..3178	19417, 30553, 30521, -2759	in gene, downstream, downstream, upstream	1	1	1	24	22.67	9.67	3	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene SLC9A5	SLC9A5, NHE5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	NM_004594, hCT19971.2, hCT2324429.0, hCT2324430.0	1559092_at, 220650_s_at, 232584_at	NP_004585.1, EAW83114.1, EAW83115.1, EAW83116.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:84342	COG6	16	69,362,524	69,373,526	11,002	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2327, 2_A375_pNL97_plus_lncRNA_AR..1..3312, 2_A375_pNL97_plus_lncRNA_AR..1..3313, 4_A375_EGR1..1..3197, 4_A375_EGR1..1..3198	-10, 8962, 54, 13782, 9702	upstream, in gene, in gene, downstream, in gene	1	1	1	21.67	24	18.33	3	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene COG6	FLJ22315, DOR1, CDG2H, COG6	component of oligomeric golgi complex 6	NM_032382		NP_115758.3
GeneID:51388	NIP7	16	69,373,546	69,377,009	3,463	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2327, 2_A375_pNL97_plus_lncRNA_AR..1..3312, 2_A375_pNL97_plus_lncRNA_AR..1..3313, 4_A375_EGR1..1..3198, 4_A375_EGR1..1..3199	-10, -9002, -74, -9722, 10246	upstream, upstream, upstream, upstream, downstream	1	1	1	22	23.67	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene NIP7	KD93, NIP7, FLJ10296, HSPC031, CGI-37	nuclear import 7 homolog (S. cerevisiae)	NM_016101, hCT19346.2, hCT2326208.0	219031_s_at, 223397_s_at	NP_057185.1, EAW83271.1, EAW83270.1
GeneID:146456	TMED6	16	69,377,149	69,385,712	8,563	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2327, 2_A375_pNL97_plus_lncRNA_AR..1..3313, 4_A375_EGR1..1..3199	12176, 12240, 1920	downstream, downstream, in gene	1	1	1	24	25	13	2	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene TMED6	PRO34237, TMED6, SPLL9146, MGC23911	transmembrane emp24 protein transport domain containing 6	NM_144676, hCT19357.2	238430_at	NP_653277.2, EAW83272.1
GeneID:7014	TERF2	16	69,389,531	69,419,873	30,342	-	1	4_A375_EGR1..1..3199	38081	downstream	0	0	1	8	8	15	1	4_A375_EGR1..1	15	Gene TERF2	TERF2, TRBF2, TRF2	telomeric repeat binding factor 2	NM_005652, hCT19345.2, hCT2326323.0	1555183_at, 1555185_x_at, 203611_at, 229790_at	NP_005643.1, EAW83273.1, EAW83274.1
GeneID:80777	CYB5B	16	69,458,498	69,500,167	41,669	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3314	62	in gene	0	1	0	13	22	9	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CYB5B	CYB5-M, DKFZp686M0619, CYPB5M, CYB5B, OMB5	cytochrome b5 type B (outer mitochondrial membrane)	NM_030579, hCT19353.2, hCT2326210.0	201633_s_at, 201634_s_at, 227382_at, 238554_at	NP_085056.2, EAW83275.1, EAW83276.1
GeneID:10725	NFAT5	16	69,598,997	69,738,553	139,556	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3316	747	in gene	0	1	0	8	14	13	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene NFAT5	NFAT5, NF-AT5, KIAA0827, OREBP, NFATL1, NFATZ, TONEBP	nuclear factor of activated T-cells 5, tonicity-responsive	NM_138714, NM_006599, NM_138713, NM_173214, NM_001113178, hCT17785.4, hCT2344109.0, hCT2344110.0, hCT2344111.0, hCT2344112.0	208003_s_at, 215092_s_at, 224984_at	NP_619728.2, NP_006590.1, NP_775321.1, NP_619727.2, NP_001106649.1, EAW83281.1, EAW83277.1, EAW83278.1, EAW83279.1, EAW83280.1
GeneID:100302119	MIR1538	16	69,599,711	69,599,771	60	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3316	27	in gene	0	1	0	8	14	13	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene MIR1538	hsa-mir-1538, MIR1538, MIRN1538	microRNA 1538	NR_031719		
GeneID:1728	NQO1	16	69,743,304	69,760,533	17,229	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3317	149	in gene	0	1	0	13	17	13	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene NQO1	DIA4, NMOR1, QR1, NMORI, NQO1, DHQU, DTD	NAD(P)H dehydrogenase, quinone 1	NM_000903, NM_001025433, NM_001025434, hCT19352.3, hCT2326321.0, hCT2356316.0	201467_s_at, 201468_s_at, 210519_s_at	NP_000894.1, NP_001020604.1, NP_001020605.1, EAW83282.1, EAW83283.1, EAW83284.1
GeneID:28987	NOB1	16	69,775,774	69,788,829	13,055	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3318, 4_A375_EGR1..1..3200	61, 16	in gene, in gene	0	1	1	11	26	19	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene NOB1	ART-4, NOB1, MST158, MSTP158, NOB1P, PSMD8BP1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	NM_014062, hCT1813234.1, hCT2324997.0	223018_at	NP_054781.1, EAW83285.1, EAW83286.1
GeneID:11060	WWP2	16	69,796,274	69,975,643	179,369	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3318, 4_A375_EGR1..1..3200	-7506, -7463	upstream, upstream	0	1	1	11	26	19	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene WWP2	WWP2, AIP2, WWp2-like	WW domain containing E3 ubiquitin protein ligase 2	NM_007014, NM_199423, NM_199424, hCT2324278.0, hCT2324279.0, hCT2324281.0	1552737_s_at, 1554580_a_at, 204022_at, 210200_at	NP_008945.2, NP_955455.1, NP_955456.1, EAW83287.1, EAW83288.1, EAW83289.1
GeneID:118460	EXOSC6	16	70,284,134	70,285,833	1,699	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2328, 2_A375_pNL97_plus_lncRNA_AR..1..3319	9, -23	in gene, upstream	1	1	0	79	82	16	1	2_A375_pNL97_plus_lncRNA_AR..1	82	Gene EXOSC6	hMtr3p, Mtr3p, EAP4, EXOSC6, p11, MTR3	exosome component 6	NM_058219, hCT1646330.3	1553947_at, 1558044_s_at, 227698_at, 231916_at	NP_478126.1, EAW51841.1
GeneID:16	AARS	16	70,286,297	70,323,412	37,115	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2328, 1_A375_pNL7_minus_lncRNA_AR..1..2329, 2_A375_pNL97_plus_lncRNA_AR..1..3319, 2_A375_pNL97_plus_lncRNA_AR..1..3320, 4_A375_EGR1..1..3201	37568, -9708, 37556, -9820, 160	downstream, upstream, downstream, upstream, in gene	1	1	1	36.33	37.33	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	82	Gene AARS	CMT2N, AARS		NM_001605, hCT1962415.1, hCT1962416.1, hCT23802.2	201000_at	NP_001596.2, EAW51838.1, EAW51839.1, EAW51840.1
GeneID:11269	DDX19B	16	70,333,072	70,367,731	34,659	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2329, 2_A375_pNL97_plus_lncRNA_AR..1..3320, 4_A375_EGR1..1..3201	48, 160, -9840	in gene, in gene, upstream	1	1	1	15	15	17	2	4_A375_EGR1..1	25	Gene DDX19B	DBP5, RNAh, DDX19, DDX19B	DEAD (Asp-Glu-Ala-As) box polypeptide 19B	NM_007242, NM_001014449, NM_001014451	230974_at	NP_009173.1, NP_001014449.1, NP_001014451.1
GeneID:100506083	LOC100506083	16	70,349,543	70,380,678	31,135	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2330, 2_A375_pNL97_plus_lncRNA_AR..1..3321, 4_A375_EGR1..1..3202	-122, -90, -218	upstream, upstream, upstream	1	1	1	24	21	23	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene LOC100506083		hypothetical LOC100506083	XR_111591, XR_109317, XR_115018		
GeneID:55308	DDX19A	16	70,380,824	70,407,284	26,460	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2330, 2_A375_pNL97_plus_lncRNA_AR..1..3321, 4_A375_EGR1..1..3202, 4_A375_EGR1..1..3203	-24, -56, 72, 34966	upstream, upstream, in gene, downstream	1	1	1	16.5	15.5	20.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene DDX19A	DDX19L, DDX19-DDX19L, DKFZp686C21137, DDX19A, FLJ11126	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	NM_018332	1570126_at, 202577_s_at, 202578_s_at	NP_060802.1
GeneID:6483	ST3GAL2	16	70,413,338	70,472,991	59,653	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2331, 2_A375_pNL97_plus_lncRNA_AR..1..3322, 4_A375_EGR1..1..3203, 4_A375_EGR1..1..3204	-257, -289, 57199, -481	upstream, upstream, in gene, upstream	1	1	1	21.5	27.5	19	2	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene ST3GAL2	ST3GAL2, ST3GALII, SIAT4B, ST3GalA.2, Gal-NAc6S	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	NM_006927, hCT2280377.0, hCT2280379.0, hCT2280380.0, hCT23556.3	217650_x_at, 229336_at	NP_008858.1, EAW51820.1, EAW51818.1, EAW51819.1, EAW51821.1
GeneID:197258	FUK	16	70,488,498	70,514,177	25,679	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2332, 1_A375_pNL7_minus_lncRNA_AR..1..2333, 2_A375_pNL97_plus_lncRNA_AR..1..3323, 4_A375_EGR1..1..3205, 4_A375_EGR1..1..3206, 4_A375_EGR1..1..3207	-130, 3070, -146, 142, 20556, 26266	upstream, in gene, upstream, in gene, in gene, downstream	1	1	1	22	25.25	18	4	2_A375_pNL97_plus_lncRNA_AR..1	71	Gene FUK	1110046B12Rik, FLJ39408, FUK	fucokinase	NM_145059, hCT1812709.2, hCT2352496.0, hCT2352497.0, hCT2352498.0	226072_at	NP_659496.2, EAW51814.1, EAW51815.1, EAW51816.1, EAW51817.1
GeneID:25839	COG4	16	70,514,472	70,557,457	42,985	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3324, 4_A375_EGR1..1..3206, 4_A375_EGR1..1..3207	-431, 48401, 42673	upstream, downstream, in gene	0	1	1	10.33	11	19.33	3	4_A375_EGR1..1	25	Gene COG4	COD1, DKFZp586E1519, CDG2J, COG4	component of oligomeric golgi complex 4	NM_015386, hCT2280370.0, hCT2280371.0, hCT2280373.0, hCT2280374.0, hCT2352493.0, hCT2352494.0, hCT2352495.0, hCT23804.2	212189_s_at	NP_056201.2, EAW51810.1, EAW51807.1, EAW51808.1, EAW51809.1, EAW51813.1, EAW51806.1, EAW51811.1, EAW51812.1
GeneID:23450	SF3B3	16	70,557,691	70,611,571	53,880	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3324	197	in gene	0	1	0	11	16	14	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SF3B3	SF3B3, KIAA0017, RSE1, STAF130, SF3b130, SAP130	splicing factor 3b, subunit 3, 130kDa	NM_012426, hCT2280811.0, hCT2280812.0, hCT2280813.0	200687_s_at, 200688_at	NP_036558.3, EAW51803.1, EAW51804.1, EAW51805.1
GeneID:100113402	SNORD111B	16	70,563,405	70,563,498	93	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3324	-5517	upstream	0	1	0	11	16	14	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SNORD111B	SNORD111B	small nucleolar RNA, C/D box 111B	NR_003698		
GeneID:146433	IL34	16	70,613,798	70,694,585	80,787	+	2	4_A375_EGR1..1..3208, 4_A375_EGR1..1..3209	76922, 82405	in gene, downstream	0	0	1	8	5.5	17	2	4_A375_EGR1..1	17	Gene IL34	C16orf77, IL34, IL-34, MGC34647	interleukin 34	NM_152456, NM_001172771, NM_001172772, hCT2280814.0, hCT2280815.0, hCT2280816.0	237046_x_at	NP_689669.2, NP_001166242.1, NP_001166243.1, EAW51800.1, EAW51801.1, EAW51802.1
GeneID:92154	MTSS1L	16	70,695,107	70,719,954	24,847	-	2	4_A375_EGR1..1..3208, 4_A375_EGR1..1..3209	29234, 23751	downstream, in gene	0	0	1	8	5.5	17	2	4_A375_EGR1..1	17	Gene MTSS1L	ABBA-1, MTSS1L	metastasis suppressor 1-like	NM_138383, hCT1812702.2, hCT1952964.1, hCT2352492.0	1555894_s_at, 1556175_at, 213978_at	NP_612392.1, EAW51798.1, EAW51797.1, EAW51799.1
GeneID:55697	VAC14	16	70,721,342	70,835,061	113,719	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3325	53	in gene	0	1	0	19	21	17	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene VAC14	FLJ46582, MGC149816, ArPIKfyve, VAC14, TRX, TAX1BP2, FLJ10305, FLJ36622, MGC149815	Vac14 homolog (S. cerevisiae)	NM_018052, hCT2280359.0, hCT2280360.0, hCT2280361.0, hCT2280363.0, hCT2280364.0	216407_at, 216501_at, 218169_at	NP_060522.3, EAW51793.1, EAW51791.1, EAW51792.1, EAW51794.1, EAW51795.1
GeneID:54768	HYDIN	16	70,841,289	71,264,569	423,280	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2334, 1_A375_pNL7_minus_lncRNA_AR..1..2335, 2_A375_pNL97_plus_lncRNA_AR..1..3325, 2_A375_pNL97_plus_lncRNA_AR..1..3326, 2_A375_pNL97_plus_lncRNA_AR..1..3327, 2_A375_pNL97_plus_lncRNA_AR..1..3328, 4_A375_EGR1..1..3210	243257, 211401, 429581, 366409, 243193, 211417, 292249	in gene, in gene, downstream, in gene, in gene, in gene, in gene	1	1	1	24.2	26.4	13	5	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene HYDIN	DKFZp434L0850, HYDIN1, FLJ12871, HYDIN, HYDIN2, DKFZp434D0513, KIAA1864, FLJ14665	hydrocephalus inducing homolog (mouse)	NM_017558, NM_032821, hCT1812574.1	1554908_at, 220098_at, 232984_at	NP_060028.2, NP_116210.2, EAW59249.1
GeneID:55783	FTSJD1	16	71,316,203	71,323,509	7,306	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2336, 2_A375_pNL97_plus_lncRNA_AR..1..3329	389, 421	in gene, in gene	1	1	0	21	17	15	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene FTSJD1	FTSJD1, AFT, FLJ11171	FtsJ methyltransferase domain containing 1	NM_018348, NM_001099642, hCT2299799.0, hCT2299800.0	222611_at	NP_060818.4, NP_001093112.1, EAW59246.1, EAW59247.1
GeneID:7571	ZNF23	16	71,481,500	71,496,117	14,617	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2337, 1_A375_pNL7_minus_lncRNA_AR..1..2338, 2_A375_pNL97_plus_lncRNA_AR..1..3331, 2_A375_pNL97_plus_lncRNA_AR..1..3332, 4_A375_EGR1..1..3211, 4_A375_EGR1..1..3212	-27, -5675, 69, -5707, 20725, 21	upstream, upstream, in gene, upstream, downstream, in gene	1	1	1	24.67	30.33	16.33	3	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene ZNF23	MGC57283, KOX16, ZNF612, ZNF23, Zfp612, ZNF359	zinc finger protein 23 (KOX 16)	NM_145911		NP_666016.1
GeneID:100506105	LOC100506105	16	71,496,198	71,497,970	1,772	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2337, 1_A375_pNL7_minus_lncRNA_AR..1..2338, 2_A375_pNL97_plus_lncRNA_AR..1..3331, 2_A375_pNL97_plus_lncRNA_AR..1..3332, 4_A375_EGR1..1..3212	-54, 5594, -150, 5626, -102	upstream, downstream, upstream, downstream, upstream	1	1	1	34.5	42	15	2	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene LOC100506105		hypothetical LOC100506105	XR_111592, XR_109318, XR_115019		
GeneID:7567	ZNF19	16	71,507,976	71,523,254	15,278	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2338, 2_A375_pNL97_plus_lncRNA_AR..1..3332, 2_A375_pNL97_plus_lncRNA_AR..1..3333, 2_A375_pNL97_plus_lncRNA_AR..1..3334	21462, 21430, 14326, 4606	downstream, downstream, in gene, in gene	1	1	0	24.33	29	9	3	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene ZNF19	KOX12, MGC51021, ZNF19	zinc finger protein 19	NM_006961	213934_s_at	NP_008892.2
GeneID:100132529	LOC100132529	16	71,599,692	71,606,341	6,649	+	2	4_A375_EGR1..1..3213, 4_A375_EGR1..1..3214	-796, -364	upstream, upstream	0	0	1	10	11.5	15	2	4_A375_EGR1..1	15	Gene LOC100132529		hypothetical LOC100132529	XR_111593, XR_109319, XR_115020		
GeneID:6898	TAT	16	71,600,754	71,610,998	10,244	-	2	4_A375_EGR1..1..3213, 4_A375_EGR1..1..3214	12102, 11670	downstream, downstream	0	0	1	10	11.5	15	2	4_A375_EGR1..1	15	Gene TAT	TAT		NM_000353, hCT1812573.1, hCT1957782.1	1555189_a_at, 206916_x_at, 214413_at	NP_000344.1, EAW59230.1, EAW59231.1
GeneID:164	AP1G1	16	71,762,903	71,842,976	80,073	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2339, 2_A375_pNL97_plus_lncRNA_AR..1..3335, 4_A375_EGR1..1..3215	96, 176, 400	in gene, in gene, in gene	1	1	1	21	26	18	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene AP1G1	ADTG, AP1G1, MGC18255, CLAPG1	adaptor-related protein complex 1 gamma 1 subunit	NM_001128, NM_001030007, hCT1963755.1, hCT2299786.0, hCT24203.4	203350_at, 225754_at, 225771_at	NP_001119.3, NP_001025178.1, EAW59222.1, EAW59223.1, EAW59224.1
GeneID:342371	ATXN1L	16	71,879,899	71,919,174	39,275	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3336, 2_A375_pNL97_plus_lncRNA_AR..1..3337	-123, 49381	upstream, downstream	0	1	0	14	23	13	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene ATXN1L	BOAT, DKFZp686D05115, DKFZp667N0214, DKFZp686O1195, ATXN1L, FLJ21686, FLJ21460	ataxin 1-like	NR_024612, NM_001137675	226095_s_at, 227373_at	NP_001131147.1
GeneID:9798	KIAA0174	16	71,929,446	71,962,906	33,460	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3337	-166	upstream	0	1	0	14	27	13	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene KIAA0174	IST1, MGC117220, KIAA0174	KIAA0174	NM_014761, hCT2301538.0, hCT2301539.0, hCT2353398.0, hCT2353399.0, hCT24204.2	200851_s_at, 215565_at	NP_055576.2, EAW59209.1, EAW59205.1, EAW59206.1, EAW59207.1, EAW59208.1
GeneID:342372	PKD1L3	16	71,963,441	72,033,877	70,436	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2340, 2_A375_pNL97_plus_lncRNA_AR..1..3338, 4_A375_EGR1..1..3216	-8843, -8843, -8907	upstream, upstream, upstream	1	1	1	25	21	22	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene PKD1L3	PKD1L3		NM_181536, hCT2349849.0, hCT2349850.0, hCT2349851.0		NP_853514.1, EAW59204.1, EAW59202.1, EAW59203.1
GeneID:1723	DHODH	16	72,042,643	72,058,955	16,312	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2340, 2_A375_pNL97_plus_lncRNA_AR..1..3338, 4_A375_EGR1..1..3216	77, 77, 141	in gene, in gene, in gene	1	1	1	25	21	22	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene DHODH	URA1, POADS, DHODH, DHOdehase	dihydroorotate dehydrogenase	NM_001361, hCT1957648.1, hCT2301541.0, hCT2301543.0, hCT24208.4	213632_at	NP_001352.2, EAW59198.1, EAW59199.1, EAW59200.1, EAW59201.1
GeneID:54957	TXNL4B	16	72,118,756	72,128,215	9,459	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2341, 2_A375_pNL97_plus_lncRNA_AR..1..3339, 4_A375_EGR1..1..3217	663, 439, 298	in gene, in gene, in gene	1	1	1	19	22	13	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene TXNL4B	DLP, FLJ20511, Dim2, TXNL4B	thioredoxin-like 4B	NM_017853, NM_001142317, NM_001142318, hCT1818721.1, hCT1957634.1	218794_s_at, 222748_s_at	NP_060323.1, NP_001135789.1, NP_001135790.1, EAW59191.1, EAW59192.1
GeneID:9785	DHX38	16	72,127,615	72,146,811	19,196	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2341, 2_A375_pNL97_plus_lncRNA_AR..1..3339, 4_A375_EGR1..1..3217	-63, 161, 302	upstream, in gene, in gene	1	1	1	19	22	13	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene DHX38	PRP16, DDX38, PRPF16, KIAA0224, DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	NM_014003, hCT2301557.0, hCT2301558.1, hCT2350472.0, hCT2350473.0, hCT2350474.0, hCT2350475.0, hCT2350476.0, hCT2350477.0, hCT2350478.0, hCT2350479.0, hCT24206.2	209178_at	NP_054722.2, EAW59180.1, EAW59182.1, EAW59183.1, EAW59186.1, EAW59188.1, EAW59181.1, EAW59184.1, EAW59185.1, EAW59187.1, EAW59189.1, EAW59190.1
GeneID:463	ZFHX3	16	72,816,784	73,092,534	275,750	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2342, 2_A375_pNL97_plus_lncRNA_AR..1..3341, 2_A375_pNL97_plus_lncRNA_AR..1..3342, 4_A375_EGR1..1..3218, 4_A375_EGR1..1..3219	36006, 130742, 36086, 42785, -8541	in gene, in gene, in gene, in gene, upstream	1	1	1	12.75	16.75	13	4	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene ZFHX3	ZFHX3, ATBT, ATBF1, ZNF927	zinc finger homeobox 3	NM_006885, NM_001164766, hCT2293728.0, hCT2293729.0, hCT23632.3	208033_s_at, 226137_at, 233751_at, 233752_s_at, 242738_s_at, 243323_s_at	NP_008816.3, NP_001158238.1, EAW59168.1, EAW59169.1, EAW59170.1
GeneID:100506152	LOC100506152	16	73,045,573	73,046,278	705	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2342, 2_A375_pNL97_plus_lncRNA_AR..1..3342, 4_A375_EGR1..1..3218	-8250, -8170, -3471	upstream, upstream, upstream	1	1	1	17	16.5	13	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene LOC100506152		hypothetical LOC100506152	XR_111594, XR_109320, XR_115021		
GeneID:5713	PSMD7	16	74,330,681	74,340,186	9,505	+	1	4_A375_EGR1..1..3221	55	in gene	0	0	1	23	19	24	1	4_A375_EGR1..1	24	Gene PSMD7	S12, MOV34, P40, Rpn8, PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	NM_002811, hCT2293656.0, hCT2293657.0	201705_at, 238738_at, 244515_at	NP_002802.2, EAW59163.1, EAW59162.1
GeneID:100506201	LOC100506201	16	74,339,025	74,354,270	15,245	-	1	4_A375_EGR1..1..3221	23534	downstream	0	0	1	23	19	24	1	4_A375_EGR1..1	24	Gene LOC100506201		hypothetical LOC100506201	XR_109323		
GeneID:440348	NPIPL2	16	74,411,872	74,426,013	14,141	+	1	4_A375_EGR1..1..3222	-4266	upstream	0	0	1	8	3	18	1	4_A375_EGR1..1	18	Gene NPIPL2	NPIPL2, A-761H5.4	nuclear pore complex interacting protein-like 2	XM_002344099	221992_at	XP_002344140.1
GeneID:100507666	LOC100507666	16	74,411,872	74,426,013	14,141	+	1	4_A375_EGR1..1..3222	-4266	upstream	0	0	1	8	3	18	1	4_A375_EGR1..1	18	Gene LOC100507666		nuclear pore complex-interacting protein-like 2-like	XM_003118720		XP_003118768.1
GeneID:2734	GLG1	16	74,481,325	74,641,042	159,717	-	1	4_A375_EGR1..1..3223	62	in gene	0	0	1	15	10	21	1	4_A375_EGR1..1	21	Gene GLG1	FLJ23967, ESL-1, MG160, DKFZp686L08213, CFR-1, GLG1, MG-160, FLJ23319, FLJ32797	golgi apparatus protein 1	NM_012201, NM_001145666, NM_001145667, NR_027264, NR_027265, hCT2252266.0, hCT2252267.0, hCT2357661.0, hCT2357662.0, hCT2357663.0	207966_s_at, 212045_at, 214730_s_at	NP_036333.2, NP_001139138.1, NP_001139139.1, EAW95682.1, EAW95683.1, EAW95686.1, EAW95684.1, EAW95685.1
GeneID:100132346	LOC100132346	16	74,646,491	74,647,119	628	-	1	4_A375_EGR1..1..3223	6159	downstream	0	0	1	15	10	21	1	4_A375_EGR1..1	21	Gene LOC100132346		10 kDa heat shock protein, mitochondrial-like	XM_001726790		XP_001726842.1
GeneID:55159	RFWD3	16	74,655,297	74,700,779	45,482	-	1	4_A375_EGR1..1..3224	251	in gene	0	0	1	15	14	15	1	4_A375_EGR1..1	15	Gene RFWD3	RFWD3, RNF201, FLJ10520	ring finger and WD repeat domain 3	NM_018124, hCT2252263.0, hCT2252264.0	218564_at	NP_060594.3, EAW95680.1, EAW95681.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A3SS_2_A3SS_gNG7_wt_gNU97_all_lncRNA_AR_1 Percent	4_A3SS_EGR1_gNU97_all_lncRNA_AR_1 Percent	1_A3SS_gNG7_mxe_lncRNA_AR_1 Avg Reads	2_A3SS_gNU97_all_lncRNA_AR_1 Avg Reads	4_A3SS_EGR1_gNU97_all_lncRNA Avg Reads	Adj Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
GeneID:19789289	MLK1	19	74,705,755	74,734,769	29,015	+	1	4_A3SS_EGR1.1..3224	54261	Downstream	0	0	1	15	14	15	1	4_A3SS_EGR1.1..3	15	Gene MLK1	FLJ32689, MLK1	mixed lineage kinase domain-l	NM_152497, NM_001143297, NCT01582223.4	238029_at	NP_689592.1, NP_001135997.1, ENSP00000...
GeneID:19791522	FAIM	19	74,748,653	74,806,729	58,076	+	1	4_A3SS_EGR1.1..3225	80940	Downstream gene	0	0	1	9	8	17	1	4_A3SS_EGR1.1..1	17	Gene FAIM	FAIM3C1, FAIM3, FAIM, SPG35, FLJ25257, SCI27, FAH1	fatty acid 2-hydroxylase	NM_024308, NCT01136443.3, NCT02522777.0	219429_at, 234983_s_at	NP_077322.3, ENSP00000...
GeneID:19792726	WDR39	19	74,807,471	75,019,017	211,546	+	1	4_A3SS_EGR1.1..3226	264	Downstream gene	0	0	1	16	16	15	1	4_A3SS_EGR1.1..1	15	Gene WDR39	FLJ12270, WDR39, PP977, MGC112230	WD repeat domain 39	NM_030581, NCT02529300.0, NCT02529364.0, NCT02529355.0, NCT02529386.0, NCT02529397.0	215693_at, 219966_at, 221901_s_at, 222259_at	NP_569056.3, ENSP00000...
GeneID:64219317	ZNRF1	19	75,032,915	75,144,892	111,977	+	1	4_A3SS_EGR1.1..3227	114733	Downstream	0	0	1	3	8	16	1	4_A3SS_EGR1.1..1	16	Gene ZNRF1	ZNRF1, DKFZp434E229, MN053, MGC15430, FLJ14545	zinc and ring finger 1	NM_032480, NCT01263773, NCT02376560.0, NCT02376590.0, NCT02376600.0	223382_s_at, 223383_at, 223555_s_at, 223990_at, 231962_x_at	NP_115844.1, ENSP00000...
GeneID:19793237	LDHD	19	75,149,766	75,190,965	41,200	-	1	4_A3SS_EGR1.1..3227	3017	Downstream gene	0	0	1	3	8	16	1	4_A3SS_EGR1.1..1	16	Gene LDHD	LDHD, MGC37739, DLD	lactate dehydrogenase D	NM_152439, NM_194436, NCT02449..., NCT02509000.0, NCT02509010.0, NCT02509030.0	229241_at	NP_705930.2, NP_919477..., ENSP00000...
GeneID:18992239	ZFP1	19	75,162,421	75,206,152	43,731	+	1	2_A3SS_all_lncRNA_AR_1.3343	-133	upstream	0	1	0	16	25	13	1	2_A3SS_all_lncRNA_AR_1	23	Gene ZFP1	ZFP1, ZNF473, FLJ36241	zinc finger protein 1 homolog (mouse)	NM_135653, NCT02535..., NCT02535000.0	229837_at, 234455_at, 234510_at	NP_742153.2, ENSP00000...
GeneID:44237697	CTR9J	19	75,237,994	75,241,072	3,078	+	1	4_A3SS_EGR1.1..3228	443	Downstream gene	0	0	1	9	7	16	1	4_A3SS_EGR1.1..1	16	Gene CTR9J	CTR9J	ctr9 homolog J (S. cerevisiae)	NM_031232.3, NCT01912219.1	214411_x_at	NP_001129271.2, ENSP00000...
GeneID:10163580351	LOC100...	19	75,240,907	75,262,097	21,190	+	2	4_A3SS_EGR1.1..3229, 4_A3SS_EGR1.1..3230	6497, 11641	Downstream, Downstream	0	0	1	12	11.5	16.5	2	4_A3SS_EGR1.1..1	22	Gene LOC100506831	hypothetical LOC100506831	XR_109324		
GeneID:89795545	BCAR1	19	75,262,926	75,301,951	39,025	-	8	4_A3SS_EGR1.1..3229, 4_A3SS_EGR1.1..3230, 4_A3SS_EGR1.1..3231, 4_A3SS_EGR1.1..3232, 4_A3SS_EGR1.1..3233, 4_A3SS_EGR1.1..3234	32567, 29423, 23911, 22495, 20845, 2731	Downstream, Downstream, Downstream, Downstream, Downstream, Downstream, Downstream	0	0	1	9.63	11.67	19.67	6	4_A3SS_EGR1.1..1	22	Gene BCAR1	CRKAS, CAS1, BCAR1, FLJ10176, P130Cas, CAS, CASS1, FLJ45039	breast cancer anti-estrogen resistance 1	NM_031774, NM_001170715, NM_001170716, NM_001170717, NM_001170718, NM_014567, NM_001170719, NM_001170720, NM_001170721, NCT01668..., NCT01912127, NCT01912163, NCT02279418, NCT02579941.0, NCT02579965.0	225116_at, 232442_at	NP_001164155.1, NP_001164156.1, NP_001164157.1, NP_001164158.1, NP_001164159.1, NP_001164160.1, NP_001164161.1, NP_001164162.1, ENSP00000...
GeneID:18992545	CFDP1	16	75,227,806	75,497,387	269,582	+	1	4_A3SS_EGR1.1..3233	363	Downstream gene	0	0	1	12	11	24	1	4_A3SS_EGR1.1..1	24	Gene CFDP1	bM7, Yeh, BMCA, CFDP1, BUCENTA-LIR, CP27, BCNT	craniofacial development protein 1	NM_006324, NCT01298032, NCT02527672.0, NCT02527690.0	203166_at, 210761_at	NP_006315.1, ENSP00000...
GeneID:19794494	TMEM70A	19	75,440,917	75,496,904	57,987	-	2	2_A3SS_gNU97_all_lncRNA_AR_1.3343, 2_A3SS_gNU97_all_lncRNA_AR_1.3344	24, 66	Downstream gene, Downstream gene	1	1	0	16	23	15	1	2_A3SS_all_lncRNA_AR_1	23	Gene TMEM70A	TMEM70, FLJ27011, TMEM70A	transmembrane protein 70A	NM_145334, NCT01048711.1, NCT01951274.1, NCT01964931.1	227906_at, 229263_s_at, 230414_s_at	NP_660257.1, ENSP00000...
GeneID:41997688	CHST8	19	75,507,022	75,520,928	21,904	-	2	2_A3SS_gNG7_mxe_lncRNA_AR_1.3344, 2_A3SS_gNU97_all_lncRNA_AR_1.3344	20866, 20430	Downstream, Downstream	1	1	0	16	23	15	1	2_A3SS_all_lncRNA_AR_1	23	Gene CHST8	MCDC1, CHST8	carbohydrate (N-acetylgalactosamine 6-O) sulfotransferase 8	NM_021615, NCT01841692.2, NCT02527680.0	222158_at	NP_065426.1, ENSP00000...
GeneID:79783931	TMEM231	19	75,572,015	75,590,070	18,155	-	2	1_A3SS_gNG7_mxe_lncRNA_AR_1.3344, 2_A3SS_gNU97_all_lncRNA_AR_1.3343	90, 199	Downstream gene, Downstream gene	1	1	0	21	24	15	1	2_A3SS_all_lncRNA_AR_1	24	Gene TMEM231	ALY1870, PRO1888, FLJ22167, TMEM231	transmembrane protein 231	NM_031774.16, NM_001077416, NM_001077419	219182_at, 64490_at	NP_001070884.1, NP_001070886.1, NP_001070887.1
GeneID:11594545	GNB5IP1	19	75,800,249	75,811,779	11,530	+	3	1_A3SS_gNG7_mxe_lncRNA_AR_1.3344, 2_A3SS_gNU97_all_lncRNA_AR_1.3343, 4_A3SS_EGR1.1..3237	-10695, -10283, 599	upstream, upstream, exon	1	1	1	14.3	16	16	2	2_A3SS_all_lncRNA_AR_1	24	Gene GNB5AP1L2	GNB5AP1L2	GNB5IP1 encoded protein GNTR-19, GNB5IP1L2	NM_027255, NCT02289..., NCT01961479.1	220946_s_at	NP_339216.1, ENSP00000...
GeneID:53533	KARS	19	75,861,822	75,891,565	29,743	-	2	2_A3SS_gNU97_all_lncRNA_AR_1.3348, 4_A3SS_EGR1.1..3238	-599, 30	upstream, gene	1	1	1	14	20	22	1	4_A3SS_EGR1.1..1	22	Gene KARS	KARS2	lysyl-tRNA synthetase	NM_005548, NM_001130009, NCT02552..., NCT01912221.1, NCT01912231.1, NCT01912251.1, NCT02570930.0	200079_s_at, 200960_at	NP_005539.1, NP_001123561.1, NP_001123562.1, ENSP00000...
GeneID:84701	TERF2IP	19	75,861,835	75,891,340	29,506	+	2	2_A3SS_gNU97_all_lncRNA_AR_1.3348, 4_A3SS_EGR1.1..3236	541, -83	gene, upstream	0	1	1	14	20	22	1	4_A3SS_EGR1.1..1	22	Gene TERF2IP	DKFZp, RAP1, TERF2IP	telomeric repeat binding factor 2, interacting protein	NM_018975, NCT02296021.0, NCT02550022.0, NCT02550032.0	220174_s_at	NP_061944.2, ENSP00000...
GeneID:10130938	SYCE1L	19	77,233,349	77,249,976	16,627	+	2	2_A3SS_gNU97_all_lncRNA_AR_1.3349, 4_A3SS_EGR1.1..3239	14171, 13611	Downstream, gene	0	1	1	9.5	16	9.5	2	2_A3SS_all_lncRNA_AR_1	23	Gene SYCE1L	SYCE1L, MRP2	synaptonemal complex central element protein 1-like	NM_032129079		NP_001123651.1
GeneID:83977	VATIL	19	77,822,483	78,014,001	191,518	+	2	2_A3SS_gNU97_all_lncRNA_AR_1.3349, 4_A3SS_EGR1.1..3240	-222, -3611	upstream, upstream	0	1	1	10	12	13.5	2	2_A3SS_all_lncRNA_AR_1	16	Gene VATIL	VATIL, EVA1137	vacuolar ATP synthase intermediate subunit C, lumenal (Tetrahymena)	NM_020927, NCT01844423.0	226419_at	NP_065979.1, ENSP00000...
GeneID:83941	WWOX	16	78,133,851	79,249,364	1,115,513	-	3	1_A3SS_gNU97_mxe1_lncRNA_AR_1.2347, 1_A3SS_gNU97_all_lncRNA_AR_1.3351, 4_A3SS_EGR1.1..3242	-111, -79, -143	upstream, upstream, upstream	1	1	1	30	42	22	1	2_A3SS_all_lncRNA_AR_1	42	Gene WWOX	2DRA1C1, WWOX, WOX1, FRA16D, HHCMA39, SWSAS22.8, FOR, PRO1023	WW domain containing oxidoreductase	NM_016373, NM_130791, NM_130944	210869_s_at, 211077_s_at, 221147_s_at, 222747_s_at, 223982_s_at	NP_057457.1, NP_570907.1, NP_570559.1
GeneID:23493	MAP	19	79,827,743	79,834,823	6,877	-	2	2_A3SS_gNU97_all_lncRNA_AR_1.3353, 4_A3SS_EGR1.1..3243	-130, -402	upstream, upstream	0	1	1	12	21	16	1	2_A3SS_all_lncRNA_AR_1	21	Gene MAP	u-MAP, MGC71853, MAP	u-map	NM_033390, NM_001031804	1568822_at, 1568826_s_at, 206982_at, 209547_s_at, 209345_s_at	NP_262331.2, NP_001026074.1
GeneID:83573	DYNLRB2	19	80,574,854	80,584,541	9,687	+	1	2_A3SS_gNU97_all_lncRNA_AR_1.3355	-102	upstream	0	1	0	20	25	13	1	2_A3SS_all_lncRNA_AR_1	25	Gene DYNLRB2	DYNLRB2, MGC63332, DNCL2B, ROBLD2, DNLC2B	dynein, light chain, roadblock-type 2	NM_130397, NCT7766.2	235116_at	NP_570987.1, ENSP00000...
GeneID:84611	C19orf81	19	81,809,899	81,849,902	39,003	-	3	1_A3SS_gNG7_mxe1_lncRNA_AR_1.2352, 2_A3SS_gNU97_all_lncRNA_AR_1.3359, 4_A3SS_EGR1.1..3244	-138, -170, -490	upstream, upstream, upstream	1	1	1	93	76	29	1	1_A3SS_gNG7_mxe_lncRNA_AR_1	93	Gene C19orf81	C19orf81, DC13, 2310061C15Rik	ubiquitin conjugation enzyme E2 variant 1	NM_030188, NCT01961507.2, NCT01961201.1, NCT01912241.1, NCT01912391.1, NCT02519361.0	218447_at	NP_396373.1, ENSP00000...
GeneID:55768	CENPN	16	81,849,103	81,866,712	36,809	+	3	1_A3SS_gNG7_mxe1_lncRNA_AR_1.2352, 2_A3SS_gNU97_all_lncRNA_AR_1.3359, 4_A3SS_EGR1.1..3244	537, 589, 689	gene, gene, gene, gene	1	1	1	93	76	29	1	1_A3SS_gNG7_mxe_lncRNA_AR_1	93	Gene CENPN	CENP-N, 8h6003, CENPN, FLJ22850, C16orf61, FLJ13927	centromere protein N	NM_018455, NM_001100634, NM_001100635, NCT01912211.1, NCT02529910.0, NCT02529930.0	219555_s_at, 222116_at, 234911_at	NP_060925.1, NP_001090494.1, NP_001094055.1, ENSP00000...
GeneID:64399	GAN	19	81,946,571	81,970,003	23,432	+	3	1_A3SS_gNG7_mxe1_lncRNA_AR_1.2353, 2_A3SS_gNU97_all_lncRNA_AR_1.3360, 4_A3SS_EGR1.1..3245	65, -125, -155	gene, upstream, upstream	1	1	1	14	24	19	1	4_A3SS_EGR1.1..1	24	Gene GAN	GAN2, GAN, KLHL16, FLJ38359	gigaxonin	NM_022041, NCT13209.2	220124_at	NP_071324.1, ENSP00000...
GeneID:83986	C4RF	19	81,476,775	81,745,367	268,592	+	1	4_A3SS_EGR1.1..3249	282697	gene	0	0	1	5	7	16	1	4_A3SS_EGR1.1..1	16	Gene C4RF	TCAIP, KIAA1894	cell-adhesion protein	NM_033629, NM_176390, NCT15932.0, NCT02524036.1, NCT02524237.1	224991_at, 224992_s_at, 225...., 231943_s_at, 243720_at	NP_388132.1, NP_788204.2, ENSP00000...
GeneID:10980200	MPHOSPH8	19	82,161,787	82,203,629	22,062	-	2	2_A3SS_gNU97_mxe1_lncRNA_AR_1.2356, 2_A3SS_gNU97_all_lncRNA_AR_1.3362	277, 213	gene, gene	0	1	1	9	16	21	1	2_A3SS_all_lncRNA_AR_1	21	Gene MPHOSPH8	MPHOSPH8, MPP8, MPP-8, KIF20	M-phase phosphoprotein 8	NM_032792, NCT02546378.0, NCT02546379.0, NCT29716.3	1554906_a_at, 203760_at	NP_076063.2, ENSP00000...
GeneID:10981712	CDH13	19	82,660,676	83,030,301	1,369,625	-	6	1_A3SS_gNU97_mxe1_lncRNA_AR_1.2357, 1_A3SS_gNU97_mxe2_lncRNA_AR_1.2358, 1_A3SS_gNU97_mxe3_lncRNA_AR_1.2359, 1_A3SS_gNU97_mxe4_lncRNA_AR_1.2360, 2_A3SS_gNU97_all_lncRNA_AR_1.3361, 2_A3SS_gNU97_all_lncRNA_AR_1.3364, 2_A3SS_gNU97_all_lncRNA_AR_1.3365, 2_A3SS_gNU97_all_lncRNA_AR_1.3366	7262, 606230, 928699, 1074782, 1022, 919430, 928699, 1091102	gene, gene, gene, gene, gene, gene, gene, gene	1	1	0	17	18.14	8.43	7	2_A3SS_all_lncRNA_AR_1	24	Gene CDH13	CDH13, CDHH	cadherin 13, H-cadherin (heart)	NM_001257, NCT02707.3	204726_at	NP_001240.1, ENSP00000...
GeneID:10981842	MIR3182	19	83,041,931	83,042,013	82	+	1	4_A3SS_EGR1.1..3256	4083	Downstream	0	0	0	15	11	3	1	4_A3SS_EGR1.1..1	15	Gene MIR3182	MIR3182	microRNA 3182	NR_038147		
GeneID:23493	MLYCD	16	83,932,700	83,949,767	17,067	+	1	4_A3SS_EGR1.1..3249	27269	Downstream	0	0	1	7	8	15	1	4_A3SS_EGR1.1..1	15	Gene MLYCD	MLYCD, MCD, MGC29758	malonyl-CoA decarboxylase	NM_012213, NCT01366.0	210589_at	NP_036345.2, ENSP00000...
GeneID:29945	OSGIN1	16	83,952,672	83,999,937	47,265	+	2	2_A3SS_gNU97_mxe1_lncRNA_AR_1.2361, 2_A3SS_gNU97_all_lncRNA_AR_1.3367	3586, 3963	gene, gene	1	1	0	29	32	12	1	2_A3SS_all_lncRNA_AR_1	32	Gene OSGIN1	BDU1, OKL56, OSGIN1	oxidative stress induced growth inhibitory 1	NM_013376, NM_182983, NM_182991, NCT01959302.1, NCT01999..2	219479_at	NP_037502.3, NP_892026.1, NP_892028.1, ENSP00000...
GeneID:57019	MBTPS1	16	84,087,366	84,160,917	80,149	-	2	2_A3SS_gNU97_mxe1_lncRNA_AR_1.3366, 4_A3SS_EGR1.1..3251	-107, -299	upstream, upstream	0	1	1	14	17	19	1	4_A3SS_EGR1.1..1	19	Gene MBTPS1	MBTPS1, PCSK8, S1P, MGC135711, SIAH2091, MGC135712, SKI-1	membrane-bound transcription factor peptidase, site 1	NM_003791, NCT02387636.0, NCT11981.2	201420_at, 217543_s_at	NP_003781.1, ENSP00000...
GeneID:83989	HSDL1	19	84,155,744	84,176,900	20,856	-	3	2_A3SS_gNU97_all_lncRNA_AR_1.3369, 4_A3SS_EGR1.1..3254, 4_A3SS_EGR1.1..3252	20178, 27964, -272	Downstream, Downstream, Downstream	0	1	1	12	13	16	2	4_A3SS_EGR1.1..1	19	Gene HSDL1	MGC129953, HSDL1, SDR12C3, MGC129952, MGC129994	hydroxysteroid dehydrogenase like 1	NM_031483, NM_001145031, NCT02535514.0, NCT02535963.0, NCT11999.3	223245_at	NP_113551.4, NP_001139123.1, ENSP00000...
GeneID:12705972	DKFZP434...	19	84,176,985	84,211,324	32,839	+	2	2_A3SS_gNU97_all_lncRNA_AR_1.3369, 4_A3SS_EGR1.1..3252	41997, 207	Downstream, gene	0	1	1	11	14	13	2	2_A3SS_all_lncRNA_AR_1	19	Gene LRRC59	DKFZp434A115, LRRC59, ODN7, FLJ38359	leucine rich repeat containing 59	NM_178452, NCT02534110.0, NCT02534410.0	219713_at, 222955_s_at	NP_848547.2, ENSP00000...
GeneID:84787	TAF1C	16	84,211,461	84,220,862	9,401	-	2	2_A3SS_gNU97_mxe1_lncRNA_AR_1.3369, 4_A3SS_EGR1.1..3253	-230, -4105	gene, upstream	0	1	1	7	12.5	15.5	2	2_A3SS_all_lncRNA_AR_1	19	Gene TAF1C	MGC.39176, TAF9B, TAF1C, SL1, TAF110	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kDa	NM_139153, NM_003879, NCT2325247.0, NCT02525300.0, NCT02576170.0, NCT02576174.0, NCT29711.2	202937_s_at, 203955_s_at	NP_647610.1, NP_003179.2, ENSP00000...
GeneID:16842042	ADAD2	19	84,224,703	84,230,772	6,069	+	2	2_A3SS_gNU97_mxe1_lncRNA_AR_1.3369, 4_A3SS_EGR1.1..3255	-4291, 45	upstream, gene	0	1	1	7	12.5	15.5	2	2_A3SS_all_lncRNA_AR_1	19	Gene ADAD2	TENR/L, ADAD2, FLJ40227	adenosine deaminase, tRNA-specific, 3 domain-containing 2	NM_139174, NM_001145400, NCT01992022.2, NCT01992082.2, NCT02496802.0, NCT51070.0	236462_at	NP_631913.3, NP_001138072.1, ENSP00000...
GeneID:84787	LOC84870	19	84,226,164	84,230,669	4,506	-	2	2_A3SS_gNU97_mxe1_lncRNA_AR_1.3369, 4_A3SS_EGR1.1..3253	10227, 5691	Downstream, Downstream	0	1	1	7	12.5	15.5	2	2_A3SS_all_lncRNA_AR_1	19	Gene LOC654760	FLJ41555, FLJ39012	SPRY domain containing SOCS box protein 4	XR_111902, XR_109329, XR_110030	1562426_at	
GeneID:93747107	KCNG4	16	84,255,623	84,273,356	17,733	-	1	4_A3SS_gNU97_mxe1_lncRNA_AR_1.3370	10624	gene	0	1	0	15	20	10	1	2_A3SS_all_lncRNA_AR_1	20	Gene KCNG4	MGC129809, Kv6.4, MGC4155, Kv6.2, KCNG4	potassium voltage-gated channel, subfamily G, member 4	NM_172347, NCT2325345.0, NCT2376562.0, NCT31044.2	1552595_at	NP_758557.1, ENSP00000...
GeneID:56169	WIPDC1	19	84,326,401	84,385,450	59,049	+	1	4_A3SS_EGR1.1..3254	341	upstream	0	0	1	12	7	16	1	4_A3SS_EGR1.1..1	16	Gene WIPDC1	FE20, WIPDC1	WAP four-disulfide core domain 13	NM_031197, NCT02376681.0, NCT31043.2	219476_at	NP_001120.2, ENSP00000...
GeneID:83989707	KIAA1809	19	84,809,998	84,838,265	28,222	+	1	4_A3SS_EGR1.1..3255	-804	upstream	0	0	1	13	13	16	1	4_A3SS_EGR1.1..1	16	Gene KIAA1809	MGC29329, KIAA1809	KIAA1809	NM_030947, NCT01961982.2, NCT01962061.1, NCT02376503.0	221643_s_at, 222361_at, 233423_at, 234136_at	NP_569116.1, ENSP00000...
GeneID:23768405	COTL1	16	84,899,202	84,901,869	52,467	+	1	1_A3SS_gNU97_mxe1_lncRNA_AR_1.2362	14709	gene	1	0	0	25	16	10	1	1_A3SS_all_lncRNA_AR_1	25	Gene COTL1	CLP, MGC19731, FLJ43657	coactosin-like 1 (Dictyostelium)	NM_021149, NCT2325221.0, NCT2325253.0, NCT31042.2	221209_s_at, 224362_at	NP_066772.1, ENSP00000...
GeneID:83989718	CRISPLD2	16	84,955,167	84,965,116	99,929	+	2	2_A3SS_gNU97_mxe1_lncRNA_AR_1.3372, 4_A3SS_EGR1.1..3258	64677, 16749	gene, gene	0	1	1	10.5	13	14.5	2	4_A3SS_EGR1.1..1	19	Gene CRISPLD2	MGC74585, dJ3F2a.5.B014, LCRISP2, CRISPLD2, CRISP11	cysteine-rich secretory protein LCCL domain containing 2	NM_031476, NCT17894.2, NCT2325354.0	1558609_at, 231541_at	NP_113684.1, ENSP00000...
GeneID:83989823	ZDHHC7	16	85,000,086	85,049,141	57,073	+	1	4_A3SS_EGR1.1..3259	408	gene	0	0	1	10	8	14	1	4_A3SS_EGR1.1..1	14	Gene ZDHHC7	FLJ13753, SERF2, B, ZDHHC7, DKFZp762E1312, FLJ38279	zinc finger, DHHC-type containing 7	NM_017740, NM_001143845, NCT19301.1, NCT19077.1, NCT31041.2	210606_at	NP_060210.2, NP_001139320.1, ENSP00000...
GeneID:97153	KIAA0319	16	85,061,410	85,127,836	66,426	+	1	4_A3SS_EGR1.1..3260	61756	gene	0	0	1	8	9	16	1	4_A3SS_EGR1.1..1	16	Gene KIAA0319	KIAA0319	KIAA0319	NM_014732, NCT19501.0, NCT19501.1, NCT29700.1	1554440_at, 208548_at	NP_055547.1, ENSP00000...
GeneID:83989140	PAM16	16	85,131,965	85,146,114	14,149	-	2	4_A3SS_EGR1.1..3260, 4_A3SS_EGR1.1..3261	22946, 2176, -8258	Downstream, gene, upstream	0	0	1	5	8	13.67	3	4_A3SS_EGR1.1..1	16	Gene PAM16	PAM16, FLJ44299, MGC133149	family with sequence similarity 92, member B	NM_199491, NCT19727.1, NCT2325249.0		NP_940953.1, ENSP00000...
GeneID:10163580351	LOC100...	19	85,160,939	85,202,995	21,836	-	2	4_A3SS_EGR1.1..3263, 4_A3SS_EGR1.1..3266	8263, -2493	gene, upstream	0	0	1	9.5	7.5	21	2	4_A3SS_EGR1.1..1	22	Gene LOC100505467	hypothetical LOC100505467	XR_111801, XR_109329, XR_110031		
GeneID:10163580555	LOC1229...	19	85,203,131	85,220,903	17,772	+	2	4_A3SS_EGR1.1..3263, 4_A3SS_EGR1.1..3266	-8779, 1957	upstream, gene	0	0	1	9.5	7.5	21	2	4_A3SS_EGR1.1..1	22	Gene LOC122855	hypothetical protein LOC122855	XM_001715590, XM_083271, XM_167996		NP_001719942.2, NP_085771.2, NP_940991.2
GeneID:19794199	TMEM49	19	85,216,291	85,217,090	800	+	1	4_A3SS_EGR1.1..3266	4701	Downstream gene	0	0	1	10	20	22	1	4_A3SS_EGR1.1..1	22	Gene TMEM49	MGC22005, TMEM49	transmembrane protein 49	NM_030938.3	1552898_at	NP_694594.1
GeneID:23493199	KIAA0195	19	85,845,039	85,879,612	34,763	+	3	2_A3SS_gNU97_mxe1_lncRNA_AR_1.3374, 4_A3SS_EGR1.1..3270, 4_A3SS_EGR1.1..3276, 4_A3SS_EGR1.1..3278, 4_A3SS_EGR1.1..3279, 4_A3SS_EGR1.1..3280, 4_A3SS_EGR1.1..3277, 4_A3SS_EGR1.1..3278	-599, 35371, 23943, 40835, 43670, 44139, 55427	upstream, gene, upstream, gene, gene, gene, gene	0	1	1	7.43	8	13.66	7	4_A3SS_EGR1.1..1	19	Gene KIAA0182	QSER1, KIAA0182	KIAA0182	NM_014815, NM_001134473, NCT01959169.1, NCT2325293.0, NCT2376576.0, NCT2376583.0, NCT6955.3	212056_at, 212057_at, 232808_at	NP_055635.1, NP_001127945.1, ENSP00000...
GeneID:49C19orf34590	C19orf34	19	85,741,123	85,764,869	43,966	-	2	4_A3SS_EGR1.1..3279, 4_A3SS_EGR1.1..3280	19865, 769	gene, gene	0	0	1	7	8.5	19	2	4_A3SS_EGR1.1..1	21	Gene C19orf34	MGC17636, C19orf34	UPF0556 protein C19orf34	NM_030967, NCT2325230.0, NCT6956.2	227808_at	NP_996550.1, ENSP00000...
GeneID:19810302	MIR1910	19	85,775,227	85,775,308	81	-	2	4_A3SS_EGR1.1..3279, 4_A3SS_EGR1.1..3280	6902, -6814	Downstream, Downstream	0	0	1	7	8.5	19	2	4_A3SS_EGR1.1..1	21	Gene MIR1910	hsa-mir-1910, MIRN1910, MIR1910	microRNA 1910	NR_035731		



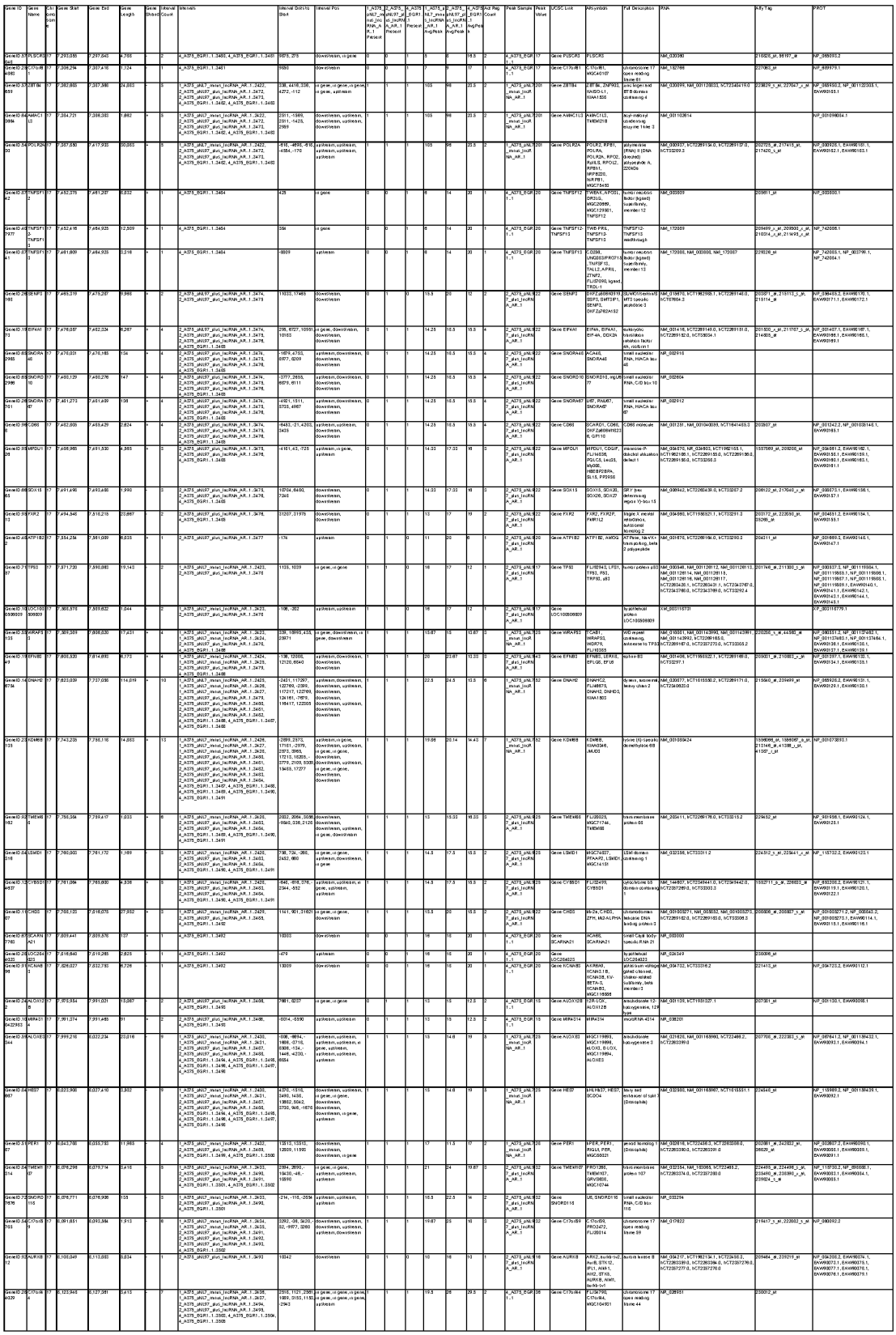
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Start	Interval Pos	1_A375_2_A375_2_A375_3_A375_4_A375_	Peak Value	Peak Sample	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
Gene ID:10326	Gene Name: COX4NB	Chromosome: 16	Gene Start: 85,612,220	Gene End: 85,633,145	Gene Length: 20,916	Gene Strand: -	Interval Count: 1	Intervals: 2_A375_shU87_plus_lacRNA_NR_1.3375	Interval Start: -305	Interval Pos: upstream	0	26	Peak Sample: 2_A375_shU820_plus_lacRNA_NR_1	UCSC Link: Gene COX4NB	Alt symbols: C16orf2, C16orf9, FNM16/9, COX4NB, NOC4	Full Description: COX4 neighbor	RNA: NM_030987, NM_001142295, NC_000016.9:1, NC_018930.2	Affy Tag: 210057_x_at, 222504_s_at, 227383_s_at	PROT: NP_076355.1, NP_001139760.1, EAW56439.1, EAW56440.1
Gene ID:10535521	Gene Name: LOC105352161	Chromosome: 16	Gene Start: 85,626,021	Gene End: 85,626,939	Gene Length: 918	Gene Strand: +	Interval Count: 1	Intervals: 2_A375_shU87_plus_lacRNA_NR_1.3375	Interval Start: 7435	Interval Pos: downstream	0	26	Peak Sample: 2_A375_shU820_plus_lacRNA_NR_1	UCSC Link: Gene LOC105352161	Alt symbols:	Full Description: hypothetical LOC105352161	RNA: XR_111827, XR_109231, XR_115033	Affy Tag:	PROT:
Gene ID:1327	Gene Name: COX4I1	Chromosome: 16	Gene Start: 85,633,198	Gene End: 85,640,908	Gene Length: 7,412	Gene Strand: +	Interval Count: 1	Intervals: 2_A375_shU87_plus_lacRNA_NR_1.3375	Interval Start: 290	Interval Pos: in gene	0	26	Peak Sample: 2_A375_shU820_plus_lacRNA_NR_1	UCSC Link: Gene COX4I1	Alt symbols: COX4, COX4I1, COX4-1, FLJ20463, COX IV, MGC72316	Full Description: cytochrome c oxidase subunit 4I1 precursor	RNA: NM_001861, NC_000019.9:1, NC_018930.2	Affy Tag: 200008_s_at, 200009_s_at, 213756_at	PROT: NP_001852.1, EAW56438.1, EAW56439.1, EAW56437.1
Gene ID:338	Gene Name: RPS6	Chromosome: 16	Gene Start: 85,932,774	Gene End: 85,936,212	Gene Length: 3,439	Gene Strand: +	Interval Count: 1	Intervals: 4_A375_EGR1.1.3281	Interval Start: -550	Interval Pos: upstream	0	8	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene RPS	Alt symbols: RPS6, PPS6P, IGSBP1, IGSBP, RPS6	Full Description: ribosomal protein S6 kinase, 240kDa	RNA: NM_001183, NC_018930.2	Affy Tag: 204387_at	PROT: NP_001174.1, EAW56428.1
Gene ID:2278	Gene Name: LOC112679	Chromosome: 16	Gene Start: 86,369,436	Gene End: 86,379,265	Gene Length: 10,829	Gene Strand: -	Interval Count: 1	Intervals: 4_A375_EGR1.1.3287	Interval Start: 6021	Interval Pos: in gene	0	5	Peak Sample: 4_A375_EGR1.1.2	UCSC Link: Gene LOC112679	Alt symbols: DKFZp434O0320, FLJ39123	Full Description: similar to KIAA4922	RNA: NR_024498	Affy Tag:	PROT:
Gene ID:3330	Gene Name: FLJ43103	Chromosome: 16	Gene Start: 86,908,131	Gene End: 86,942,486	Gene Length: 34,355	Gene Strand: -	Interval Count: 3	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2385, 2_A375_shU87_plus_lacRNA_NR_1.3377, 4_A375_EGR1.1.3289	Interval Start: 13410, 17534, 0922	Interval Pos: in gene, in gene, upstream	1	12	Peak Sample: 2_A375_shU818_plus_lacRNA_NR_1	UCSC Link: Gene FLJ43103	Alt symbols: FLJ43103, DKFZp686B08215, FLJ39983	Full Description: hypothetical LOC430530	RNA: NR_033923, NR_039444	Affy Tag:	PROT:
Gene ID:2291	Gene Name: FOXF1	Chromosome: 16	Gene Start: 86,944,103	Gene End: 86,946,070	Gene Length: 1,937	Gene Strand: +	Interval Count: 1	Intervals: 4_A375_EGR1.1.3289	Interval Start: 958	Interval Pos: in gene	0	8	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene FOXF1	Alt symbols: FOXF1, FKHL5, MGC103125, ICOMVH1, FREK1	Full Description: forkhead box F1	RNA: NM_001451, NC_018927.2	Affy Tag: 205935_at	PROT: NP_001442.2, EAW56424.1
Gene ID:7779	Gene Name: MTHFS	Chromosome: 16	Gene Start: 86,980,782	Gene End: 86,988,941	Gene Length: 8,159	Gene Strand: -	Interval Count: 1	Intervals: 4_A375_EGR1.1.3290	Interval Start: 26550	Interval Pos: downstream	0	8	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene MTHFSD	Alt symbols: FLJ12990, FLJ10955, MTHFSD, MGC103284, MGC119282	Full Description: methenyltetrahydrofolate synthetase domain containing	RNA: NM_022764, NM_001134277, NM_001134278, NC_000016.9:1, NC_018930.2	Affy Tag: 1554494_at, 1554495_s_at, NM_001135251.1, NP_001128723.1, EAW56415.1, EAW56416.1, EAW56420.1, EAW56421.1, EAW56422.1	PROT: NP_073911.2, NP_001128264.1, NP_001135251.1, NP_001128722.1, EAW56415.1, EAW56416.1, EAW56420.1, EAW56421.1, EAW56422.1
Gene ID:5308361	Gene Name: LOC105369361	Chromosome: 16	Gene Start: 87,236,430	Gene End: 87,260,993	Gene Length: 24,563	Gene Strand: -	Interval Count: 3	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2389, 2_A375_shU87_plus_lacRNA_NR_1.3381, 4_A375_EGR1.1.3292	Interval Start: 230, 284, 118	Interval Pos: in gene, in gene, upstream	1	14	Peak Sample: 2_A375_shU818_plus_lacRNA_NR_1	UCSC Link: Gene LOC105369361	Alt symbols: DKFZp434J1813	Full Description: hypothetical LOC105369361	RNA: XM_003119935, XM_003119936, XM_003119735, XM_003119736, XM_003116734, XM_003120086, XM_003120087, XM_003120088	Affy Tag:	PROT: XP_003119983.1, XP_003119984.1, XP_003119735.1, XP_003119736.1, XP_003119737.1, XP_003120034.1, XP_003120035.1
Gene ID:791	Gene Name: FBXO31	Chromosome: 16	Gene Start: 87,362,962	Gene End: 87,425,705	Gene Length: 62,744	Gene Strand: -	Interval Count: 5	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2392, 2_A375_shU87_plus_lacRNA_NR_1.3382, 3_A375_shU87_plus_lacRNA_NR_1.3383, 4_A375_EGR1.1.3293, 4_A375_EGR1.1.3294	Interval Start: 52, 6012, -199, 48025, 6044	Interval Pos: upstream, in gene, upstream, in gene, in gene	1	14	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene FBXO31	Alt symbols: pp3366, DKFZp434B0231, FBXO1a, Fbx31, MGC19327, MGC13419, FBX031, DKFZp434J1813, FBX14, FLJ22477	Full Description: F-box protein 31	RNA: 224735, NR_024595, NC_000016.9:1, NC_018930.2, NC_000083.6, NC_000084.6, NC_018930.2	Affy Tag: 219764_at, 219765_s_at, 222345_at, 224182_s_at	PROT: NP_079013.2, EAW56403.1, EAW56404.1, EAW56402.1, EAW56403.1, EAW56404.1
Gene ID:831	Gene Name: MAP1LC3B	Chromosome: 16	Gene Start: 87,425,891	Gene End: 87,435,390	Gene Length: 12,379	Gene Strand: +	Interval Count: 4	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2393, 2_A375_shU87_plus_lacRNA_NR_1.3382, 3_A375_shU87_plus_lacRNA_NR_1.3383, 4_A375_EGR1.1.3294	Interval Start: -41, -6103, 103, 6137	Interval Pos: upstream, upstream, in gene, upstream	1	19	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene MAP1LC3B	Alt symbols: LC3B, ATG8F, MAP1LC3B, MAP1ALVEC3	Full Description: microtubule-associated protein 1 light chain 3 beta	RNA: NM_022818, NC_000016.9:1, NC_018930.2, NC_000083.6, NC_000084.6, NC_018930.2	Affy Tag: 208763_s_at, 208768_s_at	PROT: NP_073729.1, EAW56397.1, EAW56398.1, EAW56393.1, EAW56394.1, EAW56395.1, EAW56396.1, EAW56398.1
Gene ID:2530	Gene Name: ZCCHC14	Chromosome: 16	Gene Start: 87,559,852	Gene End: 87,625,460	Gene Length: 65,608	Gene Strand: +	Interval Count: 1	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2391	Interval Start: -1309	Interval Pos: upstream	1	19	Peak Sample: 1_A375_shU819_minus_lacRNA_NR_1	UCSC Link: Gene ZCCHC14	Alt symbols: ZCCHC14, KIAA1849, MGC126527, MGC14139, BDG28, BDG-28	Full Description: zinc finger, CCHC domain containing 14	RNA: NM_015144, NC_018930.2, NC_018930.2, NC_000083.6, NC_000084.6, NC_018930.2	Affy Tag: 213655_at, 215428_at, 215427_s_at	PROT: NP_055959.1, EAW56390.1, EAW56391.1, EAW56392.1, EAW56393.1, EAW56391.1
Gene ID:336	Gene Name: JPH3	Chromosome: 16	Gene Start: 87,636,499	Gene End: 87,731,762	Gene Length: 95,263	Gene Strand: +	Interval Count: 9	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2372, 2_A375_shU87_minus_lacRNA_NR_1.3373, 3_A375_shU87_plus_lacRNA_NR_1.3383, 4_A375_shU87_plus_lacRNA_NR_1.3386, 4_A375_EGR1.1.3295, 4_A375_EGR1.1.3296, 4_A375_EGR1.1.3298, 4_A375_EGR1.1.3299, 4_A375_EGR1.1.3300	Interval Start: 5757, 36925, 5741, 36929, 24645, 63415, 24653, 64653, 64645, 91213	Interval Pos: in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	11.87	14.66	15.43	7	2_A375_shU8461_plus_lacRNA_NR_1	Gene JPH3	JPH, JP-3, TNRC22, JPH3, HDL2, FLJ44707, CAG1.27	Full Description: junctophilin 3	RNA: NM_020655, NC_018931.2, NC_018930.2	Affy Tag: 220958_at, 229294_at, 234706_at, 243879_at	PROT: NP_065706.2, EAW56398.1, EAW56397.1
Gene ID:1202215	Gene Name: LOC100202151	Chromosome: 16	Gene Start: 87,727,145	Gene End: 87,729,765	Gene Length: 2,620	Gene Strand: +	Interval Count: 4	Intervals: 1_A375_EGR1.1.3299, 4_A375_EGR1.1.3300, 4_A375_EGR1.1.3301	Interval Start: 10641, 6801, 4781, 2641	Interval Pos: downstream, downstream, downstream, in gene	0	6.23	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene LOC100129215	Alt symbols:	Full Description: hypothetical LOC100129215	RNA: XR_111810, XR_109254, XR_115036	Affy Tag:	PROT:
Gene ID:1129937	Gene Name: LOC100129937	Chromosome: 16	Gene Start: 87,731,749	Gene End: 87,739,290	Gene Length: 7,541	Gene Strand: -	Interval Count: 2	Intervals: 4_A375_EGR1.1.3300, 4_A375_EGR1.1.3301	Interval Start: 14266, 11916	Interval Pos: downstream, downstream	0	8	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene LOC100129937	Alt symbols: FLJ43755, FLJ43576, FLJ45154	Full Description: hypothetical LOC100129937	RNA: NR_039488	Affy Tag:	PROT:
Gene ID:80	Gene Name: SLC7A5	Chromosome: 16	Gene Start: 87,960,829	Gene End: 87,965,100	Gene Length: 39,271	Gene Strand: +	Interval Count: 4	Intervals: 1_A375_EGR1.1.3305, 4_A375_EGR1.1.3306, 4_A375_EGR1.1.3307, 4_A375_EGR1.1.3308	Interval Start: 43648, 40966, 34172, 33116	Interval Pos: downstream, downstream, in gene, in gene	0	7.5	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene SLC7A5	Alt symbols: BTO1C, MPE16, SLC7A5, hLAT1, D16S469E, E16, CD98, LAT1	Full Description: solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	RNA: NM_003486, NC_018930.2, NC_018930.2, NC_000083.6, NC_000084.6, NC_018930.2	Affy Tag: 201195_s_at	PROT: NP_003477.4, EAW56370.1, EAW56374.1, EAW56373.1
Gene ID:1050976	Gene Name: LOC105097670	Chromosome: 16	Gene Start: 87,965,961	Gene End: 87,994,903	Gene Length: 972	Gene Strand: +	Interval Count: 4	Intervals: 4_A375_EGR1.1.3306, 4_A375_EGR1.1.3307, 4_A375_EGR1.1.3308	Interval Start: -6809, -1817, 4967, 6023	Interval Pos: upstream, upstream, downstream, downstream	0	7.3	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene LOC105097670	Alt symbols:	Full Description: hypothetical LOC105097670	RNA: XR_111861, XR_109533, XR_115037	Affy Tag:	PROT:
Gene ID:79	Gene Name: CASA2	Chromosome: 16	Gene Start: 87,921,825	Gene End: 87,970,112	Gene Length: 48,287	Gene Strand: -	Interval Count: 1	Intervals: 2_A375_shU87_plus_lacRNA_NR_1.3365	Interval Start: 4326	Interval Pos: in gene	0	19	Peak Sample: 2_A375_shU817_plus_lacRNA_NR_1	UCSC Link: Gene CASA	Alt symbols: CAS, CAV2, CAVA, CASA	Full Description: calicolarin alpha/beta VA, endothelial	RNA: NM_001759, NC_018927.2, NC_018930.2	Affy Tag: 209721_at	PROT: NP_001735.1, EAW56371.1, EAW56372.1
Gene ID:54	Gene Name: BNIP3	Chromosome: 16	Gene Start: 87,963,035	Gene End: 88,110,924	Gene Length: 123,888	Gene Strand: +	Interval Count: 2	Intervals: 3_A375_shU87_minus_lacRNA_NR_1.2374, 2_A375_shU87_plus_lacRNA_NR_1.3369	Interval Start: -398, -430	Interval Pos: upstream, upstream	1	25	Peak Sample: 2_A375_shU818_plus_lacRNA_NR_1	UCSC Link: Gene BNIP	Alt symbols: FLJ11277, DKFZp781H172, BNIP3R1, BNIP1, FLJ20535, BNIP, BENI01	Full Description: BCL2/adenovirus E1B 19kDa interacting protein 3	RNA: NM_004052, NM_170667, NM_001173839, NM_001173840, NM_001173841, NM_001173842, NM_001173843, NC_018927.2, NC_018930.2, NC_000083.6, NC_000084.6, NC_018930.2	Affy Tag: 209060_x_at	PROT: NP_982293.2, NP_004322.2, NP_001157611.1, NP_001157612.1, NP_001157613.1, NP_001157614.1, EAW56364.1, EAW56365.1, EAW56366.1, EAW56367.1, EAW56368.1, EAW56370.1
Gene ID:9271	Gene Name: ZNF469	Chromosome: 16	Gene Start: 88,480,879	Gene End: 88,497,165	Gene Length: 16,286	Gene Strand: +	Interval Count: 2	Intervals: 2_A375_shU87_plus_lacRNA_NR_1.3391, 4_A375_EGR1.1.3311	Interval Start: 13651, -1331	Interval Pos: downstream, upstream	0	8	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene ZNF469	Alt symbols: KIAA1886, BCS, ZNF469	Full Description: zinc finger protein 469	RNA: XM_001127484	Affy Tag: 233440_at	PROT: XP_001128618.1
Gene ID:1682	Gene Name: ZFP91	Chromosome: 16	Gene Start: 88,520,014	Gene End: 88,591,874	Gene Length: 81,860	Gene Strand: +	Interval Count: 8	Intervals: 2_A375_shU87_plus_lacRNA_NR_1.3391, 4_A375_EGR1.1.3312, 4_A375_EGR1.1.3313, 4_A375_EGR1.1.3314, 4_A375_EGR1.1.3315, 4_A375_EGR1.1.3316, 4_A375_EGR1.1.3317, 4_A375_EGR1.1.3318	Interval Start: -10834, -976, 9714, 19998, 29116, 47292, 73922, 81934	Interval Pos: downstream, upstream, in gene, in gene, in gene, in gene, in gene, in gene	0	8.66	8.38	17.25	8	4_A375_EGR1.1.3	Gene ZFP91	ZFP91, ZNF489, FOG1, ZNF804, FOG	Full Description: zinc finger protein, multitype 1	RNA: NM_153813, NC_018930.2, NC_018930.2, NC_000083.6, NC_000084.6, NC_018930.2	Affy Tag: 242282_at	PROT: NP_722120.2, EAW56358.1, EAW56359.1, EAW56360.1, EAW56361.1, EAW56362.1
Gene ID:4345	Gene Name: ZCSH18	Chromosome: 16	Gene Start: 88,636,769	Gene End: 88,696,372	Gene Length: 61,603	Gene Strand: +	Interval Count: 6	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2376, 2_A375_shU87_plus_lacRNA_NR_1.3392, 4_A375_EGR1.1.3319, 4_A375_EGR1.1.3320, 4_A375_EGR1.1.3321, 4_A375_EGR1.1.3322	Interval Start: 6493, -9385, 82507, 82507, 89497, 89497	Interval Pos: upstream, upstream, downstream, downstream, downstream, downstream	1	11.8	11.4	13.6	5	1_A375_shU817_minus_lacRNA_NR_1	Gene ZCSH18	FLJ32804, ZCSH18, NHN1, FLJ46330	Full Description: zinc finger CCCH-type and SEL-10 domain containing 18	RNA: NM_144984, NC_018927.2, NC_018930.2, NC_000083.6, NC_000084.6, NC_018930.2	Affy Tag: 226168_at, 235418_s_at	PROT: NP_659233.2, EAW56356.1, EAW56357.1, EAW56358.1, EAW56359.1, EAW56360.1, EAW56361.1
Gene ID:27190	Gene Name: IL17C	Chromosome: 16	Gene Start: 88,700,001	Gene End: 88,706,902	Gene Length: 6,901	Gene Strand: +	Interval Count: 6	Intervals: 4_A375_EGR1.1.3320, 4_A375_EGR1.1.3321, 4_A375_EGR1.1.3322, 4_A375_EGR1.1.3323, 4_A375_EGR1.1.3324	Interval Start: -6105, -4393, 55, 830, 4163, 9111	Interval Pos: upstream, upstream, in gene, downstream, downstream, downstream	0	4.83	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene IL17C	Alt symbols: interleukin 17C	Full Description: interleukin 17C	RNA: NM_013278, NC_018927.1	Affy Tag: 224379_at	PROT: NP_037410.1, EAW56798.1
Gene ID:55	Gene Name: CYBA	Chromosome: 16	Gene Start: 88,709,897	Gene End: 88,717,457	Gene Length: 7,560	Gene Strand: -	Interval Count: 7	Intervals: 4_A375_EGR1.1.3320, 4_A375_EGR1.1.3321, 4_A375_EGR1.1.3322, 4_A375_EGR1.1.3323, 4_A375_EGR1.1.3324, 4_A375_EGR1.1.3325, 4_A375_EGR1.1.3326	Interval Start: 18649, 12401, 11901, 8273, 5343, 4223, -4498	Interval Pos: downstream, downstream, downstream, downstream, in gene, upstream, upstream	0	8	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene CYBA	Alt symbols: CYBA, p22-PHOX	Full Description: cytochrome b-245, alpha polypeptide	RNA: NM_000101, NC_018930.2, NC_018927.2, NC_018930.2, NC_018927.2, NC_018930.2	Affy Tag: 203035_s_at, 229443_at	PROT: NP_000092.2, EAW56794.1, EAW56795.1, EAW56796.1, EAW56797.1, EAW56798.1
Gene ID:4598	Gene Name: MVD	Chromosome: 16	Gene Start: 88,716,345	Gene End: 88,729,493	Gene Length: 11,147	Gene Strand: +	Interval Count: 4	Intervals: 4_A375_EGR1.1.3323, 4_A375_EGR1.1.3324, 4_A375_EGR1.1.3325, 4_A375_EGR1.1.3326	Interval Start: 20011, 11535, 11415, 7543	Interval Pos: downstream, downstream, downstream, in gene	0	8	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene MVD	Alt symbols: FPP1780, MPD, MVD	Full Description: mevalonate (diphospho) decarboxylase	RNA: NM_002461, NC_018927.2, NC_018930.2, NC_018927.2, NC_018930.2	Affy Tag: 202437_s_at	PROT: NP_002452.1, EAW56790.1, EAW56791.1, EAW56792.1
Gene ID:2197	Gene Name: MGC23284	Chromosome: 16	Gene Start: 88,729,701	Gene End: 88,753,994	Gene Length: 23,615	Gene Strand: +	Interval Count: 2	Intervals: 4_A375_EGR1.1.3326, 4_A375_EGR1.1.3327	Interval Start: -7629, 51638	Interval Pos: upstream, downstream	0	9.5	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene MGC23284	Alt symbols:	Full Description: hypothetical LOC157457	RNA: NR_024299, NR_024402	Affy Tag: 1559154_s_at, 1560863_at	PROT:
Gene ID:7029	Gene Name: SNAI3	Chromosome: 16	Gene Start: 88,744,090	Gene End: 88,762,862	Gene Length: 8,792	Gene Strand: -	Interval Count: 1	Intervals: 4_A375_EGR1.1.3327	Interval Start: -6729	Interval Pos: upstream	0	12	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene SNAI3	Alt symbols: ZNF295, SNAH3, Zfp295, SNAI3, MGC129898, SHUC	Full Description: snail homolog 3 (Drosophila)	RNA: NM_176510	Affy Tag: 1569220_at	PROT: NP_840101.1
Gene ID:9932	Gene Name: RNF166	Chromosome: 16	Gene Start: 88,762,903	Gene End: 88,772,629	Gene Length: 9,726	Gene Strand: -	Interval Count: 2	Intervals: 4_A375_EGR1.1.3327, 4_A375_EGR1.1.3328	Interval Start: 11216, 7317	Interval Pos: downstream, in gene	0	13	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene RNF166	Alt symbols: MGC14351, RNF166, MGC2647	Full Description: ring finger protein 166	RNA: NM_178541, NM_001171618, NM_001171619, NM_001171620, NC_018930.2, NC_018927.2, NC_018930.2, NC_018927.2, NC_018930.2	Affy Tag: 227726_at	PROT: NP_849185.1, NP_001158207.1, NP_001158208.1, EAW56783.1, EAW56784.1, EAW56785.1, EAW56786.1, EAW56787.1, EAW56788.1, EAW56789.1, EAW56790.1, EAW56791.1, EAW56792.1, EAW56793.1, EAW56794.1
Gene ID:8180	Gene Name: CTU2	Chromosome: 16	Gene Start: 88,772,891	Gene End: 88,781,794	Gene Length: 8,903	Gene Strand: +	Interval Count: 2	Intervals: 4_A375_EGR1.1.3328, 4_A375_EGR1.1.3329	Interval Start: -7679, 17197	Interval Pos: upstream, downstream	0	9.3	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene CTU2	Alt symbols: NCS2, UPF0420, C16orf54, CTU2, MGC119851, MGC140993, MGC149894	Full Description: cytosolic thiouridylase subunit 2 homolog (S. pombe)	RNA: NM_001012709, NM_001012782, NC_018930.2, NC_018927.2, NC_018930.2, NC_018927.2, NC_018930.2	Affy Tag: 1561600_at, 1561601_s_at, 1561602_s_at, 239410_at	PROT: NP_001012727.1, NP_001012783.1, EAW56776.1, EAW56777.1, EAW56778.1, EAW56779.1, EAW56780.1, EAW56781.1, EAW56782.1, EAW56783.1, EAW56784.1
Gene ID:60	Gene Name: FAM35A	Chromosome: 16	Gene Start: 88,781,748	Gene End: 88,831,372	Gene Length: 49,624	Gene Strand: -	Interval Count: 9	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2377, 2_A375_shU87_plus_lacRNA_NR_1.3393, 3_A375_shU87_plus_lacRNA_NR_1.3393, 4_A375_EGR1.1.3330, 4_A375_EGR1.1.3331, 4_A375_EGR1.1.3332, 4_A375_EGR1.1.3333, 4_A375_EGR1.1.3334, 4_A375_EGR1.1.3335	Interval Start: -586, -743, 61224, 57930, 52595, 50534, 40868, 34406, 16099	Interval Pos: upstream, upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	7.75	8.46	17.83	9	4_A375_EGR1.1.3	Gene FAM35A	FAM35A, PIEZO1-Mib, KIAA0233	Full Description: Family with sequence similarity 35, member A	RNA: NM_031142994	Affy Tag: 232791_at	PROT: NP_001138138.2
Gene ID:1050960	Gene Name: LOC105096960	Chromosome: 16	Gene Start: 88,797,598	Gene End: 88,805,998	Gene Length: 8,400	Gene Strand: +	Interval Count: 5	Intervals: 4_A375_EGR1.1.3329, 4_A375_EGR1.1.3330, 4_A375_EGR1.1.3331, 4_A375_EGR1.1.3332, 4_A375_EGR1.1.3333	Interval Start: 7365, -4119, 1276, 3450, 12186	Interval Pos: upstream, upstream, in gene, downstream, downstream	0	8.2	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene LOC105096960	Alt symbols: FLJ45121	Full Description: hypothetical LOC105096960	RNA: XR_109356	Affy Tag:	PROT:
Gene ID:9039	Gene Name: FLJ44048	Chromosome: 16	Gene Start: 88,809,175	Gene End: 88,812,973	Gene Length: 3,800	Gene Strand: +	Interval Count: 3	Intervals: 4_A375_EGR1.1.3332, 4_A375_EGR1.1.3333, 4_A375_EGR1.1.3334	Interval Start: -6137, 1605, 7969	Interval Pos: upstream, in gene, downstream	0	8.33	Peak Sample: 4_A375_EGR1.1.3	UCSC Link: Gene FLJ44048	Alt symbols: MGC135175	Full Description: hypothetical protein FLJ44048	RNA: XR_111861, XR_109533, XR_115189	Affy Tag:	PROT:
Gene ID:820	Gene Name: CDT1	Chromosome: 16	Gene Start: 88,870,159	Gene End: 88,879,999	Gene Length: 9,840	Gene Strand: +	Interval Count: 11	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2378, 2_A375_shU87_plus_lacRNA_NR_1.3394, 3_A375_shU87_plus_lacRNA_NR_1.3394, 4_A375_EGR1.1.3335, 4_A375_EGR1.1.3336, 4_A375_EGR1.1.3337, 4_A375_EGR1.1.3338, 4_A375_EGR1.1.3339, 4_A375_EGR1.1.3340, 4_A375_EGR1.1.3341, 4_A375_EGR1.1.3342	Interval Start: -386, 3435, -386, 8210, 9348, 23167, 3960, 3698, 7796, 6422, 12470	Interval Pos: upstream, downstream, upstream, downstream, downstream, in gene, in gene, upstream, downstream, downstream, downstream, downstream, downstream	1	11	10.68	15.29	17.29	7	4_A375_shU819_plus_lacRNA_NR_1	Gene CDT1	KIS2, CDT1, DUP	Full Description: chromatin licensing and DNA replication factor 1	RNA: NM_030925, NC_018927.2, NC_018930.2, NC_018927.2, NC_018930.2	Affy Tag: 209922_s_at, 223991_s_at	PROT: NP_112150.2, EAW56780.1, EAW56782.1, EAW56784.1
Gene ID:353	Gene Name: APRT	Chromosome: 16	Gene Start: 88,873,977	Gene End: 88,876,342	Gene Length: 2,365	Gene Strand: -	Interval Count: 11	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2379, 2_A375_shU87_minus_lacRNA_NR_1.3379, 2_A375_shU87_plus_lacRNA_NR_1.3394, 2_A375_shU87_plus_lacRNA_NR_1.3395, 3_A375_shU87_plus_lacRNA_NR_1.3395, 4_A375_EGR1.1.3336, 4_A375_EGR1.1.3337, 4_A375_EGR1.1.3338, 4_A375_EGR1.1.3339, 4_A375_EGR1.1.3340, 4_A375_EGR1.1.3341, 4_A375_EGR1.1.3342	Interval Start: 6422, -202, 6422, 156, 7115, 5835, 4185, 2195, 390, 285, -4514	Interval Pos: downstream, upstream, downstream, upstream, downstream, upstream, in gene, upstream, upstream	1	11	10.68	15.29	17.29	7	4_A375_shU819_plus_lacRNA_NR_1	Gene APRT	APRT, MGC125586, APRT, DKFZp686D0317, MGC126557, MGC129961	Full Description: adenine phosphoribosyltransferase	RNA: NM_000485, NM_001030018, NC_018927.2, NC_018930.2	Affy Tag: 200319_s_at, 213902_s_at	PROT: NP_000476.1, NP_001029189.1, EAW56781.1
Gene ID:2595	Gene Name: GALNS	Chromosome: 16	Gene Start: 88,890,142	Gene End: 88,933,074	Gene Length: 43,232	Gene Strand: +	Interval Count: 14	Intervals: 1_A375_shU87_minus_lacRNA_NR_1.2376, 2_A375_shU87_minus_lacRNA_NR_1.3379, 2_A375_shU87_plus_lacRNA_NR_1.3394, 2_A375_shU87_plus_lacRNA_NR_1.3395, 2_A375_shU87_plus_lacRNA_NR_1.3396, 4_A375_EGR1.1.3338, 4_A375_EGR1.1.3339, 4_A375_EGR1.1.3340, 4_A375_EGR1.1.3341, 4_A375_EGR1.1.3342, 4_A375_EGR1.1.3343, 4_A375_EGR1.1.3344	Interval Start: 53634, 44780, 53634, 44676, 148, 92142, 39870, 49196, 47230, 45422, 44786, 40716, 7926, 6516	Interval Pos: downstream, downstream, downstream, downstream, upstream, downstream, downstream, downstream, downstream, downstream, in gene, upstream, upstream	1	13.5	14.1	17.2	10	1_A375_shU819_minus_lacRNA_NR_1	Gene GALNS	GALNAC6S, FLJ42844, MPS4A, GALNS, FLJ90731, FLJ11734, GAS	Full Description: galactosamine (N-acetyl)-6-sulfate sulfatase	RNA: NM_000512, NC_018927.2, NC_018930.2, NC_018927.2, NC_018930.2	Affy Tag: 208325_s_at, 236986_at	PROT: NP_000503.1, EAW56789.1, EAW56787.1, EAW56788.1
Gene ID:9935	Gene Name: TRAPPC2L	Chromosome: 16	Gene Start: 88,925,936	Gene End: 88,927,520	Gene Length: 4,614	Gene Strand: +	Interval Count: 5	Intervals: 2_A375_shU87_plus_lacRNA_NR_1.3395, 4_A375_EGR1.1.3343, 4_A375_EGR1.1.3344	Interval Start: 14, 7694, 6968	Interval Pos: in gene, downstream, downstream	0	7.33	Peak Sample: 2_A375_shU823_plus_lacRNA_NR_1	UCSC Link: Gene TRAPPC2L	Alt symbols: HSPC175, TRAPPC2L, FLJ44227, MGC111198	Full Description: trafficking protein particle complex 2-like	RNA: NM_016209, NC_018966.2	Affy Tag: 218394_at, 239827_at, 239828_s_at	PROT: NP_057293.1, EAW56795.1
Gene ID:8748	Gene Name: PABPN1L	Chromosome: 16	Gene Start: 88,926,034	Gene End: 88,933,014	Gene Length: 6,980	Gene Strand: -	Interval Count: 3	Intervals: 2_A375_shU87_plus_lacRNA_NR_1.3396, 4_A375_EGR1.1.3343, 4_A375_EGR1.1.3344	Interval Start: 9484, 1614, 622	Interval Pos: downstream, in gene, in gene	0	7.33	Peak Sample: 2_A375_shU823_plus_lacRNA_NR_1	UCSC Link: Gene PABPN1L	Alt symbols: EPAB2, PABPN1L, PABPN1	Full Description: poly(A) binding protein, nuclear 1-like (cytoplasmic)	RNA: NM_031036.5	Affy Tag:	PROT: NP_001073858.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.863	CBFA2T3	16	88,941,267	89,043,401	102,134	-	20	4_A375_EGR1..1..3343, 4_A375_EGR1..1..3344, 4_A375_EGR1..1..3345, 4_A375_EGR1..1..3346, 4_A375_EGR1..1..3347, 4_A375_EGR1..1..3348, 4_A375_EGR1..1..3349, 4_A375_EGR1..1..3350, 4_A375_EGR1..1..3351, 4_A375_EGR1..1..3352, 4_A375_EGR1..1..3353, 4_A375_EGR1..1..3354, 4_A375_EGR1..1..3355, 4_A375_EGR1..1..3356, 4_A375_EGR1..1..3357, 4_A375_EGR1..1..3358, 4_A375_EGR1..1..3359, 4_A375_EGR1..1..3360, 4_A375_EGR1..1..3361, 4_A375_EGR1..1..3362	112201, 111209, 95305, 92009, 85001, 79529, 78965, 75145, 73652, 69721, 66921, 54409, 48857, 43681, 38729, 36553, 20313, 18009, 3929, -6967	downstream, downstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	0	0	1	5.9	7	17.65	20	4_A375_EGR1..1	23	Gene CBFA2T3	ZMYND4, MTG16, CBFA2T3, MTGR2, ETO2	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	NM_005187, NM_175931, hCT2253356.0, hCT2253357.0, hCT2253358.0, hCT2253359.0, hCT2253360.0, hCT2253361.0, hCT2253362.0	208056_s_at	NP_005178.4, NP_787127.1, EAW66746.1, EAW66747.1, EAW66749.1, EAW66752.1, EAW66748.1, EAW66750.1, EAW66751.1
GeneID.100129697	LOC100129697	16	89,006,549	89,017,932	11,383	+	5	4_A375_EGR1..1..3356, 4_A375_EGR1..1..3357, 4_A375_EGR1..1..3358, 4_A375_EGR1..1..3359, 4_A375_EGR1..1..3360	-7029, -1877, 299, 16539, 18843	upstream, upstream, in gene, downstream, downstream	0	0	1	7	8.4	16.2	5	4_A375_EGR1..1	17	Gene LOC100129697		hypothetical LOC100129697	XR_111614, XR_109340		
GeneID.100506183	LOC100506183	16	89,112,580	89,119,373	6,793	-	6	2_A375_pNL97_plus_lncRNA_AR..1..3399, 4_A375_EGR1..1..3364, 4_A375_EGR1..1..3365, 4_A375_EGR1..1..3366, 4_A375_EGR1..1..3367, 4_A375_EGR1..1..3368	15181, 13101, 797, -2003, -2675, -5587	downstream, downstream, in gene, upstream, upstream, upstream	0	1	1	7.83	9.17	16.17	6	4_A375_EGR1..1	21	Gene LOC100506183		hypothetical LOC100506183	XR_111619, XR_109341, XR_115040		
GeneID.197322	ACSF3	16	89,160,254	89,222,169	61,915	+	3	4_A375_EGR1..1..3370, 4_A375_EGR1..1..3371, 4_A375_EGR1..1..3372	60098, 63298, 67282	in gene, downstream, downstream	0	0	1	6.33	8	20.67	3	4_A375_EGR1..1	22	Gene ACSF3	ACSF3, FLJ39242	acyl-CoA synthetase family member 3	NM_174917, NM_001127214, NR_023316, hCT2348998.0	1556552_s_at, 227464_at	NP_777577.2, NP_001120686.1, EAW66744.1
GeneID.283860	C16orf81	16	89,225,628	89,230,083	4,455	+	5	4_A375_EGR1..1..3370, 4_A375_EGR1..1..3371, 4_A375_EGR1..1..3372, 4_A375_EGR1..1..3373, 4_A375_EGR1..1..3374	-5276, -2076, 1908, 7940, 13476	upstream, upstream, in gene, downstream, downstream	0	0	1	7.8	9	19.4	5	4_A375_EGR1..1	22	Gene C16orf81	FLJ38701, C16orf81	chromosome 16 open reading frame 81	NR_024347		
GeneID.1013	CDH15	16	89,238,163	89,261,900	23,737	+	5	4_A375_EGR1..1..3373, 4_A375_EGR1..1..3374, 4_A375_EGR1..1..3375, 4_A375_EGR1..1..3376, 4_A375_EGR1..1..3377	-4595, 941, 4717, 7053, 23277	upstream, in gene, in gene, in gene, in gene	0	0	1	8.8	7.4	17.8	5	4_A375_EGR1..1	19	Gene CDH15	CDH15, CDH3, CDH14, MCAD, MRD3, CDHM	cadherin 15, type 1, M-cadherin (myotubule)	NM_004933, hCT2257251.0, hCT23660.4	206327_s_at, 206328_at	NP_004924.1, EAW66741.1, EAW66742.1
GeneID.146429	LOC146429	16	89,262,407	89,266,529	4,122	-	1	4_A375_EGR1..1..3377	5069	downstream	0	0	1	9	5	17	1	4_A375_EGR1..1	17	Gene LOC146429		putative solute carrier family 22 member ENSG00000182157	XM_370997, XM_946336	232765_x_at	XP_370997.5, XP_951429.3
GeneID.100506202	LOC100506202	16	89,262,565	89,266,726	4,161	-	1	4_A375_EGR1..1..3377	5266	downstream	0	0	1	9	5	17	1	4_A375_EGR1..1	17	Gene LOC100506202		putative solute carrier family 22 member ENSG00000182157-like	XM_003118727, XM_003120858		XP_003118775.1, XP_003120906.1
GeneID.197320	ZNF778	16	89,284,111	89,295,363	11,252	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3400	193	in gene	0	1	0	14	16	15	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ZNF778	MGC150573, ZNF778, FLJ31875	zinc finger protein 778	NM_182531	1556581_at	NP_872337.2
GeneID.29123	ANKRD11	16	89,334,035	89,556,969	222,934	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3402, 4_A375_EGR1..1..3379, 4_A375_EGR1..1..3380	170281, 216281, 195081	in gene, in gene, in gene	0	1	1	10	10.67	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ANKRD11	ANCO-1, ANCO1, ANKRD11, LZ16, T13	ankyrin repeat domain 11	NM_013275, hCT2253337.0, hCT2253338.0, hCT2253341.0, hCT2253342.0	219437_s_at, 226012_at, 228356_at, 231999_at, 234701_at, 238538_at	NP_037407.4, EAW66732.1, EAW66731.1, EAW66733.1, EAW66734.1
GeneID.100506251	LOC100506251	16	89,363,916	89,364,725	809	+	1	4_A375_EGR1..1..3380	-2028	upstream	0	0	1	5	3	15	1	4_A375_EGR1..1	15	Gene LOC100506251		hypothetical LOC100506251	XR_111618, XR_109343, XR_115042		
GeneID.100287036	LOC100287036	16	89,387,541	89,391,518	3,977	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3402	-853	upstream	0	1	0	13	22	11	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100287036		hypothetical LOC100287036	XR_111616, XR_109342, XR_115041		
GeneID.100506266	LOC100506266	16	89,557,733	89,565,693	7,960	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3403, 4_A375_EGR1..1..3381	17547, 16299	downstream, downstream	0	1	1	8.5	13	12	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC100506266		hypothetical LOC100506266	XR_109344		
GeneID.6687	SPG7	16	89,574,805	89,624,174	49,369	+	7	2_A375_pNL97_plus_lncRNA_AR..1..3403, 2_A375_pNL97_plus_lncRNA_AR..1..3404, 2_A375_pNL97_plus_lncRNA_AR..1..3405, 4_A375_EGR1..1..3381, 4_A375_EGR1..1..3382, 4_A375_EGR1..1..3383, 4_A375_EGR1..1..3384	475, 52331, 57067, -773, 37051, 52107, 57547	in gene, downstream, downstream, upstream, in gene, downstream, downstream	0	1	1	11.2	12.8	15.8	5	4_A375_EGR1..1	20	Gene SPG7	SPG7, CAR, CMAR, FLJ37308, PGN, MGC126332, MGC126331, SPG5C	spastic paraplegia 7 (pure and complicated autosomal recessive)	NM_003119, NM_199367, hCT1953800.1, hCT2257273.0, hCT2257274.0, hCT6628.3	202104_s_at, 214494_s_at, 230684_s_at, 235325_at, 238286_at	NP_003110.1, NP_955399.1, EAW66726.1, EAW66727.1, EAW66728.1, EAW66729.1
GeneID.6137	RPL13	16	89,627,090	89,629,848	2,758	+	5	2_A375_pNL97_plus_lncRNA_AR..1..3404, 2_A375_pNL97_plus_lncRNA_AR..1..3405, 4_A375_EGR1..1..3383, 4_A375_EGR1..1..3384, 4_A375_EGR1..1..3385	46, 4782, -178, 5282, 10830	in gene, downstream, upstream, downstream, downstream	0	1	1	14.33	15	19	3	4_A375_EGR1..1	20	Gene RPL13	FLJ27454, BBC1, FLJ27453, L13, RPL13, MGC117342, MGC71373, D16S444E	ribosomal protein L13	NM_033251, NM_000977, hCT1964145.1, hCT1964146.1	1565758_at, 1565759_at, 208929_x_at, 212191_x_at, 212734_x_at, 212933_x_at, 229590_at	NP_150254.1, NP_000968.2, EAW66724.1, EAW66725.1
GeneID.606500	SNORD68	16	89,627,838	89,627,909	71	+	5	2_A375_pNL97_plus_lncRNA_AR..1..3404, 2_A375_pNL97_plus_lncRNA_AR..1..3405, 4_A375_EGR1..1..3383, 4_A375_EGR1..1..3384, 4_A375_EGR1..1..3385	-702, 4034, -926, 4514, 10082	upstream, downstream, upstream, downstream, downstream	0	1	1	14.33	15	19	3	4_A375_EGR1..1	20	Gene SNORD68	HBII-202, SNORD68	small nucleolar RNA, C/D box 68	NR_002450		
GeneID.27132	CPNE7	16	89,642,176	89,663,654	21,478	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3405, 4_A375_EGR1..1..3384, 4_A375_EGR1..1..3385, 4_A375_EGR1..1..3386	-10304, -9824, -4256, 26660	upstream, upstream, upstream, downstream	0	1	1	11.67	12.67	18.33	3	4_A375_EGR1..1	20	Gene CPNE7	CPNE7, MGC34192	copine VII	NM_014427, NM_153636, hCT2344205.0, hCT6734.4	219707_at	NP_055242.1, NP_705900.1, EAW66721.1, EAW66722.1
GeneID.1800	DPEP1	16	89,679,716	89,704,839	25,123	+	2	4_A375_EGR1..1..3387, 4_A375_EGR1..1..3388	2172, 32764	in gene, downstream	0	0	1	6	10	17	2	4_A375_EGR1..1	19	Gene DPEP1	MBD1, MDP, DPEP1, RDP	dipeptidase 1 (renal)	NM_004413, NM_001128141, hCT2257280.0, hCT2257281.0	205983_at	NP_004404.1, NP_001121613.1, EAW66719.1, EAW66720.1
GeneID.5119	CHMP1A	16	89,710,843	89,724,129	13,286	-	1	4_A375_EGR1..1..3388	11649	in gene	0	0	1	6	12	19	1	4_A375_EGR1..1	19	Gene CHMP1A	Vps46A, VPS46A, KIAA0047, PCOLN3, CHMP1A, CHMP1, PRSM1, VPS46-1	chromatin modifying protein 1A	NM_002768, NM_001083314, hCT1966645.1, hCT1966646.1, hCT201168.3	201933_at	NP_002759.2, NP_001076783.1, EAW66715.1, EAW66716.1, EAW66717.1
GeneID.8558	CDK10	16	89,753,076	89,762,772	9,696	+	3	4_A375_EGR1..1..3389, 4_A375_EGR1..1..3390, 4_A375_EGR1..1..3391	7340, 10764, 13676	in gene, downstream, downstream	0	0	1	10	9.67	19.67	3	4_A375_EGR1..1	21	Gene CDK10	PISSLRE, CDK10	cyclin-dependent kinase 10	NM_052988, NM_052987, NM_001098533, NM_001160367, NR_027702, NR_027703, hCT1953801.1, hCT1953802.1, hCT1965640.1, hCT2257289.0, hCT2257293.0, hCT2257294.0, hCT2354338.0, hCT2354339.0, hCT2354340.0, hCT2354341.0, hCT2354342.0, hCT6735.3	203468_at, 203469_s_at, 210622_x_at	NP_443714.3, NP_443713.2, NP_001092003.2, NP_001153839.1, EAW66700.1, EAW66709.1, EAW66701.1, EAW66702.1, EAW66703.1, EAW66704.1, EAW66705.1, EAW66706.1, EAW66707.1, EAW66708.1, EAW66710.1, EAW66711.1
GeneID.124044	SPATA2L	16	89,762,765	89,768,099	5,334	-	5	4_A375_EGR1..1..3389, 4_A375_EGR1..1..3390, 4_A375_EGR1..1..3391, 4_A375_EGR1..1..3392, 4_A375_EGR1..1..3393	7663, 4259, 1347, -6665, -9549	downstream, in gene, in gene, upstream, upstream	0	0	1	8.8	8.6	19.4	5	4_A375_EGR1..1	21	Gene SPATA2L	tamo, MGC26885, C16orf76, SPATA2L	spermatogenesis associated 2-like	NM_152339, hCT2253316.0, hCT2253318.0, hCT6736.2	214965_at	NP_689552.2, EAW66699.1, EAW66697.1, EAW66698.1
GeneID.9605	C16orf7	16	89,773,541	89,787,394	13,853	-	9	1_A375_pNL7_minus_lncRNA_AR..1..2382, 2_A375_pNL97_plus_lncRNA_AR..1..3406, 4_A375_EGR1..1..3390, 4_A375_EGR1..1..3391, 4_A375_EGR1..1..3392, 4_A375_EGR1..1..3393, 4_A375_EGR1..1..3394, 4_A375_EGR1..1..3395, 4_A375_EGR1..1..3396	-110, -62, 23554, 20642, 12610, 9746, 8946, -1566, -2334	upstream, upstream, downstream, downstream, in gene, in gene, in gene, upstream, upstream	1	1	1	12.13	11.13	17.75	8	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene C16orf7	ATP-BL, C16orf7	chromosome 16 open reading frame 7	NM_004913, hCT2253311.0, hCT2253312.0, hCT6627.3	205781_at	NP_004904.2, EAW66695.1, EAW66694.1, EAW66696.1
GeneID.100128881	LOC100128881	16	89,778,264	89,784,573	6,309	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2382, 2_A375_pNL97_plus_lncRNA_AR..1..3406, 4_A375_EGR1..1..3392, 4_A375_EGR1..1..3393, 4_A375_EGR1..1..3394, 4_A375_EGR1..1..3395, 4_A375_EGR1..1..3396	9240, 9192, -3480, -616, 184, 10696, 11464	downstream, downstream, upstream, upstream, in gene, downstream, downstream	1	1	1	12.33	11.5	17.33	6	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene LOC100128881	FLJ38967	hypothetical LOC100128881	NR_038480		
GeneID.92822	ZNF276	16	89,787,393	89,807,333	19,940	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2382, 2_A375_pNL97_plus_lncRNA_AR..1..3406, 4_A375_EGR1..1..3393, 4_A375_EGR1..1..3394, 4_A375_EGR1..1..3395, 4_A375_EGR1..1..3396	111, 63, -9745, 8945, 1567, 2335	in gene, in gene, upstream, upstream, in gene, in gene	1	1	1	13.8	12	16.8	5	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene ZNF276	MGC45417, FLJ77609, MGC111410, MGC126400, ZNF477, ZFP276, ZNF276, FLJ39885	zinc finger protein 276	NM_152287, NM_001113525, hCT1955545.2, hCT2253268.1, hCT2257297.1, hCT2344206.0, hCT2354322.0, hCT2354323.0, hCT7391.4	213776_x_at, 231922_at	NP_689500.2, NP_001106997.1, EAW66687.1, EAW66688.1, EAW66690.1, EAW66692.1, EAW66689.1, EAW66693.1
GeneID.2175	FANCA	16	89,803,959	89,883,065	79,106	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2383, 4_A375_EGR1..1..3397	-39, 26473	upstream, in gene	1	0	1	10.5	10	14	2	4_A375_EGR1..1	16	Gene FANCA	MGC75158, FANCH, FAH, FACA, FAA, FA1, FANCA, FA-H, FA	Fanconi anemia, complementation group A	NM_001018112, NM_000135, hCT2253307.0, hCT6693.3	203805_s_at, 203806_s_at, 215530_at, 236976_at	NP_001018122.1, NP_000126.2, EAW66683.1, EAW66686.1
GeneID.84501	SPIRE2	16	89,894,907	89,937,727	42,820	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3407, 4_A375_EGR1..1..3398, 4_A375_EGR1..1..3399	149, 3733, 44229	in gene, in gene, downstream	0	1	1	9.33	10.67	18.3	3	4_A375_EGR1..1	19	Gene SPIRE2	MGC117166, SPIRE2, Spir-2	spire homolog 2 (Drosophila)	NM_032451, hCT2257296.0, hCT2354331.0, hCT7784.3	1560916_at, 1560733_a_at, 227706_at, 243394_x_at	NP_115827.1, EAW66661.1, EAW66662.1
GeneID.22980	TCF25	16	89,939,994	89,977,792	37,798	+	4	4_A375_EGR1..1..3399, 4_A375_EGR1..1..3400, 4_A375_EGR1..1..3401, 4_A375_EGR1..1..3402	-536, 17694, 38950, 45670	upstream, in gene, downstream, downstream	0	0	1	9	10.5	17.25	4	4_A375_EGR1..1	19	Gene TCF25	KIAA1049, FKSG26, PRO2620, Hulp1, TCF25, KIAA1049	transcription factor 25 (basic helix-loop-helix)	NM_014972, hCT1953607.1, hCT2257301.0, hCT7393.2	213311_s_at, 214704_at, 221455_s_at	NP_055787.1, EAW66677.1, EAW66679.1
GeneID.4157	MC1R	16	89,984,287	89,987,385	3,098	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3408, 4_A375_EGR1..1..3401, 4_A375_EGR1..1..3402, 4_A375_EGR1..1..3403	4225, -5343, 1277, 4641	downstream, upstream, in gene, downstream	0	1	1	10.33	14	16.33	3	4_A375_EGR1..1	21	Gene MC1R	MGC14337, CMM5, MSH-R, MC1R, SHEP2	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	NM_002386, hCT2257302.1	205458_at	NP_002377.4, EAW66676.1
GeneID.10381	TUBB3	16	89,989,745	90,002,505	12,760	+	3	4_A375_EGR1..1..3401, 4_A375_EGR1..1..3402, 4_A375_EGR1..1..3403	-1233, -4061, -617	upstream, upstream, upstream	0	0	1	13	13	19	2	4_A375_EGR1..1	21	Gene TUBB3	TUBB4, beta-4, TUBB3, MC1R, CFEOM3A	tubulin, beta 3	NM_006086	202154_x_at, 213476_x_at	NP_006077.2
GeneID.54849	DEF8	16	90,015,151	90,034,467	19,316	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2384, 2_A375_pNL97_plus_lncRNA_AR..1..3409, 4_A375_EGR1..1..3404, 4_A375_EGR1..1..3405, 4_A375_EGR1..1..3406	-79, -79, 5137, 13233, 23393	upstream, upstream, in gene, in gene, downstream	1	1	1	16	20.5	14	4	2_A375_pNL97_plus_lncRNA_AR..1	56	Gene DEF8	MGC104549, DEF8, FLJ20186	differentially expressed in FDCP 8 homolog (mouse)	NM_207514, NM_017702, hCT1953829.1, hCT2257310.0	219568_at, 225637_at	NP_997397.1, NP_060172.1, EAW66667.1, EAW66668.1
GeneID.92806	CENPBD1	16	90,036,201	90,038,942	2,741	-	2	4_A375_EGR1..1..3405, 4_A375_EGR1..1..3406	10555, 396	downstream, in gene	0	0	1	12	10.5	16	2	4_A375_EGR1..1	17	Gene CENPBD1	MGC13198, LL22771, CENPBD1, FLJ31569, MGC16385	CENPB DNA-binding domains containing 1	NM_145039	1552330_at, 225728_at, 229171_at	NP_659476.2
GeneID.79007	DBNDD1	16	90,071,279	90,085,927	14,656	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2385, 2_A375_pNL97_plus_lncRNA_AR..1..3410	-1519, -1674	upstream, upstream	1	1	0	21	15	7	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene DBNDD1	FLJ12582, MGC3101, DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1	NM_024043, NM_001042610, hCT1953606.1, hCT2353007.1, hCT2354325.0, hCT7393.2	222234_s_at	NP_076948.2, NP_001036075.1, EAW66664.1, EAW66665.1
GeneID.2622	GAS8	16	90,089,008	90,111,079	22,071	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2385, 2_A375_pNL97_plus_lncRNA_AR..1..3410, 4_A375_EGR1..1..3406	-15552, -1397, 24571	upstream, upstream, downstream	1	1	1	14	13	10.5	3	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene GAS8	GAS8, MGC138326, GAS11	growth arrest-specific 8	NM_001481, hCT1953682.1, hCT2354317.0, hCT7389.3	204921_at	NP_001472.1, EAW66659.1, EAW66660.1, EAW66661.1
GeneID.750	C16orf3	16	90,098,316	90,099,309	993	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2385, 2_A375_pNL97_plus_lncRNA_AR..1..3410	6653, 6698	downstream, downstream	1	1	0	21	15	7	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene C16orf3	MGC132909, C16orf3	chromosome 16 open reading frame 3	NM_001214, hCT1950151.2	207613_s_at	NP_001205.3, EAW66662.1
GeneID.100130015	LOC100130015	16	90,105,169	90,114,181	9,012	+	1	4_A375_EGR1..1..3406	802	in gene	0	0	1	7	11	14	1	4_A375_EGR1..1	14	Gene LOC100130015		3-hydroxyisobutyryl-CoA hydrolase pseudogene	NR_027335, NR_027336		
GeneID.11105	PRDM7	16	90,122,974	90,142,338	19,364	-	1	4_A375_EGR1..1..3406	20759	downstream	0	0	1	7	11	14	1	4_A375_EGR1..1	14	Gene PRDM7	PFM4, MGC129525, ZNF910, PRDM7	PR domain containing 7	NM_052996, NM_001098173, hCT2252270.0, hCT2252272.0, hCT2252273.0, hCT2252274.0, hCT7367.2	224226_s_at	NP_443722.2, NP_001091643.1, EAW66653.1, EAW66654.1, EAW66656.1, EAW66657.1, EAW66655.1
GeneID.9801	RPH3AL	17	62,180	202,633	140,453	-	1	4_A375_EGR1..1..3410	-3559	upstream	0	0	1	1	2	20	1	4_A375_EGR1..1	20	Gene RPH3AL	RPH3AL, NOC2	rabphilin 3A-like (without C2 domains)	NM_006987, NM_001190411, NM_001190412, hCT1964196.1, hCT2260263.0, hCT2260257.0	221614_s_at, 233134_at, 235120_at	NP_001177340.1, NP_001177341.1, NP_008918.1, EAW90669.1, EAW90670.1, EAW90671.1, EAW90672.1
GeneID.55275	VPS53	17	411,906	618,096	206,190	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2386, 2_A375_pNL97_plus_lncRNA_AR..1..3411	46, 46	in gene, in gene	1	1	0	36	26	12	1	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene VPS53	FLJ10979, VPS53, FLJ45757, MGC39512, FLJ41112, HCCS1, hVps53L, pp13624	vacuolar protein sorting 53 homolog (S. cerevisiae)	NM_018289, NM_001128159, hCT1958933.2, hCT2264569.0, hCT2264570.0, hCT2337274.0, hCT2337275.0	219794_at, 221707_s_at, 233710_at	NP_060759.2, NP_001121631.1, EAW90658.1, EAW90659.1, EAW90662.1, EAW90660.1
GeneID.51031	GLOD4	17	662,549	685,571	23,022	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2387, 2_A375_pNL97_plus_lncRNA_AR..1..3412, 2_A375_pNL97_plus_lncRNA_AR..1..3412	0, -29, 3	in gene, upstream, in gene	1	1	0	19	26	19	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene GLOD4	GLOD4, C17orf25, CGI-150, HC71	glyoxalase domain containing 4	NM_016080, hCT2264547.0, hCT2264548.0, hCT2264530.0, hCT2264533.0, hCT2337244.0, hCT2337245.0, hCT29857.4	209092_s_at	NP_057164.3, EAW90643.1, EAW90644.1, EAW90646.1, EAW90647.1, EAW90650.1, EAW90645.1, EAW90648.1, EAW90649.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.55178	RNMTL1	17	885,513	895,741	10,228	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2387, 2_A375_pNL97_plus_lncRNA_AR..1..3412, 4_A375_EGR1..1..3412	55, 87, 55	in gene, in gene, in gene	1	1	1	19	28	19	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene RNMTL1	FLJ10581, HC90, RNMTL1	RNA methyltransferase like 1	NM_018146, hCT23869.2	218993_at	NP_060616.1, EAW90642.1
GeneID.84359	NXN	17	702,585	883,010	180,425	-	1	4_A375_EGR1..1..3413	178548	in gene	0	0	1	6	3	20	1	4_A375_EGR1..1	20	Gene NXN	TRG-4, FLJ12614, NRX, NXN	nucleoredoxin	NM_022463, hCT1952469.1, hCT2264528.0, hCT2264530.0	219489_s_at	NP_071908.2, EAW90639.1, EAW90640.1, EAW90641.1
GeneID.29928	TIMM22	17	900,357	905,407	5,050	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3413, 4_A375_EGR1..1..3414	-469, -133	upstream, upstream	0	1	1	18	24	20	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene TIMM22	TEX4, TIM22, TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	NM_013337, hCT2264846.0, hCT2264847.0	219184_x_at, 222841_s_at, 229100_s_at, 231400_s_at	NP_037469.2, EAW90638.1, EAW90637.1
GeneID.100506836	LOC100506836	17	905,807	909,265	3,458	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3413, 4_A375_EGR1..1..3414	-5919, -5583	upstream, upstream	0	1	1	18	24	20	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LOC100506836		hypothetical LOC100506836	XR_109362		
GeneID.29	ABR	17	906,759	1,090,616	183,857	-	9	1_A375_pNL7_minus_lncRNA_AR..1..2388, 1_A375_pNL7_minus_lncRNA_AR..1..2389, 2_A375_pNL97_plus_lncRNA_AR..1..3413, 2_A375_pNL97_plus_lncRNA_AR..1..3414, 4_A375_EGR1..1..3414, 4_A375_EGR1..1..3415, 4_A375_EGR1..1..3416, 4_A375_EGR1..1..3417, 4_A375_EGR1..1..3418	36056, 56, 190728, 76280, 190392, 166168, 159880, 115736, 79192	in gene, in gene, downstream, in gene, downstream, in gene, in gene, in gene, in gene	1	1	1	14.38	12	13.86	8	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene ABR	ABR, FLJ45954, MDB	active BCR-related gene	NM_001092, NM_021962, NM_001159746, hCT1971514.1, hCT2264503.0, hCT2264508.0, hCT2264511.0, hCT2264512.0	212895_s_at, 214671_s_at	NP_001083.2, NP_068781.2, NP_001153218.1, EAW90631.1, EAW90632.1, EAW90634.1, EAW90633.1, EAW90635.1
GeneID.100422835	MIR3183	17	925,716	925,799	83	-	2	4_A375_EGR1..1..3415, 4_A375_EGR1..1..3416	3351, -4937	downstream, upstream	0	0	1	5	5	15.5	2	4_A375_EGR1..1	16	Gene MIR3183	MIR3183	microRNA 3183	NR_036146		
GeneID.7531	YWHAE	17	1,247,834	1,303,556	55,722	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3417, 4_A375_EGR1..1..3420	340, 36	in gene, in gene	0	1	1	12	16	21	1	4_A375_EGR1..1	21	Gene YWHAE	YWHAE, MDS, FLJ53559, 14-3-3E, KCIP-1, MDCR, FLJ45465	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	NM_006761, NR_024058, hCT2264471.0, hCT2264473.0, hCT2357331.0	210317_s_at, 210996_s_at, 213655_at	NP_006752.1, EAW90628.1, EAW90627.1, EAW90629.1
GeneID.4641	MYO1C	17	1,367,480	1,396,001	28,521	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2390, 2_A375_pNL97_plus_lncRNA_AR..1..3418, 4_A375_EGR1..1..3421, 4_A375_EGR1..1..3422	6561, 6593, 6401, 1537	in gene, in gene, in gene, in gene	1	1	1	19.5	23.5	18.5	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene MYO1C	FLJ23903, NMI, MYO1C, MMIb, myr2, MMI-beta	myosin IC	NM_001080779, NM_033375, NM_001080950, hCT19877.3, hCT2264459.0	214656_x_at, 225080_at, 32811_at	NP_001074248.1, NP_203693.3, NP_001074419.1, EAW90619.1, EAW90620.1
GeneID.51763	INPP5K	17	1,397,871	1,420,182	22,311	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2390, 2_A375_pNL97_plus_lncRNA_AR..1..3418, 4_A375_EGR1..1..3421, 4_A375_EGR1..1..3422	30742, 30774, 30582, 25718	downstream, downstream, downstream, downstream	1	1	1	19.5	23.5	18.5	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene INPP5K	SKIP, PPS, INPP5K	inositol polyphosphate-5-phosphatase K	NM_016532, NM_130766, NM_001135642, hCT1814645.2, hCT2264454.0, hCT2264455.0, hCT2264456.0, hCT2264458.1	202781_s_at, 202782_s_at	NP_057616.2, NP_570122.1, NP_001129114.1, EAW90614.1, EAW90615.1, EAW90617.1, EAW90616.1, EAW90618.1
GeneID.5306	PITPNA	17	1,421,283	1,466,110	44,827	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2391, 2_A375_pNL97_plus_lncRNA_AR..1..3419	-98, -50	upstream, upstream	1	1	0	36	30	7	1	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene PITPNA	PITPN, VIB1A, MGC99649, PI-TPalpha, PITPNA	phosphatidylinositol transfer protein, alpha	NM_006224, hCT1815693.2, hCT2264453.0, hCT2357330.0	201190_s_at, 201191_at, 201192_s_at	NP_006215.1, EAW90610.1, EAW90611.1, EAW90612.1
GeneID.100507036	LOC100507036	17	1,452,559	1,473,094	20,535	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2391, 2_A375_pNL97_plus_lncRNA_AR..1..3419	13649, 13601	in gene, in gene	1	1	0	36	30	7	1	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene LOC100507036		hypothetical LOC100507036	XR_111664, XR_111665, XR_109368, XR_109369, XR_115047, XR_115048		
GeneID.124935	SLC43A2	17	1,477,896	1,532,130	54,434	-	3	4_A375_EGR1..1..3423, 4_A375_EGR1..1..3424, 4_A375_EGR1..1..3425	37866, 7298, -1278	in gene, in gene, upstream	0	0	1	8	9	18	3	4_A375_EGR1..1	19	Gene SLC43A2	MGC34680, SLC43A2, FLJ23848, LAT4	solute carrier family 43, member 2	NM_152346, hCT19874.2, hCT2264446.0, hCT2264447.0, hCT2264448.0, hCT2264450.0, hCT2264451.0, hCT2357316.0	226629_at	NP_689559.1, EAW90602.1, EAW90601.1, EAW90603.1, EAW90604.1, EAW90606.1, EAW90605.1, EAW90607.1
GeneID.8578	SCARF1	17	1,537,152	1,549,041	11,889	-	3	4_A375_EGR1..1..3425, 4_A375_EGR1..1..3426, 4_A375_EGR1..1..3427	15633, -2631, -4047	downstream, upstream, upstream	0	0	1	9.33	12	17	3	4_A375_EGR1..1	19	Gene SCARF1	SREC, MGC47738, KIAA0149, SCARF1, SREC1, SREC-I	scavenger receptor class F, member 1	NM_003693, NM_145350, NM_145352, NR_028075, NR_028076, hCT19868.3, hCT2357306.0, hCT2357307.0, hCT2357308.0, hCT2357309.0	1555021_a_at, 206995_x_at	NP_003684.2, NP_663325.1, NP_663327.2, EAW90596.1, EAW90597.1, EAW90598.1, EAW90599.1, EAW90600.1
GeneID.83547	RILP	17	1,549,444	1,553,392	3,948	-	2	4_A375_EGR1..1..3426, 4_A375_EGR1..1..3427	1520, 304	in gene, in gene	0	0	1	10.5	13.5	16	2	4_A375_EGR1..1	17	Gene RILP	PP10141, FLJ31193, RILP	Rab interacting lysosomal protein	NM_031430, hCT19879.3	227386_at	NP_113618.2, EAW90595.1
GeneID.10594	PRPF8	17	1,553,923	1,588,176	34,253	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3420, 4_A375_EGR1..1..3426, 4_A375_EGR1..1..3427, 4_A375_EGR1..1..3428	-48, 36304, 35086, 144	upstream, downstream, downstream, in gene	0	1	1	10	15	16.33	3	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PRPF8	HPRP8, PRPC8, RP13, PRP8, PRPF8	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	NM_006445, hCT19870.3, hCT2261329.0, hCT2350281.0, hCT2350282.0, hCT2350283.0, hCT2350284.0, hCT2350285.0	200000_s_at	NP_006436.3, EAW90593.1, EAW90588.1, EAW90589.1, EAW90591.1, EAW90594.1, EAW90590.1, EAW90592.1
GeneID.727910	TLCD2	17	1,606,084	1,613,662	7,578	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2392, 2_A375_pNL97_plus_lncRNA_AR..1..3421, 4_A375_EGR1..1..3429	-6946, -6898, -5714	upstream, upstream, upstream	1	1	1	24	28	22	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene TLCD2	TLCD2	TLC domain containing 2	NM_001164407		NP_001157879.1
GeneID.84981	C17orf91	17	1,614,798	1,619,566	4,768	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2392, 2_A375_pNL97_plus_lncRNA_AR..1..3421, 4_A375_EGR1..1..3429	-1042, -994, 190	upstream, upstream, in gene	1	1	1	24	28	22	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene C17orf91	MGC14376, C17orf91, MGC149751, DKFZp686O06159	chromosome 17 open reading frame 91	NR_026502, NR_026503, NR_026504, NR_026505, hCT1970576.1, hCT2261315.0	214696_at	EAW90566.1, EAW90565.1
GeneID.407004	MIR22	17	1,617,197	1,617,281	84	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2392, 2_A375_pNL97_plus_lncRNA_AR..1..3421, 4_A375_EGR1..1..3429	-3327, -3279, -2095	upstream, upstream, upstream	1	1	1	24	28	22	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene MIR22	miR-22, hsa-mir-22, MIRN22, MIR22	microRNA 22	NR_029494		
GeneID.124997	WDR81	17	1,619,817	1,641,893	22,076	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2392, 2_A375_pNL97_plus_lncRNA_AR..1..3421, 4_A375_EGR1..1..3429, 4_A375_EGR1..1..3430, 4_A375_EGR1..1..3431	791, 743, -441, 10903, 17367	in gene, in gene, upstream, in gene, in gene	1	1	1	12.67	14.67	19.67	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene WDR81	WDR81, FLJ23776, FLJ33817	WD repeat domain 81	NM_001163673, NM_001163809, NM_152348, NM_001163811, hCT2289074.1, hCT2289075.1, hCT2349376.0	226738_at	NP_001157145.1, NP_001157281.1, NP_689561.2, NP_001157283.1, EAW90563.1, EAW90564.1, EAW90562.1
GeneID.5345	SERPINF2	17	1,646,130	1,658,559	12,429	+	2	4_A375_EGR1..1..3431, 4_A375_EGR1..1..3432	-8946, 19630	upstream, downstream	0	0	1	6	9.5	19	2	4_A375_EGR1..1	21	Gene SERPINF2	ALPHA-2-PI, PLI, AAP, A2AP, API, SERPINF2	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2	NM_000934, NM_001165920, NM_001165921, hCT19873.3, hCT2289008.0, hCT2289012.0, hCT2289013.0	205075_at	NP_000925.2, NP_001159392.1, NP_001159393.1, EAW90576.1, EAW90580.1, EAW90581.1, EAW90579.1
GeneID.5176	SERPINF1	17	1,665,259	1,680,868	15,609	+	1	4_A375_EGR1..1..3432	501	in gene	0	0	1	6	11	17	1	4_A375_EGR1..1	17	Gene SERPINF1	PEDF, PIG35, EPC-1, SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	NM_002615, hCT19871.3	202283_at	NP_002606.3, EAW90577.1
GeneID.146760	RTN4RL1	17	1,837,971	1,928,178	90,207	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2393, 2_A375_pNL97_plus_lncRNA_AR..1..3422, 4_A375_EGR1..1..3433, 4_A375_EGR1..1..3434	-5230, -5230, 81746, -5390	upstream, upstream, in gene, upstream	1	1	1	35	41.5	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	77	Gene RTN4RL1	RTN4RL1, NGRH2, NgR3, DKFZp547J144	reticulon 4 receptor-like 1	NM_178568, hCT1815706.1, hCT2261378.0	230700_at	NP_848663.1, EAW90570.1, EAW90571.1
GeneID.1801	DPH1	17	1,933,431	1,946,725	13,294	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2393, 1_A375_pNL7_minus_lncRNA_AR..1..2394, 2_A375_pNL97_plus_lncRNA_AR..1..3422, 2_A375_pNL97_plus_lncRNA_AR..1..3423, 4_A375_EGR1..1..3434, 4_A375_EGR1..1..3435	-23, 11945, -23, 11945, 137, 21417	upstream, in gene, upstream, in gene, in gene, downstream	1	1	1	29.33	36.33	16.33	3	2_A375_pNL97_plus_lncRNA_AR..1	77	Gene DPH1	DPH1, FLJ33211, DPH2L1, DPH2L, OVCA1	DPH1 homolog (S. cerevisiae)	NM_001383	202632_at	NP_001374.3
GeneID.124641	OVCA2	17	1,945,277	1,946,725	1,448	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2394, 2_A375_pNL97_plus_lncRNA_AR..1..3423, 4_A375_EGR1..1..3435	99, 99, 9571	in gene, in gene, downstream	1	1	1	13.5	16	16	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene OVCA2	OVCA2		NM_080822	222041_at	NP_543012.1
GeneID.406921	MIR132	17	1,953,202	1,953,302	100	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2394, 2_A375_pNL97_plus_lncRNA_AR..1..3423, 4_A375_EGR1..1..3435	7926, 7926, -1546	downstream, downstream, upstream	1	1	1	13.5	16	16	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene MIR132	miRNA132, MIR132, MIRN132	microRNA 132	NR_029674		
GeneID.406994	MIR212	17	1,953,565	1,953,674	109	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2394, 2_A375_pNL97_plus_lncRNA_AR..1..3423, 4_A375_EGR1..1..3435	8298, 8298, -1174	downstream, downstream, upstream	1	1	1	13.5	16	16	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene MIR212	MIR212, mir-212, MIRN212	microRNA 212	NR_029625		
GeneID.3090	HIC1	17	1,958,393	1,962,981	4,588	+	1	4_A375_EGR1..1..3435	-3545	upstream	0	0	1	6	6	15	1	4_A375_EGR1..1	15	Gene HIC1	ZNF901, ZBTB29, HIC1, hic-1	hypermethylated in cancer 1	NM_006497, NM_001098202, hCT2289048.0, hCT2289052.0, hCT24169.2	208461_at	NP_006488.2, NP_001091672.1, EAW90562.1, EAW90563.1, EAW90564.1
GeneID.23293	SMG6	17	1,963,133	2,207,069	243,936	-	1	4_A375_EGR1..1..3435	252221	downstream	0	0	1	6	6	15	1	4_A375_EGR1..1	15	Gene SMG6	SMG-6, EST1A, C17orf31, SMG6, KIAA0732	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	NM_017575, NM_001170957	214940_s_at, 220347_at	NP_060045.4, NP_001164428.1
GeneID.55720	TSR1	17	2,225,972	2,240,678	14,706	-	1	4_A375_EGR1..1..3436	774	in gene	0	0	1	16	19	17	1	4_A375_EGR1..1	17	Gene TSR1	TSR1, KIAA1401, FLJ10534, MGC131829	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	NM_018128, hCT2261364.1, hCT2261365.1, hCT2349409.0, hCT2349410.0, hCT24172.4	218155_x_at, 218156_s_at, 221987_s_at, 239042_at	NP_060598.3, EAW90548.1, EAW90549.1, EAW90550.1, EAW90551.1, EAW90552.1
GeneID.692208	SNORD91B	17	2,232,419	2,232,504	85	-	1	4_A375_EGR1..1..3436	-7400	upstream	0	0	1	16	19	17	1	4_A375_EGR1..1	17	Gene SNORD91B	SNORD91B, HBII-296b	small nucleolar RNA, C/D box 91B	NR_003073		
GeneID.692207	SNORD91A	17	2,233,573	2,233,664	91	-	1	4_A375_EGR1..1..3436	-8240	upstream	0	0	1	16	19	17	1	4_A375_EGR1..1	17	Gene SNORD91A	SNORD91A, HBII-296a	small nucleolar RNA, C/D box 91A	NR_003072		
GeneID.9905	SGSM2	17	2,240,806	2,284,348	43,542	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2395, 4_A375_EGR1..1..3436, 4_A375_EGR1..1..3437, 4_A375_EGR1..1..3438	21946, -902, 25242, 42362	in gene, upstream, in gene, in gene	1	0	1	12	12.75	13.75	4	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene SGSM2	RUTBC1, KIAA0397, SGSM2	small G protein signaling modulator 2	NM_014853, NM_001098509, hCT2289065.0, hCT2357254.0, hCT24173.3	212319_at, 217538_at, 36129_at	NP_055668.2, NP_001091979.1, EAW90545.1, EAW90546.1, EAW90547.1
GeneID.4335	MNT	17	2,287,354	2,304,258	16,904	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2396, 2_A375_pNL97_plus_lncRNA_AR..1..3424, 2_A375_pNL97_plus_lncRNA_AR..1..3425, 4_A375_EGR1..1..3438, 4_A375_EGR1..1..3439	-734, 7426, -734, 21090, 4002	upstream, in gene, upstream, downstream, in gene	1	1	1	27	39.75	13.5	4	2_A375_pNL97_plus_lncRNA_AR..1	116	Gene MNT	bHLHd3, ROX, MAD6, MXD6, MNT	MAX binding protein	NM_020310, hCT2261359.0, hCT2261360.0, hCT24175.3	204206_at, 236749_at	NP_064706.1, EAW90541.1, EAW90542.1, EAW90543.1
GeneID.284009	LOC284009	17	2,310,275	2,318,730	8,455	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2396, 2_A375_pNL97_plus_lncRNA_AR..1..3425, 4_A375_EGR1..1..3439, 4_A375_EGR1..1..3440	13736, 13736, 18474, 650	downstream, downstream, downstream, in gene	1	1	1	30.67	44.67	14	3	2_A375_pNL97_plus_lncRNA_AR..1	116	Gene LOC284009	MGC138239	hypothetical LOC284009	NR_026335, hCT2342777.0		EAW90540.1
GeneID.79066	METT10D	17	2,319,343	2,415,200	95,857	-	1	4_A375_EGR1..1..3440	97120	downstream	0	0	1	3	8	16	1	4_A375_EGR1..1	16	Gene METT10D	METT10D, MGC3329, METTL16	methyltransferase 10 domain containing	NM_024086, hCT2261357.1, hCT2357338.0, hCT2357339.0	220797_at, 226744_at, 238931_at	NP_076991.3, EAW90537.1, EAW90538.1, EAW90539.1
GeneID.5048	PAFAH1B1	17	2,496,923	2,588,909	91,986	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3426, 4_A375_EGR1..1..3441	-283, 98693	upstream, downstream	0	1	1	8.5	14.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PAFAH1B1	PAFAH1B1, MDS, LIS1, LIS2, PAFAH, MDCR	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	NM_000430, hCT24167.2	200813_s_at, 200815_s_at, 200816_s_at, 211547_s_at	NP_000421.1, EAW90536.1
GeneID.23277	KIAA0664	17	2,592,680	2,614,927	22,247	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2397, 2_A375_pNL97_plus_lncRNA_AR..1..3427, 4_A375_EGR1..1..3441	-209, -225, 21311	upstream, upstream, in gene	1	1	1	13.5	16	13	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene KIAA0664	DKFZp686M09233, KIAA0664, FLJ23672, DKFZp686L05242, CLU1	KIAA0664	NM_015229, hCT2261346.0, hCT2357312.0, hCT24166.3	212456_at, 243256_at	NP_056044.3, EAW90534.1, EAW90532.1, EAW90533.1
GeneID.100302208	MIR1253	17	2,651,372	2,651,476	104	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3428	-1604	upstream	0	1	0	18	25	6	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene MIR1253	MIRN1253, MIR1253, hsa-mir-1253	microRNA 1253	NR_031654		
GeneID.23108	RAP1GAP2	17	2,699,732	2,941,035	241,303	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2398, 1_A375_pNL7_minus_lncRNA_AR..1..2399, 2_A375_pNL97_plus_lncRNA_AR..1..3429, 2_A375_pNL97_plus_lncRNA_AR..1..3430, 2_A375_pNL97_plus_lncRNA_AR..1..3431	156924, 179116, 156812, 163946, 179146	in gene, in gene, in gene, in gene, in gene	1	1	0	18	21.67	8.67	3	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene RAP1GAP2	KIAA1039, DKFZp686O238, GARNL4, RAP1GAP2, RAP1GA3	RAP1 GTPase activating protein 2	NM_015085, NM_001100398, hCT1814367.2, hCT2336411.1, hCT2340621.0, hCT2340622.0	213280_at	NP_055900.4, NP_001093868.1, EAW90526.1, EAW90527.1, EAW90528.1, EAW90529.1
GeneID.8387	OR1E1	17	3,300,760	3,301,704	944	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3433	392	in gene	0	1	0	17	20	7	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene OR1E1	OST547, OR1E1, HGM071, OR1E8P, OR1E5, OR1E9P, OR17-2, OR17-32, OR13-66, OR1E6	olfactory receptor, family 1, subfamily E, member 1	NM_003553, hCT23823.3	208587_s_at, 214515_at	NP_003544.2, EAW90515.1
GeneID.8388	OR1E2	17	3,336,164	3,337,135	971	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3434	431	in gene	0	1	0	14	18	7	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene OR1E2	OR1E4, OR17-93, OST529, OR1E2, OR17-135, OR1E7	olfactory receptor, family 1, subfamily E, member 2	NM_003554, hCT1814346.0		NP_003545.1, EAW90513.1
GeneID.84890	SPATA22	17	3,343,305	3,375,142	31,837	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3434	38438	downstream	0	1	0	14	18	7	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SPATA22	SPATA22, NYD-SP20, NYDSP20	spermatogenesis associated 22	NM_001170696, NM_001170695, NM_001170697, NM_001170698, NM_032598, NM_001170699, hCT1644982.3, hCT2336335.0, hCT2357317.0, hCT2357318.0, hCT2357319.0	1558667_at, 1558668_s_at, 231114_at	NP_001164167.1, NP_001164166.1, NP_001164168.1, NP_001164169.1, NP_115987.2, NP_001164170.1, EAW90508.1, EAW90509.1, EAW90510.1, EAW90511.1, EAW90512.1
GeneID.162514	TRPV3	17	3,416,486	3,461,289	44,803	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2400, 4_A375_EGR1..1..3442	26153, 25385	in gene, in gene	1	0	1	16	14	21	1	4_A375_EGR1..1	21	Gene TRPV3	VRL3, TRPV3	transient receptor potential cation channel, subfamily V, member 3	NM_145068, hCT1815450.2, hCT2336333.1, hCT2343282.1, hCT2357268.0	1552566_at, 1555291_at	NP_659505.1, EAW90503.1, EAW90502.1, EAW90504.1, EAW90505.1
GeneID.1497	CTNS	17	3,539,762	3,566,397	26,635	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3435, 4_A375_EGR1..1..3443, 4_A375_EGR1..1..3444, 4_A375_EGR1..1..3445	32366, 19054, 24046, 32046	downstream, in gene, in gene, downstream	0	1	1	8.33	11	17.33	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CTNS	CTNS-LSB, PQLC4, CTNS	cystinosis, nephropathic	NM_004937, NM_001031681, hCT2336430.0, hCT2357349.0, hCT24393.3	204925_at, 215459_at, 36566_at	NP_004928.2, NP_001026851.2, EAW90494.1, EAW90495.1, EAW90496.1

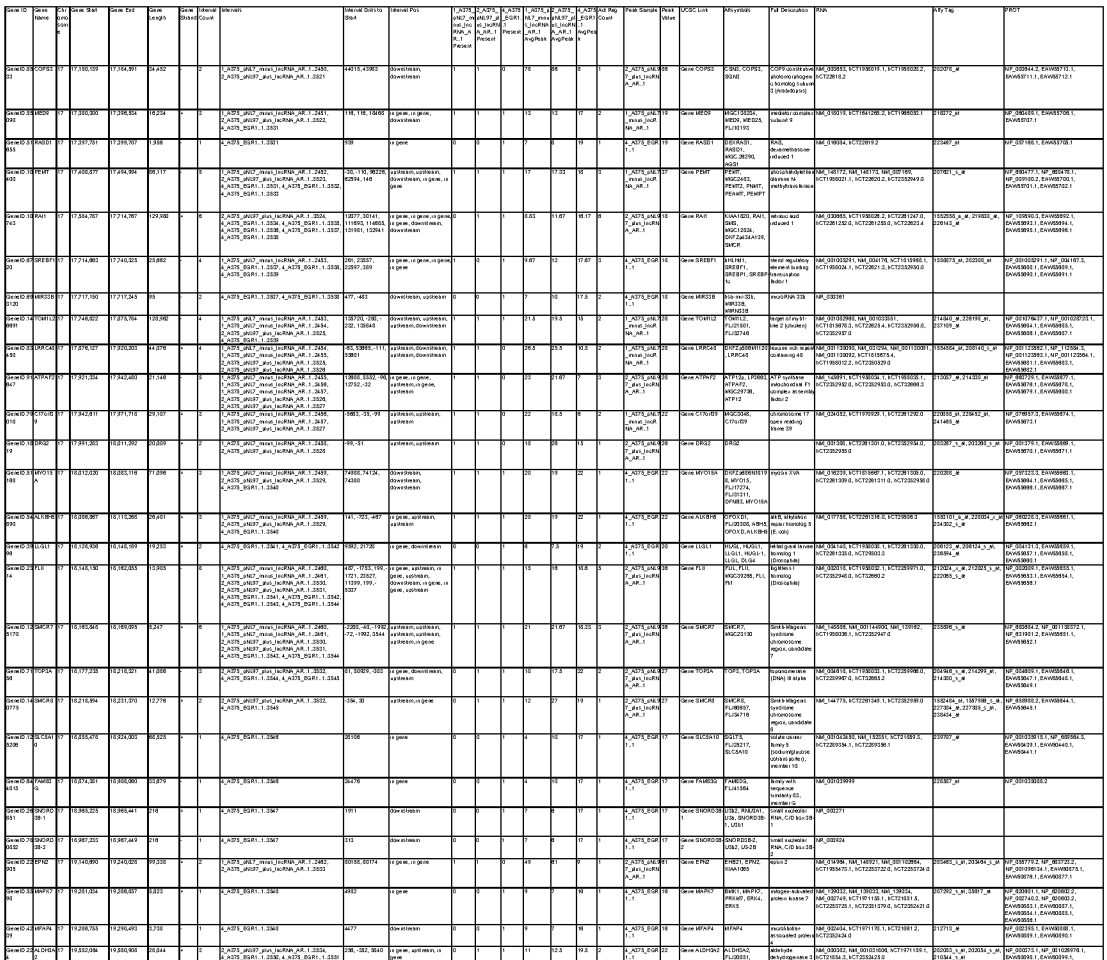
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:30851	TAX1BP3	17	3,566,189	3,571,973	5,784	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3435, 4_A375_EGR1..1..3443, 4_A375_EGR1..1..3444, 4_A375_EGR1..1..3445	-155, 13157, 8165, 165	upstream, downstream, downstream, in gene	0	1	1	8.33	11	17.33	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TAX1BP3	TAX1BP3, TIP-1	Tax1 (human T-cell leukemia virus type I) binding protein 3	NM_014604, hCT2338320.0, hCT2357315.0, hCT24409.2	209154_at, 215464_s_at	NP_055419.1, EAW90492.1, EAW90491.1, EAW90493.1
GeneID:83460	TMEM93	17	3,572,090	3,572,962	872	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3435, 4_A375_EGR1..1..3444, 4_A375_EGR1..1..3445	38, -8262, -262	in gene, upstream, upstream	0	1	1	9.5	13	18.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TMEM93	MGC2963, TMEM93	transmembrane protein 93	NM_031298, NM_001014764, hCT24408.2	221255_s_at	NP_112588.1, NP_001014764.1, EAW90490.1
GeneID:5026	P2RX5	17	3,576,521	3,599,583	23,062	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3435, 4_A375_EGR1..1..3445	27455, 27775	downstream, downstream	0	1	1	13	20	20	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene P2RX5	P2X5R, P2X5, P2RX5, LRH-1, MGC47755	purinergic receptor P2X, ligand-gated ion channel, 5	NM_002561, NM_175080, NM_175081, hCT2336314.0, hCT2336315.0, hCT2336317.0, hCT2336316.0, hCT2357250.0, hCT2357251.0, hCT24394.2	210448_s_at	NP_002552.2, NP_778255.1, NP_778256.1, EAW90482.1, EAW90485.1, EAW90486.1, EAW90483.1, EAW90484.1, EAW90487.1, EAW90488.1
GeneID:100506616	LOC100506616	17	3,580,976	3,582,570	1,594	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3435, 4_A375_EGR1..1..3445	10442, 10762	downstream, downstream	0	1	1	13	20	20	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100506616		hypothetical protein LOC100506616	XM_003118730, XM_003120861		XP_003118778.1, XP_003120909.1
GeneID:3682	ITGAE	17	3,617,919	3,704,537	86,618	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2401, 2_A375_pNL97_plus_lncRNA_AR..1..3436, 4_A375_EGR1..1..3446	77449, 77401, 77433	in gene, in gene, in gene	1	1	1	47	52	20	1	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene ITGAE	ITGAE, CD103, HUMINAE, MGC141996	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	NM_002208, hCT24396.3	205055_at	NP_002199.3, EAW90480.1
GeneID:83903	GSG2	17	3,627,197	3,629,993	2,796	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2401, 2_A375_pNL97_plus_lncRNA_AR..1..3436, 4_A375_EGR1..1..3446	-109, -61, -93	upstream, upstream, upstream	1	1	1	47	52	20	1	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene GSG2	GSG2, HASPIN	germ cell associated 2 (haspin)	NM_031965, hCT1640001.3	223759_s_at	NP_114171.2, EAW90481.1
GeneID:55421	C17orf85	17	3,714,460	3,749,540	35,080	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3437	-28	upstream	0	1	0	18	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene C17orf85	ELG, HSA277841, C17orf85	chromosome 17 open reading frame 85	NM_001114118, NM_018553, hCT2336309.0, hCT2336310.0, hCT2336312.0	218896_s_at, 222779_s_at	NP_001107590.1, NP_061023.1, EAW90477.1, EAW90478.1, EAW90479.1
GeneID:5023	P2RX1	17	3,799,885	3,819,960	20,075	-	1	4_A375_EGR1..1..3447	11992	in gene	0	0	1	9	3	14	1	4_A375_EGR1..1	14	Gene P2RX1	P2X1, P2RX1	purinergic receptor P2X, ligand-gated ion channel, 1	NM_002558, hCT1957916.1, hCT2357268.0, hCT24392.2	210401_at	NP_002549.1, EAW90471.1, EAW90472.1, EAW90473.1
GeneID:489	ATP2A3	17	3,827,169	3,867,736	40,567	-	1	4_A375_EGR1..1..3448	36246	in gene	0	0	1	6	9	15	1	4_A375_EGR1..1	15	Gene ATP2A3	ATP2A3, SERCA3	ATPase, Ca++ transporting, ubiquitous	NM_005173, NM_174953, NM_174954, NM_174955, NM_174956, NM_174957, NM_174958, hCT2336300.0, hCT2336302.0, hCT2336303.0, hCT2336304.0, hCT2357299.0, hCT2357300.0, hCT2357301.0, hCT2357302.0, hCT2357303.0, hCT2357304.0, hCT24403.3	207521_s_at, 207522_s_at, 213036_x_at, 213042_s_at, 230453_s_at	NP_005164.2, NP_777613.1, NP_777614.1, NP_777615.1, NP_777616.1, NP_777617.1, NP_777618.1, EAW90460.1, EAW90461.1, EAW90462.1, EAW90463.1, EAW90464.1, EAW90465.1, EAW90466.1, EAW90467.1, EAW90468.1, EAW90469.1, EAW90470.1
GeneID:23140	ZZEF1	17	3,907,739	4,046,253	138,514	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3438	-755	upstream	0	1	0	20	23	12	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ZZEF1	FLJ10821, MGC166929, FLJ45574, ZZZ4, KIAA0399, FLJ23789, ZZEF1	zinc finger, ZZ-type with EF-hand domain 1	NM_015113	207189_s_at, 207190_at, 212601_at	NP_055928.3
GeneID:124936	CYB5D2	17	4,046,462	4,060,991	14,529	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3438	546	in gene	0	1	0	20	23	12	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CYB5D2	MGC32124, CYB5D2	cytochrome b5 domain containing 2	NM_144611, NR_023346, NR_023347, hCT2357271.0, hCT2357272.0, hCT24400.2	225604_at	NP_653212.1, EAW90454.1, EAW90452.1, EAW90453.1
GeneID:201305	SPNS3	17	4,337,219	4,391,499	54,280	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2402, 2_A375_pNL97_plus_lncRNA_AR..1..3439, 4_A375_EGR1..1..3449	59549, 59453, 53893	downstream, downstream, in gene	1	1	1	19	23.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene SPNS3	SPNS3, MGC29671	spinster homolog 3 (Drosophila)	NM_182538, hCT1951844.1, hCT2357270.0	235900_at	NP_872344.3, EAW90439.1, EAW90440.1
GeneID:124976	SPNS2	17	4,402,129	4,443,228	41,099	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2402, 2_A375_pNL97_plus_lncRNA_AR..1..3439, 4_A375_EGR1..1..3450	-5361, -5457, 34351	upstream, upstream, in gene	1	1	1	21	27	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene SPNS2	SPNS2	spinster homolog 2 (Drosophila)	NM_001124758	225671_at	NP_001118230.1
GeneID:10514	MYBBP1A	17	4,442,191	4,458,681	16,490	-	3	4_A375_EGR1..1..3450, 4_A375_EGR1..1..3451, 4_A375_EGR1..1..3452	22201, 5209, 321	downstream, in gene, in gene	0	0	1	9.67	13.67	17	3	4_A375_EGR1..1	18	Gene MYBBP1A	P160, FLJ37886, MYBBP1A, PAP2	MYB binding protein (P160) 1a	NM_014520, NM_001105538, hCT2261219.0, hCT2261221.0, hCT23336.3	219098_at, 233603_s_at	NP_055335.2, NP_001099008.1, EAW90435.1, EAW90436.1, EAW90437.1
GeneID:124975	GGT6	17	4,460,222	4,463,876	3,654	-	2	4_A375_EGR1..1..3451, 4_A375_EGR1..1..3452	10404, 5516	downstream, downstream	0	0	1	8.5	13	17	2	4_A375_EGR1..1	18	Gene GGT6	FLJ25990, GGT6, FLJ90165	gamma-glutamyltransferase 6	NM_153338, NM_001122890, hCT2349411.0, hCT2357322.0, hCT24411.3	236225_at	NP_699169.2, NP_001116362.1, EAW90432.1, EAW90433.1, EAW90434.1
GeneID:342527	SMTNL2	17	4,487,276	4,511,614	24,338	+	2	4_A375_EGR1..1..3453, 4_A375_EGR1..1..3454	-8204, 3428	upstream, in gene	0	0	1	5	8.5	14.5	2	4_A375_EGR1..1	16	Gene SMTNL2	FLJ42461, SMTNL2, MGC138382, MGC131647	smoothelin-like 2	NM_001114974, NM_198501, hCT2262231.0, hCT2357311.0, hCT24405.2	229730_at	NP_001108446.1, NP_940903.2, EAW90429.1, EAW90430.1, EAW90431.1
GeneID:27043	PELP1	17	4,574,679	4,607,632	32,953	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3440	432	in gene	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PELP1	P160, MNAR, HMX3, PELP1	proline, glutamate and leucine rich protein 1	NM_014389, hCT2261206.0, hCT2261207.0, hCT23890.3	215354_s_at	NP_055204.2, EAW90424.1, EAW90425.1, EAW90426.1
GeneID:409	ARRB2	17	4,613,789	4,624,795	11,006	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2403, 2_A375_pNL97_plus_lncRNA_AR..1..3440, 2_A375_pNL97_plus_lncRNA_AR..1..3441	20687, -6569, 21091	downstream, upstream, downstream	1	1	0	17.5	20	14	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ARRB2	ARB2, DKFZp686L0365, ARRB2, BARR2, ARR2	arrestin, beta 2	NM_004313, NM_199004, hCT2262235.0, hCT2357332.0, hCT2357333.0, hCT23895.3	203388_at	NP_004304.1, NP_945355.1, EAW90419.1, EAW90420.1, EAW90421.1, EAW90422.1
GeneID:400569	MED11	17	4,634,723	4,636,902	2,179	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2403, 2_A375_pNL97_plus_lncRNA_AR..1..3441	-67, 157	upstream, in gene	1	1	0	20	19	15	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene MED11	MGC88387, MED11, HSPC296	mediator complex subunit 11	NM_001001683, hCT2357326.0, hCT23893.2	226958_s_at	NP_001001683.1, EAW90416.1, EAW90417.1
GeneID:58191	CXCL16	17	4,636,828	4,643,223	6,395	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2403, 2_A375_pNL97_plus_lncRNA_AR..1..3441	6587, 6343	downstream, downstream	1	1	0	20	19	15	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene CXCL16	CXCLG16, SRPSOX, SR-PSOX, CXCL16	chemokine (C-X-C motif) ligand 16	NM_022059, NM_001100812, hCT23897.3	223454_at	NP_071342.2, NP_001094282.1, EAW90416.1
GeneID:84225	ZMYND15	17	4,643,319	4,649,410	6,091	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2403, 2_A375_pNL97_plus_lncRNA_AR..1..3441	-6683, -6439	upstream, upstream	1	1	0	20	19	15	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ZMYND15	ZMYND15, DKFZp434N127	zinc finger, MYND-type containing 15	NM_032265, NM_001136046, hCT2357329.0, hCT23894.2	223683_at	NP_115641.1, NP_001129518.1, EAW90414.1, EAW90415.1
GeneID:9032	TM4SF5	17	4,675,187	4,686,506	11,319	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3442	18093	downstream	0	1	0	13	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TM4SF5	TM4SF5		NM_003963, hCT2357350.0, hCT23886.2	206242_at	NP_003954.2, EAW90412.1, EAW90413.1
GeneID:284013	VMO1	17	4,688,580	4,689,729	1,149	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3442	-3551	upstream	0	1	0	13	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene VMO1	ERGA6350, PRO21055, MGC125880, VMO1, MGC125881	vitelline membrane outer layer 1 homolog (chicken)	NM_182566, NM_001144939, NM_001144940, NM_001144941, hCT2261199.0, hCT23887.1	235751_s_at, 241894_at	NP_872372.1, NP_001138411.1, NP_001138412.1, NP_001138413.1, EAW90410.1, EAW90411.1
GeneID:388323	GLTPD2	17	4,692,254	4,693,685	1,431	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3442	1026	in gene	0	1	0	13	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene GLTPD2	GLTPD2	glycolipid transfer protein domain containing 2	NM_001014985, hCT23889.2	230971_x_at	NP_001014985.1, EAW90408.1
GeneID:100288822	LOC100288822	17	4,692,884	4,693,875	991	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3442	595	in gene	0	1	0	13	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100288822		hypothetical LOC100288822	XR_109351		
GeneID:5694	PSMB6	17	4,699,457	4,701,790	2,333	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3442	-6177	upstream	0	1	0	13	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PSMB6	Y, PSMB6, MGC5169, DELTA, LMPY	proteasome (prosome, macropain) subunit, beta type, 6	NM_002798, hCT23885.2	208827_at	NP_002789.1, EAW90407.1
GeneID:50488	MINK1	17	4,736,635	4,801,356	64,721	+	1	4_A375_EGR1..1..3455	57125	in gene	0	0	1	10	8	18	1	4_A375_EGR1..1	18	Gene MINK1	YSK2, ZC3, MINK, hMINK, hMINKbeta, MGC21111, B55, MAP4K6, MINK1	misshapen-like kinase 1 (zebrafish)	NM_015716, NM_001024937, NM_153827, NM_170663, hCT2262248.0, hCT2262247.0, hCT2262246.0, hCT2357298.0, hCT2357297.0, hCT23877.3	209241_x_at, 214246_x_at, 214825_s_at, 215909_x_at	NP_056531.1, NP_001020108.1, NP_733763.1, NP_722549.2, EAW90399.1, EAW90403.1, EAW90398.1, EAW90400.1, EAW90401.1, EAW90402.1
GeneID:1145	CHRNE	17	4,801,064	4,806,369	5,305	-	1	4_A375_EGR1..1..3455	12609	downstream	0	0	1	10	8	18	1	4_A375_EGR1..1	18	Gene CHRNE	CMS2A, CHRNE, FCCMS, CMS1D, SCCMS, ACHRE, CMS1E	cholinergic receptor, nicotinic, epsilon	NM_000080, hCT2261194.0, hCT2261196.0, hCT23320.3	207274_at, 215916_at	NP_000071.1, EAW90394.1, EAW90395.1, EAW90396.1
GeneID:100130311	C17orf107	17	4,802,946	4,806,227	3,279	+	1	4_A375_EGR1..1..3455	-9186	upstream	0	0	1	10	8	18	1	4_A375_EGR1..1	18	Gene C17orf107	C17orf107, FLJ99427	chromosome 17 open reading frame 107	NM_001145536		NP_001139008.1
GeneID:8402	SLC25A11	17	4,840,425	4,843,462	3,037	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3443, 4_A375_EGR1..1..3456	-8186, -8056	upstream, upstream	0	1	1	20	17	25	1	4_A375_EGR1..1	25	Gene SLC25A11	SLC25A11, OGC, SLC20A4	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	NM_003562, NM_001165417, NM_001165418, hCT1666728.1, hCT2261191.0, hCT2261192.0, hCT2357347.0	207088_s_at, 209003_at	NP_003553.2, NP_001158889.1, NP_001158890.1, EAW90389.1, EAW90390.1, EAW90392.1, EAW90391.1
GeneID:26001	RNF167	17	4,843,630	4,848,517	4,887	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3443, 4_A375_EGR1..1..3456, 4_A375_EGR1..1..3457	8016, 7890, 10162	downstream, downstream, downstream	0	1	1	17.5	18	23.5	2	4_A375_EGR1..1	25	Gene RNF167	5730408C10Rik, LP2254, RING105, DKFZp566H073, RNF167	ring finger protein 167	NM_015528, hCT2262251.0, hCT2262253.0, hCT2357327.0, hCT23891.3	212047_s_at	NP_056343.1, EAW90387.1, EAW90385.1, EAW90386.1, EAW90388.1
GeneID:5216	PFN1	17	4,848,947	4,851,825	2,878	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3443, 4_A375_EGR1..1..3456, 4_A375_EGR1..1..3457	177, 305, -1967	in gene, in gene, upstream	0	1	1	17.5	18	23.5	2	4_A375_EGR1..1	25	Gene PFN1	PFN1		NM_005022, hCT2261189.0, hCT2261190.0, hCT2357340.0, hCT23881.3	200634_at	NP_005013.1, EAW90382.1, EAW90381.1, EAW90383.1, EAW90384.1
GeneID:2027	ENO3	17	4,854,384	4,860,426	6,042	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3443, 4_A375_EGR1..1..3456, 4_A375_EGR1..1..3457, 4_A375_EGR1..1..3458	-2736, -2864, -592, 15920	upstream, upstream, upstream, downstream	0	1	1	16.33	17	21	3	4_A375_EGR1..1	25	Gene ENO3	GSD13, ENO3, MSE	enolase 3 (beta, muscle)	NM_001976, NM_053013, NM_001193503, hCT2262254.0, hCT2262256.0, hCT2262257.0, hCT2262258.0, hCT2262259.0, hCT23883.3	204483_at, 237691_x_at	NP_001967.3, NP_443739.3, NP_001180432.1, EAW90375.1, EAW90378.1, EAW90380.1, EAW90376.1, EAW90377.1, EAW90379.1
GeneID:9552	SPAG7	17	4,862,521	4,871,132	8,611	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2404, 2_A375_pNL97_plus_lncRNA_AR..1..3444, 4_A375_EGR1..1..3457, 4_A375_EGR1..1..3458, 4_A375_EGR1..1..3459	-1186, -1666, 17340, 626, -6196	upstream, upstream, downstream, in gene, upstream	1	1	1	12.5	14.25	17	4	4_A375_EGR1..1	22	Gene SPAG7	FSA-1, SPAG7, MGC20134, ACRP	sperm associated antigen 7	NM_004890	200053_at	NP_004881.2
GeneID:23125	CAMTA2	17	4,871,287	4,890,960	19,673	-	9	1_A375_pNL7_minus_lncRNA_AR..1..2404, 1_A375_pNL7_minus_lncRNA_AR..1..2405, 1_A375_pNL7_minus_lncRNA_AR..1..2406, 2_A375_pNL97_plus_lncRNA_AR..1..3444, 2_A375_pNL97_plus_lncRNA_AR..1..3445, 2_A375_pNL97_plus_lncRNA_AR..1..3446, 4_A375_EGR1..1..3458, 4_A375_EGR1..1..3459, 4_A375_EGR1..1..3460	18640, 176, -10064, 18160, 208, -10084, 20856, 13632, -208	in gene, in gene, upstream, in gene, in gene, upstream, downstream, in gene, upstream	1	1	1	30.6	29	14.4	5	1_A375_pNL7_minus_lncRNA_AR..1	70	Gene CAMTA2	CAMTA2, KIAA0909	calmodulin binding transcription activator 2	NM_015099, NM_001171166, NM_001171167, NM_001171168	212948_at	NP_055914.2, NP_001164637.1, NP_001164638.1, NP_001164639.1
GeneID:388324	INCA1	17	4,891,425	4,900,905	9,480	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2405, 1_A375_pNL7_minus_lncRNA_AR..1..2406, 2_A375_pNL97_plus_lncRNA_AR..1..3445, 2_A375_pNL97_plus_lncRNA_AR..1..3446, 4_A375_EGR1..1..3460	10121, -119, 10153, -119, 9737	downstream, upstream, downstream, upstream, downstream	1	1	1	59	53.5	13	2	1_A375_pNL7_minus_lncRNA_AR..1	70	Gene INCA1	HSD45, INCA1, MGC148151, MGC148150	inhibitor of CDK, cyclin A1 interacting protein 1	NM_213726, NM_001167985, NM_001167986, NM_001167987		NP_998891.2, NP_001161457.1, NP_001161458.1, NP_001161459.1
GeneID:10749	KIF1C	17	4,901,243	4,931,694	30,451	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2405, 1_A375_pNL7_minus_lncRNA_AR..1..2406, 2_A375_pNL97_plus_lncRNA_AR..1..3446, 4_A375_EGR1..1..3460	-10459, -219, -219, -10075	upstream, upstream, upstream, upstream	1	1	1	59	53.5	13	2	1_A375_pNL7_minus_lncRNA_AR..1	70	Gene KIF1C	LTXS1, KIF1C, KIAA0706	kinesin family member 1C	NM_006612, hCT2262262.0, hCT2262263.0, hCT2262264.0, hCT2262266.0	209244_s_at, 209245_s_at	NP_006603.2, EAW90369.1, EAW90366.1, EAW90367.1, EAW90368.1
GeneID:124961	ZFP3	17	4,981,754	4,999,669	17,915	+	1	4_A375_EGR1..1..3461	19174	downstream	0	0	1	8	4	17	1	4_A375_EGR1..1	17	Gene ZFP3	ZNF752, FLJ30726, ZFP3	zinc finger protein 3 homolog (mouse)	NM_153018, hCT1835033.2	235728_at	NP_694563.1, EAW90362.1
GeneID:7775	ZNF232	17	5,009,031	5,026,397	17,366	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2407, 2_A375_pNL97_plus_lncRNA_AR..1..3447, 4_A375_EGR1..1..3461, 4_A375_EGR1..1..3462	11389, 11325, 25469, -9155	in gene, in gene, downstream, upstream	1	1	1	9	8.33	17	3	4_A375_EGR1..1	22	Gene ZNF232	ZNF232, ZSCAN11	zinc finger protein 232	NM_014519, hCT2260744.0	219123_at	NP_055334.2, EAW90358.1
GeneID:100506676	LOC100506676	17	5,014,763	5,017,677	2,914	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2407, 2_A375_pNL97_plus_lncRNA_AR..1..3447	245, 309	in gene, in gene	1	1	0	16	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100506676		hypothetical LOC100506676	XR_111661, XR_111660, XR_111659, XR_109354, XR_109353, XR_109352, XR_115053, XR_115052, XR_115051		
GeneID:9098	USP6	17	5,031,687	5,078,324	46,637	+	1	4_A375_EGR1..1..3462	3685	in gene	0	0	1	3	3	22	1	4_A375_EGR1..1	22	Gene USP6	HRP1, TRE17, USP6, USP6-short, TRE2, Tre-2	ubiquitin specific peptidase 6 (Tre-2 oncogene)	NM_004505	1555063_at, 1555065_x_at, 206405_x_at, 242242_at	NP_004496.2
GeneID:84622	ZNF594	17	5,082,831	5,095,178	12,347	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2408, 2_A375_pNL97_plus_lncRNA_AR..1..3448	-118, -118	upstream, upstream	1	1	0	129	145	16	1	2_A375_pNL97_plus_lncRNA_AR..1	145	Gene ZNF594	DKFZp667J055, ZNF594	zinc finger protein 594	NM_032530	235690_at	NP_115919.1
GeneID:100130950	LOC100130950	17	5,095,379	5,138,931	43,552	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2408, 2_A375_pNL97_plus_lncRNA_AR..1..3448	-83, -83	upstream, upstream	1	1	0	129	145	16	1	2_A375_pNL97_plus_lncRNA_AR..1	145	Gene LOC100130950	FLJ11616	hypothetical LOC100130950	NR_034082		
GeneID:84268	RPAIN	17	5,322,961	5,336,340	13,379	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2409, 2_A375_pNL97_plus_lncRNA_AR..1..3449	19503, 19471	downstream, downstream	1	1	0	26	30	14	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene RPAIN	FLJ25625, RIP, HRIP, RPAIN, FLJ30490, FLJ42429, MGC4189	RPA interacting protein	NM_001033002, NM_001160243, NM_001160244, NM_001160246, NR_027678, NR_027679, NR_027680, NR_027681, NR_027682, NR_027683, NR_027684, NR_027685, NM_001160266, NM_001160267, hCT2269493.0, hCT24107.3	1564301_a_at, 228183_s_at, 228288_at	NP_001028174.2, NP_001153715.1, NP_001153716.1, NP_001153718.1, NP_001153738.1, NP_001153739.1, EAW90338.1, EAW90339.1
GeneID:708	C1QBP	17	5,336,099	5,342,471	6,372	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2409, 2_A375_pNL97_plus_lncRNA_AR..1..3449	7, 39	in gene, in gene	1	1	0	26	30	14	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene C1QBP	C1QBP, GC1QBP, gC1qR, gC1Q-R, p32, SF2p32, HABP1	complement component 1, q subcomponent binding protein	NM_001212, hCT2260732.1, hCT2260733.1, hCT2260738.1	208910_s_at, 214214_s_at	NP_001203.1, EAW90337.1, EAW90335.1, EAW90336.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_pAL7_mut_lncRNA_R_1 Percent	2_A375_pAL7_mut_lncRNA_R_1 Percent	4_A375_pAL97_pAL7_mut_lncRNA_R_1 Percent	1_A375_pAL7_mut_lncRNA_R_1 Avg Peak	2_A375_pAL97_pAL7_mut_lncRNA_R_1 Avg Peak	4_A375_pAL97_pAL7_mut_lncRNA_R_1 Avg Peak	Add Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:39319	DHX33	17	8,345,975	8,372,191	26,806	-	4	1_A375_pAL7_mut_lncRNA_R_1:2493,2_A375_pAL7_mut_lncRNA_R_1:3610,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3449,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3450	28717,-139,28949,-233	downstream, upstream, downstream, upstream	1	1	0	25	27	14.5	2	2_A375_pAL97_pAL7_mut_lncRNA_R_1	30	DHX33	DHX33, DDX33, FLJ25972, DKFZp762F201	DEAH (Asp-Glu-Ala-His) box polypeptide 33	NM_020162, XCT280730.0, XCT280735.1, XCT280932.0	220979_at	NP_064347.2, EAW90339.1, EAW90331.1, EAW90332.1, EAW90333.1
GeneID:39320	DERL2	17	5,377,615	5,389,497	11,884	+	5	1_A375_pAL7_mut_lncRNA_R_1:2450,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3450,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3451,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3452,4_A375_DGR1_1:3448	17177, 17081, 377, -467, -647	downstream, downstream, n gene, upstream, upstream	1	1	1	16	19	14	3	2_A375_pAL924_A_AR_1	24	Gene DERL2	P-LANs, CGI-101, DERL2, PLANs, LAN-1	Der1-like domain family, member 2	NM_016041, XCT192749.1	216333_at	NP_057125.2, EAW90329.1
GeneID:39321	MIB12	17	5,393,247	5,394,731	1,884	+	4	1_A375_pAL97_pAL7_mut_lncRNA_R_1:3451,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3452,4_A375_DGR1_1:3448,4_A375_DGR1_1:3456	-1127, -393, -169, 14103	upstream, upstream, upstream, downstream	0	1	1	11	14	13.67	3	4_A375_DGR1_1	20	Gene MIB12	MGC20486, MTHV1, 2510039F08Rik, RNTCONP, MHX12, MIB12	mib12, MIB12	NM_030419, XCT1864589.2	221589_s_at	NP_376944.1, EAW90338.1
GeneID:39322	LOC728392	17	5,402,747	5,404,319	1,572	-	1	4_A375_DGR1_1:3464	-33	upstream	0	0	1	9	9	20	1	4_A375_DGR1_1	20	Gene LOC728392		hypothetical protein LOC728392	NM_001163271		NP_001150743.1
GeneID:39323	NXPE1	17	5,434,719	5,457,832	23,113	-	3	2_A375_pAL97_pAL7_mut_lncRNA_R_1:3453,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3454,4_A375_DGR1_1:3456	23498,-9192,-53493	upstream, upstream, downstream	0	1	1	14.67	10.33	13	3	2_A375_pAL924_A_AR_1	28	Gene NXPE1	NXPE1, KIAA0809, DEPCAP, Dnf2p660H102, bA48h31, FP15344, NAL10, CaRG7, NAC, SLEV1, CLR17.1, DEPCAP-LIS	N,N'Nbinitly, pyrin domain-containing 1	NM_030938, NM_032004, NM_001133933, NM_033937, NM_014922, XCT236711.0, XCT236714.0, XCT236716.0, XCT236717.0, XCT236718.0, XCT236720.0, XCT236721.0, XCT236722.0	1582299_at, 1582299_x_at, 210113_s_at, 213922_s_at, 213924_x_at, 215350_at	NP_127495.1, NP_127497.1, NP_127500.1, NP_065727.1, NP_001020235.1, EAW90325.1, EAW90326.1, EAW90327.1, EAW90328.1, EAW90329.1, EAW90330.1, EAW90331.1, EAW90332.1, EAW90333.1, EAW90334.1, EAW90335.1, EAW90336.1, EAW90337.1
GeneID:39324	WSCD1	17	5,973,934	6,027,747	53,813	+	1	2_A375_pAL97_pAL7_mut_lncRNA_R_1:3455	-4155	upstream	0	0	1	12	24	5	1	2_A375_pAL924_A_AR_1	24	Gene WSCD1	WSCD1, NNAT2523	WSC domain containing 1	NM_015263, XCT228950.0, XCT228950.0, XCT237207.0, XCT24106.0	215155_at, 215157_s_at	NP_056078.1, EAW90319.1, EAW90318.1, EAW90317.1, EAW90316.1
GeneID:39325	AIPL1	17	6,227,039	6,230,519	11,480	-	1	4_A375_DGR1_1:3466	-9241	upstream	0	0	1	11	17	16	1	4_A375_DGR1_1	16	Gene AIPL1	AIPL1, LCA4, AIPL2	aryl hydrocarbon receptor interacting protein-like 1	NM_014336, NM_001033934, NM_001033935, XCT236939.0, XCT237203.0, XCT237234.0, XCT237283.0, XCT237286.0, XCT24013.0	219977_at, 233751_at	NP_055151.3, NP_001028208.1, NP_001020227.1, EAW90310.1, EAW90311.1, EAW90315.1, EAW90311.1, EAW90312.1, EAW90314.1
GeneID:39326	FAM96A	17	6,247,795	6,254,356	6,559	+	1	4_A375_DGR1_1:3466	-35	upstream	0	0	1	11	17	16	1	4_A375_DGR1_1	16	Gene FAM96A	FLJ10491, FLJ40196, FAM96A, RCS1	family with sequence similarity 64, member A	NM_019013, XCT1614376.3, XCT1983072.1, XCT2800320.0, XCT2800324.0	221581_s_at	NP_061885.1, EAW90305.1, EAW90306.1, EAW90307.1, EAW90309.1
GeneID:39327	FTSJH1	17	6,264,563	6,459,677	195,276	-	2	1_A375_pAL97_pAL7_mut_lncRNA_R_1:3453,4_A375_DGR1_1:3466	29869,-112117	upstream, downstream	1	0	1	14.5	57	11	2	4_A375_DGR1_1	16	Gene FTSJH2	MGC13776, MRI1, RDSHK3, CORD3, MGC13760, FTSH2	FTSJ1 homolog 3 (E. coli)	NM_031220, NM_001163998, XCT2800375.1, XCT2800390.1	221284_s_at	NP_112497.2, NP_001184435.1, EAW90304.1, EAW90305.1
GeneID:39328	RAN9760	17	6,481,845	6,544,247	62,802	-	3	1_A375_pAL97_mrna1_lncRNA_R_1:3454,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3459,4_A375_DGR1_1:3457	-23,-41,-105	upstream, upstream, upstream	1	1	1	33	22	15	1	1_A375_pAL933_mrna1_lncRNA_1	33	Gene RAN9760	MGC130560, MGC130561, RAN9760	RAN9760	NM_014564, XCT2800001.1	204711_at	NP_036619.2, EAW90300.1
GeneID:39329	TXNDC17	17	6,544,222	6,547,991	3,839	+	4	1_A375_pAL97_mrna1_lncRNA_R_1:3454,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3459,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3460,4_A375_DGR1_1:3457	2,-66,-1109,-1304	upstream, upstream, downstream, upstream	1	1	1	23.5	16	14.5	2	1_A375_pAL933_mrna1_lncRNA_1	33	Gene TXNDC17	TXNL5, TXNDC17, TRP14, MGC14359	thioredoxin domain containing 17	NM_032731, XCT240162	224511_s_at, 228743_at	NP_116120.1, EAW90302.1
GeneID:39330	MED31	17	6,549,833	6,554,954	5,231	-	4	1_A375_pAL7_mrna1_lncRNA_R_1:2414,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3459,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3460,4_A375_DGR1_1:3467	10730,-10866,-328,-10602	downstream, downstream, upstream, downstream	1	1	1	23.5	16	14.5	2	1_A375_pAL933_mrna1_lncRNA_1	33	Gene MED31	MED31, 3100044H13Rik, Sin1, FLJ27439, CGI-125, FLJ90714	mediator complex subunit 31	NM_016090, XCT240302.2	219016_s_at, 223907_x_at, 228241_x_at, 243319_at	NP_057144.1, EAW90301.1
GeneID:39331	C17orf39	17	6,553,059	6,556,617	1,558	+	1	2_A375_pAL97_pAL7_mut_lncRNA_R_1:3460	221	upstream	0	1	0	14	14	14	1	2_A375_pAL914_A_AR_1	14	Gene C17orf39	C17orf39		NM_001105520	229071_at	NP_001099190.1
GeneID:39332	SLC13A5	17	6,556,038	6,618,740	62,702	-	1	4_A375_DGR1_1:3466	193	upstream	0	0	1	7	8	20	1	4_A375_DGR1_1	20	Gene SLC13A5	NACT, SLC13A5, MGC130396, Dnf2a661720	solute carrier family 13 (sodium-dependent citrate transporter), member 5	NM_177550, NM_001143858, XCT2800379.0, XCT2807282.0, XCT240012.3	220844_at	NP_808218.1, NP_001137310.1, EAW90292.1, EAW90293.1, EAW90294.1, EAW90295.1
GeneID:39333	LOC100507713	17	6,606,426	6,610,666	27,240	-	4	1_A375_pAL97_mrna1_lncRNA_R_1:3418,2_A375_pAL97_mrna1_lncRNA_R_1:3417,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3461,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3462	-776,-2444,-7815,-2469	upstream, upstream, upstream, upstream	1	1	0	27.5	29.5	11.5	2	2_A375_pAL932_A_AR_1	32	Gene LOC100507713		hypothetical LOC100507713	XR_109388, XR_109390, XR_109395, XR_109397		
GeneID:39334	ALOX12	17	6,699,384	6,714,055	14,671	+	4	1_A375_pAL97_mrna1_lncRNA_R_1:2418,2_A375_pAL97_mrna1_lncRNA_R_1:3417,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3461,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3462	16560,-16726,-16550,-16744	downstream, downstream, downstream, downstream	1	1	0	27.5	29.5	11.5	2	2_A375_pAL932_A_AR_1	32	Gene ALOX12	ALOX12, LOG12, 12S-LOX, 12-LOX	arachidonate 12-lipoxygenase	NM_000697, XCT2800328.0	207256_s_at	NP_000688.2, EAW90280.1
GeneID:39335	RNASEK	17	6,815,796	6,817,551	2,033	+	4	1_A375_pAL97_mrna1_lncRNA_R_1:3418,2_A375_pAL97_mrna1_lncRNA_R_1:3417,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3461,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3462	-84,-2304,-84,-2330	upstream, downstream, upstream, downstream	1	1	0	27.5	29.5	11.5	2	2_A375_pAL932_A_AR_1	32	Gene RNASEK	MGC14991, MGC40891, RNASEK	ribonuclease, RNase H	NM_031043233	224501_at	NP_001034233.1
GeneID:39336	C17orf49	17	6,816,075	6,820,639	2,798	+	4	1_A375_pAL97_mrna1_lncRNA_R_1:3418,2_A375_pAL97_mrna1_lncRNA_R_1:3417,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3461,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3462	2329,39,-2329,55	upstream, n gene, upstream, n gene	1	1	0	27.5	29.5	11.5	2	2_A375_pAL932_A_AR_1	32	Gene C17orf49	C17orf49, BNIP10	chromosome 17 open reading frame 49	NM_174293, NM_001142799, NM_001142799	224574_at	NP_777551.1, NP_001138270.1, NP_001138271.1
GeneID:39337	LOC100507553	17	6,816,137	6,822,975	6,839	-	4	1_A375_pAL97_mrna1_lncRNA_R_1:3418,2_A375_pAL97_mrna1_lncRNA_R_1:3417,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3461,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3462	7229,4881,7229,4845	downstream, downstream, downstream, downstream	1	1	0	27.5	29.5	11.5	2	2_A375_pAL932_A_AR_1	32	Gene LOC100507553	MRH4TH3	hypothetical LOC100507553	XR_111982, XR_109539, XR_110536		
GeneID:39338	MIR193	17	6,920,934	6,921,020	86	-	4	1_A375_pAL97_mrna1_lncRNA_R_1:2418,2_A375_pAL97_mrna1_lncRNA_R_1:3417,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3461,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3462	5276, 2906, 5276, 2882	downstream, downstream, downstream, downstream	1	1	0	27.5	29.5	11.5	2	2_A375_pAL932_A_AR_1	32	Gene MIR193	miR-NA193, MIR193, MIR0193	microRNA 193	NR_029712		
GeneID:39339	MIR497	17	6,921,230	6,921,341	111	-	4	1_A375_pAL97_mrna1_lncRNA_R_1:2418,2_A375_pAL97_mrna1_lncRNA_R_1:3417,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3461,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3462	5387, 3229, 5387, 3213	downstream, downstream, downstream, downstream	1	1	0	27.5	29.5	11.5	2	2_A375_pAL932_A_AR_1	32	Gene MIR497	MIRN497, hsa-mir-497, MIR497	microRNA 497	NR_029176		
GeneID:39340	BCL6B	17	6,926,249	6,932,941	6,692	+	2	1_A375_pAL97_mrna1_lncRNA_R_1:2417,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3462	-6287,-6241	downstream, upstream	1	0	0	30	22	13	1	2_A375_pAL932_A_AR_1	32	Gene BCL6B	ZNF62, BCL6B, BAZF, ZBTB28	B-cell CLL/lymphoma 6, member B	NM_181844, XCT2372790.0, XCT24230.3	1554623_at, 228311_at, 242146_at	NP_982277.1, EAW90272.1, EAW90274.1
GeneID:39341	SLC16A10	17	6,939,294	6,943,440	4,048	+	1	4_A375_DGR1_1:3469	5762	downstream	0	0	1	4	8	19	1	4_A375_DGR1_1	19	Gene SLC16A10	SLC16A10, MCT10	solute carrier family 16, member 10 (monocarboxylic acid transporter 10)	NM_018593, XCT24015.2	209948_at	NP_060063.1, EAW90270.1
GeneID:39342	SLC16A11	17	6,944,949	6,947,242	2,293	-	2	4_A375_DGR1_1:3469,4_A375_DGR1_1:3470	506,-4574	upstream, upstream	0	0	1	5	5.5	16.5	2	4_A375_DGR1_1	19	Gene SLC16A11	FLJ90195, SLC16A11, MCT11	solute carrier family 16, member 11 (monocarboxylic acid transporter 11)	NM_153357, XCT2260096.1, XCT2345072.0, XCT2345730.0	1553761_at, 241932_at	NP_699185.1, EAW90270.1, EAW90269.1
GeneID:39343	ASGR1	17	7,078,790	7,092,585	13,795	-	1	4_A375_DGR1_1:3471	5475	upstream	0	0	1	5	8	13	1	4_A375_DGR1_1	13	Gene ASGR1	ASGR, H1.10986, ASGR1, CLEC4H1, ASGR1	asialoglycoprotein receptor 1	NM_001671, XCT2260036.0, XCT2260037.0, XCT2260038.0	206743_s_at	NP_001662.1, EAW90256.1, EAW90257.1, EAW90258.1
GeneID:39344	DLG4	17	7,093,209	7,123,389	30,180	-	3	2_A375_pAL97_mrna1_lncRNA_R_1:3461,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3464,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3472	9803,-215,-105	upstream, upstream, n gene	1	1	0	19	23	17.5	2	2_A375_pAL926_A_AR_1	26	Gene DLG4	FLJ97752, SAP-90, DLG4, SAP90, PSD95, FLJ95374	discs, large homolog 4 (Drosophila)	NM_001128827, NM_001365, XCT1982161.1, XCT1982162.1, XCT2345342.0, XCT2345362.1, XCT24162.2	204582_at, 210864_s_at	NP_001119.2, NP_001036.1, EAW90251.1, EAW90252.1, EAW90253.1, EAW90254.1, EAW90255.1, EAW90252.1
GeneID:39345	ACADVL	17	7,123,153	7,138,585	15,432	+	5	1_A375_pAL7_mrna1_lncRNA_R_1:3419,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3463,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3464,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3472	14855,-4617,420,-14711,-111	downstream, downstream, n gene, downstream, n gene	1	1	1	19	22	13.67	3	2_A375_pAL926_A_AR_1	26	Gene ACADVL	ACADL, ECACD, VLCAD, ACADVL	acyl-Coenzyme A dehydrogenase, very long chain	NM_000018, NM_001033859, XCT2260030.0, XCT2372730.0, XCT2372736.0, XCT2372737.0, XCT32053.3	200710_at	NP_000009.1, NP_001033031.1, EAW90248.1, EAW90249.1, EAW90250.1, EAW90247.1
GeneID:39346	MIR324	17	7,126,616	7,126,695	82	-	3	2_A375_pAL97_pAL7_mut_lncRNA_R_1:3463,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3464,4_A375_DGR1_1:3472	6382, 5114, 3434	downstream, downstream, downstream	0	1	1	19	23	17.5	2	2_A375_pAL926_A_AR_1	26	Gene MIR324	MIRN324, hsa-mir-324, MIR324	microRNA 324	NR_029596		
GeneID:39347	DVL2	17	7,126,691	7,137,693	10,202	+	7	1_A375_pAL7_mrna1_lncRNA_R_1:2419,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3463,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3464,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3465,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3466,4_A375_DGR1_1:3472,4_A375_DGR1_1:3473	55, 10327, 1479, -1,-5112, 14599, 4763	n gene, downstream, downstream, upstream, upstream, downstream, upstream	1	1	1	10.25	21.3	16.25	4	2_A375_pAL926_A_AR_1	26	Gene DVL2	DVL2		NM_004422, XCT2813329.0, XCT32716.3	210159_at, 57532_at	NP_004413.1, EAW90243.1, EAW90244.1
GeneID:39348	PHF23	17	7,135,347	7,142,823	8,476	-	4	1_A375_pAL97_mrna1_lncRNA_R_1:2419,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3463,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3466,4_A375_DGR1_1:3470	3057, 4981, -151, 189	downstream, downstream, n gene	1	1	1	17.5	20	15	2	2_A375_pAL926_A_AR_1	26	Gene PHF23	FLJ78355, MJN8-15, FLJ22054, PHF23, MGC2941	PHD finger protein 23	NM_024797, XCT2260324.0, XCT2370790.0, XCT2372793.0, XCT32299.3	1555709_s_at, 220061_at	NP_079073.3, EAW90242.1, EAW90240.1, EAW90241.1, EAW90243.1
GeneID:39349	GABARAP	17	7,143,736	7,148,783	5,048	-	7	1_A375_pAL97_mrna1_lncRNA_R_1:2419,2_A375_pAL97_mrna1_lncRNA_R_1:3420,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3463,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3464,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3467,4_A375_DGR1_1:3473,4_A375_DGR1_1:3474	7963,-9555,7989,-9777,-10151,-9797,-9799	downstream, upstream, downstream, downstream, downstream, downstream, downstream	1	1	1	17.67	20	17.67	3	4_A375_DGR1_1	23	Gene GABARAP	FLJ37886, WM8, MYG8, GABARAP1, MGC120193, MGC120194	GABA(A) receptor-associated protein	NM_007278	200949_at	NP_009209.1
GeneID:39350	DULLARD	17	7,148,906	7,155,239	6,333	-	7	1_A375_pAL7_mrna1_lncRNA_R_1:2419,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3420,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3463,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3466,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3467,4_A375_DGR1_1:3473,4_A375_DGR1_1:3474	17651,-453,17299,12283,-845,12803,-293	downstream, upstream, downstream, downstream, downstream, downstream, upstream	1	1	1	17.67	20	17.67	3	4_A375_DGR1_1	23	Gene DULLARD	HSH01916, CTDNEP1, DULLARD, NET36	CTD nuclear envelope phosphatase 1	NM_015343, NM_001147973	200033_at	NP_056158.2, NP_001137247.1
GeneID:39351	C17orf61	17	7,155,372	7,163,259	7,887	+	5	1_A375_pAL97_mrna1_lncRNA_R_1:3420,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3467,4_A375_DGR1_1:3474	540, 532, 160	n gene, n gene, n gene	1	1	1	16	20	23	1	4_A375_DGR1_1	23	Gene C17orf61	C17orf61, MSTP071, MSTO71, HSPC022, DERP6	chromosome 17 open reading frame 61	NM_206514, NM_202415, NM_015362, NM_206515, XCT1961582.1, XCT1961583.1, XCT32052.3	219260_s_at, 222295_at	NP_991559.1, NP_991560.1, NP_056177.3, NP_991561.1, EAW90232.1, EAW90233.1, EAW90231.1
GeneID:39352	CLDN7	17	7,163,222	7,168,512	5,290	-	3	2_A375_pAL7_mrna1_lncRNA_R_1:2420,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3467,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3474	10800,-10868,-10860	downstream, downstream, downstream	1	1	1	16	20	23	1	4_A375_DGR1_1	23	Gene CLDN7	claudin 7, Hs.84391, CLD42, CPETRL2, CPETRL2	claudin 7	NM_001184033, NM_001184035, NM_001307, XCT1961445.0, XCT2803309.0	202790_at	NP_001175951.1, NP_001175952.1, NP_001298.2, EAW90226.1, EAW90229.1
GeneID:39353	CLCN4	17	7,169,054	7,191,397	9,313	+	3	4_A375_DGR1_1:3475,4_A375_DGR1_1:3476,4_A375_DGR1_1:3477	-870, 6162, 13248	upstream, downstream, downstream	0	0	1	7.33	8.67	19	3	4_A375_DGR1_1	20	Gene SLC24A4	SLC24A, GLUT4	solute carrier family 2 (facilitated glucose transporter), member 4	NM_001042, XCT2892008.0, XCT32811.3	209603_at	NP_001033.1, EAW90227.1, EAW90228.1
GeneID:39354	LOC100507772	17	7,186,097	7,187,290	1,193	-	2	4_A375_DGR1_1:3475,4_A375_DGR1_1:3476	3006, 4828	downstream, upstream	0	0	1	6	9.5	19	2	4_A375_DGR1_1	20	Gene LOC100507772		hypothetical LOC100507772	XR_111983, XR_109390, XR_110539		NP_001178912.1, NP_001177852.1, NP_001298.2, EAW90226.1, EAW90229.1
GeneID:39355	YBX2	17	7,191,371	7,197,676	6,305	-	3	4_A375_DGR1_1:3475,4_A375_DGR1_1:3476,4_A375_DGR1_1:3477	13492,4986,-524	downstream, n gene, upstream	0	0	1	7.33	8.67	19	3	4_A375_DGR1_1	20	Gene YBX2	MGC43104, YBX2, CONTRIN, CSDA3, MSY2, CMRC	Y box binding protein 2	NM_015982, XCT1965355.1, XCT2803308.0, XCT2807260.0	219764_at	NP_057066.2, EAW90226.1, EAW90223.1, EAW90228.1
GeneID:39356	EIF5A	17	7,210,516	7,215,782	5,454	+	4	2_A375_pAL97_pAL7_mut_lncRNA_R_1:3466,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3469,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3476,4_A375_DGR1_1:3479	138, 7922, 7626, 6466	n gene, downstream, downstream, downstream	1	1	1	10.33	20.33	16.33	3	2_A375_pAL926_A_AR_1	26	Gene EIF5A	MGC29554, EIF-5A, eIF5A, MGC104253, EIF5A1, EIF5A	eukaryotic translation initiation factor 5A	NM_001142560, NM_001970, NM_001142561, NM_001142562, XCT2892120.0, XCT2892124.0, XCT2892125.0	201122_s_at, 201123_s_at, 201124_at	NP_001132033.1, NP_001961.1, NP_001132033.1, NP_001127234.1, EAW90222.1, EAW90221.1
GeneID:39357	GPS2	17	7,215,976	7,218,896	2,920	-	4	2_A375_pAL97_pAL7_mut_lncRNA_R_1:3466,4_A375_DGR1_1:3476,4_A375_DGR1_1:3479	6215, 416, 514, 138	downstream, n gene, n gene, upstream	1	1	1	10.33	20.33	16.33	3	4_A375_DGR1_1	26	Gene GPS2	MGC119397, MGC119398, MGC119399, AMF-1, GPS2, MGC104294	G protein pathway suppressor 2	NM_004489	209360_s_at	NP_004480.1
GeneID:39358	NEURL4	17	7,218,591	7,232,636	13,957	-	3	2_A375_pAL97_pAL7_mut_lncRNA_R_1:3466,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3469,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3470,4_A375_DGR1_1:3479	23190, 14396, 416, 14494, 13622	downstream, downstream, upstream, downstream, upstream	0	1	1	12.25	21.75	16.25	4	2_A375_pAL926_A_AR_1	26	Gene NEURL4	KIAA1787, FLJ38893, NEURL4	neuralized homolog 4 (Drosophila)	NM_001005495, NM_032442	226763_at	NP_001005495.1, NP_115816.2
GeneID:39359	LOC399870	17	7,233,771	7,235,482	1,711	+	1	2_A375_pAL97_pAL7_mut_lncRNA_R_1:3470	-718	upstream	0	1	0	16	26	16	1	2_A375_pAL926_A_AR_1	26	Gene LOC399760		protein phosphatase inhibitor 2-like	XM_001717760, XM_001717472, XM_001716435		XP_001717512.1, XP_001717524.1, XP_001716507.1
GeneID:39360	ACAP1	17	7,239,646	7,254,790	14,945	-	3	2_A375_pAL97_pAL7_mut_lncRNA_R_1:3421,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3470,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3471	13664, -8792, 10676	downstream, downstream, downstream	1	1	1	17.5	23.5	15.5	2	2_A375_pAL926_A_AR_1	26	Gene ACAP1	KIAA0090, ACAP1, CENTB1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	NM_014716, XCT2892117.0, XCT32059.3	203212_s_at, 203213_at, 242801_at	NP_055831.1, EAW90209.1, EAW90210.1
GeneID:39361	KCTD11	17	7,255,205	7,256,265	2,035	+	2	2_A375_pAL97_mrna1_lncRNA_R_1:2421,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3471	109, 216	n gene, n gene	1	1	0	17	25	15	1	2_A375_pAL925_A_AR_1	25	Gene KCTD11	MGC129564, REN/KCTD11, REN, KCTD11, C17orf39	potassium channel tetramerisation domain containing 11	NM_001032914, NM_170731	235357_at	NP_001028714.1, EAW90208.1
GeneID:39362	TMEM95	17	7,256,497	7,260,538	3,941	+	2	2_A375_pAL97_pAL7_mut_lncRNA_R_1:3421,2_A375_pAL97_pAL7_mut_lncRNA_R_1:3471	-3155, -3370	upstream, upstream	1	1	0	17	25	15	1	2_A375_pAL925_A_AR_1	25	Gene TMEM95	MGC129793, UNQ9390, TMEM95	transmembrane protein 95	NM_178154, XCT1965312.2, XCT2372732.0, XCT2372735.0	1560281_a_at	NP_827797.1, EAW90206.1, EAW90205.1, EAW90207.1
GeneID:39363	TNK1	17	7,264,395	7,291,092	26,727	+	2	4_A375_DGR1_1:3468,4_A375_DGR1_1:3469	5963, 13205	n gene, downstream	0	0	1	8	8	18.5	2	4_A375_DGR1_1	17	Gene TNK1	MGC45195, TNK1	tyrosine kinase, non-receptor, 1	NM_003985, XCT2892225.0, XCT32777.3	205783_s_at, 217149_at	NP_003978.2, EAW90203.1, EAW90204.1



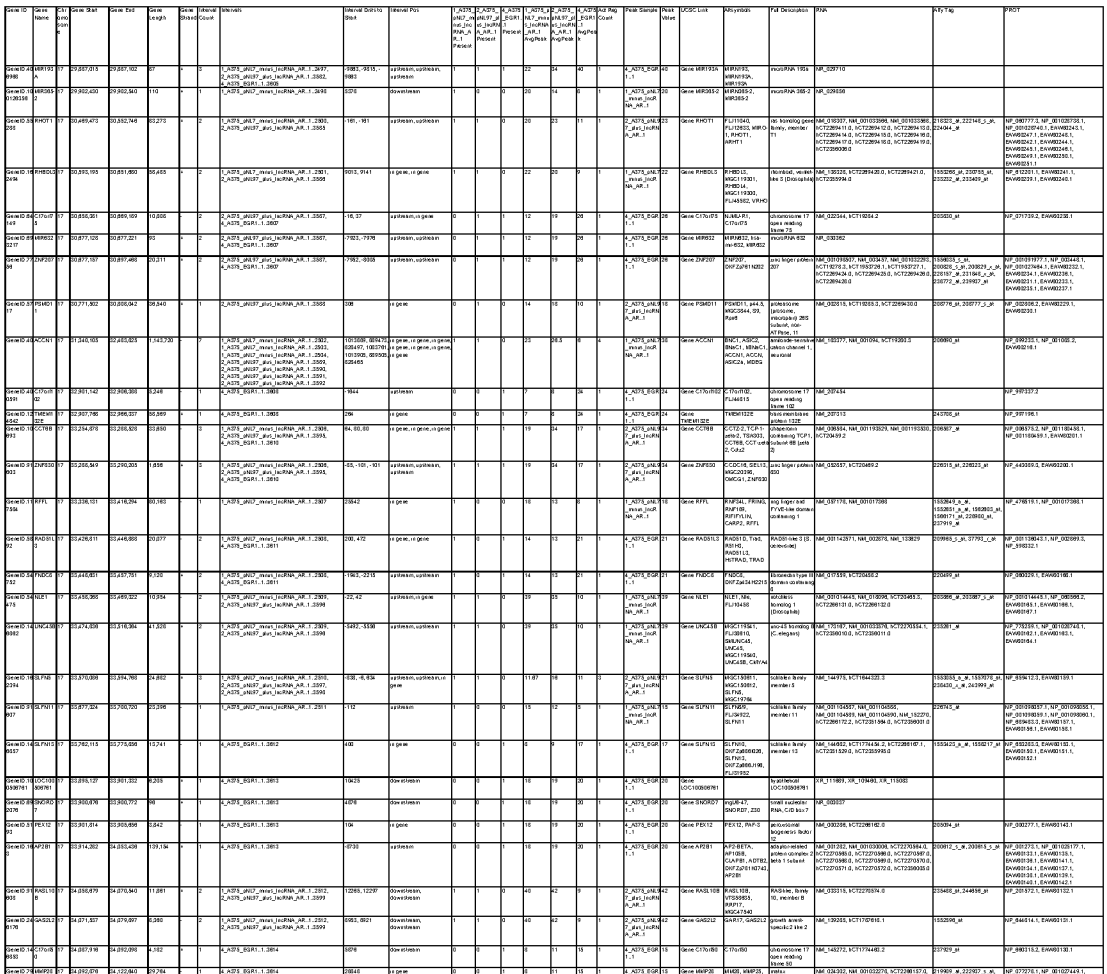
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_shN7_mycN7_shLncRNA_R_1 Percent	2_A375_shN7_shLncRNA_R_1 Percent	4_A375_SGR1_shLncRNA_R_1 Percent	1_A375_shN7_mycLncRNA_R_1 Avg Peak	2_A375_shN7_shLncRNA_R_1 Avg Peak	4_A375_SGR1_shLncRNA_R_1 Avg Peak	Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
GeneID:3778	PLSCR3	17	7,293,055	7,297,845	4,790	-	2	4_A375_SGR1_1.3480, 4_A375_SGR1_1.3481	5975, 379	Downstream, in gene	0	0	1	5	6	16.5	2	4_A375_SGR1_1.3	17	PLSCR3	PLSCR3		NM_020390	210620_at, 56797_at	NP_065093.2
GeneID:2356	C17orf81	17	7,356,294	7,357,418	1,124	+	1	4_A375_SGR1_1.3481	9980	Downstream	0	0	1	7	9	17	1	4_A375_SGR1_1.3	17	C17orf81, MGC40197	uncharacterized protein		NM_152766	227883_at	NP_689975.1
GeneID:3778	ZBTB4	17	7,382,893	7,397,396	24,503	+	5	1_A375_shN7_mycLncRNA_R_1.2422, 2_A375_shN7_shLncRNA_R_1.2472, 2_A375_shN7_shLncRNA_R_1.2473, 4_A375_SGR1_1.3482, 4_A375_SGR1_1.3483	338, 4416, 336, 4272, -112	up gene, in gene, up gene, up gene, upstream	1	1	1	105	98	23.5	2	1_A375_shN7_mycLncRNA_R_1.3	201	Gene ZBTB4	ZBTB4, ZNF903, bA80-D1.1, KIAA1356	zinc finger and BTB domain containing 4	NM_020899, NM_001128833, NCT02340116	223629_s_at, 222047_s_at	NP_065950.2, NP_001122305.1, ENSP00165.1
GeneID:8443	AMHC1	17	7,394,721	7,398,393	3,672	-	3	1_A375_shN7_mycLncRNA_R_1.2422, 2_A375_shN7_shLncRNA_R_1.2472, 2_A375_shN7_shLncRNA_R_1.2473, 4_A375_SGR1_1.3482, 4_A375_SGR1_1.3483	2301, -1589, 2301, -1423, 2969	Downstream, upstream, Downstream, upstream, Downstream	1	1	1	105	98	23.5	2	1_A375_shN7_mycLncRNA_R_1.3	201	Gene AMHC1L3	AMHC1L3, TMEM218	acyl-malonyl condensing enzyme 1-like 3	NM_001163814		NP_001093934.1
GeneID:5427	POLR2K	17	7,397,590	7,417,935	20,065	+	5	1_A375_shN7_mycLncRNA_R_1.2422, 2_A375_shN7_shLncRNA_R_1.2472, 2_A375_shN7_shLncRNA_R_1.2473, 4_A375_SGR1_1.3482, 4_A375_SGR1_1.3483	-516, -4698, -516, -4364, -176	upstream, upstream, upstream, upstream, upstream	1	1	1	105	98	23.5	2	1_A375_shN7_mycLncRNA_R_1.3	201	Gene POLR2A	POLR2, RPB1, RPB1A, POLR2A, RPO2, RpIL8, RPO12, RPB8-1, RPB220, bdf7561, MGC75455	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	NM_000937, NCT02891540, NCT02891571, NCT03209.3	200725_at, 217415_at, 217420_x_at	NP_000924.1, ENSP00181.1, ENSP00182.1, ENSP00183.1
GeneID:6742	TNFSF12-TNFSF13	17	7,452,376	7,461,297	8,932	+	1	4_A375_SGR1_1.3484	428	up gene	0	0	1	8	14	30	1	4_A375_SGR1_1.3	20	Gene TNFSF12	TWEAK, APO3L, DR3LG, MGC20989, MGC129981, TNFSF12	tumor necrosis factor (ligand) superfamily, member 12	NM_003809	209811_at	NP_003800.1
GeneID:4071	TNFSF12-TNFSF13	17	7,452,416	7,464,935	12,520	+	1	4_A375_SGR1_1.3484	356	up gene	0	0	1	8	14	30	1	4_A375_SGR1_1.3	20	Gene TNFSF12-TNFSF13	TWE-PRIL, TNFSF12-TNFSF13	TNFSF12-TNFSF13 readthrough	NM_172089	209499_x_at, 209500_x_at, 210314_x_at, 211495_x_at	NP_742058.1
GeneID:8741	TNFSF13	17	7,461,909	7,464,935	3,026	+	1	4_A375_SGR1_1.3484	-9839	upstream	0	0	1	8	14	30	1	4_A375_SGR1_1.3	20	Gene TNFSF13	CD256, UNQ383/PRO715, TNFSF13, TALL2, APRIL, ZTNF2, FLJ31090, bglap3, TRDL-1	tumor necrosis factor (ligand) superfamily, member 13	NM_172088, NM_003808, NM_172087	209629_at	NP_742055.1, NP_003799.1, NP_742084.1
GeneID:8935	SENP3	17	7,465,319	7,475,297	9,978	+	2	2_A375_shN7_plus_lncRNA_R_1.2474, 2_A375_shN7_plus_lncRNA_R_1.2475	13033, 17465	Downstream, Downstream	0	0	1	0	18.5	20	12	2	2_A375_shN7_plus_lncRNA_R_1.2	22	Gene SENP3	SENP3, MGC4850, MGC20659, MGC129981, MGC129982, SMT3IP3, DKFZp762A152	SUMO/sentrin/SMT3 specific peptidase 3	NM_015670, NCT01962168.1, NCT02891448.0, NCT07654.3	223371_at, 219113_s_at, 219114_at	NP_056453.2, ENSP00193.1, ENSP00177.1, ENSP00172.1
GeneID:1978	EIF4A1	17	7,476,037	7,482,224	6,187	+	4	2_A375_shN7_plus_lncRNA_R_1.2474, 2_A375_shN7_plus_lncRNA_R_1.2475, 2_A375_shN7_plus_lncRNA_R_1.2476, 4_A375_SGR1_1.3485	299, 6727, 1093, 10183	up gene, downstream, Downstream, Downstream, Downstream	0	1	1	14.25	16.5	15.5	4	2_A375_shN7_plus_lncRNA_R_1.2	22	Gene EIF4A1	EIF4A, EIF4A1, EIF-4A, DDX2A	eukaryotic translation initiation factor 4A, isoform 1	NM_001416, NCT02891480.0, NCT02891510, NCT02891538.0, NCT5834.1	201302_s_at, 211707_s_at, 214925_at	NP_001407.1, ENSP00187.1, ENSP00185.1, ENSP00186.1, ENSP00189.1
GeneID:8555	SNORA48	17	7,476,031	7,476,165	134	+	4	2_A375_shN7_plus_lncRNA_R_1.2474, 2_A375_shN7_plus_lncRNA_R_1.2475, 2_A375_shN7_plus_lncRNA_R_1.2476, 4_A375_SGR1_1.3485	-1879, 4793, 6077, 6209	upstream, downstream, Downstream, Downstream	0	1	1	14.25	16.5	15.5	4	2_A375_shN7_plus_lncRNA_R_1.2	22	Gene SNORA48	ACA48, SNORA48	small nucleolar RNA, H/ACA box 48	NR_002916		
GeneID:8555	SNORD10	17	7,480,129	7,480,276	147	+	4	2_A375_shN7_plus_lncRNA_R_1.2474, 2_A375_shN7_plus_lncRNA_R_1.2475, 2_A375_shN7_plus_lncRNA_R_1.2476, 4_A375_SGR1_1.3485	-3777, 2853, 6679, 6811	upstream, Downstream, Downstream, Downstream, Downstream	0	1	1	14.25	16.5	15.5	4	2_A375_shN7_plus_lncRNA_R_1.2	22	Gene SNORD10	SNORD10, mgUN77	small nucleolar RNA, C/D box 10	NR_002954		
GeneID:2661	SNORA73	17	7,481,273	7,481,409	136	+	4	2_A375_shN7_plus_lncRNA_R_1.2474, 2_A375_shN7_plus_lncRNA_R_1.2475, 2_A375_shN7_plus_lncRNA_R_1.2476, 4_A375_SGR1_1.3485	-4921, 1511, 5755, 4967	upstream, Downstream, Downstream, Downstream, Downstream	0	1	1	14.25	16.5	15.5	4	2_A375_shN7_plus_lncRNA_R_1.2	22	Gene SNORA67	U67, RNA67, SNORA67	small nucleolar RNA, H/ACA box 67	NR_002912		
GeneID:9636	C6orf60	17	7,482,033	7,483,429	2,824	+	4	2_A375_shN7_plus_lncRNA_R_1.2474, 2_A375_shN7_plus_lncRNA_R_1.2475, 2_A375_shN7_plus_lncRNA_R_1.2476, 4_A375_SGR1_1.3485	-4443, -21, 4203, 3435	upstream, upstream, Downstream, Downstream	0	1	1	14.25	16.5	15.5	4	2_A375_shN7_plus_lncRNA_R_1.2	22	Gene C6orf60	BCARD1, C6orf60, DKFZp686H09233, GPI10	C6orf60 molecule	NM_031231, NM_001040899, NCT19447455.0	230307_at	NP_001242.2, NP_001035145.1, ENSP00183.1
GeneID:9588	MPDU1	17	7,486,985	7,491,530	4,545	+	5	2_A375_shN7_plus_lncRNA_R_1.2474, 2_A375_shN7_plus_lncRNA_R_1.2475, 2_A375_shN7_plus_lncRNA_R_1.2476, 4_A375_SGR1_1.3485	-4161, 43, -725	upstream, up gene, upstream	0	1	1	14.33	17.33	16	3	2_A375_shN7_plus_lncRNA_R_1.2	22	Gene MPDU1	MPDU1, CDGIF, FLJ46156, PQLC5, Lec35, dg5B2, HBEBP28PA, SL15, P35S6	mannose-P-dolichol utilization defect 1	NM_004870, NR_024693, NCT19651051, NCT19621961, NCT02891512, NCT02891562, NCT02891580.0, NCT02266.3	1557569_at, 209205_at	NP_004861.2, ENSP00182.1, ENSP00183.1, ENSP00180.1, ENSP00183.1, ENSP00181.1
GeneID:8651	SOX15	17	7,491,496	7,493,486	1,990	-	3	2_A375_shN7_plus_lncRNA_R_1.2474, 2_A375_shN7_plus_lncRNA_R_1.2475, 2_A375_shN7_plus_lncRNA_R_1.2476, 4_A375_SGR1_1.3485	10704, 6400, 7360	Downstream, Downstream, Downstream, Downstream	0	1	1	14.33	17.33	16	3	2_A375_shN7_plus_lncRNA_R_1.2	22	Gene SOX15	SOX15, SOX20, SOX26, SOX27	SRY (sex determining region Y)-box 15	NM_006942, NCT02804318.0, NCT03267.2	208122_at, 217043_x_at	NP_006933.1, ENSP00186.1, ENSP00187.1
GeneID:3968	FXR2	17	7,494,346	7,516,218	23,867	-	2	2_A375_shN7_plus_lncRNA_R_1.2476, 4_A375_SGR1_1.3485	31207, 31975	Downstream, Downstream	0	1	1	13	17	19	2	2_A375_shN7_plus_lncRNA_R_1.2	22	Gene FXR2	FXR2, FXR2P, FMR1L2	fragile X mental retardation, autosomal homolog 2	NM_004860, NCT19983521.1, NCT02291.3	203272_at, 223350_at, 35289_at	NP_004851.2, ENSP00194.1, ENSP00193.1
GeneID:4857	ATP1B2	17	7,534,234	7,541,009	6,835	+	1	2_A375_shN7_plus_lncRNA_R_1.2477	-176	upstream	0	1	0	11	20	8	1	2_A375_shN7_plus_lncRNA_R_1.2	20	Gene ATP1B2	ATP1B2, AMOG	ATPase, Na+/K+ transporting, beta 2 polypeptide	NM_001678, NCT02891640.0, NCT02290.3	204211_at	NP_001669.3, ENSP00145.1, ENSP00147.1
GeneID:7717	TP53	17	7,571,720	7,590,868	19,149	-	2	2_A375_shN7_plus_lncRNA_R_1.2475, 2_A375_shN7_plus_lncRNA_R_1.2476	1135, 1039	up gene, in gene	1	1	0	16	17	12	1	2_A375_shN7_plus_lncRNA_R_1.2	17	Gene TP53	FLJ92943, LFS1, TP53, P53, TRP53, p53	tumor protein p53	NM_000546, NM_001126112, NM_001126113, NM_001126114, NM_001126115, NM_001126116, NM_001126117, NCT02834261.1, NCT02834311.0, NCT02437470.0, NCT02437660.0, NCT02437661.0, NCT03292.4	201746_at, 211300_s_at	NP_000537.3, NP_001119584.1, NP_001119585.1, NP_001119586.1, NP_001119587.1, NP_001119588.1, ENSP00140.1, ENSP00142.1, ENSP00143.1, ENSP00144.1, ENSP00145.1
GeneID:1810	LOC100289	17	7,585,376	7,589,822	1,044	-	2	2_A375_shN7_mycLncRNA_R_1.2423, 2_A375_shN7_plus_lncRNA_R_1.2479	-108, -302	upstream, upstream	1	1	0	16	17	12	1	2_A375_shN7_plus_lncRNA_R_1.2	17	Gene LOC100289809		hypothetical protein LOC100289809		XP_003118779.1	
GeneID:1156	WRAP53	17	7,589,309	7,606,620	17,311	+	4	1_A375_shN7_mycLncRNA_R_1.2423, 2_A375_shN7_mycLncRNA_R_1.2424, 2_A375_shN7_plus_lncRNA_R_1.2476, 4_A375_SGR1_1.3486	539, 18693, 453, 2801	up gene, downstream, up gene, downstream	1	1	1	13.67	15	13.67	3	1_A375_shN7_mycLncRNA_R_1.3	25	Gene WRAP53	TCAB1, WRAP53, WDR79, FLJ43555	WD repeat containing, antisense to TP53	NM_018081, NM_001143990, NM_001143991, NM_001142892, NCT02891653, NCT02891687.0, NCT03272710.0, NCT03305.2	220256_s_at, 44580_at	NP_060551.2, NP_001137462.1, NP_001137465.1, NP_001137464.1, ENSP00138.1, ENSP00139.1, ENSP00137.1, ENSP00139.1
GeneID:9181	EPHB3	17	7,606,520	7,614,690	8,170	+	4	1_A375_shN7_mycLncRNA_R_1.2424, 2_A375_shN7_mycLncRNA_R_1.2425, 2_A375_shN7_plus_lncRNA_R_1.2479, 4_A375_SGR1_1.3486	139, 12555, 12120, 6640	upstream, Downstream, Downstream, Downstream	1	1	1	20	23.67	13.33	3	2_A375_shN7_plus_lncRNA_R_1.2	43	Gene EPHB3	EPHB3, LERK3, EPLG6, EP3R	ephrin-B3	NM_001406, NCT19655221.1, NCT02891680.0, NCT02297.1	230031_at, 210853_x_at	NP_001397.1, ENSP00132.1, ENSP00134.1, ENSP00133.1
GeneID:1474	DNAH2	17	7,623,039	7,737,058	114,019	+	10	1_A375_shN7_mycLncRNA_R_1.2423, 1_A375_shN7_mycLncRNA_R_1.2424, 1_A375_shN7_mycLncRNA_R_1.2425, 1_A375_shN7_mycLncRNA_R_1.2426, 1_A375_shN7_mycLncRNA_R_1.2427, 1_A375_shN7_mycLncRNA_R_1.2479, 1_A375_shN7_mycLncRNA_R_1.2480, 1_A375_shN7_mycLncRNA_R_1.2481, 1_A375_shN7_mycLncRNA_R_1.2482, 4_A375_SGR1_1.3486, 4_A375_SGR1_1.3487, 4_A375_SGR1_1.3488	2431, 117297, 12780, 2286, 117217, 12780, 12461, 7879, 118417, 122003	Downstream, Downstream, Downstream, Downstream, Downstream, Downstream, Downstream, Downstream, Downstream, Downstream	1	1	1	22.5	24.5	10.5	6	2_A375_shN7_plus_lncRNA_R_1.2	52	Gene DNAH2	DNAH2, FLJ46573, DNAH2, DNHD3, KIAA1300	dynein, axonemal, heavy chain 2	NM_020877, NCT01655302.2, NCT02891711.0, NCT2940822.0	215940_at, 239499_at	NP_3689252, ENSP00131.1, ENSP00129.1, ENSP00130.1
GeneID:2310	KDM6B	17	7,743,235	7,798,116	54,882	+	13	1_A375_shN7_mycLncRNA_R_1.2426, 1_A375_shN7_mycLncRNA_R_1.2427, 1_A375_shN7_mycLncRNA_R_1.2428, 1_A375_shN7_mycLncRNA_R_1.2429, 1_A375_shN7_mycLncRNA_R_1.2430, 1_A375_shN7_mycLncRNA_R_1.2431, 1_A375_shN7_mycLncRNA_R_1.2432, 1_A375_shN7_mycLncRNA_R_1.2433, 1_A375_shN7_mycLncRNA_R_1.2434, 1_A375_shN7_mycLncRNA_R_1.2435, 4_A375_SGR1_1.3488, 4_A375_SGR1_1.3489, 4_A375_SGR1_1.3490, 4_A375_SGR1_1.3491	2899, 2573, 17161, 2979, 2913, 3165, 17215, 16825, 3779, 2105, 5359, 13465, 17277	up gene, up gene, Downstream, up gene, up gene, Downstream, Downstream, Downstream, up gene, up gene, Downstream, Downstream, Downstream	1	1	1	19.69	20.14	14.43	7	1_A375_shN7_mycLncRNA_R_1.3	52	Gene KDM6B	KDM6B, bA403A6, MLL5	lysine (K)-specific demethylase 6B	NM_0015559.24	1598899_at, 1598987_s_at, 213145_at, 41398_i_at, 41397_i_at	NP_0010739.1
GeneID:5562	TMEM66	17	7,795,384	7,799,417	4,033	+	8	1_A375_shN7_mycLncRNA_R_1.2426, 2_A375_shN7_plus_lncRNA_R_1.2453, 2_A375_shN7_plus_lncRNA_R_1.2454, 4_A375_SGR1_1.3490, 4_A375_SGR1_1.3491	2822, 3084, 5036, -6943, 336, 2126	Downstream, Downstream, Downstream, upstream, up gene, Downstream	1	1	1	15	15.33	16.33	3	2_A375_shN7_plus_lncRNA_R_1.2	23	Gene TMEM66	FLJ30323, MGC17744, TMEM66	transmembrane protein 66	NM_025411, NCT02891780.0, NCT03315.2	229452_at	NP_931958.1, ENSP00124.1, ENSP00125.1
GeneID:5443	LSM201	17	7,800,003	7,801,172	1,169	-	5	1_A375_shN7_mycLncRNA_R_1.2426, 1_A375_shN7_mycLncRNA_R_1.2427, 1_A375_shN7_mycLncRNA_R_1.2428, 4_A375_SGR1_1.3490, 4_A375_SGR1_1.3491	736, 734, -286, 2452, 660	up gene, in gene, Downstream, Downstream, up gene	1	1	1	14.3	17.3	15.5	2	2_A375_shN7_plus_lncRNA_R_1.2	23	Gene LSM201	MGC74657, PFAAP2, LSM20, MGC14139	LSM domain containing 1	NM_032356, NCT03311.2	224312_s_at, 223441_s_at	NP_115722.2, ENSP00123.1
GeneID:1357	CYB5D1	17	7,781,094	7,783,930	4,836	+	5	1_A375_shN7_mycLncRNA_R_1.2426, 2_A375_shN7_plus_lncRNA_R_1.2453, 2_A375_shN7_plus_lncRNA_R_1.2454, 4_A375_SGR1_1.3490, 4_A375_SGR1_1.3491	-642, -618, 376, 2364, -932	upstream, downstream, in gene, upstream, upstream	1	1	1	14.3	17.3	15.5	2	2_A375_shN7_plus_lncRNA_R_1.2	23	Gene CYB5D1	FLJ32499, CYB501	cytochrome b5 domain containing 1	NM_144637, NCT02494410, NCT02940442.0, NCT02972950.0, NCT03202.2	1552711_a_at, 226823_at	NP_653238.2, ENSP00121.1, ENSP00119.1, ENSP00120.1, ENSP00122.1
GeneID:1160	CHD3	17	7,795,125	7,818,075	27,932	+	3	1_A375_shN7_mycLncRNA_R_1.2427, 2_A375_shN7_plus_lncRNA_R_1.2453, 4_A375_SGR1_1.3492	1141, 901, 31621	up gene, in gene, Downstream	1	1	1	15.5	20	15.5	2	2_A375_shN7_plus_lncRNA_R_1.2	22	Gene CHD3	Mi-2a, CHD3, ZFH, Mi2-ALPHA	chromodomain helicase DNA binding protein 3	NM_001005271, NM_005852, NM_001005273, NCT02891448.0, NCT02891513.0, NCT03306.3	200936_at, 200937_s_at	NP_001005272.1, NP_005843.2, NP_001005273.1, ENSP00114.1, ENSP00115.1, ENSP00116.1
GeneID:8570	SCARA21	17	7,809,441	7,809,976	537	+	1	4_A375_SGR1_1.3492	10003	Downstream	0	0	1	16	16	30	1	4_A375_SGR1_1.3	20	Gene SCARA21	SCARA5, bA421K24.1	small Cajal body-specific RNA 21	NR_003000		
GeneID:2356	LOC2343	17	7,816,640	7,819,265	2,625	+	1	4_A375_SGR1_1.3492	-479	upstream	0	0	1	16	16	30	1	4_A375_SGR1_1.3	20	Gene LOC234023			NR_026349	235099_at	
GeneID:9181	KCNAB3	17	7,826,027	7,832,793	6,766	+	1	4_A375_SGR1_1.3492	13009	Downstream	0	0	1	16	16	30	1	4_A375_SGR1_1.3	20	Gene KCNAB3	KCNB3P, KCNA3.1.B, KCA3B, KV-BETA-3, KCAB3, MGC116895	potassium voltage-gated channel, shaker-related subfamily, beta member 3	NM_004732, NCT03316.2	221403_at	NP_004723.2, ENSP00112.1
GeneID:2242	ALOX12P2	17	7,870,934	7,891,031	19,097	-	2	4_A375_SGR1_1.3492	7981, 6237	up gene, in gene	0	1	1	13	15	12.5	2	4_A375_SGR1_1.3	15	Gene ALOX12B	12R-LOX, ALOX12B	arachidonate 12-lipoxygenase, 12R type	NM_001139, NCT01631271.1	207381_at	NP_001130.1, ENSP00098.1
GeneID:1148	MRM234	17	7,891,374	7,891,466	91	+	2	2_A375_shN7_plus_lncRNA_R_1.2478, 4_A375_SGR1_1.3492	-5014, -5090	upstream, upstream	0	1	1	13	15	12.5	2	4_A375_SGR1_1.3	15	Gene MRM234	MRM234	mrnaSR fch 4214	NR_038201		
GeneID:3964	ALOX8E3	17	7,999,216	8,022,234	23,018	+	9	1_A375_shN7_mycLncRNA_R_1.2430, 1_A375_shN7_mycLncRNA_R_1.2431, 1_A375_shN7_mycLncRNA_R_1.2432, 1_A375_shN7_mycLncRNA_R_1.2433, 1_A375_shN7_mycLncRNA_R_1.2434, 1_A375_shN7_mycLncRNA_R_1.2435, 4_A375_SGR1_1.3494, 4_A375_SGR1_1.3495, 4_A375_SGR1_1.3496, 4_A375_SGR1_1.3497, 4_A375_SGR1_1.3498	-938, -9894, -8956, -5716, 5939, -134, 1446, 4230, 6884	upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream, upstream	1	1	1	15	14.8	19	5	4_A375_SGR1_1.3	25	Gene ALOX8E3	MGC119885, MGC119886, ALOX8, ALOX8E3, MGC119884, ALOXE3	arachidonate hydroxylase 3	NM_021838, NM_001163990, NCT02489.2, NCT02833990.0	207768_at, 222383_s_at	NP_068441.2, NP_001156422.1, ENSP00163.1, ENSP00394.1
GeneID:8477	HES7	17	8,023,906	8,027,416	3,510	-	8	1_A375_shN7_mycLncRNA_R_1.2430, 1_A375_shN7_mycLncRNA_R_1.2431, 1_A375_shN7_mycLncRNA_R_1.2432, 1_A375_shN7_mycLncRNA_R_1.2433, 1_A375_shN7_mycLncRNA_R_1.2434, 1_A375_shN7_mycLncRNA_R_1.2435, 4_A375_SGR1_1.3494, 4_A375_SGR1_1.3495, 4_A375_SGR1_1.3496, 4_A375_SGR1_1.3497, 4_A375_SGR1_1.3498	4376, -1516, 3460, 1456, 13802, 5542, 5700, 948, -1675	downstream, upstream, in gene, in gene, Downstream, Downstream, Downstream, in gene, upstream	1	1	1	15	14.8	19	5	1_A375_shN7_mycLncRNA_R_1.3	23	Gene HES7	bHLHB37, HES7	hairy and enhancer of split 7 (Drosophila)	NM_032300, NM_001163997, NCT01155511.1	224348_at	NP_115999.2, NP_001138439.1, ENSP00092.1
GeneID:5511	PER1	17	8,043,790	8,053,793	11,983	-	4	1_A375_shN7_mycLncRNA_R_1.2432, 1_A375_shN7_plus_lncRNA_R_1.2455, 1_A375_shN7_plus_lncRNA_R_1.2456, 4_A375_SGR1_1.3500	13813, 13515, 12699, 11592	Downstream, Downstream, Downstream, in gene	1	1	1	17	11.3	17	2	1_A375_shN7_plus_lncRNA_R_1.3	26	Gene PER1	hPER, PER1, PAS1, PER, MGC99221	period homolog 1 (Drosophila)	NM_002616, NCT02349.3, NCT02833860.0, NCT02903900.0, NCT02903911.0	202861_at, 242032_at, 38623_at	NP_002607.2, ENSP00093.1, ENSP00099.1, ENSP00201.1
GeneID:5464	TMEM37	17	8,078,298	8,079,774	3,476	-	5	2_A375_shN7_mycLncRNA_R_1.2433, 2_A375_shN7_plus_lncRNA_R_1.2490, 2_A375_shN7_plus_lncRNA_R_1.2491, 4_A375_SGR1_1.3501, 4_A375_SGR1_1.3502	2884, 2890, -10630, -48, -10890	up gene, in gene, upstream, upstream, upstream	1	1	1	21	24	19.67	3	2_A375_shN7_plus_lncRNA_R_1.2	52	Gene TMEM107	PRO1369, TMEM107, MRVSR02, MGC10744	transmembrane protein 107	NM_032334, NM_183065, NCT22485.2, NCT02803374.0, NCT02872800.0	224489_at, 224498_s_at, 233480_at, 233890_x_at, 229824_s_at	NP_115720.2, NP_899058.1, ENSP00331.1, ENSP00334.1, ENSP00335.1
GeneID:7283	SNORD11	17	8,084,771	8,084,906	135	-	2	2_A375_shN7_plus_lncRNA_R_1.2433, 2_A375_shN7_plus_lncRNA_R_1.2492, 4_A375_SGR1_1.3501	-214, -115, -2056	upstream, upstream, upstream	1	1	1	16.5	22.5	14	2	2_A375_shN7_plus_lncRNA_R_1.2	52	Gene SNORD116	U8, SNORD116	small nucleolar RNA, C/D box 116	NR_003284		
GeneID:5462	C17orf59	17	8,091,851	8,093,364	1,513	-	6	1_A375_shN7_mycLncRNA_R_1.2434, 1_A375_shN7_mycLncRNA_R_1.2435, 1_A375_shN7_mycLncRNA_R_1.2491, 2_A375_shN7_plus_lncRNA_R_1.2492, 4_A375_SGR1_1.3502, 4_A375_SGR1_1.3503	3292, -38, 3420, 62, -1807, 3260	downstream, upstream, Downstream, upstream, downstream, downstream	1	1	1	19.67	25	16	3	2_A375_shN7_plus_lncRNA_R_1.2	52	Gene C17orf59	C17orf59, FLJ20212, FLJ30014	chromosome 17 open reading frame 59	NM_017622	219417_s_at, 223002_s_at	NP_060292.2
GeneID:9324	AURKB	17	8,103,049	8,113,893	9,834	-	1	2_A375_shN7_plus_lncRNA_R_1.2493	10842	Downstream	0	0	0	10	18	10	1	2_A375_shN7_plus_lncRNA_R_1.2	18	Gene AURKB	AIK2, ArcN-1b2, AurB, STK12, IPL1, AIM1, AIK2, STK5, AURKB, AIM1, ArcN-1v1	aurora kinase B	NM_004217, NCT19621341.1, NCT20458.3, NCT20533910, NCT20533941.0, NCT20727610.0, NCT20727720.0, NCT20727760.0	209464_at, 239219_at	NP_3962032, ENSP00074.1, ENSP00073.1, ENSP00077.1, ENSP00076.1, ENSP00078.1
GeneID:2356	C17orf49	17	8,123,948	8,127,391	3,443	-	7	1_A375_shN7_mycLncRNA_R_1.2436, 1_A375_shN7_mycLncRNA_R_1.2437, 1_A375_shN7_mycLncRNA_R_1.2494, 2_A375_shN7_plus_lncRNA_R_1.2495, 4_A375_SGR1_1.3504, 4_A375_SGR1_1.3505	2818, 1121, 2591, 1004, 3153, 1153, 2943	up gene, in gene, up gene, up gene, in gene, in gene, up gene, upstream	1	1	1	19.5	28	29.5	2	4_A375_SGR1_1.3	38	Gene C17orf49	FLJ39160, C17orf49, MGC104161	chromosome 17 open reading frame 44	NR_026951	230012_at	

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.80169	C17orf68	17	8,128,139	8,151,413	23,274	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2436, 1_A375_pNL7_minus_lncRNA_AR..1..2437, 2_A375_pNL97_plus_lncRNA_AR..1..3494, 2_A375_pNL97_plus_lncRNA_AR..1..3495, 4_A375_EGR1..1..3503, 4_A375_EGR1..1..3504, 4_A375_EGR1..1..3505	26570, 25173, 26613, 25141, 27205, 25205, 21109	downstream, downstream, downstream, downstream, downstream, downstream, in gene	1	1	1	19.5	26	29.5	2	4_A375_EGR1..1	36	Gene C17orf68	AAF132, MGC133331, CTC1, C17orf68, AAF-132, FLJ22170	CTS telomere maintenance complex component 1	NM_025099, hCT2263346.0, hCT2263351.0	219435_at, 240875_at	NP_079375.3, EAW90070.1, EAW90071.1
GeneID.399512	SLC25A35	17	8,191,082	8,198,170	7,088	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3496	5946	in gene	0	1	0	10	18	15	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SLC25A35	SLC25A35, FLJ40217, MGC120446, MGC120448	solute carrier family 25, member 35	NM_201520, hCT22461.2, hCT2357279.0	228836_at, 236084_at	NP_958928.1, EAW90082.1, EAW90083.1
GeneID.29098	RANGRF	17	8,191,969	8,193,409	1,440	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3496	255	in gene	0	1	0	10	18	15	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene RANGRF	RANGRF, DKFZp686F02139, MOG1, HSPC236, RANGNRF, MGC110973, HSPC165	RAN guanine nucleotide release factor	NM_001177801, NM_001177802, NM_016492, hCT1962136.1, hCT1962137.1, hCT22459.3	218526_s_at, 223554_s_at	NP_001171272.1, NP_001171273.1, NP_057576.2, EAW90084.1, EAW90085.1, EAW90086.1
GeneID.22899	ARHGEF15	17	8,213,558	8,225,834	12,276	+	1	4_A375_EGR1..1..3506	892	in gene	0	0	1	7	7	15	1	4_A375_EGR1..1	15	Gene ARHGEF15	ARHGEF15, FLJ13791, KIAA0915, E5, MGC44868, Ephexin5, Vsm-RhoGEF, ARGEF15	Rho guanine nucleotide exchange factor (GEF) 15	NM_173728, NM_025014, hCT2260337.0, hCT2260340.0	205507_at, 217348_x_at	NP_776089.2, NP_079290.1, EAW90080.1, EAW90081.1
GeneID.6154	RPL26	17	8,280,834	8,286,565	5,731	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2438, 2_A375_pNL97_plus_lncRNA_AR..1..3497, 4_A375_EGR1..1..3507, 4_A375_EGR1..1..3508	-59, -59, 101, -9487	upstream, upstream, in gene, upstream	1	1	1	81	89	19.5	2	2_A375_pNL97_plus_lncRNA_AR..1	171	Gene RPL26	L26, RPL26	ribosomal protein L26	NM_000987		NP_000978.1
GeneID.643904	RNF222	17	8,294,022	8,301,144	7,122	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2438, 2_A375_pNL97_plus_lncRNA_AR..1..3497, 4_A375_EGR1..1..3507, 4_A375_EGR1..1..3508	14520, 14520, 14680, 5112	downstream, downstream, downstream, in gene	1	1	1	81	89	19.5	2	2_A375_pNL97_plus_lncRNA_AR..1	171	Gene RNF222	RNF222		NM_001146684		NP_001140156.1
GeneID.146850	PIK3R6	17	8,706,055	8,770,994	64,939	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2439, 2_A375_pNL97_plus_lncRNA_AR..1..3498	8338, 8242	in gene, in gene	1	1	0	28	29	8	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene PIK3R6	PIK3R6, p87(PIKAP), FLJ34500, p84, p87PIKAP, DKFZp666P158, HsT41028, C17orf38	phosphoinositide-3-kinase, regulatory subunit 6	NM_001010855, hCT2260149.1, hCT2340631.0, hCT2340632.0, hCT2357310.0	1558770_a_at	NP_001010855.1, EAW90039.1, EAW90038.1, EAW90040.1, EAW90041.1
GeneID.23533	PIK3R5	17	8,782,233	8,869,024	86,791	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2440, 2_A375_pNL97_plus_lncRNA_AR..1..3499, 4_A375_EGR1..1..3509	49886, 49886, 77419	in gene, in gene, in gene	1	1	1	11	14	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PIK3R5	p101, P101-PI3K, FOAP-2, F730038I15Rik, PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_014308, NM_001142633, hCT19513.3, hCT2260143.0, hCT2260146.0	220566_at, 227645_at	NP_055123.2, NP_001136105.1, EAW90035.1, EAW90036.1, EAW90037.1
GeneID.9423	NTN1	17	8,924,859	9,147,317	222,458	+	3	4_A375_EGR1..1..3510, 4_A375_EGR1..1..3511, 4_A375_EGR1..1..3512	-587, 69317, 156773	upstream, in gene, in gene	0	0	1	4.67	6.67	17.33	3	4_A375_EGR1..1	20	Gene NTN1	NTN1, NTN1L	netrin 1	NM_004822, hCT1951329.1	208005_at	NP_004813.2, EAW90032.1
GeneID.9482	STX8	17	9,153,768	9,479,275	325,487	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2441, 2_A375_pNL97_plus_lncRNA_AR..1..3500	267, 123	in gene, in gene	1	1	0	18	15	7	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene STX8	CARB, STX8	syntaxin 8	NM_004853, NR_033656, hCT2259762.1, hCT2259763.0, hCT2349370.0, hCT2349371.0	1570357_at, 204690_at	NP_004844.1, EAW90029.1, EAW90028.1, EAW90030.1, EAW90031.1
GeneID.146845	WDR16	17	9,479,944	9,546,776	66,832	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2441, 2_A375_pNL97_plus_lncRNA_AR..1..3500	-938, -792	upstream, upstream	1	1	0	18	15	7	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene WDR16	WDRPUH, FLJ37528, WDR16	WD repeat domain 16	NM_001080556, NM_145054, hCT20368.2, hCT2259940.0, hCT2357293.0, hCT2357294.0	237755_s_at, 239916_at	NP_001074025.1, NP_659491.4, EAW90024.1, EAW90025.1, EAW90026.1, EAW90027.1
GeneID.124739	USP43	17	9,546,950	9,633,004	84,054	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2442	31336	in gene	1	0	0	16	20	11	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene USP43	USP43, FLJ30626	ubiquitin specific peptidase 43	NM_153210	237439_at	NP_694942.3
GeneID.8522	GAS7	17	9,813,926	10,101,868	287,942	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2443, 2_A375_pNL97_plus_lncRNA_AR..1..3501, 4_A375_EGR1..1..3513, 4_A375_EGR1..1..3514	221164, 83068, 261404, 812	in gene, in gene, in gene, in gene	1	1	1	12.75	10.75	15	4	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene GAS7	KIAA0394, MLL/GAS7, MGC1348, GAS7	growth arrest-specific 7	NM_003644, NM_201432, NM_201433, NM_001130831, hCT2259766.0, hCT2259767.0, hCT46316.3	202191_s_at, 202192_s_at, 207704_s_at, 210872_x_at, 211067_s_at	NP_003635.2, NP_958636.1, NP_001124303.1, NP_958639.1, EAW90011.1, EAW90013.1, EAW90012.1
GeneID.6341	SCO1	17	10,583,649	10,600,885	17,236	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3503	85	in gene	0	1	0	14	28	14	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene SCO1	SCOD1, SCO1	SCO cytochrome oxidase deficient homolog 1 (yeast)	NM_004589, hCT19412.3	223221_at	NP_004580.1, EAW89997.1
GeneID.56985	C17orf48	17	10,600,927	10,614,875	13,948	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3503	-127	upstream	0	1	0	14	28	14	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene C17orf48	C17orf48, NBLA03831, MDS006	chromosome 17 open reading frame 48	NM_020233, hCT22250.3, hCT2262194.0	220606_s_at, 223401_at	NP_064618.3, EAW89995.1, EAW89996.1
GeneID.644139	hCG_1776018	17	10,725,792	10,741,418	15,626	-	1	4_A375_EGR1..1..3515	-7062	upstream	0	0	1	6	9	14	1	4_A375_EGR1..1	14	Gene hCG_1776018	PIRT	phosphoinositide-interacting regulator of transient receptor potential channels	NM_001101387	232687_at	NP_001094857.1
GeneID.388336	SHISA6	17	11,144,740	11,467,380	322,640	+	1	4_A375_EGR1..1..3517	317820	in gene	0	0	1	4	5	13	1	4_A375_EGR1..1	13	Gene SHISA6	FLJ45455, SHISA6, FLJ37030, FLJ37733	shisa homolog 6 (Xenopus laevis)	NM_001173461, NM_001173462, NM_207386		NP_001166932.1, NP_001166933.1, NP_997269.2
GeneID.1770	DNAH9	17	11,501,748	11,873,065	371,317	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3504	255660	in gene	0	1	0	15	19	8	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene DNAH9	DNEL1, DNAH17L, HL-20, Dnahc9, DYH9, DNAH9, KIAA0357, HL20	dynein, axonemal, heavy chain 9	NM_001372, NM_004662, hCT1963561.1, hCT1963562.1, hCT1963563.1, hCT2259850.0, hCT2259856.0, hCT2259858.0	207959_s_at, 210345_s_at, 240857_at	NP_001363.2, NP_004653.2, EAW89978.1, EAW89979.1, EAW89981.1, EAW89982.1, EAW89980.1, EAW89983.1
GeneID.7566	ZNF18	17	11,880,762	11,900,689	19,927	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2445, 2_A375_pNL97_plus_lncRNA_AR..1..3505	81, 177	in gene, in gene	1	1	0	16	17	12	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ZNF18	KOX11, Zfp535, ZNF18, HDSG1, ZKSCAN6, ZNF535	zinc finger protein 18	NM_144680, hCT33087.2	226787_at	NP_653281.2, EAW89977.1
GeneID.9912	RICH2	17	12,692,829	12,894,960	202,131	+	1	4_A375_EGR1..1..3516	403	in gene	0	0	1	12	9	19	1	4_A375_EGR1..1	19	Gene RICH2	RICH2, KIAA0672, ARHGAP44, NPC-A-10	Rho GTPase activating protein 44	NM_014859, hCT20899.3, hCT2259861.0, hCT2259863.0, hCT2259864.0, hCT2357320.0	205414_s_at, 215232_at	NP_055674.4, EAW89967.1, EAW89965.1, EAW89966.1, EAW89968.1, EAW89969.1
GeneID.60528	ELAC2	17	12,894,929	12,921,381	26,452	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2446, 2_A375_pNL97_plus_lncRNA_AR..1..3506	389, 261	in gene, in gene	1	1	0	19	22	13	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ELAC2	ELAC2, FLJ36693, HPC2, FLJ10530, ELC2, FLJ42848	elaC homolog 2 (E. coli)	NM_018127, NM_001165962, NM_173717, hCT20901.3, hCT2357324.0, hCT2357325.0, hCT2357326.0	201766_at, 201767_s_at	NP_060597.4, NP_001159434.1, NP_776065.1, EAW89961.1, EAW89962.1, EAW89963.1, EAW89964.1
GeneID.9955	HS3ST3A1	17	13,399,006	13,505,244	106,238	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3507, 2_A375_pNL97_plus_lncRNA_AR..1..3508, 4_A375_EGR1..1..3519	40060, 1276, 524	in gene, in gene, in gene	0	1	1	12.33	16.67	12	3	4_A375_EGR1..1	23	Gene HS3ST3A1	HS3ST3A1, 3OST3A1, 30ST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	NM_006042, hCT1951326.1	219985_at	NP_006033.1, EAW89959.1
GeneID.100506989	LOC100506989	17	13,932,609	13,972,775	40,166	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3509, 4_A375_EGR1..1..3520	-57, -121	upstream, upstream	0	1	1	17	19	25	1	4_A375_EGR1..1	25	Gene LOC100506989		hypothetical LOC100506989	XR_109366, XR_115063		
GeneID.1352	COX10	17	13,972,719	14,111,996	139,277	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3509, 4_A375_EGR1..1..3520	113, 177	in gene, in gene	0	1	1	17	19	25	1	4_A375_EGR1..1	25	Gene COX10	COX10		NM_001303, hCT2259565.1, hCT2259566.0	203858_s_at	NP_001294.2, EAW89957.1, EAW89958.1
GeneID.5376	PMP22	17	15,133,096	15,168,644	35,548	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3511, 4_A375_EGR1..1..3521	2020, 2420	in gene, in gene	0	1	1	15	16	20	1	4_A375_EGR1..1	20	Gene PMP22	CMT1A, CMT1E, HNPP, MGC20769, Sp110, DSS, PMP22, GAS-3, HMSNIA	peripheral myelin protein 22	NM_000304, NM_153321, NM_153322, hCT19376.2, hCT1955001.1, hCT2357291.0, hCT2357292.0	210139_s_at	NP_000295.1, NP_696996.1, NP_696997.1, EAW89946.1, EAW89947.1, EAW89948.1, EAW89949.1
GeneID.284040	CDRT4	17	15,339,338	15,370,925	31,587	-	1	4_A375_EGR1..1..3522	37405	downstream	0	0	1	4	4	16	1	4_A375_EGR1..1	16	Gene CDRT4	NBLA10383, FLJ36674, CDRT4, MGC33988	CMT1A duplicated region transcript 4	NM_173622	228482_at, 244698_at	NP_775893.2
GeneID.57335	ZNF286A	17	15,602,891	15,624,101	21,210	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2449	-27	upstream	1	0	0	13	12	10	1	1_A375_pNL7_minus_lncRNA_AR..1	13	Gene ZNF286A	MGC149827, MGC156161, ZNF286A, KIAA1874, ZNF286	zinc finger protein 286A	NM_020652, NM_001130842	1557684_at, 220250_at, 227077_at, 239898_x_at	NP_065703.1, NP_001124314.1
GeneID.125150	ZSWIM7	17	15,879,874	15,903,006	23,132	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3514	30	in gene	0	1	0	21	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ZSWIM7	SWS1, ZSWIM7	zinc finger, SWIM-type containing 7	NM_001042698, NM_001042697	228719_at, 229119_s_at	NP_001036163.1, NP_001036162.1
GeneID.54902	TTC19	17	15,902,782	15,932,096	29,314	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3514	194	in gene	0	1	0	21	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene TTC19	MGC19520, 2010204O13Rik, FLJ20343, MGC138312, TTC19	tetratricopeptide repeat domain 19	NM_017775, hCT20098.3, hCT2281443.0	217964_at	NP_060245.2, EAX04490.1, EAX04491.1
GeneID.9611	NCOR1	17	15,933,408	16,118,874	185,466	-	1	4_A375_EGR1..1..3523	-654	upstream	0	0	1	8	8	14	1	4_A375_EGR1..1	14	Gene NCOR1	MGC104216, hCIT529I10, KIAA1047, N-CoR, NCOR1, hN-CoR, TRAC1	nuclear receptor co-repressor 1	NM_001190438, NM_001190440, NM_006311, hCT2282060.0, hCT2282061.0, hCT2282062.0, hCT2282063.0, hCT2358665.0	200854_at, 200857_s_at, 234313_at	NP_001177367.1, NP_001177369.1, NP_006302.2, EAX04492.1, EAX04495.1, EAX04496.1, EAX04493.1, EAX04494.1
GeneID.9487	PIGL	17	16,120,509	16,229,573	109,064	+	1	4_A375_EGR1..1..3523	-781	upstream	0	0	1	8	8	14	1	4_A375_EGR1..1	14	Gene PIGL	PIGL		NM_004278, hCT1971006.1, hCT2358668.0	205873_at, 232282_at	NP_004269.1, EAX04498.1, EAX04497.1
GeneID.7314	UBB	17	16,284,367	16,286,054	1,687	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3515, 4_A375_EGR1..1..3524	273, -79	in gene, upstream	0	1	1	12	16	14	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene UBB	RPS27A, UBC, UBB, MGC8385, FLJ25987, UBA52	ubiquitin B	NM_018955, hCT2281446.0, hCT2281447.0, hCT2281448.0, hCT2281449.0, hCT2281450.0, hCT2281451.0	200633_at	NP_061828.1, EAX04503.1, EAX04501.1, EAX04504.1, EAX04505.1, EAX04506.1, EAX04502.1
GeneID.51393	TRPV2	17	16,318,856	16,340,317	21,461	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3516, 4_A375_EGR1..1..3525	23384, 23608	downstream, downstream	0	1	1	14	19	21	1	4_A375_EGR1..1	21	Gene TRPV2	TRPV2, VRL1, VRL-1, MGC12549, VRL	transient receptor potential cation channel, subfamily V, member 2	NM_016113, hCT1812517.1, hCT1955974.1, hCT2358887.0	219282_s_at, 222855_s_at	NP_057197.2, EAX04508.1, EAX04507.1, EAX04509.1
GeneID.125144	NCRNA00188	17	16,342,301	16,373,982	31,681	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3516, 4_A375_EGR1..1..3525	-61, 163	upstream, in gene	0	1	1	14	19	21	1	4_A375_EGR1..1	21	Gene NCRNA00188	NCRNA00188, MGC40157, TSAP19, FLJ25777, C17orf45	non-protein coding RNA 188	NR_027158, NR_027159, NR_027160, NR_027161, NR_027162, NR_027163, NR_027164, NR_027165, NR_027166, NR_027167, NR_027168, NR_027169, NR_027170, NR_027171, NR_027172, NR_027173, NR_027174, NR_027175, NR_027176, NR_027177, NR_027178, NR_027179, NR_027667, hC	225085_x_at	EAX04511.1, EAX04510.1, EAX04512.1, EAX04513.1, EAX04514.1, EAX04515.1
GeneID.692087	SNORD49B	17	16,342,823	16,342,870	47	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3516, 4_A375_EGR1..1..3525	-583, -359	upstream, upstream	0	1	1	14	19	21	1	4_A375_EGR1..1	21	Gene SNORD49B	U49B, SNORD49B	small nucleolar RNA, C/D box 49B	NR_003043		
GeneID.26800	SNORD49A	17	16,343,350	16,343,420	70	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3516, 4_A375_EGR1..1..3525	-1110, -886	upstream, upstream	0	1	1	14	19	21	1	4_A375_EGR1..1	21	Gene SNORD49A	U49A, RNU49, SNORD49A, U49	small nucleolar RNA, C/D box 49A	NR_002744		
GeneID.692106	SNORD65	17	16,344,540	16,344,612	72	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3516, 4_A375_EGR1..1..3525	-2300, -2076	upstream, upstream	0	1	1	14	19	21	1	4_A375_EGR1..1	21	Gene SNORD65	HBII-135, SNORD65	small nucleolar RNA, C/D box 65	NR_003054		
GeneID.388341	C17orf76	17	16,345,328	16,395,480	50,152	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3516, 4_A375_EGR1..1..3525	53240, 53016	downstream, downstream	0	1	1	14	19	21	1	4_A375_EGR1..1	21	Gene C17orf76	C17orf76, FLJ35696	chromosome 17 open reading frame 76	NM_207387, NM_001113567, hCT20099.2, hCT2358686.0	229889_at	NP_997270.2, NP_001107039.1, EAX04516.1, EAX04517.1
GeneID.57336	ZNF287	17	16,453,631	16,472,520	18,889	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3517, 4_A375_EGR1..1..3526	232, 392	in gene, in gene	0	1	1	15	20	15	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ZNF287	MGC126536, MGC141923, ZKSCAN13, ZNF287	zinc finger protein 287	NM_020653, hCT1770372.1	216453_at, 216710_x_at, 220055_at	NP_065704.2, EAX04518.1
GeneID.57547	ZNF624	17	16,524,048	16,557,167	33,119	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3518, 4_A375_EGR1..1..3526	79, -17	in gene, upstream	0	1	1	19	18	20	1	4_A375_EGR1..1	20	Gene ZNF624	MGC119605, MGC119603, KIAA1349, MGC119602, ZNF624	zinc finger protein 624	NM_020787, hCT2282069.0	232272_at	NP_065838.2, EAX04519.1
GeneID.96597	TBC1D27	17	16,761,220	16,835,818	74,598	-	1	4_A375_EGR1..1..3529	-2102	upstream	0	0	1	6	9	13	1	4_A375_EGR1..1	13	Gene TBC1D27	TBC1D27	TBC1 domain family, member 27	XM_002345003, XM_002343461, XM_002347724	233483_at	XP_002345044.1, XP_002343522.1, XP_002347765.2
GeneID.23495	TNFRSF13B	17	16,842,398	16,875,402	33,004	-	1	4_A375_EGR1..1..3529	37462	downstream	0	0	1	6	9	13	1	4_A375_EGR1..1	13	Gene TNFRSF13B	CD267, CVID2, FLJ39942, MGC133214, CVID, TNFRSF14B, TACI, MGC39952, TNFRSF13B	tumor necrosis factor receptor superfamily, member 13B	NM_012452, hCT19445.3, hCT2352951.0	207641_at	NP_036584.1, EAW55728.1, EAW55729.1
GeneID.23164	MPRIP	17	16,946,107	17,088,874	142,767	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3519	533	in gene	0	1	0	10	14	5	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene MPRIP	p116Rip, MRIP, KIAA0864, RIP3, RHOIP3, M-RIP, MPRIP	myosin phosphatase Rho interacting protein	NM_201274, NM_015134, hCT2257592.0, hCT2257593.0, hCT2257594.0, hCT2257595.0	212197_x_at, 214771_x_at, 233278_at, 233414_at, 238328_at, 238329_at, 238330_s_at	NP_958431.2, NP_055949.2, EAW55721.1, EAW55722.1, EAW55723.1, EAW55724.1
GeneID.201164	PLD6	17	17,104,309	17,109,646	5,337	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3520	-178	upstream	0	1	0	17	24	15	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PLD6	PLD6		NM_178836, hCT2347534.0	227037_at, 244430_at	NP_849158.2, EAW55718.1
GeneID.201163	FLCN	17	17,115,526	17,140,502	24,976	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2450, 2_A375_pNL97_plus_lncRNA_AR..1..3520, 2_A375_pNL97_plus_lncRNA_AR..1..3521	-74, 30878, -106	upstream, downstream, upstream	1	1	0	47.5	55	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	66	Gene FLCN	FLJ45004, FLCL, MGC17998, FLCN, DKFZp547A118, MGC23445, BHD, FLJ99377	folliculin	NM_144997, NM_144606, hCT1814090.4, hCT1958009.2	1552864_at, 215645_at, 235250_at, 243082_at	NP_659434.2, NP_653207.1, EAW55715.1, EAW55716.1

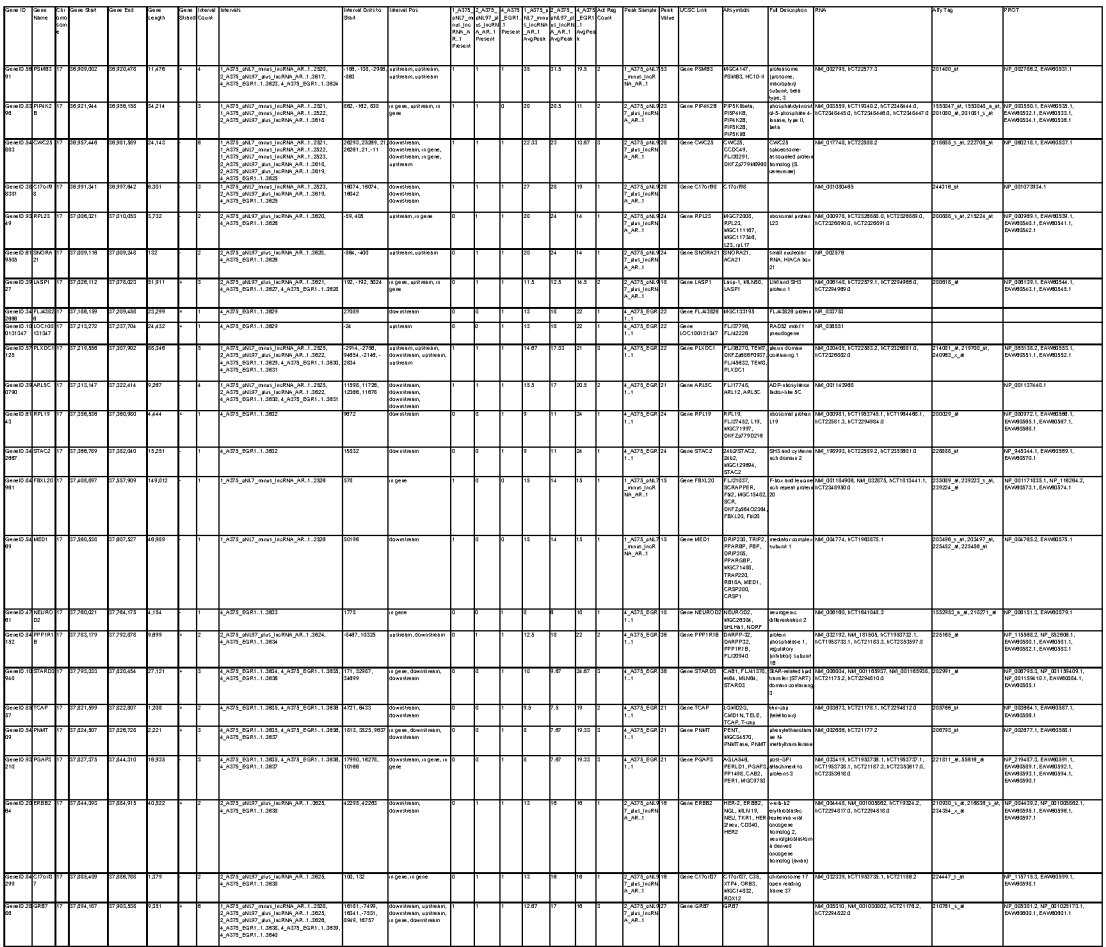


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_2_A375_4_EGFR_1_NLF_mrna_incRNA_RR_1_Percent	2_A375_2_A375_2_A375_4_EGFR_1_NLF_mrna_incRNA_RR_1_Percent	3_A375_2_A375_2_A375_4_EGFR_1_NLF_mrna_incRNA_RR_1_Avg Peak	4_A375_2_A375_2_A375_4_EGFR_1_NLF_mrna_incRNA_RR_1_Avg Peak	Ad Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:8533	COPS3	17	17,150,109	17,154,991	4882	-	2	1_A375_uNU7_mrust_lncRNA_RR_1:2450, 2_A375_uNU37_plus_lncRNA_RR_1:3321	44813, 43993	downstream, downstream		1	1	0	76	66	8	1	2_A375_uNU7_plus_lncRNA_RR_1	968	Gene COPS3	COPS3, COPS3, BGN3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	NM_003653, XCT1190019.1, XCT1190020.2, XCT226162.2	202076_at	NP_003644.2, EAW58712.1, EAW58711.1, EAW58712.1
GeneID:5534	MED9	17	17,350,930	17,356,834	16,254	+	3	1_A375_uNU7_mrust_lncRNA_RR_1:2451, 2_A375_uNU37_plus_lncRNA_RR_1:3322, 4_A375_RGR1_1:3331	118, 118, 15668	yr gene, rs gene, downstream		1	1	1	10	13	17	2	1_A375_uNU7_mrust_lncRNA_RR_1	919	Gene MED9	MGC132354, MED9, MED23, FLJ10193	mediator complex subunit 9	NM_015019, XCT1561268.2, XCT1966033.1	218572_at	NP_055834.1, EAW53706.1, EAW53707.1
GeneID:5187	RASD1	17	17,397,761	17,399,707	1,956	-	1	4_A375_RGR1_1:3331	938	up gene		0	0	1	7	8	19	1	4_A375_RGR1_1.1	19	Gene RASD1	DEXRAS1, RASD1, MGC26290, dexS1	RAS, dexamethasone-induced 1	NM_016084, XCT2281612	223487_at	NP_057168.1, EAW53709.1
GeneID:1869	PEMT	17	17,455,677	17,494,994	66,117	-	5	1_A375_uNU7_mrust_lncRNA_RR_1:2452, 2_A375_uNU37_plus_lncRNA_RR_1:3323, 3_A375_RGR1_1:3330, 4_A375_RGR1_1:3332, 5_A375_RGR1_1:3333	-35, -110, 90228, 62594, 146	upstream, upstream, downstream, rs gene, rs gene		1	1	1	17	17.33	18	3	1_A375_uNU37_mrust_lncRNA_RR_1	527	Gene PEMT	PEMT, MGC24451, PEMT2, PNMT, PEMPT, PEMPT	phosphatidylethanolamine N-methyltransferase	NM_148172, NM_148173, NM_007169, XCT1995021.1, XCT2262.2, XCT2352949.0	207621_s_at	NP_694477.1, NP_982478.1, NP_009000.2, EAW58700.1, EAW58701.1, EAW58702.1
GeneID:1074	RAI1	17	17,564,767	17,714,767	129,992	+	6	2_A375_uNU37_plus_lncRNA_RR_1:3324, 4_A375_RGR1_1:3334, 4_A375_RGR1_1:3335, 4_A375_RGR1_1:3337, 4_A375_RGR1_1:3338	13277, 30141, 116993, 114653, 13161, 13264	up gene, rs gene, rs gene, up gene, downstream, downstream	0	1	1	6.83	11.67	16.17	6	2_A375_uNU37_plus_lncRNA_RR_1	616	Gene RAI1	KIAA1820, RAI1, SMS, MGC11034, SNF2alpha1H39, SMCR	retinoic acid induced 1	NM_030665, XCT1993028.2, XCT2261247.0, XCT2261252.0, XCT2261255.0, XCT23622.4	1553552_a_at, 214920_at, 228145_at	NP_109593.3, EAW58692.1, EAW58693.1, EAW58694.1, EAW58695.1, EAW58696.1
GeneID:6721	SREBF1	17	17,714,993	17,740,325	25,882	-	4	1_A375_uNU7_mrust_lncRNA_RR_1:2453, 2_A375_RGR1_1:3337, 4_A375_RGR1_1:3339, 5_A375_RGR1_1:3339	261, 23357, 23997, 369	up gene, rs gene, rs gene, up gene	1	0	1	9.67	12	17.67	3	4_A375_EGFR_1.1	16	Gene SREBF1	bHLH61, SREBF1, SREBP1, SREBP1c, sterol regulatory element binding transcription factor 1	NM_001005291, NM_004176, XCT1519966.1, XCT1519024.1, XCT2621.2, XCT2323930.0	1539873_at, 202308_at	NP_001005291.1, NP_004167.3, EAW58688.1, EAW58689.1, EAW58690.1, EAW58691.1
GeneID:8991	MRS2B	17	17,717,150	17,717,243	93	-	2	4_A375_RGR1_1:3337, 4_A375_RGR1_1:3338	477, 463	downstream, upstream	0	0	1	7	10	17.5	2	4_A375_EGFR_1.1	16	Gene MRS2B	Mrs-mm-2Bs, MRS2B, MRS2B	mrs2/MRS 2Bs	NR_033361		
GeneID:1427	TOM1L2	17	17,746,822	17,875,764	128,942	+	4	1_A375_uNU7_mrust_lncRNA_RR_1:2453, 2_A375_uNU37_mrust_lncRNA_RR_1:3434, 3_A375_uNU37_plus_lncRNA_RR_1:3323, 4_A375_RGR1_1:3339	138703, -288, 232, 128648	downstream, upstream, upstream, downstream	1	1	1	21.5	19.5	15	2	1_A375_uNU7_mrust_lncRNA_RR_1	328	Gene TOM1L2	TOM1L2, FLJ21911, FLJ32746	target of myb1 like 2 (chicken)	NM_001032998, NM_001033031, XCT1819870.2, XCT2629.4, XCT2352998.0, XCT2352937.0	214940_at, 226190_at, 227182_at	NP_001027667.1, NP_001029723.1, EAW58934.1, EAW58935.1, EAW58936.1, EAW58937.1
GeneID:1552	SMCR7	17	17,876,127	17,920,303	44,076	+	4	1_A375_uNU7_mrust_lncRNA_RR_1:2454, 2_A375_uNU37_mrust_lncRNA_RR_1:3435, 3_A375_uNU37_plus_lncRNA_RR_1:3323, 4_A375_RGR1_1:3339	-83, 53693, -111, 53801	upstream, downstream, upstream, downstream	1	1	0	26.5	23.5	10.5	2	1_A375_uNU7_mrust_lncRNA_RR_1	328	Gene LRRC45	DKFZp686M01120, LRRC45	leucine rich repeat containing 45	NM_001130892, NM_001294, NM_001130891, XCT1519024.1, XCT1960122.2, XCT2352929.0	1554564_at, 208140_s_at	NP_001123812.1, NP_112264.3, NP_001123813.1, NP_001122564.1, EAW58911.1, EAW58913.1, EAW58912.1
GeneID:8147	ATPAF2	17	17,921,224	17,942,480	21,348	-	3	1_A375_uNU7_mrust_lncRNA_RR_1:2455, 2_A375_uNU37_mrust_lncRNA_RR_1:3436, 3_A375_uNU37_plus_lncRNA_RR_1:3437, 4_A375_RGR1_1:3339, 5_A375_RGR1_1:3339	13668, 5552, -99, 12732, -22	up gene, rs gene, upstream, rs gene, upstream	1	1	0	23	21.67	7	3	2_A375_uNU37_plus_lncRNA_RR_1	926	Gene ATPAF2	ATP12p, LP5663, ATPAF2, MGC29739, ATP12	ATP synthase mitochondrial F1 complex assembly factor 2	NM_145991, XCT1519039.1, XCT1519038.1, XCT2352932.0, XCT2352933.0, XCT23999.3	213057_at, 214330_at	NP_665725.1, EAW58977.1, EAW58978.1, EAW58979.1, EAW58980.1
GeneID:7918	C17orf59	17	17,942,811	17,971,716	29,107	+	3	1_A375_uNU7_mrust_lncRNA_RR_1:2456, 2_A375_uNU37_mrust_lncRNA_RR_1:3437, 3_A375_uNU37_plus_lncRNA_RR_1:3327	-9863, -35, -99	upstream, upstream, upstream	1	1	0	22	16.5	8	2	1_A375_uNU7_mrust_lncRNA_RR_1	522	Gene C17orf59	MGC3046, C17orf59	chromosome 17 open reading frame 59	NM_024052, XCT1970929.1, XCT2261292.0	220650_at, 229452_at, 241469_at	NP_076957.3, EAW58674.1, EAW58673.1
GeneID:1819	DRG2	17	17,991,393	18,011,392	20,000	+	2	1_A375_uNU37_plus_lncRNA_RR_1:2455, 2_A375_uNU37_plus_lncRNA_RR_1:3325	-99, -31	upstream, upstream	1	1	0	16	26	15	1	2_A375_uNU37_plus_lncRNA_RR_1	926	Gene DRG2	DRG2		NM_001386, XCT2261301.0, XCT2352954.0, XCT2352955.0	200397_s_at, 200398_s_at	NP_001376.1, EAW58699.1, EAW58700.1, EAW58701.1
GeneID:5311	MYO1B	17	18,012,030	18,083,116	71,086	+	5	1_A375_uNU7_mrust_lncRNA_RR_1:2459, 2_A375_uNU37_plus_lncRNA_RR_1:3329, 4_A375_RGR1_1:3340	74956, 74124, 74269	downstream, downstream, downstream	1	1	1	20	19	22	1	4_A375_EGFR_1.1	22	Gene MYO1BA	DKFZp686N0619, MYO1B, FLJ17274, FLJ18311, DFNB83, MYO1BA	myosin IXA	NM_012339, XCT1519997.1, XCT2261008.0, XCT2611299.0, XCT2611311.0, XCT2352960.0	220282_at	NP_036471.2, EAW58982.1, EAW58983.1, EAW58984.1, EAW58985.1, EAW58986.1, EAW58987.1
GeneID:3430	ALKBH8	17	18,056,997	18,113,366	56,401	+	3	1_A375_uNU7_mrust_lncRNA_RR_1:2459, 2_A375_uNU37_plus_lncRNA_RR_1:3329, 4_A375_RGR1_1:3340	141, -723, -497	up gene, upstream, upstream	1	1	1	20	19	22	1	4_A375_EGFR_1.1	22	Gene ALKBH8	CPOX01, FLJ33335, ATS-1, CPOX/D, ALKBH8	alkB, alkylation repair homolog 8 (E. coli)	NM_017758, XCT2261316.0, XCT2352963.0	1553101_a_at, 220524_s_at, 224302_s_at	NP_060228.3, EAW58981.1, EAW58982.1
GeneID:2661	LGL1	17	18,126,508	18,145,169	19,293	+	2	1_A375_RGR1_1:3341, 4_A375_RGR1_1:3342	6982, 21720	up gene, downstream	0	0	1	8	7.5	19	2	4_A375_EGFR_1.1	20	Gene LGL1	HUGL, HUGL1, LLGL1, HUGL-1, LLGL, DLG14	lethal giant larvae homolog 1 (Drosophila)	NM_004140, XCT1519039.1, XCT2261330.0, XCT2611333.0, XCT29003.3	208125_at, 208124_s_at, 236894_at	NP_004131.3, EAW58999.1, EAW58970.1, EAW58980.1, EAW58981.1
GeneID:23	FLII	17	18,148,130	18,182,055	33,926	-	6	1_A375_uNU7_mrust_lncRNA_RR_1:2460, 2_A375_uNU7_mrust_lncRNA_RR_1:3441, 2_A375_uNU37_plus_lncRNA_RR_1:3330, 3_A375_uNU37_plus_lncRNA_RR_1:3331, 4_A375_RGR1_1:3341, 4_A375_RGR1_1:3342, 4_A375_RGR1_1:3343, 4_A375_RGR1_1:3344	4021, -1753, 199, 1721, 23327, 11399, 199, -5237	up gene, upstream, rs gene, upstream, downstream, rs gene, rs gene, upstream	1	1	1	15	16	16.6	5	2_A375_uNU37_plus_lncRNA_RR_1	926	Gene FLII	FLII, FLII, FLJ39189, FLJ40289, FLJ41	fli-leucine rich gene (Drosophila)	NM_002018, XCT1519022.1, XCT2259977.0, XCT2352940.0, XCT29962.2	212024_s_at, 212025_s_at, 222853_s_at	NP_002008.1, EAW58553.1, EAW58554.1, EAW58555.1, EAW58556.1
GeneID:1757	SMCR7	17	18,185,545	18,189,995	5,247	+	6	1_A375_uNU7_mrust_lncRNA_RR_1:2460, 2_A375_uNU7_mrust_lncRNA_RR_1:3441, 2_A375_uNU37_plus_lncRNA_RR_1:3330, 3_A375_uNU37_plus_lncRNA_RR_1:3331, 4_A375_RGR1_1:3343, 4_A375_RGR1_1:3344	-2393, -93, -1992, -72, -1992, 3544	up gene, upstream, upstream, upstream, upstream, up gene	1	1	1	21	21.67	16.33	5	2_A375_uNU37_plus_lncRNA_RR_1	926	Gene SMCR7	SMCR7, MGC23130	Smith-Magenis syndrome chromosome region, candidate 7	NM_145059, NM_001144900, NM_139162, XCT1959328.1, XCT2352947.0	235896_s_at	NP_659454.2, NP_001139372.1, NP_631901.2, EAW58551.1, EAW58552.1
GeneID:7518	TOP3A	17	18,177,235	18,216,321	41,086	-	3	1_A375_uNU37_plus_lncRNA_RR_1:3332, 3_A375_RGR1_1:3344, 4_A375_RGR1_1:3345	51, 50929, -203	up gene, downstream, upstream	0	1	1	10	17.5	22	2	4_A375_EGFR_1.1	927	Gene TOP3A	TOP3, TOP3A	topoisomerase (DNA) III alpha	NM_004618, XCT1519033.1, XCT2259998.0, XCT2259987.0, XCT23993.2	204745_x_at, 214299_at, 214300_s_at	NP_004609.1, EAW58643.1, EAW58642.1, EAW58641.1, EAW58640.1
GeneID:1440	SMCR8	17	18,216,974	18,231,370	12,778	+	2	1_A375_uNU37_plus_lncRNA_RR_1:3332, 4_A375_RGR1_1:3345	-394, 30	upstream, rs gene	0	1	1	12	27	19	1	2_A375_uNU37_plus_lncRNA_RR_1	927	Gene SMCR8	SMCR8, FLJ40697, FLJ34718	Smith-Magenis syndrome chromosome region, candidate 8	NM_144773, XCT2261349.1, XCT2259939.0	1552464_at, 1557988_s_at, 227384_at, 227393_s_at, 235404_at	NP_658955.2, EAW58644.1, EAW58645.1
GeneID:1335	SLC5A10	17	18,555,076	18,924,003	368,928	+	1	4_A375_RGR1_1:3346	35106	up gene	0	0	1	4	10	17	1	4_A375_EGFR_1.1	17	Gene SLC5A10	SGLT5, FLJ25317, SLC5A10	sodium/glucose transporter 5 (sodium/glucose cotransporter) member 10	NM_001042450, NM_152351, XCT2161859.2, XCT2259394.1, XCT2259396.1	235707_at	NP_001035915.1, NP_689564.3, EAW58429.1, EAW58430.1, EAW58431.1
GeneID:8443	FAM83G	17	18,974,361	18,980,080	37,879	+	1	4_A375_RGR1_1:3348	36476	up gene	0	0	1	4	10	17	1	4_A375_EGFR_1.1	17	Gene FAM83G	FAM83G, FLJ41564	family with sequence similarity 83, member G	NM_031919999	235367_at	NP_001035082.2
GeneID:2663	SNORD38-1	17	18,985,223	18,985,441	218	+	1	4_A375_RGR1_1:3347	1191	downstream	0	0	1	7	8	17	1	4_A375_EGFR_1.1	17	Gene SNORD38-1, U38	SNORD38, RNU38, U38, SNORD38-1, U38-1	small nucleolar RNA, C/D box 38-1	NR_002371		
GeneID:3582	SNORD38-2	17	18,987,233	18,987,449	216	+	1	4_A375_RGR1_1:3347	212	downstream	0	0	1	7	8	17	1	4_A375_EGFR_1.1	17	Gene SNORD38-2	SNORD38-2, U38-2	small nucleolar RNA, C/D box 38-2	NR_002324		
GeneID:2230	EPN2	17	19,140,690	19,240,026	99,336	+	2	1_A375_uNU37_mrust_lncRNA_RR_1:2462, 2_A375_uNU37_plus_lncRNA_RR_1:3333	69156, 69174	down, rs gene	1	1	0	49	61	9	1	2_A375_uNU37_plus_lncRNA_RR_1	961	Gene EPN2	EHSD1, EPN2, KIAA1065	epsin 2	NM_014796, NM_145021, NM_001172864, XCT1959753.1, XCT2257724.0, XCT2257734.0	205465_s_at, 205464_s_at	NP_055770.2, NP_663723.2, NP_001159754.1, EAW58375.1, EAW58376.1, EAW58377.1
GeneID:1153	MAPK7	17	19,261,024	19,286,657	8,633	+	1	4_A375_RGR1_1:3348	4982	up gene	0	0	1	9	7	18	1	4_A375_EGFR_1.1	18	Gene MAPK7	BMK1, MAPK7, PRKM7, ERK5, ERK5	mitogen-activated protein kinase 7	NM_139032, NM_139033, NM_139034, XCT1971158.1, XCT1971159.1, XCT2257325.1, XCT2611579.0, XCT2352421.0	207292_s_at, 33917_at	NP_620081.1, NP_620082.2, NP_620083.2, NP_002740.2, NP_620082.2, EAW58553.1, EAW58554.1, EAW58555.1, EAW58556.1
GeneID:4313	MAP4	17	19,286,765	19,290,493	3,728	-	1	4_A375_RGR1_1:3348	4477	downstream	0	0	1	9	7	18	1	4_A375_EGFR_1.1	18	Gene MAP4	MTAP4	microtubule-associated protein 4	NM_002374, XCT1971178.1, XCT2181812.2, XCT2352424.0	212713_at	NP_002365.1, EAW58388.1, EAW58389.1, EAW58390.1
GeneID:2268	ALDH3A2	17	19,552,956	19,600,900	56,644	+	3	1_A375_uNU37_plus_lncRNA_RR_1:3334, 4_A375_RGR1_1:3339, 5_A375_RGR1_1:3339	296, -352, 3640	up gene, upstream, rs gene	0	1	1	11	12.5	19.5	2	4_A375_EGFR_1.1	22	Gene ALDH3A2	ALDH3A2, DKFZp686B03287, FLJ40351, FLJ41564, SLS, ALDH10	aldehyde dehydrogenase 3 family, member A2	NM_000382, NM_001031806, XCT1971159.1, XCT2181834.2, XCT2352433.0	202053_s_at, 203354_s_at, 210364_s_at	NP_000373.1, NP_001026976.1, EAW58381.1, EAW58382.1, EAW58383.1
GeneID:2716	ALDH3A1	17	19,841,297	19,851,748	10,449	-	2	1_A375_uNU37_plus_lncRNA_RR_1:3353, 4_A375_RGR1_1:3352	4808, 3234	up gene, rs gene	0	1	1	15	15	17	2	4_A375_EGFR_1.1	24	Gene ALDH3A1	ALDH3, MGC10499, ALDH3A1, ALDH10	aldehyde dehydrogenase 3 family, member A1	NM_000691, NM_001135167, NM_001135168, XCT2181862.2, XCT2352417.0	209823_at	NP_000682.2, NP_001129639.1, NP_001129640.1, EAW58365.1, EAW58366.1
GeneID:1616	AXAP1	17	19,900,749	19,951,129	72,380	+	1	4_A375_RGR1_1:3353	343	upstream	0	0	1	10	11	17	1	4_A375_EGFR_1.1	17	Gene AXAP1	MGC9414, D-AMINO_ACID_OXIDASE_PROTEIN	A kinase (PRKA) anchor protein 10	NM_027302, XCT1212853.0	205345_at, 219038_s_at, 236857_at	NP_009133.2, EAW58913.1
GeneID:1005	LOC10039	17	20,799,982	20,833,334	37,892	+	1	2_A375_uNU37_plus_lncRNA_RR_1:3337	30748	up gene	0	0	1	10	17	2	1	2_A375_uNU37_plus_lncRNA_RR_1	917	Gene LOC100507263	LOC100507263	hypothetical LOC100507263	XR_111873, XR_111874, XR_111876, XR_111875, XR_110374, XR_925276, XR_110899, XR_110898, XR_110870		
GeneID:2306	USP22	17	20,932,908	20,946,352	13,445	+	4	1_A375_uNU7_mrust_lncRNA_RR_1:2464, 2_A375_RGR1_1:3339, 4_A375_RGR1_1:3355, 5_A375_RGR1_1:3356	-539, 30450, 48502, -326	upstream, downstream, downstream, upstream	1	0	1	13.33	11.33	16.67	3	1_A375_uNU7_mrust_lncRNA_RR_1	920	Gene USP22	USP22, USP22, NAH1063	ubiquitin specific peptidase 22	NM_015276	220083_at, 218537_at, 220082_s_at	NP_056091.1
GeneID:2399	DHRS7B	17	21,030,236	21,094,839	64,376	+	1	1_A375_uNU37_mrust_lncRNA_RR_1:2465	-16	upstream	1	0	0	17	16	11	1	1_A375_uNU37_mrust_lncRNA_RR_1	517	Gene DHRS7B	C-SRS5, DKFZp686K0284, SDR32C1, DHRS7B, MGC2916	dehydrogenase/reductase (SDR family) member 7B	NM_015510, XCT1959666.1, XCT1959513	220860_s_at	NP_056335.2, EAW58397.1, EAW58398.1
GeneID:8764	TMEM161A	17	21,161,285	21,317,906	156,845	-	3	1_A375_uNU37_mrust_lncRNA_RR_1:2466, 2_A375_uNU37_plus_lncRNA_RR_1:3339, 3_A375_RGR1_1:3337	598, 598, 596	up gene, rs gene, rs gene	1	1	1	31	29	13	1	1_A375_uNU7_mrust_lncRNA_RR_1	931	Gene TMEM161A	TMEM161, C17orf33, PM1, PM1	transmembrane protein 11	NM_025076, NR_024547, XCT1972.5, XCT1959630.1	205437_at	NP_079352.1, EAW58360.1, EAW58361.1
GeneID:3800	MAP2K3	17	21,187,960	21,216,932	30,084	+	6	1_A375_uNU37_plus_lncRNA_RR_1:2467, 2_A375_uNU7_mrust_lncRNA_RR_1:3440, 2_A375_uNU37_plus_lncRNA_RR_1:3340, 3_A375_uNU37_plus_lncRNA_RR_1:3339, 4_A375_RGR1_1:3356, 4_A375_RGR1_1:3357, 4_A375_RGR1_1:3358	3304, 30400, 3265, 16912, 12224, 20032, 33821, 33312	up gene, downstream, rs gene, rs gene, rs gene, downstream, downstream	1	1	1	15.67	14.33	30.33	6	4_A375_EGFR_1.1	26	Gene MAP2K3	MAP2K3, PRKMK3, MAPKK3, MAP2K3, MEK3	mitogen-activated protein kinase kinase 3	NM_145109, NM_002756, XCT2232659.1	207807_s_at, 213478_s_at, 213479_at	NP_619731.1, NP_002747.2, EAW58288.1
GeneID:3351	KCNJ12	17	21,276,899	21,322,079	45,180	+	11	1_A375_RGR1_1:3357, 4_A375_RGR1_1:3358, 4_A375_RGR1_1:3359, 4_A375_RGR1_1:3370, 4_A375_RGR1_1:3371, 4_A375_RGR1_1:3372, 4_A375_RGR1_1:3374, 4_A375_RGR1_1:3376, 4_A375_RGR1_1:3378, 4_A375_RGR1_1:3377	18077, 24141, 24855, 26546, 20865, 33521, 37589, 39205, 40037, 44545, 49013	up gene, rs gene, up gene, rs gene, up gene, rs gene, up gene, rs gene, up gene, rs gene, downstream, downstream, downstream	0	1	1	14.82	14.55	28.46	11	4_A375_EGFR_1.1	34	Gene KCNJ12	IRK2, Kir2.2, bIRK1, KCNJ12, hxp12c, Kir2.2v, KCNJ12, FLJ16187, Kir2.2c, KIR2	potassium inwardly-rectifying channel, subfamily J, member 12	NM_021012, XCT1786692.1	207110_at, 205898_at, 205897_s_at, 212209_at	NP_066552.2, EAW58109.1
GeneID:3235	C17orf61	17	21,431,571	21,454,941	23,370	-	2	1_A375_uNU37_plus_lncRNA_RR_1:3341, 4_A375_RGR1_1:3378	381, 221	up gene, rs gene	0	1	1	7	17	15	1	2_A375_uNU37_plus_lncRNA_RR_1	917	Gene C17orf61	FLJ41148, FLJ42377, FLJ31674, FLJ38707, C17orf61, FLJ39616	chromosome 17 open reading frame 61	NM_031115#34	225145_at, 228166_s_at, 236857_at	NP_001108955.1
GeneID:2618	FAM27L	17	21,823,370	21,826,499	1,129	+	1	4_A375_RGR1_1:3361	5960	downstream	0	0	1	5	9	17	1	4_A375_EGFR_1.1	17	Gene FAM27L	FAM27L, MGC35181	family with sequence similarity 27-like	NR_026356, XCT2252932.0		EAW58114.1
GeneID:2661	FLJ39006	17	21,904,082	21,913,070	8,988	+	2	4_A375_RGR1_1:3362, 4_A375_RGR1_1:3363	-694, 816	up/stream, rs gene	0	0	1	21.5	19.5	26.5	2	4_A375_EGFR_1.1	49	Gene FLJ39006		hypothetical FLJ39006	NR_027084		
GeneID:2665	WSB1	17	23,821,108	23,845,643	19,329	+	2	1_A375_uNU37_plus_lncRNA_RR_1:2469, 2_A375_uNU37_plus_lncRNA_RR_1:3342	482, 46	up gene, rs gene	1	1	0	16	21	14	1	2_A375_uNU37_plus_lncRNA_RR_1	921	Gene WSB1	WSB-1, SWIP1, WSB1	WD repeat and SOCS box-containing 1	NM_134263, NM_015626, XCT1990812.2, XCT1961087.1, XCT1961088.1, XCT2264080.0, XCT2264070.0	231294_s_at, 231295_at, 231308_at	NP_599027.1, NP_056441.0, EAW59308.1, EAW59309.1, EAW59310.1, EAW59311.1, EAW59312.1, EAW59313.1
GeneID:5888	RSRC1	17	23,799,038	23,930,716	131,682	+	2	1_A375_uNU37_plus_lncRNA_RR_1:2470, 4_A375_RGR1_1:3344	199, -80	upstream, upstream	1	1	0	16	20	5	1	2_A375_uNU37_plus_lncRNA_RR_1	920	Gene RSRC1	RSRC, RSUZ, RDR1	arginine/serine-rich 1	NM_014238, XCT1931498.1, XCT2264078.0	213787_at, 212769_at, 212770_at, 233252_at	NP_055833.1, EAW59333.1, EAW59334.1
GeneID:4843	NOS2	17	25,855,792	26,127,355	45,795	+	4	1_A375_uNU7_mrust_lncRNA_RR_1:2471, 1_A375_uNU37_mrust_lncRNA_RR_1:2472, 2_A375_uNU37_plus_lncRNA_RR_1:3343, 3_A375_uNU37_plus_lncRNA_RR_1:3348	37643, 23091, 37479, 23043	up gene, rs gene, rs gene, up gene	1	1	0	19	20.5	5.5	2	2_A375_uNU37_plus_lncRNA_RR_1	940	Gene NOS2	NOS, INOS, HEP-NOS, NOS2, NOS2A	nitric oxide synthase 2, inducible	NM_000625, XCT1940423.2, XCT2265131.0, XCT2265133.0	210037_at, 210037_s_at	NP_000616.3, EAW59340.1, EAW59341.1, EAW59350.1
GeneID:5310	NUK	17	26,369,868	26,523,407	153,719	+	2	1_A375_uNU37_plus_lncRNA_RR_1:2474, 2_A375_uNU37_plus_lncRNA_RR_1:3349	1112, -1090	upstream, upstream	1	1	0	24	26	9	1	2_A375_uNU37_plus_lncRNA_RR_1	928	Gene NUK	DKFZp761G1231, FLJ20033, NUK	serine/threonine kinase	NM_199331, XCT2264098.0, XCT2264099.0, XCT22662.2, XCT2352448.0	216316_s_at, 222369_at, 222380_s_at	NP_001157153.1, EAW59365.1, EAW59366.1, EAW59367.1, EAW59368.1
GeneID:2778	TMEM97	17	26,646,121	26,655,711	9,590	+	5	1_A375_uNU7_mrust_lncRNA_RR_1:2475, 1_A375_uNU37_mrust_lncRNA_RR_1:3478, 2_A375_uNU37_plus_lncRNA_RR_1:3350, 3_A375_uNU37_plus_lncRNA_RR_1:3351, 4_A375_RGR1_1:3357	55, 18425, 119, 18579, 119	up gene, downstream, rs gene, downstream, rs gene	1	1	1	16	22	19	2	4_A375_EGFR_1.1	24	Gene TMEM97	TMEM97, MAC30	transmembrane protein 97	NM_014573, XCT1960027.0, XCT2265071.1, XCT22692.1	212279_at, 212281_s_at, 212282_at, 214283_at	NP_055850.2, EAW59365.1, EAW59366.1, EAW59367.1
GeneID:9361	PTD	17	26,655,353	26,662,495	7,142	-	5	1_A375_uNU7_mrust_lncRNA_RR_1:2475, 1_A375_uNU37_mrust_lncRNA_RR_1:3478, 2_A375_uNU37_plus_lncRNA_RR_1:3350, 3_A375_uNU37_plus_lncRNA_RR_1:3351, 4_A375_RGR1_1:3357	18619, -49, 18619, 99, 18291	up/stream, upstream, downstream, rs gene, rs gene, downstream	1	1	1	16	22	19	2	4_A375_EGFR_1.1	24	Gene PTD	PTD		NM_174357, XCT1960032.1, XCT1960033.1, XCT1960034.1, XCT2259980.0, XCT2349987.0	210312_s_at	NP_777943.1, EAW59376.1, EAW59378.1, EAW59377.1, EAW59378.1, EAW59379.1, EAW59372.1, EAW59373.1
GeneID:7179	TNFAIP8	17	26,862,545	26,874,255	11,687	+	2	1_A375_uNU7_mrust_lncRNA_RR_1:2476, 2_A375_uNU37_plus_lncRNA_RR_1:3351	-4, -146	upstream, upstream	1	1	0	20	22	14	1	2_A375_uNU37_plus_lncRNA_RR_1	922	Gene TNFAIP8	EDP1, NCU00202, 981, TNFAIP1, WDZ2317, B12	tumor necrosis factor, alpha-induced protein 8	NM_021137, XCT2259953	201207_at, 201208_s_at	NP_066965.1, EAW59377.1
GeneID:2872	POLDIP2	17	26,873,699	26,884,903	10,944	-	2	1_A375_uNU7_mrust_lncRNA_RR_1:2477, 2_A375_uNU37_plus_lncRNA_RR_1:3352	99, 99	up gene, rs gene	1	1	0	50	54	11	1	2_A375_uNU37_plus_lncRNA_RR_1	934	Gene POLDIP2	POLDIP2, DKFZp686F1532, POLD4, PDIP38	polymerase (DNA-directed), delta interacting protein 2	NM_015584, XCT2259614	217886_s_at, 222423_s_at	NP_056399.1, EAW59378.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:147007	TMEM199	17	26,684,687	26,689,089	4,402	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2477, 2_A375_pNL97_plus_lncRNA_AR..1..3552	-143, -143	upstream, upstream	1	1	0	50	54	11	1	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene TMEM199	TMEM199, C17orf32, MGC45714	transmembrane protein 199	NM_152464, hCT2285076.1, hCT23000.3	225374_at, 225375_at	NP_689677.1, EAW51080.1, EAW51079.1
GeneID:645832	SEBOX	17	26,691,290	26,692,265	975	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2477, 2_A375_pNL97_plus_lncRNA_AR..1..3552, 2_A375_pNL97_plus_lncRNA_AR..1..3553	7721, 7721, -8599	downstream, downstream, upstream	1	1	0	31.5	39	8	2	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene SEBOX	OG9X, SEBOX, OG9, OG-9	SEBOX homeobox	NM_001080837	234256_at	NP_001074306.2
GeneID:7448	VTN	17	26,694,298	26,697,373	3,075	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2477, 2_A375_pNL97_plus_lncRNA_AR..1..3552, 2_A375_pNL97_plus_lncRNA_AR..1..3553	12829, 12829, -3491	downstream, downstream, upstream	1	1	0	31.5	39	8	2	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene VTN	V75, VNT, VN, VTN	vitronectin	NM_000638, hCT22991.3	204534_at	NP_000629.3, EAW51082.1
GeneID:23098	SARM1	17	26,698,987	26,728,065	29,078	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2478, 2_A375_pNL97_plus_lncRNA_AR..1..3553, 4_A375_EGR1..1..3588, 4_A375_EGR1..1..3589	34845, 1877, 12549, 33317	downstream, in gene, in gene, downstream	1	1	1	10.25	12	12.25	4	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SARM1	SAMD2, KIAA0524, FLJ36296, SARM1, SARM	sterile alpha and TIR motif containing 1	NM_015077, hCT2285078.0, hCT22990.3	213257_at, 213259_s_at	NP_055892.2, EAW51083.1, EAW51084.1
GeneID:113235	SLC46A1	17	26,721,661	26,733,228	11,567	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2478, 4_A375_EGR1..1..3588, 4_A375_EGR1..1..3589	-404, 21692, 924	upstream, downstream, in gene	1	0	1	9.33	6	14.67	3	4_A375_EGR1..1	18	Gene SLC46A1	MGC9564, FLJ39875, HCP1, PCFT, SLC46A1	solute carrier family 46 (folate transporter), member 1	NM_080669, hCT1966026.1, hCT2281326.0, hCT2281327.0, hCT2281329.0, hCT22993.2	1552278_a_at, 1552279_a_at, 1558703_at, 233531_at	NP_542400.2, EAW51088.1, EAW51085.1, EAW51086.1, EAW51087.1, EAW51089.1
GeneID:8456	FOXN1	17	26,850,959	26,865,175	14,216	+	1	4_A375_EGR1..1..3590	11121	in gene	0	0	1	3	7	22	1	4_A375_EGR1..1	22	Gene FOXN1	RONU, WHN, FOXN1, FKHL20	forkhead box N1	NM_003593, hCT22976.2	207683_at	NP_003584.2, EAW51092.1
GeneID:10615	SPAG5	17	26,904,563	26,926,036	21,473	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2479	-424	upstream	1	0	0	20	14	16	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene SPAG5	MAP126, hMAP126, DEEPEST, SPAG5	sperm associated antigen 5	NM_006461, hCT22977.3	203145_at	NP_006452.3, EAW51106.1
GeneID:100506436	LOC100506436	17	26,925,808	26,944,679	18,871	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2479	672	in gene	1	0	0	20	14	16	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LOC100506436		hypothetical LOC100506436	XR_111662, XR_111661, XR_109449, XR_109448, XR_115073, XR_115072		
GeneID:124923	FLJ25006	17	26,934,982	26,941,211	6,229	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2479	14731	downstream	1	0	0	20	14	16	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene FLJ25006	SGK494, MGC39533, FLJ25006, FLJ78978	uncharacterized serine/threonine-protein kinase SgK494	NM_001174103, hCT2281315.1, hCT2281316.1, hCT22988.4, hCT2346115.1	1553292_s_at	NP_001167574.1, EAW51108.1, EAW51109.1, EAW51110.1, EAW51111.1
GeneID:6388	SDF2	17	26,975,607	26,988,933	13,326	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3554	-347	upstream	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SDF2	SDF2	stromal cell-derived factor 2	NM_006923, hCT2344356.1, hCT2344359.1, hCT2344364.0, hCT2349500.0	203090_at	NP_008854.2, EAW51122.1, EAW51121.1, EAW51123.1, EAW51124.1
GeneID:6830	SUPT6H	17	26,989,302	27,029,249	39,947	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3554	-22	upstream	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SUPT6H	KIAA0162, emb-5, SPT6H, MGC87943, SPT6, SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	NM_003170, hCT1956386.1, hCT2285085.0, hCT2285086.0, hCT22997.3	1554311_a_at, 208420_x_at, 208830_s_at, 208831_x_at	NP_003161.2, EAW51119.1, EAW51116.1, EAW51117.1, EAW51118.1
GeneID:147011	PROCA1	17	27,030,534	27,038,872	8,338	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2480, 2_A375_pNL97_plus_lncRNA_AR..1..3555, 4_A375_EGR1..1..3591	-8200, -5592, -5688	upstream, upstream, upstream	1	1	1	17.5	16	18.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene PROCA1	MGC39650, PROCA1	protein interacting with cyclin A1	NM_152465, hCT2348116.1, hCT2350934.0	232647_at, 236286_at	NP_689678.1, EAW51125.1, EAW51126.1
GeneID:83871	RAB34	17	27,041,299	27,045,286	3,987	-	8	1_A375_pNL7_minus_lncRNA_AR..1..2480, 2_A375_pNL97_plus_lncRNA_AR..1..3555, 2_A375_pNL97_plus_lncRNA_AR..1..3556, 2_A375_pNL97_plus_lncRNA_AR..1..3557, 2_A375_pNL97_plus_lncRNA_AR..1..3558, 4_A375_EGR1..1..3591, 4_A375_EGR1..1..3592, 4_A375_EGR1..1..3593	-1786, 822, -6330, -7770, -8442, 726, -7386, -8378	upstream, in gene, upstream, upstream, upstream, in gene, upstream, upstream	1	1	1	15.5	17.25	19	4	4_A375_EGR1..1	23	Gene RAB34	RAH, RAB39, RAB34	RAB34, member RAS oncogene family	NR_024575, NR_024579, NM_031934, NM_001142624, NM_001142625, NM_001144942, NM_001144943, hCT2281299.0, hCT2281300.0, hCT2281302.0, hCT22995.2	1555630_a_at, 224710_at	NP_114140.4, NP_001136096.2, NP_001136097.2, NP_001138414.1, NP_001138415.1, EAW51127.1, EAW51128.1, EAW51129.1, EAW51130.1
GeneID:6147	RPL23A	17	27,047,000	27,051,374	4,374	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2480, 2_A375_pNL97_plus_lncRNA_AR..1..3555, 2_A375_pNL97_plus_lncRNA_AR..1..3556, 2_A375_pNL97_plus_lncRNA_AR..1..3557, 2_A375_pNL97_plus_lncRNA_AR..1..3558, 4_A375_EGR1..1..3591, 4_A375_EGR1..1..3592, 4_A375_EGR1..1..3593	72, -2536, 4616, 6056, 6728, -2440, 5672, 6664	in gene, upstream, downstream, downstream, downstream, upstream, downstream, downstream	1	1	1	15.5	17.25	19	4	4_A375_EGR1..1	23	Gene RPL23A	FLJ27455, MDA20, RPL23A, L23A	ribosomal protein L23a	NM_000984, hCT2285090.1, hCT2285091.1	203012_x_at, 208825_x_at, 208834_x_at, 213084_x_at	NP_000975.2, EAW51131.1, EAW51132.1
GeneID:26808	SNORD42B	17	27,047,566	27,047,634	68	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2480, 2_A375_pNL97_plus_lncRNA_AR..1..3555, 2_A375_pNL97_plus_lncRNA_AR..1..3556, 2_A375_pNL97_plus_lncRNA_AR..1..3557, 2_A375_pNL97_plus_lncRNA_AR..1..3558, 4_A375_EGR1..1..3591, 4_A375_EGR1..1..3592, 4_A375_EGR1..1..3593	-496, -3104, 4048, 5488, 6160, -3008, 5104, 6096	upstream, upstream, downstream, downstream, downstream, upstream, downstream, downstream	1	1	1	15.5	17.25	19	4	4_A375_EGR1..1	23	Gene SNORD42B	RNU42B, U42B, SNORD42B	small nucleolar RNA, C/D box 42B	NR_000013		
GeneID:26773	SNORD4A	17	27,049,600	27,049,671	71	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2480, 2_A375_pNL97_plus_lncRNA_AR..1..3555, 2_A375_pNL97_plus_lncRNA_AR..1..3556, 2_A375_pNL97_plus_lncRNA_AR..1..3557, 2_A375_pNL97_plus_lncRNA_AR..1..3558, 4_A375_EGR1..1..3591, 4_A375_EGR1..1..3592, 4_A375_EGR1..1..3593	-2528, -5136, 2016, 3456, 4128, -5040, 3072, 4064	upstream, upstream, downstream, downstream, downstream, upstream, downstream, downstream	1	1	1	15.5	17.25	19	4	4_A375_EGR1..1	23	Gene SNORD4A	Z17A, mgh18S-121, SNORD4A, RNU101A	small nucleolar RNA, C/D box 4A	NR_000010		
GeneID:26809	SNORD42A	17	27,050,446	27,050,509	63	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2480, 2_A375_pNL97_plus_lncRNA_AR..1..3555, 2_A375_pNL97_plus_lncRNA_AR..1..3556, 2_A375_pNL97_plus_lncRNA_AR..1..3557, 2_A375_pNL97_plus_lncRNA_AR..1..3558, 4_A375_EGR1..1..3591, 4_A375_EGR1..1..3592, 4_A375_EGR1..1..3593	-3376, -5984, 1168, 2608, 3280, -5888, 2224, 3216	upstream, upstream, downstream, downstream, downstream, upstream, downstream, downstream	1	1	1	15.5	17.25	19	4	4_A375_EGR1..1	23	Gene SNORD42A	RNU42A, SNORD42A, U42, U42A	small nucleolar RNA, C/D box 42A	NR_000014		
GeneID:26772	SNORD4B	17	27,050,699	27,050,772	73	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2480, 2_A375_pNL97_plus_lncRNA_AR..1..3555, 2_A375_pNL97_plus_lncRNA_AR..1..3556, 2_A375_pNL97_plus_lncRNA_AR..1..3557, 2_A375_pNL97_plus_lncRNA_AR..1..3558, 4_A375_EGR1..1..3591, 4_A375_EGR1..1..3592, 4_A375_EGR1..1..3593	-3627, -6235, 917, 2357, 3029, -6139, 1973, 2965	upstream, upstream, downstream, downstream, downstream, upstream, downstream, downstream	1	1	1	15.5	17.25	19	4	4_A375_EGR1..1	23	Gene SNORD4B	RNU101B, Z17B, SNORD4B	small nucleolar RNA, C/D box 4B	NR_000009		
GeneID:116238	TLCD1	17	27,051,366	27,053,949	2,583	-	8	1_A375_pNL7_minus_lncRNA_AR..1..2480, 2_A375_pNL97_plus_lncRNA_AR..1..3555, 2_A375_pNL97_plus_lncRNA_AR..1..3556, 2_A375_pNL97_plus_lncRNA_AR..1..3557, 2_A375_pNL97_plus_lncRNA_AR..1..3558, 4_A375_EGR1..1..3591, 4_A375_EGR1..1..3592, 4_A375_EGR1..1..3593	6577, 9465, 2333, 893, 221, 9369, 1277, 285	downstream, downstream, in gene, in gene, in gene, downstream, in gene, in gene	1	1	1	15.5	17.25	19	4	4_A375_EGR1..1	23	Gene TLCD1	TLCD1	TLC domain containing 1	NM_138463, NM_001160407, hCT1968029.1, hCT22994.2	227604_at	NP_612472.1, NP_001153879.1, EAW51133.1, EAW51134.1
GeneID:284086	NEK8	17	27,055,832	27,069,784	13,952	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2480, 2_A375_pNL97_plus_lncRNA_AR..1..3556, 2_A375_pNL97_plus_lncRNA_AR..1..3557, 2_A375_pNL97_plus_lncRNA_AR..1..3558, 4_A375_EGR1..1..3592, 4_A375_EGR1..1..3593	-8760, -4216, -2776, -2104, -3160, -2168	upstream, upstream, upstream, upstream, upstream, upstream	1	1	1	15.33	16	19.33	3	4_A375_EGR1..1	23	Gene NEK8	JCK, NEK8, MGC138445, NEK12A, NPHP9	NIMA (never in mitosis gene a)-related kinase 8	NM_178170, hCT2285093.1, hCT2352450.0, hCT2352451.0	1557170_at, 1557172_x_at	NP_835464.1, EAW51135.1, EAW51136.1, EAW51137.1
GeneID:9618	TRAF4	17	27,071,023	27,077,976	6,953	+	1	4_A375_EGR1..1..3594	14737	downstream	0	0	1	5	7	23	1	4_A375_EGR1..1	23	Gene TRAF4	TRAF4, CART1, RNF83, MLN62	TNF receptor-associated factor 4	NM_004295, hCT19429.3, hCT1966014.1, hCT1966015.1, hCT2285096.0, hCT2285099.0	202871_at, 211899_s_at, 235668_s_at, 242473_at	NP_004286.2, EAW51138.1, EAW51139.1, EAW51140.1, EAW51141.1, EAW51142.1
GeneID:55731	C17orf63	17	27,082,996	27,169,841	86,845	-	1	4_A375_EGR1..1..3594	84081	in gene	0	0	1	5	7	23	1	4_A375_EGR1..1	23	Gene C17orf63	FLJ10700, C17orf63	chromosome 17 open reading frame 63	NM_001077498, NM_018182, hCT2281294.0, hCT2281295.0, hCT2281298.0	218484_s_at, 222641_s_at, 229418_at	NP_001070966.1, NP_060652.2, EAW51143.1, EAW51144.1, EAW51145.1
GeneID:26284	ERAL1	17	27,182,043	27,188,072	6,029	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2481, 2_A375_pNL97_plus_lncRNA_AR..1..3559	65, 5	in gene, in gene	1	1	0	16	27	13	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene ERAL1	HERA-A, ERA, ERAL1, HERA-B, H-ERA, ERAL1A	Era G-protein-like 1 (E. coli)	NM_005702, hCT1810255.2, hCT2285101.0, hCT2285102.0, hCT2352446.0	212087_s_at	NP_005693.1, EAW51146.1, EAW51147.1, EAW51148.1, EAW51149.1
GeneID:574411	MIR451	17	27,188,387	27,188,458	71	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2481, 2_A375_pNL97_plus_lncRNA_AR..1..3559	6330, 6410	downstream, downstream	1	1	0	16	27	13	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene MIR451	hsa-mir-451, MIRN451, MIR451	microRNA 451	NR_029970		
GeneID:406936	MIR144	17	27,188,551	27,188,636	85	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2481, 2_A375_pNL97_plus_lncRNA_AR..1..3559	6508, 6588	downstream, downstream	1	1	0	16	27	13	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene MIR144	MIR144, MIRN144	microRNA 144	NR_029665		
GeneID:57649	PHF12	17	27,232,271	27,278,508	46,237	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2482	-948	upstream	1	0	0	16	20	12	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene PHF12	PHF12, PF1, FLJ34122, KIAA1523, MGC131914	PHD finger protein 12	NM_020889, NM_001033561, hCT1810260.3, hCT2281276.0, hCT2352444.0, hCT2352445.0	231815_at, 234939_s_at	NP_065940.1, NP_001028733.1, EAW51164.1, EAW51165.1, EAW51166.1, EAW51167.1
GeneID:124925	SEZ6	17	27,281,923	27,333,081	51,158	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2482, 1_A375_pNL7_minus_lncRNA_AR..1..2483, 1_A375_pNL7_minus_lncRNA_AR..1..2484, 2_A375_pNL97_plus_lncRNA_AR..1..3560, 2_A375_pNL97_plus_lncRNA_AR..1..3561, 2_A375_pNL97_plus_lncRNA_AR..1..3562	53825, -71, -1991, 1369, -71, -1927	downstream, upstream, upstream, in gene, upstream, upstream	1	1	0	25.5	22.5	9.5	4	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene SEZ6	SEZ6		NM_178860, NM_001098635, hCT20246.3, hCT2281272.0, hCT2281274.0, hCT2281275.0, hCT2352441.0	229851_at, 243430_at	NP_849191.3, NP_001092105.1, EAW51171.1, EAW51172.1, EAW51173.1, EAW51174.1, EAW51170.1
GeneID:399687	MYO18A	17	27,400,528	27,507,407	106,879	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2485, 2_A375_pNL97_plus_lncRNA_AR..1..3563, 2_A375_pNL97_plus_lncRNA_AR..1..3564, 4_A375_EGR1..1..3595, 4_A375_EGR1..1..3596	47247, 26719, 25327, 65119, 47503	in gene, in gene, in gene, in gene, in gene	1	1	1	15.5	16.25	13	4	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MYO18A	KIAA0216, MYO18A, MYSPDZ, DKFZp686I0243, SPR210	myosin XVIIIA	NM_078471, NM_203318	202039_at	NP_510880.2, NP_976063.1
GeneID:1411	CRYBA1	17	27,573,875	27,581,512	7,637	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3566	-5555	upstream	0	1	0	11	20	6	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CRYBA1	CRYB1, CRYBA1	crystallin, beta A1	NM_005208, hCT20243.3	206982_at	NP_005199.2, EAW51165.1
GeneID:57532	NUFIP2	17	27,582,854	27,621,166	38,312	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3567	-146	upstream	0	1	0	16	26	14	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene NUFIP2	PIG1, MGC117262, 182-FIP, FIP-82, 82-FIP, NUFIP2, FLJ10976, KIAA1321	nuclear fragile X mental retardation protein interacting protein 2	NM_020772, hCT20247.3, hCT2288838.0	224956_at, 224958_at	NP_065823.1, EAW51186.1, EAW51187.1
GeneID:116236	ABHD15	17	27,887,679	27,894,042	6,363	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3568	314	in gene	0	1	0	7	17	14	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ABHD15	ABHD15	abhydrolase domain containing 15	NM_198147, hCT1783298.2	226796_at	NP_937790.2, EAW51191.1
GeneID:90313	TP53I13	17	27,895,739	27,900,175	4,436	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3568	-2011	upstream	0	1	0	7	17	14	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TP53I13	TP53I13, DSCP1	tumor protein p53 inducible protein 13	NM_138349, hCT2271784.1, hCT2271785.1, hCT2271786.1, hCT2351206.0	225605_at, 229056_at	NP_612358.3, EAW51192.1, EAW51193.1, EAW51194.1, EAW51195.1
GeneID:28964	GIT1	17	27,900,487	27,916,610	16,123	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3568, 2_A375_pNL97_plus_lncRNA_AR..1..3569, 2_A375_pNL97_plus_lncRNA_AR..1..3570	22682, -286, -4734	downstream, upstream, upstream	0	1	0	13.33	19.33	9.67	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene GIT1	GIT1		NM_014030, NM_001085454, hCT20244.3, hCT2352433.0	218030_at	NP_054749.2, NP_001078923.1, EAW51196.1, EAW51197.1
GeneID:124930	ANKRD13B	17	27,920,527	27,941,779	21,252	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3569, 2_A375_pNL97_plus_lncRNA_AR..1..3570	-3631, 817	upstream, in gene	0	1	0	16.5	20.5	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ANKRD13B	FLJ25555, FLJ20418, ANKRD13B	ankyrin repeat domain 13B	NM_152345, hCT20248.3, hCT2271789.0, hCT2271790.0, hCT2352439.0, hCT2352440.0	227720_at	NP_689558.4, EAW51203.1, EAW51199.1, EAW51200.1, EAW51201.1, EAW51202.1
GeneID:85464	SSH2	17	27,952,965	28,257,018	304,053	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3571, 2_A375_pNL97_plus_lncRNA_AR..1..3572, 4_A375_EGR1..1..3597, 4_A375_EGR1..1..3598	168794, -294, 168826, -182	in gene, upstream, in gene, upstream	0	1	1	15	17	19	2	4_A375_EGR1..1	20	Gene SSH2	SSH2, MGC78568, KIAA1725, SSH-2	slingshot homolog 2 (Drosophila)	NM_033389, hCT2288617.1, hCT2288618.0, hCT2288619.0, hCT2288622.0, hCT2288623.1	1554114_s_at, 1555423_at, 1555425_x_at, 226080_at	NP_203747.2, EAW51210.1, EAW51209.1, EAW51211.1, EAW51212.1, EAW51213.1
GeneID:374786	EFCAB5	17	28,256,874	28,435,470	178,596	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3572, 4_A375_EGR1..1..3598	438, 328	in gene, in gene	0	1	1	14	15	20	1	4_A375_EGR1..1	20	Gene EFCAB5	FLJ46247, DKFZp686I0638, EFCAB5, DKFZp434G2420	EF-hand calcium binding domain 5	NM_198529, NM_001145053, NR_026738	1558300_at, 1558301_a_at	NP_940931.2, NP_001138525.1
GeneID:1362	CPD	17	28,705,984	28,795,699	89,715	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2486, 1_A375_pNL7_minus_lncRNA_AR..1..2487, 2_A375_pNL97_plus_lncRNA_AR..1..3573, 2_A375_pNL97_plus_lncRNA_AR..1..3574, 2_A375_pNL97_plus_lncRNA_AR..1..3575, 4_A375_EGR1..1..3599, 4_A375_EGR1..1..3600	-160, 98366, -2048, -128, 98336, 144, 9816	upstream, downstream, upstream, upstream, downstream, in gene, in gene	1	1	1	34.5	37.5	11	4	1_A375_pNL7_minus_lncRNA_AR..1	102	Gene CPD	CPD, GP180	carboxypeptidase D	NM_001304, hCT19108.3, hCT2273897.0	201940_at, 201941_at, 201942_s_at, 201943_s_at, 229600_s_at	NP_001295.2, EAW51226.1, EAW51227.1
GeneID:9527	GOSR1	17	28,804,426	28,853,832	49,406	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2487, 2_A375_pNL97_plus_lncRNA_AR..1..3575	-74, -106	upstream, upstream	1	1	0	102	100	10	1	1_A375_pNL7_minus_lncRNA_AR..1	102	Gene GOSR1	GOS28/P28, GOS-28, GOS28, GOSR1, GS28, P28, GOLIM2	golgi SNAP receptor complex member 1	NM_001007024, NM_001007025, NM_004871, hCT1788807.2, hCT1961767.1, hCT2352438.0	1555199_at, 204830_s_at, 213020_at, 213021_at	NP_001007025.1, NP_001007026.1, NP_004862.1, EAW51229.1, EAW51230.1, EAW51231.1
GeneID:26083	TBC1D29	17	28,886,584	28,890,511	3,927	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2488, 4_A375_EGR1..1..3601, 4_A375_EGR1..1..3602	-8440, -3864, 12166	upstream, upstream, downstream	1	0	1	9.33	9.33	14	3	4_A375_EGR1..1	16	Gene TBC1D29	TBC1D29, DKFZp434O047	TBC1 domain family, member 29	NM_015594, hCT19109.4, hCT2273886.0	208008_at	NP_056409.1, EAW51236.1, EAW51237.1
GeneID:100506460	LOC100506460	17	28,900,488	28,903,499	3,011	-	1	4_A375_EGR1..1..3602	4747	downstream	0	0	1	7	7	16	1	4_A375_EGR1..1	16	Gene LOC100506460		hypothetical LOC100506460	XR_111679, XR_109451, XR_115075		
GeneID:51379	CRLF3	17	29,109,702	29,151,778	42,076	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2491, 1_A375_pNL7_minus_lncRNA_AR..1..2492, 2_A375_pNL97_plus_lncRNA_AR..1..3579	178, -7166, -7198	in gene, upstream, upstream	1	1	0	23	24	11	2	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene CRLF3	CREME9, CYTOR4, p48.2, CRLF3, FRWS, MGC20661	cytokine receptor-like factor 3	NM_015986, hCT1814758.1	205474_at	NP_057070.3, EAW80297.1
GeneID:79915	ATAD5	17	29,159,020	29,222,295	63,275	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2491, 1_A375_pNL7_minus_lncRNA_AR..1..2492, 2_A375_pNL97_plus_lncRNA_AR..1..3579	-7420, -76, -44	upstream, upstream, upstream	1	1	0	23	24	11	2	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene ATAD5	FRAG1, ELG1, C17orf41, FLJ12735, ATAD5	ATPase family, AAA domain containing 5	NM_024857	220223_at	NP_079133.3
GeneID:79736	C17orf42	17	29,226,001	29,233,286	7,285	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2493, 2_A375_pNL97_plus_lncRNA_AR..1..3580	54, -122	in gene, upstream	1	1	0	18	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C17orf42	MGC24674, TEFM, C17orf42, FLJ22729	chromosome 17 open reading frame 42	NM_024663, hCT1812231.2, hCT1980741.1, hCT1980742.1	219146_at, 238295_at	NP_078959.3, EAW80291.1, EAW80290.1, EAW80292.1
GeneID:84440	RAB11FIP4	17	29,718,642	29,865,232	146,590	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2495, 1_A375_pNL7_minus_lncRNA_AR..1..2496, 2_A375_pNL97_plus_lncRNA_AR..1..3581, 4_A375_EGR1..1..3603, 4_A375_EGR1..1..3604	22478, 80654, 106666, 96910, 133294	in gene, in gene, in gene, in gene, in gene	1	1	1	12.6	13.6	11.2	5	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene RAB11FIP4	RAB11-FIP4, MGC11316, FLJ00131, MGC126586, KIAA1821, RAB11FIP4	RAB11 family interacting protein 4 (class II)	NM_032932, hCT19960.2	224482_s_at, 225739_at, 225746_at	NP_116321.2, EAW80285.1



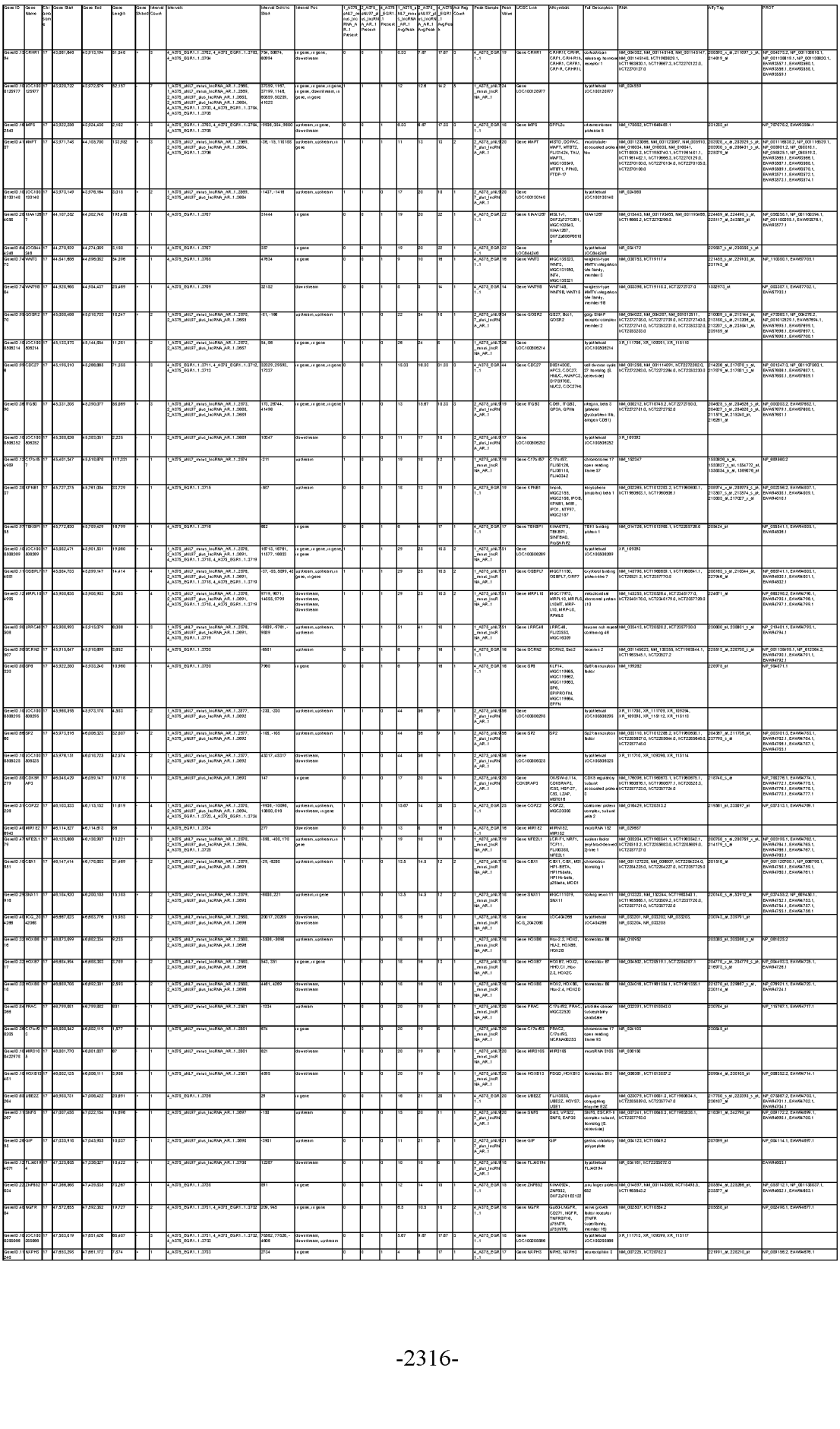
Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_pfd7_mrna_lncRNA_R_1 Percent	2_A375_pfd7_mrna_lncRNA_R_1 Percent	4_A375_EGFR_1 Percent	1_A375_pfd7_mrna_lncRNA_R_1 Avg Peak	2_A375_pfd7_mrna_lncRNA_R_1 Avg Peak	4_A375_EGFR_1 Avg Peak	Add Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:49 8986	MIR193A	17	29,857,015	29,857,102	87	+	3	1_A375_pfd7_mrna_lncRNA_R_1:-3497, 2_A375_pfd7_dist_lncRNA_R_1:3362, 4_A375_EGFR_1:3862	-3862, -3515, -3362	upstream, upstream, upstream	1	1	1	22	34	40	1	4_A375_EGFR_1_1	40	Gene MIR193A	MIR0193, MIRN193A, MIR193A	microRNA 193a	NR_029710		
GeneID:10 31383	MIR365-2	17	29,902,430	29,902,540	110	+	1	1_A375_pfd7_mrna_lncRNA_R_1:2490	5376	downstream	1	0	0	20	14	8	1	1_A375_pfd7_mrna_lncRNA_R_1	20	Gene MIR365-2	MIR0365-2, MIR365-2	microRNA 365-2	NR_029558		
GeneID:55 255	RHOT1	17	30,489,472	30,552,748	63,276	+	2	1_A375_pfd7_mrna_lncRNA_R_1:2303, 2_A375_pfd7_dist_lncRNA_R_1:3553	-181, -181	upstream, upstream	1	1	0	20	23	11	1	2_A375_pfd4_dist_lncRNA_R_1	23	Gene RHOT1	FLJ10340, FLJ12833, MIRO-1, RHOT1, shmt1	mit. homolog gene (yeast)	NM_018337, NM_001033986, NM_001033966, NCT02869413.0, NCT02869412.0, NCT02869410.0, NCT02869414.0, NCT02904183.0, NCT02869416.0, NCT02869417.0, NCT02869418.0, NCT02869419.0, NCT02869420.0	2183221_at, 222145_s_at, 224364_at		NP_060777.3, NP_001028758.1, NP_001028740.1, NP_001028741.1, EAW48243.1, EAW48247.1, EAW48245.1, EAW48244.1, EAW48243.1, EAW48245.1, EAW48245.1, EAW48245.1, EAW48243.1
GeneID:16 2494	RHBDL2	17	30,595,165	30,651,860	56,695	+	2	1_A375_pfd4_mrna_lncRNA_R_1:2303, 2_A375_pfd37_dist_lncRNA_R_1:3356	9913, 9141	up gene, up gene	1	1	0	22	20	9	1	1_A375_pfd2_mrna_lncRNA_R_1	22	Gene RHBDL2	RHBD12, bA521I9.1, MGC119301, RHBD14, MGC119300, FLJ40502, VIPAC	rhomboid, veinlet-like 5 (Drosophila)	NM_133326, NCT02894220.0, NCT02894221.0, NCT02894222.0	1552265_at, 230755_at, 233222_at, 233409_at		NP_612351.1, EAW48241.1, EAW48239.1, EAW48240.1
GeneID:84 149	C17orf7 5	17	30,650,391	30,669,169	18,806	-	2	2_A375_pfd37_dist_lncRNA_R_1:3357, 4_A375_EGFR_1:3857	-16, 37	upstream, up gene	0	1	1	12	19	26	1	4_A375_EGFR_1_1	26	Gene C17orf75	NUMA1P1, C17orf75	chromosome 17 open reading frame 75	NM_022344, NCT18264.2	2053030_at		NP_071729.2, EAW60238.1
GeneID:89 3217	MIR632	17	30,877,125	30,877,221	96	+	2	2_A375_pfd37_dist_lncRNA_R_1:3357, 4_A375_EGFR_1:3857	-7823, -7976	upstream, upstream	0	1	1	12	19	26	1	4_A375_EGFR_1_1	26	Gene MIR632	MIR0632, bladder-mir-632, MIR632	microRNA 632	NR_030182			
GeneID:77 98	ZNF207	17	30,877,197	30,897,466	20,111	+	2	2_A375_pfd37_dist_lncRNA_R_1:3357, 4_A375_EGFR_1:3857	-7982, -8058	upstream, upstream	0	1	1	12	19	26	1	4_A375_EGFR_1_1	26	Gene ZNF207	ZNF207, DKFZp761H203	zinc finger protein 207	NM_001018057, NM_003457, NM_001032293, NCT18270.2, NCT18272.0, NCT18273.1, NCT02894324.0, NCT02894325.0, NCT02894326.0, NCT02894327.0, NCT02894328.0	1559833_s_at, 200926_s_at, 200926_s_at_203829_x_at, 226157_at, 231845_x_at, 236772_x_at, 239957_at		NP_001018057.1, NP_003448.3, EAW60232.1, EAW60234.1, EAW60236.1, EAW60231.1, EAW60233.1, EAW60237.1
GeneID:57 117	PSMD1 1	17	30,771,502	30,805,942	99,540	+	1	2_A375_pfd37_dist_lncRNA_R_1:3366	598	up gene	0	1	0	14	16	10	1	2_A375_pfd4_dist_lncRNA_R_1	16	Gene PSMD11	PSMD11, p44.5, MSS4944, 09, Rpn6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	NM_002815, NCT18263.2, NCT02894300.0	208778_s_at, 208777_s_at		NP_002802.2, EAW68229.1, EAW68230.1
GeneID:49 4162	ACCN1	17	31,349,103	32,493,625	1,143,730	-	7	1_A375_pfd4_mrna_lncRNA_R_1:2322, 1_A375_pfd37_mrna_lncRNA_R_1:3503, 1_A375_pfd37_mrna_lncRNA_R_1:3504, 2_A375_pfd37_dist_lncRNA_R_1:3359, 2_A375_pfd37_dist_lncRNA_R_1:3360, 2_A375_pfd37_dist_lncRNA_R_1:3361, 2_A375_pfd37_dist_lncRNA_R_1:3362, 4_A375_EGFR_1:3862	-1013088, -889470, -628497, -1083781, -1013088, -889080, -628495	up gene, up gene, up gene, up gene, up gene, up gene, up gene	1	1	0	23	26.5	6	4	1_A375_pfd3_mrna_lncRNA_R_1	6	Gene ACCN1	BNC1, ASIC2, BNaC1, MDH4C1, ACCN1, ASIC2a, MDEG	amiloride-sensitive cation channel 1, neuronal	NM_183377, NM_001094, NCT19283.0	206690_at		NP_899233.1, NP_001088.2, EAW62618.1
GeneID:49 3391	C17orf3 2	17	32,361,142	32,906,303	5,248	-	1	4_A375_EGFR_1:3863	-1844	upstream	0	0	1	7	8	24	1	4_A375_EGFR_1_1	24	Gene C17orf32	C17orf32, FLJ44015	chromosome 17 open reading frame 32	NM_207434			NP_997237.2
GeneID:12 4542	TMEM1 52E	17	32,907,786	32,996,337	88,389	+	1	4_A375_EGFR_1:3866	256	up gene	0	0	1	7	8	24	1	4_A375_EGFR_1_1	24	Gene TMEM132E	TMEM132E	transmembrane protein 132E	NM_207310	243708_at		NP_997196.1
GeneID:10 993	CCT6B	17	33,254,976	33,268,928	33,950	-	3	1_A375_pfd37_mrna_lncRNA_R_1:2306, 2_A375_pfd37_dist_lncRNA_R_1:3355, 4_A375_EGFR_1:3855	64, 60, 60	up gene, up gene, up gene	1	1	1	19	34	17	1	2_A375_pfd4_dist_lncRNA_R_1	34	Gene CCT6B	CCT2.2, TCP-1-beta2, TSHG3, CCT6B, CCT-zeta-2, Cctz2	chaperonin containing TCP1, subunit 6B (zeta 2)	NM_006584, NM_001193329, NM_001193330, NCT00439.2	206367_at		NP_006575.2, NP_001180458.1, NP_001180459.1, EAW62201.1
GeneID:91 600	ZNF830	17	33,266,549	33,290,305	1,656	-	3	1_A375_pfd37_mrna_lncRNA_R_1:2306, 2_A375_pfd37_dist_lncRNA_R_1:3355, 4_A375_EGFR_1:3855	-65, -101, -101	upstream, upstream, upstream	1	1	1	19	34	17	1	2_A375_pfd4_dist_lncRNA_R_1	34	Gene ZNF830	CCDC16, SEL10, MGC20336, CMSC41, ZNF830	zinc finger protein 830	NM_032537, NCT20469.2	226018_at, 238223_at		NP_443093.3, EAW60200.1
GeneID:11 7956	RFFL	17	33,336,131	33,416,294	80,163	-	1	1_A375_pfd37_mrna_lncRNA_R_1:2307	23842	up gene	1	0	0	16	13	8	1	1_A375_pfd3_mrna_lncRNA_R_1	16	Gene RFFL	RNF194L, FRING, RNF186, RFFL/Y-LIN, CeRF2, RFFL	ring finger and FYVE-like domain containing 1	NM_017178, NM_001017986	1553647_s_at, 1553651_a_at, 1568903_at, 1568971_at, 229892_at, 237919_at		NP_476519.1, NP_001017986.1
GeneID:38 92	RASD1 3	17	33,426,611	33,446,888	20,277	-	2	1_A375_pfd37_mrna_lncRNA_R_1:2308, 4_A375_EGFR_1:3811	280, 472	up gene, up gene	1	0	1	14	13	21	1	4_A375_EGFR_1_1	21	Gene RASD1/3	RASD1/3, Tc4, RSH/3, RASH1/3, HSTRA3, TRAD	RASD1 family, member 3 (S. cerevisiae)	NM_031412571, NM_002870, NM_133829	209663_s_at, 37793_r_at	NP_002089.3, NP_598332.1		NP_001129843.1, NP_002089.3, NP_598332.1
GeneID:54 752	FNDC8	17	33,446,851	33,457,791	10,939	+	2	1_A375_pfd37_mrna_lncRNA_R_1:2303, 4_A375_EGFR_1:3811	-1963, -2215	upstream, upstream	1	0	1	14	13	21	1	4_A375_EGFR_1_1	21	Gene FNDC8	FNDC8, DKFZp434D2215	fibronectin type III domain containing 8	NM_017559, NCT20455.2	225689_at		NP_060029.1, EAW65186.1
GeneID:54 475	NLE1	17	33,456,366	33,489,322	10,954	-	2	1_A375_pfd37_mrna_lncRNA_R_1:2309, 2_A375_pfd37_dist_lncRNA_R_1:3359	-22, 42	upstream, up gene	1	1	0	39	35	10	1	1_A375_pfd3_mrna_lncRNA_R_1	39	Gene NLE1	NLE1, Nle, FLJ14436	notchless homolog 1 (Drosophila)	NM_031014445, NM_018096, NCT20455.2, NCT20861312.0, NCT20861312.0	2035966_at, 203987_s_at		NP_001014445.1, NP_060566.2, EAW65185.1, EAW65186.1, EAW65187.1
GeneID:14 9882	UNC45B	17	33,474,836	33,516,364	41,529	+	2	1_A375_pfd37_mrna_lncRNA_R_1:2309, 2_A375_pfd37_dist_lncRNA_R_1:3358	-5492, -5536	upstream, upstream	1	1	0	39	35	10	1	1_A375_pfd3_mrna_lncRNA_R_1	39	Gene UNC45B	MGC119541, FLJ38910, SMUNC45, UNC45, MGC119560, UNC45B, CAN4a	unc-45 homolog B (C. elegans)	NM_173187, NM_001033576, NCT20793.1, NCT20861310.0, NCT20861311.0	2332261_at		NP_775459.1, NP_001026748.1, EAW65182.1, EAW65183.1, EAW65184.1
GeneID:18 2394	SLFN5	17	33,570,898	33,594,766	24,952	+	3	1_A375_pfd37_mrna_lncRNA_R_1:2305, 2_A375_pfd37_dist_lncRNA_R_1:3357, 4_A375_EGFR_1:3856	-938, -8,934	upstream, upstream, up gene	1	1	0	11.67	16	11	1	2_A375_pfd3_dist_lncRNA_R_1	11	Gene SLFN5	MGC130981, MGC130982, SLFN5, MGC19786	schlafen family member 5	NM_144775, NCT18443.3	1553553_s_at, 1553570_at, 235430_s_at, 242999_at	NP_659412.3, EAW68199.1	
GeneID:91 997	SLFN11	17	33,677,324	33,702,720	25,396	-	1	4_A375_EGFR_1:3861	-112	upstream	0	0	1	15	12	5	1	4_A375_EGFR_1_1	15	Gene SLFN11	SLFN11, FLJ39722, SLFN11	schlafen family member 11	NM_001104587, NM_001104588, NM_001104589, NM_152270, NCT22667122.2, NCT22818842.0, NCT22839931.0	1553553_s_at, 1553570_at, 235430_s_at, 242999_at	228745_at	NP_001098057.1, NP_001098058.1, NP_001098059.1, NP_689433.3, EAW68197.1, EAW68198.1
GeneID:14 8657	SLFN13	17	33,782,115	33,775,656	13,741	-	1	4_A375_EGFR_1:3862	400	up gene	0	0	1	8	9	17	1	4_A375_EGFR_1_1	17	Gene SLFN13	SLFN13, DKFZp686D06206, SLFN13, DKFZp686J196, FLJ27352	schlafen family member 13	NM_144682, NCT17744.5l, 2, NCT22866167.1, NCT22815209.0, NCT22839955.0	1553553_s_at, 1553570_at		NP_653283.2, EAW68130.1, EAW68150.1, EAW68151.1, EAW68152.1
GeneID:10 9369761	LOC1009 69761	17	33,899,127	33,901,322	2,195	+	1	1_A375_pfd37_mrna_lncRNA_R_1:3863	10629	downstream	0	0	1	16	19	20	1	4_A375_EGFR_1_1	20	Gene LOC100369761	hypothetical LOC100369761	XR_111869, XR_179493, XR_115083				
GeneID:89 2076	SNORD7 7	17	33,900,976	33,900,972	98	+	1	4_A375_EGFR_1:3863	4076	downstream	0	0	1	16	19	20	1	4_A375_EGFR_1_1	20	Gene SNORD7	snoRA47, SNORD7, Z30	small nucleolar RNA, C/D box 7	NR_002937			
GeneID:91 93	PEX12	17	33,901,814	33,903,656	1,842	-	1	1_A375_pfd37_mrna_lncRNA_R_1:3863	104	up gene	0	0	1	16	19	20	1	4_A375_EGFR_1_1	20	Gene PEX12	PEX12, PAF-5	peroxisomal biogenesis factor 12	NM_000286, NCT20861162.0	230094_at		NP_000277.1, EAW65142.1
GeneID:16 3	AP2B1	17	33,914,282	34,003,439	109,158	+	1	4_A375_EGFR_1:3863	-9730	upstream	0	0	1	16	19	20	1	4_A375_EGFR_1_1	20	Gene AP2B1	AP2-BETA, HP1BB, CLAPB1, ADTB1, DKFZp761H0742, AP2B1	adaptor-related protein complex 2, beta 1 subunit	NM_001282, NM_001030004, NCT21700444.0, NCT22709883.0, NCT22709882.0, NCT22709881.0, NCT22709880.0, NCT22709879.0, NCT22709878.0, NCT22709877.0, NCT22709876.0, NCT22709875.0, NCT22709874.0, NCT22709873.0, NCT22709872.0, NCT22709871.0, NCT22709870.0, NCT22709869.0	200612_s_at, 200613_s_at		NP_001272.1, NP_001020177.1, EAW65133.1, EAW65134.1, EAW65141.1, EAW65134.1, EAW65137.1, EAW65136.1, EAW65139.1, EAW65140.1, EAW65142.1
GeneID:91 955	RASL10B	17	34,036,679	34,070,540	11,861	+	2	1_A375_pfd37_mrna_lncRNA_R_1:2312, 2_A375_pfd37_dist_lncRNA_R_1:3369	12265, 12297	downstream, downstream	1	1	0	40	42	9	1	2_A375_pfd4_dist_lncRNA_R_1	42	Gene RASL10B	RASL10B, bA521I9.1, MGC119301, RIP/17, MGC43140	RAS-like, family 10, member B	NM_033315, NCT22705974.0	233408_at, 244696_at		NP_203572.1, EAW65132.1
GeneID:24 8176	GAS2L2	17	34,071,537	34,079,997	8,460	-	2	1_A375_pfd37_mrna_lncRNA_R_1:2312, 2_A375_pfd37_dist_lncRNA_R_1:3369	6953, 6921	downstream, downstream	1	1	0	40	42	9	1	2_A375_pfd4_dist_lncRNA_R_1	42	Gene GAS2L2	GAR17, GAS212	growth arrest-specific 2 like 2	NM_139255, NCT17676.1	1552296_at		NP_644614.1, EAW65131.1
GeneID:14 8930	C17orf58	17	34,087,918	34,092,896	4,982	+	1	4_A375_EGFR_1:3864	5878	downstream	0	0	1	8	11	15	1	4_A375_EGFR_1_1	15	Gene C17orf58	C17orf58	chromosome 17 open reading frame 58	NM_145272, NCT17744.2	237829_at		NP_660315.2, EAW65130.1
GeneID:79 148	MMP28	17	34,092,878	34,122,840	29,764	-	1	4_A375_EGFR_1:3864	28848	up gene	0	0	1	8	11	15	1	4_A375_EGFR_1_1	15	Gene MMP28	epilysin, MMP28, MMP28, EPILYSIN, MMP-28	matrix metallopeptidase 28	NM_024302, NM_001032378, NCT23861677.0, NCT23861680.0	219909_at, 222927_x_at, 224267_x_at, 239072_at, 239073_s_at		NP_077276.1, NP_001027449.1, EAW60126.1, EAW60126.1
GeneID:51 65	TNFS13	17	34,136,466	34,174,356	37,890	+	2	2_A375_pfd37_mrna_lncRNA_R_1:2313, 2_A375_pfd37_dist_lncRNA_R_1:3800	-232, -195	upstream, upstream	1	1	0	27	56	14	1	2_A375_pfd4_dist_lncRNA_R_1	56	Gene TNFS13	Tall1, TALL1, TALL-1, TALL1a, TNFSF13, TNFSF13a, TNFSF13b, zTNF4	TNF (ligand) superfamily, member 13	NM_003457, NM_172213, NCT22705783.0, NCT22705777.0, NCT22705763.0, NCT22705939.0	202562_at, 227864_at, 227281_s_at, 234165_at		NP_003796.1, NP_751951.1, EAW60124.1, EAW60125.1, EAW60126.1, EAW60127.1
GeneID:93 28	ZNRF3	17	34,642,475	34,651,992	9,518	+	3	1_A375_pfd37_mrna_lncRNA_R_1:2315, 2_A375_pfd37_dist_lncRNA_R_1:3802, 2_A375_pfd37_dist_lncRNA_R_1:3803	-715, -3401, -73	upstream, upstream, upstream	1	1	0	29	32.5	9.5	2	2_A375_pfd4_dist_lncRNA_R_1	9.5	Gene ZNRF3	FRP5, ZNRF3	zinc finger, RING finger 3	NM_032773, NCT19854.1, NCT21893.2, NCT23022.0, NCT23022.0	212544_at		NP_056764.1, EAW67554.1, EAW67553.1, EAW67555.1, EAW67553.1
GeneID:88 179	MYO1F	17	34,851,999	34,891,303	39,708	+	6	1_A375_pfd37_mrna_lncRNA_R_1:2315, 2_A375_pfd37_mrna_lncRNA_R_1:2316, 2_A375_pfd37_dist_lncRNA_R_1:3803, 2_A375_pfd37_dist_lncRNA_R_1:3804, 2_A375_pfd37_dist_lncRNA_R_1:3805, 2_A375_pfd37_dist_lncRNA_R_1:3806, 4_A375_EGFR_1:3815	48855, -10135, 48855, -7, -10011, -9143	downstream, upstream, downstream, downstream, upstream, upstream	1	1	1	28.28	23.78	19.75	4	2_A375_pfd4_dist_lncRNA_R_1	4	Gene MYO1F	MYOH01, FLJ22855, MYO1F	myosin IF	NM_001033593, NM_001167735, NM_031555, NCT19856.2, NCT19901981.1, NCT19901971.1, NCT20115040.0, NCT20115131.0, NCT22611522.0	213120_at, 225947_at, 236622_at		NP_001028921.1, NP_001157207.1, NP_076053.2, EAW67556.1, EAW67560.1, EAW67557.1, EAW67559.1, EAW67561.1
GeneID:28 4096	PIGW	17	34,891,493	34,899,160	7,747	+	4	1_A375_pfd37_mrna_lncRNA_R_1:2316, 2_A375_pfd37_dist_lncRNA_R_1:3804, 2_A375_pfd37_dist_lncRNA_R_1:3805, 2_A375_pfd37_dist_lncRNA_R_1:3806, 4_A375_EGFR_1:3815	10037, -91, 10210, 9043	downstream, upstream, downstream, downstream	1	1	1	16.33	13.67	10.33	3	1_A375_pfd3_dist_lncRNA_R_1	3	Gene PIGW	Ipw1, PIGW, PIG-W, FLJ27420	phosphatidylinositol glycan anchor biosynthesis, class W	NM_178157, NCT22709891.1, NCT22849547.0	1568292_s_at		NP_848927.3, EAW67564.1, EAW67563.1
GeneID:79 992	GGNBP2	17	34,900,707	34,946,276	45,341	+	4	1_A375_pfd37_mrna_lncRNA_R_1:2316, 2_A375_pfd37_dist_lncRNA_R_1:3804, 2_A375_pfd37_dist_lncRNA_R_1:3805, 2_A375_pfd37_dist_lncRNA_R_1:3806, 4_A375_EGFR_1:3815	700, -9425, 679, 339	up gene, upstream, up gene, upstream	1	1	1	16.33	13.67	10.33	3	1_A375_pfd3_dist_lncRNA_R_1	3	Gene GGNBP2	DIP12, ZFP403, GGNBP2, ICRG1, FLJ22581, DIP3, LDI1, ZNF403, FLJ42050, FLJ21200	gametogenetin binding protein 2	NM_024535, NCT22709894.0, NCT22709896.0	1554419_x_at, 219078_s_at, 220306_s_at, 233967_at		NP_079111.1, EAW67567.1, EAW67566.1
GeneID:79 154	DHRS11	17	34,948,228	34,957,355	9,127	+	1	4_A375_EGFR_1:3866	9962	downstream	0	0	1	23	17	24	1	4_A375_EGFR_1_1	24	Gene DHRS11	MGC4172, SDR4C41, MRPGD58, DHRS11, DHRS11	dehydrogenase/reductase (SDR family) member 11	NM_024305, NCT22907.0, NCT22907.0	219756_s_at		NP_077304.2, EAW67568.1, EAW67570.1
GeneID:79 922	MRM1	17	34,958,028	34,965,407	7,380	+	1	4_A375_EGFR_1:3866	162	up gene	0	0	1	23	17	24	1	4_A375_EGFR_1_1	24	Gene MRM1	MTM1, FLJ22376	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	NM_024384, NCT19820.1, NCT21271.3	219967_at		NP_079140.2, EAW67571.1, EAW67572.1
GeneID:51 78	HCA1	17	35,294,499	35,300,494	5,995	+	2	2_A375_pfd37_dist_lncRNA_R_1:3811, 4_A375_EGFR_1:3817	11849, 8053	downstream, downstream	0	1	1	10	16.5	15	2	2_A375_pfd3_dist_lncRNA_R_1	15	Gene LHX1	MGC126723, MGC126741, LIM1, LIM1, LHX1	LIM homeobox 1	NM_005568, NCT18824.3	206230_at		NP_005559.2, EAW67574.1
GeneID:28 574	AATF	17	35,306,975	35,314,371	107,396	+	2	2_A375_pfd37_dist_lncRNA_R_1:3811, 4_A375_EGFR_1:3817	-127, -3523	upstream, upstream	0	1	1	10	16.5	15	2	2_A375_pfd4_dist_lncRNA_R_1	15	Gene AATF	DED, CHE1, CHE-1, AATF,	apoptosis antagonizing transcription factor	NM_012138, NCT21387.4	200165_at		NP_036270.1, EAW67575.1
GeneID:51 9	ACACA	17	35,441,827	35,789,902	324,976	-	2	4_A375_EGFR_1:3816, 4_A375_EGFR_1:3819	59350, -458	up gene, upstream	0	0	1	11	11.5	19.5	2	4_A375_EGFR_1_1	21	Gene ACACA	ACC, ACAC, ACC1, ACACA, ACCA	acetyl-CoA carboxylase alpha	NM_198834, NM_198839, NM_198837, NM_198836, NM_198839	212189_at, 214389_at		NP_742131.1, NP_942133.1, NP_942134.1, NP_942135.1, NP_742136.1
GeneID:88 71	TADA2A	17	35,786,977	35,837,328	50,249	+	2	2_A375_pfd37_mrna_lncRNA_R_1:2319, 2_A375_pfd37_dist_lncRNA_R_1:3819	79615, 283	downstream, up gene	1	0	1	15	12.5	13	2	4_A375_EGFR_1_1	21	Gene TADA2A	TADA2A, ADA2, TADA2, FLJ12705, SUPF, ADA2A	transcriptional adaptor 2A	NM_139430, NM_001406, NM_001166105, NCT19853.3, NCT19901291.1, NCT22907272.0, NCT22907300.0, NCT23023221.0	2050026_at, 210307_s_at		NP_001388553.2, NP_001479.3, NP_001159977.1, EAW67567.1, EAW67568.1, EAW67569.1, EAW67570.1, EAW67591.1
GeneID:11 7956	DUSP14	17	35,845,931	35,873,900	28,037	+	1	1_A375_pfd37_mrna_lncRNA_R_1:2319	-6199	upstream	1	0	0	17	14	8	1	1_A375_pfd3_mrna_lncRNA_R_1	17	Gene DUSP14	MKP6, DUSP14, MKP-L	dual specificity phosphatase 14	NM_007026, NCT19823.3, NCT19901251.1	203267_at		NP_008957.1, EAW67593.1, EAW67592.1
GeneID:11 2778	SYNRG	17	35,874,900	35,999,468	94,568	+	1	2_A375_pfd37_dist_lncRNA_R_1:3812	55	up gene	0	1	0	11	17	8	1	2_A375_pfd4_dist_lncRNA_R_1	17	Gene SYNRG	MGC104589, SYNG, KIAA1287, SYNRG, FLJ39402	synergin, gamma	NM_007247, NM_080550, NM_199052, NM_001163844, NM_001163845, NM_001163846, NM_001163847, NCT19836.2, NCT19901241.1, NCT22903532.0, NCT22903533.0, NCT22903534.0	1553163_at, 222713_s_at, 222357_at, 232901_s_at		NP_009745.3, NP_542177.2, NP_942053.1, NP_001129216.1, NP_001157018.1, NP_001157019.1, EAW67594.1, EAW67595.1, EAW67597.1, EAW67596.1
GeneID:11 556	DDX52	17	35,972,413	35,993,467	21,074	-	2	2_A375_pfd37_dist_lncRNA_R_1:3812, 2_A375_pfd37_dist_lncRNA_R_1:3813	54531, 65	downstream, up gene	0	0	1	10	17.5	8	2	2_A375_pfd4_dist_lncRNA_R_1	8	Gene DDX52	ROK1, HUSSY-19, DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	NM_182300, NM_007010, NCT19336.3, NCT22905300.0, NCT22905322.0	1570115_at, 210220_s_at, 212234_at		NP_859152.2, NP_009141.2, EAW67599.1, EAW67600.1, EAW67601.1
GeneID:44 8435	GPR179	17	36,021,453	36,039,893	18,200	-	1	4_A375_EGFR_1:3813	-7937	upstream	0	0	1	10	21	14	1	4_A375_EGFR_1_1	21	Gene GPR179	GPR180L1, GPR179	G protein-coupled receptor 179	NM_001004334			NP_001004334.2
GeneID:33 637	SOCS7	17	36,935,005	36,936,019	46,014	+	1	2_A375_pfd37_dist_lncRNA_R_1:3815	-403	upstream	0	0	1	10	21	14	1	2_A375_pfd4_dist_lncRNA_R_1	21	Gene SOCS7	NCKAP4, SOCS7, NAP4	nucleocytoplasmic shuttling protein 2	NM_014998, NCT20037.2	214019_at, 226872_at		NP_938413.1, EAW69312.1
GeneID:83 725	SRCIN1	17	36,898,239	36,962,163	63,924	-	2	4_A375_EGFR_1:3821, 4_A375_EGFR_1:3822	1383, 791	up gene, up gene	0	0	1	7	7.5	17	2	4_A375_EGFR_1_1	16	Gene SRCIN1	SNIP, FNI0, SRCIN1, KIAA1854	SRC kinase signaling inhibitor 1	NM_020340, NCT22688.3	1553799_at, 232647_at, 236656_at		NP_376324.2, EAW69316.1
GeneID:10 9170041	C17orf68	17	36,927,956	36,931,167	3,211	-	1	2_A375_pfd37_dist_lncRNA_R_1:3816	287	up gene	0	0	1	10	17	8	1	2_A375_pfd4_dist_lncRNA_R_1	17	Gene C17orf68	C17orf68		NM_031330877			NP_001124149.1
GeneID:79 03	PCGF2	17	36,950,150	36,954,356	14,206	-	4	1_A375_pfd4_mrna_lncRNA_R_1:2320, 2_A375_pfd37_dist_lncRNA_R_1:3817, 2_A375_pfd37_dist_lncRNA_R_1:3824, 4_A375_EGFR_1:3824	-4286, -4286, -1486, -3561	upstream, upstream, upstream, upstream	1	1	1	35	31.5	19.5	2	1_A375_pfd4_mrna_lncRNA_R_1	53	Gene PCGF2	RNF110, MEL-18, MGC10345, PCGF2, ZNF144	polycomb group ring finger 2	NM_007144, NCT01960081.1, NCT22876.2, NCT22869950.0, NCT23039950.0	203762_x_at, 203791_x_at, 213351_x_at, 214239_x_at, 240762_at	NP_009175.1, EAW69327.1, EAW69328.1, EAW69329.1, EAW69330.1	



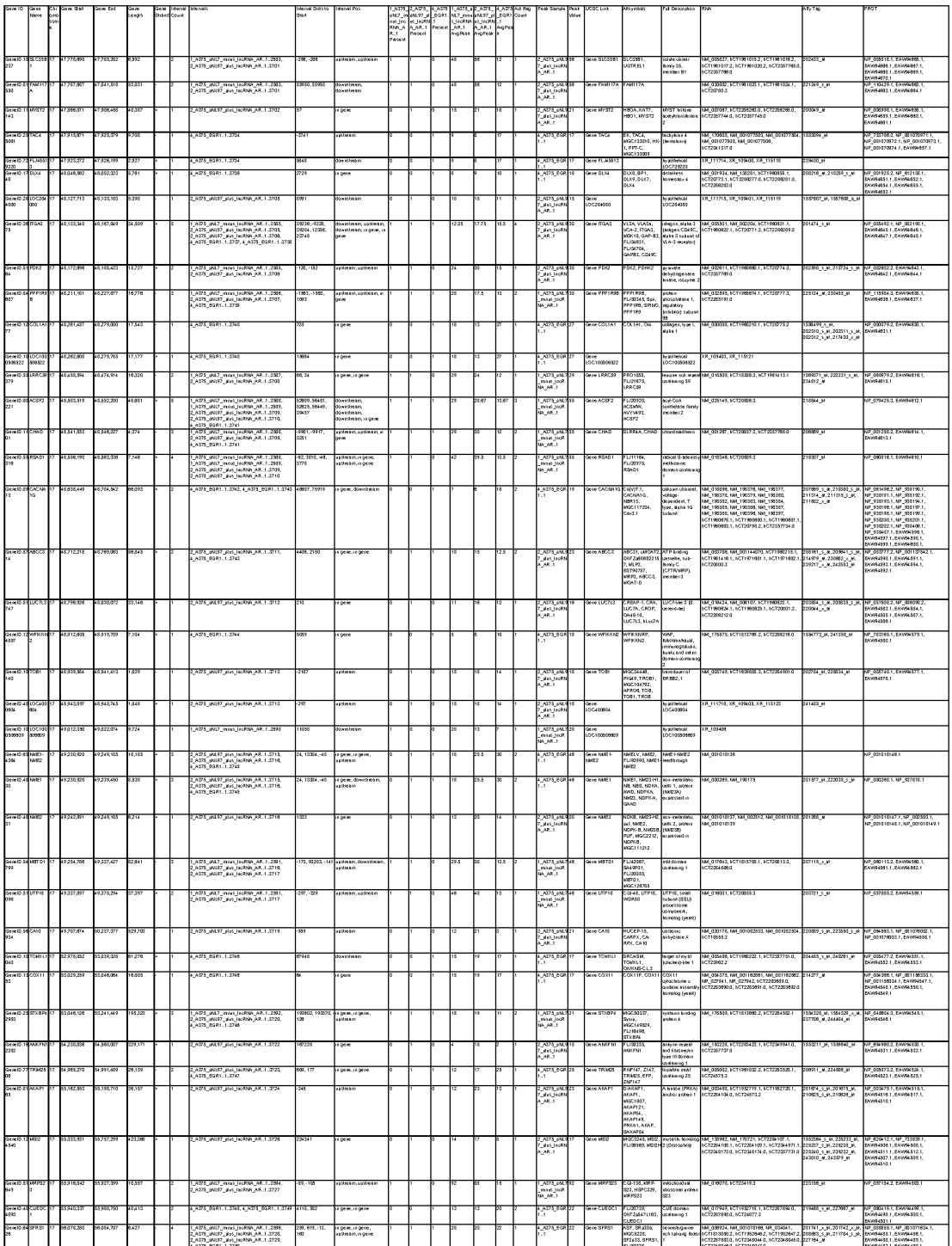
Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Exon Count	Intervals	Intervall Distnce	Intervall Pos	1_A375_2_A375_uNG7_myUG7_pl_ncRNA_R_1 Percent	2_A375_uNG7_pl_EGR1_1 Percent	3_A375_NG7_myUG7_pl_ncRNA_R_1 Avg Peak	4_A375_pl_EGR1_ncRNA_R_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
GeneID:3691	PSMB3	17	38,959,002	38,970,476	11,476	+	4	1_A375_uNG7_mrvol_lncRNA_AR_1..2320, 2_A375_uNG7_plvol_lncRNA_AR_1..2817, 3_A375_EGR1_1..3625, 4_A375_EGR1_1..3624	-188, -135, -2936, -660	upstream, upstream, upstream, upstream	1	1	1	35	51.5	19.5	2	1_A375_uNG7_mrvol_lncRNA_AR_1	53	Gene PSMB3	WGC1477, PSMB3, HC10-II	proteasome (prosome, macropain) subunit, beta type, 3	NM_002795, XR_002777.3	5314400_at	NP_002786.2, EAW65331.1
GeneID:55	PIP4K2B	17	35,921,944	35,956,156	34,214	-	5	1_A375_uNG7_mrvol_lncRNA_AR_1..2321, 2_A375_uNG7_plvol_lncRNA_AR_1..2322, 3_A375_uNG7_plvol_lncRNA_AR_1..3616	662, -152, 630	up gene, upstream, up gene	1	1	0	20	20.5	11	2	2_A375_uNG7_plvol_lncRNA_AR_1	23	Gene PIP4K2B	PIP5K1beta, PIP5K2B, PIP5K2, PIP5K2B, PIP5K3, PIP5K-III	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	NM_003559, XR_001592462, XR_001592464.0, XR_001592465.0, XR_001592466.0, XR_001592467.0	1553247_at, 1553248_a_at, 2010802_at, 2010811_s_at	NP_003550.1, EAW65538.1, EAW65532.1, EAW65533.1, EAW65534.1, EAW65536.1
GeneID:84	CWC23	17	35,937,448	35,981,889	44,143	-	8	1_A375_uNG7_mrvol_lncRNA_AR_1..2321, 1_A375_uNG7_mrvol_lncRNA_AR_1..2322, 1_A375_uNG7_mrvol_lncRNA_AR_1..2323, 2_A375_uNG7_plvol_lncRNA_AR_1..3616, 2_A375_uNG7_plvol_lncRNA_AR_1..3619, 4_A375_EGR1_1..3625	29293, 29289, 21, 21, -11	downstream, downstream, up gene, downstream, up gene, upstream	1	1	1	22.33	23	13.67	3	2_A375_uNG7_plvol_lncRNA_AR_1	78	Gene CWC23	CWC23, CCDC49, FLJ20291, DKFZp779M0982	CWC23 spliceosome-associated protein homolog (S. cerevisiae)	NM_197748, XR_039868.2	2160683_s_at, 2227068_at	NP_060718.1, EAW65537.1
GeneID:3382	C17orf49	17	36,991,341	36,997,842	6,501	-	3	1_A375_uNG7_mrvol_lncRNA_AR_1..2323, 2_A375_uNG7_plvol_lncRNA_AR_1..2619, 4_A375_EGR1_1..3625	16674, 16674, 16642	downstream, downstream, downstream	1	1	1	27	26	19	1	2_A375_uNG7_plvol_lncRNA_AR_1	26	Gene C17orf66	C17orf66		NM_031030.3,	2442316_at	NP_301073934.1
GeneID:93	RPL23	17	37,906,321	37,910,053	3,732	-	2	2_A375_uNG7_plvol_lncRNA_AR_1..3630, 4_A375_EGR1_1..3626	-99, -408	upstream, up gene	0	1	1	20	24	14	1	2_A375_uNG7_plvol_lncRNA_AR_1	24	Gene RPL23	MGC72005, RPL23, MGC111167, MGC117349, L23, WLT1	ribosomal protein L23	NM_000978, NCT02326608.0, NCT02326609.0, NCT02326610.0	2000955_s_at, 2118224_at	NP_000969.1, EAW65539.1, EAW65540.1, EAW65542.1
GeneID:81	SNORA21	17	37,909,148	37,909,348	152	-	2	2_A375_uNG7_plvol_lncRNA_AR_1..3630, 4_A375_EGR1_1..3626	-696, -400	upstream, upstream	0	1	1	20	24	14	1	2_A375_uNG7_plvol_lncRNA_AR_1	24	Gene SNORA21	SNORA21, ACA21	small nucleolar RNA, H/ACA box 21	NR_002976		
GeneID:59	LASP1	17	37,926,112	37,970,023	51,911	+	3	2_A375_uNG7_plvol_lncRNA_AR_1..3621, 4_A375_EGR1_1..3627, 4_A375_EGR1_1..3626	182, -182, 3024	up gene, upstream, up gene	0	1	1	11.5	12.5	16.5	2	2_A375_uNG7_plvol_lncRNA_AR_1	16	Gene LASP1	Lasp-1, MLN50, LASP1	LIM and SH3 protein 1	NM_006148, NCT02297911, NCT02299868.0, NCT02299869.0	2009816_at	NP_006139.1, EAW65544.1, EAW65543.1, EAW65545.1
GeneID:54	FLJ43827	17	37,998,189	37,999,488	23,299	+	1	4_A375_EGR1_1..3629	37689	downstream	0	0	1	13	16	22	1	4_A375_EGR1_1	22	Gene FLJ43827	MGC133193	FLJ43827 protein	NR_033738		
GeneID:1013	LOC100131347	17	37,213,272	37,237,704	24,432	+	1	4_A375_EGR1_1..3629	-24	upstream	0	0	1	13	16	22	1	4_A375_EGR1_1	22	Gene LOC100131347	FLJ27156, FLJ42226	RAS2 viral-1 pseudogene	NR_038551		
GeneID:125	PLXDC1	17	37,219,556	37,237,902	56,346	-	5	1_A375_uNG7_mrvol_lncRNA_AR_1..2325, 1_A375_uNG7_plvol_lncRNA_AR_1..3622, 1_A375_uNG7_plvol_lncRNA_AR_1..3630, 4_A375_EGR1_1..3631	-3914, -2799, 54654, -2146, -1, 2854	upstream, upstream, downstream, upstream, upstream	1	1	1	14.67	17.33	21	3	4_A375_EGR1_1	22	Gene PLXDC1	FLJ39270, TEM7, DKFZp686P09227, FLJ45822, TEM7, PLXDC1	plexin domain containing 1	NM_020405, NCT02295312, NCT02295651.0, NCT02295652.0	2140891_at, 2197992_at, 2140892_s_at	NP_065138.2, EAW65533.1, EAW65531.1, EAW65532.1
GeneID:3780	ARL5C	17	37,313,147	37,322,414	9,267	-	4	1_A375_uNG7_mrvol_lncRNA_AR_1..2325, 2_A375_uNG7_plvol_lncRNA_AR_1..3622, 2_A375_uNG7_plvol_lncRNA_AR_1..3630, 4_A375_EGR1_1..3631	11555, 11726, 12566, 11676	downstream, downstream, downstream, downstream	1	1	1	15.5	17	20.5	2	4_A375_EGR1_1	21	Gene ARL5C	FLJ37145, ARL12, ARL5C	ADP-ribosylation factor-like 5C	NM_031143966		NP_001137440.1
GeneID:81	RPL19	17	37,356,536	37,360,960	4,444	+	1	4_A375_EGR1_1..3632	9672	downstream	0	0	1	9	11	24	1	4_A375_EGR1_1	24	Gene RPL19	RPL19, FLJ37452, L19, MGC71997, DKFZp779G0216	ribosomal protein L19	NM_000981, NCT01937743.1, NCT01964468.1, NCT02861.2, NCT02294894.0	2000029_at	NP_000972.1, EAW65596.1, EAW65597.1, EAW65598.1
GeneID:54	STAC2	17	37,366,769	37,382,940	16,251	-	1	4_A375_EGR1_1..3632	15532	downstream	0	0	1	9	11	24	1	4_A375_EGR1_1	24	Gene STAC2	DKFZP547C2, SH3, MGC129994, STAC2	SH3 and cysteine rich domains 2	NM_198993, NCT02295912, NCT02295951.0	2295668_at	NP_945344.1, EAW65569.1, EAW65570.1
GeneID:84	FBXL20	17	37,456,897	37,537,909	149,012	-	1	1_A375_uNG7_mrvol_lncRNA_AR_1..2326	576	up gene	1	0	0	15	14	13	1	1_A375_uNG7_mrvol_lncRNA_AR_1	15	Gene FBXL20	FLJ21627, SCRAP1ER, FBG, MGC16402.01, SCR, DKFZp564O239, FBXL20, Fbl20	F-box and leucine-rich repeat protein 20	NM_001164936, NM_033573, NCT01133441.1, NCT02459930.0	2336809_at, 2336223_s_at, 2339224_at	NP_001171938.1, NP_116264.2, EAW65573.1, EAW65574.1
GeneID:54	MED31	17	37,560,336	37,607,327	46,989	-	1	1_A375_uNG7_mrvol_lncRNA_AR_1..2326	50166	downstream	1	0	0	15	14	13	1	1_A375_uNG7_mrvol_lncRNA_AR_1	13	Gene MED31	SRP120, TRIP2, PPARBP, PBP, SRAP120, PPARGBP, MGC71480, TRAP220, RB18A, MED31, CASP2030, CASP1	mediator complex subunit 31	NM_053774, NCT01960875.1	2024496_s_at, 2024497_at, 2234622_at, 2234496_at	NP_056765.2, EAW65575.1
GeneID:81	NEURD2	17	37,660,021	37,784,175	4,154	-	1	4_A375_EGR1_1..3633	1775	up gene	0	0	1	8	8	16	1	4_A375_EGR1_1	16	Gene NEUROD2	NEUROD2, MGC29539, bHLHb1, NDRF	neuroprotective differentiation 2	NM_006160, NCT01641048.3	1552653_a_at, 2102211_at	NP_006151.2, EAW65579.1
GeneID:54	PPP1R13B	17	37,703,179	37,792,876	9,699	+	2	2_A375_uNG7_plvol_lncRNA_AR_1..3624, 4_A375_EGR1_1..3634	-5447, 10325	upstream, downstream	0	1	1	12.5	16	22	2	4_A375_EGR1_1	22	Gene PPP1R13B	DKFZP-32, DKFP122, PPP1R13, FLJ20940	protein phosphatase 1, regulatory (inhibitor) subunit 13B	NM_022192, NM_181813, NCT1932732.1, NCT1933733.1, NCT2118833.3, NCT2533977.0	2231969_at	NP_115588.2, NP_852606.1, EAW65600.1, EAW65601.1, EAW65602.1, EAW65603.1
GeneID:1015	STARD3	17	37,795,533	37,820,454	27,121	+	5	4_A375_EGR1_1..3634, 4_A375_EGR1_1..3635, 4_A375_EGR1_1..3636	171, 32667, 54899	up gene, downstream, downstream	0	0	1	10	8.67	26.67	3	4_A375_EGR1_1	26	Gene STARD3	CAB1, FLJ41275, MLN64, MLN64, STARD3	START-related lipid transfer (START) domain containing 3	NM_206944, NM_001165937, NM_001165938, NCT1171.2, NCT2294810.0	2352991_at	NP_008775.5, NP_001159049.1, NP_001159051.1, EAW65604.1, EAW65605.1
GeneID:837	TCAP	17	37,821,999	37,822,907	1,208	+	2	4_A375_EGR1_1..3635, 4_A375_EGR1_1..3636	4721, 6433	downstream, downstream	0	0	1	6.5	7.5	19	2	4_A375_EGR1_1	21	Gene TCAP	TCAP, TELCAP, TCAP_Telo	titin-cap (telethonin)	NM_003673, NCT1217761.7, NCT2294812.0	2057699_at	NP_003994.1, EAW65607.1, EAW65608.1
GeneID:54	PNMT	17	37,824,307	37,826,726	2,221	+	3	4_A375_EGR1_1..3635, 4_A375_EGR1_1..3636, 4_A375_EGR1_1..3637	1813, 3525, 9637	up gene, downstream, downstream	0	0	1	6	7.67	19.33	3	4_A375_EGR1_1	21	Gene PNMT	PENT, MGC34370, PNMT-like, PNMT	phenylethanolamine N-methyltransferase	NM_002686, NCT2117772	2067673_s_at	NP_002677.1, EAW65588.1
GeneID:89	PGAP3	17	37,827,373	37,844,310	16,938	-	3	4_A375_EGR1_1..3635, 4_A375_EGR1_1..3636, 4_A375_EGR1_1..3637	17990, 16276, 10186	downstream, up gene, up gene	0	0	1	6	7.67	19.33	3	4_A375_EGR1_1	21	Gene PGAP3	Kiaa1624, PERLD1, PGAP3, PP1486, CAB2, PERT, MGC9753	post-GPI attachment to proteins 3	NM_033419, NCT1933738.1, NCT1933737.1, NCT1933738.1, NCT2118733.1, NCT2533917.0, NCT2533918.0	2231611_at, 33618_at	NP_219487.3, EAW65591.1, EAW65593.1, EAW65592.1, EAW65594.1, EAW65595.1
GeneID:2064	ERBB2	17	37,844,393	37,884,915	40,522	+	2	2_A375_uNG7_plvol_lncRNA_AR_1..3623, 4_A375_EGR1_1..3638	42293, 42295	downstream, downstream	0	1	1	13	16	16	1	2_A375_uNG7_plvol_lncRNA_AR_1	16	Gene ERBB2	HER-2, ERBB2, NGL, MLN19, MGL, TKR1, HER2, Erbv, CD340, HER2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	NM_004448, NM_001003892, NCT1932421.2, NCT2294517.0, NCT2294518.0	2100832_s_at, 2116839_s_at, 2344394_x_at	NP_004439.2, NP_001005862.1, EAW65596.1, EAW65597.1
GeneID:2353	C17orf37	17	37,883,489	37,886,768	3,279	-	2	2_A375_uNG7_plvol_lncRNA_AR_1..3623, 4_A375_EGR1_1..3638	100, 132	up gene, up gene	0	1	1	13	16	16	1	2_A375_uNG7_plvol_lncRNA_AR_1	16	Gene C17orf37	C17orf37, CGI5, HTPA, OPB2, MGC14432, RGD1	chromosome 17 open reading frame 37	NM_032339, NCT1933738.1, NCT2118582.0	2344477_s_at	NP_115715.3, EAW65599.1, EAW65598.1
GeneID:2353	GRB7	17	37,894,167	37,905,556	11,511	+	6	1_A375_uNG7_mrvol_lncRNA_AR_1..2328, 2_A375_uNG7_plvol_lncRNA_AR_1..3623, 2_A375_uNG7_plvol_lncRNA_AR_1..3626, 4_A375_EGR1_1..3639, 4_A375_EGR1_1..3640	16151, -7499, 16541, -7320, 6969, 16757	downstream, upstream, downstream, upstream, up gene, downstream	1	1	1	12.67	17	18	3	2_A375_uNG7_plvol_lncRNA_AR_1	27	Gene GRB7	GRB7		NM_005310, NM_001030002, NCT2117762.2, NCT2294522.0	2107821_s_at	NP_005301.2, NP_001029173.1, EAW65600.1, EAW65601.1
GeneID:2236	IK2F3	17	37,921,195	38,020,441	99,245	-	1	4_A375_EGR1_1..3640	109497	downstream	0	0	1	22	27	18	1	4_A375_EGR1_1	27	Gene IK2F3	IKZF3, ZNFN1A2, AIO, AIOLOS	IKAROS family zinc finger 3 (Aiolos)	NM_012481, NM_183228, NM_183229, NM_183230, NM_183231, NM_183232, NCT2117612.2, NCT2294570.1, NCT2294572.1, NCT2294573.1, NCT2533916.0, NCT2533919.0	2210952_at	NP_036913.2, NP_899351.1, NP_899352.1, NP_899353.1, NP_899354.1, NP_899355.1, EAW65604.1, EAW65605.1, EAW65606.1, EAW65607.1, EAW65608.1, EAW65609.1
GeneID:5580	GSDMB	17	38,060,543	38,074,903	14,361	-	1	2_A375_uNG7_plvol_lncRNA_AR_1..3627	-6921	upstream	0	1	0	14	20	12	1	2_A375_uNG7_plvol_lncRNA_AR_1	20	Gene GSDMB	GSDMB, GSDML, PRO1852, PRO3321	gasdermin B	NM_031047.1, NM_018530, NM_001318856, NM_001318939, NCT1933739.1, NCT2117692.2, NCT2294549.0, NCT2533921.0	2139859_at, 2139233_s_at	NP_001035.2, NP_061000.2, NP_001159630.1, NP_001159631.1, EAW65611.1, EAW65612.1, EAW65613.1, EAW65614.1, EAW65615.1
GeneID:1031	ORMDL3	17	38,077,296	38,093,884	16,589	-	1	2_A375_uNG7_plvol_lncRNA_AR_1..3627	50	up gene	0	1	0	14	20	12	1	2_A375_uNG7_plvol_lncRNA_AR_1	20	Gene ORMDL3	ORMDL3		NM_139280, NCT2117662.2, NCT2295461.0, NCT2295465.0, NCT2535619.0, NCT2535630.0	2232259_at, 233156_at, 2240701_at	NP_644681.1, EAW65619.1, EAW65617.1, EAW65618.1, EAW65620.1
GeneID:2146	GSDMA	17	38,119,226	38,134,019	14,793	-	3	1_A375_uNG7_mrvol_lncRNA_AR_1..2329, 2_A375_uNG7_plvol_lncRNA_AR_1..3626, 4_A375_EGR1_1..3641	17762, 17788, 590	downstream, downstream, up gene	1	1	1	44.3	48	13.5	2	2_A375_uNG7_plvol_lncRNA_AR_1	53	Gene GSDMA	GSDMA, FLJ39120, GSDM1, FKSG5, GSDM, MGC13998	gasdermin A	NM_178171, NCT1927649.4		NP_835483.2, EAW65624.1
GeneID:5371	PSMD3	17	38,137,060	38,154,212	17,152	+	2	2_A375_uNG7_plvol_lncRNA_AR_1..2329, 2_A375_uNG7_plvol_lncRNA_AR_1..3628	-52, -66	upstream, upstream	1	1	0	63	65	11	1	2_A375_uNG7_plvol_lncRNA_AR_1	55	Gene PSMD3	SIN, P58, TSTA2, PSMD2, RPN3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	NM_002809, NCT2117792	2013368_at	NP_002800.2, EAW65625.1
GeneID:1435	CSF3	17	38,171,814	38,174,998	3,185	+	1	4_A375_EGR1_1..3642	-4208	upstream	0	0	1	4	8	15	1	4_A375_EGR1_1	15	Gene CSF3	C17orf33, CSF3OS, CSF3, MGC14707, CSF, G-CSF	colony stimulating factor 3 (granulocyte)	NM_000759, NM_001178147, NM_172219, NM_172220, NR_033992, NCT1933731.1, NCT2118802.2, NCT2533922.0	2027442_at	NP_000750.1, NP_001170618.1, NP_757373.1, NP_757374.2, NP_001159626.1, EAW65627.1, EAW65628.1
GeneID:9846	MED24	17	38,175,330	38,210,889	35,559	-	3	1_A375_uNG7_mrvol_lncRNA_AR_1..2330, 2_A375_uNG7_plvol_lncRNA_AR_1..3629, 4_A375_EGR1_1..3642	-5899, -5831, 43481	upstream, upstream, downstream	1	1	1	12.5	13.5	15	2	2_A375_uNG7_plvol_lncRNA_AR_1	23	Gene MED24	THRAP4, DRIP130, MED24, CASP1050, RTA-AP100, nuvA0100, ARC100, MGC9745, TRAP100, CASP4	mediator complex subunit 24	NM_015775618, NM_014815, NCT1933734.1, NCT2118642.2, NCT2294544.0	2130453_s_at, 213537_at	NP_001072968.1, NP_056830.2, EAW65629.1, EAW65630.1, EAW65631.1
GeneID:7067	THRA	17	38,215,448	38,250,120	34,674	+	4	1_A375_uNG7_mrvol_lncRNA_AR_1..2330, 1_A375_uNG7_mrvol_lncRNA_AR_1..2331, 2_A375_uNG7_plvol_lncRNA_AR_1..3629, 4_A375_EGR1_1..3643	1062, 36290, 1074, 10114	up gene, downstream, up gene, up gene	1	1	1	17	17	14.67	3	2_A375_uNG7_plvol_lncRNA_AR_1	25	Gene THRA	EAR7, THRA1, THRA, c-ERBA-1, ERBA-1, ERBA, EAR7, MGC22240, MGC000281, ERBA1, THRA, NR1A1	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	NM_001190916, NM_001190919, NM_003250, NM_199334, NCT1797977.1, NCT2294531.0, NCT2294532.0	1316_at, 204160_at, 204825_at, 35548_at	NP_001177847.1, NP_001177848.1, NP_003224.2, NP_953586.1, EAW65632.1, EAW65633.1, EAW65634.1
GeneID:80	NR1D1	17	38,249,037	38,256,973	7,938	-	1	1_A375_uNG7_mrvol_lncRNA_AR_1..2321	237	up gene	1	0	0	21	14	11	1	1_A375_uNG7_mrvol_lncRNA_AR_1	21	Gene NR1D1	THRA1, EAR1, THRA, hRev, rev-1, NR1D1	nuclear receptor subfamily 1, group D, member	NM_021724, NCT1651981.2		NP_068370.1, EAW65636.1
GeneID:33	MSL1	17	38,276,760	38,293,942	14,252	+	1	2_A375_uNG7_plvol_lncRNA_AR_1..3630	1062	up gene	0	1	0	15	16	14	1	2_A375_uNG7_plvol_lncRNA_AR_1	16	Gene MSL1	MSL1, MGC141881, MGC141883, DKFZp686J1721	male-specific lethal 1 homolog, (Drosophila)	NM_031012241	2127808_at, 2242565_at, 2330153_s_at	NP_001012241.1
GeneID:58	RARA	17	38,465,423	38,513,893	48,472	+	2	2_A375_uNG7_mrvol_lncRNA_AR_1..2332, 2_A375_uNG7_plvol_lncRNA_AR_1..3631	9861, 9617	up gene, up gene	1	1	0	16	19	11	1	2_A375_uNG7_plvol_lncRNA_AR_1	19	Gene RARA	NR1B1, RAR, RARA	retinoic acid receptor, alpha	NM_000964, NM_001024809, NM_001145831, NM_001145832, NCT2294541.1, NCT2294542.1, NCT2294543.1, NCT2294544.1, NCT2294545.1, NCT2294546.0, NCT2534539.0	1565256_at, 202745_s_at, 2037950_s_at, 213953_x_at	NP_000955.1, NP_001019993.1, NP_001139270.1, NP_001139274.1, EAW65652.1, EAW65650.1, EAW65654.1, EAW65655.1, EAW65656.1, EAW65657.1
GeneID:7167	TOP2A	17	38,544,775	38,574,302	29,429	-	2	1_A375_uNG7_mrvol_lncRNA_AR_1..2333, 2_A375_uNG7_plvol_lncRNA_AR_1..3632	-76, 55	upstream, up gene	1	1	0	20	25	10	1	2_A375_uNG7_plvol_lncRNA_AR_1	25	Gene TOP2A	TOP2, TOP2A, TP2A	topoisomerase (DNA) II alpha 170kDa	NM_001067, NCT1936697.1, NCT2294547.0, NCT2294549.0	2201291_s_at, 201292_at, 2274851_at	NP_001153.2, EAW65663.1, EAW65661.1, EAW65662.1
GeneID:8467	SMARCE1	17	38,703,972	38,804,103	20,131	-	1	2_A375_uNG7_plvol_lncRNA_AR_1..3633	-313	upstream	0	1	0	11	15	14	1	2_A375_uNG7_plvol_lncRNA_AR_1	15	Gene SMARCE1	BAF57, SMARCE1, FLJ39448	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	NM_003079, NCT2292319.0, NCT2292320.0	211958_at, 211959_at, 229311_at	NP_003070.3, EAW65670.1, EAW65671.1
GeneID:1211	KRT222	17	38,811,872	38,821,416	9,544	-	1	2_A375_uNG7_plvol_lncRNA_AR_1..3633	17600	downstream	0	0	1	11	15	14	1	2_A375_uNG7_plvol_lncRNA_AR_1	15	Gene KRT222	KA21, KRT222P, MGC45382, KRT222	keratin 222	NM_152349, NCT1965247.3, NCT2535139.0	243968_at, 244111_at	NP_689362.1, EAW65672.1, EAW65673.1
GeneID:3886	KRTAP4-5	17	38,853,253	38,854,375	1,122	-	1	2_A375_uNG7_plvol_lncRNA_AR_1..3634	-337	upstream	0	1	0	8	10	8	1	2_A375_uNG7_plvol_lncRNA_AR_1	13	Gene KRTAP4-5	KRTAP4.5, KAP4.5, KRTAP4-5	keratin associated protein 4-5	NM_031960		NP_1141661
GeneID:8369	KRTAP4-9	17	38,861,841	38,862,740	1,899	+	1	4_A375_EGR1_1..3634	-6729	upstream	0	1	0	8	8.5	8	1	4_A375_EGR1_1	13	Gene KRTAP4-9	KRTAP4.9, KAP4.9	keratin associated protein 4-9	NM_033148641		NP_0011396121
GeneID:8371	KRTAP4-11	17	38,895,691	38,896,709	1,018	+	1	4_A375_EGR1_1..3637	-9117	upstream	0	0	1	5	8	16	1	4_A375_EGR1_1	16	Gene KRTAP4-11	KRTAP4.11, KAP4.11, KRTAP4-11, KAP4.13, KRTAP4.13	keratin associated protein 4-11	NM_033119989, XM_003116707, XM_017001152	2348653_at	NP_003107977.1, XP_003116755.1, XP_16723.4
GeneID:8359	KRTAP4-5	17	38,905,178	38,906,054	876	-	1	4_A375_EGR1_1..3637	196	up gene	0	1	1	5	8	16	1	4_A375_EGR1_1	16	Gene KRTAP4-5	KAP4.3, KRTAP4-5, KRTAP4.3	keratin associated protein 4-5	NM_033160, NCT1960944.2	2348637_at	NP_149443.2, EAW65711.1

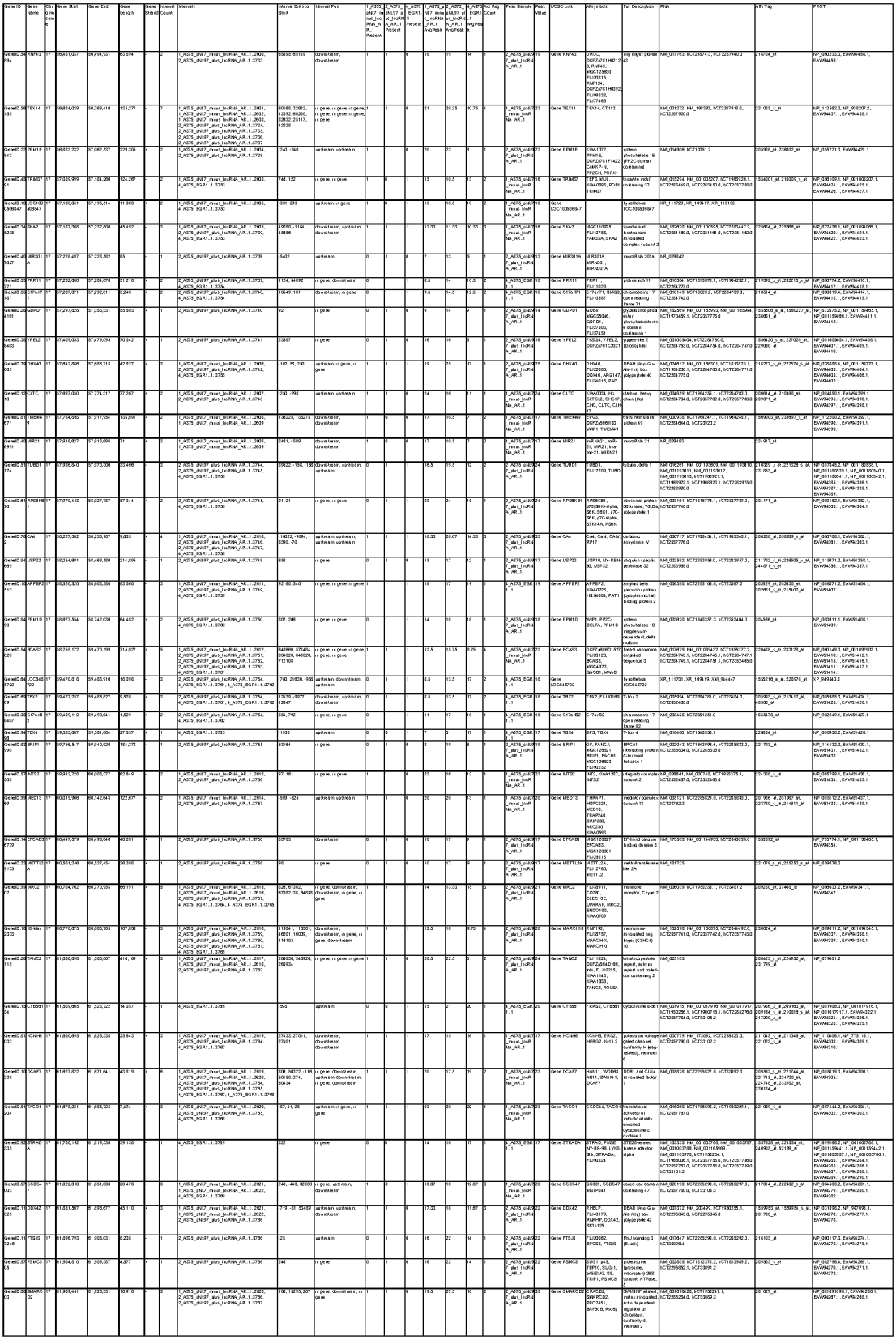
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:84616	KRTAP4-4	17	39,315,905	39,316,983	1,078	-	1	4_A375_EGR1..1..3647	11127	downstream	0	0	1	5	8	16	1	4_A375_EGR1..1	16	Gene KRTAP4-4	KRTAP4-4, KRTAP4.13, KAP4.13, KRTAP4.4, KAP4.4, KRTAP4-13	keratin associated protein 4-4	NM_032524, hCT1971463.0	234684_s_at	NP_115913.1, EAW60712.1
GeneID:3881	KRT31	17	39,549,976	39,553,844	3,868	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2534, 2_A375_pNL97_plus_lncRNA_AR..1..3635	-6540, -6478	upstream, upstream	1	1	0	16	24	8	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene KRT31	KRT31, KRTHA1, MGC138630, HA1, hHa1, Ha-1	keratin 31	NM_002277, hCT32841.1	206677_at	NP_002268.2, EAW60730.1
GeneID:100505782	LOC100505782	17	39,556,668	39,566,840	10,172	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2534, 2_A375_pNL97_plus_lncRNA_AR..1..3635	1716, 1652	in gene, in gene	1	1	0	16	24	8	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LOC100505782		hypothetical LOC100505782	XR_111690, XR_109383, XR_115101, XR_108273		
GeneID:3868	KRT16	17	39,766,030	39,769,079	3,049	-	1	4_A375_EGR1..1..3646	-1449	upstream	0	0	1	8	10	24	1	4_A375_EGR1..1	24	Gene KRT16	CK16, K1CP, K16, KRT16, NEPPK, KRT16A, FNEPPK	keratin 16	NM_005557, hCT2292256.0	209800_at	NP_005548.2, EAW60749.1
GeneID:3872	KRT17	17	39,775,692	39,780,882	5,190	-	1	4_A375_EGR1..1..3646	10354	downstream	0	0	1	8	10	24	1	4_A375_EGR1..1	24	Gene KRT17	PC2, PC, PCHC1, K17, KRT17	keratin 17	NM_000422, hCT1961149.1, hCT2292248.0, hCT2292249.0, hCT2353604.0	205157_s_at, 212236_x_at	NP_000413.1, EAW60750.1, EAW60751.1, EAW60752.1, EAW60753.1
GeneID:10209	EIF1	17	39,845,127	39,847,898	2,771	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2536, 2_A375_pNL97_plus_lncRNA_AR..1..3637, 4_A375_EGR1..1..3652	-9799, -9703, 25	upstream, upstream, in gene	1	1	1	24	24	18.5	2	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene EIF1	EIF1, A121, ISO1, EIF1A, EIF-1, SUI1	eukaryotic translation initiation factor 1	NM_005801, hCT1810075.3, hCT1983860.2	202021_x_at, 211956_s_at, 212130_x_at, 212225_at, 212227_x_at, 228967_at	NP_005792.1, EAW60754.1, EAW60755.1
GeneID:9001	HAP1	17	39,878,891	39,890,898	12,007	-	1	4_A375_EGR1..1..3653	82	in gene	0	0	1	10	9	21	1	4_A375_EGR1..1	21	Gene HAP1	HIP5, HAP2, HLP, hHLP1, HAP1	huntingtin-associated protein 1	NM_177977, NM_001079870, NM_001079871, hCT10027.1, hCT1954489.1, hCT1954490.1, hCT2295282.0, hCT2353586.0	211222_s_at, 211604_x_at, 238275_at	NP_817084.2, NP_001073339.1, NP_001073340.1, EAW60757.1, EAW60758.1, EAW60760.1, EAW60759.1, EAW60761.1
GeneID:10609	SC65	17	39,956,205	39,966,451	10,246	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2537, 2_A375_pNL97_plus_lncRNA_AR..1..3638, 4_A375_EGR1..1..3654, 4_A375_EGR1..1..3655	-285, 35, 10755, 1395	upstream, in gene, downstream, in gene	1	1	1	14	24	18	2	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene SC65	LEPREL4, NOL55, SC65, NO55	leprecan-like 4	NM_006455, hCT10045.2	204076_at	NP_006446.1, EAW60766.1
GeneID:60681	FKBP10	17	39,968,982	39,979,489	10,507	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2537, 2_A375_pNL97_plus_lncRNA_AR..1..3638, 4_A375_EGR1..1..3655	-226, -546, -1906	upstream, upstream, upstream	1	1	1	19	36	14	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene FKBP10	FLJ22041, FLJ20683, OI6, PPIASE, FKBP10, FLJ23833, hFKBP65, FKBP65	FK506 binding protein 10, 65 kDa	NM_021939, hCT1810071.2, hCT2292104.0, hCT2292105.0, hCT2353583.0	219249_s_at	NP_068758.3, EAW60770.1, EAW60767.1, EAW60768.1, EAW60769.1
GeneID:55175	KLHL11	17	40,009,799	40,021,629	11,830	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3639, 4_A375_EGR1..1..3656	93, 413	in gene, in gene	0	1	1	13	18	19	1	4_A375_EGR1..1	19	Gene KLHL11	KLHL11, FLJ10572	kelch-like 11 (Drosophila)	NM_018143, hCT10793.2, hCT2295356.0	220857_at	NP_060613.1, EAW60776.1, EAW60775.1
GeneID:47	ACLY	17	40,023,179	40,075,272	52,093	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3639, 4_A375_EGR1..1..3656, 4_A375_EGR1..1..3657	53736, 54056, 72	downstream, downstream, in gene	0	1	1	14	15	21.5	2	4_A375_EGR1..1	24	Gene ACLY	CLATP, ACL, ACLY, ATPCL	ATP citrate lyase	NM_001096, NM_198830, hCT10790.3, hCT2295354.0, hCT2295355.0, hCT2353605.0, hCT2353606.0	201127_s_at, 201128_s_at, 210337_s_at	NP_001087.2, NP_942127.1, EAW60777.1, EAW60779.1, EAW60780.1, EAW60781.1, EAW60778.1
GeneID:83538	TTC25	17	40,086,888	40,117,669	30,781	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2538, 2_A375_pNL97_plus_lncRNA_AR..1..3640	-72, -360	upstream, upstream	1	1	0	14	15	8	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene TTC25	DKFZp434H0115, TTC25	tetratricopeptide repeat domain 25	NM_031421, hCT10795.2, hCT2292108.0, hCT2353582.0	223924_at	NP_113609.1, EAW60784.1, EAW60782.1, EAW60783.1
GeneID:7266	DNAJC7	17	40,128,439	40,169,715	41,276	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2539, 1_A375_pNL7_minus_lncRNA_AR..1..2540, 2_A375_pNL97_plus_lncRNA_AR..1..3641, 2_A375_pNL97_plus_lncRNA_AR..1..3642	115, -2349, 275, -2317	in gene, upstream, in gene, upstream	1	1	0	64.5	70	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	108	Gene DNAJC7	TTC2, DJC7, TPR2, DJ11, DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	NR_029431, NM_003315, NM_001144766, hCT2353627.0, hCT7620.3	1556053_at, 202416_at	NP_003306.3, NP_001138238.1, EAW60788.1, EAW60789.1
GeneID:28511	NKIRAS2	17	40,169,594	40,177,659	8,065	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2539, 1_A375_pNL7_minus_lncRNA_AR..1..2540, 2_A375_pNL97_plus_lncRNA_AR..1..3641, 2_A375_pNL97_plus_lncRNA_AR..1..3642	6, 2470, -154, 2438	in gene, in gene, upstream, in gene	1	1	0	64.5	70	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	108	Gene NKIRAS2	MGC74742, KBRAS2, DKFZp434N1526, NKIRAS2, kappaB-Ras2	NFKB inhibitor interacting Ras-like 2	NM_001001349, NM_017595, NM_001144927, NM_001144928, NM_001144929, hCT1810080.2, hCT1960762.1, hCT1987546.1, hCT1987548.1, hCT2353607.0	218240_at, 222105_s_at	NP_001001349.1, NP_060065.2, NP_001138399.1, NP_001138400.1, NP_001138401.1, EAW60794.1, EAW60790.1, EAW60791.1, EAW60792.1, EAW60793.1
GeneID:201181	ZNF385C	17	40,177,594	40,180,707	3,113	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2539, 1_A375_pNL7_minus_lncRNA_AR..1..2540, 2_A375_pNL97_plus_lncRNA_AR..1..3641, 2_A375_pNL97_plus_lncRNA_AR..1..3642	11107, 8643, 11267, 8675	downstream, downstream, downstream, downstream	1	1	0	64.5	70	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	108	Gene ZNF385C	ZNF385C	zinc finger protein 385C	XM_002345029, XM_002343558, XM_002347765	241383_at	XP_002345070.2, XP_002343599.2, XP_002347808.2
GeneID:100507628	LOC100507628	17	40,178,915	40,190,044	11,129	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2539, 1_A375_pNL7_minus_lncRNA_AR..1..2540, 2_A375_pNL97_plus_lncRNA_AR..1..3641, 2_A375_pNL97_plus_lncRNA_AR..1..3642, 4_A375_EGR1..1..3658	20444, 17980, 20604, 18012, -2500	downstream, downstream, downstream, downstream, upstream	1	1	1	44.33	49.33	18.33	3	2_A375_pNL97_plus_lncRNA_AR..1	108	Gene LOC100507628		zinc finger protein 385C-like	XM_003119678, XM_003118752, XM_003120881		XP_003119724.1, XP_003118800.1, XP_003120929.1
GeneID:100507656	LOC100507656	17	40,191,471	40,195,129	3,658	-	1	4_A375_EGR1..1..3658	2585	in gene	0	0	1	4	8	28	1	4_A375_EGR1..1	28	Gene LOC100507656		hypothetical protein LOC100507656	XM_003119675, XM_003118753, XM_003120882		XP_003119723.1, XP_003118801.1, XP_003120930.1
GeneID:5878	RAB5C	17	40,276,997	40,307,022	30,025	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3643, 4_A375_EGR1..1..3659	-114, 48	upstream, in gene	0	1	1	13	18	17	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene RAB5C	RAB5CL, MGC117217, RABL, RAB5C, MGC138857	RAB5C, member RAS oncogene family	NM_004583, NM_201434, hCT2295335.1, hCT2295338.0, hCT2295340.0, hCT2353598.0	201140_s_at, 201156_s_at	NP_004574.2, NP_958842.1, EAW60805.1, EAW60806.1, EAW60807.1, EAW60808.1
GeneID:23415	KCNH4	17	40,308,910	40,333,296	24,386	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2541, 2_A375_pNL97_plus_lncRNA_AR..1..3643, 2_A375_pNL97_plus_lncRNA_AR..1..3644, 4_A375_EGR1..1..3659	1008, 26160, 944, 26320	in gene, downstream, in gene, downstream	1	1	1	19.5	29	16	2	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene KCNH4	KCNH4, BEC2, Kv12.3, ELK1	potassium voltage-gated channel, subfamily H (eag-related), member 4	NM_012285, hCT7611.1	220802_at	NP_036417.1, EAW60809.1
GeneID:3060	HCRT	17	40,336,078	40,337,470	1,392	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2541, 1_A375_pNL7_minus_lncRNA_AR..1..2542, 2_A375_pNL97_plus_lncRNA_AR..1..3644, 2_A375_pNL97_plus_lncRNA_AR..1..3645	5182, -9058, 5118, -9058	downstream, upstream, downstream, upstream	1	1	0	47.5	84.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	89	Gene HCRT	OX, NRCLP1, PPOX, HCRT	hypocretin (orexin) neuropeptide precursor	NM_001524, hCT7613.1	207642_at	NP_001515.1, EAW60810.1
GeneID:84514	GHDC	17	40,341,105	40,346,550	5,445	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2541, 1_A375_pNL7_minus_lncRNA_AR..1..2542, 2_A375_pNL97_plus_lncRNA_AR..1..3644, 2_A375_pNL97_plus_lncRNA_AR..1..3645	14262, 22, 14198, 22	downstream, in gene, downstream, in gene	1	1	0	47.5	84.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	89	Gene GHDC	GHDC, LGP1, D11LGP1	GH3 domain containing	NR_024573, NM_001142622, NM_001142623, NM_032484, hCT2295328.0, hCT2295329.0, hCT2295330.0, hCT2353625.0, hCT2353626.0, hCT7619.2	227159_at	NP_001136094.1, NP_001136095.1, NP_115873.1, EAW60812.1, EAW60813.1, EAW60816.1, EAW60811.1, EAW60814.1, EAW60815.1
GeneID:6777	STAT5B	17	40,351,195	40,428,424	77,229	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2542, 1_A375_pNL7_minus_lncRNA_AR..1..2543, 2_A375_pNL97_plus_lncRNA_AR..1..3645	81896, 9320, 81896	downstream, in gene, downstream	1	1	0	42.5	52	4	2	2_A375_pNL97_plus_lncRNA_AR..1	89	Gene STAT5B	STAT5B, STAT5	signal transducer and activator of transcription 5B	NM_012448, hCT7616.3	1555086_at, 1555088_x_at, 205026_at, 212549_at, 212550_at	NP_036580.2, EAW60817.1
GeneID:6776	STAT5A	17	40,439,565	40,463,961	24,396	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3646, 4_A375_EGR1..1..3660	-109, 1611	upstream, in gene	0	1	1	13	16.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene STAT5A	STAT5, MGF, STAT5A	signal transducer and activator of transcription 5A	NM_003152, hCT7610.2	203010_at	NP_003143.2, EAW60819.1
GeneID:6774	STAT3	17	40,465,343	40,540,513	75,170	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2544, 2_A375_pNL97_plus_lncRNA_AR..1..3647	-31, -79	upstream, upstream	1	1	0	45	54	17	1	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene STAT3	APRF, STAT3, MGC16063, FLJ20882, HIES	signal transducer and activator of transcription 3 (acute-phase response factor)	NM_139276, NM_003150, NM_213662, hCT1956866.1, hCT2295316.0, hCT2295320.0, hCT2295321.0, hCT2295322.0, hCT2353589.0, hCT2353590.0, hCT2353591.0	208991_at, 208992_s_at, 225289_at, 243213_at	NP_644805.1, NP_003141.2, NP_998827.1, EAW60820.1, EAW60821.1, EAW60826.1, EAW60822.1, EAW60823.1, EAW60824.1, EAW60825.1, EAW60827.1
GeneID:284119	PTRF	17	40,554,467	40,575,338	20,871	-	1	4_A375_EGR1..1..3661	18298	in gene	0	0	1	5	7	17	1	4_A375_EGR1..1	17	Gene PTRF	CAVIN1, CGL4, FLJ90031, cavin-1, FKSG13, PTRF, CAVIN	polymerase I and transcript release factor	NM_012232, hCT2349023.0	1557938_s_at, 208789_at, 208790_s_at	NP_036364.2, EAW60828.1
GeneID:535	ATP6V0A1	17	40,610,862	40,674,597	63,735	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3648, 4_A375_EGR1..1..3662	50, -62	in gene, upstream	0	1	1	16	16	28	1	4_A375_EGR1..1	28	Gene ATP6V0A1	VPP1, DKFZp781J1951, ATP6N1A, Vph1, ATP6N1, Stv1, a1, ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	NM_005177, NM_001130020, NM_001130021, hCT2353599.0, hCT7609.1	205095_s_at, 212383_at	NP_005168.2, NP_001123492.1, NP_001123493.1, EAW60830.1, EAW60831.1
GeneID:4669	NAGLU	17	40,687,951	40,696,467	8,516	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2545, 2_A375_pNL97_plus_lncRNA_AR..1..3649, 4_A375_EGR1..1..3663, 4_A375_EGR1..1..3664	18857, 17521, 2433, 18841	downstream, downstream, in gene, downstream	1	1	1	10.33	13	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NAGLU	NAG, UFHSD, MPS3B, MPS-IIIB, NAGLU	N-acetylglucosaminidase, alpha	NM_000263, hCT2292126.0, hCT8704.2	204360_s_at, 215680_at	NP_000254.2, EAW60832.1, EAW60833.1
GeneID:3292	HSD17B1	17	40,703,984	40,707,232	3,248	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2545, 2_A375_pNL97_plus_lncRNA_AR..1..3649, 4_A375_EGR1..1..3664	2624, 1488, 2608	in gene, in gene, in gene	1	1	1	11	17	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene HSD17B1	HSD17, EDH17B2, MGC138140, HSD17B1, SDR28C1, EDHB17	hydroxysteroid (17-beta) dehydrogenase 1	NM_000413, hCT7987.2	205829_at, 228595_at	NP_000404.2, EAW60836.1
GeneID:100290566	LOC100290566	17	40,704,454	40,706,766	2,312	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2545, 2_A375_pNL97_plus_lncRNA_AR..1..3649, 4_A375_EGR1..1..3664	158, 1294, 174	in gene, in gene, in gene	1	1	1	11	17	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100290566		hypothetical LOC100290566	XR_111701, XR_109384, XR_115104		
GeneID:80347	COASY	17	40,714,092	40,718,295	4,203	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2545, 2_A375_pNL97_plus_lncRNA_AR..1..3649, 2_A375_pNL97_plus_lncRNA_AR..1..3650, 4_A375_EGR1..1..3664	-7484, -8820, 4916, -7500	upstream, upstream, downstream, upstream	1	1	1	12.67	16.67	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene COASY	COASY, FLJ35179, UKR1, NBP, PPAT, pOV-2, DPCK	CoA synthase	NM_001042529, NM_025233, NM_001042530, NM_001042531, NM_001042532, hCT2292131.0, hCT2292133.0, hCT8010.2	201913_s_at	NP_001035994.1, NP_079509.5, NP_001035995.1, NP_001035996.1, NP_001035997.2, EAW60838.1, EAW60839.1, EAW60840.1
GeneID:6945	MLX	17	40,719,076	40,725,221	6,143	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3650	-70	upstream	0	1	0	16	16	17	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene MLX	MLX, MXD7, MAD7, TCFL4, bHLHd13	MAX-like protein X	NM_170607, NM_198204, NM_198205, hCT1987575.1, hCT1987577.1, hCT2353580.0, hCT2353581.0, hCT8695.2	1570347_at, 210752_s_at, 213708_s_at, 217909_s_at, 217910_x_at	NP_733752.1, NP_937847.1, NP_937848.1, EAW60841.1, EAW60842.1, EAW60845.1, EAW60843.1, EAW60844.1
GeneID:29893	PSMC3IP	17	40,724,329	40,729,747	5,418	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3650	10739	downstream	0	1	0	16	16	17	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene PSMC3IP	HOP2, TBPIP, GT198, HUMGT198A, PSMC3IP	PSMC3 interacting protein	NM_013290, NM_016556, hCT1958863.1, hCT1987512.1, hCT1987513.1, hCT2353585.0, hCT7990.2	205956_x_at, 213951_s_at	NP_037422.2, NP_057640.1, EAW60846.1, EAW60848.1, EAW60849.1, EAW60850.1, EAW60847.1
GeneID:162427	FAM134C	17	40,731,526	40,761,445	29,919	-	1	4_A375_EGR1..1..3665	-523	upstream	0	0	1	13	12	18	1	4_A375_EGR1..1	18	Gene FAM134C	FAM134C, FLJ33606	family with sequence similarity 134, member C	NM_178126, NR_026697, hCT2349024.0, hCT2353616.0	212697_at	NP_835227.1, EAW60852.1, EAW60851.1
GeneID:7283	TUBG1	17	40,761,358	40,767,256	5,898	+	1	4_A375_EGR1..1..3665	610	in gene	0	0	1	13	12	18	1	4_A375_EGR1..1	18	Gene TUBG1	TUBGCP1, TUBG, TUBG1, GCP-1	tubulin, gamma 1	NM_001070	201714_at	NP_001061.2
GeneID:27175	TUBG2	17	40,811,266	40,819,024	7,758	+	1	4_A375_EGR1..1..3666	190	in gene	0	0	1	11	9	17	1	4_A375_EGR1..1	17	Gene TUBG2	TUBG2, MGC131994	tubulin, gamma 2	NM_016437	203894_at	NP_057521.1
GeneID:79990	PLEKHH3	17	40,819,932	40,829,048	9,116	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2546, 2_A375_pNL97_plus_lncRNA_AR..1..3651, 2_A375_pNL97_plus_lncRNA_AR..1..3652, 4_A375_EGR1..1..3666	-2888, -848, -2696, 17592	upstream, upstream, upstream, downstream	1	1	1	18.33	18.33	13	3	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene PLEKHH3	FLJ21019, PLEKHH3	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	NM_024927, hCT1954482.1, hCT2295289.0, hCT2295290.0, hCT8008.3	220259_at, 227248_at	NP_079203.3, EAW60864.1, EAW60862.1, EAW60863.1, EAW60865.1
GeneID:2826	CCR10	17	40,831,420	40,833,845	2,425	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2546, 2_A375_pNL97_plus_lncRNA_AR..1..3651, 2_A375_pNL97_plus_lncRNA_AR..1..3652	1909, 4149, 2101	in gene, downstream, in gene	1	1	0	22	23	11	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene CCR10	GPR2, CCR10	chemokine (C-C motif) receptor 10	NM_016602, hCT1646365.2	220565_at	NP_057686.2, EAW60866.1
GeneID:8506	CNTNAP1	17	40,834,632	40,852,011	17,379	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2546, 2_A375_pNL97_plus_lncRNA_AR..1..3651, 2_A375_pNL97_plus_lncRNA_AR..1..3652	-2696, -4936, -2888	upstream, upstream, upstream	1	1	0	22	23	11	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene CNTNAP1	CNTNAP, NRXN4, CNTNAP1, P190, CASPR	contactin associated protein 1	NM_003632, hCT2292154.0, hCT2292157.0, hCT7986.3	219400_at	NP_003623.1, EAW60869.1, EAW60867.1, EAW60868.1
GeneID:100190938	LOC100190938	17	40,905,932	40,913,275	7,343	-	1	4_A375_EGR1..1..3667	-261	upstream	0	0	1	5	8	17	1	4_A375_EGR1..1	17	Gene LOC100190938	FLJ32559	hypothetical LOC100190938	NR_024461, NR_024462		
GeneID:10266	RAMP2	17	40,913,212	40,915,059	1,847	+	1	4_A375_EGR1..1..3667	324	in gene	0	0	1	5	8	17	1	4_A375_EGR1..1	17	Gene RAMP2	RAMP2		NM_005854, hCT2291238.0, hCT2291239.0	205779_at	NP_005845.2, EAW60877.1, EAW60878.1
GeneID:84313	VPS25	17	40,925,454	40,931,617	6,163	+	1	4_A375_EGR1..1..3668	11170	downstream	0	0	1	9	11	17	1	4_A375_EGR1..1	17	Gene VPS25	FAP20, EAP20, MGC10540, DERP9, VPS25	vacuolar protein sorting 25 homolog (S. cerevisiae)	NM_032353, hCT1987516.1, hCT8011.3	224808_s_at	NP_115729.1, EAW60880.1, EAW60879.1
GeneID:65266	WNK4	17	40,932,649	40,949,084	16,435	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3653, 4_A375_EGR1..1..3668	18103, 3975	downstream, in gene	0	1	1	13	16	13	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene WNK4	WNK4, PRKWNK4, PHA2B	WNK lysine deficient protein kinase 4	NM_032387, hCT1816276.1, hCT2291246.0	229158_at, 244344_at	NP_115763.2, EAW60881.1, EAW60882.1
GeneID:28958	CCDC56	17	40,949,652	40,950,704	1,052	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3653	-48	upstream	0	1	0	17	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CCDC56	CCDC56, HSPC009, FLJ50764	coiled-coil domain containing 56	NM_001040431	218026_at, 236998_at	NP_001035521.1
GeneID:124817	CNTD1	17	40,950,854	40,963,605	12,751	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3653	-102	upstream	0	1	0	17	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CNTD1	CNTD, CNTD1, FLJ40137	cyclin N-terminal domain containing 1	NM_173478, hCT2291252.1, hCT8013.3	231463_at	NP_775749.2, EAW60887.1, EAW60886.1
GeneID:8678	BECN1	17	40,962,150	40,976,310	14,160	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2547, 1_A375_pNL7_minus_lncRNA_AR..1..2548, 2_A375_pNL97_plus_lncRNA_AR..1..3654	54, -8906, -9130	in gene, upstream, upstream	1	1	0	20.5	15.5	13	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene BECN1	ATG6, VPS30, beclin1, BECN1	beclin 1, autophagy related	NM_003766, hCT2292726.0, hCT2353609.0, hCT8001.3	1561652_at, 208945_s_at, 208946_s_at	NP_003757.1, EAW60888.1, EAW60889.1, EAW60890.1
GeneID:10197	PSME3	17	40,985,423	40,995,777	10,354	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2547, 1_A375_pNL7_minus_lncRNA_AR..1..2548, 2_A375_pNL97_plus_lncRNA_AR..1..3654	-9167, -207, 17	upstream, upstream, in gene	1	1	0	20.5	15.5	13	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene PSME3	REG-GAMMA, Ki, PA28-gamma, PSME3, PA28G	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma, Ki)	NM_005789, NM_176863, hCT2291256.0, hCT2291258.0, hCT2353603.0, hCT7994.2	200987_x_at, 200988_s_at, 209852_x_at, 209853_s_at	NP_005780.2, NP_789839.1, EAW60891.1, EAW60892.1, EAW60893.1, EAW60894.1
GeneID:146923	RUNDC1	17	41,132,582	41,145,707	13,125	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2549, 2_A375_pNL97_plus_lncRNA_AR..1..3655, 4_A375_EGR1..1..3669	17768, 17637, 17994	downstream, downstream, downstream	1	1	1	24	20	28	1	4_A375_EGR1..1	28	Gene RUNDC1	RUNDC1, DKFZp761H0421	RUN domain containing 1	NM_173079, hCT2291280.0, hCT2291282.0	226298_at, 235040_at	NP_775102.2, EAW60908.1, EAW60907.1
GeneID:6155	RPL27	17	41,150,446	41,154,976	4,530	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2549, 2_A375_pNL97_plus_lncRNA_AR..1..3655, 2_A375_pNL97_plus_lncRNA_AR..1..3656, 4_A375_EGR1..1..3669	-78, -227, 12914, 130	upstream, upstream, downstream, in gene	1	1	1	17.5	17	15	2	4_A375_EGR1..1	28	Gene RPL27	RPL27, L27	ribosomal protein L27	NM_000988, hCT2348226.0, hCT2348227.0, hCT2348228.0, hCT2348229.0, hCT8002.2	200025_s_at	NP_000979.1, EAW60909.1, EAW60910.1, EAW60911.1, EAW60912.1, EAW60913.1
GeneID:3430	IFI35	17	41,158,769	41,166,476	7,707	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2549, 1_A375_pNL7_minus_lncRNA_AR..1..2550, 2_A375_pNL97_plus_lncRNA_AR..1..3655, 2_A375_pNL97_plus_lncRNA_AR..1..3656, 2_A375_pNL97_plus_lncRNA_AR..1..3657, 4_A375_EGR1..1..3669	-8401, 15183, -8550, 4591, 15599, -8193	upstream, downstream, upstream, in gene, downstream, upstream	1	1	1	19.67	18	14.33	3	4_A375_EGR1..1	28	Gene IFI35	IFI35, FLJ21753, IFP35	interferon-induced protein 35	NM_005533, hCT2353567.0, hCT2353568.0, hCT8016.3	209417_s_at	NP_005524.1, EAW60915.1, EAW60914.1, EAW60916.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:10493	VAT1	17	41,166,622	41,174,459	7,837	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2550, 2_A375_pNL97_plus_lncRNA_AR..1..3656, 2_A375_pNL97_plus_lncRNA_AR..1..3657	507, 11099, 91	in gene, downstream, in gene	1	1	0	17.5	17	8.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene VAT1	FLJ20230, VAT1, VATI	vesicle amine transport protein 1 homolog (T. californica)	NM_006373, hCT2292716.0, hCT8000.2	208626_s_at	NP_006364.2, EAW60917.1, EAW60918.1
GeneID:8153	RND2	17	41,177,256	41,184,056	6,800	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2550, 2_A375_pNL97_plus_lncRNA_AR..1..3657	-3306, -2690	upstream, upstream	1	1	0	24	20	13	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene RND2	RHO7, RhoN, RND2, ARHN	Rho family GTPase 2	NM_005440, hCT1962360.1, hCT7999.2	213467_at, 214393_at	NP_005431.1, EAW60919.1, EAW60920.1
GeneID:672	BRCA1	17	41,196,312	41,277,500	81,188	-	1	4_A375_EGR1..1..3670	-1188	upstream	0	0	1	7	10	24	1	4_A375_EGR1..1	24	Gene BRCA1	BRCA1, BROVCA1, PNCA4, PSCP, RNF53, IRIS, BRCAI, BRCC1	breast cancer 1, early onset	NM_007300, NM_007297, NM_007298, NM_007299, NR_027676, NM_007294, hCT1987502.1, hCT1987503.1, hCT1987504.1, hCT1987505.1, hCT1987506.1, hCT1987507.1, hCT2292699.0, hCT2292702.0, hCT2292703.0, hCT2292706.0, hCT2292707.0, hCT2292709.0, hCT2292710.0, hCT2292	204531_s_at, 211851_x_at	NP_009231.2, NP_009228.2, NP_009229.2, NP_009230.2, NP_009225.1, EAW60922.1, EAW60923.1, EAW60924.1, EAW60925.1, EAW60926.1, EAW60927.1, EAW60928.1, EAW60930.1, EAW60940.1, EAW60929.1, EAW60931.1, EAW60932.1, EAW60933.1, EAW60934.1, EAW60935.1, EAW60936.1
GeneID:10230	NBR2	17	41,277,600	41,297,130	19,530	+	1	4_A375_EGR1..1..3670	1088	in gene	0	0	1	7	10	24	1	4_A375_EGR1..1	24	Gene NBR2	MGC104305, NCRNA00192, DKFZp686F081, NBR2	neighbor of BRCA1 gene 2 (non-protein coding)	NR_003108, hCT1788663.1, hCT2291303.0, hCT2291304.0	1553992_s_at, 207631_at	EAW60943.1, EAW60944.1, EAW60945.1
GeneID:100130581	LOC100130581	17	41,447,213	41,466,266	19,053	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2552, 1_A375_pNL7_minus_lncRNA_AR..1..2553, 2_A375_pNL97_plus_lncRNA_AR..1..3659, 2_A375_pNL97_plus_lncRNA_AR..1..3660, 4_A375_EGR1..1..3671, 4_A375_EGR1..1..3672	27482, 20794, 27498, 20782, 27738, -10102	downstream, downstream, downstream, downstream, downstream, upstream	1	1	1	23.33	25.67	15.67	3	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene LOC100130581	DKFZp686H1819, FLJ41591, FLJ18727	hypothetical LOC100130581	NR_027412, NR_027413		
GeneID:379	ARL4D	17	41,476,353	41,478,504	2,151	+	1	4_A375_EGR1..1..3672	15	in gene	0	0	1	12	12	18	1	4_A375_EGR1..1	18	Gene ARL4D	ARF4L, ARL4D, ARL6	ADP-ribosylation factor-like 4D	NM_001661, hCT19537.2, hCT1965858.1	203586_s_at, 203587_at	NP_001652.2, EAW51662.1, EAW51661.1
GeneID:100313779	MIR2117	17	41,522,174	41,522,253	79	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3662	-1654	upstream	0	1	0	15	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MIR2117	MIR2117	microRNA 2117	NR_031751		
GeneID:1659	DHX8	17	41,561,334	41,601,680	40,346	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2554, 2_A375_pNL97_plus_lncRNA_AR..1..3663	-150, -118	upstream, upstream	1	1	0	45	37	12	1	1_A375_pNL7_minus_lncRNA_AR..1	45	Gene DHX8	PRPF22, DDX8, HRH1, PRP22, DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	NM_004941, hCT1957152.2, hCT1957154.1, hCT19891.2, hCT2350279.0, hCT2350280.0	203334_at, 227079_at	NP_004932.1, EAW51678.1, EAW51676.1, EAW51677.1, EAW51679.1, EAW51680.1
GeneID:4356	MPP3	17	41,878,167	41,910,547	32,380	-	1	4_A375_EGR1..1..3674	-269	upstream	0	0	1	7	11	16	1	4_A375_EGR1..1	16	Gene MPP3	MPP3, DLG3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	NM_001932, NR_003562, hCT19383.1, hCT1985652.0, hCT1985654.0, hCT1985655.1, hCT2352473.0, hCT2352474.0	206186_at	NP_001923.2, EAW51661.1, EAW51662.1, EAW51663.1, EAW51664.1, EAW51666.1, EAW51665.1
GeneID:4355	MPP2	17	41,952,727	41,985,113	32,386	-	1	4_A375_EGR1..1..3675	-587	upstream	0	0	1	5	7	16	1	4_A375_EGR1..1	16	Gene MPP2	DKFZp761D0712, MPP2, DKFZp686A06252, DKFZp686J2189, DLG2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	NM_005374, hCT1952669.1, hCT1952670.1, hCT21459.2, hCT2352479.0	207984_s_at, 213270_at	NP_005365.3, EAW51656.1, EAW51653.1, EAW51654.1, EAW51655.1
GeneID:23591	C17orf88	17	41,994,576	41,995,355	779	+	1	4_A375_EGR1..1..3675	-8896	upstream	0	0	1	5	7	16	1	4_A375_EGR1..1	16	Gene C17orf88	APR-2, C17orf88	chromosome 17 open reading frame 88	NR_026770	221129_at	
GeneID:5697	PYY	17	42,030,106	42,081,837	51,731	-	2	4_A375_EGR1..1..3676, 4_A375_EGR1..1..3677	50989, -2931	in gene, upstream	0	0	1	7.5	10	15.5	2	4_A375_EGR1..1	16	Gene PYY	PYY, PYY1	peptide YY	NM_004160, hCT1963592.1, hCT1965799.1, hCT2289264.0	207080_s_at, 211253_x_at	NP_004151.3, EAW51646.1, EAW51644.1, EAW51645.1
GeneID:162417	NAGS	17	42,082,032	42,086,436	4,404	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3664, 4_A375_EGR1..1..3677	10304, 2736	downstream, in gene	0	1	1	14.5	22.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene NAGS	NAGS, ARGA, AGAS, MGC133025	N-acetylglutamate synthase	NM_153006, hCT21475.2	229432_at	NP_694551.1, EAW51643.1
GeneID:84336	TMEM101	17	42,088,556	42,092,345	3,789	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3664, 4_A375_EGR1..1..3677	9, 7577	in gene, downstream	0	1	1	14.5	22.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene TMEM101	MGC4251, FLJ23987, TMEM101	transmembrane protein 101	NM_032376, hCT1952693.1, hCT21477.3	225004_at	NP_115752.1, EAW51642.1, EAW51641.1
GeneID:10014	HDAC5	17	42,154,121	42,201,014	46,893	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2555, 2_A375_pNL97_plus_lncRNA_AR..1..3665, 4_A375_EGR1..1..3678, 4_A375_EGR1..1..3679, 4_A375_EGR1..1..3680	-266, -250, 32310, 12567, 614	upstream, upstream, in gene, in gene, in gene	1	1	1	14.5	10	15.5	4	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene HDAC5	HD5, HDAC5, FLJ90614, NY-CO-9	histone deacetylase 5	NM_005474, NM_001015053, hCT2269317.0, hCT2269316.0	202455_at, 229408_at	NP_005465.2, NP_001015053.1, EAW51633.1, EAW51634.1
GeneID:78995	C17orf53	17	42,219,274	42,239,844	20,570	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2556, 1_A375_pNL7_minus_lncRNA_AR..1..2557, 2_A375_pNL97_plus_lncRNA_AR..1..3666, 2_A375_pNL97_plus_lncRNA_AR..1..3667	-3626, 22, -3578, 6	upstream, in gene, upstream, in gene	1	1	0	19	26	9	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene C17orf53	MGC3130, C17orf53, FLJ11594	chromosome 17 open reading frame 53	NM_001171251, NM_024032, hCT1952699.1, hCT1952700.1, hCT21479.2, hCT2352482.0	219879_s_at	NP_001164722.1, NP_076937.2, EAW51629.1, EAW51630.1, EAW51631.1, EAW51632.1
GeneID:7343	UBTF	17	42,282,401	42,298,250	15,849	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2558, 2_A375_pNL97_plus_lncRNA_AR..1..3668	-550, 12234	upstream, in gene	1	1	0	17.5	14.5	7.5	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene UBTF	UBTF, UBF, NOR-90	upstream binding transcription factor, RNA polymerase I	NM_001076684, NM_001076683, NM_014233, hCT1952679.1, hCT1952680.1, hCT21465.2, hCT2269308.0, hCT2269312.0	1558215_s_at, 202692_s_at, 214861_s_at, 225982_at	NP_001070152.1, NP_001070151.1, NP_055048.1, EAW51617.1, EAW51618.1, EAW51619.1, EAW51616.1, EAW51620.1
GeneID:6521	SLC4A1	17	42,325,758	42,345,502	19,744	-	1	4_A375_EGR1..1..3681	3310	in gene	0	0	1	4	3	15	1	4_A375_EGR1..1	15	Gene SLC4A1	MGC126623, WD, AE1, RTA1A, SW, EPB3, FR, EMPB3, WD1, DI, SLC4A1, CD233, MGC116750, WR, BND3, MGC116753, MGC126619	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	NM_000342, hCT1964443.1	1552713_a_at	NP_000333.1, EAW51614.1
GeneID:10900	RUNDC3A	17	42,385,927	42,396,038	10,111	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2559, 1_A375_pNL7_minus_lncRNA_AR..1..2560, 1_A375_pNL7_minus_lncRNA_AR..1..2561, 2_A375_pNL97_plus_lncRNA_AR..1..3669, 2_A375_pNL97_plus_lncRNA_AR..1..3670, 2_A375_pNL97_plus_lncRNA_AR..1..3671, 4_A375_EGR1..1..3682, 4_A375_EGR1..1..3683	-71, 16366, 18457, -183, 16345, 18457, -135, 15929	upstream, downstream, downstream, upstream, downstream, downstream, upstream, downstream	1	1	1	32.33	26	16	3	1_A375_pNL7_minus_lncRNA_AR..1	43	Gene RUNDC3A	RUNDC3A, RPIP-8, RPIP8, RAP2IP	RUN domain containing 3A	NM_006695, NM_001144825, NM_001144826, hCT1952682.1, hCT1952683.1, hCT21467.3, hCT2269794.0, hCT2352478.0	206196_s_at, 213439_x_at	NP_006686.1, NP_001138297.1, NP_001138298.1, EAW51608.1, EAW51609.1, EAW51612.1, EAW51610.1, EAW51611.1
GeneID:51629	SLC25A39	17	42,396,993	42,402,217	5,224	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2560, 1_A375_pNL7_minus_lncRNA_AR..1..2561, 2_A375_pNL97_plus_lncRNA_AR..1..3670, 2_A375_pNL97_plus_lncRNA_AR..1..3671, 4_A375_EGR1..1..3683	-76, -2167, -55, -2167, 361	upstream, upstream, upstream, upstream, in gene	1	1	1	37.5	33.5	15	2	1_A375_pNL7_minus_lncRNA_AR..1	43	Gene SLC25A39	CGI-69, CGI69, SLC25A39, FLJ22407	solute carrier family 25, member 39	NM_001143780, NM_016016, hCT1964438.1, hCT1964439.1, hCT1964440.1, hCT1964441.1, hCT1964442.1, hCT2269297.0	223649_s_at	NP_001137252.1, NP_057100.1, EAW51602.1, EAW51603.1, EAW51606.1, EAW51607.1, EAW51604.1, EAW51605.1
GeneID:2896	GRN	17	42,422,491	42,430,470	7,979	+	1	4_A375_EGR1..1..3684	7665	in gene	0	0	1	6	9	16	1	4_A375_EGR1..1	16	Gene GRN	GRN, PEPI, PGRN, GP88, GEP, PCDGF	granulin	NM_002087, hCT1952685.1, hCT1952686.1, hCT21468.1	200678_x_at, 211284_s_at, 216041_x_at	NP_002078.1, EAW51601.1, EAW51599.1, EAW51600.1
GeneID:284069	FAM171A2	17	42,431,101	42,441,235	10,134	-	2	4_A375_EGR1..1..3684, 4_A375_EGR1..1..3685	11059, -5261	downstream, upstream	0	0	1	5.5	8.5	19.5	2	4_A375_EGR1..1	21	Gene FAM171A2	MGC34829, FAM171A2	family with sequence similarity 171, member A2	NM_198475	235544_x_at	NP_940877.2
GeneID:3674	ITGA2B	17	42,449,550	42,466,873	17,323	-	1	4_A375_EGR1..1..3685	20377	downstream	0	0	1	5	8	21	1	4_A375_EGR1..1	21	Gene ITGA2B	GP2B, CD41, HPA3, GPIIb, CD41B, ITGA2B, GTA	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	NM_000419, hCT1964242.0, hCT2269291.0, hCT2269292.0, hCT2269293.0	206493_at, 206494_s_at, 216956_s_at, 216966_at	NP_000410.2, EAW51596.1, EAW51594.1, EAW51595.1, EAW51597.1
GeneID:23131	GPATCH8	17	42,472,645	42,580,957	108,312	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3672	253	in gene	0	1	0	11	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene GPATCH8	GPATCH8, KIAA0553, GPATC8	G patch domain containing 8	NM_001002909, NR_036474, hCT21481.2	212485_at, 212487_at	NP_001002909.1, EAW51593.1
GeneID:2535	FZD2	17	42,634,925	42,636,907	1,982	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2562, 2_A375_pNL97_plus_lncRNA_AR..1..3673	-525, -797	upstream, upstream	1	1	0	16	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene FZD2	FZD2, Fz2		NM_001466, hCT1809893.1	210220_at	NP_001457.1, EAW51591.1
GeneID:124808	CCDC43	17	42,754,805	42,767,165	12,360	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2563, 2_A375_pNL97_plus_lncRNA_AR..1..3674, 4_A375_EGR1..1..3686	-142, -35, 29	upstream, upstream, in gene	1	1	1	14	20	21	1	4_A375_EGR1..1	21	Gene CCDC43	FLJ31795, CCDC43	coiled-coil domain containing 43	NM_001099225, NM_144609, hCT1809912.1, hCT2271681.0	225607_at	NP_001092695.1, NP_653210.2, EAW51588.1, EAW51589.1
GeneID:80174	DBF4B	17	42,785,976	42,829,832	43,856	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2564, 2_A375_pNL97_plus_lncRNA_AR..1..3675, 4_A375_EGR1..1..3687, 4_A375_EGR1..1..3688, 4_A375_EGR1..1..3689	8, 40, 40424, 49944, 50984	in gene, in gene, in gene, downstream, downstream	1	1	1	10	12	14.25	4	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene DBF4B	MGC15009, chifb, ASKL1, DRF1, ZDBF1B, DBF4B, CHIFB, FLJ13087	DBF4 homolog B (S. cerevisiae)	NM_025104, NM_145663, hCT2344381.0, hCT2344382.0, hCT2344383.0, hCT2344384.0, hCT2344385.0, hCT2344832.0, hCT2352472.0	1555376_at, 206661_at, 238508_at, 238757_at	NP_079380.1, NP_663696.1, EAW51581.1, EAW51583.1, EAW51585.1, EAW51587.1, EAW51582.1, EAW51584.1, EAW51586.1
GeneID:100505943	LOC100505943	17	42,826,331	42,827,917	1,586	+	3	4_A375_EGR1..1..3687, 4_A375_EGR1..1..3688, 4_A375_EGR1..1..3689	69, 9589, 10629	in gene, downstream, downstream	0	0	1	7	5.67	15.67	3	4_A375_EGR1..1	17	Gene LOC100505943		hypothetical protein LOC100505943	XM_003118740		XP_003118788.1
GeneID:4185	ADAM11	17	42,836,568	42,859,214	22,646	+	4	4_A375_EGR1..1..3687, 4_A375_EGR1..1..3688, 4_A375_EGR1..1..3689, 4_A375_EGR1..1..3690	-10168, -648, 392, 15784	upstream, upstream, in gene, in gene	0	0	1	8.5	7.75	16.75	4	4_A375_EGR1..1	20	Gene ADAM11	MDC, ADAM11	ADAM metallopeptidase domain 11	NM_002390, hCT19380.2, hCT1952664.1, hCT1952665.1	207680_at, 239837_at	NP_002381.2, EAW51580.1, EAW51578.1, EAW51579.1
GeneID:9343	EFTUD2	17	42,927,655	42,976,993	49,338	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3676	113	in gene	0	1	0	23	20	12	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene EFTUD2	Snrp116, EFTUD2, U5-116KD, FLJ44695, Snu114, KIAA0031, DKFZp686E24196	elongation factor Tu GTP binding domain containing 2	NM_004247, NM_001142605, hCT19382.3, hCT2352477.0	222397_at, 222398_s_at	NP_004238.3, NP_001136077.1, EAW51573.1, EAW51574.1
GeneID:388389	CCDC103	17	42,977,154	42,980,629	3,475	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3676	-274	upstream	0	1	0	23	20	12	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CCDC103	FLJ34211, FLJ13094, CCDC103	coiled-coil domain containing 103	NM_213607, hCT19383.2		NP_998772.1, EAW51572.1
GeneID:2670	GFAP	17	42,982,993	42,992,914	9,921	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3676	16034	downstream	0	1	0	23	20	12	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene GFAP	GFAP, FLJ45472	glial fibrillary acidic protein	NM_002055, NM_001131019, hCT18686.1, hCT1952653.1, hCT1952654.1, hCT2271675.0, hCT2352475.0	203540_at, 229259_at	NP_002046.1, NP_001124491.1, EAW51567.1, EAW51568.1, EAW51570.1, EAW51571.1, EAW51569.1
GeneID:146909	KIF18B	17	43,003,448	43,025,082	21,634	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3677, 4_A375_EGR1..1..3691	-166, 19594	upstream, in gene	0	1	1	10.5	16	18.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene KIF18B	KIF18B	kinesin family member 18B	NM_001080443	222039_at	NP_001073912.1
GeneID:10882	C1QL1	17	43,037,061	43,045,644	8,583	-	2	4_A375_EGR1..1..3692, 4_A375_EGR1..1..3693	812, -596	in gene, upstream	0	0	1	6	9	17	2	4_A375_EGR1..1	18	Gene C1QL1	C1QRF, CRF, C1QTNF14, C1QL1	complement component 1, q subcomponent-like 1	NM_006688, hCT19378.2	205575_at, 214346_at	NP_006679.1, EAW51563.1
GeneID:79877	DCAKD	17	43,100,706	43,138,473	37,767	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3678	-247	upstream	0	1	0	20	23	6	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene DCAKD	FLJ22955, DCAKD	dephospho-CoA kinase domain containing	NM_024819, NM_001128631, hCT1809897.1, hCT1984228.1, hCT2271665.0, hCT2271667.0, hCT2352470.0	221224_s_at, 221225_at, 224522_s_at	NP_079095.3, NP_001122103.1, EAW51559.1, EAW51560.1, EAW51561.1, EAW51562.1, EAW51558.1
GeneID:4836	NMT1	17	43,138,680	43,186,384	47,704	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3678	40	in gene	0	1	0	20	23	6	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene NMT1	NMT, NMT1	N-myristoyltransferase 1	NM_021079, hCT19216.3, hCT1952655.1, hCT1952656.1, hCT1952657.1, hCT2275293.0	201157_s_at, 201158_at, 201159_s_at	NP_066565.1, EAW51554.1, EAW51553.1, EAW51555.1, EAW51556.1, EAW51557.1
GeneID:113026	PLCD3	17	43,189,008	43,209,891	20,883	-	1	4_A375_EGR1..1..3694	547	in gene	0	0	1	8	15	14	1	4_A375_EGR1..1	14	Gene PLCD3	PLCD3, MGC71172	phospholipase C, delta 3	NM_133373, hCT19218.2, hCT2271658.0, hCT2271659.0, hCT2271662.0	1552476_s_at, 234971_x_at	NP_588614.1, EAW51546.1, EAW51544.1, EAW51545.1, EAW51547.1
GeneID:79777	ACBD4	17	43,209,967	43,221,543	11,576	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3679, 4_A375_EGR1..1..3694, 4_A375_EGR1..1..3695, 4_A375_EGR1..1..3696	15261, -623, 12337, 15869	downstream, upstream, downstream, downstream	0	1	1	14.67	19.33	18.33	3	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene ACBD4	HMFT0700, FLJ13322, FLJ90623, ACBD4	acyl-CoA binding domain containing 4	NM_001135704, NM_024722, NM_001135705, NM_001135706, NM_001135707, hCT19220.2, hCT1952660.1, hCT1952661.1, hCT2275299.0, hCT2275302.0	219413_at	NP_001129176.1, NP_078998.1, NP_001129177.1, NP_001129178.1, NP_001129179.1, EAW51552.1, EAW51548.1, EAW51549.1, EAW51550.1, EAW51551.1
GeneID:10614	HEXIM1	17	43,224,684	43,229,468	4,784	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2565, 2_A375_pNL97_plus_lncRNA_AR..1..3679, 4_A375_EGR1..1..3695, 4_A375_EGR1..1..3696, 4_A375_EGR1..1..3697	14164, 564, -2360, 1172, 13951	downstream, in gene, upstream, in gene, downstream	1	1	1	16.67	19.67	19.67	3	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene HEXIM1	FLJ13562, EDG1, MAQ1, HIS1, CLP1, HEXIM1	hexamethylene bis-acetamide inducible 1	NM_006460	202814_s_at, 202815_s_at, 214186_at, 238442_at	NP_006451.1
GeneID:124790	HEXIM2	17	43,238,264	43,247,406	9,142	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2565, 1_A375_pNL7_minus_lncRNA_AR..1..2566, 2_A375_pNL97_plus_lncRNA_AR..1..3680, 2_A375_pNL97_plus_lncRNA_AR..1..3681, 4_A375_EGR1..1..3697	584, 11784, 10056, 11600, 371	in gene, downstream, downstream, downstream, in gene	1	1	1	20	24.33	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene HEXIM2	FLJ32384, HEXIM2, L3	hexamethylene bis-acetamide inducible 2	NM_144608, hCT19219.2, hCT1952658.1	238547_at, 243796_at	NP_653209.1, EAW51542.1, EAW51541.1
GeneID:100505972	LOC100505972	17	43,246,167	43,248,852	2,685	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2565, 1_A375_pNL7_minus_lncRNA_AR..1..2566, 2_A375_pNL97_plus_lncRNA_AR..1..3680, 2_A375_pNL97_plus_lncRNA_AR..1..3681, 4_A375_EGR1..1..3697	10004, -1196, 532, -1212, 10217	downstream, upstream, in gene, upstream, downstream	1	1	1	20	24.33	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene LOC100505972		hypothetical LOC100505972	XR_109387		
GeneID:752	FMNL1	17	43,299,292	43,324,665	25,393	+	1	4_A375_EGR1..1..3698	-524	upstream	0	0	1	5	6	16	1	4_A375_EGR1..1	16	Gene FMNL1	FMNL, MGC133052, FMNL1, KW-13, C17orf1B, FHOD4, MGC21878, MGC1894, C17orf1	formin-like 1	NM_005892, hCT2275310.0, hCT2275311.0, hCT2275312.0, hCT2275313.0, hCT2275314.0	1569257_at, 204789_at	NP_005883.2, EAW51537.1, EAW51534.1, EAW51535.1, EAW51536.1, EAW51538.1
GeneID:9020	MAP3K14	17	43,340,488	43,394,414	53,926	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2567	-242	upstream	1	0	0	17	16	13	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene MAP3K14	MAP3K14, HSNIK, FTDCR1B, HS, NIK	mitogen-activated protein kinase kinase kinase 14	NM_003954, hCT18746.1, hCT1952652.1	205192_at	NP_003945.2, EAW51529.1, EAW51530.1
GeneID:201176	ARHGAP27	17	43,471,268	43,503,012	31,744	-	3	4_A375_EGR1..1..3699, 4_A375_EGR1..1..3700, 4_A375_EGR1..1..3701	28932, 22484, 19892	in gene, in gene, in gene	0	0	1	4	7	16.67	3	4_A375_EGR1..1	21	Gene ARHGAP27	ARHGAP27, SH3P20, FLJ43547, MGC120624, CAMGAP1, FLJ35572, MGC78393, PP905, FLJ78025, SH3D20	Rho GTPase activating protein 27	NM_199282, NM_001159330, hCT19221.2	225618_at, 227057_at, 229424_s_at	NP_954976.1, NP_001152802.1, EAW51528.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A2T5_2_A2T5_3_A2T5_4_A2T5_1_A2T7_2_A2T7_3_A2T7_4_A2T7_Adjusted Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
GeneID:15534	CRHR1	17	43,661,648	43,815,194	153,546	+	3	1_A2T5_EGR1..3702, 4_A2T5_EGR1..3702, 4_A2T5_EGR1..3704	79e..50874, 60894	vs gene, vs gene, downstream	0 0 1 6.33 7.97 17.67 3	4_A2T5_EGR1..1	19	Gene CRHR1	CRHR1, CAR1R, CAR1, CRHR1A, CRHR1, CRFR1, CAR-R, CRHR1	corticotropin releasing hormone receptor 1	NM_004382, NM_001145145, NM_001145147, NM_001145148, XCT1682629.1, XCT1682630.1, XCT1682631.1, XCT1682632.1, XCT2072127.0	230895_x_at, 211977_s_at, 214919_at	NP_004373.2, NP_001138615.1, NP_001138616.1, NP_001138617.1, NP_001138618.1, NP_001138620.1, EAW45387.1, EAW45960.1, EAW45961.1, EAW45965.1, EAW45966.1, EAW45967.1
GeneID:10120777	LOC100120977	17	43,920,732	43,972,879	52,157	+	7	1_A2T5_gh37_rivus_lncRNA_AR..1.2865, 1_A2T5_gh37_duo_lncRNA_AR..1.2869, 2_A2T5_gh37_duo_lncRNA_AR..1.2865, 2_A2T5_gh37_duo_lncRNA_AR..1.2864, 4_A2T5_EGR1..1.3720, 4_A2T5_EGR1..1.3726, 4_A2T5_EGR1..1.3728	37599, 1187, 37599, 1145, 80839, 80239, 41923	vs gene, vs gene, vs gene, downstream, vs gene, vs gene	1 1 1 12 12.6 14.2 5	1_A2T5_gh37_rivus_lncRNA_AR..1	24	Gene LOC100120977		hypothetical LOC100120977	NM_024359		
GeneID:1815	MIPS	17	43,922,256	43,924,436	2,182	+	3	4_A2T5_EGR1..1.3703, 4_A2T5_EGR1..1.3706, 4_A2T5_EGR1..1.3708	-9908, 264, 9600	upstream, vs gene, downstream	0 0 1 8.33 8.97 17.33 3	4_A2T5_EGR1..1	16	Gene MIP3	EFP12c	vitamin k dependent protein S	NM_175552, XCT1684849.1	231205_at	NP_787078.2, EAW45596.1
GeneID:4141	MAPT	17	43,971,746	44,105,700	133,932	+	3	1_A2T5_gh37_rivus_lncRNA_AR..1.2869, 2_A2T5_gh37_duo_lncRNA_AR..1.2864, 4_A2T5_EGR1..1.3708	-136, -13, 118168	upstream, upstream, vs gene	1 1 1 11 11 11 2	2_A2T3_gh37_duo_lncRNA_AR..1	20	Gene MAPT	MSTD, DDPAC, MAPT, MTBT2, FLJ31424, TAU, MAPTL, MSTD1, MSTD1594, MTBT1, PPND, FTDP-17	microtubule-associated protein tau	NM_001123066, NM_001123067, NM_005910, NM_016834, NM_016835, NM_016841, NCT1683033.1, NCT1683043.1, NCT1683044.1, NCT1683422.1, NCT1683663.1, XCT2270129.0, XCT2270130.0, XCT2270131.0, XCT2270136.0	202092_s_at, 202093_s_at, 202094_at, 202095_s_at, 209400_s_at, 209401_s_at, 209402_s_at, 209403_x_at, 209404_s_at, 209405_s_at, 209406_s_at, 209407_s_at, 209408_at, 209409_at, 209410_at, 209411_s_at, 209412_at, 209413_at, 209414_s_at, 209415_at, 209416_at, 209417_s_at, 209418_s_at, 209419_at	NP_001119322.2, NP_001119323.1, NP_005901.2, NP_058519.1, NP_058520.1, NP_058521.1, EAW45965.1, EAW45966.1, EAW45967.1, EAW45968.1, EAW45969.1, EAW45970.1, EAW45971.1, EAW45972.1, EAW45973.1, EAW45974.1
GeneID:1013014	LOC100130146	17	43,973,149	43,976,164	3,016	+	2	1_A2T5_gh37_rivus_lncRNA_AR..1.2869, 2_A2T5_gh37_duo_lncRNA_AR..1.2864	-1427, -1418	upstream, upstream	1 1 1 0 17 20 10 1	2_A2T3_gh37_duo_lncRNA_AR..1	20	Gene LOC100130146		hypothetical LOC100130146	NR_024360		
GeneID:2851	KIAA1267	17	44,167,282	44,202,740	155,458	+	1	4_A2T5_EGR1..1.3707	31444	vs gene	0 0 1 19 20 22 1	4_A2T5_EGR1..1	22	Gene KIAA1267	MSL1v1, DKFZp727C081, MGC102362, KIAA1267, bA425I9.1 (novel protein)	KIAA1267	NM_015443, NM_001195655, NM_001195656, XCT1686622.1, XCT2072366.0	224469_at, 224490_s_at, 224491_s_at, 231177_at, 243369_at	NP_056258.1, NP_001182584.1, NP_001182585.1, EAW45876.1, EAW45877.1
GeneID:8464	LOC84464	17	44,270,929	44,274,089	3,160	+	1	4_A2T5_EGR1..1.3707	287	vs gene	0 0 1 19 20 22 1	4_A2T5_EGR1..1	22	Gene LOC84464		hypothetical LOC84464	NR_034172	229857_s_at, 230555_s_at	
GeneID:7474	WNT3	17	44,641,866	44,696,982	54,396	+	1	4_A2T5_EGR1..1.3708	47834	vs gene	0 0 1 9 10 16 1	4_A2T5_EGR1..1	16	Gene WNT3	MGC133323, WNT3, MGC131990, INT4, MGC133321	wingless-type MMTV integration site family, member 3	NM_030753, XCT1911774	221453_s_at, 221923_at, 231743_at	NP_110393.1, EAW57703.1
GeneID:7474	WNT9B	17	44,926,960	44,934,427	23,469	+	1	4_A2T5_EGR1..1.3709	32152	downstream	0 0 1 8 9 14 1	4_A2T5_EGR1..1	14	Gene WNT9B	WNT14B, WNT9B, WNT14	wingless-type MMTV integration site family, member 9B	NM_003396, XCT1911813, XCT2727377.0	1552972_at	NP_003387.1, EAW57702.1, EAW57703.1
GeneID:5932	GOSR2	17	45,000,466	45,016,703	16,247	+	2	1_A2T5_gh37_rivus_lncRNA_AR..1.2855, 2_A2T5_gh37_duo_lncRNA_AR..1.2853	-51, -198	upstream, upstream	1 1 1 0 22 34 16 1	2_A2T3_gh37_duo_lncRNA_AR..1	34	Gene GOSR2	GS27, Bos1, GOSR2	golgi SNAP receptor complex member 2	NM_004727, NM_004297, NM_005015811, NCT2727730.0, XCT2727731.0, XCT2727740.0, XCT2727741.0, XCT2832231.0, XCT2832232.0, XCT2832233.0	210093_s_at, 212144_at, 213393_s_at, 213395_at, 213397_x_at, 213398_s_at, 219184_s_at, 229190_at	NP_473365.1, NP_004291.2, NP_005115291.1, EAW57694.1, EAW57695.1, EAW57699.1, EAW57698.1, EAW57697.1, EAW57692.1, EAW57700.1
GeneID:1005214	LOC100506214	17	45,133,575	45,144,884	11,261	-	2	1_A2T5_gh37_rivus_lncRNA_AR..1.2872, 2_A2T5_gh37_duo_lncRNA_AR..1.2867	54, 66	vs gene, vs gene	1 1 1 0 26 24 6 1	1_A2T5_gh37_rivus_lncRNA_AR..1	26	Gene LOC100506214		hypothetical LOC100506214	XR_111709, XR_109291, XR_115110		
GeneID:9662	CDC27	17	45,195,310	45,288,865	71,555	-	3	4_A2T5_EGR1..1.3711, 4_A2T5_EGR1..1.3712, 4_A2T5_EGR1..1.3713	22029, 29398, 17537	vs gene, vs gene, vs gene	0 0 1 18.33 18.33 31.33 3	4_A2T5_EGR1..1	44	Gene CDC27	D0S1420E, APC3, CDC27, HNUC, ANAPC3, D17S978E, NUC2, CDC27Hs	cell division cycle 27 homolog (S. cerevisiae)	NM_001256, NM_001114091, XCT2722362.0, XCT2722363.0, XCT2722364.0, XCT2832330.0	214228_at, 217070_s_at, 217079_s_at, 217081_s_at	NP_001247.3, NP_001107983.1, EAW57686.1, EAW57687.1, EAW57688.1, EAW57689.1
GeneID:3689	ITGB3	17	45,231,200	45,290,077	58,889	+	3	1_A2T3_gh37_rivus_lncRNA_AR..1.2873, 2_A2T3_gh37_duo_lncRNA_AR..1.2868, 2_A2T5_gh37_duo_lncRNA_AR..1.2869	170, 24744, 14186	vs gene, vs gene, vs gene	1 1 1 0 13 13.67 10.33 3	2_A2T3_gh37_duo_lncRNA_AR..1	19	Gene ITGB3	CD61, ITGB3, GPIIIa, GPIIIa	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	NM_000212, XCT1676432, XCT2727350.0, XCT2727781.0, XCT2727782.0	204753_s_at, 204626_s_at, 204627_s_at, 204628_s_at, 211579_at, 213294_at, 216281_at	NP_000203.2, EAW57682.1, EAW57679.1, EAW57680.1, EAW57681.1
GeneID:1005252	LOC100506252	17	45,260,826	45,263,051	2,225	-	1	2_A2T5_gh37_duo_lncRNA_AR..1.2869	10047	downstream	0 0 1 0 11 17 10 1	2_A2T3_gh37_duo_lncRNA_AR..1	17	Gene LOC100506252		hypothetical LOC100506252	XR_109392		
GeneID:4908	CTXN3	17	45,481,347	45,516,676	117,331	+	1	1_A2T3_gh37_rivus_lncRNA_AR..1.2874	211	upstream	1 1 0 0 19 16 12 1	1_A2T3_gh37_rivus_lncRNA_AR..1	19	Gene CTXN3	CTXN3Y, FLJ38126, FLJ38110, FLJ43342	chromosome 17 open reading frame 67	NM_152347	1553629_a_at, 1553627_s_at, 1554772_at, 1558354_s_at, 1559678_at	NP_689480.2
GeneID:3845	KPNB1	17	45,727,273	45,761,004	33,729	+	1	4_A2T5_EGR1..1.3715	987	upstream	0 0 1 16 13 19 1	4_A2T5_EGR1..1	19	Gene KPNB1	Impnb, MGC2155, MGC2156, IPOB, KPNB1, IMB1, IPO1, NTF97, MGC12167	karyopherin (importin) beta 1	NM_002265, XCT1612283.2, XCT1969680.1, XCT1969682.1, XCT1969683.1, XCT1969685.1	208974_x_at, 208975_s_at, 210987_s_at, 211074_s_at, 211075_s_at, 211076_at, 211077_x_at, 211078_s_at, 211079_at, 211080_at, 211081_x_at, 211082_x_at, 211083_s_at, 211084_x_at, 211085_x_at, 211086_x_at, 211087_x_at	NP_002256.2, EAW54607.1, EAW54608.1, EAW54609.1, EAW54610.1
GeneID:9755	TBX6BP1	17	45,772,630	45,789,429	16,799	+	1	4_A2T5_EGR1..1.3716	862	vs gene	0 0 1 8 8 17 1	4_A2T5_EGR1..1	17	Gene TBX6BP1	KIAA0775, TBX6P1, SHOT6HD, Rogdi-h.P2	TBX1 binding protein 1	NM_014726, XCT1610168.1, XCT2255726.0	205624_at	NP_055541.1, EAW54605.1, EAW54606.1
GeneID:1005369	LOC100506369	17	45,802,471	45,901,531	99,060	+	4	1_A2T5_gh37_rivus_lncRNA_AR..1.2876, 1_A2T5_gh37_duo_lncRNA_AR..1.2861, 4_A2T5_EGR1..1.3716, 4_A2T5_EGR1..1.3719	16712, 16791, 11677, 16632	vs gene, vs gene, vs gene	1 1 1 1 29 25 16.5 2	1_A2T5_gh37_rivus_lncRNA_AR..1	51	Gene LOC100506369		hypothetical LOC100506369	XR_109393		
GeneID:1159	OSBPL7	17	45,854,703	45,899,147	14,414	-	4	1_A2T5_gh37_rivus_lncRNA_AR..1.2876, 1_A2T5_gh37_duo_lncRNA_AR..1.2861, 4_A2T5_EGR1..1.3716, 4_A2T5_EGR1..1.3719	-37, -93, 5099, 42	upstream, upstream, vs gene, vs gene	1 1 1 1 29 25 16.5 2	1_A2T5_gh37_rivus_lncRNA_AR..1	51	Gene OSBPL7	MGC71150, OSBPL7, ORP7	oxysterol binding protein-like 7	NM_145795, XCT1965831.1, XCT1965841.1, XCT2072021.2, XCT2077702.0	220165_s_at, 219544_at, 227845_at	NP_665741.1, EAW54603.1, EAW54604.1, EAW54631.1, EAW54632.1
GeneID:1293	MRPL10	17	45,900,650	45,906,903	6,253	+	4	1_A2T5_gh37_rivus_lncRNA_AR..1.2876, 1_A2T5_gh37_duo_lncRNA_AR..1.2861, 4_A2T5_EGR1..1.3716, 4_A2T5_EGR1..1.3719	5719, 9671, 14535, 5799	downstream, downstream, downstream, downstream	1 1 1 1 29 25 16.5 2	1_A2T5_gh37_rivus_lncRNA_AR..1	51	Gene MRPL10	mitochondrial ribosomal protein L10, MRPL10, L10MT, MRP-L10, MRP-L0, RPWL6	mitochondrial ribosomal protein L10	NM_145253, XCT1933814, XCT2340177.0, XCT2340179.0, XCT2340179.2, XCT2377298.0	224871_at	NP_660156.2, EAW54796.1, EAW54797.1, EAW54798.1, EAW54799.1
GeneID:9861	LRRC46	17	45,906,993	45,915,079	8,086	+	3	1_A2T5_gh37_rivus_lncRNA_AR..1.2876, 1_A2T5_gh37_duo_lncRNA_AR..1.2861, 4_A2T5_EGR1..1.3716, 4_A2T5_EGR1..1.3891, 4_A2T5_EGR1..1.3719	-9905, -9791, 9909	upstream, upstream, upstream	1 1 1 1 51 41 16 1	1_A2T5_gh37_rivus_lncRNA_AR..1	51	Gene LRRC46	LRRC46, FLJ23333, MGC16039	leucine rich repeat containing 46	NM_033413, XCT2032812.2, XCT2337330.0	230800_at, 239851_s_at	NP_219481.1, EAW54793.1, EAW54794.1
GeneID:8027	SCRN2	17	45,915,047	45,916,899	3,852	-	1	4_A2T5_EGR1..1.3720	4851	upstream	0 0 1 8 7 16 1	4_A2T5_EGR1..1	16	Gene SCRN2	SCRN2, Sec2	secernin 2	NM_001145023, NM_138555, XCT1958544.1, XCT1963451.1, XCT2032827.2	225512_at, 228752_s_at	NP_001138615.1, NP_612354.2, EAW54790.1, EAW54791.1, EAW54792.1
GeneID:8839	SPI1	17	45,922,260	45,933,340	10,960	-	1	4_A2T5_EGR1..1.3720	7960	vs gene	0 0 1 8 7 16 1	4_A2T5_EGR1..1	16	Gene SPI1	KLF14, MGC119985, MGC119982, MGC119983, SPI5, SFPI1PROFIN, MGC119984, SFPI1	Spi-1 leukemia virus 1 homolog (mouse)	NM_139292	229979_at	NP_954771.1
GeneID:1005369	LOC100506293	17	45,966,595	45,973,178	6,583	-	2	1_A2T3_gh37_rivus_lncRNA_AR..1.2877, 2_A2T3_gh37_duo_lncRNA_AR..1.2872	-230, -200	upstream, upstream	1 1 1 0 44 56 9 1	2_A2T3_gh37_duo_lncRNA_AR..1	56	Gene LOC100506293		hypothetical LOC100506293	XR_111708, XR_111709, XR_109294, XR_109393, NR_110112, XR_111110		
GeneID:6667	SP2	17	45,973,516	46,006,523	32,807	+	2	1_A2T3_gh37_rivus_lncRNA_AR..1.2877, 2_A2T3_gh37_duo_lncRNA_AR..1.2872	-198, -168	upstream, upstream	1 1 1 0 44 56 9 1	2_A2T3_gh37_duo_lncRNA_AR..1	56	Gene SP2	SP2	Sp2 transcription factor	NM_003110, XCT1610288.2, XCT1969690.1, XCT2036972.0, XCT2036984.0, XCT2036985.0, XCT2036986.0, XCT2377046.0	204387_at, 211736_at, 211737_s_at, 237795_s_at	NP_003101.3, EAW54783.1, EAW54784.1, EAW54785.1, EAW54786.1, EAW54787.1, EAW54788.1
GeneID:1005369	LOC100506323	17	45,976,131	46,016,703	42,574	-	2	1_A2T3_gh37_rivus_lncRNA_AR..1.2877, 2_A2T3_gh37_duo_lncRNA_AR..1.2872	43817, 43317	downstream, downstream	1 1 1 0 44 56 9 1	2_A2T3_gh37_duo_lncRNA_AR..1	56	Gene LOC100506323		hypothetical LOC100506323	XR_111710, XR_109296, XR_115114		
GeneID:1027	CDK5RAP1	17	46,045,429	46,059,147	10,718	+	1	2_A2T3_gh37_duo_lncRNA_AR..1.2893	147	vs gene	0 0 1 0 17 20 14 1	2_A2T3_gh37_duo_lncRNA_AR..1	20	Gene CDK5RAP3	CN59W-114, CDK5RAP3, ICI3, HSF27, C6, LZAP, MST016	CDK5 regulatory subunit associated protein 3	NM_176096, XCT1965875.1, XCT1965876.1, XCT1965877.1, XCT2032823.1, XCT2377234.0, XCT2377236.0	219740_s_at	NP_788276.1, EAW54774.1, EAW54772.1, EAW54773.1, EAW54775.1, EAW54776.1, EAW54777.1
GeneID:2208	COPZ2	17	46,103,533	46,115,152	11,619	-	4	1_A2T3_gh37_rivus_lncRNA_AR..1.2876, 2_A2T3_gh37_duo_lncRNA_AR..1.2894, 4_A2T5_EGR1..1.3721, 4_A2T5_EGR1..1.3724	-9906, -10098, 13830, 518	upstream, upstream, downstream, vs gene	1 1 1 1 15.67 14 20 3	4_A2T5_EGR1..1	25	Gene COPZ2	COPZ2, MGC20398	coatomer protein complex, subunit zeta 2	NM_016429, XCT2035122	219381_at, 233697_at	NP_057615.1, EAW54789.1
GeneID:4508	MIR152	17	46,114,527	46,114,613	86	+	1	4_A2T3_EGR1..1.3724	277	downstream	0 0 1 13 8 16 1	4_A2T5_EGR1..1	16	Gene MIR152	MIR0152, MIR152	microRNA 152	NR_029657		
GeneID:4791	NFE2L1	17	46,125,806	46,139,907	13,221	+	3	1_A2T3_gh37_rivus_lncRNA_AR..1.2876, 2_A2T3_gh37_duo_lncRNA_AR..1.2894, 4_A2T5_EGR1..1.3725	-596, -439, 170	upstream, upstream, vs gene	1 1 1 1 19 16 19 1	1_A2T3_gh37_rivus_lncRNA_AR..1	19	Gene NFE2L1	LCR-F1, NRF1, TCF11, FLJ40350, NFE2L1	nuclear factor (erythroid-derived 2)-like 1	NM_003204, XCT1965841.1, XCT1965842.1, XCT2035112, XCT2036903.0, XCT2036909.0, XCT2036911.0, XCT2377127.0	200785_s_at, 200786_s_at, 214179_s_at, 214180_s_at	NP_003195.1, EAW54782.1, EAW54784.1, EAW54785.1, EAW54786.1, EAW54787.1, EAW54788.1
GeneID:1053	CBX1	17	46,147,414	46,176,861	31,469	-	2	1_A2T3_gh37_rivus_lncRNA_AR..1.2879, 2_A2T3_gh37_duo_lncRNA_AR..1.2893	-29, -8255	upstream, upstream	1 1 1 0 13.5 14.5 12 2	2_A2T3_gh37_duo_lncRNA_AR..1	16	Gene CBX1	C-Bx1, C-Bx, HP1-BETA, HP1-Hsbeta, HP1Hs-beta, p25beta, MOD1	chromobox homolog 1	NM_127220, NM_006807, XCT2364224.0, XCT2364225.0, XCT2364227.0, XCT2377725.0	201516_at	NP_001117220.1, NP_008795.1, EAW54780.1, EAW54781.1, EAW54782.1, EAW54783.1
GeneID:2908	SNX11	17	46,184,920	46,200,103	15,183	+	2	1_A2T3_gh37_rivus_lncRNA_AR..1.2879, 2_A2T3_gh37_duo_lncRNA_AR..1.2893	-8005, 221	upstream, vs gene	1 1 1 0 13.5 14.5 12 2	2_A2T3_gh37_duo_lncRNA_AR..1	16	Gene SNX11	MGC11079, SNX11	sorting nexin 11	NM_013323, NM_152244, XCT1983540.1, XCT1983660.1, XCT2035912.2, XCT2377720.0, XCT2377721.0, XCT2377722.0	220140_s_at, 220312_at	NP_037455.2, NP_689480.1, EAW54752.1, EAW54753.1, EAW54754.1, EAW54757.1, EAW54758.1
GeneID:4298	KCNJ2	17	46,887,923	46,893,778	15,855	+	2	1_A2T3_gh37_rivus_lncRNA_AR..1.2880, 2_A2T3_gh37_duo_lncRNA_AR..1.2896	20017, 20269	downstream, downstream	1 1 1 0 16 16 10 1	1_A2T3_gh37_rivus_lncRNA_AR..1	16	Gene KCNJ2	CCDC49, IRK2	potassium inwardly-rectifying channel, subfamily J, member 2	NM_000891, NM_033292, NM_033293, NM_033294, NR_033295	230742_at, 239791_at	
GeneID:3316	HOXB9	17	46,870,899	46,882,334	11,435	-	2	1_A2T3_gh37_rivus_lncRNA_AR..1.2880, 2_A2T3_gh37_duo_lncRNA_AR..1.2896	-5806, -5896	upstream, upstream	1 1 1 0 16 16 13 1	1_A2T3_gh37_rivus_lncRNA_AR..1	16	Gene HOXB9	Hox-2.2, HOX2, HLA2, HOXB6, HOX2B	homeobox B9	NM_183392	203383_at, 203384_s_at	NP_061825.2
GeneID:3217	HOXB7	17	46,884,394	46,890,393	5,999	-	2	1_A2T3_gh37_rivus_lncRNA_AR..1.2880, 2_A2T3_gh37_duo_lncRNA_AR..1.2896	643, 331	vs gene, vs gene	1 1 1 0 16 16 13 1	1_A2T3_gh37_rivus_lncRNA_AR..1	16	Gene HOXB7	HOXB7, HOX2, HHO.C1, Hox-2.3, HOX2C	homeobox B7	NM_004502, XCT2035917.1, XCT2224267.1	204779_s_at, 204779_s_at, 204779_s_at	NP_004493.3, EAW54723.1, EAW54725.1, EAW54726.1
GeneID:3218	HOXB6	17	46,889,706	46,892,301	2,595	-	2	1_A2T3_gh37_rivus_lncRNA_AR..1.2880, 2_A2T3_gh37_duo_lncRNA_AR..1.2896	4481, 4269	downstream, downstream	1 1 1 0 16 16 13 1	1_A2T3_gh37_rivus_lncRNA_AR..1	16	Gene HOXB6	HOX2, HOX2B, Hox-2.4, HOX2D	homeobox B6	NM_024015, XCT1961334.1, XCT1961335.1	221276_at, 221687_s_at, 230114_at	NP_276031.1, EAW54722.1, EAW54724.1
GeneID:5464	PRAC	17	46,799,861	46,799,992	851	-	1	1_A2T3_gh37_rivus_lncRNA_AR..1.2881	1034	upstream	1 0 0 20 19 8 1	1_A2T3_gh37_rivus_lncRNA_AR..1	20	Gene PRAC	C17orf52, PRAC, MGC23320	prostate cancer susceptibility candidate	NM_032391, XCT1610043.0	230764_at	NP_115787.1, EAW54717.1
GeneID:5863	C17orf61	17	46,800,942	46,802,119	1,177	+	1	1_A2T3_gh37_rivus_lncRNA_AR..1.2881	874	vs gene	1 0 0 20 19 8 1	1_A2T3_gh37_rivus_lncRNA_AR..1	20	Gene C17orf61	PRAC2, C17orf61, NCRNA00253	chromosome 17 open reading frame 61	NR_026103	230945_at	
GeneID:1042978	MIR3188	17	46,801,770	46,801,837	67	-	1	1_A2T3_gh37_rivus_lncRNA_AR..1.2881	621	downstream	1 0 0 20 19 8 1	1_A2T3_gh37_rivus_lncRNA_AR..1	20	Gene MIR3188	MIR3188	microRNA 3188	NR_036190		
GeneID:1005611	HOXB15	17	46,802,125	46,806,111	3,986	-	1	1_A2T3_gh37_rivus_lncRNA_AR..1.2881	4885	downstream	1 0 0 20 19 8 1	1_A2T3_gh37_rivus_lncRNA_AR..1	20	Gene HOXB15	PSHD, HOXB15	homeobox B15	NM_030581, XCT1610357.2	209644_at, 230535_at	NP_598352.2, EAW54714.1
GeneID:6845	UBE2Z	17	46,805,731	47,006,423	20,691	+	1	4_A2T3_EGR1..1.3726	29	vs gene	0 0 1 0 16 21 20 1	4_A2T3_EGR1..1.3	20	Gene UBE2Z	FLJ13855, UBE2Z, HOYS7, USE1	ubiquitin-conjugating enzyme E2Z (putative)	NM_020379, XCT1610881.2, XCT1960834.1, XCT2365369.0, XCT2377747.0	217750_s_at, 222393_s_at, 238167_at	NP_065421.2, EAW54703.1, EAW54701.1, EAW54702.1, EAW54704.1
GeneID:1011267	SNF8	17	47,007,456	47,022,154	14,699	+	1	4_A2T3_gh37_duo_lncRNA_AR..1.2897	-132	upstream	1 0 0 15 20 11 1	2_A2T3_gh37_duo_lncRNA_AR..1	20	Gene SNF8	Dit3, VPS22, SNF8, EAP30	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	NM_006178, XCT1610913.1, XCT1960838.1, XCT2377750.0	218391_at, 242790_at	NP_006169.2, EAW54699.1, EAW54700.1
GeneID:2896	GIP	17	47,033,916	47,045,955	10,037	-	1	2_A2T3_gh37_duo_lncRNA_AR..1.2894	-3901	upstream	0 0 1 0 11 21 5 1	2_A2T3_gh37_duo_lncRNA_AR..1	21	Gene GIP	GIP	gastric inhibitory polypeptide	NM_004123, XCT1684912	207869_at	NP_004114.1, EAW54697.1
GeneID:1287	FLJ40194	17	47,035,935	47,036,027	10,222	+	1	2_A2T3_gh37_duo_lncRNA_AR..1.2700	12287	downstream	0 0 1 0 10 16 8 1	2_A2T3_gh37_duo_lncRNA_AR..1	16	Gene FLJ40194		hypothetical FLJ40194	NR_038161, XCT2355572.0		EAW54695.1
GeneID:6534	ZNF652	17	47,366,966	47,439,833	72,867	-	1	4_A2T3_EGR1..1.3728	891	vs gene	0 0 1 12 14 15 1	4_A2T3_EGR1..1	15	Gene ZNF652	KIAA0924, ZNF652, DKFZp761E123	zinc finger protein 652	NM_014897, NM_001145083, XCT1949.5, XCT1960442	203594_at, 223288_at, 233577_at	NP_055712.1, NP_001138037.1, EAW54682.1, EAW54683.1
GeneID:4804	NGFR	17	47,572,655	47,592,392	19,737	+	2	4_A2T3_EGR1..1.3731, 4_A2T3_EGR1..1.3732	209, 945	vs gene, vs gene	0 0 1 8.5 10.5 15 2	4_A2T3_EGR1..1	16	Gene NGFR	p75(NGFR), CD271, NGFR, TNFRSF16, (p75NTR, (p75(NTR)	nerve growth factor receptor (TNFR superfamily, member 16)	NM_002507, XCT1610954.2	205859_at	NP_002498.1, EAW54677.1
GeneID:1005369	LOC100506369	17	47,585,019	47,851,426	66,407	-	3	4_A2T3_EGR1..1.3731, 4_A2T3_EGR1..1.3732, 4_A2T3_EGR1..1.3733	76882, 77636, 4808	downstream, downstream, upstream	0 0 1 5.67 9.67 17.67 3	4_A2T3_EGR1..1	16	Gene LOC100506369		hypothetical LOC100506369	XR_111710, XR_109299, XR_115117		
GeneID:1173	NXPH2	17	47,853,295	47,861,172	7,874	+	1	4_A2T3_EGR1..1.3733	2734	vs gene	0 0 1 4 8 17 1	4_A2T3_EGR1..1	17	Gene NXPH3	NPH3, NXPH3	neurexophilin 3	NM_007225, XCT2702.0	221991_at, 226210_at	NP_009156.2, EAW54678.1





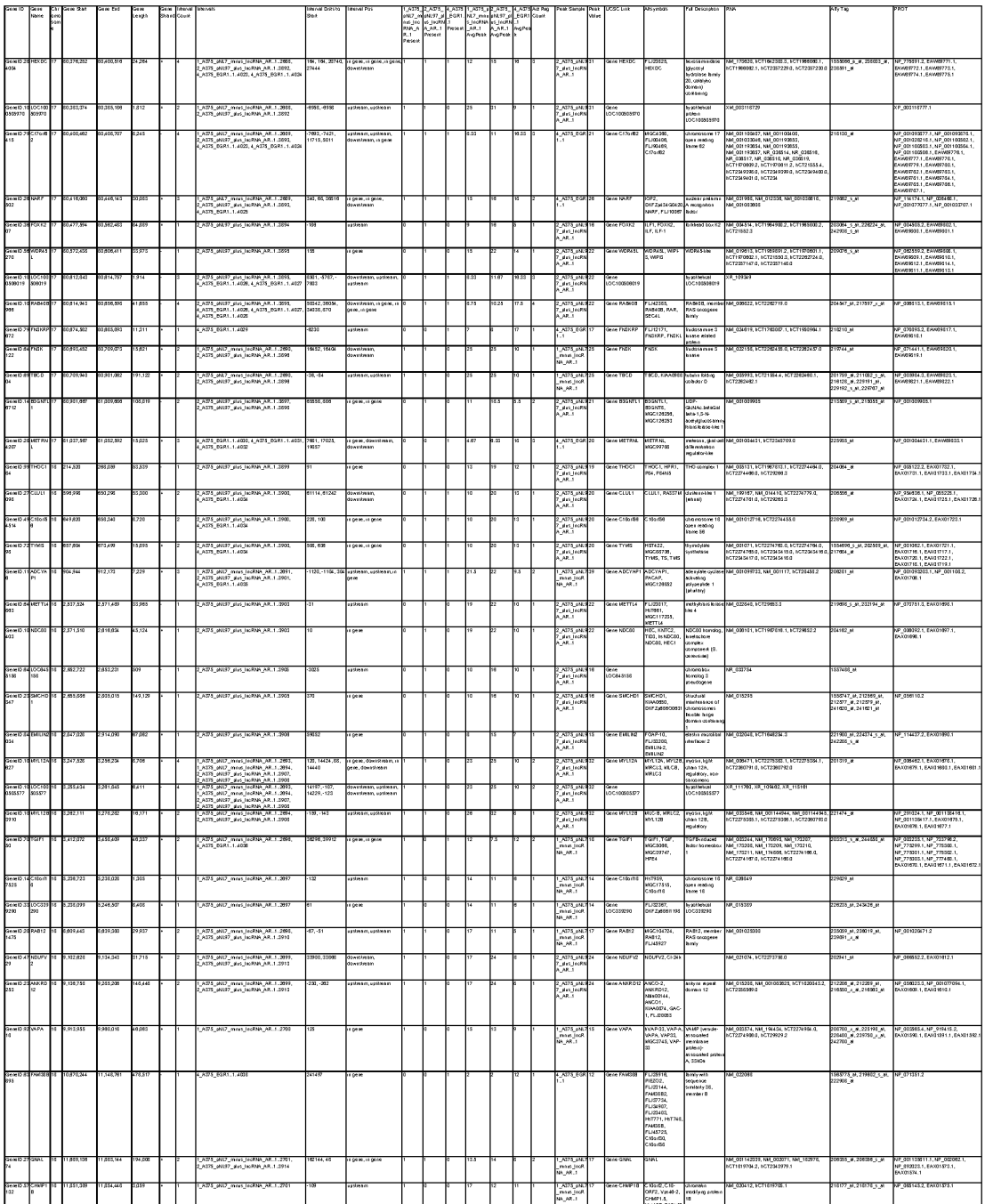
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:1444	CSHL1	17	61,986,965	61,988,618	1,653	-	1	4_A375_EGR1..1..3770	-5614	upstream	0	0	1	7	2	60	1	4_A375_EGR1..1	60	Gene CSHL1	CSL, hCS-L, CSHL1, CS-5, CSHP1, MGC149868	chorionic somatomammotropin hormone-like 1	NM_001318, NM_022579, NM_022580, NM_022581	205958_x_at, 207285_x_at, 208293_x_at, 208294_x_at, 208295_x_at	NP_001309.3, NP_072101.1, NP_072102.1, NP_072103.1
GeneID:2688	GH1	17	61,994,563	61,996,198	1,635	-	1	4_A375_EGR1..1..3770	1766	downstream	0	0	1	7	2	60	1	4_A375_EGR1..1	60	Gene GH1	GH, hGH-N, IGHD1B, GH1, GHN, GH-N	growth hormone 1	NM_000515, NM_022559, NM_022560, NM_022561, NM_022562	205840_x_at, 206685_x_at, 211151_x_at	NP_000506.2, NP_072053.1, NP_072054.1, NP_072055.1, NP_072056.1
GeneID:6329	SCN4A	17	62,015,914	62,050,278	34,364	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2624, 2_A375_pNL97_plus_lncRNA_AR..1..3768, 4_A375_EGR1..1..3771, 4_A375_EGR1..1..3772	-1786, -1487, 24836, -154	upstream, upstream, in gene, upstream	1	1	1	10	12	14.33	3	4_A375_EGR1..1	20	Gene SCN4A	HYPP, SkM1, Na(V)1.4, HOKPP2, NAC1A, HYKPP, Nav1.4, SCN4A	sodium channel, voltage-gated, type IV, alpha subunit	NM_000334, hCT2286741.0, hCT33068.2	206981_at	NP_000325.4, EAW94226.1, EAW94225.1
GeneID:92340	C17orf72	17	62,075,711	62,081,645	5,934	+	2	4_A375_EGR1..1..3773, 4_A375_EGR1..1..3774	-7999, 721	upstream, in gene	0	0	1	9	7	16	2	4_A375_EGR1..1	17	Gene C17orf72	DKFZp761M2312, FLJ11724, C17orf72	chromosome 17 open reading frame 72	NM_001164257, NM_001191029, NM_001191030, NM_001191031	232972_at	NP_001157729.1, NP_001177958.1, NP_001177959.1, NP_001177960.1
GeneID:3384	ICAM2	17	62,079,955	62,097,994	18,039	-	1	4_A375_EGR1..1..3774	21562	downstream	0	0	1	6	4	17	1	4_A375_EGR1..1	17	Gene ICAM2	CD102, ICAM2	intercellular adhesion molecule 2	NM_001099786, NM_000873, NM_001099787, NM_001099788, NM_001099789, hCT1950778.1, hCT1963245.1, hCT1963246.1, hCT2286716.0, hCT2286733.0	204683_at, 213620_s_at	NP_001093256.1, NP_000864.2, NP_001093257.1, NP_001093258.1, NP_001093259.1, EAW94216.1, EAW94217.1, EAW94218.1, EAW94219.1, EAW94220.1
GeneID:692227	SNORD104	17	62,223,438	62,223,517	79	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2625, 2_A375_pNL97_plus_lncRNA_AR..1..3769, 4_A375_EGR1..1..3775	-350, -110, -46	upstream, upstream, upstream	1	1	1	23	27	34	1	4_A375_EGR1..1	34	Gene SNORD104	U104, SNORD104	small nucleolar RNA, C/D box 104	NR_004380		
GeneID:677842	SNORA76	17	62,223,699	62,223,831	132	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2625, 2_A375_pNL97_plus_lncRNA_AR..1..3769, 4_A375_EGR1..1..3775	-611, -371, -307	upstream, upstream, upstream	1	1	1	23	27	34	1	4_A375_EGR1..1	34	Gene SNORA76	SNORA76, ACA62	small nucleolar RNA, H/ACA box 76	NR_002995	228879_at	
GeneID:55852	TEX2	17	62,224,795	62,340,653	115,858	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2625, 1_A375_pNL7_minus_lncRNA_AR..1..2626, 2_A375_pNL97_plus_lncRNA_AR..1..3769, 2_A375_pNL97_plus_lncRNA_AR..1..3770, 4_A375_EGR1..1..3775	117565, -179, 117325, -179, 117261	downstream, upstream, downstream, upstream, downstream	1	1	1	40	49	22	2	2_A375_pNL97_plus_lncRNA_AR..1	71	Gene TEX2	TMEM96, TEX2, HT008, DKFZp761G0721, KIAA1738	testis expressed 2	NM_018469, hCT2357746.0, hCT33095.3	218099_at	NP_060939.3, EAW94210.1, EAW94211.1
GeneID:100506981	LOC100506981	17	62,396,775	62,398,041	1,266	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3771	-6087	upstream	0	1	0	12	18	6	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100506981		hypothetical LOC100506981	XR_109420		
GeneID:5175	PECAM1	17	62,399,863	62,401,205	1,342	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3771	-2923	upstream	0	1	0	12	18	6	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PECAM1	FLJ58394, CD31, PECAM-1, PECAM1, FLJ34100	platelet/endothelial cell adhesion molecule	NM_000442, hCT2286665.0, hCT2286667.0	1559921_at, 208981_at, 208982_at, 208983_s_at	NP_000433.3, EAW94207.1, EAW94208.1
GeneID:11232	POLG2	17	62,473,902	62,493,184	19,282	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3772, 2_A375_pNL97_plus_lncRNA_AR..1..3773, 4_A375_EGR1..1..3776, 4_A375_EGR1..1..3777	-84, -10046, -9166, -10000	upstream, upstream, upstream, upstream	0	1	1	12.67	19.67	20.33	3	4_A375_EGR1..1	30	Gene POLG2	POLG2, HP55, MTPOLB, PEOA4, POLB, POLG-BETA, POLGB	polymerase (DNA directed), gamma 2, accessory subunit	NM_007215, hCT19316.2	205811_at	NP_009146.2, EAW94204.1
GeneID:1655	DDX5	17	62,494,374	62,502,484	8,110	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3772, 2_A375_pNL97_plus_lncRNA_AR..1..3773, 4_A375_EGR1..1..3776, 4_A375_EGR1..1..3777	9236, -748, 132, -700	downstream, upstream, in gene, upstream	0	1	1	12.67	19.67	20.33	3	4_A375_EGR1..1	30	Gene DDX5	DDX5, HLR1, p68, HUMP68, DKFZp686J01190, G17P1, DKFZp434E109	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	NM_004396, hCT18784.3, hCT1971014.1	200033_at	NP_004387.1, EAW94203.1, EAW94202.1
GeneID:90799	CCDC45	17	62,503,158	62,534,064	30,906	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3772, 2_A375_pNL97_plus_lncRNA_AR..1..3773, 4_A375_EGR1..1..3776, 4_A375_EGR1..1..3777	-9910, 74, -806, 26	upstream, in gene, upstream, in gene	0	1	1	12.67	19.67	20.33	3	4_A375_EGR1..1	30	Gene CCDC45	CCDC45, DKFZp667E1824	coiled-coil domain containing 45	NM_138363, hCT2287128.0, hCT2287129.0, hCT2287130.0, hCT2287131.0, hCT2357764.0	223815_at, 225705_at	NP_612372.1, EAW94196.1, EAW94197.1, EAW94198.1, EAW94199.1, EAW94200.1
GeneID:146880	LOC146880	17	62,745,780	62,778,117	32,337	-	1	4_A375_EGR1..1..3778	1093	in gene	0	0	1	3	2	15	1	4_A375_EGR1..1	15	Gene LOC146880	FLJ30780, FLJ40381, MGC40489	hypothetical LOC146880	NR_026899, NR_027487	229747_x_at	
GeneID:5578	PRKCA	17	64,298,926	64,806,862	507,936	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2632, 1_A375_pNL7_minus_lncRNA_AR..1..2633, 2_A375_pNL97_plus_lncRNA_AR..1..3781, 2_A375_pNL97_plus_lncRNA_AR..1..3782, 4_A375_EGR1..1..3782	190754, 237570, 208738, 237850, 626	in gene, in gene, in gene, in gene, in gene	1	1	1	15.25	18	6.25	4	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene PRKCA	AAG6, MGC129900, PRKACA, PKC-alpha, PKCA, PRKCA, MGC129901	protein kinase C, alpha	NM_002737, hCT20429.3	1560074_at, 206923_at, 213093_at, 215194_at, 215195_at	NP_002728.1, EAW89014.1
GeneID:27092	CACNG4	17	64,961,013	65,029,518	68,505	+	2	4_A375_EGR1..1..3783, 4_A375_EGR1..1..3784	32587, 59787	in gene, in gene	0	0	1	4.5	5	16	2	4_A375_EGR1..1	16	Gene CACNG4	MGC11138, MGC24983, CACNG4	calcium channel, voltage-dependent, gamma subunit 4	NM_014405, hCT1960748.1, hCT20401.3	221585_at, 231737_at, 62987_r_at	NP_055220.1, EAW89020.1, EAW89021.1
GeneID:5718	PSMD12	17	65,336,619	65,362,721	26,102	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3784, 4_A375_EGR1..1..3785	129, 1	in gene, in gene	0	1	1	21	24	24	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PSMD12	MGC75406, p55, Rpn5, PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	NM_002816, NM_174871, hCT1787864.3, hCT2284157.1, hCT2357209.0, hCT2357210.0	202352_s_at, 202353_s_at	NP_002807.1, NP_777360.1, EAW89026.1, EAW89027.1, EAW89028.1, EAW89029.1
GeneID:100507049	LOC100507049	17	65,671,272	65,713,744	42,472	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3785	-336	upstream	0	1	0	19	21	14	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100507049		hypothetical LOC100507049	XR_111744, XR_109422, XR_115138		
GeneID:25926	NOL11	17	65,714,061	65,740,266	26,205	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3785	19	in gene	0	1	0	19	21	14	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NOL11	NOL11, DKFZp586L0724	nucleolar protein 11	NM_015462, hCT2263087.0, hCT2263088.0, hCT2263091.0, hCT2263093.0, hCT2263094.0	221970_s_at	NP_056277.2, EAW89036.1, EAW89033.1, EAW89034.1, EAW89035.1, EAW89037.1
GeneID:2186	BPTF	17	65,821,780	65,980,494	158,714	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2634	-212	upstream	1	0	0	16	11	7	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene BPTF	NURF301, FALZ, BPTF, FAC1	bromodomain PHD finger transcription factor	NM_182641, NM_004459, hCT2263098.1, hCT2263104.1	207186_s_at, 209271_at, 230056_at, 231953_at, 232909_s_at	NP_872579.2, NP_004450.3, EAW89038.1, EAW89039.1
GeneID:3838	KPNA2	17	66,031,848	66,042,970	11,122	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3787, 4_A375_EGR1..1..3787	280, 120	in gene, in gene	0	1	1	14	22	19	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene KPNA2	RCH1, IPOA1, SRP1alpha, QIP2, KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	NM_002266, hCT2263099.1, hCT2346834.0	201088_at, 211762_s_at	NP_002257.1, EAW89041.1, EAW89040.1
GeneID:100499466	LOC100499466	17	66,097,696	66,132,070	34,374	+	1	4_A375_EGR1..1..3788	-1952	upstream	0	0	1	5	3	19	1	4_A375_EGR1..1	19	Gene LOC100499466	FLJ33831, FLJ35479	hypothetical LOC100499466	NR_027416		
GeneID:51321	AMZ2	17	66,244,145	66,253,305	9,160	+	1	4_A375_EGR1..1..3789	-241	upstream	0	0	1	16	13	24	1	4_A375_EGR1..1	24	Gene AMZ2	AMZ2		NM_016627, NM_001033569, NM_001033570, NM_001033571, NM_001033572, NM_001033574, hCT1954126.1, hCT1954129.1, hCT19818.3, hCT2261321.0, hCT2261323.0	218167_at, 227567_at	NP_057711.3, NP_001028741.1, NP_001028742.1, NP_001028743.1, NP_001028744.1, NP_001028746.1, EAW89047.1, EAW89048.1, EAW89049.1, EAW89050.1, EAW89051.1
GeneID:22901	ARSG	17	66,255,323	66,417,000	161,677	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2636, 1_A375_pNL7_minus_lncRNA_AR..1..2637, 2_A375_pNL97_plus_lncRNA_AR..1..3788, 2_A375_pNL97_plus_lncRNA_AR..1..3789	122053, 140965, 122005, 141269	in gene, in gene, in gene, in gene	1	1	0	17	17.5	6	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ARSG	ARSG, KIAA1001	arylsulfatase G	NM_014960, hCT1954101.1, hCT19813.3	1552632_a_at	NP_055775.2, EAW89056.1, EAW89055.1
GeneID:55062	WIPI1	17	66,417,422	66,453,653	36,231	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2636	21665	in gene	1	0	0	16	12	9	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene WIPI1	ATG18A, WIPI1, FLJ10055, ATG18, WIPI49	WD repeat domain, phosphoinositide interacting 1	NM_017983, hCT1954131.1, hCT1954132.1, hCT19820.3	203827_at, 213836_s_at	NP_060453.3, EAW89059.1, EAW89057.1, EAW89058.1
GeneID:5573	PRKAR1A	17	66,508,110	66,528,911	20,801	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2639, 2_A375_pNL97_plus_lncRNA_AR..1..3790	530, 308	in gene, in gene	1	1	0	21	26	9	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene PRKAR1A	TSE1, CAR, PRKAR1, CNC1, PRKAR1A, DKFZp779L0468, MGC17251, CNC, PKR1, PPNAD1	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	NM_002734, NM_212471, NM_212472, hCT1954118.1, hCT1954120.1, hCT19814.3, hCT2357168.0, hCT2357169.0, hCT2357170.0	200603_at, 200604_s_at, 200605_s_at, 242462_at	NP_002725.1, NP_997636.1, NP_997637.1, EAW89060.1, EAW89063.1, EAW89065.1, EAW89061.1, EAW89062.1, EAW89064.1
GeneID:54757	FAM20A	17	66,531,257	66,597,095	65,838	-	1	4_A375_EGR1..1..3790	679	in gene	0	0	1	11	13	21	1	4_A375_EGR1..1	21	Gene FAM20A	FP2747, DKFZp434F2322, FAM20A	family with sequence similarity 20, member A	NM_017565, NR_027751, hCT2261554.0	226804_at, 241981_at, 242945_at	NP_060035.2, EAW89066.1
GeneID:10351	ABCA8	17	66,863,430	66,951,533	88,103	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3792	46189	in gene	0	1	0	14	14	4	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene ABCA8	KIAA0822, MGC163152, ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	NM_007168, hCT1954125.1, hCT19816.3	1565778_at, 1565780_at, 204719_at	NP_009099.1, EAW89068.1, EAW89069.1
GeneID:5608	MAP2K6	17	67,410,838	67,538,470	127,632	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3793	125194	in gene	0	1	0	11	15	3	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene MAP2K6	MAP2K6, MEK6, MKK6, MAPKK6, PRKMK6, SAPKK3	mitogen-activated protein kinase kinase 6	NM_002758, hCT1954133.1, hCT1954134.1, hCT19927.3	205698_s_at, 205699_at	NP_002749.2, EAW89084.1, EAW89085.1, EAW89086.1
GeneID:400617	FLJ36644	17	68,163,102	68,165,543	2,441	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3796	359	in gene	0	1	0	11	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene FLJ36644		hypothetical LOC400617	NR_036534	1558234_at	
GeneID:3759	KCNJ2	17	68,165,676	68,176,185	10,509	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3796	-492	upstream	0	1	0	11	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene KCNJ2	SQT3, LQT7, KCNJ2, HHBIRK1, KIR2.1, IRK1, HHIRK1	potassium inwardly-rectifying channel, subfamily J, member 2	NM_000891, hCT18441.3	206765_at	NP_000882.1, EAW89092.1
GeneID:400618	FLJ37644	17	70,067,183	70,112,157	44,974	-	1	4_A375_EGR1..1..3791	-5539	upstream	0	0	1	9	9	14	1	4_A375_EGR1..1	14	Gene FLJ37644	DKFZp313A2240, FLJ31667	hypothetical LOC400618	XR_111743, XR_109424, XR_115139	1564466_at, 230419_at	
GeneID:6662	SOX9	17	70,117,161	70,122,561	5,400	+	1	4_A375_EGR1..1..3791	535	in gene	0	0	1	9	9	14	1	4_A375_EGR1..1	14	Gene SOX9	CMD1, SOX9, SRA1, CMPD1	SRY (sex determining region Y)-box 9	NM_000346, hCT18449.2	202935_s_at, 202936_s_at	NP_000337.1, EAW89102.1
GeneID:100499467	LOC100499467	17	70,399,463	70,588,943	189,480	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2645, 2_A375_pNL97_plus_lncRNA_AR..1..3802	127119, 20735	in gene, in gene	1	1	0	16.5	13.5	6.5	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100499467	FLJ20470, FLJ26252	hypothetical LOC100499467	NR_036466		
GeneID:400619	FLJ26484	17	70,594,180	70,636,611	42,431	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3803, 2_A375_pNL97_plus_lncRNA_AR..1..3804, 2_A375_pNL97_plus_lncRNA_AR..1..3805	24675, 21955, 8035	in gene, in gene, in gene	0	1	0	16	23.33	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene FLJ26484		hypothetical LOC400619	NR_033876		
GeneID:201266	SLC39A11	17	70,642,085	71,088,853	446,768	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2646, 1_A375_pNL7_minus_lncRNA_AR..1..2647, 1_A375_pNL7_minus_lncRNA_AR..1..2648, 2_A375_pNL97_plus_lncRNA_AR..1..3806, 2_A375_pNL97_plus_lncRNA_AR..1..3807, 2_A375_pNL97_plus_lncRNA_AR..1..3808, 2_A375_pNL97_plus_lncRNA_AR..1..3809	436261, 430997, 406389, 436261, 430933, 406501, 366117	in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	0	17.25	18	6	4	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SLC39A11	ZIP11, SLC39A11, C17orf26	solute carrier family 39 (metal ion transporter), member 11	NM_139177, NM_001159770, hCT2261740.1, hCT2261741.1, hCT2344419.0	227046_at	NP_631916.2, NP_001153242.1, EAW89107.1, EAW89108.1, EAW89109.1
GeneID:9382	COG1	17	71,189,173	71,204,646	15,473	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3810	123	in gene	0	1	0	12	20	6	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene COG1	KIAA1381, COG1, LDLB, CDG2G, DKFZp762L1710	component of oligomeric golgi complex 1	NM_018714, hCT1953331.1, hCT20152.3	227784_s_at, 230876_s_at, 231813_s_at	NP_061184.1, EAW89114.1, EAW89113.1
GeneID:23580	CDC42EP4	17	71,279,763	71,308,143	28,380	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3811, 4_A375_EGR1..1..3792, 4_A375_EGR1..1..3793	19855, 26511, 79	in gene, in gene, in gene	0	1	1	11.67	15.67	14	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CDC42EP4	CDC42EP4, BORG4, MGC17125, MGC3740, CEP4, KAIA1777	CDC42 effector protein (Rho GTPase binding) 4	NM_012121, hCT18977.3, hCT2261732.0	214721_x_at, 218062_x_at, 218063_s_at	NP_036253.2, EAW89123.1, EAW89124.1
GeneID:54549	SDK2	17	71,330,523	71,640,227	309,704	-	4	4_A375_EGR1..1..3794, 4_A375_EGR1..1..3795, 4_A375_EGR1..1..3796, 4_A375_EGR1..1..3797	188515, 86891, 72291, -61	in gene, in gene, in gene, upstream	0	0	1	5.5	5.75	16	4	4_A375_EGR1..1	17	Gene SDK2	SDK2, KIAA1514, FLJ10832	sidekick homolog 2 (chicken)	NM_001144952, hCT20153.3, hCT2261410.0, hCT2261411.0, hCT2357235.0	220628_s_at, 232061_at, 233585_at, 242064_at	NP_001138424.1, EAW89128.1, EAW89127.1, EAW89126.1, EAW89129.1
GeneID:283982	C17orf54	17	71,745,409	71,824,676	79,267	-	1	4_A375_EGR1..1..3798	36132	in gene	0	0	1	6	7	15	1	4_A375_EGR1..1	15	Gene C17orf54	MGC120127, C17orf54, FLJ40319	chromosome 17 open reading frame 54	NR_027146, hCT2261402.1, hCT2349089.0		EAW89135.1, EAW89134.1
GeneID:6169	RPL38	17	72,199,795	72,208,019	8,224	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2649, 2_A375_pNL97_plus_lncRNA_AR..1..3812, 4_A375_EGR1..1..3800	-51, -63, 77	upstream, upstream, in gene	1	1	1	53	71	17	1	2_A375_pNL97_plus_lncRNA_AR..1	71	Gene RPL38	RPL38, L38	ribosomal protein L38	NM_000999, NM_001035258, hCT2261218.1, hCT2261220.1, hCT2261223.1, hCT2344418.0	202028_s_at, 202029_x_at, 221943_x_at	NP_000990.1, NP_001030335.1, EAW89137.1, EAW89138.1, EAW89139.1, EAW89140.1
GeneID:85001	MGC16275	17	72,206,119	72,209,460	3,341	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2649, 2_A375_pNL97_plus_lncRNA_AR..1..3812, 4_A375_EGR1..1..3800	9716, 9748, 9586	downstream, downstream, downstream	1	1	1	53	71	17	1	2_A375_pNL97_plus_lncRNA_AR..1	71	Gene MGC16275		hypothetical protein MGC16275	NR_026914	1558166_at, 1558167_a_at	
GeneID:94015	TTYH2	17	72,209,696	72,258,159	48,463	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2649, 2_A375_pNL97_plus_lncRNA_AR..1..3812, 4_A375_EGR1..1..3800	-9952, -9984, -9824	upstream, upstream, upstream	1	1	1	53	71	17	1	2_A375_pNL97_plus_lncRNA_AR..1	71	Gene TTYH2	C17orf29, MGC126172, MGC4837, TTYH2	tweety homolog 2 (Drosophila)	NM_032646, NM_052869, hCT2261225.1, hCT2261227.0	223741_s_at, 232042_at	NP_116035.5, NP_443101.1, EAW89142.1, EAW89143.1
GeneID:124602	KIF19	17	72,322,351	72,351,959	29,608	+	2	4_A375_EGR1..1..3801, 4_A375_EGR1..1..3802	26097, 27281	in gene, in gene	0	0	1	5.5	6.5	17	2	4_A375_EGR1..1	18	Gene KIF19	KIF19, FLJ37300, KIF19A	kinesin family member 19	NM_153209, hCT1957157.2, hCT2349167.0, hCT2349168.0, hCT2349169.0	1553314_a_at, 236426_at	NP_694941.2, EAW89150.1, EAW89151.1, EAW89152.1, EAW89153.1
GeneID:388419	BTBD17	17	72,352,555	72,357,958	5,403	-	2	4_A375_EGR1..1..3801, 4_A375_EGR1..1..3802	9510, 8326	downstream, downstream	0	0	1	5.5	6.5	17	2	4_A375_EGR1..1	18	Gene BTBD17	BTBD17A, BTBD17, LGALS3BPL	BTB (POZ) domain containing 17	NM_001080466	230445_at	NP_001073935.1
GeneID:350383	GPR142	17	72,363,645	72,368,739	5,094	+	1	4_A375_EGR1..1..3803	4739	in gene	0	0	1	6	7	18	1	4_A375_EGR1..1	18	Gene GPR142	PGR2, GPR142	G protein-coupled receptor 142	NM_181790, hCT2261849.1, hCT2349090.0		NP_861455.1, EAW89156.1, EAW89157.1
GeneID:55890	GPRC5C	17	72,427,667	72,443,568	15,901	+	2	4_A375_EGR1..1..3805, 4_A375_EGR1..1..3806	109, 11645	in gene, in gene	0	0	1	6.5	6.5	16.5	2	4_A375_EGR1..1	18	Gene GPRC5C	MGC131820, RAIG3, RAIG-3, GPRC5C	G protein-coupled receptor, family C, group 5, member C	NM_022036, NM_018653, hCT1953272.1, hCT1953273.1, hCT1953274.1, hCT2261853.0, hCT2261855.0	219327_s_at, 230907_at	NP_071319.2, NP_061123.3, EAW89160.1, EAW89162.1, EAW89163.1, EAW89164.1, EAW89161.1
GeneID:342510	CD300E	17	72,608,712	72,619,801	11,089	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3813	13465	downstream	0	1	0	14	20	4	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CD300E	CD300E, IREM2, CLM2, CD300LE	CD300e molecule	NM_181449, hCT1813932.2, hCT2357208.0		NP_852114.1, EAW89175.1, EAW89176.1
GeneID:326624	RAB37	17	72,667,256	72,743,474	76,218	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2650, 2_A375_pNL97_plus_lncRNA_AR..1..3814	264, 296	in gene, in gene	1	1	0	79	79	14	1	2_A375_pNL97_plus_lncRNA_AR..1	79	Gene RAB37	FLJ30284, RAB37, FLJ32507	RAB37, member RAS oncogene family	NM_175738, NM_001006638, NM_001163989, NM_001163990, hCT2261866.1, hCT2348810.0, hCT2349091.0, hCT2349092.0, hCT2349093.0, hCT2357186.0	228113_at, 244124_at	NP_783865.1, NP_001006639.1, NP_001157461.1, NP_001157462.1, EAW89178.1, EAW89181.1, EAW89177.1, EAW89179.1, EAW89180.1, EAW89182.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9368	SLC9A3R1	17	72,744,763	72,765,499	20,736	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3815	27665	downstream	0	1	0	15	23	17	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene SLC9A3R1	NHERF1, NPHLOP2, SLC9A3R1, NHERF, EBP50	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	NM_004252, hCT1954141.1, hCT1954142.1, hCT21000.2	201349_at	NP_004243.1, EAW89191.1, EAW89189.1, EAW89190.1
GeneID:26151	NAT9	17	72,766,686	72,772,470	5,784	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3815	22	in gene	0	1	0	15	23	17	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene NAT9	DKFZp564C103, EBSP, EBSP, hNATL, NAT9	N-acetyltransferase 9 (GCN5-related, putative)	NM_015654, hCT2262802.0, hCT2262803.0, hCT2357204.0, hCT2357205.0, hCT2357206.0	204382_at	NP_056469.2, EAW89193.1, EAW89194.1, EAW89195.1, EAW89196.1, EAW89197.1
GeneID:54866	TMEM104	17	72,772,622	72,835,922	63,300	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3815, 4_A375_EGR1..1..3807	-174, 62514	upstream, in gene	0	1	1	9	15	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TMEM104	TMEM104, FLJ00021, FLJ20255	transmembrane protein 104	NM_017728, hCT1954149.1, hCT21003.3, hCT2357156.0, hCT2357157.0	220097_s_at	NP_060198.3, EAW89198.1, EAW89199.1, EAW89200.1, EAW89201.1
GeneID:2905	GRIN2C	17	72,838,168	72,856,007	17,839	-	3	4_A375_EGR1..1..3807, 4_A375_EGR1..1..3808, 4_A375_EGR1..1..3809	20871, -1113, -6425	downstream, upstream, upstream	0	0	1	7	8	19.67	3	4_A375_EGR1..1	22	Gene GRIN2C	GRIN2C, NR2C, NMDAR2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	NM_000835, hCT1954138.1, hCT20999.3, hCT2357149.0	1569268_at, 210400_at, 217573_at	NP_000826.2, EAW89204.1, EAW89202.1, EAW89203.1
GeneID:2232	FDXR	17	72,858,619	72,869,156	10,537	-	2	4_A375_EGR1..1..3808, 4_A375_EGR1..1..3809	12036, 6724	downstream, in gene	0	0	1	9	5.5	21.5	2	4_A375_EGR1..1	22	Gene FDXR	FDXR, ADXR	ferredoxin reductase	NM_024417, NM_004110, hCT1954144.1, hCT21001.2, hCT2357153.0, hCT2357154.0, hCT2357155.0	207813_s_at	NP_077728.2, NP_004101.2, EAW89205.1, EAW89206.1, EAW89208.1, EAW89209.1, EAW89207.1
GeneID:347741	OTOP3	17	72,931,897	72,945,511	13,614	+	2	4_A375_EGR1..1..3810, 4_A375_EGR1..1..3811	13991, 16775	downstream, downstream	0	0	1	5	8.5	17	2	4_A375_EGR1..1	17	Gene OTOP3	OTOP3	otopetrin 3	NM_178233, hCT21012.3, hCT2261875.0, hCT2357184.0		NP_839947.1, EAW89214.1, EAW89215.1, EAW89216.1
GeneID:283987	C17orf28	17	72,946,839	72,968,900	22,061	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3816, 4_A375_EGR1..1..3810, 4_A375_EGR1..1..3811	-9468, 23012, 20226	upstream, downstream, in gene	0	1	1	7.67	10	15.67	3	4_A375_EGR1..1	17	Gene C17orf28	FLJ43526, DMC1, C17orf28	chromosome 17 open reading frame 28	NM_030630, hCT2262856.0, hCT2262857.0, hCT2346611.0, hCT2357167.0	225981_at, 244593_at	NP_085133.1, EAW89218.1, EAW89217.1, EAW89219.1, EAW89220.1, EAW89221.1
GeneID:30850	CDR2L	17	72,983,727	73,001,895	18,168	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2651, 2_A375_pNL97_plus_lncRNA_AR..1..3816, 2_A375_pNL97_plus_lncRNA_AR..1..3817, 4_A375_EGR1..1..3812	25121, -5359, 25153, 25073	downstream, upstream, downstream, downstream	1	1	1	16	19.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CDR2L	HUMPPA, CDR2L	cerebellar degeneration-related protein 2-like	NM_014603, hCT21007.2, hCT2261860.0, hCT2261862.0, hCT2357181.0	213230_at	NP_055418.2, EAW89226.1, EAW89223.1, EAW89224.1, EAW89225.1
GeneID:3396	ICT1	17	73,008,780	73,017,356	8,576	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2651, 2_A375_pNL97_plus_lncRNA_AR..1..3817, 4_A375_EGR1..1..3812	66, 100, 20	in gene, in gene, in gene	1	1	1	19	22	20	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ICT1	DS-1, ICT1	immature colon carcinoma transcript 1	NM_001545, hCT21011.3	204868_at	NP_001536.1, EAW89227.1
GeneID:10476	ATP5H	17	73,034,955	73,043,074	8,119	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2652, 2_A375_pNL97_plus_lncRNA_AR..1..3818, 2_A375_pNL97_plus_lncRNA_AR..1..3819, 4_A375_EGR1..1..3813	11690, 12582, 2, 12462	downstream, downstream, in gene, downstream	1	1	1	23	19.5	22	2	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene ATP5H	ATP5H, ATPQ, ATP5JD	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	NM_006356, NM_001003785, hCT1954147.1, hCT21002.2	1555998_at, 210149_s_at	NP_006347.1, NP_001003785.1, EAW89228.1, EAW89229.1
GeneID:23510	KCTD2	17	73,043,279	73,061,981	18,702	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3819	-207	upstream	0	1	0	15	15	13	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene KCTD2	KCTD2, KIAA0176	potassium channel tetramerisation domain containing 2	NM_015353, hCT1643661.3	212564_at, 34856_at	NP_056168.1, EAW89230.1
GeneID:79637	ARMC7	17	73,106,082	73,126,360	20,278	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3820, 2_A375_pNL97_plus_lncRNA_AR..1..3821, 4_A375_EGR1..1..3814	14526, 21550, 18676	in gene, downstream, in gene	0	1	1	11.33	15	14.67	3	4_A375_EGR1..1	23	Gene ARMC7	ARMC7, FLJ22160	armadillo repeat containing 7	NM_024585, hCT2261666.0, hCT2345066.0, hCT2345067.0, hCT2345068.0	219096_at, 229906_at	NP_078861.1, EAW89236.1, EAW89237.1, EAW89238.1, EAW89239.1
GeneID:30833	NT5C	17	73,126,323	73,127,877	1,554	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3820, 2_A375_pNL97_plus_lncRNA_AR..1..3821, 4_A375_EGR1..1..3814	7289, 245, 2917	downstream, in gene, downstream	0	1	1	11.33	15	14.67	3	4_A375_EGR1..1	23	Gene NT5C	UMPH2, PN-II, NT5C, dNT-1, P5N2, DNT, PN-I, cdN, DNT1	5', 3'-nucleotidase, cytosolic	NM_014595, hCT18606.2, hCT1954115.2, hCT1954117.2	1557303_at, 219214_s_at	NP_055410.1, EAW89243.1, EAW89241.1, EAW89242.1
GeneID:51155	HN1	17	73,131,343	73,150,775	19,432	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3821, 4_A375_EGR1..1..3814	23143, 25815	downstream, downstream	0	1	1	10	13.5	16.5	2	4_A375_EGR1..1	23	Gene HN1	ARM2, HN1A, HN1	hematological and neurological expressed 1	NM_016185, NM_001002033, NM_001002032, hCT2262844.0, hCT2262845.0, hCT2357164.0, hCT2357165.0	217755_at, 222396_at	NP_057269.1, NP_001002033.1, NP_001002032.1, EAW89244.1, EAW89246.1, EAW89247.1, EAW89245.1
GeneID:6613	SUMO2	17	73,163,825	73,179,098	15,273	-	1	4_A375_EGR1..1..3815	762	in gene	0	0	1	3	11	19	1	4_A375_EGR1..1	19	Gene SUMO2	SUMO2, MGC117191, SMT3B, HSMT3, SMT3H2, Smt3A, SUMO3	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	NM_006937, NM_001005849, hCT2262842.0, hCT2262843.0	208739_x_at, 213881_x_at	NP_008868.3, NP_001005849.1, EAW89249.1, EAW89250.1
GeneID:79902	NUP85	17	73,201,597	73,231,854	30,257	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2653, 2_A375_pNL97_plus_lncRNA_AR..1..3822, 4_A375_EGR1..1..3816, 4_A375_EGR1..1..3817	3, 35, 131, 34467	in gene, in gene, in gene, downstream	1	1	1	29.5	31.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene NUP85	FLJ12549, Nup75, NUP85	nucleoporin 85kDa	NM_024844, hCT18605.3	218014_at	NP_079120.1, EAW89251.1
GeneID:23163	GGA3	17	73,232,694	73,258,444	25,750	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2654, 2_A375_pNL97_plus_lncRNA_AR..1..3823, 4_A375_EGR1..1..3817, 4_A375_EGR1..1..3818, 4_A375_EGR1..1..3819	492, 612, 22380, 556, -8340	in gene, in gene, in gene, in gene, upstream	1	1	1	11.67	12.67	20.33	3	4_A375_EGR1..1	28	Gene GGA3	KIAA0154, GGA3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	NM_138619, NM_014001, NM_001172703, NM_001172704, NR_033345, hCT18603.2, hCT1954107.1, hCT1954108.1, hCT1954109.1, hCT2262838.0, hCT2262841.0, hCT2357215.0, hCT2357216.0, hCT2357217.0	209411_s_at, 211815_s_at	NP_619525.1, NP_054720.1, NP_001166174.1, NP_001166175.1, EAW89252.1, EAW89260.1, EAW89253.1, EAW89254.1, EAW89255.1, EAW89256.1, EAW89257.1, EAW89258.1, EAW89259.1
GeneID:51081	MRPS7	17	73,257,749	73,262,457	4,708	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2654, 2_A375_pNL97_plus_lncRNA_AR..1..3823, 4_A375_EGR1..1..3818, 4_A375_EGR1..1..3819	203, -117, 139, 9035	in gene, upstream, in gene, downstream	1	1	1	14.5	15	23.5	2	4_A375_EGR1..1	28	Gene MRPS7	bMRP27a, MRPS7, MRP-S, S7mt, RP-S7, RPMS7, MRP-S7	mitochondrial ribosomal protein S7	NM_015971, hCT18598.3, hCT1954098.1	217932_at	NP_057055.2, EAW89261.1, EAW89262.1
GeneID:57409	MIF4GD	17	73,262,309	73,267,303	4,994	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2654, 2_A375_pNL97_plus_lncRNA_AR..1..3823, 4_A375_EGR1..1..3818, 4_A375_EGR1..1..3819	9351, 9871, 9415, 519	downstream, downstream, downstream, in gene	1	1	1	14.5	15	23.5	2	4_A375_EGR1..1	28	Gene MIF4GD	AD023, MGC45027, MIFD, MIF4GD, SLIP1	MIF4G domain containing	NM_020679, hCT18604.2, hCT1954111.1, hCT1954112.1, hCT1954113.1	223411_at, 231727_s_at	NP_065730.2, EAW89263.1, EAW89264.1, EAW89265.1, EAW89266.1
GeneID:100287042	LOC100287042	17	73,267,380	73,269,976	2,596	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2654, 2_A375_pNL97_plus_lncRNA_AR..1..3823, 4_A375_EGR1..1..3818, 4_A375_EGR1..1..3819	-9428, -9748, -9492, -596	upstream, upstream, upstream, upstream	1	1	1	14.5	15	23.5	2	4_A375_EGR1..1	28	Gene LOC100287042		hypothetical LOC100287042	NR_036520		
GeneID:60386	SLC25A19	17	73,269,061	73,285,530	16,469	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2655, 2_A375_pNL97_plus_lncRNA_AR..1..3824, 4_A375_EGR1..1..3819, 4_A375_EGR1..1..3820, 4_A375_EGR1..1..3821	-262, 154, 18746, 2714, 136	upstream, in gene, downstream, in gene, in gene	1	1	1	13.67	10	20.67	3	4_A375_EGR1..1	28	Gene SLC25A19	DNC, TPC, SLC25A19, MUP1, MCPHA	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	NM_021734, NM_001126121, NM_001126122, hCT18601.3, hCT1961008.1, hCT1961010.1	223222_at	NP_068380.3, NP_001119593.1, NP_001119594.1, EAW89267.1, EAW89268.1, EAW89269.1
GeneID:9772	KIAA0195	17	73,452,664	73,496,533	43,869	+	3	4_A375_EGR1..1..3822, 4_A375_EGR1..1..3823, 4_A375_EGR1..1..3824	298, 29656, 47944	in gene, in gene, downstream	0	0	1	10	8.67	15	3	4_A375_EGR1..1	17	Gene KIAA0195	DKFZp781M1056, KIAA0195, FLJ37545, TMEM94	KIAA0195	NM_014738, hCT1812358.1, hCT1954081.1, hCT2262869.0, hCT2262870.0	202650_s_at, 222210_at	NP_055553.3, EAW89274.1, EAW89275.1, EAW89276.1, EAW89277.1
GeneID:57513	CASKIN2	17	73,496,342	73,511,627	15,285	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2656, 2_A375_pNL97_plus_lncRNA_AR..1..3825, 4_A375_EGR1..1..3824	-597, -789, 11019	upstream, upstream, in gene	1	1	1	17.5	23.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene CASKIN2	ANKS5B, CASKIN2, KIAA1139, FLJ21609	CASK interacting protein 2	NM_020753, NM_001142643, hCT2266316.0	221846_s_at, 61297_at	NP_065804.2, NP_001136115.1, EAW89278.1
GeneID:283989	TSEN54	17	73,512,609	73,520,820	8,211	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2656, 2_A375_pNL97_plus_lncRNA_AR..1..3825	-365, -193	upstream, upstream	1	1	0	28	36	12	1	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene TSEN54	PCH2A, sen54, SEN54L, TSEN54, PCH4, FLJ37147	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	NM_207346	1558304_s_at, 225879_at, 241402_at	NP_997229.2
GeneID:3993	LLGL2	17	73,521,783	73,571,290	49,507	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2656, 2_A375_pNL97_plus_lncRNA_AR..1..3825, 4_A375_EGR1..1..3825	-9559, -9367, 49033	upstream, upstream, in gene	1	1	1	17.5	22.5	16	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene LLGL2	HGL, LGL2, LLGL2	lethal giant larvae homolog 2 (Drosophila)	NM_004524, NM_001015002, NM_001031803, hCT18678.3, hCT2262872.0, hCT2357221.0, hCT2357222.0	1554006_a_at, 203713_s_at	NP_004515.2, NP_001015002.1, NP_001026973.1, EAW89281.1, EAW89282.1, EAW89283.1, EAW89280.1
GeneID:9400	RECQL5	17	73,622,950	73,663,269	40,319	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3826, 4_A375_EGR1..1..3828, 4_A375_EGR1..1..3829	-27, 35717, 33893	upstream, in gene, in gene	0	1	1	13	14.33	14.67	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene RECQL5	FLJ90603, RECQL5, RECQ5	RecQ protein-like 5	NM_001003715, NM_004259, NM_001003716, hCT2266306.0, hCT2266308.0, hCT2266309.0, hCT2266311.0, hCT2266312.0, hCT2266314.0, hCT2357182.0	1561720_at, 210309_at, 211468_s_at, 221686_s_at, 34063_at	NP_001003715.1, NP_004250.4, NP_001003716.1, EAW89289.1, EAW89290.1, EAW89294.1, EAW89291.1, EAW89292.1, EAW89293.1, EAW89295.1
GeneID:643008	LOC643008	17	73,629,514	73,637,486	7,972	+	2	4_A375_EGR1..1..3828, 4_A375_EGR1..1..3829	-1962, -136	upstream, upstream	0	0	1	10.5	10.5	18	2	4_A375_EGR1..1	18	Gene LOC643008	DKFZp451K2118, FLJ31206, PP12104	hypothetical protein LOC643008	NM_001162995, NR_028439	229740_at	NP_001156467.1
GeneID:29115	SAP30BP	17	73,663,399	73,704,139	40,740	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3826, 2_A375_pNL97_plus_lncRNA_AR..1..3827	-103, 24249	upstream, in gene	0	1	0	14.5	20.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SAP30BP	HTRP, HTRG, DKFZp586L2022, HCNGP, SAP30BP	SAP30 binding protein	NM_013260, hCT18661.3, hCT2357236.0, hCT2357237.0, hCT2357238.0, hCT2357239.0, hCT2357240.0, hCT2357241.0	217965_s_at, 222475_at	NP_037392.1, EAW89298.1, EAW89299.1, EAW89300.1, EAW89302.1, EAW89304.1, EAW89301.1, EAW89303.1
GeneID:3691	ITGB4	17	73,717,516	73,753,899	36,383	+	4	4_A375_EGR1..1..3830, 4_A375_EGR1..1..3831, 4_A375_EGR1..1..3832, 4_A375_EGR1..1..3833	212, 22292, 32684, 36980	in gene, in gene, in gene, downstream	0	0	1	7.75	9.5	18.75	4	4_A375_EGR1..1	20	Gene ITGB4	CD104, ITGB4	integrin, beta 4	NM_001005619, NM_001005731, NM_000213, hCT1813723.1, hCT1813724.1, hCT18677.2, hCT2262894.0, hCT2262896.0, hCT2262898.0, hCT2262900.0, hCT2262901.0, hCT2262903.0, hCT2262904.0, hCT2357220.0	204989_s_at, 204990_s_at, 211905_s_at, 214292_at, 230704_s_at	NP_001005619.1, NP_001005731.1, NP_000204.3, EAW89305.1, EAW89306.1, EAW89312.1, EAW89307.1, EAW89308.1, EAW89309.1, EAW89310.1, EAW89311.1, EAW89313.1, EAW89314.1, EAW89315.1
GeneID:2584	GALK1	17	73,754,018	73,761,280	7,262	-	2	4_A375_EGR1..1..3832, 4_A375_EGR1..1..3833	10680, 6784	downstream, in gene	0	0	1	7.5	9.5	19	2	4_A375_EGR1..1	20	Gene GALK1	GALK, GK1, GALK1	galactokinase 1	NM_000154, hCT18679.3	204374_s_at, 229456_s_at	NP_000145.1, EAW89316.1
GeneID:3021	H3F3B	17	73,772,515	73,775,860	3,345	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2657, 1_A375_pNL7_minus_lncRNA_AR..1..2658, 2_A375_pNL97_plus_lncRNA_AR..1..3828, 2_A375_pNL97_plus_lncRNA_AR..1..3829	-76, -5356, 52, -5292	upstream, upstream, in gene, upstream	1	1	0	21.5	21.5	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene H3F3B	H3.3B, H3F3A, H3F3B	H3 histone, family 3B (H3.3B)	NM_005324, hCT2266299.1, hCT2266301.1, hCT2266303.1	209069_s_at, 211997_x_at, 211998_at, 211999_at	NP_005315.1, EAW89317.1, EAW89318.1, EAW89319.1
GeneID:85451	UNK	17	73,780,681	73,821,886	41,205	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2657, 1_A375_pNL7_minus_lncRNA_AR..1..2658, 2_A375_pNL97_plus_lncRNA_AR..1..3828, 2_A375_pNL97_plus_lncRNA_AR..1..3829, 4_A375_EGR1..1..3834, 4_A375_EGR1..1..3835, 4_A375_EGR1..1..3836	-4745, 535, -4873, 471, 25399, 38956, 41431	upstream, in gene, upstream, in gene, in gene, in gene, downstream	1	1	1	11.4	13.8	16	5	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene UNK	ZC3HDC5, KIAA1753, UNK, ZC3H5	unkempt homolog (Drosophila)	NM_001080419	1562434_at, 226376_at, 228357_at	NP_001073888.1
GeneID:100507191	LOC100507191	17	73,817,325	73,818,071	746	-	2	4_A375_EGR1..1..3835, 4_A375_EGR1..1..3836	-1586, -4041	upstream, upstream	0	0	1	3	5	17	2	4_A375_EGR1..1	17	Gene LOC100507191	FLJ40144	hypothetical protein LOC100507191	XM_003119668, XM_003118746, XM_003120898		XP_003119736.1, XP_003118794.1, XP_003120944.1
GeneID:201294	UNC13D	17	73,823,306	73,840,798	17,492	-	2	4_A375_EGR1..1..3835, 4_A375_EGR1..1..3836	21161, 18686	downstream, downstream	0	0	1	3	5	17	2	4_A375_EGR1..1	17	Gene UNC13D	FHL3, UNC13D, HLH3, HPLH3, Munc13-4	unc-13 homolog D (C. elegans)	NM_199242, hCT1814768.1, hCT2266294.0, hCT2266298.0	226678_at, 228350_at, 228352_at	NP_954712.1, EAW89323.1, EAW89322.1, EAW89324.1
GeneID:23558	WBP2	17	73,841,780	73,851,501	9,721	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2659	-275	upstream	1	0	0	17	15	14	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene WBP2	WBP-2, WBP2, MGC18269	WW domain binding protein 2	NM_012478, hCT1814765.1, hCT1960515.1, hCT2266291.0, hCT2357161.0, hCT2357162.0	209117_at	NP_036610.2, EAW89326.1, EAW89325.1, EAW89327.1, EAW89328.1, EAW89329.1
GeneID:91107	TRIM47	17	73,870,245	73,874,656	4,411	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3830, 2_A375_pNL97_plus_lncRNA_AR..1..3831, 4_A375_EGR1..1..3837	2046, 126, 2272	in gene, in gene, in gene	0	1	1	15	19	15	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TRIM47	TRIM47, GOA, RNF100	tripartite motif containing 47	NM_033452, hCT1814784.1, hCT2266288.0, hCT2357160.0	225688_at	NP_258411.2, EAW89330.1, EAW89331.1, EAW89332.1
GeneID:85302	FBF1	17	73,906,618	73,937,119	30,501	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3832, 4_A375_EGR1..1..3838, 4_A375_EGR1..1..3839	-33, 23263, 20975	upstream, in gene, in gene	0	1	1	11.33	11.33	18	3	4_A375_EGR1..1	18	Gene FBF1	KIAA1863, FBF-1, FLJ00103, FLJ13996, Alb, FBF1	Fas (TNFRSF6) binding factor 1	NM_001080542	1554468_s_at, 1555288_s_at, 1556131_s_at	NP_001074011.1
GeneID:51	ACOX1	17	73,937,588	73,975,515	37,927	-	3	2_A375_pNL97_plus_lncRNA_AR..1..3832, 2_A375_pNL97_plus_lncRNA_AR..1..3833, 4_A375_EGR1..1..3840	38363, 635, 299	downstream, in gene, in gene	0	1	1	13.5	15.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ACOX1	PALMCOX, SCOX, ACOX, ACOX1, MGC1198	acyl-CoA oxidase 1, palmitoyl	NM_001185039, NM_004035, NM_007292, hCT1814777.2, hCT1984295.1, hCT2266274.0, hCT2266276.0	207656_s_at, 209600_s_at, 209601_at, 213501_at, 227962_at	NP_001171968.1, NP_004026.2, NP_009223.2, EAW89350.1, EAW89351.1, EAW89352.1, EAW89349.1
GeneID:100134934	C17orf108	17	73,975,301	73,996,687	21,386	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3833, 4_A375_EGR1..1..3840, 4_A375_EGR1..1..3841	-421, -85, 21627	upstream, upstream, downstream	0	1	1	9.5	11	15	2	4_A375_EGR1..1	16	Gene C17orf108	TEN1, MGC54300, DKFZp686C0493, FLJ39785, C17orf106, DKFZp686G1463	chromosome 17 open reading frame 106	NM_001113324		NP_001106795.1
GeneID:1018	CDK3	17	73,996,987	74,002,080	5,093	+	1	4_A375_EGR1..1..3841	-59	upstream	0	0	1	8	8	16	1	4_A375_EGR1..1	16	Gene CDK3	CDK3	cyclin-dependent kinase 3	NM_001258, hCT2262914.0, hCT2262917.0, hCT32152.3	207166_at, 226396_at, 229468_at	NP_001249.1, EAW89355.1, EAW89353.1, EAW89354.1
GeneID:2125	EVPL	17	74,002,927	74,023,507	20,580	-	3	4_A375_EGR1..1..3841, 4_A375_EGR1..1..3842, 4_A375_EGR1..1..3843	26579, 9555, 4683	downstream, in gene, in gene	0	0	1	5	8.33	17.67	3	4_A375_EGR1..1	20	Gene EVPL	EVPL, EVPK	envoplakin	NM_001988, hCT2266272.0, hCT2266273.0	204503_at	NP_001979.2, EAW89357.1, EAW89356.1
GeneID:6730	SRP68	17	74,035,191	74,068,607	33,416	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2660, 2_A375_pNL97_plus_lncRNA_AR..1..3834, 4_A375_EGR1..1..3844, 4_A375_EGR1..1..3845	31, 31, -161, -3625	in gene, in gene, upstream, upstream	1	1	1	19	22	16	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene SRP68	SRP68	signal recognition particle 68kDa	NM_014230, hCT2266260.1, hCT2266261.1, hCT2266262.1, hCT2266263.1, hCT2266266.1, hCT2357226.0	224607_s_at	NP_055045.2, EAW89358.1, EAW89359.1, EAW89360.1, EAW89361.1, EAW89363.1, EAW89362.1
GeneID:8811	GALR2	17	74,070,892	74,073,573	2,681	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2660, 2_A375_pNL97_plus_lncRNA_AR..1..3834, 4_A375_EGR1..1..3844, 4_A375_EGR1..1..3845	-2316, -2316, -2124, 1540	upstream, upstream, upstream, in gene	1	1	1	19	22	16	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene GALR2	GALNR2, MGC125983, GALR2, MGC125984	galanin receptor 2	NM_003857, hCT32150.1	211226_at	NP_003848.1, EAW89364.1
GeneID:353174	ZACN	17	74,075,263	74,078,885	3,622	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2660, 2_A375_pNL97_plus_lncRNA_AR..1..3834, 4_A375_EGR1..1..3844, 4_A375_EGR1..1..3845, 4_A375_EGR1..1..3846	-6687, -6687, -6495, -2831, 10065	upstream, upstream, upstream, upstream, downstream	1	1	1	13	17.67	18.67	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene ZACN	LGICZ, ZAC, MGC129841, LGICZ1, L2, ZACN, ZAC1	zinc activated ligand-gated ion channel	NM_180990, hCT1649968.3, hCT2357163.0	1555550_at	NP_851321.2, EAW89365.1, EAW89366.1
GeneID:23265	EXOC7	17	74,077,086	74,099,866	22,782	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2660, 2_A375_pNL97_plus_lncRNA_AR..1..3834, 4_A375_EGR1..1..3844, 4_A375_EGR1..1..3845, 4_A375_EGR1..1..3846	31292, 31292, 31100, 27436, 14540	downstream, downstream, downstream, downstream, in gene	1	1	1	13	17.67	18.67	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene EXOC7	FLJ40965, DKFZp686J04253, Exo70p, EXO70, 2-5-3p, FLJ46415, EXO70, EXOC7, YJL085W, EXOC1	exocyst complex component 7	NM_001013839, NM_001145297, NM_001145298, NM_001145299, NM_015219, NR_028133, hCT2266267.1, hCT2266268.1, hCT2266269.1, hCT2351235.0, hCT2351236.0, hCT2351237.0, hCT2357219.0, hCT32154.3	212026_s_at, 212034_s_at, 212035_s_at, 214802_at, 215413_at	NP_001013861.1, NP_001138769.1, NP_001138770.1, NP_001138771.1, NP_056034.2, EAW89372.1, EAW89367.1, EAW89368.1, EAW89369.1, EAW89370.1, EAW89371.1, EAW89373.1, EAW89374.1
GeneID:2302	FOXJ1	17	74,132,414	74,137,380	4,966	-	1	4_A375_EGR1..1..3847	9140	downstream	0	0	1	7	4	17	1	4_A375_EGR1..1	17	Gene FOXJ1	FOXJ1, HFH-4, MGC35202, FKHL13, HFH4	forkhead box J1	NM_001454, hCT2266264.1, hCT2266265.0	205906_at	NP_001445.2, EAW89376.1, EAW89375.1
GeneID:100507218	LOC100507218	17	74,136,637	74,150,729	14,092	+	1	4_A375_EGR1..1..3847	-8397	upstream	0	0	1	7	4	17	1	4_A375_EGR1..1	17	Gene LOC100507218		hypothetical LOC100507218	XR_111740, XR_109427, XR_115142		
GeneID:114804	RNF157	17	74,138,534	74,236,390	97,856	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2661, 2_A375_pNL97_plus_lncRNA_AR..1..3835, 4_A375_EGR1..1..3848	-794, -802, -794	upstream, upstream, upstream	1	1	1	20	18	15	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene RNF157	RNF157	ring finger protein 157	NM_052916, hCT1960711.1, hCT2266256.0, hCT2266258.0, hCT2357211.0, hCT2357212.0	1569775_at, 226433_at	NP_443148.1, EAW89378.1, EAW89379.1, EAW89380.1, EAW89381.1, EAW89382.1
GeneID:283991	FAM100B	17	74,261,286	74,267,379	6,093	+	2	4_A375_EGR1..1..3849, 4_A375_EGR1..1..3850	8966, 15250	downstream, downstream	0	0	1	10	7	16	2	4_A375_EGR1..1	17	Gene FAM100B	MGC29814, FAM100B, MGC71792	family with sequence similarity 100, member B	NM_182565, hCT22076.2	224783_at, 224785_at	NP_872371.1, EAW89383.1
GeneID:84074	QRICH2	17	74,270,130	74,303,761	33,631	-	2	4_A375_EGR1..1..3849, 4_A375_EGR1..1..3850	33489, 27225	in gene, in gene	0	0	1	10	7	16	2	4_A375_EGR1..1	17	Gene QRICH2	QRICH2, DKFZp434P0316	glutamine rich 2	NM_032134, hCT22079.2, hCT2266254.0	232532_at	NP_115510.1, EAW89384.1, EAW89385.1

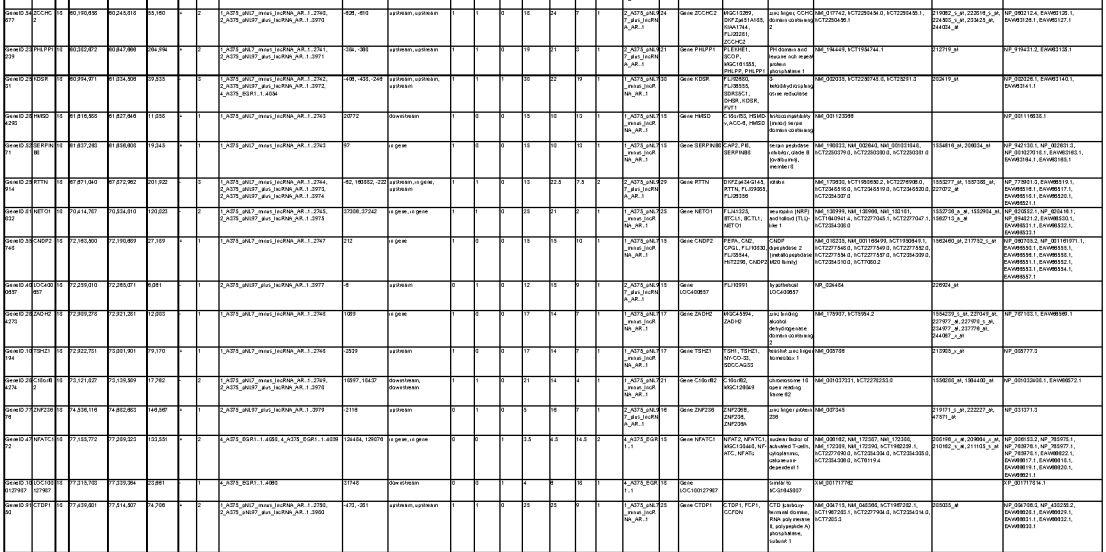
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.6877	SPHK1	17	74,380,690	74,383,941	3,251	+	2	4_A375_EGR1..1..3651, 4_A375_EGR1..1..3652	-850, 2638	upstream, in gene	0	0	1	9	10.5	19	2	4_A375_EGR1..1	20	Gene SPHK1	SPHK1, SPHK	sphingosine kinase 1	NM_182965, NM_001142601, NM_001142602, NM_021972, hCT22075.4, hCT2262923.1, hCT2262924.1, hCT2351616.0, hCT2351617.0, hCT2351618.0, hCT2351619.0	219257_s_at	NP_892010.2, NP_001136073.1, NP_068807.2, NP_001136074.1, EAW89389.1, EAW89393.1, EAW89388.1, EAW89390.1, EAW89391.1, EAW89392.1, EAW89394.1
GeneID.63893	UBE2O	17	74,385,613	74,449,288	63,675	-	2	4_A375_EGR1..1..3651, 4_A375_EGR1..1..3652	69448, 65980	downstream, downstream	0	0	1	9	10.5	19	2	4_A375_EGR1..1	20	Gene UBE2O	FLJ12878, UBE2O, E2-230K, KIAA1734	ubiquitin-conjugating enzyme E2O	NM_022066, hCT22066.3, hCT2266245.0, hCT2266246.0, hCT2266247.0, hCT2266249.0	1554814_at, 218141_at	NP_071349.3, EAW89396.1, EAW89395.1, EAW89397.1, EAW89398.1, EAW89399.1
GeneID.15	AANAT	17	74,449,433	74,466,199	16,766	+	1	4_A375_EGR1..1..3653	19079	downstream	0	0	1	12	8	17	1	4_A375_EGR1..1	17	Gene AANAT	SNAT, AANAT	arylalkylamine N-acetyltransferase	NM_001088, NM_001166579, hCT22086.1	207225_at	NP_001079.1, NP_001160051.1, EAW89400.1
GeneID.79651	RHBDF2	17	74,466,975	74,497,508	30,533	-	2	4_A375_EGR1..1..3653, 4_A375_EGR1..1..3654	28998, 3078	in gene, in gene	0	0	1	9	7	18	2	4_A375_EGR1..1	17	Gene RHBDF2	FLJ22341, RHBDL6, RHBDL5, RHBDF2	rhomboid 5 homolog 2 (Drosophila)	NM_001005498, NM_024599, hCT2266240.0, hCT2266242.0, hCT2266243.0, hCT2266244.0	219202_at	NP_001005498.2, NP_078875.4, EAW89401.1, EAW89402.1, EAW89403.1, EAW89404.1
GeneID.100507230	LOC100507230	17	74,541,700	74,549,680	7,980	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..3637	11932, 12092	downstream, downstream	1	1	0	18	17	13	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100507230		hypothetical LOC100507230	XR_111739, XR_109428, XR_115143		
GeneID.100507246	LOC100507246	17	74,553,846	74,561,430	7,584	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..3637	-214, -54	upstream, upstream	1	1	0	18	17	13	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100507246		hypothetical LOC100507246	XR_111734, XR_111735, XR_111737, XR_111736, XR_111738, XR_109429, XR_109430, XR_109432, XR_109431, XR_109433, XR_115144, XR_115145, XR_115147, XR_115146, XR_115148		
GeneID.677850	SNORD1C	17	74,554,874	74,554,951	77	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..3637	-1242, -1082	upstream, upstream	1	1	0	18	17	13	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene SNORD1C	SNORD1C, R38C, snR38C	small nucleolar RNA, C/D box 1C	NR_004397		
GeneID.677849	SNORD1B	17	74,557,190	74,557,275	85	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..3637	-3558, -3398	upstream, upstream	1	1	0	18	17	13	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene SNORD1B	snR38B, SNORD1B, R38B	small nucleolar RNA, C/D box 1B	NR_004396		
GeneID.677848	SNORD1A	17	74,557,715	74,557,788	73	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..3637	-4083, -3923	upstream, upstream	1	1	0	18	17	13	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene SNORD1A	SNORD1A, R38A, snR38A	small nucleolar RNA, C/D box 1A	NR_004395		
GeneID.10610	ST6GALNAC2	17	74,561,461	74,582,145	20,684	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..3637, 2_A375_pNL97_plus_lncRNA_AR..1..3638, 4_A375_EGR1..1..3655	28513, 28353, 129, 1089	downstream, downstream, in gene, in gene	1	1	1	12.67	12.67	12.67	3	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ST6GALNAC2	SIAT7, ST6GalNAII, SAITL1, SIAT7B, FLJ45660, ST6GALNAC2, SIATL1, STHM	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	NM_006456, hCT1962331.1, hCT22084.3, hCT2357190.0	204542_at	NP_006447.2, EAW89416.1, EAW89417.1, EAW89418.1
GeneID.23210	JMJD6	17	74,708,914	74,722,881	13,967	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3639, 4_A375_EGR1..1..3656	641, -10159	in gene, upstream	0	1	1	16	21	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene JMJD6	PTDSR, PTDSR1, PSR, JMJD6, KIAA0585	jumonji domain containing 6	NM_015167, NM_001081461, hCT22074.2, hCT2262629.1, hCT2349170.0, hCT2349171.0, hCT2349172.0, hCT2349173.0	1552629_a_at, 212722_s_at, 212723_at, 215233_at	NP_055982.2, NP_001074930.1, EAW89430.1, EAW89431.1, EAW89433.1, EAW89434.1, EAW89429.1, EAW89432.1
GeneID.124512	C17orf95	17	74,722,950	74,729,962	7,012	+	2	2_A375_pNL97_plus_lncRNA_AR..1..3639, 4_A375_EGR1..1..3656	-710, 10090	upstream, downstream	0	1	1	16	21	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene C17orf95	C17orf95, METTL23	chromosome 17 open reading frame 95	NM_001080510	225608_at	NP_001073979.2
GeneID.6427	SFRS2	17	74,730,197	74,733,412	3,215	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3639, 4_A375_EGR1..1..3656	11172, 372	downstream, in gene	0	1	1	16	21	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SFRS2	SFRS2A, SC35, PR264, SC-35, SRp30b, SFRS2, SRSF2	serine/arginine-rich splicing factor 2	NM_003016, hCT18984.3, hCT1956832.1, hCT2348059.0, hCT2348060.0, hCT2348061.0, hCT2348062.0, hCT2348063.0, hCT2348064.0, hCT2348065.0, hCT2357172.0	200753_x_at, 200754_x_at, 214882_s_at	NP_003007.2, EAW89439.1, EAW89440.1, EAW89441.1, EAW89443.1, EAW89445.1, EAW89442.1, EAW89444.1, EAW89446.1, EAW89447.1, EAW89448.1
GeneID.693221	MIR636	17	74,732,532	74,732,630	98	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3639, 4_A375_EGR1..1..3656	10390, -410	downstream, upstream	0	1	1	16	21	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene MIR636	MIRN636, hsa-mir-636, MIR636	microRNA 636	NR_030366		
GeneID.79157	MFSD11	17	74,733,783	74,775,356	41,573	+	1	4_A375_EGR1..1..3656	-743	upstream	0	0	1	16	18	23	1	4_A375_EGR1..1	23	Gene MFSD11	MFSD11, FLJ20226, ET, FLJ22196	major facilitator superfamily domain containing 11	NM_024311, hCT1956635.1, hCT1960730.1, hCT22071.3, hCT2262156.0, hCT2357193.0, hCT2357194.0	221192_x_at, 223242_s_at	NP_077287.1, EAW89449.1, EAW89450.1, EAW89451.1, EAW89452.1, EAW89453.1, EAW89454.1
GeneID.146664	MGAT5B	17	74,864,798	74,946,471	81,673	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2664, 2_A375_pNL97_plus_lncRNA_AR..1..3641, 2_A375_pNL97_plus_lncRNA_AR..1..3642, 4_A375_EGR1..1..3657	4034, 3966, 41376, 34498	in gene, in gene, in gene, in gene	1	1	1	15.67	16.33	11	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene MGAT5B	FLJ25132, GnT-IX, GnT-VB, KIAA2008, MGAT5B	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	NM_144677, NM_198955, hCT22067.3, hCT2262120.0, hCT2262122.0, hCT2357191.0	1563137_at, 236445_x_at	NP_653278.2, NP_945193.1, EAW89457.1, EAW89458.1, EAW89459.1, EAW89460.1
GeneID.654434	C17orf86	17	75,084,725	75,091,068	6,343	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2665, 2_A375_pNL97_plus_lncRNA_AR..1..3643	27, 75	in gene, in gene	1	1	0	38	43	13	1	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene C17orf86	PRO0872, FLJ25582, C17orf86, DKFZp686L05235	chromosome 17 open reading frame 86	NR_027056	221621_at	
GeneID.677761	SCARNA16	17	75,085,389	75,085,575	186	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2665, 2_A375_pNL97_plus_lncRNA_AR..1..3643	-637, -589	upstream, upstream	1	1	0	38	43	13	1	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene SCARNA16	ACA47, SCARNA16	small Cajal body-specific RNA 16	NR_003013		
GeneID.6397	SEC14L1	17	75,137,005	75,213,183	76,178	+	1	4_A375_EGR1..1..3659	-573	upstream	0	0	1	12	14	14	1	4_A375_EGR1..1	14	Gene SEC14L1	SEC14L1, PRELID4A, DKFZp686C08176, SEC14L	SEC14-like 1 (S. cerevisiae)	NM_001143998, NM_001143999, NM_003003, NM_001039573, NM_001144001, hCT2262123.0, hCT2262124.0	202082_s_at, 202083_s_at, 202084_s_at, 240038_at	NP_001137470.1, NP_001137471.1, NP_002994.3, NP_001034662.2, NP_001137473.1, EAW89470.1, EAW89469.1
GeneID.10801	9-Sep	17	75,277,492	75,496,678	219,186	+	12	1_A375_pNL7_minus_lncRNA_AR..1..2668, 1_A375_pNL7_minus_lncRNA_AR..1..2669, 1_A375_pNL7_minus_lncRNA_AR..1..2670, 2_A375_pNL97_plus_lncRNA_AR..1..3645, 2_A375_pNL97_plus_lncRNA_AR..1..3646, 2_A375_pNL97_plus_lncRNA_AR..1..3647, 2_A375_pNL97_plus_lncRNA_AR..1..3648, 2_A375_pNL97_plus_lncRNA_AR..1..3649, 4_A375_EGR1..1..3661, 4_A375_EGR1..1..3662, 4_A375_EGR1..1..3663, 4_A375_EGR1..1..3664	41148, 84428, 144524, 4398, 5680, 6692, 41420, 174380, 4636, 40460, 42236, 82844	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	15.44	16	13.22	9	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SEPT9	SINT1, FLJ75490, NAPB, MSF1, PNUTL4, SEPT9, MSF, KIAA0991, AF17q25, SeptD1	septin 9	NM_006640, NM_001113491, NM_001113492, NM_001113493, NM_001113494, NM_001113495, NM_001113496, hCT2262128.1, hCT2262129.1, hCT2262130.1, hCT2262131.1, hCT2262133.1, hCT2262134.1, hCT2345069.0, hCT2349049.0	1559025_at, 207425_s_at, 208657_s_at, 41220_at	NP_006631.2, NP_001106963.1, NP_001106964.1, NP_001106965.1, NP_001106966.1, NP_001106967.1, NP_001106968.1, EAW89461.1, EAW89462.1, EAW89463.1, EAW89464.1, EAW89465.1, EAW89466.1, EAW89467.1, EAW89468.1
GeneID.100507304	LOC100507304	17	75,440,766	75,444,561	3,795	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3649	11086	downstream	0	1	0	19	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100507304	FLJ40569	hypothetical protein LOC100507304	XM_003119667, XM_003118747, XM_003120897		XP_003119735.1, XP_003118795.1, XP_003120945.1
GeneID.400624	FLJ45079	17	75,875,083	75,880,169	5,086	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3650	-3943	upstream	0	1	0	14	20	8	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene FLJ45079	FLJ46474	FLJ45079 protein	NR_026337, hCT2360334.0		EAW89479.1
GeneID.57690	TNRC6C	17	76,000,318	76,104,916	104,598	+	2	4_A375_EGR1..1..3668, 4_A375_EGR1..1..3669	100548, 107682	in gene, downstream	0	0	1	7	8	15.5	2	4_A375_EGR1..1	16	Gene TNRC6C	KIAA1582, FLJ20015, TNRC6C	trinucleotide repeat containing 6C	NM_018996, NM_001142640, hCT2336663.1, hCT2336664.1, hCT2336665.1, hCT2336666.1, hCT2349107.0, hCT2357142.0	222820_at, 227149_at, 228591_at, 242314_at	NP_061869.2, NP_001136112.1, EAW89480.1, EAW89482.1, EAW89483.1, EAW89484.1, EAW89481.1, EAW89485.1
GeneID.11322	TMC6	17	76,108,999	76,128,488	19,489	-	4	4_A375_EGR1..1..3668, 4_A375_EGR1..1..3669, 4_A375_EGR1..1..3670, 4_A375_EGR1..1..3671	27824, 20468, 7580, 4915	downstream, downstream, in gene, in gene	0	0	1	9	7.75	15.75	4	4_A375_EGR1..1	18	Gene TMC6	LAK-4P, EVER1, EVIN1, EV1, FLJ17776, TMC6	transmembrane channel-like 6	NM_007267, NM_001127198, hCT1958584.0, hCT1958585.0, hCT20558.3, hCT2336690.0, hCT2336691.0, hCT2336694.0, hCT2336695.0	204328_at, 214958_s_at, 236482_at	NP_009198.4, NP_001120670.1, EAW89487.1, EAW89488.1, EAW89491.1, EAW89492.1, EAW89489.1, EAW89490.1, EAW89493.1
GeneID.147138	TMC8	17	76,126,859	76,139,049	12,190	+	2	4_A375_EGR1..1..3670, 4_A375_EGR1..1..3671	-5931, -3288	upstream, upstream	0	0	1	11	7.5	16	2	4_A375_EGR1..1	18	Gene TMC8	FLJ43684, FLJ40666, MGC40121, TMC8, MGC102701, EVER2, EV2, EVIN2	transmembrane channel-like 8	NM_152468, hCT2336669.1, hCT2336670.1, hCT2336671.1, hCT2348750.0	227353_at, 236554_x_at, 242644_at	NP_689681.2, EAW89495.1, EAW89494.1, EAW89496.1, EAW89497.1
GeneID.100141515	C17orf99	17	76,142,434	76,162,364	19,930	+	1	4_A375_EGR1..1..3672	24382	downstream	0	0	1	7	10	14	1	4_A375_EGR1..1	14	Gene C17orf99	FLJ50084, C17orf99	chromosome 17 open reading frame 99	NM_001163075		NP_001156547.1
GeneID.9144	SYNGR2	17	76,164,671	76,169,009	4,338	+	1	4_A375_EGR1..1..3672	2145	in gene	0	0	1	7	10	14	1	4_A375_EGR1..1	14	Gene SYNGR2	MGC102914, SYNGR2	synaptogyrin 2	NM_004710, hCT18975.3, hCT1956830.1, hCT1956831.1, hCT2336676.0, hCT2336678.0, hCT2336679.0	201079_at	NP_004701.1, EAW89503.1, EAW89499.1, EAW89501.1, EAW89502.1, EAW89504.1, EAW89500.1
GeneID.7083	TK1	17	76,170,160	76,183,285	13,125	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3651, 4_A375_EGR1..1..3672	149, 16469	in gene, downstream	0	1	1	15	27	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene TK1	TK2, TK1	thymidine kinase 1, soluble	NM_003258, hCT1962330.1, hCT1967444.1, hCT20555.2, hCT2336686.0	1554408_a_at, 202338_at, 243103_at	NP_003249.3, EAW89506.1, EAW89505.1, EAW89507.1, EAW89508.1
GeneID.125061	AFMID	17	76,183,398	76,203,782	20,384	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2671, 2_A375_pNL97_plus_lncRNA_AR..1..3651, 2_A375_pNL97_plus_lncRNA_AR..1..3652, 4_A375_EGR1..1..3673	26922, -262, 27002, 27194	downstream, upstream, downstream, downstream	1	1	1	23	36	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene AFMID	MGC167083, DKFZp686F03259, KF, AFMID	arylformamidase	NM_001010982, NR_027083, NM_001145526, hCT20560.4, hCT2351985.0	240318_at	NP_001010982.2, NP_001138998.1, EAW89509.1, EAW89510.1
GeneID.332	BIRC5	17	76,210,277	76,221,716	11,439	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2671, 2_A375_pNL97_plus_lncRNA_AR..1..3652, 4_A375_EGR1..1..3673	43, 123, 315	in gene, in gene, in gene	1	1	1	23	28	20	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene BIRC5	EPR-1, BIRC5, API4	baculoviral IAP repeat containing 5	NM_001168, NM_001012270, NM_001012271, hCT18953.2, hCT1958829.1, hCT1962326.1, hCT1962327.2	202094_at, 202095_s_at, 210334_x_at	NP_001159.2, NP_001012270.1, NP_001012271.1, EAW89511.1, EAW89513.1, EAW89514.1, EAW89512.1
GeneID.8475	EPR1	17	76,210,321	76,220,783	10,462	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2671, 2_A375_pNL97_plus_lncRNA_AR..1..3652, 4_A375_EGR1..1..3673	10463, 10383, 10191	downstream, in gene, in gene	1	1	1	23	28	20	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene EPR1	BIRC5AS, NCRNA00007, EPR-1, EPR1, BIRC5OS, BIRC5-AS1	effector cell peptidase receptor 1 (non-protein coding)	NR_002219	1555826_at	
GeneID.283999	LOC283999	17	76,227,391	76,237,068	9,677	+	1	4_A375_EGR1..1..3674	5095	in gene	0	0	1	4	11	15	1	4_A375_EGR1..1	15	Gene LOC283999	ARGM1, TMEM235	transmembrane protein 235	NM_001145529	1564040_a_at	NP_001139001.1
GeneID.9021	SOCS3	17	76,352,859	76,356,158	3,299	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3655, 2_A375_pNL97_plus_lncRNA_AR..1..3656	-770, -5026	upstream, upstream	0	1	0	15.5	20	14	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SOCS3	CIS3, SSI3, Cish3, MGC71791, SOCS3, SOCS-3, ATOD4, SSI-3	suppressor of cytokine signaling 3	NM_003955, hCT1815063.2, hCT2336905.0	206359_at, 206360_s_at, 214105_at, 227697_at	NP_003946.3, EAW89522.1, EAW89521.1
GeneID.8632	DNAH17	17	76,419,778	76,573,476	153,698	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3657	110692	in gene	0	1	0	13	21	11	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene DNAH17	MGC138489, DNAHL1, DNEL2, DNAH17, FLJ40457, MGC132787	dynein, axonemal, heavy chain 17	NM_173628	214229_at	NP_775899.3
GeneID.57602	USP36	17	76,792,985	76,836,989	44,004	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2673, 2_A375_pNL97_plus_lncRNA_AR..1..3658	9, -7	in gene, upstream	1	1	0	98	101	15	1	2_A375_pNL97_plus_lncRNA_AR..1	101	Gene USP36	USP36, DUB1	ubiquitin specific peptidase 36	NM_025090, hCT2263688.0, hCT2263690.0, hCT2357168.0, hCT86665.3	1554836_at, 220370_s_at, 224978_s_at, 224979_s_at, 227093_at	NP_079366.3, EAW89534.1, EAW89533.1, EAW89535.1, EAW89536.1
GeneID.7077	TIMP2	17	76,849,059	76,921,472	72,413	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3659, 2_A375_pNL97_plus_lncRNA_AR..1..3660, 4_A375_EGR1..1..3677, 4_A375_EGR1..1..3678	41861, -8272, 69216, -4592	in gene, upstream, in gene, upstream	0	1	1	8.5	13.5	12.5	4	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TIMP2	TIMP2, CSC-21K	TIMP metallopeptidase inhibitor 2	NM_003255, hCT1958640.1, hCT1958641.1, hCT2357197.0, hCT86672.3	203167_at, 224560_at, 231579_s_at	NP_003246.1, EAW89540.1, EAW89538.1, EAW89539.1, EAW89541.1
GeneID.3959	LGALS3BP	17	76,967,335	76,976,061	8,726	-	1	4_A375_EGR1..1..3679	6941	in gene	0	0	1	10	13	19	1	4_A375_EGR1..1	19	Gene LGALS3BP	MAC-2-BP, BTBD17B, 90K, LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	NM_005567, hCT1958626.1, hCT1958627.1, hCT1967333.1, hCT2357192.0	200923_at	NP_005558.1, EAW89544.1, EAW89543.1, EAW89545.1, EAW89546.1
GeneID.124583	CANT1	17	76,987,798	77,005,899	18,101	-	1	4_A375_EGR1..1..3680	9067	in gene	0	0	1	5	5	15	1	4_A375_EGR1..1	15	Gene CANT1	SCAN1, SHAPY, CANT1, SCAN-1, DBQD	calcium activated nucleotidase 1	NM_138793, NM_001159772, NM_001159773, hCT19760.4, hCT2344837.0, hCT2349124.0, hCT2349125.0, hCT2349126.0, hCT2349127.0, hCT2349128.0, hCT2349129.0	1554327_a_at, 221732_at, 46323_at	NP_620148.1, NP_001153244.1, NP_001153245.1, EAW89548.1, EAW89549.1, EAW89550.1, EAW89551.1, EAW89552.1, EAW89553.1, EAW89554.1, EAW89555.1
GeneID.100507410	LOC100507410	17	77,015,298	77,023,702	8,404	-	2	4_A375_EGR1..1..3681, 4_A375_EGR1..1..3682	3462, 2614	in gene, in gene	0	0	1	6	7.5	20	2	4_A375_EGR1..1	22	Gene LOC100507410		hypothetical LOC100507410	XR_111746, XR_109435, XR_115150		
GeneID.114897	C1QTNF1	17	77,020,251	77,045,870	25,619	+	2	4_A375_EGR1..1..3681, 4_A375_EGR1..1..3682	-11, 837	upstream, in gene	0	0	1	6	7.5	20	2	4_A375_EGR1..1	22	Gene C1QTNF1	ZSIG37, FLJ90694, C1QTNF1, GIP, CTRP1	C1q and tumor necrosis factor related protein 1	NM_198594, NM_030968, NM_198593, hCT19127.3, hCT2261623.0	220975_s_at, 224197_s_at	NP_940996.1, NP_112230.1, NP_940995.1, EAW89557.1, EAW89558.1
GeneID.64772	ENGASE	17	77,071,019	77,084,881	13,862	+	2	4_A375_EGR1..1..3683, 4_A375_EGR1..1..3684	16170, 22069	downstream, downstream	0	0	1	4.5	3.5	14.5	2	4_A375_EGR1..1	16	Gene ENGASE	ENGASE, FLJ21865, DKFZp434P174	endo-beta-N-acetylglucosaminidase	NM_001042573, hCT1958642.0, hCT2261627.0, hCT2261631.0, hCT87730.2	220349_s_at, 65635_at	NP_001036038.1, EAW89559.1, EAW89560.1, EAW89561.1, EAW89562.1
GeneID.146713	hCG_1776007	17	77,085,427	77,478,563	393,136	-	15	1_A375_pNL7_minus_lncRNA_AR..1..2674, 2_A375_pNL97_plus_lncRNA_AR..1..3661, 2_A375_pNL97_plus_lncRNA_AR..1..3662, 4_A375_EGR1..1..3683, 4_A375_EGR1..1..3684, 4_A375_EGR1..1..3685, 4_A375_EGR1..1..3686, 4_A375_EGR1..1..3687, 4_A375_EGR1..1..3688, 4_A375_EGR1..1..3689, 4_A375_EGR1..1..3690, 4_A375_EGR1..1..3691, 4_A375_EGR1..1..3692, 4_A375_EGR1..1..3693, 4_A375_EGR1..1..3694	187643, 269795, 187779, 391374, 385475, 375643, 372035, 365263, 338371, 331427, 327635, 325603, 296563, 68771, 24835	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	7.07	8.64	16.14	14	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene hCG_1776007	HRNBP3, FOX-3, RBFOX3, FOX3, NEUN, FLJ58356, FLJ56884	RNA binding protein, fox-1 homolog (C. elegans) 3	NM_001082575	229406_at, 235466_at, 240975_x_at	NP_001076044.1
GeneID.339221	ENPP7	17	77,704,882	77,716,021	11,139	+	1	4_A375_EGR1..1..3696	-68	upstream	0	0	1	4	8	17	1	4_A375_EGR1..1	17	Gene ENPP7	MGC50179, ENPP7, ALK-SMase	ectonucleotide pyrophosphatase/phosphodiesterase 7	NM_178543, hCT2340749.0	238245_at	NP_848638.2, EAW89566.1
GeneID.84733	CBX2	17	77,751,977	77,761,449	9,472	+	1	4_A375_EGR1..1..3697	17175	downstream	0	0	1	8	10	13	1	4_A375_EGR1..1	13	Gene CBX2	CDCA6, CBX2, M33, MGC10561	chromobox homolog 2 (Pc class homolog, Drosophila)	NM_005189, NM_032647, hCT19723.2, hCT2263651.0	215989_at, 224138_at, 226473_at	NP_005180.1, NP_116036.1, EAW89568.1, EAW89569.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:57332	CBX8	17	77,766,176	77,770,915	2,739	-	2	4_A375_EGR1..1..3897, 4_A375_EGR1..1..3898	1763, -4018	in gene, upstream	0	0	1	7.5	12	14.5	2	4_A375_EGR1..1	16	Gene CBX8	RC1, CBX8, HPC3, PC3	chromobox homolog 8 (Pc class homolog, Drosophila)	NM_020649, hCT19724.3	219755_at	NP_065700.1, EAW89571.1
GeneID:100507425	LOC100507425	17	77,774,397	77,776,328	1,931	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3863, 4_A375_EGR1..1..3897, 4_A375_EGR1..1..3898, 4_A375_EGR1..1..3899	11075, -5245, 536, 10915	downstream, upstream, in gene, downstream	0	1	1	8.67	14.33	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100507425		hypothetical LOC100507425	XR_111748, XR_109436, XR_115152		
GeneID:125058	TBC1D16	17	77,913,819	78,009,647	95,828	-	2	4_A375_EGR1..1..3900, 4_A375_EGR1..1..3901	81167, 44943	in gene, in gene	0	0	1	5	6	17	2	4_A375_EGR1..1	18	Gene TBC1D16	TBC1D16, MGC25082, FLJ20746	TBC1 domain family, member 16	NM_019020, hCT19721.3, hCT2270915.0, hCT2270917.0, hCT2270920.0	1554701_a_at, 1558066_s_at, 222116_s_at, 222848_at, 226468_at	NP_061893.2, EAW89574.1, EAW89575.1, EAW89576.1, EAW89577.1
GeneID:55036	CCDC40	17	78,010,435	78,074,412	63,977	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2675, 2_A375_pNL97_plus_lncRNA_AR..1..3864	27773, 27837	in gene, in gene	1	1	0	24	19	15	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene CCDC40	FLJ32021, FLJ20753, CCDC40, KIAA1640	coiled-coil domain containing 40	NM_017950	1563563_at, 220592_at, 220593_s_at, 229918_at, 239254_at	NP_060420.2
GeneID:2548	GAA	17	78,075,355	78,093,679	18,324	+	1	4_A375_EGR1..1..3902	11701	in gene	0	0	1	6	6	19	1	4_A375_EGR1..1	19	Gene GAA	LYAG, GAA	glucosidase, alpha; acid	NM_000152, NM_001079803, NM_001079804, hCT19083.3, hCT1958833.1, hCT2357201.0	202812_at	NP_000143.2, NP_001073271.1, NP_001073272.1, EAW89581.1, EAW89582.1, EAW89583.1
GeneID:79092	CARD14	17	78,152,281	78,182,851	30,570	+	3	4_A375_EGR1..1..3903, 4_A375_EGR1..1..3904, 4_A375_EGR1..1..3905	3047, 15143, 32263	in gene, in gene, downstream	0	0	1	6	6.67	16.67	3	4_A375_EGR1..1	24	Gene CARD14	CARD14, BIMP2, CARMA2	caspase recruitment domain family, member 14	NM_024110, NM_052819, hCT19726.3, hCT2263867.0, hCT2263866.0, hCT2357173.0	1555308_at, 1555309_a_at, 220598_at, 220599_s_at, 224113_at, 232608_x_at	NP_077015.1, NP_438170.1, EAW89586.1, EAW89587.1, EAW89588.1, EAW89589.1
GeneID:6448	SGSH	17	78,183,079	78,194,199	11,120	-	2	2_A375_pNL97_plus_lncRNA_AR..1..3865, 4_A375_EGR1..1..3905	151, 9655	in gene, in gene	0	1	1	9	14.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SGSH	HSS, SGSH, MPS3A, SFMD	N-sulfoglucosamine sulfohydrolase	NM_000199, hCT19722.3, hCT2357146.0	204293_at, 35626_at	NP_000190.1, EAW89591.1, EAW89590.1
GeneID:284129	SLC26A11	17	78,194,200	78,227,308	33,108	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3865, 2_A375_pNL97_plus_lncRNA_AR..1..3866, 4_A375_EGR1..1..3905	-152, 41084, -9656	upstream, downstream, upstream	0	1	1	9	14.67	12	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SLC26A11	MGC46523, SLC26A11	solute carrier family 26, member 11	NM_001166347, NM_001166348, NM_001166349, NM_173626, hCT1814680.2	226679_at	NP_001159819.1, NP_001159820.1, NP_001159821.1, NP_775897.3, EAW89592.1
GeneID:57674	RNF213	17	78,234,667	78,370,086	135,419	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3866	597	in gene	0	1	0	9	15	13	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene RNF213	KIAA1618, MGC9929, FLJ13051, C17orf27, KIAA1554, DKFZp762N1115, RNF213, NET57, MGC46622	ring finger protein 213	NM_020954, NM_020914, hCT2343543.1, hCT2347539.0, hCT2350173.0, hCT2350174.0, hCT2350175.0, hCT2350176.0	1569078_at, 225929_s_at, 225931_s_at, 230000_at, 233880_at, 241460_at	NP_066005.2, NP_065965.4, EAW89595.1, EAW89596.1, EAW89597.1, EAW89599.1, EAW89598.1, EAW89600.1
GeneID:100294362	LOC100294362	17	78,325,630	78,368,966	63,336	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2676, 2_A375_pNL97_plus_lncRNA_AR..1..3867, 4_A375_EGR1..1..3906	-726, -13, -472	upstream, upstream, upstream	1	1	1	19	20	19	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100294362		hypothetical LOC100294362	NR_029376		
GeneID:284131	FLJ35220	17	78,388,967	78,411,886	22,919	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2676, 2_A375_pNL97_plus_lncRNA_AR..1..3867, 2_A375_pNL97_plus_lncRNA_AR..1..3868, 4_A375_EGR1..1..3906, 4_A375_EGR1..1..3907, 4_A375_EGR1..1..3908	729, 14, 26073, 473, 29753, 30233	in gene, in gene, downstream, in gene, downstream, downstream	1	1	1	11.25	14.25	16	4	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene FLJ35220	MGC74455	hypothetical protein FLJ35220	NM_173627, NM_001164637, NM_001164638, hCT2341046.1, hCT2341047.0, hCT2341048.0, hCT2341049.0, hCT2341050.1, hCT2341051.1, hCT2349108.0, hCT2349109.0, hCT2349110.0, hCT2349111.0, hCT2349112.0, hCT2357225.0, hCT2357226.0, hCT2357227.0	238400_at, 238401_at, 238402_s_at	NP_775898.2, NP_001158109.1, NP_001158110.1, EAW89602.1, EAW89612.1, EAW89615.1, EAW89603.1, EAW89604.1, EAW89605.1, EAW89606.1, EAW89607.1, EAW89608.1, EAW89609.1, EAW89610.1, EAW89611.1, EAW89613.1, EAW89614.1
GeneID:100507440	LOC100507440	17	78,391,217	78,392,679	1,462	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2676, 2_A375_pNL97_plus_lncRNA_AR..1..3867, 4_A375_EGR1..1..3906	-1521, -2236, -1777	upstream, upstream, upstream	1	1	1	19	20	19	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100507440		hypothetical LOC100507440	XR_111750, XR_109437, XR_115153		
GeneID:4884	NPTX1	17	78,440,633	78,450,404	9,771	-	1	4_A375_EGR1..1..3909	-4626	upstream	0	0	1	7	7	19	1	4_A375_EGR1..1	19	Gene NPTX1	MGC105123, DKFZp686J2446, NP1, NPTX1	neuronal pentraxin I	NM_002522, hCT87947.3	204684_at	NP_002513.2, EAW89617.1
GeneID:57521	RPTOR	17	78,518,625	78,940,173	421,548	+	11	1_A375_pNL7_minus_lncRNA_AR..1..2677, 2_A375_pNL97_plus_lncRNA_AR..1..3870, 2_A375_pNL97_plus_lncRNA_AR..1..3871, 2_A375_pNL97_plus_lncRNA_AR..1..3872, 2_A375_pNL97_plus_lncRNA_AR..1..3873, 2_A375_pNL97_plus_lncRNA_AR..1..3874, 4_A375_EGR1..1..3910, 4_A375_EGR1..1..3911, 4_A375_EGR1..1..3912, 4_A375_EGR1..1..3913, 4_A375_EGR1..1..3914	95, 191, 105119, 288367, 328943, 347663, 256559, 395967, 396607, 419263, 420287	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	10.5	13.9	14.2	10	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene RPTOR	KIAA1303, KOG1, Mip1, RPTOR	regulatory associated protein of MTOR, complex 1	NM_020761, NM_001163034, hCT18416.4, hCT2263678.1	225715_at	NP_065812.1, NP_001156506.1, EAW89618.1, EAW89619.1
GeneID:100128105	LOC100128105	17	78,914,218	78,915,833	1,615	-	2	4_A375_EGR1..1..3911, 4_A375_EGR1..1..3912	1241, 601	in gene, in gene	0	0	1	7	6	20.5	2	4_A375_EGR1..1	22	Gene LOC100128105		hypothetical LOC100128105	XM_001716364, XM_001721678, XM_001726781		XP_001716416.1, XP_001721730.1, XP_001726833.1
GeneID:79643	CHMP6	17	78,965,641	78,973,933	8,292	+	4	4_A375_EGR1..1..3915, 4_A375_EGR1..1..3916, 4_A375_EGR1..1..3917, 4_A375_EGR1..1..3918	-9449, 5679, 8471, 11255	upstream, in gene, downstream, downstream	0	0	1	6.75	6	19	4	4_A375_EGR1..1	23	Gene CHMP6	VPS20, FLJ11749, CHMP6	chromatin modifying protein 6	NM_024591, hCT16663.3	218743_at	NP_078867.2, EAW89622.1
GeneID:100129503	LOC100129503	17	78,976,059	78,976,411	352	+	3	4_A375_EGR1..1..3916, 4_A375_EGR1..1..3917, 4_A375_EGR1..1..3918	-6539, -3947, -1163	upstream, upstream, upstream	0	0	1	6	6	16.67	3	4_A375_EGR1..1	23	Gene LOC100129503	PP13	hypothetical LOC100129503	XR_111751, XR_109438		
GeneID:440465	FLJ90757	17	79,002,933	79,008,519	5,586	-	1	4_A375_EGR1..1..3919	-3977	upstream	0	0	1	6	6	16	1	4_A375_EGR1..1	16	Gene FLJ90757	FLJ31993, FLJ39290, FLJ42772, FLJ14444, MGC131745	hypothetical LOC440465	NR_026857	1558147_a_at, 1558148_x_at, 1566555_at, 1566557_at, 1566558_x_at	
GeneID:10458	BAIAP2	17	79,008,947	79,091,232	82,285	+	10	4_A375_EGR1..1..3919, 4_A375_EGR1..1..3920, 4_A375_EGR1..1..3921, 4_A375_EGR1..1..3922, 4_A375_EGR1..1..3923, 4_A375_EGR1..1..3924, 4_A375_EGR1..1..3925, 4_A375_EGR1..1..3926, 4_A375_EGR1..1..3927, 4_A375_EGR1..1..3928	3549, 13869, 32605, 60333, 62253, 63565, 85981, 86749, 89465, 91597	in gene, in gene, in gene, in gene, in gene, downstream, downstream, downstream, downstream, downstream	0	0	1	7.5	8.7	18.3	10	4_A375_EGR1..1	21	Gene BAIAP2	IRSP53, BAIAP2, FLAF3, BAP2	BAI1-associated protein 2	NM_017451, NM_017450, NM_006340, NM_001144888, hCT1850194.3, hCT1850198.3, hCT1965871.1, hCT2263639.0	205293_x_at, 205294_at, 207832_at, 209502_s_at	NP_059345.1, NP_059344.1, NP_001138360.1, NP_006331.1, EAW89625.1, EAW89628.1, EAW89626.1, EAW89627.1
GeneID:9625	AATK	17	79,091,095	79,139,872	48,777	-	7	4_A375_EGR1..1..3924, 4_A375_EGR1..1..3925, 4_A375_EGR1..1..3926, 4_A375_EGR1..1..3927, 4_A375_EGR1..1..3928, 4_A375_EGR1..1..3929, 4_A375_EGR1..1..3930	47360, 44944, 44176, 41440, 39328, 37698, 21660	in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	5.71	7	17.43	7	4_A375_EGR1..1	20	Gene AATK	AATYK, KIAA0641, AATYK1, AATK, LMR1, p35BP, LMTK1	apoptosis-associated tyrosine kinase	NM_001080395	205986_at	NP_001073864.2
GeneID:724027	MIR657	17	79,099,076	79,099,173	97	-	6	4_A375_EGR1..1..3924, 4_A375_EGR1..1..3925, 4_A375_EGR1..1..3926, 4_A375_EGR1..1..3927, 4_A375_EGR1..1..3928, 4_A375_EGR1..1..3929	6661, 4245, 3477, 741, -1371, -3003	downstream, downstream, downstream, downstream, upstream, upstream	0	0	1	5.83	7.5	17.5	6	4_A375_EGR1..1	20	Gene MIR657	MIR657, MIRN657, hsa-mir-657	microRNA 657	NR_030394		
GeneID:100422915	MIR3065	17	79,099,677	79,099,755	78	+	6	4_A375_EGR1..1..3924, 4_A375_EGR1..1..3925, 4_A375_EGR1..1..3926, 4_A375_EGR1..1..3927, 4_A375_EGR1..1..3928, 4_A375_EGR1..1..3929	-7165, -4749, -3981, -1245, 867, 2499	upstream, upstream, upstream, upstream, downstream, downstream	0	0	1	5.83	7.5	17.5	6	4_A375_EGR1..1	20	Gene MIR3065	MIR3065	microRNA 3065	NR_036151		
GeneID:442906	MIR338	17	79,099,683	79,099,749	66	-	6	4_A375_EGR1..1..3924, 4_A375_EGR1..1..3925, 4_A375_EGR1..1..3926, 4_A375_EGR1..1..3927, 4_A375_EGR1..1..3928, 4_A375_EGR1..1..3929	7237, 4821, 4053, 1317, -795, -2427	downstream, downstream, downstream, downstream, upstream, upstream	0	0	1	5.83	7.5	17.5	6	4_A375_EGR1..1	20	Gene MIR338	hsa-mir-338, MIR338, MIRN338	microRNA 338	NR_029897		
GeneID:100302229	MIR1250	17	79,106,996	79,107,108	112	-	3	4_A375_EGR1..1..3927, 4_A375_EGR1..1..3928, 4_A375_EGR1..1..3929	8676, 6564, 4932	downstream, downstream, downstream	0	0	1	6	7.67	16	3	4_A375_EGR1..1	18	Gene MIR1250	hsa-mir-1250, MIR1250, MIRN1250	microRNA 1250	NR_031652		
GeneID:100507494	LOC100507494	17	79,117,967	79,118,838	871	-	1	4_A375_EGR1..1..3930	446	in gene	0	0	1	5	4	17	1	4_A375_EGR1..1	17	Gene LOC100507494		hypothetical protein LOC100507494	XM_003119694, XM_003118750, XM_003120901		XP_003119742.1, XP_003118798.1, XP_003120949.1
GeneID:388428	LOC388428	17	79,139,307	79,156,964	17,657	+	3	4_A375_EGR1..1..3931, 4_A375_EGR1..1..3932, 4_A375_EGR1..1..3933	22213, 24341, 27573	downstream, downstream, downstream	0	0	1	7	6.33	17.67	3	4_A375_EGR1..1	23	Gene LOC388428	FLJ44881	hypothetical LOC388428	NR_027255, hCT2360335.0		EAW89630.1
GeneID:22994	AZI1	17	79,163,393	79,196,751	33,358	-	5	4_A375_EGR1..1..3931, 4_A375_EGR1..1..3932, 4_A375_EGR1..1..3933, 4_A375_EGR1..1..3934, 4_A375_EGR1..1..3935	35231, 33103, 29871, 27823, 22863	downstream, in gene, in gene, in gene, in gene	0	0	1	6.6	7	18.2	5	4_A375_EGR1..1	23	Gene AZI1	AZ1, AZI1, Cep131, ZA1	5-azacytidine induced 1	NM_014984, NM_001009811, hCT1953024.1, hCT2270861.0	214742_at	NP_055799.2, NP_001009811.2, EAW89631.1, EAW89632.1
GeneID:146705	C17orf56	17	79,202,077	79,212,891	10,814	-	3	4_A375_EGR1..1..3936, 4_A375_EGR1..1..3937, 4_A375_EGR1..1..3938	5531, -6757, -7525	in gene, upstream, upstream	0	0	1	7.67	8.33	18.33	3	4_A375_EGR1..1	20	Gene C17orf56	DKFZp451M1616, C17orf56, FLJ31528	chromosome 17 open reading frame 56	NM_144679, hCT2270876.0, hCT2270877.0, hCT2270878.0, hCT2270879.0, hCT2357195.0	227668_at, 236737_at, 236960_x_at, 239861_at	NP_653280.1, EAW89635.1, EAW89634.1, EAW89636.1, EAW89637.1, EAW89638.1
GeneID:284184	C17orf89	17	79,213,111	79,215,098	1,987	+	3	4_A375_EGR1..1..3936, 4_A375_EGR1..1..3937, 4_A375_EGR1..1..3938	-5751, 6537, 7305	upstream, downstream, downstream	0	0	1	7.67	8.33	18.33	3	4_A375_EGR1..1	20	Gene C17orf89	C17orf89	chromosome 17 open reading frame 89	NM_001086521	225986_at, 225987_s_at, 230199_at	NP_001079990.1
GeneID:124565	SLC38A10	17	79,218,799	79,269,096	50,297	-	4	4_A375_EGR1..1..3937, 4_A375_EGR1..1..3938, 4_A375_EGR1..1..3939, 4_A375_EGR1..1..3940	49448, 48680, 34488, 520	in gene, in gene, in gene, in gene	0	0	1	11	10.25	18.75	4	4_A375_EGR1..1	20	Gene SLC38A10	FLJ35718, MGC15523, PP1744, SLC38A10, FLJ46399	solute carrier family 38, member 10	NM_001037984, NM_138570, hCT1643269.4, hCT2289851.1, hCT2340369.0	91703_at	NP_001033073.1, NP_612637.1, EAW89641.1, EAW89642.1, EAW89643.1
GeneID:284185	C17orf55	17	79,276,624	79,283,048	6,424	-	2	4_A375_EGR1..1..3940, 4_A375_EGR1..1..3941	14472, -6040	downstream, upstream	0	0	1	12.5	9	19.5	2	4_A375_EGR1..1	20	Gene C17orf55	MGC120556, C17orf55, FLJ39421, MGC120553	chromosome 17 open reading frame 55	NM_178519, hCT2269847.1, hCT2349094.0	243263_at	NP_848614.1, EAW89645.1, EAW89646.1
GeneID:284186	TMEM105	17	79,285,074	79,304,474	19,400	-	1	4_A375_EGR1..1..3941	15386	in gene	0	0	1	10	6	19	1	4_A375_EGR1..1	19	Gene TMEM105	TMEM105, FLJ38792	transmembrane protein 105	NM_178520, hCT2343208.0	1561243_at	NP_848615.1, EAW89647.1
GeneID:100130370	LOC100130370	17	79,352,934	79,357,447	4,513	-	1	4_A375_EGR1..1..3943	-4991	upstream	0	0	1	5	6	17	1	4_A375_EGR1..1	17	Gene LOC100130370		hypothetical protein LOC100130370	XM_001715409, XM_001719466, XM_001714098		XP_001715461.1, XP_001719518.1, XP_001714146.2
GeneID:100507520	LOC100507520	17	79,361,922	79,364,687	2,765	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2678, 1_A375_pNL7_minus_lncRNA_AR..1..2679, 2_A375_pNL97_plus_lncRNA_AR..1..3875, 2_A375_pNL97_plus_lncRNA_AR..1..3876, 4_A375_EGR1..1..3943	-3153, -4129, -3345, -5745, 2249	upstream, upstream, upstream, upstream, in gene	1	1	1	14.5	12.75	9.5	4	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene LOC100507520		hypothetical LOC100507520	XR_109439, XR_109440		
GeneID:57597	BAHCC1	17	79,373,540	79,433,358	59,818	+	12	1_A375_pNL7_minus_lncRNA_AR..1..2678, 1_A375_pNL7_minus_lncRNA_AR..1..2679, 2_A375_pNL97_plus_lncRNA_AR..1..3875, 2_A375_pNL97_plus_lncRNA_AR..1..3876, 4_A375_EGR1..1..3944, 4_A375_EGR1..1..3945, 4_A375_EGR1..1..3946, 4_A375_EGR1..1..3947, 4_A375_EGR1..1..3948, 4_A375_EGR1..1..3949, 4_A375_EGR1..1..3950, 4_A375_EGR1..1..3951	-5700, -4724, -5508, -3108, 7036, 17212, 20796, 27852, 28756, 46076, 51964, 61020	upstream, upstream, upstream, upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, downstream	1	1	1	9.36	8.46	14.91	11	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene BAHCC1	BAHCC1, BAHD2, FLJ23058, KIAA1447	BAH domain and coiled-coil containing 1	NM_001080519	1559048_at, 1559049_a_at, 1559075_s_at, 219218_at, 236604_at	NP_001073988.2
GeneID:100422944	MIR3186	17	79,418,130	79,418,214	84	-	2	4_A375_EGR1..1..3949, 4_A375_EGR1..1..3950	-1402, -7290	upstream, upstream	0	0	1	6.5	5	18	2	4_A375_EGR1..1	19	Gene MIR3186	MIR3186	microRNA 3186	NR_036152		
GeneID:100507545	LOC100507545	17	79,454,310	79,493,204	38,894	+	9	2_A375_pNL97_plus_lncRNA_AR..1..3877, 2_A375_pNL97_plus_lncRNA_AR..1..3878, 4_A375_EGR1..1..3952, 4_A375_EGR1..1..3953, 4_A375_EGR1..1..3954, 4_A375_EGR1..1..3955, 4_A375_EGR1..1..3956, 4_A375_EGR1..1..3957, 4_A375_EGR1..1..3958	25018, 26170, 12410, 25082, 26778, 37114, 38949, 41434, 47594	in gene, in gene, in gene, in gene, in gene, in gene, downstream, downstream, downstream	0	1	1	9.71	12	16.14	7	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100507545		hypothetical LOC100507545	XR_109444, XR_109445, XR_109441, XR_109442, XR_109443, XR_109446		
GeneID:71	ACTG1	17	79,476,999	79,479,827	2,828	-	5	2_A375_pNL97_plus_lncRNA_AR..1..3877, 2_A375_pNL97_plus_lncRNA_AR..1..3878, 4_A375_EGR1..1..3952, 4_A375_EGR1..1..3953, 4_A375_EGR1..1..3954	499, -653, 13107, 435, -1261	in gene, upstream, downstream, in gene, upstream	0	1	1	11.33	14	16	3	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ACTG1	DFNA20, ACT, ACTG1, ACTG, DFNA26	actin, gamma 1	NM_001614	201550_x_at, 211970_x_at, 211983_x_at, 211995_x_at, 212363_x_at, 212988_x_at, 213214_x_at, 221607_x_at, 224585_x_at	NP_001605.1
GeneID:25794	FSCN2	17	79,495,417	79,504,156	8,739	+	7	4_A375_EGR1..1..3955, 4_A375_EGR1..1..3956, 4_A375_EGR1..1..3957, 4_A375_EGR1..1..3958, 4_A375_EGR1..1..3959, 4_A375_EGR1..1..3960, 4_A375_EGR1..1..3961	-3993, -2158, 327, 6487, 10759, 12775, 16823	upstream, upstream, in gene, in gene, downstream, downstream, downstream	0	0	1	7.43	9.43	16.86	7	4_A375_EGR1..1	19	Gene FSCN2	FSCN2, RFSN, RP30	fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus)	NM_012418, NM_001077182, hCT1850198.1	207204_at	NP_036550.1, NP_001070650.1, EAW89654.1
GeneID:80233	C17orf70	17	79,506,911	79,519,429	12,518	-	4	4_A375_EGR1..1..3958, 4_A375_EGR1..1..3959, 4_A375_EGR1..1..3960, 4_A375_EGR1..1..3961	17525, 13253, 11237, 5189	downstream, downstream, in gene, in gene	0	0	1	6.5	8.25	17.5	4	4_A375_EGR1..1	19	Gene C17orf70	FAAP100, C17orf70, FLJ30151, FLJ22175	chromosome 17 open reading frame 70	NM_025161, NR_033338, hCT1850197.3, hCT1953021.1, hCT1963297.1, hCT1963298.1, hCT1963299.1, hCT2357180.0	221600_s_at, 225322_s_at	NP_079437.5, EAW89657.1, EAW89655.1, EAW89656.1, EAW89659.1, EAW89660.1, EAW89658.1
GeneID:55666	NPLOC4	17	79,523,913	79,604,138	80,225	-	3	4_A375_EGR1..1..3961, 4_A375_EGR1..1..3962, 4_A375_EGR1..1..3963	89898, -150, -8214	downstream, upstream, upstream	0	0	1	9	10.67	19.33	3	4_A375_EGR1..1	20	Gene NPLOC4	FLJ20657, NPLOC4, KIAA1499, NPL4, FLJ23742	nuclear protein localization 4 homolog (S. cerevisiae)	NM_017921, hCT1953007.1, hCT2289620.0, hCT2289622.0	217796_s_at	NP_060391.2, EAW89662.1, EAW89661.1, EAW89663.1
GeneID:83882	TSPAN10	17	79,609,349	79,615,779	6,430	+	4	4_A375_EGR1..1..3962, 4_A375_EGR1..1..3963, 4_A375_EGR1..1..3964, 4_A375_EGR1..1..3965	-5081, 3003, 13051, 13651	upstream, in gene, downstream, downstream	0	0	1	7.75	8	19.75	4	4_A375_EGR1..1	21	Gene TSPAN10	FLJ39807, OCSP, TSPAN10	tetraspanin 10	NM_031945, hCT1850203.1	223795_at	NP_114151.3, EAW89665.1

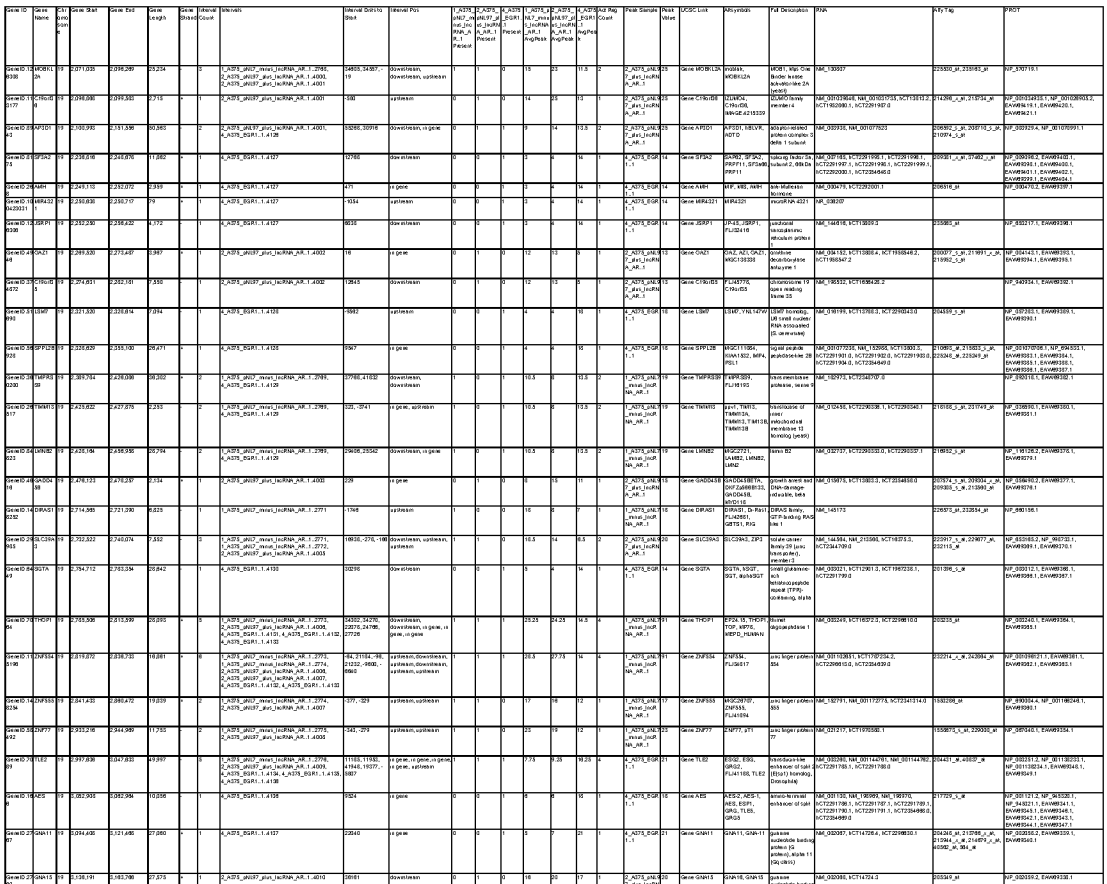
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:5148	PDE6G	17	79,617,489	79,623,607	6,118	-	5	2_A375_pNL97_plus_lncRNA_AR..1..3879, 4_A375_EGR1..1..3963, 4_A375_EGR1..1..3964, 4_A375_EGR1..1..3965, 4_A375_EGR1..1..3966	-10121, 11255, 1207, 407, -6969	upstream, downstream, in gene, in gene, upstream	0	1	1	8.4	10.6	19.4	5	4_A375_EGR1..1	21	Gene PDE6G	DKFZp686C0587, PDE6G, RP57, PDEG, MGC125749	phosphodiesterase 6G, cGMP-specific, rod, gamma	NM_002602, NR_026872, hCT29293.3	210060_at	NP_002593.1, EAW89668.1
GeneID:339229	C17orf90	17	79,632,066	79,633,618	1,552	-	5	2_A375_pNL97_plus_lncRNA_AR..1..3879, 4_A375_EGR1..1..3964, 4_A375_EGR1..1..3965, 4_A375_EGR1..1..3966, 4_A375_EGR1..1..3967	-110, 11216, 10418, 1042, -494	upstream, downstream, downstream, in gene, upstream	0	1	1	8.75	11.5	19.25	4	4_A375_EGR1..1	21	Gene C17orf90	MGC104712, C17orf90	chromosome 17 open reading frame 90	NM_001039842	221797_at, 50374_at	NP_001034931.1
GeneID:339230	CCDC137	17	79,633,761	79,640,937	7,176	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2660, 2_A375_pNL97_plus_lncRNA_AR..1..3879, 2_A375_pNL97_plus_lncRNA_AR..1..3880, 4_A375_EGR1..1..3966, 4_A375_EGR1..1..3967, 4_A375_EGR1..1..3968	17151, -33, 17327, -1165, 351, 16959	downstream, upstream, downstream, upstream, in gene, downstream	1	1	1	14.67	17	18.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CCDC137	MGC16597, CCDC137	coiled-coil domain containing 137	NM_199287	225933_at	NP_954981.1
GeneID:339231	ARL16	17	79,648,224	79,650,954	2,730	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2660, 2_A375_pNL97_plus_lncRNA_AR..1..3880, 4_A375_EGR1..1..3968, 4_A375_EGR1..1..3969	42, -134, 234, -3302	in gene, upstream, in gene, upstream	1	1	1	13.5	14	17.5	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ARL16	ARL16	ADP-ribosylation factor-like 16	NM_001040025	234972_at	NP_001035114.1
GeneID:9146	HGS	17	79,651,020	79,669,146	18,126	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2660, 1_A375_pNL7_minus_lncRNA_AR..1..2661, 2_A375_pNL97_plus_lncRNA_AR..1..3880, 2_A375_pNL97_plus_lncRNA_AR..1..3881, 4_A375_EGR1..1..3968, 4_A375_EGR1..1..3969, 4_A375_EGR1..1..3970, 4_A375_EGR1..1..3971	-106, 19476, 66, 19360, -300, 3236, 24180, 26420	upstream, downstream, in gene, downstream, upstream, in gene, downstream, downstream	1	1	1	13	14.2	19	5	4_A375_EGR1..1	24	Gene HGS	Vps27, FLJ11421, FLJ39878, HRS, ZFYVE8, HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	NM_004712, hCT2263545.1, hCT2263546.1, hCT2263548.1, hCT2263549.1, hCT2263550.1	210428_s_at	NP_004703.1, EAW89678.1, EAW89675.1, EAW89676.1, EAW89677.1, EAW89679.1
GeneID:6182	MRPL12	17	79,670,407	79,674,548	4,141	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2661, 2_A375_pNL97_plus_lncRNA_AR..1..3881, 4_A375_EGR1..1..3970, 4_A375_EGR1..1..3971, 4_A375_EGR1..1..3972	89, -7, 4793, 7033, 13049	in gene, upstream, downstream, downstream, downstream	1	1	1	10.5	12.25	20	4	4_A375_EGR1..1	24	Gene MRPL12	RPML12, 5c5-2, MRPL12, L12mt, MGC8610, MRP-L31/34, MRPL7/L12, FLJ60124, MRPL7	mitochondrial ribosomal protein L12	NM_002949, hCT2263543.1	203931_s_at, 229165_at	NP_002940.2, EAW89680.1
GeneID:1468	SLC25A10	17	79,679,371	79,688,042	8,671	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2661, 2_A375_pNL97_plus_lncRNA_AR..1..3881, 4_A375_EGR1..1..3970, 4_A375_EGR1..1..3971, 4_A375_EGR1..1..3972	-8875, -8971, -4171, -1931, 4085	upstream, upstream, upstream, upstream, in gene	1	1	1	10.5	12.25	20	4	4_A375_EGR1..1	24	Gene SLC25A10	SLC25A10, DIC	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	NM_012140, hCT2263556.0, hCT29163.3	218275_at	NP_036272.2, EAW89681.1, EAW89682.1
GeneID:2642	GCGR	17	79,762,010	79,771,889	9,879	+	2	4_A375_EGR1..1..3973, 4_A375_EGR1..1..3974	4017, 9350	in gene, in gene	0	0	1	6.5	7	14.5	2	4_A375_EGR1..1	15	Gene GCGR	MGC138246, FLJ97182, GCGR, GGR	glucagon receptor	NM_000160, hCT87190.2	210565_at	NP_000151.1, EAW89684.1
GeneID:348262	FAM195B	17	79,780,293	79,791,167	10,874	-	3	4_A375_EGR1..1..3974, 4_A375_EGR1..1..3975, 4_A375_EGR1..1..3976	19807, 8335, 639	downstream, in gene, in gene	0	0	1	6.67	9.33	15	3	4_A375_EGR1..1	16	Gene FAM195B	DKFZp686A17165, MGC133184, FAM195B	family with sequence similarity 195, member B	NM_207368, NM_001093767	225329_at	NP_997251.2, NP_001087236.1
GeneID:118729	DYSFIP1	17	79,791,368	79,792,926	1,558	-	2	4_A375_EGR1..1..3975, 4_A375_EGR1..1..3976	10094, 2398	downstream, downstream	0	0	1	7.5	9	15	2	4_A375_EGR1..1	16	Gene DYSFIP1	MGC138299, DYSFIP1	dysferlin interacting protein 1	NM_001007533	1557480_a_at	NP_001007534.1
GeneID:100505927	LOC100505927	17	79,791,970	79,801,705	9,735	+	3	4_A375_EGR1..1..3975, 4_A375_EGR1..1..3976, 4_A375_EGR1..1..3977	-9136, -1442, 17550	upstream, upstream, downstream	0	0	1	6.67	9	16.33	3	4_A375_EGR1..1	19	Gene LOC100505927		hypothetical LOC100505927	XR_109347		
GeneID:5034	P4HB	17	79,801,034	79,818,544	17,510	-	4	2_A375_pNL97_plus_lncRNA_AR..1..3882, 2_A375_pNL97_plus_lncRNA_AR..1..3883, 4_A375_EGR1..1..3977, 4_A375_EGR1..1..3978	-432, -8624, 9024, -8576	upstream, upstream, in gene, upstream	0	1	1	12	17	18.33	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene P4HB	P4HB, PO4DB, PDI, GIT, PDIA1, DSI, PROHB, PHDB, P4Hbeta, PO4HB, ERBA2L	prolyl 4-hydroxylase, beta polypeptide	NM_000918, hCT2289585.0, hCT2289587.0, hCT2289591.0, hCT2289593.0, hCT2289595.0, hCT2357183.0, hCT87194.3	1564494_s_at, 200654_at, 200656_s_at	NP_000909.2, EAW89691.1, EAW89690.1, EAW89693.1, EAW89695.1, EAW89696.1, EAW89692.1, EAW89694.1
GeneID:396	ARHGDIA	17	79,825,597	79,829,282	3,685	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2662, 2_A375_pNL97_plus_lncRNA_AR..1..3882, 2_A375_pNL97_plus_lncRNA_AR..1..3883, 2_A375_pNL97_plus_lncRNA_AR..1..3884, 4_A375_EGR1..1..3978, 4_A375_EGR1..1..3979	-94, 10306, 4114, -158, 4162, -766	upstream, downstream, downstream, upstream, downstream, upstream	1	1	1	24	27.33	17.67	3	1_A375_pNL7_minus_lncRNA_AR..1	41	Gene ARHGDIA	RHOGDI-1, MGC117248, ARHGDIA, RHOGDI, GDIA1	Rho GDP dissociation inhibitor (GDI) alpha	NM_001185077, NM_001185078, NM_004309, hCT1968278.1, hCT1968279.1	201167_x_at, 211716_x_at, 213606_s_at	NP_001172006.1, NP_001172007.1, NP_004300.1, EAW89697.1, EAW89698.1
GeneID:51529	ANAPC11	17	79,849,599	79,858,363	8,764	+	2	4_A375_EGR1..1..3980, 4_A375_EGR1..1..3981	11377, 14985	downstream, downstream	0	0	1	9.5	7.5	15	2	4_A375_EGR1..1	17	Gene ANAPC11	HSPC214, APC11, MGC882, ANAPC11, Apc11p	anaphase promoting complex subunit 11	NM_001002249, NM_001002247, NM_001002248, NM_001002245, NM_001002246, NM_001002244, NM_016476, hCT1963688.2, hCT1963689.2, hCT1963690.2, hCT2263572.1	224010_at	NP_001002249.1, NP_001002247.1, NP_001002248.1, NP_001002245.1, NP_001002246.1, NP_001002244.1, NP_057560.8, EAW89700.1, EAW89701.1, EAW89702.1, EAW89703.1
GeneID:256933	NPB	17	79,860,072	79,860,781	709	+	3	4_A375_EGR1..1..3980, 4_A375_EGR1..1..3981, 4_A375_EGR1..1..3982	904, 4512, 10344	downstream, downstream, downstream	0	0	1	6.33	8	16	3	4_A375_EGR1..1	16	Gene NPB	PPNPB, NPB, PPL7	neuropeptide B	NM_148896, hCT2341198.0		NP_683694.1, EAW89704.1
GeneID:5833	PCYT2	17	79,860,777	79,869,340	8,563	-	4	4_A375_EGR1..1..3980, 4_A375_EGR1..1..3981, 4_A375_EGR1..1..3982, 4_A375_EGR1..1..3983	8384, 4756, -1076, -9252	in gene, in gene, upstream, upstream	0	0	1	6.5	7.5	16.75	4	4_A375_EGR1..1	19	Gene PCYT2	PCYT2, ET	phosphate cytidylyltransferase 2, ethanolamine	NM_001184917, NM_002861, NR_033681, NR_033682, NR_033683, NR_033685, hCT2289575.0	209577_at	NP_001171846.1, NP_002852.1, EAW89705.1
GeneID:51547	SIRT7	17	79,869,815	79,876,058	6,243	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..3885, 4_A375_EGR1..1..3980, 4_A375_EGR1..1..3981, 4_A375_EGR1..1..3982, 4_A375_EGR1..1..3983	-9636, -9590, 15082, 11474, 5642, -2534	upstream, upstream, downstream, downstream, in gene, upstream	1	1	1	11	11	14.8	5	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene SIRT7	SIRT7, MGC126840, MGC126842, SIR2L7	sirtuin (silent mating type information regulation 2 homolog) 7 (S. cerevisiae)	NM_016538	218797_s_at	NP_057622.1
GeneID:4097	MAFG	17	79,876,146	79,885,588	9,442	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..3885, 4_A375_EGR1..1..3982, 4_A375_EGR1..1..3983, 4_A375_EGR1..1..3984, 4_A375_EGR1..1..3985	-108, -60, 15172, 6998, -676, -7438	upstream, upstream, downstream, in gene, upstream, upstream	1	1	1	10.6	12.4	15.6	5	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene MAFG	MAFG, MGC20149, MGC13090	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	NM_032711, NM_002359	204970_s_at, 224468_s_at	NP_116100.2, NP_002350.1
GeneID:92659	LOC92659	17	79,885,705	79,888,629	2,924	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..3885, 4_A375_EGR1..1..3983, 4_A375_EGR1..1..3984, 4_A375_EGR1..1..3985, 4_A375_EGR1..1..3986	-9, -57, -7113, 759, 7319, 12247	upstream, upstream, upstream, in gene, downstream, downstream	1	1	1	10.8	11.6	15.6	5	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC92659		hypothetical LOC92659	NR_015454	1559352_a_at	
GeneID:5831	PYCR1	17	79,890,267	79,894,968	4,701	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2663, 2_A375_pNL97_plus_lncRNA_AR..1..3885, 4_A375_EGR1..1..3984, 4_A375_EGR1..1..3985, 4_A375_EGR1..1..3986	9272, 9320, 8504, 1944, -2984	downstream, downstream, downstream, in gene, upstream	1	1	1	11.25	13	14.75	4	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene PYCR1	P5C, PYCR1, PIG45, PP222, ARCL2B, PYCR, P5CR, PRO3	pyrroline-5-carboxylate reductase 1	NM_153824, NM_006907, hCT1963925.2, hCT1963926.2, hCT1963927.2, hCT2289558.1, hCT2289560.1, hCT2289562.1, hCT2289563.1, hCT2349174.0, hCT2349175.0, hCT30049.3	202148_s_at	NP_722546.1, NP_008838.2, EAW89717.1, EAW89718.1, EAW89719.1, EAW89720.1, EAW89721.1, EAW89722.1, EAW89723.1, EAW89724.1, EAW89725.1, EAW89726.1
GeneID:255275	MYADML2	17	79,897,521	79,905,109	7,588	-	3	4_A375_EGR1..1..3985, 4_A375_EGR1..1..3986, 4_A375_EGR1..1..3987	12085, 7157, -9728	downstream, in gene, upstream	0	0	1	7	7.33	16.33	3	4_A375_EGR1..1	19	Gene MYADML2	MYADML2	myeloid-associated differentiation marker-like 2	NM_001145113	242378_at	NP_001138585.2
GeneID:147111	NOTUM	17	79,910,383	79,919,057	8,674	-	3	4_A375_EGR1..1..3987, 4_A375_EGR1..1..3988, 4_A375_EGR1..1..3989	4220, 1841, -1615	in gene, in gene, upstream	0	0	1	6.33	9.33	17	3	4_A375_EGR1..1	19	Gene NOTUM	NOTUM	notum pectinacetylesterase homolog (Drosophila)	NM_178493, hCT1786291.2	228649_at	NP_848588.3, EAW89729.1
GeneID:79058	ASPSCR1	17	79,935,426	79,975,282	39,856	+	12	1_A375_pNL7_minus_lncRNA_AR..1..2664, 2_A375_pNL97_plus_lncRNA_AR..1..3886, 4_A375_EGR1..1..3990, 4_A375_EGR1..1..3991, 4_A375_EGR1..1..3992, 4_A375_EGR1..1..3993, 4_A375_EGR1..1..3994, 4_A375_EGR1..1..3995, 4_A375_EGR1..1..3996, 4_A375_EGR1..1..3997, 4_A375_EGR1..1..3998, 4_A375_EGR1..1..3999	26270, 26366, 14878, 18313, 27966, 30798, 35086, 38142, 40798, 42830, 45086, 47534	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, downstream, downstream, downstream, downstream	1	1	1	7.55	9.46	17.55	11	4_A375_EGR1..1	21	Gene ASPSCR1	ASPS, TUG, UBXN9, ASPL, UBXD9, RCC17, ASPSCR1, ASPCR1, FLJ45380	alveolar soft part sarcoma chromosome region, candidate 1	NM_024083, hCT87197.3	218908_at	NP_076988.1, EAW89731.1
GeneID:201254	STRA13	17	79,976,579	79,980,773	4,194	-	9	2_A375_pNL97_plus_lncRNA_AR..1..3887, 4_A375_EGR1..1..3993, 4_A375_EGR1..1..3994, 4_A375_EGR1..1..3995, 4_A375_EGR1..1..3996, 4_A375_EGR1..1..3997, 4_A375_EGR1..1..3998, 4_A375_EGR1..1..3999, 4_A375_EGR1..1..4000	-7835, 14549, 10261, 7205, 4549, 2517, 261, -2167, -7371	upstream, downstream, downstream, downstream, downstream, in gene, in gene, upstream, upstream	0	1	1	9.13	10.25	16.63	8	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene STRA13	STRA13, MHF2, CENP-X, MGC14480	stimulated by retinoic acid 13 homolog (mouse)	NM_144998		NP_659435.2
GeneID:201255	LRRC45	17	79,981,280	79,989,027	7,747	+	10	1_A375_pNL7_minus_lncRNA_AR..1..2665, 2_A375_pNL97_plus_lncRNA_AR..1..3887, 2_A375_pNL97_plus_lncRNA_AR..1..3888, 4_A375_EGR1..1..3995, 4_A375_EGR1..1..3996, 4_A375_EGR1..1..3997, 4_A375_EGR1..1..3998, 4_A375_EGR1..1..3999, 4_A375_EGR1..1..4000, 4_A375_EGR1..1..4001	14112, 7328, 13840, -7712, -5056, -3024, -768, 1680, 6664, 10176	downstream, in gene, downstream, upstream, upstream, upstream, upstream, in gene, in gene, downstream	1	1	1	11.13	11.88	18.13	8	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LRRC45	MGC20806, LRRC45	leucine rich repeat containing 45	NM_144999	226253_at	NP_659436.1
GeneID:5881	RAC3	17	79,989,532	79,992,080	2,548	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2665, 2_A375_pNL97_plus_lncRNA_AR..1..3887, 2_A375_pNL97_plus_lncRNA_AR..1..3888, 4_A375_EGR1..1..3998, 4_A375_EGR1..1..3999, 4_A375_EGR1..1..4000, 4_A375_EGR1..1..4001	5880, -924, 5586, -9020, -6572, -1388, 1924	downstream, upstream, downstream, upstream, upstream, upstream, in gene	1	1	1	13.4	14.4	19.2	5	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene RAC3	RAC3		NM_005052	206103_at	NP_005043.1
GeneID:51181	DCXR	17	79,993,757	79,995,573	1,816	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2665, 2_A375_pNL97_plus_lncRNA_AR..1..3887, 2_A375_pNL97_plus_lncRNA_AR..1..3888, 4_A375_EGR1..1..4000, 4_A375_EGR1..1..4001	181, 6985, 453, 7429, 4117	in gene, downstream, in gene, downstream, downstream	1	1	1	16	15.33	19.33	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene DCXR	KIDCR, P34H, HCR2, DCXR, SDR20C1, HCRII, DCR	dicarbonyl/L-xylulose reductase	NM_016286, hCT1957261.0, hCT31656.3	217973_at	NP_057370.1, EAW89732.1, EAW89733.1
GeneID:5986	RFNG	17	80,005,778	80,009,650	3,872	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2665, 4_A375_EGR1..1..4002, 4_A375_EGR1..1..4003, 4_A375_EGR1..1..4004, 4_A375_EGR1..1..4005	14258, 3362, -4238, -4694, -7054	downstream, in gene, upstream, upstream, upstream	1	0	1	10.2	9.8	17.2	5	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene RFNG	RFNG		NM_002917, hCT1970473.0, hCT2289547.0, hCT2289548.0, hCT2289549.0, hCT2289550.0, hCT2357207.0	212968_at	NP_002908.1, EAW89735.1, EAW89736.1, EAW89737.1, EAW89738.1, EAW89739.1, EAW89740.1
GeneID:2873	GPS1	17	80,009,763	80,015,346	5,583	+	5	4_A375_EGR1..1..4002, 4_A375_EGR1..1..4003, 4_A375_EGR1..1..4004, 4_A375_EGR1..1..4005, 4_A375_EGR1..1..4006	-3475, 4125, 4781, 6941, 12845	upstream, in gene, in gene, downstream, downstream	0	0	1	8	8.4	17.4	5	4_A375_EGR1..1	21	Gene GPS1	COPS1, CSN1, MGC71287, GPS1	G protein pathway suppressor 1	NM_212492, NM_004127, hCT2263480.0, hCT2263483.0	217782_s_at	NP_997657.1, NP_004118.3, EAW89741.1, EAW89742.1
GeneID:64118	DUS1L	17	80,015,751	80,023,680	7,929	-	5	4_A375_EGR1..1..4002, 4_A375_EGR1..1..4003, 4_A375_EGR1..1..4004, 4_A375_EGR1..1..4005, 4_A375_EGR1..1..4006	17392, 9792, 9136, 6976, 1072	downstream, downstream, downstream, in gene, in gene	0	0	1	8	8.4	17.4	5	4_A375_EGR1..1	21	Gene DUS1L	PP3111, DUS1, DUS1L	dihydrouridine synthase 1-like (S. cerevisiae)	NM_022156, hCT2289544.0, hCT2289546.0	217912_at	NP_071439.3, EAW89744.1, EAW89743.1
GeneID:2194	FASN	17	80,036,214	80,056,106	19,892	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2666, 4_A375_EGR1..1..4007, 4_A375_EGR1..1..4008, 4_A375_EGR1..1..4009, 4_A375_EGR1..1..4010, 4_A375_EGR1..1..4011, 4_A375_EGR1..1..4012	826, 17578, 10122, 4618, 1914, 1162, -6902	in gene, in gene, in gene, in gene, in gene, in gene, upstream	1	0	1	9.67	10.5	19.83	6	4_A375_EGR1..1	23	Gene FASN	MGC14367, FAS, FASN, MGC15706, OA-519, SDR27X1	fatty acid synthase	NM_004104, hCT31647.3	212218_s_at	NP_004095.4, EAW89745.1
GeneID:284001	CCDC57	17	80,059,346	80,170,689	111,343	-	9	1_A375_pNL7_minus_lncRNA_AR..1..2666, 2_A375_pNL97_plus_lncRNA_AR..1..3889, 2_A375_pNL97_plus_lncRNA_AR..1..3890, 4_A375_EGR1..1..4009, 4_A375_EGR1..1..4010, 4_A375_EGR1..1..4011, 4_A375_EGR1..1..4012, 4_A375_EGR1..1..4013, 4_A375_EGR1..1..4014	115409, 17, -4511, 119201, 116497, 115745, 107681, 98374, -3135	downstream, in gene, upstream, downstream, downstream, downstream, in gene, in gene, upstream	1	1	1	10.71	12.14	16.86	7	4_A375_EGR1..1	23	Gene CCDC57	FLJ23754, CCDC57, FLJ00130, MGC102869, FLJ43953	coiled-coil domain containing 57	NM_198082	1553248_at, 1554554_at, 214818_at, 234681_at	NP_932348.2
GeneID:9123	SLC16A3	17	80,186,293	80,197,369	11,076	+	2	4_A375_EGR1..1..4015, 4_A375_EGR1..1..4016	-3509, 7371	upstream, in gene	0	0	1	6	7.5	15.5	2	4_A375_EGR1..1	16	Gene SLC16A3	SLC16A3, MGC138474, MCT4, MGC138472, MCT3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	NM_004207, NM_001042423, NM_001042422, hCT1984206.1, hCT1984207.1, hCT2263487.0, hCT2263492.0, hCT2263493.0	202855_s_at, 202856_s_at, 213522_s_at, 217665_at, 217691_x_at	NP_004198.1, NP_001035888.1, NP_001035887.1, EAW89753.1, EAW89754.1, EAW89755.1, EAW89756.1, EAW89757.1
GeneID:1453	CSNK1D	17	80,202,238	80,231,573	29,335	-	1	4_A375_EGR1..1..4016	37909	downstream	0	0	1	8	8	15	1	4_A375_EGR1..1	15	Gene CSNK1D	CSNK1D, HCKID	casein kinase 1, delta	NM_001893, NM_139062, hCT1984208.1, hCT2289529.0, hCT2289531.0, hCT2289532.0, hCT9888.2	207945_s_at, 208774_at	NP_001884.2, NP_620693.1, EAW89758.1, EAW89759.1, EAW89761.1, EAW89762.1, EAW89760.1
GeneID:924	CD7	17	80,272,746	80,275,480	2,734	-	2	4_A375_EGR1..1..4018, 4_A375_EGR1..1..4019	6776, -72	downstream, upstream	0	0	1	7.5	8	15.5	2	4_A375_EGR1..1	16	Gene CD7	CD7, LEU-9, Tp40, TP41, GP40	CD7 molecule	NM_006137, hCT1984204.1, hCT1984205.1, hCT9721.3	214049_x_at, 214551_s_at	NP_006128.1, EAW89764.1, EAW89763.1, EAW89765.1
GeneID:6398	SECTM1	17	80,278,900	80,291,921	13,021	-	2	4_A375_EGR1..1..4018, 4_A375_EGR1..1..4019	23217, 16389	downstream, downstream	0	0	1	7.5	8	15.5	2	4_A375_EGR1..1	16	Gene SECTM1	K12, SECTM1	secreted and transmembrane 1	NM_003004, hCT1812302.1	213716_s_at	NP_002995.1, EAW89766.1
GeneID:2837	UTS2R	17	80,332,201	80,333,370	1,169	+	1	4_A375_EGR1..1..4020	10639	downstream	0	0	1	9	17	18	1	4_A375_EGR1..1	18	Gene UTS2R	UTS2R, UTR2, GPR14, UR-2-R, UTR	urotensin 2 receptor	NM_018949, hCT1641538.2	1553262_a_at	NP_061822.1, EAW89768.1
GeneID:79701	C17orf101	17	80,347,086	80,376,513	29,427	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2666, 2_A375_pNL97_plus_lncRNA_AR..1..3892, 4_A375_EGR1..1..4020, 4_A375_EGR1..1..4021, 4_A375_EGR1..1..4022	97, 97, 33473, 31681, 30465	in gene, in gene, downstream, downstream, downstream	1	1	1	12.25	17.25	17	4	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene C17orf101	C17orf101, FLJ22222	chromosome 17 open reading frame 101	NM_175902, NM_024648, NR_033265, hCT1950963.1, hCT2289516.0	219254_at, 53071_s_at, 64438_at	NP_787096.3, NP_078924.1, EAW89769.1, EAW89770.1



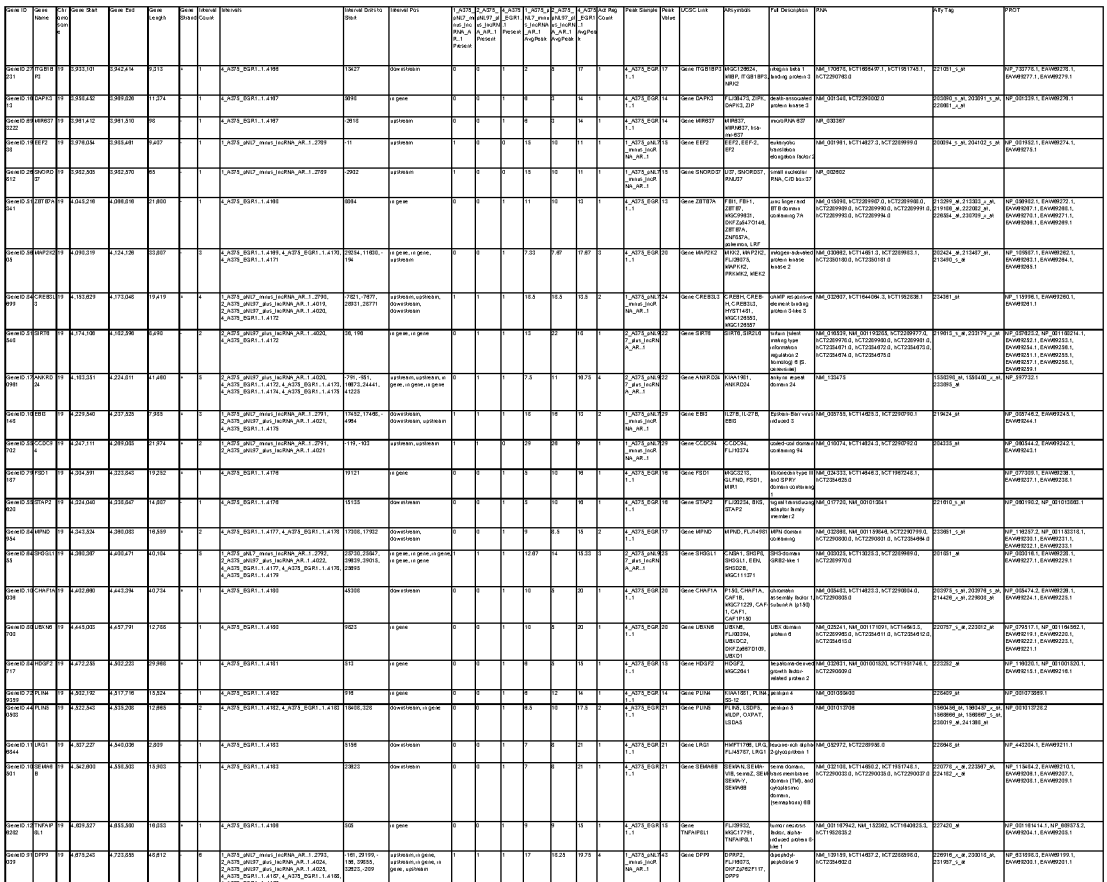
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:753	C18orf1	18	13,218,786	13,652,753	433,967	+	1	4_A375_EGR1..1..4040	233438	in gene	0	0	1	5	4	15	1	4_A375_EGR1..1	15	Gene C18orf1	C18orf1		NM_001003674, NM_001003675, NM_181482, NM_181483, NM_004338, NM_181481, hCT2278098.0, hCT2278097.0, hCT2358583.0, hCT28423.3	207996_s_at, 209573_s_at, 209574_s_at, 233138_at	NP_001003674.1, NP_001003675.1, NP_004329.1, NP_852146.1, NP_852148.1, NP_852147.1, EAX01511.1, EAX01512.1, EAX01513.1, EAX01514.1
GeneID:125228	C18orf19	18	13,663,346	13,726,591	63,245	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3920	63	in gene	0	1	0	15	28	9	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene C18orf19	C18orf19, HsT2329, MGC24180	chromosome 18 open reading frame 19	NM_152352, NM_001098801, hCT2348915.0, hCT29756.3	235022_at	NP_689565.2, NP_001092271.1, EAX01508.1, EAX01509.1
GeneID:8731	RNMT	18	13,726,704	13,764,554	37,850	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3920	-176	upstream	0	1	0	15	28	9	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene RNMT	KIAA0398, hCMT1c, MET, RG7MT1, RNMT, DKFZp686H1252	RNA (guanine-7-) methyltransferase	NM_003799, hCT2278103.0, hCT2278104.0, hCT29757.2	202683_s_at, 202684_s_at	NP_003790.1, EAX01506.1, EAX01505.1, EAX01507.1
GeneID:114799	ESCO1	18	19,109,262	19,180,693	71,431	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3921	117	in gene	0	1	0	13	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ESCO1	ESO1, CTF, EFO1, KIAA1911, ECO1, A930014I12Rik, ESCO1, MGC105022	establishment of cohesion 1 homolog 1 (S. cerevisiae)	NM_052911, hCT2351063.0, hCT2358558.0, hCT28835.4	226686_at, 235216_at, 235645_at	NP_443143.2, EAX01127.1, EAX01128.1, EAX01129.1
GeneID:6632	SNRPD1	18	19,192,260	19,210,208	17,948	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2703, 2_A375_pNL97_plus_lncRNA_AR..1..3922	-4, -36	upstream, upstream	1	1	0	75	75	10	1	2_A375_pNL97_plus_lncRNA_AR..1	75	Gene SNRPD1	SNRPD, SMD1, Sm-D1, SNRPD1, HsT2456	small nuclear ribonucleoprotein D1 polypeptide 16kDa	NM_006938, hCT2316776.0	202690_s_at, 202691_at	NP_008869.1, EAX01130.1
GeneID:100128893	LOC100128893	18	19,746,859	19,748,929	2,070	-	1	4_A375_EGR1..1..4041	-191	upstream	0	0	1	8	5	15	1	4_A375_EGR1..1	15	Gene LOC100128893		hypothetical LOC100128893	XR_111780, XR_109470, XR_115172		
GeneID:2627	GATA6	18	19,749,416	19,782,227	32,811	+	1	4_A375_EGR1..1..4041	-298	upstream	0	0	1	8	5	15	1	4_A375_EGR1..1	15	Gene GATA6	GATA6		NM_005257, hCT2315655.0	210002_at, 229282_at	NP_005248.2, EAX01137.1
GeneID:85019	C18orf45	18	20,875,977	21,017,925	141,948	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3926	85	in gene	0	1	0	8	16	5	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C18orf45	C18orf45, MGC11386, MGC138577, FLJ44259	chromosome 18 open reading frame 45	NM_032933, hCT2317958.0	224493_x_at, 244495_x_at	NP_116322.3, EAX01150.1
GeneID:29919	C18orf8	18	21,083,462	21,111,746	28,284	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2706, 2_A375_pNL97_plus_lncRNA_AR..1..3927	-134, -102	upstream, upstream	1	1	0	27	41	8	1	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene C18orf8	C18orf8, FLJ23453, HsT2591, MIC1	chromosome 18 open reading frame 8	NM_013326, hCT2317844.0, hCT2317845.0, hCT28990.3	221190_s_at, 232345_at, 232346_at	NP_037458.3, EAX01156.1, EAX01155.1, EAX01157.1
GeneID:3909	LAMA3	18	21,269,562	21,535,030	265,468	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2707, 2_A375_pNL97_plus_lncRNA_AR..1..3928	27078, 27110	in gene, in gene	1	1	0	47	36	0	1	1_A375_pNL7_minus_lncRNA_AR..1	47	Gene LAMA3	LAMA3, lama3a, LOCS, LAMNA, BM600, E170	laminin, alpha 3	NM_198129, NM_000227, NM_001127717, NM_001127718	1560078_at, 1563772_a_at, 1568879_a_at, 203726_s_at, 234608_at, 234719_at	NP_937762.1, NP_000218.2, NP_001121189.1, NP_001121190.1
GeneID:125488	TTC39C	18	21,572,737	21,715,574	142,837	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3929	83815	in gene	0	1	0	8	20	2	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TTC39C	FLJ33761, FLJ90394, C18orf17, TTC39C, HsT2697	tetratricopeptide repeat domain 39C	NM_153211, NM_001135993, NR_024232, hCT2317855.1, hCT2317857.1, hCT29561.4	1552307_a_at, 230747_s_at	NP_694943.2, NP_001129465.1, EAX01169.1, EAX01170.1, EAX01171.1
GeneID:114876	OSBPL1A	18	21,742,009	21,977,790	235,781	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3930	46	in gene	0	1	0	12	15	8	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene OSBPL1A	ORP1, ORP-1, OSBPL1A, FLJ10217, OSBPL1B	oxysterol binding protein-like 1A	NM_080597, NM_018030, hCT2315784.0, hCT2315785.0, hCT2315786.0, hCT2315787.0	1554846_at, 208158_s_at, 209485_s_at	NP_542164.2, NP_060500.3, EAX01180.1, EAX01181.1, EAX01182.1, EAX01183.1
GeneID:55364	IMPACT	18	22,006,609	22,033,495	26,886	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2708	-198	upstream	1	0	0	16	10	8	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene IMPACT	MGC33718, IMPACT	Impact homolog (mouse)	NM_018439, hCT1813052.1, hCT1951982.1, hCT2315723.0, hCT2358537.0, hCT29559.3	218637_at, 222698_s_at	NP_060909.1, EAX01188.1, EAX01184.1, EAX01185.1, EAX01186.1, EAX01187.1
GeneID:6760	SS18	18	23,596,217	23,670,611	74,394	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2709, 2_A375_pNL97_plus_lncRNA_AR..1..3932	-77, -381	upstream, upstream	1	1	0	30	25	12	1	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene SS18	MGC116875, SSXT, SYT, SS18	synovial sarcoma translocation, chromosome 18	NM_005637, NM_001007559, hCT1951955.1, hCT2315894.0, hCT2315896.0, hCT2315897.0, hCT28405.3	202816_s_at, 202817_s_at, 209954_x_at, 216684_s_at, 217051_s_at	NP_005628.2, NP_001007560.1, EAX01209.1, EAX01210.1, EAX01211.1, EAX01212.1, EAX01213.1
GeneID:6875	TAF4B	18	23,806,409	23,971,649	165,240	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3933	471	in gene	0	1	0	11	14	14	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene TAF4B	TAF4B, TAF2C2, TAFII105	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	NM_005640	216226_at, 235020_at	NP_005631.1
GeneID:1825	DSC3	18	28,570,052	28,622,781	52,729	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2711	31261	in gene	1	0	0	16	9	2	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene DSC3	DSC3, CDHF3, DSC4, DSC1, HT-CP, DSC2, DSC	desmocollin 3	NM_001941, NM_024423, hCT2319338.0, hCT2319339.0, hCT2319340.0	206032_at, 206033_s_at	NP_001932.2, NP_077741.2, EAX01247.1, EAX01248.1, EAX01249.1
GeneID:9331	B4GALT6	18	29,202,209	29,264,686	62,477	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3934	5246	in gene	0	1	0	9	15	2	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene B4GALT6	B4GALT6, beta4Gal-T6, B4Gal-T6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	NM_004775, hCT16800.3, hCT2316355.0, hCT2358562.0	206232_s_at, 206233_at, 235333_at	NP_004766.2, EAX01267.1, EAX01268.1, EAX01269.1
GeneID:100507120	LOC100507120	18	29,265,049	29,266,701	1,652	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3934	-5609	upstream	0	1	0	9	15	2	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LOC100507120		hypothetical protein LOC100507120	XM_003118759, XM_003120905		XP_003118807.1, XP_003120953.1
GeneID:22878	KIAA1012	18	29,409,136	29,523,091	113,955	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3935	19	in gene	0	1	0	6	17	7	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene KIAA1012	TRS85, HsT2706, KIAA1012, TRAPPC8, MGC71660, GSG1	KIAA1012	NM_014939, hCT1951986.1, hCT2316347.0, hCT2316348.0, hCT2316349.0, hCT2316350.0, hCT2358541.0	207305_s_at	NP_055754.2, EAX01273.1, EAX01271.1, EAX01272.1, EAX01274.1, EAX01276.1, EAX01275.1
GeneID:64762	FAM59A	18	29,847,463	30,050,447	202,984	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2712	97823	in gene	1	0	0	16	13	2	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene FAM59A	Gm944, GAREM, C18orf11, FAM59A	family with sequence similarity 59, member A	NM_022751, hCT16205.3, hCT2358552.0	219377_at	NP_073588.1, EAX01286.1, EAX01287.1
GeneID:10982	MAPRE2	18	32,556,892	32,722,378	165,486	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2713, 2_A375_pNL97_plus_lncRNA_AR..1..3936	2244, 64644	in gene, in gene	1	1	0	13	12	6.5	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene MAPRE2	RP1, EB2, EB1, MAPRE2	microtubule-associated protein, RP/EB family, member 2	NM_014268, NM_001143826, NM_001143827, NR_026570, hCT15400.3, hCT1951939.1, hCT2316441.0, hCT2316443.0, hCT2316444.0	202501_at, 211558_at, 213489_at	NP_055083.1, NP_001137298.1, NP_001137299.1, EAX01338.1, EAX01337.1, EAX01339.1, EAX01336.1, EAX01340.1
GeneID:100101467	ZNF397OS	18	32,831,023	32,870,196	39,173	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2714, 2_A375_pNL97_plus_lncRNA_AR..1..3937	-124, -140	upstream, upstream	1	1	0	34	34	9	1	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene ZNF397OS	ZSCAN30, ZNF917, ZNF397OS, FLJ46864, FLJ16245	zinc finger and SCAN domain containing 30	NM_001112734, NM_001166012		NP_001106205.1, NP_001159484.1
GeneID:7572	ZNF24	18	32,912,178	32,924,426	12,248	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2715	268	in gene	1	0	0	14	5	6	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene ZNF24	ZSCAN3, RSG-A, ZNF24, ZNF191, Zfp191, KOX17	zinc finger protein 24	NM_006965, hCT13807.2, hCT1951936.0, hCT2316553.0	1554045_at, 203247_s_at, 203248_at, 242210_at	NP_008896.2, EAX01350.1, EAX01348.1, EAX01349.1
GeneID:125476	INO80C	18	33,048,291	33,077,955	29,664	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2716, 2_A375_pNL97_plus_lncRNA_AR..1..3938	275, 259	in gene, in gene	1	1	0	15	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene INO80C	IES6, C18orf37, FLJ38183, hIes6, INO80C	INO80 complex subunit C	NM_001098817, NM_194281, hCT2316542.0, hCT2358556.0	1559716_at, 229582_at	NP_001092287.1, NP_919257.2, EAX01357.1, EAX01356.1
GeneID:55197	RPRD1A	18	33,569,791	33,647,373	77,582	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2718	173	in gene	1	0	0	17	13	10	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene RPRD1A	FLJ10656, HsT3101, P15RS, MGC19513, RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	NM_018170, hCT15983.3, hCT1951947.1, hCT1951948.1, hCT2316178.0, hCT2316179.0, hCT2358561.0	1555202_a_at, 218209_s_at, 222558_at, 222559_s_at, 225953_at, 228566_at	NP_060640.2, EAX01368.1, EAX01365.1, EAX01366.1, EAX01369.1, EAX01370.1, EAX01367.1
GeneID:25800	SLC39A6	18	33,688,494	33,709,357	20,863	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2719, 2_A375_pNL97_plus_lncRNA_AR..1..3939	-403, -403	upstream, upstream	1	1	0	20	29	12	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene SLC39A6	LIV-1, SLC39A6	solute carrier family 39 (zinc transporter), member 6	NM_012319, NM_001099406, hCT14916.3, hCT2358553.0	1555460_a_at, 1556551_s_at, 202088_at, 202089_s_at	NP_036451.3, NP_001092876.1, EAX01371.1, EAX01372.1
GeneID:55250	ELP2	18	33,709,887	33,754,607	44,720	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2719, 2_A375_pNL97_plus_lncRNA_AR..1..3939, 2_A375_pNL97_plus_lncRNA_AR..1..3940	-127, -127, 47009	upstream, upstream, downstream	1	1	0	13.5	22	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene ELP2	SHINC-2, FLJ10879, ELP2, StIP, STATIP1	elongation protein 2 homolog (S. cerevisiae)	NM_018255, hCT14917.3, hCT2316062.0, hCT2316063.0, hCT2358554.0	231713_s_at, 235623_at	NP_060725.1, EAX01373.1, EAX01374.1, EAX01375.1, EAX01376.1
GeneID:56853	BRUNOL4	18	34,823,003	35,146,000	322,997	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2720, 1_A375_pNL7_minus_lncRNA_AR..1..2721, 2_A375_pNL97_plus_lncRNA_AR..1..3941, 2_A375_pNL97_plus_lncRNA_AR..1..3942, 2_A375_pNL97_plus_lncRNA_AR..1..3943	295760, 82352, 295792, 82256, 1088	in gene, in gene, in gene, in gene, in gene	1	1	0	27.67	36.67	7	3	2_A375_pNL97_plus_lncRNA_AR..1	74	Gene BRUNOL4	CELF4, BRUNOL4, BRUNOL-4	CUGBP, Elav-like family member 4	NM_020180, NM_001025087, NM_001025088, NM_001025089, hCT13544.3, hCT2316027.0, hCT2316030.0, hCT2316031.0	223653_x_at, 223654_s_at, 231220_at, 232719_at, 238966_at	NP_064565.1, NP_001020258.1, NP_001020259.1, NP_001020260.1, EAX01395.1, EAX01397.1, EAX01394.1, EAX01396.1
GeneID:57724	KIAA1632	18	43,427,574	43,547,305	119,731	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2727, 4_A375_EGR1..1..4044	41, 249	in gene, in gene	1	0	1	22	16	14	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene KIAA1632	hEPG5, DKFZp667P2311, KIAA1632, HEEW1, EPG5	KIAA1632	NM_020964, hCT2348838.0	1563471_at, 227636_at, 228453_at, 232030_at, 232031_s_at, 234046_s_at, 236108_at	NP_066015.2, EAX01465.1
GeneID:498	ATP5A1	18	43,664,110	43,684,199	20,089	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3946	-121	upstream	0	1	0	6	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ATP5A1	ATP5A1, MOM2, ATPM, ATP5A, ATP5AL2, OMR, hATP1, ORM	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	NM_004046, NM_001001937	1569891_at, 213738_s_at	NP_004037.1, NP_001001937.1
GeneID:115106	HAUS1	18	43,684,298	43,708,299	24,001	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3946	22	in gene	0	1	0	6	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene HAUS1	HAUS1, FLJ21094, HEIC, HEI-C, FLJ40084, CCDC5, HsT1461	HAUS augmin-like complex, subunit 1	NR_026976, NM_138443, hCT1816418.1	225297_at	NP_612452.1, EAX01469.1
GeneID:147339	C18orf25	18	43,753,988	43,846,955	92,967	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2728, 2_A375_pNL97_plus_lncRNA_AR..1..3949	-66, -66	upstream, upstream	1	1	0	64	63	10	1	1_A375_pNL7_minus_lncRNA_AR..1	64	Gene C18orf25	C18orf25, MGC87799, ARKL1, MGC12909	chromosome 18 open reading frame 25	NM_001008239, NM_145055, hCT2316570.0, hCT2316572.0	1553688_at, 217508_s_at, 217539_at, 226406_at	NP_001008240.1, NP_659492.1, EAX01472.1, EAX01473.1
GeneID:125336	LOXHD1	18	44,056,935	44,236,996	180,061	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2729, 1_A375_pNL7_minus_lncRNA_AR..1..2730, 1_A375_pNL7_minus_lncRNA_AR..1..2731, 2_A375_pNL97_plus_lncRNA_AR..1..3950, 2_A375_pNL97_plus_lncRNA_AR..1..3951, 2_A375_pNL97_plus_lncRNA_AR..1..3952	159748, 120324, 24068, 159716, 154436, 24066	in gene, in gene, in gene, in gene, in gene, in gene	1	1	0	17.75	17.25	5	4	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene LOXHD1	FLJ32670, LOXHD1, LH2D1, DFNB77	lipoxygenase homology domains 1	NM_144612, NM_001173129, NM_001145472, NM_001145473, hCT2341094.1, hCT2341095.1, hCT2348909.0, hCT2358555.0	241117_at	NP_653213.6, NP_001166600.1, NP_001138944.1, NP_001138945.1, EAX01477.1, EAX01480.1, EAX01478.1, EAX01479.1
GeneID:29906	ST8SIA5	18	44,259,081	44,337,039	77,958	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3953	-529	upstream	0	1	0	11	16	4	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ST8SIA5	SIAT8E, MGC119671, ST8SiaV, ST8SIA5, MGC119670	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	NM_013305, hCT1950755.1, hCT2316288.0	206258_at	NP_037437.2, EAX01482.1, EAX01483.1
GeneID:83473	KATNAL2	18	44,526,787	44,628,614	101,827	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3954	-7043	upstream	0	1	0	12	19	2	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene KATNAL2	KATNAL2, DKFZp667C165, MGC33211	katanin p60 subunit A-like 2	NM_031303, hCT14934.4, hCT2348442.0, hCT2348443.0, hCT2353878.0	1554234_at, 233844_at, 233849_at	NP_112593.2, EAW62903.1, EAW62901.1, EAW62902.1, EAW62904.1
GeneID:9811	KIAA0427	18	46,065,427	46,389,588	324,161	+	4	2_A375_pNL97_plus_lncRNA_AR..1..3956, 4_A375_EGR1..1..4045, 4_A375_EGR1..1..4046, 4_A375_EGR1..1..4047	2157, 797, 100941, 191213	in gene, in gene, in gene, in gene	0	1	1	7.25	7.5	14.75	4	4_A375_EGR1..1	20	Gene KIAA0427	Gm672, CTIF, KIAA0427	KIAA0427	NM_014772, NM_001142397, hCT15756.3, hCT2250284.0, hCT2250286.0, hCT2353882.0	204302_s_at, 204303_s_at	NP_055587.1, NP_001135869.1, EAW62925.1, EAW62926.1, EAW62927.1, EAW62928.1
GeneID:9388	LIPG	18	47,088,427	47,119,278	30,851	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3957	24005	in gene	0	1	0	8	23	4	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LIPG	EL, LIPG, PRO719, EDL	lipase, endothelial	NM_006033, hCT15805.3, hCT2250318.0, hCT2250319.0	219181_at	NP_006024.1, EAW62949.1, EAW62947.1, EAW62948.1
GeneID:10449	ACAA2	18	47,309,874	47,340,251	30,377	-	1	4_A375_EGR1..1..4048	315	in gene	0	0	1	9	12	18	1	4_A375_EGR1..1	18	Gene ACAA2	FLJ35992, ACAA2, DSAEC, FLJ95265	acetyl-CoA acyltransferase 2	NM_006111, hCT2250981.0, hCT2250982.0, hCT2250983.0, hCT2250984.0, hCT2250985.0, hCT2250986.0, hCT2250987.0	202002_at, 202003_s_at	NP_006102.2, EAW62954.1, EAW62950.1, EAW62951.1, EAW62955.1, EAW62956.1, EAW62952.1, EAW62953.1
GeneID:677769	SCARNA17	18	47,340,393	47,340,813	420	+	1	4_A375_EGR1..1..4048	-457	upstream	0	0	1	9	12	18	1	4_A375_EGR1..1	18	Gene SCARNA17	U91, SCARNA17	small Cajal body-specific RNA 17	NR_003003	240830_at	
GeneID:4645	MYO5B	18	47,349,156	47,721,451	372,295	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2732, 2_A375_pNL97_plus_lncRNA_AR..1..3958, 4_A375_EGR1..1..4048	298491, 298459, 381515	in gene, in gene, downstream	1	1	1	14.5	20	10	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene MYO5B	KIAA1119, MYO5B	myosin VB	NM_001080467	1570141_at, 225299_at, 225301_s_at	NP_001073936.1
GeneID:220136	CCDC11	18	47,753,583	47,792,885	39,302	-	1	4_A375_EGR1..1..4049	-2090	upstream	0	0	1	4	2	15	1	4_A375_EGR1..1	15	Gene CCDC11	FLJ32743, CCDC11	coiled-coil domain containing 11	NM_145020, hCT1954675.1, hCT2250978.0	1552325_at, 1552326_a_at	NP_659457.2, EAW62960.1, EAW62961.1
GeneID:4152	MBD1	18	47,795,216	47,808,144	12,928	-	1	4_A375_EGR1..1..4049	13169	downstream	0	0	1	4	2	15	1	4_A375_EGR1..1	15	Gene MBD1	MBD1, RFT, PCM1, CXXC3	methyl-CpG binding domain protein 1	NM_015844, NM_015846, NM_015847, NM_002384, NM_015845, hCT14798.3, hCT1814510.2, hCT1814511.2, hCT1814512.2, hCT1814513.2, hCT2353880.0	1555611_s_at, 203353_s_at, 208595_s_at, 226682_at, 241813_at	NP_056669.2, NP_056671.2, NP_056670.2, NP_056723.2, NP_002375.1, EAW62966.1, EAW62962.1, EAW62963.1, EAW62964.1, EAW62965.1, EAW62967.1
GeneID:55520	ELAC1	18	48,494,387	48,514,490	20,103	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2733	77	in gene	1	0	0	19	12	2	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene ELAC1	D29, FLJ59261, ELAC1	elaC homolog 1 (E. coli)	NM_018696, hCT14601.1, hCT2353881.0	219325_s_at, 222869_s_at	NP_061166.1, EAW62984.1, EAW62983.1
GeneID:51320	MEX3C	18	48,700,920	48,724,051	23,131	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3959	-557	upstream	0	1	0	12	16	9	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene MEX3C	MEX-3C, FLJ38871, BM-013, MEX3C, RKHD2, RNF194	mex-3 homolog C (C. elegans)	NM_016626, hCT1640425.3	1556873_at, 1556874_a_at, 218247_s_at, 222567_s_at, 227275_at	NP_057710.3, EAW62989.1
GeneID:11201	POLI	18	51,795,849	51,824,604	28,755	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3962	71	in gene	0	1	0	11	14	10	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene POLI	RAD30B, POLI, RAD3OB	polymerase (DNA directed) iota	NM_007195, hCT13763.2, hCT2250226.0	219317_at, 238992_at	NP_009126.2, EAW63000.1, EAW63001.1
GeneID:147323	STARD6	18	51,851,062	51,880,943	29,881	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3963	-3217	upstream	0	1	0	10	15	11	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene STARD6	STARD6		NM_139171, hCT2250244.1, hCT2250245.1, hCT2340510.0, hCT2340511.0	1553084_at	NP_631910.1, EAW63002.1, EAW63003.1, EAW63004.1, EAW63005.1
GeneID:162681	C18orf54	18	51,885,171	51,908,404	23,233	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3963	-1011	upstream	0	1	0	10	15	11	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene C18orf54	MGC33382, C18orf54, LAS2	chromosome 18 open reading frame 54	NM_173529, hCT14350.3	1553651_at, 1553652_a_at, 229442_at, 241733_at, 244324_at	NP_775800.3, EAW63006.1

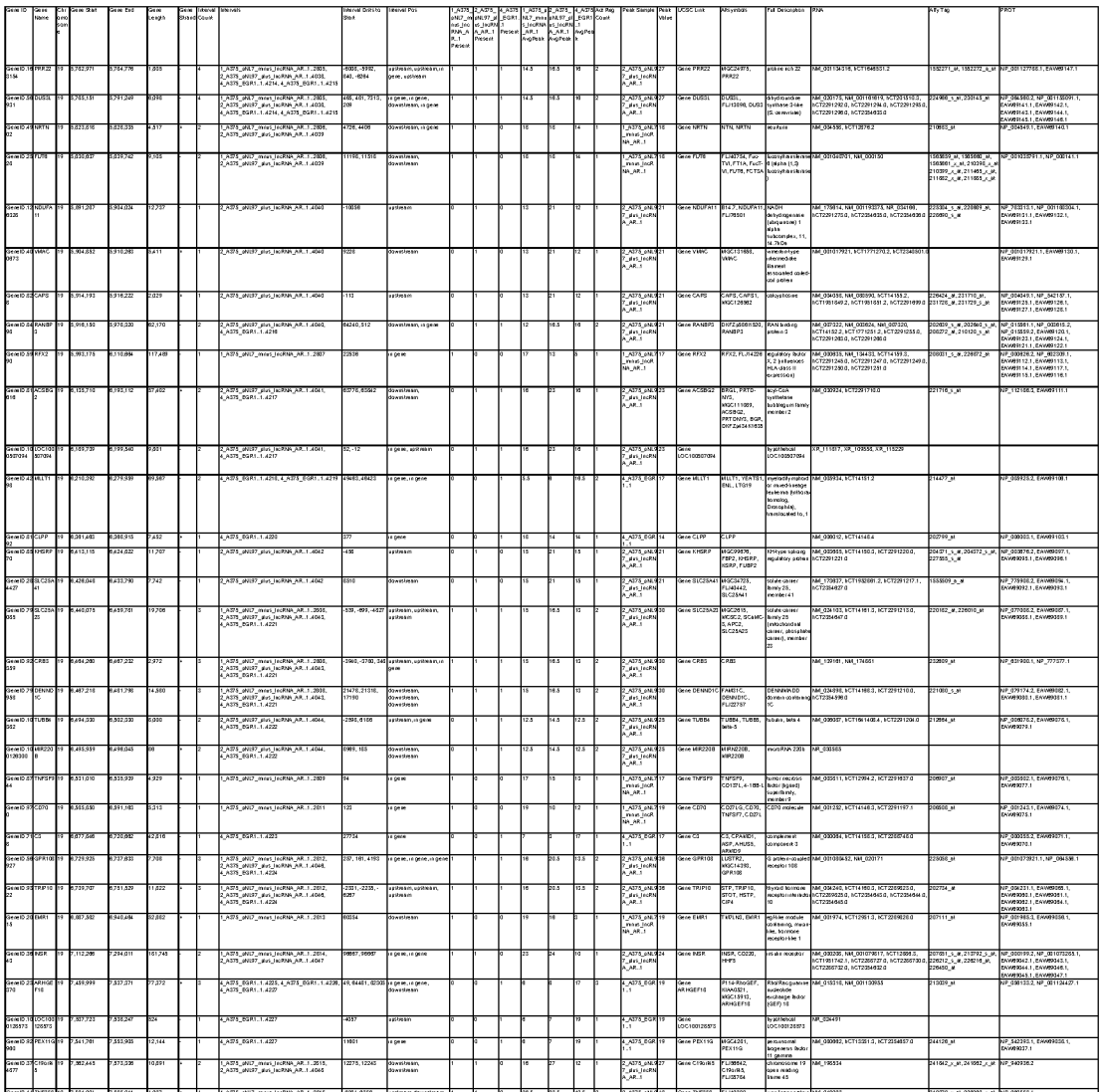


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.5725	PTBP1	19	797,392	812,327	14,935	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2755, 2_A375_pNL97_plus_lncRNA_AR..1..3987, 4_A375_EGR1..1..4093, 4_A375_EGR1..1..4094	-432, -448, 1376, 3920	upstream, upstream, in gene, in gene	1	1	1	13	13	18	3	4_A375_EGR1..1	24	Gene PTBP1	HNRNP-I, PTB4, PTB3, pPTB, PTB, HNRPI, PTB-1, MGC10830, HNRNPI, PTB-T, MGC8461, PTB2, PTBP1	polypyrimidine tract binding protein 1	NM_002819, NM_031990, NM_031991, NM_175847, hCT11639.2, hCT1955356.1, hCT1955357.1, hCT2251619.0, hCT2251620.0, hCT2251622.0, hCT2353656.0	202189_x_at, 211270_x_at, 211271_x_at, 212015_x_at, 212016_s_at, 216306_x_at, 226491_x_at, 231158_x_at, 236819_at	NP_002810.1, NP_114367.1, NP_114368.1, NP_787041.1, EAW61154.1, EAW61155.1, EAW61152.1, EAW61153.1, EAW61156.1, EAW61157.1, EAW61158.1
GeneID.79948	LPPR3	19	812,518	821,952	9,434	-	1	4_A375_EGR1..1..4095	-9868	upstream	0	0	1	8	9	19	1	4_A375_EGR1..1	19	Gene LPPR3	PRG-2, LPR3, PRG2	lipid phosphate phosphatase-related protein type 3	NM_024888, hCT11644.3, hCT1961686.1, hCT2251030.0	220798_x_at	NP_079164.1, EAW61149.1, EAW61150.1, EAW61151.1
GeneID.566	AZU1	19	827,831	832,017	4,186	+	1	4_A375_EGR1..1..4095	4009	in gene	0	0	1	8	9	19	1	4_A375_EGR1..1	19	Gene AZU1	AZAMP, AZU, AZU1, NAZC, HUMAZUR, CAP37, HBP	azurocidin 1	NM_001700, hCT201410.3	214575_s_at	NP_001691.1, EAW69592.1
GeneID.5657	PRTN3	19	840,985	848,175	7,190	+	2	4_A375_EGR1..1..4095, 4_A375_EGR1..1..4096	-9145, 5495	upstream, in gene	0	0	1	8.5	8.5	18.5	2	4_A375_EGR1..1	19	Gene PRTN3	P29, ACPA, C-ANCA, PRTN3, NP4, MBT, AGP7, MBN, PR3, PR-3, CANCA	proteinase 3	NM_002777, hCT1952851.0, hCT1952852.0	207341_at	NP_002768.3, EAW69591.1, EAW69590.1
GeneID.1991	ELANE	19	852,291	856,246	3,955	+	1	4_A375_EGR1..1..4096	-5811	upstream	0	0	1	9	8	18	1	4_A375_EGR1..1	18	Gene ELANE	ELANE, HNE, SCN1, GE, PMN-E, NE, ELA2, HLE	elastase, neutrophil expressed	NM_001972, hCT12871.2	206871_at	NP_001963.1, EAW69589.1
GeneID.1675	CFD	19	859,865	863,824	3,959	+	1	4_A375_EGR1..1..4097	14127	downstream	0	0	1	7	8	19	1	4_A375_EGR1..1	19	Gene CFD	ADIPSIN, DF, CFD, PFD, ADN	complement factor D (adipsin)	NM_001928, hCT12872.2	205382_s_at	NP_001919.2, EAW69588.1
GeneID.10025	MED16	19	867,962	893,218	25,256	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2756, 2_A375_pNL97_plus_lncRNA_AR..1..3988, 4_A375_EGR1..1..4097, 4_A375_EGR1..1..4098, 4_A375_EGR1..1..4099, 4_A375_EGR1..1..4100, 4_A375_EGR1..1..4101	-126, -142, 19426, 16130, 13058, 11202, -126	upstream, upstream, in gene, in gene, in gene, in gene, upstream	1	1	1	9.2	8	18	5	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene MED16	TRAP95, DRIP92, THRAP5, MED16	mediator complex subunit 16	NM_005481, hCT2286791.0, hCT2286792.0	221418_s_at, 221544_s_at, 221545_x_at, 221936_x_at, 43544_at	NP_005472.2, EAW69586.1, EAW69587.1
GeneID.91300	C19orf22	19	896,503	913,225	16,722	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2756, 2_A375_pNL97_plus_lncRNA_AR..1..3988, 4_A375_EGR1..1..4101	19881, 19865, 19881	downstream, downstream, downstream	1	1	1	24	18	17	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene C19orf22	MGC16353, C19orf22	chromosome 19 open reading frame 22	NM_138774, hCT2286789.0	221784_at, 55705_at	NP_620129.2, EAW69584.1
GeneID.84634	KISS1R	19	917,342	921,015	3,673	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2757, 2_A375_pNL97_plus_lncRNA_AR..1..3989	8274, 8226	downstream, downstream	1	1	0	20	40	13	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene KISS1R	HOT7T175, KISS1R, GPR54, AXOR12	KISS1 receptor	NM_032551, hCT12893.3	242517_at	NP_115940.2, EAW69583.1
GeneID.1820	ARID3A	19	926,037	972,816	46,779	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2757, 2_A375_pNL97_plus_lncRNA_AR..1..3989, 4_A375_EGR1..1..4102, 4_A375_EGR1..1..4103	-421, -469, 29099, 29419	upstream, upstream, in gene, in gene	1	1	1	8.67	16	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene ARID3A	E2FBP1, DRIL3, BRIGHT, DRIL1, ARID3A	AT rich interactive domain 3A (BRIGHT-like)	NM_005224, hCT12870.2	205865_at	NP_005215.1, EAW69580.1
GeneID.57418	WDR18	19	984,328	994,569	10,241	+	2	4_A375_EGR1..1..4104, 4_A375_EGR1..1..4105	9832, 12280	in gene, downstream	0	0	1	5.5	6	15	2	4_A375_EGR1..1	16	Gene WDR18	MGC2436, WDR18, R32184_1	WD repeat domain 18	NM_024100, hCT12868.3	209461_x_at	NP_077005.2, EAW69578.1
GeneID.116444	GRIN3B	19	1,000,437	1,009,723	9,286	+	2	4_A375_EGR1..1..4104, 4_A375_EGR1..1..4105	-8277, -3829	upstream, upstream	0	0	1	5.5	6	15	2	4_A375_EGR1..1	16	Gene GRIN3B	GRIN3B, NR3B	glutamate receptor, ionotropic, N-methyl-D-aspartate 3B	NM_138690, hCT2312904.0	233892_at	NP_619635.1, EAW69576.1
GeneID.91304	C19orf6	19	1,009,650	1,021,141	11,491	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2758, 2_A375_pNL97_plus_lncRNA_AR..1..3990	-443, -107	upstream, upstream	1	1	0	21	27	11	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene C19orf6	C19orf6, R32184_3, ASBABP1, MGC4022, MEMBRALIN, MBRL	chromosome 19 open reading frame 6	NM_033420, NM_001033026, hCT12866.3, hCT1952854.1, hCT1952855.1, hCT2286782.0, hCT2354624.0	212574_x_at, 212575_at, 213985_s_at, 213986_s_at, 225247_at, 230089_s_at	NP_219488.1, NP_001028198.1, EAW69571.1, EAW69572.1, EAW69574.1, EAW69575.1, EAW69573.1
GeneID.1265	CNN2	19	1,026,298	1,039,064	12,766	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2758, 1_A375_pNL7_minus_lncRNA_AR..1..2759, 2_A375_pNL97_plus_lncRNA_AR..1..3990, 2_A375_pNL97_plus_lncRNA_AR..1..3991	-4714, 13670, -5050, 13638	upstream, downstream, upstream, downstream	1	1	0	21	27	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene CNN2	CNN2		NM_004368, NM_201277, hCT12866.3, hCT1952849.1, hCT2312906.0, hCT2312907.0, hCT2312908.0, hCT2312910.0	201605_x_at	NP_004359.1, NP_958434.1, EAW69565.1, EAW69566.1, EAW69569.1, EAW69570.1, EAW69567.1, EAW69568.1
GeneID.10347	ABCA7	19	1,040,102	1,065,571	25,469	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2759, 2_A375_pNL97_plus_lncRNA_AR..1..3991	-134, -166	upstream, upstream	1	1	0	21	27	10	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene ABCA7	ABCX, FLJ40025, ABCA7, ABCA-SSN	ATP-binding cassette, sub-family A (ABC1), member 7	NM_019112, hCT1952853.1, hCT2312911.0, hCT2312912.0, hCT2312913.0, hCT2312914.0, hCT2312915.0, hCT2312916.0, hCT2312917.0, hCT2312919.0	219577_s_at	NP_061985.2, EAW69556.1, EAW69557.1, EAW69558.1, EAW69561.1, EAW69564.1, EAW69559.1, EAW69560.1, EAW69562.1, EAW69563.1
GeneID.23526	HMHA1	19	1,067,174	1,086,627	19,453	+	1	2_A375_pNL97_plus_lncRNA_AR..1..3992	28250	downstream	0	1	0	9	16	13	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene HMHA1	HA-1, KIAA0223, HMHA1, HLA-HA1	histocompatibility (minor) HA-1	NM_012292, hCT12865.3, hCT1967234.1, hCT2312922.0, hCT2312924.0, hCT2354619.0	212873_at	NP_036424.2, EAW69551.1, EAW69552.1, EAW69553.1, EAW69554.1, EAW69555.1
GeneID.5434	POLR2E	19	1,086,578	1,095,391	8,813	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3992	-33	upstream	0	1	0	9	16	13	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene POLR2E	hsRPB5, RPB5, hRPB25, XAP4, RPABC1, POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	NM_002695, hCT12863.3, hCT1952846.1, hCT1962224.1, hCT2286780.0	213887_s_at, 217854_s_at	NP_002686.2, EAW69549.1, EAW69547.1, EAW69548.1, EAW69550.1
GeneID.2879	GPX4	19	1,103,936	1,106,787	2,851	+	3	2_A375_pNL97_plus_lncRNA_AR..1..3992, 4_A375_EGR1..1..4106, 4_A375_EGR1..1..4107	-8512, 5936, 9536	upstream, downstream, downstream	0	1	1	5.67	9	13.67	3	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene GPX4	MCSP, PHGPx, GPX4, snGPx, snPHGPx	glutathione peroxidase 4 (phospholipid hydroperoxidase)	NM_002085, NM_001039847, NM_001039848, hCT12867.3, hCT1810469.2, hCT1952848.2, hCT2312926.0	201106_at	NP_002076.2, NP_001034936.1, NP_001034937.1, EAW69544.1, EAW69545.1, EAW69546.1, EAW69543.1
GeneID.22904	SBNO2	19	1,107,633	1,174,282	66,649	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2760, 4_A375_EGR1..1..4106, 4_A375_EGR1..1..4107, 4_A375_EGR1..1..4108, 4_A375_EGR1..1..4109	3530, 64410, 60810, 42762, 13766	in gene, in gene, in gene, in gene, in gene	1	0	1	6.6	6.6	12.6	5	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene SBNO2	FLJ00173, SBNO2, STNO, SNO, KIAA0963	strawberry notch homolog 2 (Drosophila)	NM_014963, NM_001100122, hCT12863.2, hCT2286778.0	204166_at, 215760_s_at	NP_055778.2, NP_001093592.1, EAW69541.1, EAW69542.1
GeneID.255057	C19orf26	19	1,229,947	1,237,990	8,043	-	1	4_A375_EGR1..1..4110	-1016	upstream	0	0	1	4	6	15	1	4_A375_EGR1..1	15	Gene C19orf26	C19orf26, MGC40084, DOS	chromosome 19 open reading frame 26	NM_152769, hCT12890.2, hCT2286770.1, hCT2354631.0	1552354_at, 1552355_s_at, 215325_x_at	NP_689982.2, EAW69536.1, EAW69535.1, EAW69537.1
GeneID.513	ATP5D	19	1,241,749	1,244,824	3,075	+	1	4_A375_EGR1..1..4110	-2741	upstream	0	0	1	4	6	15	1	4_A375_EGR1..1	15	Gene ATP5D	ATP5D		NM_001687, NM_001001975, hCT12862.3, hCT1952312.1, hCT2312938.0, hCT2354604.0	203926_x_at, 213041_s_at	NP_001678.1, NP_001001975.1, EAW69531.1, EAW69532.1, EAW69533.1, EAW69534.1
GeneID.90007	MIDN	19	1,248,552	1,259,142	10,590	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2761, 2_A375_pNL97_plus_lncRNA_AR..1..3993, 4_A375_EGR1..1..4110, 4_A375_EGR1..1..4111	18456, 17624, -9544, 7256	downstream, downstream, upstream, in gene	1	1	1	10	12.25	13	4	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MIDN	DKFZp547M072, MIDN	midnolin	NM_177401, hCT12860.4, hCT2348703.0, hCT2348704.0	225954_s_at, 227398_s_at, 231072_at	NP_796375.3, EAW69529.1, EAW69527.1, EAW69528.1
GeneID.146046	C19orf23	19	1,267,470	1,270,259	2,789	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2761, 2_A375_pNL97_plus_lncRNA_AR..1..3993, 4_A375_EGR1..1..4112	3251, 4083, -1933	downstream, downstream, upstream	1	1	1	11.67	13	12.67	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C19orf23	MGC39336, C19orf23	chromosome 19 open reading frame 23	NR_027271, hCT2286767.1	1552868_at, 239126_at	EAW69526.1
GeneID.1153	CIRBP	19	1,269,267	1,274,809	5,542	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2761, 2_A375_pNL97_plus_lncRNA_AR..1..3993, 4_A375_EGR1..1..4112	-2259, -3091, 2925	upstream, upstream, in gene	1	1	1	11.67	13	12.67	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CIRBP	CIRBP, CIRP	cold inducible RNA binding protein	NM_001280, NR_023312, NR_023313, hCT12866.2, hCT1952314.1, hCT1952315.1, hCT1952316.1, hCT1952317.1, hCT2312944.0	200810_s_at, 200811_at, 225191_at, 228519_x_at, 230142_s_at	NP_001271.1, EAW69520.1, EAW69521.1, EAW69523.1, EAW69524.1, EAW69525.1, EAW69522.1
GeneID.55009	C19orf24	19	1,275,520	1,279,243	3,723	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2761, 2_A375_pNL97_plus_lncRNA_AR..1..3993, 4_A375_EGR1..1..4112	-6512, -9344, -3326	upstream, upstream, upstream	1	1	1	11.67	13	12.67	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C19orf24	C19orf24, FLJ20640	chromosome 19 open reading frame 24	NM_017914, hCT12865.2, hCT1952313.1	221587_s_at	NP_060384.3, EAW69518.1, EAW69519.1
GeneID.1943	EFNA2	19	1,286,168	1,299,944	13,776	+	1	4_A375_EGR1..1..4113	7080	in gene	0	0	1	4	6	13	1	4_A375_EGR1..1	13	Gene EFNA2	LERK6, HEK7-L, EFNA2, EPLG6, ELF-1	ephrin-A2	NM_001405, hCT2312957.0	1553573_s_at, 206256_at	NP_001396.2, EAW69517.1
GeneID.100506781	LOC100506781	19	1,300,266	1,325,066	24,800	+	1	4_A375_EGR1..1..4113	-7020	upstream	0	0	1	4	6	13	1	4_A375_EGR1..1	13	Gene LOC100506781		hypothetical LOC100506781	XR_111609, XR_109551, XR_115223		
GeneID.84939	MUM1	19	1,354,976	1,378,430	23,454	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2762, 2_A375_pNL97_plus_lncRNA_AR..1..3994, 4_A375_EGR1..1..4114	28752, 28632, 28416	downstream, downstream, downstream	1	1	1	16	22	30	1	4_A375_EGR1..1	30	Gene MUM1	HSPC211, EXPAND1, MUM1, MGC131891, FLJ14868, MGC163315, FLJ22263, MUM-1	melanoma associated antigen (mutated) 1	NM_032853, NR_024247, hCT2312952.1, hCT2312953.1, hCT2312954.1, hCT2312955.1, hCT2312956.1, hCT2312958.1, hCT2312959.1	221290_s_at, 223347_at, 223348_x_at, 229033_s_at, 230461_s_at	NP_116242.2, EAW69509.1, EAW69510.1, EAW69513.1, EAW69514.1, EAW69515.1, EAW69511.1, EAW69512.1
GeneID.374291	NDUFS7	19	1,383,863	1,395,568	11,705	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2762, 2_A375_pNL97_plus_lncRNA_AR..1..3994, 4_A375_EGR1..1..4114, 4_A375_EGR1..1..4115	-155, -75, -491, 4821	upstream, upstream, upstream, in gene	1	1	1	10.5	13	24	2	4_A375_EGR1..1	30	Gene NDUFS7	CI-20, FLJ46880, NDUFS7, MGC120002, MY017, CI-20KD, FLJ45860, PSST	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	NM_024407, hCT12694.3, hCT1952320.2	211752_s_at, 242168_at	NP_077718.3, EAW69507.1, EAW69508.1
GeneID.2593	GAMT	19	1,397,088	1,401,552	4,464	-	2	4_A375_EGR1..1..4115, 4_A375_EGR1..1..4116	12848, -7739	downstream, upstream	0	0	1	5.5	7	16.5	2	4_A375_EGR1..1	18	Gene GAMT	GAMT, TPS312, PIG2	guanidinoacetate N-methyltransferase	NM_000156, NM_138924, hCT11054.3, hCT1952309.3	1552473_at, 1552474_a_at, 205354_at	NP_000147.1, NP_620279.1, EAW69505.1, EAW69506.1
GeneID.26528	DAZAP1	19	1,407,564	1,435,663	28,099	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2763, 2_A375_pNL97_plus_lncRNA_AR..1..3995, 4_A375_EGR1..1..4116	30686, 30720, 1707	downstream, downstream, in gene	1	1	1	34.5	42.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	75	Gene DAZAP1	MGC19907, DAZAP1	DAZ associated protein 1	NM_018959, NM_170711, hCT12674.3, hCT2312966.0, hCT2312970.0, hCT2354665.0	218443_s_at, 226820_x_at, 229813_x_at	NP_061832.2, NP_733829.1, EAW69501.1, EAW69502.1, EAW69503.1, EAW69504.1
GeneID.6209	RPS15	19	1,438,363	1,440,492	2,129	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2763, 2_A375_pNL97_plus_lncRNA_AR..1..3995	-91, -59	upstream, upstream	1	1	0	63	75	11	1	2_A375_pNL97_plus_lncRNA_AR..1	75	Gene RPS15	RPS15, S15, MGC111130, RIG	ribosomal protein S15	NM_001018, hCT12681.3, hCT1952310.1	1563014_at, 200819_s_at	NP_001009.1, EAW69500.1, EAW69499.1
GeneID.100506822	LOC100506822	19	1,440,844	1,441,311	467	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2763, 2_A375_pNL97_plus_lncRNA_AR..1..3995	-2572, -2540	upstream, upstream	1	1	0	63	75	11	1	2_A375_pNL97_plus_lncRNA_AR..1	75	Gene LOC100506822		hypothetical protein LOC100506822	XM_003118782		XP_003118830.1
GeneID.10297	APC2	19	1,450,148	1,473,243	23,095	+	2	4_A375_EGR1..1..4117, 4_A375_EGR1..1..4118	2360, 22300	in gene, in gene	0	0	1	6	5	17	2	4_A375_EGR1..1	19	Gene APC2	APCL, APC2	adenomatosis polyposis coli 2	NM_005883, hCT2312973.0, hCT2312974.0, hCT2312975.0	205320_at, 217174_s_at	NP_005874.1, EAW69496.1, EAW69497.1, EAW69498.1
GeneID.100506848	LOC100506848	19	1,457,664	1,462,764	5,100	-	2	4_A375_EGR1..1..4117, 4_A375_EGR1..1..4118	10236, -9664	downstream, upstream	0	0	1	6	5	17	2	4_A375_EGR1..1	19	Gene LOC100506848		hypothetical LOC100506848	XR_109552, XR_115224		
GeneID.148223	C19orf25	19	1,473,200	1,479,226	6,026	-	1	4_A375_EGR1..1..4118	6780	downstream	0	0	1	4	5	19	1	4_A375_EGR1..1	19	Gene C19orf25	C19orf25, FLJ38666	chromosome 19 open reading frame 25	NM_152482, hCT2286797.1	226378_s_at, 226379_s_at	NP_689695.2, EAW69495.1
GeneID.54760	PCSK4	19	1,481,427	1,490,407	8,980	-	1	4_A375_EGR1..1..4118	17959	downstream	0	0	1	4	5	19	1	4_A375_EGR1..1	19	Gene PCSK4	MGC34749, PCSK4, PC4, SPC5, DKFZp434B217	proprotein convertase subtilisin/kexin type 4	NM_017573, hCT12682.3	230901_x_at	NP_060043.2, EAW69494.1
GeneID.92840	REEP6	19	1,491,165	1,497,924	6,759	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2764, 2_A375_pNL97_plus_lncRNA_AR..1..3996	16875, 16771	downstream, downstream	1	1	0	30	44	9	1	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene REEP6	FLJ25383, C19orf32, TB2L1, REEP6, DP1L1	receptor accessory protein 6	NM_138393, hCT12675.3, hCT1952318.1, hCT2291925.0	226597_at	NP_612402.1, EAW69491.1, EAW69492.1, EAW69493.1
GeneID.339366	ADAMTSL5	19	1,505,017	1,513,188	8,171	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2764, 2_A375_pNL97_plus_lncRNA_AR..1..3996, 4_A375_EGR1..1..4119	5348, 5252, -753	in gene, in gene, upstream	1	1	1	16.5	25.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene ADAMTSL5	ADAMTSL5, THSD6	ADAMTS-like 5	NM_213604, hCT12692.4, hCT2290424.1, hCT2348705.0, hCT2348706.0, hCT2354677.0	242200_at	NP_998769.2, EAW69487.1, EAW69486.1, EAW69488.1, EAW69489.1, EAW69490.1
GeneID.6929	TCF3	19	1,609,292	1,652,326	43,034	-	1	2_A375_pNL97_plus_lncRNA_AR..1..3997	-666	upstream	0	1	0	13	24	8	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene TCF3	E2A, TCF3, MGC129648, VDIR, bHLHb21, ITF1, MGC129647	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	NM_003200, NM_001136139, hCT13811.2, hCT1952328.1, hCT1952329.1, hCT2290403.0, hCT2290404.0, hCT2354603.0	209151_x_at, 209152_s_at, 209153_s_at, 210776_x_at, 213730_x_at, 213731_s_at, 213732_at, 213809_x_at, 213811_x_at, 215260_s_at, 216647_at, 228052_x_at	NP_003191.1, NP_001129611.1, EAW69467.1, EAW69468.1, EAW69469.1, EAW69471.1, EAW69470.1, EAW69472.1
GeneID.57455	REXO1	19	1,815,245	1,848,452	33,207	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2765, 4_A375_EGR1..1..4121	-156, 4366	upstream, in gene	1	0	1	12	11	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene REXO1	EloA-BP1, TCEB3BP1, KIAA1138, ELOABP1, REX1, REXO1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	NM_020695, hCT2290396.0, hCT2348697.0	226144_at, 233939_at	NP_065746.3, EAW69451.1, EAW69450.1
GeneID.83855	KLF16	19	1,852,398	1,863,564	11,166	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2765, 4_A375_EGR1..1..4121	14956, 19500	downstream, downstream	1	0	1	12	11	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene KLF16	DRRF, BTEB4, KLF16, NSLP2	Kruppel-like factor 16	NM_031918, hCT13792.3, hCT2290394.0	224111_x_at, 226326_at	NP_114124.1, EAW69449.1, EAW69448.1
GeneID.81926	FAM108A1	19	1,876,975	1,885,518	8,543	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2766, 2_A375_pNL97_plus_lncRNA_AR..1..3998	9262, 9326	downstream, downstream	1	1	0	27	24	14	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene FAM108A1	MGC5244, C19orf27, FAM108A1	family with sequence similarity 108, member A1	NM_031213, NM_001130111, hCT2290381.1, hCT2290382.1, hCT2290384.1, hCT2290387.1, hCT2290389.1, hCT2290390.1, hCT2354605.0, hCT2354606.0	221267_s_at	NP_112490.3, NP_001123583.1, EAW69440.1, EAW69444.1, EAW69445.1, EAW69446.1, EAW69441.1, EAW69442.1, EAW69443.1, EAW69447.1
GeneID.113178	SCAMP4	19	1,905,373	1,926,012	20,639	+	1	4_A375_EGR1..1..4122	4463	in gene	0	0	1	3	7	13	1	4_A375_EGR1..1	13	Gene SCAMP4	FLJ90105, SCAMP-4, FLJ33647, SCAMP4	secretory carrier membrane protein 4	NM_079834	213244_at, 235073_at	NP_524558.1
GeneID.113179	ADAT3	19	1,905,417	1,913,446	8,029	+	1	4_A375_EGR1..1..4122	4439	in gene	0	0	1	3	7	13	1	4_A375_EGR1..1	13	Gene ADAT3	MSTP121, S863-5, TAD3, FWP005, ADAT3, MST121	adenosine deaminase, tRNA-specific 3, TAD3 homolog (S. cerevisiae)	NM_138422	1553967_at, 1553968_a_at, 230634_x_at	NP_612431.1
GeneID.1455	CSNK1G2	19	1,941,161	1,981,337	40,176	+	2	4_A375_EGR1..1..4123, 4_A375_EGR1..1..4124	21655, 30279	in gene, in gene	0	0	1	4	5	15	2	4_A375_EGR1..1	15	Gene CSNK1G2	CSNK1G2, CK1g2	casein kinase 1, gamma 2	NM_001319, hCT13814.3, hCT1952330.2, hCT2291980.1, hCT2291982.1, hCT2347982.0, hCT2347983.0	202573_at, 202574_s_at	NP_001310.3, EAW69430.1, EAW69426.1, EAW69427.1, EAW69429.1, EAW69431.1, EAW69428.1
GeneID.255193	C19orf34	19	1,952,526	1,954,548	2,022	-	1	4_A375_EGR1..1..4123	-8266	upstream	0	0	1	5	9	15	1	4_A375_EGR1..1	15	Gene C19orf34	MGC39896, C19orf34	chromosome 19 open reading frame 34	NR_033400, hCT2290375.1	1553871_at	EAW69432.1
GeneID.2872	MKNK2	19	2,037,470	2,051,243	13,773	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2767, 2_A375_pNL97_plus_lncRNA_AR..1..3999, 4_A375_EGR1..1..4125	-8581, -8533, -4725	upstream, upstream, upstream	1	1	1	11	12.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MKNK2	GPRK7, MNK2, MKNK2	MAP kinase interacting serine/threonine kinase 2	NM_199054, NM_017572, hCT1952331.1, hCT2290366.0	218205_s_at, 223199_at	NP_951009.1, NP_060042.2, EAW69422.1, EAW69423.1

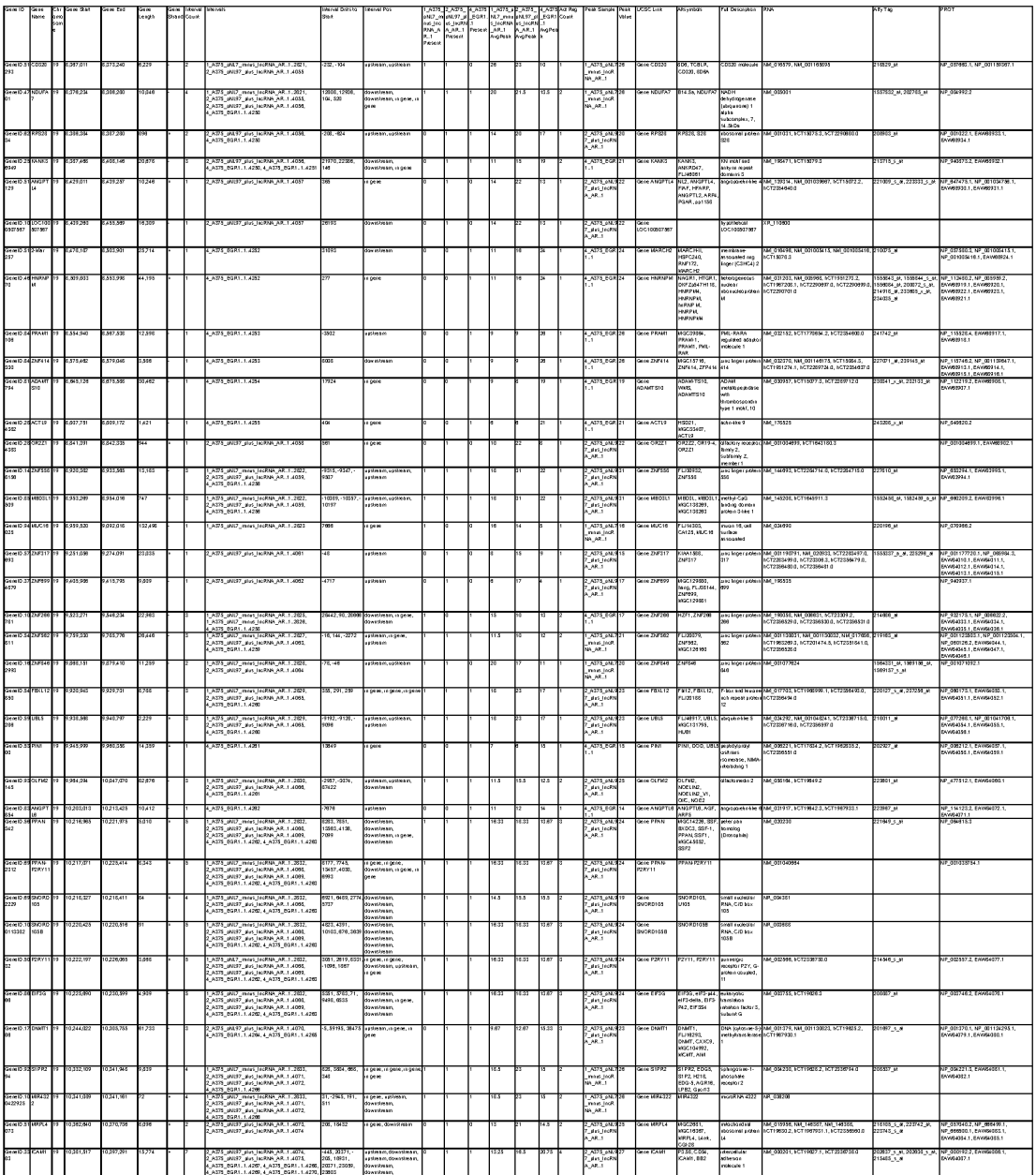


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Start	Interval Pos	1_A375_2_A375_unc_inc_RNA_R_1	2_A375_grl_lncRNA_R_1	3_A375_ESR1_lncRNA_R_1	1_A375_pLNC_lncRNA_R_1 Avg Peak	2_A375_pLNC_lncRNA_R_1 Avg Peak	3_A375_ESR1_lncRNA_R_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbol	Full Description	RNA	Alt y Tag	PROT
GeneID:10198036	MOB1A	19	2,071,035	2,099,299	28,264	-	3	1_A375_uhi07_mrvol_lncRNA_NR_1::2765, 2_A375_uhi07_dlut_lncRNA_NR_1::4093, 3_A375_uhi07_dlut_lncRNA_NR_1::4001	54853, 34587, -19	Downstream, Downstream, upstream	1	1	0	15	23	11.5	2	2_A375_uhi07_dlut_lncRNA_NR_1	23	Gene MOB1L2A	mob4/phocein, MOB1A2A	MOB1, alpha Core Motor factor, activator-like 2A (yeast)	NM_130997	225520_at, 235583_at	NP_570719.1
GeneID:10172177	CYorf15B	19	2,098,686	2,099,353	2,715	+	1	2_A375_uhi07_plus_lncRNA_NR_1::4001	-586	upstream	0	1	0	14	25	13	1	2_A375_uhi07_plus_lncRNA_NR_1	23	Gene CYorf15B	DUX4/Y-linked member 4	MAK-like-2 (C. elegans)	NM_001039648, NM_001001735, NCT13512, NCT19820803.1, NCT29191907.0	214256_x_at, 213534_at	NP_001034933.1, NP_001028903.2, EAW84191.1, EAW84230.1, EAW84241.1
GeneID:8992	AP1D1	19	2,100,990	2,151,536	50,563	-	2	2_A375_uhi07_plus_lncRNA_NR_1::4001, A_A375_EGR1_1::4126	53266, 30916	Downstream, vs gene	0	1	1	9	14	12.5	2	2_A375_uhi07_plus_lncRNA_NR_1	23	Gene AP1D1	AP1D1, HSLYR, ADTD	adaptin-related protein complex 1 delta 1 subunit	NM_003938, NM_001077623	206902_s_at, 203710_s_at, 210974_s_at	NP_003929.4, NP_001076991.1
GeneID:8189	SPSH2	19	2,236,816	2,248,676	11,860	+	1	A_A375_EGR1_1::4127	12760	Downstream	0	0	1	3	9	14	1	A_A375_EGR1_1	14	Gene SPSH2	SH3R2, SPSH2, PRPF11, SF3a60	tubulin) 2, 60kDa SS PRPF11	NM_027185, NCT22819981.1, NCT22819981.1, NCT22819981.1, NCT29203090.1, NCT29245462	205951_x_at, 37482_at	NP_839958.2, EAW84048.1, EAW84050.1, EAW84053.1, EAW84641.1, EAW84642.1, EAW85291.1, EAW85434.1
GeneID:2384	NAH	19	2,249,110	2,252,070	2,939	+	1	A_A375_EGR1_1::4127	471	vs gene	0	0	1	3	9	14	1	A_A375_EGR1_1	14	Gene NAH	ANF, ANE, ANFH	sole Multiexon Monocyte	NM_000479, NCT22820001.1	206518_at	NP_000470.2, EAW85159.1
GeneID:1018042270423031	MIR4321	19	2,250,838	2,250,717	79	-	1	A_A375_EGR1_1::4127	-1034	upstream	0	0	1	3	9	14	1	A_A375_EGR1_1	14	Gene MIR4321	MIR4321	microRNA 4321	NR_036207		
GeneID:1338338	JSRP1	19	2,252,230	2,256,422	4,172	-	1	A_A375_EGR1_1::4127	9656	Downstream	0	0	1	3	9	14	1	A_A375_EGR1_1	14	Gene JSRP1	TP-43, JSRP1, FLJ32418	junctional sarcoplasmic reticulum protein 1	NM_144618, NCT13809.3	235865_at	NP_932171.1, EAW83796.1
GeneID:2446	GNZ1	19	2,269,820	2,273,487	3,667	+	1	2_A375_uhi07_plus_lncRNA_NR_1::4002	16	vs gene	0	1	0	12	13	8	1	2_A375_uhi07_dlut_lncRNA_NR_1	13	Gene GNZ1	PAN2, NZ1, GNZ1, WGC136308	quinolinate ribotransferase isozyme 1	NM_004162, NCT19868.4, NCT19868482, NCT19683472	200977_s_at, 213991_s_at, 219952_s_at	NP_004143.1, EAW89390.1, EAW89394.1, EAW89399.1
GeneID:3572672	CYorf15B	19	2,274,851	2,282,191	7,350	-	1	2_A375_uhi07_plus_lncRNA_NR_1::4002	12643	downstream	0	1	0	12	13	8	1	2_A375_uhi07_dlut_lncRNA_NR_1	13	Gene CYorf15B	FLJ43776, CYorf15B	chromosome 19 open reading frame 35	NM_198332, NCT19364.2		NP_940934.1, EAW89392.1
GeneID:3161	LSM7	19	2,321,930	2,328,614	7,284	-	1	A_A375_EGR1_1::4128	-1682	upstream	0	0	1	4	9	16	1	A_A375_EGR1_1	16	Gene LSM7	LSM7, YNL147W	LSM7 homolog, U8 snoR nuclear RNA associated (S. cerevisiae)	NM_016199, NCT13768.2, NCT29182433	204359_s_at	NP_057283.1, EAW91609.1, EAW91610
GeneID:3892	SPTLC2B	19	2,326,829	2,355,100	28,271	+	1	A_A375_EGR1_1::4125	9367	vs gene	0	0	1	4	9	16	1	A_A375_EGR1_1	16	Gene SPTLC2B	MGC111954, SPTL2, SPTLC2	sigval peptide amidotransferase 2B	NM_031077235, NM_153956, NCT13000.3, NCT22819183.0, NCT22819183.0, NCT22819183.0, NCT22819304.0, NCT29245469.0	210952_at, 215853_s_at, 223345_s_at, 223349_at	NP_001070581.1, NP_694553.1, EAW89351.1, EAW89354.1, EAW89355.1, EAW89366.1, EAW89368.1, EAW89367.1
GeneID:3832	TMPRSS9	19	2,359,764	2,426,098	66,302	+	2	1_A375_uhi07_mrvol_lncRNA_NR_1::2769, A_A375_EGR1_1::4129	57760, 41632	Downstream, Downstream	1	0	1	10.5	8	12.5	2	2_A375_uhi07_dlut_lncRNA_NR_1	19	Gene TMPRSS9	TMPRSS9, FLJ16159	transmembrane protease, serine 9	NM_152737, NCT22340707.0		NP_932135.1, EAW89382.1
GeneID:2617517	TMM10	19	2,425,822	2,427,075	2,253	-	2	1_A375_uhi07_mrvol_lncRNA_NR_1::2769, A_A375_EGR1_1::4129	323, -1241	vs gene, upstream	1	0	1	10.5	8	12.5	2	2_A375_uhi07_dlut_lncRNA_NR_1	19	Gene TMM10	pp1, TMT2, TMM10A, TMM10_1, TMM38	transmembrane inner mitochondrial membrane 10 homolog (yeast)	NM_012455, NCT22903381.1, NCT22903547	218165_s_at, 231749_at	NP_036951.1, EAW89383.1
GeneID:6423	LMNB2	19	2,435,184	2,456,956	20,794	-	2	1_A375_uhi07_mrvol_lncRNA_NR_1::2769, A_A375_EGR1_1::4129	39408, 25542	downstream, vs gene	1	0	1	10.5	8	12.5	2	2_A375_uhi07_dlut_lncRNA_NR_1	19	Gene LMNB2	MGC27271, LMNB2, LMN2	lamin B2	NM_032737, NCT22903320.0, NCT22903321	218552_s_at	NP_116126.2, EAW89376.1, EAW89379.1
GeneID:4916	GADD45B	19	2,476,123	2,476,237	2,734	+	1	2_A375_uhi07_plus_lncRNA_NR_1::4002	229	vs gene	0	1	0	8	15	11	1	2_A375_uhi07_dlut_lncRNA_NR_1	15	Gene GADD45B	GADD45BETA, DKFZp686B133, GADD45B, MYD118	growth arrest and DNA-damage-inducible, beta	NM_015675, NCT13883.2, NCT22348560	207574_s_at, 207930_s_at, 209303_s_at, 213990_at	NP_056490.2, EAW89377.1, EAW89378.1
GeneID:1482282	DIRAS1	19	2,714,365	2,721,390	6,825	-	1	1_A375_uhi07_mrvol_lncRNA_NR_1::2771	-1748	upstream	1	0	0	16	6	7	1	1_A375_uhi07_mrvol_lncRNA_NR_1	16	Gene DIRAS1	DIRAS1, Di-Ras1, FLJ42851, GBTS1, RIG	DIRAS family, GTP-binding RAS like 1	NM_145173	226573_at, 233834_at	NP_660196.1
GeneID:2653	CLCN4	19	2,722,322	2,740,074	7,552	-	3	1_A375_uhi07_mrvol_lncRNA_NR_1::2771, 2_A375_uhi07_mrvol_lncRNA_NR_1::2772, 3_A375_uhi07_dlut_lncRNA_NR_1::4003	18636, -276, -188	downstream, upstream, upstream	1	1	0	10.5	14	8.5	2	2_A375_uhi07_dlut_lncRNA_NR_1	20	Gene SLC39A3	SLC39A3, ZIP3	solute carrier family 39 (zinc transporter), member 3	NM_144584, NM_213598, NCT18725.5, NCT23447989	222917_s_at, 223977_at, 222112_at	NP_653165.2, NP_060722.1, EAW89389.1, EAW89390.1
GeneID:8467	GSTA	19	2,754,712	2,760,394	28,642	-	1	A_A375_EGR1_1::4130	30296	downstream	0	0	1	5	9	14	1	A_A375_EGR1_1	14	Gene GSTA	GSTA, MGST, GST, alpha(GST	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	NM_000121, NCT12901.2, NCT19972361, NCT29117902	201396_s_at	NP_000112.1, EAW89386.1, EAW89388.1, EAW89387.1
GeneID:7186	THOP1	19	2,765,506	2,810,599	45,093	+	5	1_A375_uhi07_mrvol_lncRNA_NR_1::2772, 2_A375_uhi07_dlut_lncRNA_NR_1::4008, 3_A375_EGR1_1::4131, 4_A375_EGR1_1::4132, 5_A375_EGR1_1::4133	54302, 54276, 22676, 24786, 27726	downstream, downstream, vs gene, vs gene, vs gene	1	1	1	20.25	24.25	14.5	4	1_A375_uhi07_mrvol_lncRNA_NR_1	191	Gene THOP1	EP24.15, THOP1, TOP, MP78, MEPD_HUMAN	thimet oligopeptidase 1	NM_003249, NCT16372.2, NCT22988100	202235_s_at	NP_003234.1, EAW89364.1, EAW89365.1
GeneID:1119	ZNF534	19	2,819,872	2,836,733	16,861	+	6	1_A375_uhi07_mrvol_lncRNA_NR_1::2773, 2_A375_uhi07_mrvol_lncRNA_NR_1::2774, 3_A375_uhi07_dlut_lncRNA_NR_1::4008, 4_A375_uhi07_dlut_lncRNA_NR_1::4007, 5_A375_EGR1_1::4132, 6_A375_EGR1_1::4133	-84, 21184, -99, 21222, -9680, -9563	upstream, downstream, upstream, downstream, upstream, upstream	1	1	1	20.5	27.75	16	4	1_A375_uhi07_mrvol_lncRNA_NR_1	191	Gene ZNF534	ZNF534, FLJ36117	zinc finger protein 534	NM_01062851, NCT17072.2, NCT22988102.0, NCT22340939.0	232274_x_at, 243994_at	NP_001092121.1, EAW89361.1, EAW89362.1, EAW89363.1
GeneID:1423234	ZNF555	19	2,841,433	2,860,472	19,039	+	2	1_A375_uhi07_mrvol_lncRNA_NR_1::2774, 2_A375_uhi07_dlut_lncRNA_NR_1::4007	-377, -329	upstream, upstream	1	1	0	17	18	12	1	1_A375_uhi07_mrvol_lncRNA_NR_1	117	Gene ZNF555	MGC26707, ZNF555, FLJ41094	zinc finger protein 555	NM_152791, NM_001172773, NCT23413114.0	1553299_at	NP_690934.4, NP_001166048.1, EAW89360.1
GeneID:5592	ZNF77	19	2,933,216	2,944,569	11,753	-	2	1_A375_uhi07_mrvol_lncRNA_NR_1::2775, 2_A375_uhi07_plus_lncRNA_NR_1::4008	-543, -279	upstream, upstream	1	1	0	23	19	12	1	1_A375_uhi07_mrvol_lncRNA_NR_1	123	Gene ZNF77	ZNF77, pT1	zinc finger protein 77	NM_003427, NCT19795.1	1553573_s_at, 230038_at	NP_003434.1, EAW89354.1
GeneID:7811	TLE2	19	2,997,838	3,047,833	49,997	-	5	1_A375_uhi07_mrvol_lncRNA_NR_1::2776, 2_A375_uhi07_dlut_lncRNA_NR_1::4009, 3_A375_EGR1_1::4134, 4_A375_EGR1_1::4135, 5_A375_EGR1_1::4136	11193, 11193, 47946, 19377, -5857	vs gene, rt gene, rs gene, vs gene, upstream	1	1	1	7.75	9.25	10.25	4	1_A375_EGR1_1	21	Gene TLE2	ESG2, ESG, GRG2, FLJ41155, TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	NM_003260, NM_001144761, NM_001144762, NCT22971853.1, NCT22971786.0	204431_at, 40809_at	NP_003251.2, NP_001138233.1, NP_001138231.1, EAW89345.1, EAW89349.1
GeneID:1820	AES	19	3,052,905	3,082,994	30,056	-	1	A_A375_EGR1_1::4136	9324	vs gene	0	0	1	8	8	16	1	A_A375_EGR1_1	16	Gene AES	AES-2, AES-1, AES, ESP1, GRG, TLE5, GRG5	amino-terminal enhancer of split	NM_201130, NM_198969, NM_199170, NCT22971796.1, NCT22971927.1, NCT22971791.1, NCT23346986.0, NCT23346990.0	217729_s_at	NP_001121.2, NP_945320.1, NP_945321.1, EAW89344.1, EAW89343.1, EAW89346.1, EAW89342.1, EAW89341.1, EAW89344.1, EAW89347.1
GeneID:2797	GNA11	19	3,094,408	3,121,486	27,080	+	1	A_A375_EGR1_1::4127	23540	vs gene	0	0	1	5	7	21	1	A_A375_EGR1_1	21	Gene GNA11	GNA11, GNA-11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	NM_002067, NCT14726.4, NCT29868301.1	NM_002067_x_at, 212166_s_at, 212944_x_at, 214879_x_at, 40382_at, 864_at	NP_002056.2, EAW89339.1, EAW89340.1
GeneID:2797	GNA15	19	3,136,191	3,163,796	27,575	+	1	2_A375_uhi07_plus_lncRNA_NR_1::4010	28161	downstream	0	1	0	16	20	17	1	2_A375_uhi07_plus_lncRNA_NR_1	20	Gene GNA15	GNA16, GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	NM_002068, NCT14724.3	203349_at	NP_002059.2, EAW89338.1
GeneID:8613	SYPA	19	3,176,736	3,180,330	3,594	+	5	2_A375_uhi07_plus_lncRNA_NR_1::4010, A_A375_EGR1_1::4138, A_A375_EGR1_1::4139, A_A375_EGR1_1::4140, A_A375_EGR1_1::4141	-8384, -1212, 144, 696, 11000	upstream, upstream, downstream, vs gene, downstream	0	1	1	9.6	11.4	19	5	A_A375_EGR1_1	25	Gene SYPA	SYPA, LPC1, SYPA, EG98, SLP4	lysophosphatidic receptor 4	NM_002773, NCT14723.3, NCT22988103.0	209637_at	NP_002768.1, EAW89356.1, EAW89357.1
GeneID:3852	NCLN	19	3,183,075	3,209,575	25,896	+	5	A_A375_EGR1_1::4135, A_A375_EGR1_1::4139, A_A375_EGR1_1::4140, A_A375_EGR1_1::4141, A_A375_EGR1_1::4142	6443, -7283, 6443, 3949, 24545	upstream, upstream, upstream, upstream, vs gene, downstream	0	0	1	8.2	10	19.2	5	A_A375_EGR1_1	25	Gene NCLN	NIDT99, NCLN	nicalin homolog (zebrafish)	NM_020170, NCT14727.3, NCT22988400.0, NCT22988402.0, NCT22988403.0, NCT23346983.0	213837_at, 215059_at, 222266_s_at	NP_064553.2, EAW89353.1, EAW89333.1, EAW89331.1, EAW89334.1, EAW89335.1
GeneID:8890	BRUNOL5	19	3,224,701	3,297,074	72,373	+	3	1_A375_uhi07_plus_lncRNA_NR_1::2777, 2_A375_uhi07_plus_lncRNA_NR_1::4011, A_A375_EGR1_1::4143	19623, 19489, 51659	vs gene, vs gene, vs gene	1	1	1	21.5	23.5	12.5	2	2_A375_uhi07_dlut_lncRNA_NR_1	183	Gene BRUNOL5	BRUNOL5, BRUNOL-5, CELF5	CUGBP, Elav-like family member 5	NM_021938, NM_001172673, NM_033042, NCT23492693.0, NCT23492693.0	203407_at, 231744_at	NP_068707.2, NP_001166744.1, EAW89227.1, EAW89228.1
GeneID:4547	NPC	19	3,339,816	3,483,893	103,597	+	7	1_A375_uhi07_mrvol_lncRNA_NR_1::2778, 2_A375_uhi07_mrvol_lncRNA_NR_1::2779, 3_A375_uhi07_mrvol_lncRNA_NR_1::2780, 4_A375_uhi07_mrvol_lncRNA_NR_1::2781, 5_A375_uhi07_dlut_lncRNA_NR_1::4012, 6_A375_EGR1_1::4144, 7_A375_EGR1_1::4145	980, 37800, 73650, 91552, 73616, 75325, 94256	vs gene, rt gene, vs gene, vs gene, rt gene, rs gene, vs gene, vs gene	1	1	1	14.2	14.6	15	5	A_A375_EGR1_1	26	Gene NPC	C18ORF1, NPC, NP1, WGC20152, NPC, NP1	nuclear factor (erythroid-derived 2)-like 2 (CAAT box-binding transcription factor)	NM_005377, NM_208643, NCT14758.2, NCT19523351.1, NCT19523361.1, NCT23346838.0	208629_s_at, 213239_at, 229895_at	NP_005359.2, NP_955151.1, EAW89222.1, EAW89224.1, EAW89223.1, EAW89226.1
GeneID:4754	DOPEY1	19	3,492,519	3,500,936	10,119	-	5	1_A375_uhi07_mrvol_lncRNA_NR_1::2782, 2_A375_uhi07_plus_lncRNA_NR_1::4013, 3_A375_uhi07_dlut_lncRNA_NR_1::4013	136, -3048, 216	vs gene, upstream, vs gene	1	1	0	25.5	25.5	17.5	2	2_A375_uhi07_dlut_lncRNA_NR_1	198	Gene DOPEY1	DOPEY, MGC4293, HLRC1, MDDHH	dehydrogenase/reductase (SDR family) member 11	NM_031364, NM_001143165, NCT22917665.0, NCT23546013.0	205141_s_at, 213949_s_at	NP_001130.1, NP_001129857.1, EAW89218.1, EAW89217.1
GeneID:5437	FZR1	19	3,508,295	3,538,755	30,460	+	6	1_A375_uhi07_mrvol_lncRNA_NR_1::2782, 2_A375_uhi07_plus_lncRNA_NR_1::4013, 3_A375_uhi07_dlut_lncRNA_NR_1::4013, 4_A375_EGR1_1::4146, 5_A375_EGR1_1::4147, 6_A375_EGR1_1::4148	5381, -311, 5373, 30165, 31765, 26837	upstream, upstream, downstream, vs gene, downstream, upstream	1	1	1	13.2	19.2	16.2	3	2_A375_uhi07_dlut_lncRNA_NR_1	138	Gene FZR1	CDC20C, FZR2, HCDH, CDH1, KIAA1242, FZR, FZR1, HCDH	fizzy/cell division cycle 20 related 1 (Drosophila)	NM_139283, NM_001130197, NM_001130198, NCT22988703.0, NCT22988704.0, NCT22988800.0	209414_at, 209415_s_at, 209416_s_at, 211883_s_at	NP_115574.2, NP_001123669.1, NP_001123670.1, EAW89215.1, EAW89216.1, EAW89213.1
GeneID:1057	CYorf15B	19	3,508,263	3,537,371	19,308	-	5	1_A375_uhi07_mrvol_lncRNA_NR_1::2784, 2_A375_uhi07_dlut_lncRNA_NR_1::4014, 3_A375_EGR1_1::4146, 4_A375_EGR1_1::4147, 5_A375_EGR1_1::4148	141, -157, 29291, 19491, 3419	upstream, upstream, downstream, downstream, vs gene	1	1	1	13	18.75	15.5	4	1_A375_uhi07_dlut_lncRNA_NR_1	127	Gene CYorf15B	PF3S01, CYorf15B, WGC20700	chromosome 19 open reading frame 35	NM_021731, NR_174993, NR_024360, NCT22917941.0, NCT22917785.0, NCT22917786.0	220170_at, 226516_at	NP_986377.2, NP_775148.2, NP_001238451.1, EAW89309.1, EAW89310.1, EAW89311.1
GeneID:1035589	CYorf15B	19	3,539,155	3,544,026	4,872	+	3	A_A375_EGR1_1::4148, A_A375_EGR1_1::4149, A_A375_EGR1_1::4150	-1072, -1076, 5997	upstream, upstream, downstream	0	0	1	8.33	13.33	15.67	3	A_A375_EGR1_1	21	Gene CYorf15B1	CYorf15B1		NM_001135550		NP_001129522.1
GeneID:1082	HNK2B	19	3,572,943	3,579,091	6,138	+	2	1_A375_uhi07_mrvol_lncRNA_NR_1::2785, 2_A375_uhi07_dlut_lncRNA_NR_1::4015	-239, -291	upstream, upstream	1	1	0	16	24	10	1	2_A375_uhi07_dlut_lncRNA_NR_1	124	Gene HNK2B	HNK1B2, FLJ36127, dp1887, HNK2, HNK2B, BRAF29, SOX1, SHIN-RCE1, BRAF35, FP7708	high mobility group 2B	NM_006310, NCT13341.2, NCT29186853.1, NCT22989971	209113_s_at, 210719_s_at, 213989_at	NP_006301.2, EAW89307.1, EAW89308.1, EAW89306.1
GeneID:1115	TBX2R	19	3,594,304	3,606,831	12,227	-	2	A_A375_EGR1_1::4149, A_A375_EGR1_1::4150	-910, -6389	upstream, upstream	0	0	1	8	10	21.5	2	A_A375_EGR1_1	22	Gene TBX2R	T-BRAIN, TXA2-R	thromboxane A2 receptor	NM_201992, NM_201638, NCT14752.2, NCT19523341.1	207784_s_at, 207783_x_at, 211592_s_at, 336_at	NP_991331.1, NP_991967.2, EAW89311.1, EAW89322.1
GeneID:5097509	CYorf15B	19	3,615,826	3,626,615	10,167	-	8	1_A375_uhi07_mrvol_lncRNA_NR_1::2786, 2_A375_uhi07_dlut_lncRNA_NR_1::4016, 3_A375_EGR1_1::4149, 4_A375_EGR1_1::4150, 5_A375_EGR1_1::4151, 6_A375_EGR1_1::4152	-83, -35, 19069, 19815, 8193, -3	upstream, upstream, downstream, vs gene, vs gene, upstream	1	1	1	17.25	17.5	21.25	4	1_A375_uhi07_mrvol_lncRNA_NR_1	144	Gene CYorf15B	FLJ38522, FLJ17452, CYorf15A, dada, NY-REN-28	chromosome 19 open reading frame 29	NM_031655543, NM_021251	213815_s_at, 214692_x_at, 219354_s_at, 237990_x_at, 240375_at	NP_001740.2, NP_067054.1
GeneID:2350	PIP5K1C	19	3,650,162	3,700,448	50,287	-	10	1_A375_uhi07_mrvol_lncRNA_NR_1::2788, 2_A375_uhi07_dlut_lncRNA_NR_1::4016, 3_A375_EGR1_1::4152, 4_A375_EGR1_1::4153, 5_A375_EGR1_1::4154, 6_A375_EGR1_1::4155, 7_A375_EGR1_1::4156, 8_A375_EGR1_1::4157, 9_A375_EGR1_1::4158, 10_A375_EGR1_1::4159	73649, 73597, 73629, 82001, 81245, 83985, 28573, 17083, 11985, -7776	downstream, downstream, downstream, vs gene, vs gene, rs gene, vs gene, rs gene, upstream	1	1	1	11.25	10.75	17.75	6	1_A375_uhi07_mrvol_lncRNA_NR_1	144	Gene PIP5K1C	PIP5K1C, PIP5Kg, ut, CCG-32, PIP5K-Gamma, KIAA0809	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	NM_012398, NCT14733.2, NCT23546280.0	212818_at	NP_036330.1, EAW89298.1, EAW89299.1
GeneID:7154	TJP3	19	3,735,374	3,790,662	55,288	+	2	2_A375_uhi07_mrvol_lncRNA_NR_1::2787, 3_A375_uhi07_dlut_lncRNA_NR_1::4017	-6535, -6535	upstream, upstream	1	1	0	20	24	16	1	2_A375_uhi07_dlut_lncRNA_NR_1	124	Gene TJP3	ZO3, MGC119548, TJP3, ZO-3	tight junction protein 3 (zona occludens 3)	NM_014382, NCT22987043.0, NCT22987048.0	213612_at, 35143_at	NP_003248.1, EAW89293.1, EAW89292.1
GeneID:9548	APBA3	19	3,780,771	3,781,870	10,902	-	1	A_A375_EGR1_1::4160	9	vs gene	0	0	1	17	13	15	1	A_A375_EGR1_1	15	Gene APBA3	X11L3, MGC16815, APBA3, mxi2	amyloid beta (A4) precursor protein-binding, family A, member 3	NM_004886, NCT14846.2, NCT29087170	205548_s_at, 213148_s_at	NP_004477.1, EAW89290.1, EAW89291.1
GeneID:1154541	MRPL54	19	3,797,985	3,797,395	4,896	+	2	1_A375_uhi07_mrvol_lncRNA_NR_1::2788, A_A375_EGR1_1::4160	-1031, -1557	upstream, downstream	0	0	1	12	10	18.5	2	A_A375_EGR1_1	18	Gene MRPL54	L54-M, MRP-L54		NM_172231, NCT14907.2	225797_at	NP_795455.1, EAW89288.1
GeneID:6424	RAX2	19	3,799,097	3,772,219	2,122	-	2	A_A375_EGR1_1::4160, A_A375_EGR1_1::4161	10553, -5490	downstream, upstream	0	0	1	12	10	16.5	2	A_A375_EGR1_1	18	Gene RAX2	MGC15893, RAX2, CORD11, ARMD6, RAX11, QNX	retina and anterior neural fold homeobox 2	NM_032753, NCT14803.3	1553211_a_at	NP_116142.1, EAW89286.1
GeneID:4149	MNT	19	3,777,597	3,811,610	33,843	-	3	1_A375_uhi07_mrvol_lncRNA_NR_1::2789, 2_A375_uhi07_dlut_lncRNA_NR_1::4161, A_A375_EGR1_1::4162	24256, 16674, -9374	downstream, vs gene, upstream	0	0	1	8.67	8.67	13.33	3	A_A375_EGR1_1	18	Gene MNT	DXPZ4/3/4/2/12, MNT, CTS, HYLTK, LLK, MGC21021, MGC21026, HIV1-HHYLTK, CHS	peptidylprolyl cis/trans isomerase (cyclophilin)-like 4	NM_139335, NM_020310, NM_139334, NCT14829.3, NCT19822291.3, NCT19822331.1, NCT19822231.1	205267_s_at	NP_647612.1, NP_932988.2, NP_647611.1, EAW89284.1, EAW89285.1, EAW89287.1, EAW89285.1
GeneID:2517217	ZFP2	19	3,804,022	3,891,027	86,005	+	5	1_A375_uhi07_mrvol_lncRNA_NR_1::2790, 2_A375_uhi07_plus_lncRNA_NR_1::4016, 3_A375_uhi07_dlut_lncRNA_NR_1::4016, 4_A375_EGR1_1::4163, 5_A375_EGR1_1::4164, 6_A375_EGR1_1::4165	-5915, -5939, 57643, 46915, 32947	upstream, upstream, vs gene, rs gene, rs gene, upstream	1	1	1	10.75	13.75	14.5	4	2_A375_uhi07_dlut_lncRNA_NR_1	158	Gene ZFP2	ZFP2, RNA1958	zinc finger RNA binding protein 2	NM_015174, NR_001143642, NR_027149	215419_at	NP_055989.1, NP_001139112.1
GeneID:5032	ATCAY	19	3,880,816	3,926,080	47,265	+	2	1_A375_uhi07_mrvol_lncRNA_NR_1::2790, 2_A375_uhi07_dlut_lncRNA_NR_1::4016	-3976, -3982	upstream, upstream	1	1	0	16	36	8	1	2_A375_uhi07_dlut_lncRNA_NR_1	158	Gene ATCAY	BNIP-H, CLAC, MTCAY, SUA1072	ataxia, cerebellar, Cayman type	NM_033084, NCT14858.0	227385_at	NP_149355.1, EAW89280.1





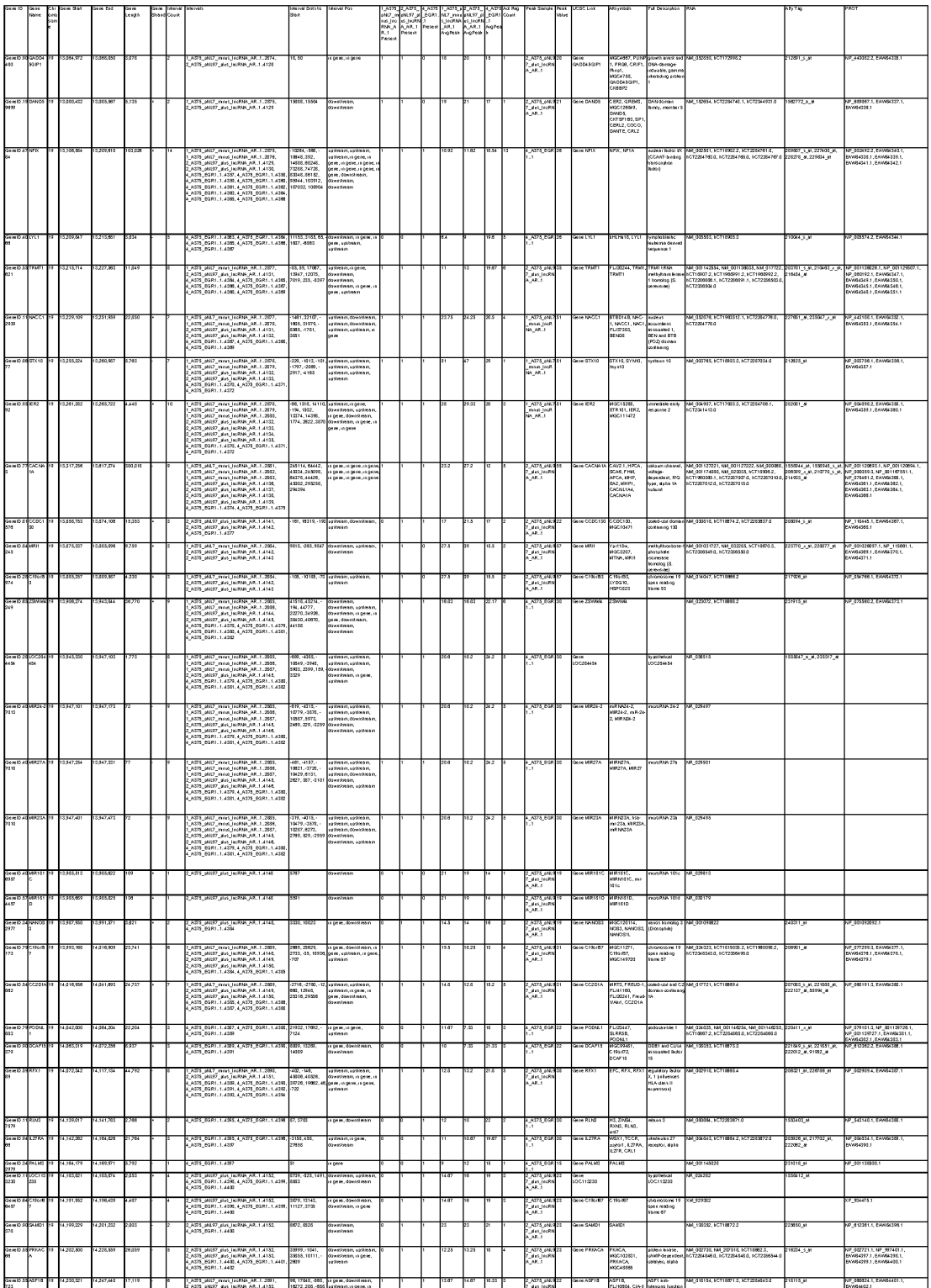
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Intervals Count	Intervals	Merged Distance Start	Merged Distance Stop	1_A375_2_A375_shN7_merged_incRNA_R_1 Present	2_A375_shN7_gRNA_incRNA_R_1 Present	3_A375_shN7_gRNA_1 Present	1_A375_shN7_merged_IncRNA_R_1 Avg Peak	2_A375_shN7_gRNA_incRNA_R_1 Avg Peak	3_A375_shN7_gRNA_1 Avg Peak	Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
Gene ID:11633134	PRR22	19	3,762,971	3,764,776	1,805	-	4	1_A375_shN7_merged_IncRNA_R_1:2003, 2_A375_shN7_plus_IncRNA_R_1:4033, 4_A375_DSR1_1:4234, 4_A375_DSR1_1:4215	-5005, -5992, 640, -6264	upstream, upstream, in gene, upstream	1	1	1	14.5	16.5	16	2	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	627	PRR22	MGC24975, PRR22	proline rich 22	NM_001134316, NCT16485531.2	1552271_at, 1552272_s_at	NP_001127788.1, ENSP00147
Gene ID:11633231	DUSP1	19	3,765,151	3,791,249	26,099	+	4	1_A375_shN7_merged_IncRNA_R_1:2003, 2_A375_shN7_plus_IncRNA_R_1:4033, 4_A375_DSR1_1:4234, 4_A375_DSR1_1:4215	486, 481, 7512, 209	in gene, in gene, downstream, in gene	1	1	1	14.5	16.5	16	2	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	627	DUSP1	DUSP1, FLJ13099, DUSP	dihydroorotate synthase 3-like (S. cerevisiae)	NM_020172, NM_001161816, NCT25105153, NCT22912782.0, NCT22912784.0, NCT22912783.0, NCT22912785.0, NCT22945310	2324668_s_at, 233143_at	NP_066550.2, NP_001158091.1, ENSP00411, ENSP00421, ENSP00441, ENSP00451, ENSP00481
Gene ID:11634972	NRTN	19	3,822,816	3,826,335	4,517	+	2	1_A375_shN7_merged_IncRNA_R_1:2005, 2_A375_shN7_plus_IncRNA_R_1:4033	4726, 4406	downstream, in gene	1	1	0	16	16	14	1	1_A375_shN7_merged_IncRNA_R_1	16	NRTN	NTN4, NRTN	neurturin	NM_004558, NCT12876.2	210663_at	NP_004549.1, ENSP00145
Gene ID:11635126	FUT8	19	3,838,837	3,859,742	20,906	-	2	1_A375_shN7_merged_IncRNA_R_1:2005, 2_A375_shN7_plus_IncRNA_R_1:4039	11166, 11516	downstream, downstream	1	1	0	16	16	14	1	1_A375_shN7_merged_IncRNA_R_1	16	FUT8	FLJ40754, Fuc-TVI, FTVI, Fuc-TVI, FUT8, FUT8A	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	NM_001041501, NM_003730	1565859_at, 1565860_at, 1565861_s_at, 210296_s_at, 210297_s_at, 211465_s_at, 211822_s_at, 211955_s_at	NP_001034991.1, NP_003141
Gene ID:11635326	NDUFA11	19	3,891,287	3,904,034	12,747	-	1	2_A375_shN7_plus_IncRNA_R_1:4040	-11658	upstream	0	1	0	13	21	12	1	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	21	NDUFA11	B14.7, NDUFA11, FLJ78501	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	NM_175614, NM_001119373, NR_034169, NCT22912753.0, NCT22945530.0, NCT22940380.0	225084_s_at, 233989_at, 235860_s_at	NP_783313.1, NP_001180304.1, ENSP00121, ENSP00132, ENSP00123.1
Gene ID:11635418	VWC	19	3,904,852	3,910,260	5,411	+	1	2_A375_shN7_plus_IncRNA_R_1:4040	5228	downstream	0	1	0	13	21	12	1	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	21	VWC	MGC131888, VWC	orthodenticle homeobox (Brachet homolog)	NM_031017921, NCT17717270.2, NCT22945501.0	NM_031017921.1, ENSP00130.1, ENSP00129.1
Gene ID:11635523	CAPS	19	3,914,193	3,918,232	4,039	-	1	2_A375_shN7_plus_IncRNA_R_1:4040	-113	upstream	0	1	0	13	21	12	1	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	21	CAPS	CAPS, CAPS1, MGC126982	calcyphosine	NM_004058, NM_033390, NCT14153.2, NCT19515492, NCT19515512, NCT22911699.0	226424_at, 231702_at, 231726_at, 231729_s_at	NP_004049.1, NP_542187.1, ENSP00123.1, ENSP00126.1, ENSP00127.1, ENSP00128.1
Gene ID:11635646	RANBP3	19	3,918,192	3,970,330	52,170	-	2	2_A375_shN7_plus_IncRNA_R_1:4040, 4_A375_DSR1_1:4216	66240, 512	downstream, in gene	0	1	1	12	16.5	10	2	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	21	RANBP3	DKFZp686I0320, RANBP3	RAN binding protein 3	NM_007322, NM_020624, NM_207220, NCT14152.2, NCT17721251.2, NCT22912753.0, NCT22912802.0, NCT22912780.0	202859_s_at, 202860_s_at, 208272_at, 210120_s_at	NP_015581.1, NP_065815.2, NP_065819.2, ENSP00120, ENSP00121, ENSP00124, ENSP00121, ENSP00122.1
Gene ID:11635990	RFX2	19	3,993,775	4,110,894	117,488	+	1	1_A375_shN7_minus_IncRNA_R_1:2007	22536	in gene	1	0	0	17	13	9	1	1_A375_shN7_minus_IncRNA_R_1	17	RFX2	RFX2, FLJ14226	regulatory factor X, 2 (influences HLA class II expression)	NM_000635, NM_134433, NCT14193.2, NCT22912458.0, NCT22912472.0, NCT22912449.0, NCT22912900.0, NCT22912931.0	209031_s_at, 226972_at	NP_000626.2, NP_602309.1, ENSP00112, ENSP00112, ENSP00113.1, ENSP00114, ENSP00117, ENSP00115.1, ENSP00116.1
Gene ID:11636316	ACSBG2	19	4,155,710	4,193,112	37,402	+	2	2_A375_shN7_plus_IncRNA_R_1:4041, 4_A375_DSR1_1:4217	63976, 65562	downstream, downstream	0	1	1	16	23	16	1	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	23	ACSBG2	BRGL, FRTD-NV2, MGC111089, ACSBG2, FRTDNV2, BGR, DKFZp434H035	acyl-CoA synthetase bubblegum family member 2	NM_020324, NCT22917102.0	221765_s_at	NP_112185.3, ENSP00111.1
Gene ID:10507094	LOC100507094	19	4,189,739	4,199,340	9,601	-	2	2_A375_shN7_plus_IncRNA_R_1:4041, 4_A375_DSR1_1:4217	52, -12	in gene, upstream	0	1	1	16	23	16	1	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	23	Gene LOC100507094	hypothetical LOC100507094		XR_111877, XR_109555, XR_115229		
Gene ID:4300	MLLT1	19	4,218,282	4,279,939	99,387	-	2	4_A375_DSR1_1:4218, 4_A375_DSR1_1:4219	44633, 48423	in gene, in gene	0	0	1	8.5	8	10.5	2	4_A375_DSR1_1	17	Gene MLLT1	MLLT1, YEATS1, ENL, LTG19	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	NM_005934, NCT14151.2	214477_at	NP_005925.2, ENSP00138.1
Gene ID:8915	CLPP	19	4,281,483	4,298,915	7,432	+	1	4_A375_DSR1_1:4220	377	in gene	0	0	1	16	14	14	1	4_A375_DSR1_1	14	Gene CLPP	CLPP		NM_006012, NCT14148.4	202799_at	NP_006003.1, ENSP00103.1
Gene ID:7170	KHSRP	19	4,412,115	4,434,822	11,707	-	1	2_A375_shN7_plus_IncRNA_R_1:4042	-156	upstream	0	1	0	15	21	15	1	2_A375_shN7_gRNA_1 A_NR_1	21	Gene KHSRP	MGC99676, FBP2, HNRNP, ISRP, FUBP2	KH-type splicing regulatory protein	NM_003685, NCT14150.3, NCT22912200.0, NCT22912201.0	204211_s_at, 204572_s_at	NP_003798.2, ENSP00097.1, ENSP00103.1, ENSP00106.1
Gene ID:4427	SLC25A19	19	4,426,048	4,433,790	7,742	-	1	2_A375_shN7_plus_IncRNA_R_1:4042	6310	downstream	0	1	0	15	21	15	1	2_A375_shN7_gRNA_1 A_NR_1	21	Gene SLC25A41	MGC34722, FLJ40442, SLC25A41	solute carrier family 25, member 41	NM_170937, NCT19320612.2, NCT22912127.1, NCT22945727.0	1553509_s_at	NP_739582.2, ENSP00094.1, ENSP00102.1, ENSP00103.1
Gene ID:7653	SLC25A20	19	4,440,078	4,459,791	19,706	-	5	1_A375_shN7_minus_IncRNA_R_1:3998, 2_A375_shN7_plus_IncRNA_R_1:4043, 4_A375_DSR1_1:4221	-539, -899, -4627	upstream, upstream, upstream	1	1	1	15	16.5	13	2	2_A375_shN7_gRNA_1 A_NR_1	20	Gene SLC25A20	MGC2615, MGC2, SCAMC, CACT, SLC25A20	solute carrier family 25 (mitochondrial carrier, allotriene shield), member 20	NM_024103, NCT14161.3, NCT22912110.0, NCT22945407.0	220162_at, 226010_at	NP_077008.2, ENSP00097.1, ENSP00098.1, ENSP00099.1
Gene ID:1393	CRB3	19	4,464,280	4,467,232	2,972	+	3	1_A375_shN7_minus_IncRNA_R_1:2003, 2_A375_shN7_plus_IncRNA_R_1:4043, 4_A375_DSR1_1:4221	-2963, -3780, 240	upstream, upstream, in gene	1	1	1	15	16.5	13	2	2_A375_shN7_gRNA_1 A_NR_1	20	Gene CRB3	CRB3		NM_139161, NM_174051	1538699_at	NP_631930.1, NP_777377.1
Gene ID:7798	DENND1C	19	4,487,218	4,651,796	14,360	-	3	1_A375_shN7_minus_IncRNA_R_1:2003, 2_A375_shN7_plus_IncRNA_R_1:4043, 4_A375_DSR1_1:4221	21476, 21316, 17160	downstream, downstream, downstream	1	1	1	15	16.5	13	2	2_A375_shN7_gRNA_1 A_NR_1	20	Gene DENND1C	FAM61C, DENND1C, FLJ22797	DENN/MADD domain containing 1C	NM_2340393, NCT14166.2, NCT22912110.0, NCT22945790.0	221800_s_at	NP_079174.2, ENSP00082.1, ENSP00083.1, ENSP00084.1
Gene ID:1002	TUBB4	19	4,644,330	4,652,230	8,000	-	2	2_A375_shN7_plus_IncRNA_R_1:4044, 4_A375_DSR1_1:4222	-2565, 6166	upstream, in gene	0	1	1	12.5	14.5	12.5	2	2_A375_shN7_gRNA_1 A_NR_1	25	Gene TUBB4	TUBB4, TUBB5, beta-5	tubulin, beta 4	NM_006087, NCT19614084.1, NCT22912904.0	212864_at	NP_006078.2, ENSP00075.1, ENSP00076.1
Gene ID:1130559	MIR2238	19	4,495,559	4,496,045	486	+	2	2_A375_shN7_plus_IncRNA_R_1:4044, 4_A375_DSR1_1:4222	6969, 165	downstream, downstream	0	1	1	12.5	14.5	12.5	2	2_A375_shN7_gRNA_1 A_NR_1	25	Gene MIR2238	MIR2238, MIR2238		NR_030565		
Gene ID:84	TNFSF9	19	6,531,010	6,535,939	4,929	+	1	1_A375_shN7_minus_IncRNA_R_1:2009	94	in gene	1	0	0	17	15	13	1	1_A375_shN7_minus_IncRNA_R_1	17	Gene TNFSF9	TNFSF9, CD137L, 4-1BBL	tumor necrosis factor (ligand) superfamily, member 9	NM_003811, NCT12994.2, NCT22916737.0	206907_at	NP_003802.1, ENSP00076.1, ENSP00077.1
Gene ID:9	CD70	19	6,555,630	6,561,180	5,313	+	1	2_A375_shN7_minus_IncRNA_R_1:2011	123	in gene	1	0	0	19	10	12	1	1_A375_shN7_minus_IncRNA_R_1	19	Gene CD70	CD70 LG, CD70, TNFSF7, CD27L	CD70 molecule	NM_001252, NCT14148.3, NCT22911971.1	206698_at	NP_001243.1, ENSP00074.1, ENSP00073.1
Gene ID:6	TCF3	19	6,677,548	6,720,682	43,135	-	1	4_A375_DSR1_1:4223	27734	in gene	0	0	1	7	5	17	1	4_A375_DSR1_1	17	Gene C3	C3, CPAMD1, ASP, AHUS5, MGC29	complement component 3	NM_000064, NCT14153.2, NCT22937451.0	NM_000333.2, ENSP00271.1, ENSP00701
Gene ID:1627	GPR108	19	6,729,925	6,737,833	7,908	-	3	1_A375_shN7_minus_IncRNA_R_1:2012, 2_A375_shN7_plus_IncRNA_R_1:4046, 4_A375_DSR1_1:4224	297, 161, 4193	in gene, in gene, in gene	1	1	1	16	20.5	13.5	2	2_A375_shN7_gRNA_1 A_NR_1	26	Gene GPR108	LUSTR2, MGC14390, GPR108	G protein-coupled receptor 108	NM_031859.02, NM_020171	223068_at	NP_031737.2, NP_064586.1
Gene ID:22	TRIP10	19	6,739,707	6,751,529	11,822	+	3	1_A375_shN7_minus_IncRNA_R_1:2012, 2_A375_shN7_plus_IncRNA_R_1:4046, 4_A375_DSR1_1:4224	-2331, -2235, 6267	upstream, upstream, upstream	1	1	1	16	20.5	13.5	2	2_A375_shN7_gRNA_1 A_NR_1	26	Gene TRIP10	STF, TRIP10, STOT, HSTF, CIP4	thyroid hormone receptor interactor 10	NM_004240, NCT14160.3, NCT22932.0, NCT22935253.0, NCT22945403.0, NCT22945454.0, NCT22945450	202734_at	NP_004231.1, ENSP00088.1, ENSP00089.1, ENSP00091.1, ENSP00092.1, ENSP00094.1, ENSP00095.1
Gene ID:2668	EMR1	19	6,887,382	6,940,484	52,882	+	1	1_A375_shN7_minus_IncRNA_R_1:2013	60034	downstream	1	0	0	19	16	5	1	1_A375_shN7_minus_IncRNA_R_1	19	Gene EMR1	TM7LN2, EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	NM_001974, NCT12961.3, NCT22936220.0	207111_at	NP_001965.3, ENSP00086.1, ENSP00087.1
Gene ID:3861	INSR	19	7,112,286	7,254,011	161,745	-	2	1_A375_shN7_minus_IncRNA_R_1:2014, 2_A375_shN7_plus_IncRNA_R_1:4047	99867, 99997	in gene, in gene	1	0	0	23	24	10	1	2_A375_shN7_gRNA_1 A_NR_1	24	Gene INSR	INSR, CD220, HHF5	insulin receptor	NM_000208, NM_001079817, NCT12968.3, NCT19517421.1, NCT22935727.0, NCT22935730.0, NCT22937220.0, NCT22945432.0	207851_s_at, 211812_s_at, 211813_s_at, 228218_at, 228450_at	NP_000199.2, ENSP00092.1, ENSP00093.1, ENSP00094.1, ENSP00095.1, ENSP00096.1, ENSP00097.1
Gene ID:3370	ARHGEF18	19	7,489,999	7,537,271	77,272	+	3	4_A375_DSR1_1:4225, 4_A375_DSR1_1:4226, 4_A375_DSR1_1:4227	49, 64461, 62930	in gene, in gene, downstream	0	0	1	8	8	17	3	4_A375_DSR1_1	19	Gene ARHGEF18	PI1a-RhoGEF, p164RhoGEF, MAY0321, MGC13912, MRHGEF18	Rho/Rac guanine nucleotide exchange factor (GEF) 18	NM_033515, NM_001130953	213029_at	NP_036133.2, NP_001129437.1
Gene ID:1002	LOC100287573	19	7,527,723	7,530,247	824	-	1	4_A375_DSR1_1:4227	-4037	upstream	0	0	1	8	7	19	1	4_A375_DSR1_1	19	Gene LOC100126573	hypothetical LOC100126573		NR_024491		
Gene ID:8	PEX11G	19	7,541,701	7,553,935	12,144	-	1	4_A375_DSR1_1:4227	11801	in gene	0	0	1	8	7	19	1	4_A375_DSR1_1	19	Gene PEX11G	MGC4261, PEX11G	peroxisomal biogenesis factor 11 gamma	NM_003662, NCT13351.3, NCT22945457.0	244126_at	NP_542393.1, ENSP00106.1, ENSP00107.1
Gene ID:6577	CYR61	19	7,562,445	7,573,336	10,891	+	2	1_A375_shN7_minus_IncRNA_R_1:2015, 2_A375_shN7_plus_IncRNA_R_1:4048	12275, 12245	downstream, downstream	1	1	0	16	27	12	1	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	27	Gene CYR61	FLJ38542, CYR61, CCN1, FLJ39754	cysteine-rich, angiogenic inducer, 61	NM_195534	2419422_x_at, 241992_x_at	NP_940936.2
Gene ID:3487	ZNF350	19	7,581,004	7,605,911	4,907	+	4	1_A375_shN7_minus_IncRNA_R_1:2015, 1_A375_shN7_minus_IncRNA_R_1:2016, 2_A375_shN7_plus_IncRNA_R_1:4048, 2_A375_shN7_plus_IncRNA_R_1:4049	-6284, 6335, 6316, 6356	downstream, downstream, upstream, downstream	1	1	1	0	26.5	23.5	12.5	2	2_A375_shN7_gRNA_1 A_NR_1	40	Gene ZNF350	FLJ10350, ZFEND, ZNF350	zinc finger protein 350	NM_019033	219379_x_at, 226260_x_at	NP_061853.4
Gene ID:192	MCOLN1	19	7,667,498	7,696,695	11,399	+	7	1_A375_shN7_minus_IncRNA_R_1:2016, 1_A375_shN7_minus_IncRNA_R_1:2017, 1_A375_shN7_minus_IncRNA_R_1:2018, 2_A375_shN7_plus_IncRNA_R_1:4049, 2_A375_shN7_plus_IncRNA_R_1:4050, 2_A375_shN7_plus_IncRNA_R_1:4051, 4_A375_DSR1_1:4228	-136, 11512, 12044, -106, 11455, 13112, 12832	upstream, downstream, downstream, upstream, downstream, downstream, downstream	1	1	1	29	34	13.67	3	4_A375_DSR1_1	40	Gene MCOLN1	MSTP150, MSTP060, TRPML1, TRPML1, MCOLN1, TRP-ML1, ML4, MLIV	mucolipin 1	NM_020533, NCT13477.2, NCT19522371.1, NCT22935422.0, NCT22945402.0	219952_s_at	NP_065394.2, ENSP00092.1, ENSP00093.1, ENSP00094.1
Gene ID:1016	PNPLA6	19	7,699,035	7,826,653	27,815	-	8	1_A375_shN7_minus_IncRNA_R_1:2017, 1_A375_shN7_minus_IncRNA_R_1:2018, 1_A375_shN7_minus_IncRNA_R_1:2019, 2_A375_shN7_plus_IncRNA_R_1:4050, 2_A375_shN7_plus_IncRNA_R_1:4051, 2_A375_shN7_plus_IncRNA_R_1:4052, 4_A375_DSR1_1:4229	-30, 1802, 26556, -82, 1910, 26566, 1060, 22630	upstream, in gene, downstream, upstream, in gene, downstream, in gene, in gene	1	1	1	19.25	26.25	10.25	4	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	38	Gene PNPLA6	PNPLA6, SPG39, NTE/NND, sws, NTE	patatin-like phospholipase domain containing 6	NM_006702, NM_001166111, NM_001166112, NM_001166113, NM_001166114, NCT12987.3, NCT22935452.0	203716_at	NP_006693.2, NP_001159553.1, NP_001159554.1, NP_001159555.1, NP_001159556.1, ENSP00229.1, ENSP00232.1
Gene ID:5741	EVSL	19	7,895,181	7,929,082	34,701	+	7	2_A375_shN7_plus_IncRNA_R_1:4053, 2_A375_shN7_plus_IncRNA_R_1:4053, 2_A375_shN7_plus_IncRNA_R_1:4054, 4_A375_DSR1_1:4235, 4_A375_DSR1_1:4236, 4_A375_DSR1_1:4237	-249, -349, 21319, 27431, 28899, 30597, 41845	upstream, upstream, in gene, in gene, in gene, downstream, in gene	1	1	1	8.83	8.67	12.83	6	2_A375_shN7_gRNA_1 T_plus_IncRNA A_NR_1	33	Gene EVSL	EVSL		NM_145343, NM_001135944, NCT13857.2, NCT22935643.0, NCT22935553.0	228411_at, 242504_at, 244350_s_at, 244351_at	NP_660325.1, NP_001128418.1, NP_001128419.1, ENSP00074.1, ENSP00075.1
Gene ID:1842	FLJ22184	19	7,933,805	7,939,230	5,721	-	4	4_A375_DSR1_1:4233, 4_A375_DSR1_1:4234, 4_A375_DSR1_1:4235, 4_A375_DSR1_1:4236, 4_A375_DSR1_1:4237, 4_A375_DSR1_1:4238	10188, 5398, 2822, 5122	downstream, in gene, in gene, upstream	0	0	1	8.25	9.5	15	4	4_A375_DSR1_1	16	Gene FLJ22184		hypothetical protein FLJ22184	NM_031196497	2203684_at	NP_001172766.1
Gene ID:1511	LRRC8E	19	7,953,290	7,966,908	13,618	+	5	2_A375_shN7_plus_IncRNA_R_1:4054, 4_A375_DSR1_1:4235, 4_A375_DSR1_1:4236, 4_A375_DSR1_1:4237, 4_A375_DSR1_1:4238	13250, -5942, 5498	downstream, upstream, downstream	0	0	1	10.5	14	16.5	2	2_A375_shN7_gRNA_1 A_NR_1	19	Gene LRRC8E	FLJ23420, LRRC8E	leucine rich repeat containing 8 family, member E	NM_032581, NCT16469388.3	2220774_at, 2236633_at	NP_379737.2, ENSP00093.1
Gene ID:9709	MAP2K7	19	7,966,765	7,979,585	10,595	+	5	2_A375_shN7_plus_IncRNA_R_1:4054, 4_A375_DSR1_1:4235, 4_A375_DSR1_1:4236, 4_A375_DSR1_1:4237, 4_A375_DSR1_1:4241, 4_A375_DSR1_1:4242	-125, -477, 11855, 16571, 17155	upstream, upstream, downstream, downstream, downstream	0	0	1	13	14.5	17.75	4	4_A375_DSR1_1	20	Gene MAP2K7	MAP2K7, MKK7, PRKMK7, JkNK2, MAPKK7	mitogen-activated protein kinase kinase 7	NM_145155, NCT13851.3, NCT19317272.1, NCT22935910.0, NCT22935951.0, NCT22935950.0, NCT22945630.0	202901_s_at, 202902_s_at, 202903_at, 216206_x_at, 228023_at, 229833_at	NP_660183.1, ENSP00085.1, ENSP00083.1, ENSP00084.1, ENSP00081.1, ENSP00087.1, ENSP00082.1, ENSP00085.1
Gene ID:1002	LOC100287868	19	7,981,153	7,982,782	1,629	+	4	4_A375_DSR1_1:4240, 4_A375_DSR1_1:4241, 4_A375_DSR1_1:4242, 4_A375_DSR1_1:4243	-1827, 3903, 4787, 11711	upstream, downstream, downstream, downstream	0	0	1	10.5	12.25	17.5	4	4_A375_DSR1_1	20	Gene LOC100287868	hypothetical protein LOC100287868		XM_002119018		XP_002119060.1
Gene ID:8655	SNAPC1	19	7,995,194	7,998,136	2,942	+	4	4_A375_DSR1_1:4240, 4_A375_DSR1_1:4241, 4_A375_DSR1_1:4242, 4_A375_DSR1_1:4243	-5976, 56, 726, 7970	upstream, upstream, in gene, downstream	0	0	1	10.5	12.25	17.5	4	4_A375_DSR1_1	20	Gene SNAPC2	SNAP45, SNAPC2, PTF DELTA	small nuclear RNA activating complex, polypeptide 2, 45kDa	NM_003083, NM_030717, NCT12960.3, NCT22935995.0	204164_at	NP_003074.1, ENSP00097.1, ENSP00098.1
Gene ID:4217	CTXN1	19	7,999,281	7,991,051	1,870	-	4	4_A375_DSR1_1:4240, 4_A375_DSR1_1:4241, 4_A375_DSR1_1:4242, 4_A375_DSR1_1:4243	11433, 5913, 5131, -5513	downstream, downstream, downstream, upstream	0	0	1	10.5	12.25	17.5	4	4_A375_DSR1_1	20	Gene CTXN1	CTXN1, CTXN, FLJ35995	cortexin 1	NM_206533, NCT23627.0	220126_s_at	NP_790894.1, ENSP00158.1
Gene ID:1951	TMEM44	19	7,991,992	8,000,708	17,105	-	5	4_A375_DSR1_1:4241, 4_A375_DSR1_1:4242, 4_A375_DSR1_1:4243	2287, 2, 22786, 19044	downstream, downstream, downstream	0	0	1	12.67	13.33	17.67	3	4_A375_DSR1_1	20	Gene TMEM44	TMM44, DKFZp686H0224, TMM44	transmembrane protein 44, endochondral ossification 44, homolog (yeast)	NM_030531, NCT13852.3, NCT22937.0	223272_at, 233293_s_at	NP_109604.2, ENSP00093.1, ENSP00094.1
Gene ID:6355	CCL25	19	8,117,934	8,127,547	9,613	+	2	2_A375_shN7_plus_IncRNA_R_1:4264, 4_A375_DSR1_1:4245	-2842, 12698	upstream, downstream	0	0	1	6.5	8	19.5	2	4_A375_DSR1_1	22	Gene CCL25	SCYA25, TECK, CCL25, MGC130327, CK-6	chemokine (C-C motif) ligand 25	NM_005624, NCT12900.3, NCT22908700.0	208568_at	NP_005615.2, ENSP00093.1, ENSP00093.1
Gene ID:8487	FBN2	19	8,130,287	8,212,395	82,099	+	4	4_A375_DSR1_1:4245, 4_A375_DSR1_1:4246, 4_A375_DSR1_1:4247, 4_A375_DSR1_1:4248	51855, 57548, 3889, -939	in gene, in gene, in gene, upstream	0	0	1	5	7.25	15	4	4_A375_DSR1_1	17	Gene FBN2	FBN2, FKN1779	fibulin 3	NM_032447, NCT16233361.1, NCT22897440.0, NCT22897445.0	240117_at	NP_115723.3, ENSP00148.1, ENSP00147.1, ENSP00148.1
Gene ID:7903	LASS4	19	8,274,217	8,327,335	53,098	+	1	4_A375_DSR1_1:4249	-743	upstream	0	0	1	7	11	10	1	4_A375_DSR1_1	16	Gene LASS4	TYH, CerS4, FLJ12089, UKS6	LAG1 homolog, ceramide synthase 4	NM_024332, NCT19382.4, NCT19622411.1, NCT19622342.1, NCT22909674.0, NCT22908760.0, NCT22945350.0	219922_s_at	NP_076028.2, ENSP00140.1, ENSP00142.1, ENSP00144.1, ENSP00145.1, ENSP00142.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_DMSO_mut_incRNA_AR_1 Percent	2_A375_DMSO_wt_incRNA_AR_1 Percent	3_A375_EGFR_1 Percent	1_A375_DMSO_NAT_incRNA_AR_1 AvgRsem	2_A375_DMSO_NAT_incRNA_AR_1 AvgPeak	3_A375_EGFR_1 AvgPeak	Adj Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbol	Full Description	RNA	Alty Tag	PROT
GeneID:3512293	IFIT3	chr10	90,997,011	91,012,240	15,229	-	2	1_A375_shG7_mrna1_lncRNA_AR_1.2021, 2_A375_shG97_dun_lncRNA_AR_1.4033	-232, -104	upstream, upstream	1	1	0	26	23	10	1	1_A375_shG7_mrna1_lncRNA_AR_1	26	Gene CD320	IFIT, TCBLR, CD320, IDWA	CD320 molecule	NM_016579, NM_001165935	218029_at	NP_057663.1, NP_001159097.1
GeneID:4717	NDUFA7	chr19	3,978,234	3,998,200	19,966	+	4	1_A375_shG7_mrna1_lncRNA_AR_1.2021, 2_A375_shG97_dun_lncRNA_AR_1.4033, 3_A375_shG97_dun_lncRNA_AR_1.4056, 4_A375_DGR1_1.4256	19966, 12606, 116, 520	downstream, downstream, upstream, gene, gene	1	1	1	20	21.5	12.5	2	1_A375_shG7_mrna1_lncRNA_AR_1	26	Gene NDUFA7	Bt.e.Sa, NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	NM_030851	1557532_at, 202765_at	NP_004992.2
GeneID:8534	RPS28	chr19	3,998,394	3,997,290	998	+	2	1_A375_shG97_dun_lncRNA_AR_1.4039, 4_A375_DGR1_1.4256	-998, -804	upstream, upstream	0	1	1	14	20	17	1	2_A375_shG97_dun_lncRNA_AR_1	30	Gene RPS28	RPS28, S28	ribosomal protein S28	NM_001031, XCT182783.3, XCT2190880.0	208883_at	NP_001022.1, EAW68933.1, EAW68934.1
GeneID:2596349	KANK2	chr19	8,397,486	8,466,146	68,676	-	3	1_A375_shG97_dun_lncRNA_AR_1.4056, 4_A375_DGR1_1.4256, 4_A375_DGR1_1.4256	21670, 22956,	downstream, downstream, gene, gene	0	1	1	11	15	19	2	4_A375_EGFR_1.1	21	Gene KANK2	KANK2, ANKRD47, FLJ46581	KN motif and ankyrin repeat domains 2	NM_138317, XCT182783.2	213715_s_at	NP_940972.2, EAW68932.1
GeneID:3310	ANGPTL4	chr19	8,429,011	8,439,287	10,276	+	1	2_A375_shG97_dun_lncRNA_AR_1.4057	598	up gene	0	1	0	14	22	13	1	2_A375_shG97_dun_lncRNA_AR_1	22	Gene ANGPTL4	HSZ, ANGPTL4, FIAF, HFARP, ANGPTL2, ARP4, PGAR, pp1158	angiopoietin-like 4	NM_139314, NM_001039987, XCT153972.2, XCT2354940.0	221809_s_at, 223333_s_at	NP_647475.1, NP_001034736.1, EAW68930.1, EAW68931.1
GeneID:1053	LOC100507867	chr19	8,429,260	8,433,599	18,339	-	1	2_A375_shG97_dun_lncRNA_AR_1.4057	28193	Downstream	0	1	0	14	22	13	1	2_A375_shG97_dun_lncRNA_AR_1	22	Gene LOC100507867		hypothetical LOC100507867	XR_110803		
GeneID:5337	PVR	chr19	8,476,187	8,503,091	26,774	+	1	4_A375_DGR1_1.4252	31893	downstream	0	0	1	11	16	24	1	4_A375_EGFR_1.1	24	Gene MARCH2	MARCH8, HSPC240, RNF172, MARCH2	membrane-associated ring finger (C3HC4) 2	NM_016498, NM_001003410, NM_001003416, NM_001003417	210079_at	NP_057583.3, NP_001003410.1, NP_001003416.1, EAW68924.1
GeneID:4488	HNRNPM	chr19	8,509,003	8,553,996	44,993	+	1	4_A375_DGR1_1.4252	277	up gene	0	0	1	11	16	24	1	4_A375_EGFR_1.1	24	Gene HNRNPM	MATR7, HTGR1, DKFZp547H165, HNRPM, HNRNPM, hnRNP M, HNRPML, HNRPAM	heterogeneous nuclear ribonucleoprotein M	NM_031303, NM_002968, XCT193270.2, XCT1967230.1, XCT2290997.0, XCT2290999.0, XCT2297001.0	1555643_at, 1558644_s_at, 1559054_at, 200072_s_at, 214316_at, 233063_s_at, 234039_at	NP_112603.2, NP_005781.2, EAW68919.1, EAW68920.1, EAW68922.1, EAW68923.1, EAW68921.1
GeneID:5447	PRAM1	chr19	8,544,940	8,567,535	22,596	-	1	4_A375_DGR1_1.4253	-3902	upstream	0	0	1	9	9	28	1	4_A375_EGFR_1.1	28	Gene PRAM1	MGC29884, PRAM-1, PRAM1, PML-RAR	PML-RARA regulated adaptor molecule 1	NM_032132, XCT179854.2, XCT2354490.0	141742_at	NP_115316.4, EAW68917.1, EAW68918.1
GeneID:3420	ZNF414	chr19	8,575,462	8,579,045	3,584	+	1	4_A375_DGR1_1.4253	6908	downstream	0	0	1	9	9	28	1	4_A375_EGFR_1.1	28	Gene ZNF414	MGC21178, ZNF414, ZFP414	zinc finger protein 414	NM_022730, NM_001145175, XCT153804.2, XCT1951274.1, XCT2297734.0, XCT2354937.0	227021_at, 239145_at	NP_073618.2, NP_001139947.1, EAW68913.1, EAW68914.1, EAW68915.1, EAW68916.1
GeneID:1794	ADAMTS10	chr19	8,845,328	8,875,595	30,662	-	1	4_A375_DGR1_1.4254	17924	up gene	0	0	1	9	8	19	1	4_A375_EGFR_1.1	19	Gene ADAMTS10	ADAMTS10, WMS, ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 motif, 10	NM_030957, XCT153972.2, XCT2297122.0	230241_s_at, 233733_at	NP_112182, EAW68905.1, EAW68907.1
GeneID:2582	ACTL9	chr19	8,937,751	8,939,172	1,421	-	1	4_A375_DGR1_1.4255	456	up gene	0	0	1	8	8	21	1	4_A375_EGFR_1.1	21	Gene ACTL9	HSD21, MGC33407, ACTL9	actin-like 9	NM_178325	243208_x_at	NP_848620.2
GeneID:2802	CIRZ2	chr19	8,941,291	8,942,335	944	+	1	2_A375_shG97_dun_lncRNA_AR_1.4056	581	up gene	0	1	0	10	22	8	1	2_A375_shG97_dun_lncRNA_AR_1	22	Gene CIRZ2	CIRZ2C, CIR19-4, CIRZ	circadian regulator, Bunyu-z, coiled-coil, Z-interacter-1	NM_031064699, XCT1643100.3		NP_001034699.1, EAW68902.1
GeneID:5184	ZNF558	chr19	8,930,582	8,933,585	13,183	-	3	1_A375_shG7_mrna1_lncRNA_AR_1.2022, 2_A375_shG97_dun_lncRNA_AR_1.4039, 4_A375_DGR1_1.4256	-9315, -9247, -7307	upstream, upstream, upstream	1	1	1	16	31	22	1	2_A375_shG97_dun_lncRNA_AR_1	31	Gene ZNF558	FLJ30152, ZNF558	zinc finger protein 558	NM_144993, XCT2259714.0, XCT2287415.0	227010_at	NP_659294.1, EAW68999.1, EAW68994.1
GeneID:5509	MBD3L1	chr19	8,933,269	8,934,016	747	+	3	1_A375_shG7_mrna1_lncRNA_AR_1.2022, 2_A375_shG97_dun_lncRNA_AR_1.4039, 4_A375_DGR1_1.4256	-10315, -10137, 10197	upstream, upstream, upstream	1	1	1	16	31	22	1	2_A375_shG97_dun_lncRNA_AR_1	31	Gene MBD3L1	MBD3L, MBD3L1, MGC133281, MGC139283	methyl-CpG binding domain protein 3-like 1	NM_145208, XCT1645911.3	1552430_at, 1552438_s_at	NP_660209.2, EAW68998.1
GeneID:5447	MUC16	chr19	8,959,520	9,092,016	132,496	+	1	1_A375_shG7_mrna1_lncRNA_AR_1.2023	7988	up gene	1	2	0	16	14	5	1	1_A375_shG7_mrna1_lncRNA_AR_1	16	Gene MUC16	FLJ14303, CA125, MUC16	mucin 16, cell surface associated	NM_024690	220198_at	NP_078966.2
GeneID:3717	ZNF317	chr19	9,251,096	9,274,091	23,015	+	1	2_A375_shG97_dun_lncRNA_AR_1.4061	-48	upstream	0	1	0	8	15	9	1	2_A375_shG97_dun_lncRNA_AR_1	15	Gene ZNF317	KIAA1808, ZNF317	zinc finger protein 317	NM_031197, NM_029931, XCT2284977.0, XCT2283499.0, XCT2290413.0, XCT2294779.0, XCT2296499.0, XCT2296501.0	1553377_s_at, 203299_s	NP_001177210.1, NP_086994.3, EAW64100.1, EAW64101.1, EAW64112.1, EAW64114.1, EAW64102.1, EAW64115.1
GeneID:3729	ZNF699	chr19	9,455,998	9,475,795	19,809	-	1	2_A375_shG97_dun_lncRNA_AR_1.4062	-4717	upstream	0	1	0	8	17	4	1	2_A375_shG97_dun_lncRNA_AR_1	17	Gene ZNF699	MGC129993, Hslig, FLJ35144, ZNF699, MGC129981	zinc finger protein 699	NM_178535		NP_849207.1
GeneID:1012	ZNF268	chr19	9,523,271	9,548,234	22,963	-	3	1_A375_shG7_mrna1_lncRNA_AR_1.2025, 2_A375_shG97_mrna1_lncRNA_AR_1.2026, 4_A375_DGR1_1.4256	28442, 80, 20998	downstream, up gene, downstream	1	0	1	15	10	13	2	4_A375_EGFR_1.1	17	Gene ZNF268	HZF1, ZNF268	zinc finger protein 268	NM_199185, NM_006631, XCT233972.2, XCT2358329.0, XCT2358330.0, XCT2358331.0	214606_at	NP_872275.1, NP_006622.2, EAW64331.1, EAW64334.1, EAW64335.1, EAW64336.1
GeneID:5427	ZNF582	chr19	9,799,230	9,793,579	35,648	-	3	1_A375_shG7_mrna1_lncRNA_AR_1.2027, 2_A375_shG97_dun_lncRNA_AR_1.4061, 4_A375_DGR1_1.4259	-16, 144, -2272	upstream, up gene, upstream	1	1	1	11.5	10	12	2	1_A375_shG7_mrna1_lncRNA_AR_1	21	Gene ZNF582	FLJ35279, ZNF582, MGC126190	zinc finger protein 582	NM_031330311, NM_031330332, NM_017666, XCT1963993.0, XCT201474.5, XCT2351641.0, XCT2356320.0	219165_at	NP_001159515.1, NT_001123004.1, NP_060126.2, EAW64044.1, EAW64045.1, EAW64047.1, EAW64048.1
GeneID:2902	ZNF646	chr19	9,886,151	9,879,410	11,259	-	2	1_A375_shG7_mrna1_lncRNA_AR_1.2028, 2_A375_shG97_dun_lncRNA_AR_1.4064	-76, -48	upstream, upstream	1	1	0	20	17	11	1	1_A375_shG7_mrna1_lncRNA_AR_1	20	Gene ZNF646	ZNF646	zinc finger protein 646	NM_031079624	1564231_at, 1569196_at, 1569197_s_at	NP_001071932.1
GeneID:5467	FBXL12	chr19	9,920,945	9,929,731	8,786	-	3	1_A375_shG7_mrna1_lncRNA_AR_1.2029, 2_A375_shG97_dun_lncRNA_AR_1.4065, 4_A375_DGR1_1.4260	358, 291, 239	up gene, up gene, up gene	1	1	1	16	23	17	1	2_A375_shG97_dun_lncRNA_AR_1	23	Gene FBXL12	FBL12, FBXL12, FLJ35165	F-box and leucine-rich repeat protein 12	NM_017703, XCT1968999.1, XCT2356492.0, XCT2356494.0	220127_s_at, 237256_at	NP_060175.1, EAW64052.1, EAW64051.1, EAW64052.1
GeneID:5988	UBL5	chr19	9,936,986	9,940,797	3,811	-	3	1_A375_shG7_mrna1_lncRNA_AR_1.2029, 2_A375_shG97_dun_lncRNA_AR_1.4065, 4_A375_DGR1_1.4260	-9192, -9128, -7699	upstream, upstream, upstream	1	1	1	16	23	17	1	2_A375_shG97_dun_lncRNA_AR_1	23	Gene UBL5	Fu48917, UBL5, MGC131793, HUB1	ubiquitin like 5	NM_024292, NM_001042541, XCT2387115.0, XCT2387116.0, XCT2387117.0	219011_at	NP_077268.1, NP_001047708.1, EAW64034.1, EAW64035.1, EAW64036.1
GeneID:5331	PIN1	chr19	9,945,999	9,960,536	14,539	+	1	4_A375_DGR1_1.4261	13649	up gene	0	0	1	7	8	15	1	4_A375_EGFR_1.1	15	Gene PIN1	PIN1, DOD, UBL5	peptidylprolyl isomerase (cyclophilin)-like 1	NM_006221, XCT177824.2, XCT1958355.2, XCT2355531.0	202297_at	NP_5982121.1, EAW68997.1, EAW64035.1, EAW64035.1
GeneID:5744	CLFM2	chr19	9,964,294	10,047,070	82,876	-	3	1_A375_shG7_mrna1_lncRNA_AR_1.2030, 2_A375_shG97_dun_lncRNA_AR_1.4066, 3_A375_DGR1_1.4261	-7987, -3074, 67622	upstream, upstream, downstream	1	1	1	11.5	15.5	12.5	2	2_A375_shG97_dun_lncRNA_AR_1	23	Gene CLFM2	CLFM2, NOELIN2, NOELIN2, V1, CMC, MOE2	calponin-like transmembrane domain protein 2	NM_053186, XCT1964.2	223801_at	NP_477112.1, EAW64060.1
GeneID:5334	ANGPTL8	chr19	10,003,013	10,013,426	10,412	+	1	4_A375_DGR1_1.4262	-7678	upstream	0	0	1	11	12	14	1	4_A375_EGFR_1.1	14	Gene ANGPTL8	ANGPTL8, AGF, UNQ1941	angiopoietin-like 8	NM_031917, XCT1964.2, XCT1967933.1	223967_at	NP_1141223.2, EAW64072.1, EAW64071.1
GeneID:3669	PPAN	chr19	10,216,965	10,221,975	5,010	+	5	1_A375_shG7_mrna1_lncRNA_AR_1.2032, 2_A375_shG97_dun_lncRNA_AR_1.4066, 3_A375_DGR1_1.4261, 4_A375_DGR1_1.4262, 4_A375_DGR1_1.4262	8263, 7831, 12855, 4136, 7089	downstream, downstream, downstream, gene, downstream	0	1	1	16.33	16.33	12.67	3	2_A375_shG97_dun_lncRNA_AR_1	24	Gene PPAN	MGC14239, SSF, BIOC2, SSF1, PPAN, SSF1, MGC43552, SSF2	peter pan homolog (Drosophila)	NM_032230	221845_s_at	NP_396418.3
GeneID:8535	PPAN-P2RY11	chr19	10,217,071	10,225,414	8,343	+	5	1_A375_shG7_mrna1_lncRNA_AR_1.2032, 2_A375_shG97_dun_lncRNA_AR_1.4066, 3_A375_DGR1_1.4261, 4_A375_DGR1_1.4262, 4_A375_DGR1_1.4262	6177, 7745, 13437, 4030, 6993	up gene, up gene, downstream, up gene, up gene	1	1	1	16.33	16.33	12.67	3	2_A375_shG97_dun_lncRNA_AR_1	24	Gene PPAN-P2RY11	PPAN-P2RY11		NM_031040994		NP_001033854.1
GeneID:8538	SNORD105	chr19	10,216,327	10,216,411	84	+	4	2_A375_shG97_dun_lncRNA_AR_1.4066, 3_A375_DGR1_1.4261, 4_A375_DGR1_1.4262, 4_A375_DGR1_1.4262	6921, 6409, 2774, 5757	downstream, downstream, downstream, downstream, downstream	1	1	1	14.5	15.5	15.5	2	2_A375_shG97_dun_lncRNA_AR_1	19	Gene SNORD105	SNORD105, U105	small nucleolar RNA, C/D box 105	NM_006351		
GeneID:6113382	SNORD105B	chr19	10,216,429	10,220,916	91	+	5	1_A375_shG7_mrna1_lncRNA_AR_1.2032, 2_A375_shG97_dun_lncRNA_AR_1.4066, 3_A375_DGR1_1.4261, 4_A375_DGR1_1.4262, 4_A375_DGR1_1.4262	4821, 4291, 10163, 876, 3639	downstream, downstream, downstream, downstream, downstream	1	1	1	16.33	16.33	12.67	3	2_A375_shG97_dun_lncRNA_AR_1	24	Gene SNORD105B	SNORD105B	small nucleolar RNA, C/D box 105B	NR_003668		
GeneID:3832	P2RY11	chr19	10,222,197	10,226,085	3,888	+	5	1_A375_shG7_mrna1_lncRNA_AR_1.2032, 2_A375_shG97_dun_lncRNA_AR_1.4066, 3_A375_DGR1_1.4261, 4_A375_DGR1_1.4262, 4_A375_DGR1_1.4262	5981, 3819, 9331, 1096, 1867	up gene, up gene, downstream, upstream, up gene	1	1	1	16.33	16.33	12.67	3	2_A375_shG97_dun_lncRNA_AR_1	24	Gene P2RY11	P2Y11, P2RY11	purinergic receptor P2Y, G-protein coupled, 11	NM_002566, XCT2387.0	214548_s_at	NP_002557.2, EAW64077.1
GeneID:1975	EIF3G	chr19	10,225,890	10,230,909	4,909	+	5	1_A375_shG7_mrna1_lncRNA_AR_1.2032, 2_A375_shG97_dun_lncRNA_AR_1.4066, 3_A375_DGR1_1.4261, 4_A375_DGR1_1.4262, 4_A375_DGR1_1.4262	5241, 5783, 71, 5495, 6533	downstream, downstream, gene, downstream, downstream, downstream	1	1	1	16.33	16.33	12.67	3	2_A375_shG97_dun_lncRNA_AR_1	24	Gene EIF3G	EIF3G, eIF3-p44, eIF3d-like, EIF3, PA2, EIF3S4	eukaryotic translation initiation factor 3, subunit G	NM_003755, XCT192683	200987_at	NP_003740.2, EAW64056.1
GeneID:1763	DNMT1	chr19	10,244,022	10,300,755	56,733	-	3	2_A375_shG97_dun_lncRNA_AR_1.4070, 4_A375_DGR1_1.4264, 4_A375_DGR1_1.4268	-9, 39193, 39475	upstream, up gene, up gene	0	1	1	9.67	12.67	15.33	3	2_A375_shG97_dun_lncRNA_AR_1	23	Gene DNMT1	DNMT1, FLJ10293, DNMT, CXJC9, MGC104992, MCMT, AIM	DNA (cytosine-5-)-methyltransferase 1	NM_001379, NM_001130823, XCT1983.2, XCT1967930.1	203697_s_at	NP_001370.2, NP_001124293.1, EAW64078.1, EAW64080.1
GeneID:3276	SIPR2	chr19	10,332,109	10,341,945	9,839	+	4	1_A375_shG7_mrna1_lncRNA_AR_1.2033, 2_A375_shG97_dun_lncRNA_AR_1.4071, 2_A375_shG97_dun_lncRNA_AR_1.4072, 4_A375_DGR1_1.4268	626, 3804, 865, 646	up gene, up gene, up gene, up gene	1	1	1	16.5	23	15	2	1_A375_shG7_mrna1_lncRNA_AR_1	26	Gene SIPR2	SIPR2, EDG5, S1P2, H218, EDG-5, AGR16, EDG5, LPB2, Gpcr03	sphingosine-1-phosphate receptor 2	NM_004230, XCT1983.2, XCT2358784.0	206537_at	NP_004221.2, EAW64061.1, EAW64062.1
GeneID:1012	MRPL42	chr19	10,341,089	10,341,161	72	+	4	2_A375_shG97_dun_lncRNA_AR_1.4071, 2_A375_shG97_dun_lncRNA_AR_1.4072, 4_A375_DGR1_1.4268	31, -2163, 191, 611	up gene, upstream, downstream, downstream	1	1	1	16.5	23	15	2	2_A375_shG97_dun_lncRNA_AR_1	26	Gene MRPL42	MRPL42	mitochondrial ribosomal protein L42	NM_022722, XCT1983.2, XCT2358784.0	218726_s_at	NP_073612.2, EAW64063.1
GeneID:5313	MRPL4	chr19	10,362,840	10,370,708	8,098	+	2	2_A375_shG97_dun_lncRNA_AR_1.4072, 4_A375_DGR1_1.4274	208, 18432	up gene, downstream	0	1	0	13	21	14.5	2	2_A375_shG97_dun_lncRNA_AR_1	25	Gene MRPL4	MGC3851, MGC16397, MRPL4, L44, CGI-28	mitochondrial ribosomal protein L4	NM_019398, NM_146557, NM_146558, XCT1965.2, XCT1967931.1, XCT2358560.0	216165_s_at, 222742_s_at, 222743_s_at	NP_057540.2, NP_665697.1, NP_665698.1, EAW64053.1, EAW64054.1, EAW64055.1
GeneID:5336	ICAM1	chr19	10,381,317	10,397,291	15,974	+	7	1_A375_shG7_mrna1_lncRNA_AR_1.2034, 2_A375_shG97_dun_lncRNA_AR_1.4073, 3_A375_DGR1_1.4267, 4_A375_DGR1_1.4268, 4_A375_DGR1_1.4268, 4_A375_DGR1_1.4269, 4_A375_DGR1_1.4270, 4_A375_DGR1_1.4271	-443, 10371, -205, 10013, 20371, 23039, 23833	upstream, downstream, upstream, downstream, downstream, downstream, downstream	0	1	1	13.25	16.5	20.75	4	2_A375_shG97_dun_lncRNA_AR_1	27	Gene ICAM1	P3.58, CD54, ICAM1, BB2	intercellular adhesion molecule 1	NM_000201, XCT19827.1, XCT2358180.0	202637_s_at, 202638_s_at, 215463_s_at	NP_000192.2, EAW64066.1, EAW64067.1
GeneID:3383	ICAM4	chr19	10,397,690	10,399,198	1,508	+	5	2_A375_shG97_dun_lncRNA_AR_1.4073, 4_A375_DGR1_1.4268, 4_A375_DGR1_1.4269, 4_A375_DGR1_1.4270, 4_A375_DGR1_1.4271	4230, 2766, 4230, 6926, 7470	downstream, downstream, downstream, downstream, downstream	0	1	1	13	16.33	22.33	3	2_A375_shG97_dun_lncRNA_AR_1	27	Gene ICAM4	ICAM4, LW	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	NM_001544, NM_022377, NM_001039132, XCT19831.2, XCT1967932.1, XCT2358741.0	207194_s_at	NP_001035.1, NP_071772.1, NP_001034231.1, EAW64065.1, EAW64069.1, EAW64066.1
GeneID:7087	ICAM5	chr19	10,400,653	10,407,434	6,799	+	5	2_A375_shG97_dun_lncRNA_AR_1.4073, 3_A375_DGR1_1.4268, 4_A375_DGR1_1.4269, 4_A375_DGR1_1.4270, 4_A375_DGR1_1.4271	1233, 207, 1233, 3021, 4483	up gene, upstream, up gene, up gene	0	1	1	13	16.33	22.33	3	2_A375_shG97_dun_lncRNA_AR_1	27	Gene ICAM5	ICAM5, TLCN, TLN	intercellular adhesion molecule 5, telencephalin	NM_003259, XCT19832.2	206908_at	NP_003250.3, EAW64091.1
GeneID:1012	ZGLP1	chr19	10,415,479	10,420,203	4,724	-	2	4_A375_DGR1_1.4271, 4_A375_DGR1_1.4272	15112, -8391	downstream, upstream	0	0	1	10	15	22	2	4_A375_EGFR_1.1	23	Gene ZGLP1	ELP1, FLJ35102, FLJ35311, ZGLP1, GLP-1	zinc finger, GATA like protein 1	NM_001103167		NP_001098637.1
GeneID:1012	FDX1L	chr19	10,420,891	10,426,991	6,100	-	2	4_A375_DGR1_1.4272, 4_A375_DGR1_1.4273	997, -6813	up gene, upstream	0	0	1	12	14.5	19.5	2	4_A375_EGFR_1.1	23	Gene FDX1L	FDX1L, MGC19896, MGC34780	ferredoxin 1 like	NM_001031734	229481_at, 239720_at	NP_001029934.1
GeneID:5930	RAVER1	chr19	10,426,955	10,444,314	17,359	-	7	1_A375_shG7_mrna1_lncRNA_AR_1.2034, 2_A375_shG97_dun_lncRNA_AR_1.4076, 3_A375_DGR1_1.4272, 4_A375_DGR1_1.4273, 4_A375_DGR1_1.4274, 4_A375_DGR1_1.4275, 4_A375_DGR1_1.4276	696, 616, 17690, 10615, 4730, 595, 1445	up gene, up gene, downstream, up gene, up gene, upstream, upstream	1	1	1	13.5	16.75	20	4	2_A375_shG97_dun_lncRNA_AR_1	30	Gene RAVER1	RAVER1, KIAA1678	ribonucleoprotein, PTB-binding, 1	NM_133452	223429_at	NP_597709.2
GeneID:3383	ICAM3	chr19	10,444,452	10,450,345	5,893	-	5	1_A375_shG7_mrna1_lncRNA_AR_1.2034, 2_A375_shG97_dun_lncRNA_AR_1.4076, 3_A375_DGR1_1.4274, 4_A375_DGR1_1.4275, 4_A375_DGR1_1.4276	6729, 6840, 10781, 5485, 4385	downstream, downstream, downstream, up gene, up gene	1	1	1	15	19	30.5	2	2_A375_shG97_dun_lncRNA_AR_1	30	Gene ICAM3	ICAM3, CD50, ICAM-R, C.CAM3	intercellular adhesion molecule 3	NM_002162	226949_at	NP_002153.2
GeneID:7272	TYK2	chr19	10,461,304	10,491,348	30,044	-	4	2_A375_shG97_dun_lncRNA_AR_1.4077, 3_A375_DGR1_1.4277, 4_A375_DGR1_1.4278, 4_A375_DGR1_1.4279	-320, 19855, 18056, 144	upstream, up gene, up gene, up gene	1	1	0	10	10.67	30	3	4_A375_EGFR_1.1	23	Gene TYK2	JTK13, TYK2	tyrosine kinase 2	NM_003331, XCT1991688.1, XCT199483.3	235348_s_at	NP_003322.3, EAW64099.1, EAW64100.1
GeneID:1101	CDC37	chr19	10,501,609	10,514,271	12,662	+	4	1_A375_shG7_mrna1_lncRNA_AR_1.2035, 2_A375_shG97_dun_lncRNA_AR_1.4077, 2_A375_shG97_dun_lncRNA_AR_1.4078, 4_A375_DGR1_1.4280	85, 22763, -17, 65	up gene, downstream, upstream, up gene	1	1	1	21	24.5	31	2	2_A375_shG97_dun_lncRNA_AR_1	30	Gene CDC37	CDC37, P50CDC37	cell division cycle 37 homolog (S. cerevisiae)	NM_007065, XCT198293.2, XCT2358270.0, XCT2359501.0	209953_s_at	NP_009196.1, EAW64102.1, EAW64101.1, EAW64102.1
GeneID:1101	MRI110	chr19	10,514,154	10,514,274	120	-	3	1_A375_shG7_mrna1_lncRNA_AR_1.2035, 2_A375_shG97_dun_lncRNA_AR_1.4078, 4_A375_DGR1_1.4280	-6, -74, 8	up gene, upstream, up gene	1	1	1	26	30	19	1	2_A375_shG97_dun_lncRNA_AR_1	30	Gene MRI1161	kiaa-rev1161, MRI1161, MRI0161	mitoNRA 1161	NM_031992		
GeneID:3176	PDE4A	chr19	10,531,333	10,580,307	48,974	+	6	1_A375_shG7_mrna1_lncRNA_AR_1.2035, 2_A375_shG97_mrna1_lncRNA_AR_1.2037, 2_A375_shG97_dun_lncRNA_AR_1.4079, 2_A375_shG97_dun_lncRNA_AR_1.4080, 4_A375_DGR1_1.4281, 4_A375_DGR1_1.4282, 4_A375_DGR1_1.4283, 4_A375_DGR1_1.4284	5303, -545, 3877, -655, 3304, -709, 155, 4011	upstream, upstream, upstream, upstream, upstream, upstream, up gene, up gene	1	1	1	19.25	24.25	16	4	2_A375_shG97_dun_lncRNA_AR_1	30	Gene PDE4A	DPDE2, PDE4A, PDE4, PDE46	phosphodiesterase 4A, cAMP-specific	NM_006202, NM_001110297, NM_001111305, NM_001111306, XCT1985.2, XCT2357460.0, XCT2357751.0, XCT2357753.0, XCT2358754.0	204753_s_at, 211447_s_at, 211591_s_at, 211901_s_at	NP_006193.1, NP_001100777.1, NP_001104770.1, NP_001104779.1, EAW64104.1, EAW64106.1, EAW64105.1, EAW64107.1, EAW64103.1, EAW64109.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9817	KEAP1	19	10,596,796	10,614,054	17,258	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2838, 2_A375_pNL97_plus_lncRNA_AR..1..4081, 4_A375_EGR1..1..4285, 4_A375_EGR1..1..4286, 4_A375_EGR1..1..4287	566, 516, 11766, 870, -216	in gene, in gene, in gene, in gene, upstream	1	1	1	15.33	17	19.33	3	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene KEAP1	MGC4407, MGC10630, KIAA0132, MGC9454, INrf2, MGC20887, KEAP1, MGC1114, KLHL19	kelch-like ECH-associated protein 1	NM_012289, NM_203500, hCT19635.2, hCT1963738.0, hCT1963739.1	202417_at	NP_036421.2, NP_987096.1, EAW84110.1, EAW84111.1, EAW84112.1
GeneID:53637	S1PR5	19	10,623,418	10,628,668	5,250	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2838, 2_A375_pNL97_plus_lncRNA_AR..1..4081, 4_A375_EGR1..1..4287	15180, 15132, 14398	downstream, downstream, downstream	1	1	1	19	19.5	19.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene S1PR5	EDG8, S1P5, S1PR5, Edg-8, SPPR-2, SPPR-1	sphingosine-1-phosphate receptor 5	NM_030760, NM_001166215, hCT1644280.2, hCT1963716.1, hCT2336821.0	221417_x_at, 230464_at, 233743_x_at	NP_110387.1, NP_001159687.1, EAW84113.1, EAW84114.1, EAW84115.1
GeneID:84971	ATG4D	19	10,654,647	10,664,094	9,447	+	1	4_A375_EGR1..1..4288	13705	downstream	0	0	1	6	7	17	1	4_A375_EGR1..1	17	Gene ATG4D	APG4D, APG4-D, AUTL4, ATG4D	ATG4 autophagy related 4 homolog D (S. cerevisiae)	NM_032885, hCT19652.3, hCT1967935.1, hCT2356519.0, hCT2356520.0	226871_s_at	NP_116274.3, EAW84118.1, EAW84116.1, EAW84117.1, EAW84119.1
GeneID:100302226	MIR1238	19	10,662,798	10,662,880	82	+	1	4_A375_EGR1..1..4288	5554	downstream	0	0	1	6	7	17	1	4_A375_EGR1..1	17	Gene MIR1238	hsa-mir-1238, MIR1238, MIRN1238	microRNA 1238	NR_031603		
GeneID:65095	KRI1	19	10,663,761	10,676,702	12,941	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2839, 2_A375_pNL97_plus_lncRNA_AR..1..4082, 2_A375_pNL97_plus_lncRNA_AR..1..4083, 4_A375_EGR1..1..4288	-3170, 208, -3202, 8350	upstream, in gene, upstream, in gene	1	1	1	19.33	19	16	3	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene KRI1	FLJ12949, KRI1	KRI1 homolog (S. cerevisiae)	NM_023008, hCT19651.3, hCT1967934.1	218798_at, 227587_at	NP_075384.3, EAW84121.1, EAW84120.1
GeneID:1032	CDKN2D	19	10,677,138	10,679,655	2,517	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2839, 2_A375_pNL97_plus_lncRNA_AR..1..4082, 2_A375_pNL97_plus_lncRNA_AR..1..4083, 4_A375_EGR1..1..4288	-217, 3159, -249, 11303	upstream, downstream, upstream, downstream	1	1	1	19.33	19	16	3	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene CDKN2D	CDKN2D, p19, INK4D, p19-INK4D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	NM_079421, NM_001800, hCT19634.3, hCT2336614.0	210240_s_at, 213586_at	NP_524145.1, NP_001791.1, EAW84122.1, EAW84123.1
GeneID:10053	AP1M2	19	10,683,347	10,697,991	14,644	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2839, 2_A375_pNL97_plus_lncRNA_AR..1..4082, 2_A375_pNL97_plus_lncRNA_AR..1..4083, 4_A375_EGR1..1..4289	18119, 21495, 18087, 5692	downstream, downstream, downstream, in gene	1	1	1	23.67	21	16	3	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene AP1M2	AP1M2, MU-1B, HSMU1B, MU1B, mu2, AP1-mu2	adaptor-related protein complex 1 mu 2 subunit	NM_005498, hCT19636.3, hCT2356602.0	218261_at, 65517_at	NP_005489.2, EAW84124.1, EAW84125.1
GeneID:57153	SLC44A2	19	10,713,121	10,755,235	42,114	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2840, 1_A375_pNL7_minus_lncRNA_AR..1..2841, 2_A375_pNL97_plus_lncRNA_AR..1..4084, 4_A375_EGR1..1..4290, 4_A375_EGR1..1..4291	191, 51583, 51711, 34047, 51359	in gene, downstream, downstream, in gene, downstream	1	1	1	23.33	20	15.33	3	1_A375_pNL7_minus_lncRNA_AR..1	44	Gene SLC44A2	FLJ44586, SLC44A2, CTL2, DKFZp666A071, PP1292	solute carrier family 44, member 2	NM_001145056, NM_020428, hCT1959864.1, hCT19647.3, hCT2336761.0, hCT2336762.0	224609_at, 225175_s_at	NP_001138528.1, NP_065161.3, EAW84126.1, EAW84127.1, EAW84128.1, EAW84129.1
GeneID:147727	LOC147727	19	10,762,538	10,764,548	2,010	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2841, 2_A375_pNL97_plus_lncRNA_AR..1..4084, 4_A375_EGR1..1..4291	-158, -284, 68	upstream, upstream, in gene	1	1	1	44	36	18	1	1_A375_pNL7_minus_lncRNA_AR..1	44	Gene LOC147727		hypothetical LOC147727	NR_024333		
GeneID:3609	ILF3	19	10,764,937	10,803,095	38,158	+	10	1_A375_pNL7_minus_lncRNA_AR..1..2841, 1_A375_pNL7_minus_lncRNA_AR..1..2842, 1_A375_pNL7_minus_lncRNA_AR..1..2843, 2_A375_pNL97_plus_lncRNA_AR..1..4084, 2_A375_pNL97_plus_lncRNA_AR..1..4085, 2_A375_pNL97_plus_lncRNA_AR..1..4086, 4_A375_EGR1..1..4291, 4_A375_EGR1..1..4292, 4_A375_EGR1..1..4293, 4_A375_EGR1..1..4294	-233, 41527, 47143, -105, 41607, 47415, -457, 33367, 41527, 47223	upstream, downstream, downstream, upstream, downstream, downstream, upstream, in gene, downstream, downstream	1	1	1	24.25	23.75	21	4	1_A375_pNL7_minus_lncRNA_AR..1	44	Gene ILF3	DRBP76, NFAR2, NFAR-1, NF110, ILF3, NF90, NF-AT-90, TCP80, CBTF, TCP110, MPP4, MMP4, MPHOSPH4, DRBF, NFAR	interleukin enhancer binding factor 3, 90kDa	NM_012218, NM_004516, NM_153464, NM_017620, NM_001137673, hCT2336765.0, hCT2336766.0, hCT2336768.0, hCT2336769.0, hCT2336770.0, hCT2336771.0, hCT2336772.0	208930_s_at, 208931_s_at, 211375_s_at, 217804_s_at, 217805_at	NP_036350.2, NP_004507.2, NP_703194.1, NP_060090.2, NP_001131145.1, EAW84133.1, EAW84131.1, EAW84132.1, EAW84134.1, EAW84135.1, EAW84136.1, EAW84137.1
GeneID:81890	QTRT1	19	10,812,112	10,824,043	11,931	+	8	1_A375_pNL7_minus_lncRNA_AR..1..2842, 1_A375_pNL7_minus_lncRNA_AR..1..2843, 2_A375_pNL97_plus_lncRNA_AR..1..4085, 2_A375_pNL97_plus_lncRNA_AR..1..4086, 2_A375_pNL97_plus_lncRNA_AR..1..4087, 4_A375_EGR1..1..4293, 4_A375_EGR1..1..4294, 4_A375_EGR1..1..4295	-5648, -32, -5568, 240, 16384, -5648, 48, 11600	upstream, upstream, upstream, in gene, downstream, upstream, in gene, in gene	1	1	1	20	20.5	18.75	4	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene QTRT1	QTRT1, FP3235, TGT	queuine tRNA-ribosyltransferase 1	NM_031209, hCT2336773.0, hCT2356582.0, hCT2356583.0, hCT2356584.0, hCT2356585.0, hCT2356586.0	221270_s_at	NP_112486.1, EAW84138.1, EAW84139.1, EAW84141.1, EAW84142.1, EAW84143.1, EAW84140.1
GeneID:1785	DNM2	19	10,828,729	10,942,586	113,857	+	11	1_A375_pNL7_minus_lncRNA_AR..1..2844, 1_A375_pNL7_minus_lncRNA_AR..1..2845, 2_A375_pNL97_plus_lncRNA_AR..1..4087, 2_A375_pNL97_plus_lncRNA_AR..1..4088, 2_A375_pNL97_plus_lncRNA_AR..1..4089, 4_A375_EGR1..1..4295, 4_A375_EGR1..1..4296, 4_A375_EGR1..1..4297, 4_A375_EGR1..1..4298, 4_A375_EGR1..1..4299, 4_A375_EGR1..1..4300	91239, 118311, -233, 90951, 118087, -5017, 31655, 85197, 98079, 113431, 118087	in gene, downstream, upstream, in gene, downstream, upstream, in gene, in gene, in gene, in gene, downstream	1	1	1	14.38	15.25	17	8	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene DNM2	CMT2M, CMTDI1, CMTDIB, DYNII, DYN2, DNM2, DI-CMTB	dynamin 2	NM_001005360, NM_001005361, NM_001005362, NM_001190716, NM_004945, hCT2336774.0, hCT2336775.0, hCT2336776.0, hCT2336777.0, hCT2336778.0, hCT2336779.0, hCT2336780.0, hCT2356588.0	1555895_at, 202253_s_at, 216024_at	NP_001005360.1, NP_001005361.1, NP_004936.2, NP_001005362.1, NP_001177645.1, EAW84144.1, EAW84145.1, EAW84146.1, EAW84147.1, EAW84148.1, EAW84149.1, EAW84150.1, EAW84151.1
GeneID:693223	MIR638	19	10,829,080	10,829,179	99	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4087, 4_A375_EGR1..1..4295	-584, -5366	upstream, upstream	0	1	1	18	19.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene MIR638	MIR638, MIRN638, hsa-mir-638	microRNA 638	NR_030366		
GeneID:100507081	LOC100507081	19	10,921,015	10,922,472	1,457	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2844, 2_A375_pNL97_plus_lncRNA_AR..1..4088, 4_A375_EGR1..1..4297, 4_A375_EGR1..1..4298	-1047, -1335, -7089, 5793	upstream, upstream, upstream, downstream	1	1	1	12.67	13	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100507081		hypothetical LOC100507081	XR_111833, XR_109560, XR_115261		
GeneID:406976	MIR199A1	19	10,928,102	10,928,172	70	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2844, 2_A375_pNL97_plus_lncRNA_AR..1..4088, 4_A375_EGR1..1..4298	8204, 8492, 1364	downstream, downstream, downstream	1	1	1	16	15	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MIR199A1	MIR199A1, MIRN199A1, MIR-199-s	microRNA 199a-1	NR_029586		
GeneID:11018	TMED1	19	10,943,114	10,946,983	3,869	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2845, 2_A375_pNL97_plus_lncRNA_AR..1..4089, 4_A375_EGR1..1..4299, 4_A375_EGR1..1..4300	-57, 167, 4823, 167	upstream, in gene, downstream, in gene	1	1	1	15	18.5	20	2	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene TMED1	Il1rl1l, IL1RL1LG, TMED1, MGC1270, ST2L	transmembrane emp24 protein transport domain containing 1	NM_006858, hCT17835.2	203679_at	NP_006849.1, EAW84152.1
GeneID:255809	C19orf38	19	10,959,106	10,980,360	21,254	+	2	4_A375_EGR1..1..4301, 4_A375_EGR1..1..4302	22236, 23955	downstream, downstream	0	0	1	9	10.5	21	2	4_A375_EGR1..1	21	Gene C19orf38	C19orf38, HIDE1	chromosome 19 open reading frame 38	NM_001136482		NP_001129954.1
GeneID:10498	CARM1	19	10,982,253	11,033,448	51,195	+	10	1_A375_pNL7_minus_lncRNA_AR..1..2846, 2_A375_pNL97_plus_lncRNA_AR..1..4090, 4_A375_EGR1..1..4301, 4_A375_EGR1..1..4302, 4_A375_EGR1..1..4303, 4_A375_EGR1..1..4304, 4_A375_EGR1..1..4305, 4_A375_EGR1..1..4306, 4_A375_EGR1..1..4307, 4_A375_EGR1..1..4308	57107, 57235, -909, 808, 37491, 42147, 43939, 48947, 52275, 57779	downstream, downstream, upstream, in gene, in gene, in gene, in gene, in gene, downstream, downstream	1	1	1	11.5	13.38	19.88	8	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene CARM1	PRMT4, CARM1	coactivator-associated arginine methyltransferase 1	NM_199141, hCT21139.3, hCT2356621.0	212512_s_at	NP_954592.1, EAW84156.1, EAW84155.1
GeneID:78992	YIPF2	19	11,033,444	11,039,357	5,913	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2846, 2_A375_pNL97_plus_lncRNA_AR..1..4090, 4_A375_EGR1..1..4304, 4_A375_EGR1..1..4305, 4_A375_EGR1..1..4306, 4_A375_EGR1..1..4307, 4_A375_EGR1..1..4308	-3, -131, 14957, 13165, 8157, 4829, -875	upstream, upstream, downstream, downstream, downstream, in gene, upstream	1	1	1	13.2	15.8	20	5	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene YIPF2	YIPF2, FinGER2, MGC3262	Yip1 domain family, member 2	NM_024029, hCT1967942.1, hCT21141.3, hCT2336807.0	219075_at, 221939_at, 65086_at	NP_076934.1, EAW84157.1, EAW84158.1, EAW84159.1
GeneID:90580	C19orf52	19	11,039,424	11,040,917	1,493	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2846, 2_A375_pNL97_plus_lncRNA_AR..1..4090, 4_A375_EGR1..1..4306, 4_A375_EGR1..1..4307, 4_A375_EGR1..1..4308	-64, 64, -8224, -4896, 808	upstream, in gene, upstream, upstream, in gene	1	1	1	14.33	17	22	3	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene C19orf52	C19orf52	chromosome 19 open reading frame 52	NM_138358, hCT1648152.2	231901_at	NP_612367.1, EAW84160.1
GeneID:6597	SMARCA4	19	11,071,598	11,172,958	101,360	+	6	2_A375_pNL97_plus_lncRNA_AR..1..4091, 4_A375_EGR1..1..4309, 4_A375_EGR1..1..4310, 4_A375_EGR1..1..4311, 4_A375_EGR1..1..4312, 4_A375_EGR1..1..4313	-270, -366, 25650, 56914, 60882, 99536	upstream, upstream, in gene, in gene, in gene, in gene	0	1	1	9.8	11.8	21.8	5	4_A375_EGR1..1	25	Gene SMARCA4	SWI2, SNF2LB, hSNF2b, SMARCA4, RTPS2, SNF2L4, SNF2, BRG1, SNF2-BETA, FLJ39786, BAF190	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	NM_003072, NM_001128844, NM_001128845, NM_001128846, NM_001128847, NM_001128848, NM_001128849, hCT2285300.0, hCT2285302.0, hCT2285304.0, hCT2285305.0, hCT2285307.0, hCT2285308.0	1569073_x_at, 208793_x_at, 208794_s_at, 212520_s_at, 213719_s_at, 213720_s_at, 214360_at, 214728_x_at, 215714_s_at	NP_003063.2, NP_001122316.1, NP_001122317.1, NP_001122318.1, NP_001122319.1, NP_001122320.1, NP_001122321.1, EAW84162.1, EAW84163.1, EAW84164.1, EAW84165.1, EAW84166.1, EAW84167.1
GeneID:3949	LDLR	19	11,200,057	11,244,506	44,449	+	11	1_A375_pNL7_minus_lncRNA_AR..1..2847, 1_A375_pNL7_minus_lncRNA_AR..1..2848, 1_A375_pNL7_minus_lncRNA_AR..1..2849, 1_A375_pNL7_minus_lncRNA_AR..1..2850, 2_A375_pNL97_plus_lncRNA_AR..1..4092, 2_A375_pNL97_plus_lncRNA_AR..1..4093, 2_A375_pNL97_plus_lncRNA_AR..1..4094, 4_A375_EGR1..1..4314, 4_A375_EGR1..1..4315, 4_A375_EGR1..1..4316, 4_A375_EGR1..1..4317	-217, 2535, 49351, 53991, 1387, 49319, 54087, 487, 1255, 38716, 53895	upstream, in gene, downstream, downstream, in gene, downstream, downstream, in gene, in gene, in gene, downstream	1	1	1	17.83	18.17	15.67	6	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene LDLR	FH, LDLCQ2, LDLR, FHC	low density lipoprotein receptor	NM_000527, hCT21132.2, hCT2285311.0, hCT2285312.0, hCT2285313.0, hCT2356561.0	202067_s_at, 202068_s_at, 217005_at, 217103_at, 217173_s_at, 217183_at	NP_000518.1, EAW84171.1, EAW84168.1, EAW84169.1, EAW84170.1, EAW84172.1
GeneID:147841	SPC24	19	11,257,831	11,266,484	8,653	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2849, 1_A375_pNL7_minus_lncRNA_AR..1..2850, 2_A375_pNL97_plus_lncRNA_AR..1..4093, 2_A375_pNL97_plus_lncRNA_AR..1..4094, 2_A375_pNL97_plus_lncRNA_AR..1..4095, 4_A375_EGR1..1..4317, 4_A375_EGR1..1..4318	17076, 12436, 17108, 12340, 84, 12532, 180	downstream, downstream, downstream, downstream, in gene, downstream, in gene	1	1	1	19	27.33	19.33	3	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene SPC24	SPBC24, SPC24, FLJ90806	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	NM_182513, hCT21147.4	235572_at	NP_872319.1, EAW84174.1
GeneID:25959	KANK2	19	11,274,943	11,308,243	33,300	-	3	2_A375_pNL97_plus_lncRNA_AR..1..4095, 4_A375_EGR1..1..4318, 4_A375_EGR1..1..4319	41843, 41939, 3498	downstream, downstream, in gene	0	1	1	12	20.5	20	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene KANK2	DKFZp434N161, SIP, MGC119707, ANKRD25, MXRA3, FLJ20004, KIAA1518, KANK2	KN motif and ankyrin repeat domains 2	NM_015493, NM_001136191, hCT2287432.0, hCT2287434.0, hCT2287435.0, hCT2287436.0	218418_s_at, 221068_at	NP_056308.3, NP_001129663.1, EAW84175.1, EAW84176.1, EAW84177.1, EAW84178.1
GeneID:57572	DOCK6	19	11,309,971	11,373,157	63,186	-	3	4_A375_EGR1..1..4319, 4_A375_EGR1..1..4320, 4_A375_EGR1..1..4321	68410, 20741, 421	downstream, in gene, in gene	0	0	1	10	11	21.33	3	4_A375_EGR1..1	25	Gene DOCK6	DOCK6, ZIR1	dedicator of cytokinesis 6	NM_020812, hCT21133.2, hCT2287422.0, hCT2287424.0, hCT2287426.0, hCT2287428.0, hCT2356587.0	221793_at, 221794_at, 222003_s_at, 222004_s_at, 55583_at	NP_065863.2, EAW84179.1, EAW84180.1, EAW84181.1, EAW84182.1, EAW84183.1, EAW84184.1
GeneID:55908	LOC55908	19	11,350,295	11,352,619	2,324	+	1	4_A375_EGR1..1..4320	2121	in gene	0	0	1	11	8	19	1	4_A375_EGR1..1	19	Gene LOC55908	PRO1185, PVPA599	hepatocellular carcinoma-associated gene TD26	NM_018687, hCT1967938.1, hCT21126.4	220437_at	NP_061157.3, EAW84185.1, EAW84186.1
GeneID:26526	TSPAN16	19	11,406,824	11,437,672	30,848	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4096	-2216	upstream	0	1	0	10	22	11	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene TSPAN16	TM4-B, TM-8, TM4SF16, TSPAN16	tetraspanin 16	NM_012466, hCT21127.2	233236_at, 242179_s_at, 242180_at	NP_036598.1, EAW84187.1
GeneID:84748	LPPR2	19	11,466,062	11,476,374	10,312	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4097, 4_A375_EGR1..1..4322	14434, 17863	downstream, downstream	0	1	1	12.5	20.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene LPPR2	FLJ13055, DKFZp761E1121, PRG4	lipid phosphate phosphatase-related protein type 2	NM_022737, NM_001170635, hCT1967943.1, hCT21142.2, hCT2285328.0, hCT2356626.0	218509_at, 64899_at	NP_073574.2, NP_001164106.1, EAW84200.1, EAW84201.1, EAW84202.1, EAW84203.1
GeneID:126074	C19orf39	19	11,485,383	11,487,627	2,244	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4097, 4_A375_EGR1..1..4322	-4887, -1456	upstream, upstream	0	1	1	12.5	20.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene C19orf39	MGC149562, FLJ35119, MGC78620, C19orf39	chromosome 19 open reading frame 39	NM_175871, hCT21145.4	227352_at	NP_787067.2, EAW84204.1
GeneID:2057	EPOR	19	11,487,881	11,495,018	7,137	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4097, 4_A375_EGR1..1..4322	14522, 11093	downstream, downstream	0	1	1	12.5	20.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene EPOR	MGC138358, EPOR	erythropoietin receptor	NM_000121, NR_033663, hCT21124.4, hCT2287405.1, hCT2287406.1, hCT2356545.1	209962_at, 209963_s_at, 215054_at, 216999_at, 37986_at, 396_f_at	NP_000112.1, EAW84205.1, EAW84206.1, EAW84207.1, EAW84208.1
GeneID:57139	RGL3	19	11,504,732	11,530,018	25,286	-	2	4_A375_EGR1..1..4323, 4_A375_EGR1..1..4324	226, -3198	in gene, upstream	0	0	1	8.5	12	19	2	4_A375_EGR1..1	20	Gene RGL3	RGL3, MGC126805, FLJ32585, FLJ44275, FLJ00153, MGC138163	ral guanine nucleotide dissociation stimulator-like 3	NM_001035223, NM_001161616, hCT21137.2, hCT2287400.0, hCT2287401.0, hCT2356617.0	1556354_s_at, 1556355_x_at, 226877_at	NP_001030300.2, NP_001155088.1, EAW84209.1, EAW84210.1, EAW84211.1, EAW84212.1
GeneID:115948	CCDC151	19	11,531,272	11,545,980	14,708	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2851, 2_A375_pNL97_plus_lncRNA_AR..1..4098, 4_A375_EGR1..1..4323, 4_A375_EGR1..1..4324	-452, -484, 16188, 12764	upstream, upstream, downstream, in gene	1	1	1	11.67	15	18	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CCDC151	CCDC151, FLJ31801, MGC20983	coiled-coil domain containing 151	NM_145045, hCT21140.2, hCT2356622.0	230807_at	NP_659482.3, EAW84213.1, EAW84214.1
GeneID:5589	PRKCSH	19	11,546,269	11,561,783	15,514	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2851, 2_A375_pNL97_plus_lncRNA_AR..1..4098, 4_A375_EGR1..1..4325, 4_A375_EGR1..1..4326, 4_A375_EGR1..1..4327	163, 195, 10883, 13059, 13891	in gene, in gene, in gene, in gene, in gene	1	1	1	12	11.75	19.5	4	4_A375_EGR1..1	24	Gene PRKCSH	AGE-R2, PLD1, PRKCSH, PCLD, G19P1	protein kinase C substrate 80K-H	NM_002743, NM_001001329, hCT21131.3, hCT2285338.0, hCT2285339.0, hCT2285340.0, hCT2356578.0	200707_at, 214080_x_at	NP_002734.2, NP_001001329.1, EAW84215.1, EAW84217.1, EAW84218.1, EAW84219.1, EAW84216.1
GeneID:1995	ELAVL3	19	11,562,143	11,591,803	29,660	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2852, 2_A375_pNL97_plus_lncRNA_AR..1..4099, 4_A375_EGR1..1..4325, 4_A375_EGR1..1..4326, 4_A375_EGR1..1..4327, 4_A375_EGR1..1..4328, 4_A375_EGR1..1..4329, 4_A375_EGR1..1..4330	-1541, -1797, 34851, 32475, 31643, 699, -1173, -5925	upstream, upstream, downstream, downstream, downstream, in gene, upstream, upstream	1	1	1	11.33	10.5	20.67	6	4_A375_EGR1..1	24	Gene ELAVL3	DKFZp547J036, PLE21, MGC20653, HUC, HUCL, ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	NM_001420, NM_032281, hCT21130.2, hCT2287392.0	1555602_a_at, 206338_at, 227612_at	NP_001411.2, NP_115657.2, EAW84220.1, EAW84221.1
GeneID:115950	ZNF653	19	11,594,242	11,616,738	22,496	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2852, 2_A375_pNL97_plus_lncRNA_AR..1..4099, 4_A375_EGR1..1..4328, 4_A375_EGR1..1..4329, 4_A375_EGR1..1..4330, 4_A375_EGR1..1..4331	23394, 23138, 25634, 23762, 19010, -446	downstream, downstream, downstream, downstream, in gene, upstream	1	1	1	11.75	12.75	19.75	4	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ZNF653	ZNF653, E430039K05Rik, ZIP67	zinc finger protein 653	NM_138783	228684_at, 244085_at	NP_620138.2
GeneID:51295	ECSIT	19	11,616,744	11,639,987	23,243	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2853, 2_A375_pNL97_plus_lncRNA_AR..1..4100, 4_A375_EGR1..1..4331, 4_A375_EGR1..1..4332	179, 200, 22803, 211	in gene, in gene, in gene, in gene	1	1	1	16.5	15	19.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene ECSIT	ECSIT, SITPEC	ECSIT homolog (Drosophila)	NM_001142464, NM_001142465, NR_024551, NM_016581	218225_at	NP_001135936.1, NP_001135937.1, NP_057665.2
GeneID:1264	CNN1	19	11,649,579	11,661,138	11,559	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2853, 2_A375_pNL97_plus_lncRNA_AR..1..4100, 2_A375_pNL97_plus_lncRNA_AR..1..4101, 4_A375_EGR1..1..4332, 4_A375_EGR1..1..4333	-9771, -9792, 20629, -9803, 15381	upstream, upstream, downstream, upstream, downstream	1	1	1	15	16.67	21.67	3	4_A375_EGR1..1	25	Gene CNN1	Sm-Calp, SMCC, CNN1	calponin 1, basic, smooth muscle	NM_001299, hCT21129.2, hCT2356575.0	203951_at	NP_001290.2, EAW84229.1, EAW84228.1
GeneID:84337	ELOF1	19	11,663,858	11,670,051	6,193	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4101, 4_A375_EGR1..1..4333	-157, 5091	upstream, in gene	0	1	1	10.5	17	21.5	2	4_A375_EGR1..1	25	Gene ELOF1	ELOF1, ELF1	elongation factor 1 homolog (S. cerevisiae)	NM_032377, hCT1967945.1, hCT1967946.1	225156_at	NP_115753.1, EAW84230.1, EAW84231.1
GeneID:54	ACP5	19	11,685,475	11,689,801	4,326	-	1	4_A375_EGR1..1..4334	521	in gene	0	0	1	14	16	17	1	4_A375_EGR1..1	17	Gene ACP5	MGC117378, ACP5, TRAP	acid phosphatase 5, tartrate resistant	NM_001611, NM_001111034, NM_001111035, NM_001111036, hCT1952538.1, hCT21128.3, hCT2287372.0	204638_at	NP_001602.1, NP_001104504.1, NP_001104505.1, NP_001104506.1, EAW84232.1, EAW84234.1, EAW84233.1

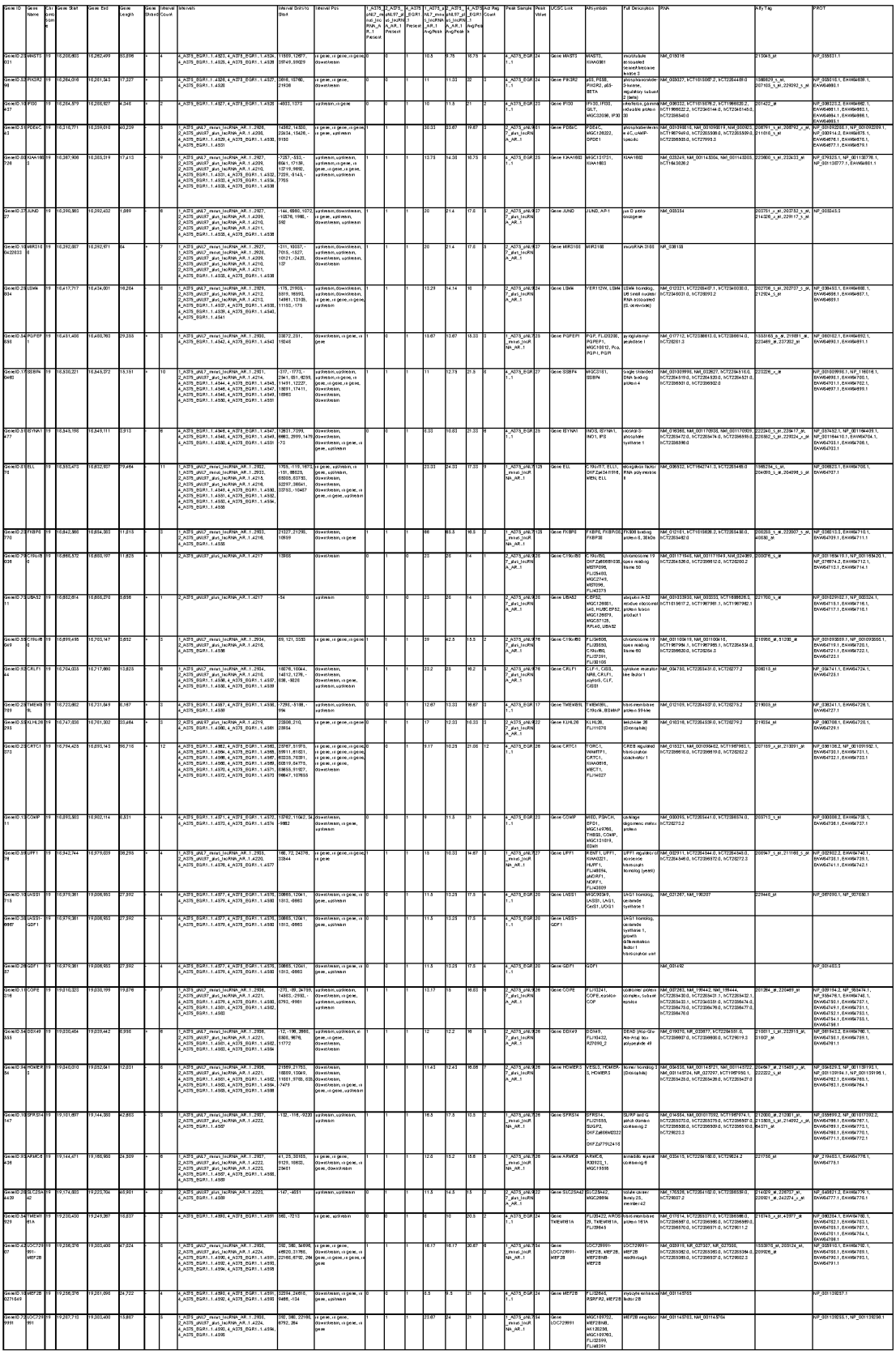
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:199692	ZNF627	19	11,706,235	11,729,974	21,739	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2854	149	in gene	1	0	0	25	21	19	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene ZNF627	FLJ90365, ZNF627	zinc finger protein 627	NM_145295, hCT21134.2, hCT2356589.0	1563204_at, 224492_s_at	NP_660338.1, EAW84237.1, EAW84236.1
GeneID:128066	ZNF441	19	11,877,815	11,894,893	17,078	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2855, 2_A375_pNL97_plus_lncRNA_AR..1..4103	41, 265	in gene, in gene	1	1	0	25	22	8	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene ZNF441	FLJ38637, ZNF441	zinc finger protein 441	NM_152355, hCT2341143.0	1553192_at, 1553193_at	NP_689568.2, EAW84240.1
GeneID:126069	ZNF491	19	11,909,391	11,919,306	9,915	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2856, 2_A375_pNL97_plus_lncRNA_AR..1..4104	220, -815	in gene, upstream	1	1	0	12.5	13	8	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ZNF491	MGC126841, FLJ34791, ZNF491, MGC126839	zinc finger protein 491	NM_152356, hCT19105.4	1562211_a_at	NP_689569.2, EAW84242.1
GeneID:100507095	LOC100507095	19	11,959,561	11,961,845	2,284	+	1	4_A375_EGR1..1..4335	183	in gene	0	0	1	9	15	17	1	4_A375_EGR1..1	17	Gene LOC100507095		hypothetical LOC100507095	XR_109561		
GeneID:7620	ZNF69	19	11,998,670	12,025,366	26,696	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2857, 2_A375_pNL97_plus_lncRNA_AR..1..4105	-206, 146	upstream, in gene	1	1	0	19	18	13	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene ZNF69	Cos5, MGC59928, ZNF69	zinc finger protein 69	NM_021915, hCT2341077.0, hCT2341078.0, hCT23476.3		NP_068734.1, EAW84249.1, EAW84248.1, EAW84250.1
GeneID:90592	ZNF700	19	12,035,900	12,061,576	25,676	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4106	66	in gene	0	1	0	19	29	15	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene ZNF700	ZNF700, DKFZp434I1610	zinc finger protein 700	NM_144566, hCT2285266.0	223590_at	NP_653167.1, EAW84251.1
GeneID:284390	ZNF763	19	12,075,869	12,091,214	15,345	+	1	4_A375_EGR1..1..4336	22787	downstream	0	0	1	10	10	19	1	4_A375_EGR1..1	19	Gene ZNF763	ZNF, ZNF763, ZNF440L	zinc finger protein 763	NM_001012753, hCT2285291.1	1558754_at, 1558755_x_at	NP_001012771.1, EAW84252.1
GeneID:100507111	LOC100507111	19	12,098,483	12,157,091	58,608	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2858, 2_A375_pNL97_plus_lncRNA_AR..1..4107, 4_A375_EGR1..1..4336, 4_A375_EGR1..1..4337, 4_A375_EGR1..1..4338	65229, 65229, 173, 47757, 65133	downstream, downstream, in gene, in gene, downstream	1	1	1	13	13.67	18.67	3	4_A375_EGR1..1	21	Gene LOC100507111		hypothetical LOC100507111	XR_111831, XR_111830, XR_109563, XR_109562, XR_115234, XR_115233		
GeneID:163059	ZNF433	19	12,125,532	12,146,525	20,993	-	1	4_A375_EGR1..1..4337	265	in gene	0	0	1	9	13	21	1	4_A375_EGR1..1	21	Gene ZNF433	ZNF433, FLJ40981	zinc finger protein 433	NM_001080411, hCT172988.3, hCT2341057.0, hCT2341058.0, hCT2341059.0		NP_001073880.1, EAW84255.1, EAW84253.1, EAW84254.1, EAW84256.1
GeneID:729747	ZNF878	19	12,154,620	12,167,127	12,507	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2858, 2_A375_pNL97_plus_lncRNA_AR..1..4107, 2_A375_pNL97_plus_lncRNA_AR..1..4108, 4_A375_EGR1..1..4337, 4_A375_EGR1..1..4338	3415, 3415, -8329, 20887, 3511	in gene, in gene, upstream, downstream, in gene	1	1	1	14	15.67	16.67	3	4_A375_EGR1..1	21	Gene ZNF878	ZNF878	zinc finger protein 878	NM_001080404		NP_001073873.1
GeneID:284391	ZNF844	19	12,175,546	12,188,626	13,080	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4108	-90	upstream	0	1	0	13	16	13	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ZNF844	MGC150553, ZNF844, FLJ14959	zinc finger protein 844	NM_001136501	1558537_x_at	NP_001129973.1
GeneID:7568	ZNF20	19	12,242,803	12,251,140	8,337	-	1	4_A375_EGR1..1..4339	356	in gene	0	0	1	9	11	18	1	4_A375_EGR1..1	18	Gene ZNF20	FLJ39241, ZNF20, KOX13	zinc finger protein 20	NM_021143, hCT1971829.1	213916_at, 244406_at	NP_066966.2, EAW84260.1
GeneID:90589	ZNF625	19	12,255,705	12,267,529	11,824	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4109, 4_A375_EGR1..1..4339	-55, 16745	upstream, downstream	0	1	1	11.5	14	15	2	4_A375_EGR1..1	18	Gene ZNF625	ZNF625	zinc finger protein 625	NM_145233, hCT2287358.1, hCT2344101.0, hCT2356472.0	1552769_at	NP_660276.1, EAW84263.1, EAW84261.1, EAW84262.1
GeneID:7695	ZNF136	19	12,273,872	12,300,064	26,192	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4109	-6266	upstream	0	1	0	14	17	12	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ZNF136	ZNF136, pHZ-20	zinc finger protein 136	NM_003437	206240_s_at	NP_003428.1
GeneID:147837	ZNF563	19	12,428,291	12,444,534	16,243	-	1	4_A375_EGR1..1..4340	436	in gene	0	0	1	13	10	18	1	4_A375_EGR1..1	18	Gene ZNF563	FLJ34797, ZNF563	zinc finger protein 563	NM_145276, hCT1971830.2, hCT2356521.0	1552770_s_at	NP_660319.1, EAW84268.1, EAW84269.1
GeneID:79973	ZNF442	19	12,460,185	12,476,475	16,290	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2859, 2_A375_pNL97_plus_lncRNA_AR..1..4110	-373, -293	upstream, upstream	1	1	0	18	20	12	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ZNF442	FLJ14356, ZNF442	zinc finger protein 442	NM_030824, hCT1827651.1	208081_s_at	NP_110451.1, EAW84270.1
GeneID:90576	ZNF799	19	12,500,826	12,512,086	11,260	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2860	173	in gene	1	0	0	17	14	14	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ZNF799	MGC71805, ZNF799, ZNF842, HIT-40	zinc finger protein 799	NM_001080821		NP_001074290.1
GeneID:10224	ZNF443	19	12,540,520	12,551,926	11,406	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2861	129	in gene	1	0	0	18	12	8	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ZNF443	ZK1, ZNF443	zinc finger protein 443	NM_005815, hCT2286993.0	205928_at	NP_005806.2, EAW84273.1
GeneID:163050	ZNF564	19	12,636,184	12,662,356	26,172	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4111	-140	upstream	0	1	0	23	32	16	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene ZNF564	FLJ38281, MGC26914, ZNF564	zinc finger protein 564	NM_144976	1553247_a_at, 1553957_at, 1562267_s_at	NP_659413.1
GeneID:57474	ZNF490	19	12,686,920	12,721,623	34,703	-	1	4_A375_EGR1..1..4342	-233	upstream	0	0	1	22	14	23	1	4_A375_EGR1..1	23	Gene ZNF490	KIAA1198, ZNF490	zinc finger protein 490	NM_020714, hCT1827649.3	231988_x_at	NP_065765.1, EAW84277.1
GeneID:163049	ZNF791	19	12,721,732	12,740,676	18,944	+	1	4_A375_EGR1..1..4342	124	in gene	0	0	1	22	14	23	1	4_A375_EGR1..1	23	Gene ZNF791	ZNF791, MGC126179, FLJ90396, MGC126180	zinc finger protein 791	NM_153358, hCT172991.3	1553703_at, 1553704_x_at	NP_699189.2, EAW84276.1
GeneID:4125	MAN2B1	19	12,757,322	12,777,591	20,269	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2862, 2_A375_pNL97_plus_lncRNA_AR..1..4112, 4_A375_EGR1..1..4343, 4_A375_EGR1..1..4344	-2673, -2633, 151, -3209	upstream, upstream, in gene, upstream	1	1	1	15.5	16	15	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MAN2B1	MAN2B1, LAMAN, MANB	mannosidase, alpha, class 2B, member 1	NM_000528, NM_001173498, hCT2286978.1, hCT2286980.1, hCT2286985.1	209166_s_at	NP_000519.2, NP_001166969.1, EAW84279.1, EAW84280.1, EAW84281.1
GeneID:84292	WDR83	19	12,777,618	12,786,646	9,028	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2862, 2_A375_pNL97_plus_lncRNA_AR..1..4112, 4_A375_EGR1..1..4343, 4_A375_EGR1..1..4344	2846, 2806, -178, 3162	in gene, in gene, upstream, in gene	1	1	1	15.5	16	15	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene WDR83	WDR83, MORG1, MGC4238	WD repeat domain 83	NM_032332, NM_001099737, NR_029375, hCT172996.3, hCT2284794.1, hCT2344866.0	224434_s_at	NP_115708.1, NP_001093207.1, EAW84282.1, EAW84283.1, EAW84284.1
GeneID:51398	C19orf56	19	12,776,881	12,780,465	1,584	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2862, 2_A375_pNL97_plus_lncRNA_AR..1..4112, 4_A375_EGR1..1..4343, 4_A375_EGR1..1..4344	1, 241, 3025, -335	in gene, in gene, downstream, upstream	1	1	1	15.5	16	15	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene C19orf56	C19orf56, PTD008	chromosome 19 open reading frame 56	NM_016145, hCT172973.2, hCT2356598.0	217780_at	NP_057229.1, EAW84285.1, EAW84286.1
GeneID:1725	DHPS	19	12,786,534	12,792,677	6,143	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2862, 2_A375_pNL97_plus_lncRNA_AR..1..4112, 4_A375_EGR1..1..4343, 4_A375_EGR1..1..4344	12213, 12453, 15237, 11677	downstream, downstream, downstream, downstream	1	1	1	15.5	16	15	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene DHPS	MIG13, DHPS	deoxyhypusine synthase	NM_013406, NM_013407, NM_001930, hCT172974.2, hCT172975.2, hCT1967981.1, hCT2286982.0, hCT2286984.0, hCT2286971.0, hCT2286974.0, hCT2286976.0	202802_at, 207831_x_at, 211558_s_at	NP_037538.1, NP_037539.1, NP_001921.1, EAW84287.1, EAW84291.1, EAW84293.1, EAW84288.1, EAW84289.1, EAW84290.1, EAW84292.1, EAW84294.1
GeneID:100507265	LOC100507265	19	12,789,617	12,800,101	10,484	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2862, 2_A375_pNL97_plus_lncRNA_AR..1..4112, 2_A375_pNL97_plus_lncRNA_AR..1..4113, 4_A375_EGR1..1..4344, 4_A375_EGR1..1..4345	-9153, -9393, 17631, -8817, 17615	upstream, upstream, downstream, upstream, downstream	1	1	1	19	21.5	22	2	4_A375_EGR1..1	30	Gene LOC100507265		hypothetical LOC100507265	XR_109566		
GeneID:646044	LOC646044	19	12,798,812	12,799,236	424	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4113, 4_A375_EGR1..1..4345	8436, 8420	downstream, downstream	0	1	1	20	22	30	1	4_A375_EGR1..1	30	Gene LOC646044		guanine nucleotide binding protein (G protein), gamma 12-like	XM_001131322		XP_001131322.3
GeneID:84261	FBXW9	19	12,799,730	12,807,455	7,725	-	3	2_A375_pNL97_plus_lncRNA_AR..1..4113, 4_A375_EGR1..1..4345, 4_A375_EGR1..1..4346	207, 223, -5089	in gene, in gene, upstream	0	1	1	14	16	26.5	2	4_A375_EGR1..1	30	Gene FBXW9	FBXW9, MGC10870, Fbw9	F-box and WD repeat domain containing 9	NM_032301, hCT172994.2, hCT1966804.1, hCT2286957.0	223419_at	NP_115677.2, EAW84295.1, EAW84296.1, EAW84297.1
GeneID:30000	TNPO2	19	12,810,006	12,834,810	24,802	-	4	2_A375_pNL97_plus_lncRNA_AR..1..4113, 2_A375_pNL97_plus_lncRNA_AR..1..4114, 4_A375_EGR1..1..4345, 4_A375_EGR1..1..4346	27562, 1274, 27578, 22286	downstream, in gene, downstream, in gene	0	1	1	17.33	19.33	21	3	4_A375_EGR1..1	30	Gene TNPO2	IPO3, TNPO2, FLJ12155, KPNB2B, TRN2	transportin 2	NM_013433, NM_001136195, NM_001136196, hCT1686323.3, hCT172976.3, hCT2286954.0	210585_s_at, 215844_at, 221506_s_at, 221507_at, 226428_at	NP_038461.2, NP_001129667.1, NP_001129668.1, EAW84299.1, EAW84300.1, EAW84301.1
GeneID:26810	SNORD41	19	12,817,263	12,817,332	69	-	3	2_A375_pNL97_plus_lncRNA_AR..1..4113, 4_A375_EGR1..1..4345, 4_A375_EGR1..1..4346	10084, 10100, 4788	downstream, downstream, downstream	0	1	1	14	16	26.5	2	4_A375_EGR1..1	30	Gene SNORD41	U41, SNORD41, RNU41	small nucleolar RNA, C/D box 41	NR_002751		
GeneID:79002	C19orf43	19	12,841,454	12,845,529	4,075	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2863, 2_A375_pNL97_plus_lncRNA_AR..1..4114, 2_A375_pNL97_plus_lncRNA_AR..1..4115	-2855, 11993, -2823	upstream, downstream, upstream	1	1	0	20	30	11	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene C19orf43	ISAP18, C19orf43, MGC2803	chromosome 19 open reading frame 43	NM_024038, hCT172995.1	223003_at, 230213_at	NP_076943.1, EAW84302.1
GeneID:439	ASNA1	19	12,848,306	12,859,137	10,831	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2863, 2_A375_pNL97_plus_lncRNA_AR..1..4115, 4_A375_EGR1..1..4347	76, 46, 9790	in gene, in gene, in gene	1	1	1	10.5	21.5	14	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene ASNA1	MGC3821, ASNA1, ARSA-I, GET3, TRC40, ARSA1	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	NM_004317, hCT172977.3	202024_at	NP_004308.2, EAW84303.1
GeneID:54831	BEST2	19	12,863,407	12,869,272	5,865	+	1	4_A375_EGR1..1..4347	-5311	upstream	0	0	1	5	9	16	1	4_A375_EGR1..1	16	Gene BEST2	FLJ20132, VMD2L1, BEST2	bestrophin 2	NM_017682, hCT2284799.0	207432_at	NP_060152.2, EAW84304.1
GeneID:29911	HOOK2	19	12,873,817	12,886,434	12,617	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2864, 1_A375_pNL7_minus_lncRNA_AR..1..2865, 2_A375_pNL97_plus_lncRNA_AR..1..4116, 2_A375_pNL97_plus_lncRNA_AR..1..4117, 2_A375_pNL97_plus_lncRNA_AR..1..4118, 4_A375_EGR1..1..4348	-94, -6910, -126, -2750, -6878, 546	upstream, upstream, upstream, upstream, upstream, in gene	1	1	1	34.67	39.33	16.33	3	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene HOOK2	FLJ26218, HOOK2, HK2	hook homolog 2 (Drosophila)	NM_013312, NM_001100176, hCT172980.2, hCT1960364.1	218780_at	NP_037444.2, NP_001093646.1, EAW84305.1, EAW84306.1
GeneID:3726	JUNB	19	12,902,310	12,904,125	1,815	+	12	1_A375_pNL7_minus_lncRNA_AR..1..2865, 1_A375_pNL7_minus_lncRNA_AR..1..2866, 1_A375_pNL7_minus_lncRNA_AR..1..2867, 1_A375_pNL7_minus_lncRNA_AR..1..2868, 1_A375_pNL7_minus_lncRNA_AR..1..2869, 2_A375_pNL97_plus_lncRNA_AR..1..4118, 2_A375_pNL97_plus_lncRNA_AR..1..4119, 2_A375_pNL97_plus_lncRNA_AR..1..4120, 2_A375_pNL97_plus_lncRNA_AR..1..4121, 2_A375_pNL97_plus_lncRNA_AR..1..4122, 4_A375_EGR1..1..4349, 4_A375_EGR1..1..4350	-6986, -70, 1016, 2410, 10394, -8996, -1362, 709, 2154, 10410, -70, 10650	upstream, upstream, in gene, downstream, downstream, upstream, upstream, in gene, downstream, downstream, upstream, downstream	1	1	1	29.5	35	22.5	4	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene JUNB	AP-1, JUNB	jun B proto-oncogene	NM_002229, hCT172978.3	201473_at	NP_002220.1, EAW84307.1
GeneID:7001	PRDX2	19	12,907,634	12,912,694	5,060	-	10	1_A375_pNL7_minus_lncRNA_AR..1..2866, 1_A375_pNL7_minus_lncRNA_AR..1..2867, 1_A375_pNL7_minus_lncRNA_AR..1..2868, 1_A375_pNL7_minus_lncRNA_AR..1..2869, 2_A375_pNL97_plus_lncRNA_AR..1..4119, 2_A375_pNL97_plus_lncRNA_AR..1..4120, 2_A375_pNL97_plus_lncRNA_AR..1..4121, 2_A375_pNL97_plus_lncRNA_AR..1..4122, 4_A375_EGR1..1..4349, 4_A375_EGR1..1..4350	10454, 9366, 7974, -10, 11766, 9675, 8230, -26, 10454, -266	downstream, downstream, downstream, upstream, downstream, downstream, downstream, upstream, downstream, upstream	1	1	1	26.33	28.67	25.33	3	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene PRDX2	TSA, TDPX1, NKEFB, PRP, PRX2, PRXII, TPX1, PRDX2, MGC4104	peroxiredoxin 2	NM_005809, NM_181738, hCT172985.2, hCT2286931.0, hCT2356490.0, hCT2356491.0, hCT2356492.0	201006_at, 211658_at, 215067_x_at, 39729_at	NP_005800.3, NP_859428.1, EAW84309.1, EAW84310.1, EAW84311.1, EAW84312.1, EAW84308.1
GeneID:10535	RNASEH2A	19	12,917,428	12,924,462	7,034	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2869, 2_A375_pNL97_plus_lncRNA_AR..1..4122, 4_A375_EGR1..1..4350	-4724, -4708, -4466	upstream, upstream, upstream	1	1	1	26	33	32	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene RNASEH2A	RNASEH2A, AGS4, RNASEHI, JUNB, RNHIA, RNHL	ribonuclease H2, subunit A	NM_006397, hCT172986.2	203022_at	NP_006388.2, EAW84313.1
GeneID:83546	RTBDN	19	12,936,296	12,946,230	9,934	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2870, 2_A375_pNL97_plus_lncRNA_AR..1..4123, 2_A375_pNL97_plus_lncRNA_AR..1..4124, 4_A375_EGR1..1..4351, 4_A375_EGR1..1..4352	2870, 2756, -1066, 950, -42	in gene, in gene, upstream, in gene, upstream	1	1	1	21.25	30.25	14.5	4	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene RTBDN	FLJ38353, RTBDN	retbindin	NM_031429, NM_001080997, hCT173003.1, hCT2356579.0, hCT2356580.0	223719_s_at	NP_113617.1, NP_001074466.1, EAW84314.1, EAW84315.1, EAW84316.1
GeneID:100507305	LOC100507305	19	12,936,525	12,943,940	7,415	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2870, 2_A375_pNL97_plus_lncRNA_AR..1..4123, 2_A375_pNL97_plus_lncRNA_AR..1..4124, 4_A375_EGR1..1..4351, 4_A375_EGR1..1..4352	6635, 6947, 10771, 6755, 9747	in gene, in gene, downstream, downstream, downstream	1	1	1	21.25	30.25	14.5	4	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene LOC100507305		hypothetical LOC100507305	XR_111826, XR_111825, XR_109566, XR_109567, XR_115239, XR_115238		
GeneID:22983	MAST1	19	12,949,259	12,985,766	36,507	+	9	1_A375_pNL7_minus_lncRNA_AR..1..2870, 1_A375_pNL7_minus_lncRNA_AR..1..2871, 2_A375_pNL97_plus_lncRNA_AR..1..4123, 2_A375_pNL97_plus_lncRNA_AR..1..4124, 2_A375_pNL97_plus_lncRNA_AR..1..4125, 4_A375_EGR1..1..4351, 4_A375_EGR1..1..4352, 4_A375_EGR1..1..4353, 4_A375_EGR1..1..4354	-5699, 9301, -5787, -1963, 42933, -3979, -2987, 29173, 42229	upstream, in gene, upstream, upstream, downstream, upstream, upstream, in gene, downstream	1	1	1	18.29	23.86	16.86	7	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene MAST1	KIAA0973, SAST170, SAST, MAST1	microtubule associated serine/threonine kinase 1	NM_014975, hCT173001.3, hCT1962983.1, hCT2284813.0	217231_s_at	NP_055790.1, EAW84317.1, EAW84318.1, EAW84319.1
GeneID:1777	DNASE2	19	12,986,025	12,992,335	6,310	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2872, 2_A375_pNL97_plus_lncRNA_AR..1..4125, 2_A375_pNL97_plus_lncRNA_AR..1..4126, 4_A375_EGR1..1..4353, 4_A375_EGR1..1..4354, 4_A375_EGR1..1..4355	-9521, 143, -9489, 13903, 847, -4497	upstream, in gene, upstream, downstream, in gene, upstream	1	1	1	26.25	29.5	20	4	1_A375_pNL7_minus_lncRNA_AR..1	63	Gene DNASE2	DNL2, DNL, DNASE2, DNASE2A	deoxyribonuclease II, lysosomal	NM_001375, hCT172983.2, hCT2286918.0, hCT2286922.0	209831_x_at, 214992_s_at	NP_001366.1, EAW84320.1, EAW84321.1, EAW84322.1
GeneID:10661	KLF1	19	12,995,236	12,998,017	2,781	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2872, 2_A375_pNL97_plus_lncRNA_AR..1..4125, 2_A375_pNL97_plus_lncRNA_AR..1..4126, 4_A375_EGR1..1..4354, 4_A375_EGR1..1..4355	-3839, 5625, -3807, 6529, 1165	upstream, downstream, upstream, downstream, in gene	1	1	1	35.33	36.67	18.33	3	1_A375_pNL7_minus_lncRNA_AR..1	63	Gene KLF1	INLU, HBFQTL6, KLF1, EKLF	Kruppel-like factor 1 (erythroid)	NM_006563, hCT172992.1	210504_at	NP_006554.1, EAW84323.1
GeneID:2639	GCDH	19	13,001,974	13,010,783	8,809	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2872, 2_A375_pNL97_plus_lncRNA_AR..1..4125, 2_A375_pNL97_plus_lncRNA_AR..1..4126, 4_A375_EGR1..1..4355	-118, -9782, -150, -5142	upstream, upstream, upstream, upstream	1	1	1	35.33	36.67	18.33	3	1_A375_pNL7_minus_lncRNA_AR..1	63	Gene GCDH	ACAD5, GCDH, GCD	glutaryl-CoA dehydrogenase	NM_000159, NM_013976, hCT172979.2, hCT2284814.0, hCT2284816.0	203500_at, 208389_s_at	NP_000150.1, NP_039663.1, EAW84324.1, EAW84325.1, EAW84326.1
GeneID:256126	SYCE2	19	13,009,894	13,030,086	20,192	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2872, 2_A375_pNL97_plus_lncRNA_AR..1..4126	26230, 26262	downstream, downstream	1	1	0	63	61	14	1	1_A375_pNL7_minus_lncRNA_AR..1	63	Gene SYCE2	CESC1, SYCE2	synaptonemal complex central element protein 2	NM_001105578	237304_at	NP_001099048.1
GeneID:2193	FARSA	19	13,033,284	13,044,558	11,274	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2873, 2_A375_pNL97_plus_lncRNA_AR..1..4127, 4_A375_EGR1..1..4356	-4976, -4530, -4682	upstream, upstream, upstream	1	1	1	34	33	27	1	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene FARSA	FRSA, FARSLA, PheHA, CML33, FARSA, FARSL	phenylalanyl-tRNA synthetase, alpha subunit	NM_004461, hCT172982.2, hCT2286910.0	202159_at, 216602_s_at	NP_004452.1, EAW84329.1, EAW84328.1
GeneID:811	CALR	19	13,049,414	13,055,304	5,890	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2873, 2_A375_pNL97_plus_lncRNA_AR..1..4127, 4_A375_EGR1..1..4356	122, -326, 26	in gene, upstream, in gene	1	1	1	34	33	27	1	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene CALR	FLJ26680, SSA, CRT, cC1qR, RO, CALR	calreticulin	NM_004343, hCT172984.2, hCT2284731.0, hCT2356489.0	200935_at, 212952_at, 212953_x_at, 214315_x_at, 214316_x_at	NP_004334.1, EAW84330.1, EAW84331.1, EAW84332.1
GeneID:100507328	LOC100507328	19	13,054,904	13,078,205	23,301	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2873, 1_A375_pNL7_minus_lncRNA_AR..1..2874, 2_A375_pNL97_plus_lncRNA_AR..1..4127, 2_A375_pNL97_plus_lncRNA_AR..1..4128, 4_A375_EGR1..1..4356	28869, 10173, 29117, 10205, 28765	downstream, in gene, downstream, in gene, downstream	1	1	1	26	26.5	21	2	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene LOC100507328		hypothetical LOC100507328	XR_109569, XR_109570		
GeneID:5886	RAD23A	19	13,056,654	13,064,455	7,801	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2873, 1_A375_pNL7_minus_lncRNA_AR..1..2874, 2_A375_pNL97_plus_lncRNA_AR..1..4127, 2_A375_pNL97_plus_lncRNA_AR..1..4128, 4_A375_EGR1..1..4356	-7118, 11376, -7566, 11346, -7214	upstream, downstream, upstream, downstream, upstream	1	1	1	26	26.5	21	2	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene RAD23A	RAD23A, HHR23A, MGC111083	RAD23 homolog A (S. cerevisiae)	NM_005053, hCT172981.3, hCT2284735.0	201039_s_at, 201046_s_at	NP_005044.1, EAW84334.1, EAW84333.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_pfd27_mut_lncRNA_AR_1 Present	2_A375_pfd27_wt_lncRNA_AR_1 Present	4_A375_EGFR1_AR_1 Present	1_A375_pfd27_mut_lncRNA_AR_1 Avg Peak	2_A375_pfd27_wt_lncRNA_AR_1 Avg Peak	4_A375_EGFR1_AR_1 Avg Peak	Add Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
GeneID:39400	GADD45GIP1	19	13,084,972	13,086,050	1078	-	2	1_A375_pfd27_mut_lncRNA_AR_1..2074, 2_A375_pfd27_plus_lncRNA_AR_1..4128	16, 50	+/- gene, +/- gene	1	1	0	18	20	18	1	2_A375_pfd27_plus_lncRNA_AR_1	620	Gene GADD45GIP1	MGC4957, PLNP, 1_PRO8, CRIP1, Plnp1, MGC4193, GADD45GIP1, CHBP2	growth arrest and DNA-damage-inducible, gamma interacting protein 1	NM_052550, XCT172956.2	212691_s_at	NP_443932.2, EAW64338.1
GeneID:1918	DAND5	19	13,860,422	13,865,997	5,576	+	12	1_A375_pfd27_mut_lncRNA_AR_1..2076, 2_A375_pfd27_plus_lncRNA_AR_1..4129	19858, 15934	downstream, downstream	1	1	0	19	21	17	1	2_A375_pfd27_plus_lncRNA_AR_1	621	Gene DAND5	C20R2, CR2MG, MGC129593, DAND5, CXTP1R2, SP1, C20L2, COCO, DANTE, CRL2	DAN domain family, member 5	NM_152654, XCT2294740.1, XCT2294931.0	1582772_s_at	NP_689997.1, EAW64337.1, EAW64338.1
GeneID:4761	NFIX	19	13,106,964	13,209,810	103,026	+	14	1_A375_pfd27_mut_lncRNA_AR_1..2075, 1_A375_pfd27_mut_lncRNA_AR_1..2076, 2_A375_pfd27_plus_lncRNA_AR_1..4129, 2_A375_pfd27_plus_lncRNA_AR_1..4130, 4_A375_EGFR1..4375 + 4_A375_EGFR1..4376, 4_A375_EGFR1..4376 + 4_A375_EGFR1..4377, 4_A375_EGFR1..4380, 4_A375_EGFR1..4382, 4_A375_EGFR1..4384, 4_A375_EGFR1..4386, 4_A375_EGFR1..4388	-10264, -586, -19643, 352, 14685, 60246, 72388, 74726, 83845, 88182, 89844, 160912, 170522, 193804	upstream, upstream, upstream, +/- gene, +/- gene, +/- gene, +/- gene, +/- gene, +/- gene, downstream, downstream, downstream	1	1	1	10.92	11.62	10.54	13	4_A375_EGFR1_AR_1	28	Gene NFIX	NFIX, NF1A	nuclear factor IX (CCAAT-binding transcription factor)	NM_002501, XCT1609022, XCT2254761.0	209307_s_at, 227403_at, 225276_at, 229264_at	NP_002492.2, EAW64340.1, EAW64338.1, EAW64339.1, EAW64341.1, EAW64342.1
GeneID:4961	LYL1	19	13,209,947	13,213,081	3,134	-	3	1_A375_EGFR1..4382, 4_A375_EGFR1..4396, 4_A375_EGFR1..4396, 4_A375_EGFR1..4398	11153, 3165, 65, 1827, -6565	downstream, +/- gene, +/- gene, upstream, upstream	0	0	1	8.4	9	19.6	5	4_A375_EGFR1_AR_1	28	Gene LYL1	bHLHb18, LYL1	lymphoblastic leukemia derived sequence 1	NM_005563, XCT169253	210044_s_at	NP_005574.2, EAW64344.1
GeneID:8317	TRMT1	19	13,219,774	13,227,993	11,849	-	6	1_A375_pfd27_mut_lncRNA_AR_1..2077, 2_A375_pfd27_plus_lncRNA_AR_1..4131, 4_A375_EGFR1..4386 + 4_A375_EGFR1..4386, 4_A375_EGFR1..4386 + 4_A375_EGFR1..4386, 4_A375_EGFR1..4386 + 4_A375_EGFR1..4386, 4_A375_EGFR1..4386 + 4_A375_EGFR1..4386, 4_A375_EGFR1..4386 + 4_A375_EGFR1..4386, 4_A375_EGFR1..4386 + 4_A375_EGFR1..4386	-69, 66, 17087, 19947, 19975, 7019, 255, -5397	upstream, +/- gene, downstream, downstream, +/- gene, +/- gene, upstream	1	1	1	11	13	19.67	6	2_A375_pfd27_plus_lncRNA_AR_1	635	Gene TRMT1	FLJ20244, TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	NM_001142594, NM_001139035, NM_017722, XCT19807.2, XCT1983912.2, XCT1983992.2, XCT2266998.1, XCT2266991.1, XCT2356503.0, XCT2356504.0	220701_s_at, 219483_x_at, 219484_at	NP_001132628.1, NP_001129807.1, NP_060182.1, EAW64347.1, EAW64349.1, EAW64350.1, EAW64345.1, EAW64346.1, EAW64351.1
GeneID:1161	NACC1	19	13,229,109	13,251,589	22,480	+	7	1_A375_pfd27_mut_lncRNA_AR_1..2077, 1_A375_pfd27_mut_lncRNA_AR_1..2078, 2_A375_pfd27_plus_lncRNA_AR_1..4131, 2_A375_pfd27_plus_lncRNA_AR_1..4132, 4_A375_EGFR1..4387 + 4_A375_EGFR1..4388, 4_A375_EGFR1..4389	-1481, 32107, -31979, -3855, -1781, 5551	upstream, downstream, downstream, downstream, upstream, upstream, +/- gene	1	1	1	23.73	24.23	20.8	4	1_A375_pfd27_plus_lncRNA_AR_1	351	Gene NACC1	BTBD14B, NACC1, MGC12551, NACC, FLJ27053, BEAG6	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing	NM_052578, XCT1983512.1, XCT2284778.0, XCT2284779.0	227681_at, 235947_x_at	NP_443105.1, EAW64352.1, EAW64353.1, EAW64354.1
GeneID:6813	STX10	19	13,255,224	13,260,967	5,743	-	7	1_A375_pfd27_mut_lncRNA_AR_1..2078, 1_A375_pfd27_mut_lncRNA_AR_1..2079, 2_A375_pfd27_plus_lncRNA_AR_1..4132, 2_A375_pfd27_plus_lncRNA_AR_1..4133, 4_A375_EGFR1..4389 + 4_A375_EGFR1..4389, 4_A375_EGFR1..4389 + 4_A375_EGFR1..4389	-229, -1613, -101, -1797, -3086, -2917, -4165	upstream, upstream, upstream, upstream, upstream, upstream	1	1	1	51	47	29	1	1_A375_pfd27_plus_lncRNA_AR_1	351	Gene STX10	STX10, SYN10, fry-like, fry10	syntaxin 10	NM_003765, XCT169203.2, XCT2357034.0	212629_at	NP_003737.1, EAW64356.1, EAW64357.1
GeneID:9915	IER2	19	13,261,202	13,265,722	4,520	+	10	1_A375_pfd27_mut_lncRNA_AR_1..2078, 1_A375_pfd27_mut_lncRNA_AR_1..2079, 1_A375_pfd27_mut_lncRNA_AR_1..2080, 2_A375_pfd27_plus_lncRNA_AR_1..4132, 2_A375_pfd27_plus_lncRNA_AR_1..4133, 2_A375_pfd27_plus_lncRNA_AR_1..4134, 2_A375_pfd27_plus_lncRNA_AR_1..4135, 4_A375_EGFR1..4389 + 4_A375_EGFR1..4389, 4_A375_EGFR1..4389 + 4_A375_EGFR1..4389	-66, 1516, 14110, -19, 1602, 13074, 14286, 1774, 2622, 3570	upstream, +/- gene, downstream, upstream, +/- gene, downstream, downstream, +/- gene, +/- gene, +/- gene	1	1	1	26	29.33	30	3	1_A375_pfd27_mut_lncRNA_AR_1	351	Gene IER2	MGC13268, IER191, IER2, MGC111472	immediate early response 2	NM_004907, XCT178833.1, XCT2284788.1, XCT2341413.0	202081_at	NP_004898.2, EAW64358.1, EAW64359.1, EAW64360.1
GeneID:7750	CACNA1I	19	13,317,256	13,617,274	300,018	-	9	1_A375_pfd27_mut_lncRNA_AR_1..2081, 1_A375_pfd27_mut_lncRNA_AR_1..2082, 1_A375_pfd27_mut_lncRNA_AR_1..2083, 1_A375_pfd27_mut_lncRNA_AR_1..2084, 1_A375_pfd27_mut_lncRNA_AR_1..2085, 1_A375_pfd27_mut_lncRNA_AR_1..2086, 2_A375_pfd27_plus_lncRNA_AR_1..4137, 2_A375_pfd27_plus_lncRNA_AR_1..4138, 2_A375_pfd27_plus_lncRNA_AR_1..4139, 4_A375_EGFR1..4375 + 4_A375_EGFR1..4375	245114, 84442, 43032, 248090, 84276, 44426, 43002, 259250, 256194	+/- gene, +/- gene, +/- gene, +/- gene, +/- gene, +/- gene, +/- gene	1	1	1	23.2	27.2	12	5	2_A375_pfd27_plus_lncRNA_AR_1	355	Gene CACNA1I	CAV2.1, HPCA, SCAR, FHM, APCA, MHP, BI2, MHP1, CACN1I4, CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	NM_001127221, NM_001127222, NM_000068, NM_001174850, NM_023035, XCT19068.2, XCT1983851.1, XCT2357067.0, XCT2357010.0, XCT2357012.0, XCT2357013.0	1558944_at, 1558948_s_at, 206399_s_at, 214103_at	NP_001120850.1, NP_001120994.1, NP_000059.2, NP_001158151.1, NP_075461.2, EAW64388.1, EAW64389.1, EAW64390.1, EAW64393.1, EAW64394.1, EAW64398.1
GeneID:5706	CCDC130	19	13,556,765	13,574,106	15,355	+	3	2_A375_pfd27_plus_lncRNA_AR_1..4141, 2_A375_pfd27_plus_lncRNA_AR_1..4142, 2_A375_pfd27_plus_lncRNA_AR_1..4377	-149, 16319, -199	upstream, downstream, upstream	0	1	1	17	21.5	17	2	2_A375_pfd27_plus_lncRNA_AR_1	622	Gene CCDC130	CCDC130, MGC10471	coiled-coil domain containing 130	NM_033518, XCT19874.2, XCT2358577.0	208894_s_at	NP_110445.1, EAW64367.1, EAW64368.1
GeneID:8441	MRI1	19	13,573,337	13,583,098	9,759	+	3	1_A375_pfd27_mut_lncRNA_AR_1..2084, 2_A375_pfd27_plus_lncRNA_AR_1..4142, 2_A375_pfd27_plus_lncRNA_AR_1..4143	5803, -383, 9547	downstream, +/- gene, downstream	1	1	0	27.5	29	15.5	2	2_A375_pfd27_plus_lncRNA_AR_1	627	Gene MRI1	Fp119e, MGC32307, MTAP, MRI1	methylthioadenosine phosphorylase interactive homolog (S. cerevisiae)	NM_031317.1, NM_032353, XCT19870.3, XCT2358549.0, XCT2358550.0	223770_s_at, 223077_at	NP_001029897.1, NP_115891.1, EAW64369.1, EAW64370.1, EAW64371.1
GeneID:2667	C19orf57	19	13,855,237	13,859,907	4,670	+	3	1_A375_pfd27_mut_lncRNA_AR_1..2084, 1_A375_pfd27_mut_lncRNA_AR_1..2085, 2_A375_pfd27_plus_lncRNA_AR_1..4142, 2_A375_pfd27_plus_lncRNA_AR_1..4143	-108, -10185, -79	upstream, upstream, upstream	1	1	0	27.5	29	15.5	2	2_A375_pfd27_plus_lncRNA_AR_1	627	Gene C19orf57	C19orf57, LYSO10, HSPC022	chromosome 19 open reading frame 57	NM_014347, XCT19866.2	217926_at	NP_036768.1, EAW64372.1
GeneID:6852	ZSWIM4	19	13,936,274	13,943,044	99,770	+	8	1_A375_pfd27_mut_lncRNA_AR_1..2085, 1_A375_pfd27_mut_lncRNA_AR_1..2086, 1_A375_pfd27_mut_lncRNA_AR_1..2087, 1_A375_pfd27_mut_lncRNA_AR_1..2088, 1_A375_pfd27_mut_lncRNA_AR_1..2089, 4_A375_EGFR1..4379 + 4_A375_EGFR1..4380, 4_A375_EGFR1..4380 + 4_A375_EGFR1..4381, 4_A375_EGFR1..4382	41518, 40214, 116, 40777, 22270, 34126, 33630, 40870, 44155	downstream, downstream, downstream, upstream, downstream, +/- gene, +/- gene, downstream, downstream, downstream	1	1	1	16.63	16.63	22.17	6	4_A375_EGFR1_AR_1	30	Gene ZSWIM4	ZSWIM4		NM_020910, XCT19882.2	231919_at	NP_065650.2, EAW64373.1
GeneID:2536	LOC284454	19	13,945,930	13,947,103	1,173	-	6	1_A375_pfd27_mut_lncRNA_AR_1..2085, 1_A375_pfd27_mut_lncRNA_AR_1..2086, 1_A375_pfd27_mut_lncRNA_AR_1..2087, 1_A375_pfd27_mut_lncRNA_AR_1..2088, 1_A375_pfd27_mut_lncRNA_AR_1..2089, 4_A375_EGFR1..4380 + 4_A375_EGFR1..4380, 4_A375_EGFR1..4380 + 4_A375_EGFR1..4382	-589, -4555, 18549, -3946, 5963, 2399, 159, 5329	upstream, upstream, upstream, downstream, downstream, +/- gene, upstream	1	1	1	20.6	18.2	24.2	5	4_A375_EGFR1_AR_1	30	Gene LOC284454		hypothetical LOC284454	NM_206513	1553647_a_at, 235597_at	
GeneID:4263	MIR24-2	19	13,947,101	13,947,173	72	-	9	1_A375_pfd27_mut_lncRNA_AR_1..2085, 1_A375_pfd27_mut_lncRNA_AR_1..2086, 1_A375_pfd27_mut_lncRNA_AR_1..2087, 1_A375_pfd27_mut_lncRNA_AR_1..2088, 1_A375_pfd27_mut_lncRNA_AR_1..2089, 4_A375_EGFR1..4380 + 4_A375_EGFR1..4380, 4_A375_EGFR1..4380 + 4_A375_EGFR1..4382	-549, -4315, 10779, -3576, 10957, 5973, 2489, 229, -2259	upstream, upstream, upstream, downstream, downstream, upstream	1	1	1	20.6	18.2	24.2	5	4_A375_EGFR1_AR_1	30	Gene MIR24-2	miR-N27-2, MIR24-2, miR-24-2, MIR1DN-2	microRNA 24-2	NR_029497		
GeneID:4263	MIR27A	19	13,947,284	13,947,351	67	-	9	1_A375_pfd27_mut_lncRNA_AR_1..2085, 1_A375_pfd27_mut_lncRNA_AR_1..2086, 1_A375_pfd27_mut_lncRNA_AR_1..2087, 1_A375_pfd27_mut_lncRNA_AR_1..2088, 1_A375_pfd27_mut_lncRNA_AR_1..2089, 4_A375_EGFR1..4380 + 4_A375_EGFR1..4380, 4_A375_EGFR1..4380 + 4_A375_EGFR1..4382	-481, -4137, 10621, -3735, 10629, 6131, 2827, 367, -2101	upstream, upstream, upstream, upstream, downstream, downstream, upstream	1	1	1	20.6	18.2	24.2	5	4_A375_EGFR1_AR_1	30	Gene MIR27A	MIRN27A, MIR27A, MIR27	microRNA 27a	NR_029501		
GeneID:4263	MIR23A	19	13,947,401	13,947,473	72	-	9	1_A375_pfd27_mut_lncRNA_AR_1..2085, 1_A375_pfd27_mut_lncRNA_AR_1..2086, 1_A375_pfd27_mut_lncRNA_AR_1..2087, 1_A375_pfd27_mut_lncRNA_AR_1..2088, 1_A375_pfd27_mut_lncRNA_AR_1..2089, 4_A375_EGFR1..4380 + 4_A375_EGFR1..4380, 4_A375_EGFR1..4380 + 4_A375_EGFR1..4382	-379, -4015, 10479, -3576, 10257, 6273, 2769, 629, -2099	upstream, upstream, upstream, upstream, downstream, downstream, upstream	1	1	1	20.6	18.2	24.2	5	4_A375_EGFR1_AR_1	30	Gene MIR23A	MIRN23A, hsa-mir-23a, MIR23A, miRNA23A	microRNA 23a	NR_029493		
GeneID:4263	MIR181C	19	13,955,813	13,955,922	109	-	1	2_A375_pfd27_plus_lncRNA_AR_1..4148	5767	downstream	0	1	0	21	19	14	1	2_A375_pfd27_plus_lncRNA_AR_1	619	Gene MIR181C	MIR181C, MIRN181C, mir-181c	microRNA 181c	NR_029613		
GeneID:4264	MIR181D	19	13,955,809	13,955,925	116	+	1	2_A375_pfd27_plus_lncRNA_AR_1..4148	5351	downstream	0	1	0	21	19	14	1	2_A375_pfd27_plus_lncRNA_AR_1	619	Gene MIR181D	MIR181D, MIR181D	microRNA 181d	NR_032179		
GeneID:3407	NANOS3	19	13,967,690	13,991,871	24,181	-	2	1_A375_pfd27_mut_lncRNA_AR_1..2148, 4_A375_EGFR1..4394	23302, 16023	+/- gene, downstream	0	1	1	14.5	14	18	2	2_A375_pfd27_plus_lncRNA_AR_1	619	Gene NANOS3	MGC126114, NOS3, NANOS3, DKFZp761D1611	nanos homolog 3 (Drosophila)	NM_001009622	244031_at	NP_001009232.1
GeneID:7961	C19orf87	19	13,993,165	14,016,909	23,741	-	8	1_A375_pfd27_mut_lncRNA_AR_1..2083, 1_A375_pfd27_mut_lncRNA_AR_1..2084, 1_A375_pfd27_mut_lncRNA_AR_1..2085, 1_A375_pfd27_mut_lncRNA_AR_1..2086, 1_A375_pfd27_mut_lncRNA_AR_1..2087, 1_A375_pfd27_mut_lncRNA_AR_1..2088, 4_A375_EGFR1..4394 + 4_A375_EGFR1..4395	2969, 25629, 2753, -55, 16936, -707	+/- gene, downstream, +/- gene, upstream, +/- gene, upstream	1	1	1	19.5	16.29	13	4	4_A375_EGFR1_AR_1	631	Gene C19orf87	MGC112721, C19orf87, MGC149720	chromosome 19 open reading frame 87	NM_024322, XCT1983038.2, XCT1983096.2, XCT2363453.0, XCT2364950.0	206901_at	NP_077299.2, EAW64377.1, EAW64378.1, EAW64379.1
GeneID:5462	CCDC21A	19	14,016,956	14,041,993	24,737	+	7	1_A375_pfd27_mut_lncRNA_AR_1..2083, 1_A375_pfd27_mut_lncRNA_AR_1..2143, 2_A375_pfd27_plus_lncRNA_AR_1..4150, 2_A375_pfd27_plus_lncRNA_AR_1..4358, 4_A375_EGFR1..4394 + 4_A375_EGFR1..4395	-2706, -2700, -12, 695, 12945, 23516, 23588	upstream, upstream, +/- gene, +/- gene, downstream, downstream	1	1	1	14.6	12.6	15.2	5	2_A375_pfd27_plus_lncRNA_AR_1	631	Gene CCDC21A	MRT3, FREUD-1, FLJ41165, FLJ30241, Freud-1/Ubi1, CCDC21A	coiled-coil and C2 domain containing 21A	NM_017721, XCT19899.4	230803_s_at, 223552_at, 223337_at, 33994_at	NP_060191.2, EAW64380.1
GeneID:7798	PODNL1	19	14,042,000	14,064,304	22,304	-	3	4_A375_EGFR1..4387, 4_A375_EGFR1..4388, 4_A375_EGFR1..4389	21932, 17982, 7124	+/- gene, +/- gene, upstream	0	0	1	11.67	7.33	10	3	4_A375_EGFR1_AR_1	622	Gene PODNL1	FLJ22447, SLRR5B, PODNL1	podocan-like 1	NM_024629, NM_001145254, NM_001145255, XCT19907.2, XCT2364655.0, XCT2364660.0	220411_x_at	NP_079161.3, NP_001139726.1, NP_001139727.1, EAW64381.1, EAW64382.1, EAW64383.1
GeneID:5594	DCAF15	19	14,065,319	14,072,256	6,937	+	5	4_A375_EGFR1..4393, 4_A375_EGFR1..4396, 4_A375_EGFR1..4397	6809, 13259, 14659	+/- gene, downstream, downstream	0	0	1	10	7.33	21.33	3	4_A375_EGFR1_AR_1	622	Gene DCAF15	MGC29661, C19orf72, DCAF15	DDB1 and CUL4 associated factor 15	NM_139343, XCT19873.2	221563_s_at, 221561_at, 222312_at, 91852_at	NP_612382.2, EAW64386.1
GeneID:8878	RFX1	19	14,072,343	14,117,104	44,762	+	8	1_A375_pfd27_mut_lncRNA_AR_1..2080, 1_A375_pfd27_mut_lncRNA_AR_1..2081, 1_A375_pfd27_mut_lncRNA_AR_1..2082, 1_A375_pfd27_mut_lncRNA_AR_1..2083, 1_A375_pfd27_mut_lncRNA_AR_1..2084, 1_A375_pfd27_mut_lncRNA_AR_1..2085, 1_A375_pfd27_mut_lncRNA_AR_1..2086, 4_A375_EGFR1..4394 + 4_A375_EGFR1..4395	-492, -149, 14806, 42626, 39726, 19982, 46, -722	upstream, upstream, downstream, +/- gene, +/- gene, +/- gene, upstream	1	1	1	12.6	13.2	25.8	5	2_A375_pfd27_plus_lncRNA_AR_1	636	Gene RFX1	EFC, RFX, RFX1	regulatory factor X, 1 (influences HLA class II expression)	NM_002918, XCT19863.4	208231_at, 228798_at	NP_002919.4, EAW64387.1
GeneID:6119	RLN3	19	14,139,017	14,141,763	2,746	+	2	4_A375_EGFR1..4393, 4_A375_EGFR1..4394	87, 3703	+/- gene, downstream	0	0	1	12	10	22	2	4_A375_EGFR1_AR_1	630	Gene RLN3	RIL, RIN3A, RIN3, RLN3, ant2	relaxin 3	NM_016568, XCT2363671.0	1553403_at	NP_542148.1, EAW64388.1
GeneID:5445	L2TRA	19	14,142,262	14,164,328	21,764	+	5	4_A375_EGFR1..4393, 4_A375_EGFR1..4396, 4_A375_EGFR1..4397	5156, 455, 27656	upstream, +/- gene, downstream	0	0	1	11	10.67	19.67	3	4_A375_EGFR1_AR_1	630	Gene L2TRA	MS11, TCCR, pum01, IL27RA, IL27R, CRL1	interleukin 27 receptor, alpha	NM_004843, XCT19864.2, XCT2363672.0	203236_at, 217702_at, 223262_at	NP_004834.1, EAW64389.1, EAW64390.1
GeneID:3429	PALM2	19	14,164,179	14,169,971	5,792	+	1	4_A375_EGFR1..4397	91	+/- gene	0	0	1	9	12	15	1	4_A375_EGFR1_AR_1	15	Gene PALM2	PALM2		NM_031430.2	231018_at	NP_001135890.1
GeneID:1123	LOC132390	19	14,165,621	14,165,674	2,053	+	4	2_A375_pfd27_plus_lncRNA_AR_1..4152, 4_A375_EGFR1..4396, 4_A375_EGFR1..4399, 4_A375_EGFR1..4400	1555, 525, 1491, 6863	downstream, upstream, +/- gene, downstream	0	1	1	14.67	16	19	3	2_A375_pfd27_plus_lncRNA_AR_1	623	Gene LOC132390		hypothetical LOC132390	NM_029352	1558612_at	
GeneID:8437	C19orf87	19	14,191,952	14,196,439	4,487	-	4	2_A375_pfd27_plus_lncRNA_AR_1..4152, 4_A375_EGFR1..4396, 4_A375_EGFR1..4399, 4_A375_EGFR1..4400	2979, 13142, 11127, 3738	+/- gene, downstream, downstream, +/- gene	0	1	1	14.67	16	19	3	2_A375_pfd27_plus_lncRNA_AR_1	623	Gene C19orf87	C19orf87	chromosome 19 open reading frame 87	NM_138352, XCT19872.2	1558612_at	NM_024473.1
GeneID:3760	SNAI3	19	14,199,329	14,201,252	2,003	-	2	2_A375_pfd27_plus_lncRNA_AR_1..4152, 4_A375_EGFR1..4400	5852, 6926	downstream, downstream	0	1	1	23	23	21	1	2_A375_pfd27_plus_lncRNA_AR_1	623	Gene SNAI3	SNAI3		NM_138352, XCT19872.2	229850_at	NP_612391.1, EAW64396.1
GeneID:8396	PRKACA	19	14,202,900	14,226,959	24,059	-	5	2_A375_pfd27_plus_lncRNA_AR_1..4152, 2_A375_pfd27_plus_lncRNA_AR_1..4153, 4_A375_EGFR1..4400, 4_A375_EGFR1..4402	23899, -1041, 23659, 10111, 2901	downstream, upstream, downstream, +/- gene, upstream	0	1	1	12.25	12.25	18	4	2_A375_pfd27_plus_lncRNA_AR_1	623	Gene PRKACA	PKACA, MGC102851, PRKACA, MGC45988	protein kinase, cAMP-dependent, catalytic, alpha	NM_002730, NM_207518, XCT19862.3, XCT2364548.0, XCT2364549.0, XCT2364554.0	216224_s_at	NP_002721.1, NP_997401.1, EAW64397.1, EAW64398.1, EAW64399.1, EAW64400.1
GeneID:5523	ASF1B	19	14,230,321	14,247,440	17,119	-	6	1_A375_pfd27_mut_lncRNA_AR_1..2081, 1_A375_pfd27_mut_lncRNA_AR_1..2082, 1_A375_pfd27_mut_lncRNA_AR_1..2083, 1_A375_pfd27_mut_lncRNA_AR_1..2084, 1_A375_pfd27_mut_lncRNA_AR_1..2085, 1_A375_pfd27_mut_lncRNA_AR_1..2086, 4_A375_EGFR1..4402, 4_A375_EGFR1..4404	98, 17560, -580, 18772, 208, -660	+/- gene, downstream, upstream, +/- gene, +/- gene, upstream	1	1	1	13.67	14.67	16.33	5	2_A375_pfd27_plus_lncRNA_AR_1	622	Gene ASF1B	ASF1B, FLJ10804, CIA-1	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	NM_018154, XCT19871.2, XCT2364543.0	218119_at	NP_060624.1, EAW64400.1, EAW64401.1, EAW64402.1
GeneID:1007	LOC100507372	19	14,247,930	14,279,914	31,984	+	6	1_A375_pfd27_mut_lncRNA_AR_1..2081, 1_A375_pfd27_mut_lncRNA_AR_1..2082, 1_A375_pfd27_mut_lncRNA_AR_1..2083, 1_A375_pfd27_mut_lncRNA_AR_1..2084, 1_A375_pfd27_mut_lncRNA_AR_1..2085, 1_A375_pfd27_mut_lncRNA_AR_1..2086, 4_A375_EGFR1..4402, 4_A375_EGFR1..4404	638, 30, -765, 145, 13172, 23124, 23716, 27796	upstream, upstream, upstream, +/- gene, +/- gene, +/- gene, +/- gene, gene	1	1	1	9.6	14.2	20.4	5	4_A375_EGFR1_AR_1	24	Gene LOC100507372		hypothetical LOC100507372	XR_925574, XR_102673		

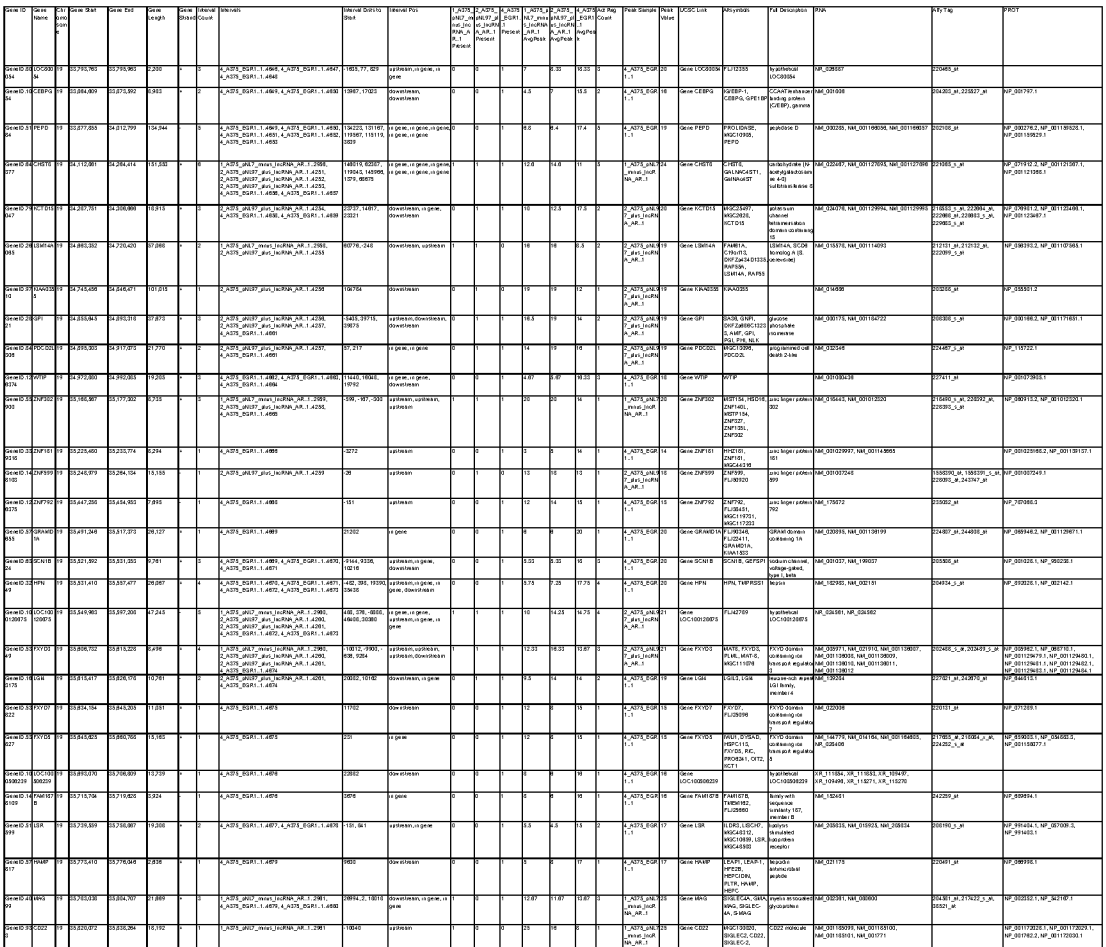
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:22859	LPHN1	19	14,258,549	14,316,997	58,448	-	9	1_A375_pNL7_minus_lncRNA_AR..1..2892, 2_A375_pNL97_plus_lncRNA_AR..1.4154, 2_A375_pNL97_plus_lncRNA_AR..1.4155, 4_A375_EGR1..1.4404, 4_A375_EGR1..1.4405, 4_A375_EGR1..1.4406, 4_A375_EGR1..1.4407, 4_A375_EGR1..1.4408, 4_A375_EGR1..1.4409	-1275, 66997, -1275, 66869, 55845, 45893, 43301, 41221, 22554	upstream, downstream, upstream, downstream, in gene, in gene, in gene, in gene, in gene	1	1	1	13.86	19.29	19.43	7	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene LPHN1	LEC2, LPHN1, CL1, CIRL1	latrophilin 1	NM_014921, NM_001008701, hCT18661.2, hCT2284835.0, hCT2284836.0, hCT2284838.0, hCT2356542.0, hCT2356543.0	203488_at, 219145_at, 47560_at	NP_055736.2, NP_001008701.1, EAW84404.1, EAW84406.1, EAW84408.1, EAW84409.1, EAW84405.1, EAW84407.1
GeneID:976	CD97	19	14,492,213	14,519,535	27,322	+	7	2_A375_pNL97_plus_lncRNA_AR..1.4156, 4_A375_EGR1..1.4410, 4_A375_EGR1..1.4411, 4_A375_EGR1..1.4412, 4_A375_EGR1..1.4413, 4_A375_EGR1..1.4414, 4_A375_EGR1..1.4415	523, -5525, 139, 12235, 24555, 25259, 29099	in gene, upstream, in gene, in gene, in gene, in gene, downstream	0	1	1	10	12	18.33	6	4_A375_EGR1..1	23	Gene CD97	TM7LN1, CD97	CD97 molecule	NM_078481, NM_001784, NM_001025160, hCT2283584.1, hCT2283587.0	202910_s_at	NP_510966.1, NP_001775.2, NP_001020331.1, EAW84412.1, EAW84413.1
GeneID:100507396	LOC100507396	19	14,495,031	14,495,672	641	+	4	2_A375_pNL97_plus_lncRNA_AR..1.4156, 4_A375_EGR1..1.4410, 4_A375_EGR1..1.4411, 4_A375_EGR1..1.4412	-2295, -8343, -2679, 9417	upstream, upstream, upstream, downstream	0	1	1	9.33	10.67	16.33	3	4_A375_EGR1..1	18	Gene LOC100507396		hypothetical protein LOC100507396	XM_003118768		XP_003118836.1
GeneID:10212	DDX39	19	14,519,631	14,530,171	10,540	-	4	4_A375_EGR1..1.4413, 4_A375_EGR1..1.4414, 4_A375_EGR1..1.4415, 4_A375_EGR1..1.4416	13403, 12699, 8859, 59	downstream, downstream, in gene, in gene	0	0	1	11.5	13.5	20.5	4	4_A375_EGR1..1	23	Gene DDX39	DDXL, MGC18203, BAT1L, URH49, DDX39A, BAT1, DDX39, MGC8417	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	NM_005804, hCT1815031.1, hCT1966929.1, hCT1966930.1, hCT2356609.0, hCT2356610.0	201584_s_at	NP_005795.2, EAW84418.1, EAW84414.1, EAW84415.1, EAW84416.1, EAW84417.1
GeneID:5585	PKN1	19	14,544,166	14,582,679	38,513	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2893, 4_A375_EGR1..1.4417, 4_A375_EGR1..1.4418, 4_A375_EGR1..1.4419, 4_A375_EGR1..1.4420	938, 506, 1178, 30725, 46970	in gene, in gene, in gene, in gene, downstream	1	0	1	15	12.67	21.33	3	4_A375_EGR1..1	27	Gene PKN1	PKN1, PKN-ALPHA, PAK-1, MGC46204, PRKCL1, PRK1, DBK, PKN, PAK1	protein kinase N1	NM_002741, NM_213560, hCT18657.3, hCT1962999.1, hCT2356527.0	202161_at	NP_002732.3, NP_998725.1, EAW84419.1, EAW84420.1, EAW84421.1
GeneID:5731	PTGER1	19	14,583,278	14,586,174	2,896	-	2	4_A375_EGR1..1.4419, 4_A375_EGR1..1.4420	11283, -4962	downstream, upstream	0	0	1	11.5	10	21	2	4_A375_EGR1..1	27	Gene PTGER1	EP1, PTGER1	prostaglandin E receptor 1 (subtype EP1), 42kDa	NM_000955, hCT18655.2	207650_x_at, 214391_x_at, 231201_at	NP_000946.2, EAW84422.1
GeneID:10755	GIPC1	19	14,588,571	14,606,944	18,373	-	1	4_A375_EGR1..1.4420	15808	in gene	0	0	1	16	10	27	1	4_A375_EGR1..1	27	Gene GIPC1	NIP, Hs.6454, GIPC1, SYNECTIIN, MGC15889, SYNECTIN, GIPC, TIP-2, RGS19IP1, GLUT1CBP, IIP-1, MGC3774, C19orf3, SEMCAP	GIPC PDZ domain containing family, member 1	NM_202470, NM_202494, NM_202468, NM_202469, NM_005716, NM_202467, hCT18654.3, hCT1967924.1, hCT1967925.1, hCT2284826.0, hCT2356522.0, hCT2356523.0, hCT2356524.0, hCT2356525.0, hCT2356526.0	207525_s_at	NP_974199.1, NP_974223.1, NP_005707.1, NP_974197.1, NP_974198.1, NP_974196.1, EAW84423.1, EAW84424.1, EAW84425.1, EAW84426.1, EAW84427.1, EAW84428.1, EAW84429.1, EAW84430.1, EAW84431.1
GeneID:100130932	LOC100130932	19	14,599,758	14,600,691	933	+	1	4_A375_EGR1..1.4420	-8622	upstream	0	0	1	16	10	27	1	4_A375_EGR1..1	27	Gene LOC100130932		small nuclear ribonucleoprotein G-like protein	NM_001146693		NP_001140165.1
GeneID:3337	DNAJB1	19	14,625,582	14,629,201	3,619	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2894, 2_A375_pNL97_plus_lncRNA_AR..1.4157, 4_A375_EGR1..1.4421	-1743, -1775, 81	upstream, upstream, in gene	1	1	1	22.5	20	21	2	4_A375_EGR1..1	32	Gene DNAJB1	HSPF1, Hsp40, DNAJB1, RSPH16B, Sis1, Hdj1	DnaJ (Hsp40) homolog, subfamily B, member 1	NM_006145, hCT1815018.2, hCT2284822.0	200664_s_at, 200666_s_at	NP_006136.1, EAW84432.1, EAW84433.1
GeneID:693224	MIR639	19	14,640,355	14,640,452	97	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2894, 2_A375_pNL97_plus_lncRNA_AR..1.4157, 4_A375_EGR1..1.4422	-9411, -9379, 77	upstream, upstream, in gene	1	1	1	21.5	21.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene MIR639	MIRN639, hsa-mir-639, MIR639	microRNA 639	NR_030369		
GeneID:9524	TECR	19	14,640,382	14,676,792	36,410	+	10	1_A375_pNL7_minus_lncRNA_AR..1..2894, 1_A375_pNL7_minus_lncRNA_AR..1..2895, 2_A375_pNL97_plus_lncRNA_AR..1.4157, 2_A375_pNL97_plus_lncRNA_AR..1.4158, 4_A375_EGR1..1.4422, 4_A375_EGR1..1.4423, 4_A375_EGR1..1.4424, 4_A375_EGR1..1.4425, 4_A375_EGR1..1.4426, 4_A375_EGR1..1.4427	-9438, 42496, -9406, 42562, 50, 31810, 33293, 33911, 35842, 42306	upstream, downstream, upstream, downstream, in gene, in gene, in gene, in gene, in gene, downstream	1	1	1	22.29	25.14	18	7	2_A375_pNL97_plus_lncRNA_AR..1	99	Gene TECR	TER, TECR, SC2, GPSN2	trans-2,3-enoyl-CoA reductase	NM_138501, hCT18659.3, hCT1967928.1	1569392_at, 208336_s_at, 231556_at	NP_612510.1, EAW84434.1, EAW84435.1
GeneID:4713	NDUFB7	19	14,676,890	14,682,886	5,996	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2895, 2_A375_pNL97_plus_lncRNA_AR..1.4158, 4_A375_EGR1..1.4423, 4_A375_EGR1..1.4424, 4_A375_EGR1..1.4425, 4_A375_EGR1..1.4426, 4_A375_EGR1..1.4427	6, -56, 10694, 9211, 8593, 6662, 196	in gene, upstream, downstream, downstream, downstream, downstream, in gene	1	1	1	22.6	26.6	19.4	5	2_A375_pNL97_plus_lncRNA_AR..1	99	Gene NDUFB7	NDUFB7, CI-B18, MGC2480, B18	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	NM_004146, hCT18660.2	202839_s_at, 211407_at	NP_004137.2, EAW84436.1
GeneID:126402	CCDC105	19	15,121,539	15,134,083	12,544	+	2	2_A375_pNL97_plus_lncRNA_AR..1.4159, 4_A375_EGR1..1.4428	5373, 289	in gene, in gene	0	1	1	16.5	22.5	16	2	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene CCDC105	CCDC105, FLJ40365	coiled-coil domain containing 105	NM_173482, hCT1646862.3	1553893_at	NP_775753.2, EAW84458.1
GeneID:126370	OR1I1	19	15,197,877	15,198,944	1,067	+	1	2_A375_pNL97_plus_lncRNA_AR..1.4160	299	in gene	0	1	0	16	25	8	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene OR1I1	OR1I1, OR19-20, OR1I1P, OR1I1Q	olfactory receptor, family 1, subfamily I, member 1	NM_001004713, hCT2351620.0	234403_at	NP_001004713.1, EAW84460.1
GeneID:85360	SYDE1	19	15,218,214	15,225,789	7,575	+	1	4_A375_EGR1..1.4429	2042	in gene	0	0	1	10	10	18	1	4_A375_EGR1..1	18	Gene SYDE1	SYDE1, FLJ13511, 7h3	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	NM_033025, hCT2282668.1, hCT2356594.0, hCT29844.4	212962_at, 216271_x_at, 216272_x_at, 44702_at	NP_149014.3, EAW84463.1, EAW84461.1, EAW84462.1
GeneID:10994	ILVBL	19	15,225,785	15,236,577	10,792	-	3	2_A375_pNL97_plus_lncRNA_AR..1.4161, 4_A375_EGR1..1.4429, 4_A375_EGR1..1.4430	161, 16321, 406	in gene, downstream, in gene	0	1	1	15.5	17.5	19.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene ILVBL	MGC1269, ILVBL, ILV2H, 209L8, AHAS, MGC19535	ilvB (bacterial acetolactate synthase)-like	NM_006844, hCT29830.3	202993_at, 210624_s_at, 216270_at	NP_006835.2, EAW84464.1
GeneID:4854	NOTCH3	19	15,270,444	15,311,792	41,348	-	3	4_A375_EGR1..1.4431, 4_A375_EGR1..1.4432, 4_A375_EGR1..1.4433	39688, 21904, 14192	in gene, in gene, in gene	0	0	1	8.67	10.67	19.33	3	4_A375_EGR1..1	21	Gene NOTCH3	NOTCH3, CADASIL, CASIL	Notch homolog 3 (Drosophila)	NM_000435, hCT29828.2	203237_s_at, 203238_s_at	NP_000426.2, EAW84466.1
GeneID:10270	AKAP8	19	15,464,335	15,490,603	26,268	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2896, 2_A375_pNL97_plus_lncRNA_AR..1.4163, 4_A375_EGR1..1.4435, 4_A375_EGR1..1.4436, 4_A375_EGR1..1.4437	11, 43, 24683, 9531, 459	in gene, in gene, in gene, in gene, in gene	1	1	1	16	13.67	20	3	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene AKAP8	DKFZp586B1222, AKAP8, AKAP95	A kinase (PRKA) anchor protein 8	NM_005858, hCT29836.3	203847_s_at, 203848_at	NP_005849.1, EAW84474.1
GeneID:26993	AKAP8L	19	15,490,859	15,529,833	38,974	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2896, 1_A375_pNL7_minus_lncRNA_AR..1..2897, 2_A375_pNL97_plus_lncRNA_AR..1.4163, 2_A375_pNL97_plus_lncRNA_AR..1.4164, 4_A375_EGR1..1.4436, 4_A375_EGR1..1.4437, 4_A375_EGR1..1.4438	39241, 233, 39273, 89, 48761, 39889, -5911	downstream, in gene, downstream, in gene, downstream, downstream, upstream	1	1	1	18.5	17	17.25	4	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene AKAP8L	AKAP8L, DKFZp434L0650, NAKAP95, NAKAP, HA95, HAP95	A kinase (PRKA) anchor protein 8-like	NM_014371, hCT2284625.1, hCT2284626.1, hCT2284627.1, hCT28011.3	215741_x_at, 218064_s_at, 222160_at, 227691_at	NP_055186.2, EAW84476.1, EAW84475.1, EAW84477.1, EAW84478.1
GeneID:58525	WIZ	19	15,532,318	15,560,762	28,444	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2897, 1_A375_pNL7_minus_lncRNA_AR..1..2898, 2_A375_pNL97_plus_lncRNA_AR..1.4164, 2_A375_pNL97_plus_lncRNA_AR..1.4165, 4_A375_EGR1..1.4438, 4_A375_EGR1..1.4439	31162, 17050, 31018, 17114, 25018, 13018	downstream, in gene, downstream, in gene, in gene, in gene	1	1	1	18.5	24.75	16	4	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene WIZ	WIZ, ZNF803	widely interspaced zinc finger motifs	NM_021241	221783_at, 221784_at, 221785_at, 52005_at	NP_067064.2
GeneID:114770	PGLYRP2	19	15,579,458	15,590,315	10,859	-	1	4_A375_EGR1..1.4440	3771	in gene	0	0	1	5	7	20	1	4_A375_EGR1..1	20	Gene PGLYRP2	tagL-alpha, HMFT0141, PGRPL, tagL-beta, PGRP-L, PGLYRP2, PGLYRPL, tagL, TAGL-like	peptidoglycan recognition protein 2	NM_052890, hCT2284612.0, hCT29841.2	242817_at	NP_443122.3, EAW84482.1, EAW84483.1
GeneID:126410	CYP4F22	19	15,619,336	15,663,128	43,792	+	2	2_A375_pNL97_plus_lncRNA_AR..1.4166, 4_A375_EGR1..1.4441	48248, 43000	downstream, in gene	0	1	1	14	19	16	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CYP4F22	FLJ39501, LI3, CYP4F22	cytochrome P450, family 4, subfamily F, polypeptide 22	NM_173483, hCT2344838.1	244692_at	NP_775754.2, EAW84484.1
GeneID:11283	CYP4F8	19	15,726,029	15,740,448	14,419	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2899, 2_A375_pNL97_plus_lncRNA_AR..1.4166, 4_A375_EGR1..1.4442	8691, 8659, 13987	in gene, in gene, in gene	1	1	1	21	25.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene CYP4F8	CYPIVF8, CYP4F8, CPF8	cytochrome P450, family 4, subfamily F, polypeptide 8	NM_007253, hCT1640352.5, hCT2356533.0	210576_at	NP_009184.1, EAW84487.1, EAW84488.1
GeneID:388514	LOC388514	19	15,870,144	15,890,798	20,654	-	1	2_A375_pNL97_plus_lncRNA_AR..1.4169	10208	in gene	0	1	0	17	30	8	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene LOC388514		cytochrome P450, family 4, subfamily F, polypeptide 24 pseudogene	NR_033864		
GeneID:652995	UCA1	19	15,939,757	15,946,230	6,473	+	2	2_A375_pNL97_plus_lncRNA_AR..1.4170, 4_A375_EGR1..1.4443	7923, 7827	downstream, downstream	0	1	1	19	27	24	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene UCA1	NCRNA00178, CUDR, UCA1	urothelial cancer associated 1 (non-protein coding)	NR_015379	227919_at	
GeneID:126536	LOC126536	19	16,126,444	16,138,272	11,828	+	4	4_A375_EGR1..1.4445, 4_A375_EGR1..1.4446, 4_A375_EGR1..1.4447, 4_A375_EGR1..1.4448	3380, 4584, 7316, 7676	in gene, in gene, in gene, in gene	0	0	1	9.25	9.5	18.75	4	4_A375_EGR1..1	24	Gene LOC126536	DKFZp686O2439, DKFZp434N1114	hypothetical LOC126536	NR_026626	1555966_a_at, 237242_at	
GeneID:100507483	LOC100507483	19	16,130,552	16,131,094	542	+	4	4_A375_EGR1..1.4445, 4_A375_EGR1..1.4446, 4_A375_EGR1..1.4447, 4_A375_EGR1..1.4448	-728, 456, 3208, 3768	upstream, in gene, downstream, downstream	0	0	1	9.25	9.5	18.75	4	4_A375_EGR1..1	24	Gene LOC100507483		3-AS protein	XM_003119721, XM_003118790, XM_003120934		XP_003119769.1, XP_003118838.1, XP_003120982.1
GeneID:148231	FLJ25328	19	16,143,286	16,152,921	9,635	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2900, 2_A375_pNL97_plus_lncRNA_AR..1.4171, 4_A375_EGR1..1.4447, 4_A375_EGR1..1.4448	19082, 19098, -9526, -8966	downstream, downstream, upstream, upstream	1	1	1	14.33	12.33	17	3	4_A375_EGR1..1	22	Gene FLJ25328	MGC126002	hypothetical LOC148231	NR_024335, NR_024336, hCT2282460.1, hCT2356482.0	1562914_a_at	EAW84520.1, EAW84519.1
GeneID:7171	TPM4	19	16,178,317	16,213,813	35,496	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2901, 2_A375_pNL97_plus_lncRNA_AR..1.4172	43827, 43811	downstream, downstream	1	1	0	18	23	12	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TPM4	TPM4		NM_003290, NM_001145160, hCT2282462.0, hCT2282463.0, hCT2282464.0, hCT2282466.0	1559989_at, 1567107_s_at, 209344_at, 212481_s_at	NP_003281.1, NP_001138632.1, EAW84521.1, EAW84522.1, EAW84523.1, EAW84524.1
GeneID:4218	RAB8A	19	16,222,490	16,244,445	21,955	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2901, 2_A375_pNL97_plus_lncRNA_AR..1.4172, 4_A375_EGR1..1.4449	-346, -362, 16518	upstream, upstream, in gene	1	1	1	13.5	17.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RAB8A	RAB8A, MEL, RAB8	RAB8A, member RAS oncogene family	NM_005370, hCT2282467.0, hCT28158.3	208819_at	NP_005361.2, EAW84526.1, EAW84527.1
GeneID:84941	HSH2D	19	16,244,838	16,269,381	24,543	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2902, 2_A375_pNL97_plus_lncRNA_AR..1.4173, 4_A375_EGR1..1.4449	27066, 27082, -5630	downstream, downstream, upstream	1	1	1	15.5	17	16	2	4_A375_EGR1..1	22	Gene HSH2D	ALX, FLJ14886, HSH2, HSH2D	hematopoietic SH2 domain containing	NM_032855, hCT1967957.1, hCT2356599.0, hCT2356600.0, hCT2356601.0, hCT28162.2	1552623_at	NP_116244.1, EAW84528.1, EAW84529.1, EAW84530.1, EAW84531.1, EAW84532.1
GeneID:117286	CIB3	19	16,272,179	16,284,286	12,107	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2902, 2_A375_pNL97_plus_lncRNA_AR..1.4173	12382, 12366	downstream, downstream	1	1	0	22	22	10	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene CIB3	MGC96922, MGC138405, KIP3, CIB3, MGC142151	calcium and integrin binding family member 3	NM_054113, hCT1814887.1, hCT2356623.0, hCT2356624.0	1552750_at, 1552751_a_at	NP_473454.1, EAW84533.1, EAW84534.1, EAW84535.1
GeneID:26017	FAM32A	19	16,296,235	16,302,857	6,622	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2903	12309	downstream	1	0	0	21	12	15	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene FAM32A	FAM32A	family with sequence similarity 32, member A	NM_014077, hCT2282471.0, hCT2356535.0, hCT28000.3	201863_at	NP_054796.1, EAW84537.1, EAW84536.1, EAW84538.1
GeneID:8907	AP1M1	19	16,308,665	16,346,156	37,491	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2903, 4_A375_EGR1..1.4450, 4_A375_EGR1..1.4451, 4_A375_EGR1..1.4452, 4_A375_EGR1..1.4453, 4_A375_EGR1..1.4454	-121, 6563, 10023, 26759, 29591, 35975	upstream, in gene, in gene, in gene, in gene, in gene	1	0	1	10.17	8.67	16.67	6	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene AP1M1	MU-1A, AP1M1, CLTNM, AP47, CLAPM2	adaptor-related protein complex 1, mu 1 subunit	NM_032493, NM_001130524, hCT2282474.0, hCT28161.2	223024_at, 223025_s_at	NP_115882.1, NP_001123996.1, EAW84539.1, EAW84540.1
GeneID:10365	KLF2	19	16,435,651	16,438,345	2,694	+	1	4_A375_EGR1..1.4455	-451	upstream	0	0	1	7	8	21	1	4_A375_EGR1..1	21	Gene KLF2	KLF2, LKLF	Kruppel-like factor 2 (lung)	NM_016270, hCT28187.3	219371_s_at, 226645_at, 226646_at	NP_057354.1, EAW84541.1
GeneID:58513	EPS15L1	19	16,472,408	16,582,762	110,354	-	3	4_A375_EGR1..1.4457, 4_A375_EGR1..1.4458, 4_A375_EGR1..1.4459	116138, 90582, 66634	downstream, in gene, in gene	0	0	1	10.67	10	17	3	4_A375_EGR1..1	20	Gene EPS15L1	EPS15R, EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	NM_021235, hCT2283393.0, hCT2356564.0, hCT2356565.0, hCT28194.3	221056_x_at, 222112_at, 222113_s_at, 231926_at, 232438_at	NP_067058.1, EAW84545.1, EAW84542.1, EAW84543.1, EAW84544.1
GeneID:125972	CALR3	19	16,589,875	16,607,003	17,128	-	2	2_A375_pNL97_plus_lncRNA_AR..1.4175, 4_A375_EGR1..1.4460	-69, -293	upstream, upstream	0	1	1	24	35	21	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene CALR3	FLJ25355, MGC26577, CRT2, CALR3, CT93	calreticulin 3	NM_145046, hCT28189.3	1552421_a_at	NP_659483.2, EAW84546.1
GeneID:84167	C19orf44	19	16,607,205	16,632,163	24,958	+	5	2_A375_pNL97_plus_lncRNA_AR..1.4175, 4_A375_EGR1..1.4460, 4_A375_EGR1..1.4461, 4_A375_EGR1..1.4462, 4_A375_EGR1..1.4463	-133, 91, 24283, 28907, 33835	upstream, in gene, in gene, downstream, downstream	0	1	1	13.25	16.25	19.25	4	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene C19orf44	C19orf44, FLJ21742, FLJ22492	chromosome 19 open reading frame 44	NM_032207, hCT2282488.0, hCT28191.3	228154_at, 232730_at	NP_115583.1, EAW84548.1, EAW84547.1
GeneID:10523	CHERP	19	16,628,700	16,653,263	24,563	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2905, 2_A375_pNL97_plus_lncRNA_AR..1.4176, 4_A375_EGR1..1.4461, 4_A375_EGR1..1.4462, 4_A375_EGR1..1.4463, 4_A375_EGR1..1.4464, 4_A375_EGR1..1.4465	175, -177, 21775, 17151, 12223, 9527, -145	in gene, upstream, in gene, in gene, in gene, in gene, upstream	1	1	1	11.4	13	19.6	5	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene CHERP	SCAF6, DAN16, CHERP, SRA1	calcium homeostasis endoplasmic reticulum protein	NM_006387, hCT2283389.0	1568704_a_at, 202229_s_at, 202230_s_at	NP_006378.3, EAW84549.1
GeneID:79939	SLC35E1	19	16,660,648	16,683,193	22,545	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2905, 2_A375_pNL97_plus_lncRNA_AR..1.4176, 4_A375_EGR1..1.4465, 4_A375_EGR1..1.4466	30105, 29753, 29785, -4535	downstream, downstream, downstream, upstream	1	1	1	12.5	17	20	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene SLC35E1	FLJ36689, DKFZp564G0462, FLJ14251, SLC35E1, MGC44954	solute carrier family 35, member E1	NM_024881, hCT2283384.0, hCT2283385.0, hCT2283386.0, hCT2283387.0	220796_x_at, 222263_at, 227518_at, 235035_at, 79005_at	NP_079157.3, EAW84553.1, EAW84550.1, EAW84551.1, EAW84552.1
GeneID:9441	MED26	19	16,685,718	16,739,015	53,297	-	4	2_A375_pNL97_plus_lncRNA_AR..1.4177, 4_A375_EGR1..1.4466, 4_A375_EGR1..1.4467, 4_A375_EGR1..1.4468	-617, 51267, 487, -569	upstream, in gene, in gene, upstream	0	1	1	10.33	16	17.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MED26	MED26, CRSP70, CRSP7	mediator complex subunit 26	NM_004831, hCT27998.3	1559382_at, 1559593_a_at, 221986_at, 227538_at, 231724_at	NP_004822.2, EAW84554.1
GeneID:100507522	LOC100507522	19	16,744,608	16,756,802	12,194	-	3	2_A375_pNL97_plus_lncRNA_AR..1.4177, 4_A375_EGR1..1.4467, 4_A375_EGR1..1.4468	17170, 18274, 17218	downstream, downstream, downstream	0	1	1	12.5	19.5	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100507522		hypothetical LOC100507522	XR_109576		
GeneID:79086	C19orf42	19	16,756,959	16,770,968	14,009	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2906, 2_A375_pNL97_plus_lncRNA_AR..1.4178	-88, -56	upstream, upstream	1	1	0	37	31	18	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene C19orf42	C19orf42, MGC2747	chromosome 19 open reading frame 42	NM_024104, hCT1967959.1, hCT2283377.0, hCT2356561.0, hCT28192.3	219097_x_at, 224712_x_at, 224717_s_at, 229850_s_at	NP_077009.2, EAW84555.1, EAW84556.1, EAW84557.1, EAW84558.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:79041	TMEM38A	19	16,771,936	16,799,830	27,892	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2906, 2_A375_pNL97_plus_lncRNA_AR..1..4178	-862, -914	upstream, upstream	1	1	0	37	31	18	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene TMEM38A	TMEM38A, TRICA, TRIC-A, MGC3169	transmembrane protein 38A	NM_024074, hCT28190.3	222896_at	NP_076979.1, EAW84559.1
GeneID:284434	NWD1	19	16,830,787	16,928,774	97,987	+	4	2_A375_pNL97_plus_lncRNA_AR..1..4179, 2_A375_pNL97_plus_lncRNA_AR..1..4180, 4_A375_EGR1..1..4469, 4_A375_EGR1..1..4470	19741, 39229, 7549, 87917	in gene, in gene, in gene, in gene	0	1	1	11	20	15.25	4	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene NWD1	MGC134940, NWD1	NACHT and WD repeat domain containing 1	NM_001007525		NP_001007526.2
GeneID:23309	SIN3B	19	16,940,216	16,991,164	50,948	+	6	4_A375_EGR1..1..4471, 4_A375_EGR1..1..4472, 4_A375_EGR1..1..4473, 4_A375_EGR1..1..4474, 4_A375_EGR1..1..4475, 4_A375_EGR1..1..4476	40054, 43782, 46870, 48614, 51666, 60214	in gene, in gene, in gene, in gene, downstream, downstream	0	0	1	9.33	10.33	19.17	6	4_A375_EGR1..1	24	Gene SIN3B	KIAA0700, SIN3B	SIN3 homolog B, transcription regulator (yeast)	NM_015260, hCT2284035.1, hCT2284036.1	209352_s_at, 39705_at	NP_056075.1, EAW84565.1, EAW84564.1
GeneID:9002	F2RL3	19	16,999,826	17,002,830	3,004	+	2	4_A375_EGR1..1..4475, 4_A375_EGR1..1..4476	-7922, 606	upstream, in gene	0	0	1	10.5	9.5	20	2	4_A375_EGR1..1	24	Gene F2RL3	F2RL3, PAR4	coagulation factor II (thrombin) receptor-like 3	NM_003950, hCT2284037.1	207221_at	NP_003941.2, EAW84566.1
GeneID:27151	CPAMD8	19	17,003,762	17,137,625	133,863	-	2	4_A375_EGR1..1..4476, 4_A375_EGR1..1..4477	137193, 11601	downstream, in gene	0	0	1	9	8.5	15	2	4_A375_EGR1..1	16	Gene CPAMD8	FLJ42058, CPAMD8, K-CAP, VIP, KIAA1283, FLJ90618	C3 and PZP-like, alpha-2-macroglobulin domain containing 8	NM_015692, hCT2286619.1, hCT2348360.0, hCT28902.3	227721_at	NP_056507.2, EAW84567.1, EAW84568.1, EAW84569.1
GeneID:93323	HAUS8	19	17,160,571	17,186,343	25,772	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2907, 2_A375_pNL97_plus_lncRNA_AR..1..4181, 2_A375_pNL97_plus_lncRNA_AR..1..4182	7, 39, -4261	in gene, in gene, upstream	1	1	0	37	51.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene HAUS8	DGT4, HICE1, MGC20533, HAUS8, NY-SAR-48	HAUS augmin-like complex, subunit 8	NM_033417, NM_001011699, hCT2356603.0, hCT28896.3	226308_at	NP_219485.1, NP_001011699.1, EAW84570.1, EAW84571.1
GeneID:4650	MYO9B	19	17,186,591	17,324,104	137,513	+	14	1_A375_pNL7_minus_lncRNA_AR..1..2907, 1_A375_pNL7_minus_lncRNA_AR..1..2908, 1_A375_pNL7_minus_lncRNA_AR..1..2909, 2_A375_pNL97_plus_lncRNA_AR..1..4181, 2_A375_pNL97_plus_lncRNA_AR..1..4182, 2_A375_pNL97_plus_lncRNA_AR..1..4183, 2_A375_pNL97_plus_lncRNA_AR..1..4184, 4_A375_EGR1..1..4478, 4_A375_EGR1..1..4479, 4_A375_EGR1..1..4480, 4_A375_EGR1..1..4481, 4_A375_EGR1..1..4482, 4_A375_EGR1..1..4483, 4_A375_EGR1..1..4484	-255, 32193, 59841, -287, 4033, 32353, 139569, 15825, 26601, 105415, 119505, 126625, 129569, 135641	upstream, in gene, in gene, upstream, in gene, in gene, downstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	16	19.08	16	12	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene MYO9B	CELIAC4, MYO9B, MYR5	myosin IXB	NM_004145, NM_001130065, hCT2284043.0, hCT28894.3	208452_x_at, 214780_s_at, 217297_s_at	NP_004136.2, NP_001123537.1, EAW84572.1, EAW84573.1
GeneID:55850	USE1	19	17,326,155	17,330,638	4,483	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2910, 2_A375_pNL97_plus_lncRNA_AR..1..4184, 2_A375_pNL97_plus_lncRNA_AR..1..4185, 4_A375_EGR1..1..4483, 4_A375_EGR1..1..4484, 4_A375_EGR1..1..4485	11029, 5, 11125, -9995, -3723, 11061	downstream, in gene, downstream, upstream, upstream, downstream	1	1	1	17	21	19.5	4	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene USE1	P31, MDS032, USE1, SLT1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	NM_018467, hCT2284048.0, hCT2284050.0, hCT28897.3	219348_at, 221706_s_at	NP_060937.1, EAW84575.1, EAW84574.1, EAW84576.1
GeneID:79629	OCEL1	19	17,337,055	17,340,028	2,973	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2910, 1_A375_pNL7_minus_lncRNA_AR..1..2911, 2_A375_pNL97_plus_lncRNA_AR..1..4185, 2_A375_pNL97_plus_lncRNA_AR..1..4186, 4_A375_EGR1..1..4485	129, 9505, 225, 9565, 161	in gene, downstream, in gene, downstream, in gene	1	1	1	30	33	19.5	2	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene OCEL1	FWP009, FLJ22709, OCEL1, S863-9	occludin/ELL domain containing 1	NM_024578, hCT2356557.0, hCT2356556.0, hCT28890.3	205441_at	NP_078854.1, EAW84577.1, EAW84578.1, EAW84579.1
GeneID:2063	NR2F6	19	17,342,694	17,356,151	13,457	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2910, 1_A375_pNL7_minus_lncRNA_AR..1..2911, 2_A375_pNL97_plus_lncRNA_AR..1..4185, 2_A375_pNL97_plus_lncRNA_AR..1..4186, 2_A375_pNL97_plus_lncRNA_AR..1..4187, 4_A375_EGR1..1..4485, 4_A375_EGR1..1..4486	18967, 9591, 18871, 9511, -3198, 18935, -1385	downstream, in gene, downstream, in gene, upstream, downstream, upstream	1	1	1	20.5	24	17.75	4	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene NR2F6	EAR-2, ERBAL2, NR2F6, EAR2	nuclear receptor subfamily 2, group F, member 6	NM_005234, hCT28895.4	209261_s_at, 209262_s_at, 213354_s_at	NP_005225.2, EAW84580.1
GeneID:83878	USHBP1	19	17,360,849	17,375,544	14,695	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4187, 4_A375_EGR1..1..4486	18195, 18008	downstream, downstream	0	1	1	11	15	16	2	4_A375_EGR1..1	20	Gene USHBP1	USHBP1, FLJ90681, FLJ38709, AIEBP, MCC2	Usher syndrome 1C binding protein 1	NM_031941, hCT2286648.1, hCT2286649.1, hCT28903.3	235510_at	NP_114147.2, EAW84581.1, EAW84582.1, EAW84583.1
GeneID:126549	ANKLE1	19	17,392,454	17,398,454	6,000	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4188, 4_A375_EGR1..1..4487	10394, 10746	downstream, downstream	0	1	1	14	17	18	1	4_A375_EGR1..1	18	Gene ANKLE1	ANKRD41, LEMD6, LEM3, ANKLE1, FLJ39369	ankyrin repeat and LEM domain containing 1	NM_152363, hCT2284054.0, hCT2284055.0, hCT2356591.0	1553136_a_at	NP_689576.4, EAW84586.1, EAW84587.1, EAW84588.1
GeneID:79575	ABHD8	19	17,402,940	17,414,282	11,342	-	9	1_A375_pNL7_minus_lncRNA_AR..1..2912, 2_A375_pNL97_plus_lncRNA_AR..1..4188, 2_A375_pNL97_plus_lncRNA_AR..1..4189, 2_A375_pNL97_plus_lncRNA_AR..1..4190, 2_A375_pNL97_plus_lncRNA_AR..1..4191, 4_A375_EGR1..1..4487, 4_A375_EGR1..1..4488, 4_A375_EGR1..1..4489, 4_A375_EGR1..1..4490	74, 11434, 31, -2006, -6198, 11082, 618, -2678, -6134	in gene, downstream, in gene, upstream, upstream, in gene, in gene, upstream, upstream	1	1	1	19.25	22.5	18.75	4	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene ABHD8	FLJ11743, MGC2512, ABHD8, MGC14280	abhydrolase domain containing 8	NM_024527, hCT28898.2	219101_x_at	NP_078803.4, EAW84589.1
GeneID:64981	MRPL34	19	17,416,477	17,417,652	1,175	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2912, 2_A375_pNL97_plus_lncRNA_AR..1..4189, 2_A375_pNL97_plus_lncRNA_AR..1..4190, 2_A375_pNL97_plus_lncRNA_AR..1..4191, 4_A375_EGR1..1..4488, 4_A375_EGR1..1..4489, 4_A375_EGR1..1..4490	-2289, -2226, -189, 4003, -2813, 483, 3939	upstream, upstream, upstream, downstream, upstream, in gene, downstream	1	1	1	21	24.33	19	3	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene MRPL34	MGC2633, L34mt, MRPL34, MGC24974	mitochondrial ribosomal protein L34	NM_023937, hCT2284056.1, hCT2284057.0, hCT2284059.1	221692_s_at	NP_076426.1, EAW84590.1, EAW84591.1, EAW84592.1
GeneID:79016	DDA1	19	17,420,337	17,434,107	13,770	+	9	1_A375_pNL7_minus_lncRNA_AR..1..2912, 2_A375_pNL97_plus_lncRNA_AR..1..4189, 2_A375_pNL97_plus_lncRNA_AR..1..4190, 2_A375_pNL97_plus_lncRNA_AR..1..4191, 4_A375_EGR1..1..4488, 4_A375_EGR1..1..4489, 4_A375_EGR1..1..4490, 4_A375_EGR1..1..4491, 4_A375_EGR1..1..4492	-6129, -6086, -4049, 143, -6673, -3377, 79, 15407, 17967	upstream, upstream, upstream, in gene, upstream, upstream, in gene, downstream, downstream	1	1	1	15.6	18.4	19.2	5	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene DDA1	MGC2594, PCIA1, C19orf58, DDA1	DET1 and DDB1 associated 1	NM_024050, hCT2284058.1, hCT2284060.1	218260_at, 227457_at, 227472_at	NP_076955.1, EAW84593.1, EAW84594.1
GeneID:57719	ANO8	19	17,434,032	17,445,838	11,806	-	7	1_A375_pNL7_minus_lncRNA_AR..1..2913, 1_A375_pNL7_minus_lncRNA_AR..1..2914, 2_A375_pNL97_plus_lncRNA_AR..1..4192, 2_A375_pNL97_plus_lncRNA_AR..1..4193, 4_A375_EGR1..1..4491, 4_A375_EGR1..1..4492, 4_A375_EGR1..1..4493	-26, -2442, -58, -2554, 9694, 7334, -2394	upstream, upstream, upstream, upstream, in gene, in gene, upstream	1	1	1	18.5	21.75	18	4	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene ANO8	TMEM16H, KIAA1623, ANO8	anoctamin 8	NM_020959, hCT2286642.1, hCT2286643.1	1563549_a_at	NP_066010.1, EAW84596.1, EAW84595.1
GeneID:84705	GTPBP3	19	17,448,356	17,453,540	5,184	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2913, 1_A375_pNL7_minus_lncRNA_AR..1..2914, 2_A375_pNL97_plus_lncRNA_AR..1..4192, 2_A375_pNL97_plus_lncRNA_AR..1..4193, 4_A375_EGR1..1..4492, 4_A375_EGR1..1..4493	-2692, -276, -2660, -164, -10052, -324	upstream, upstream, upstream, upstream, upstream, upstream	1	1	1	22	27	17.33	3	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene GTPBP3	GTPBG3, THDF1, FLJ14700, MSS1, FLJ17836, MTGP1, GTPBP3	GTP binding protein 3 (mitochondrial)	NM_133644, NM_032620, NM_001128855, hCT1951459.1, hCT2284063.0, hCT28888.3	1555062_s_at, 213835_x_at	NP_598399.2, NP_116009.2, NP_001122327.1, EAW84597.1, EAW84598.1, EAW84599.1
GeneID:83483	PLVAP	19	17,462,264	17,488,137	25,873	-	1	4_A375_EGR1..1..4494	-8663	upstream	0	0	1	9	12	20	1	4_A375_EGR1..1	20	Gene PLVAP	PLVAP, gp68, FELS, PV-1, PV1	plasmalemma vesicle associated protein	NM_031310, hCT1641342.3	221529_s_at	NP_112600.1, EAW84600.1
GeneID:100507535	LOC100507535	19	17,516,550	17,536,142	19,592	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2915, 2_A375_pNL97_plus_lncRNA_AR..1..4194	14157, 13994	in gene, in gene	1	1	0	19	22	15	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100507535		hypothetical LOC100507535	XR_111839, XR_109577, XR_115249		
GeneID:93343	FAM125A	19	17,530,912	17,536,140	5,228	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2915, 2_A375_pNL97_plus_lncRNA_AR..1..4194	-205, -366	upstream, upstream	1	1	0	19	22	15	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene FAM125A	CFBP, FAM125A, FLJ32495	family with sequence similarity 125, member A	NM_138401, hCT1951460.1, hCT28900.3	1558643_at, 227684_s_at	NP_612410.1, EAW84605.1, EAW84604.1
GeneID:376497	SLC27A1	19	17,581,300	17,616,977	35,677	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2916, 1_A375_pNL7_minus_lncRNA_AR..1..2917, 2_A375_pNL97_plus_lncRNA_AR..1..4195, 2_A375_pNL97_plus_lncRNA_AR..1..4196, 2_A375_pNL97_plus_lncRNA_AR..1..4197, 4_A375_EGR1..1..4495	5324, 41548, 5420, 37838, 41546, 41900	in gene, downstream, in gene, downstream, downstream, downstream	1	1	1	22	25.33	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene SLC27A1	MGC71751, ACSVL5, SLC27A1, FATP1, FLJ00336, FATP	solute carrier family 27 (fatty acid transporter), member 1	NM_198580, hCT2284070.0, hCT2284071.0, hCT2356626.0	226728_at	NP_940982.1, EAW84609.1, EAW84610.1, EAW84611.1
GeneID:100507551	LOC100507551	19	17,611,431	17,613,273	1,842	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2917, 2_A375_pNL97_plus_lncRNA_AR..1..4196, 2_A375_pNL97_plus_lncRNA_AR..1..4197, 4_A375_EGR1..1..4495	-9575, -5863, -9575, -9927	upstream, upstream, upstream, upstream	1	1	1	24.5	28.5	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene LOC100507551		hypothetical protein LOC100507551	XM_003118791		XP_003118839.1
GeneID:25796	PGLS	19	17,622,432	17,632,097	9,665	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2917, 2_A375_pNL97_plus_lncRNA_AR..1..4196, 2_A375_pNL97_plus_lncRNA_AR..1..4197, 4_A375_EGR1..1..4495	416, -3298, 416, 768	in gene, upstream, in gene, in gene	1	1	1	24.5	28.5	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene PGLS	6PGL, PGLS	6-phosphogluconolactonase	NM_012088, hCT1816931.2, hCT2284073.0	1554316_at, 218387_s_at, 218388_at, 230699_at	NP_036220.1, EAW84614.1, EAW84613.1
GeneID:199786	FAM129C	19	17,634,110	17,664,648	30,538	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2918, 1_A375_pNL7_minus_lncRNA_AR..1..2919, 2_A375_pNL97_plus_lncRNA_AR..1..4198, 2_A375_pNL97_plus_lncRNA_AR..1..4199, 4_A375_EGR1..1..4496, 4_A375_EGR1..1..4497, 4_A375_EGR1..1..4498	16258, 32194, 16066, 32178, 16402, 32130, 32706	in gene, downstream, in gene, downstream, in gene, downstream, downstream	1	1	1	29.5	27.5	21.5	2	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene FAM129C	BCNP1, FLJ39802, FAM129C	family with sequence similarity 129, member C	NM_173544, NM_001098524, hCT1966626.2, hCT2356498.0, hCT2356497.0, hCT2356496.0, hCT2356499.0, hCT2356500.0	1553369_at, 1569422_at, 230983_at	NP_775815.2, NP_001091994.1, EAW84615.1, EAW84617.1, EAW84618.1, EAW84620.1, EAW84616.1, EAW84619.1
GeneID:79709	GLT25D1	19	17,666,511	17,693,965	27,454	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2919, 2_A375_pNL97_plus_lncRNA_AR..1..4199, 4_A375_EGR1..1..4497, 4_A375_EGR1..1..4498, 4_A375_EGR1..1..4499, 4_A375_EGR1..1..4500	-207, -223, -271, 305, 25201, 27165	upstream, upstream, upstream, in gene, in gene, in gene	1	1	1	16.33	16.33	20.67	3	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene GLT25D1	MGC117270, FLJ22329, GLT25D1	glycosyltransferase 25 domain containing 1	NM_024656, hCT2284076.0, hCT2284077.0, hCT2284079.0, hCT2284080.0	218473_s_at, 222644_s_at	NP_078932.2, EAW84624.1, EAW84621.1, EAW84622.1, EAW84623.1
GeneID:23025	UNC13A	19	17,712,137	17,799,008	86,871	-	11	1_A375_pNL7_minus_lncRNA_AR..1..2920, 1_A375_pNL7_minus_lncRNA_AR..1..2921, 1_A375_pNL7_minus_lncRNA_AR..1..2922, 2_A375_pNL97_plus_lncRNA_AR..1..4200, 2_A375_pNL97_plus_lncRNA_AR..1..4201, 2_A375_pNL97_plus_lncRNA_AR..1..4202, 2_A375_pNL97_plus_lncRNA_AR..1..4203, 4_A375_EGR1..1..4501, 4_A375_EGR1..1..4502, 4_A375_EGR1..1..4503, 4_A375_EGR1..1..4504	7616, 6528, -224, 81952, 7688, 6448, -224, 40856, 39120, 6272, 1024	in gene, in gene, upstream, in gene, in gene, in gene, upstream, in gene, in gene, in gene, in gene	1	1	1	21	22.33	17.17	6	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene UNC13A	Munc13-1, UNC13A, KIAA1032	unc-13 homolog A (C. elegans)	NM_001080421	214617_at, 227453_at	NP_001073890.2
GeneID:55201	MAP1S	19	17,830,303	17,845,324	15,021	+	5	2_A375_pNL97_plus_lncRNA_AR..1..4204, 4_A375_EGR1..1..4505, 4_A375_EGR1..1..4506, 4_A375_EGR1..1..4507, 4_A375_EGR1..1..4508	-199, 705, 6305, 8001, 13793	upstream, in gene, in gene, in gene, in gene	0	1	1	10.4	11.2	18.2	5	4_A375_EGR1..1	20	Gene MAP1S	VCY2IP1, MAP8, C19orf5, MAP1S, BPY2IP1, MGC133087, VCY2IP-1, FLJ10669	microtubule-associated protein 1S	NM_018174, hCT2284083.0	218522_s_at	NP_060644.4, EAW84626.1
GeneID:23149	FCHO1	19	17,858,527	17,899,377	40,850	+	2	4_A375_EGR1..1..4509, 4_A375_EGR1..1..4510	16721, 22885	in gene, in gene	0	0	1	6	6	16	2	4_A375_EGR1..1	17	Gene FCHO1	FCHO1, KIAA0290	FCH domain only 1	NM_001161357, NM_015122, NM_001161358, NM_001161359, hCT2284086.0, hCT2284087.0, hCT2284088.0, hCT2356468.0	213689_at	NP_001154829.1, NP_055937.1, NP_001154830.1, NP_001154831.1, EAW84629.1, EAW84630.1, EAW84627.1, EAW84628.1
GeneID:100507578	LOC100507578	19	17,905,919	17,919,110	13,191	-	1	4_A375_EGR1..1..4511	454	in gene	0	0	1	8	8	15	1	4_A375_EGR1..1	15	Gene LOC100507578		hypothetical LOC100507578	XR_111840, XR_109578, XR_115250		
GeneID:10331	B3GNT3	19	17,905,919	17,924,385	18,466	+	2	4_A375_EGR1..1..4511, 4_A375_EGR1..1..4512	12737, 26353	in gene, downstream	0	0	1	7.5	8	15.5	2	4_A375_EGR1..1	16	Gene B3GNT3	HP10328, B3GALT8, TMEM3, B3GNT-3, beta3Gn-T3, B3GNT3, B3GN-T3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	NM_014256, hCT1816925.2	204856_at	NP_055071.2, EAW84631.1
GeneID:3640	INSL3	19	17,927,322	17,932,320	4,998	-	3	4_A375_EGR1..1..4511, 4_A375_EGR1..1..4512, 4_A375_EGR1..1..4513	13864, 48, -10016	downstream, in gene, upstream	0	0	1	7.67	8	18	3	4_A375_EGR1..1	23	Gene INSL3	RLF, MGC119819, INSL3, MGC119818, RLNL	insulin-like 3 (Leydig cell)	NM_005543, hCT1967954.2, hCT2350704.0, hCT2356506.0, hCT28101.4	1553594_a_at, 214400_at, 214572_s_at	NP_005534.2, EAW84635.1, EAW84633.1, EAW84634.1, EAW84636.1
GeneID:3718	JAK3	19	17,935,591	17,958,841	23,250	-	3	4_A375_EGR1..1..4512, 4_A375_EGR1..1..4513, 4_A375_EGR1..1..4514	26569, 16505, 5545	downstream, in gene, in gene	0	0	1	12.67	12.33	21.67	3	4_A375_EGR1..1	26	Gene JAK3	JAKL, LJAK, L-JAK, JAK3, JAK3_HUMAN, JAK-3	Janus kinase 3	NM_000215, hCT2286624.0, hCT2286625.0, hCT2286627.0, hCT28104.3	207187_at, 211108_s_at, 211109_at, 227677_at	NP_000206.2, EAW84637.1, EAW84638.1, EAW84639.1, EAW84640.1
GeneID:6142	RPL18A	19	17,970,731	17,974,124	3,393	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2923, 2_A375_pNL97_plus_lncRNA_AR..1..4205, 4_A375_EGR1..1..4515, 4_A375_EGR1..1..4516, 4_A375_EGR1..1..4517	-203, -203, 21, 4405, 13045	upstream, upstream, in gene, downstream, downstream	1	1	1	13.67	16	21.33	3	4_A375_EGR1..1	31	Gene RPL18A	RPL18A, L18A		NM_000980, hCT2284456.0, hCT28103.3		NP_000971.1, EAW84642.1, EAW84641.1
GeneID:26780	SNORA68	19	17,973,397	17,973,529	132	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2923, 2_A375_pNL97_plus_lncRNA_AR..1..4205, 4_A375_EGR1..1..4515, 4_A375_EGR1..1..4516, 4_A375_EGR1..1..4517	-2869, -2869, -2645, 1739, 10379	upstream, upstream, upstream, downstream, downstream	1	1	1	13.67	16	21.33	3	4_A375_EGR1..1	31	Gene SNORA68	U68, RNU68, SNORA68	small nucleolar RNA, H/ACA box 68	NR_000012	1566402_at, 1566403_at	
GeneID:6528	SLC5A5	19	17,982,782	18,005,983	23,201	+	7	2_A375_pNL97_plus_lncRNA_AR..1..4206, 4_A375_EGR1..1..4516, 4_A375_EGR1..1..4517, 4_A375_EGR1..1..4518, 4_A375_EGR1..1..4519, 4_A375_EGR1..1..4520, 1_A375_pNL7_minus_lncRNA_AR..1..2924	17762, -7646, 994, 2050, 6634, 9778, 17762	in gene, upstream, in gene, in gene, in gene, in gene, in gene	1	1	1	15.83	20.17	16.33	6	2_A375_pNL97_plus_lncRNA_AR..1	72	Gene SLC5A5	SLC5A5, NIS, TDH1	solute carrier family 5 (sodium iodide symporter), member 5	NM_000453, hCT28100.1	211123_at	NP_000444.1, EAW84643.1
GeneID:115098	CCDC124	19	18,043,824	18,054,794	10,970	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2925, 2_A375_pNL97_plus_lncRNA_AR..1..4207	-272, 16	upstream, in gene	1	1	0	23	24	14	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CCDC124	CCDC124	coiled-coil domain containing 124	NM_138442, NM_001136203, hCT2284466.0, hCT2284467.0	225453_x_at, 225454_at	NP_612451.1, NP_001129675.1, EAW84644.1, EAW84645.1
GeneID:3780	KCNN1	19	18,062,111	18,109,930	47,819	+	2	4_A375_EGR1..1..4521, 4_A375_EGR1..1..4522	16385, 57729	in gene, downstream	0	0	1	10.5	10	20	2	4_A375_EGR1..1	22	Gene KCNN1	hSK1, SK1, SKCA1, KCa2.1, KCNN1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	NM_002248, hCT2284469.0, hCT28108.3	206231_at	NP_002239.2, EAW84647.1, EAW84646.1
GeneID:27106	ARRDC2	19	18,111,944	18,124,911	12,967	+	1	4_A375_EGR1..1..4522	7696	in gene	0	0	1	9	11	18	1	4_A375_EGR1..1	18	Gene ARRDC2	ARRDC2, CLONE24945, PP2703	arrestin domain containing 2	NM_015683, NM_001025604, hCT2284474.0, hCT2284476.0, hCT2356536.0, hCT28110.2	226055_at	NP_056498.1, NP_001020775.1, EAW84648.1, EAW84649.1, EAW84650.1, EAW84651.1

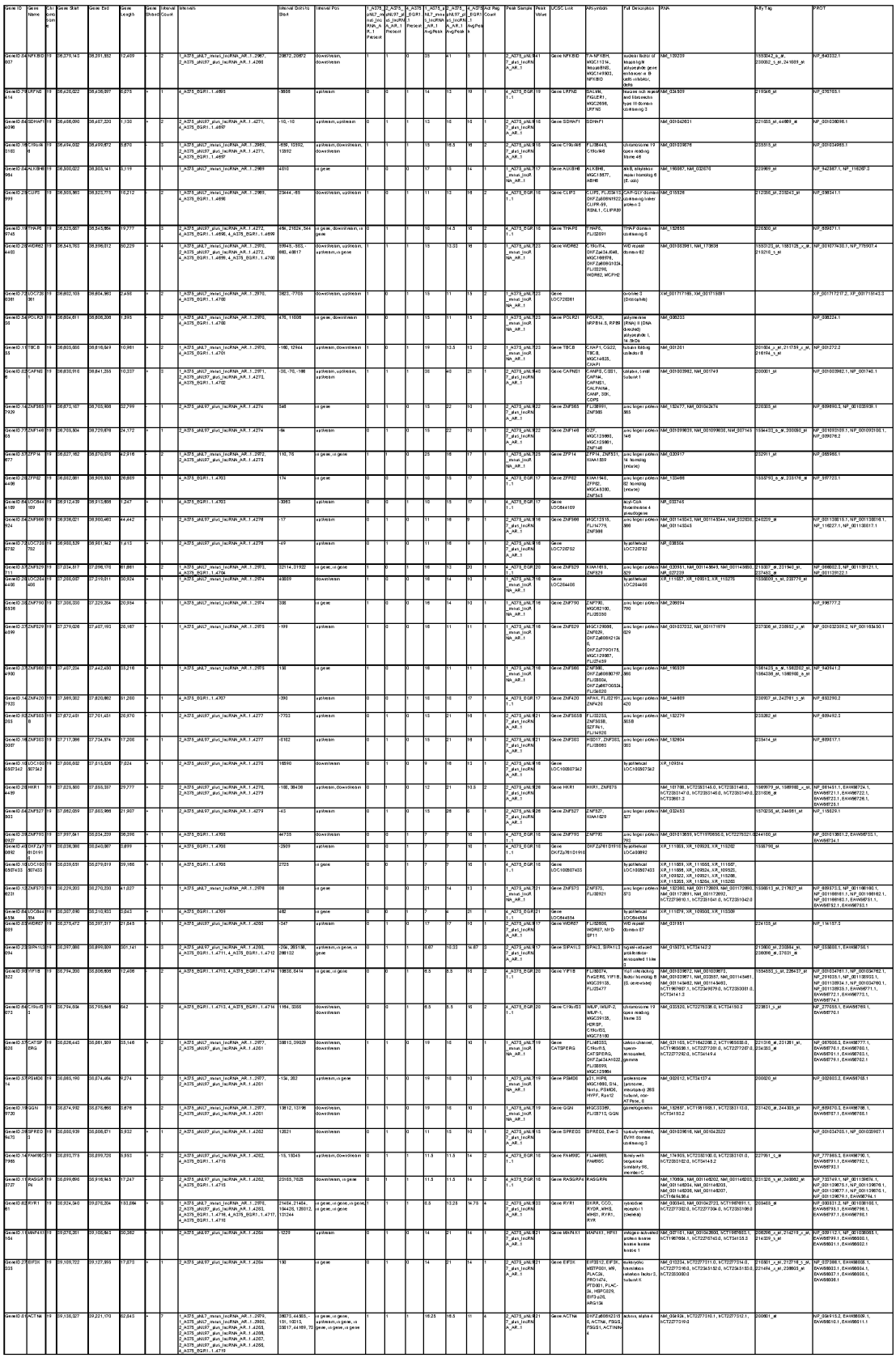


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_dN07_exon_junction_RNA_AR_1 Present	2_A375_2_A375_dN07_all_lncRNA_1 Present	4_A375_EGFR_1 Present	1_A375_2_A375_NS7_intron_lncRNA_AR_1 Avg Peak	2_A375_2_A375_dN07_all_lncRNA_AR_1 Avg Peak	4_A375_EGFR_1 Avg Peak	Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt y Tag	PROT
Gene ID-2331	MAST3	19	18,295,605	18,262,499	33,896	+	4	4_A375_EGFR1.1-4523, 4_A375_EGFR1.1-4536, 4_A375_EGFR1.1-4528, 4_A375_EGFR1.1-4538	11555, 12057, 28749, 29929			1	0	1	10.5	9.75	10.75	4	4_A375_EGFR_1.1	24	Gene MAST3	MAST3, KIAA0981	microtubule associated serine/threonine kinase 3	NM_015016	210045_at	NP_355931.1
Gene ID-3287	PI3KR2	19	18,284,018	18,261,343	17,327	+	3	4_A375_EGFR1.1-4526, 4_A375_EGFR1.1-4537, 4_A375_EGFR1.1-4538	3818, 13780, 21938		0	0	1	11	11.33	22	3	4_A375_EGFR_1.1	24	Gene PIK3R2	p85, PI3K, PIK3R2, p85-BETA	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	NM_005027, ICT-10155587-2, ICT-22844-09-0	1566620_s_at, 207163_s_at, 222932_s_at	NP_358716.1, ENSP00000389.1, ENSP00000490.1
Gene ID-1698	IP30	19	18,284,979	18,265,927	4,345	+	2	4_A375_EGFR1.1-4527, 4_A375_EGFR1.1-4538	-4693, -1373	upstream, vs gene	0	0	1	10	11.5	21	2	4_A375_EGFR_1.1	23	Gene IP30	IP30, IP30, GILT, MGC23039, IP30	interferon, gamma-inducible protein 30	NM_006332, ICT-10155676-2, ICT-19866-02-2, ICT-19866222-2, ICT-23421144-0, ICT-23421145-0, ICT-23985440-0	201422_at	NP_006323.2, ENSP00000482.1, ENSP00000490.1, ENSP00000493.1, ENSP00000494.1, ENSP00000498.1, ENSP00000495.1
Gene ID-5516	PDE4C	19	18,316,971	18,299,010	40,299	-	5	1_A375_dN07_minus_lncRNA_AR_1-2926, 2_A375_dN07_plus_lncRNA_AR_1-4209, 2_A375_dN07_plus_lncRNA_AR_1-4200, 2_A375_dN07_plus_lncRNA_AR_1-4211, 4_A375_EGFR1.1-4529, 4_A375_EGFR1.1-4532, 4_A375_EGFR1.1-4531	14882, 14500, 23634, 15426, 9160		1	1	1	20.33	23.67	19.67	3	2_A375_dN07_minus_lncRNA_AR_1	21	Gene PDE4C	PDE4C, MGC126222, DPDE1	phosphodiesterase 4C, cAMP-specific	NM_001081818, NM_001098819, NM_000922, NCT19679408, NCT22655900, NCT22655901, NCT22655902, NCT27993-3	208781_x_at, 208782_s_at, 210016_s_at	NP_001072287.1, NP_001092269.1, NP_000913.2, ENSP00000484.1, ENSP00000485.1, ENSP00000487.1, ENSP00000489.1
Gene ID-3836	KIAA1609	19	18,387,906	18,365,319	17,413	-	9	1_A375_dN07_minus_lncRNA_AR_1-2927, 1_A375_dN07_minus_lncRNA_AR_1-2928, 2_A375_dN07_plus_lncRNA_AR_1-4209, 2_A375_dN07_plus_lncRNA_AR_1-4200, 2_A375_dN07_plus_lncRNA_AR_1-4211, 4_A375_EGFR1.1-4533, 4_A375_EGFR1.1-4534, 4_A375_EGFR1.1-4535, 4_A375_EGFR1.1-4536, 4_A375_EGFR1.1-4538	7297, 533, 9861, 17186, 12019, 9892, 7235, 5145, 7765	upstream, upstream, upstream, vs gene, vs gene, vs gene, vs gene, upstream, upstream	1	1	1	13.75	14.38	10.75	6	4_A375_EGFR_1.1	23	Gene KIAA1609	MGC131731, KIAA1609	KIAA1609	NM_020349, NM_001145304, NM_001145305, NCT19432-2	223900_s_at, 223431_at	NP_079325.1, NP_001138778.1, NP_001139777.1, ENSP00000491.1
Gene ID-3778	JUND	19	18,290,983	18,282,432	7,899	-	6	1_A375_dN07_minus_lncRNA_AR_1-2927, 1_A375_dN07_minus_lncRNA_AR_1-2928, 2_A375_dN07_plus_lncRNA_AR_1-4209, 2_A375_dN07_plus_lncRNA_AR_1-4210, 2_A375_dN07_plus_lncRNA_AR_1-4211, 4_A375_EGFR1.1-4535, 4_A375_EGFR1.1-4538	-144, 6960, 1072, 10876, 1996, 592	upstream, downstream, vs gene, upstream, downstream, upstream	1	1	1	20	21.4	17.6	5	2_A375_dN07_plus_lncRNA_AR_1	27	Gene JUND	JUND, AP-1	jun D proto-oncogene	NM_005354	203751_x_at, 203752_x_at, 214326_x_at, 239117_x_at	NP_005345.5
Gene ID-1148	MIR3188	19	18,292,887	18,292,671	84	+	7	1_A375_dN07_minus_lncRNA_AR_1-2927, 1_A375_dN07_minus_lncRNA_AR_1-2928, 2_A375_dN07_plus_lncRNA_AR_1-4209, 2_A375_dN07_plus_lncRNA_AR_1-4210, 2_A375_dN07_plus_lncRNA_AR_1-4211, 4_A375_EGFR1.1-4535, 4_A375_EGFR1.1-4538	-311, 10057, 7915, 1527, 10121, 2422, 131	upstream, downstream, upstream, upstream, upstream, downstream, upstream	1	1	1	20	21.4	17.6	5	2_A375_dN07_plus_lncRNA_AR_1	27	Gene MIR3188	MIR3188	microRNA 3188	NR_036158		
Gene ID-2893	LSM4	19	18,417,717	18,414,801	18,264	-	8	1_A375_dN07_minus_lncRNA_AR_1-2928, 1_A375_dN07_minus_lncRNA_AR_1-2929, 2_A375_dN07_plus_lncRNA_AR_1-4212, 2_A375_dN07_plus_lncRNA_AR_1-4213, 4_A375_EGFR1.1-4537, 4_A375_EGFR1.1-4538, 4_A375_EGFR1.1-4539, 4_A375_EGFR1.1-4540, 4_A375_EGFR1.1-4541	-179, 21905, 5819, 16991, 14981, 13108, 11152, -173	upstream, downstream, upstream, downstream, vs gene, vs gene, upstream	1	1	1	13.29	14.14	10	7	2_A375_dN07_plus_lncRNA_AR_1	24	Gene LSM4	YER112W, LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_012321, ICT-22284-07-1, ICT-23460-00-0, ICT-23460301-0, ICT-23460302-0, ICT-27093-2	202758_s_at, 202737_s_at, 212824_x_at	NP_036453.1, ENSP00000488.1, ENSP00000489.1, ENSP00000497.1, ENSP00000499.1
Gene ID-5568	PGPEP1	19	18,451,408	18,480,760	29,353	+	3	1_A375_dN07_minus_lncRNA_AR_1-2931, 2_A375_EGFR1.1-4542, 4_A375_EGFR1.1-4543	33872, 2511, 19048	downstream, vs gene, vs gene	1	0	1	10.67	10.67	13.33	3	1_A375_dN07_minus_lncRNA_AR_1	23	Gene PGPEP1	PGP, FLJ20336, PGPEP1, MGC130612, Pca, PGP-I, PGP	pyroglutamyl-peptidase I	NM_017712, ICT-23396612-0, ICT-23396614-0, ICT-25281-2	1553165_s_at, 219891_at, 223485_s_at, 237282_at	NP_060162.1, ENSP00000492.1, ENSP00000493.1, ENSP00000491.1
Gene ID-1755	SSBP4	19	18,530,221	18,545,372	15,151	+	10	1_A375_dN07_minus_lncRNA_AR_1-2931, 1_A375_dN07_plus_lncRNA_AR_1-4214, 2_A375_dN07_plus_lncRNA_AR_1-4545, 2_A375_dN07_plus_lncRNA_AR_1-4547, 2_A375_dN07_plus_lncRNA_AR_1-4548, 2_A375_dN07_plus_lncRNA_AR_1-4549, 4_A375_EGFR1.1-4550, 4_A375_EGFR1.1-4551	337, -1772, 2341, 801, 4239, 11491, 12227, 5891, 7411, 18563	upstream, upstream, upstream, vs gene, vs gene, vs gene, downstream, downstream, downstream	1	1	1	11	12.75	21.5	8	4_A375_EGFR_1.1	27	Gene SSBP4	MGC33161, SSBP4	single stranded DNA binding protein 4	NM_001001990, NM_032827, ICT-22284-10-0, ICT-22845-01-0, ICT-22845-02-0, ICT-23985-01-0, ICT-23985-02-0	223226_x_at	NP_001001990.1, NP_116018.1, ENSP00000495.1, ENSP00000496.1, ENSP00000501.1, ENSP00000502.1, ENSP00000497.1, ENSP00000499.1
Gene ID-3192	SYNA1	19	18,545,186	18,549,111	3,913	-	8	1_A375_dN07_minus_lncRNA_AR_1-2928, 1_A375_dN07_minus_lncRNA_AR_1-2929, 1_A375_dN07_minus_lncRNA_AR_1-4547, 2_A375_dN07_minus_lncRNA_AR_1-4548, 4_A375_EGFR1.1-4549, 4_A375_EGFR1.1-4550, 4_A375_EGFR1.1-4551, 4_A375_EGFR1.1-4552, 4_A375_EGFR1.1-4553, 4_A375_EGFR1.1-4554, 4_A375_EGFR1.1-4555	13631, 7299, 6983, 2999, 1479, 723	downstream, downstream, downstream, vs gene, vs gene, upstream	0	0	1	8.33	10.83	21.33	6	4_A375_EGFR_1.1	25	Gene SYNA1	NOS, SYNA1, NOS, IPS	neuronal-specific synthase 1	NM_018386, NM_001170938, NM_001170939, NCT22284-72-0, NCT22845474, NCT23985-00-0, NCT23985-01-0	222343_s_at, 228477_at, 222352_s_at, 229262_x_at	NP_060856.1, NP_001164409.1, NP_001164410.1, ENSP00000504.1, ENSP00000505.1, ENSP00000507.1, ENSP00000508.1, ENSP00000503.1
Gene ID-8178	ELL	19	18,555,473	18,552,957	19,484	-	11	1_A375_dN07_minus_lncRNA_AR_1-2932, 1_A375_dN07_minus_lncRNA_AR_1-2933, 1_A375_dN07_plus_lncRNA_AR_1-4215, 2_A375_dN07_plus_lncRNA_AR_1-4216, 2_A375_dN07_plus_lncRNA_AR_1-4549, 2_A375_dN07_plus_lncRNA_AR_1-4550, 4_A375_EGFR1.1-4551, 4_A375_EGFR1.1-4552, 4_A375_EGFR1.1-4553, 4_A375_EGFR1.1-4554, 4_A375_EGFR1.1-4555	1705, -119, 1675, -191, 89525, 83005, 83785, 82297, 38641, 22152, -10467	vs gene, upstream, vs gene, upstream, downstream, downstream, downstream, vs gene, vs gene, upstream	1	1	1	20.33	24.33	17.33	9	1_A375_dN07_minus_lncRNA_AR_1	25	Gene ELL	C19orf17, ELL1, DKFZp434R916, ME, ELL	elongation factor RNA polymerase II	NM_006532, ICT-19427-01-3, ICT-23534-66-0	1568234_s_at, 234095_s_at, 234098_s_at	NP_006825.1, ENSP00000506.1, ENSP00000507.1
Gene ID-2357	FKBP8	19	18,842,966	18,834,383	11,815	-	3	1_A375_dN07_minus_lncRNA_AR_1-2933, 2_A375_dN07_plus_lncRNA_AR_1-4216, 4_A375_EGFR1.1-4555	21527, 21295, 10859	downstream, downstream, vs gene	1	1	1	66	83.5	66.5	2	1_A375_dN07_minus_lncRNA_AR_1	25	Gene FKBP8	FKBP8, FKBP38, MGC2741	FK506 binding protein 8, 38 kDa	NM_012181, ICT-10155628-2, ICT-22834-00-0, ICT-22834-02-0	208265_s_at, 223007_s_at, 40580_at	NP_036153.3, ENSP00000510.1, ENSP00000511.1
Gene ID-7967	C19orf39	19	18,866,572	18,850,197	11,825	+	1	2_A375_dN07_plus_lncRNA_AR_1-4217	13656	downstream	0	1	0	23	26	14	1	2_A375_dN07_plus_lncRNA_AR_1	25	Gene C19orf39	C19orf39, DKFZp686H03062, MSTP096, FLJ25493, MGC2740, MSTP096, FLJ43273	chromosome 19 open reading frame 39	NM_001177949, NM_001177947, NM_024089, NCT22842-26-0, NCT22855702-0, NCT26202-2	220276_s_at	NP_001165119, NP_001158420.1, NP_078974.2, ENSP00000712.1, ENSP00000714.1
Gene ID-7513	UBA52	19	18,862,814	18,866,270	5,856	+	1	2_A375_dN07_plus_lncRNA_AR_1-4217	-54	upstream	0	1	0	25	26	14	1	2_A375_dN07_plus_lncRNA_AR_1	26	Gene UBA52	CEP52, MGC126581, cb5, HUBC EP52, MGC126579, MGC57125, RPL40, UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	NM_001033930, NM_003333, ICT-19866-06-3, ICT-19866-07-3, ICT-19871981-1, ICT-19871982-1	231760_s_at	NP_001029032.1, NP_003324.1, ENSP00000513.1, ENSP00000514.1, ENSP00000515.1, ENSP00000517.1, ENSP00000518.1
Gene ID-3837	C19orf62	19	18,899,490	18,703,147	8,832	+	3	2_A375_dN07_plus_lncRNA_AR_1-2934, 2_A375_dN07_plus_lncRNA_AR_1-4218, 4_A375_EGFR1.1-4558	66, 121, 3335	vs gene, vs gene, upstream	1	1	1	39	42.5	15.5	2	2_A375_dN07_plus_lncRNA_AR_1	26	Gene C19orf62	FLJ39555, FLJ20350, C19orf62, FLJ21391, FLJ39105	chromosome 19 open reading frame 62	NM_001135619, NM_001130410, NCT19679941, NCT19679951, NCT22845401, NCT22855202, NCT22854-2	219582_at_s1200_at	NP_001030269.1, NP_001092555.1, ENSP00000479.1, ENSP00000480.1, ENSP00000482.1, ENSP00000722.1, ENSP00000723.1
Gene ID-8864	CRLF1	19	18,704,035	18,717,960	13,925	-	6	1_A375_dN07_minus_lncRNA_AR_1-2934, 1_A375_dN07_minus_lncRNA_AR_1-2935, 1_A375_dN07_minus_lncRNA_AR_1-4218, 1_A375_dN07_minus_lncRNA_AR_1-4557, 1_A375_dN07_minus_lncRNA_AR_1-4558, 4_A375_EGFR1.1-4559	18079, 16044, 14812, 12795, 839, -1026	downstream, downstream, downstream, vs gene, upstream, upstream	1	1	1	23.2	25	16.2	5	2_A375_dN07_plus_lncRNA_AR_1	26	Gene CRLF1	CLF-1, CISS, MRA, CRLF1, cytokine, CLF, CISS1	cytokine receptor like factor 1	NM_004750, NCT22854-31-0, ICT-22277-2	208013_at	NP_004741.1, ENSP00000724.1, ENSP00000725.1
Gene ID-2810	TMEM98	19	18,723,862	18,731,949	8,187	+	3	1_A375_dN07_minus_lncRNA_AR_1-2937, 4_A375_EGFR1.1-4559	-7295, -5199, -994	upstream, vs gene, upstream	0	0	1	12.67	13.33	10.67	3	1_A375_dN07_minus_lncRNA_AR_1	27	Gene TMEM98	TMEM98L, C19orf4, BSW17	transmembrane protein 98-like	NM_012109, ICT-22845-07-0, ICT-27275-2	219693_at	NP_036241.1, ENSP00000726.1, ENSP00000727.1
Gene ID-3858	KLHL26	19	18,747,836	18,761,302	33,464	+	3	2_A375_dN07_plus_lncRNA_AR_1-4219, 2_A375_dN07_plus_lncRNA_AR_1-4560, 4_A375_EGFR1.1-4560	23806, 210, 23854	vs gene, vs gene, vs gene	0	1	1	17	12.33	16.33	3	2_A375_dN07_plus_lncRNA_AR_1	22	Gene KLHL26	KLHL26, FLJ11276	kelch-like 26 (Drosophila)	NM_016118, ICT-22845-09-0, ICT-27277-2	219254_at	NP_057208.1, ENSP00000729.1, ENSP00000730.1
Gene ID-2330	CRTC1	19	18,794,425	18,893,143	99,718	+	12	4_A375_EGFR1.1-4561, 4_A375_EGFR1.1-4562, 4_A375_EGFR1.1-4563, 4_A375_EGFR1.1-4564, 4_A375_EGFR1.1-4565, 4_A375_EGFR1.1-4566, 4_A375_EGFR1.1-4567, 4_A375_EGFR1.1-4568, 4_A375_EGFR1.1-4569, 4_A375_EGFR1.1-4570, 4_A375_EGFR1.1-4571, 4_A375_EGFR1.1-4572, 4_A375_EGFR1.1-4573	22069, 21973, 5911, 21631, 62035, 70281, 62019, 84775, 63855, 81927, 79847, 107855	vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene, vs gene	0	1	1	9.17	10.25	21.08	12	1_A375_dN07_minus_lncRNA_AR_1	28	Gene CRTC1	TORC1, WWTR1, CRTC1, KIAA0816, MECT1, FLJ44227	CREB regulated transcription coactivator 1	NM_015321, NM_001079942, NCT19679963, NCT22866102, NCT22866103, NCT26202-2	207189_x_at, 213091_at	NP_056136.2, NP_001019932.1, ENSP00000731.1, ENSP00000732.1, ENSP00000733.1
Gene ID-2357	COMP	19	18,895,903	18,902,114	6,831	-	4	1_A375_dN07_minus_lncRNA_AR_1-4572, 1_A375_dN07_minus_lncRNA_AR_1-4573, 4_A375_EGFR1.1-4574, 4_A375_EGFR1.1-4576	13092, 11042, 3462, -6982	downstream, downstream, vs gene, upstream	0	0	1	9	11.5	21	4	4_A375_EGFR_1.1	23	Gene COMP	MED, PSACH, EPD1, MGC14785, THBS5, COMP, MGC131919, EDM4	cartilage oligomeric matrix protein	NM_000095, ICT-22845441-0, ICT-23985-04-0, ICT-27273-2	205713_s_at	NP_000086.2, ENSP00000738.1, ENSP00000739.1, ENSP00000740.1, ENSP00000741.1
Gene ID-3992	UPF1	19	18,942,744	18,979,009	36,266	+	4	1_A375_dN07_minus_lncRNA_AR_1-2938, 2_A375_dN07_plus_lncRNA_AR_1-4220, 4_A375_EGFR1.1-4576, 4_A375_EGFR1.1-4577	186, 72, 24776, 33844	vs gene, vs gene, vs gene, vs gene	1	1	1	15	16.33	14.67	3	1_A375_dN07_minus_lncRNA_AR_1	27	Gene UPF1	RENT1, UPF1, SMG2Z1, HUPF1, FLJ46894, dkfzp761, MORF1, MORF1, FLJ43009	UPF1 regulator of nonsense transcripts homolog (yeast)	NM_002911, ICT-22845-44-0, ICT-22845-45-0, ICT-23985702-0, ICT-27272-3	200937_s_at, 211166_s_at	NP_002902.2, ENSP00000742.1, ENSP00000743.1, ENSP00000744.1, ENSP00000745.1, ENSP00000746.1, ENSP00000747.1, ENSP00000748.1, ENSP00000749.1, ENSP00000750.1, ENSP00000751.1, ENSP00000752.1, ENSP00000753.1, ENSP00000754.1, ENSP00000755.1, ENSP00000756.1, ENSP00000757.1
Gene ID-3443	LNS01	19	18,979,361	19,006,953	27,592	+	4	4_A375_EGFR1.1-4577, 4_A375_EGFR1.1-4578, 4_A375_EGFR1.1-4579, 4_A375_EGFR1.1-4580	28865, 12041, 1913, -6865	downstream, vs gene, vs gene, upstream	0	0	1	11.5	13.25	17.5	4	4_A375_EGFR_1.1	20	Gene LNS01	MGC90349, LNS01, LNS1, Ceb51, UOG1	LNS1 homolog, subunit (S. cerevisiae)	NM_021397, NM_176207	229445_at	NP_067650.1, NP_787530.1
Gene ID-3443	LNS01-GDF1	19	18,979,361	19,006,953	27,592	+	4	4_A375_EGFR1.1-4577, 4_A375_EGFR1.1-4578, 4_A375_EGFR1.1-4579, 4_A375_EGFR1.1-4580	28865, 12041, 1913, -6865	downstream, vs gene, vs gene, upstream	0	0	1	11.5	13.25	17.5	4	4_A375_EGFR_1.1	20	Gene LNS01-GDF1		LNS1 homolog, subunit (S. cerevisiae) (LNS01), growth differentiation factor 1 transcription unit			
Gene ID-2857	GDF1	19	18,979,361	19,006,953	27,592	+	4	4_A375_EGFR1.1-4577, 4_A375_EGFR1.1-4578, 4_A375_EGFR1.1-4579, 4_A375_EGFR1.1-4580	28865, 12041, 1913, -6865	downstream, vs gene, vs gene, upstream	0	0	1	11.5	13.25	17.5	4	4_A375_EGFR_1.1	20	Gene GDF1	GDF1		NM_031492		NP_620450.1
Gene ID-1116	COPE	19	19,010,523	19,030,199	19,676	-	7	1_A375_dN07_minus_lncRNA_AR_1-2938, 2_A375_dN07_plus_lncRNA_AR_1-4221, 4_A375_EGFR1.1-4579, 4_A375_EGFR1.1-4580, 4_A375_EGFR1.1-4581, 4_A375_EGFR1.1-4582, 4_A375_EGFR1.1-4583	-279, -89, 34799, 14663, -2193, 6763, -9981	upstream, upstream, downstream, vs gene, upstream, upstream, upstream	1	1	1	12.17	15	18.83	6	2_A375_dN07_plus_lncRNA_AR_1	28	Gene COPE	FLJ10241, COPE, epsilon-COP	coatomer protein complex, subunit epsilon	NM_007263, NM_178442, NM_178444, NCT22854-30-0, NCT22854-31-0, NCT22854-32-0, NCT22854-33-0, NCT23534-01-0, NCT23534-76-0, NCT23984750-0, NCT23984760-0, NCT23984770-0, NCT23984780-0	201284_at_s_220489_at	NP_009194.2, NP_958474.1, NP_958476.1, ENSP00000760.1, ENSP00000761.1, ENSP00000762.1, ENSP00000763.1, ENSP00000764.1, ENSP00000765.1, ENSP00000766.1, ENSP00000767.1
Gene ID-3443	HOMER3	19	19,040,010	19,052,561	12,551	-	8	1_A375_dN07_minus_lncRNA_AR_1-2938, 2_A375_dN07_plus_lncRNA_AR_1-4221, 2_A375_dN07_plus_lncRNA_AR_1-4581, 4_A375_EGFR1.1-4582, 4_A375_EGFR1.1-4583, 4_A375_EGFR1.1-4584, 4_A375_EGFR1.1-4585, 4_A375_EGFR1.1-4586	21899, 21763, 18269, 13049, 11651, 9705, 639, -7479	downstream, downstream, downstream, downstream, downstream, vs gene, vs gene, upstream	1	1	1	11.43	12.43	16.86	7	2_A375_dN07_plus_lncRNA_AR_1	28	Gene HOMER3	VESL3, HOMER-3, HOMER3	homer homolog 3 (Drosophila)	NM_054032, NM_001145721, NM_001145722, NM_001145724, NM_027297, NCT19679951, NCT22854-33-0, NCT22854-34-0, NCT22854-37-0	204567_at_215489_x_at, 222222_s_at	NP_056370.1, NP_001139194.1, NP_001139195.1, NP_001139196.1, ENSP00000768.1, ENSP00000769.1, ENSP00000770.1, ENSP00000771.1, ENSP00000772.1
Gene ID-1016	SPATS2L	19	19,101,977	19,144,390	42,893	-	3	1_A375_dN07_minus_lncRNA_AR_1-2937, 2_A375_dN07_plus_lncRNA_AR_1-4222, 4_A375_EGFR1.1-4587	-152, -116, -9230	upstream, upstream, upstream	1	1	1	16.5	17.5	12.5	2	1_A375_dN07_minus_lncRNA_AR_1	28	Gene SPATS2	SPATS2, FLJ21555, SHZ2, DKFZp686H0222 DKFZp779Q2418	SPATS2 like	NM_014264, NM_001017092, NCT19679974, NCT22853703-0, NCT22853704-0, NCT22853705-0, NCT22853706-0, NCT23923-3	212080_at_212081_at, 215803_s_at_214092_x_at, 84371_at	NP_055099.2, NP_001017092.2, ENSP00000861.1, ENSP00000862.1, ENSP00000863.1, ENSP00000773.1, ENSP00000861.1, ENSP00000770.1, ENSP00000771.1, ENSP00000772.1
Gene ID-3554	ARMC8	19	19,144,471	19,166,900	24,309	+	6	1_A375_dN07_minus_lncRNA_AR_1-2937, 2_A375_dN07_plus_lncRNA_AR_1-4222, 2_A375_dN07_plus_lncRNA_AR_1-4223, 4_A375_EGFR1.1-4587, 4_A375_EGFR1.1-4588	41, 23, 30165, 9125, 10832, 23461	vs gene, vs gene, downstream, vs gene, vs gene, downstream	1	1	1	12.5	13.2	15.8	5	1_A375_dN07_minus_lncRNA_AR_1	28	Gene ARMC8	ARMC8, KIAA0123, MGC29896	armadillo repeat containing 8	NM_032515, NCT22561-02-0, ICT-23924-2	221758_at	NP_115903.1, ENSP00000776.1, ENSP00000778.1
Gene ID-2850	SLC35A2	19	19,174,803	19,223,704	48,901	+	2	2_A375_dN07_plus_lncRNA_AR_1-4223, 4_A375_EGFR1.1-4589	-147, -4651	upstream, upstream	0	0	1	11.5	14.5	13	2	2_A375_dN07_plus_lncRNA_AR_1	22	Gene SLC35A2	SLC35A2, MGC29896	solute carrier family 35, member A2	NM_175338, ICT-22561-03-0, ICT-23985-09-0, ICT-24027-2	214029_at_228797_at, 220921_at_242274_s_at	NP_549371.2, ENSP00000779.1, ENSP00000777.1, ENSP00000778.1
Gene ID-4444	TMEM98	19	19,230,430	19,249,397	19,037	-	2	4_A375_EGFR1.1-4590, 4_A375_EGFR1.1-4591	980, -7215	vs gene, upstream	0	0	1	8	9.5	20.5	2	4_A375_EGFR_1.1	24	Gene TMEM91A	FLJ36422, MRD5, ZN, TMEM91A, FLJ39643	transmembrane protein 91A	NM_017914, ICT-22853-07-0, ICT-23985-98-0, ICT-23985-97-0, ICT-23985-99-0, ICT-23985700-0, ICT-23985701-0, ICT-27911-2	218743_s_at_43977_at	NP_060384.1, ENSP00000780.1, ENSP00000782.1, ENSP00000783.1, ENSP00000784.1, ENSP00000787.1, ENSP00000788.1, ENSP00000789.1, ENSP00000790.1
Gene ID-4237	LOC729991-MEF2B	19	19,256,376	19,305,400	47,224	+	6	1_A375_dN07_minus_lncRNA_AR_1-2938, 1_A375_dN07_plus_lncRNA_AR_1-4224, 2_A375_dN07_plus_lncRNA_AR_1-4224, 2_A375_dN07_plus_lncRNA_AR_1-4225, 2_A375_dN07_plus_lncRNA_AR_1-4226, 4_A375_EGFR1.1-4594, 4_A375_EGFR1.1-4595	590, 590, 34696, 44920, 31765, 22165, 6702, 294	vs gene, vs gene, downstream, vs gene, vs gene, vs gene, vs gene, vs gene	1	1	1	16.17	16.17	20.67	6	1_A375_dN07_minus_lncRNA_AR_1	24	Gene LOC729991-MEF2B	LOC729991-MEF2B, MEF2B-MEF2BNB-MEF2B	LOC729991-MEF2B	NM_005919, NM_001033, NM_001033, NCT22853-08-0, NCT22853-09-0, NCT22853-10-0, NCT22853-57-0, NCT23932-3	1553976_at, 203324_at, 203326_at	NP_005910.1, ENSP00000790.1, ENSP00000791.1, ENSP00000793.1, ENSP00000794.1, ENSP00000795.1
Gene ID-3277	MEF2B	19	19,256,376	19,281,098	24,722	+	4	4_A375_EGFR1.1-4592, 4_A375_EGFR1.1-4593, 4_A375_EGFR1.1-4594, 4_A375_EGFR1.1-4595	22254, 24816, 9486, -134	downstream, vs gene, vs gene, upstream	0	0	1	8.5	8.5	21	4	4_A375_EGFR_1.1	24	Gene MEF2B	FLJ32645, RSAF32, MEF2B	myocyte enhancer factor 2B	NM_001145795		NP_001132637.1
Gene ID-7529	LOC729991	19	19,257,713	19,305,400	47,687	+	5	1_A375_dN07_minus_lncRNA_AR_1-2938, 2_A375_dN07_plus_lncRNA_AR_1-4224, 2_A375_dN07_plus_lncRNA_AR_1-4225, 4_A375_EGFR1.1-4594, 4_A375_EGFR1.1-4595	590, 590, 33166, 43782, 264	vs gene, vs gene, downstream, vs gene, vs gene	1	1	1	23.67	24	21	5	1_A375_dN07_minus_lncRNA_AR_1	24	Gene LOC729991	LOC729991	MEF2B neighbor	NM_001145793, NM_001145794	MEF2B neighbor	NP_001139265.1, NP_001139266.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.8625	RFXANK	19	19,303,008	19,312,678	9,670	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2938, 1_A375_pNL7_minus_lncRNA_AR..1..2939, 2_A375_pNL97_plus_lncRNA_AR..1.4224, 2_A375_pNL97_plus_lncRNA_AR..1.4225, 4_A375_EGR1..1.4594, 4_A375_EGR1..1.4595, 4_A375_EGR1..1.4598	0, 11296, 32, 11296, -6400, 128, 11003	in gene, downstream, in gene, downstream, upstream, in gene, downstream	1	1	1	29	26.67	19	3	1_A375_pNL7_minus_lncRNA_AR..1	54	Gene RFXANK	MGC138628, RFX-B, RFXANK, ANKRA1, BLS, F14150_1	regulatory factor X associated ankyrin-containing protein	NM_003721, NM_134440, hCT1967973.1, hCT2284184.0, hCT2284185.0, hCT2284187.0, hCT29803.2	202758_s_at	NP_003712.1, NP_604389.1, EAW84795.1, EAW84796.1, EAW84798.1, EAW84799.1, EAW84797.1
GeneID.126382	NR2C2AP	19	19,312,224	19,314,238	2,014	-	6	1_A375_pNL7_minus_lncRNA_AR..1..2938, 1_A375_pNL7_minus_lncRNA_AR..1..2939, 2_A375_pNL97_plus_lncRNA_AR..1.4224, 2_A375_pNL97_plus_lncRNA_AR..1.4225, 4_A375_EGR1..1.4595, 4_A375_EGR1..1.4598	11230, -66, 11198, -66, 11102, 227	downstream, upstream, downstream, upstream, downstream, in gene	1	1	1	39	38	18.5	2	1_A375_pNL7_minus_lncRNA_AR..1	54	Gene NR2C2AP	NR2C2AP, TRA16	nuclear receptor 2C2-associated protein	NM_176880	226839_at	NP_795361.1
GeneID.1463	NCAN	19	19,322,782	19,363,061	40,279	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2939, 1_A375_pNL7_minus_lncRNA_AR..1..2940, 2_A375_pNL97_plus_lncRNA_AR..1.4225, 4_A375_EGR1..1.4596, 4_A375_EGR1..1.4597, 4_A375_EGR1..1.4598	-8478, 3074, -8478, -8771, 12114, 26199	upstream, in gene, upstream, upstream, in gene, in gene	1	1	1	17	16	16.5	4	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene NCAN	FLJ44681, CSPG3, NCAN	neurocan	NM_004386, hCT2284189.0, hCT29801.2	205143_at	NP_004377.2, EAW84802.1, EAW84801.1
GeneID.57794	SF4	19	19,387,322	19,431,307	43,985	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2941, 2_A375_pNL97_plus_lncRNA_AR..1.4226	-85, -85	upstream, upstream	1	1	0	15	27	14	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SF4	DKFZp434E2216, SUGP1, RBP, F23858, SF4	SURP and G patch domain containing 1	NM_172231, hCT2285346.1, hCT2285348.1, hCT2285349.1, hCT2356611.0, hCT29821.3	209547_s_at, 215004_s_at	NP_757386.2, EAW84810.1, EAW84808.1, EAW84809.1, EAW84811.1, EAW84812.1
GeneID.23383	KIAA0892	19	19,431,630	19,469,563	37,933	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2941, 2_A375_pNL97_plus_lncRNA_AR..1.4226, 4_A375_EGR1..1.4599	-238, -238, 14418	upstream, upstream, in gene	1	1	1	12.5	16	15	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene KIAA0892	MAU2L, MGC75361, SCC4, KIAA0892, MAU2, mau-2	KIAA0892	NM_015329, hCT1964195.1, hCT2284192.0, hCT2284193.0, hCT2284195.0	212505_s_at, 216926_s_at, 217652_at, 227465_at	NP_056144.3, EAW84817.1, EAW84814.1, EAW84815.1, EAW84816.1
GeneID.54815	GATAD2A	19	19,496,642	19,619,741	123,099	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2942, 2_A375_pNL97_plus_lncRNA_AR..1.4227, 2_A375_pNL97_plus_lncRNA_AR..1.4228, 4_A375_EGR1..1.4600, 4_A375_EGR1..1.4601, 4_A375_EGR1..1.4602, 4_A375_EGR1..1.4603	19630, 19630, 130430, -256, 398, 117550, 130142	in gene, in gene, downstream, upstream, in gene, in gene, downstream	1	1	1	17.2	19.6	19.6	5	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene GATAD2A	FLJ21017, GATAD2A, p66alpha, FLJ20085	GATA zinc finger domain containing 2A	NM_017660, hCT2284196.0, hCT2284198.0, hCT2284199.0, hCT2284200.0, hCT2284202.0	218131_s_at, 222528_at, 229166_s_at, 234294_x_at, 236932_s_at, 238324_at	NP_060130.3, EAW84823.1, EAW84819.1, EAW84820.1, EAW84821.1, EAW84822.1
GeneID.83983	TSSK6	19	19,625,028	19,626,469	1,441	-	2	2_A375_pNL97_plus_lncRNA_AR..1.4228, 4_A375_EGR1..1.4603	-803, -315	upstream, upstream	0	1	1	20	29	24	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene TSSK6	FKSG82, TSSK6, SSTK, FLJ24002, CT72, TSSK4	testis-specific serine kinase 6	NM_032037, hCT1640514.2, hCT2285333.0	224409_s_at, 230989_s_at	NP_114426.1, EAW84824.1, EAW84825.1
GeneID.51079	NDUFA13	19	19,627,019	19,639,013	11,994	+	2	2_A375_pNL97_plus_lncRNA_AR..1.4228, 4_A375_EGR1..1.4603	53, -235	in gene, upstream	0	1	1	20	29	24	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene NDUFA13	CGI-39, GRIM-19, FLJ58045, GRIM19, CDA016, B16.6, FLJ59191, NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	NM_015965, hCT29804.2	220864_s_at	NP_057049.5, EAW84826.1
GeneID.374887	YJEFN3	19	19,639,670	19,648,393	8,723	+	3	4_A375_EGR1..1.4604, 4_A375_EGR1..1.4605, 4_A375_EGR1..1.4606	10922, 14954, 18250	downstream, downstream, downstream	0	0	1	5	6.67	20.33	3	4_A375_EGR1..1	22	Gene YJEFN3	FLJ44968, YJEFN3, MGC138490	YjeF N-terminal domain containing 3	NM_001190328, NM_198537, hCT1641673.2, hCT2356578.0, hCT2356577.0	229981_x_at	NP_001177257.1, NP_940939.2, EAW84827.1, EAW84828.1, EAW84829.1
GeneID.148113	CILP2	19	19,649,074	19,657,468	8,394	+	4	4_A375_EGR1..1.4604, 4_A375_EGR1..1.4605, 4_A375_EGR1..1.4606, 4_A375_EGR1..1.4607	1518, 5550, 8846, 11918	in gene, in gene, downstream, downstream	0	0	1	6.25	6.75	21.25	4	4_A375_EGR1..1	24	Gene CILP2	CLIP-2, MGC45771, CILP2	cartilage intermediate layer protein 2	NM_153221, hCT2356562.0, hCT29809.3		NP_694953.2, EAW84833.1, EAW84832.1
GeneID.80714	PBX4	19	19,672,522	19,729,439	56,917	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2943, 2_A375_pNL97_plus_lncRNA_AR..1.4229, 4_A375_EGR1..1.4608	27007, 27231, -10209	in gene, in gene, upstream	1	1	1	18	19.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene PBX4	PBX4		NM_025245, hCT2356605.0, hCT29815.2	230536_at	NP_079521.1, EAW84834.1, EAW84835.1
GeneID.9170	LPAR2	19	19,734,464	19,739,039	4,575	-	1	4_A375_EGR1..1.4608	-609	upstream	0	0	1	13	14	20	1	4_A375_EGR1..1	20	Gene LPAR2	LPA-2, LPAR2, EDG-4, EDG4, FLJ93869, LPA2	lysophosphatidic acid receptor 2	NM_004720, hCT2285320.0, hCT29806.3	206722_s_at, 206723_s_at	NP_004711.2, EAW84836.1, EAW84837.1
GeneID.51291	GMIP	19	19,740,285	19,754,455	14,170	-	2	4_A375_EGR1..1.4608, 4_A375_EGR1..1.4609	14807, -6201	downstream, upstream	0	0	1	10	12.5	21.5	2	4_A375_EGR1..1	23	Gene GMIP	GMIP		NM_016573, hCT1969005.1, hCT1969007.1, hCT2285408.0, hCT2285409.0, hCT2285411.0, hCT2285412.0, hCT2285413.0, hCT29814.2	218913_s_at, 222762_s_at	NP_057657.2, EAW84839.1, EAW84838.1, EAW84840.1, EAW84841.1, EAW84845.1, EAW84842.1, EAW84843.1, EAW84844.1
GeneID.57130	ATP13A1	19	19,756,007	19,774,503	18,496	-	2	4_A375_EGR1..1.4609, 4_A375_EGR1..1.4610	13647, 455	in gene, in gene	0	0	1	9	13.5	20	2	4_A375_EGR1..1	23	Gene ATP13A1	ATP13A1, ATP13A, DKFZp761L1623, FLJ43873, KIAA1825, FLJ90317, FLJ41786, FLJ31858, CGI-152	ATPase type 13A1	NM_020410, hCT1817187.1, hCT2285392.0, hCT2285394.0, hCT2285398.0, hCT2285402.0, hCT2285404.0, hCT2285405.0, hCT29817.2	218052_s_at	NP_065143.2, EAW84852.1, EAW84848.1, EAW84849.1, EAW84851.1, EAW84853.1, EAW84847.1, EAW84850.1, EAW84854.1
GeneID.94039	ZNF101	19	19,779,663	19,791,138	11,475	+	1	4_A375_EGR1..1.4610	-5615	upstream	0	0	1	11	16	17	1	4_A375_EGR1..1	17	Gene ZNF101	DKFZp570I0164, ZNF101, MGC149566, HZF12, MGC149565	zinc finger protein 101	NM_033204, hCT2284214.0, hCT2356563.0, hCT29810.2	1552633_at, 1552634_a_at	NP_149981.2, EAW84855.1, EAW84856.1, EAW84857.1
GeneID.7561	ZNF14	19	19,821,281	19,843,921	22,640	-	1	4_A375_EGR1..1.4611	-10207	upstream	0	0	1	5	6	16	1	4_A375_EGR1..1	16	Gene ZNF14	GIOT-4, KOX6, ZNF14	zinc finger protein 14	NM_021030, hCT29805.2	219854_at	NP_066358.2, EAW84858.1
GeneID.100287160	LOC100287160	19	19,855,407	19,856,269	862	-	2	4_A375_EGR1..1.4611, 4_A375_EGR1..1.4612	2141, -4819	downstream, upstream	0	0	1	7.5	7	18.5	2	4_A375_EGR1..1	21	Gene LOC100287160		hypothetical protein LOC100287160	XM_003119722, XM_002343635, XM_002347914		XP_003119770.1, XP_002343676.1, XP_002347955.1
GeneID.284440	LOC284440	19	19,867,180	19,887,222	20,042	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2944, 2_A375_pNL97_plus_lncRNA_AR..1.4230, 4_A375_EGR1..1.4612	-42, -234, 28134	upstream, upstream, downstream	1	1	1	21	23.5	20	2	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene LOC284440	MGC39821, FLJ12356	hypothetical LOC284440	NR_026956	1555363_s_at, 1569316_at	
GeneID.91120	ZNF682	19	20,115,227	20,150,277	35,050	-	1	2_A375_pNL97_plus_lncRNA_AR..1.4231	5	in gene	0	1	0	18	15	12	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene ZNF682	BC39498_3, FLJ90362, ZNF682	zinc finger protein 682	NM_033196, NM_001077349, hCT1959868.1, hCT2283180.0, hCT27970.3	216468_s_at, 242915_at	NP_149973.1, NP_001070817.1, EAW84868.1, EAW84869.1, EAW84870.1
GeneID.80264	ZNF430	19	21,203,426	21,242,852	39,426	+	1	2_A375_pNL97_plus_lncRNA_AR..1.4234	222	in gene	0	1	0	11	26	13	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ZNF430	FLJ13659, ZNF430, DKFZp762K012, MGC133232	zinc finger protein 430	NM_025189, NM_001172671, hCT28492.3	206629_x_at, 238814_x_at	NP_079465.3, NP_001166142.1, EAW84884.1
GeneID.7562	ZNF708	19	21,473,963	21,512,212	38,249	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2946	160	in gene	1	0	0	21	14	7	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ZNF708	FLJ16755, ZNF15, ZNF708, FLJ46310, ZNF15L1, KOX8, DKFZp686L10267	zinc finger protein 708	NM_021269, hCT2283892.0, hCT2356625.0	239482_x_at	NP_067092.2, EAW84892.1, EAW84891.1
GeneID.400680	LOC400680	19	21,866,517	21,886,040	19,523	+	1	4_A375_EGR1..1.4613	-8613	upstream	0	0	1	13	12	14	1	4_A375_EGR1..1	14	Gene LOC400680	DKFZp686K1636, FLJ40082	hypothetical LOC400680	XR_109581, XR_115251	1562348_at	
GeneID.163227	ZNF100	19	21,906,843	21,950,430	43,587	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2947, 2_A375_pNL97_plus_lncRNA_AR..1.4235, 4_A375_EGR1..1.4614	126, 446, 382	in gene, in gene, in gene	1	1	1	19	16	19	1	4_A375_EGR1..1	19	Gene ZNF100	FLJ44587, ZNF100	zinc finger protein 100	NM_173531, hCT1815314.2, hCT2283885.1	1569637_at, 238791_at	NP_775802.2, EAW84905.1, EAW84906.1
GeneID.7594	ZNF43	19	21,987,752	22,018,970	31,218	-	1	4_A375_EGR1..1.4615	314	in gene	0	0	1	10	15	21	1	4_A375_EGR1..1	21	Gene ZNF43	KOX27, ZNF43, ZNF39L1, HTF6, DKFZp686L1654	zinc finger protein 43	NM_003423, hCT2283882.0, hCT27966.2	206695_x_at, 222136_x_at	NP_003414.2, EAW84908.1, EAW84909.1
GeneID.148198	ZNF98	19	22,573,899	22,605,148	31,249	-	1	2_A375_pNL97_plus_lncRNA_AR..1.4236	-100	upstream	0	1	0	15	17	12	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ZNF98	ZNF98, F7175, MGC129634, ZNF739	zinc finger protein 98 (F7175)	NM_001098626	215532_x_at	NP_001092096.1
GeneID.440518	LOC440518	19	22,779,059	22,786,352	7,293	+	2	4_A375_EGR1..1.4618, 4_A375_EGR1..1.4619	6637, 14109	in gene, downstream	0	0	1	5	3.5	18	2	4_A375_EGR1..1	19	Gene LOC440518		golgin A2 pseudogene	NR_033899		
GeneID.374890	LOC374890	19	22,798,359	22,806,773	8,414	-	2	4_A375_EGR1..1.4619, 4_A375_EGR1..1.4620	13805, 501	downstream, in gene	0	0	1	5.5	7.5	17.5	2	4_A375_EGR1..1	18	Gene LOC374890		hypothetical LOC374890	XR_111642, XR_109585, XR_115254	1558405_s_at	
GeneID.100129543	ZNF730	19	23,299,883	23,329,757	29,874	+	1	4_A375_EGR1..1.4622	213	in gene	0	0	1	13	11	23	1	4_A375_EGR1..1	23	Gene ZNF730	ZNF730	zinc finger protein 730	XM_001715065, XM_001719792, XM_001718960		XP_001715117.3, XP_001719844.3, XP_001719012.3
GeneID.100132815	LOC100132815	19	23,437,855	23,457,032	19,177	-	2	2_A375_pNL97_plus_lncRNA_AR..1.4237, 4_A375_EGR1..1.4624	23736, 24152	downstream, downstream	0	1	1	16	23	20	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100132815	FLJ12978	hypothetical LOC100132815	XR_111644, XR_109587, XR_115256		
GeneID.148213	ZNF681	19	23,921,997	23,941,693	19,696	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2948, 2_A375_pNL97_plus_lncRNA_AR..1.4238	-4115, -4387	upstream, upstream	1	1	0	17	21	12	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ZNF681	ZNF681, FLJ31526	zinc finger protein 681	NM_138286, hCT1838384.2, hCT2284016.0, hCT2356532.0		NP_612143.2, EAW84946.1, EAW84947.1, EAW84949.1
GeneID.730087	ZNF726	19	24,097,684	24,106,517	8,833	+	1	2_A375_pNL97_plus_lncRNA_AR..1.4240	268	in gene	0	1	0	16	18	17	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ZNF726	ZNF726	zinc finger protein 726	NM_001190829		NP_001177758.1
GeneID.148189	LOC148189	19	28,281,401	28,284,848	3,447	-	1	2_A375_pNL97_plus_lncRNA_AR..1.4242	-528	upstream	0	1	0	17	14	11	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene LOC148189		hypothetical LOC148189	NR_027301	1558256_at, 232281_at, 242663_at	
GeneID.100506694	LOC100506694	19	28,284,375	28,296,680	12,305	+	1	2_A375_pNL97_plus_lncRNA_AR..1.4242	1001	in gene	0	1	0	17	14	11	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene LOC100506694		hypothetical LOC100506694	XR_109507		
GeneID.10775	POP4	19	30,097,170	30,108,162	10,992	+	1	2_A375_pNL97_plus_lncRNA_AR..1.4244	-194	upstream	0	1	0	10	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene POP4	POP4, RPP29	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)	NM_006627, NR_027366	202868_s_at, 227583_at	NP_006618.1
GeneID.79156	PLEKHF1	19	30,156,327	30,166,384	10,057	+	2	4_A375_EGR1..1.4631, 4_A375_EGR1..1.4632	9593, 13385	in gene, downstream	0	0	1	6.5	6.5	15.5	2	4_A375_EGR1..1	17	Gene PLEKHF1	ZFYVE15, APPD, MGC4090, PLEKHF1, PHAFIN1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	NM_024310	219566_at	NP_077286.3
GeneID.898	CCNE1	19	30,302,901	30,315,219	12,318	+	2	4_A375_EGR1..1.4633, 4_A375_EGR1..1.4634	-4584, 20907	upstream, downstream	0	0	1	5.5	5.5	13	2	4_A375_EGR1..1	13	Gene CCNE1	CCNE, CCNE1	cyclin E1	NM_001238, NM_057182	213523_at, 242105_at	NP_001229.1, NP_476530.1
GeneID.22847	ZNF507	19	32,836,514	32,878,573	42,059	+	1	2_A375_pNL97_plus_lncRNA_AR..1.4246	201	in gene	0	1	0	13	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ZNF507	ZNF507	zinc finger protein 507	NM_014910, NM_001136156	206225_at, 226327_at, 235618_at	NP_055725.2, NP_001129628.1
GeneID.147991	DPY19L3	19	32,896,655	32,976,799	80,144	+	1	4_A375_EGR1..1.4637	-159	upstream	0	0	1	10	13	14	1	4_A375_EGR1..1	14	Gene DPY19L3	DKFZp686J17135, DPY19L3, MGC35440	dpy-19-like 3 (C. elegans)	NM_207325, NM_001172774	225633_at	NP_997208.2, NP_001166245.1
GeneID.9141	PDCD5	19	33,072,104	33,078,331	6,227	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2952, 2_A375_pNL97_plus_lncRNA_AR..1.4247	344, -72	in gene, upstream	1	1	0	17	22	10	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene PDCD5	MGC9294, PDCD5, FLJ42784, TFAR19	programmed cell death 5	NM_004708	219275_at, 227751_at	NP_004699.1
GeneID.84079	ANKRD27	19	33,087,907	33,166,102	78,195	-	1	4_A375_EGR1..1.4638	22646	in gene	0	0	1	5	0	14	1	4_A375_EGR1..1	14	Gene ANKRD27	DKFZp434L0718, FLJ00040, PP12899, VARP, ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	NM_032139	221522_at	NP_115515.2
GeneID.390916	NUDT19	19	33,182,887	33,204,702	21,835	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2953	-115	upstream	1	0	0	16	13	8	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene NUDT19	RP2, NUDT19	nudix (nucleoside diphosphate linked moiety X)-type motif 19	NM_001105570		NP_001099040.1
GeneID.11136	SLC7A9	19	33,321,417	33,360,663	39,266	-	1	4_A375_EGR1..1.4639	5211	in gene	0	0	1	8	8	16	1	4_A375_EGR1..1	16	Gene SLC7A9	FLJ94301, BAT1, CSNU3, SLC7A9	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	NM_014270, NM_001126335	220135_s_at	NP_055085.1, NP_001119807.1
GeneID.84902	CCDC123	19	33,369,904	33,462,869	92,965	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2954, 2_A375_pNL97_plus_lncRNA_AR..1.4248	-123, -139	upstream, upstream	1	1	0	33	56	12	1	2_A375_pNL97_plus_lncRNA_AR..1	56	Gene CCDC123	FLJ14640, CCDC123	coiled-coil domain containing 123	NM_032816	1553732_s_at, 1554512_a_at, 1554513_s_at, 1560599_a_at, 1563919_a_at, 232106_s_at	NP_116205.3
GeneID.91442	C19orf40	19	33,463,146	33,467,974	4,828	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2954, 2_A375_pNL97_plus_lncRNA_AR..1.4248	-156, -140	upstream, upstream	1	1	0	33	56	12	1	2_A375_pNL97_plus_lncRNA_AR..1	56	Gene C19orf40	FLJ46828, MGC32020, FAAP24, C19orf40	chromosome 19 open reading frame 40	NM_152266	214816_x_at	NP_689479.1
GeneID.85415	RHPN2	19	33,469,498	33,555,824	86,326	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2954, 2_A375_pNL97_plus_lncRNA_AR..1.4248	92832, 92816	downstream, downstream	1	1	0	33	56	12	1	2_A375_pNL97_plus_lncRNA_AR..1	56	Gene RHPN2	P76RBE, RHPN2, RHOBP	rhophilin, Rho GTPase binding protein 2	NM_033103	227196_at	NP_149094.3
GeneID.126248	WDR88	19	33,622,998	33,666,705	43,707	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2955, 2_A375_pNL97_plus_lncRNA_AR..1.4249, 4_A375_EGR1..1.4640	45322, 45354, 44906	downstream, downstream, downstream	1	1	1	24	27	34	1	4_A375_EGR1..1	34	Gene WDR88	WDR88, PQWD	WD repeat domain 88	NM_173479	1552452_at, 1552453_a_at	NP_775750.3
GeneID.56301	SLC7A10	19	33,699,570	33,716,756	17,186	-	2	2_A375_pNL97_plus_lncRNA_AR..1.4250, 4_A375_EGR1..1.4641	6324, -1564	in gene, upstream	0	1	1	10	12	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SLC7A10	asc-1, FLJ20839, HASC-1, SLC7A10	solute carrier family 7, (neutral amino acid transporter, y+ system) member 10	NM_019849	220868_s_at	NP_062823.1
GeneID.1050	CEBPA	19	33,790,840	33,793,430	2,590	-	3	4_A375_EGR1..1.4646, 4_A375_EGR1..1.4647, 4_A375_EGR1..1.4648	1302, -410, -1162	in gene, upstream, upstream	0	0	1	7	8.33	18.33	3	4_A375_EGR1..1	20	Gene CEBPA	CEBP, CEBPA, C/EBP-alpha	CCAAT/enhancer binding protein (C/EBP), alpha	NM_004364	204039_at	NP_004355.2



Gene ID	Gene Name	Chr	Gene Strand	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Pos	1_A375_2_A375_3_A375_4_A375_5_A375_Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt y Tag	PROT
GeneID:39	LOC3	19	-	33,795,765	33,799,965	2,200	+	3	4_A375_EGR1..1-4648, 4_A375_EGR1..1-4647, 4_A375_EGR1..1-4646	1853, 77, 829	upstream, up gene, up gene	0 0 1 7 6.33 16.33 3	4_A375_EGR 1..1	20	Gene LOC3	FLI12355	hypothetical LOC39	NR_03	2204	
GeneID:16	CEBPG	19	+	33,864,909	33,872,992	8,983	+	2	4_A375_EGR1..1-4649, 4_A375_EGR1..1-4650	13967, 17023	downstream, downstream	0 0 1 4.5 7 15.5 2	4_A375_EGR 1..1	18	Gene CEBPG	IGEBP-1, CEBPG, GPE1 BP	CCAAT-enhancer-binding protein (C/EBP), gamma	NM_0010	2042	NP_0017
GeneID:31	FEPD	19	-	33,877,855	34,012,799	134,944	-	5	4_A375_EGR1..1-4649, 4_A375_EGR1..1-4650, 4_A375_EGR1..1-4651, 4_A375_EGR1..1-4652, 4_A375_EGR1..1-4653	134223, 131187, 119567, 113119, 3229	up gene, up gene, up gene, up gene	0 0 1 6.6 8.4 17.4 5	4_A375_EGR 1..1	19	Gene FEPD	PROLIDASE, MSCI0935, PEPD	peptidase D	NM_0002	NP_0002	NP_000119926.1, NP_001159529.1
GeneID:84	CHST6	19	-	34,112,981	34,264,414	151,433	+	6	1_A375_uhk7_rivus_lacRNA_AR..1-2566, 2_A375_uhi37_jlus_lacRNA_AR..1-4231, 2_A375_uhi37_jlus_lacRNA_AR..1-4232, 2_A375_uhi37_jlus_lacRNA_AR..1-4233, 4_A375_EGR1..1-4656, 4_A375_EGR1..1-4657	148519, 82587, 19043, 145995, 1219, 66675	up gene, up gene, up gene, up gene, up gene, up gene	1 1 1 12.8 14.8 11 5	1_A375_uhk7_rivus_lacRNA_AR..1	24	Gene CHST6	CHST6, GALNAC4ST1, GalNAc4ST	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 6	NM_0024	NM_001127693, NM_001127866	2210	NP_3701	NP_001121397.1, NP_001121395.1
GeneID:79	KCTD15	19	+	34,237,751	34,306,966	69,215	+	3	2_A393_uhk97_jlus_lacRNA_AR..1-4234, 4_A375_EGR1..1-4656, 4_A375_EGR1..1-4658	29737, 14617, 23221	downstream, up gene, downstream	0 1 1 10 12.5 17.5 2	2_A375_uhk9 7_jlus_lacRNA_AR..1	20	Gene KCTD15	MSC23497, MSC2835, KCTD15	potassium channel tetramerisation domain containing 15	NM_0304	NM_001129994, NM_001129993	2189	2189	NP_3709	NP_001124498.1, NP_001123497.1
GeneID:26	LSM14A	19	-	34,865,332	34,720,420	57,088	+	2	1_A375_uhk7_rivus_lacRNA_AR..1-2565, 2_A375_uhi37_jlus_lacRNA_AR..1-4230	60776, -248	downstream, upstream	1 1 0 16 16 8.5 2	2_A375_uhk9 7_jlus_lacRNA_AR..1	19	Gene LSM14A	FAM61A, C19orf12, DKFZp434D1330, bA61I4., 33H14A, RAP55	LSM14A, SCD6 homolog A (S. cerevisiae)	NM_0155	NM_001114093	2121	2121	NP_0963	NP_001107968.1
GeneID:97	KIAA2026	19	-	34,743,456	34,846,471	101,015	+	1	2_A375_uhi37_jlus_lacRNA_AR..1-4256	10764	downstream	0 1 0 19 19 12 1	2_A375_uhk9 7_jlus_lacRNA_AR..1	19	Gene KIAA2026	KIAA2026		NM_0145		2032	NP_3555	
GeneID:20	GPI	19	-	34,855,845	34,893,316	37,473	+	3	2_A375_uhi37_jlus_lacRNA_AR..1-4236, 2_A375_uhi37_jlus_lacRNA_AR..1-4237, 2_A375_uhi37_jlus_lacRNA_AR..1-4691	-3403, -39715, 39675	upstream, downstream, downstream	0 1 1 16.3 19 14 2	2_A375_uhk9 7_jlus_lacRNA_AR..1	19	Gene GPI	BA38, GNPI, GNPI_HUMAN, GPI, PHI, PHI1,	glucose phosphate isomerase	NM_0001	NM_001164722	2083	2083	NP_0001	NP_001116691.1
GeneID:64	PDCD2L	19	-	34,895,303	34,917,973	21,770	+	2	2_A375_uhi37_jlus_lacRNA_AR..1-4237, 4_A375_EGR1..1-4691	57, 217	up gene, up gene	0 1 1 14 19 16 1	2_A375_uhk9 7_jlus_lacRNA_AR..1	19	Gene PDCD2L	MSC13399, PDCD2L	programmed cell death 2-like	NM_0323		2244	2244	NP_1	NP_115722.1
GeneID:13	WTIP	19	+	34,972,800	34,992,963	19,203	+	3	4_A375_EGR1..1-4692, 4_A375_EGR1..1-4693, 4_A375_EGR1..1-4694	11940, 11845, 10152	up gene, up gene, downstream	0 0 1 4.67 5.67 10.33 3	4_A375_EGR 1..1	16	Gene WTIP	WTIP		NM_0310		2274	11	NP_0312	NP_001073903.1
GeneID:33	ZNF302	19	-	35,166,987	35,177,302	9,715	+	3	1_A375_uhk7_rivus_lacRNA_AR..1-2569, 2_A375_uhi37_jlus_lacRNA_AR..1-4238, 4_A375_EGR1..1-4695	-599, -957, -330	upstream, upstream, upstream	1 1 1 20 20 14 1	1_A375_uhk7_rivus_lacRNA_AR..1	20	Gene ZNF302	MGC1154, HSD18, ZNF401, MSTP154, ZNF127, ZNF1251, ZNF302	zinc finger protein 302	NM_0154	NM_001012320	2154	2154	NP_0892	NP_001012320.1
GeneID:12	ZNF161	19	-	35,225,450	35,233,774	8,294	+	1	4_A375_EGR1..1-4696	-3272	upstream	0 0 1 3 3 14 1	4_A375_EGR 1..1	14	Gene ZNF161	RHS161, ZNF161, MGC4016	zinc finger protein 161	NM_0012	NM_001278997, NM_001145665			NP_0012	NP_001265862.2, NP_001139157.1
GeneID:14	ZNF599	19	-	35,246,979	35,264,104	18,155	+	1	2_A375_uhk97_jlus_lacRNA_AR..1-4239	36	upstream	0 1 0 13 16 13 1	2_A375_uhk9 7_jlus_lacRNA_AR..1	16	Gene ZNF599	ZNF599, FLJ90320	zinc finger protein 599	NM_0310	NM_001037246	1558	1558	NP_1	NP_001037249.1
GeneID:32	HPN	19	+	35,331,410	35,337,477	29,067	+	4	4_A375_EGR1..1-4693, 4_A375_EGR1..1-4697, 4_A375_EGR1..1-4698, 4_A375_EGR1..1-4699, 4_A375_EGR1..1-4700	-462, 393, 19390, 29635	up gene, up gene, up gene, downstream	0 0 1 5.75 7.25 17.75 4	4_A375_EGR 1..1	20	Gene HPN	HPN, TMPRSS1	hepsin	NM_1829	NM_002151	2549	34_s	NP_0012	NP_002142.1
GeneID:10	LOC100	19	-	35,549,983	35,597,398	47,245	-	5	1_A375_uhk7_rivus_lacRNA_AR..1-2960, 2_A375_uhi37_jlus_lacRNA_AR..1-4240, 2_A375_uhi37_jlus_lacRNA_AR..1-4241, 4_A375_EGR1..1-4702, 4_A375_EGR1..1-4703	488, 376, -6666, 48656, 30360	up gene, up gene, upstream, up gene, up gene	1 1 1 10 14.25 14.75 4	2_A375_uhk9 7_jlus_lacRNA_AR..1	21	Gene LOC100129973	FLJ42769	hypothetical LOC100129973	NR_0245	NR_024581, NR_024582				
GeneID:33	FXYD7	19	-	35,816,417	35,826,116	10,781	+	2	2_A375_uhi37_jlus_lacRNA_AR..1-4261, 4_A375_EGR1..1-4674	20002, 10182	downstream, up gene	0 0 1 9.5 14 14 2	4_A375_EGR 1..1	19	Gene LGI4	LGI3, LGI4	leucine-rich repeat LGI family, member 4	NM_1532		2271	21	NP_2429	NP_848115.1
GeneID:33	FXYD7	19	-	35,834,184	35,845,203	11,031	+	1	4_A375_EGR1..1-4675	11702	downstream	0 0 1 12 8 15 1	4_A375_EGR 1..1	18	Gene FXYD7	FXYD7, FLJ35096	FXYD domain containing ion transport regulator 7	NM_0320		2201	31	NP_0712	NP_071269.1
GeneID:33	FXYD5	19	-	35,843,625	35,860,765	19,165	+	1	4_A375_EGR1..1-4675	231	up gene	0 0 1 12 8 15 1	4_A375_EGR 1..1	15	Gene FXYD5	WAD, DYSAD, HSPC115, FXYD5, RIC, PRO4534, DKFZp434C1	FXYD domain containing ion transport regulator 5	NM_1447	NM_014164, NM_001164805, NR_026406	2176	2176	NP_6	NP_055553.1, NP_056567.2, NP_001158077.1
GeneID:10	LOC100	19	-	35,850,570	35,706,609	10,739	+	1	4_A375_EGR1..1-4676	23852	downstream	0 0 1 8 8 16 1	4_A375_EGR 1..1	16	Gene LOC100506239	hypothetical LOC100506239		XR_1110	XR_111033, XR_109497, XR_115270				
GeneID:14	FAM167B	19	-	35,715,756	35,719,626	3,924	+	1	4_A375_EGR1..1-4676	5856	up gene	0 0 1 8 8 16 1	4_A375_EGR 1..1	16	Gene FAM167B	FAM167B, TMEM182, FLJ25860	family with sequence similarity 167, member B	NM_1526		2422	259	NP_8	NP_689994.1
GeneID:31	LSR	19	-	35,739,539	35,745,967	19,308	+	2	4_A375_EGR1..1-4677, 4_A375_EGR1..1-4678	-191, 541	upstream, up gene	0 0 1 5.5 4.5 13 2	4_A375_EGR 1..1	17	Gene LSR	ILDR3, LSR, LSR_HUMAN, MGC43312, MGC10699, LSR, MGC45893	tricellular (lipolysis-stimulated lipoprotein) receptor	NM_2056	NM_015923, NM_205834	2081	2081	NP_9	NP_991404.1, NP_057009.3, NP_991403.1
GeneID:37	HAMP	19	-	35,773,410	35,776,948	2,838	+	1	4_A375_EGR1..1-4679	9850	downstream	0 0 1 5 8 17 1	4_A375_EGR 1..1	17	Gene HAMP	LEAP1, LEAP-1, HFE2B, HEPCIDIN, PLTR, HAMP, HEPC	hepcidin antimicrobial peptide	NM_0211	NM_021175	2204	91	NP_0686	NP_068998.1
GeneID:48	MAG	19	+	35,783,038	35,804,707	21,669	+	3	1_A375_uhk7_rivus_lacRNA_AR..1-2961, 4_A375_EGR1..1-4679, 4_A375_EGR1..1-4680	28894, 2, 18018	downstream, up gene, up gene	1 1 1 12.67 11.67 13.67 3	1_A375_uhk7_rivus_lacRNA_AR..1	23	Gene MAG	SIGLEC4A, GMA, MAG, SIGLEC-4A, SAIG	myelin associated glycoprotein	NM_0023	NM_002361, NM_038600	2043	81_s	NP_3022	NP_002352.1, NP_542187.1
GeneID:39	CD22	19	-	35,820,972	35,830,364	10,192	+	1	2_A375_uhi37_jlus_lacRNA_AR..1-4241	-10040	upstream	1 2 0 25 16 8 1	1_A375_uhk7_rivus_lacRNA_AR..1	23	Gene CD22	MGC130053, SIGLEC2, CD22, SIGLEC-2, FLJ22814	CD22 molecule	NM_0011	NM_001185099, NM_001185100, NM_001185101, NM_001771			NP_0011	NP_001172026.1, NP_001172029.1, NP_001762.2, NP_001172030.1
GeneID:23	SIBLN	19	-	35,814,269	35,819,253	4,984	+	1	4_A375_EGR1..1-4681	-5739	upstream	0 0 1 4 8 20 1	4_A375_EGR 1..1	20	Gene SIBLN	SIBLN, LYNSR16, MGC75533	hyaluronan	NM_1783	NM_001166034, NM_001166033	2332	72_s	NP_7439	NP_001158061.1, NP_001158062.1
GeneID:26	GAPDH	19	-	35,824,314	35,836,221	11,907	+	1	4_A375_EGR1..1-4681	678	up gene	0 0 1 4 8 20 1	4_A375_EGR 1..1	20	Gene GAPDH	GAPD2, GAPDHS, GAPDS, GAPDH, G_HSD-2b	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	NM_0143	NM_014364	2071	16_s	NP_3361	NP_056179.1
GeneID:10	LOC100	19	-	35,831,640	35,836,417	4,777	+	1	4_A375_EGR1..1-4681	11625	downstream	0 0 1 4 8 20 1	4_A375_EGR 1..1	20	Gene LOC100506469	hypothetical LOC100506469		XR_1110	XR_110933, XR_115272				
GeneID:49	ATP4A	19	+	35,841,095	35,854,360	13,265	+	1	4_A375_EGR1..1-4682	5161	up gene	0 0 1 5 8 17 1	4_A375_EGR 1..1	17	Gene ATP4A	ATP4A, HYPA	ATPase, H+/K+ exchanging, alpha polypeptide	NM_0307		2071	59_s	NP_0306	NP_030059.2
GeneID:23	HAUS8	19	-	35,703,848	35,716,351	12,503	+	6	1_A375_uhk7_rivus_lacRNA_AR..1-2962, 1_A375_uhk7_rivus_lacRNA_AR..1-2963, 2_A375_uhi37_jlus_lacRNA_AR..1-4242, 2_A375_uhi37_jlus_lacRNA_AR..1-4243, 4_A375_EGR1..1-4684, 4_A375_EGR1..1-4685, 4_A375_EGR1..1-4686, 4_A375_EGR1..1-4687, 4_A375_EGR1..1-4688, 4_A375_EGR1..1-4689	34, 16290, 2, 16290, 34	up gene, downstream, up gene, downstream, up gene	1 1 1 22.3 27 13.5 2	2_A375_uhk9 7_jlus_lacRNA_AR..1	29	Gene HAUS8	HAUS8, dgt8, RANBS4l1	HAUS augmin-like complex, subunit 8	NM_0153	NM_015332	2109	83_s	NP_5561	NP_056117.1
GeneID:79	RBM42	19	-	35,119,900	35,126,967	6,897	+	3	1_A375_uhk7_rivus_lacRNA_AR..1-2965, 2_A375_uhi37_jlus_lacRNA_AR..1-4244, 4_A375_EGR1..1-4694	-44, -44, 19954	upstream, upstream, up gene	1 1 1 16 16 12.5 2	1_A375_uhk7_rivus_lacRNA_AR..1	28	Gene RBM42	RBM42, MGC10433	RNA binding motif protein 42	NM_0243	NM_024321	2097	43_s	NP_0778	NP_077297.2
GeneID:21	ETV2	19	-	35,132,847	35,135,773	2,926	+	1	4_A375_EGR1..1-4684	3067	up gene	0 0 1 10 11 16 1	4_A375_EGR 1..1	16	Gene ETV2	MGC129854, ETSRP71, ETV2, MGC129853, ER71	ets variant 2	NM_0142	NM_014209	2135	10_s	NP_3355	NP_055224.2
GeneID:10	COX6B1	19	+	35,139,123	35,149,866	10,981	+	1	4_A375_EGR1..1-4684	-3481	upstream	0 0 1 10 11 16 1	4_A375_EGR 1..1	16	Gene COX6B1	COX6B1, COX6, COVB1, COX6B	cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitin)	NM_0311	NM_001863	2014	41	NP_0010	NP_001854.1
GeneID:23	ZBTB32	19	-	35,203,830	35,207,940	4,110	+	6	1_A375_uhk7_rivus_lacRNA_AR..1-2965, 2_A375_uhi37_jlus_lacRNA_AR..1-4245, 2_A375_uhi37_jlus_lacRNA_AR..1-4246, 4_A375_EGR1..1-4688, 4_A375_EGR1..1-4689, 4_A375_EGR1..1-4690, 4_A375_EGR1..1-4691	4806, -10408, 4343, 2714, 4236, 5798, 7162, 5976	downstream, upstream, downstream, up gene, downstream, downstream, downstream, downstream, downstream	1 1 1 10.5 12.33 19.17 6	2_A375_uhk9 7_jlus_lacRNA_AR..1	31	Gene ZBTB32	FAZP, ZBTB32, ZNF538, TZFP, PATF, Rog	zinc finger and BTB domain containing 32	NM_0143	NM_014383	2207	18_s	NP_3551	NP_055198.1
GeneID:37	MLL4	19	-	35,200,321	35,229,779	30,036	+	8	1_A375_uhk7_rivus_lacRNA_AR..1-2965, 2_A375_uhi37_jlus_lacRNA_AR..1-4246, 2_A375_uhi37_jlus_lacRNA_AR..1-4247, 4_A375_EGR1..1-4688, 4_A375_EGR1..1-4689, 4_A375_EGR1..1-4690, 4_A375_EGR1..1-4691, 4_A375_EGR1..1-4692	928, -945, -2377, -637, -515, 2071, 4477, 20273	upstream, upstream, upstream, upstream, up gene, up gene, up gene, up gene	1 1 1 7.67 9.83 12.83 6	1_A375_uhk7_rivus_lacRNA_AR..1	31	Gene MLL4	FLJ22301, MLL4, WBP7, WAC0234, MLL2, HRX2	myeloid/lymphoid or mixed-lineage leukemia 4	NM_0147	NM_014727	2053	419	21_s	NP_3555	NP_055542.1
GeneID:79	TMEM1	19	-	35,230,191	35,233,391	3,200	-	1	4_A375_EGR1..1-4690	4085	downstream	0 0 1 9 9 16 1	4_A375_EGR 1..1	16	Gene TMEM149	TMEM149, UDAT14, FLJ23270, KIFUP1	KIF-like family receptor 1	NM_0349	NM_034980	2196	80_s	NP_0789	NP_078936.1
GeneID:19	LDAT14	19	-	35,233,435	35,236,336	2,902	-	1	4_A375_EGR1..1-4690	7040	downstream	0 0 1 9 9 16 1	4_A375_EGR 1..1	16	Gene LDAT14	LDAT1, RS3, LDAT1-DLY1, LDAT1-LY1, LDAT13, LDAT6, LDAT1FS03, FLJ38525, MGC23900	U2 small nuclear RNA auxiliary factor 1-like 4	NM_1495	NM_001040423	2267	00_s	NP_8594	NP_001035515.1
GeneID:38	PSEN2	19	+	35,236,494	35,237,903	1,409	+	1	4_A375_EGR1..1-4690	-7196	upstream	0 0 1 9 9 16 1	4_A375_EGR 1..1	16	Gene PSEN2	PSN2, MGC17994, PSENDN, MGB222, PSN2	presenilin 2 (Alzheimer disease) homolog (C. elegans)	NM_1723		2103	02_s	NP_7955	NP_795344.1
GeneID:30	UNG7	19	-	35,239,512	35,243,420	3,908	+	2	4_A375_EGR1..1-4692, 4_A375_EGR1..1-4691	-10216, 6938	upstream, downstream	0 0 1 9 9.5 17.5 2	4_A375_EGR 1..1	16	Gene LIN37	LIN37, MGC9850	lin-37 homolog (C. elegans)	NM_0191	NM_019104	2153	826_s	NP_0619	NP_061977.1
GeneID:10	HSPB6	19	-	35,245,470	35,247,930	2,460	-	1	4_A375_EGR1..1-4691	-515	upstream	0 0 1 9 10 17 1	4_A375_EGR 1..1	17	Gene HSPB6	FLJ23359, Hsp20, HSPB6	heat shock protein, alpha-crystallin-related, B6	NM_1464	NM_014241	2147	67_s	NP_6522	NP_852216.1
GeneID:14	C19orf3	19	+	35,249,044	35,260,077	11,033	+	1	4_A375_EGR1..1-4691	-396	upstream	0 0 1 9 10 17 1	4_A375_EGR 1..1	17	Gene C19orf33	DKFZp434C223, FLJ38937, C19orf33, MGC131182	chromosome 19 open reading frame 33	NM_0313	NM_031039657	1533	162_s	NP_4429	NP_001034976.1
GeneID:10	SNX26	19	-	35,266,417	35,279,724	13,307	+	1	4_A375_EGR1..1-4692	22607	downstream	0 0 1 4 8 16 1	4_A375_EGR 1..1	16	Gene SNX26	TCGAP, MDM9, SNT, SNX26, MRHGAP23, FLJ38019	Rho GTPase activating protein 35	NM_0323	NM_032545, NM_001172690	2135	27_s	21_s	NP_4431	NP_001159101.1
GeneID:38	PRDX2	19	+	35,290,092	35,294,301	13,209	-	2	4_A375_EGR1..1-4692, 4_A375_EGR1..1-4693	13077, 6905	downstream, up gene	0 0 1 7 8.5 16.5 2	4_A375_EGR 1..1	17	Gene PRDX2	PRDX2, HBP0X1	peroxiredoxin 2 (thiol specific antioxidant protein)	NM_0312	NM_021232	2166	66_s	24_s	NP_3855	NP_085033.1
GeneID:48	NPHS1	19	+	35,316,274	35,342,893	26,621	-	3	1_A375_uhk7_rivus_lacRNA_AR..1-2966, 2_A375_uhi37_jlus_lacRNA_AR..1-4247, 4_A375_EGR1..1-4694	20119, 23307, 6611	up gene, up gene, up gene	1 1 1 20 26 17 2	2_A375_uhk9 7_jlus_lacRNA_AR..1	29	Gene NPHS1	NPHS1, CNF, NPHN	nephrosis 1, congenital, Finnish type (nephrin)	NM_0045	NM_004646	2076	72_s	NP_3548	NP_004637.1
GeneID:33	APLP1	19	-	35,359,401	35,370,899	11,298	+	2	1_A375_uhk7_rivus_lacRNA_AR..1-2967, 2_A375_uhi37_jlus_lacRNA_AR..1-4265	11479, 11479	downstream, downstream	1 1 0 35 41 5 1	2_A375_uhk9 7_jlus_lacRNA_AR..1	41	Gene APLP1	APLP, APLP1	amyloid beta (A4) precursor-like protein 1	NM_0312	NM_031024857, NM_003186	2094	82_s	NP_0001	NP_001019781.1, NP_000101.1

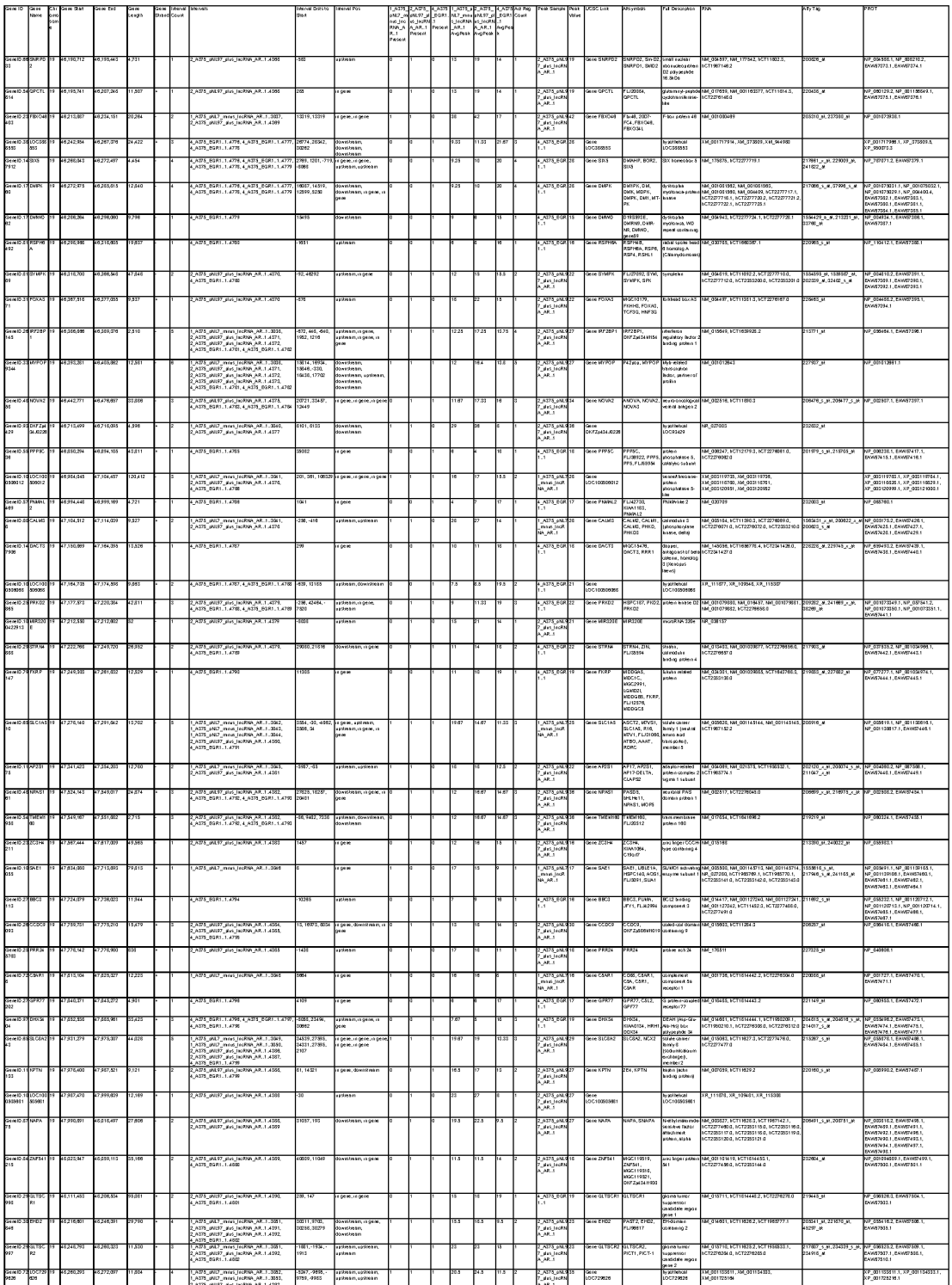


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_shN7_mes_lncRNA_R_1 Percent	2_A375_shN7_gl_lncRNA_R_1 Percent	4_A375_shN7_gl_lncRNA_R_1 Percent	1_A375_shN7_mes_lncRNA_AR_1 Avg Peak	2_A375_shN7_gl_lncRNA_AR_1 Avg Peak	4_A375_shN7_gl_lncRNA_AR_1 Avg Peak	Adj Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:64907	NFKBID	19	58,279,143	58,291,552	12,409	-	2	1_A375_shN7_mes_lncRNA_AR_1...2367, 2_A375_shN7_gl_lncRNA_AR_1...4266	20872, 20872	downstream, downstream	1	1	0	35	41	8	1	2_A375_shN7_gl_lncRNA_AR_1	941	Gene NFKBID	IFA-NFKBH, MGC11214, IkappaBNS, MGC141931, NFKBID	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	NM_139229	1553642_a_at, 230932_s_at, 2419691_at	NP_640322.1
GeneID:79187	LRFN2	19	58,426,022	58,436,007	9,986	+	1	4_A375_SGR1...4695	9658	upstream	0	0	1	14	13	19	1	4_A375_SGR1.1	19	Gene LRFN2	SALM4, FLEA21, MGC20556, LRFN2	leucine rich repeat and fibronectin type III domain containing 2	NM_024505	210548_at	NP_076765.1
GeneID:64907	SDHAF1	19	58,466,990	58,467,320	1,330	+	2	2_A375_shN7_gl_lncRNA_AR_1...4271, 4_A375_SGR1...4697	-10, -10	upstream, upstream	0	1	1	13	16	16	1	2_A375_shN7_gl_lncRNA_AR_1	916	Gene SDHAF1	SDHAF1		NM_001042631	221033_at, 44969_at	NP_001038396.1
GeneID:16815183	C19orf6	19	58,494,092	58,499,872	5,870	-	5	1_A375_shN7_mes_lncRNA_AR_1...2993, 2_A375_shN7_gl_lncRNA_AR_1...4271, 4_A375_SGR1...4697	-859, 13592, 13812	upstream, downstream, downstream	1	1	1	15	16.5	18	2	2_A375_shN7_gl_lncRNA_AR_1	916	Gene C19orf6	FLJ38445, C19orf6	chromosome 19 open reading frame 46	NM_031039576	235515_at	NP_001034985.1
GeneID:64907	ALKBH8	19	58,500,022	58,505,141	5,119	-	1	1_A375_shN7_mes_lncRNA_AR_1...2989	4850	up gene	1	0	0	17	15	14	1	1_A375_shN7_mes_lncRNA_AR	917	Gene ALKBH8	ALKBH8, MGC15877, hABH8	alkB, alkylation repair homolog 8 (E. coli)	NM_138907, NM_032670	223969_at	NP_942597.1, NP_116287.3
GeneID:23541999	CLIP3	19	58,505,963	58,522,773	16,812	-	2	1_A375_shN7_mes_lncRNA_AR_1...2993, 4_A375_SGR1...4696	23444, -65	downstream, upstream	1	0	1	11	13	16	2	4_A375_SGR1.1	19	Gene CLIP3	CLIP3, FLJ53615, DKFZp686N1922, CLIP6-91, RSN-1, CLIP4(3)	CAP-GLY domain containing linker protein 3	NM_015526	212258_at, 233243_at	NP_036341.1
GeneID:19745	TPAP6	19	58,525,907	58,545,984	19,777	-	3	1_A375_shN7_plus_lncRNA_AR_1...4272, 4_A375_SGR1...4696, 4_A375_SGR1...4699	496, 21824, 544	up gene, downstream, up gene	1	1	1	10	14.5	16	2	4_A375_SGR1.1	19	Gene TPAP6	TPAP6, FLJ32591	TPAP domain containing 6	NM_152555	235500_at	NP_689771.1
GeneID:44482	WDR62	19	58,543,765	58,596,012	90,229	+	4	1_A375_shN7_mes_lncRNA_AR_1...2992, 2_A375_shN7_gl_lncRNA_AR_1...4272, 4_A375_SGR1...4699, 4_A375_SGR1...4700	59943, -553, -660, 43817	downstream, upstream, upstream, up gene	1	1	1	15	13.33	16	3	1_A375_shN7_mes_lncRNA_AR	923	Gene WDR62	C19orf14, DKFZp434J046, MGC19978, DKFZp686I01024, FLJ32290, WDR62, MCPH2	WD repeat domain 62	NM_001083961, NM_173556	1553122_a_, 1553125_x_at, 212215_s_at	NP_001074307.1, NP_775907.4
GeneID:79187	LOC728391	19	58,602,103	58,604,963	2,860	+	2	1_A375_shN7_mes_lncRNA_AR_1...2970, 4_A375_SGR1...4700	3923, 7703	downstream, upstream	1	0	1	13	11	13	2	1_A375_shN7_mes_lncRNA_AR	923	Gene LOC728391		tyrosine 3 (Drosophila)	Xm_001717185, XM_001715891		XP_001717217.2, XP_001715413.3
GeneID:54832	POLR3G	19	58,604,811	58,606,209	1,399	-	2	1_A375_shN7_mes_lncRNA_AR_1...2970, 4_A375_SGR1...4700	439, 11606	up gene, downstream	1	0	1	15	11	13	2	1_A375_shN7_mes_lncRNA_AR	923	Gene POLR3G	POLR3, MPB14.5, RPB	polymerase (RNA) III (DNA directed) polypeptide G, 14.5kDa	NM_030233		NP_036224.1
GeneID:55	TBC1D1	19	58,803,666	58,816,949	10,981	+	2	1_A375_shN7_mes_lncRNA_AR_1...2970, 4_A375_SGR1...4701	-160, 12944	upstream, downstream	1	0	1	19	13.5	15	2	1_A375_shN7_mes_lncRNA_AR	923	Gene TBC1D	C1orf21, CG22, TBC1, MGC14825, C1orf21	tubulin folding cofactor B	NM_031201	230164_s_at, 211739_x_at, 216194_s_at	NP_001072.2
GeneID:8	EDC4PN81	19	58,830,918	58,841,355	10,337	+	5	1_A375_shN7_mes_lncRNA_AR_1...2971, 2_A375_shN7_gl_lncRNA_AR_1...4273, 4_A375_SGR1...4702	-35, -70, -186	upstream, upstream, upstream	1	1	1	36	40	21	1	2_A375_shN7_gl_lncRNA_AR_1	940	Gene CAPNS1	CAPNS, CSS1, CAPN4, CAPNS1, CALPAIN4, CAMP, 30K, CDPS	calpain, small subunit 1	NM_001003962, NM_001749	200931_at	NP_001003962.1, NP_001740.1
GeneID:14	ZNF583	19	58,875,187	58,705,908	32,799	-	1	2_A375_shN7_plus_lncRNA_AR_1...4274	548	up gene	0	1	0	15	22	10	1	2_A375_shN7_gl_lncRNA_AR_1	922	Gene ZNF583	FLJ39191, ZNF583	zinc finger protein 583	NM_152477, NM_001042474	220305_at	NP_689990.5, NP_001029391.1
GeneID:77939	ZNF148	19	58,705,304	58,729,978	24,372	+	1	2_A375_shN7_plus_lncRNA_AR_1...4274	96	upstream	0	1	0	15	22	10	1	2_A375_shN7_gl_lncRNA_AR_1	922	Gene ZNF148	ZSP, MGC133980, MGC133981, ZNF148	zinc finger protein 148	NM_001079839, NM_001079838, NM_007145	1554433_s_at, 200092_at	NP_001072039.1, NP_001072038.1, NP_009076.2
GeneID:55877	ZFP14	19	58,827,182	58,870,076	42,916	-	2	2_A375_shN7_plus_lncRNA_AR_1...2972, 2_A375_shN7_gl_lncRNA_AR_1...4275	182, 70	up gene, up gene	1	1	0	25	18	17	1	1_A375_shN7_mes_lncRNA_AR	923	Gene ZFP14	ZFP14, ZNF531, bA130J9.1	zinc finger protein 14 homolog (mouse)	NM_030917	232911_at	NP_065986.1
GeneID:44482	ZFP82	19	58,882,981	58,899,850	16,869	+	1	4_A375_SGR1...4703	174	up gene	0	0	1	10	15	17	1	4_A375_SGR1.1	17	Gene ZFP82	KIAA1845, ZFP82, MGC45390, ZNF545	zinc finger protein 82 homolog (mouse)	NM_133486	1553793_s_at, 235178_at	NP_597725.1
GeneID:84189	LOC844169	19	58,912,439	58,913,686	1,247	+	1	4_A375_SGR1...4703	3083	upstream	0	0	1	10	15	17	1	4_A375_SGR1.1	17	Gene LOC844169		acyl-CoA thioesterase 4 pseudogene	NR_033748		
GeneID:9934	ZNF598	19	58,936,021	58,950,463	44,442	-	1	2_A375_shN7_plus_lncRNA_AR_1...4276	-17	upstream	0	1	0	11	16	9	1	2_A375_shN7_gl_lncRNA_AR_1	918	Gene ZNF598	MGC13215, FLJ42779, ZNF598	zinc finger protein 598	NM_001143543, NM_001143544, NM_032828, NM_001143543	240229_at	NP_001135815.1, NP_001135816.1, NP_116277.1, NP_001135817.1
GeneID:53732	LOC728732	19	58,950,529	58,951,942	1,413	+	1	2_A375_shN7_plus_lncRNA_AR_1...4276	-49	upstream	0	1	0	11	16	9	1	2_A375_shN7_gl_lncRNA_AR_1	918	Gene LOC728732		hypothetical LOC728732	NR_028504		
GeneID:63111	ZNF529	19	58,954,317	58,996,178	41,861	-	2	2_A375_shN7_mes_lncRNA_AR_1...2973, 4_A375_SGR1...4704	32514, 31922	up gene, up gene	1	0	1	16	13	20	1	4_A375_SGR1.1	20	Gene ZNF529	KIAA1815, ZNF529	zinc finger protein 529	NM_020951, NM_001143849, NM_001143850, NM_027229	213307_at, 231940_at, 227452_at	NP_066002.3, NP_001139121.1, NP_001139122.1
GeneID:44482	LOC284440	19	58,958,087	58,216,011	59,924	+	1	2_A375_shN7_mes_lncRNA_AR_1...2974	40859	downstream	1	0	0	16	14	10	1	2_A375_shN7_mes_lncRNA_AR	918	Gene LOC284440		hypothetical LOC284440	XR_111857, XR_109515, XR_115276	1558805_s_at, 235778_at	
GeneID:55538	ZNF790	19	58,966,930	58,229,264	20,934	-	1	1_A375_shN7_mes_lncRNA_AR_1...2974	598	up gene	1	0	0	16	14	10	1	1_A375_shN7_mes_lncRNA_AR	918	Gene ZNF790	ZNF790, MGC62100, FLJ35350	zinc finger protein 790	NM_206934		NP_996777.2
GeneID:54699	ZNF829	19	57,979,928	57,987,193	35,187	-	1	1_A375_shN7_mes_lncRNA_AR_1...2975	-199	upstream	1	0	0	16	11	11	1	1_A375_shN7_mes_lncRNA_AR	918	Gene ZNF829	MGC129896, ZNF829, DKFZp686I2126, DKFZp779O175, MGC129897, FLJ27459	zinc finger protein 829	NM_031572332, NM_001171679	237308_at, 239852_x_at	NP_001032309.2, NP_001165430.1
GeneID:64930	ZNF585	19	57,987,224	57,442,480	59,216	+	1	1_A375_shN7_mes_lncRNA_AR_1...2975	138	up gene	1	0	0	16	11	11	1	1_A375_shN7_mes_lncRNA_AR	918	Gene ZNF585	ZNF585, DKFZp686B0787, FLJ35504, DKFZp686Y0534, FLJ36629	zinc finger protein 585	NM_178539	1561433_s_at, 1562282_at, 1564286_at, 1568160_s_at	NP_840041.2
GeneID:79231	ZNF420	19	57,989,302	57,920,992	31,290	+	1	4_A375_SGR1...4707	-590	upstream	0	0	1	16	16	17	1	4_A375_SGR1.1	17	Gene ZNF420	AFAH, FLJ22191, ZNF420	zinc finger protein 420	NM_144669	233007_at, 242761_s_at	NP_653290.2
GeneID:255	ZNF583	19	57,972,451	57,701,451	58,970	-	1	2_A375_shN7_plus_lncRNA_AR_1...4277	-7733	upstream	0	0	1	15	21	18	1	2_A375_shN7_gl_lncRNA_AR_1	921	Gene ZNF583B	FLJ32255, ZNF583B, SCFA1, FLJ34920	zinc finger protein 583B	NM_152279	233262_at	NP_689492.3
GeneID:3997	ZNF383	19	57,717,366	57,734,974	17,208	+	1	2_A375_shN7_gl_lncRNA_AR_1...4277	-5162	upstream	0	1	0	15	21	18	1	2_A375_shN7_gl_lncRNA_AR_1	921	Gene ZNF383	HSD17, ZNF383, FLJ39583	zinc finger protein 383	NM_152694	235414_at	NP_689917.1
GeneID:6527342	LOC100507342	19	57,666,932	57,618,626	7,224	+	1	2_A375_shN7_plus_lncRNA_AR_1...4278	16930	downstream	0	1	0	9	16	13	1	2_A375_shN7_gl_lncRNA_AR_1	919	Gene LOC100507342		hypothetical LOC100507342	XR_109364		
GeneID:4439	HIKR1	19	57,623,360	57,655,357	29,777	+	2	2_A375_shN7_plus_lncRNA_AR_1...4278, 2_A375_shN7_gl_lncRNA_AR_1...4279	-188, 38438	upstream, downstream	0	1	0	12	21	10.5	2	2_A375_shN7_gl_lncRNA_AR_1	926	Gene HIKR1	HIKR1, ZNF573		NM_181786, XC7233714.0, XC7233146.0, XC7233147.0, XC7233148.0, XC7233149.0, XC733661.3	1569979_at, 1569980_x_at	NP_861451.1, EAW68724.1, EAW68721.1, EAW68722.1, EAW68726.1, EAW68723.1, EAW68725.1
GeneID:9923	ZNF527	19	57,662,009	57,663,966	21,957	+	1	2_A375_shN7_plus_lncRNA_AR_1...4279	-413	upstream	0	1	0	15	26	6	1	2_A375_shN7_gl_lncRNA_AR_1	926	Gene ZNF527	ZNF527, KIAA1829	zinc finger protein 527	NM_032453	1570256_at, 244981_at	NP_115629.1
GeneID:3927	ZNF793	19	57,997,541	58,034,259	39,396	+	1	4_A375_SGR1...4705	44733	downstream	0	0	1	7	7	16	1	4_A375_SGR1.1	16	Gene ZNF793	ZNF793	zinc finger protein 793	NM_031013659, XC7197685.0, XC7227532.1	1244103_at	NP_001138612.2, EAW68734.1
GeneID:6992	DKFZp781D1916	19	58,036,366	58,040,997	5,899	-	1	4_A375_SGR1...4706	2939	upstream	0	0	1	7	7	16	1	4_A375_SGR1.1	16	Gene DKFZp781D1916	DKFZp781D1916	hypothetical LOC439892	XR_111853, XR_109820, XR_115282	1569798_at	
GeneID:6527433	LOC100507433	19	58,039,551	58,079,019	39,186	+	1	4_A375_SGR1...4706	2723	up gene	0	0	1	7	7	16	1	4_A375_SGR1.1	16	Gene LOC100507433		hypothetical LOC100507433	XR_111859, XR_111858, XR_111857, XR_111856, XR_109824, XR_109823, XR_109822, XR_109821, XR_115286, XR_115285, XR_115284, XR_115283	1569813_at, 219827_at	NP_689372.3, NP_001186160.1, NP_001186161.1, NP_001186162.1, NP_001186163.1, EAW68731.1, EAW68732.1, EAW68733.1
GeneID:8231	ZNF373	19	58,229,203	58,270,200	41,027	-	1	1_A375_shN7_mes_lncRNA_AR_1...2976	68	up gene	1	0	0	21	14	13	1	1_A375_shN7_mes_lncRNA_AR	921	Gene ZNF373	ZNF373, FLJ30921	zinc finger protein 373	NM_182580, NM_001173809, NM_001173810, NM_001173811, NM_001173812, NM_001173813, XC7233142.0, XC7233143.0, XC7233144.0	1569813_at, 219827_at	NP_001161081.1, NP_001161082.1, NP_001161083.1, NP_001161084.1, NP_001161085.1, NP_872295.2
GeneID:4556	LOC84455 4	19	58,267,690	58,310,803	43,113	+	1	4_A375_SGR1...4709	482	up gene	0	0	1	7	8	21	1	4_A375_SGR1.1	21	Gene LOC84455 4		hypothetical LOC84455 4	XR_111879, XR_109839, XR_115539		
GeneID:6999	WDR87	19	58,275,472	58,297,317	21,845	+	1	2_A375_shN7_plus_lncRNA_AR_1...4280	-347	upstream	0	1	0	17	17	10	1	2_A375_shN7_gl_lncRNA_AR_1	917	Gene WDR87	FLJ32605, WDR87, MYD-SP11	WD repeat domain 87	NM_031951	224155_at	NP_114157.3
GeneID:2794	SIPA1L3	19	58,297,866	58,899,009	601,141	+	3	2_A375_shN7_plus_lncRNA_AR_1...4280, 4_A375_SGR1...4711, 4_A375_SGR1...4712	-256, 265196, 298132	upstream, up gene, up gene	0	1	1	8.67	10.33	14.67	3	2_A375_shN7_gl_lncRNA_AR_1	917	Gene SIPA1L3	SPAL3, SIPA1L3	signal-induced proliferation-associated 1 like 3	NM_015073, XC7234142.2	213960_at, 235864_at, 236896_at, 37631_at	NP_055886.1, EAW68738.1
GeneID:5322	YIF1B	19	58,784,200	58,806,808	12,608	-	2	4_A375_SGR1...4713, 4_A375_SGR1...4714	10658, 5414	up gene, up gene	0	0	1	8.5	8.5	15	2	4_A375_SGR1.1	20	Gene YIF1B	FLJ30374, FLJ45765, YIF1B, MGC29135, FLJ25477	Golgi interacting factor homolog B (S. cerevisiae)	NM_001039672, NM_001039673, NM_033307, NM_001145461, NM_001145462, NM_001145463, XC7199768.1, XC7234767.0, XC7235391.0, XC754141.3	1554553_s_at, 236437_at	NP_001034741.1, NP_001034742.1, NP_001034743.1, NP_001139533.1, NP_001139534.1, NP_001034760.1, EAW68772.1, EAW68773.1, EAW68774.1
GeneID:8372	C19orf52	19	58,794,936	58,795,648	642	+	2	4_A375_SGR1...4713, 4_A375_SGR1...4714	1464, 3355	downstream, downstream	0	0	1	8.5	8.5	16	2	4_A375_SGR1.1	20	Gene C19orf52	MMLP, MMLP-2, MMLP-1, MGC29135, C19orf52, FLJ25193	chromosome 19 open reading frame 52	NM_032532, XC7227553.0, XC754150.3	229831_s_at	NP_775755.1, EAW68769.1, EAW68770.1
GeneID:5370	CATSPER4	19	58,826,443	58,861,909	35,146	+	2	2_A375_shN7_mes_lncRNA_AR_1...2977, 2_A375_shN7_plus_lncRNA_AR_1...4281	39813, 39029	downstream, downstream	1	1	0	19	16	10	1	2_A375_shN7_mes_lncRNA_AR	919	Gene CATSPER4	FLJ48353, CYNL15, CATSPER4, DKFZp434N022, FLJ38599, MGC129884	cation channel, sperm-associated, 4	NM_021183, XC7184228.2, XC7195535.0, XC7195536.1, XC7227291.0, XC7227292.0, XC754149.4	221310_at, 231261_at, 234353_at	NP_067005.3, EAW68777.1, EAW68780.1, EAW68783.1, EAW68785.1, EAW68781.1, EAW68782.1
GeneID:1114	PSMD8	19	58,865,160	58,874,484	9,274	+	2	2_A375_shN7_mes_lncRNA_AR_1...2977, 2_A375_shN7_plus_lncRNA_AR_1...4281	-134, 382	upstream, up gene	1	0	0	19	16	10	1	1_A375_shN7_mes_lncRNA_AR	919	Gene PSMD8	p31, P97S, MGC1680, S14, Nin1p, PSMD8, HYPF, Rpn12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	NM_002812, XC754137.4	200820_at	NP_002803.2, EAW68768.1
GeneID:1732	GGN	19	58,874,932	58,876,866	5,878	-	2	1_A375_shN7_mes_lncRNA_AR_1...2977, 2_A375_shN7_plus_lncRNA_AR_1...4281	13812, 13196	downstream, downstream	1	1	0	19	16	10	1	1_A375_shN7_mes_lncRNA_AR	919	Gene GGN	MGC23289, FLJ35713, GGN	gametogenetin	NM_152937, XC7191993.1, XC7233113.0, XC754152.2	231420_at, 244393_at	NP_689770.3, EAW68798.1, EAW68797.1, EAW68795.1
GeneID:3992	SPRED3	19	58,880,939	58,898,671	5,832	+	1	2_A375_shN7_plus_lncRNA_AR_1...4282	12621	downstream	0	1	0	11	15	10	1	2_A375_shN7_gl_lncRNA_AR_1	915	Gene SPRED3	SPRED3, Eve-3	sprouty-related, EVH1 domain containing 3	NM_001039616, NM_001042522		NP_001034705.1, NP_001035667.1
GeneID:7995	FAM99C	19	58,895,775	58,899,726	3,953	+	2	2_A375_shN7_plus_lncRNA_AR_1...4282, 2_A375_shN7_gl_lncRNA_AR_1...4715	-15, 18345	upstream, downstream	0	1	1	11.5	11.5	14	2	4_A375_SGR1.1	16	Gene FAM99C	FLJ44699, FAM99C	family with sequence similarity 99, member C	NM_174933, XC7233100.0, XC7233101.0, XC7235102.0, XC754143.2	227951_s_at	NP_777565.3, EAW68790.1, EAW68791.1, EAW68792.1, EAW68793.1
GeneID:5727	RAGSAP1	19	58,899,866	58,916,945	17,247	-	2	2_A375_shN7_plus_lncRNA_AR_1...4282, 2_A375_shN7_gl_lncRNA_AR_1...4715	23163, 7625	downstream, up gene	0	1	1	11.5	11.5	14	2	4_A375_SGR1.1	16	Gene RAGSAP1	RAGSAP1		NM_170684, NM_001145202, NM_001145203, NM_001145204, NM_001145205, NM_001145206, NM_001145207, XC7194384.4	231320_s_at, 243992_at	NP_733745.1, NP_001139074.1, NP_001139075.1, NP_001139076.1, NP_001139077.1, NP_001139078.1, EAW68794.1
GeneID:8398	RYR1	19	58,924,340	59,076,304	151,964	+	5	1_A375_shN7_mes_lncRNA_AR_1...2978, 2_A375_shN7_plus_lncRNA_AR_1...4283, 2_A375_shN7_gl_lncRNA_AR_1...4716, 4_A375_SGR1...4717, 4_A375_SGR1...4718	21484, 21484, 106439, 128012, 101344	up gene, up gene, up gene, up gene, up gene	1	1	1	8.3	12.25	14.75	4	2_A375_shN7_gl_lncRNA_AR_1	913	Gene RYR1	SKXR, CCO, RYDR, eRyR, sHK0, sHK01, RYR1, RYR	ryanodine receptor 1 (skeletal)	NM_000540, NM_001042723, XC7198781.1, XC7227302.0, XC7227304.0, XC7235190.0	205449_at	NP_000531.2, NP_001035193.1, EAW68793.1, EAW68796.1, EAW68797.1, EAW68798.1
GeneID:1154	MAP4K11	19	59,076,261	59,108,945	30,382	-	1	2_A375_shN7_plus_lncRNA_AR_1...4284	-1229	upstream	0	1	0	14	21	14	1	2_A375_shN7_gl_lncRNA_AR_1	921	Gene MAP4K11	MAP4K11, HPK1	mitogen-activated protein kinase kinase kinase kinase 11	NM_007181, NM_001042600, XC7195955.1, XC7197709.1, XC7227572.0, XC754153.2	206295_x_at, 216219_s_at, 214329_x_at	NP_001121.1, NP_001028055.1, EAW68799.1, EAW68800.1, EAW68801.1, EAW68802.1
GeneID:2737	EIF3I	19	59,109,722	59,127,893	17,873	+	1	2_A375_shN7_plus_lncRNA_AR_1...4284	190	up gene	0	1	0	14	21	14	1	2_A375_shN7_gl_lncRNA_AR_1	921	Gene EIF3I	EIF3S12, EIF3I, WSTF201, WS, PLAC2a, PRO1474, PTD001, PLAC2a, HSPC029, EIF3-p35, WRS136	eukaryotic translation initiation factor 3, subunit I	NM_016024, XC7227731.0, XC7227734.0, XC7227916.0, XC7234151.0, XC7234153.0, XC7235393.0	210801_s_at, 212716_s_at, 221494_x_at, 239605_at	NP_003746.1, EAW68808.1, EAW68804.1, EAW68807.1, EAW68806.1, EAW68808.1
GeneID:8574	ACTN4	19	59,135,327	59,221,170	85,843	+	7	1_A375_shN7_mes_lncRNA_AR_1...2979, 1_A375_shN7_mes_lncRNA_AR_1...2980, 2_A375_shN7_gl_lncRNA_AR_1...4285, 2_A375_shN7_gl_lncRNA_AR_1...4286, 2_A375_shN7_gl_lncRNA_AR_1...4287, 2_A375_shN7_gl_lncRNA_AR_1...4288, 4_A375_SGR1...4719	59670, 44585, -101, 10213, 53617, 44169, 75	up gene, up gene, upstream, up gene, up gene, up gene	1	1	1	16.25	16.5	11	4	2_A375_shN7_gl_lncRNA_AR_1	921	Gene ACTN4	DKFZp686I2315, ACTN4, FSGS, FSGS1, ACTN4a, 4	actinin, alpha 4	NM_004924, XC7227733.1, XC7227732.1, XC7227519.0	200801_at	NP_004915.2, EAW68809.1, EAW68810.1, EAW68811.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:3960	LGALS4	19	39,292,311	39,303,740	11,429	-	1	4_A375_EGR1..1..4720	-8473	upstream	0	0	1	7	12	20	1	4_A375_EGR1..1	20	Gene LGALS4	LGALS4, GAL4, L36LBP	lectin, galactoside-binding, soluble, 4	NM_006149, hCT11604.3, hCT2278733.0	204272_at	NP_006140.1, EAW56819.1, EAW56820.1
GeneID:1891	ECH1	19	39,306,062	39,322,497	16,435	-	1	4_A375_EGR1..1..4720	10284	in gene	0	0	1	7	12	20	1	4_A375_EGR1..1	20	Gene ECH1	HPXEL, ECH1	enoyl CoA hydratase 1, peroxisomal	NM_001398, hCT1961665.1, hCT2353191.0, hCT2353192.0, hCT2353193.0, hCT2353194.0	200789_at	NP_001389.2, EAW56824.1, EAW56821.1, EAW56822.1, EAW56823.1, EAW56825.1
GeneID:100507591	LOC100507591	19	39,306,084	39,306,587	503	+	1	4_A375_EGR1..1..4720	6149	downstream	0	0	1	7	12	20	1	4_A375_EGR1..1	20	Gene LOC100507591		hypothetical LOC100507591	XR_109528		
GeneID:100289398	LOC100289398	19	39,308,059	39,322,636	14,577	+	1	4_A375_EGR1..1..4720	4154	in gene	0	0	1	7	12	20	1	4_A375_EGR1..1	20	Gene LOC100289398		hypothetical LOC100289398	XR_111891, XR_109529, XR_115288		
GeneID:3191	HNRNPL	19	39,327,028	39,342,979	15,951	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4289	-189	upstream	0	1	0	16	21	11	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene HNRNPL	HNRNPL, FLJ35509, HNRPL, P/OKcl.14, hnRNP-L	heterogeneous nuclear ribonucleoprotein L	NM_001533, NM_001005335, hCT2278728.0, hCT2278729.0, hCT2278730.0	202072_at, 221860_at, 35201_at	NP_001524.2, NP_001005335.1, EAW56826.1, EAW56827.1, EAW56828.1
GeneID:126432	RINL	19	39,358,470	39,368,894	10,424	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2961, 2_A375_pNL97_plus_lncRNA_AR..1..4290, 4_A375_EGR1..1..4721	8288, 8254, 8894	in gene, in gene, in gene	1	1	1	35	37	17	1	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene RINL	FLJ45909, RINL, FLJ44131	Ras and Rab interactor-like	NM_198445		NP_940847.1
GeneID:22933	SIRT2	19	39,369,195	39,390,502	21,307	-	5	1_A375_pNL7_minus_lncRNA_AR..1..2961, 1_A375_pNL7_minus_lncRNA_AR..1..2962, 2_A375_pNL97_plus_lncRNA_AR..1..4290, 2_A375_pNL97_plus_lncRNA_AR..1..4291, 4_A375_EGR1..1..4721	29894, 91, 29862, 294, 30502	downstream, in gene, downstream, in gene, downstream	1	1	1	26	29.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene SIRT2	SIR2L2, SIRT2, FLJ35621, SIR2, FLJ37491, SIR2L	sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	NM_012237, NM_030593, NM_001193286, NR_034146, hCT2278720.0, hCT2278721.0, hCT2278722.0, hCT2278723.0, hCT2278724.0, hCT2353091.0	1558331_at, 220605_s_at	NP_036369.2, NP_085096.1, NP_001180215.1, EAW56834.1, EAW56837.1, EAW56838.1, EAW56833.1, EAW56835.1, EAW56836.1
GeneID:4793	NFKBIB	19	39,390,615	39,399,534	8,919	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2962, 2_A375_pNL97_plus_lncRNA_AR..1..4291, 4_A375_EGR1..1..4722	-204, -407, 11753	upstream, upstream, downstream	1	1	1	11.5	15	14	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene NFKBIB	IKBB, NFKBIB, TRIP9	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	NM_002503, NM_001001716, hCT11606.5, hCT1966665.2, hCT1966666.2, hCT1966667.2, hCT2353199.0	214062_x_at, 214448_x_at, 228388_at	NP_002494.2, NP_001001716.1, EAW56839.1, EAW56840.1, EAW56841.1, EAW56842.1, EAW56843.1
GeneID:643669	LOC643669	19	39,399,623	39,402,798	3,175	-	3	1_A375_pNL7_minus_lncRNA_AR..1..2962, 2_A375_pNL97_plus_lncRNA_AR..1..4291, 4_A375_EGR1..1..4722	12387, 12590, 430	downstream, downstream, in gene	1	1	1	11.5	15	14	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC643669		hypothetical protein LOC643669	XM_001717465, XM_933621, XM_946053		XP_001717517.1, XP_938714.3, XP_951146.3
GeneID:54938	SARS2	19	39,405,904	39,421,536	15,632	-	1	4_A375_EGR1..1..4722	19166	downstream	0	0	1	6	6	15	1	4_A375_EGR1..1	15	Gene SARS2	SARSM, SARS, mtSerRS, SerRSmt, SERS, FLJ20450, SYS, SARS2, SerRS	seryl-tRNA synthetase 2, mitochondrial	NM_001145901, NM_017827, hCT11605.3, hCT1957481.0, hCT2278719.0, hCT2353197.0, hCT2353198.0	218702_at	NP_001139373.1, NP_060297.1, EAW56845.1, EAW56846.1, EAW56847.1, EAW56848.1, EAW56844.1
GeneID:10298	PAK4	19	39,616,420	39,670,046	53,626	+	1	4_A375_EGR1..1..4724	59260	downstream	0	0	1	4	7	16	1	4_A375_EGR1..1	16	Gene PAK4	PAK4		NM_005884, NM_001014832, NM_001014835, NM_001014831, NM_001014834, hCT11358.2, hCT1957471.1, hCT1957472.1, hCT2277363.0, hCT2277364.0, hCT2353071.0, hCT2353072.0, hCT2353073.0, hCT2353074.0	203154_s_at, 215326_at, 33814_at	NP_005875.1, NP_001014832.1, NP_001014831.1, NP_001014834.1, NP_001014835.1, EAW56864.1, EAW56858.1, EAW56859.1, EAW56860.1, EAW56861.1, EAW56862.1, EAW56863.1, EAW56865.1, EAW56866.1
GeneID:282617	IL28B	19	39,734,272	39,735,611	1,339	-	1	4_A375_EGR1..1..4725	-3189	upstream	0	0	1	3	3	16	1	4_A375_EGR1..1	16	Gene IL28B	IL28C, IL28B, IL-28B, IFNL3	interleukin 28B (interferon, lambda 3)	NM_172139, hCT2278707.0		NP_742151.2, EAW56869.1
GeneID:9535	GMFG	19	39,818,999	39,826,726	7,727	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2986, 2_A375_pNL97_plus_lncRNA_AR..1..4295	-5898, -5882	upstream, upstream	1	1	0	106	116	6	1	2_A375_pNL97_plus_lncRNA_AR..1	116	Gene GMFG	GMFG, MGC126867, GMF-GAMMA	glia maturation factor, gamma	NM_004877, hCT34639.4	204220_at	NP_004868.1, EAW56874.1
GeneID:55095	SAMD4B	19	39,833,108	39,875,542	42,434	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2986, 1_A375_pNL7_minus_lncRNA_AR..1..2987, 2_A375_pNL97_plus_lncRNA_AR..1..4295, 2_A375_pNL97_plus_lncRNA_AR..1..4296	-484, 49100, -500, 49004	upstream, downstream, upstream, downstream	1	1	0	82	89	10	2	2_A375_pNL97_plus_lncRNA_AR..1	116	Gene SAMD4B	SMGB, FLJ10211, MGC99632, SAMD4B, hSmaug2	sterile alpha motif domain containing 4B	NM_018028, hCT1960832.1, hCT1960833.1, hCT2277374.0, hCT2353209.0, hCT34646.3	220457_at, 226714_at, 227511_at, 229871_at	NP_060498.2, EAW56875.1, EAW56876.1, EAW56877.1, EAW56878.1, EAW56879.1
GeneID:54623	PAF1	19	39,876,269	39,881,679	5,410	-	2	1_A375_pNL7_minus_lncRNA_AR..1..2987, 2_A375_pNL97_plus_lncRNA_AR..1..4296	-529, -433	upstream, upstream	1	1	0	18	22	12	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene PAF1	FLJ11123, PAF1, PD2, F23149_1	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	NM_019088, hCT2278699.0, hCT2278701.0, hCT2278702.0, hCT34641.3	202093_s_at	NP_061961.2, EAW56883.1, EAW56880.1, EAW56881.1, EAW56882.1
GeneID:55588	MED29	19	39,881,963	39,891,203	9,240	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2987, 2_A375_pNL97_plus_lncRNA_AR..1..4296	245, 149	in gene, in gene	1	1	0	18	22	12	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MED29	IXL, DKFZp434H247, MED29	mediator complex subunit 29	NM_017592, hCT34650.2	225708_at	NP_060062.1, EAW56884.1
GeneID:7538	ZFP36	19	39,897,487	39,900,045	2,558	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2988, 2_A375_pNL97_plus_lncRNA_AR..1..4297	5606, 5553	downstream, downstream	1	1	0	23	27	12	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene ZFP36	NUP475, GOS24, G0S24, TTP, RNF162A, TIS11, ZFP36	zinc finger protein 36, C3H type, homolog (mouse)	NM_003407, hCT2277378.0, hCT34637.3	201531_at	NP_003398.1, EAW56886.1, EAW56885.1
GeneID:64857	PLEKHG2	19	39,903,750	39,919,055	15,305	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2988, 2_A375_pNL97_plus_lncRNA_AR..1..4297, 2_A375_pNL97_plus_lncRNA_AR..1..4298	-657, -710, 22810	upstream, upstream, downstream	1	1	0	18	24	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene PLEKHG2	FLJ38638, DKFZp667J2325, FLJ22458, CLG, PLEKHG2, FLJ00018, ARHGEF42	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	NM_022835, hCT2277380.0, hCT2277382.0, hCT2277383.0, hCT2277384.0, hCT34647.3	225979_at, 233986_s_at	NP_073746.2, EAW56888.1, EAW56887.1, EAW56889.1, EAW56890.1, EAW56891.1
GeneID:6217	RPS16	19	39,923,847	39,926,618	2,771	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4298, 4_A375_EGR1..1..4726	58, -9606	in gene, upstream	0	1	1	15	17	14	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RPS16	RPS16, S16	ribosomal protein S16	NM_001020, hCT1967697.1, hCT2353169.0, hCT2353170.0, hCT2353171.0	201258_at, 213890_x_at, 226131_s_at	NP_001011.1, EAW56894.1, EAW56892.1, EAW56893.1, EAW56895.1
GeneID:6829	SUPT5H	19	39,936,186	39,967,310	31,124	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2989, 2_A375_pNL97_plus_lncRNA_AR..1..4298, 4_A375_EGR1..1..4726	35270, -9626, 36	downstream, upstream, in gene	1	1	1	15.33	17	13.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SUPT5H	SUPT5H, SPT5, Tat-CT1, SPT5H, FLJ34157	suppressor of Ty 5 homolog (S. cerevisiae)	NM_003169, NM_001111020, NM_001130824, NM_001130825, hCT1962793.1, hCT1962794.1, hCT2353151.0, hCT2353152.0, hCT34635.3	201480_s_at	NP_003160.2, NP_001104490.1, NP_001124296.1, NP_001124297.1, EAW56897.1, EAW56900.1, EAW56896.1, EAW56898.1, EAW56899.1
GeneID:92609	TIMM50	19	39,971,052	39,981,528	10,476	+	1	1_A375_pNL7_minus_lncRNA_AR..1..2989	404	in gene	1	0	0	16	17	13	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene TIMM50	TIMM50, MGC102733, TIM50, TIM50L	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	NM_001001563, hCT2277395.0, hCT2277396.0, hCT2277398.0	217612_at, 224913_s_at	NP_001001563.1, EAW56902.1, EAW56901.1, EAW56903.1
GeneID:126272	EID2B	19	40,021,630	40,023,494	1,864	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2990	-7290	upstream	1	0	0	15	14	11	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene EID2B	EID-3, FLJ38944, EID2B	EP300 interacting inhibitor of differentiation 2B	NM_152361, hCT1657237.3	242470_at	NP_689574.1, EAW56908.1
GeneID:163126	EID2	19	40,029,446	40,030,838	1,392	-	1	1_A375_pNL7_minus_lncRNA_AR..1..2990	54	in gene	1	0	0	15	14	11	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene EID2	EID2, MGC20452, CRI2, EID-2	EP300 interacting inhibitor of differentiation 2	NM_153232, hCT1970660.1	225936_at	NP_694964.3, EAW56909.1
GeneID:29124	LGALS13	19	40,093,169	40,098,114	4,945	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2991, 2_A375_pNL97_plus_lncRNA_AR..1..4299	-3233, -3169	upstream, upstream	1	1	0	21	22	1	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LGALS13	PLAC8, LGALS13, GAL13, PP13	lectin, galactoside-binding, soluble, 13	NM_013268, hCT34636.3	220440_at	NP_037400.1, EAW56910.1
GeneID:148003	LGALS16	19	40,146,558	40,151,287	4,729	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2992, 2_A375_pNL97_plus_lncRNA_AR..1..4300	-10014, -9966	upstream, upstream	1	1	0	27	36	4	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene LGALS16		beta-galactoside-binding lectin	NM_001190441		NP_001177370.1
GeneID:9149	DYRK1B	19	40,315,990	40,324,841	8,851	-	1	4_A375_EGR1..1..4727	265	in gene	0	0	1	12	11	23	1	4_A375_EGR1..1	23	Gene DYRK1B	DYRK1B, MIRK	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	NM_004714, NM_006483, NM_006484, hCT1686859.2, hCT1816458.1, hCT1967692.1, hCT1967693.1, hCT1967694.1, hCT1967695.1, hCT2276778.0, hCT2276780.0, hCT2276788.0	204954_s_at, 217270_s_at	NP_004705.1, NP_006474.1, NP_006475.1, EAW56916.1, EAW56920.1, EAW56921.1, EAW56917.1, EAW56918.1, EAW56919.1, EAW56922.1, EAW56923.1, EAW56924.1
GeneID:2091	FBL	19	40,325,093	40,337,054	11,961	-	1	4_A375_EGR1..1..4727	12476	downstream	0	0	1	12	11	23	1	4_A375_EGR1..1	23	Gene FBL	FLRN, FIB, FBL, RNU3IP1	fibrillarin	NM_001436, hCT34634.3	211623_s_at	NP_001427.2, EAW56925.1
GeneID:8857	FCGBP	19	40,353,963	40,440,533	86,570	-	1	4_A375_EGR1..1..4728	20341	in gene	0	0	1	6	5	17	1	4_A375_EGR1..1	17	Gene FCGBP	FCGBP, FC(GAMMA)BP	Fc fragment of IgG binding protein	NM_003890, hCT1951986.2	203240_at	NP_003881.2, EAW56926.1
GeneID:5704	PSMC4	19	40,477,073	40,487,353	10,280	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4301	-193	upstream	0	1	0	12	23	12	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene PSMC4	TBP7, MIP224, MGC23214, S6, MGC8570, PSMC4, MGC13687	proteasome (prosome, macropain) 26S subunit, ATPase, 4	NM_153001, NM_006503, hCT2275665.0, hCT34631.3	201252_at	NP_694546.1, NP_006494.1, EAW56928.1, EAW56929.1
GeneID:284323	ZNF780A	19	40,575,059	40,596,845	21,786	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4302	221	in gene	0	1	0	12	23	6	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ZNF780A	ZNF780A, ZNF780	zinc finger protein 780A	NM_001142577, NM_001010880, NM_001142578, NM_001142579, hCT2276861.1		NP_001136049.1, NP_001010880.2, NP_001136050.1, NP_001136051.1, EAW56936.1
GeneID:4294	MAP3K10	19	40,697,651	40,721,482	23,831	+	3	2_A375_pNL97_plus_lncRNA_AR..1..4304, 4_A375_EGR1..1..4729, 4_A375_EGR1..1..4730	26125, 397, 30829	downstream, in gene, downstream	0	1	1	12.33	13.33	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MAP3K10	MST, MLK2, MAP3K10, MEKK10	mitogen-activated protein kinase kinase kinase 10	NM_002446, hCT11318.3	206362_x_at	NP_002437.2, EAW56937.1
GeneID:148014	TTC9B	19	40,721,965	40,724,306	2,341	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4304, 4_A375_EGR1..1..4730	-1470, -4174	upstream, upstream	0	1	1	12	14	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TTC9B	FLJ30373, MGC33982, TTC9B	tetratricopeptide repeat domain 9B	NM_152479, hCT11879.3	235375_x_at, 242484_at	NP_689692.2, EAW56938.1
GeneID:79935	CNTD2	19	40,728,115	40,732,597	4,482	-	3	2_A375_pNL97_plus_lncRNA_AR..1..4304, 4_A375_EGR1..1..4730, 4_A375_EGR1..1..4731	6821, 4117, -6475	downstream, in gene, upstream	0	1	1	8.67	12	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CNTD2	CNTD2, FLJ13265	cyclin N-terminal domain containing 2	NM_024877, hCT1816468.2, hCT2276858.0	220323_at	NP_079153.2, EAW56939.1, EAW56940.1
GeneID:208	AKT2	19	40,736,224	40,791,265	55,041	-	3	2_A375_pNL97_plus_lncRNA_AR..1..4304, 4_A375_EGR1..1..4730, 4_A375_EGR1..1..4731	65489, 62785, 52193	downstream, downstream, in gene	0	1	1	8.67	12	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene AKT2	RAC-BETA, PRKBB, AKT2, PKBBETA, PKBB	v-akt murine thymoma viral oncogene homolog 2	NM_001626, hCT11881.3, hCT2276852.0, hCT2276854.0	1560689_s_at, 203809_s_at, 211453_s_at, 225471_s_at, 226156_at, 236664_at	NP_001617.1, EAW56941.1, EAW56942.1, EAW56943.1
GeneID:126526	C19orf47	19	40,826,970	40,854,293	27,323	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4305, 4_A375_EGR1..1..4732	-75, 26561	upstream, in gene	0	1	1	15	16	16	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene C19orf47	DKFZp686P0512 9, FLJ36888, C19orf47	chromosome 19 open reading frame 47	NM_178830, hCT2276845.0, hCT2276847.0, hCT2353122.0, hCT2353123.0, hCT2353124.0	1554475_a_at, 234999_at	NP_849152.1, EAW56946.1, EAW56945.1, EAW56947.1, EAW56948.1, EAW56949.1
GeneID:23646	PLD3	19	40,854,332	40,884,390	30,058	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4305	36	in gene	0	1	0	20	25	9	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene PLD3	HU-K4, PLD3, HUK4	phospholipase D family, member 3	NM_001031696, NM_012268, hCT2275873.0, hCT2275874.0, hCT2275875.0, hCT2275876.0, hCT2275877.0, hCT2275878.0, hCT2275879.0, hCT2275880.0, hCT2275881.0, hCT2275882.0	201050_at	NP_001026866.1, NP_036400.2, EAW56950.1, EAW56952.1, EAW56958.1, EAW56959.1, EAW56951.1, EAW56953.1, EAW56954.1, EAW56955.1, EAW56956.1, EAW56957.1
GeneID:57716	PRX	19	40,899,671	40,919,271	19,600	-	1	4_A375_EGR1..1..4733	-7641	upstream	0	0	1	17	16	18	1	4_A375_EGR1..1	18	Gene PRX	PRX, KIAA1620, CMT4F	periaxin	NM_181882, NM_020956, hCT11880.3, hCT2276835.0	220024_s_at, 222255_at	NP_870998.2, NP_066007.1, EAW56962.1, EAW56963.1
GeneID:29950	SERTAD1	19	40,928,408	40,931,932	3,524	-	1	4_A375_EGR1..1..4733	5020	downstream	0	0	1	17	16	18	1	4_A375_EGR1..1	18	Gene SERTAD1	TRIP-Br1, SEI1, SERTAD1	SERTA domain containing 1	NM_013376, hCT1816463.1, hCT1957460.1	223394_at	NP_037508.2, EAW56965.1, EAW56964.1
GeneID:645	BLVRB	19	40,953,691	40,971,725	18,034	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4306	-510	upstream	0	1	0	17	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene BLVRB	FLR, SDR43U1, MGC117413, BLVRB, BVRB	biliverdin reductase B (flavin reductase (NADPH))	NM_000713, hCT1966652.1, hCT201417.2, hCT2353161.0, hCT2353162.0	202201_at	NP_000704.1, EAW56972.1, EAW56969.1, EAW56970.1, EAW56971.1
GeneID:57731	SPTBN4	19	40,973,126	41,082,365	109,239	+	6	1_A375_pNL7_minus_lncRNA_AR..1..2994, 2_A375_pNL97_plus_lncRNA_AR..1..4306, 2_A375_pNL97_plus_lncRNA_AR..1..4307, 4_A375_EGR1..1..4734, 4_A375_EGR1..1..4735, 4_A375_EGR1..1..4736	109626, -891, 109626, 62074, 87194, 90074	downstream, upstream, downstream, in gene, in gene, in gene	1	1	1	11.6	16.4	14.6	5	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene SPTBN4	SPNB4, SPTBN3, KIAA1642, SPTBN4, QV	spectrin, beta, non-erythrocytic 4	NM_020971, NM_025213, hCT2275666.0, hCT2353164.0, hCT2353165.0, hCT2353166.0, hCT2353167.0, hCT2353168.0	220165_at, 224144_at, 224145_s_at, 224297_s_at, 224551_s_at	NP_066022.2, NP_079489.2, EAW56973.1, EAW56974.1, EAW56976.1, EAW56978.1, EAW56975.1, EAW56977.1
GeneID:92799	SHKBP1	19	41,082,757	41,097,305	14,548	+	2	1_A375_pNL7_minus_lncRNA_AR..1..2994, 2_A375_pNL97_plus_lncRNA_AR..1..4307	-5, -5	upstream, upstream	1	1	0	21	34	6	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene SHKBP1	PP203, Sb1, SHKBP1	SH3KBP1 binding protein 1	NM_138392, hCT2275669.0, hCT2353205.0, hCT2353206.0	224846_at	NP_612401.2, EAW56979.1, EAW56980.1, EAW56981.1
GeneID:8425	LTBP4	19	41,099,072	41,135,725	36,653	+	7	1_A375_pNL7_minus_lncRNA_AR..1..2995, 1_A375_pNL7_minus_lncRNA_AR..1..2996, 2_A375_pNL97_plus_lncRNA_AR..1..4308, 2_A375_pNL97_plus_lncRNA_AR..1..4309, 4_A375_EGR1..1..4737, 4_A375_EGR1..1..4738, 4_A375_EGR1..1..4739	12496, 17984, 18080, 21280, 11608, 16608, 20256	in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	12.6	14.4	17.6	5	4_A375_EGR1..1	23	Gene LTBP4	LTBP-4L, FLJ90018, LTBP4S, FLJ46318, LTBP-4, LTBP4, LTBP4L	latent transforming growth factor beta binding protein 4	NM_003573, NM_001042544, NM_001042545, hCT11329.3, hCT1951974.2, hCT2275690.0, hCT2275691.0	204442_x_at, 210628_x_at, 213176_s_at, 227989_at	NP_003564.2, NP_001036009.1, NP_001036010.1, EAW56982.1, EAW56983.1, EAW56985.1, EAW56984.1
GeneID:79934	ADCK4	19	41,197,434	41,222,790	25,356	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2997, 1_A375_pNL7_minus_lncRNA_AR..1..2998, 2_A375_pNL97_plus_lncRNA_AR..1..4310, 4_A375_EGR1..1..4740	1046, 6, 806, -1176	in gene, in gene, in gene, upstream	1	1	1	13.5	13	16	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ADCK4	FLJ12229, ADCK4	aarF domain containing kinase 4	NM_024876, NM_001142555, hCT2276436.1, hCT2276437.0, hCT2276438.0, hCT2345216.0, hCT2353163.0	220434_at, 227324_at	NP_079152.3, NP_001136027.1, EAW56987.1, EAW56988.1, EAW56990.1, EAW56991.1, EAW56989.1
GeneID:80271	ITPKC	19	41,223,008	41,246,765	23,757	+	4	1_A375_pNL7_minus_lncRNA_AR..1..2997, 1_A375_pNL7_minus_lncRNA_AR..1..2998, 2_A375_pNL97_plus_lncRNA_AR..1..4310, 4_A375_EGR1..1..4740	-1264, -224, -1024, 960	upstream, upstream, upstream, in gene	1	1	1	13.5	13	16	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ITPKC	IP3KC, ITPKC, IP3-3KC	inositol 1,4,5-trisphosphate 3-kinase C	NM_025194, hCT11875.3, hCT2275947.0	213076_at	NP_079470.1, EAW56992.1, EAW56993.1
GeneID:100507666	LOC100507666	19	41,223,549	41,239,209	15,660	-	4	1_A375_pNL7_minus_lncRNA_AR..1..2997, 1_A375_pNL7_minus_lncRNA_AR..1..2998, 2_A375_pNL97_plus_lncRNA_AR..1..4310, 4_A375_EGR1..1..4740	17465, 16425, 17225, 15241	downstream, downstream, downstream, in gene	1	1	1	13.5	13	16	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene LOC100507666		hypothetical LOC100507666	XR_111892, XR_109530, XR_115290		
GeneID:112398	EGLN2	19	41,305,048	41,314,337	9,289	+	1	4_A375_EGR1..1..4741	10868	downstream	0	0	1	4	9	16	1	4_A375_EGR1..1	16	Gene EGLN2	DKFZp434E026, EGLN2, PHD1, EIT6, HPH-3, HIFPH1, FLJ95603	egl nine homolog 2 (C. elegans)	NM_053046, NM_080732, hCT11869.3, hCT1958217.2, hCT1958220.2, hCT1958221.2, hCT1969289.2	220956_s_at, 223063_s_at, 227147_s_at	NP_444274.1, NP_542770.2, EAW57007.1, EAW57008.1, EAW57009.1, EAW57011.1, EAW57010.1
GeneID:1548	CYP2A	19	41,314,400	41,712,393	397,993	+	1	4_A375_EGR1..1..4741	1536	in gene	0	0	1	4	9	16	1	4_A375_EGR1..1	16	Gene CYP2A	P450C2A, CYP2, CYP1, CYP2A, P450C2, P450PB	cytochrome P450, family 2, subfamily A			

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:558	AXL	19	41,725,108	41,767,671	42,563	+	1	2_A375_pNL97_plus_lncRNA_AR..1.4311	45196	downstream	0	1	0	15	21	11	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene AXL	JTK11, UFO, AXL	AXL receptor tyrosine kinase	NM_021913, NM_001699, hCT2275923.2, hCT2275928.2	202685_s_at, 202686_s_at	NP_068713.2, NP_001690.2, EAW57022.1, EAW57023.1
GeneID:11100	HNRNPUL1	19	41,768,391	41,813,811	45,420	+	3	1_A375_pNL7_minus_lncRNA_AR..1..2999, 2_A375_pNL97_plus_lncRNA_AR..1.4311, 2_A375_pNL97_plus_lncRNA_AR..1.4312	47769, 1913, 47865	downstream, in gene, downstream	1	1	0	19.5	21.5	14	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene HNRNPUL1	HNRNPUL1, E1BAP5, HNRPUL1, FLJ12944, E1B-AP5	heterogeneous nuclear ribonucleoprotein U-like 1	NM_007040, NM_144732, hCT2275927.0, hCT2353131.0, hCT2353132.0, hCT2353133.0, hCT2353134.0, hCT2353135.0	208713_at, 209675_s_at	NP_008971.2, NP_653333.1, EAW57024.1, EAW57025.1, EAW57026.1, EAW57029.1, EAW57027.1, EAW57028.1
GeneID:90324	CCDC97	19	41,816,094	41,830,788	14,694	+	5	1_A375_pNL7_minus_lncRNA_AR..1..2999, 2_A375_pNL97_plus_lncRNA_AR..1.4312, 2_A375_pNL97_plus_lncRNA_AR..1.4313, 2_A375_pNL97_plus_lncRNA_AR..1.4314, 4_A375_EGR1..1.4742	66, 162, 11662, 13570, 17719	in gene, in gene, in gene, in gene, downstream	1	1	1	16	17	13.75	4	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene CCDC97	MGC20255, FLJ40267, CCDC97	coiled-coil domain containing 97	NM_052848, hCT13415.2, hCT2275932.0	225254_at, 225257_at, 235495_at	NP_443080.1, EAW57031.1, EAW57030.1
GeneID:7040	TGFB1	19	41,836,812	41,859,831	23,019	-	5	2_A375_pNL97_plus_lncRNA_AR..1.4313, 2_A375_pNL97_plus_lncRNA_AR..1.4314, 2_A375_pNL97_plus_lncRNA_AR..1.4315, 4_A375_EGR1..1.4742, 4_A375_EGR1..1.4743	32055, 30167, -10153, 26018, 11975	downstream, downstream, upstream, downstream, in gene	0	1	1	11.8	13.4	12.6	5	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TGFB1	TGFbeta, TGFB, LAP, DPD1, TGFB1, CED	transforming growth factor, beta 1	NM_000660, hCT13414.3, hCT2276464.0	203084_at, 203085_s_at	NP_000651.3, EAW57032.1, EAW57033.1
GeneID:80776	B9D2	19	41,860,322	41,870,078	9,756	-	1	2_A375_pNL97_plus_lncRNA_AR..1.4315	94	in gene	0	1	0	14	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene B9D2	B9D2, MKSR2, MGC4093, ICIS-1	B9 protein domain 2	NM_030578, hCT13417.3	219766_at	NP_085055.2, EAW57034.1
GeneID:641649	TMEM91	19	41,869,871	41,889,988	20,117	+	1	2_A375_pNL97_plus_lncRNA_AR..1.4315	113	in gene	0	1	0	14	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene TMEM91	IFITMD6, FLJ45695, TMEM91, FLJ27310	transmembrane protein 91	NM_001098824, NM_001098822, NM_001042595, NM_001098823, NM_001098821	229957_at	NP_001092294.1, NP_001092292.1, NP_001036060.1, NP_001092295.1, NP_001092293.1, NP_001092291.1
GeneID:55101	ATP5SL	19	41,937,223	41,945,843	8,620	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3000, 2_A375_pNL97_plus_lncRNA_AR..1.4316, 4_A375_EGR1..1.4744	-109, -45, -5917	upstream, upstream, upstream	1	1	1	34.5	31	14	2	1_A375_pNL7_minus_lncRNA_AR..1	65	Gene ATP5SL	ATP5SL, FLJ10241	ATP5S-like	NM_001167867, NM_001167868, NM_001167869, NR_030765, NM_018035, NM_001167871, NM_001167870, hCT13412.4, hCT1961718.1, hCT1961719.1, hCT1961721.0	1557759_at, 218036_at, 45828_at	NP_001161339.1, NP_001161340.1, NP_001161341.1, NP_060505.2, NP_001161343.1, NP_001161342.1, EAW57042.1, EAW57043.1, EAW57044.1, EAW57045.1
GeneID:100170765	C19orf69	19	41,949,063	41,950,670	1,607	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3000, 2_A375_pNL97_plus_lncRNA_AR..1.4316, 4_A375_EGR1..1.4744	-3111, -3175, 2697	upstream, upstream, downstream	1	1	1	34.5	31	14	2	1_A375_pNL7_minus_lncRNA_AR..1	65	Gene C19orf69	C19orf69	chromosome 19 open reading frame 69	NM_001130514		NP_001123986.1
GeneID:100505495	LOC100505495	19	41,955,425	42,006,554	51,129	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3000, 2_A375_pNL97_plus_lncRNA_AR..1.4316, 4_A375_EGR1..1.4744	60802, 60668, 54794	downstream, downstream, downstream	1	1	1	34.5	31	14	2	1_A375_pNL7_minus_lncRNA_AR..1	65	Gene LOC100505495		hypothetical LOC100505495	XR_111862, XR_111860, XR_111861, XR_109534, XR_109532, XR_109533, XR_115293, XR_115291, XR_115292		
GeneID:1089	CEACAM4	19	42,125,344	42,133,442	8,098	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3001, 2_A375_pNL97_plus_lncRNA_AR..1.4317	9842, 9922	downstream, downstream	1	1	0	18	19	9	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CEACAM4	NCA, CEACAM4, CGM7, CGM7_HUMAN	carcinoembryonic antigen-related cell adhesion molecule 4	NM_001817, hCT13401.1, hCT2353195.0, hCT2353196.0	207205_at	NP_001808.2, EAW57055.1, EAW57054.1, EAW57056.1
GeneID:1084	CEACAM3	19	42,300,534	42,315,591	15,057	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3002, 2_A375_pNL97_plus_lncRNA_AR..1.4318	17178, 17146	downstream, downstream	1	1	0	21	23	4	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CEACAM3	MGC119875, W282, CGM1, CEA, W264, CEACAM3, CD66D	carcinoembryonic antigen-related cell adhesion molecule 3	NM_001815, hCT13404.3, hCT1963667.1, hCT2276001.0, hCT2353212.0	208052_x_at, 210789_x_at	NP_001806.2, EAW57062.1, EAW57063.1, EAW57064.1, EAW57065.1
GeneID:83946	DMRTC2	19	42,349,088	42,356,398	7,312	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3003, 2_A375_pNL97_plus_lncRNA_AR..1.4319	14690, 14768	downstream, downstream	1	1	0	17	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene DMRTC2	DMRTC2	DMRT-like family C2	NM_001040283, hCT1816367.2, hCT2276003.0, hCT2353140.0	236611_at	NP_001035373.1, EAW57070.1, EAW57068.1, EAW57069.1
GeneID:6223	RPS19	19	42,363,988	42,375,484	11,496	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3003, 2_A375_pNL97_plus_lncRNA_AR..1.4319	-212, -116	upstream, upstream	1	1	0	17	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene RPS19	DBA1, S19, DBA, RPS19	ribosomal protein S19	NM_001022, hCT2276005.0, hCT2276006.0, hCT2276007.0, hCT2276008.0	202649_x_at, 213414_s_at, 242451_x_at	NP_001013.1, EAW57074.1, EAW57071.1, EAW57072.1, EAW57073.1
GeneID:100505604	LOC100505604	19	42,365,217	42,373,281	8,064	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3003, 2_A375_pNL97_plus_lncRNA_AR..1.4319	9505, 9409	downstream, downstream	1	1	0	17	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC100505604		hypothetical LOC100505604	XR_111865, XR_109537, XR_115296		
GeneID:973	CD79A	19	42,381,190	42,385,439	4,249	+	2	2_A375_pNL97_plus_lncRNA_AR..1.4320, 2_A375_pNL97_plus_lncRNA_AR..1.4321	7162, 10874	downstream, downstream	0	1	0	13.5	21	12	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CD79A	CD79A, MB-1, IGA	CD79a molecule, immunoglobulin-associated alpha	NM_001783, NM_021601, hCT13402.3, hCT1963666.1	1555779_a_at, 205049_s_at	NP_001774.1, NP_067612.1, EAW57075.1, EAW57076.1
GeneID:9138	ARHGEF1	19	42,387,267	42,411,604	24,337	+	3	2_A375_pNL97_plus_lncRNA_AR..1.4320, 2_A375_pNL97_plus_lncRNA_AR..1.4321, 4_A375_EGR1..1.4745	1065, 4797, 9277	in gene, in gene, in gene	0	1	1	12	16.67	15	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ARHGEF1	GEF1, ARHGEF1, P115-RHOGEF, SUB1.5, LBCL2, LSC	Rho guanine nucleotide exchange factor (GEF) 1	NM_004706, NM_198977, NM_199002, hCT13420.2, hCT1963676.1, hCT1963677.0, hCT1963678.1, hCT1963679.0, hCT2276012.0, hCT2353110.0, hCT2353111.0	1560445_x_at, 203055_s_at	NP_004697.2, NP_945328.1, NP_945353.1, EAW57077.1, EAW57081.1, EAW57083.1, EAW57078.1, EAW57079.1, EAW57080.1, EAW57082.1, EAW57084.1
GeneID:100505585	LOC100505585	19	42,427,246	42,434,299	7,053	+	1	4_A375_EGR1..1.4746	16914	downstream	0	0	1	12	8	14	1	4_A375_EGR1..1	14	Gene LOC100505585		hypothetical LOC100505585	XR_109538		
GeneID:10567	RABAC1	19	42,460,833	42,463,528	2,695	-	1	4_A375_EGR1..1.4747	7544	downstream	0	0	1	6	10	19	1	4_A375_EGR1..1	19	Gene RABAC1	PRA1, YIP3, PRAF1, RABAC1	Rab acceptor 1 (prenylated)	NM_006423, hCT13405.3, hCT2353216.0, hCT2353217.0	203136_at	NP_006414.2, EAW57088.1, EAW57086.1, EAW57087.1
GeneID:478	ATP1A3	19	42,470,734	42,498,382	27,648	-	2	2_A375_pNL97_plus_lncRNA_AR..1.4322, 4_A375_EGR1..1.4748	-2994, 23633	upstream, in gene	0	1	1	9.5	20.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene ATP1A3	ATP1A3, RDP, DYT12, MGC13276	ATPase, Na+/K+ transporting, alpha 3 polypeptide	NM_152296, hCT12980.3	214432_at	NP_689509.1, EAW57089.1
GeneID:2901	GRIK5	19	42,502,473	42,569,957	67,484	-	1	2_A375_pNL97_plus_lncRNA_AR..1.4322	66581	downstream	0	1	0	14	31	10	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene GRIK5	GRIK5, EAA2, KA2, GRIK2	glutamate receptor, ionotropic, kainate 5	NM_002088, hCT12986.3, hCT2278031.0	1553166_at, 214966_at, 217509_x_at	NP_002079.3, EAW57091.1, EAW57090.1
GeneID:5452	POU2F2	19	42,592,650	42,636,630	43,980	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3004, 2_A375_pNL97_plus_lncRNA_AR..1.4323	-7650, -7662	upstream, upstream	1	1	0	39	41	7	1	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene POU2F2	OCT2, OTF2, POU2F2, Oct-2	POU class 2 homeobox 2	NM_002698, hCT12984.3, hCT1963999.1, hCT1984000.1, hCT1984001.1, hCT1984002.1, hCT2278020.0, hCT2278022.0, hCT2278024.0, hCT2278026.0, hCT2278029.0	211660_at, 211771_s_at, 228343_at, 229750_at	NP_002689.1, EAW57100.1, EAW57103.1, EAW57104.1, EAW57105.1, EAW57106.1, EAW57098.1, EAW57099.1, EAW57101.1, EAW57102.1, EAW57107.1
GeneID:100505622	LOC100505622	19	42,636,707	42,641,251	4,544	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3004, 1_A375_pNL7_minus_lncRNA_AR..1..3005, 2_A375_pNL97_plus_lncRNA_AR..1.4323, 2_A375_pNL97_plus_lncRNA_AR..1.4324	7773, 11005, 7805, 10973	downstream, downstream, downstream, downstream	1	1	0	45.5	53	7	2	2_A375_pNL97_plus_lncRNA_AR..1	65	Gene LOC100505622		hypothetical LOC100505622	XR_111866, XR_109538, XR_115297		
GeneID:100422980	MIR4323	19	42,637,597	42,637,665	68	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3004, 1_A375_pNL7_minus_lncRNA_AR..1..3005, 2_A375_pNL97_plus_lncRNA_AR..1.4323, 2_A375_pNL97_plus_lncRNA_AR..1.4324	-6615, -10047, -6647, -10015	upstream, upstream, upstream, upstream	1	1	0	45.5	53	7	2	2_A375_pNL97_plus_lncRNA_AR..1	65	Gene MIR4323	MIR4323	microRNA 4323	NR_036208		
GeneID:100505639	LOC100505639	19	42,656,721	42,661,675	4,954	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3005, 2_A375_pNL97_plus_lncRNA_AR..1.4324	-9009, -9041	upstream, upstream	1	1	0	52	65	7	1	2_A375_pNL97_plus_lncRNA_AR..1	65	Gene LOC100505639		hypothetical LOC100505639	XR_109539		
GeneID:162989	DEDD2	19	42,702,752	42,721,813	19,061	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3006, 2_A375_pNL97_plus_lncRNA_AR..1.4325, 4_A375_EGR1..1.4750	-1019, 661, -2811	upstream, in gene, upstream	1	1	1	16.33	16	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene DEDD2	FLAME-3, DEDD2	death effector domain containing 2	NM_133328, hCT12961.2, hCT1963655.1, hCT1966693.1	225434_at	NP_579874.1, EAW57112.1, EAW57110.1, EAW57111.1
GeneID:116115	ZNF526	19	42,724,492	42,732,353	7,861	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3006, 2_A375_pNL97_plus_lncRNA_AR..1.4325, 4_A375_EGR1..1.4750	-1660, -3340, 132	upstream, upstream, in gene	1	1	1	16.33	16	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ZNF526	KIAA1951, ZNF526, DKFZp762O059, MGC4267	zinc finger protein 526	NM_133444, hCT12976.3	228229_at	NP_597701.1, EAW57113.1
GeneID:2931	GSK3A	19	42,734,338	42,746,736	12,398	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3007, 1_A375_pNL7_minus_lncRNA_AR..1..3006, 2_A375_pNL97_plus_lncRNA_AR..1.4326, 2_A375_pNL97_plus_lncRNA_AR..1.4327, 4_A375_EGR1..1.4750	-160, -2448, -528, -2144, 22112	upstream, upstream, upstream, upstream, downstream	1	1	1	20.33	16.67	11.67	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene GSK3A	GSK3A, DKFZp686D0638	glycogen synthase kinase 3 alpha	NM_019884, hCT12968.3, hCT2278011.0	202210_x_at, 632_at	NP_063937.2, EAW57114.1, EAW57115.1
GeneID:100132272	LOC100132272	19	42,746,927	42,749,125	2,198	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3007, 1_A375_pNL7_minus_lncRNA_AR..1..3008, 2_A375_pNL97_plus_lncRNA_AR..1.4326, 2_A375_pNL97_plus_lncRNA_AR..1.4327, 2_A375_pNL97_plus_lncRNA_AR..1.4328	-31, 2257, 337, 1953, 11393	upstream, downstream, in gene, in gene, downstream	1	1	0	17.33	21	9	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC100132272		hypothetical LOC100132272	XR_111868, XR_109540, XR_115299		
GeneID:2077	ERF	19	42,751,717	42,759,309	7,592	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3007, 1_A375_pNL7_minus_lncRNA_AR..1..3008, 2_A375_pNL97_plus_lncRNA_AR..1.4326, 2_A375_pNL97_plus_lncRNA_AR..1.4327, 2_A375_pNL97_plus_lncRNA_AR..1.4328	12413, 10125, 12045, 10429, 989	downstream, downstream, downstream, downstream, in gene	1	1	0	17.33	21	9	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene ERF	PE-2, PE2, ERF	Ets2 repressor factor	NM_006494, hCT11431.2, hCT1963651.0, hCT2278010.0	203643_at, 230388_at	NP_006485.2, EAW57116.1, EAW57117.1, EAW57118.1
GeneID:23152	CIC	19	42,788,817	42,799,949	11,132	+	7	1_A375_pNL7_minus_lncRNA_AR..1..3010, 1_A375_pNL7_minus_lncRNA_AR..1..3011, 2_A375_pNL97_plus_lncRNA_AR..1.4330, 2_A375_pNL97_plus_lncRNA_AR..1.4331, 2_A375_pNL97_plus_lncRNA_AR..1.4332, 4_A375_EGR1..1.4752, 4_A375_EGR1..1.4753	-4129, 17607, -4156, -1009, 17607, -6577, 17623	upstream, downstream, upstream, upstream, downstream, upstream, downstream	1	1	1	18.75	18.5	14.75	4	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene CIC	KIAA0306, CIC	capicua homolog (Drosophila)	NM_015125, hCT12965.3, hCT1963661.1, hCT2276036.0	212784_at	NP_055940.3, EAW57121.1, EAW57119.1, EAW57120.1
GeneID:100505682	LOC100505682	19	42,799,486	42,808,282	8,796	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3011, 2_A375_pNL97_plus_lncRNA_AR..1.4332, 2_A375_pNL97_plus_lncRNA_AR..1.4333, 4_A375_EGR1..1.4753, 4_A375_EGR1..1.4754	1658, 1658, -9558, 1642, -9830	in gene, in gene, upstream, in gene, upstream	1	1	1	15.5	17	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene LOC100505682		hypothetical LOC100505682	XR_111869, XR_109541, XR_115300		
GeneID:5050	PAFAH1B3	19	42,801,185	42,806,952	5,767	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3011, 2_A375_pNL97_plus_lncRNA_AR..1.4332, 4_A375_EGR1..1.4753	326, 326, 312	in gene, in gene, in gene	1	1	1	22	17	17	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene PAFAH1B3	PAFAHG, FLJ44990, PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)	NM_002573, NM_001145939, NM_001145940, hCT12982.2, hCT1963657.0, hCT1963658.0, hCT1963659.0, hCT2353099.0	203228_at	NP_002564.1, NP_001139411.1, NP_001139412.1, EAW57123.1, EAW57124.1, EAW57125.1, EAW57122.1, EAW57126.1
GeneID:284338	PRR19	19	42,806,284	42,814,973	8,689	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3011, 2_A375_pNL97_plus_lncRNA_AR..1.4332, 2_A375_pNL97_plus_lncRNA_AR..1.4333, 4_A375_EGR1..1.4753, 4_A375_EGR1..1.4754	340, 340, 11556, 356, 11826	in gene, in gene, downstream, in gene, downstream	1	1	1	15.5	17	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene PRR19	MGC70924, PRR19	proline rich 19	NM_199285, hCT1816368.2	231176_at	NP_954979.2, EAW57127.1
GeneID:284339	TMEM145	19	42,817,477	42,829,214	11,737	+	2	2_A375_pNL97_plus_lncRNA_AR..1.4333, 4_A375_EGR1..1.4754	363, 635	in gene, in gene	0	1	1	9	17	14	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TMEM145	FLJ90805, TMEM145	transmembrane protein 145	NM_173633, hCT12990.2, hCT1963663.1, hCT2353139.0	1553479_at	NP_775904.2, EAW57130.1, EAW57128.1, EAW57129.1
GeneID:84518	CNFN	19	42,891,171	42,894,444	3,273	-	1	2_A375_pNL97_plus_lncRNA_AR..1.4334	-6636	upstream	0	1	0	10	22	11	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CNFN	PLAC8L2, CNFN	cornifelin	NM_032488, hCT12987.2	224329_s_at	NP_115877.2, EAW57134.1
GeneID:3991	LIPE	19	42,905,666	42,931,578	25,912	-	3	2_A375_pNL97_plus_lncRNA_AR..1.4334, 2_A375_pNL97_plus_lncRNA_AR..1.4335, 4_A375_EGR1..1.4755	30298, 3562, 3994	downstream, in gene, in gene	0	1	1	9.5	20	16	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LIPE	LIPE, HSL, LHS	lipase, hormone-sensitive	NM_005357, hCT12972.3	208186_s_at, 213855_s_at	NP_005348.2, EAW57135.1
GeneID:284340	CXCL17	19	42,932,695	42,947,136	14,441	-	2	2_A375_pNL97_plus_lncRNA_AR..1.4335, 4_A375_EGR1..1.4755	19120, 19552	downstream, downstream	0	1	1	9	18	21	1	4_A375_EGR1..1	21	Gene CXCL17	VCC-1, MGC138300, VCC1, Dcip1, CXCL17, UNQ473, DMC	chemokine (C-X-C motif) ligand 17	NM_198477	226960_at	NP_940879.1
GeneID:1088	CEACAM8	19	43,084,395	43,099,082	14,687	-	1	2_A375_pNL97_plus_lncRNA_AR..1.4336	-7094	upstream	0	1	0	18	26	10	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene CEACAM8	CD66b, CD67, NCA-95, CGM6, CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	NM_001816, hCT12975.3	206676_at	NP_001807.2, EAW57144.1
GeneID:5680	PSG11	19	43,406,240	43,530,631	124,391	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3012	60935	in gene	1	0	0	13	9	4	1	1_A375_pNL7_minus_lncRNA_AR..1	13	Gene PSG11	PSG14, PSG11, MGC22484, PSG13	pregnancy specific beta-1-glycoprotein 11	NM_002785, NM_203287, NM_001113410, hCT2276196.0, hCT2276197.0, hCT2276198.0		NP_002776.3, NP_976032.2, NP_001106881.1, EAW57166.1, EAW57167.1, EAW57168.1
GeneID:23574	PRG1	19	43,853,208	43,853,700	492	+	1	4_A375_EGR1..1.4756	4552	downstream	0	0	1	4	5	16	1	4_A375_EGR1..1	16	Gene PRG1		p53-responsive gene 1	NR_026661		
GeneID:57126	CD177	19	43,857,825	43,867,480	9,655	+	1	4_A375_EGR1..1.4756	-65	upstream	0	0	1	4	5	16	1	4_A375_EGR1..1	16	Gene CD177	NB1, CD177, PRV1, HNA2A	CD177 molecule	NM_020406	219669_at	NP_065139.2
GeneID:27076	LYPD3	19	43,964,946	43,969,831	4,885	-	2	4_A375_EGR1..1.4757, 4_A375_EGR1..1.4758	1319, -9721	in gene, upstream	0	0	1	8.5	10.5	19.5	2	4_A375_EGR1..1	22	Gene LYPD3	C4.4A, LYPD3	LY6/PLAUR domain containing 3	NM_014400, hCT11353.2	204952_at	NP_055215.2, EAW57190.1
GeneID:653583	PHLDB3	19	43,979,255	44,008,985	29,730	-	2	4_A375_EGR1..1.4758, 4_A375_EGR1..1.4759	29433, 3193	in gene, in gene	0	0	1	7.5	7	18.5	2	4_A375_EGR1..1	22	Gene PHLDB3	FLJ40193, MGC67511, PHLDB3	pleckstrin homology-like domain, family B, member 3	NM_198850		NP_942147.3
GeneID:23474	ETHE1	19	44,010,871	44,031,396	20,525	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3015, 2_A375_pNL97_plus_lncRNA_AR..1.4338, 2_A375_pNL97_plus_lncRNA_AR..1.4339, 2_A375_pNL97_plus_lncRNA_AR..1.4340, 4_A375_EGR1..1.4759	36, 1524, 4, -5532, 25604	in gene, in gene, in gene, upstream, downstream	1	1	1	15.75	17.25	12.25	4	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene ETHE1	ETHE1, YF13H12, HSCO	ethylmalonic encephalopathy 1	NM_014297, hCT2276166.0, hCT2276170.0, hCT2276172.0	204034_at	NP_055112.2, EAW57195.1, EAW57196.1, EAW57197.1
GeneID:284346	ZNF575	19	44,037,340	44,040,290	2,950	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3015, 2_A375_pNL97_plus_lncRNA_AR..1.4338, 2_A375_pNL97_plus_lncRNA_AR..1.4339, 2_A375_pNL97_plus_lncRNA_AR..1.4340	-5980, -7468, -5946, -412	upstream, upstream, upstream, upstream	1	1	0	19	21.67	11.33	3	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene ZNF575	FLJ32567, ZNF575	zinc finger protein 575	NM_174945, hCT1950220.2, hCT2275358.0, hCT2275356.0	1557119_a_at	NP_777605.1, EAW57199.1, EAW57198.1, EAW57200.1
GeneID:7515	XRCC1	19	44,047,464	44,079,730	32,266	-	1	2_A375_pNL97_plus_lncRNA_AR..1.4340	42802	downstream	0	1	0	14	18	18	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene XRCC1	RCC, XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	NM_006297, hCT2276161.0, hCT2276164.0, hCT2276166.0	203655_at	NP_006288.2, EAW57202.1, EAW57201.1, EAW57203.1
GeneID:126298	IRGQ	19	44,088,519	44,100,287	11,768	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3016, 2_A375_pNL97_plus_lncRNA_AR..1.4341	31, -1	in gene, upstream	1	1	0	37	28	10	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene IRGQ	IRGQ, FLJ38849, FKSG27, IRGQ1, FLJ12521, FLJ42796, FLJ46713	immunity-related GTPase family, Q	NM_001007561, hCT1642299.0	1569310_at	NP_001007562.1, EAW57205.1
GeneID:79177	ZNF576	19	44,100,544	44,104,587	4,043	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3016, 2_A375_pNL97_plus_lncRNA_AR..1.4341	-286, -256	upstream, upstream	1	1	0	37	28	10	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene ZNF576	FLJ22700, MGC2508, ZNF576, FLJ58397	zinc finger protein 576	NM_024327, NM_001145347, hCT1967574.1, hCT2275360.0, hCT30802.3	219086_s_at, 219089_s_at	NP_077303.1, NP_001138819.1, EAW57206.1, EAW57207.1, EAW57208.1

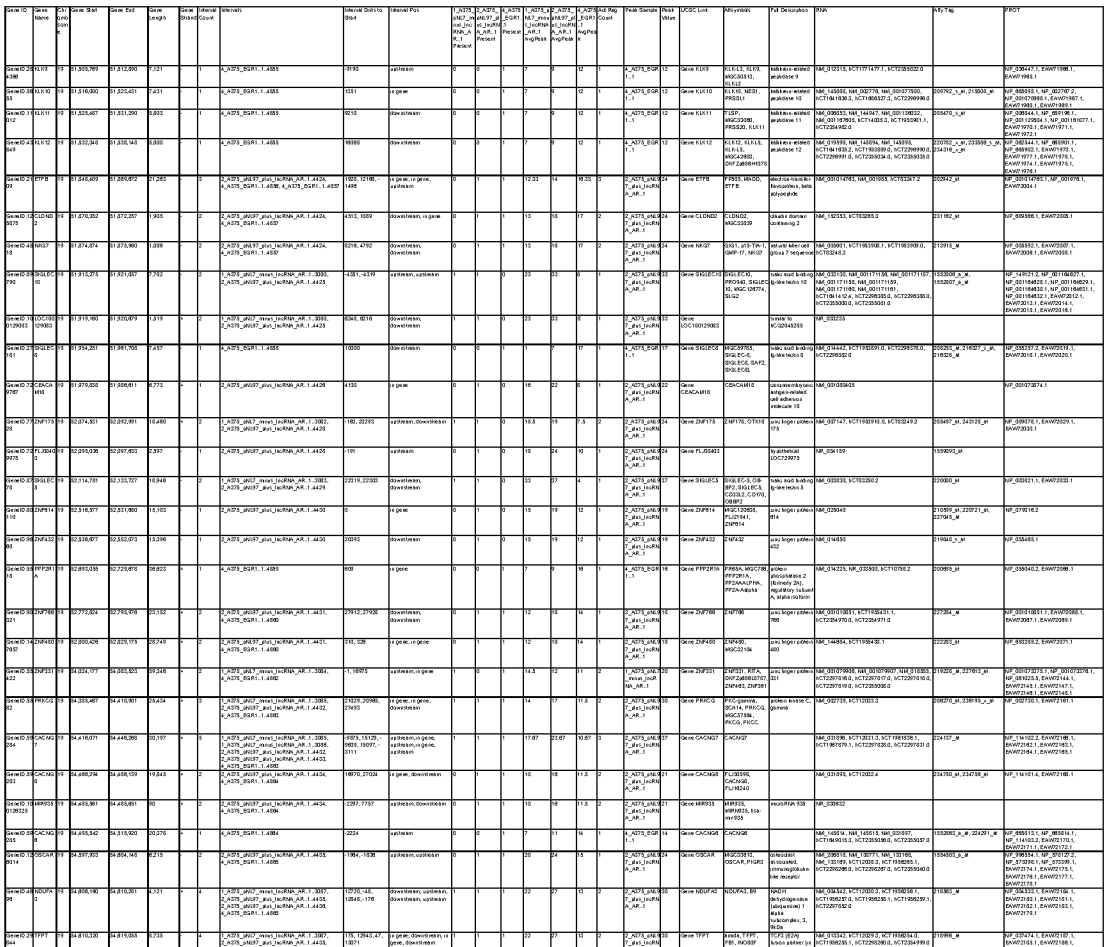
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:128299	ZNF428	19	44,111,376	44,124,014	12,638	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3017, 2_A375_pNL97_plus_lncRNA_AR..1..4342, 4_A375_EGR1..1..4760, 4_A375_EGR1..1..4761	142, 14, 558, 14	in gene, in gene, in gene, in gene	1	1	1	20	24	18	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ZNF428	C19orf37, ZNF428, MGC51082, Zfp428	zinc finger protein 428	NM_182498, hCT1641327.4, hCT2276156.1	1565848_at, 215429_s_at	NP_872304.2, EAW57209.1, EAW57210.1
GeneID:100170229	SRRM5	19	44,116,253	44,118,650	2,397	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3017, 2_A375_pNL97_plus_lncRNA_AR..1..4342, 4_A375_EGR1..1..4760, 4_A375_EGR1..1..4761	7619, 7747, 7203, 7747	downstream, downstream, downstream, downstream	1	1	1	20	24	18	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SRRM5	SRRM5, ZNF576, FLJ35737	serine/arginine repetitive matrix 5	NM_001145641		NP_001139113.1
GeneID:199731	CADM4	19	44,126,522	44,143,991	17,469	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3017, 2_A375_pNL97_plus_lncRNA_AR..1..4342, 4_A375_EGR1..1..4760, 4_A375_EGR1..1..4761	20119, 19991, 20535, 19991	downstream, downstream, downstream, downstream	1	1	1	20	24	18	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CADM4	Necl-4, synCAM4, CADM4, TSLL2, NECL4, IGSF4C	cell adhesion molecule 4	NM_145296, hCT2276151.1, hCT2276153.1, hCT2276154.1	214287_s_at, 215258_at, 215259_s_at, 222293_at, 229335_at	NP_660339.1, EAW57214.1, EAW57212.1, EAW57213.1
GeneID:5329	PLAUR	19	44,150,248	44,174,502	24,254	-	1	4_A375_EGR1..1..4762	38	in gene	0	0	1	13	14	17	1	4_A375_EGR1..1	17	Gene PLAUR	CD87, URKR, UPAR, PLAUR	plasminogen activator, urokinase receptor	NM_002659, NM_001005376, NM_001005377, hCT1950668.0, hCT2276144.0, hCT2276149.0, hCT2353083.0, hCT2353084.0, hCT30595.3	210845_s_at, 211924_s_at, 214866_at	NP_002650.1, NP_001005376.1, NP_001005377.1, EAW57216.1, EAW57217.1, EAW57219.1, EAW57215.1, EAW57218.1, EAW57220.1
GeneID:56006	C19orf61	19	44,235,301	44,259,142	23,841	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4343	-10298	upstream	0	1	0	14	25	13	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene C19orf61	C19orf61, F17127_1, FLJ12686, DKFZp564H1322, SMG9	chromosome 19 open reading frame 61	NM_019108, hCT1950222.1, hCT2276137.0, hCT2276139.0, hCT2276140.0, hCT2353114.0, hCT30605.3	221335_x_at, 223168_at, 233990_at	NP_061981.2, EAW57223.1, EAW57224.1, EAW57225.1, EAW57226.1, EAW57227.1, EAW57228.1
GeneID:3783	KCNN4	19	44,270,685	44,285,409	14,724	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3018, 2_A375_pNL97_plus_lncRNA_AR..1..4343, 2_A375_pNL97_plus_lncRNA_AR..1..4344, 2_A375_pNL97_plus_lncRNA_AR..1..4345	-7987, 15969, 257, -7951	upstream, downstream, in gene, upstream	1	1	0	20.67	27.67	9.67	3	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene KCNN4	hSK4, hIKCa1, KCNN4, KCa3.1, IK1, SK4, KCA4, IKCA1, hKCa4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	NM_002250, hCT2353156.0, hCT24567.3	204401_at	NP_002241.1, EAW57229.1, EAW57230.1
GeneID:284348	LYPD5	19	44,300,079	44,324,808	24,729	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3018, 2_A375_pNL97_plus_lncRNA_AR..1..4345	31432, 31448	downstream, downstream	1	1	0	34	40	4	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene LYPD5	PRO4356, FLJ30469, LYPD5	LY6/PLAUR domain containing 5	NM_182573, NM_001031749, hCT1950869.1	238039_at	NP_872379.2, NP_001026919.2, EAW57232.1
GeneID:100505715	LOC100505715	19	44,395,956	44,405,957	10,001	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3019	-299	upstream	1	0	0	18	16	7	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100505715		hypothetical LOC100505715	XR_111872, XR_111871, XR_109544, XR_109543, XR_115303, XR_115302		
GeneID:7711	ZNF155	19	44,488,355	44,502,477	14,122	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4346	18685	downstream	0	1	0	14	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ZNF155	pHZ-96, MGC161655, ZNF155	zinc finger protein 155	NM_003445, NM_198089, hCT2353085.0, hCT2353086.0, hCT30598.3	221201_s_at	NP_003436.2, NP_932355.1, EAW57238.1, EAW57239.1, EAW57240.1
GeneID:100505743	LOC100505743	19	44,501,048	44,506,988	5,940	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4346	-52	upstream	0	1	0	14	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100505743		hypothetical LOC100505743	XR_111874, XR_109545, XR_115305		
GeneID:7773	ZNF230	19	44,507,077	44,518,072	10,995	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4346	-37	upstream	0	1	0	14	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ZNF230	FDZF2, ZNF230	zinc finger protein 230	NM_006300, hCT30600.2	1557322_at, 1570135_at, 205791_x_at	NP_006291.2, EAW57241.1
GeneID:342909	ZNF284	19	44,576,297	44,591,623	15,326	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4347	22163	downstream	0	1	0	11	15	9	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene ZNF284	ZNF284L, ZNF284, DKFZp781F1775	zinc finger protein 284	NM_001037813	239462_at	NP_001032902.1
GeneID:7767	ZNF224	19	44,598,482	44,612,479	13,997	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3020, 2_A375_pNL97_plus_lncRNA_AR..1..4347	18830, -2	downstream, upstream	1	1	0	15	16.5	7	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene ZNF224	BMZF-2, ZNF27, BMZF2, ZNF255, ZNF224, KOX22	zinc finger protein 224	NM_013398, hCT1647899.3, hCT2277028.0, hCT2277029.0, hCT2277032.0, hCT2277033.0	216983_s_at, 216991_at, 220019_s_at, 232427_at, 244462_at	NP_037530.2, EAW57253.1, EAW57250.1, EAW57251.1, EAW57252.1, EAW57254.1
GeneID:100379224	LOC100379224	19	44,609,492	44,617,336	7,844	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3020	24	in gene	1	0	0	19	18	5	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene LOC100379224		hypothetical LOC100379224	NR_033341		
GeneID:7768	ZNF225	19	44,617,548	44,637,255	19,707	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3020	-236	upstream	1	0	0	19	18	5	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene ZNF225	ZNF225, MGC119735	zinc finger protein 225	NM_013362, hCT30601.3	207125_at, 229123_at, 235702_at	NP_037494.2, EAW57255.1
GeneID:353355	ZNF233	19	44,764,076	44,779,468	15,392	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3021, 2_A375_pNL97_plus_lncRNA_AR..1..4348	-76, -12	upstream, upstream	1	1	0	37	30	10	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene ZNF233	FLJ38032, ZNF233	zinc finger protein 233	NM_181756, hCT1646990.4, hCT2349820.0, hCT2349821.0, hCT2349822.0	230919_at, 232986_at	NP_861421.1, EAW57265.1, EAW57263.1, EAW57264.1, EAW57266.1
GeneID:9310	ZNF235	19	44,790,501	44,809,178	18,677	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4349, 4_A375_EGR1..1..4763	188, 188	in gene, in gene	0	1	1	14	16	15	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ZNF235	HZF6, ANF270, ZNF235, ZNF270, ZFP93	zinc finger protein 235	NM_004234, hCT1641537.2	210595_at, 220350_at	NP_004225.3, EAW57267.1
GeneID:7733	ZNF180	19	44,979,856	45,004,574	24,718	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3022, 2_A375_pNL97_plus_lncRNA_AR..1..4350, 4_A375_EGR1..1..4764	17, 94, 206	in gene, in gene, in gene	1	1	1	14	24	18	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ZNF180	HHZ168, ZNF180	zinc finger protein 180	NM_013256, hCT11419.3, hCT2353181.0, hCT2353182.0, hCT2353183.0, hCT2353184.0, hCT2353185.0	219495_s_at	NP_037388.2, EAW57279.1, EAW57274.1, EAW57275.1, EAW57276.1, EAW57277.1, EAW57278.1
GeneID:125931	CEACAM20	19	45,010,211	45,033,548	23,337	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3022, 2_A375_pNL97_plus_lncRNA_AR..1..4350, 2_A375_pNL97_plus_lncRNA_AR..1..4351, 4_A375_EGR1..1..4764	28991, 29068, 16426, 29180	downstream, downstream, in gene, downstream	1	1	1	11	20.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CEACAM20	CEACAM20, UNQ9366	carcinoembryonic antigen-related cell adhesion molecule 20	NM_001102597, NM_001102598, NM_001102599, NM_001102600, hCT13236.3		NP_001096067.1, NP_001096068.1, NP_001096069.1, NP_001096070.1, EAW57280.1
GeneID:602	BCL3	19	45,251,978	45,263,301	11,323	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3023	-6666	upstream	1	0	0	24	13	8	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene BCL3	D19S37, BCL3, BCL4	B-cell CLL/lymphoma 3	NM_005178, hCT13225.2	204907_s_at, 204908_s_at	NP_005169.2, EAW57291.1
GeneID:341	APOC1	19	45,417,921	45,422,606	4,685	+	1	4_A375_EGR1..1..4765	11983	downstream	0	0	1	9	5	13	1	4_A375_EGR1..1	13	Gene APOC1	APOC1		NM_001645, hCT13232.2, hCT1950218.1	204416_x_at, 213553_x_at	NP_001636.1, EAW57307.1, EAW57308.1
GeneID:346	APOC4	19	45,445,495	45,448,751	3,256	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3024, 2_A375_pNL97_plus_lncRNA_AR..1..4352	12649, 12777	downstream, downstream	1	1	0	20	24	13	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene APOC4	APOC-IV, APO-CIV, APOC4		NM_001646, hCT2277012.0	206738_at	NP_001637.1, EAW57310.1
GeneID:344	APOC2	19	45,449,243	45,452,818	3,575	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3024, 2_A375_pNL97_plus_lncRNA_AR..1..4352	8901, 9029	downstream, downstream	1	1	0	20	24	13	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene APOC2	APOC2, MGC75082, APO-CII, APOC-II	apolipoprotein C-II	NM_000483, hCT11410.3, hCT1950856.1, hCT2277015.0	204561_x_at, 231561_s_at, 231562_at	NP_000474.2, EAW57312.1, EAW57311.1, EAW57313.1
GeneID:1209	CLPTM1	19	45,458,638	45,496,599	37,961	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3024, 2_A375_pNL97_plus_lncRNA_AR..1..4352, 4_A375_EGR1..1..4766	-494, -366, 34562	upstream, upstream, in gene	1	1	1	14	18.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CLPTM1	CLPTM1	cleft lip and palate associated transmembrane protein 1	NM_001294, hCT11295.3, hCT2277018.0	201640_x_at, 211136_s_at	NP_001285.1, EAW57315.1, EAW57314.1
GeneID:11129	SFRS16	19	45,542,298	45,574,214	31,916	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4353	40230	downstream	0	1	0	22	24	11	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SFRS16	FLJ90109, CLASRP, CLASP, SFRS16, SWAP2	CLK4-associating serine/arginine rich protein	NM_007056, hCT13231.2, hCT2353077.0, hCT2353078.0	204978_at	NP_008987.2, EAW57317.1, EAW57318.1, EAW57319.1
GeneID:162979	ZNF296	19	45,574,758	45,579,688	4,930	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4353	-2640	upstream	0	1	0	22	24	11	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ZNF296	ZFP296, ZNF296, ZNF342	zinc finger protein 296	NM_145288, hCT1644650.3	236607_at	NP_660331.1, EAW57320.1
GeneID:79760	GEMIN7	19	45,582,518	45,594,782	12,264	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4353, 2_A375_pNL97_plus_lncRNA_AR..1..4354	10, 13770	in gene, downstream	0	1	0	21	25	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene GEMIN7	SIP3, GEMIN7	gem (nuclear organelle) associated protein 7	NM_024707, NM_001007269, NM_001007270, hCT13243.3	1555751_a_at, 219065_s_at, 222621_s_at	NP_078983.1, NP_001007270.1, NP_001007271.1, EAW57321.1
GeneID:284352	LRRC68	19	45,596,216	45,650,549	54,333	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4354	72	in gene	0	1	0	20	26	12	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene LRRC68	LRRC68, KIAA1988	leucine rich repeat containing 68	XM_001722969, XM_001723010, XM_001724714, XM_003119730, XM_003119732, XM_003119734, XM_003119733, XM_003119731, XM_003118775, XM_003118777, XM_003118779, XM_003118776, XM_003118778, XM_003120946, XM_003120948, XM_003120950, XM_003120949, XM_003120947	213751_at, 213781_at, 229262_at	XP_001723021.1, XP_001723062.1, XP_001724766.1, XP_003119778.1, XP_003119780.1, XP_003119782.1, XP_003119781.1, XP_003119779.1, XP_003118823.1, XP_003118825.1, XP_003118827.1, XP_003118826.1, XP_003118824.1, XP_003120994.1, XP_003120996.1, XP_003120998.1,
GeneID:90332	EXOC3L2	19	45,715,879	45,737,469	21,590	-	1	4_A375_EGR1..1..4767	21133	in gene	0	0	1	10	10	19	1	4_A375_EGR1..1	19	Gene EXOC3L2	EXOC3L2, FLJ36147, XTP7, MGC16332	exocyst complex component 3-like 2	NM_138568, hCT13242.4	1552889_a_at	NP_612635.3, EAW57331.1
GeneID:1158	CKM	19	45,809,671	45,826,233	16,562	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4355	-3335	upstream	0	1	0	12	23	9	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CKM	CKMM, CKM, M-CK	creatine kinase, muscle	NM_001824, hCT13233.3	204810_s_at	NP_001815.2, EAW57337.1
GeneID:147700	KLC3	19	45,843,998	45,854,778	10,780	+	1	4_A375_EGR1..1..4768	228	in gene	0	0	1	7	8	20	1	4_A375_EGR1..1	20	Gene KLC3	KLC2, KLC2L, KLC3, KNS2B, KLCt	kinesin light chain 3	NM_177417, hCT13241.3, hCT2276113.0, hCT2276115.0	1552749_a_at, 1570402_at, 239853_at	NP_803136.2, EAW57339.1, EAW57338.1, EAW57340.1
GeneID:2068	ERCC2	19	45,854,649	45,873,845	19,196	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3025, 2_A375_pNL97_plus_lncRNA_AR..1..4356, 4_A375_EGR1..1..4769	-43, -43, 6389	upstream, upstream, in gene	1	1	1	28	28	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	47	Gene ERCC2	MGC126218, COFS2, XPD, ERCC2, TTD, MGC126219, MGC102762, EM9	excision repair cross-complementing rodent repair deficiency, complementation group 2	NM_000400, NM_001130867, hCT11812.3, hCT2277766.0	213468_at	NP_000391.1, NP_001124339.1, EAW57341.1, EAW57342.1
GeneID:10848	PPP1R13L	19	45,882,892	45,909,607	26,715	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3025, 1_A375_pNL7_minus_lncRNA_AR..1..3026, 1_A375_pNL7_minus_lncRNA_AR..1..3027, 2_A375_pNL97_plus_lncRNA_AR..1..4356, 2_A375_pNL97_plus_lncRNA_AR..1..4357, 4_A375_EGR1..1..4770	35719, 8135, -153, 35719, -121, 615	downstream, in gene, upstream, downstream, upstream, in gene	1	1	1	66.67	66.67	13	3	2_A375_pNL97_plus_lncRNA_AR..1	146	Gene PPP1R13L	RAI, RAI4, NKIP1, IASPP, PPP1R13L	protein phosphatase 1, regulatory (inhibitor) subunit 13 like	NM_006663, NM_001142502, hCT1815489.2, hCT2277763.0, hCT2353089.0	218849_s_at	NP_006654.2, NP_001135974.1, EAW57343.1, EAW57344.1, EAW57345.1
GeneID:10849	CD3EAP	19	45,909,467	45,914,024	4,557	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3026, 1_A375_pNL7_minus_lncRNA_AR..1..3027, 2_A375_pNL97_plus_lncRNA_AR..1..4357, 4_A375_EGR1..1..4770	-7995, 293, 261, -475	upstream, in gene, in gene, upstream	1	1	1	76.5	79.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	146	Gene CD3EAP	CAST, ASE-1, MGC118851, PAF49, CD3EAP	CD3e molecule, epsilon associated protein	NM_012099, hCT11804.2, hCT2276116.1	205284_at	NP_036231.1, EAW57347.1, EAW57346.1
GeneID:2067	ERCC1	19	45,910,591	45,927,177	16,586	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3026, 1_A375_pNL7_minus_lncRNA_AR..1..3027, 2_A375_pNL97_plus_lncRNA_AR..1..4357, 2_A375_pNL97_plus_lncRNA_AR..1..4358, 4_A375_EGR1..1..4770, 4_A375_EGR1..1..4771	25705, 17417, 17449, 153, 18185, -34	downstream, downstream, downstream, in gene, downstream, upstream	1	1	1	56	60	13.67	3	2_A375_pNL97_plus_lncRNA_AR..1	146	Gene ERCC1	UV20, ERCC1, RAD10, COFS4	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	NM_001983, NM_202001, NM_001166049, hCT11808.3, hCT1950214.1, hCT1950215.1	203719_at, 203720_s_at, 228131_at	NP_001974.1, NP_973730.1, NP_001159521.1, EAW57348.1, EAW57349.1, EAW57350.1
GeneID:2354	FOSB	19	45,971,253	45,978,437	7,184	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3030, 2_A375_pNL97_plus_lncRNA_AR..1..4361, 2_A375_pNL97_plus_lncRNA_AR..1..4362	10763, 10731, 17451	downstream, downstream, downstream	1	1	0	27.5	29.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene FOSB	FOSB, GOSB, AP-1, MGC42291, G0S3, DKFZp686C0818, GOS3	FBJ murine osteosarcoma viral oncogene homolog B	NM_006732, NM_001114171, hCT11805.2, hCT2276121.0	202768_at	NP_006723.2, NP_001107643.1, EAW57351.1, EAW57352.1
GeneID:6253	RTN2	19	45,988,550	46,000,313	11,763	-	9	1_A375_pNL7_minus_lncRNA_AR..1..3030, 1_A375_pNL7_minus_lncRNA_AR..1..3031, 1_A375_pNL7_minus_lncRNA_AR..1..3032, 1_A375_pNL7_minus_lncRNA_AR..1..3033, 2_A375_pNL97_plus_lncRNA_AR..1..4361, 2_A375_pNL97_plus_lncRNA_AR..1..4362, 2_A375_pNL97_plus_lncRNA_AR..1..4363, 2_A375_pNL97_plus_lncRNA_AR..1..4364, 4_A375_EGR1..1..4773	18297, 537, -9383, -10311, 18329, 11609, 569, -10311, -9871	downstream, in gene, upstream, upstream, downstream, in gene, in gene, upstream, upstream	1	1	1	25.8	29.2	14	5	2_A375_pNL97_plus_lncRNA_AR..1	50	Gene RTN2	RTN2, NSPL1, NSP2	reticulon 2	NM_206900, NM_206901, NM_005619, hCT2277751.0, hCT2277754.0, hCT2353157.0, hCT2353158.0, hCT2353159.0, hCT2353160.0	204217_s_at, 34408_at	NP_996783.1, NP_996784.1, NP_005610.1, EAW57354.1, EAW57358.1, EAW57359.1, EAW57355.1, EAW57356.1, EAW57357.1
GeneID:147699	FLJ40125	19	46,001,731	46,005,768	4,037	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3031, 1_A375_pNL7_minus_lncRNA_AR..1..3032, 1_A375_pNL7_minus_lncRNA_AR..1..3033, 2_A375_pNL97_plus_lncRNA_AR..1..4363, 2_A375_pNL97_plus_lncRNA_AR..1..4364, 4_A375_EGR1..1..4773	-1955, 7965, 8893, -1987, 8893, 8253	upstream, downstream, downstream, upstream, downstream, downstream	1	1	1	24.67	29	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	50	Gene FLJ40125	FLJ40125, PPM1N	protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative)	NM_001080401, hCT1969106.1	229559_at, 238930_at	NP_001073870.1, EAW57360.1
GeneID:7408	VASP	19	46,010,688	46,030,241	19,553	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3032, 1_A375_pNL7_minus_lncRNA_AR..1..3033, 2_A375_pNL97_plus_lncRNA_AR..1..4364, 4_A375_EGR1..1..4773	-992, -64, -64, -704	upstream, upstream, upstream, upstream	1	1	1	27	31	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	50	Gene VASP	VASP	vasodilator-stimulated phosphoprotein	NM_003370, hCT11807.3, hCT1967148.1, hCT2276130.0, hCT2276133.0	202205_at	NP_003361.1, EAW57362.1, EAW57363.1, EAW57364.1, EAW57365.1
GeneID:80207	OPA3	19	46,031,025	46,088,122	57,097	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3034, 1_A375_pNL7_minus_lncRNA_AR..1..3035, 1_A375_pNL7_minus_lncRNA_AR..1..3036, 2_A375_pNL97_plus_lncRNA_AR..1..4365, 2_A375_pNL97_plus_lncRNA_AR..1..4366, 4_A375_EGR1..1..4774	40538, 3186, -70, 42298, -70, -6294	in gene, in gene, upstream, in gene, upstream, upstream	1	1	1	20	21.2	9.6	5	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene OPA3	FLJ22187, OPA3, MGC75494, FLJ25932, MGA3	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	NM_001017989, NM_025136, hCT2277755.0	206357_at, 238630_at	NP_001017989.2, NP_079412.1, EAW57367.1
GeneID:2828	GPR4	19	46,093,022	46,105,466	12,444	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3035, 1_A375_pNL7_minus_lncRNA_AR..1..3036, 2_A375_pNL97_plus_lncRNA_AR..1..4366, 4_A375_EGR1..1..4774	20530, 17274, 17274, 11050	downstream, downstream, downstream, in gene	1	1	1	21.67	24	11.33	3	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene GPR4	GPR4		NM_005282	206236_at, 211266_s_at	NP_005273.1
GeneID:24139	EML2	19	46,112,658	46,148,775	36,117	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4367, 4_A375_EGR1..1..4775	3191, 3351	in gene, in gene	0	1	1	15	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene EML2	EMAP-2, EMAP2, EML2, ELP70	echinoderm microtubule associated protein like 2	NM_012155, NM_001193268, NM_001193269, NR_034098, hCT11810.3, hCT1950216.1	204397_at, 204398_s_at, 204399_s_at, 234021_at, 234026_at	NP_036287.1, NP_001180197.1, NP_001180198.1, EAW57369.1, EAW57370.1
GeneID:442902	MIR330	19	46,142,252	46,142,345	93	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4367, 4_A375_EGR1..1..4775	-3239, -3079	upstream, upstream	0	1	1	15	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MIR330	hsa-mir-330, MIR330, MIRN330	microRNA 330	NR_029886		
GeneID:100287177	LOC100287177	19	46,144,948	46,146,098	1,150	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4367, 4_A375_EGR1..1..4775	636, 476	in gene, in gene	0	1	1	15	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100287177		hypothetical LOC100287177	XR_111875, XR_109547, XR_115306		
GeneID:2696	GIPR	19	46,171,502	46,185,717	14,215	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4368	24524	downstream	0	1	0	13	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene GIPR	GIPR, PGQTL2, MGC126722	gastric inhibitory polypeptide receptor	NM_000164, hCT11803.2, hCT2276145.0	208105_at	NP_000155.1, EAW57371.1, EAW57372.1



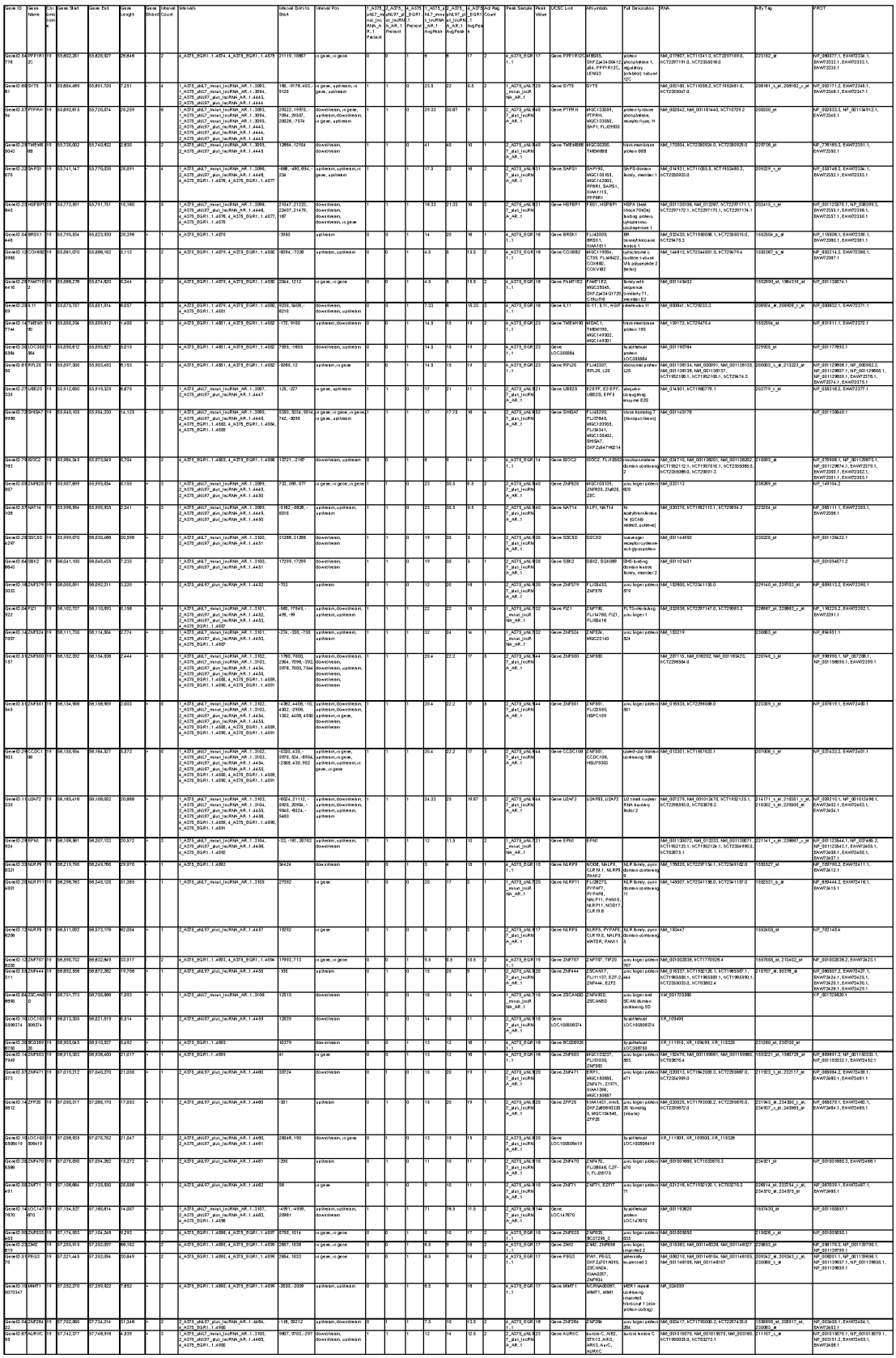
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_shN7_myA375_all_lncRNA_Junction_RNA_AR_1 Percent	2_A375_shN7_myA375_all_lncRNA_AR_1 Percent	3_A375_shN7_myA375_all_lncRNA_AR_1 Avg Peak	4_A375_shN7_myA375_all_lncRNA_AR_1 Avg Peak	Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alty Tag	PROT
GeneID:8833	SNRPD2	19	48,190,712	48,199,443	8,731	-	1	2_A375_shN7_plus_lncRNA_AR_1.4366	-583	upstream	0	1	0	13	19	14	1	2_A375_shN7_plus_lncRNA_AR_1	19	Gene SNRPD2	SNRPD2, Sm D2, SMD2,	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	NM_004597, NM_177542, NCT11802 3, NCT11967146.2	2000626_at		NP_004588.1, NP_808210.2, EAW67073.1, EAW67074.1
GeneID:54	GPCTL	19	48,195,741	48,207,045	11,307	+	1	2_A375_shN7_plus_lncRNA_AR_1.4365	255	up gene	0	1	0	13	19	14	1	2_A375_shN7_plus_lncRNA_AR_1	19	Gene GPCTL	FLJ20554, GPCTL	glutamate receptor, ionotropic, kainate-like	NM_017659, NM_001165377, NCT11814 5, NCT02781462			NP_060129.2, NP_001159564.1, EAW67075.1, EAW67076.1
GeneID:23	FBXO48	19	48,213,887	48,234,151	20,264	-	2	1_A375_shN7_minus_lncRNA_AR_1.3387, 2_A375_shN7_plus_lncRNA_AR_1.4369	13219, 13319	up gene, up gene	1	1	0	38	42	17	1	2_A375_shN7_plus_lncRNA_AR_1	42	Gene FBXO48	Fbxl48, 2007-FCA_FBXO48, FBXO48-L	F-box protein 48	NM_001080499		2053 10_at, 237380_at	NP_001073938.1
GeneID:55	LOC388553	19	48,242,954	48,267,376	24,422	+	5	1_A375_shN7_minus_lncRNA_AR_1.4777, 2_A375_shN7_plus_lncRNA_AR_1.4778	28774, 28942, 29262	downstream, downstream, downstream, downstream	0	0	1	9.33	11.33	21.67	3	4_A375_EGFR_1.1	26	Gene LOC388553		hypothetical LOC388553	XM_001717914, XM_373939, XM_944982			NP_001717995.1, XP_375939.3, XP_950053.1
GeneID:14	SIX3	19	48,266,043	48,272,497	6,454	-	4	4_A375_EGFR_1.4776, 4_A375_EGFR_1.4777, 4_A375_EGFR_1.4776, 4_A375_EGFR_1.4779	27693, 1201, 715, -6986	up gene, up gene, suppression, upstream	0	0	1	9.25	10	20	4	4_A375_EGFR_1.1	26	Gene SIX3	DMHHP, ROM2, SIX3	SIX homeobox 3	NM_175875, NCT02777116.1		217881_x_at, 223939_at, 241822_at	NP_787071.2, EAW67379.1
GeneID:17	DMPK	19	48,272,975	48,293,615	12,640	-	4	4_A375_EGFR_1.4776, 4_A375_EGFR_1.4777, 4_A375_EGFR_1.4776, 4_A375_EGFR_1.4779	18037, 14319, 12599, 5250	downstream, downstream, up gene, up gene	0	0	1	9.25	10	20	4	4_A375_EGFR_1.1	26	Gene DMPK	DMPH, DM, DM6, MDPK, DMPK, DM1, MT-PK	dystrophia myotonica-protein kinase	NM_001081560, NM_004409, NCT02777117.1, NCT02777116.1, NCT02777120.2, NCT02777121.2, NCT02777122.1, NCT02777225.1		217896_s_at, 237966_s_at	NP_001073633.1, NP_001070032.1, NP_001073629.1, NP_004400.4, EAW67352.1, EAW67353.1, EAW67355.1, EAW67356.1, EAW67357.1, EAW67358.1, EAW67359.1
GeneID:17	DMWD	19	48,288,264	48,298,960	9,796	-	1	2_A375_shN7_plus_lncRNA_AR_1.4779	13699	downstream	0	1	0	9	8	13	1	4_A375_EGFR_1.1	13	Gene DMWD	DYSWD, dystrophia myotonica, WD, DMWD, dystrophia myotonica, WD repeat containing	hypothetical LOC390853	XM_001717914, XM_373939, XM_944982		1554429_s_at, 213231_at, 237881_at	NP_001717995.1, NP_373939.3, XP_950053.1, EAW67357.1
GeneID:81	RSPH9	19	48,298,986	48,310,803	11,817	-	1	2_A375_shN7_plus_lncRNA_AR_1.4780	-9551	upstream	0	0	1	8	8	16	1	4_A375_EGFR_1.1	16	Gene RSPH9A	PSPH6B, RSPH9A, RSPH, PSPH, PSPH_RSPH1	radial spoke head 9 homolog A (Chlamydomonas)	NM_080735, NCT11680381.1		220983_s_at	NP_116412.1, EAW67386.1
GeneID:83	SYNPR	19	48,310,700	48,388,548	47,848	-	2	2_A375_shN7_plus_lncRNA_AR_1.4370, 2_A375_shN7_plus_lncRNA_AR_1.4780	-92, 48292	upstream, up gene	0	1	1	12	15	13.5	2	2_A375_shN7_plus_lncRNA_AR_1	22	Gene SYNPR	FLJ37092, SYN5, SYNPR, SYN	synaptoporin	NM_394319, NCT11819 2.2, NCT02771103, NCT02771102.0, NCT02533240.0, NCT02533241.0		1554693_at, 1559587_at, 202359_at, 224423_s_at	NP_394310.2, EAW67390.1, EAW67392.1, EAW67393.1
GeneID:33	FOXA3	19	48,387,515	48,377,055	9,537	+	1	2_A375_shN7_plus_lncRNA_AR_1.4370	-578	upstream	0	1	0	16	22	13	1	2_A375_shN7_plus_lncRNA_AR_1	22	Gene FOXA3	MGC10179, TCF3G, HNF3G	forkhead box A3	NM_004497, NCT11581 2, NCT02781672		229665_at	NP_004488.2, EAW67395.1, EAW67394.1
GeneID:29	IRF2BP1	19	48,398,986	48,399,916	2,510	-	5	1_A375_shN7_minus_lncRNA_AR_1.3035, 2_A375_shN7_plus_lncRNA_AR_1.4371, 2_A375_shN7_plus_lncRNA_AR_1.4372, 2_A375_shN7_plus_lncRNA_AR_1.4373, 2_A375_shN7_plus_lncRNA_AR_1.4782	-672, 445, 645, 1952, 1216	upstream, up gene, upstream, up gene, up gene	1	1	1	12.25	17.25	12.75	4	2_A375_shN7_plus_lncRNA_AR_1	27	Gene IRF2BP1	IRF2BP1, DKFZp434M156	interferon regulatory factor 2 binding protein 1	NM_015984, NCT11639926.2		213771_at	NP_056464.1, EAW67396.1
GeneID:33	MYPOP	19	48,399,261	48,405,962	12,881	-	8	1_A375_shN7_minus_lncRNA_AR_1.3035, 2_A375_shN7_plus_lncRNA_AR_1.4371, 2_A375_shN7_plus_lncRNA_AR_1.4372, 2_A375_shN7_plus_lncRNA_AR_1.4373, 2_A375_shN7_plus_lncRNA_AR_1.4781, 4_A375_EGFR_1.4782	18614, 18934, 13846, -330, 19635, 17702	downstream, downstream, downstream, upstream, downstream, downstream, downstream	1	1	1	12	16.4	13.6	5	2_A375_shN7_plus_lncRNA_AR_1	27	Gene MYPOP	Pa2alpy, MYPOP	Myb-related transcription factor, partner of profilin	NM_031013843		227937_at	NP_001013881.1
GeneID:48	NOVA2	19	48,442,771	48,476,697	33,926	-	3	2_A375_shN7_plus_lncRNA_AR_1.4375, 3_A375_EGFR_1.4783, 4_A375_EGFR_1.4784	29721, 23497, 12649	up gene, up gene, up gene	0	1	1	11.67	17.33	16	3	2_A375_shN7_plus_lncRNA_AR_1	34	Gene NOVA2	KNOVA, NOVA2, NOVA3	ventroneurological antigen 2	NM_002516, NCT11189 0.3		208478_s_at, 208477_s_at	NP_002507.1, EAW67397.1
GeneID:83	DKFZp434L228	19	48,712,499	48,716,095	6,396	+	2	1_A375_shN7_minus_lncRNA_AR_1.3040, 2_A375_shN7_plus_lncRNA_AR_1.4377	6101, 6133	downstream, downstream	1	1	0	29	38	6	1	2_A375_shN7_plus_lncRNA_AR_1	38	Gene DKFZp434J228		hypothetical LOC93429	NR_027003		212032_at	
GeneID:83	PPP3C	19	48,830,294	48,894,103	43,811	+	1	4_A375_EGFR_1.4785	28002	up gene	0	0	1	8	8	16	1	4_A375_EGFR_1.1	16	Gene PPP3C	PPP3C, PLIM2222, PPP3, PP3, FLJ58594	protein phosphatase 3, catalytic subunit	NM_006347, NCT12179 3, NCT27698 1.0, NCT27699 2.0		201919_s_at, 213703_at	NP_008238.1, EAW67417.1, EAW67418.1, EAW67419.1
GeneID:10	LOC100390912	19	48,984,045	47,104,457	120,412	-	5	1_A375_shN7_minus_lncRNA_AR_1.3041, 2_A375_shN7_plus_lncRNA_AR_1.4376, 4_A375_EGFR_1.4786	201, 581, 106529	up gene, up gene, up gene	1	1	1	16	17	15.5	2	1_A375_shN7_plus_lncRNA_AR_1	26	Gene LOC100390912		serine/threonine-protein phosphatase 5-like	NM_001319735, XM_001319736, XM_001316780, XM_001316781, XM_001320931, XM_001320952			XP_001319767.1, XP_001319764.1, XP_001319826.1, XP_001319827.1, XP_001320931.1, XP_001320932.1
GeneID:37	PNMA1	19	48,994,448	48,999,169	4,721	-	1	4_A375_EGFR_1.4788	1041	up gene	0	0	1	4	7	17	1	4_A375_EGFR_1.1	17	Gene PNMA2	PNMA1, PNMA2	PNMA-like 2	NM_007019		232003_at	NP_065760.1
GeneID:83	CALM3	19	47,164,512	47,114,009	9,837	-	2	1_A375_shN7_minus_lncRNA_AR_1.3041, 2_A375_shN7_plus_lncRNA_AR_1.4378	-298, -416	upstream, upstream	1	1	0	26	27	14	1	1_A375_shN7_minus_lncRNA_AR_1	26	Gene CALM3	CALM2, CALM1, CALM3, PHKD, PHKD2	calmodulin 3 (phosphorylase kinase, delta)	NM_005184, NCT11390 2, NCT02768869.0, NCT02768701.0, NCT02769702.0, NCT02532160.0		1565631_s_at, 200922_x_at, 200923_s_at	NP_005175.2, EAW67426.1, EAW67427.1, EAW67428.1, EAW67429.1
GeneID:14	DACT2	19	47,150,869	47,164,395	13,526	-	1	4_A375_EGFR_1.4787	299	up gene	0	0	1	10	11	16	1	4_A375_EGFR_1.1	16	Gene DACT2	MGC15479, DACT2, RRR1	dapper, antagonin of beta-catenin, homolog 2 (Xenopus laevis)	NM_145056, NCT11636778.4, NCT23414 28.0, NCT23414 27.0		223228_at, 229743_s_at	NP_659439.2, EAW67429.1, EAW67430.1, EAW67440.1
GeneID:10	LOC100390986	19	47,164,735	47,174,356	9,663	+	2	4_A375_EGFR_1.4787, 4_A375_EGFR_1.4788	439, 10165	upstream, downstream	0	0	1	7.5	8.5	19.5	2	4_A375_EGFR_1.1	21	Gene LOC100390986		hypothetical LOC100390986	XR_111977, XR_109945, XR_111937			
GeneID:28	PRKD2	19	47,177,973	47,220,364	42,811	-	3	2_A375_shN7_plus_lncRNA_AR_1.4379, 3_A375_EGFR_1.4788, 4_A375_EGFR_1.4789	-298, 42484, 7320	upstream, up gene, upstream	0	1	1	9	11.33	19	3	4_A375_EGFR_1.1	22	Gene PRKD2	HSPC167, PKD2, PRKD2	protein kinase D2	NM_031079888, NM_016437, NM_031079681, NM_031079682, NCT22786680.0		209202_at, 241869_x_at, 33299_at	NP_031073849.1, NP_037541.2, NP_001073360.1, NP_001073351.1, EAW67441.1
GeneID:10	MIR320D2	19	47,212,930	47,212,802	92	-	1	2_A375_shN7_plus_lncRNA_AR_1.4379	-6933	upstream	0	1	0	15	21	14	1	2_A375_shN7_plus_lncRNA_AR_1	21	Gene MIR320E	MIR320E	microRNA 320e	NR_036137			
GeneID:29	STRN4	19	47,222,765	47,249,720	26,932	-	2	2_A375_shN7_plus_lncRNA_AR_1.4379, 2_A375_shN7_plus_lncRNA_AR_1.4788	29660, 21616	downstream, up gene	0	1	1	11	14	15	2	4_A375_EGFR_1.1	22	Gene STRN4	STRN4, ZIN, FLJ58594	striatin, calmodulin binding protein 4	NM_015403, NM_001039877, NCT22786956.0, NCT27695 7.0		217903_at	NP_037535.2, NP_001034998.1, EAW67442.1, EAW67443.1
GeneID:10	FKRP	19	47,249,930	47,261,852	12,329	+	1	4_A375_EGFR_1.4790	13555	up gene	0	0	1	11	15	19	1	4_A375_EGFR_1.1	19	Gene FKRP	MDDGA5, MDC1C, MSCP91, DKFZp761D1624, MDDGB5, FKRP, FLJ13278, MDDGC5	fukutin related protein	NM_024301, NM_001039855, NCT18437685.0, NCT26531 28.0		219853_at, 227892_at	NP_377277.1, NP_001034974.1, EAW67444.1, EAW67445.1
GeneID:88	SLC1A3	19	47,276,140	47,291,942	15,802	-	5	1_A375_shN7_minus_lncRNA_AR_1.3042, 1_A375_shN7_minus_lncRNA_AR_1.3043, 1_A375_shN7_minus_lncRNA_AR_1.3044, 2_A375_shN7_plus_lncRNA_AR_1.4380, 2_A375_shN7_plus_lncRNA_AR_1.4791	2384, -32, -6982, 3308, 54	up gene, upstream, upstream, up gene, up gene	1	1	1	19.67	14.67	11.33	3	1_A375_shN7_minus_lncRNA_AR_1	23	Gene SLC1A3	ASCT2, MCVS1, SLC1A3, K16, ATV1, FLJ31466, ATBO, AIAT, EAAT, EAAC	solute carrier family 1 (neutral amino acid transporter), member 3	NM_004172, NM_001163144, NM_001163145, NCT19671 32.2		200918_at	NP_004163.1, NP_001138618.1, NP_001138619.1, EAW67446.1
GeneID:11	AP2S1	19	47,341,423	47,354,303	12,880	-	2	1_A375_shN7_minus_lncRNA_AR_1.3043, 2_A375_shN7_plus_lncRNA_AR_1.4381	-5967, -65	upstream, upstream	1	1	0	16	16	12.5	2	2_A375_shN7_plus_lncRNA_AR_1	22	Gene AP2S1	AP17, AP2S1, HP17-DELTA, CLAPS2	adaptor-related protein complex 2, sigma 1 subunit	NM_004069, NM_021573, NCT19833 32.1, NCT19837 4.1		202120_s_at, 209074_s_at, 211047_x_at	NP_004060.2, NP_067588.1, EAW67448.1, EAW67449.1
GeneID:48	NPAS1	19	47,324,143	47,349,017	24,874	+	5	2_A375_shN7_plus_lncRNA_AR_1.4382, 3_A375_EGFR_1.4792, 4_A375_EGFR_1.4792	27825, 16297, 23401	downstream, up gene, up gene	0	1	1	12	16.67	14.67	3	2_A375_shN7_plus_lncRNA_AR_1	38	Gene NPAS1	PASD5, MHLTH71, NPAS1, MOP5	neuronal PAS domain protein 1	NM_002517, NCT22786450		209899_s_at, 219975_x_at	NP_002508.2, EAW67454.1
GeneID:54	TMEM160	19	47,349,187	47,351,582	2,715	-	3	2_A375_shN7_plus_lncRNA_AR_1.4382, 3_A375_EGFR_1.4792, 4_A375_EGFR_1.4792	-58, 9482, 7338	upstream, downstream, downstream	0	1	1	12	16.67	14.67	3	2_A375_shN7_plus_lncRNA_AR_1	38	Gene TMEM160	TMEM160, FLJ35312	transmembrane protein 160	NM_017554, NCT16419582		219219_at	NP_060024.1, EAW67458.1
GeneID:23	ZC3H4	19	47,387,444	47,417,009	49,565	-	1	2_A375_shN7_plus_lncRNA_AR_1.4383	1437	up gene	0	0	1	12	16	15	1	2_A375_shN7_plus_lncRNA_AR_1	16	Gene ZC3H4	ZC3H4, KIAA1084, C16orf7	zinc finger CCCH-type containing 4	NM_033393, NCT11631 68		213280_at, 240022_at	NP_150923.1
GeneID:10	SNX11	19	47,834,060	47,715,695	79,815	+	1	1_A375_shN7_minus_lncRNA_AR_1.3045	0	up gene	1	1	0	17	15	9	1	1_A375_shN7_minus_lncRNA_AR_1	17	Gene SNX11	SNX11, LIBE16, HSPC140, hCG1, FLJ39911, DUH1	sorting nexin 11	NM_033500, NM_001147813, NM_001147814, NM_027200, NCT19857 89.1, NCT19857 70.1, NCT23531 40.0, NCT23531 41.0		1555810_s_at, 1559810_s_at, 217945_s_at, 241105_at	NP_033618.1, NP_001139183.1, EAW67460.1, EAW67461.1, EAW67462.1, EAW67464.1
GeneID:27	BBC3	19	47,724,079	47,736,023	11,944	-	1	4_A375_EGFR_1.4794	10265	upstream	0	0	1	7	9	18	1	4_A375_EGFR_1.1	18	Gene BBC3	BBC3, PUMA, JFY1, FLJ42994	BCL2 binding component 3	NM_014417, NM_001127240, NM_001127241, NM_001127242, NCT11432 .2, NCT27748 0.0, NCT27749 1.0		211692_s_at	NP_055231.2, NP_001120712.1, NP_001120713.1, NP_001120714.1, EAW67465.1, EAW67466.1, EAW67467.1
GeneID:26	CCDC9	19	47,799,751	47,778,210	13,479	+	5	2_A375_shN7_plus_lncRNA_AR_1.4384, 2_A375_shN7_plus_lncRNA_AR_1.4385, 2_A375_shN7_plus_lncRNA_AR_1.4795	15, 16972, 3054	up gene, downstream, up gene	0	1	1	13	16	14	3	4_A375_EGFR_1.1	30	Gene CCDC9	CCDC9, DKFZp686M10170	coiled-coil domain containing 9	NM_015993, NCT11126 4.3		208257_at	NP_056816.1, EAW67468.1
GeneID:28	PRR24	19	47,776,142	47,776,900	758	+	1	2_A375_shN7_plus_lncRNA_AR_1.4385	-1438	upstream	0	1	0	17	16	11	1	2_A375_shN7_plus_lncRNA_AR_1	18	Gene PRR24	PRR24	proline rich 24	NM_178511		227329_at	NP_848606.1
GeneID:72	C5AR1	19	47,815,104	47,825,327	12,223	+	1	2_A375_shN7_plus_lncRNA_AR_1.3965	9864	up gene	1	2	0	16	16	8	1	1_A375_shN7_minus_lncRNA_AR_1	16	Gene C5AR1	C5R1, C5AR1, CD88, C5AR, C5R1	complement component 5a receptor 1	NM_001736, NCT18144 42.1, NCT22458 04.0		220658_at	NP_001727.1, EAW67470.1, EAW67471.1
GeneID:72	GPR77	19	47,815,104	47,843,372	4,991	+	1	2_A375_shN7_plus_lncRNA_AR_1.4386	4169	up gene	0	0	1	8	8	17	1	4_A375_EGFR_1.1	17	Gene GPR77	GPR77, C5L2, GPF77	G protein-coupled receptor 77	NM_018483, NCT18144 43.2		221149_at	NP_060953.1, EAW67472.1
GeneID:37	DHX34	19	47,852,656	47,855,961	23,225	+	5	2_A375_shN7_plus_lncRNA_AR_1.4386, 4_A375_EGFR_1.4796	-3556, 23496, 20662	upstream, up gene, up gene	0	0	1	7.67	8	16	3	4_A375_EGFR_1.1	19	Gene DHX34	DHX34, KIAA1004, HRH1, DDX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	NM_014581, NCT18144 44.1, NCT19520 39.1, NCT27693 10.0, NCT27693 12.0		204015_s_at, 204016_s_at, 214017_s_at	NP_055396.2, EAW67473.1, EAW67474.1, EAW67475.1, EAW67476.1, EAW67477.1
GeneID:88	SLC6A20	19	47,931,279	47,979,307	44,028	-	5	1_A375_shN7_minus_lncRNA_AR_1.3049, 1_A375_shN7_minus_lncRNA_AR_1.3050, 1_A375_shN7_minus_lncRNA_AR_1.4386, 2_A375_shN7_plus_lncRNA_AR_1.4387, 2_A375_shN7_plus_lncRNA_AR_1.4796	34539, 27995, 24331, 23785, 2107	up gene, up gene, up gene, up gene, up gene	1	1	1	19.67	19	13.33	3	2_A375_shN7_plus_lncRNA_AR_1	29	Gene SLC6A20	SLC6A2, NCX2	solute carrier family 6 (neurotransmitter transporter), member 20	NM_1109 83, NCT19277 2.3, NCT27747 6.0, NCT27747 7.0		213287_s_at	NP_536378.1, EAW67481.1, EAW67482.1, EAW67483.1, EAW67484.1, EAW67485.1
GeneID:11	KPTN	19	47,976,400	47,987,921	9,521	-	2	2_A375_shN7_plus_lncRNA_AR_1.4388, 4_A375_EGFR_1.4796	61, 14321	up gene, downstream	0	1	1	16.5	17	13	2	2_A375_shN7_plus_lncRNA_AR_1	27	Gene KPTN	Dil4, KPTN	kaptin (actin binding protein)	NM_007059, NCT11629 9.2		2201 60_s_at	NP_008990.2, EAW67487.1
GeneID:10	LOC100390861	19	47,987,470	47,999,609	12,139	+	1	2_A375_shN7_plus_lncRNA_AR_1.4388	-30	upstream	0	1	0	23	27	8	1	2_A375_shN7_plus_lncRNA_AR_1	27	Gene LOC100390861		hypothetical LOC100390861	XR_111970, XR_109451, XR_111938			
GeneID:87	NAPA	19	47,990,691	48,016,497	27,806	-	2	2_A375_shN7_plus_lncRNA_AR_1.4388, 2_A375_shN7_plus_lncRNA_AR_1.4389	31557, 193	downstream, up gene	0	1	1	16.5	22.5	9.5	2	2_A375_shN7_plus_lncRNA_AR_1	27	Gene NAPA	NAPA, SNAP-A	N-ethylmaleimide-sensitive factor attachment protein, alpha	NM_003827, NCT19282 2, NCT19671 42.1, NCT27749 8.0, NCT27751 8.0, NCT27751 9.0, NCT27751 10.0, NCT27751 11.0, NCT27751 20.0, NCT27751 21.0		208691_s_at, 208731_at	NP_003816.2, EAW67489.1, EAW67490.1, EAW67491.1, EAW67492.1, EAW67495.1, EAW67496.1, EAW67497.1, EAW67498.1
GeneID:64	ZNF541	19	48,023,947	48,039,113	15,166	-	2	2_A375_shN7_plus_lncRNA_AR_1.4389, 4_A375_EGFR_1.4800	49839, 11049	downstream, up gene	0	1	1	11.3	11.3	14	2	2_A375_shN7_plus_lncRNA_AR_1	16	Gene ZNF541	MGC119519, ZNF541, MGC119516, MGC119521, DKFZp434H193	zinc finger protein 541	NM_001014919, NCT16144 55.1, NCT22745 80.0, NCT22551 44.0		232604_at	NP_001004869.1, EAW67499.1, EAW67500.1, EAW67501.1
GeneID:29	GLTSCR1	19	48,111,483	48,298,934	99,081	+	2	2_A375_shN7_plus_lncRNA_AR_1.4390, 4_A375_EGFR_1.4801	238, 147	up gene, up gene	0	1	1	19	16	19	1	4_A375_EGFR_1.1	19	Gene GLTSCR1	GLTSCR1	glioma tumor suppressor candidate region gene 1	NM_015717, NCT18144 48.2, NCT22762 76.0		217449_at	NP_056536.2, EAW67504.1, EAW67505.1
GeneID:33	EHD2	19	48,216,901	48,246,591	29,790	+	4	1_A375_shN7_minus_lncRNA_AR_1.3051, 2_A375_shN7_plus_lncRNA_AR_1.4391, 2_A375_shN7_plus_lncRNA_AR_1.4392, 2_A375_shN7_plus_lncRNA_AR_1.4802	29011, 9703, 29255, 30229	downstream, up gene, downstream, downstream	1	1	1	15.5	16.5	9.5	2	2_A375_shN7_plus_lncRNA_AR_1	23	Gene EHD2	PAST2, EHD2, FLJ99617	EH-domain containing 2	NM_014601, NCT19282 2, NCT19697 7.1		203541_at, 223170_at, 45297_at	NP_055415.2, EAW67508.1, EAW67509.1
GeneID:29	GLTSCR2	19	48,248,793	48,260,323	11,530	+	3	1_A375_shN7_minus_lncRNA_AR_1.3051, 2_A375_shN7_plus_lncRNA_AR_1.4392, 2_A375_shN7_plus_lncRNA_AR_1.4802	-1881, -1934, 1913	upstream, upstream, upstream	1	1	1	23	23	18	1	2_A375_shN7_plus_lncRNA_AR_1	23	Gene GLTSCR2	GLTSCR2, PICT1, PICT-1	glioma tumor suppressor candidate region gene 2	NM_015710, NCT19282 2, NCT19585 33.1, NCT22762 64.0, NCT22762 65.0		217807_s_at, 234239_s_at, 234310_at	NP_056533.2, EAW67509.1, EAW67510.1, EAW67510.1
GeneID:72	LOC729126	19	48,260,295	48,272,997	11,804	-	4	1_A375_shN7_minus_lncRNA_AR_1.3052, 2_A375_shN7_plus_lncRNA_AR_1.3053, 2_A375_shN7_plus_lncRNA_AR_1.4393, 2_A375_shN7_plus_lncRNA_AR_1.4803	-5267, -9895, 9781, -9953	upstream, upstream, downstream, upstream	1	1	1	20.5	24.5	11.5	2	2_A375_shN7_plus_lncRNA_AR_1	35	Gene LOC729126		hypothetical LOC729126	XM_001133511, XM_001134322, XM_001133196			XP_001133511.1, XP_001134323.1, XP_001133212.1
GeneID:84	SEPW1	19	48,261,942	48,267,939	5,997	+	4	1_A375_shN7_minus_lncRNA_AR_1.3052, 2_A375_shN7_plus_lncRNA_AR_1.3053, 2_A375_shN7_plus_lncRNA_AR_1.4393, 2_A375_shN7_plus_lncRNA_AR_1.4803	-4494, -50, 14, 238	upstream, upstream, up gene, up gene	1	1	1	20.5	24.5	11.5	2	2_A375_shN7_plus_lncRNA_AR_1	35	Gene SEPW1	SelW, SEPW1	selenoprotein W, 1	NM_0030 95, NCT12992 2, NCT27687 0, NCT25531 38.0		1553551_s_at, 201194_at	NP_003000.1, EAW67512.1, EAW67513.1, EAW67514.1
GeneID:84	PLA2G4C	19	48,331,100	48,814,109	483,009	-	1	2_A375_shN7_plus_lncRNA_AR_1.4394	221	up gene	0	1	0	13	20	8	1	2_A375_shN7_plus_lncRNA_AR_1	20	Gene PLA2G4C	DKFZp686O0625, PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)	NM_003706, NM_001159322, NM_001159323, NM_001159324, NCT19671 79.1, NCT19671 76.1, NCT23027 70.2, NCT23236 87.0, NCT27 7 4		1554810_at, 209163_s_at	NP_003697.2, NP_001152794.1, NP_001152795.1, EAW62311.1, EAW62312.1, EAW62314.1, EAW62315.1, EAW62316.1
GeneID:28	UGT8	19	48,816,703	48,873,990	54,287	-	4	1_A375_shN7_minus_lncRNA_AR_1.3054, 2_A375_shN7_plus_lncRNA_AR_1.4394, 2_A375_shN7_plus_lncRNA_AR_1.4395, 2_A375_shN7_plus_lncRNA_AR_1.4804	-230, 39972, -200, 152	upstream, downstream, upstream, up gene	1	1	1	15.5	22	10	2	2_A375_shN7_plus_lncRNA_AR_1	24	Gene UGT8	UGT8A, GAL-C, CGT, GALC, UGT8-1, UGT8-2	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)	NM_003324, NCT19535 08.1, NCT6680 3		202726_at	NP_003305.1, EAW62317.1, EAW62318.1
GeneID:37	C19orf66	19	48,875,210	48,760,916	25,206	+	3	1_A375_shN7_minus_lncRNA_AR_1.3054, 2_A375_shN7_plus_lncRNA_AR_1.4394, 2_A375_shN7_plus_lncRNA_AR_1.4804	1430, 1490, 1802	upstream, upstream, upstream	1	1	1	16	24	16	1	2_A375_shN7_plus_lncRNA_AR_1	24	Gene C19orf66	C19orf66, FLJ90339	chromosome 19 open reading frame 66	NM_0317 10790, NM_0317 13771, NM_0317 13772, NCT19 63152.4		235999_at	NP_001710732.2, NP_001710733.2, NP_001710734.2, EAW62318.1
GeneID:83	CCDC114	19	48,799,799	48,823,332	23,533	-	2	2_A375_shN7_plus_lncRNA_AR_1.4394, 2_A375_shN7_plus_lncRNA_AR_1.4805	-1054, -1916	upstream, upstream	0	1	1	13	21	22	1	4_A375_EGFR_1.1	22	Gene CCDC114	CCDC114, FLJ32926	coiled-coil domain containing 114	NM_144577, NCT22837 60.1, NCT22837 61.1, NCT22837 62.1, NCT22837 63.1, NCT22837 64.1, NCT23235 97.1		235157_x_at	NP_653178.3, EAW62332.1, EAW62327.1, EAW62328.1, EAW62329.1, EAW62330.1, EAW62331.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.2014	EMP3	19	48,828,629	48,833,810	5,181	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4396, 4_A375_EGR1..1..4805	-3413, -3381	upstream, upstream	0	1	1	13	21	22	1	4_A375_EGR1..1	22	Gene EMP3	YMP, EMP3	epithelial membrane protein 3	NM_001425, hCT1953510.1, hCT6276.2	203729_at	NP_001416.1, EAW52334.1, EAW52333.1
GeneID.55260	TMEM143	19	48,835,616	48,867,186	31,570	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3055, 2_A375_pNL97_plus_lncRNA_AR..1..4397	722, 754	in gene, in gene	1	1	0	27	25	14	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene TMEM143	TMEM143, FLJ10922	transmembrane protein 143	NM_018273, hCT1953511.3, hCT2349456.0, hCT2352579.0, hCT6280.2	219589_s_at, 222905_s_at	NP_060743.2, EAW52336.1, EAW52335.1, EAW52337.1, EAW52338.1
GeneID.23546	SYNGR4	19	48,867,657	48,879,634	11,977	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3055, 2_A375_pNL97_plus_lncRNA_AR..1..4397	-1193, -1225	upstream, upstream	1	1	0	27	25	14	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene SYNGR4	SYNGR4, MGC125805	synaptogyrin 4	NM_012451, hCT2279903.0	206719_at	NP_036583.2, EAW52339.1
GeneID.10945	KDELR1	19	48,885,827	48,894,810	8,983	-	1	4_A375_EGR1..1..4806	-5062	upstream	0	0	1	1	4	15	1	4_A375_EGR1..1	15	Gene KDELR1	ERD2.1, HDEL, KDELR1, PM23, ERD2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	NM_006801, hCT2283762.1, hCT2283763.1, hCT2283764.1, hCT2283767.1, hCT2344365.0, hCT2344366.0	1555575_a_at, 200922_at	NP_006792.1, EAW52342.1, EAW52340.1, EAW52341.1, EAW52344.1, EAW52345.1, EAW52343.1
GeneID.2906	GRIN2D	19	48,898,132	48,948,188	50,056	+	3	2_A375_pNL97_plus_lncRNA_AR..1..4398, 4_A375_EGR1..1..4806, 4_A375_EGR1..1..4807	51020, 1740, 59892	downstream, in gene, downstream	0	1	1	7.67	10.67	15	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene GRIN2D	GRIN2D, EB11, NMDAR2D, NR2D	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	NM_000836, hCT6283.3	207036_x_at, 229683_at	NP_000827.2, EAW52346.1
GeneID.83743	GRWD1	19	48,949,030	48,957,164	8,134	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4398, 4_A375_EGR1..1..4807	122, 8794	in gene, downstream	0	1	1	11	14	15	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene GRWD1	CDW4, GRWD1, GRWD, KIAA1942, WDR28, RRB1	glutamate-rich WD repeat containing 1	NM_031485, hCT6294.3	221549_at	NP_113673.3, EAW52347.1
GeneID.3770	KCNJ14	19	48,958,766	48,969,367	10,601	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4398, 4_A375_EGR1..1..4807	-9614, -942	upstream, upstream	0	1	1	11	14	15	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene KCNJ14	KCNJ14, KIAA1942, IRK4, MGC46111, KIR2.4	potassium inwardly-rectifying channel, subfamily J, member 14	NM_013348, NM_170720, hCT2279906.0	220776_at	NP_037480.1, NP_733838.1, EAW52348.1
GeneID.6820	SULT2B1	19	49,055,429	49,102,684	47,255	+	1	4_A375_EGR1..1..4808	44123	in gene	0	0	1	4	3	17	1	4_A375_EGR1..1	17	Gene SULT2B1	SULT2B1, HSST2	sulfotransferase family, cytosolic, 2B, member 1	NM_177973, NM_004605, hCT1953517.1, hCT6287.2	205759_s_at	NP_814444.1, NP_004596.2, EAW52354.1, EAW52355.1
GeneID.54854	FAM83E	19	49,103,857	49,116,694	12,837	-	4	2_A375_pNL97_plus_lncRNA_AR..1..4399, 4_A375_EGR1..1..4808, 4_A375_EGR1..1..4809, 4_A375_EGR1..1..4810	-5578, 17142, -2602, -5258	upstream, downstream, upstream, upstream	0	1	1	10.67	12	17.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene FAM83E	MGC138177, FAM83E, MGC138175, FLJ20200	family with sequence similarity 83, member E	NM_017708, hCT6290.2	220312_at	NP_060178.2, EAW52356.1
GeneID.171169	SPACA4	19	49,110,000	49,110,971	971	+	1	4_A375_EGR1..1..4809	9296	downstream	0	0	1	10	12	18	1	4_A375_EGR1..1	18	Gene SPACA4	SPACA4, SAMP14	sperm acrosome associated 4	NM_133498, hCT1829116.2	231054_at	NP_598005.1, EAW52357.1
GeneID.6141	RPL18	19	49,118,588	49,122,433	3,845	-	4	2_A375_pNL97_plus_lncRNA_AR..1..4399, 4_A375_EGR1..1..4809, 4_A375_EGR1..1..4810, 4_A375_EGR1..1..4811	161, 3137, 481, -7055	in gene, in gene, in gene, upstream	0	1	1	11.33	13.67	18.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RPL18	L18, RPL18	ribosomal protein L18	NM_000979, hCT2283744.1, hCT2283745.1, hCT2283746.1, hCT2283748.1, hCT2283749.1, hCT2283751.1, hCT2283752.1	200022_at, 214335_at	NP_000970.1, EAW52362.1, EAW52358.1, EAW52359.1, EAW52360.1, EAW52364.1, EAW52361.1, EAW52363.1
GeneID.56848	SPHK2	19	49,122,548	49,133,662	11,114	+	7	1_A375_pNL7_minus_lncRNA_AR..1..3056, 2_A375_pNL97_plus_lncRNA_AR..1..4399, 2_A375_pNL97_plus_lncRNA_AR..1..4400, 4_A375_EGR1..1..4809, 4_A375_EGR1..1..4810, 4_A375_EGR1..1..4811, 4_A375_EGR1..1..4812	18804, -276, 18568, -3252, -598, 6940, 10348	downstream, upstream, downstream, upstream, upstream, in gene, in gene	1	1	1	15.6	16.6	18	5	1_A375_pNL7_minus_lncRNA_AR..1	35	Gene SPHK2	SPHK2		NM_020126, hCT1953521.1, hCT1953522.1, hCT1953523.1, hCT2279923.0, hCT2352577.0, hCT2352578.0, hCT6295.3	209857_s_at, 40273_at	NP_064511.2, EAW52365.1, EAW52366.1, EAW52367.1, EAW52369.1, EAW52370.1, EAW52368.1, EAW52371.1
GeneID.1628	DBP	19	49,133,817	49,140,639	6,822	-	7	1_A375_pNL7_minus_lncRNA_AR..1..3056, 1_A375_pNL7_minus_lncRNA_AR..1..3057, 1_A375_pNL7_minus_lncRNA_AR..1..3058, 2_A375_pNL97_plus_lncRNA_AR..1..4400, 2_A375_pNL97_plus_lncRNA_AR..1..4401, 4_A375_EGR1..1..4811, 4_A375_EGR1..1..4812	-513, -7633, -9217, -497, -9057, 11151, 7743	upstream, upstream, upstream, upstream, upstream, downstream, downstream	1	1	1	19.8	18.2	14.8	5	1_A375_pNL7_minus_lncRNA_AR..1	35	Gene DBP	DABP, DBP	D site of albumin promoter (albumin D-box) binding protein	NM_001352, hCT2283747.1, hCT2283750.1, hCT2343387.0, hCT2343388.0	209782_s_at, 209783_at	NP_001343.2, EAW52372.1, EAW52373.1, EAW52374.1, EAW52375.1
GeneID.770	CA11	19	49,141,272	49,149,451	8,179	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3056, 1_A375_pNL7_minus_lncRNA_AR..1..3057, 1_A375_pNL7_minus_lncRNA_AR..1..3058, 2_A375_pNL97_plus_lncRNA_AR..1..4400, 2_A375_pNL97_plus_lncRNA_AR..1..4401, 4_A375_EGR1..1..4812	8299, 1179, -405, 8315, -245, 16555	downstream, in gene, upstream, downstream, upstream, downstream	1	1	1	23.25	20.75	13.25	4	1_A375_pNL7_minus_lncRNA_AR..1	35	Gene CA11	CA11, CARPX1	carbonic anhydrase XI	NM_001217, hCT1987178.1, hCT2283753.0, hCT6289.3	209726_at	NP_001208.2, EAW52378.1, EAW52376.1, EAW52377.1
GeneID.126147	NTN5	19	49,164,684	49,176,284	11,600	-	1	4_A375_EGR1..1..4813	2312	in gene	0	0	1	5	4	14	1	4_A375_EGR1..1	14	Gene NTN5	NTN5		NM_145807, hCT1771167.4, hCT2352566.0, hCT6292.3	1553890_s_at, 1558247_s_at	NP_665806.1, EAW52386.1, EAW52387.1, EAW52388.1
GeneID.284358	MAMSTR	19	49,216,255	49,222,976	6,721	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3059, 2_A375_pNL97_plus_lncRNA_AR..1..4402, 4_A375_EGR1..1..4814	-1056, -960, -6512	upstream, upstream, upstream	1	1	1	12	13	14	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MAMSTR	FLJ38070, MGC117259, MAMSTR, MASTR	MEF2 activating motif and SAP domain containing transcriptional regulator	NM_182574, NM_001130915, hCT1644137.3, hCT2349459.0, hCT2352552.0	1557091_at	NP_872380.1, NP_001124387.1, EAW52390.1, EAW52391.1, EAW52392.1
GeneID.54922	RASIP1	19	49,223,842	49,243,970	20,128	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3059, 2_A375_pNL97_plus_lncRNA_AR..1..4402, 4_A375_EGR1..1..4814	19938, 20034, 14462	in gene, in gene, in gene	1	1	1	12	13	14	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene RASIP1	RAIN, FLJ20401, RASIP1	Ras interacting protein 1	NM_017805, hCT2283737.0, hCT7264.3	220027_s_at, 244830_at	NP_060275.2, EAW52393.1, EAW52394.1
GeneID.284359	IZUMO1	19	49,244,145	49,250,166	6,021	-	1	4_A375_EGR1..1..4815	-6186	upstream	0	0	1	7	11	14	1	4_A375_EGR1..1	14	Gene IZUMO1	IZUMO, IZUMO1, FLJ61440, MGC34799	izumo sperm-egg fusion 1	NM_182575, hCT1951805.1, hCT2352568.0, hCT2352569.0, hCT7268.3	1554196_at	NP_872381.2, EAW52398.1, EAW52395.1, EAW52396.1, EAW52397.1
GeneID.2523	FUT1	19	49,251,268	49,258,647	7,379	-	1	4_A375_EGR1..1..4815	2295	in gene	0	0	1	7	11	14	1	4_A375_EGR1..1	14	Gene FUT1	FUT1, H, HSC, HH	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)	NM_000148	206109_at, 225776_at, 225778_at, 235439_at, 235558_at	NP_000139.1
GeneID.26291	FGF21	19	49,259,344	49,261,582	2,238	+	1	4_A375_EGR1..1..4815	-2992	upstream	0	0	1	7	11	14	1	4_A375_EGR1..1	14	Gene FGF21	FGF21	fibroblast growth factor 21	NM_019113, hCT2279929.0, hCT2279930.0	221433_at	NP_061986.1, EAW52402.1, EAW52401.1
GeneID.587	BCAT2	19	49,298,319	49,314,320	16,001	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3060, 2_A375_pNL97_plus_lncRNA_AR..1..4403	15800, 15552	in gene, in gene	1	1	0	46	38	10	1	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene BCAT2	BCAM, BCATM, BCAT2, BCT2, PP18	branched chain amino-acid transaminase 2, mitochondrial	NM_001190, NM_001164773, NR_028450, NR_028451, hCT7246.2	203576_at, 215654_at	NP_001181.2, NP_001158245.1, EAW52403.1
GeneID.57664	PLEKHA4	19	49,340,354	49,371,884	31,530	-	1	4_A375_EGR1..1..4816	-3844	upstream	0	0	1	11	15	16	1	4_A375_EGR1..1	16	Gene PLEKHA4	PLEKHA4, PEPP1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	NM_020904, NM_001161354, hCT2283727.0, hCT2352598.0, hCT30861.2	219011_at	NP_065955.2, NP_001154826.1, EAW52406.1, EAW52407.1, EAW52408.1
GeneID.23645	PPP1R15A	19	49,375,649	49,379,319	3,670	+	1	4_A375_EGR1..1..4816	79	in gene	0	0	1	11	15	16	1	4_A375_EGR1..1	16	Gene PPP1R15A	GADD34, PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	NM_014330, hCT30359.1	202014_at, 37028_at	NP_055145.3, EAW52409.1
GeneID.7288	TULP2	19	49,384,222	49,401,996	17,774	-	1	4_A375_EGR1..1..4816	26268	downstream	0	0	1	11	15	16	1	4_A375_EGR1..1	16	Gene TULP2	TULP2, CT65, TUBL2	tubby like protein 2	NM_003323, hCT7249.2	206733_at	NP_003314.2, EAW52410.1
GeneID.4924	NUCB1	19	49,403,307	49,426,540	23,233	+	1	4_A375_EGR1..1..4817	25957	downstream	0	0	1	8	8	15	1	4_A375_EGR1..1	15	Gene NUCB1	DKFZp686A15286, NUC, NUCB1, FLJ40471	nucleobindin 1	NM_006184, hCT1987270.1, hCT30659.3	200646_s_at, 200649_at	NP_006175.2, EAW52412.1, EAW52411.1
GeneID.27294	DHDH	19	49,436,939	49,448,226	11,287	+	1	4_A375_EGR1..1..4817	-7875	upstream	0	0	1	8	8	15	1	4_A375_EGR1..1	15	Gene DHDH	DHDH, HUM2DD, 2DD	dihydrodiol dehydrogenase (dimeric)	NM_014475, hCT30657.3	231416_at	NP_055290.1, EAW52414.1
GeneID.581	BAX	19	49,456,117	49,465,055	8,938	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3061, 2_A375_pNL97_plus_lncRNA_AR..1..4404, 4_A375_EGR1..1..4818	11051, 11099, 10427	downstream, downstream, downstream	1	1	1	21	21	21	1	4_A375_EGR1..1	21	Gene BAX	BAX, BCL2L4	BCL2-associated X protein	NM_004324, NM_138761, NM_138763, NM_138764, NR_027882, hCT1953542.1, hCT1953543.1, hCT1953544.1, hCT2279941.0, hCT2279943.0, hCT2352570.0, hCT2352571.0	208478_s_at, 211833_s_at	NP_004315.1, NP_620116.1, NP_620118.1, NP_620119.2, EAW52419.1, EAW52420.1, EAW52415.1, EAW52416.1, EAW52417.1, EAW52418.1, EAW52421.1
GeneID.2512	FTL	19	49,468,566	49,470,136	1,570	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3061, 2_A375_pNL97_plus_lncRNA_AR..1..4404, 4_A375_EGR1..1..4818	602, 650, -22	in gene, in gene, upstream	1	1	1	21	21	21	1	4_A375_EGR1..1	21	Gene FTL	MGC71996, NBIA3, FTL	ferritin, light polypeptide	NM_000146, hCT1953553.1, hCT30656.3	212788_x_at, 213187_x_at	NP_000137.2, EAW52423.1, EAW52422.1
GeneID.2997	GYS1	19	49,471,382	49,496,610	25,228	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3061, 1_A375_pNL7_minus_lncRNA_AR..1..3062, 2_A375_pNL97_plus_lncRNA_AR..1..4404, 2_A375_pNL97_plus_lncRNA_AR..1..4405, 4_A375_EGR1..1..4818	27442, -430, 27394, -494, 28086	downstream, upstream, downstream, upstream, downstream	1	1	1	24.5	21	16	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene GYS1	GSY, GYS, GYS1	glycogen synthase 1 (muscle)	NM_002103, NM_001161587, NR_027763, hCT1787823.3, hCT1787824.3	201673_s_at	NP_002094.2, NP_001155059.1, EAW52424.1, EAW52425.1
GeneID.10856	RUVBL2	19	49,497,156	49,519,182	22,026	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3062, 2_A375_pNL97_plus_lncRNA_AR..1..4405	-116, -52	upstream, upstream	1	1	0	28	21	11	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene RUVBL2	RUVBL2, TIP48, CGI-46, REPTIN, TIP49B, INO80J, ECP51, TIH2, RVB2	RuvB-like 2 (E. coli)	NM_006666, hCT1953530.2, hCT1953531.2, hCT1953532.2, hCT2352553.0, hCT2352554.0, hCT7246.4	1559945_at, 1559946_s_at, 201459_at	NP_006657.1, EAW52426.1, EAW52427.1, EAW52428.1, EAW52429.1, EAW52430.1, EAW52431.1
GeneID.6625	SNRNP70	19	49,588,465	49,611,870	23,405	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3063, 1_A375_pNL7_minus_lncRNA_AR..1..3064, 2_A375_pNL97_plus_lncRNA_AR..1..4406, 2_A375_pNL97_plus_lncRNA_AR..1..4407	399, 33759, 239, 33711	in gene, downstream, in gene, downstream	1	1	0	27.5	28.5	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene SNRNP70	SNRP70, U170K, U1RNP, RPU1, SNRNP70, U1AP, Snp1, RNPU1Z, U1-70K	small nuclear ribonucleoprotein 70kDa (U1)	NM_003089, hCT1962210.1, hCT2279957.0, hCT2279958.0, hCT2279959.0, hCT2279960.0, hCT2279962.0, hCT2352550.0, hCT2352551.0, hCT7245.3	201221_s_at, 213121_at	NP_003080.2, EAW52450.1, EAW52445.1, EAW52446.1, EAW52451.1, EAW52452.1, EAW52447.1, EAW52448.1, EAW52449.1, EAW52453.1
GeneID.64130	LIN7B	19	49,617,618	49,621,717	4,099	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3064, 2_A375_pNL97_plus_lncRNA_AR..1..4407	4606, 4558	downstream, downstream	1	1	0	37	34	15	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene LIN7B	MALS-2, MALS2, LIN7B, LIN-7B, VELI2	lin-7 homolog B (C. elegans)	NM_022165, hCT2352555.0, hCT7255.4	219760_at, 241957_x_at	NP_071448.1, EAW52454.1, EAW52455.1
GeneID.55150	C19orf73	19	49,621,654	49,622,397	743	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3064, 2_A375_pNL97_plus_lncRNA_AR..1..4407	173, 221	in gene, in gene	1	1	0	37	34	15	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene C19orf73	C19orf73, FLJ10490	chromosome 19 open reading frame 73	NM_018111, hCT1787850.1	220151_at	NP_060581.2, EAW52456.1
GeneID.8541	PPFIA3	19	49,622,663	49,654,283	31,620	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3064, 1_A375_pNL7_minus_lncRNA_AR..1..3065, 2_A375_pNL97_plus_lncRNA_AR..1..4407, 2_A375_pNL97_plus_lncRNA_AR..1..4408, 4_A375_EGR1..1..4819	-439, 31001, -487, 31033, 32665	upstream, in gene, upstream, in gene, downstream	1	1	1	23.67	22	16.33	3	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene PPFIA3	KIAA0654, MGC126569, LPNA3, MGC126567, PPFIA3	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	NM_003660, hCT1640229.2	213368_x_at, 215280_s_at	NP_003651.1, EAW52457.1
GeneID.3270	HRC	19	49,654,455	49,658,681	4,226	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3065, 2_A375_pNL97_plus_lncRNA_AR..1..4408, 4_A375_EGR1..1..4819	5017, 4985, 3353	downstream, downstream, in gene	1	1	1	17	16	17	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene HRC	HRC, MGC133236	histidine rich calcium binding protein	NM_002152, hCT2352549.0, hCT7244.3	207066_at	NP_002143.1, EAW52458.1, EAW52459.1
GeneID.54795	TRPM4	19	49,661,052	49,715,093	54,041	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3065, 2_A375_pNL97_plus_lncRNA_AR..1..4408, 4_A375_EGR1..1..4819	-7366, -7358, -5724	upstream, upstream, upstream	1	1	1	17	16	17	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene TRPM4	FLJ20041, TRPM4, PFHB1B, TRPM4B	transient receptor potential cation channel, subfamily M, member 4	NM_017636, hCT2343207.0, hCT2349457.0, hCT2352561.0, hCT7257.3	219360_s_at	NP_060106.2, EAW52463.1, EAW52460.1, EAW52461.1, EAW52462.1
GeneID.8463	TEAD2	19	49,843,852	49,865,714	21,862	-	1	4_A375_EGR1..1..4820	-1486	upstream	0	0	1	9	5	20	1	4_A375_EGR1..1	20	Gene TEAD2	TEAD2, TEF-4, ETF, TEF4	TEA domain family member 2	NM_003598, hCT2352562.0, hCT2352563.0, hCT2352564.0, hCT2352565.0, hCT7266.2	226408_at, 238321_at, 238322_s_at, 238323_at, 243766_s_at	NP_003589.1, EAW52471.1, EAW52469.1, EAW52470.1, EAW52472.1, EAW52473.1
GeneID.27120	DKKL1	19	49,867,042	49,878,373	11,331	+	1	4_A375_EGR1..1..4820	158	in gene	0	0	1	9	5	20	1	4_A375_EGR1..1	20	Gene DKKL1	SGY, DKKL1, SGY-1, SGY1, CT34	dickkopf-like 1 (soggy)	NM_014419, hCT7238.3	220284_at	NP_055234.1, EAW52475.1
GeneID.100507003	LOC100507003	19	49,929,688	49,932,075	2,387	+	1	4_A375_EGR1..1..4821	10216	downstream	0	0	1	5	5	19	1	4_A375_EGR1..1	19	Gene LOC100507003		hypothetical protein LOC100507003	XM_003119741, XM_003118789, XM_003120958		XP_003119789.1, XP_003118817.1, XP_003121004.1
GeneID.57030	SLC17A7	19	49,932,655	49,944,808	12,153	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3066, 2_A375_pNL97_plus_lncRNA_AR..1..4409, 4_A375_EGR1..1..4821	-2296, -2248, 4904	upstream, upstream, in gene	1	1	1	15	13	16	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene SLC17A7	SLC17A7, VGLUT1, BNPI	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	NM_020309, hCT7254.3	204229_at, 204230_s_at	NP_064705.1, EAW52485.1
GeneID.55011	PIH1D1	19	49,949,550	49,955,115	5,565	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3066, 1_A375_pNL7_minus_lncRNA_AR..1..3067, 2_A375_pNL97_plus_lncRNA_AR..1..4409, 4_A375_EGR1..1..4821, 4_A375_EGR1..1..4822	8011, -1761, 8059, 15211, -1461	downstream, upstream, downstream, downstream, upstream	1	1	1	18	13.33	16.33	3	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene PIH1D1	PIH1D1, FLJ20643	PIH1 domain containing 1	NM_017916, hCT1953541.2, hCT1966232.1	217872_at	NP_060386.1, EAW52486.1, EAW52487.1
GeneID.126133	ALDH16A1	19	49,956,473	49,974,305	17,832	+	8	1_A375_pNL7_minus_lncRNA_AR..1..3066, 1_A375_pNL7_minus_lncRNA_AR..1..3067, 1_A375_pNL7_minus_lncRNA_AR..1..3068, 2_A375_pNL97_plus_lncRNA_AR..1..4409, 2_A375_pNL97_plus_lncRNA_AR..1..4410, 4_A375_EGR1..1..4822, 4_A375_EGR1..1..4823, 4_A375_EGR1..1..4824	-9389, 423, 25767, -9417, 25767, 103, 10951, 20775	upstream, in gene, downstream, upstream, downstream, in gene, in gene, downstream	1	1	1	21.6	21.6	14.2	5	2_A375_pNL97_plus_lncRNA_AR..1	53	Gene ALDH16A1	MGC10204, ALDH16A1	aldehyde dehydrogenase 16 family, member A1	NM_153329, NM_001145396, hCT2279977.0, hCT2279978.0, hCT7265.3	227592_at	NP_699160.2, NP_001138868.1, EAW52482.1, EAW52483.1, EAW52484.1
GeneID.2323	FLT3LG	19	49,977,466	49,989,468	12,002	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3068, 2_A375_pNL97_plus_lncRNA_AR..1..4410, 4_A375_EGR1..1..4823, 4_A375_EGR1..1..4824, 4_A375_EGR1..1..4825, 4_A375_EGR1..1..4826	4754, 4754, -10062, -238, 13394, 22256	in gene, in gene, upstream, upstream, downstream, downstream	1	1	1	17.2	20.2	17.8	5	2_A375_pNL97_plus_lncRNA_AR..1	53	Gene FLT3LG	FL, FLT3L, FLT3LG	fms-related tyrosine kinase 3 ligand	NM_001459, hCT1953525.1, hCT1953526.2, hCT1987183.1, hCT2352546.0, hCT2352547.0, hCT2352548.0, hCT7242.3	206980_s_at, 210607_at	NP_001450.2, EAW52493.1, EAW52489.1, EAW52490.1, EAW52491.1, EAW52492.1, EAW52488.1, EAW52494.1
GeneID.23521	RPL13A	19	49,990,865	49,995,565	4,700	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3068, 2_A375_pNL97_plus_lncRNA_AR..1..4410, 4_A375_EGR1..1..4825, 4_A375_EGR1..1..4826	-8625, -8625, 15, 8879	upstream, upstream, in gene, downstream	1	1	1	22.67	27	18.67	3	2_A375_pNL97_plus_lncRNA_AR..1	53	Gene RPL13A	L13A, RPL13A, TSTA1		NM_012423, hCT2279986.0, hCT2352580.0	211942_x_at	NP_036555.1, EAW52495.1, EAW52496.1

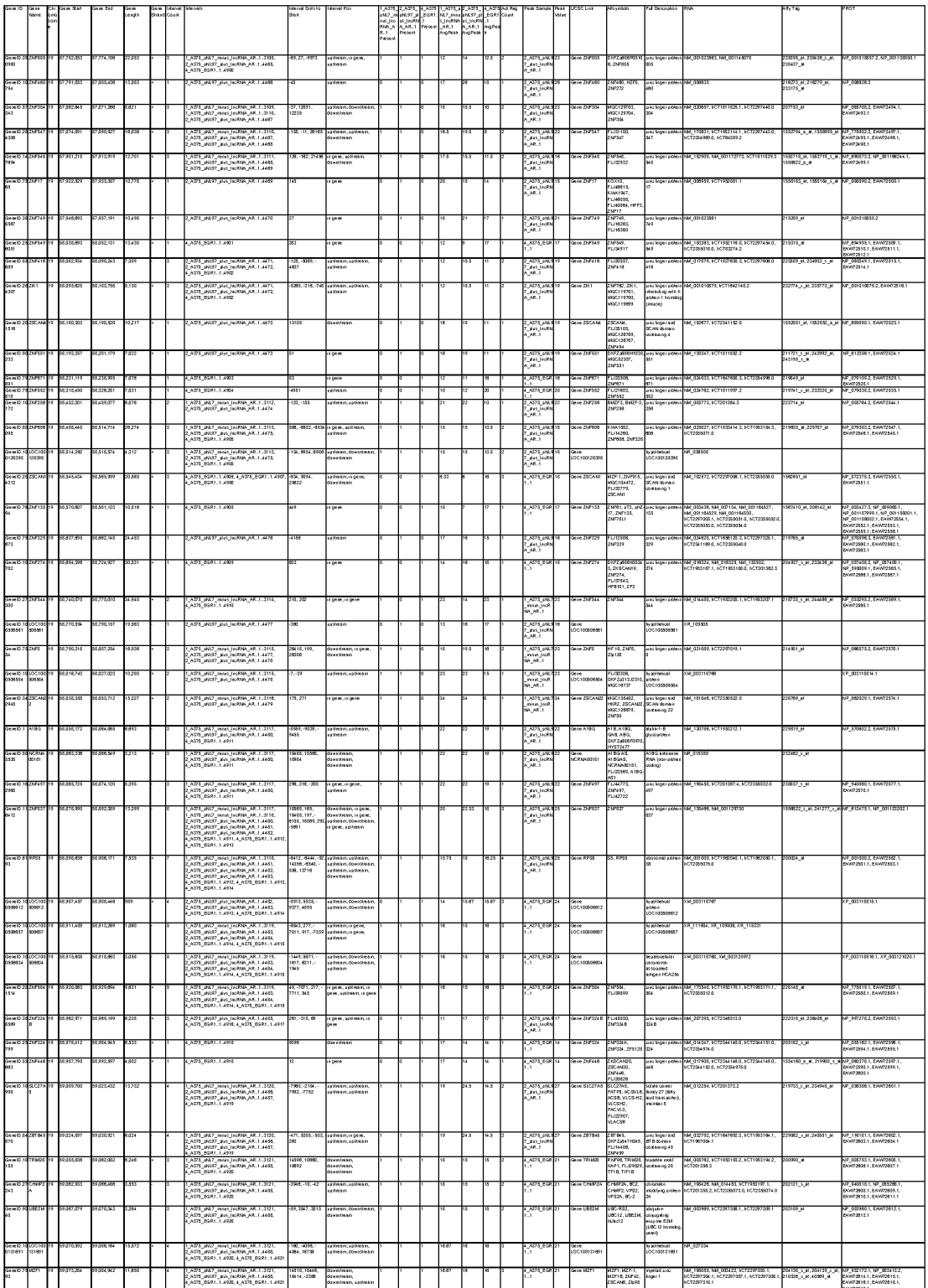
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:26819	SNORD32A	19	49,993,223	49,993,304	81	+	2	4_A375_EGR1..1.4825, 4_A375_EGR1..1.4826	-2343, 6521	upstream, downstream	0	0	1	13	14	24	2	4_A375_EGR1..1	29	Gene SNORD32A	U32, U32A, SNORD32A, RNU32	small nucleolar RNA, C/D box 32A	NR_000021		
GeneID:26818	SNORD33	19	49,993,874	49,993,956	82	+	2	4_A375_EGR1..1.4825, 4_A375_EGR1..1.4826	-2994, 5870	upstream, downstream	0	0	1	13	14	24	2	4_A375_EGR1..1	29	Gene SNORD33	RNU33, U33, SNORD33	small nucleolar RNA, C/D box 33	NR_000020		
GeneID:26817	SNORD34	19	49,994,164	49,994,229	65	+	2	4_A375_EGR1..1.4825, 4_A375_EGR1..1.4826	-3284, 5580	upstream, downstream	0	0	1	13	14	24	2	4_A375_EGR1..1	29	Gene SNORD34	RNU34, U34, SNORD34	small nucleolar RNA, C/D box 34	NR_000019		
GeneID:26816	SNORD35A	19	49,994,432	49,994,517	85	+	2	4_A375_EGR1..1.4825, 4_A375_EGR1..1.4826	-3552, 5312	upstream, downstream	0	0	1	13	14	24	2	4_A375_EGR1..1	29	Gene SNORD35A	RNU35A, SNORD35A, U35, RNU35	small nucleolar RNA, C/D box 35A	NR_000018		
GeneID:6205	RPS11	19	49,999,634	50,002,944	3,310	+	2	4_A375_EGR1..1.4825, 4_A375_EGR1..1.4826	-8754, 110	upstream, in gene	0	0	1	13	14	24	2	4_A375_EGR1..1	29	Gene RPS11	RPS11, S11	ribosomal protein S11	NM_001015, hCT7241.3	200031_s_at, 213350_at	NP_001006.1, EAW52497.1
GeneID:84546	SNORD35B	19	50,000,976	50,001,063	87	+	2	4_A375_EGR1..1.4825, 4_A375_EGR1..1.4826	-10096, -1232	upstream, upstream	0	0	1	13	14	24	2	4_A375_EGR1..1	29	Gene SNORD35B	SNORD35B, RNU35B, U35B	small nucleolar RNA, C/D box 35B	NR_001285		
GeneID:406942	MIR150	19	50,004,042	50,004,125	83	-	1	4_A375_EGR1..1.4826	4361	downstream	0	0	1	15	11	19	1	4_A375_EGR1..1	19	Gene MIR150	miRNA150, MIR150, MIRN150	microRNA 150	NR_029703		
GeneID:57479	PRR12	19	50,094,912	50,129,696	34,784	+	1	2_A375_pNL97_plus_lncRNA_AR..1.4411	22704	in gene	0	1	0	17	21	12	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PRR12	KIAA1205, PRR12	proline rich 12	NM_020719	226716_at	NP_065770.1
GeneID:6237	RRAS	19	50,138,552	50,143,400	4,848	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3069, 1_A375_pNL7_minus_lncRNA_AR..1..3070, 2_A375_pNL97_plus_lncRNA_AR..1.4412, 2_A375_pNL97_plus_lncRNA_AR..1.4413	-104, -1616, -66, -1646	upstream, upstream, upstream, upstream	1	1	0	31	22.5	14	2	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene RRAS	RRAS		NM_006270, hCT12210.3, hCT2283605.0	212647_at	NP_006261.1, EAW52507.1, EAW52506.1
GeneID:58506	SCAF1	19	50,145,382	50,161,906	16,524	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3069, 1_A375_pNL7_minus_lncRNA_AR..1..3070, 2_A375_pNL97_plus_lncRNA_AR..1.4412, 2_A375_pNL97_plus_lncRNA_AR..1.4413, 4_A375_EGR1..1.4827, 4_A375_EGR1..1.4828	-1876, -166, -1894, -134, 16056, 20056	upstream, upstream, upstream, upstream, in gene, downstream	1	1	1	16.75	15.75	16	4	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene SCAF1	SCAF1, SRA1, FLJ00034	SR-related CTD-associated factor 1	NM_021228, hCT1954374.1, hCT2280001.0	225500_x_at	NP_067051.2, EAW52509.1, EAW52508.1
GeneID:3661	IRF3	19	50,162,829	50,169,132	6,303	-	2	4_A375_EGR1..1.4827, 4_A375_EGR1..1.4828	7692, 3692	downstream, in gene	0	0	1	6.5	9	16	2	4_A375_EGR1..1	19	Gene IRF3	IRF3	interferon regulatory factor 3	NM_001571, hCT12194.4, hCT1967223.1, hCT2283602.0, hCT2352591.0	202621_at	NP_001562.1, EAW52510.1, EAW52511.1, EAW52512.1, EAW52513.1
GeneID:83596	BCL2L12	19	50,168,399	50,177,173	8,774	+	2	4_A375_EGR1..1.4827, 4_A375_EGR1..1.4828	-6959, -2959	upstream, upstream	0	0	1	6.5	9	16	2	4_A375_EGR1..1	19	Gene BCL2L12	BCL2L12, MGC120315, MGC120313, MGC120314	BCL2-like 12 (proline rich)	NM_138639, NM_001040668, hCT12208.3, hCT1953548.2, hCT1967226.0, hCT1967227.0	233110_s_at	NP_619580.1, NP_001035758.1, EAW52514.1, EAW52515.1, EAW52516.1, EAW52517.1
GeneID:126129	CPT1C	19	50,194,401	50,216,988	22,587	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3071, 2_A375_pNL97_plus_lncRNA_AR..1.4414	26527, 26463	downstream, downstream	1	1	0	28	30	12	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene CPT1C	CPT1P, CATL1, FLJ23809, CPTIC, CPT1C	carnitine palmitoyltransferase 1C	NM_152359, NM_001136052, hCT2344636.0, hCT2344639.0, hCT2344641.0, hCT2344642.0, hCT2344643.0, hCT2344644.0, hCT2344645.0, hCT2344648.0, hCT2344650.0, hCT2352592.0, hCT2352593.0	227466_at	NP_689572.1, NP_001129524.1, EAW52523.1, EAW52525.1, EAW52526.1, EAW52533.1, EAW52524.1, EAW52527.1, EAW52528.1, EAW52529.1, EAW52530.1, EAW52531.1, EAW52532.1
GeneID:60385	TSKS	19	50,243,011	50,266,515	23,504	-	1	4_A375_EGR1..1.4829	17859	in gene	0	0	1	5	5	17	1	4_A375_EGR1..1	17	Gene TSKS	TSKS, TSSKS, STK22S1, TSKS1	testis-specific serine kinase substrate	NM_021733, hCT12211.2	220544_at, 220545_s_at	NP_068379.1, EAW52534.1
GeneID:160	AP2A1	19	50,270,180	50,310,369	40,189	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3072, 2_A375_pNL97_plus_lncRNA_AR..1.4415, 4_A375_EGR1..1.4830	46556, 46716, 26028	downstream, downstream, in gene	1	1	1	16.5	15.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene AP2A1	AP2A1, CLAPA1, ADTAA, AP2-ALPHA	adaptor-related protein complex 2 alpha 1 subunit	NM_014203, NM_130787, hCT12209.3, hCT2280013.0, hCT2280015.0	1558792_x_at, 223237_x_at, 229817_x_at, 234068_s_at	NP_055018.2, NP_570603.2, EAW52535.1, EAW52536.1, EAW52537.1
GeneID:80199	FUZ	19	50,310,123	50,316,567	6,444	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3072, 2_A375_pNL97_plus_lncRNA_AR..1.4415, 4_A375_EGR1..1.4831	-169, -329, -5886	upstream, upstream, upstream	1	1	1	16	15	10	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene FUZ	FUZ, FLJ22688, FY	fuzzy homolog (Drosophila)	NM_001171937, NM_025129, NR_033269, hCT12207.3, hCT1954375.1, hCT1954376.1, hCT2283792.0, hCT2352583.0, hCT2352584.0	221187_s_at	NP_001165408.1, NP_079405.2, EAW52538.1, EAW52540.1, EAW52542.1, EAW52543.1, EAW52539.1, EAW52541.1
GeneID:81857	MED25	19	50,321,536	50,340,237	18,701	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3072, 2_A375_pNL97_plus_lncRNA_AR..1.4415, 4_A375_EGR1..1.4831, 4_A375_EGR1..1.4832	-4800, -4640, 917, 17760	upstream, upstream, in gene, in gene	1	1	1	13.67	11	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene MED25	ACID1, TCBAP0758, MED25, MGC70671, ARC92, DKFZp434K0512, PTOV2, CMT2B2, P78	mediator complex subunit 25	NM_030973, hCT2344649.0, hCT2344651.0, hCT2344652.0, hCT2344653.0, hCT2344654.0, hCT2344655.0, hCT2352594.0, hCT2352595.0	1553993_s_at, 208110_x_at, 215897_at	NP_112235.2, EAW52544.1, EAW52545.1, EAW52547.1, EAW52550.1, EAW52551.1, EAW52546.1, EAW52548.1, EAW52549.1
GeneID:100506033	LOC100506033	19	50,341,902	50,354,933	13,031	-	3	2_A375_pNL97_plus_lncRNA_AR..1.4416, 4_A375_EGR1..1.4832, 4_A375_EGR1..1.4833	565, 15637, -8139	in gene, downstream, upstream	0	1	1	10.33	9.33	14.67	3	4_A375_EGR1..1	20	Gene LOC100506033		hypothetical LOC100506033	XR_111894, XR_111893, XR_109492, XR_109491, XR_115316, XR_115315		
GeneID:53635	PTOV1	19	50,354,416	50,363,999	9,583	+	3	2_A375_pNL97_plus_lncRNA_AR..1.4416, 4_A375_EGR1..1.4833, 4_A375_EGR1..1.4834	-48, 8656, 18668	upstream, in gene, downstream	0	1	1	11.67	14.33	18.33	3	4_A375_EGR1..1	28	Gene PTOV1	MGC71475, DKFZp586I111, ACID2, PTOV1	prostate tumor overexpressed 1	NM_017432, hCT2344635.0, hCT2344637.0, hCT2344638.0, hCT2344640.0, hCT2344647.0, hCT2344646.0, hCT2349490.0, hCT2349491.0, hCT2352587.0, hCT2352588.0, hCT2352589.0	212032_s_at, 235665_at	NP_059128.2, EAW52553.1, EAW52552.1, EAW52556.1, EAW52557.1, EAW52558.1, EAW52554.1, EAW52555.1, EAW52559.1, EAW52560.1, EAW52561.1, EAW52562.1
GeneID:100506002	LOC100506002	19	50,360,984	50,362,544	1,560	-	2	2_A375_pNL97_plus_lncRNA_AR..1.4416, 4_A375_EGR1..1.4833	8176, -526	downstream, upstream	0	1	1	11	12.5	13.5	2	4_A375_EGR1..1	20	Gene LOC100506002		hypothetical protein LOC100506002	XM_003119739, XM_003118761, XM_003120954		XP_003119787.1, XP_003118809.1, XP_003121002.1
GeneID:11284	PNKP	19	50,364,461	50,370,818	6,357	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3073, 2_A375_pNL97_plus_lncRNA_AR..1.4416, 2_A375_pNL97_plus_lncRNA_AR..1.4417, 4_A375_EGR1..1.4833, 4_A375_EGR1..1.4834, 4_A375_EGR1..1.4835	-9022, 16450, -9758, 7746, -2286, -8942	upstream, downstream, upstream, downstream, upstream, upstream	1	1	1	14	15.5	18	4	4_A375_EGR1..1	28	Gene PNKP	EIEE10, MCSZ, PNKP, PNK	polynucleotide kinase 3'-phosphatase	NM_007254, hCT12191.4, hCT2283784.0, hCT2283786.0	218961_s_at	NP_009185.2, EAW52567.1, EAW52565.1, EAW52566.1
GeneID:84335	AKT1S1	19	50,372,296	50,380,644	8,348	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3073, 2_A375_pNL97_plus_lncRNA_AR..1.4417, 4_A375_EGR1..1.4833, 4_A375_EGR1..1.4834, 4_A375_EGR1..1.4835	604, 66, 17572, 7540, 684	in gene, in gene, downstream, in gene, in gene	1	1	1	14	14.67	21.67	3	4_A375_EGR1..1	28	Gene AKT1S1	AKT1S1, Lobe, MGC2865, PRAS40	AKT1 substrate 1 (proline-rich)	NM_001098633, NM_032375, NM_001098632, hCT12202.3, hCT1967224.1, hCT2273994.0, hCT2352590.0	1555821_a_at, 224962_at	NP_001092103.1, NP_115751.2, NP_001092102.1, EAW52568.1, EAW52569.1, EAW52570.1, EAW52571.1
GeneID:79735	TBC1D17	19	50,380,682	50,392,007	11,325	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3073, 2_A375_pNL97_plus_lncRNA_AR..1.4417, 4_A375_EGR1..1.4834, 4_A375_EGR1..1.4835, 4_A375_EGR1..1.4836	-842, -106, -7578, -922, 12502	upstream, upstream, upstream, upstream, downstream	1	1	1	12.33	15	21	3	4_A375_EGR1..1	28	Gene TBC1D17	TBC1D17, FLJ12168	TBC1 domain family, member 17	NM_024682, NM_001168222, hCT12203.3	218466_at	NP_078958.2, NP_001161694.1, EAW52572.1
GeneID:259307	IL4I1	19	50,392,911	50,432,762	39,851	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3074, 2_A375_pNL97_plus_lncRNA_AR..1.4418, 4_A375_EGR1..1.4836, 4_A375_EGR1..1.4837, 4_A375_EGR1..1.4838	330, 154, 39576, 21162, 522	in gene, in gene, in gene, in gene, in gene	1	1	1	9.67	15.33	16.33	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene IL4I1	IL4I1, FIG1	interleukin 4 induced 1	NM_152899, NM_172374	230966_at	NP_690863.1, NP_758962.1
GeneID:23636	NUP62	19	50,410,062	50,432,968	22,906	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3074, 2_A375_pNL97_plus_lncRNA_AR..1.4418, 4_A375_EGR1..1.4837, 4_A375_EGR1..1.4838	556, 380, 21366, 748	in gene, in gene, in gene, in gene	1	1	1	13	19	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene NUP62	FLJ20822, FLJ43869, MGC841, SNDI, IBSN, p62, DKFZp547L134, NUP62	nucleoporin 62kDa	NM_016553, NM_153719, NM_153718, NM_012346, NM_001193357	214935_at	NP_057637.2, NP_714941.1, NP_036478.2, NP_714940.1, NP_001180286.1
GeneID:22809	ATF5	19	50,431,959	50,437,193	5,234	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3074, 2_A375_pNL97_plus_lncRNA_AR..1.4418, 4_A375_EGR1..1.4838	473, 649, 281	in gene, in gene, in gene	1	1	1	16	26	15	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene ATF5	ATFX, HMFN0395, FLJ34666, ATF5	activating transcription factor 5	NM_012068, NM_001193646, hCT12190.3, hCT1954366.1, hCT2273658.0	204998_s_at, 204999_s_at, 217389_s_at, 230936_x_at	NP_036200.2, NP_001180575.1, EAW52581.1, EAW52582.1, EAW52583.1
GeneID:51231	VRK3	19	50,479,724	50,528,805	49,081	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3075, 2_A375_pNL97_plus_lncRNA_AR..1.4419	38213, 38213	in gene, in gene	1	1	0	257	320	10	1	2_A375_pNL97_plus_lncRNA_AR..1	320	Gene VRK3	VRK3		NM_016440, NM_001025778, hCT12192.2, hCT2273991.0, hCT2273993.0, hCT2352585.0, hCT2352586.0	1566700_at, 1566701_at, 218022_at, 221998_s_at, 221999_at, 239190_at	NP_057524.3, NP_001020949.1, EAW52589.1, EAW52590.1, EAW52591.1, EAW52592.1, EAW52586.1
GeneID:3748	KCNC3	19	50,818,765	50,832,634	13,869	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3076, 4_A375_EGR1..1.4839, 4_A375_EGR1..1.4840	-4196, 2986, -4102	upstream, in gene, upstream	1	0	1	18.5	14.5	21	2	4_A375_EGR1..1	23	Gene KCNC3	KSHIIID, KV3.3, SCA13, KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3	NM_004977, hCT10755.2	207600_at, 230531_at, 243893_at	NP_004968.2, EAW71844.1
GeneID:7376	NR1H2	19	50,879,685	50,886,267	6,582	+	1	4_A375_EGR1..1.4841	-149	upstream	0	0	1	14	14	17	1	4_A375_EGR1..1	17	Gene NR1H2	RIP15, NER, LXRb, UNR, NER-I, LXRB, NR1H2	nuclear receptor subfamily 1, group H, member 2	NM_007121, hCT14045.2, hCT1952531.0, hCT1987868.0, hCT2298169.0, hCT2298170.0, hCT2298173.0	218215_s_at	NP_009052.3, EAW71853.1, EAW71850.1, EAW71851.1, EAW71852.1, EAW71855.1, EAW71854.1
GeneID:5424	POLD1	19	50,887,593	50,921,271	33,678	+	2	4_A375_EGR1..1.4841, 4_A375_EGR1..1.4842	-8057, 32535	upstream, in gene	0	0	1	10	10.5	15.5	2	4_A375_EGR1..1	17	Gene POLD1	POLD, CDC2, POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	NM_002691, hCT14027.3, hCT2355072.0	203422_at	NP_002682.2, EAW71857.1, EAW71856.1
GeneID:6689	SPIB	19	50,922,195	50,932,250	10,055	+	1	4_A375_EGR1..1.4842	-2067	upstream	0	0	1	6	7	14	1	4_A375_EGR1..1	14	Gene SPIB	SPI-B, SPIB	Spi-B transcription factor (Spi-1/PU.1 related)	NM_003121, hCT14026.3, hCT1952525.1, hCT1952526.1, hCT1981838.1, hCT1987865.0, hCT2298188.0, hCT2298190.0	205861_at, 232739_at	NP_003112.2, EAW71860.1, EAW71858.1, EAW71861.1, EAW71862.1, EAW71863.1, EAW71859.1, EAW71864.1
GeneID:4608	MYBPC2	19	50,936,160	50,969,583	33,423	+	1	4_A375_EGR1..1.4843	34366	downstream	0	0	1	6	4	15	1	4_A375_EGR1..1	15	Gene MYBPC2	MYBPC2, MYBPCF, MGC163406, MYBPC	myosin binding protein C, fast type	NM_004533, hCT1952528.1, hCT2298205.0	208394_at	NP_004524.3, EAW71865.1, EAW71866.1
GeneID:112703	FAM71E1	19	50,970,045	50,980,003	9,958	-	1	4_A375_EGR1..1.4843	9475	in gene	0	0	1	6	4	15	1	4_A375_EGR1..1	15	Gene FAM71E1	FLJ27522, FAM71E1, FLJ43757	family with sequence similarity 71, member E1	NM_138411, hCT14048.4, hCT1987889.1, hCT2298972.0, hCT2355010.0	229289_at	NP_612420.1, EAW71869.1, EAW71867.1, EAW71868.1, EAW71870.1
GeneID:284361	C19orf63	19	50,979,736	50,986,608	6,872	+	1	4_A375_EGR1..1.4843	-9208	upstream	0	0	1	6	4	15	1	4_A375_EGR1..1	15	Gene C19orf63	HSM1, MGC33203, INM02, C19orf63, HSS1	chromosome 19 open reading frame 63	NM_175063, NM_206538, hCT14047.3, hCT2349288.0, hCT2355009.0	224727_at	NP_778233.4, NP_996261.1, EAW71871.1, EAW71872.1, EAW71873.1
GeneID:126119	JOSD2	19	51,009,259	51,014,345	5,086	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3077, 2_A375_pNL97_plus_lncRNA_AR..1.4420, 4_A375_EGR1..1.4844, 4_A375_EGR1..1.4845	-279, -386, 2937, 3351	upstream, upstream, in gene, upstream	1	1	1	14	14	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene JOSD2	JOSD2, FLJ29018, SBBI54	Josephin domain containing 2	NM_138334, hCT1771482.3, hCT1986758.2, hCT2355049.0, hCT2355050.0	227096_at	NP_612207.1, EAW71874.1, EAW71875.1, EAW71876.1, EAW71877.1
GeneID:554235	ASPDH	19	51,014,857	51,017,947	3,090	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3077, 2_A375_pNL97_plus_lncRNA_AR..1.4420, 4_A375_EGR1..1.4844, 4_A375_EGR1..1.4845	3323, 3216, 6539, 251	downstream, downstream, downstream, in gene	1	1	1	14	14	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ASPDH	ASPDH		NM_001024656, NM_001114598, hCT14042.3, hCT2355002.0, hCT2355003.0, hCT2355004.0, hCT2355005.0, hCT2355006.0	230912_at	NP_001019827.2, NP_001108070.1, EAW71878.1, EAW71880.1, EAW71881.1, EAW71883.1, EAW71879.1, EAW71882.1
GeneID:94030	LRRC4B	19	51,020,149	51,071,302	51,153	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3077, 2_A375_pNL97_plus_lncRNA_AR..1.4420, 4_A375_EGR1..1.4844, 4_A375_EGR1..1.4845	56678, 56571, 59694, 53606	downstream, downstream, downstream, downstream	1	1	1	14	14	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LRRC4B	DKFZp761A179, LRRC4B, HSM, LRIG4	leucine rich repeat containing 4B	NM_001080457	239320_at	NP_001073926.1
GeneID:84258	SYT3	19	51,125,234	51,143,092	17,858	-	2	4_A375_EGR1..1.4846, 4_A375_EGR1..1.4847	7364, 676	in gene, in gene	0	0	1	8	7.5	17	2	4_A375_EGR1..1	20	Gene SYT3	SYT3, DKFZp761O132, SytIII	synaptotagmin III	NM_032298, NM_001160328, NM_001160329, hCT14050.3, hCT1956267.2, hCT2298958.1, hCT2298959.1, hCT2298961.0	223901_at	NP_115674.1, NP_001153800.1, NP_001153801.1, EAW71887.1, EAW71888.1, EAW71890.1, EAW71889.1, EAW71891.1
GeneID:342918	LOC342918	19	51,152,702	51,162,587	9,885	+	1	2_A375_pNL97_plus_lncRNA_AR..1.4421	9218	in gene	0	1	0	13	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC342918		hypothetical protein LOC342918	NM_001195076	230814_at	NP_001182005.1
GeneID:50944	SHANK1	19	51,165,084	51,220,195	55,111	-	4	2_A375_pNL97_plus_lncRNA_AR..1.4421, 4_A375_EGR1..1.4848, 4_A375_EGR1..1.4849, 4_A375_EGR1..1.4850	58275, 21219, 14467, -8381	downstream, in gene, in gene, upstream	0	1	1	12.25	12	16	4	4_A375_EGR1..1	23	Gene SHANK1	SSTRIP, SHANK1, synamon, SPANK-1	SH3 and multiple ankyrin repeat domains 1	NM_016148, hCT1952523.2, hCT2298953.1	220563_s_at	NP_057232.2, EAW71893.1, EAW71894.1
GeneID:6320	CLEC11A	19	51,226,605	51,228,981	2,376	+	1	4_A375_EGR1..1.4850	1971	in gene	0	0	1	15	17	19	1	4_A375_EGR1..1	19	Gene CLEC11A	CLEC11A, LSLCL, CLECSF3, SCGF, P47	C-type lectin domain family 11, member A	NM_002975, hCT14029.3, hCT1958320.1, hCT1958321.1	205131_x_at, 210783_x_at, 211709_s_at	NP_002966.1, EAW71896.1, EAW71895.1, EAW71897.1
GeneID:93650	ACPT	19	51,293,672	51,298,481	4,809	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3078, 2_A375_pNL97_plus_lncRNA_AR..1.4422, 4_A375_EGR1..1.4851, 4_A375_EGR1..1.4852, 4_A375_EGR1..1.4853, 4_A375_EGR1..1.4854	14312, 14264, -66, 7960, 8952, 14200	downstream, downstream, upstream, downstream, downstream, downstream	1	1	1	16	21.5	20.75	4	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene ACPT	ACPT	acid phosphatase, testicular	NM_033068, hCT1770427.1, hCT2298235.0, hCT2298236.0, hCT2298237.0, hCT2298239.0	241715_x_at	NP_149059.1, EAW71902.1, EAW71900.1, EAW71901.1, EAW71903.1, EAW71904.1
GeneID:84798	C19orf48	19	51,300,961	51,307,974	7,013	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3078, 2_A375_pNL97_plus_lncRNA_AR..1.4422, 4_A375_EGR1..1.4851, 4_A375_EGR1..1.4852, 4_A375_EGR1..1.4853, 4_A375_EGR1..1.4854	-10, 38, 14390, 6342, 5350, 102	upstream, in gene, downstream, in gene, in gene, in gene	1	1	1	16	21.5	20.75	4	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene C19orf48	MGC13170, C19orf48	chromosome 19 open reading frame 48	NM_199249, NM_199250, hCT2298946.1, hCT2298947.1, hCT2298948.1, hCT2298949.1, hCT2354990.0	224468_s_at	NP_954857.1, NP_954858.1, EAW71905.1, EAW71906.1, EAW71907.1, EAW71909.1, EAW71908.1
GeneID:692203	SNORD88B	19	51,302,286	51,302,382	96	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3078, 2_A375_pNL97_plus_lncRNA_AR..1.4422, 4_A375_EGR1..1.4851, 4_A375_EGR1..1.4852, 4_A375_EGR1..1.4853, 4_A375_EGR1..1.4854	-5602, -5554, 8798, 750, -242, -5490	upstream, upstream, downstream, downstream, upstream, upstream	1	1	1	16	21.5	20.75	4	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene SNORD88B	HBII-180B, SNORD88B	small nucleolar RNA, C/D box 88B	NR_003066		
GeneID:692202	SNORD88A	19	51,302,696	51,302,792	96	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3078, 2_A375_pNL97_plus_lncRNA_AR..1.4422, 4_A375_EGR1..1.4851, 4_A375_EGR1..1.4852, 4_A375_EGR1..1.4853, 4_A375_EGR1..1.4854	-5192, -5144, 9208, 1160, 168, -5080	upstream, upstream, downstream, downstream, downstream, upstream	1	1	1	16	21.5	20.75	4	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene SNORD88A	HBII-180A, SNORD88A	small nucleolar RNA, C/D box 88A	NR_003067		
GeneID:692204	SNORD88C	19	51,305,582	51,305,678	96	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3078, 2_A375_pNL97_plus_lncRNA_AR..1.4422, 4_A375_EGR1..1.4852, 4_A375_EGR1..1.4853, 4_A375_EGR1..1.4854	-2306, -2258, 4046, 3054, -2194	upstream, upstream, downstream, downstream, upstream	1	1	1	20	27	22.33	3	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene SNORD88C	SNORD88C, HBII-180C	small nucleolar RNA, C/D box 88C	NR_003069		
GeneID:354	KLK3	19	51,358,171	51,364,020	5,849	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3079, 2_A375_pNL97_plus_lncRNA_AR..1.4423	15701, 15589	downstream, downstream	1	1	0	19	22	11	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene KLK3	KLK3, KLK2A1, PSA, hK3, APS	kallikrein-related peptidase 3	NM_001648, NM_001030047, NM_001030048, NM_001030050, hCT14028.4, hCT1952527.2, hCT1987867.2, hCT2298243.1, hCT2298244.1, hCT2298245.1, hCT2298248.1, hCT2349989.0, hCT2349990.0, hCT2349991.0, hCT2349992.0, hCT2349994.0, hCT2349995.0, hCT2349998.0, hCT23499	204582_s_at, 204583_x_at, 231629_x_at	NP_001639.1, NP_001025218.1, NP_001025219.1, NP_001025221.1, EAW71925.1, EAW71935.1, EAW71922.1, EAW71923.1, EAW71924.1, EAW71926.1, EAW71927.1, EAW71928.1, EAW71929.1, EAW71933.1, EAW71930.1, EAW71931.1, EAW71932.1, EAW71934.1, EAW71936.1
GeneID:3817	KLK2	19	51,376,689	51,383,823	7,134	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3079, 2_A375_pNL97_plus_lncRNA_AR..1.4423	-2817, -2929	upstream, upstream	1	1	0	19	22	11	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene KLK2	KLK2A2, MGC12201, hK2, KLK2	kallikrein-related peptidase 2	NM_005551, NM_001002231, hCT14031.2, hCT1981849.1, hCT1981850.1, hCT2298251.0, hCT2298252.0, hCT2354977.0	1555545_at, 209854_s_at, 209855_s_at, 210339_s_at	NP_005542.1, NP_001002231.1, EAW71937.1, EAW71938.1, EAW71939.1, EAW71941.1, EAW71940.1, EAW71942.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_3_A375_4_A375_1_A375_2_A375_3_A375_4_A375_Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	FPKM
GeneID:26	KLHL9	9	31,305,769	31,312,990	7,221	-	1	4_A375_EGR1_1.4555	5190	upstream	0 0 1 7 9 12 1	4_A375_EGR1_1.1	12	Gene KLHL9	KLHL5, KLHL9, MGC30310, KLHL5	kelch-like-related peptide 9	NM_012315, XCT177477.1, XCT235502.0		NP_036447.1, EWT1998.1, EWT1998.1
GeneID:56	KLHL10	9	31,316,930	31,323,431	7,431	-	1	4_A375_EGR1_1.4555	1351	up gene	0 0 1 7 9 12 1	4_A375_EGR1_1.1	12	Gene KLHL10	KLHL9, NESH, PRO5311	kelch-like-related peptide 10	NM_145650, NM_002758, NM_020177500, XCT164163.0, XCT160327.2, XCT229949.0	209792_s_at, 213002_at	NP_665815.1, NP_002767.2, NP_020178860.1, EWT1987.1, EWT1998.1, EWT1999.1
GeneID:1	KLHL11	9	31,325,457	31,331,260	5,803	-	1	4_A375_EGR1_1.4555	9210	downstream	0 0 1 7 9 12 1	4_A375_EGR1_1.1	12	Gene KLHL11	FLIP, MGC33980, PRO5330, KLHL11	kelch-like-related peptide 11	NM_020553, NM_144947, NM_020158032, NM_001167905, XCT140253.0, XCT195290.1, XCT235492.0	205470_s_at	NP_065144.1, NP_065196.1, NP_001139504.1, NP_001161077.1, EWT1970.1, EWT1971.1, EWT1972.1
GeneID:43	KLHL12	9	31,332,348	31,336,148	3,800	-	1	4_A375_EGR1_1.4555	99360	downstream	0 0 1 7 9 12 1	4_A375_EGR1_1.1	12	Gene KLHL12	KLHL12, KLHL5, KLHL5, MGC34892, DKFZp686H070	kelch-like-related peptide 12	NM_019390, NM_145894, NM_145895, XCT164163.2, XCT195389.0, XCT229699.0, XCT235634.0, XCT235633.0	220762_s_at, 223599_s_at, 234318_s_at	NP_062344.1, NP_665901.1, NP_665902.1, EWT1970.1, EWT1977.1, EWT1978.1, EWT1974.1, EWT1975.1, EWT1976.1
GeneID:23	ETFB	19	31,645,409	31,669,672	21,265	+	5	2_A375_chr37_plus_lncRNA_AR_1.4424, 4_A375_EGR1_1.4556, 4_A375_EGR1_1.4557	1925, 12165, -1498	up gene, up gene, upstream	0 1 1 12.33 14 16.33 5	2_A375_chr37_plus_lncRNA_AR_1	24	Gene ETFB	ETFB5, MADD, ETFB	electron transfer flavoprotein, beta polypeptide	NM_001014763, NM_001955, XCT023672	202942_at	NP_001014785.1, NP_001956.1, EWT2004.1
GeneID:12	CLCND2	19	31,670,332	31,672,257	1,925	-	2	2_A375_chr37_plus_lncRNA_AR_1.4424, 4_A375_EGR1_1.4557	4312, 1029	downstream, up gene	0 0 1 13 16 17 2	2_A375_chr37_plus_lncRNA_AR_1	24	Gene CLCND2	CLCND2, MGC33539	chloride channel nucleotide-sensitive 2	NM_152333, XCT023653	231162_at	NP_689396.1, EWT2005.1
GeneID:48	NKG7	19	31,674,974	31,679,960	1,098	-	2	2_A375_chr37_plus_lncRNA_AR_1.4424, 4_A375_EGR1_1.4557	6216, 4792	downstream, downstream	0 0 1 13 16 17 2	2_A375_chr37_plus_lncRNA_AR_1	24	Gene NKG7	GIG1, p15-TYK-1, GMP-17, NKG7	natural killer cell group 7 sequence	NM_005601, XCT163908.1, XCT163909.0, XCT023442.2	212918_at	NP_005592.1, EWT2007.1, EWT2008.1, EWT2009.1
GeneID:89	SIGLEC10	19	31,913,275	31,921,037	7,762	-	2	1_A375_chr37_minus_lncRNA_AR_1.3993, 2_A375_chr37_plus_lncRNA_AR_1.4425	-4351, -4319	upstream, upstream	1 1 0 23 33 6 1	2_A375_chr37_plus_lncRNA_AR_1	23	Gene SIGLEC10	SIGLEC10, SIGLEC10P, SIGLEC10L, SIGLEC	sialic acid binding Ig-like lectin 10	NM_033130, NM_001171136, NM_001171137, NM_001171155, NM_001171159, NM_001171160, NM_001171161, XCT164142.4, XCT229535.0, XCT229536.0, XCT235500.0, XCT235501.0	1552600_a_at, 1552607_a_at	NP_149121.2, NP_001164827.1, NP_001164828.1, NP_001164829.1, NP_001164830.1, NP_001164831.1, NP_001164832.2, EWT2012.1, EWT2013.1, EWT2014.1, EWT2015.1, EWT2016.1
GeneID:10	LOC10013	19	31,919,160	31,920,979	1,819	+	2	1_A375_chr37_minus_lncRNA_AR_1.3993, 2_A375_chr37_plus_lncRNA_AR_1.4429	6243, 6218	downstream, downstream	1 1 0 23 33 6 1	2_A375_chr37_plus_lncRNA_AR_1	23	Gene LOC100129083		similar to KIAA0430	NR_033233		
GeneID:23	SIGLEC9	19	31,934,251	31,951,705	7,457	-	1	4_A375_EGR1_1.4555	10550	downstream	0 0 1 7 9 17 1	4_A375_EGR1_1.1	17	Gene SIGLEC9	MGC29755, SIGLEC-9, SIGLEC9, SAF2, SIGLEC9L	sialic acid binding Ig-like lectin 9	NM_014442, XCT163991.0, XCT229578.0, XCT229579.0	206255_at, 219227_x_at, 219228_at	NP_055257.2, EWT2019.1, EWT2020.1, EWT2035.1
GeneID:72	CEACAM16	19	31,979,035	31,986,811	6,773	+	1	2_A375_chr37_plus_lncRNA_AR_1.4426	4150	up gene	0 1 0 16 22 6 1	2_A375_chr37_plus_lncRNA_AR_1	22	Gene CEACAM16	CEACAM16	carcinoembryonic antigen-related cell adhesion molecule 16	NM_001039845		NP_001073874.1
GeneID:77	ZNF175	19	32,074,851	32,092,991	18,460	+	2	1_A375_chr37_minus_lncRNA_AR_1.3982, 2_A375_chr37_plus_lncRNA_AR_1.4430	-160, 22293	upstream, downstream	1 1 0 16.5 19 7.5 2	2_A375_chr37_plus_lncRNA_AR_1	24	Gene ZNF175	ZNF175, OTK18	zinc finger protein 175	NM_007147, XCT163918.0, XCT023419.2	205467_at, 243120_at	NP_009178.1, EWT2029.1, EWT2030.1
GeneID:72	FLJ20400	19	32,089,036	32,097,453	8,417	-	1	4_A375_chr37_plus_lncRNA_AR_1.4426	-191	upstream	0 0 1 0 16 24 10 1	2_A375_chr37_plus_lncRNA_AR_1	24	Gene FLJ20400		hypothetical LOC27975	NR_024159	1559092_at	
GeneID:87	SIGLEC5	19	32,114,781	32,133,727	18,946	-	2	1_A375_chr37_minus_lncRNA_AR_1.3983, 2_A375_chr37_plus_lncRNA_AR_1.4429	22316, 22293	downstream, downstream	1 1 0 33 37 4 1	2_A375_chr37_plus_lncRNA_AR_1	27	Gene SIGLEC5	SIGLEC-5, OB-BP2, SIGLEC5, CD33L2, CD170, OBBP2	sialic acid binding Ig-like lectin 5	NM_003830, XCT023260.2	230600_at	NP_003831.1, EWT2032.1
GeneID:88	ZNF814	19	32,316,577	32,331,800	15,103	+	2	2_A375_chr37_plus_lncRNA_AR_1.4430	0	up gene	0 1 0 15 19 12 1	2_A375_chr37_plus_lncRNA_AR_1	19	Gene ZNF814	MGC129854, FLJ21941, ZNF814	zinc finger protein 814	NM_020940	210599_at, 220721_at, 227945_at	NP_378116.2
GeneID:96	ZNF432	19	32,336,677	32,352,073	15,396	+	1	2_A375_chr37_plus_lncRNA_AR_1.4430	20293	downstream	0 1 0 15 19 12 1	2_A375_chr37_plus_lncRNA_AR_1	19	Gene ZNF432	ZNF432	zinc finger protein 432	NM_014950	219846_s_at	NP_055465.1
GeneID:55	PPP2R1A	19	52,890,055	52,929,676	39,623	+	1	4_A375_EGR1_1.4559	609	up gene	0 0 1 7 9 16 1	4_A375_EGR1_1.1	16	Gene PPP2R1A	PR65A, MGC709, PPP2R1A, PP2AAALPHA, PP2A-Aalpha	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform	NM_014225, NM_033593, XCT10756.2	200989_at	NP_055340.2, EWT2098.1
GeneID:96	ZNF766	19	52,772,624	52,795,978	23,152	+	2	2_A375_chr37_plus_lncRNA_AR_1.4431, 4_A375_EGR1_1.4560	27612, 27936	downstream, downstream	0 1 1 12 16 14 1	2_A375_chr37_plus_lncRNA_AR_1	16	Gene ZNF766	ZNF766	zinc finger protein 766	NM_001018051, XCT158431.1, XCT235470.0, XCT234477.0	227264_at	NP_001018051.1, EWT23565.1, EWT23567.1, EWT23569.1
GeneID:14	ZNF460	19	52,800,426	52,829,173	28,749	+	2	2_A375_chr37_plus_lncRNA_AR_1.4431, 4_A375_EGR1_1.4560	530, 326	up gene, up gene	0 0 1 1 12 16 14 1	2_A375_chr37_plus_lncRNA_AR_1	16	Gene ZNF460	ZNF460, MGC32166	zinc finger protein 460	NM_144984, XCT159435.1	222283_at	NP_659203.2, EWT2077.1
GeneID:35	ZNF231	19	54,224,177	54,265,523	99,346	+	2	1_A375_chr37_minus_lncRNA_AR_1.3984, 4_A375_EGR1_1.4562	-1, 16905	upstream, up gene	1 1 0 14.5 12 11 2	2_A375_chr37_plus_lncRNA_AR_1	30	Gene ZNF231	ZNF231, RIFA, DKFZp686D15231, ZNF461, ZNF261	zinc finger protein 231	NM_031079958, NM_001079907, NM_015605, XCT229716.0, XCT229717.0, XCT229718.0, XCT235506.0	210220_at, 227613_at	NP_001073375.1, NP_001073376.1, NP_056320.5, EWT2144.1, EWT2145.1, EWT2146.1, EWT2147.1, EWT2148.1
GeneID:53	PRKCG	19	54,355,467	54,410,901	55,434	+	3	1_A375_chr37_minus_lncRNA_AR_1.3983, 2_A375_chr37_plus_lncRNA_AR_1.4432, 4_A375_EGR1_1.4563	21629, 20998, 27493	up gene, up gene, downstream	1 1 1 14 17 11.5 2	2_A375_chr37_plus_lncRNA_AR_1	29	Gene PRKCG	PKCgamma, SCA14, PRKCG, MGC37184, PKCG, PKCC	protein kinase C, gamma	NM_002739, XCT120033.0	206210_at, 238795_x_at	NP_002730.1, EWT2181.1
GeneID:59	CACNG7	19	54,416,071	54,445,266	29,197	+	5	1_A375_chr37_minus_lncRNA_AR_1.3983, 2_A375_chr37_minus_lncRNA_AR_1.3996, 2_A375_chr37_plus_lncRNA_AR_1.4432, 4_A375_chr37_plus_lncRNA_AR_1.4433, 4_A375_EGR1_1.4565	-9915, 15129, 9803, 15097, 2111	upstream, up gene, upstream, up gene, upstream	1 1 1 17.67 23.67 10.67 2	2_A375_chr37_plus_lncRNA_AR_1	27	Gene CACNG7	CACNG7		NM_031896, XCT120211.3, XCT198358.1, XCT196757.1, XCT229726.0, XCT229727.0, XCT229731.0	224137_at	NP_114102.2, EWT2196.1, EWT2197.1, EWT2198.1, EWT2164.1, EWT2165.1
GeneID:60	CACNG8	19	54,466,214	54,468,159	19,945	+	2	2_A375_chr37_plus_lncRNA_AR_1.4434, 4_A375_EGR1_1.4564	16670, 27024	up gene, downstream	0 0 1 10 16 11.5 2	2_A375_chr37_plus_lncRNA_AR_1	21	Gene CACNG8	FLJ30166, CACNG8, FLJ16240		NM_031916, XCT120224	234760_at, 234768_at	NP_114101.4, EWT2166.1
GeneID:10	MIR933	19	54,468,961	54,468,851	110	-	2	2_A375_chr37_plus_lncRNA_AR_1.4434, 4_A375_EGR1_1.4564	-2297, 7757	upstream, downstream	0 0 1 10 16 11.5 2	2_A375_chr37_plus_lncRNA_AR_1	21	Gene MIR933	MIR933, MIR933.1, hsa-mir-933	microRNA 933	NR_030632		
GeneID:56	CACNG1	19	54,495,542	54,515,920	20,378	+	1	4_A375_EGR1_1.4564	-2224	upstream	0 0 1 7 11 14 1	4_A375_EGR1_1.1	14	Gene CACNG1	CACNG1		NM_145814, NM_145815, NM_031957, XCT190905.0, XCT235096.0, XCT235097.0	1552663_a_at, 224291_at	NP_666813.1, NP_666814.1, NP_114103.2, EWT2170.1, EWT2171.1, EWT2172.1
GeneID:12	OSCAR	19	54,597,905	54,604,146	6,216	-	2	2_A375_chr37_plus_lncRNA_AR_1.4435, 4_A375_EGR1_1.4565	-1964, -1638	upstream, upstream	0 0 1 20 24 13 1	2_A375_chr37_plus_lncRNA_AR_1	24	Gene OSCAR	MGC33610, OSCAR, PIGR5	osteoclast-associated, immunoglobulin-like receptor	NM_206518, NM_130771, NM_130166, NM_153169, XCT120203.3, XCT195283.1, XCT229528.0, XCT229529.0, XCT235040.0	1554053_s_at	NP_996534.1, NP_570127.2, NP_570395.1, NP_570396.1, EWT2174.1, EWT2175.1, EWT2176.1, EWT2177.1, EWT2178.1
GeneID:48	NDUFA9	19	54,606,180	54,610,301	4,121	+	4	1_A375_chr37_minus_lncRNA_AR_1.3987, 2_A375_chr37_plus_lncRNA_AR_1.4435, 2_A375_chr37_plus_lncRNA_AR_1.4436, 2_A375_chr37_plus_lncRNA_AR_1.4437, 4_A375_EGR1_1.4566	12720, -46, 12545, -176	downstream, upstream, downstream, upstream	1 1 1 22 27 13 2	2_A375_chr37_plus_lncRNA_AR_1	30	Gene NDUFA9	NDUFA9, B9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39 kDa	NM_005342, XCT120203.3, XCT156258.1, XCT156257.0, XCT195282.1, XCT229752.0	218360_at	NP_005333.1, EWT2184.1, EWT2185.1, EWT2186.1, EWT2187.1, EWT2188.1, EWT2189.1
GeneID:29	TFPT	19	54,610,330	54,619,055	8,726	-	4	1_A375_chr37_minus_lncRNA_AR_1.3987, 2_A375_chr37_plus_lncRNA_AR_1.4435, 2_A375_chr37_plus_lncRNA_AR_1.4436, 2_A375_chr37_plus_lncRNA_AR_1.4437, 4_A375_EGR1_1.4566	176, 12643, 47, 13211	up gene, downstream, up gene, downstream	1 1 1 22 27 13 2	2_A375_chr37_plus_lncRNA_AR_1	30	Gene TFPT	smada, TFPT, FBI, MOS9	TCF3 (E2A) fusion partner (in childhood leukemia)	NM_013342, XCT120213.2, XCT198534.0, XCT198535.1, XCT229530.0, XCT229499.0	218999_at	NP_037474.3, EWT2187.1, EWT2188.1, EWT2189.1, EWT2190.1
GeneID:28	PRPF31	19	54,616,790	54,635,150	18,360	+	5	1_A375_chr37_minus_lncRNA_AR_1.3987, 2_A375_chr37_plus_lncRNA_AR_1.4435, 2_A375_chr37_plus_lncRNA_AR_1.4436, 2_A375_chr37_plus_lncRNA_AR_1.4437, 4_A375_EGR1_1.4566	90, 216, 22862	up gene, up gene, downstream	1 1 1 17.5 19.5 15 2	2_A375_chr37_plus_lncRNA_AR_1	30	Gene PRPF31	NY-BR-99, PRP31, PRP31 processing factor 31 homolog, RP11, PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	NM_015629, XCT120213.2, XCT235497.0	222407_s_at, 222408_s_at, 223604_at	NP_056443.2, EWT2190.1, EWT2191.1
GeneID:46	CNOT3	19	54,641,456	54,659,446	18,010	+	2	2_A375_chr37_plus_lncRNA_AR_1.4437, 4_A375_EGR1_1.4566	21854, 36	downstream, up gene	0 1 1 10 14 14.5 2	4_A375_EGR1_1.1	19	Gene CNOT3	CNOT3, LENG2, NOTH, NOT3,	CCR4-NOT transcription complex, subunit 3	NM_014516, XCT198238.1, XCT196238.1, XCT229709.0	203239_s_at, 211141_s_at, 229413_at	NP_055331.1, EWT2192.1, EWT2193.1, EWT2194.1
GeneID:79	LENG1	19	54,659,377	54,663,448	4,089	-	1	4_A375_EGR1_1.4437, 4_A375_EGR1_1.4567	336, -1898	up gene, upstream	0 1 1 9.5 14 14.5 2	4_A375_EGR1_1.1	19	Gene LENG1	LENG1	leukocyte receptor cluster (LRC) member 1	NM_024316, XCT120083	232016_at	NP_077292.1, EWT2199.1
GeneID:14	TMC4	19	54,665,833	54,676,944	10,111	-	2	2_A375_chr37_plus_lncRNA_AR_1.4437, 4_A375_EGR1_1.4567	13824, 4912	downstream, up gene	0 1 1 9.5 14 14.5 2	2_A375_chr37_plus_lncRNA_AR_1	19	Gene TMC4	MGC29329, TMC4	transmembrane channel-like 4	NM_001145933, NM_144856, XCT120073.2, XCT235036.0, XCT235037.0	226403_at	NP_001139775.1, NP_653207.1, EWT2195.1, EWT2196.1, EWT2197.1, EWT2198.1
GeneID:79	MBOAT7	19	54,677,108	54,690,703	19,827	-	1	4_A375_EGR1_1.4567	21701	downstream	0 1 1 10 9 10 1	4_A375_EGR1_1.1	10	Gene MBOAT7	LPAT, FLJ41264, OACT7, hMBOAT_7, BB1, MBOAT7, LRC4, LENG4	membrane bound O-acyltransferase domain-containing	NM_031148933, NM_031148932, NM_024296, NM_031148936, XCT120343.2, XCT229620.0, XCT229621.0, XCT229622.0, XCT229623.0	230179_s_at, 231027_s_at	NP_001139533.1, NP_001139534.1, NP_077274.3, NP_001139535.1, EWT2200.1, EWT2201.1, EWT2202.1, EWT2203.1, EWT2204.1
GeneID:79	TSEN34	19	54,694,119	54,696,394	4,276	+	1	4_A375_EGR1_1.4568	10734	downstream	0 0 1 14 15 15 1	4_A375_EGR1_1.1	15	Gene TSEN34	LENG5, TSEN34, SENDA, PCH2C, SEN34,	RNA splicing endonuclease 34 homolog (S. cerevisiae)	NM_031077448, NM_024073, XCT120053.2, XCT198281.1, XCT198282.1, XCT198284.1, XCT229705.0	218152_s_at	NP_001078144.1, NP_076992.2, EWT2204.1, EWT2205.1, EWT2206.1, EWT2207.1, EWT2208.1
GeneID:82	RPS9	19	54,704,726	54,711,515	6,789	+	1	4_A375_EGR1_1.4568	127	up gene	0 0 1 14 15 15 1	4_A375_EGR1_1.1	15	Gene RPS9	S9, RPS9		NM_001013, XCT207676.0, XCT229677.0, XCT207678.0, XCT207679.0, XCT207681.0, XCT229752.0, XCT229753.0	1557661_at, 214317_x_at, 217747_s_at	NP_001004.2, EWT2209.1, EWT2210.1, EWT2211.1, EWT2212.1, EWT2213.1, EWT2214.1, EWT2215.1
GeneID:79	ULK4B	19	54,740,489	54,748,724	8,235	-	1	4_A375_EGR1_1.4569	2948	up gene	0 0 1 5 9 14 1	4_A375_EGR1_1.1	14	Gene LILRA6	LILRA6, LILRB6, ILT8, LILRB3, ILT3, CD85a	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	NM_024318	206894_x_at	NP_377294.2
GeneID:10	ULK5B3	19	54,754,270	54,761,167	6,897	-	1	4_A375_EGR1_1.4569	10691	downstream	0 0 1 5 9 14 1	4_A375_EGR1_1.1	14	Gene LILRB3	LILRB3, LILRB3, ILT5, CD85e,	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	NM_006840, NM_001081442, NM_001081443, XCT229623.0, XCT229627.0, XCT229628.0, XCT229629.0, XCT235092.0	206836_at	NP_006831.1, NP_001074911.1, NP_001074912.1, EWT2215.1, EWT2216.1, EWT2217.1, EWT2218.1, EWT2222.1
GeneID:33	ULK4A3	19	54,816,353	54,824,409	8,056	-	2	1_A375_chr37_minus_lncRNA_AR_1.3988, 2_A375_chr37_plus_lncRNA_AR_1.4438	6303, 6237	downstream, downstream	1 1 0 16 16 16 1	1_A375_chr37_minus_lncRNA_AR_1.3988	16	Gene LILRA3	ILT7, ILT11, CD85, LIR5, CD85f, LILRA3	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 3	NM_181979, NM_181983, NM_181986, NM_021250	1559854_s_at, 1559943_s_at, 215838_at, 215839_at	NP_878894.1, NP_071714.1, NP_997572.1, NP_071715.1
GeneID:53	TTYH1	19	54,926,655	54,946,070	21,416	+	2	4_A375_EGR1_1.4570, 4_A375_EGR1_1.4571	10817, 19461	up gene, up gene	0 0 1 5 8 14.5 2	4_A375_EGR1_1.1	15	Gene TTYH1	TTYH1		NM_020539, NM_001003597, XCT117584.4, XCT199524.2, XCT229707.1, XCT229709.1, XCT229710.1, XCT235479.0, XCT235479.0, XCT235499.0	219419_at	NP_065710.1, NP_001003597.1, EWT2230.1, EWT2240.1, EWT2244.1, EWT2245.1, EWT2241.1, EWT2242.1, EWT2243.1, EWT2246.1
GeneID:11	LENG8	19	54,960,993	54,973,196	12,131	+	3	1_A375_chr37_minus_lncRNA_AR_1.3989, 1_A375_chr37_minus_lncRNA_AR_1.3990, 2_A375_chr37_plus_lncRNA_AR_1.4439, 2_A375_chr37_plus_lncRNA_AR_1.4440, 4_A375_EGR1_1.4572	238, 13291, 251, 12127, 22297	up gene, downstream, up gene, downstream, downstream	1 1 1 13.67 17.33 15.33 3	2_A375_chr37_plus_lncRNA_AR_1	27	Gene LENG8	KIAA1822, MGC40108, LENG8, pp10042	leukocyte receptor cluster (LRC) member 8	NM_020923, XCT229709.2, XCT235088.0, XCT235089.0	224919_s_at	NP_443137.1, EWT2230.1, EWT2240.1, EWT2244.1
GeneID:84	LENG9	19	54,972,978	54,974,894	1,916	-	3	1_A375_chr37_minus_lncRNA_AR_1.3990, 2_A375_chr37_plus_lncRNA_AR_1.4440, 4_A375_EGR1_1.4572	-582, -699, -7539	upstream, upstream, upstream	1 1 0 12.3 12.3 14 2	1_A375_chr37_minus_lncRNA_AR_1	20	Gene LENG9	LENG9	leukocyte receptor cluster (LRC) member 9	NM_198998, XCT196223.2	1554569_at	NP_943339.2, EWT2239.1
GeneID:14	CDC42EP5	19	54,976,210	54,994,422	8,212	-	3	1_A375_chr37_minus_lncRNA_AR_1.3990, 2_A375_chr37_plus_lncRNA_AR_1.4440, 4_A375_EGR1_1.4572	6966, 6830, 1990	downstream, downstream, up gene	1 1 0 12.5 12.5 14 2	1_A375_chr37_minus_lncRNA_AR_1	20	Gene CDC42EP5	Borg5, MGC21945, MGC17153, CDC42EP5, CEP5	CDC42 effector protein (Rho GTPase binding) 5	NM_145057, XCT164299.3	227850_s_at	NP_839949.2, EWT2232.1
GeneID:36	LAIR2	19	55,014,013	55,021,897	7,884	+	1	1_A375_chr37_minus_lncRNA_AR_1.3991, 2_A375_chr37_plus_lncRNA_AR_1.4441	14887, 14755	downstream, downstream	1 1 0 15 29 6 1	2_A375_chr37_plus_lncRNA_AR_1	29	Gene LAIR2	CD306, LAIR2, MGC7839	leukocyte-associated immunoglobulin-like receptor 2	NM_002350, NM_021270, XCT170039.2, XCT170097.2	207329_s_at	NP_002270.2, NP_067134.1, EWT2233.1, EWT2234.1
GeneID:53	GP6	19	55,025,073	55,049,652	24,559	-	1	4_A375_EGR1_1.4573	4936	upstream	0 0 1 5 7 15 1	4_A375_EGR1_1.1	15	Gene GP6	GPVI, GP6, GPVI	glycoprotein VI (platelet)	NM_031083899, NM_016953, XCT113373.2, XCT229716.0, XCT229720.0	220326_s_at	NP_031077885.1, NP_057447.4, EWT2224.1, EWT2225.1, EWT2226.1
GeneID:11	RDH13	19	55,035,992	55,060,914	24,922	+	1	4_A375_EGR1_1.4573	34768	up gene	0 0 1 5 8 13 1	4_A375_EGR1_1.1	13	Gene RDH13	RDH13, SDR7C2, FLJ39479, DKFZp313H0743	retinol dehydrogenase 13 (all-trans-and 9-cis)	NM_139142, NM_001143975, NR_027081, NR_027082, XCT199229.1, XCT229719.0, XCT229720.0	223449_at, 223450_s_at, 227360_at, 233049_at	NP_631911.1, NP_001137443.1, EWT2221.1, EWT2222.1, EWT2223.1
GeneID:84	EPS8L1	19	55,057,221	55,099,291	12,070	+	1	4_A375_EGR1_1.4574	20307	downstream	0 0 1 4 8 17 1	4_A375_EGR1_1.1	17	Gene EPS8L1	EPS8L1, EPS8R1, PP10866, MGC2316, FLJ20356, ORC2, MGC4542	EPS8-like 1	NM_133180, NM_017729, XCT113431.1, XCT192483.1, XCT192484.1, XCT192485.0	210776_s_at, 218779_x_at, 221605_s_at, 221955_s_at, 81628_at	NP_573447.2, NP_060190.2, EWT2230.1, EWT2231.1, EWT2232.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_2_A375_4_A375_1_A375_2_A375_4_A375_Adj Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
GeneID:5467778	PPP1R12C	19	55,802,251	55,826,927	24,676	-	2	4_A375_DSR1.1.4674, 4_A375_DSR1.1.4675	21119, 19887	vs gene, vs gene	0	0	1	8	8	17	2	4_A375_DSR1.1.1	17	Gene PPP1R12C	MBS85, DKFZp434O0612, p84, PPP1R12C, LENG3	protein phosphatase 1, regulatory (inhibitor) subunit 12C	NM_017607, ICT113411.3, ICT2297169.0, ICT2297169.1, ICT2293618.0	223152_at	NP_060077.1, ENST00236.1, ENAT02232.1, ENAT02330.1, ENAT2233.1
GeneID:8655	SYT5	19	55,864,469	55,891,720	27,251	-	4	1_A375_uhk7_mrust_lncRNA_AR..1.3393, 1_A375_uhk07_mrust_lncRNA_AR..1.3694, 2_A375_uhk07_dlust_lncRNA_AR..1.4443, 2_A375_uhk07_dlust_lncRNA_AR..1.4443, 2_A375_uhk07_dlust_lncRNA_AR..1.4444, 2_A375_uhk07_dlust_lncRNA_AR..1.4443	160, -9176, 405, 9125	vs gene, upstream, vs gene, upstream	1	1	0	23.5	22	6.5	2	1_A375_uhk7525_mrust_lncRNA_AR..1	Gene SYT5	SYT5		synaptotagmin V	NM_003180, ICT116356.2, ICT1552461.0, ICT2303047.0	206161_s_at, 206162_at	NP_003171.2, ENAT2348.1, ENAT2348.1, ENAT2347.1
GeneID:3794	PTPRH	19	55,892,815	55,720,874	28,259	-	6	1_A375_uhk7_mrust_lncRNA_AR..1.3393, 1_A375_uhk07_mrust_lncRNA_AR..1.3694, 1_A375_uhk07_dlust_lncRNA_AR..1.3695, 2_A375_uhk07_dlust_lncRNA_AR..1.4443, 2_A375_uhk07_dlust_lncRNA_AR..1.4444, 2_A375_uhk07_dlust_lncRNA_AR..1.4443	29222, 19916, 2964, 2632, 29026, -7574	downstream, vs gene, upstream,downstream, vs gene, upstream	1	1	0	29.33	30.67	9	3	2_A375_uhk448_mrust_lncRNA_AR..1	Gene PTPRH	MGC133089, PTPRH, MGC133088, SHP1, PLJ5935	protein tyrosine phosphatase, receptor type, H	NM_002842, NM_001161443, ICT107229.2	208300_at	NP_002833.3, NP_001154912.1, ENAT2346.1
GeneID:2357	TMEM88B	19	55,736,002	55,740,652	2,830	-	2	1_A375_uhk07_mrust_lncRNA_AR..1.3695, 2_A375_uhk07_dlust_lncRNA_AR..1.4443	12664, 12164	Downstream, Downstream	1	1	0	41	46	10	1	2_A375_uhk446_mrust_lncRNA_AR..1	Gene TMEM88B	MGC33036, TMEM88B	trans-membrane protein 88B	NM_175564, ICT2305924.0, ICT2305925.0	225756_at	NP_796183.3, ENAT2351.1, ENAT2350.1
GeneID:2337	SAPS1	19	55,741,147	55,770,035	28,891	-	4	1_A375_uhk7_mrust_lncRNA_AR..1.3696, 2_A375_uhk07_dlust_lncRNA_AR..1.4445, 2_A375_uhk07_dlust_lncRNA_AR..1.4676, 4_A375_DSR1..1.4677	-598, -490, 994, 256	upstream, upstream, vs gene, upstream	1	1	1	17.5	22	16	2	2_A375_uhk631_mrust_lncRNA_AR..1	Gene SAPS1	SAPS1, MGC150165, MGC142093, PPP4R1, SAPS1, SVH1115, PP2966	SAPS domain family, member 1	NM_015931, ICT111053.3, ICT1552460.1, ICT2309220.0	209229_s_at	NP_3357458.3, ENAT2336.1, ENAT2332.1, ENAT2332.1
GeneID:2339	HSPBP1	19	55,775,991	55,791,791	15,760	-	3	1_A375_uhk07_mrust_lncRNA_AR..1.3696, 2_A375_uhk07_dlust_lncRNA_AR..1.4446, 2_A375_DSR1..1.4676, 4_A375_DSR1..1.4677,	21947, 21220, 22407, 21479, 187	Downstream, Downstream, Downstream, Downstream, vs gene	1	1	1	16.33	21.33	16	3	2_A375_uhk631_mrust_lncRNA_AR..1	Gene HSPBP1	FIGC, HSPBP1	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	NM_031139.2, NM_001123576.1, NP_112099.3, ENAT2353.1, ENAT02350.1, ENAT02351.1, ENAT02350.1	202415_s_at	NP_001123578.1, NP_112099.3, ENAT2353.1, ENAT02350.1, ENAT02351.1, ENAT02350.1
GeneID:6446	BRSK1	19	55,799,934	55,823,930	23,996	+	1	4_A375_DSR1..1.4676	-3990	upstream	0	0	1	14	20	16	1	4_A375_DSR1..1.1	16	Gene BRSK1	FLJ43009, BRSK1, KIAA1011	BR serine/threonine kinase 1	NM_032430, ICT1950006.1, ICT2305015.0, ICT2947.0	1552604_a_at	NP_1150061, ENAT2338.1, ENAT02361.1, ENAT02361.1
GeneID:1088	CCDC62	19	55,861,070	55,866,162	5,112	-	2	4_A375_DSR1..1.4675, 4_A375_DSR1..1.4676	-6974, -7238	upstream, upstream	0	0	1	4.5	9	13.5	2	4_A375_DSR1..1.1	16	Gene CCDC62	MGC119084, CT95, FLJ46422, CCDC62, CCXV62	coiled-coil domain containing 62	NM_144613, ICT2344681.0, ICT2947.4	1553387_a_at	NP_6322142.2, ENAT02366.1, ENAT02367.1
GeneID:2587	FAM71E2	19	55,866,276	55,874,620	8,344	-	2	4_A375_DSR1..1.4679, 4_A375_DSR1..1.4680	2964, 1212	vs gene, vs gene	0	0	1	4.5	5	13.5	2	4_A375_DSR1..1.1	16	Gene FAM71E2	FAM71E2, MGC23545, DKFZp434G1729, C79unit8	family with sequence similarity 71, member E2	NM_031145632	1552990_at, 1564319_at	NP_5011335741
GeneID:3845	IL11	19	55,875,707	55,881,814	6,107	-	3	4_A375_DSR1..1.4679, 4_A375_DSR1..1.4680, 4_A375_DSR1..1.4681	9305, 6406, -6216	Downstream, Downstream, Downstream, vs gene	0	0	1	7.33	8	15.33	3	4_A375_DSR1..1.1	16	Gene IL11	IL11, IL11_HUMAN	interleukin 11	NM_000641, ICT2302333.3	206924_at, 206926_s_at	NP_0006222.1, ENAT02371.1
GeneID:1477	TMEM190	19	55,888,236	55,889,812	1,576	+	2	4_A375_DSR1..1.4681, 4_A375_DSR1..1.4682	-172, 9100	upstream, downstream	0	0	1	14.5	15	19	2	4_A375_DSR1..1.1	23	Gene TMEM190	MGAC1, THEM190, MGC149302, MGC149301	trans-membrane protein 190	NM_139172, ICT2294764	1552694_at	NP_6314111, ENAT02372.1
GeneID:3829	LOC3888	19	55,890,612	55,899,427	8,815	-	2	4_A375_DSR1..1.4681, 4_A375_DSR1..1.4682	7985, -1883	Downstream, upstream	0	0	1	14.5	15	19	2	4_A375_DSR1..1.1	23	Gene LOC388884		hypothetical protein LOC388884	NM_001190764	2239938_at	NP_9011179932.1
GeneID:8169	RPL26	19	55,897,300	55,903,453	6,153	+	2	4_A375_DSR1..1.4681, 4_A375_DSR1..1.4682	-9266, 12	upstream, vs gene	0	0	1	14.5	15	19	2	4_A375_DSR1..1.1	23	Gene RPL26	FLJ43107, RPL26, L26	ribosomal protein L26	NM_0011389134, NM_000991, NM_001138105, NM_001138106, NM_001138107, ICT1952108.1, ICT1952190.1, ICT2294.2	2000853_x_at_212323_at	NP_0001139616.1, NP_000982.2, NP_001123627.1, NP_001129805.1, NP_001129809.1, ENAT02376.1, ENAT02374.1, ENAT02375.1
GeneID:2737	UBE2S	19	55,912,650	55,919,325	6,675	-	2	1_A375_uhk07_mrust_lncRNA_AR..1.3397, 2_A375_uhk07_dlust_lncRNA_AR..1.4447	125, -227	vs gene, upstream	1	1	0	17	21	11	1	2_A375_uhk621_mrust_lncRNA_AR..1	Gene UBE2S	E2EFF, E2-EPF, UBE2S, EPF3	ubiquitin conjugating enzyme E2S	NM_014501, ICT1960779.1	202779_s_at	NP_0303182, ENAT2377.1
GeneID:7235	SH3GA7	19	55,940,103	55,954,200	14,725	-	3	1_A375_uhk7_mrust_lncRNA_AR..1.3398, 2_A375_uhk07_dlust_lncRNA_AR..1.4448, 2_A375_uhk07_dlust_lncRNA_AR..1.4656, 4_A375_DSR1..1.4658,	5382, 5254, 9814, 742, -9095	vs gene, vs gene, vs gene, vs gene, upstream	1	1	1	17	17.75	18	4	2_A375_uhk632_mrust_lncRNA_AR..1	Gene SH3GA7	FLJ43760, FLJ37640, MGC129355, FLJ36341, MGC154402, SH3A7, DKFZp647H0214	sh3 domain protein 7 (transcript variant 1)	NM_031145578	NP_0011338461	
GeneID:7918	SOCS2	19	55,964,345	55,970,049	5,704	-	2	4_A375_DSR1..1.4685, 4_A375_DSR1..1.4688	13721, -2187	Downstream, upstream	0	0	1	8	9	14	2	4_A375_DSR1..1.1	14	Gene SOCS2	SOCS2, FLJ10520	suppressor of cytokine signaling 2	NM_003742, NM_001135601, NM_001135602, ICT1952102.1, ICT1957618.1, ICT2293085.0, ICT2293086.0, ICT2950.2	2159951_at	NP_0709166.1, NP_001128673.1, NP_001129674.1, ENAT02378.1, ENAT02382.1, ENAT02381.1, ENAT02383.1
GeneID:9897	ZNF626	19	55,967,899	55,999,834	31,935	+	3	1_A375_uhk7_mrust_lncRNA_AR..1.3399, 2_A375_uhk07_dlust_lncRNA_AR..1.4450, 2_A375_uhk07_dlust_lncRNA_AR..1.4450	731, 299, 677	vs gene, vs gene, vs gene	1	1	0	23	30.5	9.5	2	2_A375_uhk640_mrust_lncRNA_AR..1	Gene ZNF626	MGC103179, ZNF626, ZNF626, ZBC	zinc finger protein 626	NM_033113	236289_at	NP_149154.2
GeneID:5317	NAT14	19	55,996,994	55,999,955	2,941	+	3	1_A375_uhk07_mrust_lncRNA_AR..1.3399, 2_A375_uhk07_dlust_lncRNA_AR..1.4449, 2_A375_uhk07_dlust_lncRNA_AR..1.4450	-5162, -5635, -5015	upstream, upstream, upstream	1	1	0	23	30.5	6.5	2	2_A375_uhk640_mrust_lncRNA_AR..1	Gene NAT14	KLP1, NAT14	N-acetyltransferase 14 (GCN5-related, putative)	NM_030374, ICT1952113.1, ICT2293842.2	223264_at	NP_3851111, ENAT02355.1, ENAT02358.1
GeneID:2852	SSC3D	19	55,999,070	56,030,468	30,398	+	2	1_A375_uhk7_mrust_lncRNA_AR..1.3400, 2_A375_uhk07_dlust_lncRNA_AR..1.4451	31266, 31266	Downstream, Downstream	1	1	0	19	38	5	1	2_A375_uhk636_mrust_lncRNA_AR..1	Gene SSC3D	SSC3D	suppressor of cytokine signaling sck glycoprotein	NM_001144955	2332226_at	NP_3201139622.1
GeneID:8429	SBK2	19	56,041,100	56,045,425	7,326	-	2	1_A375_uhk7_mrust_lncRNA_AR..1.3400, 2_A375_uhk07_dlust_lncRNA_AR..1.4451	17299, 17299	Downstream, Downstream	1	1	0	19	38	5	1	2_A375_uhk636_mrust_lncRNA_AR..1	Gene SBK2	SBK2, BSK089	SH3-binding domain kinase family, member 2	NM_001101401	NP_0010942712	
GeneID:1673	ZNF379	19	56,080,891	56,092,211	11,320	-	1	2_A375_uhk07_dlust_lncRNA_AR..1.4452	7203	upstream	0	0	1	12	20	16	1	2_A375_uhk620_mrust_lncRNA_AR..1	Gene ZNF379	FLJ20433, ZNF379	zinc finger protein 379	NM_152600, ICT2341136.0	229140_at, 229703_at	NP_6896112, ENAT02390.1
GeneID:5422	FIZ1	19	56,102,707	56,110,993	8,286	+	4	1_A375_uhk7_mrust_lncRNA_AR..1.3701, 1_A375_uhk07_dlust_lncRNA_AR..1.4432, 2_A375_uhk07_dlust_lncRNA_AR..1.4453, 2_A375_uhk07_dlust_lncRNA_AR..1.4697	-582, 17949, -496, -99	upstream, downstream, upstream, upstream	1	1	1	22	22	15	2	1_A375_uhk632_mrust_lncRNA_AR..1	Gene FIZ1	ZNF790, FLJ14795, FIZ1, FLJ00416	FLT3-interacting zinc finger 1	NM_032936, ICT2297147.0, ICT2296853.0	226987_at, 229983_s_at	NP_1162253.2, ENAT02392.1, ENAT02391.1
GeneID:1427	ZNF524	19	56,111,750	56,114,304	2,774	+	3	1_A375_uhk7_mrust_lncRNA_AR..1.3701, 2_A375_uhk07_dlust_lncRNA_AR..1.4452, 4_A375_DSR1..1.4697	-276, -355, -735	upstream, upstream, upstream	1	1	1	32	34	14	1	1_A375_uhk632_mrust_lncRNA_AR..1	Gene ZNF524	ZNF524, MGC22143	zinc finger protein 524	NM_152219	2239803_at	NP_6943511
GeneID:3157	ZNF350	19	56,132,202	56,134,939	2,444	+	6	1_A375_uhk7_mrust_lncRNA_AR..1.3702, 1_A375_uhk07_mrust_lncRNA_AR..1.3703, 2_A375_uhk07_dlust_lncRNA_AR..1.4454, 2_A375_uhk07_dlust_lncRNA_AR..1.4455, 4_A375_DSR1..1.4698, 4_A375_DSR1..1.4699, 4_A375_DSR1..1.4696, 4_A375_DSR1..1.4691	-1760, 7000, 5364, 7096, -352, 3976, 7000, 7344	upstream, downstream, vs gene, downstream, upstream, upstream, downstream, downstream, downstream	1	1	1	20.4	22.2	17	5	2_A375_uhk644_mrust_lncRNA_AR..1	Gene ZNF350	ZNF350		NM_207110, NM_0182002, NM_0018542S, ICT2296594.0	2207425_s_at	NP_9997851, NP_0972981, NP_0011988193, ENAT02399.1
GeneID:5437	ZNF561	19	56,134,969	56,146,969	12,000	+	8	1_A375_uhk7_mrust_lncRNA_AR..1.3702, 1_A375_uhk07_mrust_lncRNA_AR..1.3703, 2_A375_uhk07_dlust_lncRNA_AR..1.4454, 2_A375_uhk07_dlust_lncRNA_AR..1.4455, 4_A375_DSR1..1.4698, 4_A375_DSR1..1.4699, 4_A375_DSR1..1.4696, 4_A375_DSR1..1.4691	-4382, 4406, -10, 4302, -2906, 1852, 4406, 4706	upstream, downstream, upstream, downstream, upstream, downstream, downstream, downstream	1	1	1	20.4	22.2	17	5	2_A375_uhk644_mrust_lncRNA_AR..1	Gene ZNF561	ZNF561, FLJ22550, HSPC109	zinc finger protein 561	NM_018535, ICT2295598.0	223389_s_at	NP_0397419.1, ENAT02400.1
GeneID:2910	CCDC108	19	56,158,764	56,164,327	5,573	+	8	1_A375_uhk7_mrust_lncRNA_AR..1.3702, 1_A375_uhk07_mrust_lncRNA_AR..1.3703, 2_A375_uhk07_dlust_lncRNA_AR..1.4454, 2_A375_uhk07_dlust_lncRNA_AR..1.4455, 4_A375_DSR1..1.4698, 4_A375_DSR1..1.4699, 4_A375_DSR1..1.4696, 4_A375_DSR1..1.4691	-6339, 436, 3976, 934, -6954, -2366, 436, 932	upstream, vs gene, downstream, vs gene, upstream, downstream, vs gene, vs gene	1	1	1	20.4	22.2	17	5	2_A375_uhk644_mrust_lncRNA_AR..1	Gene CCDC108	ZNF591, CCDC108, HSUP020	coiled-coil domain containing 108	NM_0183391, ICT1957820.1	2207668_s_at	NP_3974332, ENAT02401.1
GeneID:1119	U2AF2	19	56,165,416	56,186,982	20,866	+	7	1_A375_uhk7_mrust_lncRNA_AR..1.3703, 1_A375_uhk07_mrust_lncRNA_AR..1.3704, 2_A375_uhk07_dlust_lncRNA_AR..1.4453, 2_A375_uhk07_dlust_lncRNA_AR..1.4456, 4_A375_DSR1..1.4698, 4_A375_DSR1..1.4699, 4_A375_DSR1..1.4691	-4924, 21112, -5928, 20992, -9363, -9324, -5440	upstream, downstream, upstream, downstream, upstream, upstream, upstream, upstream	1	1	1	24.33	25	19.67	3	2_A375_uhk644_mrust_lncRNA_AR..1	Gene U2AF2	U2AF65, U2AF2	U2 snRNP auxiliary factor 2	NM_007279, NM_0010134763, NM_0010134764, ICT1952125.1, ICT1955388.1, ICT1955389.1, ICT2296593.0, ICT53678.3	214171_s_at, 214551_s_at, 216382_s_at, 228509_at	NP_0090163.1, NP_0010014981, NP_0010134982, ENAT02403.1, ENAT02403.1, ENAT02404.1
GeneID:2918	EPN1	19	56,186,961	56,207,103	20,372	-	5	1_A375_uhk7_mrust_lncRNA_AR..1.3704, 2_A375_uhk07_dlust_lncRNA_AR..1.4456, 4_A375_DSR1..1.4692	-55, -181, 20763	upstream, upstream, upstream	1	1	1	12	11.5	10	2	1_A375_uhk621_mrust_lncRNA_AR..1	Gene EPN1	EPN1		NM_0011300721, NM_0131333, NM_0011300711, NM_0011300731, ICT1952123.1, ICT1952124.1, ICT2294998.0, ICT53673.1	2211411_x_at, 228997_x_at	NP_0011238441, NP_0743482, NP_0011238431, ENAT02403.1, ENAT02408.1, ENAT02407.1
GeneID:2338	NUP9	19	56,210,765	56,249,765	29,970	+	1	4_A375_DSR1..1.4692	36424	Downstream	0	0	1	3	9	15	1	4_A375_DSR1..1.1	15	Gene NUP9	NOD9, NALP9, CLR19.1, NLRP9, PAN12	NLR family, pyrin domain containing 12	NM_1785320, ICT2297161.1, ICT2291812.0	1553527_at	NP_7897892, ENAT02411.1, ENAT02412.1
GeneID:2339	NUP11	19	56,296,765	56,345,126	51,365	+	1	1_A375_uhk7_mrust_lncRNA_AR..1.3705	27992	vs gene	1	1	0	20	17	5	1	1_A375_uhk620_mrust_lncRNA_AR..1	Gene NUP11	FLJ39273, PYPAF7, PYPAF9, NALP11, PAN10, NLRP11, NOD17, CLR19.8	NLR family, pyrin domain containing 11	NM_149307, ICT2341136.0, ICT2341137.0	1552531_a_at	NP_6594442, ENAT02416.1, ENAT2415.1
GeneID:1237	NLRP5	19	56,311,092	56,373,178	62,084	+	1	2_A375_uhk07_dlust_lncRNA_AR..1.4457	18092	vs gene	0	0	1	8	17	5	1	2_A375_uhk617_mrust_lncRNA_AR..1	Gene NLRP5	NLRP5, PYPAF5, CLR19.5, NALP5, MATER, PAN11	NLR family, pyrin domain containing 5	NM_153447	1552455_at	NP_7851464
GeneID:1237	ZNF787	19	56,396,702	56,832,849	33,317	-	2	4_A375_DSR1..1.4693, 4_A375_DSR1..1.4694	17990, 710	vs gene, vs gene	0	0	1	9.5	8.5	16.5	2	4_A375_DSR1..1.1	19	Gene ZNF787	ZNF787, TIF20	zinc finger protein 787	NM_0010028361, ICT1705926.4	1557656_at, 213402_at	NP_0010028362, ENAT02423.1
GeneID:3111	ZNF444	19	56,852,356	56,872,362	19,706	+	1	2_A375_uhk07_dlust_lncRNA_AR..1.4458	105	upstream	0	0	1	15	26	9	1	2_A375_uhk626_mrust_lncRNA_AR..1	Gene ZNF444	ZSCAN17, FLJ11137, EZFX, ZNF444, EZF2	zinc finger protein 444	NM_0183377, ICT1952126.1, ICT1955387.1, ICT1955388.1, ICT1955389.1, ICT2296593.0, ICT53662.4	2207707_at, 50378_at	NP_3905572, ENAT02427.1, ENAT02424.1, ENAT02425.1, ENAT02426.1, ENAT02430.1, ENAT02428.1, ENAT02429.1
GeneID:9555	ZSCAN20	19	56,891,773	56,896,666	7,893	+	1	1_A375_uhk07_mrust_lncRNA_AR..1.3708	12615	Downstream	1	0	0	16	15	14	1	1_A375_uhk616_mrust_lncRNA_AR..1	Gene ZSCAN20	ZNF450, ZSC-NAD2	zinc finger and SCAN domain containing 20	NM_0012725901	2_3017259301	
GeneID:1939	LOC10030	19	56,815,305	56,821,819	6,514	+	1	2_A375_uhk07_dlust_lncRNA_AR..1.4459	12839	Downstream	0	0	1	14	16	11	1	2_A375_uhk616_mrust_lncRNA_AR..1	Gene LOC100509274		hypothetical LOC100509274	XR_103490		
GeneID:3536	BC03899	19	56,905,045	56,910,537	5,492	+	1	4_A375_DSR1..1.4695	93279	Downstream	0	0	1	15	12	16	1	4_A375_DSR1..1.1	16	Gene BC035925		hypothetical LOC388745	XR_111910, XR_103499, XR_115326	2312560_at, 2325026_at	
GeneID:7949	ZNF583	19	56,915,365	56,936,400	21,217	+	1	4_A375_DSR1..1.4695	41	vs gene	0	0	1	15	12	16	1	4_A375_DSR1..1.1	16	Gene ZNF583	MGC132237, FLJ12030, ZNF583	zinc finger protein 583	NM_152476, NM_0011539801, NM_0011539802, ICT53670.4	1552221_at, 1565725_at	NP_6896912, NP_0011539331, ENAT02432.1
GeneID:3732	ZNF471	19	57,019,212	57,040,370	21,158	+	1	2_A375_uhk07_dlust_lncRNA_AR..1.4460	30724	Downstream	0	0	1	15	20	19	1	2_A375_uhk620_mrust_lncRNA_AR..1	Gene ZNF471	ERF1, MGC150885, ZNF471, ZIR71, KIAA1356, MGC130897	zinc finger protein 471	NM_0309313, ICT1962088.3, ICT2295897.0, ICT2294999.0	2211923_s_at, 2321177_at	NP_0966984.2, ENAT02438.1, ENAT02440.1, ENAT02481.1
GeneID:1467	ZFP30	19	57,050,317	57,066,170	17,853	+	1	2_A375_uhk07_dlust_lncRNA_AR..1.4460	381	upstream	0	0	1	15	20	19	1	2_A375_uhk620_mrust_lncRNA_AR..1	Gene ZFP30	ZNF30, KIAA1431, mKIAA1431, DKFZp686I03230, MGC15634, ZFP30	zinc finger protein 30 homolog (mouse)	NM_0330230, ICT1701008.2, ICT2295870.0, ICT2295872.0	2319412_at, 2343031_s_at, 234037_x_at, 240565_at	NP_8865791, ENAT02450.1, ENAT02454.1, ENAT02455.1
GeneID:1013	LOC10030	19	57,056,935	57,076,762	21,847	-	2	2_A375_uhk07_dlust_lncRNA_AR..1.4460, 2_A375_uhk07_dlust_lncRNA_AR..1.4461	20648, 190	Downstream, vs gene	0	0	1	15	19	15	2	2_A375_uhk620_mrust_lncRNA_AR..1	Gene LOC100509419		hypothetical LOC100509419	XR_111909, XR_103503, XR_115326		
GeneID:3827	ZNF470	19	57,076,090	57,094,362	18,272	+	1	4_A375_uhk07_dlust_lncRNA_AR..1.4461	290	upstream	0	0	1	11	16	11	1	4_A375_uhk616_mrust_lncRNA_AR..1	Gene ZNF470	ZNF470, FLJ38648, CZF-1, FLJ39175	zinc finger protein 470	NM_0310031666, ICT1703876.3	2342121_at	NP_0010031666.3, ENAT02466.1
GeneID:3827	ZNF71	19	57,108,864	57,135,550	26,686	+	1	2_A375_uhk07_dlust_lncRNA_AR..1.4462	56	vs gene	0	0	1	9	16	11	1	2_A375_uhk616_mrust_lncRNA_AR..1	Gene ZNF71	ZNF71, EZF17	zinc finger protein 71	NM_0212118, ICT1952126.1, ICT53678.3	2268514_at, 2325543_x_at, 234370_at, 234375_at	NP_0010031, ENAT02487.1, ENAT02485.1
GeneID:1467	LOC14767	19	57,134,527	57,166,814	32,287	+	3	1_A375_uhk7_mrust_lncRNA_AR..1.3707, 2_A375_uhk07_dlust_lncRNA_AR..1.4463, 4_A375_DSR1..1.4696	-4491, -4939, 20861	upstream, upstream, downstream	1	1	1	71	76.3	11.3	2	2_A375_uhk644_mrust_lncRNA_AR..1	Gene LOC147670		hypothetical protein LOC147670	NM_0011936261	1557431_at	NP_9011165571
GeneID:9543	ZNF655	19	57,174,955	57,184,348	9,393	-	2	4_A375_DSR1..1.4696, 4_A375_DSR1..1.4697	6150, 1014	vs gene, vs gene	0	0	1	8	16	17	2	4_A375_DSR1..1.1	16	Gene ZNF655	ZNF655, BC27295_2	zinc finger protein 655	NM_0310035501	2155261_s_at	NP_0310035501
GeneID:2327	ZNF85	19	57,205,915	57,232,007	26,162	-	2	4_A375_DSR1..1.4696, 4_A375_DSR1..1.4697	3867, 1038	vs gene, vs gene	0	0	1	8.5	9	16	2	4_A375_DSR1..1.1	17	Gene ZIM2	ZIM2, ZNF858	zinc finger, imprinted 2	NM_0135393, NM_0011448328, NM_0011448327	2208833_at	NP_5361763, NP_0011139793.1, NP_0011337351
GeneID:5178	PEG3	19	57,321,445	57,352,094	30,649	-	2	4_A375_DSR1..1.4696, 4_A375_DSR1..1.4697	2864, 1833	vs gene, vs gene	0	0	1	8.5	9	16	2	4_A375_DSR1..1.1	17	Gene PEG3	PW1, PEG3, DKFZp434N016, ZSC-HN24, KIAA0287, ZNF904	paternally expressed 3	NM_0060210, NM_0011449184, NM_0011449183, NM_0011449186, NM_0011449187	2209242_at, 2209243_s_at, 2209860_s_at	NP_9982011.1, NP_0011396361.1, NP_0011396371.1, NP_0011396381.1, NP_0011396391.1
GeneID:7347	WNT1	19	57,352,270	57,359,922	7,652	+	2	4_A375_DSR1..1.4696, 4_A375_DSR1..1.4698	2832, -2009	upstream, upstream	1	1	1	8.5	9	16	2	4_A375_DSR1..1.1	17	Gene WNT1	WCRAVEN087, wnt01, WM1	WNT1 inducible signaling pathway protein 1 (oncogene)	NM_0264599		
GeneID:5422	ZNF264	19	57,702,966	57,754,314	51,348	+	2	2_A375_uhk07_dlust_lncRNA_AR..1.4464, 2_A375_uhk07_dlust_lncRNA_AR..1.4465	-118, 39212	upstream, downstream	0	0	1	7.5	10	12.5	2	4_A375_DSR1..1.1	16	Gene ZNF264	ZNF264	zinc finger protein 264	NM_0054171, ICT1702008.2, ICT2297435.0	1558690_at, 208517_at, 210983_at	NP_0035581, ENAT02464.1, ENAT02463.1
GeneID:6571	AURKC	19	57,742,377	57,746,916	4,539	+	3	1_A375_uhk7_mrust_lncRNA_AR..1.3708, 2_A375_uhk07_dlust_lncRNA_AR..1.4465, 4_A375_DSR1..1.4700	9867, 9703, -297	Downstream, Downstream, upstream	1	1	1	12	14	12.5	2	2_A375_uhk623_mrust_lncRNA_AR..1	Gene AURKC	aurora C, AIE2, STK12, AIK2, ARK2, AurC, AURKC	aurora kinase C	NM_0010357678, NM_0010135791, NM_003160, ICT1950035.0, ICT53273.1	211107_s_at	NP_0010135781, NP_0010135791, NP_0031512, ENAT02455.1, ENAT02458.1

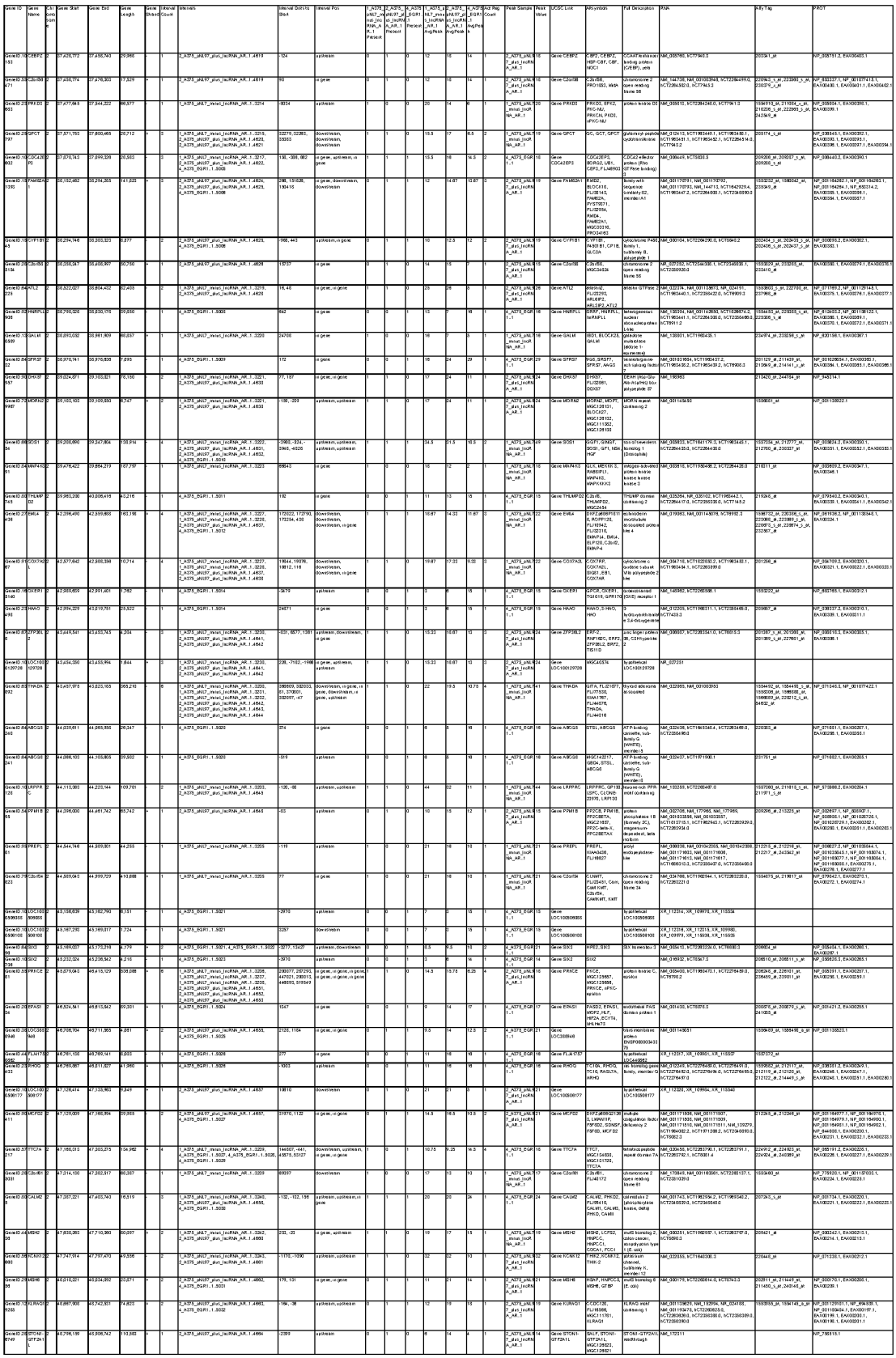


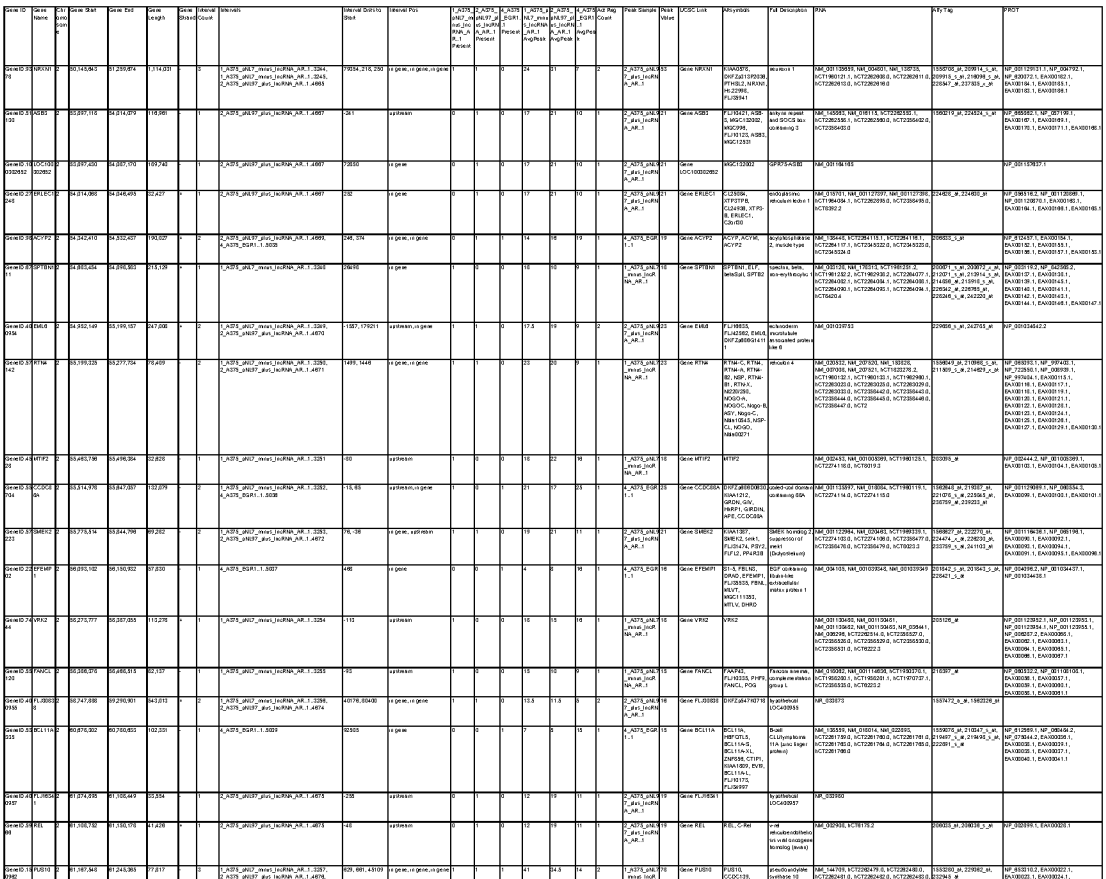
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_unk7_invasi_lncRNA_intron_RNA_AR_1 Present	2_A375_unk7_invasi_lncRNA_AR_1 Present	4_A375_EGR1_AR_1 Present	1_A375_unk7_invasi_lncRNA_AR_1 Avg Peak	2_A375_unk7_invasi_lncRNA_AR_1 Avg Peak	4_A375_EGR1_AR_1 Avg Peak	Add Tag Count	Peak Sample	Peak Value	UCSC Link	Annotation	Full Description	RNA	Ally Tag	PROT
GeneID:39 3980	ZNF800	19	57,732,035	57,774,106	42,055	+	3	1_A375_unk7_invasi_lncRNA_AR_1:3155, 2_A375_unk37_plus_lncRNA_AR_1:4468, 4_A375_EGR1_1:4468	-99, 27, -9973	upstream, in gene, downstream	1	1	1	12	14	12.3	2	2_A375_unk37_plus_lncRNA_AR_1	23	ZNF800	ENSG00000196180, ZNF800	zinc finger protein 800	NM_031223593, NM_001145076	235896_at, 235936_s_at, 235437_at	NP_001138572.2, NP_001138593.1
GeneID:40 794	ZNF480	19	57,791,553	57,805,458	13,905	+	1	2_A375_unk37_plus_lncRNA_AR_1:4469	-45	upstream	0	1	0	17	28	18	1	2_A375_unk37_plus_lncRNA_AR_1	26	ZNF480	ENSG00000197785, ZNF272	zinc finger protein 480	NM_030615	218079_at, 218079_at, 233179_s_at	NP_036236.3
GeneID:37 543	ZNF304	19	57,862,845	57,871,399	8,821	+	3	1_A375_unk7_invasi_lncRNA_AR_1:3109, 1_A375_unk7_invasi_lncRNA_AR_1:3110, 2_A375_unk37_plus_lncRNA_AR_1:4467	-37, 12091, 12235	upstream, downstream, downstream	1	1	0	16	16.5	10	2	2_A375_unk37_plus_lncRNA_AR_1	23	ZNF304	MGC129701, MGC129704, ZNF304	zinc finger protein 304	NM_030617, XM_011511628.1, XM_017297440.0	207753_at	NP_998709.2, EAW72494.1, EAW72492.1
GeneID:28 6398	ZNF547	19	57,874,991	57,890,927	16,036	+	3	1_A375_unk7_invasi_lncRNA_AR_1:3110, 2_A375_unk37_plus_lncRNA_AR_1:4467, 4_A375_EGR1_AR_1:4467	-158, -11, 26165	upstream, upstream, downstream	1	1	0	16.5	19.5	6	2	2_A375_unk37_plus_lncRNA_AR_1	23	ZNF547	FLJ35100, ZNF547	zinc finger protein 547	NM_175931, XM_011512114.1, XM_017297443.0, XM_017306359.2	1552794_a_at, 1558969_at	NP_779992.2, EAW72491.1, EAW72495.1, EAW72496.1, EAW72495.1
GeneID:14 7694	ZNF340	19	57,901,218	57,913,919	12,701	+	3	1_A375_unk7_invasi_lncRNA_AR_1:3111, 2_A375_unk37_plus_lncRNA_AR_1:4468, 2_A375_unk37_plus_lncRNA_AR_1:4469	126, -162, 21436	in gene, upstream, downstream	1	1	0	17.5	15.5	11.5	2	2_A375_unk37_plus_lncRNA_AR_1	18	ZNF340	ZNF340, FLJ22522	zinc finger protein 340	NM_152939, NM_001172773, XM_011512129.3	1553718_at, 1553719_s_at, 1558822_a_at	NP_690737.2, NP_001180244.1, EAW72499.1
GeneID:79 85	ZNF17	19	57,922,529	57,933,327	10,776	+	1	2_A375_unk37_plus_lncRNA_AR_1:4469	145	in gene	0	1	0	20	15	14	1	2_A375_unk37_plus_lncRNA_AR_1	15	ZNF17	KOX10, FLJ46615, KIAA1967, FLJ46556, FLJ46594, HPF3, ZNF17	zinc finger protein 17	NM_006959, XM_017182081.1	1555165_at, 1555166_s_at	NP_006950.2, EAW72500.1
GeneID:38 6397	ZNF749	19	57,946,660	57,957,191	10,532	+	1	2_A375_unk37_plus_lncRNA_AR_1:4470	27	in gene	0	1	0	16	21	17	1	2_A375_unk37_plus_lncRNA_AR_1	21	ZNF749	ZNF749, FLJ46265, FLJ46360	zinc finger protein 749	NM_031223561	213309_at	NP_001018555.2
GeneID:28 9931	ZNF349	19	58,036,693	58,052,131	15,439	+	1	4_A375_EGR1_1:4931	283	in gene	0	0	1	12	9	17	1	4_A375_EGR1_1.1	17	ZNF349	ZNF349, FLJ49117	zinc finger protein 349	NM_152383, XM_011512116.0, XM_017297454.0, XM_017305010.0, NC_018274.2	213319_at	NP_694959.1, EAW72509.1, EAW72510.1, EAW72511.1, EAW72512.1
GeneID:39 899	ZNF416	19	58,082,804	58,090,343	7,539	-	3	2_A375_unk37_plus_lncRNA_AR_1:4471, 2_A375_unk37_plus_lncRNA_AR_1:4472, 4_A375_EGR1_1:4932	-139, -9099, -4857	upstream, upstream, upstream	1	1	1	12	10.5	11	2	2_A375_unk37_plus_lncRNA_AR_1	19	ZNF416	FLJ35357, ZNF416	zinc finger protein 416	NM_017679, XM_017182768.2, XM_017297696.0	223889_at, 234932_s_at	NP_783624.1, EAW72513.1, EAW72514.1
GeneID:28 4307	ZIK1	19	58,095,926	58,103,766	8,130	+	3	2_A375_unk37_plus_lncRNA_AR_1:4471, 2_A375_unk37_plus_lncRNA_AR_1:4472, 4_A375_EGR1_1:4932	-5262, -318, -746	upstream, upstream, upstream	1	1	1	12	10.5	11	2	2_A375_unk37_plus_lncRNA_AR_1	19	ZIK1	ZNF792, ZIK1, MGC119701, MGC119700, MGC119899	zinc finger protein with KRAB and SCAN domains 1 (isoform 1)	NM_031018879, XM_011542143.2	232774_x_at, 232773_at	NP_001108779.2, EAW72516.1
GeneID:28 1518	ZSCAN4	19	58,160,320	58,190,920	30,217	+	1	2_A375_unk37_plus_lncRNA_AR_1:4473	13103	downstream	0	1	0	16	19	11	1	2_A375_unk37_plus_lncRNA_AR_1	19	ZSCAN4	ZSCAN4, FLJ35105, MGC126709, MGC126707, ZNF494	zinc finger and SCAN domains containing 4	NM_152677, XM_017234152.0	1552651_at, 1552652_s_at	NP_689900.1, EAW72525.1
GeneID:89 233	ZNF551	19	58,195,357	58,201,079	5,722	+	1	2_A375_unk37_plus_lncRNA_AR_1:4474	91	in gene	0	1	0	16	19	11	1	2_A375_unk37_plus_lncRNA_AR_1	19	Gene ZNF551	ENSG00000183386, MGC62307, ZNF551	zinc finger protein 551	NM_139347, XM_011511652.2	211701_s_at, 242992_at, 243195_s_at	NP_612586.1, EAW72524.1
GeneID:79 691	ZNF821	19	58,231,119	58,235,995	7,876	+	1	2_A375_unk37_plus_lncRNA_AR_1:4963	83	in gene	0	0	1	12	11	18	1	4_A375_EGR1_1.1	18	Gene ZNF821	FLJ35556, ZNF821	zinc finger protein 821	NM_024833, XM_017167468.2, XM_017234996.0	219649_at	NP_079109.2, EAW72529.1, EAW72530.1
GeneID:79 516	ZNF302	19	58,316,450	58,326,351	7,931	-	1	4_A375_EGR1_1:4964	-4931	upstream	0	0	1	10	12	20	1	4_A375_EGR1_1.1	20	Gene ZNF302	FLJ37855, ZNF302	zinc finger protein 302	NM_024782, XM_017181197.2	219741_s_at, 222228_at	NP_079358.2, EAW72535.1
GeneID:10 172	ZNF398	19	58,432,201	58,459,077	26,876	-	2	2_A375_unk37_plus_lncRNA_AR_1:3112, 2_A375_unk37_plus_lncRNA_AR_1:4474	-133, -155	upstream, upstream	1	1	0	21	22	10	1	2_A375_unk37_plus_lncRNA_AR_1	22	ZNF398	ENST0, ENST0, ZNF398	zinc finger protein 398	NM_032773, XM_017201084.3	223714_at	NP_065784.2, EAW72544.1
GeneID:88 235	ZNF808	19	58,466,440	58,514,714	48,274	-	3	2_A375_unk37_plus_lncRNA_AR_1:3113, 2_A375_unk37_plus_lncRNA_AR_1:4475, 4_A375_EGR1_1:4968	595, -6502, -6534	upstream, upstream, upstream	1	1	1	15	15	12.5	2	2_A375_unk37_plus_lncRNA_AR_1	18	ZNF808	KIAA1632, FLJ14293, ZNF808, ZNF226	zinc finger protein 808	NM_025227, XM_017182414.3, XM_017195316.3, XM_017235071.0	219935_at, 229787_at	NP_079353.2, EAW72547.1, EAW72548.1, EAW72549.1
GeneID:10 2039	LOC100129	19	58,514,282	58,516,574	4,312	+	3	1_A375_unk7_invasi_lncRNA_AR_1:3112, 2_A375_unk37_plus_lncRNA_AR_1:4473, 4_A375_EGR1_1:4968	-134, -8954, -9968	upstream, downstream, downstream	1	1	1	15	15	13.5	2	2_A375_unk37_plus_lncRNA_AR_1	18	Gene LOC100129396		hypothetical LOC100129396	NR_038508		
GeneID:28 4312	ZSCAN31	19	58,543,434	58,565,999	20,565	+	3	4_A375_EGR1_1:4968, 4_A375_EGR1_1:4967, 4_A375_EGR1_1:4968	-834, 9074, 23622	upstream, in gene, downstream	0	0	1	8.33	8	16	2	4_A375_EGR1_1.1	16	Gene ZSCAN31	MZF1_ZNF815, MGC104472, FLJ32779, ZSCAN31	zinc finger and SCAN domains containing 1	NM_152572, XM_017297008.1, XM_017235039.0	1562651_at	NP_872376.3, EAW72550.1, EAW72551.1
GeneID:74 94	ZNF133	19	58,570,607	58,581,123	10,516	+	1	4_A375_EGR1_1:4968	449	in gene	0	0	1	10	7	17	1	4_A375_EGR1_1.1	17	Gene ZNF133	ZNF81, pT2, pHZ-17, ZNF135, ZNF761	zinc finger protein 135	NM_003436, NM_007154, NM_001164327, NM_001164329, NM_001164330, XM_017297083.1, XM_017235931.0, XM_017235932.0, XM_017235933.0, XM_017235934.0	1567410_at, 208142_at	NP_003427.3, NP_009080.1, NP_001137999.1, NP_001158001.1, NP_001158002.1, EAW72554.1, EAW72552.1, EAW72553.1, EAW72555.1, EAW72556.1
GeneID:79 972	ZNF229	19	58,837,955	58,862,148	24,453	-	1	2_A375_unk37_plus_lncRNA_AR_1:4478	-4198	upstream	0	1	0	17	16	13	1	2_A375_unk37_plus_lncRNA_AR_1	18	Gene ZNF229	FLJ12599, ZNF229	zinc finger protein 229	NM_024326, XM_017169133.0, XM_017297128.1, XM_017241199.0, XM_017235040.0	219763_at	NP_378936.3, EAW72561.1, EAW72562.1, EAW72563.1
GeneID:10 7702	ZNF274	19	58,894,396	58,924,927	30,531	+	1	4_A375_EGR1_1:4969	653	in gene	0	0	1	14	16	16	1	4_A375_EGR1_1.1	16	Gene ZNF274	ENST0, ENST0, ZNF274, FLJ12543, HPF31, ZF2	zinc finger protein 274	NM_016324, NM_018523, NM_139166, XM_017182167.1, XM_017183180.0, XM_017201362.0	204937_s_at, 232436_at	NP_057408.2, NP_061981.1, NP_569059.1, EAW72565.1, EAW72566.1, EAW72567.1
GeneID:25 300	ZNF544	19	58,740,870	58,775,810	34,940	-	2	1_A375_unk7_invasi_lncRNA_AR_1:3114, 4_A375_EGR1_1:4970	-218, 202	in gene, in gene	0	1	1	20	14	20	1	1_A375_unk7_invasi_lncRNA_AR_1	23	ZNF544	ZNF544	zinc finger protein 544	NM_014498, XM_017183208.1, XM_017183207.1	218755_s_at, 244498_at	NP_055513.2, EAW72569.1, EAW72568.1
GeneID:10 5585561	LOC100	19	58,770,594	58,790,197	19,603	-	1	2_A375_unk37_plus_lncRNA_AR_1:4477	-390	upstream	0	1	0	13	16	17	1	2_A375_unk37_plus_lncRNA_AR_1	18	Gene LOC100506961		hypothetical LOC100506961	XR_109303		
GeneID:79 54	ZNF8	19	58,790,316	58,807,354	16,938	+	3	1_A375_unk7_invasi_lncRNA_AR_1:3115, 2_A375_unk37_plus_lncRNA_AR_1:4477, 4_A375_EGR1_1:4970	29618, 199, 29599	downstream, in gene, downstream	1	1	0	16	19.5	18	2	1_A375_unk7_invasi_lncRNA_AR_1	23	Gene ZNF8	HF10_ZNF8, Zfp126	zinc finger protein 8	NM_021039, XM_017297019.1	214901_at	NP_066373.2, EAW72570.1
GeneID:10 5585554	LOC100	19	58,816,743	58,827,823	10,260	+	2	1_A375_unk7_invasi_lncRNA_AR_1:3115, 2_A375_unk37_plus_lncRNA_AR_1:4478	77, -39	upstream, upstream	1	1	0	23	23	13	1	1_A375_unk7_invasi_lncRNA_AR_1	23	Gene LOC100506954	FLJ30394, DKFZp313E2310, MGC16137	hypothetical protein LOC100506954	XM_003116796		XP_003116844.1
GeneID:34 2945	ZSCAN22	19	58,836,585	58,855,712	19,127	+	2	1_A375_unk37_plus_lncRNA_AR_1:3116, 2_A375_unk37_plus_lncRNA_AR_1:4479	175, 271	in gene, in gene	0	1	0	24	24	9	1	1_A375_unk7_invasi_lncRNA_AR_1	24	Gene ZSCAN22	MGC125442, HKR2, ZSCAN22, MGC129879, ZNF305	zinc finger and SCAN domains containing 22	NM_181646, NC_018930.2	220769_at	NP_852291.1, EAW72576.1
GeneID:1 1	A1BG	19	58,858,172	58,864,865	6,693	-	3	1_A375_unk7_invasi_lncRNA_AR_1:3117, 2_A375_unk37_plus_lncRNA_AR_1:4480, 4_A375_EGR1_1:4971	-6985, -9339, 9455	upstream, upstream, upstream	1	1	1	22	22	19	1	2_A375_unk37_plus_lncRNA_AR_1	22	Gene A1BG	A1B, A1BG, GH5, HBG, DKFZp686P0270, HYST2477	alpha-1-B glycoprotein	NM_130786, NC_018932.1	229619_at	NP_570602.2, EAW72578.1
GeneID:59 3535	NCRNA	19	58,865,538	58,866,549	2,012	+	3	1_A375_unk7_invasi_lncRNA_AR_1:3117, 2_A375_unk37_plus_lncRNA_AR_1:4480, 4_A375_EGR1_1:4971	10658, 10598, 10864	downstream, downstream, downstream	1	1	1	22	22	19	1	2_A375_unk37_plus_lncRNA_AR_1	22	Gene NCRNA00161	A1BG-AS, A1BGAS, NCRNA00161, FLJ23569, A1BG-AS1	A1BG antisense RNA (non-protein coding)	NR_015380	233482_s_at	
GeneID:10 5399852	ZNF497	19	58,866,723	58,874,120	8,398	-	3	1_A375_unk7_invasi_lncRNA_AR_1:3117, 2_A375_unk37_plus_lncRNA_AR_1:4480, 4_A375_EGR1_1:4971	296, 216, -300	in gene, in gene, upstream	1	1	1	22	22	19	1	2_A375_unk37_plus_lncRNA_AR_1	22	Gene ZNF497	FLJ44773, ZNF497, FLJ47722	zinc finger protein 497	NM_198488, XM_017201987.4, XM_017286022.0	230857_s_at	NP_940990.1, EAW72577.1, EAW72578.1
GeneID:10 8412	ZNF837	19	58,876,990	58,892,389	15,399	-	6	1_A375_unk7_invasi_lncRNA_AR_1:3117, 1_A375_unk7_invasi_lncRNA_AR_1:3118, 2_A375_unk37_plus_lncRNA_AR_1:4480, 2_A375_unk37_plus_lncRNA_AR_1:4481, 2_A375_unk37_plus_lncRNA_AR_1:4482, 2_A375_unk37_plus_lncRNA_AR_1:4911, 4_A375_EGR1_1:4912, 4_A375_EGR1_1:4913	10865, 165, 10675, 197, 8155, 10099, 293, 9891	downstream, in gene, downstream, in gene, upstream, downstream, in gene, upstream	1	1	1	20	22.33	16	3	2_A375_unk37_plus_lncRNA_AR_1	23	ZNF837	ZNF837	zinc finger protein 837	NM_138498, NM_001129750	1559822_s_at, 241277_x_at	NP_612475.1, NP_001122022.1
GeneID:8 91	RPS5	19	58,890,856	58,906,171	7,335	+	7	1_A375_unk7_invasi_lncRNA_AR_1:3118, 1_A375_unk7_invasi_lncRNA_AR_1:3119, 2_A375_unk37_plus_lncRNA_AR_1:4481, 2_A375_unk37_plus_lncRNA_AR_1:4482, 2_A375_unk37_plus_lncRNA_AR_1:4483, 2_A375_unk37_plus_lncRNA_AR_1:4912, 4_A375_EGR1_1:4913, 4_A375_EGR1_1:4914	-6412, -6444, -82, 14356, -6542, 598, 13218	upstream, upstream, downstream, downstream, upstream, upstream, downstream	1	1	1	13.75	16	16.25	4	2_A375_unk37_plus_lncRNA_AR_1	23	Gene RPS5	S5, RPS5	ribosomal protein S5	NM_001009, XM_017182045.1, XM_017182036.1, XM_017235075.0	200024_at	NP_001000.2, EAW72582.1, EAW72581.1, EAW72583.1
GeneID:10 5399812	LOC100	19	58,907,437	58,908,446	969	+	4	2_A375_unk37_plus_lncRNA_AR_1:4482, 2_A375_unk37_plus_lncRNA_AR_1:4483, 4_A375_EGR1_1:4913, 4_A375_EGR1_1:4914, 4_A375_EGR1_1:4914	6913, 5535, -1027, 4899	upstream, downstream, upstream, downstream	0	1	1	14	13.67	13.67	3	4_A375_EGR1_1.1	24	Gene LOC100399812		hypothetical protein LOC100399812	XM_003116797		XP_003116845.1
GeneID:10 5399837	LOC100	19	58,911,439	58,913,389	1,950	-	5	2_A375_unk37_plus_lncRNA_AR_1:4483, 2_A375_unk37_plus_lncRNA_AR_1:4484, 2_A375_unk37_plus_lncRNA_AR_1:4485, 4_A375_EGR1_1:4914, 4_A375_EGR1_1:4915	-5943, 277, -7011, 917, -7329	upstream, in gene, downstream, in gene, upstream	1	1	1	16	15	16	3	4_A375_EGR1_1.1	24	Gene LOC100399837		hypothetical LOC100399837	XR_111904, XR_103938, XR_115331		
GeneID:10 5399834	LOC100	19	58,915,935	58,916,983	1,048	-	5	2_A375_unk37_plus_lncRNA_AR_1:4483, 2_A375_unk37_plus_lncRNA_AR_1:4484, 2_A375_unk37_plus_lncRNA_AR_1:4485, 4_A375_EGR1_1:4914, 4_A375_EGR1_1:4915	11405, 8071, 1917, 8311, 1963	upstream, downstream, downstream, downstream, upstream	1	1	1	16	15	16	3	4_A375_EGR1_1.1	24	Gene LOC100399834		hypothetical LOC100399834	XM_003116780, XM_003120972		XP_003116818.1, XP_003121932.1
GeneID:25 1514	ZNF354	19	58,920,065	58,929,894	9,831	+	3	1_A375_unk7_invasi_lncRNA_AR_1:3119, 2_A375_unk37_plus_lncRNA_AR_1:4483, 2_A375_unk37_plus_lncRNA_AR_1:4486, 4_A375_EGR1_1:4914, 4_A375_EGR1_1:4915	49, 7071, 277, 7711, 545	in gene, upstream, in gene, upstream, in gene	1	1	1	16	15	16	3	4_A375_EGR1_1.1	24	Gene ZNF354	ZNF354, FLJ39099	zinc finger protein 354	NM_175540, XM_017183761.1, XM_017183171.1, XM_017235012.0	226148_at	NP_778219.1, EAW72587.1, EAW72588.1, EAW72589.1
GeneID:38 9589	ZNF324	19	58,962,471	58,969,199	6,728	+	5	2_A375_unk37_plus_lncRNA_AR_1:4485, 4_A375_EGR1_1:4916, 4_A375_EGR1_1:4917	281, -315, 69	in gene, upstream, in gene	0	1	1	11	17	17	1	2_A375_unk37_plus_lncRNA_AR_1	17	Gene ZNF324B	FLJ45050, ZNF324B	zinc finger protein 324 B	NM_207345, XM_017234513.0	222316_at, 238698_at	NP_997262.2, EAW72593.1
GeneID:25 7191	ZNF324	19	58,976,412	58,984,945	8,533	+	1	4_A375_EGR1_1:4915	9298	downstream	0	0	1	17	14	14	1	4_A375_EGR1_1.1	14	Gene ZNF324	ZNF324, ZFS126	zinc finger protein 324	NM_014547, XM_017234148.0, XM_017234151.0, XM_017234479.0	205162_s_at	NP_055362.1, EAW72596.1, EAW72594.1, EAW72595.1
GeneID:10 6983	ZNF446	19	58,987,793	58,992,997	4,932	+	1	4_A375_EGR1_1:4918	43	in gene	0	0	1	17	14	14	1	4_A375_EGR1_1.1	14	Gene ZNF446	ENSCAN20, ZSCAN20, ZNF446, FLJ39626	zinc finger protein 446	NM_017930, XM_017234148.0, XM_017234149.0, XM_017234152.0, XM_017234975.0	1554160_a_at, 219900_s_at	NP_060376.1, EAW72597.1, EAW72598.1, EAW72600.1
GeneID:10 7293	SCAF1	19	59,009,700	59,023,432	13,732	-	4	1_A375_unk7_invasi_lncRNA_AR_1:3120, 2_A375_unk37_plus_lncRNA_AR_1:4485, 2_A375_unk37_plus_lncRNA_AR_1:4487, 4_A375_EGR1_1:4918	-7965, -2196, -7992, -7752	upstream, upstream, downstream, upstream	1	1	1	19	24.5	14.5	2	2_A375_unk37_plus_lncRNA_AR_1	27	Gene SLC27A5	SLC27A5, FATP5, HCSVL1, HCS5, VLCS-H2, VLCSH2, FACVL5, FLJ23567, VLACSR	fatty acid transporter, very long chain family member 5	NM_012254, XM_017201372.2	219702_s_at, 234946_at	NP_036386.1, EAW72601.1
GeneID:54 876	ZBTB45	19	59,024,897	59,030,921	6,024	+	4	1_A375_unk7_invasi_lncRNA_AR_1:3120, 2_A375_unk37_plus_lncRNA_AR_1:4486, 2_A375_unk37_plus_lncRNA_AR_1:4487, 4_A375_EGR1_1:4919	471, 9263, -503, 280	upstream, in gene, upstream, upstream	1	1	1	19	24.5	14.5	2	2_A375_unk37_plus_lncRNA_AR_1	27	Gene ZBTB45	ZBTB45, DKFZp547H061, FLJ14455, ZNF450	zinc finger and BTB domain containing 45	NM_032782, XM_017167852.3, XM_017183164.1, XM_017167934.1	229982_x_at, 243551_at	NP_116151.1, EAW72602.1, EAW72603.1, EAW72604.1
GeneID:10 155	TRIM28	19	59,055,836	59,062,062	6,248	+	3	1_A375_unk7_invasi_lncRNA_AR_1:3121, 2_A375_unk37_plus_lncRNA_AR_1:4488, 4_A375_EGR1_1:4920	14506, 10080, 10802	downstream, downstream, downstream	1	1	1	16	15	13	2	4_A375_EGR1_1.1	21	Gene TRIM28	RNF96, TIF1A05, TIF1A, TIF1B	tripartite motif-containing 28	NM_005762, XM_017183192.2, XM_017183194.2, XM_017201388.3	200960_at	NP_005753.1, EAW72605.1, EAW72606.1, EAW72607.1
GeneID:27 243	CHMP2	19	59,082,933	59,095,469	12,537	-	3	2_A375_unk37_plus_lncRNA_AR_1:4489, 2_A375_unk37_plus_lncRNA_AR_1:4490, 4_A375_EGR1_1:4920	-3945, -10, -42	upstream, upstream, upstream	1	1	1	15	15	13	2	4_A375_EGR1_1.1	21	Gene CHMP2A	CHMP2A, BC2, CHMP2, VPS2, VPS2A, EC-2	chromatin modifying protein 2A	NM_199426, NM_014453, XM_017183197.1, XM_017201382.2, XM_017235073.0, XM_017235074.0	202721_s_at	NP_940755.1, NP_055286.1, EAW72608.1, EAW72609.1, EAW72610.1, EAW72611.1
GeneID:84 60	UBE2H	19	59,097,079	59,270,343	5,264	+	3	1_A375_unk7_invasi_lncRNA_AR_1:3121, 2_A375_unk37_plus_lncRNA_AR_1:4489, 4_A375_EGR1_1:4920	-95, 5567, -3815	upstream, downstream, upstream	1	1	1	16	15	13	2	4_A375_EGR1_1.1	21	Gene UBE2H	UBC-RS2, UBC12, UBE2H, bcUbc12	ubiquitin conjugating enzyme E2H (UBC 12 homolog, yeast)	NM_003969, XM_017297308.1, XM_017297309.1	202109_at	NP_003949.1, EAW72612.1, EAW72613.1
GeneID:10 5131691	LOC100	19	59,270,902	59,288,184	17,282	+	4	1_A375_unk7_invasi_lncRNA_AR_1:3121, 2_A375_unk37_plus_lncRNA_AR_1:4489, 4_A375_EGR1_1:4920, 4_A375_EGR1_1:4921	-180, -4096, -4084, 16738	upstream, upstream, upstream, downstream	1	1	1	16.67	16	16	3	4_A375_EGR1_1.1	21	Gene LOC100131691		hypothetical LOC100131691	XR_037334		
GeneID:79 91	MZF1	19	59,287,354	59,294,342	11,856	+	4	1_A375_unk7_invasi_lncRNA_AR_1:3121, 2_A375_unk37_plus_lncRNA_AR_1:4489, 2_A375_unk37_plus_lncRNA_AR_1:4490, 4_A375_EGR1_1:4921	14510, 15448, 15614, -2308	downstream, downstream, downstream, upstream	1	1	1	16.67	16	16	3	4_A375_EGR1_1.1	21	Gene MZF1	MZF1, MZF-1, MZF1B, ZNF42, ZSCAN8, Zfp98	myeloid zinc finger 1	NM_198055, NM_003422, XM_017297330.1, XM_017297334.1, XM_017297337.1, XM_017297338.1, XM_017297340.0	204156_s_at, 204159_at, 204160_s_at, 40369_at	NP_932172.1, NP_003410.2, EAW72614.1, EAW72615.1, EAW72616.1, EAW72617.1
GeneID:89 998	MRGC	19	59,356,766	59,359,762	2,996	+	1	4_A375_EGR1_1:4921	582	in gene	0	0	1	14	16	16	1	4_A375_EGR1_1.1	16	Gene MRGC252	FLJ13309, MGC149825, MGC111583	hypothetical LOC83998	NM_033032, NC_018274.3	1565894_at, 219924_s_at, 222894_at, 233026_s_at	EAW72618.1
GeneID:84 2270	FAM110	2	25,814	49,566	7,774	-	1	4_A375_EGR1_1:4923	940	in gene	0	0	1	2	8	13	1	4_A375_EGR1_1.1	13	Gene FAM110C	FAM110C	family with sequence similarity 110, member C	NM_031777.10	225683_at	NP_001071176.2
GeneID:26 751	SHD1L1	2	218,138	284,886	43,932	-	1	1_A375_unk7_invasi_lncRNA_AR_1:3122	-799	upstream	1	0	0	16	12	8	1	1_A375_unk7_invasi_lncRNA_AR_1	18	Gene SHD1L1	FLJ39121, RAY1, SHD1L1, DKFZp686F1316	SHD1 domain containing, Yeast RAY1 (S. cerevisiae) ortholog-like 1	NM_018077, NM_001135097	1554169_at, 236019_s_at	NP_060547.2, NP_001128569.1
GeneID:53	ACP1	2	284,249	376,230	15,414	+	1	1_A375_unk7_invasi_lncRNA_AR_1:3122	-5	upstream	1	0	0	16	12	8	1	1_A375_unk7_invasi_lncRNA_AR_1	18	Gene ACP1	RHAP, MGC111002, ACP1, MGC2449	acid phosphatase 1, soluble	NM_001040649, NM_004300, NM_007099, NR_024000, NC_018274.2, NC_018927.1, NC_018927.2, NC_018927.3, NC_018927.4, NC_018927.5	1554000_at, 201929_s_at, 201930_s_at, 215227_x_at	NP_001035931.1, NP_004291.1, NP_009030.1, EAW31111.1, EAW31114.1, EAW31115.1, EAW31112.1, EAW31113.1, EAW31116.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.129787	TMEM18	2	667,973	677,439	9,466	-	1	4_A375_EGR1..1..4927	47	in gene	0	0	1	14	15	20	1	4_A375_EGR1..1	20	Gene TMEM18	TMEM18, DKFZp434C1714	transmembrane protein 18	NM_152834, hCT1823764.2, hCT2348899.0, hCT2348900.0, hCT2348901.0, hCT2348902.0	225487_at, 225489_at	NP_690047.2, EAX01097.1, EAX01098.1, EAX01099.1, EAX01100.1, EAX01101.1
GeneID.23040	MYT1L	2	1,792,885	2,335,045	542,160	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4489, 4_A375_EGR1..1..4931	2245, 383157	in gene, in gene	0	1	1	7.5	12	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MYT1L	MYT1L, NZF1	myelin transcription factor 1-like	NM_015025	1554633_a_at, 210016_at, 216672_s_at, 241485_at	NP_055840.2
GeneID.730811	LOC730811	2	2,323,004	2,330,880	7,876	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4489	9798	downstream	0	1	0	11	19	3	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC730811	FLJ44020, FLJ32838	hypothetical LOC730811	NR_024466		
GeneID.100132736	LOC100132736	2	3,153,392	3,185,045	31,653	+	1	4_A375_EGR1..1..4934	-3840	upstream	0	0	1	3	5	15	1	4_A375_EGR1..1	15	Gene LOC100132736		hypothetical protein LOC100132736	XM_001714359, XM_002345510		XP_001714411.2, XP_002345551.2
GeneID.7260	TSSC1	2	3,192,741	3,381,653	188,912	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3123, 2_A375_pNL97_plus_lncRNA_AR..1..4491, 2_A375_pNL97_plus_lncRNA_AR..1..4492	-267, 213, -1931	upstream, in gene, upstream	1	1	0	17.5	20	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TSSC1	TSSC1		NM_003310, hCT1983938.1, hCT1983939.1	217968_at	NP_003301.1, EAX01071.1, EAX01070.1
GeneID.51112	TTC15	2	3,383,446	3,483,342	99,896	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3123, 2_A375_pNL97_plus_lncRNA_AR..1..4491, 2_A375_pNL97_plus_lncRNA_AR..1..4492	-1526, -2008, 138	upstream, upstream, in gene	1	1	0	17.5	20	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TTC15	FLJ38662, CGI-87, TTC15, FLJ44560	tetratricopeptide repeat domain 15	NM_016030, hCT2287690.0, hCT2358467.0, hCT9597.3	203122_at, 229556_at	NP_057114.5, EAX01069.1, EAX01067.1, EAX01068.1
GeneID.55256	ADI1	2	3,501,690	3,523,350	21,660	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4493, 4_A375_EGR1..1..4935	374, 356	in gene, in gene	0	1	1	17	20	23	1	4_A375_EGR1..1	23	Gene ADI1	HMFT1638, SIPL, FLJ10913, ARD, MTCBP1, APL1, SIP-L, N-ARD, MTCBP-1, ADI1	acireductone dioxygenase 1	NM_018269, hCT1971493.1, hCT9598.2	217761_at, 222400_s_at	NP_060739.2, EAX01064.1, EAX01065.1
GeneID.100506014	LOC100506014	2	3,579,403	3,581,797	2,394	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3124	-2587	upstream	1	0	0	27	20	5	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene LOC100506014		hypothetical LOC100506014	XR_112283, XR_112282, XR_112281, XR_109909, XR_109908, XR_109907, XR_115568, XR_115567, XR_115566		
GeneID.246243	RNASEH1	2	3,592,678	3,605,940	13,262	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3124, 4_A375_EGR1..1..4936	21556, 84	downstream, in gene	1	0	1	20	19.5	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene RNASEH1	H1RNA, RNASEH1, RNH1	ribonuclease H1	NM_002936, hCT2287225.0	218496_at, 218497_s_at, 241343_at	NP_002927.2, EAX01061.1
GeneID.100506054	LOC100506054	2	3,605,976	3,609,340	3,364	+	1	4_A375_EGR1..1..4936	-120	upstream	0	0	1	13	19	20	1	4_A375_EGR1..1	20	Gene LOC100506054		hypothetical LOC100506054	XR_109912, XR_109910, XR_109911		
GeneID.6201	RPS7	2	3,622,853	3,628,509	5,656	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3125, 2_A375_pNL97_plus_lncRNA_AR..1..4494, 4_A375_EGR1..1..4937	-69, 59, -5	upstream, in gene, upstream	1	1	1	34	24	17	1	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene RPS7	RPS7, DBA8, S7	ribosomal protein S7	NM_001011, hCT1823234.2, hCT1983940.1, hCT1983941.1, hCT1983942.1	200082_s_at, 213941_x_at	NP_001002.1, EAX01059.1, EAX01056.1, EAX01057.1, EAX01058.1
GeneID.8853	ASAP2	2	9,346,894	9,545,812	198,918	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3133, 2_A375_pNL97_plus_lncRNA_AR..1..4507, 2_A375_pNL97_plus_lncRNA_AR..1..4508, 2_A375_pNL97_plus_lncRNA_AR..1..4509, 2_A375_pNL97_plus_lncRNA_AR..1..4510, 2_A375_pNL97_plus_lncRNA_AR..1..4511	81074, 27922, 28994, 81108, 81746, 171938	in gene, in gene, in gene, in gene, in gene, in gene	1	1	0	13.75	20.5	9.25	4	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene ASAP2	PAG3, CENTB3, KIAA0400, PAP, ASAP2, DDEF2, SHAG1, Pap-alpha, AMAP2, FLJ42910	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	NM_003887, NM_001135191, hCT1984190.1, hCT1987490.1, hCT2276915.0, hCT2276917.0, hCT2358456.0	206414_s_at	NP_003878.1, NP_001128663.1, EAX01003.1, EAX01004.1, EAX01005.1, EAX01006.1, EAX01002.1
GeneID.9270	ITGB1BP1	2	9,545,813	9,563,843	17,830	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4512	59	in gene	0	1	0	21	31	14	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene ITGB1BP1	ICAP1B, ICAP1A, ICAP1, ICAP-1B, ICAP-1alpha, ITGB1BP1, ICAP-1A, DKFZp686K08158	integrin beta 1 binding protein 1	NM_004763, NM_022334, hCT1690257.3, hCT1984080.2, hCT1984081.2, hCT2276418.1, hCT2343704.0, hCT2343705.0, hCT2343706.0, hCT2358508.0, hCT2358509.0, hCT2358510.0, hCT2358511.0	203336_s_at, 203337_x_at, 228227_at	NP_004754.1, NP_071729.1, EAX00991.1, EAX00992.1, EAX00997.1, EAX01000.1, EAX00993.1, EAX00994.1, EAX00995.1, EAX00996.1, EAX00998.1, EAX00999.1, EAX01001.1
GeneID.51692	CPSF3	2	9,563,868	9,613,227	49,359	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4512	-284	upstream	0	1	0	21	31	14	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene CPSF3	CPSF, CPSF73, CPSF3, CPSF-73, YSH1	cleavage and polyadenylation specific factor 3, 73kDa	NM_016207, hCT1823269.2, hCT2358381.0	225082_at	NP_057291.1, EAX00989.1, EAX00990.1
GeneID.6868	ADAM17	2	9,629,392	9,695,917	66,525	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3134, 2_A375_pNL97_plus_lncRNA_AR..1..4513	-259, -179	upstream, upstream	1	1	0	17	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ADAM17	ADAM17, MGC71942, CSVP, TACE, CD156B, ADAM18	ADAM metallopeptidase domain 17	NM_003183, hCT2278409.0, hCT2278412.0	205745_x_at, 205746_s_at, 213532_at, 237897_at	NP_003174.3, EAX00982.1, EAX00981.1
GeneID.10971	YWHAQ	2	9,724,106	9,771,106	47,000	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3135, 2_A375_pNL97_plus_lncRNA_AR..1..4514, 2_A375_pNL97_plus_lncRNA_AR..1..4515	-266, -275, -7516	upstream, upstream, upstream	1	1	0	14.5	18.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene YWHAQ	HS1, 1C5, YWHAQ, 14-3-3	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	NM_006826, hCT2278405.0, hCT2278406.0, hCT2278407.0	200693_at, 212426_s_at, 213699_s_at	NP_006817.1, EAX00978.1, EAX00977.1, EAX00979.1
GeneID.100506386	LOC100506386	2	9,897,625	9,910,470	12,845	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3136, 2_A375_pNL97_plus_lncRNA_AR..1..4516	17734, 17316	downstream, downstream	1	1	0	15	21	5	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100506386		hypothetical LOC100506386	XR_112292, XR_108392, XR_115560		
GeneID.9014	TAF1B	2	9,983,571	10,074,545	90,974	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4517	109	in gene	0	1	0	13	22	11	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene TAF1B	TAFI63, RAFI63, RAF1B, MGC:9349, TAF1B, SL1	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	NM_005680, hCT14944.3, hCT2358500.0, hCT2358501.0	214690_at, 216941_s_at, 235678_at	NP_005671.2, EAX00976.1, EAX00974.1, EAX00975.1
GeneID.29841	GRHL1	2	10,091,792	10,142,412	50,620	+	1	4_A375_EGR1..1..4941	58205	downstream	0	0	1	2	9	17	1	4_A375_EGR1..1	17	Gene GRHL1	NH32, GRHL1, TFCP2L2, LBP32, MGR	grainyhead-like 1 (Drosophila)	NM_198182, hCT2287454.0	1552665_a_at, 222830_at	NP_937825.2, EAX00973.1
GeneID.8462	KLF11	2	10,183,682	10,194,963	11,281	+	1	4_A375_EGR1..1..4942	19422	downstream	0	0	1	4	7	17	1	4_A375_EGR1..1	17	Gene KLF11	MODY7, TIEG2, KLF11, Tieg3, FKLF1, FKLF	Kruppel-like factor 11	NM_003597, NM_001177716, NM_001177718, hCT2287456.0	1553137_s_at, 218486_at	NP_003588.1, NP_001171187.1, NP_001171189.1, EAX00972.1
GeneID.192668	CYS1	2	10,196,926	10,220,538	23,612	-	2	4_A375_EGR1..1..4942, 4_A375_EGR1..1..4943	17434, 14042	in gene, in gene	0	0	1	4	7	15	2	4_A375_EGR1..1	17	Gene CYS1	FLJ33960, CYS1	cystin 1	NM_001037160, hCT1823275.1	228739_at	NP_001032237.1, EAX00971.1
GeneID.6241	RRM2	2	10,262,695	10,271,546	8,851	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3137, 1_A375_pNL7_minus_lncRNA_AR..1..3138, 2_A375_pNL97_plus_lncRNA_AR..1..4518, 2_A375_pNL97_plus_lncRNA_AR..1..4519, 4_A375_EGR1..1..4944	137, 13273, 121, 13401, 184	in gene, downstream, in gene, downstream, in gene	1	1	1	30.5	38.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	53	Gene RRM2	RR2, RRM2, RR2M, R2	ribonucleotide reductase M2	NM_001034, NM_001165931	201890_at, 209773_s_at	NP_001025.1, NP_001159403.1
GeneID.348738	C2orf48	2	10,281,509	10,351,856	70,347	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3138, 2_A375_pNL97_plus_lncRNA_AR..1..4519	-5541, -5413	upstream, upstream	1	1	0	21	24	6	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene C2orf48	FLJ25102, C2orf48	chromosome 2 open reading frame 48	NM_182626		NP_872432.1
GeneID.3241	HPCAL1	2	10,443,040	10,567,743	124,703	+	3	2_A375_pNL97_plus_lncRNA_AR..1..4521, 2_A375_pNL97_plus_lncRNA_AR..1..4522, 2_A375_pNL97_plus_lncRNA_AR..1..4523	1248, 9456, 102666	in gene, in gene, in gene	0	1	0	13	20	9.33	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene HPCAL1	HLP2, BDR1, VILIP-3, HPCAL1	hippocalcin-like 1	NM_002149, NM_134421, hCT14940.3, hCT1984978.1, hCT2287465.0, hCT2287467.0, hCT2287468.1, hCT2287470.0, hCT2287471.0	205462_s_at, 212552_at	NP_002140.2, NP_602293.1, EAX00960.1, EAX00961.1, EAX00962.1, EAX00965.1, EAX00963.1, EAX00964.1, EAX00966.1
GeneID.79954	NOL10	2	10,710,894	10,830,112	119,218	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4525	32	in gene	0	1	0	14	15	9	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene NOL10	NOL10, PQBP5, FLJ14075, FLJ13938	nucleolar protein 10	NM_024894, hCT14943.2, hCT1984192.0, hCT2286831.0	218591_s_at, 222864_s_at	NP_079170.2, EAX00953.1, EAX00954.1, EAX00955.1
GeneID.3754	KCNF1	2	11,052,063	11,054,351	2,288	+	1	4_A375_EGR1..1..4947	7217	downstream	0	0	1	6	7	17	1	4_A375_EGR1..1	17	Gene KCNF1	kH1, KV5.1, KCNF, MGC33316, KCNF1, IK8	potassium voltage-gated channel, subfamily F, member 1	NM_002236, hCT12707.2	210283_at	NP_002227.2, EAX00946.1
GeneID.130813	C2orf50	2	11,273,179	11,286,916	13,737	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4529	22501	downstream	0	1	0	13	18	9	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene C2orf50	MGC149401, FLJ25143, C2orf50	chromosome 2 open reading frame 50	NM_182500, hCT1645253.3, hCT2287929.1	1563814_at	NP_872306.1, EAX00944.1, EAX00943.1
GeneID.130814	PQLC3	2	11,295,540	11,319,000	23,460	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4529	140	in gene	0	1	0	13	18	9	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PQLC3	MGC33602, PQLC3, C2orf22	PQ loop repeat containing 3	NM_152391, hCT2287930.0, hCT2287931.0, hCT2345150.0, hCT2345151.0	218458_at, 225579_at	NP_689604.1, EAX00939.1, EAX00940.1, EAX00941.1, EAX00942.1
GeneID.9475	ROCK2	2	11,321,778	11,484,711	162,933	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4530	711	in gene	0	1	0	13	18	18	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ROCK2	KIAA0619, ROCK2	Rho-associated, coiled-coil containing protein kinase 2	NM_004850, hCT12724.3, hCT2286549.0	202762_at, 211504_x_at	NP_004841.2, EAX00936.1, EAX00937.1
GeneID.650157	LOC650157	2	11,491,753	11,512,199	20,446	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3141, 2_A375_pNL97_plus_lncRNA_AR..1..4530, 2_A375_pNL97_plus_lncRNA_AR..1..4531	23247, -7753, 23191	downstream, upstream, downstream	1	1	0	14	18	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC650157		peptidyl-prolyl cis-trans isomerase A-like	XM_001129774, XM_001726994, XM_001727011		XP_001129774.2, XP_001727046.1, XP_001727063.1
GeneID.1876	E2F6	2	11,584,501	11,606,297	21,796	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3142, 2_A375_pNL97_plus_lncRNA_AR..1..4532	-103, -23	upstream, upstream	1	1	0	20	26	14	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene E2F6	E2F6, MGC111545, E2F-6	E2F transcription factor 6	NM_198256, NR_003093, NR_003095, NR_003092, NR_003094, hCT2286545.1, hCT2286546.1, hCT2286547.1, hCT2350530.0, hCT2350531.0, hCT2358532.0	203957_at	NP_937987.2, EAX00933.1, EAX00931.1, EAX00932.1, EAX00934.1, EAX00935.1, EAX00936.1
GeneID.9687	GREB1	2	11,674,242	11,782,912	108,670	+	1	4_A375_EGR1..1..4946	84796	in gene	0	0	1	5	4	18	1	4_A375_EGR1..1	18	Gene GREB1	GREB1, KIAA0575	growth regulation by estrogen in breast cancer 1	NM_014668, NM_148903, NM_033090, hCT2287936.1, hCT2287937.1, hCT2287938.1, hCT2287939.1, hCT2351157.0, hCT2351158.0	205862_at, 210562_at, 210855_at	NP_055483.2, NP_683701.2, NP_149081.1, EAX00925.1, EAX00926.1, EAX00930.1, EAX00927.1, EAX00928.1, EAX00929.1
GeneID.23620	NTSR2	2	11,798,304	11,810,329	12,025	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3143, 2_A375_pNL97_plus_lncRNA_AR..1..4533, 4_A375_EGR1..1..4949	249, 217, 10137	in gene, in gene, in gene	1	1	1	19.5	22.5	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene NTSR2	NTR2, NTSR2	neurotensin receptor 2	NM_012344, hCT12721.3, hCT1987764.2, hCT2286539.1	206699_at	NP_036476.1, EAX00924.1, EAX00922.1, EAX00923.1
GeneID.23175	LPIN1	2	11,886,740	11,967,535	80,795	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3144, 2_A375_pNL97_plus_lncRNA_AR..1..4534, 2_A375_pNL97_plus_lncRNA_AR..1..4535	-2324, -2260, 83860	upstream, upstream, downstream	1	1	0	22.5	20.5	7	2	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene LPIN1	LPIN1, PAP1, DKFZp781P1796, KIAA0188	lipin 1	NM_145693, hCT14053.3, hCT1984189.1, hCT2287940.0	212272_at, 212274_at, 212276_at	NP_663731.1, EAX00919.1, EAX00918.1, EAX00920.1
GeneID.100422996	MIR4262	2	11,977,059	11,977,112	53	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4535	6712	downstream	0	1	0	13	20	8	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MIR4262	MIR4262	microRNA 4262	NR_036226		
GeneID.100506457	LOC100506457	2	12,246,750	12,271,711	24,961	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4536	13970	in gene	0	1	0	14	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100506457		hypothetical LOC100506457	XR_112297, XR_108396, XR_115565		
GeneID.51594	NBAS	2	15,307,032	15,701,454	394,422	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3147, 2_A375_pNL97_plus_lncRNA_AR..1..4539	14, 46	in gene, in gene	1	1	0	17	16	7	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene NBAS	NBAS, FLJ40407, NAG, DKFZp586G1219	neuroblastoma amplified sequence	NM_015909, hCT2285842.1, hCT2285843.0, hCT2285845.1, hCT2285847.1	202926_at, 240579_at, 242049_s_at	NP_056993.2, EAX00900.1, EAX00901.1, EAX00902.1, EAX00903.1
GeneID.1653	DDX1	2	15,731,770	15,771,225	39,455	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4540, 4_A375_EGR1..1..4951	36, 150	in gene, in gene	0	1	1	16	27	18	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene DDX1	UKVH5d, DDX1, DBP-RB	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	NM_004939, hCT2286081.1, hCT2286083.1, hCT2350462.0, hCT2350463.0, hCT6944.3	201241_at	NP_004930.1, EAX00894.1, EAX00895.1, EAX00896.1, EAX00897.1, EAX00898.1
GeneID.81553	FAM49A	2	16,730,727	16,805,287	74,560	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3148, 2_A375_pNL97_plus_lncRNA_AR..1..4541	77751, 77767	downstream, downstream	1	1	0	19	16	3	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene FAM49A	FLJ33961, FAM49A, DKFZp566A1524, FLJ11080	family with sequence similarity 49, member A	NM_030797, hCT1965010.1, hCT2285707.0	208092_s_at, 209683_at, 230276_at	NP_110424.1, EAX00878.1, EAX00879.1
GeneID.729475	RAD51AP2	2	17,691,988	17,699,708	7,720	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3149	106	in gene	1	0	0	16	15	6	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene RAD51AP2	RAD51AP2	RAD51 associated protein 2	NM_001099218		NP_001092688.1
GeneID.7447	VSNL1	2	17,721,807	17,837,706	115,899	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3150, 1_A375_pNL7_minus_lncRNA_AR..1..3151	-1487, -399	upstream, upstream	1	0	0	22	17	11	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene VSNL1	VSNL1, HLP3, VILIP, HPCAL3, VILIP-1, HUVISL1	visinin-like 1	NM_003385, hCT1965018.1, hCT1965019.1, hCT2285958.0, hCT23242.2, hCT2358383.0, hCT2358384.0	203797_at, 203798_s_at	NP_003376.2, EAX00872.1, EAX00871.1, EAX00873.1, EAX00874.1, EAX00875.1, EAX00870.1
GeneID.57665	RDH14	2	18,735,989	18,741,959	5,970	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3152, 2_A375_pNL97_plus_lncRNA_AR..1..4542	55, 7	in gene, in gene	1	1	0	23	23	8	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene RDH14	PAN2, RDH14, SDR7C4	retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	NM_020905, hCT1641564.1, hCT2285445.0, hCT2285446.0, hCT2285448.0	222203_s_at	NP_065956.1, EAX00857.1, EAX00855.1, EAX00856.1, EAX00858.1
GeneID.93034	NT5C1B	2	18,744,137	18,770,838	26,701	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3152, 2_A375_pNL97_plus_lncRNA_AR..1..4542	26934, 26866	downstream, downstream	1	1	0	23	23	8	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene NT5C1B	NT5C1B, AIRP, CN1B, CN-IB, MGC26640	5'-nucleotidase, cytosolic IB	NM_033253, NM_001002006, hCT2285442.0, hCT2285443.0, hCT23208.2	1554366_at, 243100_at	NP_150278.2, NP_001002006.1, EAX00852.1, EAX00853.1, EAX00854.1
GeneID.130497	OSR1	2	19,551,246	19,558,372	7,126	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3155, 2_A375_pNL97_plus_lncRNA_AR..1..4546	10612, 10521	downstream, downstream	1	1	0	19	15	14	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene OSR1	ODD, OSR1	odd-skipped related 1 (Drosophila)	NM_145260, hCT2265426.0, hCT2285428.0, hCT22919.2	228399_at	NP_660303.1, EAX00846.1, EAX00847.1, EAX00848.1
GeneID.130502	TTC32	2	20,096,514	20,101,747	5,233	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3158, 2_A375_pNL97_plus_lncRNA_AR..1..4548	19, -29	in gene, upstream	1	1	0	27	24	12	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene TTC32	TTC32		NM_001008237, hCT1966394.1, hCT23256.2	226838_at	NP_001008238.1, EAX00843.1, EAX00842.1
GeneID.57539	WDR35	2	20,110,024	20,189,884	79,860	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3158, 1_A375_pNL7_minus_lncRNA_AR..1..3159, 2_A375_pNL97_plus_lncRNA_AR..1..4548, 2_A375_pNL97_plus_lncRNA_AR..1..4549, 4_A375_EGR1..1..4955	88156, -100, 88108, 60, -148	downstream, upstream, downstream, in gene, upstream	1	1	1	24	21.5	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene WDR35	KIAA1336, WDR35, MGC33196, CED2	WD repeat domain 35	NM_001006657, NM_020779, hCT2265421.0, hCT23255.3, hCT2358429.0, hCT2358430.0	226889_at, 226890_at	NP_001006658.1, NP_065830.2, EAX00838.1, EAX00839.1, EAX00840.1, EAX00841.1
GeneID.4148	MATN3	2	20,191,813	20,212,455	20,642	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3159, 2_A375_pNL97_plus_lncRNA_AR..1..4549, 4_A375_EGR1..1..4955	22471, 22631, 22423	downstream, downstream, downstream	1	1	1	21	19	17	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene MATN3	HOA, OADIP, DIPOA, MATN3, EDM5, OS2	matrilin 3	NM_002381, hCT23276.1	206091_at	NP_002372.1, EAX00837.1
GeneID.6382	SDC1	2	20,400,558	20,425,194	24,636	-	1	4_A375_EGR1..1..4957	1418	in gene	0	0	1	13	9	15	1	4_A375_EGR1..1	15	Gene SDC1	SYND1, syndecan, SDC1, SDC, CD138	syndecan 1	NM_001006946, NM_002997, hCT2286219.0, hCT2286220.0, hCT2286221.0, hCT2286223.0	201286_at, 201287_s_at	NP_001006947.1, NP_002988.3, EAX00828.1, EAX00829.1, EAX00830.1, EAX00831.1
GeneID.100131373	LOC100131373	2	20,425,035	20,427,748	2,713	+	1	4_A375_EGR1..1..4957	-1259	upstream	0	0	1	13	9	15	1	4_A375_EGR1..1	15	Gene LOC100131373		hypothetical LOC100131373	XR_109790		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:23369	PUM2	2	20,448,453	20,527,144	78,691	-	1	4_A375_EGR1..1..4958	84680	downstream	0	0	1	8	7	14	1	4_A375_EGR1..1	14	Gene PUM2	MGC138251, PUML2, MGC138253, KIAA0235, PUMH2, PUM2, FLJ36528	pumilio homolog 2 (Drosophila)	NM_015317, hCT2266211.0, hCT2266214.0, hCT2266215.0, hCT23260.2	201493_s_at, 216221_s_at	NP_056132.1, EAX00822.1, EAX00821.1, EAX00823.1, EAX00824.1
GeneID:388	RHOB	2	20,646,835	20,649,201	2,366	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4551	925	in gene	0	1	0	17	25	13	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene RHOB	ARHB, RHOB, RHOH6, ARH6, MST081, MSTP081	ras homolog gene family, member B	NM_004040, hCT2266410.0, hCT22918.3	1553962_s_at, 1553963_at, 1553965_x_at, 212099_at, 226417_at	NP_004031.1, EAX00820.1, EAX00819.1
GeneID:64342	HS1BP3	2	20,817,584	20,850,884	33,300	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4553, 4_A375_EGR1..1..4960	-80, 5584	upstream, in gene	0	1	1	10.5	12.5	18	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene HS1BP3	HS1BP3, FLJ14249, ETM2, HS1-BP3	HCLS1 binding protein 3	NM_022460, hCT1823843.1, hCT1984360.1, hCT1987728.1, hCT1987727.1, hCT2266201.0, hCT2358413.0	1568734_s_at, 219020_at, 236530_at, 237407_at	NP_071905.3, EAX00812.1, EAX00813.1, EAX00814.1, EAX00815.1, EAX00816.1, EAX00817.1
GeneID:80526	C2orf43	2	20,884,818	21,022,827	138,009	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3162, 2_A375_pNL97_plus_lncRNA_AR..1..4554	75, 11	in gene, in gene	1	1	0	23	27	8	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene C2orf43	C2orf43, FLJ21820	chromosome 2 open reading frame 43	NM_021925, hCT1986398.1, hCT1986397.1, hCT1986396.1, hCT2266232.0, hCT23279.3	219008_at, 222192_s_at, 222193_at	NP_068744.1, EAX00807.1, EAX00806.1, EAX00808.1, EAX00809.1, EAX00810.1
GeneID:114818	KLHL29	2	23,608,298	23,931,483	323,185	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3164, 2_A375_pNL97_plus_lncRNA_AR..1..4556, 4_A375_EGR1..1..4962, 4_A375_EGR1..1..4963	139062, 138998, 189666, 305142	in gene, in gene, in gene, in gene	1	1	1	9.67	10.67	15.67	3	4_A375_EGR1..1	20	Gene KLHL29	KLHL29, KIAA1921, KBTBD9	kelch-like 29 (Drosophila)	NM_052920	1554261_at, 1554262_s_at, 220348_at, 229310_at	NP_443152.1
GeneID:54454	ATAD2B	2	23,971,534	24,149,934	178,400	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4557	-114	upstream	0	1	0	23	24	14	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ATAD2B	ATAD2B, MGC88424, KIAA1240	ATPase family, AAA domain containing 2B	NM_017552	1558807_at, 213387_at, 232908_at	NP_060022.1
GeneID:388931	MFSD2B	2	24,232,953	24,247,145	14,192	+	1	4_A375_EGR1..1..4965	7431	in gene	0	0	1	9	8	16	1	4_A375_EGR1..1	16	Gene MFSD2B	MFSD2B	major facilitator superfamily domain containing 2B	NM_001080473		NP_001073942.1
GeneID:51639	SF3B14	2	24,290,454	24,299,314	8,860	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3165, 1_A375_pNL7_minus_lncRNA_AR..1..3166, 2_A375_pNL97_plus_lncRNA_AR..1..4558, 2_A375_pNL97_plus_lncRNA_AR..1..4559, 4_A375_EGR1..1..4966	50, -7962, 34, -8206, 39	in gene, upstream, in gene, upstream, in gene	1	1	1	38	33.5	14	2	1_A375_pNL7_minus_lncRNA_AR..1	52	Gene SF3B14	HSPC175, CGI-110, Ht006, SF3B14a, SAP14, P14	splicing factor 3B, 14 kDa subunit	NM_016047, hCT13480.2	1561923_a_at, 223416_at	NP_057131.1, EAX00767.1
GeneID:9540	TP53I3	2	24,300,305	24,307,728	7,423	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3165, 1_A375_pNL7_minus_lncRNA_AR..1..3166, 2_A375_pNL97_plus_lncRNA_AR..1..4558, 2_A375_pNL97_plus_lncRNA_AR..1..4559, 4_A375_EGR1..1..4966	8484, 432, 8448, 208, 8453	downstream, in gene, downstream, in gene, downstream	1	1	1	38	33.5	14	2	1_A375_pNL7_minus_lncRNA_AR..1	52	Gene TP53I3	PIG3, TP53I3	tumor protein p53 inducible protein 3	NM_004881, NM_147184, hCT13479.2, hCT1987779.1, hCT1987780.1, hCT2265672.0, hCT2358488.0	210609_s_at	NP_004872.2, NP_671713.1, EAX00762.1, EAX00763.1, EAX00765.1, EAX00766.1, EAX00764.1
GeneID:375189	PFN4	2	24,338,244	24,346,151	7,907	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3167, 2_A375_pNL97_plus_lncRNA_AR..1..4560	39, -249	in gene, upstream	1	1	0	15	19	7	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PFN4	PFN4		NM_199346, hCT1822872.1, hCT2358380.0	1557476_at, 235827_at	NP_955378.1, EAX00760.1, EAX00761.1
GeneID:375190	LOC375190	2	24,346,350	24,392,507	46,157	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3167, 2_A375_pNL97_plus_lncRNA_AR..1..4560	-238, 50	upstream, in gene	1	1	0	15	19	7	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC375190	FLJ30851	hypothetical protein LOC375190	NM_001145710	230435_at	NP_001139182.1
GeneID:50618	ITSN2	2	24,425,735	24,583,397	157,662	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3168, 2_A375_pNL97_plus_lncRNA_AR..1..4561	128981, -123	in gene, upstream	1	1	0	17.5	12.5	5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene ITSN2	SWAP, ITSN2, SWA, PRO2015, SH3P18, SH3D1B, KIAA1256	intersectin 2	NM_006277, NM_019595, NM_147152, hCT2265659.1, hCT2265660.1, hCT2265661.1, hCT2265662.1	209898_x_at, 209907_s_at, 210545_at, 240941_at	NP_006268.2, NP_062541.3, NP_671494.2, EAX00750.1, EAX00751.1, EAX00752.1, EAX00753.1
GeneID:100507630	LOC100507630	2	24,447,506	24,449,402	1,896	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3168	-5014	upstream	1	0	0	19	12	2	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene LOC100507630		hypothetical protein LOC100507630	XM_003119858, XM_003118863, XM_003121039		XP_003119906.1, XP_003118911.1, XP_003121087.1
GeneID:8648	NCOA1	2	24,807,346	24,993,571	186,225	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3169	124302	in gene	1	0	0	19	8	2	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene NCOA1	bHLHe74, bHLHe42, SRC1, RIP160, KAT13A, MGC129720, NCOA1, F-SRC-1, MGC129719	nuclear receptor coactivator 1	NM_003743, NM_147233, NM_147223, hCT12467.3, hCT2266053.0, hCT2266054.0	209105_at, 209106_at, 209107_x_at, 210249_s_at, 231289_at	NP_003734.3, NP_671766.1, NP_671756.1, EAX00746.1, EAX00747.1, EAX00748.1
GeneID:391356	C2orf79	2	25,013,136	25,016,251	3,115	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3170, 2_A375_pNL97_plus_lncRNA_AR..1..4562	-89, -325	upstream, upstream	1	1	0	19	18	14	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene C2orf79	C2orf79	chromosome 2 open reading frame 79	NM_001013663, hCT13684.3	226243_at	NP_001013685.1, EAX00745.1
GeneID:79172	CENPO	2	25,016,333	25,042,784	26,451	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3170, 2_A375_pNL97_plus_lncRNA_AR..1..4562	-13, 243	upstream, in gene	1	1	0	19	18	14	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene CENPO	MCM21R, CENP-O, ICEN-36, CENPO, MGC11266	centromere protein O	NM_024322, hCT1815707.1, hCT1823320.3, hCT2266058.0	219472_at, 226118_at	NP_077298.1, EAX00742.1, EAX00743.1, EAX00744.1
GeneID:51277	DNAJC27	2	25,166,505	25,194,824	28,319	-	1	4_A375_EGR1..1..4968	168	in gene	0	0	1	14	15	18	1	4_A375_EGR1..1	18	Gene DNAJC27	RBJ, RabJS, DKFZp434N211, DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27	NM_016544, hCT13682.4, hCT2265471.1, hCT2265472.1, hCT2358521.0	223504_at, 223505_s_at, 227659_at, 233386_s_at	NP_057628.1, EAX00738.1, EAX00735.1, EAX00736.1, EAX00737.1
GeneID:729723	LOC729723	2	25,194,981	25,262,563	67,582	+	1	4_A375_EGR1..1..4968	-325	upstream	0	0	1	14	15	18	1	4_A375_EGR1..1	18	Gene LOC729723		hypothetical LOC729723	NR_034113	239325_at	
GeneID:22979	EFR3B	2	25,264,973	25,382,004	117,031	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4563, 4_A375_EGR1..1..4969	61283, 126915	in gene, downstream	0	1	1	9.5	13	11	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene EFR3B	EFR3B, KIAA0953	EFR3 homolog B (S. cerevisiae)	NM_014971	215326_at, 215334_at	NP_055786.1
GeneID:5443	POMC	2	25,383,722	25,391,559	7,837	-	1	4_A375_EGR1..1..4969	-329	upstream	0	0	1	4	7	14	1	4_A375_EGR1..1	14	Gene POMC	ACTH, LPH, MSH, POC, NPP, POMC, CLIP	proopiomelanocortin	NM_001035256, NM_000939, hCT13681.2, hCT1823317.1	205720_at	NP_001030333.1, NP_000930.1, EAX00729.1, EAX00730.1
GeneID:1788	DNMT3A	2	25,455,845	25,565,459	109,614	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3171, 2_A375_pNL97_plus_lncRNA_AR..1..4564, 4_A375_EGR1..1..4970, 4_A375_EGR1..1..4971	19, -13, 90723, 27811	in gene, upstream, in gene, in gene	1	1	1	10.33	14	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene DNMT3A	DNMT3A, DNMT3A2, M.HsaIIIA	DNA (cytosine-5-)-methyltransferase 3 alpha	NM_022552, NM_153759, NM_175629, NM_175630, hCT13685.2, hCT2265463.0	218457_s_at, 222640_at, 244428_at	NP_072046.2, NP_715640.2, NP_783328.1, NP_783329.1, EAX00727.1, EAX00728.1
GeneID:1838	DTNB	2	25,600,112	25,896,503	296,391	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4565, 4_A375_EGR1..1..4972	-489, 82599	upstream, in gene	0	1	1	9.5	12	12.5	2	4_A375_EGR1..1	15	Gene DTNB	MGC57126, MGC17163, DTNB	dystrobrevin, beta	NM_183360, NM_183361, NM_033147, NM_033148, NM_021907, hCT14241.3, hCT2265455.0, hCT2265456.0, hCT2265457.0, hCT2265458.0, hCT2265460.0, hCT2358418.0	214253_s_at, 215295_at, 215565_at	NP_899204.1, NP_899205.1, NP_066707.1, NP_149160.1, NP_149159.2, EAX00724.1, EAX00719.1, EAX00720.1, EAX00721.1, EAX00722.1, EAX00723.1, EAX00725.1
GeneID:729769	LOC729769	2	26,217,604	26,218,140	536	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4566	3076	downstream	0	1	0	12	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC729769	UQCRHP2	ubiquinol-cytochrome c reductase hinge protein pseudogene 2			
GeneID:391356	LOC391356	2	26,251,074	26,251,481	407	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4567	-5511	upstream	0	1	0	16	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC391356		tRNA methyltransferase 11-2 homolog (S. cerevisiae) pseudogene			
GeneID:10890	RAB10	2	26,256,729	26,360,323	103,594	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4567	263	in gene	0	1	0	16	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RAB10	RAB10		NM_016131, hCT14236.3, hCT2287373.0	222980_at, 222981_s_at	NP_057215.3, EAX00710.1, EAX00711.1
GeneID:3030	HADHA	2	26,413,504	26,467,594	54,090	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3172, 2_A375_pNL97_plus_lncRNA_AR..1..4568, 4_A375_EGR1..1..4973	10, -54, -214	in gene, upstream, upstream	1	1	1	20	30	18	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene HADHA	LCEH, HADH, LCHAD, HADHA, MTPA, ECHA, TP-ALPHA, MGC1728, GBP	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	NM_000182, hCT14237.3, hCT2280302.0	208629_s_at, 208630_at, 208631_s_at	NP_000173.2, EAX00703.1, EAX00704.1
GeneID:3032	HADHB	2	26,467,616	26,513,333	45,717	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3172, 2_A375_pNL97_plus_lncRNA_AR..1..4568, 4_A375_EGR1..1..4973	-32, 32, 192	upstream, in gene, in gene	1	1	1	20	30	18	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene HADHB	MGC87480, ECHB, HADHB, MTPB, TP-BETA, MSTP029	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	NM_000183, hCT14242.3, hCT1957722.1, hCT2358420.0	201007_at	NP_000174.1, EAX00701.1, EAX00700.1, EAX00702.1
GeneID:165082	GPR113	2	26,531,041	26,569,685	38,644	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3173, 2_A375_pNL97_plus_lncRNA_AR..1..4569, 4_A375_EGR1..1..4974	629, 717, 29877	in gene, in gene, in gene	1	1	1	12.5	11	16	2	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene GPR113	FLJ16767, GPR113, hGPCR37, PGR23	G protein-coupled receptor 113	NM_153835, NM_001145168, NM_001145169, hCT1642838.3, hCT2280299.1, hCT2343784.1, hCT2358502.0, hCT2358503.0, hCT2358504.0	1553016_at, 236808_at	NP_722577.2, NP_001138640.1, NP_001138641.1, EAX00694.1, EAX00696.1, EAX00697.1, EAX00695.1, EAX00698.1, EAX00699.1
GeneID:85465	SELI	2	26,568,954	26,618,759	49,805	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3173, 2_A375_pNL97_plus_lncRNA_AR..1..4569	102, 14	in gene, in gene	1	1	0	18	17	15	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene SELI	SELI, SEPI, EPT1, KIAA1724	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)	NM_033505, hCT1651443.3, hCT2287407.0, hCT2287411.0, hCT2358490.0	1555274_a_at, 1570371_a_at, 224686_at	NP_277040.1, EAX00690.1, EAX00691.1, EAX00692.1, EAX00693.1
GeneID:9381	OTOF	2	26,680,071	26,781,566	101,495	-	2	4_A375_EGR1..1..4975, 4_A375_EGR1..1..4976	82558, 81408	in gene, in gene	0	0	1	5.5	5	20.5	2	4_A375_EGR1..1	23	Gene OTOF	AUNB1, DFNB6, FER1L2, NSRD9, OTOF, DFNB9	otoferlin	NM_194248, NM_194323, NM_004802, NM_194322, hCT2280292.0, hCT2280293.0, hCT2280294.0, hCT2280295.0, hCT2280297.0, hCT2280298.0	1555251_a_at, 220492_s_at	NP_919224.1, NP_919304.1, NP_919303.1, NP_004793.2, EAX00683.1, EAX00687.1, EAX00682.1, EAX00684.1, EAX00685.1, EAX00686.1
GeneID:3777	KCNK3	2	26,915,581	26,954,066	38,485	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3174, 4_A375_EGR1..1..4977	3939, 787	in gene, in gene	1	0	1	14	11.5	12.5	2	4_A375_EGR1..1	18	Gene KCNK3	KCNK3, TBAK1, TASK, K2p3.1, TASK-1, OAT1	potassium channel, subfamily K, member 3	NM_002246, hCT12485.2, hCT2287433.0	205952_at	NP_002237.1, EAX00678.1, EAX00679.1
GeneID:54978	C2orf18	2	26,987,142	27,004,099	16,957	+	3	2_A375_pNL97_plus_lncRNA_AR..1..4570, 1_A375_pNL7_minus_lncRNA_AR..1..3175, 2_A375_pNL97_plus_lncRNA_AR..1..4571	-6230, 21658, 21669	upstream, downstream, downstream	1	1	0	19.5	17.5	10.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene C2orf18	FLJ20555, C2orf18, ANT2BP	chromosome 2 open reading frame 18	NM_017677, hCT2267312.0, hCT2344588.0, hCT2358373.0, hCT2358374.0	1554444_s_at, 219763_at, 225695_at	NP_060347.2, EAX00676.1, EAX00673.1, EAX00674.1, EAX00675.1
GeneID:1058	CENPA	2	27,008,882	27,017,457	8,575	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3175, 2_A375_pNL97_plus_lncRNA_AR..1..4571	-82, -71	upstream, upstream	1	1	0	24	19	16	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene CENPA	CENP-A, CENPA	centromere protein A	NM_001042426, NM_001809, hCT2267308.0, hCT2267310.1, hCT2267315.1, hCT2267316.0	204962_s_at, 210821_x_at	NP_001035891.1, NP_001800.1, EAX00669.1, EAX00670.1, EAX00671.1, EAX00672.1
GeneID:56896	DPYSL5	2	27,070,969	27,173,219	102,250	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3176, 2_A375_pNL97_plus_lncRNA_AR..1..4572, 4_A375_EGR1..1..4978	-9433, -9353, 487	upstream, upstream, in gene	1	1	1	19.5	22.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene DPYSL5	DPYSL5, Ulip6, CRMP5, FLJ45383, CRMP-5, CRAM	dihydropyrimidinase-like 5	NM_020134, hCT2267318.0, hCT2267319.0	222797_at, 224100_s_at	NP_064519.2, EAX00666.1, EAX00667.1
GeneID:22924	MAPRE3	2	27,193,525	27,250,087	56,562	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3177, 2_A375_pNL97_plus_lncRNA_AR..1..4573, 2_A375_pNL97_plus_lncRNA_AR..1..4574, 2_A375_pNL97_plus_lncRNA_AR..1..4575, 4_A375_EGR1..1..4979	23254, -85, 23179, 62347, 62835	in gene, upstream, in gene, downstream, downstream	1	1	1	19	31.33	11	3	2_A375_pNL97_plus_lncRNA_AR..1	53	Gene MAPRE3	EBF3-S, EBF3, MAPRE3, EB3, RP3	microtubule-associated protein, RP/EB family, member 3	NM_012326, hCT14820.1, hCT2267320.0, hCT2267321.0, hCT2267323.0, hCT2267324.0, hCT2358398.0, hCT2358397.0	203841_x_at, 203842_s_at, 214270_s_at, 229682_at	NP_036458.2, EAX00662.1, EAX00660.1, EAX00663.1, EAX00664.1, EAX00666.1, EAX00661.1, EAX00665.1
GeneID:54867	TMEM214	2	27,255,774	27,264,565	8,791	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3178, 2_A375_pNL97_plus_lncRNA_AR..1..4575, 2_A375_pNL97_plus_lncRNA_AR..1..4576, 4_A375_EGR1..1..4979, 4_A375_EGR1..1..4980	18338, 98, 18402, 368, 18029	downstream, in gene, downstream, in gene, downstream	1	1	1	18	22	22.5	2	4_A375_EGR1..1	27	Gene TMEM214	FLJ39682, FLJ20254, TMEM214	transmembrane protein 214	NM_001083590, NM_017727, hCT14833.3, hCT1983760.1, hCT2267327.0, hCT2267328.0, hCT2358487.0, hCT2358488.0	217899_at	NP_001077059.1, NP_060197.4, EAX00654.1, EAX00655.1, EAX00656.1, EAX00658.1, EAX00657.1, EAX00659.1
GeneID:80509	AGBL5	2	27,274,491	27,293,490	18,999	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3178, 2_A375_pNL97_plus_lncRNA_AR..1..4576, 2_A375_pNL97_plus_lncRNA_AR..1..4577, 4_A375_EGR1..1..4980	-379, -315, 20037, -666	upstream, upstream, downstream, upstream	1	1	1	16.5	20.5	17.5	2	4_A375_EGR1..1	27	Gene AGBL5	FLJ21839, AGBL5	ATP/GTP binding protein-like 5	NM_001035507, NM_021831, hCT2267329.0, hCT2267330.0, hCT2267331.0, hCT2267332.0, hCT2358454.0	218480_at, 231857_s_at, 236889_at	NP_001030584.1, NP_068603.4, EAX00649.1, EAX00650.1, EAX00651.1, EAX00653.1, EAX00652.1
GeneID:100128731	LOC100128731	2	27,293,340	27,294,567	1,227	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4577	39	in gene	0	1	0	14	19	8	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100128731	OST4, DKFZp686A0722	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4	NM_001134693		NP_001128165.1
GeneID:11117	EMILIN1	2	27,301,435	27,309,271	7,836	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3179, 2_A375_pNL97_plus_lncRNA_AR..1..4577, 2_A375_pNL97_plus_lncRNA_AR..1..4578, 4_A375_EGR1..1..4981, 4_A375_EGR1..1..4982	7269, -8907, 7429, 4085, 5157	in gene, upstream, in gene, in gene, in gene	1	1	1	13	14.25	15.5	4	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene EMILIN1	gp115, EMILIN1, DKFZp586M121, EMI, EMILIN	elastin microfibril interfacer 1	NM_007046, hCT14817.3, hCT1957724.1, hCT2267333.0, hCT2358395.0	204163_at	NP_008977.1, EAX00644.1, EAX00645.1, EAX00646.1, EAX00647.1
GeneID:3795	KHK	2	27,309,611	27,323,619	14,008	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3179, 2_A375_pNL97_plus_lncRNA_AR..1..4578, 4_A375_EGR1..1..4981, 4_A375_EGR1..1..4982	-907, -747, -4091, -3019	upstream, upstream, upstream, upstream	1	1	1	12.67	12.67	18	3	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene KHK	KHK		NM_000221, NM_006488, hCT14818.3, hCT14819.3, hCT2358437.0, hCT2358436.0	205175_s_at, 211026_s_at	NP_000212.1, NP_006479.1, EAX00640.1, EAX00641.1, EAX00642.1, EAX00643.1
GeneID:10669	CGREF1	2	27,322,221	27,341,995	19,774	-	1	4_A375_EGR1..1..4983	-8936	upstream	0	0	1	8	8	13	1	4_A375_EGR1..1	13	Gene CGREF1	CGREF1, CGR11	cell growth regulator with EF-hand domain 1	NM_006569, NM_001166239, NM_001166240, NM_001166241, hCT1822887.2, hCT2265617.0, hCT2358414.0, hCT2358415.0, hCT2358416.0	205937_at	NP_006560.3, NP_001159711.1, NP_001159712.1, NP_001159713.1, EAX00638.1, EAX00637.1, EAX00635.1, EAX00636.1, EAX00639.1
GeneID:84696	ABHD1	2	27,346,657	27,353,680	7,023	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3180, 2_A375_pNL97_plus_lncRNA_AR..1..4579, 4_A375_EGR1..1..4983, 4_A375_EGR1..1..4984	10799, 10879, 4276, 13759	downstream, downstream, in gene, downstream	1	1	1	11.67	11.67	13.33	3	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene ABHD1	LABH1, FLJ36128, ABHD1	abhydrolase domain containing 1	NM_032604, hCT14836.3, hCT2358497.0, hCT2358498.0, hCT2358499.0	1560117_at, 232550_at, 236461_at	NP_115993.3, EAX00632.1, EAX00631.1, EAX00633.1, EAX00634.1
GeneID:10113	PREB	2	27,353,624	27,357,542	3,918	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3180, 2_A375_pNL97_plus_lncRNA_AR..1..4579, 4_A375_EGR1..1..4983, 4_A375_EGR1..1..4984	86, 6, 6609, -2874	in gene, in gene, downstream, upstream	1	1	1	11.67	11.67	13.33	3	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene PREB	PREB, MGC3467, SEC12	prolactin regulatory element binding	NM_013388, hCT14821.3, hCT2265612.0, hCT2265614.0, hCT2358400.0, hCT2358401.0	217861_s_at	NP_037520.1, EAX00627.1, EAX00628.1, EAX00626.1, EAX00629.1, EAX00630.1
GeneID:339779	C2orf53	2	27,359,715	27,362,332	2,617	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3180, 2_A375_pNL97_plus_lncRNA_AR..1..4579, 4_A375_EGR1..1..4983, 4_A375_EGR1..1..4984	4876, 4796, 11399, 1916	downstream, downstream, downstream, in gene	1	1	1	11.67	11.67	13.33	3	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene C2orf53	C2orf53, MGC44505	chromosome 2 open reading frame 53	NM_178553, hCT1960496.3	237319_at	NP_848648.2, EAX00625.1
GeneID:8884	SLC5A6	2	27,422,455	27,435,175	12,720	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3181, 2_A375_pNL97_plus_lncRNA_AR..1..4580	-121, 71	upstream, in gene	1	1	0	16	16	12	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene SLC5A6	SMVT, SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	NM_021095, NR_028323, hCT14835.3, hCT1955577.1, hCT2265610.0, hCT2358491.0	204087_s_at	NP_066918.2, EAX00622.1, EAX00620.1, EAX00621.1, EAX00623.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.51374	C2orf28	2	27,434,899	27,440,046	5,147	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3181, 2_A375_pNL97_plus_lncRNA_AR..1..4580	397, 205	in gene, in gene	1	1	0	16	16	12	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene C2orf28	p18, PRO240, C2orf28, APR--3, APR3, HSPC013, APR-3	chromosome 2 open reading frame 28	NM_016085, NM_080592, NM_001170795, hCT14824.4, hCT1955576.1, hCT1970700.1, hCT2267343.0, hCT2267344.0	219329_s_at	NP_057169.2, NP_542159.3, NP_001164266.1, EAX00615.1, EAX00616.1, EAX00617.1, EAX00618.1, EAX00619.1
GeneID.790	CAD	2	27,440,258	27,466,654	26,396	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3181, 2_A375_pNL97_plus_lncRNA_AR..1..4580	-4982, -5154	upstream, upstream	1	1	0	16	16	12	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene CAD	CAD		NM_004341, hCT14822.3, hCT2267345.0, hCT2267346.0	1564064_at, 202715_at	NP_004332.2, EAX00612.1, EAX00613.1, EAX00614.1
GeneID.7781	SLC30A3	2	27,477,440	27,485,960	8,520	-	1	4_A375_EGR1..1..4985	264	in gene	0	0	1	11	12	15	1	4_A375_EGR1..1	15	Gene SLC30A3	ZNT3, SLC30A3	solute carrier family 30 (zinc transporter), member 3	NM_003459, hCT14823.2, hCT2265806.0	207035_at	NP_003450.2, EAX00611.1, EAX00610.1
GeneID.57159	TRIM54	2	27,505,297	27,530,307	25,010	+	1	4_A375_EGR1..1..4986	24367	in gene	0	0	1	7	12	17	1	4_A375_EGR1..1	17	Gene TRIM54	RNF30, MURF, TRIM54, MURF-3	tripartite motif containing 54	NM_032546, NM_187841, hCT14832.3, hCT2267349.0	233669_s_at	NP_115935.3, NP_912730.2, EAX00606.1, EAX00607.1
GeneID.7349	UCN	2	27,530,265	27,531,130	865	-	1	4_A375_EGR1..1..4986	1466	downstream	0	0	1	7	12	17	1	4_A375_EGR1..1	17	Gene UCN	MGC129975, UCN, UI, MGC129974, UROC	urocortin	NM_003353, hCT14836.3	206072_at	NP_003344.1, EAX00605.1
GeneID.4358	MPV17	2	27,532,380	27,545,989	13,609	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3182, 4_A375_EGR1..1..4986, 4_A375_EGR1..1..4987	-79, 16305, -15	upstream, downstream, upstream	1	0	1	14	16	17	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene MPV17	SYM1, MTDPS6, MPV17	MpV17 mitochondrial inner membrane protein	NM_002437, hCT14825.3, hCT1984967.1, hCT1984968.1, hCT1984969.1, hCT1984970.1, hCT1984971.1, hCT1984972.1, hCT2265797.0	203466_at	NP_002428.1, EAX00600.1, EAX00597.1, EAX00598.1, EAX00601.1, EAX00603.1, EAX00599.1, EAX00602.1, EAX00604.1
GeneID.2976	GTF3C2	2	27,548,721	27,579,868	31,147	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3182, 2_A375_pNL97_plus_lncRNA_AR..1..4581, 4_A375_EGR1..1..4987	33820, 460, 33884	downstream, in gene, downstream	1	1	1	19	18	14	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene GTF3C2	KIAA0011, GTF3C2, TFIIIC-BETA, TFIIIC110	general transcription factor IIIC, polypeptide 2, beta 110kDa	NM_001521, NM_001035521, hCT14831.3, hCT2265791.0, hCT2265794.0	204366_s_at, 210620_s_at, 212429_s_at	NP_001512.1, NP_001030598.1, EAX00594.1, EAX00595.1, EAX00596.1
GeneID.100505605	LOC100505605	2	27,579,113	27,583,123	4,010	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3183, 2_A375_pNL97_plus_lncRNA_AR..1..4581, 2_A375_pNL97_plus_lncRNA_AR..1..4582	14103, 295, 14135	downstream, in gene, downstream	1	1	0	41.5	45	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	74	Gene LOC100505605		hypothetical LOC100505605	XR_112299, XR_109962, XR_115595		
GeneID.8890	EIF2B4	2	27,587,219	27,593,324	6,105	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3183, 2_A375_pNL97_plus_lncRNA_AR..1..4581, 2_A375_pNL97_plus_lncRNA_AR..1..4582, 4_A375_EGR1..1..4988, 4_A375_EGR1..1..4989	106, 13916, 76, -6984, -8212	in gene, downstream, in gene, upstream, upstream	1	1	1	24.75	28.25	15.25	4	2_A375_pNL97_plus_lncRNA_AR..1	74	Gene EIF2B4	EIF-2B, EIF2Bdelta, EIF2B4, DKFZp586J0119, EIF2B	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa	NM_015636, NM_001034116, NM_172195, hCT1823410.1, hCT1984358.1, hCT1984359.1, hCT2358369.0, hCT2358370.0, hCT2358371.0	209429_x_at, 215482_s_at	NP_056451.3, NP_001029288.1, NP_751945.2, EAX00587.1, EAX00588.1, EAX00592.1, EAX00589.1, EAX00590.1, EAX00591.1
GeneID.9784	SNX17	2	27,593,389	27,599,994	6,605	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3183, 2_A375_pNL97_plus_lncRNA_AR..1..4582, 4_A375_EGR1..1..4988, 4_A375_EGR1..1..4989	-173, -141, 6899, 8147	upstream, upstream, downstream, downstream	1	1	1	27.33	32.33	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	74	Gene SNX17	KIAA0064, SNX17	sorting nexin 17	NM_014748, hCT1823407.1, hCT2358358.0, hCT2358359.0	200991_s_at	NP_055563.1, EAX00585.1, EAX00584.1, EAX00586.1
GeneID.130557	ZNF513	2	27,600,102	27,603,593	3,491	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3183, 2_A375_pNL97_plus_lncRNA_AR..1..4582, 4_A375_EGR1..1..4988, 4_A375_EGR1..1..4989	10377, 10345, 3305, 2057	downstream, downstream, in gene, in gene	1	1	1	27.33	32.33	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	74	Gene ZNF513	RP58, HMFT0656, ZNF513, FLJ32203	zinc finger protein 513	NM_144631, hCT1823416.2	225753_at	NP_653232.3, EAX00583.1
GeneID.5496	PPM1G	2	27,604,061	27,632,496	28,435	-	2	4_A375_EGR1..1..4988, 4_A375_EGR1..1..4989	32208, 30960	downstream, downstream	0	0	1	8	11.5	18	2	4_A375_EGR1..1	20	Gene PPM1G	PP2CG, MGC2870, MGC1675, PP2CGAMMA, PPP2CG, PPM1G	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	NM_177983, hCT12316.3	200913_at	NP_817092.1, EAX00582.1
GeneID.84450	ZNF512	2	27,805,893	27,845,963	40,070	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4583	45947	downstream	0	1	0	17	21	8	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ZNF512	MGC111046, KIAA1805, ZNF512, FLJ51176	zinc finger protein 512	NM_032434, hCT1823417.2, hCT2267299.0, hCT2358404.0, hCT2358405.0	1553218_a_at, 225050_at	NP_115810.2, EAX00562.1, EAX00563.1, EAX00564.1, EAX00565.1
GeneID.79635	CCDC121	2	27,848,506	27,851,898	3,392	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4583	56	in gene	0	1	0	17	21	8	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CCDC121	FLJ13646, FLJ43364, CCDC121	coiled-coil domain containing 121	NM_024584, NM_001142683	220321_s_at	NP_078860.2, NP_001136155.1
GeneID.11321	GPN1	2	27,851,515	27,873,713	22,198	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4583	325	in gene	0	1	0	17	21	8	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene GPN1	NTPBP, MBDIN, XAB1, GPN1, FLJ51176, ATPBD1A	GPN-loop GTPase 1	NM_007266, NM_001145047, NM_001145048, NM_001145049, NR_026735, hCT12317.3, hCT1984366.1	209313_at	NP_009197.2, NP_001138519.1, NP_001138520.1, NP_001138521.1, EAX00557.1, EAX00556.1
GeneID.9553	MRPL33	2	27,994,584	28,002,608	8,024	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3185, 2_A375_pNL97_plus_lncRNA_AR..1..4585, 4_A375_EGR1..1..4990	166, 40, 200	in gene, in gene, in gene	1	1	1	15	19	16	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MRPL33	MGC13694, C2orf1, L33mt, MGC111093, RPL33L, MRP-L33, MGC23922, MRPL33	mitochondrial ribosomal protein L33	NM_145330, NM_004891, hCT1971564.1, hCT2358466.0	203781_at	NP_663303.1, NP_004882.1, EAX00552.1, EAX00553.1
GeneID.64080	RBKS	2	28,004,266	28,113,223	108,957	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3185, 1_A375_pNL7_minus_lncRNA_AR..1..3186, 2_A375_pNL97_plus_lncRNA_AR..1..4585, 2_A375_pNL97_plus_lncRNA_AR..1..4586, 4_A375_EGR1..1..4990	118471, 19431, 118599, 19399, 118439	downstream, in gene, downstream, in gene, downstream	1	1	1	21	22.5	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene RBKS	RBSK, RBKS, DKFZp686G13268	ribokinase	NM_022128, hCT2358474.0, hCT8082.2	219222_at, 57540_at	NP_071411.1, EAX00551.1, EAX00550.1
GeneID.9577	BRE	2	28,113,482	28,561,768	448,286	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3187, 2_A375_pNL97_plus_lncRNA_AR..1..4587	123190, 123158	in gene, in gene	1	1	0	18	17	2	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene BRE	BRE, BRCC45, BRCC4	brain and reproductive organ-expressed (TNFRSF1A modulator)	NM_199193, NM_199194, NM_199192, NM_199191, NM_004899, hCT1951009.2, hCT2267967.0, hCT2267968.0, hCT2358360.0, hCT2358361.0, hCT2358362.0, hCT6849.2	1568768_s_at, 205550_s_at, 211566_x_at, 212645_x_at	NP_954663.1, NP_954664.1, NP_004890.2, NP_954662.1, NP_954661.1, EAX00548.1, EAX00542.1, EAX00543.1, EAX00544.1, EAX00545.1, EAX00546.1, EAX00547.1
GeneID.403150	FLJ31356	2	28,807,276	28,817,539	10,263	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3188, 2_A375_pNL97_plus_lncRNA_AR..1..4588, 2_A375_pNL97_plus_lncRNA_AR..1..4589	2099, 3851, 2115	in gene, in gene, in gene	1	1	0	20.5	20.5	11	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene FLJ31356		hypothetical protein FLJ31356	XR_112303, XR_109966, XR_115599	1560932_at	
GeneID.2355	FOSL2	2	28,615,779	28,637,516	21,737	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3188, 2_A375_pNL97_plus_lncRNA_AR..1..4588, 2_A375_pNL97_plus_lncRNA_AR..1..4589, 4_A375_EGR1..1..4991	-339, -1891, -355, 19197	upstream, upstream, upstream, in gene	1	1	1	16	16	13	3	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene FOSL2	FOSL2, FRA2, FLJ23306	FOS-like antigen 2	NM_005253, hCT2267971.0, hCT2267972.0, hCT2267973.0, hCT2358524.0	205409_at, 218880_at, 218881_s_at, 225262_at	NP_005244.1, EAX00537.1, EAX00538.1, EAX00539.1, EAX00540.1
GeneID.151056	PLB1	2	28,718,938	28,866,654	147,716	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3189, 2_A375_pNL97_plus_lncRNA_AR..1..4590, 4_A375_EGR1..1..4994	88118, 114630, 95942	in gene, in gene, in gene	1	1	1	15.33	17	9.33	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PLB1	PLB, PLB1, PLB/LIP, hPLB	phospholipase B1	NM_153021, NM_001170585, hCT2267975.3, hCT2342678.1, hCT2351204.0, hCT2351205.0, hCT2351206.0	235703_at	NP_694566.4, NP_001164056.1, EAX00532.1, EAX00533.1, EAX00535.1, EAX00536.1, EAX00534.1
GeneID.100505774	LOC100505774	2	28,931,916	28,959,030	27,114	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3190, 2_A375_pNL97_plus_lncRNA_AR..1..4591	18534, 18518	in gene, in gene	1	1	0	27	30	9	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene LOC100505774		hypothetical LOC100505774	XR_112304, XR_109967, XR_115600		
GeneID.5500	PPP1CB	2	28,974,614	29,025,806	51,192	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3191, 2_A375_pNL97_plus_lncRNA_AR..1..4592	-86, -150	upstream, upstream	1	1	0	22	32	9	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene PPP1CB	PP1beta, PPP1CD, MGC3672, PP-1B, PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	NM_002709, NM_206876, hCT1639990.2, hCT2267976.0, hCT2358378.0, hCT2358379.0	201407_s_at, 201408_at, 201409_s_at, 228222_at	NP_002700.1, NP_996759.1, EAX00527.1, EAX00528.1, EAX00529.1, EAX00530.1
GeneID.55006	TRMT61B	2	29,072,687	29,093,175	20,488	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3192, 2_A375_pNL97_plus_lncRNA_AR..1..4593	87, -73	in gene, upstream	1	1	0	23	24	18	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene TRMT61B	DKFZp564I2178, FLJ20628, TRMT61B	tRNA methyltransferase 61 homolog B (S. cerevisiae)	NM_017910, hCT1822715.2, hCT2264902.0	221229_s_at	NP_060380.3, EAX00525.1, EAX00524.1
GeneID.23160	WDR43	2	29,117,533	29,171,080	53,547	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3193, 2_A375_pNL97_plus_lncRNA_AR..1..4594	-157, -157	upstream, upstream	1	1	0	38	47	9	1	2_A375_pNL97_plus_lncRNA_AR..1	47	Gene WDR43	NET12, WDR43	WD repeat domain 43	NM_015131	214662_at	NP_055946.1
GeneID.79745	CLIP4	2	29,338,308	29,406,679	68,371	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4595, 2_A375_pNL97_plus_lncRNA_AR..1..4596	-766, 764	upstream, in gene	0	1	0	11.5	14.5	6	2	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene CLIP4	RSNL2, FLJ32705, FLJ21069, CLIP4	CAP-GLY domain containing linker protein family, member 4	NM_024692, hCT1822711.2, hCT2267986.0, hCT2267987.0, hCT2267988.0, hCT2267989.0, hCT2267990.0, hCT2267991.0	219944_at, 226425_at	NP_078968.3, EAX00509.1, EAX00510.1, EAX00511.1, EAX00512.1, EAX00514.1, EAX00513.1, EAX00515.1
GeneID.238	ALK	2	29,415,640	30,144,432	728,792	-	7	1_A375_pNL7_minus_lncRNA_AR..1..3194, 1_A375_pNL7_minus_lncRNA_AR..1..3195, 2_A375_pNL97_plus_lncRNA_AR..1..4597, 4_A375_EGR1..1..4995, 1_A375_pNL7_minus_lncRNA_AR..1..3196, 2_A375_pNL97_plus_lncRNA_AR..1..4598, 4_A375_EGR1..1..4996	627466, 173296, 173264, 706240, 1264, 1216, 206	in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	24.25	24.25	10.5	4	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene ALK	NBLST3, ALK, TFG/ALK, CD246	anaplastic lymphoma receptor tyrosine kinase	NM_004304, hCT1666334.3, hCT2264312.0, hCT2264313.0	208211_s_at, 208212_s_at	NP_004295.2, EAX00506.1, EAX00507.1, EAX00508.1
GeneID.51646	YPEL5	2	30,369,750	30,383,399	13,649	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4600	-310	upstream	0	1	0	22	26	7	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene YPEL5	YPEL5, CGI-127	yippee-like 5 (Drosophila)	NM_016061, NM_001127399, NM_001127400, NM_001127401, hCT1964309.1, hCT1964310.0, hCT1964311.1, hCT1964312.1, hCT1966037.1, hCT2358522.0, hCT6647.1	217783_s_at, 222408_s_at	NP_057145.1, NP_001120871.1, NP_001120872.1, NP_001120873.1, EAX00499.1, EAX00500.1, EAX00501.1, EAX00502.1, EAX00503.1, EAX00504.1, EAX00505.1
GeneID.253558	LCLAT1	2	30,670,123	30,867,091	196,968	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4602, 4_A375_EGR1..1..4997	37, 309	in gene, in gene	0	1	1	9	20	17	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LCLAT1	LCLAT1, ALCAT1, AGPAT8, HSRG1849, FLJ37965, LYCAT, 1AGPAT8, UNQ1849	lysocardiolipin acyltransferase 1	NM_001002257, NM_182551, hCT1641103.4	226996_at	NP_001002257.1, NP_872357.2, EAX00495.1
GeneID.79623	GALNT14	2	31,133,333	31,361,571	228,238	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3199, 1_A375_pNL7_minus_lncRNA_AR..1..3200, 2_A375_pNL97_plus_lncRNA_AR..1..4603, 2_A375_pNL97_plus_lncRNA_AR..1..4604, 2_A375_pNL97_plus_lncRNA_AR..1..4605	30947, 163, 30915, 29699, -29	in gene, in gene, in gene, in gene, upstream	1	1	0	21.33	23.67	6.33	3	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene GALNT14	FLJ12691, FLJ13977, GALNT14, GalNac-T14, GalNac-T10, GALNT15	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	NM_024572, hCT1822791.2, hCT2264429.0, hCT2264432.0, hCT2358538.0	1560180_at, 219271_at	NP_078848.2, EAX00487.1, EAX00488.1, EAX00488.1, EAX00489.1
GeneID.30845	EHD3	2	31,456,880	31,491,260	34,380	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3201, 2_A375_pNL97_plus_lncRNA_AR..1..4606, 4_A375_EGR1..1..4998	0, 16, 752	in gene, in gene, in gene	1	1	1	19	18	12	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene EHD3	EHD3, PAST3	EH-domain containing 3	NM_014600, hCT12598.3, hCT2264965.0	218935_at, 241267_at	NP_055415.1, EAX00480.1, EAX00481.1
GeneID.6716	SRD5A2	2	31,749,656	31,806,040	56,384	-	1	4_A375_EGR1..1..4999	72	in gene	0	0	1	3	13	16	1	4_A375_EGR1..1	16	Gene SRD5A2	SRD5A2, MGC138457	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)	NM_000348, hCT12602.3	206938_at	NP_000339.2, EAX00476.1
GeneID.51072	MEMO1	2	32,092,892	32,235,698	142,806	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3202, 2_A375_pNL97_plus_lncRNA_AR..1..4607, 4_A375_EGR1..1..5000	-366, -334, -366	upstream, upstream, upstream	1	1	1	27	43	18	1	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene MEMO1	MEMO1, C2orf4, FLJ25031, DKFZp434I0135, NS5ATP7, MEMO, CGI-27	mediator of cell motility 1	NM_015955, NM_001137602, hCT2264777.0, hCT2264778.0, hCT2264779.0, hCT2264781.1, hCT2264782.0, hCT2358439.0, hCT2358440.0, hCT2358441.0	219065_s_at	NP_057039.1, NP_001131074.1, EAX00468.1, EAX00469.1, EAX00471.1, EAX00472.1, EAX00467.1, EAX00470.1, EAX00473.1, EAX00474.1
GeneID.84661	DPY30	2	32,248,972	32,264,844	15,872	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3203, 2_A375_pNL97_plus_lncRNA_AR..1..4608, 4_A375_EGR1..1..5001	-116, -180, -116	upstream, upstream, upstream	1	1	1	16	23	18	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene DPY30	Saf19, DPY30, HDPY-30	dpy-30 homolog (C. elegans)	NM_032574, hCT2264776.0, hCT2344566.0, hCT2344567.0, hCT2358372.0	224129_s_at	NP_115963.1, EAX00463.1, EAX00464.1, EAX00465.1, EAX00466.1
GeneID.6683	SPAST	2	32,288,680	32,382,706	94,026	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3204, 2_A375_pNL97_plus_lncRNA_AR..1..4609, 4_A375_EGR1..1..5002	102136, 102104, 102200	downstream, downstream, downstream	1	1	1	25	24	20	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene SPAST	ADPSP, KIAA1083, SPG4, FSP2, SPAST	spastin	NM_014946, NM_199436, hCT14184.2, hCT1957721.1	207724_s_at, 209748_at	NP_055761.2, NP_955468.1, EAX00461.1, EAX00462.1
GeneID.55676	SLC30A6	2	32,390,910	32,449,181	58,271	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3204, 2_A375_pNL97_plus_lncRNA_AR..1..4609, 4_A375_EGR1..1..5002	-94, -126, -30	upstream, upstream, upstream	1	1	1	25	24	20	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene SLC30A6	MST103, MGC45055, MSTP103, SLC30A6, FLJ31101, ZNT6	solute carrier family 30 (zinc transporter), member 6	NM_017964, NM_001193513, NM_001193514, NM_001193515, hCT14186.3, hCT2358340.0, hCT2358341.0, hCT2358342.0, hCT2358343.0	226181_at, 226182_at, 243643_x_at	NP_060434.2, NP_001180442.1, NP_001180443.1, NP_001180444.1, EAX00456.1, EAX00459.1, EAX00457.1, EAX00458.1, EAX00460.1
GeneID.57448	BIRC6	2	32,582,096	32,843,966	261,870	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3205, 2_A375_pNL97_plus_lncRNA_AR..1..4610, 4_A375_EGR1..1..5003	-219, -48, 270592	upstream, upstream, downstream	1	1	1	14.5	15.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene BIRC6	FLJ13726, KIAA1289, FLJ13786, BRUCE, BIRC6, APOLLON	baculoviral IAP repeat containing 6	NM_016252, hCT14841.3, hCT2265371.0, hCT2265372.0, hCT2265373.0, hCT2358515.0	224635_s_at, 233093_s_at	NP_057336.3, EAX00443.1, EAX00444.1, EAX00445.1, EAX00446.1, EAX00447.1
GeneID.55622	TTC27	2	32,853,087	33,046,118	193,031	+	1	4_A375_EGR1..1..5003	-399	upstream	0	0	1	11	11	16	1	4_A375_EGR1..1	16	Gene TTC27	FLJ20272, TTC27	tetratricopeptide repeat domain 27	NM_001193509, NM_017735, hCT14840.2, hCT2264589.0	218710_at, 244248_at	NP_001180438.1, NP_060205.3, EAX00441.1, EAX00442.1
GeneID.4052	LTBP1	2	33,172,369	33,624,576	452,207	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3206, 2_A375_pNL97_plus_lncRNA_AR..1..4611, 2_A375_pNL97_plus_lncRNA_AR..1..4612, 2_A375_pNL97_plus_lncRNA_AR..1..4613, 2_A375_pNL97_plus_lncRNA_AR..1..4614	122671, 123163, 187023, 328543, 428207	in gene, in gene, in gene, in gene, in gene	1	1	0	16.25	17.5	6.5	4	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LTBP1	MGC163161, LTBP1	latent transforming growth factor beta binding protein 1	NM_206943, NM_000627, NM_001166264, NM_001166265, NM_001166266, hCT2264591.0, hCT2264592.0, hCT2264593.0, hCT2264594.0, hCT2358465.0	202728_s_at, 202729_s_at	NP_996826.2, NP_000618.3, NP_001159736.1, NP_001159737.1, NP_001159738.1, EAX00435.1, EAX00436.1, EAX00437.1, EAX00438.1, EAX00439.1
GeneID.25780	RASGRP3	2	33,661,416	33,789,798	128,382	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3207	39576	in gene	1	0	0	18	8	3	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene RASGRP3	RASGRP3, GRP3, KIAA0846	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	NM_170672, NM_001139488, NM_015376, hCT1983457.1, hCT1983458.1, hCT2264598.0	205801_s_at, 244526_at	NP_733772.1, NP_001132960.1, NP_056191.1, EAX00432.1, EAX00433.1, EAX00434.1
GeneID.25940	FAM98A	2	33,808,729	33,824,362	15,633	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3208, 2_A375_pNL97_plus_lncRNA_AR..1..4615	-374, -163	upstream, upstream	1	1	0	17	17	10	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene FAM98A	FAM98A, DKFZp686O03192, DKFZp564F0522	family with sequence similarity 98, member A	NM_015475, hCT1641750.3	212333_at, 239487_at, 241832_at	NP_056290.3, EAX00431.1
GeneID.100288911	LOC100288911	2	36,565,035	36,582,713	17,678	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3213	-2311	upstream	1	0	0	18	15	9	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100288911		hypothetical LOC100288911	XR_109968, XR_115525, XR_108260		
GeneID.51232	CRIM1	2	36,583,397	36,778,278	194,881	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3213, 2_A375_pNL97_plus_lncRNA_AR..1..4616	1627, 71659	in gene, in gene	1	1	0	15	18.5	7	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CRIM1	MGC138194, CRIM1, S52	cysteine rich transmembrane BMP regulator 1 (chordin-like)	NM_016441, hCT8309.2	202551_s_at, 202552_s_at, 228496_s_at	NP_057525.1, EAX00426.1
GeneID.5212	VIT	2	36,923,833	37,041,937	118,104	+	1	4_A375_EGR1..1..5004	111959	in gene	0	0	1	7	4	18	1	4_A375_EGR1..1	18	Gene VIT	VIT, MGC70561, MGC149746, DKFZp313L1517	vitrin	NM_001177969, NM_001177970, NM_001177971, NM_001177972, NM_053276, hCT2264225.0, hCT2358452.0, hCT2358453.0, hCT8310.2	227899_at	NP_001171440.1, NP_001171441.1, NP_444506.2, NP_001171442.1, NP_001171443.1, EAX00417.1, EAX00416.1, EAX00418.1, EAX00419.1



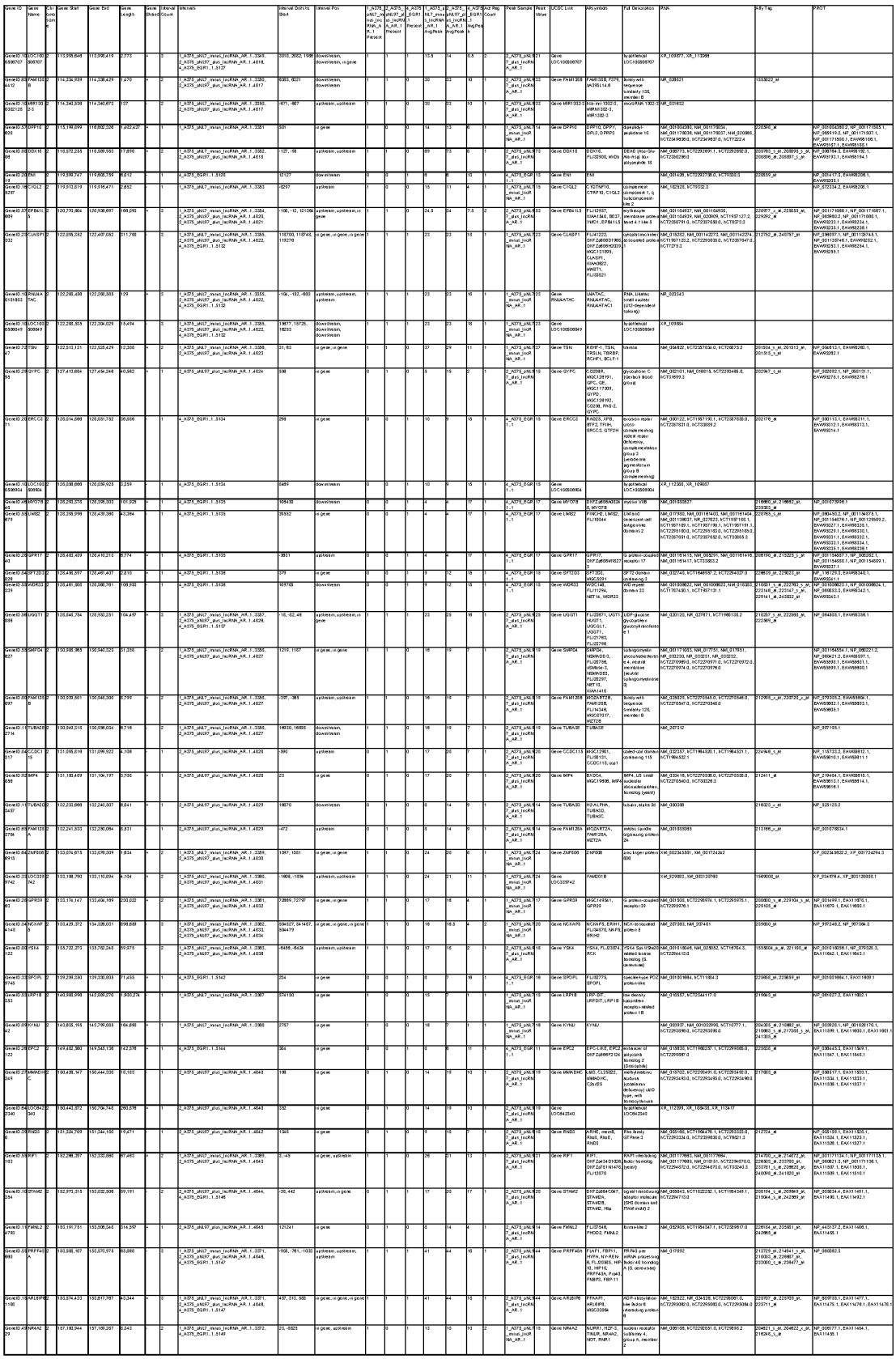


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.4211	MEIS1	2	66,662,532	66,799,891	137,359	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3272, 2_A375_pNL97_plus_lncRNA_AR..1..4699	-452, -436	upstream, upstream	1	1	0	23	22	7	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene MEIS1	MEIS1, MGC43380	Meis homeobox 1	NM_002398, hCT1961198.1, hCT2261565.0, hCT2261587.0, hCT2261566.0, hCT2358435.0	1559477_s_at, 204069_at, 242172_at	NP_002389.1, EAW99894.1, EAW99892.1, EAW99893.1, EAW99895.1, EAW99896.1
GeneID.54465	ETAA1	2	67,624,442	67,637,533	13,091	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4702	310	in gene	0	1	0	12	15	7	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene ETAA1	ETAA1, FLJ22647	Ewing tumor-associated antigen 1	NM_019002, hCT13940.3		NP_061875.2, EAW99886.1
GeneID.10436	C1D	2	68,269,332	68,290,159	20,827	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4703	63	in gene	0	1	0	13	17	15	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene C1D	SUNCOR, MGC14659, SUN-CoR, LRP1, MGC12261, C1D	C1D nuclear receptor co-repressor	NM_006333, NM_173177, NM_001190263, NM_001190265, hCT2261656.0, hCT2261657.0, hCT2261658.0	200056_s_at	NP_006324.1, NP_775269.1, NP_001177192.1, NP_001177194.1, EAW99884.1, EAW99886.1, EAW99885.1
GeneID.116143	WDR92	2	68,357,281	68,384,656	27,375	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3274, 2_A375_pNL97_plus_lncRNA_AR..1..4704	-144, -80	upstream, upstream	1	1	0	60	61	15	1	2_A375_pNL97_plus_lncRNA_AR..1	61	Gene WDR92	WDR92, FLJ31741	WD repeat domain 92	NM_138458, hCT2261668.1, hCT2261669.1, hCT2261670.1, hCT2348130.0	235071_at	NP_612467.1, EAW99883.1, EAW99880.1, EAW99881.1, EAW99882.1
GeneID.56902	PNO1	2	68,385,005	68,403,091	18,086	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3274, 2_A375_pNL97_plus_lncRNA_AR..1..4704	-205, -289	upstream, upstream	1	1	0	60	61	15	1	2_A375_pNL97_plus_lncRNA_AR..1	61	Gene PNO1	KHRBP1, RRP20, PNO1	partner of NOB1 homolog (S. cerevisiae)	NM_020143, hCT13310.3	203622_s_at, 211697_x_at, 242627_at, 242905_at	NP_064528.1, EAW99879.1
GeneID.25927	CNRIP1	2	68,511,303	68,547,183	35,880	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4705	-401	upstream	0	1	0	16	22	3	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CNRIP1	C2orf32, CNRIP1, CRIP1, DKFZp566K1924	cannabinoid receptor interacting protein 1	NM_015463, NM_001111101, hCT13308.2	226751_at	NP_056278.1, NP_001104571.1, EAW99877.1
GeneID.554251	FBXO48	2	68,689,498	68,694,390	4,892	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3275, 2_A375_pNL97_plus_lncRNA_AR..1..4706	-122, -106	upstream, upstream	1	1	0	21	30	11	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene FBXO48	FBXO48	F-box protein 48	NM_001024680, hCT1654160.4		NP_001019851.1, EAW99873.1
GeneID.200558	APLF	2	68,694,691	68,807,294	112,603	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3275, 2_A375_pNL97_plus_lncRNA_AR..1..4706	-179, -195	upstream, upstream	1	1	0	21	30	11	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene APLF	FLJ16593, C2orf13, MGC47799, PALF, APLF, APFL, Xip1	aprataxin and PNKP like factor	NM_173545, hCT2262492.2, hCT2262493.2	1555100_at, 241379_at	NP_775816.1, EAW99872.1, EAW99871.1
GeneID.9938	ARHGAP25	2	68,961,913	69,053,965	92,052	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3276	94663	downstream	1	0	0	20	10	7	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ARHGAP25	KAIA0053, ARHGAP25	Rho GTPase activating protein 25	NM_014882, NM_001007231, NM_001166276, NM_001166277, hCT1959629.1, hCT2262498.0, hCT7896.2	1555076_at, 204882_at, 38149_at	NP_055697.1, NP_001007232.2, NP_001159748.1, NP_001159749.1, EAW99866.1, EAW99868.1, EAW99867.1
GeneID.84168	ANTXR1	2	69,240,276	69,476,459	236,183	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3277, 2_A375_pNL97_plus_lncRNA_AR..1..4708	165132, 165116	in gene, in gene	1	1	0	21	20	6	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ANTXR1	ANTXR1, TEM8, FLJ10601, ATR, FLJ21776, FLJ11298	anthrax toxin receptor 1	NM_032208, NM_053034, NM_018153, hCT1950023.2, hCT1950024.2, hCT2262502.0, hCT2262504.0	220092_s_at, 220093_at, 224694_at, 227660_at, 234430_at, 234632_at	NP_115584.1, NP_444262.1, NP_060623.2, EAW99855.1, EAW99857.1, EAW99858.1, EAW99856.1
GeneID.27247	NFU1	2	69,623,252	69,664,753	41,501	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4709, 4_A375_EGR1..1..5052	119, 241	in gene, in gene	0	1	1	15	17	16	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene NFU1	NIFUC, HIRIP5, MGC142252, MGC142254, NIfU, CGI-33, NFU1, Nfu	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	NM_001002757, NM_001002755, NM_001002756, NM_015700, hCT1821367.1, hCT2358457.0	218946_at	NP_001002757.1, NP_001002755.1, NP_001002756.1, NP_056515.2, EAW99849.1, EAW99850.1
GeneID.22848	AAK1	2	69,685,127	69,870,977	185,850	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4710, 2_A375_pNL97_plus_lncRNA_AR..1..4711	1025, -863	in gene, upstream	0	1	0	10.5	18	9	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene AAK1	FLJ45252, DKFZp686F03202, FLJ23712, KIAA1048, DKFZp686K16132, MGC138170, MGC164588, FLJ25931, FLJ31060, MGC164570, FLJ42882, AAK1	AP2 associated kinase 1	NM_014911, hCT1815718.2, hCT2289968.0	205434_s_at, 205435_s_at, 211166_s_at, 214956_at, 214998_at, 225522_at, 238100_at	NP_055726.3, EAW99848.1, EAW99847.1
GeneID.307	ANXA4	2	69,969,127	70,053,596	84,469	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3278, 2_A375_pNL97_plus_lncRNA_AR..1..4712, 4_A375_EGR1..1..5053, 4_A375_EGR1..1..5054	-183, 87465, 87545, 88217	upstream, downstream, downstream, downstream	1	1	1	16	17.5	18	2	4_A375_EGR1..1	22	Gene ANXA4	PIG28, MGC75105, ZAP36, DKFZp686H02120, ANXA4, ANX4	annexin A4	NM_001153, hCT30733.3	201301_s_at, 201302_at	NP_001144.1, EAW99844.1
GeneID.64395	GMCL1	2	70,056,816	70,106,727	49,909	+	3	2_A375_pNL97_plus_lncRNA_AR..1..4712, 4_A375_EGR1..1..5053, 4_A375_EGR1..1..5054	-226, -146, 526	upstream, upstream, in gene	0	1	1	16	19	22	1	4_A375_EGR1..1	22	Gene GMCL1	BTBD13, GCL1, GCL, GMCL1	germ cell-less homolog 1 (Drosophila)	NM_178439, hCT31637.4	218458_at, 234488_s_at	NP_848526.1, EAW99842.1
GeneID.11017	SNRNP27	2	70,121,090	70,132,349	11,259	+	2	4_A375_EGR1..1..5055, 4_A375_EGR1..1..5056	20478, 21598	downstream, downstream	0	0	1	14	13.5	17	2	4_A375_EGR1..1	17	Gene SNRNP27	SNRNP27, RY1	small nuclear ribonucleoprotein 27kDa (U4/U6.U5)	NM_006857	212436_at, 212440_at	NP_006848.1
GeneID.4084	MXD1	2	70,142,203	70,170,077	27,874	+	2	4_A375_EGR1..1..5055, 4_A375_EGR1..1..5056	-835, 465	upstream, in gene	0	0	1	14	13.5	17	2	4_A375_EGR1..1	17	Gene MXD1	MAD1, MXD1, MGC104659, BHLHC58, MAD, bHLHc58	MAX dimerization protein 1	NM_002357	206877_at, 226275_at, 228846_at	NP_002348.1
GeneID.400960	LOC400960	2	70,189,395	70,314,147	124,752	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3279, 2_A375_pNL97_plus_lncRNA_AR..1..4713, 2_A375_pNL97_plus_lncRNA_AR..1..4714	547, -265, -1309	in gene, upstream, upstream	1	1	0	16.5	18	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC400960		hypothetical LOC400960	NR_033672	1566840_at, 227969_at, 235137_at, 235462_at, 235909_at, 240017_at	
GeneID.5093	PCBP1	2	70,314,585	70,316,335	1,750	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3279, 2_A375_pNL97_plus_lncRNA_AR..1..4713, 2_A375_pNL97_plus_lncRNA_AR..1..4714	-965, -153, 871	upstream, upstream, in gene	1	1	0	16.5	18	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PCBP1	hnRNP-X, HNRPE1, PCBP1, HNRPX, hnRNP-E1	poly(rC) binding protein 1	NM_006196, hCT1815722.1	208620_at	NP_006187.2, EAW99834.1
GeneID.100133985	LOC100133985	2	70,351,166	70,352,446	1,280	-	1	4_A375_EGR1..1..5057	976	in gene	0	0	1	11	5	14	1	4_A375_EGR1..1	14	Gene LOC100133985		hypothetical LOC100133985	NR_024444		
GeneID.54980	C2orf42	2	70,377,017	70,418,151	41,134	-	5	2_A375_pNL97_plus_lncRNA_AR..1..4715, 2_A375_pNL97_plus_lncRNA_AR..1..4716, 4_A375_EGR1..1..5058, 4_A375_EGR1..1..5059, 4_A375_EGR1..1..5060	46231, 327, 49063, 42631, 391	downstream, in gene, downstream, downstream, in gene	0	1	1	12.5	14.75	19.25	4	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene C2orf42	C2orf42, FLJ20558	chromosome 2 open reading frame 42	NM_017880, hCT1965751.1, hCT1965752.1, hCT1965753.0, hCT31638.4	219128_at	NP_060350.1, EAW99831.1, EAW99828.1, EAW99829.1, EAW99830.1
GeneID.7072	TIA1	2	70,436,576	70,475,779	39,203	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4717	-9893	upstream	0	1	0	11	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene TIA1	TIA1, TIA-1		NM_022173, NM_022037, hCT1954240.1, hCT1954245.1, hCT2358398.0, hCT2358399.0, hCT31841.3	1554889_at, 1554890_a_at, 201446_s_at, 201447_at, 201448_at, 201449_at, 201450_s_at	NP_071505.2, NP_071320.2, EAW99824.1, EAW99825.1, EAW99826.1, EAW99827.1, EAW99823.1
GeneID.100302268	MIR1285-2	2	70,480,050	70,480,137	87	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4717	-5335	upstream	0	1	0	11	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene MIR1285-2	MIRN1285-2, MIR1285-2, hsa-mir-1285-2	microRNA 1285-2	NR_031617		
GeneID.51449	PCYOX1	2	70,485,231	70,508,317	23,086	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4717	241	in gene	0	1	0	11	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene PCYOX1	PCYOX1, PCL1, KIAA0908	prenylcysteine oxidase 1	NM_016297, hCT1643346.3	203803_at	NP_057381.3, EAW99819.1
GeneID.6637	SNRPG	2	70,508,510	70,520,869	12,359	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3280, 2_A375_pNL97_plus_lncRNA_AR..1..4718, 2_A375_pNL97_plus_lncRNA_AR..1..4719, 4_A375_EGR1..1..5061	133, 37, -7931, -8123	in gene, in gene, upstream, upstream	1	1	1	16.5	23	16	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene SNRPG	Sm-G, SMG, SNRPG, MGC117317	small nuclear ribonucleoprotein polypeptide G	NM_003096, hCT2270014.0, hCT2270017.0	205644_s_at	NP_003087.1, EAW99818.1, EAW99817.1
GeneID.84908	FAM136A	2	70,523,108	70,529,220	6,112	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3280, 2_A375_pNL97_plus_lncRNA_AR..1..4718, 2_A375_pNL97_plus_lncRNA_AR..1..4719, 4_A375_EGR1..1..5061	8484, 8366, 420, 228	downstream, downstream, in gene, in gene	1	1	1	16.5	23	16	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene FAM136A	FLJ14668, FAM136A	family with sequence similarity 136, member A	NM_032822, hCT1954247.1, hCT1954248.1	215947_s_at	NP_116211.2, EAW99815.1, EAW99816.1
GeneID.7039	TGFA	2	70,674,416	70,781,105	106,689	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3281, 2_A375_pNL97_plus_lncRNA_AR..1..4720, 4_A375_EGR1..1..5062	-319, -303, 241	upstream, upstream, in gene	1	1	1	27	18	19	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene TGFA	TFGA, TGFA	transforming growth factor, alpha	NM_001099691, NM_003236, hCT2265719.0, hCT2265721.0, hCT2265722.0, hCT2265726.0, hCT31833.3	205015_s_at, 205016_at, 211258_s_at	NP_001093161.1, NP_003227.1, EAW99810.1, EAW99811.1, EAW99813.1, EAW99814.1, EAW99812.1
GeneID.119	ADD2	2	70,889,216	70,995,375	106,159	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4721	81167	in gene	0	1	0	9	17	6	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ADD2	ADDB, ADD2	adducin 2 (beta)	NM_001185054, NM_001185055, NM_001617, NM_017482, NM_017488, hCT1954217.1, hCT1954218.1, hCT1954219.1, hCT2265702.0, hCT2265703.0, hCT2265704.0, hCT2265712.0, hCT2265714.0, hCT2358494.0, hCT30736.2, hCT32273.2	205268_s_at, 206807_s_at, 237336_at	NP_001171983.1, NP_001171984.1, NP_059522.1, NP_001608.1, NP_059516.2, EAW99804.1, EAW99798.1, EAW99799.1, EAW99800.1, EAW99801.1, EAW99802.1, EAW99803.1, EAW99805.1, EAW99806.1, EAW99807.1, EAW99808.1
GeneID.25806	VAX2	2	71,127,720	71,160,576	32,856	+	1	4_A375_EGR1..1..5063	680	in gene	0	0	1	14	16	19	1	4_A375_EGR1..1	19	Gene VAX2	VAX2, DRES93	ventral anterior homeobox 2	NM_012476, hCT32275.2	220443_s_at	NP_036608.1, EAW99792.1
GeneID.525	ATP6V1B1	2	71,162,998	71,192,561	29,563	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4723	11946	in gene	0	1	0	11	21	5	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ATP6V1B1	VATB, RTA1B, ATP6V1B1, VMA2, ATP6B1, VPP3, MGC32642	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1	NM_001692, hCT2358526.0, hCT32276.3	1554847_at, 205473_at	NP_001683.2, EAW99791.1, EAW99790.1
GeneID.79998	ANKRD53	2	71,205,575	71,212,629	7,054	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3283, 2_A375_pNL97_plus_lncRNA_AR..1..4724	16521, 16537	downstream, downstream	1	1	0	78	99	17	1	2_A375_pNL97_plus_lncRNA_AR..1	99	Gene ANKRD53	FLJ12056, ANKRD53, FLJ38160	ankyrin repeat domain 53	NM_024933, NM_001115116, hCT1646962.5, hCT2350660.0, hCT2350661.0, hCT2350662.0	215759_at, 244453_at	NP_079209.3, NP_001108588.1, EAW99786.1, EAW99787.1, EAW99788.1, EAW99789.1
GeneID.113419	TEX261	2	71,213,068	71,222,001	8,933	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3283, 2_A375_pNL97_plus_lncRNA_AR..1..4724	-95, -111	upstream, upstream	1	1	0	78	99	17	1	2_A375_pNL97_plus_lncRNA_AR..1	99	Gene TEX261	TEG-261, MGC32043, TEX261	testis expressed 261	NM_144582, hCT1954284.1, hCT1954285.1, hCT32281.3	212083_at, 212084_at	NP_653183.2, EAW99784.1, EAW99783.1, EAW99785.1
GeneID.55577	NAGK	2	71,295,408	71,305,998	10,590	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3284, 2_A375_pNL97_plus_lncRNA_AR..1..4725, 4_A375_EGR1..1..5064	400, 368, 224	in gene, in gene, in gene	1	1	1	21	24	23	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene NAGK	GNK, HSA242910, NAGK	N-acetylglucosamine kinase	NM_017567, hCT1954279.1	218231_at	NP_060037.3, EAW99780.1
GeneID.84693	MCEE	2	71,336,808	71,357,394	20,586	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3285, 2_A375_pNL97_plus_lncRNA_AR..1..4726	146, -238	in gene, upstream	1	1	0	23	24	16	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene MCEE	MCEE, GLOD2	methylmalonyl CoA epimerase	NM_032601, hCT32282.3	226238_at	NP_115990.3, EAW99778.1
GeneID.10199	MPHOSPH10	2	71,357,444	71,377,230	19,786	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3285, 2_A375_pNL97_plus_lncRNA_AR..1..4726	-198, 188	upstream, in gene	1	1	0	23	24	16	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene MPHOSPH10	MPP10P, MPP10, MPHOSPH10, CT90	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	NM_005791, hCT1954287.1, hCT32283.3	212885_at	NP_005782.1, EAW99777.1, EAW99776.1
GeneID.27332	ZNF638	2	71,558,889	71,662,189	103,300	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3287, 1_A375_pNL7_minus_lncRNA_AR..1..3288, 2_A375_pNL97_plus_lncRNA_AR..1..4727, 4_A375_EGR1..1..5065	15911, 16695, 15927, 407	in gene, in gene, in gene, in gene	1	1	1	17.5	21	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene ZNF638	ZFML, Zfp638, ZNF638, NP220, MGC26130, DKFZp686P1231, MGC90196	zinc finger protein 638	NM_001014972, NM_014497, hCT1954280.1, hCT1954281.1, hCT1954282.1, hCT2358533.0, hCT2358534.0, hCT32278.2	1554248_at, 1554249_a_at, 211257_x_at, 213775_x_at, 239243_at	NP_001014972.1, NP_055312.2, EAW99767.1, EAW99768.1, EAW99770.1, EAW99771.1, EAW99769.1, EAW99772.1
GeneID.56603	CYP26B1	2	72,356,367	72,374,963	18,596	-	1	4_A375_EGR1..1..5066	2739	in gene	0	0	1	8	8	17	1	4_A375_EGR1..1	17	Gene CYP26B1	MGC129613, DKFZp686G0638, CYP26B1, P450RAI-2, CYP26A2	cytochrome P450, family 26, subfamily B, polypeptide 1	NM_019885, hCT32538.3	219825_at, 234721_s_at	NP_063938.1, EAW99761.1
GeneID.23233	EXOC6B	2	72,406,444	73,053,177	646,733	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3293, 2_A375_pNL97_plus_lncRNA_AR..1..4731, 2_A375_pNL97_plus_lncRNA_AR..1..4732	89, 47481, 137	in gene, in gene, in gene	1	1	0	15	19.5	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene EXOC6B	SEC15L2, SEC15B, EXOC6B, KIAA0919	exocyst complex component 6B	NM_015189	215417_at, 225900_at	NP_056004.1
GeneID.6697	SPR	2	73,114,512	73,119,289	4,777	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3294, 2_A375_pNL97_plus_lncRNA_AR..1..4733, 2_A375_pNL97_plus_lncRNA_AR..1..4734	-3824, -3858, 64	upstream, upstream, in gene	1	1	0	24	29	8	2	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene SPR	SPR, SDR38C1	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	NM_003124, hCT2278769.0, hCT30757.2	203458_at	NP_003115.1, EAW99757.1, EAW99758.1
GeneID.94097	SFXN5	2	73,169,165	73,298,965	129,800	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3295, 4_A375_EGR1..1..5069, 4_A375_EGR1..1..5070	757, 107957, 81749	in gene, in gene, in gene	1	0	1	8.67	9.33	16	3	4_A375_EGR1..1	18	Gene SFXN5	MGC120415, SFXN5, MGC120413, BBG-TCC	sideroflexin 5	NM_144579, hCT2278304.0, hCT2278305.0, hCT2358339.0	1563708_at, 226373_at, 232691_at, 241999_at	NP_653180.1, EAW99754.1, EAW99752.1, EAW99753.1
GeneID.26056	RAB11FIP5	2	73,300,510	73,340,146	39,636	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3295	41936	downstream	1	0	0	15	13	13	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene RAB11FIP5	RIP11, DKFZp434H018, KIAA0857, GAF1, pp75, RAB11FIP5	RAB11 family interacting protein 5 (class I)	NM_015470, hCT2278301.1, hCT2278302.1, hCT2278303.1	210879_s_at	NP_056285.1, EAW99750.1, EAW99749.1, EAW99751.1
GeneID.344022	NOTO	2	73,429,386	73,438,340	8,954	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3296, 2_A375_pNL97_plus_lncRNA_AR..1..4735, 4_A375_EGR1..1..5071	12182, 12102, 12054	downstream, downstream, downstream	1	1	1	18	18	29	1	4_A375_EGR1..1	29	Gene NOTO	NOTO		NM_001134462		NP_001127934.1
GeneID.10322	SMYD5	2	73,441,366	73,454,355	12,989	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3296, 1_A375_pNL7_minus_lncRNA_AR..1..3297, 2_A375_pNL97_plus_lncRNA_AR..1..4735, 2_A375_pNL97_plus_lncRNA_AR..1..4736, 4_A375_EGR1..1..5071, 4_A375_EGR1..1..5072	202, 19914, 122, 20178, 74, 20108	in gene, downstream, in gene, downstream, in gene, downstream	1	1	1	18.5	18.5	23	2	4_A375_EGR1..1	29	Gene SMYD5	NN8-4AG, ZMYND23, RRG1, RAI15, SMYD5	SMYD family member 5	NM_006062, hCT2278793.0, hCT2278794.0	209516_at	NP_006053.2, EAW99744.1, EAW99745.1
GeneID.84279	C2orf7	2	73,455,134	73,460,356	5,222	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3297, 2_A375_pNL97_plus_lncRNA_AR..1..4736, 4_A375_EGR1..1..5072	-924, -1188, -1116	upstream, upstream, upstream	1	1	1	19	19	17	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C2orf7	C2orf7, PRADC1, PAP21, MGC13004	chromosome 2 open reading frame 7	NM_032319, hCT1954235.1, hCT31620.3	223312_at	NP_115695.1, EAW99742.1, EAW99743.1
GeneID.10574	CCT7	2	73,461,364	73,480,150	18,786	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3297, 2_A375_pNL97_plus_lncRNA_AR..1..4736, 4_A375_EGR1..1..5072	-84, 180, 108	upstream, in gene, in gene	1	1	1	19	19	17	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CCT7	NIP7-1, CCT7, CCTH, CCTETA, TCP1ETA, MGC110985	chaperonin containing TCP1, subunit 7 (eta)	NM_006429, NM_001009570, NM_001166284, NM_001166285, NR_029402, NR_029403, hCT2278797.0, hCT2278798.0, hCT2278800.0	200812_at	NP_006420.1, NP_001009570.1, NP_001159756.1, NP_001159757.1, EAW99739.1, EAW99740.1, EAW99738.1
GeneID.100507133	LOC100507133	2	73,511,653	73,518,113	6,460	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3298, 2_A375_pNL97_plus_lncRNA_AR..1..4737, 4_A375_EGR1..1..5073	6651, 6683, 27	downstream, downstream, in gene	1	1	1	15	21	17	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene LOC100507133		hypothetical LOC100507133	XR_109945		
GeneID.1961	EGR4	2	73,518,057	73,520,829	2,772	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3298, 2_A375_pNL97_plus_lncRNA_AR..1..4737, 4_A375_EGR1..1..5073	2525, 2493, 9149	in gene, in gene, downstream	1	1	1	15	21	17	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene EGR4	PAT133, NGFIC, EGR4, NGFI-C	early growth response 4	NM_001965, hCT31611.3	207767_s_at, 207768_at, 231575_at	NP_001956.3, EAW99734.1

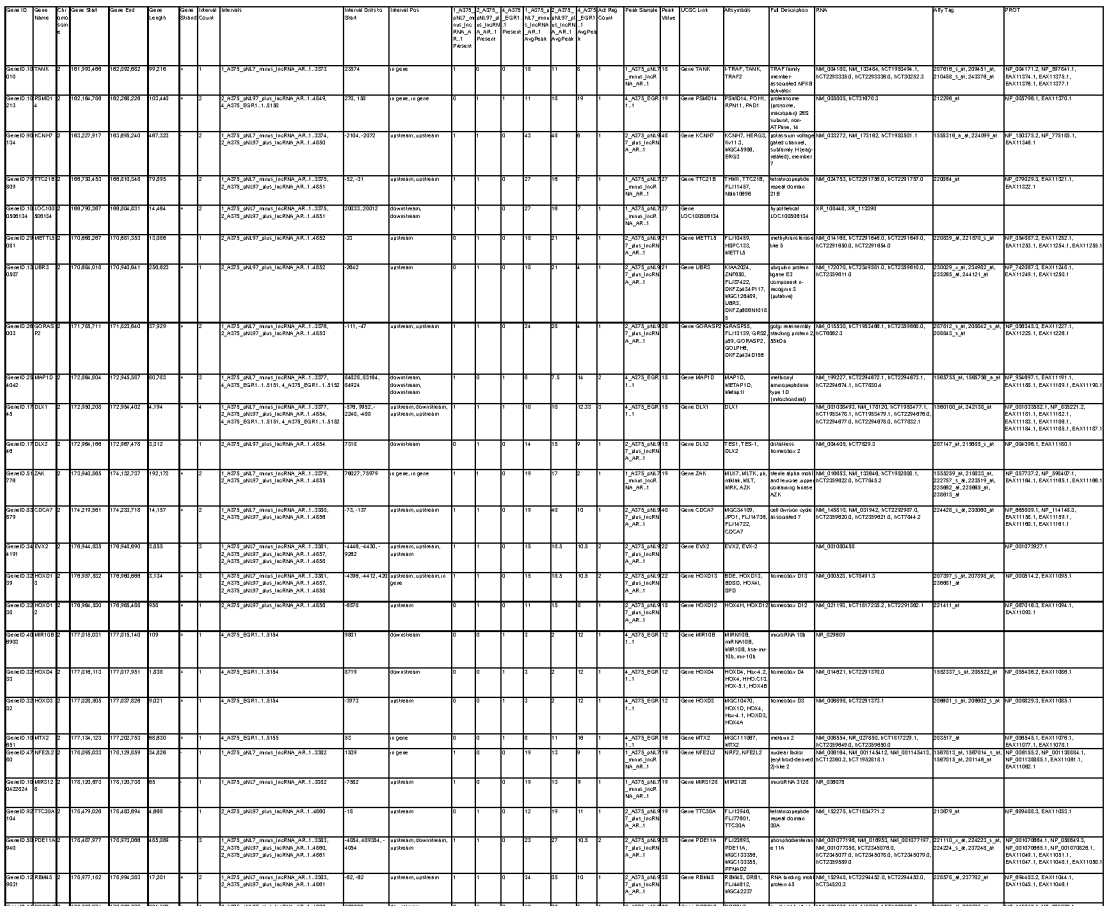
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:7840	ALMS1	2	73,612,886	73,837,046	224,160	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4736	362	in gene	0	1	0	10	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ALMS1	DKFZp686A118, DKFZp686D1828, ALMS1, ALSS, KIAA0328	Alstrom syndrome 1	NM_015120, hCT2278761.0, hCT2278762.0, hCT2278763.0, hCT2356507.0	214220_s_at, 214221_at, 214707_x_at	NP_055935.4, EAW99729.1, EAW99728.1, EAW99730.1, EAW99731.1
GeneID:51002	TPRKB	2	73,956,957	73,964,517	7,560	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3299, 2_A375_pNL97_plus_lncRNA_AR..1..4739	-123, -176	upstream, upstream	1	1	0	23	23	10	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene TPRKB	TPRKB, CGI-121	TP53RK binding protein	NM_016058, hCT1815575.1, hCT1954084.1, hCT1981377.1, hCT2356391.0	219030_at	NP_057142.1, EAW99720.1, EAW99721.1, EAW99722.1, EAW99723.1
GeneID:8446	DUSP11	2	73,989,325	74,007,284	17,959	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4740	-12	upstream	0	1	0	16	26	10	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene DUSP11	DUSP11, PIR1	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	NM_003584, hCT1954251.1, hCT30758.3	202703_at	NP_003575.2, EAW99719.1, EAW99718.1
GeneID:388960	C2orf78	2	74,011,316	74,044,274	32,958	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4740	-4020	upstream	0	1	0	16	26	10	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene C2orf78	FLJ43987, C2orf78, COG5373, hCG1989538	chromosome 2 open reading frame 78	NM_001080474		NP_001073943.1
GeneID:10617	STAMBP	2	74,056,086	74,090,011	33,925	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3300, 1_A375_pNL7_minus_lncRNA_AR..1..3301, 2_A375_pNL97_plus_lncRNA_AR..1..4741	2026, 23322, 10	in gene, in gene, in gene	1	1	0	15.33	13.33	8	3	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene STAMBP	AMSH, MGC126518, MGC126516, STAMBP	STAM binding protein	NM_006463, NM_201647, NM_213622, hCT1954256.1, hCT1954257.1, hCT31997.3	202811_at, 227515_at	NP_006454.1, NP_964010.1, NP_998787.1, EAW99714.1, EAW99715.1, EAW99716.1
GeneID:72	ACTG2	2	74,120,093	74,146,780	26,687	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4742, 4_A375_EGR1..1..5074	34051, 33971	downstream, downstream	0	1	1	11	18	20	1	4_A375_EGR1..1	20	Gene ACTG2	ACTG2, ACTSG, ACT, ACTL3, ACTA3, ACTE	actin, gamma 2, smooth muscle, enteric	NM_001615, hCT2358493.0, hCT32003.3	202274_at, 241146_at	NP_001606.1, EAW99712.1, EAW99713.1
GeneID:1716	DGUOK	2	74,153,953	74,186,088	32,135	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4742, 4_A375_EGR1..1..5074	191, 111	in gene, in gene	0	1	1	11	18	20	1	4_A375_EGR1..1	20	Gene DGUOK	MTDPS3, dGK, DGUOK	deoxyguanosine kinase	NM_080916, NM_080918	203816_at, 209549_s_at	NP_550438.1, NP_550440.1
GeneID:200424	TET3	2	74,273,450	74,335,303	61,853	+	1	4_A375_EGR1..1..5075	55574	in gene	0	0	1	7	8	15	1	4_A375_EGR1..1	15	Gene TET3	TET3, MGC22014, KIAA0401	tet oncogene family member 3	NM_144993	1554841_a_at, 214754_at, 235542_at	NP_659430.1
GeneID:388962	BOLA3	2	74,362,526	74,375,039	12,511	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3303, 2_A375_pNL97_plus_lncRNA_AR..1..4744	-1, -1	upstream, upstream	1	1	0	103	136	8	1	2_A375_pNL97_plus_lncRNA_AR..1	136	Gene BOLA3	BOLA3		NM_001035505, NM_212552, hCT2264704.0, hCT2264706.0	227291_s_at	NP_001030582.1, NP_997717.2, EAW99699.1, EAW99700.1
GeneID:100507171	LOC100507171	2	74,375,166	74,377,188	2,022	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3303, 2_A375_pNL97_plus_lncRNA_AR..1..4744	-126, -126	upstream, upstream	1	1	0	103	136	8	1	2_A375_pNL97_plus_lncRNA_AR..1	136	Gene LOC100507171		hypothetical LOC100507171	XR_112337, XR_112338, XR_109947, XR_109948, XR_115557, XR_115558		
GeneID:55233	MOBKL1B	2	74,383,211	74,405,995	22,784	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3303, 2_A375_pNL97_plus_lncRNA_AR..1..4744	30955, 30955	downstream, downstream	1	1	0	103	136	8	1	2_A375_pNL97_plus_lncRNA_AR..1	136	Gene MOBKL1B	C2orf6, MOB1, MOBK1B, MATS1, FLJ10788, MOBKL1B, Mob4B, FLJ11595	MOB1, Mps One Binder kinase activator-like 1B (yeast)	NM_018221, hCT1983553.1, hCT31999.3	201297_s_at, 201298_s_at, 201299_s_at, 214812_s_at	NP_060691.2, EAW99696.1, EAW99695.1
GeneID:10797	MTHFD2	2	74,425,690	74,442,425	16,735	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4745	54	in gene	0	1	0	17	18	10	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MTHFD2	MTHFD2, NMDMC	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	NM_006636, NR_027405, hCT1668604.3, hCT1816943.1, hCT2266666.0, hCT31994.3	201761_at	NP_006627.2, EAW99671.1, EAW99670.1, EAW99672.1, EAW99673.1
GeneID:1639	DCTN1	2	74,588,281	74,619,214	30,933	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3304	14	in gene	1	0	0	16	16	6	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene DCTN1	HMN7B, DAP-150, DCTN1, P135, DP-150	dynactin 1 (p150, glued homolog, Drosophila)	NM_001135040, NM_001135041, NM_001190836, NM_001190837, NM_004082, NM_023019, NR_033935, hCT2264671.0, hCT2264673.0, hCT2264674.0, hCT2264676.0	201082_s_at, 204298_at, 211780_x_at	NP_001128512.1, NP_001128513.1, NP_075408.1, NP_004073.2, NP_001177765.1, NP_001177766.1, EAW99684.1, EAW99685.1, EAW99686.1, EAW99687.1
GeneID:100189589	LOC100189589	2	74,612,845	74,621,008	8,163	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3304	8355	in gene	1	0	0	16	16	6	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene LOC100189589		hypothetical LOC100189589	NR_024463		
GeneID:388963	C2orf81	2	74,641,303	74,644,844	3,541	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4746	-3660	upstream	0	1	0	12	18	6	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene C2orf81	hCG40743, C2orf81	chromosome 2 open reading frame 81	NM_001145054	236070_at	NP_001138526.1
GeneID:100130009	LOC100130009	2	74,645,222	74,645,569	347	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4746	-3135	upstream	0	1	0	12	18	6	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100130009		hypothetical LOC100130009	XM_001719366, XM_001718914, XM_001720336		XP_001719440.3, XP_001718966.3, XP_001720390.3
GeneID:84058	WDR54	2	74,648,885	74,652,882	3,997	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4746	-161	upstream	0	1	0	12	18	6	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene WDR54	WDR54, FLJ12953	WD repeat domain 54	NM_032118, hCT1954265.1, hCT1954266.1, hCT2358505.0, hCT2358506.0, hCT32006.2	225698_at	NP_115494.1, EAW99680.1, EAW99677.1, EAW99678.1, EAW99679.1, EAW99681.1
GeneID:6242	RTKN	2	74,652,988	74,669,060	16,072	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3305, 2_A375_pNL97_plus_lncRNA_AR..1..4746, 2_A375_pNL97_plus_lncRNA_AR..1..4747, 4_A375_EGR1..1..5076	1264, 20356, 1252, 5156	in gene, downstream, in gene, in gene	1	1	1	15.33	23	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene RTKN	RTKN	rhotekin	NM_033046, NM_001015055, NM_001015056, hCT1954263.1, hCT1954264.1, hCT32005.3	225150_s_at, 225151_at, 239226_at	NP_149035.1, NP_001015055.1, NP_001015056.1, EAW99674.1, EAW99675.1, EAW99676.1
GeneID:83444	INO80B	2	74,682,199	74,685,087	2,888	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4748, 4_A375_EGR1..1..5077	169, 2697	in gene, in gene	0	1	1	15.5	15.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene INO80B	INO80B, PAP-1BP, ZNHIT4, IES2, HMGA1L4, hIes2, PAPA-1, HMGIYL4	INO80 complex subunit B	NM_031288	221251_x_at, 222093_s_at, 65133_i_at	NP_112578.2
GeneID:23559	WBP1	2	74,685,577	74,688,010	2,433	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4748, 4_A375_EGR1..1..5077	-3209, -681	upstream, upstream	0	1	1	15.5	15.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene WBP1	WBP1, MGC15305, WBP-1	WW domain binding protein 1	NM_012477	223072_s_at	NP_036609.1
GeneID:7841	MOGS	2	74,688,184	74,692,537	4,353	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3306, 2_A375_pNL97_plus_lncRNA_AR..1..4748, 2_A375_pNL97_plus_lncRNA_AR..1..4749, 4_A375_EGR1..1..5077, 4_A375_EGR1..1..5078	-7223, 10169, -7207, 7841, -7335	upstream, downstream, upstream, downstream, upstream	1	1	1	17	17.67	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MOGS	MOGS, CDG2B, GCS1	mannosyl-oligosaccharide glucosidase	NM_006302, NM_001146158, hCT1954255.1, hCT31995.3	210627_s_at	NP_006293.2, NP_001139630.1, EAW99652.1, EAW99653.1
GeneID:116540	MRPL53	2	74,699,109	74,699,927	818	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3306, 1_A375_pNL7_minus_lncRNA_AR..1..3307, 2_A375_pNL97_plus_lncRNA_AR..1..4749, 2_A375_pNL97_plus_lncRNA_AR..1..4750, 4_A375_EGR1..1..5078, 4_A375_EGR1..1..5079	167, -10329, 183, -10057, 55, -9841	in gene, upstream, in gene, upstream, in gene, upstream	1	1	1	19.5	22.5	20	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MRPL53	MRPL53, L53MT, FLJ90728, MGC20402	mitochondrial ribosomal protein L53	NM_053050, hCT2264643.1	225523_at	NP_444278.1, EAW99651.1
GeneID:84865	CCDC142	2	74,699,959	74,710,357	10,398	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3306, 1_A375_pNL7_minus_lncRNA_AR..1..3307, 2_A375_pNL97_plus_lncRNA_AR..1..4749, 2_A375_pNL97_plus_lncRNA_AR..1..4750, 4_A375_EGR1..1..5078, 4_A375_EGR1..1..5079	10597, 101, 10613, 373, 10465, 769	downstream, in gene, downstream, in gene, downstream, in gene	1	1	1	19.5	22.5	20	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CCDC142	FLJ14397, CCDC142, FLJ90728	coiled-coil domain containing 142	NM_032779, hCT2264650.1	239922_at	NP_116168.3, EAW99650.1
GeneID:84427	TTC31	2	74,710,200	74,721,691	11,491	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3306, 1_A375_pNL7_minus_lncRNA_AR..1..3307, 2_A375_pNL97_plus_lncRNA_AR..1..4750, 4_A375_EGR1..1..5079, 4_A375_EGR1..1..5080	-10440, 56, -216, 632, 14936	upstream, in gene, upstream, upstream, downstream	1	1	1	16.33	19.33	18.33	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TTC31	MGC120200, FLJ12788, TTC31, FLJ33201	tetratricopeptide repeat domain 31	NM_022492, NR_027749, hCT1954220.2, hCT1954222.2, hCT2341450.0, hCT2341451.0, hCT2341452.0, hCT2358424.0, hCT2358425.0, hCT2358426.0, hCT2358427.0, hCT2358428.0, hCT32002.4	218838_s_at	NP_071937.4, EAW99638.1, EAW99639.1, EAW99642.1, EAW99646.1, EAW99648.1, EAW99640.1, EAW99641.1, EAW99643.1, EAW99644.1, EAW99645.1, EAW99647.1
GeneID:85474	LBX2	2	74,724,644	74,730,443	5,799	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3308, 2_A375_pNL97_plus_lncRNA_AR..1..4751, 4_A375_EGR1..1..5080, 4_A375_EGR1..1..5081	-4005, -4021, 5307, -4245	upstream, upstream, in gene, upstream	1	1	1	19	25.5	18.5	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene LBX2	LBX2, LP3727	ladybird homeobox 2	NM_001009812		NP_001009812.1
GeneID:151534	hCG_1811732	2	74,729,744	74,732,192	2,448	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3308, 2_A375_pNL97_plus_lncRNA_AR..1..4751, 4_A375_EGR1..1..5080, 4_A375_EGR1..1..5081	4704, 4720, -4608, 4944	downstream, downstream, upstream, downstream	1	1	1	19	25.5	18.5	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene hCG_1811732	LOC151534, MGC120166	hypothetical LOC151534	NR_024606	236422_at	
GeneID:84759	PCGF1	2	74,732,170	74,734,821	2,651	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3308, 2_A375_pNL97_plus_lncRNA_AR..1..4751, 4_A375_EGR1..1..5080, 4_A375_EGR1..1..5081	373, 357, 9665, 133	in gene, in gene, downstream, in gene	1	1	1	19	25.5	18.5	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene PCGF1	MGC10882, 2010002K04Rik, PCGF1, NSPC1, RNF68, FLJ43754, RNF3A-2	polycomb group ring finger 1	NM_032673, hCT1954309.2, hCT2358470.0	210022_at, 210023_s_at	NP_116062.2, EAW99632.1, EAW99633.1
GeneID:3196	TLX2	2	74,741,596	74,744,275	2,679	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3308, 2_A375_pNL97_plus_lncRNA_AR..1..4751, 4_A375_EGR1..1..5081	-7148, -7132, -6908	upstream, upstream, upstream	1	1	1	28	36	22	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene TLX2	TLX2, NCX, Enx, HOX11L1	T-cell leukemia homeobox 2	NM_016170	207410_s_at, 211049_at	NP_057254.1
GeneID:165545	DQX1	2	74,745,256	74,753,406	8,150	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4752, 4_A375_EGR1..1..5082	-3200, -3296	upstream, upstream	0	1	1	16	27	19	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene DQX1	DQX1, FLJ23757	DEAQ box RNA-dependent ATPase 1	NM_133637, hCT1954301.1, hCT2358423.0, hCT32335.3	236055_at	NP_598376.2, EAW99627.1, EAW99626.1, EAW99628.1
GeneID:550	AUP1	2	74,753,775	74,756,974	3,199	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4752, 4_A375_EGR1..1..5082	366, 270	in gene, in gene	0	1	1	16	27	19	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene AUP1	AUP1	ancient ubiquitous protein 1	NM_181575, hCT1668578.2, hCT1954298.1, hCT1954299.1, hCT32333.3	220525_s_at	NP_853553.1, EAW99622.1, EAW99623.1, EAW99624.1, EAW99625.1
GeneID:27429	HTRA2	2	74,756,532	74,760,683	4,151	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4752, 4_A375_EGR1..1..5082	76, 172	in gene, in gene	0	1	1	16	27	19	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene HTRA2	PARK13, HTRA2, OMI, PRSS25	HtrA serine peptidase 2	NM_013247, NM_145074, hCT1954291.2, hCT1954292.2, hCT1954293.2, hCT2358417.0, hCT32331.4	203089_s_at, 211152_s_at	NP_037379.1, NP_659540.1, EAW99617.1, EAW99618.1, EAW99619.1, EAW99620.1, EAW99621.1
GeneID:84695	LOXL3	2	74,759,946	74,781,062	21,116	-	5	2_A375_pNL97_plus_lncRNA_AR..1..4752, 4_A375_EGR1..1..5082, 4_A375_EGR1..1..5083, 4_A375_EGR1..1..5084, 4_A375_EGR1..1..5085	24454, 24358, 374, -456, -1290	downstream, downstream, in gene, upstream, upstream	0	1	1	12	17	18	4	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene LOXL3	LOXL3, LOXL	lysyl oxidase-like 3	NM_032603, hCT1954302.1, hCT32337.2	228253_at	NP_115992.1, EAW99615.1, EAW99616.1
GeneID:1796	DOK1	2	74,781,880	74,784,683	2,803	+	3	4_A375_EGR1..1..5083, 4_A375_EGR1..1..5084, 4_A375_EGR1..1..5085	-1172, -340, 492	upstream, upstream, in gene	0	0	1	10.67	13.67	17.67	3	4_A375_EGR1..1	19	Gene DOK1	MGC138860, P62DOK, MGC117395, DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	NM_001381, hCT1954288.1, hCT2266726.0, hCT32329.2	211121_s_at, 216835_s_at	NP_001372.1, EAW99614.1, EAW99612.1, EAW99613.1
GeneID:130951	C2orf65	2	74,785,010	74,875,164	90,154	-	4	4_A375_EGR1..1..5083, 4_A375_EGR1..1..5084, 4_A375_EGR1..1..5085, 4_A375_EGR1..1..5086	94476, 93644, 92812, -6532	downstream, downstream, downstream, upstream	0	0	1	11	13	18.25	4	4_A375_EGR1..1	20	Gene C2orf65	D6Mm5e, C2orf65, FLJ44410	chromosome 2 open reading frame 65	NM_138804, hCT2264617.0, hCT2264619.0, hCT32336.3	1552849_at, 1555148_a_at, 234325_at, 234498_at	NP_620159.2, EAW99611.1, EAW99609.1, EAW99610.1
GeneID:10505	SEMA4F	2	74,881,393	74,909,185	27,792	+	1	4_A375_EGR1..1..5086	303	in gene	0	0	1	12	11	20	1	4_A375_EGR1..1	20	Gene SEMA4F	M-SEMA, m-Sema-M, SEMA4F, SEMAM, PRO2353, SEMAW	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	NM_004263, hCT1954289.1, hCT2266729.0, hCT2358412.0, hCT32330.3	208124_s_at, 210124_x_at, 226660_x_at	NP_004254.2, EAW99606.1, EAW99605.1, EAW99607.1, EAW99608.1
GeneID:3099	HK2	2	75,059,782	75,120,481	60,699	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4753, 4_A375_EGR1..1..5087	2330, 1650	in gene, in gene	0	1	1	16	22	18	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene HK2	DKFZp686M1669, HXK2, HKII, HK2	hexokinase 2	NM_000189, hCT2281454.0, hCT2281455.0, hCT32338.3	202934_at, 222305_at	NP_000180.2, EAW99603.1, EAW99601.1, EAW99602.1
GeneID:6869	TACR1	2	75,273,590	75,426,645	153,055	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3310, 4_A375_EGR1..1..5088	151413, -611	in gene, upstream	1	0	1	16	14	9	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene TACR1	SPR, NK1R, NKIR, TAC1R, TACR1	tachykinin receptor 1	NM_001058, NM_015727, hCT1965757.1, hCT32334.2	208048_at, 208049_s_at, 210637_at	NP_001049.1, NP_056542.1, EAW99595.1, EAW99596.1
GeneID:9801	MRPL19	2	75,873,909	75,889,334	15,425	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3312, 2_A375_pNL97_plus_lncRNA_AR..1..4756	-21, 11	upstream, in gene	1	1	0	17	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MRPL19	MGC20675, MRP-L19, KIAA0104, L19mt, MRP-L15, MRPL19, MRPL15, RPML15, RLX1	mitochondrial ribosomal protein L19	NM_014763, hCT30787.3	203465_at, 232071_at, 238448_at	NP_055578.2, EAW99590.1
GeneID:8936	C2orf3	2	75,889,831	75,938,111	48,280	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4757	143	in gene	0	1	0	19	23	12	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene C2orf3	TCF9, DNABF, C2orf3, GCF	chromosome 2 open reading frame 3	NM_003203, hCT1981443.1, hCT1981446.1, hCT2280910.0, hCT31614.4	210175_at, 218305_s_at, 237531_at	NP_003194.3, EAW99586.1, EAW99587.1, EAW99588.1, EAW99589.1
GeneID:80059	LRRTM4	2	76,974,849	77,749,502	774,653	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3314, 2_A375_pNL97_plus_lncRNA_AR..1..4759	563454, 563438	in gene, in gene	1	1	0	20	20	4	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LRRTM4	LRRTM4, FLJ12568, MGC120633, MGC120636	leucine rich repeat transmembrane neuronal 4	NM_024993, NM_001134745, hCT1645355.3	220345_at	NP_079269.4, NP_001128217.1, EAW99585.1
GeneID:8802	SUCLG1	2	84,650,647	84,686,586	35,939	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3319, 2_A375_pNL97_plus_lncRNA_AR..1..4762, 4_A375_EGR1..1..5093	26, -6, 394	in gene, upstream, in gene	1	1	1	40	37	14	1	1_A375_pNL7_minus_lncRNA_AR..1	40	Gene SUCLG1	GALPHA, MTDPS9, SUCLA1, FLJ21114, FLJ43513, SUCLG1, G-ALPHA	succinate-CoA ligase, alpha subunit	NM_003849, hCT1815055.2	217874_at	NP_003840.2, EAW99556.1
GeneID:1768	DNAH6	2	84,743,579	85,046,713	303,134	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4763	225093	in gene	0	1	0	10	25	15	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene DNAH6	KIAA1697, HL2, MGC132544, FLJ37357, HL-2, MGC141984, Dnahc6, FLJ23529, DNAH6, MGC177197, DNHL1, DKFZp667K087	dynein, axonemal, heavy chain 6	NM_001370	1561616_a_at, 1561617_at, 1565337_at, 1565338_x_at	NP_001361.1
GeneID:9168	TMSB10	2	85,132,763	85,133,799	1,036	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4764, 4_A375_EGR1..1..5094	229, 549	in gene, in gene	0	1	1	10	19	16	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TMSB10	TB10, MIG12, TMSB10	thymosin beta 10	NM_021103, hCT1815300.1, hCT2266411.0	217733_s_at	NP_066926.1, EAW99547.1, EAW99548.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.10818	TGOLN2	2	85,545,146	85,555,374	10,228	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3322, 2_A375_pNL97_plus_lncRNA_AR..1..4766	14, 142	in gene, in gene	1	1	0	20	16	16	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene TGOLN2	TGN38, TGN46, MGC14722, TTGN2, TGOLN2, TGN51, TGN48	trans-golgi network protein 2	NM_006464, hCT1954165.1, hCT1954166.1, hCT2286998.0, hCT2287001.0, hCT2358458.0, hCT25814.2	1554608_at, 203833_s_at, 203834_s_at, 212040_at, 212043_at	NP_006455.2, EAW99535.1, EAW99536.1, EAW99537.1, EAW99538.1, EAW99540.1, EAW99539.1
GeneID.54884	RETSAT	2	85,569,078	85,581,821	12,743	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4767	-35	upstream	0	1	0	14	21	11	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RETSAT	FLJ20296, RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	NM_017750, hCT1954211.1, hCT1954212.1, hCT1954214.1, hCT25829.3	1566472_s_at, 218124_at	NP_060220.3, EAW99531.1, EAW99530.1, EAW99532.1, EAW99533.1
GeneID.84173	ELMOD3	2	85,581,843	85,618,875	37,032	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4767	13	in gene	0	1	0	14	21	11	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ELMOD3	LST3, FLJ35601, RBM29, RBED1, FLJ21977, MGC111036, ELMOD3	ELMO/CED-12 domain containing 3	NM_032213, NM_001135021, NM_001135022, NM_001135023, hCT1954195.2, hCT1954197.2, hCT1989079.2, hCT1989080.2, hCT1989082.2, hCT2358516.0, hCT2358517.0, hCT2358518.0, hCT25824.3	226286_at	NP_115589.2, NP_001128493.1, NP_001128494.1, NP_001128495.1, EAW99521.1, EAW99526.1, EAW99522.1, EAW99523.1, EAW99524.1, EAW99525.1, EAW99528.1, EAW99527.1, EAW99529.1
GeneID.822	CAPG	2	85,621,871	85,637,676	15,805	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4768	-10196	upstream	0	1	0	11	21	8	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CAPG	MCP, AFCP, CAPG	capping protein (actin filament), gelsolin-like	NM_001747, hCT1954179.1, hCT1954180.1, hCT1954182.1, hCT25812.2	201850_at	NP_001738.2, EAW99519.1, EAW99517.1, EAW99518.1, EAW99520.1
GeneID.284948	SH2D6	2	85,661,918	85,664,152	2,234	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4769	2946	downstream	0	1	0	11	21	10	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SH2D6	SH2D6, FLJ35993	SH2 domain containing 6	NM_198482	242543_at	NP_940884.1
GeneID.4144	MAT2A	2	85,766,288	85,772,403	6,115	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3323, 2_A375_pNL97_plus_lncRNA_AR..1..4770, 4_A375_EGR1..1..5095	112, 656, 112	in gene, in gene, in gene	1	1	1	21	19	22	1	4_A375_EGR1..1	22	Gene MAT2A	MATII, SAMS2, MAT2A, MATA2	methionine adenosyltransferase II, alpha	NM_005911, hCT1954175.1, hCT1954176.1, hCT1954177.1, hCT25811.3	200768_s_at, 200769_s_at	NP_005902.1, EAW99511.1, EAW99512.1, EAW99513.1, EAW99514.1
GeneID.100507238	LOC100507238	2	85,770,915	85,773,392	2,477	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3323, 2_A375_pNL97_plus_lncRNA_AR..1..4770, 4_A375_EGR1..1..5095	6992, 6448, 6992	downstream, downstream, downstream	1	1	1	21	19	22	1	4_A375_EGR1..1	22	Gene LOC100507238		hypothetical LOC100507238	XR_109950		
GeneID.2677	GGCX	2	85,776,193	85,788,657	12,464	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3323, 2_A375_pNL97_plus_lncRNA_AR..1..4770, 4_A375_EGR1..1..5095, 4_A375_EGR1..1..5096	22257, 21713, 22257, 49	downstream, downstream, downstream, in gene	1	1	1	16.5	14.5	21	2	4_A375_EGR1..1	22	Gene GGCX	VKCFD1, GGCX, FLJ26629	gamma-glutamyl carboxylase	NM_000821, NM_001142269, hCT1954172.1, hCT25810.3	205351_at, 214005_at, 214006_s_at, 235413_at	NP_000812.2, NP_001135741.1, EAW99509.1, EAW99510.1
GeneID.8673	VAMP8	2	85,804,614	85,809,156	4,542	+	1	4_A375_EGR1..1..5097	7274	downstream	0	0	1	15	13	17	1	4_A375_EGR1..1	17	Gene VAMP8	EDB, VAMP8	vesicle-associated membrane protein 8 (endobrevin)	NM_003761	202546_at	NP_003752.2
GeneID.10791	VAMP5	2	85,811,531	85,820,511	8,980	+	3	2_A375_pNL97_plus_lncRNA_AR..1..4771, 2_A375_pNL97_plus_lncRNA_AR..1..4772, 4_A375_EGR1..1..5097	10965, 16389, 357	downstream, downstream, in gene	0	1	1	14.33	17.67	11.67	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene VAMP5	VAMP5		NM_006634	204929_s_at, 214115_at	NP_006625.1
GeneID.51255	RNF181	2	85,822,837	85,824,831	1,994	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4771, 2_A375_pNL97_plus_lncRNA_AR..1..4772	-341, 7083	upstream, downstream	0	1	0	14	20	9	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RNF181	RNF181, HSPC238	ring finger protein 181	NM_016494, hCT1954204.1, hCT25828.2	223084_at, 229932_at	NP_057578.1, EAW99505.1, EAW99504.1
GeneID.129303	TMEM150A	2	85,825,670	85,829,822	4,152	-	4	2_A375_pNL97_plus_lncRNA_AR..1..4771, 2_A375_pNL97_plus_lncRNA_AR..1..4772, 2_A375_pNL97_plus_lncRNA_AR..1..4773, 4_A375_EGR1..1..5098	7326, -96, -9282, 9136	downstream, upstream, upstream, upstream	0	1	1	14.67	20.33	13	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TMEM150A	FLJ90024, TM6P1, TMEM150A, TMEM150	transmembrane protein 150A	NM_001031738, NR_033179, hCT1954198.1, hCT1954199.1, hCT1954201.1, hCT1954202.1, hCT2286980.0, hCT2358519.0, hCT2358520.0, hCT25825.2	226239_at	NP_001026908.1, EAW99498.1, EAW99496.1, EAW99497.1, EAW99500.1, EAW99502.1, EAW99499.1, EAW99501.1, EAW99503.1
GeneID.388969	C2orf68	2	85,832,376	85,839,179	6,803	-	4	2_A375_pNL97_plus_lncRNA_AR..1..4771, 2_A375_pNL97_plus_lncRNA_AR..1..4772, 2_A375_pNL97_plus_lncRNA_AR..1..4773, 4_A375_EGR1..1..5098	16683, 9259, 75, 219	downstream, downstream, in gene, in gene	0	1	1	14.67	20.33	13	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene C2orf68	C2orf68, FLJ35653, FLJ14112, MGC131675	chromosome 2 open reading frame 68	NM_001013649, hCT25827.4	221878_at, 232145_at, 238766_at	NP_001013671.2, EAW99495.1
GeneID.10713	USP39	2	85,843,283	85,876,406	33,123	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4773, 4_A375_EGR1..1..5098	-4179, -4323	upstream, upstream	0	1	1	16	21	21	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene USP39	MGC75069, SNRNP65, HSPC332, CGI-21, SAD1, USP39	ubiquitin specific peptidase 39	NM_006590, hCT1954191.1, hCT2358512.0, hCT2358513.0, hCT2358514.0, hCT25823.2	217829_s_at	NP_006581.2, EAW99490.1, EAW99491.1, EAW99492.1, EAW99493.1, EAW99494.1
GeneID.6439	SFTPB	2	85,884,440	85,895,864	11,424	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4774, 4_A375_EGR1..1..5099	5666, 9048	in gene, in gene	0	1	1	9.5	18	15	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SFTPB	SFTPB, SMDP1, SFTB3, SP-B, PSP-B, SFTP3	surfactant protein B	NM_198843, NM_000542, hCT1954168.1, hCT2286971.0, hCT25808.3	209810_at, 213936_x_at, 214354_x_at, 37004_at	NP_942140.2, NP_000533.3, EAW99487.1, EAW99488.1, EAW99489.1
GeneID.84913	ATOH8	2	85,980,909	86,018,506	37,597	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3324, 2_A375_pNL97_plus_lncRNA_AR..1..4775, 4_A375_EGR1..1..5100	18835, 18739, 25363	in gene, in gene, in gene	1	1	1	15.5	17.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ATOH8	HATH6, FLJ38730, FLJ14708, bHLHa21, ATOH8	atonal homolog 8 (Drosophila)	NM_032827, hCT1954190.1, hCT25822.3	1558705_at, 1558706_a_at, 226890_at	NP_116216.2, EAW99482.1, EAW99481.1
GeneID.8869	ST3GAL5	2	86,066,271	86,116,157	49,886	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4776	-4691	upstream	0	1	0	18	19	5	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ST3GAL5	SATI, ST3GalV, ST3GAL5, SIATGM3S, SIAT9	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	NM_003896, NM_001042437, hCT1954188.1, hCT1985728.1, hCT1985731.1, hCT1985733.1, hCT1985734.1, hCT2358492.0, hCT25819.3	203217_s_at, 239755_at	NP_003887.3, NP_001035902.1, EAW99474.1, EAW99475.1, EAW99476.1, EAW99480.1, EAW99477.1, EAW99478.1, EAW99479.1
GeneID.25885	POLR1A	2	86,253,451	86,333,278	79,827	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3325, 2_A375_pNL97_plus_lncRNA_AR..1..4778	78, 510	in gene, in gene	1	1	0	25	26	14	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene POLR1A	A190, RPA194, MGC87965, FLJ21915, RPO14, RPO1-4, POLR1A, DKFZp586M0122, RPA1	polymerase (RNA) I polypeptide A, 194kDa	NM_015425, hCT2261119.0, hCT2261120.0, hCT25395.3	222704_at	NP_056240.2, EAW99468.1, EAW99467.1, EAW99469.1
GeneID.55037	PTCD3	2	86,333,305	86,369,280	35,975	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3325, 2_A375_pNL97_plus_lncRNA_AR..1..4778	-105, -537	upstream, upstream	1	1	0	25	26	14	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene PTCD3	FLJ20758, DKFZp666K071, PTCD3	Pentatricopeptide repeat domain 3	NM_017952, hCT1954991.1, hCT1954994.1, hCT25399.3	217895_at, 228020_at, 228512_at, 228590_at	NP_060422.4, EAW99464.1, EAW99465.1, EAW99466.1
GeneID.65055	REEP1	2	86,441,116	86,565,206	124,090	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3326, 2_A375_pNL97_plus_lncRNA_AR..1..4779	37190, 37014	in gene, in gene	1	1	0	22	26	9	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene REEP1	REEP1, FLJ13110, SPG31, C2orf23	receptor accessory protein 1	NM_022912, NM_001164731, NM_001164730, NM_001164732, hCT1954988.0, hCT25396.1	204364_s_at, 204365_s_at	NP_075063.1, NP_001158203.1, NP_001158202.1, NP_001158204.1, EAW99457.1, EAW99458.1
GeneID.55818	KDM3A	2	86,668,271	86,719,839	51,568	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3327, 2_A375_pNL97_plus_lncRNA_AR..1..4780	-271, 1057	upstream, in gene	1	1	0	13	18.5	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene KDM3A	DKFZp686P0711, TSGA, KIAA0742, JHDM2A, KDM3A, JMJD1A, JMJD1, DKFZp686A24246, JHMD2A	lysine (K)-specific demethylase 3A	NM_018433, NM_001146688, hCT1818953.2, hCT2358409.0, hCT2358410.0, hCT2358411.0	212689_s_at	NP_060903.2, NP_001140160.1, EAW99453.1, EAW99454.1, EAW99455.1, EAW99456.1
GeneID.51652	VPS24	2	86,730,553	86,790,620	60,067	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3328, 2_A375_pNL97_plus_lncRNA_AR..1..4781	412, 444	in gene, in gene	1	1	0	29	24	12	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene VPS24	FLJ36114, CHMP3, VPS24, CGI-149, NEDF	vacuolar protein sorting 24 homolog (S. cerevisiae)	NM_001005753, NM_016079, NM_001193517, NR_036454, hCT1954966.1, hCT2358365.0, hCT2358366.0, hCT2358367.0, hCT25393.2	217837_s_at, 222436_s_at, 222437_s_at	NP_001005753.1, NP_057163.1, NP_001180446.1, EAW99449.1, EAW99451.1, EAW99452.1, EAW99448.1, EAW99450.1
GeneID.150572	SMYD1	2	88,367,382	88,412,903	45,521	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4782	50314	downstream	0	1	0	17	17	9	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene SMYD1	KMT3D, SMYD1, ZMYND22, ZMYND18, BOP	SET and MYND domain containing 1	NM_198274, hCT1952979.1, hCT2355667.0, hCT2355668.0, hCT24468.2	228406_at, 243045_at	NP_938015.1, EAW77077.1, EAW77078.1, EAW77079.1, EAW77080.1
GeneID.2168	FABP1	2	88,422,510	88,427,576	5,066	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4782	9682	downstream	0	1	0	17	17	9	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene FABP1	L-FABP, FABP1, FABPL	fatty acid binding protein 1, liver	NM_001443, hCT2252922.0, hCT24139.1	205892_s_at, 231693_at	NP_001434.1, EAW77075.1, EAW77076.1
GeneID.9451	EIF2AK3	2	88,856,259	88,927,094	70,835	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3329	-330	upstream	1	0	0	16	14	16	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene EIF2AK3	WRS, DKFZp781H1925, EIF2AK3, HRI, PERK, PEK	eukaryotic translation initiation factor 2-alpha kinase 3	NM_004836, hCT1788243.1, hCT2252915.0	218696_at	NP_004827.4, EAW77068.1, EAW77069.1
GeneID.100507380	LOC100507380	2	88,927,039	88,931,343	4,304	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3329	365	in gene	1	0	0	16	14	16	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene LOC100507380		hypothetical LOC100507380	XR_112345, XR_109953, XR_115626		
GeneID.22934	RPIA	2	88,991,176	89,050,452	59,276	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3330, 2_A375_pNL97_plus_lncRNA_AR..1..4784	-40, -136	upstream, upstream	1	1	0	24	25	12	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene RPIA	RPIA, RPI	ribose 5-phosphate isomerase A	NM_144563, hCT2253010.0, hCT2253012.0	212973_at	NP_653164.2, EAW77067.1, EAW77066.1
GeneID.100294406	LOC100294406	2	89,148,206	89,476,123	327,917	+	1	4_A375_EGR1..1..5103	37330	in gene	0	0	1	1	3	35	1	4_A375_EGR1..1	35	Gene LOC100294406		hypothetical LOC100294406	XR_109956, XR_109957, XR_109958, XR_115625, XR_115624		
GeneID.50802	IGK@	2	89,156,874	89,630,436	473,562	-	1	4_A375_EGR1..1..5103	444900	in gene	0	0	1	1	3	35	1	4_A375_EGR1..1	35	Gene IGK@	IGK, FLJ26298, MGC22645, MGC40426, MGC27376, IGK@, MGC71990	immunoglobulin kappa locus			
GeneID.28908	IGKV4-1	2	89,185,088	89,185,669	581	+	1	4_A375_EGR1..1..5103	448	in gene	0	0	1	1	3	35	1	4_A375_EGR1..1	35	Gene IGKV4-1	B3, IGKV4-1, IGKV41	immunoglobulin kappa variable 4-1			
GeneID.100506191	LOC100506191	2	91,832,852	91,835,376	2,524	-	2	4_A375_EGR1..1..5108, 4_A375_EGR1..1..5109	-8688, -9424	upstream, upstream	0	0	1	9	9.5	20	2	4_A375_EGR1..1	23	Gene LOC100506191		hypothetical protein LOC100506191	XM_003118995		XP_003119043.1
GeneID.64969	MRPS5	2	95,752,952	95,787,754	34,802	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4787	138	in gene	0	1	0	12	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MRPS5	S5mt, MRPS5, MRP-S5	mitochondrial ribosomal protein S5	NM_031902, hCT2288427.0, hCT31039.3	224333_s_at, 224877_s_at, 236779_at, 237580_at	NP_114108.1, EAX10713.1, EAX10712.1
GeneID.84874	ZNF514	2	95,813,400	95,825,263	11,863	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4788, 4_A375_EGR1..1..5110	-6289, -6001	upstream, upstream	0	1	1	13	17	12	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ZNF514	ZNF514, MGC126230, MGC126229	zinc finger protein 514	NM_032788, hCT1784492.2	235729_at	NP_116177.1, EAX10714.1
GeneID.7549	ZNF2	2	95,831,183	95,850,065	18,882	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4788, 4_A375_EGR1..1..5110	369, 81	in gene, in gene	0	1	1	13	17	12	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ZNF2	ZNF2, Zfp661, A1-5, ZNF661	zinc finger protein 2	NM_021088, NM_001017396, hCT1784488.2, hCT1953712.1	223792_at	NP_066574.2, NP_001017396.1, EAX10715.1, EAX10716.1
GeneID.150696	PROM2	2	95,940,201	95,957,056	16,855	+	1	4_A375_EGR1..1..5111	2295	in gene	0	0	1	4	8	13	1	4_A375_EGR1..1	13	Gene PROM2	PROM2, MGC138714, PROML2	prominin 2	NM_001165978, NM_144707, NM_001165977, hCT2287992.1, hCT2287993.1, hCT2359581.0, hCT2359582.0, hCT2359583.0	1552797_s_at, 1562378_s_at, 239528_at	NP_001159450.1, NP_653308.2, NP_001159449.1, EAX10718.1, EAX10720.1, EAX10722.1, EAX10719.1, EAX10721.1
GeneID.30818	KCNIP3	2	95,963,072	96,051,825	88,753	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3332	36576	in gene	1	0	0	18	13	10	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene KCNIP3	CSEN, DREAM, MGC18289, KCNIP3, KCHIP3	Kv channel interacting protein 3, calsenilin	NM_013434, NM_001034914, hCT1963194.1, hCT1963195.1, hCT2287997.0, hCT2287998.0, hCT28121.4	1555694_a_at, 1569355_at, 228289_x_at, 231774_at, 233668_at, 234198_at, 234647_at	NP_038462.1, NP_001030086.1, EAX10723.1, EAX10724.1, EAX10725.1, EAX10727.1, EAX10726.1
GeneID.51011	FAHD2A	2	96,068,448	96,078,879	10,431	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4789	32	in gene	0	1	0	6	21	10	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene FAHD2A	CGI-105, FAHD2A, MGC131995	fumarylacetoacetate hydrolase domain containing 2A	NM_016044, hCT2288000.0, hCT2288001.0, hCT2288002.0, hCT2288003.0, hCT2288004.0	218504_at, 222056_s_at	NP_057128.2, EAX10732.1, EAX10729.1, EAX10730.1, EAX10731.1, EAX10733.1
GeneID.285033	LOC285033	2	96,905,977	96,907,701	1,724	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4790	11655	downstream	0	1	0	18	21	3	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC285033	MGC126779, MGC126781	hypothetical protein LOC285033	NM_001037228, hCT2289920.0, hCT2354906.0	235584_at	NP_001032305.1, EAW71380.1, EAW71381.1
GeneID.55654	TMEM127	2	96,916,312	96,931,751	15,439	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4790	14119	in gene	0	1	0	18	21	3	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TMEM127	FLJ22257, TMEM127, FLJ20507	transmembrane protein 127	NM_017849, NM_001193304, hCT1967805.1, hCT2289249.0, hCT2289251.0, hCT26534.3	219460_s_at, 222867_s_at	NP_060319.1, NP_001180233.1, EAW71376.1, EAW71377.1, EAW71378.1, EAW71379.1
GeneID.150771	ITPRIPL1	2	96,991,062	96,994,091	3,029	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3333, 2_A375_pNL97_plus_lncRNA_AR..1..4791	10527, 10522	downstream, downstream	1	1	0	17	15	9	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ITPRIPL1	ITPRIPL1, KIAA1754L	inositol 1,4,5-triphosphate receptor interacting protein-like 1	NM_178495, NM_001008949, NM_001163523, NM_001163524	240037_at	NP_848590.3, NP_001008949.1, NP_001156995.1, NP_001156996.1
GeneID.23397	NCAPH	2	97,001,484	97,041,274	39,790	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3333, 2_A375_pNL97_plus_lncRNA_AR..1..4791	105, 100	in gene, in gene	1	1	0	17	15	9	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene NCAPH	HCAP-H, CAP-H, NCAPH, BRRN1	non-SMC condensin I complex, subunit H	NM_015341, hCT28532.3	212949_at	NP_056156.2, EAW71370.1
GeneID.10865	ARID5A	2	97,202,464	97,218,371	15,907	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3334, 2_A375_pNL97_plus_lncRNA_AR..1..4793	20320, 20368	downstream, downstream	1	1	0	20	19	7	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ARID5A	RP11-363D14, MRF-1, ARID5A, MRF1	AT rich interactive domain 5A (MRF1-like)	NM_212481, hCT2289879.0, hCT2354918.0, hCT2354919.0, hCT2354920.0, hCT2354921.0, hCT2354922.0, hCT2354923.0, hCT26530.3	213138_at	NP_997646.1, EAW71360.1, EAW71359.1, EAW71361.1, EAW71365.1, EAW71366.1, EAW71362.1, EAW71363.1, EAW71364.1
GeneID.55683	KIAA1310	2	97,258,907	97,304,115	45,208	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3335, 2_A375_pNL97_plus_lncRNA_AR..1..4794	67, -61	in gene, upstream	1	1	0	20	24	14	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene KIAA1310	KIAA1310, FLJ10061, Rod1, FLJ23799	KIAA1310	NM_017991, NM_001115016, hCT1950358.1, hCT1950359.1, hCT2289237.0, hCT2289238.0, hCT2289241.0, hCT2354899.0, hCT2354900.0, hCT2354901.0, hCT2354902.0, hCT2354903.0, hCT2354904.0, hCT9706.3	1558852_at, 220950_s_at, 223756_at, 224316_s_at	NP_060461.3, NP_001108488.1, EAW71347.1, EAW71354.1, EAW71357.1, EAW71358.1, EAW71348.1, EAW71349.1, EAW71350.1, EAW71351.1, EAW71352.1, EAW71353.1, EAW71355.1, EAW71356.1
GeneID.90342	FER1L5	2	97,308,574	97,370,624	62,050	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3335, 2_A375_pNL97_plus_lncRNA_AR..1..4794	-4526, -4398	upstream, upstream	1	1	0	20	24	14	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene FER1L5	FER1L5	fer-1-like 5 (C. elegans)	NM_001113382	233353_at	NP_001106853.1
GeneID.26504	CNNM4	2	97,426,639	97,477,628	50,989	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3336	55377	downstream	1	0	0	20	10	5	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene CNNM4	KIAA1592, FLJ42791, CNNM4, FLJ37746, ACDP4	cyclin M4	NM_020184, hCT9245.3	218900_at	NP_064569.3, EAW71340.1
GeneID.100506036	LOC100506036	2	97,477,976	97,480,170	2,194	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3336	-1846	upstream	1	0	0	20	10	5	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LOC100506036		hypothetical LOC100506036	XR_109916		
GeneID.26505	CNNM3	2	97,481,991	97,501,121	19,130	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3336	25	in gene	1	0	0	20	10	5	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene CNNM3	ACDP3, FLJ20018, DKFZp434I1016, CNNM3	cyclin M3	NM_017623, NM_199078, hCT1771438.2, hCT1966165.1, hCT2289897.0, hCT2289900.0	220739_s_at	NP_060093.3, NP_951060.1, EAW71334.1, EAW71335.1, EAW71336.1, EAW71337.1
GeneID.51239	ANKRD39	2	97,513,722	97,523,756	10,034	-	2	4_A375_EGR1..1..5112, 4_A375_EGR1..1..5113	-2516, -3540	upstream, upstream	0	0	1	3.5	8	15	2	4_A375_EGR1..1	15	Gene ANKRD39	MGC41816, ANKRD39	ankyrin repeat domain 39	NM_016466, hCT2289228.0, hCT2289230.1, hCT2354927.0	223532_at	NP_057550.3, EAW71328.1, EAW71329.1, EAW71330.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:54910	SEMA4C	2	97,525,473	97,535,735	10,262	-	2	4_A375_EGR1..1..5112, 4_A375_EGR1..1..5113	9463, 8439	in gene, in gene	0	0	1	3.5	8	15	2	4_A375_EGR1..1	15	Gene SEMA4C	MGC126382, SEMAI, KIAA1739, MGC126383, SEMACL1, FLJ20369, SEMAF, SEMA4C, M-SEMA-F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	NM_017789, hCT2289224.0, hCT2289226.0, hCT9705.2	219039_at, 46665_at	NP_060259.4, EAW71326.1, EAW71325.1, EAW71327.1
GeneID:643615	UBTFL6	2	98,253,048	98,255,087	2,039	-	1	4_A375_EGR1..1..5114	-7441	upstream	0	0	1	7	9	15	1	4_A375_EGR1..1	15	Gene UBTFL6	UBTFL6	upstream binding transcription factor, RNA polymerase I-like 6			
GeneID:1329	COX5B	2	98,262,521	98,264,657	2,136	+	1	4_A375_EGR1..1..5114	7	in gene	0	0	1	7	9	15	1	4_A375_EGR1..1	15	Gene COX5B	COX5B, COXVB	cytochrome c oxidase subunit Vb	NM_001862, hCT1770444.2	202343_x_at, 211025_x_at, 213735_s_at, 213736_at	NP_001853.2, EAX01930.1
GeneID:10120	ACTR1B	2	98,272,402	98,280,561	8,159	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3337, 4_A375_EGR1..1..5114	-111, 18033	upstream, downstream	1	0	1	15	12	10	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene ACTR1B	ACTR1B, CTRN2, ARP1B, PC3	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	NM_005735, hCT2282763.0, hCT2282764.0, hCT2282765.0, hCT2282766.0, hCT2282767.0, hCT2282768.0	202135_s_at	NP_005726.1, EAX01923.1, EAX01925.1, EAX01926.1, EAX01927.1, EAX01928.1, EAX01924.1
GeneID:3631	INPP4A	2	99,061,321	99,207,496	146,175	+	1	4_A375_EGR1..1..5115	63143	in gene	0	0	1	4	11	18	1	4_A375_EGR1..1	18	Gene INPP4A	TVAS1, INPP4, INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	NM_004027, NM_001566, NM_001134224, NM_001134225, hCT1955215.1, hCT2266503.0, hCT2266504.0, hCT2266505.0, hCT2266506.0, hCT2266507.0, hCT29666.3	204553_x_at, 208363_s_at, 208364_at	NP_004018.1, NP_001557.1, NP_001127696.1, NP_001127697.1, EAX01905.1, EAX01910.1, EAX01904.1, EAX01906.1, EAX01907.1, EAX01908.1, EAX01909.1
GeneID:493753	C2orf64	2	99,215,865	99,224,955	9,090	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4795	187	in gene	0	1	0	9	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C2orf64	6330578E17Rik, C2orf64, MGC52110	chromosome 2 open reading frame 64	NM_001008215, hCT1955213.2	225409_at, 225410_at	NP_001008216.1, EAX01903.1
GeneID:25972	UNC50	2	99,225,042	99,234,978	9,936	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4795	-274	upstream	0	1	0	9	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene UNC50	UNCL, HSD23, URP, GMH1, UNC50, DKFZp564G0222	unc-50 homolog (C. elegans)	NM_014044, hCT1963233.2, hCT2348913.0, hCT29661.2	203583_at	NP_054763.2, EAX01900.1, EAX01901.1, EAX01902.1
GeneID:80705	TSGA10	2	99,613,724	99,771,187	157,463	-	1	4_A375_EGR1..1..5116	-445	upstream	0	0	1	12	10	11	1	4_A375_EGR1..1	11	Gene TSGA10	CT79, TSGA10, CEP4L	testis specific, 10	NM_025244, NM_182911, hCT2282987.0, hCT2282988.0, hCT2358584.0, hCT2358585.0, hCT29669.3	220623_s_at, 223638_at	NP_079520.1, NP_878915.2, EAX01888.1, EAX01890.1, EAX01891.1, EAX01892.1, EAX01889.1
GeneID:150590	C2orf15	2	99,758,165	99,767,950	9,785	+	1	4_A375_EGR1..1..5116	13447	downstream	0	0	1	12	10	11	1	4_A375_EGR1..1	11	Gene C2orf15	MGC29762, C2orf15, FLJ44438	chromosome 2 open reading frame 15	NM_144706, hCT2268490.0	1552740_at	NP_653307.1, EAX01893.1
GeneID:51601	LIPT1	2	99,771,418	99,779,620	8,202	+	1	4_A375_EGR1..1..5116	214	in gene	0	0	1	12	10	11	1	4_A375_EGR1..1	11	Gene LIPT1	MGC12290, LIPT1, MGC13378	lipoyltransferase 1	NM_145198, NM_145197, NM_145196, NM_145199, NM_015929	205571_at	NP_660197.1, NP_660198.1, NP_660199.1, NP_660200.1, NP_057013.1
GeneID:129531	MITD1	2	99,785,726	99,797,492	11,766	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4796	-76	upstream	0	1	0	14	18	9	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MITD1	MITD1	MIT, microtubule interacting and transport, domain containing 1	NM_138798, hCT2358577.0, hCT2358578.0, hCT2358579.0, hCT29667.3	226329_s_at	NP_620153.1, EAX01885.1, EAX01884.1, EAX01886.1, EAX01887.1
GeneID:51263	MRPL30	2	99,797,576	99,814,089	16,511	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4796	-10	upstream	0	1	0	14	18	9	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MRPL30	MGC3314, MRPL28, RPML28, MRP-L28, MRPL28M, L28MT, MRPL30, MGC24095, L30MT, FLJ44438	mitochondrial ribosomal protein L30	NM_145212	223998_s_at, 224173_s_at, 224971_at	NP_660213.1
GeneID:10190	TXNDC9	2	99,935,487	99,952,860	17,373	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3338	-900	upstream	1	0	0	20	14	5	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene TXNDC9	TXNDC9, APACD, PHLP3	thioredoxin domain containing 9	NM_005783, hCT1771591.1, hCT2282996.0, hCT2282997.0, hCT2358586.0	1554047_at, 203008_x_at, 211758_x_at	NP_005774.2, EAX01870.1, EAX01868.1, EAX01869.1, EAX01871.1
GeneID:9669	EIF5B	2	99,953,834	100,016,728	62,894	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3338	-74	upstream	1	0	0	20	14	5	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene EIF5B	FLJ10524, EIF5B, DKFZp434I036, IF2, KIAA0741	eukaryotic translation initiation factor 5B	NM_015904, hCT2283253.0, hCT2283255.0, hCT2283256.0, hCT29664.3	201024_x_at, 201025_at, 201026_at, 201027_s_at, 214313_s_at, 214314_s_at	NP_056988.3, EAX01864.1, EAX01865.1, EAX01866.1, EAX01867.1
GeneID:3899	AFF3	2	100,163,715	100,759,037	595,322	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3339	260573	in gene	1	0	0	14	5	4	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene AFF3	AFF3, LAF4, MLLT2-like	AF4/FMR2 family, member 3	NM_002285, NM_001025108, hCT1958876.2, hCT2283035.1, hCT2283037.1, hCT2283039.1, hCT2283040.1, hCT2283046.1	205734_s_at, 205735_s_at, 227198_at, 243987_at	NP_002276.2, NP_001020279.1, EAX01854.1, EAX01855.1, EAX01857.1, EAX01859.1, EAX01856.1, EAX01858.1
GeneID:9486	CHST10	2	101,008,322	101,034,091	25,769	-	1	4_A375_EGR1..1..5117	-8933	upstream	0	0	1	3	5	12	1	4_A375_EGR1..1	12	Gene CHST10	HNK1ST, MGC17148, HNK-1ST, CHST10	carbohydrate sulfotransferase 10	NM_004854, hCT17602.3, hCT1971001.1, hCT1971002.1, hCT1971003.1	204085_at	NP_004845.1, EAX01843.1, EAX01841.1, EAX01842.1, EAX01844.1
GeneID:129521	NMS	2	101,086,944	101,099,742	12,798	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3340, 2_A375_pNL97_plus_lncRNA_AR..1..4797	544, 576	in gene, in gene	1	1	0	17	18	2	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene NMS	NMS	neuromedin S	NM_001011717		NP_001011717.1
GeneID:4862	NPAS2	2	101,436,613	101,613,287	176,674	+	1	4_A375_EGR1..1..5118	25467	in gene	0	0	1	3	8	14	1	4_A375_EGR1..1	14	Gene NPAS2	PASD4, FLJ23138, MGC71151, MOP4, bHLHe9, NPAS2	neuronal PAS domain protein 2	NM_002518, hCT18755.4, hCT1971011.1, hCT1971012.1, hCT2283169.0, hCT2283174.0, hCT2283177.0	205459_s_at, 205460_at, 213462_at, 39548_at, 39549_at	NP_002509.2, EAX01833.1, EAX01830.1, EAX01831.1, EAX01832.1, EAX01835.1, EAX01834.1
GeneID:11138	TBC1D8	2	101,623,690	101,767,846	144,156	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3341, 2_A375_pNL97_plus_lncRNA_AR..1..4798	30876, 30534	in gene, in gene	1	1	0	16	17	5	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TBC1D8	TBC1D8, HBLP1, VRP, TBC1D8A, AD3	TBC1 domain family, member 8 (with GRAM domain)	NM_001102426, hCT18754.2, hCT2282771.0, hCT2282774.0	204526_s_at, 221592_at, 241017_at	NP_001095896.1, EAX01825.1, EAX01823.1, EAX01824.1
GeneID:731220	RFX8	2	102,013,823	102,091,165	77,342	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3342, 2_A375_pNL97_plus_lncRNA_AR..1..4799	27645, 27581	in gene, in gene	1	1	0	23	18	1	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene RFX8	FLJ16242, RFX8, FLJ42986, FLJ52890	regulatory factor X, 8	NM_001145664		NP_001139136.1
GeneID:9392	TGFBRAP1	2	105,883,529	105,946,148	62,619	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4800	-7740	upstream	0	1	0	12	18	5	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TGFBRAP1	TGFBRAP1, TRAP1, TRAP-1	transforming growth factor, beta receptor associated protein 1	NM_004257, NM_001142621, hCT2282441.0, hCT2282442.0	205210_at	NP_004248.2, NP_001136093.1, EAX01764.1, EAX01765.1
GeneID:100506473	LOC100506473	2	105,950,491	105,952,005	1,514	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4800	-1683	upstream	0	1	0	12	18	5	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100506473		hypothetical LOC100506473	XR_109933		
GeneID:79074	C2orf49	2	105,954,013	105,961,984	7,971	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4800	-125	upstream	0	1	0	12	18	5	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene C2orf49	C2orf49, MGC5509, FLJ45759, asw	chromosome 2 open reading frame 49	NM_024093, hCT1642208.2	219682_at, 226951_at, 243093_at	NP_076998.1, EAX01763.1
GeneID:80146	UXS1	2	106,709,759	106,810,795	101,036	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3345, 2_A375_pNL97_plus_lncRNA_AR..1..4801	78923, 78843	in gene, in gene	1	1	0	22	19	5	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene UXS1	FLJ23591, UGD, UXS1, SDR6E1	UDP-glucuronate decarboxylase 1	NM_025076, hCT1955977.1, hCT2266425.0, hCT2358580.0, hCT2358581.0	219675_s_at, 225583_at	NP_079352.2, EAX01750.1, EAX01747.1, EAX01748.1, EAX01749.1
GeneID:3987	LIMS1	2	109,150,857	109,303,702	152,845	+	1	4_A375_EGR1..1..5120	-340	upstream	0	0	1	9	10	14	1	4_A375_EGR1..1	14	Gene LIMS1	LIMS1, PINCH1, PINCH	LIM and senescent cell antigen-like domains 1	NM_004987, NM_001193482, NM_001193483, NM_001193484, NM_001193485, NM_001193488, hCT2274389.0, hCT2274390.0, hCT2274391.0, hCT2274392.0	1566127_at, 1566129_at, 1570259_at, 207198_s_at, 212687_at	NP_004978.2, NP_001180411.1, NP_001180412.1, NP_001180413.1, NP_001180414.1, NP_001180417.1, EAW53877.1, EAW53878.1, EAW53879.1, EAW53880.1
GeneID:5903	RANBP2	2	109,335,937	109,402,267	66,330	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4802	-17	upstream	0	1	0	17	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene RANBP2	NUP358, TRP1, RANBP2, TRP2, ANE1	RAN binding protein 2	NM_006267	201711_x_at, 201712_s_at, 201713_s_at, 226922_at	NP_006258.3
GeneID:100287216	LOC100287216	2	109,743,783	109,746,575	2,792	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4803, 4_A375_EGR1..1..5121	1183, -97	in gene, upstream	0	1	1	9.5	15.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100287216	FLJ53560	hypothetical LOC100287216	NR_029193		
GeneID:344558	SH3RF3	2	109,745,997	110,107,395	361,398	+	4	2_A375_pNL97_plus_lncRNA_AR..1..4803, 2_A375_pNL97_plus_lncRNA_AR..1..4804, 2_A375_pNL97_plus_lncRNA_AR..1..4805, 4_A375_EGR1..1..5121	-605, 84627, 113619, 675	upstream, in gene, in gene, in gene	0	1	1	9	16.25	7.75	4	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SH3RF3	SH3MD4, POSH2, FLJ00204, SH3RF3	SH3 domain containing ring finger 3	NM_001099289	228461_at	NP_001092759.1
GeneID:100506574	LOC100506574	2	109,867,678	109,868,105	227	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4805	-8262	upstream	0	1	0	8	17	3	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC100506574	SNRPGP9	small nuclear ribonucleoprotein G-like	XM_003119869, XM_003118659, XM_003120363		XP_003119917.1, XP_003118907.1, XP_003120411.1
GeneID:4867	NPHP1	2	110,880,913	110,962,639	81,726	-	1	4_A375_EGR1..1..5122	143	in gene	0	0	1	8	11	14	1	4_A375_EGR1..1	14	Gene NPHP1	FLJ97602, NPH1, JBTS4, SLSN1, NPHP1	nephronophthisis 1 (juvenile)	NM_000272, NM_207181, NM_001128178, NM_001128179, hCT2265221.0, hCT2265222.0, hCT2265223.0, hCT2352394.0, hCT2352395.0, hCT2352396.0, hCT2352397.0	206285_at, 238843_at, 238844_s_at	NP_000263.2, NP_997064.2, NP_001121650.1, NP_001121651.1, EAW50631.1, EAW50636.1, EAW50632.1, EAW50633.1, EAW50634.1, EAW50635.1, EAW50637.1
GeneID:205251	NCRNA00116	2	110,969,106	110,980,517	11,411	-	1	4_A375_EGR1..1..5122	18021	downstream	0	0	1	8	11	14	1	4_A375_EGR1..1	14	Gene NCRNA00116	NCRNA00116	non-protein coding RNA 116	NR_027063	228614_at	
GeneID:699	BUB1	2	111,395,409	111,435,684	40,275	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4806	-92	upstream	0	1	0	11	18	7	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene BUB1	BUB1L, BUB1A, BUB1, hBUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	NM_004336, hCT2255329.0	209642_at, 215508_at, 215509_s_at, 216275_at, 216277_at	NP_004327.1, EAW50355.1
GeneID:55289	ACOXL	2	111,490,150	111,875,799	385,649	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3346, 2_A375_pNL97_plus_lncRNA_AR..1..4807	368442, 368378	in gene, in gene	1	1	0	26	24	4	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene ACOXL	FLJ11042, ACOXL	acyl-CoA oxidase-like	NM_001142807, hCT2255305.0, hCT2255307.0, hCT2255309.0, hCT7660.3	220845_at	NP_001136279.1, EAW50360.1, EAW50357.1, EAW50358.1, EAW50359.1
GeneID:400997	FLJ44006	2	111,855,918	111,871,762	15,844	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3346, 2_A375_pNL97_plus_lncRNA_AR..1..4807	13170, 13234	in gene, in gene	1	1	0	26	24	4	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene FLJ44006		hypothetical FLJ44006	XR_112372, XR_109903, XR_113363		
GeneID:64682	ANAPC1	2	112,526,638	112,641,741	115,103	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4808, 4_A375_EGR1..1..5123	-115, 237	upstream, in gene	0	1	1	11	15	17	1	4_A375_EGR1..1	17	Gene ANAPC1	MCPR, TSG24, APC1, ANAPC1	anaphase promoting complex subunit 1	NM_022662, hCT1644042.3	218575_at, 231973_s_at	NP_073153.1, EAW52095.1
GeneID:376940	ZC3H6	2	113,033,178	113,097,640	64,462	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4809, 4_A375_EGR1..1..5124	-218, -18	upstream, upstream	0	1	1	13	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ZC3H6	FLJ41410, ZC3H6, FLJ16526, ZC3HDC6, FLJ45877, KIAA2035	zinc finger CCCH-type containing 6	NM_198581	227809_at, 241372_at	NP_940983.2
GeneID:150465	TTL	2	113,239,743	113,290,223	50,480	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4810, 4_A375_EGR1..1..5125	59873, 865	downstream, in gene	0	1	1	10.5	10.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TTL	TTL, MGC46235	tubulin tyrosine ligase	NM_153712, hCT7290.3	1559680_at, 224896_s_at, 224906_s_at	NP_714923.1, EAW73589.1
GeneID:84172	POLR1B	2	113,299,492	113,334,727	35,235	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4810	124	in gene	0	1	0	13	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene POLR1B	FLJ10816, RPA2, MGC131780, POLR1B, Rpo1-2, RPA135, FLJ21921	polymerase (RNA) I polypeptide B, 128kDa	NM_019014, NM_001137604, hCT1952953.1, hCT2273620.0, hCT2273622.0, hCT7291.2	1557331_at, 220113_x_at, 223403_s_at, 233341_s_at	NP_061887.2, NP_001131076.1, EAW73590.1, EAW73591.1, EAW73592.1, EAW73593.1
GeneID:400999	FLJ42351	2	113,399,407	113,401,757	2,350	-	3	2_A375_pNL97_plus_lncRNA_AR..1..4811, 2_A375_pNL97_plus_lncRNA_AR..1..4812, 4_A375_EGR1..1..5126	3229, -2003, -1875	downstream, upstream, upstream	0	1	1	12.5	16.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene FLJ42351		hypothetical LOC400999	NR_033871	230452_at	
GeneID:6574	SLC20A1	2	113,403,527	113,421,402	17,875	+	3	2_A375_pNL97_plus_lncRNA_AR..1..4811, 2_A375_pNL97_plus_lncRNA_AR..1..4812, 4_A375_EGR1..1..5126	-4999, 233, 105	upstream, in gene, in gene	0	1	1	12.5	16.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SLC20A1	Glvr-1, PIT1, DKFZp686J2397, FLJ41426, SLC20A1, GLVR1, PiT-1	solute carrier family 20 (phosphate transporter), member 1	NM_005415, hCT2273628.1, hCT2273629.1, hCT6777.3	201920_at	NP_005406.3, EAW73599.1, EAW73597.1, EAW73598.1
GeneID:150468	CKAP2L	2	113,495,444	113,522,254	26,810	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3347, 2_A375_pNL97_plus_lncRNA_AR..1..4813	-66, 78	upstream, in gene	1	1	0	15	23	9	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CKAP2L	MGC39683, FLJ40629, CKAP2L	cytoskeleton associated protein 2-like	NM_152515, hCT2343355.0, hCT7293.3	229610_at	NP_689728.3, EAW73603.1, EAW73602.1
GeneID:3552	IL1A	2	113,531,492	113,542,971	11,479	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3347, 2_A375_pNL97_plus_lncRNA_AR..1..4813	20851, 20795	downstream, downstream	1	1	0	15	23	9	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene IL1A	IL1, IL1-ALPHA, IL1F1, IL-1A, IL1A	interleukin 1, alpha	NM_000575, hCT7292.3	208200_at, 210118_s_at	NP_000566.3, EAW73604.1
GeneID:27178	IL1F7	2	113,670,548	113,676,459	5,911	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4815	6172	downstream	0	1	0	11	17	7	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene IL1F7	IL1RP1, IL-1F7, IL-1H4, FIL1, FIL1Z, FIL1(ZETA), IL-1RP1, IL1F7, IL1H4	interleukin 1 family, member 7 (zeta)	NM_014439, NM_173202, NM_173203, NM_173204, NM_173205, hCT18382.3, hCT2273787.0, hCT2273789.0, hCT2273790.0, hCT2273791.0	221470_s_at, 224555_x_at	NP_055254.2, NP_775294.1, NP_775295.1, NP_775296.1, NP_775297.1, EAW73611.1, EAW73608.1, EAW73609.1, EAW73610.1, EAW73612.1
GeneID:7849	PAX8	2	113,973,574	114,036,498	62,924	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3349, 2_A375_pNL97_plus_lncRNA_AR..1..4816, 4_A375_EGR1..1..5127	37842, 37970, 38868	in gene, in gene, in gene	1	1	1	13.5	14	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PAX8	PAX8		NM_003466, NM_013952, NM_013953, NM_013992, hCT18378.3, hCT18379.3, hCT18380.3, hCT1970998.1, hCT1970999.1, hCT1971000.1, hCT2274188.0, hCT2274191.0, hCT2274192.0, hCT2274193.0, hCT2274194.0	121_at, 207921_x_at, 207923_x_at, 207924_x_at, 209552_at, 213917_at, 214528_s_at, 221990_at	NP_003457.1, NP_039246.1, NP_039247.1, NP_054698.1, EAW73629.1, EAW73637.1, EAW73630.1, EAW73631.1, EAW73632.1, EAW73633.1, EAW73634.1, EAW73635.1, EAW73636.1, EAW73638.1, EAW73639.1
GeneID:654433	LOC654433	2	113,993,846	114,024,580	30,734	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3349, 2_A375_pNL97_plus_lncRNA_AR..1..4816, 4_A375_EGR1..1..5127	4610, 4662, 3766	in gene, in gene, in gene	1	1	1	13.5	14	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC654433	FLJ44467, DKFZp686E10196, FLJ31793, DKFZp547P134, FLJ17200	hypothetical LOC654433	NR_015377	227474_at, 228425_at	



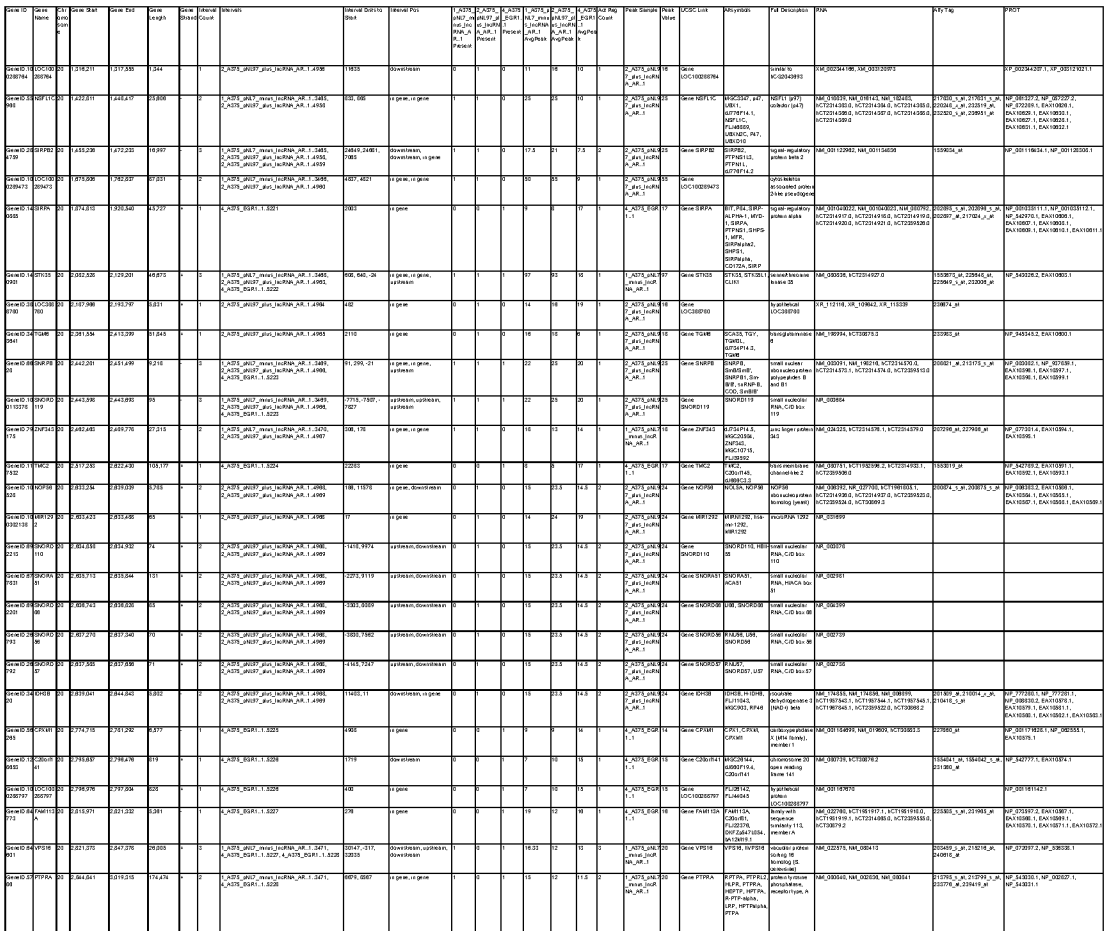
Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_uN27_eu_lncRNA_R1_1 Peaks	2_A375_uN27_eu_lncRNA_R1_1 Peaks	4_A375_EGR1_1 Peaks	1_A375_uN27_lncRNA_R1_1 Avg Peak	2_A375_uN27_lncRNA_R1_1 Avg Peak	4_A375_EGR1_1 Avg Peak	Ad2 Rag Count	Peak Sample	Peak Values	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:10 5938707	LOC1059 38707	2	113,999,648	113,998,419	2,772	+	3	1_A375_uN27_mrna1_lncRNA_NR_1:3369, 2_A375_uN27_plus_lncRNA_NR_1:4616, 4_A375_EGR1_1.3127	3010, 2662, 1998	downstream, downstream, upgene	1	1	1	13.5	14	8.5	2	2_A375_uN27_plus_lncRNA_NR_1	21	Gene LOC105938707		hypothetical protein LOC105938707	XR_109377, XR_112996		
GeneID:83 4412	FAM133 B	2	114,258,359	114,258,429	1,470	+	2	1_A375_uN27_mrna1_lncRNA_NR_1:3392, 2_A375_uN27_plus_lncRNA_NR_1:4617	6383, 6321	downstream, downstream	1	1	0	30	33	10	1	2_A375_uN27_plus_lncRNA_NR_1	33	Gene FAM133B	FAM133B, FSTL5A285L14.6	family with sequence similarity 133, member B	NR_026821		
GeneID:10 3382126	MIR1302 -2	2	114,340,536	114,340,673	137	-	2	1_A375_uN27_mrna1_lncRNA_NR_1:3393, 4_A375_EGR1_1.4617	-871, -807	upstream, upstream	1	1	0	30	33	10	1	2_A375_uN27_plus_lncRNA_NR_1	33	Gene MIR1302-2	hsa-mir-1302-2, MIRN1302-2, MIR1302-2	microRNA 1302-2	NR_031832		
GeneID:25 826	DPP10	2	115,199,899	115,802,326	1,402,427	+	1	1_A375_uN27_mrna1_lncRNA_NR_1:3351	501	upgene	1	0	0	14	0.0	8	1	1_A375_uN27_mrna1_lncRNA_NR_1	14	Gene DPP10	DPP10, DPPX, DPL2, DPRP3	dipeptidyl-peptidase 10	NM_001034880, NM_001178034, NM_001178036, NM_001178037, NM_020868, XC7349639.0, XC7349637.0, XC7372224	230898_at	NP_001034880.2, NP_001171005.1, NP_068910.2, NP_001171007.1, NP_001171006.1, EAW68166.1, EAW68167.1, EAW68165.1
GeneID:88 98	DDX18	2	118,972,233	119,088,993	117,886	+	2	1_A375_uN27_mrna1_lncRNA_NR_1:3382, 2_A375_uN27_plus_lncRNA_NR_1:4618	-127, -98	upstream, upstream	1	1	0	89	73	8	1	2_A375_uN27_plus_lncRNA_NR_1	73	Gene DDX18	DDX18, FLJ23505, MXB	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	NM_006773, XC7229269.1, XC7229268.0, XC7230236.0	203763_s_at, 203939_s_at, 208896_at, 208897_s_at	NP_006764.3, EAW68150.1, EAW93193.1, EAW95194.1
GeneID:20 19	ENI	2	119,590,747	119,605,799	15,052	+	1	4_A375_EGR1_1.5326	12127	downstream	0	0	1	18	8	10	1	4_A375_EGR1_1.5	10	Gene ENI	ENI		NM_031426, XC7229273.0, XC7233033	220859_at	NP_300417.2, EAW68208.1, EAW93255.1
GeneID:19 5237	C1QL2	2	119,913,619	119,916,471	2,852	-	1	1_A375_uN27_mrna1_lncRNA_NR_1:3393	4297	upstream	1	0	0	15	11	4	1	1_A375_uN27_mrna1_lncRNA_NR_1	15	Gene C1QL2	C1QTNF10, CTRP10, C1QL2	complement 1, q subcomponent-like 2	NM_182935, XC7233.3		NP_873234.2, EAW68206.1
GeneID:37 8869	EPB41L3	2	120,770,804	120,938,697	168,002	+	3	1_A375_uN27_mrna1_lncRNA_NR_1:3394, 2_A375_uN27_plus_lncRNA_NR_1:4620, 2_A375_uN27_plus_lncRNA_NR_1:4621	-108, -12, 121356	upstream, upstream, upgene	1	1	0	24.5	34	7.5	2	2_A375_uN27_plus_lncRNA_NR_1	33	Gene EPB41L3	FLJ12437, MGC14345, DKFZp761M1511, EPB413	erythrocyte membrane protein band 4.1 like 3	NM_001164937, NM_001164935, NM_001164939, NM_020909, XC7197127.2, XC7230791.0, XC7237630.0, XC7237.0.3	220977_s_at, 223655_at, 223656_at	NP_001157996.1, NP_001157997.1, NP_065960.2, NP_001157995.1, EAW68233.1, EAW68234.1, EAW68235.1, EAW68236.1
GeneID:23 032	CLASP1	2	122,099,352	122,407,032	311,700	-	3	1_A375_uN27_mrna1_lncRNA_NR_1:3395, 2_A375_uN27_plus_lncRNA_NR_1:4622, 4_A375_EGR1_1.5132	116700, 116745, 115276	upgene, upgene, upgene	1	1	1	23	23	16	1	1_A375_uN27_mrna1_lncRNA_NR_1	23	Gene CLASP1	FLJ41222, DKFZp685D19Rik, DKFZp686H02029, KIAA1713, KIAA0803, MUNIT1, FLJ35221	cytoskeleton-associated protein 5-like (rat)	NM_182282, NM_001142273, NM_001142274, XC7197122.2, XC7229339.0, XC7237547.0, XC7272.5	212752_at, 240797_at	NP_036397.1, NP_001130745.1, NP_001129249.1, EAW68262.1, EAW68263.1, EAW68264.1, EAW68265.1
GeneID:10 3131603	RNASA 7AC	2	122,288,499	122,288,555	129	+	3	1_A375_uN27_mrna1_lncRNA_NR_1:3155, 2_A375_uN27_plus_lncRNA_NR_1:4622, 4_A375_EGR1_1.5132	-156, -152, -693	upstream, upstream, upstream	1	1	1	23	23	16	1	1_A375_uN27_mrna1_lncRNA_NR_1	23	Gene RNASA7AC	Rhs, Lisetic RNASA7AC, RNASA7AC1	3A7AC, RNase, Lisetic (U12-dependent tuft-ring)	NM_022343		
GeneID:10 5389549	LOC1003 89549	2	122,288,555	122,306,029	19,474	-	3	1_A375_uN27_mrna1_lncRNA_NR_1:3395, 2_A375_uN27_plus_lncRNA_NR_1:4622, 4_A375_EGR1_1.5132	19677, 19725, 16253	downstream, downstream, downstream	1	1	1	23	23	16	1	1_A375_uN27_mrna1_lncRNA_NR_1	23	Gene LOC100389549		hypothetical LOC100389549	XR_109864		
GeneID:72 47	TSN	2	122,310,121	122,325,429	12,308	+	2	1_A375_uN27_mrna1_lncRNA_NR_1:3396, 2_A375_uN27_plus_lncRNA_NR_1:4623	31, 83	upgene, upgene	1	1	0	37	29	11	1	1_A375_uN27_plus_lncRNA_NR_1	37	Gene TSN	RCHY-1, TSN, TSG10L, TSH1B1, RCHY1, BCLF-1	translin	NM_004622, XC7237634.0, XC7237.5.2	201554_s_at, 201513_at, 201513_s_at	NP_004613.1, EAW68280.1, EAW93282.1
GeneID:29 93	GYPC	2	127,413,864	127,436,248	40,382	+	1	2_A375_uN27_plus_lncRNA_NR_1:4624	598	upgene	0	1	0	5	15	2	1	2_A375_uN27_plus_lncRNA_NR_1	15	Gene GYPC	C-DS28R, MGC129191, GPC, GE, MGC117309, GYPD, MGC129192, CD236, PAS-2, GYPC	glycophorin C (Gerbich blood group)	NM_002101, NM_016613, XC7229485.0, XC7.9699.3	202947_s_at	NP_002092.1, NP_057731.1, EAW68278.1, EAW68279.1
GeneID:20 71	ERCC3	2	128,014,998	128,031,732	16,735	-	1	4_A375_EGR1_1.5134	298	upgene	0	0	1	10	9	15	1	4_A375_EGR1_1.1	15	Gene ERCC3	RAD25, XPB, BTF2, TFIIH, ERCC3, GTF2H	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	NM_000122, XC7197192.1, XC7237630.0, XC7.9701.0, XC7.9699.2	202170_at	NP_000113.1, EAW68311.1, EAW93112.1, EAW93113.1, EAW93114.1
GeneID:10 5389904	LOC1003 89904	2	128,038,666	128,039,925	2,259	-	1	4_A375_EGR1_1.5134	6489	downstream	0	0	1	10	9	15	1	4_A375_EGR1_1.1	15	Gene LOC100389904		hypothetical LOC100389904	XR_112393, XR_109607		
GeneID:49 65	MYO7B	2	128,292,376	128,359,303	101,928	+	1	4_A375_EGR1_1.5135	106432	downstream	0	0	1	4	9	17	1	4_A375_EGR1_1.1	17	Gene MYO7B	DKFZp686H04235, MYO7B	myosin VIIB	NM_020985527	219982_at, 219982_at, 223252_at	NP_031079196.1
GeneID:33 679	LMO2	2	128,339,996	128,419,399	79,404	+	1	4_A375_EGR1_1.5133	39332	upgene	0	0	1	4	9	17	1	4_A375_EGR1_1.1	17	Gene LMO2	FHCRC1, LMO2, TTG-1, TTG1	LIM domain only 2 (rhombotin-like 1)	NM_017980, NM_001161403, NM_001161404, NM_001139037, NR_027623, XC7197185.1, XC7197190.1, XC7197191.1, XC7229150.0, XC7229151.0, XC7229155.0, XC7237631.0, XC7237632.0, XC7.9699.3	220765_s_at	NP_060402.2, NP_001154673.1, NP_001154676.1, NP_001129809.2, EAW68227.1, EAW68228.1, EAW68230.1, EAW68231.1, EAW68232.1, EAW68233.1, EAW68234.1, EAW68235.1, EAW68236.1
GeneID:24 828	GPR17	2	128,468,459	128,482,213	13,754	+	1	4_A375_EGR1_1.5133	3831	upstream	0	0	1	4	9	17	1	4_A375_EGR1_1.1	17	Gene GPR17	G21P17, DKFZp686H1627	G protein-coupled receptor 17	NM_001161415, NM_005291, NM_001161416, NM_001161417, XC7.9699.3	206190_at, 213223_s_at	NP_001154027.1, NP_005282.1, NP_001154028.1, NP_001154029.1, EAW68321.1
GeneID:33 239	WDR33	2	128,481,800	128,588,761	106,962	+	1	4_A375_EGR1_1.5136	109765	downstream	0	0	1	9	12	15	1	4_A375_EGR1_1.1	15	Gene WDR33	WDC148, FLJ11294, MYT14, WDR33	WD repeat domain 33	NM_001006622, NM_001006623, NM_001161833, NM_018383, XC7197430.1, XC7197131.1	219551_s_at, 222763_s_at, 223147_s_at, 223148_at, 223147_s_at, 229141_at, 243022_at	NP_001006622.1, NP_001006624.1, NP_060883.2, EAW68342.1, EAW68343.1
GeneID:38 698	UGGT1	2	128,648,784	128,693,251	104,467	+	3	1_A375_uN27_mrna1_lncRNA_NR_1:3397, 2_A375_uN27_plus_lncRNA_NR_1:4626, 4_A375_EGR1_1.5137	-15, -62, 48	upstream, upstream, upgene	1	1	1	23	25	16	1	2_A375_uN27_plus_lncRNA_NR_1	25	Gene UGGT1	FLJ23621, UGT1, HUGT1, UNQ551, UGGT, FLJ23765, FLJ23790	UDP-glucose glycoprotein glucosyltransferase 1	NM_020120, NR_027971, XC7198133.2	218257_s_at, 222369_at, 222369_s_at	NP_064505.1, EAW68356.1
GeneID:33 827	SMPD4	2	130,892,963	130,940,223	51,356	-	2	1_A375_uN27_mrna1_lncRNA_NR_1:3398, 2_A375_uN27_plus_lncRNA_NR_1:4627	1219, 1157	upgene, upgene	1	1	0	16	19	7	1	2_A375_uN27_plus_lncRNA_NR_1	19	Gene SMPD4	SMPD4, NSMASE3, FLJ20798, nSMase-3, NSMASE3, FLJ20797, MIT15, SMN1418	sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase 3)	NM_017177.1, NM_017751, NM_017951, NR_033230, NR_033231, NR_033232, XC7237088.0, XC7237971.0, XC7270972.0, XC7270974.0, XC7270976.0		NP_001164354.1, NP_060221.2, NP_059421.2, EAW68397.1, EAW68398.1, EAW68401.1, EAW68399.1, EAW68400.1
GeneID:88 097	FAM132 B	2	130,939,901	130,946,500	6,599	+	2	1_A375_uN27_mrna1_lncRNA_NR_1:3395, 2_A375_uN27_plus_lncRNA_NR_1:4627	-397, -355	upstream, upstream	1	1	0	16	19	7	1	2_A375_uN27_plus_lncRNA_NR_1	19	Gene FAM132B	MGC24172.6, FAM132B, FLJ14346, MGC20107, WET2B	family with sequence similarity 132, member B	NM_020929, XC7229549.0, XC7270546.0, XC7270547.0, XC7270549.0	212905_s_at, 220732_s_at	NP_066003.2, EAW68569.1, EAW68570.1, EAW68603.1, EAW68603.1
GeneID:11 2714	TUBA3E	2	130,949,516	130,956,034	6,518	-	2	1_A375_uN27_mrna1_lncRNA_NR_1:3395, 2_A375_uN27_plus_lncRNA_NR_1:4627	66830, 66886	downstream, downstream	1	1	0	16	19	7	1	2_A375_uN27_plus_lncRNA_NR_1	19	Gene TUBA3E	TUBA3E		NM_007112		NP_997185.1
GeneID:64 317	CCDC11 8	2	131,098,618	131,099,922	4,158	-	2	2_A375_uN27_plus_lncRNA_NR_1:4628	-993	upstream	0	1	0	17	20	7	1	2_A375_uN27_plus_lncRNA_NR_1	20	Gene CCDC118	MGC12981, FLJ30131, CCDC118, visf	coiled-coil domain containing 118	NM_032357, XC7198432.1, XC7198432.1, XC7198432.1	224948_s_at	NP_115723.2, EAW68912.1, EAW68910.1, EAW68911.1
GeneID:32 555	IMP4	2	131,100,459	131,109,197	8,739	+	1	2_A375_uN27_plus_lncRNA_NR_1:4630	23	upgene	0	1	0	17	20	7	1	2_A375_uN27_plus_lncRNA_NR_1	20	Gene IMP4	BXDC4, MGC19998, IMP4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	NM_032416, XC7229538.0, XC7229538.0, XC7270540.0, XC7270226.0	212411_at	NP_115804.1, EAW68918.1, EAW68913.1, EAW68914.1, EAW68916.1
GeneID:11 3437	TUBA3D	2	132,233,899	132,240,307	6,841	+	1	2_A375_uN27_plus_lncRNA_NR_1:4629	18670	downstream	0	1	0	8	14	9	1	2_A375_uN27_plus_lncRNA_NR_1	14	Gene TUBA3D	RD:ALPHA, TUBA3D, TUBA3C	tubulin, alpha 3d	NM_006009	210023_s_at	NP_006000.2
GeneID:88 3756	FAM126 A	2	132,241,533	132,280,054	6,331	-	1	2_A375_uN27_plus_lncRNA_NR_1:4629	-472	upstream	0	1	0	8	14	9	1	2_A375_uN27_plus_lncRNA_NR_1	14	Gene FAM126A	MGC47172A, FAM126A, MGC172A	hikDu tandfe sqdmusng pdtesc 2A	NM_031053355	213166_s_at	NP_001078934.1
GeneID:64 8915	ZNF598	2	133,074,873	133,079,309	1,834	+	2	1_A375_uN27_mrna1_lncRNA_NR_1:3399, 2_A375_uN27_plus_lncRNA_NR_1:4630	1397, 1561	upgene, upgene	1	1	0	24	20	6	1	1_A375_uN27_mrna1_lncRNA_NR_1	24	Gene ZNF598	ZNF598	zinc finger protein 598	XM_002343581, XM_001724262		XP_002343622.2, XP_001724264.3
GeneID:33 9742	LOC3319 42	2	133,106,790	133,110,934	4,164	+	2	1_A375_uN27_mrna1_lncRNA_NR_1:3393, 2_A375_uN27_plus_lncRNA_NR_1:4631	-1606, -1594	upstream, upstream	1	1	0	24	21	11	1	1_A375_uN27_mrna1_lncRNA_NR_1	24	Gene LOC331942	FAM201B		XM_929803, XM_002120760	1569002_at	XP_934978.4, XP_002120802.1
GeneID:28 83	GPR39	2	133,176,147	133,456,169	280,022	+	2	1_A375_uN27_mrna1_lncRNA_NR_1:3381, 2_A375_uN27_plus_lncRNA_NR_1:4632	72869, 72797	upgene, upgene	1	1	0	17	16	4	1	1_A375_uN27_mrna1_lncRNA_NR_1	17	Gene GPR39	MGC14459A1, GPR39	G protein-coupled receptor 39	NM_001508, XC7229579.1, XC7229579.1, XC7270976.1	230950_s_at, 231934_s_at, 231935_at	NP_001499.1, EAX11676.1, EAX11680.1
GeneID:64 4146	NCKAP 5	2	133,429,372	134,226,031	796,659	-	3	1_A375_uN27_mrna1_lncRNA_NR_1:3382, 2_A375_uN27_plus_lncRNA_NR_1:4633, 2_A375_uN27_plus_lncRNA_NR_1:4634	504427, 541457, 504479	upgene, upgene, upgene	1	1	0	16	16.5	4	2	2_A375_uN27_plus_lncRNA_NR_1	20	Gene NCKAP5	NCKAP5, ERH1, KIAA0478, NAP1-like5h2	NCK-associated protein 5	NM_207383, NM_207451	219660_at	NP_997248.2, NP_997394.3
GeneID:80 122	YSK4	2	153,732,213	153,782,248	99,975	-	2	1_A375_uN27_mrna1_lncRNA_NR_1:3383, 2_A375_uN27_plus_lncRNA_NR_1:4635	-5455, -5424	upstream, upstream	1	1	0	17	16	2	1	2_A375_uN27_plus_lncRNA_NR_1	16	Gene YSK4	YSK4, FLJ23374, RCK	YSK4 Sps1/Ste20-related kinase (yeast) homolog (S. cerevisiae)	NM_001018045, NM_020552, XC7197643.3, XC7229413.0	1555604_a_at, 221165_at	NP_001018055.1, NP_065326.3, EAX11562.1, EAX11563.1
GeneID:33 9745	SPOPL	2	159,239,530	159,330,003	71,455	+	1	4_A375_EGR1_1.5142	254	upgene	0	0	1	8	7	18	1	4_A375_EGR1_1.1	18	Gene SPOPL	FLJ30775, SPOPL	speckle-type POZ protein-like	NM_031031984, XC7119843	229868_at, 229869_at	NP_001031984.1, EAX11689.1
GeneID:53 553	LRP1B	2	140,698,998	142,689,270	1,990,274	+	1	1_A375_uN27_mrna1_lncRNA_NR_1:3387	574160	upgene	0	0	0	15	7	1	1	1_A375_uN27_mrna1_lncRNA_NR_1	15	Gene LRP1B	LRP-DIF, LRPDIT, LRP1B	low density lipoprotein receptor-related protein 1B	NM_018557, XC7234417.0	219843_at	NP_060027.2, EAX11802.1
GeneID:89 42	KYNU	2	143,835,193	143,799,555	164,696	+	1	1_A375_uN27_mrna1_lncRNA_NR_1:3388	2757	upgene	0	1	0	16	7	1	1	1_A375_uN27_mrna1_lncRNA_NR_1	16	Gene KYNU	KYNU		NM_003937, NM_031033996, XC7197777.1, XC7229396.0, XC7229396.0	204383_at, 210982_at, 210983_s_at, 215358_s_at, 215359_x_at	NP_003926.1, NP_001028170.1, NP_001028171.1, EAX11690.1, EAX11691.1, EAX11692.1, EAX11693.1
GeneID:28 122	EPC2	2	149,492,580	149,543,156	162,576	+	4	4_A375_EGR1_1.5144	304	upgene	0	0	1	8	8	11	1	4_A375_EGR1_1.1	11	Gene EPC2	EPC-LIKE, EPC2, DKFZp686F1224	enhancer of polycomb homolog 2 (Drosophila)	NM_015630, XC7198228.1, XC7229568.0, XC7229567.0	225858_at	NP_056445.3, EAX11801.1, EAX11547.1, EAX11548.1
GeneID:27 049	MAGED2	2	150,436,147	150,444,330	18,183	-	1	2_A375_uN27_plus_lncRNA_NR_1:4640	108	upgene	0	1	0	14	19	10	1	2_A375_uN27_plus_lncRNA_NR_1	19	Gene MAGED2	L3D, C12orf2, MAGE-D2, Cdc/DS	melanoma antigen family D, 2	NM_015702, XC7229549.0, XC7229549.0, XC7230549.0, XC7230549.0	217883_at	NP_056517.1, EAX11553.1, EAX11554.1, EAX11555.1, EAX11537.1
GeneID:64 2540	LOC642 540	2	150,443,972	150,706,748	262,776	+	1	2_A375_uN27_plus_lncRNA_NR_1:4640	552	upgene	0	1	0	14	19	10	1	2_A375_uN27_plus_lncRNA_NR_1	19	Gene LOC642540		hypothetical LOC642540	XR_112399, XR_109438, XR_113417		
GeneID:38 0	RND3	2	151,258,709	151,344,160	19,671	+	1	2_A375_uN27_plus_lncRNA_NR_1:4642	1368	upgene	0	1	0	9	16	2	1	2_A375_uN27_plus_lncRNA_NR_1	16	Gene RND3	ARHE, rnen8, RhoE, RhoE, RND3	Rho family GTPase 3	NM_005168, XC7198478.1, XC7229520.0, XC7229520.0, XC7229520.0, XC7229521.0	212724_at	NP_005159.1, EAX11820.1, EAX11532.1, EAX11526.1, EAX11527.1
GeneID:38 183	RIF1	2	152,296,377	152,333,690	37,483	+	2	2_A375_uN27_plus_lncRNA_NR_1:3389, 2_A375_uN27_plus_lncRNA_NR_1:4643	5, -45	upgene, upgene	1	1	0	26	31	13	1	2_A375_uN27_plus_lncRNA_NR_1	31	Gene RIF1	RIF1, DKFZp434D1828, DKFZp761N1476, FLJ12870	RAP1 interacting factor homolog (yeast)	NM_031177993, NM_031177994, XC7229470.0, XC7229470.0, XC7229470.0, XC7229470.0, XC7229470.0, XC7232.0	214702_x_at, 214972_s_at, 215983_x_at, 233760_x_at, 233761_s_at, 239820_at, 240896_at, 241820_at	NP_031177334.1, NP_001171133.1, NP_001171135.1, EAX11706.1, EAX11707.1, EAX11708.1, EAX11709.1, EAX11510.1
GeneID:10 254	STAM2	2	152,373,315	152,532,508	99,191	-	2	2_A375_uN27_plus_lncRNA_NR_1:4644, 4_A375_EGR1_1.5146	-35, 442	upstream, upgene	0	1	1	17	20	17	1	2_A375_uN27_plus_lncRNA_NR_1	20	Gene STAM2	DKFZp686C0247, STAM2h, STAM2B, STAM2, Hbp	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	NM_005843, XC7122232.1, XC7198454.1, XC7229473.0	208784_s_at, 208969_at, 210344_s_at, 242989_at	NP_005834.4, EAX11491.1, EAX11490.1, EAX11492.1
GeneID:11 4792	FMNL2	2	152,199,751	153,008,545	814,597	+	1	2_A375_uN27_plus_lncRNA_NR_1:4645	121241	upgene	0	1	0	8	14	4	1	2_A375_uN27_plus_lncRNA_NR_1	14	Gene FMNL2	FLJ37546, FHOD2, FMNL2	formin-like 2	NM_052905, XC7198457.1, XC7229517.0	226164_at, 235881_at, 242865_at	NP_443137.2, EAX11469.1, EAX11470.1
GeneID:33 880	PRPF40A	2	153,898,107	153,973,973	93,866	-	3	1_A375_uN27_mrna1_lncRNA_NR_1:3391, 2_A375_uN27_plus_lncRNA_NR_1:4646, 4_A375_EGR1_1.5147	-909, -761, -1035	upstream, upstream, upstream	1	1	1	41	44	16	1	2_A375_uN27_plus_lncRNA_NR_1	44	Gene PRPF40A	FLNT1, FBP11, HYPA, NY-REN-16, FLJ23365, HYPA, HIP10, PRP40A, Prp40, FNBP5, FBP11	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	NM_007192	213729_at, 214641_s_at, 215053_x_at, 228867_at, 233092_s_at, 239477_at	NP_983262.3
GeneID:10 1180	ARL6IP6	2	153,974,423	153,817,797	43,244	+	3	1_A375_uN27_mrna1_lncRNA_NR_1:3391, 2_A375_uN27_plus_lncRNA_NR_1:4646, 4_A375_EGR1_1.5147	437, 313, 585	upgene, upgene, upgene	1	1	1	41	44	16	1	2_A375_uN27_plus_lncRNA_NR_1	44	Gene ARL6IP6	PRA1, MGC3386	ADP-ribosylation factor-like 6 interacting protein 6	NM_152322, NR_024328, XC7229080.0, XC7229080.0, XC7229080.0, XC7229039.0	225707_at, 225709_at, 225710_at	NP_689735.1, EAX11477.1, EAX11475.1, EAX11478.1, EAX11476.1
GeneID:49 29	NRAS	2	157,180,944	157,189,287	8,343	-	2	2_A375_uN27_mrna1_lncRNA_NR_1:3372, 4_A375_EGR1_1.5149	23, -5923	upgene, upstream	1	0	1	13	10	10	2	1_A375_uN27_mrna1_lncRNA_NR_1	13	Gene NRAS	NCMP1, HRZ-1, TB3JR, NRAS2, MCT, RAS1	neuroblastoma RAS viral (v-ras) oncogene homolog	NM_0981985, XC7229283.0, XC7229283.0	204621_s_at, 209422_at, 216245_s_at	NP_008977.1, EAX11454.1, EAX11455.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:92935	MARS2	2	198,570,087	198,573,114	3,027	+	1	4_A375_EGR1..1..5162	249	in gene	0	0	1	11	11	14	1	4_A375_EGR1..1	14	Gene MARS2	mtMetRS, MARS2, MetRS	methionyl-tRNA synthetase 2, mitochondrial	NM_138395, hCT1970665.1	243529_at	NP_612404.1, EAW70170.1
GeneID:23314	SATB2	2	200,134,223	200,335,989	201,766	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3398, 2_A375_pNL97_plus_lncRNA_AR..1..4672, 2_A375_pNL97_plus_lncRNA_AR..1..4673	11665, 155653, 11661	in gene, in gene, in gene	1	1	0	18	23.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene SATB2	FLJ32076, MGC119477, KIAA1034, MGC119474, SATB2, FLJ21474	SATB homeobox 2	NM_015265, NM_001172509, NM_001172517, hCT11165.3, hCT1952884.1	213435_at, 215591_at	NP_056080.1, NP_001165980.1, NP_001165988.1, EAW70180.1, EAW70181.1
GeneID:100288092	LOC100288092	2	200,322,423	200,325,977	3,554	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3398, 2_A375_pNL97_plus_lncRNA_AR..1..4673	1661, 1705	in gene, in gene	1	1	0	27	32	13	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene LOC100288092		hypothetical LOC100288092	XR_108415		
GeneID:150538	FLJ32063	2	200,332,621	200,337,461	4,840	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3398, 2_A375_pNL97_plus_lncRNA_AR..1..4673	-8517, -8693	upstream, upstream	1	1	0	27	32	13	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene FLJ32063	MGC126831	hypothetical LOC150538	NR_026830, hCT2302364.2, hCT2351046.0	1553420_at, 1560010_a_at	EAW70183.1, EAW70182.1
GeneID:129450	C2orf60	2	200,793,834	200,820,459	26,625	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3399, 2_A375_pNL97_plus_lncRNA_AR..1..4674	75, 107	in gene, in gene	1	1	0	32	20	10	1	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene C2orf60	FLJ37953, C2orf60, hTYW5, MGC70509, TYW5	chromosome 2 open reading frame 60	NM_001039693, NR_004862, hCT12049.3, hCT2349279.0, hCT2349280.0, hCT2349281.0	235161_at, 235686_at, 241825_at	NP_001034782.1, EAW70191.1, EAW70192.1, EAW70193.1, EAW70194.1
GeneID:79568	C2orf47	2	200,820,040	200,828,848	8,808	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3399, 2_A375_pNL97_plus_lncRNA_AR..1..4674	344, 312	in gene, in gene	1	1	0	32	20	10	1	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene C2orf47	C2orf47, FLJ22555, DKFZp666A212	chromosome 2 open reading frame 47	NM_024520, hCT12048.3, hCT2354879.0	219176_at	NP_078796.2, EAW70196.1, EAW70195.1
GeneID:130535	KCTD18	2	201,353,681	201,374,792	21,111	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3400	-56	upstream	1	0	0	16	11	7	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene KCTD18	6530404F10Rik, FLJ31322, FLJ37618, KCTD18	potassium channel tetramerisation domain containing 18	NM_152387, hCT2343755.0, hCT2343756.0, hCT2343757.0, hCT7602.3	1553136_at, 226493_at	NP_689600.2, EAW70204.1, EAW70203.1, EAW70205.1, EAW70206.1
GeneID:316	AOX1	2	201,450,731	201,536,218	85,487	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4675	76653	in gene	0	1	0	8	13	5	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene AOX1	AOH1, AO, AOX1	aldehyde oxidase 1	NM_001159, hCT2302561.0, hCT7596.3	205082_s_at, 205083_at	NP_001150.3, EAW70208.1, EAW70209.1
GeneID:9689	BZW1	2	201,676,647	201,688,560	11,913	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3401, 2_A375_pNL97_plus_lncRNA_AR..1..4676, 4_A375_EGR1..1..5163, 4_A375_EGR1..1..5164	-231, -167, -551, -55	upstream, upstream, upstream, upstream	1	1	1	17	15	18	1	4_A375_EGR1..1	18	Gene BZW1	Nbla10236, KIAA0005, BZW1, BZAP45	basic leucine zipper and W2 domains 1	NM_014670, hCT2302566.0, hCT2302567.0		NP_055485.2, EAW70213.1, EAW70212.1
GeneID:1195	CLK1	2	201,717,732	201,729,467	11,735	-	1	4_A375_EGR1..1..5165	19291	downstream	0	0	1	6	6	15	1	4_A375_EGR1..1	15	Gene CLK1	CLK, CLK/STY, CLK1, STY	CDC-like kinase 1	NM_004071, NM_001162407, NR_027855, NR_027856, hCT1967292.1, hCT1967293.1, hCT1967294.1, hCT2354778.0, hCT7594.3	214683_s_at	NP_004062.2, NP_001155879.1, EAW70215.1, EAW70216.1, EAW70218.1, EAW70219.1, EAW70217.1
GeneID:285172	FAM126B	2	201,838,441	201,936,392	97,951	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3402	-136	upstream	1	0	0	20	12	9	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene FAM126B	HYCC2, FAM126B, FLJ42947, FLJ37917, MGC39518, FLJ10981	family with sequence similarity 126, member B	NM_173822, hCT1953570.2, hCT2354840.0, hCT2354841.0	1554178_a_at, 231874_at	NP_776183.1, EAW70232.1, EAW70230.1, EAW70231.1
GeneID:4709	NDUFB3	2	201,936,462	201,950,473	14,011	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3402	66	in gene	1	0	0	20	12	9	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene NDUFB3	NDUFB3, B12	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	NM_002491, hCT1815348.1, hCT1967335.1	203371_s_at	NP_002482.1, EAW70234.1, EAW70233.1
GeneID:8837	CFLAR	2	201,980,816	202,029,016	48,200	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4677	366	in gene	0	1	0	14	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CFLAR	c-FLIPS, c-FLIP, MRIT, I-FLICE, c-FLIPR, FLAME-1, FLIP, FLAME, c-FLIPL, CASH, FLAME1, CFLAR, Casper, CLARP, CASP8AP1	CASP8 and FADD-like apoptosis regulator	NM_003879, NM_001127183, NM_001127184, hCT1967289.1, hCT1967290.1, hCT2303159.0, hCT2303162.0, hCT2303164.0, hCT2303166.0, hCT2303167.0, hCT2303168.0, hCT2303171.0, hCT2354776.0, hCT7591.3	208485_x_at, 209508_x_at, 209939_x_at, 210563_x_at, 210564_x_at, 211316_x_at, 211317_s_at, 211862_x_at, 214486_x_at, 214618_at, 237367_x_at, 239629_at	NP_003870.4, NP_001120655.1, NP_001120656.1, EAW70235.1, EAW70236.1, EAW70242.1, EAW70237.1, EAW70238.1, EAW70239.1, EAW70240.1, EAW70241.1, EAW70243.1, EAW70244.1, EAW70245.1
GeneID:66008	TRAK2	2	202,241,930	202,316,319	74,389	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3403	47	in gene	1	0	0	17	12	11	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene TRAK2	GRIF1, CALS-C, KIAA0549, GRIF-1, ALS2CR3, TRAK2, OIP98	trafficking protein, kinesin binding 2	NM_015049, hCT2303293.0, hCT8039.2	202124_s_at, 202125_s_at	NP_055864.2, EAW70272.1, EAW70271.1
GeneID:55437	STRADB	2	202,316,392	202,345,574	29,182	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3403	-120	upstream	1	0	0	17	12	11	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene STRADB	ILPIPA, CALS-21, PRO1038, ALS2CR2, STRADB, MGC102916, ILPIP, PAPK	STE20-related kinase adaptor beta	NM_018571, hCT2303199.1, hCT2303201.1, hCT2303202.1, hCT2303204.1	223266_at	NP_061041.2, EAW70273.1, EAW70274.1, EAW70275.1, EAW70276.1
GeneID:57679	ALS2	2	202,564,986	202,645,895	80,909	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3404	7	in gene	1	0	0	15	12	13	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene ALS2	KIAA1563, ALS2CR6, MGC87187, IAHSP, ALSJ, FLJ31851, ALS2, PLSJ	amyotrophic lateral sclerosis 2 (juvenile)	NM_020919, NM_001135745, hCT2303279.0, hCT2303280.0, hCT8035.2	1555264_at, 226291_at, 232184_at	NP_065970.2, NP_001129217.1, EAW70291.1, EAW70292.1, EAW70293.1
GeneID:8324	FZD7	2	202,899,310	202,903,160	3,850	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4678	850	in gene	0	1	0	6	18	16	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene FZD7	FzE3, FZD7	frizzled homolog 7 (Drosophila)	NM_003507, hCT6116.2	203705_s_at, 203706_s_at	NP_003498.1, EAW70298.1
GeneID:51602	NOP58	2	203,130,515	203,168,384	37,869	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3405, 2_A375_pNL97_plus_lncRNA_AR..1..4679	-19, 141	upstream, in gene	1	1	0	16	19	9	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene NOP58	HSPC120, NOP58, NOP5, NOP5/NOP58	NOP58 ribonucleoprotein homolog (yeast)	NM_015934, hCT23687.3	223098_at	NP_057018.1, EAW70306.1
GeneID:55759	WDR12	2	203,745,323	203,776,949	31,626	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3406, 2_A375_pNL97_plus_lncRNA_AR..1..4680	661, 597	in gene, in gene	1	1	0	15	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene WDR12	WDR12, FLJ12720, FLJ10881, YTM1, FLJ12719	WD repeat domain 12	NM_018256, hCT1818766.2, hCT2348678.0	218512_at	NP_060726.3, EAW70318.1, EAW70319.1
GeneID:79800	ALS2CR8	2	203,776,978	203,851,060	74,082	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3406, 2_A375_pNL97_plus_lncRNA_AR..1..4680	-690, -626	upstream, upstream	1	1	0	15	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ALS2CR8	ALS2CR8, DKFZp667N246, FLJ12675, NYD-SP24, FLJ21579, CARF	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8	NM_024744, NM_001104586, hCT1818767.2, hCT2304423.0, hCT2304424.0, hCT2304428.0, hCT2304430.0	1555391_a_at, 219834_at	NP_079020.13, NP_001098056.1, EAW70320.1, EAW70322.1, EAW70323.1, EAW70324.1, EAW70321.1
GeneID:100507285	LOC100507285	2	204,098,609	204,102,676	4,067	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3407, 2_A375_pNL97_plus_lncRNA_AR..1..4681	-1004, -876	upstream, upstream	1	1	0	27	34	12	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene LOC100507285		hypothetical LOC100507285	XR_112429, XR_108421, XR_113424		
GeneID:57404	CYP20A1	2	204,103,164	204,170,563	67,399	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3407, 2_A375_pNL97_plus_lncRNA_AR..1..4681	516, 388	in gene, in gene	1	1	0	27	34	12	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene CYP20A1	CYP20A1, CYP-M, MGC22229	cytochrome P450, family 20, subfamily A, polypeptide 1	NM_177538, hCT10481.5, hCT1953578.3, hCT2354787.0	219565_at	NP_803882.1, EAW70334.1, EAW70332.1, EAW70333.1
GeneID:10152	ABI2	2	204,193,003	204,296,892	103,889	+	1	4_A375_EGR1..1..5166	597	in gene	0	0	1	7	8	19	1	4_A375_EGR1..1	19	Gene ABI2	ABI2B, argBPIA, ABI-2, AblBP3, SSH3BP2, AIP-1, argBPIB, ABI2	abl-interactor 2	NM_005759, hCT1967275.2, hCT1967276.2, hCT2302499.1, hCT2302501.1, hCT2302503.1, hCT2302504.1, hCT2302505.1, hCT2302506.1, hCT2302507.1	207268_x_at, 209856_x_at, 211793_s_at, 216113_at, 225098_at, 225112_at, 227631_at	NP_005750.4, EAW70343.1, EAW70335.1, EAW70337.1, EAW70338.1, EAW70342.1, EAW70336.1, EAW70339.1, EAW70340.1, EAW70341.1
GeneID:8828	NRP2	2	206,547,224	206,662,857	115,633	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3410	-2264	upstream	1	0	0	21	12	4	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene NRP2	NP2, MGC126574, VEGF165R2, NRP2, PRO2714, NPN2	neuropilin 2	NM_003872, NM_018534, NM_201264, NM_201266, NM_201267, NM_201279, hCT1967277.2, hCT1967278.2, hCT2303051.1, hCT2303052.1, hCT2303055.1, hCT2303058.1, hCT2354748.0, hCT2354749.0, hCT2354750.0, hCT2354751.0, hCT2354752.0, hCT6225.4	1555468_at, 210841_s_at, 210842_at, 211844_s_at, 214632_at, 223510_at, 225566_at, 228102_at, 228103_s_at, 228699_at, 229225_at, 230410_at	NP_003863.2, NP_061004.3, NP_957716.1, NP_957718.1, NP_957719.1, NP_958436.1, EAW70362.1, EAW70363.1, EAW70364.1, EAW70365.1, EAW70366.1, EAW70367.1, EAW70368.1, EAW70369.1, EAW70370.1, EAW70371.1, EAW70372.1, EAW70373.1
GeneID:54891	INO80D	2	206,858,445	206,950,906	92,461	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4682	216	in gene	0	1	0	9	13	6	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene INO80D	INO80D, FLJ20309	INO80 complex subunit D	NM_017759, hCT2303388.0, hCT2303389.0	220165_at, 243070_at	NP_060229.3, EAW70374.1, EAW70375.1
GeneID:729570	LOC729570	2	206,949,320	206,951,584	2,264	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4682	1366	in gene	0	1	0	9	13	6	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene LOC729570		hypothetical LOC729570	XR_112430, XR_112431, XR_108422, XR_108423, XR_113425, XR_113426	227837_at	
GeneID:151194	FAM119A	2	208,473,839	208,489,973	16,134	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3413, 2_A375_pNL97_plus_lncRNA_AR..1..4684	-11, -11	upstream, upstream	1	1	0	18	17	6	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene FAM119A	MGC45373, METTL21A, FAM119A, HCA557b	family with sequence similarity 119, member A	NM_145280, NM_001127395, hCT1953564.1, hCT2344884.0, hCT2344885.0, hCT2344886.0, hCT2344887.0, hCT2354770.0, hCT6486.3	1553743_at, 235177_at	NP_660323.3, NP_001120867.1, EAW70411.1, EAW70412.1, EAW70416.1, EAW70417.1, EAW70413.1, EAW70414.1, EAW70415.1
GeneID:100507475	LOC100507475	2	209,119,957	209,120,893	936	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3414, 2_A375_pNL97_plus_lncRNA_AR..1..4685	10795, 10891	downstream, downstream	1	1	0	47	43	10	1	1_A375_pNL7_minus_lncRNA_AR..1	47	Gene LOC100507475		hypothetical LOC100507475	XR_112434, XR_108426, XR_113429		
GeneID:200576	PIKFYVE	2	209,130,991	209,223,475	92,484	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3414, 2_A375_pNL97_plus_lncRNA_AR..1..4685	-239, -143	upstream, upstream	1	1	0	47	43	10	1	1_A375_pNL7_minus_lncRNA_AR..1	47	Gene PIKFYVE	MGC40423, KIAA0981, FLJ37746, CFD, FAB1, PIP5K3, PIP5K, PIKFYVE	phosphoinositide kinase, FYVE finger containing	NM_015040, NM_152671, NM_001178000, hCT2340612.0, hCT2340613.0, hCT2340614.0, hCT2340615.0, hCT2340616.0, hCT2354825.0	1553917_at, 1557719_at, 213111_at	NP_055855.2, NP_689884.1, NP_001171471.1, EAW70444.1, EAW70445.1, EAW70446.1, EAW70447.1, EAW70448.1, EAW70449.1
GeneID:285175	UNC80	2	210,636,717	210,864,024	227,307	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4686	-173	upstream	0	1	0	12	20	6	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene UNC80	UNC-80, FLJ33496, KIAA1843, FLJ14677, FLJ53903, UNC80, C2orf21	unc-80 homolog (C. elegans)	NM_032504, NM_182587, hCT1971839.2, hCT2302626.2, hCT2302627.2, hCT2302851.1, hCT2346139.2, hCT2346699.1		NP_115893.1, NP_872393.3, EAW70465.1, EAW70467.1, EAW70469.1, EAW70470.1, EAW70466.1, EAW70468.1
GeneID:79582	SPAG16	2	214,149,116	215,275,225	1,126,109	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4687	1126756	downstream	0	1	0	12	26	4	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene SPAG16	SPAG16, WDR29, FLJ22724, MGC87036, FLJ37717, DKFZp666P1710, PF20	sperm associated antigen 16	NM_001025436, NM_024532, hCT2349309.0	1560174_at, 219109_at, 240898_at	NP_001020607.1, NP_078808.3, EAW70515.1
GeneID:402117	VWC2L	2	215,276,461	215,440,653	164,192	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4687	-569	upstream	0	1	0	12	26	4	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene VWC2L	VWC2L	von Willebrand factor C domain-containing protein 2-like	NM_001080500		NP_001073969.1
GeneID:55686	MREG	2	216,807,314	216,878,346	71,032	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4688	7176	in gene	0	1	0	8	13	5	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene MREG	WDT2, DSU, MGC90298, FLJ10116, MREG	melanoregulin	NM_018000, hCT2302966.0, hCT2302968.0, hCT7734.2	219648_at, 232682_at	NP_060470.2, EAW70555.1, EAW70554.1, EAW70556.1
GeneID:57574	4-Mar	2	217,122,585	217,236,750	114,165	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3415, 1_A375_pNL7_minus_lncRNA_AR..1..3416, 2_A375_pNL97_plus_lncRNA_AR..1..4689, 2_A375_pNL97_plus_lncRNA_AR..1..4690	-338, -1698, -338, -1666	upstream, upstream, upstream, upstream	1	1	0	21.5	30.5	5	2	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene MARCH4	MARCH4, MARCH-IV, MGC104908, RNF174	membrane-associated ring finger (C3HC4) 4	NM_020814, hCT7419.2	230112_at	NP_065865.1, EAW70566.1
GeneID:50485	SMARCAL1	2	217,277,137	217,347,776	70,639	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3417, 2_A375_pNL97_plus_lncRNA_AR..1..4691	143, -66	in gene, upstream	1	1	0	16	16	12	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene SMARCAL1	SMARCAL1, HARP, HHARP	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	NM_014140, NM_001127207, hCT2302926.0	218452_at	NP_054859.2, NP_001120679.1, EAW70567.1
GeneID:100507554	LOC100507554	2	217,351,335	217,363,469	12,134	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3418	-115	upstream	1	0	0	24	12	14	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene LOC100507554		hypothetical LOC100507554	XR_112436, XR_108428, XR_113433		
GeneID:6168	RPL37A	2	217,363,520	217,366,190	2,670	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3418	64	in gene	1	0	0	24	12	14	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene RPL37A	L37A, RPL37A, MGC74786, FLJ13357	ribosomal protein L37a	NM_000998, hCT1688475.4, hCT1815270.3, hCT2302892.1	213459_at, 214041_x_at	NP_000989.1, EAW70569.1, EAW70570.1, EAW70571.1
GeneID:729582	DIRC3	2	218,148,746	218,621,316	472,570	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4692	478644	downstream	0	1	0	12	17	1	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene DIRC3	DIRC3, FLJ14199	disrupted in renal carcinoma 3	NR_026597		
GeneID:6556	SLC11A1	2	219,246,752	219,261,617	14,865	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3419, 1_A375_pNL7_minus_lncRNA_AR..1..3420, 2_A375_pNL97_plus_lncRNA_AR..1..4693, 2_A375_pNL97_plus_lncRNA_AR..1..4694	14240, 17776, 14272, 17744	in gene, downstream, in gene, downstream	1	1	0	25.5	37.5	7	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene SLC11A1	LSH, NRAMP1, NRAMP, SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	NM_000578, hCT2303101.0, hCT2303102.0, hCT2303104.0, hCT7337.3	1555116_s_at, 210422_x_at, 210423_s_at, 217473_x_at, 217507_at, 230382_at	NP_000569.3, EAW70611.1, EAW70612.1, EAW70613.1, EAW70614.1
GeneID:58190	CTDSP1	2	219,264,478	219,270,664	6,186	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3419, 1_A375_pNL7_minus_lncRNA_AR..1..3420, 2_A375_pNL97_plus_lncRNA_AR..1..4693, 2_A375_pNL97_plus_lncRNA_AR..1..4694	-3486, 50, -3454, 18	upstream, in gene, upstream, in gene	1	1	0	25.5	37.5	7	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene CTDSP1	CTDSP1, NLIIF, SCP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	NM_021198, NM_182642, hCT1955108.1, hCT2303107.0, hCT2303108.0, hCT7331.2	217844_at	NP_067021.1, NP_872580.1, EAW70615.1, EAW70616.1, EAW70617.1, EAW70618.1
GeneID:407017	MIR26B	2	219,267,369	219,267,445	76	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3419, 1_A375_pNL7_minus_lncRNA_AR..1..3420, 2_A375_pNL97_plus_lncRNA_AR..1..4693, 2_A375_pNL97_plus_lncRNA_AR..1..4694	-6377, -2841, -6345, -2873	upstream, upstream, upstream, upstream	1	1	0	25.5	37.5	7	2	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene MIR26B	MIR26B, hsa-mir-26b, MIRN26B, miR-26b	microRNA 26b	NR_029500		

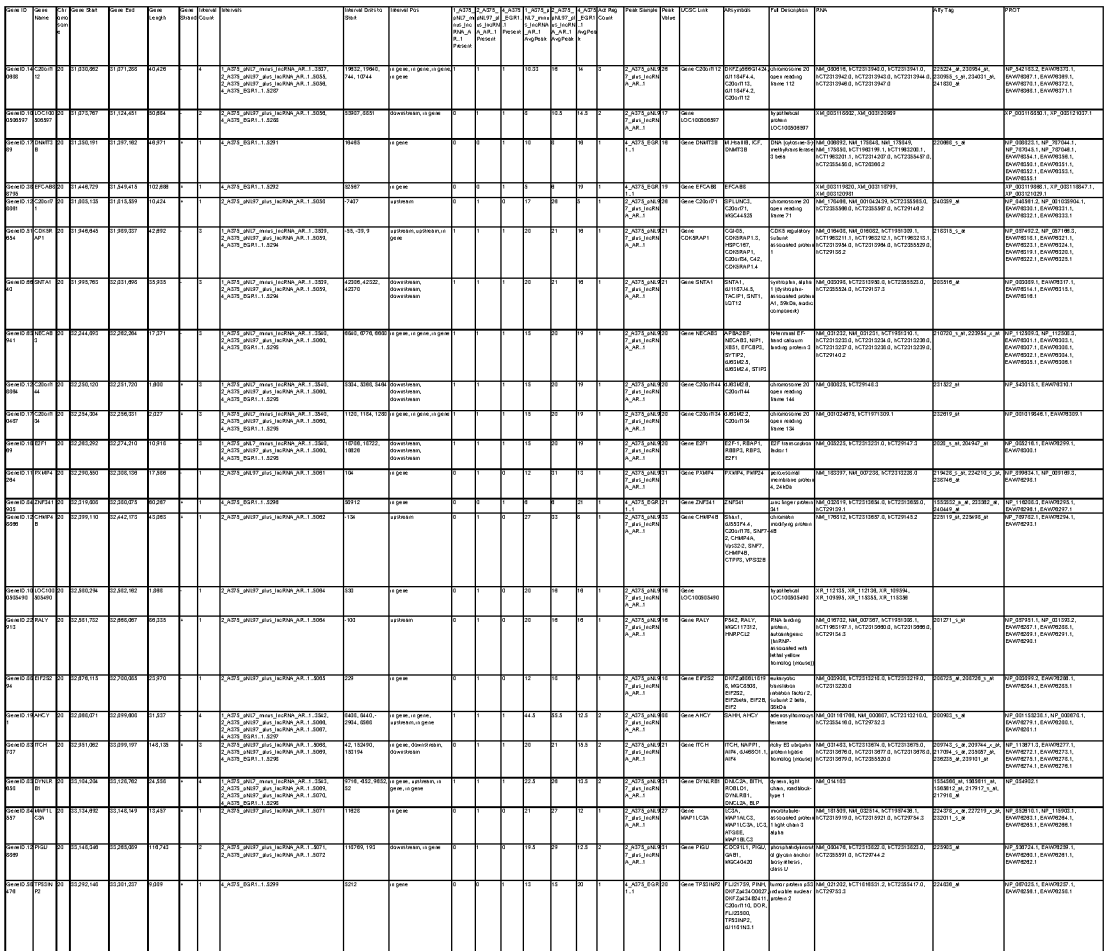
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:8941	CDK5R2	2	219,824,398	219,826,877	2,479	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3422, 2_A375_pNL97_plus_lncRNA_AR..1..4895	3410, 3330	downstream, downstream	1	1	0	22	26	10	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene CDK5R2	NCK5AI, P39, CDK5R2, p39nck5ai	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	NM_003936, hCT6592.2	205852_at	NP_003927.1, EAW70662.1
GeneID:54738	FEV	2	219,845,809	219,850,379	4,570	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3423	-6229	upstream	1	0	0	17	7	7	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene FEV	PET-1, FEV, HSRNAFEV	FEV (ETS oncogene family)	NM_017521, hCT6593.2	207260_at	NP_059991.1, EAW70664.1
GeneID:1412	CRYBA2	2	219,854,912	219,858,127	3,215	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3423	1519	in gene	1	0	0	17	7	7	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene CRYBA2	CRYBA2		NM_005209, NM_057093, NM_057094, hCT1955095.2, hCT1987464.0, hCT2304381.0	220136_s_at	NP_005200.1, NP_476434.1, NP_476435.1, EAW70665.1, EAW70666.1, EAW70667.1
GeneID:494324	MIR375	2	219,866,367	219,866,430	63	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3423	9822	downstream	1	0	0	17	7	7	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene MIR375	MIRN375, MIR375, miRNA375, hsa-mir-375	microRNA 375	NR_029867		
GeneID:255101	CCDC108	2	219,867,576	219,906,245	38,669	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3424, 2_A375_pNL97_plus_lncRNA_AR..1..4896	-4603, -4571	upstream, upstream	1	1	0	26	24	3	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene CCDC108	CCDC108, DKFZp434O0527, MGC35338	coiled-coil domain containing 108	NM_194302, NM_152389	1553686_at, 1556989_at, 1557879_at, 239506_x_at	NP_919278.2, NP_689602.2
GeneID:3549	IHH	2	219,919,142	219,925,238	6,096	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3424, 2_A375_pNL97_plus_lncRNA_AR..1..4896	14390, 14422	downstream, downstream	1	1	0	26	24	3	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene IHH	IHH, BDA1, HHG2	Indian hedgehog	NM_002181, hCT2304456.0	215420_at, 229356_at	NP_002172.2, EAW70675.1
GeneID:79840	NHEJ1	2	219,940,046	220,025,587	85,541	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3425, 2_A375_pNL97_plus_lncRNA_AR..1..4897	35491, 35411	in gene, in gene	1	1	0	14	18	4	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene NHEJ1	NHEJ1, FLJ12610, XLF	nonhomologous end-joining factor 1	NM_024782	219418_at	NP_079058.1
GeneID:130617	ZFAND2B	2	220,071,538	220,074,370	2,832	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4898	12046	downstream	0	1	0	14	14	12	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene ZFAND2B	ZFAND2B, AIRAPL		NM_138802, hCT1819607.1, hCT1966298.1, hCT2354774.0, hCT2354775.0	226166_at	NP_620157.1, EAW70690.1, EAW70691.1, EAW70692.1, EAW70693.1
GeneID:10058	ABCB6	2	220,074,494	220,083,672	9,178	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4898	66	in gene	0	1	0	14	14	12	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene ABCB6	ABCB6, ABC, ABC14, MTABC3, EST45597, umat, PRP, FLJ22414	ATP-binding cassette, sub-family B (MDR/TAP), member 6	NM_005689, hCT1966025.1, hCT2343394.0, hCT2343395.0, hCT2343396.0, hCT2343397.0, hCT2343398.0, hCT2343399.0, hCT2343400.0, hCT2343401.0, hCT2343402.0, hCT2343403.0, hCT6602.2	203191_at, 203192_at	NP_005680.1, EAW70694.1, EAW70695.1, EAW70696.1, EAW70698.1, EAW70699.1, EAW70697.1, EAW70700.1, EAW70701.1, EAW70702.1, EAW70703.1, EAW70704.1, EAW70705.1
GeneID:79065	ATG9A	2	220,084,102	220,094,361	10,259	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3426, 2_A375_pNL97_plus_lncRNA_AR..1..4898	132, 10777	in gene, downstream	1	1	0	15.5	14.5	10	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ATG9A	APG9L1, mATG9, MGD3208, ATG9A	ATG9 autophagy related 9 homolog A (S. cerevisiae)	NM_001077198, NM_024085, hCT2304441.0, hCT6608.3	202492_at	NP_001070666.1, NP_076990.4, EAW70706.1, EAW70707.1
GeneID:55139	ANKZF1	2	220,094,479	220,101,391	6,912	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3426, 2_A375_pNL97_plus_lncRNA_AR..1..4899, 4_A375_EGR1..1..5167	-250, 15857, 15729	upstream, downstream, downstream	1	1	1	13	15	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ANKZF1	ZNF744, FLJ13144, FLJ10415, ANKZF1	ankyrin repeat and zinc finger domain containing 1	NM_018089, NM_001042410, hCT1955104.1, hCT1955105.1, hCT6607.3	218274_s_at	NP_060559.2, NP_001035869.1, EAW70708.1, EAW70709.1, EAW70710.1
GeneID:79411	GLB1L	2	220,101,493	220,110,131	8,638	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3426, 2_A375_pNL97_plus_lncRNA_AR..1..4899, 4_A375_EGR1..1..5167	15902, -205, -77	downstream, upstream, upstream	1	1	1	13	15	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene GLB1L	MGC10771, GLB1L	galactosidase, beta 1-like	NM_024506, hCT1955097.1, hCT2304437.0, hCT6599.3	206540_at	NP_078782.3, EAW70713.1, EAW70711.1, EAW70712.1
GeneID:8576	STK16	2	220,110,192	220,115,059	4,867	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4899, 4_A375_EGR1..1..5167	144, 16	in gene, in gene	0	1	1	9	15	17	1	4_A375_EGR1..1	17	Gene STK16	MPSK, FLJ39635, KRCT, TSF1, MGC16211, PKL12, STK16	serine/threonine kinase 16	NM_001008910, NR_026909, hCT1955092.1, hCT1955093.1, hCT2354890.0, hCT6591.2	209622_at	NP_001008910.1, EAW70714.1, EAW70715.1, EAW70716.1, EAW70717.1
GeneID:7277	TUBA4A	2	220,115,001	220,118,838	3,837	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4899, 4_A375_EGR1..1..5167	8302, 8430	downstream, downstream	0	1	1	9	15	17	1	4_A375_EGR1..1	17	Gene TUBA4A	H2-ALPHA, FLJ30169, TUBA1, TUBA4A	tubulin, alpha 4a	NM_006000, hCT2304429.0, hCT2304431.1	212242_at	NP_005991.1, EAW70718.1, EAW70719.1
GeneID:3300	DNAJB2	2	220,144,040	220,151,622	7,582	+	1	4_A375_EGR1..1..5168	312	in gene	0	0	1	7	8	17	1	4_A375_EGR1..1	17	Gene DNAJB2	DNAJB2, HSPF3, HSJ1	DnaJ (Hsp40) homolog, subfamily B, member 2	NM_006736, NM_001039550, hCT1963115.1, hCT1963117.1	202500_at	NP_006727.2, NP_001034639.1, EAW70722.1, EAW70723.1
GeneID:5798	PTPRN	2	220,154,345	220,174,143	19,798	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3427, 2_A375_pNL97_plus_lncRNA_AR..1..4900, 4_A375_EGR1..1..5168	927, 1007, 29791	in gene, in gene, downstream	1	1	1	15.5	18	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene PTPRN	IA2, ICA512, R-PTP-N, IA-2, IA-2/PTP, PTPRN, FLJ16131	protein tyrosine phosphatase, receptor type, N	NM_002846, hCT1955091.1, hCT2354888.0, hCT6590.3	204945_at	NP_002837.1, EAW70725.1, EAW70724.1, EAW70726.1
GeneID:389075	RESP18	2	220,192,131	220,197,899	5,768	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4901	1440	in gene	0	1	0	13	19	5	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene RESP18	RESP18	regulated endocrine-specific protein 18 homolog (rat)	NM_001007089, hCT1645737.3		NP_001007090.3, EAW70727.1
GeneID:23549	DNPEP	2	220,238,180	220,252,662	14,482	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3428	-662	upstream	1	0	0	20	15	3	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene DNPEP	DNPEP, ASPEP, DAP	aspartyl aminopeptidase	NM_012100, hCT1955103.1, hCT2304416.1, hCT2304418.1, hCT2340840.0, hCT2340841.0, hCT2340842.0, hCT2340843.0, hCT2340844.0, hCT2348654.0, hCT2348655.0, hCT6606.3	201937_s_at, 215135_at, 38703_at	NP_036232.2, EAW70730.1, EAW70728.1, EAW70731.1, EAW70736.1, EAW70738.1, EAW70729.1, EAW70732.1, EAW70733.1, EAW70734.1, EAW70735.1, EAW70737.1
GeneID:10290	SPEG	2	220,299,700	220,358,354	58,654	+	2	4_A375_EGR1..1..5170, 4_A375_EGR1..1..5171	31052, 60972	in gene, downstream	0	0	1	6	5	14	2	4_A375_EGR1..1	14	Gene SPEG	SPEGalpha, SPEG, MGC12676, SPEGbeta, KIAA1297, APEG1, BPEG	SPEG complex locus	NM_005876, NM_001173476, hCT2303612.1, hCT2303613.1, hCT2303614.1, hCT2340838.0, hCT2340839.0, hCT2340840.0, hCT2340841.0, hCT2340842.0, hCT2340843.0, hCT2354844.0	205265_s_at, 232153_at	NP_005867.3, NP_001166947.1, EAW70743.1, EAW70746.1, EAW70748.1, EAW70750.1, EAW70742.1, EAW70744.1, EAW70745.1, EAW70747.1, EAW70749.1, EAW70751.1
GeneID:100507611	LOC100507611	2	220,346,454	220,381,599	35,145	-	2	4_A375_EGR1..1..5171, 4_A375_EGR1..1..5172	20927, 1791	in gene, in gene	0	0	1	5.5	5	16	2	4_A375_EGR1..1	16	Gene LOC100507611		hypothetical LOC100507611	XR_112443, XR_108431, XR_113436		
GeneID:29926	GMPPA	2	220,363,587	220,371,718	8,131	+	2	4_A375_EGR1..1..5171, 4_A375_EGR1..1..5172	-2915, 16221	upstream, downstream	0	0	1	5.5	5	16	2	4_A375_EGR1..1	16	Gene GMPPA	GMPPA		NM_205847, NM_013335, hCT1966017.1, hCT1966018.1, hCT1966020.0, hCT2354777.0, hCT6601.2	218070_s_at	NP_995319.1, NP_037467.2, EAW70755.1, EAW70756.1, EAW70758.1, EAW70759.1, EAW70757.1
GeneID:55515	ACCN4	2	220,378,892	220,403,494	24,602	+	1	4_A375_EGR1..1..5172	916	in gene	0	0	1	4	3	18	1	4_A375_EGR1..1	18	Gene ACCN4	ASIC4, MGC24860, ACCN4, BNAC4, MGC17248	amiloride-sensitive cation channel 4, pituitary	NM_018674, NM_182847, hCT2303621.0, hCT2303623.1, hCT2354818.0, hCT6612.2	221226_s_at	NP_061144.3, NP_878267.2, EAW70760.1, EAW70761.1, EAW70762.1, EAW70763.1
GeneID:10056	FARSB	2	223,436,162	223,520,827	84,665	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4904	155	in gene	0	1	0	15	19	7	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene FARSB	PheHB, HSPC173, PheRS, FARSB, FARSLB, FRSB	phenylalanyl-tRNA synthetase, beta subunit	NM_005687, hCT2303002.0, hCT2348700.0, hCT2354829.0	223035_s_at, 223036_at, 232083_x_at	NP_005678.3, EAW70802.1, EAW70803.1, EAW70804.1
GeneID:116255	MOGAT1	2	223,536,457	223,574,649	38,192	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4905	37719	in gene	0	1	0	11	14	4	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene MOGAT1	DGAT2L, MGAT1, DGAT2L1, MOGAT1	monoacylglycerol O-acyltransferase 1	NM_058165, hCT12102.3, hCT2302989.0	1553062_at	NP_477513.2, EAW70805.1, EAW70806.1
GeneID:2181	ACSL3	2	223,725,732	223,808,119	82,387	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3430	28	in gene	1	0	0	20	10	8	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ACSL3	ACSL3, ACS3, PRO2194, FACL3	acyl-CoA synthetase long-chain family member 3	NM_004457, NM_203372, hCT1955138.1, hCT2303712.0, hCT2303714.0	201661_s_at, 201662_s_at	NP_004448.2, NP_976251.1, EAW70807.1, EAW70808.1, EAW70809.1
GeneID:57590	WDFY1	2	224,740,065	224,810,052	69,987	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3432, 2_A375_pNL97_plus_lncRNA_AR..1..4906, 2_A375_pNL97_plus_lncRNA_AR..1..4907	4, 49540, -44	in gene, in gene, upstream	1	1	0	13	21	5.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene WDFY1	ZFYVE17, FENS-1, WDF1, WDFY1	WD repeat and FYVE domain containing 1	NM_020830, hCT2303142.0, hCT2303143.0	224800_at, 233559_s_at	NP_065881.1, EAW70817.1, EAW70818.1
GeneID:65080	MRPL44	2	224,822,121	224,832,431	10,310	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4906	87	in gene	0	1	0	13	21	8	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MRPL44	FLJ37668, L44MT, MRPL44, FLJ12701, MRP-L44, FLJ13990	mitochondrial ribosomal protein L44	NM_022915, hCT11133.2, hCT2303013.0	218202_x_at, 222555_s_at	NP_075066.1, EAW70820.1, EAW70819.1
GeneID:5270	SERPINE2	2	224,839,765	224,904,036	64,271	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3433	-3196	upstream	1	0	0	16	14	0	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene SERPINE2	DKFZp666A13110, PNI, GDN, SERPINE2, PI7, PI-7, PN-1, PN1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	NM_006216, NM_001136528, NM_001136530, hCT12527.2, hCT2303138.0, hCT2303139.0, hCT2354862.0	212190_at, 227487_s_at	NP_006207.1, NP_001130000.1, NP_001130002.1, EAW70822.1, EAW70823.1, EAW70824.1, EAW70821.1
GeneID:3667	IRS1	2	227,596,033	227,663,506	67,473	-	1	4_A375_EGR1..1..5173	1536	in gene	0	0	1	2	8	12	1	4_A375_EGR1..1	12	Gene IRS1	IRS1, HIRS-1	insulin receptor substrate 1	NM_005544, hCT1666484.2, hCT9420.2	204686_at	NP_005535.1, EAW70839.1, EAW70838.1
GeneID:3267	AGFG1	2	228,336,866	228,425,936	89,050	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3436, 2_A375_pNL97_plus_lncRNA_AR..1..4913	-66, -72	upstream, upstream	1	1	0	89	90	7	1	2_A375_pNL97_plus_lncRNA_AR..1	90	Gene AGFG1	MGC116940, RIP, HRB, AGFG1, MGC116938, RAB, DKFZp686I15205	ArfGAP with FG repeats 1	NM_004504, NM_001135187, NM_001135188, NM_001135189, hCT2304299.0, hCT2304300.0	213926_s_at, 213928_s_at, 218091_at, 218092_s_at	NP_004495.2, NP_001128659.1, NP_001128660.1, NP_001128661.1, EAW70871.1, EAW70872.1
GeneID:164781	WDR69	2	228,736,327	228,789,026	52,699	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4914	-8695	upstream	0	1	0	10	14	5	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene WDR69	FLJ25955, WDR69	WD repeat domain 69	NM_178821, hCT1815011.3, hCT2348672.0, hCT2348673.0, hCT2348674.0, hCT2354798.0	242162_at	NP_849143.1, EAW70884.1, EAW70880.1, EAW70881.1, EAW70882.1, EAW70883.1
GeneID:92737	DNER	2	230,222,345	230,579,286	356,941	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3437, 2_A375_pNL97_plus_lncRNA_AR..1..4915	-566, -456	upstream, upstream	1	1	0	19	19	7	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene DNER	UNQ26, bet, DNER	delta/notch-like EGF repeat containing	NM_139072, hCT2303273.0, hCT2303274.0, hCT2354864.0, hCT25012.3	226281_at	NP_620711.3, EAW70895.1, EAW70892.1, EAW70893.1, EAW70894.1
GeneID:51719	CAB39	2	231,577,557	231,685,790	108,233	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3438, 2_A375_pNL97_plus_lncRNA_AR..1..4916	-85, -53	upstream, upstream	1	1	0	37	39	8	1	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene CAB39	CGI-66, FLJ22682, CAB39, MO25	calcium binding protein 39	NM_016289, NM_001130849, NM_001130850, hCT2303766.0, hCT25537.3	217873_at, 224311_s_at	NP_057373.1, NP_001124321.1, NP_001124322.1, EAW70932.1, EAW70933.1
GeneID:81618	ITM2C	2	231,729,621	231,743,963	14,342	+	1	4_A375_EGR1..1..5174	5835	in gene	0	0	1	4	2	15	1	4_A375_EGR1..1	15	Gene ITM2C	E25, BRI3, E25C, BRICD2C, ITM3, ITM2C	integral membrane protein 2C	NM_001012514, NM_001012516, NM_030926, hCT1981988.1, hCT1981989.1, hCT2303770.0, hCT2354772.0, hCT25541.3	221004_s_at	NP_001012532.1, NP_001012534.1, NP_112188.1, EAW70934.1, EAW70935.1, EAW70937.1, EAW70936.1, EAW70938.1
GeneID:9290	GPR55	2	231,772,043	231,789,941	17,898	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4917	16325	in gene	0	1	0	12	16	2	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene GPR55	GPR55		NM_005683, hCT1645302.2, hCT2303873.1	231745_at, 237559_at	NP_005674.2, EAW70939.1, EAW70940.1
GeneID:257407	C2orf72	2	231,902,281	231,914,429	12,148	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3439, 2_A375_pNL97_plus_lncRNA_AR..1..4918, 2_A375_pNL97_plus_lncRNA_AR..1..4919	19063, 15431, 19031	downstream, downstream, downstream	1	1	0	61.5	59.5	8.5	2	1_A375_pNL7_minus_lncRNA_AR..1	113	Gene C2orf72	C2orf72	chromosome 2 open reading frame 72	NM_001144994	1556464_a_at, 213143_at, 213146_at	NP_001138466.1
GeneID:5707	PSMD1	2	231,921,578	232,037,541	115,963	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3439, 2_A375_pNL97_plus_lncRNA_AR..1..4918, 2_A375_pNL97_plus_lncRNA_AR..1..4919	-234, -3666, -266	upstream, upstream, upstream	1	1	0	61.5	59.5	8.5	2	1_A375_pNL7_minus_lncRNA_AR..1	113	Gene PSMD1	MGC133041, S1, P112, MGC133040, Rpn2, PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	NM_001191037, NM_002807, NR_034059, hCT2354765.0, hCT25536.2	201198_s_at, 201199_s_at	NP_001177966.1, NP_002798.2, EAW70947.1, EAW70948.1
GeneID:93010	B3GNT7	2	232,260,335	232,265,875	5,540	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3441, 2_A375_pNL97_plus_lncRNA_AR..1..4921	-7039, -7007	upstream, upstream	1	1	0	16	13	9	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene B3GNT7	B3GNT7, beta3GnT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	NM_145236, hCT2341139.0, hCT2341140.0	1552965_a_at, 1555962_at, 1555963_x_at, 232337_at	NP_660279.1, EAW70959.1, EAW70958.1
GeneID:4691	NCL	2	232,319,459	232,329,205	9,746	-	1	4_A375_EGR1..1..5176	517	in gene	0	0	1	7	10	13	1	4_A375_EGR1..1	13	Gene NCL	FLJ45706, NCL, FLJ59041, C23	nucleolin	NM_005381, hCT2304308.0, hCT2304309.0, hCT2354824.0, hCT25179.2	200610_s_at	NP_005372.2, EAW70960.1, EAW70961.1, EAW70962.1, EAW70963.1
GeneID:654321	SNORA75	2	232,320,511	232,320,647	136	-	1	4_A375_EGR1..1..5176	-8041	upstream	0	0	1	7	10	13	1	4_A375_EGR1..1	13	Gene SNORA75	SNORA75, U23	small nucleolar RNA, H/ACA box 75	NR_002921		
GeneID:6082	SNORD20	2	232,321,155	232,321,234	79	-	1	4_A375_EGR1..1..5176	-7454	upstream	0	0	1	7	10	13	1	4_A375_EGR1..1	13	Gene SNORD20	SNORD20, RNU20, U20	small nucleolar RNA, C/D box 20	NR_002908		
GeneID:25826	SNORD82	2	232,325,079	232,325,153	74	-	1	4_A375_EGR1..1..5176	-3535	upstream	0	0	1	7	10	13	1	4_A375_EGR1..1	13	Gene SNORD82	RNU82, SNORD82, U82, Z25	small nucleolar RNA, C/D box 82	NR_004398		
GeneID:5757	PTMA	2	232,573,235	232,578,251	5,016	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3442, 1_A375_pNL7_minus_lncRNA_AR..1..3443, 2_A375_pNL97_plus_lncRNA_AR..1..4924, 2_A375_pNL97_plus_lncRNA_AR..1..4925, 4_A375_EGR1..1..5177, 4_A375_EGR1..1..5178	-1523, -19, -1459, -195, -835, 2461	upstream, upstream, upstream, upstream, upstream, in gene	1	1	1	16	20	13.67	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene PTMA	PTMA, TMSA, MGC104802	prothymosin, alpha	NM_002823, NM_001099285, hCT2303930.0, hCT2303931.0, hCT2303933.0, hCT2303934.0, hCT2303935.0, hCT2303937.0, hCT2303938.0	200772_x_at, 211921_x_at	NP_002814.3, NP_001092755.1, EAW70969.1, EAW70970.1, EAW70974.1, EAW70975.1, EAW70971.1, EAW70972.1, EAW70973.1
GeneID:5147	PDE6D	2	232,597,147	232,645,974	48,827	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3444, 2_A375_pNL97_plus_lncRNA_AR..1..4926, 2_A375_pNL97_plus_lncRNA_AR..1..4927, 4_A375_EGR1..1..5179	-5130, 22, -5194, 328	upstream, in gene, upstream, in gene	1	1	1	15.5	20.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene PDE6D	PDED, PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta	NM_002601, hCT1981980.1, hCT24143.3	204091_at, 216663_x_at, 231085_at	NP_002592.1, EAW70977.1, EAW70976.1
GeneID:64708	COPS7B	2	232,651,162	232,673,434	22,272	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3444, 2_A375_pNL97_plus_lncRNA_AR..1..4926, 2_A375_pNL97_plus_lncRNA_AR..1..4927, 4_A375_EGR1..1..5179	-56, -5210, 6, -5514	upstream, upstream, in gene, upstream	1	1	1	15.5	20.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene COPS7B	COPS7B, CSN7B, MGC111077, FLJ12612	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	NM_022730, hCT1981985.2, hCT2348719.0, hCT2348720.0, hCT25181.4	219997_s_at, 225698_at, 243626_at	NP_073567.1, EAW70982.1, EAW70979.1, EAW70980.1, EAW70981.1
GeneID:129563	DIS3L2	2	232,826,293	233,201,908	375,615	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3445, 2_A375_pNL97_plus_lncRNA_AR..1..4928	353699, 354139	in gene, in gene	1	1	0	16	18	6	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene DIS3L2	DIS3L2, FAM6A, FLJ36974, MGC42174	DIS3 mitotic control homolog (S. cerevisiae)-like 2	NM_152383	227597_at, 238602_at	NP_689596.4
GeneID:248	ALPI	2	233,320,833	233,324,742	3,909	+	1	4_A375_EGR1..1..5181	-9569	upstream	0	0	1	2	3	14	1	4_A375_EGR1..1	14	Gene ALPI	IAP, ALPI	alkaline phosphatase, intestinal	NM_001631, hCT2303905.0, hCT24847.2	207140_at, 211618_s_at	NP_001622.2, EAW70997.1, EAW70998.1
GeneID:1146	CHRNG	2	233,404,437	233,411,038	6,601	+	1	4_A375_EGR1..1..5182	10795	downstream	0	0	1	15	13	14	1	4_A375_EGR1..1	14	Gene CHRNG	CHRNG, ACHRG, MGC133376	cholinergic receptor, nicotinic, gamma	NM_005199, hCT2303914.0, hCT24855.1	221355_at	NP_005190.4, EAW71005.1, EAW71004.1
GeneID:200765	TIGD1	2	233,412,779	233,415,226	2,447	-	1	4_A375_EGR1..1..5182	-6	upstream	0	0	1	15	13	14	1	4_A375_EGR1..1	14	Gene TIGD1	EEYORE, TIGD1	tigger transposable element derived 1	NM_145702, hCT2341138.0	1553099_at	NP_663748.1, EAW71006.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9470	EIF4E2	2	233,415,357	233,433,920	18,563	+	1	4_A375_EGR1..1..5182	-125	upstream	0	0	1	15	13	14	1	4_A375_EGR1..1	14	Gene EIF4E2	4E-LP, EIF4E2, 4EHP, EIF4EL3, IF4e	eukaryotic translation initiation factor 4E family member 2	NM_004846, hCT1961981.1, hCT1961982.1, hCT2303918.0, hCT24846.2	209393_s_at, 213570_at, 213571_s_at, 226734_at	NP_004837.1, EAW71008.1, EAW71007.1, EAW71009.1, EAW71010.1
GeneID:79054	TRPM8	2	234,826,043	234,928,166	102,123	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3446, 2_A375_pNL97_plus_lncRNA_AR..1..4929	-4443, -4475	upstream, upstream	1	1	0	23	39	4	1	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene TRPM8	LTRPC6, TRPM8, TRPP8, MGC2849	transient receptor potential cation channel, subfamily M, member 8	NM_024080, hCT2303397.0, hCT2303398.0	220226_at, 243483_at	NP_076985.4, EAW71068.1, EAW71067.1
GeneID:10920	COPS8	2	237,994,084	238,007,489	13,405	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3448, 2_A375_pNL97_plus_lncRNA_AR..1..4933	284, 444	in gene, in gene	1	1	0	18	28	10	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene COPS8	MGC43256, COP9, CSN8, COPS8, MGC1297, SGN8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	NM_006710, NM_198189, hCT1815594.2, hCT1981954.1, hCT2354866.0, hCT2354867.0	202141_s_at, 202142_at, 202143_s_at, 214260_at, 243152_at	NP_006701.1, NP_937832.1, EAW71097.1, EAW71098.1, EAW71099.1, EAW71100.1
GeneID:79083	MLPH	2	238,395,878	238,463,961	68,083	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4937	76698	downstream	0	1	0	13	17	8	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene MLPH	MGC2771, MGC59733, MLPH, SLAC2-A	melanophilin	NM_001042467, NM_024101, hCT14132.2, hCT2303728.0, hCT2303729.0, hCT2354846.0, hCT2354847.0	218211_s_at	NP_001035932.1, NP_077006.1, EAW71113.1, EAW71114.1, EAW71115.1, EAW71116.1, EAW71112.1
GeneID:51052	PRLH	2	238,475,217	238,475,818	601	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4937, 4_A375_EGR1..1..5183	-2641, 9679	upstream, downstream	0	1	1	8.5	9.5	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PRLH	PRH, PRLH, PRRP	prolactin releasing hormone	NM_015893, hCT14122.0	221443_x_at	NP_056977.1, EAW71117.1
GeneID:64284	RAB17	2	238,482,965	238,499,769	16,804	-	1	4_A375_EGR1..1..5183	14873	in gene	0	0	1	4	2	13	1	4_A375_EGR1..1	13	Gene RAB17	FLJ12538, RAB17	RAB17, member RAS oncogene family	NM_022449, NR_033308, hCT2304033.0, hCT2304034.0, hCT2354758.0	218931_at	NP_071894.1, EAW71120.1, EAW71118.1, EAW71119.1
GeneID:10267	RAMP1	2	238,768,187	238,820,756	52,569	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3450, 2_A375_pNL97_plus_lncRNA_AR..1..4938	39173, 39301	in gene, in gene	1	1	0	20	20	7	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene RAMP1	RAMP1		NM_005855, hCT14123.4	204916_at	NP_005846.1, EAW71127.1
GeneID:140739	UBE2F	2	238,875,700	238,950,684	74,984	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3451	-180	upstream	1	0	0	16	10	3	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene UBE2F	MGC18120, UBE2F, NCE2	ubiquitin-conjugating enzyme E2F (putative)	NM_080678, hCT2344156.0, hCT2344158.0, hCT2344159.0, hCT2354766.0, hCT2354767.0, hCT2354768.0, hCT2354769.0	225783_at, 225787_at, 231948_s_at	NP_542409.1, EAW71130.1, EAW71128.1, EAW71132.1, EAW71133.1, EAW71134.1, EAW71129.1, EAW71131.1
GeneID:51540	SCLY	2	238,969,632	239,008,054	38,422	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4939, 4_A375_EGR1..1..5185	-298, 320	upstream, in gene	0	1	1	8.5	13.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SCLY	SCL, SCLY	selenocysteine lyase	NM_016510, hCT2344157.1, hCT2344160.1, hCT2344161.1, hCT2344162.1, hCT2354764.1	219808_at, 221575_at, 59705_at	NP_057594.3, EAW71135.1, EAW71136.1, EAW71137.1, EAW71138.1, EAW71139.1
GeneID:339768	ESPNL	2	239,008,951	239,041,928	32,977	+	2	4_A375_EGR1..1..5186, 4_A375_EGR1..1..5187	28817, 29481	in gene, in gene	0	0	1	2	4.5	13	2	4_A375_EGR1..1	14	Gene ESPNL	ESPNL, FLJ42566, MGC99829	espin-like	NM_194312, hCT1953158.2	1557000_at, 1557002_x_at	NP_919288.2, EAW71140.1
GeneID:377007	KLHL30	2	239,047,363	239,061,547	14,184	+	2	4_A375_EGR1..1..5186, 4_A375_EGR1..1..5187	-9795, -8931	upstream, upstream	0	0	1	2	4.5	13	2	4_A375_EGR1..1	14	Gene KLHL30	FLJ43374, KLHL30	kelch-like 30 (Drosophila)	NM_198582, hCT1816196.2		NP_940984.3, EAW71141.1
GeneID:8864	PER2	2	239,152,679	239,197,207	44,528	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3452, 1_A375_pNL7_minus_lncRNA_AR..1..3453, 2_A375_pNL97_plus_lncRNA_AR..1..4940, 2_A375_pNL97_plus_lncRNA_AR..1..4941	31631, -297, 31631, -329	in gene, upstream, in gene, upstream	1	1	0	23.5	24	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene PER2	KIAA0347, PER2, FASPS	period homolog 2 (Drosophila)	NM_022817, hCT2304251.0, hCT2304252.0, hCT2304254.0	205251_at, 208518_s_at	NP_073728.1, EAW71153.1, EAW71154.1, EAW71155.1
GeneID:9759	HDAC4	2	239,969,864	240,322,643	352,779	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3457, 2_A375_pNL97_plus_lncRNA_AR..1..4943, 2_A375_pNL97_plus_lncRNA_AR..1..4944	-749, 125619, -653	upstream, in gene, upstream	1	1	0	12	16.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene HDAC4	HA6116, BDMR, HD4, AHO3, HDAC4, HDAC-A, KIAA0288, HDACA	histone deacetylase 4	NM_006037, hCT13281.3, hCT2354798.0	1554322_a_at, 204225_at, 228813_at	NP_006028.2, EAW71166.1, EAW71165.1
GeneID:4705	NDUFA10	2	240,896,789	240,964,819	68,030	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4945	-45	upstream	0	1	0	13	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene NDUFA10	NDUFA10, CI-42k, FLJ21923, CI-42KD, MGC5103	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	NM_004544, hCT11609.3, hCT2303673.0, hCT2303674.0, hCT2303675.0	1554719_at, 1555546_at	NP_004535.1, EAW71173.1, EAW71172.1, EAW71174.1, EAW71175.1
GeneID:389090	OR6B2	2	240,968,908	240,969,846	938	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4945	4982	downstream	0	1	0	13	18	8	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene OR6B2	OR6B2P, OR6B2, OR2-1	olfactory receptor, family 6, subfamily B, member 2	NM_001005853, hCT2345564.0		NP_001005853.1, EAW71176.1
GeneID:57140	RNPEPL1	2	241,508,104	241,518,144	10,040	+	1	4_A375_EGR1..1..5192	9165	in gene	0	0	1	3	9	14	1	4_A375_EGR1..1	14	Gene RNPEPL1	MGC99544, FLJ10806, RNPEPL1, FLJ26675	arginyl aminopeptidase (aminopeptidase B)-like 1	NM_018226, hCT1960550.1, hCT2304498.0, hCT23848.3	218301_at	NP_060696.3, EAW71193.1, EAW71194.1, EAW71195.1
GeneID:11132	CAPN10	2	241,526,145	241,538,520	12,375	+	1	4_A375_EGR1..1..5192	-8876	upstream	0	0	1	3	9	14	1	4_A375_EGR1..1	14	Gene CAPN10	CANP10, CAPN10, NIDDM1	calpain 10	NM_023083, NM_023085	219333_s_at, 221040_at	NP_075571.1, NP_075573.2
GeneID:547	KIF1A	2	241,653,184	241,759,624	106,440	-	1	4_A375_EGR1..1..5193	36104	in gene	0	0	1	6	10	18	1	4_A375_EGR1..1	18	Gene KIF1A	MGC133285, FLJ30229, MGC133286, ATSV, KIF1A, DKFZp686I2094, C2orf20, UNC104, HUNC-104	kinesin family member 1A	NM_004321, hCT2304924.0, hCT2304925.0, hCT2304926.0, hCT23481.2	203849_s_at, 203850_s_at, 225482_at	NP_004312.2, EAW71217.1, EAW71214.1, EAW71215.1, EAW71216.1
GeneID:79919	C2orf54	2	241,825,465	241,835,573	10,108	-	1	4_A375_EGR1..1..5194	-1227	upstream	0	0	1	6	8	16	1	4_A375_EGR1..1	16	Gene C2orf54	FLJ22671, C2orf54, MGC150431, MGC150432	chromosome 2 open reading frame 54	NM_001085437, NM_024861, hCT10514.3, hCT2304920.0, hCT2304922.0	220149_at	NP_001078906.1, NP_079137.2, EAW71218.1, EAW71219.1, EAW71220.1
GeneID:200772	LOC200772	2	241,894,034	241,906,868	12,834	-	2	4_A375_EGR1..1..5196, 4_A375_EGR1..1..5197	21266, 4052	downstream, in gene	0	0	1	3	5.5	13.5	2	4_A375_EGR1..1	14	Gene LOC200772		hypothetical LOC200772	NR_033841	241525_at	
GeneID:25992	SNED1	2	241,938,255	242,033,643	95,388	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3456, 4_A375_EGR1..1..5198	103537, -495	downstream, upstream	1	0	1	17	14	16.5	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene SNED1	FLJ00133, SST3, Snep, SNED1, DKFZp586B2420	sushi, nidogen and EGF-like domains 1	NM_001080437	1554798_at, 213488_at, 213493_at	NP_001073906.1
GeneID:130916	MTERFD2	2	242,026,509	242,041,747	15,238	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3456	-45	upstream	1	0	0	18	16	17	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene MTERFD2	MTERFD2, FLJ16261, MGC61716	MTERF domain containing 2	NM_182501, NR_026049, NR_026050, NR_026051, hCT2354863.0, hCT24247.4	1557965_at, 1557966_x_at, 214384_at, 226486_at	NP_872307.2, EAW71234.1, EAW71235.1
GeneID:23178	PASK	2	242,045,515	242,088,878	43,363	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3456	47086	downstream	1	0	0	18	16	17	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene PASK	DKFZp434O051, DKFZp686P2031, PASK, PASKIN, STK37, KIAA0135	PAS domain containing serine/threonine kinase	NM_015148, hCT1950053.1, hCT1958412.1, hCT2304907.0, hCT2304909.0, hCT2354827.0, hCT2354828.0, hCT24240.1	206594_at, 213534_s_at, 216945_x_at	NP_055963.2, EAW71236.1, EAW71237.1, EAW71240.1, EAW71241.1, EAW71242.1, EAW71238.1, EAW71239.1
GeneID:3069	HDLBP	2	242,166,679	242,255,254	88,575	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3459, 1_A375_pNL7_minus_lncRNA_AR..1..3460, 2_A375_pNL97_plus_lncRNA_AR..1..4946, 2_A375_pNL97_plus_lncRNA_AR..1..4947	43882, 502, 43798, 502	in gene, in gene, in gene, in gene	1	1	0	25	21.5	6	2	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene HDLBP	PRO2900, HDLBP, FLJ16432, VGL, HBP	high density lipoprotein binding protein	NM_005336, NM_203346, hCT1966929.1, hCT2304954.0, hCT24241.3	200643_at, 219674_s_at, 221767_x_at, 222918_s_at, 225012_at, 235624_at, 240152_at	NP_005327.1, NP_976221.1, EAW71253.1, EAW71254.1, EAW71255.1
GeneID:4735	2-Sep	2	242,254,723	242,293,442	38,719	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3460, 2_A375_pNL97_plus_lncRNA_AR..1..4947	29, 29	in gene, in gene	1	1	0	34	27	9	1	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene SEPT2	Pnutl3, SEPT2, NEDD5, DIFF6, KIAA0158, hNedd5	septin 2	NM_001008491, NM_001008492, NM_006155, NM_004404, hCT2304461.1, hCT2304462.1, hCT2304463.1, hCT2304464.1	1554747_a_at, 1559038_at, 200015_s_at, 200778_s_at, 232637_at	NP_001008491.1, NP_001008492.1, NP_004395.1, NP_006146.1, EAW71258.1, EAW71261.1, EAW71259.1, EAW71260.1
GeneID:10494	STK25	2	242,434,432	242,448,034	13,602	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4948	-94	upstream	0	1	0	15	19	7	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene STK25	SOK1, DKFZp686J1430, STK25, YSK1	serine/threonine kinase 25 (STE20 homolog, yeast)	NM_006374, hCT2304944.0, hCT2304945.0	201314_at	NP_006365.2, EAW71265.1, EAW71266.1
GeneID:100379249	BOKAS	2	242,483,799	242,498,558	14,759	-	2	4_A375_EGR1..1..5199, 4_A375_EGR1..1..5200	17406, -3234	downstream, upstream	0	0	1	6.5	8	13.5	2	4_A375_EGR1..1	15	Gene BOKAS	BOK-AS, NCRNA00151, BOK-AS1, NATOB, BOKAS	BOK antisense RNA (non-protein coding)	NR_033346		
GeneID:666	BOK	2	242,498,192	242,513,553	15,361	+	1	4_A375_EGR1..1..5200	3600	in gene	0	0	1	6	8	15	1	4_A375_EGR1..1	15	Gene BOK	MGC4631, BOK, BOKL, BCL2L9	BCL2-related ovarian killer	NM_032515, hCT1965482.1, hCT1965483.1, hCT1965484.1, hCT1965485.1, hCT2354860.0, hCT2354861.0, hCT24245.4	221454_at, 223349_s_at	NP_115904.1, EAW71269.1, EAW71268.1, EAW71270.1, EAW71272.1, EAW71274.1, EAW71271.1, EAW71273.1
GeneID:84289	ING5	2	242,641,456	242,668,896	27,440	+	1	4_A375_EGR1..1..5201	17584	in gene	0	0	1	2	4	12	1	4_A375_EGR1..1	12	Gene ING5	FLJ23842, p28ING5, ING5	inhibitor of growth family, member 5	NM_032329, hCT2349297.0, hCT2349298.0, hCT2354842.0	228672_at	NP_115705.2, EAW71288.1, EAW71287.1, EAW71289.1
GeneID:728294	D2HGDH	2	242,674,030	242,708,231	34,201	+	3	4_A375_EGR1..1..5202, 4_A375_EGR1..1..5203, 4_A375_EGR1..1..5204	9250, 17789, 42626	in gene, in gene, downstream	0	0	1	3	4	15.67	3	4_A375_EGR1..1	16	Gene D2HGDH	D2HGDH, FLJ42195, D2HGD, MGC25181	D-2-hydroxyglutarate dehydrogenase	NM_152783	228738_at	NP_689996.4
GeneID:84090	GAL3ST2	2	242,716,240	242,743,702	27,462	+	1	4_A375_EGR1..1..5204	416	in gene	0	0	1	2	8	16	1	4_A375_EGR1..1	16	Gene GAL3ST2	GP3ST, GAL3ST2, GAL3ST-2	galactose-3-O-sulfotransferase 2	NM_022134, hCT2303829.0		NP_071417.2, EAW71293.1
GeneID:5133	PDCD1	2	242,792,033	242,801,058	9,025	-	3	4_A375_EGR1..1..5205, 4_A375_EGR1..1..5206, 4_A375_EGR1..1..5207	8306, 4290, -366	in gene, in gene, upstream	0	0	1	5.67	3	15.33	3	4_A375_EGR1..1	16	Gene PDCD1	hPD-l, CD279, PD1, hPD-1, PDCD1, SLEB2, PD-1	programmed cell death 1	NM_005018, hCT1814989.0	207634_at	NP_005009.2, EAW71296.1
GeneID:285093	C2orf85	2	242,811,886	242,815,482	3,596	+	1	4_A375_EGR1..1..5208	2	in gene	0	0	1	2	3	12	1	4_A375_EGR1..1	12	Gene C2orf85	FLJ33590, MGC142077, MGC142079, C2orf85	chromosome 2 open reading frame 85	NM_173821, hCT2303835.0, hCT2303837.0, hCT2303838.0, hCT2303839.0	1560035_at	NP_776182.2, EAW71302.1, EAW71299.1, EAW71300.1, EAW71301.1
GeneID:140680	C20orf96	20	251,524	271,390	19,866	-	1	4_A375_EGR1..1..5211	-7554	upstream	0	0	1	12	12	17	1	4_A375_EGR1..1	17	Gene C20orf96	C20orf96, dJ1103G7.2, FLJ40075	chromosome 20 open reading frame 96	NM_153269, hCT2314264.0, hCT31126.2	231905_at	NP_695001.1, EAX10682.1, EAX10681.1
GeneID:85364	ZCCHC3	20	278,204	280,965	2,761	+	1	4_A375_EGR1..1..5211	740	in gene	0	0	1	12	12	17	1	4_A375_EGR1..1	17	Gene ZCCHC3	MGC104290, C20orf99, ZCCHC3	zinc finger, CCHC domain containing 3	NM_033089, hCT1641168.3	225072_at, 225091_at, 229993_at	NP_149080.2, EAX10684.1
GeneID:100507459	LOC100507459	20	300,971	305,896	4,925	-	2	2_A375_pNL97_plus_lncRNA_AR..1..4949, 4_A375_EGR1..1..5212	552, -2104	in gene, upstream	0	1	1	12	18.5	14	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100507459		hypothetical LOC100507459	XR_112112, XR_109838, XR_115335		
GeneID:6666	SOX12	20	306,239	310,868	4,629	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4949, 4_A375_EGR1..1..5212	-895, 1761	upstream, in gene	0	1	1	12	18.5	14	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SOX12	SOX12, SOX22	SRY (sex determining region Y)-box 12	NM_006943, hCT2314747.0	204432_at, 228358_at	NP_008874.2, EAX10683.1
GeneID:57761	TRIB3	20	361,308	378,203	16,895	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4950, 4_A375_EGR1..1..5213	27076, 292	downstream, in gene	0	1	1	15.5	16	14.5	2	4_A375_EGR1..1	19	Gene TRIB3	SKIP3, NIPK, TRIB3, SINK, TRB3, C20orf97	tribbles homolog 3 (Drosophila)	NM_021158, hCT2314750.2	1555788_a_at, 218145_at	NP_066981.2, EAX10678.1
GeneID:10616	RBCK1	20	388,709	411,610	22,901	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3461, 2_A375_pNL97_plus_lncRNA_AR..1..4950, 4_A375_EGR1..1..5214	23483, -325, 13019	downstream, upstream, in gene	1	1	1	15	12	14.67	3	4_A375_EGR1..1	23	Gene RBCK1	XAP3, RBCK2, HOIL-1, HOIL1, XAP4, C20orf18, UBCE7IP3, RNF54, ZRANB4, RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	NM_031229, NM_006462	207713_s_at, 221827_at	NP_112506.2, NP_006453.1
GeneID:128637	TBC1D20	20	416,124	443,187	27,063	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3461	30995	downstream	1	0	0	16	8	11	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene TBC1D20	FLJ45119, TBC1D20, C20orf140	TBC1 domain family, member 20	NM_144628, hCT2359534.0, hCT2359535.0, hCT31128.3	228409_at, 228684_at	NP_653229.1, EAX10672.1, EAX10670.1, EAX10671.1
GeneID:1457	CSNK2A1	20	463,338	524,482	61,144	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3462, 2_A375_pNL97_plus_lncRNA_AR..1..4951	228, -46	in gene, upstream	1	1	0	21	22	11	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CSNK2A1	CK2A1, CKII, CSNK2A1	casein kinase 2, alpha 1 polypeptide	NM_177559, NM_001895, NM_177560, hCT1963004.1, hCT1963005.1, hCT1963006.1, hCT1963007.1, hCT2359579.0	206075_s_at, 212072_s_at, 212075_s_at, 229212_at, 229216_s_at	NP_808227.1, NP_001886.1, NP_808228.1, EAX10665.1, EAX10668.1, EAX10669.1, EAX10666.1, EAX10667.1
GeneID:85508	SCRT2	20	642,240	656,823	14,583	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4952	727	in gene	0	1	0	12	18	10	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SCRT2	SCRT2, ZNF898B, FLJ43353		NM_033129, hCT2314449.0, hCT31125.3		NP_149120.1, EAX10660.1, EAX10661.1
GeneID:83541	FAM110A	20	814,356	826,922	12,566	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3463, 2_A375_pNL97_plus_lncRNA_AR..1..4953, 4_A375_EGR1..1..5216	-52, 108, 11292	upstream, in gene, in gene	1	1	1	17	12	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene FAM110A	C20orf55, MGC2450, F10, bA371L19.3, FAM110A, MGC4675	family with sequence similarity 110, member A	NM_031424, NM_001042353, NM_207121	226584_s_at	NP_113612.1, NP_001035812.1, NP_997004.1
GeneID:51378	ANGPT4	20	853,296	896,960	43,664	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4954	37376	in gene	0	1	0	12	22	5	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ANGPT4	ANG4, MGC138183, AGP4, ANGPT4, MGC138181, ANG-3	angiopoietin 4	NM_015985, hCT31122.1	221134_at	NP_057069.1, EAX10654.1
GeneID:9491	PSMF1	20	1,093,906	1,148,426	54,520	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3464, 2_A375_pNL97_plus_lncRNA_AR..1..4955	5262, 5230	in gene, in gene	1	1	0	23	28	16	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene PSMF1	PSMF1, PI31	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	NM_006814, NM_178578, hCT1967837.1, hCT2359498.0, hCT30868.2	201052_s_at, 201053_s_at	NP_006805.2, NP_848693.2, EAX10649.1, EAX10650.1, EAX10651.1
GeneID:642636	RAD21L1	20	1,206,764	1,235,145	28,381	+	1	4_A375_EGR1..1..5217	306	in gene	0	0	1	7	11	14	1	4_A375_EGR1..1	14	Gene RAD21L1	RAD21L1, MGC198626, dJ545L17.2	RAD21-like 1 (S. pombe)	NM_001136566	234682_at	NP_001130038.2
GeneID:9751	SNPH	20	1,246,960	1,289,971	43,011	+	3	4_A375_EGR1..1..5218, 4_A375_EGR1..1..5219, 4_A375_EGR1..1..5220	42084, 46432, 46928	in gene, downstream, downstream	0	0	1	5	7.67	18	3	4_A375_EGR1..1	19	Gene SNPH	MGC46096, SNPH, bA314N13.5, KIAA0374	syntaphilin	NM_014723, hCT2314671.0, hCT2314672.0, hCT2314673.0, hCT2314674.0, hCT2314675.0	205104_at, 215917_at	NP_055538.2, EAX10644.1, EAX10641.1, EAX10642.1, EAX10643.1, EAX10645.1
GeneID:27111	SDCBP2	20	1,290,619	1,309,838	19,219	-	4	2_A375_pNL97_plus_lncRNA_AR..1..4956, 4_A375_EGR1..1..5218, 4_A375_EGR1..1..5219, 4_A375_EGR1..1..5220	3918, 20814, 16446, 15950	in gene, downstream, in gene, in gene	0	1	1	6.5	9.75	16	4	4_A375_EGR1..1	19	Gene SDCBP2	SDCBP2, ST-2, FLJ12256, SITAC18	syndecan binding protein (syntenin) 2	NM_080489, NM_015685, hCT2314394.1, hCT2314395.1	233565_s_at	NP_536737.3, NP_056500.2, EAX10639.1, EAX10640.1
GeneID:100507495	LOC100507495	20	1,306,054	1,359,379	53,325	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4956	-134	upstream	0	1	0	11	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100507495		hypothetical LOC100507495	XR_112113, XR_112114, XR_109839, XR_109840, XR_115336, XR_115337		



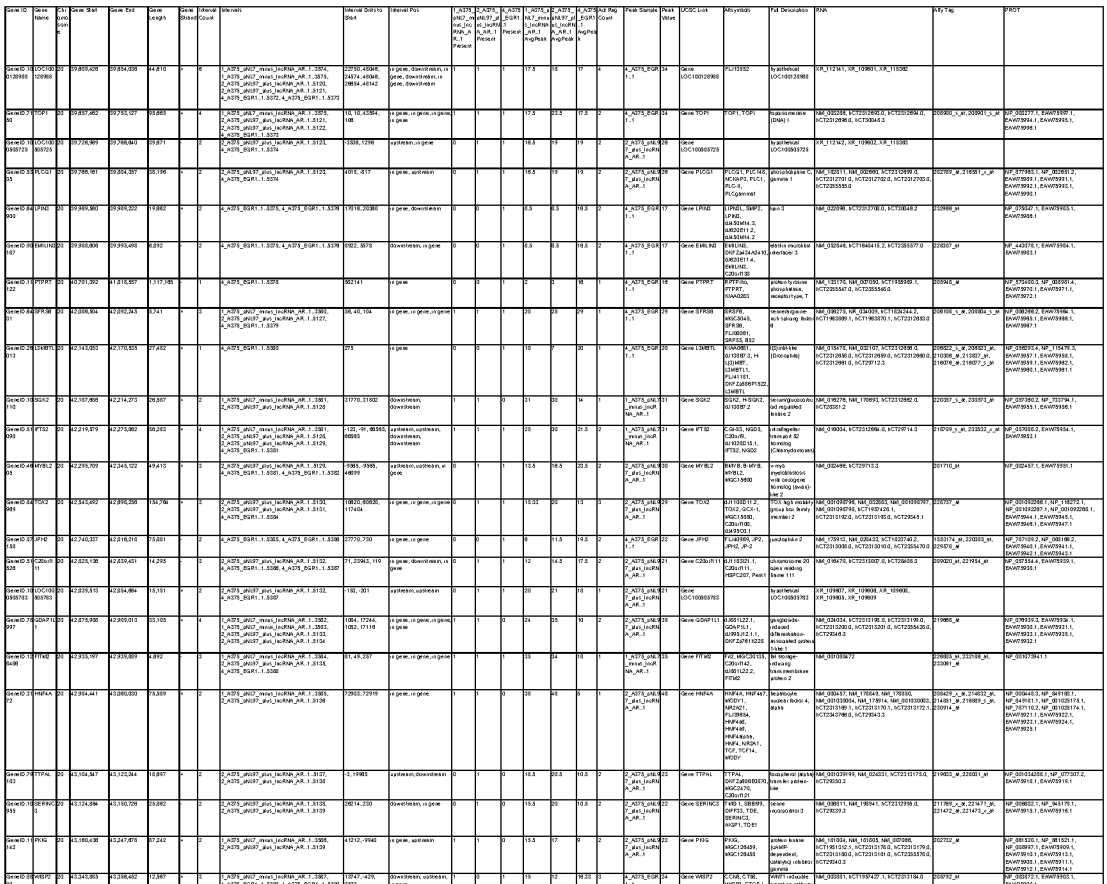
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:57506	MAVS	20	3,827,449	3,856,762	29,313	+	4	2_A375_pNL97_plus_lncRNA_AR..1..4976, 2_A375_pNL97_plus_lncRNA_AR..1..4977, 4_A375_EGR1..1..5243, 4_A375_EGR1..1..5244	-441, 119, -165, 295	upstream, in gene, upstream, in gene	0	1	1	15	18	17	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MAVS	FLJ41962, FLJ38051, FLJ35386, KIAA1271, DKFZp666M015, IPS-1, MGC3260, CARDIF, VISA, MAVS, DKFZp547C224, FLJ31698, FLJ27482, IPS1	mitochondrial antiviral signaling protein	NM_020746, hCT2314294.0, hCT30592.1	226495_at, 231629_at	NP_065797.2, EAX10481.1, EAX10482.1
GeneID:80025	PANK2	20	3,869,486	3,904,502	35,016	+	2	2_A375_pNL97_plus_lncRNA_AR..1..4978, 4_A375_EGR1..1..5245	336, 176	in gene, in gene	0	1	1	16	21	24	1	4_A375_EGR1..1	24	Gene PANK2	HSS, PKAN, C20orf48, PANK2, HARP, MGC15053, FLJ17232, NBIA1	pantothenate kinase 2	NM_153638, NM_024960, NM_153640	218809_at, 228735_s_at, 228985_s_at, 228986_at, 235130_at, 236658_s_at	NP_705902.2, NP_079236.3, NP_705904.1
GeneID:54498	SMOX	20	4,129,450	4,168,369	38,919	+	1	4_A375_EGR1..1..5246	23782	in gene	0	0	1	8	10	21	1	4_A375_EGR1..1	21	Gene SMOX	PAO, FLJ20746, SMO, SMOX, PAOH1, MGC1010, C20orf16	spermine oxidase	NM_175839, NM_175840, NM_175841, NM_175842	1555860_a_at, 210357_s_at, 217074_at	NP_787033.1, NP_787034.1, NP_787035.1, NP_787036.1
GeneID:5621	PRNP	20	4,666,797	4,682,234	15,437	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4983	-2665	upstream	0	1	0	10	19	3	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PRNP	PrPc, PrP33-35C, CJD, PRNP, CD230, PrP, MGC26679, PrP27-30, GSS, PRIP, ASCR, prion	prion protein	NM_000311, NM_183079, NM_001080121, NM_001080122, NM_001080123, hCT1824426.3, hCT2359571.0	1556190_s_at, 201300_s_at, 215707_s_at	NP_000302.1, NP_898902.1, NP_001073590.1, NP_001073591.1, NP_001073592.1, EAX10450.1, EAX10449.1
GeneID:29058	C20orf30	20	5,080,484	5,093,733	13,249	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3482, 2_A375_pNL97_plus_lncRNA_AR..1..4984, 2_A375_pNL97_plus_lncRNA_AR..1..4985	-59, 21, -6747	upstream, in gene, upstream	1	1	0	18.5	27	18	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene C20orf30	HSPC274, dJ1116H23.2.1, C20orf30	chromosome 20 open reading frame 30	NM_014145, NM_001009923, NM_001009924, NM_001009925, hCT2315408.0, hCT2315409.0, hCT2315410.0, hCT2315411.0, hCT2359574.0, hCT2359575.0, hCT2359576.0	220477_s_at, 224584_at	NP_054864.3, NP_001009923.1, NP_001009924.1, NP_001009925.1, EAX10436.1, EAX10437.1, EAX10431.1, EAX10432.1, EAX10433.1, EAX10434.1, EAX10435.1
GeneID:5111	PCNA	20	5,095,599	5,107,268	11,669	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3482, 2_A375_pNL97_plus_lncRNA_AR..1..4984, 2_A375_pNL97_plus_lncRNA_AR..1..4985	13476, 13556, 6786	downstream, downstream, in gene	1	1	0	18.5	27	18	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene PCNA	MGC8367, PCNA	proliferating cell nuclear antigen	NM_002592, NM_182649, hCT1951350.1, hCT2315404.0, hCT30362.3	201202_at	NP_002583.1, NP_872590.1, EAX10428.1, EAX10429.1, EAX10430.1
GeneID:100302739	PCNAAS	20	5,100,232	5,100,615	383	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3482, 2_A375_pNL97_plus_lncRNA_AR..1..4984, 2_A375_pNL97_plus_lncRNA_AR..1..4985	-6440, -6520, 248	upstream, upstream, in gene	1	1	0	18.5	27	18	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene PCNAAS	PCNA-AS, PCNA-AS1, PCNAAS	PCNA antisense RNA (non-protein coding)	NR_028370		
GeneID:8760	CDS2	20	5,107,482	5,171,989	64,507	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4985	-7002	upstream	0	1	0	10	22	21	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CDS2	CDS2, FLJ38111	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	NM_003818, hCT2315501.0, hCT2359519.0, hCT2359520.0	212862_at, 212864_at, 233630_at	NP_003809.1, EAX10424.1, EAX10425.1, EAX10426.1
GeneID:149840	C20orf196	20	5,731,043	5,844,558	113,515	+	1	2_A375_pNL97_plus_lncRNA_AR..1..4987	94109	in gene	0	1	0	16	24	7	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene C20orf196	RP4-784N16.1, C20orf196, FLJ25067	chromosome 20 open reading frame 196	NM_152504, hCT1951346.1, hCT2315505.0	235063_at, 235064_s_at, 243507_s_at, 243508_at	NP_689717.2, EAX10411.1, EAX10412.1
GeneID:1114	CHGB	20	5,891,974	5,906,007	14,033	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3484, 2_A375_pNL97_plus_lncRNA_AR..1..4986	314, 282	in gene, in gene	1	1	0	33	65	11	1	2_A375_pNL97_plus_lncRNA_AR..1	65	Gene CHGB	SCG1, CHGB	chromogranin B (secretogranin 1)	NM_001819, hCT29384.3	204260_at	NP_001810.2, EAX10410.1
GeneID:51605	TRMT6	20	5,918,486	5,931,173	12,687	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3485	133	in gene	1	0	0	14	14	14	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene TRMT6	CGI-09, Gcd10p, MGC5029, GCD10, TRMT6	tRNA methyltransferase 6 homolog (S. cerevisiae)	NM_015939, hCT1961803.1, hCT30773.3	222768_s_at, 233970_s_at	NP_057023.2, EAX10407.1, EAX10408.1
GeneID:84515	MCM8	20	5,931,298	5,975,833	44,535	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3485	-256	upstream	1	0	0	14	14	14	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene MCM8	REC, MGC119522, MCM8, MGC119523, C20orf154, MGC4816, MGC12866, dJ967N21.5	minichromosome maintenance complex component 8	NM_182802, NM_032485, hCT2314161.0, hCT2359521.0, hCT30778.3	224320_s_at, 233560_x_at	NP_877954.1, NP_115874.3, EAX10403.1, EAX10404.1, EAX10405.1
GeneID:55612	FERMT1	20	6,055,492	6,104,191	48,699	-	1	2_A375_pNL97_plus_lncRNA_AR..1..4989	543	in gene	0	1	0	15	16	14	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene FERMT1	UNC112A, C20orf42, FLJ23423, FLJ20116, URP1, KIND1, FERMT1, DTGCU2	fermitin family homolog 1 (Drosophila)	NM_017671, hCT1951355.1, hCT2314102.0, hCT2359536.0, hCT2359537.0	1557334_a_at, 218796_at, 229545_at, 232479_at, 60474_at	NP_060141.3, EAX10392.1, EAX10393.1, EAX10394.1, EAX10395.1
GeneID:650	BMP2	20	6,748,745	6,760,910	12,165	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3487, 4_A375_EGR1..1..5247	1943, 23	in gene, in gene	1	0	1	15.5	13.5	17	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene BMP2	BMP2A, BMP2	bone morphogenetic protein 2	NM_001200, hCT2314172.1, hCT30775.3	205289_at, 205290_s_at	NP_001191.1, EAX10366.1, EAX10367.1
GeneID:54363	HAO1	20	7,863,631	7,921,093	57,462	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3490, 2_A375_pNL97_plus_lncRNA_AR..1..4993	15429, 15509	in gene, in gene	1	1	0	21	18	3	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene HAO1	MGC142225, MGC142227, HAO1, GOX1, HAOX1, GOX	hydroxyacid oxidase (glycolate oxidase) 1	NM_017545, hCT2314176.0, hCT2314180.0, hCT30852.3	220224_at	NP_060015.1, EAX10380.1, EAX10379.1, EAX10381.1
GeneID:56255	TMX4	20	7,961,713	8,000,393	38,680	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3491, 2_A375_pNL97_plus_lncRNA_AR..1..4994, 4_A375_EGR1..1..5248	-151, 137, -39	upstream, in gene, upstream	1	1	1	16	18	20	1	4_A375_EGR1..1	20	Gene TMX4	DJ971N18.2, TMX4, TXNDC13, KIAA1162, PDIA14	thioredoxin-related transmembrane protein 4	NM_021156, hCT30850.3	201580_s_at, 201581_at, 216027_at	NP_066979.2, EAX10377.1
GeneID:23236	PLCB1	20	8,113,296	8,865,547	752,251	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3492, 2_A375_pNL97_plus_lncRNA_AR..1..4996, 2_A375_pNL97_plus_lncRNA_AR..1..4997	412668, 412624, 623668	in gene, in gene, in gene	1	1	0	16	18.5	4	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PLCB1	PLCB1, PLC154, EIEE12, FLJ45792, PLC-154, PI-PLC, PLC-I, PLCB1B, PLCB1A	phospholipase C, beta 1 (phosphoinositide-specific)	NM_182734, NM_015192, hCT1951349.1, hCT2314230.0, hCT2314231.0, hCT2314233.0, hCT2314234.0	211925_s_at, 213222_at, 215687_x_at	NP_877398.1, NP_056007.1, EAX10372.1, EAX10373.1, EAX10375.1, EAX10376.1, EAX10374.1
GeneID:5332	PLCB4	20	9,049,701	9,461,463	411,762	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3493	167	in gene	1	0	0	16	14	13	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene PLCB4	FLJ16169, PI-PLC, PLCB4	phospholipase C, beta 4	NM_000933, NM_182797, NM_001172646, hCT1951358.1, hCT2314129.0, hCT2314130.0, hCT2314133.0, hCT2314134.0, hCT2314135.0, hCT30885.2	203895_at, 203896_s_at, 240728_at	NP_000924.3, NP_877949.2, NP_001166117.1, EAX10365.1, EAX10368.1, EAX10370.1, EAX10364.1, EAX10366.1, EAX10367.1, EAX10369.1
GeneID:100131208	LOC100131208	20	10,004,460	10,200,151	195,691	-	8	1_A375_pNL7_minus_lncRNA_AR..1..3494, 1_A375_pNL7_minus_lncRNA_AR..1..3495, 1_A375_pNL7_minus_lncRNA_AR..1..3496, 2_A375_pNL97_plus_lncRNA_AR..1..4998, 2_A375_pNL97_plus_lncRNA_AR..1..4999, 2_A375_pNL97_plus_lncRNA_AR..1..5000, 2_A375_pNL97_plus_lncRNA_AR..1..5001, 4_A375_EGR1..1..5249	159063, 126231, -105, 179255, 156951, 1335, -105, 47175	in gene, in gene, upstream, in gene, in gene, in gene, upstream, in gene	1	1	1	21.5	22.67	7.67	6	2_A375_pNL97_plus_lncRNA_AR..1	57	Gene LOC100131208		similar to hCG2045625	XR_112120, XR_109646, XR_115343		
GeneID:63926	ANKRD5	20	10,015,697	10,037,407	21,710	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3494, 2_A375_pNL97_plus_lncRNA_AR..1..4998, 2_A375_pNL97_plus_lncRNA_AR..1..4999	25391, 5199, 25503	downstream, in gene, downstream	1	1	0	20.5	17.5	3	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ANKRD5	FLJ21669, ANKRD5, dJ839B4.6	ankyrin repeat domain 5	NM_022096, NM_198798, hCT1951357.1	220144_s_at, 222951_s_at	NP_071379.3, NP_942093.1, EAX10355.1
GeneID:6616	SNAP25	20	10,199,477	10,288,065	88,588	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3496, 2_A375_pNL97_plus_lncRNA_AR..1..5000, 2_A375_pNL97_plus_lncRNA_AR..1..5001	779, -661, 779	in gene, upstream, in gene	1	1	0	30	38.5	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	57	Gene SNAP25	FLJ23079, SNAP-25, RIC-4, dJ1068F16.2, RIC4, SNAP, bA416N4.2, SNAP25, SEC9	synaptosomal-associated protein, 25kDa	NM_003081, NM_130811, hCT1961808.1, hCT1961809.1, hCT1967865.1, hCT2359538.0, hCT2359539.0, hCT2359540.0, hCT2359541.0, hCT31490.3	1556629_a_at, 202507_s_at, 202508_s_at	NP_003072.2, NP_570824.1, EAX10346.1, EAX10347.1, EAX10350.1, EAX10352.1, EAX10348.1, EAX10349.1, EAX10351.1, EAX10353.1
GeneID:8195	MKKS	20	10,385,832	10,414,866	29,034	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3497, 2_A375_pNL97_plus_lncRNA_AR..1..5002	-174, 50	upstream, in gene	1	1	0	25	27	19	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene MKKS	KMS, MKS, HMCS, MKKS, BBS6	McKusick-Kaufman syndrome	NM_018848, NM_170784, hCT1951356.1, hCT2359542.0, hCT31491.3	218138_at, 222530_s_at	NP_061336.1, NP_740754.1, EAX10343.1, EAX10344.1, EAX10345.1
GeneID:128710	C20orf94	20	10,415,951	10,604,027	188,076	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3497, 1_A375_pNL7_minus_lncRNA_AR..1..3498, 2_A375_pNL97_plus_lncRNA_AR..1..5002	-911, 163313, -1135	upstream, in gene, upstream	1	1	0	19.5	19.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene C20orf94	bA254M13.1, bA204H22.1, dJ1099D15.3, C20orf94	chromosome 20 open reading frame 94	NM_001009608, hCT31492.2	236390_at	NP_001009608.1, EAX10342.1
GeneID:182	JAG1	20	10,618,332	10,654,694	36,362	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5003	-262	upstream	0	1	0	15	18	9	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene JAG1	MGC104644, CD339, HJ1, JAGL1, AWS, AGS, JAG1, AHD	jagged 1 (Alagille syndrome)	NM_000214, hCT29369.3	209097_s_at, 209098_s_at, 209099_x_at, 216268_s_at, 229924_s_at, 231183_s_at	NP_000205.1, EAX10341.1
GeneID:140862	ISM1	20	13,202,418	13,281,297	78,879	+	1	4_A375_EGR1..1..5252	-1154	upstream	0	0	1	5	9	15	1	4_A375_EGR1..1	15	Gene ISM1	isthmin, C20orf82, ISM1, ISM, bA149I16.1, dJ1077I2.1	isthmin 1 homolog (zebrafish)	NM_080826	232688_at, 235182_at	NP_543016.1
GeneID:51575	ESF1	20	13,694,969	13,765,532	70,563	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5008, 4_A375_EGR1..1..5253	-100, -132	upstream, upstream	0	1	1	15	20	17	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ESF1	C20orf6, ESF1, bA526K24.1, ABTAP, HDCMC28P, FLJ20366	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	NM_016649, hCT2313662.0	218659_s_at, 222765_x_at	NP_057733.2, EAX10313.1
GeneID:79133	C20orf7	20	13,765,672	13,799,087	33,395	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5008, 4_A375_EGR1..1..5253	-40, -8	upstream, upstream	0	1	1	15	20	17	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C20orf7	MGC90272, FLJ22324, bA526K24.2, dJ842G6.1, C20orf7	chromosome 20 open reading frame 7	NM_024120, NM_001039375, NR_029377	222894_x_at, 227160_s_at	NP_077025.2, NP_001034464.1
GeneID:140733	MACROD2	20	13,976,146	16,033,842	2,057,696	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3504, 2_A375_pNL97_plus_lncRNA_AR..1..5009, 1_A375_pNL7_minus_lncRNA_AR..1..3505	293614, 869742, 1704142	in gene, in gene, in gene	1	1	0	16	18.67	5	3	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene MACROD2	dJ631M13.5, MACROD2, C20orf133	MACRO domain containing 2	NM_001033087, NM_080676	1553564_at, 1561677_at, 1563209_a_at, 235278_at	NP_001028259.1, NP_542407.2
GeneID:55614	KIF16B	20	16,252,749	16,554,078	301,329	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3506, 2_A375_pNL97_plus_lncRNA_AR..1..5011	-1442, 14	upstream, in gene	1	1	0	18.5	17	11	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene KIF16B	KIF16B, C20orf23, KISC20ORF, SNX23	kinesin family member 16B	NM_024704, hCT1951347.1, hCT2313765.0, hCT2313768.0, hCT2313769.0	219570_at, 232083_at	NP_078980.3, EAX10287.1, EAX10288.1, EAX10289.1, EAX10290.1
GeneID:6629	SNRPB2	20	16,710,609	16,722,417	11,808	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3507, 2_A375_pNL97_plus_lncRNA_AR..1..5012	-17, 15	upstream, in gene	1	1	0	60	76	14	1	2_A375_pNL97_plus_lncRNA_AR..1	76	Gene SNRPB2	MGC24807, MGC45309, Msl1, SNRPB2	small nuclear ribonucleoprotein polypeptide B''	NM_198220, NM_003092, hCT1961785.1, hCT2313838.0, hCT29395.2	1561965_at, 202505_at	NP_937863.1, NP_003083.1, EAX10284.1, EAX10285.1, EAX10286.1
GeneID:5126	PCSK2	20	17,207,631	17,465,223	257,592	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3508, 1_A375_pNL7_minus_lncRNA_AR..1..3509, 2_A375_pNL97_plus_lncRNA_AR..1..5016, 2_A375_pNL97_plus_lncRNA_AR..1..5017, 2_A375_pNL97_plus_lncRNA_AR..1..5018	753, 190417, -335, 669, 190417	in gene, in gene, upstream, in gene, in gene	1	1	0	20.33	25.67	5.67	3	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene PCSK2	PC2, NEC2, NEC-2, PCSK2, SPC2	proprotein convertase subtilisin/kexin type 2	NM_002594, hCT2313869.0, hCT2359566.0, hCT30932.3	204869_at, 204870_s_at	NP_002585.2, EAX10279.1, EAX10280.1, EAX10281.1
GeneID:11034	DSTN	20	17,550,599	17,588,652	38,053	+	2	4_A375_EGR1..1..5254, 4_A375_EGR1..1..5255	41177, 45721	downstream, downstream	0	0	1	5.5	8.5	17.5	2	4_A375_EGR1..1	19	Gene DSTN	ACTDP, bA462D18.2, ADF, DSTN	destrin (actin depolymerizing factor)	NM_006870, NM_001011546, hCT2313872.0, hCT2313873.0, hCT2359544.0	201021_s_at, 201022_s_at, 230933_at	NP_006861.1, NP_001011546.1, EAX10274.1, EAX10275.1, EAX10276.1
GeneID:6238	RRBP1	20	17,594,323	17,662,928	68,605	-	2	4_A375_EGR1..1..5254, 4_A375_EGR1..1..5255	71152, 66608	downstream, in gene	0	0	1	5.5	8.5	17.5	2	4_A375_EGR1..1	19	Gene RRBP1	RRBP1, FLJ38146, hES, MGC157721, DKFZp586A1420, ES130, MGC157720, ES/130	ribosome binding protein 1 homolog 180kDa (dog)	NM_001042576, NM_004587, hCT30931.3	201203_s_at, 201204_s_at, 201206_s_at, 213495_s_at, 213973_at, 227686_at	NP_001036041.1, NP_004578.2, EAX10273.1
GeneID:27131	SNX5	20	17,922,244	17,949,490	27,246	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3511, 2_A375_pNL97_plus_lncRNA_AR..1..5021	210, 162	in gene, in gene	1	1	0	23	30	19	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SNX5	SNX5, FLJ10931	sorting nexin 5	NM_014426, NM_152227, hCT2313915.0, hCT2313917.0, hCT2313918.0, hCT2313920.0, hCT2313922.0, hCT2359494.0	217792_at, 222417_s_at, 223666_at, 229980_s_at, 229981_at, 238433_at	NP_055241.1, NP_689413.1, EAX10263.1, EAX10264.1, EAX10265.1, EAX10266.1, EAX10268.1, EAX10267.1
GeneID:692086	SNORD17	20	17,943,353	17,943,589	236	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3511, 2_A375_pNL97_plus_lncRNA_AR..1..5021	-5691, -5739	upstream, upstream	1	1	0	23	30	19	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SNORD17	SNORD17, HBI-43	small nucleolar RNA, C/D box 17	NR_003045		
GeneID:92667	C20orf72	20	17,949,762	17,971,761	21,999	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3511, 2_A375_pNL97_plus_lncRNA_AR..1..5021	-482, -434	upstream, upstream	1	1	0	23	30	19	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene C20orf72	C20orf72, FLJ14597, bA504H3.4	chromosome 20 open reading frame 72	NM_052865, hCT1967818.1, hCT2314015.0, hCT29766.3	225890_at	NP_443097.1, EAX10262.1, EAX10260.1, EAX10261.1
GeneID:58495	OVOL2	20	18,004,796	18,038,521	33,725	-	1	4_A375_EGR1..1..5256	313	in gene	0	0	1	6	9	16	1	4_A375_EGR1..1	16	Gene OVOL2	EUROIMAGE566589, OVOL2, ZNF339	ovo-like 2 (Drosophila)	NM_021220, hCT2313914.0, hCT2313921.0	206048_at, 211778_s_at	NP_067043.2, EAX10259.1, EAX10258.1
GeneID:100303755	PET117	20	18,118,499	18,123,813	5,314	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3512, 2_A375_pNL97_plus_lncRNA_AR..1..5022, 4_A375_EGR1..1..5257, 4_A375_EGR1..1..5258	-3, -3, -259, 109	upstream, upstream, upstream, in gene	1	1	1	44	44	17	1	1_A375_pNL7_minus_lncRNA_AR..1	44	Gene PET117		cytochrome c oxidase assembly factor-like	NM_001164811		NP_001158283.1
GeneID:57325	CSRP2BP	20	18,122,868	18,169,031	46,163	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3512, 2_A375_pNL97_plus_lncRNA_AR..1..5022, 4_A375_EGR1..1..5257, 4_A375_EGR1..1..5258	-4372, -4372, -4628, -4260	upstream, upstream, upstream, upstream	1	1	1	44	44	17	1	1_A375_pNL7_minus_lncRNA_AR..1	44	Gene CSRP2BP	CSRP2BP, PRO1194, CRP2BP, KAT14, dJ717M23.1, MGC15388	CSRP2 binding protein	NR_026402, NM_020536, hCT1823052.1, hCT1827847.3, hCT2359543.0	225432_s_at, 227316_at, 228543_at, 228544_s_at, 233396_s_at	NP_065397.3, EAX10255.1, EAX10254.1, EAX10256.1
GeneID:7692	ZNF133	20	18,269,121	18,297,640	28,519	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5023, 4_A375_EGR1..1..5259	-193, 143	upstream, in gene	0	1	1	15	21	20	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ZNF133	pHZ-66, ZNF150, ZNF133, pHZ-13	zinc finger protein 133	NM_003434, NM_001083330, hCT2349558.0, hCT2349559.0, hCT2349560.0, hCT2349561.0, hCT2349562.0	216960_s_at, 37254_at	NP_003425.2, NP_001076799.1, EAX10249.1, EAX10250.1, EAX10251.1, EAX10252.1, EAX10253.1
GeneID:55184	C20orf12	20	18,364,011	18,447,829	83,818	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3513, 1_A375_pNL7_minus_lncRNA_AR..1..3514, 2_A375_pNL97_plus_lncRNA_AR..1..5024	53893, -91, -43	in gene, upstream, upstream	1	1	0	21	17	8.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene C20orf12	FLJ10600, bA189K21.1, FLJ30892, dJ568F9.2, bA189K21.8, DKFZp761J2425, C20orf12, C20orf84	chromosome 20 open reading frame 12	NM_001099407, hCT12770.3, hCT2313905.0, hCT2313906.0, hCT2313907.0, hCT2359565.0	1554616_s_at, 219951_s_at	NP_001092877.1, EAX10244.1, EAX10242.1, EAX10243.1, EAX10245.1, EAX10246.1

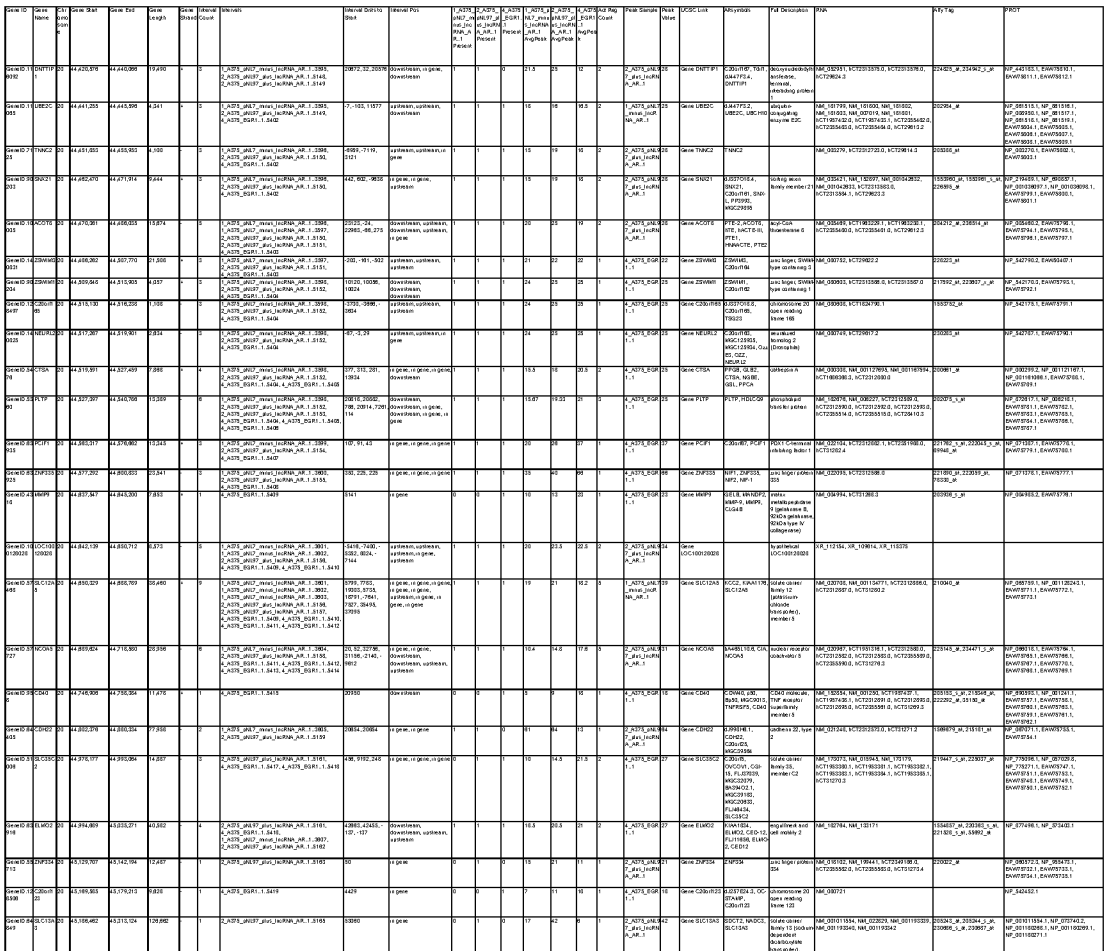
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.10621	POLR3F	20	18,448,033	18,465,287	17,254	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3514, 2_A375_pNL97_plus_lncRNA_AR..1..5024	-113, -161	upstream, upstream	1	1	0	24	24	14	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene POLR3F	RPC39, POLR3F, RPC6, MGC13517	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	NM_006466, hCT12216.2, hCT2359567.0, hCT2359568.0	205218_at	NP_006457.2, EAX10240.1, EAX10239.1, EAX10241.1
GeneID.100422875	MIR3192	20	18,451,259	18,451,335	76	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3514, 2_A375_pNL97_plus_lncRNA_AR..1..5024	-3339, -3387	upstream, upstream	1	1	0	24	24	14	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene MIR3192	MIR3192	microRNA 3192	NR_036160		
GeneID.10741	RBBP9	20	18,467,184	18,477,887	10,703	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5025	47	in gene	0	1	0	8	19	10	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene RBBP9	RBBP10, RBBP9, BOG, MGC9236	retinoblastoma binding protein 9	NM_006606, hCT12768.3, hCT2313903.0, hCT2359564.0	221439_at, 221440_s_at, 226696_at, 232751_at	NP_006597.2, EAX10236.1, EAX10237.1, EAX10238.1
GeneID.10483	SEC23B	20	18,488,188	18,542,059	53,871	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3515, 2_A375_pNL97_plus_lncRNA_AR..1..5026	198, 226	in gene, in gene	1	1	0	21	13	10	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene SEC23B	CDAN2, CDA-II, HEMPAS, CDAII, SEC23B	Sec23 homolog B (S. cerevisiae)	NM_006363, NM_032986, NM_032985, NM_001172745, NM_001172746, hCT12766.3, hCT1967765.1, hCT1967766.1, hCT2314030.0, hCT2359563.0	201582_at, 201583_s_at, 210293_s_at	NP_006354.2, NP_116781.1, NP_116780.1, NP_001166216.1, NP_001166217.1, EAX10232.1, EAX10231.1, EAX10233.1, EAX10234.1, EAX10235.1
GeneID.92675	DTD1	20	18,568,556	18,744,561	176,005	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5027	-26	upstream	0	1	0	11	16	7	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene DTD1	DUEB, MGC41905, DTD1, bA379J5.3, bA555E18.1, C20orf88, MGC119131, pqn-68, HARS2	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	NM_080820, hCT2349563.0, hCT2359553.0	1552718_at, 234107_s_at	NP_543010.3, EAX10227.1, EAX10228.1
GeneID.57419	SLC24A3	20	19,193,290	19,703,541	510,251	+	1	4_A375_EGR1..1..5260	427254	in gene	0	0	1	7	3	17	1	4_A375_EGR1..1	17	Gene SLC24A3	SLC24A3, NCKX3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	NM_020689, hCT13552.3, hCT2313594.0	219090_at, 57588_at	NP_065740.2, EAX10219.1, EAX10220.1
GeneID.51126	NAA20	20	19,997,937	20,014,269	16,332	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3517, 2_A375_pNL97_plus_lncRNA_AR..1..5029	15, 15	in gene, in gene	1	1	0	25	26	12	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene NAA20	dJ1002M8.1, NAT3, NAT5, NAA20	N(alpha)-acetyltransferase 20, NatB catalytic subunit	NM_181528, NM_181527, NM_016100, hCT12189.3, hCT1957535.2, hCT2349557.0	223040_at	NP_852669.1, NP_852668.1, NP_057184.1, EAX10213.1, EAX10214.1, EAX10215.1
GeneID.51340	CRNKL1	20	20,015,012	20,036,890	21,878	-	1	4_A375_EGR1..1..5261	3826	in gene	0	0	1	15	16	18	1	4_A375_EGR1..1	18	Gene CRNKL1	Clf1, MSTP021, HCRN, CRNKL1, CRN, SYF3, CLF	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	NM_016652, hCT13556.3, hCT1967783.1, hCT2313612.0, hCT2313613.0, hCT2313615.0, hCT2359561.0, hCT2359562.0	219913_s_at	NP_057736.4, EAX10208.1, EAX10206.1, EAX10207.1, EAX10209.1, EAX10211.1, EAX10210.1, EAX10212.1
GeneID.26074	C20orf26	20	20,033,158	20,341,346	308,188	+	1	4_A375_EGR1..1..5261	-294	upstream	0	0	1	15	16	18	1	4_A375_EGR1..1	18	Gene C20orf26	dJ1002M8.3, C20orf26, dJ1178H5.4, DKFZp434K156	chromosome 20 open reading frame 26	NM_015585, NM_001167816, hCT2349577.0, hCT2349578.0, hCT2359525.0	1554657_a_at, 233389_at, 240453_at	NP_056400.3, NP_001161288.1, EAX10202.1, EAX10203.1, EAX10204.1
GeneID.57186	RALGAPA2	20	20,373,411	20,693,266	319,855	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3518, 2_A375_pNL97_plus_lncRNA_AR..1..5030	17138, 17138	in gene, in gene	1	1	0	25	25	4	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene RALGAPA2	FLJ12819, dJ1049G11, C20orf74, KIAA1272, RALGAPA2, bA287B20.1, AS250, dJ1049G11.4	Ral GTPase activating protein, alpha subunit 2 (catalytic)	NM_020343	1559699_at, 231826_at, 232500_at, 234314_at, 234934_at, 239680_at	NP_065076.2
GeneID.22803	XRN2	20	21,283,942	21,370,463	86,521	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3519, 2_A375_pNL97_plus_lncRNA_AR..1..5031	394, -230	in gene, upstream	1	1	0	25	15	11	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene XRN2	XRN2		NM_012255, hCT12168.3, hCT2313842.0	223002_s_at, 233878_s_at	NP_036387.2, EAX10187.1, EAX10186.1
GeneID.4821	NKX2-2	20	21,491,648	21,494,664	3,016	-	1	4_A375_EGR1..1..5263	8248	downstream	0	0	1	9	13	14	1	4_A375_EGR1..1	14	Gene NKX2-2	NKX2-2, NKX2.2, NKX2B	NK2 homeobox 2	NM_002509, hCT13291.3	206915_at	NP_002500.1, EAX10183.1
GeneID.5075	PAX1	20	21,686,297	21,696,620	10,323	+	1	4_A375_EGR1..1..5264	583	in gene	0	0	1	6	5	14	1	4_A375_EGR1..1	14	Gene PAX1	PAX1, HUP48	paired box 1	NM_006192, hCT2313618.0	1553492_a_at, 214401_at	NP_006183.2, EAX10180.1
GeneID.140828	C20orf56	20	22,541,191	22,559,280	18,089	-	1	4_A375_EGR1..1..5265	-8176	upstream	0	0	1	3	4	16	1	4_A375_EGR1..1	16	Gene C20orf56	NCRNA00261, bA216C10.1, dJ788L20.2, C20orf56	chromosome 20 open reading frame 56	NR_001558	228004_at	
GeneID.3170	FOXA2	20	22,561,642	22,566,101	4,459	-	1	4_A375_EGR1..1..5265	-1355	upstream	0	0	1	3	4	16	1	4_A375_EGR1..1	16	Gene FOXA2	HNF3B, FOXA2, MGC19807, TCF3B	forkhead box A2	NM_153675, NM_021784, hCT13255.3, hCT2313314.0	210103_s_at, 214312_at, 40284_at	NP_710141.1, NP_068556.2, EAX10174.1, EAX10175.1
GeneID.29107	NXT1	20	23,331,373	23,335,408	4,035	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3521, 2_A375_pNL97_plus_lncRNA_AR..1..5035, 2_A375_pNL97_plus_lncRNA_AR..1..5036, 4_A375_EGR1..1..5267	11187, -461, 10995, 11731	downstream, upstream, downstream, downstream	1	1	1	16	16.67	12.67	3	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene NXT1	NXT1, MTR2, P15	NTF2-like export factor 1	NM_013248, hCT13460.2	218708_at	NP_037380.1, EAX10163.1
GeneID.100505683	LOC100505683	20	23,337,231	23,338,642	1,411		4	1_A375_pNL7_minus_lncRNA_AR..1..3521, 2_A375_pNL97_plus_lncRNA_AR..1..5035, 2_A375_pNL97_plus_lncRNA_AR..1..5036, 4_A375_EGR1..1..5267	-3916, 7730, -3726, -4462	upstream, downstream, upstream, upstream	1	1	1	16	16.67	12.67	3	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene LOC100505683		hypothetical LOC100505683	XR_109654, XR_115351		
GeneID.64412	GZF1	20	23,345,021	23,353,683	8,662	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3521, 2_A375_pNL97_plus_lncRNA_AR..1..5036, 4_A375_EGR1..1..5267	-2461, -2653, -1917	upstream, upstream, upstream	1	1	1	16	15	13	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene GZF1	ZNF336, GZF1, ZBTB23	GDNF-inducible zinc finger protein 1	NM_022482, hCT13462.4, hCT2313400.1, hCT2313401.1	225684_s_at, 234055_s_at	NP_071927.1, EAX10160.1, EAX10159.1, EAX10161.1
GeneID.79953	TMEM90B	20	24,449,835	24,647,167	197,332	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5037	165909	in gene	0	1	0	8	18	7	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TMEM90B	C20orf39, TMEM90B, IFITMD5, FLJ14220	transmembrane protein 90B	NM_024893, hCT8749.2	219310_at	NP_079169.1, EAX10117.1
GeneID.57136	C20orf3	20	24,943,560	24,973,425	29,845	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3522, 2_A375_pNL97_plus_lncRNA_AR..1..5038, 4_A375_EGR1..1..5269	113, 209, -79	in gene, in gene, upstream	1	1	1	24	16	17	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene C20orf3	C20orf3, BSCv, APMAP	chromosome 20 open reading frame 3	NM_020531, hCT2359577.0, hCT8667.3	206656_s_at	NP_065392.1, EAX10114.1, EAX10113.1
GeneID.84532	ACSS1	20	24,986,873	25,039,616	52,743	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3523, 2_A375_pNL97_plus_lncRNA_AR..1..5039, 4_A375_EGR1..1..5270, 4_A375_EGR1..1..5271	3808, 3792, 1664, 368	in gene, in gene, in gene, in gene	1	1	1	16	19.67	14.67	3	1_A375_pNL7_minus_lncRNA_AR..1	35	Gene ACSS1	AceCS2L, MGC33843, ACSS1, ACAS2L, FLJ45659	acyl-CoA synthetase short-chain family member 1	NM_032501, hCT2313252.0, hCT2313254.0, hCT2359531.0, hCT2359532.0, hCT2359533.0, hCT8681.2	224882_at, 234483_at, 234484_s_at, 234801_s_at, 235724_at	NP_115890.2, EAX10106.1, EAX10108.1, EAX10109.1, EAX10110.1, EAX10111.1, EAX10107.1
GeneID.955	ENTPD6	20	25,176,339	25,207,360	31,021	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3525, 2_A375_pNL97_plus_lncRNA_AR..1..5041, 2_A375_pNL97_plus_lncRNA_AR..1..5042	27597, -211, 27597	in gene, upstream, in gene	1	1	0	16	18.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ENTPD6	FLJ36711, ENTPD6, NTPDase-6, DKFZp781G2277, DKFZp781K21102, CD39L2, IL6ST2, dJ738P15.3, IL-6SAG	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	NM_001247, NM_001114089, hCT1966537.1, hCT2313387.0, hCT2359529.0, hCT2359530.0, hCT8679.3	201704_at, 234946_at	NP_001238.2, NP_001107561.1, EAX10095.1, EAX10096.1, EAX10097.1, EAX10098.1, EAX10099.1
GeneID.5834	PYGB	20	25,228,706	25,278,648	49,942	+	5	2_A375_pNL97_plus_lncRNA_AR..1..5043, 4_A375_EGR1..1..5272, 4_A375_EGR1..1..5273, 4_A375_EGR1..1..5274, 4_A375_EGR1..1..5275	-10146, 34142, 35566, 44270, 49502	upstream, in gene, in gene, in gene, in gene	0	1	1	9.8	14.2	15.8	5	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene PYGB	MGC9213, PYGB	phosphorylase, glycogen; brain	NM_002862, hCT1961632.1, hCT1966536.1, hCT8678.3	201481_s_at, 243238_at	NP_002853.2, EAX10092.1, EAX10091.1, EAX10093.1
GeneID.26090	ABHD12	20	25,275,379	25,371,477	96,098	-	4	2_A375_pNL97_plus_lncRNA_AR..1..5044, 4_A375_EGR1..1..5274, 4_A375_EGR1..1..5275, 4_A375_EGR1..1..5276	80981, 96501, 93269, 949	in gene, downstream, in gene, in gene	0	1	1	7.75	13.25	15.5	4	4_A375_EGR1..1	19	Gene ABHD12	PHARC, ABHD12, C20orf22, dJ965G21.2, BEM46L2, ABHD12A, DKFZp434P106	abhydrolase domain containing 12	NM_001042472, NM_015600, hCT1966538.1, hCT1966539.1, hCT8665.4	224742_at, 226123_s_at, 228124_at	NP_001035937.1, NP_056415.1, EAX10088.1, EAX10089.1, EAX10090.1
GeneID.9837	GINS1	20	25,388,323	25,429,191	40,868	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5045	29	in gene	0	1	0	16	26	7	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene GINS1	PSF1, KIAA0186, GINS1	GINS complex subunit 1 (Psf1 homolog)	NM_021067, hCT8668.3	206102_at	NP_066545.3, EAX10087.1
GeneID.22981	NINL	20	25,433,337	25,566,153	132,816	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3526	86249	in gene	1	0	0	26	24	5	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene NINL	NINL, KIAA0980, dJ691N24.1, FLJ11792, NLP	ninein-like	NM_025176, hCT1956868.1, hCT1956867.1, hCT2313340.0, hCT2359572.0, hCT8663.3	207705_s_at	NP_079452.3, EAX10085.1, EAX10082.1, EAX10083.1, EAX10084.1, EAX10086.1
GeneID.140838	NANP	20	25,593,571	25,604,648	11,077	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3527, 2_A375_pNL97_plus_lncRNA_AR..1..5046, 4_A375_EGR1..1..5277	-164, 232, -66	upstream, in gene, upstream	1	1	1	21	19	26	1	4_A375_EGR1..1	26	Gene NANP	MGC26833, C20orf147, NANP, HDHD4, dJ694B14.3	N-acetylneuraminic acid phosphatase	NM_152667, hCT8664.3	228073_at	NP_689880.1, EAX10081.1
GeneID.26152	ZNF337	20	25,654,851	25,677,469	22,618	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3528, 2_A375_pNL97_plus_lncRNA_AR..1..5047	-35, 253	upstream, in gene	1	1	0	27	28	9	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene ZNF337	ZNF337	zinc finger protein 337	NM_015655, hCT2313334.0, hCT8660.3	214760_at, 37860_at	NP_056470.1, EAX10077.1, EAX10078.1
GeneID.728882	FAM182B	20	25,744,102	25,781,927	37,825		1	4_A375_EGR1..1..5278	26587	in gene	0	0	1	5	2	11	1	4_A375_EGR1..1	11	Gene FAM182B	MGC51338, FAM182B, DKFZp434B104	family with sequence similarity 182, member B	NR_027061, NR_026714		
GeneID.81502	HM13	20	30,102,241	30,157,370	55,129	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3529, 1_A375_pNL7_minus_lncRNA_AR..1..3530, 2_A375_pNL97_plus_lncRNA_AR..1..5048, 4_A375_EGR1..1..5281	95, 58387, 223, 191	in gene, downstream, in gene, in gene	1	1	1	22.5	15	16.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene HM13	IMPAS, PSENL3, IMP1, HM13, PSL3, MSTP086, SPP, IMPAS-1, dJ324O17.1, H13	histocompatibility (minor) 13	NM_178580, NM_178581, NM_178582, NM_030789, hCT1964352.1, hCT2314098.0, hCT2355465.0, hCT28825.3	1557148_at, 1558581_at, 224615_x_at, 232209_x_at	NP_848695.1, NP_848696.1, NP_110416.1, NP_848697.1, EAW76435.1, EAW76436.1, EAW76437.1, EAW76438.1
GeneID.598	BCL2L1	20	30,252,261	30,310,656	58,395	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3531, 2_A375_pNL97_plus_lncRNA_AR..1..5050, 4_A375_EGR1..1..5282, 4_A375_EGR1..1..5283	-640, -664, 32, -448	upstream, upstream, in gene, upstream	1	1	1	17	21	18	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene BCL2L1	bcl-xL, BCL2L, BCLXL, BCL2L1, BCLX, Bcl-X, BCL-XL/S, DKFZp781P2092, BCLXS, bcl-xS	BCL2-like 1	NM_001191, NM_138578, hCT2313721.0, hCT2313722.0, hCT2313723.0, hCT2313724.0, hCT2313725.0, hCT30057.3	206665_s_at, 212312_at, 215037_s_at, 231228_at	NP_001182.1, NP_612815.1, EAW76424.1, EAW76425.1, EAW76426.1, EAW76427.1, EAW76428.1, EAW76429.1
GeneID.22974	TPX2	20	30,326,904	30,389,603	62,699	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3532, 2_A375_pNL97_plus_lncRNA_AR..1..5051	264, 138	in gene, in gene	1	1	0	19	18	12	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene TPX2	REPP86, C20orf2, GD:C20orf1, HCTP4, TPX2, DIL2, DIL-2, FLS353, HCA519, p100, C20orf1	TPX2, microtubule-associated, homolog (Xenopus laevis)	NM_012112, hCT1951803.1, hCT2314059.0, hCT2314060.0, hCT2355570.0, hCT30067.3	210052_s_at	NP_036244.2, EAW76419.1, EAW76418.1, EAW76420.1, EAW76421.1, EAW76422.1
GeneID.85366	MYLK2	20	30,407,178	30,422,500	15,322	+	1	4_A375_EGR1..1..5284	25398	downstream	0	0	1	5	6	17	1	4_A375_EGR1..1	17	Gene MYLK2	MLCK2, KMLC, MLCK, MYLK2, skMLCK	myosin light chain kinase 2	NM_033118, hCT2314064.0, hCT2355572.0, hCT2355573.0, hCT30068.2	231792_at	NP_149109.1, EAW76416.1, EAW76414.1, EAW76415.1, EAW76417.1
GeneID.2307	FOXS1	20	30,432,103	30,433,420	1,317	-	1	4_A375_EGR1..1..5284	644	in gene	0	0	1	5	6	17	1	4_A375_EGR1..1	17	Gene FOXS1	FREAC10, MGC4544, FKHL18, FOXS1	forkhead box S1	NM_004118	229731_at	NP_004109.1
GeneID.83747	C20orf57	20	30,436,207	30,446,117	9,910	-	1	4_A375_EGR1..1..5284	13541	downstream	0	0	1	5	6	17	1	4_A375_EGR1..1	17	Gene C20orf57	bA243J16.5, C20orf57, FLJ20645	chromosome 20 open reading frame 57	XR_112136, XR_109823, XR_115353	234629_at	
GeneID.128853	DUSP15	20	30,448,870	30,458,479	9,609	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5052	207	in gene	0	1	0	13	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene DUSP15	DUSP15, FLJ40111, VHY	dual specificity phosphatase 15	NM_080611, NM_177991, NM_001012644, hCT2313705.0, hCT30064.2	230402_at	NP_542178.2, NP_817130.1, NP_001012662.1, EAW76409.1, EAW76410.1
GeneID.164395	TTLL9	20	30,458,505	30,530,858	72,353	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5052	-233	upstream	0	1	0	13	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TTLL9	C20orf125, TTLL9, MGC120486, dJ310O13.1, MGC120487	tubulin tyrosine ligase-like family, member 9	NM_001008409, hCT2314067.0, hCT2314068.0, hCT2314069.0, hCT2314070.0, hCT2355537.0, hCT2355538.0, hCT2355539.0, hCT30059.3	232357_at, 234336_s_at, 234337_at	NP_001008409.1, EAW76405.1, EAW76402.1, EAW76404.1, EAW76407.1, EAW76406.1, EAW76401.1, EAW76403.1, EAW76408.1
GeneID.343702	XKR7	20	30,555,805	30,586,256	30,451	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3533, 2_A375_pNL97_plus_lncRNA_AR..1..5053, 4_A375_EGR1..1..5285	611, 579, 547	in gene, in gene, in gene	1	1	1	56	71	20	1	2_A375_pNL97_plus_lncRNA_AR..1	71	Gene XKR7	XKR7, C20orf159, dJ310O13.4	XK, Kell blood group complex subunit-related family, member 7	NM_001011718, hCT30063.3		NP_001011718.1, EAW76398.1
GeneID.3055	HCK	20	30,639,991	30,689,659	49,668	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3534	57449	downstream	1	0	0	22	11	6	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene HCK	JTK9, HCK	hemopoietic cell kinase	NM_002110, NM_001172129, NM_001172130, NM_001172131, NM_001172132, NM_001172133, hCT2314079.0, hCT2314080.0, hCT30056.3	208018_s_at	NP_002101.2, NP_001165600.1, NP_001165601.1, NP_001165602.1, NP_001165603.1, NP_001165604.1, EAW76392.1, EAW76393.1, EAW76394.1
GeneID.9777	TM9SF4	20	30,697,309	30,755,061	57,752	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3534	131	in gene	1	0	0	22	11	6	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene TM9SF4	KIAA0255, TM9SF4, dJ836N17.2	transmembrane 9 superfamily protein member 4	NM_014742, hCT2314082.0, hCT2355490.0, hCT30055.3	212194_s_at, 212198_s_at	NP_055557.2, EAW76391.1, EAW76389.1, EAW76390.1
GeneID.5326	PLAGL2	20	30,780,307	30,795,546	15,239	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3535, 4_A375_EGR1..1..5286	-134, 17650	upstream, downstream	1	0	1	11.5	11	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene PLAGL2	ZNF900, FLJ23283, PLAGL2	pleiomorphic adenoma gene-like 2	NM_002657, hCT2313688.0, hCT30054.3	202924_s_at, 202925_s_at	NP_002648.1, EAW76388.1, EAW76387.1
GeneID.23509	POFUT1	20	30,795,696	30,826,467	30,771	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3535	-16	upstream	1	0	0	16	15	10	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene POFUT1	O-FUT, FUT12, O-Fuc-T, O-FucT-1, MGC2482, POFUT1, KIAA0180	protein O-fucosyltransferase 1	NM_015352, NM_172236, hCT2314084.0, hCT2314086.0, hCT30065.2	210433_at, 212349_at	NP_056167.1, NP_758436.1, EAW76383.1, EAW76384.1, EAW76385.1
GeneID.100506402	LOC100506402	20	30,922,055	30,939,859	17,804	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3536, 2_A375_pNL97_plus_lncRNA_AR..1..5054	-6029, -6253	upstream, upstream	1	1	0	23	21	13	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene LOC100506402		hypothetical LOC100506402	XR_112137, XR_109831, XR_115354		
GeneID.171023	ASXL1	20	30,946,147	31,027,122	80,975	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3536, 2_A375_pNL97_plus_lncRNA_AR..1..5054	-259, -35	upstream, upstream	1	1	0	23	21	13	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene ASXL1	MGC71111, KIAA0978, ASXL1, MGC117280	additional sex combs like 1 (Drosophila)	NM_015338, NM_001164603, hCT2314198.0, hCT2355545.0, hCT2355546.0, hCT30062.3	212234_at, 212237_at, 212238_at, 244519_at	NP_056153.2, NP_001158075.1, EAW76377.1, EAW76378.1, EAW76379.1, EAW76380.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_2_A375_4_A375_1_A375_2_A375_4_A375_Adjusted Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
GeneID:14	4C20orf12	20	31,230,992	31,271,395	40,404	+	4	1_A375_shG7_mrna_lncRNA_AR_1:3327-2_A375_shG7_dun_lncRNA_AR_1:3033-3_A375_shG7_dun_lncRNA_AR_1:3098-4_A375_DGR1_1:3207	19632, 19940, 744, 10744	sr gene, sr gene, cn gene	1	1	1	10.33	16	16	3	2_A375_shLK28 T_dun_lncRNA_AR_1	Gene C20orf12	DKFZp686G1442, bA516F4.4, C20orf112, bA516F4.2, C20orf112	chromosome 20 open reading frame 112	NM_018618, NCT03139940.0, NCT03139941.0, NCT03139942.0, NCT03139943.0, NCT03139944.0, NCT03139946.0, NCT03139947.0	220324_at_220954_at, 220955_s_at_224351_at, 241630_at	NP_542163.2, EAW78339.1, EAW78340.1, EAW78341.1, EAW78360.1, EAW78372.1, EAW78383.1, EAW78371.1
GeneID:15	LOC100505937	20	31,973,787	31,124,451	50,664	+	2	2_A375_shG7_dun_lncRNA_AR_1:3056-4_A375_DGR1_1:3206	53807, 8651	downstream, sr gene	0	1	1	6	10.5	14.5	2	2_A375_shLK17 T_dun_lncRNA_AR_1	Gene LOC100505937		hypothetical protein LOC100505937		NM_033115582, NP_033120937.1		
GeneID:16	DNMT3B	20	31,350,191	31,397,162	46,971	+	1	4_A375_DGR1_1:3291	19483	sr gene	0	0	1	10	9	19	1	4_A375_DGR1.1	Gene DNMT3B	DNMT3B	DNA (cytosine-5)-methyltransferase 3 beta	NM_006892, NM_175848, NM_175849, NM_175850, NCT01983196.1, NCT01982300.1, NCT01982301.1, NCT01243070.1, NCT02554470.0, NCT02554480.0, NCT02555060.2	220985_s_at	NP_006883.1, NP_787044.1, NP_787045.1, NP_787046.1, EAW76534.1, EAW76535.1, EAW76550.1, EAW76551.1, EAW76552.1, EAW76553.1, EAW76555.1
GeneID:38	EPCAM	20	31,446,729	31,449,415	102,898	+	1	4_A375_DGR1:1.3292	92367	sr gene	0	0	1	3	8	19	1	4_A375_DGR1.1	Gene EPCAM	EPCAM6			NM_033119620, NM_033118791, NM_033120791	NP_033119396.1, NP_033118647.1, NP_033121629.1
GeneID:12	C20orf11	20	31,803,135	31,815,559	10,424	+	1	2_A375_shG7_dun_lncRNA_AR_1:3030	-7427	upstream	0	1	0	17	26	0	1	2_A375_shLK28 T_dun_lncRNA_AR_1	Gene C20orf11	EPLUNC3, C20orf11, MGC44325	chromosome 20 open reading frame 71	NM_178488, NM_001042439, NCT03355983.0, NCT03355985.0, NCT03355987.0, NCT02144402	040339_at	NP_848587.2, NP_001029904.1, EAW76530.1, EAW76531.1, EAW76532.1, EAW76533.1
GeneID:39	CDK5RAP1	20	31,946,645	31,969,357	42,892	-	3	1_A375_shG7_mrna_lncRNA_AR_1:3329-2_A375_shG7_dun_lncRNA_AR_1:3099-3_A375_DGR1_1:3294	-55, -39, 9	upstream, upstream, cn gene	1	1	1	20	21	16	1	2_A375_shLK21 T_dun_lncRNA_AR_1	Gene CDK5RAP1	CGI-85, CGI85RAP1.3, MST1067, CGI85RAP1, C20orf64, C42, CGI85RAP1.4	CDK5 regulatory subunit associated protein	NM_018450, NM_018932, NCT01991309.1, NCT01992311.1, NCT01992312.1, NCT01992313.1, NCT02131994.0, NCT02131996.0, NCT02555370.0, NCT02135122	216315_s_at	NP_060940.2, NP_061186.2, EAW76531.1, EAW76532.1, EAW76533.1, EAW76534.1, EAW76535.1, EAW76536.1, EAW76537.1, EAW76538.1, EAW76539.1, EAW76540.1, EAW76541.1, EAW76542.1, EAW76543.1
GeneID:89	SNTA1	20	31,995,765	32,031,896	36,355	+	3	1_A375_shG7_mrna_lncRNA_AR_1:3329-2_A375_shG7_dun_lncRNA_AR_1:3099-3_A375_DGR1_1:3296	42506, 42532, 42570	downstream, downstream, downstream	1	1	1	20	21	16	1	2_A375_shLK21 T_dun_lncRNA_AR_1	Gene SNTA1	SNTA1, dJ1167A5.5, TNCIP1, SNT1, IGT12	syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)	NM_003098, NCT03139930.0, NCT03555520.0, NCT02555320.0, NCT02139137.0	205516_at	NP_003089.1, EAW76517.1, EAW76514.1, EAW76515.1, EAW76516.1
GeneID:83	NECAB3	20	32,244,893	32,262,264	17,371	-	3	1_A375_shG7_mrna_lncRNA_AR_1:3362-2_A375_shG7_dun_lncRNA_AR_1:3090-3_A375_DGR1_1:3295	6960, 6976, 6993	sr gene, sr gene, cn gene	1	1	1	15	20	19	1	2_A375_shLK20 T_dun_lncRNA_AR_1	Gene NECAB3	APBA2BP, NECAB3, NIP1, KIS1, EFCBP3, SYTF2, dJ851M2.3, dJ851M2.4, SYIP2	N-terminal EF-hand calcium binding protein 3	NM_031232, NM_031231, NCT01991310.1, NCT01992330.0, NCT01992334.0, NCT01992335.0, NCT01992337.0, NCT01992338.0, NCT02144122	210720_s_at_222054_s_at	NP_112099.3, NP_112098.2, EAW76531.1, EAW76532.1, EAW76533.1, EAW76536.1, EAW76537.1, EAW76538.1, EAW76539.1, EAW76540.1, EAW76541.1, EAW76542.1, EAW76543.1
GeneID:12	C20orf144	20	32,230,120	32,231,703	1,808	+	2	1_A375_shG7_mrna_lncRNA_AR_1:3345-2_A375_shG7_dun_lncRNA_AR_1:3099-3_A375_DGR1_1:3295	6364, 8065, 8484	downstream, downstream, downstream	1	1	1	15	20	19	1	2_A375_shLK20 T_dun_lncRNA_AR_1	Gene C20orf144	dJ851M2.6, C20orf144	chromosome 20 open reading frame 144	NM_080833, NCT02144183	231322_at	NP_543018.1, EAW76310.1
GeneID:17	C20orf134	20	32,254,304	32,256,331	2,027	+	3	1_A375_shG7_mrna_lncRNA_AR_1:3345-2_A375_shG7_dun_lncRNA_AR_1:3099-3_A375_DGR1_1:3295	1120, 1154, 1288	sr gene, cn gene, cn gene	1	1	1	15	20	19	1	2_A375_shLK20 T_dun_lncRNA_AR_1	Gene C20orf134	dJ851M2.2, C20orf134	chromosome 20 open reading frame 134	NM_031224975, NCT11971329.1	232619_at	NP_001019646.1, EAW76309.1
GeneID:18	E2F1	20	32,260,392	32,274,210	10,916	-	3	1_A375_shG7_mrna_lncRNA_AR_1:3362-2_A375_shG7_dun_lncRNA_AR_1:3090-3_A375_DGR1_1:3295	10766, 10722, 10626	downstream, downstream, downstream	1	1	1	15	20	19	1	2_A375_shLK20 T_dun_lncRNA_AR_1	Gene E2F1	E2F1, RBAP1, RBBP3, RBP3, E2F1	E2F transcription factor 1	NM_005225, NCT02132310.1, NCT02147.3	2038_s_at_204947_at	NP_005216.1, EAW82999.1, EAW82930.1
GeneID:11	PXMP4	20	32,290,850	32,295,156	17,306	+	1	2_A375_shLK27 dun_lncRNA_AR_1:3081	104	sr gene	0	0	1	12	21	13	1	2_A375_shLK31 T_dun_lncRNA_AR_1	Gene PXMP4	PXMP4, PMP24	peroxisomal membrane protein 4, 24kDa	NM_153377, NM_007238, NCT02132128.0	219428_s_at_224210_s_at	NP_699154.1, NP_009188.2, EAW76246.1
GeneID:84	ZNF341	20	32,316,606	32,350,075	60,287	+	1	4_A375_DGR1:1.3298	50912	sr gene	0	0	1	8	8	21	1	4_A375_DGR1.1	Gene ZNF341	ZNF341	zinc finger protein 341	NM_020516, NCT02145836.0, NCT02155830.0, NCT02139139.1	1555502_s_at_203382_at	NP_116036.3, EAW76293.1, EAW76294.1, EAW76295.1, EAW76297.1
GeneID:12	CHMP4B	20	32,399,110	32,442,173	43,063	+	1	2_A375_shG7_dun_lncRNA_AR_1:3092	-134	upstream	0	1	0	27	33	6	1	2_A375_shLK33 T_dun_lncRNA_AR_1	Gene CHMP4B	Shax1, bA516F4.4, C20orf176, SNF7-2, CHMP4A, Vps32-2, SNF7, CHMP4B, CTPP5, VPS32B	chromatin modifying protein 4B	NM_176812, NCT02155807.0, NCT02145.2	223119_at_223695_at	NP_787762.1, EAW76294.1, EAW76293.1
GeneID:19	LOC100505490	20	32,500,274	32,502,162	1,888	+	1	2_A375_shG7_dun_lncRNA_AR_1:3094	930	sr gene	0	1	0	20	16	19	1	2_A375_shLK18 T_dun_lncRNA_AR_1	Gene LOC100505490		hypothetical LOC100505490	XR_112133, XR_112139, XR_109594, XR_109593, XR_118355, XR_118356		
GeneID:22	RALY	20	32,561,702	32,566,087	99,335	+	1	2_A375_shG7_dun_lncRNA_AR_1:3094	-100	upstream	0	1	0	20	16	18	1	2_A375_shLK18 T_dun_lncRNA_AR_1	Gene RALY	RALY, MGC117312, HNRPCL2	RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow) homolog (mouse)	NM_016732, NM_007367, NCT01991306.1, NCT01993712.1, NCT02139910.0, NCT02139986.0, NCT02154.3	201211_s_at	NP_057951.1, NP_031292.2, EAW76287.1, EAW76288.1, EAW76289.1, EAW76291.1, EAW76292.1
GeneID:23	EIF2S2	20	32,876,115	32,700,003	23,970	-	1	2_A375_shG7_dun_lncRNA_AR_1:3093	229	sr gene	0	1	0	12	16	9	1	2_A375_shLK18 T_dun_lncRNA_AR_1	Gene EIF2S2	DKFZp686I16116, IMD6, MGC5935, EIF2S2, EIF2beta, EIF2B, EIF2	eukaryotic translation initiation factor 2, subunit 2 beta, 36kDa	NM_003908, NCT02132218.0, NCT02132410.0, NCT02132230.0	200729_at_200730_s_at	NP_003899.2, EAW76398.1, EAW76264.1, EAW76265.1
GeneID:16	AHCY	20	32,880,071	32,899,806	31,827	-	4	1_A375_shG7_mrna_lncRNA_AR_1:3362-2_A375_shG7_dun_lncRNA_AR_1:3098-3_A375_shG7_dun_lncRNA_AR_1:3097-4_A375_DGR1_1:3297	6408, 6440, -2464, -5966	sr gene, cn gene, upstream, cn gene	1	1	1	44.5	53.5	12.5	2	2_A375_shLK33 T_dun_lncRNA_AR_1	Gene AHCY	DKFZp686I16116, IMD6, MGC5935, EIF2S2, EIF2beta, EIF2B, EIF2	adenosylhomocysteinase	NM_001161788, NM_000687, NCT02132110.0, NCT02154160.0, NCT02132.3	200803_s_at	NP_001153330.1, NP_000670.1, EAW76279.1, EAW76280.1, EAW76281.1
GeneID:83	ITCH	20	32,931,982	33,099,197	149,138	+	3	1_A375_shG7_mrna_lncRNA_AR_1:3098-2_A375_shG7_dun_lncRNA_AR_1:3099-3_A375_DGR1_1:3296	42, 152490, 183194	sr gene, downstream, downstream	1	1	1	20	21	19.5	2	2_A375_shLK21 T_dun_lncRNA_AR_1	Gene ITCH	ITCH, NAPP1, AIP4, dJ465O1.1, AIP4	itchy E3 ubiquitin protein ligase homolog (mouse)	NM_031483, NCT02132670.0, NCT02132680.0, NCT02139760.0, NCT02155330.0	209743_s_at_209744_s_at	NP_113971.3, EAW76277.1, EAW76272.1, EAW76273.1, EAW76275.1, EAW76276.1, EAW76274.1, EAW76278.1
GeneID:83	DYNLRB1	20	33,104,294	33,126,762	34,356	+	4	1_A375_shG7_mrna_lncRNA_AR_1:3362-2_A375_shG7_dun_lncRNA_AR_1:3099-3_A375_shG7_dun_lncRNA_AR_1:3070-4_A375_DGR1_1:3296	9716, 9752, 9852, 82	sr gene, upstream, cn gene, cn gene	1	1	1	22.5	28	13.5	2	2_A375_shLK31 T_dun_lncRNA_AR_1	Gene DYNLRB1	DNLC2A, BTH, ROBLD1, DYNLRB1, DNLC2A, BLP	dynein, light interchain, roadblock-type 1	NM_014183	1554566_at_1565611_at, 1565612_at_217917_s_at, 217916_at	NP_054902.1
GeneID:84	MAP1LC3A	20	33,134,892	33,145,149	10,257	+	1	2_A375_shG7_dun_lncRNA_AR_1:3071	11825	sr gene	0	1	0	21	27	12	1	2_A375_shLK27 T_dun_lncRNA_AR_1	Gene MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	NM_181509, NM_032514, NCT01991438.1, NCT02139119.0, NCT02139121.0, NCT02139134.0	224376_s_at_222219_s_at, 232011_s_at	NP_852610.1, NP_115903.1, EAW76354.1, EAW76355.1, EAW76356.1
GeneID:12	PXDC1	20	33,146,348	33,165,009	118,743	-	2	2_A375_shG7_dun_lncRNA_AR_1:3071-2_A375_shG7_dun_lncRNA_AR_1:3072	118789, 193	downstream, cn gene	0	1	0	19.5	29	12.5	2	2_A375_shLK31 T_dun_lncRNA_AR_1	Gene PXDC1	CDC5L11, PIG2, Cdc5l, MGC40420	phosphodiesterase 4D guanylate cyclase activator, brefeldin A-inhibited guanine nucleotide-exchange protein 3	NM_030760, NCT02132022.0, NCT02132620.0, NCT02139531.0, NCT02744.2	223603_at	NP_598734.1, EAW76239.1, EAW76240.1, EAW76241.1, EAW76242.1
GeneID:83	TPS3N2	20	33,292,148	33,301,227	9,080	+	1	4_A375_DGR1:1.3299	5212	sr gene	0	0	1	13	15	30	1	4_A375_DGR1.1	Gene TPSN2P2	FLJ27799, PNN, DKFZp434O0227, DKFZp434B0416, C20orf110, DOR, FLJ25500, TPS3NP2, bA116N3.1	tumor protein p53 inducible nuclear protein 2	NM_021202, NCT01985312.1, NCT02554170.0, NCT02793.3	224696_at	NP_067025.1, EAW76237.1, EAW76238.1, EAW76239.1
GeneID:23	NCOA6	20	33,302,976	33,415,453	110,038	+	1	4_A375_DGR1:1.3299	116073	downstream	0	0	1	13	15	30	1	4_A375_DGR1.1	Gene NCOA6	ASC2, HCA47, NRC, NCOA6, PRIP, PAIP2B, AIB3, HCA1.3, ANCP, KIAA0181, TRBP	nuclear receptor coactivator 6	NM_014071, NCT02139165.0, NCT02145.3	1555574_at_208979_at	NP_034792.2, EAW76254.1, EAW76255.1
GeneID:10	LOC100505514	20	33,302,932	33,315,195	12,263	+	1	4_A375_DGR1:1.3299	-5242	upstream	0	0	1	13	15	30	1	4_A375_DGR1.1	Gene LOC100505514		hypothetical LOC100505514	XR_112154, XR_109596, XR_115337		
GeneID:26	GGT7	20	33,432,923	33,460,991	28,156	+	1	2_A375_shG7_dun_lncRNA_AR_1:3073	-107	upstream	0	1	0	12	24	9	1	2_A375_shLK24 T_dun_lncRNA_AR_1	Gene GGT7	GGTL5, GGT5L, dJ1050.2, GGT5, GGT7L, GGT7	gamma-glutamyltransferase 7	NM_176026, NCT03139512.0, NCT03139513.1, NCT03139.0, NCT02147.2	225469_s_at_226470_at, 225471_at	NP_821156.2, EAW76249.1, EAW76250.1, EAW76251.1, EAW76252.1
GeneID:83	ACSS2	20	33,482,768	33,518,769	33,093	+	3	1_A375_shG7_mrna_lncRNA_AR_1:3364-2_A375_shG7_dun_lncRNA_AR_1:3071-3_A375_shG7_dun_lncRNA_AR_1:3074	33031, -1998, 32754	sr gene, upstream, cn gene	1	1	1	14.3	20.3	10.3	2	2_A375_shLK24 T_dun_lncRNA_AR_1	Gene ACSS2	ACECS2, ACSA, dJ1181H22.1, ACSS2, AceCS1, DKFZp762K026, ACAS2	acyl-CoA synthetase short-chain family member 2	NM_018677, NM_001076532, NM_020549, NCT01997435.1, NCT02139230.0, NCT02139232.0, NCT02139233.0, NCT02554.0	234312_x_at	NP_061147.1, NP_001076000.2, EAW76242.1, EAW76243.1, EAW76244.1, EAW76245.1, EAW76246.1, EAW76247.1, EAW76248.1
GeneID:29	GSS	20	33,516,239	33,545,901	27,385	-	3	1_A375_shG7_mrna_lncRNA_AR_1:3363-2_A375_shG7_dun_lncRNA_AR_1:3073-3_A375_shG7_dun_lncRNA_AR_1:3090	-237, 230, 199	sr gene, cn gene, cn gene	1	1	1	24	27	20	1	2_A375_shLK27 T_dun_lncRNA_AR_1	Gene GSS	GSS, GSHS, MGC14298	glutathione synthetase	NM_000178, NCT01982728.1, NCT02555580.0, NCT02744.0	201415_at_211693_x_at	NP_000169.1, EAW76239.1, EAW76240.1, EAW76241.1
GeneID:37	MYH7B	20	33,543,704	33,590,340	46,636	+	6	1_A375_shG7_mrna_lncRNA_AR_1:3363-2_A375_shG7_dun_lncRNA_AR_1:3073-3_A375_shG7_dun_lncRNA_AR_1:3090-4_A375_DGR1_1:3300-5_A375_DGR1_1:3302-6_A375_DGR1_1:3303	-340, -333, -269, 23256, 29000, 47192	upstream, upstream, upstream, cn gene, cn gene, downstream	1	1	1	12.75	12.25	16	4	2_A375_shLK27 T_dun_lncRNA_AR_1	Gene MYH7B	MGC99340, MGC99339, KIAA1512, MYH7B, MYH15	myosin, heavy chain 7B, cardiac muscle, beta	NM_020884, NCT01640782.0, NCT02155934.0, NCT02139133.0	213795_at_233963_s_at	NP_065725.2, EAW76238.1, EAW76239.1, EAW76237.1, EAW76236.1
GeneID:37	MRAS	20	33,576,179	33,576,300	121	+	2	4_A375_DGR1:1.3301, 4_A375_DGR1:1.3302	-8175, -8475	upstream, upstream	0	0	1	9	7.5	19	2	4_A375_DGR1.1	Gene MRAS	MRAS, MRAS67, bA134P9.1	muscle RAS oncogene	NR_030223		
GeneID:17	TRPC4AP	20	33,590,207	33,600,616	10,411	-	3	1_A375_shG7_mrna_lncRNA_AR_1:3362-2_A375_shG7_dun_lncRNA_AR_1:3098-3_A375_DGR1_1:3303	178, 10, 69722	sr gene, cn gene, cn gene	1	1	1	14.3	14	16	2	2_A375_shLK21 T_dun_lncRNA_AR_1	Gene TRPC4AP	TRUSS, dJ701.1.1.B2, TRPC4AP, TRPA1AP	transient receptor potential cation channel, subfamily C, member 4 associated protein	NM_015638, NM_199366, NCT02139304.0, NCT02139306.0, NCT02139307.0, NCT02554290.0, NCT02554.0, NCT02744.3	212089_s_at	NP_056453.1, NP_955402.1, EAW76229.1, EAW76230.1, EAW76234.1, EAW76233.1, EAW76231.1, EAW76232.1, EAW76233.1
GeneID:10	MMP24	20	33,814,929	33,864,904	50,265	+	6	1_A375_shG7_mrna_lncRNA_AR_1:3367-2_A375_shG7_dun_lncRNA_AR_1:3076-3_A375_shG7_dun_lncRNA_AR_1:3079-4_A375_DGR1_1:3304-5_A375_DGR1_1:3305-6_A375_DGR1_1:3306	501, 597, 58143, 58837, 61107, 80241	sr gene, cn gene, downstream, cn gene, downstream, downstream, cn gene	1	1	1	15.8	17.2	17.8	3	2_A375_shLK33 T_dun_lncRNA_AR_1	Gene MMP24	MT5-MMP, MMP24, MMP25, MT-MMP5	matrix metalloproteinase 24 (membrane-inserted)	NM_006690, NCT02144.3	230387_s_at_213171_s_at, 221993_s_at_49873_s_at	NP_006681.1, EAW76222.1
GeneID:26	EIF6	20	33,866,723	33,872,994	6,089	+	4	2_A375_shG7_dun_lncRNA_AR_1:3074-3_A375_DGR1_1:3304-4_A375_DGR1_1:3305-5_A375_DGR1_1:3306	-94, -6004, 6195, 6195	upstream, downstream, downstream, upstream	0	1	1	13.5	13.25	30	4	4_A375_DGR1.1	Gene EIF6	C4-B, EIF3A, EIF6, ITGB4BP, dJ1181H22.1, bA134P9.1	eukaryotic translation initiation factor 6	NM_181468, NM_181469, NM_002210, NCT01992216.1, NCT01992220.1, NCT02744.1	210213_s_at	NP_852133.1, NP_852132.1, NP_002201.1, EAW76219.1, EAW76220.1, EAW76221.1
GeneID:12	FAM83C	20	33,873,934	33,880,223	6,291	-	4	2_A375_shG7_dun_lncRNA_AR_1:3074-3_A375_DGR1_1:3304-4_A375_DGR1_1:3305-5_A375_DGR1_1:3306	7327, 10849, 14395, 6348	downstream, downstream, downstream, downstream, cn gene	0	1	1	13.5	13.25	30	4	4_A375_DGR1.1	Gene FAM83C	C.30.nr132, bA516F4.7, FAM83C, MGC142363	family with sequence similarity 83, member C	NM_178488, NCT16449.1	1556793_s_at, 1560803_s_at	NP_848563.1, EAW76216.1
GeneID:53	UQCC	20	33,890,389	33,899,945	109,578	-	5	1_A375_shG7_mrna_lncRNA_AR_1:3362-2_A375_shG7_dun_lncRNA_AR_1:3098-3_A375_shG7_dun_lncRNA_AR_1:3091-4_A375_DGR1_1:3307-5_A375_DGR1_1:3308	108217, 108513, 109753	sr gene, cn gene, cn gene	1	2	1	19.5	22.5	10	2	1_A375_shLK29 T_dun_lncRNA_AR_1	Gene UQCC	UQCC, C20F3, dJ1167A5.1, MGC141902, C20orf64, BF25	ubiquinol-cytochrome c reductase complex chaperone	NM_001164777, NM_018244, NM_199457, NCT01993224.1, NCT01993228.1, NCT01993593.1, NCT02555930.0, NCT02555934.0, NCT02555935.0, NCT02555950.0, NCT02744.0	217023_s_at_223470_s_at, 223972_at_244795_at	NP_001171908.1, NP_060714.3, NP_001161.2, EAW76210.1, EAW76211.1, EAW76217.1, EAW76212.1, EAW76213.1, EAW76214.1, EAW76215.1, EAW76216.1
GeneID:10	MIR1208	20	34,041,778	34,041,919	143	+	2	2_A375_shG7_mrna_lncRNA_AR_1:3349-3_A375_DGR1_1:3307	-1058, -1153	upstream, upstream	1	0	1	17	12	28	1	4_A375_DGR1.1	Gene MIR1208	hsa-mir-1208-1, MIR1208-1, MIR1208-1	microRNA 1208-1	NR_030820		
GeneID:17	CEP250	20	34,043,223	34,099,003	56,300	+	2	1_A375_shG7_mrna_lncRNA_AR_1:3345-2_A375_DGR1_1:3307-4_A375_DGR1_1:3308	212, -151, 46541	sr gene, upstream, cn gene	1	2	1	12.5	12.5	21	2	4_A375_DGR1.1	Gene CEP250	C-NAP1, CNAP1, MGC99342, CEP2B, CEP2	centrosomal protein 250kDa	NM_007186, NCT02155944.0, NCT02139145.0, NCT02139146.0, NCT02744.0.2	209469_at_210894_s_at	NP_009117.2, EAW76239.1, EAW76235.1, EAW76236.1, EAW76237.1
GeneID:83	ERGIC3	20	34,129,776	34,143,405	13,627	+	1	4_A375_DGR1:1.3309	76	sr gene	0	0	1	8	13	32	1	4_A375_DGR1.1	Gene ERGIC3	Erv46, PRO0969, Cgl-5a, bA770d.2, C20orf67, SDBCAG84, NY-BR-84, ERGIC3	ERGIC and golgi 3	NM_018988, NM_199290, NCT02555580.0, NCT02744.0.2	1555800_at_219257_at, 219832_s_at	NP_057953.1, NP_950430.1, EAW76191.1, EAW76203.1
GeneID:89	SPAG4	20	34,203,609	34,208,965	5,356	+	4	1_A375_shG7_mrna_lncRNA_AR_1:3360-2_A375_shG7_dun_lncRNA_AR_1:3092-3_A375_DGR1_1:3311-4_A375_DGR1_1:3312	76, 49, 1697, 3967	sr gene, upstream, cn gene, cn gene	1	1	1	14	11.67	18	3	2_A375_shLK23 T_dun_lncRNA_AR_1	Gene SPAG4	SPAG4, CT127, SUN4	sperm associated antigen 4	NM_003116, NCT02146.2	219888_at	NP_003107.1, EAW76191.1
GeneID:23	CPNE1	20	34,213,966	34,252,945	38,852	+	6	1_A375_shG7_mrna_lncRNA_AR_1:3362-2_A375_shG7_dun_lncRNA_AR_1:3092-3_A375_DGR1_1:3311-4_A375_DGR1_1:3312-5_A375_DGR1_1:3313-6_A375_DGR1_1:3314	48960, 49008, 47152, 45332, 15888, 208	downstream, downstream, downstream, downstream, cn gene, cn gene, cn gene	1	1	1	12.8	16.4	20.4	5	4_A375_DGR1.1	Gene CPNE1	MGC1142, COPN1, CPN1, CPNE1	copine 1	NM_152923, NM_152929, NM_152927, NM_152925, NM_152920, NM_152931, NM_002591	209918_s_at	NP_690602.1, NP_690603.1, NP_690604.1, NP_690605.1, NP_690607.1, NP_690606.1, NP_003906.2
GeneID:10	RBM12	20	34,236,077	34,252,656	16,580	-	2	4_A375_DGR1:1.3313, 4_A375_DGR1:1.3314	11878, 195	sr gene, cn gene	0	0	1	10.5	17.5	24	2	4_A375_DGR1.1	Gene RBM12	RBPHP33291, RBM12, bA442I23.1, SWAN	RNA binding motif protein 12	NM_006047, NM_152856	212166_at_212170_at	NP_006038.2, NP_690351.1
GeneID:90	NFS1	20	34,256,811	34,267,374	30,863	-	2	2_A375_shG7_dun_lncRNA_AR_1:3093-3_A375_DGR1_1:3314	-68, 34834	upstream, downstream	0	1	1	19.5	24.5	21.5	2	4_A375_DGR1.1	Gene NFS1	NFS1, NIFS, hcd, HUSSY-08	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	NM_021100, NCT02132407.0, NCT02554440.0, NCT2439.2	1554321_a_at_210455_at	NP_066923.3, EAW76170.1, EAW76171.1, EAW76172.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.140823	ROMO1	20	34,287,232	34,288,902	1,670	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5083	128	in gene	0	1	0	22	23	16	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ROMO1	MTGMP, ROMO1, MGC111180, bA353C18.2, C20orf52	reactive oxygen species modulator 1	NM_080748, hCT1824726.1, hCT1969213.1	224972_at	NP_542786.1, EAW76168.1, EAW76169.1
GeneID.9584	RBM39	20	34,291,531	34,330,193	38,662	-	3	2_A375_pNL97_plus_lncRNA_AR..1..5083, 2_A375_pNL97_plus_lncRNA_AR..1..5084, 4_A375_EGR1..1..5315	42633, -79, 49	downstream, upstream, in gene	0	1	1	21.5	22.5	18	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RBM39	DKFZp781C0423, RBM39, CAPERalpha, FLJ44170, CAPER, CC1.3, HCC1, fSAP59, RNPC2	RNA binding motif protein 39	NM_184234, NM_004902, hCT2313483.0, hCT2313485.0, hCT2313486.0, hCT2355452.0, hCT2355453.0, hCT2355454.0, hCT2355455.0, hCT2355456.0, hCT29460.3	207941_s_at, 208720_s_at, 236355_at, 236357_at	NP_909122.1, NP_004893.1, EAW76159.1, EAW76160.1, EAW76163.1, EAW76166.1, EAW76161.1, EAW76162.1, EAW76164.1, EAW76165.1, EAW76167.1
GeneID.51230	PHF20	20	34,359,923	34,538,288	178,365	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3551, 2_A375_pNL97_plus_lncRNA_AR..1..5085, 2_A375_pNL97_plus_lncRNA_AR..1..5086, 4_A375_EGR1..1..5316	182541, -2675, 182701, 181933	downstream, upstream, downstream, downstream	1	1	1	26.5	26	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene PHF20	NZF, PHF20, GLEA2, FLJ33479, HCA58, TZP, C20orf104	PHD finger protein 20	NM_016436, hCT1951313.1, hCT2315108.0, hCT2315107.0, hCT2315106.0, hCT2315109.0, hCT2315113.0	1569906_s_at, 208587_s_at, 209422_at, 209423_s_at	NP_057520.2, EAW76153.1, EAW76154.1, EAW76155.1, EAW76156.1, EAW76158.1, EAW76157.1
GeneID.51282	SCAND1	20	34,541,546	34,542,428	882	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3551, 2_A375_pNL97_plus_lncRNA_AR..1..5086, 4_A375_EGR1..1..5316	-36, -198, 572	upstream, upstream, in gene	1	1	1	31	27	21	1	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene SCAND1	SCAND1, RAZ1, SDP1	SCAN domain containing 1	NM_016558, NM_033630, hCT2313480.0, hCT2313481.0, hCT29461.3	218206_x_at, 231059_x_at, 232852_x_at	NP_057842.1, NP_361012.1, EAW76150.1, EAW76151.1, EAW76152.1
GeneID.647979	LOC647979	20	34,633,540	34,638,882	5,342	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3552, 2_A375_pNL97_plus_lncRNA_AR..1..5087, 4_A375_EGR1..1..5317	130, 98, 130	in gene, in gene, in gene	1	1	1	17	18	24	1	4_A375_EGR1..1	24	Gene LOC647979		hypothetical LOC647979	NR_027451	1558028_x_at, 224597_at	
GeneID.2036	EPB41L1	20	34,700,348	34,820,721	120,373	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3553, 2_A375_pNL97_plus_lncRNA_AR..1..5090, 4_A375_EGR1..1..5320	123716, 123988, 124057	downstream, downstream, downstream	1	1	1	19	29	23	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene EPB41L1	DKFZp686H1724 2, MGC11072, EPB41L1, 4.1N, KIAA0338	erythrocyte membrane protein band 4.1-like 1	NM_012156, NM_177996, hCT1824725.2, hCT2315116.0, hCT2315118.0	212336_at, 212339_at, 222086_at, 230289_at	NP_036288.2, NP_818932.1, EAW76144.1, EAW76145.1, EAW76146.1
GeneID.25980	C20orf4	20	34,824,447	34,844,853	20,406	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3553, 2_A375_pNL97_plus_lncRNA_AR..1..5090, 4_A375_EGR1..1..5320	-383, -111, -42	upstream, upstream, upstream	1	1	1	19	29	23	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene C20orf4	CGI-23, C20orf4, bA234K24.2, DKFZp564N1363	chromosome 20 open reading frame 4	NM_015511, hCT2315119.0, hCT2315121.0, hCT28359.3	218089_at	NP_056326.2, EAW76143.1, EAW76141.1, EAW76142.1
GeneID.22839	DLGAP4	20	34,995,444	35,157,040	161,596	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3555, 2_A375_pNL97_plus_lncRNA_AR..1..5092, 4_A375_EGR1..1..5323, 4_A375_EGR1..1..5324, 4_A375_EGR1..1..5325, 4_A375_EGR1..1..5326	17164, 17132, 34412, 69198, 73164, 80065	in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	17.6	20.8	16.4	5	2_A375_pNL97_plus_lncRNA_AR..1	60	Gene DLGAP4	KIAA0964, DLGAP4, DLP4, DAP4, RP5-977B1.6, MGC131862, SAPAP4, FLJ20566	discs, large (Drosophila) homolog-associated protein 4	NM_183006, NM_014902, NM_001042486, hCT2315123.0, hCT2315124.0, hCT2315125.0, hCT2315126.0, hCT2315127.0, hCT2315128.0	1556701_at, 1557394_at, 202570_s_at, 202571_s_at, 202572_s_at, 233056_x_at	NP_892116.1, NP_055717.2, NP_001035951.1, EAW76135.1, EAW76139.1, EAW76140.1, EAW76136.1, EAW76137.1, EAW76138.1
GeneID.10398	MYL9	20	35,169,897	35,178,226	8,329	+	2	4_A375_EGR1..1..5327, 4_A375_EGR1..1..5328	-553, 231	upstream, in gene	0	0	1	6.5	10	17	2	4_A375_EGR1..1	17	Gene MYL9	MGC3505, MYL9, MRLC1, LC20, MYRL2, MLC2	myosin, light chain 9, regulatory	NM_006097, NM_181526, hCT1845729.3, hCT1983184.1, hCT2315130.0, hCT2315132.0, hCT2315134.0, hCT2355513.0	201058_s_at	NP_006088.2, NP_852667.1, EAW76129.1, EAW76131.1, EAW76132.1, EAW76133.1, EAW76130.1, EAW76134.1
GeneID.55969	C20orf24	20	35,234,167	35,240,960	6,793	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3556, 2_A375_pNL97_plus_lncRNA_AR..1..5093	-215, -103	upstream, upstream	1	1	0	26	33	24	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene C20orf24	RIP5, PNAS-11, C20orf24	chromosome 20 open reading frame 24	NM_018840, NM_199483, NR_028562, hCT1982412.1, hCT1982413.1, hCT22971.3, hCT2315141.0, hCT2355450.0, hCT2355451.0	217835_x_at, 223880_x_at, 224376_s_at	NP_061328.1, NP_955777.1, EAW76120.1, EAW76121.1, EAW76122.1, EAW76125.1, EAW76123.1, EAW76124.1
GeneID.84174	SLA2	20	35,240,922	35,274,558	33,636	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3556, 2_A375_pNL97_plus_lncRNA_AR..1..5093	40606, 40494	downstream, downstream	1	1	0	26	33	24	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene SLA2	SLA2, MGC49845, SLAP2, FLJ21992, C20orf156, SLAP-2	Src-like-adaptor 2	NM_032214, NM_175077, hCT22972.2, hCT2313469.1, hCT2313470.1, hCT2313471.1	1555688_s_at, 232234_at	NP_115590.1, NP_778252.1, EAW76116.1, EAW76117.1, EAW76118.1, EAW76119.1
GeneID.57446	NDRG3	20	35,280,169	35,374,481	94,312	-	1	4_A375_EGR1..1..5329	69185	in gene	0	0	1	10	5	22	1	4_A375_EGR1..1	22	Gene NDRG3	FLJ13556, NDRG3	NDRG family member 3	NM_022477, NM_032013, hCT1824117.2, hCT1983867.1, hCT1983868.1, hCT2313425.0, hCT2313426.0, hCT2355426.0, hCT2355427.0	217286_s_at, 221082_s_at, 224388_s_at	NP_071922.2, NP_114402.1, EAW76109.1, EAW76113.1, EAW76114.1, EAW76115.1, EAW76110.1, EAW76111.1, EAW76112.1
GeneID.79980	DSN1	20	35,380,194	35,402,230	22,036	-	1	4_A375_EGR1..1..5330	-250	upstream	0	0	1	22	21	20	1	4_A375_EGR1..1	20	Gene DSN1	KNL3, MIS13, dJ469A13.2, DSN1, C20orf172, FLJ13346, hKNL-3, MGC32987	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	NM_001145315, NM_001145316, NM_001145317, NM_001145318, NM_024918, hCT2313419.0, hCT2313420.0, hCT2313421.0, hCT2355508.0, hCT2355509.0, hCT2355510.0, hCT2355511.0, hCT2355512.0	219512_at	NP_001138787.1, NP_001138788.1, NP_001138789.1, NP_001138790.1, NP_079194.3, EAW76103.1, EAW76101.1, EAW76102.1, EAW76104.1, EAW76105.1, EAW76106.1, EAW76107.1, EAW76108.1
GeneID.140710	C20orf117	20	35,405,845	35,492,087	86,242	-	7	4_A375_EGR1..1..5330, 4_A375_EGR1..1..5331, 4_A375_EGR1..1..5332, 4_A375_EGR1..1..5333, 4_A375_EGR1..1..5334, 4_A375_EGR1..1..5335, 4_A375_EGR1..1..5336	89807, 69687, 58471, 47815, 24487, 1063, -598	downstream, in gene, in gene, in gene, in gene, in gene, upstream	0	0	1	11.57	12.57	20.71	7	4_A375_EGR1..1	26	Gene C20orf117	FLJ44670, KIAA0889, C20orf117, SOGA, dJ132F21.1	chromosome 20 open reading frame 117	NM_199181, NM_080627, hCT1848363.3, hCT1861001.3, hCT1824119.3, hCT2313416.1, hCT2313418.1, hCT2313451.1, hCT2313452.1	207711_at, 215852_x_at, 225473_at, 241382_at	NP_954650.2, NP_542194.2, EAW76095.1, EAW76098.1, EAW76099.1, EAW76100.1, EAW76094.1, EAW76096.1, EAW76097.1
GeneID.25939	SAMHD1	20	35,520,227	35,580,246	60,019	-	2	4_A375_EGR1..1..5337, 4_A375_EGR1..1..5338	854, 22	in gene, in gene	0	0	1	14.5	13	17.5	2	4_A375_EGR1..1	21	Gene SAMHD1	MOP-5, SBBI88, DCIP, AGS5, HDDC1, SAMHD1	SAM domain and HD domain 1	NM_015474, hCT2313446.0, hCT9014.3	1559882_at, 1559883_s_at, 204502_at	NP_056289.2, EAW76091.1, EAW76090.1
GeneID.5933	RBL1	20	35,626,178	35,724,410	98,232	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3557, 2_A375_pNL97_plus_lncRNA_AR..1..5094, 4_A375_EGR1..1..5339	-8, 122, 202	upstream, in gene, in gene	1	1	1	18	24	18	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene RBL1	RBL1, PRB1, MGC40006, p107, CP107	retinoblastoma-like 1 (p107)	NM_183404, NM_002895, hCT1824110.2, hCT2355575.0	1555003_at, 1555004_a_at, 1559307_s_at, 205296_at	NP_899662.1, NP_002886.2, EAW76088.1, EAW76089.1
GeneID.140699	C20orf132	20	35,729,629	35,807,974	78,345	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3557, 1_A375_pNL7_minus_lncRNA_AR..1..3558, 2_A375_pNL97_plus_lncRNA_AR..1..5094, 2_A375_pNL97_plus_lncRNA_AR..1..5095, 4_A375_EGR1..1..5339, 4_A375_EGR1..1..5340	83556, 486, 83686, 486, 83766, 86	downstream, in gene, downstream, in gene, downstream, in gene	1	1	1	56.5	60	20	2	2_A375_pNL97_plus_lncRNA_AR..1	96	Gene C20orf132	DKFZp434N0426, FLJ38113, C20orf131, dJ621N11.4, C20orf132, dJ621N11.3	chromosome 20 open reading frame 132	NM_213631, NM_213632, NM_152503	232185_at, 236618_at	NP_998796.1, NP_998797.1, NP_689716.4
GeneID.6185	RPN2	20	35,807,456	35,870,026	62,570	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3558, 2_A375_pNL97_plus_lncRNA_AR..1..5095, 4_A375_EGR1..1..5340	32, 32, 432	in gene, in gene, in gene	1	1	1	95	96	22	1	2_A375_pNL97_plus_lncRNA_AR..1	96	Gene RPN2	RPN2, SWP1, RPN-II, RIBIIR, RPNII	ribophorin II	NM_002951, NM_001135771, hCT2313839.0, hCT2313840.0, hCT2313841.0, hCT2355505.0, hCT28372.2	208689_s_at, 213399_x_at, 213491_x_at	NP_002942.2, NP_001129243.1, EAW76073.1, EAW76074.1, EAW76076.1, EAW76077.1, EAW76075.1
GeneID.63905	MANBAL	20	35,916,051	35,945,863	27,812	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5096, 4_A375_EGR1..1..5341	45, 61	in gene, in gene	0	1	1	21	26	21	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene MANBAL	MANBAL		NM_022077, NM_001003897, hCT1983216.1, hCT2313843.0, hCT2313844.0, hCT29286.2	224689_at	NP_071360.1, NP_001003897.1, EAW76068.1, EAW76069.1, EAW76070.1, EAW76071.1
GeneID.6714	SRC	20	35,973,088	36,033,821	60,733	+	3	2_A375_pNL97_plus_lncRNA_AR..1..5097, 4_A375_EGR1..1..5342, 4_A375_EGR1..1..5343	-1024, 45200, 53920	upstream, in gene, in gene	0	1	1	12.67	16.67	14	3	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SRC	SRC1, p60-Src, SRC, c-SRC, ASV	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	NM_005417, NM_198291, hCT2313846.0, hCT2313847.0, hCT2313848.0, hCT2313849.0, hCT2355463.0, hCT29285.3	1558210_at, 1558211_s_at, 1565080_at, 1565082_x_at, 213324_at, 221281_at, 221284_s_at	NP_005408.1, NP_938033.1, EAW76062.1, EAW76063.1, EAW76065.1, EAW76067.1, EAW76064.1, EAW76066.1
GeneID.10904	BLCAP	20	36,145,819	36,156,333	10,514	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3559, 2_A375_pNL97_plus_lncRNA_AR..1..5098, 4_A375_EGR1..1..5344, 4_A375_EGR1..1..5345	-179, -147, 6733, 45	upstream, upstream, in gene, in gene	1	1	1	44.5	48	24	2	2_A375_pNL97_plus_lncRNA_AR..1	88	Gene BLCAP	BLCAP, BC10	bladder cancer associated protein	NM_006698, NM_001167820, NM_001167821, NM_001167822, NM_001167823, hCT29278.3	201032_at	NP_006689.1, NP_001161292.1, NP_001161293.1, NP_001161294.1, NP_001161295.1, EAW76056.1
GeneID.4826	NNAT	20	36,149,607	36,152,092	2,485	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3559, 2_A375_pNL97_plus_lncRNA_AR..1..5098, 4_A375_EGR1..1..5344, 4_A375_EGR1..1..5345	6905, 6873, -7, 6681	downstream, downstream, upstream, downstream	1	1	1	44.5	48	24	2	2_A375_pNL97_plus_lncRNA_AR..1	88	Gene NNAT	Peg5, MGC1439, NNAT	neuronatin	NM_005386, NM_181689, hCT1983215.1, hCT2313857.0, hCT2313860.0, hCT2355447.0, hCT29279.2	204239_s_at	NP_005377.1, NP_859017.1, EAW76057.1, EAW76058.1, EAW76059.1, EAW76061.1, EAW76060.1
GeneID.56259	CTNNBL1	20	36,322,434	36,500,520	178,086	+	1	4_A375_EGR1..1..5346	62	in gene	0	0	1	10	16	20	1	4_A375_EGR1..1	20	Gene CTNNBL1	NYD-SP19, CTNNBL1, P14L, dJ633O20.1, C20orf33, FLJ21108, PP8304, NAP	catenin, beta like 1	NM_030877, hCT1951311.1, hCT2314793.0	221021_s_at	NP_110517.2, EAW76055.1, EAW76054.1
GeneID.128434	VSTM2L	20	36,531,499	36,573,752	42,253	+	8	1_A375_pNL7_minus_lncRNA_AR..1..3562, 1_A375_pNL7_minus_lncRNA_AR..1..3563, 2_A375_pNL97_plus_lncRNA_AR..1..5101, 2_A375_pNL97_plus_lncRNA_AR..1..5102, 4_A375_EGR1..1..5349, 4_A375_EGR1..1..5350, 4_A375_EGR1..1..5351, 4_A375_EGR1..1..5352	-1547, -923, -1515, -1003, -8555, 1557, 3445, 12181	upstream, upstream, upstream, upstream, upstream, in gene, in gene, in gene	1	1	1	13.67	12.17	16.5	6	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene VSTM2L	VSTM2L, C20orf102, dJ1118M15.2	V-set and transmembrane domain containing 2 like	NM_080607, hCT2314796.0, hCT2314797.0, hCT29289.3	226973_at	NP_542174.1, EAW76053.1, EAW76051.1, EAW76052.1
GeneID.9675	KIAA0406	20	36,611,423	36,661,833	50,410	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5103, 4_A375_EGR1..1..5353	41, -503	in gene, upstream	0	1	1	15	26	18	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene KIAA0406	KIAA0406, TTI1	Tel2 interacting protein 1 homolog (S. pombe)	NM_014657, hCT2313027.0, hCT2313029.0, hCT2355461.0, hCT29283.2	212898_at	NP_055472.1, EAW76047.1, EAW76048.1, EAW76049.1, EAW76050.1
GeneID.58490	RPRD1B	20	36,661,948	36,720,766	58,818	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5103, 4_A375_EGR1..1..5353	-156, 386	upstream, in gene	0	1	1	15	26	18	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene RPRD1B	NET60, CREPT, FLJ44520, dJ1057B20.2, C20orf77, RPRD1B, DKFZp434P0735	regulation of nuclear pre-mRNA domain containing 1B	NM_021215, hCT2314799.0, hCT29284.3	225024_at, 230801_at	NP_067038.1, EAW76046.1, EAW76045.1
GeneID.7052	TGM2	20	36,756,863	36,793,700	36,837	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5104, 4_A375_EGR1..1..5354	12580, 29092	in gene, in gene	0	1	1	11.5	16.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TGM2	GNAH, G-ALPHA-h, TG2, TGM2, TGC	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	NM_004613, NM_198951, hCT2313021.0, hCT2313022.0, hCT2313024.0, hCT2313025.0, hCT2313026.0	201042_at, 211003_x_at, 211573_x_at, 216183_at	NP_004604.2, NP_945189.1, EAW76040.1, EAW76041.1, EAW76043.1, EAW76044.1, EAW76042.1
GeneID.85449	KIAA1755	20	36,838,907	36,889,174	50,267	-	1	4_A375_EGR1..1..5355	47894	in gene	0	0	1	5	7	15	1	4_A375_EGR1..1	15	Gene KIAA1755	KIAA1755		NM_001029864, hCT1645413.3, hCT2313018.0, hCT2313019.0	1561394_s_at, 231893_at	NP_001025035.1, EAW76037.1, EAW76038.1, EAW76039.1
GeneID.388796	LOC388796	20	37,049,239	37,064,018	14,779	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3566, 2_A375_pNL97_plus_lncRNA_AR..1..5105, 4_A375_EGR1..1..5356, 4_A375_EGR1..1..5357	50, 50, 16466, 82	in gene, in gene, downstream, in gene	1	1	1	26.5	28.5	22	2	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene LOC388796		hypothetical LOC388796	NR_015366, NR_027241	225857_s_at, 65588_at	
GeneID.26776	SNORA71B	20	37,053,843	37,053,978	135	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3566, 2_A375_pNL97_plus_lncRNA_AR..1..5105, 4_A375_EGR1..1..5356, 4_A375_EGR1..1..5357	-9990, -9990, 6426, -9958	upstream, upstream, downstream, upstream	1	1	1	26.5	28.5	22	2	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene SNORA71B	RNU71B, SNORA71B, U71b	small nucleolar RNA, H/ACA box 71B	NR_002910	1568248_x_at, 1568249_at	
GeneID.26777	SNORA71A	20	37,055,949	37,056,086	137	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3566, 2_A375_pNL97_plus_lncRNA_AR..1..5105, 4_A375_EGR1..1..5356, 4_A375_EGR1..1..5357	-7882, -7882, 8534, -7850	upstream, upstream, downstream, upstream	1	1	1	26.5	28.5	22	2	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene SNORA71A	U71a, RNU71A, SNORA71A	small nucleolar RNA, H/ACA box 71A	NR_002911	1565858_at, 1565859_at	
GeneID.677839	SNORA71C	20	37,058,310	37,058,447	137	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3566, 2_A375_pNL97_plus_lncRNA_AR..1..5105, 4_A375_EGR1..1..5357	-5521, -5521, -5489	upstream, upstream, upstream	1	1	1	44	45	25	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene SNORA71C	U71c, SNORA71C	small nucleolar RNA, H/ACA box 71C	NR_003017		
GeneID.677840	SNORA71D	20	37,062,505	37,062,642	137	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3566, 2_A375_pNL97_plus_lncRNA_AR..1..5105, 4_A375_EGR1..1..5357	-1326, -1326, -1294	upstream, upstream, upstream	1	1	1	44	45	25	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene SNORA71D	SNORA71D, U71d	small nucleolar RNA, H/ACA box 71D	NR_003018		
GeneID.128439	SNHG11	20	37,075,297	37,079,584	4,287	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3567, 2_A375_pNL97_plus_lncRNA_AR..1..5106, 4_A375_EGR1..1..5358	-33, -33, 479	upstream, upstream, in gene	1	1	1	69	84	20	1	2_A375_pNL97_plus_lncRNA_AR..1	84	Gene SNHG11	SNHG11, C20orf198, NCRNA00101	small nucleolar RNA host gene 11 (non-protein coding)	NR_003239, hCT2314807.0, hCT2314808.0, hCT2349453.0, hCT2355495.0, hCT2355496.0, hCT2355497.0	226149_at	EAW76027.1, EAW76029.1, EAW76025.1, EAW76026.1, EAW76028.1, EAW76030.1
GeneID.677821	SNORA39	20	37,076,726	37,076,861	135	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3567, 2_A375_pNL97_plus_lncRNA_AR..1..5106, 4_A375_EGR1..1..5358	-1462, -1462, -950	upstream, upstream, upstream	1	1	1	69	84	20	1	2_A375_pNL97_plus_lncRNA_AR..1	84	Gene SNORA39	SNORA39, ACA39	small nucleolar RNA, H/ACA box 39	NR_002972		
GeneID.677837	SNORA60	20	37,078,012	37,078,147	135	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3567, 2_A375_pNL97_plus_lncRNA_AR..1..5106, 4_A375_EGR1..1..5358	-2748, -2748, -2236	upstream, upstream, upstream	1	1	1	69	84	20	1	2_A375_pNL97_plus_lncRNA_AR..1	84	Gene SNORA60	ACA60, SNORA60	small nucleolar RNA, H/ACA box 60	NR_002986		
GeneID.343578	C20orf95	20	37,230,577	37,279,295	48,718	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5107, 4_A375_EGR1..1..5359	44303, 43983	in gene, in gene	0	1	1	19	23	19	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene C20orf95	dJ1100H13.4, ARHGAP40, C20orf95	Rho GTPase activating protein 40	NM_001164431		NP_001157903.1
GeneID.140679	SLC32A1	20	37,353,105	37,358,015	4,910	+	2	4_A375_EGR1..1..5360, 4_A375_EGR1..1..5361	-401, 3607	upstream, in gene	0	0	1	8	9.5	21.5	2	4_A375_EGR1..1	23	Gene SLC32A1	VGAT, VIAAT, SLC32A1	solute carrier family 32 (GABA vesicular transporter), member 1	NM_080552, hCT29304.2	240532_at	NP_542119.1, EAW76012.1
GeneID.79913	ACTR5	20	37,377,097	37,401,089	23,992	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5111, 2_A375_pNL97_plus_lncRNA_AR..1..5112	23, 16599	in gene, in gene	0	1	0	16	19.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ACTR5	FLJ12785, ACTR5, INO80M, Arp5	ARP5 actin-related protein 5 homolog (yeast)	NM_024855, hCT2314818.0, hCT29302.3	219623_at, 222147_s_at	NP_079131.3, EAW76011.1, EAW76010.1
GeneID.26051	PPP1R16B	20	37,434,348	37,551,667	117,319	+	8	1_A375_pNL7_minus_lncRNA_AR..1..3571, 1_A375_pNL7_minus_lncRNA_AR..1..3572, 2_A375_pNL97_plus_lncRNA_AR..1..5113, 2_A375_pNL97_plus_lncRNA_AR..1..5114, 2_A375_pNL97_plus_lncRNA_AR..1..5115, 4_A375_EGR1..1..5362, 4_A375_EGR1..1..5363, 4_A375_EGR1..1..5364	84916, 120756, 84916, 91604, 120532, -460, 30368, 121156	in gene, downstream, in gene, in gene, downstream, upstream, in gene, downstream	1	1	1	15	16.6	18.2	5	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene PPP1R16B	PPP1R16B, TIMAP, ANKRD4, KIAA0823	protein phosphatase 1, regulatory (inhibitor) subunit 16B	NM_015568, NM_001172735, hCT29300.2	212750_at, 233813_at, 41577_at	NP_056383.1, NP_001166206.1, EAW76009.1
GeneID.81610	FAM83D	20	37,554,955	37,581,703	26,748	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3572, 2_A375_pNL97_plus_lncRNA_AR..1..5115, 2_A375_pNL97_plus_lncRNA_AR..1..5116, 4_A375_EGR1..1..5364, 4_A375_EGR1..1..5365	149, -75, 35893, 549, 36245	in gene, upstream, downstream, in gene, downstream	1	1	1	20	22	22.5	2	4_A375_EGR1..1	24	Gene FAM83D	C20orf129, FAM83D, dJ616B8.3, FLJ38341, CHICA	family with sequence similarity 83, member D	NM_030919, hCT29299.3	225687_at	NP_112181.2, EAW76008.1
GeneID.60625	DHX35	20	37,590,981	37,668,366	77,385	+	4	2_A375_pNL97_plus_lncRNA_AR..1..5116, 2_A375_pNL97_plus_lncRNA_AR..1..5117, 4_A375_EGR1..1..5365, 4_A375_EGR1..1..5366	-133, 87643, 219, 76907	upstream, downstream, in gene, downstream	0	1	1	15.33	16.67	20.33	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene DHX35	DDX35, KAIA0875, C20orf15, DHX35, FLJ22759	DEAH (Asp-Glu-Ala-His) box polypeptide 35	NM_001190809, NM_021931, NR_033905, hCT2312638.0, hCT2312640.0, hCT29301.3	1561132_at, 218579_s_at, 234728_s_at	NP_001177738.1, NP_068750.2, EAW76005.1, EAW76006.1, EAW76007.1
GeneID.9935	MAFB	20	39,314,515	39,317,876	3,361	-	2	4_A375_EGR1..1..5369, 4_A375_EGR1..1..5370	5652, -732	downstream, upstream	0	0	1	8.5	10	17	2	4_A375_EGR1..1	17	Gene MAFB	KRML, MGC43127, MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	NM_005461, hCT28376.3	218559_s_at, 222670_s_at	NP_005452.2, EAW76000.1





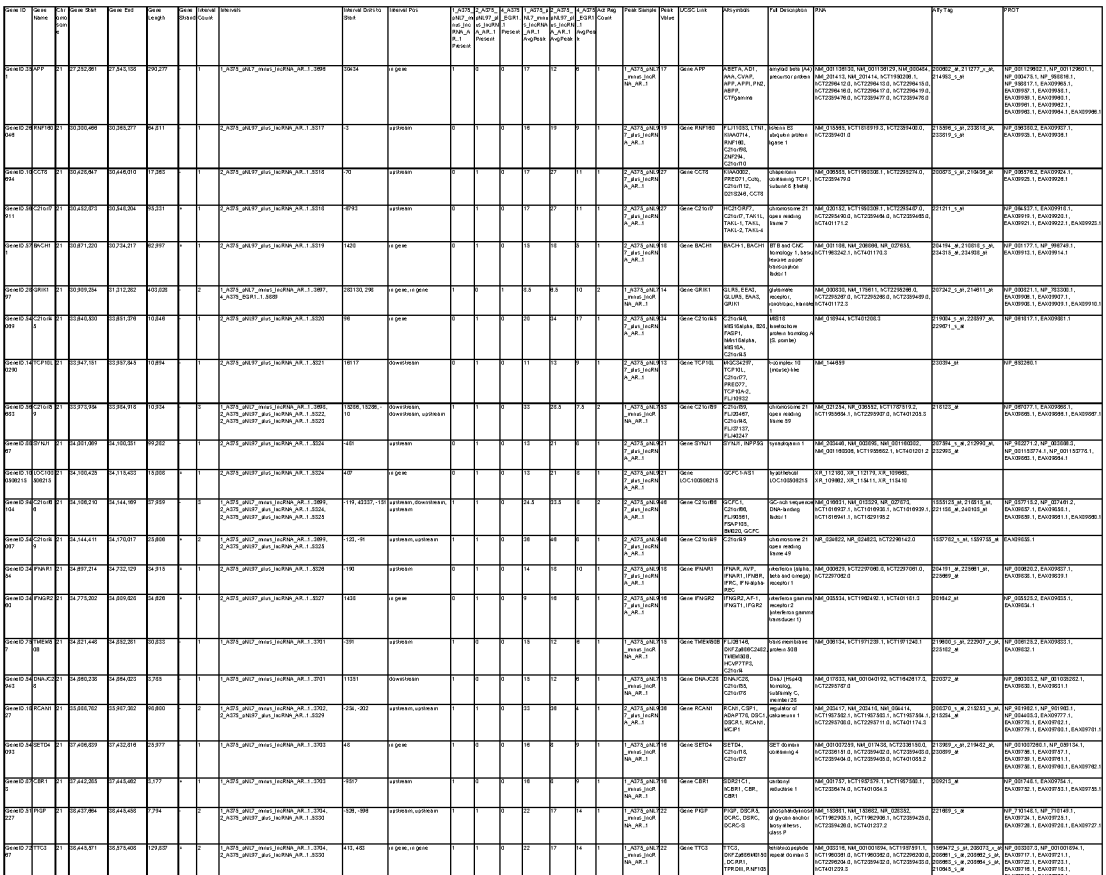
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.5740	PTGIS	20	48,120,411	48,184,707	64,296	-	2	4_A375_EGR1..1..5444, 4_A375_EGR1..1..5445	5571, 419	in gene, in gene	0	0	1	11.5	10.5	23	2	4_A375_EGR1..1	24	Gene PTGIS	PGIS, MGC126858, CYP8A1, PTGIS, PTGI, MGC126860, CYP8	prostaglandin I2 (prostacyclin) synthase	NM_000961, hCT2312298.1	208131_s_at, 210702_s_at, 211892_s_at	NP_000952.1, EAW75655.1
GeneID.728671	LOC728671	20	48,232,412	48,237,694	5,282	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3814, 2_A375_pNL97_plus_lncRNA_AR..1..5180	-4860, -4798	upstream, upstream	1	1	0	20	23	14	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC728671		hypothetical LOC728671	XM_001716479, XM_001128100, XM_001129178		XP_001716531.2, XP_001128100.2, XP_001129178.2
GeneID.9334	B4GALT5	20	48,249,482	48,330,421	80,939	-	4	2_A375_pNL97_plus_lncRNA_AR..1..5181, 2_A375_pNL97_plus_lncRNA_AR..1..5182, 4_A375_EGR1..1..5446, 4_A375_EGR1..1..5447	51941, -3915, 405, -235	in gene, upstream, in gene, upstream	0	1	1	16	15	14	4	4_A375_EGR1..1	22	Gene B4GALT5	MGC138470, B4Gal-T5, beta4GalT-V, B4GALT5, beta4Gal-T5, BETA4-GALT-IV, gt-V	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	NM_004776, hCT2312294.0, hCT29122.3	221484_at, 221485_at	NP_004767.1, EAW75654.1, EAW75653.1
GeneID.23315	SLC9A8	20	48,429,250	48,508,772	79,522	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3816, 2_A375_pNL97_plus_lncRNA_AR..1..5183, 2_A375_pNL97_plus_lncRNA_AR..1..5184, 4_A375_EGR1..1..5448, 4_A375_EGR1..1..5449, 4_A375_EGR1..1..5450	75022, -468, 75054, -2, 74206, 75326	in gene, upstream, in gene, upstream, in gene, in gene	1	1	1	15.33	16.67	17	3	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene SLC9A8	FLJ42500, MGC138418, KIAA0939, NHE8, SLC9A8, DKFZp686C03237	solute carrier family 9 (sodium/hydrogen exchanger), member 8	NM_015266, hCT2318423.0, hCT2318424.0, hCT2318425.0, hCT2318426.0, hCT2355429.0, hCT29125.3	212947_at	NP_056081.1, EAW75650.1, EAW75647.1, EAW75648.1, EAW75649.1, EAW75651.1, EAW75652.1
GeneID.9825	SPATA2	20	48,519,928	48,532,080	12,152	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3817, 2_A375_pNL97_plus_lncRNA_AR..1..5185	-112, -112	upstream, upstream	1	1	0	34	38	15	1	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene SPATA2	FLJ13167, tamo, PD1, KIAA0757, SPATA2	spermatogenesis associated 2	NM_001135773, NM_006038, hCT2312291.0, hCT28388.3	204433_s_at, 204434_at	NP_001129245.1, NP_006029.1, EAW75645.1, EAW75646.1
GeneID.55905	RNF114	20	48,552,914	48,570,422	17,508	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3818, 2_A375_pNL97_plus_lncRNA_AR..1..5186	-114, 382	upstream, in gene	1	1	0	23	19	18	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene RNF114	PSORS12, RNF114, ZNF313	ring finger protein 114	NM_018683, hCT1953355.1, hCT2355433.0, hCT2355434.0, hCT29126.3	200867_at, 200868_s_at, 211678_s_at	NP_061153.1, EAW75641.1, EAW75642.1, EAW75643.1, EAW75644.1
GeneID.8615	SNAI1	20	48,599,513	48,605,423	5,910	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5187	6919	downstream	0	1	0	14	22	14	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SNAI1	SNAH, SLUGH2, dJ710H13.1, SNAI1, SNA	snail homolog 1 (Drosophila)	NM_005985, hCT29121.2	219480_at	NP_005976.2, EAW75640.1
GeneID.7335	UBE2V1	20	48,697,661	48,732,494	34,833	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5189, 4_A375_EGR1..1..5453	-2, 41502	upstream, downstream	0	1	1	12	17	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene UBE2V1	UEV1A, CROC-1, UEV1, CROC1, UBE2V1, UBE2V, CIR1, UEV-1	ubiquitin-conjugating enzyme E2 variant 1	NM_199144, NM_001032288, NM_021988, NM_022442		NP_954595.1, NP_001027459.1, NP_071887.1, NP_068823.2
GeneID.387522	TMEM189-UBE2V1	20	48,697,661	48,770,335	72,674	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3819, 2_A375_pNL97_plus_lncRNA_AR..1..5189, 2_A375_pNL97_plus_lncRNA_AR..1..5190, 4_A375_EGR1..1..5453, 4_A375_EGR1..1..5454	15039, 37639, 14863, 79343, 12511	in gene, in gene, in gene, downstream, in gene	1	1	1	13.5	17.5	15.5	4	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene TMEM189-UBE2V1	CROC1B, TMEM189-UBE2V1, KUA-UEV, CROC-1B, UBE2V1	TMEM189-UBE2V1 readthrough	NM_199203	201001_s_at, 201002_s_at, 216315_x_at	NP_954673.1
GeneID.387521	TMEM189	20	48,740,274	48,770,335	30,061	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3819, 2_A375_pNL97_plus_lncRNA_AR..1..5189, 2_A375_pNL97_plus_lncRNA_AR..1..5190, 4_A375_EGR1..1..5454	15039, 37639, 14863, 12511	in gene, downstream, in gene, in gene	1	1	1	15.33	20.33	15	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene TMEM189	KUA, TMEM189, UBE2V1	transmembrane protein 189	NM_199129, NM_001162505, NR_027689	223186_at	NP_954580.1, NP_001155977.1
GeneID.100506115	LOC100506115	20	48,884,035	48,896,332	12,297	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3821, 2_A375_pNL97_plus_lncRNA_AR..1..5192, 4_A375_EGR1..1..5456	-211, -163, 3165	upstream, upstream, in gene	1	1	1	13	13	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100506115		hypothetical LOC100506115	XR_109821, XR_109822		
GeneID.5770	PTPN1	20	49,126,891	49,201,088	74,197	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3823, 2_A375_pNL97_plus_lncRNA_AR..1..5195	-299, 51477	upstream, in gene	1	1	0	16.5	20	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PTPN1	PTP1B, PTPN1	protein tyrosine phosphatase, non-receptor type 1	NM_002827, hCT2314155.0, hCT2314156.0, hCT28384.2	202716_at, 217686_at, 217689_at, 239526_x_at	NP_002818.1, EAW75624.1, EAW75625.1, EAW75626.1
GeneID.100506153	LOC100506153	20	49,187,512	49,194,578	7,066	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5195	16210	downstream	0	1	0	14	24	11	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LOC100506153		hypothetical LOC100506153	XR_112163, XR_109824, XR_115384		
GeneID.140876	FAM65C	20	49,202,645	49,253,426	50,781	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3824, 2_A375_pNL97_plus_lncRNA_AR..1..5196, 4_A375_EGR1..1..5459	-8734, -8582, -8622	upstream, upstream, upstream	1	1	1	18	23	18	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene FAM65C	FLJ32230, FAM65C, FLJ00360, dJ530I15.2, C20orf175	family with sequence similarity 65, member C	NM_080829, hCT1953349.2, hCT1953350.2, hCT2314055.0, hCT2314056.1, hCT28773.4	227654_at, 243978_at	NP_543019.2, EAW75618.1, EAW75619.1, EAW75620.1, EAW75621.1, EAW75622.1
GeneID.100506175	LOC100506175	20	49,262,008	49,276,828	14,820	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3824, 2_A375_pNL97_plus_lncRNA_AR..1..5196, 4_A375_EGR1..1..5459	152, 0, 40	in gene, in gene, in gene	1	1	1	18	23	18	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100506175		hypothetical LOC100506175	XR_109825		
GeneID.84612	PARD6B	20	49,348,081	49,370,278	22,197	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3825, 4_A375_EGR1..1..5460	15, -337	in gene, upstream	1	0	1	20	12	25	1	4_A375_EGR1..1	25	Gene PARD6B	PAR6B, PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	NM_032521, hCT1950760.1, hCT2314142.0, hCT28340.3	211907_s_at, 214827_at, 235165_at	NP_115910.1, EAW75617.1, EAW75615.1, EAW75616.1
GeneID.55653	BCAS4	20	49,411,467	49,493,714	82,247	+	1	4_A375_EGR1..1..5461	70709	in gene	0	0	1	7	7	17	1	4_A375_EGR1..1	17	Gene BCAS4	BCAS4, CNOL, FLJ20495	breast carcinoma amplified sequence 4	NM_001010974, NM_017843, NM_198799, hCT1953263.1, hCT2355571.0	220588_at, 228787_s_at	NP_001010974.1, NP_060313.3, NP_942094.2, EAW75613.1, EAW75614.1
GeneID.23394	ADNP	20	49,506,883	49,547,527	40,644	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3826, 2_A375_pNL97_plus_lncRNA_AR..1..5197	-745, -825	upstream, upstream	1	1	0	20	28	14	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene ADNP	KIAA0784, ADNP, ADNP1	activity-dependent neuroprotector homeobox	NM_181442, NM_015339, hCT1950768.1, hCT29337.2	201773_at	NP_852107.1, NP_056154.1, EAW75611.1, EAW75612.1
GeneID.8813	DPM1	20	49,551,405	49,575,060	23,655	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3826, 1_A375_pNL7_minus_lncRNA_AR..1..3827, 2_A375_pNL97_plus_lncRNA_AR..1..5197, 2_A375_pNL97_plus_lncRNA_AR..1..5198	26768, 122, 26708, -380	downstream, in gene, downstream, upstream	1	1	0	20	30	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene DPM1	DPM1, CDGIE, MPDS	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	NM_003859, hCT2314047.0, hCT2355553.0, hCT2355554.0	202673_at	NP_003850.1, EAW75608.1, EAW75607.1, EAW75609.1
GeneID.27304	MOCS3	20	49,575,363	49,577,820	2,457	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3827, 2_A375_pNL97_plus_lncRNA_AR..1..5198	-425, 77	upstream, in gene	1	1	0	20	32	19	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene MOCS3	MOCS3, UBA4, dJ914P20.3, MGC9252	molybdenum cofactor synthesis 3	NM_014484, hCT28383.2	206141_at	NP_055299.1, EAW75606.1
GeneID.3755	KCNG1	20	49,620,193	49,639,675	19,482	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5200, 4_A375_EGR1..1..5462	251, 379	in gene, in gene	0	1	1	16	22	20	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene KCNG1	K13, kH2, KCNG1, KV6.1, MGC12878, KCNG	potassium voltage-gated channel, subfamily G, member 1	NM_002237, hCT29333.1	211053_at, 214595_at	NP_002228.2, EAW75605.1
GeneID.4773	NFATC2	20	50,007,765	50,179,168	171,403	-	12	1_A375_pNL7_minus_lncRNA_AR..1..3831, 1_A375_pNL7_minus_lncRNA_AR..1..3832, 1_A375_pNL7_minus_lncRNA_AR..1..3833, 1_A375_pNL7_minus_lncRNA_AR..1..3834, 2_A375_pNL97_plus_lncRNA_AR..1..5207, 2_A375_pNL97_plus_lncRNA_AR..1..5208, 2_A375_pNL97_plus_lncRNA_AR..1..5209, 2_A375_pNL97_plus_lncRNA_AR..1..5210, 2_A375_pNL97_plus_lncRNA_AR..1..5211, 4_A375_EGR1..1..5464, 4_A375_EGR1..1..5465, 4_A375_EGR1..1..5466	137040, 124668, 64608, -1392, 137056, 124632, 65024, 8208, -1216, 130400, 70464, 64	in gene, in gene, in gene, upstream, in gene, in gene, in gene, in gene, upstream, in gene, in gene, in gene	1	1	1	19.25	21.83	12.63	8	2_A375_pNL97_plus_lncRNA_AR..1	47	Gene NFATC2	NFATC2, NFATP, NFAT1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	NM_173091, NM_012340, NM_001136021, hCT2312681.0, hCT2312683.0	224542_s_at, 226991_at, 231601_at	NP_775114.1, NP_036472.2, NP_001129493.1, EAW75602.1, EAW75603.1
GeneID.57167	SALL4	20	50,400,581	50,419,048	18,467	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5212	2232	in gene	0	1	0	10	22	9	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SALL4	MGC133050, dJ1112F19.1, DRRS, HSAL4, ZNF797, SALL4	sal-like 4 (Drosophila)	NM_020436, hCT2355578.0, hCT29338.2	229661_at, 236501_at	NP_065169.1, EAW75595.1, EAW75596.1
GeneID.55734	ZFP64	20	50,700,550	50,808,524	107,974	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3836, 2_A375_pNL97_plus_lncRNA_AR..1..5214	428, 492	in gene, in gene	1	1	0	25	23	14	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene ZFP64	MGC940, ZFP64, ZNF338	zinc finger protein 64 homolog (mouse)	NM_018197, NM_022088, NM_199426, NM_199427, hCT2312671.0, hCT2312672.0, hCT2312673.0, hCT2312674.0	218968_s_at, 219536_s_at, 222697_s_at, 229186_s_at	NP_060667.2, NP_071371.3, NP_955459.2, NP_955458.1, EAW75591.1, EAW75592.1, EAW75590.1, EAW75593.1
GeneID.7764	ZNF217	20	52,183,610	52,199,636	16,026	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5215	4	in gene	0	1	0	14	19	3	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ZNF217	ZNF217, ZABC1	zinc finger protein 217	NM_006526, hCT1950762.1, hCT2311964.0, hCT2311965.0, hCT28357.2	203739_at	NP_006517.1, EAW75579.1, EAW75578.1, EAW75580.1, EAW75581.1
GeneID.5203	PFDN4	20	52,824,502	52,836,492	11,990	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3842, 2_A375_pNL97_plus_lncRNA_AR..1..5221	58, 10	in gene, in gene	1	1	0	29	45	12	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene PFDN4	C1, PFD4, PFDN4	prefoldin subunit 4	NM_002623, hCT28592.2	205361_s_at, 205362_s_at	NP_002614.2, EAW75572.1
GeneID.116151	C20orf108	20	54,933,983	54,943,719	9,736	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5226	1121	in gene	0	1	0	14	25	16	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene C20orf108	5A3, DKFZp434A1114, dJ1187H4.1, C20orf108	chromosome 20 open reading frame 108	NM_080821, hCT2312006.0, hCT2312007.0, hCT30347.2	224690_at, 224693_at	NP_543011.2, EAW75563.1, EAW75564.1, EAW75565.1
GeneID.6790	AURKA	20	54,944,445	54,967,351	22,906	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3846, 2_A375_pNL97_plus_lncRNA_AR..1..5226, 2_A375_pNL97_plus_lncRNA_AR..1..5227	-265, 32247, -281	upstream, downstream, upstream	1	1	0	35	42	15	2	2_A375_pNL97_plus_lncRNA_AR..1	59	Gene AURKA	MGC34538, ARK1, AURA, AURKA, AURORA2, STK7, BTAK, AIK, STK15, STK6	aurora kinase A	NM_003600, NM_198433, NM_198434, NM_198435, NM_198436, NM_198437, hCT1950770.0, hCT1953374.1, hCT1953375.1, hCT1953376.2, hCT1965747.1, hCT2311645.0, hCT2311650.0, hCT2355418.0, hCT2355419.0, hCT2355420.0, hCT2355421.0, hCT2355423.0, hCT30342.3	204092_s_at, 208079_s_at, 208080_at	NP_003591.2, NP_940835.1, NP_940836.1, NP_940837.1, NP_940838.1, NP_940839.1, EAW75550.1, EAW75551.1, EAW75552.1, EAW75553.1, EAW75554.1, EAW75555.1, EAW75556.1, EAW75557.1, EAW75558.1, EAW75559.1, EAW75560.1, EAW75561.1, EAW75562.1
GeneID.1477	CSTF1	20	54,967,427	54,979,582	12,155	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3846, 2_A375_pNL97_plus_lncRNA_AR..1..5227	189, 205	in gene, in gene	1	1	0	58	59	14	1	2_A375_pNL97_plus_lncRNA_AR..1	59	Gene CSTF1	CstFp50, CSTF1, CstF-50	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa	NM_001033521, NM_001324, NM_001033522, hCT2312009.0, hCT30344.3	202190_at, 32723_at	NP_001028693.1, NP_001315.1, NP_001028694.1, EAW75548.1, EAW75549.1
GeneID.57091	CASS4	20	54,987,168	55,034,396	47,228	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3847, 2_A375_pNL97_plus_lncRNA_AR..1..5228, 4_A375_EGR1..1..5469	56416, 56364, 56288	downstream, downstream, downstream	1	1	1	34	26	41	1	4_A375_EGR1..1	41	Gene CASS4	HEPL, CASS4, C20orf32, HEFL, CAS4	Cas scaffolding protein family member 4	NM_020356, NM_001164114, NM_001164115, NM_001164116, hCT1950772.1, hCT1953379.1, hCT2312012.0, hCT2355498.0, hCT2355499.0, hCT2355500.0, hCT30348.2	1554786_at, 220868_s_at	NP_065089.2, NP_001157586.1, NP_001157587.1, NP_001157588.1, EAW75546.1, EAW75547.1, EAW75541.1, EAW75542.1, EAW75543.1, EAW75544.1, EAW75545.1
GeneID.51507	C20orf43	20	55,043,647	55,093,942	50,295	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3847, 2_A375_pNL97_plus_lncRNA_AR..1..5228, 4_A375_EGR1..1..5469	-63, -95, -191	upstream, upstream, upstream	1	1	1	34	26	41	1	4_A375_EGR1..1	41	Gene C20orf43	SHUJUN-3, C20orf43, CDAO5, HSPC164	chromosome 20 open reading frame 43	NM_016407	217737_x_at, 224126_at, 233842_x_at, 234926_s_at, 236702_at	NP_057491.2
GeneID.7022	TFAP2C	20	55,204,358	55,214,339	9,981	+	3	2_A375_pNL97_plus_lncRNA_AR..1..5229, 4_A375_EGR1..1..5470, 4_A375_EGR1..1..5471	1146, -2806, 1466	in gene, upstream, in gene	0	1	1	11	15.5	19.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene TFAP2C	ERF1, AP2-GAMMA, TFAP2G, TFAP2C, hAP-2g	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	NM_003222, hCT29104.2	205286_at, 205287_s_at	NP_003213.1, EAW75532.1
GeneID.655	BMP7	20	55,743,809	55,841,707	97,898	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3850, 2_A375_pNL97_plus_lncRNA_AR..1..5237, 2_A375_pNL97_plus_lncRNA_AR..1..5238, 4_A375_EGR1..1..5477, 4_A375_EGR1..1..5478	60875, 75979, 70987, 1323, 43	in gene, in gene, in gene, in gene, in gene	1	1	1	15.6	20.6	15.6	5	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene BMP7	BMP7, OP-1	bone morphogenetic protein 7	NM_001719, hCT1953393.1, hCT1953394.1, hCT31354.3	209590_at, 209591_s_at, 211259_s_at, 211260_at	NP_001710.1, EAW75529.1, EAW75530.1, EAW75531.1
GeneID.23626	SPO11	20	55,904,831	55,919,049	14,218	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5239, 4_A375_EGR1..1..5480	21633, 21393	downstream, downstream	0	1	1	19	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SPO11	MGC39953, CT35, SPO11	SPO11 meiotic protein covalently bound to DSB homolog (S. cerevisiae)	NM_012444, NM_198265, hCT1953392.1, hCT31353.2	222259_s_at	NP_036576.1, NP_937998.1, EAW75526.1, EAW75527.1
GeneID.8480	RAE1	20	55,926,145	55,953,519	27,374	+	4	2_A375_pNL97_plus_lncRNA_AR..1..5239, 4_A375_EGR1..1..5480, 4_A375_EGR1..1..5481, 4_A375_EGR1..1..5482	319, 79, 34479, 36255	in gene, in gene, downstream, downstream	0	1	1	11.67	12.33	19.67	3	4_A375_EGR1..1	25	Gene RAE1	RAE1, MGC126077, MRNP41, Mnrp41, MIG14, FLJ30608, MGC117333, MGC126076, dJ800J21.1, dJ481F12.3	RAE1 RNA export 1 homolog (S. pombe)	NM_001015885, NM_003610, hCT2312071.0, hCT2312072.0, hCT2355436.0	201558_at, 211318_s_at	NP_001015885.1, NP_003601.1, EAW75523.1, EAW75524.1, EAW75525.1
GeneID.100462983	MTRNR2L3	20	55,933,496	55,934,878	1,382	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5239, 4_A375_EGR1..1..5480	8414, 8654	downstream, downstream	0	1	1	19	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MTRNR2L3	HN3, MTRNR2L3	MT-RNR2-like 3	NM_001190472		NP_001177401.1
GeneID.100291105	LOC100291105	20	55,959,216	55,968,118	8,902	-	3	4_A375_EGR1..1..5481, 4_A375_EGR1..1..5482, 4_A375_EGR1..1..5483	7494, 5718, 614	in gene, in gene, in gene	0	0	1	8.67	8	20.33	3	4_A375_EGR1..1	25	Gene LOC100291105		hypothetical LOC100291105	XR_109827, XR_115387		
GeneID.55544	RBM38	20	55,966,463	55,984,389	17,926	+	8	4_A375_EGR1..1..5481, 4_A375_EGR1..1..5482, 4_A375_EGR1..1..5483, 4_A375_EGR1..1..5484, 4_A375_EGR1..1..5485, 4_A375_EGR1..1..5486, 4_A375_EGR1..1..5487, 4_A375_EGR1..1..5488	-5839, -4063, 1041, 13537, 14625, 20365, 23009, 23937	upstream, upstream, in gene, in gene, in gene, downstream, downstream, downstream	0	0	1	8.13	9.63	19	8	4_A375_EGR1..1	25	Gene RBM38	dJ800J21.2, SEB4B, RBM38, SEB4D, HSRNASEB, RNPC1	RNA binding motif protein 38	NM_183425, NM_017495, hCT2312074.0, hCT2312075.0, hCT2355445.0	212430_at	NP_906270.1, NP_059965.2, EAW75520.1, EAW75521.1, EAW75522.1
GeneID.81030	ZBP1	20	56,178,902	56,195,632	16,730	-	3	2_A375_pNL97_plus_lncRNA_AR..1..5241, 4_A375_EGR1..1..5491, 4_A375_EGR1..1..5492	19246, 3686, 3301	downstream, in gene, in gene	0	1	1	12.67	14.33	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ZBP1	ZBP1, DLM-1, DAI, DLM1, C20orf183	Z-DNA binding protein 1	NM_030776, NM_001160417, NM_001160418, NM_001160419, hCT1950773.1, hCT1953397.1, hCT1953398.1, hCT2355449.0, hCT31357.1	208087_s_at, 242020_s_at	NP_110403.2, NP_001153889.1, NP_001153890.1, NP_001153891.1, EAW75511.1, EAW75512.1, EAW75509.1, EAW75510.1, EAW75513.1
GeneID.56937	PMEPA1	20	56,223,452	56,286,541	63,089	-	9	1_A375_pNL7_minus_lncRNA_AR..1..3852, 1_A375_pNL7_minus_lncRNA_AR..1..3853, 1_A375_pNL7_minus_lncRNA_AR..1..3854, 2_A375_pNL97_plus_lncRNA_AR..1..5242, 2_A375_pNL97_plus_lncRNA_AR..1..5243, 2_A375_pNL97_plus_lncRNA_AR..1..5244, 4_A375_EGR1..1..5493, 4_A375_EGR1..1..5494, 4_A375_EGR1..1..5495	13101, 1325, -7187, 13005, 1277, -7155, 49517, 47661, -3347	in gene, in gene, upstream, in gene, in gene, upstream, in gene, in gene, upstream	1	1	1	22	22.17	14.5	6	2_A375_pNL97_plus_lncRNA_AR..1	48	Gene PMEPA1	PMEPA1, TMEPAI, STAG1	prostate transmembrane protein, androgen induced 1	NM_020182, NM_199169, NM_199170, NM_199171, hCT1953395.1, hCT1953396.1, hCT2355442.0, hCT2355443.0, hCT31355.2	217875_s_at, 222449_at, 222450_at, 237166_at	NP_064567.2, NP_954638.1, NP_954639.1, NP_954640.1, EAW75504.1, EAW75507.1, EAW75505.1, EAW75506.1, EAW75508.1

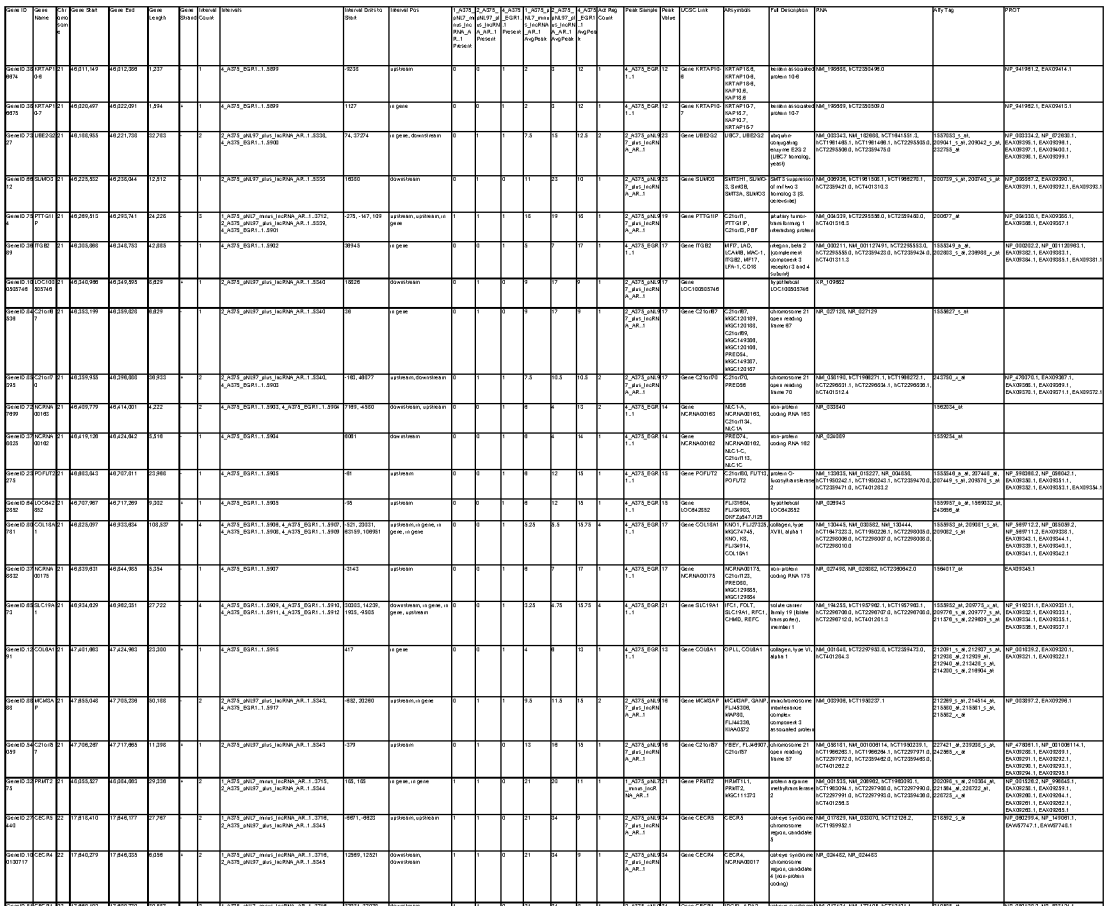
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.9217	VAPB	20	56,964,245	57,021,963	57,718	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5254	50987	in gene	0	1	0	14	21	3	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene VAPB	ALS8, VAMP-C, VAPB, VAP-C, VAP-B, VAMP-B	VAMP (vesicle-associated membrane protein)-associated protein B and C	NM_004738, hCT17825.3, hCT1953298.1, hCT2314478.0	202549_at, 202550_s_at	NP_004729.1, EAW75494.1, EAW75493.1, EAW75495.1
GeneID.164284	APCDD1L	20	57,034,426	57,089,949	55,523	-	1	4_A375_EGR1..1..5499	52805	in gene	0	0	1	8	10	19	1	4_A375_EGR1..1	19	Gene APCDD1L	MGC126809, RP4-685L9.2, APCDD1L, MGC126807, FLJ90166	adenomatosis polyposis coli down-regulated 1-like	NM_153360, hCT2311826.0, hCT2355435.0	235548_at	NP_699191.1, EAW75492.1, EAW75491.1
GeneID.149773	LOC149773	20	57,090,435	57,194,948	104,513	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3659	108621	downstream	1	0	0	29	25	17	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene LOC149773	FLJ33293, FLJ34385	hypothetical LOC149773	NR_034147	1556900_at, 1556901_s_at, 1559433_at	
GeneID.79160	MGC4294	20	57,209,827	57,210,794	967	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5255	10845	downstream	0	1	0	11	17	8	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene MGC4294		hypothetical MGC4294	XR_112170, XR_109828, XR_115388	220898_at	
GeneID.8675	STX16	20	57,226,328	57,254,582	28,254	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3660, 2_A375_pNL97_plus_lncRNA_AR..1..5255, 2_A375_pNL97_plus_lncRNA_AR..1..5256, 4_A375_EGR1..1..5500	8, -5658, -58, -184	in gene, upstream, upstream, upstream	1	1	1	21	29.5	18	2	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene STX16	SYN16, STX16, hsyn16, MGC90328	syntaxin 16	NM_001001433, NM_003763, NM_001134772, NM_001134773, hCT1953321.1, hCT1953323.1, hCT1953324.1, hCT19703.3, hCT2345028.0, hCT2345029.0, hCT2355531.0	1558249_s_at, 221499_s_at, 221500_s_at, 221638_s_at	NP_001001433.1, NP_003754.2, NP_001128244.1, NP_001128245.1, EAW75481.1, EAW75485.1, EAW75482.1, EAW75483.1, EAW75484.1, EAW75486.1, EAW75487.1
GeneID.79716	NPEPL1	20	57,267,862	57,290,900	23,038	+	2	4_A375_EGR1..1..5501, 4_A375_EGR1..1..5502	890, 26862	in gene, downstream	0	0	1	9.5	11	21.5	2	4_A375_EGR1..1	23	Gene NPEPL1	FLJ42065, NPEPL1, bA261P9.2, FLJ11583	aminopeptidase-like 1	NM_024663, hCT1953325.1, hCT1953327.1, hCT19705.3, hCT2345030.0, hCT2345031.0, hCT2345032.0, hCT2345033.0	218821_at, 218822_s_at, 235033_at, 89476_r_at	NP_078939.3, EAW75479.1, EAW75474.1, EAW75475.1, EAW75477.1, EAW75478.1, EAW75476.1, EAW75480.1
GeneID.407022	MIR296	20	57,392,670	57,392,749	79	-	2	4_A375_EGR1..1..5505, 4_A375_EGR1..1..5506	5997, 1453	downstream, downstream	0	0	1	13	12.5	24	2	4_A375_EGR1..1	28	Gene MIR296	MIR296, miRNA296, MIRN296	microRNA 296	NR_029844		
GeneID.100126296	MIR298	20	57,393,281	57,393,368	87	-	2	4_A375_EGR1..1..5505, 4_A375_EGR1..1..5506	6616, 2072	downstream, downstream	0	0	1	13	12.5	24	2	4_A375_EGR1..1	28	Gene MIR298	MIRN298, hsa-mir-298, MIR298	microRNA 298	NR_030580		
GeneID.149775	GNASAS	20	57,393,973	57,425,958	31,985	-	5	4_A375_EGR1..1..5505, 4_A375_EGR1..1..5506, 4_A375_EGR1..1..5507, 4_A375_EGR1..1..5508, 4_A375_EGR1..1..5509	39208, 34662, -1615, -3226, -4922	downstream, downstream, upstream, upstream, upstream	0	0	1	11	9.6	22.2	5	4_A375_EGR1..1	28	Gene GNASAS	GNAS-AS1, GNAS1AS, NESPAS, GNASAS, SANG, GNAS-AS, NCRNA00075	GNAS antisense RNA (non-protein coding)	NR_002785	232681_at	
GeneID.2778	GNAS	20	57,414,795	57,486,250	71,455	+	3	4_A375_EGR1..1..5507, 4_A375_EGR1..1..5508, 4_A375_EGR1..1..5509	12778, 14389, 16085	in gene, in gene, in gene	0	0	1	9.67	8	21	3	4_A375_EGR1..1	25	Gene GNAS	GPSA, AHO, GNAS, MGC33735, POH, NESP, GSA, PHP1C, C20orf45, PHP1B, GSP, GNAS1, PHP1A	GNAS complex locus	NM_000516, NM_080425, NM_080426, NM_001077488, NM_016592, NM_001077489, NR_003259, NM_001077490, hCT1827487.2, hCT1950750.0, hCT1950751.1, hCT1956027.1, hCT1956028.1, hCT1956029.1, hCT1956031.1, hCT2314435.0, hCT2314438.0, hCT2314443.0, hCT2314450.0, hCT2	200780_x_at, 200981_x_at, 211858_x_at, 212273_x_at, 214157_at, 214548_x_at, 217057_s_at, 217058_at, 217673_x_at, 229274_at, 235851_s_at, 239037_at	NP_000507.1, NP_536350.2, NP_536351.1, NP_001070956.1, NP_001070957.1, NP_057676.1, NP_001070958.1, EAW75457.1, EAW75458.1, EAW75459.1, EAW75460.1, EAW75461.1, EAW75462.1, EAW75463.1, EAW75464.1, EAW75465.1, EAW75466.1, EAW75467.1, EAW75468.1, EAW75469.1,
GeneID.1522	CTSZ	20	57,570,242	57,582,309	12,067	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5258, 4_A375_EGR1..1..5510	165, 865	in gene, in gene	0	1	1	14	19	22	1	4_A375_EGR1..1	22	Gene CTSZ	CTSZ, CTSX, FLJ17088	cathepsin Z	NM_001336, hCT1953309.1, hCT19700.2, hCT2355522.0	210042_s_at, 212562_s_at	NP_001327.2, EAW75448.1, EAW75449.1, EAW75450.1
GeneID.81027	TUBB1	20	57,594,309	57,601,709	7,400	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3661, 2_A375_pNL97_plus_lncRNA_AR..1..5259	12859, 12827	downstream, downstream	1	1	0	25	27	14	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene TUBB1	TUBB1, dJ543J19.4	tubulin, beta 1	NM_030773, hCT19704.4	208601_s_at, 230690_at	NP_110400.1, EAW75447.1
GeneID.514	ATP5E	20	57,603,733	57,607,422	3,689	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3661, 1_A375_pNL7_minus_lncRNA_AR..1..3662, 2_A375_pNL97_plus_lncRNA_AR..1..5259, 2_A375_pNL97_plus_lncRNA_AR..1..5260	254, -10562, 286, -10498	in gene, upstream, in gene, upstream	1	1	0	24.5	22.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene ATP5E	MGC104243, ATP5E, ATPE	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	NM_006886, NM_001001977, hCT1953318.1, hCT1953319.1, hCT19702.3	217801_at	NP_008817.1, NP_001001977.1, EAW75444.1, EAW75445.1, EAW75446.1
GeneID.51012	SLMO2	20	57,608,200	57,617,901	9,701	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3661, 1_A375_pNL7_minus_lncRNA_AR..1..3662, 2_A375_pNL97_plus_lncRNA_AR..1..5259, 2_A375_pNL97_plus_lncRNA_AR..1..5260	10733, -83, 10765, -19	downstream, upstream, downstream, upstream	1	1	0	24.5	22.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SLMO2	dJ543J19.5, C20orf45, SLMO2, PRELID3B	slowmo homolog 2 (Drosophila)	NM_016045, hCT1953307.1, hCT19699.3	217851_s_at, 222441_x_at	NP_057129.2, EAW75443.1, EAW75442.1
GeneID.100287547	LOC100287547	20	57,707,998	57,729,904	21,906	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3664, 1_A375_pNL7_minus_lncRNA_AR..1..3665, 2_A375_pNL97_plus_lncRNA_AR..1..5261, 2_A375_pNL97_plus_lncRNA_AR..1..5262	20464, 12528, 20496, 12464	in gene, in gene, in gene, in gene	1	1	0	34.5	42	10	2	2_A375_pNL97_plus_lncRNA_AR..1	49	Gene LOC100287547		hypothetical protein LOC100287547	XM_002343714, XM_002348049, XM_003119823		XP_002343755.1, XP_002348090.1, XP_003119871.1
GeneID.128611	ZNF831	20	57,766,075	57,834,168	68,093	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3666, 1_A375_pNL7_minus_lncRNA_AR..1..3667, 2_A375_pNL97_plus_lncRNA_AR..1..5263, 4_A375_EGR1..1..5511	30037, 57189, 51613, 677	in gene, in gene, in gene, in gene	1	1	1	12.25	15.25	7.5	4	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ZNF831	dJ492J12.1, ZNF831, C20orf174	zinc finger protein 831	NM_178457	1558826_at, 1558827_a_at	NP_848552.1
GeneID.1908	EDN3	20	57,875,499	57,901,047	25,548	+	1	4_A375_EGR1..1..5512	298	in gene	0	0	1	4	8	17	1	4_A375_EGR1..1	17	Gene EDN3	EDN3, WS4B, ET3, MGC61498, HSCR4, MGC15067	endothelin 3	NM_000114, NM_207032, NM_207033, NM_207034, hCT17824.3, hCT1953297.1, hCT2312325.0, hCT2312327.0	208399_s_at, 217154_s_at	NP_000105.1, NP_996915.1, NP_996916.1, NP_996917.1, EAW75434.1, EAW75435.1, EAW75436.1, EAW75437.1
GeneID.116154	PHACTR3	20	58,179,603	58,422,766	243,163	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3669, 2_A375_pNL97_plus_lncRNA_AR..1..5265, 4_A375_EGR1..1..5515, 4_A375_EGR1..1..5516, 4_A375_EGR1..1..5517, 4_A375_EGR1..1..5518	161229, 161325, 275, 834, 7021, 140621	in gene, in gene, upstream, in gene, in gene, in gene	1	1	1	10.6	11	16.2	5	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene PHACTR3	C20orf101, PHACTR3, SCAPININ, MGC117178, H17739, SCAPIN1	phosphatase and actin regulator 3	NM_183244, NM_183246, NM_080672, hCT18808.2, hCT1950759.0, hCT1953304.1	227949_at	NP_899067.1, NP_899069.1, NP_542403.1, EAW75428.1, EAW75429.1, EAW75430.1
GeneID.10388	SYCP2	20	58,438,618	58,507,209	68,591	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3670, 2_A375_pNL97_plus_lncRNA_AR..1..5266, 2_A375_pNL97_plus_lncRNA_AR..1..5267, 4_A375_EGR1..1..5519	-8439, -7207, -8568, -8983	upstream, upstream, upstream, upstream	1	1	1	16	17.5	18.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene SYCP2	SYCP2, SCP2	synaptonemal complex protein 2	NM_014258, hCT1953303.1, hCT2312240.0	206546_at, 237920_at	NP_055073.2, EAW75426.1, EAW75427.1
GeneID.63939	C20orf177	20	58,508,819	58,523,702	14,883	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3670, 2_A375_pNL97_plus_lncRNA_AR..1..5266, 2_A375_pNL97_plus_lncRNA_AR..1..5267, 4_A375_EGR1..1..5519	6629, 5597, 6978, 5373	in gene, in gene, in gene, in gene	1	1	1	16	17.5	18.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene C20orf177	C20orf177, dJ551D2.5	chromosome 20 open reading frame 177	NM_001190826, NM_001190827, NM_022106, hCT1644430.2	225313_at	NP_001177755.1, NP_001177756.1, NP_071389.1, EAW75424.1
GeneID.5509	PPP1R3D	20	58,511,887	58,515,352	3,465	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3670, 2_A375_pNL97_plus_lncRNA_AR..1..5266, 2_A375_pNL97_plus_lncRNA_AR..1..5267, 4_A375_EGR1..1..5519	-298, 936, -445, 1160	upstream, in gene, upstream, in gene	1	1	1	16	17.5	18.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene PPP1R3D	PPP1R3D, PPP1R6, DKFZp781L2441	protein phosphatase 1, regulatory (inhibitor) subunit 3D	NM_006242, hCT17852.3	204554_at, 204555_s_at	NP_006233.1, EAW75425.1
GeneID.284756	C20orf197	20	58,630,980	58,648,008	17,028	+	1	4_A375_EGR1..1..5520	-5172	upstream	0	0	1	7	7	19	1	4_A375_EGR1..1	19	Gene C20orf197	FLJ33860, C20orf197, MGC120498, RP5-1017F8.1	chromosome 20 open reading frame 197	NM_173644, hCT1958470.2	1553311_at	NP_775915.1, EAW75416.1
GeneID.1002	CDH4	20	59,827,559	60,512,299	684,740	+	32	4_A375_EGR1..1..5522, 4_A375_EGR1..1..5523, 4_A375_EGR1..1..5524, 2_A375_pNL97_plus_lncRNA_AR..1..5271, 2_A375_pNL97_plus_lncRNA_AR..1..5272, 4_A375_EGR1..1..5525, 4_A375_EGR1..1..5526, 4_A375_EGR1..1..5527, 4_A375_EGR1..1..5528, 4_A375_EGR1..1..5529, 4_A375_EGR1..1..5530, 4_A375_EGR1..1..5531, 4_A375_EGR1..1..5532, 4_A375_EGR1..1..5533, 4_A375_EGR1..1..5534, 4_A375_EGR1..1..5535, 4_A375_EGR1..1..5536, 4_A375_EGR1..1..5537, 4_A375_EGR1..1..5538, 4_A375_EGR1..1..5539, 4_A375_EGR1..1..5540, 4_A375_EGR1..1..5541, 4_A375_EGR1..1..5542, 4_A375_EGR1..1..5543, 4_A375_EGR1..1..5544, 4_A375_EGR1..1..5545, 4_A375_EGR1..1..5546, 4_A375_EGR1..1..5547, 4_A375_EGR1..1..5548, 4_A375_EGR1..1..5549, 4_A375_EGR1..1..5550, 4_A375_EGR1..1..5551	48025, 79353, 117561, 278361, 356025, 183353, 247513, 286137, 363593, 376121, 410713, 416569, 427470, 478329, 485337, 509433, 532985, 550297, 551417, 601881, 612377, 622233, 623241, 629001, 643993, 645561, 649617, 657961, 672377, 676849, 681753, 689145	in gene, downstream	0	1	1	7.31	6.75	17.25	32	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene CDH4	MGC138355, RCAD, CAD4, FLJ22202, FLJ40547, MGC126700, CDH4	cadherin 4, type 1, R-cadherin (retinal)	NM_001794, hCT2312091.0, hCT33046.2	1563587_at, 206866_at, 220227_at, 239485_at	NP_001785.2, EAW75410.1, EAW75409.1
GeneID.100302168	MIR1257	20	60,528,602	60,528,718	116	-	1	4_A375_EGR1..1..5552	-242	upstream	0	0	1	6	9	16	1	4_A375_EGR1..1	16	Gene MIR1257	MIRN1257, hsa-mir-1257, MIR1257	microRNA 1257	NR_031658		
GeneID.6874	TAF4	20	60,549,854	60,640,866	91,012	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3674, 4_A375_EGR1..1..5553, 4_A375_EGR1..1..5554, 4_A375_EGR1..1..5555, 4_A375_EGR1..1..5556, 4_A375_EGR1..1..5557	95341, 61954, 51330, 35682, 4578, -1982	downstream, in gene, in gene, in gene, in gene, upstream	1	0	1	8.17	9.5	16.83	6	4_A375_EGR1..1	20	Gene TAF4	TAF2C, TAF4A, TAF4, FLJ41943, TAFII135, TAF2C1, TAFII130	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	NM_003185, hCT2311878.0, hCT33044.3	206545_x_at, 213090_s_at	NP_003176.2, EAW75406.1, EAW75407.1
GeneID.149986	LSM14B	20	60,697,517	60,710,434	12,917	+	4	2_A375_pNL97_plus_lncRNA_AR..1..5273, 4_A375_EGR1..1..5559, 4_A375_EGR1..1..5560, 4_A375_EGR1..1..5561	21939, -3693, 10867, 13475	downstream, upstream, in gene, downstream	0	1	1	8.25	10	20	4	4_A375_EGR1..1	23	Gene LSM14B	FLJ25473, bA11M20.3, C20orf40, LSM14B, RAP55B, LSM13, MGC61931, FAM61B	LSM14B, SCD6 homolog B (S. cerevisiae)	NM_144703, hCT2312099.1, hCT2312101.1, hCT2312102.1, hCT2312103.1, hCT2312104.1	1553304_at, 219653_at, 224171_at, 231200_at, 244488_at	NP_653304.2, EAW75403.1, EAW75401.1, EAW75402.1, EAW75404.1, EAW75405.1
GeneID.5688	PSMA7	20	60,711,791	60,718,474	6,683	-	4	2_A375_pNL97_plus_lncRNA_AR..1..5273, 4_A375_EGR1..1..5560, 4_A375_EGR1..1..5561, 4_A375_EGR1..1..5562	-982, 10090, 7482, -5286	upstream, downstream, downstream, upstream	0	1	1	7.75	10.75	19.25	4	4_A375_EGR1..1	23	Gene PSMA7	XAPC7, PSMA7, C8, MGC3755, RC6-1, HSPC	proteasome (prosome, macropain) subunit, alpha type, 7	NM_002792	201114_x_at, 216088_s_at	NP_002783.1
GeneID.26039	SS18L1	20	60,718,822	60,757,566	38,744	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3675, 2_A375_pNL97_plus_lncRNA_AR..1..5273, 2_A375_pNL97_plus_lncRNA_AR..1..5274, 4_A375_EGR1..1..5561, 4_A375_EGR1..1..5562, 4_A375_EGR1..1..5563	39002, 634, 39375, -7630, 4938, 39130	downstream, in gene, downstream, upstream, in gene, downstream	1	1	1	12.75	17	20.5	4	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SS18L1	MGC78386, MGC26711, CREST, KIAA0693, SS18L1, LP2261	synovial sarcoma translocation gene on chromosome 18-like 1	NM_198935, hCT2312108.0, hCT2312107.0, hCT2312109.0, hCT2355466.0, hCT2355467.0, hCT2355468.0, hCT2355469.0, hCT33050.2	213140_s_at	NP_945173.1, EAW75394.1, EAW75392.1, EAW75393.1, EAW75395.1, EAW75396.1, EAW75389.1, EAW75390.1, EAW75391.1
GeneID.26164	GTPBP5	20	60,758,081	60,777,823	19,742	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3675, 2_A375_pNL97_plus_lncRNA_AR..1..5274, 4_A375_EGR1..1..5563, 4_A375_EGR1..1..5564	-257, 116, -129, 18367	upstream, in gene, upstream, in gene	1	1	1	17.5	19	23.5	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene GTPBP5	GTPBP5, FLJ10741, ObgH1, MGC29512, dJ1005F21.2	GTP binding protein 5 (putative)	NM_015666, hCT2312111.0, hCT2312113.0, hCT33049.3	1568822_at, 226598_s_at, 228606_s_at, 236890_at	NP_056481.1, EAW75386.1, EAW75387.1, EAW75388.1
GeneID.11255	HRH3	20	60,790,017	60,795,323	5,306	-	4	4_A375_EGR1..1..5565, 4_A375_EGR1..1..5566, 4_A375_EGR1..1..5567, 4_A375_EGR1..1..5568	2811, 1595, -2197, -6629	in gene, in gene, upstream, upstream	0	0	1	8.5	9.5	16.25	4	4_A375_EGR1..1	19	Gene HRH3	GPCR97, HH3R, HRH3	histamine receptor H3	NM_007232, hCT1950778.0, hCT2311861.0, hCT2311863.0, hCT2355406.0, hCT33042.3	1555215_a_at, 1555715_a_at, 220447_at, 221663_x_at	NP_009163.2, EAW75381.1, EAW75382.1, EAW75383.1, EAW75384.1, EAW75385.1
GeneID.400850	FLJ44790	20	60,807,016	60,811,355	4,339	+	3	4_A375_EGR1..1..5567, 4_A375_EGR1..1..5568, 4_A375_EGR1..1..5569	-9498, -5064, 504	upstream, upstream, in gene	0	0	1	7.67	8.33	16	3	4_A375_EGR1..1	17	Gene FLJ44790		hypothetical FLJ44790	XR_112171, XR_109835, XR_115394, hCT2380141.0		EAW75380.1
GeneID.9885	OSBPL2	20	60,813,580	60,871,269	57,689	+	7	1_A375_pNL7_minus_lncRNA_AR..1..3676, 2_A375_pNL97_plus_lncRNA_AR..1..5275, 2_A375_pNL97_plus_lncRNA_AR..1..5276, 4_A375_EGR1..1..5569, 4_A375_EGR1..1..5570, 4_A375_EGR1..1..5571, 4_A375_EGR1..1..5572	64308, 64212, 66324, -6060, 11572, 31476, 59412	downstream, downstream, downstream, upstream, in gene, in gene, downstream	1	1	1	11.17	14.83	16.67	6	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene OSBPL2	KIAA0772, OSBPL2, ORP-2, MGC8342, FLJ20223, MGC4307, ORP2	oxysterol binding protein-like 2	NM_014835, NM_144498, hCT2312614.0, hCT2312615.0, hCT2312616.0	209221_s_at, 209222_s_at	NP_055650.1, NP_653081.1, EAW75377.1, EAW75378.1, EAW75379.1
GeneID.11047	ADRM1	20	60,878,027	60,883,918	5,891	+	10	1_A375_pNL7_minus_lncRNA_AR..1..3676, 2_A375_pNL97_plus_lncRNA_AR..1..5275, 2_A375_pNL97_plus_lncRNA_AR..1..5276, 4_A375_EGR1..1..5572, 4_A375_EGR1..1..5573, 4_A375_EGR1..1..5574, 4_A375_EGR1..1..5575, 4_A375_EGR1..1..5576, 4_A375_EGR1..1..5577, 4_A375_EGR1..1..5578	-139, -235, 1877, 5035, 3829, 4725, 6689, 8181, 9397, 13973	upstream, upstream, in gene, upstream, in gene, in gene, downstream, downstream, downstream, downstream	1	1	1	11.56	14.33	21.56	9	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene ADRM1	MGC29536, ARM1, ADRM1, GP110, Rpn13	adhesion regulating molecule 1	NM_007002, NM_175573, hCT33040.3	201281_at	NP_008933.2, NP_783163.1, EAW75375.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.3911	LAMA5	20	60,884,121	60,942,368	58,247	-	27	1_A375_pNL7_minus_lncRNA_AR..1..3676, 2_A375_pNL97_plus_lncRNA_AR..1..5275, 2_A375_pNL97_plus_lncRNA_AR..1..5276, 4_A375_EGR1..1..5573, 4_A375_EGR1..1..5574, 4_A375_EGR1..1..5575, 4_A375_EGR1..1..5576, 4_A375_EGR1..1..5577, 4_A375_EGR1..1..5578, 4_A375_EGR1..1..5579, 4_A375_EGR1..1..5580, 4_A375_EGR1..1..5581, 4_A375_EGR1..1..5582, 4_A375_EGR1..1..5583, 4_A375_EGR1..1..5584, 4_A375_EGR1..1..5585, 4_A375_EGR1..1..5586, 4_A375_EGR1..1..5587, 4_A375_EGR1..1..5588, 4_A375_EGR1..1..5589, 4_A375_EGR1..1..5590, 4_A375_EGR1..1..5591, 4_A375_EGR1..1..5592, 4_A375_EGR1..1..5593, 4_A375_EGR1..1..5594, 4_A375_EGR1..1..5595, 4_A375_EGR1..1..5596	64480, 64576, 62464, 60512, 59816, 57472, 56160, 54944, 50368, 43680, 38845, 36800, 35648, 34656, 33024, 20352, 16680, 11642, 10368, 9280, 8096, 5984, -896, -1920, -2640, -3552, -6992	downstream, downstream, downstream, downstream, downstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream, upstream, upstream, upstream, upstream	1	1	1	10.62	11.96	19.89	26	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene LAMA5	LAMA5, KIAA1907	laminin, alpha 5	NM_005560, hCT2312184.0, hCT2355464.0, hCT33047.3	210150_s_at, 229570_at	NP_005551.3, EAW75374.1, EAW75372.1, EAW75373.1
GeneID.100506553	LOC100506553	20	60,928,062	60,931,536	3,474	+	7	4_A375_EGR1..1..5585, 4_A375_EGR1..1..5586, 4_A375_EGR1..1..5587, 4_A375_EGR1..1..5588, 4_A375_EGR1..1..5589, 4_A375_EGR1..1..5590, 4_A375_EGR1..1..5591	-6046, -2574, 2664, 3938, 5026, 6210, 8322	upstream, upstream, in gene, downstream, downstream, downstream, downstream	0	0	1	10	10	17.86	7	4_A375_EGR1..1	20	Gene LOC100506553		hypothetical LOC100506553	XR_109636, XR_115395		
GeneID.6227	RPS21	20	60,962,121	60,963,576	1,455	+	6	2_A375_pNL97_plus_lncRNA_AR..1..5277, 4_A375_EGR1..1..5597, 4_A375_EGR1..1..5598, 4_A375_EGR1..1..5599, 4_A375_EGR1..1..5600, 4_A375_EGR1..1..5601	-297, -8617, -105, 4535, 5943, 9671	upstream, upstream, upstream, downstream, downstream, downstream	0	1	1	10.6	12.8	22.4	5	4_A375_EGR1..1	24	Gene RPS21	S21, RPS21		NM_001024, hCT1950775.1, hCT2312621.0, hCT2312622.0, hCT2312623.0, hCT33041.3	200834_s_at, 214097_at	NP_001015.1, EAW75367.1, EAW75368.1, EAW75369.1, EAW75370.1, EAW75371.1
GeneID.81928	CABLES2	20	60,963,686	60,982,339	18,653	-	16	1_A375_pNL7_minus_lncRNA_AR..1..3677, 2_A375_pNL97_plus_lncRNA_AR..1..5277, 2_A375_pNL97_plus_lncRNA_AR..1..5278, 4_A375_EGR1..1..5597, 4_A375_EGR1..1..5598, 4_A375_EGR1..1..5599, 4_A375_EGR1..1..5600, 4_A375_EGR1..1..5601, 4_A375_EGR1..1..5602, 4_A375_EGR1..1..5603, 4_A375_EGR1..1..5604, 4_A375_EGR1..1..5605, 4_A375_EGR1..1..5606, 4_A375_EGR1..1..5607, 4_A375_EGR1..1..5608, 4_A375_EGR1..1..5609	-157, 20515, -189, 28835, 20323, 15663, 14275, 10547, 4483, 2139, 1507, -4109, -5533, -6973, -7901, -9277	upstream, downstream, upstream, downstream, downstream, in gene, in gene, in gene, in gene, in gene, in gene, upstream, upstream, upstream, upstream, upstream	1	1	1	11.29	13	21	14	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene CABLES2	C20orf150, CABLES2, ik3-2, dJ908M14.2	Cdk5 and Abl enzyme substrate 2	NM_031215, hCT2312180.0, hCT2312182.0, hCT33052.2	226004_at	NP_112492.2, EAW75364.1, EAW75365.1, EAW75366.1
GeneID.140893	C20orf151	20	60,985,293	61,002,629	17,336	-	15	1_A375_pNL7_minus_lncRNA_AR..1..3677, 2_A375_pNL97_plus_lncRNA_AR..1..5278, 4_A375_EGR1..1..5602, 4_A375_EGR1..1..5603, 4_A375_EGR1..1..5604, 4_A375_EGR1..1..5605, 4_A375_EGR1..1..5606, 4_A375_EGR1..1..5607, 4_A375_EGR1..1..5608, 4_A375_EGR1..1..5609, 4_A375_EGR1..1..5610, 4_A375_EGR1..1..5611, 4_A375_EGR1..1..5612, 4_A375_EGR1..1..5613, 4_A375_EGR1..1..5614	20133, 20101, 24773, 22429, 21797, 16181, 14757, 13317, 12389, 11013, 8117, 4549, 2085, 133, -1627	downstream, downstream, downstream, downstream, downstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	1	1	1	10.43	10.93	19.86	14	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene C20orf151	C20orf151	chromosome 20 open reading frame 151	NM_080833, hCT2312179.1, hCT2344645.0	236256_at	NP_543023.2, EAW75362.1, EAW75363.1
GeneID.140626	GATA5	20	61,038,553	61,051,026	12,473	-	10	4_A375_EGR1..1..5620, 4_A375_EGR1..1..5621, 4_A375_EGR1..1..5622, 4_A375_EGR1..1..5623, 4_A375_EGR1..1..5624, 4_A375_EGR1..1..5625, 4_A375_EGR1..1..5626, 4_A375_EGR1..1..5627, 4_A375_EGR1..1..5628, 4_A375_EGR1..1..5629	17138, 11618, 9714, 7122, 5117, 3570, 402, -291, -4926, -8398	downstream, in gene, in gene, in gene, in gene, in gene, in gene, upstream, upstream, upstream	0	0	1	7.7	7.3	18.6	10	4_A375_EGR1..1	26	Gene GATA5	bB379O24.1, GATA5	GATA binding protein 5	NM_080473, hCT2312174.0, hCT2312176.0	238095_at, 238197_at	NP_536721.1, EAW75361.1, EAW75360.1
GeneID.253868	C20orf200	20	61,141,436	61,148,766	7,330	-	7	4_A375_EGR1..1..5635, 4_A375_EGR1..1..5636, 4_A375_EGR1..1..5637, 4_A375_EGR1..1..5638, 4_A375_EGR1..1..5639, 4_A375_EGR1..1..5640, 4_A375_EGR1..1..5641	5552, 4288, 3712, 2464, -3392, -6464, -9664	in gene, in gene, in gene, in gene, upstream, upstream, upstream	0	0	1	8.57	9.14	19.29	7	4_A375_EGR1..1	21	Gene C20orf200	C20orf200, DKFZp313D1936, MGC138143, FLJ30313	chromosome 20 open reading frame 200	NR_033263, hCT2344138.0, hCT2344139.0, hCT2344140.0, hCT2355552.0	1553204_at, 1553205_at	EAW75356.1, EAW75357.1, EAW75358.1, EAW75359.1
GeneID.128826	C20orf166	20	61,147,660	61,167,971	20,311	+	13	1_A375_pNL7_minus_lncRNA_AR..1..3678, 2_A375_pNL97_plus_lncRNA_AR..1..5280, 4_A375_EGR1..1..5635, 4_A375_EGR1..1..5636, 4_A375_EGR1..1..5637, 4_A375_EGR1..1..5638, 4_A375_EGR1..1..5639, 4_A375_EGR1..1..5640, 4_A375_EGR1..1..5641, 4_A375_EGR1..1..5642, 4_A375_EGR1..1..5643, 4_A375_EGR1..1..5644, 4_A375_EGR1..1..5645	26580, 26164, -4444, -3180, -2604, -1356, 4500, 7572, 10772, 15748, 24361, 25343, 29972	downstream, downstream, upstream, upstream, upstream, upstream, in gene, in gene, in gene, in gene, downstream, downstream, downstream	1	1	1	10.18	11.27	19.09	11	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene C20orf166	C20orf166, MGC129808, dJ353C17.1, FLJ32423	chromosome 20 open reading frame 166	NM_178463, hCT9735.3	232892_at	NP_848558.1, EAW75355.1
GeneID.406904	MIR1-1	20	61,151,513	61,151,583	70	+	7	4_A375_EGR1..1..5635, 4_A375_EGR1..1..5636, 4_A375_EGR1..1..5637, 4_A375_EGR1..1..5638, 4_A375_EGR1..1..5639, 4_A375_EGR1..1..5640, 4_A375_EGR1..1..5641	-8297, -7033, -6457, -5209, 647, 3719, 6919	upstream, upstream, upstream, upstream, downstream, downstream, downstream	0	0	1	8.57	9.14	19.29	7	4_A375_EGR1..1	21	Gene MIR1-1	MIRN1-1, miRNA1-1, MIR1-1, hsa-mir-1-1	microRNA 1-1	NR_029780		
GeneID.406923	MIR133A2	20	61,162,119	61,162,220	101	+	5	4_A375_EGR1..1..5639, 4_A375_EGR1..1..5640, 4_A375_EGR1..1..5641, 4_A375_EGR1..1..5642, 4_A375_EGR1..1..5643	-9959, -6687, -3687, 1289, 9902	upstream, upstream, upstream, downstream, downstream	0	0	1	7.8	12	20.4	5	4_A375_EGR1..1	24	Gene MIR133A2	MIRN133A2, MIR133A2	microRNA 133a-2	NR_029676		
GeneID.100131174	LOC100131174	20	61,172,797	61,174,714	1,917	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3678, 2_A375_pNL97_plus_lncRNA_AR..1..5280, 4_A375_EGR1..1..5642, 4_A375_EGR1..1..5643, 4_A375_EGR1..1..5644, 4_A375_EGR1..1..5645	1443, 1027, -9389, -776, 206, 4835	in gene, in gene, upstream, upstream, in gene, downstream	1	1	1	13	15	18.75	4	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene LOC100131174		hypothetical LOC100131174	XR_112174, XR_109637, XR_115397		
GeneID.100505735	LOC100505735	20	61,265,124	61,267,214	2,090	+	4	4_A375_EGR1..1..5648, 4_A375_EGR1..1..5649, 4_A375_EGR1..1..5650, 4_A375_EGR1..1..5651	798, 1612, 7324, 9532	in gene, in gene, downstream, downstream	0	0	1	10.25	10	21.5	4	4_A375_EGR1..1	24	Gene LOC100505735		hypothetical LOC100505735	XR_109589		
GeneID.149650	RP11-93B14.6	20	61,272,071	61,274,656	2,585	-	5	4_A375_EGR1..1..5648, 4_A375_EGR1..1..5649, 4_A375_EGR1..1..5650, 4_A375_EGR1..1..5651, 4_A375_EGR1..1..5652	8736, 7920, 2208, 0, -9856	downstream, downstream, in gene, in gene, upstream	0	0	1	10	10.6	21.4	5	4_A375_EGR1..1	24	Gene RP11-93B14.6	FLJ32154	hypothetical protein FLJ32154	XM_003119625, XR_109590, XR_115399	235933_at	XP_003119673.1
GeneID.28231	SLCO4A1	20	61,273,797	61,303,647	29,850	+	11	1_A375_pNL7_minus_lncRNA_AR..1..3679, 2_A375_pNL97_plus_lncRNA_AR..1..5282, 4_A375_EGR1..1..5648, 4_A375_EGR1..1..5649, 4_A375_EGR1..1..5650, 4_A375_EGR1..1..5651, 4_A375_EGR1..1..5652, 4_A375_EGR1..1..5653, 4_A375_EGR1..1..5654, 4_A375_EGR1..1..5655, 4_A375_EGR1..1..5656	24539, 26299, -7877, -7061, -1349, 859, 10715, 13531, 14363, 15035, 26747	in gene, in gene, upstream, upstream, upstream, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	12.33	12.67	22	9	4_A375_EGR1..1	27	Gene SLCO4A1	OATPRP1, SLC21A12, OATPE, SLCO4A1, OATP-E, POAT, OATP4A1, OATP1	solute carrier organic anion transporter family, member 4A1	NM_016354, hCT2312641.0, hCT2312642.0, hCT2312643.0, hCT2312644.0	219911_s_at, 229239_x_at	NP_057438.3, EAW75351.1, EAW75348.1, EAW75349.1, EAW75350.1
GeneID.100127888	NCG_2018279	20	61,294,379	61,297,973	3,594	-	7	1_A375_pNL7_minus_lncRNA_AR..1..3679, 2_A375_pNL97_plus_lncRNA_AR..1..5282, 4_A375_EGR1..1..5652, 4_A375_EGR1..1..5653, 4_A375_EGR1..1..5654, 4_A375_EGR1..1..5655, 4_A375_EGR1..1..5656	-363, -2123, 13461, 10645, 9813, 9141, -2571	upstream, upstream, downstream, downstream, downstream, downstream, upstream	1	1	1	14	14.6	22.4	5	4_A375_EGR1..1	27	Gene NCG_2018279	LOC100127888, MGC39393	hypothetical LOC100127888	NR_024470		
GeneID.4923	NTSR1	20	61,340,189	61,394,123	53,934	+	14	1_A375_pNL7_minus_lncRNA_AR..1..3680, 2_A375_pNL97_plus_lncRNA_AR..1..5283, 2_A375_pNL97_plus_lncRNA_AR..1..5284, 4_A375_EGR1..1..5659, 4_A375_EGR1..1..5660, 4_A375_EGR1..1..5661, 4_A375_EGR1..1..5662, 4_A375_EGR1..1..5663, 4_A375_EGR1..1..5664, 4_A375_EGR1..1..5665, 4_A375_EGR1..1..5666, 4_A375_EGR1..1..5667, 4_A375_EGR1..1..5668, 4_A375_EGR1..1..5669	32227, -4569, 31651, -6877, 3171, 3779, 8099, 15267, 19011, 32163, 35011, 53705, 54659, 56163	in gene, upstream, in gene, upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, downstream, downstream	1	1	1	10.42	12.33	19.58	12	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene NTSR1	NTR, NTSR1	neurotensin receptor 1 (high affinity)	NM_002531, hCT1786414.2	207360_s_at	NP_002522.2, EAW75345.1
GeneID.100505843	LOC100505843	20	61,409,070	61,409,552	482	+	3	4_A375_EGR1..1..5670, 4_A375_EGR1..1..5671, 4_A375_EGR1..1..5672	-2446, -1198, 8978	upstream, upstream, downstream	0	0	1	11.33	10.67	19	3	4_A375_EGR1..1	25	Gene LOC100505843		hypothetical protein LOC100505843	XM_003119626, XM_003118798, XM_003120991		XP_003119674.1, XP_003118846.1, XP_003121039.1
GeneID.55257	C20orf20	20	61,427,805	61,431,945	4,140	+	6	2_A375_pNL97_plus_lncRNA_AR..1..5285, 4_A375_EGR1..1..5672, 4_A375_EGR1..1..5673, 4_A375_EGR1..1..5674, 4_A375_EGR1..1..5675, 4_A375_EGR1..1..5676	-845, -9757, -7213, -2573, -1757, 13507	upstream, upstream, upstream, upstream, upstream, downstream	0	1	1	12.4	14.6	23	5	4_A375_EGR1..1	26	Gene C20orf20	C20orf20, MRGBP, MRG15BP, FLJ10914, Eaf7, URCC4	chromosome 20 open reading frame 20	NM_018270, hCT14524.3, hCT2312653.0	218586_at	NP_060740.1, EAW75342.1, EAW75343.1
GeneID.11054	OGFR	20	61,436,177	61,445,352	9,175	+	10	2_A375_pNL97_plus_lncRNA_AR..1..5285, 2_A375_pNL97_plus_lncRNA_AR..1..5286, 4_A375_EGR1..1..5675, 4_A375_EGR1..1..5676, 4_A375_EGR1..1..5677, 4_A375_EGR1..1..5678, 4_A375_EGR1..1..5679, 4_A375_EGR1..1..5680, 4_A375_EGR1..1..5681, 4_A375_EGR1..1..5682	-9217, 13295, -10129, 5135, 8175, 9551, 11711, 14191, 15455, 17055	upstream, downstream, upstream, in gene, in gene, downstream, downstream, downstream, downstream, downstream	0	1	1	12.86	15.25	21	8	4_A375_EGR1..1	26	Gene OGFR	OGFR		NM_007346, hCT12108.2, hCT1950754.2, hCT2312659.0, hCT2312660.0, hCT2312661.0, hCT2312662.0, hCT2355492.0	202841_x_at, 210443_x_at, 211512_s_at, 211513_s_at	NP_031372.2, EAW75337.1, EAW75336.1, EAW75338.1, EAW75340.1, EAW75341.1, EAW75335.1, EAW75339.1
GeneID.1299	COL9A3	20	61,448,414	61,472,511	24,097	+	12	2_A375_pNL97_plus_lncRNA_AR..1..5286, 4_A375_EGR1..1..5676, 4_A375_EGR1..1..5677, 4_A375_EGR1..1..5678, 4_A375_EGR1..1..5679, 4_A375_EGR1..1..5680, 4_A375_EGR1..1..5681, 4_A375_EGR1..1..5682, 4_A375_EGR1..1..5683, 4_A375_EGR1..1..5684, 4_A375_EGR1..1..5685, 4_A375_EGR1..1..5686	1058, -7102, -4062, -2686, -526, 1954, 3218, 4618, 9570, 10802, 12130, 23522	in gene, upstream, upstream, upstream, upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	1	1	10.55	12.62	20.18	11	4_A375_EGR1..1	26	Gene COL9A3	MED, DJ885L7.4.1, FLJ90759, EDM3, IDD, COL9A3	collagen, type IX, alpha 3	NM_001853, hCT1962387.1, hCT1962388.1	204724_s_at	NP_001844.3, EAW75334.1, EAW75333.1
GeneID.10732	TCFL5	20	61,472,467	61,493,115	20,648	-	1	4_A375_EGR1..1..5686	21179	downstream	0	0	1	9	12	22	1	4_A375_EGR1..1	22	Gene TCFL5	bHLHe82, CHA, Figlb, E2BP-1, MGC46135, TCFL5	transcription factor-like 5 (basic helix-loop-helix)	NM_006602, hCT14517.3, hCT2355474.0, hCT2355475.0	204849_at, 235694_at	NP_006593.2, EAW75330.1, EAW75329.1, EAW75331.1
GeneID.100132911	DPH3B	20	61,476,476	61,477,543	1,067	+	1	4_A375_EGR1..1..5686	-4540	upstream	0	0	1	9	12	22	1	4_A375_EGR1..1	22	Gene DPH3B	dJ885L7.5, DPH3P1, C20orf143, DPH3B, ZCSL1	DPH3, KTI11 homolog (S. cerevisiae) pseudogene 1	NM_080750		NP_542788.1
GeneID.11083	DIDO1	20	61,509,090	61,569,304	60,214	-	9	1_A375_pNL7_minus_lncRNA_AR..1..3681, 2_A375_pNL97_plus_lncRNA_AR..1..5287, 2_A375_pNL97_plus_lncRNA_AR..1..5288, 2_A375_pNL97_plus_lncRNA_AR..1..5289, 4_A375_EGR1..1..5687, 4_A375_EGR1..1..5688, 4_A375_EGR1..1..5689, 4_A375_EGR1..1..5690, 4_A375_EGR1..1..5691	312, 11976, 152, -520, 57560, 56896, 55912, 26531, 472	in gene, in gene, in gene, upstream, in gene, in gene, in gene, in gene, in gene	1	1	1	11.86	12	16.86	7	4_A375_EGR1..1	23	Gene DIDO1	DIO-1, DIDO1, DATF1, DIDO2, BYE1, MGC16140, DIDO3, C20orf158, DKFZp434P1115, FLJ11265, dJ885L7.8, DIO1, KIAA0333	death inducer-obliterator 1	NM_033081, NM_080797, NM_080796, NM_022105, NM_001193369, NM_001193370, hCT2312150.2, hCT2344531.1, hCT2344532.1, hCT2344534.0, hCT2344535.1, hCT2348135.0	213213_at, 218325_s_at, 222595_s_at, 227335_at	NP_149072.2, NP_542987.2, NP_071388.2, NP_542988.1, NP_001180298.1, NP_001180299.1, EAW75321.1, EAW75322.1, EAW75323.1, EAW75324.1, EAW75325.1, EAW75326.1
GeneID.54994	C20orf11	20	61,569,441	61,579,827	10,386	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3681, 2_A375_pNL97_plus_lncRNA_AR..1..5288, 2_A375_pNL97_plus_lncRNA_AR..1..5289, 4_A375_EGR1..1..5691, 4_A375_EGR1..1..5692, 4_A375_EGR1..1..5693	-449, -289, 383, -609, 16159, 18751	upstream, upstream, in gene, upstream, downstream, downstream	1	1	1	11.25	14	16.5	4	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene C20orf11	C20orf11, TWA1	chromosome 20 open reading frame 11	NM_017896, hCT14530.3, hCT2312657.1	218448_at, 225376_at	NP_060366.1, EAW75318.1, EAW75319.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.63910	SLC17A9	20	61,583,999	61,599,949	15,950	+	6	4_A375_EGR1..1..5692, 4_A375_EGR1..1..5693, 4_A375_EGR1..1..5694, 4_A375_EGR1..1..5695, 4_A375_EGR1..1..5696, 4_A375_EGR1..1..5697	1601, 4193, 9249, 10913, 20433, 25809	in gene, in gene, in gene, in gene, downstream, downstream	0	0	1	8.33	8.83	18.17	6	4_A375_EGR1..1	22	Gene SLC17A9	C20orf59, SLC17A9, FLJ23412	solute carrier family 17, member 9	NM_022082, hCT1826724.2, hCT1950908.1, hCT1950909.1, hCT1950910.1, hCT2312872.0	219559_at, 232922_s_at, 233328_x_at	NP_071365.3, EAW75313.1, EAW75314.1, EAW75315.1, EAW75316.1, EAW75317.1
GeneID.128408	BHLHE23	20	61,637,331	61,638,387	1,056	-	3	4_A375_EGR1..1..5700, 4_A375_EGR1..1..5701, 4_A375_EGR1..1..5702	10979, 979, -1453	downstream, in gene, upstream	0	0	1	9.67	10	20.67	3	4_A375_EGR1..1	27	Gene BHLHE23	BHLHE23, bA305P22.3, BHLHB4, BETA4	basic helix-loop-helix family, member e23	NM_080606, hCT1826794.1, hCT2312141.0	234045_x_at	NP_542173.1, EAW75311.1, EAW75312.1
GeneID.63930	LOC63930	20	61,640,735	61,716,423	75,688	+	20	1_A375_pNL7_minus_lncRNA_AR..1..3682, 1_A375_pNL7_minus_lncRNA_AR..1..3683, 2_A375_pNL97_plus_lncRNA_AR..1..5290, 2_A375_pNL97_plus_lncRNA_AR..1..5291, 4_A375_EGR1..1..5701, 4_A375_EGR1..1..5702, 4_A375_EGR1..1..5703, 4_A375_EGR1..1..5704, 4_A375_EGR1..1..5705, 4_A375_EGR1..1..5706, 4_A375_EGR1..1..5707, 4_A375_EGR1..1..5708, 4_A375_EGR1..1..5709, 4_A375_EGR1..1..5710, 4_A375_EGR1..1..5711, 4_A375_EGR1..1..5712, 4_A375_EGR1..1..5713, 4_A375_EGR1..1..5714, 4_A375_EGR1..1..5715, 4_A375_EGR1..1..5716	60577, 73057, 60841, 73121, -3327, -895, 8513, 16401, 21313, 25857, 46625, 47393, 51617, 64065, 73025, 73617, 74625, 76145, 77585, 82945	in gene, in gene, in gene, in gene, upstream, upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, downstream, downstream, downstream	1	1	1	12.13	14.69	18.63	16	2_A375_pNL97_plus_lncRNA_AR..1	47	Gene LOC63930	FLJ46471, FLJ17646	hypothetical LOC63930	NR_033370, hCT1963168.1, hCT2355530.0	231760_at	EAW75309.1, EAW75310.1
GeneID.100144596	NCRNA00029	20	61,665,569	61,668,380	2,811	-	3	4_A375_EGR1..1..5704, 4_A375_EGR1..1..5705, 4_A375_EGR1..1..5706	11244, 8332, 1788	downstream, downstream, in gene	0	0	1	8	12.33	18	3	4_A375_EGR1..1	23	Gene NCRNA00029	DKFZp434E222, bA305P22.4, NCRNA00029, MGC133146, C20orf51	non-protein coding RNA 29	NR_026295		
GeneID.100144597	LOC100144597	20	61,669,363	61,685,215	15,852	+	5	4_A375_EGR1..1..5705, 4_A375_EGR1..1..5706, 4_A375_EGR1..1..5707, 4_A375_EGR1..1..5708, 4_A375_EGR1..1..5709	-7315, -2771, 17997, 18765, 22989	upstream, upstream, downstream, downstream, downstream	0	0	1	8	10.4	20.8	5	4_A375_EGR1..1	26	Gene LOC100144597		hypothetical LOC100144597	NR_033369		
GeneID.768097	HAR1B	20	61,726,845	61,733,671	6,826	-	9	4_A375_EGR1..1..5714, 4_A375_EGR1..1..5715, 4_A375_EGR1..1..5716, 4_A375_EGR1..1..5717, 4_A375_EGR1..1..5718, 4_A375_EGR1..1..5719, 4_A375_EGR1..1..5720, 4_A375_EGR1..1..5721, 4_A375_EGR1..1..5722	16791, 15351, 9991, 5127, 1383, 7, -2489, -3577, -5085	downstream, downstream, downstream, in gene, in gene, in gene, upstream, upstream, upstream	0	0	1	8.44	9.33	18.22	9	4_A375_EGR1..1	21	Gene HAR1B	HAR1R, NCRNA00065, HAR1B	highly accelerated region 1B (non-protein coding)	NR_003245		
GeneID.768096	HAR1A	20	61,732,644	61,735,737	3,093	+	7	4_A375_EGR1..1..5716, 4_A375_EGR1..1..5717, 4_A375_EGR1..1..5718, 4_A375_EGR1..1..5719, 4_A375_EGR1..1..5720, 4_A375_EGR1..1..5721, 4_A375_EGR1..1..5722	-8984, -4100, -356, 1020, 3516, 4604, 6092	upstream, upstream, upstream, in gene, downstream, downstream, downstream	0	0	1	7.86	9.43	18.29	7	4_A375_EGR1..1	21	Gene HAR1A	HAR1F, HAR1A, NCRNA00064	highly accelerated region 1A (non-protein coding)	NR_003244	1557098_s_at	
GeneID.406909	MIR124-3	20	61,809,852	61,809,938	86	+	2	4_A375_EGR1..1..5730, 4_A375_EGR1..1..5731	-1959, 4436	upstream, downstream	0	0	1	11	12	20.5	2	4_A375_EGR1..1	24	Gene MIR124-3	MIRN124-3, MIR124-3, MIRN124A3	microRNA 124-3	NR_029670		
GeneID.54915	YTHDF1	20	61,826,781	61,847,538	20,757	-	2	4_A375_EGR1..1..5732, 4_A375_EGR1..1..5733	25266, -318	downstream, upstream	0	0	1	10.5	11.5	22	2	4_A375_EGR1..1	22	Gene YTHDF1	FLJ20391, YTHDF1, C20orf21	YTH domain family, member 1	NM_017798, hCT14531.3, hCT2312131.0	221741_s_at	NP_060268.2, EAW75305.1, EAW75306.1
GeneID.79444	BIRC7	20	61,867,276	61,871,854	4,578	+	3	4_A375_EGR1..1..5734, 4_A375_EGR1..1..5735, 4_A375_EGR1..1..5736	-76, 11092, 12196	upstream, downstream, downstream	0	0	1	8.33	11.67	25.33	3	4_A375_EGR1..1	31	Gene BIRC7	LIVIN, KIAP, ML-IAP, BIRC7, MLIAP, RNF50	baculoviral IAP repeat containing 7	NM_022161, NM_139317, hCT14526.3, hCT2312804.0, hCT2312806.0	220451_s_at	NP_071444.1, NP_647478.1, EAW75302.1, EAW75303.1, EAW75304.1
GeneID.100423014	MIR3196	20	61,870,131	61,870,194	63	+	3	4_A375_EGR1..1..5734, 4_A375_EGR1..1..5735, 4_A375_EGR1..1..5736	-2931, 8237, 9341	upstream, downstream, downstream	0	0	1	8.33	11.67	25.33	3	4_A375_EGR1..1	31	Gene MIR3196	MIR3196	microRNA 3196	NR_036163		
GeneID.128414	NKAIN4	20	61,872,136	61,885,892	13,756	-	5	4_A375_EGR1..1..5734, 4_A375_EGR1..1..5735, 4_A375_EGR1..1..5736, 4_A375_EGR1..1..5737, 4_A375_EGR1..1..5738	16892, 7524, 6420, -396, -6524	downstream, in gene, in gene, upstream, upstream	0	0	1	8.2	10.2	24.6	5	4_A375_EGR1..1	31	Gene NKAIN4	bA261N11.2, NKAIN4, C20orf58, FAM77A	Na+/K+ transporting ATPase interacting 4	NM_152864, hCT14532.3, hCT2355532.0, hCT2355533.0, hCT2355534.0, hCT2355535.0	228017_s_at, 228018_at, 230688_at, 230771_at	NP_690603.3, EAW75297.1, EAW75298.1, EAW75299.1, EAW75300.1, EAW75301.1
GeneID.100192386	FLJ16779	20	61,885,330	61,892,967	7,637	+	4	4_A375_EGR1..1..5735, 4_A375_EGR1..1..5736, 4_A375_EGR1..1..5737, 4_A375_EGR1..1..5738	-6962, -5856, 958, 7066	upstream, upstream, in gene, in gene	0	0	1	7.75	9.75	23	4	4_A375_EGR1..1	25	Gene FLJ16779		hypothetical LOC100192386	NR_024389		
GeneID.55738	ARFGAP1	20	61,904,165	61,921,142	16,977	+	4	4_A375_EGR1..1..5739, 4_A375_EGR1..1..5740, 4_A375_EGR1..1..5741, 4_A375_EGR1..1..5742	12987, 18268, 22299, 24251	in gene, downstream, downstream, downstream	0	0	1	8.5	8.25	18.25	4	4_A375_EGR1..1	23	Gene ARFGAP1	MGC39924, ARF1GAP, ARFGAP1, HRIHFB2281	ADP-ribosylation factor GTPase activating protein 1	NM_018209, NM_175609, hCT14518.3, hCT1962389.1, hCT1962390.1, hCT2312808.0, hCT2312811.0, hCT2355477.0, hCT2355476.0	217686_s_at, 234001_s_at	NP_060679.1, NP_783202.1, EAW75290.1, EAW75291.1, EAW75292.1, EAW75295.1, EAW75293.1, EAW75294.1, EAW75296.1
GeneID.100422945	MIR4326	20	61,918,160	61,918,218	58	+	4	4_A375_EGR1..1..5739, 4_A375_EGR1..1..5740, 4_A375_EGR1..1..5741, 4_A375_EGR1..1..5742	-1006, 4293, 8304, 10256	upstream, downstream, downstream, downstream	0	0	1	8.5	8.25	18.25	4	4_A375_EGR1..1	23	Gene MIR4326	MIR4326	microRNA 4326	NR_036220		
GeneID.57642	COL20A1	20	61,924,538	61,962,285	37,747	+	11	4_A375_EGR1..1..5739, 4_A375_EGR1..1..5740, 4_A375_EGR1..1..5741, 4_A375_EGR1..1..5742, 4_A375_EGR1..1..5743, 4_A375_EGR1..1..5744, 4_A375_EGR1..1..5745, 4_A375_EGR1..1..5746, 4_A375_EGR1..1..5747, 4_A375_EGR1..1..5748, 4_A375_EGR1..1..5749	-7366, -2065, 1926, 3876, 13814, 16390, 18534, 27494, 29190, 33666, 37350	upstream, upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	7.36	8.27	18.46	11	4_A375_EGR1..1	23	Gene COL20A1	KIAA1510, COL20A1, bA261N11.4	collagen, type XX, alpha 1	NM_020882, hCT14529.2, hCT2317355.0, hCT2355526.0, hCT2355527.0, hCT2355528.0	232636_at, 232733_s_at	NP_065933.2, EAW75265.1, EAW75266.1, EAW75267.1, EAW75268.1, EAW75269.1
GeneID.1137	CHRNA4	20	61,974,665	61,992,695	18,030	-	11	4_A375_EGR1..1..5750, 4_A375_EGR1..1..5751, 4_A375_EGR1..1..5752, 4_A375_EGR1..1..5753, 4_A375_EGR1..1..5754, 4_A375_EGR1..1..5755, 4_A375_EGR1..1..5756, 4_A375_EGR1..1..5757, 4_A375_EGR1..1..5758, 4_A375_EGR1..1..5759, 4_A375_EGR1..1..5760	17655, 16002, 14695, 13623, 11367, 9767, 4587, 3063, 2092, -649, -5449	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream, upstream	0	0	1	6.46	7.36	20.27	11	4_A375_EGR1..1	26	Gene CHRNA4	FLJ95812, NACHRA4, NACHR, EBN1, NACRA4, BFNC, EBN, CHRNA4	cholinergic receptor, nicotinic, alpha 4	NM_000744, hCT14519.3, hCT2312453.0	206735_at, 206736_x_at, 216666_at, 216900_s_at	NP_000735.1, EAW75269.1, EAW75270.1
GeneID.3785	KCNQ2	20	62,037,542	62,103,993	66,451	-	22	1_A375_pNL7_minus_lncRNA_AR..1..3684, 4_A375_EGR1..1..5766, 4_A375_EGR1..1..5767, 4_A375_EGR1..1..5768, 4_A375_EGR1..1..5769, 4_A375_EGR1..1..5770, 4_A375_EGR1..1..5771, 4_A375_EGR1..1..5772, 4_A375_EGR1..1..5773, 4_A375_EGR1..1..5774, 4_A375_EGR1..1..5775, 4_A375_EGR1..1..5776, 4_A375_EGR1..1..5777, 4_A375_EGR1..1..5778, 4_A375_EGR1..1..5779, 4_A375_EGR1..1..5780, 4_A375_EGR1..1..5781, 4_A375_EGR1..1..5782, 4_A375_EGR1..1..5783, 4_A375_EGR1..1..5784, 4_A375_EGR1..1..5785, 4_A375_EGR1..1..5786	-2823, 72633, 67993, 66905, 64537, 62425, 61401, 54777, 53561, 50649, 42623, 32153, 20665, 17542, 14169, 6377, 6846, 2121, -967, -6204, -7207, -9607	upstream, downstream, downstream, downstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream, upstream, upstream, upstream	1	0	1	9.5	9.27	19.09	22	4_A375_EGR1..1	25	Gene KCNQ2	KVEBN1, KCNA11, EBN1, KV7.2, ENB1, EIEE7, BFNC, EBN, KCNQ2, BFNS1, HNSPC	potassium voltage-gated channel, KQT-like subfamily, member 2	NM_172106, NM_172109, NM_172107, NM_172108, NM_004518, hCT14533.2, hCT1950304.0, hCT1962391.1, hCT1962392.1, hCT2312456.0, hCT2312460.0, hCT2312461.0, hCT2312462.0, hCT2312463.0, hCT2355542.0, hCT2355543.0, hCT2355544.0	205737_at, 210506_s_at, 211486_s_at	NP_742104.1, NP_742107.1, NP_004509.2, NP_742105.1, NP_742106.1, EAW75281.1, EAW75271.1, EAW75272.1, EAW75273.1, EAW75274.1, EAW75275.1, EAW75276.1, EAW75277.1, EAW75278.1, EAW75279.1, EAW75280.1, EAW75282.1
GeneID.1917	EEF1A2	20	62,119,366	62,130,505	11,139	-	10	2_A375_pNL97_plus_lncRNA_AR..1..5293, 4_A375_EGR1..1..5784, 4_A375_EGR1..1..5785, 4_A375_EGR1..1..5786, 4_A375_EGR1..1..5787, 4_A375_EGR1..1..5788, 4_A375_EGR1..1..5789, 4_A375_EGR1..1..5790, 4_A375_EGR1..1..5791, 4_A375_EGR1..1..5792	809, 20306, 19305, 16905, 14009, 12569, 10377, 4105, -951, -3767	in gene, downstream, downstream, downstream, downstream, downstream, in gene, in gene, upstream, upstream	0	1	1	10.1	9.4	19.3	10	4_A375_EGR1..1	24	Gene EEF1A2	FLJ41696, EEF1A2, STNL, HS1, EF1A, STN, EF-1-alpha-2, EEF1AL	eukaryotic translation elongation factor 1 alpha 2	NM_001958, hCT14522.3, hCT2312440.0	204540_at	NP_001949.1, EAW75260.1, EAW75259.1
GeneID.79144	PPDPF	20	62,152,133	62,153,524	1,391	+	3	4_A375_EGR1..1..5793, 4_A375_EGR1..1..5794, 4_A375_EGR1..1..5795	-3141, 1723, 10075	upstream, downstream, downstream	0	0	1	11.33	11.33	23	3	4_A375_EGR1..1	24	Gene PPDPF	PPDPF, FLJ21046, dJ697K14.9, MGC2479, C20orf149	pancreatic progenitor cell differentiation and proliferation factor homolog (zebrafish)	NM_024299, hCT14534.3, hCT1962929.1	218010_x_at, 227994_x_at, 233571_x_at	NP_077275.1, EAW75265.1, EAW75264.1
GeneID.5753	PTK6	20	62,159,766	62,168,707	8,941	-	8	4_A375_EGR1..1..5793, 4_A375_EGR1..1..5794, 4_A375_EGR1..1..5795, 4_A375_EGR1..1..5796, 4_A375_EGR1..1..5797, 4_A375_EGR1..1..5798, 4_A375_EGR1..1..5799, 4_A375_EGR1..1..5800	19715, 14851, 6499, -701, -2525, -3901, -6973, -10221	downstream, downstream, in gene, upstream, upstream, upstream, upstream, upstream	0	0	1	11.38	11	22.88	8	4_A375_EGR1..1	28	Gene PTK6	FLJ42088, BRK, PTK6	PTK6 protein tyrosine kinase 6	NM_005975, hCT1950298.1, hCT2312445.0	1553114_a_at, 206482_at	NP_005966.1, EAW75262.1, EAW75263.1
GeneID.6725	SRMS	20	62,172,163	62,178,857	6,694	-	6	4_A375_EGR1..1..5795, 4_A375_EGR1..1..5796, 4_A375_EGR1..1..5797, 4_A375_EGR1..1..5798, 4_A375_EGR1..1..5799, 4_A375_EGR1..1..5800	16849, 9449, 7625, 6249, 3177, -71	downstream, downstream, downstream, in gene, in gene, upstream	0	0	1	11.5	10.67	23	6	4_A375_EGR1..1	28	Gene SRMS	SRMS, SRM, C20orf148, dJ697K14.1	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	NM_080823, hCT14523.2	234514_at	NP_543013.1, EAW75261.1
GeneID.79025	C20orf195	20	62,184,373	62,188,036	3,663	+	5	4_A375_EGR1..1..5799, 4_A375_EGR1..1..5800, 4_A375_EGR1..1..5801, 4_A375_EGR1..1..5802, 4_A375_EGR1..1..5803	-8693, -5445, 9435, 10635, 12411	upstream, upstream, downstream, downstream, downstream	0	0	1	10	11	20.6	5	4_A375_EGR1..1	24	Gene C20orf195	MGC5356, C20orf195	chromosome 20 open reading frame 195	NM_024059, hCT1645389.3	220426_at	NP_076964.1, EAW75258.1
GeneID.85441	PRIC285	20	62,189,439	62,205,592	16,153	-	6	4_A375_EGR1..1..5801, 4_A375_EGR1..1..5802, 4_A375_EGR1..1..5803, 4_A375_EGR1..1..5804, 4_A375_EGR1..1..5805, 4_A375_EGR1..1..5806	11764, 10584, 6806, 7224, 1944, -360	in gene, in gene, in gene, in gene, in gene, upstream	0	0	1	12	12.5	21.33	6	4_A375_EGR1..1	24	Gene PRIC285	KIAA1769, MGC132634, MGC138228, PDIP-1, FLJ00244	peroxisomal proliferator-activated receptor A interacting complex 285	NM_001037335, NM_033405, hCT14525.3, hCT2312438.0, hCT2355467.0	226230_at, 232517_s_at, 232518_at, 232787_at	NP_001032412.2, NP_208384.3, EAW75255.1, EAW75256.1, EAW75257.1
GeneID.26205	GMEB2	20	62,218,955	62,258,381	39,426	-	3	2_A375_pNL97_plus_lncRNA_AR..1..5294, 4_A375_EGR1..1..5807, 4_A375_EGR1..1..5808	-435, 38845, -387	upstream, in gene, upstream	0	1	1	13	13	24.5	2	4_A375_EGR1..1	25	Gene GMEB2	KIAA1269, P79PIF, GMEB2, PIF79	glucocorticoid modulatory element binding protein 2	NM_012384, hCT14521.3, hCT2312435.0, hCT2312436.0	222251_s_at, 44146_at	NP_036516.1, EAW75253.1, EAW75252.1, EAW75254.1
GeneID.100505771	LOC100505771	20	62,258,587	62,260,061	1,474	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5294, 4_A375_EGR1..1..5808	229, 181	in gene, in gene	0	1	1	15	20	24	1	4_A375_EGR1..1	24	Gene LOC100505771		hypothetical LOC100505771	XR_109591, XR_109592, XR_115400, XR_115401		
GeneID.50861	STMN3	20	62,271,061	62,284,780	13,719	-	6	2_A375_pNL97_plus_lncRNA_AR..1..5295, 2_A375_pNL97_plus_lncRNA_AR..1..5296, 2_A375_pNL97_plus_lncRNA_AR..1..5297, 4_A375_EGR1..1..5809, 4_A375_EGR1..1..5810, 4_A375_EGR1..1..5811	7960, 140, -5044, 10604, 1132, -4652	in gene, in gene, upstream, in gene, in gene, upstream	0	1	1	13.2	19.8	19.8	5	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene STMN3	SCLIP, STMN3	stathmin-like 3	NM_015894, hCT2312418.1, hCT2312420.1	218207_s_at, 222557_at	NP_056978.2, EAW75250.1, EAW75249.1
GeneID.51750	RTEL1	20	62,289,647	62,327,601	37,954	+	13	1_A375_pNL7_minus_lncRNA_AR..1..3685, 2_A375_pNL97_plus_lncRNA_AR..1..5296, 2_A375_pNL97_plus_lncRNA_AR..1..5297, 4_A375_EGR1..1..5810, 4_A375_EGR1..1..5811, 4_A375_EGR1..1..5812, 4_A375_EGR1..1..5813, 4_A375_EGR1..1..5814, 4_A375_EGR1..1..5815, 4_A375_EGR1..1..5816, 4_A375_EGR1..1..5817, 4_A375_EGR1..1..5818, 4_A375_EGR1..1..5819	40913, -5007, 177, -5999, -15, 6449, 23633, 27729, 32913, 37169, 38833, 39793, 42289	downstream, upstream, in gene, upstream, upstream, in gene, in gene, in gene, in gene, in gene, downstream, downstream, downstream	1	1	1	11.25	15.08	21.56	12	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene RTEL1	RTEL, DKFZp434C013, KIAA1088, bK3184A7.3, RTEL1, C20orf41, NHL	regulator of telomere elongation helicase 1	NM_016434, NM_032957	208467_x_at	NP_057518.1, NP_116575.2
GeneID.8771	TNFRSF6B	20	62,326,288	62,330,037	3,749	+	10	1_A375_pNL7_minus_lncRNA_AR..1..3685, 1_A375_pNL7_minus_lncRNA_AR..1..3686, 2_A375_pNL97_plus_lncRNA_AR..1..5298, 4_A375_EGR1..1..5814, 4_A375_EGR1..1..5815, 4_A375_EGR1..1..5816, 4_A375_EGR1..1..5817, 4_A375_EGR1..1..5818, 4_A375_EGR1..1..5819, 4_A375_EGR1..1..5820	4272, 12944, 12944, -8912, -3728, 528, 2192, 3152, 5848, 13552	downstream, downstream, downstream, upstream, upstream, in gene, in gene, in gene, downstream, downstream	1	1	1	13.33	15.67	22.11	9	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene TNFRSF6B	DCR3, DJ583P15.1.1, M68, TR6, TNFRSF6B	tumor necrosis factor receptor superfamily, member 6b, decoy	NM_003823, NM_032945		NP_003814.1, NP_116563.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.10139	ARFRP1	20	62,329,995	62,339,355	9,360	-	9	1_A375_pNL7_minus_lncRNA_AR..1..3665, 1_A375_pNL7_minus_lncRNA_AR..1..3666, 2_A375_pNL97_plus_lncRNA_AR..1..5298, 4_A375_EGR1..1..5815, 4_A375_EGR1..1..5816, 4_A375_EGR1..1..5817, 4_A375_EGR1..1..5818, 4_A375_EGR1..1..5819, 4_A375_EGR1..1..5820	8795, 123, 123, 16795, 12539, 10875, 9915, 7419, -485	in gene, in gene, in gene, downstream, downstream, downstream, downstream, in gene, upstream	1	1	1	13.88	15.75	21.5	8	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene ARFRP1	ARP, ARFRP1, ARL18, Arp1	ADP-ribosylation factor related protein 1	NM_003224, NM_001134758, hCT12109.4, hCT1970952.1, hCT1970953.1, hCT1970955.1, hCT2312422.0, hCT2312423.0, hCT2312427.0, hCT2312429.0	203174_s_at, 215984_s_at	NP_003215.1, NP_001128230.1, EAW75230.1, EAW75232.1, EAW75235.1, EAW75236.1, EAW75231.1, EAW75233.1, EAW75234.1, EAW75237.1
GeneID.84619	ZGPAT	20	62,338,794	62,367,494	28,700	+	10	1_A375_pNL7_minus_lncRNA_AR..1..3665, 1_A375_pNL7_minus_lncRNA_AR..1..3666, 2_A375_pNL97_plus_lncRNA_AR..1..5298, 4_A375_EGR1..1..5817, 4_A375_EGR1..1..5818, 4_A375_EGR1..1..5819, 4_A375_EGR1..1..5820, 4_A375_EGR1..1..5821, 4_A375_EGR1..1..5822, 4_A375_EGR1..1..5823	-8234, 436, 436, -10314, -9354, -6858, 1046, 31238, 33398, 37718	upstream, in gene, in gene, upstream, upstream, upstream, in gene, downstream, downstream, downstream	1	1	1	13.89	15	21.78	9	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene ZGPAT	GPATC6, GPATCH6, ZC3H9, KIAA1847, ZC3HDC9, ZIP, MGC44880, ZGPAT	zinc finger, CCCH-type with G patch domain	NM_181485, NM_032527, NM_001083113, hCT2344173.0, hCT2344174.0, hCT2344175.0, hCT2344177.0, hCT2344185.0, hCT2344187.0, hCT2355501.0, hCT2355502.0, hCT2355503.0, hCT2355504.0	221848_at, 238398_s_at, 238399_x_at, 57539_at	NP_852150.2, NP_115916.3, NP_001076582.1, EAW75220.1, EAW75222.1, EAW75228.1, EAW75221.1, EAW75223.1, EAW75224.1, EAW75225.1, EAW75226.1, EAW75227.1, EAW75229.1
GeneID.54923	LIME1	20	62,367,978	62,370,460	2,482	+	4	4_A375_EGR1..1..5821, 4_A375_EGR1..1..5822, 4_A375_EGR1..1..5823, 4_A375_EGR1..1..5824	2054, 4214, 8534, 11158	in gene, downstream, downstream, downstream	0	0	1	10.25	10.25	21.75	4	4_A375_EGR1..1	24	Gene LIME1	LIME, dJ583P15.4, FLJ20406, LIME1, LP8067	Lck interacting transmembrane adaptor 1	NM_017806, hCT2344176.0, hCT2344178.0, hCT2344181.0, hCT2344184.0, hCT2355549.0, hCT2355550.0, hCT2355551.0	219541_at	NP_060276.2, EAW75217.1, EAW75213.1, EAW75214.1, EAW75215.1, EAW75218.1, EAW75216.1, EAW75219.1
GeneID.56731	SLC2A4RG	20	62,371,211	62,375,403	4,192	+	5	4_A375_EGR1..1..5821, 4_A375_EGR1..1..5822, 4_A375_EGR1..1..5823, 4_A375_EGR1..1..5824, 4_A375_EGR1..1..5825	-1179, 981, 5301, 7925, 13462	upstream, in gene, downstream, downstream, downstream	0	0	1	9.2	10.2	20.2	5	4_A375_EGR1..1	24	Gene SLC2A4RG	SLC2A4RG, Si-1-2-19, HDBP1, Si-1-2, GEF	SLC2A4 regulator	NM_020062, hCT13858.2, hCT1957411.1, hCT2317424.0	1555500_s_at, 218494_s_at, 222650_s_at, 227362_at	NP_064446.2, EAW75210.1, EAW75211.1, EAW75212.1
GeneID.140685	ZBTB46	20	62,375,878	62,436,856	60,978	-	8	4_A375_EGR1..1..5821, 4_A375_EGR1..1..5822, 4_A375_EGR1..1..5823, 4_A375_EGR1..1..5824, 4_A375_EGR1..1..5825, 4_A375_EGR1..1..5826, 4_A375_EGR1..1..5827, 4_A375_EGR1..1..5828	66824, 64664, 60344, 57720, 52163, 29752, 14904, 4726	downstream, downstream, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	9.25	9.88	20.63	8	4_A375_EGR1..1	24	Gene ZBTB46	dJ583P15.7, RINZF, ZBTB46, ZNF340, BTBD4, FLJ13502, dJ583P15.8	zinc finger and BTB domain containing 46	NM_025224, hCT2312415.1, hCT2351667.0	227329_at, 227358_at, 243214_at	NP_079500.1, EAW75205.1, EAW75206.1
GeneID.100128998	C20orf181	20	62,463,962	62,479,665	15,703	-	6	4_A375_EGR1..1..5829, 4_A375_EGR1..1..5830, 4_A375_EGR1..1..5831, 4_A375_EGR1..1..5832, 4_A375_EGR1..1..5833, 4_A375_EGR1..1..5834	13905, 4476, 2993, 1969, -6255, -7335	in gene, in gene, in gene, in gene, upstream, upstream	0	0	1	8.5	10.5	18.67	6	4_A375_EGR1..1	23	Gene C20orf181	dJ824A14.1, C20orf181	chromosome 20 open reading frame 181	XR_109593, XR_115402		
GeneID.140701	C20orf135	20	62,492,566	62,494,341	1,775	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3667, 2_A375_pNL97_plus_lncRNA_AR..1..5299, 4_A375_EGR1..1..5833, 4_A375_EGR1..1..5834, 4_A375_EGR1..1..5835, 4_A375_EGR1..1..5836	3882, 3322, -6646, -5566, 1082, 4410	downstream, downstream, upstream, upstream, in gene, downstream	1	1	1	10.25	11.5	21.5	4	4_A375_EGR1..1	33	Gene C20orf135	dJ591C20.1, ABHD16B, MGC42974, C20orf135	abhydrolase domain containing 16B	NM_080622, hCT2312411.0	234002_at	NP_542189.1, EAW75203.1
GeneID.7165	TPD52L2	20	62,496,590	62,522,891	26,301	+	7	1_A375_pNL7_minus_lncRNA_AR..1..3667, 1_A375_pNL7_minus_lncRNA_AR..1..3668, 2_A375_pNL97_plus_lncRNA_AR..1..5299, 4_A375_EGR1..1..5834, 4_A375_EGR1..1..5835, 4_A375_EGR1..1..5836, 4_A375_EGR1..1..5837	-142, 29778, -702, -9590, -2942, 386, 20338	upstream, downstream, upstream, upstream, upstream, in gene, in gene	1	1	1	13.4	11.6	19.6	5	4_A375_EGR1..1	33	Gene TPD52L2	D54, DKFZp686A1765, hD54, TPD52L2	tumor protein D52-like 2	NM_003288, NM_199359, NM_199360, NM_199361, NM_199362, NM_199363, hCT13853.3, hCT1962381.1, hCT1962382.1, hCT1962383.1, hCT2317439.0, hCT2317442.0, hCT2355431.0, hCT2355432.0	201379_s_at	NP_003279.2, NP_955391.1, NP_955392.1, NP_955393.1, NP_955394.1, NP_955395.1, EAW75194.1, EAW75195.1, EAW75196.1, EAW75197.1, EAW75198.1, EAW75199.1, EAW75200.1, EAW75201.1
GeneID.80331	DNAJC5	20	62,526,518	62,565,395	38,877	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3668, 2_A375_pNL97_plus_lncRNA_AR..1..5300, 4_A375_EGR1..1..5837, 4_A375_EGR1..1..5838, 4_A375_EGR1..1..5839, 4_A375_EGR1..1..5840	-150, 45130, -9590, 25290, 44362, 45634	upstream, downstream, upstream, in gene, downstream, downstream	1	1	1	10.8	12.6	19.6	5	4_A375_EGR1..1	29	Gene DNAJC5	CSP, DNAJC5A, DKFZp761N1221, FLJ13070, DKFZp434N1429, FLJ00118, DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5	NM_025219, hCT2317443.0, hCT2317444.0, hCT2355521.0	224611_s_at, 224612_s_at, 224613_s_at, 244601_at	NP_079495.1, EAW75193.1, EAW75191.1, EAW75192.1
GeneID.100126339	MIR941-2	20	62,550,906	62,550,994	88	+	1	4_A375_EGR1..1..5838	902	downstream	0	0	1	5	12	15	1	4_A375_EGR1..1	15	Gene MIR941-2	MIRN941-2, MIR941-2	microRNA 941-2	NR_030638		
GeneID.100126329	MIR941-1	20	62,551,437	62,551,493	56	+	1	4_A375_EGR1..1..5838	371	downstream	0	0	1	5	12	15	1	4_A375_EGR1..1	15	Gene MIR941-1	MIR941-1, MIRN941-1	microRNA 941-1	NR_030637		
GeneID.54963	UCKL1	20	62,571,182	62,587,800	16,618	-	10	1_A375_pNL7_minus_lncRNA_AR..1..3669, 2_A375_pNL97_plus_lncRNA_AR..1..5300, 2_A375_pNL97_plus_lncRNA_AR..1..5301, 4_A375_EGR1..1..5839, 4_A375_EGR1..1..5840, 4_A375_EGR1..1..5841, 4_A375_EGR1..1..5842, 4_A375_EGR1..1..5843, 4_A375_EGR1..1..5844, 4_A375_EGR1..1..5845	24, 16152, -166, 16920, 15446, 11752, 7176, 5060, -776, -7507	in gene, in gene, upstream, downstream, in gene, in gene, in gene, in gene, upstream, upstream	1	1	1	11.75	14.75	19.75	8	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene UCKL1	URKL1, UCK1L, UCK1-LIKE, UCKL1	uridine-cytidine kinase 1-like 1	NM_017859, NM_001193379, hCT13861.3, hCT1970981.1, hCT2312407.0, hCT2355493.0, hCT2355494.0	218533_s_at, 232675_s_at, 232727_at	NP_060329.2, NP_001180308.1, EAW75185.1, EAW75186.1, EAW75188.1, EAW75189.1, EAW75187.1
GeneID.100302137	MIR1914	20	62,572,818	62,572,897	79	-	6	2_A375_pNL97_plus_lncRNA_AR..1..5300, 4_A375_EGR1..1..5839, 4_A375_EGR1..1..5840, 4_A375_EGR1..1..5841, 4_A375_EGR1..1..5842, 4_A375_EGR1..1..5843	1249, 2017, 545, -3151, -7727, -9823	downstream, downstream, downstream, upstream, upstream, upstream	0	1	1	8.8	12.8	20.4	5	4_A375_EGR1..1	29	Gene MIR1914	MIRN1914, hsa-mir-1914, MIR1914	microRNA 1914	NR_031735		
GeneID.693232	MIR647	20	62,573,984	62,574,079	95	-	6	2_A375_pNL97_plus_lncRNA_AR..1..5300, 4_A375_EGR1..1..5839, 4_A375_EGR1..1..5840, 4_A375_EGR1..1..5841, 4_A375_EGR1..1..5842, 4_A375_EGR1..1..5843	2431, 3199, 1727, -1989, -6545, -8641	downstream, downstream, downstream, upstream, upstream, upstream	0	1	1	8.8	12.8	20.4	5	4_A375_EGR1..1	29	Gene MIR647	MIR647, hsa-mir-647, MIRN647	microRNA 647	NR_030377		
GeneID.100113386	UCKL1AS	20	62,584,737	62,588,338	3,601	+	8	1_A375_pNL7_minus_lncRNA_AR..1..3669, 2_A375_pNL97_plus_lncRNA_AR..1..5301, 4_A375_EGR1..1..5841, 4_A375_EGR1..1..5842, 4_A375_EGR1..1..5843, 4_A375_EGR1..1..5844, 4_A375_EGR1..1..5845, 4_A375_EGR1..1..5846	3039, 3231, -8689, -4113, -2017, 3839, 10570, 13631	in gene, in gene, upstream, upstream, upstream, downstream, downstream, downstream	1	1	1	12.43	14	18.43	7	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene UCKL1AS	UCKL1OS, UCKL1-AS, UCKL1-AS1, FLJ46847, UCKL1AS	UCKL1 antisense RNA (non-protein coding)	NR_027287		
GeneID.57473	ZNF512B	20	62,588,055	62,601,218	13,163	-	7	1_A375_pNL7_minus_lncRNA_AR..1..3669, 2_A375_pNL97_plus_lncRNA_AR..1..5301, 4_A375_EGR1..1..5842, 4_A375_EGR1..1..5843, 4_A375_EGR1..1..5844, 4_A375_EGR1..1..5845, 4_A375_EGR1..1..5846	13442, 13250, 20594, 18498, 12642, 5911, 2850	downstream, downstream, downstream, downstream, in gene, in gene, in gene	1	1	1	12.83	14.33	18.5	6	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene ZNF512B	KIAA1196, MGC149846, GM632, ZNF512B, MGC149845	zinc finger protein 512B	NM_020713	221889_at, 55872_at	NP_065764.1
GeneID.140700	SAMD10	20	62,605,466	62,610,995	5,529	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3690, 2_A375_pNL97_plus_lncRNA_AR..1..5302, 4_A375_EGR1..1..5845, 4_A375_EGR1..1..5846	-1357, -1357, 15868, 12627	upstream, upstream, downstream, downstream	1	1	1	14.33	22.67	18.33	3	2_A375_pNL97_plus_lncRNA_AR..1	47	Gene SAMD10	C20orf136, SAMD10, dJ591C20.7, dJ591C20	sterile alpha motif domain containing 10	NM_080621, hCT13863.2, hCT1950301.1	227773_at, 233001_at	NP_542188.1, EAW75180.1, EAW75181.1
GeneID.24148	PRPF6	20	62,612,431	62,664,453	52,022	+	8	1_A375_pNL7_minus_lncRNA_AR..1..3690, 2_A375_pNL97_plus_lncRNA_AR..1..5302, 2_A375_pNL97_plus_lncRNA_AR..1..5303, 4_A375_EGR1..1..5847, 4_A375_EGR1..1..5848, 4_A375_EGR1..1..5849, 4_A375_EGR1..1..5850, 4_A375_EGR1..1..5851	-79, -79, 57649, 46641, 57761, 58417, 59457, 60945	upstream, upstream, downstream, in gene, downstream, downstream, downstream, downstream	1	1	1	13.8	19.4	19.4	5	2_A375_pNL97_plus_lncRNA_AR..1	47	Gene PRPF6	C20orf14, ANT-1, TOM, Prp6, PRPF6, hPrp6, U5-102K	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	NM_012469, hCT13855.2, hCT1957410.2, hCT2317328.1, hCT2317330.1, hCT2350264.0, hCT2355444.0	208879_x_at, 208880_s_at	NP_036601.2, EAW75174.1, EAW75175.1, EAW75176.1, EAW75177.1, EAW75179.1, EAW75178.1
GeneID.284739	NCRNA00176	20	62,665,697	62,671,315	5,618	+	7	2_A375_pNL97_plus_lncRNA_AR..1..5303, 4_A375_EGR1..1..5847, 4_A375_EGR1..1..5848, 4_A375_EGR1..1..5849, 4_A375_EGR1..1..5850, 4_A375_EGR1..1..5851, 4_A375_EGR1..1..5852	4363, -6625, 4495, 5151, 6191, 7679, 16607	in gene, upstream, in gene, in gene, downstream, downstream, downstream	0	1	1	9.8	12.8	21	5	4_A375_EGR1..1	27	Gene NCRNA00176	DKFZp434G015, PRR17, NCRNA00176, FLJ27267, FLJ17673	non-protein coding RNA 176	NR_027666, NR_027667	233355_at	
GeneID.54345	SOX18	20	62,679,079	62,680,979	1,900	-	8	2_A375_pNL97_plus_lncRNA_AR..1..5303, 4_A375_EGR1..1..5848, 4_A375_EGR1..1..5849, 4_A375_EGR1..1..5850, 4_A375_EGR1..1..5851, 4_A375_EGR1..1..5852, 4_A375_EGR1..1..5853, 4_A375_EGR1..1..5854	10899, 10787, 10131, 9091, 7603, -1325, -2157, -6413	downstream, downstream, downstream, downstream, downstream, upstream, upstream, upstream	0	1	1	10.33	12.67	19.67	6	4_A375_EGR1..1	27	Gene SOX18	HLTS, SOX18	SRY (sex determining region Y)-box 18	NM_018419	219568_x_at	NP_060889.1
GeneID.6919	TCEA2	20	62,688,439	62,703,700	15,261	+	13	1_A375_pNL7_minus_lncRNA_AR..1..3691, 2_A375_pNL97_plus_lncRNA_AR..1..5304, 4_A375_EGR1..1..5852, 4_A375_EGR1..1..5853, 4_A375_EGR1..1..5854, 4_A375_EGR1..1..5855, 4_A375_EGR1..1..5856, 4_A375_EGR1..1..5857, 4_A375_EGR1..1..5858, 4_A375_EGR1..1..5859, 4_A375_EGR1..1..5860, 4_A375_EGR1..1..5861, 4_A375_EGR1..1..5862	5961, 5961, -6135, -5303, -1047, 5657, 6441, 8649, 12361, 15753, 16553, 21209, 22409	in gene, in gene, upstream, upstream, upstream, in gene, in gene, in gene, in gene, downstream, downstream, downstream, downstream	1	1	1	11.6	14.1	17.9	10	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene TCEA2	TFIIS, TCEA2	transcription elongation factor A (SII), 2	NM_003195, NM_198723, hCT2317338.0, hCT2317339.0, hCT2355574.0	203919_at, 238173_at, 241428_x_at	NP_003186.1, NP_942016.1, EAW75168.1, EAW75169.1, EAW75170.1
GeneID.10287	RGS19	20	62,704,534	62,711,324	6,790	-	9	1_A375_pNL7_minus_lncRNA_AR..1..3691, 2_A375_pNL97_plus_lncRNA_AR..1..5304, 4_A375_EGR1..1..5856, 4_A375_EGR1..1..5857, 4_A375_EGR1..1..5858, 4_A375_EGR1..1..5859, 4_A375_EGR1..1..5860, 4_A375_EGR1..1..5861, 4_A375_EGR1..1..5862	16924, 16924, 16444, 14236, 10524, 7132, 6332, 1676, 476	downstream, downstream, downstream, downstream, downstream, downstream, downstream, in gene, in gene	1	1	1	12.57	15	17.86	7	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene RGS19	RGS19, GAIP, RGSGAIP	regulator of G-protein signaling 19	NM_005873, NM_001039467, hCT2312397.0, hCT2312399.0	204336_s_at	NP_005864.1, NP_001034556.1, EAW75166.1, EAW75167.1
GeneID.4987	OPRL1	20	62,711,488	62,731,996	20,508	+	8	4_A375_EGR1..1..5858, 4_A375_EGR1..1..5859, 4_A375_EGR1..1..5860, 4_A375_EGR1..1..5861, 4_A375_EGR1..1..5862, 4_A375_EGR1..1..5863, 4_A375_EGR1..1..5864, 4_A375_EGR1..1..5865	-10686, -7296, -6496, -1640, -840, 25056, 25984, 29344	upstream, upstream, upstream, upstream, upstream, downstream, downstream, downstream	0	0	1	8.5	10.75	17.75	8	4_A375_EGR1..1	22	Gene OPRL1	NOCIR, KOR-3, OOR, MGC34578, OPRL1, ORL1	opiate receptor-like 1	NM_182647, NM_000913, hCT13852.2, hCT2317336.1	206563_s_at, 206564_at	NP_872588.1, NP_000904.1, EAW75162.1, EAW75163.1
GeneID.198437	C20orf201	20	62,714,733	62,715,712	979	-	3	4_A375_EGR1..1..5860, 4_A375_EGR1..1..5861, 4_A375_EGR1..1..5862	10720, 6064, 4864	downstream, downstream, downstream	0	0	1	7.33	10.67	16.33	3	4_A375_EGR1..1	18	Gene C20orf201	C20orf201		NM_001007125, hCT2312390.0, hCT2312391.0	1554977_at	NP_001007126.1, EAW75164.1, EAW75165.1
GeneID.2832	NPBWR2	20	62,737,183	62,738,184	1,001	-	4	4_A375_EGR1..1..5863, 4_A375_EGR1..1..5864, 4_A375_EGR1..1..5865, 4_A375_EGR1..1..5866	1640, 712, -2648, -5304	downstream, in gene, upstream, upstream	0	0	1	9.5	9.75	18.5	4	4_A375_EGR1..1	21	Gene NPBWR2	GPR8, NPBWR2	neuropeptides B/W receptor 2	NM_005286, hCT1647131.3	221356_at	NP_005277.2, EAW75161.1
GeneID.4661	MYT1	20	62,795,827	62,873,606	77,779	+	9	1_A375_pNL7_minus_lncRNA_AR..1..3692, 2_A375_pNL97_plus_lncRNA_AR..1..5305, 2_A375_pNL97_plus_lncRNA_AR..1..5306, 2_A375_pNL97_plus_lncRNA_AR..1..5307, 2_A375_pNL97_plus_lncRNA_AR..1..5308, 4_A375_EGR1..1..5868, 4_A375_EGR1..1..5869, 4_A375_EGR1..1..5870, 4_A375_EGR1..1..5871	-2403, -2419, 2477, 28088, 41229, -10131, 1997, 21421, 67805	upstream, upstream, in gene, in gene, in gene, upstream, in gene, in gene, in gene	1	1	1	14.14	18.86	15.86	7	2_A375_pNL97_plus_lncRNA_AR..1	38	Gene MYT1	MYT1, C20orf36, MYTI, PLPB1, MTF1	myelin transcription factor 1	NM_004535	1556269_at, 210341_at, 215822_x_at	NP_004526.1
GeneID.55251	PCMTD2	20	62,887,048	62,907,579	20,531	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3693, 2_A375_pNL97_plus_lncRNA_AR..1..5309	-40, -72	upstream, upstream	1	1	0	29	33	7	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene PCMTD2	FLJ10883, C20orf36, KIAA0835, KIAA1050, PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	NM_018257, NM_001104925	212406_s_at	NP_060727.2, NP_001098395.1
GeneID.100132288	LOC100132288	21	9,907,194	9,968,585	61,391	-	5	4_A375_EGR1..1..5877, 4_A375_EGR1..1..5878, 4_A375_EGR1..1..5879, 4_A375_EGR1..1..5880, 4_A375_EGR1..1..5881	64665, 60329, 59561, 58761, 56425	downstream, in gene, in gene, in gene, in gene	0	0	1	9.8	13.2	23.4	5	4_A375_EGR1..1	31	Gene LOC100132288	FLJ00219, MGC90442, FLJ35473, FLJ39633	hypothetical protein LOC100132288	NM_001033515		NP_001028687.1
GeneID.7179	TPTE	21	10,906,741	10,990,920	84,179	-	1	4_A375_EGR1..1..5882	-440	upstream	0	0	1	5	8	15	1	4_A375_EGR1..1	15	Gene TPTE	TPTE, CT44, PTEN2	transmembrane phosphatase with tensin homology	NM_199261, NM_199259, NM_199260	220205_at	NP_954870.2, NP_954868.1, NP_954869.1
GeneID.85318	BAGE3	21	11,020,842	11,058,323	37,481	-	1	4_A375_EGR1..1..5883	-1421	upstream	0	0	1	9	13	31	1	4_A375_EGR1..1	31	Gene BAGE3	CT2.3, BAGE3	B melanoma antigen family, member 3	NM_182481		NP_872287.1
GeneID.574	BAGE	21	11,057,796	11,059,817	2,021	-	1	4_A375_EGR1..1..5883	73	in gene	0	0	1	9	13	31	1	4_A375_EGR1..1	31	Gene BAGE	CT2.1, BAGE1, BAGE	B melanoma antigen	NM_001187	1555369_at, 1555603_at, 1555605_x_at, 207712_at	
GeneID.8204	NRIP1	21	16,333,556	16,437,126	103,570	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5311	-1002	upstream	0	1	0	10	14	6	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene NRIP1	RIP140, NRIP1, FLJ77253	nuclear receptor interacting protein 1	NM_003489	202599_s_at, 202600_s_at	NP_003480.2
GeneID.54149	C21orf91	21	19,161,284	19,191,703	30,419	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3695, 2_A375_pNL97_plus_lncRNA_AR..1..5314	-105, -105	upstream, upstream	1	1	0	48	42	6	1	1_A375_pNL7_minus_lncRNA_AR..1	48	Gene C21orf91	DKFZp781D1223, EURL, C21orf38, YG81, C21orf14, C21orf91	chromosome 21 open reading frame 91	NM_001100421, NM_017447, NM_001100420, hCT2298264.0, hCT2298265.0, hCT2359465.0	220941_s_at, 226109_at	NP_001093891.1, NP_059143.3, NP_001093890.1, EAX10020.1, EAX10021.1, EAX10022.1
GeneID.54148	MRPL39	21	26,957,968	26,979,801	21,833	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5315	-7	upstream	0	1	0	14	21	10	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MRPL39	FLJ20451, MGC104174, PRED22, PRED66, MRPL5, C21orf92, MRPL39, MSTP003, RPML5, MGC3400, L39mt, MRP-L5	mitochondrial ribosomal protein L39	NM_080794, NM_017446, hCT1958517.1, hCT1958518.1, hCT2295879.0, hCT401157.3	218558_s_at, 236910_at	NP_542984.2, NP_059142.2, EAX09979.1, EAX09980.1, EAX09981.1, EAX09982.1

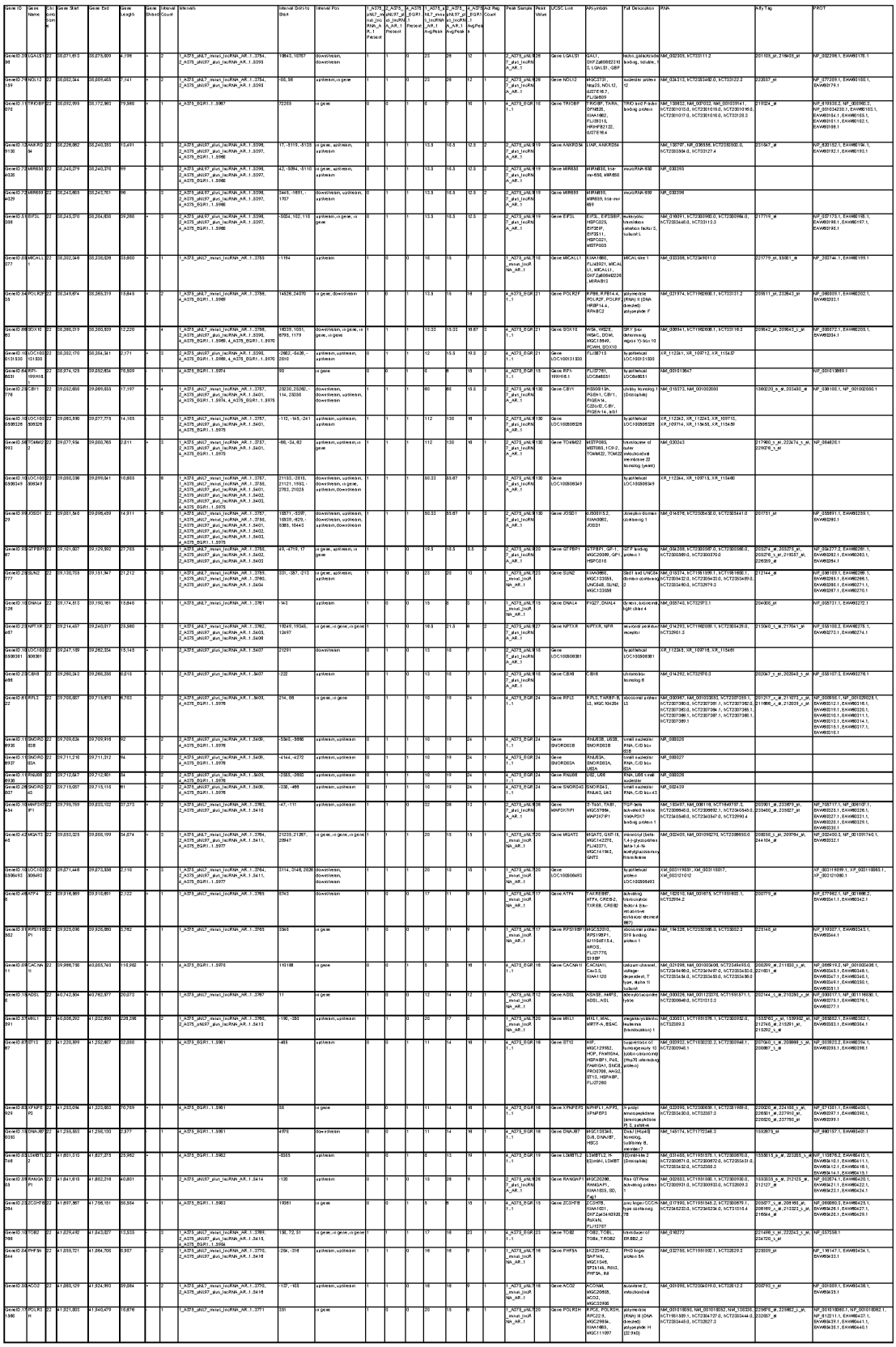




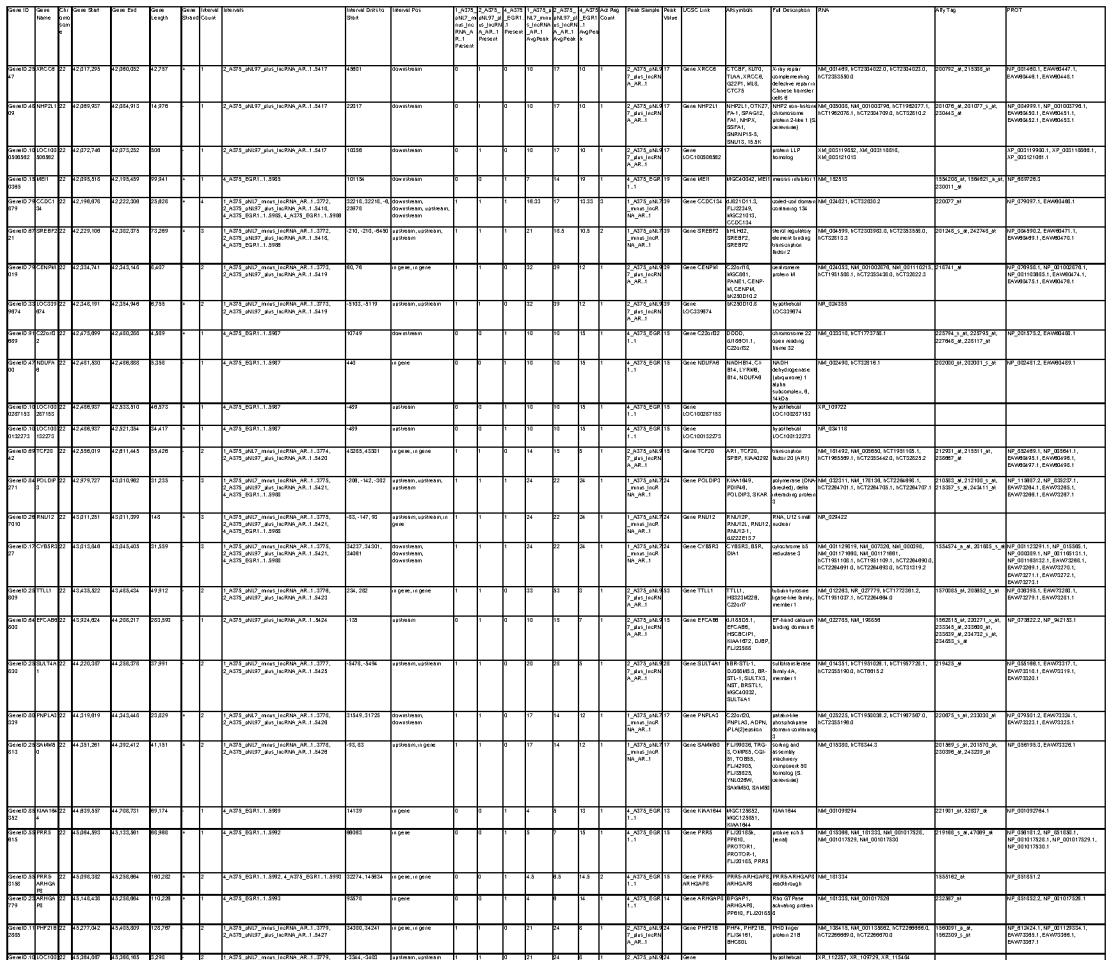
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_shN7_shRNA_AR_1 Percent	2_A375_shN7_shRNA_AR_1 Percent	4_A375_EGFR_shRNA_AR_1 Percent	1_A375_shN7_shRNA_AR_1 Avg Peak	2_A375_shN7_shRNA_AR_1 Avg Peak	4_A375_EGFR_shRNA_AR_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:3976	KRTAP10-6	21	46,011,149	46,012,399	1,237	-	1	4_A375_EGR1...1.5899	9238	upstream	0	0	1	2	3	12	1	4_A375_EGR1...1	12	Gene KRTAP10-6	KRTAP10.6, KRTAP10-6, KRTAP16-1, KAP16.1	keratin associated protein 10-6	NM_199565, XCT2350496.0			NP_941982.1
GeneID:9975	KRTAP10-7	21	46,020,497	46,022,091	1,594	+	1	4_A375_EGR1...1.5899	1127	up gene	0	0	1	2	3	12	1	4_A375_EGR1...1	12	Gene KRTAP10-7	KRTAP10.7, KAP10.7, KRTAP16-7	keratin associated protein 10-7	NM_199569, XCT2350509.0			NP_941982.1, EAX09410.1
GeneID:7377	UBE2G2	21	46,166,953	46,221,708	52,763	-	2	2_A375_shN7_plus_lacRNA_AR_1.3336, 4_A375_EGR1...1.5900	74, 37274	up gene, downstream	0	1	1	7.5	15	12.5	2	2_A375_shN7_plus_lacRNA_AR_1	23	Gene UBE2G2	UBC7, UBE2G2	ubiquitin conjugating enzyme E2 G2 (UBC7 homolog, yeast)	NM_003343, NM_182688, XCT1841531.3, XCT1961489.1, XCT1961486.1, XCT2353935.0, XCT2355936.0, XCT2359476.0	1557653_s_at, 2009411_s_at, 2009412_s_at, 232753_at	NP_003334.2, NP_872638.1, EAX09396.1, EAX09397.1, EAX09400.1, EAX09396.1, EAX09399.1
GeneID:113	SUMO3	21	46,235,552	46,236,064	12,512	-	1	2_A375_shN7_plus_lacRNA_AR_1.3336	18560	downstream	0	1	0	11	23	10	1	2_A375_shN7_plus_lacRNA_AR_1	23	Gene SUMO3	SMT3H1, SUMO3, SLS1418, SMT3A, SUMO3	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	NM_006936, XCT1961508.1, XCT1962782.1, XCT2359421.0, XCT4310116.3	2009729_s_at, 2009742_s_at	NP_006927.2, EAX09390.1, EAX09392.1, EAX09393.1
GeneID:7373	PTTG1IP	21	46,269,513	46,293,741	24,228	-	3	1_A375_shN7_minus_lacRNA_AR_1.3712, 2_A375_shN37_plus_lacRNA_AR_1.3339, 4_A375_EGR1...1.5901	-279, -147, 109	upstream, upstream, up gene	1	1	1	16	19	16	1	2_A375_shN37_plus_lacRNA_AR_1	19	Gene PTTG1IP	C21orf1, PTTG1IP, C21orf5, PBF	pituitary tumor-transforming 1 interacting protein	NM_004339, XCT2355380.0, XCT2359480.0, XCT4310116.3	200977_at	NP_004330.1, EAX09365.1, EAX09367.1
GeneID:3678	ITGB2	21	46,305,966	46,348,793	42,828	-	1	4_A375_EGR1...1.5902	38943	up gene	0	0	1	5	7	17	1	4_A375_EGR1...1	17	Gene ITGB2	MFI7, LAD, CD18, MAC-1, ITGB2, MF17, LFA-1, CD18	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	NM_000211, NM_001127491, XCT2355533.0, XCT2355535.0, XCT2359425.0, XCT2359434.0, XCT4311311.3	1553549_s_at, 202803_s_at, 239998_x_at	NP_000202.2, NP_001120983.1, EAX09353.1, EAX09354.1, EAX09355.1, EAX09351.1
GeneID:1005	LOC100505748	21	46,346,998	46,349,993	6,829	+	1	2_A375_shN37_plus_lacRNA_AR_1.3340	18026	downstream	0	1	0	9	17	9	1	2_A375_shN37_plus_lacRNA_AR_1	17	Gene LOC100505748	hypothetical LOC100505748	XR_109982			
GeneID:8396	C21orf67	21	46,353,199	46,359,828	6,629	-	1	2_A375_shN37_plus_lacRNA_AR_1.3340	98	up gene	0	0	1	9	17	9	1	2_A375_shN37_plus_lacRNA_AR_1	17	Gene C21orf67	C21orf67, MGC120189, MGC120190, C21orf69, MGC149398, MGC120188, PRED54, MGC149397, MGC120187	chromosome 21 open reading frame 67	NR_027126, NR_027129	1559627_s_at	
GeneID:3395	C21orf33	21	46,359,935	46,396,860	36,925	+	2	2_A375_shN37_plus_lacRNA_AR_1.3340, 4_A375_EGR1...1.5902	-180, 46577	upstream, downstream	0	1	1	7.5	10.5	10.5	2	2_A375_shN37_plus_lacRNA_AR_1	17	Gene C21orf33	C21orf33, PRED56	chromosome 21 open reading frame 33	NM_006180, XCT1960271.1, XCT1960272.1, XCT2356531.1, XCT2359536.1, XCT4311312.4	242750_x_at	NP_476705.1, EAX09387.1, PRED56
GeneID:7699	NCRNA00160	21	46,409,779	46,414,001	4,222	-	2	4_A375_EGR1...1.5903, 4_A375_EGR1...1.5904	7193, 4350	downstream, upstream	0	0	1	8	9	13	2	4_A375_EGR1...1	14	Gene NCRNA00160	NCI-1-A, NCRNA00160, C21orf134, NCI1A	non-protein coding RNA 160	NR_033540	1562054_at	
GeneID:6035	NCRNA00162	21	46,416,136	46,424,842	8,706	-	1	4_A375_EGR1...1.5904	6061	downstream	0	0	1	8	9	14	1	4_A375_EGR1...1	14	Gene NCRNA00162	PRED74, NCRNA00162, NCI-1-C, C21orf13, NCI1C	non-protein coding RNA 162	NR_033659	1559234_at	
GeneID:2375	POFUT2	21	46,663,643	46,707,811	33,966	-	1	4_A375_EGR1...1.5905	-89	upstream	0	0	1	8	12	15	1	4_A375_EGR1...1	15	Gene POFUT2	C21orf80, FUT12, POFUT2	protein O-fucosyltransferase 2	NM_133933, NM_018227, NR_036836, XCT1960242.1, XCT1960243.1, XCT2359470.0, XCT2359471.0, XCT4312813.2	1553548_s_at, 207446_s_at, 207447_s_at, 209876_s_at	NP_598368.2, NP_060642.1, EAX09386.1, EAX09531.1, EAX09534.1
GeneID:8492	LOC642852	21	46,707,997	46,717,369	9,372	+	1	4_A375_EGR1...1.5905	-95	upstream	0	0	1	8	12	15	1	4_A375_EGR1...1	15	Gene LOC642852	FLJ31804, FLJ34002, DKFZp547J125	hypothetical LOC642852	NM_028943	1559937_s_at, 1569032_at, 243695_at	
GeneID:7851	COL18A1	21	46,828,097	46,933,454	105,357	+	4	4_A375_EGR1...1.5906, 4_A375_EGR1...1.5907, 4_A375_EGR1...1.5908, 4_A375_EGR1...1.5909	4321, 20031, 83139, 106991	upstream, up gene, up gene, up gene	0	0	1	5.25	8.5	13.75	4	4_A375_EGR1...1	17	Gene COL18A1	KNO1, FLJ37228, MGC74748, KNO, KNO_HS, FLJ34914, COL19A1	collagen, type XVIII, alpha 1	NM_130445, NM_030582, NM_130444, XCT1961722.0, XCT1962236.1, XCT2359335.0, XCT2359336.0, XCT2359337.0, XCT2359338.0, XCT2359339.0	1559552_at, 209651_s_at, 209652_s_at	NP_848112.2, NP_085089.2, NP_848111.2, EAX09328.1, EAX09340.1, EAX09338.1, EAX09340.1, EAX09341.1, EAX09342.1
GeneID:3737	NCRNA00175	21	46,839,631	46,844,365	8,354	-	1	4_A375_EGR1...1.5907	-3143	upstream	0	0	1	8	7	17	1	4_A375_EGR1...1	17	Gene NCRNA00175	NCRNA00175, C21orf125, PRED60, MGC129985, MGC129984	non-protein coding RNA 175	NR_027496, NR_028062, XCT2359342.0	1564017_at	EAX09343.1
GeneID:8915	SLC19A1	21	46,934,829	46,992,351	57,722	+	4	4_A375_EGR1...1.5908, 4_A375_EGR1...1.5910, 4_A375_EGR1...1.5911, 4_A375_EGR1...1.5912	33003, 14239, 4935, 4505	downstream, up gene, up gene, upstream	0	0	1	3.25	6.75	13.75	4	4_A375_EGR1...1	21	Gene SLC19A1	RFC1, FOLT, SLC19A1, RFC1, CHMD, RFC	solute carrier family 19 (folate transporter), member 1	NM_194255, XCT1957982.1, XCT1957983.1, XCT2360760.0, XCT2360761.0, XCT2360762.0, XCT4312610.2	1559552_at, 209715_s_at, 209776_s_at, 209777_s_at, 211359_s_at, 229809_s_at	NP_914031.1, EAX09331.1, EAX09332.1, EAX09333.1, EAX09335.1, EAX09336.1, EAX09337.1
GeneID:1301	COL8A1	21	47,481,993	47,524,963	43,200	+	1	4_A375_EGR1...1.5915	417	up gene	0	0	1	4	9	13	1	4_A375_EGR1...1	13	Gene COL8A1	CFL1, COL8A1	collagen, type VIII, alpha 1	NM_001848, XCT2357933.0, XCT2359470.0, XCT4310264.3	212091_s_at, 212927_s_at, 212928_at, 212929_at, 212940_at, 213425_s_at, 214260_s_at, 218964_at	NP_001839.2, EAX09320.1, EAX09321.1, EAX09322.1
GeneID:8566	MCM3AP	21	47,855,048	47,905,208	50,160	-	2	2_A375_shN37_plus_lacRNA_AR_1.3343, 4_A375_EGR1...1.5917	-692, 20260	upstream, up gene	0	1	1	9.5	11.5	13	2	2_A375_shN37_plus_lacRNA_AR_1	16	Gene MCM3AP	MCM3AP, GANP	mitotic-spindle organizing protein associated with a polo-like kinase 1	NM_033398, XCT1960231.1	212289_s_at, 214514_at, 215350_at, 215981_s_at, 215982_x_at	NP_003897.2, EAX09296.1
GeneID:8477	C21orf67	21	47,706,287	47,717,993	11,706	+	1	2_A375_shN37_plus_lacRNA_AR_1.3343	-379	upstream	0	0	0	13	16	13	1	2_A375_shN37_plus_lacRNA_AR_1	16	Gene C21orf67	FB97, FLJ40937, C21orf67	chromosome 21 open reading frame 67	NM_018161, NM_001009814, XCT1960229.1, XCT1960230.1, XCT1960231.1, XCT2357972.0, XCT2359482.0, XCT2359483.0, XCT4312652.2	227421_at, 239265_s_at, 242953_x_at	NP_476881.1, NP_001008114.1, EAX09288.1, EAX09289.1, EAX09291.1, EAX09292.1, EAX09290.1, EAX09293.1, EAX09294.1, EAX09295.1
GeneID:7475	PRMT2	21	48,055,527	48,064,965	29,208	+	2	1_A375_shN37_minus_lacRNA_AR_1.3715, 2_A375_shN37_plus_lacRNA_AR_1.3344	105, 105	up gene, up gene	1	1	0	21	20	11	1	1_A375_shN37_minus_lacRNA_AR_1	21	Gene PRMT2	PRMT1-L, PRMT2, MGC111273	protein arginine methyltransferase 2	NM_001535, NM_206962, XCT1960360.1, XCT1960361.1, XCT1960362.1, XCT2357980.0, XCT2357981.0, XCT2357982.0, XCT2359438.0, XCT2359439.0, XCT4312258.2	200056_s_at, 210384_at, 221864_at, 222032_at, 226725_s_at	NP_001526.2, NP_996042.1, EAX09280.1, EAX09281.1, EAX09284.1, EAX09282.1, EAX09285.1
GeneID:440	CERCAM	22	17,818,410	17,846,177	27,767	-	2	1_A375_shN37_minus_lacRNA_AR_1.3716, 2_A375_shN37_plus_lacRNA_AR_1.3343	-6971, -6823	upstream, upstream	1	1	0	21	34	9	1	1_A375_shN37_minus_lacRNA_AR_1	34	Gene CERCAM	CERCAM, NCRNA00017	cerebellar degeneration-related protein 1 (non-protein coding)	NM_024652, NR_024483	219272_s_at, 219273_at	NP_078928.1, NP_001001714.1, EAX07447.1, EAX07448.1
GeneID:8183	CERCAM	22	17,860,192	17,890,779	30,587	-	2	1_A375_shN37_minus_lacRNA_AR_1.3716, 2_A375_shN37_plus_lacRNA_AR_1.3343	37931, 37979	downstream, downstream	1	1	0	21	34	9	1	2_A375_shN37_plus_lacRNA_AR_1	34	Gene CERCAM	CERCAM, NCRNA00017	cerebellar degeneration-related protein 1 (non-protein coding)	NM_024652, NR_024483	219272_s_at, 219273_at	NP_078928.1, NP_001001714.1, EAX07447.1, EAX07448.1
GeneID:8183	CERCAM	22	17,860,192	17,890,779	30,587	-	2	1_A375_shN37_minus_lacRNA_AR_1.3716, 2_A375_shN37_plus_lacRNA_AR_1.3343	37931, 37979	downstream, downstream	1	1	0	21	34	9	1	2_A375_shN37_plus_lacRNA_AR_1	34	Gene CERCAM	CERCAM, NCRNA00017	cerebellar degeneration-related protein 1 (non-protein coding)	NM_024652, NR_024483	219272_s_at, 219273_at	NP_078928.1, NP_001001714.1, EAX07447.1, EAX07448.1
GeneID:8183	CERCAM	22	17,860,192	17,890,779	30,587	-	2	1_A375_shN37_minus_lacRNA_AR_1.3716, 2_A375_shN37_plus_lacRNA_AR_1.3343	37931, 37979	downstream, downstream	1	1	0	21	34	9	1	2_A375_shN37_plus_lacRNA_AR_1	34	Gene CERCAM	CERCAM, NCRNA00017	cerebellar degeneration-related protein 1 (non-protein coding)	NM_024652, NR_024483	219272_s_at, 219273_at	NP_078928.1, NP_001001714.1, EAX07447.1, EAX07448.1
GeneID:8183	CERCAM	22	17,860,192	17,890,779	30,587	-	2	1_A375_shN37_minus_lacRNA_AR_1.3716, 2_A375_shN37_plus_lacRNA_AR_1.3343	37931, 37979	downstream, downstream	1	1	0	21	34	9	1	2_A375_shN37_plus_lacRNA_AR_1	34	Gene CERCAM	CERCAM, NCRNA00017	cerebellar degeneration-related protein 1 (non-protein coding)	NM_024652, NR_024483	219272_s_at, 219273_at	NP_078928.1, NP_001001714.1, EAX07447.1, EAX07448.1
GeneID:8183	CERCAM	22	17,860,192	17,890,779	30,587	-	2	1_A375_shN37_minus_lacRNA_AR_1.3716, 2_A375_shN37_plus_lacRNA_AR_1.3343	37931, 37979	downstream, downstream	1	1	0	21	34	9	1	2_A375_shN37_plus_lacRNA_AR_1	34	Gene CERCAM	CERCAM, NCRNA00017	cerebellar degeneration-related protein 1 (non-protein coding)	NM_024652, NR_024483	219272_s_at, 219273_at	NP_078928.1, NP_001001714.1, EAX07447.1, EAX07448.1
GeneID:8183	CERCAM	22	17,860,192	17,890,779	30,587	-	2	1_A375_shN37_minus_lacRNA_AR_1.3716, 2_A375_shN37_plus_lacRNA_AR_1.3343	37931, 37979	downstream, downstream	1	1	0	21	34	9	1	2_A375_shN37_plus_lacRNA_AR_1	34	Gene CERCAM	CERCAM, NCRNA00017	cerebellar degeneration-related protein 1 (non-protein coding)	NM_024652, NR_024483	219272_s_at, 219273_at	NP_078928.1, NP_001001714.1, EAX07447.1, EAX07448.1
GeneID:8183	CERCAM	22	17,860,192	17,890,779	30,587	-	2	1_A375_shN37_minus_lacRNA_AR_1.3716, 2_A375_shN37_plus_lacRNA_AR_1.3343	37931, 37979	downstream, downstream	1	1	0	21	34	9	1	2_A375_shN37_plus_lacRNA_AR_1	34	Gene CERCAM	CERCAM, NCRNA00017	cerebellar degeneration-related protein 1 (non-protein coding)	NM_024652, NR_024483	219272_s_at, 219273_at	NP_078928.1, NP_001001714.1, EAX07447.1, EAX07448.1
GeneID:8183	CERCAM	22	17,860,192	17,890,779	30,587	-	2	1_A375_shN37_minus_lacRNA_AR_1.3716, 2_A375_shN37_plus_lacRNA_AR_1.3343	37931, 37979	downstream, downstream	1	1	0	21	34	9	1	2_A375_shN37_plus_lacRNA_AR_1	34	Gene CERCAM	CERCAM, NCRNA00017	cerebellar degeneration-related protein 1 (non-protein coding)	NM_024652, NR_024483	219272_s_at, 219273_at	NP_078928.1, NP_001001714.1, EAX07447.1, EAX07448.1
GeneID:8183	CERCAM	22	17,860,192	17,890,779	30,587	-	2	1_A375_shN37_minus_lacRNA_AR_1.3716, 2_A375_shN37_plus_lacRNA_AR_1.3343	37931, 37979	downstream, downstream	1	1	0	21	34	9	1	2_A375_shN37_plus_lacRNA_AR_1	34	Gene CERCAM	CERCAM, NCRNA00017	cerebellar degeneration-related protein 1 (non-protein coding)	NM_024652, NR_024483	219272_s_at, 219273_at	NP_078928.1, NP_001001714.1, EAX07447.1, EAX07448.1
GeneID:4439	MRPA4	22	18,480,604	18,480,727	123	-	1	2_A375_shN37_plus_lacRNA_AR_1.3348	6067	downstream	0	1	0	9	19	8	1	2_A375_shN37_plus_lacRNA_AR_1	19	Gene MRPA4	MRPA4, RNA-binding region (RNP1, RRM) 4	mitochondrial ribosomal protein A4	NM_033776		
GeneID:8979	PEX26	22	18,580,866	18,672,207	91,341	+	1	2_A375_shN37_plus_lacRNA_AR_1.3349	16	up gene	0	1	0	14	19	11	1	2_A375_shN37_plus_lacRNA_AR_1	19	Gene PEX26	PEX26, PEX26IRF7, FLJ20905, PEX26HT	peroxisomal biogenesis factor 26	NM_017929, NM_001127649, XCT1959937.1, XCT1959938.0, XCT2332334.0	219160_s_at, 233092_at	NP_060399.1, NP_001121121.1, EAX07522.1, EAX07523.1, EAX07754.1
GeneID:9311	TUBA8	22	18,593,483	18,614,496	21,045	+	1	2_A375_shN37_plus_lacRNA_AR_1.3919	-333	upstream	0	0	1	7	7	21	1	4_A375_EGR1...1	21	Gene TUBA8	TUBA12, TUBA8	tubulin, alpha 8	NM_001166414, NM_018943, XCT1962825.2, XCT2332348.0	220089_at	NP_001153431.1, NP_061818.1, EAX07503.1, EAX07505.1
GeneID:8742	DGCR8	22	18,893,706	18,899,801	6,095	+	1	4_A375_EGR1...1.5920	-343	upstream	0	0	1	8	10	16	1	4_A375_EGR1...1	16	Gene DGCR8	DGCR8	DiGeorge syndrome critical region gene 8	NM_022720, XCT2351576.0, XCT2351577.0, XCT2351578.0, XCT2357107.0	2060024_s_at	NP_036466.2, EAX09370.1, EAX09371.1, EAX09376.1, EAX09377.1
GeneID:5829	PRODH	22	18,900,264	18,923,814	23,550	-	1	4_A375_EGR1...1.5920	30228	downstream	0	0	1	8	10	16	1	4_A375_EGR1...1	16	Gene PRODH	HSPO12, PRODH, PRODH2, FLJ37744, TP53I6, MGC142076, PRODH1, SCZD4, POX, PIG6, MGC142077	proline dehydrogenase (oxidase) 1	NM_016335, XCT2358750.0, XCT4312855.3	214203_s_at	NP_057419.3, EAX09374.1, EAX09373.1
GeneID:5309	LOC100288434	22	19,001,986	19,016,742	16,876	+	1	4_A375_EGR1...1.5921	13950	up gene	0	0	1	0	2	13	1	4_A375_EGR1...1	13	Gene LOC100288434	hypothetical LOC100288434	XR_109703			
GeneID:2222	DGCR10	22	19,016,197	19,211,983	195,787	+	1	4_A375_EGR1...1.5921	7718	downstream	0	0	1	0	2	13	1	4_A375_EGR1...1	13	Gene DGCR10	DGCR10, DGS-B	DiGeorge syndrome critical region gene 10	NR_028651	1557431_at	
GeneID:2038	LOC643239	22	19,019,641	19,020,962	1,321	-	1	4_A375_EGR1...1.5921	3766	downstream	0	0	1	0	2	13	1	4_A375_EGR1...1	13	Gene LOC643239		XM_001719223, XM_002545484, XM_002349300	XP_001719275.2, XP_002545533.1, XP_002345121.1
GeneID:993	DGCR2	22	19,023,763	19,109,997	86,172	-	2	2_A375_shN37_plus_lacRNA_AR_1.3349, 4_A375_EGR1...1.5921	615, 92111	up gene, downstream	0	1	1	8	8.5	10.5	2	2_A375_shN37_plus_lacRNA_AR_1	15	Gene DGCR2	SED2-LAN, KIAA0163, DGS-C, IDD, DKFZp686H130, DGCR2	DiGeorge syndrome critical region gene 2	NM_001137, NM_001173533, NM_001173534, NM_001164761, NR_023874, XCT1958894.1, XCT2357989.0, XCT2358.2	202899_s_at, 214199_s_at, 220328_s_at	NP_001164233.1, NP_001167004.1, NP_001167005.1, NP_001171710.1, EAX09361.1, EAX09363.1, EAX09361.1
GeneID:20	DGCR14	22	19,117,792	19,132,100	14,309	+	1	2_A375_shN37_plus_lacRNA_AR_1.3349	23035	downstream	0	0	1	8	15	8	1	2_A375_shN37_plus_lacRNA_AR_1	15	Gene DGCR14	DGS-11, DGCR14, DGCR12, DGS11, DGS1, ES2, Es2rel	DiGeorge syndrome critical region gene 14	NM_022719, XCT1958595.1, XCT1961782.1, XCT1964793.1, XCT6234.3	224365_at, 216365_at, 217283_at, 239730_at, 241746_x_at, 32032_at	NP_073615.1, EAX09353.1, EAX09354.1, EAX09356.1
GeneID:617	TBX22	23	19,116,521	19,120,158	3,638	+	1	2_A375_shN37_plus_lacRNA_AR_1.3349	-9489	upstream	0	0	1	8	8.5	8	1	2_A375_shN37_plus_lacRNA_AR_1	15	Gene TBX22	BTK129, DGS-5, SPOXA2, FLJ38813, TBX22	tbx-box protein tissue biome 2	NM_032208	214251_at, 217279_at	NP_443732.3
GeneID:8913	SLC25A1	22	19,183,094	19,196,391	13,297	-	1	1_A375_shN37_minus_lacRNA_AR_1.3716	7261	downstream	0	0	0	16	13	12	1	1_A375_shN37_minus_lacRNA_AR_1	16	Gene SLC25A1	CTP, SLC25A1, SEA, SLC20A3	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	NM_005984, NR_033937, XCT1958595.1, XCT1958599.1, XCT2357035.0, XCT6299.1	210010_s_at	NP_005975.1, EAX09345.1, EAX09346.1, EAX09351.1
GeneID:1571	CLTCL1	22	19,366,906	19,479,339	112,433	-	3	1_A375_shN37_minus_lacRNA_AR_1.3716, 1_A375_shN37_minus_lacRNA_AR_1.3719, 2_A375_shN37_plus_lacRNA_AR_1.3350	126199, 99899, 69845	downstream, up gene, up gene	1	1	0	16	16.5	10.5	2	2_A375_shN37_plus_lacRNA_AR_1	24	Gene CLTCL1	CLTCL1, CLH22, CLTD, CHC22, CLTCL	clathrin, heavy chain-like 1	NM_007098, NM_001033, XCT1958579.1, XCT6266.2	200944_s_at	NP_009229.3, NP_001828.2, EAX09348.1, EAX09347.1
GeneID:23	HIRA	22	19,716,224	19,719,319	100,096	-	3	1_A375_shN37_minus_lacRNA_AR_1.3720, 2_A375_shN37_plus_lacRNA_AR_1.3351, 4_A375_EGR1...1.5922	-768, -761, -909	upstream, upstream, upstream	1	1	1	15	15	13	1	1_A375_shN37_minus_lacRNA_AR_1	13	Gene HIRA	DUP1.E1, HIRA, TUP1, D22S1	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	NM_003325, XCT1958358.2, XCT2357032.0	1569560_at, 217427_s_at	NP_003316.3, EAX09344.1, EAX09342.1
GeneID:9768	MRPL40	22	19,720,039	19,723,998	3,960	+	3	1_A375_shN37_minus_lacRNA_AR_1.3720, 2_A375_shN37_plus_lacRNA_AR_1.3351, 4_A375_EGR1...1.5922	-92, -38, 92	upstream, upstream, up gene	1	1	1	15	15	13	1	1_A375_shN37_minus_lacRNA_AR_1	13	Gene MRPL40	MRP-L22, MGC9450, MRPL40, NLVCF, FLJ43774, URM1	mitochondrial ribosomal protein L40	NM_032776, XCT1958948.3	1555162_at	NP_076407.2, EAX09342.1
GeneID:8977	C22orf29	22	19,726,459	19,735,753	7,346	-	4	1_A375_shN37_minus_lacRNA_AR_1.3720, 1_A375_shN37_minus_lacRNA_AR_1.3721, 2_A375_shN37_plus_lacRNA_AR_1.3351, 4_A375_EGR1...1.5922	13971, 1179, 10165, 10827	downstream, up gene, downstream, downstream	1	1	1	14.5	10	8.5	2	1_A375_shN37_minus_lacRNA_AR_1	15	Gene C22orf29	MGC7444, DKFZp686D22022, C22orf29	chromosome 22 open reading frame 29	NM_170733, NM_001168242, XCT2357035.1, XCT2440350.0, XCT6299.2	1553974_at, 221956_at	NP_736154.2, NP_001159714.1, EAX09338.1, EAX09340.1, EAX09341.1
GeneID:5358	LOC100505803	22	19,838,418	19,837,826	2,212	+	1	1_A375_shN37_minus_lacRNA_AR_1.3721	-540	upstream	1	0	0	14	9	4	1	1_A375_shN37_minus_lacRNA_AR_1	14	Gene LOC100505803	hypothetical LOC100505803	XR_112200, XR_109701, XR_115442	
GeneID:53	UPD1	22	19,837,464	19,868,705	29,274	-	3	1_A375_shN37_minus_lacRNA_AR_1.3721, 2_A375_shN37_plus_lacRNA_AR_1.3722, 4_A375_EGR1...1.5922	52182, -350, -94	downstream, upstream, upstream	1	1	0	15.5	11.5	8	2	2_A375_shN37_plus_lacRNA_AR_1	15	Gene UPD1	UPD1, UPS1	uroporphyrinogen III synthase (congenital erythropoietic porphyria)	NM_000375, NM_001035247, XCT1958953.1, XCT6555.3	209103_s_at	NP_000363.2, NP_001028324.2, EAX09332.1, EAX09335.1
GeneID:1116	CDC45L	22	19,897,414	19,905,153	40,721	+	2	1_A375_shN37_minus_lacRNA_AR_1.3722, 2_A375_shN37_plus_lacRNA_AR_1.3352	-398, -992	upstream, upstream	1	1	0	17	16	8	1	2_A375_shN37_plus_lacRNA_AR_1	16	Gene CDC45L	CDC45L2, CDC45, PORD, PH-1, CDC45	CDC45 cell division cycle 45 homolog (S. cerevisiae)	NM_003504, NM_001179010, NM_001179011, XCT6299.3	204126_s_at	NP_003475.1, NP_001171451.1, NP_001171452.1, EAX09339.1
GeneID:9544	GNB11	22	19,779,954	19,842,462	62,508	-	2	2_A375_shN37_plus_lacRNA_AR_1.3353, 4_A375_EGR1...1.5923	-182, 96549	upstream, up gene	0	1	1	8.5	10	13	2	2_A375_shN37_plus_lacRNA_AR_1	18	Gene GNB11	FKSG1, DGCR12, GNAI1K1, GNB11L, WDR14, WDVCF-SV2	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	NM_030594	220762_s_at, 223963_at, 223964_s_at	NP_443126.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1.1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1.1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:79880	C22orf29	22	19,833,661	19,842,371	8,710	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5353	-253	upstream	0	1	0	12	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C22orf29	C22orf29, FLJ21125	chromosome 22 open reading frame 29	NM_024627	219560_at, 226204_at	NP_078903.3
GeneID:421	ARVCF	22	19,957,402	20,004,309	46,907	-	1	4_A375_EGR1..1..5924	-395	upstream	0	0	1	5	4	16	1	4_A375_EGR1..1	16	Gene ARVCF	FLJ35345, ARVCF	armadillo repeat gene deleted in velocardiofacial syndrome	NM_001670, hCT1955631.2, hCT1955632.2, hCT8941.4	1556149_at, 205784_x_at, 216204_at, 217516_x_at	NP_001661.1, EAX03009.1, EAX03007.1, EAX03008.1
GeneID:128989	C22orf25	22	20,008,631	20,053,447	44,816	+	1	4_A375_EGR1..1..5924	-3927	upstream	0	0	1	5	4	16	1	4_A375_EGR1..1	16	Gene C22orf25	DKFZp761P1121, C22orf25	chromosome 22 open reading frame 25	NM_152906, hCT2286387.1, hCT2286388.1, hCT2286389.1, hCT2358706.0, hCT2358707.0, hCT2358708.0	235396_at	NP_690870.3, EAX03001.1, EAX03002.1, EAX03003.1, EAX03004.1, EAX03005.1, EAX03006.1
GeneID:54487	DGCR8	22	20,067,755	20,099,400	31,645	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3723, 2_A375_pNL97_plus_lncRNA_AR..1..5354	36917, 36949	downstream, downstream	1	1	0	24	20	2	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene DGCR8	C22orf12, Gy1, pasha, DGCR8, DGCRK6	DiGeorge syndrome critical region gene 8	NM_001190326, NM_022720, hCT2286392.0, hCT2286393.0, hCT2286395.0	218650_at, 219611_at, 64474_g_at, 91617_at	NP_001177255.1, NP_073557.3, EAX02998.1, EAX02999.1, EAX03000.1
GeneID:27037	TRMT2A	22	20,099,398	20,104,768	5,370	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3723, 2_A375_pNL97_plus_lncRNA_AR..1..5354	96, 64	in gene, in gene	1	1	0	24	20	2	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene TRMT2A	MGC102728, TRMT2A, HTF9C	TRM2 tRNA methyltransferase 2 homolog A (S. cerevisiae)	NM_022727, NM_182984, hCT1783543.2, hCT1813407.1, hCT1813406.1	218475_at	NP_073564.3, NP_892029.2, EAX02995.1, EAX02996.1, EAX02997.1
GeneID:5902	RANBP1	22	20,105,024	20,114,704	9,680	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3723, 2_A375_pNL97_plus_lncRNA_AR..1..5354, 2_A375_pNL97_plus_lncRNA_AR..1..5355, 4_A375_EGR1..1..5925	-352, -320, 13632, 14646	upstream, upstream, downstream, downstream	1	1	1	14.67	20	7.67	3	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene RANBP1	RANBP1, HTF9A, MGC88701	RAN binding protein 1	NM_002882, hCT1955627.2, hCT1955628.1, hCT1955629.1, hCT1955630.2, hCT2340553.0, hCT2340554.0, hCT2340555.0, hCT2358713.0, hCT8940.4	202482_x_at, 202483_s_at, 221915_s_at	NP_002873.1, EAX02986.1, EAX02988.1, EAX02989.1, EAX02992.1, EAX02994.1, EAX02987.1, EAX02990.1, EAX02991.1, EAX02993.1
GeneID:29801	ZDHHC8	22	20,119,384	20,135,530	16,166	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5355, 4_A375_EGR1..1..5925	-706, 508	upstream, in gene	0	1	1	10	20	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene ZDHHC8	ZDHHC8, ZDHHCL1, DHHC8, ZNF378	zinc finger, DHHC type containing 8	NM_001185024, NM_013373, hCT1783546.2, hCT2286404.0, hCT2286406.0	225744_at	NP_001171953.1, NP_037505.1, EAX02982.1, EAX02983.1, EAX02984.1
GeneID:150197	LOC150197	22	20,193,855	20,196,060	2,205	+	2	4_A375_EGR1..1..5927, 4_A375_EGR1..1..5928	-1871, 5489	upstream, downstream	0	0	1	5	5	18.5	2	4_A375_EGR1..1	21	Gene LOC150197	FLJ32575	hypothetical LOC150197	NR_026919	1553656_at	
GeneID:65078	RTN4R	22	20,228,938	20,255,816	26,878	-	1	4_A375_EGR1..1..5929	35800	downstream	0	0	1	2	7	14	1	4_A375_EGR1..1	14	Gene RTN4R	RTN4R, NOGOR, NGR	reticulon 4 receptor	NM_023004, hCT1770151.3, hCT1984135.1	228550_at	NP_075380.1, EAX02976.1, EAX02975.1
GeneID:51586	MED15	22	20,861,886	20,941,919	80,033	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3724, 2_A375_pNL97_plus_lncRNA_AR..1..5356	2, 10	in gene, in gene	1	1	0	16	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MED15	CAG7A, CTG7A, ARC105, TIG1, DKFZp686A2214, TNRC7, TIG-1, MED15, PCQAP, DKFZp762B1216, FLJ42935, FLJ42282	mediator complex subunit 15	NM_015889, NM_001003891, hCT2286422.0, hCT2286423.0, hCT2286425.0, hCT2286426.0, hCT2358700.0, hCT2358701.0, hCT2358702.0, hCT2358703.0, hCT32547.3	222175_s_at	NP_056973.2, NP_001003891.1, EAX02950.1, EAX02952.1, EAX02955.1, EAX02956.1, EAX02948.1, EAX02949.1, EAX02951.1, EAX02953.1, EAX02954.1
GeneID:5297	PI4KA	22	21,061,979	21,213,070	151,091	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3725, 2_A375_pNL97_plus_lncRNA_AR..1..5357	-114, -82	upstream, upstream	1	1	0	25	21	3	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene PI4KA	FLJ16556, PI4KA, pi4K230, PIK4CA, PI4K-ALPHA	phosphatidylinositol 4-kinase, catalytic, alpha	NM_058004, NM_002650	207061_s_at	NP_477352.2, NP_002641.1
GeneID:9342	SNAP29	22	21,213,292	21,245,502	32,210	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3725, 2_A375_pNL97_plus_lncRNA_AR..1..5357	-108, -140	upstream, upstream	1	1	0	25	21	3	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene SNAP29	SNAP29, FLJ21051, CEDNIK, SNAP-29	synaptosomal-associated protein, 29kDa	NM_004782, hCT32543.3	218327_s_at, 222597_at	NP_004773.1, EAX02935.1
GeneID:100507329	LOC100507329	22	21,311,380	21,318,967	7,587	+	1	4_A375_EGR1..1..5930	6700	downstream	0	0	1	2	5	15	1	4_A375_EGR1..1	15	Gene LOC100507329		hypothetical LOC100507329	XR_109747		
GeneID:150209	AIFM3	22	21,319,418	21,335,649	16,231	+	3	2_A375_pNL97_plus_lncRNA_AR..1..5358, 4_A375_EGR1..1..5930, 4_A375_EGR1..1..5931	17190, 662, 16934	downstream, in gene, downstream	0	1	1	8.5	11.5	17.5	2	4_A375_EGR1..1	20	Gene AIFM3	FLJ45137, AIFM3, FLJ30473, AIFL	apoptosis-inducing factor, mitochondrion-associated, 3	NM_144704, NM_001018060, NM_001146288, NR_027464, hCT1970625.1, hCT1970632.1, hCT1970633.1, hCT1970635.1, hCT1970636.1, hCT2286436.0, hCT2358711.0, hCT32550.3	244084_at	NP_653305.1, NP_001018070.1, NP_001139760.1, EAX02924.1, EAX02925.1, EAX02929.1, EAX02926.1, EAX02927.1, EAX02928.1, EAX02930.1, EAX02931.1
GeneID:8216	LZTR1	22	21,336,558	21,353,326	16,768	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3726, 2_A375_pNL97_plus_lncRNA_AR..1..5358, 2_A375_pNL97_plus_lncRNA_AR..1..5359, 4_A375_EGR1..1..5931, 4_A375_EGR1..1..5932, 4_A375_EGR1..1..5933	19426, 50, 19698, -208, 15250, 19922	downstream, in gene, downstream, upstream, in gene, downstream	1	1	1	12.67	14	18	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LZTR1	MGC21205, LZTR1, LZTR-1	leucine-zipper-like transcription regulator 1	NM_006767, hCT32540.3	203412_at	NP_006758.2, EAX02923.1
GeneID:80764	THAP7	22	21,354,061	21,356,404	2,343	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3726, 2_A375_pNL97_plus_lncRNA_AR..1..5359, 2_A375_pNL97_plus_lncRNA_AR..1..5360, 4_A375_EGR1..1..5932, 4_A375_EGR1..1..5933	420, 148, -7598, 4598, -76	in gene, in gene, upstream, downstream, upstream	1	1	1	12.33	15	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene THAP7	THAP7, MGC10963	THAP domain containing 7	NM_030573, NM_001008695, hCT2282952.1, hCT2282954.1, hCT2282963.1, hCT2282965.1	218492_s_at	NP_085050.2, NP_001008695.1, EAX02918.1, EAX02919.1, EAX02920.1, EAX02921.1
GeneID:439931	FLJ39582	22	21,356,211	21,364,663	8,452	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3726, 2_A375_pNL97_plus_lncRNA_AR..1..5359, 2_A375_pNL97_plus_lncRNA_AR..1..5360, 4_A375_EGR1..1..5932, 4_A375_EGR1..1..5933	-227, 45, 7789, -4403, 289	upstream, in gene, in gene, upstream, in gene	1	1	1	12.33	15	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene FLJ39582	FLJ40420	hypothetical LOC439931	NR_027051, NR_027052	236403_at, 239015_at	
GeneID:9127	P2RX6	22	21,369,442	21,382,302	12,860	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5360	-5442	upstream	0	1	0	14	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene P2RX6	P2X6, P2XM, MGC129625, P2RXL1, P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6	NM_005446, NM_001159554, hCT1970624.1, hCT2358714.0, hCT2358715.0, hCT2358716.0, hCT32544.1	206680_at, 211147_s_at	NP_005437.2, NP_001153026.1, EAX02910.1, EAX02911.1, EAX02912.1, EAX02913.1, EAX02914.1
GeneID:23119	HIC2	22	21,771,693	21,805,752	34,059	+	1	4_A375_EGR1..1..5934	28979	in gene	0	0	1	4	2	14	1	4_A375_EGR1..1	14	Gene HIC2	ZBTB30, HRG22, KIAA1020, HIC2, ZNF907	hypermethylated in cancer 2	NM_015094, hCT2274792.0	212964_at, 212965_at, 212966_at, 216911_s_at	NP_055909.2, EAW59621.1
GeneID:7332	UBE2L3	22	21,921,957	21,978,323	56,366	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3727, 2_A375_pNL97_plus_lncRNA_AR..1..5361	61691, 61767	downstream, downstream	1	1	0	42	36	12	1	1_A375_pNL7_minus_lncRNA_AR..1	42	Gene UBE2L3	E2-F1, UbcM4, UBE2L3, UBCH7, L-UBC	ubiquitin-conjugating enzyme E2L 3	NM_003347, NR_028436, NR_028437, hCT1962722.1, hCT1967644.1	200676_s_at, 200682_s_at, 200683_s_at, 200684_s_at	NP_003338.1, EAW59459.1, EAW59460.1
GeneID:150223	YDJC	22	21,982,378	21,984,340	1,962	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3727, 2_A375_pNL97_plus_lncRNA_AR..1..5361	692, 598	in gene, in gene	1	1	0	42	36	12	1	1_A375_pNL7_minus_lncRNA_AR..1	42	Gene YDJC	YDJC, MGC133160	YdjC homolog (bacterial)	NM_001017964, hCT1953847.1, hCT2353491.0, hCT2353492.0, hCT23752.2	227042_at	NP_001017964.1, EAW59461.1, EAW59462.1, EAW59463.1, EAW59464.1
GeneID:164592	CCDC116	22	21,987,086	21,991,616	4,530	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3727, 2_A375_pNL97_plus_lncRNA_AR..1..5361	-3436, -3342	upstream, upstream	1	1	0	42	36	12	1	1_A375_pNL7_minus_lncRNA_AR..1	42	Gene CCDC116	FLJ36046, CCDC116	coiled-coil domain containing 116	NM_152612, hCT1649121.3, hCT2300037.1	1555792_a_at	NP_689825.2, EAW59466.1, EAW59465.1
GeneID:23753	SDF2L1	22	21,996,542	21,998,588	2,046	+	1	4_A375_EGR1..1..5935	10306	downstream	0	0	1	3	9	17	1	4_A375_EGR1..1	17	Gene SDF2L1	SDF2L1		NM_022044, hCT23751.3	218681_s_at	NP_071327.2, EAW59467.1
GeneID:100126318	MIR301B	22	22,007,270	22,007,347	77	+	1	4_A375_EGR1..1..5935	-422	upstream	0	0	1	3	9	17	1	4_A375_EGR1..1	17	Gene MIR301B	MIR301B, MIRN301B	microRNA 301b	NR_030622		
GeneID:406920	MIR130B	22	22,007,593	22,007,674	81	+	1	4_A375_EGR1..1..5935	-745	upstream	0	0	1	3	9	17	1	4_A375_EGR1..1	17	Gene MIR130B	mir-130b, MIR130B, MIRN130B	microRNA 130b	NR_029845		
GeneID:23759	PPIL2	22	22,020,273	22,052,202	31,929	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3728, 4_A375_EGR1..1..5936	79, 207	in gene, in gene	1	0	1	17	13	14	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene PPIL2	hCyP-60, MGC787, PPIL2, FLJ39930, CYP60, Cyp-60, MGC33174, CYC4	peptidylprolyl isomerase (cyclophilin)-like 2	NM_014337, NM_148175, NM_148176, hCT1963280.1, hCT1963282.1, hCT1963283.1, hCT2353449.0, hCT2353450.0, hCT2353451.0, hCT2353452.0, hCT23748.3	208063_x_at, 208064_s_at, 209299_x_at, 214988_x_at, 217407_x_at, 223999_at, 243414_at	NP_055152.1, NP_680480.1, NP_680481.1, EAW59469.1, EAW59474.1, EAW59475.1, EAW59470.1, EAW59471.1, EAW59472.1, EAW59473.1, EAW59476.1
GeneID:8940	TOP3B	22	22,311,403	22,337,147	25,744	-	1	4_A375_EGR1..1..5937	91	in gene	0	0	1	2	9	16	1	4_A375_EGR1..1	16	Gene TOP3B	TOP3B, FLJ39376	topoisomerase (DNA) III beta	NM_003935, hCT2300834.1, hCT2300835.1, hCT2300836.0, hCT2300837.1, hCT2353458.0	213660_s_at, 215781_s_at	NP_003926.1, EAW59487.1, EAW59488.1, EAW59489.1, EAW59490.1, EAW59491.1
GeneID:649179	PRAMEL	22	22,345,496	22,385,393	39,897	-	1	4_A375_EGR1..1..5937	48337	downstream	0	0	1	2	9	16	1	4_A375_EGR1..1	16	Gene PRAMEL	FLJ16327, PRAMEL	preferentially expressed antigen in melanoma-like	XR_112255, XR_109745, XR_115472		
GeneID:3535	IGL@	22	22,380,474	23,265,085	884,611	+	1	4_A375_EGR1..1..5938	849734	in gene	0	0	1	1	2	14	1	4_A375_EGR1..1	14	Gene IGL@	IGLC6, IGL, MGC88804, IGL@	immunoglobulin lambda locus		216365_x_at	
GeneID:28809	IGLV3-1	22	23,223,092	23,223,572	480	+	1	4_A375_EGR1..1..5938	7116	downstream	0	0	1	1	2	14	1	4_A375_EGR1..1	14	Gene IGLV3-1	IGLV3-1, V2-1, IGLV31	immunoglobulin lambda variable 3-1			
GeneID:100423062	IGLL5	22	23,229,960	23,238,014	8,054	+	1	4_A375_EGR1..1..5938	248	in gene	0	0	1	1	2	14	1	4_A375_EGR1..1	14	Gene IGLL5	IGLL5		NM_001178126, NR_033661		NP_001171597.1
GeneID:28833	IGLJ1	22	23,235,961	23,235,998	37	+	1	4_A375_EGR1..1..5938	-5753	upstream	0	0	1	1	2	14	1	4_A375_EGR1..1	14	Gene IGLJ1	J1, IGLJ1	immunoglobulin lambda joining 1			
GeneID:3537	IGLC1	22	23,237,555	23,237,874	319	+	1	4_A375_EGR1..1..5938	-7347	upstream	0	0	1	1	2	14	1	4_A375_EGR1..1	14	Gene IGLC1	IGLC, IGLC2, IGLC1	immunoglobulin lambda constant 1 (Mcg marker)			
GeneID:9609	RAB36	22	23,487,513	23,506,531	19,018	+	1	4_A375_EGR1..1..5939	12487	in gene	0	0	1	4	3	14	1	4_A375_EGR1..1	14	Gene RAB36	RAB36		NM_004914, hCT1955487.1, hCT2353433.0	211471_s_at	NP_004905.2, EAW59562.1, EAW59561.1
GeneID:7621	ZNF70	22	24,083,772	24,093,279	9,507	-	1	4_A375_EGR1..1..5940	-225	upstream	0	0	1	14	8	14	1	4_A375_EGR1..1	14	Gene ZNF70	MGC46959, Cos17, ZNF70	zinc finger protein 70	NM_021916, hCT2342498.0	1554578_at, 243616_at	NP_068735.1, EAW59597.1
GeneID:29802	VPREB3	22	24,094,930	24,096,630	1,700	-	1	4_A375_EGR1..1..5940	3126	downstream	0	0	1	14	8	14	1	4_A375_EGR1..1	14	Gene VPREB3	N27C7-2, VPREB3, 8HS20	pre-B lymphocyte 3	NM_013378, hCT32368.1	220068_at	NP_037510.1, EAW59598.1
GeneID:150248	C22orf15	22	24,105,208	24,108,050	2,842	+	1	4_A375_EGR1..1..5941	5128	downstream	0	0	1	9	11	15	1	4_A375_EGR1..1	15	Gene C22orf15	C22orf15, N27C7-3, FLJ36561	chromosome 22 open reading frame 15	NM_182520, hCT2349008.0, hCT2353520.0, hCT2353521.0	1556333_at, 1556334_a_at	NP_872326.2, EAW59600.1, EAW59599.1, EAW59601.1
GeneID:400916	CHCHD10	22	24,108,021	24,110,141	2,120	-	1	4_A375_EGR1..1..5941	-195	upstream	0	0	1	9	11	15	1	4_A375_EGR1..1	15	Gene CHCHD10	N27C7-4, MGC70631, CHCHD10, C22orf16	coiled-coil-helix-coiled-coil-helix domain containing 10	NM_213720, hCT32373.3	224932_at	NP_998885.1, EAW59602.1
GeneID:4320	MMP11	22	24,115,036	24,126,503	11,467	+	1	4_A375_EGR1..1..5941	-4700	upstream	0	0	1	9	11	15	1	4_A375_EGR1..1	15	Gene MMP11	ST3, STMY3, MMP11, SL-3	matrix metallopeptidase 11 (stromelysin 3)	NM_005940, hCT2353477.0, hCT32364.3	203876_s_at, 203878_s_at, 235908_at	NP_005931.2, EAW59604.1, EAW59603.1
GeneID:66035	SLC2A11	22	24,199,059	24,227,738	28,679	+	1	4_A375_EGR1..1..5942	-7187	upstream	0	0	1	9	6	12	1	4_A375_EGR1..1	12	Gene SLC2A11	MGC118833, MGC118830, SLC2A11-a, GLUT10, GLUT11, SLC2A11, SLC2A11-c	solute carrier family 2 (facilitated glucose transporter), member 11	NM_001024939, NM_001024938, NM_030807, hCT1966534.1, hCT2300270.0, hCT2300271.0, hCT2353546.0, hCT2353547.0, hCT32376.3	1558540_s_at, 221262_s_at, 232167_at	NP_001020110.1, NP_001020109.1, NP_110434.3, EAW59614.1, EAW59616.1, EAW59618.1, EAW59613.1, EAW59615.1, EAW59617.1
GeneID:729632	LOC729632	22	24,350,106	24,352,079	1,973	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5362	-7665	upstream	0	1	0	16	19	6	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC729632		glutathione S-transferase theta-1-like			
GeneID:23523	CABIN1	22	24,407,765	24,574,596	166,831	+	1	4_A375_EGR1..1..5944	143835	in gene	0	0	1	5	6	14	1	4_A375_EGR1..1	14	Gene CABIN1	PPP3IN, CAIN, CABIN1, KIAA0330	calcineurin binding protein 1	NM_012295, hCT2300284.0, hCT2353473.0, hCT2353474.0, hCT32362.2	202624_s_at, 37652_at	NP_036427.1, EAW59640.1, EAW59637.1, EAW59638.1, EAW59639.1
GeneID:23384	CYTSA	22	24,666,786	24,813,708	146,922	+	1	4_A375_EGR1..1..5945	154110	downstream	0	0	1	3	3	16	1	4_A375_EGR1..1	16	Gene CYTSA	KIAA0376, CYTSA, SPECC1L	cytospin A	NM_015330, NM_001145468, hCT1955485.0, hCT2300295.0	212480_at	NP_056145.2, NP_001138940.1, EAW59656.1, EAW59657.1
GeneID:135	ADORA2A	22	24,823,530	24,838,325	14,795	+	2	4_A375_EGR1..1..5945, 4_A375_EGR1..1..5946	-2634, 13174	upstream, in gene	0	0	1	4	4	16.5	2	4_A375_EGR1..1	17	Gene ADORA2A	hA2aR, ADORA2, ADORA2A, RDC8	adenosine A2a receptor	NM_000675, hCT2300299.0	205013_s_at	NP_000666.2, EAW59658.1
GeneID:646023	C22orf45	22	24,825,178	24,890,783	65,605	-	2	4_A375_EGR1..1..5945, 4_A375_EGR1..1..5946	69667, 54079	downstream, in gene	0	0	1	4	4	16.5	2	4_A375_EGR1..1	17	Gene C22orf45	C22orf45, FLJ34651	chromosome 22 open reading frame 45	NR_026463, NR_026464	237447_at	
GeneID:83606	C22orf13	22	24,936,406	24,951,275	14,869	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5363, 4_A375_EGR1..1..5947	-613, -533	upstream, upstream	0	1	1	9	16	14	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C22orf13	C22orf13, LLN4, MGC1842	chromosome 22 open reading frame 13	NM_031444, hCT1951848.2, hCT2353506.0, hCT2353507.0, hCT2353508.0, hCT32472.4	223039_at	NP_113632.2, EAW59665.1, EAW59666.1, EAW59667.1, EAW59668.1, EAW59669.1
GeneID:6634	SNRPD3	22	24,951,618	24,968,509	16,891	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5363, 4_A375_EGR1..1..5947	270, 190	in gene, in gene	0	1	1	9	16	14	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SNRPD3	SNRPD3, Sm-D3, SMD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	NM_004175, hCT2300316.1	202567_at	NP_004166.1, EAW59670.1
GeneID:129049	SGSM1	22	25,202,136	25,322,813	120,677	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5364	69976	in gene	0	1	0	14	23	5	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene SGSM1	MGC133298, KIAA1941, SGSM1, RUTBC2	small G protein signaling modulator 1	NM_133454, NM_001098497, NM_001039948, NM_001098498	1562239_at, 230287_at, 242921_at	NP_597711.1, NP_001091967.1, NP_001091968.1, NP_001035037.1
GeneID:84700	MYO18B	22	26,138,120	26,427,007	288,887	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3729	5304	in gene	1	0	0	16	14	6	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene MYO18B	FLJ41942, DKFZp779C1666, MYO18B, DKFZp434C2422	myosin XVIIIB	NM_032608, hCT2301174.0, hCT2301175.0, hCT2301176.0, hCT2301177.0, hCT2353423.0, hCT2353424.0, hCT2353425.0	1554579_a_at	NP_115997.5, EAW59707.1, EAW59702.1, EAW59703.1, EAW59705.1, EAW59706.1, EAW59704.1, EAW59708.1
GeneID:24144	TFIP11	22	26,887,893	26,908,437	20,544	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5365	5	in gene	0	1	0	14	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene TFIP11	hNtr1, NTR1, TIP39, TFIP11, FLJ22086, Spp382, bK445C9.6	tuftelin interacting protein 11	NM_012143, NM_001008697, hCT2301316.0, hCT2353515.0, hCT31342.3	202750_s_at, 202751_at	NP_036275.1, NP_001008697.1, EAW59722.1, EAW59723.1, EAW59724.1
GeneID:100507599	LOC100507599	22	26,908,476	26,910,531	2,055	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5365	-44	upstream	0	1	0	14	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LOC100507599		hypothetical LOC100507599	XR_112230, XR_109753, XR_115478		
GeneID:129080	EMID1	22	29,801,953	29,855,586	53,633	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3733, 2_A375_pNL97_plus_lncRNA_AR..1..5369, 4_A375_EGR1..1..5949	62175, 62143, 61375	downstream, downstream, downstream	1	1	1	20	25	12	2	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene EMID1	EMI5, MGC50657, EMU1, hEmu1, EMID1	EMI domain containing 1	NM_133455, hCT1644223.3, hCT2300848.0	1564251_at, 213779_at	NP_597712.2, EAW59776.1, EAW59777.1
GeneID:25807	RHBDD3	22	29,855,844	29,863,914	8,070	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3733, 2_A375_pNL97_plus_lncRNA_AR..1..5369, 4_A375_EGR1..1..5949	-214, -182, 586	upstream, upstream, in gene	1	1	1	20	25	12	2	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene RHBDD3	RHBDD3, PTAG, C22orf3, HS984G1A	rhomboid domain containing 3	NM_012265, hCT1967611.1, hCT32910.3	204402_at, 217822_at	NP_036397.1, EAW59778.1, EAW59779.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:2130	EWSR1	22	29,663,998	29,696,515	32,517	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3733, 1_A375_pNL7_minus_lncRNA_AR..1..3734, 2_A375_pNL97_plus_lncRNA_AR..1..5369, 2_A375_pNL97_plus_lncRNA_AR..1..5370, 4_A375_EGR1..1..5949	130, 38306, 98, 38818, -670	in gene, downstream, in gene, downstream, upstream	1	1	1	16.67	23	11	3	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene EWSR1	bK984G1.4, EWSR1, EWS	Ewing sarcoma breakpoint region 1	NM_005243, NM_013986, NM_001163285, NM_001163286, NM_001163287, hCT2300850.0, hCT2300851.0, hCT2300852.0, hCT2300853.0, hCT2300854.0, hCT2353499.0, hCT2353500.0, hCT2353501.0	209214_s_at, 210011_s_at, 210012_s_at, 229966_at	NP_005234.1, NP_053733.2, NP_001156757.1, NP_001156758.1, NP_001156759.1, EAW59780.1, EAW59781.1, EAW59782.1, EAW59783.1, EAW59784.1, EAW59785.1, EAW59786.1, EAW59787.1
GeneID:10634	GAS2L1	22	29,702,997	29,708,774	5,777	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3734, 2_A375_pNL97_plus_lncRNA_AR..1..5370, 4_A375_EGR1..1..5950	-893, -161, 11339	upstream, upstream, downstream	1	1	1	9.5	12.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene GAS2L1	GAS2L1, MGC17243, GAR22	growth arrest-specific 2 like 1	NM_006478, NM_152236, NM_152237, hCT1951342.1, hCT1967610.1, hCT2300855.0, hCT2300858.0, hCT2353484.0, hCT2353485.0, hCT2353486.0, hCT32905.2	208256_s_at, 209729_at, 31874_at	NP_006469.2, NP_689422.1, NP_689423.1, EAW59789.1, EAW59793.1, EAW59795.1, EAW59788.1, EAW59790.1, EAW59791.1, EAW59792.1, EAW59794.1
GeneID:10633	RASL10A	22	29,708,922	29,711,748	2,826	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3734, 2_A375_pNL97_plus_lncRNA_AR..1..5370, 4_A375_EGR1..1..5950	9444, 8932, -2586	downstream, downstream, upstream	1	1	1	9.5	12.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene RASL10A	RASL10A, RRP22	RAS-like, family 10, member A	NM_006477, NM_001007279, hCT2301165.0, hCT32906.3	206850_at	NP_006468.1, NP_001007280.1, EAW59796.1, EAW59797.1
GeneID:162	AP1B1	22	29,723,669	29,784,572	60,903	-	1	4_A375_EGR1..1..5950	70236	downstream	0	0	1	3	8	16	1	4_A375_EGR1..1	16	Gene AP1B1	CLAPB2, ADTB1, AP1B1, BAM22, AP105A	adaptor-related protein complex 1 beta 1 subunit	NM_145730, NM_001127, NM_001166019, hCT2301160.0, hCT2301162.0, hCT2301163.0	205423_at	NP_663782.2, NP_001118.3, NP_001159491.1, EAW59798.1, EAW59799.1, EAW59800.1
GeneID:8563	THOC5	22	29,904,156	29,949,736	45,580	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3735, 2_A375_pNL97_plus_lncRNA_AR..1..5371	-40, -72	upstream, upstream	1	1	0	24	25	8	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene THOC5	PK1.3, C22orf19, THOC5, Fmip, ISAP79	THO complex 5	NM_003678, NM_001002877, NM_001002878, NM_001002879	209418_s_at, 209419_at	NP_003669.4, NP_001002877.1, NP_001002878.1, NP_001002879.1
GeneID:8508	NIPSNAP1	22	29,950,797	29,977,144	26,347	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3735, 2_A375_pNL97_plus_lncRNA_AR..1..5371	27368, 27336	downstream, downstream	1	1	0	24	25	8	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene NIPSNAP1	NIPSNAP1		NM_003634	201708_s_at, 201709_s_at	NP_003625.2
GeneID:4771	NF2	22	29,999,545	30,094,589	95,044	+	1	4_A375_EGR1..1..5951	231	in gene	0	0	1	11	7	16	1	4_A375_EGR1..1	16	Gene NF2	BANF, SCH, ACN, NF2	neurofibromin 2 (merlin)	NM_000268, NM_016418, NM_181828, NM_181829, NM_181830, NM_181832, NM_181833, NM_181825, NM_181831, hCT2300870.0, hCT2300871.0, hCT2300872.0, hCT2300873.0, hCT2300874.0, hCT2300875.0, hCT2300876.0, hCT2300878.0, hCT2300879.0, hCT2300880.0, hCT2300881.0, hC	204991_s_at, 210767_at, 211017_s_at, 211091_s_at, 211092_s_at, 217150_s_at, 218915_at, 236618_at	NP_000259.1, NP_057502.2, NP_861966.1, NP_861967.1, NP_861968.1, NP_861970.1, NP_861546.1, NP_861971.1, NP_861969.1, EAW59814.1, EAW59815.1, EAW59816.1, EAW59817.1, EAW59820.1, EAW59818.1, EAW59819.1, EAW59821.1, EAW59822.1, EAW59823.1, EAW59824.1, EAW598
GeneID:164633	CABP7	22	30,116,344	30,127,822	11,478	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3736, 2_A375_pNL97_plus_lncRNA_AR..1..5372	-3480, -3512	upstream, upstream	1	1	0	52	55	12	1	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene CABP7	CALN2, MGC57793, CABP7	calcium binding protein 7	NM_182527, hCT2300885.0, hCT2300887.0	234798_at, 243173_at	NP_872333.1, EAW59835.1, EAW59834.1
GeneID:55954	ZMAT5	22	30,126,945	30,162,969	36,024	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5373	-455	upstream	0	1	0	14	24	8	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ZMAT5	ZMAT5		NM_019103, NM_001003692, hCT2301148.0, hCT2301149.0	218752_at	NP_061976.1, NP_001003692.1, EAW59837.1, EAW59838.1
GeneID:29796	UQCR10	22	30,163,358	30,166,402	3,044	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5373	66	in gene	0	1	0	14	24	8	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene UQCR10	HSPC151, UCCR7.2, UCRC, HSPC119, QCR9, HSPC051, UQCR10	ubiquinol-cytochrome c reductase, complex III subunit X	NM_013387, NM_001003684, hCT1641845.2, hCT2300889.0, hCT2300891.0	218190_s_at, 228142_at	NP_037519.2, NP_001003684.1, EAW59839.1, EAW59840.1, EAW59841.1
GeneID:84164	ASCC2	22	30,184,600	30,234,254	49,654	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3737	36990	in gene	1	0	0	15	10	8	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene ASCC2	ASCC2, ASC1p100	activating signal cointegrator 1 complex subunit 2	NM_032204, hCT1951343.1, hCT1967612.1, hCT1967613.1, hCT1967614.1, hCT2301146.0, hCT2353525.0, hCT32912.3	215684_s_at	NP_115580.2, EAW59846.1, EAW59842.1, EAW59843.1, EAW59844.1, EAW59846.1, EAW59845.1, EAW59847.1
GeneID:10291	SF3A1	22	30,727,977	30,752,913	24,936	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5375	145	in gene	0	1	0	11	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SF3A1	SF3A120, SF3A1, PRPF21, SAP114, PRP21	splicing factor 3a, subunit 1, 120kDa	NM_005877, NM_001005409, hCT2300790.0, hCT32566.3	1566796_at, 201356_at, 201357_s_at, 216457_s_at, 227516_at, 232920_at, 242949_x_at	NP_005868.1, NP_001005409.1, EAW59878.1, EAW59879.1
GeneID:550631	CCDC157	22	30,752,627	30,772,818	20,191	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5375	141	in gene	0	1	0	11	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CCDC157	CCDC157	coiled-coil domain containing 157	NM_001017437		NP_001017437.2
GeneID:23541	SEC14L2	22	30,792,933	30,821,278	28,345	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3738	27291	in gene	1	0	0	21	18	8	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene SEC14L2	C22orf6, MGC65053, KIAA1186, TAP1, SEC14L2, SPF, KIAA1658, TAP	SEC14-like 2 (S. cerevisiae)	NM_012429, NM_033382, hCT2300543.0, hCT2353566.0, hCT2353567.0, hCT32567.3	204541_at, 230316_at, 232400_at, 232894_at, 232895_s_at, 240024_at	NP_036561.1, NP_203740.1, EAW59885.1, EAW59886.1, EAW59887.1, EAW59888.1
GeneID:51537	MTP18	22	30,821,720	30,825,041	3,321	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3738	-1496	upstream	1	0	0	21	18	8	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene MTP18	MTFP1, MTP18, HSPC242	mitochondrial fission process 1	NM_016498, NM_001003704, hCT1967593.1, hCT2300504.0, hCT32580.4	223172_s_at	NP_057582.2, NP_001003704.1, EAW59889.1, EAW59890.1, EAW59891.1
GeneID:266629	SEC14L3	22	30,855,216	30,868,034	12,818	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3739, 2_A375_pNL97_plus_lncRNA_AR..1..5376	12578, 12610	in gene, in gene	1	1	0	19	20	5	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SEC14L3	SEC14L3, MGC119387, MGC119386, TAP2, MGC119388	SEC14-like 3 (S. cerevisiae)	NM_174975, hCT1818305.1, hCT2300782.0	216346_at, 240899_at, 241221_at	NP_777635.1, EAW59894.1, EAW59893.1
GeneID:23762	OSBP2	22	31,090,793	31,303,811	213,018	+	6	1_A375_pNL7_minus_lncRNA_AR..1..3740, 1_A375_pNL7_minus_lncRNA_AR..1..3741, 2_A375_pNL97_plus_lncRNA_AR..1..5377, 2_A375_pNL97_plus_lncRNA_AR..1..5378, 4_A375_EGR1..1..5952, 4_A375_EGR1..1..5953	108119, 111751, 108119, 111735, 375, 189863	in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	15.75	16.75	10.25	4	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene OSBP2	OSBPL4, ORP-4, OSBPL1, ORP4, OSBP2	oxysterol binding protein 2	NM_030758, hCT2300515.0, hCT2300516.0, hCT2353465.0, hCT32573.3	1569817_at, 221237_s_at, 223432_at	NP_110385.1, EAW59919.1, EAW59916.1, EAW59917.1, EAW59918.1
GeneID:22880	MORC2	22	31,322,600	31,364,187	41,587	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3742, 2_A375_pNL97_plus_lncRNA_AR..1..5379	-1125, -1093	upstream, upstream	1	1	0	33	20	12	1	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene MORC2	ZCW3, MORC2, ZCWCC1	MORC family CW-type zinc finger 2	NM_014941, hCT2300760.0, hCT31329.3	203958_at, 216863_s_at	NP_055756.1, EAW59922.1, EAW59921.1
GeneID:55000	TUG1	22	31,365,634	31,375,381	9,747	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3742, 2_A375_pNL97_plus_lncRNA_AR..1..5379	-322, -354	upstream, upstream	1	1	0	33	20	12	1	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene TUG1	FLJ20618, TI-227H, TUG1, MGC46067, NCRNA00080	taurine upregulated 1 (non-protein coding)	NR_002323	222244_s_at, 228397_at, 230635_at	
GeneID:6525	SMTN	22	31,477,305	31,500,609	23,304	+	1	4_A375_EGR1..1..5954	3751	in gene	0	0	1	11	10	16	1	4_A375_EGR1..1	16	Gene SMTN	SMTN, FLJ35365, FLJ38597	smoothelin	NM_006932, NM_134269, NM_134270, hCT2300521.0, hCT2300522.0, hCT2300523.0, hCT2300524.0, hCT2300525.0, hCT2348324.0, hCT2348325.0, hCT32583.3	1556030_at, 207390_s_at, 209427_at	NP_008863.3, NP_599031.1, NP_599032.1, EAW59925.1, EAW59926.1, EAW59932.1, EAW59927.1, EAW59928.1, EAW59929.1, EAW59930.1, EAW59931.1
GeneID:56478	EIF4ENIF1	22	31,835,345	31,885,874	50,529	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5380	-174	upstream	0	1	0	13	19	3	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene EIF4ENIF1	FLJ26551, EIF4ENIF1, Clast4, FLJ21601, 4E-T	eukaryotic translation initiation factor 4E nuclear import factor 1	NM_019843, NM_001164501, NM_001164502, hCT1951335.1, hCT2300200.0, hCT32790.3	218626_at, 242291_at	NP_062817.2, NP_001157973.1, NP_001157974.1, EAW59977.1, EAW59978.1, EAW59979.1
GeneID:9814	SFI1	22	31,892,261	32,014,534	122,273	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5380	-6213	upstream	0	1	0	13	19	3	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SFI1	MGC57874, hSfi1p, RP5-858B16.1, MGC131712, MGC150663, SFI1, PISD, MGC156263	Sfi1 homolog, spindle assembly associated (yeast)	NM_014775, NM_001007467, hCT2300078.0, hCT2300079.0, hCT2300081.0, hCT2353552.0	213431_x_at, 214402_s_at, 215699_x_at, 36545_s_at	NP_055590.2, NP_001007468.1, EAW59980.1, EAW59981.1, EAW59982.1, EAW59983.1
GeneID:23761	PISD	22	32,014,477	32,026,810	12,333	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3743, 2_A375_pNL97_plus_lncRNA_AR..1..5381, 4_A375_EGR1..1..5955	-230, -198, 138	upstream, upstream, in gene	1	1	1	16	20	18	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PISD	PSSC, DKFZp566G2246, DJ858B16, PSDC, dJ858B16.2, PISD, PSD	phosphatidylserine decarboxylase	NM_014338, hCT2300193.0, hCT2300194.0, hCT2300195.0, hCT2300196.0, hCT2300197.0, hCT2300198.0, hCT2300199.0, hCT2353545.0	202392_s_at	NP_055153.1, EAW59984.1, EAW59985.1, EAW59989.1, EAW59990.1, EAW59991.1, EAW59986.1, EAW59987.1, EAW59988.1
GeneID:253143	C22orf30	22	32,077,333	32,146,120	68,787	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3744, 2_A375_pNL97_plus_lncRNA_AR..1..5382	-152, -88	upstream, upstream	1	1	0	17	25	10	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene C22orf30	MGC50372, DKFZp761P2326, PRR14L, FLJ33247, FLJ23059, FLJ31368, C22orf30	chromosome 22 open reading frame 30	NM_173566, hCT1815995.4, hCT2300189.2, hCT2300190.2, hCT2300192.1	1553761_at, 1556097_at, 216555_at, 236941_at	NP_775837.2, EAW59995.1, EAW59992.1, EAW59993.1, EAW59994.1
GeneID:9681	DEPDC5	22	32,150,069	32,303,001	152,932	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3744, 2_A375_pNL97_plus_lncRNA_AR..1..5382	-3797, -3861	upstream, upstream	1	1	0	17	25	10	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene DEPDC5	DEP.5, DKFZp779P2027, DEPDC5	DEP domain containing 5	NM_014662, NM_001007188, NM_001136029, hCT1967602.0, hCT2300084.0, hCT2300085.0, hCT2300086.0	205223_at	NP_055477.1, NP_001007189.1, NP_001129501.1, EAW59996.1, EAW59997.1, EAW59999.1, EAW59998.1
GeneID:6523	SLC5A1	22	32,439,019	32,509,016	69,997	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5383, 2_A375_pNL97_plus_lncRNA_AR..1..5384	61173, 64085	in gene, in gene	0	1	0	12.5	20.5	4.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SLC5A1	NAGT, D22S675, SLC5A1, SGLT1	solute carrier family 5 (sodium/glucose cotransporter), member 1	NM_000343, NR_033411, hCT32782.2	206628_at	NP_000334.1, EAW60006.1
GeneID:150297	C22orf42	22	32,545,519	32,555,243	9,724	-	1	4_A375_EGR1..1..5956	-53	upstream	0	0	1	2	2	13	1	4_A375_EGR1..1	13	Gene C22orf42	dJ90G24.6, C22orf42	chromosome 22 open reading frame 42	NM_001010859, hCT2342989.0, hCT2353559.0	1555990_at, 1555991_s_at	NP_001010859.1, EAW60007.1, EAW60008.1
GeneID:10739	RFPL2	22	32,586,422	32,600,718	14,296	-	1	4_A375_EGR1..1..5957	-1842	upstream	0	0	1	4	11	16	1	4_A375_EGR1..1	16	Gene RFPL2	RFPL2, RNF79	ret finger protein-like 2	NM_001098527, NM_006605, NM_001159545, NM_001159546, hCT1774277.2, hCT2300182.0, hCT2300183.0, hCT2353554.0, hCT2353555.0	207227_x_at	NP_001091997.2, NP_006596.2, NP_001153017.1, NP_001153018.1, EAW60012.1, EAW60013.1, EAW60009.1, EAW60010.1, EAW60011.1
GeneID:25793	FBXO7	22	32,870,707	32,894,818	24,111	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3745, 2_A375_pNL97_plus_lncRNA_AR..1..5385, 4_A375_EGR1..1..5958	125, -35, 125	in gene, upstream, in gene	1	1	1	14	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene FBXO7	FBX, DKFZp686B08113, FBX07, PKPS, FBXO7, FBX7, PARK15	F-box protein 7	NM_012179, NM_001033024, hCT1982587.1, hCT1982588.1, hCT2353469.0, hCT32883.3	1554423_a_at, 201178_at, 243649_at	NP_036311.3, NP_001028196.1, EAW60023.1, EAW60024.1, EAW60025.1, EAW60026.1
GeneID:8224	SYN3	22	32,908,539	33,454,377	545,838	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5386, 1_A375_pNL7_minus_lncRNA_AR..1..3746	528057, 261385	in gene, in gene	1	1	0	18	13.5	9	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene SYN3	SYN3		NM_003490, NM_133633, NM_001135774, hCT1955488.2, hCT2300906.1, hCT2300907.1, hCT2300908.1, hCT2300910.0, hCT2300911.1, hCT2300912.1, hCT2300913.0, hCT2300914.1	206322_at	NP_003481.3, NP_598344.2, NP_001129246.1, EAW60034.1, EAW60035.1, EAW60036.1, EAW60029.1, EAW60030.1, EAW60031.1, EAW60032.1, EAW60033.1, EAW60037.1
GeneID:7078	TIMP3	22	33,196,802	33,259,028	62,226	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3746	-3610	upstream	1	0	0	20	10	4	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene TIMP3	SFD, K222TA2, K222, HSMRK222, TIMP3	TIMP metallopeptidase inhibitor 3	NM_000362, hCT32685.2	201147_s_at, 201148_s_at, 201149_s_at, 201150_s_at	NP_000353.1, EAW60038.1
GeneID:9215	LARGE	22	33,669,062	34,316,416	647,354	-	1	4_A375_EGR1..1..5959	-1966	upstream	0	0	1	4	4	12	1	4_A375_EGR1..1	12	Gene LARGE	LARGE, KIAA0609, MDDGA6, MDC1D, MDDGB6	like-glycosyltransferase	NM_004737, NM_133642, hCT1815498.2, hCT2300902.0, hCT2353476.0	204414_at, 215543_s_at	NP_004728.1, NP_598397.1, EAW60041.1, EAW60042.1, EAW60043.1
GeneID:10042	HMGXB4	22	35,653,445	35,691,800	38,355	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3747, 1_A375_pNL7_minus_lncRNA_AR..1..3748, 2_A375_pNL97_plus_lncRNA_AR..1..5387, 2_A375_pNL97_plus_lncRNA_AR..1..5388	-69, 42603, 11, 42635	upstream, downstream, in gene, downstream	1	1	0	15	25.5	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene HMGXB4	HMG2L1, HMGBCG, HMGXB4, THC211630	HMG box domain containing 4	NM_001003681, NR_027760, hCT2300114.0, hCT2300116.0, hCT2353522.0, hCT32605.3	212596_s_at, 212597_s_at	NP_001003681.1, EAW60048.1, EAW60049.1, EAW60050.1, EAW60051.1
GeneID:10043	TOM1	22	35,695,268	35,743,987	48,719	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3748, 2_A375_pNL97_plus_lncRNA_AR..1..5388	780, 812	in gene, in gene	1	1	0	13	20	11	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TOM1	TOM1, FLJ33404	target of myb1 (chicken)	NM_005488, NM_001135729, NM_001135730, NR_024194, NR_024195, NM_001135732, hCT1950809.1, hCT2300117.0, hCT2300120.0, hCT2353479.0, hCT2353480.0, hCT32798.3	202807_s_at	NP_005479.1, NP_001129201.1, NP_001129202.1, NP_001129204.1, EAW60056.1, EAW60058.1, EAW60053.1, EAW60054.1, EAW60055.1, EAW60057.1
GeneID:3162	HMOX1	22	35,777,060	35,790,207	13,147	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3749	-4020	upstream	1	0	0	17	9	11	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene HMOX1	bK286B10, HO-1, HSP32, HMOX1	heme oxygenase (decycling) 1	NM_002133, hCT2300122.0	203665_at	NP_002124.1, EAW60059.1
GeneID:4627	MYH9	22	36,677,323	36,784,063	106,740	-	1	4_A375_EGR1..1..5960	103743	in gene	0	0	1	4	3	14	1	4_A375_EGR1..1	14	Gene MYH9	MGC104539, FTNS, MYH9, DFNA17, MHA, NMHC-II-A, NMMHCA, EPSTS	myosin, heavy chain 9, non-muscle	NM_002473, hCT2301108.0, hCT2301111.0, hCT32725.3	211926_s_at	NP_002464.1, EAW60097.1, EAW60096.1, EAW60098.1
GeneID:25828	TXN2	22	36,863,093	36,877,687	14,594	-	3	2_A375_pNL97_plus_lncRNA_AR..1..5389, 4_A375_EGR1..1..5962, 4_A375_EGR1..1..5963	151, 17719, 87	in gene, downstream, in gene	0	1	1	9	11	17.5	2	4_A375_EGR1..1	18	Gene TXN2	TRX2, MT-TRX, MTRX, TXN2	thioredoxin 2	NM_012473, hCT2301099.0, hCT2301105.0	209077_at, 209078_s_at	NP_036605.2, EAW60104.1, EAW60103.1
GeneID:80020	FOXRED2	22	36,883,233	36,903,148	19,915	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5389, 4_A375_EGR1..1..5963	25612, 25548	downstream, downstream	0	1	1	12	17	18	1	4_A375_EGR1..1	18	Gene FOXRED2	ERFAD, FLJ23322, FLJ33734, FOXRED2	FAD-dependent oxidoreductase domain containing 2	NM_024955, NM_001102371, hCT2301103.0, hCT2301104.1, hCT2353446.0, hCT2353447.0	220707_s_at, 231846_at, 233250_x_at	NP_079231.4, NP_001095841.1, EAW60105.1, EAW60106.1, EAW60107.1, EAW60108.1
GeneID:8664	EIF3D	22	36,906,897	36,925,277	18,380	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3750	125	in gene	1	0	0	15	11	8	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene EIF3D	eIF3-p66, MGC126526, EIF3S7, MGC17258, EIF3D, eIF3-zeta	eukaryotic translation initiation factor 3, subunit D	NM_003753, hCT1815324.2, hCT2301098.0	200005_at	NP_003744.1, EAW60109.1, EAW60110.1
GeneID:10369	CACNG2	22	36,960,104	37,098,903	138,799	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3751, 1_A375_pNL7_minus_lncRNA_AR..1..3752, 2_A375_pNL97_plus_lncRNA_AR..1..5391, 2_A375_pNL97_plus_lncRNA_AR..1..5392, 2_A375_pNL97_plus_lncRNA_AR..1..5393	58423, -649, 58455, 42727, -601	in gene, upstream, in gene, in gene, upstream	1	1	0	20.33	23.67	4.67	3	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene CACNG2	MGC138502, FLJ41437, MGC138504, CACNG2	calcium channel, voltage-dependent, gamma subunit 2	NM_006078, hCT1827810.3	214495_at	NP_006069.1, EAW60113.1
GeneID:114904	C1QTNF6	22	37,576,206	37,584,330	8,124	-	1	4_A375_EGR1..1..5965	306	in gene	0	0	1	4	6	12	1	4_A375_EGR1..1	12	Gene C1QTNF6	ZACRP6, CTRP6, C1QTNF6	C1q and tumor necrosis factor related protein 6	NM_031910, NM_182486, hCT2301261.0, hCT2301264.0	223571_at, 242444_at	NP_114116.3, NP_872292.1, EAW60145.1, EAW60146.1
GeneID:26088	GGA1	22	38,004,481	38,029,571	25,090	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3753, 2_A375_pNL97_plus_lncRNA_AR..1..5394	127, 191	in gene, in gene	1	1	0	32	36	6	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene GGA1	GGA1		NM_013365, NM_001001560, NM_001001561, NM_001172687, NM_001172688, hCT2300998.0, hCT2301002.0, hCT33108.3	1554870_at, 217560_at, 218114_at, 45572_s_at, 50277_at	NP_037497.1, NP_001001560.1, NP_001001561.1, NP_001166158.1, NP_001166159.1, EAW60168.1, EAW60169.1, EAW60170.1



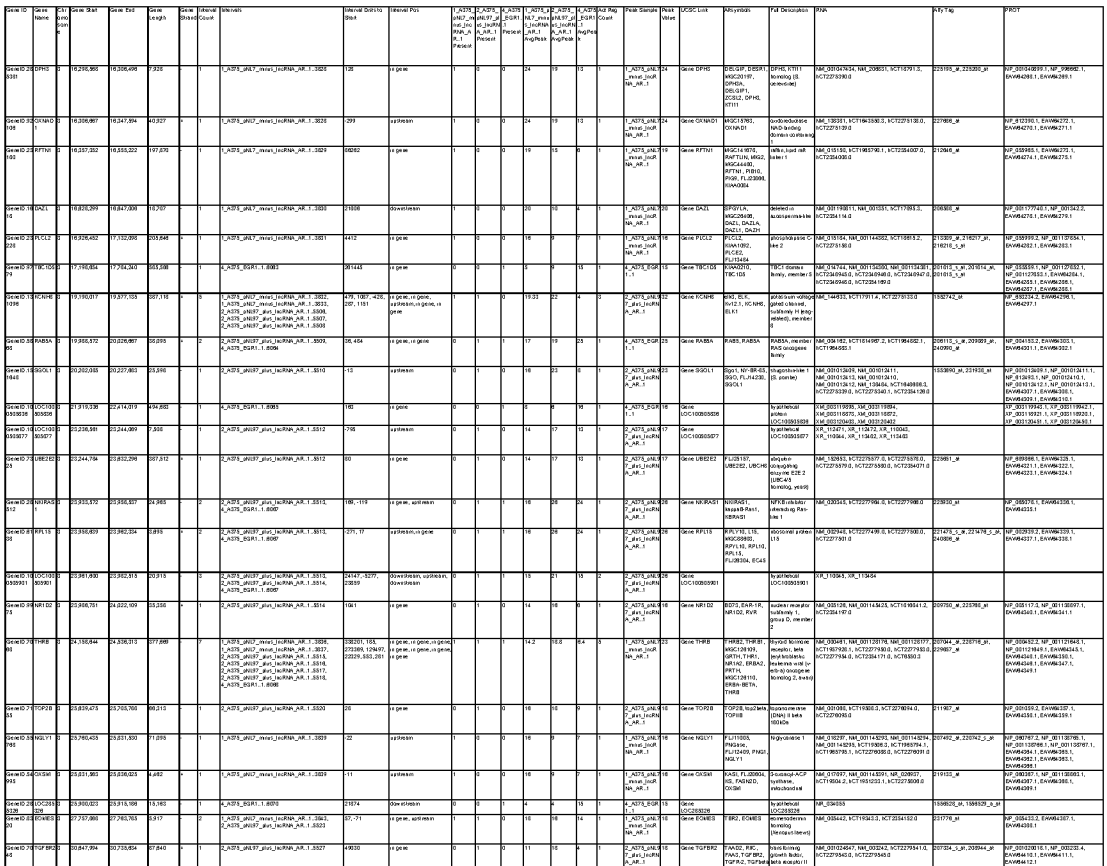
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_pfa7_mrna_junction_RNA_AR_1 Percent	2_A375_pfa7_mrna_junction_RNA_AR_1 Percent	4_A375_pfa7_mrna_junction_RNA_AR_1 Percent	1_A375_pfa7_mrna_junction_RNA_AR_1 Avg Peak	2_A375_pfa7_mrna_junction_RNA_AR_1 Avg Peak	4_A375_pfa7_mrna_junction_RNA_AR_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
Gene ID:39156	LGALS1	22	35,071,615	35,073,909	2,196	+	2	1_A375_pfa7_mrna_lncRNA_AR_1:3764, 2_A375_pfa7_dun_lncRNA_AR_1:3293											2_A375_pfa7_dun_lncRNA_AR_1	26	Gene LGALS1	GAL1, SHFEM6B2.10, LGALS1, GBP	lectin, galactoside-binding, soluble, 1	NM_002305, NC_000011.2	2311609_at, 2196639_at	NP_002296.1, EAW66178.1
Gene ID:79139	NOL12	22	35,692,344	35,699,485	7,141	+	2	1_A375_pfa7_mrna_lncRNA_AR_1:3764, 2_A375_pfa7_dun_lncRNA_AR_1:3293											2_A375_pfa7_dun_lncRNA_AR_1	26	Gene NOL12	MGC3731, Nop25, NOL12, dJ207E10.7, FLJ36509	nucleolar protein 12	NM_024313, NC_000011.9, NC_018922.2	223857_at	NP_077265.1, EAW63160.1, EAW63179.1
Gene ID:1170	TRIOBP	22	35,992,955	35,172,963	79,986	+	1	4_A375_DGR1..3997	72283	in gene	0	0	1	0	7	10	1	4_A375_DGR	10	Gene TRIOBP	TRIOBP, TARA, DFNB28, KIAA1862, FLJ39115, MRHFB2122, dJ207E16.4	TRIO and F-actin binding protein	NM_138932, NM_007032, NM_001039941, NC_000022.10, NC_018930.2, NC_000022.11, NC_018930.2, NC_000022.10, NC_018930.2	219224_at	NP_619530.2, NP_009083.2, NP_001034230.1, EAW63163.1, EAW63164.1, EAW63165.1, EAW63161.1, EAW63162.1, EAW63166.1
Gene ID:9138	ANKRD54	22	35,226,982	35,240,355	13,491	-	5	2_A375_pfa37_dun_lncRNA_AR_1:3396, 2_A375_pfa37_dun_lncRNA_AR_1:3397, 4_A375_DGR1..3998	17,-5119,-5125	in gene, upstream, upstream	0	1	1	13.5	16.5	12.5	2	2_A375_pfa37_dun_lncRNA_AR_1	19	Gene ANKRD54	LIAR, ANKRD54		NM_139197, NR_038538, NC_000022.10, NC_018930.2, NC_000022.11, NC_018930.2	231547_at	NP_620125.1, EAW66196.1, EAW66192.1, EAW66193.1
Gene ID:7231	MIR633	22	35,240,279	35,240,378	99	+	3	2_A375_pfa37_dun_lncRNA_AR_1:3396, 2_A375_pfa37_dun_lncRNA_AR_1:3397, 4_A375_DGR1..3998		in gene, upstream, upstream	0	1	1	13.5	16.5	12.5	2	2_A375_pfa37_dun_lncRNA_AR_1	19	Gene MIR633	MIR633, bta-mir-633, MIR633	microRNA 633	NR_032195		
Gene ID:7231	MIR633	22	35,240,805	35,240,761	96	-	3	2_A375_pfa37_dun_lncRNA_AR_1:3396, 2_A375_pfa37_dun_lncRNA_AR_1:3397, 4_A375_DGR1..3998	3445,-1691,-1767	downstream, upstream, upstream	0	1	1	13.5	16.5	12.5	2	2_A375_pfa37_dun_lncRNA_AR_1	19	Gene MIR633	MIR633, MIR699, bta-mir-699	microRNA 699	NR_032196		
Gene ID:5181	EIF3L	22	35,245,370	35,264,855	19,286	+	3	2_A375_pfa37_dun_lncRNA_AR_1:3396, 2_A375_pfa37_dun_lncRNA_AR_1:3397, 4_A375_DGR1..3998	-5004,-102,-116	upstream, in gene, in gene	0	1	1	13.5	16.5	12.5	2	2_A375_pfa37_dun_lncRNA_AR_1	19	Gene EIF3L	EIF3L, EIF3S6IP, HSPC023, EIF6IP, EIF3S11, HSPC021, MSTP005	eukaryotic translation initiation factor 3, subunit L	NM_019091, NC_000022.10, NC_018930.2, NC_000022.11, NC_018930.2	217719_at	NP_057175.1, EAW66198.1, EAW66199.1, EAW66197.1, EAW66195.1
Gene ID:8817	MICALL1	22	35,302,348	35,338,028	35,680	+	1	1_A375_pfa37_mrna_lncRNA_AR_1:3755	-1194	upstream	1	0	0	16	15	7	1	1_A375_pfa37_mrna_junction_NA_AR_1	16	Gene MICALL1	KIAA1966, FLJ45921, MICAL-L1, MICALL1, DKFZp686H02261, MRIP-B1G	MICAL-like 1	NM_033398, NC_018930.2, NC_000022.11	221779_at, 55681_at	NP_203744.1, EAW66199.1
Gene ID:3415	POLR2F	22	35,349,674	35,365,319	15,645	+	2	1_A375_pfa37_mrna_lncRNA_AR_1:3756, 4_A375_DGR1..3999	14526,24070	in gene, downstream	1	0	1	13.5	15	10	2	4_A375_DGR	21	Gene POLR2F	RPB8, RPB14.4, RPABC2	polymerase (RNA) II (DNA directed) polypeptide F	NM_021974, NC_018930.2, NC_000022.11	209611_at, 212643_at	NP_068593.1, EAW62202.1, EAW62203.1
Gene ID:8651	SOX10	22	35,366,319	35,393,539	27,220	-	4	1_A375_pfa37_mrna_lncRNA_AR_1:3756, 2_A375_pfa37_dun_lncRNA_AR_1:3396, 4_A375_DGR1..3999, 4_A375_DGR1..3999	18039,1651,8793,1179	downstream, in gene, in gene, in gene	1	1	1	13.33	13.33	10.67	3	4_A375_DGR	21	Gene SOX10	WS4, WS2E, WSC, DOM, MGC15649, PCWH, SOX10	SRY (sex determining region Y)-box 10	NM_006941, NC_018930.2, NC_000022.11	209642_at, 209643_s_at	NP_008872.1, EAW62205.1, EAW62204.1
Gene ID:1013530	LOC100131530	22	35,382,170	35,384,341	2,171	+	3	2_A375_pfa37_dun_lncRNA_AR_1:3396, 2_A375_pfa37_dun_lncRNA_AR_1:3397, 4_A375_DGR1..3998, 4_A375_DGR1..3999	-3982,-5439,-2010	upstream, upstream, upstream	0	1	1	12	13.5	11.5	2	4_A375_DGR	21	Gene LOC100131530	FLJ39713	hypothetical LOC100131530	XR_112361, XR_109712, XR_115497		
Gene ID:8651	RPS15	22	35,974,125	35,952,854	16,509	-	1	4_A375_DGR1..3994	90	in gene	0	0	1	8	8	15	1	4_A375_DGR	15	Gene RPS15	FLJ37761, LOC646551	hypothetical LOC646551	NM_001013647		NP_001013669.1
Gene ID:2387778	CBY1	22	35,952,856	35,969,653	17,197	+	4	1_A375_pfa37_mrna_lncRNA_AR_1:3757, 2_A375_pfa37_dun_lncRNA_AR_1:3401, 4_A375_DGR1..3974, 4_A375_DGR1..3975	23230,23282,114,23336	downstream, downstream, upstream, downstream	1	1	1	80	86	13.5	2	2_A375_pfa37_dun_lncRNA_AR_1	30	Gene CBY1	HSB3BTA, PGEH1, CBY1, PHSH1a, C22orf2, CBY, PHSH1a, sb51	ubiquitin homolog 1 (Drosophila)	NM_015373, NM_001003890	1560220_a_at, 203480_at	NP_056188.1, NP_001002890.1
Gene ID:1013530	LOC100128226	22	35,965,590	35,977,775	14,185	-	3	2_A375_pfa37_mrna_lncRNA_AR_1:3757, 2_A375_pfa37_dun_lncRNA_AR_1:3401, 4_A375_DGR1..3975	-115,-145,-241	upstream, upstream, upstream	1	1	1	112	130	98	1	2_A375_pfa37_dun_lncRNA_AR_1	30	Gene LOC100128226		hypothetical LOC100128226	XR_112362, XR_112363, XR_109715, XR_109714, XR_115435, XR_115436		
Gene ID:7046	TOMM22	22	35,977,934	35,980,763	2,811	+	3	2_A375_pfa37_mrna_lncRNA_AR_1:3757, 2_A375_pfa37_dun_lncRNA_AR_1:3401, 4_A375_DGR1..3975	-66,-34,-82	upstream, upstream, in gene	1	1	1	112	130	98	1	2_A375_pfa37_dun_lncRNA_AR_1	30	Gene TOMM22	MSTP065, MSTP083, TOM22, TOMM22, TOM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	NM_020243	217980_s_at, 223474_s_at, 224076_s_at	NP_064628.1
Gene ID:1013530	LOC100130549	22	35,980,596	35,999,941	19,865	+	8	1_A375_pfa37_mrna_lncRNA_AR_1:3757, 1_A375_pfa37_mrna_lncRNA_AR_1:3758, 2_A375_pfa37_dun_lncRNA_AR_1:3401, 2_A375_pfa37_dun_lncRNA_AR_1:3402, 2_A375_pfa37_dun_lncRNA_AR_1:3403, 4_A375_DGR1..3975	21153,-2615,21121,1953,2783,21023	downstream, upstream, downstream, in gene, upstream, downstream	1	1	1	50.33	53.67	9	3	2_A375_pfa37_dun_lncRNA_AR_1	30	Gene LOC100130549		hypothetical LOC100130549	XR_112364, XR_109715, XR_115498		
Gene ID:9929	JOSD1	22	35,981,345	35,996,459	14,911	-	8	1_A375_pfa37_mrna_lncRNA_AR_1:3757, 1_A375_pfa37_mrna_lncRNA_AR_1:3758, 2_A375_pfa37_dun_lncRNA_AR_1:3401, 2_A375_pfa37_dun_lncRNA_AR_1:3402, 2_A375_pfa37_dun_lncRNA_AR_1:3403, 4_A375_DGR1..3975	18071,-3397,18039,-829,5383,16442	downstream, upstream, downstream, upstream, upstream, downstream	1	1	1	50.33	53.67	9	3	2_A375_pfa37_dun_lncRNA_AR_1	30	Gene JOSD1	JOSD1L2, KIAA0983, JOSD1	Josephin domain containing 1	NM_014978, NC_018924.10, NC_018944.11	203781_at	NP_055991.1, EAW62259.1, EAW62260.1
Gene ID:8767	NPTXR	22	35,214,457	35,240,017	25,560	-	3	1_A375_pfa37_mrna_lncRNA_AR_1:3762, 2_A375_pfa37_dun_lncRNA_AR_1:3403, 4_A375_DGR1..3409	18049,19545,12697	in gene, in gene, in gene	1	1	0	16.5	21.5	9	2	2_A375_pfa37_dun_lncRNA_AR_1	27	Gene NPTXR	NPTXR, NPR	neuronal pentraxin receptor	NM_014293, NC_018920.10, NC_018944.29, NC_032961.2	213040_s_at, 217041_at	NP_055108.2, EAW66275.1, EAW66274.1
Gene ID:1013530	LOC100130361	22	35,247,189	35,262,354	15,145	+	1	4_A375_DGR1..3407	21291	in gene	0	0	0	12	16	7	1	4_A375_DGR	16	Gene LOC100130361		hypothetical LOC100130361	XR_112363, XR_109718, XR_115481		
Gene ID:8612	CBX8	22	35,260,343	35,262,356	2,013	+	1	4_A375_DGR1..3407	-722	upstream	0	1	0	13	16	7	1	4_A375_DGR	16	Gene CBX8	C3X8	chromobox homolog 8	NM_014292, NC_018920.3	202047_s_at, 202048_s_at	NP_055107.2, EAW62276.1
Gene ID:22	RPL3	22	39,708,997	39,715,870	6,793	-	2	2_A375_pfa37_dun_lncRNA_AR_1:3403, 4_A375_DGR1..3978	214, 66	in gene, in gene	0	1	1	10	19	24	1	4_A375_DGR	24	Gene RPL3	RPL3, TARBP-B, MGC164354	ribosomal protein L3	NM_000967, NM_001033553, NC_018919.10, NC_018944.29, NC_032961.2, NC_018919.10, NC_018944.29, NC_032961.2, NC_018919.10, NC_018944.29, NC_032961.2	201377_s_at, 211072_x_at, 211073_s_at, 211966_x_at, 213029_x_at	NP_000958.1, NP_001029023.1, EAW66312.1, EAW66316.1, EAW66320.1, EAW66311.1, EAW66314.1, EAW66313.1, EAW66317.1, EAW66318.1
Gene ID:1155	SNORD38	22	39,709,924	39,709,916	62	-	2	2_A375_pfa37_dun_lncRNA_AR_1:3436, 4_A375_DGR1..3978	-5949,-5956	upstream, upstream	0	1	1	10	19	24	1	4_A375_DGR	24	Gene SNORD38	RNU38, U38, SNORD38	small nucleolar RNA, C/D box 38	NR_000026		
Gene ID:8937	SNORD3A	22	39,711,216	39,711,312	94	-	2	2_A375_pfa37_dun_lncRNA_AR_1:3436, 4_A375_DGR1..3978	-4144,-4272	upstream, upstream	0	1	1	10	19	24	1	4_A375_DGR	24	Gene SNORD3A	RNU3A, SNORD3A, U83A	small nucleolar RNA, C/D box 3A	NR_000027		
Gene ID:6223	RNU68	22	39,712,247	39,712,301	54	-	2	2_A375_pfa37_dun_lncRNA_AR_1:3436, 4_A375_DGR1..3978	-5185,-5892	upstream, upstream	0	1	1	10	19	24	1	4_A375_DGR	24	Gene RNU68	U68, U68	RNA, U68 small nucleolar	NR_000028		
Gene ID:6227	SNORD45	22	39,715,057	39,715,116	60	-	2	2_A375_pfa37_dun_lncRNA_AR_1:3436, 4_A375_DGR1..3978	-230,-466	upstream, upstream	0	1	1	10	19	24	1	4_A375_DGR	24	Gene SNORD45	SNORD45, RNA45, U45	small nucleolar RNA, C/D box 45	NR_002439		
Gene ID:654	MAP3K7IP1	22	39,799,709	39,833,152	37,373	+	2	1_A375_pfa37_mrna_lncRNA_AR_1:3763, 2_A375_pfa37_dun_lncRNA_AR_1:3410	-47,-111	upstream, upstream	1	1	0	32	58	13	1	2_A375_pfa37_dun_lncRNA_AR_1	28	Gene MAP3K7IP1	3-Tab1, TAB1, MAP3K7IP1	PDZ-LIM domain binding factor	NM_152497, NM_006116, NC_018949.7, NC_018944.29, NC_032961.2, NC_018949.7, NC_018944.29, NC_032961.2	230301_at, 233979_at	NP_689710.1, NP_006107.1, EAW66225.1, EAW66224.1, EAW66221.1, EAW66220.1, EAW66223.1, EAW66222.1
Gene ID:45	MGAT3	22	39,853,325	39,866,199	34,874	+	3	1_A375_pfa37_mrna_lncRNA_AR_1:3764, 2_A375_pfa37_dun_lncRNA_AR_1:3411, 4_A375_DGR1..3977	21233,21287,22847	in gene, in gene, in gene	1	1	1	20	15	15	1	1_A375_pfa37_mrna_junction_NA_AR_1	20	Gene MGAT3	MGAT3, GNT-III, MGC142275, FLJ43271, MGC141963, GNT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	NM_002409, NM_001092270, NC_018936.10, NC_018944.29, NC_032965.2, NC_018936.10, NC_018944.29, NC_032965.2	209365_s_at, 209764_at, 244164_at	NP_002400.3, NP_001091743.1, EAW63222.1
Gene ID:6383	LOC100130549	22	39,871,448	39,873,568	2,110	+	3	1_A375_pfa37_mrna_lncRNA_AR_1:3764, 2_A375_pfa37_dun_lncRNA_AR_1:3411, 4_A375_DGR1..3977	3114,3140,2028	downstream, downstream, downstream	1	1	1	20	15	15	1	1_A375_pfa37_mrna_junction_NA_AR_1	20	Gene LOC100130549		hypothetical protein LOC100130549	XM_003119931, XM_003116817, XM_003121012		XP_003119979.1, XP_003116865.1, XP_003121060.1
Gene ID:4763	ATF4	22	39,916,569	39,916,691	2,122	+	1	1_A375_pfa37_mrna_lncRNA_AR_1:3765	8763	downstream	1	0	0	17	11	9	1	1_A375_pfa37_mrna_junction_NA_AR_1	17	Gene ATF4	TAXREB67, CREB2A, TXREB, CREB2	activating transcription factor 4 (tax-responsive enhancer element B67)	NM_182810, NM_001675, NC_018930.2, NC_018944.29, NC_032964.2	200779_at	NP_877362.1, NP_001666.2, EAW66241.1, EAW66242.1
Gene ID:5591	RPS19BP1	22	39,925,036	39,932,960	7,782	+	1	1_A375_pfa37_mrna_lncRNA_AR_1:3765	3965	in gene	1	0	0	17	11	9	1	1_A375_pfa37_mrna_junction_NA_AR_1	17	Gene RPS19BP1	MGC53210, RPS19BP1, bA110J13.4, HROS, FLJ20770, bA13F	ribosomal protein S19 binding protein 1	NM_194228, NC_018930.2, NC_018944.29, NC_032964.2	225162_at	NP_919321.1, EAW63343.1, EAW63344.1
Gene ID:8910	CACNA1I	22	39,966,756	40,005,740	118,982	+	1	4_A375_DGR1..3976	19108	in gene	0	0	1	5	5	10	1	4_A375_DGR	16	Gene CACNA1I	CACNA1I, Cav3.3, bA441.G20	calcium channel, voltage-dependent, T type, alpha 1I subunit	NM_021096, NM_001003406, NC_018949.7, NC_018944.29, NC_032967.2, NC_018949.7, NC_018944.29, NC_032967.2	206289_at, 211650_s_at, 221631_at	NP_066919.2, NP_001003406.1, EAW63245.1, EAW63246.1, EAW63247.1, EAW63248.1, EAW63249.1, EAW63250.1, EAW63251.1
Gene ID:1315	ADSL	22	40,742,904	40,762,977	20,073	+	1	1_A375_pfa37_mrna_lncRNA_AR_1:3767	11	in gene	1	0	0	12	14	12	1	1_A375_pfa37_mrna_junction_NA_AR_1	12	Gene ADSL	ASASE, AMPS2, ASL, ASL	adenylosuccinate lyase	NM_000026, NM_001127378, NC_018931.10, NC_018944.29, NC_032965.2, NC_018931.10, NC_018944.29, NC_032965.2	202144_s_at, 210292_at	NP_000017.1, NP_001116536.1, EAW62215.1, EAW62216.1, EAW62217.1
Gene ID:5591	MRLC1	22	40,936,292	41,032,800	206,296	+	2	2_A375_pfa37_dun_lncRNA_AR_1:3765, 2_A375_pfa37_dun_lncRNA_AR_1:3412	3965	in gene	1	0	0	17	11	9	1	1_A375_pfa37_mrna_junction_NA_AR_1	17	Gene MRLC1	MRL1, MRL, MRTF-A, BSHC	myosin regulatory light chain (translocation) 1	NM_006551, NC_018931.10, NC_018944.29, NC_032965.2, NC_018931.10, NC_018944.29, NC_032965.2	1553763_at, 1559782_at, 1559782_s_at, 212745_s_at, 212751_at, 212752_s_at	NP_006542.1, EAW63352.1, EAW63353.1, EAW63354.1, EAW63355.1, EAW63356.1
Gene ID:8772	STT3B	22	41,235,599	41,252,807	22,868	+	1	4_A375_DGR1..3981	-483	upstream	0	0	1	11	14	10	1	4_A375_DGR	16	Gene STT3	HIP, MGC131992, HOP, FMS004, HSPAB1, FeLV, FAM108A1, SWAP, PRO0768, AA52, STT3, HSTT3, HSPABP, FLJ27260	oligosaccharyltransferase 3 (homologous)	NM_033302, NC_018922.22, NC_032964.2, NC_018922.23, NC_032964.2	202743_s_at, 202999_s_at	NP_036523.2, EAW66294.1, EAW66293.1, EAW66296.1
Gene ID:8539	XRNPEP3	22	41,253,094	41,325,955	70,769	+	1	4_A375_DGR1..3981	56	in gene	0	0	1	11	14	10	1	4_A375_DGR	16	Gene XRNPEP3	NPEPL1, APP3, EPAEP3	X-ray repair complementing defective repair in Chinese hamster cells 3 (putative)	NM_020399, NC_018936.9, NC_032965.2, NC_018936.10, NC_018944.29, NC_032965.2	220020_at, 224166_s_at, 226081_at, 227912_at, 229220_at, 237750_at	NP_371351.1, EAW66400.1, EAW66397.1, EAW66398.1, EAW66399.1
Gene ID:1053	DNAJB7	22	41,255,553	41,266,100	10,577	+	1	4_A375_DGR1..3981	4956	downstream	0	0	1	11	14	10	1	4_A375_DGR	16	Gene DNAJB7	HSJ1, HSPAB7, hSJ1, DNAJB7, HSC3	DnaJ (Hsp40) homolog, subfamily B, member 7	NM_145174, NC_018922.23, NC_032964.2, NC_018922.23, NC_032964.2	1553879_at	NP_660157.1, EAW66400.1
Gene ID:7486	LSM8	22	41,801,315	41,827,373	25,982	+	1	4_A375_DGR1..3982	-5555	upstream	0	0	1	5	13	10	1	4_A375_DGR	19	Gene LSM8	LSM8TU3, rb, EG:rb6H1, LSM8	U6 snRNA-associated Sm-like protein LSm8	NM_031468, NC_018931.10, NC_018944.29, NC_032965.2, NC_018931.10, NC_018944.29, NC_032965.2	1553815_s_at, 223205_s_at	NP_112736.2, EAW66410.1, EAW66411.1, EAW66412.1, EAW66416.1, EAW66414.1, EAW66415.1
Gene ID:6908	RANGAP1	22	41,841,815	41,852,218	10,861	+	1	1_A375_pfa37_mrna_lncRNA_AR_1:3414	-120	upstream	0	1	0	15	28	9	1	2_A375_pfa37_dun_lncRNA_AR_1	28	Gene RANGAP1	MGC20289, RANGAP1, KIAA1963, SD, FLJ	Ran GTPase activating protein 1	NM_002883, NC_018931.10, NC_018944.29, NC_032965.2, NC_018931.10, NC_018944.29, NC_032965.2	1553833_s_at, 212127_at	NP_002874.1, EAW66420.1, EAW66421.1, EAW66422.1, EAW66423.1, EAW66424.1
Gene ID:2354	ZC3HR1	22	41,897,967	41,756,151	56,554	+	1	4_A375_DGR1..3983	19561	in gene	0	0	1	5	8	15	1	4_A375_DGR	15	Gene ZC3HR1	ZC3HR, KIAA1031, DKFZp434D0306, Rakkin, FLJ12767	zinc finger CCCH-type containing, R	NM_015590, NC_018931.10, NC_018944.29, NC_032965.2, NC_018931.10, NC_018944.29, NC_032965.2	205577_s_at, 206165_at, 206169_s_at, 213323_s_at, 219564_at	NP_056405.3, EAW66425.1, EAW66426.1, EAW66427.1, EAW66428.1, EAW66429.1
Gene ID:7682	TOB2	22	41,829,492	41,843,027	13,535	-	3	1_A375_pfa37_mrna_lncRNA_AR_1:3765, 2_A375_pfa37_dun_lncRNA_AR_1:3415, 4_A375_DGR1..3996	136,72,51	in gene, in gene, in gene	1	1	1	17	16	23	1	4_A375_DGR	23	Gene TOB2	TOB2, TOB1, TOB4, TOBD2	transducer of TOB1, 2	NM_016272	221486_s_at, 222043_s_at, 224350_s_at	NP_057356.1
Gene ID:5644	PHF5A	22	41,855,721	41,864,706	8,987	-	2	1_A375_pfa37_mrna_lncRNA_AR_1:3772, 2_A375_pfa37_dun_lncRNA_AR_1:3416	-259,-316	upstream, upstream	1	1	0	16	16	9	1	1_A375_pfa37_mrna_junction_NA_AR_1	16	Gene PHF5A	bA222H9.2, SAP14b, MGC13548, SF3b14b, Rds3, PHF5A, p14	PHD finger protein 5A	NM_022758, NC_018931.10, NC_018929.3	223309_at	NP_116147.1, EAW66434.1, EAW66433.1
Gene ID:8070	ACO2	22	41,865,129	41,924,993	59,864	+	2	1_A375_pfa37_mrna_lncRNA_AR_1:3770, 2_A375_pfa37_dun_lncRNA_AR_1:3416	-137,-193	upstream, upstream	1	1	0	16	16	9	1	1_A375_pfa37_mrna_junction_NA_AR_1	16	Gene ACO2	ACONM, MGC20955, ACO2, MGC23996	aconitase 2, mitochondrial	NM_001098, NC_018944.10, NC_018912.3	200763_s_at	NP_001089.1, EAW66438.1, EAW66435.1
Gene ID:1798	POLR3H	22	41,921,803	41,940,479	18,676	-	1	1_A375_pfa37_mrna_lncRNA_AR_1:3771	331	in gene	1	0	0	20	15	8	1	1_A375_pfa37_mrna_junction_NA_AR_1	20	Gene POLR3H	RPC8, POLR3H, MGC29814, KIAA1803, MGC111097	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	NM_001018050, NM_001018052, NM_016310, NC_018931.10, NC_018944.10, NC_032965.2, NC_018931.10, NC_018944.10, NC_032965.2	229870_at, 229962_s_at, 232057_at	NP_001018060.1, NP_001018062.1, NP_057411.1, EAW66430.1, EAW66431.1, EAW66441.1, EAW66432.1, EAW66440.1



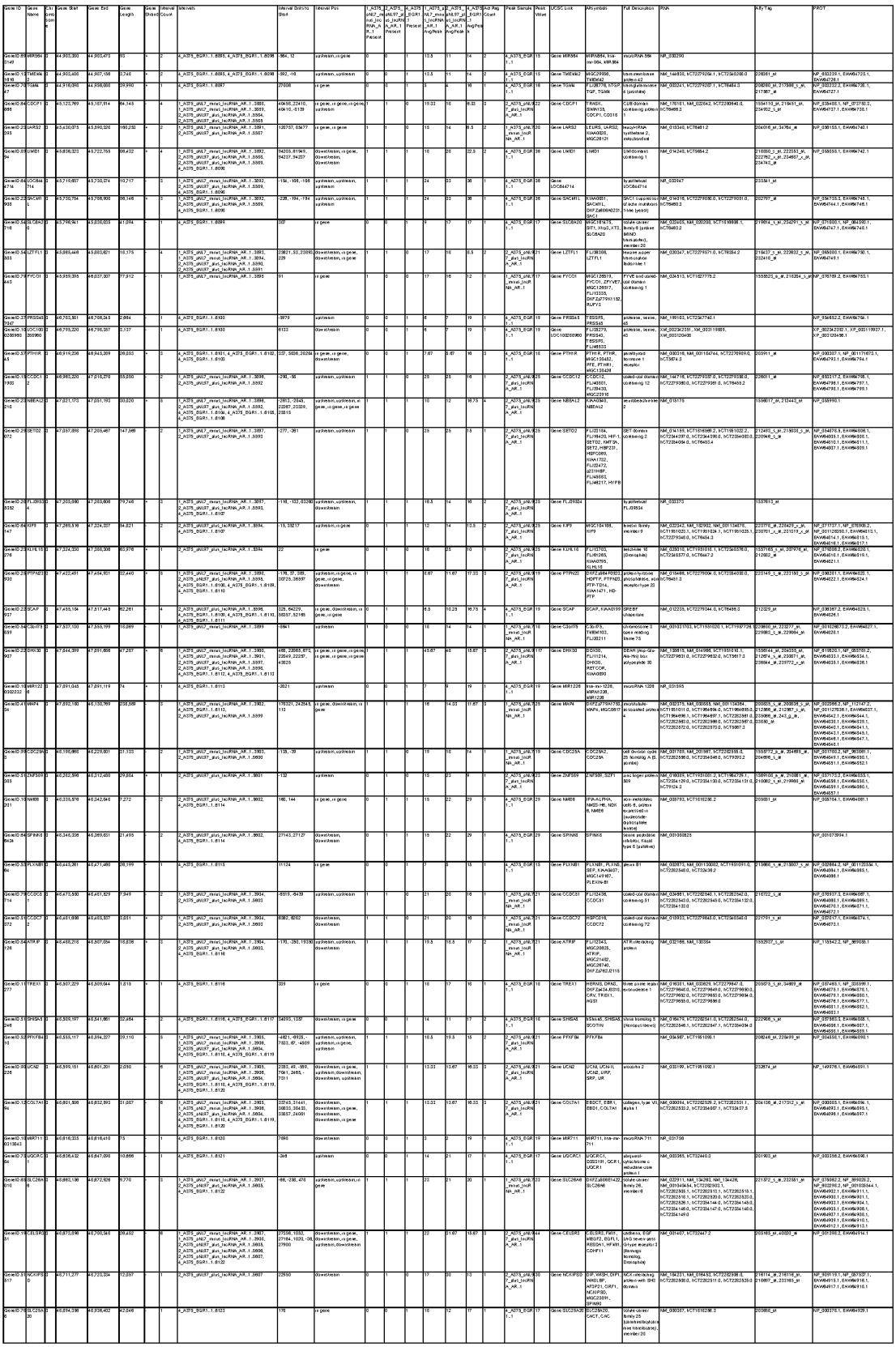
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_4_A375_1_A375_p_A375_4_A375 Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt-symbols	Full Description	RNA	Ally Tag	PROT
GeneID:2597	XRCC6	22	42,017,255	42,060,052	42,797	+	1	2_A375_shU97_plus_lncRNA_NR_1:3417	43651	downstream	0 1 0 10 17 10 1	2_A375_shU97_plus_lncRNA_NR_1	17	Gene XRCC6	CTC87, KU70, TLAA, XRCC6, bB22P1, ML6, CTC75	X-ray repair complementing defective repair in Chinese hamster cells 6	NM_001469, NCT02804022.0, NCT03340423.0, NCT02355360.0	2307792_at_215358_at	NP_001450.1, EAW66447.1, EAW66448.1, EAW66449.1
GeneID:4689	NHP2L1	22	42,069,937	42,084,915	14,978	+	1	2_A375_shU97_plus_lncRNA_NR_1:3417	22617	downstream	0 1 0 10 17 10 1	2_A375_shU97_plus_lncRNA_NR_1	17	Gene NHP2L1	NHP2L1, OTK27, Rh1, SNU482, FAI, NHPX, SNU41, SNRNP9-5, SNU13, 15.5K	NHP2 ribonucleoprotein homolog (yeast)	NM_002606, NM_001003796, NCT01983277.1, NCT01983705.1, NCT02647972.0, NCT02810122	2001276_at_201077_s_at, 2036443_at	NP_004990.1, NP_001003796.1, EAW66450.1, EAW66451.1, EAW66452.1, EAW66453.1
GeneID:1081	LOC1003	22	42,072,746	42,075,252	2506	-	1	2_A375_shU97_plus_lncRNA_NR_1:3417	10256	downstream	0 1 0 10 17 10 1	2_A375_shU97_plus_lncRNA_NR_1	17	Gene LOC100506862	protein LLP homolog	XM_003119532, XM_003316816, XM_003131010		XP_003119580.1, XP_003316864.1, XP_003131091.1
GeneID:1534	MET	22	42,095,516	42,195,459	99,943	+	1	4_A375_DSR1_1:3965	100156	downstream	0 0 1 7 14 19 1	4_A375_DSR1_1	19	Gene MET	MGC49042, MET	mesoss ctatolic t	NM_152513	1554200_at, 1566521_s_at, 2030011_at	NP_869258.3
GeneID:7941	CCDC1	22	42,166,676	42,222,306	55,630	+	4	1_A375_shU7_mirart_lncRNA_NR_1:3772, 2_A375_shU97_plus_lncRNA_NR_1:3416, 4_A375_DSR1_1:3958, 4_A375_DSR1_1:3958	33218, 22216, -6, 23876	downstream, downstream, upstream, downstream	1 1 1 16.33 17 13.33 3	1_A375_shU539_mirart_lncRNA_NR_1	17	Gene CCDC134	KIAA1011-3, FLJ22349, MGC21610, CCDC134	coiled-coil domain containing 134	NM_024321, NCT02302022	233077_at	NP_079397.1, EAW66448.1
GeneID:8715	SREBF2	22	42,229,106	42,302,013	73,269	+	3	1_A375_shU7_mirart_lncRNA_NR_1:3772, 2_A375_shU97_plus_lncRNA_NR_1:3416, 4_A375_DSR1_1:3958	-210, -210, -6430	upstream, upstream, upstream	1 1 1 21 16.5 10.5 2	1_A375_shU539_mirart_lncRNA_NR_1	17	Gene SREBF2	KIAA1652, SREBF2, SREBF2	sterol regulatory element binding transcription factor 2	NM_004599, NCT02302022.0, NCT02355360.0, NCT02302122.0	2012345_s_at_242745_at	NP_004590.2, EAW66451.1, EAW66470.1
GeneID:7942	CENPH	22	42,234,741	42,245,146	10,405	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3772, 2_A375_shU97_plus_lncRNA_NR_1:3419	-60, 76	cr gene, cr gene	1 1 1 0 32 39 12 1	2_A375_shU439_mirart_lncRNA_NR_1	17	Gene CENPH	C-20orf16, MGC981, FAAE1, CENP-H, CENPH, MGC92012	centromere protein H	NM_024533, NM_001002876, NM_001110215, NCT01931385.1, NCT02334380.0, NCT02622.3	218741_at	NP_079556.1, NP_001002876.1, NP_001103685.1, EAW66474.1, EAW66476.1
GeneID:3315	LOC339	22	42,248,191	42,254,948	6,758	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3772, 2_A375_shU97_plus_lncRNA_NR_1:3419	-5193, -5119	upstream, upstream	1 1 1 0 32 39 12 1	2_A375_shU439_mirart_lncRNA_NR_1	17	Gene LOC339974	MGC90102	hypothetical LOC339974	NM_024355		
GeneID:8315	C22orf3	22	42,275,899	42,280,266	4,368	+	1	4_A375_DSR1_1:3967	32749	downstream	0 0 1 10 10 15 1	4_A375_DSR1_1	15	Gene C22orf32	DC06, bA185O1.1, C22orf32	chromosome 22 open reading frame 32	NM_033318, NCT01737361	223764_s_at, 223793_at, 227862_at, 228117_at	NP_203753.2, EAW66488.1
GeneID:4700	NDUFA	22	42,281,820	42,286,985	5,166	-	1	4_A375_DSR1_1:3967	440	cr gene	0 0 1 10 10 15 1	4_A375_DSR1_1	15	Gene NDUFA6	NADHBH4, C1 6H+, LYRM6, 8H+, NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	NM_002490, NCT02816161	202600_at, 202031_s_at	NP_002481.2, EAW66489.1
GeneID:1810	LOC1003	22	42,456,927	42,533,510	76,573	+	1	4_A375_DSR1_1:3967	-469	upstream	0 0 1 10 10 15 1	4_A375_DSR1_1	15	Gene LOC100287153		hypothetical LOC100287153	XR_109722		
GeneID:1810	LOC1003	22	42,456,927	42,521,354	64,417	+	1	4_A375_DSR1_1:3967	-469	upstream	0 0 1 10 10 15 1	4_A375_DSR1_1	15	Gene LOC100132273		hypothetical LOC100132273	NR_034118		
GeneID:8977	TCF20	22	42,506,019	42,611,445	65,426	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3774, 2_A375_shU97_plus_lncRNA_NR_1:3420	43255, 43261	cr gene, cr gene	1 1 1 0 14 15 5 1	2_A375_shU615_mirart_lncRNA_NR_1	15	Gene TCF20	AR1, TCF20, SPBP, KIAA0282	transcription factor 20 (AR1)	NM_181492, NM_005650, NCT01991105.1, NCT01955859.1, NCT02535452.0, NCT02352.2	212931_at, 215831_at, 233867_at	NP_852489.1, NP_005641.1, EAW66495.1, EAW66496.1, EAW66497.1, EAW66498.1
GeneID:5471	POLDIP	22	42,979,727	43,010,962	31,235	-	3	1_A375_shU7_mirart_lncRNA_NR_1:3775, 2_A375_shU97_plus_lncRNA_NR_1:3421, 4_A375_DSR1_1:3958	-298, -142, -382	upstream, upstream, upstream	1 1 1 24 22 24 1	1_A375_shU524_mirart_lncRNA_NR_1	24	Gene POLDIP3	KIAA1647, PDIP46, POLDIP3, SKAR	polymerase (DNA-directed), delta interacting protein 3	NM_023311, NM_178139, NCT02849490.1, NCT02864707.1, NCT02864708.1, NCT02864707.1	219383_at_212393_s_at, 219387_s_at, 243411_at	NP_115807.2, NP_835237.1, EAW72264.1, EAW72265.1, EAW72266.1, EAW72267.1
GeneID:2619	RNU12	22	43,011,251	43,011,399	148	+	3	1_A375_shU7_mirart_lncRNA_NR_1:3775, 2_A375_shU97_plus_lncRNA_NR_1:3421, 4_A375_DSR1_1:3958	-65, -147, -95	upstream, upstream, cr gene	1 1 1 24 22 24 1	1_A375_shU524_mirart_lncRNA_NR_1	24	Gene RNU12	RNU12P, RNA12, RNU12, RNU12-1, U2D2SEQ7	RNA, U12 small nuclear	NR_029422		
GeneID:1757	CYBSR3	22	43,013,549	43,045,403	31,859	-	3	1_A375_shU7_mirart_lncRNA_NR_1:3775, 2_A375_shU97_plus_lncRNA_NR_1:3421, 4_A375_DSR1_1:3958	54237, 54301, 54361	downstream, downstream, downstream	1 1 1 24 22 24 1	1_A375_shU524_mirart_lncRNA_NR_1	24	Gene CYBSR3	CYBSR2, BSR, Dia1	cytochrome b5 reductase 3	NM_001134616, NM_007326, NM_000290, NM_001174980, NM_001174981, NCT01951180.1, NCT01951199.1, NCT02864990.0, NCT02864991.0, NCT02864993.0, NCT03131.2	1554574_a_at, 201883_s_at	NP_001122911.1, NP_015356.1, NP_000281.1, NP_001158131.1, NP_001158132.1, EAW72265.1, EAW72266.1, EAW72267.1, EAW72270.1, EAW72271.1, EAW72272.1, EAW72273.1
GeneID:2397	TTLL1	22	43,435,922	43,485,434	49,512	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3776, 2_A375_shU97_plus_lncRNA_NR_1:3423	294, 292	cr gene, cr gene	1 1 1 0 33 33 3 1	2_A375_shU693_mirart_lncRNA_NR_1	23	Gene TTLL1	TTLL1, HB2314B2B, C20orf7	tubulin tyrosine ligase-like family, member 1	NM_012263, NR_027779, NCT01722561.2, NCT01910371.1, NCT02864984.0	1570693_at, 209832_s_at	NP_036393.1, EAW70280.1, EAW70279.1, EAW70281.1
GeneID:8464	EPCAM	22	43,924,824	44,206,217	283,393	+	1	2_A375_shU97_plus_lncRNA_NR_1:3424	-108	upstream	0 1 0 10 15 7 1	2_A375_shU615_mirart_lncRNA_NR_1	15	Gene EPCAM	EVR5/CE1, EPCAM6, HEBCBP1, KMA1672, DJB7, FLJ20500	EP-bind cell adhesion binding domain 8	NM_002763, NM_139058	1562815_at_232271_x_at, 233365_at_233860_at, 233859_at_234752_x_at, 234353_x_at	NP_078832.2, NP_942133.1
GeneID:2383	SULT4A1	22	44,226,397	44,236,376	37,991	-	2	1_A375_shU7_mirart_lncRNA_NR_1:3777, 2_A375_shU97_plus_lncRNA_NR_1:3425	-5476, -5494	upstream, upstream	1 1 1 0 20 20 3 1	2_A375_shU626_mirart_lncRNA_NR_1	26	Gene SULT4A1	KBR-STI-1, DJ358H5.2, BR-STI-1, SULT4, NST, BRSTI-1, MGC40312, SULT4A1	sulfotransferase family 4A, member 1	NM_014351, NCT01931036.1, NCT01977738.1, NCT02551590.0, NCT0915.2	1515429_at	NP_055166.1, EAW72317.1, EAW72318.1, EAW72319.1, EAW72320.1
GeneID:8859	PNPLA3	22	44,319,819	44,345,446	25,629	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3776, 2_A375_shU97_plus_lncRNA_NR_1:3426	51549, 51735	downstream, downstream	1 1 1 0 17 14 12 1	2_A375_shU517_mirart_lncRNA_NR_1	17	Gene PNPLA3	C20orf20, PNPLA3, ADPN, iPLA(2)epsilon	patatin-like phospholipase domain containing	NM_025225, NCT01930038.2, NCT01967487.0, NCT02551190.0	2206015_s_at, 219330_at	NP_076931.2, EAW72324.1, EAW72325.1
GeneID:2338	SHMT2	22	44,351,261	44,392,412	41,151	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3776, 2_A375_shU97_plus_lncRNA_NR_1:3426	90, 83	upstream, cr gene	1 1 1 0 17 14 12 1	2_A375_shU517_mirart_lncRNA_NR_1	17	Gene SHMT2	FLJ90939, TRG-3, CHRF53, CGI-31, TCBS3, FLJ42503, FLJ58525, YNL028W, SHMT2, SHMT2	5-drug and ionizing radiation-resistance conspicuous 32 homolog (S cerevisiae)	NM_013290, NCT0344.3	2019659_s_at_201970_at, 2030396_at_243239_at	NP_036169.3, EAW72326.1
GeneID:8381	KIAA1644	22	44,839,597	44,706,701	99,174	-	1	4_A375_DSR1_1:3969	14139	cr gene	0 0 1 4 9 13 1	4_A375_DSR1_1	13	Gene KIAA1644	MGC129552, MGC129551, KIAA1644	KIAA1644	NM_031939294	2221901_at_52827_at	NP_940992.2, EAW70294.1
GeneID:5313	PRR5	22	43,984,993	43,133,961	148,968	+	1	4_A375_DSR1_1:3992	98083	cr gene	0 0 1 9 7 13 1	4_A375_DSR1_1	13	Gene PRR5	FLJ31159, PRR5, PROTOR1, PROTOR-1, FLJ31165, PRR5	protein rich 5 (brain)	NM_015366, NM_181333, NM_020317826, NM_031017529, NM_031017530	1219165_s_at_47389_at	NP_056181.2, NP_851567.1, NP_031017526.1, NP_031017527.1, NP_001017529.1, NP_001017530.1
GeneID:5591	PRKR-AR	22	45,096,382	45,286,994	190,282	+	2	1_A375_DSR1_1:3992, 4_A375_DSR1_1:3992	32274, 149834	cr gene, cr gene	0 0 1 4.3 8.5 14.5 2	4_A375_DSR1_1	15	Gene PRKR-AR;HQ4PE	PRKR-AR;HQ4PE	PRKR-AR;HQ4PE	NM_181334	1555162_at	NP_851851.2
GeneID:2339	ARHGA	22	45,148,439	45,216,864	110,238	+	1	4_A375_DSR1_1:3993	99878	cr gene	0 0 1 4 9 14 1	4_A375_DSR1_1	14	Gene ARHGAP8	BPGAP1, ARHGAP8, PRO1510, FLJ20105	Rho GTPase activating protein PR05, FLJ20105	NM_181333, NM_001017826	232367_at	NP_851852.2, NP_001017836.1
GeneID:2555	PHF21B	22	45,277,942	45,455,909	178,767	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3779, 2_A375_shU97_plus_lncRNA_NR_1:3427	54300, 54241	cr gene, cr gene	1 1 1 0 21 24 6 1	2_A375_shU624_mirart_lncRNA_NR_1	24	Gene PHF21B	PHF4, PHF21B, FLJ36161, BHC80L	PHD finger protein 21B	NM_138419, NM_001135992, NCT02869990.0, NCT02869993.0, NCT02869970.0	1560891_s_at, 1562009_s_at	NP_612624.1, NP_001129054.1, EAW72365.1, EAW72366.1, EAW72367.1
GeneID:1030	LOC1003	22	43,384,997	43,386,163	1,166	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3779, 2_A375_shU97_plus_lncRNA_NR_1:3427	-3364, -3450	upstream, upstream	1 1 1 0 21 24 6 1	2_A375_shU624_mirart_lncRNA_NR_1	24	Gene LOC100509865		hypothetical LOC100509865	XR_112287, XR_109729, XR_115494		
GeneID:1030	LOC1003	22	43,829,839	43,849,992	20,023	-	1	4_A375_DSR1_1:3994	110	cr gene	0 0 1 10 7 16 1	4_A375_DSR1_1	16	Gene LOC100506714		hypothetical LOC100506714	XR_112295, XR_112293, XR_109730, XR_109731, NR_115455, XR_115496		
GeneID:1070	NUP50	22	43,859,728	43,865,892	24,166	+	1	4_A375_DSR1_1:3994	-174	upstream	0 0 1 10 7 16 1	4_A375_DSR1_1	16	Gene NUP50	NPAP60, NUP50, NPAP60L	nucleoporin 50kDa	NM_007172, NM_130845	213982_at_218293_s_at, 218294_s_at_218293_s_at, 222363_s_at	NP_009103.2, NP_751931.1
GeneID:3387	FAM118A	22	45,769,081	43,737,838	32,758	+	1	4_A375_DSR1_1:3995	343	cr gene	0 0 1 5 12 17 1	4_A375_DSR1_1	17	Gene FAM118A	C.20orf6, FLJ38653, FAM118A	family with sequence similarity 118, member A	NM_001104589, NM_017911, NCT01937733.1, NCT02355180.0, NCT1900.2	219079_at_220473_at	NP_001098681.1, NP_060361.2, EAW72781.1, EAW72779.1, EAW72780.1
GeneID:2286	ATXN10	22	45,867,876	46,241,167	373,309	+	1	2_A375_shU97_plus_lncRNA_NR_1:3429	788	cr gene	0 1 0 8 15 8 1	2_A375_shU615_mirart_lncRNA_NR_1	15	Gene ATXN10	ATX10, HUMSEP, SCA10, E46L, FLJ27090	ataxin 10	NM_012236, NM_001167621, NCT01931227.1, NCT02355127.0	206522_at_206523_s_at	NP_037366.1, NP_001161092.1, EAW72262.1, EAW72263.1
GeneID:7477	WNT7B	22	46,316,245	46,373,005	56,762	-	3	2_A375_shU97_plus_lncRNA_NR_1:3430, 4_A375_DSR1_1:3997, 4_A375_DSR1_1:3998	7952, 41904, 54512	cr gene, cr gene, cr gene	0 1 1 6.33 13.67 13.67 3	2_A375_shU616_mirart_lncRNA_NR_1	16	Gene WNT7B	WNT7B	wingless-type MMTV integration site family, member 7B	NM_058238, NCT0722.2		NP_476979.1, EAW70339.1
GeneID:1030	LOC1003	22	46,345,936	46,373,005	27,172	+	2	2_A375_shU97_plus_lncRNA_NR_1:3430, 4_A375_DSR1_1:3996	19220, -7340	cr gene, upstream	0 1 1 6.5 12.5 13 2	2_A375_shU616_mirart_lncRNA_NR_1	16	Gene LOC100506756		hypothetical LOC100506756	XR_109733, XR_109735, XR_109734		
GeneID:4034	LOC4034	22	46,461,077	46,509,008	27,931	+	4	1_A375_shU7_mirart_lncRNA_NR_1:3780, 4_A375_DSR1_1:4000, 4_A375_DSR1_1:4002, 4_A375_DSR1_1:4003	-21, -921, 303, 27243	upstream, upstream, cr gene, cr gene	1 1 1 12.33 9 10.67 3	4_A375_shU616_mirart_lncRNA_NR_1	16	Gene OGA00931	FLJ27365	hypothetical LOC439931	NR_027033, NCT01931036.1, NCT02551319.0	233460_at	EAW72390.1, EAW72399.1
GeneID:4050	MRLET7A	22	46,505,629	46,505,702	73	+	1	4_A375_DSR1_1:4003	491	downstream	0 0 1 5 8 16 1	4_A375_DSR1_1	16	Gene MIRLET7A3	let-7a-3, MIRLET7A3, LET7A3, MIRLET7A3	microRNA let-7a-3	NR_029476		
GeneID:4050	MRLET7B	22	46,509,566	46,509,648	82	+	1	4_A375_DSR1_1:4003	-448	upstream	0 0 1 5 8 16 1	4_A375_DSR1_1	16	Gene MIRLET7B	MIRNLET7B, let-7b, MIRLET7B, let-7b-mir-7b	microRNA let-7b	NR_029479		
GeneID:3387	TTC33	22	46,865,991	46,869,903	28,044	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3781, 2_A375_shU97_plus_lncRNA_NR_1:3431	28807, 28923	downstream, downstream	1 1 1 0 22 20 6 1	1_A375_shU522_mirart_lncRNA_NR_1	22	Gene TTC33	TTC33, FLJ20999	tetratricopeptide repeat domain 33	NM_017931, NCT01985976.1, NCT02714100.0, NCT02877.2	218434_at_218766_s_at, 218272_at	NP_060401.2, EAW75412.1, EAW75413.1, EAW75414.1, EAW75415.1
GeneID:1060	NCN3H6	22	46,891,040	46,892,857	1,817	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3781, 2_A375_shU97_plus_lncRNA_NR_1:3431	-211, -227	upstream, upstream	1 1 1 0 22 20 6 1	1_A375_shU522_mirart_lncRNA_NR_1	22	Gene CNDH6		hypothetical LOC153084	NM_026009	1559661_at	
GeneID:5512	GTSE1	22	46,892,836	46,926,707	34,089	+	3	1_A375_shU7_mirart_lncRNA_NR_1:3781, 2_A375_shU97_plus_lncRNA_NR_1:3431, 4_A375_DSR1_1:3997	130, 148, 33979	cr gene, cr gene, downstream	1 1 1 0 16 24.5 7.5 2	2_A375_shU629_mirart_lncRNA_NR_1	29	Gene GTSE1	B99, GTSE1	G-2 and S-phase expressed 1	NM_016426, NCT02714151.0, NCT02714160.0, NCT02714150.0, NCT02714119.0	204315_s_at_204317_at, 204316_s_at_211340_s_at, 211342_s_at_223343_at	NP_057510.4, EAW75419.1, EAW74310.1, EAW75420.1, EAW74321.1
GeneID:5588	TRMU	22	46,731,296	46,783,237	51,939	+	1	2_A375_shU97_plus_lncRNA_NR_1:3432	316	cr gene	0 0 1 0 14 20 7 1	2_A375_shU629_mirart_lncRNA_NR_1	29	Gene TRMU	TRMU, TRNT1, MTU1, TRMT, MGC99627, TRMT1, MTO2	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	NM_018006, NCT02714121.0, NCT02714122.0, NCT02551451.0, NCT02551452.0, NCT02551453.0	219084_x_at	NP_060176.2, EAW75426.1, EAW75422.1, EAW75423.1, EAW75424.1, EAW75425.1
GeneID:5981	CELSR1	22	46,758,751	46,933,997	175,238	+	1	2_A375_shU97_plus_lncRNA_NR_1:3433	63827	cr gene	0 0 1 0 10 15 4 1	2_A375_shU615_mirart_lncRNA_NR_1	15	Gene CELSR1	FMI2, ME2, CDHF8, CELSR1, Dor2a1a-R0726, HPMI2	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	NM_014246, NCT02298232.0, NCT02355864.0	1554539_s_at_217092_s_at, 41660_at	NP_055061.1, EAW75429.1, EAW75428.1
GeneID:2597	TBC1D22	22	47,156,516	47,371,342	412,826	+	2	1_A375_shU7_mirart_lncRNA_NR_1:3782, 2_A375_shU97_plus_lncRNA_NR_1:3434	-56, -54	upstream, upstream	1 1 1 0 17 16 11 1	2_A375_shU616_mirart_lncRNA_NR_1	16	Gene TBC1D22A	C.20orf6, HBC79B021, TBC1D22A	TBC1 domain family, member 22A	NM_014346, NCT01722982.2, NCT02714136.0, NCT02714139.0	209660_s_at_210144_at, 23776_at	NP_055861.1, EAW75443.1, EAW75444.1, EAW75445.1
GeneID:4911	RPI1-191L9.1	22	48,016,792	48,027,316	10,525	+	1	2_A375_shU97_plus_lncRNA_NR_1:3435	-366	upstream	0 0 1 0 12 23 5 1	2_A375_shU623_mirart_lncRNA_NR_1	23	Gene RPI1-191L9.1	FLJ46257	hypothetical LOC439932	NR_033377, NCT2540900.1		EAW75451.1
GeneID:2397	FAM19A5	22	48,055,355	48,147,744	92,389	+	6	1_A375_shU7_mirart_lncRNA_NR_1:3783, 2_A375_shU97_plus_lncRNA_NR_1:3436, 4_A375_DSR1_1:4004, 4_A375_DSR1_1:4005, 4_A375_DSR1_1:4006, 4_A375_DSR1_1:4007, 4_A375_DSR1_1:4008	213240, 134596, 147648, 160072, 231660, 280344	cr gene, cr gene, cr gene, cr gene, cr gene, cr gene	1 1 1 8.67 7.33 11 6 1	2_A375_shU616_mirart_lncRNA_NR_1	16	Gene FAM19A5	UNQ6266, QLL4339, TAFA-5, TAFA5, FAM19A5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	NM_001082497, NM_015551, NCT01931012.1, NCT5675.2	229489_at_229683_at, 237094_at	NP_001076387.1, NP_056136.2, EAW75463.1, EAW75465.1
GeneID:1030	LOC1003	22	50,006,395	50,009,364	2,970	+	1	4_A375_DSR1_1:4013	398	cr gene	0 0 1 4 9 16 1	4_A375_DSR1_1	16	Gene LOC100509932		hypothetical LOC100509932	XR_112287, XR_109743, XR_115494		
GeneID:3943	LOC22ch5	22	50,013,230	50,051,160	37,930	-	2	4_A375_DSR1_1:4013, 4_A375_DSR1_1:4014	42162, 16328	downstream, cr gene	0 0 1 3.5 8.5 13 2	4_A375_DSR1_1	16	Gene C22ch54	C.20orf54	chromosome 22 open reading frame 54	NR_028997		
GeneID:4734	TTLL8	22	50,450,552	50,470,055	19,503	-	2	2_A375_shU97_plus_lncRNA_NR_1:3435, 4_A375_DSR1_1:4015	28647, 23199	cr gene, cr gene	0 1 1 0 10 10 12 2	2_A375_shU617_mirart_lncRNA_NR_1	17	Gene TTLL8	TTLL8		NM_031930447		NP_001073816.1
GeneID:5866	PANX2	22	50,809,160	50,816,704	7,544	+	1	4_A375_DSR1_1:4016	5984	cr gene	0 0 1 1 9 16 1	4_A375_DSR1_1	16	Gene PANX2	MGC119432, MGC119433, PANX2, PX2	pannexin 2	NM_052839, NM_001168200, NR_027691, NCT02535750.0, NCT02354.1.0, NCT02551166.0	1552644_a_at, 239087_s_at_244471_x_at	NP_443731.2, NP_001153772.1, EAW74349.1, EAW75495.1, EAW74348.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:80305	TRABD	22	50,624,360	50,638,027	13,667	+	2	4_A375_EGR1..1..8016, 4_A375_EGR1..1..8017	-9336, 4600	upstream, in gene	0	0	1	2.5	3.5	14	2	4_A375_EGR1..1	16	Gene TRABD	TRABD, LP6054, MGC110928, PP2447	TraB domain containing	NM_025204, hCT2263677.1, hCT2263680.0, hCT23037.3, hCT2355193.0, hCT2355194.0, hCT2355195.0	221807_s_at, 225360_at, 232706_s_at	NP_079480.2, EAW73497.1, EAW73498.1, EAW73499.1, EAW73501.1, EAW73502.1, EAW73500.1
GeneID:85378	TUBGCP6	22	50,656,118	50,683,400	27,282	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5439, 4_A375_EGR1..1..8018	-88, -104	upstream, upstream	0	1	1	13	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TUBGCP6	TUBGCP6, GCP6	tubulin, gamma complex associated protein 6	NM_020461, hCT1965012.1, hCT2264513.0, hCT23032.2, hCT2355184.0	225758_s_at, 234306_at	NP_065194.2, EAW73508.1, EAW73507.1, EAW73509.1, EAW73510.1
GeneID:83933	HDAC10	22	50,683,612	50,689,834	6,222	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5439, 4_A375_EGR1..1..8018	6346, 6330	downstream, downstream	0	1	1	13	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene HDAC10	HD10, DKFZp761B039, HDAC10, MGC149722	histone deacetylase 10	NM_032019, NM_001159286, hCT1965013.1, hCT1965014.1, hCT1965015.1, hCT1965016.1, hCT1965017.1, hCT2264496.0, hCT2264497.0, hCT2264507.0, hCT23036.3, hCT2355197.0	226672_s_at, 232870_at	NP_114408.3, NP_001152758.1, EAW73511.1, EAW73516.1, EAW73517.1, EAW73519.1, EAW73512.1, EAW73513.1, EAW73514.1, EAW73515.1, EAW73518.1, EAW73520.1
GeneID:6300	MAPK12	22	50,691,331	50,700,089	8,758	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5439, 4_A375_EGR1..1..8018	16601, 16585	downstream, downstream	0	1	1	13	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MAPK12	ERK3, SAPK-3, ERK6, MAPK12, SAPK3, P38GAMMA, PRKM12	mitogen-activated protein kinase 12	NM_002969, hCT2264476.0, hCT2355180.0	1556340_at, 1556341_s_at, 206106_at	NP_002960.2, EAW73522.1, EAW73521.1
GeneID:5600	MAPK11	22	50,702,142	50,708,779	6,637	-	1	4_A375_EGR1..1..8019	-5733	upstream	0	0	1	5	3	15	1	4_A375_EGR1..1	15	Gene MAPK11	P38B, SAPK2B, PRKM11, MAPK11, SAPK2, p38-2, p38Beta, P38BETA2	mitogen-activated protein kinase 11	NM_002751, hCT2264480.0, hCT2355178.0, hCT2355179.0	206040_s_at, 211499_s_at, 211500_at	NP_002742.3, EAW73526.1, EAW73524.1, EAW73525.1
GeneID:23654	PLXNB2	22	50,713,408	50,746,001	32,593	-	4	4_A375_EGR1..1..8019, 4_A375_EGR1..1..8020, 4_A375_EGR1..1..8021, 4_A375_EGR1..1..8022	31489, 23281, 21265, 10449	in gene, in gene, in gene, in gene	0	0	1	5.5	4.25	14.75	4	4_A375_EGR1..1	17	Gene PLXNB2	MM1, dJ402G11.3, PLXNB2, Nbla00445, KIAA0315, PLEXB2	plexin B2	NM_012401	208890_s_at, 211472_at	NP_036533.2
GeneID:414918	FAM116B	22	50,750,392	50,765,489	15,097	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3784, 2_A375_pNL97_plus_lncRNA_AR..1..5440	-207, -527	upstream, upstream	1	1	0	19	17	6	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene FAM116B	FAM116B, MGC33692	family with sequence similarity 116, member B	NM_001001794, hCT1613361.1, hCT2355192.0	228678_at, 229739_s_at	NP_001001794.3, EAW73529.1, EAW73528.1
GeneID:6305	SBF1	22	50,883,429	50,913,464	30,035	-	1	4_A375_EGR1..1..8023	-7032	upstream	0	0	1	7	7	15	1	4_A375_EGR1..1	15	Gene SBF1	DKFZp761D0422, MTMR5, MGC99700, SBF1	SET binding factor 1	NM_002972, hCT2264367.0, hCT2264370.0, hCT2355172.0, hCT2355173.0, hCT7921.1	212389_at, 212393_at, 222084_s_at, 39835_at	NP_002963.2, EAW73539.1, EAW73536.1, EAW73537.1, EAW73538.1, EAW73540.1
GeneID:79924	ADM2	22	50,920,012	50,924,866	4,854	+	1	4_A375_EGR1..1..8023	464	in gene	0	0	1	7	7	15	1	4_A375_EGR1..1	15	Gene ADM2	AM2, FLJ21135, ADM2, dJ579N16.4	adrenomedullin 2	NM_024866	220536_at	NP_079142.2
GeneID:55586	MIOX	22	50,925,213	50,928,750	3,537	+	1	4_A375_EGR1..1..8023	-4717	upstream	0	0	1	7	7	15	1	4_A375_EGR1..1	15	Gene MIOX	MGC90217, MIOX, ALDRL6	myo-inositol oxygenase	NM_017584, hCT2264034.0, hCT2355161.0, hCT2355162.0, hCT7918.3	224179_s_at	NP_060054.4, EAW73544.1, EAW73545.1, EAW73546.1, EAW73547.1
GeneID:29781	NCAPH2	22	50,946,645	50,963,209	16,564	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5441, 4_A375_EGR1..1..8024	18187, 22795	downstream, downstream	0	1	1	11	11	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene NCAPH2	384D8_6, CAP-H2, MGC2455, hCAP-H2, 384D8-2, MGC4133, MGC8840, MGC18000, NCAPH2, MGC5305, CAPH2, MGC15858	non-SMC condensin II complex, subunit H2	NM_014551, NM_001185011, NM_152299, hCT2263998.0, hCT2263999.0, hCT2264000.0, hCT2264002.0, hCT2264003.0, hCT2355159.0, hCT2355160.0, hCT7925.2	205066_s_at, 209718_at, 221633_at, 40640_at	NP_055366.3, NP_001171940.1, NP_689512.2, EAW73552.1, EAW73555.1, EAW73559.1, EAW73553.1, EAW73554.1, EAW73556.1, EAW73557.1, EAW73558.1
GeneID:9997	SCO2	22	50,961,997	50,964,868	2,871	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5441, 4_A375_EGR1..1..8024	36, -4572	in gene, upstream	0	1	1	11	11	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SCO2	MGC125825, MGC125823, SCO1L, SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	NM_005138, NM_001169109, NM_001169110, NM_001169111	205241_at	NP_005129.2, NP_001162580.1, NP_001162581.1, NP_001162582.1
GeneID:1890	TYMP	22	50,964,181	50,968,514	4,333	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5441, 4_A375_EGR1..1..8024	3662, -926	in gene, upstream	0	1	1	11	11	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene TYMP	MEDPS1, MTDPS1, ECGF, MNGIE, TP, hPD-ECGF, PDECGF, ECGF1, TYMP	thymidine phosphorylase	NM_001113755, NM_001953, NM_001113756	204858_s_at, 217497_at	NP_001107227.1, NP_001944.1, NP_001107228.1
GeneID:440836	ODF3B	22	50,968,836	50,971,006	2,170	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5441, 4_A375_EGR1..1..8024	6176, 1566	downstream, in gene	0	1	1	11	11	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ODF3B	ODF3L3, ODF3B	outer dense fiber of sperm tails 3B	NM_001014440	235257_at, 238325_s_at, 238326_at, 238327_at	NP_001014440.2
GeneID:23542	MAPK8IP2	22	51,039,131	51,049,979	10,848	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3785, 2_A375_pNL97_plus_lncRNA_AR..1..5442	-507, -523	upstream, upstream	1	1	0	20	23	6	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MAPK8IP2	JIP2, MAPK8IP2, PRKM8IPL, IB2	mitogen-activated protein kinase 8 interacting protein 2	NM_016431, NM_012324, hCT2264008.0, hCT2264009.0, hCT2264010.0, hCT7914.3	205050_s_at, 208603_s_at	NP_057515.1, NP_036456.1, EAW73577.1, EAW73578.1, EAW73579.1, EAW73580.1
GeneID:100506900	LOC100506900	22	51,061,182	51,062,326	1,144	-	1	4_A375_EGR1..1..8025	-3914	upstream	0	0	1	5	7	12	1	4_A375_EGR1..1	12	Gene LOC100506900		hypothetical LOC100506900	XR_109757		
GeneID:410	ARSA	22	51,063,449	51,066,607	3,158	-	1	4_A375_EGR1..1..8025	367	in gene	0	0	1	5	7	12	1	4_A375_EGR1..1	12	Gene ARSA	ARSA, MLD	arylsulfatase A	NM_001085425, NM_000487, NM_001085428, NM_001085426, NM_001085427, hCT1961563.1, hCT7912.3	204443_at	NP_001078894.1, NP_000478.2, NP_001078897.1, NP_001078895.1, NP_001078896.1, EAW73562.1, EAW73563.1
GeneID:642891	LOC642891	3	237,441	239,090	1,649	-	1	4_A375_EGR1..1..8026	82	in gene	0	0	1	4	6	20	1	4_A375_EGR1..1	20	Gene LOC642891		hypothetical LOC642891	XM_001714956, XM_931146, XM_943602	243432_at	XP_001715008.1, XP_936241.3, XP_948695.2
GeneID:10752	CHL1	3	238,650	451,096	212,446	+	1	4_A375_EGR1..1..8026	358	in gene	0	0	1	4	6	20	1	4_A375_EGR1..1	20	Gene CHL1	MGC132578, CALL, L1CAM2, CHL1, FLJ44930	cell adhesion molecule with homology to L1CAM (close homolog of L1)	NM_006614, hCT2275009.0, hCT2275010.0	204591_at, 234563_at	NP_006605.2, EAW63669.1, EAW63668.1
GeneID:27255	CNTN6	3	1,134,629	1,445,278	310,649	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3786	86139	in gene	1	0	0	16	12	6	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene CNTN6	CNTN6, MGC133256, NB3	contactin 6	NM_014461, hCT2354138.0, hCT31376.2	207195_at	NP_055276.1, EAW63672.1, EAW63671.1
GeneID:152330	CNTN4	3	2,142,247	3,099,645	957,398	+	1	4_A375_EGR1..1..8028	251769	in gene	0	0	1	5	7	19	1	4_A375_EGR1..1	19	Gene CNTN4	MGC33615, CNTN4, BIG-2, AXCAM, CNTN4A	contactin 4	NM_175607, NM_175612, NM_175613, hCT1957351.2, hCT2349777.0, hCT2349778.0, hCT2349779.0, hCT2349780.0, hCT31372.3	229084_at, 237177_at	NP_783200.1, NP_783301.1, NP_783302.1, EAW63873.1, EAW63876.1, EAW63878.1, EAW63874.1, EAW63875.1, EAW63877.1
GeneID:51095	TRNT1	3	3,168,600	3,190,707	22,107	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5444, 4_A375_EGR1..1..8029	72, 168	in gene, in gene	0	1	1	18	27	16	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene TRNT1	CGI-47, TRNT1, CCA1, MtCCA	tRNA nucleotidyl transferase, CCA-adding, 1	NM_182916, hCT2274314.1, hCT2274315.1, hCT2274317.0, hCT2274316.0, hCT2354092.0	1552625_a_at, 222754_at, 223814_at	NP_886552.2, EAW63885.1, EAW63886.1, EAW63887.1, EAW63888.1, EAW63889.1
GeneID:51185	CRBN	3	3,191,317	3,221,401	30,084	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3789, 2_A375_pNL97_plus_lncRNA_AR..1..5445	25, 25	in gene, in gene	1	1	0	102	127	13	1	2_A375_pNL97_plus_lncRNA_AR..1	127	Gene CRBN	MRT2A, CRBN, DKFZp781K0715, MGC27358	cereblon	NM_001173482, NM_016302, hCT2274405.0, hCT2274408.0, hCT2274406.0, hCT2274409.0, hCT2274411.0, hCT2274412.0, hCT2354025.0, hCT2354026.0	218142_s_at, 222533_at	NP_001166953.1, NP_057386.2, EAW63890.1, EAW63894.1, EAW63895.1, EAW63896.1, EAW63891.1, EAW63892.1, EAW63893.1, EAW63897.1
GeneID:6419	SETMAR	3	4,344,988	4,358,949	13,961	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3790	36	in gene	1	0	0	16	13	9	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene SETMAR	SETMAR, METNASE	SET domain and mariner transposase fusion gene	NM_006515, NR_024022, hCT1956760.0, hCT2277769.0, hCT5743.2	1554059_at, 1554060_s_at, 206554_x_at	NP_006506.3, EAW63904.1, EAW63903.1, EAW63905.1
GeneID:285362	SUMF1	3	4,402,829	4,508,966	106,137	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3791, 2_A375_pNL97_plus_lncRNA_AR..1..5446	70, 102	in gene, in gene	1	1	0	34	35	11	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene SUMF1	MGC150436, AAPA3037, SUMF1, FGE, MGC131853	sulfatase modifying factor 1	NM_182760, NM_001164674, NM_001164675, hCT1956761.1, hCT6226.3	226850_at	NP_877437.2, NP_001158146.1, NP_001158147.1, EAW63906.1, EAW63907.1
GeneID:3708	ITPR1	3	4,535,032	4,889,524	354,492	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3792, 2_A375_pNL97_plus_lncRNA_AR..1..5447	-168, -77	upstream, upstream	1	1	0	19	16	16	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene ITPR1	SCA15, INSP3R1, DKFZp313E1334, ITPR1, SCA16, IP3R1, DKFZp313N1434, IP3R	inositol 1,4,5-triphosphate receptor, type 1	NM_001099952, NM_002222, NM_001168272, hCT12824.3, hCT1956801.1, hCT2277792.0, hCT2277793.0, hCT2277795.0, hCT2277796.0, hCT2277797.0, hCT2277799.0	203710_at, 211323_s_at, 216944_s_at, 240052_at	NP_001093422.2, NP_002213.5, NP_001161744.1, EAW63910.1, EAW63913.1, EAW63915.1, EAW63908.1, EAW63909.1, EAW63911.1, EAW63912.1, EAW63914.1
GeneID:8553	BHLHE40	3	5,021,097	5,026,866	5,769	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5449	-1177	upstream	0	1	0	11	20	15	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene BHLHE40	STRA13, FLJ99214, BHLHE40, Stra14, SHARP-2, BHLHB2, DEC1, HLHB2	basic helix-loop-helix family, member e40	NM_003670, hCT11435.2, hCT2277802.0	201169_s_at, 201170_s_at	NP_003661.1, EAW63916.1, EAW63917.1
GeneID:55207	ARL8B	3	5,163,930	5,222,801	58,871	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3794, 2_A375_pNL97_plus_lncRNA_AR..1..5450	-56, -26	upstream, upstream	1	1	0	189	203	13	1	2_A375_pNL97_plus_lncRNA_AR..1	203	Gene ARL8B	ARL8B, FLJ10702, ARL10C, Gie1	ADP-ribosylation factor-like 8B	NM_018184, hCT12825.2, hCT1965391.1, hCT1965392.1, hCT2354015.0	217852_s_at, 222442_s_at	NP_060654.1, EAW63920.1, EAW63919.1, EAW63921.1, EAW63922.1
GeneID:2917	GRM7	3	6,902,802	7,783,218	880,416	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3795, 1_A375_pNL7_minus_lncRNA_AR..1..3796, 2_A375_pNL97_plus_lncRNA_AR..1..5451, 2_A375_pNL97_plus_lncRNA_AR..1..5452, 4_A375_EGR1..1..8030	49502, 128636, 49596, 644270, 707790	in gene, in gene, in gene, in gene, in gene	1	1	1	12	12	6.5	4	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene GRM7	MGLUR7, GPRC1G, FLJ40498, GRM7, GLUR7, MGLU7	glutamate receptor, metabotropic 7	NM_000844, NM_181874, hCT1643937.3, hCT2354051.0, hCT2354052.0	207548_at, 217006_s_at, 241049_at	NP_000835.1, NP_870989.1, EAW63933.1, EAW63934.1, EAW63935.1
GeneID:100288428	LOC100288428	3	8,282,834	8,543,344	260,510	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5454	-60	upstream	0	1	0	11	22	9	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100288428	FLJ42094	hypothetical LOC100288428	NR_033378		
GeneID:29995	LMCD1	3	8,543,511	8,609,806	66,295	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5454	-67	upstream	0	1	0	11	22	9	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LMCD1	LMCD1		NM_014583, hCT12835.2, hCT1966377.1	218574_s_at, 227317_at, 242787_at	NP_055398.1, EAW63936.1, EAW63937.1
GeneID:51066	C3orf32	3	8,861,317	8,893,737	32,420	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3797, 2_A375_pNL97_plus_lncRNA_AR..1..5455	22457, 22361	in gene, in gene	1	1	0	23	32	11	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene C3orf32	fls485, C3orf32	chromosome 3 open reading frame 32	NM_015931, hCT12833.2, hCT2274756.0, hCT2354081.0	206741_at	NP_057015.1, EAW63941.1, EAW63942.1, EAW63943.1
GeneID:56852	RAD18	3	8,918,880	9,005,159	86,279	-	1	1_A375_pNL7_minus_lncRNA_AR..1..3798	87	in gene	1	0	0	21	19	11	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene RAD18	RNF73, RAD18	RAD18 homolog (S. cerevisiae)	NM_020165, hCT12846.2, hCT2274749.0	223417_at, 224200_s_at	NP_064550.3, EAW63949.1, EAW63948.1
GeneID:25917	THUMPD3	3	9,404,717	9,428,475	23,758	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5457	34099	downstream	0	1	0	18	21	14	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene THUMPD3	DKFZp434F091, THUMPD3	THUMP domain containing 3	NM_015453, NM_001114092, hCT1797614.1, hCT1958785.1, hCT1958786.1, hCT2276212.0, hCT2276214.0, hCT2276215.0	223804_s_at, 225730_s_at, 225741_at, 242377_x_at	NP_056268.2, NP_001107564.1, EAW63954.1, EAW63955.1, EAW63956.1, EAW63958.1, EAW63957.1, EAW63959.1
GeneID:440944	LOC440944	3	9,430,537	9,439,174	8,637	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5457, 4_A375_EGR1..1..8031	356, -536	in gene, upstream	0	1	1	15	16.5	16	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC440944		hypothetical LOC440944	NR_027007	1557357_at, 232052_at	
GeneID:100507618	LOC100507618	3	9,435,634	9,438,752	3,118	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5457, 4_A375_EGR1..1..8031	-64, -960	upstream, upstream	0	1	1	15	16.5	16	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC100507618		putative uncharacterized protein FLJ46541-like	XM_003118871		XP_003118919.1
GeneID:55209	SETD5	3	9,439,403	9,519,838	80,435	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3799, 2_A375_pNL97_plus_lncRNA_AR..1..5457, 4_A375_EGR1..1..8031	25205, -587, 309	in gene, upstream, in gene	1	1	1	15.33	15.33	12	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SETD5	SETD5, FLJ10707, KIAA1757, DKFZp686J18276	SET domain containing 5	NM_001080517	1569105_at, 1569106_s_at, 221806_s_at, 222575_at, 244691_at	NP_001073986.1
GeneID:375323	LHFPL4	3	9,540,045	9,595,486	55,441	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5458	1390	in gene	0	1	0	13	42	6	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene LHFPL4	LHFPL4, MGC133162	lipoma HMGIC fusion partner-like 4	NM_198560, hCT12651.2	228422_at	NP_940962.1, EAW63964.1
GeneID:151835	CPNE9	3	9,745,510	9,771,592	26,082	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5459	27770	downstream	0	1	0	10	16	19	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CPNE9	KIAA4217, CPNE9	copine family member IX	NM_153635	239139_at	NP_705899.2
GeneID:7862	BRPF1	3	9,773,434	9,789,699	16,265	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5459	-154	upstream	0	1	0	10	16	19	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene BRPF1	BR140, BRPF1	bromodomain and PHD finger containing, 1	NM_001003694, NM_004634, hCT12637.4, hCT2276236.0, hCT2276237.0, hCT2276238.0, hCT2276239.0	204461_at	NP_001003694.1, NP_004625.2, EAW63972.1, EAW63973.1, EAW63975.1, EAW63976.1, EAW63974.1
GeneID:10474	TADA3	3	9,821,651	9,834,420	12,769	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5460, 4_A375_EGR1..1..8032	-204, 340	upstream, in gene	0	1	1	15	21	17	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TADA3	NGG1, ADA3, FLJ20221, FLJ21329, TADA3L, hADA3, TADA3	transcriptional adaptor 3	NM_006354, NM_133480, hCT12641.3, hCT2277616.0, hCT2277617.0, hCT2277618.0	211221_at, 215273_s_at	NP_006345.1, NP_597814.1, EAW63994.1, EAW63995.1, EAW63996.1, EAW63997.1
GeneID:10093	ARPC4	3	9,834,227	9,848,789	14,562	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5460, 4_A375_EGR1..1..8032	397, -147	in gene, upstream	0	1	1	15	21	17	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ARPC4	P20-ARC, ARC20, MGC13544, ARPC4, p20-Arc	actin related protein 2/3 complex, subunit 4, 20kDa	NM_005718, NM_001024959, NM_001024960	211672_s_at, 217817_at, 217818_s_at	NP_005709.1, NP_001020130.1, NP_001020131.1
GeneID:84522	JAGN1	3	9,932,271	9,936,033	3,762	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3800, 2_A375_pNL97_plus_lncRNA_AR..1..5461	81, 81	in gene, in gene	1	1	0	23	29	14	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene JAGN1	FLJ14602, GL009, JAGN1	jagunal homolog 1 (Drosophila)	NM_032492, hCT11665.1	223104_at	NP_115881.3, EAW64015.1
GeneID:84818	IL17RC	3	9,958,764	9,975,314	16,550	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3801, 2_A375_pNL97_plus_lncRNA_AR..1..5462	16692, 16692	downstream, downstream	1	1	0	19	36	13	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene IL17RC	MGC10763, FLJ98005, FLJ95963, IL17RC, IL17RL, IL17-RL	interleukin 17 receptor C	NM_153460, NM_032732, NM_153461, hCT2276270.1, hCT2276271.0, hCT2348419.0, hCT2348420.0, hCT2348421.0, hCT2348422.0, hCT2348423.0, hCT2348424.0, hCT2348425.0, hCT2348426.0, hCT2354088.0, hCT2354089.0	221926_s_at, 224514_x_at, 64440_at	NP_703190.1, NP_116121.2, NP_703191.1, EAW64022.1, EAW64023.1, EAW64024.1, EAW64021.1, EAW64025.1, EAW64026.1, EAW64027.1, EAW64028.1, EAW64029.1, EAW64030.1, EAW64032.1, EAW64031.1
GeneID:78987	CRELD1	3	9,975,524	9,987,097	11,573	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3801, 1_A375_pNL7_minus_lncRNA_AR..1..3802, 2_A375_pNL97_plus_lncRNA_AR..1..5462, 2_A375_pNL97_plus_lncRNA_AR..1..5463, 4_A375_EGR1..1..8033	-66, 12796, -66, 12760, 13116	upstream, downstream, upstream, downstream, downstream	1	1	1	39	60	17	2	2_A375_pNL97_plus_lncRNA_AR..1	64	Gene CRELD1	AVSD2, CRELD1, CIRRIN, DKFZp566D213	cysteine-rich with EGF-like domains 1	NM_001031717, NM_001077415, NM_015513, hCT2276251.1, hCT2276262.1, hCT2276263.0, hCT2348430.0, hCT2348431.0, hCT2348432.0, hCT2348433.0, hCT2348434.0, hCT2348435.0, hCT2354123.0	203368_at	NP_001026887.1, NP_001070883.1, NP_056328.2, EAW64034.1, EAW64036.1, EAW64043.1, EAW64035.1, EAW64037.1, EAW64038.1, EAW64039.1, EAW64040.1, EAW64041.1, EAW64042.1

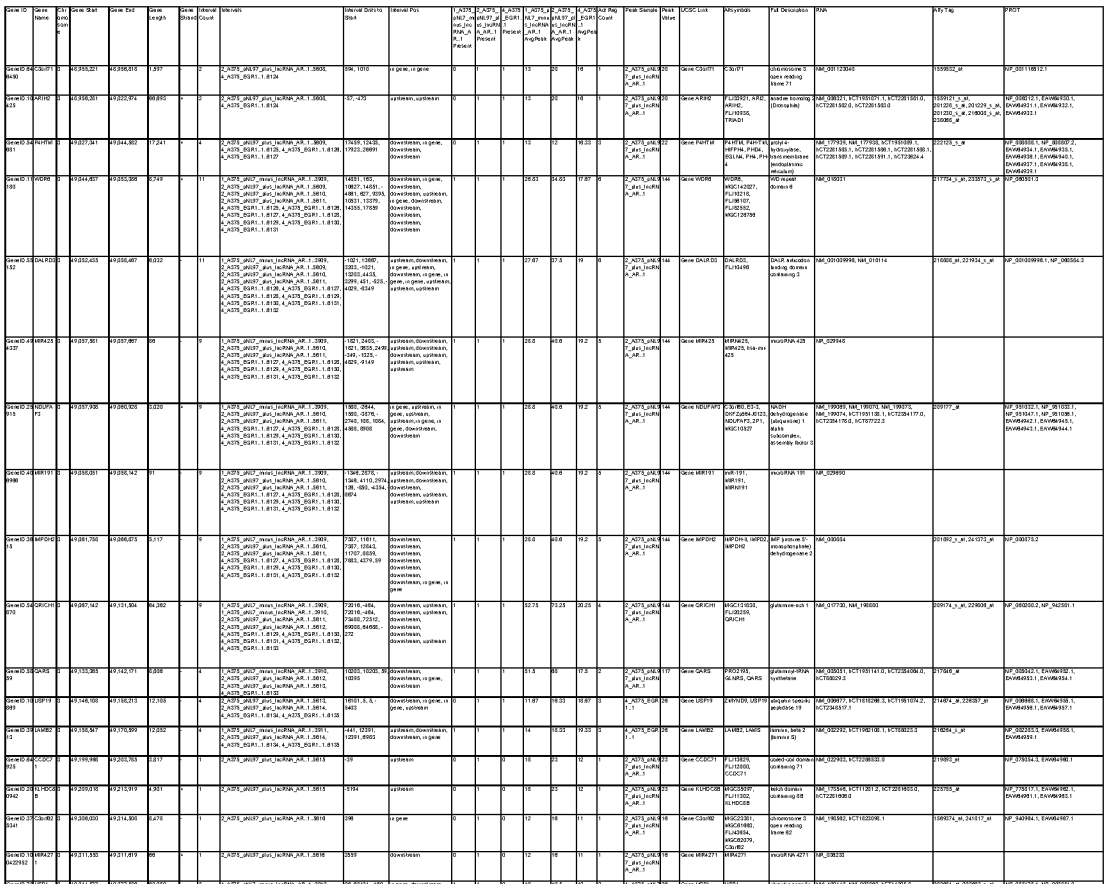
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:285368	PRRT3	3	9,987,226	9,994,078	6,852	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3802, 2_A375_pNL97_plus_lncRNA_AR..1..5463, 4_A375_EGR1..1..6033	5756, 5774, 5436	in gene, in gene, in gene	1	1	1	59	64	21	1	2_A375_pNL97_plus_lncRNA_AR..1	64	Gene PRRT3	FLJ33674, PRRT3, MGC105134, MGC33990	proline-rich transmembrane protein 3	NM_207351, hCT1642996.3, hCT2277607.0	1558308_at	NP_997234.3, EAW64044.1, EAW64045.1
GeneID:55831	TMEM111	3	10,005,636	10,028,522	22,886	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3803, 2_A375_pNL97_plus_lncRNA_AR..1..5464	10, -11	in gene, upstream	1	1	0	26	31	11	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene TMEM111	POB, TMEM111	transmembrane protein 111	NM_018447	215250_at, 217882_at	NP_060917.1
GeneID:442075	LOC442075	3	10,028,595	10,046,944	18,349	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3803, 2_A375_pNL97_plus_lncRNA_AR..1..5464	-83, -82	upstream, upstream	1	1	0	26	31	11	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene LOC442075	FLJ43570	hypothetical LOC442075	XR_112457, XR_110030, XR_113459	237005_at	
GeneID:2177	FANCD2	3	10,068,113	10,143,614	75,501	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3804, 2_A375_pNL97_plus_lncRNA_AR..1..5465	-65, -33	upstream, upstream	1	1	0	33	43	11	1	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene FANCD2	FACD, FLJ23826, FANCD2, FA4, FAD, FAD2, DKFZp762A223, FANCD, FA-D2	Fanconi anemia, complementation group D2	NM_033084, NM_001018115, hCT1952810.1, hCT2274945.0, hCT2274946.0, hCT2354166.0	1566889_at, 1566891_x_at, 223545_at, 242560_at	NP_149075.2, NP_001018125.1, EAW64055.1, EAW64056.1, EAW64057.1, EAW64058.1
GeneID:7428	VHL	3	10,183,319	10,193,762	10,443	+	1	4_A375_EGR1..1..6034	393	in gene	0	0	1	16	13	19	1	4_A375_EGR1..1	19	Gene VHL	RCA1, VHL, VHL1, HRCA1	von Hippel-Lindau tumor suppressor	NM_000551, NM_198156, hCT2274955.0, hCT2274957.0, hCT2274958.0, hCT2274960.0, hCT2354134.0	1559227_s_at, 203844_at	NP_000542.1, NP_937799.1, EAW64064.1, EAW64065.1, EAW64066.1, EAW64067.1, EAW64068.1
GeneID:3656	IRAK2	3	10,206,563	10,285,427	78,864	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5466, 4_A375_EGR1..1..6035	41469, 189	in gene, in gene	0	1	1	14.5	16	14	2	4_A375_EGR1..1	19	Gene IRAK2	IRAK2, MGC150550, IRAK-2	interleukin-1 receptor-associated kinase 2	NM_001570, hCT2274962.0	1553739_at, 1553740_a_at, 231779_at	NP_001561.3, EAW64069.1
GeneID:6396	SEC13	3	10,342,615	10,362,858	20,243	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5467	42	in gene	0	1	0	18	29	8	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene SEC13	npp-20, SEC13R, D3S1231E, SEC13L1, SEC13	SEC13 homolog (S. cerevisiae)	NM_183352, NM_001136232, NR_024272, NR_024273, hCT1962202.1, hCT1962203.1	207707_s_at	NP_899195.1, NP_001129704.1, EAW64077.1, EAW64078.1
GeneID:491	ATP2B2	3	10,365,707	10,547,288	181,581	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3805, 2_A375_pNL97_plus_lncRNA_AR..1..5467, 2_A375_pNL97_plus_lncRNA_AR..1..5468, 4_A375_EGR1..1..6036, 4_A375_EGR1..1..6037	45220, 184452, 45204, 162660, 6766	in gene, downstream, in gene, in gene, in gene	1	1	1	36.75	40.5	13.75	4	2_A375_pNL97_plus_lncRNA_AR..1	119	Gene ATP2B2	PMCA2, PMCA2i, ATP2B2, PMCA2a	ATPase, Ca++ transporting, plasma membrane 2	NM_001001331, NM_001683, hCT1952827.1, hCT1964891.1, hCT2277646.0, hCT2277647.0, hCT2277648.0, hCT2277650.0	204685_s_at, 211586_s_at, 216120_s_at, 234714_x_at, 234741_at	NP_001001331.1, NP_001674.2, EAW64079.1, EAW64080.1, EAW64082.1, EAW64083.1, EAW64081.1, EAW64084.1
GeneID:100422933	MIR378B	3	10,371,913	10,371,969	56	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5467	-9097	upstream	0	1	0	18	29	8	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene MIR378B	MIR378B	microRNA 378b	NR_036084		
GeneID:285370	LOC285370	3	10,801,169	10,805,877	4,708	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3809, 2_A375_pNL97_plus_lncRNA_AR..1..5473	10037, 10037	downstream, downstream	1	1	0	25	43	8	1	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene LOC285370		hypothetical LOC285370	NR_027102	1556447_at, 1556448_a_at	
GeneID:9686	VGLL4	3	11,597,544	11,762,220	164,676	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3811, 2_A375_pNL97_plus_lncRNA_AR..1..5476, 2_A375_pNL97_plus_lncRNA_AR..1..5477	152380, 152460, 110700	in gene, in gene, in gene	1	1	0	21	24.5	5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene VGLL4	KIAA0121, VGL-4, VGLL4	vestigial like 4 (Drosophila)	NM_014667, NM_001128219, NM_001128220, NM_001128221, hCT1816009.3, hCT1952811.2, hCT2287349.1, hCT2287350.1, hCT2287351.0, hCT2287352.1, hCT2287353.0, hCT2287354.1, hCT2354151.0	212399_s_at, 214004_s_at	NP_055482.2, NP_001121691.1, NP_001121692.1, NP_001121693.1, EAW64099.1, EAW64100.1, EAW64098.1, EAW64101.1, EAW64102.1, EAW64103.1, EAW64104.1, EAW64105.1, EAW64106.1
GeneID:100133039	LOC100133039	3	11,802,886	11,805,949	3,063	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3811, 2_A375_pNL97_plus_lncRNA_AR..1..5476	-3891, -3811	upstream, upstream	1	1	0	26	26	8	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene LOC100133039		hypothetical LOC100133039	XR_112484, XR_110031, XR_113469		
GeneID:132001	C3orf31	3	11,831,919	11,888,352	56,433	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3812, 2_A375_pNL97_plus_lncRNA_AR..1..5478	-64, -64	upstream, upstream	1	1	0	193	174	13	1	1_A375_pNL7_minus_lncRNA_AR..1	193	Gene C3orf31	MGC16471, C3orf31, DKFZp434E0519	chromosome 3 open reading frame 31	NM_138807, hCT19191.1, hCT2287346.0, hCT2344411.0, hCT2344412.0, hCT2344413.0, hCT2344414.0, hCT2344415.0	226815_at, 231956_at, 234697_x_at	NP_620162.1, EAW64113.1, EAW64108.1, EAW64109.1, EAW64110.1, EAW64111.1, EAW64112.1, EAW64114.1
GeneID:6854	SYN2	3	12,045,862	12,233,532	187,670	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3813, 2_A375_pNL97_plus_lncRNA_AR..1..5479	151642, 151642	in gene, in gene	1	1	0	20	25	9	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene SYN2	SYNIIb, SYNII, SYNIIa, SYN2	synapsin II	NM_133625, NM_003178, hCT19487.2, hCT2274906.0, hCT2274907.0, hCT2274908.0, hCT2354053.0	1553037_a_at, 210247_at, 210315_at, 229039_at, 240197_at	NP_598328.1, NP_003169.2, EAW64118.1, EAW64119.1, EAW64120.1, EAW64121.1, EAW64117.1
GeneID:7079	TIMP4	3	12,194,568	12,200,647	6,079	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3813, 2_A375_pNL97_plus_lncRNA_AR..1..5479	3143, 3143	in gene, in gene	1	1	0	20	25	9	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene TIMP4	TIMP4		NM_003256, hCT19466.3	206243_at	NP_003247.1, EAW64122.1
GeneID:5468	PPARG	3	12,329,349	12,475,855	146,506	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3814, 2_A375_pNL97_plus_lncRNA_AR..1..5480	107963, 118043	in gene, in gene	1	1	0	10.5	12	5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PPARG	PPARG2, PPARG1, CIMT1, NR1C3, PPARG, PPARgamma, GLM1	peroxisome proliferator-activated receptor gamma	NM_005037, NM_138712, NM_015869, NM_138711, hCT19464.2, hCT1951704.1, hCT2275109.0	208510_s_at	NP_005028.4, NP_619726.2, NP_056953.2, NP_619725.2, EAW64124.1, EAW64125.1, EAW64123.1
GeneID:80746	TSEN2	3	12,525,931	12,574,820	48,889	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3815, 2_A375_pNL97_plus_lncRNA_AR..1..5481	165, 133	in gene, in gene	1	1	0	19	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TSEN2	SEN2L, TSEN2, MGC4440, MGC2776, SEN2, PCH2B	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	NM_025265, NM_001145392, NM_001145393, NM_001145394, NM_001145395, hCT19470.3, hCT2275119.0, hCT2275120.0, hCT2354093.0	219581_at, 244391_at	NP_079541.1, NP_001138864.1, NP_001138865.1, NP_001138866.1, NP_001138867.1, EAW64130.1, EAW64127.1, EAW64128.1, EAW64129.1
GeneID:23609	MKRN2	3	12,598,594	12,625,212	26,618	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3816, 2_A375_pNL97_plus_lncRNA_AR..1..5482	156, -66	in gene, upstream	1	1	0	22	26	13	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene MKRN2	RNF62, MKRN2, HSPC070	makorin ring finger protein 2	NM_014160, hCT19469.3, hCT2275122.0	216995_x_at, 218071_s_at, 222510_s_at	NP_054879.3, EAW64132.1, EAW64133.1
GeneID:5894	RAF1	3	12,625,100	12,705,700	80,600	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3817, 2_A375_pNL97_plus_lncRNA_AR..1..5483, 4_A375_EGR1..1..6038	-12, 4, -76	upstream, in gene, upstream	1	1	1	35	45	17	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene RAF1	Raf-1, RAF1, c-Raf, NS5, CRAF	v-raf-1 murine leukemia viral oncogene homolog 1	NM_002880, hCT19462.3, hCT2300428.0	1557675_at, 201244_s_at	NP_002871.1, EAW64134.1, EAW64135.1
GeneID:23066	CAND2	3	12,838,171	12,876,313	38,142	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5484	45013	downstream	0	1	0	13	26	13	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene CAND2	KIAA0667, TIP120B, CAND2, Tp120b	cullin-associated and neddylation-dissociated 2 (putative)	NM_012298, NM_001162499	213547_at	NP_036430.1, NP_001155971.1
GeneID:6161	RPL32	3	12,876,444	12,883,081	6,637	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5484	-103	upstream	0	1	0	13	26	13	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene RPL32	PP9932, RPL32, L32	ribosomal protein L32	NM_001007073, NM_001007074, NM_000994, hCT19461.3, hCT1951717.1	200674_s_at	NP_001007074.1, NP_001007075.1, NP_000985.1, EAW64144.1, EAW64145.1
GeneID:619563	SNORA7A	3	12,881,811	12,881,949	138	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5484	-1235	upstream	0	1	0	13	26	13	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene SNORA7A	ACA7, SNORA7A	small nucleolar RNA, H/ACA box 7A	NR_002582		
GeneID:9922	IQSEC1	3	12,938,719	13,114,617	175,898	-	8	1_A375_pNL7_minus_lncRNA_AR..1..3818, 2_A375_pNL97_plus_lncRNA_AR..1..5485, 2_A375_pNL97_plus_lncRNA_AR..1..5486, 2_A375_pNL97_plus_lncRNA_AR..1..5487, 4_A375_EGR1..1..6039, 4_A375_EGR1..1..6040, 4_A375_EGR1..1..6041, 4_A375_EGR1..1..6042	78009, 124505, 78009, 18073, 137769, 120526, 80057, 78457	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	17.5	22.17	15.33	6	2_A375_pNL97_plus_lncRNA_AR..1	71	Gene IQSEC1	ARFGEP100, IQSEC1, KIAA0763	IQ motif and Sec7 domain 1	NM_014869, NM_001134382, hCT17904.2, hCT1951716.1	203906_at, 203907_s_at, 243523_at	NP_055684.3, NP_001127854.1, EAW64147.1, EAW64148.1
GeneID:79885	HDAC11	3	13,521,715	13,547,924	26,209	+	1	4_A375_EGR1..1..6046	13053	in gene	0	0	1	4	5	15	1	4_A375_EGR1..1	15	Gene HDAC11	FLJ22237, HDAC11, HD11	histone deacetylase 11	NM_001136041, NM_024827, hCT1951719.1, hCT1951720.1, hCT1951721.1, hCT1951722.1, hCT1951723.1, hCT19543.3, hCT1965797.1, hCT2354065.0, hCT2354066.0, hCT2354067.0, hCT2354068.0, hCT2354069.0, hCT2354070.0	219847_at	NP_001129513.1, NP_079103.2, EAW64157.1, EAW64160.1, EAW64164.1, EAW64166.1, EAW64158.1, EAW64159.1, EAW64161.1, EAW64162.1, EAW64163.1, EAW64165.1, EAW64167.1, EAW64168.1, EAW64169.1
GeneID:2199	FBLN2	3	13,590,625	13,679,922	89,297	+	1	4_A375_EGR1..1..6046	22267	in gene	0	0	1	5	5	15	1	4_A375_EGR1..1	15	Gene FBLN2	FBLN2		NM_001004019, NM_001998, NM_001165035, hCT1951698.2, hCT2275105.1	203886_s_at	NP_001004019.1, NP_001989.2, NP_001158507.1, EAW64170.1, EAW64171.1
GeneID:100293612	LOC100293612	3	13,889,246	13,895,947	6,701	-	1	4_A375_EGR1..1..6049	715	in gene	0	0	1	6	5	16	1	4_A375_EGR1..1	16	Gene LOC100293612		hypothetical LOC100293612	XR_112482, XR_110033, XR_113471		
GeneID:285375	LOC285375	3	13,692,221	13,788,132	95,911	+	1	4_A375_EGR1..1..6049	3011	in gene	0	0	1	6	5	16	1	4_A375_EGR1..1	16	Gene LOC285375		hypothetical LOC285375	NR_027103	1563043_at	
GeneID:7476	WNT7A	3	13,860,082	13,921,618	61,536	-	1	4_A375_EGR1..1..6050	1442	in gene	0	0	1	4	7	16	1	4_A375_EGR1..1	16	Gene WNT7A	WNT7A		NM_004625, hCT17903.3, hCT1951703.1	210248_at	NP_004616.2, EAW64173.1, EAW64174.1
GeneID:100132526	LOC100132526	3	13,974,553	13,978,444	3,891	+	1	4_A375_EGR1..1..6051	1959	in gene	0	0	1	4	3	17	1	4_A375_EGR1..1	17	Gene LOC100132526		FYVE, RhoGEF and PH domain containing 5 pseudogene	NR_036461		
GeneID:131474	CHCHD4	3	14,153,577	14,166,371	12,794	-	3	2_A375_pNL97_plus_lncRNA_AR..1..5489, 4_A375_EGR1..1..6053, 4_A375_EGR1..1..6054	-629, -528, -9085	upstream, upstream, upstream	0	1	1	9	16	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CHCHD4	MIA40, CHCHD4, TIMM40, FLJ31709	coiled-coil-helix-coiled-coil-helix domain containing 4	NM_001098502, NM_144636, hCT1640260.3, hCT1951690.1, hCT1964863.1, hCT2275226.0	229595_at	NP_001091972.1, NP_653237.1, EAW64180.1, EAW64181.1, EAW64182.1, EAW64183.1
GeneID:79188	TMEM43	3	14,166,440	14,185,180	18,740	+	3	2_A375_pNL97_plus_lncRNA_AR..1..5489, 4_A375_EGR1..1..6053, 4_A375_EGR1..1..6054	760, 459, 9016	in gene, in gene, in gene	0	1	1	9	16	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TMEM43	LUMA, ARVD5, TMEM43, DKFZp586G1919, MGC3222, ARVC5	transmembrane protein 43	NM_024334, hCT18374.3, hCT2275076.0, hCT2275077.0, hCT2354094.0	217795_s_at, 222418_s_at, 233480_at, 233489_at	NP_077310.1, EAW64184.1, EAW64185.1, EAW64186.1, EAW64187.1
GeneID:7508	XPC	3	14,186,647	14,220,172	33,525	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3820, 2_A375_pNL97_plus_lncRNA_AR..1..5490	204, 204	in gene, in gene	1	1	0	21	24	11	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene XPC	XPC, RAD4, XP3, XPCC	xeroderma pigmentosum, complementation group C	NM_004628, NM_001145769, NR_027299, hCT18373.3, hCT2275219.0	209375_at	NP_004619.3, NP_001139241.1, EAW64188.1, EAW64189.1
GeneID:27258	LSM3	3	14,220,228	14,239,869	19,641	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3820, 2_A375_pNL97_plus_lncRNA_AR..1..5490	-260, -260	upstream, upstream	1	1	0	21	24	11	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LSM3	USS2, SMX4, YLR438C, LSM3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_014463, hCT17683.3	202209_at	NP_055278.1, EAW64190.1
GeneID:6533	SLC6A6	3	14,444,106	14,530,857	86,751	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3821, 2_A375_pNL97_plus_lncRNA_AR..1..5492, 2_A375_pNL97_plus_lncRNA_AR..1..5493, 4_A375_EGR1..1..6057	29814, 29814, 50358, 10454	in gene, in gene, in gene, in gene	1	1	1	14	14	14.33	3	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene SLC6A6	MGC131729, SLC6A6, TAUT, MGC10619	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	NM_003043, NM_001134367, NM_001134368, hCT2275545.0, hCT2275547.0, hCT2275548.0, hCT2275549.0	205920_at, 205921_s_at, 211030_s_at, 228754_at, 228756_at	NP_003034.2, NP_001127839.1, NP_001127840.1, EAW64192.1, EAW64194.1, EAW64195.1, EAW64193.1
GeneID:80852	GRIP2	3	14,530,619	14,583,588	52,969	-	1	4_A375_EGR1..1..6058	32628	in gene	0	0	1	13	14	18	1	4_A375_EGR1..1	18	Gene GRIP2	GRIP2		NM_001080423	216481_at	NP_001073892.2
GeneID:84077	C3orf20	3	14,716,606	14,814,543	97,937	+	1	4_A375_EGR1..1..6060	97698	in gene	0	0	1	4	5	15	1	4_A375_EGR1..1	15	Gene C3orf20	DKFZp434N1817, C3orf20	chromosome 3 open reading frame 20	NM_001184957, NM_001184958, NM_032137, hCT1644238.3, hCT2348935.0, hCT2354085.0	224273_at	NP_001171886.1, NP_001171887.1, NP_115513.4, EAW64204.1, EAW64205.1, EAW64206.1
GeneID:152273	FGD5	3	14,860,469	14,976,072	115,603	+	1	4_A375_EGR1..1..6061	58539	in gene	0	0	1	7	7	21	1	4_A375_EGR1..1	21	Gene FGD5	ZFYVE23, FGD5	FYVE, RhoGEF and PH domain containing 5	NM_152536, hCT2348959.0, hCT2348960.0	226984_at, 226985_at	NP_689749.3, EAW64208.1, EAW64209.1
GeneID:100505673	LOC100505673	3	14,961,857	14,989,931	28,074	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5496	1227	in gene	0	1	0	8	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100505673		hypothetical LOC100505673	XR_112481, XR_110037, XR_113476		
GeneID:100505641	LOC100505641	3	14,984,287	14,989,400	5,113	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5496	696	in gene	0	1	0	8	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC100505641		hypothetical LOC100505641	XR_110036, XR_110034, XR_110035		
GeneID:7182	NR2C2	3	14,989,236	15,090,780	101,544	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5496	-532	upstream	0	1	0	8	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene NR2C2	TAK1, hTAK1, NR2C2, TR4, TR2R1	nuclear receptor subfamily 2, group C, member 2	NM_003298, hCT1951707.1, hCT2275559.0, hCT2275560.0	206038_s_at, 225477_s_at	NP_003289.2, EAW64215.1, EAW64213.1, EAW64214.1
GeneID:64145	ZFYVE20	3	15,111,580	15,140,655	29,075	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3823, 2_A375_pNL97_plus_lncRNA_AR..1..5497	-1, -49	upstream, upstream	1	1	0	46	43	14	1	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene ZFYVE20	Rabenosyn-5, MGC126210, FLJ34993, ZFYVE20	zinc finger, FYVE domain containing 20	NM_022340, hCT18974.3, hCT2276756.0	1569714_at, 226561_at, 231785_at	NP_071735.2, EAW64221.1, EAW64220.1
GeneID:23473	CAPN7	3	15,247,733	15,294,423	46,690	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5498	235	in gene	0	1	0	13	23	7	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CAPN7	FLJ36423, PALBH, CALPAIN7, CAPN7	calpain 7	NM_014296, hCT18962.3, hCT1965791.1	203356_at, 203357_s_at	NP_055111.1, EAW64223.1, EAW64224.1
GeneID:100505696	LOC100505696	3	15,295,159	15,305,995	10,836	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3824	15945	downstream	1	0	0	24	19	8	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene LOC100505696		hypothetical LOC100505696	XR_112477, XR_110038, XR_113477		
GeneID:9467	SH3BP5	3	15,296,357	15,382,901	86,544	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3824, 1_A375_pNL7_minus_lncRNA_AR..1..3825, 1_A375_pNL7_minus_lncRNA_AR..1..3826, 2_A375_pNL97_plus_lncRNA_AR..1..5499, 2_A375_pNL97_plus_lncRNA_AR..1..5500, 2_A375_pNL97_plus_lncRNA_AR..1..5501	71797, 40437, 9173, 40465, 30517, 9365	in gene, in gene, in gene, in gene, in gene, in gene	1	1	0	22.5	23	7.75	4	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene SH3BP5	SAB, SH3BP5	SH3-domain binding protein 5 (BTK-associated)	NM_004844, NM_001018009, hCT17896.3, hCT1951702.1, hCT2276739.0, hCT2354115.0	201810_s_at, 201811_x_at, 227591_at	NP_004835.2, NP_001018009.2, EAW64225.1, EAW64226.1, EAW64227.1, EAW64228.1
GeneID:131965	METTL6	3	15,451,377	15,469,042	17,665	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5502	434	in gene	0	1	0	10	14	11	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene METTL6	METTL6, MGC24132	methyltransferase like 6	NM_152396, hCT1640278.4, hCT1964861.1	1553668_at, 1553669_s_at, 1557991_at, 232102_at	NP_689609.2, EAW64232.1, EAW64233.1
GeneID:85403	EAF1	3	15,469,064	15,484,120	15,056	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5502	-456	upstream	0	1	0	10	14	11	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene EAF1	EAF1		NM_033083, hCT18969.4	226952_at	NP_149074.3, EAW64234.1
GeneID:686	BTD	3	15,643,255	15,687,325	44,070	+	1	4_A375_EGR1..1..6062	50841	downstream	0	0	1	5	7	12	1	4_A375_EGR1..1	12	Gene BTD	BTD	biotinidase	NM_000060, hCT18789.3, hCT1951705.1, hCT1951706.1	204167_at, 214117_s_at	NP_000051.1, EAW64254.1, EAW64255.1, EAW64256.1
GeneID:100505737	LOC100505737	3	15,676,947	15,683,820	6,873	-	1	4_A375_EGR1..1..6062	-10076	upstream	0	0	1	5	7	12	1	4_A375_EGR1..1	12	Gene LOC100505737		hypothetical LOC100505737	XR_110040		
GeneID:23243	ANKRD28	3	15,708,743	15,901,053	192,310	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5503, 2_A375_pNL97_plus_lncRNA_AR..1..5504	413, -707	in gene, upstream	0	1	0	14.5	18	11	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ANKRD28	PITK, KIAA0379, ANKRD28	ankyrin repeat domain 28	NM_015199, NM_001195098, NM_001195099, hCT1951695.1, hCT2348854.0, hCT2348855.0, hCT2348856.0, hCT2348857.0, hCT2348858.0, hCT2348859.0, hCT2348860.0, hCT2348861.0	1561079_at, 213035_at, 226025_at, 229307_at	NP_056014.2, NP_001182027.1, NP_001182028.1, EAW64258.1, EAW64259.1, EAW64262.1, EAW64257.1, EAW64260.1, EAW64261.1, EAW64263.1, EAW64264.1, EAW64265.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:30	ACAA1	3	38,164,201	38,178,733	14,532	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3862, 1_A375_pNL7_minus_lncRNA_AR..1..3863	-259, -1427	upstream, upstream	1	0	0	17	16.5	8	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ACAA1	THIO, ACAA, ACAA1, PTHIO	acetyl-CoA acyltransferase 1	NM_001607, NM_001130410, NR_024024, hCT1967980.1, hCT2278964.0, hCT2278965.0, hCT2278968.0, hCT2278966.0, hCT33702.3	202025_x_at, 214274_s_at	NP_001598.1, NP_001123882.1, EAW64513.1, EAW64515.1, EAW64516.1, EAW64517.1, EAW64514.1, EAW64518.1
GeneID:4615	MYD88	3	38,179,969	38,184,513	4,544	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3862, 1_A375_pNL7_minus_lncRNA_AR..1..3863	-977, 191	upstream, in gene	1	0	0	17	16.5	8	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene MYD88	MYD88D, MYD88	myeloid differentiation primary response gene (88)	NM_002468, NM_001172566, NM_001172567, NM_001172568, NM_001172569, hCT2354031.0, hCT33703.2	209124_at	NP_002459.2, NP_001166037.1, NP_001166038.1, NP_001166039.1, NP_001166040.1, EAW64520.1, EAW64521.1
GeneID:9942	XYLB	3	38,388,251	38,456,467	68,216	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3864, 2_A375_pNL97_plus_lncRNA_AR..1..5552	37, 101	in gene, in gene	1	1	0	22	27	14	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene XYLB	XYLB, FLJ12539, FLJ22075, FLJ10343	xylulokinase homolog (H. influenzae)	NM_005108, hCT2278368.0, hCT2278370.0, hCT2354024.0, hCT33700.1	1569683_at, 208317_at, 208318_s_at, 214778_x_at	NP_005099.2, EAW64531.1, EAW64532.1, EAW64533.1, EAW64534.1
GeneID:93	ACVR2B	3	38,495,790	38,534,633	38,843	+	1	4_A375_EGR1..1..8078	25570	in gene	0	0	1	11	10	16	1	4_A375_EGR1..1	16	Gene ACVR2B	ACTRIIB, ACVR2B, ActR-IIB, MGC116908	activin A receptor, type IIB	NM_001106, hCT33897.2	1559548_at, 220028_at, 236126_at	NP_001097.2, EAW64536.1
GeneID:6331	SCN5A	3	38,589,553	38,691,164	101,611	-	1	4_A375_EGR1..1..8079	380	in gene	0	0	1	5	8	16	1	4_A375_EGR1..1	16	Gene SCN5A	CDCD2, HB2, PFHB1, Nav1.5, VF1, HH1, ICCD, HBBD, HB1, CMD1E, SCN5A, LQT3, SSS1, IVF, CMPD2	sodium channel, voltage-gated, type V, alpha subunit	NM_198056, NM_000335, NM_001099404, NM_001099405, NM_001160160, NM_001160161, hCT2278957.1, hCT2278959.1, hCT33707.4	207413_s_at	NP_932173.1, NP_000326.2, NP_001092874.1, NP_001092875.1, NP_001153632.1, NP_001153633.1, EAW64540.1, EAW64541.1, EAW64542.1
GeneID:57599	WDR48	3	39,093,507	39,137,882	44,375	+	1	4_A375_EGR1..1..8080	52157	downstream	0	0	1	8	5	16	1	4_A375_EGR1..1	16	Gene WDR48	DKFZp686G1794, P80, KIAA1449, WDR48, UAF1	WD repeat domain 48	NM_020839, hCT10094.3, hCT2279898.0, hCT2279899.0, hCT2354044.0	221735_at, 222157_s_at, 56919_at, 65591_at	NP_065890.1, EAW64550.1, EAW64548.1, EAW64549.1, EAW64551.1
GeneID:64689	GORASP1	3	39,138,091	39,149,130	11,039	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3866, 2_A375_pNL97_plus_lncRNA_AR..1..5555, 4_A375_EGR1..1..8080	10, 74, 3466	in gene, in gene, in gene	1	1	1	16	13	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene GORASP1	P65, GORASP1, MGC118894, GOLPH5, GRASP65, FLJ23443, MGC118897	golgi reassembly stacking protein 1, 65kDa	NM_031899, hCT10093.3, hCT1967892.1, hCT2280039.0, hCT2280040.0, hCT2280043.0, hCT2354039.0, hCT2354040.0, hCT2354041.0, hCT2354042.0	215749_s_at, 243677_at	NP_114105.1, EAW64559.1, EAW64552.1, EAW64553.1, EAW64554.1, EAW64558.1, EAW64555.1, EAW64556.1, EAW64557.1, EAW64560.1
GeneID:199223	TTC21A	3	39,149,152	39,180,394	31,242	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3866, 2_A375_pNL97_plus_lncRNA_AR..1..5555, 2_A375_pNL97_plus_lncRNA_AR..1..5556, 4_A375_EGR1..1..8080	-32, -98, 39403, -3466	upstream, upstream, downstream, upstream	1	1	1	16.33	15	14	3	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene TTC21A	TTC21A, STI2, MGC70523, DKFZp686P18239, MGC156293	tetratricopeptide repeat domain 21A	NM_145755, NM_001105513, hCT10095.3, hCT2344910.0, hCT2344911.0, hCT2344912.0	230997_at, 232308_at	NP_665698.2, NP_001098983.2, EAW64561.1, EAW64562.1, EAW64563.1, EAW64564.1
GeneID:64651	CSRNP1	3	39,183,342	39,195,102	11,760	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3867, 2_A375_pNL97_plus_lncRNA_AR..1..5556, 2_A375_pNL97_plus_lncRNA_AR..1..5557	862, 6547, 750	in gene, in gene, in gene	1	1	0	23	24	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene CSRNP1	DKFZp566F164, CSRNP-1, URAX1, FAM130B, TAIP-3, AXUD1, CSRNP1	cysteine-serine-rich nuclear protein 1	NM_033027, hCT1640204.3, hCT2280035.0, hCT2280036.0, hCT2280037.0, hCT2354013.0, hCT2354014.0	225557_at	NP_149016.2, EAW64568.1, EAW64565.1, EAW64567.1, EAW64569.1, EAW64570.1, EAW64566.1
GeneID:165904	XIRP1	3	39,224,707	39,234,077	9,370	-	1	4_A375_EGR1..1..8081	5309	in gene	0	0	1	4	8	19	1	4_A375_EGR1..1	19	Gene XIRP1	CMYA1, XIRP1, Xin, DKFZp779C1947, DKFZp451D042, DKFZp779C1255	xin actin-binding repeat containing 1	NM_194293, hCT1645271.3, hCT2354124.0, hCT2354125.0	235042_at	NP_919269.2, EAW64572.1, EAW64573.1, EAW64574.1
GeneID:54977	SLC25A38	3	39,424,815	39,438,819	14,004	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3868, 1_A375_pNL7_minus_lncRNA_AR..1..3869, 2_A375_pNL97_plus_lncRNA_AR..1..5559, 4_A375_EGR1..1..8082	209, 23505, 401, 209	in gene, downstream, in gene, in gene	1	1	1	16.5	18	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SLC25A38	SLC25A38, FLJ22703, FLJ20551	solute carrier family 25, member 38	NM_017875, hCT2279708.0, hCT2279709.0, hCT8068.3	217961_at	NP_060345.2, EAW64579.1, EAW64580.1, EAW64581.1
GeneID:3921	RPSA	3	39,448,204	39,454,033	5,829	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3869	116	in gene	1	0	0	16	14	12	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene RPSA	p40, LAMBR, 67LR, SA, LBP, LRP, RPSA, LAMR1, 37LRP	ribosomal protein SA	NM_001012321, NM_002295, hCT2279710.0, hCT2279711.1, hCT2279712.1, hCT2279713.1, hCT2279714.1, hCT2279715.1	212955_s_at	NP_001012321.1, NP_002286.2, EAW64582.1, EAW64585.1, EAW64586.1, EAW64587.1, EAW64583.1, EAW64584.1
GeneID:574040	SNORA6	3	39,449,882	39,450,030	148	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3869	-1582	upstream	1	0	0	16	14	12	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene SNORA6	ACA6, SNORA6	small nucleolar RNA, H/ACA box 6	NR_002325		
GeneID:6044	SNORA62	3	39,452,545	39,452,698	153	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3869	-4225	upstream	1	0	0	16	14	12	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene SNORA62	RNU106, E2, E2-1, RNE2, SNORA62	small nucleolar RNA, H/ACA box 62	NR_002324		
GeneID:25924	MYRIP	3	39,851,303	40,301,812	450,509	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3871	449017	in gene	1	0	0	21	14	4	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene MYRIP	SLAC2C, MGC130034, MGC130035, DKFZp586F1018, SLAC2-C, MYRIP, FLJ44025	myosin VIIA and Rab interacting protein	NM_015460, hCT2344791.0, hCT2354188.0	214156_at	NP_056275.2, EAW64596.1, EAW64595.1
GeneID:440952	FLJ33065	3	40,214,636	40,351,189	136,553	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3871, 1_A375_pNL7_minus_lncRNA_AR..1..3872, 2_A375_pNL97_plus_lncRNA_AR..1..5560	50689, 101, 65	in gene, in gene, in gene	1	1	0	23	22	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene FLJ33065		hypothetical LOC440952	NR_033965	1556248_at, 1556249_a_at, 1557212_at, 242730_at	
GeneID:10289	EIF1B	3	40,351,173	40,353,915	2,742	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3872, 2_A375_pNL97_plus_lncRNA_AR..1..5560	-65, -69	upstream, upstream	1	1	0	25	30	13	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene EIF1B	GC20, EIF1B	eukaryotic translation initiation factor 1B	NM_005875, hCT2278072.0, hCT7455.2	201738_at, 237968_at	NP_005866.1, EAW64598.1, EAW64599.1
GeneID:285267	ZNF619	3	40,518,604	40,531,728	13,124	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5561	-44	upstream	0	1	0	8	19	9	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ZNF619	FLJ90764, ZNF619	zinc finger protein 619	NM_001145083, NM_001145082, NM_001145093, NR_026746, hCT1816430.2, hCT2354021.0	1552636_at	NP_001138555.1, NP_001138554.1, NP_001138565.1, EAW64611.1, EAW64612.1
GeneID:253639	ZNF620	3	40,547,530	40,559,200	11,670	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3873, 2_A375_pNL97_plus_lncRNA_AR..1..5562	18891, 18846	downstream, downstream	1	1	0	21	20	15	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ZNF620	MGC50836, ZNF620	zinc finger protein 620	NM_175888, NR_024114, hCT2348396.1, hCT2348397.1, hCT2348398.1, hCT2354168.0	1558743_at	NP_787084.1, EAW64615.1, EAW64613.1, EAW64614.1, EAW64616.1
GeneID:285268	ZNF621	3	40,566,376	40,581,043	14,667	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3873, 2_A375_pNL97_plus_lncRNA_AR..1..5562	45, -200	in gene, upstream	1	1	0	21	20	15	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ZNF621	ZNF621, DKFZp686B11107, MGC126666, FLJ45246, FLJ23786	zinc finger protein 621	NM_198484, NM_001098414	1558820_at, 230164_at, 241499_at	NP_940886.1, NP_001091884.1
GeneID:1499	CTNNB1	3	41,240,942	41,281,939	40,997	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3875, 2_A375_pNL97_plus_lncRNA_AR..1..5564, 4_A375_EGR1..1..8083	82, 82, 82	in gene, in gene, in gene	1	1	1	16	18	21	1	4_A375_EGR1..1	21	Gene CTNNB1	DKFZp686D02253, CTNNB, CTNNB1, FLJ25606, FLJ37923	catenin (cadherin-associated protein), beta 1, 88kDa	NM_001098210, NM_001904, NM_001098209, hCT18957.3, hCT2277743.0, hCT2277748.0, hCT2354113.0	1554411_at, 201533_at, 223679_at	NP_001091680.1, NP_001895.1, NP_001091679.1, EAW64625.1, EAW64626.1, EAW64628.1, EAW64627.1
GeneID:54986	ULK4	3	41,288,090	42,003,660	715,570	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3876, 2_A375_pNL97_plus_lncRNA_AR..1..5565	76, 76	in gene, in gene	1	1	0	27	28	9	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene ULK4	DKFZp434E1822, REC01035, FAM7C1, ULK4, FLJ20574	unc-51-like kinase 4 (C. elegans)	NM_017886	220958_at, 231149_s_at, 232206_at, 244166_s_at	NP_060356.2
GeneID:100287063	LOC100287063	3	42,002,914	42,128,865	125,951	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3876, 1_A375_pNL7_minus_lncRNA_AR..1..3877, 2_A375_pNL97_plus_lncRNA_AR..1..5565	670, 119246, 670	in gene, in gene, in gene	1	1	0	21	18	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene LOC100287063		hypothetical protein LOC100287063	XM_003119897, XM_002342327, XM_002346486		XP_003119945.1, XP_002342368.2, XP_002346529.2
GeneID:7433	VIPR1	3	42,544,104	42,579,085	34,981	+	2	4_A375_EGR1..1..8084, 4_A375_EGR1..1..8085	-4264, 37624	upstream, downstream	0	0	1	5.5	8.5	15.5	2	4_A375_EGR1..1	18	Gene VIPR1	PACAP-R-2, VPAC1, VPCAP1R, VAPC1, V1RG, VIRG, RDC1, FLJ41949, HVR1, II, VIPR, VIPR1	vasoactive intestinal peptide receptor 1	NM_004624, hCT20008.3, hCT2283223.0, hCT2283225.0, hCT2354022.0	205019_s_at	NP_004615.2, EAW64652.1, EAW64649.1, EAW64650.1, EAW64651.1
GeneID:9117	SEC22C	3	42,589,472	42,623,428	33,956	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3878, 2_A375_pNL97_plus_lncRNA_AR..1..5567, 4_A375_EGR1..1..8085	-252, -492, 41700	upstream, upstream, downstream	1	1	1	13	14.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SEC22C	DKFZp761F2321, MGC13261, SEC22L3, SEC22C, MGC5373	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	NM_032970, NM_004206, hCT2283842.0, hCT2283843.0, hCT2283844.0, hCT2283845.0	224470_at, 225460_at, 235120_at, 236268_at, 239013_at, 239056_at	NP_116752.1, NP_004197.1, EAW64653.1, EAW64654.1, EAW64655.1, EAW64656.1
GeneID:51188	SS18L2	3	42,632,298	42,636,490	4,192	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3878, 1_A375_pNL7_minus_lncRNA_AR..1..3879, 2_A375_pNL97_plus_lncRNA_AR..1..5567, 4_A375_EGR1..1..8086	-8618, 9670, -8378, 9614	upstream, downstream, upstream, downstream	1	1	1	18	17	20.5	2	4_A375_EGR1..1	26	Gene SS18L2	SS18L2, KIAA-iso	synovial sarcoma translocation gene on chromosome 18-like 2	NM_016305, hCT20016.2, hCT2283228.0	218283_at	NP_057389.1, EAW64658.1, EAW64657.1
GeneID:4820	NKTR	3	42,642,147	42,690,233	48,086	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3879, 4_A375_EGR1..1..8086, 4_A375_EGR1..1..8087	-179, -35, 53309	upstream, upstream, downstream	1	0	1	13.5	12.5	22	2	4_A375_EGR1..1	26	Gene NKTR	DKFZp686G0426, DKFZp686F1754, MGC90527, DKFZp686N24126, NKTR, p104, DKFZp686J06106	natural killer-tumor recognition sequence	NM_005385, hCT2283230.0, hCT2283231.0, hCT2354019.0	1557736_at, 1557737_s_at, 1570342_at, 202379_s_at, 202380_s_at, 215338_s_at, 215339_at, 231235_at	NP_005376.2, EAW64661.1, EAW64659.1, EAW64660.1
GeneID:92999	ZBTB47	3	42,695,176	42,709,072	13,896	+	2	4_A375_EGR1..1..8087, 4_A375_EGR1..1..8088	280, 9240	in gene, in gene	0	0	1	7.5	9.5	16.5	2	4_A375_EGR1..1	18	Gene ZBTB47	KIAA1190, ZNF651, DKFZp434N0615, ZBTB47	zinc finger and BTB domain containing 47	NM_145166, hCT1818660.1	226484_at, 226500_at, 234336_s_at	NP_660149.2, EAW64662.1
GeneID:131377	KBTBD5	3	42,727,011	42,733,938	6,927	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3880, 2_A375_pNL97_plus_lncRNA_AR..1..5568, 4_A375_EGR1..1..8089	16093, 16040, 11624	downstream, downstream, downstream	1	1	1	16	15	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene KBTBD5	SRYP, MGC125350, KBTBD5, FLJ32015	kelch repeat and BTB (POZ) domain containing 5	NM_152393, hCT20012.3, hCT2348560.1	1555044_a_at	NP_689606.2, EAW64664.1, EAW64665.1
GeneID:57467	HHATL	3	42,734,155	42,744,319	10,164	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3880, 2_A375_pNL97_plus_lncRNA_AR..1..5568, 4_A375_EGR1..1..8089	1215, 1268, 5684	in gene, in gene, in gene	1	1	1	16	15	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene HHATL	KIAA1173, MBOAT3, C3orf3, MSTP002, HHATL, OACT3, GUP1	hedgehog acyltransferase-like	NM_020707, NR_027753, hCT1959886.1, hCT20015.2, hCT2354043.0	223572_at	NP_065758.3, EAW64668.1, EAW64666.1, EAW64667.1
GeneID:152206	CCDC13	3	42,749,874	42,814,745	64,871	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3880, 1_A375_pNL7_minus_lncRNA_AR..1..3881, 2_A375_pNL97_plus_lncRNA_AR..1..5568	71641, 9, 71694	downstream, in gene, downstream	1	1	0	24	18	10.5	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene CCDC13	FLJ25467, CCDC13	coiled-coil domain containing 13	NM_144719, hCT2283837.1, hCT2344199.0, hCT2344201.0	1553396_a_at, 1553397_at, 1554022_at, 1554023_s_at	NP_653320.3, EAW64670.1, EAW64669.1, EAW64671.1
GeneID:25994	HIGD1A	3	42,824,400	42,846,027	21,627	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3881, 2_A375_pNL97_plus_lncRNA_AR..1..5569	31291, 27	downstream, in gene	1	1	0	17	14	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene HIGD1A	HIGD1A, HIG1, DKFZp564K247	HIG1 hypoxia inducible domain family, member 1A	NM_001099668, NM_014056, NM_001099669, hCT2283836.1, hCT2283838.0, hCT2344200.0, hCT2354186.0, hCT2354187.0	217845_x_at, 221896_s_at	NP_001093138.1, NP_054775.2, NP_001093139.1, EAW64673.1, EAW64676.1, EAW64677.1, EAW64674.1, EAW64675.1
GeneID:1238	CCBP2	3	42,850,984	42,908,775	57,811	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5569, 2_A375_pNL97_plus_lncRNA_AR..1..5570	-4984, 10636	upstream, in gene	0	1	0	10.5	14.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene CCBP2	CMKBR9, D6, CCR9, MGC138250, CCBP2, CCR10, MGC126678, hD6	chemokine binding protein 2	NM_001296, hCT2283239.1, hCT2283240.1, hCT2344210.0, hCT2344211.0	1559432_at, 1566850_at, 206887_at	NP_001287.2, EAW64678.1, EAW64679.1, EAW64680.1, EAW64681.1
GeneID:1582	CYP8B1	3	42,913,684	42,917,633	3,949	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5571	-4991	upstream	0	1	0	13	17	12	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene CYP8B1	CYP12, CP8B, CYP8B1, FLJ17826	cytochrome P450, family 8, subfamily B, polypeptide 1	NM_004391, hCT1640852.2	232494_at	NP_004382.2, EAW64682.1
GeneID:55129	ANO10	3	43,407,818	43,663,560	255,742	-	1	4_A375_EGR1..1..8090	257907	downstream	0	0	1	5	3	16	1	4_A375_EGR1..1	16	Gene ANO10	FLJ10375, ANO10, SCAR10, MGC47890, TMEM16K	anoctamin 10	NM_018075, hCT1968277.1, hCT2279759.0, hCT2354057.0, hCT2354058.0	218910_at	NP_060545.3, EAW64696.1, EAW64695.1, EAW64697.1, EAW64698.1
GeneID:375337	C3orf77	3	44,283,378	44,373,590	90,212	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3885, 4_A375_EGR1..1..8092, 4_A375_EGR1..1..8093	96750, -50, 96782	downstream, upstream, downstream	1	0	1	11.5	13	23	2	4_A375_EGR1..1	26	Gene C3orf77	C3orf77, FLJ36157	chromosome 3 open reading frame 77	NM_001145030		NP_001138502.1
GeneID:285343	C3orf23	3	44,379,611	44,450,940	71,329	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3885, 4_A375_EGR1..1..8093	517, 549	in gene, in gene	1	0	1	20	18	28	1	4_A375_EGR1..1	28	Gene C3orf23	FLJ41686, DKFZp313N0621, MGC119532, MGC119531, C3orf23, MGC119533, TOAG1, MGC119530	chromosome 3 open reading frame 23	NM_001029840, NM_001029839, NM_173826, hCT17936.3, hCT1960094.2, hCT2348536.0, hCT2348537.0	1555905_a_at, 1555906_s_at, 228668_at, 241686_at	NP_001025011.1, NP_001025010.1, NP_776187.2, EAW64703.1, EAW64704.1, EAW64706.1, EAW64705.1
GeneID:353274	ZNF445	3	44,481,262	44,519,162	37,900	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5579	-102	upstream	0	1	0	7	13	8	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene ZNF445	ZKSCAN15, MGC126535, ZNF168, ZNF445	zinc finger protein 445	NM_181489, hCT2349013.0	229786_at, 233992_x_at	NP_852466.1, EAW64708.1
GeneID:285346	ZNF852	3	44,540,462	44,552,132	11,670	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5580	100	in gene	0	1	0	8	19	8	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ZNF852	ZNF852	zinc finger protein 852	XM_001717544, XM_001725070	1564662_at	XP_001717596.2, XP_001725122.2
GeneID:10168	ZNF197	3	44,666,511	44,689,963	23,452	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3887, 2_A375_pNL97_plus_lncRNA_AR..1..5582	-79, -47	upstream, upstream	1	1	0	16	20	8	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ZNF197	VHLaK, ZNF197, ZNF166, ZKSCAN9, ZNF20, D3S1363E, P18	zinc finger protein 197	NM_006991, NM_001024855, hCT2279277.0	205855_at, 233070_at	NP_008922.1, NP_001020026.1, EAW64714.1
GeneID:91392	ZNF502	3	44,754,135	44,765,323	11,188	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5583	-87	upstream	0	1	0	13	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ZNF502	FLJ14855, FLJ12515, ZNF502	zinc finger protein 502	NM_033210, NM_001134440, NM_001134441, NM_001134442, hCT2279280.0, hCT2279281.0	229532_at, 232247_at	NP_149987.2, NP_001127912.1, NP_001127913.1, NP_001127914.1, EAW64718.1, EAW64719.1
GeneID:57456	KIAA1143	3	44,790,236	44,803,173	12,937	-	1	4_A375_EGR1..1..8094	-59	upstream	0	0	1	18	16	19	1	4_A375_EGR1..1	19	Gene KIAA1143	KIAA1143		NM_020696, hCT1814783.1, hCT2280648.0	226616_s_at, 227493_s_at	NP_065747.1, EAW64723.1, EAW64722.1
GeneID:56992	KIF15	3	44,803,209	44,894,746	91,539	+	3	4_A375_EGR1..1..8094, 4_A375_EGR1..1..8095, 4_A375_EGR1..1..8096	23, 99607, 100163	in gene, downstream, downstream	0	0	1	15	12.67	15.67	3	4_A375_EGR1..1	19	Gene KIF15	HKLP2, FLJ25667, KIF15, NY-BR-62, KNSL7	kinesin family member 15	NM_020242, hCT8465.1	219306_at	NP_064627.1, EAW64724.1

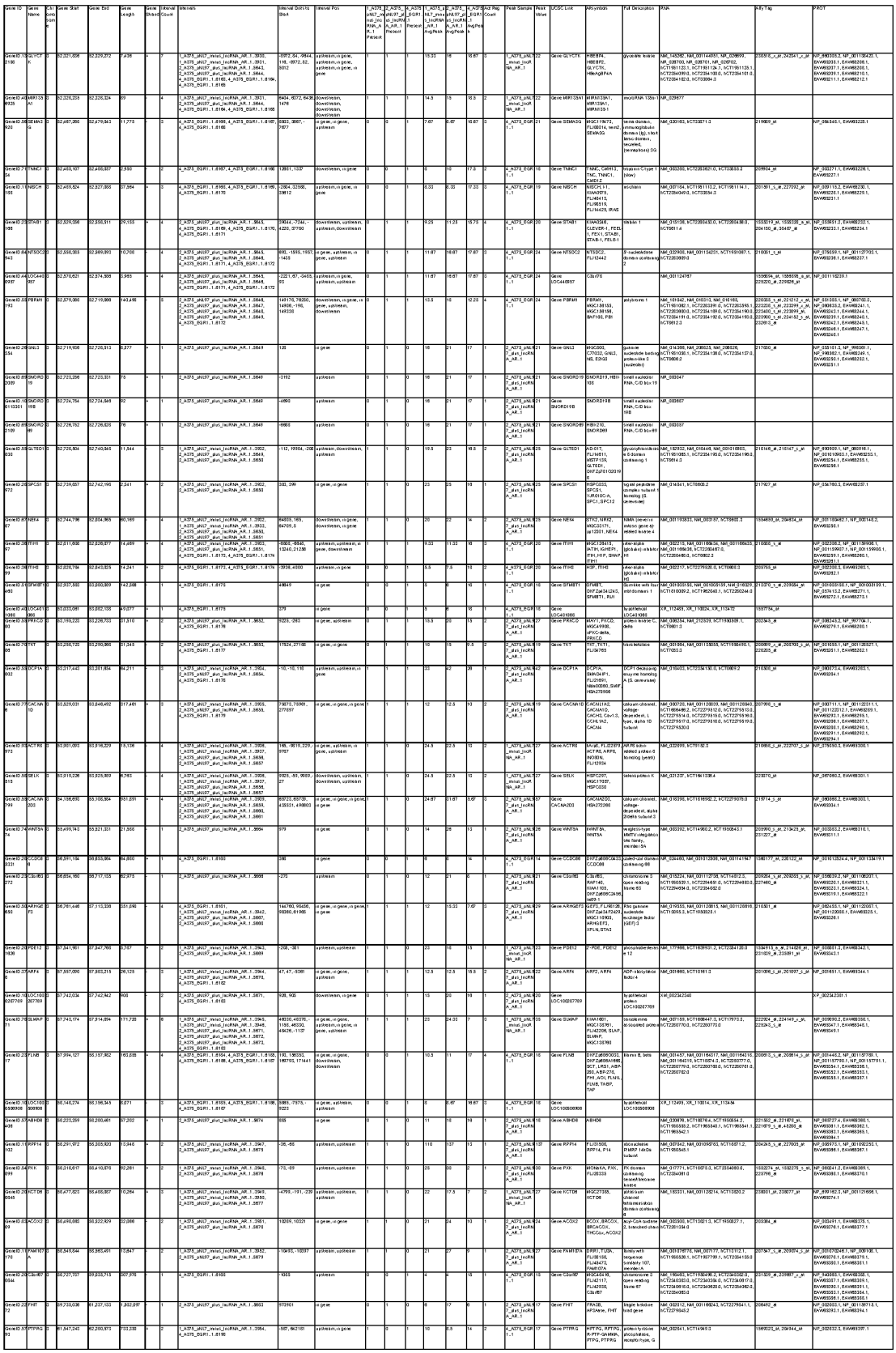


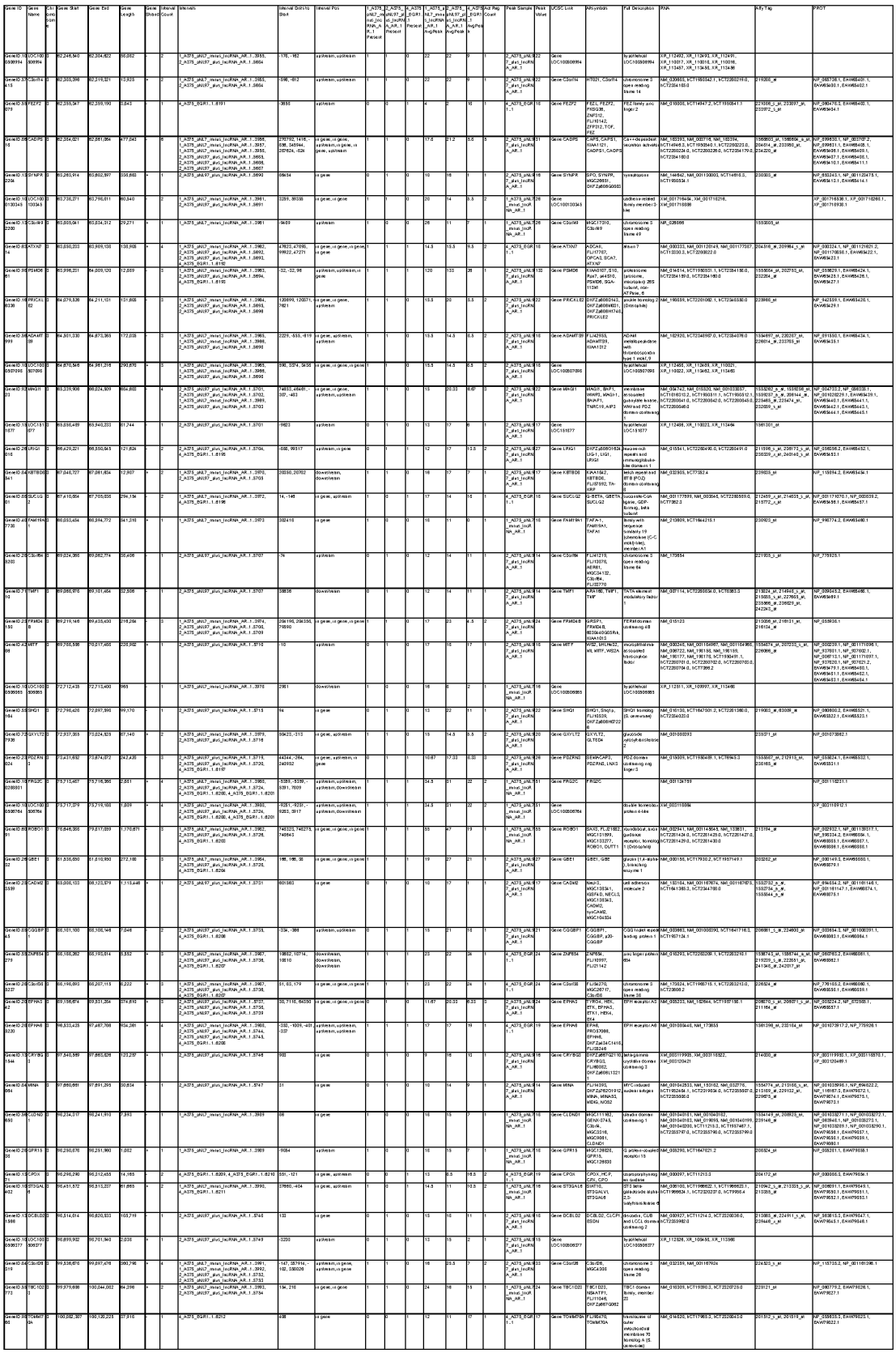
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Start	Interval Pos	1_A3'5_ uNG7_ ins_loc ation_A_R_1 Percent	2_A3'5_ uNG7_ins_ location_A_R_1 Percent	4_A3'5_ SGR1_ NA7_ins ertion_A_R_1 Percent	1_A3'5_ uNG7_ins_ location_A_R_1 Avg Peak	2_A3'5_ SGR1_ins_ location_A_R_1 Avg Peak	4_A3'5_ SGR1_ins_ location_A_R_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
Gene:ID:89 3149	MIR596	2	44,903,350	44,903,473	93	+	2	4_A3'5_EGR1..1.8093, 4_A3'5_EGR1..1.8096	-984, 12	upstream, up gene	0	0	1	13.5	11	14	2	4_A3'5_EGR1..1	15	Gene:MIR596	MIR596, hsa-mir-596, MIR596	microRNA 596	NR_030290			
Gene:ID:10 4818	TMEM8 2	2	44,903,400	44,907,158	3,758	+	2	4_A3'5_EGR1..1.8093, 4_A3'5_EGR1..1.8096	-592, -16	upstream, upstream	0	0	1	13.5	11	14	2	4_A3'5_EGR1..1	15	Gene:TMEM82	TMEM82	transmembrane protein 82	NM_144630, NCT22792084.1, NCT25403208.0	226581_at		NP_653239.1, EAW64723.1, EAW64726.1
Gene:ID:70 7044	TGM4	3	44,916,696	44,936,868	20,173	+	1	4_A3'5_EGR1..1.8097	27088	up gene	0	0	1	5	4	16	1	4_A3'5_EGR1..1	16	Gene:TGM4	TGM4, TGM, TGM4	transglutaminase 4 (prostate)	NM_003241, NCT22792071.1, NCT16844.3	206260_at, 217588_s_at, 217587_at	NP_003232.2, EAW64728.1, EAW64727.1
Gene:ID:84 6997	CDCP1	3	45,123,769	45,167,914	44,145	-	4	1_A3'5_uNG7_invert_lncRNA_AR..1.3885, 1_A3'5_uNG7_invert_lncRNA_AR..1.3899, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8894, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8965	45098,22410, 45810,-6139	up gene, up gene, up gene, upstream	1	1	0	19.33	16	6.33	3	2_A3'5_uNG7_ilun_lncRNA_AR..1	22	Gene:CDCP1	TRASK, SIMA135, CDCP1, CD318	CUB domain containing protein 1	NM_178181, NM_022842, NCT22809640.0, NCT6466.3	1554110_at, 219631_at, 234202_s_at	NP_839485.1, NP_073783.2, EAW64727.1, EAW64738.1
Gene:ID:23 395	LARS2	3	45,430,075	45,590,326	160,252	+	2	1_A3'5_uNG7_invert_lncRNA_AR..1.3891, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8967	126707, 69477	up gene, up gene	1	1	0	15	14	8.5	2	1_A3'5_uNG7_invert_lncRNA_AR..1	20	Gene:LARS2	LEURS, LARS2, RIARS025, MSC26121	leucyl-tRNA synthetase 2, mitochondrial	NM_015340, NCT19481.2	204016_at, 34764_at	NP_056155.1, EAW64740.1
Gene:ID:89 94	LIMD1	3	45,836,323	45,722,755	99,432	+	4	1_A3'5_uNG7_invert_lncRNA_AR..1.3892, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8966, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8993, 4_A3'5_EGR1..1.8096	94205,81949, 94237,94237	5downstream, up gene, 5downstream, 5downstream	1	1	1	16	26	22.5	2	4_A3'5_EGR1..1	38	Gene:LIMD1	LIMD1	LIM domain containing 1	NM_014240, NCT19484.2	216850_s_at, 222353_at, 222782_s_at, 234957_x_at, 234763_at	NP_056059.1, EAW64742.1
Gene:ID:84 4774	LOC644 714	3	45,719,657	45,730,374	10,717	-	3	1_A3'5_uNG7_invert_lncRNA_AR..1.3892, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8966, 4_A3'5_EGR1..1.8096	-156, -156, -156	upstream, upstream, upstream	1	1	1	24	33	36	1	4_A3'5_EGR1..1	38	Gene:LOC644714	LOC644714	hypothetical LOC644714	NM_033947	233541_at	
Gene:ID:23 595	SACM1 L	3	45,730,754	45,768,900	38,146	+	3	1_A3'5_uNG7_invert_lncRNA_AR..1.3892, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8966, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8993, 4_A3'5_EGR1..1.8096	-236, -194, -194	upstream, upstream, upstream	1	1	1	24	33	36	1	4_A3'5_EGR1..1	38	Gene:SACM1L	KIAA0261, SACM1L, DKFZp686N0331, SAC1	SAC1 suppressor of actin mutations 1-like (yeast)	NM_014816, NCT22793030.0, NCT22793031.0, NCT6480.3	202797_at	NP_234733.2, EAW64748.1, EAW64744.1, EAW64745.1
Gene:ID:54 718	CLEC18 B	3	45,798,941	45,830,033	41,094	-	1	4_A3'5_EGR1..1.8099	207	up gene	0	0	1	9	17	17	1	4_A3'5_EGR1..1	17	Gene:SCGB420	MGC16475, SFT, hlug1, XTS, SLC6A20	solute carrier family 6 (proline IMINO transporter), member 20	NM_032403, NM_020200, NCT16199808.1, NCT6483.2	219814_s_at, 232491_s_at	NP_071890.1, NP_064592.1, EAW64747.1, EAW64748.1
Gene:ID:54 555	LZTFL1	3	45,866,448	45,883,621	16,175	-	4	1_A3'5_uNG7_invert_lncRNA_AR..1.3893, 1_A3'5_uNG7_invert_lncRNA_AR..1.3894, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8990, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8991	23621,,53,,23093 229	5downstream, up gene, 5downstream, up gene	1	1	0	17	16	6.5	2	2_A3'5_uNG7_ilun_lncRNA_AR..1	21	Gene:LZTFL1	FLJ38386, LZTFL1	leucine zipper transcription factor-like 1	NM_020347, NCT22791671.0, NCT6584.2	219437_s_at, 223932_s_at, 232410_at	NP_066993.1, EAW64730.1, EAW64749.1
Gene:ID:79 443	FYCO1	3	45,959,355	46,037,307	77,952	+	1	4_A3'5_uNG7_invert_lncRNA_AR..1.3883	91	up gene	1	0	0	17	16	12	1	1_A3'5_uNG7_invert_lncRNA_AR..1	17	Gene:FYCO1	MGC126819, FYCO1, ZFYVE7, MGC126817, FLJ13333, DKFZp779X1152, RUFY2	FYVE and coiled-coil domain containing 1	NM_024513, NCT19277752	1553923_a_at, 219284_s_at	NP_076799.2, EAW64753.1
Gene:ID:37 7047	PRSS43	2	48,763,561	48,766,345	2,884	-	1	4_A3'5_EGR1..1.8100	-3979	upstream	0	0	1	8	7	19	1	4_A3'5_EGR1..1	19	Gene:PRSS43	TESSP5, PRSS43	protease, serine, 43	NM_199183, NCT22677451.1		NP_938032.2, EAW64759.1
Gene:ID:18 0260960	LOC100 260960	2	48,765,220	48,766,357	1,137	-	1	4_A3'5_EGR1..1.8100	-6133	downstream	0	0	1	8	7	19	1	Gene LOC100260960	FLJ35279, PRSS43, TESSP5, FLJ40533	protease, serine, 43	NM_002342331, NM_033119889, XM_005312406		XP_002342392.1, XP_033119937.1, XP_005312463.1
Gene:ID:37 45	PTH1R	3	45,916,256	46,045,389	129,033	+	3	4_A3'5_EGR1..1.8101, 4_A3'5_EGR1..1.8102, 4_A3'5_EGR1..1.8103	237, 9008, 29284	up gene, up gene, downstream	0	0	1	7.67	5.67	18	3	4_A3'5_EGR1..1	18	Gene:PTH1R	PTHR, PTH1R, MGC133432, PTR, PTHR1, MGC133428	parathyroid hormone 1 receptor	NM_000316, NM_001163744, NCT22795970.0, NCT5974.3	203911_at	NP_000307.1, NP_001171673.1, EAW64762.1, EAW64764.1
Gene:ID:19 1903	CCDC61	2	46,965,250	47,016,270	50,020	-	2	1_A3'5_uNG7_invert_lncRNA_AR..1.3898, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8992	-290, -56	upstream, upstream	1	1	0	25	25	18	1	2_A3'5_uNG7_ilun_lncRNA_AR..1	25	Gene:CCDC12	CCDC12, FLJ40001, FLJ39420, MGC22315	coiled-coil domain containing 12	NM_144718, NCT22795970.0, NCT22795836.0, NCT22793980.0, NCT22793981.0, NCT6483.2	236011_at	NP_653117.2, EAW64756.1, EAW64757.1, EAW64758.1, EAW64759.1
Gene:ID:23 216	NBEAL2	3	47,021,073	47,091,193	69,020	+	3	1_A3'5_uNG7_invert_lncRNA_AR..1.3898, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8992, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8109, 4_A3'5_EGR1..1.8102, 4_A3'5_EGR1..1.8108	-2803, -2845, 22587, 23339, 23515	upstream, upstream, up gene, up gene, up gene	1	1	1	10	12	10.75	4	2_A3'5_uNG7_ilun_lncRNA_AR..1	25	Gene:NBEAL2	KIAA0341, NBEAL2	neurobeachin-like 2	NM_015175	1559817_at, 212443_at	NP_056991.1
Gene:ID:29 372	SETD2	3	47,057,856	47,205,467	147,611	+	2	1_A3'5_uNG7_invert_lncRNA_AR..1.3897, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8993	-277, -261	upstream, upstream	1	1	0	25	25	13	1	2_A3'5_uNG7_ilun_lncRNA_AR..1	25	Gene:SETD2	FLJ21184, FLJ16425, HIF1, SET02, HMTase SET2, HIF120, HIF0069, KIAA1732, FLJ20473, dJ211H8F, FLJ44893, FLJ46217, HYP8	SET domain containing 2	NM_014159, NCT16189988.2, NCT19516022.2, NCT22443397.0, NCT22443390.0, NCT22443050.0, NCT6483.2	212453_s_at, 219033_s_at, 220946_s_at	NP_054878.5, EAW64806.1, EAW64809.1, EAW64830.1, EAW64831.1, EAW64833.1, EAW64837.1
Gene:ID:84 147	KIF9	3	47,269,516	47,324,327	54,811	-	2	1_A3'5_uNG7_ilun_lncRNA_AR..1.3894, 4_A3'5_EGR1..1.8107	-15, 13217	upstream, up gene	0	1	1	12	14	12.5	2	2_A3'5_uNG7_ilun_lncRNA_AR..1	25	Gene:KIF9	MGC104166, KIF9	kinesin family member 9	NM_022342, NM_182902, NM_001134476, NCT19510231.1, NCT19510234.1, NCT19510235.1, NCT22793440.0, NCT6634.2	223776_at, 225429_x_at, 227251_x_at, 233701_x_at, 233719_x_at	NP_071727.1, NP_876082.2, NP_001122630.1, EAW64813.1, EAW64814.1, EAW64815.1, EAW64816.1, EAW64817.1
Gene:ID:23 278	KLHL18	2	47,324,230	47,366,308	80,978	+	1	4_A3'5_uNG7_ilun_lncRNA_AR..1.3894	22	up gene	0	1	0	16	25	10	1	2_A3'5_uNG7_ilun_lncRNA_AR..1	25	Gene:KLHL18	FLJ13103, FLJ00263, KIAA0709, KLHL18	kelch-like 18 (Drosophila)	NM_020810, NCT19510155.1, NCT22455576.0, NCT22455577.0, NCT6647.2	1557165_s_at, 220776_at, 212802_at	NP_065862.2, EAW64820.1, EAW64819.1, EAW64818.1, EAW64821.1
Gene:ID:28 932	PTPN23	3	47,422,491	47,454,931	32,440	+	9	1_A3'5_uNG7_invert_lncRNA_AR..1.3895, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8995, 4_A3'5_EGR1..1.8108, 4_A3'5_EGR1..1.8109, 4_A3'5_EGR1..1.8110	-178, 37, 226, 33013, 36597	upstream, up gene, up gene, up gene, up gene	1	1	1	8.67	11.67	17.33	3	2_A3'5_uNG7_ilun_lncRNA_AR..1	19	Gene:PTPN23	DKFZp686H1823, HDPTP, PTPN23, PTP-TD14, WAH1471, HD-PTP	potein tyrosine phosphatase, non-receptor type 23	NM_015466, NCT22795004.0, NCT22845030.0, NCT6481.3	223749_s_at, 223182_s_at	NP_036201.1, EAW64823.1, EAW64822.1, EAW64824.1
Gene:ID:22 937	SCAP	3	47,453,154	47,517,445	62,291	-	4	2_A3'5_uNG7_ilun_lncRNA_AR..1.3896, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8109, 4_A3'5_EGR1..1.8110, 4_A3'5_EGR1..1.8111	525, 64229	up gene, downstream, up gene, up gene	0	1	1	8.5	10.25	10.75	4	4_A3'5_EGR1..1	19	Gene:SCAP	SCAP, KIAA0190	SREBF chaperone	NM_012235, NCT22795344.0, NCT6498.3	212379_at	NP_036367.2, EAW64825.1, EAW64826.1
Gene:ID:54 599	C3orf15	3	47,537,100	47,553,199	16,099	-	1	4_A3'5_uNG7_invert_lncRNA_AR..1.3899	-6941	upstream	1	0	0	16	14	14	1	1_A3'5_uNG7_invert_lncRNA_AR..1	16	Gene:C3orf15	C3orf15, THEM183, FLJ22211	chromosome 3 open reading frame 15	NM_031317031, NCT19510201.1, NCT19577258.1	2209830_at, 223277_at, 223983_s_at, 229994_at	NP_001278772.2, EAW64827.1, EAW64828.1
Gene:ID:22 907	DHX32	3	47,644,599	47,691,866	47,267	+	8	1_A3'5_uNG7_invert_lncRNA_AR..1.3900, 1_A3'5_uNG7_invert_lncRNA_AR..1.3901, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8997, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8998, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8999, 4_A3'5_EGR1..1.8112, 4_A3'5_EGR1..1.8113	448, 22685,,673, 22549,,22257, 43025	up gene, up gene, up gene, up gene, up gene	1	1	1	43.67	66	13.67	12	2_A3'5_uNG7_ilun_lncRNA_AR..1	17	Gene:DHX32	DDX32, FLJ11214, DHX32, RETCOR, KIAA0950	DEAH (Asp-Glu-Ala-His) box polypeptide 32	NM_139018, NM_014998, NCT19531912.1, NCT19577259.1, NCT22795910.0, NCT22795922.0, NCT6617.3	1559144_at, 204355_at, 212674_x_at, 233071_at, 236944_at, 239772_x_at	NP_612627.1, NP_057972.2, EAW64833.1, EAW64834.1, EAW64835.1, EAW64836.1
Gene:ID:10 0302232	MIR122	3	47,691,045	47,691,119	74	+	1	4_A3'5_EGR1..1.8113	-2821	upstream	0	0	1	7	9	19	1	4_A3'5_EGR1..1	19	Gene:MIR122	MIR122, miR122a, MIR122B	microRNA 122	NR_031595		
Gene:ID:41 54	MAP4	3	47,692,180	48,130,769	438,589	-	3	1_A3'5_uNG7_invert_lncRNA_AR..1.3902, 1_A3'5_uNG7_invert_lncRNA_AR..1.3903, 1_A3'5_uNG7_invert_lncRNA_AR..1.3899	180321, 24254,,5 112	up gene, downstream, up gene	1	1	1	16	14.33	11.67	3	1_A3'5_uNG7_invert_lncRNA_AR..1	25	Gene:MAP4	MAP4, MAP190, MGC8871	microtubule-associated protein 4	NM_002375, NM_030555, NM_001134084, NCT19510181.1, NCT19545945.0, NCT19545946.1, NCT19545947.1, NCT22623460.0, NCT22623466.0, NCT22623467.0, NCT22623702.0, NCT22623703.0, NCT6807.2	200835_s_at, 200836_s_at, 212365_at, 212367_s_at, 212368_at, 242_at, 36590_at	NP_002366.2, NP_112147.2, NP_001127636.1, EAW64837.1, EAW64838.1, EAW64844.1, EAW64839.1, EAW64840.1, EAW64841.1, EAW64843.1, EAW64845.1, EAW64846.1, EAW64847.1, EAW64848.1
Gene:ID:39 5054	CDC25A	3	48,196,966	48,229,901	31,155	-	2	1_A3'5_uNG7_ilun_lncRNA_AR..1.3903, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8930	-139, -39	upstream, upstream	1	1	0	19	16	14	1	1_A3'5_uNG7_invert_lncRNA_AR..1	19	Gene:CDC25A	CDC25A2, CDC25A	cell division cycle 25 homolog A (S. pombe)	NM_001789, NM_201567, NCT22823330.0, NCT22823566.0, NCT22840460.0, NCT19393.2	1553772_a_at, 204695_at, 204696_s_at	NP_001778.2, NP_963861.1, EAW64849.1, EAW64850.1, EAW64851.1, EAW64852.1
Gene:ID:83 355	ZNF589	3	48,282,998	48,312,460	29,464	+	1	4_A3'5_uNG7_ilun_lncRNA_AR..1.3901	-132	upstream	0	1	0	15	23	9	1	2_A3'5_uNG7_ilun_lncRNA_AR..1	23	Gene:ZNF589	ZNF589, dZF1	zinc finger protein 589	NM_018089, NCT19510081.2, NCT19547291.1, NCT22541129.0, NCT22541130.0, NCT22541131.0, NCT6124.3	1559160_a_at, 210081_at, 210082_s_at, 219960_at	NP_060559.2, EAW64853.1, EAW64854.1, EAW64855.1, EAW64856.1, EAW64857.1
Gene:ID:10 0331	NAIP8	3	48,233,376	48,242,948	9,572	-	2	4_A3'5_uNG7_ilun_lncRNA_AR..1.3902, 4_A3'5_EGR1..1.8114	180, 144	up gene, up gene	0	1	1	15	22	29	1	4_A3'5_EGR1..1	29	Gene:NAIP8	BIRHLH1HA, NAIP2-H6, NOL6, NAIP8	neuronal apoptosis inhibitory protein 8, pseudogene 1	NM_003793, NCT16192.2	209831_at	NP_003784.1, EAW64861.1
Gene:ID:84 2438	SPINK5	3	48,346,336	48,389,831	21,495	-	2	2_A3'5_uNG7_ilun_lncRNA_AR..1.3902, 4_A3'5_EGR1..1.8114	27143,,27127	5downstream, 5downstream	0	1	1	15	22	29	1	4_A3'5_EGR1..1	29	Gene:SPINK5	SPINK5	lekine protease inhibitor, Kazal type 5 (putative)	NM_031850525		NP_031073894.1
Gene:ID:83 84	PLXNB1	3	48,445,861	48,571,480	98,199	-	1	4_A3'5_EGR1..1.8115	11124	up gene	0	0	1	7	9	18	1	4_A3'5_EGR1..1	18	Gene:PLXNB1	PLXNB1, PLXNB, SEP, KIAA0407, MGC149187, PLEXIN-B1	plexin B1	NM_002673, NM_001130002, NCT19531911.0, NCT22823445.0, NCT23436.2	210869_s_at, 213007_s_at	NP_002664.2, NP_001123554.1, EAW64864.1, EAW64865.1, EAW64866.1
Gene:ID:79 714	CCDC51	3	48,475,530	48,481,829	7,949	-	2	1_A3'5_uNG7_invert_lncRNA_AR..1.3904, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8993	-6919, -6439	upstream, upstream	1	1	0	21	20	18	1	1_A3'5_uNG7_invert_lncRNA_AR..1	21	Gene:CCDC51	FLJ12436, CCDC51	coiled-coil domain containing 51	NM_024981, NCT22823445.1, NCT22823542.0, NCT22823443.0, NCT22823443.1, NCT22841320.0	219722_s_at	NP_079257.3, EAW64867.1, EAW64868.1, EAW64869.1, EAW64870.1, EAW64871.1, EAW64872.1
Gene:ID:57 372	CCDC72	2	48,681,838	48,685,557	3,851	+	2	1_A3'5_uNG7_invert_lncRNA_AR..1.3904, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8993	6982, 6202	5downstream, 5downstream	1	1	0	21	20	18	1	1_A3'5_uNG7_invert_lncRNA_AR..1	21	Gene:CCDC72	HSPC018, CCDC72	coiled-coil domain containing 72	NM_018932, NCT22795453.0, NCT22845548.0	221791_s_at	NP_061705.1, EAW64874.1, EAW64873.1
Gene:ID:11 128	ATRIP	3	48,685,218	48,807,854	16,636	+	3	1_A3'5_uNG7_invert_lncRNA_AR..1.3904, 1_A3'5_uNG7_invert_lncRNA_AR..1.3905, 1_A3'5_uNG7_invert_lncRNA_AR..1.3906	-176, -250, 19136	upstream, upstream, 5downstream	1	1	1	19.5	18.5	17	2	1_A3'5_uNG7_invert_lncRNA_AR..1	21	Gene:ATRIP	FLJ12343, MGC20825, ATRIP, MGC21482, MGC26740, DKFZp762J0115	ATR-interacting protein	NM_032166, NM_130384	1552937_s_at	NP_115542.2, NP_569038.1
Gene:ID:11 077	TREX1	3	48,807,229	48,809,044	1,815	+	1	4_A3'5_EGR1..1.8116	329	up gene	0	0	1	16	17	18	1	4_A3'5_EGR1..1	18	Gene:TREX1	HERN3, DRN2, DKFZp434J035, CRV, TREX1, mp31	three prime repair exonuclease 1	NM_016311, NM_033629, NCT22795947.0, NCT22795948.0, NCT22795951.0, NCT22795952.0, NCT22795953.0, NCT22795954.0, NCT22795955.0, NCT22795956.0	209573_s_at, 34869_at	NP_057404.1, NP_150599.1, EAW64876.1, EAW64878.1, EAW64880.1, EAW64876.1, EAW64877.1, EAW64881.1, EAW64882.1, EAW64883.1
Gene:ID:51 048	SH3BA5	3	48,809,197	48,841,961	32,764	-	2	4_A3'5_EGR1..1.8116, 4_A3'5_EGR1..1.8117	54895, 1557	5downstream, up gene	0	0	1	14	11	17	2	4_A3'5_EGR1..1	18	Gene:SH3BA5	SH3KBP5, SH3BA5, SCOTIN	SH3 domain binding 5 (Wnt-specific)	NM_016479, NCT22823541.0, NCT22823542.0, NCT22823445.1, NCT22823547.1, NCT22840439.0	222906_s_at	NP_057563.3, EAW64885.1, EAW64886.1, EAW64887.1, EAW64888.1
Gene:ID:32 10	PPYR1	3	48,833,117	48,894,227	59,110	-	3	1_A3'5_uNG7_invert_lncRNA_AR..1.3905, 1_A3'5_uNG7_invert_lncRNA_AR..1.3906, 1_A3'5_uNG7_invert_lncRNA_AR..1.3907, 1_A3'5_uNG7_invert_lncRNA_AR..1.3908, 4_A3'5_EGR1..1.8116, 4_A3'5_EGR1..1.8119	44821,,4935,,, 7833,,67,,,4509	upstream, upstream, upstream, up gene, upstream	1	1	1	16.5	19.5	13	2	4_A3'5_EGR1..1	21	Gene:PPYR1	PPYR1		NM_004567, NCT19510981.1	209248_at, 229699_at	NP_004558.1, EAW64890.1
Gene:ID:56 228	UCN2	2	48,899,151	48,901,301	2,150	-	6	1_A3'5_uNG7_invert_lncRNA_AR..1.3905, 1_A3'5_uNG7_invert_lncRNA_AR..1.3906, 1_A3'5_uNG7_invert_lncRNA_AR..1.3907, 1_A3'5_uNG7_invert_lncRNA_AR..1.3908, 1_A3'5_uNG7_invert_lncRNA_AR..1.3909, 4_A3'5_EGR1..1.8116, 4_A3'5_EGR1..1.8119, 4_A3'5_EGR1..1.8120	2383, 49,,,389, 7041, 2465,,,7251	5downstream, up gene, upstream, 5downstream, 5downstream, upstream	1	1	1	13.33	13.67	16.33	3	2_A3'5_uNG7_ilun_lncRNA_AR..1	21	Gene:UCN2	UCN, UCN-II, UCN2, URP, SRP, UR	urocortin 2	NM_033199, NCT19510921.1	232874_at	NP_149978.1, EAW64891.1
Gene:ID:13 94	COL7A1	3	48,931,906	48,932,993	31,087	-	6	1_A3'5_uNG7_invert_lncRNA_AR..1.3905, 1_A3'5_uNG7_invert_lncRNA_AR..1.3906, 1_A3'5_uNG7_invert_lncRNA_AR..1.3907, 1_A3'5_uNG7_invert_lncRNA_AR..1.3908, 1_A3'5_uNG7_invert_lncRNA_AR..1.3909, 4_A3'5_EGR1..1.8116, 4_A3'5_EGR1..1.8119, 4_A3'5_EGR1..1.8120	32143,,31441, 30833,,30433, 23837,,24001	5downstream, 5downstream, 5downstream, 5downstream, 5downstream	1	1	1	13.33	13.67	16.33	3	2_A3'5_uNG7_ilun_lncRNA_AR..1	21	Gene:COL7A1	EBDCT, EBR1, EBD1, COL7A1	collagen, type VII, alpha 1	NM_000094, NCT22823528.2, NCT22823531.1, NCT22823532.2, NCT22840457.1, NCT22847.5	204109_at, 217312_s_at	NP_000085.1, EAW64896.1, EAW64893.1, EAW64895.1, EAW64897.1
Gene:ID:10 0302225	MIR711	3	48,816,333	48,816,410	78	-	1	4_A3'5_EGR1..1.8120	7892	downstream	0	0	1	3	2	19	1	4_A3'5_EGR1..1	19	Gene:MIR711	MIR711, hsa-mir-711	microRNA 711	NR_031758		
Gene:ID:73 54	UQCRC2	3	48,836,432	48,847,995	10,866	+	1	4_A3'5_EGR1..1.8121	-348	upstream	0	0	1	14	21	17	1	4_A3'5_EGR1..1	17	Gene:UQCRC1	UQCRC1, QCR1, UQCR1	ubiquinol-cytochrome c reductase core protein I	NM_003365, NCT22446.3	201903_at	NP_003356.2, EAW64899.1
Gene:ID:83 010	SLC26A8	3	48,865,136	48,872,928	7,770	-	3	1_A3'5_uNG7_invert_lncRNA_AR..1.3907, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8993, 4_A3'5_EGR1..1.8122	-66, -238, 479	upstream, upstream, up gene	1	1	1	23	21	30	1	1_A3'5_uNG7_invert_lncRNA_AR..1	23	Gene:SLC26A8	DKFZp686E1420, SLC26A8	solute carrier family 26, member 8	NM_022911, NM_134263, NM_134426, AK_091049434, NCT22823503.1, NCT22823505.1, NCT22823510.1, NCT22823523.0, NCT22823536.1, NCT22841446.0, NCT22841447.0, NCT22841448.0, NCT22841449.0, NCT22841450.0	221572_s_at, 233581_at	NP_075382.2, NP_599028.2, NP_852276.2, NP_001028944.1, EAW64900.1, EAW64911.1, EAW64903.1, EAW64901.1, EAW64904.1, EAW64905.1, EAW64906.1, EAW64907.1, EAW64909.1, EAW64910.1, EAW64912.1, EAW64913.1
Gene:ID:19 51	CLEC18B	3	48,873,696	48,880,348	36,652	+	6	1_A3'5_uNG7_invert_lncRNA_AR..1.3907, 1_A3'5_uNG7_invert_lncRNA_AR..1.3908, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8993, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8994, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8995, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8996, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8997, 2_A3'5_uNG7_ilun_lncRNA_AR..1.8998	27556, 1552, 27184, 1520, -56, 27900	5downstream, up gene, 5downstream, up gene, upstream, downstream	1	1	1	22	31.67	13.67	3	2_A3'5_uNG7_ilun_lncRNA_AR..1	44	Gene:CLEC18B	C4SR3, FM12, MRG12, EGFL1, RBSDA1, HFW8, CDHF11	C-type (calcium dependent, carbohydrate-recognition domain) lectin, EGF-like domain and fibronectin type III domain containing 1	NM_031407, NCT22447.2	203183_at, 40920_at	NP_001358.2, EAW64914.1
Gene:ID:57 517	NCKIPSD	3	48,711,277	48,720,204	12,037	-	1	4_A3'5_uNG7_ilun_lncRNA_AR..1.3907	23910	5downstream	0	1	0	17	20	13	1	2_A3'5_uNG7_ilun_lncRNA_AR..1	30	Gene:NCKIPSD	DIP, WASH_DIP1, WASLBP, AF3P21, ORF1, NCKIPSD, MGC23991, SPIN90	NCK-interacting protein with SH3 domain	NM_139231, NM_018449, NCT22823398.0, NCT22823399.0, NCT22823528.0	218114_at, 218116_at, 218117_at, 219897_at, 233169_at	NP_569191.1, NP_060727.1, EAW64913.1, EAW64916.1, EAW64917.1, EAW64918.1
Gene:ID:78 6	SLC25A20	3	48,894,196	48,936,402	42,246	+	1	4_A3'5_EGR1..1.8123	176	up gene	0	0	1	16	12	17	1	4_A3'5_EGR1..1	17	Gene:SLC25A20	SLC25A20, CACT, CAC	solute carrier family 25 (beta-tic/alpha-ketoglutarate transporter), member 20	NM_000387, NCT16192.3	209582_at	NP_000378.1, EAW64929.1



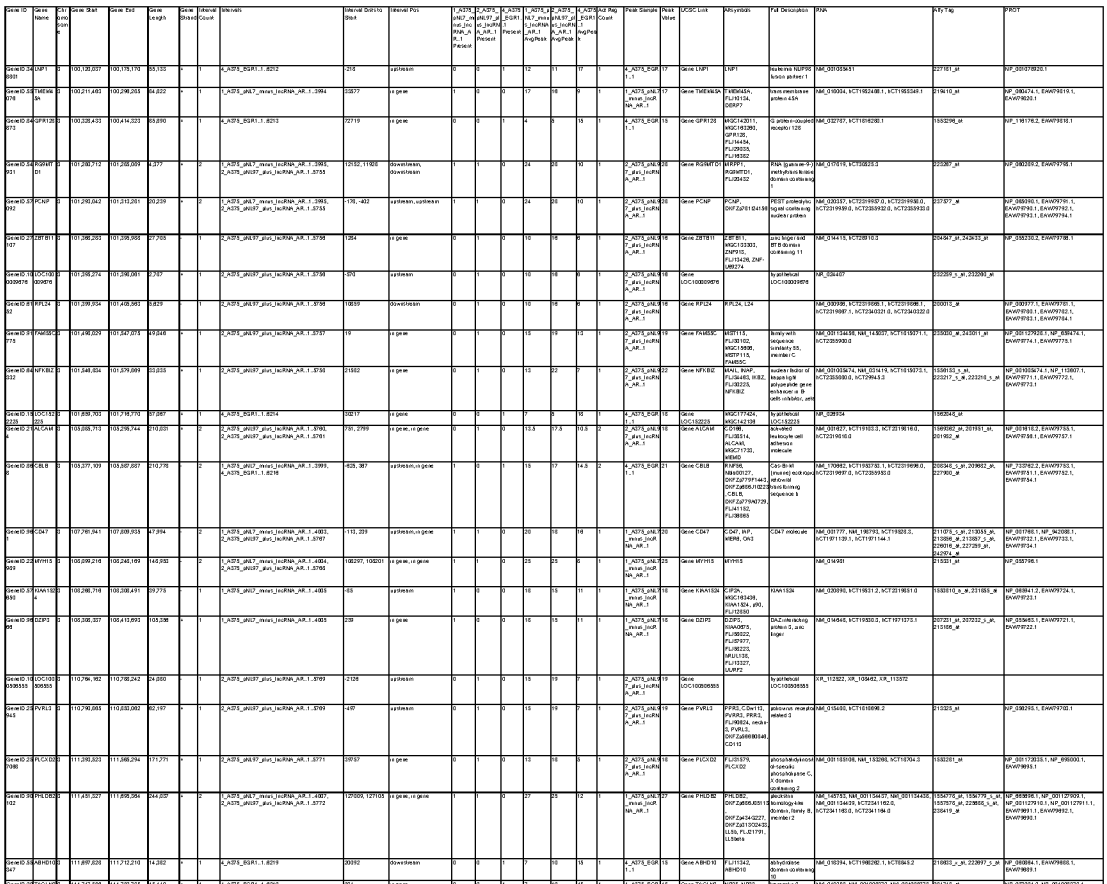
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_pHL97_plus_lncRNA_IR_1 Present	2_A375_pHL97_plus_lncRNA_IR_1 Present	4_A375_pHL97_plus_lncRNA_IR_1 Present	1_A375_pHL97_plus_lncRNA_IR_1 Avg Reads	2_A375_pHL97_plus_lncRNA_IR_1 Avg Peak	4_A375_pHL97_plus_lncRNA_IR_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbol	Full Description	RNA	Ally Tag	PROT
GeneID:84435	C3orf71	3	49,355,221	49,356,615	1,397	-	2	2_A375_pHL97_plus_lncRNA_IR_1.3855, A_A375_EGR1_1.8124	596, 1010	vs gene, vs gene	0	1	1	13	20	18	1	2_A375_pHL97_plus_lncRNA_IR_1	20	Gene C3orf71	C3orf71	chromosome 3 open reading frame 71	NM_001123045	1539532_at	NP_001117517.1
GeneID:10	ARI2	3	49,356,281	49,622,974	66,693	+	2	2_A375_pHL97_plus_lncRNA_IR_1.3855, A_A375_EGR1_1.8124	-57, +75	upstream, upstream	0	1	1	13	20	18	1	2_A375_pHL97_plus_lncRNA_IR_1	20	Gene ARI2	FLJ23521, ARI2, ARIH2, FLJ16556, TRAD1	ariadne homolog (Drosophila)	NM_006321, NCT1551071.1, NCT2251551.0, NCT2251922.0, NCT2251933.0	1539121_s_at, 201226_s_at, 201227_s_at, 219305_s_at, 239095_at	NP_006312.1, ENSP00000..., ENSP00000..., ENSP00000...
GeneID:84	PHTF1	3	49,627,341	49,644,382	17,041	+	4	2_A375_pHL97_plus_lncRNA_IR_1.3859, A_A375_EGR1_1.8125, A_A375_EGR1_1.8126, A_A375_EGR1_1.8127	17439, 12438, 17923, 28691	downstream, vs gene, downstream, downstream	0	1	1	13	12	18.33	3	2_A375_pHL97_plus_lncRNA_IR_1	22	Gene PHTF1	PHTF1, PHTF1A, HPH4, PHTA, EULHd, PHL, PHTA4	putative homeodomain transcription factor 1	NM_177939, NM_177938, NCT1551039.1, NCT2251585.1, NCT2251588.1, NCT2251589.1, NCT2251591.1, NCT23634.4	222123_s_at	NP_808858.1, NP_808857.2, ENSP00000..., ENSP00000..., ENSP00000..., ENSP00000...
GeneID:11	WDR6	3	49,644,657	49,653,356	8,749	+	11	1_A375_pHL97_minus_lncRNA_IR_1.3909, 2_A375_pHL97_plus_lncRNA_IR_1.3909, 2_A375_pHL97_plus_lncRNA_IR_1.3910, 2_A375_pHL97_plus_lncRNA_IR_1.3911, A_A375_EGR1_1.8125, A_A375_EGR1_1.8126, A_A375_EGR1_1.8127, A_A375_EGR1_1.8128, A_A375_EGR1_1.8129, A_A375_EGR1_1.8130, A_A375_EGR1_1.8131	14551, 183, 19027, 14331, 4981, 927, 9393, 10831, 13276, 14355, 17539	downstream, vs gene, downstream, downstream, upstream, vs gene, downstream, downstream, downstream, downstream, downstream, downstream	1	1	1	26.63	34.83	17.67	6	2_A375_pHL97_plus_lncRNA_IR_1	144	Gene WDR6	WDR6, MGC142027, FLJ10210, FLJ98107, FLJ32932, MGC126756	WD repeat domain 6	NM_018031	217754_s_at, 233573_s_at	NP_060501.3
GeneID:58	DALRD3	3	49,652,455	49,656,467	6,012	-	11	1_A375_pHL97_minus_lncRNA_IR_1.3909, 2_A375_pHL97_plus_lncRNA_IR_1.3909, 2_A375_pHL97_plus_lncRNA_IR_1.3910, 2_A375_pHL97_plus_lncRNA_IR_1.3911, A_A375_EGR1_1.8126, A_A375_EGR1_1.8127, A_A375_EGR1_1.8128, A_A375_EGR1_1.8129, A_A375_EGR1_1.8130, A_A375_EGR1_1.8131, A_A375_EGR1_1.8132	-1621, -1607, -1621, -1621, 12203, 4433, 3269, 481, -625, 4029, -5349	upstream, downstream, vs gene, upstream, downstream, vs gene, vs gene, vs gene, vs gene, upstream, upstream, upstream, upstream, upstream	1	1	1	27.67	37.3	19	6	2_A375_pHL97_plus_lncRNA_IR_1	144	Gene DALRD3	DALRD3, FLJ10490	DALR ASCIZ duplicated domain containing 3	NM_030929998, NM_018114	219808_at, 221934_s_at	NP_001009816.1, NP_060564.3
GeneID:49	MIR423	3	49,657,561	49,657,667	106	-	9	1_A375_pHL97_minus_lncRNA_IR_1.3909, 2_A375_pHL97_plus_lncRNA_IR_1.3910, 2_A375_pHL97_plus_lncRNA_IR_1.3911, A_A375_EGR1_1.8127, A_A375_EGR1_1.8128, A_A375_EGR1_1.8129, A_A375_EGR1_1.8130, A_A375_EGR1_1.8131, A_A375_EGR1_1.8132	-1621, 2403, -1621, 3653, 2491, 4029, -5149	upstream, downstream, upstream, downstream, downstream, upstream, upstream, upstream, upstream	1	1	1	26.6	40.6	19.2	5	2_A375_pHL97_plus_lncRNA_IR_1	144	Gene MIR423	MIR1423, MIR425, bta-mir-425	mouse RNA 425	NR_029945		
GeneID:25	NDUFA13	3	49,657,561	49,657,667	106	-	9	1_A375_pHL97_minus_lncRNA_IR_1.3909, 2_A375_pHL97_plus_lncRNA_IR_1.3910, 2_A375_pHL97_plus_lncRNA_IR_1.3911, A_A375_EGR1_1.8127, A_A375_EGR1_1.8128, A_A375_EGR1_1.8129, A_A375_EGR1_1.8130, A_A375_EGR1_1.8131, A_A375_EGR1_1.8132	1800, 3944, 1800, -2076, 2745, 168, 1656, 4988, 6908	vs gene, upstream, vs gene, upstream, vs gene, vs gene, vs gene, downstream, downstream	1	1	1	26.6	40.6	19.2	5	2_A375_pHL97_plus_lncRNA_IR_1	144	Gene NDUFA13	C3orf60, E3-3, DKFZp564J0123, NDUFA13, GRIM-19, MGC10327	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 (cerebellar fold) 3	NM_199080, NM_198070, NM_198073, NM_199074, NCT1551138.1, NCT2341177.0, NCT2341750.0, NCT07722.2	220177_at	NP_510332.1, NP_510333.1, NP_510334.1, NP_115386.1, ENSP00000..., ENSP00000..., ENSP00000...
GeneID:49	MIR191	3	49,656,051	49,656,142	91	-	9	1_A375_pHL97_minus_lncRNA_IR_1.3909, 2_A375_pHL97_plus_lncRNA_IR_1.3910, 2_A375_pHL97_plus_lncRNA_IR_1.3911, A_A375_EGR1_1.8127, A_A375_EGR1_1.8128, A_A375_EGR1_1.8129, A_A375_EGR1_1.8130, A_A375_EGR1_1.8131, A_A375_EGR1_1.8132	1396, 2876, 1396, 4110, 2974, 126, -580, -4334, 6864	upstream, downstream, upstream, downstream, downstream, downstream, upstream, upstream, upstream	1	1	1	26.6	40.6	19.2	5	2_A375_pHL97_plus_lncRNA_IR_1	144	Gene MIR191	miR-191, MIR191, MIRN191	mouse RNA 191	NR_029890		
GeneID:38	MPDH2	3	49,661,700	49,666,675	5,117	-	9	1_A375_pHL97_minus_lncRNA_IR_1.3909, 2_A375_pHL97_plus_lncRNA_IR_1.3910, 2_A375_pHL97_plus_lncRNA_IR_1.3911, A_A375_EGR1_1.8127, A_A375_EGR1_1.8128, A_A375_EGR1_1.8129, A_A375_EGR1_1.8130, A_A375_EGR1_1.8131, A_A375_EGR1_1.8132	2327, -1851, 2327, 12843, 11707, 6839, 7983, 4379, 99	downstream, downstream, downstream, downstream, downstream, downstream, downstream, vs gene, vs gene	1	1	1	26.6	40.6	19.2	5	2_A375_pHL97_plus_lncRNA_IR_1	144	Gene MPDH2	MPDH4, MPD2, MPDH2	MP protein 5-monocistronic(alpha) dehydrogenase 2	NM_030864	201992_s_at, 241373_at	NP_0900075.2
GeneID:54	GRHCH1	3	49,667,142	49,731,904	64,762	-	9	1_A375_pHL97_minus_lncRNA_IR_1.3909, 1_A375_pHL97_minus_lncRNA_IR_1.3910, 2_A375_pHL97_plus_lncRNA_IR_1.3911, 2_A375_pHL97_plus_lncRNA_IR_1.3912, A_A375_EGR1_1.8126, A_A375_EGR1_1.8130, A_A375_EGR1_1.8131, A_A375_EGR1_1.8132	72616, -484, 72616, -484, 73468, 72312, 69606, 64695, 272	downstream, upstream, downstream, upstream, downstream, downstream, downstream, downstream, upstream	1	1	1	52.75	73.25	30.25	4	2_A375_pHL97_plus_lncRNA_IR_1	144	Gene GRHCH1	MGC131655, FLJ30299, GRHCH1	glutamine-rich 1	NM_017730, NM_186690	209974_s_at, 229606_at	NP_060200.2, NP_942501.1
GeneID:59	QARS	3	49,135,365	49,142,171	6,806	-	4	1_A375_pHL97_minus_lncRNA_IR_1.3910, 2_A375_pHL97_plus_lncRNA_IR_1.3912, 2_A375_pHL97_plus_lncRNA_IR_1.3913, A_A375_EGR1_1.8134, A_A375_EGR1_1.8135	19503, 10230, 9810293	downstream, vs gene, vs gene, downstream	1	1	1	51.5	65	17.5	2	2_A375_pHL97_plus_lncRNA_IR_1	117	Gene QARS	PRO2193, GLNRS, QARS	glutaminyl-tRNA synthetase	NM_005051, NCT1551141.0, NCT2340590.0, NCT60229.2	217568_at	NP_005042.1, ENSP00000..., ENSP00000...
GeneID:10	USP19	3	49,148,106	49,185,213	37,108	+	4	2_A375_pHL97_plus_lncRNA_IR_1.3913, 2_A375_pHL97_plus_lncRNA_IR_1.3914, A_A375_EGR1_1.8134, A_A375_EGR1_1.8135	18697, 5, 5, -5403	downstream, vs gene, vs gene, upstream	0	1	1	11.67	16.33	10.67	3	4_A375_EGR1_1.1	28	Gene USP19	CANYON, USP19	ubiquitin specific peptidase 19	NM_006677, NCT1616288.3, NCT1551074.2, NCT2345317.1	214874_at, 228537_at	NP_006666.1, ENSP00000..., ENSP00000...
GeneID:39	LIAS	3	49,155,347	49,170,599	15,252	+	4	1_A375_pHL97_minus_lncRNA_IR_1.3911, 2_A375_pHL97_plus_lncRNA_IR_1.3914, A_A375_EGR1_1.8134, A_A375_EGR1_1.8135	4441, 12391, 12391, 6993	upstream, downstream, vs gene, downstream, vs gene	1	1	1	14	16.33	19.33	3	4_A375_EGR1_1.1	28	Gene LIAS	LIAS2, LIAS	lipoyl synthase, beta S (Bernus S)	NM_032302, NCT1982108.1, NCT60222.3	218264_s_at	NP_0322303.2, ENSP00000..., ENSP00000...
GeneID:84	CCDC71	3	49,199,988	49,203,765	3,817	-	1	2_A375_pHL97_plus_lncRNA_IR_1.3915	-39	upstream	0	1	0	16	23	12	1	2_A375_pHL97_plus_lncRNA_IR_1	23	Gene CCDC71	FLJ13629, FLJ12600, CCDC71	coiled-coil domain containing 71	NM_032903, NCT0238633.0	219883_at	NP_3769344.3, ENSP00000...
GeneID:23	KLHDC8B	3	49,209,916	49,213,919	4,003	+	1	2_A375_pHL97_plus_lncRNA_IR_1.3915	-5784	upstream	0	1	0	16	23	12	1	2_A375_pHL97_plus_lncRNA_IR_1	23	Gene KLHDC8B	MGC23597, FLJ11002, KLHDC8B	kelch domain containing 8B	NM_173548, NCT1612812, NCT2251803.0, NCT2251830.0	223783_at	NP_7758171.1, ENSP00000..., ENSP00000...
GeneID:37	C3orf62	3	49,209,230	49,214,308	5,078	-	1	2_A375_pHL97_plus_lncRNA_IR_1.3916	298	vs gene	0	1	0	12	16	11	1	2_A375_pHL97_plus_lncRNA_IR_1	16	Gene C3orf62	MGC23281, MGC61980, FLJ43654, MGC62079, C3orf62	chromosome 3 open reading frame 62	NM_176582, NCT1622096.1	1569274_at, 241617_at	NP_7429644.1, ENSP00000...
GeneID:10	MIR4271	3	49,211,185	49,211,819	635	+	1	2_A375_pHL97_plus_lncRNA_IR_1.3916	3539	downstream	0	1	0	12	16	11	1	2_A375_pHL97_plus_lncRNA_IR_1	16	Gene MIR4271	MIR4271	mouse RNA 4271	NR_039733		
GeneID:75	USP4	3	49,314,877	49,377,836	62,959	-	3	2_A375_pHL97_minus_lncRNA_IR_1.3912, 2_A375_pHL97_plus_lncRNA_IR_1.3916, 2_A375_pHL97_plus_lncRNA_IR_1.3917	98, 65424, -160	vs gene, downstream, upstream	1	1	0	19	19.5	12	2	2_A375_pHL97_minus_lncRNA_IR_1	28	Gene USP4	USP4, MGC149868, MGC149869, Unph, UNP	ubiquitin specific peptidase 4 (proto-oncogene)	NM_199443, NM_003363, NCT11303.0, NCT1551035.1, NCT2356533.0, NCT2356536.0, NCT2356539.0, NCT2354172.0	202861_at, 202862_s_at, 202863_at	NP_9356751.1, NP_003354.2, ENSP00000..., ENSP00000..., ENSP00000...
GeneID:10	LOC100289130	3	49,365,351	49,397,760	32,409	+	2	2_A375_pHL97_minus_lncRNA_IR_1.3912, 2_A375_pHL97_plus_lncRNA_IR_1.3917	-7911, -7655	upstream, upstream	1	1	0	26	23	13	1	1_A375_pHL97_minus_lncRNA_IR_1	28	Gene LOC100289130		hypothetical LOC100289130	XR_112309, XR_112303, XR_110035, XR_110004, XR_113497		
GeneID:38	RHOA	3	49,396,576	49,449,926	52,945	-	2	2_A375_pHL97_minus_lncRNA_IR_1.3913, A_A375_EGR1_1.8136	-330, -330	upstream, upstream	1	2	1	20	11	17	1	1_A375_pHL97_minus_lncRNA_IR_1	20	Gene RHOA	RHOH12, ARH6, ARH12, ARH12	ras homolog gene family, member A	NM_001664, NCT1112112, NCT1551060.0, NCT2265220.0	1555814_a_at, 200083_s_at, 240327_at	NP_0016655.1, ENSP00000..., ENSP00000...
GeneID:69	TCTA	3	49,449,639	49,453,909	4,270	+	2	2_A375_pHL97_minus_lncRNA_IR_1.3913, A_A375_EGR1_1.8136	217, 217	vs gene, vs gene	1	2	1	20	11	17	1	1_A375_pHL97_minus_lncRNA_IR_1	20	Gene TCTA	TCTA		NM_022171, NCT112081, NCT1551060.0, NCT2251622.0	200084_s_at	NP_071923.1, ENSP00000..., ENSP00000...
GeneID:25	AIRT	3	49,454,211	49,460,111	5,900	-	2	2_A375_pHL97_minus_lncRNA_IR_1.3913, A_A375_EGR1_1.8136	10253, 10235	downstream, downstream	1	2	1	20	11	17	1	1_A375_pHL97_minus_lncRNA_IR_1	20	Gene AIRT	QC2, AIRT, QC3T, NKH, QC4T	aminoacetylhistamine uptake	NM_030561, NM_001164710, NM_001164711, NM_001164712, NR_029635	204264_at	NP_0904172.2, NP_0011639162.1, NP_0011639163.1, NP_0011639164.1, ENSP00000...
GeneID:64	NICN1	3	49,459,799	49,466,797	6,991	-	2	2_A375_pHL97_minus_lncRNA_IR_1.3913, A_A375_EGR1_1.8136	16931, 16931	downstream, downstream	1	2	1	20	11	17	1	1_A375_pHL97_minus_lncRNA_IR_1	20	Gene NICN1	MGC12939, NICN1	nicolin 1	NM_032116	223442_at	NP_1139921.1
GeneID:89	BSN	3	49,591,932	49,709,982	117,050	+	2	A_A375_EGR1_1.8138, A_A375_EGR1_1.8139	109573, 119902	vs gene, downstream	0	0	1	11	9	17.5	2	4_A375_EGR1_1.1	16	Gene BSN	BSN, ZNF231	bassoon (cytomatrix active zone)	NM_003458, NCT2201628.0, VCT6987.2	204568_at	NP_3854492.2, ENSP00000...
GeneID:22	APEH	3	49,711,435	49,720,904	9,470	+	3	2_A375_pHL97_plus_lncRNA_IR_1.3916, A_A375_EGR1_1.8138, A_A375_EGR1_1.8140	13073, 389, 13803	downstream, vs gene, downstream	0	0	1	16	20	16	2	2_A375_pHL97_plus_lncRNA_IR_1	28	Gene APEH	DNF1802, D3F1802, D3S4456, APH, ACP15, MGC2178, OPH, APEH	N-acetylneuraminoyl-peptide hydrolase	NM_001640, NCT1615837.1, NCT1615838.1, NCT1623077.2, NCT1623078.2, NCT2261631.0	200264_s_at, 243013_x_at	NP_3304813.3, ENSP00000..., ENSP00000..., ENSP00000...
GeneID:44	MST1	3	49,721,360	49,726,196	4,836	-	3	2_A375_pHL97_plus_lncRNA_IR_1.3916, A_A375_EGR1_1.8139, A_A375_EGR1_1.8140	-612, 14372, -644	upstream, downstream, upstream	0	1	1	16	20	16	2	2_A375_pHL97_plus_lncRNA_IR_1	28	Gene MST1	NPT1822, D3F1822, D3F1822, MST1, HGFL, HEP	macrophage stimulating 1 (hepatocyte growth factor-like)	NM_0209990, NCT2269436.0, NCT2269501.0, NCT2269502.0, NCT2269504.0, NCT2269509.0	209914_x_at, 216232_x_at	NP_3962763, ENSP00000..., ENSP00000..., ENSP00000...
GeneID:85	RNF123	3	49,726,960	49,765,962	31,972	+	4	2_A375_pHL97_plus_lncRNA_IR_1.3916, 2_A375_pHL97_plus_lncRNA_IR_1.3919, A_A375_EGR1_1.8140, A_A375_EGR1_1.8141	10, 34264, 50, 12022	vs gene, downstream, vs gene, vs gene	0	1	1	16	16.33	17	3	2_A375_pHL97_plus_lncRNA_IR_1	28	Gene RNF123	FP1479, DKFZp686C2222, KPC1, MGC163504, FLJ12565, RNF123	ring finger protein 123	NM_032584	221085_s_at, 224158_s_at	NP_0715437.2
GeneID:38	AMIGO2	3	49,754,267	49,757,356	2,971	-	1	2_A375_pHL97_plus_lncRNA_IR_1.3919	-4108	upstream	0	1	0	19	22	18	1	2_A375_pHL97_plus_lncRNA_IR_1	22	Gene AMIGO2	AMIGO2, MGC120552, AMIGO-2	adhesion molecule with Ig-like domain 2	NM_181722	229717_at	NP_9425151
GeneID:25	GMFPB	3	49,756,922	49,761,364	4,442	-	1	2_A375_pHL97_plus_lncRNA_IR_1.3919	440	vs gene	0	1	0	19	22	18	1	2_A375_pHL97_plus_lncRNA_IR_1	22	Gene GMFPB	KIAA1851, GMFPB	GDP-mannose pyrophosphorylase B	NM_013334, NM_021971, NCT11197.3, NCT1197797.1, NCT1197796.1, NCT2269457.0	219203_s_at, 222710_at	NP_0374462, NP_0660967, ENSP00000..., ENSP00000..., ENSP00000...
GeneID:90	IP6K1	3	49,761,726	49,822,473	62,215	-	2	2_A375_pHL97_plus_lncRNA_IR_1.3919, A_A375_EGR1_1.8142	62629, -251	downstream, upstream	0	1	1	16.5	16.5	16.5	2	2_A375_pHL97_plus_lncRNA_IR_1	22	Gene IP6K1	PLCB, MGC29023, IP6K1, IHP61	inositol hexakisphosphate kinase 1	NM_153373, NM_201803115, NCT11197.3, NCT2262630.0, NCT2262634.0, NCT2341181.0, NCT2341182.0	212439_at	NP_8560335.1, NP_8010981113, ENSP00000..., ENSP00000..., ENSP00000...
GeneID:10	LOC100289738	3	49,822,913	49,823,705	792	-	1	A_A375_EGR1_1.8142	-519	upstream	0	0	1	14	11	17	1	4_A375_EGR1_1.1	17	Gene LOC100289738		hypothetical LOC100289738	XR_112304, XR_110009		
GeneID:38	C3orf64	3	49,826,163	49,837,264	11,089	-	3	2_A375_pHL97_plus_lncRNA_IR_1.3920, A_A375_EGR1_1.8142, A_A375_EGR1_1.8143	-3002, 13530, 4074	upstream, downstream, upstream	0	1	1	11.33	14.67	13	3	2_A375_pHL97_plus_lncRNA_IR_1	24	Gene C3orf64	PRO34293, MGC164962, C3orf64	cadherin-related family member 4	NM_0310734		NP_0010734.2
GeneID:38	C3orf54	3	49,840,807	49,842,481	1,778	-	2	2_A375_pHL97_plus_lncRNA_IR_1.3920, A_A375_EGR1_1.8143	-431, 941	upstream, vs gene	0	1	1	10	16.5	14	2	2_A375_pHL97_plus_lncRNA_IR_1	24	Gene C3orf54	C3orf54, HAKAI, MGC20418	chromosome 3 open reading frame 54	NM_033770, NCT1622094.1	225807_at	NP_3782451, ENSP00000...
GeneID:73	UBA7	3	49,842,856	49,881,391	38,535	-	2	2_A375_pHL97_plus_lncRNA_IR_1.3920, A_A375_EGR1_1.8143	11133, 10080	downstream, downstream	0	1	1	10	16.5	14	2	2_A375_pHL97_plus_lncRNA_IR_1	24	Gene UBA7	E1, UBE2, UBA7, UBE1L, UBA1B, MGC12712	ubiquitin-like modifier-activating enzyme 7	NM_003335, NCT1622058.2, NCT2262622.0	1294_at, 203230_s_at	NP_0033262, ENSP00000..., ENSP00000...
GeneID:10	TRAIP	3	49,866,026	49,870,992	27,964	-	1	2_A375_pHL97_plus_lncRNA_IR_1.3921	197	vs gene	0	1	0	20	17	11	1	4_A375_EGR1_1.1	17	Gene TRAIP	RNF206, TRIP, TRAIP	TRAF interacting protein	NM_005879, NCT1982108.2, NCT62779.4	203898_at	NP_3597763, ENSP00000...
GeneID:79	CAMKV	3	49,895,422	49,907,399	11,947	-	3	2_A375_pHL97_minus_lncRNA_IR_1.3914, 2_A375_pHL97_plus_lncRNA_IR_1.3921, 2_A375_pHL97_plus_lncRNA_IR_1.3922	3287, 13554, 1885	vs gene, downstream, vs gene	1	1	0	22.5	22.5	16	2	2_A375_pHL97_plus_lncRNA_IR_1	28	Gene CAMKV	VACAM03, MGC45407, VGL, CAMKV	CaM kinase-like vesicle-associated	NM_0204349, NCT1982108.1, NCT1982107.1, NCT2354185.0, NCT2354186.0, NCT2354187.0, NCT2354188.0, NCT2354189.0, NCT07060.3	219385_s_at	NP_0769512, ENSP00000..., ENSP00000..., ENSP00000..., ENSP00000...
GeneID:64	MONTA1	3	49,948,932	49,987,443	31,143	-	3	2_A375_pHL97_plus_lncRNA_IR_1.3921, 2_A375_pHL97_plus_lncRNA_IR_1.3944, A_A375_EGR1_1.8145	-10123, 243, 10219	upstream, vs gene, upstream	0	1	1	14	22	19.5	2	2_A375_pHL97_plus_lncRNA_IR_1	25	Gene MONTA	FLJ90566, SAND1, MGC13272, MONTA	MONT1 homolog 1 (yeast)	NM_032355, NM_001142501, NCT1985594.1, NCT67454.2	224300_s_at	NP_1107012, NP_0011139731, ENSP00000...
GeneID:10	RBM6	3	49,977,477	50,114,865	137,388	+	5	2_A375_pHL97_plus_lncRNA_IR_1.3921, A_A375_EGR1_1.8144, A_A375_EGR1_1.8145	91, -19277, 187	vs gene, upstream, vs gene	1	1	1	14	22	19.5	2	2_A375_pHL97_plus_lncRNA_IR_1	25	Gene RBM6	DKFZp686B03077, RBM6, FLJ90317, g16, NY-LU-12, DEF2, DEF-2, HLC-11, FLJ39445, FLJ42036	RNA binding motif protein 6	NM_0211672, NM_003777, NCT62526.4	1558972_a_at, 201967_at, 220029_at	NP_0011619541.1, NP_0207651, ENSP00000...
GeneID:84	SEMA3F	3	50,192,540	50,226,908	33,860	-	3	A_A375_EGR1_1.8146, A_A375_EGR1_1.8147, A_A375_EGR1_1.8148	21549, 29072, 2247	vs gene, vs gene, vs gene	0	1	1	9	9	17.33	3	4_A375_EGR1_1.1	19	Gene SEMA3F	SEMAH-IV, SEMPA, SEMAA, SEMA3F	semaphorin domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	NM_004186, NCT1551098.1, NCT2259089.0, NCT62326.3	206552_s_at, 209733_at, 239998_at	NP_0041773, ENSP00000..., ENSP00000..., ENSP00000...
GeneID:89	MIR598	3	50,210,709	50,210,802	93	-	1	A_A375_EGR1_1.8148	3438	downstream	0	0	1	3	3	15	1	4_A375_EGR1_1.1	15	Gene MIR598	MIR598, MIRN598, bta-mir-598	mouse RNA 598	NR_030291		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:2779	GNAT1	3	50,229,043	50,235,129	6,086	+	2	4_A375_EGR1..1..6147, 4_A375_EGR1..1..6148	-7123, -3846	upstream, upstream	0	0	1	8	8	18.5	2	4_A375_EGR1..1	19	Gene GNAT1	CSNBAD3, GNATR, GNAT1, GBT1	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1	NM_000172, NM_144499, hCT2279592.0, hCT2279594.0	207514_s_at, 214268_at	NP_000163.2, NP_653082.1, EAW65047.1, EAW65048.1
GeneID:10991	SLC38A3	3	50,242,692	50,258,406	15,714	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3915, 2_A375_pNL97_plus_lncRNA_AR..1..5624, 4_A375_EGR1..1..6149	22384, 22384, 7838	downstream, downstream, in gene	1	1	1	19	17.5	14	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene SLC38A3	NAT1, SN1, G17, SLC38A3	solute carrier family 38, member 3	NM_006841, hCT2279595.0, hCT8514.3	205972_at	NP_006832.1, EAW65049.1, EAW65050.1
GeneID:2771	GNAI2	3	50,273,647	50,296,786	23,139	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3915, 2_A375_pNL97_plus_lncRNA_AR..1..5624, 4_A375_EGR1..1..6150	-8591, -8591, 1905	upstream, upstream, in gene	1	1	1	19	18.5	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene GNAI2	H_LUCA15.1, GNAI2B, H_LUCA16.1, GIP, GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	NM_002070, NM_001166425, hCT2279597.0, hCT2279598.1, hCT2344929.0, hCT2344930.0, hCT2354127.0, hCT2354128.0	201040_at	NP_002061.1, NP_001159897.1, EAW65051.1, EAW65052.1, EAW65055.1, EAW65056.1, EAW65053.1, EAW65054.1
GeneID:7869	SEMA3B	3	50,305,040	50,314,573	9,533	+	2	4_A375_EGR1..1..6151, 4_A375_EGR1..1..6152	6352, 19131	in gene, downstream	0	0	1	9.5	9	18.5	2	4_A375_EGR1..1	21	Gene SEMA3B	SEMA3B, LUCA-1, semaV, SEMA5, SEMAA, SemA, FLJ34863	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	NM_004636, NM_001005914, hCT1951050.1, hCT1951051.1, hCT2279604.0, hCT2279605.0, hCT2354055.0, hCT8516.3	203070_at, 203071_at	NP_004627.1, NP_001005914.1, EAW65062.1, EAW65063.1, EAW65065.1, EAW65066.1, EAW65064.1, EAW65067.1
GeneID:132228	C3orf45	3	50,316,518	50,325,545	9,027	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3916, 2_A375_pNL97_plus_lncRNA_AR..1..5625, 4_A375_EGR1..1..6151, 4_A375_EGR1..1..6152	13434, 13468, -5126, 7853	downstream, downstream, upstream, in gene	1	1	1	24.67	24.33	18.33	3	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene C3orf45	C3orf45, FLJ38608	chromosome 3 open reading frame 45	NM_153215, hCT8529.4	237024_at	NP_694947.1, EAW65068.1
GeneID:7866	IFRD2	3	50,325,163	50,330,026	4,863	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3916, 1_A375_pNL7_minus_lncRNA_AR..1..3917, 2_A375_pNL97_plus_lncRNA_AR..1..5625, 2_A375_pNL97_plus_lncRNA_AR..1..5626, 4_A375_EGR1..1..6152	74, -6678, 42, -6678, 5855	in gene, upstream, in gene, upstream, downstream	1	1	1	33.33	34.33	16	3	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene IFRD2	IFRD2, SKMc15, FLJ40446, IFNRP, SM15	interferon-related developmental regulator 2	NM_006764, hCT2344548.1, hCT2344550.1	209100_at	NP_006755.4, EAW65069.1, EAW65070.1
GeneID:8372	HYAL3	3	50,330,262	50,336,899	6,637	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3916, 1_A375_pNL7_minus_lncRNA_AR..1..3917, 2_A375_pNL97_plus_lncRNA_AR..1..5625, 2_A375_pNL97_plus_lncRNA_AR..1..5626, 4_A375_EGR1..1..6152	6947, 195, 6915, 195, 12726	downstream, in gene, downstream, in gene, downstream	1	1	1	33.33	34.33	16	3	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene HYAL3	Minna14, LUCA3, LUCA-3, LUCA14, HYAL3, HYAL-3	hyaluronoglucosaminidase 3	NM_003549, hCT2344547.1, hCT2344549.1, hCT2344551.1, hCT2348436.0, hCT2348437.0, hCT2348438.0	211728_s_at	NP_003540.2, EAW65075.1, EAW65072.1, EAW65073.1, EAW65074.1, EAW65076.1, EAW65071.1
GeneID:24142	NAT6	3	50,333,833	50,336,712	2,879	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3916, 1_A375_pNL7_minus_lncRNA_AR..1..3917, 2_A375_pNL97_plus_lncRNA_AR..1..5625, 2_A375_pNL97_plus_lncRNA_AR..1..5626, 4_A375_EGR1..1..6152	6760, 8, 6728, 8, 12541	downstream, in gene, downstream, in gene, downstream	1	1	1	33.33	34.33	16	3	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene NAT6	NAT6, FUS2, FUS-2	N-acetyltransferase 6 (GCN5-related)	NM_012191, hCT2344537.1, hCT2344538.1, hCT2344539.1, hCT2344540.1, hCT2344543.1, hCT2350364.0	210874_s_at	NP_036323.2, EAW65077.1, EAW65078.1, EAW65079.1, EAW65081.1, EAW65082.1, EAW65080.1
GeneID:3373	HYAL1	3	50,337,320	50,349,812	12,492	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3916, 1_A375_pNL7_minus_lncRNA_AR..1..3917, 1_A375_pNL7_minus_lncRNA_AR..1..3918, 2_A375_pNL97_plus_lncRNA_AR..1..5625, 2_A375_pNL97_plus_lncRNA_AR..1..5626, 2_A375_pNL97_plus_lncRNA_AR..1..5627	19860, 13108, -9228, 19828, 13108, -9228	downstream, downstream, upstream, downstream, downstream, upstream	1	1	0	80	86	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	163	Gene HYAL1	NAT6, HYAL-1, MGC45987, LUCA1, HYAL1	hyaluronoglucosaminidase 1	NM_007312, NM_033159, NM_153281, NM_153282, NM_153283, NM_153285, hCT1951042.2, hCT1951043.2, hCT2350328.0, hCT2350329.0, hCT2350330.0, hCT2350331.0, hCT2350332.0, hCT2350333.0, hCT8509.3	210619_s_at	NP_009296.1, NP_149349.2, NP_695013.1, NP_695014.1, NP_695015.1, NP_695017.1, EAW65083.1, EAW65084.1, EAW65085.1, EAW65086.1, EAW65087.1, EAW65088.1, EAW65089.1, EAW65091.1, EAW65090.1
GeneID:8692	HYAL2	3	50,355,221	50,360,281	5,060	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3918, 2_A375_pNL97_plus_lncRNA_AR..1..5627	1241, 1241	in gene, in gene	1	1	0	149	163	18	1	2_A375_pNL97_plus_lncRNA_AR..1	163	Gene HYAL2	HYAL2, LUCA2, LuCa-2	hyaluronoglucosaminidase 2	NM_003773, NM_033158, hCT2282771.0, hCT2282772.1, hCT2282773.0	206855_s_at	NP_003764.3, NP_149348.2, EAW65092.1, EAW65093.1, EAW65094.1
GeneID:11334	TUSC2	3	50,362,341	50,365,668	3,327	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3918, 2_A375_pNL97_plus_lncRNA_AR..1..5627, 2_A375_pNL97_plus_lncRNA_AR..1..5628, 4_A375_EGR1..1..6153	6628, 6628, -9004, -9452	downstream, downstream, upstream, upstream	1	1	1	85.5	93	22.5	2	2_A375_pNL97_plus_lncRNA_AR..1	163	Gene TUSC2	PAP, PDAP2, C3orf11, TUSC2, FUS1	tumor suppressor candidate 2	NM_007275, hCT2282769.1, hCT2282774.0, hCT2344197.0	203272_s_at, 203273_s_at	NP_009206.1, EAW65096.1, EAW65095.1, EAW65097.1
GeneID:11186	RASSF1	3	50,367,217	50,378,367	11,150	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3918, 1_A375_pNL7_minus_lncRNA_AR..1..3919, 2_A375_pNL97_plus_lncRNA_AR..1..5627, 2_A375_pNL97_plus_lncRNA_AR..1..5628, 2_A375_pNL97_plus_lncRNA_AR..1..5629, 4_A375_EGR1..1..6153	19327, -10113, 19327, 3695, -10097, 3247	downstream, upstream, downstream, in gene, upstream, in gene	1	1	1	67.33	71.67	19.67	3	2_A375_pNL97_plus_lncRNA_AR..1	163	Gene RASSF1	RASSF1, 123F2, RDA32, NORE2A, RASSF1A, REH3P21	Ras association (RalGDS/AF-6) domain family member 1	NM_007182, NM_170714, NM_170713, NM_170712, hCT1951045.1, hCT1951046.1, hCT1957764.1, hCT1957765.1, hCT1957766.1	204346_s_at, 240278_at	NP_009113.3, NP_733832.1, NP_733830.1, NP_733831.1, EAW65100.1, EAW65101.1, EAW65098.1, EAW65099.1, EAW65102.1
GeneID:51364	ZMYND10	3	50,378,537	50,383,156	4,619	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3919, 2_A375_pNL97_plus_lncRNA_AR..1..5628, 2_A375_pNL97_plus_lncRNA_AR..1..5629, 4_A375_EGR1..1..6153	-5324, 8484, -5308, 8036	upstream, downstream, upstream, downstream	1	1	1	26.5	26	20.5	2	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene ZMYND10	ZMYND10, BLU, FLU	zinc finger, MYND-type containing 10	NM_015896, hCT1961317.1, hCT1961318.1, hCT8519.3	205714_s_at, 216663_s_at	NP_056980.2, EAW65103.1, EAW65104.1, EAW65105.1
GeneID:10641	TUSC4	3	50,384,919	50,388,486	3,567	-	7	1_A375_pNL7_minus_lncRNA_AR..1..3919, 1_A375_pNL7_minus_lncRNA_AR..1..3920, 2_A375_pNL97_plus_lncRNA_AR..1..5628, 2_A375_pNL97_plus_lncRNA_AR..1..5629, 2_A375_pNL97_plus_lncRNA_AR..1..5630, 4_A375_EGR1..1..6153, 4_A375_EGR1..1..6154	6, -8602, 13814, 22, -8698, 13366, -7450	in gene, upstream, downstream, in gene, upstream, downstream, upstream	1	1	1	21.25	21	17.5	4	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene TUSC4	NPR2, NPR2L, NPRL2, TUSC4	nitrogen permease regulator-like 2 (S. cerevisiae)	NM_006545, hCT1951055.1, hCT2354103.0, hCT2354104.0, hCT2354105.0, hCT2354106.0, hCT2354107.0, hCT8523.3	203246_s_at, 210373_at	NP_006536.3, EAW65106.1, EAW65108.1, EAW65109.1, EAW65110.1, EAW65112.1, EAW65107.1, EAW65111.1
GeneID:11068	CYB561D2	3	50,388,297	50,391,500	3,203	+	5	1_A375_pNL7_minus_lncRNA_AR..1..3919, 1_A375_pNL7_minus_lncRNA_AR..1..3920, 2_A375_pNL97_plus_lncRNA_AR..1..5629, 2_A375_pNL97_plus_lncRNA_AR..1..5630, 4_A375_EGR1..1..6154	183, 8791, 167, 8687, 7839	in gene, downstream, in gene, downstream, downstream	1	1	1	21	20.33	14.33	3	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene CYB561D2	101F6, TSP10, CYB561D2	cytochrome b-561 domain containing 2	NM_007022, hCT1951053.1, hCT1951054.1	209665_at	NP_008953.1, EAW65113.1, EAW65114.1
GeneID:11070	TMEM115	3	50,392,180	50,396,939	4,759	-	5	1_A375_pNL7_minus_lncRNA_AR..1..3919, 1_A375_pNL7_minus_lncRNA_AR..1..3920, 2_A375_pNL97_plus_lncRNA_AR..1..5629, 2_A375_pNL97_plus_lncRNA_AR..1..5630, 4_A375_EGR1..1..6154	8459, -149, 8475, -245, 1003	downstream, upstream, downstream, upstream, in gene	1	1	1	21	20.33	14.33	3	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene TMEM115	PL6, TMEM115	transmembrane protein 115	NM_007024, hCT2282746.0, hCT2282751.0, hCT8515.3	218267_s_at	NP_008955.1, EAW65115.1, EAW65116.1, EAW65117.1
GeneID:9254	CACNA2D2	3	50,400,230	50,540,892	140,662	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3920, 2_A375_pNL97_plus_lncRNA_AR..1..5630, 4_A375_EGR1..1..6154	143804, 143708, 144956	downstream, downstream, downstream	1	1	1	16	16	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CACNA2D2	KIAA0558, CACNA2D, LUAC11.1, CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	NM_001005505, NM_006030, NM_001174051, hCT2282744.0, hCT2282748.0, hCT2354111.0, hCT8527.3	204811_s_at	NP_001005505.1, NP_006021.2, NP_001167522.1, EAW65118.1, EAW65120.1, EAW65121.1, EAW65119.1
GeneID:100506825	LOC100506825	3	50,402,761	50,404,894	2,133	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3920, 2_A375_pNL97_plus_lncRNA_AR..1..5630, 4_A375_EGR1..1..6154	-5673, -5577, -6825	upstream, upstream, upstream	1	1	1	16	16	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LOC100506825		hypothetical LOC100506825	XR_110010		
GeneID:100506802	LOC100506802	3	50,404,933	50,405,828	895	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3920, 2_A375_pNL97_plus_lncRNA_AR..1..5630, 4_A375_EGR1..1..6154	-7845, -7749, -8997	upstream, upstream, upstream	1	1	1	16	16	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene LOC100506802		hypothetical LOC100506802	XR_110009, XR_113500		
GeneID:51161	C3orf18	3	50,595,456	50,608,458	13,002	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3922, 2_A375_pNL97_plus_lncRNA_AR..1..5632, 4_A375_EGR1..1..6155	1642, 1578, 1594	in gene, in gene, in gene	1	1	1	24	31	22	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene C3orf18	G20, C3orf18	chromosome 3 open reading frame 18	NM_001171740, NM_001171741, NM_001171743, NM_016210, hCT1951038.1, hCT1951039.1, hCT8506.1	219114_at	NP_001165211.1, NP_001165212.1, NP_057294.2, NP_001165214.2, EAW65122.1, EAW65124.1, EAW65123.1
GeneID:51409	HEMK1	3	50,606,909	50,622,422	15,513	+	3	1_A375_pNL7_minus_lncRNA_AR..1..3922, 2_A375_pNL97_plus_lncRNA_AR..1..5632, 4_A375_EGR1..1..6155	-93, -29, -45	upstream, upstream, upstream	1	1	1	24	31	22	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene HEMK1	MTQ1, FLJ22320, HEMK1, HEMK	HemK methyltransferase family member 1	NM_016173, hCT1951015.1, hCT2279613.0	1556092_s_at, 218820_s_at, 218821_at, 52159_at	NP_057257.1, EAW65126.1, EAW65125.1
GeneID:1154	CISH	3	50,643,885	50,649,262	5,377	-	1	4_A375_EGR1..1..6156	-5442	upstream	0	0	1	9	7	20	1	4_A375_EGR1..1	20	Gene CISH	CISH, CIS-1, G18, CIS, SOCS	cytokine inducible SH2-containing protein	NM_013324, NM_145071, hCT1961314.1, hCT1984716.1, hCT2354194.0, hCT8507.4	221223_x_at, 223377_x_at, 223961_s_at	NP_037456.5, NP_659508.1, EAW65127.1, EAW65128.1, EAW65129.1, EAW65130.1
GeneID:7867	MAPKAPK3	3	50,654,601	50,686,719	32,118	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5633, 4_A375_EGR1..1..6156	10295, 103	in gene, in gene	0	1	1	11.5	11.5	15.5	2	4_A375_EGR1..1	20	Gene MAPKAPK3	MAPKAP3, MAPKAPK3, 3PK	mitogen-activated protein kinase-activated protein kinase 3	NM_004635, hCT1951041.1, hCT2279616.0, hCT8508.3	202787_s_at, 202788_at	NP_004626.1, EAW65132.1, EAW65131.1, EAW65133.1
GeneID:9730	VPRBP	3	51,433,298	51,534,018	100,720	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5634	418	in gene	0	1	0	14	15	14	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene VPRBP	VPRBP, MGC102804, KIAA0800, DCAF1	Vpr (HIV-1) binding protein	NM_014703, NM_001171904, hCT1951016.1, hCT2279214.0, hCT2279215.0, hCT8380.3	204376_at, 204377_s_at, 226476_s_at, 226477_at, 226481_at	NP_055518.1, NP_001165375.1, EAW65140.1, EAW65141.1, EAW65142.1, EAW65143.1
GeneID:23132	RAD54L2	3	51,575,596	51,697,634	122,038	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3923, 2_A375_pNL97_plus_lncRNA_AR..1..5635, 4_A375_EGR1..1..6157, 4_A375_EGR1..1..6158	-2986, -2988, -3052, 130015	upstream, upstream, upstream, downstream	1	1	1	15.5	18	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene RAD54L2	KIAA0809, ARIP4, FLJ22400, HSPC325, FLJ21396, SRISNF2L, RAD54L2	RAD54-like 2 (S. cerevisiae)	NM_015106	213205_s_at	NP_055921.2
GeneID:51368	TEX264	3	51,705,222	51,738,339	33,117	+	1	4_A375_EGR1..1..6158	389	in gene	0	0	1	14	14	14	1	4_A375_EGR1..1	14	Gene TEX264	SIG11, FLJ13935, ZSIG11, TEX264, DKFZp451H0417	testis expressed 264	NM_015926, NM_001129884, NR_024012	218548_x_at, 233350_s_at	NP_057010.1, NP_001123356.1
GeneID:2912	GRM2	3	51,741,081	51,752,629	11,548	+	1	4_A375_EGR1..1..6159	8727	in gene	0	0	1	4	6	23	1	4_A375_EGR1..1	23	Gene GRM2	mGlu2, MGLUR2, GPRC1B, GLUR2, GRM2	glutamate receptor, metabotropic 2	NM_000839, NM_001130063, hCT33862.3	208465_at, 241802_x_at	NP_000830.2, NP_001123535.1, EAW65150.1
GeneID:100506840	LOC100506840	3	51,851,620	51,864,874	13,254	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5636	19292	downstream	0	1	0	11	15	5	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LOC100506840		hypothetical LOC100506840	XR_112498, XR_110011, XR_113451		
GeneID:401067	IQCF3	3	51,862,569	51,864,876	2,307	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5636	8343	downstream	0	1	0	11	15	5	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene IQCF3	IQCF3	IQ motif containing F3	NM_001085479	1555235_s_at, 236671_s_at	NP_001078948.1
GeneID:9136	RRP9	3	51,967,446	51,975,922	8,476	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3924, 1_A375_pNL7_minus_lncRNA_AR..1..3925, 2_A375_pNL97_plus_lncRNA_AR..1..5637	12274, -430, 12210	downstream, upstream, downstream	1	1	0	24.5	26.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene RRP9	RRP9, U3-55K, RNU3IP2	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)	NM_004704, hCT33861.2	204133_at	NP_004695.1, EAW65159.1
GeneID:10039	PARP3	3	51,976,361	51,982,883	6,522	+	1	1_A375_pNL7_minus_lncRNA_AR..1..3925	-9	upstream	1	0	0	23	14	15	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene PARP3	PADPRT-3, ADPRT3, ADPRTL3, IRT1, PARP3, ADPRTL2	poly (ADP-ribose) polymerase family, member 3	NM_001003931, NM_005485, hCT1951118.1, hCT2348571.0, hCT2354058.0, hCT33859.3	209940_at	NP_001003931.2, NP_005476.3, EAW65160.1, EAW65161.1, EAW65162.1, EAW65163.1
GeneID:84836	ABHD14B	3	52,002,526	52,008,646	6,120	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3926, 2_A375_pNL97_plus_lncRNA_AR..1..5638	-8090, -8666	upstream, upstream	1	1	0	25	19	14	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene ABHD14B	ABHD14B, MGC15429, CIB	abhydrolase domain containing 14B	NR_027476, NM_032750, NM_001146314, hCT2283542.0, hCT33875.3	224821_at	NP_116139.1, NP_001139786.1, EAW65178.1, EAW65179.1
GeneID:25864	ABHD14A	3	52,009,042	52,015,216	6,174	+	2	1_A375_pNL7_minus_lncRNA_AR..1..3926, 2_A375_pNL97_plus_lncRNA_AR..1..5638	7694, 8270	downstream, downstream	1	1	0	25	19	14	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene ABHD14A	FLJ60467, DORZ1, ABHD14A, DKFZp564O243, FLJ60317	abhydrolase domain containing 14A	NM_015407, hCT33870.1	210006_at	NP_056222.2, EAW65180.1
GeneID:95	ACY1	3	52,017,583	52,023,218	5,635	+	4	1_A375_pNL7_minus_lncRNA_AR..1..3926, 1_A375_pNL7_minus_lncRNA_AR..1..3927, 2_A375_pNL97_plus_lncRNA_AR..1..5638, 2_A375_pNL97_plus_lncRNA_AR..1..5639	-827, 12357, -251, 12309	upstream, downstream, upstream, downstream	1	1	0	22.5	20.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene ACY1	ACY1D, ACYLASE, ACY1	aminoacylase 1	NM_000666, hCT33858.3	202740_at, 238649_at	NP_000657.1, EAW65181.1
GeneID:6159	RPL29	3	52,027,644	52,029,958	2,314	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3926, 1_A375_pNL7_minus_lncRNA_AR..1..3927, 2_A375_pNL97_plus_lncRNA_AR..1..5639	13222, 38, 86	downstream, in gene, in gene	1	1	0	22.5	20.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene RPL29	HUMRPL29, HIP, RPL29, MGC88589, L29	ribosomal protein L29	NM_000992, hCT2283669.0, hCT2283670.0	200823_x_at, 213969_x_at	NP_000983.1, EAW65182.1, EAW65183.1
GeneID:1849	DUSP7	3	52,082,935	52,090,461	7,526	-	2	1_A375_pNL7_minus_lncRNA_AR..1..3928, 2_A375_pNL97_plus_lncRNA_AR..1..5640	-767, -843	upstream, upstream	1	1	0	20	26	12	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene DUSP7	DKFZp586F2224, PYST2, MKPX, DUSP7	dual specificity phosphatase 7	NM_001947, hCT33866.3	214793_at	NP_001938.2, EAW65184.1
GeneID:100128378	C3orf74	3	52,096,110	52,099,126	3,016	-	3	1_A375_pNL7_minus_lncRNA_AR..1..3928, 2_A375_pNL97_plus_lncRNA_AR..1..5640, 4_A375_EGR1..1..6160	7660, 8024, -2952	downstream, downstream, upstream	1	1	1	13	17.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene C3orf74	C3orf74	chromosome 3 open reading frame 74	NR_027331		
GeneID:25866	WDR51A	3	52,109,249	52,188,706	79,457	-	4	1_A375_pNL7_minus_lncRNA_AR..1..3929, 2_A375_pNL97_plus_lncRNA_AR..1..5641, 4_A375_EGR1..1..6160, 4_A375_EGR1..1..6161	205, 226, 66626, -7774	in gene, in gene, downstream, upstream	1	1	1	21.67	31.67	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	76	Gene WDR51A	PIX2, WDR51A, POC1A, MGC131902, DKFZp434C245	POC1 centriolar protein homolog A (Chlamydomonas)	NM_015426, NM_001161580, NM_001161581, hCT1985585.1, hCT33873.2	226355_at, 234749_s_at	NP_056241.3, NP_001155052.1, NP_001155053.1, EAW65185.1, EAW65186.1
GeneID:211	ALAS1	3	52,232,116	52,248,343	16,227	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5642, 4_A375_EGR1..1..6162	60, 23596	in gene, downstream	0	1	1	16	15.5	18.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ALAS1	MIG4, ALASH, ALAS1, ALAS, ALAS3	aminolevulinate, delta-, synthase 1	NM_199166, NM_000688, hCT1951115.1, hCT1985584.1, hCT33857.3	205633_s_at	NP_954635.1, NP_000679.1, EAW65188.1, EAW65189.1, EAW65190.1
GeneID:54106	TLR9	3	52,255,096	52,260,179	5,081	-	1	4_A375_EGR1..1..6162	4487	in gene	0	0	1	8	12	17	1	4_A375_EGR1..1	17	Gene TLR9	TLR9, CD289	toll-like receptor 9	NM_017442, hCT2283654.0	223903_at	NP_059138.1, EAW65191.1
GeneID:11344	TWF2	3	52,262,626	52,273,183	10,557	-	1	4_A375_EGR1..1..6162	17471	downstream	0	0	1	8	12	17	1	4_A375_EGR1..1	17	Gene TWF2	PTK9L, TWF2, MSTP011, A6r, A6RP, FLJ56277	twinfilin, actin-binding protein, homolog 2 (Drosophila)	NM_007284	202009_at	NP_009215.1
GeneID:80335	WDR82	3	52,288,438	52,312,659	24,221	-	6	1_A375_pNL7_minus_lncRNA_AR..1..3930, 1_A375_pNL7_minus_lncRNA_AR..1..3931, 2_A375_pNL97_plus_lncRNA_AR..1..5643, 2_A375_pNL97_plus_lncRNA_AR..1..5644, 4_A375_EGR1..1..6163, 4_A375_EGR1..1..6164	-205, -9261, 467, -9293, -205, -9229	upstream, upstream, in gene, upstream, upstream, upstream	1	1	1	19.5	20	19.5	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene WDR82	MST107, PRO34047, SWD2, TMEM113, MSTP107, WDR82, WDR82A, PRO2730	WD repeat domain 82	NM_025222, hCT2283643.0, hCT2283647.0	201934_at	NP_079498.2, EAW65202.1, EAW65203.1
GeneID:406890	MIRLET7G	3	52,302,294	52,302,377	83	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5643	-9815	upstream	0	1	0	17	18	19	1	4_A375_EGR1..1	19	Gene MIRLET7G	MIRLET7G, MIRNLET7G, LET7G, hsa-let-7g	microRNA let-7g	NR_029660		

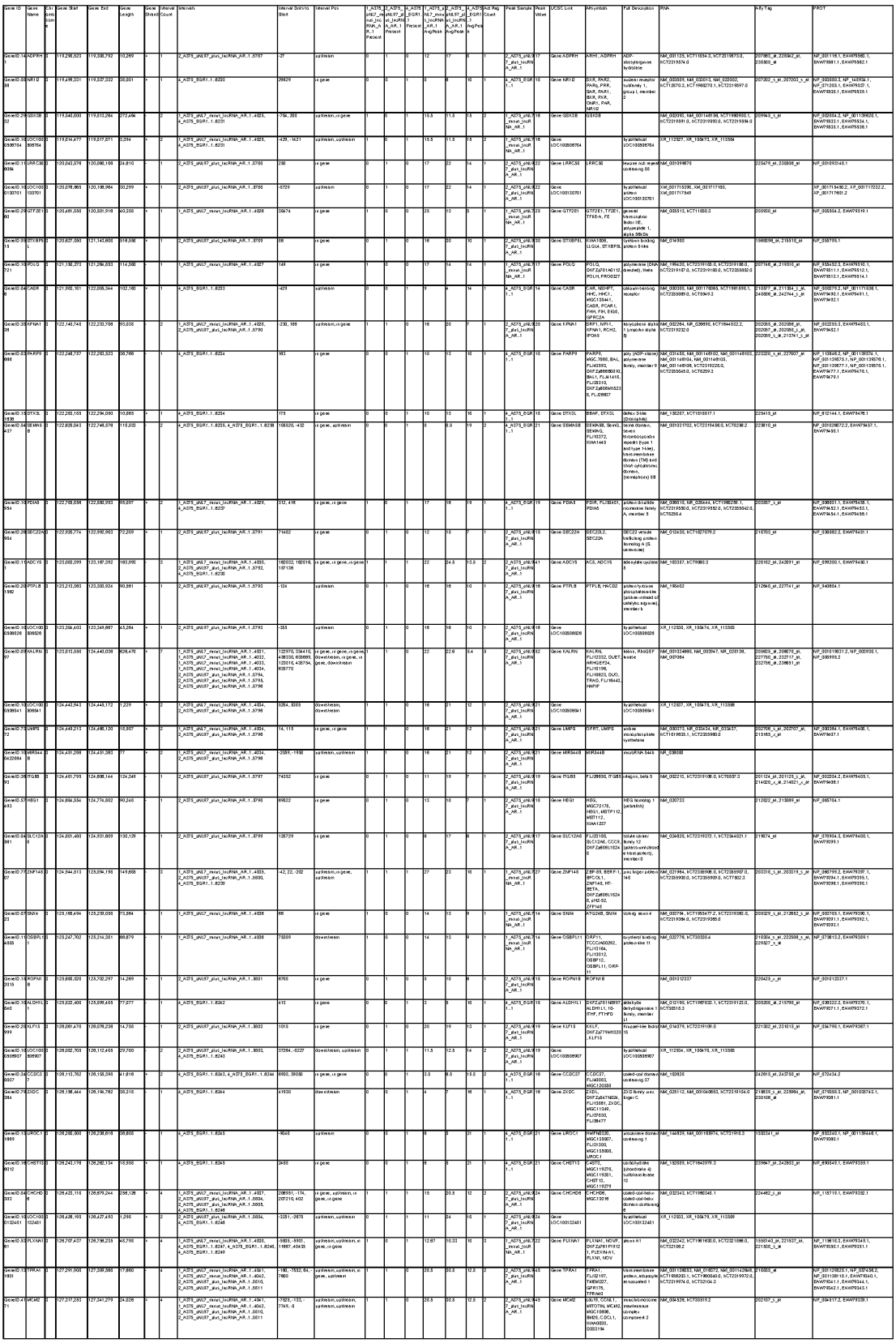




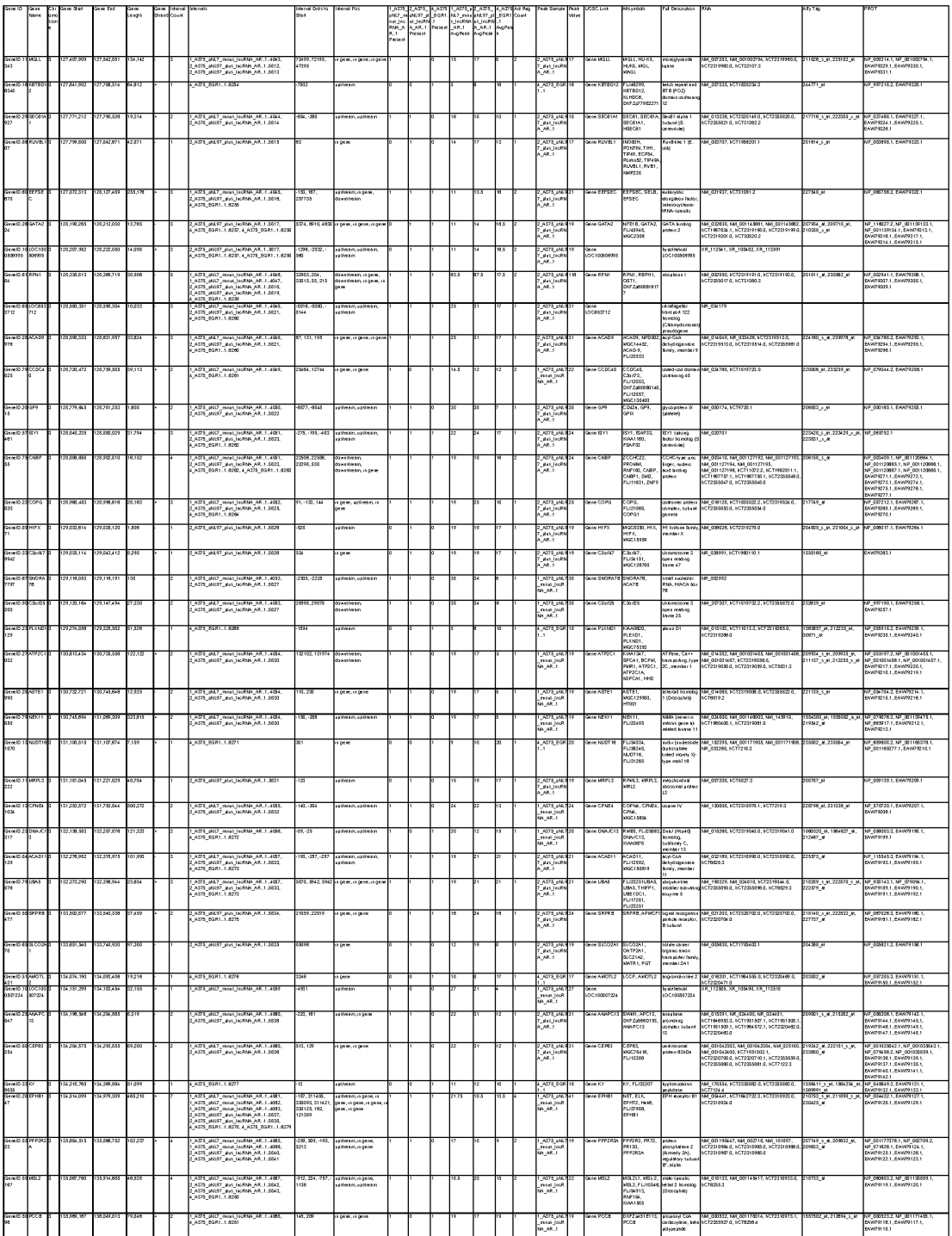
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_shN7_mrna_lncRNA_AR_1 Percent	2_A375_shN7_mrna_lncRNA_AR_1	3_A375_shN7_mrna_lncRNA_AR_1 Avg Peak	4_A375_shN7_mrna_lncRNA_AR_1 Avg Peak	Ad Tag Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:10539894	LOC100	2	82,246,540	82,304,822	58,282	-	2	1_A375_shN7_mrna_lncRNA_AR_1:3955, 2_A375_shN7_dun_lncRNA_AR_1:3864		-176, -182	upstream,upstream	1	1	0	22	22	9	1	2_A375_shN7_dun_lncRNA_AR_1	22	Gene LOC100509994		hypothetical LOC100509994	XR_112492, XR_113493, XR_112491, XR_110917, XR_110018, XR_110016, XR_113457, XR_113455, XR_113456		
GeneID:37	C2orf14	2	82,355,396	82,370,321	14,925	+	2	1_A375_shN7_mrna_lncRNA_AR_1:3955, 2_A375_shN7_dun_lncRNA_AR_1:3864		-596, -612	upstream,upstream	1	1	0	22	22	9	1	2_A375_shN7_dun_lncRNA_AR_1	22	Gene C2orf14	PTD21, C2orf14	chromosome 2 open reading frame 14	NM_030883, NCT01605421, NCT02021810, NCT02841453	210500_at		NP_598738.1, EAW56400.1, EAW56403.1, EAW56402.1
GeneID:33	FEZF2	2	82,355,347	82,399,190	43,843	-	1	4_A375_EGR1.1.6991		-3656	upstream	0	0	1	4	2	10	1	4_A375_EGR1.1.1	10	Gene FEZF2	FEZ1, FEZF2, FEZ homolog 2 (zebrafish), FEZ homolog 2	FEZ family zinc finger 2	NM_018008, NCT01749472, NCT01508841	221056_s_at, 233977_s_at, 233972_s_at		NP_990476.3, EAW56400.1, EAW56404.1
GeneID:38	CADPS2	2	82,354,021	82,661,964	477,943	-	6	1_A375_shN7_mrna_lncRNA_AR_1:3956, 1_A375_shN7_mrna_lncRNA_AR_1:3957, 1_A375_shN7_mrna_lncRNA_AR_1:3958, 1_A375_shN7_dun_lncRNA_AR_1:3853, 2_A375_shN7_dun_lncRNA_AR_1:3856, 2_A375_shN7_dun_lncRNA_AR_1:3857		276792, 1416, 596, 545944, 207604, -629	up gene, ut gene, upstream, up gene, up gene, upstream	1	1	0	17.6	21.2	5.5	5	2_A375_shN7_dun_lncRNA_AR_1	21	Gene CADPS	CADPS, CAPS1, KIAA1121, CADPS1, CADPS	Ca++-dependent secretion activator	NM_183393, NM_003716, NM_183394, NCT04645.2, NCT01925451.1, NCT02002222.0, NCT02002234.0, NCT02002363, NCT02041579.0, NCT02841803	1569803_at, 1569804_s_at, 204314_at, 233962_at, 234250_at		NP_599021.1, NP_003707.2, NP_599031.1, EAW56408.1, EAW56409.1, EAW56407.1, EAW56405.1, EAW56410.1, EAW56411.1
GeneID:13	SYNPR	3	85,262,914	85,802,997	539,883	+	1	2_A375_shN7_dun_lncRNA_AR_1:3890		6964	up gene	0	1	0	10	16	1	1	2_A375_shN7_dun_lncRNA_AR_1	16	Gene SYNPR	SPD, SYNPR, MGC29659, DKFZp686G0955	basophilin-like	NM_144642, NM_001139003, NCT14851.0, NCT19035.1	230303_at		NP_653243.1, NP_001125475.1, EAW56413.1, EAW56414.1
GeneID:10130343	LOC100	3	85,736,271	85,796,611	60,340	-	2	1_A375_shN7_mrna_lncRNA_AR_1:3991, 2_A375_shN7_dun_lncRNA_AR_1:3891		3299, 59338	up gene, ut gene	1	1	0	20	14	5.5	2	1_A375_shN7_mrna_lncRNA_AR_1	28	Gene LOC100130343		sodium-iodide symporter member 3 (pseudogene)	XM_001716439, XM_001716298, XM_001716690		XP_001716189.1, XP_001716298.1, XP_001716938.1
GeneID:15	C3orf49	3	85,805,941	85,834,312	29,271	+	1	1_A375_shN7_mrna_lncRNA_AR_1:3961		-9459	upstream	1	0	0	26	11	7	1	1_A375_shN7_mrna_lncRNA_AR_1	26	Gene C3orf49	MGC17310, C3orf49	chromosome 3 open reading frame 49	NR_026666	1553055_at		
GeneID:83	ATXN7	3	63,850,233	63,899,138	138,906	+	4	1_A375_shN7_mrna_lncRNA_AR_1:3962, 2_A375_shN7_dun_lncRNA_AR_1:3892, 2_A375_shN7_dun_lncRNA_AR_1:3893, 2_A375_EGR1.1.6192		47623, 47698, 99922, 47271	up gene, up gene, up gene, up gene	1	1	1	14.3	15.5	6.5	2	4_A375_EGR1.1.1	16	Gene ATXN7	ADCA4, FLJ17707, OPCA3, SCA7, ataxin7	ataxin 7	NM_000333, NM_001128149, NM_001177387, NCT15392.3, NCT20002220.0	204316_at, 209964_s_at		NP_000324.1, NP_001178058.1, EAW56422.1, EAW56423.1
GeneID:39	PSMD8	3	63,896,231	64,009,120	12,889	-	5	1_A375_shN7_mrna_lncRNA_AR_1:3963, 1_A375_shN7_mrna_lncRNA_AR_1:3964, 2_A375_shN7_dun_lncRNA_AR_1:3894, 4_A375_EGR1.1.6192		-32, -32, 98	upstream,upstream,up gene	1	1	1	120	133	28	1	2_A375_shN7_dun_lncRNA_AR_1	33	Gene PSMD8	KIAA0107, S10, p40.5, Rpn7, p40.01, PSMD8, SGA-113M	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	NM_014814, NCT01903531.1, NCT02841780.0, NCT02841790.0, NCT02841800.0	1555564_at, 202753_at, 202754_at		NP_002801.1, EAW56424.1, EAW56425.1, EAW56426.1, EAW56427.1
GeneID:18	PRKCA1	3	64,279,536	64,311,101	131,565	-	3	1_A375_shN7_mrna_lncRNA_AR_1:3964, 2_A375_shN7_dun_lncRNA_AR_1:3895, 2_A375_shN7_dun_lncRNA_AR_1:3896		126999, 120371, 7921	up gene, up gene, upstream	1	1	0	15.5	20	5.5	2	2_A375_shN7_dun_lncRNA_AR_1	22	Gene PRKCA1	DKFZp686D1431, DKFZp686H0743, PRKCA1E2	protein kinase C (Drosophila) 2	NM_190599, NCT22010821.1, NCT24553.0	223968_at		NP_942359.1, EAW56428.1, EAW56429.1
GeneID:98	ADAMT	3	64,901,330	64,973,365	172,035	-	3	1_A375_shN7_mrna_lncRNA_AR_1:3965, 2_A375_shN7_mrna_lncRNA_AR_1:3966, 2_A375_shN7_dun_lncRNA_AR_1:3898		2229, -555, -619	up gene, upstream, upstream	1	1	0	15.5	14.5	6.5	2	2_A375_shN7_dun_lncRNA_AR_1	16	Gene ADAMTS9	FLJ42555, ADAMTS9, KIAA1312	ADAM metallopeptidase with thrombospondin type 1 motif, 9	NM_182920, NCT23349907.0, NCT23349709.0	1564697_at, 230207_at, 236014_at, 233763_at		NP_6915561, EAW56434.1, EAW56435.1
GeneID:10507096	LOC1003	3	64,970,548	64,981,216	260,670	+	3	1_A375_shN7_mrna_lncRNA_AR_1:3965, 1_A375_shN7_mrna_lncRNA_AR_1:3966, 2_A375_shN7_dun_lncRNA_AR_1:3899		590, 5324, 5155	up gene, ut gene, up gene	1	1	0	15.5	14.5	6.5	2	2_A375_shN7_dun_lncRNA_AR_1	16	Gene LOC100507096		hypothetical LOC100507096	XR_112495, XR_113499, XR_110021, XR_110022, XR_113462, XR_113461		
GeneID:83	MAGI1	3	65,229,908	66,024,309	664,802	-	4	1_A375_shN7_mrna_lncRNA_AR_1:3701, 2_A375_shN7_dun_lncRNA_AR_1:3702, 2_A375_shN7_dun_lncRNA_AR_1:3900, 2_A375_shN7_dun_lncRNA_AR_1:3702		748832, 48481, 307, -483	up gene, ut gene, upstream, upstream	1	1	0	19	20.33	6.67	3	2_A375_shN7_dun_lncRNA_AR_1	22	Gene MAGI1	MAGI1, BAP1, WAP3, WAS1, BAIAP1, WHAP, MAGI-1, WHAP1, TNRC19, AIP3	membrane-associated guanylate kinase, WW and PDZ domain containing 1	NM_0397422, NM_018539, NM_001203837, NCT21653102, NCT19503511.1, NCT19503512.1, NCT20035410.0, NCT20035422.0, NCT20035430.0, NCT22005460.0	1553282_s_at, 1553658_at, 1553659_at, 1553660_at, 208144_s_at, 233473_at, 233659_s_at		NP_0047232, NP_0603281, NP_001302029.1, EAW56439.1, EAW56440.1, EAW56441.1, EAW56442.1, EAW56443.1, EAW56444.1, EAW56445.1
GeneID:26	LRIG1	3	66,429,221	66,550,945	121,824	-	2	2_A375_shN7_dun_lncRNA_AR_1:3704, 4_A375_EGR1.1.6195		-698, 99517	upstream,up gene	0	1	1	12	17	13.5	2	2_A375_shN7_dun_lncRNA_AR_1	27	Gene LRIG1	DKFZp686O162, LIG-1, LIG1	leucine-rich repeats and immunoglobulin-like domains 1	NM_015541, NCT22028490.0, NCT22020491.0	211595_s_at, 239772_s_at, 239720_x_at, 240145_s_at		NP_0356362, EAW56452.1, EAW56453.1
GeneID:64	KBTBD3	3	67,045,727	67,081,834	12,907	+	2	1_A375_shN7_mrna_lncRNA_AR_1:3970, 2_A375_shN7_dun_lncRNA_AR_1:3703		20250, 20702	downstream, downstream	1	1	0	16	17	7	1	2_A375_shN7_dun_lncRNA_AR_1	17	Gene KBTBD3	KIAA1842, KBTBD6, FLJ37932, TA-BTB	kelch repeat and BTB (POZ) domain containing 3	NM_032935, ICT73824	219033_at		NP_1158942, EAW56436.1
GeneID:58	SLIC1G2	3	67,410,954	67,705,055	294,154	-	2	1_A375_shN7_mrna_lncRNA_AR_1:3972, 4_A375_EGR1.1.6196		14, -146	up gene, upstream	1	0	1	17	14	10	1	4_A375_EGR1.1.1	16	Gene SLIC1G2	G-BETA, GBETA, SLIC1G2	brain/testis-CAM kinase, GDP-forming, beta subunit	NM_001177999, NM_003645, NCT22005509.0, NCT7362.2	212459_x_at, 214653_x_at, 212372_s_at		NP_0026292, EAW56438.1, EAW56437.1
GeneID:73	FAM19A2	3	68,055,454	68,594,772	541,318	+	1	1_A375_shN7_mrna_lncRNA_AR_1:3973		332416	up gene	1	0	0	16	11	5	1	1_A375_shN7_dun_lncRNA_AR_1	16	Gene FAM19A1	TAFA-1, FAM19A1, TAFA1	family with sequence similarity 19 (chemokine (C-C motif)-like), member A1	NM_213609, NCT16421.1	230923_at		NP_1907742, EAW56439.1
GeneID:20	C3orf56	3	69,224,366	69,262,774	38,408	-	1	2_A375_shN7_dun_lncRNA_AR_1:3707		-74	upstream	0	1	0	12	14	11	1	2_A375_shN7_dun_lncRNA_AR_1	14	Gene C3orf56	FLJ14173, FLJ13076, MDS81, MGC34132, C3orf56, FLJ22770	chromosome 3 open reading frame 56	NM_175954	221935_s_at		NP_7792251
GeneID:71	TMPT	3	69,986,976	69,991,464	22,506	+	1	2_A375_shN7_dun_lncRNA_AR_1:3707		59838	downstream	0	1	0	12	14	11	1	2_A375_shN7_dun_lncRNA_AR_1	14	Gene TMPT	KIAA1186, TMPT, TMP	TATA element modulatory factor 1	NM_007114, NCT22005509.0, ICT6383.2	213224_at, 214945_s_at, 215053_s_at, 227655_at, 233366_at, 239521_at, 242243_at		NP_9305453, EAW56456.1, EAW56459.1
GeneID:23	FRMD4	3	69,219,149	69,435,430	216,294	-	5	1_A375_shN7_mrna_lncRNA_AR_1:3974, 2_A375_shN7_dun_lncRNA_AR_1:3708, 2_A375_shN7_dun_lncRNA_AR_1:3709		206190, 204355, 79590	downstream, up gene, up gene, up gene	1	1	0	17	23	4.5	2	2_A375_shN7_dun_lncRNA_AR_1	24	Gene FRMD4B	GRSP1, FRMD4B, MGC9049035RA, SWAP-70	FERM domain containing 4B	NM_015123	210209_at, 216131_at, 216134_at		NP_5538351
GeneID:42	MITF	3	69,795,596	70,017,465	220,592	+	1	2_A375_shN7_dun_lncRNA_AR_1:3710		-10	upstream	0	1	0	17	16	17	1	2_A375_shN7_dun_lncRNA_AR_1	16	Gene MITF	WS2, bHLHe32, MI, MITF, WS2A	microphthalmia-associated transcription factor	NM_000248, NM_001184097, NM_001184966, NM_006722, NM_198136, NM_198189, NM_198177, NM_198178, NCT19930491, NCT20007010.0, NCT20007021.0, NCT22007050.0, NCT22007040.0, NCT7366.2	1554574_at, 207233_s_at, 209369_at		NP_5982351, NP_0011710961, NP_1978511, NP_0011721, NP_000697.3, NP_001171697.1, NP_0011721, NP_001178058.1, NP_001721.2, EAW56793.1, EAW56450.1, EAW56451.1, EAW56452.1, EAW56453.1, EAW56454.1
GeneID:10	LOC1003	3	72,712,435	72,713,400	965	-	1	1_A375_shN7_mrna_lncRNA_AR_1:3976		2961	downstream	1	1	0	16	8	2	1	1_A375_shN7_mrna_lncRNA_AR_1	16	Gene LOC100509985		hypothetical LOC100509985	XR_112511, XR_109997, XR_113486		
GeneID:33	SHQ1	3	72,799,426	72,897,996	99,170	-	1	2_A375_shN7_dun_lncRNA_AR_1:3715		94	up gene	0	1	0	13	22	11	1	2_A375_shN7_dun_lncRNA_AR_1	22	Gene SHQ1	SHQ1, Shq1p, FLJ45329, DKFZp686H0220	SHQ1 homolog (S. cerevisiae)	NM_018130, NCT16475012, NCT22010980.0, NCT22010990.0	219083_at, 83009_at		NP_0600502, EAW56521.1, EAW56522.1, EAW56523.1
GeneID:72	GXYLT2	3	72,937,365	73,024,823	87,140	+	2	1_A375_shN7_mrna_lncRNA_AR_1:3979, 2_A375_shN7_dun_lncRNA_AR_1:3716		93425, -313	up gene, upstream	1	1	0	19	14.5	8.5	2	2_A375_shN7_dun_lncRNA_AR_1	20	Gene GXYLT2	GXYLT2, GLT8D4	glycoside xylosyltransferase 2	NM_001093093	233231_at		NP_0010739622
GeneID:23	PDZRN3	3	73,431,832	73,874,972	442,430	-	3	2_A375_shN7_dun_lncRNA_AR_1:3719, 4_A375_shN7_dun_lncRNA_AR_1:3720, 4_A375_EGR1.1.6197		44844, -264, 240552	up gene, upstream, up gene	0	1	1	10.67	17.33	6.33	3	2_A375_shN7_dun_lncRNA_AR_1	28	Gene PDZRN3	SEMCAP3, PDZRN2, LNX3	PDZ domain containing ring finger 3	NM_015009, NCT19304681.1, ICT6954.3	1555667_at, 212913_at, 233165_at		NP_3158274, EAW56532.1, EAW56533.1
GeneID:10	FRG2C	3	73,715,467	73,716,366	2,851	+	4	1_A375_shN7_mrna_lncRNA_AR_1:3992, 1_A375_shN7_dun_lncRNA_AR_1:3724, 4_A375_EGR1.1.6200, 4_A375_EGR1.1.6201		-3393, -3399, 5391, 7609	upstream, upstream, upstream, downstream	1	1	1	34.5	51	22	2	2_A375_shN7_dun_lncRNA_AR_1	51	Gene FRG2C	FRG2C		NM_201247.59			NP_3011102.1
GeneID:10	LOC1003	3	73,717,379	73,718,188	1,809	+	4	1_A375_shN7_mrna_lncRNA_AR_1:3993, 1_A375_shN7_dun_lncRNA_AR_1:3724, 4_A375_EGR1.1.6200, 4_A375_EGR1.1.6201		-5351, -9251, 9263, 5917	upstream, upstream, upstream, downstream	1	1	1	34.5	51	22	2	2_A375_shN7_dun_lncRNA_AR_1	51	Gene LOC100509764			XM_003116994			XP_0031169121
GeneID:89	ROBO1	3	78,646,955	79,017,559	1,370,671	-	3	1_A375_shN7_mrna_lncRNA_AR_1:3982, 2_A375_shN7_dun_lncRNA_AR_1:3728, 2_A375_EGR1.1.6202		745323, 746273, 746843	up gene, ut gene, up gene	1	1	1	55	67	79	1	1_A375_shN7_mrna_lncRNA_AR_1	93	Gene ROBO1	SAX3, PLAUR2, MGC131999, MGC132277, ROBO1, DUTT1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	NM_002941, NM_001143854, NM_133631, NCT22014240.0, NCT22014253.0, NCT22014270.0, NCT22014293.0, NCT22014303.0	212164_at		NP_3029321.1, NP_0011780171, NP_5953342, EAW56556.1, EAW56557.1, EAW56558.1, EAW56559.1, EAW56560.1
GeneID:26	GBE1	3	81,535,650	81,610,950	272,100	-	5	1_A375_shN7_mrna_lncRNA_AR_1:3984, 2_A375_shN7_dun_lncRNA_AR_1:3726, 4_A375_EGR1.1.6204		186, 186, 36	up gene, up gene, up gene	1	1	1	19	27	21	1	2_A375_shN7_dun_lncRNA_AR_1	27	Gene GBE1	GBE1, GBE	glucan (1,4-alpha-), alpha, glycosyltransferase, enzyme 1	NM_003156, NCT19302.2, NCT19571449.1	203262_at		NP_3001493, EAW56560.1, EAW56579.1
GeneID:23	CADM2	3	85,006,103	86,123,579	1,113,448	+	1	2_A375_shN7_dun_lncRNA_AR_1:3731		600363	up gene	0	1	0	10	17	1	1	2_A375_shN7_dun_lncRNA_AR_1	17	Gene CADM2	Necl-3, MGC139361, KIAA1463, NECL3, MGC139343, CADM2, hpCAM2, MGC104354	cell adhesion molecule 2	NM_153184, NM_001167674, NM_001167675, NCT19413883.0, NCT23447080.0	1553732_a_at, 1553734_s_at, 1553744_s_at		NP_6963342, NP_0011671481, EAW56874.1, EAW56875.1
GeneID:85	CGGBP1	3	85,161,100	85,185,148	73,648	-	2	1_A375_shN7_mrna_lncRNA_AR_1:3733, 4_A375_EGR1.1.6208		-334, -388	upstream, upstream	0	1	1	15	21	10	1	4_A375_shN7_dun_lncRNA_AR_1	21	Gene CGGBP1	CGGBP1, CGGBP, p20-CGGBP	CGG triplet repeat binding protein 1	NM_033993, NM_001003690, NCT19471783, NCT19571241.1	209881_s_at, 224693_at		NP_3395343, NP_0010039911, EAW56983.1, EAW56984.1
GeneID:58	ZNF654	3	85,166,262	85,193,014	26,752	+	3	1_A375_shN7_mrna_lncRNA_AR_1:3987, 2_A375_shN7_dun_lncRNA_AR_1:3736, 4_A375_EGR1.1.6207		10652, 10714, 10810	downstream, downstream, downstream	1	1	1	23	22	24	1	4_A375_EGR1.1.1	24	Gene ZNF654	ZNF654, FLJ10997, FLJ21142	zinc finger protein 654	NM_0182932, NCT22032081.1, NCT22032161	1538743_at, 1558744_s_at, 212035_s_at, 223531_at, 241346_at, 242207_at		NP_5807653, EAW56981.1, EAW56982.1
GeneID:20	C3orf58	3	85,196,693	86,207,115	8,222	+	5	1_A375_shN7_mrna_lncRNA_AR_1:3987, 2_A375_shN7_dun_lncRNA_AR_1:3736, 4_A375_EGR1.1.6207		51, 63, 179	up gene, up gene, up gene	1	1	1	23	22	24	1	4_A375_EGR1.1.1	24	Gene C3orf58	FLJ36270, MGC27017, C3orf58	chromosome 3 open reading frame 58	NM_173524, NCT19857151.1, NCT22032310.0, NCT19969.2	226524_at		NP_7761053, EAW56580.1, EAW56581.1, EAW56582.1
GeneID:23	EPHA2	3	89,156,674	89,331,364	174,810	+	3	1_A375_shN7_mrna_lncRNA_AR_1:3737, 2_A375_shN7_dun_lncRNA_AR_1:3738, 2_A375_shN7_dun_lncRNA_AR_1:3739		50, 7116, 64250	up gene, up gene, up gene	0	1	1	11.67	20.33	6.33	3	2_A375_shN7_dun_lncRNA_AR_1	24	Gene EPHA2	EPHA2, HEK, ETK, EPHA2, ETK1, HEK4, SK4	EPH receptor A2	NM_0283232, NM_182564, NCT19391182.1	209470_s_at, 209207_s_at, 211164_at		NP_0035242, NP_0025821, EAW56537.1
GeneID:28	EPHA8	3	89,833,435	97,467,768	634,281	+	4	1_A375_shN7_mrna_lncRNA_AR_1:3993, 2_A375_shN7_dun_lncRNA_AR_1:3744, 2_A375_shN7_dun_lncRNA_AR_1:3743, 4_A375_EGR1.1.6208		-332, -1935, -237	upstream, upstream, upstream, upstream	1	1	1	17	17	19	1	4_A375_EGR1.1.1	19	Gene EPHA8	EPHA8, PRO37098, EPHA8L, DKFZp434C1416, FLJ25249	EPH receptor A8	NM_0010054481, NM_173655	1561398_at, 233164_at		NP_0010739172, NP_775936.1
GeneID:10	CRYBG3	3	97,840,589	97,865,626	123,257	-	1	2_A375_shN7_dun_lncRNA_AR_1:3745		993	up gene	0	1	0	9	16	13	1	2_A375_shN7_dun_lncRNA_AR_1	16	Gene CRYBG3	DKFZp667F021[0], CRYBG3, FLJ38302, DKFZp686I1221	beta/gamma crystallin domain containing 3	XM_003119935, XM_003316522, XM_003120421	214002_at		XP_0031199321, XP_0031157701, XP_0031203491
GeneID:64	MINA	3	97,860,661	97,891,295	30,634	-	1	2_A375_shN7_dun_lncRNA_AR_1:3747		21	up gene	0	1	0	10	14	9	1	2_A375_shN7_dun_lncRNA_AR_1	14	Gene MINA	FLJ14295, DKFZp762D019[2], MINA, MINA53, MDIG, NO52	MYC-induced nuclear antigen	NM_0010425331, NM_153182, NM_032776, NCT19525494.1, NCT19536436, NCT23559507.0, NCT23559520.0	1554774_at, 213165_s_at, 213166_at, 223152_at, 229879_at		NP_0010359901.1, NP_694622.2, NP_1165872, EAW56972.1, EAW56974.1, EAW56975.1, EAW56973.1
GeneID:39	C1GNB1	3	98,234,317	98,241,910	7,593	-	1	1_A375_shN7_mrna_lncRNA_AR_1:3988		68	up gene	0	0	1	16	16	7	1	1_A375_shN7_mrna_lncRNA_AR_1	16	Gene C1GNB1	MGC111182, GEM-9743, C3GLN, MGC3316, MGC3981, C1GNB1	ankyrin domain containing 1	NM_0010435511, NM_0010431021, NM_0010431031, NM_0010431041, NM_0010431051, NCT11913.2, NCT19374871.1, NCT23537470.0, NCT23537490.0	1554149_at, 208928_at, 239149_at		NP_0010327711, NP_0010327721, NP_0010328731, NP_0010328751, NP_0010328771, EAW56961.1, EAW56962.1, EAW56963.1, EAW56964.1, EAW56965.1
GeneID:26	GPR15	3	98,290,976	98,291,990	1,012	+	1	1_A375_shN7_mrna_lncRNA_AR_1:3989		9084	upstream	1	0	0	16	16	7	1	1_A375_shN7_mrna_lncRNA_AR_1	16	Gene GPR15	MGC126820, GPR15, MGC126820	G protein-coupled receptor 15	NM_0053202, NCT18470.2	206524_at		NP_0052611.1, EAW56981.1
GeneID:13	CPOX	3	98,290,290	98,312,455	14,165	-	2	2_A375_EGR1.1.6209, 4_A375_EGR1.1.6210		551, -121	up gene, upstream	0	0	1	13	8.5	16.5	2	4_A375_EGR1.1.1	19	Gene CPOX	CPOX, HCP, CPO, CPO	coproporphyrinogen oxidase	NM_0004972, NCT11213.0	204172_at		NP_0008881.2, EAW56984.1
GeneID:10	ST3GAL3	3	98,451,572	98,515,257	81,865	+	2	1_A375_shN7_mrna_lncRNA_AR_1:3990, 2_A375_shN7_dun_lncRNA_AR_1:3211		37860, -404	up gene, upstream	1	0	1	14.5	11	10.5	2	2_A375_shN7_dun_lncRNA_AR_1	16	Gene ST3GAL3	SIAT3C, FLJ20341, V1, ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	NM_0061002, NCT19986221.1, NCT19986241.1, NCT19986251.1, NCT19986271.1, NCT19995.4	210942_s_at, 213355_s_at, 213356_at		NP_0060911.1, EAW56943.1, EAW56944.1, EAW56945.1, EAW56946.1, EAW56947.1
GeneID:15	DCBLD2	3	98,514,914	98,620,833	103,719	-	1	2_A375_shN7_dun_lncRNA_AR_1:3743		133	up gene	0	0	1	15	16	11	1	2_A375_shN7_dun_lncRNA_AR_1	16	Gene DCBLD2	DCBLD2, CCCP, ESDN	discoidin, CUB and LCCL domain containing 2	NM_080927, NCT11214.2, NCT22036360.0, NCT23559482.0	213883_at, 224911_s_at, 239446_s_at		NP_5838153, EAW56747.1, EAW56748.1, EAW56749.1
GeneID:10	LOC1003	3	98,899,932	98,901,940	2,038	+	1	2_A375_shN7_dun_lncRNA_AR_1:3749		-2230	upstream	0	1	0	13	15	2	1	2_A375_shN7_dun_lncRNA_AR_1	15	Gene LOC100509377		hypothetical LOC100509377	XR_112329, XR_110435, XR_113398		
GeneID:64	C3orf26	3	99,836,676	99,897,476	360,795	+	4	1_A375_shN7_mrna_lncRNA_AR_1:3991, 1_A375_shN7_mrna_lncRNA_AR_1:3992, 2_A375_shN7_dun_lncRNA_AR_1:3732, 2_A375_shN7_dun_lncRNA_AR_1:3731		-147, 157914, -102, 336026	upstream, up gene, upstream, up gene	1	0	0	16	23.5	7	2	2_A375_shN7_dun_lncRNA_AR_1	33	Gene C3orf26	C3orf26, MGC4309	chromosome 3 open reading frame 26	NM_0223359, NM_0011679241	224523_s_at		NP_1157352, NP_0011612961
GeneID:58	TBC1D23	3	99,979,699	100,044,092	64,394	+	2	1_A375_shN7_mrna_lncRNA_AR_1:3993, 2_A375_shN7_dun_lncRNA_AR_1:3734		194, 216	up gene, up gene	1	1	0	24	16	13	1	1_A375_shN7_mrna_lncRNA_AR_1	24	Gene TBC1D23	TBC1D23, KIAA1791, FLJ11046, DKFZp667G062	TBC1 domain family, member 23	NM_0163093, NCT19393.2, NCT22020120.0	223121_at		NP_0607792, EAW56261.1, EAW56262.1
GeneID:89	TOMM70	3	100,092,307	100,130,223	37,916	-	1	1_A375_EGR1.1.6212		498	up gene	0	0	1	12	11	10	1	4_A375_EGR1.1.1	17	Gene TOMM70A	FLJ90170, TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	NM_0145202, NCT19653.2, NCT22030410.0	201512_s_at, 201519_at		NP_1555153.2, EAW56225.1, EAW56226.1



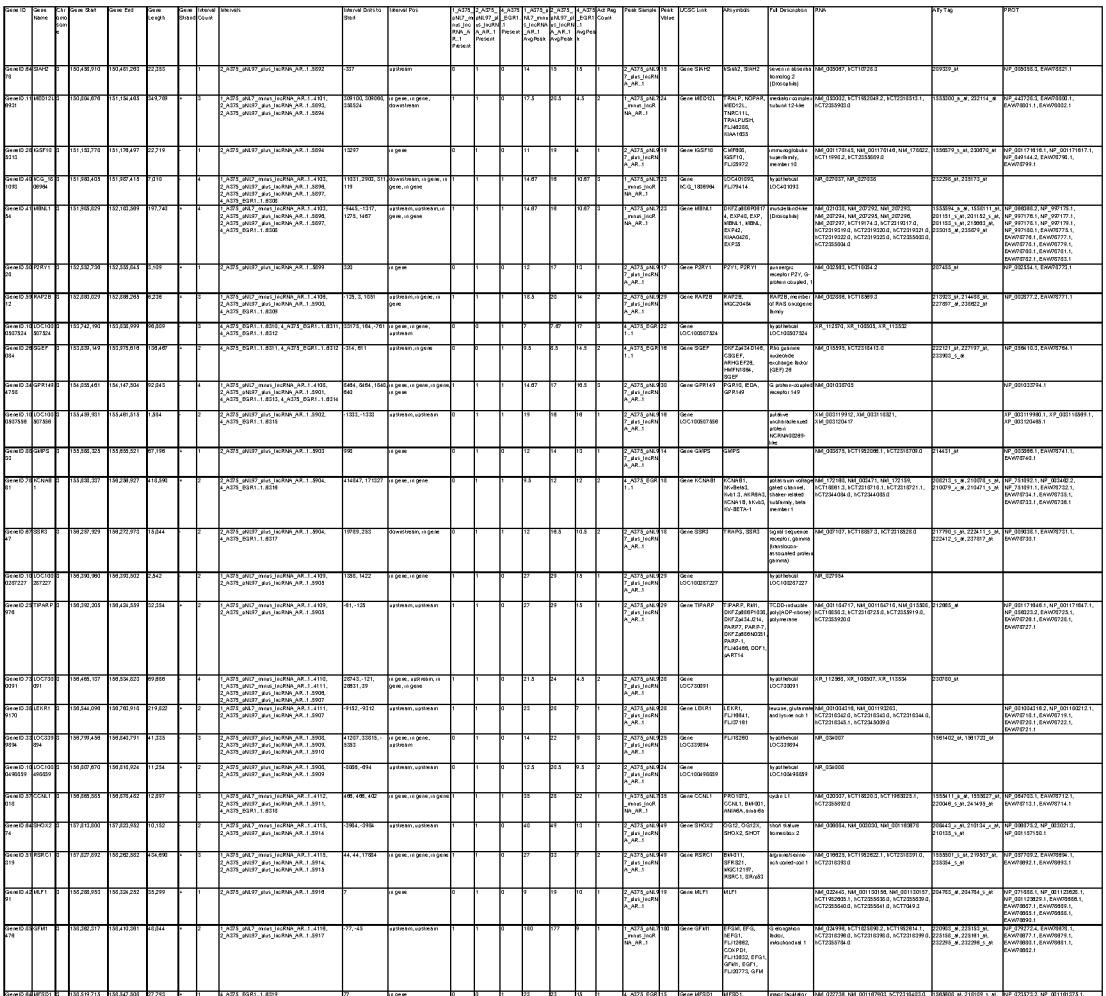
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Start	Interval Pos	1_A375_2_A375_3_A375_4_A375_1_A375_2_A375_3_A375_4_A375_Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
GeneID:34993091	LNP1	2	100,120,037	100,179,170	59,133	+	1	4_A375_EGR1..1_8212	-218	upstream	0 0 1 12 11 17 1	4_A375_EGR1..1	17	Gene LNP1	LNP1	leutamine NUP98 fusion partner 1	NM_031035v31	227161_at	NP_031073920.1
GeneID:33978778	TMEM45A	3	100,211,463	100,296,265	84,802	+	1	1_A375_shL7_mirvI_lncRNA_AR..1..3994	33577	sr gene	1 0 0 17 16 9 1	1_A375_shL7_mirvI_lncRNA_AR..1	17	Gene TMEM45A	TMEM45A, FLJ10134, DERP7	transmembrane protein 45A	NM_018004, XCT16224081, XCT16553491	219410_at	NP_060174.1, EAW78919.1, EAW78920.1
GeneID:34993873	GPR128	3	100,328,433	100,414,323	85,890	+	1	4_A375_EGR1..1_8213	72719	sr gene	0 0 1 4 3 15 1	4_A375_EGR1..1	15	Gene GPR128	MGC143011, MGC163392, GPR128, FLJ14454, FLJ29035, FLJ40302	G protein-coupled receptor 128	NM_032787, XCT16162981	1553296_at	NP_116176.2, EAW78918.1
GeneID:34993931	RGMB	3	101,280,712	101,295,089	14,377	+	2	1_A375_shL7_mirvI_lncRNA_AR..1..3995, 2_A375_shL07_plus_lncRNA_AR..1..3755	12532, 11926	downstream, downstream	1 1 0 24 26 10 1	2_A375_shL07_plus_lncRNA_AR..1	26	Gene RGMB	RGMBT01, FLJ35452	RGM (guidance-like) family member B (dorsal inhibitory axon guidance protein)	NM_017619, XCT13825.3	223287_at	NP_060089.2, EAW79795.1
GeneID:33978107	PCNP	3	101,292,042	101,312,261	20,219	+	2	1_A375_shL7_mirvI_lncRNA_AR..1..3995, 2_A375_shL07_plus_lncRNA_AR..1..3755	-170, -422	upstream, upstream	1 1 0 24 26 10 1	2_A375_shL07_plus_lncRNA_AR..1	26	Gene PCNP	PCNP, ONFZ2810415	PEST proteolytic signal containing nuclear protein	NM_030337, XCT23199801.0, XCT23199800.0, XCT23199490.0, XCT23539322.0, XCT23539331.0	227377_at	NP_068090.1, EAW79790.1, EAW79792.1, EAW79793.1, EAW79794.1
GeneID:33978107	ZBTB11	2	101,298,293	101,399,998	27,705	-	1	2_A375_shL07_plus_lncRNA_AR..1..3756	1264	sr gene	0 1 0 10 16 8 1	2_A375_shL07_plus_lncRNA_AR..1	16	Gene ZBTB11	ZBTB11, MGC132303, ZNF512, FLJ10426, ZNF-MIZ74	zinc finger and BTB domain containing 11	NM_014413, XCT28110.3	204497_at, 242433_at	NP_036230.2, EAW79798.1
GeneID:33978107	LOC100009976	2	101,298,274	101,298,661	2,757	+	1	2_A375_shL07_plus_lncRNA_AR..1..3756	-210	upstream	0 1 0 10 16 8 1	2_A375_shL07_plus_lncRNA_AR..1	16	Gene LOC100009976		hypothetical LOC100009976	NR_024407	232200_s_at, 232200_at	
GeneID:33978132	RPL24	3	101,299,954	101,408,583	8,629	-	1	2_A375_shL07_plus_lncRNA_AR..1..3756	10659	downstream	0 1 0 10 16 8 1	2_A375_shL07_plus_lncRNA_AR..1	16	Gene RPL24	RPL24, L24		NM_000986, XCT23199681.1, XCT23199681.2, XCT23199681.3, XCT23410320.0, XCT23410322.0	200012_at	NP_000977.1, EAW79781.1, EAW79782.1, EAW79783.1, EAW79784.1
GeneID:33978775	FAM65C	3	101,406,029	101,547,075	49,048	+	1	2_A375_shL07_plus_lncRNA_AR..1..3757	19	sr gene	0 1 0 15 19 13 1	2_A375_shL07_plus_lncRNA_AR..1	19	Gene FAM65C	MST113, FLJ35102, MGC15896, MST113, FAM65C	family with sequence similarity 65, member C	NM_001134436, NM_145057, XCT15197.1, XCT23539930.0	235000_at, 243011_at	NP_001127920.1, NP_689474.1, EAW79774.1, EAW79775.1
GeneID:33978332	NFKBIZ	3	101,548,634	101,579,099	30,035	+	1	2_A375_shL07_plus_lncRNA_AR..1..3758	21802	sr gene	0 1 0 13 22 7 1	2_A375_shL07_plus_lncRNA_AR..1	22	Gene NFKBIZ	MAIL, INAP, FLJ34463, IKBZ, FLJ36233, NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	NM_031357, XCT23539574, XCT23539573.0, XCT23539930.0, XCT2943.3	1559152_s_at, 223217_s_at, 223218_s_at	NP_113507.1, EAW79772.1, EAW79773.1
GeneID:33982228	LOC100132247	3	101,859,703	101,716,770	57,067	+	1	4_A375_EGR1..1_8214	33217	sr gene	0 0 1 7 9 16 1	4_A375_EGR1..1	16	Gene LOC100132247	MGC147239	hypothetical LOC100132247	NR_026954	1562048_at	
GeneID:21463	ALCAM	3	103,088,713	103,298,744	210,031	+	2	2_A375_shL07_plus_lncRNA_AR..1..3760, 2_A375_shL07_plus_lncRNA_AR..1..3761	791, 2799	sr gene, sr gene	0 1 0 13.5 17.5 10.5 2	2_A375_shL16_plus_lncRNA_AR..1	16	Gene ALCAM	CD166, FLJ38514, ALCAM, MGC17720, MEMD	activated leukocyte cell adhesion molecule	NM_001627, XCT11933.3, XCT23199160.0, XCT23160.0	1569062_at, 201951_at, 201952_at	NP_001618.2, EAW79733.1, EAW79736.1, EAW79737.1
GeneID:8856	CBLB	3	105,277,109	105,507,007	210,776	-	2	1_A375_shL7_mirvI_lncRNA_AR..1..3999, 2_A375_shL07_plus_lncRNA_AR..1..8216	429, 387	upstream, sr gene	1 1 0 1 15 17 14.5 2	4_A375_EGR1..1	21	Gene CBLB	RNF56, Nbla00127, DKFZp779F1442, DKFZp686J10220, CBLB, DKFZp779A0729, FLJ41152, FLJ38665	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	NM_170662, XCT11937.82.1, XCT23199690.0, XCT23199700.0, XCT23539330.0	206346_s_at, 209682_at, 227900_at	NP_732622.2, EAW79753.1, EAW79751.1, EAW79752.1, EAW79754.1
GeneID:8856	CD47	3	107,791,541	107,809,935	47,994	-	2	1_A375_shL7_mirvI_lncRNA_AR..1..4003, 2_A375_shL07_plus_lncRNA_AR..1..3767	113, 239	upstream, upstream	1 1 0 20 16 10 1	1_A375_shL16_mirvI_lncRNA_AR..1	20	Gene CD47	CD47, IAP, MER6, Ort3	CD47 molecule	NM_001777, NM_198793, XCT19828.3, XCT19711.93.1, XCT19711.44.1	211075_s_at, 215333_at, 215334_at, 215335_at, 226816_at, 227291_at, 242374_at	NP_001768.1, NP_942088.1, EAW79722.1, EAW79723.1, EAW79724.1
GeneID:2259	MYH15	3	108,099,216	108,245,169	145,953	+	2	1_A375_shL7_mirvI_lncRNA_AR..1..4004, 2_A375_shL07_plus_lncRNA_AR..1..3768	108297, 108201	sr gene, sr gene	1 1 0 25 25 5 1	1_A375_shL16_mirvI_lncRNA_AR..1	25	Gene MYH15	MYH15		NM_014981	215321_at	NP_055798.1
GeneID:3378	KIAA1324	3	108,298,718	108,398,491	99,773	-	1	1_A375_shL7_mirvI_lncRNA_AR..1..4005	-65	upstream	1 0 0 16 15 11 1	1_A375_shL16_mirvI_lncRNA_AR..1	16	Gene KIAA1324	C3P2k, MGC163439, KIAA1324, p80, FLJ12830	KIAA1324	NM_020990, XCT19831.2, XCT23199831.0	1553810_s_at, 231083_at	NP_065841.2, EAW79724.1, EAW79723.1
GeneID:3378	DZIP3	3	108,398,327	108,413,893	103,536	+	1	1_A375_shL7_mirvI_lncRNA_AR..1..4005	239	sr gene	1 0 0 16 15 11 1	1_A375_shL16_mirvI_lncRNA_AR..1	16	Gene DZIP3	DZIP3, KIAA0675, FLJ36022, FLJ37977, FLJ38223, MGC1135, FLJ13327, ULF2	DAZ interacting protein 3, zinc finger	NM_014648, XCT19303.2, XCT19713.73.1	207231_at, 207232_s_at, 215166_at	NP_055625.1, EAW79721.1, EAW79722.1
GeneID:1005935	LOC100505655	3	110,794,162	110,795,242	24,080	-	1	2_A375_shL07_plus_lncRNA_AR..1..3769	-2126	upstream	0 1 0 15 19 7 1	2_A375_shL19_plus_lncRNA_AR..1	19	Gene LOC100505655		hypothetical LOC100505655	NR_112822, XR_109462, XR_113372		
GeneID:2365	PVRL3	3	110,740,665	110,832,062	92,197	+	1	2_A375_shL07_plus_lncRNA_AR..1..3769	-107	upstream	0 1 0 15 19 7 1	2_A375_shL19_plus_lncRNA_AR..1	19	Gene PVRL3	PVR3, CDw110, PVRR3, PRR3, FLJ40824, nectin-3, PVRL3, ONFZa66880340, CD113	poliovirus receptor-related 3	NM_015480, XCT16109.2	213323_at	NP_036295.1, EAW79710.1
GeneID:2365	PLCXD2	3	111,280,323	111,369,294	171,771	+	1	2_A375_shL07_plus_lncRNA_AR..1..3771	29137	sr gene	0 0 1 13 16 6 1	2_A375_shL16_mirvI_lncRNA_AR..1	16	Gene PLCXD2	FLJ10379, PLCXD2	phosphatidylinositol-specific phospholipase C, X domain containing 2	NM_001165108, NM_152366, XCT16704.3	1552261_at	NP_001172035.1, NP_689500.1, EAW79693.1
GeneID:2365	PHLDB2	3	111,430,527	111,695,564	265,037	+	2	1_A375_shL7_mirvI_lncRNA_AR..1..4007, 2_A375_shL07_plus_lncRNA_AR..1..3772	125009, 127105	sr gene, sr gene	1 1 0 27 25 12 1	1_A375_shL16_mirvI_lncRNA_AR..1	27	Gene PHLDB2	PHLDB2, ONFZa66JE031, ONFZa43422?, ONFZa81302433, LLSL, FLJ11791, LLSlets	pleckstrin homology-like domain, family B, member 2	NM_145153, NM_001134437, NM_001134438, NM_001134439, XCT23411852.0, XCT23411853.0, XCT23411854.0, XCT23411194.0	1554779_at, 1554779_s_at, 1557579_at, 229855_s_at, 238419_at	NP_663596.1, NP_001127939.1, NP_001127951.1, NP_001127911.1, EAW79692.1, EAW79690.1
GeneID:1148	ABHD10	3	111,697,826	111,712,210	14,382	+	1	4_A375_EGR1..1_8219	20092	downstream	0 0 1 7 10 15 1	4_A375_EGR1..1	15	Gene ABHD10	FLJ11342, ABHD10	abhydrolase domain containing 10	NM_018194, XCT19882921.1, XCT1954.2	219803_s_at, 222977_s_at	NP_060864.1, EAW79668.1, EAW79669.1
GeneID:2911	TAGLN2	3	111,717,568	111,732,733	15,149	+	1	4_A375_EGR1..1_8219	334	sr gene	0 0 1 7 10 15 1	4_A375_EGR1..1	15	Gene TAGLN2	NP25, NP22, TAGLN2	transgelin 2	NM_003186, NM_001003712, NM_001003713, XCT19529942.2, XCT19710303.1, XCT19710291.1	200743_at	NP_037391.2, NP_001003713.1, NP_001003714.1, EAW79663.1, EAW79664.1, EAW79667.1
GeneID:5335	SLC9A10	3	111,839,752	112,012,074	172,322	-	1	2_A375_shL07_plus_lncRNA_AR..1..4008	94402	sr gene	1 0 0 24 11 2 1	2_A375_shL34_plus_lncRNA_AR..1	34	Gene SLC9A10	SLC9A10		NM_182981, XCT23199857.1		NP_896554.1, EAW79679.1
GeneID:422	ATG3	3	112,291,399	112,280,465	59,126	-	2	1_A375_shL7_mirvI_lncRNA_AR..1..4009, 2_A375_shL07_plus_lncRNA_AR..1..3773	-398, -356	upstream, upstream	1 1 0 25 21 10 1	1_A375_shL16_mirvI_lncRNA_AR..1	25	Gene ATG3	ATG3, PC3-96, FLJ22126, KPG3, UHE, MGC15201, KPG3L, ONFZa66JH0176, APG3	ATG3 autophagy related 3 homolog (S. cerevisiae)	NM_022488, XCT23199878.0, XCT23199780.0, XCT23539330.0, XCT6943.3	220227_at, 221492_s_at	NP_071933.2, EAW79686.1, EAW79687.1, EAW79678.1, EAW79677.1
GeneID:3378	SLC35A3	3	112,280,893	112,302,003	22,108	+	2	1_A375_shL7_mirvI_lncRNA_AR..1..4009, 2_A375_shL07_plus_lncRNA_AR..1..3773	-202, -52	upstream, upstream	1 1 0 25 21 10 1	1_A375_shL16_mirvI_lncRNA_AR..1	25	Gene SLC35A3	ONFZa43422, FLJ35773, SLC35A3, FLJ35730, FLJ11330	solute carrier family 35, member A3	NM_017943, XCT19824.1, XCT6941.2	218319_at	NP_060415.1, EAW79666.1, EAW79667.1
GeneID:1687	CCDC50	3	112,333,407	112,339,977	56,570	-	1	2_A375_shL07_plus_lncRNA_AR..1..3774	-260	upstream	0 1 0 16 21 4 1	2_A375_shL21_plus_lncRNA_AR..1	21	Gene CCDC50	CCDC50, MGC134551, MGC151933, URB, tubulaire, SGG1, DRO1	coiled-coil domain containing 50	NM_199311, NM_199312, XCT19829.3, XCT23455551.1, XCT23494491.1	225321_at, 225322_s_at, 243284_at	NP_955803.1, NP_955808.1, EAW79662.1, EAW79664.1, EAW79665.1
GeneID:693	BOC	3	112,931,315	113,008,308	74,931	+	1	4_A375_EGR1..1_8220	-79	upstream	0 0 1 14 13 10 1	4_A375_EGR1..1	10	Gene BOC	BOC	Boc homolog (mouse)	NM_033254, XCT23203.0, XCT23203.0, XCT23203.0, XCT23203.0, XCT6383.2	224164_s_at, 225990_at, 230053_at	NP_150276.1, EAW79643.1, EAW79644.1, EAW79645.1, EAW79646.1
GeneID:2165	CCDC32	3	113,161,565	113,230,054	72,489	-	1	4_A375_EGR1..1_8221	114	sr gene	0 0 1 13 12 10 1	4_A375_EGR1..1	10	Gene CCDC32	EPCE, EPC-ET, FLJ44949, CCDC32, FLJ30054	coiled-coil domain containing 32	NM_144718, XCT23197905.0, XCT23539516.0, XCT23555190.0, XCT6509.2	219384_at, 234968_at	NP_653319.1, EAW79656.1, EAW79655.1, EAW79656.1, EAW79657.1
GeneID:5717	KIAA2018	3	113,287,202	113,413,493	140,291	+	1	2_A375_shL07_mirvI_lncRNA_AR..1..4011	-347	upstream	1 0 0 25 23 9 1	2_A375_shL16_mirvI_lncRNA_AR..1	25	Gene KIAA2018	KIAA2018, ONFZa81C0144	KIAA2018	NM_031309699	1559801_at, 227433_at, 227439_s_at, 242369_at, 242512_x_at	NP_001309699.2
GeneID:1005935	LOC100505655	3	113,425,826	113,436,570	10,844	+	1	2_A375_shL07_mirvI_lncRNA_AR..1..4011	20730	downstream	1 0 0 25 23 9 1	2_A375_shL16_mirvI_lncRNA_AR..1	25	Gene LOC100505655		hypothetical LOC100505655	NR_112816, XR_109457, XR_113376		
GeneID:2165	KIAA0182	3	113,437,641	113,448,096	27,255	-	2	1_A375_shL7_mirvI_lncRNA_AR..1..4012, 2_A375_shL07_plus_lncRNA_AR..1..8222	-932, 364	upstream, sr gene	1 1 0 14 14.5 13 2	2_A375_shL16_mirvI_lncRNA_AR..1	20	Gene KIAA0	KIAA, KIAA18, MAN3, FLJ12194, NAT13, BAA, NAT12, MAN3	N(4)-acetylaminoadenosine 18S rRNA synthase, homolog	NM_020148, XCT16402396.2, XCT19884231.1, XCT23539870.0	217743_s_at, 222393_s_at	NP_064532.1, EAW79630.1, EAW79631.1
GeneID:2911	ATP6V1A	3	113,448,908	113,530,903	84,995	+	2	1_A375_shL7_mirvI_lncRNA_AR..1..4012, 4_A375_EGR1..1_8222	140, -1076	sr gene, upstream	1 0 1 14 14.3 13 2	2_A375_shL16_mirvI_lncRNA_AR..1	20	Gene ATP6V1A	VVA1, VMB, ATP6V1A, HO68, ATP6V1A1, ATP6A1, VPF2	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	NM_001690, XCT23539581.0, XCT23539582.0, XCT23539583.0, XCT9837.3	201991_s_at, 201972_at	NP_001681.2, EAW79626.1, EAW79627.1, EAW79628.1
GeneID:5462	GRAMD1C	3	113,537,951	113,598,021	105,540	+	1	4_A375_EGR1..1_8223	108455	downstream	0 0 1 10 11 22 1	4_A375_EGR1..1	22	Gene GRAMD1C	FLJ40454, ONFZa66H0491, FLJ30982, ONFZa43C0224, GRAM01C	GRAM domain containing 1C	NM_015377, NM_001172105, XCT23539556.0, XCT23539752.0, XCT23539753.0, XCT9553.2	219315_at	NP_056192.2, NP_001165576.1, EAW79621.1, EAW79622.1, EAW79624.1
GeneID:2811	ZDHHC20	3	113,898,748	113,931,829	33,081	+	1	4_A375_EGR1..1_8223	388	sr gene	0 0 1 10 11 22 1	4_A375_EGR1..1	22	Gene ZDHHC20	ZDHHC20, NIDD	zinc finger, DHHC-type containing 20	NM_175310, XCT18764491.4, XCT23539514.0, XCT23539513.0, XCT23539931.0	229912_at	NP_778241.2, EAW79617.1, EAW79618.1, EAW79619.1, EAW79620.1
GeneID:5775	KIAA1407	3	113,952,364	113,975,490	22,276	-	2	1_A375_shL07_mirvI_lncRNA_AR..1..4013, 2_A375_shL07_plus_lncRNA_AR..1..3775	-26, -12	upstream, upstream	1 1 0 25 22 4 1	1_A375_shL16_mirvI_lncRNA_AR..1	25	Gene KIAA1407	KIAA1407, FLJ42314	KIAA1407	NM_030617, XCT9557.3	225478_at	NP_085155.1, EAW79615.1
GeneID:7991	GTPBP10	3	113,979,481	113,997,269	31,856	+	2	1_A375_shL7_mirvI_lncRNA_AR..1..4013, 2_A375_shL07_plus_lncRNA_AR..1..3775	-123, -109	upstream, upstream	1 1 0 25 22 4 1	1_A375_shL16_mirvI_lncRNA_AR..1	25	Gene GTPBP10	GTPBP01, FLJ12980	guanine nucleotide binding protein 10 (putative)	NM_024838, XCT23539539.0, XCT9550.3	1560893_at, 1560896_x_at	NP_079114.1, EAW79614.1, EAW79616.1
GeneID:1814	DRD5	4	113,847,587	113,897,699	50,342	-	3	1_A375_shL7_mirvI_lncRNA_AR..1..4014, 2_A375_shL07_plus_lncRNA_AR..1..3776, 4_A375_EGR1..1_8224	139, 139, 28219	sr gene, sr gene, sr gene	1 1 1 19 23 9.5 2	2_A375_shL16_mirvI_lncRNA_AR..1	23	Gene DRD5	FBT1, MGC149204, ETM1, DRD5, MGC149205, D5R	dopamine receptor D5	NM_000798, NM_033660, XCT19829.44.1, XCT23197485.0, XCT23197483.0, XCT23197820.0, XCT23197821.0, XCT23197860.0, XCT9934.3	211825_s_at, 214359_at	NP_000787.2, NP_387512.2, EAW79608.1, EAW79607.1, EAW79609.1, EAW79612.1, EAW79605.1, EAW79606.1, EAW79610.1, EAW79611.1
GeneID:2812	ZBTB20	3	114,038,541	114,096,127	609,198	-	1	1_A375_shL7_mirvI_lncRNA_AR..1..4015	734767	sr gene	1 0 0 17 12 4 1	1_A375_shL16_mirvI_lncRNA_AR..1	17	Gene ZBTB20	HOF, FLJ20435, DKFZ, ONFZa66F1231, ZBTB20, CGI-68, ZNF288	zinc finger and BTB domain containing 20	NM_001164542, NM_001164543, NM_015962, NM_001164544, NM_001164543, NM_001164545, NM_001164547, XCT23199809.0	203353_s_at, 222357_at, 233306_at	NP_001157614.1, NP_001157615.1, NP_056837.2, NP_001157616.1, NP_001157617.1, NP_001157618.1, NP_001157619.1, EAW79599.1
GeneID:4313	LSAMP	3	115,521,210	116,164,365	643,175	+	4	1_A375_shL7_mirvI_lncRNA_AR..1..4020, 2_A375_shL07_plus_lncRNA_AR..1..4021, 3_A375_shL7_mirvI_lncRNA_AR..1..4022, 4_A375_shL07_plus_lncRNA_AR..1..3781	539777, 443933, 296365, 539713	sr gene, sr gene, sr gene, sr gene	1 1 0 10.67 16.33 4 3	1_A375_shL34_plus_lncRNA_AR..1	34	Gene LSAMP	FLJ32334, FLJ38296, LSAMP, FLJ40856, FLJ32116, LAMP, WUCH2	limbic system-associated membrane protein	NM_002338, XCT23199816.1, XCT23440777.0, XCT23440760.0, XCT23440779.0	1570190_at, 214480_at	NP_002329.2, EAW79590.1, EAW79591.1, EAW79589.1, EAW79591.1
GeneID:5962	KSR1	3	116,619,477	116,694,696	243,421	-	1	4_A375_EGR1..1_8228	72334	sr gene	0 0 1 5 4 15 1	4_A375_EGR1..1	15	Gene KSR1	CXADR11, KSR1, VSK23, CT119, MGC33227, Ipg53, BT-IgSF	coxsackie adenovirus receptor-like membrane protein	NM_152335, NM_001013857, XCT13967.4, XCT23539707.0	229379_at	NP_689751.2, NP_001103687.1, EAW79781.1, EAW79583.1
GeneID:5755	CDGAP	3	119,013,200	119,138,323	125,103	+	2	2_A375_shL07_plus_lncRNA_AR..1..3765, 4_A375_EGR1..1_8227	29764, 29838	sr gene, sr gene	0 1 0 9 10 20 1	4_A375_EGR1..1	20	Gene CDGAP	MGC133270, CDGAP, RAM1204, MGC133266, MNGAP51	CDC42 GTPase-activating protein	NM_020754, XCT19862.2, XCT1972.1	229858_at, 229857_at	NP_065805.2, EAW79573.1, EAW79574.1
GeneID:3378	TMEM38A	3	119,149,701	119,192,471	42,770	-	3	2_A375_shL07_plus_lncRNA_AR..1..3766, 4_A375_EGR1..1_8226, 4_A375_EGR1..1_8229	-25, 7, -3468	upstream, sr gene, upstream	1 0 1 12.5 19.5 10 2	2_A375_shL16_mirvI_lncRNA_AR..1	20	Gene TMEM38A	TMEM38A, FLJ10902	transmembrane protein 38A	NM_018298, XCT13964.3, XCT11937.60	219813_s_at, 222993_s_at, 241392_at	NP_060736.1, EAW79571.1, EAW79572.1
GeneID:5861	NTELC1	3	119,187,755	119,213,535	25,780	+	3	2_A375_shL07_plus_lncRNA_AR..1..3766, 4_A375_EGR1..1_8226, 4_A375_EGR1..1_8229	-3269, -3321, 19	upstream, upstream, sr gene	1 0 1 12.5 19.5 10 2	2_A375_shL16_mirvI_lncRNA_AR..1	20	Gene NTELC1	CLP48, Rum, KC1P48, MGC22709, KTELC1, MGC807, WDS010, C2orf9, KIAA1254, RGLUT1	RTEL (Lyn-Tyr-like-Leu) containing 1	NM_152335, NR_024265, XCT16109.2	218587_s_at, 223651_at	NP_689516.1, EAW79570.1



Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_uNG7_ev_incRNA_AR_1 Percent	2_A375_uNG7_sh_lncRNA_AR_1 Percent	3_A375_uNG7_shRNA_AR_1 Percent	4_A375_1_A375_NG7_shRNA_lncRNA_AR_1 Avg Peak	5_A375_2_A375_uNG7_shRNA_lncRNA_AR_1 Avg Peak	6_A375_EGFR_lncRNA_AR_1 Avg Peak	Add Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
GeneID:1644	ADPRH	3	119,298,523	119,308,792	10,269	+	1	2_A375_uNG7_plus_lncRNA_AR_1..5707	-27	upstream	0	1	0	12	17	8	1	2_A375_uNG7_plus_lncRNA_AR_1	17	Gene ADPRH	ARH1, ADPRH	ADP-ribosylarginine hydrolase	NM_001123, NCT11554.3, NCT21997.0, NCT21997.0	207985_at, 226942_at, 235809_at	NP_001116.1, EAW79580.1, EAW79581.1, EAW79582.1
GeneID:8856	NR1D2	3	119,499,351	119,537,232	38,881	+	1	4_A375_EGR1..6230	39829	up gene	0	0	1	0	8	16	1	4_A375_EGR1..1	16	Gene NR1D2	BHR, RAR2, PARg, PXR, SHP, RXR1, BHR, RXR, ONR1, PAR, NR1D2	nuclear receptor subfamily 1, group I, member 2	NM_005000, NM_033013, NM_033032, NCT12670.3, NCT19982.0, NCT21997.0	207302_s_at, 207303_x_at	NP_004991.2, NP_149094.1, NP_371265.1, EAW79537.1, EAW79538.1, EAW79539.1
GeneID:2915	GSK3B	3	119,948,000	119,811,264	772,484	-	2	1_A375_uNG7_minus_lncRNA_AR_1..4303, 4_A375_EGR1..8231	-756, 366	upstream, up gene	1	0	1	10.5	11.5	13	2	1_A375_uNG7_minus_lncRNA_AR_1	16	Gene GSK3B	GSK3B		NM_002093, NM_001146156, NCT11990.1, NCT21999.0, NCT21999.0, NCT21999.0	3599.1_s_at	NP_002084.2, NP_001139605.1, EAW79533.1, EAW79534.1, EAW79535.1, EAW79536.1
GeneID:1810	LOC100506764	3	119,814,477	119,817,871	3,394	+	2	1_A375_uNG7_plus_lncRNA_AR_1..4023, 4_A375_EGR1..8231	-429, -1421	upstream, upstream	1	0	1	15.5	11.5	13	2	1_A375_uNG7_minus_lncRNA_AR_1	16	Gene LOC100506764		hypothetical LOC100506764	XR_112327, XR_109476, XR_113556		
GeneID:1119	LRRC58	3	120,643,376	120,686,198	54,810	-	1	2_A375_uNG7_plus_lncRNA_AR_1..5765	230	up gene	0	1	0	17	22	14	1	2_A375_uNG7_plus_lncRNA_AR_1	22	Gene LRRC58	LRRC58	leucine rich repeat containing 58	NM_001079676	223479_at, 235898_at	NP_001034246.1
GeneID:1013	LOC100130701	3	120,679,865	120,686,984	50,299	+	1	2_A375_uNG7_plus_lncRNA_AR_1..5765	-5729	upstream	0	1	0	17	22	14	1	2_A375_uNG7_plus_lncRNA_AR_1	22	Gene LOC100130701		hypothetical protein LOC100130701	XM_001715390, XM_001717165, XM_001717549		XP_001715492.2, XP_001717222.2, XP_001717601.2
GeneID:2907	GTF2E1	3	120,481,556	120,501,916	40,356	+	1	1_A375_uNG7_minus_lncRNA_AR_1..4026	33674	up gene	1	0	0	25	13	5	1	1_A375_uNG7_minus_lncRNA_AR_1	23	Gene GTF2E1	GTF2E1, TF2E1, TFIIEA, FE	general transcription factor IIE, polypeptide 1, alpha 56kDa	NM_005513, NCT11656.0	203900_at	NP_005504.2, EAW74519.1
GeneID:8878	STXBP5L	3	120,827,690	121,143,908	316,538	+	1	2_A375_uNG7_plus_lncRNA_AR_1..5769	66	up gene	0	1	0	16	20	10	1	2_A375_uNG7_plus_lncRNA_AR_1	20	Gene STXBP5L	KIAA1006, LLG14, STXBP5L	syntaxin binding protein 5-like	NM_014900	1568096_at, 215316_at	NP_055784.1
GeneID:1870	POLQ	3	121,180,373	121,256,553	114,580	+	1	1_A375_uNG7_minus_lncRNA_AR_1..4027	149	up gene	1	0	0	17	14	14	1	1_A375_uNG7_minus_lncRNA_AR_1	17	Gene POLQ	POLQ, DNFZp001A012, POLH, PRO0327	polymerase (DNA directed), theta	NM_199420, NCT20191805.0, NCT20191807.0, NCT20191809.0, NCT20191810.0, NCT20559302.0	220748_at, 219509_at	NP_955472.3, EAW79512.1, EAW79513.1, EAW79514.1
GeneID:8442	CASR	3	121,903,161	122,008,344	102,183	+	1	4_A375_EGR1..8223	-429	upstream	0	0	1	9	4	14	1	4_A375_EGR1..1	14	Gene CASR	CASR, NSHPT, HHC, HHC1, MGC104441, CaSR, PCAR1, FHH, FHH, EGE, GPRC2A	calcium-sensing receptor	NM_000388, NM_001178065, NCT19813.1, NCT20559910.0, NCT9749.0	210879_at, 211784_s_at, 240899_at, 242764_s_at	NP_000379.2, NP_001170581.1, EAW79493.1, EAW79491.1, EAW79492.1
GeneID:2887	KPNA1	3	122,140,745	122,233,799	93,055	-	2	1_A375_uNG7_minus_lncRNA_AR_1..4025, 2_A375_uNG7_plus_lncRNA_AR_1..5790	-230, 166	upstream, up gene	1	1	0	16	20	7	1	2_A375_uNG7_plus_lncRNA_AR_1	20	Gene KPNA1	SRP1, NPI-1, KPNA1, RCH1, IPOA5	karyopherin alpha 1 (importin alpha 5)	NM_002264, NP_036956, NCT16445522.2, NCT21972.0	202005_at, 202086_at, 202087_at, 202088_s_at, 202089_s_at, 212741_s_at	NP_002255.3, EAW79465.1, EAW79462.1
GeneID:8893	PARP9	3	122,248,737	122,283,323	39,766	-	1	4_A375_EGR1..8224	983	up gene	0	0	1	10	13	10	1	4_A375_EGR1..1	10	Gene PARP9	PARP9, MGC7880, BAL, FLJ43593, DKFZp686B0310, BAL1, FLJ41412, FLJ33510, DKFZp686H01523, FLJ20627	poly (ADP-ribose) polymerase family, member 9	NM_031458, NM_001148102, NM_001148103, NM_001148105, NCT21972.0, NCT22226.0, NCT22556.0, NCT6259.0	223220_s_at, 227007_at	NP_115648.2, NP_001138974.1, NP_001139273.1, NP_001139275.1, NP_001139276.1, EAW79476.1, EAW79477.1, EAW79478.1, EAW79479.1
GeneID:1839	DTX3L	3	122,293,165	122,334,000	40,835	+	1	4_A375_EGR1..8224	113	up gene	0	0	1	10	13	10	1	4_A375_EGR1..1	10	Gene DTX3L	BBAP, DTX3L	deltex 3-like (Drosophila)	NM_138287, NCT10165017.1	223418_at	NP_612144.1, EAW79478.1
GeneID:3427	SEMA3B	3	122,828,043	122,746,576	118,533	-	2	4_A375_EGR1..8218, 4_A375_EGR1..8238	108320, 1432	up gene, upstream	0	0	1	8	8.5	19	2	4_A375_EGR1..1	21	Gene SEMA3B	SEMA5B, Sema5, SEMG, FLJ43722, KIAA1445	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	NM_001031702, NCT20194.0, NCT6236.2	223810_at	NP_001026872.2, EAW79437.1, EAW79438.1
GeneID:1854	PDIA5	3	122,768,556	122,882,953	99,397	+	2	1_A375_uNG7_minus_lncRNA_AR_1..4029, 4_A375_EGR1..8227	312, 418	up gene, up gene	1	0	1	17	16	19	1	4_A375_EGR1..1	19	Gene PDIA5	PDIR, FLJ30401, PDIA5	protein disulfide isomerase family A, member 5	NM_006810, NP_036444, NCT19982.0, NCT21953.0, NCT21955.0, NCT22554.0, NCT6266.4	205857_s_at	NP_006801.1, EAW79435.1, EAW79436.1, EAW79437.1, EAW79438.1
GeneID:2894	SEC22A	3	122,930,374	122,992,893	72,209	+	1	2_A375_uNG7_plus_lncRNA_AR_1..5791	71462	up gene	0	1	0	12	15	7	1	2_A375_uNG7_plus_lncRNA_AR_1	13	Gene SEC22A	SEC22L2, SEC22A	SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	NM_012439, NCT10270.2	218703_at	NP_036362.2, EAW79439.1
GeneID:1161	ADCY9	3	123,003,099	123,187,392	183,993	-	3	1_A375_uNG7_minus_lncRNA_AR_1..4033, 2_A375_uNG7_plus_lncRNA_AR_1..5792, 4_A375_EGR1..8236	160332, 160016, 150136	up gene, up gene, up gene	1	1	1	22	24.5	13.5	2	2_A375_uNG7_plus_lncRNA_AR_1	41	Gene ADCY9	AC9, ADCY9	adenylate cyclase 9	NM_183357, NCT19983.3	226162_at, 242891_at	NP_899208.1, EAW79440.1
GeneID:2869	PTPLB	3	123,213,565	123,260,924	90,581	-	1	2_A375_uNG7_plus_lncRNA_AR_1..5793	-124	upstream	0	1	0	16	16	10	1	2_A375_uNG7_plus_lncRNA_AR_1	16	Gene PTPLB	PTPLB, HACD2	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	NM_196402	212940_at, 227741_at	NP_940854.1
GeneID:1010	LOC100506828	3	123,259,403	123,349,887	90,485	+	1	2_A375_uNG7_plus_lncRNA_AR_1..5793	-353	upstream	0	1	0	16	16	10	1	2_A375_uNG7_plus_lncRNA_AR_1	16	Gene LOC100506828		hypothetical LOC100506828	XR_112355, XR_109474, XR_113555		
GeneID:8997	KALRN	3	123,810,500	124,440,038	629,478	+	7	1_A375_uNG7_minus_lncRNA_AR_1..4031, 1_A375_uNG7_minus_lncRNA_AR_1..4032, 1_A375_uNG7_minus_lncRNA_AR_1..4033, 1_A375_uNG7_minus_lncRNA_AR_1..4034, 2_A375_uNG7_plus_lncRNA_AR_1..5794, 2_A375_uNG7_plus_lncRNA_AR_1..5795, 2_A375_uNG7_plus_lncRNA_AR_1..5796	132970, 334410, 436330, 639669, 725016, 435794, 835770	up gene, up gene, up gene, down-stream, up gene, down-stream	1	1	0	22	22.8	5.4	3	2_A375_uNG7_plus_lncRNA_AR_1	22	Gene KALRN	KALRN, FLJ12322, DUET, MRNEF24, FLJ16199, FLJ16823, CAD, TRAD, FLJ19442, HAPIP	kalirin, RhoGEF kinase	NM_001024980, NM_003947, NR_020150, NM_007064	209459_s_at, 209870_at, 227792_at, 232717_at, 232796_s_at, 239851_at	NP_001019631.2, NP_003930.1, NP_009059.2
GeneID:1010	LOC100506841	3	124,443,943	124,445,172	1,229	+	2	2_A375_uNG7_minus_lncRNA_AR_1..4034, 2_A375_uNG7_plus_lncRNA_AR_1..5796	5264, 6355	down-stream, down-stream	1	1	0	16	21	12	1	2_A375_uNG7_minus_lncRNA_AR_1	21	Gene LOC100506841		hypothetical LOC100506841	XR_112357, XR_109476, XR_113558		
GeneID:2795	LNPEP	3	124,449,213	124,490,130	16,907	+	2	1_A375_uNG7_minus_lncRNA_AR_1..4034, 2_A375_uNG7_plus_lncRNA_AR_1..5796	14,115	up gene, up gene	1	1	0	16	21	12	1	2_A375_uNG7_plus_lncRNA_AR_1	21	Gene LNPEP	CPRT, LNPEP	prolyl cis-trans isomerase/cytokine synthetase	NM_005377, NR_035434, NR_035437, NCT10196.5, NCT22559.0	202706_s_at, 202707_at, 213165_s_at	NP_005366.1, EAW79436.1, EAW79437.1
GeneID:1184	MIR3648	3	124,491,099	124,491,993	77	+	2	1_A375_uNG7_minus_lncRNA_AR_1..4034, 2_A375_uNG7_plus_lncRNA_AR_1..5796	-2691, -1798	upstream, upstream	1	1	0	16	21	12	1	2_A375_uNG7_plus_lncRNA_AR_1	21	Gene MIR3648	MIR3648	microRNA 3648	NR_039188		
GeneID:2887	ITGB5	3	124,491,795	124,606,144	124,349	-	1	2_A375_uNG7_plus_lncRNA_AR_1..5797	74252	up gene	0	1	0	11	19	7	1	2_A375_uNG7_plus_lncRNA_AR_1	19	Gene ITGB5	FLJ26550, ITGB5	integrin, beta 5	NM_002213, NCT22319106.0, NCT6537.2	201124_at, 201125_s_at, 214020_x_at, 214021_x_at	NP_002204.2, EAW79405.1, EAW79406.1
GeneID:3791	HEG1	3	124,569,554	124,774,002	180,248	-	1	2_A375_uNG7_plus_lncRNA_AR_1..5798	69822	up gene	0	1	0	13	16	7	1	2_A375_uNG7_plus_lncRNA_AR_1	16	Gene HEG1	HEG, MGC72175, HEG1, MSTP112, MSTI112, 10A11237	HEG homolog 1 (zebrafish)	NM_020733	212922_at, 213089_at	NP_065784.1
GeneID:6481	SLC12A9	3	124,931,490	124,931,609	130,129	-	1	2_A375_uNG7_plus_lncRNA_AR_1..5799	126729	up gene	0	1	0	8	17	9	1	2_A375_uNG7_plus_lncRNA_AR_1	17	Gene SLC12A9	FLJ20185, SLC12A6, CCCE, DKFZp686L162A	solute carrier family 12 (potassium/chloride transporters), member 9	NM_024826, NCT23193.2, NCT23440.1	219674_at	NP_079094.3, EAW79400.1, EAW79399.1
GeneID:2757	ZNF148	3	124,944,513	125,004,198	149,688	-	3	1_A375_uNG7_minus_lncRNA_AR_1..4035, 2_A375_uNG7_plus_lncRNA_AR_1..5800, 4_A375_EGR1..8239	-42, 22, -202	up-stream, up gene, up-stream	1	1	1	27	23	16	1	1_A375_uNG7_minus_lncRNA_AR_1	27	Gene ZNF148	ZBP-99, BERF-1, BFCL1, ZNF148, HT-BETA, DKFZp686L1624, HSD-52, ZFP148	zinc finger protein 148	NM_021964, NCT23389.8, NCT23393.0, NCT23395.0, NCT23399.0, NCT7802.3	209316_s_at, 209319_s_at	NP_067795.2, EAW79397.1, EAW79394.1, EAW79395.1, EAW79396.1, EAW79398.1
GeneID:8701	SNX4	3	125,168,494	125,239,035	70,564	-	1	2_A375_uNG7_minus_lncRNA_AR_1..4036	66	up gene	0	0	0	14	13	9	1	1_A375_uNG7_minus_lncRNA_AR_1	14	Gene SNX4	ATG24B, SNX4	sorting nexin 4	NM_020774, NCT19347.2, NCT23193.0, NCT23193.0, NCT23195.0	205279_s_at, 213532_at	NP_065827.1, EAW79388.1, EAW79389.1, EAW79390.1, EAW79391.1, EAW79392.1, EAW79393.1
GeneID:1010	OSBPL11	3	125,247,702	125,314,361	66,659	-	1	1_A375_uNG7_minus_lncRNA_AR_1..4026	73269	down-stream	1	0	0	14	13	9	1	1_A375_uNG7_minus_lncRNA_AR_1	14	Gene OSBPL11	ORP11, TCCAN00292, FLJ13184, FLJ35310, OSBP12, OSBPL11, ORP-11	oxysterol binding protein-like 11	NM_032776, NCT23020.4	218364_s_at, 222698_s_at, 225827_s_at	NP_079152.2, EAW79369.1
GeneID:1810	ROPN1B	3	125,898,020	125,702,297	14,289	+	1	2_A375_uNG7_plus_lncRNA_AR_1..5801	6760	up gene	0	1	0	5	16	9	1	2_A375_uNG7_plus_lncRNA_AR_1	16	Gene ROPN1B	ROPN1B		NM_001012337	229429_x_at	NP_001012337.1
GeneID:1810	ALDH1L1	3	125,822,400	125,899,465	77,077	-	1	4_A375_EGR1..8242	412	up gene	0	0	1	3	8	16	1	4_A375_EGR1..1	16	Gene ALDH1L1	DKFZp781N0997, ALDH1L1, 10-FTHF, FTHFD	aldehyde dehydrogenase 1 family, member L1	NM_012190, NCT19810.1, NCT23191.0, NCT9516.3	203326_at, 215756_at	NP_036222.2, EAW79370.1, EAW79372.1
GeneID:2887	KLF13	3	126,080,478	126,079,238	14,756	-	1	2_A375_uNG7_plus_lncRNA_AR_1..5803	1013	up gene	0	1	0	20	19	13	1	2_A375_uNG7_plus_lncRNA_AR_1	19	Gene KLF13	KLF7, DKFZp779H1320, KLF13	Kruppel-like factor 13	NM_015995, NCT23191.0	221302_at, 231410_at	NP_056810.2, EAW79367.1
GeneID:1010	LOC100506907	3	126,082,705	126,112,483	29,760	-	2	2_A375_uNG7_plus_lncRNA_AR_1..5803, 4_A375_EGR1..8242	37264, -5227	down-stream, up-stream	0	1	1	11.5	12.5	14	2	2_A375_uNG7_plus_lncRNA_AR_1	19	Gene LOC100506907		hypothetical LOC100506907	XR_112354, XR_109476, XR_113556		
GeneID:3427	CCDC37	3	126,113,762	126,155,396	41,635	+	2	4_A375_EGR1..8243, 4_A375_EGR1..8244	6603, 39030	up gene, up gene	0	0	1	3.5	8.5	13.5	2	4_A375_EGR1..1	16	Gene CCDC37	CCDC37, FLJ40503, MGC120588	coiled-coil domain containing 37	NM_152626	242615_at, 243756_at	NP_870434.2
GeneID:2794	ZXDC	3	126,156,444	126,194,782	38,339	-	1	4_A375_EGR1..8264	41930	down-stream	0	0	1	4	7	16	1	4_A375_EGR1..1	16	Gene ZXDC	ZXDC, DKFZp547M024, FLJ10581, ZXDC, MGC11349, FLJ20320, FLJ38477	ZXD family zinc finger C	NM_025112, NM_001040653, NCT21918.0	218839_s_at, 223964_at, 230106_at	NP_079068.3, NP_001029743.1, EAW79361.1
GeneID:1369	UROC1	3	126,200,300	126,238,618	38,805	+	1	4_A375_EGR1..8265	-9648	upstream	0	0	1	8	8	21	1	4_A375_EGR1..1	21	Gene UROC1	UROD1, DKFZp313D1320, MGC13307, FLJ31300, MGC119301, UROC1	urocanate domain containing 1	NM_144939, NM_001165974, NCT21918.0	1553241_at	NP_653245.1, NP_001159446.1, EAW79360.1
GeneID:9612	CHST13	3	126,242,176	126,282,134	39,959	+	1	4_A375_EGR1..8245	3456	up gene	0	0	1	8	8	21	1	4_A375_EGR1..1	21	Gene CHST13	C4ST3, MGC119278, MGC119281, CHST13, MGC119279	carbohydrate (chondroitin 4) sulfotransferase 13	NM_152889, NCT18429.3	233947_at, 242833_at	NP_690418.1, EAW79359.1
GeneID:5303	CHCHD6	3	126,428,116	126,879,244	299,128	+	4	1_A375_uNG7_minus_lncRNA_AR_1..4037, 2_A375_uNG7_plus_lncRNA_AR_1..5804, 2_A375_uNG7_plus_lncRNA_AR_1..5805, 4_A375_EGR1..8248	208951, -174, 207210, 402	up gene, up-stream, up gene, up gene	1	1	1	15	20.5	12	2	2_A375_uNG7_plus_lncRNA_AR_1	24	Gene CHCHD6	CHCHD6, MGC13216	coiled-coil-helix-coiled-coil-helix domain containing 6	NM_032343, NCT19834.1	224462_s_at	NP_115719.1, EAW79332.1
GeneID:1132	LOC100132461	3	126,438,193	126,457,491	19,298	-	2	2_A375_uNG7_plus_lncRNA_AR_1..5804, 4_A375_EGR1..8248	-3251, -3676	up-stream, up-stream	0	1	1	11	24	16	1	2_A375_uNG7_plus_lncRNA_AR_1	24	Gene LOC100132461		hypothetical LOC100132461	XR_112323, XR_109476, XR_113559		
GeneID:8331	PLXNA1	3	126,707,437	126,798,235	90,799	+	4	1_A375_uNG7_minus_lncRNA_AR_1..4028, 1_A375_uNG7_minus_lncRNA_AR_1..8247, 4_A375_EGR1..8246, 4_A375_EGR1..8249	-5803, -5901, 11867, 40435	up-stream, up-stream, up gene, up gene	1	0	1	12.67	10.33	16	3	1_A375_uNG7_minus_lncRNA_AR_1	22	Gene PLXNA1	PLXNA1, NOV3, DKFZp781P1912, PLEXIN-1, PLXN1, NOV	plexin A1	NM_032242, NCT19618.0, NCT22109.0, NCT22109.0	1555140_at, 221537_at, 221539_s_at	NP_115618.3, EAW79349.1, EAW79350.1, EAW79351.1
GeneID:1551	TPRA1	3	127,291,005	127,328,000	37,995	+	4	1_A375_uNG7_minus_lncRNA_AR_1..4061, 1_A375_uNG7_minus_lncRNA_AR_1..4062, 2_A375_uNG7_plus_lncRNA_AR_1..5810, 2_A375_uNG7_plus_lncRNA_AR_1..5811	-180, -7532, 84, 7803	up-stream, up-stream, up gene, up-stream	1	1	0	20.5	20.5	12.5	2	2_A375_uNG7_plus_lncRNA_AR_1	24	Gene TPRA1	TPRA1, FLJ22107, THEM027, GPR178, TPRA40	transmembrane protein, adipocyte-associated 1	NM_001136053, NM_018372, NM_001142968, NCT19832.1, NCT19834.0, NCT21972.0, NCT21974.0, NCT22104.2	210559_at	NP_001129525.1, NP_060745.2, NP_001136116.1, EAW79343.1, EAW79344.1, EAW79342.1, EAW79343.1
GeneID:4171	MCM2	3	127,317,253	127,341,279	24,026	+	4	1_A375_uNG7_minus_lncRNA_AR_1..4061, 1_A375_uNG7_minus_lncRNA_AR_1..4062, 2_A375_uNG7_plus_lncRNA_AR_1..5810, 2_A375_uNG7_plus_lncRNA_AR_1..5811	-7525, -133, -7346, -9	up-stream, up-stream, up-stream, up-stream	1	1	0	26.5	30.5	12.5	2	2_A375_uNG7_plus_lncRNA_AR_1	24	Gene MCM2	CCA19, CCNL1, MTS7/8, MCM2, MGC10696, BM28, CCNL1, HsMCM2	minichromosome maintenance complex component 2	NM_004526, NCT20519.2	202107_s_at	NP_004517.2, EAW79339.1

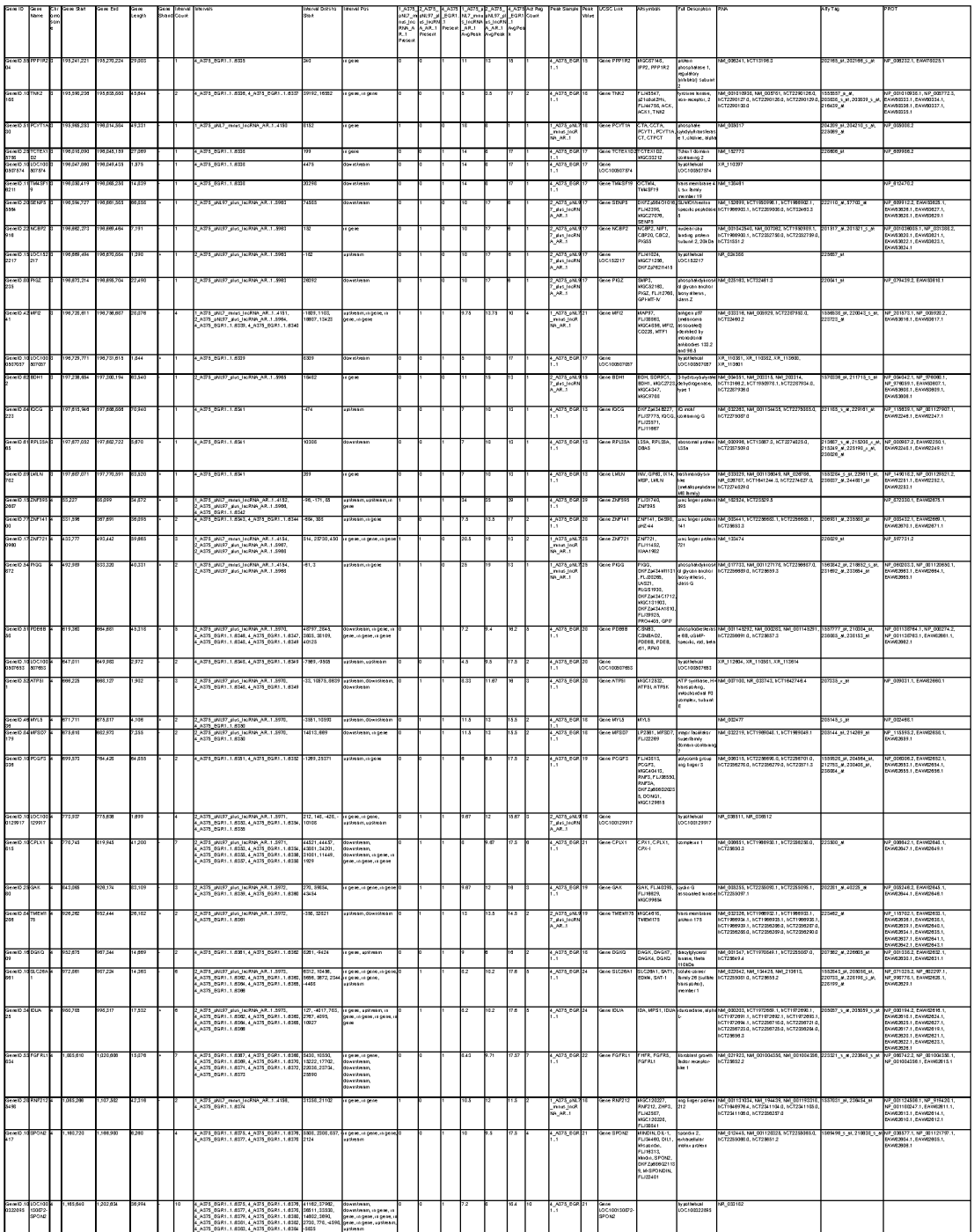


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:25852	ARMC8	3	137,906,148	138,016,219	110,071	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5847	135	in gene	0	1	0	14	22	11	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ARMC8	ARMC8, HSPC056, MGC10058, MGC4880, S863-2	armadillo repeat containing 8	NM_213654, NM_014154, NM_015396, hCT1951512.1, hCT1961935.1, hCT1961936.1, hCT2319292.0, hCT2319294.0, hCT2319297.0, hCT2319298.0, hCT2355855.0	1555279_at, 1555281_x_at, 203486_s_at, 203487_s_at, 219094_at, 236986_at, 244528_at	NP_998819.1, NP_054873.2, NP_056211.2, EAW79078.1, EAW79077.1, EAW79081.1, EAW79075.1, EAW79076.1, EAW79079.1, EAW79080.1, EAW79082.1
GeneID:22808	MRAS	3	138,066,825	138,124,377	57,752	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4071, 2_A375_pNL97_plus_lncRNA_AR..1..5848	575, 363	in gene, in gene	1	1	0	19	18	10	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene MRAS	M-RAs, FLJ42964, MRAS, RRAS3, R-RAS3	muscle RAS oncogene homolog	NM_001085049, NM_012219, hCT1951513.1, hCT1951514.1, hCT2319301.0, hCT8152.3	206538_at, 225185_at	NP_001078518.1, NP_036351.3, EAW79068.1, EAW79069.1, EAW79070.1, EAW79071.1
GeneID:80321	CEP70	3	138,213,186	138,313,129	99,943	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5849	-247	upstream	0	1	0	14	15	8	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene CEP70	CEP70, FLJ13036, BITE	centrosomal protein 70kDa	NM_024491, hCT1951516.1, hCT2318815.0, hCT2355868.0, hCT8269.3	1554488_at, 1554489_a_at, 219036_at, 224150_s_at, 238154_at	NP_077817.2, EAW79060.1, EAW79061.1, EAW79062.1, EAW79063.1
GeneID:55179	FAIM	3	138,327,542	138,352,218	24,676	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5850	-22	upstream	0	1	0	15	23	15	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene FAIM	FAIM1, FAIM	Fas apoptotic inhibitory molecule	NM_018147, NM_001033032, NM_001033030, NM_001033031, hCT1951517.1, hCT2319307.0, hCT8270.3	220643_s_at	NP_060617.1, NP_001028204.1, NP_001028202.1, NP_001028203.1, EAW79058.1, EAW79059.1, EAW79057.1
GeneID:668	FOXL2	3	138,663,066	138,665,982	2,916	-	1	4_A375_EGR1..1..8285	-3202	upstream	0	0	1	8	9	21	1	4_A375_EGR1..1	21	Gene FOXL2	BPES1, BPES, PFRK, PINTO, FOXL2, POF3	forkhead box L2	NM_023067	220102_at	NP_075555.1
GeneID:401089	C3orf72	3	138,866,076	138,872,830	6,754	+	1	4_A375_EGR1..1..8285	3108	in gene	0	0	1	8	9	21	1	4_A375_EGR1..1	21	Gene C3orf72	C3orf72, FLJ52231	chromosome 3 open reading frame 72	NM_001040081		NP_001035150.1
GeneID:9276	COPB2	3	139,076,433	139,108,522	32,089	-	1	4_A375_EGR1..1..8286	202	in gene	0	0	1	15	12	14	1	4_A375_EGR1..1	14	Gene COPB2	beta'-COP, COPB2	coatomer protein complex, subunit beta 2 (beta prime)	NM_004766, NR_023350, hCT2318895.0, hCT8267.3	201098_at	NP_004757.1, EAW79040.1, EAW79039.1
GeneID:100507291	LOC100507291	3	139,108,657	139,163,446	54,789	+	1	4_A375_EGR1..1..8286	-337	upstream	0	0	1	15	12	14	1	4_A375_EGR1..1	14	Gene LOC100507291		hypothetical LOC100507291	XR_112579, XR_112577, XR_112580, XR_112578, XR_108497, XR_108495, XR_108498, XR_108496, XR_113525, XR_113523, XR_113526, XR_113524		
GeneID:64084	CLSTN2	3	139,654,027	140,286,919	632,892	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4075, 2_A375_pNL97_plus_lncRNA_AR..1..5855, 4_A375_EGR1..1..8287	271701, 358149, 661	in gene, in gene, in gene	1	1	1	14.33	12.33	8.67	3	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene CLSTN2	FLJ39113, CSTN2, CDHR13, ALC-GAMMA, CS2, MGC119560, CLSTN2, alcagamma, FLJ39499	calsyntenin 2	NM_022131, hCT2319018.0, hCT2355865.0, hCT7091.3	219414_at	NP_071414.2, EAW79016.1, EAW79017.1, EAW79018.1
GeneID:55186	SLC25A36	3	140,660,662	140,698,785	38,123	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4077, 4_A375_EGR1..1..8288	106, 10	in gene, in gene	1	0	1	13	11	13	1	1_A375_pNL7_minus_lncRNA_AR..1	13	Gene SLC25A36	SLC25A36, DKFZp564C053, FLJ10618	solute carrier family 25, member 36	NM_001104647, NM_018155, hCT2319015.0, hCT2355801.0, hCT8654.3	201917_s_at, 201918_at, 201919_at, 223698_at, 237741_at	NP_001098117.1, NP_060625.2, EAW79011.1, EAW79012.1, EAW79013.1
GeneID:92370	ACPL2	3	140,950,662	141,013,466	62,804	+	4	2_A375_pNL97_plus_lncRNA_AR..1..5857, 4_A375_EGR1..1..8289, 1_A375_pNL7_minus_lncRNA_AR..1..4078, 2_A375_pNL97_plus_lncRNA_AR..1..5858	8566, -314, 70758, 70918	in gene, upstream, downstream, downstream	1	1	1	13.67	19.33	10	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ACPL2	ACPL2, FLJ23751	acid phosphatase-like 2	NM_001037172, NM_152282, hCT2318937.0, hCT2355795.0, hCT8652.3	226925_at, 239475_at	NP_001032249.1, NP_689495.1, EAW79007.1, EAW79008.1, EAW79009.1
GeneID:253461	ZBTB38	3	141,043,055	141,168,634	125,579	+	5	1_A375_pNL7_minus_lncRNA_AR..1..4079, 1_A375_pNL7_minus_lncRNA_AR..1..4080, 2_A375_pNL97_plus_lncRNA_AR..1..5860, 2_A375_pNL97_plus_lncRNA_AR..1..5861, 2_A375_pNL97_plus_lncRNA_AR..1..5862	43165, 43873, 11409, 43261, 44177	in gene, in gene, in gene, in gene, in gene	1	1	0	13	18	7	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ZBTB38	FLJ22332, FLJ31131, ZNF921, CIBZ, FLJ35036, ZBTB38	zinc finger and BTB domain containing 38	NM_001080412	1558733_at, 219221_at, 225512_at, 230754_at, 236557_at	NP_001073881.2
GeneID:5922	RASA2	3	141,205,926	141,331,197	125,271	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5863	602	in gene	0	1	0	12	13	11	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene RASA2	GAP1M, RASA2	RAS p21 protein activator 2	NM_006506, hCT1961930.1, hCT7092.4	206636_at, 230669_at	NP_006497.2, EAW78998.1, EAW78999.1
GeneID:9616	RNF7	3	141,457,051	141,465,243	8,192	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4081, 2_A375_pNL97_plus_lncRNA_AR..1..5864	5, -11	in gene, upstream	1	1	0	23	26	11	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene RNF7	ROC2, RNF7, CKBBP1, SAG	ring finger protein 7	NM_183237, NM_014245, hCT1951510.1, hCT1951511.1, hCT2318947.0, hCT2318949.0, hCT2355942.0, hCT7578.3	218286_s_at, 224394_at, 224395_s_at, 224439_x_at, 239820_at	NP_899060.1, NP_055060.1, EAW78991.1, EAW78992.1, EAW78993.1, EAW78994.1, EAW78995.1, EAW78996.1
GeneID:483	ATP1B3	3	141,595,470	141,645,382	49,912	+	1	4_A375_EGR1..1..8290	-318	upstream	0	0	1	10	12	17	1	4_A375_EGR1..1	17	Gene ATP1B3	ATP1B3, CD298, FLJ29027, ATPB-3	ATPase, Na+/K+ transporting, beta 3 polypeptide	NM_001679, hCT1951528.1, hCT1985319.1, hCT1985320.1, hCT1985321.1, hCT2318954.0, hCT2318955.0, hCT2318958.0, hCT2318960.0	208836_at, 226570_at, 229709_at	NP_001670.1, EAW78989.1, EAW78982.1, EAW78983.1, EAW78985.1, EAW78986.1, EAW78984.1, EAW78988.1, EAW78987.1
GeneID:100507375	LOC100507375	3	141,595,485	141,622,572	27,087	-	1	4_A375_EGR1..1..8290	27420	downstream	0	0	1	10	12	17	1	4_A375_EGR1..1	17	Gene LOC100507375		hypothetical LOC100507375	XR_112575, XR_108500		
GeneID:7029	TFDP2	3	141,663,270	141,868,386	205,116	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4082, 2_A375_pNL97_plus_lncRNA_AR..1..5865, 2_A375_pNL97_plus_lncRNA_AR..1..5866, 4_A375_EGR1..1..8291	209186, 209170, 98, -30	downstream, downstream, in gene, upstream	1	1	1	16	15	12	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene TFDP2	DP2, FLJ39131, Dp-2, DKFZp313O196, TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	NM_001178138, NM_001178139, NM_001178140, NM_001178141, NM_001178142, NM_006286, hCT1951526.1, hCT1951527.1, hCT2318695.0, hCT2318698.0, hCT2355963.0	203588_s_at, 203589_s_at, 226157_at	NP_001171609.1, NP_001171610.1, NP_006277.1, NP_001171611.1, NP_001171612.1, NP_001171613.1, EAW78977.1, EAW78978.1, EAW78979.1, EAW78980.1, EAW78981.1
GeneID:256356	GK5	3	141,876,369	141,944,449	68,080	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5866, 4_A375_EGR1..1..8291	76161, 76033	downstream, downstream	0	1	1	11	14	14	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene GK5	FLJ45739, FLJ33582, MGC40579, GK5	glycerol kinase 5 (putative)	NM_001039547, NR_033289, hCT1826043.3, hCT2355910.0, hCT2355911.0	1553772_at, 238121_at, 241384_x_at	NP_001034636.1, EAW78976.1, EAW78974.1, EAW78975.1
GeneID:545	ATR	3	142,168,077	142,297,668	129,591	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4083, 2_A375_pNL97_plus_lncRNA_AR..1..5867	-12, -28	upstream, upstream	1	1	0	49	53	17	1	2_A375_pNL97_plus_lncRNA_AR..1	53	Gene ATR	SCKL, SCKL1, ATR, FRP1, MEC1	ataxia telangiectasia and Rad3 related	NM_001184, hCT1951523.1, hCT2318691.0	209902_at	NP_001175.2, EAW78970.1, EAW78969.1
GeneID:5357	PLS1	3	142,315,229	142,432,506	117,277	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5868	51	in gene	0	1	0	17	19	10	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PLS1	Plastin-1, FIMBRIN, PLS1	plastin 1 (I isoform)	NM_002670, NM_001145319, NM_001172312, hCT13076.2, hCT1952058.0, hCT2319535.0	205190_at	NP_002661.2, NP_001138791.1, NP_001165783.1, EAW78965.1, EAW78966.1, EAW78967.1
GeneID:26577	PCOLCE2	3	142,536,702	142,608,045	71,343	-	3	2_A375_pNL97_plus_lncRNA_AR..1..5869, 2_A375_pNL97_plus_lncRNA_AR..1..5870, 4_A375_EGR1..1..8292	1037, -7134, 493	in gene, upstream, in gene	0	1	1	12.67	15	11	3	4_A375_EGR1..1	19	Gene PCOLCE2	PCPE2, PCOLCE2	procollagen C-endopeptidase enhancer 2	NM_013363, hCT12595.2, hCT2318687.0	219295_s_at	NP_037495.1, EAW78961.1, EAW78962.1
GeneID:344838	PAQR9	3	142,680,073	142,682,178	2,105	-	1	4_A375_EGR1..1..8293	665	in gene	0	0	1	11	12	18	1	4_A375_EGR1..1	18	Gene PAQR9	PAQR9, FLJ41938	progestin and adipoQ receptor family member IX	NM_198504, hCT2318686.0	1558322_a_at, 1560467_at	NP_940906.1, EAW78959.1
GeneID:100289361	LOC100289361	3	142,719,687	142,720,309	622	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4085, 2_A375_pNL97_plus_lncRNA_AR..1..5871	-75, 5	upstream, in gene	1	1	0	36	42	12	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene LOC100289361		hypothetical LOC100289361	NR_034032		
GeneID:23350	SR140	3	142,720,372	142,779,567	59,195	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4085, 2_A375_pNL97_plus_lncRNA_AR..1..5871	12, -66	in gene, upstream	1	1	0	36	42	12	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene SR140	SR140, KIAA0332, MGC133197, fSAPa, U2SURP	U2 snRNP-associated SURP domain containing	NM_001080415	212058_at, 212060_at, 212061_at, 238431_at, 236896_at	NP_001073884.1
GeneID:9435	CHST2	3	142,838,668	142,841,812	3,144	+	1	4_A375_EGR1..1..8294	1652	in gene	0	0	1	14	12	21	1	4_A375_EGR1..1	21	Gene CHST2	GST-2, GST2, C6ST, Gn6ST-1, CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	NM_004267, hCT2319542.0, hCT2319543.0	203921_at	NP_004258.2, EAW78953.1, EAW78952.1
GeneID:285195	SLC9A9	3	142,984,064	143,567,373	583,309	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4086, 2_A375_pNL97_plus_lncRNA_AR..1..5872, 2_A375_pNL97_plus_lncRNA_AR..1..5873	161645, 405773, 161741	in gene, in gene, in gene	1	1	0	16	17.5	3	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene SLC9A9	Nbla00118, FLJ35613, NHE9, AUTS16, SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	NM_173653, hCT2343785.0, hCT2343788.0	227791_at, 242587_at	NP_775924.1, EAW78950.1, EAW78951.1
GeneID:205428	C3orf58	3	143,690,640	143,711,210	20,570	+	6	1_A375_pNL7_minus_lncRNA_AR..1..4087, 1_A375_pNL7_minus_lncRNA_AR..1..4088, 1_A375_pNL7_minus_lncRNA_AR..1..4089, 2_A375_pNL97_plus_lncRNA_AR..1..5874, 2_A375_pNL97_plus_lncRNA_AR..1..5875, 2_A375_pNL97_plus_lncRNA_AR..1..5876	-668, 160, 1072, -795, 672, 1520	upstream, in gene, in gene, upstream, in gene, in gene	1	1	0	15.5	16.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C3orf58	MGC33365, DIA1, C3orf58	chromosome 3 open reading frame 58	NM_173552, NM_001134470, hCT1964553.2, hCT1964554.1, hCT5808.3	226464_at, 228079_at, 235653_at	NP_775823.1, NP_001127942.1, EAW78946.1, EAW78947.1, EAW78948.1
GeneID:5352	PLOD2	3	145,787,227	145,879,282	92,055	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5877, 4_A375_EGR1..1..8296	29376, 594	in gene, in gene	0	1	1	11	15.5	12	2	4_A375_EGR1..1	22	Gene PLOD2	LH2, PLOD2, TLH	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	NM_182943, NM_000935, hCT2318729.0, hCT2355805.0, hCT7119.3	202619_s_at, 202620_s_at	NP_891988.1, NP_000926.2, EAW78939.1, EAW78940.1, EAW78941.1
GeneID:57088	PLSCR4	3	145,910,122	145,968,966	58,844	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5878	390	in gene	0	1	0	10	19	9	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PLSCR4	PLSCR4, TRA1	phospholipid scramblase 4	NM_020353, NM_001128306, NM_001177304, NR_033438, NR_033439, hCT1961934.1, hCT2355928.0, hCT2355929.0, hCT7840.3	218901_at	NP_065086.2, NP_001121778.1, NP_001170775.1, EAW78935.1, EAW78937.1, EAW78938.1, EAW78936.1
GeneID:57047	PLSCR2	3	146,151,082	146,213,722	62,640	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4090, 4_A375_EGR1..1..8297	-8036, 26554	upstream, in gene	1	0	1	14	9.5	12.5	2	4_A375_EGR1..1	21	Gene PLSCR2	PLSCR2		NM_020359, hCT1640638.2, hCT2318561.0	207374_at	NP_065092.1, EAW78932.1, EAW78931.1
GeneID:84107	ZIC4	3	147,103,835	147,124,407	20,572	-	1	4_A375_EGR1..1..8299	13047	in gene	0	0	1	5	16	21	1	4_A375_EGR1..1	21	Gene ZIC4	FLJ42609, FLJ45833, ZIC4	Zic family member 4	NM_032153, NM_001168378, NM_001168379, NR_033118, NR_033119, hCT2318521.0, hCT2355852.0, hCT8155.3	211483_at, 236711_at	NP_115529.2, NP_001161850.1, NP_001161851.1, EAW78917.1, EAW78918.1, EAW78919.1
GeneID:7545	ZIC1	3	147,127,181	147,134,506	7,325	+	1	4_A375_EGR1..1..8300	11955	downstream	0	0	1	7	2	15	1	4_A375_EGR1..1	15	Gene ZIC1	ZIC1, ZNF201, ZIC	Zic family member 1 (odd-paired homolog, Drosophila)	NM_003412, hCT1957083.1, hCT7102.2	1557154_at, 1557155_a_at, 206373_at, 234716_at, 238696_at	NP_003403.2, EAW78916.1, EAW78915.1
GeneID:440982	FLJ30375	3	147,137,609	147,139,986	2,377	+	1	4_A375_EGR1..1..8300	1527	in gene	0	0	1	7	2	15	1	4_A375_EGR1..1	15	Gene FLJ30375		hypothetical LOC440982	XR_112573, XR_108502, XR_113529		
GeneID:2992	GYG1	3	148,709,195	148,745,456	36,261	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4091	19381	in gene	1	0	0	16	14	4	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene GYG1	GYG, GYG1, GSD15	glycogenin 1	NM_001184720, NM_001184721, NM_004130, hCT12297.2, hCT1952050.0, hCT1983020.1, hCT1983021.1, hCT1983022.1, hCT2318603.0, hCT2318607.0, hCT2318610.0	201554_x_at, 211275_s_at	NP_001171649.1, NP_001171650.1, NP_004121.2, EAW78895.1, EAW78898.1, EAW78896.1, EAW78894.1, EAW78897.1, EAW78899.1, EAW78900.1, EAW78901.1
GeneID:6596	HLTF	3	148,747,904	148,804,341	56,437	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5880	-171	upstream	0	1	0	14	21	7	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene HLTF	SMARCA3, HLTF1, HLTF, SNF2L3, HIP116, ZBU1, RNF80, HIP116A	helicase-like transcription factor	NM_139048, NM_003071, hCT12299.3, hCT1952051.1, hCT2318582.0, hCT2318584.0, hCT2355905.0	202983_at	NP_620636.1, NP_003062.2, EAW78889.1, EAW78890.1, EAW78892.1, EAW78893.1, EAW78891.1
GeneID:84343	HPS3	3	148,847,371	148,891,305	43,934	+	3	2_A375_pNL97_plus_lncRNA_AR..1..5881, 2_A375_pNL97_plus_lncRNA_AR..1..5882, 4_A375_EGR1..1..8301	149, 50837, -11	in gene, downstream, upstream	0	1	1	15	21	14	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene HPS3	DKFZp686F0413, SUTAL, FLJ22704, HPS3	Hermansky-Pudlak syndrome 3	NM_032383, hCT1826064.2, hCT2318612.0, hCT2318614.0, hCT2318615.0	227139_s_at, 231121_at, 238539_at	NP_115759.2, EAW78886.1, EAW78885.1, EAW78887.1, EAW78888.1
GeneID:1356	CP	3	148,890,286	148,939,832	49,546	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5882	41624	in gene	0	1	0	13	19	8	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CP	CP-2, CP	ceruloplasmin (ferroxidase)	NM_000096, hCT1820064.2, hCT2318579.0, hCT2355814.0	1558034_s_at, 204846_at, 227253_at	NP_000087.1, EAW78882.1, EAW78883.1, EAW78884.1
GeneID:4071	TM4SF1	3	149,086,805	149,095,568	8,763	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4092	-9120	upstream	1	0	0	19	17	2	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene TM4SF1	H-L6, L6, TM4SF1, TAAL6, M3S1	transmembrane 4 L six family member 1	NM_014220, hCT12304.3, hCT1985325.1, hCT2318572.0	209386_at, 209387_s_at, 215033_at, 215034_s_at, 238168_at	NP_055035.1, EAW78875.1, EAW78874.1, EAW78876.1
GeneID:25937	WWTR1	3	149,235,022	149,421,060	186,038	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4093, 1_A375_pNL7_minus_lncRNA_AR..1..4094, 2_A375_pNL97_plus_lncRNA_AR..1..5883, 4_A375_EGR1..1..8302	45316, 24740, 24788, 45668	in gene, in gene, in gene, in gene	1	1	1	16.5	19	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene WWTR1	FLJ27004, FLJ45718, DKFZp586I1419, TAZ, WWTR1	WW domain containing transcription regulator 1	NM_015472, NM_001168278, NM_001168280, hCT12303.3, hCT2319086.0	202132_at, 202133_at, 202134_s_at	NP_056287.1, NP_001161750.1, NP_001161752.1, EAW78868.1, EAW78869.1
GeneID:51122	COMMD2	3	149,456,257	149,470,286	14,029	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4095, 2_A375_pNL97_plus_lncRNA_AR..1..5884, 4_A375_EGR1..1..8303	78, 14, 46	in gene, in gene, in gene	1	1	1	20	21	18	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene COMMD2	MGC57611, COMMD2, HSPC042	COMM domain containing 2	NM_016094, hCT10727.3, hCT1952816.1	223491_at	NP_057178.2, EAW78867.1, EAW78866.1
GeneID:389161	C3orf16	3	149,478,887	149,510,610	31,723	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4095, 2_A375_pNL97_plus_lncRNA_AR..1..5884, 4_A375_EGR1..1..8303	40402, 40338, 40370	downstream, downstream, downstream	1	1	1	20	21	18	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene C3orf16	FLJ40759, C3orf16	chromosome 3 open reading frame 16	NM_001144960	1561927_at, 1561928_s_at	NP_001138432.1
GeneID:11342	RNF13	3	149,530,475	149,679,926	149,451	+	5	1_A375_pNL7_minus_lncRNA_AR..1..4096, 1_A375_pNL7_minus_lncRNA_AR..1..4097, 2_A375_pNL97_plus_lncRNA_AR..1..5885, 2_A375_pNL97_plus_lncRNA_AR..1..5886, 4_A375_EGR1..1..8304	1413, 158677, 373, 158693, 158653	in gene, downstream, in gene, downstream, downstream	1	1	1	16	19.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RNF13	FLJ93617, RNF13, MGC13689, RZF	ring finger protein 13	NM_183381, NM_007282, hCT12430.3, hCT1952052.1, hCT2319138.0, hCT2319140.0, hCT2355823.0, hCT2355824.0	201779_s_at, 201780_s_at	NP_899237.1, NP_009213.1, EAW78859.1, EAW78860.1, EAW78861.1, EAW78863.1, EAW78858.1, EAW78862.1
GeneID:5217	PFN2	3	149,682,691	149,688,741	6,050	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4097, 2_A375_pNL97_plus_lncRNA_AR..1..5886, 4_A375_EGR1..1..8304	-411, -427, -587	upstream, upstream, upstream	1	1	1	16	18	17	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PFN2	D3S1319E, PFL, PFN2	profilin 2	NM_002628, NM_053024, hCT12431.3, hCT1952053.1, hCT1983023.1, hCT1985326.1, hCT2319075.0, hCT2319078.0, hCT2319080.0	204992_s_at	NP_002619.1, NP_444252.1, EAW78852.1, EAW78853.1, EAW78854.1, EAW78855.1, EAW78850.1, EAW78851.1, EAW78856.1
GeneID:646903	LOC646903	3	149,689,066	149,691,029	1,963	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4097, 2_A375_pNL97_plus_lncRNA_AR..1..5886, 4_A375_EGR1..1..8304	86, 102, 262	in gene, in gene, in gene	1	1	1	16	18	17	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC646903		hypothetical LOC646903	NR_038536	237116_at	
GeneID:653659	TMEM183B	3	149,699,448	149,701,153	1,705	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5886, 4_A375_EGR1..1..8304	11985, 11825	downstream, downstream	0	1	1	16	18	17	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TMEM183B	C1orf37-DUP, TMEM183B	transmembrane protein 183B	NM_001079809	212165_at	NP_001073277.1
GeneID:9819	TSC22D2	3	150,126,788	150,177,631	50,843	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4098, 2_A375_pNL97_plus_lncRNA_AR..1..5889, 4_A375_EGR1..1..8305	-132, -612, -484	upstream, upstream, upstream	1	1	1	17	17	16	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TSC22D2	TILZ4a, TILZ4c, KIAA0669, TILZ4b, TSC22D2	TSC22 domain family, member 2	NM_014779, hCT12432.2, hCT1952054.1, hCT1952055.1, hCT2319152.0, hCT2319153.0	204094_s_at, 210953_at, 210954_s_at, 215547_at	NP_055594.1, EAW78839.1, EAW78837.1, EAW78838.1, EAW78840.1, EAW78841.1
GeneID:27230	SERP1	3	150,259,780	150,264,428	4,648	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4099, 2_A375_pNL97_plus_lncRNA_AR..1..5890	76, 12	in gene, in gene	1	1	0	18	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene SERP1	MGC133321, RAMP4, MGC133322, MGC117327, SERP1	stress-associated endoplasmic reticulum protein 1	NM_014445, hCT12434.3, hCT1952056.1, hCT1952057.1, hCT2319067.0	200969_at, 200970_s_at, 200971_s_at, 235475_at	NP_055260.1, EAW78836.1, EAW78833.1, EAW78834.1, EAW78835.1
GeneID:83939	EIF2A	3	150,264,574	150,303,803	39,229	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4099, 2_A375_pNL97_plus_lncRNA_AR..1..5890	-222, -158	upstream, upstream	1	1	0	18	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene EIF2A	MSTP089, EIF-2A, EIF2A, MST089, CDA02, MSTP004	eukaryotic translation initiation factor 2A, 65kDa	NM_032025, hCT1825726.2, hCT2319156.0, hCT2355765.0	223015_at	NP_114414.2, EAW78831.1, EAW78830.1, EAW78832.1
GeneID:51714	SELT	3	150,321,066	150,348,234	27,168	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4100, 2_A375_pNL97_plus_lncRNA_AR..1..5891, 4_A375_EGR1..1..8306	246, 206, -42	in gene, in gene, upstream	1	1	1	22	26	28	1	4_A375_EGR1..1	28	Gene SELT		selenoprotein T	NM_016275, hCT11995.3, hCT1952047.1, hCT2319158.0	217811_at, 225581_at	NP_057359.2, EAW78827.1, EAW78828.1, EAW78829.1

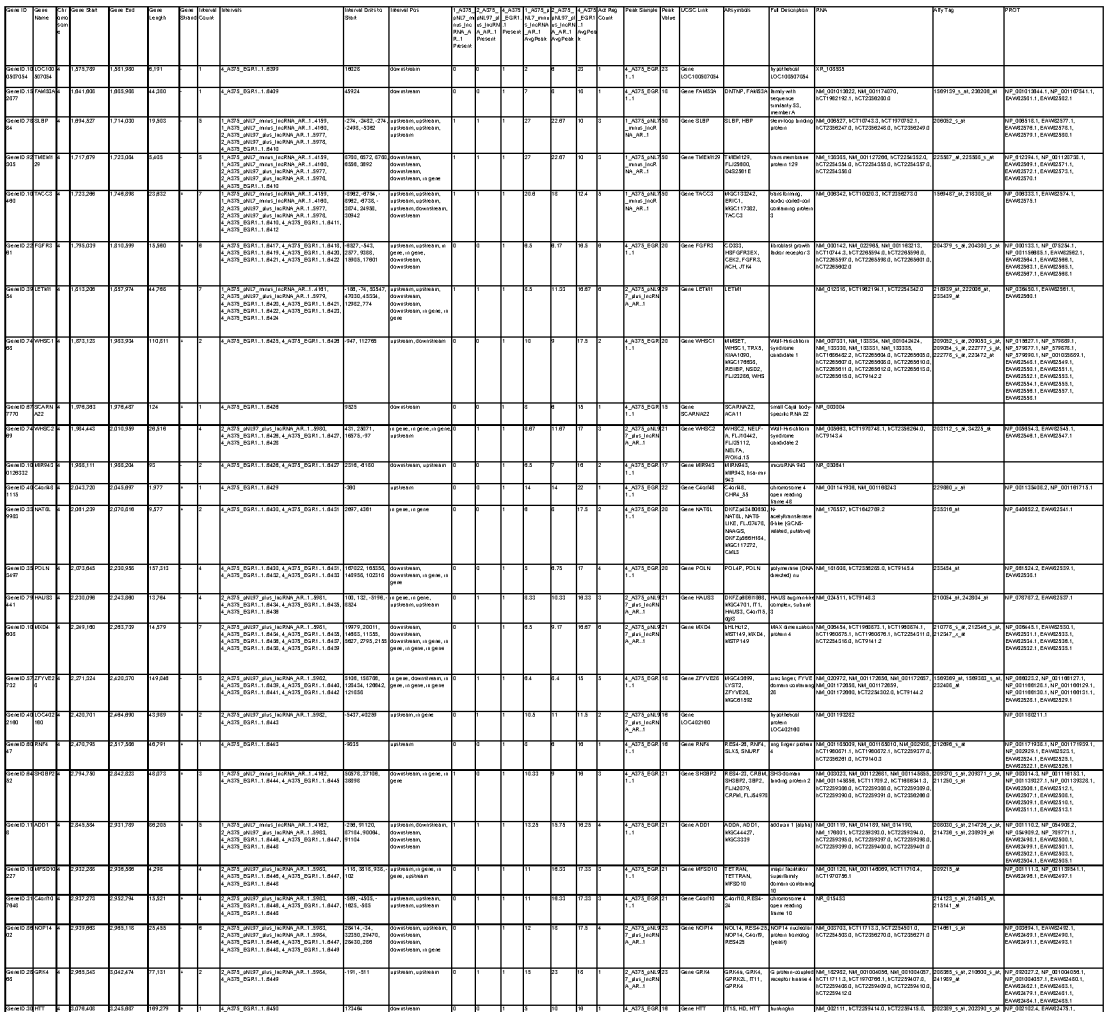


Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_2_A375_3_A375_4_A375_1_A375_2_A375_3_A375_4_A375_Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
GeneID:84476	SAMD1	1	150,456,310	150,481,265	22,955	-	1	2_A375_uNU97_plus_lncRNA_NR_1:5092	597	upstream	0 1 0 14 15 15 1	2_A375_uNU97_plus_lncRNA_NR_1	15	Gene SAMD1	SAM domain containing 1	NM_030967, XM_005249	209939_at	NP_109585.3, ENAH5621
GeneID:11	MED12L	3	150,656,876	151,156,455	549,799	+	3	1_A375_uNU7_minus_lncRNA_NR_1:4151, 2_A375_uNU97_plus_lncRNA_NR_1:5092, 3_A375_uNU97_plus_lncRNA_NR_1:5094	398100, 599099, 336324	upstream, downstream	1 1 0 17.3 20.3 4.5 2	2_A375_uNU97_minus_lncRNA_NR_1	24	Gene MED12L	FRALP, NCPAM, MED12L, THRC111, TRALPUSH, FLJ46255, KIAA1053	mediator complex subunit 12-like	NM_005302, XM_011562049.2, XM_011565151.1, XM_012309302.0	1555300_a_at, 232114_at	NP_443725.3, ENAH5990.1, ENAH79911.1, ENAH79922.1
GeneID:26	IGSF10	3	151,132,776	151,179,497	22,719	-	1	2_A375_uNU97_plus_lncRNA_NR_1:5094	19297	upstream	0 1 0 11 19 4 1	2_A375_uNU97_minus_lncRNA_NR_1	19	Gene IGSF10	C3MRS8, IGSF10, FLJ29972	immunoglobulin superfamily, member 10	NM_001178145, NM_001178149, NM_178822, XM_011519992.2, XM_011530909.2	1556379_s_at, 230870_at	NP_001178161.1, NP_001178167.1, NP_549144.2, ENAH5746.1, ENAH7949.1
GeneID:40	SCG_10	3	151,998,405	151,997,415	7,010	-	4	1_A375_uNU7_minus_lncRNA_NR_1:4103, 2_A375_uNU97_plus_lncRNA_NR_1:5096, 3_A375_uNU97_plus_lncRNA_NR_1:5097, 4_A375_uNU97_plus_lncRNA_NR_1:5098	11031, 2992, 511, 119	downstream, upstream, gene, intragene	1 1 1 14.67 16 10.67 3	1_A375_uNU97_plus_lncRNA_NR_1	23	Gene SCG10	SCG10, SCG10	superior cervical ganglia-10 protein	NM_020357, NR_027555	232296_at, 235573_at	
GeneID:41	MBNL1	3	151,998,029	152,152,399	197,740	+	4	1_A375_uNU7_minus_lncRNA_NR_1:4103, 2_A375_uNU97_plus_lncRNA_NR_1:5096, 3_A375_uNU97_plus_lncRNA_NR_1:5097, 4_A375_uNU97_plus_lncRNA_NR_1:5098	-1645, -1317, 1215, 1467	upstream, upstream, gene, intragene	1 1 1 14.67 16 10.67 3	1_A375_uNU97_plus_lncRNA_NR_1	23	Gene MBNL1	EXP2, MBNH, MBNL, EXP42, hmh0425, EXP38	muscleblind-like (Drosophila)	NM_021038, NM_207292, NM_207293, NM_207294, NM_207295, NM_207296, NM_207297, XR_001197412, XR_001197413, XR_001197414, XR_001197415, XR_001197416, XR_001197417, XR_001197418, XR_001197419, XR_001197420, XR_001197421, XR_001197422, XR_001197423, XR_001197424, XR_001197425, XR_001197426, XR_001197427, XR_001197428, XR_001197429, XR_001197430, XR_001197431, XR_001197432, XR_001197433, XR_001197434, XR_001197435, XR_001197436, XR_001197437, XR_001197438, XR_001197439, XR_001197440, XR_001197441, XR_001197442, XR_001197443, XR_001197444, XR_001197445, XR_001197446, XR_001197447, XR_001197448, XR_001197449, XR_001197450, XR_001197451, XR_001197452, XR_001197453, XR_001197454, XR_001197455, XR_001197456, XR_001197457, XR_001197458, XR_001197459, XR_001197460, XR_001197461, XR_001197462, XR_001197463, XR_001197464, XR_001197465, XR_001197466, XR_001197467, XR_001197468, XR_001197469, XR_001197470, XR_001197471, XR_001197472, XR_001197473, XR_001197474, XR_001197475, XR_001197476, XR_001197477, XR_001197478, XR_001197479, XR_001197480, XR_001197481, XR_001197482, XR_001197483, XR_001197484, XR_001197485, XR_001197486, XR_001197487, XR_001197488, XR_001197489, XR_001197490, XR_001197491, XR_001197492, XR_001197493, XR_001197494, XR_001197495, XR_001197496, XR_001197497, XR_001197498, XR_001197499, XR_001197500, XR_001197501, XR_001197502, XR_001197503, XR_001197504, XR_001197505, XR_001197506, XR_001197507, XR_001197508, XR_001197509, XR_001197510, XR_001197511, XR_001197512, XR_001197513, XR_001197514, XR_001197515, XR_001197516, XR_001197517, XR_001197518, XR_001197519, XR_001197520, XR_001197521, XR_001197522, XR_001197523, XR_001197524, XR_001197525, XR_001197526, XR_001197527, XR_001197528, XR_001197529, XR_001197530, XR_001197531, XR_001197532	1555894_a_at, 1556011_at, 201151_s_at, 201152_s_at, 201153_s_at, 213663_at, 233015_at, 233019_at	NP_066988.2, NP_997176.1, NP_997177.1, NP_997178.1, NP_997179.1, NP_997180.1, ENAH5773.1, ENAH7878.1, ENAH7877.1, ENAH7876.1, ENAH7779.1, ENAH7893.1, ENAH7891.1, ENAH7892.1, ENAH7883.1
GeneID:55	P2RY1	3	152,332,756	152,338,845	6,089	+	1	2_A375_uNU97_plus_lncRNA_NR_1:5099	330	upstream	0 1 0 12 17 13 1	2_A375_uNU97_plus_lncRNA_NR_1	17	Gene P2RY1	P2Y1, P2RY1	purinergic receptor P2Y, G-protein coupled, 1	NM_002563, ENST10084.2	207455_at	NP_002154.1, ENAH7973.1
GeneID:59	RAP2B	3	152,698,029	152,698,265	6,236	+	0	1_A375_uNU7_minus_lncRNA_NR_1:4106, 2_A375_uNU97_plus_lncRNA_NR_1:5900, 3_A375_uNU97_plus_lncRNA_NR_1:5099	-128, 0, 1031	upstream, upstream, gene, upstream	1 1 1 16.3 20 14 2	2_A375_uNU97_plus_lncRNA_NR_1	29	Gene RAP2B	RAP2B, MGC20459	RAP2B, member of RAS oncogene family	NM_002886, NT_167693.2	213923_at, 214468_at, 227877_at, 236822_at	NP_002877.2, ENAH7771.1
GeneID:10	LOC1003	3	153,742,190	153,838,999	96,809	-	3	4_A375_BGR1.1_8302, 4_A375_BGR1.1_8311, 4_A375_BGR1.1_8312	53978, 164, -781	upstream, gene, upstream	0 0 1 7 7.67 17 3	4_A375_BGR1.1_1	22	Gene LOC100507324		hypothetical LOC100507324	XR_112243, XR_108303, XR_113332		
GeneID:26	SGEF	3	153,838,149	153,979,816	139,667	+	2	4_A375_BGR1.1_8311, 4_A375_BGR1.1_8312	-314, -811	upstream, upstream	0 0 1 9.5 8.5 14.5 2	4_A375_BGR1.1_1	18	Gene SGEF	DKFZp434D1446, C3orf17, HPH-EEF28, Hef-N1/Nbla, Sgef	Rho guanine nucleotide exchange factor (GEF) 28	NM_015595, NT_022184.13,	222121_at, 227197_at, 233903_s_at	NP_559610.3, ENAH8764.1
GeneID:34	GPR149	3	154,035,461	154,147,504	92,043	-	4	1_A375_uNU7_minus_lncRNA_NR_1:4105, 2_A375_uNU97_plus_lncRNA_NR_1:5901, 3_A375_BGR1.1_8312, 4_A375_BGR1.1_8314	6464, 6464, 1640, 640	upstream, gene, upstream, gene, upstream	1 1 1 14.67 17 16.5 3	2_A375_uNU97_plus_lncRNA_NR_1	30	Gene GPR149	PCLB10, BDA, GPR149	G protein-coupled receptor 149	NM_001033705		NP_001032794.1
GeneID:10	LOC1003	3	155,499,161	155,491,015	1,994	-	2	2_A375_uNU97_plus_lncRNA_NR_1:5902, 3_A375_BGR1.1_8315	-1333, -1333	upstream, upstream	0 0 1 19 16 16 1	2_A375_uNU97_plus_lncRNA_NR_1	16	Gene LOC100507306		putative ankyrin repeat and protein-NCRNA00269-like	XM_003119912, XM_003318521, XM_003133417		XP_003119960.1, XP_003118989.1, XP_003133449.1
GeneID:58	GIPR	3	155,598,325	155,838,521	97,196	+	1	2_A375_uNU97_plus_lncRNA_NR_1:5903	996	upstream	0 0 1 12 14 13 1	2_A375_uNU97_plus_lncRNA_NR_1	14	Gene GIPR	GIPR		NM_000164, ENST10109.0	214431_at	NP_000155.1, ENAH7941.1, ENAH7940.1
GeneID:79	KCNAB	3	155,838,387	156,238,927	410,540	+	2	2_A375_uNU97_plus_lncRNA_NR_1:5904, 4_A375_BGR1.1_8316	414547, 171027	upstream, gene	0 0 1 9.3 12 12 2	4_A375_BGR1.1_1	16	Gene KCNAB1	KCNAB1, MVP-like3, Kvb1.2, KVBETA3, KCNA1B, kVb3, Kv-BETA-1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	NM_172160, NM_002471, NM_172159, NT_167691.3, XC7231F215.1, XC7231F221.1, XC7234439.0, XC7234439.0	205213_s_at, 210976_s_at, 210273_s_at, 210419_s_at, 214741_s_at	NP_751892.1, NP_002462.2, NP_751891.1, ENAH7732.1, ENAH7734.1, ENAH7733.1, ENAH7723.1, ENAH7736.1
GeneID:87	SSR3	3	156,237,929	156,272,973	19,044	-	2	2_A375_uNU97_plus_lncRNA_NR_1:5904, 4_A375_BGR1.1_8317	19959, 293	downstream, upstream	0 0 1 12 16.3 10.3 2	2_A375_uNU97_plus_lncRNA_NR_1	16	Gene SSR3	TRAP2, SSR3	signal sequence receptor, gamma (translocation-associated protein gamma)	NM_007107, XT_011697.2, XC7231826.0	217750_s_at, 222411_s_at, 222412_s_at, 237877_at	NP_009036.1, ENAH7731.1, ENAH7730.1
GeneID:10	LOC1003	3	156,330,960	156,330,502	2,542	-	2	1_A375_uNU7_minus_lncRNA_NR_1:4109, 2_A375_uNU97_plus_lncRNA_NR_1:5905	1355, 1422	upstream, gene	1 1 0 27 29 15 1	2_A375_uNU97_plus_lncRNA_NR_1	29	Gene LOC100287227		hypothetical LOC100287227	NR_027954		
GeneID:26	TIPARP	3	156,392,353	156,434,559	42,204	+	2	1_A375_uNU7_minus_lncRNA_NR_1:4109, 2_A375_uNU97_plus_lncRNA_NR_1:5905	-91, -125	upstream, upstream	1 1 0 27 29 15 1	2_A375_uNU97_plus_lncRNA_NR_1	29	Gene TIPARP	TIPARP, RiH1, DKFZp686P0130, DKFZp834L014, PARP7, PARP-7, DKFZp686N0351, PARP-1, FLJ46495, DDF1, pART14	TCDD-inducible poly(ADP-ribose) polymerase	NM_001184717, NM_001184718, NM_015508, XC7231825.0, XC7235919.0, XC7235920.0	212983_at	NP_001171646.1, NP_001171647.1, NP_056520.2, ENAH7725.1, ENAH7726.1, ENAH7728.1, ENAH7727.1
GeneID:73	LOC7300	3	156,488,107	156,834,823	99,808	-	4	1_A375_uNU7_minus_lncRNA_NR_1:4110, 1_A375_uNU7_minus_lncRNA_NR_1:4111, 2_A375_uNU97_plus_lncRNA_NR_1:5906, 3_A375_uNU97_plus_lncRNA_NR_1:5907	23743, -121, 28831, 39	upstream, upstream, gene, upstream, gene, upstream	1 1 0 21.3 24 4.3 2	2_A375_uNU97_plus_lncRNA_NR_1	26	Gene LOC730091		hypothetical LOC730091	XR_112865, XR_108907, XR_113534	230160_at	
GeneID:26	LEXR1	3	156,844,096	156,740,916	219,022	+	2	1_A375_uNU7_minus_lncRNA_NR_1:4111, 2_A375_uNU97_plus_lncRNA_NR_1:5907	-9132, -9212	upstream, upstream	1 1 0 23 26 7 1	2_A375_uNU97_plus_lncRNA_NR_1	26	Gene LEXR1	LEXR1, FLJ46841, FLJ21181	leucine_glutamate and lysine sub 1	NM_001004316, NM_001119202, XC7231834.0, XC7231834.0, XC7231834.0, XC7231834.0, XC7233039.0		NP_001004316.2, NP_001102212.1, ENAH7745.1, ENAH7745.1, ENAH7744.1, ENAH7722.1, ENAH7721.1
GeneID:33	LOC3393	3	156,799,496	156,840,791	41,235	-	2	2_A375_uNU97_plus_lncRNA_NR_1:5908, 2_A375_uNU97_plus_lncRNA_NR_1:5909, 2_A375_uNU97_plus_lncRNA_NR_1:5910	41207, 33515, -, 9353	upstream, gene, gene, upstream	0 1 0 14 22 9 2	2_A375_uNU97_plus_lncRNA_NR_1	23	Gene LOC339894	FLJ10260	hypothetical LOC339894	NR_024007	1561402_at, 1561722_at	
GeneID:10	LOC1003	3	156,837,870	156,816,924	11,254	+	2	2_A375_uNU97_plus_lncRNA_NR_1:5908, 2_A375_uNU97_plus_lncRNA_NR_1:5909	-5908, -994	upstream, upstream	0 1 0 12.5 20.5 9.5 2	2_A375_uNU97_plus_lncRNA_NR_1	24	Gene LOC100419559		hypothetical LOC100419559	NR_024006		
GeneID:37	CCNL1	3	156,898,565	156,976,462	12,897	-	3	1_A375_uNU7_minus_lncRNA_NR_1:4112, 2_A375_uNU97_plus_lncRNA_NR_1:5911, 3_A375_BGR1.1_8318	486, 486, 402	upstream, gene, upstream, gene	1 1 1 35 26 22 1	1_A375_uNU97_plus_lncRNA_NR_1	33	Gene CCNL1	PRO1073, CCNL1, RH-ST, RNH6BA, bm-86	cyclin L1	NM_020307, NT_019220.3, NT_196925.1, XC7233092.0	1555611_s_at, 1555627_at, 230406_s_at, 241459_at	NP_064705.1, ENAH7712.1, ENAH7713.1, ENAH7714.1
GeneID:84	SHOX2	3	157,013,000	157,035,532	10,102	-	2	2_A375_uNU97_plus_lncRNA_NR_1:4115, 2_A375_uNU97_plus_lncRNA_NR_1:5914	-3984, -3996	upstream, upstream	1 1 0 40 49 13 1	2_A375_uNU97_plus_lncRNA_NR_1	49	Gene SHOX2	OG12, OG12X, SHOX2, SHOT	short stature homeobox 2	NM_006884, NM_030703, NM_001159870	209643_s_at, 210134_x_at, 210135_s_at	NP_008815.2, NP_001157150.1
GeneID:51	RSRC1	3	157,227,692	157,282,582	454,890	+	3	1_A375_uNU7_minus_lncRNA_NR_1:4115, 2_A375_uNU97_plus_lncRNA_NR_1:5914, 3_A375_uNU97_plus_lncRNA_NR_1:5915	44, 44, 17984	gene, gene, upstream, gene	1 1 0 27 33 7 2	2_A375_uNU97_plus_lncRNA_NR_1	49	Gene RSRC1	Brh011, SFRS21, MGC12197, RSRC1, SRrp53	arginine/serine-rich coiled-coil 1	NM_016823, XT_011626.2, XC7231839.0, XC7231839.0	1555601_s_at, 219307_at, 233834_s_at	NP_057709.2, ENAH5696.1, ENAH8912.1, ENAH8913.1
GeneID:42	MLF1	3	158,298,953	158,329,252	55,299	+	1	2_A375_uNU97_plus_lncRNA_NR_1:5916	7	gene	0 1 0 9 19 10 1	2_A375_uNU97_plus_lncRNA_NR_1	19	Gene MLF1	MLF1		NM_022440, NM_001130156, NM_001130157, XC7235539.0, XC7235539.0, XC7235539.0, XC7235541.0, XC7736.0	204702_at, 204764_s_at	NP_071905.1, NP_001123626.1, NP_001123629.1, ENAH8868.1, ENAH8867.1, ENAH8869.1, ENAH8865.1, ENAH8866.1, ENAH8870.1
GeneID:89	GFAP	3	161,282,317	161,419,061	49,844	+	2	2_A375_uNU97_plus_lncRNA_NR_1:4118, 2_A375_uNU97_plus_lncRNA_NR_1:5917	-77, -43	upstream, upstream	1 1 0 160 177 9 1	1_A375_uNU97_plus_lncRNA_NR_1	30	Gene GFAP	EPGM, EPG, NEFG1, FLJ21860, COXDFL, FLJ10832, EPG1, GFAP, EGF1, FLJ20772, GFM	Alexander disease, astrocytic hair	NM_024998, NT_167699.2, NT_196264.1, XC7231839.0, XC7231839.0, XC7231839.0, XC7233079.0	203820_at, 223103_at, 223186_at, 223861_at, 232282_s_at, 232282_x_at	NP_079272.4, ENAH8878.1, ENAH8877.1, ENAH8876.1, ENAH8881.1, ENAH8861.1, ENAH8862.1
GeneID:84	MPSS1	3	158,519,713	158,547,308	27,793	+	1	4_A375_BGR1.1_8319	-77	upstream	0 0 1 23 23 15 1	4_A375_BGR1.1_1	15	Gene MPSS1	MPSS1, FLJ14153, SMAP4	major facilitator superfamily domain containing 6	NM_022738, NM_001197903, XC7231840.0, XC7235576.0, XC7663.3	1565600_at, 218109_s_at, 244008_at	NP_073737.2, NP_001183073.1, ENAH7872.1, ENAH7873.1, ENAH7874.1
GeneID:85	IQCJ	3	158,797,117	158,892,492	199,375	+	4	1_A375_uNU7_minus_lncRNA_NR_1:4117, 2_A375_uNU97_plus_lncRNA_NR_1:5918, 3_A375_uNU97_plus_lncRNA_NR_1:5919, 4_A375_uNU97_plus_lncRNA_NR_1:5920	29499, 13580, 59079, 204451	downstream, upstream, gene, upstream, gene, downstream	1 1 1 17.67 17.67 2.67 3	1_A375_uNU97_minus_lncRNA_NR_1	23	Gene IQCJ	IQCJ		NM_001042705, NM_001042703		NP_001035171.1, NP_001035170.1
GeneID:29	SCHIP1	3	158,991,544	159,015,139	623,596	+	4	1_A375_uNU7_minus_lncRNA_NR_1:4117, 2_A375_uNU97_plus_lncRNA_NR_1:5920, 3_A375_uNU7_minus_lncRNA_NR_1:4116, 4_A375_uNU97_plus_lncRNA_NR_1:5921	72, 24, 497004, 499400	upstream, gene, upstream, gene, upstream	1 1 1 22.3 20.3 6.5 2	1_A375_uNU97_minus_lncRNA_NR_1	23	Gene SCHIP1	SCHIP1, FLJ39160, SCHIP	schwannomin interacting protein 1	NM_014575, NT_022184.9, NT_022184.10, XC7234437.0, XC7234439.0	204050_s_at	NP_055390.1, ENAH8886.1, ENAH8889.1, ENAH8890.1, ENAH8892.1
GeneID:23	PTS	3	159,374,774	160,117,320	742,546	-	2	2_A375_uNU97_plus_lncRNA_NR_1:5923, 2_A375_uNU97_plus_lncRNA_NR_1:5924	19102, -160	upstream, upstream	0 0 1 13.3 21 8 2	2_A375_uNU97_plus_lncRNA_NR_1	23	Gene PTS	PTSD, ATD2, WDR56, PTPS, MGC12563	6-pyruvoyltetrahydropterin synthase	NM_000317, NM_001190241, NM_001190242, NM_030800, XC7231844.0, XC7231844.0, XC7231844.0, XC7233099.0, XC7233099.0, XC7233099.0, XC7233099.0, XC7237.0	1553898_s_at, 1564233_at, 205177_s_at, 205551_s_at, 205552_s_at, 205553_s_at, 240251_at	NP_000308.1, NP_001177177.1, NP_001177171.1, NP_955551.1, ENAH8842.1, ENAH8846.1, ENAH8845.1, ENAH8844.1, ENAH8843.1, ENAH8847.1
GeneID:10	SMC4	3	160,117,450	160,132,741	33,211	+	1	2_A375_uNU97_plus_lncRNA_NR_1:5924	98	gene	0 1 0 16 23 8 1	2_A375_uNU97_plus_lncRNA_NR_1	23	Gene SMC4	BCAP-C, SMC4L1, SMC4	structural maintenance of chromosomes 4	NM_001002800, NM_005496, NT_113511.15, XC7231844.0, XC7231844.0, XC7231844.0, XC7233099.0, XC7237.0	201663_s_at, 201664_at, 201665_at	NP_001002800.1, NP_005487.3, ENAH8849.1, ENAH8848.1, ENAH8850.1, ENAH8851.1, ENAH8852.1
GeneID:45	MIR155	3	160,132,378	160,132,473	97	+	1	2_A375_uNU97_plus_lncRNA_NR_1:5924	-4698	upstream	0 1 0 16 23 8 1	2_A375_uNU97_plus_lncRNA_NR_1	23	Gene MIR155	MIRN155, hsa-mir-155, miR-155, MIR155	microRNA 155	NR_029839		
GeneID:35	C3orf80	3	161,282,660	161,699,671	27,291	-	1	4_A375_BGR1.1_8321	-961	upstream	0 0 1 7 9 14 1	4_A375_BGR1.1_1	14	Gene C3orf80	UNQ1124/2229, C3orf80, SSSP1760	ubiquitin conjugating enzyme E2 variant 3	NM_031042.3, NT_022184.9, NT_022184.10, XC7231844.0, XC7231844.0, XC7231844.0, XC7233099.0, XC7237.0	230762_at	NP_001035169.1, ENAH9817.1, ENAH9815.1, ENAH9816.1
GeneID:27	GOLIM4	3	167,727,654	167,813,417	85,763	-	1	2_A375_uNU97_plus_lncRNA_NR_1:5926	-67	upstream	0 1 0 10 21 9 1	2_A375_uNU97_plus_lncRNA_NR_1	21	Gene GOLIM4	GOLIM4, GPP130, GMPP130, GOLPH4, PI3K	golgi integral membrane protein	NM_014498, XC7183121.1, XC7237580.0, XC7237580.0, XC7237580.0	204322_at, 204324_s_at, 235662_at	NP_055315.1, ENAH8564.1, ENAH8565.1, ENAH8566.1
GeneID:33	C3orf80	3	167,967,310	168,846,397	861,077	+	2	1_A375_uNU7_minus_lncRNA_NR_1:4120, 2_A375_uNU97_plus_lncRNA_NR_1:5929	23126, 496	upstream, gene, upstream	1 1 0 13 15.5 8.5 2	2_A375_uNU97_plus_lncRNA_NR_1	19	Gene C3orf80	C3orf80, DKFZp686P19254, NCRNA00239	DKFZp686P19254 protein	NM_021455	1558411_at	
GeneID:23	MECOM	3	168,806,267	169,291,560	560,278	-	1	4_A375_BGR1.1_8323	491	upstream	0 0 1 8 8 17 1	4_A375_BGR1.1_1	17	Gene MECOM	PRDM3, MGC17556, MGC103392, EVI1, MECOM, MDS1-EVI1, MDS1-EVI1, MDS	MDS1 and EVI1 complex locus	NM_001105077, NM_005241, NM_001105076, NM_001164769, NM_001164770, NM_001164771, NM_001164800, XC7231844.0, XC7231844.0, XC7231844.0, XC7234140.0, XC7234141.0, XC7234142.0	210551_at, 221084_at, 226420_at, 242277_x_at	NP_001092473.3, NP_005232.2, NP_001092474.2, NP_004982.2, NP_001157471.1, NP_001157472.1, ENAH8542.1, ENAH8543.1, ENAH8544.1, ENAH8545.1, ENAH8546.1, ENAH8547.1, ENAH8548.1, ENAH8549.1
GeneID:54	PRKCI	3	169,840,230	170,025,770	93,330	+	2	1_A375_uNU7_minus_lncRNA_NR_1:4121, 2_A375_uNU97_plus_lncRNA_NR_1:5930	-230, -220	upstream, upstream	1 1 0 22 26 5 1	2_A375_uNU97_plus_lncRNA_NR_1	26	Gene PRKCI	aPKC-iota, PKCI, DXS1179E, PRKCI, MGC8538	protein kinase C, iota	NM_002740, XT_012068.2, XC7231863.0, XC7231863.0, XC7237.0	209677_at, 209678_s_at, 213916_at	NP_002721.4, ENAH8514.1, ENAH8513.1, ENAH8515.1
GeneID:37	SLC7A1	3	170,177,542	170,300,693	109,521	-	3	1_A375_uNU7_minus_lncRNA_NR_1:4122, 2_A375_uNU97_plus_lncRNA_NR_1:5931, 3_A375_uNU97_plus_lncRNA_NR_1:5932	1803, 1351, -6625	upstream, gene, upstream, gene, upstream	1 1 0 16.3 17.3 6.3 2	1_A375_uNU97_minus_lncRNA_NR_1	21	Gene SLC7A14	FLJ37226, KIAA1813, SLC7A14	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14	NM_030949, XT_009312	232904_at	NP_996330.2, ENAH8510.1
GeneID:53	PLD1	3	171,316,816	171,528,273	209,657	-	1	4_A375_BGR1.1_8324	61	upstream	0 0 1 11 10 15 1	4_A375_BGR1.1_1	15	Gene PLD1	PLD1		NM_002662, NM_001130851, XC7238.3	1557126_s_at, 177_at, 205253_at, 215072_s_at, 215724_at, 226656_at, 232551_at	NP_002653.3, NP_001123553.1, ENAH8452.1
GeneID:26	GHSR	3	172,161,051	172,186,248	9,198	-	2	2_A375_uNU97_plus_lncRNA_NR_1:4123, 2_A375_uNU97_plus_lncRNA_NR_1:5933	-1434, -1402	upstream, upstream	1 1 0 23 30 8 1	2_A375_uNU97_plus_lncRNA_NR_1	30	Gene GHSR	GHSER		NM_004122, NM_198407, XC7181.8.2, XC7182127.0	221380_s_at, 224354_at	NP_004113.1, NP_940798.1, ENAH8468.1, ENAH8469.1
GeneID:57	NCEH1	3	172,346,455	172,439,005	92,573	-	2	2_A375_uNU97_plus_lncRNA_NR_1:4124, 2_A375_uNU97_plus_lncRNA_NR_1:5934	16, 64	gene, upstream	1 1 0 20 23 11 1	2_A375_uNU97_plus_lncRNA_NR_1	23	Gene NCEH1	NCEH, AKGNC1, NCEH1	neutral cholesterol ester hydrolase 1	NM_001146278, NT_022792, NM_001146277, NM_001146276, XC7112262	225567_at	NP_001139418.1, NP_065643.2, NP_001139419.1, NP_001139780.1, ENAH7942.1
GeneID:10	LOC1003	3	172,437,787	172,443,593	16,166	+	2	1_A375_uNU7_minus_lncRNA_NR_1:4124, 2_A375_uNU97_plus_lncRNA_NR_1:5934	1305, 1157	gene, upstream	1 1 0 20 23 11 1	1_A375_uNU97_minus_lncRNA_NR_1	23	Gene LOC100505326		hypothetical LOC100505326	XR_112363, XR_108513, XR_113540		
GeneID:10	ECT2	3	172,472,299	172,539,283	66,984	+	1	2_A375_uNU97_minus_lncRNA_NR_1:4125	-3951	upstream	0 1 0 16 9 4 1	2_A375_uNU97_plus_lncRNA_NR_1	16	Gene ECT2	FLJ10481, ECT2, MGC102291, MKHLEP21	epithelial cell transforming sequence 2 oncogene	NM_018098, XT_009312.1, XC7232094.0	210187_s_at, 234992_x_at, 237241_at	NP_060568.3, ENAH5460.1, ENAH7945.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:22871	NLGN1	3	173,116,244	174,001,116	884,872	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4126	-564	upstream	1	0	0	17	8	5	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene NLGN1	NLGN1, KIAA1070, MGC45115, NL1	neuroligin 1	NM_014932, hCT2317276.0, hCT2317454.1, hCT2344055.0, hCT2344056.0	205893_at, 231361_at	NP_055747.1, EAW78455.1, EAW78453.1, EAW78454.1, EAW78456.1
GeneID:79718	TBL1XR1	3	176,738,542	176,915,048	176,506	-	1	4_A375_EGR1..1..8325	-6868	upstream	0	0	1	6	4	12	1	4_A375_EGR1..1	12	Gene TBL1XR1	DC42, TBLR1, IRA1, TBL1XR1, FLJ12894, C21	transducin (beta)-like 1 X-linked receptor 1	NM_024665, hCT2317365.1, hCT2317369.1	221428_s_at, 222633_at, 222634_s_at, 223013_at, 233633_at	NP_078941.2, EAW78436.1, EAW78437.1
GeneID:10242	KCNMB2	3	178,254,224	178,562,217	307,993	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4128, 2_A375_pNL97_plus_lncRNA_AR..1..5936, 2_A375_pNL97_plus_lncRNA_AR..1..5937	148624, 148640, 154256	in gene, in gene, in gene	1	1	0	19	19.5	2.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene KCNMB2	KCNMB2, MGC22431	potassium large conductance calcium-activated channel, subfamily M, beta member 2	NM_005832, NM_181361, hCT2319031.0, hCT8020.2	221097_s_at, 223823_at	NP_005823.1, NP_852006.1, EAW78428.1, EAW78429.1
GeneID:27094	KCNMB3	3	178,957,537	178,984,838	27,301	-	1	4_A375_EGR1..1..8327	3862	in gene	0	0	1	1	4	14	1	4_A375_EGR1..1	14	Gene KCNMB3	SLOBETA3, BKBETA3, KCNMB2, KCNMBL, HBETA3, KCNMB3	potassium large conductance calcium-activated channel, subfamily M beta member 3	NM_014407, NM_171828, NM_171830, NM_001163677, NM_171829, NR_028135, hCT2318981.1, hCT2318982.2, hCT2318983.2, hCT2318984.2, hCT2349039.0	221125_s_at	NP_055222.3, NP_741979.1, NP_741980.1, NP_741981.1, NP_001157149.1, EAW78417.1, EAW78418.1, EAW78419.1, EAW78420.1, EAW78421.1
GeneID:8087	FXR1	3	180,630,234	180,700,541	70,307	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4129	77156	downstream	1	0	0	18	14	7	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene FXR1	FXR1, FXR1P		NM_001013438, NM_001013439, NM_005087, hCT2317115.0, hCT2317116.0, hCT2317117.0, hCT2317118.0, hCT2317119.0, hCT2317120.0, hCT2317121.0, hCT2355833.0	1569171_a_at, 201635_s_at, 201636_at, 201637_s_at, 229519_at	NP_001013456.1, NP_001013457.1, NP_005078.2, EAW78365.1, EAW78368.1, EAW78369.1, EAW78366.1, EAW78367.1, EAW78370.1, EAW78371.1, EAW78372.1
GeneID:131118	DNAJC19	3	180,701,497	180,707,562	6,065	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4129	170	in gene	1	0	0	18	14	7	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene DNAJC19	TIM14, Pam18, TIMM14, DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	NM_001190233, NM_145261, NR_033721, NR_033722, NR_033723, NR_033724, NR_033725, hCT1954025.1, hCT1954026.2, hCT1954027.0, hCT1965291.1, hCT1965292.1, hCT2318991.0, hCT8563.2	225358_at, 225359_at	NP_001177162.1, NP_660304.1, EAW78358.1, EAW78359.1, EAW78360.1, EAW78363.1, EAW78361.1, EAW78362.1, EAW78364.1
GeneID:56922	MCCC1	3	182,733,006	182,817,365	84,359	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5939	373	in gene	0	1	0	8	17	8	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene MCCC1	MCC-B, FLJ25545, MCCC1, DKFZp686B20267, MCCA	methylcrotonoyl-CoA carboxylase 1 (alpha)	NM_020166, hCT1954032.0, hCT2355693.0	218440_at, 242223_at	NP_064551.3, EAW78340.1, EAW78339.1
GeneID:55689	YEATS2	3	183,415,606	183,530,413	114,807	+	1	4_A375_EGR1..1..8328	618	in gene	0	0	1	3	10	14	1	4_A375_EGR1..1	14	Gene YEATS2	FLJ12841, FLJ33401, YEATS2, FLJ34335, FLJ13308, FLJ10201, KIAA1197	YEATS domain containing 2	NM_018023, hCT1954024.1, hCT2318264.0, hCT7702.3	1557047_at, 221203_s_at	NP_060493.3, EAW78317.1, EAW78315.1, EAW78316.1
GeneID:55486	PARL	3	183,547,173	183,602,693	55,520	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4131, 2_A375_pNL97_plus_lncRNA_AR..1..5940	21, -91	in gene, upstream	1	1	0	19	23	11	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene PARL	RHBDS1, PSARL1, PSENIP2, PRO2207, PSARL, PARL	presenilin associated, rhomboid-like	NM_001037639, NM_018622, hCT1961932.1, hCT7703.2	218271_s_at, 228681_at	NP_001032728.1, NP_061092.3, EAW78311.1, EAW78312.1
GeneID:8893	EIF2B5	3	183,852,810	183,863,099	10,289	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4132, 2_A375_pNL97_plus_lncRNA_AR..1..5941	342, 118	in gene, in gene	1	1	0	23	14	13	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene EIF2B5	EIF2Bepsilon, EIF2B, LVWM, CLE, EIF2B5, CACH	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	NM_003907, hCT1817120.2, hCT1954030.1, hCT1954031.1, hCT2318284.0, hCT2355675.0	1558050_at, 212351_at	NP_003898.2, EAW78299.1, EAW78298.1, EAW78300.1, EAW78301.1, EAW78302.1
GeneID:1857	DVL3	3	183,873,284	183,891,314	18,030	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5942	19452	downstream	0	1	0	14	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene DVL3	KIAA0208, DVL3	dishevelled, dsh homolog 3 (Drosophila)	NM_004423, hCT2318293.0, hCT2318295.1, hCT2318296.1, hCT31755.3	201907_x_at, 201908_at	NP_004414.3, EAW78296.1, EAW78293.1, EAW78294.1, EAW78295.1
GeneID:1173	AP2M1	3	183,892,634	183,901,879	9,245	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5942	102	in gene	0	1	0	14	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene AP2M1	CLAPM1, AP2M1, AP50, mu2	adaptor-related protein complex 2 mu 1 subunit	NM_004068, NM_001025205, hCT2318301.0, hCT2318303.0, hCT31753.3	200613_at	NP_004059.2, NP_001020376.1, EAW78290.1, EAW78291.1, EAW78292.1
GeneID:90113	VWA5B2	3	183,948,317	183,960,117	11,800	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4133, 4_A375_EGR1..1..8329	18339, 2595	downstream, in gene	1	0	1	12.5	10	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene VWA5B2	VWA5B2	von Willebrand factor A domain containing 5B2	NM_138345	1554850_at, 232642_at	NP_612354.1
GeneID:100187716	MIR1224	3	183,959,193	183,959,277	84	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4133, 4_A375_EGR1..1..8329	7463, -8281	downstream, upstream	1	0	1	12.5	10	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene MIR1224	MIR1224, MIRN1224	microRNA 1224	NR_030410		
GeneID:10195	ALG3	3	183,960,117	183,967,313	7,196	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4133, 4_A375_EGR1..1..8329	657, 16401	in gene, downstream	1	0	1	12.5	10	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene ALG3	CDG1D, D16Ertd36e, NOT56L, Not56, ALG3, CDGS4	asparagine-linked glycosylation 3, alpha-1,3-mannosyltransferase homolog (S. cerevisiae)	NM_005787, NM_001006941, NR_024533, NR_024534, hCT1963026.1, hCT31554.3	207396_s_at	NP_005778.1, NP_001006942.1, EAW78282.1, EAW78283.1
GeneID:9718	ECE2	3	183,967,445	184,010,819	43,374	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4133	-789	upstream	1	0	0	22	15	12	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene ECE2	MGC2408, MGC17664, ECE2, KIAA0604, MGC78487	endothelin converting enzyme 2	NM_032331, NM_014693, NM_001100120, NM_001037324, NM_001100121	1555306_a_at, 206728_at	NP_115707.2, NP_055508.3, NP_001093590.1, NP_001093591.1, NP_001032401.1
GeneID:94032	CAMK2N2	3	183,977,003	183,979,251	2,248	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4133	12595	downstream	1	0	0	22	15	12	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene CAMK2N2	CAMKIIN, CAMK2N2, CAM-KIIN	calcium/calmodulin-dependent protein kinase II inhibitor 2	NM_033259, hCT2317142.0, hCT2317143.0	1552693_at, 230706_s_at	NP_150284.1, EAW78280.1, EAW78281.1
GeneID:2049	EPHB3	3	184,279,587	184,300,196	20,609	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5944	61	in gene	0	1	0	10	15	9	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene EPHB3	HEK2, EPHB3, ETK2, TYRO6	EPH receptor B3	NM_004443, hCT2318252.0, hCT7681.3	1438_at, 204600_at	NP_004434.2, EAW78237.1, EAW78236.1
GeneID:90407	TMEM41A	3	185,207,389	185,216,845	9,456	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4134	61	in gene	1	0	0	20	16	6	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene TMEM41A	TMEM41A, DKFZp686N0614 9, 2900010K02Rik, MGC15397, DKFZp686N107	transmembrane protein 41A	NM_080652, hCT11761.3, hCT1954038.1, hCT1954039.1, hCT1954040.1, hCT2316920.0	225991_at, 229771_at, 235037_at	NP_542383.1, EAW78221.1, EAW78219.1, EAW78220.1, EAW78222.1, EAW78223.1
GeneID:200879	LIPH	3	185,225,570	185,270,369	44,799	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4134	53565	downstream	1	0	0	20	16	6	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LIPH	LAH2, mPA-PLA1, ARWH2, LIPH, AH, PLA1B, LPDLR	lipase, member H	NM_139248, hCT11760.3	235871_at	NP_640341.1, EAW78218.1
GeneID:59343	SENP2	3	185,304,031	185,348,889	44,858	+	1	4_A375_EGR1..1..8331	273	in gene	0	0	1	12	14	15	1	4_A375_EGR1..1	15	Gene SENP2	AXAM2, DKFZp762A2316, SMT3IP2, KIAA1331, SENP2	SUMO1/sentrin/SMT3 specific peptidase 2	NM_021627, hCT11762.3, hCT1965322.1, hCT2317006.0, hCT2317008.0	218122_s_at, 222523_at	NP_067640.2, EAW78215.1, EAW78214.1, EAW78216.1, EAW78217.1
GeneID:2119	ETV5	3	185,764,106	185,826,901	62,795	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4135, 2_A375_pNL97_plus_lncRNA_AR..1..5946	-167, -51	upstream, upstream	1	1	0	21	13	4	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ETV5	ETV5, ERM	ets variant 5	NM_004454	203348_s_at, 203349_s_at, 216375_s_at, 230102_at	NP_004445.1
GeneID:1606	DGKG	3	185,864,990	186,080,023	215,033	-	3	2_A375_pNL97_plus_lncRNA_AR..1..5947, 1_A375_pNL7_minus_lncRNA_AR..1..4136, 2_A375_pNL97_plus_lncRNA_AR..1..5948	141735, 54471, 54455	in gene, in gene, in gene	1	1	0	16.5	16	3	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene DGKG	DGKG, MGC133330, MGC104993, DGK-GAMMA, DAGK3	diacylglycerol kinase, gamma 90kDa	NM_001080744, NM_001346, NM_001080745	206395_at, 235643_at, 242319_at	NP_001074213.1, NP_001337.2, NP_001074214.1
GeneID:55171	TBCCD1	3	186,263,856	186,288,332	24,476	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4137	3404	in gene	1	0	0	16	12	10	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene TBCCD1	TBCCD1, FLJ10560	TBCC domain containing 1	NM_018138, NM_001134415, hCT2316680.0, hCT2355789.0, hCT7189.3	206451_at	NP_060608.1, NP_001127887.1, EAW78191.1, EAW78192.1, EAW78193.1
GeneID:51726	DNAJB11	3	186,288,467	186,303,589	15,122	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4137	-3539	upstream	1	0	0	16	12	10	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene DNAJB11	DNAJB11, ABBP-2, EDJ, UNQ537, hDj9, HEDJ, DJ9, ERdj3, ABBP2, PRO1080, ERj3	DnaJ (Hsp40) homolog, subfamily B, member 11	NM_016306, hCT2317216.0	223054_at	NP_057390.1, EAW78190.1
GeneID:1974	EIF4A2	3	186,501,361	186,507,686	6,325	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5949	-61	upstream	0	1	0	9	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene EIF4A2	BM-010, EIF4A, eIF-4A-II, EIF4F, EIF4A2, DDX2B, eIF4A-II	eukaryotic translation initiation factor 4A, isoform 2	NM_001967, hCT1823010.2, hCT1823011.2, hCT1954858.1, hCT1965307.1, hCT2317229.0, hCT2317230.0, hCT2317231.0	1555998_s_at, 1556350_a_at, 200912_s_at	NP_001958.2, EAW78173.1, EAW78172.1, EAW78174.1, EAW78176.1, EAW78178.1, EAW78175.1, EAW78177.1
GeneID:619567	SNORD2	3	186,502,585	186,502,654	69	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5949	-1305	upstream	0	1	0	9	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene SNORD2	SNR39B, SNORD2, R39B	small nucleolar RNA, C/D box 2	NR_002567		
GeneID:677847	SNORA81	3	186,504,464	186,504,641	177	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5949	-3184	upstream	0	1	0	9	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene SNORA81	HBI-61, SNORA81	small nucleolar RNA, H/ACA box 81	NR_002989		
GeneID:6043	SNORA63	3	186,505,088	186,505,222	134	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5949	-3808	upstream	0	1	0	9	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene SNORA63	E3, RNU107, SNORA63, RNE3, E3-2	small nucleolar RNA, H/ACA box 63	NR_002586		
GeneID:619566	SNORA4	3	186,505,402	186,505,538	136	+	1	2_A375_pNL97_plus_lncRNA_AR..1..5949	-4122	upstream	0	1	0	9	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene SNORA4	SNORA4, ACA4	small nucleolar RNA, H/ACA box 4	NR_002588		
GeneID:5984	RFC4	3	186,507,681	186,524,484	16,803	-	2	2_A375_pNL97_plus_lncRNA_AR..1..5949, 2_A375_pNL97_plus_lncRNA_AR..1..5950	23204, 84	downstream, in gene	0	1	0	13	16	8	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RFC4	A1, MGC27291, RFC37, RFC4	replication factor C (activator 1) 4, 37kDa	NM_002916, NM_181573, hCT2316671.0, hCT2316672.0, hCT2316673.0	204023_at	NP_002907.1, NP_853551.1, EAW78169.1, EAW78170.1, EAW78171.1
GeneID:6480	ST6GAL1	3	186,648,315	186,796,341	148,026	+	1	4_A375_EGR1..1..8332	-27	upstream	0	0	1	4	10	18	1	4_A375_EGR1..1	18	Gene ST6GAL1	ST6GalI, MGC48859, ST6N, SIAT1, ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	NM_003032, NM_173216, NM_173217, hCT2317241.0, hCT2317242.0, hCT2317243.0, hCT2317244.0, hCT2317245.0, hCT2317246.0, hCT2355825.0	201998_at, 214970_s_at, 214971_s_at	NP_003023.1, NP_775323.1, NP_775324.1, EAW78161.1, EAW78162.1, EAW78163.1, EAW78158.1, EAW78159.1, EAW78160.1, EAW78164.1
GeneID:64108	RTP4	3	187,086,168	187,089,372	3,204	+	1	4_A375_EGR1..1..8333	-600	upstream	0	0	1	4	5	17	1	4_A375_EGR1..1	17	Gene RTP4	IFRG28, RTP4	receptor (chemosensory) transporter protein 4	NM_022147, hCT1653760.2	219684_at	NP_071430.2, EAW78148.1
GeneID:6750	SST	3	187,386,694	187,388,201	1,507	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4138, 2_A375_pNL97_plus_lncRNA_AR..1..5951	585, 585	in gene, in gene	1	1	0	21	31	12	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene SST	SST, SMST	somatostatin	NM_001048, hCT2316610.0, hCT8261.2	213921_at	NP_001039.1, EAW78146.1, EAW78145.1
GeneID:604	BCL6	3	187,439,165	187,463,513	24,348	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4139, 2_A375_pNL97_plus_lncRNA_AR..1..5952	89, 41	in gene, in gene	1	1	0	23	22	5	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene BCL6	BCL5, BCL6, LAZ3, ZNF51, BCL6A, ZBTB27	B-cell CLL/lymphoma 6	NM_001130845, NM_001134738, NM_001706, hCT1954830.1, hCT7052.3	203140_at, 215990_s_at, 228758_at, 239249_at	NP_001124317.1, NP_001128210.1, NP_001697.2, EAW78140.1, EAW78141.1
GeneID:3556	IL1RAP	3	190,231,840	190,374,986	143,146	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4141, 2_A375_pNL97_plus_lncRNA_AR..1..5954	71968, -363	in gene, upstream	1	1	0	13.5	11.5	7	2	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene IL1RAP	C3orf13, IL-1RAcP, IL1RAP, FLJ37788, IL1R3	interleukin 1 receptor accessory protein	NM_002182, NM_134470, NM_001167928, NM_001167929, NM_001167930, NM_001167931, hCT1954834.1, hCT2316592.0, hCT2316593.0, hCT7081.1	205227_at, 210233_at	NP_002173.1, NP_608273.1, NP_001161400.1, NP_001161401.1, NP_001161402.1, NP_001161403.1, EAW78100.1, EAW78101.1, EAW78102.1, EAW78103.1
GeneID:2257	FGF12	3	191,859,684	192,445,388	585,704	-	1	2_A375_pNL97_plus_lncRNA_AR..1..5956	539766	in gene	0	1	0	10	17	0	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene FGF12	FHF1, FGF12B, FGF12	fibroblast growth factor 12	NM_021032, NM_004113, hCT2316392.0, hCT2344053.0, hCT2344054.0	207501_s_at, 214589_at	NP_066360.1, NP_004104.3, EAW78084.1, EAW78085.1, EAW78086.1
GeneID:4976	OPA1	3	193,310,933	193,415,600	104,667	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4142, 2_A375_pNL97_plus_lncRNA_AR..1..5958	-21, -53	upstream, upstream	1	1	0	25	26	7	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene OPA1	KIAA0567, MGM1, NPG, largeG, FLJ12460, OPA1, NTG	optic atrophy 1 (autosomal dominant)	NM_015560, NM_130831, NM_130832, NM_130833, NM_130834, NM_130835, NM_130836, NM_130837, hCT1954850.1, hCT2317768.0, hCT2317769.0, hCT2355944.0, hCT2355945.0, hCT2355946.0, hCT2355947.0, hCT2355948.0, hCT8320.2	212213_x_at, 212214_at, 214306_at, 241027_at	NP_056375.2, NP_570844.1, NP_570845.1, NP_570846.1, NP_570848.1, NP_570847.2, NP_570849.2, NP_570850.2, EAW78064.1, EAW78065.1, EAW78066.1, EAW78067.1, EAW78068.1, EAW78069.1, EAW78070.1, EAW78071.1, EAW78072.1
GeneID:647323	LOC647323	3	193,675,161	193,721,448	46,287	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4145, 2_A375_pNL97_plus_lncRNA_AR..1..5959	136, -152	in gene, upstream	1	1	0	20	20	10	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LOC647323		hypothetical LOC647323	NR_033944	1564539_at	
GeneID:100505902	LOC100505902	3	193,727,752	193,788,741	60,989	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4145, 2_A375_pNL97_plus_lncRNA_AR..1..5959	67429, 67141	downstream, downstream	1	1	0	20	20	10	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LOC100505902		hypothetical LOC100505902	XR_112543, XR_108533, XR_113560		
GeneID:3280	HES1	3	193,853,934	193,856,396	2,462	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4146	-1022	upstream	1	0	0	19	11	7	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene HES1	FLJ20408, HHL, HES-1, bHLHb39, HRY, HES1	hairy and enhancer of split 1, (Drosophila)	NM_005524, hCT7353.2	203393_at, 203394_s_at, 203395_s_at	NP_005515.1, EAW78058.1
GeneID:55341	LSG1	3	194,361,517	194,393,206	31,689	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4147, 2_A375_pNL97_plus_lncRNA_AR..1..5960	54, 22	in gene, in gene	1	1	0	28	20	5	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene LSG1	FLJ27294, LSG1, FLJ11301	large subunit GTPase 1 homolog (S. cerevisiae)	NM_018385, hCT13478.3, hCT1961003.1, hCT1961004.1, hCT1967081.1, hCT2316477.0, hCT2316479.0	221535_at, 221536_s_at, 223200_s_at	NP_060855.2, EAW78036.1, EAW78035.1, EAW78037.1, EAW78038.1, EAW78039.1, EAW78034.1
GeneID:100507391	LOC100507391	3	194,429,150	194,502,897	73,747	+	2	2_A375_pNL97_plus_lncRNA_AR..1..5961, 4_A375_EGR1..1..8334	32498, 71234	in gene, in gene	0	1	1	7	9	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100507391		hypothetical LOC100507391	XR_112592, XR_112593, XR_110393, XR_110392, XR_113565, XR_113566		
GeneID:152002	C3orf21	3	194,789,013	194,991,895	202,882	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4149, 2_A375_pNL97_plus_lncRNA_AR..1..5962	-169, -105	upstream, upstream	1	1	0	20	26	8	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene C3orf21	C3orf21, FLJ35155	chromosome 3 open reading frame 21	NM_152531, hCT13931.2, hCT1950189.1, hCT2316490.0	226891_at	NP_689744.3, EAW78028.1, EAW78029.1, EAW78030.1
GeneID:23527	ACAP2	3	194,995,465	195,163,817	168,352	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4149, 2_A375_pNL97_plus_lncRNA_AR..1..5962	171753, 171817	downstream, downstream	1	1	0	20	26	8	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ACAP2	ACAP2, CENTB2, CNT-B2, KIAA0041	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	NM_012287, hCT13930.3, hCT2316487.0	1552472_a_at, 212476_at, 212477_at	NP_036419.3, EAW78027.1, EAW78026.1

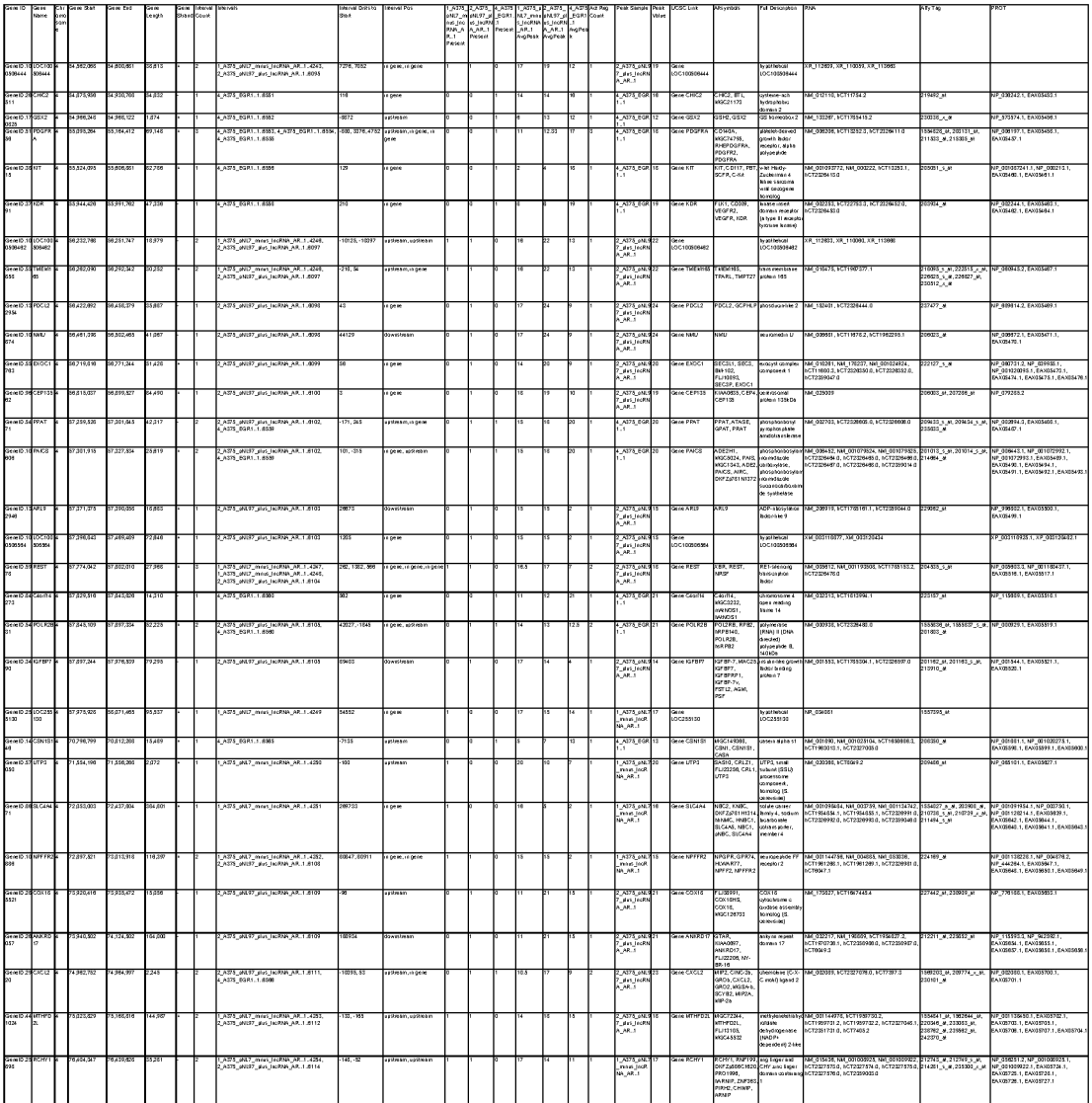


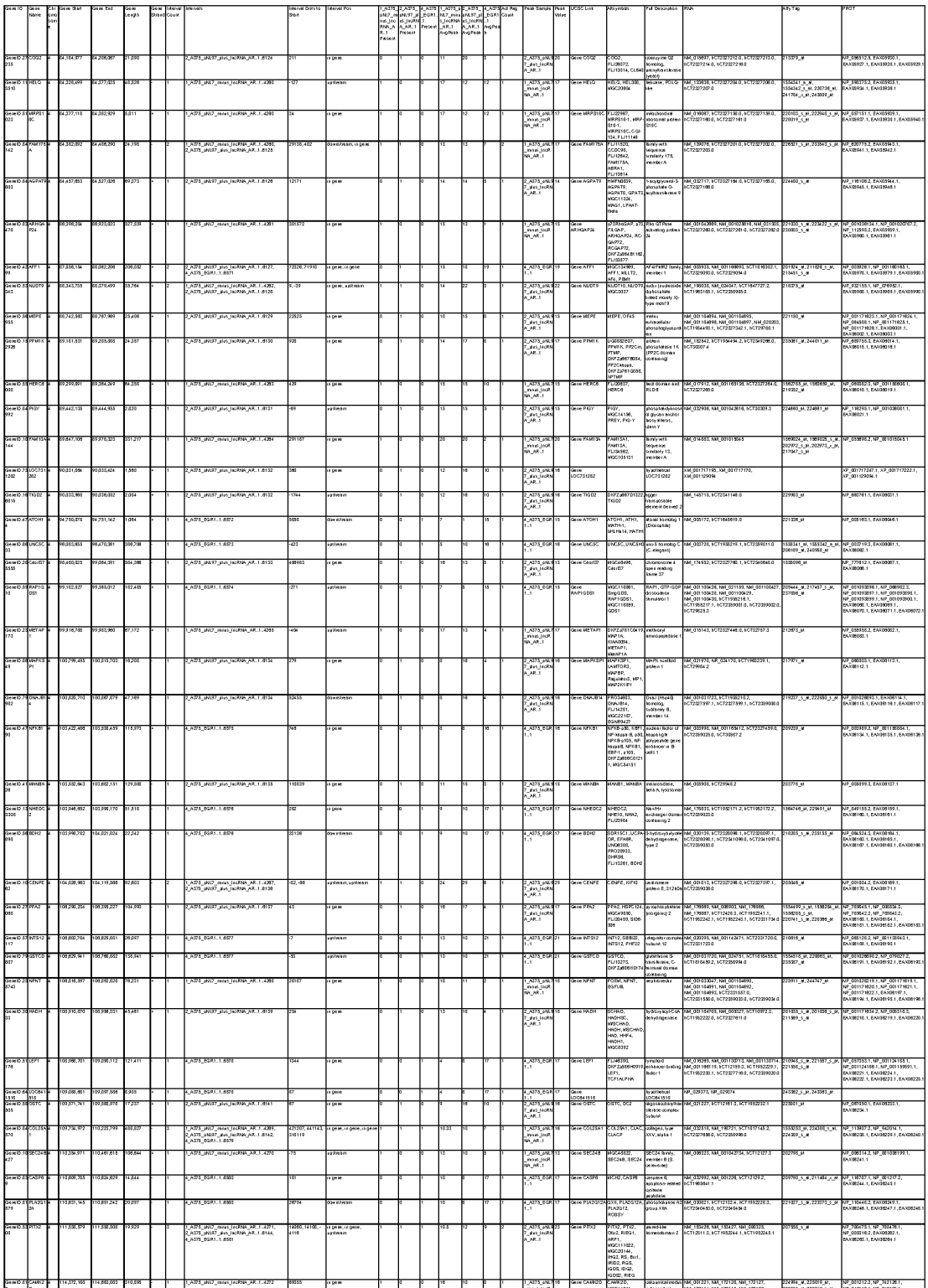
Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_uNG7_minus_lncRNA_R1_1 Percent	2_A375_2_A375_uNG7_plus_lncRNA_R1_1 Percent	4_A375_EGFR1_lncRNA_R1_1 Percent	1_A375_plus_NG7_minus_lncRNA_R1_1 Avg Peak	2_A375_plus_NG7_plus_lncRNA_R1_1 Avg Peak	4_A375_EGFR1_lncRNA_R1_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:3594	PPP1R2	2	193,241,221	193,279,224	38,003	-	1	4_A375_EGR1_1_6535	3kb	vs gene	0	0	1	11	13	18	1	4_A375_EGFR1_1	18	Gene PPP1R2	WGC97145, PP2, PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2	NM_006241, XCT13196.3	2021B5_at_202166_s_at	NP_006232.1, EAW75025.1
GeneID:1078	TNK2	3	195,590,256	195,635,500	45,644	+	2	4_A375_EGR1_1_6536, 4_A375_EGR1_1_6537	39192, 16552	vs gene, vs gene	0	0	1	5	3.5	17	2	4_A375_EGFR1_1	16	Gene Tnk2	FLJ45547, activated CDC42 kinase 1, FLJ44756, ACK, ACK1, TNK2	tyrosine kinase, non-receptor, 2	NM_001010930, NM_005781, XCT2290126.0, XCT2290127.0, XCT2290128.0, XCT2290129.0, XCT2290130.0	1555857_s_at, 2058555_s_at, 203939_s_at, 216439_at	NP_001010930.1, NP_005772.3, EAW59233.1, EAW59234.1, EAW59235.1, EAW59237.1, EAW59238.1
GeneID:3150	PCYT1A	3	193,968,233	193,814,364	49,231	-	1	1_A375_uNG7_minus_lncRNA_NR_1_4150	6152	vs gene	1	0	0	16	9	7	1	1_A375_uNG7_minus_lncRNA_NR_1_4150	16	Gene PCYT1A	CTA, CCTA, PCYT1, PCYT1A, CT, CYTCT	phosphate cytidylyltransferase 1, choline, alpha isoform	NM_005017	204309_at, 204310_s_at, 223089_at	NP_005008.2
GeneID:2357	TCTEX1D2	2	190,010,090	190,045,193	37,089	+	1	4_A375_EGR1_1_6535	999	vs gene	0	0	1	14	8	17	1	4_A375_EGFR1_1	17	Gene TCTEX1D2	DYNLT3, MGC23212	Tctex1 domain containing 2	NM_152773	235808_at	NP_689488.2
GeneID:1057	LOC100132	2	190,047,990	190,049,433	1,373	-	1	4_A375_EGR1_1_6535	4478	downstream	0	0	1	14	8	17	1	4_A375_EGFR1_1	17	Gene LOC100507974	hypothetical LOC100507974	XR_112397		
GeneID:1011	MSH3	5	79,930,419	79,998,256	74,839	-	1	4_A375_EGR1_1_6535	30256	downstream	0	0	1	14	8	17	1	4_A375_EGFR1_1	17	Gene TMEM79	QCTM4, TMEM79	transmembrane protein 79	NM_139481		NP_612470.2
GeneID:2015	SENP3	3	196,594,727	196,661,565	66,838	+	1	2_A375_uNG7_plus_lncRNA_NR_1_5983	74565	downstream	0	0	0	10	17	8	1	2_A375_uNG7_plus_lncRNA_NR_1_5983	17	Gene SENP3	DKFZp686O10193, FLJ42395, MGC27079, SENP3	SUMO/sentrin specific peptidase 3	NM_015935, NCT1950596.1, NCT1969002.1, NCT1969003.1, NCT2294563.3	222110_at, 577Gt_at	NP_056912.2, EAW59825.1, EAW59826.1, EAW59827.1, EAW59828.1, EAW59829.1
GeneID:2215	NCBP2	3	196,662,272	196,689,484	27,191	-	1	2_A375_uNG7_plus_lncRNA_NR_1_5983	192	vs gene	0	1	0	10	17	8	1	2_A375_uNG7_plus_lncRNA_NR_1_5983	17	Gene NCBP2	NCBP2, NMP1, CBP20, CBC2, FHS5	nuclear cap binding protein subunit 2, 20kDa	NM_001042540, NM_007362, XCT1969935.1, NCT1969936.1, NCT2302789.0, NCT2302790.0, NCT2302791.0	201917_at, 201921_s_at	NP_001036005.1, NP_031388.2, EAW59832.1, EAW59833.1, EAW59834.1
GeneID:1511	LOC1332	3	196,686,494	196,870,884	1,390	+	1	2_A375_uNG7_plus_lncRNA_NR_1_5983	-192	upstream	0	1	0	10	17	8	1	2_A375_uNG7_plus_lncRNA_NR_1_5983	17	Gene LOC152217	FLJ41024, MGC71298, DKFZp762H415	hypothetical LOC152217	NR_026555	225957_at	
GeneID:8319	PI3C	3	196,870,314	196,896,704	22,490	+	1	2_A375_uNG7_plus_lncRNA_NR_1_5983	29292	downstream	0	1	0	10	17	8	1	2_A375_uNG7_plus_lncRNA_NR_1_5983	17	Gene PI3C	SHIP1, MGC32185, PI3C, FLJ12760, GPHRT-V	phosphatidylinositol 3'-phosphate 5'-phosphatase, type I	NM_020183, XCT324811.3	220041_at	NP_879439.2, EAW93818.1
GeneID:4216	IDCG	3	197,815,968	197,898,598	70,940	-	1	4_A375_EGR1_1_6541	-474	upstream	0	0	1	7	10	13	1	4_A375_EGFR1_1	13	Gene IDCG	DKFZp434B231, FLJ37775, IGCG, FLJ23371, FLJ11667	IG mu chain C region G	NM_032383, NM_001134435, XCT2279383.0, XCT2279387.0	221183_s_at, 229161_at	NP_115589.1, NP_001129407.1, EAW92248.1, EAW92247.1
GeneID:4216	RPL35A	3	197,877,052	197,892,722	15,670	+	1	4_A375_EGR1_1_6541	93366	downstream	0	0	1	7	10	13	1	4_A375_EGFR1_1	13	Gene RPL35A	L35A, RPL35A, DBA3	ribosomal protein L35A	NM_000996, NCT13867.2, XCT2274825.0, XCT2279389.0	213987_s_at, 215305_x_at, 215306_at, 222192_x_at, 229026_at	NP_000987.2, EAW92250.1, EAW92246.1, EAW92245.1
GeneID:3991	LMLN	3	197,897,077	197,970,591	93,520	+	1	4_A375_EGR1_1_6541	289	vs gene	0	0	1	7	10	13	1	4_A375_EGFR1_1	13	Gene LMLN	RAY, GPR5, 0114, MSP, LMLN	leishmanolysin-like (metallopeptidase M10 family)	NM_033035, NM_001136941, NM_020798, NR_026767, XCT1641244.3, XCT2274827.0, XCT2274829.0	1553254_s_at, 239911_at, 239917_at, 240037_s_at, 244881_at	NP_149116.2, NP_001129021.2, EAW92253.1, EAW92252.1, EAW92253.1
GeneID:1512	ZNF595	6	53,227	58,099	54,872	+	3	1_A375_uNG7_minus_lncRNA_NR_1_4152, 2_A375_uNG7_plus_lncRNA_NR_1_5986, 4_A375_EGR1_1_6542	-96, -171, 55	upstream, upstream, vs gene	1	1	1	34	35	39	1	4_A375_EGFR1_1	39	Gene ZNF595	FLJ20740, ZNF595	zinc finger protein 595	NM_152524, XCT2325279.5		NP_370130.1, EAW92675.1
GeneID:7791	ZNF141	6	331,396	387,891	56,495	+	2	4_A375_EGR1_1_6543, 4_A375_EGR1_1_6544	-856, 305	upstream, vs gene	0	0	1	7.5	13.5	17	2	4_A375_EGFR1_1	20	Gene ZNF141	ZNF141, D43R5, shE44	zinc finger protein 141	NM_006641, XCT2296682.1, XCT2296683.1, XCT2296683.2, XCT2296683.3	206951_at, 233582_at	NP_006632.1, EAW92689.1, EAW92870.1, EAW92871.1
GeneID:1572	ZNF721	6	453,277	493,442	99,865	-	3	1_A375_uNG7_minus_lncRNA_NR_1_4154, 2_A375_uNG7_plus_lncRNA_NR_1_5987, 2_A375_uNG7_plus_lncRNA_NR_1_5988	514, 23700, 4,450	vs gene, vs gene, vs gene	1	1	0	20.5	19	13	2	1_A375_uNG7_minus_lncRNA_NR_1_4154	25	Gene ZNF721	ZNF721, FLJ11432, RIAN1982	zinc finger protein 721	NM_133474	229229_at	NP_597731.2
GeneID:5412	PIGQ	9	402,969	533,220	40,231	+	2	1_A375_uNG7_minus_lncRNA_NR_1_4154, 2_A375_uNG7_plus_lncRNA_NR_1_5985	-61, 3	upstream, vs gene	1	1	0	29	19	13	1	1_A375_uNG7_minus_lncRNA_NR_1_4154	29	Gene PIGQ	PIGQ, DKFZp434H132, FLJ20298, UNQ21, RUSS1930, DKFZp434C2112, MGC131901, DKFZp434K192, FLJ39925, PRO0453, GPP	phosphatidylinositol glycan anchor biosynthesis, class Q	NM_017733, NM_001127715, XCT2296697.0, XCT2296699.0, XCT2296699.2	1563242_at, 210852_s_at, 231852_s_at, 231852_at, 232864_at	NP_060203.3, NP_001120690.1, EAW92663.1, EAW92664.1, EAW92665.1
GeneID:5518	PDE8B	5	6,119,280	6,264,881	45,218	+	3	2_A375_uNG7_plus_lncRNA_NR_1_5970, 4_A375_EGR1_1_6546, 4_A375_EGR1_1_6547, 4_A375_EGR1_1_6548, 4_A375_EGR1_1_6549	48797, 2643, 3803, 38109, 40128	downstream, vs gene, vs gene, vs gene, vs gene	0	1	1	7.2	9.4	16.2	3	4_A375_EGFR1_1	20	Gene PDE8B	CGI-83, CGI-83/MAD, PDE8B, PDE8, 401, RPA0	phosphodiesterase 8B, cGMP-specific, not, beta	NM_001142292, NM_003605, NM_001142291, XCT2296691.0, XCT2296692.3	1557777_at, 210054_at, 230805_at, 230153_at	NP_001135764.1, NP_003274.2, NP_001135763.1, EAW63861.1, EAW63862.1
GeneID:1012	LOC1023	6	647,011	649,983	2,972	-	2	4_A375_EGR1_1_6545, 4_A375_EGR1_1_6549	-7991, -9555	upstream, upstream	0	0	1	4.5	9.5	17.5	2	4_A375_EGFR1_1	20	Gene LOC100507853	hypothetical LOC100507853	XR_112804, XR_113551, XR_113614		
GeneID:3324	ATP5I	4	999,228	999,127	1,902	-	3	2_A375_uNG7_plus_lncRNA_NR_1_5979, 4_A375_EGR1_1_6546, 4_A375_EGR1_1_6549	-33, 10979, 8829	upstream, downstream, downstream	0	1	1	8.33	11.67	16	3	4_A375_EGFR1_1	20	Gene ATP5I	MGC12332, ATP5I, ATP5K	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	NM_007100, NR_023743, XCT1642748.4	207533_s_at	NP_009031.1, EAW92660.1
GeneID:4469	MYL3	4	977,711	973,217	4,708	-	2	4_A375_EGR1_1_6545, 4_A375_EGR1_1_6550	-3381, 10590	upstream, downstream	0	1	1	11.5	13	13.5	2	4_A375_EGFR1_1	16	Gene MYL3	MYL3	NM_002477	203143_s_at	NP_002466.1
GeneID:1794	MPSD7	4	873,816	862,870	7,233	-	2	2_A375_uNG7_plus_lncRNA_NR_1_5979, 4_A375_EGR1_1_6550	14613, 689	downstream, vs gene	0	1	1	11.5	13	13.5	2	4_A375_EGFR1_1	16	Gene MPSD7	LP2391, MPSD7, FLJ22269	major facilitator superfamily domain containing	NM_022319, XCT1989048.1, XCT1989049.1	203144_at, 214289_at	NP_115595.2, EAW92666.1, EAW92669.1
GeneID:1012	PCGF3	4	999,970	784,426	84,855	+	2	4_A375_EGR1_1_6551, 4_A375_EGR1_1_6552	1289, 25371	upstream, vs gene	0	0	1	8	8.5	17.5	2	4_A375_EGFR1_1	19	Gene PCGF3	FLJ43515, PCGF3, MGC40410, RNF3, FLJ36550, RNF3A, DKFZp686D023 5, DGNG1, MGC129851	polycomb group ring finger 3	NM_006315, XCT2296696.0, XCT2296701.0, XCT2296776.0, XCT2296779.2, XCT2297131.2	1559525_at, 204864_at, 212762_at, 228456_at, 230804_at	NP_006306.2, EAW92652.1, EAW92653.1, EAW92654.1, EAW92655.1, EAW92656.1
GeneID:1012	LOC1002	4	773,207	775,838	1,899	-	4	2_A375_uNG7_plus_lncRNA_NR_1_5971, 4_A375_EGR1_1_6553, 4_A375_EGR1_1_6554, 4_A375_EGR1_1_6555	212, 142, -428, -10166	vs gene, vs gene, upstream, upstream	0	1	1	9.67	12	15.67	3	2_A375_uNG7_plus_lncRNA_NR_1_5971	16	Gene LOC100129917	hypothetical LOC100129917	NR_038511, NR_038512		
GeneID:1012	CFLV1	4	770,743	819,943	41,200	-	7	4_A375_EGR1_1_6551, 4_A375_EGR1_1_6553, 4_A375_EGR1_1_6554, 4_A375_EGR1_1_6555, 4_A375_EGR1_1_6556, 4_A375_EGR1_1_6557, 4_A375_EGR1_1_6558	44527, 44437, 43881, 34201, 31651, 11446, 1929	downstream, downstream, downstream, downstream, vs gene, vs gene, vs gene	0	1	1	8	9.67	17.5	6	4_A375_EGFR1_1	21	Gene CFLV1	CFV1, CFLV1, CFV-1	cofilin-like 1	NM_030931, NCT1969930.1, XCT2298239.0, XCT2298390.2	223300_at	NP_038942.1, EAW92648.1, EAW92647.1, EAW92649.1
GeneID:2264	GAX	4	943,088	929,174	63,109	-	3	2_A375_uNG7_plus_lncRNA_NR_1_5972, 4_A375_EGR1_1_6556, 4_A375_EGR1_1_6560	279, 39834, 45434	vs gene, vs gene, vs gene	0	1	1	9.67	12	16	3	4_A375_EGFR1_1	19	Gene GAX	GAX, FLJ40395, FLJ98629, MSX3, FLJ39854	cyclin G associated kinase	NM_053355, XCT2298091.1, XCT2298096.1, XCT2298097.1	202281_at, 40228_at	NP_058248.2, EAW92643.1, EAW92644.1, EAW92646.1
GeneID:5447	TMEM1	4	926,282	952,444	26,162	+	2	2_A375_uNG7_plus_lncRNA_NR_1_5972, 4_A375_EGR1_1_6561	-356, 32521	upstream, downstream	0	1	1	10	13.5	14.5	2	2_A375_uNG7_plus_lncRNA_NR_1_5972	19	Gene TMEM175	DKFZp686I15175, TMEM175	transmembrane protein 175	NM_032326, XCT1989032.1, XCT1989033.1, XCT1989034.1, XCT1989035.1, XCT1989036.1, XCT2298280.0, XCT2298280.2, XCT2298290.0	1557702.1, EAW92630.1, EAW92631.1, EAW92632.1, EAW92633.1, EAW92634.1, EAW92635.1, EAW92636.1, EAW92637.1, EAW92641.1, EAW92642.1, EAW92643.1	
GeneID:1012	DGKG	9	852,878	867,244	14,889	-	2	4_A375_EGR1_1_6561, 4_A375_EGR1_1_6562	6261, 4424	vs gene, upstream	0	0	1	9	8	16	2	4_A375_EGFR1_1	16	Gene DGKG	DAGK, DAGK7, DKFZp564J064, DGKG	diacylglycerol kinase, theta	NM_001347, XCT1970549.1, XCT2295007.0, XCT2295449.4	207962_at, 226803_at	NP_001338.2, EAW92632.1, EAW92633.1, EAW92631.1
GeneID:1012	SLC26A1	4	972,691	987,224	14,265	-	6	2_A375_uNG7_plus_lncRNA_NR_1_5973, 4_A375_EGR1_1_6562, 4_A375_EGR1_1_6563, 4_A375_EGR1_1_6564, 4_A375_EGR1_1_6565, 4_A375_EGR1_1_6566	6012, 5456, 5888, 3812, 2544, -4455	vs gene, vs gene, vs gene, vs gene, vs gene, upstream	0	1	1	8.2	10.2	17.8	5	4_A375_EGFR1_1	24	Gene SLC26A1	SLC26A1, SAT1, SO4a, SAT-1	solute carrier family 26 (sulfate transporter), member 1	NM_022042, NM_134425, NM_213815, XCT2295001.0, XCT2295002.2	1552843_at, 203650_at, 203733_at, 203732_s_at, 220192_s_at, 220199_at	NP_071325.2, NP_602297.1, NP_990776.1, EAW92626.1, EAW92629.1
GeneID:5412	IDUA	4	980,768	998,217	17,332	+	6	2_A375_uNG7_plus_lncRNA_NR_1_5973, 4_A375_EGR1_1_6562, 4_A375_EGR1_1_6563, 4_A375_EGR1_1_6564, 4_A375_EGR1_1_6565, 4_A375_EGR1_1_6566	127, -4017, 765, 2797, 4093, 10627	vs gene, upstream, vs gene, vs gene, vs gene, vs gene	0	1	1	8.2	10.2	17.8	5	4_A375_EGFR1_1	24	Gene IDUA	IDA, MPS1, IDUA	alpha-L-iduronidase, alpha-	NM_000203, XCT1972668.1, XCT1972690.1, XCT1972691.1, XCT1972692.1, XCT1972694.1, XCT2295720.0, XCT2295721.0, XCT2295722.0, XCT2295723.0, XCT2295724.0, XCT2295725.0	1553843_at, 203650_at, 203733_at, 203732_s_at, 220192_s_at, 220199_at	NP_000194.2, EAW92618.1, EAW92619.1, EAW92620.1, EAW92621.1, EAW92622.1, EAW92623.1, EAW92624.1, EAW92625.1
GeneID:5533	FGFRL1	4	1,805,810	1,830,696	15,076	+	7	4_A375_EGR1_1_6567, 4_A375_EGR1_1_6568, 4_A375_EGR1_1_6569, 4_A375_EGR1_1_6570, 4_A375_EGR1_1_6571, 4_A375_EGR1_1_6572, 4_A375_EGR1_1_6573	5430, 10550, 13222, 17702, 23516, 25734, 29550	vs gene, vs gene, downstream, downstream, downstream, downstream, downstream	0	0	1	8.43	9.71	17.57	7	4_A375_EGFR1_1	22	Gene FGFRL1	FYRF, FGFR5, FGFRL1	fibroblast growth factor receptor-like 1	NM_021923, NM_001004356, NM_001004358, XCT2295091.0, XCT2295092.2	223321_s_at, 223645_s_at	NP_068742.2, NP_001004356.1, NP_001004358.1, EAW63815.1
GeneID:2387	RNF212	4	1,865,288	1,707,382	42,316	-	2	2_A375_uNG7_minus_lncRNA_NR_1_4158, 4_A375_EGR1_1_6574	313358, 21102	vs gene, vs gene	1	0	1	10.5	12	11.5	2	1_A375_uNG7_minus_lncRNA_NR_1_4158	16	Gene RNF212	MGC120227, RNF212, ZHF3, FLJ42307, MGC120226, FLJ38541	ring finger protein 212	NM_001139334, NM_194439, NM_001159318, XCT1649764.4, XCT2411084.0, XCT2411103.0, XCT2411082.0, XCT2295237.0	1557831_at, 239634_at	NP_001132806.1, NP_919430.1, NP_001159247.1, EAW92611.1, EAW92614.1, EAW92610.1, EAW92612.1
GeneID:1012	SPON2	4	1,160,720	1,168,930	8,280	+	4	4_A375_EGR1_1_6575, 4_A375_EGR1_1_6576, 4_A375_EGR1_1_6577, 4_A375_EGR1_1_6578	5305, 2205, 637, 2124	downstream, vs gene, vs gene, upstream	0	0	1	10	9.5	17.5	4	4_A375_EGFR1_1	21	Gene SPON2	MINDIN, DIL-1, FLJ34481, DIL1, Mindin/ spondin, FLJ40113, Mindin, SPON2, DKFZp686I21010, M-SPONDIN, FLJ22401	spondin 2, extracellular matrix protein	NM_012445, NM_001012833, XCT2295080.0, XCT2295081.2	1569498_s_at, 219931_s_at	NP_036977.1, NP_001129797.1, EAW63864.1, EAW63865.1, EAW63866.1
GeneID:1012	LOC1003	4	1,165,840	1,202,834	36,994	-	10	4_A375_EGR1_1_6575, 4_A375_EGR1_1_6576, 4_A375_EGR1_1_6577, 4_A375_EGR1_1_6578, 4_A375_EGR1_1_6579, 4_A375_EGR1_1_6580, 4_A375_EGR1_1_6581, 4_A375_EGR1_1_6582, 4_A375_EGR1_1_6583, 4_A375_EGR1_1_6584	41182, 37982, 36811, 33330, 14602, 2690, 2730, 776, -4356, -5825	downstream, downstream, vs gene, vs gene, vs gene, vs gene, vs gene, upstream, upstream	0	0	1	7.2	8	16.4	10	4_A375_EGFR1_1	21	Gene LOC100130872-SPON2	hypothetical LOC100130872	NR_033162		
GeneID:2615	LOC2835	4	1,203,936	1,212,379	8,471	+	6	4_A375_EGR1_1_6580, 4_A375_EGR1_1_6581, 4_A375_EGR1_1_6582, 4_A375_EGR1_1_6583, 4_A375_EGR1_1_6584, 4_A375_EGR1_1_6585	-1464, -4056, 3082, 3224, 4961, 12116	upstream, upstream, upstream, vs gene, vs gene, downstream	0	0	1	5.5	8.17	16.83	6	4_A375_EGFR1_1	21	Gene LOC283663	hypothetical LOC283663	XR_112800, XR_113553, XR_113616	1562571_at	
GeneID:1012	CTBP1	4	1,205,226	1,242,936	37,850	-	8	4_A375_EGR1_1_6580, 4_A375_EGR1_1_6581, 4_A375_EGR1_1_6582, 4_A375_EGR1_1_6583, 4_A375_EGR1_1_6584, 4_A375_EGR1_1_6585, 4_A375_EGR1_1_6586, 4_A375_EGR1_1_6587	43884, 43004, 41832, 33676, 34439, 29859	downstream, downstream, downstream, downstream, vs gene, vs gene, vs gene, vs gene	0	0	1	5.5	8.17	16.83	8	4_A375_EGFR1_1	21	Gene CTBP1	MGC104884, BARS, CTBP1	C-terminal binding protein 1	NM_001328, NM_001013614, XCT2295049.0, XCT2295051.0, XCT2295052.0, XCT2295053.0, XCT2295054.0, XCT2295055.0, XCT2295056.0, XCT2295057.0	1557714_at, 202982_s_at, 202983_at, 212663_x_at, 213992_s_at	NP_001310.1, NP_001012632.1, EAW92599.1, EAW92600.1, EAW92601.1, EAW92602.1
GeneID:1012	MAEA	4	1,203,872	1,233,935	30,253	+	2	1_A375_uNG7_minus_lncRNA_NR_1_4157, 2_A375_uNG7_plus_lncRNA_NR_1_5975	58938, 56964	downstream, downstream	1	1	0	16	29	10	1	2_A375_uNG7_plus_lncRNA_NR_1_5975	29	Gene MAEA	FKSG, EMLP, HEC-10, EMP, MAEA	macrophage erythroblast attacher	NM_005932, NM_001017405, NCT1949978.3, NCT1969026.1, NCT1969027.1, NCT2296782.0, NCT2296786.0, NCT2296787.0, NCT2296788.0, NCT2296789.0, NCT2296274.0, NCT2296275.0, NCT2296276.0, NCT2296277.0	207922_s_at	NP_005923.2, NP_001017405.1, EAW62598.1, EAW62599.1, EAW62594.1, EAW62596.1, EAW62597.1, EAW62593.1, EAW62591.1, EAW62592.1, EAW62595.1
GeneID:3757	KIAA1539	4	1,341,704	1,381,837	40,133	+	6	1_A375_uNG7_minus_lncRNA_NR_1_4157, 2_A375_uNG7_plus_lncRNA_NR_1_5975, 4_A375_EGR1_1_6588, 4_A375_EGR1_1_6589, 4_A375_EGR1_1_6590	-496, -443, 22702, 22016, 22579	upstream, upstream, vs gene, vs gene, vs gene	1	1	1	7.75	12.75	13.25	4	2_A375_uNG7_plus_lncRNA_NR_1_5975	29	Gene KIAA1539	KIAA1539, MGC117169	KIAA1539	NM_020894, XCT1653221.3	1558107_s_at, 233052_s_at, 241201_at	NP_065943.2, EAW62596.1
GeneID:2615	CRIPAK	4	1,359,540	1,359,782	4,442	+	1	4_A375_EGR1_1_6589	10420	downstream	0	0	1	6	7	20	1	4_A375_EGFR1_1	20	Gene CRIPAK	FLJ39443, CRIPAK, MGC130520	cysteine-rich PAK1 inhibitor	NM_175918, XCT2295772.1	229316_s_at, 244908_at	NP_787114.2, EAW62585.1
GeneID:3477	NKX1-1	4	1,398,720	1,400,119	2,399	-	3	1_A375_uNG7_minus_lncRNA_NR_1_4158, 2_A375_uNG7_plus_lncRNA_NR_1_5976, 4_A375_EGR1_1_6590	-4265, -4233, 4389	upstream, upstream, downstream	1	1	1	49.5	83	15.5	2	2_A375_uNG7_plus_lncRNA_NR_1_5976	119	Gene NKX1-1	NKX1-1, SAX2, HBFX1S3	NK1 homeobox 1	XM_928641, XM_937699	1566537_at	XP_931434.4, XP_942752.3



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:7466	WFS1	4	6,271,577	6,304,992	33,415	+	1	4_A375_EGR1..1..6486	7991	in gene	0	0	1	4	5	19	1	4_A375_EGR1..1	19	Gene WFS1	WFS1, FLJ51211, WFS, WFRS, WOLFRAMIN	Wolfram syndrome 1 (wolframin)	NM_006005, NM_001145853, hCT2254558.0, hCT2254559.0, hCT29319.3	1555270_a_at, 202908_at	NP_005996.2, NP_001139325.1, EAW82396.1, EAW82397.1, EAW82398.1
GeneID:5522	PPP2R2C	4	6,322,305	6,474,326	152,021	-	6	1_A375_pNL7_minus_lncRNA_AR..1..4171, 1_A375_pNL7_minus_lncRNA_AR..1..4172, 2_A375_pNL97_plus_lncRNA_AR..1..5995, 2_A375_pNL97_plus_lncRNA_AR..1..5996, 4_A375_EGR1..1..6487, 4_A375_EGR1..1..6488	128470, 109494, 109462, -5503, 133910, 51451	in gene, in gene, in gene, upstream, in gene, in gene	1	1	1	16.2	16.6	10.6	5	2_A375_pNL97_plus_lncRNA_AR..1	48	Gene PPP2R2C	IMYPNO1, PR52, B55-GAMMA, IMYPNO, MGC33570, PR55G, PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	NM_020416, NM_181876, hCT1837937.1, hCT2254142.1, hCT30893.3	223573_s_at, 223574_x_at, 226010_at, 226025_s_at, 226137_s_at, 226140_s_at	NP_065149.2, NP_870991.1, EAW82393.1, EAW82394.1, EAW82395.1
GeneID:23324	MAN2B2	4	6,576,902	6,624,188	47,286	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4173, 4_A375_EGR1..1..6489	122, 170	in gene, in gene	1	0	1	19	10	14	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene MAN2B2	MAN2B2, KIAA0935	mannosidase, alpha, class 2B, member 2	NM_015274, hCT2254770.0, hCT2254772.0, hCT2254773.0, hCT2254776.0	214703_s_at	NP_056089.1, EAW82390.1, EAW82389.1, EAW82391.1, EAW82392.1
GeneID:93621	MRFAP1	4	6,642,445	6,644,449	2,004	+	1	4_A375_EGR1..1..6490	-301	upstream	0	0	1	10	10	17	1	4_A375_EGR1..1	17	Gene MRFAP1	PAM14, MRFAP1, PGR1	Morf4 family associated protein 1	NM_033296, hCT1828208.3, hCT1960547.2	226091_s_at	NP_150638.1, EAW82386.1, EAW82387.1
GeneID:114932	MRFAP1L1	4	6,709,428	6,711,606	2,178	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4174, 2_A375_pNL97_plus_lncRNA_AR..1..5997, 2_A375_pNL97_plus_lncRNA_AR..1..5998, 4_A375_EGR1..1..6491	-6250, 470, -6782, -6218	upstream, in gene, upstream, upstream	1	1	1	16	21.5	15.5	2	4_A375_EGR1..1	23	Gene MRFAP1L1	MGC9651, PP784, MRFAP1L1	Morf4 family associated protein 1-like 1	NM_203462, hCT2350911.0	212199_at	NP_982287.1, EAW82383.1
GeneID:55330	CNO	4	6,717,842	6,719,387	1,545	+	5	1_A375_pNL7_minus_lncRNA_AR..1..4174, 2_A375_pNL97_plus_lncRNA_AR..1..5997, 2_A375_pNL97_plus_lncRNA_AR..1..5998, 2_A375_pNL97_plus_lncRNA_AR..1..5999, 4_A375_EGR1..1..6491	14, -6706, 526, 11310, -16	in gene, upstream, in gene, downstream, upstream	1	1	1	12.67	20.33	15	3	4_A375_EGR1..1	23	Gene CNO	FLJ11230, BCAS4L, CNO	cappuccino homolog (mouse)	NM_018366	223431_at	NP_060836.1
GeneID:9778	KIAA0232	4	6,784,459	6,885,899	101,440	+	1	4_A375_EGR1..1..6492	629	in gene	0	0	1	9	13	22	1	4_A375_EGR1..1	22	Gene KIAA0232	KIAA0232		NM_014743, NM_001100590, hCT30895.3	212441_at, 232366_at	NP_055558.2, NP_001094060.1, EAW82378.1
GeneID:57533	TBC1D14	4	6,911,171	7,034,845	123,674	+	7	1_A375_pNL7_minus_lncRNA_AR..1..4175, 1_A375_pNL7_minus_lncRNA_AR..1..4176, 1_A375_pNL7_minus_lncRNA_AR..1..4177, 2_A375_pNL97_plus_lncRNA_AR..1..6000, 2_A375_pNL97_plus_lncRNA_AR..1..6001, 2_A375_pNL97_plus_lncRNA_AR..1..6002, 4_A375_EGR1..1..6493	-63, 7309, 77741, -35, 7261, 77637, 6045	upstream, in gene, in gene, upstream, in gene, in gene, in gene	1	1	1	20	21.75	11	4	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene TBC1D14	KIAA1322, TBC1D14, FLJ32400	TBC1 domain family, member 14	NM_020773, NM_001113361, NM_001113363, hCT2254797.0, hCT2356254.0, hCT30890.3	224822_at	NP_065824.2, NP_001106832.1, NP_001106834.1, EAW82375.1, EAW82376.1, EAW82377.1
GeneID:93624	TADA2B	4	7,045,156	7,059,679	14,523	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6003	24540	downstream	0	1	0	21	19	19	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TADA2B	ADA2B, ADA2(beta), MGC21874, TADA2B	transcriptional adaptor 2B	NM_152293	226240_at, 236248_x_at	NP_689506.2
GeneID:80273	GRPEL1	4	7,061,780	7,069,800	8,020	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6003	104	in gene	0	1	0	21	19	19	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene GRPEL1	GRPEL1, HMGE, FLJ25609	GrpE-like 1, mitochondrial (E. coli)	NM_025196, hCT2349958.1, hCT30891.3	212432_at, 212434_at	NP_079472.1, EAW82370.1, EAW82371.1
GeneID:57537	SORCS2	4	7,194,374	7,744,564	550,190	+	12	1_A375_pNL7_minus_lncRNA_AR..1..4178, 1_A375_pNL7_minus_lncRNA_AR..1..4179, 1_A375_pNL7_minus_lncRNA_AR..1..4180, 2_A375_pNL97_plus_lncRNA_AR..1..6004, 2_A375_pNL97_plus_lncRNA_AR..1..6005, 2_A375_pNL97_plus_lncRNA_AR..1..6006, 4_A375_EGR1..1..6494, 4_A375_EGR1..1..6495, 4_A375_EGR1..1..6496, 4_A375_EGR1..1..6497, 4_A375_EGR1..1..6498, 4_A375_EGR1..1..6499	14042, 103066, 544442, 14376, 457162, 544376, 6394, 102776, 241274, 266456, 353626, 543962	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	15.25	16.66	15.66	6	2_A375_pNL97_plus_lncRNA_AR..1	56	Gene SORCS2	SORCS2		NM_020777, hCT2254805.1, hCT2254807.0	228720_at	NP_065828.2, EAW82364.1, EAW82363.1
GeneID:768239	PSAPL1	4	7,432,021	7,436,700	4,679	-	1	4_A375_EGR1..1..6496	1052	in gene	0	0	1	4	9	20	1	4_A375_EGR1..1	20	Gene PSAPL1	FLJ40379, PSAPL1	prosaposin-like 1	NM_001085382	1564333_a_at	NP_001078851.1
GeneID:60312	AFAP1	4	7,760,440	7,941,653	181,213	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4181, 2_A375_pNL97_plus_lncRNA_AR..1..6007	362, 309	in gene, in gene	1	1	0	22	24	13	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene AFAP1	AFAP, FLJ56849, AFAP-110, AFAP1	actin filament associated protein 1	NM_198595, NM_001134647, hCT2254075.0	203563_at	NP_940997.1, NP_001128119.1, EAW82360.1
GeneID:84448	ABLIM2	4	7,967,037	8,160,559	193,522	-	8	1_A375_pNL7_minus_lncRNA_AR..1..4182, 2_A375_pNL97_plus_lncRNA_AR..1..6008, 4_A375_EGR1..1..6500, 4_A375_EGR1..1..6501, 4_A375_EGR1..1..6502, 4_A375_EGR1..1..6503, 4_A375_EGR1..1..6504, 4_A375_EGR1..1..6505	202415, 202351, 134363, 112959, 111667, 6423, 463, -401	downstream, downstream, in gene, in gene, in gene, in gene, in gene, upstream	1	1	1	10.43	10.43	16	7	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ABLIM2	MGC141918, FLJ39684, KIAA1808, DKFZp761F129, FLJ26534, ABLIM2	actin binding LIM protein family, member 2	NM_001130083, NM_001130084, NM_001130085, NM_001130086, NM_001130087, NM_032432, NM_001130088, hCT2254071.0, hCT2254072.0, hCT22761.3	1567622_at, 1567623_at, 228132_at, 236087_at, 242624_at	NP_001123555.1, NP_001123556.1, NP_115808.3, NP_001123557.1, NP_001123558.1, NP_001123559.1, NP_001123560.1, EAW82357.1, EAW82358.1, EAW82359.1
GeneID:54436	SH3TC1	4	8,201,060	8,242,830	41,770	+	3	4_A375_EGR1..1..6507, 4_A375_EGR1..1..6508, 4_A375_EGR1..1..6509	2412, 23740, 46124	in gene, in gene, downstream	0	0	1	6	7	16.67	3	4_A375_EGR1..1	22	Gene SH3TC1	SH3TC1, FLJ46394, FLJ36243, FLJ20356, FLJ32999	SH3 domain and tetratricopeptide repeats 1	NM_018986, hCT2254326.0, hCT2254327.0, hCT2254329.0, hCT2254330.0, hCT2356293.0, hCT2356294.0, hCT8436.2	219256_s_at, 229632_x_at	NP_061859.3, EAW82347.1, EAW82348.1, EAW82349.1, EAW82351.1, EAW82352.1, EAW82350.1, EAW82353.1
GeneID:94031	HTRA3	4	8,271,492	8,308,834	37,342	+	1	4_A375_EGR1..1..6510	-2532	upstream	0	0	1	7	6	15	1	4_A375_EGR1..1	15	Gene HTRA3	Tasp, Prsp, HTRA3	HtrA serine peptidase 3	NM_053044, hCT2356295.0, hCT8437.2	226944_at, 226580_at	NP_444272.1, EAW82346.1, EAW82345.1
GeneID:8310	ACOX3	4	8,368,009	8,442,452	74,443	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4183, 1_A375_pNL7_minus_lncRNA_AR..1..4184, 2_A375_pNL97_plus_lncRNA_AR..1..6009, 4_A375_EGR1..1..6511	12306, -172, 116, 12084	in gene, upstream, in gene, in gene	1	1	1	18	16.5	16	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ACOX3	ACOX3		NM_003501, NM_001101667, hCT1950283.1, hCT2254064.0, hCT2356245.0, hCT8438.3	204241_at, 204242_s_at	NP_003492.2, NP_001095137.1, EAW82339.1, EAW82340.1, EAW82341.1, EAW82342.1
GeneID:152992	C4orf23	4	8,442,532	8,478,282	35,750	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4184, 2_A375_pNL97_plus_lncRNA_AR..1..6009	92, -196	in gene, upstream	1	1	0	16	16	15	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C4orf23	C4orf23, METTL19, FLJ35725, FLJ12891	chromosome 4 open reading frame 23	NM_152544	1554192_s_at, 220691_at, 235097_at	NP_689757.2
GeneID:27201	GPR78	4	8,582,291	8,589,520	7,229	+	1	4_A375_EGR1..1..6513	461	in gene	0	0	1	15	13	23	1	4_A375_EGR1..1	23	Gene GPR78	GPR78	G protein-coupled receptor 78	NM_080819, hCT8439.3	1553063_at	NP_543009.2, EAW82336.1
GeneID:8532	CPZ	4	8,594,435	8,621,488	27,053	+	1	4_A375_EGR1..1..6514	15037	in gene	0	0	1	6	7	16	1	4_A375_EGR1..1	16	Gene CPZ	MGC99682, CPZ	carboxypeptidase Z	NM_003652, NM_001014447, NM_001014448, hCT2254351.0, hCT2356259.0, hCT2356260.0, hCT7485.2	211062_s_at	NP_003643.2, NP_001014447.1, NP_001014448.1, EAW82332.1, EAW82333.1, EAW82334.1, EAW82335.1
GeneID:3166	HMX1	4	8,868,773	8,873,543	4,770	-	1	4_A375_EGR1..1..6516	7271	downstream	0	0	1	3	7	16	1	4_A375_EGR1..1	16	Gene HMX1	HMX1, NKX5-3, H6	H6 family homeobox 1	NM_018942	207353_s_at, 214366_at	NP_061815.2
GeneID:1816	DRD5	4	9,783,258	9,785,633	2,375	+	1	4_A375_EGR1..1..6518	196	in gene	0	0	1	3	4	16	1	4_A375_EGR1..1	16	Gene DRD5	DRD5, DRD1L2, MGC10601, DBDR, DRD1B	dopamine receptor D5	NM_000798, hCT1642343.2	208486_at	NP_000789.1, EAW92679.1
GeneID:9948	WDR1	4	10,075,963	10,118,573	42,610	-	1	4_A375_EGR1..1..6519	34093	in gene	0	0	1	4	6	17	1	4_A375_EGR1..1	17	Gene WDR1	AIP1, WDR1, NORI-1	WD repeat domain 1	NM_017491, NM_005112, hCT10446.3, hCT2326080.0, hCT2326081.0, hCT2326083.0	200609_s_at, 200611_s_at, 210935_s_at, 210936_at, 240282_at, 244672_at	NP_059830.1, NP_005103.2, EAW92666.1, EAW92667.1, EAW92668.1, EAW92669.1
GeneID:100423011	MIR3138	4	10,080,235	10,080,316	81	-	1	4_A375_EGR1..1..6519	-4164	upstream	0	0	1	4	6	17	1	4_A375_EGR1..1	17	Gene MIR3138	MIR3138	microRNA 3138	NR_036090		
GeneID:85460	ZNF518B	4	10,441,504	10,459,032	17,528	-	1	4_A375_EGR1..1..6520	-3784	upstream	0	0	1	6	11	15	1	4_A375_EGR1..1	15	Gene ZNF518B	ZNF518B, KIAA1729	zinc finger protein 518B	NM_053042, hCT2342814.0	226909_at, 230715_at, 241580_at	NP_444270.2, EAW92692.1
GeneID:693157	MIR572	4	11,370,451	11,370,545	94	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4186, 2_A375_pNL97_plus_lncRNA_AR..1..6013	-1171, -1235	upstream, upstream	1	1	0	19	17	3	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene MIR572	MIR572, MIRN572, hsa-mir-572	microRNA 572	NR_030298		
GeneID:643446	LOC643446	4	11,370,535	11,375,359	4,824	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4186, 2_A375_pNL97_plus_lncRNA_AR..1..6013	-1255, -1319	upstream, upstream	1	1	0	19	17	3	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene LOC643446		RNA binding protein S1, serine-rich domain pseudogene			
GeneID:9364	RAB28	4	13,369,347	13,485,989	116,642	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6015	-155	upstream	0	1	0	19	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RAB28	RAB28, MGC41862	RAB28, member RAS oncogene family	NM_004249, NM_001017979, NM_001159601, hCT1961602.1, hCT7412.2	207495_at, 209084_s_at, 227003_at	NP_004240.2, NP_001017979.1, NP_001153073.1, EAW92711.1, EAW92712.1
GeneID:259282	BOD1L	4	13,570,366	13,629,328	58,962	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4187, 4_A375_EGR1..1..6522	-96, -112	upstream, upstream	1	0	1	22	13	15	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene BOD1L	BOD1L, FLJ33215, KIAA1327, FAM44A	biorientation of chromosomes in cell division 1-like	NM_148894, hCT2325866.0	225821_s_at, 235009_at, 242594_at	NP_683692.2, EAW92716.1
GeneID:441009	LOC441009	4	15,003,373	15,003,964	591	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4192, 2_A375_pNL97_plus_lncRNA_AR..1..6023	-260, -132	upstream, upstream	1	1	0	17	21	12	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC441009		hypothetical LOC441009	XM_001723280, XM_498965, XM_944416	1561471_at	XP_001723332.1, XP_498965.3, XP_949511.2
GeneID:132864	CPEB2	4	15,004,298	15,071,777	67,479	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4192, 2_A375_pNL97_plus_lncRNA_AR..1..6023	-74, -202	upstream, upstream	1	1	0	17	21	12	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CPEB2	CPEB-2, MGC119577, CPEB2, MGC119575, MGC119576	cytoplasmic polyadenylation element binding protein 2	NM_001177381, NM_001177382, NM_001177383, NM_001177384, NM_182485, NM_182646, hCT2346793.1, hCT2349392.0, hCT2349393.0, hCT2349394.0	226939_at, 235482_at, 235479_at	NP_001170852.1, NP_001170853.1, NP_001170854.1, NP_001170855.1, NP_872291.2, NP_872587.2, EAW92727.1, EAW92728.1, EAW92729.1, EAW92730.1
GeneID:57545	CC2D2A	4	15,471,489	15,603,180	131,691	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6024	92575	in gene	0	1	0	17	24	5	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CC2D2A	JBTS9, MKS6, CC2D2A, KIAA1345	coiled-coil and C2 domain containing 2A	NM_001080522, NM_001164720, NM_020785	1559409_a_at, 234933_at, 234936_s_at, 236473_at	NP_001073991.2, NP_001158192.1, NP_065836.2
GeneID:285550	LOC285550	4	15,683,352	15,692,070	8,718	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4193, 2_A375_pNL97_plus_lncRNA_AR..1..6025, 2_A375_pNL97_plus_lncRNA_AR..1..6026, 4_A375_EGR1..1..6523	13784, -24, 13666, -296	downstream, upstream, downstream, upstream	1	1	1	16.5	19.5	13	2	4_A375_EGR1..1	22	Gene LOC285550	FAM200B	family with sequence similarity 200, member B	NM_001145191	227270_at, 227466_at, 236321_at	NP_001138663.1
GeneID:683	BST1	4	15,704,573	15,733,796	29,223	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4193, 2_A375_pNL97_plus_lncRNA_AR..1..6026	-7437, -7533	upstream, upstream	1	1	0	19	20	4	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene BST1	BST1, CD157	bone marrow stromal cell antigen 1	NM_004334, hCT30656.2	205715_at	NP_004325.2, EAW92744.1
GeneID:952	CD38	4	15,779,931	15,850,706	70,775	+	1	4_A375_EGR1..1..6524	6773	in gene	0	0	1	6	6	16	1	4_A375_EGR1..1	16	Gene CD38	CD38, T10	CD38 molecule	NM_001775, hCT1816708.2, hCT2357591.0	205692_s_at	NP_001766.2, EAW92746.1, EAW92745.1
GeneID:9079	LDB2	4	16,503,164	16,900,424	397,260	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4195	325416	in gene	1	0	0	16	6	3	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene LDB2	LDB2, LDB1, CLIM1	LIM domain binding 2	NM_001290, NM_001130834, hCT1953751.2, hCT1953752.2, hCT2325901.0	206481_s_at, 242380_at	NP_001281.1, NP_001124306.1, EAW92765.1, EAW92766.1, EAW92767.1
GeneID:5860	QDPR	4	17,488,016	17,513,857	25,841	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4196, 2_A375_pNL97_plus_lncRNA_AR..1..6029, 4_A375_EGR1..1..6525	1, -31, 353	in gene, upstream, in gene	1	1	1	24	36	19	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene QDPR	FLJ42391, PKU2, DHPR, QDPR, SDR33C1	quinoid dihydropteridine reductase	NM_000320, hCT1962487.2, hCT1971220.2, hCT2357574.0, hCT2357575.0, hCT2357576.0	209123_at, 238616_at	NP_000311.2, EAW92775.1, EAW92774.1, EAW92776.1, EAW92777.1, EAW92778.1
GeneID:645104	CLRN2	4	17,516,788	17,528,727	11,939	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4196, 2_A375_pNL97_plus_lncRNA_AR..1..6029, 4_A375_EGR1..1..6525	-2932, -2900, -3284	upstream, upstream, upstream	1	1	1	24	36	19	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene CLRN2	CLRN2		NM_001079827		NP_001073296.1
GeneID:51056	LAP3	4	17,578,927	17,609,590	30,663	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6030, 4_A375_EGR1..1..6526	37361, -271	downstream, upstream	0	1	1	12.5	16.5	15	2	4_A375_EGR1..1	23	Gene LAP3	LAPEP, LAP, LAP3, PEPS	leucine aminopeptidase 3	NM_015907, hCT32195.3	217933_s_at	NP_056991.2, EAW92780.1
GeneID:80306	MED28	4	17,616,273	17,626,160	9,887	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6030	15	in gene	0	1	0	13	17	7	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene MED28	magicin, DKFZp434N185, MED28, 1500003D12Rik, EG1	mediator complex subunit 28	NM_025205, hCT2325923.0, hCT2325924.0	214831_at, 218438_s_at, 222635_s_at, 222636_at, 224416_s_at, 228992_at, 243666_at	NP_079481.2, EAW92782.1, EAW92781.1
GeneID:27146	FAM184B	4	17,633,696	17,783,135	149,439	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4197, 1_A375_pNL7_minus_lncRNA_AR..1..4198, 2_A375_pNL97_plus_lncRNA_AR..1..6031, 2_A375_pNL97_plus_lncRNA_AR..1..6032	93770, 90527, 93791, 90463	in gene, in gene, in gene, in gene	1	1	0	22.5	26	9	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene FAM184B	FAM184B, KIAA1276	family with sequence similarity 184, member B	NM_015688	233823_at	NP_056503.1
GeneID:54876	DCAF16	4	17,802,278	17,812,381	10,103	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4199, 2_A375_pNL97_plus_lncRNA_AR..1..6033	-163, 93	upstream, in gene	1	1	0	16	16	13	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene DCAF16	MGC126767, C4orf30, DCAF16, MGC126765, FLJ20260	DDB1 and CUL4 associated factor 16	NM_017741, hCT2326004.0	219717_at, 228106_at, 239187_at	NP_060211.3, EAW92784.1
GeneID:64151	NCAPG	4	17,812,525	17,846,488	33,963	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4199, 2_A375_pNL97_plus_lncRNA_AR..1..6033	19, -237	in gene, upstream	1	1	0	16	16	13	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene NCAPG	CHCG, HCAP-G, MGC126525, NY-MEL-3, CAPG, NCAPG, FLJ12450	non-SMC condensin I complex, subunit G	NM_022346, hCT32197.3	218662_s_at, 218663_at	NP_071741.2, EAW92785.1
GeneID:254251	LCORL	4	17,844,639	18,023,483	178,844	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4200, 2_A375_pNL97_plus_lncRNA_AR..1..6034	-191, -325	upstream, upstream	1	1	0	17	22	10	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LCORL	MLR1, FLJ30696, LCORL	ligand dependent nuclear receptor corepressor-like	NM_153686, NM_001166139, hCT1660901.3, hCT2349345.0, hCT2349346.0, hCT2349347.0	232293_at, 235970_at, 240592_at	NP_710153.2, NP_001159611.1, EAW92786.1, EAW92787.1, EAW92788.1, EAW92789.1
GeneID:9353	SLIT2	4	20,255,235	20,620,788	365,553	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4201, 2_A375_pNL97_plus_lncRNA_AR..1..6035, 2_A375_pNL97_plus_lncRNA_AR..1..6036, 4_A375_EGR1..1..6527	220646, -1619, 220733, -371	in gene, upstream, in gene, upstream	1	1	1	11	15.67	13.33	3	4_A375_EGR1..1	24	Gene SLIT2	SLIL3, Slit-2, SLIT2, FLJ14420	slit homolog 2 (Drosophila)	NM_004787, hCT1954498.1, hCT2325983.0	209897_s_at, 230130_at	NP_004778.1, EAW92792.1, EAW92793.1
GeneID:80333	KCNIP4	4	20,730,239	21,950,374	1,220,135	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4202, 2_A375_pNL97_plus_lncRNA_AR..1..6037, 1_A375_pNL7_minus_lncRNA_AR..1..4203, 2_A375_pNL97_plus_lncRNA_AR..1..6038, 2_A375_pNL97_plus_lncRNA_AR..1..6039	1089702, 1089734, 46162, 935142, 60086	in gene, in gene, in gene, in gene, in gene	1	1	0	19.25	17.5	2.5	4	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene KCNIP4	CALP, MGC44947, KCNIP4, KCHIP4	Kv channel interacting protein 4	NM_025221, NM_147181, NM_147182, NM_147183, NM_001035003, NM_001035004, hCT1954497.1, hCT2326016.0	224530_s_at, 236783_at, 240591_at	NP_079497.2, NP_671710.1, NP_671711.1, NP_671712.1, NP_001030175.1, NP_001030176.1, EAW92797.1, EAW92798.1
GeneID:10891	PPARGC1A	4	23,793,644	23,891,700	98,056	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4207	33568	in gene	1	0	0	19	15	6	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene PPARGC1A	PGC1A, PGC-1v, PGC1, LEM6, PGC-1(alpha), PPARGC1A, PPARGC1	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	NM_013261, hCT1954499.1, hCT2326025.0	1569141_a_at, 219195_at	NP_037393.1, EAW92812.1, EAW92811.1
GeneID:729175	LOC729175	4	24,473,456	24,484,502	11,046	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6044	9494	in gene	0	1	0	15	21	6	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene LOC729175		hypothetical LOC729175	XM_001129556, XM_001131204, XM_001717514		XP_001129556.1, XP_001131204.1, XP_001717566.1
GeneID:1665	DHX15	4	24,529,087	24,586,184	57,097	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6045	72	in gene	0	1	0	13	16	15	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene DHX15	DBP1, PrPp43p, DHX15, PRP43, DDX15, PRPF43, HRH2	DEAH (Asp-Glu-Ala-His) box polypeptide 15	NM_001358, hCT2350293.0, hCT2350294.0, hCT2350295.0, hCT2350296.0, hCT2350482.0, hCT2350483.0, hCT2350484.0, hCT30900.2	201385_at, 201386_s_at	NP_001349.2, EAW92817.1, EAW92814.1, EAW92816.1, EAW92819.1, EAW92821.1, EAW92815.1, EAW92818.1, EAW92820.1

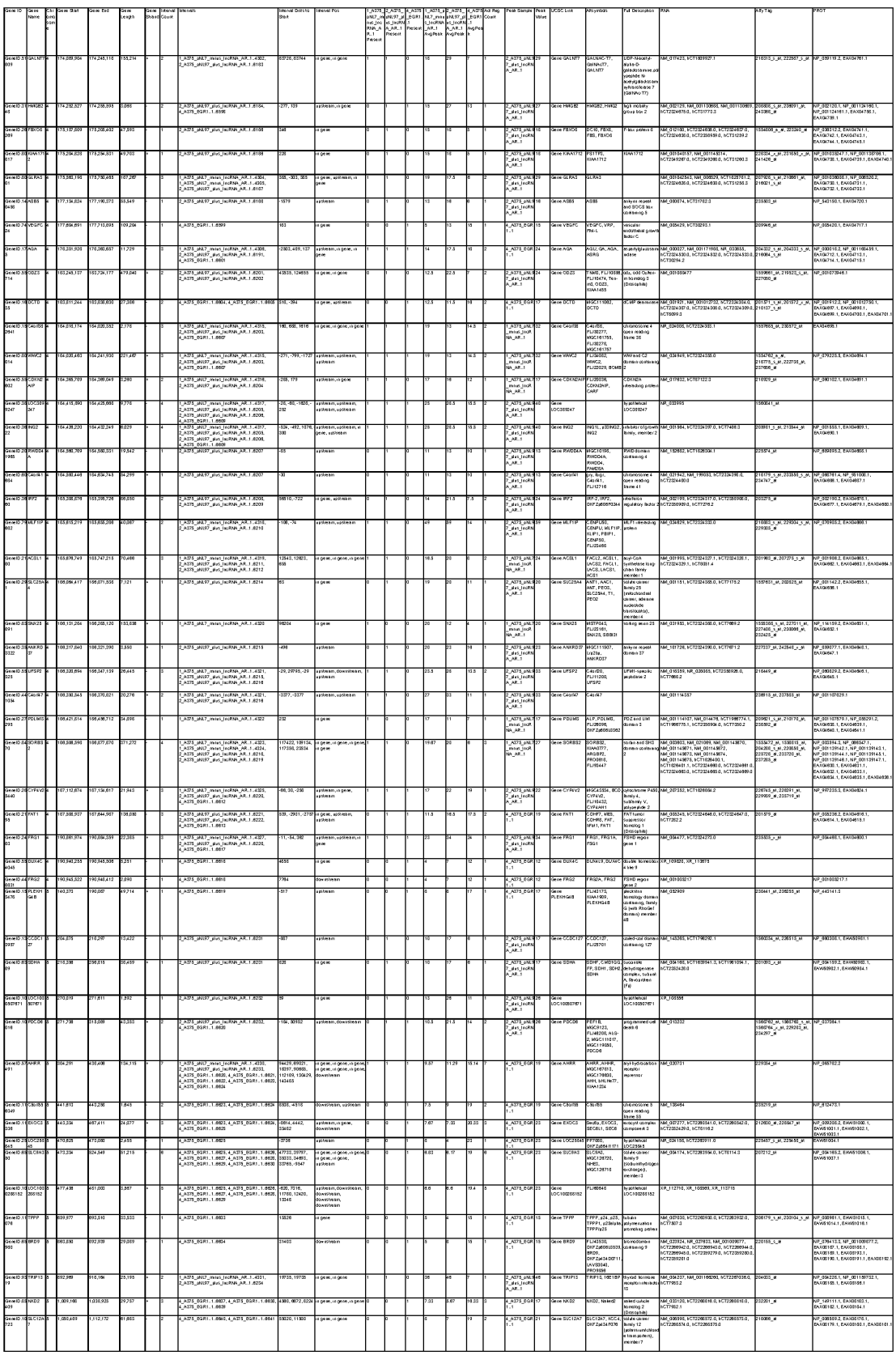
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.51091	SEPSECS	4	25,121,627	25,162,204	40,577	-	2	2_A375_pNL97_plus_lncRNA_AR..1..6047, 4_A375_EGR1..1..6526	60, 124	in gene, in gene	0	1	1	15	18	15	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SEPSECS	LP, SLA/LP, SEPSECS, SLA, DKFZp434B1417, MGC161491	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	NM_016955, hCT1954502.1, hCT2326132.0, hCT2326133.0, hCT2326135.0, hCT9307.3	1553167_a_at, 1569834_at, 231730_at, 235516_at	NP_058651.3, EAW92832.1, EAW92831.1, EAW92833.1, EAW92834.1, EAW92835.1
GeneID.285540	LOC285540	4	25,162,294	25,200,128	37,834	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6047, 2_A375_pNL97_plus_lncRNA_AR..1..6048, 4_A375_EGR1..1..6526	-150, 12906, -214	upstream, in gene, upstream	0	1	1	16.5	21.5	9	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC285540		hypothetical LOC285540	XR_112624, XR_108552, XR_113627	1559479_at	
GeneID.55300	PI4K2B	4	25,235,653	25,280,831	45,178	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6049, 4_A375_EGR1..1..6529	347, 5531	in gene, in gene	0	1	1	8.5	11	11.5	2	4_A375_EGR1..1	16	Gene PI4K2B	PI4KIIB, PI4K2B, PIK42B, FLJ11105	phosphatidylinositol 4-kinase type 2 beta	NM_018323, hCT10866.2	222631_at	NP_060793.2, EAW92838.1
GeneID.29063	ZCCHC4	4	25,314,398	25,372,005	57,609	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4209, 2_A375_pNL97_plus_lncRNA_AR..1..6050, 2_A375_pNL97_plus_lncRNA_AR..1..6051	-28, 4, 64692	upstream, in gene, downstream	1	1	0	42.5	52	8	2	2_A375_pNL97_plus_lncRNA_AR..1	68	Gene ZCCHC4	MGC21108, HSPC052, ZCCHC4	zinc finger, CCHC domain containing 4	NM_024936	219917_at, 220472_at, 220473_s_at	NP_079212.2
GeneID.29945	ANAPC4	4	25,378,848	25,420,120	41,272	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6051	240	in gene	0	1	0	14	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ANAPC4	ANAPC4, APC4	anaphase promoting complex subunit 4	NM_013367, hCT10862.3, hCT2326112.0	226917_s_at, 232524_x_at	NP_037499.2, EAW92839.1, EAW92840.1
GeneID.100506024	LOC100506024	4	25,906,314	25,908,462	2,148	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4210, 2_A375_pNL97_plus_lncRNA_AR..1..6052, 4_A375_EGR1..1..6530	-1776, -1938, -7106	upstream, upstream, upstream	1	1	1	12.5	16.5	14.5	2	4_A375_EGR1..1	21	Gene LOC100506024		hypothetical LOC100506024	XR_112625, XR_108553, XR_113628		
GeneID.389203	C4orf52	4	25,915,814	25,931,501	15,687	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4210, 2_A375_pNL97_plus_lncRNA_AR..1..6052, 4_A375_EGR1..1..6530	-5574, -5414, -248	upstream, upstream, upstream	1	1	1	12.5	16.5	14.5	2	4_A375_EGR1..1	21	Gene C4orf52	C4orf52	chromosome 4 open reading frame 52	NM_001145432	225014_at	NP_001138904.1
GeneID.3516	RBPJ	4	26,321,332	26,433,278	111,946	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4212, 1_A375_pNL7_minus_lncRNA_AR..1..4213, 2_A375_pNL97_plus_lncRNA_AR..1..6055	-420, 956, 1036	upstream, in gene, in gene	1	1	0	26	36	12	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene RBPJ	csl, RBPJ, RBPJK, CBF1, KBF2, IGKJRB, IGKJRB1, RBP-J, SUH, RBPSUH, MGC61669	recombination signal binding protein for immunoglobulin kappa J region	NM_203284, NM_203283, NM_005349, NM_015874, hCT1954500.1, hCT2326122.0, hCT2326123.0, hCT8168.3	207785_s_at, 211974_x_at	NP_976029.1, NP_976028.1, NP_005340.2, NP_056958.3, EAW92848.1, EAW92849.1, EAW92846.1, EAW92847.1
GeneID.55296	TBC1D19	4	26,585,546	26,756,917	171,371	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4214, 2_A375_pNL97_plus_lncRNA_AR..1..6056	-10, 150	upstream, in gene	1	1	0	23	26	8	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene TBC1D19	TBC1D19, FLJ11082	TBC1 domain family, member 19	NM_018317, hCT1968256.0, hCT8167.2	220260_at	NP_060787.2, EAW92851.1, EAW92852.1
GeneID.100506048	LOC100506048	4	26,861,246	26,862,221	975	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4215, 1_A375_pNL7_minus_lncRNA_AR..1..4216, 2_A375_pNL97_plus_lncRNA_AR..1..6057	2701, 141, 3053	downstream, in gene, downstream	1	1	0	17	14.5	10	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100506048		hypothetical LOC100506048	XR_112627, XR_112626, XR_108555, XR_108554, XR_113630, XR_113629		
GeneID.57620	STIM2	4	26,862,313	27,027,003	164,690	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4215, 1_A375_pNL7_minus_lncRNA_AR..1..4216, 2_A375_pNL97_plus_lncRNA_AR..1..6057	-2793, -233, -3145	upstream, upstream, upstream	1	1	0	17	14.5	10	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene STIM2	FLJ39527, STIM2, KIAA1482	stromal interaction molecule 2	NM_020860, NM_001169117, NM_001169118, hCT2326049.0, hCT2357600.0, hCT7622.3	225248_at, 225250_at, 234140_s_at	NP_065911.3, NP_001162588.1, NP_001162589.1, EAW92853.1, EAW92854.1, EAW92855.1
GeneID.5099	PCDH7	4	30,722,037	31,148,423	426,386	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6063, 4_A375_EGR1..1..6532	-2805, -693	upstream, upstream	0	1	1	10.5	13.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene PCDH7	FLJ97161, BH-Pcdh, PCDH7, BHPCDH	protocadherin 7	NM_002589, NM_032456, NM_001173523, NM_032457, hCT2326070.0, hCT2326071.0, hCT2326072.0, hCT2326073.0, hCT2326074.0	205534_at, 205535_s_at, 210273_at, 210941_at, 226840_at	NP_002580.2, NP_115832.1, NP_001166994.1, NP_115833.2, EAW92863.1, EAW92864.1, EAW92861.1, EAW92862.1, EAW92865.1
GeneID.57495	KIAA1239	4	37,246,690	37,451,087	204,397	+	1	4_A375_EGR1..1..6534	62	in gene	0	0	1	6	5	24	1	4_A375_EGR1..1	24	Gene KIAA1239	KIAA1239		NM_001144990	230765_at	NP_001138462.1
GeneID.55286	C4orf19	4	37,455,552	37,595,132	139,580	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4225	23403	in gene	1	0	0	15	15	2	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene C4orf19	C4orf19, FLJ11017	chromosome 4 open reading frame 19	NM_001104629, NM_018302, hCT1640834.1, hCT1950224.1	219450_at	NP_001098099.1, NP_060772.2, EAW92882.1, EAW92883.1
GeneID.768211	RELL1	4	37,592,422	37,687,999	95,577	-	3	2_A375_pNL97_plus_lncRNA_AR..1..6068, 2_A375_pNL97_plus_lncRNA_AR..1..6069, 2_A375_pNL97_plus_lncRNA_AR..1..6070	57279, 38079, 287	in gene, in gene, in gene	0	1	0	14.67	24.33	4.33	3	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene RELL1	FLJ21778, RELL1, MGC50583	RELT-like 1	NM_001085399, NM_001085400	1554714_at, 226430_at	NP_001078868.1, NP_001078869.1
GeneID.55276	PGM2	4	37,828,282	37,864,559	36,277	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4226, 4_A375_EGR1..1..6535	262, 262	in gene, in gene	1	0	1	14	14	20	1	4_A375_EGR1..1	20	Gene PGM2	MSTP006, PGM2, FLJ10983	phosphoglucomutase 2	NM_018290, hCT30128.3	223738_s_at, 225366_at, 225367_at	NP_060760.2, EAW92886.1
GeneID.23216	TBC1D1	4	37,892,720	38,140,794	248,074	+	2	4_A375_EGR1..1..6536, 4_A375_EGR1..1..6537	-304, 215664	upstream, in gene	0	0	1	6.5	7	17	2	4_A375_EGR1..1	17	Gene TBC1D1	TBC1D1, KIAA1108, TBC1, TBC	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	NM_015173	1566713_a_at, 1569566_at, 212350_at, 214013_s_at, 227945_at	NP_055988.2
GeneID.79667	FLJ13197	4	38,614,322	38,666,249	51,927	-	2	2_A375_pNL97_plus_lncRNA_AR..1..6072, 4_A375_EGR1..1..6539	43873, 37673	in gene, in gene	0	1	1	6	12	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene FLJ13197		hypothetical FLJ13197	NR_026804, hCT2326621.0, hCT30270.3	1570414_x_at, 219871_at	EAW92894.1, EAW92893.1
GeneID.92689	FAM114A1	4	38,869,354	38,947,365	78,011	+	1	4_A375_EGR1..1..6540	502	in gene	0	0	1	12	12	18	1	4_A375_EGR1..1	18	Gene FAM114A1	Noxp20, FLJ33151, FAM114A1	family with sequence similarity 114, member A1	NM_138389, NR_033290, hCT1950693.1, hCT30266.3	213455_at, 226697_at	NP_612398.2, EAW92904.1, EAW92903.1
GeneID.693159	MIR574	4	38,869,653	38,869,748	95	+	1	4_A375_EGR1..1..6540	203	downstream	0	0	1	12	12	18	1	4_A375_EGR1..1	18	Gene MIR574	MIR574, MIRN574, hsa-mir-574	microRNA 574	NR_030300		
GeneID.5981	RFC1	4	39,289,076	39,367,995	78,919	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6074	123	in gene	0	1	0	16	15	15	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene RFC1	MHCBFB, A1, RFC, RECC1, MGC51786, RFC140, RFC1, PO-GA	replication factor C (activator 1) 1, 145kDa	NM_002913, hCT2350365.0, hCT2357565.0, hCT29790.3	208021_s_at, 208133_at, 209085_x_at	NP_002904.3, EAW92922.1, EAW92923.1, EAW92924.1
GeneID.152831	KLB	4	39,408,473	39,453,153	44,680	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4228, 2_A375_pNL97_plus_lncRNA_AR..1..6075, 4_A375_EGR1..1..6541	52103, 52039, 52199	downstream, downstream, downstream	1	1	1	31	28	17	1	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene KLB	KLB, BKL, MGC142213	klotho beta	NM_175737, hCT29793.4	235708_at, 244276_at	NP_783864.1, EAW92925.1
GeneID.6133	RPL9	4	39,455,744	39,460,568	4,824	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4228, 2_A375_pNL97_plus_lncRNA_AR..1..6075, 4_A375_EGR1..1..6541	-8, 56, -104	upstream, in gene, upstream	1	1	1	31	28	17	1	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene RPL9	RPL9P9, RPL9P7, RPL9P8, RPL9, MGC15545, FLJ27456, DKFZp313J1510, NPC-A-16, L9	ribosomal protein L9	NM_001024921, NM_000661, hCT1950690.1, hCT1981484.2, hCT1981485.2, hCT2326519.1, hCT2326522.1, hCT28694.3	200032_s_at	NP_001020092.1, NP_000652.2, EAW92926.1, EAW92927.1, EAW92929.1, EAW92930.1, EAW92928.1, EAW92931.1
GeneID.11019	LIAS	4	39,460,665	39,479,273	18,608	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4228, 2_A375_pNL97_plus_lncRNA_AR..1..6075, 4_A375_EGR1..1..6541	-89, -153, 7	upstream, upstream, in gene	1	1	1	31	28	17	1	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene LIAS	LS, LAS, MGC23245, HUSSY-01, LIP1, LIAS	lipoic acid synthetase	NM_194451, NM_006859, hCT2326294.0, hCT2357568.0, hCT29798.2	214045_at	NP_919433.1, NP_006850.2, EAW92932.1, EAW92933.1, EAW92934.1
GeneID.7358	UGDH	4	39,500,375	39,529,218	28,843	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4229, 2_A375_pNL97_plus_lncRNA_AR..1..6076, 4_A375_EGR1..1..6542	-158, -222, 366	upstream, upstream, in gene	1	1	1	20	27	20	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene UGDH	UDP-GlcDH, UGDH, UDPGDH, UGD, GDH	UDP-glucose dehydrogenase	NM_001184700, NM_001184701, NM_003359, hCT2326516.0, hCT2357583.0, hCT29797.3	203343_at	NP_001171629.1, NP_001171630.1, NP_003350.1, EAW92936.1, EAW92937.1, EAW92938.1
GeneID.201895	C4orf34	4	39,552,550	39,640,481	87,931	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4230	-810	upstream	1	0	0	15	14	10	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene C4orf34	FLJ13289, C4orf34	chromosome 4 open reading frame 34	NM_174921, hCT1965808.2, hCT2357577.0, hCT29796.4	222336_at, 224990_at	NP_777581.1, EAW92942.1, EAW92940.1, EAW92941.1
GeneID.3093	UBE2K	4	39,699,664	39,784,412	84,748	+	1	4_A375_EGR1..1..6543	72112	in gene	0	0	1	5	4	19	1	4_A375_EGR1..1	19	Gene UBE2K	E2-25K, HIP2, UBE2K, DKFZp564C1216, LIG, DKFZp686J24237, HYPG	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	NM_005339, NM_001111112, NM_001111113, hCT1950891.1, hCT1950892.1, hCT1965805.1, hCT2357573.0, hCT29795.3	202346_at, 202347_s_at	NP_005330.1, NP_001104582.1, NP_001104583.1, EAW92946.1, EAW92948.1, EAW92949.1, EAW92947.1, EAW92950.1
GeneID.23244	PDS5A	4	39,824,483	39,979,576	155,093	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4231, 2_A375_pNL97_plus_lncRNA_AR..1..6077	8, -40	in gene, upstream	1	1	0	45	42	6	1	1_A375_pNL7_minus_lncRNA_AR..1	45	Gene PDS5A	PDS5A, PIG54, MGC131948, DKFZp686B19246, FLJ41012, SCC-112, MGC161503, KIAA0648	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	NM_001100399, NM_001100400, hCT2326508.0, hCT2326509.0, hCT2357572.0, hCT29794.3	212138_at, 212140_at, 213983_s_at, 213984_at	NP_001093869.1, NP_001093870.1, EAW92952.1, EAW92953.1, EAW92954.1, EAW92955.1
GeneID.55728	N4BP2	4	40,058,524	40,157,028	98,504	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4232, 2_A375_pNL97_plus_lncRNA_AR..1..6078	-892, -876	upstream, upstream	1	1	0	17	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene N4BP2	KIAA1413, B3BP, N4BP2, FLJ10680	NEDD4 binding protein 2	NM_018177, hCT2326304.0, hCT2326305.0, hCT28816.3	231996_at	NP_060647.2, EAW92959.1, EAW92957.1, EAW92958.1
GeneID.54502	RBM47	4	40,425,272	40,631,883	206,611	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6080	75	in gene	0	1	0	14	18	5	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene RBM47	RBM47, DKFZp686F02235, FLJ21643, NET18, FLJ21344, FLJ20273	RNA binding motif protein 47	NM_019027, NM_001098634, hCT1950686.1, hCT22910.2, hCT2326501.0, hCT2326504.0, hCT2326505.0, hCT2357598.0	218035_s_at, 222496_s_at, 229421_s_at, 229439_s_at, 229440_at	NP_061900.2, NP_001092104.1, EAW92965.1, EAW92967.1, EAW92968.1, EAW92969.1, EAW92964.1, EAW92966.1
GeneID.79730	NSUN7	4	40,751,914	40,812,002	60,088	+	1	4_A375_EGR1..1..6544	-74	upstream	0	0	1	4	3	17	1	4_A375_EGR1..1	17	Gene NSUN7	NSUN7, FLJ14001	NOP2/Sun domain family, member 7	NM_024677, hCT1950887.0, hCT2343313.1, hCT23485.4, hCT2349385.0	220194_at, 238983_at	NP_078953.3, EAW92971.1, EAW92970.1, EAW92972.1, EAW92973.1
GeneID.323	APBB2	4	40,812,044	41,216,635	404,591	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4234, 2_A375_pNL97_plus_lncRNA_AR..1..6081, 2_A375_pNL97_plus_lncRNA_AR..1..6082, 2_A375_pNL97_plus_lncRNA_AR..1..6083	305227, 316923, 123, -2064	in gene, in gene, in gene, upstream	1	1	0	16.75	19.25	8	4	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene APBB2	FE65L1, APBB2, MGC35575, FE65L, DKFZp434E033	amyloid beta (A4) precursor protein-binding, family B, member 2	NM_173075, NM_004307, NM_001166050, NM_001166051, NM_001166052, NM_001166053, NM_001166054, hCT2357592.0, hCT2357593.0, hCT24282.3	213419_at, 216747_at, 216750_at, 40148_at	NP_775098.2, NP_004298.1, NP_001159522.1, NP_001159523.1, NP_001159524.1, NP_001159525.1, NP_001159526.1, EAW92975.1, EAW92976.1, EAW92977.1
GeneID.8929	PHOX2B	4	41,746,099	41,750,987	4,888	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4235, 4_A375_EGR1..1..6545	14411, -2213	downstream, upstream	1	0	1	11	9.5	10	2	4_A375_EGR1..1	18	Gene PHOX2B	PMX2B, PHOX2B, NBPhox, NBLST2	paired-like homeobox 2b	NM_003924, hCT23489.1	207009_at	NP_003915.2, EAW92989.1
GeneID.285429	DCAF4L1	4	41,983,713	41,988,484	4,771	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6084	8631	downstream	0	1	0	21	20	14	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene DCAF4L1	MGC126021, WDR21B, DCAF4L1, MGC126022	DDB1 and CUL4 associated factor 4-like 1	NM_001029955, hCT1643188.3	1562209_at, 233491_at	NP_001025126.2, EAW92995.1
GeneID.10463	SLC30A9	4	41,992,523	42,089,551	97,028	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6084	21	in gene	0	1	0	21	20	14	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SLC30A9	GAC63, HUEL, ZNT9, C4orf1, SLC30A9	solute carrier family 30 (zinc transporter), member 9	NM_006345, hCT1640889.3, hCT2326233.0, hCT2326235.0, hCT2357597.0	202614_at	NP_006336.3, EAW92999.1, EAW92996.1, EAW92997.1, EAW92998.1
GeneID.10396	ATP8A1	4	42,410,390	42,659,122	248,732	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4236, 2_A375_pNL97_plus_lncRNA_AR..1..6085	-238, -302	upstream, upstream	1	1	0	37	27	12	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene ATP8A1	ATPP2, MGC26327, ATPIA, MGC130042, MGC130043, ATP8A1, ATPASEII	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	NM_006095, NM_001105529, hCT1950326.1, hCT2326283.0	1569773_at, 210192_at	NP_006086.1, NP_001098999.1, EAW93003.1, EAW93004.1
GeneID.60558	GUF1	4	44,680,433	44,702,697	22,264	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6086	15	in gene	0	1	0	13	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene GUF1	GUF1, FLJ13220, EF-4	GUF1 GTPase homolog (S. cerevisiae)	NM_021927, hCT2326193.0, hCT24099.3	218884_s_at, 222770_s_at	NP_068746.2, EAW93018.1, EAW93017.1
GeneID.54951	COMMD8	4	47,452,815	47,465,676	12,861	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6087	140	in gene	0	1	0	13	22	12	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene COMMD8	FLJ20502, COMMD8	COMM domain containing 8	NM_017845, hCT1950968.1, hCT2326368.0	218351_at	NP_060315.1, EAW93033.1, EAW93034.1
GeneID.10699	CORIN	4	47,596,018	47,840,059	244,041	-	1	4_A375_EGR1..1..6549	475	in gene	0	0	1	10	7	15	1	4_A375_EGR1..1	15	Gene CORIN	MGC119742, ATC2, TMPRSS10, Lrp4, CRN, CORIN	corin, serine peptidase	NM_006587, hCT1950965.1, hCT2326361.0	220356_at, 239260_at, 239261_s_at	NP_006578.2, EAW93038.1, EAW93039.1
GeneID.100506842	LOC100506842	4	47,842,139	47,844,789	2,650	-	1	4_A375_EGR1..1..6549	5205	downstream	0	0	1	10	7	15	1	4_A375_EGR1..1	15	Gene LOC100506842		hypothetical LOC100506842	XR_112632, XR_108546, XR_113620		
GeneID.152518	NFXL1	4	47,849,257	47,916,633	67,376	-	2	4_A375_EGR1..1..6549, 4_A375_EGR1..1..6550	77049, 265	downstream, in gene	0	0	1	13	12	15.5	2	4_A375_EGR1..1	18	Gene NFXL1	HOZFP, NFXL1, URCC5, FLJ16294	nuclear transcription factor, X-box binding-like 1	NM_152995, hCT1957698.1, hCT2326377.0, hCT2326378.0, hCT2357578.0, hCT2357579.0, hCT2357580.0	227220_at	NP_694540.3, EAW93044.1, EAW93041.1, EAW93042.1, EAW93045.1, EAW93046.1, EAW93043.1
GeneID.285527	FRYL	4	48,499,380	48,782,316	282,936	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4238, 2_A375_pNL97_plus_lncRNA_AR..1..6088	268, 204	in gene, in gene	1	1	0	19	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene FRYL	FRYL, KIAA0826, FLJ16177, DKFZp686E205	FRY-like	NM_015030	1554260_a_at, 1562625_at, 1562650_at, 1563687_a_at, 212546_s_at, 212548_s_at	NP_055845.1
GeneID.54940	OCIAD1	4	48,833,060	48,863,834	30,774	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4239, 2_A375_pNL97_plus_lncRNA_AR..1..6089	-198, 92	upstream, in gene	1	1	0	18	22	12	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene OCIAD1	OCIA, MGC111072, FLJ20455, ASRIJ, TPA018, OCIAD1	OCIA domain containing 1	NM_017830, NM_001079839, NM_001079840, NM_001079841, NM_001168254, NM_001079842, hCT1641699.3, hCT1957674.1, hCT1957676.1, hCT1957677.1	223010_s_at, 223011_s_at, 232644_x_at, 235537_at, 239748_x_at	NP_060300.1, NP_001073308.1, NP_001073309.1, NP_001073310.1, NP_001161726.1, NP_001073311.2, EAW93070.1, EAW93071.1, EAW93072.1, EAW93073.1
GeneID.23142	DCUN1D4	4	52,709,276	52,783,003	73,727	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6090	60036	downstream	0	1	0	11	15	4	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene DCUN1D4	KIAA0276, FLJ42355, DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	NM_001040402, NM_015115, hCT12509.3, hCT1967380.1, hCT2359050.0, hCT2359051.0, hCT2359052.0	212851_at, 212853_at, 212855_at	NP_001035492.1, NP_055930.2, EAX05425.1, EAX05426.1, EAX05427.1, EAX05428.1, EAX05424.1
GeneID.57291	KIAA0114	4	53,578,621	53,580,305	1,684	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6091	67	in gene	0	1	0	10	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene KIAA0114	KIAA00167, KIAA0114	KIAA0114	NR_024031	224870_at	
GeneID.677810	SNORA26	4	53,579,416	53,579,537	121	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6091	-726	upstream	0	1	0	10	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SNORA26	HBI-6, SNORA26	small nucleolar RNA, H/ACA box 26	NR_003016		
GeneID.152579	SCFD2	4	53,739,149	54,232,242	493,093	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4241, 2_A375_pNL97_plus_lncRNA_AR..1..6092	-46, -14	upstream, upstream	1	1	0	19	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SCFD2	FLJ39514, SCFD2, FLJ21060, STXBP1L1	sec1 family domain containing 2	NM_152540, hCT12606.3, hCT2358968.0	226923_at, 236834_at	NP_689753.2, EAX05442.1, EAX05443.1
GeneID.81608	FIP1L1	4	54,243,820	54,326,103	82,283	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4242, 2_A375_pNL97_plus_lncRNA_AR..1..6093	426, 100	in gene, in gene	1	1	0	12	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene FIP1L1	Rhe, DKFZp586K0717, FLJ33619, FIP1L1, hFip1	FIP1 like 1 (S. cerevisiae)	NM_030917, NM_001134937, NM_001134938, hCT1957989.1, hCT2326360.0, hCT2326361.0, hCT2326363.0, hCT2326364.0	1554424_at, 221007_s_at	NP_112179.2, NP_001128409.1, NP_001128410.1, EAX05445.1, EAX05446.1, EAX05449.1, EAX05447.1, EAX05448.1
GeneID.84708	LNX1	4	54,326,437	54,457,724	131,287	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6094	63516	in gene	0	1	0	12	18	3	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LNX1	PDZRN2, MPDZ, LNX1, LNX	ligand of numb-protein X 1	NM_032622, NM_001126328, hCT12609.3, hCT2326387.0	223811_s_at, 223812_s_at	NP_116011.2, NP_001119800.1, EAX05450.1, EAX05451.1



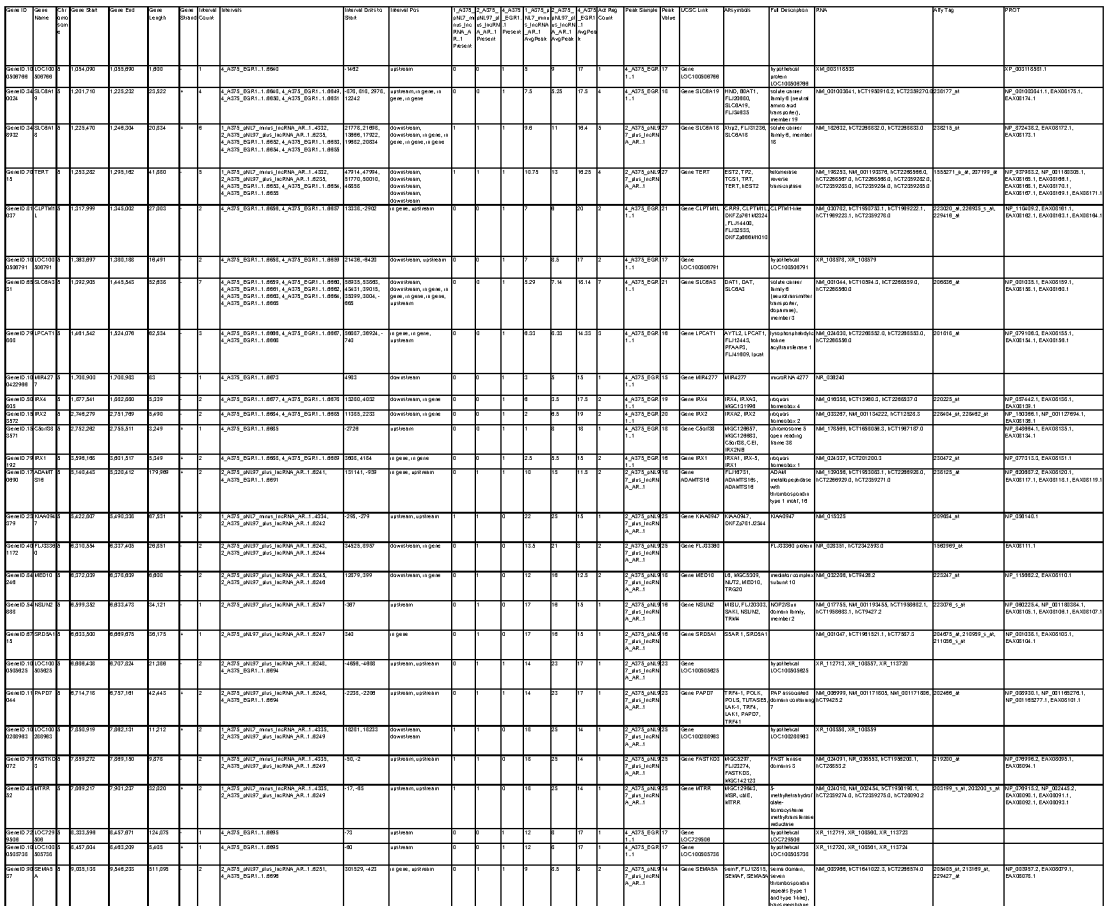


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_shN7_minLncRNA_R1_1 Percent	2_A375_shN7_plusLncRNA_R1_1 Percent	3_A375_1_shN7_minLncRNA_R1_1 Avg Peak	4_A375_2_shN7_plusLncRNA_R1_1 Avg Peak	5_A375_1_shEGFR_minLncRNA_R1_1 Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
GeneID:2352235	COQ2	4	84,164,977	84,206,987	41,990	-	1	2_A375_shN7_plus_lncRNA_R1_1:8124	211	sv gene	0	1	0	11	20	0	1	2_A375_shN7_plus_lncRNA_R1_1	620	Gene COQ2	COQ2, PLSM372, FLJ13014, CL640	coenzyme Q2 homolog, prenyltransferase (yeast)	NM_015697, NCT02372212.0, NCT02372110.0, NCT02372714.0, NCT02372716.0	213279_at	NP_056512.3, EAX05900.1, EAX05927.1, EAX05928.1, EAX05929.1
GeneID:161193510	HELQ	4	84,226,499	84,277,325	48,826	-	1	1_A375_shN7_minus_lncRNA_R1_1:4280	-127	upstream	1	0	0	17	12	12	1	1_A375_shN7_minus_lncRNA_R1_1	317	Gene HELQ	HELQ, HEL30B, WGC20998	helicase, POU-like	NM_139038, NCT02372508.0, NCT02372508.0, NCT02372707.0	1554041_s_at, 1554042_s_at, 230738_at, 241764_x_at, 242929_at	NP_569715.2, EAX05933.1, EAX05934.1, EAX05936.1
GeneID:8123023	MRPS11	4	84,277,118	84,302,929	25,811	+	1	1_A375_shN7_minus_lncRNA_R1_1:4280	34	sv gene	1	0	0	17	12	12	1	1_A375_shN7_minus_lncRNA_R1_1	317	Gene MRPS11	28S ribosomal protein S11, mitochondrial, MRP-S11, MRPS11C, CGI-134, FLJ11148	mitochondrial ribosomal protein S11C	NM_019097, NCT02371980.0, NCT02372180.0, NCT02372180.0, NCT02372181.0	220163_s_at, 222945_s_at, 229319_s_at	NP_037151.1, EAX05939.1, EAX05937.1, EAX05938.1, EAX05940.1
GeneID:84142	FAM173A	4	84,302,992	84,406,290	24,199	+	2	1_A375_shN7_minus_lncRNA_R1_1:4280, 2_A375_shN7_plus_lncRNA_R1_1:8125	29138,402	downstream, sv gene	1	1	0	13	13	7	2	1_A375_shN7_minus_lncRNA_R1_1	317	Gene FAM173A	FLJ11320, CCDC92, FLJ12842, FAM173A, MRN1, FLJ13614	family with sequence similarity 173, member A	NM_139074, NCT02372201.0, NCT02372082.0, NCT02372203.0	236821_s_at, 243543_s_at	NP_639773.2, EAX05943.1, EAX05941.1, EAX05942.1
GeneID:84602	AGPAT9	4	84,457,853	84,527,026	69,173	+	1	2_A375_shN7_plus_lncRNA_R1_1:8126	12171	sv gene	0	1	0	14	14	5	1	2_A375_shN7_plus_lncRNA_R1_1	614	Gene AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	1-acylglycerol-3-phosphate O-acyltransferase 9	NM_032717, NCT02372186.0, NCT02372186.0, NCT02372186.0	224460_s_at	NP_116106.2, EAX05944.1, EAX05945.1, EAX05946.1
GeneID:83478	ARHGAP24	4	85,096,256	85,203,623	107,368	+	1	1_A375_shN7_minus_lncRNA_R1_1:4361	550372	sv gene	1	0	0	15	13	1	1	1_A375_shN7_minus_lncRNA_R1_1	315	Gene ARHGAP24	p73H-associated protein, p73 H2-GAP, ARHGAP24, RC-GAP72, RCGAP72, DKFZp564B182, FLJ20277	Rho GTPase activating protein 24	NM_033423899, NM_001323810, NM_031383, NCT02372800.0, NCT02372081.0, NCT02372082.0	231050_s_at, 233422_s_at	NP_001307814.1, NP_001032707.2, NP_112553.2, EAX05949.1, EAX05946.1, EAX05961.1
GeneID:42144	AFF1	4	87,896,154	88,082,308	186,032	+	2	2_A375_shN7_plus_lncRNA_R1_1:8127, 3_A375_EGR1_1:8571	72226,71910	sv gene, cr gene	0	1	1	15	16	19	1	4_A375_EGR1_1	319	Gene AFF1	MGC134369, AF4/FMR2 family, member 1	AF4/FMR2 family, member 1	NM_005935, NM_001169893, NCT16393251, NCT02369503, NCT02369504.0	201924_at, 211028_s_at, 213441_x_at	NP_005926.1, NP_001160165.1, EAX05978.1, EAX05980.1
GeneID:83539	NUDT9	4	88,343,725	88,379,499	35,774	+	2	1_A375_shN7_minus_lncRNA_R1_1:4282, 2_A375_shN7_plus_lncRNA_R1_1:8126	0,-39	sv gene, upstream	1	1	0	14	22	5	1	2_A375_shN7_plus_lncRNA_R1_1	622	Gene NUDT9	NUDT16, NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	NM_199332, NM_024047, NCT16477727.2, NCT19651651.1, NCT23559955.0	219229_at	NP_742155.1, NP_076932.1, EAX05995.1, EAX05993.1, EAX05990.1
GeneID:84555	MEPE	4	89,042,580	89,067,989	25,409	+	1	2_A375_shN7_plus_lncRNA_R1_1:8129	22825	sv gene	0	1	0	10	15	0	1	2_A375_shN7_plus_lncRNA_R1_1	615	Gene MEPE	MEPE, OF45	matrix extracellular phosphoglycoprotein	NM_031164994, NM_001164955, NM_031164998, NM_001164997, NM_020302, NCT19644951.1, NCT23727342.1, NCT29783.1	221150_at	NP_001171923.1, NP_001171924.1, NP_064585.1, NP_001171923.1, NP_001171926.1, EAX06031.1, EAX06032.1, EAX06033.1
GeneID:162972926	PPM1K	4	89,161,531	89,205,956	44,357	-	1	2_A375_shN7_plus_lncRNA_R1_1:8130	926	sv gene	0	1	0	14	17	6	1	2_A375_shN7_plus_lncRNA_R1_1	617	Gene PPM1K	bA395E8.2, PPM1K, PP2Cm, PTMP, DKFZp667B054, PP2Cmitoch, DKFZp761G059, MPTMP	protein phosphatase 1K (PP2C domain containing)	NM_152542, NCT19644194.2, NCT23429286.0, NCT29307.4	235081_at, 244011_at	NP_689733.5, EAX06004.1, EAX06015.1, EAX06016.1
GeneID:8554955	HERC6	4	89,299,991	89,364,349	64,358	+	1	1_A375_shN7_minus_lncRNA_R1_1:4283	429	sv gene	1	0	0	15	15	10	1	1_A375_shN7_minus_lncRNA_R1_1	15	Gene HERC6	FLJ39837, HERC6	hect domain and RLD 6	NM_017912, NM_001165156, NCT23729364.0, NCT23729365.0	1562765_at, 1565858_at, 1565859_at	NP_060382.5, NP_001156955.1, EAX06016.1, EAX06018.1
GeneID:8442992	PIGY	4	89,442,135	89,444,955	2,820	-	1	2_A375_shN7_plus_lncRNA_R1_1:8131	-89	upstream	0	1	0	15	15	5	1	2_A375_shN7_plus_lncRNA_R1_1	615	Gene PIGY	PIGY, MGC14199, PREY, PIG-Y	phosphatidylinositol glycan anchor biosynthesis, class Y	NM_032908, NM_001042818, NCT03309.3	224860_at, 224861_at	NP_116755.1, NP_001038051.1, EAX06021.1
GeneID:10144	FAM193A	4	89,847,106	89,976,323	537,217	+	1	1_A375_shN7_minus_lncRNA_R1_1:4284	2991107	sv gene	1	0	0	20	20	2	1	1_A375_shN7_minus_lncRNA_R1_1	320	Gene FAM193A	FAM193A1, FAM193A, FLJ39362, WGC103531	family with sequence similarity 193, member A	NM_014955, NM_001013043	1569824_at, 1569825_s_at, 202972_s_at, 202973_s_at, 217047_s_at	NP_055992.2, NP_001010043.1
GeneID:731201282	LOC731202	4	90,031,856	90,033,424	1,569	+	1	2_A375_shN7_plus_lncRNA_R1_1:8132	980	sv gene	0	1	0	12	16	10	1	2_A375_shN7_plus_lncRNA_R1_1	616	Gene LOC731202		hypothetical LOC731202	XM_001717185, XM_037717170, XM_001129094		XP_001717247.1, XP_037717222.1, XP_001129094.1
GeneID:8611968	TIG02	4	90,033,969	90,036,052	2,084	+	1	2_A375_shN7_plus_lncRNA_R1_1:8132	-1764	upstream	0	1	0	12	16	10	1	2_A375_shN7_plus_lncRNA_R1_1	616	Gene TIG02	DKFZp667D1020, TIG02	tigger transposable element-derived 2	NM_145715, XCT16344148.0	229983_at	NP_660761.1, EAX06031.1
GeneID:4764	ATOH1	4	94,750,976	94,751,142	1,054	+	1	4_A375_EGR1_1:8572	5550	downstream	0	0	1	7	1	15	1	4_A375_EGR1_1	15	Gene ATOH1	ATOH1, ATH1, MATH-1, BHLH14, HATH1	atonal homolog 1 (Drosophila)	NM_005172, NCT16458619.0	221326_at	NP_005163.1, EAX06049.1
GeneID:8893333	UNC5C	4	95,053,653	95,470,391	399,738	+	1	4_A375_EGR1_1:8573	-423	upstream	0	0	1	3	10	18	1	4_A375_EGR1_1	16	Gene UNC5C	UNC5C, UNC5H3	unc-5 homolog C (C. elegans)	NM_003728, NCT19382219.1, NCT23559011.0	1558241_at, 1558342_s_at	NP_003727.3, EAX06061.1, EAX06062.1
GeneID:2355533	Cdc42	4	95,460,925	95,664,391	564,266	-	1	2_A375_shN7_plus_lncRNA_R1_1:8133	489903	sv gene	0	1	0	16	13	5	1	2_A375_shN7_plus_lncRNA_R1_1	613	Gene Cdc42	MGC4549, Cdc42	cell division cycle 42 (GTP binding protein, 25kDa)	NM_174152, NCT23277961.1, NCT23560640.0	1558096_at	NP_776121.1, EAX06067.1, EAX06066.1
GeneID:5893810	RAP1GDS1	4	99,162,527	99,285,012	122,485	+	1	4_A375_EGR1_1:8574	-271	upstream	0	0	1	7	5	15	1	4_A375_EGR1_1	15	Gene RAP1GDS1	MGC118881, SmgGDS, RHP120021, MGC118889, GDS1	RAP1, GTP-GDP dissociation stimulator 1	NM_001100426, NM_021159, NM_001100427, NM_001109425, NM_001109429, NM_001109430, NCT19382161.1, NCT19382171.1, NCT19382181.1, NCT19382191.1, NCT23559302.0, NCT23629.2	209444_at, 217437_s_at, 237696_at	NP_001093897.1, NP_066932.3, NP_001093895.1, NP_001093896.1, NP_001093900.1, EAX06085.1, EAX06086.1, EAX06089.1, EAX06090.1, EAX06075.1, EAX06077.1, EAX06072.1
GeneID:2355173	METAP1	4	99,916,786	99,963,960	47,172	+	1	1_A375_shN7_minus_lncRNA_R1_1:4285	-404	upstream	1	0	0	17	13	4	1	1_A375_shN7_minus_lncRNA_R1_1	617	Gene METAP1	D12S2451E, MNP1A, 60kDa, METAP1, MetAP1A	methionyl aminopeptidase 1	NM_015143, NCT23527446.0, NCT23727.3	212673_at	NP_056958.2, EAX06052.1, EAX06053.1
GeneID:8889549	MAPK8IP3	4	100,799,493	100,815,703	16,206	-	1	2_A375_shN7_plus_lncRNA_R1_1:8134	279	sv gene	0	1	0	8	16	4	1	2_A375_shN7_plus_lncRNA_R1_1	618	Gene MAPK8IP3	MAPK8IP3, JIP3, JIP-3, KIAA0783, MAPBP, Rag-ulating, MP1, MAP2K7IP1	MAPK scaffold protein 1	NM_201270, NR_024176, XCT19882291.1, XCT29954.2	217971_at	NP_598035.1, EAX06112.1, EAX06112.1, EAX06112.1
GeneID:7982	DNAJB14	4	100,830,710	100,887,879	57,169	-	1	2_A375_shN7_plus_lncRNA_R1_1:8134	53633	downstream	0	1	0	8	16	4	1	2_A375_shN7_plus_lncRNA_R1_1	618	Gene DNAJB14	FKSG48B3, DNAJB14, FLJ14251, MGC22187, EG:BAC22187.1	DnaJ (Hsp40) homolog, subfamily B, member 14	NM_001031731, XCT19882113.2, NCT23727397.1, NCT23727399.1, NCT23599030.0	219237_s_at, 222580_s_at	NP_001029859.1, EAX06134.1, EAX06115.1, EAX06116.1, EAX06117.1
GeneID:4790	NFKB1	4	103,422,469	103,538,459	115,991	+	1	4_A375_EGR1_1:8575	748	sv gene	1	0	0	8	16	1	1	4_A375_EGR1_1	16	Gene NFKB1	NFKB-p105, KBF1, NF-kappa-B, p50, NFKB-p105, NF-kappaB, NFKB1, EBP-1, p105, DKFZp686C0121, MGC34151	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	NM_003998, NM_001165412, NCT23724593.0, NCT23599253.0, NCT30567.2	209239_at	NP_003989.2, NP_001158054.1, EAX06134.1, EAX06133.1, EAX06136.1
GeneID:4144	MAN1B1	4	103,532,843	103,692,151	159,308	-	1	2_A375_shN7_plus_lncRNA_R1_1:8135	116839	sv gene	0	1	0	11	15	5	1	2_A375_shN7_plus_lncRNA_R1_1	615	Gene MAN1B1	MAN1, MAN1B	mannosidase, alpha A, lysosomal	NM_016219, NCT23594.2	203779_at	NP_057303.3, EAX06137.1
GeneID:3308	NHEDC2	4	103,948,552	103,996,170	51,618	-	1	4_A375_EGR1_1:8576	282	sv gene	0	0	1	9	10	17	1	4_A375_EGR1_1	17	Gene NHEDC2	NHEDC2, NHE10, NHA2, FLJ20954	Na+/H+ exchanger domain containing 2	NM_176533, NCT19521171.2, NCT19521712.2, NCT23599223.0	1564748_at, 229491_at	NP_549153.2, EAX06159.1, EAX06160.1, EAX06161.1
GeneID:3098	BDH2	4	103,996,702	104,021,024	22,242	-	1	4_A375_EGR1_1:8576	23138	downstream	0	0	1	9	10	17	1	4_A375_EGR1_1	17	Gene BDH2	SDR15C1, UCP4, ER-MRP, SMR3035, PRO32823, DHRS6, FLJ12281, BDH2	3-hydroxybutyrate dehydrogenase, type 2	NM_020139, XCT23280961.1, NCT23280971.1, NCT23280971.1, NCT23410787.0, NCT23599353.0	210353_s_at, 231555_at	NP_064524.3, EAX06164.1, EAX06165.1, EAX06165.1, EAX06167.1, EAX06166.1, EAX06166.1
GeneID:8422	CENPE	4	104,028,960	104,119,598	90,603	-	2	1_A375_shN7_minus_lncRNA_R1_1:4287, 2_A375_shN7_plus_lncRNA_R1_1:8136	-62,-68	upstream, upstream	1	1	0	24	29	8	1	1_A375_shN7_minus_lncRNA_R1_1	629	Gene CENPE	CENPE, KIF10	centromere protein E, 312 kDa	NM_001813, NCT23727998.0, NCT23727997.1, NCT23599039.0	205046_at	NP_001804.2, EAX06169.1, EAX06170.1, EAX06171.1
GeneID:5864	PPA2	4	106,290,354	106,336,227	104,592	+	1	2_A375_shN7_plus_lncRNA_R1_1:8137	43	sv gene	0	1	0	16	17	4	1	2_A375_shN7_plus_lncRNA_R1_1	617	Gene PPA2	PPA2, HSPC124, MGC49690, FLJ30499, SIDK338	pyrophosphatase (inorganic) 2	NM_176566, NM_006903, NM_176566, NM_176567, NCT12428.2, NCT19522411.1, NCT19522421.1, NCT23727434.0	1554499_s_at, 1559256_at, 1559258_x_at, 220741_s_at, 220396_at	NP_789845.1, NP_008829.2, NP_789842.2, NP_789843.2, EAX06180.1, EAX06184.1, EAX06181.1, EAX06182.1, EAX06183.1
GeneID:3117	INT512	4	106,603,764	106,629,651	26,007	-	1	4_A375_EGR1_1:8577	-7	upstream	0	0	1	13	10	21	1	4_A375_EGR1_1	21	Gene INT512	INT12, SIB1522, INT512, IFAP22	integrator complex subunit 12	NM_020395, NM_001142471, NCT23377200.0, NCT23377220.0	210816_at	NP_065126.2, NP_001139943.1, EAX06189.1, EAX06190.1
GeneID:2597	GSTCD	4	106,629,941	106,795,552	165,941	+	1	4_A375_EGR1_1:8577	-55	upstream	0	0	1	13	10	21	1	4_A375_EGR1_1	21	Gene GSTCD	GSTCD5, FLJ13275, DKFZp686I0215	glutathione S-transferase, C-terminal domain containing	NM_001301720, NM_022491, NCT19164559.0, NCT19164592.0, NCT23599294.0	1554018_at, 220865_at, 235807_at	NP_001288649.2, NP_072087.2, EAX06191.1, EAX06192.1, EAX06193.1
GeneID:3733	NPNT	4	106,816,997	106,892,026	76,231	+	1	2_A375_shN7_minus_lncRNA_R1_1:4288	20167	sv gene	1	0	0	16	11	2	1	1_A375_shN7_minus_lncRNA_R1_1	616	Gene NPNT	POEM, NPNT, EGFL6	preferentially expressed in melanocytes	NM_031033047, NM_001164690, NM_001164691, NM_001164692, NM_001164693, NCT23215370.0, NCT23215371.0, NCT23599334.0	223911_at, 224757_at	NP_001032219.1, NP_001171619.1, NP_001171620.1, NP_001171621.1, NP_001171622.1, EAX06197.1, EAX06198.1, EAX06199.1
GeneID:3952	HADH	4	106,910,870	106,936,331	45,461	+	1	2_A375_shN7_plus_lncRNA_R1_1:8139	256	sv gene	0	1	0	13	10	4	1	2_A375_shN7_plus_lncRNA_R1_1	618	Gene HADH	SCHAD, HHDHSC, MSCHAD, HHDH, MSCHAD, HHD, HHF4, HHDH1, MGC3932	hydroxyacyl-CoA dehydrogenase	NM_005327, NCT19382.3, NCT19522.2, NCT19522.3, NCT27811.0	201853_s_at, 201854_s_at, 211389_s_at	NP_005318.1, EAX06210.1, EAX06219.1, EAX06220.1
GeneID:1761	LEF1	4	108,998,701	109,090,112	121,411	+	1	4_A375_EGR1_1:8578	1344	sv gene	0	0	1	4	6	17	1	4_A375_EGR1_1	17	Gene LEF1	FLJ46370, DKFZp686H0715, TCF1, TCF1ALPHA	lymphoid enhancer-binding factor 1	NM_016269, NM_001130713, NM_001130714, NM_001166119, XCT12159.2, XCT19522291.1, NCT19522330.1, NCT23777160.0, NCT23599330.0	210949_s_at, 221557_s_at, 221558_s_at	NP_057353.1, NP_001124193.1, NP_001124194.1, NP_001159931.1, EAX06231.1, EAX06234.1, EAX06222.1, EAX06223.1, EAX06225.1
GeneID:1516	LOC84151516	4	109,098,961	109,097,998	6,935	+	1	4_A375_EGR1_1:8578	67	sv gene	0	0	1	4	6	17	1	4_A375_EGR1_1	17	Gene LOC84151516		hypothetical LOC84151516	NR_029370, NR_029374	243282_s_at, 243583_at	
GeneID:5503	CSTC	4	109,097,741	109,098,976	71,237	+	1	2_A375_shN7_plus_lncRNA_R1_1:8141	67	sv gene	0	1	0	9	16	10	1	2_A375_shN7_plus_lncRNA_R1_1	618	Gene CSTC	CSTC, DC2	oligosaccharyltransferase complex subunit (catalytic)	NM_031227, NCT12161.2, NCT19522322.1	223801_at	NP_598355.1, EAX06233.1, EAX06234.1
GeneID:5703	COL3A1	4	109,734,172	110,233,799	499,627	-	2	1_A375_shN7_minus_lncRNA_R1_1:4289, 2_A375_shN7_plus_lncRNA_R1_1:8142, 4_A375_EGR1_1:8579	420,207, 441143, 316119	sv gene, cr gene, cr gene	1	1	1	10.33	10	7	3	1_A375_shN7_minus_lncRNA_R1_1	618	Gene COL3A1	COL3A1, CLAC	collagen, type XXV, alpha 1	NM_000090, NM_009119, NCT19522.4, NCT23504510.0, NCT23504534.0	1553293_at, 224358_s_at, 224359_s_at	NP_000081.1, NP_032145.1, EAX06238.1, EAX06239.1, EAX06240.1
GeneID:8627	SEC24B	4	110,294,371	110,491,815	198,844	+	1	1_A375_shN7_minus_lncRNA_R1_1:4290	-75	upstream	1	0	0	13	10	5	1	1_A375_shN7_minus_lncRNA_R1_1	613	Gene SEC24B	SEC24B, SEC24	SEC24 family, member B (S. cerevisiae)	NM_006323, NM_001042754, NCT12127.3	202766_at	NP_006314.2, NP_001038199.1, EAX06241.1
GeneID:9	CASP8	4	110,809,765	110,834,629	24,844	+	1	4_A375_EGR1_1:8580	-161	sv gene	0	0	1	10	8	17	1	4_A375_EGR1_1	17	Gene CASP8	MCH5, CASP8	caspase 8, apoptosis-related cysteine peptidase	NM_032992, NM_001228, NCT12129.2, NCT19636411	202763_s_at, 211483_x_at	NP_116701.1, NP_001217.2, EAX06244.1, EAX06245.1
GeneID:5879	PLA2G12A	4	110,831,143	110,831,242	20,097	-	1	4_A375_EGR1_1:8580	29794	downstream	0	0	1	10	8	17	1	4_A375_EGR1_1	17	Gene PLA2G12A	PLA2G12A, PLA2G12, FLA2G12, ROSSY	phospholipase A2, group XIIA	NM_030821, NCT12122.4, NCT19522.5, NCT23504503.0, NCT23504534.0	221027_s_at, 223013_s_at	NP_110444.2, EAX06247.1, EAX06246.1
GeneID:5833	PITX2	4	111,538,979	111,598,508	59,529	-	2	1_A375_shN7_minus_lncRNA_R1_1:4271, 2_A375_shN7_plus_lncRNA_R1_1:8144, 3_A375_EGR1_1:8581	14060, 14106, -4118	sv gene, cr gene, upstream	1	1	1	10.5	12	9	2	1_A375_shN7_minus_lncRNA_R1_1	623	Gene PITX2	PITX2, PTX2, RIEG1, RIEG1.1, RIEG1.2, MRF1, MGC111022, MGC20144, RGS, RS, Bot1, RIEG, RGS, GDS, IDG2, IDG2, RIEG	paired-like homeodomain 2	NM_153426, NM_153427, NM_000325, NCT12511.2, NCT19522441.1, NCT19522451.1	207555_s_at	NP_700475.1, NP_700476.1, NP_000316.2, EAX06282.1, EAX06284.1
GeneID:8727	CAMK2D	4	114,372,165	114,692,883	320,696	+	1	2_A375_shN7_plus_lncRNA_R1_1:8142	69033	sv gene	1	0	0	16	10	0	1	2_A375_shN7_plus_lncRNA_R1_1	618	Gene CAMK2D	CAMK2D, MGC44911, DKFZp686I2356, CAMK-II, DKFZp686G2311	calcium/calmodulin-dependent protein kinase II delta	NM_001221, NM_172128, NM_172127, NM_172114, NM_172115, NM_172129, NCT19777.3, NCT19522451.1, NCT23559214.0, NCT23559310.0, NCT23559310.0, NCT23559321.0	224364_at, 225059_at, 225059_s_at, 230749_s_at, 231042_s_at, 231793_s_at	NP_001212.2, NP_742126.1, NP_742125.1, NP_742124.1, NP_742127.1, EAX06295.1, EAX06296.1, EAX06297.1, EAX06300.1, EAX06301.1
GeneID:5413	USP53	4	120,133,762	120,218,873	82,891	+	1	2_A375_shN7_plus_lncRNA_R1_1:8147	-3382	upstream	0	1	0	12	17	5	1	2_A375_shN7_plus_lncRNA_R1_1	617	Gene USP53	USP53, DKFZp761E141	ubiquitin specific peptidase 53	NM_019050, XCT22764268.0	218773_at, 233617_at, 237463_at	NP_061923.2, EAX07564.1
GeneID:100507308	LOC100507308	4	120,219,722	120,279,764	60,042	-	2	1_A375_shN7_minus_lncRNA_R1_1:4273, 2_A375_shN7_plus_lncRNA_R1_1:8145	-66,-66	upstream, upstream	1	1	0	45	87	11	1	2_A375_shN7_plus_lncRNA_R1_1	667	Gene LOC100507308		hypothetical LOC100507308	XR_109826, XR_113693		
GeneID:5845513	LOC645513	4	120,219,944	120,432,003	97,981	+	2	1_A375_shN7_minus_lncRNA_R1_1:4273, 2_A375_shN7_plus_lncRNA_R1_1:8145	-72,-72	upstream, upstream	1	1	0	45	87	11	1	2_A375_shN7_plus_lncRNA_R1_1	667	Gene LOC645513		hypothetical LOC645513	XR_112895, XR_109826, XR_113688	1566237_at, 1567758_at, 1567760_s_at, 1567761_at, 232955_at, 235956_at, 242303_at	

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:4085	MAD2L1	4	120,980,577	120,988,013	7,436	-	1	4_A375_EGR1..1..8583	-51	upstream	0	0	1	15	17	18	1	4_A375_EGR1..1	18	Gene MAD2L1	MAD2, MAD2L1, HSMAD2	MAD2 mitotic arrest deficient-like 1 (yeast)	NM_002358, hCT1957608.1, hCT1957609.1, hCT1982931.1, hCT28584.3	1554768_a_at, 203362_s_at	NP_002349.1, EAX05271.1, EAX05270.1, EAX05272.1, EAX05273.1
GeneID:11107	PRDM5	4	121,615,929	121,844,013	228,084	-	1	4_A375_EGR1..1..8584	82629	in gene	0	0	1	5	2	15	1	4_A375_EGR1..1	15	Gene PRDM5	PRDM5, PFM2	PR domain containing 5	NM_018699, hCT1957613.1, hCT1957614.1, hCT29936.3	1569508_at, 220792_at	NP_061169.2, EAX05269.1, EAX05267.1, EAX05268.1
GeneID:5393	EXOSC9	4	122,722,472	122,738,176	15,704	+	1	4_A375_EGR1..1..8585	22488	downstream	0	0	1	17	18	15	1	4_A375_EGR1..1	15	Gene EXOSC9	PM/Scl-75, RRP45, p5, PMSCL1, EXOSC9, Rrp45p, p8	exosome component 9	NM_005033, NM_001034194, hCT1958402.1, hCT1958403.1, hCT1958404.1, hCT2325582.0, hCT2358905.0, hCT30076.2	205061_s_at	NP_005024.2, NP_001029366.1, EAX05247.1, EAX05248.1, EAX05249.1, EAX05250.1, EAX05251.1, EAX05252.1
GeneID:890	CCNA2	4	122,737,599	122,745,068	7,469	-	1	4_A375_EGR1..1..8585	128	in gene	0	0	1	17	18	15	1	4_A375_EGR1..1	15	Gene CCNA2	CCNA2, CCN1, CCNA	cyclin A2	NM_001237, hCT30072.2	203418_at, 213226_at	NP_001228.1, EAX05246.1
GeneID:55212	BBS7	4	122,745,835	122,791,842	46,007	-	1	4_A375_EGR1..1..8585	46662	downstream	0	0	1	17	18	15	1	4_A375_EGR1..1	15	Gene BBS7	FLJ10715, BBS2L1, BBS7	Bardet-Biedl syndrome 7	NM_018190, NM_176824, hCT2325508.0, hCT30079.3	219688_at, 235007_at	NP_060660.2, NP_789794.1, EAX05244.1, EAX05245.1
GeneID:2247	FGF2	4	123,747,863	123,819,390	71,527	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8149	777	in gene	0	1	0	7	17	7	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene FGF2	BFGF, FGF2, HBGF-2, FGFB	fibroblast growth factor 2 (basic)	NM_002006, hCT28598.2	204421_s_at, 204422_s_at	NP_001997.5, EAX05222.1
GeneID:11162	NUDT6	4	123,813,799	123,844,123	30,324	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4274, 1_A375_pNL7_minus_lncRNA_AR..1..4275, 2_A375_pNL97_plus_lncRNA_AR..1..8150	443, -117, 411	in gene, upstream, in gene	1	1	0	22	23	11	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene NUDT6	bFGF, FGF-2, gfg, NUDT6, FGF2AS, FGF-AS, gfg-1, ASFGF2	nudix (nucleoside diphosphate linked moiety X)-type motif 6	NM_198041, NM_007083, hCT1958395.1, hCT2325428.0, hCT2325426.0, hCT2358899.0, hCT29425.4	220183_s_at, 230329_s_at	NP_932158.1, NP_009014.2, EAX05217.1, EAX05218.1, EAX05219.1, EAX05220.1, EAX05221.1
GeneID:166378	SPATA5	4	123,844,225	124,240,605	396,380	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4274, 1_A375_pNL7_minus_lncRNA_AR..1..4275, 2_A375_pNL97_plus_lncRNA_AR..1..8150	-545, 15, -513	upstream, in gene, upstream	1	1	0	22	23	11	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene SPATA5	SPATA5, SPAF, AFG2	spermatogenesis associated 5	NM_145207, hCT1958398.0, hCT2326494.0, hCT2326495.0, hCT2358937.0	241546_at	NP_660208.2, EAX05213.1, EAX05214.1, EAX05215.1, EAX05216.1
GeneID:79633	FAT4	4	126,237,567	126,414,087	176,520	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8152	1313	in gene	0	1	0	14	15	13	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene FAT4	FATJ, NBLA00548, CDHF14, FLJ23056, FAT-J, FAT4, FLJ77878, CDHR11	FAT tumor suppressor homolog 4 (Drosophila)	NM_024582, hCT2348137.0	219427_at	NP_078858.4, EAX05203.1
GeneID:256471	MFSD8	4	128,838,960	128,887,139	48,179	-	1	4_A375_EGR1..1..8586	115	in gene	0	0	1	5	7	14	1	4_A375_EGR1..1	14	Gene MFSD8	CLN7, MGC33302, MFSD8	major facilitator superfamily domain containing 8	NM_152778, hCT1817345.2, hCT1986207.1, hCT1986208.1	226282_at, 229509_at, 243407_at	NP_689991.1, EAX05195.1, EAX05193.1, EAX05194.1
GeneID:80167	C4orf29	4	128,886,461	128,952,468	66,007	+	1	4_A375_EGR1..1..8586	583	in gene	0	0	1	5	7	14	1	4_A375_EGR1..1	14	Gene C4orf29	MGC149227, FLJ21106, C4orf29, MGC149228	chromosome 4 open reading frame 29	NM_001039717, hCT1958341.1, hCT1958342.1, hCT1958343.1, hCT1989317.1	219980_at, 236240_at	NP_001034806.1, EAX05189.1, EAX05190.1, EAX05191.1, EAX05192.1
GeneID:100507487	LOC100507487	4	129,437,032	129,440,553	3,521	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4278	1992	in gene	1	0	0	18	9	2	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100507487		hypothetical LOC100507487	XR_112671, XR_109634, XR_113672		
GeneID:132320	SCLT1	4	129,805,152	130,014,764	209,612	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8154	92	in gene	0	1	0	9	18	5	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SCLT1	CAP-1A, CAP1A, FLJ36042, SCLT1, FLJ30655, MGC70542, hCAP-1A	sodium channel and clathrin linker 1	NM_144643, hCT2325298.0, hCT2325299.0, hCT2325300.0	1569190_at, 1569495_at, 236487_at	NP_653244.2, EAX05168.1, EAX05167.1, EAX05169.1
GeneID:132321	C4orf33	4	130,014,829	130,033,843	19,014	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8154	-157	upstream	0	1	0	9	18	5	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene C4orf33	C4orf33, FLJ33703	chromosome 4 open reading frame 33	NM_001099783, NM_173487, hCT1640614.2, hCT1958330.1, hCT1958331.1, hCT1980383.1, hCT1980384.1, hCT2358960.0	1552370_at, 1552372_at, 1552373_s_at	NP_001093253.1, NP_775758.2, EAX05161.1, EAX05164.1, EAX05165.1, EAX05166.1, EAX05162.1, EAX05163.1
GeneID:25819	CCRN4L	4	139,936,943	139,967,093	30,150	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8157	-271	upstream	0	1	0	10	14	12	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene CCRN4L	MGC142054, CCR4L, CCRN4L, MGC4120817, MGC142080, MGC78549, NOC	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	NM_012118, hCT1773626.2, hCT2325616.0, hCT2325618.0	1554283_at, 220671_at	NP_036250.2, EAX05129.1, EAX05130.1, EAX05131.1
GeneID:4717	NDUFC1	4	140,211,071	140,223,705	12,634	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8158	889	in gene	0	1	0	9	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NDUFC1	MGC138288, MGC126847, NDUFC1, MGC117464, KFYI	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	NM_001184986, NM_001184987, NM_001184988, NM_001184989, NM_001184990, NM_001184991, NM_002494, hCT29188.4	203478_at, 232146_at	NP_001171915.1, NP_001171916.1, NP_001171917.1, NP_001171918.1, NP_001171919.1, NP_001171920.1, NP_002485.1, EAX05121.1
GeneID:80155	NAA15	4	140,222,676	140,311,935	89,259	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8158	140	in gene	0	1	0	9	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NAA15	NARG1, TBDN100, NATH, NAA15, Ga19	N(alpha)-acetyltransferase 15, NatA auxiliary subunit	NM_057175, hCT1950433.1, hCT2325821.0, hCT2325823.0	1556381_at, 1556382_a_at, 219158_s_at, 222636_at, 222637_s_at, 226996_at	NP_476516.1, EAX05118.1, EAX05119.1, EAX05120.1
GeneID:80854	SETD7	4	140,427,192	140,477,577	50,385	-	2	2_A375_pNL97_plus_lncRNA_AR..1..8159, 4_A375_EGR1..1..8588	153, 9	in gene, in gene	0	1	1	11	16	13	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SETD7	KMT7, SET7/9, FLJ21193, SETD7, SET7, KIAA1717, SET9	SET domain containing (lysine methyltransferase) 7	NM_030648, hCT29187.2	224928_at	NP_085151.1, EAX05114.1
GeneID:55534	MAML3	4	140,637,545	141,075,233	437,688	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4280, 1_A375_pNL7_minus_lncRNA_AR..1..4281, 2_A375_pNL97_plus_lncRNA_AR..1..8160, 2_A375_pNL97_plus_lncRNA_AR..1..8161, 4_A375_EGR1..1..8589	58017, -175, 2897, 97, 3201	in gene, upstream, in gene, in gene, in gene	1	1	1	15.33	14.33	8.33	3	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MAML3	ERDA3, MAM2, TNRC3, GDN, MAM-2, CAGH3, MAML3	mastermind-like 3 (Drosophila)	NM_018717, hCT1950435.2	228508_at, 242794_at	NP_061187.2, EAX05107.1
GeneID:23158	TBC1D9	4	141,541,938	141,677,471	135,535	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4282, 4_A375_EGR1..1..8590	-385, 111263	upstream, in gene	1	0	1	10	8.5	15	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene TBC1D9	TBC1D9, MDR1, KIAA0882	TBC1 domain family, member 9 (with GRAM domain)	NM_015130, hCT2325236.0, hCT2325238.0, hCT29972.1	212956_at, 212960_at	NP_055945.2, EAX05093.1, EAX05092.1, EAX05094.1
GeneID:8821	INPP4B	4	142,949,181	143,767,604	818,423	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4283, 2_A375_pNL97_plus_lncRNA_AR..1..8162	282564, 282612	in gene, in gene	1	1	0	21	14	1	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene INPP4B	MGC132014, INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	NM_003866, NM_001101669, hCT2325719.0	205376_at, 223876_at	NP_003857.2, NP_001095139.1, EAX05081.1
GeneID:84640	USP38	4	144,106,070	144,143,141	37,071	+	2	2_A375_pNL97_plus_lncRNA_AR..1..8163, 4_A375_EGR1..1..8591	-342, 426	upstream, in gene	0	1	1	10.5	9.5	11	2	4_A375_EGR1..1	15	Gene USP38	KIAA1891, FLJ35970, HP43.8KD, USP38	ubiquitin specific peptidase 38	NM_032557, hCT1950439.3, hCT2358921.0, hCT2358922.0	223288_at, 223289_s_at	NP_115946.2, EAX05075.1, EAX05076.1, EAX05077.1
GeneID:10393	ANAPC10	4	145,916,310	146,019,366	103,056	-	1	4_A375_EGR1..1..8592	83928	in gene	0	0	1	7	2	12	1	4_A375_EGR1..1	12	Gene ANAPC10	ANAPC10, DKFZp564L0562, DOC1, APC10	anaphase promoting complex subunit 10	NM_014885, hCT1971209.1, hCT1971210.1, hCT2358947.0, hCT30017.1	241959_at	NP_055700.2, EAX05053.1, EAX05050.1, EAX05051.1, EAX05052.1
GeneID:54726	OTUD4	4	146,054,802	146,100,832	46,030	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4284	-898	upstream	1	0	0	20	11	12	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene OTUD4	KIAA1046, OTUD4, HIN1, HSHIN1, DUBA6, DKFZp434I0721	OTU domain containing 4	NM_001102653, NM_017493, hCT2325181.1, hCT2325182.1, hCT2325183.1, hCT2325184.1, hCT2325185.0, hCT2325186.1, hCT2358938.0	203479_s_at, 203480_s_at, 220689_at, 238848_at	NP_001096123.1, NP_059963.1, EAX05043.1, EAX05045.1, EAX05046.1, EAX05047.1, EAX05042.1, EAX05044.1, EAX05048.1
GeneID:166785	MMAA	4	146,540,540	146,581,187	40,647	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8164	-124	upstream	0	1	0	12	16	11	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene MMAA	MGC120010, MGC120013, MGC120012, MMAA, cblA, MGC120011	methylmalonic aciduria (cobalamin deficiency) cblA type	NM_172250, hCT2341295.0	236347_at, 237631_x_at, 239852_at, 242750_at	NP_758454.1, EAX05036.1
GeneID:646603	C4orf51	4	146,601,356	146,653,949	52,593	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8165	54740	downstream	0	1	0	13	16	7	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C4orf51	C4orf51	chromosome 4 open reading frame 51	NM_001080531		NP_001074000.1
GeneID:84068	SLC10A7	4	147,175,137	147,443,123	267,986	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4285, 2_A375_pNL97_plus_lncRNA_AR..1..8166, 4_A375_EGR1..1..8593	-29, -29, 278035	upstream, upstream, downstream	1	1	1	12.5	17	12	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SLC10A7	DKFZp779O2438, C4orf13, MGC25043, SLC10A7, DKFZp566M114, DKFZp313H0531, P7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7	NM_001029998, NM_032128	1555108_at, 224126_at, 235143_at	NP_001025169.1, NP_115504.1
GeneID:5458	POU4F2	4	147,560,045	147,563,623	3,578	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4286, 1_A375_pNL7_minus_lncRNA_AR..1..4287, 2_A375_pNL97_plus_lncRNA_AR..1..8167	-1773, 5139, -1805	upstream, downstream, upstream	1	1	0	17.5	20	3.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene POU4F2	BRN3.2, BRN3B, Brn-3b, POU4F2	POU class 4 homeobox 2	NM_004575, hCT30290.3	207725_at	NP_004566.2, EAX05025.1
GeneID:166614	DCLK2	4	151,000,080	151,178,609	178,529	+	1	4_A375_EGR1..1..8595	16	in gene	0	0	1	6	7	13	1	4_A375_EGR1..1	13	Gene DCLK2	CL2, DCAMKL2, MGC45428, DCLK2, CLICK-II, DCDC3B, DCK2, CLICK2, DCDC3, CLIK2, DKFZp761I032	doublecortin-like kinase 2	NM_001040260, NM_001040261, hCT2358910.0, hCT2358911.0, hCT9098.3	216724_at, 216725_at, 227666_at	NP_001035350.2, NP_001035351.3, EAX05001.1, EAX05002.1, EAX05003.1
GeneID:987	LRBA	4	151,185,594	151,936,879	751,285	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8169	514527	in gene	0	1	0	11	16	4	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LRBA	FLJ16600, DKFZp686A09128, LAB300, DKFZp686P2258, CDC4L, FLJ25686, BGL, LRBA, DKFZp686K03100, LBA, MGC72098	LPS-responsive vesicle trafficking, beach and anchor containing	NM_006726, hCT1959776.1	212692_s_at, 214109_at	NP_006717.2, EAX04996.1
GeneID:6189	RPS3A	4	152,020,754	152,025,804	5,050	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8170	14	in gene	0	1	0	15	27	11	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene RPS3A	FTE1, S3A, MGC23240, RPS3A, MFTL	ribosomal protein S3A	NM_001006, hCT2325156.0, hCT2325157.0, hCT2325158.0, hCT2325159.0, hCT2325160.0, hCT2325161.0, hCT2325162.0, hCT2325163.0	201257_x_at, 212391_x_at	NP_000997.1, EAX04988.1, EAX04989.1, EAX04990.1, EAX04991.1, EAX04995.1, EAX04992.1, EAX04993.1, EAX04994.1
GeneID:8944	SNORD73A	4	152,024,979	152,025,043	64	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8170	-4211	upstream	0	1	0	15	27	11	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SNORD73A	RNU73, U73, U73a, RNU73A, SNORD73A	small nucleolar RNA, C/D box 73A	NR_000007		
GeneID:729830	FAM160A1	4	152,330,398	152,584,784	254,386	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4289, 4_A375_EGR1..1..8596	-478, -510	upstream, upstream	1	0	1	14	10	12	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene FAM160A1	FAM160A1, FLJ43373	family with sequence similarity 160, member A1	NM_001109977	1569465_at, 242687_at	NP_001103447.1
GeneID:5188	PET112L	4	152,591,808	152,682,175	90,367	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4290	-1	upstream	1	0	0	21	11	5	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene PET112L	PET112, HSPC199, PET112L	PET112-like (yeast)	NM_004564, hCT18117.3, hCT1959579.1, hCT1959580.1	204300_at	NP_004555.1, EAX04981.1, EAX04982.1, EAX04983.1
GeneID:201798	TIGD4	4	153,690,506	153,700,877	10,371	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4292	-227	upstream	1	0	0	20	12	3	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene TIGD4	MGC43837, TIGD4	tigger transposable element derived 4	NM_145720, hCT1648440.3	1552522_at, 1552523_a_at	NP_663772.1, EAX04973.1
GeneID:27236	ARFIP1	4	153,701,112	153,833,064	131,952	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4292	-8	upstream	1	0	0	20	12	3	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ARFIP1	MGC117369, ARFIP1, HSU52521	ADP-ribosylation factor interacting protein 1	NM_014447, NM_001025593, NM_001025595, hCT1772843.2, hCT18114.3, hCT1959578.1, hCT2325064.0, hCT2325066.0	214463_s_at, 218230_at	NP_055262.1, NP_001020764.1, NP_001020766.1, EAX04968.1, EAX04970.1, EAX04971.1, EAX04969.1, EAX04972.1
GeneID:85462	FHDC1	4	153,864,135	153,900,848	36,713	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4293, 2_A375_pNL97_plus_lncRNA_AR..1..8171	40537, 40601	downstream, downstream	1	1	0	22	32	3	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene FHDC1	KIAA1727, FHDC1	FH2 domain containing 1	NM_033393, hCT19231.3	226599_at	NP_203751.2, EAX04967.1
GeneID:54798	DCHS2	4	155,155,527	155,412,930	257,403	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8172	158706	in gene	0	1	0	3	15	8	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene DCHS2	PCDHJ, CDHR7, CDH27, CDHJ, DCHS2, FLJ20047, PCDH23	dachsous 2 (Drosophila)	NM_017639, NM_001142552, NM_001142553, hCT1782315.2, hCT2325378.1, hCT2325379.1, hCT2325380.1, hCT2325381.1, hCT2325382.1	220373_at, 242764_at	NP_060109.2, NP_001136024.1, NP_001136025.1, EAX04942.1, EAX04943.1, EAX04945.1, EAX04944.1, EAX04946.1, EAX04947.1
GeneID:2891	GRIA2	4	158,141,736	158,287,227	145,491	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8173	-200	upstream	0	1	0	22	26	5	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene GRIA2	GluA2, GRIA2, HBGR2, GluR-K2, GLUR2, GLURB	glutamate receptor, ionotropic, AMPA 2	NM_001083619, NM_000826, NM_001083620, hCT18060.3, hCT1955228.1, hCT2325192.0, hCT2325194.0, hCT2325196.0, hCT2325197.0, hCT2325198.0	205358_at, 236538_at, 241172_at	NP_001077088.1, NP_000817.2, NP_001077089.1, EAX04868.1, EAX04867.1, EAX04870.1, EAX04865.1, EAX04866.1, EAX04869.1, EAX04871.1
GeneID:201725	C4orf46	4	159,587,831	159,593,202	5,371	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4294, 2_A375_pNL97_plus_lncRNA_AR..1..8175	-238, -254	upstream, upstream	1	1	0	119	124	4	1	2_A375_pNL97_plus_lncRNA_AR..1	124	Gene C4orf46	C4orf46	chromosome 4 open reading frame 46	NM_001008393	235088_at, 236015_at	NP_001008394.1
GeneID:2110	ETFDH	4	159,593,277	159,629,842	36,565	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4294, 2_A375_pNL97_plus_lncRNA_AR..1..8175	163, 179	in gene, in gene	1	1	0	119	124	4	1	2_A375_pNL97_plus_lncRNA_AR..1	124	Gene ETFDH	ETFQO, ETFDH, MADD	electron-transferring-flavoprotein dehydrogenase	NM_004453, hCT1955220.1	205530_at, 33494_at	NP_004444.2, EAX04854.1
GeneID:5481	PPID	4	159,630,279	159,644,552	14,273	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8176	104	in gene	0	1	0	8	14	7	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene PPID	CYP-40, CYPD, MGC33096, PPID	peptidylprolyl isomerase D	NM_005038, hCT7442.2	204185_x_at, 204186_s_at, 228469_at	NP_005029.1, EAX04853.1
GeneID:56884	FSTL5	4	162,305,049	163,085,186	780,137	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4296, 2_A375_pNL97_plus_lncRNA_AR..1..8177	34, 66	in gene, in gene	1	1	0	22	28	9	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene FSTL5	KIAA1263, DKFZp566D234, FSTL5	follistatin-like 5	NM_020116, NM_001128427, NM_001128428, hCT1961916.2	232010_at	NP_064501.2, NP_001121899.1, NP_001121900.1, EAX04846.1
GeneID:55319	C4orf43	4	164,415,873	164,441,891	26,018	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4297, 2_A375_pNL97_plus_lncRNA_AR..1..8178	135, 7	in gene, in gene	1	1	0	14	19	13	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C4orf43	FLJ52950, C4orf43, FLJ11184	chromosome 4 open reading frame 43	NM_018352, hCT18753.4, hCT1971109.1	218513_at	NP_060822.2, EAX04836.1, EAX04837.1
GeneID:55601	DDX60	4	169,137,442	169,239,958	102,516	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8179	44774	in gene	0	1	0	13	16	4	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene DDX60	FLJ10787, DDX60, FLJ20035	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	NM_017631, hCT1782733.3, hCT1952480.1, hCT2324715.0, hCT2324716.0	218986_s_at	NP_060101.3, EAX04806.1, EAX04807.1, EAX04808.1, EAX04809.1
GeneID:9848	MFAP3L	4	170,907,748	170,947,429	39,681	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4300, 2_A375_pNL97_plus_lncRNA_AR..1..8181, 4_A375_EGR1..1..8597	-1163, -1147, 453	upstream, upstream, in gene	1	1	1	13	13	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MFAP3L	NYD-sp9, MFAP3L	microfibrillar-associated protein 3-like	NM_021647, NM_001009554, hCT2324823.0, hCT2324824.0, hCT8380.3	205442_at, 210492_at, 210493_s_at, 210843_s_at	NP_067679.6, NP_001009554.1, EAX04773.1, EAX04774.1, EAX04775.1



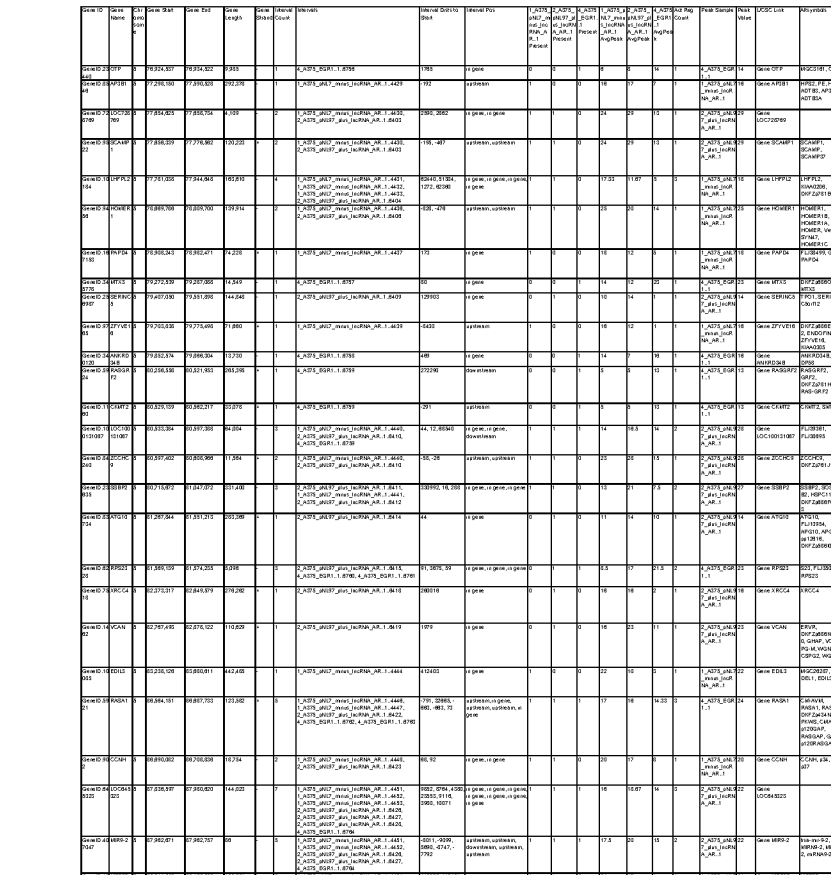
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_pAL7_invasion_lncRNA_RR_1 Percent	2_A375_pAL7_invasion_lncRNA_AR_1 Percent	3_A375_pAL7_EGR1_lncRNA_AR_1 Percent	4_A375_pAL7_invasion_lncRNA_RR_1 Avg Peak	5_A375_pAL7_pAL97_pAL7_invasion_lncRNA_AR_1 Avg Peak	6_A375_pAL7_EGR1_lncRNA_AR_1 Avg Peak	Add Tag Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:339509	GALNT7	+	174,209,004	174,245,118	153,214	+	2	1_A375_pAL7_invasion_lncRNA_RR_1:4302, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8163	03F26, 03T44	cr gene, cr gene	1	1	0	16	29	7	1	2_A375_pAL9 29_invasion_lncRNA_AR_1	29	GALNT7	GALNAC-T7, GalNAcT7, GalNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	NM_017423, XCT1809927.1	210313_s_at, 222567_s_at	NP_059119.2, EAX04761.1
GeneID:374648	HAGE	+	174,232,527	174,236,593	3,986	+	2	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8154, 2_A375_EGR1_1:8596	229, 139	upstream, cr gene	0	1	1	15	27	13	1	2_A375_pAL9 27_pAL7_invasion_lncRNA_AR_1	27	Gene HAGE	HAGE2, HAH2	high mobility group box 2	NM_002129, NM_001130855, NM_001130869, XCT2249758.0, XCT3773.3	205955_s_at, 239091_at, 243366_at	NP_002120.1, NP_001124160.1, NP_001124161.1, EAX04786.1, EAX04787.1
GeneID:2899	FBXO6	+	175,157,609	175,258,402	47,393	+	1	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8159	548	cr gene	0	1	0	15	16	8	1	2_A375_pAL9 16_pAL7_invasion_lncRNA_AR_1	16	Gene FBXO6	DC10, FBX6, FBG, FBXO6	F-box protein 6	NM_012160, XCT2324858.0, XCT2324859.0, XCT2324930.0, XCT2356999.0, XCT3129.2	1554000_a_at, 223368_at	NP_036172.2, EAX04741.1, EAX04742.1, EAX04743.1, EAX04744.1, EAX04745.1
GeneID:8317	KIAA1712	+	175,234,828	175,294,931	60,103	+	1	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8160	228	cr gene	0	1	0	19	16	8	1	2_A375_pAL9 16_pAL7_invasion_lncRNA_AR_1	16	Gene KIAA1712	PSTPIP2, KIAA1712	KIAA1712	NM_001045537, NM_001143314, XCT2342587.0, XCT2342926.0, XCT2342928.0, XCT2342986.0, XCT3129.3	1235224_s_at, 231930_s_at	NP_001038627.1, NP_001139798.1, EAX04736.1, EAX04739.1, EAX04740.1
GeneID:8501	GLRA3	+	175,580,196	175,730,465	150,269	+	3	1_A375_pAL7_invasion_lncRNA_AR_1:4304, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:4355, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8167	355, 302, 355	cr gene, upstream, cr gene	1	1	0	19	17.5	8	2	2_A375_pAL9 29_pAL7_invasion_lncRNA_AR_1	29	Gene GLRA3	GLRA3		NM_021042543, NM_006829, XCT1537811.2, XCT2342620.0, XCT2342630.0, XCT3129.5	1557826_s_at, 213991_at, 216021_s_at	NP_001038003.1, NP_006820.2, EAX04730.1, EAX04731.1, EAX04732.1, EAX04733.1
GeneID:5436	ASB3	+	177,139,824	177,190,373	50,549	+	1	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8168	1579	upstream	0	1	0	13	16	8	1	2_A375_pAL9 16_pAL7_invasion_lncRNA_AR_1	16	Gene ASB3	ASB3	ankyrin repeat and SOCS box-containing 3	NM_080874, XCT317762.3	235803_at	NP_542150.1, EAX04720.1
GeneID:74	VEGFC	+	177,899,691	177,712,695	103,204	+	1	4_A375_EGR1_1:8599	953	cr gene	0	0	1	5	13	15	1	4_A375_EGR 1_1	15	Gene VEGFC	VEGFC, VRP, Flt4-L	vascular endothelial growth factor C	NM_005429, XCT322951.1	209946_at	NP_005420.1, EAX04717.1
GeneID:5	AGA	+	178,091,926	178,260,837	11,729	+	3	1_A375_pAL7_invasion_lncRNA_AR_1:4306, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8151, 4_A375_EGR1_1:8601	-2303, 489, 137	upstream, cr gene, cr gene	1	1	1	14	17.5	10	2	4_A375_EGR 1_1	24	Gene AGA	AGU, GA, AGA, ASRG	N-acetylglucosaminidase	NM_000027, NM_001171668, NR_033635, XCT2342330.0, XCT2342332.0, XCT2342333.0, XCT3229.2	204332_s_at, 204333_s_at, 216684_s_at	NP_000018.2, NP_001164491.1, EAX04712.1, EAX04713.1, EAX04714.1, EAX04715.1
GeneID:5501	ODZ3	+	183,245,137	183,736,177	479,040	+	2	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8201, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8202	43835, 124655	cr gene, cr gene	0	1	0	12.5	22.5	7	2	2_A375_pAL9 24_pAL7_invasion_lncRNA_AR_1	24	Gene ODZ3	TNM3, FLJ10358, FLJ10474, Ten-m3, ODZ3, KIAA1455	teneurin transmembrane protein 3 (Drosophila)	NM_031956477	1559961_at, 219325_s_at, 227282_at	NP_001073946.1
GeneID:1855	DCTD	+	183,811,244	183,838,930	27,686	-	2	4_A375_EGR1_1:8604, 4_A375_EGR1_1:8608	516, -384	cr gene, upstream	0	0	1	12.5	11.5	10	2	4_A375_EGR 1_1	17	Gene DCTD	MGC21002, DCTD	dCMP deaminase	NM_001921, NM_001012732, XCT2336304.0, XCT2342307.0, XCT2342309.0, XCT3699.2	201571_s_at, 201572_x_at, 210107_x_at, 214697_x_at, 214698_s_at, 214699_s_at, 214700.1	NP_001912.2, NP_001027563.1, EAX04697.1, EAX04698.1, EAX04700.1, EAX04701.1
GeneID:2641	C4orf58	+	184,016,174	184,030,552	2,378	-	3	1_A375_pAL7_invasion_lncRNA_AR_1:4355, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8203, 4_A375_EGR1_1:8607	160, 668, 1616	cr gene, cr gene, cr gene	1	1	1	19	13	14.5	2	1_A375_pAL9 32_invasion_lncRNA_AR_1	32	Gene C4orf58	C4orf58, FLJ90277, MGC161755, FLJ90276, MGC161757	chromosome 4 open reading frame 58	NM_024808, XCT2324393.1	1557663_at, 230372_at	EAX04699.1
GeneID:114	WWC2	+	184,239,483	184,241,930	231,067	+	3	1_A375_pAL7_invasion_lncRNA_AR_1:4353, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8203, 4_A375_EGR1_1:8607	-291, -799, -1729	upstream, upstream, upstream	1	1	1	19	13	14.5	2	1_A375_pAL9 32_invasion_lncRNA_AR_1	32	Gene WWC2	FLJ90855, WWC2, FLJ22736, KIAA1412	WW and C2 domain containing	NM_0309349, XCT2324358.0	1554762_a_at, 218775_s_at, 222758_at, 237868_at	NP_079225.5, EAX04694.1
GeneID:1902	CDKN2AIP	+	184,368,769	184,389,049	20,280	+	2	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:4356, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8204	-289, 179	upstream, cr gene	1	1	0	17	16	12	1	1_A375_pAL9 17_invasion_lncRNA_AR_1	17	Gene CDKN2AIP	FLJ20036, CDK2AIP, CARF	CDK2A/interacting protein	NM_017622, XCT677122.3	219329_at	NP_060102.1, EAX04691.1
GeneID:9247	LOC55918 247	+	184,413,992	184,425,666	11,775	+	4	1_A375_pAL7_invasion_lncRNA_AR_1:4357, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8203, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8206, 4_A375_EGR1_1:8609	-245, -80, -1823, 252	upstream, upstream, upstream, upstream	1	1	1	25	28.5	15.5	2	2_A375_pAL9 40_invasion_lncRNA_AR_1	40	Gene LOC559247		hypothetical LOC559247	NR_032955	1559641_at	
GeneID:22	IN02	+	184,439,230	184,452,249	13,020	+	4	1_A375_pAL7_invasion_lncRNA_AR_1:4357, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8203, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8206, 4_A375_EGR1_1:8609	-53k, -492, 1076, 330	upstream, upstream, cr gene, upstream	1	1	1	25	28.5	15.5	2	4_A375_pAL9 40_pAL7_invasion_lncRNA_AR_1	40	Gene IN02	IN02L, JID:IN02, ING2	inhibitor of growth family, member 2	NM_001984, XCT2324397.0, XCT7488.3	203851_s_at, 213944_at	NP_001555.1, EAX04689.1, EAX04690.1
GeneID:1985	RWDD4A	+	184,580,769	184,590,331	19,342	-	1	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8207	-65	upstream	0	1	0	11	13	10	1	2_A375_pAL9 13_pAL7_invasion_lncRNA_AR_1	13	Gene RWDD4A	MGC10766, RWDD4A, RWDD4, FLJ40024	RWD domain containing 4	NM_152662, XCT1628594.1	1235874_at	NP_689695.2, EAX04685.1
GeneID:8604	C4orf41	+	184,598,448	184,634,743	34,299	+	1	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8207	-30	upstream	0	1	0	11	13	10	1	2_A375_pAL9 13_pAL7_invasion_lncRNA_AR_1	13	Gene C4orf41	gry, Rgc, C4orf41, FLJ12716	chromosome 4 open reading frame 41	NM_021942, NM_199353, XCT2324390.0, XCT2324400.0	210170_s_at, 233551_s_at, 234747_at	NP_068761.4, NP_951008.1, EAX04686.1, EAX04687.1
GeneID:90	IRF2	+	183,208,576	183,256,726	48,650	-	2	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8208, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8209	98610, -722	cr gene, upstream	0	1	0	14	21.5	7.5	2	2_A375_pAL9 24_pAL7_invasion_lncRNA_AR_1	24	Gene IRF2	IRF-2, IRF2, DKFZp686P02264	interferon regulatory factor 2	NM_002199, XCT2324317.0, XCT2356908.0, XCT2356909.0, XCT729.2	202379_at	NP_002190.2, EAX04676.1, EAX04677.1, EAX04678.1, EAX04680.1
GeneID:2911	MLF1IP	+	183,813,219	183,838,266	40,087	-	2	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:4358, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8210	-198, -74	upstream, upstream	1	1	0	49	59	14	1	2_A375_pAL9 59_pAL7_invasion_lncRNA_AR_1	59	Gene MLF1IP	CENPU, MLF1IP, KLIP1, PBIP1, CENP30, FLJ23466	MLF1 interacting protein	NM_024629, XCT2324330.0	219563_s_at, 229504_s_at, 229505_at	NP_376553.2, EAX04699.1
GeneID:6907	ACSL1	+	185,678,749	185,747,213	70,466	-	3	1_A375_pAL7_invasion_lncRNA_AR_1:4359, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8211, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8212	12643, 12623, 858	cr gene, cr gene, cr gene	1	1	0	16.5	20	8	2	1_A375_pAL9 24_invasion_lncRNA_AR_1	24	Gene ACSL1	FACL2, ACSL1, LACS2, FACL1, LACS, LACS1, ACS1	acyl-CoA synthetase long-chain family member 1	NM_001995, XCT2324327.1, XCT2324328.1, XCT2324329.1, XCT6931.4	201963_at, 207273_s_at	NP_001986.2, EAX04683.1, EAX04684.1, EAX04694.1
GeneID:1	SLC25A34	+	186,099,417	186,871,556	7,121	+	1	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8214	65	cr gene	0	1	0	19	20	11	1	2_A375_pAL9 20_pAL7_invasion_lncRNA_AR_1	20	Gene SLC25A4	KIAT1, AAC1, ANT, PEO2, SLC25A4, T1, PEO2	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	NM_001151, XCT2324358.0, XCT7175.2	1557851_at, 202625_at	NP_001142.2, EAX04655.1, EAX04656.1
GeneID:6991	SNX25	+	186,101,264	186,208,120	103,838	+	1	1_A375_pAL7_invasion_lncRNA_AR_1:4360	96024	cr gene	1	0	0	20	12	4	1	1_A375_pAL9 20_invasion_lncRNA_AR_1	20	Gene SNX25	MSTP043, FLJ23181, SNX25, SSB631	sorting nexin 25	NM_031953, XCT2324356.0, XCT7689.2	1553356_s_at, 227511_at, 227456_s_at, 233099_at, 233425_at	NP_114159.2, EAX04651.1, EAX04652.1
GeneID:3332	ANKRD37	+	186,317,640	186,321,290	3,650	+	1	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8215	-499	upstream	0	1	0	20	23	16	1	2_A375_pAL9 23_pAL7_invasion_lncRNA_AR_1	23	Gene ANKRD37	MGC111907, bA379a.1, ANKRD37	ankyrin repeat domain 37	NM_181726, XCT2324390.0, XCT7612.2	227737_at, 242648_x_at	NP_859771.1, EAX04648.1, EAX04647.1
GeneID:325	UPSP2	+	186,330,894	186,347,129	29,445	-	3	1_A375_pAL7_invasion_lncRNA_AR_1:4321, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8213, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8216	-29, 29795, -29	upstream, downstream, upstream	1	1	0	23.5	26	12.5	2	2_A375_pAL9 33_pAL7_invasion_lncRNA_AR_1	33	Gene UPSP2	C4orf30, FLJ11200, UPSP2	UPA1-specific peptidase 2	NM_015559, NR_029055, XCT2356926.0, XCT7666.2	218449_at	NP_056370.2, EAX04645.1, EAX04646.1
GeneID:1034	C4orf47	+	186,330,543	186,370,021	39,479	-	2	1_A375_pAL7_invasion_lncRNA_AR_1:4321, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8216	-3377, -3377	upstream, upstream	1	1	0	27	33	11	1	2_A375_pAL9 33_pAL7_invasion_lncRNA_AR_1	33	Gene C4orf47	C4orf47		NM_031144357	238819_at, 237555_at	NP_001107291.1
GeneID:295	PDLIM5	+	186,421,814	186,498,712	54,899	-	1	1_A375_pAL7_invasion_lncRNA_AR_1:4322	232	cr gene	1	0	0	17	11	7	1	1_A375_pAL9 17_invasion_lncRNA_AR_1	17	Gene PDLIM5	ALP, PDLIM5, PLIM5995, DKFZp686J0562	PDZ and LIM domain 5	NM_031144107, NM_014476, XCT1998774.1, XCT1998775.1, XCT2356934.0, XCT7350.2	209621_s_at, 210170_at, 235892_at	NP_001078779, NP_006291.2, EAX04641.1, EAX04642.1, EAX04643.1, EAX04644.1
GeneID:7070	SORBS2	+	186,598,594	186,677,870	271,272	-	4	1_A375_pAL7_invasion_lncRNA_AR_1:4323, 1_A375_pAL7_invasion_lncRNA_AR_1:4324, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8216, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8219	117422, 109154, 11356, 23034	cr gene, cr gene, cr gene, cr gene	1	1	0	19.67	20	6	3	1_A375_pAL9 27_invasion_lncRNA_AR_1	27	Gene SORBS2	SORBS2, KIAA0777, ARGBP2, PRO0810, FLJ90447	vinculin and SH3 domain containing protein 2	NM_003603, NM_021069, NM_001143870, NM_001143871, NM_001143872, NM_001143874, NM_001143875, XCT1626400.1, XCT1626401.1, XCT2324980.0, XCT2324981.0, XCT2324983.0, XCT2324985.0, XCT2324989.0	1553472_at, 1556515_at, 204265_s_at, 228536_at, 228537_at, 233720_at, 237269_at	NP_003594.3, NP_996547.1, NP_001139421.1, NP_001139423.1, NP_001139424.1, NP_001139425.1, NP_001139426.1, NP_001139427.1, EAX04631.1, EAX04632.1, EAX04633.1, EAX04634.1, EAX04635.1, EAX04636.1
GeneID:5937	CCDC127	+	187,112,674	187,156,817	31,943	+	3	2_A375_pAL7_invasion_lncRNA_AR_1:4325, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8220, 4_A375_EGR1_1:8612	-486, 30, -238	upstream, cr gene, upstream	1	1	1	17	22	19	1	4_A375_pAL9 22_pAL7_invasion_lncRNA_AR_1	22	Gene CYFIP2	MGC42054, BCD, CYFIP42, FLJ16433, CYFIP41	cytochrome P450, family 4, subfamily V, polypeptide 2	NM_207352, XCT1626604.2	235745_at, 235291_at, 229993_at, 233719_at	NP_997235.2, EAX04624.1
GeneID:2191	FAT1	+	187,395,927	187,644,997	199,890	-	3	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8221, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8222, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8613	839, -2901, -2791	cr gene, upstream, upstream	0	1	1	11.5	16.5	17.5	2	4_A375_EGR 1_1	19	Gene FAT1	CDHF7, KIES, CDHR8, FNT, hFat1, FAT1	FAT tumor suppressor homolog 1 (Drosophila)	NM_005245, XCT2324646.0, XCT2324647.0, XCT7352.2	201979_at	NP_005226.2, EAX04616.1, EAX04614.1, EAX04615.1
GeneID:2483	FRS1	+	190,681,974	190,854,339	172,365	+	3	1_A375_pAL7_invasion_lncRNA_AR_1:4327, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8223, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8617	-11, -94, 392	upstream, upstream, cr gene	1	1	1	23	34	24	1	2_A375_pAL9 34_pAL7_invasion_lncRNA_AR_1	34	Gene FRS1	FRS1, FRS1A, FSG1	FSHD region gene 1	NM_004477, XCT2324272.0	235833_s_at	NP_004460.1, EAX04600.1
GeneID:4045	DUX4C	+	190,948,255	190,948,508	6,251	+	1	4_A375_EGR1_1:8618	4658	cr gene	0	0	1	4	7	12	1	4_A375_EGR 1_1	12	Gene DUX4C	DUX4L9, DUX4C	double homeobox 4 like 9	XR_109825, XR_113675		
GeneID:9931	FRG2	+	190,948,322	190,948,412	2,090	+	1	4_A375_EGR1_1:8618	3784	downstream	0	0	1	4	7	12	1	4_A375_EGR 1_1	12	Gene FRG2	FRG2A, FRG2	FSHD region gene 2	NM_001033217		NP_001033217.1
GeneID:5476	PLEKHG6	+	140,375	190,007	49,714	+	1	4_A375_EGR1_1:8619	-517	upstream	0	0	1	6	6	17	1	4_A375_EGR 1_1	17	Gene PLEKHG6	FLJ43173, RAH1909, PLEKHG6	pleckstrin homology domain containing, family G (with RhoGef domain) member 6	NM_032909	233441_at, 238555_at	NP_445141.3
GeneID:5937	CCDC127	+	204,875	219,290	13,222	-	1	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8231	-807	upstream	0	1	0	10	17	8	1	2_A375_pAL9 17_pAL7_invasion_lncRNA_AR_1	17	Gene CCDC127	CCDC127, FLJ35701	coiled-coil domain containing 127	NM_145265, XCT1796292.1	1560354_at, 236513_at	NP_660338.1, EAX05961.1
GeneID:8803	SDHA	+	218,836	256,815	38,459	+	1	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8231	626	cr gene	0	1	0	10	17	8	1	2_A375_pAL9 17_pAL7_invasion_lncRNA_AR_1	17	Gene SDHA	SDHF, CMDS1G2, FP, SDH1, SDH2, SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	NM_004168, XCT1639941.3, XCT1961094.1, XCT2352420.0	201092_s_at	NP_004159.2, EAX05992.1, EAX05993.1, EAX05994.1
GeneID:5501	LOC100507871	-	270,019	271,811	1,892	+	1	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8232	59	cr gene	0	1	0	13	26	11	1	2_A375_pAL9 26_pAL7_invasion_lncRNA_AR_1	26	Gene LOC100507871		hypothetical LOC100507871	XR_103555		
GeneID:1779	PDCD6	+	271,738	313,269	43,532	+	2	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8232, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8626	-156, 30552	upstream, downstream	0	1	1	10.5	21.5	14	2	2_A375_pAL9 28_pAL7_invasion_lncRNA_AR_1	28	Gene PDCD6	PEF1B, MGC9123, FLJ46205, AIG5-1, MGC110317, MGC119393, PDCD6	programmed cell death 6	NM_013232	1569782_at, 1569780_s_at, 1569784_x_at, 229283_at, 234267_at	NP_037384.1
GeneID:4351	AHRR	+	334,291	439,408	104,118	+	7	1_A375_pAL7_invasion_lncRNA_AR_1:4330, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8231, 4_A375_EGR1_1:8626, 4_A375_EGR1_1:8627, 4_A375_EGR1_1:8628, 4_A375_EGR1_1:8629, 4_A375_EGR1_1:8630, 4_A375_EGR1_1:8631, 4_A375_EGR1_1:8634	94429, 89021, 16097, 99988, 112169, 109429, 143453	cr gene, cr gene, cr gene, cr gene, cr gene, cr gene, downstream	1	1	1	9.57	11.29	13.14	7	4_A375_EGR 1_1	19	Gene AHRR	AHRR, AHRR, MGC167852, MGC167853, MGC179893, bHH, bHLHe77, KIAA1234	aryl hydrocarbon receptor repressor	NM_020731	229354_at	NP_065782.2
GeneID:1707	C5orf53	+	441,810	443,236	1,845	-	2	4_A375_EGR1_1:8623, 4_A375_EGR1_1:8624	5935, 4316	downstream, upstream	0	0	1	7.5	9	19	2	4_A375_EGR 1_1	19	Gene C5orf53	C5orf53	chromosome 5 open reading frame 53	NM_138464	233219_at	NP_612472.1
GeneID:5136	EXOSC3	+	443,234	487,411	24,077	+	3	4_A375_EGR1_1:8623, 4_A375_EGR1_1:8629, 4_A375_EGR1_1:8625	-5954, 4442, 53452	upstream, cr gene, downstream	0	0	1	7.67	7.33	20.33	3	4_A375_EGR 1_1	23	Gene EXOSC3	Skedly, EXOSC3, SEC8L1, SEC8	exosome complex component 3	NM_016236, XCT2356541.0, XCT2356542.0, XCT2356543.0, XCT6116.2	212609_at, 226567_at	NP_057320.2, EAX05000.1, EAX05002.1, EAX05003.1, EAX05022.1, EAX05023.1
GeneID:5155	LOC23549	+	470,825	475,080	4,435	-	1	4_A375_EGR1_1:8625	-2739	upstream	0	0	1	6	9	23	1	4_A375_EGR 1_1	23	Gene LOC23549	FFPSD1, DKFZp564J157	hypothetical LOC23549	NM_015155, XCT2356911.0	235497_s_at, 239455_at	EAX05034.1
GeneID:9900	SLC9A3R1	+	470,234	524,349	51,218	-	6	4_A375_EGR1_1:8625, 4_A375_EGR1_1:8626, 4_A375_EGR1_1:8627, 4_A375_EGR1_1:8628, 4_A375_EGR1_1:8629, 4_A375_EGR1_1:8630	47723, 39797, 39033, 34853, 33765, 9547	cr gene, cr gene, cr gene, cr gene, cr gene, upstream	0	0	1	6.83	8.17	19	6	4_A375_EGR 1_1	23	Gene SLC9A3	SLC9A3, MGC126720, NHE2, MGC126716	solute carrier family 9 (sodium/hydrogen exchanger), member 3	NM_004174, XCT2363934.0, XCT6114.3	202122_at	NP_004165.2, EAX05006.1, EAX05007.1
GeneID:2535	LOC10050 2552	-	477,438	481,000	3,997	+	5	4_A375_EGR1_1:8625, 4_A375_EGR1_1:8626, 4_A375_EGR1_1:8627, 4_A375_EGR1_1:8628, 4_A375_EGR1_1:8629	420, 7216, 11700, 12420, 13246	upstream, downstream, downstream, downstream, downstream	0	0	1	6.6	8.6	19.4	5	4_A375_EGR 1_1	23	Gene LOC100250152	FLJ90646	hypothetical LOC100250152	XR_112710, XR_108599, XR_113715		
GeneID:1178	TPPP	+	609,977	660,510	50,533	-	1	4_A375_EGR1_1:8633	19826	cr gene	0	0	1	5	9	15	1	4_A375_EGR 1_1	15	Gene TPPP	TPPP, p24, p25, TPPP1, p25alpha, TPPP/p25	tubulin polymerization-promoting protein	NM_007030, XCT2369930.0, XCT2369932.0, XCT7907.3	208079_s_at, 233034_s_at	NP_009061.1, EAW51015.1, EAW51014.1, EAW51016.1
GeneID:9989	RPD3	+	660,830	692,939	32,109	-	1	4_A375_EGR1_1:8634	31403	downstream	0	0	1	3	8	15	1	4_A375_EGR 1_1	15	Gene RPD3	FLJ43530, DKFZp686I05353, RPD3, DKFZp434D0711, UNQ5840, PRO9396	histone deacetylase 3	NM_003924, NR_027632, NM_001003677, XCT2369942.0, XCT2369943.0, XCT2369944.0, XCT2369945.0, XCT2370279.0, XCT2370280.0, XCT2370281.0	1220183_s_at	NP_076413.3, NP_001009677.2, EAW58187.1, EAW58188.1, EAW58189.1, EAW58190.1, EAW58191.1, EAW58192.1
GeneID:7189	TRIP13	+	692,989	916,196	25,195	+	2	2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:4331, 2_A375_pAL97_pAL7_invasion_lncRNA_AR_1:8234	19735, 19735	cr gene, cr gene	1	1	0	36	46	7	1	2_A375_pAL9 46_pAL7_invasion_lncRNA_AR_1	46	Gene TRIP13	TRIP13, HEL187	thyroid hormone receptor interactor 13	NM_004237, NM_001166280, XCT2370126.0, XCT7955.2	204033_at	NP_004228.1, NP_001159732.1, EAW58185.1, EAW58186.1
GeneID:4859	NKD2	-	1,009,166	1,030,935	29,737	+	3	4_A375_EGR1_1:8637, 4_A375_EGR1_1:8638, 4_A375_EGR1_1:8639	4386, 6872, 8224	cr gene, cr gene, cr gene	0	0	1	7.33	5.67	16.33	3	4_A375_EGR 1_1	17	Gene NKD2	NKD2, Naked2	naked cuticle homolog 2 (Drosophila)	NM_033120, XCT2366016.0, XCT2366018.0, XCT7952.1	232201_at	NP_149111.1, EAX05162.1, EAX05163.1, EAX05164.1
GeneID:1723	SLC12A7	-	1,092,669	1,112,172	61,883	+	2	4_A375_EGR1_1:8640, 4_A375_EGR1_1:8641	59020, 11503	cr gene, cr gene	0	0	1	8	7	19	2	4_A375_EGR 1_1	21	Gene SLC12A7	SLC12A7, KCC4, DKFZp434F0706	solute carrier family 12 (potassium/chloride transporters), member 7	NM_006598, XCT2365572.0, XCT2365573.0, XCT2365574.0, XCT2365575.0	210866_at	NP_006589.2, EAX05170.1, EAX05171.1, EAX05180.1, EAX05181.1



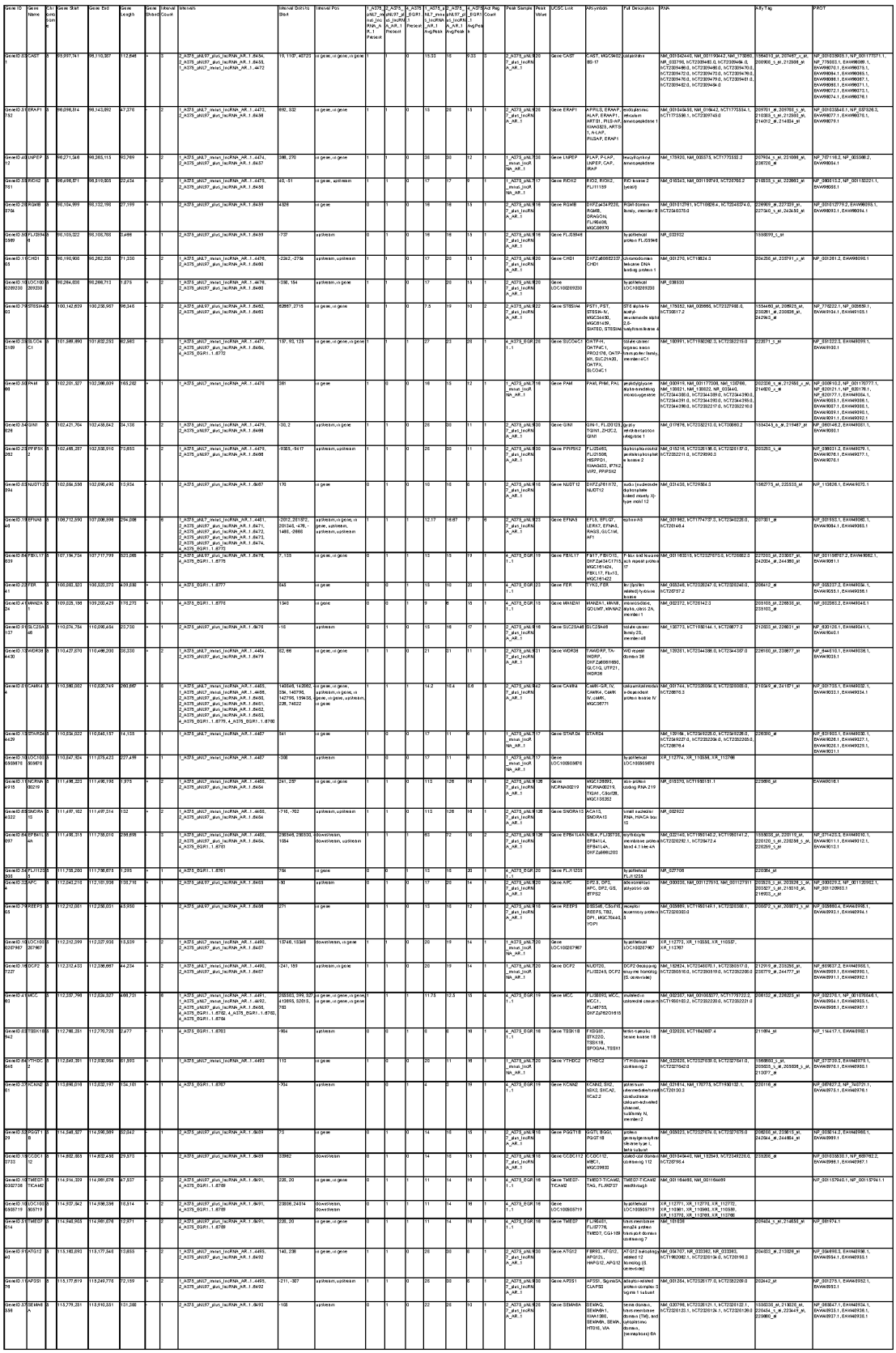
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.64083	GOLPH3	5	32,124,824	32,174,425	49,601	-	1	2_A375_pNL97_plus_lncRNA_AR..1.8279	-39	upstream	0	1	0	17	24	16	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene GOLPH3	FLJ90675, MIDAS, GOPP1, GPP34, GOLPH3	golgi phosphoprotein 3 (coat-protein)	NM_022130, hCT13923.2, hCT1952506.1, hCT1958295.1	217803_at	NP_071413.1, EAX10780.1, EAX10781.1, EAX10782.1
GeneID.51663	ZFR	5	32,354,456	32,444,844	90,388	-	1	2_A375_pNL97_plus_lncRNA_AR..1.8280	53676	in gene	0	1	0	16	20	3	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ZFR	FLJ41312, ZFR1, ZFR	zinc finger RNA binding protein	NM_016107, hCT2289945.0, hCT2289947.0, hCT2289946.0	201856_s_at, 201857_at, 213286_at, 33146_at	NP_057191.2, EAX10790.1, EAX10789.1, EAX10791.1
GeneID.693164	MIR579	5	32,394,484	32,394,581	97	-	1	2_A375_pNL97_plus_lncRNA_AR..1.8280	3413	downstream	0	1	0	16	20	3	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MIR579	MIR579, MIRN579, hsa-mir-579	microRNA 579	NR_030305		
GeneID.4883	NPR3	5	32,711,665	32,787,256	75,591	+	2	4_A375_EGR1..1.8710, 4_A375_EGR1..1.8711	847, 2511	in gene, in gene	0	0	1	8	10	18.5	2	4_A375_EGR1..1	20	Gene NPR3	NPRC, MGC22189, NPR3, FLJ14054, ANPRC, C5orf23, GUCY2B	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	NM_000908, hCT1952514.1, hCT2359588.0, hCT28455.2	219789_at, 219790_s_at	NP_000899.1, EAX10797.1, EAX10798.1, EAX10799.1
GeneID.6897	TARS	5	33,440,898	33,468,196	27,298	+	1	2_A375_pNL97_plus_lncRNA_AR..1.8282	-226	upstream	0	1	0	16	17	16	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TARS	ThrRS, MGC9344, TARS	threonyl-tRNA synthetase	NM_152295, hCT2289499.0, hCT28056.3	201263_at, 240206_at	NP_689508.3, EAX10803.1, EAX10804.1
GeneID.81792	ADAMTS12	5	33,527,286	33,892,124	364,838	-	1	2_A375_pNL97_plus_lncRNA_AR..1.8283	200986	in gene	0	1	0	12	17	0	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ADAMTS12	ADAMTS12, PRO4389	ADAM metallopeptidase with thrombospondin type 1 motif, 12	NM_030955, hCT1957567.2, hCT2289678.0	221421_s_at	NP_112217.2, EAX10808.1, EAX10809.1
GeneID.51289	RXFP3	5	33,936,491	33,939,023	2,532	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4348, 2_A375_pNL97_plus_lncRNA_AR..1.8284	-267, -331	upstream, upstream	1	1	0	33	29	18	1	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene RXFP3	RLN3R1, MGC142000, SALPR, GPCR135, RXFP3, RXFPR3, MGC141998	relaxin/insulin-like family peptide receptor 3	NM_016568, hCT1645300.2	221088_at	NP_057652.1, EAX10810.1
GeneID.51151	SLC45A2	5	33,944,721	33,984,780	40,059	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4348, 2_A375_pNL97_plus_lncRNA_AR..1.8284, 4_A375_EGR1..1.8712	48556, 48620, 266	downstream, downstream, in gene	1	1	1	19.5	22	18	2	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene SLC45A2	1A1, SHEP5, SLC45A2, MATP, AIM1	solute carrier family 45, member 2	NM_016180, NM_001012509, hCT1952515.1, hCT2359585.0, hCT2359586.0, hCT28644.2	220245_at, 221644_s_at	NP_057264.3, NP_001012527.1, EAX10811.1, EAX10812.1, EAX10813.1, EAX10814.1
GeneID.23600	AMACR	5	33,987,091	34,008,220	21,129	-	4	2_A375_pNL97_plus_lncRNA_AR..1.8285, 2_A375_pNL97_plus_lncRNA_AR..1.8286, 4_A375_EGR1..1.8712, 4_A375_EGR1..1.8713	6732, 66, 23706, 44	in gene, in gene, downstream, in gene	0	1	1	9.33	15.67	12	3	4_A375_EGR1..1	16	Gene AMACR	RACE, RM, AMACR, CBAS4	alpha-methylacyl-CoA racemase	NM_014324, NM_203382, NM_001167595, NM_001167598, NM_001167597, NM_001167596, hCT1952511.1, hCT1958301.1, hCT2289659.0, hCT28298.2	209424_s_at, 209425_at, 209426_s_at, 217111_at, 217113_at, 236365_at	NP_055139.4, NP_976316.1, NP_001161067.1, NP_001161068.1, NP_001161069.1, NP_001161070.1, EAX10815.1, EAX10816.1, EAX10817.1, EAX10818.1
GeneID.114899	C1QTNF3	5	34,017,963	34,043,317	25,354	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4349, 1_A375_pNL7_minus_lncRNA_AR..1..4350, 2_A375_pNL97_plus_lncRNA_AR..1.8286, 4_A375_EGR1..1.8713	-4123, -10219, 35165, 35141	upstream, upstream, downstream, downstream	1	1	1	16	14	8.33	3	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene C1QTNF3	FLJ37576, CORS, CORS-26, C1QTNF3, Cors-26, CTRP3, C1ATNF3, Cors, CORS26, Cors, CORCS	C1q and tumor necrosis factor related protein 3	NM_181435, NM_030945, hCT2289652.0, hCT2289654.0, hCT2289656.0	1561263_at, 220988_s_at	NP_852100.3, NP_112207.1, EAX10819.1, EAX10820.1, EAX10821.1
GeneID.26064	RAI14	5	34,656,433	34,832,717	176,284	+	1	2_A375_pNL97_plus_lncRNA_AR..1.8287	182943	downstream	0	1	0	12	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene RAI14	RAI13, RAI14, KIAA1334, DKFZp564G013, NORPEG	retinoic acid induced 14	NM_015577, NM_001145520, NM_001145521, NM_001145522, NM_001145523, NM_001145525, hCT2292780.0	202052_s_at	NP_056392.2, NP_001138992.1, NP_001138993.1, NP_001138994.1, NP_001138995.1, NP_001138997.1, EAW55898.1
GeneID.153657	TTC23L	5	34,839,289	34,899,587	60,298	+	1	2_A375_pNL97_plus_lncRNA_AR..1.8287	107	in gene	0	1	0	12	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TTC23L	FLJ25439, TTC23L	tetratricopeptide repeat domain 23-like	NM_144725, hCT2344497.0, hCT2344501.0	1557003_at, 239620_at	NP_653326.3, EAW55900.1, EAW55901.1
GeneID.5810	RAD1	5	34,905,365	34,915,780	10,415	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4351, 2_A375_pNL97_plus_lncRNA_AR..1.8288, 4_A375_EGR1..1.8714	4, -60, -124	in gene, upstream, upstream	1	1	1	21	34	19	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene RAD1	HRAD1, RAD1, REC1	RAD1 homolog (S. pombe)	NM_002853, NR_026591	204460_s_at, 204461_x_at, 210216_x_at, 226535_at, 235253_at	NP_002844.1
GeneID.55299	BRIX1	5	34,915,820	34,925,787	9,967	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4351, 2_A375_pNL97_plus_lncRNA_AR..1.8288, 4_A375_EGR1..1.8714	-44, 20, 84	upstream, in gene, in gene	1	1	1	21	34	19	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene BRIX1	BRIX1, BXDC2, FLJ11100	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)	NM_018321, hCT2344499.0, hCT2344500.0	219177_at	NP_060791.3, EAW55909.1, EAW55910.1
GeneID.79925	SPEF2	5	35,617,989	35,814,713	196,724	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4352, 2_A375_pNL97_plus_lncRNA_AR..1.8290	-101, -69	upstream, upstream	1	1	0	94	96	9	1	2_A375_pNL97_plus_lncRNA_AR..1	96	Gene SPEF2	FLJ25395, KPL2, KIAA1770, CT122, MGC102842, FLJ23577, SPEF2, FLJ23164	sperm flagellar 2	NM_144722, NM_024867, hCT2292758.0, hCT2292760.0, hCT2292761.0, hCT2292762.0	1552716_at, 232745_x_at, 233429_at	NP_653323.1, NP_079143.3, EAW55920.1, EAW55921.1, EAW55922.1, EAW55923.1
GeneID.92255	LMBRD2	5	36,103,414	36,152,015	48,601	-	1	2_A375_pNL97_plus_lncRNA_AR..1.8291	-61	upstream	0	1	0	16	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LMBRD2	MGC125692, MGC125693, DKFZp434H2226, DKFZp686G1057, LMBRD2	LMBR1 domain containing 2	NM_001007527, hCT2293043.0, hCT28813.3	232893_at	NP_001007528.1, EAW55933.1, EAW55932.1
GeneID.693165	MIR580	5	36,147,994	36,148,090	96	-	1	2_A375_pNL97_plus_lncRNA_AR..1.8291	-4006	upstream	0	1	0	16	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MIR580	MIR580, hsa-mir-580, MIRN580	microRNA 580	NR_030306		
GeneID.6502	SKP2	5	36,152,189	36,184,147	31,958	+	1	2_A375_pNL97_plus_lncRNA_AR..1.8291	-93	upstream	0	1	0	16	18	11	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SKP2	FLB1, FBL1, MGC1366, SKP2, FBXL1	S-phase kinase-associated protein 2 (p45)	NM_032637, NM_005983, hCT2292772.0, hCT2292774.0, hCT2292775.0, hCT2292776.0, hCT28123.3	203626_s_at, 210567_s_at	NP_116026.1, NP_005974.2, EAW55934.1, EAW55935.1, EAW55936.1, EAW55937.1, EAW55938.1
GeneID.133686	C5orf33	5	36,192,694	36,242,258	49,564	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4353, 2_A375_pNL97_plus_lncRNA_AR..1.8292, 2_A375_pNL97_plus_lncRNA_AR..1.8293	50, 925, -94	in gene, in gene, upstream	1	1	0	19.5	17.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene C5orf33	FLJ30596, C5orf33, MGC43298	chromosome 5 open reading frame 33	NM_001085411, NM_153013, hCT2352981.0, hCT2352982.0, hCT28815.3	226946_at, 228594_at, 229299_at	NP_001078880.1, NP_694558.1, EAW55939.1, EAW55940.1, EAW55941.1
GeneID.202151	RANBP3L	5	36,249,104	36,302,011	52,907	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4353, 2_A375_pNL97_plus_lncRNA_AR..1.8292, 2_A375_pNL97_plus_lncRNA_AR..1.8293	59603, 60676, 59659	downstream, downstream, downstream	1	1	0	19.5	17.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene RANBP3L	FLJ25422, RANBP3L	RAN binding protein 3-like	NM_145000, NM_001161429, hCT2293038.1, hCT2293039.1, hCT2352977.0	1553147_at	NP_659437.3, NP_001154901.1, EAW55942.1, EAW55943.1, EAW55944.1
GeneID.6507	SLC1A3	5	36,606,457	36,688,436	81,979	+	1	2_A375_pNL97_plus_lncRNA_AR..1.8294	51367	in gene	0	1	0	12	27	4	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SLC1A3	FLJ25094, GLAST, GLAST1, SLC1A3, EA6, EAAT1	solute carrier family 1 (glial high affinity glutamate transporter), member 3	NM_004172, NM_001166695, NM_001166696, hCT2293436.0, hCT28085.3	1569054_at, 202800_at	NP_004163.3, NP_001160167.1, NP_001160168.1, EAW55945.1, EAW55946.1
GeneID.646719	LOC646719	5	36,864,527	36,876,796	12,269	-	1	4_A375_EGR1..1.8715	-596	upstream	0	0	1	8	8	15	1	4_A375_EGR1..1	15	Gene LOC646719		hypothetical LOC646719	XR_112726, XR_108571, XR_113733		
GeneID.25836	NIPBL	5	36,876,861	37,065,921	189,060	+	1	4_A375_EGR1..1.8715	531	in gene	0	0	1	8	8	15	1	4_A375_EGR1..1	15	Gene NIPBL	FLJ13354, CDLS, FLJ44854, FLJ11203, CDLS1, IDN3-B, IDN3, FLJ12597, NIPBL, FLJ13648, Scc2, DKFZp434L1319	Nipped-B homolog (Drosophila)	NM_133433, NM_015384, hCT2293444.0, hCT2293446.0, hCT2293447.0	207108_s_at, 212469_at, 212483_at, 213918_s_at, 242352_at	NP_597677.2, NP_056199.2, EAW55948.1, EAW55949.1, EAW55950.1
GeneID.9631	NUP155	5	37,291,941	37,371,197	79,256	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4354, 1_A375_pNL7_minus_lncRNA_AR..1..4355, 2_A375_pNL97_plus_lncRNA_AR..1.8295, 2_A375_pNL97_plus_lncRNA_AR..1.8296	-3, -8099, -3, -8099	upstream, upstream, upstream, upstream	1	1	0	91	96	8	2	2_A375_pNL97_plus_lncRNA_AR..1	166	Gene NUP155	N155, NUP155, KIAA0791	nucleoporin 155kDa	NM_004298, NM_153485, hCT2293835.0, hCT2293837.0, hCT28791.4	206550_s_at	NP_004289.1, NP_705618.1, EAW55957.1, EAW55958.1, EAW55959.1
GeneID.55100	WDR70	5	37,379,412	37,752,774	373,362	+	5	1_A375_pNL7_minus_lncRNA_AR..1..4354, 1_A375_pNL7_minus_lncRNA_AR..1..4355, 1_A375_pNL7_minus_lncRNA_AR..1..4356, 2_A375_pNL97_plus_lncRNA_AR..1.8295, 2_A375_pNL97_plus_lncRNA_AR..1.8296	-6212, -116, 343772, -6212, -116	upstream, upstream, in gene, upstream, upstream	1	1	0	67.33	87.33	7	3	2_A375_pNL97_plus_lncRNA_AR..1	166	Gene WDR70	WDR70, FLJ10233	WD repeat domain 70	NM_018034, hCT2293453.0, hCT2352980.0	219193_at	NP_060504.1, EAW55961.1, EAW55960.1
GeneID.3977	LIFR	5	38,475,065	38,595,507	120,442	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4356, 2_A375_pNL97_plus_lncRNA_AR..1.8299	-6589, -6557	upstream, upstream	1	1	0	16	20	2	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LIFR	LIFR, FLJ99923, SWS, LIF-R, STWS, FLJ98106, CD118, SJS2	leukemia inhibitory factor receptor alpha	NM_001127671, NM_002310, hCT28083.3	205876_at, 225571_at, 225575_at, 227771_at	NP_001121143.1, NP_002301.1, EAW55972.1
GeneID.100506495	LOC100506495	5	38,556,864	38,608,964	52,100	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4356, 2_A375_pNL97_plus_lncRNA_AR..1.8299	45232, 45200	in gene, in gene	1	1	0	16	20	2	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100506495		hypothetical LOC100506495	XR_108573		
GeneID.9180	OSMR	5	38,845,960	38,935,743	89,783	+	1	2_A375_pNL97_plus_lncRNA_AR..1.8302	75512	in gene	0	1	0	14	16	3	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene OSMR	MGC150626, MGC150627, OSMR, MGC75127, OSMRB	oncostatin M receptor	NM_001168355, NM_003999, hCT2292868.0, hCT28778.3	1554008_at, 205729_at	NP_001161827.1, NP_003990.1, EAW55976.1, EAW55977.1
GeneID.253260	RICTOR	5	38,938,022	39,074,501	136,479	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4359, 4_A375_EGR1..1.8717	-251, -251	upstream, upstream	1	0	1	22	15	16	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene RICTOR	mAVO3, RICTOR, KIAA1999, DKFZp686B11164, PIA, MGC39830	RPTOR independent companion of MTOR, complex 2	NM_152756, hCT2293413.1, hCT2293416.1, hCT2352978.0	1552734_at, 226310_at, 226312_at, 228248_at	NP_689969.2, EAW55978.1, EAW55979.1, EAW55980.1
GeneID.2533	FYB	5	39,105,357	39,219,667	114,310	-	1	2_A375_pNL97_plus_lncRNA_AR..1.8303	22803	in gene	0	1	0	9	16	5	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene FYB	PRO0823, ADAP, SLAP-130, FYB	FYN binding protein	NM_199335, NM_001465, hCT1958011.1, hCT2293408.0, hCT2293409.0, hCT2293412.0, hCT28779.3	205285_s_at, 211794_at, 211795_s_at, 227266_s_at	NP_955367.1, NP_001456.3, EAW55982.1, EAW55983.1, EAW55984.1, EAW55985.1, EAW55981.1
GeneID.1601	DAB2	5	39,371,780	39,425,335	53,555	-	2	2_A375_pNL97_plus_lncRNA_AR..1.8304, 2_A375_pNL97_plus_lncRNA_AR..1.8305	25527, 247	in gene, in gene	0	1	0	13.5	18.5	5.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene DAB2	DOC2, FLJ26626, DOC-2, DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	NM_001343, hCT1816997.3, hCT1963174.2, hCT2293389.1, hCT2293390.1, hCT2293393.1, hCT2293395.1	1559370_at, 201278_at, 201279_s_at, 201280_s_at, 210757_x_at, 232898_at, 240873_x_at	NP_001334.2, EAW55989.1, EAW55990.1, EAW55991.1, EAW55993.1, EAW55994.1, EAW55992.1
GeneID.23548	TTC33	5	40,711,676	40,756,072	44,394	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4360, 2_A375_pNL97_plus_lncRNA_AR..1.8308	-88, 272	upstream, in gene	1	1	0	20	18	7	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene TTC33	TTC33, OSRF	tetratricopeptide repeat domain 33	NM_012382, hCT2352979.0, hCT28059.3	219421_at, 231479_at	NP_036514.1, EAW55999.1, EAW55998.1
GeneID.5562	PRKAA1	5	40,759,481	40,798,297	38,816	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4360, 2_A375_pNL97_plus_lncRNA_AR..1.8308	42137, 42497	downstream, downstream	1	1	0	20	18	7	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene PRKAA1	AMPK, MGC33776, MGC57364, PRKAA1, AMPKa1	protein kinase, AMP-activated, alpha 1 catalytic subunit	NM_206907, NM_006251, hCT2298181.0, hCT28571.3	1555177_at, 209799_at, 214917_at, 225984_at, 225985_at	NP_996790.3, NP_006242.5, EAW56000.1, EAW56001.1
GeneID.100506546	LOC100506546	5	40,819,488	40,830,556	11,068	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4361, 2_A375_pNL97_plus_lncRNA_AR..1.8309, 4_A375_EGR1..1.8716	-4740, -4804, -4836	upstream, upstream, upstream	1	1	1	23	20	31	1	4_A375_EGR1..1	31	Gene LOC100506546		hypothetical LOC100506546	XR_112729, XR_108574, XR_113736		
GeneID.6167	RPL37	5	40,831,430	40,835,387	3,957	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4361, 2_A375_pNL97_plus_lncRNA_AR..1.8309, 4_A375_EGR1..1.8716	91, 27, -5	in gene, in gene, upstream	1	1	1	23	20	31	1	4_A375_EGR1..1	31	Gene RPL37	DKFZp686G1699, MGC99572, RPL37, L37	ribosomal protein L37	NM_000997, hCT2298166.1, hCT2298168.1, hCT2298171.1, hCT28572.4	200092_s_at, 224763_at, 224766_at, 224767_at	NP_000988.1, EAW56005.1, EAW56002.1, EAW56003.1, EAW56004.1
GeneID.619564	SNORD72	5	40,832,758	40,832,837	79	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4361, 2_A375_pNL97_plus_lncRNA_AR..1.8309, 4_A375_EGR1..1.8716	-2459, -2523, -2555	upstream, upstream, upstream	1	1	1	23	20	31	1	4_A375_EGR1..1	31	Gene SNORD72	HBII-240, SNORD72	small nucleolar RNA, C/D box 72	NR_002583		
GeneID.84674	CARD6	5	40,841,410	40,855,456	14,046	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4361, 2_A375_pNL97_plus_lncRNA_AR..1.8309, 4_A375_EGR1..1.8716	-6114, -6050, -6018	upstream, upstream, upstream	1	1	1	23	20	31	1	4_A375_EGR1..1	31	Gene CARD6	CARD6, CINCIN1	caspase recruitment domain family, member 6	NM_032587, hCT28573.2	224414_s_at	NP_115976.2, EAW56006.1
GeneID.5019	OXCT1	5	41,730,167	41,870,791	140,624	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4363	391	in gene	1	0	0	21	13	13	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene OXCT1	OXCT, SCOT, OXCT1	3-oxoacid CoA transferase 1	NM_000436, hCT2293185.0, hCT28770.2	202780_at, 244134_at	NP_000427.1, EAW56014.1, EAW56015.1
GeneID.285636	C5orf51	5	41,904,470	41,921,736	17,266	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4364, 1_A375_pNL7_minus_lncRNA_AR..1..4365, 2_A375_pNL97_plus_lncRNA_AR..1.8310	-422, 20936, 20776	upstream, downstream, downstream	1	1	0	19.5	21.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene C5orf51	C5orf51		NM_175921, hCT2293090.0, hCT28477.2	226159_at, 238609_at	NP_787117.3, EAW56016.1, EAW56017.1
GeneID.26272	FBXO4	5	41,925,356	41,941,672	16,316	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4365, 2_A375_pNL97_plus_lncRNA_AR..1.8310	52, -108	in gene, upstream	1	1	0	23	29	15	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene FBXO4	FBX4, FLJ10141, FBXO4, DKFZp547N213	F-box protein 4	NM_012176, NM_033484, hCT1950293.1, hCT1969221.1	220550_at, 223493_at, 233386_at	NP_036308.1, NP_277019.1, EAW56019.1, EAW56020.1
GeneID.2690	GHR	5	42,424,026	42,721,926	297,900	+	2	2_A375_pNL97_plus_lncRNA_AR..1.8311, 2_A375_pNL97_plus_lncRNA_AR..1.8312	-346, 107942	upstream, in gene	0	1	0	9.5	16	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene GHR	GHR, GHBP	growth hormone receptor	NM_000163, hCT1950292.1	205498_at	NP_000154.1, EAW56023.1
GeneID.643977	FLJ32255	5	42,985,503	42,993,468	7,965	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4367, 2_A375_pNL97_plus_lncRNA_AR..1.8313, 2_A375_pNL97_plus_lncRNA_AR..1.8314	1132, 11196, 1244	in gene, downstream, in gene	1	1	0	13	18.5	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene FLJ32255		hypothetical LOC643977	XR_112730, XR_108575, XR_113737	235291_s_at, 235292_at	
GeneID.646987	LOC646987	5	43,014,831	43,018,913	4,082	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4368, 2_A375_pNL97_plus_lncRNA_AR..1.8315	673, 737	in gene, in gene	1	1	0	31	30	16	1	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene LOC646987		hypothetical LOC646987	NR_034085, NR_034086	227901_at	
GeneID.100132356	hCG_2039146	5	43,065,289	43,067,073	1,784	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4369	2017	downstream	1	0	0	24	21	8	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene hCG_2039146	LOC100132356, FLJ90723	hypothetical LOC100132356	NR_034127		
GeneID.100506639	LOC100506639	5	43,067,128	43,093,660	26,532	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4369	-2072	upstream	1	0	0	24	21	8	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene LOC100506639		hypothetical LOC100506639	XR_108576		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.167359	MGC42105	5	43,192,327	43,280,952	88,625	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6317, 2_A375_pNL97_plus_lncRNA_AR..1..6318, 2_A375_pNL97_plus_lncRNA_AR..1..6319, 4_A375_EGR1..1..6719	-1255, 165, 1545, 585	upstream, in gene, in gene, in gene	0	1	1	12	15.33	6.67	3	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene MGC42105	MGC42105, NIM1	serine/threonine-protein kinase NIM1	NM_153361, hCT2293394.1, hCT2293398.0, hCT2293399.1, hCT28035.4	230884_at	NP_699192.1, EAW56052.1, EAW56050.1, EAW56051.1, EAW56053.1
GeneID.56477	CCL28	5	43,381,600	43,412,488	30,888	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6320	15432	in gene	0	1	0	16	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CCL28	MGC71902, CCK1, SCYA28, CCL28, MEC	chemokine (C-C motif) ligand 28	NM_148672, hCT2293567.0, hCT2293566.0, hCT2352988.0, hCT28167.2	224027_at, 224240_s_at	NP_683513.1, EAW56057.1, EAW56058.1, EAW56059.1, EAW56060.1
GeneID.64417	C5orf28	5	43,444,354	43,483,992	39,638	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4371, 2_A375_pNL97_plus_lncRNA_AR..1..6321, 4_A375_EGR1..1..6720	296, 216, 280	in gene, in gene, in gene	1	1	1	16	29	20	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene C5orf28	FLJ21657, MGC149524, MGC90228, C5orf28	chromosome 5 open reading frame 28	NM_022483, hCT1817364.2, hCT2299987.0, hCT2299988.0, hCT2299989.0	219029_at, 236635_at	NP_071928.2, EAW56063.1, EAW56061.1, EAW56062.1, EAW56064.1
GeneID.375444	C5orf34	5	43,486,810	43,515,187	28,377	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4371, 2_A375_pNL97_plus_lncRNA_AR..1..6321, 4_A375_EGR1..1..6720	31491, 31411, 31475	downstream, downstream, downstream	1	1	1	16	29	20	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene C5orf34	C5orf34, MGC48446, FLJ32363	chromosome 5 open reading frame 34	NM_198566, hCT1817367.2	229886_at	NP_940968.1, EAW56065.1
GeneID.10605	PAIP1	5	43,526,369	43,557,521	31,152	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4372, 2_A375_pNL97_plus_lncRNA_AR..1..6322, 2_A375_pNL97_plus_lncRNA_AR..1..6323	417, 1105, 433	in gene, in gene, in gene	1	1	0	52	61	13	1	2_A375_pNL97_plus_lncRNA_AR..1	61	Gene PAIP1	PAIP1, MGC12360	poly(A) binding protein interacting protein 1	NM_006451, NM_182789, NM_183323, hCT1790135.2, hCT2350215.0, hCT2350216.0, hCT2350217.0	208051_s_at, 209063_x_at, 209064_x_at, 210283_x_at, 213754_s_at	NP_006442.2, NP_877590.1, NP_899152.1, EAW56067.1, EAW56068.1, EAW56070.1, EAW56069.1
GeneID.100506674	LOC100506674	5	44,744,517	44,808,862	64,345	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4373, 2_A375_pNL97_plus_lncRNA_AR..1..6324, 4_A375_EGR1..1..6721	14, -34, -496	in gene, upstream, upstream	1	1	1	39	37	26	1	1_A375_pNL7_minus_lncRNA_AR..1	39	Gene LOC100506674		hypothetical LOC100506674	XR_112732, XR_108577, XR_113739		
GeneID.10884	MRPS30	5	44,809,027	44,815,616	6,589	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4373, 2_A375_pNL97_plus_lncRNA_AR..1..6324, 4_A375_EGR1..1..6721	-179, -131, 333	upstream, upstream, in gene	1	1	1	39	37	26	1	1_A375_pNL7_minus_lncRNA_AR..1	39	Gene MRPS30	DKFZp566B2024, PAP, MRPS30, PDCD9, MRP-S30	mitochondrial ribosomal protein S30	NM_016640, hCT8415.3	218398_at	NP_057724.2, EAW56076.1
GeneID.348980	HCN1	5	45,259,352	45,696,220	436,868	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4374, 2_A375_pNL97_plus_lncRNA_AR..1..6325	1660, 1660	in gene, in gene	1	1	0	18	22	1	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene HCN1	BCNG-1, HCN1, HAC-2, BCNG1	hyperpolarization activated cyclic nucleotide-gated potassium channel 1	NM_021072, hCT2348119.0, hCT2348120.0	1558351_at, 1562563_at	NP_066550.2, EAW56077.1, EAW56078.1
GeneID.133418	EMB	5	49,692,031	49,737,234	45,203	-	1	4_A375_EGR1..1..6722	114	in gene	0	0	1	22	15	20	1	4_A375_EGR1..1	20	Gene EMB	MGC71745, EMB	embigin homolog (mouse)	NM_198449, hCT2287655.0, hCT2287656.0, hCT2352898.0		NP_940851.1, EAW54854.1, EAW54852.1, EAW54853.1
GeneID.642366	LOC642366	5	50,872,902	50,879,488	6,586	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6326	240	in gene	0	1	0	14	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene LOC642366		hypothetical LOC642366	XR_112735, XR_108597, XR_113744		
GeneID.3670	ISL1	5	50,678,958	50,690,564	11,606	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6326	290	in gene	0	1	0	14	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ISL1	ISLET1, Isl-1, ISL1	ISL LIM homeobox 1	NM_002202, hCT7708.2	206104_at	NP_002193.2, EAW54861.1
GeneID.53918	PELO	5	52,083,774	52,098,451	14,677	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6328	450	in gene	0	1	0	16	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PELO	PRO1770, CGI-17, PELO	pelota homolog (Drosophila)	NM_015946	1553140_at, 1560359_at, 214660_at, 218472_s_at, 226731_at	NP_057030.3
GeneID.3672	ITGA1	5	52,084,136	52,249,485	165,349	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6328	88	in gene	0	1	0	16	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ITGA1	VLA1, ITGA1, CD49a	integrin, alpha 1	NM_181501		NP_852478.1
GeneID.3673	ITGA2	5	52,285,156	52,390,609	105,453	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4377, 2_A375_pNL97_plus_lncRNA_AR..1..6329	34732, 572	in gene, in gene	1	1	0	18.5	14.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ITGA2	ITGA2, CD49B, GPIa, BR, VLAA2, VLA-2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	NM_002203, hCT1963523.1, hCT31944.3	205032_at, 227314_at	NP_002194.2, EAW54873.1, EAW54872.1
GeneID.4338	MOCS2	5	52,393,892	52,405,598	11,706	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6330	-130	upstream	0	1	0	15	20	13	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MOCS2	MOCS2A, MOCS2B, MCBPE, MOCS2, MPTS, MOCO1	molybdenum cofactor synthesis 2	NM_004531, NM_176806, hCT1813842.1, hCT2287823.0, hCT2352889.0, hCT31945.2	218212_s_at	NP_004522.1, NP_789776.1, EAW54874.1, EAW54875.1, EAW54876.1, EAW54877.1
GeneID.257396	LOC257396	5	52,405,687	52,410,953	5,266	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6330	41	in gene	0	1	0	15	20	13	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC257396		hypothetical LOC257396	NR_034107	236076_at	
GeneID.10468	FST	5	52,776,595	52,781,923	5,328	+	1	4_A375_EGR1..1..6723	1293	in gene	0	0	1	10	11	15	1	4_A375_EGR1..1	15	Gene FST	FST, FS	follistatin	NM_013409, NM_006350, hCT1965559.1, hCT1965560.1, hCT2287716.0, hCT32159.3	204948_s_at, 207345_at, 226847_at	NP_037541.1, NP_006341.1, EAW54880.1, EAW54881.1, EAW54882.1, EAW54883.1
GeneID.54622	ARL15	5	53,180,614	53,606,403	425,789	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4376, 2_A375_pNL97_plus_lncRNA_AR..1..6331, 2_A375_pNL97_plus_lncRNA_AR..1..6332	-317, 217283, -61	upstream, in gene, upstream	1	1	0	17	19.5	9	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ARL15	ARL15, ARFRP2, FLJ20051	ADP-ribosylation factor-like 15	NM_019087, hCT12290.3, hCT2287726.0, hCT2287727.0	219842_at	NP_061960.1, EAW54891.1, EAW54889.1, EAW54890.1
GeneID.112574	SNX18	5	53,813,589	53,842,416	28,827	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4379, 2_A375_pNL97_plus_lncRNA_AR..1..6333	-149, -133	upstream, upstream	1	1	0	37	42	5	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene SNX18	FLJ32560, SH3PX2, FLJ11997, FLJ61062, MGC150829, MGC150827, SNAG1, SH3PXD3B, SNX18	sorting nexin 18	NM_052870, NM_001102575, NM_001145427	1552628_at, 226883_at	NP_443102.2, NP_001096045.1, NP_001138899.1
GeneID.11082	ESM1	5	54,273,695	54,281,414	7,719	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4381	70	in gene	1	0	0	18	13	10	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ESM1	ESM1, endocan	endothelial cell-specific molecule 1	NM_001135604, NM_007036, hCT2288262.0, hCT30831.3	208394_x_at	NP_001129076.1, NP_008967.1, EAW54896.1, EAW54897.1
GeneID.345643	LOC345643	5	54,515,425	54,523,143	7,718	-	3	2_A375_pNL97_plus_lncRNA_AR..1..6336, 4_A375_EGR1..1..6724, 4_A375_EGR1..1..6725	-5361, 359, -6073	upstream, in gene, upstream	0	1	1	16	16.5	21.5	2	4_A375_EGR1..1	26	Gene LOC345643		hypothetical LOC345643	NM_001190787		NP_001177716.1
GeneID.10309	CCNO	5	54,526,980	54,529,508	2,528	-	3	2_A375_pNL97_plus_lncRNA_AR..1..6336, 4_A375_EGR1..1..6724, 4_A375_EGR1..1..6725	1004, 6724, 292	in gene, downstream, in gene	0	1	1	16	16.5	21.5	2	4_A375_EGR1..1	26	Gene CCNO	UDG2, UNG2, FLJ22422, CCNU, CCNO	cyclin O	NM_021147, hCT1954066.1, hCT31711.3	210021_s_at	NP_066970.3, EAW54912.1, EAW54913.1
GeneID.54505	DHX29	5	54,552,073	54,603,521	51,448	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4382	-159	upstream	1	0	0	20	15	15	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene DHX29	DHX29, FLJ21492, DDX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	NM_019030, hCT2349721.0, hCT2349722.0, hCT2352897.0, hCT31708.4	212648_at	NP_061903.2, EAW54916.1, EAW54915.1, EAW54917.1, EAW54918.1
GeneID.23517	SKIV2L2	5	54,603,576	54,721,409	117,833	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4382	104	in gene	1	0	0	20	15	15	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene SKIV2L2	Mtr4, KIAA0052, fSAP118, MGC142069, Dob1, SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	NM_015360, hCT32259.3	1562142_at, 212696_at, 227447_at	NP_056175.3, EAW54919.1
GeneID.8611	PPAP2A	5	54,720,682	54,830,873	110,191	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4383, 2_A375_pNL97_plus_lncRNA_AR..1..6337	121, 377	in gene, in gene	1	1	0	22	16	12	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene PPAP2A	LPP1, LLP1a, PAPalpha1, PPAP2A, PAP2, PAP2alpha2, PAP2a, PAP2a2	phosphatidic acid phosphatase type 2A	NM_003711, NM_176895, hCT1954059.1, hCT1954060.1, hCT2352881.0, hCT30832.3	209147_s_at, 210946_at	NP_003702.2, NP_795714.1, EAW54920.1, EAW54921.1, EAW54922.1, EAW54923.1
GeneID.54514	DDX4	5	55,033,845	55,112,974	79,129	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4384	35147	in gene	1	0	0	17	10	7	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene DDX4	DDX4, VASA, MGC111074	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	NM_001142549, NM_024415, NM_001166534, NM_001166533, hCT2287660.0	221630_s_at	NP_001136021.1, NP_077726.1, NP_001160006.1, NP_001160005.1, EAW54929.1
GeneID.3572	IL6ST	5	55,230,923	55,290,821	59,898	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4385, 2_A375_pNL97_plus_lncRNA_AR..1..6338	-251, -443	upstream, upstream	1	1	0	17	15	13	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene IL6ST	GP130, CD130, GP130-RAPS, CDW130, CDw130, IL6R-beta, IL6ST, DKFZp564F053	interleukin 6 signal transducer (gp130, oncostatin M receptor)	NM_001190981, NM_002184, NM_175767, hCT2288057.1, hCT2288060.1, hCT2288064.1	204863_s_at, 204864_s_at, 211000_s_at, 212195_at, 212196_at, 234474_x_at, 234967_at	NP_001177910.1, NP_002175.2, NP_786943.1, EAW54936.1, EAW54937.1, EAW54938.1
GeneID.441072	FLJ31104	5	55,290,989	55,299,471	8,482	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4385, 2_A375_pNL97_plus_lncRNA_AR..1..6338	83, 275	in gene, in gene	1	1	0	17	15	13	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene FLJ31104		hypothetical LOC441072	XR_112737, XR_108600, XR_113742	1557466_at	
GeneID.79722	ANKRD55	5	55,395,507	55,529,186	133,679	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4386, 1_A375_pNL7_minus_lncRNA_AR..1..4387, 2_A375_pNL97_plus_lncRNA_AR..1..6339	109394, 49666, 120594	in gene, in gene, in gene	1	1	0	17	14.33	6	3	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ANKRD55	MGC126013, ANKRD55, MGC126014, FLJ11795	ankyrin repeat domain 55	NM_024669	220112_at, 240456_at	NP_078945.2
GeneID.10769	PLK2	5	57,749,809	57,755,913	6,104	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4389, 2_A375_pNL97_plus_lncRNA_AR..1..6346, 4_A375_EGR1..1..6728, 4_A375_EGR1..1..6729	9, -487, 41, -535	in gene, upstream, in gene, upstream	1	1	1	19	22	20	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene PLK2	SNK, PLK2	polo-like kinase 2 (Drosophila)	NM_006622, hCT2287616.0, hCT30636.2	201939_at	NP_006613.2, EAW54973.1, EAW54972.1
GeneID.100289379	LOC100289379	5	57,756,088	57,756,766	678	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4389, 2_A375_pNL97_plus_lncRNA_AR..1..6346, 4_A375_EGR1..1..6728, 4_A375_EGR1..1..6729	862, 366, 894, 316	downstream, in gene, downstream, in gene	1	1	1	19	22	20	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100289379		hypothetical protein LOC100289379	XM_002342510		XP_002342551.1
GeneID.115827	RAB3C	5	57,878,939	58,147,406	268,467	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4390, 2_A375_pNL97_plus_lncRNA_AR..1..6349	-91, -107	upstream, upstream	1	1	0	39	45	7	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene RAB3C	RAB3C	RAB3C, member RAS oncogene family	NM_138453, hCT1952951.0, hCT2287750.0	241977_s_at	NP_612462.1, EAW54978.1, EAW54979.1
GeneID.5144	PDE4D	5	58,264,865	59,783,925	1,519,060	-	11	1_A375_pNL7_minus_lncRNA_AR..1..4391, 1_A375_pNL7_minus_lncRNA_AR..1..4392, 1_A375_pNL7_minus_lncRNA_AR..1..4393, 1_A375_pNL7_minus_lncRNA_AR..1..4394, 1_A375_pNL7_minus_lncRNA_AR..1..4395, 1_A375_pNL7_minus_lncRNA_AR..1..4396, 2_A375_pNL97_plus_lncRNA_AR..1..6350, 2_A375_pNL97_plus_lncRNA_AR..1..6351, 2_A375_pNL97_plus_lncRNA_AR..1..6352, 2_A375_pNL97_plus_lncRNA_AR..1..6353, 4_A375_EGR1..1..6730	1448565, 1380213, 1188853, 594005, 291509, 155221, 1380389, 1293973, 593973, 395221, 1448565	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	17	19	6.5	8	2_A375_pNL97_plus_lncRNA_AR..1	44	Gene PDE4D	STRK1, DKFZp686M11213, PDE4DN2, FLJ97311, DPDE3, PDE4D, HSPDE4D	phosphodiesterase 4D, cAMP-specific	NM_006203, NM_001104631, NM_001165899, hCT1952950.2, hCT2288589.1, hCT2288591.1, hCT2288599.1, hCT2288602.1, hCT2348493.0, hCT2348494.0, hCT2348495.0, hCT2348868.0, hCT2348869.0, hCT2348870.0	1554717_a_at, 204491_at, 210836_x_at, 210837_s_at, 211840_s_at	NP_006194.2, NP_001098101.1, NP_001159371.1, EAW54983.1, EAW54988.1, EAW54989.1, EAW54982.1, EAW54984.1, EAW54985.1, EAW54986.1, EAW54987.1, EAW54990.1, EAW54991.1, EAW54992.1
GeneID.642781	LOC642781	5	58,335,035	58,336,614	1,579	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4391, 4_A375_EGR1..1..6730	325, 325	in gene, in gene	1	0	1	13	14	17	1	4_A375_EGR1..1	17	Gene LOC642781		hypothetical LOC642781	XR_112733, XR_108601, XR_113743		
GeneID.55789	DEPDC1B	5	59,892,739	59,995,993	103,254	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6354	-23	upstream	0	1	0	14	24	14	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene DEPDC1B	FLJ11252, BRCC3, XTP1, DEPDC1B	DEP domain containing 1B	NM_001145208, NM_018369, hCT31642.3	226980_at	NP_001138680.1, NP_060839.2, EAW54998.1
GeneID.91942	NDUFAF2	5	60,240,956	60,448,864	207,908	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4397, 2_A375_pNL97_plus_lncRNA_AR..1..6355, 4_A375_EGR1..1..6731	217092, 217188, 217124	downstream, downstream, downstream	1	1	1	20	17	14	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene NDUFAF2	FLJ22398, B17.2L, NDUFA12L, NDUFAF2, MMTN, mimitin	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2	NM_174889, hCT31644.3	228355_s_at	NP_777549.1, EAW55008.1
GeneID.643155	C5orf43	5	60,453,536	60,458,302	4,766	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4397, 2_A375_pNL97_plus_lncRNA_AR..1..6355, 4_A375_EGR1..1..6731	254, 156, 222	in gene, in gene, in gene	1	1	1	20	17	14	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene C5orf43	C5orf43, DKFZp686E2158, DKFZp686O1365	chromosome 5 open reading frame 43	NM_001048249	224740_at	NP_001041714.1
GeneID.57688	ZSWIM6	5	60,628,100	60,841,999	213,899	+	5	1_A375_pNL7_minus_lncRNA_AR..1..4398, 1_A375_pNL7_minus_lncRNA_AR..1..4399, 2_A375_pNL97_plus_lncRNA_AR..1..6356, 2_A375_pNL97_plus_lncRNA_AR..1..6357, 2_A375_pNL97_plus_lncRNA_AR..1..6358	-932, -132, -4004, -1026, -100	upstream, upstream, upstream, upstream, upstream	1	1	0	22	24.67	7.33	3	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene ZSWIM6	DKFZp779P0344, ZSWIM6, KIAA1577	zinc finger, SWIM-type containing 6	NM_020928	226208_at	NP_065979.1
GeneID.285668	FLJ37543	5	60,933,636	61,002,362	68,726	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4400	7516	in gene	1	0	0	20	12	2	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene FLJ37543	MGC138187, FLJ45901, MGC138213	hypothetical protein FLJ37543	NM_173667, hCT2341297.0	1553426_at	NP_775938.1, EAW51393.1
GeneID.27292	DIMT1L	5	61,684,351	61,699,728	15,377	-	3	2_A375_pNL97_plus_lncRNA_AR..1..6359, 2_A375_pNL97_plus_lncRNA_AR..1..6360, 4_A375_EGR1..1..6733	32, -6660, 16	in gene, upstream, in gene	0	1	1	16.5	22	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene DIMT1L	DIMT1L, HUSSY5, DIMT1, DIM1, HSA9761	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	NM_014473, hCT1963565.1, hCT2285631.0, hCT9073.2	204405_x_at, 210802_s_at, 213598_at, 217106_x_at	NP_055288.1, EAW51386.1, EAW51384.1, EAW51385.1
GeneID.51194	IPO11	5	61,708,573	61,924,416	215,843	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6359, 2_A375_pNL97_plus_lncRNA_AR..1..6360, 4_A375_EGR1..1..6733	-6677, 35, -6661	upstream, in gene, upstream	0	1	1	16.5	22	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene IPO11	RanBP11, IPO11	importin 11	NM_016338, NM_001134779, hCT2286585.1, hCT2286586.0, hCT8787.3	1557770_at, 222859_at, 234304_s_at, 238488_at	NP_057422.3, NP_001128251.1, EAW51379.1, EAW51380.1, EAW51381.1
GeneID.3350	HTR1A	5	63,256,278	63,257,546	1,268	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4401, 2_A375_pNL97_plus_lncRNA_AR..1..6361	-1494, -1494	upstream, upstream	1	1	0	18	23	2	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene HTR1A	ADRBRL1, 5-HT1A, HTR1A, ADRB2RL1, 5HT1a	5-hydroxytryptamine (serotonin) receptor 1A	NM_000524, hCT7678.2	221351_at	NP_000515.2, EAW51377.1
GeneID.285671	RNF180	5	63,461,671	63,668,696	207,025	+	1	4_A375_EGR1..1..6735	70937	in gene	0	0	1	2	2	14	1	4_A375_EGR1..1	14	Gene RNF180	RNF180, MGC120328, MGC120326	ring finger protein 180	NM_178532, NM_001113561, hCT1785663.3, hCT2349465.0, hCT2349466.0	236644_at, 242033_at, 242985_x_at	NP_848627.1, NP_001107033.1, EAW51373.1, EAW51374.1, EAW51375.1
GeneID.285672	SFRS12IP1	5	64,013,975	64,064,496	50,521	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4402, 2_A375_pNL97_plus_lncRNA_AR..1..6362	-80, -48	upstream, upstream	1	1	0	44	35	6	1	1_A375_pNL7_minus_lncRNA_AR..1	44	Gene SFRS12IP1	FLJ36754, P18SRP, SREK1IP1, MGC150549, MGC150548, MGC131910, SFRS12IP1	SFRS12-interacting protein 1	NM_173829, hCT2285279.1, hCT2285280.1, hCT8930.3	1553581_s_at, 217606_at, 227266_at, 235390_at	NP_776190.1, EAW51366.1, EAW51367.1, EAW51368.1
GeneID.10283	CWC27	5	64,064,755	64,314,590	249,835	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4402, 2_A375_pNL97_plus_lncRNA_AR..1..6362	-179, -211	upstream, upstream	1	1	0	44	35	6	1	1_A375_pNL7_minus_lncRNA_AR..1	44	Gene CWC27	NY-CO-10, CWC27, SDCCAG10	CWC27 spliceosome-associated protein homolog (S. cerevisiae)	NM_005869, hCT2352456.0, hCT8929.2	1555495_a_at, 1556841_at, 223337_at	NP_005860.2, EAW51364.1, EAW51365.1
GeneID.11174	ADAMTS6	5	64,444,563	64,777,704	333,141	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4403	283144	in gene	1	0	0	15	9	5	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene ADAMTS6	ADAM-TS6, ADAMTS-6, ADAMTS6, ADAM-TS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	NM_197941	1570351_at, 220866_at, 237411_at	NP_922932.2
GeneID.64105	CENPK	5	64,813,593	64,858,995	45,402	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6363	-109	upstream	0	1	0	13	24	16	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CENPK	P33, AF5alpha, CENP-K, Solt, FKSG14, CENPK	centromere protein K	NM_022145, hCT1785461.3, hCT1966906.1	222848_at	NP_071426.2, EAW51353.1, EAW51354.1

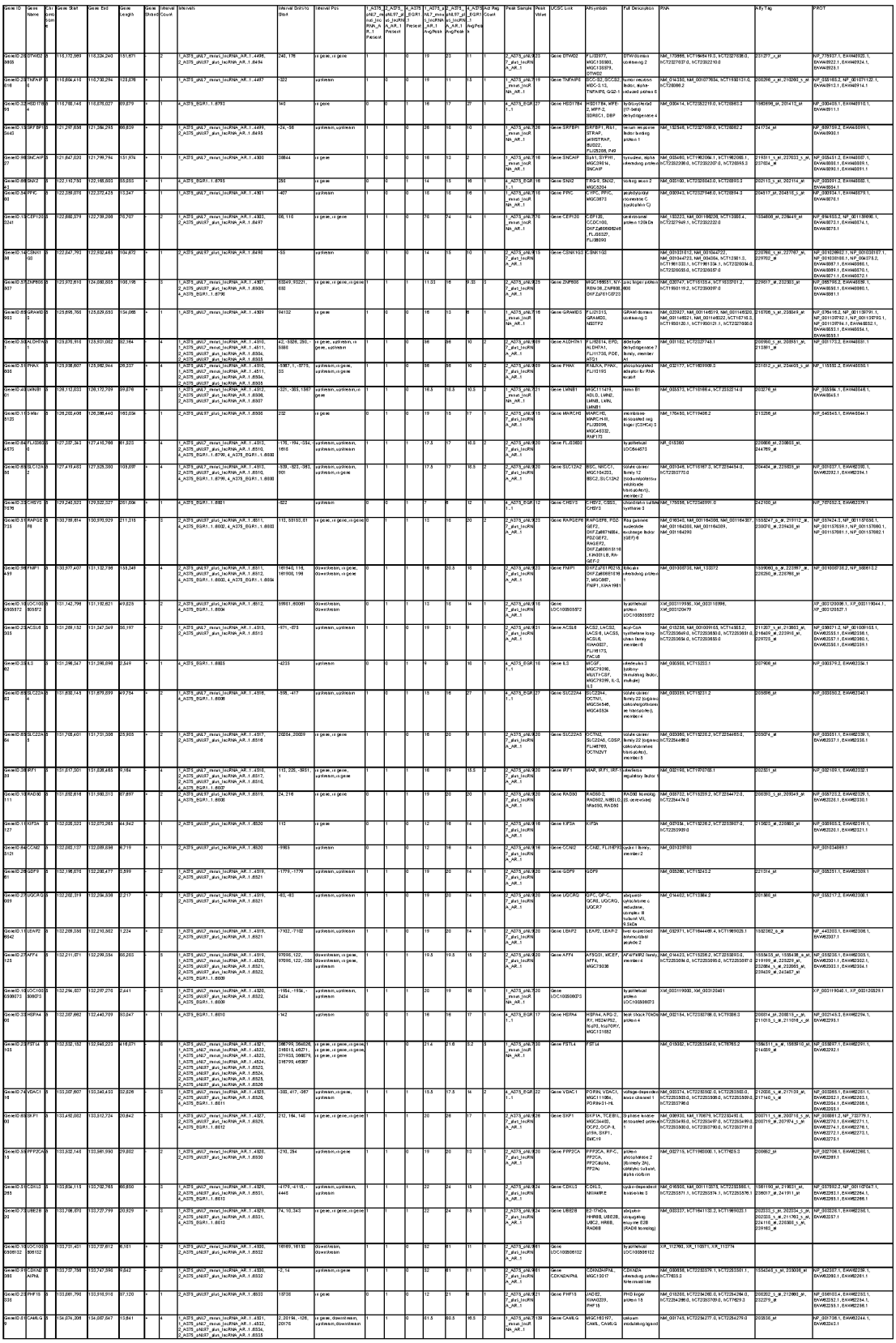
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:23398	PPWD1	5	64,859,131	64,883,373	24,242	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6363	-27	upstream	0	1	0	13	24	16	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PPWD1	PPWD1, KIAA0073	peptidylprolyl isomerase domain and WD repeat containing 1	NM_015342, hCT8916.2	213463_at	NP_056157.1, EAW51352.1
GeneID:54557	SGTB	5	64,961,755	65,017,941	56,186	-	1	4_A375_EGR1..1..6736	149	in gene	0	0	1	13	16	14	1	4_A375_EGR1..1	14	Gene SGTB	SGTB, FLJ39002, SGT2	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	NM_019072, hCT8915.4	228745_at, 232084_at	NP_061945.1, EAW51342.1
GeneID:57486	NLN	5	65,018,023	65,125,111	107,088	+	1	4_A375_EGR1..1..6736	-231	upstream	0	0	1	13	16	14	1	4_A375_EGR1..1	14	Gene NLN	EP24.16, KIAA1226, AGTBP, FLJ23002, MOP, DKFZp564F123, NLN	neurolysin (metallopeptidase M3 family)	NM_020726, hCT1967726.1, hCT2266653.0, hCT8918.3	224083_at, 225942_at, 225943_at, 225944_at, 234762_x_at	NP_065777.1, EAW51338.1, EAW51339.1, EAW51340.1
GeneID:55914	ERBB2IP	5	65,222,384	65,376,850	154,466	+	1	4_A375_EGR1..1..6737	-1360	upstream	0	0	1	14	11	16	1	4_A375_EGR1..1	16	Gene ERBB2IP	ERBB2IP, LAP2, ERBIN	erbb2 interacting protein	NM_001006600, NM_018695, hCT1963048.1, hCT2266660.1, hCT2266662.1, hCT8913.3	217941_s_at, 222473_s_at, 232896_at	NP_001006600.1, NP_061165.1, EAW51332.1, EAW51333.1, EAW51334.1, EAW51335.1
GeneID:140890	SFRS12	5	65,440,085	65,476,716	36,631	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4404, 2_A375_pNL97_plus_lncRNA_AR..1..6364	43, 43	in gene, in gene	1	1	0	14	19	10	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SFRS12	SREK1, DKFZp564B176, SRrp86, SFRS12, MGC133045, SRrp508	splicing factor, arginine/serine-rich 12	NM_139168, NM_001077199, hCT2266675.0, hCT2266678.0, hCT2352462.0, hCT8917.3	1568763_at, 212721_at, 243381_at, 244287_at	NP_631907.1, NP_001070667.1, EAW51328.1, EAW51329.1, EAW51330.1, EAW51331.1
GeneID:401191	FLJ46010	5	65,492,117	65,867,801	375,684	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4405	36555	in gene	1	0	0	23	16	5	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene FLJ46010		FLJ46010 protein	XR_112740, XR_108603, XR_113746		
GeneID:375449	MAST4	5	65,892,176	66,465,423	573,247	+	1	4_A375_EGR1..1..6738	569808	in gene	0	0	1	8	8	16	1	4_A375_EGR1..1	16	Gene MAST4	KIAA0303, MAST4, DKFZp686N1467, FLJ16540, DKFZp686E18148, FLJ33039	microtubule associated serine/threonine kinase family member 4	NM_198828, NM_015183, NM_001164664, hCT1950015.1, hCT2265415.0, hCT2265417.0	1554652_s_at	NP_942123.1, NP_055998.1, NP_001158136.1, EAW51319.1, EAW51320.1, EAW51321.1
GeneID:891	CCNB1	5	68,462,913	68,474,072	11,159	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6371	-65	upstream	0	1	0	15	24	15	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene CCNB1	CCNB1, CCNB	cyclin B1	NM_031966, hCT16307.3	214710_s_at, 228729_at	NP_114172.1, EAW51306.1
GeneID:64946	CENPH	5	68,485,375	68,506,184	20,809	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6372, 4_A375_EGR1..1..6740	193, 28385	in gene, downstream	0	1	1	13	18.5	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CENPH	CENPH, PMF1, NNF1	centromere protein H	NM_022909, hCT18305.3, hCT2352463.0	231772_x_at	NP_075060.1, EAW51304.1, EAW51305.1
GeneID:92259	MRPS36	5	68,513,573	68,525,985	12,412	+	1	4_A375_EGR1..1..6740	187	in gene	0	0	1	14	16	17	1	4_A375_EGR1..1	17	Gene MRPS36	MGC22896, DC47, MRP-S36, MRPS36	mitochondrial ribosomal protein S36	NM_033281, hCT2265527.0, hCT2265529.0	224302_s_at	NP_150597.1, EAW51302.1, EAW51303.1
GeneID:6880	TAF9	5	68,647,553	68,665,840	18,287	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4406, 2_A375_pNL97_plus_lncRNA_AR..1..6374, 4_A375_EGR1..1..6743, 4_A375_EGR1..1..6744	288, 272, 347, -112	in gene, in gene, in gene, upstream	1	1	1	21	23	16	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TAF9	AD-004, TAF9, MGC.1603, CGI-137, MGC1603, MGC.5067, MGC5067, CINAP, TAFII32, TAF2G, TAFII31, MGC.3647, AK6, CIP, hCINAP, TAFIID32, MGC3647	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	NM_001015891, NM_001015892, NM_016283, NM_003187, hCT2265305.0, hCT2265307.0, hCT2265309.0, hCT2265310.0, hCT2348066.0, hCT2348067.0, hCT2352461.0, hCT28432.2	202168_at, 203893_at	NP_001015891.1, NP_001015892.1, NP_003178.1, NP_057367.1, EAW51292.1, EAW51296.1, EAW51290.1, EAW51291.1, EAW51293.1, EAW51294.1, EAW51295.1, EAW51297.1
GeneID:5884	RAD17	5	68,665,124	68,710,628	45,504	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4406, 2_A375_pNL97_plus_lncRNA_AR..1..6374, 4_A375_EGR1..1..6743, 4_A375_EGR1..1..6744	428, 444, 369, 628	in gene, in gene, in gene, in gene	1	1	1	21	23	16	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RAD17	RAD24, RAD17, FLJ41520, RAD17SP, R24L, HRAD17, CCYC	RAD17 homolog (S. pombe)	NM_002873, NM_133338, NM_133339, NM_133340, NM_133341, NM_133342, NM_133343, NM_133344, hCT1959762.1, hCT1981992.1, hCT1981993.1, hCT1986941.1, hCT2265538.0, hCT2265541.0, hCT2265544.0, hCT2265546.0, hCT2265547.0, hCT2265550.0, hCT28290.2	207405_s_at, 210826_x_at, 211228_s_at	NP_002864.1, NP_579916.1, NP_579917.1, NP_579918.1, NP_579919.1, NP_579920.1, NP_579921.1, NP_579922.1, EAW51279.1, EAW51280.1, EAW51281.1, EAW51282.1, EAW51283.1, EAW51284.1, EAW51285.1, EAW51286.1, EAW51287.1, EAW51288.1, EAW51289.1
GeneID:153562	MARVELD2	5	68,710,939	68,737,890	26,951	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4407	35237	downstream	1	0	0	19	10	3	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene MARVELD2	MARVELD2, FLJ30532, MARVD2, DFNB49, MRVLDC2, Tric	MARVEL domain containing 2	NM_001038603, hCT1781389.3, hCT2349464.0	235141_at, 235955_at	NP_001033692.2, EAW51277.1, EAW51276.1
GeneID:100505674	LOC100505674	5	70,647,682	70,742,169	94,487	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4408, 2_A375_pNL97_plus_lncRNA_AR..1..6375, 4_A375_EGR1..1..6745	-9287, -9351, -9351	upstream, upstream, upstream	1	1	1	18	17	17	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene LOC100505674		hypothetical LOC100505674	XR_108564		
GeneID:55814	BDP1	5	70,751,442	70,863,649	112,207	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4408, 2_A375_pNL97_plus_lncRNA_AR..1..6375, 4_A375_EGR1..1..6745	14, 78, 78	in gene, in gene, in gene	1	1	1	18	17	17	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene BDP1	KIAA1241, BDP1, TFIIIB", TFC5, TFIIIB150, DKFZp686C01233, HSA238520, TFIIIB90, DKFZp686K0631, KIAA1689, TFNR, TAF3B1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	NM_018429, hCT2308214.1, hCT29087.3	224227_s_at, 226290_at, 231939_s_at	NP_060899.2, EAW95688.1, EAW95689.1
GeneID:9607	CARTPT	5	71,014,990	71,016,875	1,885	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4409, 2_A375_pNL97_plus_lncRNA_AR..1..6376	402, 265	in gene, in gene	1	1	0	25	26	9	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene CARTPT	CARTPT, CART	CART prepropeptide	NM_004291, hCT28342.1	206339_at	NP_004282.1, EAW95694.1
GeneID:4131	MAP1B	5	71,403,118	71,505,397	102,279	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4412, 4_A375_EGR1..1..6746, 4_A375_EGR1..1..6747	413, -174, 402	in gene, upstream, in gene	1	0	1	15	12.5	17	2	4_A375_EGR1..1	19	Gene MAP1B	FUTSCH, DKFZp686F1345, FLJ38954, DKFZp686E1099, MAP1B, MAP5	microtubule-associated protein 1B	NM_005909, hCT2308221.0, hCT2308223.0, hCT2357900.0, hCT2357901.0, hCT29083.3	214577_at, 226084_at	NP_005900.2, EAW95697.1, EAW95698.1, EAW95696.1, EAW95699.1, EAW95700.1
GeneID:23107	MRPS27	5	71,515,236	71,616,084	100,848	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4413, 2_A375_pNL97_plus_lncRNA_AR..1..6379, 4_A375_EGR1..1..6748	11668, 11748, 11956	in gene, in gene, in gene	1	1	1	21	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MRPS27	MRPS27, FLJ23348, FLJ21764, KIAA0264, MRP-S27, S27mt	mitochondrial ribosomal protein S27	NM_015084, hCT2308240.0, hCT2357898.0, hCT29088.3	1563970_at, 212145_at	NP_055899.2, EAW95701.1, EAW95702.1, EAW95703.1
GeneID:100130998	LOC100130998	5	71,801,740	71,804,201	2,461	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4413, 2_A375_pNL97_plus_lncRNA_AR..1..6379, 4_A375_EGR1..1..6748	-215, -135, 73	upstream, upstream, in gene	1	1	1	21	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100130998		hypothetical protein LOC100130998	XM_003119951, XM_003118537, XM_003120464		XP_003119999.1, XP_003118585.1, XP_003120512.1
GeneID:167465	ZNF366	5	71,739,234	71,803,249	64,015	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4414, 4_A375_EGR1..1..6749	41425, 46929	in gene, in gene	1	0	1	14	14.5	9	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ZNF366	DCSCRIPT, FLJ39798, ZNF366	zinc finger protein 366	NM_152625, hCT28939.4	238570_at	NP_689838.1, EAW95707.1
GeneID:3842	TNPO1	5	72,112,418	72,210,215	97,797	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4415, 2_A375_pNL97_plus_lncRNA_AR..1..6380, 2_A375_pNL97_plus_lncRNA_AR..1..6381	31586, -226, 31486	in gene, upstream, in gene	1	1	0	20	24	13	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene TNPO1	MIP, MIP1, TNPO1, IPO2, KPNB2, TRN	transportin 1	NM_153188, NM_002270, hCT2308251.0, hCT2308252.0, hCT2308253.0	1557278_s_at, 207657_x_at, 209225_x_at, 209226_s_at, 221829_s_at	NP_694858.1, NP_002261.3, EAW95713.1, EAW95714.1, EAW95715.1
GeneID:115548	FCHO2	5	72,251,808	72,386,349	134,541	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6382	-224	upstream	0	1	0	12	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene FCHO2	FCHO2	FCH domain only 2	NM_138782, NM_001146032, hCT1797265.2	1555153_s_at, 226220_at	NP_620137.2, NP_001139504.1, EAW95716.1
GeneID:2297	FOXD1	5	72,742,083	72,744,352	2,269	-	1	4_A375_EGR1..1..6751	-808	upstream	0	0	1	10	7	14	1	4_A375_EGR1..1	14	Gene FOXD1	FOXD1, FKHL8, FREAC4	forkhead box D1	NM_004472, hCT29078.3	206307_s_at, 213972_at	NP_004463.1, EAW95721.1
GeneID:689	BTF3	5	72,794,250	72,801,446	7,196	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4417, 2_A375_pNL97_plus_lncRNA_AR..1..6385, 4_A375_EGR1..1..6752	310, 310, -136	in gene, in gene, upstream	1	1	1	20	22	26	1	4_A375_EGR1..1	26	Gene BTF3	BTF3a, NACB, BETA-NAC, BTF3b, BTF3	basic transcription factor 3	NM_001207, NM_001037637, hCT1950011.1, hCT1950012.1, hCT2308325.0, hCT2308332.0, hCT2357895.0, hCT29079.3	208517_x_at, 211939_x_at, 214800_x_at, 217461_x_at, 243165_at	NP_001198.2, NP_001032726.1, EAW95723.1, EAW95726.1, EAW95727.1, EAW95728.1, EAW95724.1, EAW95725.1
GeneID:57763	ANKRA2	5	72,848,025	72,861,511	13,486	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6386	327	in gene	0	1	0	13	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene ANKRA2	ANKRA2, ANKRA	ankyrin repeat, family A (RFXANK-like), 2	NM_023039, hCT2308369.0, hCT29082.3	218769_s_at	NP_075526.1, EAW95730.1, EAW95729.1
GeneID:84135	UTP15	5	72,861,598	72,877,794	16,196	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6386	-414	upstream	0	1	0	13	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene UTP15	FLJ12787, UTP15, NET21	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	NM_032175, hCT29081.3	228043_at, 228050_at	NP_115551.2, EAW95731.1
GeneID:8507	ENC1	5	73,923,234	73,937,249	14,015	-	1	4_A375_EGR1..1..6753	993	in gene	0	0	1	15	19	21	1	4_A375_EGR1..1	21	Gene ENC1	KLHL37, ENC1, KLHL35, TP53I10, ENC-1, CCL28, NRPB, FLJ39259, PIG10	ectodermal-neural cortex (with BTB-like domain)	NM_003633, hCT28334.2	201340_s_at, 201341_at	NP_003624.1, EAW95740.1
GeneID:84340	GFM2	5	74,017,031	74,063,042	46,011	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4419, 2_A375_pNL97_plus_lncRNA_AR..1..6390, 4_A375_EGR1..1..6754	66, 34, 194	in gene, in gene, in gene	1	1	1	51	49	16	1	1_A375_pNL7_minus_lncRNA_AR..1	51	Gene GFM2	hEFG2, RRF2mt, GFM2, mEF-G 2, EF-G2mt, EFG2, MRRF2, MST027, RRF2	G elongation factor, mitochondrial 2	NM_032380, NM_170681, NM_170691, hCT1951688.1, hCT1989088.1, hCT2308719.0, hCT2308720.0, hCT2357904.0, hCT29439.3	225392_at, 231917_at, 231918_s_at	NP_115756.2, NP_733781.1, NP_733792.1, EAW95743.1, EAW95747.1, EAW95748.1, EAW95744.1, EAW95745.1, EAW95746.1
GeneID:10412	NSA2	5	74,063,103	74,072,734	9,631	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4419, 2_A375_pNL97_plus_lncRNA_AR..1..6390, 4_A375_EGR1..1..6754	-127, -95, -255	upstream, upstream, upstream	1	1	1	51	49	16	1	1_A375_pNL7_minus_lncRNA_AR..1	51	Gene NSA2	TINP1, YR-29, NSA2, HUSSY-29, HCLG1, CDK105, HUSSY29, HCL-G1	NSA2 ribosome biogenesis homolog (S. cerevisiae)	NM_014886, hCT29438.3	201922_at	NP_055701.1, EAW95749.1
GeneID:26049	FAM169A	5	74,073,399	74,162,615	89,216	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4419, 4_A375_EGR1..1..6755	99839, 1047	downstream, in gene	1	0	1	29.5	29.5	15	2	1_A375_pNL7_minus_lncRNA_AR..1	51	Gene FAM169A	KIAA0888, FAM169A	family with sequence similarity 169, member A	NM_015566	213954_at, 235048_at	NP_056381.1
GeneID:3156	HMGCR	5	74,632,993	74,657,926	24,933	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6391	-321	upstream	0	1	0	16	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene HMGCR	HMGCR, LDLCQ3	3-hydroxy-3-methylglutaryl-CoA reductase	NM_000859, NM_001130996, hCT1795806.2, hCT2308397.0, hCT2357902.0	202539_s_at, 202540_s_at	NP_000850.1, NP_001124468.1, EAW95754.1, EAW95755.1, EAW95756.1
GeneID:10087	COL4A3BP	5	74,666,928	74,807,806	140,878	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4420, 2_A375_pNL97_plus_lncRNA_AR..1..6392	46, -18	in gene, upstream	1	1	0	20	23	15	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene COL4A3BP	CERTL, COL4A3BP, FLJ20597, STARD11, CERT, GPBP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	NM_001130105, NM_031361, NM_005713, hCT1987070.2, hCT2357887.0, hCT2357888.0, hCT2357889.0, hCT9879.4	219625_s_at, 223465_at, 223466_x_at	NP_001123577.1, NP_112729.1, NP_005704.1, EAW95757.1, EAW95758.1, EAW95760.1, EAW95759.1, EAW95761.1
GeneID:51426	POLK	5	74,807,657	74,895,646	87,989	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4420, 2_A375_pNL97_plus_lncRNA_AR..1..6392	103, 167	in gene, in gene	1	1	0	20	23	15	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene POLK	DINP, POLQ, POLK, DINB1	polymerase (DNA directed) kappa	NM_016218, hCT1951642.1, hCT2308400.0, hCT2357906.0, hCT9412.3	1555317_at, 223260_s_at, 223261_at	NP_057302.1, EAW95763.1, EAW95762.1, EAW95764.1, EAW95765.1
GeneID:728780	ANKDD1B	5	74,907,460	74,965,449	57,989	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4421	52124	in gene	1	0	0	17	15	6	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ANKDD1B	ANKDD1B	ankyrin repeat and death domain containing 1B	XM_001714463, XM_001128459, XM_001715633		XP_001714535.2, XP_001128459.3, XP_001715685.2
GeneID:134359	C5orf37	5	74,970,023	75,013,313	43,290	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4421, 1_A375_pNL7_minus_lncRNA_AR..1..4422, 2_A375_pNL97_plus_lncRNA_AR..1..6393	53729, 97, 145	downstream, in gene, in gene	1	1	0	17	17.5	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C5orf37	C5orf37, MGC120443, MGC120442, POC5, FLJ35779, MGC120444	POC5 centriolar protein homolog (Chlamydomonas)	NM_152408, NM_001099271, hCT2350225.0, hCT2350226.0, hCT9880.4	227287_at	NP_689621.2, NP_001092741.1, EAW95767.1, EAW95768.1, EAW95769.1
GeneID:22987	SV2C	5	75,379,305	75,621,416	242,111	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4423, 2_A375_pNL97_plus_lncRNA_AR..1..6396	20695, 20759	in gene, in gene	1	1	0	41	65	3	1	2_A375_pNL97_plus_lncRNA_AR..1	65	Gene SV2C	MGC118675, MGC118677, SV2C, MGC118676, MGC118674	synaptic vesicle glycoprotein 2C	NM_014979, hCT10295.3, hCT2308383.0	1562372_at, 216086_at	NP_055794.1, EAW95772.1, EAW95771.1
GeneID:2150	F2RL1	5	76,114,833	76,131,140	16,307	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6398	20047	downstream	0	1	0	15	20	5	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene F2RL1	F2RL1, PAR2, GPR11	coagulation factor II (thrombin) receptor-like 1	NM_005242, hCT28289.3	206429_at, 213506_at	NP_005233.3, EAW95782.1
GeneID:170591	S100Z	5	76,145,826	76,217,056	71,230	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4424	24366	in gene	1	0	0	16	12	0	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene S100Z	Gm625, S100-zeta, S100Z	S100 calcium binding protein Z	NM_130772, hCT1797346.1, hCT2308559.0	1554876_a_at	NP_570128.2, EAW95783.1, EAW95784.1
GeneID:84327	ZBED3	5	76,372,532	76,383,030	10,498	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4425, 2_A375_pNL97_plus_lncRNA_AR..1..6399	214, 374	in gene, in gene	1	1	0	18	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ZBED3	ZBED3, MGC15435	zinc finger, BED-type containing 3	NM_032367, hCT1646174.3, hCT2308684.0	228402_at	NP_115743.1, EAW95791.1, EAW95790.1
GeneID:677828	SNORA47	5	76,376,259	76,376,396	137	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4425, 2_A375_pNL97_plus_lncRNA_AR..1..6399	-6420, -6260	upstream, upstream	1	1	0	18	19	11	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SNORA47	HBI-115, SNORA47	small nucleolar RNA, H/ACA box 47	NR_003014		
GeneID:728723	LOC728723	5	76,382,623	76,444,176	61,553	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4425, 1_A375_pNL7_minus_lncRNA_AR..1..4426, 2_A375_pNL97_plus_lncRNA_AR..1..6399	193, 46809, 33	in gene, in gene, in gene	1	1	0	18	18	11	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC728723		hypothetical LOC728723	NR_024398	241423_at	
GeneID:55255	WDR41	5	76,728,089	76,788,332	60,263	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4427, 2_A375_pNL97_plus_lncRNA_AR..1..6401	204, 119	in gene, in gene	1	1	0	17	15	11	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene WDR41	MSTP048, WDR41, FLJ10904	WD repeat domain 41	NM_018268, hCT1951665.1, hCT2308678.0, hCT29327.3	218055_s_at, 222503_s_at, 240637_at	NP_060738.2, EAW95806.1, EAW95805.1, EAW95807.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_uN27_mi_lncRNA_R_1 Present	2_A375_uN27_mi_lncRNA_R_1 Present	3_A375_1_A375_NL7_mi_lncRNA_R_1 Present	4_A375_2_A375_uN37_pl_lncRNA_R_1 Avg Peak	4_A375_pl_EGFR_lncRNA_R_1 Avg Peak	Add Tag Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
Gene ID:2357	FP	5	78,324,327	78,334,322	9,995	-	1	4_A375_EGFR:1..6756	1785	nr gene	0	0	1	8	8	14	1	4_A375_EGFR:1..1	14	Gene:OFP	MGC3181, OTF	orthopedia homeobox	NM_032109, XM_005272	225855_s_at	231455_at	NP_115485.1, EAW65899.1
Gene ID:8	AP1B1	5	77,296,150	77,310,525	14,376	-	1	1_A375_uN37_mirvol_lncRNA_AR:1..4429	192	upstream	1	0	0	16	17	7	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	16	Gene:AP1B1	HIP92, IFE, HIP92, ADTB1, AP1B1, ADTB1A	adaptor-related protein complex 1 beta 1 subunit	NM_003664, XM_005	230141_s_at	203142_s_at	NP_003655.3, EAW66112.1, EAW66111.1, EAW66112.1
Gene ID:7	LOC728	5	77,854,825	77,855,764	940	+	2	1_A375_uN37_mirvol_lncRNA_AR:1..4430, 2_A375_uN37_plvol_lncRNA_AR:1..6403	2980, 2682	nr gene, nr gene	1	1	0	24	29	13	1	2_A375_uN37_plvol_lncRNA_AR:1..1	29	Gene:LOC728769		hypothetical LOC728769	XR_112763, XR_105558, XR_112750	238239_at		
Gene ID:8	SCAMP1	5	77,856,329	77,776,962	130,233	+	2	1_A375_uN37_mirvol_lncRNA_AR:1..4430, 2_A375_uN37_plvol_lncRNA_AR:1..6403	-106, -497	upstream, upstream	1	1	0	24	29	13	1	2_A375_uN37_plvol_lncRNA_AR:1..1	29	Gene:SCAMP1	SCAMP1, SCAMP, SCAMP37	secretory carrier membrane protein 1	NM_004866, NT_01861	1552970_s_at, 239887_s_at, 239888_s_at, 213418_at, 213427_at, 212425_at		NP_004857.4, EAW66817.1, EAW66814.1, EAW66815.1, EAW66816.1
Gene ID:10	HPLP2	5	77,761,656	77,744,945	183,830	-	4	1_A375_uN37_mirvol_lncRNA_AR:1..4431, 1_A375_uN37_mirvol_lncRNA_AR:1..4432, 1_A375_uN37_mirvol_lncRNA_AR:1..4433, 2_A375_uN37_plvol_lncRNA_AR:1..6404	62640, 51364, 1212, 62366	nr gene, nr gene, nr gene, nr gene	1	1	0	17.33	11.67	6	3	1_A375_uN37_mirvol_lncRNA_AR:1..1	16	Gene:LHPL2	LHPL2, KIAA1934, DKFZp761B0312	lipoma HMGIC fusion partner-like	NM_020779, XM_005	212858_at		NP_065710.1, EAW65818.1, EAW65819.1
Gene ID:84	HOMER1	5	75,899,708	75,899,700	139,814	-	2	1_A375_uN37_mirvol_lncRNA_AR:1..4436, 2_A375_uN37_plvol_lncRNA_AR:1..6408	-638, -476	upstream, upstream	1	1	0	25	20	14	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	25	Gene:HOMER1	HOMER1, HOMER1B, HOMER1A, HOMER, Ves-1, Dyn47, HOMER1C	homer homolog 1 (Drosophila)	NM_004272, XM_005	213763_s_at, 239851_at		NP_004263.1, EAW66386.1, EAW66383.1
Gene ID:16	PAFP4	5	75,898,243	75,892,471	74,228	+	1	1_A375_uN37_mirvol_lncRNA_AR:1..4437	170	nr gene	0	0	0	16	12	8	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	16	Gene:PAFP4	FLJ38499, G1/2, PAFP	PAF acetylhydrolase domain containing	NM_170797, NM_0011	1556977_s_at, 237761_at		NP_776182.2, NP_001107985.1, NP_001107986.1, EAW66836.1, EAW66837.1, EAW66838.1
Gene ID:54	MTX3	5	79,272,539	79,287,865	15,349	-	1	2_A375_uN37_plvol_lncRNA_AR:1..6397	60	nr gene	1	0	0	14	12	33	1	2_A375_uN37_plvol_lncRNA_AR:1..1	14	Gene:MTX3	DKFZp686D1780, MTX3	metaxin 3	NM_031018, NM_0011	226529_at, 241779_at		NP_030118.1, NP_001182123.1, EAW66540.1
Gene ID:23	SERINC5	5	79,407,030	79,381,895	144,846	-	1	2_A375_uN37_plvol_lncRNA_AR:1..6409	129903	nr gene	0	0	1	10	14	1	1	2_A375_uN37_plvol_lncRNA_AR:1..1	14	Gene:SERINC5	TPO1, SERINC5, C9orf12	serine incorporator 5	NM_001174071, NM_0011	1554852_at, 1555011_at, 203691_at		NP_001167543.1, NP_001167543.1, NP_443180.1, EAW66543.1, EAW66544.1, EAW66545.1
Gene ID:85	ZFYVE1	5	79,703,838	79,775,490	71,660	+	1	1_A375_uN37_mirvol_lncRNA_AR:1..4439	-6430	upstream	1	0	0	16	12	1	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	16	Gene:ZFYVE1	DKFZp686E1218, ENDOFIN, ZFYVE18, WAD933	zinc finger, FYVE domain containing 1	NM_015742, NM_0011	1554858_at, 1555011_at, 203691_at		NP_056615.3, NP_001092721.1, EAW66550.1, EAW66551.1
Gene ID:24	ANKRD	5	79,932,574	79,996,304	63,730	-	1	4_A375_EGR1:1..6759	448	nr gene	0	0	0	14	7	16	1	4_A375_EGR1:1..1	16	Gene:ANKRD24	ANKRD24B, SP58	ankyrin repeat domain 24	NM_031044.4, NT_0	235855.1, AI		NP_001034441.2, EAW66537.1, EAW66538.1
Gene ID:24	RASGA	5	80,266,536	80,321,853	383,296	+	1	4_A375_EGR1:1..6759	272240	downstream	0	0	0	5	5	13	1	4_A375_EGR1:1..1	13	Gene:RASGRF2	RASGRF2, GRF2, DKFZp761H175, RAS-GRF2	Ras protein-specific guanine nucleotide-releasing factor 2	NM_006909, NT_0167	1556120_a_at, 226109_at		NP_008840.1, EAW65883.1
Gene ID:11	CAMT2	5	80,329,109	80,362,317	33,208	+	1	4_A375_EGR1:1..6759	-291	upstream	0	0	1	9	9	13	1	4_A375_EGR1:1..1	13	Gene:CAMT2	C9orf72, SMRCK	calmin (calponin-like, transmembrane) 2 (predicted)	NM_031223, NM_0010	230259_at		NP_001076152, NP_001092203.1, NP_001092206.1, EAW65863.1, EAW65867.1
Gene ID:10	LOC100	5	80,333,364	80,397,398	64,034	-	3	1_A375_uN37_mirvol_lncRNA_AR:1..4440, 2_A375_uN37_plvol_lncRNA_AR:1..6410, 4_A375_EGR1:1..6759	44, 12, 66540	nr gene, nr gene, downstream	1	1	1	14	16.3	14	2	2_A375_uN37_plvol_lncRNA_AR:1..1	16	Gene:LOC100131087	FLJ39381, FLJ38893	hypothetical LOC100131087	NR_034121, NR_0341			
Gene ID:54	ZCCHC	5	80,397,402	80,806,966	11,564	+	2	1_A375_uN37_mirvol_lncRNA_AR:1..4440, 2_A375_uN37_plvol_lncRNA_AR:1..6410	-56, -26	upstream, upstream	1	1	0	25	26	15	1	2_A375_uN37_plvol_lncRNA_AR:1..1	25	Gene:ZCCHC9	ZCCHC9, DKFZp761J139	zinc finger, CCHC domain containing 9	NM_032350, NM_0011	1555355_at, 228272_at		NP_115958.1, NP_001124307.1, NP_001124308.1, EAW66570.1, EAW66571.1, EAW66572.1, EAW66573.1
Gene ID:23	SSBP3	5	80,716,872	81,047,072	331,200	-	3	1_A375_uN37_mirvol_lncRNA_AR:1..6411, 2_A375_uN37_mirvol_lncRNA_AR:1..6411, 2_A375_uN37_plvol_lncRNA_AR:1..6412	338992, 16, 288	nr gene, nr gene, nr gene, nr gene	1	1	0	13	21	7.5	2	2_A375_uN37_plvol_lncRNA_AR:1..1	21	Gene:SSBP2	SSBP2, SSSB, IBD, HSPC116, DKFZp686F0327	single-stranded DNA binding protein 2	NM_012446, NT_0167	203767_at, 210529_s_at		NP_036578.3, EAW66779.1, EAW66780.1, EAW66781.1, EAW66782.1
Gene ID:8	ATG10	5	81,287,564	81,351,215	63,652	-	1	2_A375_uN37_plvol_lncRNA_AR:1..6414	44	nr gene	0	1	0	11	14	10	1	2_A375_uN37_plvol_lncRNA_AR:1..1	14	Gene:ATG10	ATG10, FLJ10134, APG10, APG10L, bs13816, DKFZp686I4410	ATG10 autophagy related 10 homolog (S. cerevisiae)	NM_031482, NM_0011	1559020_at, 1559020_s_at, 227774_at, 243477_at		NP_113701.1, NP_001124500.1, EAW66522.1, EAW66523.1, EAW66524.1, EAW66525.1, EAW66526.1, EAW66527.1, EAW66528.1, EAW66529.1, EAW66530.1, EAW66531.1, EAW66533.1
Gene ID:8	RASA1	5	86,884,151	86,887,703	123,582	+	3	1_A375_uN37_mirvol_lncRNA_AR:1..4445, 1_A375_uN37_mirvol_lncRNA_AR:1..4447, 2_A375_uN37_plvol_lncRNA_AR:1..6422, 4_A375_EGR1:1..6760	-799, 32665, 665, -663, 73	upstream, nr gene, upstream, upstream, nr gene	1	1	1	17	16	14.33	3	4_A375_EGR1:1..1	24	Gene:RASA1	CMAR4, RASA1, RASA, DKFZp434J071, PIK4S_CMAR4, p120GAP, RASGAP, GAP, p120RASGAP	RAS p21 protein activator (GTPase activating protein) 1	NM_002890, NM_0026	1557193_s_at, 207279_at, 202627_at, 210821_s_at		NP_002881.1, NP_872179.1, EAW66912.1, EAW66932.1, EAW66933.1
Gene ID:89	CCAH	5	88,890,802	88,708,839	10,754	-	2	1_A375_uN37_mirvol_lncRNA_AR:1..4445, 2_A375_uN37_plvol_lncRNA_AR:1..6423	66, 92	nr gene, nr gene	1	1	0	20	17	9	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	20	Gene:CCAH	CCAH, p38, CAP, a37	cyclin H	NM_001239, NT_0167	209369_at, 209370_s_at		NP_001230.1, EAW66934.1, EAW66935.1
Gene ID:84	LOC643	5	87,836,197	87,950,820	144,622	+	7	1_A375_uN37_mirvol_lncRNA_AR:1..4451, 1_A375_uN37_mirvol_lncRNA_AR:1..4452, 1_A375_uN37_mirvol_lncRNA_AR:1..4453, 1_A375_uN37_mirvol_lncRNA_AR:1..4526, 1_A375_uN37_mirvol_lncRNA_AR:1..4527, 2_A375_uN37_plvol_lncRNA_AR:1..6426, 2_A375_uN37_plvol_lncRNA_AR:1..6776	9952, 8764, 4356, 23853, 9116, 2863, 10271	nr gene, nr gene, nr gene, nr gene, nr gene, nr gene, nr gene	1	1	1	16	10.67	14	2	2_A375_uN37_plvol_lncRNA_AR:1..1	16	Gene:LOC643223		hypothetical LOC643223	NR_015435, NR_0245	235272_at, 238830_at		
Gene ID:40	MIR9-2	5	87,982,671	87,982,757	86	+	5	1_A375_uN37_mirvol_lncRNA_AR:1..4451, 1_A375_uN37_mirvol_lncRNA_AR:1..4452, 1_A375_uN37_mirvol_lncRNA_AR:1..4526, 1_A375_uN37_mirvol_lncRNA_AR:1..4527, 1_A375_uN37_mirvol_lncRNA_AR:1..6776	-5011, -9099, 5860, -4747, -5792	upstream, upstream, downstream, upstream, upstream	1	1	1	17.5	20	15	2	2_A375_uN37_plvol_lncRNA_AR:1..1	20	Gene:MIR9-2	hsa-mir-9-2, MIR9-2, miRNA9-2	microRNA 9-2	NR_030741			
Gene ID:42	MEF2C	5	88,014,036	88,199,922	185,886	-	2	1_A375_uN37_mirvol_lncRNA_AR:1..4454, 2_A375_uN37_plvol_lncRNA_AR:1..6429	119026, 11934	nr gene, nr gene	1	1	0	21	17	7	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	21	Gene:MEF2C	MEF2C, DKFZp686H0611, DEL9q14.3	myocyte enhancer factor 2C	NM_001131005, NM_0	2007960_s_at, 2019191_s_at, 207961_x_at, 207962_s_at, 207963_at, 207964_s_at, 207965_at, 207966_x_at, 207967_s_at, 207968_s_at, 207969_x_at, 207970_s_at, 207971_x_at, 207972_at, 207973_x_at, 207974_s_at, 207975_at, 207976_x_at, 207977_s_at, 207978_at, 207979_x_at, 207980_s_at, 207981_x_at, 207982_at, 207983_x_at, 207984_s_at, 207985_at, 207986_x_at, 207987_s_at, 207988_at, 207989_x_at, 207990_s_at, 207991_at, 207992_x_at, 207993_s_at, 207994_at, 207995_x_at, 207996_s_at, 207997_at, 207998_x_at, 207999_s_at, 208000_at, 208001_x_at, 208002_s_at	NP_001124777.1, NP_002388.2, NP_001119245.1, NP_001119246.1, NP_001119247.1, NP_001119248.1, NP_001119249.1, NP_001119250.1, NP_001119251.1, NP_001119252.1, NP_001119253.1, NP_001119254.1, NP_001119255.1, NP_001119256.1, NP_001119257.1, NP_001119258.1, NP_001119259.1, NP_001119260.1, NP_001119261.1, NP_001119262.1, NP_001119263.1, NP_001119264.1, NP_001119265.1, NP_001119266.1, NP_001119267.1, NP_001119268.1, NP_001119269.1, NP_001119270.1, NP_001119271.1, NP_001119272.1, NP_001119273.1, NP_001119274.1, NP_001119275.1, NP_001119276.1, NP_001119277.1, NP_001119278.1, NP_001119279.1, EAW66962.1, EAW66963.1, EAW66964.1, EAW66965.1, EAW66966.1, EAW66967.1, EAW66968.1
Gene ID:33	MBLAC	5	89,754,030	89,770,365	16,335	-	3	1_A375_uN37_mirvol_lncRNA_AR:1..4455, 2_A375_uN37_plvol_lncRNA_AR:1..6430, 4_A375_EGR1:1..6758	343, 69, 165	nr gene, nr gene, nr gene	1	1	1	21	24	19	1	2_A375_uN37_plvol_lncRNA_AR:1..1	24	Gene:MBLAC2	MGC4570A, DKFZp686P515, MBLAC2	metallo-beta-lactamase domain containing 2	NM_205456, NT_0167	1554619_at, 230295_at		NP_001001.1, EAW65979.1
Gene ID:10	POLR3	5	89,770,891	89,810,399	39,508	+	3	1_A375_uN37_mirvol_lncRNA_AR:1..4455, 2_A375_uN37_plvol_lncRNA_AR:1..6430, 4_A375_EGR1:1..6758	-441, -183, -281	upstream, upstream, upstream	1	1	1	21	24	19	1	2_A375_uN37_plvol_lncRNA_AR:1..1	24	Gene:POLR3G	RPC32, POLR3G, RPC3	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	NM_006467, NT_0167	200863_at, 200864_s_at, 231344_s_at		NP_006458.2, EAW66980.1, EAW66981.1, EAW66982.1
Gene ID:11	LYSM3	5	89,811,444	89,825,401	13,957	-	1	4_A375_EGR1:1..6758	199	nr gene	0	0	1	15	14	30	1	4_A375_EGR1:1..1	30	Gene:LYSM3D	FLJ11542, LYSM3D, DKFZp686F0735	lysM, putative peptidoglycan-binding domain containing 3	NM_182773	226321_at		NP_839014.1
Gene ID:54	GPR95	5	89,834,817	90,460,833	603,416	+	2	1_A375_uN37_mirvol_lncRNA_AR:1..4457, 2_A375_uN37_plvol_lncRNA_AR:1..6432	-182, -199	upstream, upstream	1	1	0	52	62	14	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	52	Gene:GPR95	GPR95, KIAA0695, LB-828, VLGR1a, VLGR1, FEB4, DKFZp761P0210, MASS1, USH2C	G protein-coupled receptor 98	NM_032119, NR_0351	213396_at, 223362_at, 224275_at, 234251_at, 240851_at		NP_115493.3, EAW65992.1, EAW65993.1, EAW65997.1, EAW65998.1, EAW65999.1, EAW66000.1, EAW66001.1, EAW66002.1, EAW66004.1
Gene ID:72	LOC729	5	90,579,914	90,579,959	1,045	-	1	2_A375_uN37_plvol_lncRNA_AR:1..6433	658	nr gene	0	0	0	17	17	12	1	2_A375_uN37_plvol_lncRNA_AR:1..1	17	Gene:LOC729040		hypothetical LOC729040	XR_112752, XR_1052	239119_at		
Gene ID:83	ARRDC	5	90,864,341	90,879,149	14,808	-	1	1_A375_uN37_mirvol_lncRNA_AR:1..4458	-337	upstream	1	0	0	17	13	13	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	17	Gene:ARRDC3	FLJ34R, ARRDC3, KIAA1276	arrestin domain containing 3	NM_020801, NT_0167	223797_at		NP_065852.1, EAW65997.1
Gene ID:10	LOC100	5	90,876,156	90,716,932	40,366	+	1	1_A375_uN37_mirvol_lncRNA_AR:1..4458	3262	nr gene	1	0	0	17	13	13	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	17	Gene:LOC100129716		hypothetical LOC100129716	NR_027455			
Gene ID:44	FLJ42709	5	92,743,985	92,917,903	171,938	-	3	1_A375_uN37_mirvol_lncRNA_AR:1..4462, 2_A375_uN37_plvol_lncRNA_AR:1..6437, 2_A375_uN37_plvol_lncRNA_AR:1..6438	-229, 875, -245	upstream, nr gene, upstream	1	1	1	22.3	25.5	6	2	2_A375_uN37_plvol_lncRNA_AR:1..1	22	Gene:FLJ42709	DKFZp686H0151	hypothetical LOC441994	NR_015389, NR_0241	1559853_s_at, 1559890_s_at, 229014_at		
Gene ID:76	NRZF1	5	92,919,945	92,929,766	10,745	+	3	1_A375_uN37_mirvol_lncRNA_AR:1..4462, 2_A375_uN37_plvol_lncRNA_AR:1..6437, 2_A375_uN37_plvol_lncRNA_AR:1..6438	-1011, -2915, -1793	upstream, upstream, upstream	1	1	1	22.3	25.5	6	2	1_A375_uN37_mirvol_lncRNA_AR:1..1	22	Gene:NRZF1	COUP-TF1, MGC72, MRZF1, TFCOUP1, TFCOUP1, ERBAL3, EAR-3, SVP44, SVP3	nuclear receptor zinc finger protein, zinc finger 1	NM_030854, NT_0167	205803_at, 205958_s_at		NP_109643.1, EAW66008.1, EAW66009.1
Gene ID:85	FAM172	5	92,933,431	93,047,404	493,973	-	7	1_A375_uN37_mirvol_lncRNA_AR:1..4459, 1_A375_uN37_mirvol_lncRNA_AR:1..4460, 1_A375_uN37_mirvol_lncRNA_AR:1..4461, 1_A375_uN37_mirvol_lncRNA_AR:1..4462, 1_A375_uN37_mirvol_lncRNA_AR:1..4463, 1_A375_uN37_mirvol_lncRNA_AR:1..4464, 2_A375_uN37_plvol_lncRNA_AR:1..6444	489305, 489504, 489504, 490195, 235, 90105, 239	downstream, downstream, downstream, upstream, nr gene, nr gene, nr gene, nr gene	1	1	0	13.67	19.5	6.33	6	2_A375_uN37_plvol_lncRNA_AR:1..1	25	Gene:FAM172A	DKFZp686I0172, C9orf61, FAM172A	family with sequence similarity 172, member A	NM_032042, NM_0011	1557416, 212936_at, 223822_at		NP_115493.2, NP_001159911.1, NP_001159912.1, EAW66010.1, EAW66011.1, EAW66012.1
Gene ID:10	MIR227	5	92,956,402	92,956,494	92	+	4	1_A375_uN37_mirvol_lncRNA_AR:1..4459, 1_A375_uN37_mirvol_lncRNA_AR:1..4460, 2_A375_uN37_plvol_lncRNA_AR:1..6441, 2_A375_uN37_plvol_lncRNA_AR:1..6442, 2_A375_uN37_plvol_lncRNA_AR:1..6443, 2_A375_uN37_plvol_lncRNA_AR:1..6444	6381, 6014, 94, 756	downstream, downstream, downstream, upstream	1	1	0	12	21	6.75	4	2_A375_uN37_plvol_lncRNA_AR:1..1	25	Gene:MIR2277	MIR2277	microRNA 2277	NR_031756			
Gene ID:28	C9orf84	5	93,088,556	92,934,309	467,783	-	3	1_A375_uN37_mirvol_lncRNA_AR:1..4464, 2_A375_uN37_plvol_lncRNA_AR:1..6443, 4_A375_EGR1:1..6760	-5, -203, 69	nr gene, upstream, nr gene	1	1	1	16	14	10	1	4_A375_EGR1:1..1	16	Gene:C9orf84	DKFZp686R0272, chromosome 9 open reading frame 84, KIAA0825, FLJ37431, C9orf84	chromosome 9 open reading frame 84	NM_173693, NM_0011	1553880_s_at		NP_775939.1, NP_001139190.1, EAW66825.1
Gene ID:54	ANKRD	5	93,954,391	94,031,873	77,102	+	3	1_A375_uN37_mirvol_lncRNA_AR:1..4464, 2_A375_uN37_plvol_lncRNA_AR:1..6443, 4_A375_EGR1:1..6760	-67, 201, -151	upstream, nr gene, upstream	1	1	1	16	14	10	1	4_A375_EGR1:1..1	16	Gene:ANKRD32	DKFZp761C121, DKFZp684C0409, BKCT1, BKCT01, ANKRD32	ankyrin repeat domain 32	NM_032290, XM_0052	1559079_at, 223842_at		NP_115866.2, EAW66827.1, EAW66828.1, EAW66829.1
Gene ID:79	MCTP1	5	94,042,264	94,820,279	777,995	+	2	1_A375_uN37_mirvol_lncRNA_AR:1..4465, 4_A375_EGR1:1..6761	499079, 505	nr gene, nr gene	1	0	1	11	8	9.5	2	4_A375_EGR1:1..1	17	Gene:MCTP1	MCTP1, FLJ23344	multiple C2 domains, transmembrane 1	NM_024717, NM_0010	1554792_at, 220122_at		NP_079093.4, NP_001002796.1, NP_001002797.1, EAW66832.1, EAW66833.1
Gene ID:16	FAM81B	5	94,727,048	94,768,144	99,096	+	1	1_A375_uN37_mirvol_lncRNA_AR:1..4466	29800	nr gene	1	0	0	16	8	2	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	16	Gene:FAM81B	FAM81B, FLJ23333	family with sequence similarity 81, member B	NM_152445, NT_0167	1557021_at, 1557869_at		NP_689791.2, EAW66833.1, EAW66838.1
Gene ID:9	TTC37	5	94,799,599	94,890,709	91,110	-	2	1_A375_uN37_mirvol_lncRNA_AR:1..4467, 2_A375_uN37_plvol_lncRNA_AR:1..6445	-11, -56	upstream, upstream	1	1	0	33	26	16	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	33	Gene:TTC37	TTC37, KIAA0722, MGC23327	tetratricopeptide repeat domain 37	NM_014939, NT_0151	1554529_a_at, 203345_s_at, 203349_s_at		NP_055754.1, EAW66837.1, EAW66838.1
Gene ID:15	ARSK	5	94,890,625	94,940,606	49,981	+	2	1_A375_uN37_mirvol_lncRNA_AR:1..4467, 2_A375_uN37_plvol_lncRNA_AR:1..6445	-108, -30	upstream, upstream	1	1	0	33	26	16	1	1_A375_uN37_mirvol_lncRNA_AR:1..1	33	Gene:ARSK	ARSK, DKFZp313G1733	arylsulfatase family, member K	NM_198150, XM_0052	1559122_s_at, 1559123_x_at, 229147_at		NP_937762.1, EAW66839.1, EAW66840.1
Gene ID:23	RFESD	5	94,922,451	94,932,949	10,366	+	1	4_A375_EGR1:1..6770	-17	upstream	0	0	1	9	15	20	1	4_A375_EGR1:1..1	20	Gene:RFESD	RFESD		NM_173282, NM_0011	1553093_at, 223932_at, 223742_at		NP_775405.1, NP_001124027.1, NP_001124028.1, EAW66843.1, EAW66844.1, EAW66845.1, EAW66842.1
Gene ID:22	RHOBT	5	93,966,930	93,132,071	80,221	-	1	2_A375_uN37_plvol_lncRNA_AR:1..6445	788	nr gene	0	0	0	11	20	14	1	2_A375_uN37_plvol_lncRNA_AR:1..1	20	Gene:RHOBTB3	KIAA0676, RHOBTB3	Rho-related BTB domain containing 3	NM_014899, NT_0167	202873_s_at, 202876_s_at, 210965_s_at, 215959_at, 223352_at, 240111_at		NP_055734.3, EAW66849.1, EAW66850.1, EAW66851.1, EAW66852.1
Gene ID:2	C9orf27	5	93,167,936	93,176,837	7,901	+	1	2_A375_uN37_plvol_lncRNA_AR:1..6449	6762	nr gene	0	0	1	11	16	7	1	2_A375_uN37_plvol_lncRNA_AR:1..1	16	Gene:C9orf27	MGC129828, FLJ38221, C9orf27, FIS	chromosome 9 open reading frame 27	NR_028936, NT_0167	239350_at		EAW66935.1, EAW66939.1
Gene ID:8	PCSK1	5	93,726,040	93,766,953	42,914	-	5	1_A375_uN37_mirvol_lncRNA_AR:1..4465, 1_A375_uN37_mirvol_lncRNA_AR:1..4466, 1_A375_uN37_mirvol_lncRNA_AR:1..4467, 2_A375_uN37_plvol_lncRNA_AR:1..6451, 2_A375_uN37_plvol_lncRNA_AR:1..6452	1981, -967, 40729, 1577, -1031	nr gene, upstream, downstream, nr gene, upstream	1	1	0	20.67	36	7.33	3	2_A375_uN37_plvol_lncRNA_AR:1..1	36	Gene:PCSK1	PC1, SPC3, Bdt3H2, NEC1, PCSK1, PC3	proprotein convertase subtilisin/kexin type 1	NM_000439, NM_0011	1557376, 205029_at		NP_000430.3, NP_001171548.1, NP_001171547.1, EAW66062.1, EAW66063.1



Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distrib Start	Interval Pos	1_A375_pfk27_mut_lncRNA_AR_1 Percent	2_A375_pfk37_plus_lncRNA_AR_1 Percent	4_A375_EGR1_lncRNA_AR_1 Percent	1_A375_pfk27_mut_lncRNA_AR_1 Avg Peak	2_A375_pfk37_plus_lncRNA_AR_1 Avg Peak	4_A375_EGR1_lncRNA Avg Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:8355	CAST	5	95,997,741	96,110,397	112,656	+	3	2_A375_pfk37_plus_lncRNA_AR_1:8454, 2_A375_pfk37_plus_lncRNA_AR_1:8455, 2_A375_pfk37_mut_lncRNA_AR_1:4472	19, 1107, 40723	vs gene, vs gene, vs gene	1	1	0	15.33	16	9.33	3	2_A375_pfk37_plus_lncRNA_AR_1	9.20	Gene CAST	CAST, HKZ5HG2	calpastatin	80-17	NM_001042445, NM_001190442, NM_173357, NM_203795, XC7339481.0, XC7339482.0, XC7339470.0, XC7339472.0, XC7339473.0, XC7339476.0, XC7339478.0, XC7339479.0, XC7339481.0, XC7339482.0, XC7339484.0	1864610_at, 207497_x_at, 209930_s_at, 212898_at	NP_001035935.1, NP_001117571.1, NP_776023.1, EAW96986.1, EAW96970.1, EAW96973.1, EAW96984.1, EAW96985.1, EAW96986.1, EAW96987.1, EAW96970.1, EAW96971.1, EAW96972.1, EAW96973.1, EAW96974.1, EAW96976.1
GeneID:3.61	ERAP1	5	96,896,514	96,143,892	47,378	-	2	1_A375_pfk7_mixed_lncRNA_AR_1:4473, 2_A375_pfk37_plus_lncRNA_AR_1:8439	692, 832	vs gene, vs gene	1	1	0	15	26	15	1	2_A375_pfk37_plus_lncRNA_AR_1	9.20	Gene ERAP1	APPILS, ERAP1, KIAA0525, ARTS1, ERAP1, ARTS1, A-LAP, PILSAP, ERAP1	endoplasmic reticulum aminopeptidase 1	NM_001040636, NM_016442, XC7177554.1, XC7177539.1, XC7339743.0	209701_at, 209702_s_at, 210083_s_at, 212393_at, 214012_at, 214034_at	NP_001033546.1, NP_057028.3, EAW96777.1, EAW96778.1, EAW96779.1
GeneID:4.61	LNPEP	5	96,271,349	96,365,115	93,769	+	2	1_A375_pfk7_mixed_lncRNA_AR_1:4474, 2_A375_pfk37_plus_lncRNA_AR_1:8437	586, 270	vs gene, vs gene	1	1	0	36	30	12	1	1_A375_pfk7_mixed_lncRNA_AR_1	9.30	Gene LNPEP	P-LAP, P-LAP, LNPEP, CAP, IRAP	leucyl/cystinyl aminopeptidase	NM_173930, NM_005575, XC7177553.2	207904_s_at, 213999_at, 228705_at	NP_747116.2, NP_005566.2, EAW80934.1
GeneID:5.61	RXRG	5	96,456,871	96,519,005	62,134	-	2	1_A375_pfk7_mixed_lncRNA_AR_1:4475, 2_A375_pfk37_plus_lncRNA_AR_1:8436	45, -51	vs gene, upstream	1	1	0	17	17	9	1	1_A375_pfk7_mixed_lncRNA_AR_1	9.17	Gene RXRG	RXG, RXRG, FLJ11109	RXG license 2 (yeast)	NM_006545, NM_001159749, XC7339562.2	210853_s_at, 222693_at	NP_006535.2, NP_001153221.1, EAW98550.1
GeneID:6.61	RGMB	5	96,564,999	96,632,198	67,199	+	1	2_A375_pfk37_plus_lncRNA_AR_1:8439	4328	vs gene	0	1	0	16	16	13	1	2_A375_pfk37_plus_lncRNA_AR_1	9.18	Gene RGMB	DKFZp434P228, RGMB, DRAGON, FLJ40406, MGC28970	RGM domain family, member B	NM_031127791, XC7166874.4, XC7339743.0, XC7339750.0	229909_at, 237709_at, 227360_s_at, 242963_at	NP_001127791.2, EAW98995.1, EAW98993.1, EAW98994.1
GeneID:7.61	FLJ37453	5	96,169,322	96,169,768	5,466	-	1	2_A375_pfk37_plus_lncRNA_AR_1:8439	-737	upstream	0	1	0	16	16	13	1	2_A375_pfk37_plus_lncRNA_AR_1	9.16	Gene FLJ37453		hypothetical protein FLJ37453	NR_033932	1559899_s_at	
GeneID:8.61	CHD1	5	96,190,906	96,262,356	71,450	-	2	1_A375_pfk7_mixed_lncRNA_AR_1:4476, 2_A375_pfk37_plus_lncRNA_AR_1:8440	-2262, -2756	upstream, upstream	1	1	0	17	20	15	1	2_A375_pfk37_plus_lncRNA_AR_1	9.20	Gene CHD1	DKFZp686B22320, CHD1	chromodomain helicase DNA binding protein 1	NM_001270, XC7118824.3	204256_at, 235791_x_at	NP_001261.2, EAW99096.1
GeneID:9.61	LOC100289230	5	96,264,838	96,266,713	1,876	+	2	1_A375_pfk37_mixed_lncRNA_AR_1:4476, 2_A375_pfk37_plus_lncRNA_AR_1:8440	-338, 154	upstream, vs gene	1	1	0	17	20	13	1	2_A375_pfk37_plus_lncRNA_AR_1	9.20	Gene LOC100289230		hypothetical LOC100289230	NR_038330		
GeneID:7.61	STS5M4	5	100,142,699	100,238,907	96,345	-	2	2_A375_pfk37_plus_lncRNA_AR_1:8452, 2_A375_pfk37_plus_lncRNA_AR_1:8453	62867, 2715	vs gene, vs gene	0	1	0	7.5	19	10	2	2_A375_pfk37_plus_lncRNA_AR_1	9.22	Gene STS5M4	PST1, PST, STS5A-V, MGC34490, MGC81480, SHTS5, STS5M4	STS alpha-to acetyl-transferase alpha 5 (dihydrosphingosine alpha-N-acetyltransferase a	NM_175052, NM_030665, XC7237998.0, XC7339017.2	1554460_at, 208925_at, 233281_at, 233836_at, 242943_at	NP_778222.1, NP_005839.1, EAW99104.1, EAW99105.1
GeneID:8.61	SLCO4C1	5	101,389,890	101,632,293	242,883	-	3	1_A375_pfk7_mixed_lncRNA_AR_1:4477, 2_A375_pfk37_plus_lncRNA_AR_1:8454, 4_A375_EGR1_1:8772	197, 93, 123	vs gene, vs gene, vs gene	1	1	1	27	23	20	1	4_A375_EGR1_1.1	20	Gene SLCO4C1	OATP-H, OATP4C1, PRO2178, OATP-H, SLC21A20, OATPX, SLCO4C1	solute carrier organic anion transporter family, member 4C1	NM_180991, XC7199292.3, XC7232218.0	223071_s_at	NP_631922.3, EAW99099.1, EAW99100.1
GeneID:9.61	PAI4	5	102,291,527	102,386,609	163,282	+	1	1_A375_pfk7_mixed_lncRNA_AR_1:4478	581	vs gene	1	0	0	16	15	12	1	1_A375_pfk7_mixed_lncRNA_AR_1	9.16	Gene PAI4	PAI4, PI4K, PAI	phosphatidylinositol 4-kinase type 2 alpha	NM_030919, NM_001177306, NM_130766, NM_139021, NM_139022, NR_033440, XC7234388.0, XC7234389.0, XC7234390.0, XC7234391.0, XC7234392.0, XC7234393.0, XC7234394.0, XC7232217.0, XC7232218.0	202236_s_at, 212562_s_at, 214480_x_at	NP_030910.2, NP_001170777.1, NP_620121.1, NP_620176.1, NP_620177.1, EAW99084.1, EAW99085.1, EAW99086.1, EAW99087.1, EAW99088.1, EAW99089.1, EAW99090.1, EAW99091.1, EAW99092.1
GeneID:8.62	GINI	5	102,421,704	102,438,842	34,138	-	2	1_A375_pfk7_mixed_lncRNA_AR_1:4479, 2_A375_pfk37_plus_lncRNA_AR_1:8455	-30, 2	upstream, vs gene	1	1	0	26	30	11	1	2_A375_pfk37_plus_lncRNA_AR_1	9.30	Gene GINI	GINI-1, FLJ20133, TGINI, DKFZp, GINI	Gyrin	NM_017976, XC7232213.0, XC7339862.2	1554343_s_at, 219487_at	NP_060436.2, EAW99081.1, EAW99082.1
GeneID:2.62	PRPF8	5	102,488,257	102,535,910	73,655	+	2	1_A375_pfk7_mixed_lncRNA_AR_1:4479, 2_A375_pfk37_plus_lncRNA_AR_1:8456	-9365, -9417	upstream, upstream	1	1	0	26	30	11	1	2_A375_pfk37_plus_lncRNA_AR_1	9.30	Gene PRPF8	PRPF8, FLJ25465, FLJ35306, HSPP31, WAYAD3, IPT52, p912, PPIF5H2	pre-mRNA processing factor 8 homolog B isoform 2	NM_006445, XC7232219.0, XC7232220.0, XC7232221.0, XC7339562.3	202252_s_at	NP_006437.2, EAW99079.1, EAW99077.1, EAW99078.1
GeneID:6.62	NUDT12	5	102,664,596	102,690,490	25,934	-	1	2_A375_pfk37_plus_lncRNA_AR_1:8457	170	vs gene	0	1	0	10	16	6	1	2_A375_pfk37_plus_lncRNA_AR_1	9.16	Gene NUDT12	DKFZp761I172, NUDT12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	NM_031438, XC7239364.3	1562775_at, 225535_at	NP_115826.1, EAW99070.1
GeneID:1.62	EPHA3	5	106,712,590	107,009,596	294,006	+	6	1_A375_pfk7_mixed_lncRNA_AR_1:4481, 2_A375_pfk37_plus_lncRNA_AR_1:8471, 2_A375_pfk37_plus_lncRNA_AR_1:8472, 2_A375_pfk37_plus_lncRNA_AR_1:8473, 2_A375_pfk37_plus_lncRNA_AR_1:8474, 4_A375_EGR1_1:8775	3312, 331972, 201348, 476, -1488, -2668	upstream, vs gene, vs gene, upstream, upstream	1	1	1	12.17	16.67	7	6	2_A375_pfk37_plus_lncRNA_AR_1	9.23	Gene EPHA3	EPH3, EPLG7, EK97, ETHA3, RAGS, GLC1M, HTI	ephrin-A3	NM_031982, XC7177473.3, XC7234228.0, XC7239148.4	207351_at	NP_031953.1, EAW99085.1, EAW99084.1, EAW99083.1
GeneID:8.64	FBXL17	5	107,194,754	107,717,799	523,046	-	2	2_A375_pfk37_plus_lncRNA_AR_1:8476, 4_A375_EGR1_1:8775	-7, 133	vs gene, vs gene	0	1	1	13	15	19	1	4_A375_EGR1_1.1	19	Gene FBXL17	FBXL17, FBOX13, DKFZp434C1713, MGC161454, FBXL17, Fbx13, MGC161422	F-box and leucine-rich repeat protein 17	NM_001163115, XC7232707.0, XC7239582.3	227203_at, 233057_at, 242204_at, 244380_at	NP_001156587.2, EAW99062.1, EAW99063.1
GeneID:2.63	FER	5	108,683,923	108,823,373	439,450	+	1	4_A375_EGR1_1:8777	643	vs gene	0	0	1	15	10	20	1	4_A375_EGR1_1.1	23	Gene FER	TYK3, FER	fer (tyrosine kinase) tyrosine kinase	NM_005246, XC7233824.0, XC7232624.0, XC7237572.2	206412_at	NP_005127.2, EAW99058.1, EAW99059.1
GeneID:4.64	MANEA	5	109,029,166	109,230,429	179,273	+	1	4_A375_EGR1_1:8776	1368	vs gene	0	0	1	9	8	15	1	4_A375_EGR1_1.1	15	Gene MANEA	MANEA1, MANA, GOLIM7, MANA2	mannosidase, alpha, class 2A, member 1	NM_032772, XC7261423	203103_at, 229838_at, 233103_s_at	NP_002363.2, EAW99046.1
GeneID:9.64	SLC35A5	5	110,074,764	110,096,454	23,730	+	1	2_A375_pfk37_plus_lncRNA_AR_1:8476	-16	upstream	0	1	0	15	16	17	1	2_A375_pfk37_plus_lncRNA_AR_1	9.18	Gene SLC35A5	SLC35A5	solute carrier family 35, member A5	NM_130773, XC7160744.1, XC7239577.3	212033_at, 229831_at	NP_630126.1, EAW99041.1, EAW99042.1
GeneID:10.64	WDR36	5	110,427,870	110,498,200	69,330	+	2	2_A375_pfk37_plus_lncRNA_AR_1:8484, 2_A375_pfk37_plus_lncRNA_AR_1:8479	62, 66	vs gene, vs gene	0	1	0	21	21	11	1	2_A375_pfk37_plus_lncRNA_AR_1	9.31	Gene WDR36	FAM24A, TA-WDRP, DKFZp686H80, GLC1G, UTP21, WDR36	WD repeat domain 36	NM_139281, XC7244398.0, XC7244397.0	229160_at, 239877_at	NP_644810.1, EAW99036.1, EAW99038.1
GeneID:8.65	CA4864	5	110,580,882	110,630,749	280,867	+	6	1_A375_pfk7_mixed_lncRNA_AR_1:4483, 2_A375_pfk37_mixed_lncRNA_AR_1:4486, 2_A375_pfk37_plus_lncRNA_AR_1:8480, 2_A375_pfk37_plus_lncRNA_AR_1:8481, 2_A375_pfk37_plus_lncRNA_AR_1:8482, 2_A375_pfk37_plus_lncRNA_AR_1:8483, 4_A375_EGR1_1:8779, 4_A375_EGR1_1:8780	142048, 142662, 394, 140795, 142795, 159456, 226, 74622	vs gene, vs gene, upstream, vs gene, vs gene, upstream, vs gene	1	1	1	14.2	16.4	6.8	5	2_A375_pfk37_plus_lncRNA_AR_1	9.42	Gene CA4864	CA4R, CAR_IV, CA4R, IV, ca4R1, MGC39771	carbonic anhydrase IV precursor	NM_000717, XC7232609.0, XC7232608.0, XC7239576.2	210349_at, 241721_at	NP_000708.1, EAW99052.1, EAW99053.1, EAW99054.1
GeneID:10.65	STARD9	5	110,836,022	110,848,157	14,135	-	1	1_A375_pfk7_mixed_lncRNA_AR_1:4487	541	vs gene	1	0	0	17	11	8	1	1_A375_pfk7_mixed_lncRNA_AR_1	9.17	Gene STARD9	STARD9	START domain containing 9	NM_139156, XC7239220.0, XC7239220.0, XC7244027.0, XC7232236.0, XC7232235.0, XC7239576.4	229390_at	NP_631993.1, EAW99030.1, EAW99031.1, EAW99027.1, EAW99028.1, EAW99029.1, EAW99031.1
GeneID:10.66	LOC100505978	5	110,847,924	111,079,423	227,499	+	1	2_A375_pfk37_mixed_lncRNA_AR_1:4487	-398	upstream	1	0	0	17	11	8	1	2_A375_pfk37_mixed_lncRNA_AR_1	9.17	Gene LOC100505978		hypothetical LOC100505978	XR_112774, XR_113598, XR_113786		
GeneID:10.67	NCRNA00219	5	111,498,223	111,498,195	1,978	+	2	1_A375_pfk37_mixed_lncRNA_AR_1:4488, 2_A375_pfk37_plus_lncRNA_AR_1:8484	241, 237	vs gene, vs gene	1	1	0	113	126	68	1	2_A375_pfk37_plus_lncRNA_AR_1	9.26	Gene NCRNA00219	MGC126991, NCRNA00219, TIGA1, CAI4CB, MGC126992	actin-filament binding RNA 219	NR_015370, XC7159751.1	225866_at	EAW99015.1
GeneID:8.66	SNORA13	5	111,497,162	111,497,314	152	+	2	1_A375_pfk37_mixed_lncRNA_AR_1:4488, 2_A375_pfk37_plus_lncRNA_AR_1:8484	-716, -702	upstream, upstream	1	1	0	113	126	68	1	2_A375_pfk37_plus_lncRNA_AR_1	9.26	Gene SNORA13	ACA13, SNORA13	small nucleolar RNA, H/ACA box 13	NR_002922		
GeneID:8.67	EPB41L5	5	111,498,315	111,758,010	259,696	-	3	1_A375_pfk7_mixed_lncRNA_AR_1:4488, 2_A375_pfk37_plus_lncRNA_AR_1:8485, 4_A375_EGR1_1:8781	238546, 258550, 1064	downstream, downstream, upstream	1	1	1	85	72	55	2	4_A375_EGR1_1.1	26	Gene EPB41L5	NBL4, FLJ38734, EPB41L5, EPB41L4A, DKFZp686J203	erythrocyte membrane protein band 4.1 like 4A	NM_022140, XC7160140.2, XC7160141.2, XC7239292.1, XC7239472.4	1553656_at, 220119_at, 220120_s_at, 238298_s_at	NP_071423.3, EAW99010.1, EAW99011.1, EAW99012.1, EAW99013.1
GeneID:8.68	FLJ31235	5	111,758,280	111,758,673	1,395	+	1	4_A375_EGR1_1:8561	796	vs gene	0	0	1	13	16	20	1	4_A375_EGR1_1.1	20	Gene FLJ31235		hypothetical FLJ31235	NR_027706	220384_at	
GeneID:3.68	APC	5	112,043,218	112,181,936	138,718	+	1	2_A375_pfk37_plus_lncRNA_AR_1:8485	50	upstream	0	1	0	17	20	14	1	2_A375_pfk37_plus_lncRNA_AR_1	9.20	Gene APC	DP2.5, DP3, FAP2, GS, BTPS2	adenomatosis polyposis coli	NM_000038, NM_001127510, NM_001127511	203525_s_at, 203526_s_at, 203527_s_at, 213510_at, 213933_s_at	NP_000129.2, NP_001120982.1, NP_001120983.1
GeneID:7.68	REEP3	5	112,212,051	112,238,031	25,980	-	1	2_A375_pfk37_plus_lncRNA_AR_1:8486	271	vs gene	0	1	0	13	16	12	1	2_A375_pfk37_plus_lncRNA_AR_1	9.16	Gene REEP3	DP1, MGC70445, YOP1	receptor accessory protein 3	NM_030899, XC7160149.1, XC7232030.1, XC7232033.0	226059_s_at, 233073_s_at	NP_036550.4, EAW99048.1, EAW99049.1, EAW99044.1
GeneID:10.68	LOC100507967	5	112,212,099	112,227,935	15,839	-	2	1_A375_pfk7_mixed_lncRNA_AR_1:4489, 2_A375_pfk37_plus_lncRNA_AR_1:8487	13648, 13548	downstream, vs gene	1	1	0	20	19	14	1	1_A375_pfk7_mixed_lncRNA_AR_1	9.20	Gene LOC100507967		hypothetical LOC100507967	XR_112773, XR_113533, XR_113537, XR_113767		
GeneID:10.69	DCP2	5	112,212,433	112,238,997	44,224	+	2	1_A375_pfk7_mixed_lncRNA_AR_1:4490, 2_A375_pfk37_plus_lncRNA_AR_1:8487	-241, 159	upstream, vs gene	1	1	0	20	19	14	1	1_A375_pfk7_mixed_lncRNA_AR_1	9.20	Gene DCP2	NUDT20, FLJ33245, DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	NM_152624, XC7234607.1, XC7235017.0, XC7239351.0, XC7232238.0	212919_at, 233262_at, 238779_at, 244777_at	NP_689937.2, EAW99066.1, EAW99067.1, EAW99068.1, EAW99069.1, EAW99070.1, EAW99071.1, EAW99072.1
GeneID:4.69	MCC	5	112,237,799	112,526,327	488,731	+	6	1_A375_pfk7_mixed_lncRNA_AR_1:4491, 1_A375_pfk7_mixed_lncRNA_AR_1:4492, 2_A375_pfk37_plus_lncRNA_AR_1:8488, 2_A375_pfk37_plus_lncRNA_AR_1:8489, 2_A375_pfk37_plus_lncRNA_AR_1:8490, 4_A375_EGR1_1:8782, 4_A375_EGR1_1:8784	295560, 299, 525, 415893, 52010, 703	vs gene, vs gene, vs gene, vs gene, vs gene, vs gene	1	1	1	11.75	12.5	15	4	4_A375_EGR1_1.1	19	Gene MCC	FLJ36550, MCC, MCC1, FLJ46755, DKFZp762E0516	mutated in colorectal cancers	NM_002387, NM_001085377, XC7197202.3, XC7199202.2, XC7232232.0, XC7232231.0	206132_at, 226229_at	NP_002378.1, NP_001076648.1, NP_001076649.1, EAW99084.1, EAW99085.1, EAW99087.1
GeneID:8.69	TSSK1B	5	112,786,351	112,770,720	2,477	-	1	4_A375_EGR1_1:8783	-984	upstream	0	0	1	8	8	16	1	4_A375_EGR1_1.1	16	Gene TSSK1B	FSSG97, STK2232, TSSK1B, SPOG44, TSSK1	testis-specific serine kinase 1B	NM_032035, XC7164268.4	211694_at	NP_115417.1, EAW99082.1
GeneID:8.70	YTHDC2	5	112,849,391	112,930,954	81,393	+	1	1_A375_pfk37_mixed_lncRNA_AR_1:4493	113	vs gene	1	0	0	20	11	16	1	1_A375_pfk37_mixed_lncRNA_AR_1	9.20	Gene YTHDC2	YTHDC2	YTH domain containing 2	NM_022828, XC7227639.0, XC7227641.0, XC7227642.0	1569950_s_at, 205883_s_at, 205884_x_at, 213977_at	NP_073733.3, EAW99079.1, EAW99078.1, EAW99080.1
GeneID:2.70	KCNN2	5	113,896,016	113,932,197	134,181	+	1	4_A375_EGR1_1:8567	-704	upstream	0	0	1	4	3	19	1	4_A375_EGR1_1.1	19	Gene KCNN2	KCNN2, SK2, SKA3, SKCA2, KCa2.2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	NM_021614, NM_170775, XC7160132.1, XC7239130.3	210189_at	NP_067637.2, NP_787121.1, EAW99078.1, EAW99079.1
GeneID:5.70	PGGT1B	5	114,548,527	114,596,599	52,042	-	1	2_A375_pfk37_plus_lncRNA_AR_1:8499	93	vs gene	0	1	0	14	16	13	1	2_A375_pfk37_plus_lncRNA_AR_1	9.18	Gene PGGT1B	PGGT1, PGGI, PGGT1B	protein geranylgeranyltransferase type I, beta subunit	NM_005023, XC7232787.0, XC7232787.0	208266_at, 233615_at, 242564_at, 244854_at	NP_005013.2, EAW99060.1, EAW99061.1
GeneID:10.70	CCDC112	5	114,802,553	114,832,436	29,883	-	1	2_A375_pfk37_plus_lncRNA_AR_1:8499	33862	downstream	0	1	0	14	16	13	1	2_A375_pfk37_plus_lncRNA_AR_1	9.16	Gene CCDC112	CCDC112, MBC1, MGC29833	coiled-coil domain containing 112	NM_001040440, NM_152349, XC7249220.0, XC7237950.4	233208_at	NP_001035530.1, NP_689702.2, EAW99087.1, EAW99097.1
GeneID:10.71	TMED7-TICAM2	5	114,916,329	114,960,876	47,227	-	2	1_A375_pfk7_plus_lncRNA_AR_1:4501, 2_A375_pfk37_plus_lncRNA_AR_1:8709	226, 20	vs gene, vs gene	0	1	1	11	14	16	1	4_A375_EGR1_1.1	16	Gene TMED7-TICAM2	TMED7-TICAM2, TAG, FLJ90737	TMED7-TICAM2 readthrough	NM_001164455, NM_001164469		NP_001157940.1, NP_001157941.1
GeneID:10.72	LOC100505719	5	114,917,942	114,938,598	16,914	+	2	1_A375_pfk7_plus_lncRNA_AR_1:4501, 2_A375_pfk37_plus_lncRNA_AR_1:8709	23658, 24014	downstream, downstream	0	1	1	11	14	16	1	4_A375_EGR1_1.1	16	Gene LOC100505719		hypothetical LOC100505719	XR_112771, XR_112770, XR_112772, XR_113961, XR_113993, XR_113599, XR_112770, XR_112769, XR_112766		
GeneID:8.71	TMED7	5	114,948,905	114,960,876	12,971	-	2	2_A375_pfk37_plus_lncRNA_AR_1:8491, 4_A375_EGR1_1:8709	226, 20	vs gene, vs gene	0	1	1	11	14	16	1	4_A375_EGR1_1.1	16	Gene TMED7	FLJ90401, FLJ90776, TMED7, CGI-109	trans-membrane emp24 protein transport domain containing 7	NM_181838	209454_s_at, 214656_at	NP_861974.1
GeneID:9.71	ATG12	5	115,182,693	115,177,548	10,855	+	2	2_A375_pfk37_plus_lncRNA_AR_1:8493, 2_A375_pfk37_plus_lncRNA_AR_1:8492	140, 238	vs gene, vs gene	0	1	0	26	30	8	1	2_A375_pfk37_plus_lncRNA_AR_1	9.30	Gene ATG12	FBW93, ATG12, APG12L, WAP012, APG12	ATG12 autophagy related 12 homolog (S. cerevisiae)	NM_004707, NM_033392, NR_033393, XC7190982.1, XC7232134.0, XC7239193.3	203439_at, 213029_at	NP_004698.3, EAW99098.1, EAW99094.1, EAW99095.1
GeneID:10.71	AP3S1	5	115,177,819	115,249,775	72,159	+	2	2_A375_pfk37_plus_lncRNA_AR_1:8493, 2_A375_pfk37_plus_lncRNA_AR_1:8492	-211, -307	upstream, upstream	1	1	0	26	30	8	1	2_A375_pfk37_plus_lncRNA_AR_1	9.30	Gene AP3S1	AP3S1, Sigma3A, CLAPS3	adaptin-related protein complex 3 sigma 1 subunit	NM_001284, XC7232617.0, XC7232209.0	202442_at	NP_001275.1, EAW99052.1, EAW99053.1
GeneID:8.72	SEMA6A	5	115,779,351	115,810,351	131,000	-	1	2_A375_pfk37_plus_lncRNA_AR_1:8493	-108	upstream	0	1	0	22	26	10	1	2_A375_pfk37_plus_lncRNA_AR_1	9.20	Gene SEMA6A	SEMA6Q, SEMA6A1, KIAA1395, SEMA6A, SEMA, HTG16, VIA	semaphorin-like domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	NM_020796, XC7232612.1, XC7232612.1, XC7232123.1, XC7232124.1, XC7232126.0	1555330_at, 213626_at, 220454_s_at, 223449_at, 229862_at	NP_068471.1, EAW99054.1, EAW99055.1, EAW99056.1, EAW99057.1, EAW99058.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_uNG7_myNG7_gRNA_1_Patient	2_A375_2_A375_myNG7_gRNA_1_Patient	3_A375_2_A375_NG7_mimic_lncRNA_NR_1_Patient	4_A375_2_A375_gRNA_lncRNA_NR_1_Patient	1_A375_2_A375_gRNA_lncRNA_NR_1_Avg Read	2_A375_2_A375_gRNA_lncRNA_NR_1_Avg Read	3_A375_2_A375_gRNA_lncRNA_NR_1_Avg Read	4_A375_2_A375_gRNA_lncRNA_NR_1_Avg Read	Adj Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alty Tag	PROT
GeneID:2887 5693	DTWD2	3	110,172,599	110,226,240	151,671	+	2	1_A375_uNG7_mvat_lncRNA_NR_1:4498, 2_A375_uNG7_plus_lncRNA_NR_1:8494			240, 176	cr:gene, cr:gene	1	1	0	19	23	11	1	2_A375_uNG7_plus_lncRNA_NR_1	23	Gene DTWD2	FLJ33977, MGC130891, MGC130899, DTWD2	DTW domain containing 2	NM_175988, ICT19484419.0, ICT23276596.0, NCT23276597.0, NCT23223210.0	231277_x_at		NP_779321.1, EHA48922.1, EHA48923.1, EHA49924.1, EHA49925.1
GeneID:2387 6318	TNFAIP8	3	110,656,410	110,730,294	123,578	+	1	1_A375_uNG7_mvat_lncRNA_NR_1:4497	-323	upstream	1	0	0	19	11	13	1	2_A375_uNG7_plus_lncRNA_NR_1	19	Gene TNFAIP8	SCC-S2, SCC32, MDC-0.53, TNFAIP8, GG2-1	tumor necrosis factor, alpha-induced protein 8	NM_014350, NM_001077654, NCT19301311.0, NCT28088.2	206256_x_at, 210260_s_at		NP_055165.2, NP_001071122.1, EHA49913.1, EHA49914.1
GeneID:3351 95	HS01784 4	3	110,788,148	110,878,027	89,879	+	1	1_A375_DGR1.1:8793	143	cr:gene	0	0	1	16	17	29	1	4_A375_DGR1.1	27	Gene HS01784	HS01784, MFE-2, MFP-2, SDR8C1, DBP	hydroxysteroid (17-beta) dehydrogenase 4	NM_000414, ICT23222310.0, NCT28983.3	1983896_at, 205413_at		NP_000405.1, EHA49910.1, EHA49911.1
GeneID:1587 3443	SRFBP1	3	121,297,858	121,356,293	58,839	+	2	1_A375_uNG7_mvat_lncRNA_NR_1:4499, 2_A375_uNG7_plus_lncRNA_NR_1:8495	-24, -58	upstream, upstream	1	1	0	26	16	10	1	1_A375_uNG7_mvat_lncRNA_NR_1	26	Gene SRFBP1	SRFBP1, RS1, STRAP, antiSTRAP, BUD22, FLJ35205, P49	serum response factor binding protein 1	NM_152548, ICT23276810.0, NCT28982.2	241754_at		NP_689759.2, EHA48999.1, EHA48900.1
GeneID:5663 27	SNCAIP	3	121,847,620	121,799,794	151,974	+	1	1_A375_DGR1.1:4300	59844	cr:gene	1	0	0	16	13	2	1	1_A375_uNG7_mvat_lncRNA_NR_1	16	Gene SNCAIP	Syt11, SYT11, MGC20614, SNCAIP	synuclein, alpha interacting protein	NM_005460, NCT19620084.1, NCT19620085.1, NCT23222080.0, NCT23223072.0, NCT28083.3	219311_s_at, 227653_s_at, 227654_at		NP_005451.2, EHA48997.1, EHA48998.1, EHA48999.1, EHA49000.1, EHA49001.1
GeneID:8893 60	SNX2	5	122,193,750	122,198,003	53,853	+	1	4_A375_DGR1.1:8795	255	cr:gene	0	0	1	14	15	16	1	4_A375_DGR1.1	16	Gene SNX2	FAP4, SNX2, MGC3334	sorting nexin 2	NM_003100, ICT23205013.0, NCT28993.3	202113_s_at, 202114_at		NP_003087.2, EHA48588.1, EHA48594.1
GeneID:5477 60	PPIC	5	122,338,076	122,372,423	10,347	-	1	1_A375_uNG7_mvat_lncRNA_NR_1:4501	-407	upstream	1	0	0	16	16	16	1	1_A375_uNG7_mvat_lncRNA_NR_1	16	Gene PPIC	CYPC, PPIC, MGC3973	peptidylprolyl isomerase C (cyclophilin C)	NM_000943, ICT23277448.0, NCT28984.3	204317_at, 204318_s_at		NP_000934.1, EHA48779.1, EHA48780.1
GeneID:1587 3241	CEP120	5	122,880,979	122,739,298	79,707	-	2	1_A375_uNG7_mvat_lncRNA_NR_1:4503, 2_A375_uNG7_plus_lncRNA_NR_1:8497	66, 116	cr:gene, cr:gene	1	1	0	26	24	14	1	1_A375_uNG7_mvat_lncRNA_NR_1	26	Gene CEP120	CEP120, CCDC100, DKFZp686D0245, FLJ35327, FLJ36309	centrosomal protein 120kDa	NM_153223, NM_001166026, NCT13060.4, NCT23279491.1, NCT23222222.0	1554808_at, 228649_at		NP_694753.2, NP_001138696.1, EHA48870.1, EHA48874.1, EHA48875.1
GeneID:1427 99	CSNK1G3	5	122,847,793	122,932,465	104,672	+	1	2_A375_uNG7_plus_lncRNA_NR_1:8498	-55	upstream	0	0	0	14	15	10	1	2_A375_uNG7_plus_lncRNA_NR_1	14	Gene CSNK1G3	CSNK1G3		NM_001319152, NM_001044722, NM_001044723, NM_004354, NCT12981.3, NCT19613120.1, NCT19613134.1, NCT23209364.0, NCT23209365.0, NCT23209367.0	220768_s_at, 227797_at,		NP_001306081.1, NP_001030187.1, NP_001030188.1, NP_004373.2, EHA48997.1, EHA48998.1, EHA48999.1, EHA49000.1, EHA49870.1, EHA49871.1, EHA49872.1
GeneID:5707 607	ZNF605	5	123,972,810	124,080,555	108,196	-	3	1_A375_uNG7_mvat_lncRNA_NR_1:4507, 2_A375_uNG7_plus_lncRNA_NR_1:8500, 3_A375_DGR1.1:8796	63549, 81221, 630	cr:gene, cr:gene, cr:gene	1	1	1	11.33	16	8.25	3	2_A375_uNG7_plus_lncRNA_NR_1	23	Gene ZNF605	MGC189851, NY-REN-58, ZNF605, DKFZp781C0123	zinc finger protein 605	NM_020747, ICT19151.5, NCT19537012, NCT19601192, NCT23200972	229817_at, 232393_at		NP_065798.2, EHA48589.1, EHA48590.1, EHA48860.1, EHA48861.1
GeneID:4917 01	UNK581	3	126,112,033	126,172,709	99,676	+	3	1_A375_uNG7_mvat_lncRNA_NR_1:4502, 2_A375_uNG7_plus_lncRNA_NR_1:8496, 3_A375_DGR1.1:8797	-321, -383, 1587	upstream, upstream, cr:gene	1	1	0	16.3	16.3	10.3	2	2_A375_uNG7_plus_lncRNA_NR_1	21	Gene UNK581	MGC111419, KIDLO, UNK2, UNK8, UNK, UNK581	taiman B1	NM_033373, ICT19188.4, NCT23322114.0	203276_at		NP_358596.1, EHA48848.1, EHA48849.1, EHA48845.1
GeneID:1153 5125	Mar 3	3	126,230,406	126,288,440	165,034	-	1	2_A375_uNG7_plus_lncRNA_NR_1:8500	232	cr:gene	0	1	0	19	15	17	1	2_A375_uNG7_plus_lncRNA_NR_1	15	Gene MARCH6	MARCH6, MARCH-VI, FLJ20056, MGC40332, RNF172	membrane-associated ring finger (C3HC4) 6	NM_1 75450, ICT19408.2	213256_at		NP_545345.1, EHA49344.1
GeneID:4447 4575	FLJ33630	3	127,207,343	127,410,799	61,323	-	4	1_A375_uNG7_mvat_lncRNA_NR_1:4503, 2_A375_uNG7_plus_lncRNA_NR_1:8510, 4_A375_DGR1.1:8799, 4_A375_DGR1.1:8800	-176, -194, -354, 1616	upstream, upstream, upstream, upstream	1	1	1	17.5	17	16.5	2	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene FLJ33630		hypothetical LOC646673	NR_015360	230909_at, 230955_at, 244789_at		
GeneID:8895 56	SLC12A9	3	127,419,483	127,528,350	103,697	+	4	1_A375_uNG7_mvat_lncRNA_NR_1:4503, 2_A375_uNG7_plus_lncRNA_NR_1:8510, 4_A375_DGR1.1:8799, 4_A375_DGR1.1:8800	-539, -923, -983, 901	upstream, upstream, upstream, cr:gene	1	1	1	17.5	17	16.5	2	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene SLC12A2	BSC, NKCC1, MGC104222, BSC2, SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	NM_001046, ICT19187.2, NCT23443.0, NCT23937.0	204464_s_at, 225853_at		NP_001037.1, EHA48299.1, EHA48299.2, EHA48294.1
GeneID:3356 7676	CHSY3	3	129,240,523	129,532,527	291,856	+	1	4_A375_DGR1.1:8801	-822	upstream	0	0	1	7	8	12	1	4_A375_DGR1.1	12	Gene CHSY3	CHSY2, CSS3, CHSY3	chondroitin sulfate synthase 3	NM_175856, NCT23546991.0	242160_at		NP_787932.2, EHA49279.1
GeneID:5311 733	RAPGEF6	5	130,736,614	130,976,929	211,315	+	3	1_A375_uNG7_plus_lncRNA_NR_1:8511, 3_A375_DGR1.1:8802, 4_A375_DGR1.1:8800	110, 53153, 51	cr:gene, cr:gene, cr:gene	0	1	1	13	16	20	2	2_A375_uNG7_plus_lncRNA_NR_1	23	Gene RAPGEF6	RAPGEF6, PDZ, GEF2, DKFZp686D14064, PDZGEF2, RAGEF2, DKFZp686I15116, FLJ00118, RA-GEF-2	Rap guanine nucleotide exchange factor (GEF) 6	NM_016340, NM_001164398, NM_001164397, NM_001164399, NM_001164400	1553247_s_at, 213112_at, 213113_s_at, 213432_at		NP_057424.3, NP_001157653.1, NP_001157654.1, NP_001157655.1, NP_001157660.1, EHA48360.1, EHA48361.1, NP_001157661.1, NP_001157662.1
GeneID:8461 439	PNPT1	3	130,977,407	131,132,798	155,349	+	4	1_A375_uNG7_plus_lncRNA_NR_1:8511, 2_A375_uNG7_plus_lncRNA_NR_1:8512, 3_A375_DGR1.1:8803, 4_A375_DGR1.1:8804	169940, 116, 169906, 198	downstream, cr:gene, downstream, cr:gene	0	1	1	16	20.5	16	2	2_A375_uNG7_plus_lncRNA_NR_1	23	Gene PNPT1	PNPT1, DKFZp781P0210, DKFZp686E16116, FLJ00108, RNA-GEF-2	ribonuclease (RNase) polynucleotide phosphorylase	NM_033109, NM_133372	1569060_a_at, 223997_at, 223260_at, 226260_at		NP_001030182.2, NP_596013.2
GeneID:1012 7552	LOC10013 3655572	5	131,142,796	131,192,821	49,025	-	2	2_A375_uNG7_plus_lncRNA_NR_1:8512, 4_A375_DGR1.1:8804	59661, 60091	downstream, downstream	0	1	1	13	16	14	1	2_A375_uNG7_plus_lncRNA_NR_1	16	Gene LOC100505572		hypothetical protein LOC100505572	XM_003119980, XM_003116996, XM_003120479			XP_003120028.1, XP_003119044.1, XP_003120027.1
GeneID:2332 4312	ACSL6	5	131,259,152	131,347,549	88,197	-	2	1_A375_uNG7_mvat_lncRNA_NR_1:4515, 2_A375_uNG7_plus_lncRNA_NR_1:8513	-971, -978	upstream, upstream	1	1	0	19	31	9	1	2_A375_uNG7_plus_lncRNA_NR_1	31	Gene ACSL6	ACS2, LACS2, LACS-6, LACS2, ACSL6, KIAA0827, FLJ46172, FACL6	acyl-CoA synthetase long-chain family member 6	NM_015256, NM_001009165, NCT14363.2, NCT23539649.0, NCT23539650.0, NCT23539651.0, NCT23539654.0, NCT23539655.0	211207_s_at, 213602_at, 216409_at, 222916_at, 229725_at		NP_056071.2, NP_001009165.1, EHA48155.1, EHA48156.1, EHA48360.1, EHA48156.1, EHA48359.1
GeneID:3384 82	IL3	5	131,396,347	131,398,698	2,349	+	1	4_A375_DGR1.1:8805	-4235	upstream	0	0	0	9	9	10	1	4_A375_DGR1.1	10	Gene IL3	MCGF, MGC79396, MGC172251, MGC79399, IL-3	interleukin 3 (colony-stimulating factor, multiple)	NM_000588, NCT13222.1	207908_at		NP_000579.2, EHA48236.1
GeneID:8895 53	SLC22A4	5	131,830,143	131,879,899	49,756	+	2	1_A375_uNG7_mvat_lncRNA_NR_1:4516, 4_A375_DGR1.1:8806	-506, -417	upstream, upstream	1	1	0	15	16	27	1	4_A375_DGR1.1	27	Gene SLC22A4	SLC22A4, OCTN1, MGC34546, MGC45324	solute carrier family 22 (organic cation/zwitterion transporter), member 4	NM_003059, ICT19211.2	205896_at		NP_003050.2, EHA48234.1
GeneID:8895 54	SLC22A5	5	131,708,401	131,751,506	43,305	+	2	1_A375_uNG7_mvat_lncRNA_NR_1:4517, 2_A375_uNG7_plus_lncRNA_NR_1:8516	29264, 29039	cr:gene, cr:gene	1	1	0	16	20	9	1	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene SLC22A5	SCN2, SLC22A5, CDSP, FLJ46789, OCTN2/T	solute carrier family 22 (organic cation/zwitterion transporter), member 5	NM_003060, ICT19226.2, NCT23544853.0, NCT23544854.0	205074_at		NP_003051.1, EHA48238.1, EHA48239.1, EHA48235.1
GeneID:3854 59	IRF1	5	131,817,501	131,828,465	10,964	+	4	1_A375_uNG7_mvat_lncRNA_NR_1:4518, 2_A375_uNG7_plus_lncRNA_NR_1:8517, 3_A375_uNG7_plus_lncRNA_NR_1:8516, 4_A375_DGR1.1:8807	135, 226, -3851, 1	cr:gene, cr:gene, upstream, cr:gene	1	1	1	16	19	13.5	2	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene IRF1	MAR, IRF1, IRF-1	interferon regulatory factor 1	NM_002198, ICT19707.1	202531_at		NP_002189.1, EHA48232.1
GeneID:1048 111	RAD50	5	131,892,818	131,980,313	87,897	+	2	1_A375_uNG7_plus_lncRNA_NR_1:8519, 4_A375_DGR1.1:8808	24, 216	cr:gene, cr:gene	0	1	1	19	20	20	1	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene RAD50	RAD50 homolog, RAD50, MRE50, RAD50	RAD50 homolog (S. cerevisiae)	NM_005732, ICT15299.2, NCT23447.0, NCT23447.1	208302_s_at, 208303_s_at		NP_005723.2, EHA48229.1, EHA48230.1
GeneID:1127 127	KIF3A	5	132,028,323	132,072,265	44,942	-	1	2_A375_uNG7_plus_lncRNA_NR_1:8520	112	cr:gene	0	1	0	12	16	14	1	2_A375_uNG7_plus_lncRNA_NR_1	16	Gene KIF3A	KIF3A		NM_007054, ICT19236.2, NCT23539570.0, NCT23539900.0	215825_at, 220660_at		NP_002583.3, EHA48219.1, EHA48220.1, EHA48221.1
GeneID:8444 3121	CCN2	5	132,083,137	132,089,536	6,719	+	1	2_A375_uNG7_plus_lncRNA_NR_1:8520	-9965	upstream	0	1	0	12	16	14	1	2_A375_uNG7_plus_lncRNA_NR_1	16	Gene CCN2	CCN2, FLJ16790	cyclin I family, member 2	NM_010709			NP_010340.1
GeneID:2662 81	GDF9	5	132,196,676	132,200,477	3,802	-	2	1_A375_uNG7_mvat_lncRNA_NR_1:4519, 2_A375_uNG7_plus_lncRNA_NR_1:8521	-1779, -1779	upstream, upstream	1	1	0	19	20	14	1	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene GDF9	GDF9		NM_005260, ICT15243.2	221374_at		NP_005251.1, EHA48230.1
GeneID:2751 599	UQCRQ	5	132,202,319	132,206,539	22,317	-	2	1_A375_uNG7_mvat_lncRNA_NR_1:4519, 2_A375_uNG7_plus_lncRNA_NR_1:8521	-83, -83	upstream, upstream	1	1	0	19	20	14	1	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene UQCRQ	QPC, QPC-, QCR6, UQCR2, UQCR7	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	NM_014402, ICT13964.2	201366_at		NP_055217.2, EHA48238.1
GeneID:1152 8542	LEAP2	3	132,209,388	132,210,582	1,224	+	2	1_A375_uNG7_mvat_lncRNA_NR_1:4519, 2_A375_uNG7_plus_lncRNA_NR_1:8521	-7102, -7102	upstream, upstream	1	1	0	19	20	14	1	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene LEAP2	LEAP2, LEAP-2	liver expressed antimicrobial peptide 2	NM_052971, ICT19444.4, NCT19619.1	1552362_a_at		NP_443203.1, EHA48208.1, EHA48237.1
GeneID:2751 125	APY4	3	132,211,071	132,299,334	88,263	-	3	1_A375_uNG7_mvat_lncRNA_NR_1:4519, 2_A375_uNG7_plus_lncRNA_NR_1:4520, 3_A375_uNG7_plus_lncRNA_NR_1:8521, 4_A375_DGR1.1:8809	97899, 122, 97899, 122, -356	downstream, cr:gene, downstream, cr:gene, upstream	1	1	1	19.5	19.5	15	2	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene APY4	APY4P, APY4P2 family, member 4	APY4P/NP2 family, member 4	NM_014423, ICT15268.2, NCT23539910.0, NCT23539940.0, NCT23539957.0, NCT23539958.0	1555435_at, 1558438_s_at, 219199_at, 223229_at, 223864_s_at, 223865_at, 239429_at, 243487_at		NP_055235.1, EHA48305.1, EHA48306.1, EHA48307.1, EHA48304.1
GeneID:1012 7552	LOC10013 3655572	5	132,294,327	132,297,276	2,641	-	3	1_A375_uNG7_mvat_lncRNA_NR_1:4520, 2_A375_uNG7_plus_lncRNA_NR_1:8522, 4_A375_DGR1.1:8809	-1954, -1954, -2434	upstream, upstream, upstream	1	1	1	20	19	18	1	1_A375_uNG7_mvat_lncRNA_NR_1	20	Gene LOC100509072		hypothetical protein LOC100509072	XM_003119930, XM_003120481			XP_003119048.1, XP_003120029.1
GeneID:3384 06	HSPA4	5	132,397,662	132,440,709	93,047	+	1	4_A375_DGR1.1:8810	-142	upstream	0	0	0	16	16	17	1	4_A375_DGR1.1	17	Gene HSPA4	HSPH4, APG-2, RY, HSX/PS2, HSJP1, NJ/OTK1, MGC131582	heat shock 70 kDa protein 4	NM_002154, ICT23307.8, NCT9396.3	200814_at, 209813_x_at, 211015_s_at, 211016_x_at		NP_002145.3, EHA48294.1, EHA48293.1
GeneID:2751 103	FBTL4	3	132,532,152	132,648,223	116,071	+	8	1_A375_uNG7_mvat_lncRNA_NR_1:4521, 1_A375_uNG7_mvat_lncRNA_NR_1:4522, 1_A375_uNG7_mvat_lncRNA_NR_1:4523, 1_A375_uNG7_mvat_lncRNA_NR_1:4524, 1_A375_uNG7_mvat_lncRNA_NR_1:8523, 2_A375_uNG7_plus_lncRNA_NR_1:8524, 2_A375_uNG7_plus_lncRNA_NR_1:8525, 2_A375_uNG7_plus_lncRNA_NR_1:8526, 4_A375_DGR1.1:8811	198799, 284526, 316815, 48271, 271653, 198874, 316799, 48287	cr:gene, cr:gene, cr:gene, cr:gene, cr:gene, cr:gene, cr:gene	1	1	0	21.4	21.6	15.2	5	2_A375_uNG7_plus_lncRNA_NR_1	30	Gene FBTL4	FBTL4		NM_030592, ICT23233469.0, NCT8763.2	1564511_s_at, 1565810_at		NP_085091.1, EHA48291.1, EHA48292.1
GeneID:7474 16	VDAC1	5	133,207,607	133,240,453	32,826	-	3	1_A375_uNG7_mvat_lncRNA_NR_1:4523, 2_A375_uNG7_plus_lncRNA_NR_1:8526, 4_A375_DGR1.1:8811	-392, 417, -987	upstream, cr:gene, upstream	1	1	1	15.3	17.3	14	2	4_A375_DGR1.1	22	Gene VDAC1	PORIN, VDAC1, MGC119384, FLJ39213,	voltage-dependent anion channel 1	NM_003374, ICT23235502.0, NCT23539300.0, NCT23539503.0, NCT23539510.0, NCT23539790.0	212005_s_at, 217139_at, 217140_s_at		NP_003365.1, EHA48261.1, EHA48262.1, EHA48263.1, EHA48264.1, EHA48265.1
GeneID:8883 00	SKP1	5	133,480,082	133,512,724	30,642	-	3	1_A375_uNG7_mvat_lncRNA_NR_1:4527, 2_A375_uNG7_plus_lncRNA_NR_1:8529, 4_A375_DGR1.1:8812	212, 194, 148	cr:gene, cr:gene, cr:gene	1	1	1	20	26	17	1	2_A375_uNG7_plus_lncRNA_NR_1	26	Gene SKP1	SKP1A, TCEB1L, MGC34483, OCP2, OCP-II, p19A, SKP1, SIP1	S-phase kinase-associated protein 1	NM_006930, NM_170679, NCT23539430.0, NCT23539455.0, NCT23539472.0, NCT23539490.0, NCT23539491.0, NCT23539790.0	200711_s_at, 200712_s_at, 200713_s_at, 200719_at, 200797_s_at		NP_036841.2, NP_733799.1, EHA48270.1, EHA48271.1, EHA48274.1, EHA48276.1, EHA48272.1, EHA48273.1, EHA48275.1
GeneID:5687 15	PPP2CA	5	133,532,145	133,561,930	29,802	-	2	1_A375_uNG7_mvat_lncRNA_NR_1:4528, 2_A375_uNG7_plus_lncRNA_NR_1:8530	-219, 284	upstream, cr:gene	1	1	0	19	20	13	1	2_A375_uNG7_plus_lncRNA_NR_1	20	Gene PPP2CA	PPP2CA, PP-C, PP2CA, PP2Calpha, PP2Cb	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	NM_002715, ICT19600.1, NCT7823.3	200662_at		NP_002706.1, EHA48266.1, EHA48269.1
GeneID:1012 7283	CDK13	5	133,654,113	133,702,765	48,653	-	3	1_A375_uNG7_mvat_lncRNA_NR_1:4529, 2_A375_uNG7_plus_lncRNA_NR_1:8531, 4_A375_DGR1.1:8813	-1178, -1113, -1445	upstream, upstream, upstream	1	1	1	22	24	15	1	2_A375_uNG7_plus_lncRNA_NR_1	24	Gene CDK13	CDK13, MGC4848	cyclin-dependent kinase 13	NM_003718, NM_001113373, NCT23539565.1, NCT23539571.1, NCT23539574.1, NCT23539576.1	1561190_at, 219631_at, 239617_at, 241391_at		NP_003709.2, NP_001107377.1, EHA48284.1, EHA48285.1, EHA48286.1
GeneID:7320 00	UBE2B	5	133,796,670	133,797,799	20,329	+	3	1_A375_uNG7_mvat_lncRNA_NR_1:4529, 2_A375_uNG7_plus_lncRNA_NR_1:8531, 4_A375_DGR1.1:8813	74, 10,343	cr:gene, cr:gene, cr:gene	1	1	1	22	24	13	1	2_A375_uNG7_plus_lncRNA_NR_1	24	Gene UBE2B	E2-17kDa, HHR6B, UBE2B, UBC2, HR6B, RAD6B	ubiquitin conjugating enzyme E2B (RAD6 homolog)	NM_003337, ICT19411.2, NCT19902.1	202333_s_at, 202334_s_at, 202335_s_at, 211760_s_at, 224116_at, 226366_s_at, 239162_at		NP_003327.1, EHA48288.1, EHA48286.1, EHA48287.1
GeneID:1012 7552	LOC10013 3655572	5	133,791,451	133,797,872	6,581	+	2	2_A375_uNG7_plus_lncRNA_NR_1:4530, 2_A375_uNG7_plus_lncRNA_NR_1:8532	16989, 16153	downstream, downstream	1	1	0	52	81	11	1	2_A375_uNG7_plus_lncRNA_NR_1	81	Gene LOC100505572		hypothetical protein LOC100505572	XR_112760, XR_110371, XR_112774			
GeneID:8543 388	CDK5RAP3	5	133,797,799	133,747,995	9,842	-	2	1_A375_uNG7_mvat_lncRNA_NR_1:4530, 2_A375_uNG7_plus_lncRNA_NR_1:8532	-2, 14	upstream, cr:gene	1	1	0	52	81	11	1	2_A375_uNG7_plus_lncRNA_NR_1	81	Gene CDK5RAP3	CDK5RAP3, MGC13217	CDK5RAP3 interacting protein	NM_080656, ICT23235579.1, NCT23539581.1, NCT7833.2	1554345_at, 213038_at		NP_542387.1, EHA48239.1, EHA48288.1, EHA48286.1
GeneID:2237 338	PHF15	3	133,891,795	133,918,918	97,120	+	1	2_A375_uNG7_plus_lncRNA_NR_1:8533	19700	cr:gene	0	1	0	12	21	9	1	2_A375_uNG7_plus_lncRNA_NR_1	21	Gene PHF15	JADE2, KIAA0239, PHF15	PHD finger protein 15	NM_015280, ICT23342.0, NCT23542784.0, NCT23542986.0, NCT23573709.0, NCT7829.3	206302_s_at, 212980_at, 232279_at		NP_056095.2, EHA48233.1, EHA48234.1, EHA48235.1, EHA48236.1
GeneID:8573 9	CAMLG	5	134,076,308	134,097,847	21,541	+	4	1_A375_uNG7_mvat_lncRNA_NR_1:4531, 1_A375_uNG7_mvat_lncRNA_NR_1:4532, 1_A375_uNG7_mvat_lncRNA_NR_1:8534, 2_A375_uNG7_plus_lncRNA_NR_1:8535	2, 20194, -126, 20176	cr:gene, downstream, upstream, downstream	1	1	0	51.5	50.5	16.5	2	1_A375_uNG7_mvat_lncRNA_NR_1	139	Gene CAMLG	CAML, CAMLG	calcium modulating ligand	NM_001745, ICT23342770.0, NCT23542789.0	203536_at		NP_001736.1, EHA48244.1, EHA48242.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9879	DDX46	5	134,094,461	134,166,811	72,350	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4532, 2_A375_pNL97_plus_lncRNA_AR..1..6535	-81, -77	upstream, upstream	1	1	0	139	132	18	1	1_A375_pNL7_minus_lncRNA_AR..1	139	Gene DDX46	PRPF5, FLJ25329, MGC9936, KIAA0801, DDX46, Prp5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	NM_014829, hCT2254261.0, hCT2254265.0, hCT2353713.0, hCT2353714.0, hCT7634.2	202462_s_at, 226039_at	NP_055644.2, EAW62238.1, EAW62239.1, EAW62240.1, EAW62241.1, EAW62242.1
GeneID:134553	C5orf24	5	134,181,370	134,195,425	14,055	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6536	358	in gene	0	1	0	13	24	13	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene C5orf24	C5orf24, FLJ37562	chromosome 5 open reading frame 24	NM_152409, NM_001135586	1553106_at, 1553107_s_at, 1553108_at, 224875_at, 224876_at, 229098_s_at	NP_689622.2, NP_001129058.1
GeneID:79770	TXNDC15	5	134,209,460	134,237,323	27,863	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4533, 1_A375_pNL7_minus_lncRNA_AR..1..4534, 2_A375_pNL97_plus_lncRNA_AR..1..6537	1484, 31084, 31148	in gene, downstream, downstream	1	1	0	16.5	15.5	7.5	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene TXNDC15	FLJ22625, UNQ335, C5orf14, TXNDC15	thioredoxin domain containing 15	NM_024715, hCT1784313.2, hCT2353792.0, hCT2353793.0	220495_s_at, 227873_at	NP_078991.3, EAW62231.1, EAW62232.1, EAW62233.1
GeneID:84105	PCBD2	5	134,240,810	134,298,336	57,526	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4534, 2_A375_pNL97_plus_lncRNA_AR..1..6537	-266, -202	upstream, upstream	1	1	0	15	17	6	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PCBD2	PCBD2, DCOH2, DCOHM, PHS2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	NM_032151, hCT2349005.0	1554894_a_at, 223712_at, 240646_at	NP_115527.3, EAW62229.1
GeneID:5307	PITX1	5	134,363,424	134,369,964	6,540	-	4	4_A375_EGR1..1..6614, 4_A375_EGR1..1..6615, 4_A375_EGR1..1..6616, 4_A375_EGR1..1..6617	6798, 5260, 2988, -5106	downstream, in gene, in gene, upstream	0	0	1	6.25	6.5	18.75	4	4_A375_EGR1..1	20	Gene PITX1	POTX, BFT, CCF, PITX1, PTX1	paired-like homeodomain 1	NM_002653, hCT2253534.0, hCT30950.3	208502_s_at, 209587_at	NP_002644.4, EAW62227.1, EAW62226.1
GeneID:9555	H2AFY	5	134,670,071	134,735,577	65,506	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6539	665	in gene	0	1	0	12	19	5	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene H2AFY	mH2A1, H2A.y, MACROH2A1.1, H2AF12M, H2AFJ, H2A/y, H2AFY, macroH2A1.2	H2A histone family, member Y	NM_004893, NM_138609, NM_138610, NM_001040158, hCT1954327.2, hCT1970650.2, hCT1970653.2, hCT2253492.1, hCT29569.2	1558779_at, 1558780_a_at, 207168_s_at, 214500_at, 214501_s_at, 226640_at	NP_004884.1, NP_613075.1, NP_613258.2, NP_001035248.1, EAW62220.1, EAW62222.1, EAW62218.1, EAW62219.1, EAW62221.1
GeneID:4762	NEUROG1	5	134,869,972	134,871,639	1,667	-	1	4_A375_EGR1..1..6619	55	in gene	0	0	1	4	6	19	1	4_A375_EGR1..1	19	Gene NEUROG1	NEUROG1, ngn1, AKA, bHLHa6, Math4C, NEUROD3	neurogenin 1	NM_006161, hCT1784311.1	208497_x_at	NP_006152.2, EAW62214.1
GeneID:9547	CXCL14	5	134,906,369	134,914,969	8,600	-	1	4_A375_EGR1..1..6620	441	in gene	0	0	1	6	5	18	1	4_A375_EGR1..1	18	Gene CXCL14	SCYB14, BMAC, KS1, KEC, MGC10687, MIP-2g, BRAK, MIP2G, NJAC, CXCL14	chemokine (C-X-C motif) ligand 14	NM_004887	218002_s_at, 222484_s_at, 237038_at	NP_004878.2
GeneID:7045	TGFBI	5	135,364,584	135,399,507	34,923	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4535, 1_A375_pNL7_minus_lncRNA_AR..1..4536, 2_A375_pNL97_plus_lncRNA_AR..1..6540, 2_A375_pNL97_plus_lncRNA_AR..1..6541	-8312, 24868, -8296, 24888	upstream, in gene, upstream, in gene	1	1	0	18	20	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TGFBI	CDB1, CSD, BIGH3, CSD3, CDGG1, EBMD, TGFBI, CSD1, LCD1, CSD2, CDG2	transforming growth factor, beta-induced, 68kDa	NM_000358, hCT2253103.0, hCT2353684.0, hCT32670.3	201506_at	NP_000349.1, EAW62199.1, EAW62198.1, EAW62200.1
GeneID:9597	SMAD5OS	5	135,465,202	135,470,579	5,377	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4537, 2_A375_pNL97_plus_lncRNA_AR..1..6542	1971, 1843	in gene, in gene	1	1	0	24	17	9	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene SMAD5OS	SMAD5AS, SMAD5OS, DAMS	SMAD family member 5 opposite strand	NR_026763	220263_at	
GeneID:4090	SMAD5	5	135,468,536	135,518,422	49,886	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4537, 2_A375_pNL97_plus_lncRNA_AR..1..6542	72, 200	in gene, in gene	1	1	0	24	17	9	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene SMAD5	SMAD5, DKFZp781O1323, Dwfc, MADH5, DKFZp781C1895, DWFC, JV5-1	SMAD family member 5	NM_005903, NM_001001419, NM_001001420, hCT2253108.0, hCT2253113.0, hCT32672.2	205187_at, 205188_s_at, 225219_at, 225223_at, 235451_at	NP_005894.3, NP_001001419.1, NP_001001420.1, EAW62194.1, EAW62195.1, EAW62196.1
GeneID:57113	TRPC7	5	135,548,999	135,701,164	152,165	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4538, 2_A375_pNL97_plus_lncRNA_AR..1..6543	92, 108	in gene, in gene	1	1	0	35	43	3	1	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene TRPC7	TRP7, TRPC7	transient receptor potential cation channel, subfamily C, member 7	NM_020389, NM_001167576, NM_001167577, hCT2353685.0, hCT2353686.0, hCT2353687.0, hCT2353688.0, hCT2353689.0, hCT32674.3	208589_at, 234407_s_at	NP_065122.1, NP_001161048.1, NP_001161049.1, EAW62187.1, EAW62188.1, EAW62192.1, EAW62189.1, EAW62190.1, EAW62191.1
GeneID:8695	SPOCK1	5	136,310,987	136,835,018	524,031	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4539, 1_A375_pNL7_minus_lncRNA_AR..1..4540, 1_A375_pNL7_minus_lncRNA_AR..1..4541, 2_A375_pNL97_plus_lncRNA_AR..1..6544, 2_A375_pNL97_plus_lncRNA_AR..1..6545	358410, 45674, 28426, 45674, 28426	in gene, in gene, in gene, in gene, in gene	1	1	0	25.33	27.67	7	3	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene SPOCK1	TESTICAN, SPOCK1, SPOCK, FLJ37170, TIC1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	NM_004598, hCT2353752.0, hCT30730.3	202363_at	NP_004589.1, EAW62185.1, EAW62186.1
GeneID:10949	HNRNPA0	5	137,087,073	137,090,039	2,966	-	2	2_A375_pNL97_plus_lncRNA_AR..1..6546, 4_A375_EGR1..1..6621	7, 23	in gene, in gene	0	1	1	16	23	21	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene HNRNPA0	HNRPA0, HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	NM_006805, hCT1640078.4	201054_at, 201055_s_at	NP_006796.1, EAW62182.1
GeneID:51306	FAM13B	5	137,273,636	137,368,802	95,164	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6547	594	in gene	0	1	0	10	17	14	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene FAM13B	N61, KHCHP, FAM13B1, MGC57159, DKFZp667F249, C5orf5, FLJ26735, FAM13B	family with sequence similarity 13, member B	NM_016603, NM_001101800, NM_001101801, hCT1821582.1, hCT2254836.0, hCT2353734.0, hCT2353735.0	218518_at	NP_057687.2, NP_001095270.1, NP_001095271.1, EAW62170.1, EAW62171.1, EAW62172.1, EAW62173.1
GeneID:100130172	LOC100130172	5	137,368,482	137,373,321	4,839	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6547	-274	upstream	0	1	0	10	17	14	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC100130172		hypothetical LOC100130172	XR_112756, XR_110574, XR_113779		
GeneID:995	CDC25C	5	137,620,959	137,667,516	46,557	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4542, 1_A375_pNL7_minus_lncRNA_AR..1..4543, 2_A375_pNL97_plus_lncRNA_AR..1..6548, 4_A375_EGR1..1..6622	92, -6052, -6020, 6466	in gene, upstream, upstream, upstream	1	1	1	71	88.5	21	2	2_A375_pNL97_plus_lncRNA_AR..1	164	Gene CDC25C	CDC25C, CDC25	cell division cycle 25 homolog C (S. pombe)	NM_022809, NM_001790, hCT1821564.2, hCT2254621.0, hCT2254622.0, hCT2254623.0, hCT2353753.0, hCT2353754.0	205167_s_at, 216914_at, 217010_s_at	NP_073720.1, NP_001781.2, EAW62146.1, EAW62147.1, EAW62149.1, EAW62150.1, EAW62145.1, EAW62148.1
GeneID:51307	FAM53C	5	137,673,224	137,685,418	12,194	+	7	1_A375_pNL7_minus_lncRNA_AR..1..4542, 1_A375_pNL7_minus_lncRNA_AR..1..4543, 1_A375_pNL7_minus_lncRNA_AR..1..4544, 1_A375_pNL7_minus_lncRNA_AR..1..4545, 2_A375_pNL97_plus_lncRNA_AR..1..6548, 2_A375_pNL97_plus_lncRNA_AR..1..6549, 4_A375_EGR1..1..6622	-5800, 344, 14952, 15898, 312, 14936, 760	upstream, in gene, downstream, downstream, in gene, downstream, in gene	1	1	1	58	89.33	18	3	2_A375_pNL97_plus_lncRNA_AR..1	164	Gene FAM53C	C5orf6, FAM53C	family with sequence similarity 53, member C	NM_001135647, NM_016605, hCT1954332.1, hCT9646.2	218023_s_at	NP_001129119.1, NP_057689.1, EAW62143.1, EAW62144.1
GeneID:51780	KDM3B	5	137,688,285	137,772,716	84,431	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4544, 1_A375_pNL7_minus_lncRNA_AR..1..4545, 2_A375_pNL97_plus_lncRNA_AR..1..6549, 4_A375_EGR1..1..6623	-109, 835, -125, 92707	upstream, in gene, upstream, downstream	1	1	1	17.5	19	14	2	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene KDM3B	KDM3B, KIAA1082, JMJD1B, NET22, 5qNCA, C5orf7	lysine (K)-specific demethylase 3B	NM_016604, hCT2256307.0, hCT9636.2	201643_x_at, 210878_s_at	NP_057688.2, EAW62141.1, EAW62142.1
GeneID:51308	REEP2	5	137,774,776	137,782,658	7,882	+	1	4_A375_EGR1..1..6623	6216	in gene	0	0	1	3	7	16	1	4_A375_EGR1..1	16	Gene REEP2	C5orf19, SGC32445, REEP2	receptor accessory protein 2	NM_016606, hCT1813927.1, hCT1954333.1, hCT1954334.1, hCT9647.3	205331_s_at	NP_057690.2, EAW62137.1, EAW62138.1, EAW62139.1, EAW62140.1
GeneID:1958	EGR1	5	137,801,181	137,805,004	3,823	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4546, 2_A375_pNL97_plus_lncRNA_AR..1..6550, 4_A375_EGR1..1..6624	-361, -125, -733	upstream, upstream, upstream	1	1	1	36	43	30	1	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene EGR1	ZIF-268, ZNF225, KROX-24, TIS8, EGR1, NGFI-A, G0S30, AT225	early growth response 1	NM_001964, hCT2256315.1, hCT9839.1	201693_s_at, 201694_s_at, 227404_s_at	NP_001955.1, EAW62136.1, EAW62135.1
GeneID:2107	ETF1	5	137,841,784	137,878,932	37,148	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4548, 2_A375_pNL97_plus_lncRNA_AR..1..6551, 4_A375_EGR1..1..6625	116, 148, 532	in gene, in gene, in gene	1	1	1	18	26	25	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ETF1	MGC111066, ETF1, D5S1995, ERF1, TB3-1, SUP45L1, ERF, RF1	eukaryotic translation termination factor 1	NM_004730, hCT2254611.0, hCT2254612.0, hCT2254613.0, hCT2353728.0, hCT2353729.0	201573_s_at, 201574_at	NP_004721.1, EAW62134.1, EAW62130.1, EAW62131.1, EAW62132.1, EAW62133.1
GeneID:3313	HSPA9	5	137,890,571	137,911,318	20,747	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4549, 2_A375_pNL97_plus_lncRNA_AR..1..6552, 4_A375_EGR1..1..6626	102, 182, 230	in gene, in gene, in gene	1	1	1	24	31	20	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene HSPA9	HSPA9B, GRP75, MTHSP75, PBP74, CSA, HSPA9, MOT, mot-2, MGC4500, MOT2	heat shock 70kDa protein 9 (mortalin)	NM_004134, hCT1954329.2, hCT9841.3	200690_at, 200691_s_at, 200692_s_at, 232200_at	NP_004125.3, EAW62129.1, EAW62128.1
GeneID:724102	SNHG4	5	138,609,441	138,618,873	9,432	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4552	159	in gene	1	0	0	17	16	14	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene SNHG4	U19H, NCRNA00059, SNHG4	small nucleolar RNA host gene 4 (non-protein coding)	NR_036536, NR_003141	1564906_at, 1564911_at, 1565325_at	
GeneID:9782	MATR3	5	138,609,441	138,667,366	57,925	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4552, 2_A375_pNL97_plus_lncRNA_AR..1..6555, 4_A375_EGR1..1..6627, 4_A375_EGR1..1..6628	159, 68111, 20159, 68255	in gene, downstream, in gene, downstream	1	1	1	15	15.33	20.33	3	4_A375_EGR1..1	24	Gene MATR3	MGC9105, KIAA0723, MPD2, DKFZp686K23100, VCPDM, DKFZp686K0542, MATR3	matrin 3	NM_018834, NM_199189, NM_001194954, NM_001194955, NM_001194956, NR_036535	1558093_s_at, 200624_s_at, 200626_s_at, 214363_s_at, 228012_at, 242260_at	NP_061322.2, NP_954659.1, NP_001181883.1, NP_001181884.1, NP_001181885.1
GeneID:26821	SNORA74A	5	138,614,469	138,614,668	199	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4552	-4869	upstream	1	0	0	17	16	14	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene SNORA74A	SNORA74A, U19, RNU19	small nucleolar RNA, H/ACA box 74A	NR_002915	1567679_at, 1567681_at, 1567682_x_at	
GeneID:51247	PAIP2	5	138,677,519	138,705,409	27,890	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6555, 4_A375_EGR1..1..6628	33, 177	in gene, in gene	0	1	1	15	19	23	1	4_A375_EGR1..1	23	Gene PAIP2	PAIP2A, MGC72018, PAIP2	poly(A) binding protein interacting protein 2	NM_016480, NM_001033112, hCT2253795.0, hCT2253796.0, hCT2353704.0, hCT2353705.0, hCT2353706.0, hCT7701.1	222983_s_at, 222984_at	NP_057564.3, NP_001028284.1, EAW62107.1, EAW62108.1, EAW62110.1, EAW62112.1, EAW62109.1, EAW62111.1
GeneID:389333	LOC389333	5	138,727,635	138,730,885	3,250	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6556	-8923	upstream	0	1	0	17	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC389333		hypothetical protein LOC389333	NM_001161546		NP_001155018.1
GeneID:202051	SPATA24	5	138,732,456	138,739,776	7,320	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6556	-32	upstream	0	1	0	17	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SPATA24	T6441, CCDC161, SPATA24	spermatogenesis associated 24	NM_194296	1556841_at, 238027_at	NP_919272.1
GeneID:202052	DNAJC18	5	138,745,892	138,775,214	29,322	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4553, 2_A375_pNL97_plus_lncRNA_AR..1..6556	-18, 35406	upstream, downstream	1	1	0	17.5	17	9	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene DNAJC18	MGC29463, DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	NM_152686, hCT7699.3	227166_at, 227169_at	NP_689899.1, EAW62102.1
GeneID:641700	ECSCR	5	138,784,245	138,784,863	618	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4553	9631	downstream	1	0	0	18	14	6	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ECSCR	ARIA, ECSCR, ECSM2	endothelial cell-specific chemotaxis regulator	NM_001077693	227780_s_at, 228339_at	NP_001071161.1
GeneID:7322	UBE2D2	5	138,940,751	139,008,019	67,268	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6557	76481	downstream	0	1	0	17	32	6	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene UBE2D2	UBC4/5, PUBC1, UBCH5B, UBC4, E2(17)KB2, UBE2D2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	NM_181838, NM_003339, hCT2253808.0, hCT2253809.0, hCT2253811.0	201343_at, 201344_at, 201345_s_at	NP_862821.1, NP_003330.1, EAW62095.1, EAW62096.1, EAW62097.1
GeneID:51523	CXXC5	5	139,028,301	139,062,680	34,379	+	2	4_A375_EGR1..1..6630, 4_A375_EGR1..1..6631	7347, 10611	in gene, in gene	0	0	1	8.5	10	16.5	2	4_A375_EGR1..1	17	Gene CXXC5	WID, HSPC195, CXXC5, CF5, RINF	CXXC finger 5	NM_016463, hCT1640331.3, hCT2253778.0, hCT2253777.0, hCT2253780.0	222996_s_at, 224516_s_at, 233955_x_at	NP_057547.5, EAW62090.1, EAW62091.1, EAW62092.1, EAW62093.1
GeneID:9542	NRG2	5	139,226,364	139,422,884	196,520	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4554, 1_A375_pNL7_minus_lncRNA_AR..1..4555, 2_A375_pNL97_plus_lncRNA_AR..1..6559, 2_A375_pNL97_plus_lncRNA_AR..1..6560	57476, -300, 57508, -268	in gene, upstream, in gene, upstream	1	1	0	17.5	18	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene NRG2	Don-1, NRG2, DON1, NTAK, HRG2	neuregulin 2	NM_001184935, NM_004883, NM_013981, NM_013982, NM_013983, hCT2252851.0, hCT2252852.0, hCT2252853.0, hCT2252855.0, hCT2252856.0, hCT2252857.0, hCT2252859.0, hCT2252860.0, hCT2353746.0, hCT2353747.0	206679_s_at, 208062_s_at	NP_001171864.1, NP_004874.1, NP_053584.1, NP_053585.1, NP_053586.1, EAW62084.1, EAW62078.1, EAW62079.1, EAW62080.1, EAW62081.1, EAW62082.1, EAW62083.1, EAW62085.1, EAW62086.1, EAW62087.1
GeneID:100505636	LOC100505636	5	139,482,505	139,488,150	5,645	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4556, 1_A375_pNL7_minus_lncRNA_AR..1..4557, 2_A375_pNL97_plus_lncRNA_AR..1..6561, 2_A375_pNL97_plus_lncRNA_AR..1..6562, 4_A375_EGR1..1..6634	822, -5946, -5062, -6042, -4690	in gene, upstream, upstream, upstream, upstream	1	1	1	13.67	16.67	13	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100505636		hypothetical LOC100505636	XR_112789, XR_112788, XR_110310, XR_110309, XR_113783, XR_113782		
GeneID:5813	PURA	5	139,493,708	139,496,321	2,613	+	5	1_A375_pNL7_minus_lncRNA_AR..1..4556, 1_A375_pNL7_minus_lncRNA_AR..1..4557, 2_A375_pNL97_plus_lncRNA_AR..1..6561, 2_A375_pNL97_plus_lncRNA_AR..1..6562, 4_A375_EGR1..1..6634	-6380, 388, -476, 484, -686	upstream, in gene, upstream, in gene, upstream	1	1	1	13.67	16.67	13	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene PURA	PURALPHA, PUR1, PUR-ALPHA, PURA	purine-rich element binding protein A	NM_005859	204020_at, 204021_s_at, 213806_at	NP_005850.1
GeneID:84418	C5orf32	5	139,554,653	139,623,374	68,721	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6563, 4_A375_EGR1..1..6635	46979, 451	in gene, in gene	0	1	1	13.5	16	9	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene C5orf32	ORF1-FL49, C5orf32	chromosome 5 open reading frame 32	NM_032412, hCT1690270.1, hCT36801.2	224707_at	NP_115788.1, EAW62073.1, EAW62074.1
GeneID:1839	HBEGF	5	139,712,428	139,726,188	13,760	-	1	4_A375_EGR1..1..6636	204	in gene	0	0	1	12	11	19	1	4_A375_EGR1..1	19	Gene HBEGF	DTS, HEGFL, HBEGF, DTSF, DTR	heparin-binding EGF-like growth factor	NM_001945, hCT36568.2	203821_at, 222076_at, 244657_at, 38037_at	NP_001936.1, EAW62069.1
GeneID:404734	ANKHD1-EIF4EBP3	5	139,781,429	139,929,163	147,734	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4558, 2_A375_pNL97_plus_lncRNA_AR..1..6564	-293, -1093	upstream, upstream	1	1	0	30	34	12	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene ANKHD1-EIF4EBP3	MASK-BP3ARF, MASK-BP3arf, MASK-BP3, ANKHD1-EIF4EBP3	ANKHD1-EIF4EBP3 readthrough	NM_020690	208772_at, 208773_s_at, 214919_s_at, 233292_s_at	NP_065741.3
GeneID:54882	ANKHD1	5	139,781,429	139,919,441	138,012	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4558, 2_A375_pNL97_plus_lncRNA_AR..1..6564	-293, -1093	upstream, upstream	1	1	0	30	34	12	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene ANKHD1	ANKHD1, MASK, VBARP	ankyrin repeat and KH domain containing 1	NM_017747, NM_017978, NM_024668	219061_at, 229457_at	NP_060217.1, NP_060448.1, NP_078944.2
GeneID:10011	SRA1	5	139,929,653	139,937,678	8,025	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4559, 2_A375_pNL97_plus_lncRNA_AR..1..6565	-6450, -6482	upstream, upstream	1	1	0	33	39	12	1	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene SRA1	MGC87674, STRAA1, SRAP, SRA, SRA1, pp7684	steroid receptor RNA activator 1	NM_001035235, hCT11375.2, hCT1953450.1, hCT2353720.0	224130_s_at, 224664_at	NP_001030312.2, EAW62052.1, EAW62051.1, EAW62053.1
GeneID:10307	APBB3	5	139,937,853	139,944,189	6,336	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4559, 2_A375_pNL97_plus_lncRNA_AR..1..6565	61, 29	in gene, in gene	1	1	0	33	39	12	1	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene APBB3	MGC87674, SRA, FE65L2, APBB3, MGC150555	amyloid beta (A4) precursor protein-binding, family B, member 3	NM_133172, NM_006051, NM_133173, NM_133174, hCT2252827.0, hCT2252828.0, hCT2252829.0, hCT2252830.0, hCT2252832.0, hCT2252833.0, hCT2252835.0, hCT2252836.0, hCT2252837.0, hCT2353703.0	204650_s_at	NP_573418.2, NP_006042.3, NP_573419.2, NP_573420.2, EAW62046.1, EAW62050.1, EAW62041.1, EAW62042.1, EAW62043.1, EAW62044.1, EAW62045.1, EAW62047.1, EAW62048.1, EAW62049.1
GeneID:113829	SLC35A4	5	139,944,420	139,948,683	4,263	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4559, 2_A375_pNL97_plus_lncRNA_AR..1..6565	-292, -260	upstream, upstream	1	1	0	33	39	12	1	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene SLC35A4	SLC35A4, MGC2541	solute carrier family 35, member A4	NM_080670, hCT1821826.0	224628_at	NP_542401.1, EAW62040.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.100505798	LOC100505798	5	139,949,833	139,971,877	22,044	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4559, 2_A375_pNL97_plus_lncRNA_AR..1..6565	27549, 27517	downstream, downstream	1	1	0	33	39	12	1	2_A375_pNL97_plus_lncRNA_AR..1	39	Gene LOC100505798		hypothetical protein LOC100505798	XM_003118935		XP_003118983.1
GeneID.929	CD14	5	140,011,313	140,013,286	1,973	-	2	2_A375_pNL97_plus_lncRNA_AR..1..6566, 4_A375_EGR1..1..6837	-8010, 1606	upstream, in gene	0	1	1	9	10	13.5	2	4_A375_EGR1..1	18	Gene CD14	CD14		NM_000591, NM_001040021, NM_001174104, NM_001174105, hCT2252825.0	201743_at	NP_000582.1, NP_001035110.1, NP_001167575.1, NP_001167576.1, EAW62037.1
GeneID.55374	TMCO6	5	140,019,012	140,024,989	5,977	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4560, 2_A375_pNL97_plus_lncRNA_AR..1..6566, 4_A375_EGR1..1..6837	8012, 284, -7332	downstream, in gene, upstream	1	1	1	12	12	11.67	3	4_A375_EGR1..1	18	Gene TMCO6	TMCO6, PRO1580, FLJ39769	transmembrane and coiled-coil domains 6	NM_018502, hCT11377.2, hCT1953451.1, hCT2255734.0, hCT2353750.0, hCT2353751.0	221098_s_at	NP_060972.3, EAW62033.1, EAW62032.1, EAW62034.1, EAW62035.1, EAW62036.1
GeneID.4695	NDUFA2	5	140,024,948	140,027,370	2,422	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4560, 2_A375_pNL97_plus_lncRNA_AR..1..6566	346, 8074	in gene, downstream	1	1	0	15.5	16	8.5	2	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene NDUFA2	B8, CD14, CIB8, NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	NM_001185012, NM_002488, NR_033697, hCT1953449.1	209223_at, 209224_s_at, 222971_at	NP_001171941.1, NP_002479.1, EAW62031.1
GeneID.3550	IK	5	140,027,384	140,042,065	14,681	+	5	1_A375_pNL7_minus_lncRNA_AR..1..4560, 1_A375_pNL7_minus_lncRNA_AR..1..4561, 2_A375_pNL97_plus_lncRNA_AR..1..6566, 2_A375_pNL97_plus_lncRNA_AR..1..6567, 4_A375_EGR1..1..6838	-360, 16712, -8068, 16648, 17084	upstream, downstream, upstream, downstream, downstream	1	1	1	16	18.33	11	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene IK	IK, MGC59741, RED, CSA2	IK cytokine, down-regulator of HLA II	NM_006083, hCT1821814.1, hCT2255740.0, hCT2255742.0	200066_at	NP_006074.2, EAW62028.1, EAW62029.1, EAW62030.1
GeneID.54853	WDR55	5	140,044,384	140,050,553	6,169	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4561, 2_A375_pNL97_plus_lncRNA_AR..1..6567, 4_A375_EGR1..1..6838	-288, -352, 84	upstream, upstream, in gene	1	1	1	17	23	16	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene WDR55	FLJ20195, FLJ21702, WDR55	WD repeat domain 55	NM_017706, hCT1821813.2, hCT2255744.0, hCT2255752.0	219809_at, 222114_x_at, 223833_at	NP_060176.2, EAW62024.1, EAW62025.1, EAW62026.1
GeneID.373863	DND1	5	140,050,381	140,053,171	2,790	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4561, 2_A375_pNL97_plus_lncRNA_AR..1..6567, 4_A375_EGR1..1..6838	9075, 9139, 8723	downstream, downstream, downstream	1	1	1	17	23	16	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene DND1	RBMS4, MGC34750, DND1	dead end homolog 1 (zebrafish)	NM_194249, hCT2351851.0	57739_at	NP_919225.1, EAW62027.1
GeneID.3035	HARS	5	140,053,490	140,070,971	17,481	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4561, 1_A375_pNL7_minus_lncRNA_AR..1..4562, 2_A375_pNL97_plus_lncRNA_AR..1..6567, 4_A375_EGR1..1..6838	26875, -101, 26939, 26523	downstream, upstream, downstream, downstream	1	1	1	19	19.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene HARS	HARS, FLJ20491, HRS	histidyl-tRNA synthetase	NM_002109, hCT1821805.3, hCT2252820.1, hCT2353741.0	202042_at	NP_002100.2, EAW62023.1, EAW62021.1, EAW62022.1
GeneID.23438	HARS2	5	140,071,016	140,078,890	7,872	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4562	54	in gene	1	0	0	21	16	10	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene HARS2	HARSR, HARSL, HO3, HARS2	histidyl-tRNA synthetase 2, mitochondrial (putative)	NM_012208, hCT2255764.0, hCT2353763.0	209252_at	NP_036340.1, EAW62020.1, EAW62019.1
GeneID.153527	ZMAT2	5	140,080,032	140,088,239	8,207	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4562, 1_A375_pNL7_minus_lncRNA_AR..1..4563, 2_A375_pNL97_plus_lncRNA_AR..1..6568, 4_A375_EGR1..1..6839	-8960, 10658, 10720, 10816	upstream, downstream, downstream, downstream	1	1	1	25	21	18	2	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene ZMAT2	hSNU23, FLJ31121, Snu23, ZMAT2	zinc finger, matrin type 2	NM_144723, hCT2255766.1, hCT2344113.0, hCT2353717.0	224782_at	NP_653324.1, EAW62016.1, EAW62017.1, EAW62018.1
GeneID.56147	PCDHA1	5	140,165,876	140,391,929	226,053	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6571, 4_A375_EGR1..1..6841, 4_A375_EGR1..1..6842	140396, 10700, 49452	in gene, in gene, in gene	0	1	1	10.67	12.33	18.67	3	4_A375_EGR1..1	24	Gene PCDHA1	PCDH-ALPHA1, PCDHA1	protocadherin alpha 1	NM_018900, NM_031410, NM_031411		NP_061723.1, NP_113598.1, NP_113599.1
GeneID.56117	PCDHA@	5	140,165,876	140,391,929	226,053	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6571, 4_A375_EGR1..1..6841, 4_A375_EGR1..1..6842	140396, 10700, 49452	in gene, in gene, in gene	0	1	1	10.67	12.33	18.67	3	4_A375_EGR1..1	24	Gene PCDHA@	PCDHA@, CNR1, CNRS1	protocadherin alpha cluster			
GeneID.56146	PCDHA2	5	140,174,444	140,391,929	217,485	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6571, 4_A375_EGR1..1..6841, 4_A375_EGR1..1..6842	131828, 2132, 40884	in gene, in gene, in gene	0	1	1	10.67	12.33	18.67	3	4_A375_EGR1..1	24	Gene PCDHA2	PCDH-ALPHA2, PCDHA2	protocadherin alpha 2	NM_018905, NM_031495	210572_at, 211365_s_at	NP_061728.1, NP_113683.1
GeneID.56145	PCDHA3	5	140,180,783	140,391,929	211,146	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6571, 4_A375_EGR1..1..6841, 4_A375_EGR1..1..6842	125489, -4207, 34545	in gene, upstream, in gene	0	1	1	10.67	12.33	18.67	3	4_A375_EGR1..1	24	Gene PCDHA3	MGC141869, PCDH-ALPHA3, PCDHA3	protocadherin alpha 3	NM_018906, NM_031497	211870_s_at	NP_061729.1, NP_113685.1
GeneID.56144	PCDHA4	5	140,186,872	140,391,929	205,257	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6571, 4_A375_EGR1..1..6841, 4_A375_EGR1..1..6842	119800, -10098, 28856	in gene, upstream, in gene	0	1	1	10.67	12.33	18.67	3	4_A375_EGR1..1	24	Gene PCDHA4	CNR1, PCDH-ALPHA4, MGC138307, PCDHA4, MGC142169, CNRN1, CRNR1	protocadherin alpha 4	NM_018907, NM_031500		NP_061730.1, NP_113688.1
GeneID.56143	PCDHA5	5	140,201,361	140,391,929	190,568	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6571, 4_A375_EGR1..1..6842	104911, 13967	in gene, in gene	0	1	1	11.5	14.5	16	2	4_A375_EGR1..1	19	Gene PCDHA5	CRNR6, PCDHA5, CNRS6, CNR6, CNRN6, PCDH-ALPHA5	protocadherin alpha 5	NM_018908, NM_031501	211836_x_at	NP_061731.1, NP_113689.1
GeneID.56142	PCDHA6	5	140,207,850	140,391,929	184,279	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6571, 4_A375_EGR1..1..6842	98822, 7678	in gene, in gene	0	1	1	11.5	14.5	16	2	4_A375_EGR1..1	19	Gene PCDHA6	CNRN2, CRNR2, PCDH-ALPHA6, CNRS2, PCDHA6, CNR2	protocadherin alpha 6	NM_018909, NM_031848, NM_031849	211811_s_at	NP_061732.1, NP_114036.1, NP_114037.1
GeneID.56141	PCDHA7	5	140,213,969	140,391,929	177,960	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6571, 4_A375_EGR1..1..6842	92303, 1359	in gene, in gene	0	1	1	11.5	14.5	16	2	4_A375_EGR1..1	19	Gene PCDHA7	CRNR4, CNRN4, PCDHA7, CNRS4, PCDH-ALPHA7, CNR4	protocadherin alpha 7	NM_018910, NM_031852		NP_061733.1, NP_114040.1
GeneID.56140	PCDHA8	5	140,220,907	140,391,929	171,022	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6571, 4_A375_EGR1..1..6842	85365, -5579	in gene, upstream	0	1	1	11.5	14.5	16	2	4_A375_EGR1..1	19	Gene PCDHA8	PCDHA8, PCDH-ALPHA8	protocadherin alpha 8	NM_018911, NM_031856		NP_061734.1, NP_114062.1
GeneID.9752	PCDHA9	5	140,227,357	140,391,929	164,572	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6571	78915	in gene	0	1	0	16	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PCDHA9	PCDH-ALPHA9, KIAA0345, PCDHA9	protocadherin alpha 9	NM_031857, NM_014005	208205_at	NP_114063.1, NP_054724.1
GeneID.56139	PCDHA10	5	140,235,634	140,391,929	156,295	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6571	70636	in gene	0	1	0	16	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PCDHA10	PCDHA10, CNR8, CRNR8, CNRN8, CNRS8, PCDH-ALPHA10	protocadherin alpha 10	NM_018901, NM_031859, NM_031860	211867_s_at	NP_061724.1, NP_114065.1, na.2919
GeneID.56138	PCDHA11	5	140,247,831	140,391,929	144,098	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6571	58441	in gene	0	1	0	16	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PCDHA11	CRNR7, CNRS7, PCDH-ALPHA11, PCDHA11, CNRN7, CNR7	protocadherin alpha 11	NM_031861, NM_018902		NP_114067.1, NP_061725.1
GeneID.56137	PCDHA12	5	140,254,931	140,391,929	136,998	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6571	51341	in gene	0	1	0	16	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PCDHA12	PCDHA12, MGC138485, MGC141932, PCDH-ALPHA12	protocadherin alpha 12	NM_018903, NM_031864		NP_061726.1, NP_114070.1
GeneID.56136	PCDHA13	5	140,261,854	140,391,929	130,075	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6571	44418	in gene	0	1	0	16	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PCDHA13	CNR5, PCDHA13, CNRN5, PCDH-ALPHA13, CRNR5, CNRS5	protocadherin alpha 13	NM_018904, NM_031865		NP_061727.1, NP_114071.1
GeneID.56135	PCDHAC1	5	140,306,302	140,391,929	85,627	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6571	-30	upstream	0	1	0	16	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PCDHAC1	PCDHAC1, PCDH-ALPHA-C1	protocadherin alpha subfamily C, 1	NM_018898, NM_031882	1553235_at, 1553237_x_at	NP_061721.2, NP_114088.2
GeneID.29930	PCDHB1	5	140,430,979	140,433,512	2,533	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4566, 2_A375_pNL97_plus_lncRNA_AR..1..6572, 2_A375_pNL97_plus_lncRNA_AR..1..6573	-10403, -10275, 189	upstream, upstream, in gene	1	1	0	17	21	7	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene PCDHB1	MGC138303, PCDHB1, MGC138301, PCDH-BETA1	protocadherin beta 1	NM_013340, hCT33793.3	221303_at	NP_037472.2, EAW61985.1
GeneID.56116	PCDHB@	5	140,430,979	140,627,802	196,823	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4566, 2_A375_pNL97_plus_lncRNA_AR..1..6572, 2_A375_pNL97_plus_lncRNA_AR..1..6573, 2_A375_pNL97_plus_lncRNA_AR..1..6574	-10403, -10275, 189, 43245	upstream, upstream, in gene, in gene	1	1	0	16	20.33	6	3	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene PCDHB@	PCDHB@, PCDH3	protocadherin beta cluster			
GeneID.56133	PCDHB2	5	140,474,237	140,476,964	2,727	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6574	-13	upstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PCDHB2	MGC111392, PCDHB2, PCDH-BETA2	protocadherin beta 2	NM_018936, hCT1963271.1	231725_at	NP_061759.1, EAW61983.1
GeneID.56132	PCDHB3	5	140,480,234	140,483,406	3,172	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6574	-6010	upstream	0	1	0	14	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PCDHB3	PCDHB3, PCDH-BETA3	protocadherin beta 3	NM_018937, hCT33798.3	221410_x_at, 244163_x_at	NP_061760.1, EAW61981.1
GeneID.6879	TAF7	5	140,698,057	140,700,351	2,294	-	1	4_A375_EGR1..1..6843	335	in gene	0	0	1	13	10	18	1	4_A375_EGR1..1	18	Gene TAF7	TAF2F, TAF7, TAFII55	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	NM_005642, hCT33792.2	201023_at	NP_005633.2, EAW61968.1
GeneID.56114	PCDHGA1	5	140,710,252	140,892,546	182,294	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	145492, 183284, 54100, 145876	in gene, downstream, in gene, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGA1	PCDHGA1, PCDH-GAMMA-A1, MGC138287, MGC138289	protocadherin gamma subfamily A, 1	NM_018912, NM_031993	211880_x_at	NP_061735.1, NP_114382.1
GeneID.56113	PCDHGA2	5	140,718,354	140,892,546	174,192	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	137390, 175182, 45998, 137774	in gene, downstream, in gene, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGA2	PCDHGA2, PCDH-GAMMA-A2	protocadherin gamma subfamily A, 2	NM_018915, NM_032009		NP_061738.1, NP_114398.1
GeneID.56112	PCDHGA3	5	140,723,601	140,892,546	168,945	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	132143, 169935, 40751, 132527	in gene, downstream, in gene, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGA3	PCDH-GAMMA-A3, PCDHGA3	protocadherin gamma subfamily A, 3	NM_032011, NM_018916	211879_x_at, 216343_at, 216352_x_at	NP_114400.1, NP_061739.2
GeneID.56104	PCDHGB1	5	140,729,828	140,892,546	162,718	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	125916, 163708, 34524, 126300	in gene, downstream, in gene, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGB1	MGC119469, PCDHGB1, MGC119467, PCDH-GAMMA-B1, MGC119468	protocadherin gamma subfamily B, 1	NM_018922, NM_032095		NP_061745.1, NP_115266.1
GeneID.56111	PCDHGA4	5	140,734,768	140,892,546	157,778	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	120976, 158768, 29584, 121360	in gene, downstream, in gene, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGA4	PCDH-GAMMA-A4, PCDHGA4	protocadherin gamma subfamily A, 4	NM_018917, NM_032053	1552735_at	NP_061740.1, NP_114442.1
GeneID.56103	PCDHGB2	5	140,739,703	140,892,546	152,843	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	116041, 153833, 24649, 116425	in gene, downstream, in gene, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGB2	PCDHGB2, PCDH-GAMMA-B2, MGC126854	protocadherin gamma subfamily B, 2	NM_018923, NM_032096		NP_061746.1, NP_115267.1
GeneID.56110	PCDHGA5	5	140,743,698	140,892,546	148,848	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	111846, 149838, 20454, 112230	in gene, downstream, in gene, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGA5	PCDH-GAMMA-A5, ME3, MGC142020, PCDHGA5, CDH-GAMMA-A5	protocadherin gamma subfamily A, 5	NM_018918, NM_032054		NP_061741.1, NP_114443.1
GeneID.56102	PCDHGB3	5	140,749,962	140,892,546	142,584	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	105782, 143574, 14390, 106166	in gene, downstream, in gene, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGB3	PCDH-GAMMA-B3, PCDHGB3	protocadherin gamma subfamily B, 3	NM_018924, NM_032097		NP_061747.1, NP_115268.1
GeneID.56109	PCDHGA6	5	140,753,651	140,892,546	138,895	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	102093, 139885, 10701, 102477	in gene, downstream, in gene, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGA6	PCDH-GAMMA-A6, PCDHGA6	protocadherin gamma subfamily A, 6	NM_018919, NM_032086		NP_061742.1, NP_114475.1
GeneID.56108	PCDHGA7	5	140,762,467	140,892,546	130,079	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	93277, 131069, 1885, 93661	in gene, downstream, in gene, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGA7	PCDH-GAMMA-A7, PCDHGA7	protocadherin gamma subfamily A, 7	NM_018920, NM_032087		NP_061743.1, NP_114476.1
GeneID.8641	PCDHGB4	5	140,767,452	140,892,546	125,094	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	88292, 126084, -3100, 88676	in gene, downstream, upstream, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGB4	CDH20, MGC142167, PCDH-GAMMA-B4, FIB2, PCDHGB4, MGC138293	protocadherin gamma subfamily B, 4	NM_003736, NM_032098	210388_at	NP_003727.1, NP_115269.1
GeneID.9708	PCDHGA8	5	140,771,483	140,892,546	121,063	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6844, 4_A375_EGR1..1..6845	84261, 122053, -7131, 84645	in gene, downstream, upstream, in gene	0	1	1	10	13	14.67	3	4_A375_EGR1..1	17	Gene PCDHGA8	PCDHGA8, KIAA0327, PCDH-GAMMA-A8	protocadherin gamma subfamily A, 8	NM_014004, NM_032088		NP_054723.1, NP_114477.1
GeneID.56101	PCDHGB5	5	140,777,695	140,892,546	114,851	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6845	78049, 115841, 78433	in gene, downstream, in gene	0	1	1	13	16.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PCDHGB5	PCDHGB5, PCDH-GAMMA-B5	protocadherin gamma subfamily B, 5	NM_018925, NM_032099	211807_x_at	NP_061748.1, NP_115270.1
GeneID.56107	PCDHGA9	5	140,782,520	140,892,546	110,026	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6845	73224, 111016, 73608	in gene, downstream, in gene	0	1	1	13	16.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PCDHGA9	PCDHGA9, PCDH-GAMMA-A9	protocadherin gamma subfamily A, 9	NM_018921, NM_032089	211873_s_at	NP_061744.1, NP_114478.1
GeneID.56100	PCDHGB6	5	140,787,770	140,892,546	104,776	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6845	67974, 105766, 68358	in gene, downstream, in gene	0	1	1	13	16.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PCDHGB6	PCDHGB6, PCDH-GAMMA-B6	protocadherin gamma subfamily B, 6	NM_018926, NM_032100	221682_s_at	NP_061749.1, NP_115271.1
GeneID.56106	PCDHGA10	5	140,792,743	140,892,546	99,803	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6845	63001, 100793, 63385	in gene, downstream, in gene	0	1	1	13	16.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PCDHGA10	PCDH-GAMMA-A10, PCDHGA10	protocadherin gamma subfamily A, 10	NM_018913, NM_032090	211875_x_at	NP_061736.1, NP_114479.1
GeneID.56099	PCDHGB7	5	140,797,282	140,892,546	95,264	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6845	58462, 96254, 58846	in gene, downstream, in gene	0	1	1	13	16.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PCDHGB7	ME6, PCDHGB7, PCDH-GAMMA-B7	protocadherin gamma subfamily B, 7	NM_018927, NM_032101	1552861_at, 1552862_a_at	NP_061750.1, NP_115272.1
GeneID.56105	PCDHGA11	5	140,800,537	140,892,546	92,009	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6845	55207, 92999, 55591	in gene, downstream, in gene	0	1	1	13	16.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PCDHGA11	PCDHGA11, PCDH-GAMMA-A11	protocadherin gamma subfamily A, 11	NM_018914, NM_032091, NM_032092	211877_s_at	NP_061737.1, NP_114480.1, NP_114481.1
GeneID.26025	PCDHGA12	5	140,810,158	140,892,546	82,388	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6575, 2_A375_pNL97_plus_lncRNA_AR..1..6576, 4_A375_EGR1..1..6845	45566, 83378, 45970	in gene, downstream, in gene	0	1	1	13	16.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PCDHGA12	FIB3, CDH21, PCDH-GAMMA-A12, PCDHGA12, KIAA0588	protocadherin gamma subfamily A, 12	NM_003735, NM_032094	205717_x_at, 209079_x_at, 211066_x_at, 211876_x_at, 215836_s_at	NP_003726.1, NP_115265.1

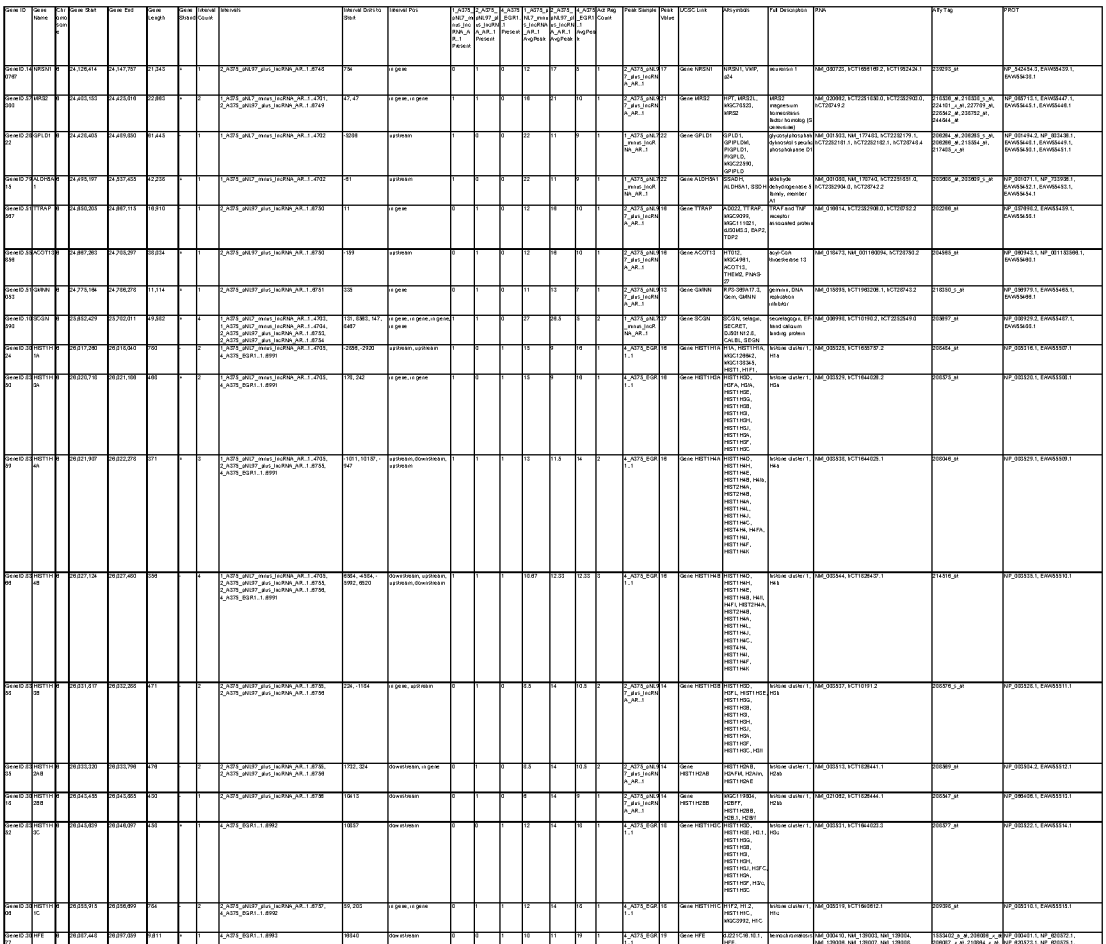
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.5098	PCDHGC3	5	140,855,569	140,892,546	36,977	+	3	2_A375_pNL97_plus_lncRNA_AR..1.6575, 2_A375_pNL97_plus_lncRNA_AR..1.6576, 4_A375_EGR1..1.6645	175, 37967, 559	in gene, downstream, in gene	0	1	1	13	16.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PCDHGC3	PCDH2, PCDH-GAMMA-C3, PC43, PCDHGC3	protocadherin gamma subfamily C, 3	NM_002588, NM_032402, NM_032403	214563_at, 214564_s_at	NP_002579.2, NP_115778.1, NP_115779.1
GeneID.56098	PCDHGC4	5	140,864,741	140,892,546	27,805	+	3	2_A375_pNL97_plus_lncRNA_AR..1.6575, 2_A375_pNL97_plus_lncRNA_AR..1.6576, 4_A375_EGR1..1.6645	-8997, 28795, -8613	upstream, downstream, upstream	0	1	1	13	16.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PCDHGC4	MGC24976, PCDHGC4, PCDH-GAMMA-C4, MGC119489	protocadherin gamma subfamily C, 4	NM_018928, NM_032406	231753_s_at, 231754_at	NP_061751.1, NP_115782.1
GeneID.56097	PCDHGC5	5	140,868,808	140,892,546	23,738	+	1	2_A375_pNL97_plus_lncRNA_AR..1.6576	24728	downstream	0	1	0	12	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene PCDHGC5	MGC138288, PCDHGC5, PCDH-GAMMA-C5, MGC138286	protocadherin gamma subfamily C, 5	NM_018929, NM_032407	224536_s_at, 224537_at	NP_061752.1, NP_115783.1
GeneID.1729	DIAPH1	5	140,894,588	140,998,622	104,034	-	8	1_A375_pNL7_minus_lncRNA_AR..1..4567, 1_A375_pNL7_minus_lncRNA_AR..1..4568, 1_A375_pNL7_minus_lncRNA_AR..1..4569, 1_A375_pNL7_minus_lncRNA_AR..1..4570, 2_A375_pNL97_plus_lncRNA_AR..1.6576, 2_A375_pNL97_plus_lncRNA_AR..1.6577, 2_A375_pNL97_plus_lncRNA_AR..1.6578, 2_A375_pNL97_plus_lncRNA_AR..1.6579	94110, 61246, 54750, -82, 105086, 61278, 54782, -114	in gene, in gene, in gene, upstream, downstream, in gene, in gene, upstream	1	1	0	43.8	39.2	7	5	1_A375_pNL7_minus_lncRNA_AR..1	111	Gene DIAPH1	DIAPH1, hDIA1, LFHL1, DRF1, DFNA1, FLJ25265, DIA1	diaphanous homolog 1 (Drosophila)	NM_005219, NM_001079812, hCT2253167.0, hCT33805.3	1560080_at, 209190_s_at, 213514_s_at, 215541_s_at	NP_005210.3, NP_001073280.1, EAW61919.1, EAW61920.1
GeneID.100505658	LOC100505658	5	140,937,878	140,944,827	6,949	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4568, 1_A375_pNL7_minus_lncRNA_AR..1..4569, 2_A375_pNL97_plus_lncRNA_AR..1.6577, 2_A375_pNL97_plus_lncRNA_AR..1.6578	-502, 5994, -534, 5962	upstream, in gene, upstream, in gene	1	1	0	70.5	64	4	2	1_A375_pNL7_minus_lncRNA_AR..1	111	Gene LOC100505658		hypothetical LOC100505658	XR_112787, XR_110311, XR_113784		
GeneID.8841	HDAC3	5	141,000,443	141,016,423	15,980	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4570, 2_A375_pNL97_plus_lncRNA_AR..1.6579, 1_A375_pNL7_minus_lncRNA_AR..1..4571, 2_A375_pNL97_plus_lncRNA_AR..1.6580, 4_A375_EGR1..1.6646	17719, 17687, -1145, -1113, -745	downstream, downstream, upstream, upstream, upstream	1	1	1	33.5	36	18	2	1_A375_pNL7_minus_lncRNA_AR..1	47	Gene HDAC3	HD3, RPD3-2, HDAC3, RPD3	histone deacetylase 3	NM_003883, hCT1817569.1, hCT2253159.0, hCT2253162.0, hCT28566.2	216326_s_at	NP_003874.2, EAW61918.1, EAW61915.1, EAW61916.1, EAW61917.1
GeneID.285613	RELL2	5	141,016,517	141,020,631	4,114	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4571, 2_A375_pNL97_plus_lncRNA_AR..1.6580, 4_A375_EGR1..1.6646	1051, 1019, 651	in gene, in gene, in gene	1	1	1	20	29	24	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene RELL2	C5orf16, FLJ90583, RELL2	RELT-like 2	NM_173828, NM_001130029, hCT2255499.0, hCT2353777.0, hCT2353778.0, hCT33804.2	1564031_a_at	NP_776189.3, NP_001123501.1, EAW61911.1, EAW61912.1, EAW61913.1, EAW61914.1
GeneID.89848	FCHSD1	5	141,018,869	141,030,986	12,117	-	6	1_A375_pNL7_minus_lncRNA_AR..1..4571, 1_A375_pNL7_minus_lncRNA_AR..1..4572, 2_A375_pNL97_plus_lncRNA_AR..1.6580, 2_A375_pNL97_plus_lncRNA_AR..1.6581, 4_A375_EGR1..1.6646, 4_A375_EGR1..1.6647	13418, -6868, 13450, -6870, 13818, 26	downstream, upstream, downstream, upstream, downstream, in gene	1	1	1	16.67	20.67	15.67	3	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene FCHSD1	NWK2, FLJ00007, FCHSD1	FCH and double SH3 domains 1	NM_033449, hCT2353771.0, hCT2353772.0, hCT33802.4	226698_at, 226699_at	NP_258260.1, EAW61908.1, EAW61909.1, EAW61910.1
GeneID.64411	ARAP3	5	141,032,968	141,061,800	28,832	-	6	1_A375_pNL7_minus_lncRNA_AR..1..4572, 1_A375_pNL7_minus_lncRNA_AR..1..4573, 2_A375_pNL97_plus_lncRNA_AR..1.6581, 2_A375_pNL97_plus_lncRNA_AR..1.6582, 2_A375_pNL97_plus_lncRNA_AR..1.6583, 4_A375_EGR1..1.6647	23928, -10392, 23944, -312, -10408, 30840	in gene, upstream, in gene, upstream, upstream, downstream	1	1	1	21.25	23.5	11.25	4	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene ARAP3	ARAP3, CENTD3, FLJ21065, DRAG1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	NM_022481, hCT2253152.0, hCT2253154.0, hCT2253155.0, hCT2353696.0	218950_at, 235606_at	NP_071926.4, EAW61905.1, EAW61904.1, EAW61906.1, EAW61907.1
GeneID.5097	PCDH1	5	141,232,672	141,257,944	25,272	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4577, 1_A375_pNL7_minus_lncRNA_AR..1..4578, 1_A375_pNL7_minus_lncRNA_AR..1..4579, 2_A375_pNL97_plus_lncRNA_AR..1.6589, 2_A375_pNL97_plus_lncRNA_AR..1.6590	28120, 1528, -5144, -664, -5160	downstream, in gene, upstream, upstream, upstream	1	1	0	18.75	19	13.5	4	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene PCDH1	PCDH1, MGC45991, PCDH42, PC42, FLJ53887	protocadherin 1	NM_002587, NM_032420, hCT1641260.2, hCT1811578.1, hCT2252411.0, hCT2252413.0	203918_at, 215277_at	NP_002578.2, NP_115796.2, EAW61900.1, EAW61901.1, EAW61902.1, EAW61903.1
GeneID.9812	KIAA0141	5	141,303,385	141,321,612	18,227	+	1	4_A375_EGR1..1.6649	-57	upstream	0	0	1	12	12	22	1	4_A375_EGR1..1	22	Gene KIAA0141	DELE, KIAA0141		NM_014773, NM_001142603, hCT2252658.0	201977_s_at, 201978_s_at, 227056_at	NP_055588.3, NP_001136075.1, EAW61899.1
GeneID.80762	NDFIP1	5	141,488,324	141,534,008	45,684	+	1	2_A375_pNL97_plus_lncRNA_AR..1.6592	-4	upstream	0	1	0	13	14	8	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene NDFIP1	N4WBP5, MGC10924, NDFIP1	Nedd4 family interacting protein 1	NM_030571, hCT2252668.0, hCT28223.2	217800_s_at, 222422_s_at, 222423_at	NP_085048.1, EAW61888.1, EAW61889.1
GeneID.81848	SPRY4	5	141,689,992	141,704,820	14,828	-	3	2_A375_pNL97_plus_lncRNA_AR..1.6594, 4_A375_EGR1..1.6650, 4_A375_EGR1..1.6651	10780, 683, -356	in gene, in gene, upstream	0	1	1	11.67	15.33	12.33	3	4_A375_EGR1..1	16	Gene SPRY4	SPRY4		NM_030964, NM_001127496	220983_s_at, 221489_s_at	NP_112226.2, NP_001120968.1
GeneID.23092	ARHGAP26	5	142,150,292	142,608,572	458,280	+	5	1_A375_pNL7_minus_lncRNA_AR..1..4582, 1_A375_pNL7_minus_lncRNA_AR..1..4583, 2_A375_pNL97_plus_lncRNA_AR..1.6597, 2_A375_pNL97_plus_lncRNA_AR..1.6598, 4_A375_EGR1..1.6652	51436, 56558, 558, 51468, 384	in gene, in gene, in gene, in gene, in gene	1	1	1	21	23	7.67	3	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene ARHGAP26	GRAF, OPHN1L, FLJ42530, KIAA0621, ARHGAP26, OPHN1L1	Rho GTPase activating protein 26	NM_001135608, NM_015071, hCT1821273.2, hCT2263474.0	205068_s_at, 205069_s_at, 215955_x_at, 226576_at	NP_001129080.1, NP_055886.1, EAW61876.1, EAW61877.1
GeneID.2908	NR3C1	5	142,657,496	142,815,077	157,581	-	4	2_A375_pNL97_plus_lncRNA_AR..1.6600, 2_A375_pNL97_plus_lncRNA_AR..1.6601, 2_A375_pNL97_plus_lncRNA_AR..1.6602, 4_A375_EGR1..1.6653	32133, 31269, 29893, 30245	in gene, in gene, in gene, in gene	0	1	1	15	18.33	10.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NR3C1	GR, GCCR, NR3C1, GRL, GCR	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NM_000176, NM_001018074, NM_001018075, NM_001018076, NM_001018077, NM_001020825, NM_001024094, hCT2283081.1, hCT2353707.0, hCT2353708.0, hCT28834.3	201865_x_at, 201866_s_at, 211671_s_at, 216321_s_at	NP_000167.1, NP_001018084.1, NP_001018085.1, NP_001018086.1, NP_001018087.1, NP_001018661.1, NP_001019265.1, EAW61870.1, EAW61871.1, EAW61872.1, EAW61873.1
GeneID.153769	SH3RF2	5	145,316,126	145,442,879	126,753	+	1	2_A375_pNL97_plus_lncRNA_AR..1.6603	10016	in gene	0	1	0	14	16	5	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SH3RF2	MGC90410, RNF158, MGC149789, FLJ23654, SH3RF2, HEPP1, MGC149788	SH3 domain containing ring finger 2	NM_152550, hCT2251972.0, hCT2353727.0, hCT29358.3	228892_at, 235786_at, 243582_at	NP_689763.3, EAW61853.1, EAW61852.1, EAW61854.1
GeneID.51520	LARS	5	145,492,589	145,562,294	69,705	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4585, 2_A375_pNL97_plus_lncRNA_AR..1.6604	-10, -74	upstream, upstream	1	1	0	26	36	9	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene LARS	LEUS, LEURS, FLJ21788, RNTLS, KIAA1352, PIG44, HSPC192, hr025Cl, FLJ10595, LARS1, LARS, LRS	leucyl-tRNA synthetase	NM_020117, hCT1821149.2, hCT2251913.0, hCT2251915.0	217810_x_at, 222427_s_at, 222428_s_at, 223868_s_at	NP_064502.9, EAW61849.1, EAW61848.1, EAW61850.1
GeneID.54439	RBM27	5	145,583,163	145,668,786	85,623	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4586, 2_A375_pNL97_plus_lncRNA_AR..1.6605	-187, -139	upstream, upstream	1	1	0	32	36	11	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene RBM27	Psc1, KIAA1311, RBM27, ARRS1	RNA binding motif protein 27	NM_018989	225326_at, 243295_at	NP_061862.1
GeneID.5459	POU4F3	5	145,718,587	145,720,083	1,496	+	1	4_A375_EGR1..1.6655	773	in gene	0	0	1	8	10	15	1	4_A375_EGR1..1	15	Gene POU4F3	DFNA15, MGC138412, BRN3C, POU4F3	POU class 4 homeobox 3	NM_002700, hCT2252268.0, hCT2252269.0, hCT2252271.0, hCT2252274.0	208554_at	NP_002691.1, EAW61844.1, EAW61843.1, EAW61845.1, EAW61846.1
GeneID.10915	TCERG1	5	145,826,873	145,891,069	64,196	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4587, 2_A375_pNL97_plus_lncRNA_AR..1.6606	-217, -185	upstream, upstream	1	1	0	56	50	9	1	1_A375_pNL7_minus_lncRNA_AR..1	56	Gene TCERG1	TCERG1, Urn1, TAF2S, MGC133200, CA150	transcription elongation regulator 1	NM_006706, NM_001040006, hCT2252281.0, hCT2353700.0, hCT29354.2	202396_at, 229706_at, 236838_at	NP_006697.2, NP_001035095.1, EAW61840.1, EAW61841.1, EAW61842.1
GeneID.5521	PPP2R2B	5	145,969,067	146,461,033	491,966	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4588, 2_A375_pNL97_plus_lncRNA_AR..1.6607, 4_A375_EGR1..1.6656, 4_A375_EGR1..1.6657	258265, 258265, 203641, 202697	in gene, in gene, in gene, in gene	1	1	1	16.67	26.67	11.33	3	2_A375_pNL97_plus_lncRNA_AR..1	59	Gene PPP2R2B	PP2AB-BETA, PR2APR55BETA, PP2APR55BETA, SCA12, MGC24888, B55-BETA, PR2APR55-BETA, FLJ95686, PR2AB55BETA, PP2A-PR55B, PP2ABBETA, PP2A-B55BETA, PR2ABBETA, PR55-BETA, PR52B, PP2APR55-BETA, PP2APR55B, PPP2R2B, PR2AB55-BETA, PP2AB55BETA, PR2AB-BETA, B55BETA, P	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	NM_004576, NM_181674, NM_181675, NM_181676, NM_181677, NM_181678, NM_001127381, hCT2252050.1, hCT2252051.1, hCT2252052.1, hCT2344918.0, hCT2344919.0, hCT2344920.0, hCT2353743.0	205643_s_at, 213849_s_at	NP_004567.1, NP_858060.1, NP_858061.1, NP_858062.1, NP_858063.1, NP_858064.1, NP_001120853.1, EAW61829.1, EAW61830.1, EAW61831.1, EAW61832.1, EAW61833.1, EAW61834.1, EAW61835.1
GeneID.79628	SH3TC2	5	148,361,713	148,442,737	81,024	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4589, 1_A375_pNL7_minus_lncRNA_AR..1..4590, 2_A375_pNL97_plus_lncRNA_AR..1.6609, 2_A375_pNL97_plus_lncRNA_AR..1.6610	61265, 657, 61201, 657	in gene, in gene, in gene, in gene	1	1	0	22	19	7.5	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene SH3TC2	MNMN, SH3TC2, KIAA1985, FLJ13605, CMT4C	SH3 domain and tetratricopeptide repeats 2	NM_024577	219710_at, 233561_at, 240966_at	NP_078853.2
GeneID.693169	MIR584	5	148,441,876	148,441,972	96	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4590, 2_A375_pNL97_plus_lncRNA_AR..1.6610	-108, -108	upstream, upstream	1	1	0	28	22	12	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene MIR584	MIR584, hsa-mir-584, MIRN584	microRNA 584	NR_030310		
GeneID.255187	hCG_1980447	5	148,443,066	148,446,548	3,482	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4590, 2_A375_pNL97_plus_lncRNA_AR..1.6610	-986, -986	upstream, upstream	1	1	0	28	22	12	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene hCG_1980447	FLJ32218, LOC255187	hCG1980447	XR_112784, XR_110313, XR_113786		
GeneID.22885	ABLIM3	5	148,521,054	148,639,999	118,945	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4591, 2_A375_pNL97_plus_lncRNA_AR..1.6611, 4_A375_EGR1..1.6658	-6876, 21570, 34402	upstream, in gene, in gene	1	1	1	15.67	13.67	10.67	3	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene ABLIM3	ABLIM3, HMFN1661	actin binding LIM protein family, member 3	NM_014945, hCT2252747.0, hCT2252748.0, hCT2353690.0, hCT2353691.0, hCT28725.3	205730_s_at	NP_055760.1, EAW61788.1, EAW61789.1, EAW61790.1, EAW61791.1, EAW61792.1
GeneID.134265	AFAP1L1	5	148,651,401	148,721,368	69,967	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4592	73527	downstream	1	0	0	17	16	12	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene AFAP1L1	FLJ38748, MGC149773, AFAP1L1	actin filament associated protein 1-like 1	NM_152406, NM_001146337, hCT1821379.2	1555542_at, 226955_at	NP_689619.1, NP_001139809.1, EAW61787.1
GeneID.134266	GRPEL2	5	148,724,977	148,734,146	9,169	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4592	-49	upstream	1	0	0	17	16	12	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene GRPEL2	Mt-GrpE#2, FLJ23713, FLJ33918, GRPEL2, DKFZp451C205	GrpE-like 2, mitochondrial (E. coli)	NM_152407, hCT28723.3	226881_at, 238427_at	NP_689620.2, EAW61786.1
GeneID.728264	LOC728264	5	148,786,440	148,812,399	25,959	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4593	-2056	upstream	1	0	0	23	15	11	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene LOC728264	DKFZp586C0721, FLJ38638, DKFZp781L018	hypothetical LOC728264	NR_027180	1558828_s_at, 231987_at	
GeneID.1452	CSNK1A1	5	148,874,845	148,931,007	56,162	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4597, 2_A375_pNL97_plus_lncRNA_AR..1.6613, 2_A375_pNL97_plus_lncRNA_AR..1.6614, 4_A375_EGR1..1.6659	-129, 65183, -209, 239	upstream, downstream, upstream, in gene	1	1	1	16.5	17.5	11	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene CSNK1A1	CSNK1A1, HLCDGP1, PRO2975, CK1	casein kinase 1, alpha 1	NM_001892, NM_001025105, hCT1962993.1, hCT1962994.1, hCT1984753.1, hCT1984754.1, hCT1984755.1, hCT201515.3, hCT2260944.0, hCT2260947.0, hCT2260949.0, hCT2260950.0	1556006_s_at, 1556007_s_at, 208562_s_at, 208865_at, 208866_at, 208867_s_at, 213086_s_at, 213860_x_at, 226920_at, 235464_at, 240221_at, 243338_at	NP_001883.4, NP_001020276.1, EAW61768.1, EAW61771.1, EAW61772.1, EAW61775.1, EAW61767.1, EAW61769.1, EAW61770.1, EAW61773.1, EAW61774.1, EAW61776.1
GeneID.1836	SLC26A2	5	149,340,300	149,366,963	26,663	+	2	2_A375_pNL97_plus_lncRNA_AR..1.6615, 4_A375_EGR1..1.6660	124, 116	in gene, in gene	0	1	1	16	17	15	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene SLC26A2	D5S1708, DTDST, MSTP157, SLC26A2, EDM4, MST153, DTD	solute carrier family 26 (sulfate transporter), member 2	NM_000112	205097_at, 224959_at, 224963_at	NP_000103.2
GeneID.81789	TIGD6	5	149,372,681	149,380,217	7,536	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4598, 2_A375_pNL97_plus_lncRNA_AR..1.6616, 4_A375_EGR1..1.6661	-7, -71, -103	upstream, upstream, upstream	1	1	1	24	24	18	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene TIGD6	DKFZp761E2110, TIGD6	tigger transposable element derived 6	NM_030953, hCT29858.2	220986_s_at	NP_112215.1, EAW61753.1
GeneID.22993	HMGXB3	5	149,380,169	149,432,706	52,537	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4598, 1_A375_pNL7_minus_lncRNA_AR..1..4599, 2_A375_pNL97_plus_lncRNA_AR..1.6616, 4_A375_EGR1..1.6661	55, 36215, 119, 151	in gene, in gene, in gene, in gene	1	1	1	25	17	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene HMGXB3	HMGX3, KIAA0194, HMGXB3, SMF	HMG box domain containing 3	NM_014983	212431_at, 34221_at	NP_055798.2
GeneID.1436	CSF1R	5	149,432,854	149,492,935	60,081	-	2	4_A375_EGR1..1.6662, 4_A375_EGR1..1.6663	231, -689	in gene, upstream	0	0	1	9	7.5	19.5	2	4_A375_EGR1..1	21	Gene CSF1R	FIM2, CD115, CSFR, C-FMS, CSF1R, FMS	colony stimulating factor 1 receptor	NM_005211, hCT2260927.0, hCT29855.3	203104_at	NP_005202.2, EAW61749.1, EAW61750.1
GeneID.5159	PDGFRB	5	149,493,402	149,535,422	42,020	-	2	4_A375_EGR1..1.6662, 4_A375_EGR1..1.6663	42718, 41598	downstream, in gene	0	0	1	9	7.5	19.5	2	4_A375_EGR1..1	21	Gene PDGFRB	PDGFR1, JTK12, PDGFRB, CD140B, PDGFR	platelet-derived growth factor receptor, beta polypeptide	NM_002609, hCT2260923.0, hCT2260924.0, hCT2260925.0	202273_at	NP_002600.1, EAW61748.1, EAW61746.1, EAW61747.1
GeneID.6534	SLC6A7	5	149,569,520	149,590,635	21,115	+	1	4_A375_EGR1..1.6664	14096	in gene	0	0	1	6	3	18	1	4_A375_EGR1..1	18	Gene SLC6A7	PROT, SLC6A7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	NM_014228, hCT2261926.0, hCT29853.3	208494_at	NP_055043.2, EAW61744.1, EAW61743.1
GeneID.815	CAMK2A	5	149,599,054	149,669,403	70,349	-	1	4_A375_EGR1..1.6665	25307	in gene	0	0	1	16	12	17	1	4_A375_EGR1..1	17	Gene CAMK2A	KIAA0968, CAMK2A, CAMKA	calcium/calmodulin-dependent protein kinase II alpha	NM_015981, NM_171825, hCT2260919.1, hCT2260920.1	207613_s_at, 213108_at	NP_057065.2, NP_741960.1, EAW61741.1, EAW61742.1
GeneID.6949	TCOF1	5	149,737,202	149,779,871	42,669	+	2	2_A375_pNL97_plus_lncRNA_AR..1.6618, 4_A375_EGR1..1.6666	446, 49102	in gene, downstream	0	1	1	11	14.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TCOF1	MFD1, TCS1, TCOF1, treacle	Treacher Collins-Franceschetti syndrome 1	NM_001008657, NM_000356, NM_001135243, NM_001135244, NM_001135245, hCT2261930.0, hCT2261931.0, hCT2261933.0, hCT2261934.0, hCT2353766.0, hCT2353767.0, hCT2353768.0, hCT29852.3	202384_s_at, 202385_s_at, 244686_at	NP_001008657.1, NP_000347.2, NP_001128715.1, NP_001128716.1, NP_001128717.1, EAW61734.1, EAW61732.1, EAW61733.1, EAW61735.1, EAW61736.1, EAW61737.1, EAW61738.1, EAW61739.1
GeneID.972	CD74	5	149,781,200	149,792,332	11,132	-	1	4_A375_EGR1..1.6666	6026	in gene	0	0	1	6	9	19	1	4_A375_EGR1..1	19	Gene CD74	HLADG, DHLAG, Ia-GAMMA, II, CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	NM_004355, NM_001025158, NM_001025159, hCT2253206.0, hCT2253207.0, hCT2253208.0, hCT2253209.0, hCT2353798.0	1567627_at, 1567628_at, 209619_at	NP_004346.1, NP_001020329.1, NP_001020330.1, EAW61728.1, EAW61730.1, EAW61731.1, EAW61727.1, EAW61729.1

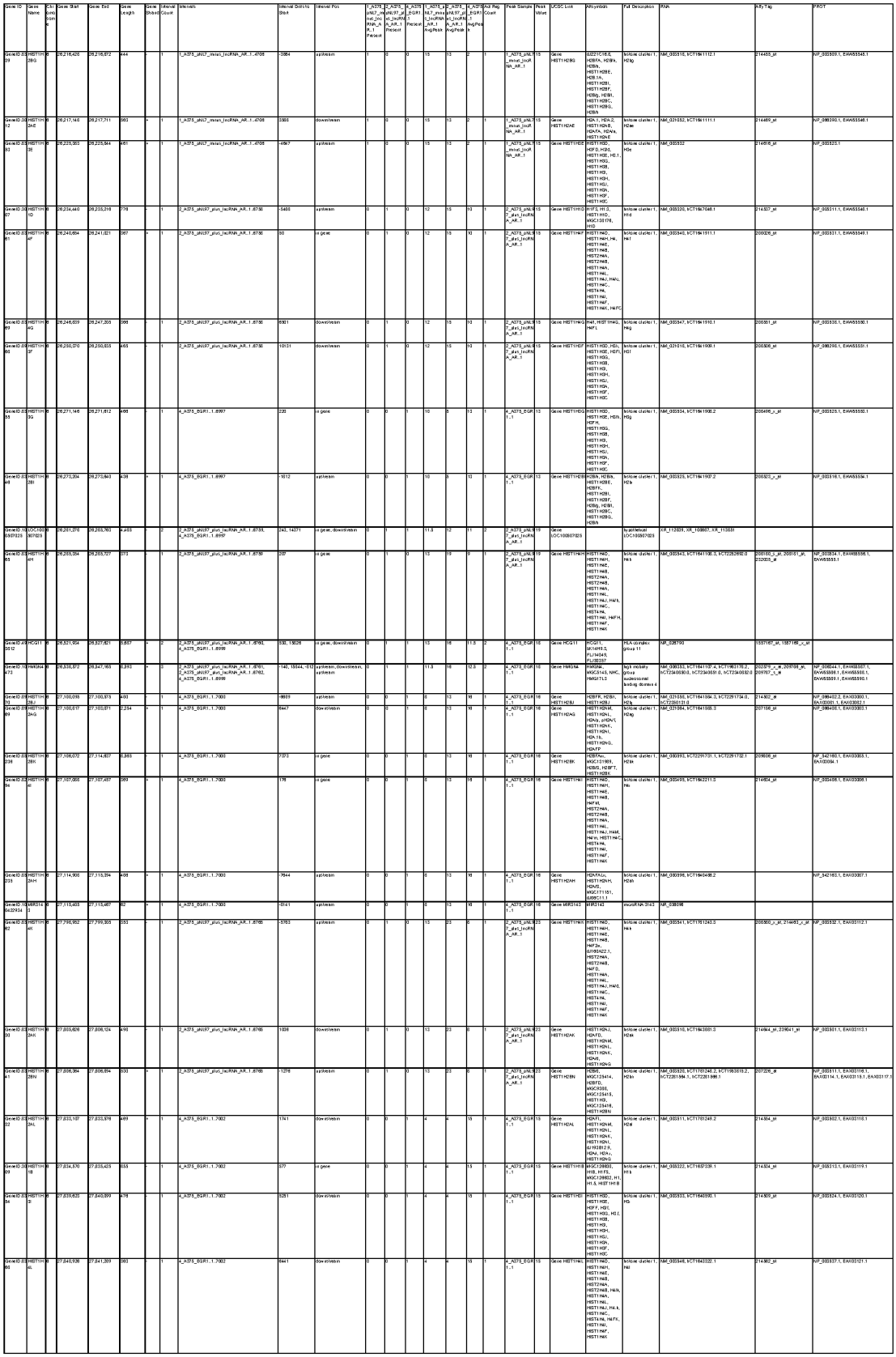
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:6208	RPS14	5	149,823,792	149,829,319	5,527	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4601, 2_A375_pNL97_plus_lncRNA_AR..1..6619, 4_A375_EGR1..1..6666	-121, -249, 167	upstream, upstream, in gene	1	1	1	31	51	21	1	2_A375_pNL97_plus_lncRNA_AR..1	51	Gene RPS14	S14, RPS14, EMTB	ribosomal protein S14	NM_005617, NM_001025070, NM_001025071, hCT1952785.1, hCT2253202.0, hCT2253204.0, hCT29864.4	208645_s_at, 214245_at, 217298_at, 241241_at	NP_005608.1, NP_001020241.1, NP_001020242.1, EAW61723.1, EAW61726.1, EAW61725.1, EAW61724.1
GeneID:3340	NDST1	5	149,887,674	149,937,773	50,099	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4602, 4_A375_EGR1..1..6669	-7066, 27646	upstream, in gene	1	0	1	16	10.5	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene NDST1	HSST, NST1, NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	NM_001543, hCT2256227.0, hCT2256229.0, hCT29850.3	1554010_at, 202607_at, 202608_s_at	NP_001534.1, EAW61722.1, EAW61720.1, EAW61721.1
GeneID:11346	SYNPO	5	149,980,642	150,038,792	58,150	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6620, 4_A375_EGR1..1..6670	39466, 49342	in gene, in gene	0	1	1	9	11.5	14.5	2	4_A375_EGR1..1	17	Gene SYNPO	KIAA1029, SYNPO	synaptopodin	NM_007286, NM_001109974, NM_001166208, NM_001166209, hCT2256234.0, hCT2256235.0	202796_at, 235128_at, 235914_at	NP_009217.3, NP_001103444.1, NP_001159680.1, NP_001159681.1, EAW61715.1, EAW61716.1
GeneID:91977	MYOZ3	5	150,040,404	150,058,925	18,521	+	1	4_A375_EGR1..1..6671	10676	in gene	0	0	1	4	7	17	1	4_A375_EGR1..1	17	Gene MYOZ3	FRP3, CS-3, MYOZ3, CS3	myozenin 3	NM_133371, NM_001122853, hCT2348978.0, hCT2353697.0	1553070_a_at, 1553071_a_at, 1562002_at, 1562004_x_at, 213955_at	NP_588612.2, NP_001116325.1, EAW61713.1, EAW61714.1
GeneID:55696	RBM22	5	150,070,352	150,080,669	10,317	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4603, 2_A375_pNL97_plus_lncRNA_AR..1..6621	-67, 477	upstream, in gene	1	1	0	21	20	12	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene RBM22	RBM22, Cwc2, FLJ10290, ZC3H16, fSAP47	RNA binding motif protein 22	NM_018047, hCT1829130.3, hCT2253193.0, hCT29863.4	218134_s_at, 222527_s_at, 224066_x_at, 236872_at	NP_060517.1, EAW61711.1, EAW61710.1, EAW61712.1
GeneID:51164	DCTN4	5	150,088,309	150,138,657	50,348	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4603, 1_A375_pNL7_minus_lncRNA_AR..1..4604, 2_A375_pNL97_plus_lncRNA_AR..1..6621	57921, 33, 58465	downstream, in gene, downstream	1	1	0	19	17.5	13.5	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene DCTN4	DCTN4		NM_016221, NM_001135643, NM_001135644, hCT2253189.0, hCT2253191.0, hCT2353692.0, hCT29862.3	218013_x_at, 222466_s_at, 233490_at	NP_057305.1, NP_001129115.1, NP_001129116.1, EAW61706.1, EAW61707.1, EAW61708.1, EAW61709.1
GeneID:85027	C5orf62	5	150,157,508	150,176,298	18,790	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6622	23356	downstream	0	1	0	11	19	9	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C5orf62	C5orf62, NID67, MGC117221, MST150, MGC126887, MGC126889	chromosome 5 open reading frame 62	NM_032947, hCT1642802.5	223276_at	NP_116565.3, EAW61705.1
GeneID:91975	ZNF300	5	150,273,954	150,284,545	10,591	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4605, 2_A375_pNL97_plus_lncRNA_AR..1..6623	-127, -95	upstream, upstream	1	1	0	38	52	9	1	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene ZNF300	ZNF300, DKFZp686B24204	zinc finger protein 300	NM_052860, NM_001172831, NM_001172832, hCT2253185.0, hCT2253186.0, hCT2253187.0, hCT2253188.0, hCT2353757.0	228144_at	NP_443092.1, NP_001166302.1, NP_001166303.1, EAW61699.1, EAW61701.1, EAW61702.1, EAW61698.1, EAW61700.1
GeneID:2760	GM2A	5	150,632,613	150,649,955	17,342	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6625	59	in gene	0	1	0	19	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene GM2A	GM2A, SAP-3	GM2 ganglioside activator	NM_000405, NM_001167607, hCT1668597.3, hCT2256222.0	209727_at, 212737_at, 215890_at, 215891_s_at, 235678_at, 33646_g_at, 35820_at	NP_000396.2, NP_001161079.1, EAW61680.1, EAW61681.1
GeneID:206358	SLC36A1	5	150,827,163	150,871,940	44,777	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6626, 4_A375_EGR1..1..6672	69, 69	in gene, in gene	0	1	1	17	21	25	1	4_A375_EGR1..1	25	Gene SLC36A1	LYAAT1, TRAMD3, Dct1, SLC36A1, PAT1	solute carrier family 36 (proton/amino acid symporter), member 1	NM_078483, hCT2253237.0, hCT2253238.0, hCT2253239.0, hCT2353760.0	1553272_at, 213119_at	NP_510968.2, EAW61676.1, EAW61674.1, EAW61675.1, EAW61677.1
GeneID:2196	FAT2	5	150,883,653	150,948,505	64,852	-	1	4_A375_EGR1..1..6673	37369	in gene	0	0	1	4	3	19	1	4_A375_EGR1..1	19	Gene FAT2	FAT2, CDHR9, MEGF1, HFAT2, CDHF8	FAT tumor suppressor homolog 2 (Drosophila)	NM_001447, hCT1641743.2	208153_s_at	NP_001438.1, EAW61673.1
GeneID:6678	SPARC	5	151,041,008	151,066,517	25,509	-	2	4_A375_EGR1..1..6674, 4_A375_EGR1..1..6675	3669, 65	in gene, in gene	0	0	1	8.5	9	17.5	2	4_A375_EGR1..1	21	Gene SPARC	ON, SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	NM_003118, hCT1952791.1, hCT2252321.0, hCT2252324.0, hCT2252325.0, hCT2252330.0, hCT30395.2	200665_s_at, 212667_at	NP_003109.1, EAW61669.1, EAW61667.1, EAW61668.1, EAW61671.1, EAW61672.1, EAW61670.1
GeneID:475	ATOX1	5	151,122,383	151,138,210	15,827	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4606, 1_A375_pNL7_minus_lncRNA_AR..1..4607	15490, 13026	in gene, in gene	1	0	0	21.5	16.5	7	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene ATOX1	ATOX1, HAH1, MGC138455, ATX1, MGC138453	ATX1 antioxidant protein 1 homolog (yeast)	NM_004045, hCT1952790.1, hCT30394.1	203454_s_at	NP_004036.1, EAW61663.1, EAW61664.1
GeneID:10146	G3BP1	5	151,151,476	151,184,915	33,439	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4608, 4_A375_EGR1..1..6676	-52, -1444	upstream, upstream	1	0	1	13.5	11.5	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene G3BP1	MGC111040, HDH-VIII, G3BP, G3BP1	GTPase activating protein (SH3 domain) binding protein 1	NM_005754, NM_198395, hCT1821762.1, hCT2253219.0, hCT2253222.0, hCT2253226.0	1557350_at, 201503_at, 201514_s_at, 222187_x_at, 244396_at	NP_005745.1, NP_938405.1, EAW61659.1, EAW61660.1, EAW61661.1, EAW61662.1
GeneID:2741	GLRA1	5	151,202,074	151,304,397	102,323	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4609, 2_A375_pNL97_plus_lncRNA_AR..1..6627	141, 125	in gene, in gene	1	1	0	48	67	11	1	2_A375_pNL97_plus_lncRNA_AR..1	67	Gene GLRA1	STHE, GLRA1, MGC138878, MGC138879	glycine receptor, alpha 1	NM_000171, NM_001146040, hCT2252309.0, hCT30393.3	207972_at	NP_000162.2, NP_001139512.1, EAW61656.1, EAW61657.1
GeneID:10827	FAM114A2	5	153,371,263	153,418,497	47,234	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6628	-63	upstream	0	1	0	16	25	15	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene FAM114A2	FAM114A2, 133K02, C5orf3	family with sequence similarity 114, member A2	NM_018691, hCT1971880.1, hCT2251771.0, hCT2251772.0	218588_s_at, 222662_s_at	NP_061161.2, EAW61648.1, EAW61646.1, EAW61647.1
GeneID:4238	MFAP3	5	153,418,519	153,437,014	18,495	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6628	41	in gene	0	1	0	16	25	15	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene MFAP3	DKFZp586F0219, MFAP3	microfibrillar-associated protein 3	NM_005927, NM_001135037, NR_024152, hCT1971098.1	1552312_a_at, 213123_at, 214583_s_at	NP_005918.1, NP_001128509.1, EAW61645.1
GeneID:55568	GALNT10	5	153,570,295	153,800,544	230,249	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4610, 2_A375_pNL97_plus_lncRNA_AR..1..6629, 2_A375_pNL97_plus_lncRNA_AR..1..6630	-311, 7529, 86505	upstream, in gene, in gene	1	1	0	16.33	17	8.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene GALNT10	GALNACT10, pp-GalNAc-T10, GalNAcT10, FLJ11715, DKFZp586H0623, PPGANTASE10, GALNT10, FLJ00205, PPGALNACT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	NM_198321, hCT1821190.3, hCT1828948.4, hCT2257016.2, hCT2257018.0, hCT2353718.0, hCT28038.5	207357_s_at, 212256_at, 220296_at, 230906_at	NP_938080.1, EAW61639.1, EAW61640.1, EAW61642.1, EAW61643.1, EAW61644.1, EAW61641.1
GeneID:79685	SAP30L	5	153,825,517	153,840,613	15,096	+	1	4_A375_EGR1..1..6677	-686	upstream	0	0	1	9	13	12	1	4_A375_EGR1..1	12	Gene SAP30L	FLJ23595, DKFZp667L2214, FLJ11526, SAP30L, NS4ATP2, FLJ36497	SAP30-like	NM_001131062, NM_001131063, NR_024084, NM_024632, hCT28118.2	219129_s_at, 222631_at, 226772_s_at	NP_001124534.1, NP_001124535.1, NP_078908.1, EAW61637.1
GeneID:9421	HAND1	5	153,854,532	153,857,824	3,292	-	2	4_A375_EGR1..1..6678, 4_A375_EGR1..1..6679	-1184, -4460	upstream, upstream	0	0	1	4.5	6	17	2	4_A375_EGR1..1	18	Gene HAND1	eHand, Thing1, Hxt, HAND1, bHLHa27	heart and neural crest derivatives expressed 1	NM_004821, hCT28026.2	220138_at	NP_004812.1, EAW61636.1
GeneID:23367	LARP1	5	154,092,462	154,197,165	104,703	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4611, 2_A375_pNL97_plus_lncRNA_AR..1..6631	42096, 42096	in gene, in gene	1	1	0	21	29	14	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene LARP1	LARP1, MGC19556, LARP, KIAA0731	La ribonucleoprotein domain family, member 1	NM_015315, hCT2254109.1, hCT2344691.0, hCT28082.4	210966_x_at, 212137_at, 212193_s_at, 239663_x_at	NP_056130.2, EAW61634.1, EAW61632.1, EAW61633.1
GeneID:100505647	LOC100505647	5	154,135,135	154,166,244	31,109	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4611, 2_A375_pNL97_plus_lncRNA_AR..1..6631	-575, -575	upstream, upstream	1	1	0	21	29	14	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene LOC100505647		la-related protein 1-like	XM_003118936		XP_003118984.1
GeneID:10826	C5orf4	5	154,198,052	154,230,213	32,161	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4612, 2_A375_pNL97_plus_lncRNA_AR..1..6632, 4_A375_EGR1..1..6682	-7771, -7867, -7035	upstream, upstream, upstream	1	1	1	19	17	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene C5orf4	C5orf4, FLJ13758	chromosome 5 open reading frame 4	NM_032385, hCT2251697.0, hCT2251698.0, hCT2251699.0	220751_s_at, 48030_i_at, 48031_r_at	NP_115761.2, EAW61629.1, EAW61630.1, EAW61631.1
GeneID:9337	CNOT8	5	154,238,198	154,256,352	18,154	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4612, 2_A375_pNL97_plus_lncRNA_AR..1..6632, 4_A375_EGR1..1..6682	-214, -118, -950	upstream, upstream, upstream	1	1	1	19	17	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene CNOT8	POP2, hCAF1, CNOT8, CAF1, CALIF	CCR4-NOT transcription complex, subunit 8	NM_004779, hCT1952778.1, hCT1952779.1, hCT2254112.0, hCT28227.2	202162_s_at, 202163_s_at, 202164_s_at	NP_004770.4, EAW61625.1, EAW61626.1, EAW61627.1, EAW61628.1
GeneID:25929	GEMIN5	5	154,266,976	154,317,776	50,800	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4613, 2_A375_pNL97_plus_lncRNA_AR..1..6633, 2_A375_pNL97_plus_lncRNA_AR..1..6634	-16, -48, -2928	upstream, upstream, upstream	1	1	0	17	21.5	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene GEMIN5	GEMIN5, MGC142174, DKFZp586M1824	gem (nuclear organelle) associated protein 5	NM_015465, hCT2251694.0, hCT2251695.0	225712_at	NP_056280.2, EAW61623.1, EAW61624.1
GeneID:29093	MRPL22	5	154,320,633	154,346,971	26,338	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4613, 2_A375_pNL97_plus_lncRNA_AR..1..6633, 2_A375_pNL97_plus_lncRNA_AR..1..6634	-2841, -2809, 71	upstream, upstream, in gene	1	1	0	17	21.5	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MRPL22	DKFZp781F1071, HSPC158, MRP-L22, L22mt, MRPL22, MRP-L25, RPML25	mitochondrial ribosomal protein L22	NM_014180, NM_001014990, hCT28228.2	218339_at	NP_054899.2, NP_001014990.1, EAW61622.1
GeneID:100289098	LOC100289098	5	157,097,409	157,098,447	1,038	-	1	4_A375_EGR1..1..6684	127	in gene	0	0	1	11	9	15	1	4_A375_EGR1..1	15	Gene LOC100289098		hypothetical LOC100289098	XR_112790, XR_110062, XR_113796		
GeneID:100190949	C5orf52	5	157,098,561	157,107,162	8,601	+	1	4_A375_EGR1..1..6684	-241	upstream	0	0	1	11	9	15	1	4_A375_EGR1..1	15	Gene C5orf52	C5orf52	chromosome 5 open reading frame 52	NM_001145132		NP_001138604.1
GeneID:54974	THG1L	5	157,158,323	157,166,772	8,449	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4614, 2_A375_pNL97_plus_lncRNA_AR..1..6636, 2_A375_pNL97_plus_lncRNA_AR..1..6637	125, 77, 12413	in gene, in gene, downstream	1	1	0	27.5	29	9	2	1_A375_pNL7_minus_lncRNA_AR..1	44	Gene THG1L	FLJ11601, FLJ20546, THG1L, ICF45	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	NM_017872, hCT1952293.1, hCT6874.3	219122_s_at	NP_060342.2, EAW61590.1, EAW61591.1
GeneID:134353	LSM11	5	157,170,755	157,183,746	12,991	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6637	-19	upstream	0	1	0	11	15	3	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LSM11	FLJ38273, LSM11	LSM11, U7 small nuclear RNA associated	NM_173491, hCT6875.3	241599_at, 242112_at	NP_775762.1, EAW61589.1
GeneID:1879	EBF1	5	158,122,923	158,526,788	403,865	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4616, 1_A375_pNL7_minus_lncRNA_AR..1..4617, 1_A375_pNL7_minus_lncRNA_AR..1..4618, 2_A375_pNL97_plus_lncRNA_AR..1..6640	382948, 372628, -604, 372663	in gene, in gene, upstream, in gene	1	1	0	17.67	13	5.33	3	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene EBF1	FLJ39389, O/E-1, FLJ41763, OLF1, COE1, EBF, EBF1	early B-cell factor 1	NM_024007, hCT2349019.0, hCT2349020.0, hCT2353769.0	232204_at, 233261_at	NP_076870.1, EAW61582.1, EAW61580.1, EAW61581.1
GeneID:134510	UBLCP1	5	158,690,089	158,713,048	22,959	+	1	4_A375_EGR1..1..6686	311	in gene	0	0	1	14	17	19	1	4_A375_EGR1..1	19	Gene UBLCP1	UBLCP1, FLJ25267, CPUB1, MGC10067	ubiquitin-like domain containing CTD phosphatase 1	NM_145049, hCT2353722.0, hCT7089.3	227413_at, 243916_x_at	NP_659486.2, EAW61576.1, EAW61577.1
GeneID:147	ADRA1B	5	159,343,740	159,400,017	56,277	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6644	11684	in gene	0	1	0	12	19	5	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ADRA1B	ADRA1B, ADRA1, ALPHA1BAR	adrenergic, alpha-1B-, receptor	NM_000679, hCT5771.2	207589_at	NP_000670.1, EAW61572.1
GeneID:7265	TTC1	5	159,436,180	159,492,550	56,370	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6645	-84	upstream	0	1	0	12	19	10	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TTC1	TPR1, FLJ46404, TTC1	tetratricopeptide repeat domain 1	NM_003314, hCT2251528.0, hCT2251529.0	201434_at	NP_003305.1, EAW61570.1, EAW61571.1
GeneID:114825	PWWP2A	5	159,502,889	159,546,452	43,563	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6646	180	in gene	0	1	0	14	15	11	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene PWWP2A	MGC132770, MST101, PWWP2A, KIAA1935	PWWP domain containing 2A	NM_052927, NM_001130864	226720_at, 228336_at, 228337_at, 236544_at	NP_443159.1, NP_001124336.1
GeneID:79616	CCNJL	5	159,678,671	159,739,573	60,902	-	1	4_A375_EGR1..1..6687	261	in gene	0	0	1	16	23	17	1	4_A375_EGR1..1	17	Gene CCNJL	CCNJL, FLJ14166	cyclin J-like	NM_024565, hCT2251453.0	219227_at	NP_078841.3, EAW61562.1
GeneID:10569	SLU7	5	159,828,848	159,846,168	17,320	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6648	-2824	upstream	0	1	0	12	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SLU7	9G8, hSlu7, MGC9280, SLU7	SLU7 splicing factor homolog (S. cerevisiae)	NM_006425, hCT1964842.1, hCT2251446.0, hCT7344.3	227990_at, 231718_at	NP_006416.3, EAW61554.1, EAW61555.1, EAW61556.1
GeneID:9232	PTTG1	5	159,848,865	159,855,746	6,881	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6648	127	in gene	0	1	0	12	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PTTG1	EAP1, PTTG1, MGC138276, HPTTG, MGC126883, PTTG, TUTR1	pituitary tumor-transforming 1	NM_004219, hCT1952294.1, hCT1981458.1, hCT7343.3	203554_x_at	NP_004210.1, EAW61551.1, EAW61552.1, EAW61553.1
GeneID:100422938	MIR3142	5	159,901,451	159,901,532	81	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6650	-6347	upstream	0	1	0	17	15	13	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene MIR3142	MIR3142	microRNA 3142	NR_036095		
GeneID:2566	GABRG2	5	161,494,648	161,582,545	87,897	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4621, 2_A375_pNL97_plus_lncRNA_AR..1..6651	1000, 1000	in gene, in gene	1	1	0	51	64	3	1	2_A375_pNL97_plus_lncRNA_AR..1	64	Gene GABRG2	CAE2, GEFSP3, GABRG2, ECA2	gamma-aminobutyric acid (GABA) A receptor, gamma 2	NM_198904, NM_000816, NM_198903, hCT2353774.0, hCT2353775.0, hCT2353776.0, hCT28201.3	1568612_at, 206849_at	NP_944494.1, NP_000807.2, NP_944493.2, EAW61532.1, EAW61534.1, EAW61535.1, EAW61533.1
GeneID:134492	NUDCD2	5	162,880,586	162,887,143	6,557	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6652	-57	upstream	0	1	0	14	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene NUDCD2	DKFZp686E10109, NUDCD2	NudC domain containing 2	NM_145266, hCT2251151.0	1558124_at, 226642_s_at, 226643_s_at	NP_660309.1, EAW61527.1
GeneID:3161	HMMR	5	162,887,517	162,918,951	31,434	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6652	-317	upstream	0	1	0	14	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene HMMR	MGC119495, MGC119494, IHABP, HMMR, CD168, RHAMM	hyaluronan-mediated motility receptor (RHAMM)	NM_001142556, NM_001142557, NM_012484, NM_012485, hCT2251253.0, hCT2251254.0, hCT2251255.0, hCT2353764.0, hCT28206.3	207165_at, 209709_s_at	NP_001136028.1, NP_001136029.1, NP_036616.2, NP_036617.2, EAW61523.1, EAW61524.1, EAW61521.1, EAW61522.1, EAW61525.1
GeneID:27430	MAT2B	5	162,930,231	162,946,328	16,097	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4622, 2_A375_pNL97_plus_lncRNA_AR..1..6653, 4_A375_EGR1..1..6689	2377, 2313, 2313	in gene, in gene, in gene	1	1	1	24	32	17	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene MAT2B	MATIIbeta, TGR, MAT2B, MGC12237, SDR23E1, MAT-II, Nbla02999	methionine adenosyltransferase II, beta	NM_182796, NM_013283, hCT2251245.0, hCT2251246.0, hCT2353715.0, hCT28945.2	217993_s_at, 229284_at	NP_877725.1, NP_037415.1, EAW61517.1, EAW61518.1, EAW61519.1, EAW61520.1
GeneID:100507193	LOC100507193	5	163,724,057	164,598,619	874,562	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6654	303591	in gene	0	1	0	9	16	3	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100507193		hypothetical LOC100507193	XR_112798, XR_110063, XR_113797		
GeneID:5917	RARS	5	167,913,463	167,946,311	32,848	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4625, 2_A375_pNL97_plus_lncRNA_AR..1..6657, 2_A375_pNL97_plus_lncRNA_AR..1..6658	-71, -23, 42217	upstream, upstream, downstream	1	1	0	54.5	47	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	95	Gene RARS	MGC8641, ArgRS, RARS, DALRD1	arginyl-tRNA synthetase	NM_002887, hCT29844.3	201330_at	NP_002878.2, EAW61507.1
GeneID:79646	PANK3	5	167,982,630	168,006,586	23,956	-	1	4_A375_EGR1..1..6690	346	in gene	0	0	1	12	10	16	1	4_A375_EGR1..1	16	Gene PANK3	MGC16883, DKFZp686O22247, PANK3, FLJ12899	pantothenate kinase 3	NM_024594, hCT2251263.0, hCT2251264.0, hCT2251266.0	218433_at	NP_078870.1, EAW61505.1, EAW61503.1, EAW61504.1
GeneID:6586	SLIT3	5	168,093,071	168,728,133	635,062	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4626, 2_A375_pNL97_plus_lncRNA_AR..1..6659, 2_A375_pNL97_plus_lncRNA_AR..1..6660, 4_A375_EGR1..1..6691	126053, 644709, 126053, 609061	in gene, downstream, in gene, in gene	1	1	1	12.67	16.67	8.33	3	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SLIT3	SLIT1, MEGF5, SLIL2, slit2, FLJ10764, Slit-3, SLIT3	slit homolog 3 (Drosophila)	NM_003062, hCT2251260.0, hCT2251261.0, hCT28216.3	203813_s_at, 216216_at	NP_003053.1, EAW61499.1, EAW61500.1, EAW61501.1
GeneID:54908	CCDC99	5	169,010,638	169,031,782	21,144	+	1	4_A375_EGR1..1..6692	370	in gene	0	0	1	12	12	14	1	4_A375_EGR1..1	14	Gene CCDC99	FLJ20364, CCDC99, FLJ40690	coiled-coil domain containing 99	NM_017785, hCT2250659.0, hCT2250660.0	221685_s_at	NP_060255.3, EAW61496.1, EAW61495.1
GeneID:1794	DOCK2	5	169,064,251	169,510,386	446,135	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4627	13733	in gene	1	0	0	15	12	3	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene DOCK2	FLJ46592, DOCK2, KIAA0209	dedicator of cytokinesis 2	NM_004946, hCT2353716.0, hCT28946.3	1554325_at, 213160_at	NP_004937.1, EAW61492.1, EAW61491.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:30820	KCNIP1	5	169,780,881	170,163,636	382,755	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4629, 2_A375_pNL97_plus_lncRNA_AR..1..8661, 2_A375_pNL97_plus_lncRNA_AR..1..8662, 2_A375_pNL97_plus_lncRNA_AR..1..8663	243439, 98287, 139359, 327375	in gene, in gene, in gene, in gene	1	1	0	14.5	18.5	6.75	4	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene KCNIP1	KCNIP1, VABP, KCHIP1, MGC95	Kv channel interacting protein 1	NM_014592, NM_001034838, NM_001034837, hCT2251111.0, hCT28983.3	221307_at	NP_055407.1, NP_001030010.1, NP_001030009.1, EAW61470.1, EAW61471.1
GeneID:4869	NPM1	5	170,814,708	170,837,888	23,180	+	1	4_A375_EGR1..1..8894	140	in gene	0	0	1	14	15	16	1	4_A375_EGR1..1	16	Gene NPM1	NPM1, B23, NPM, MGC104254	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	NM_002520, NM_199185, NM_001037738, hCT2251124.0, hCT2251128.0, hCT2251127.0, hCT2251129.0, hCT2251130.0, hCT2251132.0, hCT2353742.0	200063_s_at, 221691_x_at, 221923_s_at	NP_002511.1, NP_954654.1, NP_001032827.1, EAW61444.1, EAW61447.1, EAW61446.1, EAW61443.1, EAW61445.1, EAW61448.1, EAW61449.1
GeneID:8817	FGF18	5	170,846,667	170,884,630	37,963	+	1	4_A375_EGR1..1..8895	8805	in gene	0	0	1	4	9	15	1	4_A375_EGR1..1	15	Gene FGF18	ZFGF5, FGF18, FGF-18	fibroblast growth factor 18	NM_003862, hCT2251109.0, hCT28827.3	206987_x_at, 211029_x_at, 211485_s_at, 214284_s_at, 231382_at	NP_003853.1, EAW61441.1, EAW61442.1
GeneID:23291	FBXW11	5	171,288,556	171,433,877	145,321	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8664	69	in gene	0	1	0	27	42	18	1	2_A375_pNL97_plus_lncRNA_AR..1	42	Gene FBXW11	BTRC2, FBW1B, BTRCP2, KIAA0696, FBXW11, Fbw11, Hos, FBXW1B	F-box and WD repeat domain containing 11	NM_033644, NM_033645, NM_012300, hCT1987355.1	209455_at, 209456_s_at	NP_387448.2, NP_387449.2, NP_036432.2, EAW61440.1
GeneID:6793	STK10	5	171,469,074	171,615,346	146,272	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4630, 2_A375_pNL97_plus_lncRNA_AR..1..8665, 4_A375_EGR1..1..8897	-110, -398, 434	upstream, upstream, in gene	1	1	1	17	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene STK10	PRO2729, LOK, STK10	serine/threonine kinase 10	NM_005990, hCT32021.4	203047_at, 226394_at, 40420_at	NP_005981.3, EAW61439.1
GeneID:285588	EFCAB9	5	171,621,176	171,630,458	9,282	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4630, 2_A375_pNL97_plus_lncRNA_AR..1..8665, 4_A375_EGR1..1..8897	-5720, -5432, -6284	upstream, upstream, upstream	1	1	1	17	20	16	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene EFCAB9	EFCAB9		NM_001171183		NP_001164654.1
GeneID:92181	UBTD2	5	171,636,650	171,710,795	74,145	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4631	8715	in gene	1	0	0	14	4	6	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene UBTD2	MGC30022, DCUBP, UBTD2	ubiquitin domain containing 2	NM_152277, hCT2256333.0, hCT32020.2	224827_at, 224834_at	NP_689490.2, EAW61436.1, EAW61437.1
GeneID:1843	DUSP1	5	172,195,093	172,198,203	3,110	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4632, 2_A375_pNL97_plus_lncRNA_AR..1..8666, 4_A375_EGR1..1..8899	411, 27, 251	in gene, in gene, in gene	1	1	1	16	21	17	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene DUSP1	CL100, MKP1, HVH1, PTPN10, MKP-1, DUSP1	dual specificity phosphatase 1	NM_004417, hCT1952301.1, hCT32515.2	201041_s_at, 201044_x_at, 226578_s_at	NP_004408.1, EAW61425.1, EAW61426.1
GeneID:57222	ERGIC1	5	172,261,223	172,379,688	118,465	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4633, 2_A375_pNL97_plus_lncRNA_AR..1..8667	125113, 125113	downstream, downstream	1	1	0	149	141	11	1	1_A375_pNL7_minus_lncRNA_AR..1	149	Gene ERGIC1	FLJ39684, ERGIC-32, ERGIC32, KIAA1181, MGC14345, ERGIC1, NET24	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	NM_001031711, hCT2251071.1, hCT2251072.1	223847_s_at, 224024_at, 224576_at, 224577_at	NP_001026881.1, EAW61422.1, EAW61423.1
GeneID:100268168	LOC100268168	5	172,381,785	172,386,371	4,586	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4633, 2_A375_pNL97_plus_lncRNA_AR..1..8667	35, 35	in gene, in gene	1	1	0	149	141	11	1	1_A375_pNL7_minus_lncRNA_AR..1	149	Gene LOC100268168	FLJ43741	hypothetical LOC100268168	NR_026662, NR_026663		
GeneID:51121	RPL26L1	5	172,388,439	172,398,774	10,335	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4633, 2_A375_pNL97_plus_lncRNA_AR..1..8667	-103, -103	upstream, upstream	1	1	0	149	141	11	1	1_A375_pNL7_minus_lncRNA_AR..1	149	Gene RPL26L1	RPL26P1, FLJ46904, RPL26L1	ribosomal protein L26-like 1	NM_016093, hCT2251076.0, hCT2251077.0	218830_at	NP_057177.1, EAW61420.1, EAW61421.1
GeneID:8992	ATP6V0E1	5	172,410,763	172,461,900	51,137	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4634, 2_A375_pNL97_plus_lncRNA_AR..1..8668	21, 53	in gene, in gene	1	1	0	19	19	13	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ATP6V0E1	Vma21p, M9.2, ATP6V0E, Vma21, ATP6H, ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	NM_003945, hCT2251080.0, hCT32521.3	200096_s_at, 201171_at, 201172_x_at, 214149_s_at, 214150_x_at, 214244_s_at	NP_003936.1, EAW61417.1, EAW61418.1
GeneID:153222	C5orf41	5	172,483,355	172,566,291	82,936	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4635, 2_A375_pNL97_plus_lncRNA_AR..1..8669	88133, 88149	downstream, downstream	1	1	0	28	28	11	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene C5orf41	DKFZp313F2319, C5orf41, DKFZp686G2059, LRF	chromosome 5 open reading frame 41	NM_153607, NM_001166393, NM_001166394, hCT2348978.0, hCT2353695.0, hCT2353698.0	1554229_at, 225956_at, 225957_at, 238476_at	NP_705835.2, NP_001161865.1, NP_001161866.1, EAW61414.1, EAW61415.1, EAW61416.1
GeneID:662	BNIP1	5	172,571,445	172,591,390	19,945	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4635, 2_A375_pNL97_plus_lncRNA_AR..1..8669	43, 59	in gene, in gene	1	1	0	28	28	11	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene BNIP1	NIP1, SEC20, TRG-8, BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	NM_013979, NM_001205, NM_013978, NM_013980, hCT1952302.1, hCT1958537.1, hCT2251050.0, hCT2251053.0, hCT2251055.0, hCT2251058.0, hCT2251056.0, hCT2353745.0, hCT32518.2	204930_s_at, 207829_s_at, 37226_at	NP_053582.2, NP_001196.2, NP_053581.2, NP_053583.2, EAW61408.1, EAW61413.1, EAW61405.1, EAW61406.1, EAW61407.1, EAW61409.1, EAW61410.1, EAW61411.1, EAW61412.1
GeneID:1482	NKX2-5	5	172,659,107	172,662,315	3,208	-	2	2_A375_pNL97_plus_lncRNA_AR..1..8670, 4_A375_EGR1..1..8900	219, 427	in gene, in gene	0	1	1	15	22	13	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene NKX2-5	FLJ97195, CSX1, NKX2E, NKX4-1, NKX2.5, NKX2-5, FLJ97166, CHNG5, FLJ97197, FLJ99536, CSX, FLJ52202	NK2 transcription factor related, locus 5 (Drosophila)	NM_004387, NM_001166175, NM_001166176, hCT32513.3	206578_at	NP_004378.1, NP_001159647.1, NP_001159648.1, EAW61404.1
GeneID:91272	BOD1	5	173,034,148	173,043,666	9,518	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4638, 2_A375_pNL97_plus_lncRNA_AR..1..8673	-110, -78	upstream, upstream	1	1	0	45	35	8	1	1_A375_pNL7_minus_lncRNA_AR..1	45	Gene BOD1	BOD1, FAM44B	biorientation of chromosomes in cell division 1	NM_138369, NM_001159651, hCT32401.4	225030_at	NP_612378.1, NP_001153123.1, EAW61396.1
GeneID:80315	CPEB4	5	173,315,331	173,387,313	71,982	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4639	29725	in gene	1	0	0	31	17	8	1	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene CPEB4	KIAA1673, CPEB4	cytoplasmic polyadenylation element binding protein 4	NM_030627, hCT2254638.0, hCT2353780.0, hCT2353781.0, hCT2353782.0, hCT31534.3	224828_at, 224829_at, 224831_at, 242280_x_at	NP_085130.2, EAW61391.1, EAW61389.1, EAW61390.1, EAW61392.1, EAW61393.1
GeneID:51617	HMP19	5	173,472,724	173,536,182	63,458	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4640, 1_A375_pNL7_minus_lncRNA_AR..1..4641, 2_A375_pNL97_plus_lncRNA_AR..1..8674	-20, 36884, 28	upstream, in gene, in gene	1	1	0	25.5	19.5	4	2	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene HMP19		HMP19 protein	NM_015980, hCT2254644.0, hCT2254646.0, hCT2254647.0, hCT32400.3	218623_at	NP_057064.1, EAW61386.1, EAW61383.1, EAW61384.1, EAW61385.1
GeneID:94081	SFXN1	5	174,905,514	174,955,621	50,107	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4644	39446	in gene	1	0	0	20	9	5	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene SFXN1	SFXN1, FLJ12876	sideroflexin 1	NM_022754, hCT1821032.3, hCT2251939.1, hCT2251942.2, hCT2251943.2, hCT2353763.0, hCT2353764.0	218392_x_at, 230069_at	NP_073591.2, EAW61372.1, EAW61370.1, EAW61371.1, EAW61373.1, EAW61375.1, EAW61374.1
GeneID:3274	HRH2	5	175,085,040	175,113,245	28,205	+	1	4_A375_EGR1..1..8903	29008	downstream	0	0	1	6	6	17	1	4_A375_EGR1..1	17	Gene HRH2	H2R, HRH2	histamine receptor H2	NM_022304, NM_001131055, hCT1646125.2	220605_at	NP_071640.1, NP_001124527.1, EAW61369.1
GeneID:10814	CPLX2	5	175,223,610	175,311,023	87,413	+	7	1_A375_pNL7_minus_lncRNA_AR..1..4645, 1_A375_pNL7_minus_lncRNA_AR..1..4646, 2_A375_pNL97_plus_lncRNA_AR..1..8676, 2_A375_pNL97_plus_lncRNA_AR..1..8677, 2_A375_pNL97_plus_lncRNA_AR..1..8678, 4_A375_EGR1..1..8904, 4_A375_EGR1..1..8905	422, 75254, 454, 15030, 75190, 134, 75142	in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	50.33	53	13.67	3	2_A375_pNL97_plus_lncRNA_AR..1	99	Gene CPLX2	CPX2, 921-L, CPLX2, CPX-2, Hfb1, MGC138492	complexin 2	NM_001008220, NM_006650, hCT2251948.0, hCT31541.2	206366_at, 225615_at	NP_001008221.1, NP_006641.1, EAW61366.1, EAW61367.1
GeneID:643201	LOC643201	5	175,570,088	175,626,298	56,210		1	4_A375_EGR1..1..8906	6618	in gene	0	0	1	9	5	16	1	4_A375_EGR1..1	16	Gene LOC643201		centrosomal protein 192kDa pseudogene	NR_036494	1570444_at, 1570445_a_at	
GeneID:51491	NOP16	5	175,811,232	175,815,540	4,308	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4647, 2_A375_pNL97_plus_lncRNA_AR..1..8679	-316, -332	upstream, upstream	1	1	0	21	25	14	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene NOP16	NOP16, HSPC185, HSPC111	NOP16 nucleolar protein homolog (yeast)	NM_016391, hCT2252391.0, hCT2356630.0, hCT2356631.0	203023_at, 209327_s_at, 214011_s_at	NP_057475.2, EAW65083.1, EAW65084.1, EAW65085.1
GeneID:192286	HIGD2A	5	175,815,764	175,816,751	987	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4647, 2_A375_pNL97_plus_lncRNA_AR..1..8679	72, 88	in gene, in gene	1	1	0	21	25	14	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene HIGD2A	HIGD2A, MGC2198	HIG1 hypoxia inducible domain family, member 2A	NM_138820, hCT2253105.0, hCT2253107.0	209328_x_at, 209329_x_at, 213833_x_at	NP_620175.1, EAW65082.1, EAW65081.1
GeneID:1212	CLTB	5	175,819,456	175,843,540	24,084	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4647, 1_A375_pNL7_minus_lncRNA_AR..1..4648, 2_A375_pNL97_plus_lncRNA_AR..1..8679, 2_A375_pNL97_plus_lncRNA_AR..1..8680	27884, -204, 27868, -140	downstream, upstream, downstream, upstream	1	1	0	26	31.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene CLTB	LCB, CLTB	clathrin, light chain (Lcb)	NM_001834, NM_007097, hCT2252387.0, hCT2252389.0, hCT31539.2, hCT32049.2	205172_x_at, 206284_x_at, 211043_s_at, 221996_s_at	NP_001825.1, NP_009028.1, EAW65077.1, EAW65078.1, EAW65079.1, EAW65080.1
GeneID:23197	FAF2	5	175,875,356	175,937,075	61,719	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4649	-188	upstream	1	0	0	16	14	8	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene FAF2	KIAA0887, FAF2, ETEA, UBXN3B, UBXD8	Fas associated factor family member 2	NM_014613, hCT2253112.0, hCT2253114.0, hCT2356645.0	212106_at, 212108_at	NP_055428.1, EAW65074.1, EAW65073.1, EAW65075.1
GeneID:22838	RNF44	5	175,953,700	175,964,421	10,721	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4650, 2_A375_pNL97_plus_lncRNA_AR..1..8681, 4_A375_EGR1..1..8907, 4_A375_EGR1..1..8908	-315, -571, 6621, 5285	upstream, upstream, in gene, in gene	1	1	1	12	16	15	3	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene RNF44	KIAA1100, RNF44	ring finger protein 44	NM_014901, hCT1966946.1, hCT1966947.1, hCT32055.3	203286_at	NP_055716.1, EAW65070.1, EAW65071.1, EAW65072.1
GeneID:54825	CDHR2	5	175,969,512	176,022,769	53,257	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4650, 2_A375_pNL97_plus_lncRNA_AR..1..8681	-4776, -4520	upstream, upstream	1	1	0	27	28	11	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene CDHR2	CDHR2, FLJ20383, FLJ20124, PCLKC, PCDH24, MGC183154	cadherin-related family member 2	NM_001171976, NM_017675, hCT1953079.2, hCT2253119.0, hCT2253121.0, hCT2253122.0	220186_s_at	NP_001165447.1, NP_060145.3, EAW65066.1, EAW65067.1, EAW65068.1, EAW65069.1
GeneID:114787	GPRIN1	5	176,022,803	176,037,131	14,328	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4651, 2_A375_pNL97_plus_lncRNA_AR..1..8682, 2_A375_pNL97_plus_lncRNA_AR..1..8683	-1461, -901, -1477	upstream, upstream, upstream	1	1	0	13.5	21	4	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene GPRIN1	KIAA1893, GPRIN1, GRIN1	G protein regulated inducer of neurite outgrowth 1	NM_052899, hCT1650598.4	227975_at, 229922_at	NP_443131.2, EAW65065.1
GeneID:6620	SNCB	5	176,047,210	176,057,557	10,347	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4651, 2_A375_pNL97_plus_lncRNA_AR..1..8682, 2_A375_pNL97_plus_lncRNA_AR..1..8683	18965, 19525, 18949	downstream, downstream, downstream	1	1	0	13.5	21	4	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SNCB	SNCB	synuclein, beta	NM_003085, NM_001001502, hCT1810323.3, hCT2351715.0	207653_s_at	NP_003076.1, NP_001001502.1, EAW65063.1, EAW65064.1
GeneID:253314	EIF4E1B	5	176,057,863	176,073,842	15,959	+	1	4_A375_EGR1..1..8909	16301	downstream	0	0	1	12	12	15	1	4_A375_EGR1..1	15	Gene EIF4E1B	EIF4E1B, FLJ38951	eukaryotic translation initiation factor 4E family member 1B	NM_001099408		NP_001092878.1
GeneID:26262	TSPAN17	5	176,074,388	176,086,059	11,671	+	1	4_A375_EGR1..1..8909	-404	upstream	0	0	1	12	12	15	1	4_A375_EGR1..1	15	Gene TSPAN17	TSPAN17, MGC14859, MGC71255, TM4SF17, FBX23, FBXO23	tetraspanin 17	NM_001006616, NM_012171, NM_130465, hCT2255139.0, hCT2255141.0, hCT2255142.0, hCT2356646.0, hCT2356647.0, hCT2356648.0, hCT2356649.0, hCT2356650.0, hCT32870.2	1558119_at, 225235_at	NP_001006617.2, NP_036303.1, NP_569732.2, EAW65053.1, EAW65056.1, EAW65058.1, EAW65054.1, EAW65055.1, EAW65057.1, EAW65059.1, EAW65060.1, EAW65061.1
GeneID:90249	UNC5A	5	176,237,560	176,307,899	70,339	+	15	1_A375_pNL7_minus_lncRNA_AR..1..4654, 1_A375_pNL7_minus_lncRNA_AR..1..4655, 1_A375_pNL7_minus_lncRNA_AR..1..4656, 2_A375_pNL97_plus_lncRNA_AR..1..8684, 2_A375_pNL97_plus_lncRNA_AR..1..8685, 2_A375_pNL97_plus_lncRNA_AR..1..8686, 2_A375_pNL97_plus_lncRNA_AR..1..8687, 4_A375_EGR1..1..8911, 4_A375_EGR1..1..8912, 4_A375_EGR1..1..8913, 4_A375_EGR1..1..8914, 4_A375_EGR1..1..8915, 4_A375_EGR1..1..8916, 4_A375_EGR1..1..8917, 4_A375_EGR1..1..8918	-6376, -4184, 27206, -6376, -4920, -4248, 27240, 2360, 12184, 40552, 57992, 58776, 59720, 67320, 68968	upstream, upstream, in gene, upstream, upstream, upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	19.64	24.27	14	11	2_A375_pNL97_plus_lncRNA_AR..1	117	Gene UNC5A	FLJ16449, UNC5A, UNC5H1, KIAA1976	unc-5 homolog A (C. elegans)	NM_133369, hCT2255145.0, hCT2255146.0, hCT32858.2	238448_at, 243833_at	NP_588610.2, EAW65052.1, EAW65050.1, EAW65051.1
GeneID:3101	HK3	5	176,307,870	176,326,333	18,463	-	2	4_A375_EGR1..1..8917, 4_A375_EGR1..1..8918	21453, 19805	downstream, downstream	0	0	1	6.5	7.5	16.5	2	4_A375_EGR1..1	18	Gene HK3	HXK3, HKIII, HK3	hexokinase 3 (white cell)	NM_002115, hCT2253999.0, hCT2254000.0, hCT32855.3	205936_s_at	NP_002106.2, EAW65047.1, EAW65048.1, EAW65049.1
GeneID:51720	UIMC1	5	176,332,006	176,433,443	101,437	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4657, 2_A375_pNL97_plus_lncRNA_AR..1..8688	-349, -285	upstream, upstream	1	1	0	16	21	11	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene UIMC1	RAP80, UIMC1, X2HRIP110	ubiquitin interaction motif containing 1	NM_016290, hCT1961260.1, hCT1961261.1, hCT1961262.1, hCT2253997.0, hCT2356632.0, hCT32854.3	220746_s_at	NP_057374.3, EAW65046.1, EAW65041.1, EAW65042.1, EAW65043.1, EAW65044.1, EAW65045.1
GeneID:23567	ZNF346	5	176,449,697	176,493,758	44,061	+	1	4_A375_EGR1..1..8919	-65	upstream	0	0	1	19	21	15	1	4_A375_EGR1..1	15	Gene ZNF346	Zfp346, JAZ, DKFZp547M223, ZNF346	zinc finger protein 346	NM_012279, hCT1962017.1, hCT2356634.0, hCT32856.3	222884_at, 232753_at, 236287_at	NP_036411.1, EAW65038.1, EAW65039.1, EAW65040.1
GeneID:2264	FGFR4	5	176,513,921	176,525,127	11,206	+	1	4_A375_EGR1..1..8920	271	in gene	0	0	1	13	17	14	1	4_A375_EGR1..1	14	Gene FGFR4	FGFR4, MGC20292, JTK2, CD334, TKF	fibroblast growth factor receptor 4	NM_002011, NM_213647, NM_022963, hCT1972611.1, hCT1972612.1, hCT2255152.0, hCT2255153.0	1554961_at, 1554962_a_at, 204579_at, 211237_s_at	NP_002002.3, NP_998812.1, NP_075252.2, EAW65035.1, EAW65036.1, EAW65037.1, EAW65034.1
GeneID:64324	NSD1	5	176,560,080	176,727,214	167,134	+	3	2_A375_pNL97_plus_lncRNA_AR..1..8689, 2_A375_pNL97_plus_lncRNA_AR..1..8690, 4_A375_EGR1..1..8921	170144, 176544, 174928	downstream, downstream, downstream	0	1	1	9	14.33	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene NSD1	ARA267, NSD1, FLJ44628, DKFZp666C163, STO, FLJ10684, SOTOS, FLJ22263, KMT3B	nuclear receptor binding SET domain protein 1	NM_022455, NM_172349, hCT1960928.1, hCT1960929.1, hCT2255158.0	219064_at, 243612_at	NP_071900.2, NP_758859.1, EAW65031.1, EAW65032.1, EAW65033.1
GeneID:53917	RAB24	5	176,728,199	176,730,744	2,545	-	3	2_A375_pNL97_plus_lncRNA_AR..1..8689, 2_A375_pNL97_plus_lncRNA_AR..1..8690, 4_A375_EGR1..1..8921	520, -5880, -4264	in gene, upstream, upstream	0	1	1	9	14.33	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene RAB24	RAB24	RAB24, member RAS oncogene family	NM_001031677, NM_130781, hCT2253977.1, hCT2253979.1, hCT2253983.1, hCT2253984.1, hCT2253985.1, hCT2344093.0	225251_at	NP_001026847.1, NP_570137.2, EAW65024.1, EAW65025.1, EAW65028.1, EAW65029.1, EAW65026.1, EAW65027.1
GeneID:27166	PRELID1	5	176,730,835	176,733,950	3,115	+	3	2_A375_pNL97_plus_lncRNA_AR..1..8689, 2_A375_pNL97_plus_lncRNA_AR..1..8690, 4_A375_EGR1..1..8921	-611, 5789, 4173	upstream, downstream, downstream	0	1	1	9	14.33	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PRELID1	PRELID1, MGC87972, CGI-106, PRELI, PX19	PRELI domain containing 1	NM_013237, hCT1810304.2, hCT2255163.0, hCT2255164.0	223032_x_at, 224232_s_at	NP_037369.1, EAW65023.1, EAW65021.1, EAW65022.1
GeneID:83463	MXD3	5	176,732,501	176,739,292	6,791	-	3	2_A375_pNL97_plus_lncRNA_AR..1..8689, 2_A375_pNL97_plus_lncRNA_AR..1..8690, 4_A375_EGR1..1..8921	9088, 2868, 4284	downstream, in gene, in gene	0	1	1	9	14.33	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MXD3	MYX, FLJ35523, MAD3, MXD3, MGC2383, BHLHC13	MAX dimerization protein 3	NM_031300, NM_001142935, hCT2253961.1, hCT2253962.1, hCT2344094.0, hCT2344095.0, hCT2344096.0	221250_s_at	NP_112590.1, NP_001136407.1, EAW65016.1, EAW65018.1, EAW65019.1, EAW65020.1, EAW65017.1
GeneID:10960	LMAN2	5	176,758,563	176,778,885	20,322	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4658, 2_A375_pNL97_plus_lncRNA_AR..1..8691, 4_A375_EGR1..1..8922	229, 133, 16165	in gene, in gene, in gene	1	1	1	14.5	15.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene LMAN2	C5orf8, LMAN2, GP36B, VIP36	lectin, mannose-binding 2	NM_006816, hCT2253978.0, hCT2253980.1	200805_at, 215656_at	NP_006807.1, EAW65014.1, EAW65015.1
GeneID:10636	RGS14	5	176,784,844	176,799,599	14,755	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4658, 2_A375_pNL97_plus_lncRNA_AR..1..8691, 4_A375_EGR1..1..8923	-6188, -6092, 14436	upstream, upstream, in gene	1	1	1	14	17	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene RGS14	RGS14	regulator of G-protein signaling 14	NM_006480, hCT2255165.0, hCT2255167.0, hCT32872.3	204280_at, 211021_s_at, 38290_at	NP_006471.2, EAW65012.1, EAW65011.1, EAW65013.1
GeneID:6569	SLC34A1	5	176,811,432	176,825,849	14,417	+	2	4_A375_EGR1..1..8924, 4_A375_EGR1..1..8925	1666, 19666	in gene, downstream	0	0	1	10.5	10	19	2	4_A375_EGR1..1	20	Gene SLC34A1	SLC17A2, SLC34A1, FRTS2, NAPI-3, SLC11, NPHLOP1, NPTIIa, NPT2	solute carrier family 34 (sodium phosphate), member 1	NM_003052, NM_001167579, hCT2255169.0, hCT2356636.0, hCT2356637.0, hCT32849.3	206177_s_at, 217530_at	NP_003043.3, NP_001161051.1, EAW65007.1, EAW65008.1, EAW65009.1, EAW65010.1
GeneID:345456	PFN3	5	176,827,108	176,827,637	529	-	1	4_A375_EGR1..1..8925	-3483	upstream	0	0	1	14	13	18	1	4_A375_EGR1..1	18	Gene PFN3	PFN3		NM_001029886, hCT1640772.2		NP_001025057.1, EAW65006.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:2161	F12	5	176,829,139	176,836,577	7,438	-	1	4_A375_EGR1..1..6925	5457	in gene	0	0	1	14	13	18	1	4_A375_EGR1..1	18	Gene F12	HAEX, HAF, F12, HAE3	coagulation factor XII (Hageman factor)	NM_000505, hCT2253971.0, hCT2253972.0, hCT2253973.0, hCT32651.3	205774_at, 215981_at	NP_000496.2, EAW85003.1, EAW85002.1, EAW85004.1, EAW85005.1
GeneID:2870	GRK6	5	176,853,687	176,869,850	16,163	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4659, 4_A375_EGR1..1..6926, 4_A375_EGR1..1..6927	21401, 14889, 15873	downstream, in gene, in gene	1	0	1	10	12	15	3	4_A375_EGR1..1	18	Gene GRK6	GPRK6, FLJ32135, GRK6	G protein-coupled receptor kinase 6	NM_002082, NM_001004106, NM_001004105, hCT1971524.1, hCT1971525.1, hCT2255173.0, hCT2356638.0, hCT31538.3	202848_s_at, 202849_x_at, 210981_s_at, 211543_s_at	NP_002073.2, NP_001004106.1, NP_001004105.1, EAW84997.1, EAW84999.1, EAW85001.1, EAW84998.1, EAW85000.1
GeneID:80758	PRR7	5	176,873,796	176,883,287	9,491	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4659, 4_A375_EGR1..1..6926, 4_A375_EGR1..1..6927, 4_A375_EGR1..1..6928	1292, -5220, -4436, 13308	in gene, upstream, upstream, downstream	1	0	1	8.5	11.25	15.5	4	4_A375_EGR1..1	18	Gene PRR7	PRR7, MGC10772	proline rich 7 (synaptic)	NM_001174101, NM_001174102, NM_030567, hCT1965507.1, hCT1965508.1, hCT32863.2	219742_at	NP_001167572.1, NP_001167573.1, NP_085044.2, EAW84994.1, EAW84995.1, EAW84996.1
GeneID:1627	DBN1	5	176,883,814	176,900,894	17,080	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4659, 4_A375_EGR1..1..6928	25806, 13590	downstream, in gene	1	0	1	10	14.5	14.5	2	4_A375_EGR1..1	17	Gene DBN1	D0S117E, DKFZp434D064, DBN1	drebrin 1	NM_004395, NM_080881, hCT2253941.1, hCT2253948.1, hCT2253951.1, hCT2253954.1, hCT2356629.0	202806_at, 217025_s_at	NP_004386.2, NP_543157.1, EAW84989.1, EAW84990.1, EAW84991.1, EAW84993.1, EAW84992.1
GeneID:9260	PDLIM7	5	176,910,395	176,924,602	14,207	-	2	2_A375_pNL97_plus_lncRNA_AR..1..6692, 4_A375_EGR1..1..6929	828, 56	in gene, in gene	0	1	1	15	21	21	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PDLIM7	PDLIM7, LMP1	PDZ and LIM domain 7 (enigma)	NM_005451, NM_203352, NM_213636, hCT2253963.0, hCT2253965.0, hCT2253966.0, hCT2253967.0	1569149_at, 1569150_x_at, 203369_x_at, 203370_s_at, 214121_x_at, 214122_at, 214266_s_at	NP_005442.2, NP_976227.1, NP_998801.1, EAW84985.1, EAW84986.1, EAW84988.1, EAW84987.1
GeneID:79930	DOK3	5	176,928,905	176,937,427	8,522	-	6	1_A375_pNL7_minus_lncRNA_AR..1..4660, 2_A375_pNL97_plus_lncRNA_AR..1..6692, 2_A375_pNL97_plus_lncRNA_AR..1..6693, 4_A375_EGR1..1..6929, 4_A375_EGR1..1..6930, 4_A375_EGR1..1..6931	-6701, 13651, -6701, 12683, 2067, -6253	upstream, downstream, upstream, downstream, in gene, upstream	1	1	1	17.67	22.67	19.33	3	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene DOK3	FLJ22570, DOK3, DOKL, FLJ39939	docking protein 3	NM_024872, NM_001144875, NM_001144876, hCT1962022.1, hCT1962023.1, hCT32861.2	220320_at, 223553_s_at	NP_079148.2, NP_001138347.1, NP_001138348.1, EAW84982.1, EAW84983.1, EAW84984.1
GeneID:51428	DDX41	5	176,938,578	176,943,967	5,389	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4660, 2_A375_pNL97_plus_lncRNA_AR..1..6693, 4_A375_EGR1..1..6930, 4_A375_EGR1..1..6931, 4_A375_EGR1..1..6932	-161, -161, 6607, 287, -7217	upstream, upstream, downstream, in gene, upstream	1	1	1	14.33	16	16.67	3	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene DDX41	MGC8828, ABS, DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	NM_016222, hCT2253940.1, hCT2253949.1, hCT2344089.0, hCT2344090.0, hCT2344091.0	217840_at	NP_057306.2, EAW84977.1, EAW84978.1, EAW84979.1, EAW84980.1, EAW84981.1
GeneID:54540	FAM193B	5	176,946,790	176,981,546	34,756	-	6	1_A375_pNL7_minus_lncRNA_AR..1..4660, 2_A375_pNL97_plus_lncRNA_AR..1..6693, 2_A375_pNL97_plus_lncRNA_AR..1..6694, 4_A375_EGR1..1..6931, 4_A375_EGR1..1..6932, 4_A375_EGR1..1..6933	37420, 37420, 7684, 37866, 30364, 556	downstream, downstream, in gene, downstream, in gene, in gene	1	1	1	16.25	20.5	16.25	4	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene FAM193B	DKFZp313I142, FAM193B, FLJ10404, IRIZIO, KIAA1931	family with sequence similarity 193, member B	NM_001190946, NR_024019, hCT2253943.0, hCT2253945.0, hCT2253948.1, hCT2253952.1, hCT2253955.1, hCT2344087.0, hCT2344088.0, hCT2344092.0	218920_at, 243047_at	NP_001177875.1, EAW84969.1, EAW84970.1, EAW84971.1, EAW84974.1, EAW84976.1, EAW84972.1, EAW84973.1, EAW84975.1
GeneID:23138	N4BP3	5	177,540,556	177,553,107	12,551	+	1	4_A375_EGR1..1..6934	8308	in gene	0	0	1	6	7	18	1	4_A375_EGR1..1	18	Gene N4BP3	KIAA0341, N4BP3	NEDD4 binding protein 3	NM_015111, hCT1773345.2, hCT2256866.0, hCT2256870.0, hCT2256872.0	214775_at	NP_055926.1, EAW53854.1, EAW53851.1, EAW53852.1, EAW53853.1
GeneID:84777	RMND5B	5	177,558,028	177,575,479	17,451	+	1	4_A375_EGR1..1..6934	-9164	upstream	0	0	1	6	7	18	1	4_A375_EGR1..1	18	Gene RMND5B	DKFZp434K0926, FLJ22318, RMND5B	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	NM_022762, hCT2256876.0, hCT2256878.0	213297_at, 218262_at	NP_073599.2, EAW53849.1, EAW53850.1
GeneID:3182	HNRNPAB	5	177,631,508	177,638,184	6,676	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6695, 2_A375_pNL97_plus_lncRNA_AR..1..6696, 4_A375_EGR1..1..6935	-132, 1740, 28	upstream, in gene, in gene	0	1	1	10.5	16.5	18	2	4_A375_EGR1..1	22	Gene HNRNPAB	HNRNPAB, FLJ40338, HNRPAB, ABBP1	heterogeneous nuclear ribonucleoprotein A/B	NM_031266, NM_004499, hCT2256882.0, hCT2256883.0, hCT2256884.0, hCT2352772.0	201277_s_at, 231060_at, 235889_at	NP_112556.2, NP_004490.2, EAW53842.1, EAW53843.1, EAW53844.1, EAW53845.1
GeneID:85007	AGXT2L2	5	177,635,540	177,659,803	24,263	-	4	2_A375_pNL97_plus_lncRNA_AR..1..6695, 2_A375_pNL97_plus_lncRNA_AR..1..6696, 4_A375_EGR1..1..6935, 4_A375_EGR1..1..6936	28427, 26555, 28267, -8437	downstream, downstream, downstream, upstream	0	1	1	8.67	13.33	18	3	4_A375_EGR1..1	22	Gene AGXT2L2	MGC117348, AGXT2L2, MGC45484, MGC15875	alanine-glyoxylate aminotransferase 2-like 2	NM_153373, hCT2256744.0, hCT2256747.0, hCT2256749.0, hCT2352780.0, hCT2352781.0, hCT2352782.0, hCT2352783.0	226519_s_at, 226763_at, 232488_at	NP_699204.1, EAW53836.1, EAW53835.1, EAW53837.1, EAW53840.1, EAW53841.1, EAW53838.1, EAW53839.1
GeneID:91522	COL23A1	5	177,664,617	178,017,556	352,939	-	5	4_A375_EGR1..1..6936, 4_A375_EGR1..1..6937, 4_A375_EGR1..1..6938, 4_A375_EGR1..1..6939, 4_A375_EGR1..1..6940	351316, 342484, 310132, 218916, 174676	in gene, in gene, in gene, in gene, in gene	0	0	1	4.8	8.4	17.6	5	4_A375_EGR1..1	20	Gene COL23A1	COL23A1, DKFZp434K0621	collagen, type XXIII, alpha 1	NM_173465, hCT11171.4, hCT2349714.0	229168_at	NP_775736.2, EAW53833.1, EAW53834.1
GeneID:57396	CLK4	5	178,029,865	178,054,054	24,389	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4661, 2_A375_pNL97_plus_lncRNA_AR..1..6697	390, 678	in gene, in gene	1	1	0	18	16	11	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene CLK4	CLK4, DKFZp686A20267	CDC-like kinase 4	NM_020666, hCT11173.1, hCT2352777.0	1566836_at, 210346_s_at, 226751_at, 241403_at	NP_065717.1, EAW53831.1, EAW53832.1
GeneID:117608	ZNF354B	5	178,286,954	178,311,424	24,470	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4662	-138	upstream	1	0	0	18	11	6	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene ZNF354B	FLJ25008, MGC138316, KID2, ZNF354B	zinc finger protein 354B	NM_058230, hCT1957974.1		NP_478137.1, EAW53828.1
GeneID:80108	ZFP2	5	178,322,916	178,360,210	37,294	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6698, 4_A375_EGR1..1..6942, 4_A375_EGR1..1..6943	-12, 28, 44828	upstream, in gene, downstream	0	1	1	9.5	13.5	16	2	4_A375_EGR1..1	17	Gene ZFP2	ZFP2, FLJ21628, ZNF751	zinc finger protein 2 homolog (mouse)	NM_030613	207757_at	NP_085116.2
GeneID:285676	ZNF454	5	178,368,194	178,393,218	25,024	+	1	4_A375_EGR1..1..6943	-450	upstream	0	0	1	7	14	17	1	4_A375_EGR1..1	17	Gene ZNF454	MGC138481, ZNF454, FLJ37444	zinc finger protein 454	NM_001178089, NM_001178090, NM_182594, hCT2343131.0, hCT2345368.1, hCT2347992.0		NP_001171560.1, NP_001171561.1, NP_872400.2, EAW53822.1, EAW53823.1, EAW53824.1
GeneID:30832	ZNF354C	5	178,487,607	178,507,695	20,088	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4663, 2_A375_pNL97_plus_lncRNA_AR..1..6699	-311, -327	upstream, upstream	1	1	0	18	34	6	1	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene ZNF354C	KID3, ZNF354C	zinc finger protein 354C	NM_014594, hCT11305.3	234409_at	NP_055409.1, EAW53817.1
GeneID:9509	ADAMTS2	5	178,537,852	178,772,431	234,579	-	6	4_A375_EGR1..1..6944, 4_A375_EGR1..1..6945, 4_A375_EGR1..1..6946, 4_A375_EGR1..1..6947, 4_A375_EGR1..1..6948, 4_A375_EGR1..1..6949	149775, 136255, 132335, 86047, 54095, 14927	in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	4.5	5.67	17	6	4_A375_EGR1..1	20	Gene ADAMTS2	hPCPNI, NPI, PCINP, ADAM-TS2, PCPNI, DKFZp686F12218, PCI-NP, ADAMTS-3, ADAMTS2, PNPI	ADAM metallopeptidase with thrombospondin type 1 motif, 2	NM_014244, NM_021599, hCT1775598.2, hCT7586.3	214454_at, 214535_s_at	NP_055059.2, NP_067610.1, EAW53815.1, EAW53816.1
GeneID:100507476	LOC100507476	5	178,816,523	178,820,682	4,159	-	1	4_A375_EGR1..1..6944	-1974	upstream	0	0	1	5	10	17	1	4_A375_EGR1..1	17	Gene LOC100507476		hypothetical protein LOC100507476	XM_003118879		XP_003118927.1
GeneID:80230	RUFY1	5	178,977,571	179,037,019	59,448	+	2	4_A375_EGR1..1..6952, 4_A375_EGR1..1..6953	9373, 59561	in gene, downstream	0	0	1	15.5	14	15.5	2	4_A375_EGR1..1	16	Gene RUFY1	ZFYVE12, FLJ22251, RUFY1, RABIP4	RUN and FYVE domain containing 1	NM_001040452, NM_001040451, NM_025158, hCT2261067.0	218243_at, 229179_at, 233380_s_at, 233381_at	NP_001035542.1, NP_001035541.1, NP_079434.3, EAW53810.1
GeneID:3187	HNRNPH1	5	179,041,179	179,050,722	9,543	-	4	2_A375_pNL97_plus_lncRNA_AR..1..6700, 4_A375_EGR1..1..6953, 4_A375_EGR1..1..6954, 4_A375_EGR1..1..6955	178, 13570, 67, -478	in gene, downstream, in gene, upstream	0	1	1	14	15.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene HNRNPH1	HNRNPH1, hnRNPH, DKFZp686A15170, HNRPH, HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	NM_005520, hCT2257899.0, hCT2257903.0, hCT87455.1	201031_s_at, 213470_s_at, 213472_at, 213619_at	NP_005511.1, EAW53807.1, EAW53808.1, EAW53809.1
GeneID:646019	CBY3	5	179,105,559	179,107,975	2,416	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4664, 4_A375_EGR1..1..6956, 4_A375_EGR1..1..6957	2055, 2359, 1735	in gene, in gene, in gene	1	0	1	21	19	21	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene CBY3	CBY3		NM_001164444		NP_001157916.1
GeneID:729595	LOC729595	5	179,121,198	179,121,743	545	+	1	4_A375_EGR1..1..6958	4258	downstream	0	0	1	11	14	19	1	4_A375_EGR1..1	19	Gene LOC729595	HMGB3P22	high mobility group box 3 pseudogene 22	XM_001717176, XM_001130734, XM_001714426		XP_001717228.2, XP_001130734.2, XP_001714478.2
GeneID:821	CANX	5	179,125,930	179,158,642	32,712	+	1	4_A375_EGR1..1..6958	-474	upstream	0	0	1	11	14	19	1	4_A375_EGR1..1	19	Gene CANX	P90, CNX, FLJ26570, IP90, CANX	calnexin	NM_001746, NM_001024649, hCT2261070.0, hCT2261071.0, hCT2352773.0, hCT2352774.0	200068_s_at, 208852_s_at, 208853_s_at, 238034_at, 241712_at	NP_001737.1, NP_001019820.1, EAW53802.1, EAW53803.1, EAW53804.1, EAW53805.1
GeneID:4056	LTC4S	5	179,220,986	179,223,513	2,527	+	1	4_A375_EGR1..1..6959	11606	downstream	0	0	1	10	12	20	1	4_A375_EGR1..1	20	Gene LTC4S	MGC33147, LTC4S	leukotriene C4 synthase	NM_145867, hCT1960372.1, hCT1960373.1, hCT2352779.0, hCT8301.2	206480_at	NP_665874.1, EAW53796.1, EAW53797.1, EAW53798.1, EAW53799.1
GeneID:11282	MGAT4B	5	179,224,597	179,233,952	9,355	-	3	2_A375_pNL97_plus_lncRNA_AR..1..6701, 4_A375_EGR1..1..6959, 4_A375_EGR1..1..6960	-523, 1360, -512	upstream, in gene, upstream	0	1	1	11	12.5	17.5	2	4_A375_EGR1..1	20	Gene MGAT4B	GNT-IVB, GNT-IV, MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	NM_014275, NM_054013, hCT1960374.1, hCT1960375.1, hCT2257878.0, hCT2257879.0, hCT2257880.0, hCT2257882.0, hCT2257884.0, hCT2257887.0	220189_s_at, 224598_at	NP_055090.1, NP_463459.1, EAW53788.1, EAW53789.1, EAW53790.1, EAW53795.1, EAW53791.1, EAW53792.1, EAW53793.1, EAW53794.1
GeneID:100302156	MIR1229	5	179,225,278	179,225,346	68	-	3	2_A375_pNL97_plus_lncRNA_AR..1..6701, 4_A375_EGR1..1..6959, 4_A375_EGR1..1..6960	-9129, -7246, -9116	upstream, upstream, upstream	0	1	1	11	12.5	17.5	2	4_A375_EGR1..1	20	Gene MIR1229	hsa-mir-1229, MIRN1229, MIR1229	microRNA 1229	NR_031598		
GeneID:8878	SQSTM1	5	179,233,388	179,265,078	31,690	+	7	1_A375_pNL7_minus_lncRNA_AR..1..4665, 1_A375_pNL7_minus_lncRNA_AR..1..4666, 2_A375_pNL97_plus_lncRNA_AR..1..6701, 2_A375_pNL97_plus_lncRNA_AR..1..6702, 2_A375_pNL97_plus_lncRNA_AR..1..6703, 4_A375_EGR1..1..6959, 4_A375_EGR1..1..6960	13332, 14420, 1067, 13268, 14516, -798, 1076	in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	18.25	16.25	15.5	4	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene SQSTM1	PDB3, OSIL, p60, SQSTM1, p62, A170, ZIP3, p62B	sequestosome 1	NM_003900, NM_001142298, NM_001142299, hCT1960371.1, hCT8300.3	201471_s_at, 213112_s_at, 217252_at, 217255_at, 239004_at, 244804_at	NP_003891.1, NP_001135770.1, NP_001135771.1, EAW53786.1, EAW53787.1
GeneID:51149	C5orf45	5	179,264,266	179,285,840	21,574	-	1	4_A375_EGR1..1..6961	80	in gene	0	0	1	19	11	22	1	4_A375_EGR1..1	22	Gene C5orf45	MGC65027, MGC78537, C5orf45, DKFZp686L2452	chromosome 5 open reading frame 45	NM_016175, NM_001017987, hCT1960367.1, hCT1960369.1	220341_s_at	NP_057259.2, NP_001017987.1, EAW53764.1, EAW53765.1
GeneID:23061	TBC1D9B	5	179,289,071	179,334,856	45,785	-	2	4_A375_EGR1..1..6961, 4_A375_EGR1..1..6962	49096, 29484	downstream, in gene	0	0	1	12.5	8.5	20.5	2	4_A375_EGR1..1	22	Gene TBC1D9B	TBC1D9B, FLJ41660, MGC157757, KIAA0676	TBC1 domain family, member 9B (with GRAM domain)	NM_198868, NM_015043, hCT1960381.1, hCT1960382.1, hCT2257930.0, hCT2352767.0, hCT2352768.0, hCT8309.3	206431_x_at, 212052_s_at, 212054_x_at, 215994_x_at	NP_942568.2, NP_055858.2, EAW53777.1, EAW53778.1, EAW53779.1, EAW53781.1, EAW53780.1, EAW53782.1
GeneID:55819	RNF130	5	179,382,474	179,499,109	116,635	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6704	645	in gene	0	1	0	14	19	5	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene RNF130	GP, RNF130, MGC99542, MGC117241, MGC138647, GOLIATH, G1RZFP	ring finger protein 130	NM_018434, hCT1960379.1, hCT1960380.1, hCT2258998.0, hCT8308.3	1563975_at, 217865_at, 236292_at	NP_060904.2, EAW53774.1, EAW53772.1, EAW53773.1, EAW53775.1
GeneID:255426	RASGEF1C	5	179,527,795	179,636,130	108,335	-	2	4_A375_EGR1..1..6963, 4_A375_EGR1..1..6964	89122, 29698	in gene, in gene	0	0	1	6.5	5	19	2	4_A375_EGR1..1	20	Gene RASGEF1C	FLJ35841, RASGEF1C	RasGEF domain family, member 1C	NM_175062, hCT1966180.2, hCT2349698.0, hCT8307.3	238748_at	NP_778232.2, EAW53771.1, EAW53769.1, EAW53770.1
GeneID:9945	GFPT2	5	179,727,700	179,780,315	52,615	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4667, 2_A375_pNL97_plus_lncRNA_AR..1..6705	107, 507	in gene, in gene	1	1	0	20	20	12	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene GFPT2	FLJ10380, GFPT2, GFAT2	glutamine-fructose-6-phosphate transaminase 2	NM_005110, hCT2259060.0, hCT8298.3	205100_at, 237352_at	NP_005101.1, EAW53755.1, EAW53756.1
GeneID:57472	CNOT6	5	179,921,417	180,005,353	83,936	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4668, 2_A375_pNL97_plus_lncRNA_AR..1..6706	-153, -137	upstream, upstream	1	1	0	25	35	6	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene CNOT6	CCR4, CNOT6, KIAA1194	CCR4-NOT transcription complex, subunit 6	NM_015455, hCT2259723.1, hCT2259725.1, hCT2349984.0	217970_s_at, 222476_at	NP_056270.2, EAW53753.1, EAW53752.1, EAW53754.1
GeneID:2324	FLT4	5	180,028,506	180,076,624	48,118	-	1	4_A375_EGR1..1..6967	23086	in gene	0	0	1	5	6	16	1	4_A375_EGR1..1	16	Gene FLT4	PCL, FLT4, VEGFR3, LMPH1A, FLT41	fms-related tyrosine kinase 4	NM_002020, NM_182925, hCT1960378.2, hCT8304.3	210316_at, 229902_at, 234379_at	NP_002011.2, NP_891555.2, EAW53749.1, EAW53750.1
GeneID:4245	MGAT1	5	180,217,541	180,237,137	19,596	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4669, 2_A375_pNL97_plus_lncRNA_AR..1..6707	-175, -591	upstream, upstream	1	1	0	16	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MGAT1	GNT-1, GLYT1, MGAT1, GLCT1, GLCNAC-TI, MGAT, GNT-I	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	NM_002406, NM_001114617, NM_001114618, NM_001114619, NM_001114620, hCT1641756.2, hCT1960385.1, hCT1960386.1, hCT1960387.1, hCT1987984.1, hCT2259027.0, hCT2259026.0	201126_s_at	NP_002397.2, NP_001108089.1, NP_001108090.1, NP_001108091.1, NP_001108092.1, EAW53739.1, EAW53740.1, EAW53741.1, EAW53742.1, EAW53743.1, EAW53744.1, EAW53745.1
GeneID:643836	ZFP62	5	180,274,611	180,288,286	13,675	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4670, 2_A375_pNL97_plus_lncRNA_AR..1..6708, 4_A375_EGR1..1..6969	94, -402, -130	in gene, upstream, upstream	1	1	1	16	19	15	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene ZFP62	MGC176438, ZET, FLJ58781, ZNF755, FLJ34231, ZFP62, FLJ34057, FLJ59694, FLJ11344, DKFZp667F2013	zinc finger protein 62 homolog (mouse)	NM_152283, NM_001172638	227796_at	NP_689496.4, NP_001166109.1
GeneID:153579	BTNL9	5	180,467,225	180,488,523	21,298	+	1	4_A375_EGR1..1..6970	-3001	upstream	0	0	1	8	8	17	1	4_A375_EGR1..1	17	Gene BTNL9	VDLS1900, BTNL9, BTN3	butyrophilin-like 9	NM_152547, hCT2259734.1, hCT2259735.1, hCT2340514.0, hCT2352770.0, hCT2352771.0	1553279_at, 228434_at, 230992_at, 241496_at	NP_689760.2, EAW53728.1, EAW53724.1, EAW53725.1, EAW53726.1, EAW53727.1
GeneID:81786	TRIM7	5	180,620,924	180,632,177	11,253	-	8	1_A375_pNL7_minus_lncRNA_AR..1..4671, 2_A375_pNL97_plus_lncRNA_AR..1..6711, 2_A375_pNL97_plus_lncRNA_AR..1..6712, 2_A375_pNL97_plus_lncRNA_AR..1..6713, 4_A375_EGR1..1..6973, 4_A375_EGR1..1..6974, 4_A375_EGR1..1..6975, 4_A375_EGR1..1..6976	13457, 17553, 13425, 17, 17425, 16241, 13425, -2639	downstream, downstream, downstream, in gene, downstream, downstream, downstream, upstream	1	1	1	15.2	19.6	20.2	5	4_A375_EGR1..1	28	Gene TRIM7	GNIP, TRIM7, RNF90	tripartite motif containing 7	NM_033342, NM_203293, NM_203294, NM_203295, NM_203296, NM_203297, hCT1773618.3, hCT1960390.2, hCT1960391.0, hCT2259014.1, hCT2351992.0, hCT2351993.0	1554735_a_at, 223694_at, 239694_at	NP_203126.1, NP_976038.1, NP_976039.1, NP_976040.1, NP_976041.1, NP_976042.1, EAW53715.1, EAW53716.1, EAW53717.1, EAW53718.1, EAW53719.1, EAW53720.1
GeneID:100507546	LOC100507546	5	180,625,202	180,630,117	4,915	+	6	1_A375_pNL7_minus_lncRNA_AR..1..4671, 2_A375_pNL97_plus_lncRNA_AR..1..6712, 2_A375_pNL97_plus_lncRNA_AR..1..6713, 4_A375_EGR1..1..6974, 4_A375_EGR1..1..6975, 4_A375_EGR1..1..6976	-6482, -6450, 6958, -9266, -6450, 9814	upstream, upstream, downstream, upstream, upstream, downstream	1	1	1	16	20	18.25	4	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene LOC100507546		hypothetical LOC100507546	XR_112804, XR_112802, XR_112803, XR_110079, XR_110077, XR_110078, XR_113812, XR_113813, XR_113811		
GeneID:90933	TRIM41	5	180,650,306	180,662,808	12,502	+	9	1_A375_pNL7_minus_lncRNA_AR..1..4672, 1_A375_pNL7_minus_lncRNA_AR..1..4673, 1_A375_pNL7_minus_lncRNA_AR..1..4674, 1_A375_pNL7_minus_lncRNA_AR..1..4675, 2_A375_pNL97_plus_lncRNA_AR..1..6714, 2_A375_pNL97_plus_lncRNA_AR..1..6715, 4_A375_EGR1..1..6977, 4_A375_EGR1..1..6978, 4_A375_EGR1..1..6979	-4962, -1058, 190, 20542, -962, 30, -666, -34, 20574	upstream, upstream, in gene, downstream, upstream, in gene, upstream, upstream, downstream	1	1	1	20.5	19.75	21	4	4_A375_EGR1..1	31	Gene TRIM41	MGC31991, TRIM41, MGC1127, RINCK	tripartite motif containing 41	NM_033549, NM_201627, hCT11046.2, hCT1960402.1, hCT1960403.0, hCT2259742.0, hCT2259743.0, hCT2259744.0, hCT2259747.0, hCT2352769.0	228445_s_at	NP_291027.3, NP_963921.1, EAW53707.1, EAW53712.1, EAW53713.1, EAW53714.1, EAW53708.1, EAW53709.1, EAW53710.1, EAW53711.1
GeneID:10399	GNB2L1	5	180,663,928	180,670,906	6,978	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4675, 4_A375_EGR1..1..6979, 4_A375_EGR1..1..6980	58, 26, -2694	in gene, in gene, upstream	1	0	1	18.5	11.5	18	2	4_A375_EGR1..1	20	Gene GNB2L1	Gnb2-rs1, H12.3, PIG21, GNB2L1, RACK1, HLC-7	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	NM_006098, hCT10125.4, hCT1960398.3, hCT1960399.2, hCT1960400.3, hCT1960401.3, hCT2349976.1, hCT2349977.1, hCT2349978.1, hCT2349979.1, hCT2349980.1, hCT2349982.1	200651_at, 222034_at	NP_006089.1, EAW53694.1, EAW53692.1, EAW53695.1, EAW53700.1, EAW53702.1, EAW53693.1, EAW53696.1, EAW53697.1, EAW53698.1, EAW53699.1, EAW53701.1
GeneID:619571	SNORD96A	5	180,666,818	180,666,889	71	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4675, 4_A375_EGR1..1..6979, 4_A375_EGR1..1..6980	-1959, -1991, -4711	upstream, upstream, upstream	1	0	1	18.5	11.5	18	2	4_A375_EGR1..1	20	Gene SNORD96A	SNORD96A, U96A	small nucleolar RNA, C/D box 96A	NR_002592		
GeneID:100289627	LOC100289627	5	180,668,965	180,670,914	1,949	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4675, 4_A375_EGR1..1..6979, 4_A375_EGR1..1..6980	1883, 1915, 4635	in gene, in gene, downstream	1	0	1	18.5	11.5	18	2	4_A375_EGR1..1	20	Gene LOC100289627		hypothetical LOC100289627	XR_112805, XR_110080, XR_113814		
GeneID:619570	SNORD95	5	180,670,314	180,670,376	62	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4675, 4_A375_EGR1..1..6979, 4_A375_EGR1..1..6980	-472, -504, -3224	upstream, upstream, upstream	1	0	1	18.5	11.5	18	2	4_A375_EGR1..1	20	Gene SNORD95	U95, SNORD95	small nucleolar RNA, C/D box 95	NR_002591		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.100507619	LOC100507619	5	180,873,507	180,884,587	11,080	+	7	1_A375_pNL7_minus_lncRNA_AR..1..4675, 1_A375_pNL7_minus_lncRNA_AR..1..4676, 2_A375_pNL97_plus_lncRNA_AR..1..8716, 4_A375_EGR1..1..8979, 4_A375_EGR1..1..8980, 4_A375_EGR1..1..8981, 4_A375_EGR1..1..8982	-2659, 14621, 14573, -2627, 93, 14853, 15421	upstream, downstream, downstream, upstream, in gene, downstream, downstream	1	1	1	21	13.67	18.67	3	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene LOC100507619		hypothetical LOC100507619	XR_112807, XR_110062, XR_113616		
GeneID.84851	TRIM52	5	180,683,373	180,688,119	4,746	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4676, 2_A375_pNL97_plus_lncRNA_AR..1..8716, 4_A375_EGR1..1..8980, 4_A375_EGR1..1..8981, 4_A375_EGR1..1..8982	-9, 39, 14519, -41, -809	upstream, in gene, downstream, upstream, upstream	1	1	1	22	14.5	18	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene TRIM52	RNF102, TRIM52, MGC16175	tripartite motif containing 52	NM_032765, hCT1832619.3, hCT1960397.0, hCT2259005.1	1566594_s_at, 221897_at	NP_116154.1, EAW53704.1, EAW53703.1, EAW53705.1
GeneID.100507602	LOC100507602	5	180,888,213	180,891,259	3,046	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4676, 2_A375_pNL97_plus_lncRNA_AR..1..8716, 4_A375_EGR1..1..8981, 4_A375_EGR1..1..8982	-85, -133, -53, 715	upstream, upstream, upstream, in gene	1	1	1	26	18	20	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene LOC100507602		hypothetical LOC100507602	XR_112806, XR_110061, XR_113615		
GeneID.56940	DUSP22	6	292,101	351,355	59,254	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8717	187	in gene	0	1	0	15	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene DUSP22	VHX, LMWDSP2, JSP1, JKAP, MKPX, FLJ35864, DUSP22	dual specificity phosphatase 22	NM_020185, hCT2343655.0	218845_at, 226440_at	NP_064570.1, EAW53895.1
GeneID.55770	EXOC2	6	485,138	693,109	207,971	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4677, 2_A375_pNL97_plus_lncRNA_AR..1..8718	10, -43	in gene, upstream	1	1	0	37	40	9	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene EXOC2	EXOC2, SEC5L1, Sec5p, SEC5, FLJ11026	exocyst complex component 2	NM_018303, hCT13746.4, hCT2251308.0	219349_s_at, 226270_at	NP_060773.3, EAW55062.1, EAW55061.1
GeneID.340156	MYLK4	6	2,663,863	2,751,154	87,291	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8721	91966	downstream	0	1	0	15	21	5	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MYLK4	SgK085, MYLK4	myosin light chain kinase family, member 4	NM_001012418, hCT13977.4, hCT2351884.0	1558136_at, 1561503_at, 1561504_s_at	NP_001012418.2, EAW55083.1, EAW55084.1
GeneID.56897	WRNIP1	6	2,765,666	2,785,979	20,313	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4678, 2_A375_pNL97_plus_lncRNA_AR..1..8722, 4_A375_EGR1..1..8983	14, -50, -1922	in gene, upstream, upstream	1	1	1	11	15.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene WRNIP1	RP11-420G6.2, WHIP, WRNIP1, FLJ22526, bA420G6.2	Werner helicase interacting protein 1	NM_020135, NM_130395, hCT13979.2, hCT1962922.0, hCT1962923.1, hCT2250669.0	218015_s_at, 222469_s_at, 227619_at	NP_064520.2, NP_569079.1, EAW55085.1, EAW55086.1, EAW55087.1, EAW55088.1
GeneID.401232	DKFZP686I15217	6	2,988,201	2,991,405	3,204	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8723	1655	in gene	0	1	0	13	13	3	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene DKFZP686I15217		hypothetical LOC401232	NR_026655, NR_026656		
GeneID.4835	NQO2	6	3,000,067	3,019,994	19,927	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8723	-10211	upstream	0	1	0	13	13	3	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene NQO2	NQO2, QR2, DHQV, DIA6, NMOR2	NAD(P)H dehydrogenase, quinone 2	NM_000904, hCT13974.2, hCT1953936.1, hCT2250674.0, hCT2250675.0, hCT2250679.0	203814_s_at	NP_000895.2, EAW55109.1, EAW55107.1, EAW55108.1, EAW55110.1, EAW55111.1
GeneID.8737	RIPK1	6	3,077,058	3,115,421	38,363	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8724	-7767	upstream	0	1	0	11	12	8	1	2_A375_pNL97_plus_lncRNA_AR..1	12	Gene RIPK1	RIP, RIP1, RIPK1, FLJ39204	receptor (TNFRSF)-interacting serine-threonine kinase 1	NM_003804, hCT13972.3, hCT1960109.0, hCT2250662.0, hCT2250665.0	209941_at, 226551_at	NP_003795.2, EAW55115.1, EAW55116.1, EAW55117.1, EAW55118.1
GeneID.347733	TUBB2B	6	3,224,495	3,227,968	3,473	-	1	4_A375_EGR1..1..8984	-266	upstream	0	0	1	5	9	17	1	4_A375_EGR1..1	17	Gene TUBB2B	FLJ98847, bA506K6.1, MGC8685, DKFZp566F223, TUBB2B, TUBB-PARALOG	tubulin, beta 2B	NM_178012, hCT1822143.2, hCT1953928.1, hCT1980104.1, hCT2255284.0	214023_x_at	NP_821080.1, EAW55125.1, EAW55126.1, EAW55127.1, EAW55128.1
GeneID.100507294	LOC100507294	6	3,228,159	3,287,301	59,142	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4679, 2_A375_pNL97_plus_lncRNA_AR..1..8725, 4_A375_EGR1..1..8984	31020, 31041, 97	in gene, in gene, in gene	1	1	1	11.5	18	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene LOC100507294		hypothetical LOC100507294	XR_112809, XR_108898, XR_113619		
GeneID.389362	PSMG4	6	3,259,162	3,268,300	9,138	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4679, 2_A375_pNL97_plus_lncRNA_AR..1..8725	17, 36	in gene, in gene	1	1	0	16	27	12	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene PSMG4	C6orf86, PAC4, PSMG4, bA506K6.2	proteasome (prosome, macropain) assembly chaperone 4	NM_001128591, NM_001128592, NM_001135750	1561304_a_at, 226217_s_at, 233443_at, 233447_at, 242055_at, 242623_x_at	NP_001122063.1, NP_001122064.1, NP_001129222.1
GeneID.63027	SLC22A23	6	3,269,207	3,456,793	187,586	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4679, 2_A375_pNL97_plus_lncRNA_AR..1..8725, 2_A375_pNL97_plus_lncRNA_AR..1..8726	197614, 197593, 131929	downstream, downstream, in gene	1	1	0	15	22	9	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SLC22A23	C6orf85, SLC22A23, DKFZp434F011, FLJ22174	solute carrier family 22, member 23	NM_021945, NM_015482, hCT13976.2, hCT2255257.0, hCT2255258.0, hCT2255260.0	1566718_at, 1566719_s_at, 223194_s_at, 233206_at	NP_068764.3, NP_056297.1, EAW55132.1, EAW55133.1, EAW55134.1, EAW55135.1
GeneID.10799	RPP40	6	4,995,280	5,004,271	8,991	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8728	239	in gene	0	1	0	10	15	8	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene RPP40	RPP40, bA428J1.3, RNASEP1	ribonuclease P/MRP 40kDa subunit	NM_006638, hCT1958278.1, hCT1983393.1, hCT1983394.1, hCT2250904.0, hCT2250906.0	213427_at	NP_006629.2, EAW55170.1, EAW55171.1, EAW55172.1, EAW55173.1, EAW55174.1
GeneID.57128	LYRM4	6	5,108,653	5,261,172	152,519	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8729	-444	upstream	0	1	0	8	20	13	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LYRM4	LYRM4, ISD11, C6orf149, CGI-203	LYR motif containing 4	NM_020408, NM_001164840, NM_001164841, hCT1640219.3, hCT2250900.0, hCT2250901.0	218581_s_at, 222872_at	NP_065141.3, NP_001158312.1, NP_001158313.1, EAW55176.1, EAW55177.1, EAW55178.1
GeneID.10667	FARS2	6	5,261,584	5,771,816	510,232	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8729	32	in gene	0	1	0	8	20	13	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene FARS2	HSPC320, PheRS, FARS1, dJ520B18.2, FARS2	phenylalanyl-tRNA synthetase 2, mitochondrial	NM_006567, hCT2250616.0	204282_s_at, 204283_at, 215414_at	NP_006558.1, EAW55179.1
GeneID.6745	SSR1	6	7,281,283	7,313,541	32,258	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8730	218	in gene	0	1	0	14	14	11	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene SSR1	SSR1, FLJ93042, DKFZp781N23103, FLJ22100, TRAPA, FLJ14232, FLJ78242, FLJ23034	signal sequence receptor, alpha	NM_003144, hCT2254020.0, hCT2254021.0, hCT2254022.0	200889_s_at, 200890_s_at, 200891_s_at, 201894_s_at, 225435_at	NP_003135.2, EAW55204.1, EAW55202.1, EAW55203.1
GeneID.100505680	LOC100505680	6	7,540,684	7,543,149	2,465	-	1	4_A375_EGR1..1..8985	941	in gene	0	0	1	4	8	13	1	4_A375_EGR1..1	13	Gene LOC100505680		hypothetical LOC100505680	XR_112633, XR_112632, XR_108655, XR_108654, XR_113630, XR_113629		
GeneID.1832	DSP	6	7,541,870	7,586,946	45,076	+	1	4_A375_EGR1..1..8985	336	in gene	0	0	1	4	8	13	1	4_A375_EGR1..1	13	Gene DSP	DPI, DPII, DSP	desmoplakin	NM_004415, NM_001008844, hCT5698.2	200606_at	NP_004406.2, NP_001008844.1, EAW55215.1
GeneID.347744	C6orf52	6	10,671,651	10,695,030	23,379	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4680	54	in gene	1	0	0	14	10	10	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene C6orf52	C6orf52	chromosome 6 open reading frame 52	NM_001145020, NR_026736, NR_026737	236504_x_at, 239417_x_at, 243943_x_at	NP_001138492.1
GeneID.55003	PAK1IP1	6	10,695,188	10,709,972	14,784	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4680	-212	upstream	1	0	0	14	10	10	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene PAK1IP1	PIP1, FLJ20624, RP11-421M1.5, WDR84, PAK1IP1, hPIP1, MAK11, bA421M1.5	PAK1 interacting protein 1	NM_017906, hCT1816839.1, hCT1954768.1, hCT1983392.1, hCT2352910.0	218886_at	NP_060376.2, EAW55267.1, EAW55268.1, EAW55269.1, EAW55270.1
GeneID.51522	TMEM14C	6	10,723,148	10,731,362	8,214	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4681, 2_A375_pNL97_plus_lncRNA_AR..1..8731	20, -26	in gene, upstream	1	1	0	22	21	4	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene TMEM14C	HSPC194, bA421M1.6, C6orf53, MSTP073, NET26, TMEM14C	transmembrane protein 14C	NM_016462, NM_001165258, hCT1821900.2, hCT1954767.1, hCT1983391.1, hCT2251174.0, hCT2251177.0	223105_s_at	NP_057546.1, NP_001158730.1, EAW55271.1, EAW55272.1, EAW55274.1, EAW55275.1, EAW55273.1
GeneID.100506379	LOC100506379	6	10,743,557	10,747,896	4,339	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4682, 2_A375_pNL97_plus_lncRNA_AR..1..8732	104, 66	in gene, in gene	1	1	0	16	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100506379		hypothetical LOC100506379	XR_112617, XR_112616, XR_108672, XR_108671, XR_113638, XR_113637		
GeneID.81853	TMEM14B	6	10,747,995	10,757,214	9,219	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4682, 2_A375_pNL97_plus_lncRNA_AR..1..8732	-203, -187	upstream, upstream	1	1	0	16	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TMEM14B	FLJ60466, TMEM14B, MGC1223	transmembrane protein 14B	NM_030969, NM_001127711, hCT1821899.2, hCT1983387.1, hCT1983388.1, hCT1983389.1, hCT1983390.1, hCT2251182.0	221452_s_at, 223133_at	NP_112231.3, NP_001121183.1, EAW55276.1, EAW55278.1, EAW55280.1, EAW55281.1, EAW55277.1, EAW55279.1
GeneID.9247	GCM2	6	10,873,456	10,882,098	8,642	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4683, 2_A375_pNL97_plus_lncRNA_AR..1..8733	-5166, -5166	upstream, upstream	1	1	0	36	33	6	1	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene GCM2	GCM2, GCMB, hGCMb	glial cells missing homolog 2 (Drosophila)	NM_004752, hCT27966.3	220799_at	NP_004743.1, EAW55287.1
GeneID.221711	SYCP2L	6	10,887,064	10,974,542	87,478	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4683, 2_A375_pNL97_plus_lncRNA_AR..1..8733	200, 200	in gene, in gene	1	1	0	36	33	6	1	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene SYCP2L	NO145, C6orf177, SYCP2L, dJ82D2.1	synaptonemal complex protein 2-like	NM_001040274, hCT1815433.1	236337_at	NP_001035364.2, EAW55288.1
GeneID.221710	LOC221710	6	11,094,266	11,138,971	44,705	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4684, 1_A375_pNL7_minus_lncRNA_AR..1..4685, 2_A375_pNL97_plus_lncRNA_AR..1..8734, 2_A375_pNL97_plus_lncRNA_AR..1..8735	-250, 49894, -56, 49862	upstream, downstream, upstream, downstream	1	1	0	25	22	7	2	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene LOC221710		hypothetical protein LOC221710	NM_001135575	1564651_at, 227124_at, 235707_at	NP_001129047.1
GeneID.405754	HERV-FRD	6	11,102,722	11,112,071	9,349	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4684, 2_A375_pNL97_plus_lncRNA_AR..1..8734	18055, 17883	downstream, downstream	1	1	0	18	17	12	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene HERV-FRD	FLJ41944, HERV-FRD, UNQ6191, GLLL6191, FLJ90611, MGC87565	HERV-FRD provirus ancestral Env polyprotein	NM_207582	1555680_at	NP_997465.1
GeneID.4739	NEDD9	6	11,183,531	11,382,581	199,050	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4686	175061	in gene	1	0	0	17	12	4	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene NEDD9	dJ761I2.1, dJ49G10.2, NEDD9, CASL, CASS2, CAS2, CAS-L, HEF1	neural precursor cell expressed, developmentally down-regulated 9	NM_182966, NM_006403, NM_001142393, hCT1956286.1, hCT1956288.1, hCT2251366.0, hCT2352914.0, hCT27987.1	1569020_at, 202149_at, 202150_s_at	NP_892011.2, NP_006394.1, NP_001135865.1, EAW55299.1, EAW55300.1, EAW55302.1, EAW55301.1, EAW55303.1
GeneID.100506431	LOC100506431	6	11,196,541	11,199,708	1,167	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4686	-7612	upstream	1	0	0	17	12	4	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene LOC100506431		B2 RNA	XR_108674		
GeneID.100113407	TMEM170B	6	11,538,511	11,583,757	45,246	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4687, 2_A375_pNL97_plus_lncRNA_AR..1..8736	-2383, -2415	upstream, upstream	1	1	0	18	23	1	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene TMEM170B	TMEM170B	transmembrane protein 170B	NM_001100629		NP_001094299.1
GeneID.51256	TBC1D7	6	13,305,183	13,328,787	23,604	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8738	19	in gene	0	1	0	9	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TBC1D7	TBC7, TBC1D7, FLJ32666, dJ257A7.3, PIG51, DKFZp686N2317	TBC1 domain family, member 7	NM_001143966, NM_001143964, NM_001143965, NM_016495, hCT1956296.1, hCT1966053.1, hCT1966054.1, hCT2251655.0, hCT28654.3	1563839_at, 223461_at	NP_001137438.1, NP_001137436.1, NP_001137437.1, NP_057579.1, EAW55323.1, EAW55326.1, EAW55324.1, EAW55325.1, EAW55327.1
GeneID.23408	SIRT5	6	13,574,792	13,614,790	39,998	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4688, 2_A375_pNL97_plus_lncRNA_AR..1..8739, 2_A375_pNL97_plus_lncRNA_AR..1..8740, 4_A375_EGR1..1..8988	40726, 566, 40744, 168	downstream, in gene, downstream, in gene	1	1	1	31.67	32.33	11.33	3	1_A375_pNL7_minus_lncRNA_AR..1	77	Gene SIRT5	SIR2L5, FLJ36950, SIRT5	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	NM_012241, NM_031244, NM_001193267, hCT1954773.2, hCT1966050.1, hCT1966051.1, hCT1966052.0, hCT2251419.0, hCT2251420.0, hCT28652.3	1569938_at, 219185_at, 221010_s_at	NP_036373.1, NP_112534.1, NP_001180196.1, EAW55333.1, EAW55335.1, EAW55336.1, EAW55332.1, EAW55334.1, EAW55338.1, EAW55337.1
GeneID.51406	NOL7	6	13,615,559	13,621,127	5,568	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4688, 2_A375_pNL97_plus_lncRNA_AR..1..8740	-39, -23	upstream, upstream	1	1	0	77	76	16	1	1_A375_pNL7_minus_lncRNA_AR..1	77	Gene NOL7	MGC71933, dJ223E5.2, C6orf90, NOL7, RARG-1, PQBP3	nucleolar protein 7, 27kDa	NM_016167, hCT2251427.0, hCT28650.2	202882_x_at, 210097_s_at, 213838_at	NP_057251.2, EAW55339.1, EAW55340.1
GeneID.10048	RANBP9	6	13,621,730	13,711,796	90,066	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4688, 1_A375_pNL7_minus_lncRNA_AR..1..4689, 2_A375_pNL97_plus_lncRNA_AR..1..8740	96276, -620, 96260	downstream, upstream, downstream	1	1	0	47	43.5	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	77	Gene RANBP9	RANBPM, RANBP9, BPM90, BPM-L, RanBP7	RAN binding protein 9	NM_005493, hCT1961876.1, hCT1961877.1, hCT2251642.0, hCT2352912.0, hCT27985.4	202582_s_at, 202583_s_at, 216125_s_at	NP_005484.2, EAW55344.1, EAW55341.1, EAW55342.1, EAW55343.1, EAW55345.1
GeneID.3720	JARID2	6	15,246,527	15,522,253	275,726	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4691, 2_A375_pNL97_plus_lncRNA_AR..1..8741	-511, -575	upstream, upstream	1	1	0	24	21	3	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene JARID2	JMJ, JARID2	jumonji, AT rich interactive domain 2	NM_004973, hCT1954770.1, hCT2251275.0	203297_s_at, 203298_s_at	NP_004964.2, EAW55357.1, EAW55358.1
GeneID.100506681	LOC100506681	6	15,248,048	15,248,887	839	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4691, 2_A375_pNL97_plus_lncRNA_AR..1..8741	2871, 2935	downstream, downstream	1	1	0	24	21	3	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene LOC100506681		hypothetical LOC100506681	XR_108680, XR_113645		
GeneID.84062	DTNBP1	6	15,523,032	15,663,289	140,257	-	1	4_A375_EGR1..1..8989	265	in gene	0	0	1	10	6	12	1	4_A375_EGR1..1	12	Gene DTNBP1	SDY, MGC20210, FLJ30031, DKFZp564K192, DTNBP1, DBND, HPS7, My031	dystrobrevin binding protein 1	NM_032122, NM_183040, NR_036448, hCT1958391.2, hCT1958392.2, hCT1966045.1, hCT2352936.0, hCT2352937.0, hCT28365.3	223445_at, 223446_s_at, 223763_at	NP_115498.2, NP_898861.1, EAW55359.1, EAW55360.1, EAW55361.1, EAW55364.1, EAW55362.1, EAW55363.1
GeneID.6310	ATXN1	6	16,299,343	16,761,721	462,378	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4693, 1_A375_pNL7_minus_lncRNA_AR..1..4694, 1_A375_pNL7_minus_lncRNA_AR..1..4695, 2_A375_pNL97_plus_lncRNA_AR..1..8742, 2_A375_pNL97_plus_lncRNA_AR..1..8743	426633, 79737, -4871, 426633, 79601	in gene, in gene, upstream, in gene, in gene	1	1	0	14.67	13.67	4	3	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ATXN1	D6S504E, ATX1, SCA1, ATXN1	ataxin 1	NM_000332, NM_001128164, hCT1983398.1, hCT1983399.1, hCT2251554.0, hCT2352907.0, hCT27979.4	1559249_at, 203231_s_at, 203232_s_at, 230507_at, 242230_at	NP_000323.2, NP_001121636.1, EAW55370.1, EAW55371.1, EAW55372.1, EAW55373.1, EAW55374.1
GeneID.9972	NUP153	6	17,615,269	17,706,818	91,549	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8744	-302	upstream	0	1	0	16	26	8	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene NUP153	NUP153, HNUP153, N153	nucleoporin 153kDa	NM_005124, hCT2252377.0, hCT28538.2	1559084_at, 202097_at, 239946_at	NP_005115.2, EAW55385.1, EAW55384.1
GeneID.63971	KIF13A	6	17,760,585	17,987,799	227,214	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8745	79839	in gene	0	1	0	11	20	5	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene KIF13A	FLJ27232, bA500C11.2, KIF13A	kinesin family member 13A	NM_022113, NM_001105566, NM_001105567, NM_001105568, hCT2252370.0, hCT2252371.0, hCT2252372.0, hCT2252373.0, hCT2252374.0	220777_at, 223520_s_at, 230990_at, 232637_at	NP_071396.4, NP_001099036.1, NP_001099037.1, NP_001099038.1, EAW55389.1, EAW55391.1, EAW55387.1, EAW55388.1, EAW55390.1
GeneID.378884	NHLRC1	6	18,120,718	18,122,851	2,133	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4696	35	in gene	1	0	0	14	12	3	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene NHLRC1	EPM2A, MGC119262, MALIN, NHLRC1, MGC119265, bA204B7.2, EPM2B, MGC119264	NHL repeat containing 1	NM_198586, hCT2345217.0		NP_940988.2, EAW55392.1
GeneID.7172	TPMT	6	18,128,542	18,155,374	26,832	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4696	32556	downstream	1	0	0	14	12	3	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene TPMT	TPMT	thiopurine S-methyltransferase	NM_000367, hCT1828356.3, hCT2251477.1, hCT2251478.1, hCT2343408.0, hCT2343409.0, hCT2343410.0, hCT2343411.0	203671_at, 203672_x_at, 236272_at	NP_000358.1, EAW55396.1, EAW55393.1, EAW55395.1, EAW55397.1, EAW55398.1, EAW55394.1, EAW55399.1
GeneID.54901	CDKAL1	6	20,534,688	21,232,635	697,947	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4698, 1_A375_pNL7_minus_lncRNA_AR..1..4699, 2_A375_pNL97_plus_lncRNA_AR..1..8747, 1_A375_pNL7_minus_lncRNA_AR..1..4700	-64, 343184, 343072, 488112	upstream, in gene, in gene, in gene	1	1	0	15.67	13	2.5	3	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene CDKAL1	FLJ20342, FLJ46705, MGC75469, CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	NM_017774, hCT1956010.1, hCT2251813.0, hCT2352922.0	214877_at, 220039_s_at	NP_060244.2, EAW55426.1, EAW55425.1, EAW55427.1

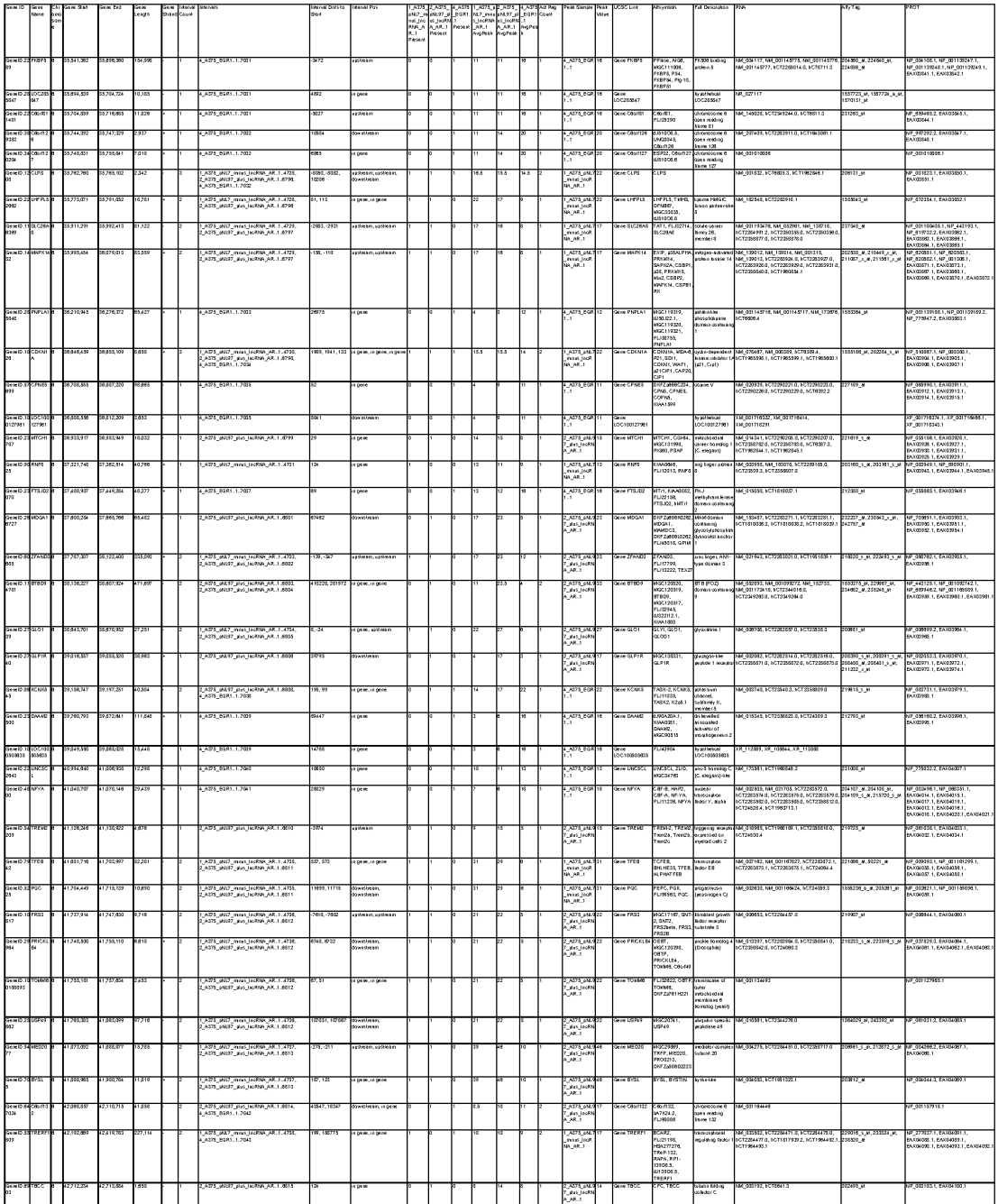




Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_uhl27_mrna_lncRNA_AR_1 Present	2_A375_uhl27_plus_lncRNA_AR_1 Present	4_A375_EGR1_AR_1 Present	1_A375_uhl27_mrna_lncRNA_AR_1 AvgPeak	2_A375_uhl27_plus_lncRNA_AR_1 AvgPeak	4_A375_EGR1_AR_1 AvgPeak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
GeneID:8339	HIST1H2BG	6	26,216,426	26,216,972	444	-	1	1_A375_uhl27_mrna_lncRNA_AR_1:-4706	-3984	upstream	1	0	0	15	13	2	1	1_A375_uhl27_mrna_lncRNA_AR_1	15	Gene HIST1H2BG	D2C1C1E2, H2BFA, H2BFA, H2BFA, H2BFB, HIST1H2BE, H2BJ, HIST1H2BI, HIST1H2BF, H2Bg, H2BI, HIST1H2BC, HIST1H2BG, H2BH	histone cluster 1, H2bg	NM_003518, XCT1961112.1	2144459_at	NP_003509.1, EAW65348.1
GeneID:3852	HIST1H2AE	6	26,217,146	26,217,711	566	+	1	1_A375_uhl27_mrna_lncRNA_AR_1:-4706	3366	downstream	1	0	0	15	13	2	1	1_A375_uhl27_mrna_lncRNA_AR_1	15	Gene HIST1H2AE	H2A.1, H2A.2, H2A.3, H2A.I, H2AFA, H2AFA, H2AFA, HIST1H2AE	histone cluster 1, H2ae	NM_021052, XCT1961111.1	2144459_at	NP_066390.1, EAW65348.1
GeneID:3230	HIST1H1E	6	26,225,365	26,225,944	581	+	1	1_A375_uhl27_mrna_lncRNA_AR_1:-4706	-4967	upstream	1	0	0	15	13	2	1	1_A375_uhl27_mrna_lncRNA_AR_1	15	Gene HIST1H1E	HIST1H1D, H1F3, H1.3, HIST1H1E, H1.4, HIST1H1B, H1.5, HIST1H1C, H1.2, HIST1H1A, H1.1, HIST1H1D, H1.3, HIST1H1B, H1.5, HIST1H1C, H1.2, HIST1H1A, H1.1	histone cluster 1, H1e	NM_005322	2146818_at	NP_005525.1
GeneID:3387	HIST1H1D	6	26,234,440	26,235,216	776	-	1	2_A375_uhl27_plus_lncRNA_AR_1:-5736	-5488	upstream	0	1	0	12	15	10	1	2_A375_uhl27_plus_lncRNA_AR_1	15	Gene HIST1H1D	H1F3, H1.3, HIST1H1D, MGC130178, H1D	histone cluster 1, H1d	NM_005320, XCT1967048.1	2143527_at	NP_005311.1, EAW65348.1
GeneID:3385	HIST1H1C	6	26,240,694	26,241,021	327	+	1	2_A375_uhl27_plus_lncRNA_AR_1:-5736	50	ex gene	0	1	0	12	15	10	1	2_A375_uhl27_plus_lncRNA_AR_1	15	Gene HIST1H1C	HIST1H1D, HIST1H1A, H1.1, HIST1H1E, HIST1H1B, H1.5, HIST2H1A, HIST2H1B, HIST1H1A, H1.1, HIST1H1C, H1.2, HIST1H1B, H1.5, HIST1H1E, H1.4, HIST1H1D, H1.3, HIST2H1A, HIST2H1B	histone cluster 1, H1c	NM_005340, XCT1961911.1	2000229_at	NP_005331.1, EAW65349.1
GeneID:3388	HIST1H1T	6	26,246,639	26,247,205	566	-	1	2_A375_uhl27_plus_lncRNA_AR_1:-5736	6301	downstream	0	1	0	12	15	10	1	2_A375_uhl27_plus_lncRNA_AR_1	15	Gene HIST1H1T	H1.6, HIST1H1T, H1.6	histone cluster 1, H1g	NM_005327, XCT1961910.1	2105501_at	NP_005318.1, EAW65350.1
GeneID:3387	HIST1H1B	6	26,250,370	26,250,835	465	-	1	2_A375_uhl27_plus_lncRNA_AR_1:-5736	10131	downstream	0	1	0	12	15	10	1	2_A375_uhl27_plus_lncRNA_AR_1	15	Gene HIST1H1B	HIST1H2D, H2d, HIST1H1B, H1.5, HIST1H2G, HIST1H2B, HIST1H3, HIST1H3H, HIST1H2J, HIST1H2A, HIST1H2F, HIST1H1C	histone cluster 1, H1d	NM_021058, XCT1961908.1	2105706_at	NP_066266.1, EAW65351.1
GeneID:3385	HIST1H1C	6	26,271,146	26,271,612	466	-	1	4_A375_EGR1_1.8997	235	ex gene	0	0	1	10	9	13	1	4_A375_EGR1_1.1	13	Gene HIST1H2G	HIST1H2D, HIST1H1B, H1.5, HIST1H2G, HIST1H2B, HIST1H3, HIST1H3H, HIST1H2J, HIST1H2A, HIST1H2F, HIST1H1C	histone cluster 1, H2g	NM_003534, XCT1961908.2	2105498_s_at	NP_003525.1, EAW65353.1
GeneID:3389	HIST1H2BN	6	26,273,304	26,273,940	636	+	1	4_A375_EGR1_1.8997	-1612	upstream	0	0	1	10	9	13	1	4_A375_EGR1_1.1	13	Gene HIST1H2BN	H2BH, H2Bb, HIST1H2BE, H2BFS, H2BFP, HIST1H2BI, HIST1H2BF, H2Bg, H2BI, HIST1H2BC, HIST1H2BG, H2BN	histone cluster 1, H2b	NM_003533, XCT1961907.2	2105523_r_at	NP_003516.1, EAW65354.1
GeneID:1001 93007035	LOC100507023	6	26,281,276	26,283,763	2,488	-	2	2_A375_uhl27_plus_lncRNA_AR_1:-5739, 4_A375_EGR1_1.8997	242, 14371	ex gene, downstream	0	1	1	11.5	12	11	2	2_A375_uhl27_plus_lncRNA_AR_1	19	Gene LOC100507023		hypothetical LOC100507023	XR_112829, XR_139897, XR_111531			
GeneID:3387	HIST1H1H	6	26,285,354	26,285,727	373	+	1	2_A375_uhl27_plus_lncRNA_AR_1:-5739	207	ex gene	0	1	0	12	19	8	1	2_A375_uhl27_plus_lncRNA_AR_1	19	Gene HIST1H1H	HIST1H2D, HIST1H1I, HIST1H1E, HIST1H2I, HIST1H2A, HIST2H2A, HIST2H2B, HIST1H1A, HIST1H1L, HIST1H1J, HAI3, HIST1H1C, HIST4H4, HIST1H2J, HAF1, HIST1H1T, HIST1H1H	histone cluster 1, h1h	NM_005343, XCT1961108.3, XCT2252992.0	2000150_s_at, 2031511_at, 232033_at	NP_005334.1, EAW65356.1, EAW65355.1
GeneID:4599	HCG11	6	26,321,954	26,327,821	5,867	+	2	2_A375_uhl27_plus_lncRNA_AR_1:-5760, 4_A375_EGR1_1.8999	532, 18026	ex gene, downstream	0	1	1	13	16	11.5	2	4_A375_EGR1_1.1	16	Gene HCG11	HCG11, bA134P9.3, FLJ14049, FLJ90337	HLA complex group 11	NR_026790	1557167_at, 1557168_x_at	
GeneID:1766 473	HIST2H2AA3	6	26,335,572	26,347,165	11,593	+	3	2_A375_uhl27_plus_lncRNA_AR_1:-5761, 3_A375_uhl27_plus_lncRNA_AR_1:-5762, 4_A375_EGR1_1.8999	140, 13544, -612	upstream, downstream, upstream	0	1	1	11.5	16	12.3	2	4_A375_EGR1_1.1	16	Gene HIST2H2A	HIST2H2A, MGC3045, NIRC, HIST2L1	high mobility group nucleosomal binding domain 4	NM_030533, XCT1961107.4, XCT1963176.2, XCT2345930.0, XCT2345931.0, XCT2345932.0	232570_x_at, 207058_at, 209787_s_at	NP_109844.1, EAW65357.1, EAW65358.1, EAW65359.1, EAW65360.1, EAW65390.1
GeneID:3387	HIST1H1B	6	27,100,095	27,100,978	883	-	1	4_A375_EGR1_1.7900	-6939	upstream	0	0	1	8	13	16	1	4_A375_EGR1_1.1	16	Gene HIST1H2BJ	H2BFR, H2Bv, HIST1H2BJ	histone cluster 1, H2bj	NM_021058, XCT1961599.3, XCT2291734.0, XCT2300131.0	2147502_at	NP_066402.2, EAW65360.1, EAW65361.1, EAW65362.1
GeneID:3390	HIST1H2AG	6	27,100,617	27,103,071	2,254	+	1	4_A375_EGR1_1.7900	6447	downstream	0	0	1	8	13	16	1	4_A375_EGR1_1.1	16	Gene HIST1H2AG	H2AFX, HIST1H2AM, HDAV, pHDV1, HIST1H2AV, HDA1b, HIST1H2AG, H2AFZ	histone cluster 1, H2ag	NM_021084, XCT1961598.3	2207158_at	NP_066408.1, EAW65363.1
GeneID:3389	HIST1H2BK	6	27,106,072	27,114,827	8,755	-	1	4_A375_EGR1_1.7900	7203	ex gene	0	0	1	8	13	16	1	4_A375_EGR1_1.1	16	Gene HIST1H2BK	H2BFAm, MGC131899, H2BFT, HIST1H2BK	histone cluster 1, H2bk	NM_080593, XCT2291731.1, XCT2291732.1	2209608_at	NP_542165.1, EAW65365.1, EAX03094.1
GeneID:3391	HIST1H1T	6	27,107,855	27,107,457	599	+	1	4_A375_EGR1_1.7900	178	ex gene	0	0	1	8	13	16	1	4_A375_EGR1_1.1	16	Gene HIST1H1I	HIST1H2D, HIST1H1I, HIST1H1E, HIST1H1T, HAF4, HIST2H1A, HIST2H2B, HIST1H1A, HIST1H1L, HIST1H1J, HAI4, HIST1H1C, HIST4H4, HIST1H2J, HAF1, HIST1H1T, HIST1H1H	histone cluster 1, h1i	NM_005435, XCT1962211.3	2144824_at	NP_005426.1, EAX03099.1
GeneID:3392	HIST1H1H	6	27,114,908	27,115,394	486	+	1	4_A375_EGR1_1.7900	7644	upstream	0	0	1	8	13	16	1	4_A375_EGR1_1.1	16	Gene HIST1H2AH	H2AFA1c, HIST1H2AH, HDAS, MGC171151, MGC171.1	histone cluster 1, H2ah	NM_003509, XCT1961948.2		NP_542182.1, EAX03097.1
GeneID:1016 3420934	MIR5143	6	27,115,403	27,115,487	85	+	1	4_A375_EGR1_1.7900	-8141	upstream	0	0	1	8	13	16	1	4_A375_EGR1_1.1	16	Gene MIR5143	MIR5143	microRNA 5143	NR_039796		
GeneID:3393	HIST1H1I	6	27,790,932	27,790,305	553	-	1	2_A375_uhl27_plus_lncRNA_AR_1:-5785	-5763	upstream	0	1	0	13	23	8	1	2_A375_uhl27_plus_lncRNA_AR_1	23	Gene HIST1H1I	HIST1H2D, HIST1H1I, HIST1H1E, HIST1H1T, HAF2n, GTRNADC1, HIST2H1A, HIST2H2B, HAF3, HIST1H1A, HIST1H1L, HIST1H1J, HAI3, HIST1H1C, HIST4H4, HIST1H2J, HAF1, HIST1H1T, HIST1H1H	histone cluster 1, h1i	NM_005541, XCT1761243.5	2005600_s_at, 2144953_x_at	NP_005532.1, EAX03112.1
GeneID:3391	HIST1H1H	6	27,805,828	27,806,124	296	-	1	2_A375_uhl27_plus_lncRNA_AR_1:-5785	1038	downstream	0	1	0	13	23	8	1	2_A375_uhl27_plus_lncRNA_AR_1	23	Gene HIST1H2AJ	HIST1H2AJ, HDAT3, HIST1H2AM, HIST1H2AL, HIST1H2AH, HDA2, HIST1H2AG	histone cluster 1, H2aj	NM_003510, XCT1963551.3	2144844_at, 2390411_at	NP_003501.1, EAX03113.1
GeneID:3395	HIST1H2BH	6	27,806,364	27,806,894	530	+	1	2_A375_uhl27_plus_lncRNA_AR_1:-5785	-1276	upstream	0	1	0	13	23	8	1	2_A375_uhl27_plus_lncRNA_AR_1	23	Gene HIST1H2BH	H2BG, MGC124414, H2BFD, MGC8355, MGC132413, HIST1H3I, MGC132416, HIST1H2BH	histone cluster 1, H2bh	NM_003520, XCT1761242.2, XCT1963615.2, XCT2351594.1, XCT2351595.1	2207226_at	NP_003511.1, EAX03116.1, EAX03114.1, EAX03115.1, EAX03117.1
GeneID:3394	HIST1H2AL	6	27,833,197	27,833,678	481	+	1	4_A375_EGR1_1.7902	1741	downstream	0	0	1	4	4	15	1	4_A375_EGR1_1.1	15	Gene HIST1H2AL	H2AFI, HIST1H2AM, HIST1H2AL, HIST1H2AI, HIST1H2AI, MGC138803, H2AB1.2, H2AJ, H2Ar, HIST1H2AL	histone cluster 1, H2al	NM_003511, XCT1761249.2	2143494_at	NP_003502.1, EAX03118.1
GeneID:3396	HIST1H1B	6	27,834,570	27,835,423	853	-	1	4_A375_EGR1_1.7902	677	ex gene	0	0	1	4	4	15	1	4_A375_EGR1_1.1	15	Gene HIST1H1B	MGC126803, H1E, H1.5, MGC126802, H1.5, HIST1H1B	histone cluster 1, H1b	NM_005322, XCT1937231.1	2143524_at	NP_005313.1, EAX03119.1
GeneID:3397	HIST1H1D	6	27,839,425	27,840,099	675	-	1	4_A375_EGR1_1.7902	5251	downstream	0	0	1	4	4	15	1	4_A375_EGR1_1.1	15	Gene HIST1H1D	HIST1H2D, HIST1H1D, H1F, H3/t, HIST1H2G, H2J, HIST1H2B, HIST1H3, HIST1H3H, HIST1H2J, HIST1H2A, HIST1H2F, HIST1H1C	histone cluster 1, H1d	NM_005323, XCT1940590.1	2143509_at	NP_005324.1, EAX03120.1
GeneID:3398	HIST1H1E	6	27,840,938	27,841,269	332	-	1	4_A375_EGR1_1.7902	6441	downstream	0	0	1	4	4	15	1	4_A375_EGR1_1.1	15	Gene HIST1H1E	HIST1H2D, HIST1H1I, HIST1H1E, HIST1H1B, HIST2H1A, HIST2H2B, H4/b, HIST1H1A, HIST1H1L, HIST1H1J, H4.k, HIST1H1C, HIST4H4, H4/m, HIST1H1T, HIST1H1H	histone cluster 1, h1e	NM_005348, XCT1943322.1	2143902_at	NP_005337.1, EAX03121.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_pAS7_mut_lncRNA_R1_1 Percent	2_A375_pAS7_plus_lncRNA_R1_1 Percent	3_A375_pAS7_EGFR1_lncRNA_R1_1 Percent	1_A375_pAS7_plus_lncRNA_R1_1 Avg Peak	2_A375_pAS7_plus_lncRNA_R1_1 Avg Peak	3_A375_pAS7_EGFR1_lncRNA_R1_1 Avg Peak	Ad Tag Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:8366	HIST1H1B	6	27,856,093	27,856,970	877	-	1	1_A375_pAS7_mrna1_lncRNA_R1_1:-4705	-2466	upstream	1	0	0	19	15	9	1	1_A375_pAS7_mrna1_lncRNA_R1_1	19	Gene HIST1H1B	HIST1H1B, HIST1H1, H1B, HISTH1B, HIST1H1B, HIST1H1C, HIST1H1D, HIST1H1E, HIST1H1T, HIST1H1A, HIST1H1C	histone cluster 1, H1b	NM_005325, ICT196355.2	214648_at	NP_005316.1, EAX03122.1
GeneID:8358	HIST1H1A	6	27,860,477	27,860,963	486	-	2	1_A375_pAS7_mrna1_lncRNA_R1_1:-4705, 4_A375_EGR1_1.7002	-90, -9905	upstream, upstream	1	0	1	14.5	12	16	2	4_A375_EGR1_1.1	23	Gene HIST1H2AI	H2AN, H2A.1, H2A/N, HIST1H2AM, HIST1H2AI, HIST1H2AK, HIST1H2AH, HIST1H2AG, bb183812.1	histone cluster 1, H2ai	NM_003514, ICT196359.3	214481_at	NP_003505.1, EAX03123.1
GeneID:8358	HIST1H1E	6	27,861,203	27,861,969	486	+	2	1_A375_pAS7_mrna1_lncRNA_R1_1:-4705, 4_A375_EGR1_1.7002	-147, 9965	upstream, downstream	1	0	1	14.5	12	16	2	4_A375_EGR1_1.1	23	Gene HIST1H2BC	MGC119808, HIST1H2BO, H2Be, H2B.2, bb183812.2, H2BFN	histone cluster 1, H2bc	NM_003537, ICT2351376.1	214540_at	NP_003518.2, EAX03124.1
GeneID:8355	OR2B2	11	27,876,963	27,880,174	3,211	-	1	4_A375_EGR1_1.7003	9436	downstream	0	0	1	10	9	23	1	4_A375_EGR1_1.1	23	Gene OR2B2	bb183812.4, OR2B2U, OR6-1, bb1811-10, OR2B6, OR2B2	olfactory receptor, family 2, subfamily B, member 2	NM_033357, ICT196370.2	216408_at	NP_149948.2, EAX03125.1
GeneID:1050724	LOC100507241	9	28,048,970	28,048,997	2,357	+	1	1_A375_pAS7_mrna1_lncRNA_R1_1:-4709	283	sv gene	1	0	0	15	12	9	1	1_A375_pAS7_mrna1_lncRNA_R1_1	15	Gene LOC100507241	hypothetical LOC100507241	XR_112563, XR_108959, XR_113581			
GeneID:7716	ZNF169	9	28,048,482	28,057,341	8,859	+	1	1_A375_pAS7_mrna1_lncRNA_R1_1:-4709	222	sv gene	1	0	0	15	12	9	1	1_A375_pAS7_mrna1_lncRNA_R1_1	15	Gene ZNF169	CTG5, ZNF169, ZSCAN7, LD86	zinc finger protein 169	NM_030447, ICT23807.3	206803_at	NP_030438.1, EAX03151.1
GeneID:1012919	LOC100129195	10	28,056,356	28,103,071	46,715	-	4	1_A375_pAS7_mrna1_lncRNA_R1_1:-4709, 1_A375_pAS7_mrna1_lncRNA_R1_1:-4710, 2_A375_pAS7_plus_lncRNA_R1_1:8795, 2_A375_pAS7_plus_lncRNA_R1_1:8797	58587, -4625, 12855, -4529	downstream, upstream, sv gene, upstream	1	1	0	13	16	6	2	1_A375_pAS7_mrna1_lncRNA_R1_1	19	Gene LOC100129195	FLJ90227	hypothetical LOC100129195	XR_112971, XR_108954, XR_113582		
GeneID:8845	ZSCAN18	18	28,092,307	28,097,857	5,670	+	1	2_A375_pAS7_plus_lncRNA_R1_1:8788	29	sv gene	0	1	0	11	16	9	1	2_A375_pAS7_plus_lncRNA_R1_1	16	Gene ZSCAN18	ZSCAN18, ZNF382, ZNF433, FLJ23141, bb0693.24.3	zinc finger and SCAN domain containing 18	NM_022331, ICT196359.2	219876_at	NP_376937.1, EAX03154.1
GeneID:7752	ZNF192	6	28,109,716	28,125,256	15,520	+	2	1_A375_pAS7_mrna1_lncRNA_R1_1:-4710, 2_A375_pAS7_plus_lncRNA_R1_1:8787	-25, -116	upstream, upstream	1	1	0	19	16	8	1	1_A375_pAS7_mrna1_lncRNA_R1_1	19	Gene ZNF192	ZNF192, LD51-2, ZSCAN46	zinc finger protein 192	NM_006298, ICT23808.2, ICT2251900.0	206879_at	NP_006289.2, EAX03153.1, EAX03156.1
GeneID:8420	ZNF223	19	28,292,914	28,324,946	31,334	-	1	2_A375_pAS7_plus_lncRNA_R1_1:8788	272	sv gene	0	1	0	8	14	8	1	2_A375_pAS7_plus_lncRNA_R1_1	14	Gene ZNF223	bb1474c20.2, ZNF223, FLJ25497, ZNF190P, ZNF22-like	zinc finger protein 223	NM_145909, NM_001135813, NM_001135816, NM_030999, NR_024164, NR_024165, ICT1800796.2, ICT1800772.2, ICT1954682.1, ICT2305580.0, ICT2305599.0	2220016_s_at	NP_668918.1, NP_001128687.1, NP_001128688.1, NP_112161.3, EAX03153.1, EAX03154.1, EAX03155.1, EAX03156.1
GeneID:8839	ZKSCAN3	6	28,317,891	28,334,324	16,433	+	1	2_A375_pAS7_plus_lncRNA_R1_1:8788	6083	sv gene	0	1	0	8	14	6	1	2_A375_pAS7_plus_lncRNA_R1_1	14	Gene ZKSCAN3	FLJ33998, ZNF398, ZFP398, ZNSCAN6, ZFA7, bb1474c20.1, KIAA0629, ZSCAN13, ZNF309, ZNA7, bb1474c20.1	zinc finger with KRAB and SCAN domains 3	NM_024493, ICT229809.3, ICT2358727.0	1982393_at, 1982308_x_at, 211773_s_at	NP_079119.2, EAX03158.1, EAX03187.1
GeneID:1011542	SCAND3	6	28,539,497	28,555,112	15,765	-	2	2_A375_pAS7_plus_lncRNA_R1_1:8789, 4_A375_EGR1_1.7006	-72, -10058	sv gene, upstream	0	1	1	7	15	12	2	2_A375_pAS7_plus_lncRNA_R1_1	16	Gene SCAND3	ZNF452, MGC131702, ZNF309P2, FLJ12087, DKFZp434N092, MGC133311, SCAND3, ZFP35-L, KIAA1923, MGC133312, bb1186N24.3	SCAN domain containing 3	NM_032923, ICT2292038.1	244758_at	NP_443155.1, EAX03170.1
GeneID:8939	LOC401242	20	28,627,482	28,631,454	3,952	-	2	2_A375_pAS7_plus_lncRNA_R1_1:8791, 4_A375_EGR1_1.7007	-2994, 14	upstream, sv gene	0	1	1	7.5	12	12.5	2	4_A375_EGR1_1.1	16	Gene LOC401242		hypothetical LOC401242	NR_033379			
GeneID:8368	RFS-DT7H4	9	29,894,376	29,716,626	22,446	-	1	4_A375_EGR1_1.7009	330	sv gene	0	0	1	9	13	14	1	4_A375_EGR1_1.1	14	Gene RFS-DT7H4	LOC285830, FLJ38429	hypothetical LOC285830	NR_038972, NR_038973, ICT2300369.0	1582351_at, 222279_at	EAX03226.1
GeneID:7719	TRIM28	19	30,152,232	30,181,153	28,921	-	1	4_A375_EGR1_1.7011	161	sv gene	0	0	1	6	9	16	1	4_A375_EGR1_1.1	16	Gene TRIM28	ZNF175, TRIM28, KAP1, RNF95	tripartite motif containing 28	NM_005449, ICT1480.5, ICT2294320.1, ICT2294023.1, ICT2294025.1, ICT2351954.0	1559967_s_at, 202702_at, 202975_s_at, 242916_at, 242912_at	NP_005440.1, EAX03272.1, EAX03274.1, EAX03275.1, EAX03276.1
GeneID:4777	HCG15	19	30,255,174	30,294,927	39,755	-	2	2_A375_pAS7_plus_lncRNA_R1_1:8772, 4_A375_EGR1_1.7012	-129, 387	upstream, sv gene	0	1	1	7.5	13	11.5	2	4_A375_EGR1_1.1	17	Gene HCG15	FLJ10355, FLJ10356, FLJ35550, HCG15	HLA-complex group 15	NR_024052, NR_024053	225577_at, 235554_at	
GeneID:8858	TRIM39	6	30,294,821	30,311,906	16,865	+	2	2_A375_pAS7_plus_lncRNA_R1_1:8772, 4_A375_EGR1_1.7012	435, -61	sv gene, upstream	0	1	1	7.5	13	11.5	2	4_A375_EGR1_1.1	17	Gene TRIM39	RNF23, TFP, MGC32956, D6S200, TRIM39	tripartite motif containing 39	NM_021253, NM_172018, NCT148514, NCT2291539.1, NCT2291980.1, NCT2291981.1	222702_at	NP_067078.2, NP_742012.1, EAX03283.1, EAX03284.1, EAX03285.1, EAX03286.1
GeneID:2731	GNL1	9	30,309,134	30,325,371	16,217	-	1	2_A375_pAS7_plus_lncRNA_R1_1:8774	1115	sv gene	0	0	0	13	22	13	1	2_A375_pAS7_plus_lncRNA_R1_1	22	Gene GNL1	PSR1, GNL1, DKFZp547E126, FLJ27152, DKFZp547B036	guanine nucleotide binding protein-like 1	NM_008275, ICT1771193.2, ICT2294079.0	203307_at, 233844_at	NP_008266.2, EAX03293.1, EAX03294.1
GeneID:5620	PRPS1	X	30,324,499	30,332,473	7,987	+	1	2_A375_pAS7_plus_lncRNA_R1_1:8774	-230	upstream	0	1	0	13	22	13	1	2_A375_pAS7_plus_lncRNA_R1_1	22	Gene PRPS1	PRPS, CAY56, MGC161703, MGC161733	ribose-ph 3	NM_002683, NM_001077497, NCT1713.3, ICT2291370.0	204769_at	NP_379519.3, NP_001070953.1, EAX03297.1, EAX03298.1
GeneID:7369	C6orf153	6	30,394,813	30,814,366	19,553	+	1	4_A375_EGR1_1.7013	20715	downstream	0	0	1	6	10	19	1	4_A375_EGR1_1.1	19	Gene C6orf134	MEC17, FLJ11130, Nbla00457, TAT, DKFZp547J097, C6orf134, ATAT1	alpha tubulin acetyltransferase 1	NM_024939, NM_001031722, NM_001190704, NCT2291503.0, ICT2291503.1, ICT2291504.0, ICT2356786.0, ICT2356789.0	219274_s_at, 225950_at	NP_079193.2, NP_001026892.1, NP_001178951.1, EAX03299.1, EAX03307.1, EAX03308.1, EAX03309.1
GeneID:1545	C6orf153	6	30,814,516	30,820,967	6,371	+	1	4_A375_EGR1_1.7013	512	sv gene	0	0	1	6	10	19	1	4_A375_EGR1_1.1	19	Gene C6orf153	MGC13556, C6orf153	chromosome 6 open reading frame 138	NM_031189032, NM_143629, NM_001161376, ICT2344279.0, ICT2358741.0	227455_at, 227456_s_at	NP_001159436.1, NP_689498.2, NP_001159445.1, EAX03310.1, EAX03311.1
GeneID:8449	DHX16	6	30,820,990	30,840,650	19,934	-	3	1_A375_pAS7_mrna1_lncRNA_R1_1:-4713, 2_A375_pAS7_plus_lncRNA_R1_1:8773, 4_A375_EGR1_1.7013	-99, -2, 23502	upstream, upstream, downstream	1	1	1	20	20	13	2	1_A375_pAS7_mrna1_lncRNA_R1_1	32	Gene DHX16	Prp8, DEP2, PRPF2, DDX16, Dnx16, PRP2, PRO2014	DEAH (Asp-Glu-Ala-His) box polypeptide 16	NM_003587, NM_001164239, ICT2294369.1, ICT2294372.1, ICT2350270.0, ICT2350276.0, ICT1713.0, ICT1609933.2	203964_s_at	NP_003578.2, NP_001157711.1, EAX03312.1, EAX03314.1, EAX03315.1, EAX03317.1, EAX03318.1
GeneID:9939	KIAA1949	9	30,844,166	30,855,872	11,706	-	2	1_A375_pAS7_mrna1_lncRNA_R1_1:-4713, 4_A375_EGR1_1.7013	14744, 14540	downstream, downstream	1	0	1	32	30	7	1	1_A375_pAS7_mrna1_lncRNA_R1_1	32	Gene KIAA1949	HIWIP1099, KIAA1949	KIAA1949	NM_001134870, NM_133471	224927_at	NP_001128421.1, NP_597726.1
GeneID:1011211	FLOT1	9	30,895,511	30,910,453	14,942	-	2	4_A375_EGR1_1.7014, 4_A375_EGR1_1.7015	-267, -1627	upstream, upstream	0	0	1	11.5	10.5	13.5	2	4_A375_EGR1_1.1	17	Gene FLOT1	FLOT1		NM_005803, ICT2294081.0, ICT2294082.0, ICT2294083.0	208745_s_at, 208749_s_at, 210142_s_at, 213819_s_at	NP_005794.1, EAX03329.1, EAX03330.1, EAX03327.1
GeneID:8841	IER3	6	30,710,976	30,712,327	1,351	-	2	4_A375_EGR1_1.7014, 4_A375_EGR1_1.7015	1907, 247	downstream, sv gene	0	0	1	11.5	10.5	13.5	2	4_A375_EGR1_1.1	17	Gene IER3	PRG1, IER-1, IEX1, GLY96, IER3, IER1, IEX-1, GRP2, DP1	immediate early response 3	NM_003897, ICT2294086.0, ICT2294088.0, ICT1710.3	201631_s_at	NP_003888.2, EAX03330.1, EAX03329.1, EAX03331.1
GeneID:7412	DDR1	6	30,851,861	30,867,853	16,072	+	1	2_A375_pAS7_plus_lncRNA_R1_1:8776	23947	downstream	0	1	0	17	24	13	1	2_A375_pAS7_plus_lncRNA_R1_1	24	Gene DDR1	RTK6, NTRK4, PTK3, EDDR1, CD167, PTK3A, DDR1, CAK, NEP, DDR, TRKE, MCK10	discoidin domain receptor tyrosine kinase 1	NM_013993, NM_013994, NM_033954, NCT2291500.0, ICT2291500.2, ICT2291500.3, ICT2291501.0, ICT2291503.0, ICT2291690.0, ICT2356932.0, ICT1711.3, ICT1954732.1, ICT1954731.1, ICT1960332.1	1007_s_at, 207180_s_at, 208779_s_at, 210749_x_at, NP_001945.3, EAX03333.1, EAX03337.1, EAX03340.1, EAX03338.1, EAX03339.1, EAX03341.1, EAX03342.1, EAX03343.1, EAX03344.1, EAX03345.1, EAX03346.1	NP_036890.2, NP_054782.2, NP_001945.3, EAX03333.1, EAX03337.1, EAX03340.1, EAX03338.1, EAX03339.1, EAX03341.1, EAX03342.1, EAX03343.1, EAX03344.1, EAX03345.1, EAX03346.1
GeneID:2967	QTF2H6	9	30,875,977	30,881,660	5,683	+	2	2_A375_pAS7_plus_lncRNA_R1_1:8776, 2_A375_pAS7_plus_lncRNA_R1_1:8777	-169, 8295	upstream, downstream	0	1	0	14	16.5	11	2	2_A375_pAS7_plus_lncRNA_R1_1	24	Gene QTF2H6	QTF2H6, TFIIH, TFB2	general transcription factor IIH, polypeptide 4, 52kDa	NM_031517, ICT1713.2	205577_at	NP_001026.1, EAX03347.1
GeneID:1761	VARS2	6	30,881,962	30,894,209	12,248	+	2	2_A375_pAS7_plus_lncRNA_R1_1:8776, 2_A375_pAS7_plus_lncRNA_R1_1:8777	-8174, 290	upstream, sv gene	0	1	0	14	16.5	11	2	2_A375_pAS7_plus_lncRNA_R1_1	24	Gene VARS2	VARS2L, MGC142165, VARS2, VARSL, MGC19229	valyl-tRNA synthetase 2, mitochondrial (putative)	NM_020442, NM_001167733, NM_001167734, ICT2291618.0, ICT1677782.2	224500_at	NP_065175.4, NP_001161233.1, NP_001161234.1, EAX03348.1, EAX03349.1
GeneID:3135	HLA-C	6	31,236,529	31,239,655	3,326	-	1	4_A375_EGR1_1.7016	350	sv gene	0	0	1	7	9	12	1	4_A375_EGR1_1.1	12	Gene HLA-C	PSORS1C1, FLJ27052, HLA-JVC, HLC-C, HLA-Cw12, HLA-C, D6S204	major histocompatibility complex, class I, C	NM_002117, ICT2358000.0, ICT2358000.0, ICT2358000.0, ICT2358000.1, ICT2358000.2, ICT2358000.3, ICT2358012.0, ICT2358014.0	200812_x_at	NP_002108.4, EAX03376.1, EAX03377.1, EAX03378.1, EAX03380.1, EAX03381.1, EAX03382.1
GeneID:5707438	LOC100507438	18	31,367,581	31,455,566	88,025	+	1	4_A375_EGR1_1.7017	247	sv gene	0	0	1	6	8	16	1	4_A375_EGR1_1.1	16	Gene LOC100507438	PERB11.1, MGC21250, MHC class I polypeptide-related sequence A, FLJ38910, MICA, MGC111007, FLJ96320	MHC class I polypeptide-related sequence A	XM_005116582, XM_005116584, XM_005116585, XM_005116588, XM_005119085, XM_005119087, XM_005119285, XM_005119287, XM_005119290, XM_005119293, XM_005119379, XM_005119377, XM_005119376, XM_005119378, XM_005120312, XM_005120314, XM_005120313		XP_005116639.1, XP_005116612.1, XP_005116611.1, XP_005119134.1, XP_005119136.1, XP_005119135.1, XP_005119139.1, XP_005119138.1, XP_005119332.1, XP_005119327.1, XP_005119422.1, XP_005119423.1, XP_005120313.1, XP_005120962.1,
GeneID:8931	BAT1	6	31,497,996	31,510,223	12,229	-	2	1_A375_pAS7_mrna1_lncRNA_R1_1:-4715, 2_A375_pAS7_plus_lncRNA_R1_1:8779	497, 112	sv gene, sv gene	0	1	0	16	20	9	1	2_A375_pAS7_plus_lncRNA_R1_1	20	Gene BAT1	D6S298, D6S51E, BAT1, UHF96	HLA-B associated transcript 1	NM_004639, NM_004640	200041_s_at, 212355_at	NP_542185.1, NP_004631.1
GeneID:8931	SNORD117	6	31,504,131	31,504,239	109	+	2	1_A375_pAS7_mrna1_lncRNA_R1_1:-4715, 2_A375_pAS7_plus_lncRNA_R1_1:8779	-9382, -9598	upstream, upstream	1	1	0	16	20	9	1	2_A375_pAS7_plus_lncRNA_R1_1	20	Gene SNORD117	SNORD117, U83	small nucleolar RNA, C/D box 117	NR_003140		
GeneID:8931	SNORD99	6	31,505,976	31,506,055	79	-	2	1_A375_pAS7_mrna1_lncRNA_R1_1:-4715, 2_A375_pAS7_plus_lncRNA_R1_1:8779	-772, -1157	upstream, upstream	1	1	0	16	20	9	1	2_A375_pAS7_plus_lncRNA_R1_1	20	Gene SNORD99	SNORD99, U58	small nucleolar RNA, C/D box 99	NR_003085		
GeneID:8355	ATP6V1G2	6	31,512,239	31,514,827	2,589	-	2	1_A375_pAS7_mrna1_lncRNA_R1_1:-4715, 2_A375_pAS7_plus_lncRNA_R1_1:8779	4389, 4515	downstream, downstream	1	1	0	16	20	9	1	2_A375_pAS7_plus_lncRNA_R1_1	20	Gene ATP6V1G2	VMA10, NG38, ATP6V1G2	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2	NM_130463, NM_138282	214762_at	NP_569730.1, NP_612138.1
GeneID:4790	NFKBIL1	6	31,514,838	31,526,808	11,970	+	2	1_A375_pAS7_mrna1_lncRNA_R1_1:-4715, 2_A375_pAS7_plus_lncRNA_R1_1:8779	-4903, -4518	upstream, upstream	1	1	0	16	20	9	1	2_A375_pAS7_plus_lncRNA_R1_1	20	Gene NFKBIL1	NFKBIL1, LST1, IKBL, NFKBIL	leukocyte factor of kappa light polypeptide gene enhancer in B cells-inhibitor-like	NM_030937, NM_001144961, NM_001144962, NM_001144963, NCT2358044.0, NCT1647967.2, NCT1952782.0, NCT1952784.0, NCT1952785.0	209972_x_at	NP_036916.3, NP_001138433.1, NP_001138434.1, NP_001138435.1, EAX03420.1, EAX03421.1, EAX03417.1, EAX03418.1, EAX03419.1
GeneID:8355	APOM	6	31,822,971	31,825,907	2,936	+	1	2_A375_pAS7_plus_lncRNA_R1_1:8780	9945	downstream	0	1	0	8	15	7	1	2_A375_pAS7_plus_lncRNA_R1_1	15	Gene APOM	NG20, APOM, G3a, MGC22495, HSPC036	lipocalin protein M	NM_019101, ICT1558752, ICT1955193.0, ICT1953420.1, ICT1953421.1	203982_s_at, 214910_s_at	NP_061974.2, EAX03463.1, EAX03461.1, EAX03462.1, EAX03464.1
GeneID:5707	C6orf47	6	31,826,075	31,826,949	2,874	+	1	2_A375_pAS7_plus_lncRNA_R1_1:8780	9387	downstream	0	1	0	8	15	7	1	2_A375_pAS7_plus_lncRNA_R1_1	15	Gene C6orf47	G4, D6S316, C6orf47, NG24	chromosome 6 open reading frame 47	NM_021184, ICT2292508.1	204968_at	NP_067037.2, EAX03465.1
GeneID:7916	BAT4	6	31,829,982	31,833,183	3,201	+	1	2_A375_pAS7_plus_lncRNA_R1_1:8780	4182	upstream	0	1	0	8	15	7	1	2_A375_pAS7_plus_lncRNA_R1_1	15	Gene BAT4	GPANK1, D6S2700E, D6S345, G3, HMOX6R, BAT4	HLA-B associated transcript 4	NM_033177, ICT2292507.0, ICT2355997.0, ICT2355997.2, ICT1953435.1, ICT1953439.2	225472_at, 225479_at	NP_149417.1, EAX03470.1, EAX03469.1, EAX03468.1, EAX03471.1
GeneID:1460	CSN2B	6	31,833,687	31,837,643	4,156	+	1	2_A375_pAS7_plus_lncRNA_R1_1:8780	-41	upstream	0	1	0	8	15	7	1	2_A375_pAS7_plus_lncRNA_R1_1	15	Gene CSN2B	MGC150224, CSK2B, CSK2B, CK2N, CK2B, MGC150222, CBA	casein kinase 2, beta polypeptide	NM_001320, ICT2350102, NCT1953442.1, ICT1953444.0, ICT1953444.0	201320_s_at, 201777_at	NP_001311.3, EAX03472.1, EAX03474.1, EAX03475.1
GeneID:8881	LY6G5B	6	31,836,726	31,840,027	3,302	+	1	2_A375_pAS7_plus_lncRNA_R1_1:8780	-1112	upstream	0	1	0	8	15	7	1	2_A375_pAS7_plus_lncRNA_R1_1	15	Gene LY6G5B	G5b, C6orf191, LY6G5B	lymphocyte antigen 6 complex, locus G5B	NM_031221, ICT2350823.2, ICT1953437.1		NP_997044.2, EAX03477.1, EAX03476.1
GeneID:2322	DDAH2	6	31,894,017	31,899,039	5,022	+	1	2_A375_pAS7_plus_lncRNA_R1_1:8781	9565	upstream	0	1	0	10	15	8	1	2_A375_pAS7_plus_lncRNA_R1_1	15	Gene DDAH2	DDAH, DDAH-II, NG30, DDAH2	dimethylarginine dimethylaminohydrolase 2	NM_013974, ICT2354555.0, ICT2358739.0, ICT2358740.0	202362_s_at, 214909_s_at	NP_037906.1, EAX03501.1, EAX03501.1, EAX03502.1
GeneID:1011	CUC1	6	31,898,356	31,904,341	5,983	-	1	2_A375_pAS7_plus_lncRNA_R1_1:8781	3343	upstream	0	1	0	10	15	8	1	2_A375_pAS7_plus_lncRNA_R1_1	15	Gene C1C1	C1C1, G6, NCC27	cytosolic ethanolamine kinase 1	NM_031286, ICT2292474.1, ICT2358726.0, ICT2358730.0	209869_at	NP_001278.2, EAX03504.1, EAX03505.1, EAX03503.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:4439	MSH5	6	31,707,725	31,730,455	22,730	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6761	-141	upstream	0	1	0	10	15	6	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene MSH5	MUTSH5, NG23, DKFZp434C1615, MSH5, G7, MGC2939	mutS homolog 5 (E. coli)	NM_002441, NM_172166, NM_025259, NM_172165, hCT2285764.0, hCT2285765.0, hCT2285767.0, hCT2285769.0, hCT2285771.0, hCT2285773.0, hCT2285774.0, hCT2285776.0, hCT2285778.0, hCT2285780.0, hCT2285782.0, hCT2356847.0, hCT2356848.0, hCT2356849.0, hCT2356850.0	210410_s_at	NP_002432.1, NP_751898.1, NP_751897.1, NP_079535.4, EAX03514.1, EAX03519.1, EAX03506.1, EAX03507.1, EAX03508.1, EAX03509.1, EAX03510.1, EAX03511.1, EAX03512.1, EAX03513.1, EAX03515.1, EAX03516.1, EAX03517.1, EAX03518.1, EAX03520.1
GeneID:4758	NEU1	6	31,826,829	31,830,709	3,880	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6762	-43	upstream	0	1	0	13	14	5	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene NEU1	SIAL1, NEU1, NANH, NEU, FLJ93471	sialidase 1 (lysosomal sialidase)	NM_000434, hCT34977.3, hCT1953422.1	208926_at	NP_000425.1, EAX03536.1, EAX03537.1
GeneID:80736	SLC44A4	6	31,830,969	31,846,823	15,854	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6762	16071	downstream	0	1	0	13	14	5	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene SLC44A4	SLC44A4, C6orf29, FLJ14491, CTL4, NG22	solute carrier family 44, member 4	NM_025257, NM_001178044, NM_001178045, hCT35012.3, hCT1953445.1	1555203_s_at, 205597_at	NP_079533.2, NP_001171515.1, NP_001171516.1, EAX03538.1, EAX03539.1
GeneID:6499	SKIV2L	6	31,926,581	31,937,532	10,951	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4716, 2_A375_pNL97_plus_lncRNA_AR..1..6763	13483, 13265	downstream, downstream	1	1	0	18	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SKIV2L	SKI2, SKIV2, DDX13, SKI2W, 170A, HLP, SKIV2L	superkiller viralicidic activity 2-like (S. cerevisiae)	NM_006929, hCT2285616.0, hCT2285619.0, hCT34963.3, hCT1953428.1	203727_at	NP_008860.4, EAX03555.1, EAX03554.1, EAX03556.1, EAX03557.1
GeneID:1797	DOM3Z	6	31,937,566	31,940,032	2,444	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4716, 2_A375_pNL97_plus_lncRNA_AR..1..6763	-32, 166	upstream, in gene	1	1	0	18	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene DOM3Z	DOM3Z, DOM3L, NG6, RAI1	dom-3 homolog Z (C. elegans)	NM_005510, hCT2292437.0, hCT2292438.0, hCT2356795.0, hCT2356796.0, hCT2356797.0, hCT34991.3, hCT1956524.1, hCT1956525.1	204522_at, 215962_s_at, 38157_at	NP_005501.2, EAX03559.1, EAX03560.1, EAX03561.1, EAX03562.1, EAX03563.1, EAX03558.1, EAX03564.1, EAX03565.1
GeneID:8859	STK19	6	31,938,952	31,949,223	10,271	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4716, 2_A375_pNL97_plus_lncRNA_AR..1..6763	1112, 914	in gene, in gene	1	1	0	18	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene STK19	RP1, G11, STK19, D6S60E, HLA-RP1, MGC117388, D6S60	serine/threonine kinase 19	NM_004197, NM_032454, NR_026717, hCT1953432.1, hCT1953433.1, hCT1953434.1	204090_at, 36019_at	NP_004188.1, NP_115830.1, EAX03566.1, EAX03567.1, EAX03568.1
GeneID:720	C4A	6	31,949,834	31,970,457	20,623	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4716, 2_A375_pNL97_plus_lncRNA_AR..1..6763	-9770, -9966	upstream, upstream	1	1	0	18	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C4A	C4S, C4A4, C4A, CPAMD2, C4A6, RG, C4A2, MGC164979, C4, C4A3, CO4	complement component 4A (Rodgers blood group)	NM_007293	208451_s_at, 214428_x_at	NP_009224.2
GeneID:7148	TNXB	6	32,008,932	32,077,153	68,221	-	2	2_A375_pNL97_plus_lncRNA_AR..1..6784, 4_A375_EGR1..1..7018	3777, 52665	in gene, in gene	0	1	1	5	12.5	9	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TNXB	TNXB1, TNXBS, TNXB2, TENX, HXBL, XB, TNXB, TNX, XBS	tenascin XB	NM_019105, NM_032470, hCT2285740.0, hCT2285742.0, hCT2285744.0, hCT2285746.0, hCT2285748.0, hCT2285749.0, hCT2285751.0, hCT2285753.0	1565242_at, 206093_x_at, 213451_x_at, 216333_x_at, 216654_at, 217413_s_at	NP_061978.6, NP_115859.2, EAX03572.1, EAX03573.1, EAX03576.1, EAX03577.1, EAX03574.1, EAX03575.1, EAX03578.1, EAX03579.1
GeneID:1388	ATF6B	6	32,083,045	32,096,030	12,985	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4717, 2_A375_pNL97_plus_lncRNA_AR..1..6784, 2_A375_pNL97_plus_lncRNA_AR..1..6785	-2242, 22654, -2178	upstream, downstream, upstream	1	1	0	15.5	22.5	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene ATF6B	CREB-RP, FLJ10066, G13, CREBL1, ATF6B	activating transcription factor 6 beta	NM_004381, NM_001136153, hCT2285729.0, hCT2285733.0, hCT2285735.0, hCT34989.2, hCT1953431.0	211611_s_at	NP_004372.3, NP_001129625.1, EAX03582.1, EAX03583.1, EAX03584.1, EAX03585.1, EAX03581.1
GeneID:63943	FKBPL	6	32,096,484	32,098,067	1,583	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4717, 2_A375_pNL97_plus_lncRNA_AR..1..6785	-205, -141	upstream, upstream	1	1	0	24	28	10	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene FKBPL	FKBPL, DIR1, WISP39, NG7	FK506 binding protein like	NM_022110, hCT2285724.0, hCT1643244.3	219187_at	NP_071393.2, EAX03586.1, EAX03587.1
GeneID:3112	HLA-DOB	6	32,780,540	32,784,825	4,285	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6786	-2823	upstream	0	1	0	15	24	2	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene HLA-DOB	DOB, HLA-DOB, FLJ57033	major histocompatibility complex, class II, DO beta	NM_002120, hCT2285805.1, hCT2285808.1, hCT2285810.0, hCT2343625.0	1554984_a_at, 205671_s_at	NP_002111.1, EAX03640.1, EAX03638.1, EAX03639.1, EAX03641.1
GeneID:6891	TAP2	6	32,789,610	32,806,547	16,937	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6786	16899	downstream	0	1	0	15	24	2	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene TAP2	APT2, PSF2, RING11, ABC18, ABCB3, D6S217E, TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	NM_000544, NM_018833, hCT2285803.0, hCT2285806.0	204769_s_at, 204770_at, 208428_at, 225973_at	NP_000535.3, NP_061313.2, EAX03642.1, EAX03643.1
GeneID:6046	BRD2	6	32,936,437	32,949,282	12,845	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4718, 4_A375_EGR1..1..7019	1163, 4235	in gene, in gene	1	0	1	10.5	10.5	12	2	4_A375_EGR1..1	17	Gene BRD2	RING3, FLJ31942, NAT, FSRG1, D6S113E, RNF3, FSH, BRD2, DKFZp686N0336, KIAA9001	bromodomain containing 2	NM_005104, NM_001113182, hCT2283115.0, hCT2283117.0, hCT2356784.0, hCT2356785.0, hCT5872.3	208685_x_at, 208686_s_at, 214911_s_at	NP_005095.1, NP_001106653.1, EAX03662.1, EAX03663.1, EAX03664.1, EAX03665.1, EAX03666.1
GeneID:6257	RXRB	6	33,161,365	33,168,432	7,067	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4719, 4_A375_EGR1..1..7020	-7664, -7744	upstream, upstream	1	0	1	25	14	19	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene RXRB	MGC1831, H-2RIIBP, RCoR-1, RXRB, NR2B2, DAUDI6	retinoid X receptor, beta	NM_021976, hCT2347458.1	209148_at, 215096_at, 215099_s_at	NP_068811.1, EAX03679.1
GeneID:7922	SLC39A7	6	33,168,603	33,172,214	3,611	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4719, 4_A375_EGR1..1..7020	7493, 7573	downstream, downstream	1	0	1	25	14	19	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene SLC39A7	ZIP7, D6S115E, KE4, D6S2244E, H2-KE4, RING5, HKE4, SLC39A7	solute carrier family 39 (zinc transporter), member 7	NM_006979, NM_001077516, hCT2347463.1, hCT2349265.0	202667_s_at	NP_008910.2, NP_001070984.1, EAX03660.1, EAX03661.1
GeneID:7923	HSD17B8	6	33,172,419	33,174,607	2,188	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4719, 4_A375_EGR1..1..7020	3677, 3757	downstream, downstream	1	0	1	25	14	19	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene HSD17B8	FABG, FABGL, dJ1033B10.9, RING2, SDR30C1, D6S2245E, HKE6, HSD17B8, KE6, H2-KE6	hydroxysteroid (17-beta) dehydrogenase 8	NM_014234, hCT2344275.0	213540_at	NP_055049.1, EAX03662.1
GeneID:407002	MIR219-1	6	33,175,612	33,175,721	109	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4719, 4_A375_EGR1..1..7020	484, 564	downstream, downstream	1	0	1	25	14	19	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene MIR219-1	MIR219-1, MIRI219-1, mir-219, MIRN219-1	microRNA 219-1	NR_029633		
GeneID:6015	RING1	6	33,176,286	33,180,499	4,213	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4719, 4_A375_EGR1..1..7020	-190, -110	upstream, upstream	1	0	1	25	14	19	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene RING1	RNF1, RING1, RING1A	ring finger protein 1	NM_002931, hCT2284167.0, hCT8584.4	206371_s_at, 35685_at	NP_002922.2, EAX03683.1, EAX03684.1
GeneID:6293	VPS52	6	33,218,049	33,239,662	21,613	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4720, 1_A375_pNL7_minus_lncRNA_AR..1..4721, 2_A375_pNL97_plus_lncRNA_AR..1..6787, 4_A375_EGR1..1..7021	21036, -242, -210, -370	in gene, upstream, upstream, upstream	1	1	1	16	12	11	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene VPS52	SAC2, DKFZp547I194, ARE1, VPS52, RP5-1033B10, SACM2L, dJ1033B10.5	vacuolar protein sorting 52 homolog (S. cerevisiae)	NM_022553, hCT2286068.0, hCT2286069.0, hCT2286071.0, hCT2286072.0, hCT2286073.0, hCT2286075.0, hCT2356779.0, hCT2356780.0	214565_s_at	NP_072047.4, EAX03687.1, EAX03686.1, EAX03688.1, EAX03691.1, EAX03692.1, EAX03689.1, EAX03690.1, EAX03693.1
GeneID:6222	RPS18	6	33,239,852	33,244,261	4,429	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4721, 2_A375_pNL97_plus_lncRNA_AR..1..6787, 4_A375_EGR1..1..7021	52, 20, 180	in gene, in gene, in gene	1	1	1	17	17	14	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene RPS18	KE3, D6S218E, MGC126837, KE-3, HKE3, MGC126835, S18, MGC117351, RPS18	ribosomal protein S18	NM_022551, hCT1640294.3, hCT1983723.1, hCT1983724.0, hCT1983725.1, hCT1983726.0, hCT1983727.0	201049_s_at	NP_072045.1, EAX03695.1, EAX03694.1, EAX03696.1, EAX03698.1, EAX03699.1, EAX03697.1
GeneID:8705	B3GALT4	6	33,244,917	33,246,602	1,685	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4721, 2_A375_pNL97_plus_lncRNA_AR..1..6787, 4_A375_EGR1..1..7021	-5013, -5045, -4685	upstream, upstream, upstream	1	1	1	17	17	14	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene B3GALT4	BETA3GALT4, GALT4, B3GALT4, GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	NM_003782, hCT8562.3	210205_at	NP_003773.1, EAX03700.1
GeneID:9277	WDR46	6	33,246,880	33,257,304	10,424	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4721, 1_A375_pNL7_minus_lncRNA_AR..1..4722, 2_A375_pNL97_plus_lncRNA_AR..1..6787, 2_A375_pNL97_plus_lncRNA_AR..1..6788, 4_A375_EGR1..1..7021	17400, -9864, 17432, -9960, 17272	downstream, upstream, downstream, upstream, downstream	1	1	1	20	16	13	2	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene WDR46	WDR46, BING4, C6orf11, FP221	WD repeat domain 46	NM_005452, NM_001164267, hCT1966763.1, hCT2286135.0, hCT8575.3, hCT1962875.1	209196_at	NP_005443.3, NP_001157739.1, EAX03701.1, EAX03702.1, EAX03703.1, EAX03704.1
GeneID:10471	PFDN6	6	33,257,376	33,258,711	1,333	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4722, 2_A375_pNL97_plus_lncRNA_AR..1..6788	9790, 9686	downstream, downstream	1	1	0	23	15	12	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene PFDN6	PFD6, H2-KE2, KE-2, MGC70744, HKE2, PFDN6	prefoldin subunit 6	NM_014260, NM_001165181, hCT2284130.0, hCT8578.3, hCT1962676.1	222019_at, 222029_x_at, 233568_x_at, 242046_at	NP_055075.1, NP_001172110.1, EAX03705.1, EAX03706.1, EAX03707.1
GeneID:5863	RGL2	6	33,259,431	33,267,176	7,745	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4722, 2_A375_pNL97_plus_lncRNA_AR..1..6788	8, -88	in gene, upstream	1	1	0	23	15	12	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene RGL2	RAB2L, KE1.5, HKE1.5, RGL2	ral guanine nucleotide dissociation stimulator-like 2	NR_026387, NM_004761, hCT2286129.0, hCT2286130.0, hCT2286131.0, hCT2356862.0, hCT2356863.0, hCT2356864.0, hCT8571.3	209110_s_at	NP_004752.1, EAX03713.1, EAX03708.1, EAX03709.1, EAX03710.1, EAX03711.1, EAX03712.1, EAX03714.1
GeneID:6892	TAPBP	6	33,267,471	33,282,164	14,693	-	6	1_A375_pNL7_minus_lncRNA_AR..1..4722, 1_A375_pNL7_minus_lncRNA_AR..1..4723, 2_A375_pNL97_plus_lncRNA_AR..1..6788, 2_A375_pNL97_plus_lncRNA_AR..1..6789, 2_A375_pNL97_plus_lncRNA_AR..1..6790, 4_A375_EGR1..1..7022	14996, -3468, 14900, -3420, -9100, -812	downstream, upstream, downstream, upstream, upstream, upstream	1	1	1	16.25	17.75	11	4	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene TAPBP	TPSN, TPN, NGS17, TAPA, TAPBP	TAP binding protein (tapasin)	NM_003190, NM_172208, NM_172209, hCT2286123.0, hCT2286125.0, hCT2286126.0, hCT8570.4, hCT1962673.1, hCT1962674.1	1555565_s_at, 208829_at, 210294_at	NP_003181.3, NP_757345.2, NP_757346.2, EAX03715.1, EAX03716.1, EAX03719.1, EAX03717.1, EAX03718.1, EAX03720.1
GeneID:9278	ZBTB22	6	33,282,182	33,285,719	3,537	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4723, 2_A375_pNL97_plus_lncRNA_AR..1..6789, 2_A375_pNL97_plus_lncRNA_AR..1..6790, 4_A375_EGR1..1..7022	87, 135, -5545, 2743	in gene, in gene, upstream, in gene	1	1	1	14	16.67	10.67	3	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene ZBTB22	ZBTB22A, ZNF297, ZNF297A, BING1, ZBTB22, fruitless, fru	zinc finger and BTB domain containing 22	NM_005453, NM_001145338, hCT2286120.0	213081_at	NP_005444.4, NP_001138810.1, EAX03721.1
GeneID:1616	DAXX	6	33,286,335	33,290,793	4,458	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4723, 2_A375_pNL97_plus_lncRNA_AR..1..6789, 2_A375_pNL97_plus_lncRNA_AR..1..6790, 4_A375_EGR1..1..7022	5161, 5209, -471, 7817	downstream, downstream, upstream, downstream	1	1	1	14	16.67	10.67	3	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene DAXX	MGC126245, EAP1, BING2, DAP6, DAXX, MGC126246	death-domain associated protein	NR_024517, NM_001141970, NM_001141969, NM_001350, hCT1967013.1, hCT2356826.0, hCT8566.2	201763_s_at, 216038_x_at	NP_001135442.1, NP_001135441.1, NP_001341.1, EAX03722.1, EAX03723.1, EAX03724.1
GeneID:221496	LEMD2	6	33,738,990	33,756,906	17,916	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4724, 4_A375_EGR1..1..7023	-22, 17194	upstream, in gene	1	0	1	13.5	9.5	7.5	2	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene LEMD2	NET25, LEMD2, dJ482C21.1	LEM domain containing 2	NM_001143944, NM_181336, hCT2356858.0, hCT32527.3	224980_at	NP_001137416.1, NP_851853.1, EAX03750.1, EAX03751.1
GeneID:4295	MLN	6	33,762,449	33,771,793	9,344	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4724, 1_A375_pNL7_minus_lncRNA_AR..1..4725, 2_A375_pNL97_plus_lncRNA_AR..1..6791	14865, -8763, -8783	downstream, upstream, upstream	1	1	0	17.5	17.5	6	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MLN	MGC138519, MLN	motilin	NM_001040109, NM_002418, NM_001184698, hCT32524.2, hCT1963737.0	207473_at	NP_001035198.1, NP_002409.1, NP_001171627.1, EAX03752.1, EAX03753.1
GeneID:100507584	LOC100507584	6	33,857,288	33,864,684	7,396	-	1	4_A375_EGR1..1..7024	4156	in gene	0	0	1	2	5	13	1	4_A375_EGR1..1	13	Gene LOC100507584		hypothetical LOC100507584	XR_108631		
GeneID:2914	GRM4	6	33,989,628	34,101,443	111,815	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4726, 2_A375_pNL97_plus_lncRNA_AR..1..6792, 2_A375_pNL97_plus_lncRNA_AR..1..6793	915, 18163, 931	in gene, in gene, in gene	1	1	0	14.5	22.5	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene GRM4	GPRC1D, GRM4, MGLUR4, MGC177594, mGlu4	glutamate receptor, metabotropic 4	NM_000841, hCT2286086.0, hCT32525.3	210234_at	NP_000832.1, EAX03759.1, EAX03760.1
GeneID:3159	HMGA1	6	34,204,577	34,214,008	9,431	+	1	4_A375_EGR1..1..7026	12127	downstream	0	0	1	6	6	22	1	4_A375_EGR1..1	22	Gene HMGA1	HMGIY, MGC4242, HMG-R, HMGA1, MGC4854, MGC12816, HMGA1A	high mobility group AT-hook 1	NM_145903, NM_002131, NM_145899, NM_145902, NM_145901, NM_145905, hCT2282636.0, hCT2282637.0, hCT2282638.0, hCT2282639.0, hCT2282640.0, hCT2282641.0, hCT2282642.0, hCT2282643.0, hCT2356762.0, hCT2356763.0, hCT2356764.0, hCT2356765.0, hCT2356766.0	206074_s_at, 210457_x_at	NP_665910.1, NP_002122.1, NP_665906.1, NP_665908.1, NP_665909.1, NP_665912.1, EAX03762.1, EAX03763.1, EAX03764.1, EAX03765.1, EAX03766.1, EAX03767.1, EAX03768.1, EAX03772.1, EAX03769.1, EAX03770.1, EAX03771.1, EAX03773.1, EAX03774.1
GeneID:221491	C6orf1	6	34,214,157	34,216,904	2,747	-	1	4_A375_EGR1..1..7026	200	in gene	0	0	1	6	6	22	1	4_A375_EGR1..1	22	Gene C6orf1	C6orf1, MGC57858, LBH	chromosome 6 open reading frame 1	NM_001006703, NM_001006704, NM_178508, hCT1966962.1, hCT2356733.0, hCT2356734.0, hCT7117.3	226306_at	NP_001006703.1, NP_001006704.1, NP_848603.2, EAX03775.1, EAX03776.1, EAX03778.1, EAX03777.1
GeneID:54887	UHRF1BP1	6	34,759,794	34,845,291	85,497	+	1	4_A375_EGR1..1..7027	430	in gene	0	0	1	9	6	11	1	4_A375_EGR1..1	11	Gene UHRF1BP1	ICBP90, dJ349A12.1, FLJ20302, UHRF1BP1, C6orf107	UHRF1 binding protein 1	NM_017754, hCT2356728.0, hCT1666470.3	1566789_at, 226135_at, 233245_at	NP_060224.3, EAX03798.1, EAX03799.1
GeneID:6882	TAF11	6	34,845,555	34,855,819	10,264	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6794	11	in gene	0	1	0	13	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TAF11	PRO2134, TAFII28, TAF11, MGC:15243, TAF2I	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	NM_005643	1558135_at, 1558136_s_at, 209358_at	NP_005634.1
GeneID:23294	ANKS1A	6	34,857,038	35,059,190	202,152	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6794	-1230	upstream	0	1	0	13	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ANKS1A	KIAA0229, MGC42354, ANKS1A, ANKS1	ankyrin repeat and sterile alpha motif domain containing 1A	NM_015245, hCT2282657.0, hCT2282659.0, hCT2282660.0, hCT2356731.0, hCT7113.3	212747_at	NP_056060.2, EAX03801.1, EAX03800.1, EAX03802.1, EAX03803.1, EAX03804.1
GeneID:6954	TCP11	6	35,085,849	35,109,187	23,338	-	1	4_A375_EGR1..1..7028	531	in gene	0	0	1	4	1	16	1	4_A375_EGR1..1	16	Gene TCP11	KIAA0229, TCP11, D6S230E, MGC111103	t-complex 11 homolog (mouse)	NM_018679, NM_001093728, hCT1967038.1, hCT8715.3	220376_at	NP_061149.1, NP_001087197.1, EAX03808.1, EAX03809.1
GeneID:2178	FANCE	6	35,420,138	35,434,881	14,743	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4727, 2_A375_pNL97_plus_lncRNA_AR..1..6795, 4_A375_EGR1..1..7029	15974, 16026, -8970	downstream, downstream, upstream	1	1	1	9	6.5	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene FANCE	FAE, FACE, FANCE	Fanconi anemia, complementation group E	NM_021922, hCT1643777.3	220255_at	NP_068741.1, EAX03830.1
GeneID:4736	RPL10A	6	35,436,178	35,438,558	2,380	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4727, 2_A375_pNL97_plus_lncRNA_AR..1..6795	-66, -12	upstream, upstream	1	1	0	17	14	15	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene RPL10A	Csa-19, RPL10A, NEDD6, L10A	ribosomal protein L10a	NM_007104, hCT8712.5, hCT1983313.2, hCT1983314.1, hCT1983315.2	200036_s_at, 229563_s_at	NP_009035.3, EAX03831.1, EAX03832.1, EAX03833.1, EAX03834.1
GeneID:7005	TEAD3	6	35,441,374	35,464,861	23,487	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4727, 2_A375_pNL97_plus_lncRNA_AR..1..6795, 4_A375_EGR1..1..7030	28749, 28695, 5453	downstream, downstream, in gene	1	1	1	10	10	14	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene TEAD3	ETFR-1, TEAD3, TEAD5, TEF5, DTEF-1, TEF-5	TEA domain family member 3	NM_003214, hCT2285017.0, hCT2285018.0, hCT2356843.0, hCT8717.3	209454_s_at	NP_003205.2, EAX03835.1, EAX03836.1, EAX03837.1, EAX03838.1
GeneID:7287	TULP1	6	35,465,651	35,480,647	14,996	-	1	4_A375_EGR1..1..7030	21239	downstream	0	0	1	3	6	13	1	4_A375_EGR1..1	13	Gene TULP1	TUBL1, RP14, TULP1	tubby like protein 1	NM_003322, hCT2356801.0, hCT8709.3	206705_at	NP_003313.3, EAX03839.1, EAX03840.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_shN7_mycN7_shRNA_1	2_A375_shN7_gfp_lncRNA_1 Percent	4_A375_EGFR_lncRNA_1 Percent	1_A375_shN7_mycN7_lncRNA_1 Avg Peak	2_A375_shN7_gfp_lncRNA_1 Avg Peak	4_A375_EGFR_lncRNA_1 Avg Peak	Ad Tag Count	Peak Sample	Peak Values	UCSC Link	Annotation	Full Description	RNA	Ally Tag	PROT
Gene:ID:23999	FKBP3	14	55,541,392	55,896,960	164,896	+	1	4_A375_EGR1_1.7021	5472	upstream	0	0	1	11	11	16	1	4_A375_EGR1_1.1	16	Gene FKBP3	FKbox, AnSR, MGC110308, FKBP3, P54, FKBP54, Pig10, FKBP59	FK506 binding protein 3	NM_004117, NM_001145973, NM_001145976, NM_001145977, XC_T220880140.0, XC70711.3	2394560_at_2249545_at, 2249696_at	NP_004108.1, NP_001139247.1, NP_001139248.1, NP_001139249.1, EAX05841.1, EAX05842.1
Gene:ID:26455647	LOC26455647	8	55,694,509	55,704,724	10,165	+	1	4_A375_EGR1_1.7021	4852	in gene	0	0	1	11	11	16	1	4_A375_EGR1_1.1	16	Gene LOC26455647		hypothetical LOC26455647	NR_027117	1557723_at, 1557726_a_at, 1570131_at	
Gene:ID:23401401	C8orf81	8	55,704,659	55,716,863	11,226	+	1	4_A375_EGR1_1.7021	5027	upstream	0	0	1	11	11	16	1	4_A375_EGR1_1.1	16	Gene C8orf81	C8orf81, FLJ25390	chromosome 8 open reading frame 81	NM_145028, XC_T220492440.0, XC76611.3	231260_at	NP_659463.2, EAX03945.1, EAX03944.1
Gene:ID:23999338	C8orf128	8	55,744,392	55,747,329	2,937	+	1	4_A375_EGR1_1.7022	10604	downstream	0	0	1	11	14	20	1	4_A375_EGR1_1.1	20	Gene C8orf128	dJ510E05.3, UNQ3043, C8orf128	chromosome 8 open reading frame 128	NM_207409, XC_T220391110.0, XC116430981.1		NP_997232.2, EAX03947.1, EAX03946.1
Gene:ID:34025284	C8orf127	8	55,746,651	55,753,961	7,310	+	1	4_A375_EGR1_1.7022	8965	in gene	0	0	1	11	14	20	1	4_A375_EGR1_1.1	20	Gene C8orf127	EG:FLJ22477, C8orf127, dJ510E05.6	chromosome 8 open reading frame 127	NM_031018556		NP_001018556.1
Gene:ID:1292893	CLPS	8	55,782,760	55,785,102	2,342	-	3	1_A375_shN7_mycL_lncRNA_NR_1..4725, 2_A375_shN37_gfpL_lncRNA_NR_1.8796, 4_A375_EGR1_1.7022	-9992, -9302, 10238	upstream, upstream, downstream	1	1	1	16.5	15.5	14.5	2	1_A375_shL822_mycL_lncRNA_NR_1	22	Gene CLPS	CLPS		NM_031932, NT_167693.3, XC_T1962948.1	209131_at	NP_001025.1, EAX03800.1, EAX03801.1
Gene:ID:23999282	LHFPL5	8	55,773,071	55,791,852	18,781	+	2	1_A375_shN7_mycL_lncRNA_NR_1..4726, 2_A375_shN37_gfpL_lncRNA_NR_1.8796	51, 113	in gene, in gene	1	1	0	22	17	9	1	1_A375_shL822_mycL_lncRNA_NR_1	22	Gene LHFPL5	LHFPL5, TMHS, DFNB67, MGC33535, dJ510E05.2	tetraspan membrane protein 5	NM_182548, XC_T220291151	1553042_at	NP_570154.1, EAX03802.1
Gene:ID:11798399	GLC2B4N	8	55,811,291	55,892,413	81,122	-	2	1_A375_shN7_mycL_lncRNA_NR_1..4729, 2_A375_shN37_gfpL_lncRNA_NR_1.8797	-2883, -2931	upstream, upstream	1	1	0	17	16	8	1	1_A375_shL817_mycL_lncRNA_NR_1	17	Gene SLC2B4	FAT1, FLJ22714, SLC2B4	solute carrier family 2B, member 4	NM_001193478, NM_032961, NM_139118, XC_T2264991.2, XC72393360.0, XC72393360.1, XC72395570.0, XC72395570.1	2373A0_at	NP_001180633.1, NP_443193.1, NP_619132.2, EAX03962.1, EAX03961.1, EAX03960.1, EAX03959.1, EAX03958.1, EAX03955.1
Gene:ID:14399	MAPK14	6	55,995,454	56,079,015	83,559	+	2	1_A375_shN7_mycL_lncRNA_NR_1..4729, 2_A375_shN37_gfpL_lncRNA_NR_1.8797	-106, -110	upstream, upstream	1	1	0	17	16	8	1	1_A375_shL817_mycL_lncRNA_NR_1	17	Gene MAPK14	EXIP, p38ALPHA, PRKM14, SAPK2A, CSBP1, p38, PRKAR5, Mxi2, CSBP2, MAPK14, CSPB1, Kin	mitogen-activated protein kinase 14	NM_139012, NM_139013, NM_001315, NM_139013, XC72392924.0, XC72392927.0, XC72392928.0, XC72392929.0, XC72392930.0, XC72395640.0, XC71960854.1	202550_at, 210449_x_at, 211027_x_at, 211561_x_at	NP_620581.1, NP_620582.1, NP_620583.1, NP_620582.1, NP_001336.1, EAX03971.1, EAX03972.1, EAX03967.1, EAX03966.1, EAX03965.1, EAX03963.1, EAX05572.1
Gene:ID:26468546	PNPLA1	6	56,210,945	56,276,572	65,627	+	1	4_A375_EGR1_1.7023	29875	in gene	0	0	1	4	3	12	1	4_A375_EGR1_1.1	12	Gene PNPLA1	MGC119329, dJ982J21.1, MGC119320, MGC119321, FLJ38755, PNPLA1	patatin-like phospholipase domain containing 1	NM_001145716, NM_001145717, NM_173816, XC76926.4	1553364_at	NP_001139183.1, NP_001139189.2, NP_775847.2, EAX03953.1
Gene:ID:10420	CDKN1A	6	36,644,439	36,655,109	10,670	+	3	1_A375_shN7_mycL_lncRNA_NR_1..4730, 2_A375_shN37_gfpL_lncRNA_NR_1.8798, 4_A375_EGR1_1.7024	1909, 1941, 153	in gene, in gene, in gene	1	1	1	15.5	13.5	14	2	1_A375_shL822_mycL_lncRNA_NR_1	22	Gene CDKN1A	CDKN1A, WDNM1, SDI1, SDI1, CAP20, WAF1, p21CIP1, CAP20, CIP1	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_078467, NM_000389, XC76399.4, XC71963399.1, XC71963900.1	1555166_at, 202284_s_at	NP_510867.1, NP_000380.1, EAX03964.1, EAX03965.1, EAX03966.1, EAX03967.1
Gene:ID:57654	CPNE8	19	56,766,553	56,807,220	66,668	-	1	4_A375_EGR1_1.7025	92	in gene	0	0	1	4	9	11	1	4_A375_EGR1_1.1	11	Gene CPNE8	DKFZp686C254, CPN8, C8FWB, COPN8, bA441.B9	copine V	NM_020939, XC72390222.0, XC72390223.0, XC72390226.0, XC76392.2	227189_at	NP_066960.1, EAX03911.1, EAX03912.1, EAX03913.1, EAX03914.1, EAX03915.1
Gene:ID:10127961	LOC100127961	19	56,806,196	56,812,309	5,893	-	1	4_A375_EGR1_1.7025	5561	downstream	0	0	1	4	9	11	1	4_A375_EGR1_1.1	11	Gene LOC100127961		hypothetical LOC100127961	XM_001716232, XM_001716614, XM_001716231		XP_001716274.1, XP_001716498.1, XP_001716340.1
Gene:ID:23787167	MTCH1	19	58,833,917	58,853,949	18,032	-	1	2_A375_shN37_gfpL_lncRNA_NR_1..6799	29	in gene	0	1	0	14	15	8	1	2_A375_shL818_gfpL_lncRNA_NR_1	18	Gene MTCH1	MTCH1, CGI-64, MGC131996, PQBP, PSAP	mitochondrial carrier homolog 1 (C. elegans)	NM_014341, XC72390208.0, XC72390207.0, XC72390782.0, XC72390783.0, XC71960284.1, XC71962648.1	221819_s_at	NP_055156.1, EAX03928.1, EAX03926.1, EAX03927.1, EAX03930.1, EAX03931.1, EAX03929.1, EAX03932.1
Gene:ID:23999	RNF5	19	57,321,745	57,362,814	40,766	+	1	1_A375_shN7_mycL_lncRNA_NR_1..4751	126	in gene	1	0	0	13	11	9	1	1_A375_shL813_mycL_lncRNA_NR_1	13	Gene RNF5	RNF5, RMA1, MGC10955, dJ1093J23.6, FLJ12013, RNF5	ring finger protein 5	NM_007055, NM_145057, XC72391165.0, XC72391172.2, XC72395007.0	203160_s_at, 203161_s_at	NP_009049.1, NP__859001.1, EAX03943.1, EAX03944.1, EAX03945.1
Gene:ID:23787570	FTSJD2	19	57,400,907	57,449,364	48,277	+	1	4_A375_EGR1_1.7027	69	in gene	0	0	1	13	12	16	1	4_A375_EGR1_1.1	16	Gene FTSJD2	MTF1, KIAA0852, FLJ22186, FTSJD2, NMT1	Rho / methyltransferase fold domain containing	NM_015355, XC71961003.1	212350_at	NP_056155.1, EAX03948.1
Gene:ID:26472227	MDGA1	19	57,850,254	57,865,766	65,512	-	1	2_A375_shL837_gfpL_lncRNA_NR_1..6801	67462	downstream	0	1	0	17	23	5	1	2_A375_shL823_gfpL_lncRNA_NR_1	23	Gene MDGA1	DKFZp686H2282, MDGA1, MAMDC2, DKFZp686H02052, FLJ45515, GPI-8	MAM domain containing glycosylphosphatidylinositol anchor 1	NM_153487, XC72392271.1, XC72392291.1, XC71960362.0, XC71960362.2, XC71960391.1	232237_at, 235943_x_at, 242797_at	NP_705891.1, EAX03953.1, EAX03950.1, EAX03951.1, EAX03952.1, EAX03954.1
Gene:ID:89855655	ZFAND3	6	37,757,307	38,122,400	353,093	+	2	1_A375_shN7_mycL_lncRNA_NR_1..4733, 2_A375_shN37_gfpL_lncRNA_NR_1.8802	-139, -367	upstream, upstream	1	1	0	17	23	12	1	2_A375_shL823_gfpL_lncRNA_NR_1	23	Gene ZFAND3	ZFAND3, FLJ17799, FLJ12222, TEX27	zinc finger, AN1-type domain 3	NM_031943, XC72392021.0, XC71961639.1	218620_s_at, 223493_s_at	NP_036782.1, EAX03953.1, EAX03958.1
Gene:ID:11798399	BTBD9	6	55,136,227	55,607,924	471,697	-	2	1_A375_shN7_mycL_lncRNA_NR_1..8803, 2_A375_shN37_gfpL_lncRNA_NR_1.8804	418228, 281972	in gene, in gene	0	1	0	11	23.5	4	2	2_A375_shL823_gfpL_lncRNA_NR_1	23	Gene BTBD9	MGC132530, MGC120319, BTBD9, MGC120317, FLJ22943, 6322J12.1, MGC131803	BTB (POZ) domain containing 9	NM_032993, NM_001099272, NM_152733, NM_001172416, XC72340416.0, XC72340760.0, XC72410394.0	1553273_at, 229687_at, 234802_at, 235246_at	NP_443125.1, NP_001092742.1, NP_689946.2, NP_001185699.1, EAX03980.1, EAX03981.1
Gene:ID:27500	GLO1	6	35,845,701	35,870,952	27,251	-	4	1_A375_shN7_mycL_lncRNA_NR_1..4754, 2_A375_shN37_gfpL_lncRNA_NR_1.8693	6, -24	in gene, upstream	1	1	0	22	27	8	1	2_A375_shL827_gfpL_lncRNA_NR_1	27	Gene GLO1	GLYL, GLO1, GLOD1	glyoxalase I	NM_006708, XC72325697.0, XC72325853	200681_at	NP_006699.2, EAX03964.1, EAX03965.1
Gene:ID:27500	GLP1R	6	39,016,837	39,055,520	38,683	+	1	2_A375_shN37_gfpL_lncRNA_NR_1.8699	39793	downstream	0	1	0	4	7	3	1	2_A375_shL817_gfpL_lncRNA_NR_1	17	Gene GLP1R	MGC138331, GLP1R	glucagon-like peptide 1 receptor	NM_002062, XC72323514.0, XC72323518.0, XC72356571.0, XC72356572.0, XC72356573.0	206393_s_at, 209291_s_at, 209400_at, 209401_s_at, 211252_x_at	NP_002053.3, EAX03970.1, EAX03971.1, EAX03972.1, EAX03973.1, EAX03974.1
Gene:ID:23787	KCNK5	6	39,156,747	39,197,351	40,604	-	2	2_A375_shL837_gfpL_lncRNA_NR_1.6800, 4_A375_EGR1_1.7028	196, 99	in gene, in gene	0	1	1	14	17	22	1	4_A375_EGR1_1.1	22	Gene KCNK5	TASK-2, KCNK5, FLJ11033, TASK2, K2p5.1	potassium channel, subfamily K, member 5	NM_033347, XC72334403.1, XC72356859.0	219913_s_at	NP_003731.1, EAX03979.1, EAX03980.1
Gene:ID:23787	DAAM2	6	39,780,793	39,872,961	111,646	+	1	4_A375_EGR1_1.7029	69447	in gene	0	0	1	3	8	16	1	4_A375_EGR1_1.1	16	Gene DAAM2	dJ982A20.1, KIAA0261, DAAM2, MGC30115	dishevelled associated activator of morphogenesis 2	NM_015345, XC72356622.0, XC72435693	212795_at	NP_056160.2, EAX03995.1, EAX03996.1
Gene:ID:10639638	LOC100639638	19	39,849,580	39,860,028	10,448	-	1	4_A375_EGR1_1.7029	14788	in gene	0	0	1	3	8	16	1	4_A375_EGR1_1.1	16	Gene LOC100639638	FLJ43904	hypothetical LOC100639638	XR_112889, XR_110844, XR_113558		
Gene:ID:23787	LNCSCL1	22	40,994,840	41,006,955	12,295	-	1	4_A375_EGR1_1.7030	10850	in gene	0	0	1	10	11	13	1	4_A375_EGR1_1.1	13	Gene LNCSCL1	LNCSCL1, ZUD, MGC34785	zinc finger with UBP domain in Drosophila and C. elegans-like	NM_175581, XC71960548.2	231008_at	NP_783322.2, EAX03927.1
Gene:ID:44	NFYA	6	41,640,707	41,670,148	29,439	+	1	4_A375_EGR1_1.7041	28829	in gene	0	0	1	7	8	16	1	4_A375_EGR1_1.1	16	Gene NFYA	CBF-B, HAP2, NFYA, NFYA, FLJ11236, NFYA	nuclear transcription factor-Y alpha	NM_002505, NM_021703, XC72351572.0, XC72353574.0, XC72353576.0, XC72353579.0, XC72353582.0, XC72353583.0, XC72356512.0, XC74029.4, XC71962713.1	204167_at, 234168_at, 234169_s_at, 234170_s_at, 235703_s_at	NP_002496.1, NP__085351.1, EAX04014.1, EAX04015.1, EAX04017.1, EAX04019.1, EAX04012.1, EAX04018.1, EAX04016.1, EAX04020.1, EAX04021.1
Gene:ID:54209	TREML2	6	41,126,348	41,130,922	4,575	+	1	2_A375_shN37_gfpL_lncRNA_NR_1.6810	-3974	upstream	0	1	0	9	15	5	1	2_A375_shL815_gfpL_lncRNA_NR_1	15	Gene TREML2	TREM-2, TREM2, TREM2a, TREM2b, Trem2u	triggering receptor expressed on myeloid cells 2	NM_018965, XC71961581.1, XC72355510.0, XC74030.4	219725_at	NP_061836.1, EAX04033.1, EAX04032.1, EAX04034.1
Gene:ID:79178	TFEB	6	41,651,746	41,703,997	52,251	-	2	1_A375_shN7_mycL_lncRNA_NR_1.4703, 2_A375_shN37_gfpL_lncRNA_NR_1.6811	537, 372	in gene, in gene	1	1	0	21	29	6	1	1_A375_shL831_mycL_lncRNA_NR_1	31	Gene TFEB	TCFE3, BHLHE35, TFEB, bHLH-ZIP-137, FLJ44709	transcription factor EB	NM_007162, NM_001167627, XC72323372.1, XC72353573.1, XC72353575.0, XC72406644, XLFH07728	221666_at, 50221_at	NP_009193.1, NP_001160299.1, EAX04038.1, EAX04036.1, EAX04037.1, EAX04035.1
Gene:ID:5329	PGC	6	41,764,449	41,713,109	50,660	-	2	1_A375_shN7_mycL_lncRNA_NR_1.4703, 2_A375_shN37_gfpL_lncRNA_NR_1.6811	18899, 11715	downstream, downstream	1	1	0	21	29	6	1	1_A375_shL831_mycL_lncRNA_NR_1	31	Gene PGC	PEPC, PGA, FLJ95983, PGC	progastricsin (pepsinogen C)	NM_002630, NM_001166924, XC72405893	1568296_a_at, 205281_at	NP_002621.1, NP_001156096.1, EAX04039.1
Gene:ID:10170	FRS3	6	41,737,914	41,747,650	9,736	-	2	1_A375_shN7_mycL_lncRNA_NR_1.4705, 2_A375_shN37_gfpL_lncRNA_NR_1.6812	-7815, -7892	upstream, upstream	1	1	0	21	22	5	1	2_A375_shL822_gfpL_lncRNA_NR_1	22	Gene FRS3	MGC71187, SNT-2, SNT2, FRS2beta, FRS3, FRS2B	fibroblast growth factor receptor substrate 3	NM_006653, XC72329457.0	219927_at	NP_006644.1, EAX04060.1
Gene:ID:26468	PRKCL1	6	41,746,500	41,785,110	38,610	+	2	1_A375_shN7_mycL_lncRNA_NR_1.4706, 2_A375_shN37_gfpL_lncRNA_NR_1.6812	6748, 6732	downstream, downstream	1	1	0	21	22	5	1	2_A375_shL822_gfpL_lncRNA_NR_1	22	Gene PRKCL1	CrE87, MGC133395, C8TP, PRKCL64, TOMM6, C8orf49	protein kinase C and casein kinase substrate in neurons 1 (Drosophila)	NM_013297, XC72329596.0, XC72356541.0, XC72356542.0, XC74099.3	218233_s_at, 223518_s_at	NP_037378.3, EAX04084.1, EAX04081.1, EAX04082.1, EAX04083.1
Gene:ID:11080693	TOMM6	6	41,755,151	41,757,854	2,703	+	2	1_A375_shN7_mycL_lncRNA_NR_1.4706, 2_A375_shN37_gfpL_lncRNA_NR_1.6812	97, 51	in gene, in gene	1	1	0	21	22	5	1	2_A375_shL822_gfpL_lncRNA_NR_1	22	Gene TOMM6	FLJ32022, C8TP, TOMM6, DKFZp681H221	translocase of outer mitochondrial membrane 6 homolog (yeast)	NM_031134, XC72329471.0, XC72356475.0, XC72356477.0, XC71917932.2, XC71964482.3, XC71964483.1	220016_s_at, 233224_at, 233520_at	NP_277031.1, EAX04091.1, EAX04089.1, EAX04090.1, EAX04093.1, EAX04092.1
Gene:ID:23999	USP49	6	41,765,303	41,800,099	37,716	-	2	1_A375_shN7_mycL_lncRNA_NR_1.4706, 2_A375_shN37_gfpL_lncRNA_NR_1.6812	107631, 107067	downstream, downstream	1	1	0	21	22	5	1	2_A375_shL822_gfpL_lncRNA_NR_1	22	Gene USP49	MGC20741, USP49	ubiquitin specific peptidase 49	NM_015561, XC72344278.0	1564629_at, 243292_at	NP_056391.2, EAX04085.1
Gene:ID:54465	MED20	6	41,870,092	41,886,877	16,785	-	2	1_A375_shN7_mycL_lncRNA_NR_1.4707, 2_A375_shN37_gfpL_lncRNA_NR_1.6813	-276, -251	upstream, upstream	1	1	0	39	48	10	1	2_A375_shL848_gfpL_lncRNA_NR_1	48	Gene MED20	MGC29989, TRFP, MED20, PRO2213, DKFZp686D2223	mediator complex subunit 20	NM_019274, XC72394431.0, XC72397717.0	208981_s_at, 213072_s_at	NP_001265.2, EAX04087.1, EAX04086.1
Gene:ID:7018	BYSL	6	41,898,965	41,900,764	11,819	+	2	1_A375_shN7_mycL_lncRNA_NR_1.4707, 2_A375_shN37_gfpL_lncRNA_NR_1.6813	167, 120	in gene, in gene	1	1	0	39	48	10	1	2_A375_shL848_gfpL_lncRNA_NR_1	48	Gene BYSL	BYSL, BYSTIN	bystin-like	NM_004053, XC71961322.1	203812_at	NP_892044.2, EAX04089.1
Gene:ID:44	C8orf33	8	42,086,697	42,110,715	41,898	+	2	2_A375_shN37_gfpL_lncRNA_NR_1.6814, 4_A375_EGR1_1.7042	42847, 18347	downstream, in gene	0	1	1	8.5	10	11	2	2_A375_shL817_gfpL_lncRNA_NR_1	17	Gene C8orf33	C8orf33, bA374.2, FLJ90068	chromosome 8 open reading frame 132	NM_001164448		NP_001157916.1
Gene:ID:55909	TRERF1	6	42,192,869	42,319,763	127,114	+	2	1_A375_shN7_mycL_lncRNA_NR_1.4708, 2_A375_shN37_gfpL_lncRNA_NR_1.7043	199, 192773	in gene, in gene	1	1	0	10	10	9	2	1_A375_shL817_gfpL_lncRNA_NR_1	17	Gene TRERF1	BCAR2, FLJ31195, HSA277276, TReP-132, RreKa, RP1-120G6.5, dJ1310G6.5, TRERF1	transcriptional regulating factor 1	NM_033532, XC72394171.0, XC72394479.0, XC72394770.0, XC71917932.2, XC71964482.3, XC71964483.1	229016_s_at, 233324_at, 233520_at	NP_277031.1, EAX04091.1, EAX04089.1, EAX04090.1, EAX04093.1, EAX04092.1
Gene:ID:23999	TBCC	6	42,212,254	42,215,864	3,610	+	1	2_A375_shN37_gfpL_lncRNA_NR_1.6815	126	in gene	0	1	0	8	14	8	1	2_A375_shL814_gfpL_lncRNA_NR_1	14	Gene TBCC	CFC, TBCC	tubulin folding cofactor C	NM_003192, XC76841.3	202489_at	NP_003183.1, EAX04100.1
Gene:ID:23999	RPUTL1	6	42,847,871	42,894,761	46,890	+	2	1_A375_shN7_mycL_lncRNA_NR_1.4709, 2_A375_shN37_gfpL_lncRNA_NR_1.6817	-160, 11113	upstream, downstream	1	1	0	10.5	17	8	2	2_A375_shL822_gfpL_lncRNA_NR_1	22	Gene RPUTL1	RPUTL1, MGC62039, dJ475H6.4	ribonuclease P/MRP 38kDa subunit	NM_198498, XC72396312.1, XC72396313.1, XC71917930.3	224768_s_at	NP_940958.2, EAX04106.1, EAX04104.1, EAX04105.1
Gene:ID:44	C8orf22	8	42,856,953	42,858,854	1,901	-	1	4_A375_EGR1_1.7044	9425	in gene	0	0	1	12	12	9	1	4_A375_EGR1_1.1	12	Gene C8orf22	C8orf22	chromosome 8 open reading frame 22	NM_031301, XC71962736.1	225458_at	NP_001301719.1
Gene:ID:17	PTCRA	9	42,853,727	42,893,978	40,249	+	1	4_A375_EGR1_1.7044	9425	in gene	0	0	1	8	8	13	1	4_A375_EGR1_1.1	13	Gene PTCRA	PT-ALPHA, PTA, PTCRA	pre T-cell antigen receptor alpha	NM_130398, XC71962026.1, XC72395816.0, XC72395816.1, XC71962026.2, XC76767.4	211352_s_at, 211827_s_at, 211828_x_at	NP_612153.2, EAX04108.1, EAX04107.1, EAX04109.1, EAX04110.1
Gene:ID:26468	CNPY3	6	42,896,660	42,907,005	10,345	+	1	4_A375_EGR1_1.7044	2958	upstream	0	2	1	8	8	15	1	4_A375_EGR1_1.1	15	Gene CNPY3	ERDS-5, PRATA, CASA, TARCA, CAPY3	canopy 3 homolog (zebrafish)	NM_006355, XC71962707.1, XC71962708.1, XC72395222.0, XC72395223.0, XC72395224.0, XC72395225.0, XC72395227.0, XC72395730.0, XC76994.2, XC71965052.1, XC71965053.1, XC71961022.1	1553777_s_at, 1558539_at, 211701_at, 220389_at	NP_006767.2, EAX04120.1, EAX04112.1, EAX04118.1, EAX04119.1, EAX04111.1, EAX04114.1, EAX04115.1, EAX04116.1, EAX04117.1, EAX04121.1, EAX04122.1
Gene:ID:85477	SRF	6	43,130,930	43,149,344	18,224	+	1	2_A375_shN37_gfpL_lncRNA_NR_1.6816	10866	downstream	0	1	0	11	17	10	1	2_A375_shL817_gfpL_lncRNA_NR_1	17	Gene SRF	SRF, MCM1	serum response factor (c-fos serum response element-binding transcription factor)	NM_003131, XC72395536.0, XC76995.3	202400_s_at, 202401_s_at	NP_003122.1, EAX04161.1, EAX04160.1
Gene:ID:23787	CUL9	6	43,149,922	43,192,325	42,403	+	1	2_A375_shN37_gfpL_lncRNA_NR_1.6816	-54	upstream	0	1	0	11	17	10	1	2_A375_shL817_gfpL_lncRNA_NR_1	17	Gene CUL9	KIAA0708, FLJ12113, DKFZp686F0353, DKFZp686G1642, PARC1, PARC, CUL9	cullin 9	NM_015089, XC72395537.0, XC71963326.1	213204_at, 238392_at	NP_853654.1, EAX04164.1, EAX04165.1
Gene:ID:26468	ABCC10	6	43,299,489	43,416,163	116,674	+	1	1_A375_shN7_mycL_lncRNA_NR_1.4729	-4289	upstream	1	0	0	23	9	9	1	1_A375_shL823_mycL_lncRNA_NR_1	23	Gene ABCC10	EST162793, MRP7, ABCC10, SMRP	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	NM_033450, XC71962674.1, XC71965081.1, XC71965091.1, XC72350521.0, XC72350522.0, XC71962674.4	213453_s_at, 213573_s_at	NP_872585.2, EAX04169.1, EAX04168.1, EAX04170.1, EAX04167.1, EAX04166.1, EAX04165.1, EAX04162.1
Gene:ID:83943	TJAP1	6	43,443,261	43,474,294	29,033	+	2	1_A375_shN7_mycL_lncRNA_NR_1.4740, 2_A375_EGR1_1.7045	31939, 33076	downstream, downstream	1	1	0	13	14	12.5	2	1_A375_shL818_mycL_lncRNA_NR_1	18	Gene TJAP1	FILT, TJP4, DKFZp686F0851.1, TJAP1	tight junction associated protein 1 (peripheral)	NM_001146106, NM_001146107, NM_001146110, NM_080604, NM_001146019, NM_001146020, NR_027294, XC71969574.1, XC71969575.1, XC72350792.0, XC72350793.0, XC72350727.0, XC72350728.0, XC72350729.0, XC72350730.0	221557_s_at, 47803_at	NP_001139466.1, NP_001139467.1, NP_001139468.1, NP_542177.2, NP_001139469.1, NP_001139470.1, EAX04182.1, EAX04183.1, EAX04184.1, EAX04185.1, EAX04186.1, EAX04187.1, EAX04188.1, EAX04189.1, EAX04190.1, EAX04191.1

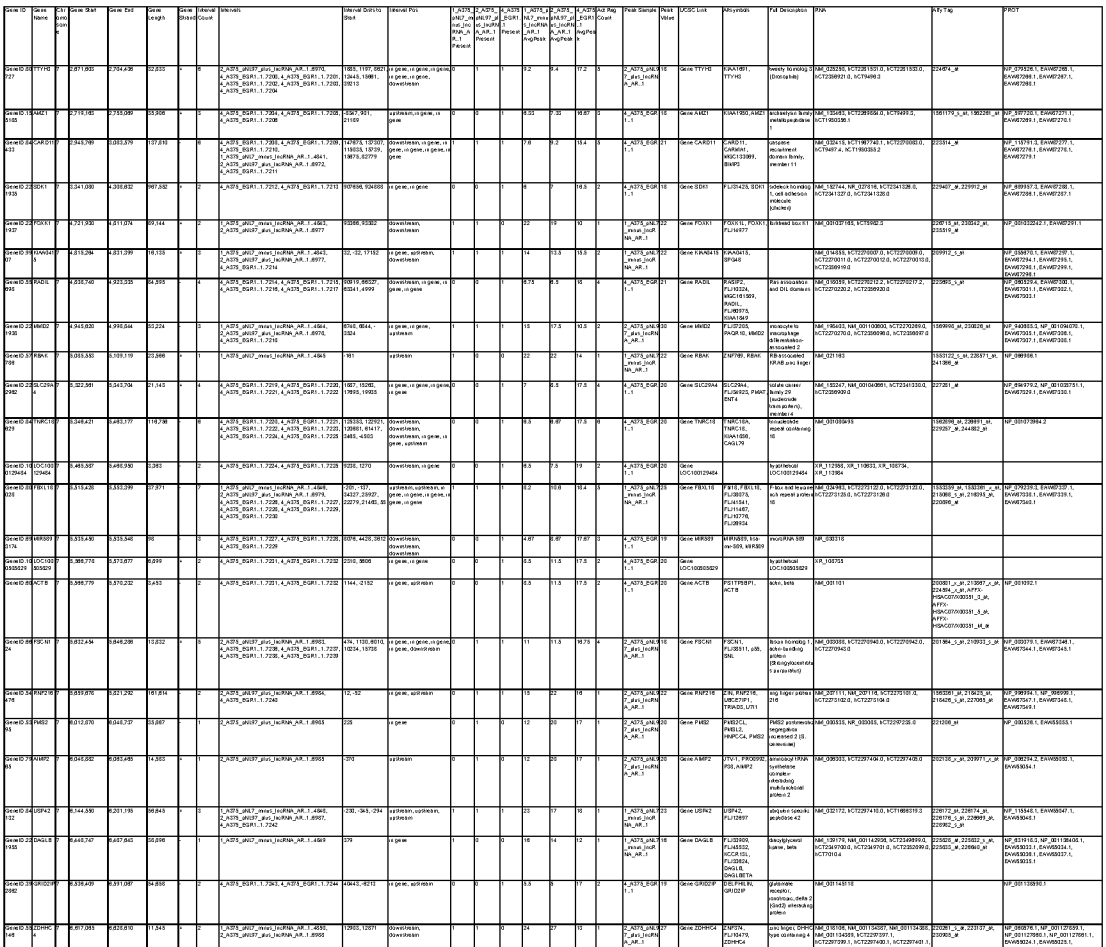
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:221424	C6orf154	6	43,474,707	43,478,424	3,717	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4740, 4_A375_EGR1..1..7045	1224, 68	in gene, in gene	1	0	1	13	14	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene C6orf154	C6orf154, FLJ44636, dJ337H4.2, MGC131666	chromosome 6 open reading frame 154	NM_001012974, hCT10061.2	235935_at	NP_001012992.1, EAX04202.1
GeneID:25844	YIPF3	6	43,479,565	43,484,728	5,163	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4740, 4_A375_EGR1..1..7045	7528, 6392	downstream, downstream	1	0	1	13	14	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene YIPF3	FinGER3, C6orf109, KLIP1, dJ337H4.3, YIPF3, DKFZp566C243	Yip1 domain family, member 3	NM_015388, hCT10072.3	216338_s_at	NP_056203.2, EAX04203.1
GeneID:9533	POLR1C	6	43,484,791	43,497,114	12,323	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4740, 4_A375_EGR1..1..7045	-7591, -6455	upstream, upstream	1	0	1	13	14	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene POLR1C	RPA39, TCS3, POLR1C, RPA5, RPA40, RPAC1	polymerase (RNA) I polypeptide C, 30kDa	NM_203290, NM_004875, hCT2286377.0, hCT2286378.0	207515_s_at, 209317_at	NP_976035.1, NP_004866.1, EAX04204.1, EAX04205.1
GeneID:54676	GTPBP2	6	43,588,218	43,596,936	8,718	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6619	-8728	upstream	0	1	0	6	18	10	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene GTPBP2	GTPBP2, MGC74725	GTP binding protein 2	NM_019096, hCT2286299.0, hCT2286300.0, hCT2286301.0, hCT2286302.0, hCT2286303.0, hCT10073.3	221050_s_at, 223789_s_at	NP_061969.3, EAX04218.1, EAX04213.1, EAX04214.1, EAX04216.1, EAX04217.1, EAX04215.1
GeneID:9587	MAD2L1BP	6	43,597,279	43,608,689	11,410	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6619, 2_A375_pNL97_plus_lncRNA_AR..1..6620	6385, 10977	in gene, in gene	0	1	0	5.5	16	6	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene MAD2L1BP	CMT2, MGC11282, MAD2L1BP, KIAA0110, RP1-261G23.6	MAD2L1 binding protein	NM_014628, NM_001003690, hCT10082.3	203094_at	NP_055443.1, NP_001003690.1, EAX04219.1
GeneID:221421	RSPH9	6	43,612,767	43,638,748	25,981	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6619, 2_A375_pNL97_plus_lncRNA_AR..1..6620	-9103, -4511	upstream, upstream	0	1	0	5.5	16	6	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene RSPH9	C6orf206, MRPS18AL1, FLJ30845, RSPH9, CILD12	radial spoke head 9 homolog (Chlamydomonas)	NM_152732, NM_001193341, hCT1966134.1, hCT1966135.1, hCT10079.2	230695_s_at	NP_689945.2, NP_001180270.1, EAX04220.1, EAX04221.1, EAX04222.1
GeneID:64928	MRPL14	6	44,081,372	44,095,191	13,819	-	1	4_A375_EGR1..1..7047	-377	upstream	0	0	1	5	6	13	1	4_A375_EGR1..1	13	Gene MRPL14	MRPL14, L14mt, L32mt, MGC70566, MRP-L32, RMPL32, RPML32, MRP-L14, MRPL32	mitochondrial ribosomal protein L14	NM_032111, hCT2349245.0, hCT2349246.0, hCT2349247.0, hCT1641363.3	225201_s_at	NP_115487.2, EAX04243.1, EAX04242.1, EAX04244.1, EAX04245.1
GeneID:55362	TMEM63B	6	44,095,376	44,123,256	27,880	+	1	4_A375_EGR1..1..7047	192	in gene	0	0	1	5	6	13	1	4_A375_EGR1..1	13	Gene TMEM63B	DKFZp666N2275, TMEM63B, C6orf110, RP3-421H19.2	transmembrane protein 63B	NM_018426, hCT2285917.0, hCT2285918.0, hCT10080.3	225271_at	NP_060896.1, EAX04248.1, EAX04246.1, EAX04247.1
GeneID:100505819	LOC100505819	6	44,209,727	44,221,620	11,893	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4741, 2_A375_pNL97_plus_lncRNA_AR..1..6621, 2_A375_pNL97_plus_lncRNA_AR..1..6622	6820, 6932, -3452	in gene, in gene, upstream	1	1	0	22	26	12	2	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene LOC100505819		hypothetical LOC100505819	XR_112682, XR_108852, XR_113895		
GeneID:3326	HSP90AB1	6	44,214,849	44,221,614	6,765	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4741, 2_A375_pNL97_plus_lncRNA_AR..1..6621, 2_A375_pNL97_plus_lncRNA_AR..1..6622	-49, -161, 10223	upstream, upstream, downstream	1	1	0	22	26	12	2	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene HSP90AB1	HSP90-BETA, D6S182, HSP90AB1, HSP90B, HSPC2, HSPCB, FLJ26984	heat shock protein 90kDa alpha (cytosolic), class B member 1	NM_007355, hCT2285894.1, hCT2285895.1, hCT2358808.0, hCT10066.3	1557910_at, 200064_at, 214359_s_at	NP_031381.2, EAX04257.1, EAX04258.1, EAX04259.1, EAX04260.1
GeneID:347734	SLC35B2	6	44,221,836	44,225,283	3,445	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4741, 2_A375_pNL97_plus_lncRNA_AR..1..6621, 2_A375_pNL97_plus_lncRNA_AR..1..6622	10483, 10595, 211	downstream, downstream, in gene	1	1	0	22	26	12	2	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene SLC35B2	PAPST1, UGTrel4, SLC35B2, SLL	solute carrier family 35, member B2	NM_178148, hCT10087.3	224716_at	NP_835361.1, EAX04261.1
GeneID:4794	NFKBIE	6	44,225,903	44,233,525	7,622	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6622	8453	downstream	0	1	0	13	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NFKBIE	NFKBIE, IKBE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	NM_004556, hCT2286055.0, hCT10064.4, hCT1983327.1	203927_at	NP_004547.2, EAX04262.1, EAX04263.1, EAX04264.1
GeneID:441151	TMEM151B	6	44,238,480	44,247,182	8,702	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4742, 2_A375_pNL97_plus_lncRNA_AR..1..6623	15048, 14992	downstream, downstream	1	1	0	20	21	6	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TMEM151B	TMEM151B, FLJ42511, FLJ44891, TMEM193, C6orf137, FLJ37046, bA444E17.5, FLJ44683	transmembrane protein 151B	NM_001137560	213676_at, 213678_at	NP_001131032.1
GeneID:202500	TCTE1	6	44,247,897	44,265,458	17,561	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4742, 2_A375_pNL97_plus_lncRNA_AR..1..6623	11930, 11986	in gene, in gene	1	1	0	20	21	6	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TCTE1	FLJ50041, TCTE1, D6S46, MGC33600	t-complex-associated-testis-expressed 1	NM_182539, hCT2347546.0	237280_at	NP_872345.2, EAX04266.1
GeneID:57505	AARS2	6	44,266,463	44,281,063	14,600	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4743, 2_A375_pNL97_plus_lncRNA_AR..1..6624	7, -25	in gene, upstream	1	1	0	62	66	9	1	2_A375_pNL97_plus_lncRNA_AR..1	66	Gene AARS2	AARSL, KIAA1270, MTALARS, AARS2, bA444E17.1, MT-ALARS	alanyl-tRNA synthetase 2, mitochondrial (putative)	NM_020745, hCT9577.3	231845_at	NP_065796.1, EAX04268.1
GeneID:100128935	LOC100128935	6	44,440,641	44,445,639	4,998	+	1	4_A375_EGR1..1..7048	-2913	upstream	0	0	1	7	6	14	1	4_A375_EGR1..1	14	Gene LOC100128935		similar to hCG2041342	XM_001723560, XM_001725735, XM_003120005		XP_001723632.1, XP_001725787.1, XP_003120053.1
GeneID:51302	CYP39A1	6	46,517,445	46,620,523	103,078	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4744, 2_A375_pNL97_plus_lncRNA_AR..1..6625	-501, -469	upstream, upstream	1	1	0	15	14	6	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene CYP39A1	CYP39A1		NM_016593, hCT9824.3	1553977_a_at, 220432_s_at, 244407_at	NP_057677.2, EAX04297.1
GeneID:9481	SLC25A27	6	46,620,679	46,645,927	25,248	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4744, 2_A375_pNL97_plus_lncRNA_AR..1..6625	345, 313	in gene, in gene	1	1	0	15	14	6	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene SLC25A27	UCP4, SLC25A27, FLJ33552	solute carrier family 25, member 27	NM_004277, hCT7934.4, hCT1982852.1	1552774_a_at, 1554161_at, 229381_at, 230624_at, 231787_at	NP_004268.3, EAX04299.1, EAX04298.1
GeneID:266977	GPR110	6	46,967,813	47,010,082	42,269	-	1	4_A375_EGR1..1..7049	9101	in gene	0	0	1	4	7	12	1	4_A375_EGR1..1	12	Gene GPR110	KPG_012, hGPCR36, PGR19, FLJ22684, MGC125952, GPR110, FLJ30646	G protein-coupled receptor 110	NM_025048, NM_153840, hCT2284307.0, hCT2284308.1, hCT2343794.0	220907_at, 235988_at, 236689_at	NP_079324.2, NP_722582.2, EAX04311.1, EAX04312.1, EAX04313.1
GeneID:83741	TFAP2D	6	50,681,257	50,740,746	59,489	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6626	7191	in gene	0	1	0	9	17	2	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TFAP2D	TFAP2D, TFAP2BL1	transcription factor AP-2 delta (activating enhancer binding protein 2 delta)	NM_172238, hCT1817639.3	233987_at	NP_758438.2, EAX04354.1
GeneID:114327	EFHC1	6	52,284,994	52,360,583	75,589	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6629	3986	in gene	0	1	0	6	18	3	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene EFHC1	FLJ37290, EFHC1, EJM, EJM1, dJ304B14.2, FLJ10466, JAE, EJA1	EF-hand domain (C-terminal) containing 1	NM_018100, NR_033327, NM_001172420, hCT2286825.0, hCT12282.4, hCT1983344.1	219833_s_at, 225656_at, 231026_at	NP_060570.2, NP_001165891.1, EAX04370.1, EAX04371.1, EAX04372.1
GeneID:2941	GSTA4	6	52,842,746	52,860,178	17,432	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6630	162	in gene	0	1	0	10	14	6	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene GSTA4	GSTA4, DKFZp686D21185, GSTA4-4, GTA4	glutathione S-transferase alpha 4	NM_001512, hCT2287508.0, hCT2358859.0, hCT2358860.0, hCT13033.3, hCT1983352.1, hCT1983353.1, hCT1983354.1	202967_at, 235405_at	NP_001503.1, EAX04394.1, EAX04395.1, EAX04396.1, EAX04398.1, EAX04399.1, EAX04393.1, EAX04397.1
GeneID:125050	RN7SK	6	52,860,418	52,860,749	331	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6630	-402	upstream	0	1	0	10	14	6	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene RN7SK	RN7SK, 7SK	RNA, 7SK small nuclear	NR_001445		
GeneID:22858	ICK	6	52,866,098	52,926,600	60,502	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4750, 2_A375_pNL97_plus_lncRNA_AR..1..6630, 2_A375_pNL97_plus_lncRNA_AR..1..6631	-3048, 66584, -3084	upstream, downstream, upstream	1	1	0	14	17.5	5.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ICK	LCK2, MGC46090, ICK, ECO, KIAA0936, MRK	intestinal cell (MAK-like) kinase	NM_014920, NM_016513, hCT2287502.1, hCT2287503.1, hCT11897.4, hCT1983340.2, hCT1983341.2	1552837_at, 204589_at	NP_055735.1, NP_057597.2, EAX04400.1, EAX04401.1, EAX04402.1, EAX04403.1, EAX04404.1
GeneID:26268	FBXO9	6	52,929,796	52,965,671	35,875	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4750, 2_A375_pNL97_plus_lncRNA_AR..1..6631	-146, -132	upstream, upstream	1	1	0	18	21	5	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene FBXO9	NY-REN-57, FBXO9, DKFZp434C0118, FBX9, dJ341E18.2, KIAA0936, VCIA1	F-box protein 9	NM_012347, NM_033481, NM_033480, hCT2286839.0, hCT2286840.0, hCT2286842.0, hCT2286843.0, hCT2286844.0, hCT1950794.1	1559094_at, 1559096_x_at, 1566507_a_at, 1566509_s_at, 1566511_at, 210638_s_at, 212987_at, 212991_at, 236472_at	NP_036479.1, NP_258442.2, NP_258441.1, EAX04406.1, EAX04407.1, EAX04408.1, EAX04405.1, EAX04409.1, EAX04410.1
GeneID:60481	ELOVL5	6	53,132,196	53,213,942	81,746	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4751, 1_A375_pNL7_minus_lncRNA_AR..1..4752, 2_A375_pNL97_plus_lncRNA_AR..1..6632	454, -10506, -10616	in gene, upstream, upstream	1	1	0	18.5	18.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ELOVL5	ELOVL5, dJ483K16.1, HELO1	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	NM_021814, hCT2285388.0, hCT2285390.0, hCT2285391.0, hCT2285393.0, hCT2285395.0, hCT2285397.0, hCT2285399.0, hCT2285401.0, hCT2285403.0, hCT2358833.0	1567222_x_at, 208788_at, 214153_at, 215062_at	NP_068586.1, EAX04419.1, EAX04413.1, EAX04417.1, EAX04421.1, EAX04422.1, EAX04414.1, EAX04415.1, EAX04416.1, EAX04418.1, EAX04420.1
GeneID:2729	GCLC	6	53,362,139	53,409,831	47,692	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4753, 1_A375_pNL7_minus_lncRNA_AR..1..4754, 2_A375_pNL97_plus_lncRNA_AR..1..6633, 2_A375_pNL97_plus_lncRNA_AR..1..6634	-25, -3033, -57, -2989	upstream, upstream, upstream, upstream	1	1	0	34.5	29.5	6.5	2	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene GCLC	GCL, GLCLC, GCS, GCLC, GLCL	glutamate-cysteine ligase, catalytic subunit	NM_001498, hCT2285384.0, hCT13035.3	1555330_at, 202922_at, 202923_s_at	NP_001489.1, EAX04425.1, EAX04426.1
GeneID:55227	LRRC1	6	53,659,778	53,788,919	129,141	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6635	-130	upstream	0	1	0	9	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LRRC1	LRRC1, FLJ11834, LANO, FLJ10775, dJ523E19.1	leucine rich repeat containing 1	NM_018214, hCT2284977.0, hCT1817829.1	207790_at	NP_060684.4, EAX04430.1, EAX04429.1
GeneID:3062	HCRTR2	6	55,039,071	55,147,418	108,347	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4755, 2_A375_pNL97_plus_lncRNA_AR..1..6637	2881, 2881	in gene, in gene	1	1	0	29	19	2	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene HCRTR2	OX2R, HCRTR2	hypocretin (orexin) receptor 2	NM_001526, hCT2284958.0	207393_at	NP_001517.2, EAX04440.1
GeneID:202559	KHDRBS2	6	62,389,865	62,996,100	606,235	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4757, 2_A375_pNL97_plus_lncRNA_AR..1..6640, 4_A375_EGR1..1..7052	-76, -156, 58580	upstream, upstream, in gene	1	1	1	15	12	14	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene KHDRBS2	SLM-1, MGC26664, KHDRBS2, bA535F17.1, SLM1, FLJ38664	KH domain containing, RNA binding, signal transduction associated 2	NM_152688, hCT2280880.1, hCT2280881.1, hCT1953078.2	215527_at	NP_689901.2, EAW48490.1, EAW48489.1, EAW48491.1
GeneID:7803	PTP4A1	6	64,281,920	64,293,489	11,569	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4758, 1_A375_pNL7_minus_lncRNA_AR..1..4759, 2_A375_pNL97_plus_lncRNA_AR..1..6641, 2_A375_pNL97_plus_lncRNA_AR..1..6642	-128, 2432, 1552, 2464	upstream, in gene, in gene, in gene	1	1	0	21.33	17.67	7.67	3	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene PTP4A1	PRL1, PTP4A1, DKFZp779M0721, PRL-1, PTPCAAX1, HH72, PTP(CAAX1)	protein tyrosine phosphatase type IVA, member 1	NM_003463, hCT2281169.0, hCT1797443.1	200730_s_at, 200731_s_at, 200732_s_at, 200733_s_at, 240329_at	NP_003454.1, EAW48495.1, EAW48494.1
GeneID:346007	EYS	6	64,429,876	66,417,118	1,987,242	-	1	4_A375_EGR1..1..7054	79598	in gene	0	0	1	6	7	20	1	4_A375_EGR1..1	20	Gene EYS	C6orf179, bA74E24.1, EYS, C6orf178, RP25, bA307F22.3, dJ303F19.1, SPAM, dJ1018A4.2, EGFL11, dJ22I17.2, bA166P24.2, C6orf180, KIAA0663, EGFL10	eyes shut homolog (Drosophila)	NM_198283, NM_001142800, NM_001142801		NP_938024.1, NP_001136272.1, NP_001136273.1
GeneID:577	BAI3	6	69,345,632	70,099,403	753,771	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4765, 2_A375_pNL97_plus_lncRNA_AR..1..6647	597298, 597248	in gene, in gene	1	1	0	27	35	5	1	2_A375_pNL97_plus_lncRNA_AR..1	35	Gene BAI3	KIAA0550, BAI3, MGC133100	brain-specific angiogenesis inhibitor 3	NM_001704, hCT2332673.0, hCT1959844.1	205638_at, 211566_at	NP_001695.1, EAW48837.1, EAW48836.1
GeneID:1310	COL19A1	6	70,576,446	70,922,157	345,709	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4766	51456	in gene	1	0	0	16	10	3	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene COL19A1	COL19A1, COL9A1L, D6S228E	collagen, type XIX, alpha 1	NM_001858, hCT2332678.0, hCT2332680.0, hCT6078.3	211011_at	NP_001849.2, EAW48828.1, EAW48829.1, EAW48830.1
GeneID:57579	FAM135A	6	71,123,107	71,270,877	147,770	+	1	4_A375_EGR1..1..7059	153661	downstream	0	0	1	12	11	15	1	4_A375_EGR1..1	15	Gene FAM135A	FAM135A, KIAA1411, FLJ13577, DKFZp781H2319	family with sequence similarity 135, member A	NM_001105531, NM_020819, NM_001162529, hCT2332749.0, hCT2332750.0, hCT2332752.0, hCT2332754.0, hCT1959836.1, hCT1959837.1, hCT1959838.1, hCT1959839.1	221233_s_at, 223497_at, 233730_at	NP_001099001.1, NP_065870.3, NP_001156001.1, EAW48814.1, EAW48817.1, EAW48819.1, EAW48815.1, EAW48816.1, EAW48818.1, EAW48820.1, EAW48821.1
GeneID:135154	C6orf57	6	71,276,625	71,298,606	21,981	+	1	4_A375_EGR1..1..7059	143	in gene	0	0	1	12	11	15	1	4_A375_EGR1..1	15	Gene C6orf57	C6orf57, MGC104225	chromosome 6 open reading frame 57	NM_145267, hCT2349195.0, hCT2349196.0, hCT1817613.3	238504_at	NP_660310.2, EAW48810.1, EAW48811.1, EAW48812.1
GeneID:56479	KCNQ5	6	73,331,571	73,908,574	577,003	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4767, 2_A375_pNL97_plus_lncRNA_AR..1..6648	499949, 499865	in gene, in gene	1	1	0	21	28	3	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene KCNQ5	Kv7.5, KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5	NM_019842, NM_001160130, NM_001160132, NM_001160133, NM_001160134, hCT2344244.0, hCT2344246.0	223891_at	NP_062816.2, NP_001153602.1, NP_001153604.1, NP_001153605.1, NP_001153606.1, EAW48782.1, EAW48783.1
GeneID:1915	EEF1A1	6	74,225,473	74,230,755	5,282	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4768, 2_A375_pNL97_plus_lncRNA_AR..1..6649, 4_A375_EGR1..1..7060	-141, -61, 83	upstream, upstream, in gene	1	1	1	20	17	29	1	4_A375_EGR1..1	29	Gene EEF1A1	EF-Tu, FLJ25721, MGC131894, EEF-1, GRAF-1EF, CCS-3, MGC102687, CCS3, eEF1A-1, LENG7, EF1A, HNGC:16303, EEF1A, EEF1A1, MGC16224, EE1A1, PTI1	eukaryotic translation elongation factor 1 alpha 1	NM_001402, hCT2336043.1	1557120_at, 204892_x_at, 206559_x_at, 213477_x_at, 213614_x_at, 227708_at	NP_001393.1, EAW48759.1
GeneID:100506740	LOC100506740	6	74,403,615	74,405,854	2,239	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4769, 2_A375_pNL97_plus_lncRNA_AR..1..6650	318, 126	in gene, in gene	1	1	0	13	14	5	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene LOC100506740		hypothetical LOC100506740	XR_108807		

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:135228	CD109	6	74,405,508	74,538,041	132,533	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4769, 2_A375_pNL97_plus_lncRNA_AR..1..6650	28, 220	in gene, in gene	1	1	0	13	14	5	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene CD109	RP11-525G3.1, DKFZp762L1111, CPAMD7, FLJ38569, CD109, FLJ41966	CD109 molecule	NM_133493, NM_001159587, NM_001159588, hCT2336059.0, hCT2336060.0, hCT2336061.0, hCT2352078.0	226545_at, 229900_at, 239719_at	NP_598000.2, NP_001153059.1, NP_001153060.1, EAW48752.1, EAW48753.1, EAW48755.1, EAW48754.1
GeneID:55603	FAM46A	6	82,455,447	82,462,428	6,981	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4770	-560	upstream	1	0	0	24	13	10	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene FAM46A	FLJ20037, C6orf37, FAM46A, FLJ31495, XTP11	family with sequence similarity 46, member A	NM_017633, hCT401094.3, hCT1959598.1	221766_s_at, 224973_at, 229737_at	NP_060103.2, EAW48692.1, EAW48691.1
GeneID:5238	PGM3	6	83,878,628	83,902,935	24,307	-	1	4_A375_EGR1..1..7062	23	in gene	0	0	1	8	11	19	1	4_A375_EGR1..1	19	Gene PGM3	PAGM, FLJ13623, DKFZp434B187, FLJ11614, PGM3, AGM1	phosphoglucomutase 3	NM_015599, hCT2332333.0, hCT2352194.0, hCT401115.3, hCT1959602.1, hCT1959603.1	210041_s_at	NP_056414.1, EAW48667.1, EAW48668.1, EAW48669.1, EAW48670.1, EAW48671.1
GeneID:112611	RWDD2A	6	83,903,032	83,906,256	3,224	+	1	4_A375_EGR1..1..7062	-120	upstream	0	0	1	8	11	19	1	4_A375_EGR1..1	19	Gene RWDD2A	MGC138208, dJ747H23.2, RWDD2A, RWDD2, MGC13523	RWD domain containing 2A	NM_033411, hCT401119.3, hCT1959606.1	213555_at	NP_219479.2, EAW48665.1, EAW48666.1
GeneID:134701	RIPPLY2	6	84,562,985	84,567,234	4,249	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4771, 2_A375_pNL97_plus_lncRNA_AR..1..6652	6231, 6247	downstream, downstream	1	1	0	45	62	7	1	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene RIPPLY2	RIPPLY2, C6orf159, dJ237I15.1	ripply2 homolog (zebrafish)	NM_001009994	236771_at	NP_001009994.1
GeneID:51167	CYB5R4	6	84,569,370	84,670,146	100,776	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4771, 2_A375_pNL97_plus_lncRNA_AR..1..6652	-154, -138	upstream, upstream	1	1	0	45	62	7	1	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene CYB5R4	cb5/cb5R, dJ676J13.1, RP4-676J13.1, CYB5R4, NCB5OR	cytochrome b5 reductase 4	NM_016230	219079_at	NP_057314.2
GeneID:9096	TBX18	6	85,444,157	85,473,899	29,742	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6654	-533	upstream	0	1	0	10	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene TBX18	TBX18		NM_001080508	1559639_at, 1559640_s_at, 233839_at	NP_001073977.1
GeneID:4907	NT5E	6	86,159,302	86,205,498	46,196	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6656	15274	in gene	0	1	0	13	17	4	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene NT5E	NT, CD73, eNT, NT5E, eN, E5NT, NTE, NT5	5'-nucleotidase, ecto (CD73)	NM_002526, hCT2352189.0, hCT401111.1, hCT1959599.1	1553994_at, 1553995_a_at, 203939_at, 227486_at	NP_002517.1, EAW48635.1, EAW48634.1, EAW48636.1
GeneID:387066	SNHG5	6	86,386,725	86,388,451	1,726	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4772, 2_A375_pNL97_plus_lncRNA_AR..1..6657, 4_A375_EGR1..1..7063, 4_A375_EGR1..1..7064	131, 35, 371, -445	in gene, in gene, in gene, upstream	1	1	1	16	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SNHG5	NCRNA00044, MGC16382, bA33E24.2, SNHG5, U50HG, C6orf160	small nucleolar RNA host gene 5 (non-protein coding)	NR_003038	225155_at	
GeneID:26799	SNORD50A	6	86,387,012	86,387,086	74	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4772, 2_A375_pNL97_plus_lncRNA_AR..1..6657, 4_A375_EGR1..1..7063, 4_A375_EGR1..1..7064	-1234, -1330, -994, -1610	upstream, upstream, upstream, upstream	1	1	1	16	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SNORD50A	SNORD50A, RNU50, U50	small nucleolar RNA, C/D box 50A	NR_002743	244669_at	
GeneID:692088	SNORD50B	6	86,387,307	86,387,377	70	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4772, 2_A375_pNL97_plus_lncRNA_AR..1..6657, 4_A375_EGR1..1..7063, 4_A375_EGR1..1..7064	-943, -1039, -703, -1519	upstream, upstream, upstream, upstream	1	1	1	16	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SNORD50B	U50', U50B, SNORD50B	small nucleolar RNA, C/D box 50B	NR_003044		
GeneID:375519	GJB7	6	87,992,697	88,038,996	46,299	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4773, 2_A375_pNL97_plus_lncRNA_AR..1..6658	6772, 6740	in gene, in gene	1	1	0	64	62	5	1	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene GJB7	bA136M9.1, connexin25, CX25, GJB7, MGC71746	gap junction protein, beta 7, 25kDa	NM_198568		NP_940970.1
GeneID:57150	C6orf162	6	88,032,306	88,052,043	19,737	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4773, 2_A375_pNL97_plus_lncRNA_AR..1..6658	-82, -50	upstream, upstream	1	1	0	64	62	5	1	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene C6orf162	DKFZp566E1923, dJ102H19.2, C6orf162	chromosome 6 open reading frame 162	NM_020425, NM_001042493, hCT2349211.0, hCT2349212.0, hCT2349213.0	213312_at, 213314_at, 236178_at	NP_065158.3, NP_001035958.1, EAW48601.1, EAW48602.1, EAW48603.1
GeneID:154313	C6orf165	6	88,117,690	88,174,191	56,501	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4774, 1_A375_pNL7_minus_lncRNA_AR..1..4775, 2_A375_pNL97_plus_lncRNA_AR..1..6659, 2_A375_pNL97_plus_lncRNA_AR..1..6660	28846, 64902, 28814, 64790	in gene, downstream, in gene, downstream	1	1	0	30	37	6	2	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene C6orf165	dJ382I10.1, FLJ46091, FLJ25974, C6orf165	chromosome 6 open reading frame 165	NM_001031743	230273_at	NP_001026913.1
GeneID:10559	SLC35A1	6	88,182,643	88,222,057	39,414	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4775, 2_A375_pNL97_plus_lncRNA_AR..1..6660	-51, -163	upstream, upstream	1	1	0	19	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SLC35A1	CMPST, SLC35A1, FLJ76955, CST, hCST, CDG2F	solute carrier family 35 (CMP-sialic acid transporter), member A1	NM_006416, NM_001168398	203306_s_at	NP_006407.1, NP_001161870.1
GeneID:2570	GABRR2	6	89,967,239	90,024,967	57,728	-	1	4_A375_EGR1..1..7065	12087	in gene	0	0	1	3	2	15	1	4_A375_EGR1..1	15	Gene GABRR2	GABRR2		NM_002043, hCT24263.1	208217_at	NP_002034.2, EAW48557.1
GeneID:51465	UBE2J1	6	90,036,344	90,062,619	26,275	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6662	187	in gene	0	1	0	11	15	9	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene UBE2J1	HSPC205, NCUBE1, HSU93243, CGI-76, NCUBE-1, HSPC153, UBE2J1, Ubc6p, MGC12555	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	NM_016021, hCT2333110.0, hCT24262.3	217823_s_at, 217824_at, 217825_s_at, 217826_s_at, 222435_s_at, 226924_s_at	NP_057105.2, EAW48556.1, EAW48555.1
GeneID:23195	MDN1	6	90,353,231	90,529,442	176,211	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6663	2	in gene	0	1	0	12	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MDN1	KIAA0301, FLJ23395, FLJ42031, FLJ25587, MDN1, FLJ43191, DKFZp686H16106	MDN1, midasin homolog (yeast)	NM_014611, hCT2340243.0, hCT2340244.1	1569484_s_at, 212693_at, 234854_at	NP_055426.1, EAW48545.1, EAW48546.1
GeneID:9994	CASP8AP2	6	90,539,619	90,584,155	44,536	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6663	-10179	upstream	0	1	0	12	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CASP8AP2	FLJ11208, CED-4, FLASH, CASP8AP2, RIP25, KIAA1315	caspase 8 associated protein 2	NM_001137666, NM_012115, NM_001137667, hCT2333142.1, hCT2348015.0, hCT2348016.0, hCT2352062.0, hCT23591.2	1570001_at, 222201_s_at	NP_001131140.1, NP_036247.1, NP_001131139.1, EAW48540.1, EAW48542.1, EAW48543.1, EAW48541.1, EAW48544.1
GeneID:84694	GJA10	6	90,604,188	90,605,819	1,631	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4777, 2_A375_pNL97_plus_lncRNA_AR..1..6664	1028, 996	in gene, in gene	1	1	0	43	56	5	1	2_A375_pNL97_plus_lncRNA_AR..1	56	Gene GJA10	CX62, GJA10, RP11-63K6.6	gap junction protein, alpha 10, 62kDa	NM_032602, hCT1646356.1	1553044_at	NP_115991.1, EAW48537.1
GeneID:60468	BACH2	6	90,636,247	91,006,627	370,380	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6665	74019	in gene	0	1	0	14	20	1	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene BACH2	BACH2		NM_021813, NM_001170794, hCT2333070.1, hCT2333074.1, hCT2340902.0, hCT2340903.0, hCT24268.2	221234_s_at, 227173_s_at, 236796_at	NP_068585.1, NP_001164265.1, EAW48530.1, EAW48531.1, EAW48533.1, EAW48534.1, EAW48532.1
GeneID:6885	MAP3K7	6	91,225,353	91,296,907	71,554	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6666	-181	upstream	0	1	0	15	25	10	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene MAP3K7	TAK1, MAP3K7, MEKK7, TGF1a	mitogen-activated protein kinase kinase kinase 7	NM_003188, NM_145331, NM_145332, NM_145333, hCT2332198.0, hCT2352058.0, hCT2352059.0, hCT23590.3, hCT1956063.1	206853_s_at, 206854_s_at, 211536_x_at, 211537_x_at	NP_003179.1, NP_663304.1, NP_663305.1, NP_663306.1, EAW48526.1, EAW48528.1, EAW48525.1, EAW48527.1, EAW48529.1
GeneID:23376	KIAA0776	6	96,969,702	97,003,152	33,450	+	1	4_A375_EGR1..1..7066	-36	upstream	0	0	1	6	13	14	1	4_A375_EGR1..1	14	Gene KIAA0776	KIAA0776, NLBP, RP3-393D12.1	KIAA0776	NM_015323, hCT2352051.0, hCT2352052.0, hCT1956052.1	212633_at, 212634_at	NP_056138.1, EAW48508.1, EAW48506.1, EAW48507.1
GeneID:81491	GPR63	6	97,245,888	97,285,353	39,465	-	1	4_A375_EGR1..1..7067	329	in gene	0	0	1	9	11	19	1	4_A375_EGR1..1	19	Gene GPR63	PSP24(beta), GPR63, PSP24B	G protein-coupled receptor 63	NM_001143957, NM_030784, hCT1646440.3	220993_s_at	NP_001137429.1, NP_110411.1, EAW48502.1
GeneID:29078	NDUFAF4	6	97,337,187	97,345,767	8,580	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4778, 2_A375_pNL97_plus_lncRNA_AR..1..6668	-9, -9	upstream, upstream	1	1	0	46	40	6	1	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene NDUFAF4	NDUFAF4, My013, bA22L21.1, HRPAP20, C6orf66, HSPC125	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	NM_014165, hCT7745.2	219006_at	NP_054884.1, EAW48501.1
GeneID:84553	C6orf168	6	99,720,793	99,797,531	76,738	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4780, 2_A375_pNL97_plus_lncRNA_AR..1..6670	-3621, -3685	upstream, upstream	1	1	0	14	16	2	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C6orf168	C6orf168, dJ273F20, MGC2817, FLJ30539	chromosome 6 open reading frame 168	NM_032511, hCT2331975.0, hCT2352064.0, hCT2352065.0, hCT1660090.3, hCT1963908.1	232067_at	NP_115900.1, EAW48483.1, EAW48484.1, EAW48485.1, EAW48486.1, EAW48487.1
GeneID:85015	USP45	6	99,880,182	99,963,252	83,070	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6671	20	in gene	0	1	0	9	15	6	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene USP45	USP45, MGC14793	ubiquitin specific peptidase 45	NM_001080481	224441_s_at, 238057_at	NP_001073950.1
GeneID:10973	ASCC3	6	100,956,608	101,329,224	372,616	-	1	4_A375_EGR1..1..7069	104	in gene	0	0	1	7	14	15	1	4_A375_EGR1..1	15	Gene ASCC3	dJ121G13.4, HELIC1, RNAH, ASCC3, DJ467N11.1, MGC26074, ASC1p200	activating signal cointegrator 1 complex subunit 3	NM_006828, NM_022091, hCT2344462.1, hCT2344463.1	212815_at, 231289_at	NP_006819.2, NP_071374.1, EAW48449.1, EAW48450.1
GeneID:2898	GRIK2	6	101,846,861	102,517,958	671,097	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4781, 2_A375_pNL97_plus_lncRNA_AR..1..6672, 1_A375_pNL7_minus_lncRNA_AR..1..4782, 2_A375_pNL97_plus_lncRNA_AR..1..6673	-5421, -5469, 215939, 267411	upstream, upstream, in gene, in gene	1	1	0	14.67	16.67	5	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene GRIK2	MGC74427, GLR6, GLUR6, EAA4, GLUK6, GRIK2, MRT6	glutamate receptor, ionotropic, kainate 2	NM_021956, NM_175768, NM_001166247, hCT2331868.2, hCT2331869.2, hCT2341428.1	1555375_at, 1560142_at, 1560265_at, 1563754_at, 213845_at, 215655_at	NP_068775.1, NP_786944.1, NP_001159719.1, EAW48446.1, EAW48447.1, EAW48448.1
GeneID:57531	HACE1	6	105,175,968	105,307,794	131,826	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6674	274	in gene	0	1	0	15	17	7	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene HACE1	HACE1		NM_020771, hCT2349187.0, hCT2349188.0, hCT2349189.0	227471_at	NP_065822.2, EAW48438.1, EAW48437.1, EAW48439.1
GeneID:5550	PREP	6	105,725,442	105,850,999	125,557	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4783, 2_A375_pNL97_plus_lncRNA_AR..1..6677	23, -355	in gene, upstream	1	1	0	22	14	4	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene PREP	MGC16060, PE, PEP, PREP	prolyl endopeptidase	NM_002726, hCT1955484.1	204117_at, 229644_at, 37950_at	NP_002717.3, EAW48426.1
GeneID:100506148	LOC100506148	6	105,825,260	105,851,000	25,740	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4783, 2_A375_pNL97_plus_lncRNA_AR..1..6677	25716, 26094	in gene, downstream	1	1	0	22	14	4	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene LOC100506148		hypothetical LOC100506148	XR_112906, XR_110205, XR_113966		
GeneID:639	PRDM1	6	106,534,195	106,557,814	23,619	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6678	-3	upstream	0	1	0	10	13	6	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene PRDM1	MGC118922, PRDM1, MGC118923, MGC118924, PRDI-BF1, BLIMP1, MGC118925	PR domain containing 1, with ZNF domain	NM_182907, NM_001198, hCT2332068.1, hCT2332067.1, hCT2352163.0, hCT24713.4	217192_s_at, 228964_at, 235686_at	NP_878911.1, NP_001189.2, EAW48419.1, EAW48420.1, EAW48421.1, EAW48422.1
GeneID:9474	ATG5	6	106,632,352	106,773,695	141,343	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6679	116	in gene	0	1	0	13	13	6	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene ATG5	hAPG5, APG5-LIKE, ATG5, ASP, APG5L, APG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	NM_004849, hCT2331941.0, hCT2352093.0, hCT2352094.0, hCT24151.3, hCT1962562.1	202511_s_at, 202512_s_at, 210639_s_at	NP_004840.1, EAW48415.1, EAW48414.1, EAW48416.1, EAW48417.1, EAW48418.1
GeneID:202	AIM1	6	106,959,730	107,018,335	58,605	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6680	-1170	upstream	0	1	0	12	23	7	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene AIM1	CRYBG1, ST4, AIM1	absent in melanoma 1	NM_001624, hCT2332070.0, hCT24714.3	212543_at	NP_001615.1, EAW48412.1, EAW48413.1
GeneID:84816	RTN4IP1	6	107,018,903	107,077,373	58,470	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6681	-3	upstream	0	1	0	9	20	6	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene RTN4IP1	MGC12934, NIMP, RTN4IP1	reticulon 4 interacting protein 1	NM_032730, hCT2331938.0, hCT2352057.0, hCT35127.3	1555879_a_at, 224509_s_at	NP_116119.2, EAW48409.1, EAW48410.1, EAW48411.1
GeneID:55278	QRSL1	6	107,077,441	107,116,292	38,851	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6681	-65	upstream	0	1	0	9	20	6	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene QRSL1	DKFZp564C1278, QRSL1, GatA, FLJ12169, FLJ13447, FLJ10989	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	NM_018292, hCT2332071.0, hCT35123.3	218948_at, 218949_s_at, 233089_at, 241933_at	NP_060762.3, EAW48408.1, EAW48407.1
GeneID:51250	C6orf203	6	107,349,407	107,372,546	23,139	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4784, 2_A375_pNL97_plus_lncRNA_AR..1..6682	-95, -63	upstream, upstream	1	1	0	57	72	6	1	2_A375_pNL97_plus_lncRNA_AR..1	72	Gene C6orf203	FLJ34245, C6orf203, PRED31, RP11-59I9.1	chromosome 6 open reading frame 203	NM_016487, NM_001142468, NM_001142470, hCT2331908.0	223576_at	NP_057571.1, NP_001135940.1, NP_001135942.1, EAW48402.1
GeneID:57673	BEND3	6	107,386,385	107,435,636	49,251	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6683	20	in gene	0	1	0	9	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene BEND3	KIAA1553, BEND3, RP11-59I9.2	BEN domain containing 3	NM_001080450	227920_at	NP_001073919.1
GeneID:55084	SOBP	6	107,811,317	107,982,513	171,196	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6684	-437	upstream	0	1	0	7	15	9	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene SOBP	FLJ10159, SOBP, JXC1, MRAMS	sine oculis binding protein homolog (Drosophila)	NM_018013, hCT2331921.0, hCT2331923.0, hCT2331924.0	1563906_at, 1569351_at, 218974_at, 229034_at, 229646_at, 233786_at, 234098_at, 244279_at	NP_060483.3, EAW48399.1, EAW48397.1, EAW48398.1
GeneID:2309	FOXO3	6	108,881,026	109,005,971	124,945	+	1	4_A375_EGR1..1..7070	766	in gene	0	0	1	11	6	16	1	4_A375_EGR1..1	16	Gene FOXO3	FOXO3A, MGC31925, FKHRL1P2, AF6q21, FOXO2, FKHRL1, FOXO3, DKFZp781A0677, MGC12739	forkhead box O3	NM_001455, NM_201559, hCT2352099.0, hCT25324.3	204131_s_at, 204132_s_at, 210655_s_at, 217399_s_at, 224889_at, 224891_at, 231548_at	NP_001446.1, NP_963853.1, EAW48373.1, EAW48374.1
GeneID:8763	CD164	6	109,687,717	109,703,762	16,045	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6685	-46	upstream	0	1	0	12	20	14	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CD164	MGC-24, MUC-24, CD164, endolyn	CD164 molecule, sialomucin	NM_006016, NM_001142401, NM_001142402, NM_001142403, NM_001142404, hCT2331843.0, hCT2331844.0, hCT2352095.0, hCT2352096.0, hCT2352097.0, hCT25321.3, hCT1962572.1, hCT1966512.1	208405_s_at, 208653_s_at, 208654_s_at	NP_006007.2, NP_001135873.1, NP_001135874.1, NP_001135875.1, NP_001135876.1, EAW48355.1, EAW48348.1, EAW48349.1, EAW48350.1, EAW48351.1, EAW48352.1, EAW48353.1, EAW48354.1
GeneID:285755	PPIL6	6	109,711,416	109,762,374	50,958	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6685	58566	downstream	0	1	0	12	20	14	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PPIL6	dJ919F19.1, RSPH12, MGC27054, MGC41939, bA425D10.6, PPIL6, MGC27056	peptidylprolyl isomerase (cyclophilin)-like 6	NM_173672, NM_001111298, hCT25327.3	1553684_at, 1560910_at, 236187_s_at	NP_775943.1, NP_001104768.2, EAW48347.1
GeneID:2830	GPR6	6	110,300,298	110,301,923	1,625	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4785, 2_A375_pNL97_plus_lncRNA_AR..1..6686	-410, -394	upstream, upstream	1	1	0	18	22	5	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene GPR6	GPR6		NM_005284	1553507_a_at, 214655_at	NP_005275.1
GeneID:8936	WASF1	6	110,421,022	110,501,207	80,185	-	2	2_A375_pNL97_plus_lncRNA_AR..1..6687, 2_A375_pNL97_plus_lncRNA_AR..1..6688	6295, 183	in gene, in gene	0	1	0	9.5	17	5	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene WASF1	WAVE1, KIAA0269, SCAR1, FLJ31482, WASF1, WAVE	WAS protein family, member 1	NM_003931, NM_001024934, NM_001024935, NM_001024936, hCT2331807.0, hCT2331809.0, hCT33166.3, hCT1952470.1, hCT1952471.1, hCT1952472.1	204165_at	NP_003922.1, NP_001020105.1, NP_001020106.1, NP_001020107.1, EAW48325.1, EAW48329.1, EAW48326.1, EAW48327.1, EAW48328.1, EAW48330.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:51362	CDC40	6	110,501,624	110,553,423	51,799	+	2	2_A375_pNL97_plus_lncRNA_AR..1..6887, 2_A375_pNL97_plus_lncRNA_AR..1..6888	-6712, -600	upstream, upstream	0	1	0	9.5	17	5	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CDC40	MGC102802, EHB3, CDC40, PRPF17, FLJ10564, PRP17	cell division cycle 40 homolog (S. cerevisiae)	NM_015891, hCT2332039.2, hCT2332040.1, hCT2348022.0, hCT2348023.1, hCT2350507.0, hCT1960520.3	203376_at, 203377_s_at	NP_056975.1, EAW48324.1, EAW48319.1, EAW48320.1, EAW48322.1, EAW48323.1, EAW48321.1
GeneID:728464	C6orf186	6	110,567,149	110,679,475	112,326	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4786, 2_A375_pNL97_plus_lncRNA_AR..1..6889	102771, 102771	in gene, in gene	1	1	0	20	24	7	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene C6orf186	C6orf186, dJ71D21.2, FLJ45203	chromosome 6 open reading frame 186	NM_001123364		NP_001116836.1
GeneID:23097	CDK19	6	110,931,161	111,136,412	205,251	-	2	2_A375_pNL97_plus_lncRNA_AR..1..6891, 2_A375_pNL97_plus_lncRNA_AR..1..6892	412, -196	in gene, upstream	0	1	0	12.5	14.5	10	2	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene CDK19	bA346C16.3, CDK19, CDC2L6, CDK11, KIAA1028	cyclin-dependent kinase 19	NM_015076, hCT25091.3	211706_s_at, 212897_at, 212899_at, 235226_at	NP_055891.1, EAW48312.1
GeneID:84154	RPF2	6	111,303,291	111,346,794	43,503	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6893	53	in gene	0	1	0	10	16	7	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene RPF2	RPF2, BXDC1, bA397G5.4, FLJ21087	ribosome production factor 2 homolog (S. cerevisiae)	NM_032194, hCT2348140.0, hCT2348141.0, hCT2352063.0, hCT25092.5	225686_at	NP_115570.1, EAW48302.1, EAW48301.1, EAW48303.1, EAW48304.1
GeneID:5980	REV3L	6	111,620,234	111,804,414	184,180	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4787, 2_A375_pNL97_plus_lncRNA_AR..1..6894	-308, -194	upstream, upstream	1	1	0	14	17	14	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene REV3L	POLZ, REV3, REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	NM_002912, hCT2331963.0, hCT2331966.0, hCT1960519.1	208070_s_at, 238736_at	NP_002903.3, EAW48292.1, EAW48293.1, EAW48294.1
GeneID:643749	LOC643749	6	111,804,675	111,923,498	118,823	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4787, 2_A375_pNL97_plus_lncRNA_AR..1..6894	45, -67	in gene, upstream	1	1	0	14	17	14	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC643749		hypothetical LOC643749	NR_034108, NR_034109, NR_034110, NR_034111	1562566_at, 236555_at	
GeneID:2534	FYN	6	111,982,465	112,194,827	212,142	-	1	4_A375_EGR1..1..7072	-77	upstream	0	0	1	8	10	19	1	4_A375_EGR1..1	19	Gene FYN	FYN, SYN, SLK, MGC45350	FYN oncogene related to SRC, FGR, YES	NM_002037, NM_153047, NM_153048, hCT2331948.0, hCT2331949.0, hCT2331950.0, hCT2331951.0, hCT2331953.0, hCT2331954.0, hCT28018.2	1559101_at, 210105_s_at, 212486_s_at, 216033_s_at	NP_002028.1, NP_694592.1, NP_694593.1, EAW48282.1, EAW48283.1, EAW48284.1, EAW48278.1, EAW48279.1, EAW48280.1, EAW48281.1
GeneID:3910	LAMA4	6	112,429,134	112,575,828	146,694	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6896	-558	upstream	0	1	0	6	15	1	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LAMA4	LAMA3, LAMA4, LAMA4*-1, DKFZp686D23145	laminin, alpha 4	NM_002290, NM_001105206, NM_001105207, NM_001105208, NM_001105209, hCT2331765.0, hCT2331766.0, hCT2331767.0, hCT2352087.0, hCT24147.3	202202_s_at, 210089_s_at, 210989_at, 210990_s_at, 216061_at	NP_002281.2, NP_001098676.1, NP_001098677.1, NP_001098678.1, NP_001098679.1, EAW48266.1, EAW48267.1, EAW48268.1, EAW48269.1, EAW48270.1
GeneID:100506430	LOC100506430	6	112,557,797	112,627,885	70,088	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6896	18587	in gene	0	1	0	6	15	1	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LOC100506430		hypothetical LOC100506430	XR_112921, XR_110211, XR_113909		
GeneID:3066	HDAC2	6	114,257,320	114,292,359	35,039	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4789, 2_A375_pNL97_plus_lncRNA_AR..1..6898, 4_A375_EGR1..1..7073	-57, 231, 647	upstream, in gene, in gene	1	1	1	13	18.5	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene HDAC2	YAF1, HDAC2, RPD3	histone deacetylase 2	NM_001527, NR_033441, hCT2331725.0, hCT2352103.0, hCT2352104.0, hCT12472.3	201833_at, 242141_at	NP_001518.3, EAW48255.1, EAW48252.1, EAW48253.1, EAW48254.1
GeneID:51389	RWDD1	6	116,892,583	116,914,438	21,855	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4790, 1_A375_pNL7_minus_lncRNA_AR..1..4791, 2_A375_pNL97_plus_lncRNA_AR..1..6899, 2_A375_pNL97_plus_lncRNA_AR..1..6900	-103, 25593, -103, 25561	upstream, downstream, upstream, downstream	1	1	0	34	38	4.5	2	2_A375_pNL97_plus_lncRNA_AR..1	63	Gene RWDD1	PTD013, CGI-24, RWDD1	RWD domain containing 1	NM_015952, NM_016104, NM_001007464, hCT2352070.0, hCT11949.2	219598_s_at	NP_057036.2, NP_057188.2, NP_001007465.1, EAW48221.1, EAW48222.1
GeneID:221302	ZUFSP	6	116,956,781	116,989,973	33,192	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6901	149	in gene	0	1	0	13	13	7	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene ZUFSP	dJ412I7.3, ZUFSP, C6orf113	zinc finger with UFM1-specific peptidase domain	NM_145062, hCT2332371.0, hCT12855.3	228330_at	NP_659499.2, EAW48217.1, EAW48218.1
GeneID:3841	KPNA5	6	117,002,367	117,083,030	80,663	+	1	4_A375_EGR1..1..7075	-191	upstream	0	0	1	10	7	18	1	4_A375_EGR1..1	18	Gene KPNA5	IPOA6, SRP6, KPNA5	karyopherin alpha 5 (importin alpha 6)	NM_002269, hCT1953794.1	206241_at	NP_002260.2, EAW48216.1
GeneID:6098	ROS1	6	117,609,530	117,747,018	137,488	-	1	4_A375_EGR1..1..7076	52415	in gene	0	0	1	3	4	15	1	4_A375_EGR1..1	15	Gene ROS1	MCF3, ROS, c-ros-1, ROS1	c-ros oncogene 1, receptor tyrosine kinase	NM_002944, hCT2331700.1, hCT1953788.1	207569_at	NP_002935.2, EAW48209.1, EAW48208.1
GeneID:116150	NUS1	6	117,996,617	118,031,890	35,273	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4792, 2_A375_pNL97_plus_lncRNA_AR..1..6902	-105, -105	upstream, upstream	1	1	0	116	137	6	1	2_A375_pNL97_plus_lncRNA_AR..1	137	Gene NUS1	NgBR, MGC.7199, MGC117249, MGC7199, C6orf68, NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	NM_138459, hCT1640994.2	225070_at, 225071_at	NP_612468.1, EAW59309.1
GeneID:387119	C6orf204	6	118,781,935	119,031,238	249,303	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4793, 2_A375_pNL97_plus_lncRNA_AR..1..6903, 2_A375_pNL97_plus_lncRNA_AR..1..6904	-90, 214246, 59174	upstream, in gene, in gene	1	1	0	19	16.33	5.67	3	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene C6orf204	C6orf204, bA57K17.2, NY-BR-15, MGC131785	chromosome 6 open reading frame 204	NM_206921, NM_001042475, NM_001178035, hCT2331605.0, hCT12046.3	228007_at, 232444_at	NP_996804.2, NP_001035940.1, NP_001171506.1, EAW48196.1, EAW48197.1
GeneID:25842	ASF1A	6	119,215,241	119,230,336	15,095	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4794, 2_A375_pNL97_plus_lncRNA_AR..1..6905	23, 23	in gene, in gene	1	1	0	81	80	6	1	1_A375_pNL7_minus_lncRNA_AR..1	81	Gene ASF1A	CGI-98, HSPC146, ASF1A, CIA, DKFZp547E2110	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	NM_014034, hCT6593.2	203427_at, 203428_s_at, 213561_at	NP_054753.1, EAW48193.1
GeneID:221322	C6orf170	6	121,400,627	121,655,644	255,017	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6906	-36	upstream	0	1	0	10	13	13	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene C6orf170	C6orf170, dJ310J6.1, bA57L9.1, C6orf171, bA301B7.2, BROMI, FLJ30899, FLJ34235	chromosome 6 open reading frame 170	NM_152730, hCT2331463.1, hCT2331464.1, hCT10866.3	1553726_s_at, 232036_at	NP_689943.4, EAW48182.1, EAW48180.1, EAW48181.1
GeneID:7164	TPD52L1	6	125,474,679	125,584,644	109,765	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4795	1	in gene	1	0	0	14	12	3	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene TPD52L1	TPD52L2, TPD52L1, hD53, MGC8556, D53	tumor protein D52-like 1	NM_003287, NM_001003395, NM_001003396, NM_001003397, hCT1970951.1, hCT2352108.0, hCT2352109.0, hCT12023.2, hCT1951799.1, hCT1951800.1	203786_s_at, 210372_s_at	NP_003278.1, NP_001003395.1, NP_001003396.1, NP_001003397.1, EAW48144.1, EAW48147.1, EAW48142.1, EAW48143.1, EAW48145.1, EAW48146.1
GeneID:51020	HDDC2	6	125,596,496	125,623,282	26,786	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6907	162	in gene	0	1	0	13	17	6	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene HDDC2	NS5ATP2, HDDC2, dJ167O5.2, MGC87330, C6orf74, CGI-130	HD domain containing 2	NM_016063, hCT1969242.2, hCT1969243.2, hCT2340250.0, hCT2340251.0, hCT11060.3, hCT1951798.2	203259_s_at, 203260_at	NP_057147.2, EAW48141.1, EAW48136.1, EAW48137.1, EAW48139.1, EAW48140.1, EAW48138.1
GeneID:135112	NCOA7	6	126,112,001	126,252,266	140,265	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4796, 2_A375_pNL97_plus_lncRNA_AR..1..6908	21951, 21983	in gene, in gene	1	1	0	15	19	5	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene NCOA7	NCOA7, MGC88425, dJ187J11.3, ESNA1, Nbla10993, ERAP140, Nbla00052, FLJ45605	nuclear receptor coactivator 7	NM_181782, NM_001122842, hCT2331523.0, hCT2331524.0, hCT2331525.0, hCT2352173.0, hCT2352174.0	1566605_at, 225344_at, 243807_at	NP_861447.3, NP_001116314.1, EAW48130.1, EAW48131.1, EAW48132.1, EAW48133.1, EAW48134.1
GeneID:135114	HINT3	6	126,277,861	126,301,390	23,529	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4797, 2_A375_pNL97_plus_lncRNA_AR..1..6909	27, 27	in gene, in gene	1	1	0	28	27	9	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene HINT3	HINT3, FLJ33126, HINT4, FLJ99898, MGC22976	histidine triad nucleotide binding protein 3	NM_138571, hCT2331526.0, hCT12418.3	226533_at, 226537_at, 228697_at	NP_612638.3, EAW48129.1, EAW48128.1
GeneID:81847	RNF146	6	127,588,020	127,609,507	21,487	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6911	204	in gene	0	1	0	13	17	5	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene RNF146	dJ351K20.1, RP3-351K20.1, RNF146, DKFZp434O1427	ring finger protein 146	NM_030963, hCT2352186.0, hCT2352187.0, hCT1825330.2, hCT1951792.1, hCT1951793.1	221430_s_at, 223686_s_at	NP_112225.2, EAW48109.1, EAW48110.1, EAW48111.1, EAW48112.1, EAW48113.1
GeneID:387104	C6orf174	6	127,759,551	127,840,500	80,949	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4800, 2_A375_pNL97_plus_lncRNA_AR..1..6912	2996, 2932	in gene, in gene	1	1	0	15	20	9	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C6orf174	C6orf174, dJ403A15.3	chromosome 6 open reading frame 174	NM_001012279	1569146_s_at, 233050_at	NP_001012279.1
GeneID:9439	MED23	6	131,895,106	131,949,363	54,257	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4801, 2_A375_pNL97_plus_lncRNA_AR..1..6913	-109, -45	upstream, upstream	1	1	0	29	47	10	1	2_A375_pNL97_plus_lncRNA_AR..1	47	Gene MED23	MED23, CRSP3, SUR2, DRIP130, CRSP133, DKFZp434H0117, SUR-2, CRSP130	mediator complex subunit 23	NM_015979, NM_004830, hCT2331416.0, hCT2331417.0, hCT2352135.0, hCT12114.3	218846_at, 223946_at, 223947_s_at, 242706_s_at, 242707_at	NP_057063.2, NP_004821.2, EAW48049.1, EAW48050.1, EAW48051.1, EAW48052.1
GeneID:5169	ENPP3	6	131,958,442	132,068,550	110,108	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4801, 2_A375_pNL97_plus_lncRNA_AR..1..6913	-8970, -9034	upstream, upstream	1	1	0	29	47	10	1	2_A375_pNL97_plus_lncRNA_AR..1	47	Gene ENPP3	NPP3, B10, PDNP3, ENPP3, CD203c, PD-IBETA	ectonucleotide pyrophosphatase/phosphodiesterase 3	NM_005021, hCT2331597.0, hCT2331598.0, hCT2331599.0	222936_x_at, 232737_s_at	NP_005012.2, EAW48045.1, EAW48044.1, EAW48046.1
GeneID:100131774	LOC100131774	6	132,266,630	132,269,801	3,171	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6914	5086	downstream	0	1	0	17	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100131774		hypothetical LOC100131774	XR_112914, XR_110171, XR_113917		
GeneID:1490	CTGF	6	132,269,316	132,272,518	3,202	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6914	822	in gene	0	1	0	17	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CTGF	IGFBP8, CTGF, CCN2, HCS24, MGC102839, NOV2	connective tissue growth factor	NM_001901, hCT2331409.0, hCT13202.3	209101_at	NP_001892.1, EAW48038.1, EAW48039.1
GeneID:6206	RPS12	6	133,135,708	133,138,703	2,995	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4802, 2_A375_pNL97_plus_lncRNA_AR..1..6915, 4_A375_EGR1..1..7077	-236, -220, -26	upstream, upstream, upstream	1	1	1	37	32	18	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene RPS12	S12, RPS12		NM_001016, hCT2331681.0, hCT2331682.0, hCT2331683.0, hCT2331684.0	213377_x_at	NP_001007.2, EAW48008.1, EAW48009.1, EAW48010.1, EAW48011.1
GeneID:594837	SNORD101	6	133,136,446	133,136,518	72	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4802, 2_A375_pNL97_plus_lncRNA_AR..1..6915, 4_A375_EGR1..1..7077	-974, -958, -766	upstream, upstream, upstream	1	1	1	37	32	18	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene SNORD101	SNORD101, U101	small nucleolar RNA, C/D box 101	NR_002434		
GeneID:594838	SNORD100	6	133,137,941	133,138,016	75	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4802, 2_A375_pNL97_plus_lncRNA_AR..1..6915, 4_A375_EGR1..1..7077	-2469, -2453, -2261	upstream, upstream, upstream	1	1	1	37	32	18	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene SNORD100	SNORD100, HBII-429	small nucleolar RNA, C/D box 100	NR_002435		
GeneID:594839	SNORA33	6	133,138,358	133,138,490	132	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4802, 2_A375_pNL97_plus_lncRNA_AR..1..6915, 4_A375_EGR1..1..7077	-2886, -2870, -2678	upstream, upstream, upstream	1	1	1	37	32	18	1	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene SNORA33	ACA33, SNORA33	small nucleolar RNA, H/ACA box 33	NR_002436		
GeneID:9519	TBPL1	6	134,274,301	134,308,629	34,328	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4803, 4_A375_EGR1..1..7078	-957, 195	upstream, in gene	1	0	1	14	12	10	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene TBPL1	TLF, STUD, MGC.8389, MGC.9620, TRF2, TBPL1, TLP	TBP-like 1	NM_004865, hCT2331230.0, hCT2331231.0, hCT2331232.0, hCT2352066.0	208398_s_at	NP_004856.1, EAW47996.1, EAW47995.1, EAW47997.1, EAW47998.1
GeneID:54806	AHI1	6	135,605,110	135,818,903	213,793	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4806, 2_A375_pNL97_plus_lncRNA_AR..1..6916, 4_A375_EGR1..1..7079	71, 87, 151	in gene, in gene, in gene	1	1	1	18	17	14	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene AHI1	FLJ20069, JBTS3, dJ71N10.1, AHI1, ORF1, FLJ14023, AHI-1, DKFZp686J1653	Abelson helper integration site 1	NM_017651, NM_001134830, NM_001134831, NM_001134832, hCT2331254.0, hCT2331256.0, hCT2331257.0, hCT2331258.0, hCT2331259.0	220841_s_at, 220842_at, 221569_at, 232461_at, 244699_at	NP_060121.3, NP_001128302.1, NP_001128303.1, NP_001128304.1, EAW47962.1, EAW47966.1, EAW47963.1, EAW47964.1, EAW47965.1
GeneID:100131814	C6orf217	6	135,818,939	136,011,976	193,037	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4806, 2_A375_pNL97_plus_lncRNA_AR..1..6916, 4_A375_EGR1..1..7079	-107, -123, -187	upstream, upstream, upstream	1	1	1	18	17	14	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene C6orf217	C6orf217, NCRNA00271	chromosome 6 open reading frame 217	NR_026805		
GeneID:113115	FAM54A	6	136,552,168	136,571,449	19,281	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6918	-103	upstream	0	1	0	12	22	6	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene FAM54A	DUFD1, FAM54A	family with sequence similarity 54, member A	NM_138419, NM_001099286, hCT2331245.0, hCT2331246.0, hCT24553.2	228069_at, 234944_s_at, 234945_at	NP_612428.2, NP_001092756.1, EAW47953.1, EAW47954.1, EAW47955.1
GeneID:9774	BCLAF1	6	136,578,001	136,610,989	32,988	-	2	2_A375_pNL97_plus_lncRNA_AR..1..6918, 4_A375_EGR1..1..7080	39437, 13	downstream, in gene	0	1	1	13.5	16	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene BCLAF1	KIAA0164, BCLAF1, BTF, bK211L9.1	BCL2-associated transcription factor 1	NM_001077440, NM_014739, NM_001077441, hCT2331242.0, hCT2331244.0, hCT2352069.0, hCT24550.3	201083_s_at, 201084_s_at, 201101_s_at, 214499_s_at, 229454_at, 239897_at	NP_001070908.1, NP_055554.1, NP_001070909.1, EAW47949.1, EAW47951.1, EAW47952.1, EAW47950.1
GeneID:4217	MAP3K5	6	136,878,187	137,113,656	235,469	-	1	4_A375_EGR1..1..7081	-424	upstream	0	0	1	8	12	16	1	4_A375_EGR1..1	16	Gene MAP3K5	MAP3K5, MEKK5, ASK1, MAPKKK5	mitogen-activated protein kinase kinase kinase 5	NM_005923, hCT24551.4	203837_at	NP_005914.1, EAW47942.1
GeneID:3459	IFNGR1	6	137,518,621	137,540,567	21,946	-	1	4_A375_EGR1..1..7082	39	in gene	0	0	1	7	13	16	1	4_A375_EGR1..1	16	Gene IFNGR1	CD119, IFNGR, IFNGR1, FLJ45734	interferon gamma receptor 1	NM_000416, hCT2331366.0, hCT7835.3	202727_s_at, 211676_s_at, 242903_at	NP_000407.1, EAW47931.1, EAW47932.1
GeneID:85021	REPS1	6	139,225,620	139,309,398	83,778	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6919	54	in gene	0	1	0	13	15	14	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene REPS1	RALBP1, REPS1	RALBP1 associated Eps domain containing 1	NM_031922, NM_001128617, hCT2331167.0, hCT2352180.0, hCT2352181.0, hCT9340.2, hCT1951797.1	215201_at, 215922_at, 224366_s_at	NP_114128.3, NP_001122089.1, EAW47904.1, EAW47905.1, EAW47906.1, EAW47907.1, EAW47903.1
GeneID:10370	CITED2	6	139,693,396	139,695,785	2,389	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4807, 2_A375_pNL97_plus_lncRNA_AR..1..6920	-759, -151	upstream, upstream	1	1	0	25	31	13	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene CITED2	MRG1, P35SRJ, CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	NM_006079, NM_001168388, NM_001168389, hCT2331154.0, hCT2331156.0, hCT2331157.0, hCT2331158.0, hCT24122.3	207980_s_at, 209357_at, 227287_at	NP_006070.2, NP_001161860.1, NP_001161861.1, EAW47891.1, EAW47893.1, EAW47894.1, EAW47892.1, EAW47895.1
GeneID:51534	VTA1	6	142,468,410	142,542,085	73,675	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4808, 2_A375_pNL97_plus_lncRNA_AR..1..6923	-154, -186	upstream, upstream	1	1	0	18	25	13	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene VTA1	DRG-1, C6orf55, My012, VTA1, DRG1, SBP1, HSPC228, LIP5, FLJ27228	Vps20-associated 1 homolog (S. cerevisiae)	NM_016485, hCT1969226.2, hCT9175.5, hCT1962368.2	223021_x_at, 223022_s_at, 224437_s_at	NP_057569.2, EAW47884.1, EAW47883.1, EAW47885.1
GeneID:57211	GPR126	6	142,623,056	142,767,403	144,347	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4809	16	in gene	1	0	0	16	15	10	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene GPR126	GPR126, APG1, PS1TP2, VIGR, DREG	G protein-coupled receptor 126	NM_001032395, NM_001032394, NM_020455, NM_198569, hCT2331298.0, hCT2331304.0, hCT2331309.1, hCT2352107.0, hCT9176.3, hCT1824738.3, hCT1824736.1	1553025_at, 213094_at, 233887_at	NP_001027567.1, NP_001027566.1, NP_940971.1, NP_065188.4, EAW47878.1, EAW47881.1, EAW47875.1, EAW47876.1, EAW47877.1, EAW47879.1, EAW47880.1
GeneID:134637	ADAT2	6	143,743,969	143,771,841	27,872	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4810, 2_A375_pNL97_plus_lncRNA_AR..1..6924	-15, -15	upstream, upstream	1	1	0	18	23	10	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ADAT2	FLJ44213, dJ20N2, ADAT2, DKFZp686L1118, DEADC1, dJ20N2.1, TAD2	adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. cerevisiae)	NM_182503, hCT2349197.0, hCT9154.3	227213_at, 236817_at	NP_872309.2, EAW47866.1, EAW47867.1

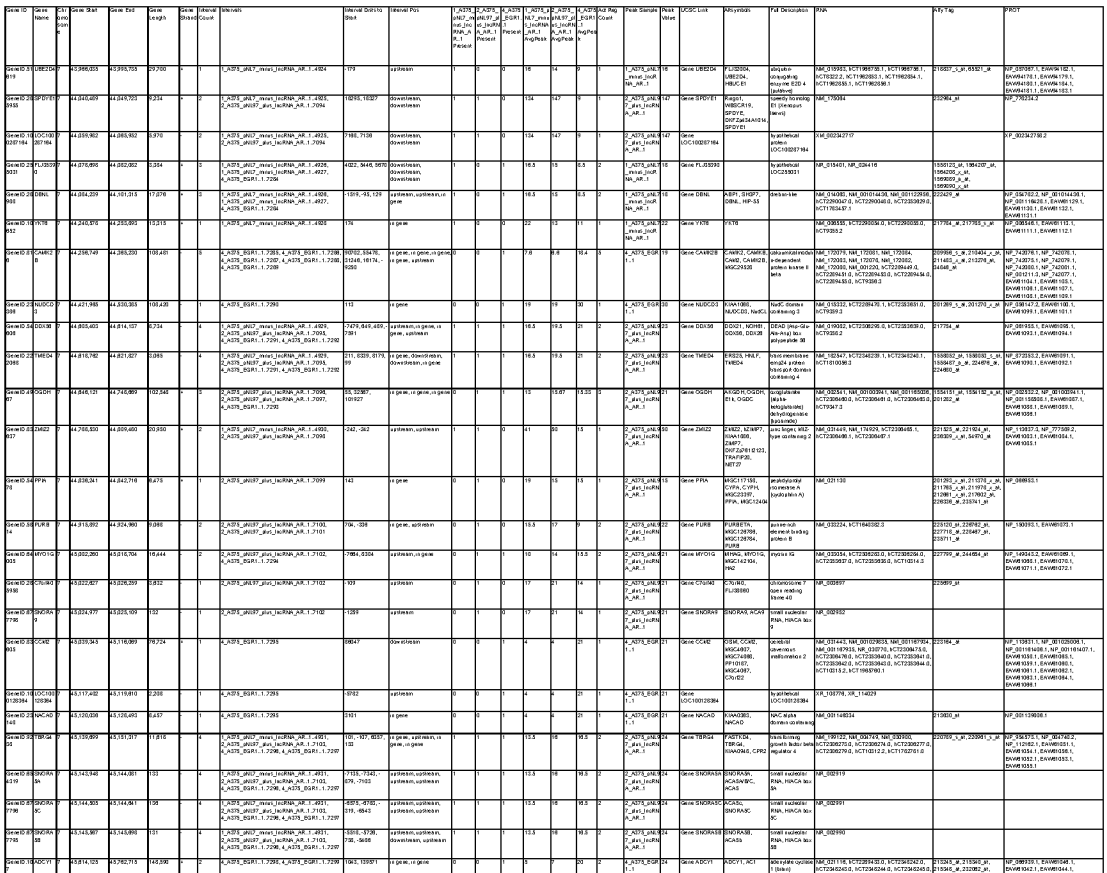
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:8504	PEX3	6	143,771,916	143,811,753	39,835	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4810, 2_A375_pNL97_plus_lncRNA_AR..1..6924	-62, -62	upstream, upstream	1	1	0	16	23	10	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene PEX3	DKFZp686N14184, TRG18, FLJ13531, PEX3	peroxisomal biogenesis factor 3	NM_003630, hCT9157.4	203970_s_at, 203972_s_at	NP_003621.1, EAW47666.1
GeneID:7957	EPM2A	6	145,946,440	146,056,991	110,551	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6925	863	in gene	0	1	0	9	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene EPM2A	EPM2A, EPM2, MELF	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	NM_005670, NM_001018041, hCT2352164.0, hCT2352165.0, hCT9116.3	205231_s_at, 210870_s_at, 216079_at	NP_005661.1, NP_001018051.1, EAW47642.1, EAW47643.1, EAW47644.1
GeneID:100507557	LOC100507557	6	146,056,008	146,208,186	152,178	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6925	120	in gene	0	1	0	9	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100507557		hypothetical LOC100507557	XR_112933, XR_112934, XR_112935, XR_110184, XR_110183, XR_110185, XR_113930, XR_113929, XR_113931		
GeneID:2911	GRM1	6	146,348,782	146,758,731	409,949	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4811, 2_A375_pNL97_plus_lncRNA_AR..1..6926	722, 618	in gene, in gene	1	1	0	15	29	3	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene GRM1	MGLUR1, GRM1A, GPRC1A, mGlu1, GRM1, MGLUR1A	glutamate receptor, metabotropic 1	NM_000838, NM_001114329, hCT2331330.0, hCT7807.3	207299_s_at, 210939_s_at, 210940_s_at	NP_000829.2, NP_001107801.1, EAW47634.1, EAW47635.1
GeneID:23328	SASH1	6	148,663,729	148,873,184	209,455	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6927	175	in gene	0	1	0	8	15	3	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene SASH1	dJ323M4, KIAA0790, SH3D6A, SASH1, RP3-323M4.1, dJ323M4.1	SAM and SH3 domain containing 1	NM_015278, hCT2330910.0, hCT7809.3	213236_at, 226022_at, 41644_at	NP_056093.3, EAW47815.1, EAW47816.1
GeneID:10090	UST	6	149,068,271	149,398,126	329,855	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4812, 1_A375_pNL7_minus_lncRNA_AR..1..4813, 2_A375_pNL97_plus_lncRNA_AR..1..6928	188785, 265073, 265073	in gene, in gene, in gene	1	1	0	16	12.5	1	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene UST	2OST, UST	uronyl-2-sulfotransferase	NM_005715, hCT2330916.0	205138_s_at, 205139_s_at	NP_005706.1, EAW47812.1
GeneID:23118	MAP3K7IP2	6	149,639,436	149,732,747	93,311	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6929	-1088	upstream	0	1	0	14	18	7	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MAP3K7IP2	FLJ21885, MAP3K7IP2, TAB2, CHTD2, KIAA0733	TGF-beta activated kinase 1/MAP3K7 binding protein 2	NM_015093, hCT2330924.0, hCT2330926.0, hCT13825.3	210284_s_at, 212184_s_at	NP_055908.1, EAW47805.1, EAW47806.1, EAW47807.1
GeneID:85313	PPIL4	6	149,825,631	149,867,171	41,540	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4814, 2_A375_pNL97_plus_lncRNA_AR..1..6930	-29, 3	upstream, in gene	1	1	0	19	22	8	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene PPIL4	HDCME13P, PPIL4	peptidylprolyl isomerase (cyclophilin)-like 4	NM_139126, hCT2330712.1, hCT13823.4	226472_at	NP_624311.1, EAW47800.1, EAW47799.1
GeneID:348995	NUP43	6	150,045,457	150,067,688	22,231	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6931	-3320	upstream	0	1	0	9	14	10	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene NUP43	NUP43, bA350J20.1, p42, FLJ13287	nucleoporin 43kDa	NM_198887	219007_at, 238474_at	NP_942590.1
GeneID:5110	PCMT1	6	150,070,831	150,132,557	61,726	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6931	177	in gene	0	1	0	9	14	10	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene PCMT1	PCMT1		NM_005389, hCT2330960.0, hCT12094.2, hCT1953605.1	205202_at, 208857_s_at, 210156_s_at	NP_005380.2, EAW47788.1, EAW47786.1, EAW47787.1
GeneID:353091	RAET1G	6	150,236,014	150,244,214	8,200	-	1	4_A375_EGR1..1..7084	118	in gene	0	0	1	10	10	19	1	4_A375_EGR1..1	19	Gene RAET1G	ULBP5, RAET1G	retinoic acid early transcript 1G	NM_001001788, hCT13172.4		NP_001001788.2, EAW47779.1
GeneID:79465	ULBP3	6	150,385,743	150,390,202	4,459	-	2	4_A375_EGR1..1..7085, 4_A375_EGR1..1..7086	11386, 58	downstream, in gene	0	0	1	6.5	7.5	15	2	4_A375_EGR1..1	17	Gene ULBP3	ULBP3, RAET1N	UL16 binding protein 3	NM_024518, hCT2330868.0	231748_at	NP_078794.1, EAW47772.1
GeneID:55005	RMND1	6	151,725,989	151,773,316	47,327	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4815	-60	upstream	1	0	0	21	14	10	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene RMND1	bA351K16.3, MGC88260, MGC117362, RMND1, FLJ20627, bA351K16, RMD1, MGC149570, C6orf96	required for meiotic nuclear division 1 homolog (S. cerevisiae)	NM_017909, hCT2330734.0, hCT2352200.0, hCT13079.3, hCT1953609.1	1555201_a_at, 220329_s_at	NP_060379.2, EAW47749.1, EAW47746.1, EAW47747.1, EAW47748.1
GeneID:79624	C6orf211	6	151,773,422	151,791,232	17,810	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4815	-46	upstream	1	0	0	21	14	10	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene C6orf211	C6orf211, DKFZp566I174, FLJ12910	chromosome 6 open reading frame 211	NM_024573, hCT2352203.0, hCT1953611.1	218195_at	NP_078849.1, EAW47744.1, EAW47745.1
GeneID:2099	ESR1	6	152,011,631	152,424,409	412,778	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4816	156669	in gene	1	0	0	19	12	3	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene ESR1	ESRA, ESR, DKFZp686N23123, ER, NR3A1, Era, ESR1	estrogen receptor 1	NM_000125, NM_001122740, NM_001122741, NM_001122742, hCT2331066.0, hCT1953606.1	205225_at, 211233_x_at, 211234_x_at, 211235_s_at, 211627_x_at, 215552_s_at, 217163_at, 217190_x_at	NP_000116.2, NP_001116212.1, NP_001116213.1, NP_001116214.1, EAW47740.1, EAW47741.1
GeneID:7432	VIP	6	153,071,933	153,080,900	8,967	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4817	19	in gene	1	0	0	14	13	2	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene VIP	PHM27, VIP, MGC13587	vasoactive intestinal peptide	NM_003381, NM_194435, hCT2352148.0, hCT13142.2	206577_at	NP_003372.1, NP_919416.1, EAW47724.1, EAW47725.1
GeneID:4988	OPRM1	6	154,331,636	154,568,001	236,365	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4818, 2_A375_pNL97_plus_lncRNA_AR..1..6932	29066, 29100	in gene, in gene	1	1	0	45	76	8	1	2_A375_pNL97_plus_lncRNA_AR..1	76	Gene OPRM1	LMOR, MOR1, OPRM, OPRM1, KIAA0403, MOR	opioid receptor, mu 1	NM_001008503, NM_001008505, NM_000914, NM_001008504, NM_001145279, NM_001145280, NM_001145281, NM_001145284, NM_001145287, NM_001145286, NM_001145282, NM_001145283, hCT2330621.0, hCT23523.1	207994_s_at, 211359_s_at	NP_001008503.2, NP_001008505.2, NP_001008504.2, NP_000905.3, NP_001138757.1, NP_001138751.1, NP_001138752.1, NP_001138753.1, NP_001138756.1, NP_001138759.1, NP_001138758.1, NP_001138754.1, NP_001138755.1, EAW47704.1, EAW47705.1
GeneID:22826	RBM16	6	155,054,512	155,155,194	100,682	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6933	64	in gene	0	1	0	17	15	6	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene RBM16	KIAA1116, RBM16, SCAF8	RNA binding motif protein 16	NM_014892, hCT2330614.0, hCT24177.3	203250_at	NP_055707.3, EAW47696.1, EAW47697.1
GeneID:26230	TIAM2	6	155,411,423	155,578,857	167,434	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4819, 2_A375_pNL97_plus_lncRNA_AR..1..6934	36961, 81137	in gene, in gene	1	1	0	18.5	14.5	2.5	2	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene TIAM2	TIAM-2, STEF, FLJ41865, TIAM2	T-cell lymphoma invasion and metastasis 2	NM_012454, NM_001010927, hCT2330615.0, hCT1953628.2	219950_s_at, 222942_s_at	NP_036586.2, NP_001010927.1, EAW47692.1, EAW47693.1
GeneID:57492	ARID1B	6	157,099,064	157,531,913	432,849	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4820, 2_A375_pNL97_plus_lncRNA_AR..1..6935	371016, 243656	in gene, in gene	1	1	0	12.5	13.5	6	2	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene ARID1B	OSA2, KIAA1235, ARID1B, ELD/OSA1, BRIGHT, 6A3-5, p250R, P250R, BAF250B, DAN15, BAF250b	AT rich interactive domain 1B (SWI1-like)	NM_017519, NM_020732, hCT2332458.1, hCT2332459.1, hCT2332460.1, hCT2332461.1, hCT2332462.1, hCT2332463.1, hCT2332467.1, hCT2352061.0	1566989_at, 1566990_x_at, 1566991_at, 233339_s_at	NP_059989.2, NP_065783.3, EAW47679.1, EAW47683.1, EAW47684.1, EAW47685.1, EAW47678.1, EAW47680.1, EAW47681.1, EAW47682.1
GeneID:729515	C6orf35	6	157,710,054	157,745,253	35,199	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6936	764	in gene	0	1	0	16	22	13	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene C6orf35	FLJ10029, BM033, MGC34308, C6orf35	chromosome 6 open reading frame 35	NM_018452	218453_s_at, 222638_s_at, 230457_at	NP_060922.2
GeneID:79683	ZDHHC14	6	157,802,557	158,094,977	292,420	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4821, 2_A375_pNL97_plus_lncRNA_AR..1..6937	147939, 74563	in gene, in gene	1	1	0	14.5	13	7	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ZDHHC14	FLJ20984, ZDHHC14, NEW1CP	zinc finger, DHHC-type containing 14	NM_024630, NM_153746, hCT2332472.0, hCT2332474.0, hCT2332475.0, hCT2352162.0, hCT8453.3, hCT1814540.1	1556967_at, 219247_s_at	NP_078906.2, NP_714968.1, EAW47670.1, EAW47671.1, EAW47672.1, EAW47675.1, EAW47673.1, EAW47674.1
GeneID:57583	TMEM181	6	158,957,468	159,056,467	98,999	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4823, 2_A375_pNL97_plus_lncRNA_AR..1..6939, 1_A375_pNL7_minus_lncRNA_AR..1..4824, 4_A375_EGR1..1..7087	-252, -156, 108132, 108132	upstream, upstream, downstream, downstream	1	1	1	20.5	18	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene TMEM181	GPR178, KIAA1423, TMEM181	transmembrane protein 181	NM_020823	225127_at	NP_065874.1
GeneID:6993	DYNLT1	6	159,057,506	159,065,804	8,298	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4824, 4_A375_EGR1..1..7087	204, 204	in gene, in gene	1	0	1	17	9	21	1	4_A375_EGR1..1	21	Gene DYNLT1	DYNLT1, MGC111571, tctex-1, CW-1, TCTEL1	dynein, light chain, Tctex-type 1	NM_006519, hCT2343703.0, hCT2352178.0, hCT7663.3, hCT1953582.2, hCT1963141.2	201999_s_at	NP_006510.1, EAW47658.1, EAW47655.1, EAW47657.1, EAW47656.1, EAW47659.1
GeneID:94120	SYTL3	6	159,071,046	159,185,901	114,855	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4824, 4_A375_EGR1..1..7087	-5446, -5446	upstream, upstream	1	0	1	17	9	21	1	4_A375_EGR1..1	21	Gene SYTL3	MGC118883, MGC118885, SYTL3, MGC105130, MGC118884, SLP3	synaptotagmin-like 3	NM_001009991, hCT2330940.0, hCT2352078.0, hCT2352079.0, hCT2352080.0, hCT9214.4, hCT1966347.1, hCT1966348.1	1561882_at, 1562255_at, 236884_at, 238423_at, 242109_at	NP_001009991.2, EAW47650.1, EAW47648.1, EAW47651.1, EAW47652.1, EAW47654.1, EAW47649.1, EAW47653.1
GeneID:83861	RSPH3	6	159,398,266	159,421,198	22,932	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6940	225	in gene	0	1	0	11	11	16	1	2_A375_pNL97_plus_lncRNA_AR..1	11	Gene RSPH3	dJ111C20.1, RSHL2, RSPH3, RSP3	radial spoke 3 homolog (Chlamydomonas)	NM_031924, hCT25232.3, hCT1953636.1, hCT1953637.1	1566613_at, 223713_at	NP_114130.3, EAW47643.1, EAW47641.1, EAW47642.1
GeneID:6648	SOD2	6	160,100,148	160,114,353	14,205		2	2_A375_pNL97_plus_lncRNA_AR..1..6941, 2_A375_pNL97_plus_lncRNA_AR..1..6942	417, -207	in gene, upstream	0	1	0	13	17.5	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SOD2	MNSOD, MVCD6, Mn-SOD, IPOB, IPO-B, SOD2	superoxide dismutase 2, mitochondrial	NM_000636, NM_001024465, NM_001024466, hCT2330550.0, hCT25235.3, hCT1953639.1	1566342_at, 215078_at, 215223_s_at, 216841_s_at	NP_000627.2, NP_001019636.1, NP_001019637.1, EAW47629.1, EAW47630.1, EAW47631.1
GeneID:9589	WTAP	6	160,148,152	160,177,351	29,199	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4825, 2_A375_pNL97_plus_lncRNA_AR..1..6943	-72, 35246	upstream, downstream	1	1	0	12	11	10	2	1_A375_pNL7_minus_lncRNA_AR..1	13	Gene WTAP	WTAP, MGC3925, KIAA0105, DKFZp686F20131	Wilms tumor 1 associated protein	NM_004906, NM_152857, NM_152858, hCT2330634.1, hCT2330637.1, hCT2330638.1, hCT2350292.0, hCT2352159.0, hCT25228.3, hCT1953629.2	1560274_at, 203137_at, 210285_x_at, 214759_at, 229630_s_at, 241626_at	NP_004897.2, NP_690596.1, NP_690597.1, EAW47625.1, EAW47627.1, EAW47628.1, EAW47622.1, EAW47623.1, EAW47624.1, EAW47626.1
GeneID:100129518	LOC100129518	6	160,181,290	160,183,364	2,074	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6943	-34	upstream	0	1	0	11	10	9	1	2_A375_pNL97_plus_lncRNA_AR..1	10	Gene LOC100129518	FLJ40076	hypothetical LOC100129518	XR_112942, XR_110194, XR_113939		
GeneID:39	ACAT2	6	160,182,989	160,200,087	17,098	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6943	409	in gene	0	1	0	11	10	9	1	2_A375_pNL97_plus_lncRNA_AR..1	10	Gene ACAT2	ACAT2		NM_005891, hCT25231.1, hCT1953633.1	209608_s_at	NP_005882.2, EAW47620.1, EAW47619.1
GeneID:4216	MAP3K4	6	161,412,822	161,538,417	125,595	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4826, 2_A375_pNL97_plus_lncRNA_AR..1..6944	-22, 46456	upstream, in gene	1	1	0	15.5	17	7	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MAP3K4	MEKK4, PRO0412, MAP3K4, MTK1, MAPKKK4, KIAA0213, FLJ42439	mitogen-activated protein kinase kinase kinase 4	NM_006724, NM_005922, hCT24617.3, hCT1950009.1	204089_x_at, 216199_s_at	NP_006715.2, NP_005913.2, EAW47586.1, EAW47587.1
GeneID:9444	QKI	6	163,835,675	163,999,628	163,953	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6945	-1083	upstream	0	1	0	16	19	5	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene QKI	QK1, Hqk, QK3, QKI, DKFZp586I0923, QK	quaking homolog, KH domain RNA binding (mouse)	NM_006775, NM_206853, NM_206854, NM_206855, hCT2331178.0, hCT2331179.0, hCT2331180.0, hCT2331181.0, hCT2331182.0, hCT2331183.0, hCT1950075.1	1555154_a_at, 212262_at, 212263_at, 212265_at, 212636_at, 214541_s_at, 214543_x_at, 241938_at	NP_006766.1, NP_996735.1, NP_996736.1, NP_996737.1, EAW47554.1, EAW47556.1, EAW47555.1, EAW47557.1, EAW47558.1, EAW47559.1, EAW47560.1
GeneID:10846	PDE10A	6	165,740,776	166,075,584	334,808	-	1	4_A375_EGR1..1..7088	-1344	upstream	0	0	1	7	7	17	1	4_A375_EGR1..1	17	Gene PDE10A	PDE10A, HSPDE10A, FLJ25677, FLJ11894	phosphodiesterase 10A	NM_001130690, NM_006661, hCT25259.3	211170_s_at, 211171_s_at	NP_001124162.1, NP_006652.1, EAW47546.1
GeneID:100505705	LOC100505705	6	166,307,330	166,309,725	2,395	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4827, 2_A375_pNL97_plus_lncRNA_AR..1..6948	477, 653	in gene, in gene	1	1	0	18	22	3	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100505705	SDIM1	hypothetical protein LOC100505705	XM_003120019, XM_003118900, XM_003120536		XP_003120067.1, XP_003118948.1, XP_003120586.1
GeneID:90632	C6orf176	6	166,337,536	166,401,527	63,991	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4828, 2_A375_pNL97_plus_lncRNA_AR..1..6949	-9, 7	upstream, in gene	1	1	0	17	15	5	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene C6orf176	bA142J11.1, C6orf176	chromosome 6 open reading frame 176	NR_026680, NR_026681	230251_at	
GeneID:441177	LOC441177	6	166,401,039	166,403,103	2,064	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4828, 2_A375_pNL97_plus_lncRNA_AR..1..6949	497, 461	in gene, in gene	1	1	0	17	15	5	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene LOC441177	MGC131672	hypothetical LOC441177	NR_027264		
GeneID:51660	BRP44L	6	166,778,407	166,796,486	18,079	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6950	630	in gene	0	1	0	13	16	9	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene BRP44L	BRP44L, CGI-129, dJ68L15.3	brain protein 44-like	NM_016098, hCT1968330.2, hCT2330320.1, hCT8037.2, hCT1981265.2, hCT1981266.1	218024_at	NP_057182.1, EAW47527.1, EAW47528.1, EAW47529.1, EAW47530.1, EAW47531.1
GeneID:6196	RPS6KA2	6	166,822,854	167,275,771	452,917	-	1	4_A375_EGR1..1..7089	449563	in gene	0	0	1	3	2	14	1	4_A375_EGR1..1	14	Gene RPS6KA2	S6K-alpha, HU-2, RSK, MAPKAPK1C, S6K-alpha2, RPS6KA2, RSK3, p90-RSK3, pp90RSK3	ribosomal protein S6 kinase, 90kDa, polypeptide 2	NM_001006932, NM_021135, hCT2330308.0, hCT2330310.0, hCT2330311.0	1557970_s_at, 204906_at, 212912_at	NP_001006933.1, NP_066958.2, EAW47522.1, EAW47523.1, EAW47524.1
GeneID:11116	FGFR1OP	6	167,412,816	167,454,066	41,250	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6951	112	in gene	0	1	0	11	19	8	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene FGFR1OP	FGFR1OP, FOP	FGFR1 oncogene partner	NM_007045, NM_194429	1568678_s_at, 205587_at, 205588_s_at	NP_008976.1, NP_919410.1
GeneID:401286	LOC401286	6	168,067,520	168,079,903	12,383	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6952	-4001	upstream	0	1	0	11	15	7	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LOC401286		hypothetical LOC401286	XR_112949, XR_110199, XR_113944, hCT2359785.0		EAW47492.1
GeneID:253769	WDR27	6	169,857,307	170,102,159	244,852	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4829, 2_A375_pNL97_plus_lncRNA_AR..1..6955	-65, -81	upstream, upstream	1	1	0	14	20	13	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene WDR27	MGC43690, WDR27	WD repeat domain 27	NM_182552, hCT2330187.1, hCT2330189.1, hCT2330190.1, hCT2330192.1	226326_at, 235298_at, 235576_at, 238074_at, 238239_at	NP_872358.3, EAW47448.1, EAW47447.1, EAW47449.1, EAW47450.1
GeneID:387263	C6orf120	6	170,102,257	170,106,402	4,145	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4829, 2_A375_pNL97_plus_lncRNA_AR..1..6955	-33, -17	upstream, upstream	1	1	0	14	20	13	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C6orf120	C6orf120, bA160E12.4	chromosome 6 open reading frame 120	NM_001029863	221786_at, 221787_at	NP_001025034.1
GeneID:55274	PHF10	6	170,104,001	170,124,106	20,105	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4829, 2_A375_pNL97_plus_lncRNA_AR..1..6955	21882, 21866	downstream, downstream	1	1	0	14	20	13	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PHF10	FLJ10975, PHF10, BAF45A, XAP135, MGC111009	PHD finger protein 10	NM_018288, NM_133325, hCT2330175.0, hCT2330178.0, hCT2330181.0	219126_at, 225046_at	NP_060758.2, NP_579866.2, EAW47442.1, EAW47443.1, EAW47444.1
GeneID:6991	TCTE3	6	170,140,215	170,151,638	11,423	-	1	2_A375_pNL97_plus_lncRNA_AR..1..6956	-138	upstream	0	1	0	13	16	16	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene TCTE3	TCTE3, TCTEX1D3, MGC142199	t-complex-associated-testis-expressed 3	NM_174910, hCT1640662.3	1554400_at, 1554401_a_at, 1557945_at, 232258_at	NP_777570.1, EAW47439.1
GeneID:55780	C6orf70	6	170,151,721	170,181,617	29,896	+	1	2_A375_pNL97_plus_lncRNA_AR..1..6956	55	in gene	0	1	0	13	16	16	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C6orf70	C6orf70, FLJ11152, dJ266L20.3	chromosome 6 open reading frame 70	NM_018341, hCT2352160.0, hCT6211.3, hCT1950066.1	227656_at	NP_060811.1, EAW47437.1, EAW47436.1, EAW47438.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:80069	C6orf208	6	170,190,169	170,202,969	12,800	+	1	4_A375_EGR1..1..7093	21667	downstream	0	0	1	3	2	14	1	4_A375_EGR1..1	14	Gene C6orf208	RP1-266L20.3, MGC120218, C6orf208, FLJ13162, dJ162D15.1	chromosome 6 open reading frame 208	NR_026780, hCT1820126.2	220904_at	EAW47434.1
GeneID:28514	DLL1	6	170,591,294	170,599,697	8,403	-	2	4_A375_EGR1..1..7094, 4_A375_EGR1..1..7095	6785, -1007	in gene, upstream	0	0	1	4.5	4.5	14.5	2	4_A375_EGR1..1	15	Gene DLL1	DELTA1, DL1, Delta, DLL1	delta-like 1 (Drosophila)	NM_005618, hCT5627.3	224215_s_at, 227938_s_at	NP_005609.3, EAW47425.1
GeneID:5689	PSMB1	6	170,844,204	170,862,417	18,213	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4830, 2_A375_pNL97_plus_lncRNA_AR..1..6958	-879, -1231	upstream, upstream	1	1	0	15	16	7	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene PSMB1	PSC5, PSMB1, FLJ25321, KIAA1838, HC5, PMSB1	proteasome (prosome, macropain) subunit, beta type, 1	NM_002793, hCT2330138.0, hCT2330139.0, hCT2330140.0, hCT2330142.0	200876_s_at, 214288_s_at, 214289_at	NP_002784.1, EAW47422.1, EAW47420.1, EAW47421.1, EAW47423.1
GeneID:6908	TBP	6	170,863,421	170,881,958	18,537	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4830, 2_A375_pNL97_plus_lncRNA_AR..1..6958	-125, 227	upstream, in gene	1	1	0	15	16	7	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene TBP	GTF2D1, TBP, TFIID, MGC126055, GTF2D, HDL4, SCA17, MGC117320, MGC126054	TATA box binding protein	NM_003194, NM_001172085, hCT2330398.0, hCT2330396.0	203135_at	NP_003185.1, NP_001165556.1, EAW47418.1, EAW47419.1
GeneID:100507642	LOC100507642	7	149,597	154,990	5,393	+	1	4_A375_EGR1..1..7097	10275	downstream	0	0	1	7	10	40	1	4_A375_EGR1..1	40	Gene LOC100507642		hypothetical LOC100507642	XR_112952, XR_110819, XR_108720, XR_113970		
GeneID:56975	FAM20C	7	192,969	300,711	107,742	+	4	4_A375_EGR1..1..7098, 4_A375_EGR1..1..7099, 4_A375_EGR1..1..7100, 4_A375_EGR1..1..7101	13335, 18839, 108519, 114327	in gene, in gene, downstream, downstream	0	0	1	5	5.75	16.5	4	4_A375_EGR1..1	17	Gene FAM20C	DMP4, RNS, DKFZp547C074, FAM20C	family with sequence similarity 20, member C	NM_020223, hCT2271338.1, hCT2271339.0, hCT2271340.1, hCT2271341.1, hCT2349095.0, hCT2349096.0, hCT2349097.0, hCT2356902.0, hCT2356903.0	226722_at, 229438_at, 234342_at, 234486_at	NP_064608.2, EAW87149.1, EAW87150.1, EAW87154.1, EAW87155.1, EAW87156.1, EAW87151.1, EAW87152.1, EAW87153.1, EAW87157.1
GeneID:100288496	LOC100288496	7	301,855	304,070	2,215	+	2	4_A375_EGR1..1..7100, 4_A375_EGR1..1..7101	-387, 5441	upstream, downstream	0	0	1	5	7	16.5	2	4_A375_EGR1..1	17	Gene LOC100288496		hypothetical LOC100288496			
GeneID:442497	LOC442497	7	419,391	422,845	3,454	+	2	4_A375_EGR1..1..7105, 4_A375_EGR1..1..7106	-2463, 12225	upstream, downstream	0	0	1	7.5	4	19	2	4_A375_EGR1..1	22	Gene LOC442497		hypothetical LOC442497	NR_033960		
GeneID:100131372	LOC100131372	7	467,033	471,873	4,840	-	1	4_A375_EGR1..1..7109	-4879	upstream	0	0	1	7	12	15	1	4_A375_EGR1..1	15	Gene LOC100131372		hypothetical LOC100131372	XR_112955, XR_110820, XR_108721, XR_113971		
GeneID:5154	PDGFA	7	536,895	559,481	22,586	-	2	2_A375_pNL97_plus_lncRNA_AR..1..6960, 4_A375_EGR1..1..7113	889, -2007	in gene, upstream	0	1	1	7	13	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene PDGFA	PDGF-A, PDGFA, PDGF1	platelet-derived growth factor alpha polypeptide	NM_002607, NM_033023, hCT2272389.0, hCT2272390.0, hCT1963868.1	1564472_at, 205463_s_at, 216867_s_at	NP_002598.4, NP_148983.1, EAW87160.1, EAW87161.1, EAW87162.1
GeneID:441307	FLJ44511	7	560,028	564,869	4,841	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6960, 4_A375_EGR1..1..7113, 4_A375_EGR1..1..7114	-1436, 1460, 10436	upstream, in gene, downstream	0	1	1	5.33	9.67	13	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene FLJ44511		hypothetical LOC441307	NR_033963		
GeneID:5575	PRKAR1B	7	588,834	767,313	178,479	-	6	4_A375_EGR1..1..7115, 4_A375_EGR1..1..7116, 4_A375_EGR1..1..7117, 4_A375_EGR1..1..7118, 4_A375_EGR1..1..7119, 4_A375_EGR1..1..7120	188765, 177849, 137473, 133777, 122481, 111249	downstream, in gene, in gene, in gene, in gene, in gene	0	0	1	6.83	6.5	16.33	6	4_A375_EGR1..1	20	Gene PRKAR1B	PRKAR1, PRKAR1B	protein kinase, cAMP-dependent, regulatory, type I, beta	NM_002735, NM_001164758, NM_001164759, NM_001164760, NM_001164762, NM_001164761, hCT2272383.0, hCT2272384.0, hCT2272385.0, hCT2272386.0	212555_at, 212559_at	NP_002726.1, NP_001158230.1, NP_001158231.1, NP_001158232.1, NP_001158234.1, NP_001158233.1, EAW87163.1, EAW87164.1, EAW87165.1, EAW87166.1
GeneID:100505500	LOC100505500	7	842,482	848,139	5,657	+	3	4_A375_EGR1..1..7118, 4_A375_EGR1..1..7119, 4_A375_EGR1..1..7120	-8946, 2350, 13582	upstream, in gene, downstream	0	0	1	6.67	5.33	18.33	3	4_A375_EGR1..1	20	Gene LOC100505500		hypothetical LOC100505500	XR_112960, XR_112961, XR_110821, XR_110822, XR_108722, XR_108723, XR_113972, XR_113973		
GeneID:23353	SUN1	7	855,194	914,557	59,363	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4831, 2_A375_pNL97_plus_lncRNA_AR..1..6961, 4_A375_EGR1..1..7121	60902, 60758, 52790	downstream, downstream, in gene	1	1	1	14.5	16	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene SUN1	SUN1, KIAA0810, UNC84A, FLJ12407, MGC176649	Sad1 and UNC84 domain containing 1	NM_001130965, NM_025154, NM_001171944, NM_001171945, NM_001171946, hCT2271241.1, hCT2271242.1, hCT2271243.1, hCT2271244.1, hCT1955830.2	208487_at, 212074_at, 230210_at	NP_001124437.1, NP_079430.3, NP_001165415.1, NP_001165416.1, NP_001165417.1, EAW87174.1, EAW87175.1, EAW87176.1, EAW87177.1, EAW87178.1
GeneID:51608	C7orf20	7	916,191	936,071	19,880	+	5	1_A375_pNL7_minus_lncRNA_AR..1..4831, 2_A375_pNL97_plus_lncRNA_AR..1..6961, 4_A375_EGR1..1..7121, 4_A375_EGR1..1..7122, 4_A375_EGR1..1..7123	-95, -239, -8207, 22081, 24529	upstream, upstream, upstream, downstream, downstream	1	1	1	10.25	11.75	15.5	4	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene C7orf20	GET4, CEE, C7orf20, CGI-20, TRC35	chromosome 7 open reading frame 20	NM_015949, hCT1786064.1, hCT1955831.1	223811_s_at, 224608_s_at, 224616_at, 227568_s_at	NP_057033.2, EAW87180.1, EAW87179.1
GeneID:100505531	LOC100505531	7	919,586	921,830	2,244	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4831, 2_A375_pNL97_plus_lncRNA_AR..1..6961	-3490, -3634	upstream, upstream	1	1	0	24	23	7	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene LOC100505531		hypothetical LOC100505531	XR_112963, XR_110823, XR_108724, XR_113974		
GeneID:11033	ADAP1	7	937,537	994,289	56,752	-	9	4_A375_EGR1..1..7122, 4_A375_EGR1..1..7123, 4_A375_EGR1..1..7124, 4_A375_EGR1..1..7125, 4_A375_EGR1..1..7126, 4_A375_EGR1..1..7127, 4_A375_EGR1..1..7128, 4_A375_EGR1..1..7129, 4_A375_EGR1..1..7130	56017, 53569, 45121, 34449, 32177, 28753, 19228, 8561, -7743	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	0	0	1	6.44	7.89	17.67	9	4_A375_EGR1..1	20	Gene ADAP1	GCS1L, ADAP1, CENTA1, p42IP4	ArfGAP with dual PH domains 1	NM_006869, hCT2272373.0, hCT1786065.2, hCT1955832.1	219150_s_at, 90265_at	NP_006860.1, EAW87183.1, EAW87182.1, EAW87184.1
GeneID:90639	COX19	7	1,004,486	1,015,235	10,749	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4832, 2_A375_pNL97_plus_lncRNA_AR..1..6962, 4_A375_EGR1..1..7130, 4_A375_EGR1..1..7131	67, 35, 13203, 307	in gene, in gene, downstream, in gene	1	1	1	21.5	25.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene COX19	COX19, MGC104475	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	NM_001031617, hCT1646068.3	231831_at, 235533_at	NP_001026788.1, EAW87185.1
GeneID:54905	CYP2W1	7	1,022,835	1,029,276	6,441	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4832, 2_A375_pNL97_plus_lncRNA_AR..1..6962, 4_A375_EGR1..1..7131	-7667, -7635, -7907	upstream, upstream, upstream	1	1	1	40	43	16	1	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene CYP2W1	MGC34287, CYP2W1	cytochrome P450, family 2, subfamily W, polypeptide 1	NM_017781, hCT2356923.0, hCT1786066.1	220562_at	NP_060251.2, EAW87187.1, EAW87186.1
GeneID:84310	C7orf50	7	1,036,623	1,177,893	141,270	-	3	4_A375_EGR1..1..7132, 4_A375_EGR1..1..7133, 4_A375_EGR1..1..7134	116245, 55077, 15237	in gene, in gene, in gene	0	0	1	5.67	5.67	17.33	3	4_A375_EGR1..1	19	Gene C7orf50	C7orf50, YCR016W, MGC11257	chromosome 7 open reading frame 50	NM_032350, NM_001134395, NM_001134396, hCT2272445.0, hCT1786069.2	224478_s_at, 240147_at, 240900_at	NP_115726.1, NP_001127867.1, NP_001127868.1, EAW87188.1, EAW87189.1
GeneID:442907	MIR339	7	1,062,569	1,062,662	93	-	1	4_A375_EGR1..1..7132	3014	downstream	0	0	1	7	8	19	1	4_A375_EGR1..1	19	Gene MIR339	hsa-mir-339, MIR339, MIRN339	microRNA 339	NR_029898		
GeneID:2852	GPER	7	1,126,443	1,133,451	7,008	+	1	4_A375_EGR1..1..7133	-3627	upstream	0	0	1	7	4	18	1	4_A375_EGR1..1	18	Gene GPER	MGC99678, GPER, LERGU2, GPR30, CEPR, DRY12, LyGPR, CMKRL2, GPCR-Br, FEG-1, LERGU	G protein-coupled estrogen receptor 1	NM_001505, NM_001039966, NM_001098201, hCT1642574.3, hCT1961765.1	210640_s_at, 211829_s_at	NP_001496.1, NP_001035055.1, NP_001091671.1, EAW87194.1, EAW87195.1
GeneID:90637	ZFAND2A	7	1,192,543	1,199,855	7,312	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4833	175	in gene	1	0	0	15	16	7	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene ZFAND2A	ZFAND2A, AIRAP	zinc finger, AN1-type domain 2A	NM_182491, hCT2356895.0, hCT1783095.2	226650_at	NP_872297.2, EAW87197.1, EAW87196.1
GeneID:340260	UNCX	7	1,272,854	1,276,813	3,959	+	3	4_A375_EGR1..1..7135, 4_A375_EGR1..1..7136, 4_A375_EGR1..1..7137	-7534, 2002, 10114	upstream, in gene, downstream	0	0	1	5.33	7	18.33	3	4_A375_EGR1..1	17	Gene UNCX	UNCX, UNCX4.1	UNC homeobox	NM_001080461		NP_001073930.1
GeneID:79778	MICALL2	7	1,473,995	1,499,109	25,114	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4834, 4_A375_EGR1..1..7153, 4_A375_EGR1..1..7154, 4_A375_EGR1..1..7155	325, 29061, 1317, 437	in gene, downstream, in gene, in gene	1	0	1	14.67	9	19.33	3	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene MICALL2	FLJ44858, MICALL2, MGC48023, FLJ23471, FLJ41998, MICALL2, FLJ45410, JRAB	MICAL-like 2	NM_182924, hCT2356924.0, hCT8782.3	1555862_s_at, 219332_at	NP_891554.1, EAW87201.1, EAW87200.1
GeneID:26173	INTS1	7	1,509,913	1,544,018	34,105	-	10	1_A375_pNL7_minus_lncRNA_AR..1..4835, 2_A375_pNL97_plus_lncRNA_AR..1..6963, 2_A375_pNL97_plus_lncRNA_AR..1..6964, 4_A375_EGR1..1..7156, 4_A375_EGR1..1..7157, 4_A375_EGR1..1..7158, 4_A375_EGR1..1..7159, 4_A375_EGR1..1..7160, 4_A375_EGR1..1..7161, 4_A375_EGR1..1..7162	-78, -78, -9022, 25626, 24050, 23005, 2722, -7534, -8270, -8846	upstream, upstream, upstream, in gene, in gene, in gene, in gene, upstream, upstream, upstream	1	1	1	17.75	20.5	16.75	8	2_A375_pNL97_plus_lncRNA_AR..1	107	Gene INTS1	FLJ46624, KIAA1440, INTS1, INT1, NET28, DKFZp586J0619	integrator complex subunit 1	NM_001080453	212210_at, 212212_s_at	NP_001073922.2
GeneID:7975	MAFK	7	1,570,368	1,582,679	12,311	+	4	2_A375_pNL97_plus_lncRNA_AR..1..6965, 4_A375_EGR1..1..7163, 4_A375_EGR1..1..7164, 4_A375_EGR1..1..7165	1952, 3472, 7904, 19840	in gene, in gene, in gene, downstream	0	1	1	7	11.25	15	4	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene MAFK	NFE2U, FLJ32205, MAFK, MGC71717, P18	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	NM_002360, hCT2271316.1, hCT9983.3	206750_at, 226206_at	NP_002351.1, EAW87206.1, EAW87207.1
GeneID:100128653	LOC100128653	7	1,572,090	1,574,516	2,426	-	3	2_A375_pNL97_plus_lncRNA_AR..1..6965, 4_A375_EGR1..1..7163, 4_A375_EGR1..1..7164	2196, 676, -3756	in gene, in gene, upstream	0	1	1	8	12.33	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100128653		hypothetical LOC100128653	XR_112966, XR_110826, XR_108727, XR_113977		
GeneID:202915	TMEM184A	7	1,581,871	1,596,066	14,195	-	8	2_A375_pNL97_plus_lncRNA_AR..1..6965, 4_A375_EGR1..1..7163, 4_A375_EGR1..1..7164, 4_A375_EGR1..1..7165, 4_A375_EGR1..1..7166, 4_A375_EGR1..1..7167, 4_A375_EGR1..1..7168, 4_A375_EGR1..1..7169	23746, 22226, 17794, 5858, 2, -1982, -3358, -7646	downstream, downstream, downstream, in gene, in gene, upstream, upstream, upstream	0	1	1	6.88	9.38	16.38	8	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene TMEM184A	FLJ24011, MGC9712, TMEM184A	transmembrane protein 184A	NM_001097620, hCT2272412.0, hCT2356894.0, hCT10533.2	1558281_a_at, 235817_at	NP_001091089.1, EAW87210.1, EAW87209.1, EAW87211.1
GeneID:84262	PSMG3	7	1,606,966	1,609,666	2,700	-	5	2_A375_pNL97_plus_lncRNA_AR..1..6966, 4_A375_EGR1..1..7167, 4_A375_EGR1..1..7168, 4_A375_EGR1..1..7169, 4_A375_EGR1..1..7170	-92, 11620, 10244, 5956, -284	upstream, downstream, downstream, downstream, upstream	0	1	1	7.5	10.75	17.25	4	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PSMG3	MGC10911, PSMG3, PAC3, C7orf48	proteasome (prosome, macropain) assembly chaperone 3	NM_032302, NM_001134340, hCT10534.3, hCT1960838.1	223363_at	NP_115678.1, NP_001127812.1, EAW87212.1, EAW87213.1
GeneID:114798	KIAA1908	7	1,609,709	1,629,262	19,553	+	3	2_A375_pNL97_plus_lncRNA_AR..1..6966, 4_A375_EGR1..1..7169, 4_A375_EGR1..1..7170	51, -5997, 243	in gene, upstream, in gene	0	1	1	8	12.5	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene KIAA1908		hypothetical LOC114798	NR_027328, NR_027329, NR_021487	1561666_a_at	
GeneID:392617	ELFN1	7	1,748,798	1,787,590	38,792	+	5	4_A375_EGR1..1..7172, 4_A375_EGR1..1..7173, 4_A375_EGR1..1..7174, 4_A375_EGR1..1..7175, 4_A375_EGR1..1..7176	-4318, 16130, 32210, 40194, 42002	upstream, in gene, in gene, downstream, downstream	0	0	1	5.8	7.2	18.6	5	4_A375_EGR1..1	22	Gene ELFN1	ELFN1		NM_001128636	229561_at	NP_001122108.1
GeneID:100505644	LOC100505644	7	1,778,266	1,781,940	3,674	-	3	4_A375_EGR1..1..7174, 4_A375_EGR1..1..7175, 4_A375_EGR1..1..7176	932, -7052, -8860	in gene, upstream, upstream	0	0	1	5.67	6.67	19.33	3	4_A375_EGR1..1	22	Gene LOC100505644		hypothetical LOC100505644	XR_112968, XR_110828, XR_108729, XR_113979		
GeneID:8379	MAD1L1	7	1,855,428	2,272,583	417,155	-	8	1_A375_pNL7_minus_lncRNA_AR..1..4836, 4_A375_EGR1..1..7178, 4_A375_EGR1..1..7179, 4_A375_EGR1..1..7180, 4_A375_EGR1..1..7181, 4_A375_EGR1..1..7182, 4_A375_EGR1..1..7183, 4_A375_EGR1..1..7184	-89, 409319, 367975, 267495, 259363, 243175, 240467, 175647	upstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	0	1	8	7.75	16	8	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene MAD1L1	MAD1, TP53I9, TXBP181, PIG9, HsMAD1, MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	NM_003550, NM_001013836, NM_001013837, hCT2281848.0, hCT2281849.0	204857_at	NP_003541.2, NP_001013858.1, NP_001013859.1, EAW87219.1, EAW87220.1
GeneID:100128374	LOC100128374	7	1,876,222	1,889,567	11,345	+	1	4_A375_EGR1..1..7179	6386	in gene	0	0	1	7	8	17	1	4_A375_EGR1..1	17	Gene LOC100128374		hypothetical LOC100128374	XR_112969, XR_110829, XR_108730, XR_113980		
GeneID:29960	FTSJ2	7	2,273,926	2,281,833	7,907	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4836, 4_A375_EGR1..1..7185	9161, -5527	downstream, upstream	1	0	1	15.5	14	15	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene FTSJ2	DKFZp686J14194, FJH1, FTSJ2	FtsJ homolog 2 (E. coli)	NM_013393	218356_at, 222130_s_at	NP_037525.1
GeneID:4521	NUDT1	7	2,281,857	2,290,780	8,923	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4836, 4_A375_EGR1..1..7185	-9185, 5503	upstream, in gene	1	0	1	15.5	14	15	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene NUDT1	MTH1, NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	NM_002452, NM_198948, NM_198949, NM_198950, NM_198952, NM_198953, NM_198954, hCT2356910.0, hCT2356911.0, hCT2356912.0, hCT2356913.0, hCT2356914.0, hCT2356915.0, hCT9490.2, hCT1962602.1	204766_s_at	NP_002443.3, NP_945186.1, NP_945187.1, NP_945188.1, NP_945190.1, NP_945191.1, NP_945192.1, EAW87225.1, EAW87226.1, EAW87227.1, EAW87228.1, EAW87229.1, EAW87230.1, EAW87231.1, EAW87232.1
GeneID:29886	SNX8	7	2,294,638	2,354,099	59,461	-	2	4_A375_EGR1..1..7185, 4_A375_EGR1..1..7186	66739, 31155	downstream, in gene	0	0	1	4.5	9	15.5	2	4_A375_EGR1..1	17	Gene SNX8	DKFZp761E1721, Mvp1, SNX8	sorting nexin 8	NM_013321, hCT2281841.0, hCT9494.2, hCT1950353.1	223241_at	NP_037453.1, EAW87236.1, EAW87234.1, EAW87235.1
GeneID:8662	EIF3B	7	2,394,474	2,420,380	25,906	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4837, 2_A375_pNL97_plus_lncRNA_AR..1..6967	-138, -170	upstream, upstream	1	1	0	52	59	19	1	2_A375_pNL97_plus_lncRNA_AR..1	59	Gene EIF3B	EIF3-P116, EIF3-ETA, MGC104664, EIF3-P110, PRT1, EIF3B, MGC131875, EIF3S9	eukaryotic translation initiation factor 3, subunit B	NM_001037283, NM_003751, hCT2281510.0, hCT2356898.0, hCT2356899.0, hCT2356900.0, hCT2356901.0	203462_x_at, 208688_x_at, 211501_s_at, 236274_at, 237457_at, 242550_at	NP_001032360.1, NP_003742.2, EAW87237.1, EAW87238.1, EAW87240.1, EAW87241.1, EAW87239.1
GeneID:55501	CHST12	7	2,443,259	2,474,240	30,981	+	1	4_A375_EGR1..1..7187	14629	in gene	0	0	1	6	3	17	1	4_A375_EGR1..1	17	Gene CHST12	C4ST2, CHST12, C4ST-2, C4S-2	carbohydrate (chondroitin 4) sulfotransferase 12	NM_018641, hCT2281514.0, hCT2281516.0, hCT1639901.3	218927_s_at, 222788_at	NP_061111.1, EAW87243.1, EAW87244.1, EAW87245.1
GeneID:100288594	LOC100288594	7	2,480,699	2,486,315	5,616	+	2	4_A375_EGR1..1..7188, 4_A375_EGR1..1..7189	10117, 10741	downstream, downstream	0	0	1	10	11	19.5	2	4_A375_EGR1..1	22	Gene LOC100288594	FLJ00049	hypothetical LOC100288594	XR_112982, XR_110863, XR_108779, XR_113989		
GeneID:3955	LFNG	7	2,552,163	2,568,811	16,648	+	4	4_A375_EGR1..1..7195, 4_A375_EGR1..1..7196, 4_A375_EGR1..1..7197, 4_A375_EGR1..1..7198	-6995, -2755, -1827, 12477	upstream, upstream, upstream, in gene	0	0	1	7.25	7.75	20.25	4	4_A375_EGR1..1	24	Gene LFNG	SCDO3, LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	NM_001040167, NM_001040168, NM_001166355, NM_002304, hCT2281525.0, hCT2281526.0, hCT2281527.0, hCT9495.3, hCT1950354.1	215270_at, 228762_at	NP_001035257.1, NP_001035258.1, NP_001159827.1, NP_002295.1, EAW87250.1, EAW87253.1, EAW87251.1, EAW87252.1, EAW87254.1
GeneID:221927	C7orf27	7	2,577,511	2,595,146	17,635	-	5	1_A375_pNL7_minus_lncRNA_AR..1..4838, 1_A375_pNL7_minus_lncRNA_AR..1..4839, 2_A375_pNL97_plus_lncRNA_AR..1..6968, 2_A375_pNL97_plus_lncRNA_AR..1..6969, 4_A375_EGR1..1..7199	106, -3462, -86, -3446, -8	in gene, upstream, upstream, upstream, upstream	1	1	1	17.5	23	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene C7orf27	BRAT1, C7orf27, BAAT1, MGC22916	BRCA1-associated ATM activator 1	NM_152743, hCT1967739.1, hCT2281828.0, hCT2281831.0, hCT2281832.0, hCT2356918.0, hCT9492.2	225437_s_at	NP_689956.1, EAW87259.1, EAW87255.1, EAW87256.1, EAW87258.1, EAW87260.1, EAW87257.1
GeneID:23288	IQCE	7	2,598,632	2,654,368	55,736	+	5	1_A375_pNL7_minus_lncRNA_AR..1..4838, 1_A375_pNL7_minus_lncRNA_AR..1..4839, 2_A375_pNL97_plus_lncRNA_AR..1..6968, 2_A375_pNL97_plus_lncRNA_AR..1..6969, 4_A375_EGR1..1..7199	-3592, -24, -3400, -40, -3480	upstream, upstream, upstream, upstream, upstream	1	1	1	17.5	23	12.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene IQCE	MGC41907, KIAA1023, IQCE, 1700028P05Rik	IQ motif containing E	NM_152558, NM_001100390, hCT2281529.0, hCT2356916.0, hCT2356917.0, hCT1828117.2	204202_at, 217124_at	NP_689771.3, NP_001093860.1, EAW87261.1, EAW87262.1, EAW87263.1, EAW87264.1



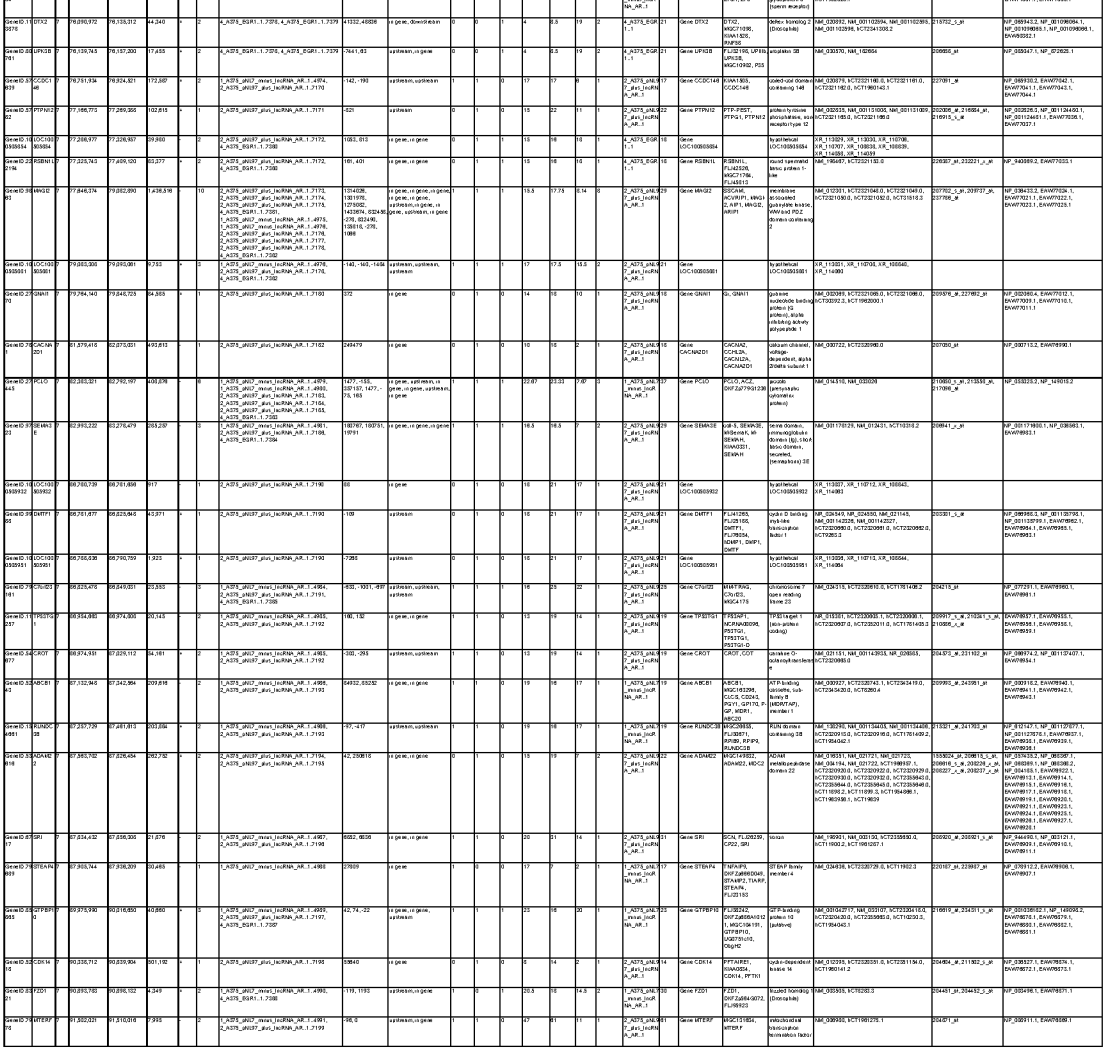
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9734	HDAC9	7	18,535,369	19,036,993	501,624	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7014	371063	in gene	0	1	0	9	23	4	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene HDAC9	HDAC9B, HDAC7B, HD7b, HDAC9, HDAC9FL, DKFZp779K1053, HDAC7, HDAC, MITR, HDRP, KIAA0744, HD9, HD7	histone deacetylase 9	NM_014707, NM_178423, NM_178425, NM_058176, hCT2298892.0, hCT2298893.0, hCT2298894.0, hCT2298895.0, hCT2298896.0, hCT2298897.0, hCT2298898.0, hCT2298899.0, hCT2298900.0, hCT2298901.0	1552758_at, 1552760_at, 205659_at, 234393_at	NP_055522.1, NP_848510.1, NP_478056.1, NP_848512.1, EAW93703.1, EAW93709.1, EAW93701.1, EAW93702.1, EAW93704.1, EAW93705.1, EAW93706.1, EAW93707.1, EAW93708.1, EAW93710.1
GeneID:221830	TWISTNB	7	19,735,065	19,748,680	13,575	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7015	132	in gene	0	1	0	16	20	12	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TWISTNB	TWISTNB		NM_001002926, hCT29154.2	214729_at, 226784_at	NP_001002926.1, EAW93714.1
GeneID:100422967	MIR3146	7	19,744,981	19,745,059	78	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7015	-3469	upstream	0	1	0	16	20	12	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MIR3146	MIR3146	microRNA 3146	NR_036101		
GeneID:256130	TMEM196	7	19,758,938	19,812,404	53,466	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4869, 2_A375_pNL97_plus_lncRNA_AR..1..7015, 2_A375_pNL97_plus_lncRNA_AR..1..7016	-268, 63676, -364	upstream, downstream, upstream	1	1	0	19	20.5	10	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene TMEM196	TMEM196, DKFZp686K0753, DKFZp686H19205, MGC42090	transmembrane protein 196	NM_152774, hCT2298997.1, hCT2357697.0, hCT1657084.3	1552293_at, 236705_at	NP_689987.3, EAW93716.1, EAW93715.1, EAW93717.1
GeneID:346389	MACC1	7	20,174,276	20,257,013	82,735	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4871, 1_A375_pNL7_minus_lncRNA_AR..1..4872, 2_A375_pNL97_plus_lncRNA_AR..1..7016	57909, -2731, -2427	in gene, upstream, upstream	1	1	0	20.5	18.5	3	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MACC1	SH3BP4L, MACC1, 7A5	metastasis associated in colon cancer 1	NM_182762, hCT30175.3		NP_877439.3, EAW93719.1
GeneID:100506098	LOC100506098	7	20,257,200	20,261,326	4,126	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4872, 2_A375_pNL97_plus_lncRNA_AR..1..7016	2544, 2240	in gene, in gene	1	1	0	22	22	2	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOC100506098		hypothetical LOC100506098	XR_112981, XR_112980, XR_112982, XR_110647, XR_110646, XR_110648, XR_108745, XR_108744, XR_108746, XR_113997, XR_113996, XR_113998		
GeneID:100506130	LOC100506130	7	20,367,924	20,371,370	3,446	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4873, 2_A375_pNL97_plus_lncRNA_AR..1..7019, 4_A375_EGR1..1..7253	1050, 1354, 1002	in gene, in gene, in gene	1	1	1	16	19	28	1	4_A375_EGR1..1	28	Gene LOC100506130		hypothetical LOC100506130	XR_112983, XR_112984, XR_110649, XR_110650, XR_108747, XR_108748, XR_113999, XR_114000		
GeneID:3696	ITGB8	7	20,370,725	20,455,382	84,657	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4873, 2_A375_pNL97_plus_lncRNA_AR..1..7019, 2_A375_pNL97_plus_lncRNA_AR..1..7020, 4_A375_EGR1..1..7253	-405, -709, 21995, -357	upstream, upstream, in gene, upstream	1	1	1	16.5	16.5	17	2	4_A375_EGR1..1	28	Gene ITGB8	ITGB8	integrin, beta 8	NM_002214, hCT2303791.0, hCT28543.3	205816_at, 211488_s_at, 226189_at, 242962_x_at	NP_002205.1, EAW93724.1, EAW93725.1
GeneID:221833	SP8	7	20,821,894	20,826,508	4,614	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7022	1836	in gene	0	1	0	10	18	12	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene SP8	BTD, SP8	Sp8 transcription factor	NM_198956, NM_182700, hCT2303801.1, hCT2349677.0, hCT2357665.0, hCT30173.3	237449_at, 239743_at	NP_945194.1, NP_874359.2, EAW93729.1, EAW93730.1, EAW93731.1, EAW93732.1
GeneID:8701	DNAH11	7	21,582,833	21,941,457	358,624	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4875	224175	in gene	1	0	0	15	7	4	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene DNAH11	CILD7, DPL11, FLJ37699, DNAH11, FLJ30095, DNAHC11, DNHBL, DNAHBL	dynein, axonemal, heavy chain 11	NM_003777, hCT2298990.0, hCT2298991.0, hCT2298992.0, hCT1961201.2	1553159_at, 1560416_at, 237804_at	NP_003768.2, EAW93737.1, EAW93736.1, EAW93738.1, EAW93739.1
GeneID:55536	CDCA7L	7	21,940,517	21,985,542	45,025	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4876, 2_A375_pNL97_plus_lncRNA_AR..1..7023	-122, -74	upstream, upstream	1	1	0	45	58	10	1	2_A375_pNL97_plus_lncRNA_AR..1	58	Gene CDCA7L	JPO2, CDCA7L, DKFZp762L0311, R1, RAM2	cell division cycle associated 7-like	NM_018719, NM_001127370, NM_001127371, hCT1986944.1, hCT2349681.0, hCT2349682.0, hCT2357710.0, hCT31255.5	225081_s_at	NP_061189.2, NP_001120842.1, NP_001120843.1, EAW93740.1, EAW93741.1, EAW93744.1, EAW93742.1, EAW93743.1
GeneID:256227	MGC87042	7	22,459,063	22,539,901	80,838	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7025	61	in gene	0	1	0	14	16	12	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene MGC87042		STEAP family protein MGC87042	NM_207342, NM_001164460	217553_at	NP_997225.1, NP_001157932.1
GeneID:54543	TOMM7	7	22,852,251	22,862,421	10,170	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7026	-43	upstream	0	1	0	14	20	9	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TOMM7	TOM7, TOMM7	translocase of outer mitochondrial membrane 7 homolog (yeast)	NM_019059, hCT1659702.2, hCT1983307.0, hCT1983308.1, hCT1985963.0		NP_061932.1, EAW93761.1, EAW93760.1, EAW93762.1, EAW93763.1
GeneID:692210	SNORD93	7	22,896,232	22,896,305	73	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4877, 2_A375_pNL97_plus_lncRNA_AR..1..7027	1960, 2104	downstream, downstream	1	1	0	19	21	6	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SNORD93	HBII-336, SNORD93	small nucleolar RNA, C/D box 93	NR_003075		
GeneID:84668	FAM126A	7	22,980,878	23,053,770	72,892	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4878	-7156	upstream	1	0	0	16	17	5	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene FAM126A	HCC, HYCC1, DRCTNNB1A, HLD5, FAM126A	family with sequence similarity 126, member A	NM_032581, hCT2322590.0, hCT29470.3	223825_at, 227239_at, 231398_s_at, 244115_at	NP_115970.2, EAW93767.1, EAW93768.1
GeneID:100506198	LOC100506198	7	23,126,671	23,140,052	13,381	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4879, 2_A375_pNL97_plus_lncRNA_AR..1..7029	18873, 18737	downstream, downstream	1	1	0	20	17	12	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene LOC100506198		hypothetical LOC100506198	XR_112987, XR_110653, XR_108751, XR_114003		
GeneID:55975	KLHL7	7	23,145,353	23,215,040	69,687	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4879, 1_A375_pNL7_minus_lncRNA_AR..1..4880, 2_A375_pNL97_plus_lncRNA_AR..1..7029, 2_A375_pNL97_plus_lncRNA_AR..1..7030	-9, 76183, 55, 76151	upstream, downstream, in gene, downstream	1	1	0	22	20.5	12	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene KLHL7	RP42, SBBI26, KLHL6, KLHL7	kelch-like 7 (Drosophila)	NM_001031710, NM_018846, NR_033328, NR_033329, NM_001172428, hCT2357676.0, hCT1827997.2, hCT1982890.0, hCT1982891.1, hCT1982892.1	220238_s_at, 220239_at, 223250_at	NP_001026880.2, NP_061334.4, NP_001165899.1, EAW93770.1, EAW93771.1, EAW93773.1, EAW93772.1, EAW93774.1
GeneID:11097	NUPL2	7	23,221,446	23,240,630	19,184	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4880, 2_A375_pNL97_plus_lncRNA_AR..1..7030, 4_A375_EGR1..1..7254	90, 56, 12090	in gene, in gene, in gene	1	1	1	16.5	16	17	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene NUPL2	NLP-1, hCG1, NUPL2, CG1, NLP_1	nucleoporin like 2	NM_007342, hCT2299127.0, hCT2357669.0, hCT28547.4, hCT1963714.1, hCT1963715.1	204003_s_at	NP_031368.1, EAW93778.1, EAW93775.1, EAW93776.1, EAW93777.1, EAW93779.1
GeneID:10457	GPNMB	7	23,286,316	23,314,729	28,413	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7031	532	in gene	0	1	0	11	18	16	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene GPNMB	GPNMB, NMB, HGFIN	glycoprotein (transmembrane) nmb	NM_002510, NM_001005340, hCT2299130.0, hCT2299133.0, hCT2357714.0, hCT29213.3	1554018_at, 201141_at	NP_002501.1, NP_001005340.1, EAW93781.1, EAW93782.1, EAW93783.1, EAW93784.1
GeneID:115416	C7orf30	7	23,338,940	23,349,180	10,240	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4881	-26	upstream	1	0	0	19	19	15	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene C7orf30	C7orf30	chromosome 7 open reading frame 30	NM_138446, hCT29220.3	226385_s_at, 226386_at, 230516_at, 244641_at	NP_612455.1, EAW93785.1
GeneID:10643	IGF2BP3	7	23,349,828	23,509,995	160,167	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4882, 2_A375_pNL97_plus_lncRNA_AR..1..7032	-949, -3861	upstream, upstream	1	1	0	16.5	14	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene IGF2BP3	VICKZ3, IMP-3, KOC1, DKFZp686F1078, IGF2BP3, IMP3, CT98	insulin-like growth factor 2 mRNA binding protein 3	NM_006547, hCT2299349.0, hCT2299350.0	1569033_at, 203819_s_at, 203820_s_at	NP_006538.2, EAW93787.1, EAW93786.1
GeneID:29896	TRA2A	7	23,544,399	23,571,656	27,257	-	1	4_A375_EGR1..1..7255	169	in gene	0	0	1	12	16	13	1	4_A375_EGR1..1	13	Gene TRA2A	HSU53209, TRA2A	transformer 2 alpha homolog (Drosophila)	NM_013293, hCT2299345.0, hCT29216.3	204658_at, 213575_at, 213593_s_at, 227939_s_at, 229574_at	NP_037425.1, EAW93789.1, EAW93788.1
GeneID:4852	NPY	7	24,323,807	24,331,484	7,677	+	1	4_A375_EGR1..1..7256	337	in gene	0	0	1	8	3	14	1	4_A375_EGR1..1	14	Gene NPY	PYY4, NPY	neuropeptide Y	NM_000905, hCT28545.3	206001_at	NP_000896.1, EAW93807.1
GeneID:1687	DFNA5	7	24,737,974	24,797,639	59,665	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4883, 2_A375_pNL97_plus_lncRNA_AR..1..7033	247, 103	in gene, in gene	1	1	0	17	15	12	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene DFNA5	ICERE-1, DFNA5	deafness, autosomal dominant 5	NM_004403, NM_001127453, NM_001127454, hCT30081.3, hCT1963734.1, hCT1963735.1	203695_s_at	NP_004394.1, NP_001120925.1, NP_001120926.1, EAW93812.1, EAW93813.1, EAW93814.1
GeneID:26031	OSBPL3	7	24,836,159	25,019,760	183,601	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4884, 1_A375_pNL7_minus_lncRNA_AR..1..4885, 2_A375_pNL97_plus_lncRNA_AR..1..7034	193008, 158432, -240	downstream, in gene, upstream	1	1	0	18	14	7.67	3	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene OSBPL3	MGC21526, DKFZp667P1518, OSBPL3, KIAA0704, ORP-3, ORP3, OSBP3	oxysterol binding protein-like 3	NM_015550, NM_145320, NM_145321, NM_145322	209626_s_at, 209627_s_at	NP_056365.1, NP_663160.1, NP_663161.1, NP_663162.1
GeneID:54205	CYCS	7	25,158,270	25,164,980	6,710	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4886, 2_A375_pNL97_plus_lncRNA_AR..1..7035	-108, -12	upstream, upstream	1	1	0	28	25	14	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene CYCS	CYCS, HCS, CYC, THC4	cytochrome c, somatic	NM_018947, hCT2299206.1, hCT2299207.1, hCT2299209.1	208905_at, 229415_at, 244546_at	NP_061820.1, EAW93824.1, EAW93822.1, EAW93823.1
GeneID:136895	C7orf31	7	25,174,316	25,219,817	45,501	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4886, 2_A375_pNL97_plus_lncRNA_AR..1..7035	54729, 54825	downstream, downstream	1	1	0	28	25	14	1	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene C7orf31	C7orf31		NM_138811, hCT2349678.0, hCT2349679.0, hCT2349680.0, hCT30275.3	229146_at	NP_620166.3, EAW93825.1, EAW93826.1, EAW93827.1, EAW93828.1
GeneID:3181	HNRNPA2B1	7	26,229,556	26,240,413	10,857	-	3	2_A375_pNL97_plus_lncRNA_AR..1..7037, 4_A375_EGR1..1..7257, 4_A375_EGR1..1..7258	-1059, 29, -1091	upstream, in gene, upstream	0	1	1	14	15.5	17.5	2	4_A375_EGR1..1	19	Gene HNRNPA2B1	HNRPB1, HNRPA2B1, DKFZp779B0244, HNRNPA2B1, HNRNPB1, HNRPA2, SNRPB1, RNPA2, HNRNPA2, FLJ22720	heterogeneous nuclear ribonucleoprotein A2/B1	NM_002137, NM_031243, hCT2299295.0, hCT2299296.0, hCT2299297.0, hCT2299298.0, hCT2299299.0, hCT2357674.0, hCT2357675.0, hCT29630.3	205292_s_at, 225107_at, 225932_s_at, 235454_at, 244131_at	NP_002128.1, NP_112533.1, EAW93834.1, EAW93835.1, EAW93836.1, EAW93839.1, EAW93837.1, EAW93838.1, EAW93840.1, EAW93841.1
GeneID:11335	CBX3	7	26,241,099	26,252,976	11,877	+	3	2_A375_pNL97_plus_lncRNA_AR..1..7037, 4_A375_EGR1..1..7257, 4_A375_EGR1..1..7258	373, -715, 405	in gene, upstream, in gene	0	1	1	14	15.5	17.5	2	4_A375_EGR1..1	19	Gene CBX3	HECH, HP1-GAMMA, HP1Hs-gamma, CBX3	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	NM_016587, NM_007276, hCT1967003.2, hCT1967005.2, hCT2357670.0, hCT1783632.4, hCT1952443.2	1555920_at, 200037_s_at	NP_057671.2, NP_009207.2, EAW93843.1, EAW93844.1, EAW93845.1, EAW93846.1, EAW93842.1
GeneID:3198	HOXA1	7	27,132,612	27,135,625	3,013	-	1	4_A375_EGR1..1..7260	-855	upstream	0	0	1	11	14	16	1	4_A375_EGR1..1	16	Gene HOXA1	HOX1F, HOXA1, BSAS, MGC45232, HOX1	homeobox A1	NM_153620, NM_005522, hCT30278.4, hCT1963716.1	214639_s_at	NP_705873.2, NP_005513.1, EAW93861.1, EAW93862.1
GeneID:100506311	LOC100506311	7	27,135,984	27,139,883	3,899	+	1	4_A375_EGR1..1..7260	498	in gene	0	0	1	11	14	16	1	4_A375_EGR1..1	16	Gene LOC100506311		hypothetical LOC100506311	XR_112990, XR_110656, XR_108754, XR_114006		
GeneID:3199	HOXA2	7	27,139,973	27,142,394	2,421	-	1	4_A375_EGR1..1..7260	5914	downstream	0	0	1	11	14	16	1	4_A375_EGR1..1	16	Gene HOXA2	HOXA2, HOX1K	homeobox A2	NM_006735, hCT1640456.4	1557051_s_at, 214457_at, 228642_at	NP_006726.1, EAW93864.1
GeneID:3200	HOXA3	7	27,145,809	27,166,639	20,830	-	2	4_A375_EGR1..1..7260, 4_A375_EGR1..1..7261	30159, -2913	downstream, upstream	0	0	1	9	11.5	16	2	4_A375_EGR1..1	16	Gene HOXA3	HOXA3, HOX1, HOX1E, MGC10155	homeobox A3	NM_030661, NM_153631, hCT2349030.0, hCT1640754.4	208604_s_at, 235521_at	NP_109377.1, NP_705895.1, EAW93865.1, EAW93866.1
GeneID:285943	LOC285943	7	27,150,039	27,163,437	13,398	+	1	4_A375_EGR1..1..7261	19513	downstream	0	0	1	7	9	16	1	4_A375_EGR1..1	16	Gene LOC285943		hypothetical LOC285943	XR_112991, XR_110657, XR_108755, XR_114007	1562840_at	
GeneID:3201	HOXA4	7	27,168,126	27,170,399	2,273	-	1	4_A375_EGR1..1..7261	847	in gene	0	0	1	7	9	16	1	4_A375_EGR1..1	16	Gene HOXA4	HOX1D, HOXA4, HOX1	homeobox A4	NM_002141, hCT30277.4	206289_at	NP_002132.3, EAW93872.1
GeneID:100133311	LOC100133311	7	27,179,983	27,195,547	15,564	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7039	10561	in gene	0	1	0	16	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100133311		hypothetical LOC100133311	XR_112992, XR_112993, XR_112994, XR_110658, XR_110659, XR_110660, XR_108756, XR_108757, XR_108758, XR_114008, XR_114009, XR_114010		
GeneID:3202	HOXA5	7	27,180,996	27,183,287	2,291	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7039	-7257	upstream	0	1	0	16	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene HOXA5	HOX1.3, HOX1, MGC9376, HOXA5, HOX1C	homeobox A5	NM_019102, hCT1640753.3	213844_at	NP_061975.2, EAW93873.1
GeneID:3203	HOXA6	7	27,185,116	27,187,366	2,252	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7039	-3176	upstream	0	1	0	16	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene HOXA6	HOX1B, HOXA6, HOX1, HOX1.2	homeobox A6	NM_024014, hCT2299374.1, hCT1640752.3	208557_at	NP_076919.1, EAW93875.1, EAW93874.1
GeneID:3204	HOXA7	7	27,193,335	27,196,296	2,961	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7039	5752	downstream	0	1	0	16	23	13	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene HOXA7	HOXA7, HOX1, HOX1A, HOX1.1, ANTP	homeobox A7	NM_006896, hCT1640455.3	206847_s_at, 206848_at, 235753_at	NP_008827.2, EAW93877.1
GeneID:3205	HOXA9	7	27,202,057	27,205,149	3,092	-	1	4_A375_EGR1..1..7262	-8899	upstream	0	0	1	12	7	20	1	4_A375_EGR1..1	20	Gene HOXA9	MGC1934, ABD-B, HOX1, HOXA9, HOX1.7, HOX1G	homeobox A9	NM_152739	209905_at, 214651_s_at	NP_689952.1
GeneID:442920	MIR196B	7	27,209,099	27,209,182	83	-	1	4_A375_EGR1..1..7262	-4666	upstream	0	0	1	12	7	20	1	4_A375_EGR1..1	20	Gene MIR196B	miR-196b, MIR196B, MIRN196B, miRNA196B	microRNA 196b	NR_029911		
GeneID:3206	HOXA10	7	27,210,210	27,219,676	9,666	-	2	4_A375_EGR1..1..7262, 4_A375_EGR1..1..7263	5626, -4604	in gene, upstream	0	0	1	11.5	9	18	2	4_A375_EGR1..1	20	Gene HOXA10	PL, MGC12859, HOX1, HOX1.8, HOX1H, HOXA10	homeobox A10	NM_018951, NM_153715, hCT2349319.0, hCT2349320.0, hCT2349321.0, hCT1783952.3	213147_at, 213150_at	NP_061824.3, NP_714926.1, EAW93883.1, EAW93884.1, EAW93885.1, EAW93886.1
GeneID:3207	HOXA11	7	27,220,776	27,224,835	4,059	-	2	4_A375_EGR1..1..7262, 4_A375_EGR1..1..7263	10787, 355	downstream, in gene	0	0	1	11.5	9	18	2	4_A375_EGR1..1	20	Gene HOXA11	HOX1, HOXA11, HOX1I	homeobox A11	NM_005523, hCT2357668.0, hCT1783950.2	208493_at, 213823_at	NP_005514.1, EAW93887.1, EAW93888.1
GeneID:221883	HOXA11AS	7	27,225,027	27,228,912	3,885	+	2	4_A375_EGR1..1..7263, 4_A375_EGR1..1..7264	-547, 13917	upstream, downstream	0	0	1	8.5	12.5	17	2	4_A375_EGR1..1	18	Gene HOXA11AS	HOXA11-AS, HOXA11-AS1, NCRNA00076, HOXA11S, HOXA11AS	HOXA11 antisense RNA (non-protein coding)	NR_002795	230686_at, 239950_at	
GeneID:3209	HOXA13	7	27,236,499	27,239,725	3,226	-	1	4_A375_EGR1..1..7264	781	in gene	0	0	1	6	14	18	1	4_A375_EGR1..1	18	Gene HOXA13	HOXA13, HOX1, HOX1J	homeobox A13	NM_000522, hCT1783949.2	231786_at	NP_000513.2, EAW93890.1
GeneID:100316868	NCRNA00213	7	27,240,058	27,242,449	2,393	+	1	4_A375_EGR1..1..7264	-1112	upstream	0	0	1	6	14	18	1	4_A375_EGR1..1	18	Gene NCRNA00213	HOTTIP, FLJ38668, NCRNA00213	non-protein coding RNA 213	XR_112995, XR_110661, XR_108759, XR_114011		
GeneID:100129463	LOC100129463	7	27,278,862	27,280,847	1,985	-	3	4_A375_EGR1..1..7265, 4_A375_EGR1..1..7266, 4_A375_EGR1..1..7267	5743, -1545, -2300	downstream, upstream, upstream	0	0	1	8	11.67	18	3	4_A375_EGR1..1	22	Gene LOC100129463		hypothetical LOC100129463	XR_112996, XR_110662, XR_108760, XR_114012		
GeneID:2128	EVX1	7	27,282,164	27,286,192	4,028	+	3	4_A375_EGR1..1..7265, 4_A375_EGR1..1..7266, 4_A375_EGR1..1..7267	-7080, 228, 983	upstream, in gene, in gene	0	0	1	8	11.67	18	3	4_A375_EGR1..1	22	Gene EVX1	EVX1		NM_001989, hCT28552.2	207914_x_at, 231708_s_at	NP_001980.1, EAW93892.1
GeneID:11112	HIBADH	7	27,565,059	27,702,620	137,561	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4889, 2_A375_pNL97_plus_lncRNA_AR..1..7040	28, 28	in gene, in gene	1	1	0	44	34	10	1	1_A375_pNL7_minus_lncRNA_AR..1	44	Gene HIBADH	NS5ATP1, HIBADH, MGC40361	3-hydroxyisobutyrate dehydrogenase	NM_152740, hCT1969095.1, hCT1969096.1, hCT2357715.0, hCT30281.4	224812_at, 231955_s_at, 234452_at	NP_689953.1, EAW93898.1, EAW93897.1, EAW93899.1, EAW93900.1
GeneID:8887	TAX1BP1	7	27,779,738	27,869,386	89,648	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7041	22	in gene	0	1	0	11	24	11	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene TAX1BP1	CALCOCO3, TAX1BP1, T6BP, TXBP151	Tax1 (human T-cell leukemia virus type I) binding protein 1	NM_001079864, NM_006024, hCT2299137.0, hCT2299140.0, hCT30279.3, hCT1961211.1	200976_s_at, 200977_s_at, 213786_at	NP_001073333.1, NP_006015.4, EAW93901.1, EAW93902.1, EAW93903.1, EAW93904.1
GeneID:221895	JAZF1	7	27,870,192	28,220,437	350,245	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4890, 2_A375_pNL97_plus_lncRNA_AR..1..7042	118437, 118293	in gene, in gene	1	1	0	18	22	9	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene JAZF1	TIP27, ZNF802, JAZF1, DKFZp761K2222	JAZF zinc finger 1	NM_175061, hCT30282.2	225798_at, 225800_at	NP_778231.2, EAW93905.1
GeneID:9586	CREB5	7	28,338,940	28,865,511	526,571	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7043	388652	in gene	0	1	0	9	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CREB5	CREB5, CRE-BPA	cAMP responsive element binding protein 5	NM_182898, NM_182899, NM_004904, NM_001011666, hCT2299254.1, hCT1783344.3, hCT1982664.1	205931_s_at, 229228_at	NP_878901.2, NP_878902.2, NP_004895.2, NP_001011666.1, EAW93908.1, EAW93910.1, EAW93909.1

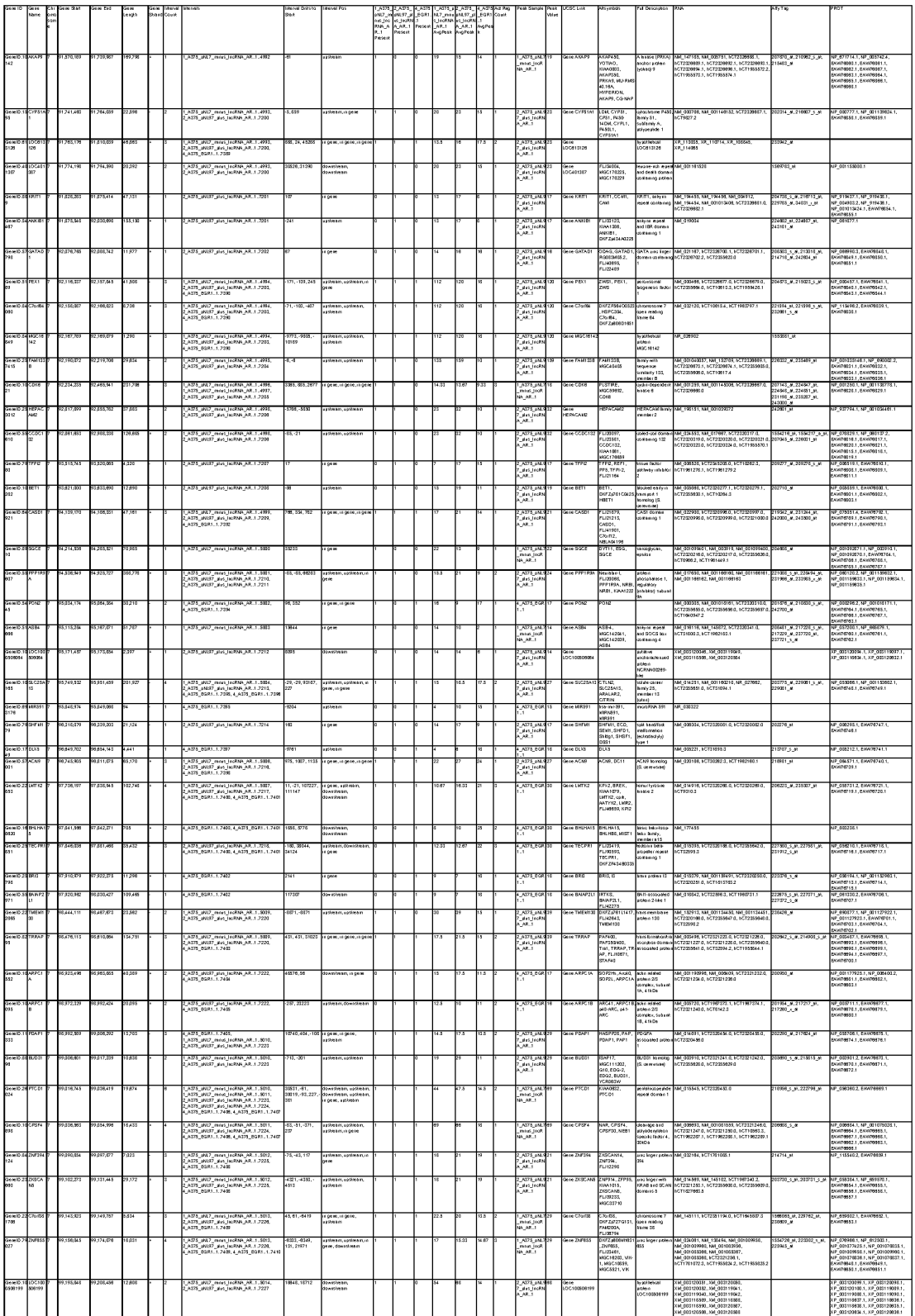
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:9865	TRIL	7	28,992,974	28,998,029	5,055	-	1	4_A375_EGR1..1..7266	1069	in gene	0	0	1	10	6	20	1	4_A375_EGR1..1	20	Gene TRIL	KIAA0644, TRIL	TLR4 interactor with leucine rich repeats	NM_014817, hCT29676.3	205150_s_at, 205151_s_at	NP_055632.2, EAW93913.1
GeneID:54504	CPVL	7	29,035,247	29,186,153	150,906	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7045	110857	in gene	0	1	0	14	26	2	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene CPVL	HVLP, CPVL, MGC10029	carboxypeptidase, vitellogenic-like	NM_031311, NM_019029, hCT1966998.1, hCT1966999.0, hCT1967000.1, hCT1967001.1, hCT1783341.2	1555710_at, 1555711_x_at, 208146_s_at, 211678_at	NP_112601.3, NP_061902.2, EAW93914.1, EAW93915.1, EAW93917.1, EAW93916.1, EAW93918.1
GeneID:1124	CHN2	7	29,234,121	29,553,944	319,823	+	1	4_A375_EGR1..1..7269	99191	in gene	0	0	1	0	3	15	1	4_A375_EGR1..1	15	Gene CHN2	ARHGAP3, RHOGAP3, BCH, CHN2, MGC138360	chimerin (chimaerin) 2	NM_001039936, NM_004067, hCT29551.3	1557769_at, 207486_x_at, 211419_s_at, 213385_at	NP_001035025.1, NP_004058.1, EAW93919.1
GeneID:222171	PRR15	7	29,603,427	29,606,911	3,484	+	1	4_A375_EGR1..1..7270	2461	in gene	0	0	1	6	6	19	1	4_A375_EGR1..1	19	Gene PRR15	PRR15	proline rich 15	NM_175887, hCT2301810.0	226961_at	NP_787083.1, EAW93920.1
GeneID:9805	SCRN1	7	29,959,719	30,029,905	70,186	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7046	1009	in gene	0	1	0	9	14	10	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene SCRN1	KIAA0193, SES1, SCRN1	secernin 1	NM_014766, NM_001145514, NM_001145515, NM_001145513, hCT2301908.0, hCT2301910.0, hCT28557.3	201462_at	NP_055581.3, NP_001138986.1, NP_001138987.1, NP_001138985.1, EAW93926.1, EAW93927.1, EAW93928.1
GeneID:55033	FKBP14	7	30,052,884	30,066,268	13,384	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4892, 1_A375_pNL7_minus_lncRNA_AR..1..4893, 2_A375_pNL97_plus_lncRNA_AR..1..7047, 2_A375_pNL97_plus_lncRNA_AR..1..7048	-68, -1668, -132, -1604	upstream, upstream, upstream, upstream	1	1	0	36	43	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene FKBP14	FLJ20731, FKBP22, FKBP14	FK506 binding protein 14, 22 kDa	NM_017946, hCT29554.3	219390_at, 235311_at	NP_060416.1, EAW93929.1
GeneID:84725	PLEKHA8	7	30,066,288	30,130,360	62,072	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4892, 1_A375_pNL7_minus_lncRNA_AR..1..4893, 2_A375_pNL97_plus_lncRNA_AR..1..7047, 2_A375_pNL97_plus_lncRNA_AR..1..7048	-1952, -352, -1868, -416	upstream, upstream, upstream, upstream	1	1	0	36	43	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	43	Gene PLEKHA8	DKFZp686J09164, MGC3358, FAPP2, DKFZp313M1034, PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	NM_032639, hCT2301819.0, hCT2301820.0, hCT28559.3, hCT1955376.1	1560556_a_at, 224208_at, 231543_at, 232212_at, 233943_x_at	NP_116028.1, EAW93930.1, EAW93931.1, EAW93932.1, EAW93933.1
GeneID:223082	ZNRF2	7	30,323,923	30,407,308	83,385	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7049, 2_A375_pNL97_plus_lncRNA_AR..1..7050	445, 1693	in gene, in gene	0	1	0	12	14.5	9	2	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene ZNRF2	ZNRF2, RNF202	zinc and ring finger 2	NM_147128, hCT1840663.3, hCT1966581.2	226261_at	NP_667339.1, EAW93938.1, EAW93939.1
GeneID:693133	MIR550-1	7	30,329,410	30,329,506	96	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7049, 2_A375_pNL97_plus_lncRNA_AR..1..7050	-5042, -3794	upstream, upstream	0	1	0	12	14.5	9	2	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene MIR550-1	MIR550-1, hsa-mir-550a-1, MIR550A1, MIRN550-1	microRNA 550-1	NR_030319		
GeneID:10392	NOD1	7	30,464,143	30,518,393	54,250	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7051, 4_A375_EGR1..1..7271	-151, 26553	upstream, in gene	0	1	1	10.5	11	12.5	2	4_A375_EGR1..1	18	Gene NOD1	NOD1, CLR7.1, NLRC1, CARD4	nucleotide-binding oligomerization domain containing 1	NM_006092, hCT2301899.0, hCT2301901.0, hCT2301902.0, hCT2357702.0, hCT2357703.0, hCT30385.3	221073_s_at, 224190_x_at	NP_006083.1, EAW93946.1, EAW93944.1, EAW93945.1, EAW93947.1, EAW93948.1, EAW93949.1
GeneID:401320	LOC401320	7	30,587,974	30,617,375	29,401	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7052	26543	in gene	0	1	0	12	16	3	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC401320		hypothetical LOC401320	XR_113001, XR_110667, XR_108765, XR_114017	1558458_at, 1558459_s_at, 233732_at, 238540_at, 239313_at, 239640_at	
GeneID:2617	GARS	7	30,634,161	30,673,649	39,488	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7053	235	in gene	0	1	0	15	29	10	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene GARS	GlyRS, DSMAV, CMT2D, SMAD1, HMN5, GARS	glycyl-tRNA synthetase	NM_002047, hCT2301809.0, hCT30383.3	208693_s_at	NP_002038.2, EAW93960.1, EAW93961.1
GeneID:1395	CRHR2	7	30,692,863	30,722,140	29,277	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4894, 2_A375_pNL97_plus_lncRNA_AR..1..7054, 4_A375_EGR1..1..7272	10476, 10426, 33532	in gene, in gene, downstream	1	1	1	56	72	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	139	Gene CRHR2	CRHR2, CRF2, CRFR2	corticotropin releasing hormone receptor 2	NM_001883, hCT2299480.0, hCT2299481.0, hCT2299482.0, hCT1955337.1	207897_at, 211510_s_at	NP_001874.2, EAW93964.1, EAW93962.1, EAW93963.1, EAW93965.1
GeneID:84182	FAM188B	7	30,811,033	30,932,002	120,969	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7055	28423	in gene	0	1	0	14	24	5	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene FAM188B	FLJ51453, FAM188B, FLJ22374, MGC44277, C7orf67	family with sequence similarity 188, member B	NM_032222	1557141_at, 235559_at	NP_115598.2
GeneID:117	ADCYAP1R1	7	31,092,142	31,146,311	54,169	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4896, 2_A375_pNL97_plus_lncRNA_AR..1..7056	62610, 62594	downstream, downstream	1	1	0	51	96	7	1	2_A375_pNL97_plus_lncRNA_AR..1	96	Gene ADCYAP1R1	PACAPRI, PAC1, PACAPR, ADCYAP1R1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	NM_001118, hCT1641237.3	207151_at, 226690_at	NP_001109.2, EAW93978.1
GeneID:5137	PDE1C	7	31,792,632	32,338,383	545,751	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4897, 2_A375_pNL97_plus_lncRNA_AR..1..7057	247567, 437679	in gene, in gene	1	1	0	13.5	20	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene PDE1C	PDE1C, Hcam3	phosphodiesterase 1C, calmodulin-dependent 70kDa	NM_005020, NM_001191056, NM_001191057, NM_001191058, NM_001191059, hCT2299408.0, hCT2299407.0, hCT2299406.0, hCT2299409.0	1554378_a_at, 207303_at, 216869_at	NP_005011.1, NP_001177985.1, NP_001177986.1, NP_001177987.1, NP_001177988.1, EAW93984.1, EAW93985.1, EAW93986.1, EAW93987.1
GeneID:23658	LSM5	7	32,524,945	32,534,870	9,925	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4899, 2_A375_pNL97_plus_lncRNA_AR..1..7060	4918, 4838	in gene, in gene	1	1	0	42	49	17	1	2_A375_pNL97_plus_lncRNA_AR..1	49	Gene LSM5	YER146W, FLJ12710, LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_001130710, NM_012322, NM_001139499, NR_024466, hCT28560.3, hCT1955379.0	202903_at, 202904_s_at, 211747_s_at	NP_001124182.1, NP_036454.1, NP_001132971.1, EAW93990.1, EAW93991.1
GeneID:23080	AVL9	7	32,535,176	32,623,779	88,603	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4899, 2_A375_pNL97_plus_lncRNA_AR..1..7060	-5224, -5144	upstream, upstream	1	1	0	42	49	17	1	2_A375_pNL97_plus_lncRNA_AR..1	49	Gene AVL9	AVL9, DKFZp686G0344, KIAA0241	AVL9 homolog (S. cerevisiase)	NM_015060, hCT2299340.0, hCT2299344.0, hCT2357684.0, hCT29002.3, hCT1955380.1, hCT1955381.1	1555055_at, 212471_at, 212474_at, 212475_at	NP_055875.1, EAW93992.1, EAW93993.1, EAW93995.1, EAW93996.1, EAW93997.1, EAW93994.1
GeneID:25948	KBTBD2	7	32,907,776	32,931,466	23,690	-	1	4_A375_EGR1..1..7274	-356	upstream	0	0	1	6	6	16	1	4_A375_EGR1..1	16	Gene KBTBD2	KBTBD2, BKLHD1	kelch repeat and BTB (POZ) domain containing 2	NM_015483, hCT1967448.1, hCT2299561.0, hCT28578.3	212447_at, 223584_s_at, 223585_x_at, 234232_at, 234233_s_at, 234793_at	NP_056298.2, EAW94000.1, EAW94001.1, EAW94002.1
GeneID:11328	FKBP9	7	32,997,005	33,046,543	49,538	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4900, 2_A375_pNL97_plus_lncRNA_AR..1..7062	243, 243	in gene, in gene	1	1	0	17	21	6	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene FKBP9	PPIase, FKBP60, FKBP63, FKBP9, MGC126772, MGC138258, DKFZp586B1723	FK506 binding protein 9, 63 kDa	NM_007270	212169_at	NP_009201.2
GeneID:51251	NT5C3	7	33,053,742	33,102,409	48,667	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7063	73	in gene	0	1	0	15	21	13	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NT5C3	PSN1, P5'N-1, cN-III, MGC27337, MGC87828, UMPH, NT5C3, PN-I, MGC87109, UMPH1	5'-nucleotidase, cytosolic III	NM_001002010, NM_016489, NR_029372, NM_001166118, hCT2299556.1, hCT2299557.1, hCT2357698.1, hCT2357699.1, hCT2357700.1	223298_s_at	NP_001002010.1, NP_057573.2, NP_001159590.1, EAW94007.1, EAW94008.1, EAW94009.1, EAW94010.1, EAW94011.1
GeneID:6100	RP9	7	33,134,409	33,149,002	14,593	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4901, 1_A375_pNL7_minus_lncRNA_AR..1..4902, 1_A375_pNL7_minus_lncRNA_AR..1..4903, 2_A375_pNL97_plus_lncRNA_AR..1..7064	1462, 234, -150, -182	in gene, in gene, upstream, upstream	1	1	0	27.5	36	5.5	2	2_A375_pNL97_plus_lncRNA_AR..1	61	Gene RP9	PAP-1, RP9	retinitis pigmentosa 9 (autosomal dominant)	NM_203288, hCT2348338.0, hCT2348339.0, hCT1957377.2	227649_at, 227652_at	NP_976033.1, EAW94014.1, EAW94012.1, EAW94013.1
GeneID:27241	BBS9	7	33,169,152	33,645,680	476,528	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7065	144	in gene	0	1	0	10	21	9	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene BBS9	PTHB1, BBS9, D1, MGC118917, C18, B1	Bardet-Biedl syndrome 9	NM_014451, NM_198428, NM_001033604, NM_001033605, hCT2299422.0, hCT2299423.0, hCT2299426.0, hCT1782568.2	1555555_at, 209958_s_at, 216239_at, 37547_at, 37549_g_at	NP_055266.2, NP_940820.1, NP_001028776.1, NP_001028777.1, EAW94017.1, EAW94018.1, EAW94015.1, EAW94016.1
GeneID:168667	BMPER	7	33,945,112	34,194,112	249,000	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4904, 2_A375_pNL97_plus_lncRNA_AR..1..7066	82008, 81928	in gene, in gene	1	1	0	20	27	4	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene BMPER	CV2, CRIM3, CV-2, BMPER	BMP binding endothelial regulator	NM_133468	241986_at	NP_597725.1
GeneID:23333	DPY19L1	7	34,968,493	35,077,653	109,160	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7067	34005	in gene	0	1	0	15	19	4	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene DPY19L1	KIAA0877, DPY19L1	dpy-19-like 1 (C. elegans)	NM_015283	1560915_at, 1560916_a_at, 1570355_a_at, 212792_at, 215433_at	NP_056098.1
GeneID:57057	TBX20	7	35,242,042	35,293,711	51,669	-	1	4_A375_EGR1..1..7276	-7953	upstream	0	0	1	4	5	17	1	4_A375_EGR1..1	17	Gene TBX20	ASD4, TBX20	T-box 20	NM_001077653, NM_001166220, hCT8923.4	1564945_at	NP_001071121.1, NP_001159692.1, EAW94048.1
GeneID:64224	HERPUD2	7	35,672,269	35,734,772	62,503	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4905, 2_A375_pNL97_plus_lncRNA_AR..1..7069	132, -12	in gene, upstream	1	1	0	26	25	16	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene HERPUD2	HERPUD2, FLJ22313, FLJ31032	HERPUD family member 2	NM_022373, hCT2299725.0, hCT2299726.0, hCT2357668.0, hCT2357669.0, hCT8925.2, hCT1981202.0	1552628_a_at, 1558699_a_at, 222751_at, 236170_x_at	NP_071768.3, EAW94051.1, EAW94052.1, EAW94053.1, EAW94054.1, EAW94055.1, EAW94050.1
GeneID:989	7-Sep	7	35,840,627	35,944,917	104,290	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7070	941	in gene	0	1	0	11	17	9	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene SEPT7	CDC10, NBla02942, SEPT7, CDC3, SEPT7A	septin 7	NM_001011553, NM_001788, hCT2299578.0, hCT2299580.0, hCT2299581.0, hCT2299582.0	1565623_at, 213151_s_at, 244508_at	NP_001011553.2, NP_001779.3, EAW94059.1, EAW94060.1, EAW94061.1, EAW94062.1
GeneID:23366	KIAA0895	7	36,363,759	36,429,734	65,975	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4906, 2_A375_pNL97_plus_lncRNA_AR..1..7073	22774, 22950	in gene, in gene	1	1	0	16	23	6	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene KIAA0895	KIAA0895		NM_015314, NM_001100425, hCT2299601.0, hCT2299602.0, hCT8181.2	213424_at	NP_056129.2, NP_001093895.1, EAW94064.1, EAW94065.1, EAW94066.1
GeneID:313	AOAH	7	36,552,549	36,764,154	211,605	-	1	1_A375_pNL7_minus_lncRNA_AR..1..4907	217578	downstream	1	0	0	17	15	7	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene AOAH	AOAH	acyloxyacyl hydrolase (neutrophil)	NM_001177506, NM_001177507, NM_001637, hCT8771.2	205639_at	NP_001170977.1, NP_001170978.1, NP_001628.1, EAW94073.1
GeneID:9844	ELMO1	7	36,893,961	37,488,511	594,550	-	7	1_A375_pNL7_minus_lncRNA_AR..1..4908, 1_A375_pNL7_minus_lncRNA_AR..1..4909, 1_A375_pNL7_minus_lncRNA_AR..1..4910, 2_A375_pNL97_plus_lncRNA_AR..1..7074, 2_A375_pNL97_plus_lncRNA_AR..1..7075, 2_A375_pNL97_plus_lncRNA_AR..1..7076, 4_A375_EGR1..1..7277	398031, 93687, 951, 416598, 395999, -81, -97	in gene, in gene, in gene, in gene, in gene, upstream, upstream	1	1	1	15.2	16.2	7.6	5	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ELMO1	ELMO1, MGC126406, ELMO-1, CED-12, KIAA0281, CED12	engulfment and cell motility 1	NM_014800, NM_001039459, NM_130442, hCT2299593.0, hCT2299594.0, hCT2299595.0, hCT2357712.0, hCT9236.3	204513_s_at	NP_055615.8, NP_001034548.1, NP_569709.1, EAW94075.1, EAW94076.1, EAW94079.1, EAW94077.1, EAW94078.1
GeneID:11281	POU6F2	7	39,017,609	39,504,390	486,781	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4911, 1_A375_pNL7_minus_lncRNA_AR..1..4912, 2_A375_pNL97_plus_lncRNA_AR..1..7077, 2_A375_pNL97_plus_lncRNA_AR..1..7078	27575, 436439, 27671, 436535	in gene, in gene, in gene, in gene	1	1	0	19.5	16.5	6	2	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene POU6F2	WTSL, RPF-1, WT5, POU6F2	POU class 6 homeobox 2	NM_007252, NM_001166018, hCT2300166.0, hCT1955234.1	207450_s_at	NP_009183.3, NP_001159490.1, EAW94116.1, EAW94117.1
GeneID:57002	C7orf36	7	39,806,003	39,812,480	6,477	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7079	77	in gene	0	1	0	12	24	7	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene C7orf36	C7orf36, GK003	chromosome 7 open reading frame 36	NM_020192, hCT8262.1	223433_at	NP_064577.1, EAW94120.1
GeneID:5898	RALA	7	39,663,162	39,747,719	84,557	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4913, 4_A375_EGR1..1..7278	-56, -90	upstream, upstream	1	0	1	17	16	16	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene RALA	RAL, MGC48949, RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	NM_005402, hCT8261.2, hCT1983577.1	214435_x_at, 224660_at	NP_005393.2, EAW94123.1, EAW94122.1
GeneID:8621	CDK13	7	39,989,959	40,136,733	146,774	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4915, 4_A375_EGR1..1..7279	-263, 233	upstream, in gene	1	0	1	20	14	19	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene CDK13	CHED, FLJ35215, CDC2L, KIAA1791, CDC2L5, CDK13, hCDK13	cyclin-dependent kinase 13	NM_003718, NM_031267, hCT2299608.0, hCT2299609.0, hCT2299610.0, hCT2299611.0, hCT2299612.0, hCT2299613.0	207318_s_at, 207319_s_at, 210965_x_at, 213987_s_at, 214287_s_at, 232266_x_at	NP_003709.3, NP_112557.2, EAW94129.1, EAW94130.1, EAW94131.1, EAW94132.1, EAW94128.1, EAW94133.1
GeneID:136647	C7orf11	7	40,172,342	40,174,251	1,909	-	2	1_A375_pNL7_minus_lncRNA_AR..1..4916, 2_A375_pNL97_plus_lncRNA_AR..1..7080	-373, -85	upstream, upstream	1	1	0	15	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C7orf11	ABHS, TTDN1, ORF20, C7orf11	chromosome 7 open reading frame 11	NM_138701, hCT1819417.1	225419_at	NP_619646.1, EAW94134.1
GeneID:79783	C7orf10	7	40,174,575	40,900,366	725,791	+	4	1_A375_pNL7_minus_lncRNA_AR..1..4916, 1_A375_pNL7_minus_lncRNA_AR..1..4917, 2_A375_pNL97_plus_lncRNA_AR..1..7080, 2_A375_pNL97_plus_lncRNA_AR..1..7081	49, 416977, -239, 416689	in gene, in gene, upstream, in gene	1	1	0	16.5	18.5	8.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C7orf10	DERP13, FLJ11806, ORF19, FLJ53672, C7orf10	chromosome 7 open reading frame 10	NM_024728, NM_001193311, NM_001193312, NM_001193313, hCT2299620.0, hCT2299622.0, hCT2299624.0	219655_at	NP_079004.1, NP_001180240.1, NP_001180241.1, NP_001180242.1, EAW94136.1, EAW94137.1, EAW94135.1
GeneID:2737	GLI3	7	42,000,547	42,276,618	276,071	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7087, 4_A375_EGR1..1..7280	4662, 271594	in gene, in gene	0	1	1	13	12.5	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene GLI3	PAPA1, GLI3FL, GCPS, GLI3, PAPA, PAPB, PAP-A, GLI3-190, ACLS, PPDIV, PHS	GLI family zinc finger 3	NM_000168, hCT2299656.0, hCT8318.3	1569342_at, 205201_at, 227376_at	NP_000159.3, EAW94144.1, EAW94145.1
GeneID:5683	PSMA2	7	42,956,460	42,971,805	15,345	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7088	-291	upstream	0	1	0	11	18	5	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene PSMA2	PSC2, PMSA2, HC3, PSMA2, MU	proteasome (prosome, macropain) subunit, alpha type, 2	NM_002787, hCT2357709.0, hCT10955.2, hCT1950325.1	201316_at, 201317_s_at	NP_002778.1, EAW94151.1, EAW94152.1, EAW94153.1
GeneID:64983	MRPL32	7	42,971,939	42,977,456	5,517	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7088	157	in gene	0	1	0	11	18	5	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene MRPL32	L32mt, HSPC283, MRP-L32, bMRP-59b, MRPL32	mitochondrial ribosomal protein L32	NM_031903, hCT10958.3, hCT1963337.0, hCT1963338.0, hCT1963339.0	225260_s_at	NP_114109.1, EAW94157.1, EAW94154.1, EAW94155.1, EAW94156.1
GeneID:23072	HECW1	7	43,152,198	43,602,938	450,740	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4921, 2_A375_pNL97_plus_lncRNA_AR..1..7089	107634, 457062	in gene, downstream	1	1	0	19	19	7	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene HECW1	HECW1, NEDL1, KIAA0322	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	NM_015052, hCT2349644.0, hCT2349645.0, hCT10492.3	210331_at, 215584_at	NP_055867.3, EAW94158.1, EAW94159.1, EAW94160.1
GeneID:9263	STK17A	7	43,622,692	43,666,978	44,286	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7090	412	in gene	0	1	0	11	22	9	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene STK17A	DRAK1, STK17A	serine/threonine kinase 17a	NM_004760, hCT2299694.0, hCT10495.3	202693_s_at, 202694_at, 202695_s_at	NP_004751.2, EAW94162.1, EAW94163.1
GeneID:55744	C7orf44	7	43,678,859	43,769,083	90,224	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4922, 1_A375_pNL7_minus_lncRNA_AR..1..4923, 2_A375_pNL97_plus_lncRNA_AR..1..7091, 2_A375_pNL97_plus_lncRNA_AR..1..7092	61403, -181, 54715, -69	in gene, upstream, in gene, upstream	1	1	0	16.67	21.67	7.67	3	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene C7orf44	C7orf44, FLJ10803	chromosome 7 open reading frame 44	NM_018224, hCT2299736.0, hCT2357695.0, hCT10496.3, hCT1983330.1, hCT1983331.1, hCT1983332.1	208497_at, 209445_x_at, 209446_s_at, 232330_at, 239490_at	NP_060694.2, EAW94167.1, EAW94165.1, EAW94166.1, EAW94168.1, EAW94169.1, EAW94170.1
GeneID:644	BLVRA	7	43,798,272	43,846,941	48,669	+	1	4_A375_EGR1..1..7282	-8432	upstream	0	0	1	6	4	22	1	4_A375_EGR1..1	22	Gene BLVRA	BLVR, BVR, BLVRA, BVRA	biliverdin reductase A	NM_000712, hCT2299697.0	203771_s_at, 203772_at, 203773_x_at, 211729_x_at, 229109_s_at	NP_000703.2, EAW94171.1
GeneID:64951	MRPS24	7	43,906,157	43,909,145	2,988	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7093, 4_A375_EGR1..1..7283	89, -8055	in gene, upstream	0	1	1	10	15	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene MRPS24	MRP-S24, HSPC335, MRPS24	mitochondrial ribosomal protein S24	NM_032014, hCT1969067.1, hCT1819209.0	224946_at	NP_114403.1, EAW94172.1, EAW94173.1
GeneID:55665	URGCP	7	43,915,501	43,965,996	50,495	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4924, 2_A375_pNL97_plus_lncRNA_AR..1..7093, 4_A375_EGR1..1..7283	140, 56940, 48798	in gene, downstream, in gene	1	1	1	12	14.67	13.33	3	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene URGCP	DKFZp686O0457, URGCP, URG4, DKFZp686G166	upregulator of cell proliferation	NM_001077663, NM_001077664, NM_017920, hCT2299750.0, hCT2357694.0, hCT10493.3	218601_at, 244046_at	NP_001071131.1, NP_001071132.1, NP_060390.3, EAW94174.1, EAW94175.1, EAW94176.1



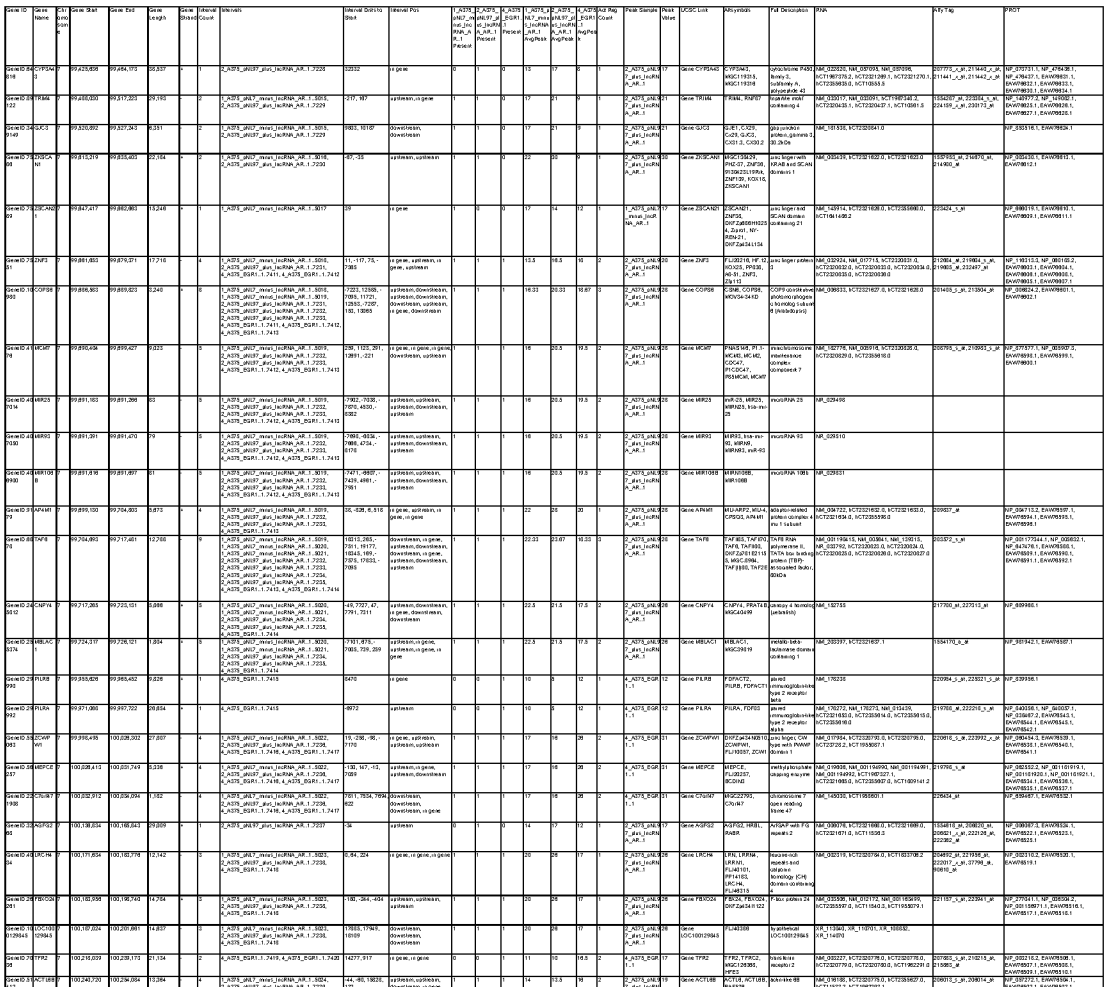
Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_DMSO_MK87_plus_lncRNA_RUN_A_R_1 Peaks	2_A375_DMSO_MK87_plus_lncRNA_RUN_A_R_1 Present	4_A375_EGFR_MK87_plus_lncRNA_RUN_A_R_1 Present	1_A375_plus_MK87_plus_lncRNA_RUN_A_R_1 Avg Peak	2_A375_plus_MK87_plus_lncRNA_RUN_A_R_1 Avg Peak	4_A375_EGFR_plus_lncRNA_RUN_A_R_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:3119	UBE2D3	7	43,966,025	43,999,705	33,700	+	1	2_A375_plus7_minus_lncRNA_RUN_A_R_1:4164	-179	upstream	1	0	0	16	14	9	1	2_A375_plus7_minus_lncRNA_RUN_A_R_1	16	Gene UBE2D3	FLJ20054, UBE2D4, HBUCE1	ubiquitin-conjugating enzyme E2D 4 (putative)	NM_015983, NCT1968735.1, NCT1968784.1, NCT1968804.1, NCT1968825.1, NCT1968836.1	116837_s_at:65321_at	NP_3370971, ENAW94182.1, ENAW94183.1, ENAW94179.1, ENAW94180.1, ENAW94184.1, ENAW94181.1, ENAW94182.1
GeneID:2823	SPDYE1	7	44,040,489	44,045,703	5,234	+	2	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4163, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7094	18793, 18527	downstream, downstream	1	1	0	134	147	9	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	147	Gene SPDYE1	Rapid1, WBSCR19, SPDYE, DKFZp434A016, SPDYE1	family homolog E1 (Drosophila)	NM_170984	232984_at	NP_7702342
GeneID:1023719	LOC100287164	7	44,099,902	44,099,932	8,970	-	2	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4163, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7094	7165, 7136	downstream, downstream	1	1	0	134	147	9	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	147	Gene LOC100287164		hypothetical protein LOC100287164	XM_002342717		XP_002342758.2
GeneID:2837	FLJ35397	7	44,076,695	44,092,862	16,164	+	5	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4158, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:4927, 4_A375_EGFR_1:7294	4002, 3446, 5676	downstream, downstream, downstream, downstream	1	0	1	16.5	15	6.5	2	1_A375_plus7_minus_lncRNA_RUN_A_R_1	16	Gene FLJ35397		hypothetical LOC283501	NR_015401, NR_024416	1550125_at, 1564297_at, 1564302_at, 1569093_a_at, 1569090_s_at	222429_at	
GeneID:2819	DBNL	7	44,084,229	44,101,315	17,086	+	3	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4926, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:4927, 4_A375_EGFR_1:7294	-1919, -93, 129	upstream, upstream, gene	1	0	1	16.5	15	6.5	2	1_A375_plus7_minus_lncRNA_RUN_A_R_1	16	Gene DBNL	ABP1, SH3P7, DBNL, HIP-55	drebrin-like	NM_014383, NM_001014436, NM_001127698, NCT02000427.0, NCT02003408.0, NCT02030829.0, NCT1783477.1	222429_at	NP_5567022, NP_001014436.1, NP_001116228.1, ENAW91129.1, ENAW91130.1, ENAW91132.1, ENAW91131.1
GeneID:1076	TK2	7	44,240,876	44,253,993	13,118	+	1	2_A375_plus7_minus_lncRNA_RUN_A_R_1:4925	176	upstream	1	0	0	22	13	11	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	22	Gene TK2	TK19		NM_206535, NCT02900530.0, NCT02900539.0, NCT9355.2	217764_at, 217765_s_at	NP_3985451, ENAW91112.1, ENAW91111.1, ENAW91112.1
GeneID:8744	CAMK2B	7	44,256,749	44,285,200	100,451	+	5	1_A375_plus7_minus_lncRNA_RUN_A_R_1:7288, 4_A375_EGFR_1:7287, 4_A375_EGFR_1:7288, 4_A375_EGFR_1:7289	69102, 55476, 31248, 16174, -9280	downstream, downstream, upstream, upstream, upstream	0	0	1	7.8	8.8	10.4	3	4_A375_EGFR_1.1	19	Gene CAMK2B	CaMK2, CaMK2B, CAMK, CaMK2-dependent protein kinase II beta	calcium/calmodulin-dependent protein kinase II beta	NM_172079, NM_172081, NM_172084, NM_172083, NM_172078, NM_001220, NCT02284649.0, NCT02284911.0, NCT02894353.0, NCT02894354.0, NCT02894353.0, NCT9389.2	209968_s_at, 211404_x_at, 211405_s_at, 211276_at, 244846_at	NP_7438761, NP_742076.1, NP_742075.1, NP_742079.1, NP_742081.1, NP_742081.1, NP_001211.3, NP_742077.1, ENAW91104.1, ENAW91105.1, ENAW91106.1, ENAW91107.1, ENAW91108.1, ENAW91109.1
GeneID:2316	NUDCD3	7	44,321,985	44,330,355	108,430	-	1	4_A375_EGFR_1.1:7290	113	gene	0	0	1	19	19	30	1	4_A375_EGFR_1.1	30	Gene NUDCD3	KIAA1060, NudC domain containing 3	NudC domain containing 3	NM_015332, NCT2289479.1, NCT2283691.0, NCT9389.2	201289_s_at, 201270_x_at	NP_5961473, ENAW91100.1, ENAW91101.1, ENAW91101.1
GeneID:5406	DDX58	9	44,805,403	44,814,107	8,704	-	4	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4929, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7293, 4_A375_EGFR_1:7291, 4_A375_EGFR_1:7292	-7479, 849, 459, 7391	upstream, upstream, gene, upstream	1	1	1	16.5	19.5	21	2	2_A375_plus7_plus_lncRNA_RUN_A_R_1	23	Gene DDX58	DDX21, NOH61, DDX56, DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	NM_019032, NCT02382295.0, NCT02383639.0, NCT9355.2	217764_at	NP_0859551, ENAW91096.1, ENAW91093.1, ENAW91094.1
GeneID:2237	TMED4	7	44,816,782	44,821,827	5,045	+	4	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4929, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7293, 4_A375_EGFR_1:7291, 4_A375_EGFR_1:7292	211, 6329, 8179, 99	upstream, downstream, downstream, upstream	1	1	1	16.5	19.5	21	2	2_A375_plus7_plus_lncRNA_RUN_A_R_1	23	Gene TMED4	ERS29, HHLF, TMED4	transmembrane emp24 domain trafficking protein 4	NM_183047, NCT02402291.1, NCT02402401.1, NCT01810936.3	1559352_at, 1559353_s_at, 1559467_s_at, 224676_at, 224601_at	NP_5725353.2, ENAW91091.1, ENAW91093.1, ENAW91092.1
GeneID:4904	OGDH	7	44,848,121	44,745,969	102,848	+	3	1_A375_plus7_minus_lncRNA_RUN_A_R_1:7099, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7097, 4_A375_EGFR_1:7295	55, 32387, 10127	gene, gene, gene, gene	0	0	1	13	13.67	13.33	3	4_A375_EGFR_1.1	21	Gene OGDH	AKGDH, OGDH, E1k, OGDC	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	NM_002541, NM_001030941, NM_001165036, NCT02906480.0, NCT02906481.0, NCT9347.2	1554151_at, 1554152_a_at, 201262_at	NP_2523332.2, NP_001029941.1, NP_001165036.1, ENAW91097.1, ENAW91095.1, ENAW91098.1
GeneID:4832	MED22	7	44,766,930	44,809,460	20,950	+	2	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4930, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7096	-242, -242	upstream, upstream	1	1	0	41	50	15	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	50	Gene MED22	MED22, SOH1, SMAP100, Med22, DKFZp761Q123, TRAP/SMCC subunit MED22	yeast, large) Mediator complex 2	NM_031449, NM_174929, NCT2306485.1, NCT2306486.1, NCT2306487.1	221525_at, 221924_at, 236520_x_at, 242572_at	NP_1139873.2, NP_775589.2, ENAW91034.1, ENAW91035.1, ENAW91033.1
GeneID:84	MYO1G	7	45,002,260	45,016,704	16,444	-	2	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7102, 4_A375_EGFR_1:7294	-7864, 6304	upstream, upstream	0	1	1	10	14	15.5	2	2_A375_plus7_plus_lncRNA_RUN_A_R_1	21	Gene MYO1G	MYH42, MYO1G	myosin IG	NM_033054, NCT2306265.0, NCT2306294.0, NCT2306307.0, NCT2306306.0, NCT1021.0	227799_at, 244854_at	NP_1499452, ENAW91089.1, ENAW91090.1, ENAW91070.1, ENAW91071.1, ENAW91072.1
GeneID:2815	C7orf40	7	45,022,427	45,026,359	3,932	-	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7102	109	upstream	0	1	0	17	21	14	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	21	Gene C7orf40	C7orf40, FLJ35393	chromosome 7 open reading frame 40	NR_026997	229689_at	
GeneID:7795	SNORA9	9	45,024,977	45,025,109	132	+	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7102	-1259	upstream	0	1	0	17	21	14	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	21	Gene SNORA9	SNORA9, ACA9	small nucleolar RNA, H/ACA box 9	NR_002982		
GeneID:8330	CCAR2	7	45,039,345	45,116,969	76,724	+	1	4_A375_EGFR_1.1:7293	69647	downstream	0	0	1	4	4	21	1	4_A375_EGFR_1.1	21	Gene CCAR2	DBC1, CCAR2, MGC4697, MGC74986, PP10187, MGC4087, CIA/E2	cell division cycle and apoptosis regulator 2	NM_0314443, NM_001078935, NM_001178764, NM_001187933, NM_032735, NCT02994753.0, NCT02994754.0, NCT02994753.0, NCT02994754.0, NCT1021.5, NCT1983760.1	223164_at	NP_113931.1, NP_001029595.1, NP_001178235.1, NP_001187407.1, ENAW91085.1, ENAW91083.1, ENAW91086.1, ENAW91081.1, ENAW91082.1, ENAW91083.1, ENAW91084.1, ENAW91086.1
GeneID:1023719	LOC100287164	7	45,117,402	45,119,810	2,308	+	1	4_A375_EGFR_1.1:7295	8762	upstream	0	0	1	4	4	21	1	4_A375_EGFR_1.1	21	Gene LOC100287164		hypothetical LOC100287164	XR_110778, XR_114029		
GeneID:2316	NACAD	7	45,120,056	45,126,493	6,437	-	1	4_A375_EGFR_1.1:7295	3161	gene	0	0	1	4	4	21	1	4_A375_EGFR_1.1	21	Gene NACAD	KIAA0363, NACAD	NAC alpha domain containing	NM_0311468334	213650_at	NP_5011396.1
GeneID:9276	TBRG4	9	45,159,899	45,181,317	21,818	-	4	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4931, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7103, 4_A375_EGFR_1:7296, 4_A375_EGFR_1:7297	101, -107, 6557, 133	gene, upstream, gene, gene	1	1	1	13.5	16	16.5	2	2_A375_plus7_plus_lncRNA_RUN_A_R_1	24	Gene TBRG4	FAST(X)4, TBRG4, KIAA0948, CPR2	transforming growth factor beta regulator 4	NM_199122, NM_004743, NM_030900, NCT2306270.0, NCT2306274.0, NCT2306277.0, NCT2306279.0, NCT1021.2, NCT1782761.0	220769_s_at, 220961_s_at	NP_9543751, NP_0047482.2, NP_112582.1, ENAW91031.1, ENAW91034.1, ENAW91035.1, ENAW91032.1, ENAW91033.1, ENAW91033.1
GeneID:8319	SNORA73A	9	45,143,948	45,144,081	133	+	4	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4931, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7103, 4_A375_EGFR_1:7296, 4_A375_EGFR_1:7297	-7133, -7342, -679, -7103	upstream, upstream, upstream, upstream	1	1	1	13.5	16	16.5	2	2_A375_plus7_plus_lncRNA_RUN_A_R_1	24	Gene SNORA73A	SNORA9A, ACA58/9C, SNORA9C, ACA58	small nucleolar RNA, H/ACA box 9A	NR_002919		
GeneID:7796	SNORA73B	9	45,144,805	45,144,941	136	+	4	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4931, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7103, 4_A375_EGFR_1:7296, 4_A375_EGFR_1:7297	-6875, -6782, 319, -6643	upstream, upstream, upstream, upstream	1	1	1	13.5	16	16.5	2	2_A375_plus7_plus_lncRNA_RUN_A_R_1	24	Gene SNORA73B	SNORA9B, ACA58/9C, SNORA9C	small nucleolar RNA, H/ACA box 9C	NR_002990		
GeneID:7795	SNORA73A	9	45,143,987	45,144,098	111	+	4	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4931, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7103, 4_A375_EGFR_1:7296, 4_A375_EGFR_1:7297	-6685, -6736, 736, -6685	upstream, upstream, downstream, upstream	1	1	1	13.5	16	16.5	2	2_A375_plus7_plus_lncRNA_RUN_A_R_1	24	Gene SNORA58	SNORA58, ACA58	small nucleolar RNA, H/ACA box 58	NR_002990		
GeneID:1074	ADCY1	7	45,814,125	45,762,715	148,590	+	2	4_A375_EGFR_1.1:7298, 4_A375_EGFR_1.1:7299	1063, 139571	gene, gene	0	0	1	5	7	20	2	4_A375_EGFR_1.1	24	Gene ADCY1	ADCY1, AC1	adenylate cyclase 1 (brain)	NM_0211116, NCT2359420.0, NCT2364242.0, NCT2364243.0, NCT2364244.0, NCT2364245.0, NCT10313.4	213345_at, 213346_at, 213347_at, 213348_at, 213349_at	NP_0989391, ENAW91048.1, ENAW91042.1, ENAW91044.1, ENAW91043.1, ENAW91047.1, ENAW91045.1
GeneID:5474	KIFBP	7	45,951,944	43,980,871	8,027	-	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7107	102	gene	0	0	1	13	16	8	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	16	Gene KIFBP3	BPAP, BPS, KIFBP3	serine-threonine growth factor-binding protein 3	NM_003391, NM_001013240, NCT2359434.0, NCT2359435.0, NCT1773271.0, NCT1961110.1, NCT1961111.1	210953_s_at, 212143_s_at	NP_0003382, NP_001013416.1, ENAW91026.1, ENAW91027.1, ENAW91029.1, ENAW91028.1
GeneID:8477	TNS3	7	47,314,752	47,379,199	264,447	+	6	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4928, 2_A375_plus7_minus_lncRNA_RUN_A_R_1:4927, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7114, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7115, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7116, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7117	247999, 236015, 247993, 211551, 176799, 64239	gene, gene, gene, gene, gene, gene, gene, gene	1	1	0	19	20.8	7.6	5	2_A375_plus7_plus_lncRNA_RUN_A_R_1	29	Gene TNS3	FLJ17722, DKFZp686H04(HH), TENS1, TENS, DKFZp686I2122S, MGC89434, FLJ39443, TNS3, H_NH0493I22.2	tensin 3	NM_0227481, NCT2342281.1, NCT2342289.0, NCT2342290.1, NCT2342291.0, NCT2342292.0	217853_at, 234257_at	NP_0753355.6, ENAW91011.1, ENAW91013.1, ENAW91014.1, ENAW91015.1
GeneID:1679	PKD1L1	7	47,814,290	47,868,057	173,747	-	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7118	189689	gene	0	1	0	10	19	8	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	19	Gene PKD1L1	PKD1L1, PKD1R63	polycystic kidney disease 1 like 1	NM_138295, NCT2365613.0, NCT2365614.0, NCT2365616.0, NCT2342228.0, NCT1949391.2	1553004_at, 1560486_at	NP_8121521, ENAW91036.1, ENAW91033.1, ENAW91034.1, ENAW91037.1
GeneID:3399	CTic/B9	7	47,834,869	47,859,443	24,356	+	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7118	-6821	upstream	0	1	0	10	19	8	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	19	Gene C7orf99	FLJ21075, C7orf99	chromosome 7 open reading frame 99	NM_0250311, NCT1782422.1	221172_at	NP_0793372.2, ENAW91038.1
GeneID:3364	HUS1	7	45,003,763	45,019,348	15,585	-	3	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4963, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7119, 4_A375_EGFR_1.1:7300	142, 48, 110	gene, gene, gene, gene	1	1	1	19	16	22	1	4_A375_EGFR_1.1	22	Gene HUS1	HUS1		NM_004507, NCT1983852.1, NCT1973251.1	204663_s_at, 204664_s_at	NP_0044981, ENAW91002.1, ENAW91001.1
GeneID:8979	SUN3	7	45,026,745	45,066,716	41,971	+	5	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4963, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7119, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7120, 4_A375_EGFR_1.1:7300, 4_A375_EGFR_1.1:7301	40612, 49516, 8567, 49582, 6804	downstream, downstream, upstream, downstream, upstream	1	1	1	14.5	16.5	19	2	4_A375_EGFR_1.1	22	Gene SUN3	MGC33329, SUN3, SUNC1	Sad1 and UNC84 domain containing 3	NM_152732, NM_001039319, NCT2359536.0, NCT2359537.0, NCT9375.1	231816_s_at	NP_6999355, NP_001029190.1, ENAW91018.1, ENAW91020.1
GeneID:1310	C7orf87	7	45,075,117	45,100,894	25,777	+	2	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7120, 4_A375_EGFR_1.1:7301	446, 430	gene, gene	0	1	0	10	15	16	1	4_A375_EGFR_1.1	16	Gene C7orf87	C7orf87	chromosome 7 open reading frame 87	NM_0311035.1	1557838_a_at	NP_0013038.1
GeneID:7291	UPF1	7	45,126,355	45,145,330	19,975	+	2	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7121, 4_A375_EGFR_1.1:7302	-3775, 61	upstream, gene	0	1	1	14	14.5	10	2	4_A375_EGFR_1.1	16	Gene UPF1	UP, UPHSE, UPF1L, KIAA0416, UPF1, UPF	antiviral phosphorylase 1	NM_003364, NM_1161997, NCT2299111.0, NCT2299112.0, NCT2299114.0, NCT2299115.0	200224_at	NP_0033551, NP_0036281, ENAW91021.1, ENAW91014.1, ENAW91022.1, ENAW91023.1
GeneID:1810	ABCA13	7	48,211,097	48,667,691	478,034	+	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7122	73851	gene	0	1	0	14	25	12	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	25	Gene ABCA13	FLJ23091, DKFZp761D241, FLJ32078, ABCA13, FLJ16395	ATP-binding cassette, sub-family A (ABC1), member 13	NM_1527011, NCT2299116.0, NCT2341138.1, NCT9389.4	1553259_at, 1559896_at, 1553803_a_at	NP_8378142, ENAW91031.1, ENAW91030.1, ENAW91032.1
GeneID:2597	VWC2	7	49,815,257	49,932,155	150,681	+	1	4_A375_EGFR_1.1:7306	727	gene	0	0	1	3	9	13	1	4_A375_EGFR_1.1	13	Gene VWC2	MGC131645, PSST739, UNQ739, VWC2	von Willebrand factor C domain containing 2	NM_1965701, NCT2389980.0		NP_9429722, ENAW91058.1
GeneID:1103	RIZP1	7	50,044,376	50,087,397	22,979	-	1	4_A375_EGFR_1.1:7307	1630	upstream	0	0	1	4	7	18	1	4_A375_EGFR_1.1	18	Gene RIZP1	RIZP1, bTB-1, ZNFN1A1, IK1, PRO0750, LYP1, Ht.54452, IKAROS	IKAROS family zinc finger 1 (Ikaros)	NM_0990360, NCT2299439.0, NCT2299440.0, NCT2299500.0, NCT1774839.3, NCT1965997.1, NCT1965998.1	1565818_at, 1565817_at, 1565816_s_at, 209036_at, 209035_s_at, 209801_x_at, 220764_at, 227344_at, 227345_at	NP_0966511, ENAW91062.1, ENAW91076.1, ENAW91079.1, ENAW91063.1, ENAW91061.1, ENAW91077.1
GeneID:3579	FSHL1	7	50,311,651	50,316,985	5,335	-	3	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4961, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7123, 4_A375_EGFR_1.1:7308	72, 156, 200	gene, gene, gene, gene	1	1	1	19	22	19	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	22	Gene FSHL1	FSHL1		NM_0013427821, NM_022118, NCT2359523.0, NCT1943189.2	1553721_a_at, 222943_at	NP_0013392271, NP_071359.2, ENAW91073.1, ENAW91078.1
GeneID:1678	DDC	7	50,526,134	50,633,184	107,050	-	7	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4961, 2_A375_plus7_minus_lncRNA_RUN_A_R_1:4942, 2_A375_plus7_minus_lncRNA_RUN_A_R_1:4943, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7123, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7124, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7125, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7126	118155, 20462, 12522, 115302, 39616, 1534, 115266	downstream, gene, gene, gene, downstream, gene, downstream	1	1	1	27.67	28.33	13	3	1_A375_plus7_plus_lncRNA_RUN_A_R_1	38	Gene DDC	AADC, DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	NM_0010329711, NM_000790, NCT2392926.0, NCT2392935.0, NCT9324.1	205311_at, 214767_s_at	NP_0010294493, NP_000781.1, ENAW91070.1, ENAW91071.1, ENAW91072.1
GeneID:1023719	LOC100287164	7	50,599,457	50,611,161	11,704	+	4	1_A375_plus7_minus_lncRNA_RUN_A_R_1:4962, 2_A375_plus7_minus_lncRNA_RUN_A_R_1:4963, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7124, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7125, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7126	3215, 21375, 3195, 21343	gene, downstream, gene, downstream	1	1	0	32	26.5	10	2	1_A375_plus7_plus_lncRNA_RUN_A_R_1	36	Gene LOC100129427		hypothetical LOC100129427	NR_033545		
GeneID:2815	GRB10	7	50,837,780	50,861,189	303,299	+	1	4_A375_EGFR_1.1:7309	10603	gene	0	0	1	8	12	17	1	4_A375_EGFR_1.1	17	Gene GRB10	GRB-IR, ME01, Grb-10, GRB10, IRBP, KIAA0207, RSS	growth factor receptor-bound protein 10	NM_0055311, NM_001001549, NM_001001550, NCT2389010.0, NCT2389012.0, NCT1969813.1, NCT1969814.1, NCT1969815.1	209409_at, 209410_s_at, 210991_x_at, 215364_at	NP_0030022.3, NP_001001549.1, NP_001001550.1, NP_001001551.1, ENAW91067.1, ENAW91068.1, ENAW91064.1, ENAW91065.1, ENAW91066.1
GeneID:2322	COBL	7	51,062,939	51,264,513	200,808	-	2	2_A375_plus7_minus_lncRNA_RUN_A_R_1:4965, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7127	190027, 192501	gene, gene	1	1	0	31	25	5	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	31	Gene COBL	MGC131893, DKFZp686G1322, COBL, bA440I23	cordon-bleu homolog (mouse)	NM_0151951, NCT2389688.0, NCT1775502.2	1552496_a_at, 213050_at	NP_0561522, ENAW91065.1, ENAW91062.1
GeneID:2815	PCWI21	7	53,103,349	53,104,818	1,269	+	1	4_A375_EGFR_1.1:7310	63	gene	0	0	1	4	5	13	1	4_A375_EGFR_1.1	13	Gene PCWI21L12	PCWI21	pectin methylesterase glycoprotein-like 12 (sp)	NM_182995	1558291_at, 1558292_x_at	NP_8724013
GeneID:1027	PLA2R1	7	55,723,252	55,879,624	156,422	-	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7129	40	gene	0	1	0	10	20	10	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	20	Gene PLA2R1	PLA2R74	PLA2R74 isoform	XR_113351, XR_116893, XR_110543, XR_114031		
GeneID:2303	VSTM2	7	54,810,019	54,836,945	26,926	+	3	2_A375_plus7_plus_lncRNA_RUN_A_R_1:7131, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7132, 4_A375_EGFR_1.1:7312	93, 1008, 4013	gene, gene, gene, gene	0	1	1	8	16.33	11	3	2_A375_plus7_plus_lncRNA_RUN_A_R_1	23	Gene VSTM2A	VSTM2A, MGC33330, VSTM2	V-set and transmembrane domain containing 2A	NM_1825481, NCT2349480.0, NCT2382427.0, NCT1844444.4	1554550_at	NP_8733322, ENAW90956.1, ENAW90953.1, ENAW90953.1
GeneID:2815	SEC61G	7	54,819,940	54,826,939	6,999	+	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1:4965	101	upstream	1	0	0	24	21	16	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	24	Gene SEC61G	SEC61G, Sec61	Sec61 gamma subunit	NM_0143323, NM_001013496, NCT1839927.2, NCT1962227.1	220464_at	NP_0381171, NP_001012474.1, ENAW90961.1, ENAW90961.1
GeneID:1956	EGFR	7	55,086,725	55,275,031	188,306	+	2	2_A375_plus7_minus_lncRNA_RUN_A_R_1:4965, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7133	116043, 114073	gene, gene	1	1	0	19	20	11	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	20	Gene EGFR	ERBB, HER1, EGFR, mENA, Prp81, ERBB1	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	NM_201282, NM_201283, NM_201284, NM_005228, NCT2391410.0, NCT2391412.0, NCT2391440.0, NCT9523761.1	1565633_at, 1565636_s_at, 201983_s_at, 201984_s_at, 211550_at, 211551_at, 211607_x_at	NP_9586351, NP_5584401, NP_0052282, NP_5584411, ENAW90963.1, ENAW90965.1, ENAW90962.1, ENAW90964.1
GeneID:8315	LANCL2	7	55,433,141	55,501,435	68,294	+	2	2_A375_plus7_minus_lncRNA_RUN_A_R_1:4965, 2_A375_plus7_plus_lncRNA_RUN_A_R_1:7135	179, 427	gene, gene	1	1	0	26	29	14	1	2_A375_plus7_plus_lncRNA_RUN_A_R_1	29	Gene LANCL2	FAST, MGC27139, LANCL2, GPR69B	lanC lantibiotic synthetase component C-like 2 (bacterial)	NM_1769971, NCT2382853.1	218219_s_at, 222360_at	NP_0011671.1, ENAW90966.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:51373	MRPS17	7	56,019,611	56,023,034	3,423	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4951, 2_A375_pNL97_plus_lncRNA_AR..1..7136	-155, -155	upstream, upstream	1	1	0	17	22	14	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MRPS17	HSPC011, MRP-S17, MRPS17, RPMS17	mitochondrial ribosomal protein S17	NM_015969	218982_s_at	NP_057053.1
GeneID:908	CCT6A	7	56,119,376	56,131,682	12,304	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7137, 4_A375_EGR1..1..7316	12854, 12558	downstream, downstream	0	1	1	16	23	26	1	4_A375_EGR1..1	26	Gene CCT6A	CCT6A, MGC126214, HTR3, TCPZ, MoDP-2, TTCP20, TCP20, CCT6, MGC126215, CCT-zeta, Cctz, CCT-zeta-1, TCP-1-zeta	chaperonin containing TCP1, subunit 6A (zeta 1)	NM_001762, NM_001009186, hCT2258389.0, hCT2258390.0, hCT9893.2	201326_at, 201327_s_at	NP_001753.1, NP_001009186.1, EAX07972.1, EAX07973.1, EAX07974.1
GeneID:677803	SNORA15	7	56,128,163	56,128,295	132	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7137, 4_A375_EGR1..1..7316	3889, 3773	downstream, downstream	0	1	1	16	23	26	1	4_A375_EGR1..1	26	Gene SNORA15	SNORA15, ACA15	small nucleolar RNA, H/ACA box 15	NR_002957		
GeneID:25870	SUMF2	7	56,131,917	56,148,365	16,448	+	3	2_A375_pNL97_plus_lncRNA_AR..1..7137, 4_A375_EGR1..1..7316, 4_A375_EGR1..1..7317	115, 19, 17779	in gene, in gene, downstream	0	1	1	11	15.5	22	2	4_A375_EGR1..1	26	Gene SUMF2	SUMF2, MGC99485, DKFZp781L1035, pFGE, DKFZp566I1024, DKFZp686I1024, DKFZp686L17160	sulfatase modifying factor 2	NM_015411, NM_001042469, NM_001042470, NM_001130069, NM_001146333, hCT1987529.1, hCT1987530.1, hCT1987531.1, hCT1987532.1, hCT2359262.0, hCT2359263.0, hCT2359264.0, hCT2359265.0, hCT2359266.0, hCT2359267.0, hCT2359268.0, hCT1774525.1	225002_s_at	NP_056226.2, NP_001035934.2, NP_001035935.2, NP_001123541.1, NP_001139805.1, EAX07975.1, EAX07976.1, EAX07977.1, EAX07978.1, EAX07979.1, EAX07980.1, EAX07981.1, EAX07982.1, EAX07983.1, EAX07984.1, EAX07985.1, EAX07986.1
GeneID:5260	PHKG1	7	56,148,675	56,160,689	12,014	-	1	4_A375_EGR1..1..7317	10993	in gene	0	0	1	6	6	18	1	4_A375_EGR1..1	18	Gene PHKG1	PHKG1, PHKG	phosphorylase kinase, gamma 1 (muscle)	NM_006213	207312_at, 234729_at	NP_006204.1
GeneID:51142	CHCHD2	7	56,169,266	56,174,187	4,921	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7138	-117	upstream	0	1	0	17	19	10	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene CHCHD2	C7orf17, CHCHD2	coiled-coil-helix-coiled-coil-helix domain containing 2	NM_016139	217720_at	NP_057223.1
GeneID:389493	LOC389493	7	56,182,374	56,184,090	1,716	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7138	9786	downstream	0	1	0	17	19	10	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC389493		hypothetical protein LOC389493	NM_001145712		NP_001139184.1
GeneID:222029	DKFZp434L192	7	56,563,916	56,564,977	1,061	+	1	4_A375_EGR1..1..7318	564	in gene	0	0	1	7	2	12	1	4_A375_EGR1..1	12	Gene DKFZp434L192		hypothetical protein DKFZp434L192	NR_026929	1553698_a_at	
GeneID:100422939	MIR3147	7	57,472,731	57,472,796	65	+	1	4_A375_EGR1..1..7320	-6267	upstream	0	0	1	4	6	19	1	4_A375_EGR1..1	19	Gene MIR3147	MIR3147	microRNA 3147	NR_036102		
GeneID:100287633	LOC100287633	7	57,710,228	57,712,559	2,331	+	1	4_A375_EGR1..1..7322	5066	downstream	0	0	1	9	10	16	1	4_A375_EGR1..1	16	Gene LOC100287633		protein FAM27D1-like	XM_003120037, XM_002344315, XM_002342728, XM_003120560		XP_003120085.1, XP_002344356.2, XP_002342769.2, XP_003120608.1
GeneID:100506050	LOC100506050	7	63,484,794	63,490,480	5,686	-	1	4_A375_EGR1..1..7326	-7040	upstream	0	0	1	3	6	14	1	4_A375_EGR1..1	14	Gene LOC100506050		hypothetical LOC100506050	XR_113018, XR_110698, XR_108847, XR_114033		
GeneID:442319	ZNF727	7	63,505,821	63,538,927	33,106	+	1	4_A375_EGR1..1..7326	-8301	upstream	0	0	1	3	6	14	1	4_A375_EGR1..1	14	Gene ZNF727	ZNF727	zinc finger protein 727	NM_001159522		NP_001152994.1
GeneID:7697	ZNF138	7	64,254,771	64,294,026	39,255	+	1	4_A375_EGR1..1..7328	45293	downstream	0	0	1	6	2	13	1	4_A375_EGR1..1	13	Gene ZNF138	ZNF138, pHZ-32	zinc finger protein 138	NM_006524, NM_001160183, NR_027660, NR_027661, hCT1811841.1, hCT1960180.1, hCT1960182.1, hCT1960183.1, hCT1960184.1		NP_006515.2, NP_001153655.1, EAW77979.1, EAW77980.1, EAW77981.1, EAW77983.1, EAW77982.1
GeneID:10793	ZNF273	7	64,363,620	64,391,955	28,335	+	1	4_A375_EGR1..1..7329	316	in gene	0	0	1	7	11	17	1	4_A375_EGR1..1	17	Gene ZNF273	HZF9, MGC12518, ZNF273	zinc finger protein 273	NR_003099, NM_021148, hCT2344897.0, hCT2355778.0, hCT1960177.2	215239_x_at, 243661_at	NP_066971.2, EAW77992.1, EAW77993.1, EAW77994.1
GeneID:168374	ZNF92	7	64,838,768	64,865,998	27,230	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7144	60	in gene	0	1	0	13	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene ZNF92	ZNF92, HPF12, HTF12, TF12	zinc finger protein 92	NM_152626, NM_007139, hCT1950713.1	1564962_at, 1564963_x_at, 235170_at	NP_689839.1, NP_009070.2, EAW52301.1
GeneID:677807	SNORA22	7	65,220,513	65,220,646	133	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7145, 4_A375_EGR1..1..7333	-4633, -4193	upstream, upstream	0	1	1	12	21	18	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SNORA22	SNORA22, ACA22	small nucleolar RNA, H/ACA box 22	NR_002961		
GeneID:84214	DKFZp434F142	7	65,305,198	65,305,588	390	+	1	1_A375_pNL7_minus_lncRNA_AR..1..4955	-7790	upstream	1	0	0	24	19	6	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene DKFZp434F142		hypothetical DKFZp434F142	XR_113022, XR_110687, XR_108609, XR_114040	224123_at	
GeneID:27297	CRCP	7	65,579,805	65,619,555	39,750	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4956, 2_A375_pNL97_plus_lncRNA_AR..1..7146, 4_A375_EGR1..1..7334	195, 195, 19	in gene, in gene, in gene	1	1	1	20	23	19	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene CRCP	CGRP-RCP, RCP, MGC111194, RCP9, CRCP	CGRP receptor component	NM_014478, NM_001040647, NM_001040648, NM_001142414, NR_024548, hCT1970694.1, hCT9765.4, hCT1982133.1	203698_at, 203699_s_at	NP_055293.1, NP_001035737.1, NP_001035738.1, NP_001135886.1, EAX07941.1, EAX07943.1, EAX07942.1
GeneID:8460	TPST1	7	65,670,259	65,825,438	155,179	+	1	4_A375_EGR1..1..7335	26306	in gene	0	0	1	3	3	13	1	4_A375_EGR1..1	13	Gene TPST1	TPST1		NM_003596, hCT2257773.0, hCT30868.4	204140_at	NP_003587.1, EAX07937.1, EAX07938.1
GeneID:285908	NCRNA00174	7	65,841,031	65,865,395	24,364	-	1	4_A375_EGR1..1..7336	23027	in gene	0	0	1	4	5	17	1	4_A375_EGR1..1	17	Gene NCRNA00174	NCRNA00174	non-protein coding RNA 174	NR_026673, hCT1656997.2	235397_at	EAX07935.1
GeneID:100289098	LOC100289098	7	65,958,693	65,960,461	1,768	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4957, 2_A375_pNL97_plus_lncRNA_AR..1..7147, 4_A375_EGR1..1..7337	-101, 171, 107	upstream, in gene, in gene	1	1	1	19	21	21	1	4_A375_EGR1..1	21	Gene LOC100289098		hypothetical LOC100289098	XR_113021, XR_113020, XR_110669, XR_110668, XR_108825, XR_108824, XR_114039, XR_114038		
GeneID:27342	RABGEF1	7	66,205,643	66,276,451	70,808	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7151, 4_A375_EGR1..1..7340	369, 364	in gene, in gene	0	1	1	15	16	15	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene RABGEF1	FLJ32302, rabex-5, RABGEF1, RABEX5	RAB guanine nucleotide exchange factor (GEF) 1	NM_014504, hCT2359269.0, hCT30865.3, hCT1813474.1, hCT1815833.1	218310_at	NP_055319.1, EAX07915.1, EAX07913.1, EAX07914.1, EAX07916.1
GeneID:644794	LOC644794	7	66,368,444	66,370,643	2,199	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7153, 4_A375_EGR1..1..7342	-6668, -1233	upstream, upstream	0	1	1	11	12	10	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC644794		hypothetical LOC644794	XR_110690, XR_108626, XR_114037		
GeneID:55069	C7orf42	7	66,386,203	66,423,538	37,335	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4959, 4_A375_EGR1..1..7343	-167, 46085	upstream, downstream	1	0	1	17	16.5	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene C7orf42	C7orf42, FLJ13090, FLJ10099	chromosome 7 open reading frame 42	NM_017994, hCT2257796.0, hCT2359254.0, hCT1818329.2	218006_at, 224668_at	NP_060464.1, EAX07907.1, EAX07908.1, EAX07909.1
GeneID:51119	SBDS	7	66,452,690	66,460,588	7,898	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7154	844	in gene	0	1	0	15	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SBDS	CGI-97, SDS, SWDS, FLJ10917, SBDS	Shwachman-Bodian-Diamond syndrome	NM_016038, hCT87096.3	222689_s_at	NP_057122.2, EAX07906.1
GeneID:55253	TYW1	7	66,461,817	66,704,499	242,682	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7154	-2073	upstream	0	1	0	15	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene TYW1	MGC60291, FLJ10900, RSAFD1, YPL207W, TYW1A, MGC23001, TYW1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	NM_018264, hCT2359259.0, hCT2359260.0, hCT1640407.3	218347_at	NP_060734.2, EAX07904.1, EAX07903.1, EAX07905.1
GeneID:26053	AUTS2	7	69,063,905	70,257,885	1,193,980	+	1	4_A375_EGR1..1..7347	309631	in gene	0	0	1	4	1	13	1	4_A375_EGR1..1	13	Gene AUTS2	MGC13140, KIAA0442, FBRSL2, AUTS2	autism susceptibility candidate 2	NM_015570, NM_001127231, NM_001127232, hCT2256959.0, hCT2256960.0	212599_at, 243384_at, 243385_s_at	NP_056385.1, NP_001120703.1, NP_001120704.1, EAX07895.1, EAX07896.1
GeneID:84409	WBSCR17	7	70,597,789	71,178,584	580,795	+	1	4_A375_EGR1..1..7348	52611	in gene	0	0	1	5	3	12	1	4_A375_EGR1..1	12	Gene WBSCR17	GALNT16, DKFZp434I216, DKFZp761D2324, GALNT20, GALNTL3, WBSCR17	Williams-Beuren syndrome chromosome region 17	NM_022479, hCT2257194.0, hCT2257196.0, hCT2257197.0, hCT10423.3	227434_at	NP_071924.1, EAX07898.1, EAX07897.1, EAX07899.1, EAX07900.1
GeneID:441250	TYW1B	7	72,039,492	72,298,813	259,321	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7155	-1263	upstream	0	1	0	11	15	11	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene TYW1B	NCRNA00069, MGC87315, TYW1B, RSAFD2	tRNA-yW synthesizing protein 1 homolog B (S. cerevisiae)	NM_001145440, NM_001145441		NP_001138912.1, NP_001138913.1
GeneID:9883	POM121	7	72,349,936	72,418,838	68,902	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7156, 4_A375_EGR1..1..7349	45552, 63584	in gene, in gene	0	1	1	6	6.5	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene POM121	POM121, MGC3792, POM121A, DKFZp586G1822, DKFZp586P2220, KIAA0618, FLJ41820	POM121 membrane glycoprotein	NM_172020, hCT1775372.5	205098_at	NP_742017.1, EAW69698.1
GeneID:260294	NSUN5C	7	72,416,832	72,425,302	8,470	-	1	4_A375_EGR1..1..7349	11762	downstream	0	0	1	5	2	10	1	4_A375_EGR1..1	10	Gene NSUN5C	FLJ11626, DKFZp686P104, WBSCR20C, WBSCR20B, MGC129801, MGC15057, NSUN5P2, NSUN5C, DKFZp434K056, NOL1R2	NOP2/Sun domain family, member 5 pseudogene 2	NR_033323	213460_x_at, 213642_x_at	
GeneID:8326	FZD9	7	72,848,109	72,850,450	2,341	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7157	-109	upstream	0	1	0	16	29	7	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene FZD9	FZD9, FZD3, CD349	frizzled homolog 9 (Drosophila)	NM_003508, hCT9410.2	207639_at	NP_003499.1, EAW69682.1
GeneID:9031	BAZ1B	7	72,854,728	72,936,615	81,887	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4960, 2_A375_pNL97_plus_lncRNA_AR..1..7157, 2_A375_pNL97_plus_lncRNA_AR..1..7158	-313, 66615, -185	upstream, downstream, upstream	1	1	0	17.5	28	6	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene BAZ1B	WSTF, BAZ1B, WBSCR9, WBSCR10	bromodomain adjacent to zinc finger domain, 1B	NM_032408, hCT10055.2, hCT1961276.1, hCT1961277.1	208445_s_at, 211313_s_at, 213336_at, 229658_at	NP_115784.1, EAW69681.1, EAW69679.1, EAW69680.1
GeneID:84277	DNAJC30	7	73,095,248	73,097,781	2,533	-	1	4_A375_EGR1..1..7350	373	in gene	0	0	1	12	16	18	1	4_A375_EGR1..1	18	Gene DNAJC30	MGC12943, DNAJC30, WBSCR18	DnaJ (Hsp40) homolog, subfamily C, member 30	NM_032317, hCT1832271.2	223387_at, 239018_at, 239194_at	NP_115693.2, EAW69658.1
GeneID:114049	WBSCR22	7	73,097,898	73,112,542	14,644	+	2	4_A375_EGR1..1..7350, 4_A375_EGR1..1..7351	-490, 16406	upstream, downstream	0	0	1	10	15.5	17	2	4_A375_EGR1..1	18	Gene WBSCR22	FLJ44236, MGC2022, WBMT, HUSSY-3, HASJ4442, MGC5140, MGC19709, WBSCR22, PP3381	Williams Beuren syndrome chromosome region 22	NM_017528, hCT10056.3, hCT1963482.1	207628_s_at, 231415_at	NP_059998.2, EAW69656.1, EAW69657.1
GeneID:6804	STX1A	7	73,113,535	73,134,017	20,482	-	4	1_A375_pNL7_minus_lncRNA_AR..1..4961, 1_A375_pNL7_minus_lncRNA_AR..1..4962, 2_A375_pNL97_plus_lncRNA_AR..1..7159, 4_A375_EGR1..1..7351	3873, 1521, 3905, 19713	in gene, in gene, in gene, in gene	1	1	1	18	18.33	11.67	3	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene STX1A	STX1, SYN1A, STX1A, HPC-1, p35-1, P35-1	syntaxin 1A (brain)	NM_001165903, NM_004603, hCT1966952.1, hCT1966953.1, hCT1966954.1, hCT2257116.0, hCT2354698.0, hCT87408.3, hCT1963485.1	204729_s_at	NP_001159375.1, NP_004594.1, EAW69649.1, EAW69651.1, EAW69654.1, EAW69655.1, EAW69650.1, EAW69652.1, EAW69653.1
GeneID:100505484	LOC100505484	7	73,119,184	73,119,493	309	+	1	4_A375_EGR1..1..7351	-4660	upstream	0	0	1	6	15	16	1	4_A375_EGR1..1	16	Gene LOC100505484		hypothetical LOC100505484	XR_113023, XR_110696, XR_108631, XR_114042		
GeneID:100422948	MIR4284	7	73,125,647	73,125,727	80	+	3	1_A375_pNL7_minus_lncRNA_AR..1..4961, 1_A375_pNL7_minus_lncRNA_AR..1..4962, 2_A375_pNL97_plus_lncRNA_AR..1..7159	4497, 6849, 4465	downstream, downstream, downstream	1	1	0	23	20	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene MIR4284	MIR4284	microRNA 4284	NR_036247		
GeneID:1364	CLDN4	7	73,245,193	73,247,015	1,822	+	3	4_A375_EGR1..1..7352, 4_A375_EGR1..1..7353, 4_A375_EGR1..1..7354	3959, 10983, 11447	downstream, downstream, downstream	0	0	1	10.67	9.33	15.33	3	4_A375_EGR1..1	16	Gene CLDN4	CLDN4, CPE-R, CPETR, CPETR1, hCPE-R, WBSCR8, CPER	claudin 4	NM_001305, hCT1775365.1	1569421_at, 201428_at	NP_001296.1, EAW69639.1
GeneID:100128031	LOC100128031	7	73,245,343	73,247,020	1,677	-	3	4_A375_EGR1..1..7352, 4_A375_EGR1..1..7353, 4_A375_EGR1..1..7354	-2132, -9156, -9620	upstream, upstream, upstream	0	0	1	10.67	9.33	15.33	3	4_A375_EGR1..1	16	Gene LOC100128031		hypothetical LOC100128031	XM_002346008, XM_002344327, XM_002342735, XM_002346890		XP_002346047.1, XP_002344368.1, XP_002342776.1, XP_002346931.1
GeneID:155368	WBSCR27	7	73,248,920	73,256,855	7,935	-	3	4_A375_EGR1..1..7352, 4_A375_EGR1..1..7353, 4_A375_EGR1..1..7354	7703, 679, 215	in gene, in gene, in gene	0	0	1	10.67	9.33	15.33	3	4_A375_EGR1..1	16	Gene WBSCR27	MGC40131, WBSCR27	Williams Beuren syndrome chromosome region 27	NM_152559, hCT1775374.2	1553778_at	NP_689772.2, EAW69638.1
GeneID:2006	ELN	7	73,442,427	73,484,237	41,810	+	1	4_A375_EGR1..1..7359	33957	in gene	0	0	1	17	6	13	1	4_A375_EGR1..1	13	Gene ELN	SVAS, FLJ38671, WBS, ELN, FLJ43523, WS	elastin	NM_001081753, NM_000501, NM_001081754, NM_001081755, NM_001081752, hCT2354678.0, hCT2354679.0, hCT2354680.0, hCT2354681.0, hCT2354682.0, hCT2354683.0, hCT2354684.0, hCT2354685.0, hCT2354686.0, hCT2354687.0, hCT2354688.0, hCT9092.3, hCT1963478.1	212670_at, 216289_s_at	NP_001075222.1, NP_000492.2, NP_001075223.1, NP_001075224.1, NP_001075221.1, EAW69633.1, EAW69624.1, EAW69625.1, EAW69626.1, EAW69627.1, EAW69628.1, EAW69629.1, EAW69630.1, EAW69632.1, EAW69631.1, EAW69634.1, EAW69635.1, EAW69636.1
GeneID:3984	LIMK1	7	73,498,156	73,536,854	38,698	+	2	1_A375_pNL7_minus_lncRNA_AR..1..4984, 2_A375_pNL97_plus_lncRNA_AR..1..7160	10516, 14306	in gene, in gene	1	1	0	10	15	6	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LIMK1	LIMK1, LIMK	LIM domain kinase 1	NM_002314, hCT2259324.0, hCT7893.2, hCT1984601.1, hCT1984602.1	204356_at, 204357_s_at, 208372_s_at	NP_002305.1, EAW69622.1, EAW69620.1, EAW69621.1, EAW69623.1
GeneID:7462	LAT2	7	73,624,087	73,644,164	20,077	+	1	4_A375_EGR1..1..7360	10585	in gene	0	0	1	4	4	17	1	4_A375_EGR1..1	17	Gene LAT2	LAT2, LAB, WSCR5, WBSCR15, HSPC046, NTAL, WBSCR5	linker for activation of T cells family, member 2	NM_032463, NM_014146, NM_032464, hCT2259342.0, hCT2354697.0, hCT9088.3, hCT1963475.1, hCT1984628.1, hCT1984629.1	211768_at, 221581_s_at	NP_115852.1, NP_054865.2, NP_115853.2, EAW69612.1, EAW69613.1, EAW69614.1, EAW69609.1, EAW69610.1, EAW69611.1
GeneID:5982	RFC2	7	73,645,832	73,668,738	22,906	-	3	1_A375_pNL7_minus_lncRNA_AR..1..4965, 2_A375_pNL97_plus_lncRNA_AR..1..7161, 4_A375_EGR1..1..7361	-94, 34, 50	upstream, in gene, in gene	1	1	1	26	22	18	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene RFC2	RFC40, A1, RFC2, MGC3665	replication factor C (activator 1) 2, 40kDa	NM_181471, NM_002914, hCT2256829.0, hCT2256831.0, hCT9089.2, hCT1983476.1	1053_at, 203696_s_at	NP_852136.1, NP_002905.2, EAW69605.1, EAW69606.1, EAW69607.1, EAW69608.1



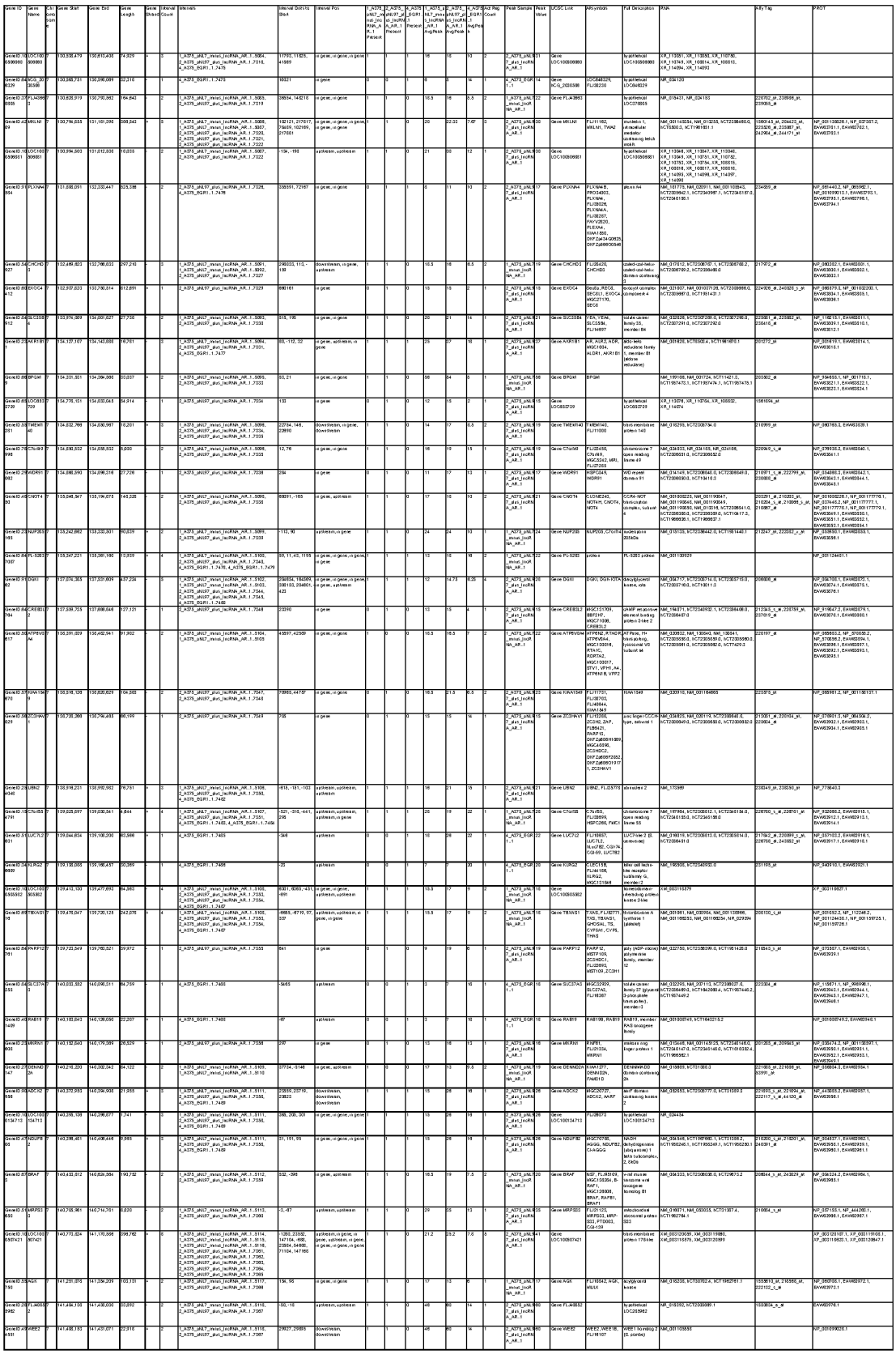


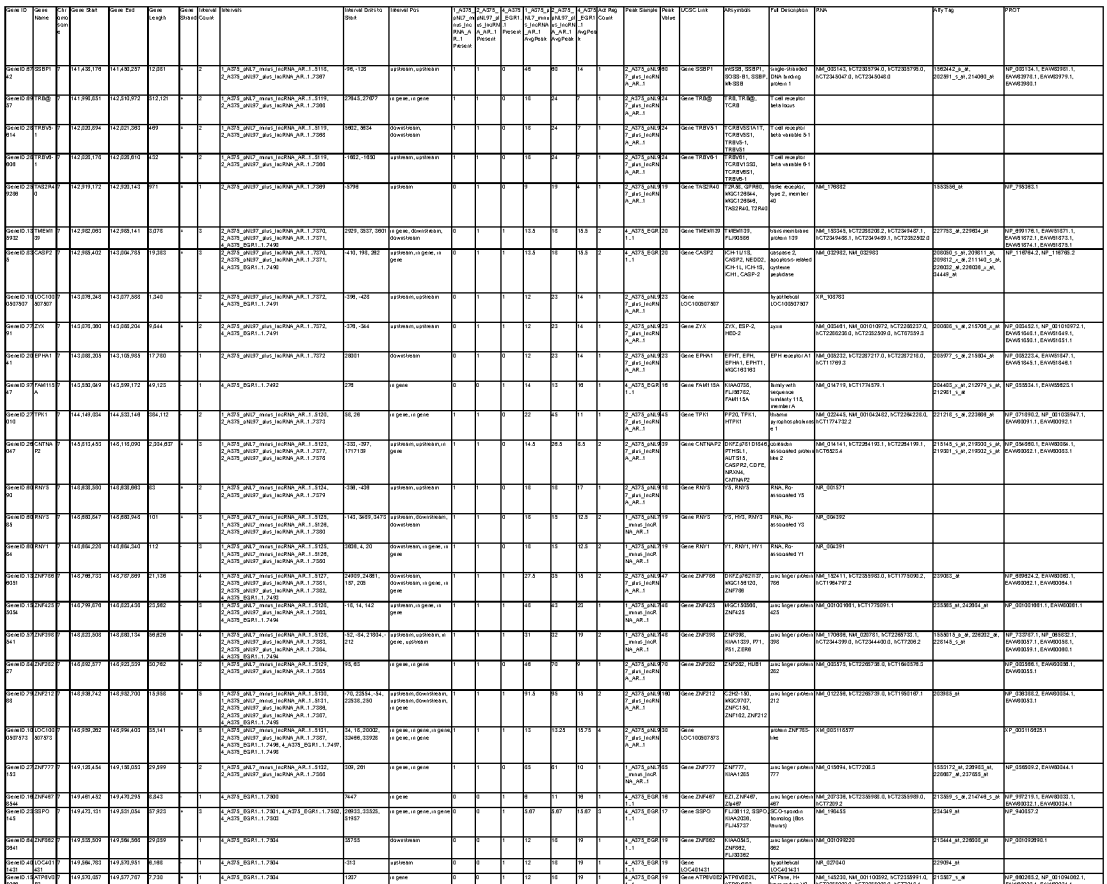
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_shN7_shLR7_all_nuc_inc_lncRNA_R_1 Percent	1_A375_shN7_shLR7_all_lncRNA_R_1 Percent	1_A375_shN7_shLR7_all_lncRNA_R_1 Avg Peak	1_A375_shN7_shLR7_all_lncRNA_R_1 Avg Peak	1_A375_shN7_shLR7_all_lncRNA_R_1 Avg Peak	Add Tag Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
Gene ID:142	AXAP1	7	91,370,169	91,739,967	369,798	+	1	1_A375_shN7_mnat_lncRNA_R_1:-4992	-81	upstream	1	0	0	19	15	14	1	2_A375_shN7_mnat_lncRNA_R_1	19	Gene AXAP1	AXAP450, KIAA0653, MGC4536, PRKWS, MU-PMS 40.19A, HYPERION, NXAP5, CG-NAP	A kinase (PRKA) anchor protein 5	NM_147155, NM_003751, XCT223999B.1, XCT223999B.2, XCT223999B.3, XCT223999B.4, XCT223999B.5, XCT1993572.2, XCT1993570.1, XCT1993574.1	207870_at_210992_s_at, 213403_at	NP_877714.1, NP_003742.4, EAW76893.1, EAW76891.1, EAW76892.1, EAW76897.1, EAW76894.1, EAW76896.1, EAW76895.1, EAW76898.1, EAW76899.1
Gene ID:1836	CYP51A1	7	91,741,483	91,764,359	22,876	-	2	1_A375_shN7_mnat_lncRNA_R_1:-4993, 2_A375_shN7_plus_lncRNA_R_1:7200	-5,859	upstream,cis gene	1	1	0	20	23	13	1	2_A375_shN7_plus_lncRNA_R_1	23	Gene CYP51A1	LDM, CYP51, CYP51A1, P450 14DM, CYPL1, RASL1, CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	NM_000786, NM_001146192, XCT223999T.1, XCT223999T.2	202314_at_216967_s_at	NP_000767.1, NP_001139624.1, EAW76830.1, EAW76835.1
Gene ID:3126	LOC81312	7	91,765,176	91,810,059	44,883	+	3	1_A375_shN7_mnat_lncRNA_R_1:-4993, 2_A375_shN7_plus_lncRNA_R_1:7200, 4_A375_SGR1_1:7200	656, 24, 43305	cis gene, nr gene, cis gene	1	1	1	13.5	16	17.5	2	2_A375_shN7_plus_lncRNA_R_1	23	Gene LOC81312		hypothetical LOC81126	XR_113253, XR_112714, XR_108545, XR_114855	233942_at	
Gene ID:1387	LOC401387	7	91,774,190	91,794,990	20,292	-	2	1_A375_shN7_mnat_lncRNA_R_1:-4993, 2_A375_shN7_plus_lncRNA_R_1:7200	30026, 31190	downstream, downstream	1	1	0	20	23	13	1	2_A375_shN7_plus_lncRNA_R_1	23	Gene LOC401387	FLJ36054, MGC176223, MGC176229	hexose-ish aspartate and dec83 domain containing protein	NM_001161526	1569763_at	NP_001153030.1
Gene ID:9	KIF71	7	91,825,253	91,875,414	47,161	-	1	2_A375_shN7_plus_lncRNA_R_1:7201	107	nr gene	0	1	0	13	17	8	1	2_A375_shN7_plus_lncRNA_R_1	17	Gene KIF71	KIF71, CCAR1, CAR1	KIF71, kinesin family member 71	NM_194435, NM_178455, NM_058112, NM_194434, NM_001013436, XCT223991T.0, XCT223991T.2	204725_s_at_219713_at, 229769_at_234031_at	NP_919437.1, NP_919438.1, NP_004503.2, NP_919439.1, XP_001131624.1, EAW76834.1, EAW76835.1
Gene ID:5487	ANKIB1	7	91,875,845	92,030,896	155,130	+	1	2_A375_shN7_plus_lncRNA_R_1:7201	-241	upstream	0	1	0	10	17	8	1	2_A375_shN7_plus_lncRNA_R_1	17	Gene ANKIB1	FLJ35125, RIAM1306, ANKIB1, DKFZp434A0225	ankyrin repeat and IBR domain containing 1	NM_019064	224802_at_224857_at, 243161_at	NP_061977.1
Gene ID:7706	GATAD1	7	92,076,765	92,095,742	11,977	+	1	2_A375_shN7_plus_lncRNA_R_1:7202	87	nr gene	0	1	0	14	16	10	1	2_A375_shN7_plus_lncRNA_R_1	16	Gene GATAD1	DGAG, GATAD1, RMB39A9.2, FLJ40855, FLJ22491	GATA zinc finger domain containing 1	NM_021187, XCT223870E.1, XCT223870T.1, XCT223870Z.2, XCT223962D.0	206363_s_at_213016_at, 214716_at_242864_at	NP_066960.3, EAW76848.1, EAW76846.1, EAW76850.1, EAW76851.1
Gene ID:7415	FAM133B	7	92,160,972	92,210,708	49,804	-	2	1_A375_shN7_mnat_lncRNA_R_1:-4993, 2_A375_shN7_plus_lncRNA_R_1:7204	-6, -8	upstream, upstream	1	1	0	135	159	10	1	2_A375_shN7_plus_lncRNA_R_1	159	Gene FAM133B	FAM133B, MGC40455	family with sequence similarity 133, member B	NM_001040057, NM_152769, XCT223999S.1, XCT223970.1, XCT223974.1, XCT223959S.0, XCT223959S.2, XCT19817.4	230322_at_235489_at	NP_001035146.1, NP_690002.2, EAW76811.1, EAW76822.1, EAW76824.1, EAW76825.1, EAW76823.1, EAW76826.1
Gene ID:21	CDK6	7	92,234,253	92,453,941	231,708	-	3	1_A375_shN7_mnat_lncRNA_R_1:4998, 1_A375_shN7_mnat_lncRNA_R_1:4997, 2_A375_shN7_plus_lncRNA_R_1:7203	3383, 883, 2877	nr gene, nr gene, cis gene	1	1	0	14.33	17.67	9.33	3	1_A375_shN7_mnat_lncRNA_R_1	18	Gene CDK6	PLSTIRF2, MGC99892, CDK6	cyclin-dependent kinase 6	NM_001259, NM_001145306, XCT223997D.2, XCT223997D.3	207423_at_224297_at, 224456_at_224481_at, 231166_at_233357_at, 243009_at	NP_001020.1, NP_001139776.1, EAW76826.1, EAW76829.1
Gene ID:3312	HEPACAM2	7	92,617,899	92,653,762	37,863	-	2	1_A375_shN7_mnat_lncRNA_R_1:4998, 2_A375_shN7_plus_lncRNA_R_1:7206	-5788, -5830	upstream, upstream	1	1	0	23	22	10	1	2_A375_shN7_plus_lncRNA_R_1	22	Gene HEPACAM2	HEPACAM2	HEPACAM family member 2	NM_152531, NM_001032372	243681_at	NP_722794.1, NP_001034491.1
Gene ID:810	CCDC132	7	92,861,693	92,895,338	139,668	+	2	1_A375_shN7_mnat_lncRNA_R_1:4999, 2_A375_shN7_plus_lncRNA_R_1:7208	-65, -21	upstream, upstream	1	1	0	23	22	10	1	2_A375_shN7_plus_lncRNA_R_1	22	Gene CCDC132	FLJ35997, FLJ33501, CCDC132, KIAA1861, MGC176689	coiled-coil domain containing 132	NM_024353, NM_017697, XCT223237.0, XCT223219.0, XCT223233.0, XCT223231.0, XCT223202.0, XCT223224.0, XCT19555703	1554218_at_1554217_a_at, 207949_at_226031_at	NP_076029.1, NP_060127.2, EAW76818.1, EAW76817.1, EAW76820.1, EAW76821.1, EAW76815.1, EAW76816.1, EAW76819.1
Gene ID:7794	TFPI2	7	93,515,745	93,520,065	4,320	+	1	2_A375_shN7_plus_lncRNA_R_1:7207	17	nr gene	0	1	0	7	17	13	1	2_A375_shN7_plus_lncRNA_R_1	17	Gene TFPI2	TFPI2, PP5171, PP5, TFPI-2, FLJ21164	tissue factor pathway inhibitor 2	NM_006528, XCT223232B.0, XCT1992621, XCT1991276.1, XCT1991279.2	209277_at_209278_s_at	NP_006519.1, EAW76810.1, EAW76809.1, EAW76808.1, EAW76811.1
Gene ID:202	BET1	7	93,821,600	93,833,890	12,890	-	1	2_A375_shN7_plus_lncRNA_R_1:7208	-98	upstream	0	1	0	15	19	11	1	2_A375_shN7_plus_lncRNA_R_1	19	Gene BET1	BET1, DKFZp761C0420, HBET1	blocked early in transport 1 homolog (S. cerevisiae)	NM_005868, XCT223227T.1, XCT223227R.1, XCT223963D.1, XCT10264.2	202710_at	NP_005859.1, EAW76830.1, EAW76832.1, EAW76831.1
Gene ID:321	CASD1	7	94,139,170	94,196,351	57,181	+	3	1_A375_shN7_mnat_lncRNA_R_1:4999, 2_A375_shN7_plus_lncRNA_R_1:7209, 4_A375_SGR1_1:7209	796, 834, 762	nr gene, nr gene, cis gene	1	1	1	17	21	14	3	2_A375_shN7_plus_lncRNA_R_1	21	Gene CASD1	FLJ20279, FLJ21213, CASD1, FLJ41901, CNJ172, MBLAK0196	CASD1 domain containing 1	NM_022930, XCT223999E.0, XCT223999F.0, XCT223999S.0, XCT223935.0, XCT223936.0, XCT223935F.0, XCT19429472	219342_at_231264_at, 242000_at_243000_at	NP_076281.4, EAW76792.1, EAW76793.1, EAW76790.1, EAW76791.1, EAW76793.1
Gene ID:10	SGCE	7	94,214,356	94,265,521	50,965	-	1	2_A375_shN7_mnat_lncRNA_R_1:5000	53233	nr gene	1	0	0	22	23	9	1	2_A375_shN7_plus_lncRNA_R_1	22	Gene SGCE	DYT11, EPSG, SGCE	sarcoglycan, epsilon	NM_031919/31, NM_003919, NM_001099400, XCT223021E.0, XCT223021T.0, XCT223936.0, XCT19966.2, XCT1991449.1	204856_at	NP_001092117, NP_003910.1, NP_001092070.1, EAW76764.1, EAW76765.1, EAW76766.1, EAW76767.1
Gene ID:997	PPP1R9A	7	94,536,949	94,629,727	269,778	+	3	1_A375_shN7_mnat_lncRNA_R_1:5001, 2_A375_shN7_plus_lncRNA_R_1:7210, 2_A375_shN7_plus_lncRNA_R_1:7211	-69, -69, 99203	upstream, upstream, cis gene	1	1	0	15.5	21	9	2	2_A375_shN7_plus_lncRNA_R_1	24	Gene PPP1R9A	Neurabin-I, FLJ20995, PPP1R9A, NRB1, KIAA1220	protein phosphatase 1, regulatory (inhibitor) subunit 9A	NM_017650, NM_001166180, NM_001166181, NM_001166182, NM_001166183	221060_s_at_223494_at, 231966_at_233563_s_at	NP_060120.2, NP_001158102.1, NP_001158103.1, NP_001158104.1, NP_001158105.1, NP_001139634.1, NP_001139633.1
Gene ID:45	PON2	7	95,054,174	95,064,364	20,210	-	2	1_A375_shN7_mnat_lncRNA_R_1:5002, 4_A375_SGR1_1:7294	96, 552	nr gene, nr gene	1	1	1	16	9	17	1	4_A375_SGR1_1.1	17	Gene PON2	PON2	CADD domain containing 1	NM_000305, NM_001018161, XCT223031D.0, XCT223935D.0, XCT223936D.0, XCT223935F.0, XCT19429472	205979_at_210020_s_at, 242700_at	NP_000296.2, NP_001018171.1, EAW76764.1, EAW76765.1, EAW76766.1, EAW76767.1, EAW76763.1
Gene ID:666	ASB4	7	95,115,734	95,167,071	51,737	+	1	1_A375_shN7_mnat_lncRNA_R_1:5003	13644	nr gene	1	0	0	14	10	2	1	1_A375_shN7_plus_lncRNA_R_1	14	Gene ASB4	ASB4, MGC142061, MGC142089, ASB4	ankyrin repeat and SOCS box containing 4	NM_016116, NM_145872, XCT223034T.0, XCT19300.3, XCT1992165.1	205481_at_217203_s_at, 217229_at_237720_at, 237721_s_at	NP_057200.1, NP_665979.1, EAW76780.1, EAW76781.1, EAW76782.1
Gene ID:5508954	LOC100509364	7	95,171,457	95,172,854	2,397	+	1	2_A375_shN7_plus_lncRNA_R_1:7212	6083	downstream	0	1	0	14	14	6	1	2_A375_shN7_plus_lncRNA_R_1	14	Gene LOC100509364		pathway enrichment used probes NCRAN(0269-bp	XM_005120548, XM_002319969, XM_005115595, XM_003120564	NP_001120036.1, XP_002319977.1, XP_001119958.1, XP_003129952.1
Gene ID:165	SLC25A13	7	95,749,532	95,951,459	201,927	-	4	1_A375_shN7_mnat_lncRNA_R_1:5004, 2_A375_shN7_plus_lncRNA_R_1:7213, 4_A375_SGR1_1:7395, 4_A375_SGR1_1:7396	-29, -29, 93157, 227	upstream, upstream, cis gene, cis gene	1	1	1	15	15.5	17.5	2	2_A375_shN7_plus_lncRNA_R_1	27	Gene SLC25A13	C7LN2, SLC25A13, AGXLM2, CITRIN	solute carrier family 25, member 13 (citrin)	NM_014251, NM_001162110, NM_027662, XCT223558T.0, XCT19594.1	220775_at_229081_s_at, 229081_at	NP_036866.1, NP_001136662.1, EAW76845.1, EAW76849.1
Gene ID:3178	MRS2	7	95,845,974	95,849,980	14	-	1	4_A375_SGR1_1:7395	-1934	upstream	0	0	1	4	10	15	1	4_A375_SGR1_1.1	15	Gene MRS2	mrs2-like (S1, MRNS01, MRS01	mrs2-like (S. cerevisiae)	NM_033322		
Gene ID:79	SHFM1	7	96,216,079	96,339,303	21,124	-	1	2_A375_shN7_plus_lncRNA_R_1:7214	160	nr gene	0	1	0	14	17	9	1	2_A375_shN7_plus_lncRNA_R_1	17	Gene SHFM1	SHFM1, ECD, SEM5, SHFD1, Dlb6p1, SHSF1, DSS1	split hand/foot malformation (ectrodactyly) type 1	NM_006304, XCT223020D.0, XCT223020D.2	202276_at	NP_006285.1, EAW76747.1, EAW76748.1
Gene ID:9	DLX5	7	96,649,702	96,654,143	4,441	-	1	4_A375_SGR1_1:7397	-9741	upstream	0	0	1	4	8	16	1	4_A375_SGR1_1.1	16	Gene DLX5	DLX5		NM_005221, XCT10193.3	212507_s_at	NP_005212.1, EAW76741.1
Gene ID:551	ACN9	7	96,743,903	96,811,075	83,173	+	3	1_A375_shN7_mnat_lncRNA_R_1:5005, 2_A375_shN7_plus_lncRNA_R_1:7216, 4_A375_SGR1_1:7398	979, 1007, 1153	cis gene, nr gene, cis gene	1	1	1	22	27	24	1	2_A375_shN7_plus_lncRNA_R_1	27	Gene ACN9	ACN9, DC11	ACN9 homolog (S. cerevisiae)	NM_020188, XCT223822.3, XCT1992180.1	218801_at	NP_064711.1, EAW76740.1, EAW76739.1
Gene ID:553	LMTK2	7	97,736,197	97,836,943	102,746	+	4	1_A375_shN7_mnat_lncRNA_R_1:5007, 2_A375_shN7_plus_lncRNA_R_1:7217, 4_A375_SGR1_1:7400, 4_A375_SGR1_1:7401	11, -21, 107227, 111147	cis gene, upstream, downstream, downstream	1	1	1	10.67	16.33	21	3	4_A375_SGR1_1.1	30	Gene LMTK2	KPK2, SREK, KIAA1079, LMTK2, clk, MATYK2, LMK2, FLJ46559, KPK2	serine/threonine kinase 2	NM_014916, XCT223029E.0, XCT223029R.0, XCT9310.3	206223_at_235397_at	NP_055713.2, EAW76721.1, EAW76719.1, EAW76720.1
Gene ID:5930	BHLHA15	7	97,841,588	97,842,271	703	+	2	4_A375_SGR1_1:7400, 4_A375_SGR1_1:7401	1686, 5776	downstream, downstream	0	0	1	8	10	25	2	4_A375_SGR1_1.1	30	Gene BHLHA15	BHLHA15, BHLHB5, MIST1	basic helix-loop-helix family, member a15	NM_177455		NP_803236.1
Gene ID:551	TECPR1	7	97,846,056	97,881,466	35,432	-	3	2_A375_shN7_plus_lncRNA_R_1:7218, 4_A375_SGR1_1:7400, 4_A375_SGR1_1:7401	-180, 32044, 54124	downstream, downstream, cis gene	1	1	1	12.33	12.67	22	3	4_A375_SGR1_1.1	30	Gene TECPR1	FLJ25419, FLJ90350, TECPR1, DKFZp434B033	tectonin beta-propeller repeat containing 1	NM_018335, XCT223018B.0, XCT223564D.0, XCT22595.3	227560_s_at_227561_at, 231912_s_at	NP_059131.1, EAW76716.1, EAW76717.1, EAW76718.1, EAW76719.1
Gene ID:7706	BRI3	7	97,910,979	97,922,275	11,296	+	1	4_A375_SGR1_1:7402	2141	cis gene	0	0	1	8	9	16	1	4_A375_SGR1_1.1	16	Gene BRI3	BRI3, IS	brain protein 13	NM_015379, NM_001159491, XCT223023D.0, XCT223023D.2, XCT10127.2	223276_s_at	NP_056194.1, NP_001152963.1, EAW76713.1, EAW76714.1, EAW76715.1
Gene ID:971	BNIP2	7	97,920,062	98,020,427	109,466	-	1	4_A375_SGR1_1:7402	117207	downstream	0	0	1	9	7	10	1	4_A375_SGR1_1.1	10	Gene BNIP2L1	HTKS, BNIP2L1, FLJ40279	BNIP-associated protein 2-like 1	NM_138422, XCT223963.2, XCT1992731.1	223873_s_at_227271_at, 227272_s_at	NP_001193202.1, EAW76706.1, EAW76707.1
Gene ID:3988	TMEM130	7	98,444,111	98,487,873	43,862	-	2	1_A375_shN7_mnat_lncRNA_R_1:5009, 2_A375_shN7_plus_lncRNA_R_1:7220	-5971, -5971	upstream, upstream	1	1	0	30	39	13	1	2_A375_shN7_plus_lncRNA_R_1	39	Gene TMEM130	DKFZp761I1147, FLJ40843, TMEM130	transmembrane protein 130	NM_152313, NM_001134430, NM_001134431, XCT223019B.0, XCT223954T.0, XCT223954D.0, XCT223962.2	230429	NP_690077.1, NP_001127922.1, NP_001127923.1, EAW76703.1, EAW76704.1, EAW76702.1
Gene ID:9365	TRRAP	7	98,476,113	98,610,864	134,751	+	3	1_A375_shN7_mnat_lncRNA_R_1:5009, 2_A375_shN7_plus_lncRNA_R_1:7220, 4_A375_SGR1_1:7402	431, 431, 51023	nr gene, nr gene, cis gene	1	1	1	17.5	21.5	15	2	4_A375_SGR1_1.1	39	Gene TRRAP	PAF60, PRKDC-interacting protein, Tra1, TRRAP, TR-AF, FLJ30871, STAF42	transformation/transcription domain-associated protein	NM_003496, XCT223212D.0, XCT223212B.0, XCT223212T.0, XCT223212S.0, XCT223940.0, XCT223954.0, XCT223954.2, XCT19536.4.1	202942_s_at_214093_s_at	NP_003487.1, EAW76698.1, EAW76699.1, EAW76700.1, EAW76701.1, EAW76702.1, EAW76697.1, EAW76696.1, EAW76703.1
Gene ID:5532	ARPC1A	7	98,923,498	98,965,953	40,359	+	2	1_A375_shN7_plus_lncRNA_R_1:7222, 4_A375_SGR1_1:7404	48576, 56	downstream, cis gene	0	1	1	15	17.5	11.5	2	4_A375_SGR1_1.1	17	Gene ARPC1A	SOP2H, Arc/p-20, SOP2L, ARPC1A	actin related protein 2/3 complex, subunit 1A, 41kDa	NM_001199998, NM_006409, XCT223122Q.0, XCT223123d.0, XCT223123d.0	200950_at	NP_001177215.1, NP_006390.2, EAW76801.1, EAW76802.1, EAW76803.1
Gene ID:5533	ARPC1B	7	98,972,329	98,992,424	20,095	+	2	1_A375_shN7_plus_lncRNA_R_1:7222, 4_A375_SGR1_1:7405	-237, 22223	upstream, downstream	0	1	1	12.5	10	11	2	4_A375_SGR1_1.1	18	Gene ARPC1B	ARC41, ARPC1B, actin-ARC, p41-ARC	actin related protein 2/3 complex, subunit 1B, 41kDa	NM_005720, XCT199727L.1, XCT199727H.1, XCT223124D.0, XCT9124.2	201964_at_217277_at, 217280_x_at	NP_005711.1, EAW76677.1, EAW76678.1, EAW76679.1, EAW76680.1
Gene ID:3312	PDAP1	7	98,992,569	99,006,262	13,693	-	3	4_A375_SGR1_1:7405, 1_A375_shN7_mnat_lncRNA_R_1:5010, 2_A375_shN7_plus_lncRNA_R_1:7223	10140, 454, -108	cis gene, nr gene, upstream	1	1	1	14.5	17.5	12.5	2	2_A375_shN7_plus_lncRNA_R_1	29	Gene PDAP1	HSPP35, PAP, PDAP1, PAP1	HCGPA bi-located protein	NM_014391, XCT223024E.0, XCT223024S.0, XCT223040.0	202290_at_217824_at	NP_038706.1, EAW76675.1, EAW76674.1, EAW76676.1
Gene ID:98	BUD31	7	99,006,801	99,017,209	10,808	+	2	1_A375_shN7_plus_lncRNA_R_1:5010, 2_A375_shN7_plus_lncRNA_R_1:7223	-712, -201	upstream, upstream	1	1	0	19	29	11	1	2_A375_shN7_plus_lncRNA_R_1	29	Gene BUD31	G10P17, MGC111202, G10, EDG-2, EDG2, BUD31, HCA66DW	BUD31 homolog (S. cerevisiae)	NM_003910, XCT223123J.0, XCT223124J.0, XCT223562D.0, XCT223562D.2	200960_s_at_213613_at	NP_003901.2, EAW76672.1, EAW76670.1, EAW76671.1, EAW76672.1
Gene ID:6024	PTCD1	7	99,016,743	99,036,419	19,674	-	8	1_A375_shN7_mnat_lncRNA_R_1:5010, 1_A375_shN7_mnat_lncRNA_R_1:5011, 2_A375_shN7_plus_lncRNA_R_1:7223, 2_A375_shN7_plus_lncRNA_R_1:7224, 4_A375_SGR1_1:7406, 4_A375_SGR1_1:7407	33831, -81, 33819, -93, 227, 351	downstream, upstream, downstream, upstream, cis gene, upstream	1	1	1	44	47.3	14.5	2	2_A375_shN7_plus_lncRNA_R_1	49	Gene PTCD1	KIAA0822, PTCD1	pentatricopeptide repeat domain 1	NM_015345, XCT223240.0	210998_s_at_222796_at	NP_056360.2, EAW76669.1
Gene ID:696	CPSF4	7	99,036,963	99,054,998	18,035	+	4	1_A375_shN7_mnat_lncRNA_R_1:5011, 2_A375_shN7_plus_lncRNA_R_1:7224, 4_A375_SGR1_1:7408, 4_A375_SGR1_1:7407	-83, -31, -371, 237	upstream, upstream, upstream, cis gene	1	1	1	69	86	16	1	1_A375_shN7_mnat_lncRNA_R_1	69	Gene CPSF4	hNIK, CPSF4, CPSF30, NEB1	cleavage and polyadenylation specific factor 4, 30kDa	NM_006693, NM_001005509, XCT223124E.0, XCT223123.0, XCT19622.3, XCT19622297.1, XCT19622300.1, XCT19622299.1	209695_s_at	NP_006684.1, NP_001070025.1, EAW76664.1, EAW76665.1, EAW76667.1, EAW76666.1, EAW76662.1, EAW76663.1, EAW76668.1
Gene ID:124	ZNF394	7	99,090,854	99,097,677	7,823	-	3	1_A375_shN7_mnat_lncRNA_R_1:5012, 2_A375_shN7_plus_lncRNA_R_1:7223, 4_A375_SGR1_1:7408	-75, -43, 117	upstream, upstream, cis gene	1	1	1	16	21	19	1	2_A375_shN7_plus_lncRNA_R_1	21	Gene ZNF394	ENSCAN14, ZNF394, FLJ12290	zinc finger protein 394	NM_032184, XCT151005.1	214714_at	NP_115340.2, EAW76639.1
Gene ID:660	ZNF36	7	99,102,273	99,131,443	29,172	+	3	1_A375_shN7_mnat_lncRNA_R_1:5012, 2_A375_shN7_plus_lncRNA_R_1:7223, 4_A375_SGR1_1:7408	-4321, -4350, 4913	upstream, upstream, upstream	1	1	1	16	21	19	1	2_A375_shN7_plus_lncRNA_R_1	21	Gene ZNF36	ZNF914, ZFP36, KIAA1015, ZNSCAN8, FLJ39233, MGC2210	zinc finger protein 36, C3H type, homolog (mouse)	NM_014369, NM_145102, XCT199T340.2, XCT223113D.1, XCT223539D.0, XCT223539D.2, XCT19627985.3	203707_s_at_203731_s_at	NP_055354.1, NP_659707.1, EAW76644.1, EAW76643.1, EAW76645.1, EAW76646.1, EAW76647.1
Gene ID:1795	CTIF	7	99,143,923	99,149,757	5,834	-	3	1_A375_shN7_mnat_lncRNA_R_1:5013, 2_A375_shN7_plus_lncRNA_R_1:7226, 2_A375_shN7_plus_lncRNA_R_1:7228, 4_A375_SGR1_1:7409	45, 61, -5419	nr gene, nr gene, upstream	1	1	0	22.5	20	10.5	2	1_A375_shN7_mnat_lncRNA_R_1	29	Gene CTIF	CTIF, CBP/CBP-interacting protein, 20S	chromosome 7 open reading frame 26	NM_145111, XCT223119A.0, XCT19650.3	1568565_at_229762_at, 229809_at	NP_659032.1, EAW76652.1, EAW76653.1
Gene ID:6427	ZNF853	7	99,166,945	99,174,078	10,231	-	4	1_A375_shN7_mnat_lncRNA_R_1:5013, 2_A375_shN7_plus_lncRNA_R_1:7226, 4_A375_SGR1_1:7409, 4_A375_SGR1_1:7410	-6522, -6349, 121, 21971	upstream, upstream, cis gene, downstream	1	1	1	17	15.33	14.67	3	1_A375_shN7_mnat_lncRNA_R_1	29	Gene ZNF853	ZNF853, MGC142091, ZNF853, FLJ32491, MGC16203, Vlv 1, MGC16939, MGC5521, V1K	zinc finger protein 853	NM_024091, NM_138464, NM_001009856, AK001009980, NM_001003396, NM_001003397, NM_001003398, XCT223129E.1, XCT19702.0, XCT19538.2, XCT19538.3	1554720_at_223002_s_at, 223945_at	NP_076988.1, NP_612322.1, NP_001078035.1, NP_001009856.1, NP_001009980.1, NP_001078036.1, NP_001078037.1, EAW76643.1, EAW76649.1, EAW76650.1, EAW76651.1
Gene ID:5930199	LOC100509199	7	99,195,845	99,208,456	12,611	+	2	1_A375_shN7_mnat_lncRNA_R_1:5014, 2_A375_shN7_plus_lncRNA_R_1:7227	18645, 16712	downstream, downstream	1	1	0	54	86	14	1	2_A375_shN7_plus_lncRNA_R_1	86	Gene LOC100509199		hypothetical protein LOC100509199	XM_003120391, XM_003120095, XM_003120092, XM_003119761, XM_003119940, XM_003119942, XM_003119939, XM_003119955, XM_003119590, XM_003120097, XM_003120098, XM_003120096	XP_003120399.1, XP_003120093.1, XP_003119938.1, XP_003119939.1, XP_003119937.1, XP_003119938.1, XP_003119935.1, XP_003120938.1
Gene ID:1705	ZNF492	7	99,214,871	99,230,830	15,959	-	2	1_A375_shN7_mnat_lncRNA_R_1:5014, 2_A375_shN7_plus_lncRNA_R_1:7227	-75, -11	upstream, upstream	1	1	0	54	86	14	1	2_A375_shN7_plus_lncRNA_R_1	86	Gene ZNF492	ZSCAN25, ZNF492	zinc finger protein 492	NM_145115, XCT3445431.1, XCT231196.0, XCT231197.0, XCT223561H.0, XCT1701691.2	226156_at_242801_at	NP_660350.2, EAW76643.1, EAW76644.1, EAW76645.1, EAW76647.1
Gene ID:74	CYP2A7	7	99,245,613	99,264,173	218,560	-	1	1_A375_shN7_plus_lncRNA_R_1:7228	6255	nr gene	0	1	0	13	17	8	1	2_A375_shN7_plus_lncRNA_R_1	17	Gene CYP2A	CYP2, CYP2A	cytochrome P450, family 2, subfamily A			



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.10467	ZNHIT1	7	100,860,985	100,867,471	6,486	+	1	4_A375_EGR1..1..7431	-25	upstream	0	0	1	12	16	24	1	4_A375_EGR1..1	24	Gene ZNHIT1	ZNHIT1, CG1I, ZNFN4A1	zinc finger, HIT type 1	NM_006349, hCT2352374.0, hCT8397.3, hCT1950175.1, hCT1950176.1	201541_s_at	NP_006340.1, EAW50207.1, EAW50206.1, EAW50208.1, EAW50209.1
GeneID.24146	CLDN15	7	100,875,373	100,882,101	6,728	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5030, 2_A375_pNL97_plus_lncRNA_AR..1..7250, 4_A375_EGR1..1..7432	-5995, -5995, -6219	upstream, upstream, upstream	1	1	1	24	25	20	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene CLDN15	FLJ42715, CLDN15, MGC19536	claudin 15	NM_001185080, NM_014343, hCT2267600.0, hCT1950174.1	1552845_at, 219640_at	NP_001172009.1, NP_055158.1, EAW50210.1, EAW50211.1
GeneID.51024	FIS1	7	100,882,893	100,888,371	5,478	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5030, 1_A375_pNL7_minus_lncRNA_AR..1..5031, 2_A375_pNL97_plus_lncRNA_AR..1..7250, 2_A375_pNL97_plus_lncRNA_AR..1..7251, 4_A375_EGR1..1..7432	275, -7149, 275, -7117, 51	in gene, upstream, in gene, upstream, in gene	1	1	1	23	28.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene FIS1	CGI-135, FIS1, TTC11	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)	NM_016068, hCT2352368.0, hCT8399.2, hCT1960989.1	218034_at	NP_057152.2, EAW50213.1, EAW50212.1, EAW50214.1
GeneID.100506507	LOC100506507	7	100,942,894	100,944,625	1,731	+	1	4_A375_EGR1..1..7433	6834	downstream	0	0	1	10	8	13	1	4_A375_EGR1..1	13	Gene LOC100506507		hypothetical LOC100506507	XR_108653		
GeneID.64792	RABL5	7	100,956,648	100,965,093	8,445	-	1	4_A375_EGR1..1..7433	13365	downstream	0	0	1	10	8	13	1	4_A375_EGR1..1	13	Gene RABL5	FLJ13225, RABL5, FLJ14117, DKFZp761N0823	RAB, member RAS oncogene family-like 5	NM_022777, NM_001130820, NM_001130821, NM_001130822, hCT2352372.0, hCT2352373.0, hCT8404.2, hCT1950178.1, hCT1981370.1	218785_s_at, 222742_s_at	NP_073614.1, NP_001124292.1, NP_001124293.1, NP_001124294.1, EAW50217.1, EAW50220.1, EAW50216.1, EAW50218.1, EAW50219.1
GeneID.136227	EMID2	7	101,006,122	101,202,304	196,182	+	3	4_A375_EGR1..1..7434, 4_A375_EGR1..1..7435, 4_A375_EGR1..1..7436	152198, 184166, 196406	in gene, in gene, downstream	0	0	1	5	5.67	16.33	3	4_A375_EGR1..1	19	Gene EMID2	SH2B, hEmu2, EMI6, COL26A1, EMID2, EMU2, MGC129648	EMI domain containing 2	NM_133457, hCT10107.3, hCT1963536.1	229080_at, 233894_x_at	NP_597714.2, EAW50221.1, EAW50222.1
GeneID.100506527	LOC100506527	7	101,208,597	101,212,230	3,633	-	1	4_A375_EGR1..1..7436	9702	downstream	0	0	1	4	5	19	1	4_A375_EGR1..1	19	Gene LOC100506527		hypothetical LOC100506527	XR_113044, XR_110719, XR_108654, XR_114072		
GeneID.1523	CUX1	7	101,459,292	101,927,250	467,958	+	8	1_A375_pNL7_minus_lncRNA_AR..1..5032, 1_A375_pNL7_minus_lncRNA_AR..1..5033, 2_A375_pNL97_plus_lncRNA_AR..1..7252, 2_A375_pNL97_plus_lncRNA_AR..1..7253, 2_A375_pNL97_plus_lncRNA_AR..1..7254, 4_A375_EGR1..1..7438, 4_A375_EGR1..1..7439, 4_A375_EGR1..1..7440	-1584, -668, -1532, -60, 303300, -732, 365444, 470132	upstream, upstream, upstream, upstream, in gene, upstream, in gene, downstream	1	1	1	11.17	15.33	9.5	8	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CUX1	CUX1, Nbla10317, CUX, p110, CUTL1, p200, GOLIM6, Clox, FLJ31745, CDP, CDP1, CDP/Cut, CASP, p100, Cux/CDP, p75, COY1	cut-like homeobox 1	NM_001913, NM_181500, NM_181552, hCT2267142.0, hCT2267144.0	202367_at, 214743_at	NP_001904.2, NP_852477.1, NP_853530.2, EAW50227.1, EAW50228.1
GeneID.10603	SH2B2	7	101,928,405	101,962,178	33,773	+	1	4_A375_EGR1..1..7440	1019	in gene	0	0	1	8	11	17	1	4_A375_EGR1..1	17	Gene SH2B2	SH2B2, APS	SH2B adaptor protein 2	NM_020979, hCT10108.3, hCT1960208.1	205367_at	NP_066189.3, EAW50232.1, EAW50233.1
GeneID.100422858	MIR4285	7	101,938,389	101,938,453	64	+	1	4_A375_EGR1..1..7440	-6945	upstream	0	0	1	8	11	17	1	4_A375_EGR1..1	17	Gene MIR4285	MIR4285	microRNA 4285	NR_036245		
GeneID.729597	SPDYE6	7	101,988,192	101,998,889	10,697	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5034, 2_A375_pNL97_plus_lncRNA_AR..1..7255	-7287, -7367	upstream, upstream	1	1	0	25	18	6	1	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene SPDYE6	SPDYE6	speedy homolog E6 (Xenopus laevis)	NM_001146210		NP_001139682.1
GeneID.79706	PRKRIP1	7	102,036,804	102,067,129	30,325	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5035, 2_A375_pNL97_plus_lncRNA_AR..1..7256, 4_A375_EGR1..1..7441	-132, -198, 156	upstream, upstream, in gene	1	1	1	25	25	20	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene PRKRIP1	C114, KRBOX3, FLJ13902, PRKRIP1, FLJ40957	PRKR interacting protein 1 (IL11 inducible)	NM_024653, hCT2265995.0, hCT2265996.0, hCT2352369.0	1564165_at, 1564166_s_at, 218378_s_at, 222615_s_at	NP_078929.1, EAW50243.1, EAW50241.1, EAW50242.1
GeneID.100313829	MIR548O	7	102,046,189	102,046,302	113	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5035, 2_A375_pNL97_plus_lncRNA_AR..1..7256, 4_A375_EGR1..1..7441	9630, 9694, 9342	downstream, downstream, downstream	1	1	1	25	25	20	1	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene MIR548O	MIRN548O, MIR548O	microRNA 548o	NR_031669		
GeneID.80228	ORAI2	7	102,073,996	102,097,268	23,272	+	4	4_A375_EGR1..1..7442, 4_A375_EGR1..1..7443, 4_A375_EGR1..1..7444, 4_A375_EGR1..1..7445	12980, 13760, 18985, 21556	in gene, in gene, in gene, in gene	0	0	1	5.75	8.5	16.5	4	4_A375_EGR1..1	23	Gene ORAI2	FLJ44818, ORAI2, FLJ14733, TMEM142B, C7orf19, MEM142B, CBCIP2, FLJ12474	ORAI calcium release-activated calcium modulator 2	NM_032831, NM_001126340, hCT2265998.0, hCT2266001.0, hCT2266002.0, hCT2352370.0, hCT1774798.2	1558426_x_at, 218611_at, 218612_s_at, 230347_at	NP_116220.1, NP_001119812.1, EAW50245.1, EAW50246.1, EAW50247.1, EAW50248.1, EAW50244.1
GeneID.54784	ALKBH4	7	102,096,667	102,105,321	8,654	-	5	4_A375_EGR1..1..7442, 4_A375_EGR1..1..7443, 4_A375_EGR1..1..7444, 4_A375_EGR1..1..7445, 4_A375_EGR1..1..7446	18345, 17545, 12340, 9769, -8007	downstream, downstream, downstream, downstream, upstream	0	0	1	6	8.4	16.2	5	4_A375_EGR1..1	23	Gene ALKBH4	FLJ20013, ABH4, ALKBH4	alkB, alkylation repair homolog 4 (E. coli)	NM_017621, hCT1774793.1	222228_s_at	NP_060091.1, EAW50249.1
GeneID.222229	LRWD1	7	102,105,390	102,113,612	8,222	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5036, 2_A375_pNL97_plus_lncRNA_AR..1..7257, 4_A375_EGR1..1..7445, 4_A375_EGR1..1..7446	13954, 13938, -9838, 7936	downstream, downstream, upstream, in gene	1	1	1	19	25.33	11.33	3	2_A375_pNL97_plus_lncRNA_AR..1	64	Gene LRWD1	ORCA, LRWD1, DKFZp434K1815	leucine-rich repeats and WD repeat domain containing 1	NM_152892, hCT1774802.3	225680_at	NP_690852.1, EAW50250.1
GeneID.5439	POLR2J	7	102,113,547	102,119,381	5,834	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5036, 2_A375_pNL97_plus_lncRNA_AR..1..7257, 4_A375_EGR1..1..7446	37, 53, 6053	in gene, in gene, downstream	1	1	1	26.5	35	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	64	Gene POLR2J	POLR2J, RPB11, MGC71910, hRPB14, RPB11m, POLR2J1, RPB11A	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa	NM_006234	212782_x_at	NP_006225.1
GeneID.100506726	LOC100506726	7	102,122,205	102,123,513	1,308	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5036, 2_A375_pNL97_plus_lncRNA_AR..1..7257, 4_A375_EGR1..1..7446	4169, 4185, 10185	downstream, downstream, downstream	1	1	1	26.5	35	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	64	Gene LOC100506726		hypothetical LOC100506726	XR_110725, XR_108660		
GeneID.100271927	RASA4B	7	102,123,588	102,158,224	34,636	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5036, 2_A375_pNL97_plus_lncRNA_AR..1..7257, 4_A375_EGR1..1..7446	36680, 36696, 44696	downstream, downstream, downstream	1	1	1	26.5	35	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	64	Gene RASA4B	FLJ59902, RASA4B	RAS p21 protein activator 4B	XM_003119052, XM_003119055, XM_003119054, XM_003119053, XM_003119056, XM_003118597, XM_003118600, XM_003118598, XM_003118599, XM_003118596		XP_003119100.1, XP_003119103.1, XP_003119102.1, XP_003119101.1, XP_003119104.1, XP_003118645.1, XP_003118648.1, XP_003118644.1, XP_003118647.1, XP_003118646.1
GeneID.222235	FBXL13	7	102,453,308	102,715,288	261,980	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5037, 1_A375_pNL7_minus_lncRNA_AR..1..5038, 2_A375_pNL97_plus_lncRNA_AR..1..7258	198858, 82968, 198938	in gene, in gene, in gene	1	1	0	21	20	4	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene FBXL13	FBXL13, Fbl13, FLJ38068, MGC21636	F-box and leucine-rich repeat protein 13	NM_145032, NM_001111038, hCT2305303.0, hCT2305304.0, hCT2356430.0, hCT2356431.0, hCT2356432.0, hCT2356433.0, hCT2356434.0, hCT2356435.0, hCT1646378.2	1553798_a_at, 1556770_a_at	NP_659469.3, NP_001104508.1, EAW83298.1, EAW83301.1, EAW83302.1, EAW83306.1, EAW83299.1, EAW83300.1, EAW83303.1, EAW83304.1, EAW83305.1
GeneID.222236	NAPEPLD	7	102,740,023	102,789,569	49,546	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5039, 2_A375_pNL97_plus_lncRNA_AR..1..7259	-47, -63	upstream, upstream	1	1	0	15	17	9	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene NAPEPLD	FMP30, NAPEPLD, NAPE-PLD, DKFZp781D1098	N-acyl phosphatidylethanolamine phospholipase D	NM_198990, NM_001122838, hCT2305300.0, hCT9251.3	226041_at, 233539_at, 238722_x_at, 242229_at, 242635_s_at	NP_945341.3, NP_001116310.1, EAW83314.1, EAW83315.1
GeneID.9512	PMPCB	7	102,937,873	102,955,133	17,260	+	1	4_A375_EGR1..1..7447	79	in gene	0	0	1	16	16	18	1	4_A375_EGR1..1	18	Gene PMPCB	Beta-MPP, MPPB, MPPP52, MPP11, P-52, PMPCB	peptidase (mitochondrial processing) beta	NM_004279, hCT2305050.0, hCT2356423.0, hCT2356424.0, hCT9247.2	201682_at	NP_004270.2, EAW83326.1, EAW83325.1, EAW83327.1, EAW83328.1
GeneID.27000	DNAJC2	7	102,952,921	102,985,320	32,399	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5040, 2_A375_pNL97_plus_lncRNA_AR..1..7260	232, 232	in gene, in gene	1	1	0	20	19	12	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene DNAJC2	DNAJC2, MPP11, ZRF1, ZUO1, MPHOSPH11	DnaJ (Hsp40) homolog, subfamily C, member 2	NM_014377, NM_001129887	1566884_at, 213097_s_at	NP_055192.1, NP_001123359.1
GeneID.5701	PSMC2	7	102,988,089	103,008,656	20,567	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5040, 2_A375_pNL97_plus_lncRNA_AR..1..7260	-3001, -3001	upstream, upstream	1	1	0	20	19	12	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene PSMC2	Nbla10058, MSS1, MGC3004, S7, PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	NM_002803, hCT2305051.0, hCT2305052.0, hCT2305053.0	201068_s_at, 238020_at	NP_002794.1, EAW83332.1, EAW83331.1, EAW83333.1
GeneID.375611	SLC26A5	7	102,993,177	103,086,624	93,447	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5040, 2_A375_pNL97_plus_lncRNA_AR..1..7260	101536, 101536	downstream, downstream	1	1	0	20	19	12	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene SLC26A5	DFNB61, MGC118887, SLC26A5, MGC118888, MGC118889, MGC118886, PRES	solute carrier family 26, member 5 (prestin)	NM_206883, NM_206884, NM_206885, NM_198999, NM_001167962, hCT2305291.0, hCT1952587.1		NP_996766.1, NP_996767.1, NP_001161434.1, NP_945350.1, NP_996768.1, EAW83334.1, EAW83335.1
GeneID.5649	RELN	7	103,112,231	103,629,963	517,732	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5041, 2_A375_pNL97_plus_lncRNA_AR..1..7261	353163, 353163	in gene, in gene	1	1	0	16	24	3	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene RELN	PRO1598, RL, RELN	reelin	NM_005045, NM_173054, hCT2305275.0, hCT2305279.0, hCT9253.3	205923_at	NP_005036.2, NP_774959.1, EAW83336.1, EAW83337.1, EAW83338.1
GeneID.5001	ORC5L	7	103,766,788	103,848,463	81,675	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5042, 2_A375_pNL97_plus_lncRNA_AR..1..7262	15, -1	in gene, upstream	1	1	0	23	22	9	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene ORC5L	ORC5P, ORC5T, ORC5, ORC5L	origin recognition complex, subunit 5	NM_002553, NM_181747, hCT2306225.1, hCT2341398.0, hCT8046.4	204957_at, 211212_s_at, 211213_at	NP_002544.1, NP_859531.1, EAW83341.1, EAW83342.1, EAW83343.1
GeneID.375612	LHFPL3	7	103,969,104	104,549,005	579,901	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5043, 2_A375_pNL97_plus_lncRNA_AR..1..7263, 2_A375_pNL97_plus_lncRNA_AR..1..7264	299008, 223600, 299024	in gene, in gene, in gene	1	1	0	18.5	26	3.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene LHFPL3	LHFPL4, LHFPL3	lipoma HMGIC fusion partner-like 3	NM_199000	236781_at	NP_945351.1
GeneID.100216545	LOC100216545	7	104,650,989	104,654,588	3,599	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7265, 4_A375_EGR1..1..7448	1212, 604	in gene, in gene	0	1	1	16	16	16	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100216545	FLJ37053, FLJ42052, FLJ41482	hypothetical LOC100216545	NR_024586		
GeneID.55904	MLL5	7	104,654,637	104,754,532	99,895	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7265, 4_A375_EGR1..1..7448	-1261, -653	upstream, upstream	0	1	1	16	16	16	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene MLL5	MLL5, FLJ10078, MGC70452, FLJ14026, KMT2E, HDCMC04P	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	NM_182931, NM_018682, hCT2306194.0, hCT2306195.0, hCT2306198.0, hCT2306199.0	223189_x_at, 223190_s_at, 226100_at	NP_891847.1, NP_061152.3, EAW83355.1, EAW83356.1, EAW83357.1, EAW83358.1
GeneID.8733	SRPK2	7	104,756,823	105,029,341	272,518	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7266	84429	in gene	0	1	0	15	15	3	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene SRPK2	SRPK2, FLJ36101, SFRSK2	SFRS protein kinase 2	NM_182691, NM_182692, hCT2305118.0, hCT2305119.0, hCT2356429.0	1558254_s_at, 203181_x_at, 203182_s_at, 214931_s_at, 217517_x_at	NP_872633.1, NP_872634.1, EAW83359.1, EAW83360.1, EAW83361.1
GeneID.54517	PUS7	7	105,096,958	105,162,685	65,727	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5044, 2_A375_pNL97_plus_lncRNA_AR..1..7267	-10035, -9907	upstream, upstream	1	1	0	23	31	16	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene PUS7	PUS7, KIAA1897, MGC17720, FLJ20485	pseudouridylate synthase 7 homolog (S. cerevisiae)	NM_019042, hCT2305113.0, hCT1953072.1	218984_at	NP_061915.2, EAW83364.1, EAW83363.1
GeneID.80561	RINT1	7	105,172,532	105,208,124	35,592	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5044, 2_A375_pNL97_plus_lncRNA_AR..1..7267	168, 60	in gene, in gene	1	1	0	23	31	16	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene RINT1	DKFZp667H2324, RINT1, RINT-1	RAD50 interactor 1	NM_021930, hCT2304679.0, hCT1818538.2	218598_at	NP_068749.3, EAW83366.1, EAW83367.1
GeneID.222255	ATXN7L1	7	105,245,221	105,517,031	271,810	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5045, 2_A375_pNL97_plus_lncRNA_AR..1..7268	100327, 100327	in gene, in gene	1	1	0	28	36	4	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene ATXN7L1	FLJ40255, MGC33190, FLJ58242, ATXN7L4, MGC10760, KIAA1218, ATXN7L1	ataxin 7-like 1	NM_152749, NM_020725, NM_138495, hCT2305092.1, hCT2305094.1, hCT2305096.1, hCT2305097.1, hCT2344936.0	214342_at, 214343_s_at	NP_689962.1, NP_065776.1, NP_612504.1, EAW83370.1, EAW83371.1, EAW83373.1, EAW83372.1, EAW83374.1
GeneID.6856	SYPL1	7	105,730,951	105,753,057	22,106	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5046, 2_A375_pNL97_plus_lncRNA_AR..1..7270	-63, 185	upstream, in gene	1	1	0	18	15	6	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene SYPL1	H-SP1, SYPL, SYPL1	synaptophysin-like 1	NM_006754, NM_182715, hCT2305085.0, hCT7975.3, hCT1981683.1	201259_s_at, 201260_s_at	NP_006745.1, NP_874384.1, EAW83379.1, EAW83380.1, EAW83381.1
GeneID.168455	FLJ36031	7	106,299,149	106,301,591	2,442	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7271, 4_A375_EGR1..1..7449	903, 1015	in gene, in gene	0	1	1	12	17	16	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene FLJ36031	FLJ25556, MGC16181, FLJ11436	hypothetical protein FLJ36031	NM_175884	227883_at, 228686_x_at, 229521_at	NP_787080.2
GeneID.5294	PIK3CG	7	106,505,924	106,547,592	41,668	+	1	4_A375_EGR1..1..7450	2508	in gene	0	0	1	5	7	27	1	4_A375_EGR1..1	27	Gene PIK3CG	PIK3CG, PIK3, PI3Kgamma, PI3K, PI3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	NM_002649, hCT1968320.1, hCT2356437.0, hCT7976.2	206369_s_at, 206370_at	NP_002640.2, EAW83389.1, EAW83387.1, EAW83388.1
GeneID.10466	COG5	7	106,842,189	107,204,959	362,770	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5048, 1_A375_pNL7_minus_lncRNA_AR..1..5049, 2_A375_pNL97_plus_lncRNA_AR..1..7273, 4_A375_EGR1..1..7451	238255, 767, 671, 511	in gene, in gene, in gene, in gene	1	1	1	23.5	26	20	2	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene COG5	GTC90, COG5, FLJ41732, GOLTC1, FLJ44289, CDG2I	component of oligomeric golgi complex 5	NM_006348, NM_181733, NM_001161520, hCT2305494.0, hCT2356413.0, hCT1953971.1	203629_s_at, 203630_s_at	NP_006339.3, NP_859422.2, NP_001154992.1, EAW83395.1, EAW83396.1, EAW83397.1
GeneID.11062	DUS4L	7	107,204,432	107,218,968	14,536	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5049, 2_A375_pNL97_plus_lncRNA_AR..1..7273, 4_A375_EGR1..1..7451	-240, -144, 16	upstream, upstream, in gene	1	1	1	30	41	20	1	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene DUS4L	PP35, MGC133233, DUS4, DUS4L	dihydrouridine synthase 4-like (S. cerevisiae)	NM_181581, hCT1968321.1, hCT1968322.1, hCT7977.3, hCT1955453.1, hCT1981684.1, hCT1981685.1	205761_s_at, 205762_s_at	NP_853559.1, EAW83400.1, EAW83399.1, EAW83401.1, EAW83402.1, EAW83404.1, EAW83403.1
GeneID.100128737	LOC100128737	7	107,383,198	107,385,026	1,828	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7274	256	in gene	0	1	0	17	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100128737		hypothetical LOC100128737	XR_113067, XR_113066, XR_113068, XR_110731, XR_110730, XR_110732, XR_108796, XR_108795, XR_108797, XR_114078, XR_114077, XR_114079		
GeneID.79872	CBLL1	7	107,384,279	107,402,083	17,804	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7274	489	in gene	0	1	0	17	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CBLL1	MGC163401, FLJ23109, MGC163403, CBLL1, RNF188, HAKAI	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	NM_024814, NR_024199, hCT8165.3, hCT1953974.1	220018_at	NP_079090.2, EAW83417.1, EAW83416.1
GeneID.4897	NRCAM	7	107,788,071	108,096,841	308,770	-	5	2_A375_pNL97_plus_lncRNA_AR..1..7275, 1_A375_pNL7_minus_lncRNA_AR..1..5050, 2_A375_pNL97_plus_lncRNA_AR..1..7276, 2_A375_pNL97_plus_lncRNA_AR..1..7277, 4_A375_EGR1..1..7452	108585, 14105, 25065, 1225, 393	in gene, in gene, in gene, in gene, in gene	1	1	1	14.6	17.6	7.6	5	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene NRCAM	MGC138845, NRCAM, MGC138846, KIAA0343	neuronal cell adhesion molecule	NM_001037132, NM_005010, NM_001193582, NM_001193583, NM_001193584, hCT2305461.0, hCT2356392.0, hCT8159.3, hCT1953973.1	204105_s_at, 216959_x_at	NP_001032209.1, NP_005001.3, NP_001180511.1, NP_001180512.1, NP_001180513.1, EAW83430.1, EAW83427.1, EAW83428.1, EAW83429.1
GeneID.50640	PNPLA8	7	108,112,071	108,166,638	54,567	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7278	-210	upstream	0	1	0	15	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene PNPLA8	PNPLA8, IPLA2-2, IPLA2(GAMMA), IPLA2G	patatin-like phospholipase domain containing 8	NM_015723, hCT2356402.0, hCT2356403.0, hCT2356404.0, hCT8164.3	223309_x_at, 223310_x_at, 223982_s_at	NP_056538.1, EAW83433.1, EAW83432.1, EAW83434.1, EAW83435.1
GeneID.168451	THAP5	7	108,202,671	108,210,167	7,496	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5051, 2_A375_pNL97_plus_lncRNA_AR..1..7279, 4_A375_EGR1..1..7453	-169, -41, -425	upstream, upstream, upstream	1	1	1	16	19	20	1	4_A375_EGR1..1	20	Gene THAP5	DKFZp313O1132, THAP5	THAP domain containing 5	NM_001130475, NM_182529, hCT2304826.0, hCT2349616.0	227636_at, 244190_at	NP_001123947.1, NP_872335.2, EAW83436.1, EAW83437.1
GeneID.4189	DNAJB9	7	108,210,356	108,215,294	4,938	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5051, 2_A375_pNL97_plus_lncRNA_AR..1..7279, 4_A375_EGR1..1..7453	-20, -148, 236	upstream, upstream, in gene	1	1	1	16	19	20	1	4_A375_EGR1..1	20	Gene DNAJB9	MST049, MSTP049, ERdj4, DNAJB9, DKFZp564F1862, MDG1, MDG-1	DnaJ (Hsp40) homolog, subfamily B, member 9	NM_012328, hCT2304807.0, hCT8161.2, hCT1981686.0, hCT1981687.0	1554462_a_at, 202842_s_at, 202843_at	NP_036460.1, EAW83439.1, EAW83438.1, EAW83440.1, EAW83441.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:83943	IMMP2L	7	110,303,110	111,202,347	899,237	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5052	-357	upstream	1	0	0	16	11	10	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene IMMP2L	IMMP2L, IMP2-LIKE, IMP2	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	NM_032549, hCT2344102.0, hCT2344103.0, hCT2344104.0, hCT2344105.0	1555571_at, 227153_at	NP_115938.1, EAW83445.1, EAW83444.1, EAW83446.1, EAW83447.1
GeneID:9732	DOCK4	7	111,366,164	111,846,462	480,298	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5053, 2_A375_pNL97_plus_lncRNA_AR..1..7280, 2_A375_pNL97_plus_lncRNA_AR..1..7281	-66, 205198, -2	upstream, in gene, upstream	1	1	0	14.5	19	8	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene DOCK4	MGC134912, KIAA0716, FLJ34238, MGC134911, DOCK4	dedicator of cytokinesis 4	NM_014705, hCT2305066.0, hCT2305067.0, hCT2305068.0, hCT2305069.0, hCT2305070.0, hCT2305072.0	1558891_a_at, 205003_at, 241313_at, 244840_x_at	NP_055520.3, EAW83452.1, EAW83451.1, EAW83453.1, EAW83454.1, EAW83455.1, EAW83456.1
GeneID:11179	ZNF277	7	111,846,643	111,983,989	137,346	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5053, 2_A375_pNL97_plus_lncRNA_AR..1..7281	-115, -179	upstream, upstream	1	1	0	19	23	14	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ZNF277	NRIF4, ZNF277, ZNF277P	zinc finger protein 277	NM_021994, hCT2304966.0, hCT2356416.0, hCT5774.3, hCT1981879.1, hCT1966253.1	1555192_at, 1555193_a_at, 215887_at, 216645_at	NP_068834.2, EAW83457.1, EAW83458.1, EAW83459.1, EAW83460.1, EAW83461.1
GeneID:3475	IFRD1	7	112,063,226	112,116,247	53,021	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5054, 1_A375_pNL7_minus_lncRNA_AR..1..5055, 2_A375_pNL97_plus_lncRNA_AR..1..7282, 2_A375_pNL97_plus_lncRNA_AR..1..7283	27870, 58638, 27206, 61734	in gene, downstream, in gene, downstream	1	1	0	15.33	17	6.67	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene IFRD1	TIS7, PC4, IFRD1	interferon-related developmental regulator 1	NM_001550, NM_001007245, hCT2304958.0, hCT6798.3	202146_at, 202147_s_at	NP_001541.2, NP_001007246.1, EAW83462.1, EAW83463.1
GeneID:286006	C7orf53	7	112,120,908	112,130,943	10,035	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5055, 2_A375_pNL97_plus_lncRNA_AR..1..7283	1156, 4052	in gene, in gene	1	1	0	12.5	13	3	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene C7orf53	MGC161427, C7orf53, MGC163440, FLJ39575, MGC42850	chromosome 7 open reading frame 53	NM_182597, NM_001134468, hCT2304960.0, hCT2349817.0	1569852_at, 239203_at	NP_872403.1, NP_001127940.1, EAW83464.1, EAW83465.1
GeneID:64418	TMEM168	7	112,405,787	112,430,478	24,691	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5056, 4_A375_EGR1..1..7455	462, 78	in gene, in gene	1	0	1	19	12	20	1	4_A375_EGR1..1	20	Gene TMEM168	TMEM168, DKFZp564C012, FLJ13576	transmembrane protein 168	NM_022484, hCT2356470.0, hCT6795.3, hCT1807969.1	218962_s_at, 234726_s_at	NP_071929.3, EAW83472.1, EAW83470.1, EAW83471.1
GeneID:401397	LOC401397	7	112,756,773	112,758,637	1,864	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7284	-179	upstream	0	1	0	13	14	7	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene LOC401397	MGC104490	hypothetical LOC401397	NR_024412, NR_015442	224723_x_at	
GeneID:93986	FOXP2	7	113,726,365	114,333,827	607,462	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7286	299427	in gene	0	1	0	7	14	10	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene FOXP2	SPCH1, FOXP2, TNRC10, DKFZp686H1726, CAGH44	forkhead box P2	NM_001172766, NM_001172767, NM_014491, NM_148898, NM_148899, NM_148900, NR_033766, NR_033767, hCT2304975.0, hCT2304976.0, hCT2304977.0, hCT2356425.0, hCT2356426.0, hCT2356427.0, hCT2356428.0, hCT1813365.1	1552902_a_at, 1555352_at, 1555516_at, 1555647_a_at, 1555648_at, 1562139_a_at, 1564676_s_at	NP_001166237.1, NP_001166238.1, NP_055306.1, NP_683696.2, NP_683698.2, NP_683697.2, EAW83479.1, EAW83480.1, EAW83481.1, EAW83482.1, EAW83483.1, EAW83484.1, EAW83485.1, EAW83486.1
GeneID:857	CAV1	7	116,164,839	116,201,239	36,400	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5061, 2_A375_pNL97_plus_lncRNA_AR..1..7289	1849, 1785	in gene, in gene	1	1	0	27	19	9	1	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene CAV1	CAV1, BSCL3, CGL3, CAV, MSTP085, VIP21	caveolin 1, caveolae protein, 22kDa	NM_001753, NM_001172895, NM_001172896, NM_001172897, hCT2305358.0, hCT30335.3, hCT1962974.1	203065_s_at, 212097_at	NP_001744.2, NP_001166366.1, NP_001166367.1, NP_001166368.1, EAW83503.1, EAW83504.1, EAW83505.1
GeneID:4233	MET	7	116,312,459	116,438,440	125,981	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5064, 1_A375_pNL7_minus_lncRNA_AR..1..5065	44293, 104117	in gene, in gene	1	0	0	18	14.5	8	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene MET	RCCP2, HGFR, MET, c-Met, AUTS9	met proto-oncogene (hepatocyte growth factor receptor)	NM_000245, NM_001127500, hCT2305360.0, hCT2305362.0, hCT2305363.0, hCT2356398.0, hCT29949.3	203510_at, 211599_x_at, 213807_x_at, 213816_s_at	NP_000236.2, NP_001120972.1, EAW83508.1, EAW83509.1, EAW83510.1, EAW83511.1, EAW83507.1
GeneID:830	CAPZA2	7	116,502,563	116,559,313	56,750	+	1	4_A375_EGR1..1..7457	157	in gene	0	0	1	13	16	15	1	4_A375_EGR1..1	15	Gene CAPZA2	CAPPA2, CAPZ, CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2	NM_006136, hCT1971516.1, hCT2305342.0, hCT29119.1, hCT1962970.0	1569450_at, 201237_at, 201238_s_at	NP_006127.1, EAW83514.1, EAW83512.1, EAW83513.1, EAW83515.1
GeneID:93653	ST7OT1	7	116,592,500	116,594,388	1,888	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5066	66	in gene	1	0	0	15	13	3	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene ST7OT1	ST7AS1, ST7OT1	ST7 overlapping transcript 1 (non-protein coding)	NR_002330	1555912_at	
GeneID:7982	ST7	7	116,593,381	116,870,077	276,696	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5066	939	in gene	1	0	0	15	13	3	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene ST7	DKFZp762O2113, HELG, FAM4A, ETS7q, FAM4A1, RAY1, ST7, TSG7, SEN4	suppression of tumorigenicity 7	NM_021908, NM_018412, hCT2305155.0, hCT2305157.0, hCT2305156.0, hCT2305160.0, hCT6965.3, hCT1952565.1	207524_at, 207871_s_at	NP_068708.1, NP_060882.2, EAW83518.1, EAW83519.1, EAW83520.1, EAW83521.1, EAW83516.1, EAW83517.1
GeneID:338069	ST7OT4	7	116,593,953	116,599,867	5,914	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5066	367	in gene	1	0	0	15	13	3	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene ST7OT4	NCRNA00042, ST7OT4	ST7 overlapping transcript 4 (non-protein coding)	NR_002329	1559208_at	
GeneID:7472	WNT2	7	116,916,685	116,963,343	46,658	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5067, 2_A375_pNL97_plus_lncRNA_AR..1..7291, 4_A375_EGR1..1..7458	53711, 53711, -721	downstream, downstream, upstream	1	1	1	17.5	13.5	11	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene WNT2	WNT2, INT1L1, IRP	wingless-type MMTV integration site family member 2	NM_003391, NR_024047, hCT5668.3	205648_at	NP_003382.1, EAW83525.1
GeneID:1080	CFTR	7	117,120,017	117,308,719	188,702	+	1	4_A375_EGR1..1..7459	116335	in gene	0	0	1	7	5	19	1	4_A375_EGR1..1	19	Gene CFTR	ABCC7, MRP7, TNR-CFTR, dJ760C5.1, CFTR/MRP, CFTR, CF, ABC35	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	NM_000492, hCT2305162.0, hCT2305163.0, hCT6982.2	205043_at, 215702_s_at, 215703_at, 217026_at, 234702_x_at, 234706_x_at	NP_000483.3, EAW83529.1, EAW83530.1, EAW83531.1
GeneID:54556	ING3	7	120,590,817	120,615,711	24,894	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5068, 2_A375_pNL97_plus_lncRNA_AR..1..7292	-97, -97	upstream, upstream	1	1	0	22	22	11	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene ING3	FLJ20089, ING3, p47ING3, MEAF4, Eaf4, ING2	inhibitor of growth family, member 3	NM_019071, NM_198267, hCT2305177.0, hCT2305179.0, hCT2305180.0, hCT24278.3	205070_at, 231883_at, 242293_at	NP_061944.2, NP_938008.1, EAW83546.1, EAW83547.1, EAW83548.1, EAW83549.1
GeneID:79974	C7orf58	7	120,628,751	120,937,498	308,747	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5069	216081	in gene	1	0	0	15	11	1	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene C7orf58	FLJ21986, FLJ26813, C7orf58	chromosome 7 open reading frame 58	NM_024913, NM_001105533, hCT2305181.0, hCT2305185.0, hCT2356471.0, hCT1958418.1, hCT1958419.1, hCT1958420.1	220032_at, 228728_at	NP_079189.4, NP_001099003.1, EAW83550.1, EAW83552.1, EAW83554.1, EAW83555.1, EAW83551.1, EAW83553.1
GeneID:10447	FAM3C	7	120,988,905	121,036,422	47,517	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5070, 2_A375_pNL97_plus_lncRNA_AR..1..7293	-10, -56	upstream, upstream	1	1	0	26	41	7	1	2_A375_pNL97_plus_lncRNA_AR..1	41	Gene FAM3C	GS3786, FAM3C, ILEI	family with sequence similarity 3, member C	NM_014888, NM_001040020, hCT23515.3	201889_at, 236316_at, 240082_at	NP_055703.1, NP_001035109.1, EAW83558.1
GeneID:10157	AASS	7	121,713,598	121,784,344	70,746	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5071	120	in gene	1	0	0	15	14	10	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene AASS	AASS, LKRSDH, LORSDH, LKR/SDH	aminoadipate-semialdehyde synthase	NM_005763, hCT2305311.0, hCT24806.3	210852_s_at, 214829_at	NP_005754.2, EAW83564.1, EAW83565.1
GeneID:4698	NDUFA5	7	123,181,083	123,197,958	16,875	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5072, 2_A375_pNL97_plus_lncRNA_AR..1..7295	70, 70	in gene, in gene	1	1	0	29	24	7	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene NDUFA5	FLJ12147, NDUFA5, B13, UQOR13, DKFZp781K1356, CI-13kB, CI-13KD-B, NUFM	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	NM_005000, hCT1971475.1, hCT2305321.0, hCT2305323.0, hCT2305326.0, hCT1817741.2, hCT1982955.1, hCT1982956.2	201304_at, 215850_s_at	NP_004991.1, EAW83590.1, EAW83587.1, EAW83588.1, EAW83591.1, EAW83592.1, EAW83589.1, EAW83593.1
GeneID:8976	WASL	7	123,321,997	123,389,116	67,119	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5073, 2_A375_pNL97_plus_lncRNA_AR..1..7296, 4_A375_EGR1..1..7461	60, 252, 220	in gene, in gene, in gene	1	1	1	18	19	23	1	4_A375_EGR1..1	23	Gene WASL	WASL, DKFZp779G0847, NWASP, MGC48327, N-WASP	Wiskott-Aldrich syndrome-like	NM_003941, hCT24112.4	205809_s_at, 205810_s_at, 224813_at, 230340_s_at	NP_003932.3, EAW83599.1
GeneID:730130	TMEM229A	7	123,670,970	123,673,523	2,553	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7297	723	in gene	0	1	0	14	18	16	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TMEM229A	MGC189723, TMEM229A	transmembrane protein 229A	NM_001136002		NP_001129474.1
GeneID:2861	GPR37	7	124,386,114	124,405,681	19,567	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5075, 2_A375_pNL97_plus_lncRNA_AR..1..7299	-175, -239	upstream, upstream	1	1	0	16	22	12	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene GPR37	GPR37, EDNRBL, hET(B)R-LP, PAELR	G protein-coupled receptor 37 (endothelin receptor type B-like)	NM_005302, hCT23509.3	209631_s_at, 214586_at	NP_005293.1, EAW83613.1
GeneID:2918	GRM8	7	126,078,652	126,892,428	813,776	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5077, 1_A375_pNL7_minus_lncRNA_AR..1..5078, 2_A375_pNL97_plus_lncRNA_AR..1..7302, 4_A375_EGR1..1..7463	144556, -1524, 144524, 316	in gene, upstream, in gene, in gene	1	1	1	22	24.33	9.67	3	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene GRM8	GLUR8, MGLUR8, GPRC1H, MGC126724, GRM8, mGlu8, FLJ41058	glutamate receptor, metabotropic 8	NM_000845, NM_001127323, NR_028041, hCT2305308.0, hCT2356454.0, hCT2356455.0, hCT1952026.1	216255_s_at, 216256_at, 216992_s_at	NP_000836.2, NP_001120795.1, EAW83621.1, EAW83622.1, EAW83623.1, EAW83624.1
GeneID:168850	ZNF800	7	127,010,353	127,032,767	22,414	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7303, 2_A375_pNL97_plus_lncRNA_AR..1..7304	639, -289	in gene, upstream	0	1	0	14	15.5	6.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene ZNF800	MGC130032, ZNF800, MGC130033, FLJ43301	zinc finger protein 800	NM_176814, hCT2305845.0, hCT2305846.0, hCT2305847.0	227101_at, 227104_x_at	NP_789784.2, EAW83625.1, EAW83626.1, EAW83627.1
GeneID:100506682	LOC100506682	7	127,116,932	127,125,858	8,926	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7305	-2292	upstream	0	1	0	15	23	3	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100506682		hypothetical LOC100506682	XR_113056, XR_110741, XR_108605, XR_114066		
GeneID:27044	SND1	7	127,292,202	127,732,659	440,457	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5079, 2_A375_pNL97_plus_lncRNA_AR..1..7306	-426, -266	upstream, upstream	1	1	0	18	15	12	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene SND1	TDRD11, SND1, p100	staphylococcal nuclease and tudor domain containing 1	NM_014390, hCT2305516.0, hCT23514.4, hCT1980571.2	201622_at	NP_055205.2, EAW83635.1, EAW83636.1, EAW83637.1
GeneID:55131	RBM28	7	127,950,436	127,983,962	33,526	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7309	74	in gene	0	1	0	16	23	12	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RBM28	RBM28, FLJ10377	RNA binding motif protein 28	NM_018077, NM_001166135, hCT2305629.0, hCT24198.3	218593_at	NP_060547.2, NP_001159607.1, EAW83643.1, EAW83644.1
GeneID:401399	PRRT4	7	127,990,379	128,001,739	11,360	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7309, 4_A375_EGR1..1..7466	17851, 763	downstream, in gene	0	1	1	12.5	15	14	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene PRRT4	PRRT4	proline-rich transmembrane protein 4	NM_001114726, NM_001174164		NP_001108198.2, NP_001167635.1
GeneID:29923	C7orf68	7	128,095,884	128,098,472	2,588	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7310, 4_A375_EGR1..1..7467	212, 198	in gene, in gene	0	1	1	13	16	22	1	4_A375_EGR1..1	22	Gene C7orf68	HIG2, MGC138388, C7orf68, FLJ21076, HIG-2	chromosome 7 open reading frame 68	NM_001098786, NM_013332, hCT2305880.0, hCT2305881.0, hCT24195.2	1554452_a_at, 218507_at	NP_001092256.1, NP_037464.1, EAW83854.1, EAW83855.1, EAW83856.1
GeneID:55798	METTL2B	7	128,116,783	128,142,978	26,195	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7311	49	in gene	0	1	0	13	19	12	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene METTL2B	PSENIP1, METTL2B, METTL2A, METL, FLJ12760, METTL2, FLJ11350	methyltransferase like 2B	NM_018396		NP_060866.2
GeneID:84691	FAM71F1	7	128,355,443	128,371,797	16,354	+	1	4_A375_EGR1..1..7468	24189	downstream	0	0	1	13	16	21	1	4_A375_EGR1..1	21	Gene FAM71F1	FAM71F1, FAM137A, NYD-SP18	family with sequence similarity 71, member F1	NM_032599	231466_at, 236214_at	NP_115988.1
GeneID:813	CALU	7	128,379,346	128,411,531	32,185	+	1	4_A375_EGR1..1..7468	288	in gene	0	0	1	13	16	21	1	4_A375_EGR1..1	21	Gene CALU	FLJ90608, CALU	calumenin	NM_001219, NM_001130674, hCT2305897.0, hCT2305899.0, hCT2356466.0, hCT2356467.0, hCT32928.4, hCT1816563.1	200755_s_at, 200756_x_at, 200757_s_at, 214845_s_at, 238908_at	NP_001210.1, NP_001124146.1, EAW83675.1, EAW83676.1, EAW83678.1, EAW83679.1, EAW83674.1, EAW83677.1
GeneID:64753	CCDC136	7	128,432,099	128,462,183	30,084	+	1	4_A375_EGR1..1..7469	39293	downstream	0	0	1	6	3	16	1	4_A375_EGR1..1	16	Gene CCDC136	CCDC136, NAG6, MGC129657, MGC176632, DKFZp434G156	coiled-coil domain containing 136	NM_022742, hCT2305900.0, hCT2305901.0, hCT2305902.0, hCT2305904.0, hCT2305905.0, hCT2356419.0, hCT2356420.0, hCT32937.2	226971_at, 226972_s_at, 232969_s_at	NP_073579.3, EAW83686.1, EAW83681.1, EAW83683.1, EAW83687.1, EAW83688.1, EAW83682.1, EAW83684.1, EAW83685.1
GeneID:2318	FLNC	7	128,470,483	128,499,328	28,845	+	2	4_A375_EGR1..1..7469, 4_A375_EGR1..1..7470	909, 18317	in gene, in gene	0	0	1	5	5.5	16.5	2	4_A375_EGR1..1	17	Gene FLNC	FLJ10186, ABP-280, ABPL, ABPA, ABP280A, FLNC, FLN2	filamin C, gamma	NM_001458, NM_001127487, hCT2356464.0, hCT2356465.0, hCT32927.3	207876_s_at	NP_001449.3, NP_001120959.1, EAW83689.1, EAW83690.1, EAW83691.1
GeneID:23534	TNPO3	7	128,594,234	128,695,227	100,993	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5080, 2_A375_pNL97_plus_lncRNA_AR..1..7312	59, 219	in gene, in gene	1	1	0	20	24	11	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene TNPO3	TRN-SR, TRN-SR2, TRNSR, TNPO3, MTR10A, IPO12	transportin 3	NM_012470, NM_001191028, NR_034053, hCT2305969.0, hCT2305971.0, hCT32936.3	212317_at, 212318_at, 214550_s_at	NP_036602.1, NP_001177957.2, EAW83708.1, EAW83709.1, EAW83710.1
GeneID:100127891	LOC100127891	7	129,232,744	129,251,495	18,751	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7313	-41	upstream	0	1	0	13	20	11	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100127891		hypothetical LOC100127891	XR_113053, XR_110746, XR_108612, XR_114091		
GeneID:4899	NRF1	7	129,251,555	129,396,922	145,367	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7313, 4_A375_EGR1..1..7471	-19, 150797	upstream, downstream	0	1	1	8.5	12	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene NRF1	NRF1, ALPHA-PAL	nuclear respiratory factor 1	NM_005011, NM_001040110, hCT2307025.0, hCT2356400.0, hCT2356401.0, hCT1951448.2, hCT1966589.1, hCT1966590.1	204651_at, 204652_s_at, 211279_at, 211280_s_at	NP_005002.3, NP_001035199.1, EAW83726.1, EAW83727.1, EAW83729.1, EAW83730.1, EAW83728.1, EAW83731.1
GeneID:406958	MIR182	7	129,410,223	129,410,332	109	-	2	4_A375_EGR1..1..7471, 4_A375_EGR1..1..7472	7980, -10132	downstream, upstream	0	0	1	5.5	7.5	16.5	2	4_A375_EGR1..1	17	Gene MIR182	miRNA182, MIRN182, MIR182	microRNA 182	NR_029614		
GeneID:407053	MIR96	7	129,414,532	129,414,609	77	-	1	4_A375_EGR1..1..7472	-5655	upstream	0	0	1	7	11	17	1	4_A375_EGR1..1	17	Gene MIR96	hsa-mir-96, miRNA96, MIRN96, DFNA50, MIR96, mir-96	microRNA 96	NR_029512		
GeneID:406959	MIR183	7	129,414,745	129,414,854	109	-	1	4_A375_EGR1..1..7472	-5810	upstream	0	0	1	7	11	17	1	4_A375_EGR1..1	17	Gene MIR183	miR-183, miRNA183, MIRN183, MIR183	microRNA 183	NR_029615		
GeneID:51530	ZC3HC1	7	129,658,126	129,691,233	33,107	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5081, 2_A375_pNL97_plus_lncRNA_AR..1..7315, 4_A375_EGR1..1..7473	40665, 41025, 34305	downstream, downstream, downstream	1	1	1	12.5	12.5	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ZC3HC1	ZC3HC1, NIPA, 1110054L24Rik, FBXO50, HSPC216	zinc finger, C3HC-type containing 1	NM_016478, hCT2307934.0, hCT2307936.0, hCT2356453.0, hCT1818287.3, hCT1966559.1, hCT1966560.1	223163_s_at	NP_057562.3, EAW83743.1, EAW83738.1, EAW83739.1, EAW83740.1, EAW83741.1, EAW83742.1
GeneID:23008	KLHDC10	7	129,710,349	129,775,560	65,211	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5082, 2_A375_pNL97_plus_lncRNA_AR..1..7316	-173, -141	upstream, upstream	1	1	0	44	34	10	1	1_A375_pNL7_minus_lncRNA_AR..1	44	Gene KLHDC10	KIAA0265, slim, KLHDC10	kelch domain containing 10	NM_014997, hCT1969287.1, hCT2356415.0, hCT10034.4	209254_at, 209255_at, 209256_s_at, 210111_s_at, 242746_at	NP_055812.1, EAW83746.1, EAW83744.1, EAW83745.1
GeneID:1358	CPA2	7	129,906,703	129,929,638	22,935	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7317	12669	in gene	0	1	0	13	16	6	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CPA2	CPA2	carboxypeptidase A2 (pancreatic)	NM_001869, hCT8499.3	206212_at	NP_001860.2, EAW83751.1
GeneID:93979	CPA5	7	129,984,630	130,008,571	23,941	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5083, 4_A375_EGR1..1..7474	12458, 19754	in gene, in gene	1	0	1	10.5	10.5	11	2	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene CPA5	FLJ35989, CPA5	carboxypeptidase A5	NM_080385, NM_001127441, NM_001127442, hCT2307046.0, hCT2307047.1, hCT2356447.0, hCT2356448.0, hCT2356449.0, hCT2356450.0, hCT1640572.4	240744_at	NP_525124.3, NP_001120913.1, NP_001120914.1, EAW83754.1, EAW83756.1, EAW83758.1, EAW83755.1, EAW83757.1, EAW83759.1, EAW83760.1





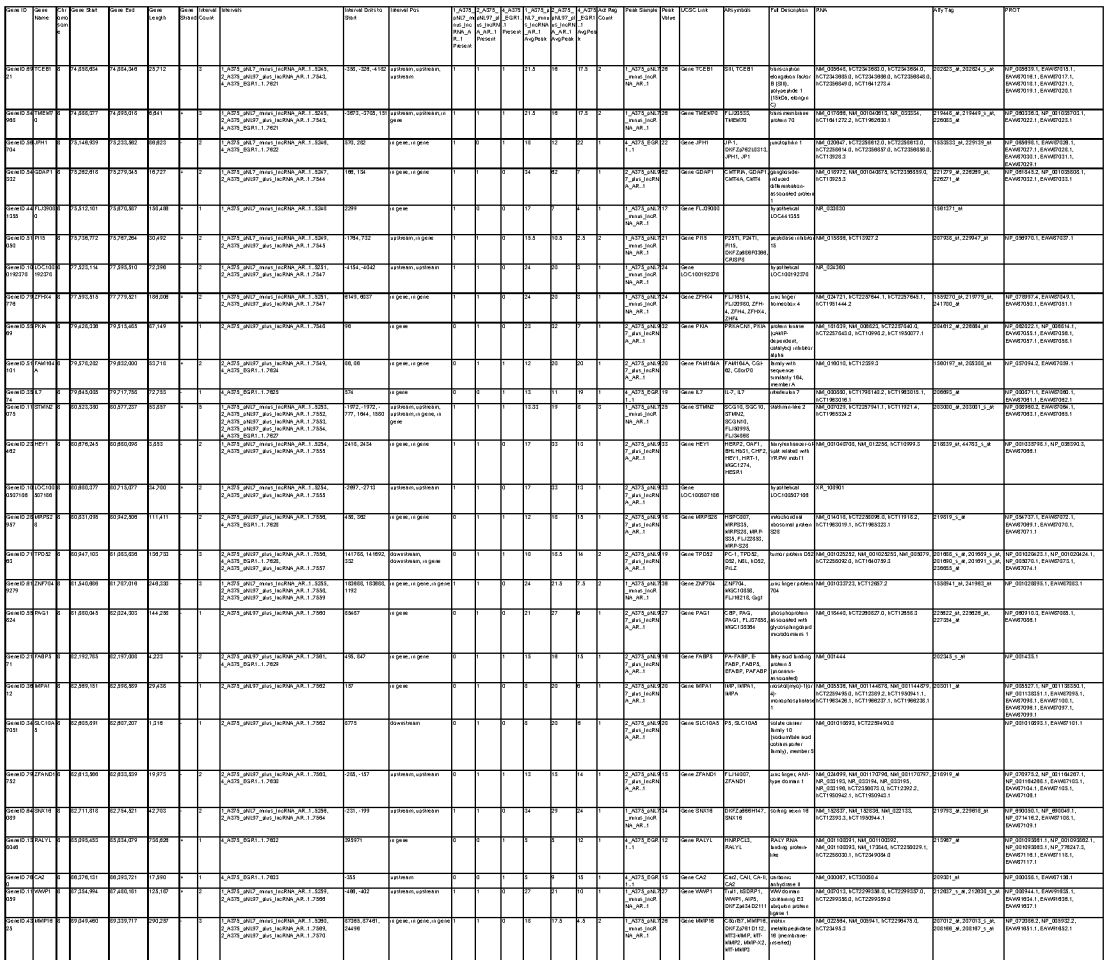
Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_pAG7_mrna_lncRNA_AR_1 Percent	2_A375_pAG7_mrna_lncRNA_AR_1 Percent	3_A375_pAG7_mrna_lncRNA_AR_1 Percent	4_A375_pAG7_mrna_lncRNA_AR_1 Percent	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Affy Tag	PROT
GeneID:85 42	SSBP1	7	141,436,178	141,490,237	12,061	+	2	1_A375_pAG7_mrut_lncRNA_AR_1:5116, 2_A375_pAG37_plus_lncRNA_AR_1:7367				1	1	0	46	80	14	1	2_A375_pAG:80 7_plus_lncRNA_AR_1	SSBP1	single-stranded DNA binding protein 1	ssDSB, SSBP1, SSBP-1, SSBP, MI-SSB	NM_003143, NCT03839784, 0, NCT03357796, 0, NCT03439047, 0, NCT03439048 0	1563442_a_at, 202891_s_at, 214090_at	NP_003134.1, ENSP0000, 1, ENSP0000, 1, ENSP0000, 1, ENSP0000, 1
GeneID:85 57	TRBJ	7	141,996,551	142,010,972	13,121	+	2	1_A375_pAG7_mrut_lncRNA_AR_1:5119, 2_A375_pAG37_plus_lncRNA_AR_1:7368				1	1	0	16	24	7	1	2_A375_pAG:24 7_plus_lncRNA_AR_1	TRBJ	T cell receptor beta locus	TRB, TRBJ@, TCR@			
GeneID:28 614	TRBV5 1	7	142,020,094	142,021,093	999	+	2	1_A375_pAG7_mrut_lncRNA_AR_1:5119, 2_A375_pAG37_plus_lncRNA_AR_1:7368				1	1	0	16	24	7	1	2_A375_pAG:24 7_plus_lncRNA_AR_1	TRBV5-1	T cell receptor beta variable 5-1	TCRBV5S1A1T, TCRBV5S1, TRBV5-1, TRBV5S1			
GeneID:28 606	TRBV6 1	7	142,026,176	142,026,810	634	+	2	1_A375_pAG7_mrut_lncRNA_AR_1:5119, 2_A375_pAG37_plus_lncRNA_AR_1:7368				1	1	0	16	24	7	1	2_A375_pAG:24 7_plus_lncRNA_AR_1	TRBV6-1	T cell receptor beta variable 6-1	TCRBV6S1, TCRBV6S1A1, TRBV6-1			
GeneID:28 9238	TNS2	7	142,919,172	142,920,143	971	+	1	2_A375_pAG37_plus_lncRNA_AR_1:7369		-5798	upstream	0	0	0	9	19	4	1	2_A375_pAG:19 7_plus_lncRNA_AR_1	TNS2	tensin 2	TENS2, DFNB8, KIAA1288, KIAA1288L, TNS2-PAK1, TNS2-PAK1, TNS2	NM_178022	1553398_at	NP_783863.1
GeneID:10 3932	TMEM1 39	7	142,992,065	142,993,141	1,076	+	3	1_A375_pAG37_plus_lncRNA_AR_1:7370, 2_A375_pAG37_plus_lncRNA_AR_1:7371, 3_A375_pAG37_plus_lncRNA_AR_1:7372		2929, 3937, 3961	cg gene, downstream, downstream	0	1	1	13.5	16	15.5	2	4_A375_EGFR 1_1	20	Gene TMEM139	TMEM139, FLJ90586	transmembrane protein 139	NM_152343, NCT02852238 2, NCT03494471, NCT03494489 1, NCT02852502 0	227753_at, 229684_at	NP_689776.1, ENSP0001, 1, ENSP0001, 1, ENSP0001, 1, ENSP0001, 1
GeneID:28 41	CASP2	7	142,998,402	143,054,765	19,363	+	3	1_A375_pAG37_plus_lncRNA_AR_1:7370, 2_A375_pAG37_plus_lncRNA_AR_1:7371, 3_A375_pAG37_plus_lncRNA_AR_1:7372		-410, 186, 282	upstream, cg gene, cg gene	0	1	1	13.5	16	15.5	2	4_A375_EGFR 1_1	20	Gene CASP2	ICH-1/ICH-1L, CASP2, NEDD2, NEDD2-like caspase, ICH-1, ICH-1L, CASP-2	activator 2, apoptosis-related cysteine peptidase	NM_032982, NM_032982	206893_s_at, 209611_at, 209612_s_at, 211144_s_at, 226932_at, 226936_s_at, 244449_at	NP_116784.2, NP_116786.2
GeneID:10 0507937	LOC1003 907937	7	143,018,343	143,077,388	1,340	-	2	2_A375_pAG37_plus_lncRNA_AR_1:7372, 4_A375_EGFR_1:7491		-396, -426	upstream, upstream	0	1	1	12	23	14	1	2_A375_pAG:23 7_plus_lncRNA_AR_1	Gene LOC100507937	hypothetical LOC100507937		XR_93763		
GeneID:72 91	ZYX	7	143,078,390	143,088,204	9,844	+	2	2_A375_pAG37_plus_lncRNA_AR_1:7372, 4_A375_EGFR_1:7491		-378, -344	upstream, upstream	0	1	1	12	23	14	1	2_A375_pAG:23 7_plus_lncRNA_AR_1	Gene ZYX	ZYX, ESP-2, HES-2	zyxin	NM_003461, NM_001010972, NCT02362377, 0, NCT02662436, 0, NCT02825909, 0, NCT03539, 0	200808_s_at, 215708_s_at	NP_003452.1, NP_001010972.1, ENSP0001, ENSP0001, ENSP0001, ENSP0001
GeneID:28 41	EPHA1	7	143,088,355	143,106,565	17,760	-	1	2_A375_pAG37_plus_lncRNA_AR_1:7372		29801	downstream	0	0	0	12	23	14	1	2_A375_pAG:23 7_plus_lncRNA_AR_1	Gene EPHA1	EPHT, EPH, EPHT1, EPHT1, HEK, MGC161991	EPH receptor A1	NM_005232, NCT02827217, 0, NCT02702716, 0, NCT17993	203977_s_at, 213804_at	NP_005223.4, ENSP0001, ENSP0001, ENSP0001
GeneID:97 47	FAM115 A	7	143,530,049	143,599,172	69,123	-	1	4_A375_EGFR_1:7492		2798	cg gene	0	0	1	14	13	16	1	4_A375_EGFR 1_1	16	Gene FAM115A	KIAA0702, FLJ38702, FAM115A	family with sequence similarity 115, member A	NM_014719, NCT01774579, 1	204405_x_at, 212979_s_at, 212981_s_at	
GeneID:27 0110	TPK1	7	144,149,654	144,532,148	384,112	-	2	1_A375_pAG7_mrut_lncRNA_AR_1:5120, 2_A375_pAG37_plus_lncRNA_AR_1:7373		56, 29	upstream, cg gene	1	1	0	22	45	11	1	2_A375_pAG:45 7_plus_lncRNA_AR_1	Gene TPK1	PP20, TPK1, HTPK1	thiamin pyrophosphokinase 1	NM_022445, NM_001043482, NCT02842216, 0, NCT01774722 2, e 1	221216_s_at, 223989_at	NP_071990.2, NP_001035947.1, ENSP0001, ENSP0001
GeneID:26 047	CNTNAP2	7	145,810,453	145,110,090	2,304,637	+	3	1_A375_pAG7_mrut_lncRNA_AR_1:5123, 2_A375_pAG37_plus_lncRNA_AR_1:7376, 3_A375_pAG37_plus_lncRNA_AR_1:7376		-332, -397, 17117,99	upstream, upstream, cg gene	0	1	0	14.5	26.5	6.5	2	2_A375_pAG:26 7_plus_lncRNA_AR_1	Gene CNTNAP2	DKFZp781D1644, PTHS1, AUTS15, CASPR2, CDFS, KIAA0, CNTNAP2	contactin associated protein-like 2	NM_014141, NCT02841921, 1, NCT02842179 0, 1, NCT02842205 1	215145_s_at, 219302_s_at, 219381_s_at, 219382_s_at	NP_0549551, ENSP0000, ENSP0000, ENSP0000
GeneID:80 90	RNY5	7	145,838,560	145,838,683	83	+	2	1_A375_pAG7_mrut_lncRNA_AR_1:5124, 2_A375_pAG37_plus_lncRNA_AR_1:7379		-338, -438	upstream, upstream	1	1	0	16	16	17	1	2_A375_pAG:16 7_plus_lncRNA_AR_1	Gene RNY5	Y5, RNY5	RNA, Ro-associated Y5	NR_001571		
GeneID:80 53	RNY3	7	145,850,547	145,850,945	101	+	3	1_A375_pAG7_mrut_lncRNA_AR_1:5125, 2_A375_pAG37_plus_lncRNA_AR_1:7378, 3_A375_pAG37_plus_lncRNA_AR_1:7380		-143, 3459, 3475	upstream, downstream, downstream	1	1	0	16	15	12.5	2	2_A375_pAG:15 7_plus_lncRNA_AR_1	Gene RNY3	Y3, RNY3, RNY3	RNA, Ro-associated Y3	NR_004392		
GeneID:80 54	RNY1	7	145,856,235	145,856,348	113	+	3	1_A375_pAG7_mrut_lncRNA_AR_1:5125, 2_A375_pAG37_plus_lncRNA_AR_1:7378, 3_A375_pAG37_plus_lncRNA_AR_1:7380		3808, 4, 20	downstream, cg gene, cg gene	1	1	0	16	15	12.5	2	2_A375_pAG:15 7_plus_lncRNA_AR_1	Gene RNY1	Y1, RNY1, HY1	RNA, Ro-associated Y1	NR_004391		
GeneID:15 6031	ZNF709	7	145,798,733	145,797,899	21,156	-	4	1_A375_pAG7_mrut_lncRNA_AR_1:5127, 2_A375_pAG37_plus_lncRNA_AR_1:7381, 3_A375_pAG37_plus_lncRNA_AR_1:7382, 4_A375_EGFR_1:7492		-24809, -24881, 197, 205	downstream, downstream, cg gene, cg gene	1	1	0	27.5	33	19	2	2_A375_pAG:33 7_plus_lncRNA_AR_1	Gene ZNF709	DKFZp781F197, MGC139120, ZNF709	zinc finger protein 709	NM_152411, NCT02859883, 0, NCT17939062, 2, NCT19647972	239063_at	NP_689824.2, ENSP0001, ENSP0001
GeneID:15 5054	ZNF425	7	145,799,878	145,822,436	23,082	-	3	1_A375_pAG7_mrut_lncRNA_AR_1:5126, 2_A375_pAG37_plus_lncRNA_AR_1:7383, 4_A375_EGFR_1:7494		-16, 14, 142	upstream, cg gene, cg gene	1	1	0	46	63	33	1	1_A375_pAG:63 7_plus_lncRNA_AR_1	Gene ZNF425	MGC135595, ZNF425	zinc finger protein 425	NM_001201681, NCT17550911, 1	233583_at, 242864_at	NP_001201681.1, ENSP0001
GeneID:15 541	ZNF396	7	145,823,593	145,838,154	99,826	+	4	1_A375_pAG7_mrut_lncRNA_AR_1:5128, 2_A375_pAG37_plus_lncRNA_AR_1:7383, 3_A375_pAG37_plus_lncRNA_AR_1:7384, 4_A375_EGFR_1:7494		-52, -64, 21604, 212	upstream, upstream, cg gene, upstream	1	1	0	31	52	19	2	1_A375_pAG:52 7_plus_lncRNA_AR_1	Gene ZNF396	ZNF396, KIAA1329, PT1-251, ZER6	zinc finger protein 396	NM_178068, NM_020751, NCT02858732, 1, NCT02944399 0, NCT02944400 0, NCT17206 2	1553019_s_at, 226302_at, 228145_s_at	NP_722527.1, NP_9585321, ENSP0001, ENSP0001, ENSP0001
GeneID:54 27	ZNF282	7	145,892,377	145,922,339	29,962	+	2	1_A375_pAG7_mrut_lncRNA_AR_1:5129, 2_A375_pAG37_plus_lncRNA_AR_1:7385		93, 63	cg gene, cg gene	1	1	0	46	70	9	1	2_A375_pAG:70 7_plus_lncRNA_AR_1	Gene ZNF282	ZNF282, HUB1	zinc finger protein 282	NM_020375, NCT02867838, 0, NCT16505758, 5	1553598_s_at, 244553_at	NP_065098.1, ENSP0001, ENSP0001
GeneID:78 5998	ZNF212	7	145,938,742	145,952,700	13,958	+	5	1_A375_pAG7_mrut_lncRNA_AR_1:5130, 2_A375_pAG7_mrut_lncRNA_AR_1:5131, 3_A375_pAG37_plus_lncRNA_AR_1:7386, 4_A375_EGFR_1:7496, 5_A375_EGFR_1:7497		770, 22854, -54, 22836, 250	upstream, downstream, upstream, downstream, cg gene	1	1	1	61.8	65	15	2	2_A375_pAG:65 7_plus_lncRNA_AR_1	Gene ZNF212	C2H2-180, MGC9707, ZNFC190, ZNFN2, ZNF212	zinc finger protein 212	NM_012396, NCT02867838, 0, NCT16501671 0	203869_at	NP_036356.2, ENSP0003, ENSP0003
GeneID:10 5507973	LOC1003 907973	7	145,959,382	145,994,403	35,141	+	5	1_A375_pAG7_mrut_lncRNA_AR_1:5131, 2_A375_pAG37_plus_lncRNA_AR_1:7387, 3_A375_pAG37_plus_lncRNA_AR_1:7388, 4_A375_EGFR_1:7497, 5_A375_EGFR_1:7498		34, 16, 20002, 32468, 33926	upstream, cg gene, cg gene, cg gene, cg gene	1	1	1	13	13.25	13.75	4	2_A375_pAG:13 7_plus_lncRNA_AR_1	Gene LOC100507973		pseudo ZNF765-like	NM_0031155577		XP_003119925.1
GeneID:23 777	ZNF777	7	149,126,454	149,136,053	29,599	+	2	1_A375_pAG7_mrut_lncRNA_AR_1:5132, 2_A375_pAG37_plus_lncRNA_AR_1:7388		309, 291	cg gene, cg gene	1	1	0	65	81	10	1	1_A375_pAG:65 7_plus_lncRNA_AR_1	Gene ZNF777	ZNF777, KIAA1203	zinc finger protein 777	NM_015994, NCT17206 3	1553172_at, 236963_at, 239887_at, 237353_at	NP_056809.2, ENSP0003, ENSP0003
GeneID:16 5344	ZNF467	7	149,481,432	149,479,295	8,843	-	1	4_A375_EGFR_1:7493		1647	cg gene	0	0	1	8	11	10	1	4_A375_EGFR 1_1	10	Gene ZNF467	EZI, ZNF467, ZNF467	zinc finger protein 467	NM_201236, NCT02369168, 0, NCT02369981, 0, NCT17209 2	213569_s_at, 214748_s_at	NP_9772151, ENSP0003, ENSP0003
GeneID:23 143	SSPO	7	149,475,151	149,531,034	57,923	+	3	1_A375_pAG7_mrut_lncRNA_AR_1:5133, 2_A375_pAG37_plus_lncRNA_AR_1:7389, 3_A375_pAG37_plus_lncRNA_AR_1:7392		29803, 33525, 51637	upstream, cg gene, cg gene, cg gene	0	1	1	5.67	5.67	13.67	3	4_A375_EGFR 1_1	17	Gene SSPO	FLJ38112, SSPO, KIAA0339, FLJ43737	SCO-spondin homolog (Bos taurus)	NM_198455	234349_at	NP_9403572
GeneID:64 5941	ZNF582	7	149,558,309	149,566,366	29,059	+	1	4_A375_EGFR_1:7504		35755	downstream	0	0	1	12	16	19	1	4_A375_EGFR 1_1	19	Gene ZNF582	KIAA0543, ZNF582, FLJ32352	zinc finger protein 582	NM_031019220	213444_at, 229838_at	NP_0010192201
GeneID:40 1431	LOC4317 401	7	149,564,763	149,570,551	6,189	-	1	4_A375_EGFR_1:7504		-313	upstream	0	0	1	12	16	19	1	4_A375_EGFR 1_1	19	Gene LOC431431	hypothetical LOC431431	NR_027040	229094_at	
GeneID:15 5049	ATP6V0E2	7	149,570,057	149,577,707	7,730	+	1	4_A375_EGFR_1:7504		1267	cg gene	0	0	1	12	16	19	1	4_A375_EGFR 1_1	19	Gene ATP6V0E2	ATP6V0E2L, ATP6V0E2, C7orf32	ATPase, H+ transporting, V0 subunit e2	NM_145230, NM_001100092, NCT02359911, 0, NCT02359902, 0, NCT02359903, 0, NCT17213 1, NCT02359904 1	213307_s_at	NP_8602852, NP_001040082, ENSP0003, ENSP0003, ENSP0003
GeneID:23 601	REPIN1	7	150,068,879	150,071,133	2,254	+	1	2_A375_pAG37_plus_lncRNA_AR_1:7391		377	cg gene	0	0	1	10	19	10	1	2_A375_pAG:19 7_plus_lncRNA_AR_1	Gene REPIN1	REPIN1, RIP60, AP4_Z1484, ZNF484	activation-induced cytidine deaminase-dependent chromosomal translocation to	NM_015450, NM_014374, NM_001099955, 1, NM_001099956	219041_s_at, 222501_s_at, 225015_s_at	NP_0375222, NP_0551892, NP_001091685.1, NP_001091615.1
GeneID:23 5971	ZNF773	7	150,078,408	150,089,719	11,312	+	3	1_A375_pAG7_mrut_lncRNA_AR_1:5134, 2_A375_pAG37_plus_lncRNA_AR_1:7391, 3_A375_pAG37_plus_lncRNA_AR_1:7393		23890, -10155, 23898	downstream, upstream, downstream	1	1	0	22.5	27.5	10	2	2_A375_pAG:28 7_plus_lncRNA_AR_1	Gene ZNF773	ZNF773, MGC33586	zinc finger protein 773	NM_173800	229228_s_at, 229294_s_at, 229921_at, 233489_at	NP_776991.2
GeneID:27 5742	Clorf96	7	150,102,640	150,109,556	6,916	+	2	1_A375_pAG7_mrut_lncRNA_AR_1:5134, 2_A375_pAG37_plus_lncRNA_AR_1:7392		-539, -556	upstream, upstream	1	1	0	25	26	10	1	2_A375_pAG:26 7_plus_lncRNA_AR_1	Gene lclorf96	FLJ12702, FLJ12702, LOC128745	family for GLI-Kruppel family member HKR1	NM_022737	223907_at, 223909_at	
GeneID:28 559	TMEM7 8B	7	150,486,078	150,496,448	10,073	-	1	4_A375_EGFR_1:7505		144	cg gene	0	0	1	3	9	17	1	4_A375_EGFR 1_1	17	Gene TMEM76B	TMEM76B, LOC100287, FLJ39614, LR6	transmembrane protein 176B	NM_2140332, NM_0011031 1, NM_0011031 2, NM_0011031 3, NM_0011031 4, NCT02885111 0, NCT02885112 0, NCT17611773 0, NCT18153493 1	229302_s_at	NP_3547393, NP_0010976 1, NP_0010976 2, NP_0010976 3, NP_0010976 4, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003
GeneID:55 566	TMEM1 76A	7	150,497,834	150,502,205	4,354	+	1	4_A375_EGFR_1:7505		430	cg gene	0	0	1	3	8	17	1	4_A375_EGFR 1_1	17	Gene TMEM176A	HCA112, GS183, TMEM176A	transmembrane protein 176A	NM_018487, NCT02857230, 0, NCT17823, 0, NCT19920151, 1, NCT19960031 1	219563_at	NP_2607372, ENSP0003, ENSP0003, ENSP0003, 1
GeneID:37 7	KCNH2	7	150,642,049	150,679,014	22,965	-	2	1_A375_pAG7_mrut_lncRNA_AR_1:5135, 2_A375_pAG37_plus_lncRNA_AR_1:7393		-6002, -6138	upstream, upstream	1	1	0	30	29	8	1	1_A375_pAG:29 7_plus_lncRNA_AR_1	Gene KCNH2	SQT1, HERG, KCNH2, ERG1, LQT2, Kv11.1, HERG1	potassium voltage-gated channel, subfamily H (eag-related), member 2	NM_000238, NM_172057, NM_172057, NM_0010 60, NCT02859936, 0, NCT02859937, 0, NCT17611 3	209362_at, 210058_s_at	NP_0002291, NP_7620381, NP_7620391, NP_7620401, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003
GeneID:40 44	NOS3	7	150,688,144	150,711,897	23,843	+	2	2_A375_pAG37_plus_lncRNA_AR_1:5135, 2_A375_pAG37_plus_lncRNA_AR_1:7393		-6925, -6992	upstream, upstream	1	1	0	30	29	8	1	1_A375_pAG:29 7_plus_lncRNA_AR_1	Gene NOS3	eNOS, ECNOS, NOS3	nitric oxide synthase 3 (endothelial cell)	NM_000603, NM_0011607 00, NM_0011607 10, NCT02859 11, NCT17735 2	205581_s_at, 221093_at	NP_0006942, NP_0011535 61, NP_0011535 62, ENSP0003, ENSP0003
GeneID:28 5970	ATG5	7	150,709,297	150,721,556	12,259	-	2	2_A375_pAG37_plus_lncRNA_AR_1:5136, 2_A375_pAG37_plus_lncRNA_AR_1:7394		-4356, -4156	upstream, upstream	1	1	0	17	19	14	1	2_A375_pAG:19 7_plus_lncRNA_AR_1	Gene ATG5	ATG5, APG5L, APG5-LIKE, MGC5245	ATG5 autophagy related 5 homolog (S. cerevisiae)	NM_175061	1553390_at, 229252_at	NP_7795524
GeneID:10 0507614	LOC1003 907614	7	150,729,510	150,731,698	16,776	+	4	1_A375_pAG7_mrut_lncRNA_AR_1:5136, 2_A375_pAG37_plus_lncRNA_AR_1:7394, 3_A375_pAG37_plus_lncRNA_AR_1:7395, 4_A375_EGFR_1:7505		3884, 3942, -4036, -4038	cg gene, cg gene, upstream, upstream	1	1	1	11.33	16	14.67	3	2_A375_pAG:16 7_plus_lncRNA_AR_1	19	Gene LOC100507614	hypothetical LOC100507614	XR_112089, XR_113008, XR_113768, XR_113769, XR_113768, XR_113768, XR_113769, XR_114110, XR_114109		
GeneID:11 794	ABCB6	7	150,735,510	150,744,089	19,259	+	7	1_A375_pAG7_mrut_lncRNA_AR_1:5136, 2_A375_pAG7_mrut_lncRNA_AR_1:5137, 3_A375_pAG37_plus_lncRNA_AR_1:7394, 4_A375_pAG37_plus_lncRNA_AR_1:7395, 5_A375_pAG37_plus_lncRNA_AR_1:7396, 6_A375_pAG37_plus_lncRNA_AR_1:7397, 7_A375_EGFR_1:7506		292, 29650, 254, 19352, 29686, 12714, 20232	cg gene, downstream, cg gene, cg gene, downstream, cg gene, downstream	1	1	1	12.4	18.4	14.4	5	2_A375_pAG:18 7_plus_lncRNA_AR_1	26	Gene ABCB6	ABC6, MTABC3, ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	NM_005166, NCT02545830, 0, NCT02563630, 0, NCT02439031 0, NCT02439032, 0, NCT02439033, 0, NCT02439034, 0, NCT02439035 0, NCT02439036 0, NCT02439037 0, NCT17543, 2, NCT19320011 1	208317_s_at	NP_5991102, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003
GeneID:11 11	ACCN2	7	150,743,693	150,749,843	6,230	+	7	1_A375_pAG7_mrut_lncRNA_AR_1:5137, 2_A375_pAG37_plus_lncRNA_AR_1:7395, 3_A375_pAG37_plus_lncRNA_AR_1:7396, 4_A375_pAG37_plus_lncRNA_AR_1:7397, 5_A375_pAG37_plus_lncRNA_AR_1:7397, 6_A375_EGFR_1:7506, 7_A375_EGFR_1:7506		9383, -9393, 9383, 12559, 7301, 107, 12107	upstream, downstream, downstream, upstream, cg gene, downstream	1	1	1	11.2	13.6	15.2	5	2_A375_pAG:13 7_plus_lncRNA_AR_1	20	Gene ACCN2	ACCN2, GNASC, SLNAC1, TNAC1, ASIC3	amiloride-sensitive cation channel 3	NM_020322, NM_020323, NM_006769, NCT02527917, 0, NCT02711 3, NCT17735462, 0, NCT19962 2	207981_s_at	NP_0067161, NP_0647772, NP_0647861, ENSP0003, ENSP0003, ENSP0003, ENSP0003
GeneID:10 0507937	CDK5	7	150,792,099	150,795,032	4,193	-	3	1_A375_pAG7_mrut_lncRNA_AR_1:5137, 2_A375_pAG37_plus_lncRNA_AR_1:7396, 3_A375_pAG37_plus_lncRNA_AR_1:7398, 4_A375_EGFR_1:7506, 5_A375_EGFR_1:7508		-148, -118, -3092, 9360, -2660	upstream, upstream, upstream, downstream, upstream	1	1	1	13	16.33	13.33	3	2_A375_pAG:16 7_plus_lncRNA_AR_1	Gene CDK5	C2K5, PSSALRE	cyclin-dependent kinase 5	NM_0041849, NM_0049351, NCT02869553, 0, NCT17522, 3, NCT19662 24	204267_s_at	NP_0041752, NP_0049261, ENSP0003, ENSP0003, ENSP0003
GeneID:85 22	SLC4A2	7	150,796,857	150,772,874	19,937	+	7	1_A375_pAG7_mrut_lncRNA_AR_1:5137, 2_A375_pAG37_plus_lncRNA_AR_1:7396, 3_A375_pAG37_plus_lncRNA_AR_1:7397, 4_A375_pAG37_plus_lncRNA_AR_1:7398, 5_A375_pAG37_plus_lncRNA_AR_1:7399, 6_A375_EGFR_1:7509, 7_A375_EGFR_1:7510, 8_A375_EGFR_1:7511		1437, -1489, 1437, 21029, 1053, 17693, 21103	upstream, upstream, cg gene, downstream, cg gene, downstream, downstream	1	1	1	15.75	16.5	16.5	4	2_A375_pAG:16 7_plus_lncRNA_AR_1	26	Gene SLC4A2	AE2, HKB1, BND3L, NBND3, FLJ39525, EPB3.1, SLC4A2	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	NM_0035401, NCT02887483, 0, NCT02897460, 0, NCT02897830, 0, NCT17503212 3	202111_at	NP_0035311, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003
GeneID:10 5507927	TNFSF 13	7	150,995,857	150,996,857	1,001	-	1	4_A375_EGFR_1:7511		6677	upstream	0	0	1	8	8	17	1	4_A375_EGFR 1_1	17	Gene GBX1	GBX1		NM_0010785534		
GeneID:13 8371	ADSS2	7	150,852,765	150,856,919	12,154	-	2	4_A375_EGFR_1:7510, 4_A375_EGFR_1:7510		13078, -4689	downstream, upstream	0	0	1	8.5	8.5	17	2	4_A375_EGFR 1_1	17	Gene ADSS2	ADSS2	adenylo succinate synthase 2, brain	NM_2835711, NM_0011423 59, NM_0011423 60, NCT02866501 0, NCT02527961 0, NCT19520093 1	1553239_a_at, 1554358_at, 1554537_a_at	NP_5438732, NP_0011395 12, NP_0011395 13, ENSP0003, ENSP0003, ENSP0003, ENSP0003
GeneID:10 591	ABCF2	7	150,894,523	150,926,217	19,284	-	3	1_A375_pAG7_mrut_lncRNA_AR_1:5138, 2_A375_pAG37_plus_lncRNA_AR_1:7400, 3_A375_pAG37_plus_lncRNA_AR_1:7517		-53, -51, 5123	upstream, upstream, upstream	1	1	1	16.3	20	13.3	2	1_A375_pAG:20 7_plus_lncRNA_AR_1	24	Gene ABCF2	ABC25, GCN20, HUSSY-19, MGC1, OTTHUMP00000162, ABCF2, HUSSY-19	ATP-binding cassette, sub-family F (GCN20), member 2	NM_005997, NM_0011953, NCT02869572, 0, NCT02869574, 0, NCT02869576, 0, NCT19514793, 1, NCT19514901 2	207822_s_at, 207823_s_at, 209346_at, 209347_s_at, 214252_at	NP_0051872, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003, ENSP0003
GeneID:54 4453	CHPF2	7	150,929,955	150,938,905	8,950	+	4	1_A375_pAG7_mrut_lncRNA_AR_1:5138, 2_A375_pAG37_plus_lncRNA_AR_1:7400, 3_A375_pAG37_plus_lncRNA_AR_1:7517, 4_A375_EGFR_1:7516		5165, -5217, -145, 5219	upstream, upstream, upstream, cg gene	1	1	1	14.67	16.67	14.33	3	1_A375_pAG:24 7_plus_lncRNA_AR_1	24	Gene CHPF2	CHPF2, CSG1CA, T_C-like-3, C9orf47, bA41A22	chondroitin polymerizing factor 2	NM_0199315, NCT19736 3, NCT19660 01, 1, NCT19660 32 1	221799_at, 35092_at	NP_3951881, ENSP0003, ENSP0003, ENSP0003
GeneID:79 8215	MRPS1 7	7	150,958,507	150,958,624	117	+	2	4_A375_EGFR_1:7517, 4_A375_EGFR_1:7516		-6097, -547	upstream, upstream	0	0	1	10	13.5	13	2	4_A375_EGFR 1_1	16	Gene MRPS17	bicaudal-like 1, MRP-S17, MRP17, MRS17	mitochondrial 28S ribosomal protein S17	NR_033407		

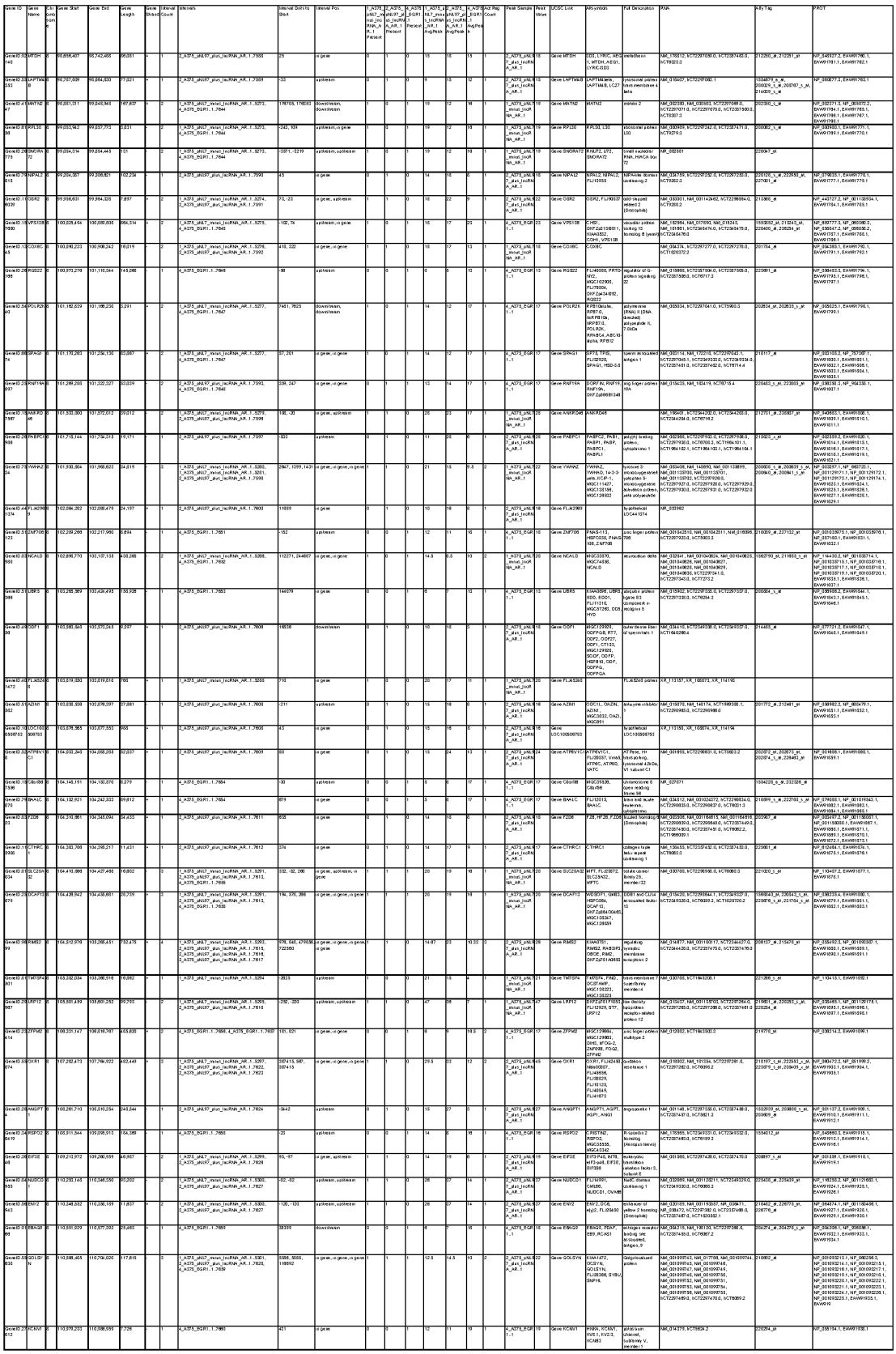
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.8604	SMARCD3	7	150,936,059	150,974,231	38,172	-	3	4_A375_EGR1..1..7517, 4_A375_EGR1..1..7518, 4_A375_EGR1..1..7519	44791, 39271, 15335	downstream, downstream, in gene	0	0	1	8.33	12	15.33	3	4_A375_EGR1..1	18	Gene SMARCD3	MGC111010, CRACD3, BAF60C, SMARCD3, Rsc6p	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	NM_001003801, NM_001003802, NM_003078, hCT2266862.0, hCT2266863.1, hCT2344954.0, hCT2352792.0, hCT1775538.3	204099_at, 231144_at	NP_001003801.1, NP_001003802.1, NP_003069.2, EAW54005.1, EAW54006.1, EAW54008.1, EAW54007.1, EAW54009.1
GeneID.349136	WDR86	7	151,078,207	151,107,124	28,917	-	1	4_A375_EGR1..1..7520	-151	upstream	0	0	1	3	7	15	1	4_A375_EGR1..1	15	Gene WDR86	WDR86, FLJ51355, MGC129839	WD repeat domain 86	NM_198285, hCT2344955.0, hCT2344956.0, hCT2352791.0, hCT10662.4	243526_at	NP_938026.2, EAW53996.1, EAW53995.1, EAW53997.1, EAW53998.1
GeneID.100507673	LOC100507673	7	151,103,955	151,106,058	2,103	-	1	4_A375_EGR1..1..7520	-1217	upstream	0	0	1	3	7	15	1	4_A375_EGR1..1	15	Gene LOC100507673		hypothetical LOC100507673	XR_108790		
GeneID.100131176	LOC100131176	7	151,106,322	151,110,134	3,812	+	1	4_A375_EGR1..1..7520	953	in gene	0	0	1	3	7	15	1	4_A375_EGR1..1	15	Gene LOC100131176		hypothetical LOC100131176	NR_034012, NR_034013		
GeneID.155051	CRYGN	7	151,127,056	151,137,099	10,043	-	1	4_A375_EGR1..1..7521	4203	in gene	0	0	1	4	5	18	1	4_A375_EGR1..1	18	Gene CRYGN	MGC119044, CRYGN, MGC119042, MGC119045, MGC119043	crystallin, gamma N	NM_144727, hCT2266853.1, hCT10663.3	1553082_at	NP_653328.1, EAW53992.1, EAW53993.1
GeneID.6009	RHEB	7	151,163,098	151,217,010	53,912	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5139, 1_A375_pNL7_minus_lncRNA_AR..1..5140, 4_A375_EGR1..1..7522	51506, 47954, 51536	in gene, in gene, in gene	1	0	1	19	15	12.5	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene RHEB	RHEB, RHEB2, MGC111559	Ras homolog enriched in brain	NM_005614, hCT2266851.0, hCT10658.4, hCT1966235.1, hCT1966236.1	1555780_a_at, 201451_x_at, 201452_at, 201453_x_at, 213404_s_at, 213409_s_at, 227633_at, 241795_at	NP_005605.1, EAW53986.1, EAW53987.1, EAW53988.1, EAW53989.1
GeneID.51422	PRKAG2	7	151,253,200	151,574,316	321,116	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5141, 1_A375_pNL7_minus_lncRNA_AR..1..5142, 2_A375_pNL97_plus_lncRNA_AR..1..7401, 2_A375_pNL97_plus_lncRNA_AR..1..7402, 4_A375_EGR1..1..7523	94060, 80666, 131652, 80636, 94172	in gene, in gene, in gene, in gene, in gene	1	1	1	16	17.33	10	3	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene PRKAG2	CMH6, AAKG2, PRKAG2, H91620p, AAKG, WPWS	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	NM_024429, NM_016203, NM_001040633, hCT2349965.0, hCT2352804.0	215231_at, 218292_s_at, 222562_at, 231224_x_at, 233748_x_at	NP_077747.1, NP_057287.2, NP_001035723.1, EAW53983.1, EAW53984.1
GeneID.168391	GALNTL5	7	151,653,464	151,717,019	63,555	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7403, 4_A375_EGR1..1..7524	68966, 69000	downstream, downstream	0	1	1	16	16	17	1	4_A375_EGR1..1	17	Gene GALNTL5	GALNTL5, GALNT15	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 5	NM_145292, NR_033169, hCT2266117.1, hCT2266118.0, hCT2344959.0, hCT2344960.0, hCT2352802.0	233150_at	NP_660335.2, EAW53978.1, EAW53977.1, EAW53979.1, EAW53980.1, EAW53981.1
GeneID.63917	GALNT11	7	151,722,778	151,819,427	96,649	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7403, 4_A375_EGR1..1..7524	-346, -314	upstream, upstream	0	1	1	16	16	17	1	4_A375_EGR1..1	17	Gene GALNT11	FLJ21634, MGC71630, GALNT11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)	NM_022087, hCT2266120.0, hCT2266121.0	219013_at	NP_071370.2, EAW53975.1, EAW53976.1
GeneID.58508	MLL3	7	151,832,010	152,133,090	301,080	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5143, 2_A375_pNL97_plus_lncRNA_AR..1..7404	-846, -796	upstream, upstream	1	1	0	22	30	3	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene MLL3	HALR, KIAA1506, MGC119853, FLJ12625, MGC119852, KMT2C, DKFZp686C08112, FLJ38309, MLL3, MGC119851	myeloid/lymphoid or mixed-lineage leukemia 3	NM_170606	1555409_a_at	NP_733751.2
GeneID.100128822	LOC100128822	7	152,161,209	152,162,630	1,421	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5144, 2_A375_pNL97_plus_lncRNA_AR..1..7405	487, 359	in gene, in gene	1	1	0	39	32	18	1	1_A375_pNL7_minus_lncRNA_AR..1	39	Gene LOC100128822		hypothetical LOC100128822	NR_027387		
GeneID.1804	DPP6	7	153,584,419	154,264,035	679,616	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7406	166317	in gene	0	1	0	11	18	2	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene DPP6	FLJ55680, MGC46605, DPPX, VF2, DPP6	dipeptidyl-peptidase 6	NM_130797, NM_001936, NM_001039350, hCT2281718.0, hCT1950436.1	1554796_at, 207789_s_at, 228546_at	NP_570629.2, NP_001927.3, NP_001034439.1, EAX04521.1, EAX04522.1
GeneID.22976	PAXIP1	7	154,735,400	154,794,682	59,282	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5147, 2_A375_pNL97_plus_lncRNA_AR..1..7409	-326, -356	upstream, upstream	1	1	0	24	27	10	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene PAXIP1	CAGF28, CAGF29, FLJ41049, PAXIP1L, TNRC2, PAXIP1, PTIP, PACIP1	PAX interacting (with transcription-activation domain) protein 1	NM_007349, hCT2281610.0, hCT10597.3	212825_at	NP_031375.3, EAX04525.1, EAX04524.1
GeneID.202781	LOC202781	7	154,795,143	154,797,413	2,270	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5147, 2_A375_pNL97_plus_lncRNA_AR..1..7409	-135, -103	upstream, upstream	1	1	0	24	27	10	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene LOC202781		hypothetical LOC202781	NR_026090	235587_at	
GeneID.100128264	LOC100128264	7	154,858,777	154,863,267	4,490	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5149, 2_A375_pNL97_plus_lncRNA_AR..1..7411, 2_A375_pNL97_plus_lncRNA_AR..1..7412, 2_A375_pNL97_plus_lncRNA_AR..1..7413	1443, 4947, 1443, 163	in gene, downstream, in gene, in gene	1	1	0	53.67	76	10	3	2_A375_pNL97_plus_lncRNA_AR..1	194	Gene LOC100128264	FLJ50036	hypothetical LOC100128264	XR_113090, XR_110773, XR_108707, XR_114117		
GeneID.3361	HTR5A	7	154,862,546	154,877,459	14,913	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5149, 2_A375_pNL97_plus_lncRNA_AR..1..7411, 2_A375_pNL97_plus_lncRNA_AR..1..7412, 2_A375_pNL97_plus_lncRNA_AR..1..7413	-722, -4226, -722, 558	upstream, upstream, upstream, in gene	1	1	0	53.67	76	10	3	2_A375_pNL97_plus_lncRNA_AR..1	194	Gene HTR5A	MGC138226, HTR5A, 5-HT5A	5-hydroxytryptamine (serotonin) receptor 5A	NM_024012, hCT6200.2	221362_at	NP_076917.1, EAX04526.1
GeneID.3638	INSIG1	7	155,089,486	155,101,945	12,459	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5150	-622	upstream	1	0	0	17	16	12	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene INSIG1	MGC1405, CL6, CL-6, INSIG1	insulin induced gene 1	NM_005542, NM_198336, NM_198337, hCT2351193.0, hCT1642107.5, hCT1962635.2, hCT1962636.2	201625_s_at, 201626_at, 201627_s_at	NP_005533.2, NP_938150.2, NP_938151.1, EAX04529.1, EAX04531.1, EAX04532.1, EAX04530.1
GeneID.100286906	LOC100286906	7	155,174,771	155,188,078	13,307	+	2	4_A375_EGR1..1..7527, 4_A375_EGR1..1..7528	-9696, -6063	upstream, upstream	0	0	1	5	6	19	2	4_A375_EGR1..1	21	Gene LOC100286906		hypothetical protein LOC100286906	XM_002342607, XM_002344413, XM_002346958, XM_003120066		XP_002342648.1, XP_002344454.1, XP_002346997.1, XP_003120116.1
GeneID.2020	EN2	7	155,250,824	155,257,526	6,702	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5151, 2_A375_pNL97_plus_lncRNA_AR..1..7414, 4_A375_EGR1..1..7530, 4_A375_EGR1..1..7531	-744, -712, -2024, 1366	upstream, upstream, upstream, in gene	1	1	1	18	21.67	14	3	2_A375_pNL97_plus_lncRNA_AR..1	49	Gene EN2	EN2		NM_001427, hCT11166.3	207060_at	NP_001418.2, EAX04535.1
GeneID.100506302	LOC100506302	7	155,434,610	155,437,074	2,464	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5152, 1_A375_pNL7_minus_lncRNA_AR..1..5153, 2_A375_pNL97_plus_lncRNA_AR..1..7415	176, -590, 176	in gene, upstream, in gene	1	1	0	19	20	10	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene LOC100506302		hypothetical LOC100506302	XR_113096, XR_110774, XR_108708, XR_114118		
GeneID.155435	RBM33	7	155,437,203	155,574,179	136,976	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5152, 1_A375_pNL7_minus_lncRNA_AR..1..5153, 1_A375_pNL7_minus_lncRNA_AR..1..5154, 2_A375_pNL97_plus_lncRNA_AR..1..7415	-307, 461, 16045, -307	upstream, in gene, in gene, upstream	1	1	0	20	16	8	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene RBM33	PRR8, DKFZp434D1319, RBM33, MGC20460	RNA binding motif protein 33	NM_053043, hCT1822159.1	225839_at, 226732_at, 238601_at	NP_444271.2, EAX04541.1
GeneID.6469	SHH	7	155,595,558	155,604,967	9,409	-	3	4_A375_EGR1..1..7532, 4_A375_EGR1..1..7533, 4_A375_EGR1..1..7534	15351, 14568, 6215	downstream, downstream, in gene	0	0	1	4.33	6.67	17.33	3	4_A375_EGR1..1	18	Gene SHH	TPT, MCOPCB5, HLP3, HPE3, SMMCI, TPTPS, HHG1, SHH	sonic hedgehog homolog (Drosophila)	NM_000193, hCT9434.3	207586_at, 236263_at	NP_000184.1, EAX04543.1
GeneID.389602	tcag7.1275	7	155,755,251	155,759,037	3,786	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7417	-787	upstream	0	1	0	16	16	12	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene tcag7.1275	FLJ42330, LOC389602	hypothetical LOC389602	XR_113095, XR_110775, XR_108709, XR_114119		
GeneID.100506380	LOC100506380	7	156,264,795	156,398,461	133,666	-	1	4_A375_EGR1..1..7536	-1635	upstream	0	0	1	6	6	16	1	4_A375_EGR1..1	16	Gene LOC100506380		hypothetical LOC100506380	XR_113093, XR_113092, XR_110779, XR_110776, XR_108713, XR_108712, XR_114123, XR_114122		
GeneID.129790	C7orf13	7	156,431,060	156,433,348	2,288	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7418	228	in gene	0	1	0	13	16	12	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C7orf13	MY040, C7orf13	chromosome 7 open reading frame 13	NR_026865, hCT1841604.3	223630_at	EAX04550.1
GeneID.140545	RNF32	7	156,433,401	156,469,824	36,423	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7418	-261	upstream	0	1	0	13	16	12	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene RNF32	RNF32, HSD15, FKSG33	ring finger protein 32	NM_030936, NM_001184996, NM_001184997, hCT2282008.0, hCT2282009.0, hCT2358891.0, hCT2358892.0, hCT9921.3, hCT1950336.0, hCT1950337.0, hCT1950338.0	1554642_at, 220991_s_at, 232830_at	NP_112198.1, NP_001171925.1, NP_001171926.1, EAX04551.1, EAX04553.1, EAX04557.1, EAX04552.1, EAX04554.1, EAX04555.1, EAX04556.1, EAX04558.1
GeneID.64327	LMBR1	7	156,473,570	156,685,902	212,332	-	1	4_A375_EGR1..1..7537	-194	upstream	0	0	1	15	16	36	1	4_A375_EGR1..1	36	Gene LMBR1	TPT, DIF14, LMBR1, ACHP, PPD2, FLJ11665, C7orf2	limb region 1 homolog (mouse)	NM_022458, hCT2282078.0, hCT2282079.0, hCT2282081.0, hCT9919.3	222505_at, 222506_at, 224036_s_at, 224410_s_at	NP_071903.2, EAX04561.1, EAX04559.1, EAX04560.1, EAX04562.1
GeneID.64434	NOM1	7	156,742,417	156,765,876	23,459	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5156, 2_A375_pNL97_plus_lncRNA_AR..1..7419, 4_A375_EGR1..1..7538	15, -17, 319	in gene, upstream, in gene	1	1	1	47	33	16	1	1_A375_pNL7_minus_lncRNA_AR..1	47	Gene NOM1	FLJ16401, C7orf3, SGD1, NOM1	nucleolar protein with MIF4G domain 1	NM_138400, hCT9920.3	227161_at, 229220_x_at	NP_612409.1, EAX04563.1
GeneID.3110	MNX1	7	156,797,547	156,803,347	5,800	-	2	4_A375_EGR1..1..7539, 4_A375_EGR1..1..7540	4211, 1491	in gene, in gene	0	0	1	6	5.5	18	2	4_A375_EGR1..1	21	Gene MNX1	HLXB9, MNX1, HOXHB9, HB9, SCRA1	motor neuron and pancreas homeobox 1	NM_005515, NM_001165255, hCT9918.3	214614_at	NP_005506.3, NP_001158727.1, EAX04564.1
GeneID.100506410	LOC100506410	7	156,799,001	156,799,814	813	+	2	4_A375_EGR1..1..7539, 4_A375_EGR1..1..7540	135, 2655	in gene, downstream	0	0	1	6	5.5	18	2	4_A375_EGR1..1	21	Gene LOC100506410		hypothetical LOC100506410	XR_113091, XR_110780, XR_108714, XR_114124		
GeneID.645249	LOC645249	7	156,803,208	156,809,118	5,910	+	2	4_A375_EGR1..1..7539, 4_A375_EGR1..1..7540	-4072, -1352	upstream, upstream	0	0	1	6	5.5	18	2	4_A375_EGR1..1	21	Gene LOC645249		hypothetical LOC645249	XR_113097, XR_110785, XR_108719, XR_114128	236987_at	
GeneID.10049	DNAJB6	7	157,129,710	157,210,133	80,423	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5157, 2_A375_pNL97_plus_lncRNA_AR..1..7420, 4_A375_EGR1..1..7543, 4_A375_EGR1..1..7544	66130, 66210, 87154, 89650	in gene, in gene, downstream, downstream	1	1	1	8	12	14	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene DNAJB6	HSJ-2, MSJ-1, HSJ2, DKFZp566D0824, MGC117297, DnaJ, DJ4, MRJ, MGC1152, HHDJ1, DNAJB6, FLJ42837	DnaJ (Hsp40) homolog, subfamily B, member 6	NM_005494, NM_058246, hCT2282244.0, hCT2282248.0	208811_s_at, 209015_s_at	NP_005485.1, NP_490647.1, EAX04570.1, EAX04571.1
GeneID.5799	PTPRN2	7	157,331,750	158,380,482	1,048,732	-	14	1_A375_pNL7_minus_lncRNA_AR..1..5158, 1_A375_pNL7_minus_lncRNA_AR..1..5159, 2_A375_pNL97_plus_lncRNA_AR..1..7421, 2_A375_pNL97_plus_lncRNA_AR..1..7422, 4_A375_EGR1..1..7545, 4_A375_EGR1..1..7546, 4_A375_EGR1..1..7547, 4_A375_EGR1..1..7548, 4_A375_EGR1..1..7549, 4_A375_EGR1..1..7550, 4_A375_EGR1..1..7551, 4_A375_EGR1..1..7552, 4_A375_EGR1..1..7553, 4_A375_EGR1..1..7554	1022818, 33490, 1022882, 33442, 974658, 897602, 727682, 702530, 679682, 525015, 142322, 140682, 112962, 98987	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	8.58	10.25	14.08	12	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene PTPRN2	PTPRP, IAR, PTPRN2, ICAAR, IA-2beta	protein tyrosine phosphatase, receptor type, N polypeptide 2	NM_130842, NM_002847, NM_130843, hCT2282984.0, hCT2282989.0	203029_s_at, 203030_s_at, 211534_x_at	NP_570857.2, NP_002838.2, NP_570858.2, EAX04577.1, EAX04578.1
GeneID.406945	MIR153-2	7	157,367,028	157,367,114	86	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5158, 2_A375_pNL97_plus_lncRNA_AR..1..7421	9450, 9514	downstream, downstream	1	1	0	27	33	8	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene MIR153-2	MIR153-2, MIRN153-2	microRNA 153-2	NR_029689		
GeneID.100506585	LOC100506585	7	157,847,277	157,858,784	11,507	+	1	4_A375_EGR1..1..7547	5523	in gene	0	0	1	1	7	13	1	4_A375_EGR1..1	13	Gene LOC100506585		hypothetical LOC100506585	XR_108716		
GeneID.57488	ESYT2	7	158,523,689	158,622,319	98,630	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5160, 1_A375_pNL7_minus_lncRNA_AR..1..5161, 2_A375_pNL97_plus_lncRNA_AR..1..7423, 4_A375_EGR1..1..7555	11023, -49, 10663, -401	in gene, upstream, in gene, upstream	1	1	1	19	21	15	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ESYT2	ESYT2, E-Syt2, KIAA1228, CHR2SYT, FAM62B	extended synaptotagmin-like protein 2	NM_020728, hCT2282315.0, hCT11253.4	1555829_at, 1555830_s_at, 1556511_s_at, 224698_at, 224699_s_at, 239334_at	NP_065779.1, EAX04590.1, EAX04591.1
GeneID.55112	WDR60	7	158,649,269	158,738,883	89,614	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5162, 2_A375_pNL97_plus_lncRNA_AR..1..7424	-85, -117	upstream, upstream	1	1	0	46	55	8	1	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene WDR60	FLJ23575, FLJ10300, WDR60	WD repeat domain 60	NM_018051, hCT1959855.1	1562516_at, 219251_s_at, 229008_at	NP_060521.4, EAX04592.1
GeneID.154822	tcag7.1307	7	158,801,045	158,818,929	17,884	+	2	4_A375_EGR1..1..7556, 4_A375_EGR1..1..7557	21227, 22523	downstream, downstream	0	0	1	5	10	16.5	2	4_A375_EGR1..1	20	Gene tcag7.1307	LOC154822	hypothetical LOC154822	NR_024394	1559712_at, 1570378_at, 236753_at, 237471_at, 243261_at	
GeneID.7434	VIPR2	7	158,820,866	158,937,649	116,783	-	4	4_A375_EGR1..1..7556, 4_A375_EGR1..1..7557, 4_A375_EGR1..1..7558, 4_A375_EGR1..1..7559	115377, 114081, 80929, 53265	in gene, in gene, in gene, in gene	0	0	1	3.25	6.75	16.5	4	4_A375_EGR1..1	20	Gene VIPR2	FLJ16511, VPCAP2R, VPAC2, VIPR2	vasoactive intestinal peptide receptor 2	NM_003382, hCT9110.3	205946_at, 205947_s_at, 211598_x_at	NP_003373.2, EAX04596.1
GeneID.100507448	LOC100507448	8	1,710,788	1,712,750	1,962	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5163, 2_A375_pNL97_plus_lncRNA_AR..1..7425	1406, 8974	in gene, downstream	1	1	0	13	11.5	4	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene LOC100507448		hypothetical LOC100507448	XR_113103, XR_113104, XR_113102, XR_110091, XR_110092, XR_114132, XR_114133, XR_114134		
GeneID.2055	CLN8	8	1,711,870	1,734,736	22,866	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5163, 2_A375_pNL97_plus_lncRNA_AR..1..7425	-526, -8094	upstream, upstream	1	1	0	13	11.5	4	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CLN8	C8orf61, CLN8, FLJ39417, EPMR	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	NM_018941, hCT2291976.1, hCT2351272.0, hCT6131.3	219340_s_at, 219341_at, 222874_s_at, 223912_s_at, 229958_at	NP_061764.2, EAW51478.1, EAW51477.1, EAW51479.1
GeneID.64478	CSMD1	8	2,792,875	4,852,328	2,059,453	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7426	1811720	in gene	0	1	0	11	16	0	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CSMD1	CSMD1, KIAA1890	CUB and Sushi multiple domains 1	NM_033225, hCT2344401.2, hCT2350239.0	1553405_a_at, 1562329_at, 1562330_s_at, 231223_at, 241980_at	NP_150094.5, EAW80463.1, EAW80464.1
GeneID.389610	XKR5	8	6,666,038	6,693,166	27,128	-	1	4_A375_EGR1..1..7563	23830	in gene	0	0	1	1	2	14	1	4_A375_EGR1..1	14	Gene XKR5	XRG5BM, XRG5A, UNQ2754, XRG5a, XRG5b, XKR5	XK, Kell blood group complex subunit-related family, member 5	NM_207411, hCT13376.4, hCT1818073.2		NP_997294.3, EAW80480.1, EAW80479.1
GeneID.157285	PRAGMIN	8	8,175,258	8,239,257	63,999	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5164, 1_A375_pNL7_minus_lncRNA_AR..1..5165, 2_A375_pNL97_plus_lncRNA_AR..1..7428, 2_A375_pNL97_plus_lncRNA_AR..1..7429	70745, 29257, 70681, 29230	downstream, in gene, downstream, in gene	1	1	0	17	17.5	3	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene PRAGMIN	DKFZp761P0423, PRAGMIN	homolog of rat pragma of Rnd2	NM_001080826	235085_at	NP_001074295.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:4482	MSRA	8	9,911,830	10,286,401	374,571	+	1	4_A375_EGR1..1..7564	350868	in gene	0	0	1	4	4	15	1	4_A375_EGR1..1	15	Gene MSRA	MSRA		NM_012331, NM_001135670, NM_001135671, hCT2354202.0, hCT1950652.1	219281_at	NP_036463.1, NP_001129142.1, NP_001129143.1, EAW65584.1, EAW65585.1
GeneID:83595	SOX7	8	10,581,278	10,588,022	6,744	-	2	4_A375_EGR1..1..7565, 4_A375_EGR1..1..7566	4214, -2954	in gene, upstream	0	0	1	3	3.5	16.5	2	4_A375_EGR1..1	20	Gene SOX7	MGC10895, SOX7	SRY (sex determining region Y)-box 7	NM_031439	224013_s_at, 226898_at	NP_113627.1
GeneID:54984	PINX1	8	10,622,884	10,697,299	74,415	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7431	83	in gene	0	1	0	9	15	11	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene PINX1	LPTL, LPTS, MGC8850, FLJ20565, PINX1	PIN2-interacting protein 1	NM_017884, hCT10467.4, hCT1963980.1, hCT1984747.1	223907_s_at	NP_060354.4, EAW65596.1, EAW65595.1, EAW65597.1
GeneID:286046	XKR6	8	10,753,654	11,058,875	305,221	-	6	1_A375_pNL7_minus_lncRNA_AR..1..5167, 1_A375_pNL7_minus_lncRNA_AR..1..5168, 1_A375_pNL7_minus_lncRNA_AR..1..5169, 2_A375_pNL97_plus_lncRNA_AR..1..7432, 2_A375_pNL97_plus_lncRNA_AR..1..7433, 2_A375_pNL97_plus_lncRNA_AR..1..7434	211003, 108699, -325, 210971, 108663, -229	in gene, in gene, upstream, in gene, in gene, upstream	1	1	0	32	40	5	3	2_A375_pNL97_plus_lncRNA_AR..1	55	Gene XKR6	FLJ31557, XRG6, C8orf7, C8orf21, XKR6, C8orf5	XK, Kell blood group complex subunit-related family, member 6	NM_173683, hCT1647103.4	1553840_at, 1557436_at	NP_775954.2, EAW65599.1
GeneID:66036	MTMR9	8	11,142,000	11,185,655	43,655	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5170, 2_A375_pNL97_plus_lncRNA_AR..1..7435	-144, 46	upstream, in gene	1	1	0	19	17	6	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene MTMR9	MTMR9, MTMR8, DKFZp434K171, MGC126672, C8orf9, LIP-STYX	myotubularin related protein 9	NM_015458, hCT2268668.0, hCT2354201.0, hCT10465.3	204837_at, 213278_at, 233101_at	NP_056273.2, EAW65608.1, EAW65607.1, EAW65609.1
GeneID:83648	FAM167A	8	11,278,973	11,324,276	45,303	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7436	-266	upstream	0	1	0	9	15	10	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene FAM167A	DKFZp761G151, MGC120650, D8S265, MGC120651, MGC120649, C8orf13, FAM167A	family with sequence similarity 167, member A	NM_053279, hCT2349276.0	226614_s_at, 233641_s_at	NP_444509.2, EAW65616.1
GeneID:100506990	LOC100506990	8	12,294,549	12,408,558	114,009	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7439	123195	downstream	0	1	0	6	15	1	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LOC100506990		hypothetical LOC100506990	XR_110881		
GeneID:51201	ZDHHC2	8	17,013,836	17,080,241	66,405	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5172	-412	upstream	1	0	0	16	13	3	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene ZDHHC2	ZDHHC2, ZNF372, DHHC2	zinc finger, DHHC-type containing 2	NM_016353, hCT2274220.0, hCT18264.3	1563502_at, 222730_s_at, 222731_at	NP_057437.1, EAW63824.1, EAW63825.1
GeneID:5157	PDGFRL	8	17,433,942	17,500,642	66,700	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5173	46986	in gene	1	0	0	15	9	3	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene PDGFRL	PDGRL, PRLTS, PDGFRL	platelet-derived growth factor receptor-like	NM_006207, hCT16894.3	205226_at	NP_006198.1, EAW63811.1
GeneID:5108	PCM1	8	17,780,366	17,887,457	107,091	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5174, 2_A375_pNL97_plus_lncRNA_AR..1..7440	-174, -46	upstream, upstream	1	1	0	16	14	13	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene PCM1	PTC4, PCM1	pericentriolar material 1	NM_006197, hCT2274262.0, hCT2274265.0, hCT19402.3	202174_s_at, 209996_x_at, 209997_x_at, 214118_x_at, 214937_x_at, 226905_at	NP_006188.3, EAW63796.1, EAW63797.1, EAW63798.1
GeneID:427	ASAH1	8	17,913,925	17,942,507	28,582	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7441, 4_A375_EGR1..1..7567	766, 619	in gene, in gene	0	1	1	13	15	16	1	4_A375_EGR1..1	16	Gene ASAH1	PHP32, FLJ21558, ACDase, ASAH, PHP, ASAH1, FLJ22079, AC	N-acylsphingosine amidohydrolase (acid ceramidase) 1	NM_004315, NM_177924, NM_001127505, hCT2273573.0, hCT2273576.0, hCT2273579.0, hCT19403.3, hCT1958859.1	1555419_a_at, 210979_at, 210980_s_at, 213702_x_at, 213902_at	NP_004306.3, NP_808592.2, NP_001120977.1, EAW63793.1, EAW63794.1, EAW63795.1, EAW63791.1, EAW63792.1
GeneID:55790	CSGALNACT1	8	19,261,672	19,540,261	278,589	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7443	177221	in gene	0	1	0	8	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CSGALNACT1	beta4GalNAcT, CSGalNAcT-1, ChGn, CSGALNACT1, FLJ13760, FLJ11264	chondroitin sulfate N-acetylgalactosaminyltransferase 1	NM_018371, NM_001130518, NR_024040, hCT2273325.0, hCT2273328.0, hCT1824454.2	219049_at	NP_060841.5, NP_001123990.1, EAW63770.1, EAW63771.1, EAW63772.1
GeneID:55174	INTS10	8	19,674,918	19,709,589	34,671	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5175, 2_A375_pNL97_plus_lncRNA_AR..1..7445	-102, -70	upstream, upstream	1	1	0	24	27	7	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene INTS10	C8orf35, INT10, INTS10, FLJ10569	integrator complex subunit 10	NM_018142, hCT2274273.0, hCT2274274.0, hCT2274276.0, hCT14667.3, hCT1956858.1	1560172_at, 229832_s_at, 229833_at, 237504_at	NP_060612.2, EAW63765.1, EAW63766.1, EAW63767.1, EAW63768.1, EAW63769.1
GeneID:526	ATP6V1B2	8	20,054,704	20,079,207	24,503	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5176	-48	upstream	1	0	0	20	16	6	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene ATP6V1B2	ATP6B1B2, VATB, ATP6B2, Vma2, HO57, ATP6V1B2, VPP3	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	NM_001693, hCT2274287.0, hCT14665.3	201089_at	NP_001684.2, EAW63758.1, EAW63759.1
GeneID:11178	LZTS1	8	20,103,676	20,112,803	9,127	-	1	4_A375_EGR1..1..7568	5107	in gene	0	0	1	3	2	12	1	4_A375_EGR1..1	12	Gene LZTS1	FEZ1, LZTS1, F37	leucine zipper, putative tumor suppressor 1	NM_021020, hCT2273317.0, hCT2273319.0, hCT2273320.0, hCT2273321.0, hCT2273322.0	219042_at, 221719_s_at, 221721_s_at, 221722_x_at, 222107_x_at, 47550_at	NP_066300.1, EAW63752.1, EAW63753.1, EAW63754.1, EAW63755.1, EAW63756.1
GeneID:55806	HR	8	21,971,932	21,988,565	16,633	-	3	4_A375_EGR1..1..7569, 4_A375_EGR1..1..7570, 4_A375_EGR1..1..7571	9989, 1442, 69	in gene, in gene, in gene	0	0	1	6.67	6.67	14.33	3	4_A375_EGR1..1	16	Gene HR	HSA277165, ALUNC, MUHH, AU, FLJ98860, MUHH1, HR	hairless homolog (mouse)	NM_018411, NM_005144, hCT2274634.0, hCT2353921.0, hCT14911.3	210086_at, 220163_s_at, 241355_at	NP_060881.2, NP_005135.2, EAW63716.1, EAW63717.1, EAW63718.1
GeneID:80346	REEP4	8	21,995,533	21,999,448	3,915	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5177, 2_A375_pNL97_plus_lncRNA_AR..1..7446, 4_A375_EGR1..1..7570, 4_A375_EGR1..1..7571	-40, -40, 12325, 10952	upstream, upstream, downstream, downstream	1	1	1	12.67	13	14.33	3	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene REEP4	PP432, FLJ22246, C8orf20, REEP4, FLJ22277	receptor accessory protein 4	NM_025232, hCT2274624.0, hCT2274629.0, hCT2353892.0, hCT14912.3, hCT1984976.1, hCT1984977.1	218777_at	NP_079508.2, EAW63712.1, EAW63710.1, EAW63713.1, EAW63714.1, EAW63715.1, EAW63711.1
GeneID:203190	LGI3	8	22,004,343	22,014,344	10,001	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5177, 2_A375_pNL97_plus_lncRNA_AR..1..7446	14856, 14856	downstream, downstream	1	1	0	22	19	14	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene LGI3	LGIL4, LGI3	leucine-rich repeat LGI family, member 3	NM_139278, hCT2341193.0, hCT2353935.0	238061_at	NP_644807.1, EAW63708.1, EAW63709.1
GeneID:407037	MIR320A	8	22,102,475	22,102,556	81		2	2_A375_pNL97_plus_lncRNA_AR..1..7447, 4_A375_EGR1..1..7572	-15, 26	upstream, in gene	0	1	1	13	14	18	1	4_A375_EGR1..1	18	Gene MIR320A	MIRN320A, MIRN320, hsa-mir-320a, MIR320A	microRNA 320a	NR_029714		
GeneID:661	POLR3D	8	22,102,619	22,108,680	6,061	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7447, 4_A375_EGR1..1..7572	-48, -91	upstream, upstream	0	1	1	13	14	18	1	4_A375_EGR1..1	18	Gene POLR3D	TSBN51, RPC53, BN51T, POLR3D, RPC4	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	NM_001722, hCT2275706.0, hCT2275707.0, hCT2353919.0, hCT1825216.3	208361_s_at	NP_001713.2, EAW63692.1, EAW63689.1, EAW63690.1, EAW63691.1
GeneID:100507071	LOC100507071	8	22,112,089	22,132,675	20,586		2	2_A375_pNL97_plus_lncRNA_AR..1..7447, 4_A375_EGR1..1..7572	30104, 30147	downstream, downstream	0	1	1	13	14	18	1	4_A375_EGR1..1	18	Gene LOC100507071		hypothetical LOC100507071	XR_113112, XR_110863, XR_114151		
GeneID:23516	SLC39A14	8	22,224,762	22,291,642	66,880	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7448	26022	in gene	0	1	0	15	21	2	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SLC39A14	cig19, NET34, SLC39A14, LZT-Hs4, ZIP14, KIAA0062	solute carrier family 39 (zinc transporter), member 14	NM_015359, NM_001128431, NM_001135153, NM_001135154, hCT2275710.0, hCT2275712.0, hCT7028.2, hCT1984912.1	1555433_at, 1555434_a_at, 212110_at	NP_056174.2, NP_001121903.1, NP_001128625.1, NP_001128626.1, EAW63660.1, EAW63662.1, EAW63661.1, EAW63663.1
GeneID:57805	KIAA1967	8	22,462,145	22,477,984	15,839	+	1	4_A375_EGR1..1..7573	25439	downstream	0	0	1	2	1	14	1	4_A375_EGR1..1	14	Gene KIAA1967	KIAA1967, p30DBC, NET35, p30 DBC, DBC-1, DBC1	KIAA1967	NM_021174, NR_033902, hCT2349016.0, hCT2349017.0, hCT2349018.0, hCT2353927.0, hCT2353928.0	221070_s_at, 225187_at, 225193_at	NP_066997.3, EAW63660.1, EAW63658.1, EAW63659.1, EAW63661.1, EAW63662.1
GeneID:55909	BIN3	8	22,477,931	22,526,661	48,730	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7449, 4_A375_EGR1..1..7573	101, 39077	in gene, in gene	0	1	1	7	12	11	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene BIN3	MGC14978, BIN3	bridging integrator 3	NM_018688, hCT2274144.0, hCT2274149.0, hCT1984905.1, hCT1984906.1, hCT1984907.0, hCT1984908.1, hCT1984909.1	1557582_at, 222199_s_at	NP_061156.1, EAW63655.1, EAW63650.1, EAW63651.1, EAW63652.1, EAW63654.1, EAW63653.1, EAW63656.1
GeneID:1960	EGR3	8	22,545,174	22,550,815	5,641	-	1	4_A375_EGR1..1..7574	-1441	upstream	0	0	1	5	6	16	1	4_A375_EGR1..1	16	Gene EGR3	PILOT, EGR3, MGC138484	early growth response 3	NM_004430, hCT7022.3	206115_at	NP_004421.2, EAW63649.1
GeneID:157310	PEBP4	8	22,570,765	22,785,421	214,656	-	3	2_A375_pNL97_plus_lncRNA_AR..1..7450, 2_A375_pNL97_plus_lncRNA_AR..1..7451, 4_A375_EGR1..1..7575	183293, 178813, 149773	in gene, in gene, in gene	0	1	1	6.67	11.33	8.67	3	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PEBP4	PRO4408, MGC22776, CORK-1, hPEBP4, PEBP-4, GWTM1933, PEBP4, CORK1	phosphatidylethanolamine-binding protein 4	NM_144962, hCT7029.3	227848_at	NP_659399.2, EAW63647.1
GeneID:100507139	LOC100507139	8	22,812,323	22,815,705	3,382	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7450, 2_A375_pNL97_plus_lncRNA_AR..1..7451	-10195, -3715	upstream, upstream	0	1	0	9	15	5.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC100507139		hypothetical LOC100507139	XR_110867		
GeneID:8795	TNFRSF10B	8	22,877,646	22,926,700	49,054	-	1	4_A375_EGR1..1..7576	364	in gene	0	0	1	5	13	17	1	4_A375_EGR1..1	17	Gene TNFRSF10B	TRICK2A, TRAIL-R2, KILLER/DR5, TNFRSF10B, TRICK2B, TRAILR2, CD262, TRICK2, KILLER, TRICKB, ZTNFR9, DR5	tumor necrosis factor receptor superfamily, member 10b	NM_003842, NM_147187, NR_027140, hCT1989297.1, hCT2274134.0, hCT2274135.0, hCT1645199.2	209294_x_at, 209295_at, 210405_x_at	NP_003833.4, NP_671716.2, EAW63640.1, EAW63641.1, EAW63642.1, EAW63643.1
GeneID:203069	R3HCC1	8	23,145,612	23,153,792	8,180	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5178, 2_A375_pNL97_plus_lncRNA_AR..1..7452, 4_A375_EGR1..1..7577	52, 20, 212	in gene, in gene, in gene	1	1	1	22	22	14	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene R3HCC1	R3HCC1, DKFZp564N123	R3H domain and coiled-coil containing 1	NM_001136108	212686_at, 35156_at	NP_001129580.1
GeneID:4017	LOXL2	8	23,154,410	23,261,722	107,312	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5178, 2_A375_pNL97_plus_lncRNA_AR..1..7452, 4_A375_EGR1..1..7577	116058, 116090, 115896	downstream, downstream, downstream	1	1	1	22	22	14	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene LOXL2	LOXL2, LOR2, WS9-14	lysyl oxidase-like 2	NM_002318, hCT2274126.0, hCT2274129.0, hCT7729.3	1562263_at, 202997_s_at, 202998_s_at, 202999_s_at, 228808_s_at	NP_002309.1, EAW63625.1, EAW63626.1, EAW63627.1
GeneID:51312	SLC25A37	8	23,386,363	23,430,063	43,700	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5179	12773	in gene	1	0	0	19	13	6	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene SLC25A37	HT015, MSCP, MFRN, MFRN1, PRO1278, MSC, SLC25A37, PRO1584, PRO2217	solute carrier family 25, member 37	NM_016612	218136_s_at, 218978_s_at, 221920_s_at, 222528_s_at, 222529_at, 226179_at, 226928_x_at, 228527_s_at, 231274_s_at, 242335_at	NP_057696.2
GeneID:80005	DOCK5	8	25,042,287	25,270,619	228,332	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7454	3081	in gene	0	1	0	9	18	4	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene DOCK5	DKFZp761J211, DKFZp779M164, DOCK5, DKFZp451J181	dedicator of cytokinesis 5	NM_024940, hCT2273023.0, hCT2273026.0, hCT6517.3	1561276_at, 1569590_at, 1570078_a_at, 219921_s_at, 222721_at, 230206_at, 230207_s_at, 230263_s_at	NP_079216.4, EAW63595.1, EAW63593.1, EAW63594.1
GeneID:54793	KCTD9	8	25,285,363	25,315,984	30,621	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5180, 2_A375_pNL97_plus_lncRNA_AR..1..7455	-640, -624	upstream, upstream	1	1	0	33	36	6	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene KCTD9	FLJ20038, KCTD9	potassium channel tetramerisation domain containing 9	NM_017634, hCT2272952.0, hCT2272954.0, hCT2272955.0, hCT1814491.2	218823_s_at, 224316_at	NP_060104.2, EAW63589.1, EAW63587.1, EAW63588.1, EAW63590.1
GeneID:157313	CDCA2	8	25,316,513	25,365,425	48,912	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5180, 2_A375_pNL97_plus_lncRNA_AR..1..7455	111, 95	in gene, in gene	1	1	0	33	36	6	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene CDCA2	MGC129907, Repo-Man, CDCA2, MGC129906, FLJ25804	cell division cycle associated 2	NM_152562	226661_at, 236957_at	NP_689775.2
GeneID:5520	PPP2R2A	8	26,149,007	26,230,196	81,189	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5181	91393	downstream	1	0	0	17	15	12	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene PPP2R2A	FLJ41727, PR55A, PR52A, B55A, MGC52248, B55-ALPHA, B55ALPHA, PPP2R2A, FLJ26613, DKFZp686N05117	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	NM_001177591, NM_002717, hCT2274996.0, hCT2274998.0, hCT8210.3, hCT1984921.1	202313_at, 236492_at, 237636_at	NP_001171062.1, NP_002708.1, EAW63577.1, EAW63578.1, EAW63579.1, EAW63580.1
GeneID:665	BNIP3L	8	26,240,523	26,270,644	30,121	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5181	-123	upstream	1	0	0	17	15	12	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene BNIP3L	NIX, BNIP3a, BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	NM_004331, hCT1690263.3	221478_at, 221479_s_at	NP_004322.1, EAW63576.1
GeneID:10687	PNMA2	8	26,362,196	26,371,483	9,287	-	1	4_A375_EGR1..1..7578	1275	in gene	0	0	1	5	3	14	1	4_A375_EGR1..1	14	Gene PNMA2	MA2, PNMA2, KIAA0883, MM2, RGAG2	paraneoplastic antigen MA2	NM_007257, hCT2348934.0	209597_s_at, 209598_at	NP_009188.1, EAW63575.1
GeneID:1808	DPYSL2	8	26,435,421	26,515,693	80,272	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7456	-957	upstream	0	1	0	5	18	6	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene DPYSL2	CRMP2, DHPRP2, DRP-2, DPYSL2, DRP2	dihydropyrimidinase-like 2	NM_001386, hCT2275002.0, hCT8209.3	200762_at	NP_001377.1, EAW63573.1, EAW63574.1
GeneID:55872	PBK	8	27,667,138	27,695,349	28,211	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5182, 2_A375_pNL97_plus_lncRNA_AR..1..7457	37, 53	in gene, in gene	1	1	0	23	20	10	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene PBK	CT84, Nori-3, TOPK, PBK, SPK, FLJ14385	PDZ binding kinase	NM_018492, hCT8338.4, hCT1981592.1	219148_at	NP_060962.2, EAW63536.1, EAW63537.1
GeneID:286133	SCARA5	8	27,727,736	27,850,198	122,462	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7458	120162	in gene	0	1	0	10	16	3	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene SCARA5	SCARA5, Tesr, NET33, FLJ23907, MGC45780	scavenger receptor class A, member 5 (putative)	NM_173833, hCT2350912.0, hCT2353939.0, hCT1648131.3	1554705_at, 229839_at, 235849_at	NP_776194.2, EAW63534.1, EAW63532.1, EAW63533.1
GeneID:55756	INTS9	8	28,625,175	28,747,698	122,523	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5185, 2_A375_pNL97_plus_lncRNA_AR..1..7461	-121, -110	upstream, upstream	1	1	0	18	24	10	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene INTS9	CPSF2L, RC-74, INT9, FLJ10871, RC74, INTS9	integrator complex subunit 9	NM_001172562, NM_018250, NM_001145159, NR_026626, hCT2275721.0, hCT2353946.0, hCT7770.3	203941_at, 237286_at	NP_001166033.1, NP_060720.2, NP_001138631.1, EAW63504.1, EAW63505.1, EAW63506.1
GeneID:79618	HMBOX1	8	28,747,911	28,910,242	162,331	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5185, 2_A375_pNL97_plus_lncRNA_AR..1..7461	-92, -103	upstream, upstream	1	1	0	18	24	10	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene HMBOX1	HMBOX1, PBHNF, FLJ21616, HNF1LA	homeobox containing 1	NM_024567, NM_001135726, hCT2273643.1, hCT2273646.1, hCT2273647.1, hCT2273648.1, hCT2343357.0, hCT2353945.0, hCT7769.4	219269_at	NP_078843.2, NP_001129198.1, EAW63496.1, EAW63498.1, EAW63501.1, EAW63502.1, EAW63497.1, EAW63499.1, EAW63500.1
GeneID:1846	DUSP4	8	29,193,611	29,208,185	14,574	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7462	1689	in gene	0	1	0	8	15	7	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene DUSP4	TYP, MKP2, HVH2, MKP-2, DUSP4	dual specificity phosphatase 4	NM_057158, NM_001394, hCT2273426.0, hCT1639905.3, hCT1981543.1, hCT1984913.1	204014_at, 204015_s_at	NP_476499.1, NP_001385.1, EAW63481.1, EAW63482.1, EAW63483.1, EAW63484.1
GeneID:10671	DCTN6	8	30,013,613	30,041,060	27,247	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5189, 2_A375_pNL97_plus_lncRNA_AR..1..7463	75, 123	in gene, in gene	1	1	0	22	18	7	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene DCTN6	WS3, DCTN6, p27, WS-3	dynactin 6	NM_006571, hCT7539.4	203261_at	NP_006562.1, EAW63466.1

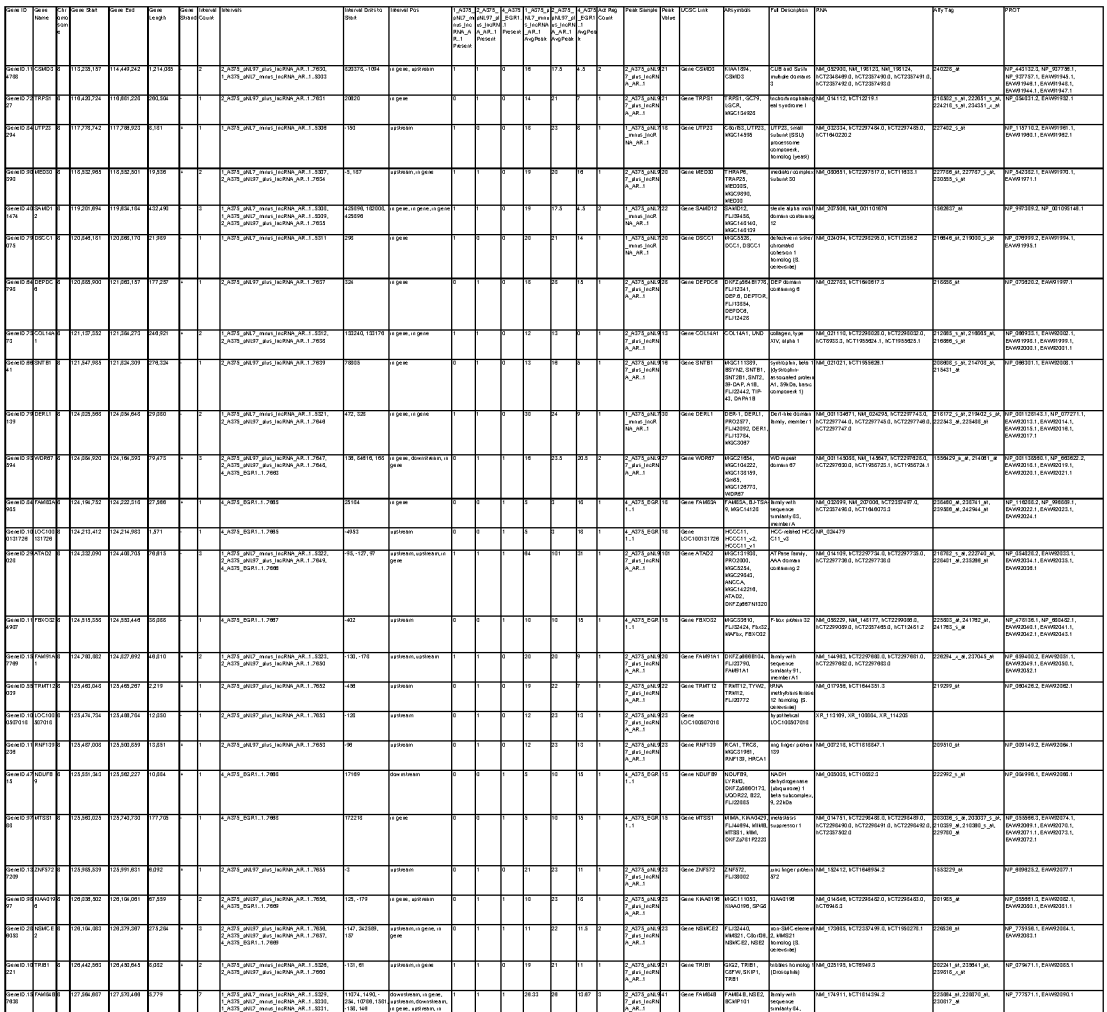
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:5516	PPP2CB	8	30,643,126	30,670,352	27,226	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5190, 2_A375_pNL97_plus_lncRNA_AR..1..7464	16, -60	in gene, upstream	1	1	0	36	52	6	1	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene PPP2CB	PP2CB, PPP2CB, PP2Abeta	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	NM_001009552, hCT2336253.0, hCT2336254.0, hCT2336255.0, hCT2336256.0	201374_x_at, 201375_s_at	NP_001009552.1, EAW63436.1, EAW63433.1, EAW63434.1, EAW63435.1
GeneID:84750	FUT10	8	33,228,342	33,330,664	102,322	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5191, 2_A375_pNL97_plus_lncRNA_AR..1..7465	-24, -56	upstream, upstream	1	1	0	22	23	7	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene FUT10	MGC11141, FUT10	fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	NM_032664, hCT2271736.0, hCT2353891.0, hCT1824885.1, hCT1984946.1	223976_at, 235472_at, 239020_at	NP_116053.3, EAW63403.1, EAW63401.1, EAW63402.1, EAW63404.1
GeneID:80185	C8orf41	8	33,356,233	33,370,703	14,470	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5192, 2_A375_pNL97_plus_lncRNA_AR..1..7466	-193, -145	upstream, upstream	1	1	0	51	40	7	1	1_A375_pNL7_minus_lncRNA_AR..1	51	Gene C8orf41	C8orf41, FLJ23263	chromosome 8 open reading frame 41	NM_025115, NM_001102401, hCT1824881.1, hCT1984944.1, hCT1984945.1	219124_at	NP_079391.2, NP_001095871.1, EAW63397.1, EAW63398.1, EAW63399.1
GeneID:692084	SNORD13	8	33,370,993	33,371,096	103	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5192, 2_A375_pNL97_plus_lncRNA_AR..1..7466	-97, -145	upstream, upstream	1	1	0	51	40	7	1	1_A375_pNL7_minus_lncRNA_AR..1	51	Gene SNORD13	SNORD13, U13, RNU13	small nucleolar RNA, C/D box 13	NR_003041		
GeneID:80139	ZNF703	8	37,553,301	37,556,396	3,095	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5194, 2_A375_pNL97_plus_lncRNA_AR..1..7467	-161, -161	upstream, upstream	1	1	0	21	20	4	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ZNF703	ZNF503L, ZNF703, FLJ14299	zinc finger protein 703	NM_025069, hCT13468.2	222760_at, 230586_s_at	NP_079345.1, EAW63370.1
GeneID:25960	GPR124	8	37,654,401	37,701,504	47,103	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5195, 2_A375_pNL97_plus_lncRNA_AR..1..7468	53087, 53119	downstream, downstream	1	1	0	17	19	6	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene GPR124	TEM5, FLJ14390, GPR124, DKFZp434J0911, DKFZp434C211, KIAA1531	G protein-coupled receptor 124	NM_032777, hCT2272687.0, hCT2272689.0, hCT2272691.0, hCT2353944.0, hCT14217.3, hCT1961335.1	221814_at, 65718_at	NP_116166.9, EAW63355.1, EAW63354.1, EAW63356.1, EAW63357.1, EAW63359.1, EAW63358.1
GeneID:55290	BRF2	8	37,701,398	37,707,431	6,033	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5195, 2_A375_pNL97_plus_lncRNA_AR..1..7468	-57, -89	upstream, upstream	1	1	0	17	19	6	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene BRF2	FLJ11052, TFIIIB50, BRF2, BRFU	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	NM_018310, hCT2271633.0, hCT2271635.0, hCT14216.2	218954_s_at, 218955_at	NP_060780.2, EAW63353.1, EAW63351.1, EAW63352.1
GeneID:80223	RAB11FIP1	8	37,716,465	37,757,015	40,550	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5195, 2_A375_pNL97_plus_lncRNA_AR..1..7468	49527, 49495	downstream, downstream	1	1	0	17	19	6	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene RAB11FIP1	MGC78448, rab11-FIP1, DKFZp686E2214, FLJ22524, NOEL1A, RCP, FLJ22622, RAB11FIP1	RAB11 family interacting protein 1 (class I)	NM_001002814, NM_025151, hCT2271630.1, hCT2271631.1, hCT14212.4	219681_s_at, 225177_at, 231830_x_at	NP_001002814.2, NP_079427.4, EAW63347.1, EAW63348.1, EAW63349.1
GeneID:9070	ASH2L	8	37,963,011	37,997,228	34,217	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5196, 2_A375_pNL97_plus_lncRNA_AR..1..7469	-35, -99	upstream, upstream	1	1	0	22	24	9	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ASH2L	ASH2L2, ASH2L1, ASH2L, Bre2, ASH2	ash2 (absent, small, or homeotic)-like (Drosophila)	NM_004674, NM_001105214, hCT2353890.0, hCT14208.3, hCT1958812.1, hCT1958813.1, hCT1958856.1	209517_s_at	NP_004665.2, NP_001098684.1, EAW63336.1, EAW63337.1, EAW63339.1, EAW63340.1, EAW63338.1
GeneID:27257	LSM1	8	38,020,857	38,034,026	13,169	-	1	4_A375_EGR1..1..7579	90	in gene	0	0	1	6	12	13	1	4_A375_EGR1..1	13	Gene LSM1	CASM, YJL124C, LSM1	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_014462, hCT2271622.0, hCT2353895.0	203534_at	NP_055277.1, EAW63332.1, EAW63333.1
GeneID:9530	BAG4	8	38,034,106	38,068,537	34,431	+	1	4_A375_EGR1..1..7579	-170	upstream	0	0	1	6	12	13	1	4_A375_EGR1..1	13	Gene BAG4	SODD, DKFZp586O2022, BAG4, BAG-4	BCL2-associated athanogene 4	NM_004874, hCT2272712.0, hCT2272714.0	219624_at, 222909_s_at, 228189_at	NP_004865.1, EAW63330.1, EAW63331.1
GeneID:23259	DDHD2	8	38,089,009	38,120,287	31,278	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5197, 2_A375_pNL97_plus_lncRNA_AR..1..7470	47, 175	in gene, in gene	1	1	0	20	21	7	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene DDHD2	SAMWD1, DDHD2, KIAA0725	DDHD domain containing 2	NM_015214, NM_001164232, NM_001164234, hCT2272716.0, hCT1825442.2	212690_at	NP_056029.2, NP_001157704.1, NP_001157706.1, EAW63323.1, EAW63324.1
GeneID:2260	FGFR1	8	38,268,656	38,326,352	57,696	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7471	144	in gene	0	1	0	11	15	6	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene FGFR1	N-SAM, CEK, FGFBR, FLJ99988, FLG, CD331, FLT2, FGFR1, OGD, KAL2, HBGFR, BFGFR	fibroblast growth factor receptor 1	NM_015850, NM_023106, NM_023105, NM_023110, NM_001174063, NM_001174064, NM_001174065, NM_001174066, NM_001174067, hCT2271922.0, hCT2271926.0, hCT2353910.0, hCT2353911.0, hCT2353912.0, hCT2353913.0, hCT2353914.0, hCT14209.2, hCT1961539.1, hCT1961540.1, hCT	207822_at, 207937_x_at, 210973_s_at, 211535_s_at, 215404_x_at, 222164_at, 226705_at	NP_056934.2, NP_075594.1, NP_075593.1, NP_075598.2, NP_001167534.1, NP_001167535.1, NP_001167536.1, NP_001167537.1, NP_001167538.1, EAW63303.1, EAW63304.1, EAW63305.1, EAW63306.1, EAW63307.1, EAW63308.1, EAW63309.1, EAW63310.1, EAW63311.1, EAW63312.1, EAW
GeneID:286	ANK1	8	41,510,744	41,754,280	243,536	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5201, 1_A375_pNL7_minus_lncRNA_AR..1..5202, 2_A375_pNL97_plus_lncRNA_AR..1..7474	176824, 660, 712	in gene, in gene, in gene	1	1	0	22	18.5	5.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ANK1	SPH1, ANK, ANK1, SPH2	ankyrin 1, erythrocytic	NM_020475, NM_020477, NM_000037, NM_020476, NM_001142445, NM_001142446, NM_020478, NM_020480, hCT2273031.1, hCT2273032.1, hCT2273034.1, hCT2273036.1, hCT2273037.1, hCT2273039.1, hCT2273040.1, hCT2273041.1, hCT2273044.1, hCT2273045.1	205389_s_at, 205390_s_at, 205391_x_at, 207087_x_at, 208352_x_at, 208353_x_at, 240363_at	NP_065208.2, NP_065210.2, NP_001135917.1, NP_001135918.1, NP_000028.3, NP_065209.2, NP_065213.2, NP_065211.2, EAW63241.1, EAW63242.1, EAW63243.1, EAW63244.1, EAW63245.1, EAW63246.1, EAW63247.1, EAW63248.1, EAW63249.1, EAW63250.1
GeneID:3551	IKBKB	8	42,128,820	42,190,171	61,351	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5203	67146	downstream	1	0	0	15	10	9	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene IKBKB	FLJ40509, IKK-beta, FLJ36218, MGC131801, FLJ33771, IKK2, NFKBIKB, FLJ38368, IKKB, IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	NM_001190720, NM_001190721, NM_001190722, NM_001556, NR_033818, NR_033819, NR_033820, hCT2272520.0, hCT2272521.0, hCT2353917.0, hCT2353918.0, hCT6445.1	209341_s_at, 209342_s_at, 211027_s_at	NP_001177649.1, NP_001177650.1, NP_001547.1, NP_001177651.1, EAW63222.1, EAW63225.1, EAW63223.1, EAW63224.1, EAW63226.1
GeneID:5423	POLB	8	42,196,030	42,229,313	33,283	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5203	-62	upstream	1	0	0	15	10	9	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene POLB	MGC125976, POLB	polymerase (DNA directed), beta	NM_002690, hCT6443.3	203616_at	NP_002681.1, EAW63221.1
GeneID:2339	FNTA	8	42,911,442	42,940,931	29,489	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5204, 2_A375_pNL97_plus_lncRNA_AR..1..7475	37582, 37582	downstream, downstream	1	1	0	21	23	6	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene FNTA	MGC99680, FNTA, PGGT1A, FPTA, PTAR2	farnesyltransferase, CAAX box, alpha	NM_002027, NR_033698, hCT2272180.0, hCT2272181.0, hCT2272182.0, hCT2353936.0, hCT2353937.0	200090_at, 209471_s_at, 230608_at	NP_002018.1, EAW63188.1, EAW63189.1, EAW63190.1, EAW63191.1, EAW63192.1
GeneID:84197	SGK196	8	42,946,657	42,976,323	29,666	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5204, 2_A375_pNL97_plus_lncRNA_AR..1..7475	367, 367	in gene, in gene	1	1	0	21	23	6	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene SGK196	MGC126597, FLJ23356	protein kinase-like protein SgK196	NM_032237, hCT1641972.2	1553246_a_at	NP_115613.1, EAW63187.1
GeneID:23514	KIAA0146	8	48,173,542	48,648,475	474,933	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7476	477962	downstream	0	1	0	9	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene KIAA0146	KIAA0146		NM_001080394	212523_s_at, 228325_at, 236284_at	NP_001073863.1
GeneID:1052	CEBPD	8	48,649,476	48,650,726	1,250	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7476	-776	upstream	0	1	0	9	16	10	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene CEBPD	CRP3, C/EBP-delta, NF-IL6-beta, CEBPD, CELF	CCAAT/enhancer binding protein (C/EBP), delta	NM_005195, hCT9382.3	203973_s_at, 213003_s_at, 213006_at	NP_005186.2, EAW86679.1
GeneID:5591	PRKDC	8	48,685,669	48,872,743	187,074	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7477	-601	upstream	0	1	0	23	36	9	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene PRKDC	XRCC7, HYRC, DNPK1, DNA-PKcs, DNAPK, p350, PRKDC, HYRC1	protein kinase, DNA-activated, catalytic polypeptide	NM_006904, NM_001081640, hCT2257125.1, hCT2257127.1, hCT2356850.0, hCT1951438.2	208694_at, 210543_s_at, 215757_at	NP_008835.5, NP_001075109.1, EAW86680.1, EAW86681.1, EAW86682.1, EAW86683.1
GeneID:4173	MCM4	8	48,873,494	48,890,068	16,574	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7477	-150	upstream	0	1	0	23	36	9	1	2_A375_pNL97_plus_lncRNA_AR..1	36	Gene MCM4	CDC54, MCM4, hCdc21, P1-CDC21, CDC21, MGC33310	minichromosome maintenance complex component 4	NM_182746, NM_005914, hCT2356865.0, hCT2356866.0, hCT10871.3	212141_at, 212142_at, 222036_s_at, 222037_at	NP_877423.1, NP_005905.2, EAW86684.1, EAW86685.1, EAW86686.1
GeneID:7336	UBE2V2	8	48,920,995	48,974,454	53,459	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5205	29	in gene	1	0	0	21	19	15	1	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene UBE2V2	UBE2V2, UEV2, DDVit-1, EDAF-1, EDPF1, DDVIT1, UEV-2, EDPF-1, MMS2	ubiquitin-conjugating enzyme E2 variant 2	NM_003350, hCT2256532.0, hCT2256534.0, hCT2356847.0, hCT1640632.3	209096_at	NP_003341.1, EAW86689.1, EAW86687.1, EAW86688.1, EAW86690.1
GeneID:644334	LOC644334	8	49,820,194	49,826,830	6,636	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5206, 2_A375_pNL97_plus_lncRNA_AR..1..7480, 2_A375_pNL97_plus_lncRNA_AR..1..7481	-7586, -7536, 13662	upstream, upstream, downstream	1	1	0	18	19	7	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene LOC644334		band 4.1-like protein 5-like	XM_001714497, XM_927497, XM_937001		XP_001714549.2, XP_932590.4, XP_942094.4
GeneID:6591	SNAI2	8	49,830,236	49,833,988	3,752	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7481	132	in gene	0	1	0	11	15	9	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene SNAI2	SNAI2, SLUG, WS2D, MGC10182, SLUGH1	snail homolog 2 (Drosophila)	NM_003068, hCT23486.3	213139_at	NP_003059.1, EAW86700.1
GeneID:54212	SNTG1	8	50,824,597	51,705,427	880,830	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5207, 2_A375_pNL97_plus_lncRNA_AR..1..7482, 2_A375_pNL97_plus_lncRNA_AR..1..7483, 2_A375_pNL97_plus_lncRNA_AR..1..7484, 4_A375_EGR1..1..7583	-293, -309, 144635, 651371, 579531	upstream, upstream, in gene, in gene, in gene	1	1	1	11.75	16	7.25	4	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene SNTG1	SNTG1, SYN4, G1SYN	syntrophin, gamma 1	NM_018967, hCT2256444.0, hCT2256447.0, hCT18216.2	1562287_at, 220405_at, 234919_s_at	NP_061840.1, EAW86704.1, EAW86705.1, EAW86706.1
GeneID:137902	PXDNL	8	52,232,137	52,722,005	489,868	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5208, 2_A375_pNL97_plus_lncRNA_AR..1..7485	414421, 414357	in gene, in gene	1	1	0	24	23	4	1	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene PXDNL	PXDNL, VPO2, FLJ25471	peroxidasin homolog (Drosophila)-like	NM_144651, hCT2356868.0, hCT1950898.2	241942_at	NP_653252.3, EAW86708.1, EAW86707.1
GeneID:115294	PCMTD1	8	52,730,140	52,811,735	81,595	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7486, 4_A375_EGR1..1..7585	-281, -137	upstream, upstream	0	1	1	14	16	20	1	4_A375_EGR1..1	20	Gene PCMTD1	PCMTD1, FLJ10883	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	NM_052937, hCT2256604.0, hCT2256605.0, hCT2356874.0, hCT18213.3	226119_at, 232382_s_at, 235507_at, 238114_at, 244706_at	NP_443169.2, EAW86711.1, EAW86710.1, EAW86712.1, EAW86713.1
GeneID:100287313	LOC100287313	8	52,811,842	52,859,733	47,891	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7486, 4_A375_EGR1..1..7585	174, 30	in gene, in gene	0	1	1	14	16	20	1	4_A375_EGR1..1	20	Gene LOC100287313		hypothetical protein LOC100287313	XM_002342851		XP_002342892.2
GeneID:389658	FAM150A	8	53,446,597	53,478,021	31,424	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7487, 4_A375_EGR1..1..7587	29157, 165	in gene, in gene	0	1	1	9	12.5	14	2	4_A375_EGR1..1	22	Gene FAM150A	MGC163515, FAM150A, UNQ9433, MGC163513	family with sequence similarity 150, member A	NM_207413		NP_997296.1
GeneID:9821	RB1CC1	8	53,535,018	53,627,026	92,008	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7488, 2_A375_pNL97_plus_lncRNA_AR..1..7489	1170, -302	in gene, upstream	0	1	0	13	19.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene RB1CC1	FIP200, CC1, RB1CC1	RB1-inducible coiled-coil 1	NM_014781, NM_001083617, hCT2256600.0, hCT2356864.0, hCT18217.3	202033_s_at, 202034_x_at	NP_055596.3, NP_001077086.1, EAW86719.1, EAW86720.1, EAW86721.1
GeneID:2831	NPBWR1	8	53,852,468	53,853,454	986	+	1	4_A375_EGR1..1..7588	1244	downstream	0	0	1	9	8	16	1	4_A375_EGR1..1	16	Gene NPBWR1	GPR7, MGC129755, NPBWR1	neuropeptides B/W receptor 1	NM_005285, hCT1646408.3	231752_at	NP_005276.2, EAW86722.1
GeneID:8601	RGS20	8	54,764,366	54,871,863	107,495	+	6	1_A375_pNL7_minus_lncRNA_AR..1..5210, 2_A375_pNL97_plus_lncRNA_AR..1..7491, 2_A375_pNL97_plus_lncRNA_AR..1..7492, 4_A375_EGR1..1..7591, 4_A375_EGR1..1..7592, 4_A375_EGR1..1..7593	29840, 28720, 29376, 28219, 29136, 30736	in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	13.5	14	19	2	4_A375_EGR1..1	22	Gene RGS20	ZGAP1, RGSZ1, RGS20	regulator of G-protein signaling 20	NM_170587, NM_003702, hCT2256642.0, hCT1826267.3, hCT1962680.1, hCT1962681.1, hCT1962682.1	1569303_s_at, 210138_at	NP_733466.1, NP_003693.2, EAW86734.1, EAW86736.1, EAW86737.1, EAW86738.1, EAW86735.1
GeneID:6917	TCEA1	8	54,879,116	54,935,008	55,892	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5211, 2_A375_pNL97_plus_lncRNA_AR..1..7493	96, 64	in gene, in gene	1	1	0	63	65	6	1	2_A375_pNL97_plus_lncRNA_AR..1	65	Gene TCEA1	TCEA, GTF2S, SII, TFIIS, TF2S, TCEA1	transcription elongation factor A (SII), 1	NM_006756, NM_201437, hCT2257345.0, hCT2257346.0, hCT1951437.1	1566207_at, 1566208_at, 216241_s_at	NP_006747.1, NP_958845.1, EAW86739.1, EAW86740.1, EAW86741.1
GeneID:29088	MRPL15	8	55,047,761	55,061,074	13,293	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5212, 2_A375_pNL97_plus_lncRNA_AR..1..7494	18171, 18287	downstream, downstream	1	1	0	26	17	5	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene MRPL15	MRP-L15, MRPL15, RPML7, L15mt, MRP-L7, HSPC145	mitochondrial ribosomal protein L15	NM_014175, hCT31676.2	218027_at	NP_054894.1, EAW86747.1
GeneID:114786	XKR4	8	56,015,017	56,438,714	423,697	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5214, 2_A375_pNL97_plus_lncRNA_AR..1..7495, 4_A375_EGR1..1..7594, 4_A375_EGR1..1..7595, 4_A375_EGR1..1..7596	471, 535, 348727, 349271, 395991	in gene, in gene, in gene, in gene, in gene	1	1	1	12.25	17	15.5	4	2_A375_pNL97_plus_lncRNA_AR..1	46	Gene XKR4	XKR4, KIAA1889, XRG4	XK, Kell blood group complex subunit-related family, member 4	NM_052898	237802_at	NP_443130.1
GeneID:137695	TMEM68	8	56,651,320	56,685,885	34,565	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5215, 2_A375_pNL97_plus_lncRNA_AR..1..7496	61, 13	in gene, in gene	1	1	0	16	21	10	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TMEM68	TMEM68, FLJ32370, MGC87778	transmembrane protein 68	NM_152417, hCT2257245.0, hCT2356867.0, hCT32270.3	226483_at, 227936_at	NP_689630.1, EAW86760.1, EAW86758.1, EAW86759.1
GeneID:96764	TGS1	8	56,685,791	56,738,005	52,214	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5215, 2_A375_pNL97_plus_lncRNA_AR..1..7496	33, 81	in gene, in gene	1	1	0	16	21	10	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene TGS1	FLJ22995, NCOA6IP, PIPMT, DKFZp762A163, PIMT, TGS1	trimethylguanosine synthase 1	NM_024831, hCT2257001.0, hCT2356854.0, hCT1951449.2	219231_at, 236371_s_at, 238346_s_at	NP_079107.6, EAW86763.1, EAW86761.1, EAW86762.1
GeneID:6224	RPS20	8	56,980,739	56,987,140	6,401	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5216, 2_A375_pNL97_plus_lncRNA_AR..1..7497	-26, -26	upstream, upstream	1	1	0	130	143	11	1	2_A375_pNL97_plus_lncRNA_AR..1	143	Gene RPS20	MGC102930, RPS20, S20, FLJ27451	ribosomal protein S20	NM_001023, NM_001146227, hCT32015.3, hCT1958251.1, hCT1958253.1	200949_x_at, 214003_x_at	NP_001014.1, NP_001139699.1, EAW86770.1, EAW86771.1, EAW86772.1
GeneID:26795	SNORD54	8	56,986,398	56,986,460	62	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5216, 2_A375_pNL97_plus_lncRNA_AR..1..7497	-708, -708	upstream, upstream	1	1	0	130	143	11	1	2_A375_pNL97_plus_lncRNA_AR..1	143	Gene SNORD54	U54, SNORD54, RNU54	small nucleolar RNA, C/D box 54	NR_002437		
GeneID:5324	PLAG1	8	57,073,468	57,123,859	50,391	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7498	-877	upstream	0	1	0	10	13	13	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene PLAG1	PLAG1, PSA, ZNF912, SGPA	pleiomorphic adenoma gene 1	NM_002655, NM_001114634, NM_001114635, hCT2259207.0, hCT32013.2	205372_at	NP_002646.2, NP_001108106.1, NP_001108107.1, EAW86774.1, EAW86775.1
GeneID:79145	CHCHD7	8	57,124,315	57,131,178	6,863	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7498	421	in gene	0	1	0	10	13	13	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene CHCHD7	CHCHD7, MGC2217, FLJ40966	coiled-coil-helix-coiled-coil-helix domain containing 7	NM_001011667, NM_001011668, NM_001011669, NM_001011670, NM_001011671, NM_024300, hCT2356868.0, hCT2356869.0, hCT2356870.0, hCT32019.3	218642_s_at, 222701_s_at	NP_001011667.1, NP_001011668.1, NP_001011669.1, NP_001011670.1, NP_001011671.1, NP_077276.2, EAW86776.1, EAW86777.1, EAW86778.1, EAW86779.1
GeneID:5179	PENK	8	57,353,513	57,359,282	5,769	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7499, 4_A375_EGR1..1..7597	1234, 754	in gene, in gene	0	1	1	9	21	17	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PENK	PENK		NM_006211, NM_001135690, hCT2259232.0, hCT2259233.0, hCT32018.3	213791_at	NP_006202.1, NP_001129162.1, EAW86785.1, EAW86786.1, EAW86787.1
GeneID:100507651	LOC100507651	8	58,131,648	58,145,380	13,732	+	1	4_A375_EGR1..1..7598	-6600	upstream	0	0	1	21	21	40	1	4_A375_EGR1..1	40	Gene LOC100507651		hypothetical LOC100507651	XR_108908		
GeneID:26136	C8orf71	8	58,192,102	58,197,290	5,188	+	2	4_A375_EGR1..1..7600, 4_A375_EGR1..1..7601	-326, 314	upstream, in gene	0	0	1	4	5.5	13.5	2	4_A375_EGR1..1	14	Gene C8orf71	C8orf71, DKFZp434F122	chromosome 8 open reading frame 71	NR_026772	210464_at	

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	1_A375_2_A375_untU7_minus_lncRNA_R1_1 Percent	2_A375_untU7_minus_lncRNA_R1_1 Percent	3_A375_1_untU7_plus_lncRNA_R1_1 Percent	1_A375_plus_lncRNA_R1_1 Avg Peak	2_A375_plus_lncRNA_R1_1 Avg Peak	3_A375_plus_lncRNA_R1_1 Avg Peak	Ad Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:1617096	UBXN2B	8	99,225,625	99,264,960	40,227	+	1	2_A375_untU7_plus_lncRNA_R1_1:7500	51	cr gene	0	1	0	5	15	7	1	2_A375_untU7_plus_lncRNA_R1_1	15	Gene UBXN2B	UBXN2B, p37	UBX domain protein 2B	NM_031077619		212934_at, 218933_at	NP_001073557.1
GeneID:8390599	SIDCBP	8	99,265,726	99,295,419	29,691	+	1	4_A375_DGR1.1:7903	-299	upstream	0	0	1	14	13	16	1	4_A375_DGR1.1	15	Gene SIDCBP	SYCL, TACIP18, sIBP+, SIT1, SIDCBP	syntaxuin binding protein thyroiocyte	NM_001007097, NM_001007095, NM_001007089, NM_001007070, NM_003953, XCT229554.2, XCT229554.3, XCT229554.4, XCT1620834.1, XCT1620834.1	200955_s_at	NP_001007098.1, NP_001007095.1, NP_001007089.1, NP_001007070.1, NP_003944.2, EAW68512.1, EAW68513.1, EAW68514.1, EAW68515.1, EAW68516.1
GeneID:8409399	NSMAF	8	99,446,983	99,572,404	99,341	-	1	2_A375_untU7_plus_lncRNA_R1_1:7501	98k	cr gene	0	1	0	16	16	10	1	2_A375_untU7_plus_lncRNA_R1_1	15	Gene NSMAF	FAN, NSMAF	acidic sphingomyelinase (N-SMase) activator associated factor	NM_0035900, NM_001144772, XCT1910445.1	1558773_s_at, 203398_at, 232145_at, 232149_s_at, 240696_at	NP_0035912, NP_001138244.1, EAW68517.1
GeneID:3977	TOX	8	99,717,977	99,831,767	113,790	+	1	1_A375_untU7_minus_lncRNA_R1_1:5218	3174/95	downstream	1	0	0	14	16	4	1	1_A375_untU7_minus_lncRNA_R1_1	14	Gene TOX	TOX, KIAA0930, TOX1	thymocyte selection-associated high mobility group box	NM_014729, XCT2257978.0, XCT30999.3	204429_s_at, 204430_s_at	NP_0536944.1, EAW68819.1, EAW68818.1
GeneID:7852	CAS	8	81,161,425	81,193,954	32,531	-	1	4_A375_DGR1.1:7905	452	cr gene	0	0	1	8	9	10	1	4_A375_DGR1.1	15	Gene CAS	CAS, CAS3, CAS-L, NSLCAPR22, MGC130922, MGC99399, CasBP	substrate trap for	NM_0364358, XCT2258701.1, XCT2307077.0, XCT1900990.3	1558445_at, 220234_at	NP_3963473, EAW68826.1, EAW68825.1, EAW68826.1
GeneID:1810555332	LOC100505332	8	81,318,771	81,326,377	10,606	-	2	1_A375_untU7_minus_lncRNA_R1_1:8219, 2_A375_untU7_plus_lncRNA_R1_1:7501	205, -3551	cr gene, upstream	1	1	0	14	15	8	2	2_A375_untU7_plus_lncRNA_R1_1	16	Gene LOC100505332		hypothetical LOC100505332	XR_112143, XR_109312, XR_114176		
GeneID:8396836	CHD7	8	61,691,339	61,779,465	169,126	+	1	4_A375_DGR1.1:7907	39797	cr gene	0	0	1	9	8	12	1	4_A375_DGR1.1	12	Gene CHD7	KIAA, CHD7, FLJ20337, ISS, FLJ20391, KIAA1416	chromodomain helicase DNA binding protein 7	NM_017780, XCT229474.0, XCT2284741.0, XCT2284742.0, XCT2284743.0, XCT2284744.0	219629_s_at, 239819_at, 222793_s_at, 226123_at	NP_3982832, EAW68831.1, EAW68830.1, EAW68832.1, EAW68833.1, EAW68834.1
GeneID:1907	CLVS1	8	62,200,925	62,414,304	213,379	+	4	1_A375_untU7_minus_lncRNA_R1_1:8222, 2_A375_untU7_minus_lncRNA_R1_1:8223, 3_A375_untU7_plus_lncRNA_R1_1:7506, 4_A375_untU7_plus_lncRNA_R1_1:7507	207, 208273, 243, 208371	cr gene, cr gene, cr gene, cr gene	1	1	0	32	30.5	7	2	2_A375_untU7_plus_lncRNA_R1_1	643	Gene CLVS1	CLVS1, RLBP1L1	clavesin 1	NM_175519, XCT2345727.0, XCT1862297.3	230217_at	NP_7757911, EAW68839.1, EAW68838.1
GeneID:4444	ASPH	8	62,415,113	62,627,199	214,894	+	8	1_A375_untU7_minus_lncRNA_R1_1:8223, 2_A375_untU7_minus_lncRNA_R1_1:8224, 3_A375_untU7_minus_lncRNA_R1_1:8225, 4_A375_untU7_plus_lncRNA_R1_1:7501, 5_A375_untU7_plus_lncRNA_R1_1:7508, 6_A375_untU7_plus_lncRNA_R1_1:7509	218399, 122643, 95845, 219332, 129643, 207	downstream, cr gene, upstream, downstream, cr gene, cr gene	1	1	0	22.75	22.3	8.25	4	2_A375_untU7_plus_lncRNA_R1_1	643	Gene ASPH	HAH1, CASQBP1, JCTN, AAH, ASPH, BAH, junctin	aspartate beta-hydroxylase	NM_004318, NM_032466, NM_032466, NM_001164780, NM_020164, NM_001164781, NM_001164782, NM_032467, NM_001164783, NM_001164784, NM_001164785, NM_001164786, XCT2171262.0, XCT2171264.0, XCT2171266.0, XCT2171269.0, XCT2212191.0, XCT2171263.0, XCT2171267.0, XCT2	209956_at, 209764_s_at, 209765_at, 209766_s_at	NP_3943092, NP_115583.1, NP_001159222.1, NP_001159223.1, NP_064349.1, NP_115836.1, NP_001159224.1, NP_001159225.1, NP_001159226.1, NP_001159227.1, NP_001159228.1, EAW68840.1, EAW68841.1, EAW68842.1, EAW68843.1, EAW68844.1, EAW68845.1, EAW688
GeneID:3943	YTHDF3	8	64,081,101	64,125,346	44,225	+	3	2_A375_untU7_plus_lncRNA_R1_1:7511, 3_A375_untU7_plus_lncRNA_R1_1:7512, 4_A375_DGR1.1:7908	-140, 91551, 267	upstream, downstream, cr gene	0	1	1	14.5	19	11.5	2	2_A375_untU7_plus_lncRNA_R1_1	21	Gene YTHDF3	FLJ10557, YTHDF3	YT521-B homolog family, member 3	NM_152758, XCT2336551.0, XCT2336552.0, XCT2336553.0, XCT2347.3	1564553_a_at, 221749_at	NP_689774.4, EAW68598.1, EAW68597.1, EAW68596.1, EAW68595.1, EAW68
GeneID:1301555	LOC100505155	8	65,255,775	65,291,395	5,613	+	2	1_A375_untU7_minus_lncRNA_R1_1:8226, 2_A375_untU7_plus_lncRNA_R1_1:7512	6983, 6769	downstream, downstream	1	1	0	16	26	8	1	2_A375_untU7_plus_lncRNA_R1_1	26	Gene LOC100505155		hypothetical LOC100505155	NR_024102, NR_034103		
GeneID:4438	MIR124-2	8	65,291,796	65,291,914	102	+	2	1_A375_untU7_minus_lncRNA_R1_1:8228, 2_A375_untU7_plus_lncRNA_R1_1:7512	934, 838	downstream, downstream	1	1	0	16	26	8	1	2_A375_untU7_plus_lncRNA_R1_1	26	Gene MIR124-2	MIRN124A2, MIRN124-2, MIR124-2	microRNA 124-2	NR_029869		
GeneID:1388	ARMC1	8	99,814,491	99,846,452	31,781	-	2	1_A375_untU7_minus_lncRNA_R1_1:8230, 2_A375_untU7_plus_lncRNA_R1_1:7513	100, 116	cr gene, cr gene	1	1	0	17	20	12	1	2_A375_untU7_plus_lncRNA_R1_1	20	Gene ARMC1	FLJ10311, MNAC1, Armc	armadillo repeat containing 1	NM_018120, XCT31765.3	218165_s_at, 222593_at	NP_3963901, EAW68600.1
GeneID:5150	PDE7A	8	86,829,905	86,955,755	123,850	-	5	1_A375_untU7_minus_lncRNA_R1_1:8231, 2_A375_untU7_plus_lncRNA_R1_1:7514, 3_A375_DGR1.1:7909	-932, -561, -933	upstream, upstream, upstream	1	1	1	19	16	17	1	1_A375_untU7_plus_lncRNA_R1_1	19	Gene PDE7A	PDE7, HCP1, PDE7A	phosphodiesterase 7A	NM_002603, NM_002604, XCT1995677.2, XCT2307727.1, XCT2307730.1, XCT31764.2	1552243_s_at, 223359_s_at, 224548_s_at	NP_0025944.1, NP_002598.1, EAW68554.1, EAW68553.1, EAW68555.1
GeneID:6859479	DNAJC3IB	8	88,933,791	87,012,765	78,944	+	1	1_A375_untU7_minus_lncRNA_R1_1:8232	6057	cr gene	1	0	0	22	12	6	1	1_A375_untU7_plus_lncRNA_R1_1	22	Gene DNAJC3IB	DNAJC3IB, CSPI, beta, MGC26226	DnaJ (Hsp40) homolog, subfamily C, member 3 beta	NM_032105, XCT2236423.0, XCT2236424.0, XCT9447.2	1554256_a_at, 222790_at	NP_1490362, EAW68699.1, EAW68697.1, EAW68698.1
GeneID:8475	TRIM55	8	87,039,276	87,087,720	48,442	+	5	1_A375_untU7_minus_lncRNA_R1_1:8234, 2_A375_untU7_plus_lncRNA_R1_1:7515, 3_A375_untU7_plus_lncRNA_R1_1:7520, 4_A375_DGR1.1:7911, 4_A375_DGR1.1:7912	59632, -2936, 59645, 6109, 59194	downstream, upstream, downstream, cr gene, downstream	1	1	1	23.67	27	12	3	2_A375_untU7_plus_lncRNA_R1_1	23	Gene TRIM55	TRIM55, MURF2, E, RNF29	tripartite motif containing 55	NM_033058, NM_184083, NM_184084, NM_184087, XCT2236432.0, XCT2236540.0, XCT9446.5	232721_at, 236179_at	NP_1490472.2, NP_9695751, NP_9695752, NP_9695753, EAW68693.1, EAW68692.1, EAW68694.1
GeneID:1363	CRH	8	87,666,612	87,690,948	2,234	-	3	1_A375_untU7_minus_lncRNA_R1_1:8234, 2_A375_untU7_plus_lncRNA_R1_1:7520, 3_A375_DGR1.1:7912	1808, 1022, 1374	cr gene, cr gene, cr gene	1	1	1	33	33	19	1	2_A375_untU7_plus_lncRNA_R1_1	33	Gene CRH	CRH, CRF	corticotropin releasing hormone	NM_000756, XCT1639998.3	203629_s_at, 203630_at	NP_000747.1, EAW68697.1
GeneID:1005976	LOC100505976	8	87,231,622	87,241,212	9,590	-	3	1_A375_untU7_minus_lncRNA_R1_1:8235, 2_A375_untU7_plus_lncRNA_R1_1:7521, 3_A375_DGR1.1:7910	76, 92, -420	cr gene, cr gene, upstream	1	1	1	19	26	20	1	2_A375_untU7_plus_lncRNA_R1_1	26	Gene LOC100505976		hypothetical LOC100505976	XR_112143, XR_109317, XR_114180		
GeneID:2212	RRS1	8	87,241,240	87,342,966	1,705	+	3	1_A375_untU7_minus_lncRNA_R1_1:8233, 2_A375_untU7_plus_lncRNA_R1_1:7521, 3_A375_DGR1.1:7913	-127, -143, 399	upstream, upstream, cr gene	1	1	1	19	26	20	1	2_A375_untU7_plus_lncRNA_R1_1	26	Gene RRS1	RRS1, KIAA0112	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	NM_015189, XCT1639902.2	209587_at	NP_0559664.1, EAW68900.1
GeneID:7672	ADHFE1	8	87,344,716	87,351,944	99,228	+	3	1_A375_untU7_minus_lncRNA_R1_1:8235, 2_A375_untU7_plus_lncRNA_R1_1:7521, 3_A375_DGR1.1:7913	-3982, -3596, -3066	upstream, upstream, upstream	1	1	1	19	26	20	1	2_A375_untU7_plus_lncRNA_R1_1	26	Gene ADHFE1	HOT, ADHE, MGC40950, FLJ32430, ADHFE1, HeFT2282	alcohol dehydrogenase, iron-containing, 1	NM_144650, XCT2236436.0, XCT2236435.0, XCT2236439.0, XCT2236552.0, XCT2236553.0, XCT2236554.0, XCT2236555.0	227112_at	NP_6322912, EAW68916.1, EAW68915.1, EAW68912.1, EAW68913.1, EAW68914.1, EAW68907.1
GeneID:4486	MYBL1	8	87,474,410	87,525,450	51,070	-	2	1_A375_untU7_minus_lncRNA_R1_1:8236, 2_A375_untU7_plus_lncRNA_R1_1:7522	-45, -130	upstream, upstream	1	1	0	17	20	12	1	2_A375_untU7_plus_lncRNA_R1_1	20	Gene MYBL1	A-MYB, MGC120081, MYB, MYBL1, MGC120083	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	NM_0015584.16, NM_001144755	213906_at	NP_3010736.5, NP_001138227.1
GeneID:8357	VCPIP1	8	87,542,486	87,579,452	36,966	-	2	1_A375_untU7_minus_lncRNA_R1_1:8237, 2_A375_untU7_plus_lncRNA_R1_1:7523	-102, -148	upstream, upstream	1	1	0	22	29	9	1	2_A375_untU7_plus_lncRNA_R1_1	29	Gene VCPIP1	EUBH2, FLJ40894, DKFZp686I09232, FLJ23122, VCPIP1, VCIP135, KIAA1555	valosin containing protein (p97)/p47 complex-interacting protein 1	NM_025054, XCT1844812.3	1558227_at, 1558228_a_at, 219610_at, 234868_at	NP_0792302, EAW68916.1
GeneID:7777	C8orf84	8	87,655,454	87,693,255	4,781	+	2	1_A375_untU7_minus_lncRNA_R1_1:8237, 2_A375_untU7_plus_lncRNA_R1_1:7523	-9995, -9956	upstream, upstream	1	1	0	22	29	9	1	2_A375_untU7_plus_lncRNA_R1_1	29	Gene C8orf84	C8orf84, FLJ11267	chromosome 8 open reading frame 84	NM_019097, XCT1810228.1, XCT1810230.2	220218_at	NP_9823551, EAW68917.1, EAW68918.1
GeneID:2305	SIGIRR	8	87,824,991	87,974,297	149,306	+	1	4_A375_untU7_plus_lncRNA_R1_1:7524	91	upstream	0	1	0	12	19	4	1	4_A375_untU7_plus_lncRNA_R1_1	19	Gene SIGIRR	DKFZp761M2910, SIGI2, SIGI2, C9ID, SIgIL	interleukin one receptor antagonist	NM_152237, NM_178709, NM_001033576, XCT2255445.0, XCT9446.0	219058_at, 227627_at	NP_6313894, NP_7552972, NP_9312375.1, EAW68919.1, EAW68920.1
GeneID:7777	C8orf84	8	87,762,164	87,834,393	81,299	+	2	1_A375_untU7_minus_lncRNA_R1_1:8238, 4_A375_DGR1.1:7914	54744, 54594	downstream, downstream	1	1	0	19	14	16	1	1_A375_untU7_minus_lncRNA_R1_1	19	Gene C8orf43	C8orf43, FLJ25892	chromosome 8 open reading frame 43	NM_173518, NM_001130190, NM_001130191, XCT2344086.0, XCT2346932.0, XCT2346933.0	1553259_at, 1558677_a_at	NP_7767853, NP_0011296321, NP_001129633.1, EAW68921.1, EAW68922.1, EAW68923.1
GeneID:1635	SNHG8	8	87,834,165	87,837,777	3,612	+	2	1_A375_untU7_minus_lncRNA_R1_1:8238, 4_A375_DGR1.1:7914	410, 209	cr gene, cr gene	1	1	0	19	14	16	1	1_A375_untU7_minus_lncRNA_R1_1	19	Gene SNHG8	NCRNA00095, U87HG, SNHG8, HBI-27HG	small nucleolar RNA host gene 8 (non-protein coding)	NR_002599	223547_at	
GeneID:1640	SNORD87	8	87,834,709	87,834,764	55	-	2	1_A375_untU7_minus_lncRNA_R1_1:8238, 4_A375_DGR1.1:7914	-2944, -2756	upstream, upstream	1	1	0	19	14	16	1	1_A375_untU7_minus_lncRNA_R1_1	19	Gene SNORD87	U87, SNORD87, HBI-278	small nucleolar RNA, C/D box 87	NR_002598		
GeneID:2810	LRRC8D	8	87,900,366	87,940,766	40,420	-	1	4_A375_untU7_plus_lncRNA_R1_1:7523	20862	cr gene	0	1	0	12	20	9	1	2_A375_untU7_plus_lncRNA_R1_1	20	Gene LRRC8D	LRRC8F, dh	leucine rich repeat containing 8D	NM_0010136826, XCT1616661.2		NP_0010136461, EAW68927.1
GeneID:1007	COPS5	8	87,955,314	87,974,362	19,048	-	5	1_A375_untU7_minus_lncRNA_R1_1:8239, 2_A375_untU7_minus_lncRNA_R1_1:7526, 3_A375_untU7_plus_lncRNA_R1_1:7527, 4_A375_untU7_plus_lncRNA_R1_1:7528, 4_A375_DGR1.1:7915	-1962, 194, -1950, -3695, 430	upstream, cr gene, upstream, upstream, cr gene	1	1	1	33.33	43.33	11.33	3	2_A375_untU7_plus_lncRNA_R1_1	643	Gene COPS5	MOV-34, COPS5, JAB1, MGC3141, SGN5, CSN5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	NM_006837, XCT2257621.0, XCT2257622.0, XCT2257624.0, XCT9447.3	201952_at	NP_0068202.2, EAW68920.1, EAW68919.1, EAW68929.1, EAW68930.1
GeneID:3445	CSPP1	8	87,976,603	88,108,649	132,248	+	5	1_A375_untU7_minus_lncRNA_R1_1:8239, 2_A375_untU7_plus_lncRNA_R1_1:7526, 3_A375_untU7_plus_lncRNA_R1_1:7527, 4_A375_untU7_plus_lncRNA_R1_1:7528, 4_A375_DGR1.1:7915	-39, -2251, -91, 643, -3491	upstream, upstream, upstream, cr gene, upstream	1	1	1	33.33	43.33	11.33	3	2_A375_untU7_plus_lncRNA_R1_1	643	Gene CSPP1	CSPP, FLJ32449, FLJ38598, CSPP1	centrosome and spindle pole associated protein	NM_024790, XCT2257176.0, XCT2257180.0, XCT2257183.0	1554573_a_at, 220072_at, 221303_s_at, 221103_at, 242041_at	NP_3740883, EAW68922.1, EAW68923.1, EAW68924.1
GeneID:5565	ARFGEF1	8	66,109,597	66,255,912	146,315	-	1	4_A375_untU7_plus_lncRNA_R1_1:7529	6	cr gene	0	1	0	6	16	6	1	2_A375_untU7_plus_lncRNA_R1_1	16	Gene ARFGEF1	ARFGEF1, D75S2E01EH4, BIG1, ARFGEF1, D75S2D1EH4, MFGEF1, DKFZp434I037, BIG1, P200	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	NM_006421, XCT1619464.4, XCT1962100.1	202953_s_at, 202936_at, 216295_s_at	NP_0096122, EAW68933.1, EAW68934.1
GeneID:7848	SLCO3A1	8	70,864,986	70,747,299	182,791	-	2	1_A375_untU7_minus_lncRNA_R1_1:7530, 4_A375_DGR1.1:7917	63823, 2574	cr gene, cr gene	0	1	1	11	13.5	11	2	2_A375_untU7_plus_lncRNA_R1_1	15	Gene SLCO3A1	OATP-J, SLCO3A1, SLC21A10, OATP3A1, FLJ38565, OATPRPN	solute carrier organic anion transporter family, member 3A1	NM_013355, NM_001145809, NM_001145808, XCT2356772.0, XCT6424.2	220964_s_at	NP_1223202, NP_0011394511, NP_0011394501, EAW68937.1, EAW68936.1
GeneID:1007760	LOC100505760	8	70,746,394	70,750,994	2,700	+	1	4_A375_DGR1.1:7917	-1639	upstream	0	0	1	8	12	15	1	4_A375_DGR1.1	15	Gene LOC100505760		hypothetical LOC100505760	XR_103923		
GeneID:8357	PRDM14	8	70,984,021	70,993,982	10,541	-	2	1_A375_DGR1.1:7918, 4_A375_DGR1.1:7919	1658, 286	cr gene, cr gene	0	0	1	5.5	8.5	10	2	4_A375_DGR1.1	19	Gene PRDM14	PRDM14, PFM11, MGC29730	PR domain containing 14	NM_024504, XCT9507.2	220714_at	NP_5767051, EAW68982.1
GeneID:1007	NCOA2	8	71,224,287	71,316,020	91,733	-	2	1_A375_untU7_minus_lncRNA_R1_1:7532, 2_A375_untU7_plus_lncRNA_R1_1:7533	276020, 1444	cr gene, cr gene	0	1	0	9	19	8	2	2_A375_untU7_plus_lncRNA_R1_1	19	Gene NCOA2	KAT13C, MGC139893, GRIP1, TIF2, bHLHe75, NCOA2, hNCoA-62, SRT1SC	nuclear receptor coactivator 2	NM_006540, XCT9508.3	202731_s_at, 202732_s_at, 219853_at	NP_3068311, EAW68983.1
GeneID:2271	TRAM1	8	71,455,455	71,520,894	65,241	-	2	1_A375_untU7_minus_lncRNA_R1_1:8240, 2_A375_untU7_plus_lncRNA_R1_1:7534	-10, 6	upstream, cr gene	1	1	0	61	66	16	1	2_A375_untU7_plus_lncRNA_R1_1	66	Gene TRAM1	PNAS5, TRAM1, PRO1292, TRAM-1	translocation associated membrane protein 1	NM_014294, XCT2259140.0, XCT2259507.0, XCT9508.2	201395_s_at, 201099_s_at, 210752_at	NP_0559351, EAW68987.1, EAW68986.1, EAW68985.1
GeneID:1110	LACTB2	8	71,849,901	71,881,447	31,546	-	2	1_A375_untU7_minus_lncRNA_R1_1:8241, 2_A375_untU7_plus_lncRNA_R1_1:7535	187, 67	cr gene, cr gene	1	1	0	16	16	14	1	1_A375_untU7_minus_lncRNA_R1_1	16	Gene LACTB2	LACTB2, CGI-43	lactamase, beta 2	NM_016027, XCT2259148.0, XCT1988088.2	218701_at, 222714_s_at	NP_057111.1, EAW68990.1, EAW68989.1
GeneID:9986	XIRP2	8	71,881,800	71,946,177	64,377	+	2	1_A375_untU7_minus_lncRNA_R1_1:8241, 2_A375_untU7_plus_lncRNA_R1_1:7535	-320, -240	upstream, upstream	1	1	0	16	16	14	1	1_A375_untU7_minus_lncRNA_R1_1	16	Gene XIRP2	XIRP2, XIRP	XI-, fast blood glucose variation-related Bckdy, member B	NM_031117120, XCT1647422.2		NP_0010117201, EAW68971.1
GeneID:2271	EYA1	8	72,109,966	72,274,467	164,798	+	3	1_A375_untU7_minus_lncRNA_R1_1:8242, 2_A375_untU7_plus_lncRNA_R1_1:7536, 3_A375_DGR1.1:7920	98131, 98131, 165819	cr gene, cr gene, cr gene	1	1	1	17	14.5	9	2	2_A375_untU7_plus_lncRNA_R1_1	29	Gene EYA1	MGC141975, EYA1, BOR, BOR	eyes absent homolog 1 (Drosophila)	NM_172065, NM_172058, NM_000503, NM_172059, XCT2257475.0, XCT2356559.0, XCT2356560.0, XCT2356561.0, XCT2356562.0, XCT5429.2, XCT1961849.1, XCT1961850.1	214656_s_at	NP_7420371, NP_7420381, NP_0094942, NP_7420391, EAW68975.1, EAW68974.1, EAW68973.1, EAW68972.1, EAW68976.1, EAW68977.1, EAW68978.1, EAW68980.1
GeneID:9053	MSC	8	72,753,777	72,756,701	2,934	+	1	4_A375_untU7_plus_lncRNA_R1_1:7535	411	cr gene	0	1	0	21	23	10	1	2_A375_untU7_plus_lncRNA_R1_1	23	Gene MSC	MYOR, AMY-1, MSC, bHLHb22, HBF1	myocardin	NM_0309016, XCT9712.3	209605_s_at	NP_9359892, EAW68994.1
GeneID:1102391	LOC100132891	8	72,755,336	72,966,947	210,189	+	1	2_A375_untU7_plus_lncRNA_R1_1:7535	982	cr gene	0	1	0	21	23	10	1	2_A375_untU7_plus_lncRNA_R1_1	23	Gene LOC100132891	FLJ35545	hypothetical LOC100132891	NR_033851, NR_033852		
GeneID:9179	RPL7	8	74,202,874	74,205,989	3,115	-	3	1_A375_untU7_minus_lncRNA_R1_1:8243, 2_A375_untU7_plus_lncRNA_R1_1:7539, 3_A375_untU7_plus_lncRNA_R1_1:7540	-487, -251, -1795	upstream, upstream, upstream	1	1	0	13	16.5	13	2	2_A375_untU7_plus_lncRNA_R1_1	21	Gene RPL7	L7, fam17-1, MGC117376, RPL7	ribosomal protein L7	NM_000971, XCT2236080.0, XCT2236084.0	200717_x_at, 213042_x_at	NP_0009622, EAW68999.1, EAW68998.1
GeneID:7936	RDH10	8	74,207,265	74,237,516	30,251	+	3	1_A375_untU7_minus_lncRNA_R1_1:8243, 2_A375_untU7_plus_lncRNA_R1_1:7539, 3_A375_untU7_plus_lncRNA_R1_1:7540	929, 1023, 399	upstream, upstream, cr gene	1	1	0	13	16.5	13	2	2_A375_untU7_plus_lncRNA_R1_1	21	Gene RDH10	RDH10, SDR16C4	retinol dehydrogenase 10 (all-trans)	NM_172037, XCT1625212, XCT1998833.1	1552376_s_at, 1552379_at, 229621_at, 237467_at	NP_7420341, EAW68702.1, EAW68701.1
GeneID:2757	STAU2	8	74,332,804	74,859,943	527,239	+	2	1_A375_untU7_plus_lncRNA_R1_1:7541, 2_A375_untU7_plus_lncRNA_R1_1:7542	256765, 257015	cr gene, cr gene	0	1	0	13	16.5	8	2	2_A375_untU7_plus_lncRNA_R1_1	17	Gene STAU2	DKFZp781B2311, MGC119808, SHL2, SHL2, STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)	NM_014393, NM_001164393, NM_001164391, NM_001164392, NM_001164394, NM_001164395, XCT2356562.0, XCT2356561.0, XCT1900555.1, XCT1900559.1, XCT1955545.1	1554899_at, 204236_at, 227179_at	NP_0330552, NP_0011570531, NP_0011570541, NP_0011570551, NP_0011570561, NP_0011570571, EAW68703.1, EAW68705.1, EAW68706.1, EAW68707.1
GeneID:2843	UBE2W	8	74,702,640	74,791,110	88,270	-	1	1_A375_untU7_minus_lncRNA_R1_1:8244	134	cr gene	1	0	0	16	15	13	1	1_A375_untU7_minus_lncRNA_R1_1	16	Gene UBE2W	FLJ11011, hUBC, W, UBE2W	ubiquitin conjugating enzyme E2W (putative)	NM_0315015.1, NM_018299, XCT2356553.0, XCT2356553.0, XCT1961732.3, XCT1965553.1	1553517_at, 1560436_at, 218521_s_at, 222686_at, 223927_s_at	NP_7420741.1, NP_060793.3, EAW67699.1, EAW67700.1, EAW67701.1, EAW67702.1





Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_uNU7_wuNU97_all_incRNA_R_1 Percent	2_A375_uNU97_all_lncRNA_1 Percent	3_A375_1_NU7_intro_lncRNA_R_1 Avg Peak	4_A375_2_uNU97_all_lncRNA_1 Avg Peak	4_A375_2_uNU97_all_lncRNA_1 Peak Count	Adj Avg Peak Value	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:3351401	MTDH	8	98,836,407	98,742,465	99,881	+	1	2_A375_uNU97_plus_lncRNA_NR_1:7555	25	sr:gene	0	1	0	15	15	15	1	2_A375_uNU97_all_lncRNA_NR_1	16	Gene MTDH	1D3, LYRIC, AEG-1, MTDH, AEG1, LYRIC/3D3	metadherin	NM_178512, hCT2297059.0, hCT2337482.0, hCT6223.3	212250_at, 212251_at	NP_549227.2, ENW91790.1, ENW91781.1, ENW91782.1
GeneID:3351402	LAPTM4B	8	55,757,539	56,884,350	77,221	+	1	2_A375_uNU97_plus_lncRNA_NR_1:7559	-33	upstream	0	1	0	9	15	12	1	2_A375_uNU97_all_lncRNA_NR_1	15	Gene LAPTM4B	LAPTM4B-beta, LAPTM4B, LC27	lysosomal protein transmembrane 4 beta	NM_018407, hCT2297068.1	1554879_s_at, 206029_s_at, 206787_s_at, 214339_s_at	NP_060977.3, ENW91765.1
GeneID:4147	MINT2	8	65,661,311	65,645,945	107,857	+	2	1_A375_uNU7_mixed_lncRNA_NR_1:5273, 4_A375_DGR1_1.7644	1787103, 1788353	downstream, downstream	1	0	1	19	12	16	1	1_A375_uNU7_mixed_lncRNA_NR_1	19	Gene MINT2	MINT2	mstone 2	NM_002390, NM_030965, hCT2297089.0, hCT2297071.0, hCT2297075.0, hCT2337500.0, hCT6307.2	202260_s_at	NP_002371.3, NP_110372.2, ENW91764.1, ENW91765.1, ENW91766.1, ENW91767.1, ENW91768.1
GeneID:8819598	RPL39	8	99,655,942	99,657,773	2,831	+	2	1_A375_uNU7_mixed_lncRNA_NR_1:5273, 4_A375_DGR1_1.7644	-243, 109	upstream, sr:gene	1	0	1	19	12	16	1	1_A375_uNU7_mixed_lncRNA_NR_1	19	Gene RPL39	RPL39, L39	ribosomal protein L39	NM_000999, hCT2297242.0, hCT2337471.0, hCT6279.0	200062_s_at	NP_000990.1, ENW91771.1, ENW91769.1, ENW91770.1
GeneID:2687775	SNORA72	8	99,654,314	99,654,445	131	+	2	1_A375_uNU7_mixed_lncRNA_NR_1:5273, 4_A375_DGR1_1.7644	-1371, -2219	upstream, upstream	1	0	1	19	12	16	1	1_A375_uNU7_mixed_lncRNA_NR_1	19	Gene SNORA72	RNA72, U72, SNORA72	small nucleolar RNA, H/ACA box 72	NR_002581	223947_at	
GeneID:7969615	NIPAL3	8	99,204,307	99,306,821	102,256	-	1	2_A375_uNU97_plus_lncRNA_NR_1:7590	43	sr:gene	0	1	0	14	16	8	1	2_A375_uNU97_all_lncRNA_NR_1	16	Gene NIPAL3	NIPA3, NIPAL3, FLI12955	NIPA-like domain containing 2	NM_033195, hCT2297232.0, hCT2297230.0, hCT6262.2	220326_s_at, 223930_at	NP_376815.1, ENW91776.1, ENW91777.1, ENW91778.1
GeneID:1010639	OSBI2	8	99,596,631	99,964,326	7,897	+	2	1_A375_uNU7_mixed_lncRNA_NR_1:5274, 2_A375_uNU97_plus_lncRNA_NR_1:7591	73, -23	sr:gene, upstream	1	1	0	16	22	9	1	2_A375_uNU97_all_lncRNA_NR_1	22	Gene OSBI2	OSBI2, FLJ40032	oxysterol-binding protein 2 (Donaldson)	NM_030931, NM_001143482, hCT2298994.0, hCT6300.2	213969_at	NP_443727.2, NP_001139934.1, ENW91784.1, ENW91785.1
GeneID:1510597930	VPS13B	8	100,025,494	100,089,606	864,314	+	2	1_A375_uNU7_mixed_lncRNA_NR_1:5275, 4_A375_DGR1_1.7645	-102, 74	upstream, sr:gene	1	0	1	16	17	20	1	4_A375_DGR1_1.1	23	Gene VPS13B	COH1, VPS13B, hCT2336519.1, hVAN0522 COH1, VPS13B	vacuolar protein sorting 13 homolog B (yeast)	NM_152564, NM_017890, NM_015243, NM_181981, hCT2336474.0, hCT2336475.0, hCT2340476.0	1553552_at, 212243_at, 220400_at, 228254_at	NP_689777.3, NP_060360.2, NP_056067.2, NP_689536.2, ENW91787.1, ENW91788.1, ENW91789.1
GeneID:1310443	CCNB1IP1	8	100,690,223	100,698,242	18,019	-	2	1_A375_uNU7_mixed_lncRNA_NR_1:5276, 2_A375_uNU97_plus_lncRNA_NR_1:7592	418, 322	sr:gene, sr:gene	1	1	0	16	17	13	1	1_A375_uNU7_mixed_lncRNA_NR_1	16	Gene CCNB1IP1	CCNB1IP1	NM_020374, hCT2297277.0, hCT2297278.0, hCT1503772.2	201754_at	NP_064365.1, ENW91790.1, ENW91791.1, ENW91792.1
GeneID:2681965	RGS22	8	100,970,276	101,116,344	145,068	-	1	4_A375_DGR1_1.7646	96	upstream	0	0	1	8	8	13	1	4_A375_DGR1_1.1	13	Gene RGS22	FLJ40050, PRTG, MYG, MGC102806, FLJ40054, DKFZp434D192, RGS22	regulator of G-protein signaling 22	NM_015985, hCT2297509.0, hCT2337505.0, hCT2337506.0, hCT6317.2	223991_at	NP_056853.3, ENW91794.1, ENW91793.1, ENW91795.1, ENW91797.1
GeneID:5460	POLR2K	8	101,182,039	101,199,230	2,091	+	2	1_A375_uNU7_mixed_lncRNA_NR_1:5277, 4_A375_DGR1_1.7647	7451, 7625	downstream, downstream	1	0	1	14	12	17	1	4_A375_DGR1_1.1	17	Gene POLR2K	RPB10(alpha, RPB7.2, hsRPB10a, MGC8730, POLR2K, RPABC4, ABC10-alpha, RPB10	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	NM_005034, hCT2297041.0, hCT5900.3	208534_at, 208535_s_at	NP_005025.1, ENW91796.1, ENW91799.1
GeneID:8887474	SPAG1	8	101,179,283	101,254,130	69,087	+	2	1_A375_uNU7_mixed_lncRNA_NR_1:5277, 4_A375_DGR1_1.7647	97, 201	sr:gene, sr:gene	1	0	1	14	12	17	1	4_A375_DGR1_1.1	17	Gene SPAG1	SPT3, TFIIS, FLJ32320, SPAG1, HSD-2.0	sperm associated antigen 1	NM_003114, NM_172218, hCT2297043.1, hCT2297045.1, hCT2349333.0, hCT2349334.0, hCT2357481.0, hCT2357482.0, hCT6714.4	210117_at	NP_003105.2, NP_757387.1, ENW91800.1, ENW91801.1, ENW91802.1, ENW91805.1, ENW91803.1, ENW91804.1, ENW91806.1
GeneID:2387697	RNF19A	8	101,269,288	101,322,227	53,039	-	2	1_A375_uNU7_mixed_lncRNA_NR_1:7593, 4_A375_DGR1_1.7648	339, 247	sr:gene, sr:gene	0	1	1	13	14	17	1	4_A375_DGR1_1.1	17	Gene RNF19A	DORF IN, RNF19A, DKFZp686B0349	ring finger protein 19A	NM_015435, NM_183419, hCT6715.4	220483_s_at, 223065_at	NP_056230.3, NP_904350.1, ENW91807.1
GeneID:1507587	ANKRD46	8	101,533,000	101,572,012	39,012	-	2	1_A375_uNU7_mixed_lncRNA_NR_1:5278, 2_A375_uNU97_plus_lncRNA_NR_1:7596	105, -20	sr:gene, upstream	1	1	0	26	23	17	1	1_A375_uNU7_mixed_lncRNA_NR_1	26	Gene ANKRD46	ANKRD46	NM_199450, hCT2342420.0, hCT2342421.0, hCT2344204.0, hCT6716.2	212731_at, 235837_at	NP_940953.1, ENW91808.1, ENW91809.1, ENW91810.1, ENW91811.1
GeneID:2687698	PABPC1L	8	101,713,144	101,734,315	19,171	+	1	2_A375_uNU97_plus_lncRNA_NR_1:7597	-533	upstream	0	1	0	11	20	8	1	2_A375_uNU97_all_lncRNA_NR_1	20	Gene PABPC1	PABPC2, PABP2, PABP, PABPC1, PABP1	poly(A) binding protein, cytoplasmic 1	NM_002568, hCT2297033.0, hCT2297038.0, hCT2297039.0, hCT2297040.0, hCT6700.3, hCT1964101.1, hCT1964102.1, hCT1964103.1, hCT1964104.1	215923_s_at	NP_002559.2, ENW91826.1, ENW91814.1, ENW91815.1, ENW91817.1, ENW91818.1, ENW91819.1, ENW91821.1
GeneID:7734	YWHAZ	8	101,930,934	101,968,823	34,019	-	3	1_A375_uNU7_mixed_lncRNA_NR_1:5280, 1_A375_uNU7_mixed_lncRNA_NR_1:5281, 2_A375_uNU97_plus_lncRNA_NR_1:7598	2967, 1399, 1431	sr:gene, sr:gene, sr:gene	1	1	0	21	15	9.3	2	1_A375_uNU7_mixed_lncRNA_NR_1	22	Gene YWHAZ	YWHAZ, YWHAD, 14-3-3-zeta, HCP-1, MGC111427, MGC131936, MGC126822	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	NM_003406, NM_145690, NM_001135699, NM_001135700, NM_001135701, NM_001135702, hCT2297026.0, hCT2297027.0, hCT2297029.0, hCT2297030.0, hCT2297031.0, hCT2297032.0	200809_s_at, 200809_s_at, 200640_at, 200641_s_at	NP_003397.1, NP_663723.1, NP_001129711.1, NP_001129712.1, NP_001129713.1, NP_001129714.1, ENW91823.1, ENW91824.1, ENW91825.1, ENW91826.1, ENW91827.1, ENW91828.1, ENW91829.1
GeneID:4441274	FLJ42969	9	102,094,352	102,098,479	24,197	+	1	2_A375_uNU97_plus_lncRNA_NR_1:7600	11659	sr:gene	0	1	0	10	16	8	1	2_A375_uNU97_all_lncRNA_NR_1	16	Gene FLJ42969	FLJ42969	hypothetical LOC441274	NR_033962		
GeneID:5151723	ZNF706	8	102,208,266	102,217,990	9,894	-	1	4_A375_DGR1_1.7651	-152	upstream	0	2	1	12	11	16	1	4_A375_DGR1_1.1	16	Gene ZNF706	PNAS-110, RSFD338, PNAS-108, ZNF706	zinc finger protein 706	NM_031425.10, NM_001042511, NM_016066, NM_172370.2, NC_000003.3	210059_at, 227132_at	NP_001033975.1, NP_112598.1, NP_001035976.1, NP_357483.1, ENW91831.1, ENW91832.1
GeneID:8851	NCALD	8	102,898,770	103,137,133	438,286	-	2	1_A375_uNU7_mixed_lncRNA_NR_1:5286, 4_A375_DGR1_1.7652	112271, 244697	sr:gene, sr:gene	1	0	1	14.3	8.5	10	2	1_A375_uNU7_mixed_lncRNA_NR_1	20	Gene NCALD	MGC33570, MGC74656, NCALD	neurocalcin delta	NM_033041, NM_001042824, NM_001042825, NM_001042826, NM_001042827, NM_001042828, NM_001042829, NM_001042830, hCT2297124.0, hCT2357540.0, hCT2372.2	1562790_at, 211955_s_at	NP_114430.2, NP_001033714.1, NP_001033715.1, NP_001033716.1, NP_001033717.1, NP_001033718.1, NP_001033719.1, NP_001033720.1, ENW91833.1, ENW91834.1, ENW91835.1, ENW91836.1, ENW91837.1
GeneID:5111398	UBR5	8	103,268,389	103,434,493	150,928	-	1	4_A375_DGR1_1.7653	144879	sr:gene	0	0	1	8	7	10	1	4_A375_DGR1_1.1	13	Gene UBR5	KIAA0896, UBR5, EDD, EDD1, FLJ11310, MGC97280, DD5, HYD	ubiquitin protein ligase E3 component n-recognin 5	NM_015902, hCT2297028.0, hCT2297029.0, hCT2297030.0, hCT6294.3	200564_s_at	NP_056987.2, ENW91844.1, ENW91843.1, ENW91845.1
GeneID:4967	ODF1	8	103,580,545	103,579,245	91,297	+	1	2_A375_uNU97_plus_lncRNA_NR_1:7606	18838	downstream	0	1	0	10	16	8	1	2_A375_uNU97_all_lncRNA_NR_1	16	Gene ODF1	MGC129929, ODFPGB, RT7, ODF2, ODF27, ODF1, CT133, MGC129931, SDDY, ODFP, HSPB10, ODF, ODFPG, ODFPGA	outer dense fiber of sperm tails 1	NM_033418, hCT2349338.0, hCT2349337.0, hCT1642086.4	214455_at	NP_377712.2, ENW91847.1, ENW91848.1, ENW91849.1
GeneID:4762	FLJ45224	8	103,619,050	103,619,515	466	+	1	1_A375_uNU7_mixed_lncRNA_NR_1:5288	-712	sr:gene	1	0	0	20	17	11	1	1_A375_uNU7_mixed_lncRNA_NR_1	20	Gene FLJ45224	FLJ45224	FLJ45224 protein	XR_113157, XR_130873, XR_114190		
GeneID:5502	AZIN1	8	103,838,509	103,879,397	37,981	-	1	2_A375_uNU97_plus_lncRNA_NR_1:7608	-211	upstream	0	1	0	15	16	8	1	2_A375_uNU97_all_lncRNA_NR_1	16	Gene AZIN1	CDC1L, CHZN, AZIN1, MGC3032, OAZ1, MGC691	ornithine decarboxylase antizyme inhibitor 1	NM_015878, NM_148174, hCT1999330.1, hCT2309985.0, hCT2309986.0	201772_at, 212481_at	NP_056962.2, NP_680479.1, ENW91851.1, ENW91852.1, ENW91853.1
GeneID:1010639693	LOC100506763	8	103,879,365	103,877,553	666	-	1	2_A375_uNU97_plus_lncRNA_NR_1:7609	43	sr:gene	0	1	0	15	16	8	1	2_A375_uNU97_all_lncRNA_NR_1	16	Gene LOC100506763	LOC100506763	hypothetical LOC100506763	XR_113155, XR_130874, XR_114194		
GeneID:8837	ATP6V1C1	8	104,038,348	104,088,255	50,037	+	1	2_A375_uNU97_plus_lncRNA_NR_1:7609	60	sr:gene	0	0	1	18	24	13	1	2_A375_uNU97_all_lncRNA_NR_1	24	Gene ATP6V1C1	ATP6V1C1, FLJ00037, VMA5, ATP6C, ATP6D, VATC	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	NM_001696, hCT2298631.0, hCT5823.2	202873_at, 202873_at, 202874_s_at, 228463_at	NP_001686.1, ENW91860.1, ENW91859.1
GeneID:7896	C8orf88	8	104,149,191	104,150,570	2,379	-	1	4_A375_DGR1_1.7654	-30	upstream	0	2	1	5	8	17	1	4_A375_DGR1_1.1	17	Gene C8orf88	MGC29539, C8orf88	uncharacterized bone marrow stromal antigen	NM_025071	1554235_a_at, 232328_at	
GeneID:8701	BAALC	8	104,192,921	104,242,533	99,612	+	1	4_A375_DGR1_1.7654	679	sr:gene	0	0	1	5	8	17	1	4_A375_DGR1_1.1	17	Gene BAALC	FLJ10213, BAALC	brain and acute leukemia, cytoplasmic	NM_024112, NM_001024722, hCT2298843.0, hCT2298833.0, hCT2298837.0, hCT6031.3	216899_s_at, 222700_s_at	NP_079388.1, NP_001019453.1, ENW91862.1, ENW91863.1, ENW91864.1, ENW91865.1
GeneID:8553223	FZD8	10	104,210,981	104,245,994	34,933	+	1	2_A375_uNU97_plus_lncRNA_NR_1:7611	605	sr:gene	0	1	0	14	16	8	1	2_A375_uNU97_all_lncRNA_NR_1	16	Gene FZD8	FZ8, hFZ8, FZD8	frizzled homolog 8 (Drosophila)	NM_007238, NM_001164613, NM_001164618, hCT2298930.0, hCT2298940.0, hCT2370449.0, hCT2370450.0, hCT2370451.0, hCT6392.2, hCT1966030.1	203357_at	NP_003497.2, NP_001155931.1, ENW91867.1, ENW91868.1, ENW91869.1, ENW91870.1, ENW91871.1, ENW91872.1, ENW91873.1
GeneID:3993	CTHRC1	8	104,268,766	104,298,217	31,451	+	1	2_A375_uNU97_plus_lncRNA_NR_1:7612	574	sr:gene	0	0	0	14	17	9	1	2_A375_uNU97_all_lncRNA_NR_1	17	Gene CTHRC1	CTHRC1	collagen triple helix repeat containing 1	NM_138455, hCT2337432.0, hCT2337433.0, hCT6083.2	223681_at	NP_612464.1, ENW91876.1, ENW91875.1, ENW91878.1
GeneID:8537234	SLC25A32	8	104,410,999	104,427,466	16,602	-	3	1_A375_uNU7_mixed_lncRNA_NR_1:5291, 2_A375_uNU97_plus_lncRNA_NR_1:7612, 4_A375_DGR1_1.7655	332, -92, 290	sr:gene, sr:gene, sr:gene	1	1	1	20	19	16	1	1_A375_uNU7_mixed_lncRNA_NR_1	20	Gene SLC25A32	MFT, FLJ23972, SLC25A32, MFTC	solute carrier family 25, member 32	NM_030780, hCT2298936.0, hCT6080.3	221020_s_at	NP_110407.2, ENW91877.1, ENW91878.1
GeneID:2387379	DCAF13	8	104,438,942	104,439,851	39,729	+	3	1_A375_uNU7_mixed_lncRNA_NR_1:5291, 2_A375_uNU97_plus_lncRNA_NR_1:7612, 4_A375_DGR1_1.7655	196, 376, 266	sr:gene, sr:gene, sr:gene	1	1	1	20	19	16	1	1_A375_uNU7_mixed_lncRNA_NR_1	20	Gene DCAF13	WD3071, GWD, WDR21, DCAF13, DKFZp564J0463, MGC13267, MGC126589	DDB1 and Cul4 associated factor 13	NM_015420, hCT2298944.1, hCT2298927.0, hCT2349328.0, hCT6029.3, hCT1627020.2	1569840_at, 230543_s_at, 223676_s_at, 231054_s_at	NP_056235.4, ENW91881.1, ENW91879.1, ENW91880.1, ENW91882.1, ENW91883.1
GeneID:8969	RAB52	8	104,512,976	103,288,431	732,475	-	4	1_A375_uNU7_mixed_lncRNA_NR_1:5293, 2_A375_uNU97_plus_lncRNA_NR_1:7613, 2_A375_uNU97_plus_lncRNA_NR_1:7616, 2_A375_uNU97_plus_lncRNA_NR_1:7617	978, 648, 479536, 722560	sr:gene, sr:gene, sr:gene, sr:gene	1	1	1	14.67	23	10.33	3	2_A375_uNU97_all_lncRNA_NR_1	28	Gene RAB52	KIAA0751, RAB52, RAB52P1, DB32, RAB2, DKFZp681A0852	regulating synaptic membrane exocytosis 2	NM_014877, NM_001100117, hCT2344427.0, hCT2344435.0, hCT2357475.0, hCT2357476.0	208137_at, 215470_at	NP_055692.3, NP_001093587.1, ENW91885.1, ENW91886.1, ENW91887.1, ENW91888.1
GeneID:8611501	TMEM184A	8	104,538,034	103,288,918	16,882	+	1	1_A375_uNU7_mixed_lncRNA_NR_1:5294	3829	upstream	1	0	0	21	15	4	1	1_A375_uNU7_mixed_lncRNA_NR_1	21	Gene TMEM184A	TMEM184, FIND, DCSTAMP, MGC129221, MGC129223	transmembrane 7 superfamily member 4	NM_030788, hCT1643208.1	221366_s_at	NP_110415.1, ENW91892.1
GeneID:2387697	LRP12	8	103,520,439	103,501,232	992,793	-	2	1_A375_uNU7_mixed_lncRNA_NR_1:5293, 2_A375_uNU97_plus_lncRNA_NR_1:7615	-232, -229	upstream, upstream	1	0	0	47	36	7	1	1_A375_uNU7_mixed_lncRNA_NR_1	47	Gene LRP12	DKFZp761P1024, FLJ12929, ST7, LRP12	low density lipoprotein receptor-related protein 12	NM_013437, NM_001135702, hCT2297284.0, hCT2297285.0, hCT2297282.0, hCT2297281.0	219681_at, 220253_s_at, 220254_at	NP_038465.1, NP_001129173.1, ENW91895.1, ENW91896.1, ENW91897.1, ENW91898.1
GeneID:2387698	ZFP462	8	104,031,147	104,016,797	453,830	-	2	4_A375_DGR1_1.7656, 4_A375_DGR1_1.7657	181, 621	sr:gene, sr:gene	0	0	1	8	9	16.5	2	4_A375_DGR1_1.1	17	Gene ZFP462	MGC129984, MGC129983, DKFZp686C19124, ZNF462, FOG2, ZFP462	zinc finger protein 462 homolog (mouse)	NM_173082, hCT1643503.3	219778_at	NP_938124.2, ENW91899.1
GeneID:8304774	GIXR1	8	107,282,473	107,784,922	502,449	+	3	1_A375_uNU7_mixed_lncRNA_NR_1:5297, 2_A375_uNU97_plus_lncRNA_NR_1:7622, 2_A375_uNU97_plus_lncRNA_NR_1:7623	307415, 997, 307415	sr:gene, sr:gene, sr:gene	1	1	0	29.5	33	12	2	2_A375_uNU97_all_lncRNA_NR_1	33	Gene GIXR1	GIXR1, FLJ42436, MGC20397, FLJ43698, FLJ38029, FLJ10125, FLJ43654, FLJ41873	cytokine receptor 1	NM_018002, NM_181554, hCT2297261.0, hCT2297262.0, hCT6399.2	219197_s_at, 222537_at, 223593_s_at, 223973_s_at	NP_060472.2, NP_851997.2, ENW91902.1, ENW91904.1, ENW91903.1
GeneID:8603	ANGPTL6	8	108,291,710	108,510,254	218,544	+	1	1_A375_uNU97_plus_lncRNA_NR_1:7624	-3642	upstream	0	1	0	19	27	8	1	2_A375_uNU97_all_lncRNA_NR_1	27	Gene ANGPTL6	ANGPTL6, ASPT, ASPT1, ANG1	angiopoietin 1	NM_031149, hCT2297259.0, hCT2337436.0, hCT2357437.0, hCT6621.3	1553259_at, 203605_s_at, 203606_at	NP_001137.2, ENW91908.1, ENW91910.1, ENW91911.1, ENW91912.1
GeneID:8434709	RSPO2	8	109,011,544	109,099,913	154,389	+	1	4_A375_DGR1_1.7658	-20	upstream	0	2	1	14	8	16	1	4_A375_DGR1_1.1	16	Gene RSPO2	C8ORF62, RSPO2, MGC15555, MGC43542	R-spondin 2 homolog (Mus musculus)	NM_178565, hCT2298933.0, hCT2349332.0, hCT2357483.0, hCT6109.2	1554012_at	NP_848563.3, ENW91915.1, ENW91913.1, ENW91914.1, ENW91916.1
GeneID:3681748	EIF3E	8	109,213,372	109,280,939	68,567	-	2	1_A375_uNU7_mixed_lncRNA_NR_1:5299, 2_A375_uNU97_plus_lncRNA_NR_1:7626	65, -67	sr:gene, upstream	1	0	1	14	19	8	1	2_A375_uNU97_all_lncRNA_NR_1	19	Gene EIF3E	EIF3-P48, INT6, eIF3-p48, EIF3E, EIF3S6	eukaryotic translation initiation factor 3, subunit E	NM_001568, hCT2297428.0, hCT2357479.0	200897_s_at	NP_001559.1, ENW91916.1, ENW91918.1
GeneID:8541555	NUDCD1	8	110,282,145	110,348,330	66,202	-	2	1_A375_uNU7_mixed_lncRNA_NR_1:5300, 2_A375_uNU97_plus_lncRNA_NR_1:7627	-62, -62	upstream, upstream	1	0	1	26	27	14	1	2_A375_uNU97_all_lncRNA_NR_1	27	Gene NUDCD1	FLJ14991, Cat986, KIAA0237, CVAK98	NudC domino subfamily 1	NM_032899, NM_001128211, hCT2349329.0, hCT2349330.0, hCT6366.3	223435_at, 223439_at	NP_116358.2, NP_001121682.1, ENW91924.1, ENW91925.1, ENW91926.1
GeneID:8643	ENY2	8	110,348,532	110,336,189	11,827	+	2	1_A375_uNU7_mixed_lncRNA_NR_1:5300, 2_A375_uNU97_plus_lncRNA_NR_1:7627	-120, -120	upstream, upstream	1	0	1	26	27	14	1	2_A375_uNU97_all_lncRNA_NR_1	27	Gene ENY2	ENY2, DC8, sus1p, SUS1P	enhancer of yellow 2 homolog (Drosophila)	NM_030189, NM_001193537, NM_039471, NM_039472, hCT2297382.0, hCT2357480.0, hCT2357481.0, hCT1633592.1	218422_at, 226703_at	NP_084474.1, NP_001180498.1, ENW91927.1, ENW91928.1, ENW91929.1, ENW91930.1
GeneID:8189	EBAG9	8	110,551,929	110,577,592	25,663	+	1	4_A375_DGR1_1.7659	35399	downstream	0	0	1	8	7	10	1	4_A375_DGR1_1.1	10	Gene EBAG9	EBAG9, RCAS1	estrogen receptor binding site associated, antigen, 9	NM_005714, hCT2357485.0, hCT6367.2	204274_at, 204275_s_at	NP_036206.1, NP_005087.1, ENW91932.1, ENW91933.1, ENW91934.1
GeneID:8589	GOLSYN	8	110,598,403	110,779,020	177,615	-	3	1_A375_uNU7_mixed_lncRNA_NR_1:5301, 2_A375_uNU97_plus_lncRNA_NR_1:7628, 4_A375_DGR1_1.7659	5566, 5555, 116892	sr:gene, sr:gene, sr:gene	1	1	1	12.5	14.5	10	2	2_A375_uNU97_all_lncRNA_NR_1	22	Gene GOLSYN	KIAA1472, GOLSYN, GOLGYN, SYBU, SNPH4,	Golgi-localized protein	(NM_031997)*43, NM_017795, NM_001009764, (NM_001009745, NM_001009746, NM_001009747, NM_001009749, NM_001009748, NM_001009750, NM_001009752, NM_001009751, NM_001009753, NM_001009754, NM_001009755, NM_001009756, hCT2297489.0, hCT2297490.0, hCT6369.2	210892_at	NP_001029212.1, NP_060295.3, NP_001029213.1, NP_001029214.1, NP_001029215.1, NP_001029216.1, NP_001029217.1, NP_001029218.1, NP_001029219.1, NP_001029220.1, NP_001029221.1, NP_001029222.1, NP_001029223.1, NP_001029224.1, NP_001029225.1, ENW91935.1, ENW91936.1
GeneID:2757012	RCNW1	8	110,979,233	110,998,959	7,726	-	1	4_A375_DGR1_1.7660	451	sr:gene	0	2	1	12	11	10	1	4_A375_DGR1_1.1	10	Gene RCNW1	RNN4, RCNW1, RVS1, KIV2.3, KIAA0	adducin subunit, subfamily V, member 1	NM_014279, hCT5824.2	220284_at	NP_055194.1, ENW91938.1

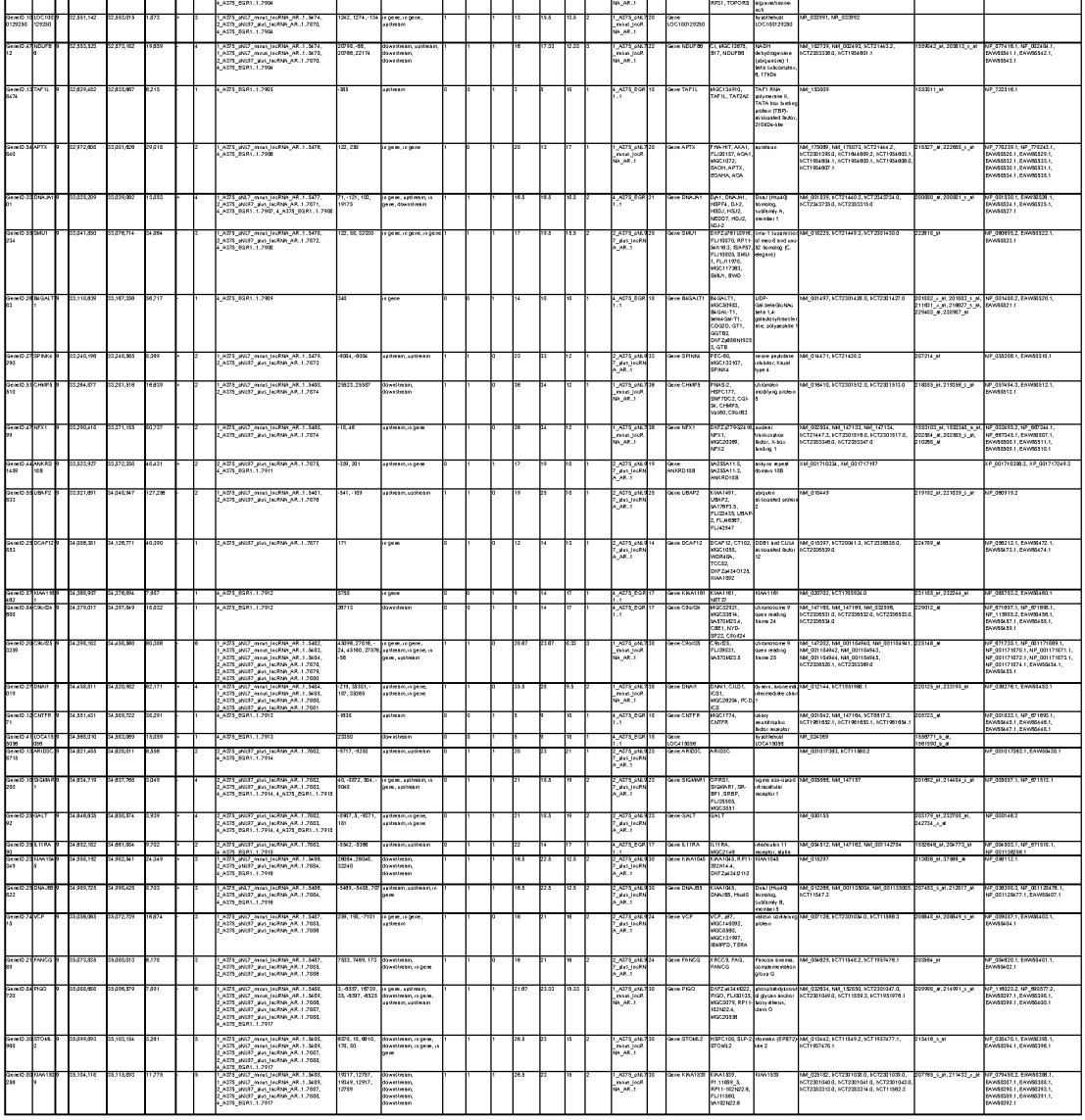


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:169044	COL22A1	8	139,600,478	139,926,236	325,758	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5352, 2_A375_pNL97_plus_lncRNA_AR..1..7706, 2_A375_pNL97_plus_lncRNA_AR..1..7707, 4_A375_EGR1..1..7674, 4_A375_EGR1..1..7675	271804, 271852, 82924, 54252, 38220	in gene, in gene, in gene, in gene, in gene	1	1	1	11.75	13.75	10.25	4	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene COL22A1	COL22A1	collagen, type XXII, alpha 1	NM_152888, hCT2343736.0, hCT2343737.0, hCT2348478.0	228873_at, 243301_at	NP_690848.1, EAW92194.1, EAW92193.1, EAW92195.1
GeneID:51305	KCNK9	8	140,624,804	140,715,299	90,495	-	4	2_A375_pNL97_plus_lncRNA_AR..1..7711, 2_A375_pNL97_plus_lncRNA_AR..1..7712, 4_A375_EGR1..1..7677, 4_A375_EGR1..1..7678	44227, -2909, 49363, -2472	in gene, upstream, in gene, upstream	0	1	1	9.33	14.67	12.67	3	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene KCNK9	TASK-3, KCNK9, TASK3, MGC138268, MGC138270, KT3.2, K2p9.1	potassium channel, subfamily K, member 9	NM_016601, hCT2306625.0, hCT2306626.0, hCT13630.2	224072_s_at	NP_057685.1, EAW92196.1, EAW92197.1, EAW92198.1
GeneID:83696	TRAPPC9	8	140,742,586	141,468,678	726,092	-	13	1_A375_pNL7_minus_lncRNA_AR..1..5356, 1_A375_pNL7_minus_lncRNA_AR..1..5357, 2_A375_pNL97_plus_lncRNA_AR..1..7713, 2_A375_pNL97_plus_lncRNA_AR..1..7714, 1_A375_pNL7_minus_lncRNA_AR..1..5358, 1_A375_pNL7_minus_lncRNA_AR..1..5359, 1_A375_pNL7_minus_lncRNA_AR..1..5360, 2_A375_pNL97_plus_lncRNA_AR..1..7715, 2_A375_pNL97_plus_lncRNA_AR..1..7716, 2_A375_pNL97_plus_lncRNA_AR..1..7717, 2_A375_pNL97_plus_lncRNA_AR..1..7718, 4_A375_EGR1..1..7679, 4_A375_EGR1..1..7680	736086, 559670, 736038, 559670, 148622, 870, -5834, 148670, 64630, 756, -5914, 381158, 358246	downstream, in gene, downstream, in gene, in gene, in gene, upstream, in gene, in gene, in gene, upstream, in gene, in gene	1	1	1	21.75	23.75	10.25	8	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene TRAPPC9	IKBKBBP, NIBP, KIAA1882, TRAPPC9, TRS120, MRT13, MGC4737, MGC4769, IBP, T1	trafficking protein particle complex 9	NM_031466, NM_001160372, hCT2306636.0, hCT2306638.0	221872_s_at, 221836_s_at, 56829_at	NP_113654.4, NP_001153844.1, EAW92200.1, EAW92201.1
GeneID:100507278	LOC100507278	8	141,105,058	141,107,742	2,684	-	2	4_A375_EGR1..1..7679, 4_A375_EGR1..1..7680	222, -2690	in gene, upstream	0	0	1	6.5	6	18.5	2	4_A375_EGR1..1	19	Gene LOC100507278		hypothetical LOC100507278	XR_108894		
GeneID:54108	CHRAC1	8	141,521,401	141,527,252	5,851	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7719, 2_A375_pNL97_plus_lncRNA_AR..1..7720	-409, 1015	upstream, in gene	0	1	0	13	16	13.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene CHRAC1	YCL1, CHARC15, CHRAC1, CHARC1, CHRAC15	chromatin accessibility complex 1	NM_017444, NR_023360, hCT13133.2	231784_at	NP_059140.1, EAW92206.1
GeneID:27161	EIF2C2	8	141,541,264	141,645,646	104,382	-	6	1_A375_pNL7_minus_lncRNA_AR..1..5381, 2_A375_pNL97_plus_lncRNA_AR..1..7721, 2_A375_pNL97_plus_lncRNA_AR..1..7722, 2_A375_pNL97_plus_lncRNA_AR..1..7723, 4_A375_EGR1..1..7681, 4_A375_EGR1..1..7682	14137, 45742, 14094, 1166, 66662, 45422	in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	13.5	14	14.25	4	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene EIF2C2	EIF2C2, MGC3183, AGO2, Q10	eukaryotic translation initiation factor 2C, 2	NM_012154, NM_001164623, hCT2306631.0, hCT9194.3	213310_at, 225569_at, 225827_at	NP_036286.2, NP_001158095.1, EAW92207.1, EAW92208.1
GeneID:22898	DENND3	8	142,138,720	142,205,901	67,181	+	3	2_A375_pNL97_plus_lncRNA_AR..1..7726, 4_A375_EGR1..1..7685, 4_A375_EGR1..1..7686	25392, -498, 61184	in gene, upstream, in gene	0	1	1	9.67	11.67	15.67	3	4_A375_EGR1..1	19	Gene DENND3	KIAA0870, DENND3	DENN/MADD domain containing 3	NM_014957, hCT2348480.1, hCT2348481.1, hCT2351373.0, hCT11620.5, hCT1953930.3	212974_at, 212975_at	NP_055772.2, EAW92216.1, EAW92217.1, EAW92218.1, EAW92219.1, EAW92220.1
GeneID:57210	SLC45A4	8	142,220,870	142,238,673	17,803	-	4	4_A375_EGR1..1..7687, 4_A375_EGR1..1..7688, 4_A375_EGR1..1..7689, 4_A375_EGR1..1..7690	21713, 20625, 5841, -4303	downstream, downstream, in gene, upstream	0	0	1	4.75	6	17.25	4	4_A375_EGR1..1	19	Gene SLC45A4	SLC45A4, KIAA1126	solute carrier family 45, member 4	NM_001080431	225597_at, 225598_at	NP_001073900.1
GeneID:2843	GPR20	8	142,366,585	142,377,365	10,780	-	1	4_A375_EGR1..1..7692	-9275	upstream	0	0	1	6	3	16	1	4_A375_EGR1..1	16	Gene GPR20	GPR20	G protein-coupled receptor 20	NM_005293, hCT1767425.2	214510_at	NP_005284.2, EAW92227.1
GeneID:389690	FLJ43860	8	142,443,929	142,517,330	73,401	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5384, 2_A375_pNL97_plus_lncRNA_AR..1..7727, 4_A375_EGR1..1..7694, 4_A375_EGR1..1..7695, 4_A375_EGR1..1..7696	-9582, -9550, 58962, 29090, 17682	upstream, upstream, in gene, in gene, in gene	1	1	1	14	17	15	4	2_A375_pNL97_plus_lncRNA_AR..1	47	Gene FLJ43860		FLJ43860 protein	NM_207414, hCT2340761.0, hCT2340762.0, hCT2340763.0		NP_997297.2, EAW92232.1, EAW92233.1, EAW92234.1
GeneID:619434	NCRNA00051	8	143,279,717	143,290,364	10,647	+	3	2_A375_pNL97_plus_lncRNA_AR..1..7731, 4_A375_EGR1..1..7707, 4_A375_EGR1..1..7708	19099, -10021, 251	downstream, upstream, in gene	0	1	1	10	12	16	3	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene NCRNA00051	NCRNA00051, C8orf43	non-protein coding RNA 51	NR_024376	1554976_a_at	
GeneID:203062	TSNARE1	8	143,293,441	143,484,543	191,102	-	13	1_A375_pNL7_minus_lncRNA_AR..1..5367, 2_A375_pNL97_plus_lncRNA_AR..1..7731, 2_A375_pNL97_plus_lncRNA_AR..1..7732, 2_A375_pNL97_plus_lncRNA_AR..1..7733, 4_A375_EGR1..1..7709, 4_A375_EGR1..1..7710, 4_A375_EGR1..1..7711, 4_A375_EGR1..1..7712, 4_A375_EGR1..1..7713, 4_A375_EGR1..1..7714, 4_A375_EGR1..1..7715, 4_A375_EGR1..1..7716, 4_A375_EGR1..1..7717	152287, 185727, 152223, 19863, 183423, 170367, 153247, 151551, 110319, 107455, 100447, 83866, 49375	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	8.33	10.75	14.25	12	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene TSNARE1	FLJ31164, MGC142116, TSNARE1	t-SNARE domain containing 1	NM_145003, hCT1804112.2	1552799_at, 228862_at	NP_659440.2, EAW82324.1
GeneID:575	BAI1	8	143,545,377	143,626,368	80,991	+	7	4_A375_EGR1..1..7719, 4_A375_EGR1..1..7720, 4_A375_EGR1..1..7721, 4_A375_EGR1..1..7722, 4_A375_EGR1..1..7723, 4_A375_EGR1..1..7724, 4_A375_EGR1..1..7725	-9665, 7775, 60399, 64383, 64927, 71551, 77655	upstream, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	6.71	7.29	17.43	7	4_A375_EGR1..1	20	Gene BAI1	GDAIF, BAI1, FLJ41988	brain-specific angiogenesis inhibitor 1	NM_001702, hCT1953049.1	206083_at	NP_001693.2, EAW82323.1
GeneID:23237	ARC	8	143,692,410	143,695,833	3,423	-	4	4_A375_EGR1..1..7730, 4_A375_EGR1..1..7731, 4_A375_EGR1..1..7732, 4_A375_EGR1..1..7733	2745, 505, -4999, -7387	in gene, in gene, upstream, upstream	0	0	1	6.5	7.75	18	4	4_A375_EGR1..1	21	Gene ARC	KIAA0278, ARC, Arg3.1	activity-regulated cytoskeleton-associated protein	NM_015193, hCT2268325.0, hCT1830230.2	210090_at	NP_056008.1, EAW82321.1, EAW82320.1
GeneID:8629	JRK	8	143,738,874	143,751,401	12,527	-	3	2_A375_pNL97_plus_lncRNA_AR..1..7734, 4_A375_EGR1..1..7735, 4_A375_EGR1..1..7736	-23, 5209, 4233	upstream, in gene, in gene	0	1	1	11.33	17	13.67	3	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene JRK	JRK, DKFZp686C24207, FLJ45729, JH8	jerky homolog (mouse)	NM_003724, NM_001077527, hCT2268322.0, hCT1841648.3, hCT1965968.1	1554916_a_at, 1566805_at, 214692_s_at, 216309_x_at, 217146_at, 37872_at	NP_003715.2, NP_001070995.1, EAW82315.1, EAW82316.1, EAW82317.1
GeneID:8000	PSCA	8	143,751,726	143,764,145	12,419	+	4	2_A375_pNL97_plus_lncRNA_AR..1..7734, 2_A375_pNL97_plus_lncRNA_AR..1..7735, 4_A375_EGR1..1..7735, 4_A375_EGR1..1..7736	-302, 11666, -5534, -4556	upstream, in gene, upstream, upstream	0	1	1	12.75	16.25	14.5	4	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene PSCA	PRO232, PSCA	prostate stem cell antigen	NM_005672, NR_033343, hCT2268513.0, hCT29980.2	1560011_at, 205319_at	NP_005663.2, EAW82313.1, EAW82312.1
GeneID:100288181	LOC100288181	8	143,783,670	143,808,391	24,721	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5366, 2_A375_pNL97_plus_lncRNA_AR..1..7736, 4_A375_EGR1..1..7737	8743, 8775, 263	in gene, in gene, in gene	1	1	1	21.5	17.5	13	2	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene LOC100288181		hypothetical LOC100288181	XR_113191, XR_108895, XR_114229		
GeneID:51337	C8orf55	8	143,808,621	143,818,350	9,729	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5366, 2_A375_pNL97_plus_lncRNA_AR..1..7736, 2_A375_pNL97_plus_lncRNA_AR..1..7737, 4_A375_EGR1..1..7737	-8973, -9005, 12211, -493	upstream, upstream, downstream, upstream	1	1	1	20.67	18.33	13.33	3	1_A375_pNL7_minus_lncRNA_AR..1	30	Gene C8orf55	DSCD75, C8orf55	chromosome 8 open reading frame 55	NM_016647, hCT30559.3	218500_at	NP_057731.1, EAW82309.1
GeneID:57152	SLURP1	8	143,822,362	143,823,829	1,467	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7737, 4_A375_EGR1..1..7738	2997, -9163	downstream, upstream	0	1	1	13	12.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene SLURP1	MDM, ANUP, ARS, LY6LS, SLURP1, ArsB	secreted LY6/PLAUR domain containing 1	NM_020427, hCT30561.2	214536_at	NP_065160.1, EAW82308.1
GeneID:137797	LYPD2	8	143,831,628	143,833,952	2,324	-	2	4_A375_EGR1..1..7738, 4_A375_EGR1..1..7739	960, -1552	in gene, upstream	0	0	1	6	7	17	2	4_A375_EGR1..1	16	Gene LYPD2	UNQ430, LYPDC2, LYPD2, MGC148108	LY6/PLAUR domain containing 2	NM_205545, hCT30565.2		NP_991108.1, EAW82307.1
GeneID:66004	LYNX1	8	143,845,756	143,859,640	13,884	-	7	4_A375_EGR1..1..7739, 4_A375_EGR1..1..7740, 4_A375_EGR1..1..7741, 4_A375_EGR1..1..7742, 4_A375_EGR1..1..7743, 4_A375_EGR1..1..7744, 4_A375_EGR1..1..7745	24136, 9400, 5176, 4280, 2104, 1624, -4584	downstream, in gene, in gene, in gene, in gene, in gene, upstream	0	0	1	5.71	6	17.57	7	4_A375_EGR1..1	20	Gene LYNX1	MGC40384, SLURP2, LYNX1	Ly6/neurotoxin 1	NM_177458, NM_177457, NM_177476, NM_177477, NM_023946	1554179_s_at, 1559388_a_at, 226305_at, 244224_x_at	NP_803253.1, NP_803252.1, NP_803430.1, NP_076435.1, NP_803429.1
GeneID:8581	LY6D	8	143,866,298	143,868,008	1,710	-	3	4_A375_EGR1..1..7743, 4_A375_EGR1..1..7744, 4_A375_EGR1..1..7745	10472, 9992, 3784	downstream, downstream, downstream	0	0	1	6.67	9	17	3	4_A375_EGR1..1	19	Gene LY6D	LY6D, Ly-6D, E48	lymphocyte antigen 6 complex, locus D	NM_003695, hCT2268311.0, hCT30560.3	206276_at	NP_003686.1, EAW82297.1, EAW82298.1
GeneID:100288207	LOC100288207	8	143,877,674	143,887,558	9,884	-	1	4_A375_EGR1..1..7746	7078	in gene	0	0	1	5	11	17	1	4_A375_EGR1..1	17	Gene LOC100288207		hypothetical protein LOC100288207	XM_002342860, XM_002347029		XP_002342921.1, XP_002347070.1
GeneID:2765	GML	8	143,916,217	143,928,262	12,045	+	2	4_A375_EGR1..1..7748, 4_A375_EGR1..1..7749	-473, 39	upstream, in gene	0	0	1	5.5	2.5	15.5	2	4_A375_EGR1..1	16	Gene GML	GML, LY6DL	glycosylphosphatidylinositol anchored molecule like protein	NM_002066, hCT30557.3	208000_at	NP_002057.1, EAW82296.1
GeneID:1585	CYP11B2	8	143,991,975	143,999,259	7,284	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7738	5755	in gene	0	1	0	13	21	12	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene CYP11B2	CPN2, P450C18, CYP11BL, CYP11B2, ALDOS, P-450C18, CYP11B, P450aldo	cytochrome P450, family 11, subfamily B, polypeptide 2	NM_000498, hCT1952554.1	214630_at	NP_000489.3, EAW82292.1
GeneID:286122	C8orf31	8	144,120,679	144,135,720	15,041	+	1	4_A375_EGR1..1..7751	-407	upstream	0	0	1	6	9	18	1	4_A375_EGR1..1	18	Gene C8orf31	C8orf31, FLJ37131, MGC90155	chromosome 8 open reading frame 31	NM_173687, hCT2275045.2, hCT2351040.0, hCT2356235.0	1552793_at	NP_775958.1, EAW82282.1, EAW82281.1, EAW82283.1
GeneID:4062	LY6H	8	144,239,331	144,242,053	2,722	-	3	4_A375_EGR1..1..7753, 4_A375_EGR1..1..7754, 4_A375_EGR1..1..7755	3205, 2405, 805	downstream, in gene, in gene	0	0	1	3.33	6	16.33	3	4_A375_EGR1..1	17	Gene LY6H	LY6H, NMLY6	lymphocyte antigen 6 complex, locus H	NM_001130478, NM_002347, NM_001135655, hCT2274487.0, hCT2274488.0, hCT22770.3	206773_at	NP_001123950.1, NP_002338.3, NP_001129127.1, EAW82277.1, EAW82278.1, EAW82279.1
GeneID:338328	GPIHBP1	8	144,295,068	144,299,044	3,976	+	2	4_A375_EGR1..1..7757, 4_A375_EGR1..1..7758	1700, 6836	in gene, downstream	0	0	1	7	6	17.5	2	4_A375_EGR1..1	19	Gene GPIHBP1	GPI-HBP1, GPIHBP1	glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	NM_178172, hCT1808836.2	236062_at	NP_835466.1, EAW82276.1
GeneID:286128	ZFP41	8	144,329,109	144,344,875	15,766	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5371, 2_A375_pNL97_plus_lncRNA_AR..1..7742, 4_A375_EGR1..1..7759, 4_A375_EGR1..1..7760	20427, 20395, 11, 23435	downstream, downstream, in gene, downstream	1	1	1	17.67	16	14.67	3	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene ZFP41	FLJ00028, ZNF753, FLJ38705, ZFP41, DKFZp761O1618	zinc finger protein 41 homolog (mouse)	NM_173832	227898_s_at, 227902_at, 237382_at	NP_776193.1
GeneID:2738	GLI4	8	144,349,607	144,359,101	9,494	+	9	1_A375_pNL7_minus_lncRNA_AR..1..5371, 1_A375_pNL7_minus_lncRNA_AR..1..5372, 2_A375_pNL97_plus_lncRNA_AR..1..7742, 2_A375_pNL97_plus_lncRNA_AR..1..7743, 4_A375_EGR1..1..7760, 4_A375_EGR1..1..7761, 4_A375_EGR1..1..7762, 4_A375_EGR1..1..7763, 4_A375_EGR1..1..7764	-71, 14313, -103, 14297, 2937, 7789, 9049, 10057, 11461	upstream, downstream, upstream, downstream, in gene, in gene, in gene, downstream, downstream	1	1	1	29.57	33.43	15	7	2_A375_pNL97_plus_lncRNA_AR..1	150	Gene GLI4	ZNF928, HKR4, GLI4	GLI family zinc finger 4	NM_138465	227023_at	NP_612474.1
GeneID:100507316	LOC100507316	8	144,362,331	144,363,860	1,529	-	9	1_A375_pNL7_minus_lncRNA_AR..1..5372, 1_A375_pNL7_minus_lncRNA_AR..1..5373, 2_A375_pNL97_plus_lncRNA_AR..1..7743, 2_A375_pNL97_plus_lncRNA_AR..1..7744, 4_A375_EGR1..1..7760, 4_A375_EGR1..1..7761, 4_A375_EGR1..1..7762, 4_A375_EGR1..1..7763, 4_A375_EGR1..1..7764	-60, -9644, -44, -9644, 11316, 6484, 5204, 4196, 2772	upstream, upstream, upstream, upstream, downstream, downstream, downstream, downstream, downstream	1	1	1	29.86	32.57	15.71	7	2_A375_pNL97_plus_lncRNA_AR..1	150	Gene LOC100507316		hypothetical LOC100507316	XR_108896, XR_108897, XR_108898		
GeneID:79943	ZNF696	8	144,373,559	144,382,122	8,563	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5372, 1_A375_pNL7_minus_lncRNA_AR..1..5373, 2_A375_pNL97_plus_lncRNA_AR..1..7743, 2_A375_pNL97_plus_lncRNA_AR..1..7744	-9639, -55, -9655, -55	upstream, upstream, upstream, upstream	1	1	0	82.5	86.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	150	Gene ZNF696	ZNF696, FLJ14129	zinc finger protein 696	NM_030895	220987_s_at, 232162_at	NP_112157.2
GeneID:116447	TOP1MT	8	144,391,526	144,417,050	25,524	-	2	4_A375_EGR1..1..7765, 4_A375_EGR1..1..7766	17818, 314	in gene, in gene	0	0	1	10	6	15.5	2	4_A375_EGR1..1	17	Gene TOP1MT	TOP1MT	topoisomerase (DNA) I, mitochondrial	NM_052963, hCT2274577.1, hCT2274578.0, hCT2345003.0, hCT2345004.0, hCT2345005.0, hCT2345006.0, hCT2345007.0, hCT2345008.0	225602_at	NP_443195.1, EAW82265.1, EAW82259.1, EAW82260.1, EAW82264.1, EAW82266.1, EAW82261.1, EAW82262.1, EAW82263.1
GeneID:78996	C8orf51	8	144,448,793	144,450,805	2,012	-	1	4_A375_EGR1..1..7767	-6659	upstream	0	0	1	7	7	21	1	4_A375_EGR1..1	21	Gene C8orf51	MGC3113, C8orf51	chromosome 8 open reading frame 51	NR_026785, hCT1808826.1	207456_at	EAW82257.1
GeneID:114822	RHPN1	8	144,451,025	144,466,390	15,365	+	3	4_A375_EGR1..1..7767, 4_A375_EGR1..1..7768, 4_A375_EGR1..1..7769	6639, 14927, 16559	in gene, in gene, downstream	0	0	1	6.67	12	18.67	3	4_A375_EGR1..1	21	Gene RHPN1	KIAA1929, RHPN, RHPN1, ODF5, RHOPHILIN	rhophilin, Rho GTPase binding protein 1	NM_052924, hCT2275065.0, hCT23248.3, hCT2358215.0, hCT1953944.1, hCT1953945.1, hCT1953946.1	228405_at, 235998_at	NP_443156.2, EAW82258.1, EAW82252.1, EAW82253.1, EAW82254.1, EAW82255.1, EAW82251.1
GeneID:100507344	LOC100507344	8	144,510,230	144,511,261	1,031	-	1	4_A375_EGR1..1..7773	3581	downstream	0	0	1	9	7	13	1	4_A375_EGR1..1	13	Gene LOC100507344		hypothetical LOC100507344	XR_113187, XR_108899, XR_114233		
GeneID:389692	MAFA	8	144,511,515	144,512,576	1,061	-	1	4_A375_EGR1..1..7773	4896	downstream	0	0	1	9	7	13	1	4_A375_EGR1..1	13	Gene MAFA	MAFA, hMafA, RIPE3b1	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian)	NM_201589		NP_963883.2
GeneID:23144	ZC3H3	8	144,519,825	144,623,620	103,795	-	6	2_A375_pNL97_plus_lncRNA_AR..1..7745, 4_A375_EGR1..1..7774, 4_A375_EGR1..1..7775, 4_A375_EGR1..1..7776, 4_A375_EGR1..1..7777, 4_A375_EGR1..1..7778	-172, 99966, 78260, 29604, 23108, -5116	upstream, in gene, in gene, in gene, in gene, upstream	0	1	1	8.33	9.83	15.83	6	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene ZC3H3	ZC3H3, ZC3HDC3, KIAA0150	zinc finger CCCH-type containing 3	NM_015117, hCT23253.1	213445_at	NP_055932.2, EAW82249.1
GeneID:79792	GSDMD	8	144,635,557	144,645,232	9,675	+	3	4_A375_EGR1..1..7778, 4_A375_EGR1..1..7779, 4_A375_EGR1..1..7780	-6621, 939, 8715	upstream, in gene, in gene	0	0	1	9	6.33	18	3	4_A375_EGR1..1	21	Gene GSDMD	GSDMD, FKSG10, FLJ12150, GSDMDC1, DFNA5L, DF5L	gasdermin D	NM_024736, NM_001166237, hCT2275013.0, hCT2275015.0, hCT23251.3, hCT2358220.0, hCT2358221.0, hCT2358222.0, hCT2358223.0	218154_at	NP_079012.3, NP_001159709.1, EAW82243.1, EAW82245.1, EAW82247.1, EAW82248.1, EAW82242.1, EAW82244.1, EAW82246.1
GeneID:642475	C8orf73	8	144,648,362	144,654,928	6,566	-	1	4_A375_EGR1..1..7780	10856	downstream	0	0	1	4	11	17	1	4_A375_EGR1..1	17	Gene C8orf73	C8orf73	chromosome 8 open reading frame 73	NM_001100878	227672_at	NP_001094348.1

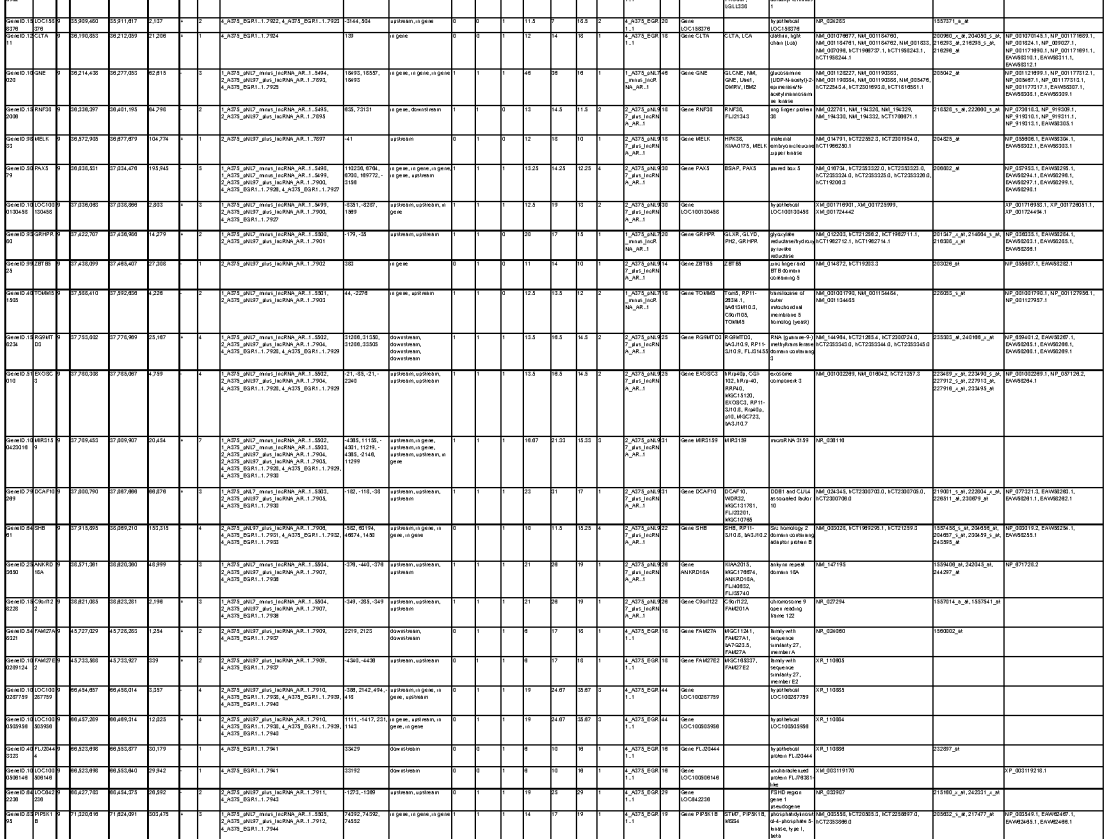
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.1936	EEF1D	8	144,661,898	144,679,845	17,947	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5374, 2_A375_pNL97_plus_lncRNA_AR..1..7746, 2_A375_pNL97_plus_lncRNA_AR..1..7747, 4_A375_EGR1..1..7781, 4_A375_EGR1..1..7782	133, 133, -603, 6037, -3619	in gene, in gene, upstream, in gene, upstream	1	1	1	17.75	24	15.75	4	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene EEF1D	EF1D, EF-1D, FP1047, FLJ20897, EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	NM_032378, NM_001960, NM_001130053, NM_001130055, NM_001130056, NM_001130057, hCT2274544.0, hCT2274545.0, hCT2274547.0, hCT2274548.0, hCT2274550.0, hCT2274552.0, hCT2274554.0, hCT2274558.0, hCT2356228.0	203113_s_at	NP_115754.2, NP_001951.2, NP_001123525.1, NP_001123527.1, NP_001123528.1, NP_001123529.1, EAW82227.1, EAW82228.1, EAW82229.1, EAW82230.1, EAW82231.1, EAW82232.1, EAW82233.1, EAW82234.1, EAW82235.1
GeneID.84946	TIGD5	8	144,680,074	144,682,485	2,411	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5374, 2_A375_pNL97_plus_lncRNA_AR..1..7746, 2_A375_pNL97_plus_lncRNA_AR..1..7747, 4_A375_EGR1..1..7781, 4_A375_EGR1..1..7782	-362, -362, 374, -8268, 3590	upstream, upstream, in gene, upstream, downstream	1	1	1	17.75	24	15.75	4	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene TIGD5	MGC44883, FLJ14926, TIGD5	tigger transposable element derived 5	NM_032862, hCT1971207.1	229758_at	NP_116251.4, EAW82226.1
GeneID.65263	PYCRL	8	144,686,083	144,691,784	5,701	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5374, 2_A375_pNL97_plus_lncRNA_AR..1..7746, 2_A375_pNL97_plus_lncRNA_AR..1..7747, 2_A375_pNL97_plus_lncRNA_AR..1..7748, 4_A375_EGR1..1..7782	12072, 12072, 11336, -8568, 8120	downstream, downstream, downstream, upstream, downstream	1	1	1	20.25	26.5	13.5	4	2_A375_pNL97_plus_lncRNA_AR..1	54	Gene PYCRL	PYCRL, FLJ13852	pyrroline-5-carboxylate reductase-like	NM_023078, hCT1966035.1, hCT2274541.0, hCT23245.3	218944_at	NP_075566.2, EAW82223.1, EAW82224.1, EAW82225.1
GeneID.7264	TSTA3	8	144,694,788	144,699,732	4,944	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7748	-620	upstream	0	1	0	13	18	9	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TSTA3	SDR4E1, P35B, TSTA3, FX	tissue specific transplantation antigen P35B	NM_003313, hCT2274532.0, hCT2274533.0, hCT2274537.0, hCT23243.3, hCT1952560.1, hCT1952561.1	201644_at, 36936_at	NP_003304.1, EAW82219.1, EAW82217.1, EAW82218.1, EAW82220.1, EAW82222.1, EAW82221.1
GeneID.9831	ZNF623	8	144,718,373	144,735,900	17,527	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5375, 2_A375_pNL97_plus_lncRNA_AR..1..7749	-581, -517	upstream, upstream	1	1	0	18	18	13	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene ZNF623	MGC104128, MGC103985, ZNF623	zinc finger protein 623	NM_001082480, NM_014789, hCT2274531.0	206188_at	NP_001075949.1, NP_055604.3, EAW82215.1
GeneID.286075	ZNF707	8	144,766,622	144,777,555	10,933	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5376, 2_A375_pNL97_plus_lncRNA_AR..1..7750	-110, 50	upstream, in gene	1	1	0	19	23	20	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ZNF707	ZNF707	zinc finger protein 707	NM_173831, NM_001100598, NM_001100599, hCT2349691.0, hCT2356236.0, hCT1808838.3, hCT1952551.1, hCT1952552.1	232078_at	NP_776192.2, NP_001094068.1, NP_001094069.1, EAW82210.1, EAW82211.1, EAW82212.1, EAW82213.1, EAW82214.1
GeneID.225689	MAPK15	8	144,796,507	144,804,633	8,126	+	2	4_A375_EGR1..1..7763, 4_A375_EGR1..1..7764	5109, 6421	in gene, downstream	0	0	1	5	8	15.5	2	4_A375_EGR1..1	17	Gene MAPK15	MAPK15, ERK7, ERK8	mitogen-activated protein kinase 15	NM_139021, hCT2275037.0, hCT22884.3, hCT2349693.0	241357_at, 241528_at	NP_620590.2, EAW82203.1, EAW82204.1, EAW82205.1
GeneID.286077	FAM83H	8	144,806,103	144,815,914	9,811	-	4	4_A375_EGR1..1..7763, 4_A375_EGR1..1..7764, 4_A375_EGR1..1..7765, 4_A375_EGR1..1..7766	12298, 10986, -438, -4150	downstream, downstream, upstream, upstream	0	0	1	8.25	8.5	16.75	4	4_A375_EGR1..1	19	Gene FAM83H	AI3, FAM83H, FLJ46072	family with sequence similarity 83, member H	NM_198488	226129_at, 241406_at	NP_940890.3
GeneID.100128338	hCG_1995004	8	144,816,310	144,828,507	12,197	+	2	4_A375_EGR1..1..7765, 4_A375_EGR1..1..7766	42, 3754	in gene, in gene	0	0	1	7.5	7	18	2	4_A375_EGR1..1	19	Gene hCG_1995004	LOC100128338, FLJ33892, FLJ43864, FLJ42065	hypothetical LOC100128338	NR_033849		
GeneID.642574	LOC642574	8	144,853,300	144,872,776	19,476	+	2	4_A375_EGR1..1..7787, 4_A375_EGR1..1..7788	18700, 20236	in gene, downstream	0	0	1	3.5	8	16.5	2	4_A375_EGR1..1	18	Gene LOC642574		IQ motif and ankyrin repeat domain-containing protein LOC642574	XM_926080		XP_931153.5
GeneID.23513	SCRIB	8	144,873,090	144,897,549	24,459	-	7	4_A375_EGR1..1..7787, 4_A375_EGR1..1..7788, 4_A375_EGR1..1..7789, 4_A375_EGR1..1..7790, 4_A375_EGR1..1..7791, 4_A375_EGR1..1..7792, 4_A375_EGR1..1..7793	25549, 24013, 11085, 6445, 2781, 2253, -4755	downstream, in gene, in gene, in gene, in gene, in gene, upstream	0	0	1	5.86	7.29	16.57	7	4_A375_EGR1..1	21	Gene SCRIB	Vartul, SCRB1, SCRIB, CRIB1, SCRIB1	scribbled homolog (Drosophila)	NM_182706, NM_015356, hCT2274525.0, hCT2356229.0, hCT31977.2	212556_at	NP_874365.2, NP_056171.2, EAW82196.1, EAW82197.1, EAW82198.1
GeneID.100126338	MIR937	8	144,895,127	144,895,212	85	-	5	4_A375_EGR1..1..7789, 4_A375_EGR1..1..7790, 4_A375_EGR1..1..7791, 4_A375_EGR1..1..7792, 4_A375_EGR1..1..7793	8748, 4108, 444, -84, -7092	downstream, downstream, downstream, upstream, upstream	0	0	1	6.8	7.6	16.6	5	4_A375_EGR1..1	21	Gene MIR937	hsa-mir-937, MIRN937, MIR937	microRNA 937	NR_030633		
GeneID.22827	PUF60	8	144,898,547	144,911,537	12,990	-	5	2_A375_pNL97_plus_lncRNA_AR..1..7751, 4_A375_EGR1..1..7790, 4_A375_EGR1..1..7791, 4_A375_EGR1..1..7792, 4_A375_EGR1..1..7793	113, 20433, 16769, 16241, 9233	in gene, downstream, downstream, downstream, in gene	0	1	1	8.8	10	18	5	4_A375_EGR1..1	21	Gene PUF60	FLJ31379, RoBPI, SIAHBP1, FIR, PUF60	poly-U binding splicing factor 60KDa	NM_014281, NM_078480, NM_001136033, hCT1966843.1, hCT1966844.1, hCT2274516.0, hCT2274517.0, hCT2274521.0, hCT2274522.0, hCT2356232.0, hCT2356233.0, hCT2356234.0, hCT31979.2, hCT1952566.1, hCT1952567.1	209899_s_at	NP_055096.2, NP_510965.1, NP_001129505.1, EAW82184.1, EAW82187.1, EAW82192.1, EAW82185.1, EAW82186.1, EAW82188.1, EAW82189.1, EAW82190.1, EAW82191.1, EAW82193.1, EAW82194.1, EAW82195.1
GeneID.340371	NRBP2	8	144,915,755	144,923,146	7,391	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7751	11722	downstream	0	1	0	16	19	14	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene NRBP2	pp9320, DKFZp434P086, TRG16, NRBP2, MGC138699	nuclear receptor binding protein 2	NM_178564, hCT2274512.0, hCT2274514.0, hCT2356230.0, hCT2356231.0, hCT31978.3, hCT1952565.1	225949_at	NP_848659.2, EAW82178.1, EAW82179.1, EAW82180.1, EAW82181.1, EAW82182.1, EAW82183.1
GeneID.5339	PLEC1	8	144,989,321	145,050,913	61,592	-	25	1_A375_pNL7_minus_lncRNA_AR..1..5377, 1_A375_pNL7_minus_lncRNA_AR..1..5378, 1_A375_pNL7_minus_lncRNA_AR..1..5379, 1_A375_pNL7_minus_lncRNA_AR..1..5380, 2_A375_pNL97_plus_lncRNA_AR..1..7752, 2_A375_pNL97_plus_lncRNA_AR..1..7753, 2_A375_pNL97_plus_lncRNA_AR..1..7754, 2_A375_pNL97_plus_lncRNA_AR..1..7755, 4_A375_EGR1..1..7795, 4_A375_EGR1..1..7796, 4_A375_EGR1..1..7797, 4_A375_EGR1..1..7798, 4_A375_EGR1..1..7799, 4_A375_EGR1..1..7800, 4_A375_EGR1..1..7801, 4_A375_EGR1..1..7802, 4_A375_EGR1..1..7803, 4_A375_EGR1..1..7804, 4_A375_EGR1..1..7805, 4_A375_EGR1..1..7806, 4_A375_EGR1..1..7807, 4_A375_EGR1..1..7808, 4_A375_EGR1..1..7809, 4_A375_EGR1..1..7810, 4_A375_EGR1..1..7811	40033, 32633, 28129, 1649, 33889, 26085, 27201, 1633, 63777, 56273, 48993, 46769, 44929, 41457, 38065, 35937, 33793, 31673, 30913, 28321, 27137, 4577, 1665, -6634, -9215	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, downstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream, upstream	1	1	1	12.22	14.39	18.28	18	4_A375_EGR1..1	30	Gene PLEC1	LGMD2Q, PLTN, EBSO, PLEC1b, PCN, PLEC1, PLEC, EBS1, HD1	plectin 1, intermediate filament binding protein 500kDa	NM_201379, NM_201381, NM_201383, NM_201384, NM_201380, NM_201382, NM_201378, NM_000445, hCT2274504.0, hCT2274505.0, hCT2274506.0, hCT2274507.0, hCT2356224.0	201373_at, 216971_s_at	NP_958781.1, NP_958783.1, NP_958785.1, NP_958782.1, NP_958784.1, NP_958786.1, NP_958780.1, NP_000436.2, EAW82170.1, EAW82171.1, EAW82172.1, EAW82173.1, EAW82174.1
GeneID.724031	MIR661	8	145,019,359	145,019,447	88	-	14	1_A375_pNL7_minus_lncRNA_AR..1..5377, 1_A375_pNL7_minus_lncRNA_AR..1..5378, 1_A375_pNL7_minus_lncRNA_AR..1..5379, 2_A375_pNL97_plus_lncRNA_AR..1..7752, 2_A375_pNL97_plus_lncRNA_AR..1..7753, 2_A375_pNL97_plus_lncRNA_AR..1..7754, 4_A375_EGR1..1..7800, 4_A375_EGR1..1..7801, 4_A375_EGR1..1..7802, 4_A375_EGR1..1..7803, 4_A375_EGR1..1..7804, 4_A375_EGR1..1..7805, 4_A375_EGR1..1..7806, 4_A375_EGR1..1..7807	8587, 1367, -3337, 2423, -3401, -4265, 9991, 6599, 4471, 2327, 407, -553, -3145, -4329	downstream, downstream, upstream, downstream, upstream, upstream, downstream, downstream, downstream, downstream, upstream, upstream, upstream	1	1	1	15.56	16.89	17.78	9	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene MIR661	hsa-mir-661, MIR661, MIRN661	microRNA 661	NR_030363		
GeneID.84875	PARP10	8	145,051,320	145,060,635	9,315	-	6	1_A375_pNL7_minus_lncRNA_AR..1..5380, 2_A375_pNL97_plus_lncRNA_AR..1..7755, 4_A375_EGR1..1..7808, 4_A375_EGR1..1..7809, 4_A375_EGR1..1..7810, 4_A375_EGR1..1..7811	11371, 11355, 14299, 11387, 3068, 507	downstream, downstream, downstream, downstream, in gene, in gene	1	1	1	10.25	15.75	15.75	4	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene PARP10	FLJ14464, PARP10	poly (ADP-ribose) polymerase family, member 10	NM_032789, hCT2274501.1	226401_at, 228669_x_at, 229350_x_at, 238063_at	NP_116178.2, EAW82169.1
GeneID.2907	GRINA	8	145,064,226	145,067,583	3,357	+	2	4_A375_EGR1..1..7810, 4_A375_EGR1..1..7811	-6679, -4098	upstream, upstream	0	0	1	9.5	12.5	15	2	4_A375_EGR1..1	17	Gene GRINA	NMDARA1, LFG1, TMBIM3, MGC99687, GRINA, HNRGW	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	NM_000837, NM_001009184, hCT2251631.0, hCT2251632.0, hCT2251634.0	212090_at	NP_000828.1, NP_001009184.1, EAW52304.1, EAW52305.1, EAW52306.1
GeneID.392275	LOC392275	8	145,104,023	145,106,107	2,084	+	1	4_A375_EGR1..1..7812	9145	downstream	0	0	1	8	9	18	1	4_A375_EGR1..1	18	Gene LOC392275		sphingomyelin phosphodiesterase 5	XM_001714032		XP_001714084.1
GeneID.26873	OPLAH	8	145,106,167	145,115,584	9,417	-	2	4_A375_EGR1..1..7812, 4_A375_EGR1..1..7813	2418, -3328	in gene, upstream	0	0	1	10.5	5.5	18.5	2	4_A375_EGR1..1	19	Gene OPLAH	OPLAH, OPLA, DKFZp434H244, 5-Opase	5-oxoprolinase (ATP-hydrolysing)	NM_017570	222025_s_at	NP_060040.1
GeneID.54512	EXOSC4	8	145,133,522	145,135,551	2,029	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5381, 2_A375_pNL97_plus_lncRNA_AR..1..7756, 4_A375_EGR1..1..7814, 4_A375_EGR1..1..7815	195, 462, 110, 7374	in gene, in gene, in gene, downstream	1	1	1	13	16.5	22	2	4_A375_EGR1..1	23	Gene EXOSC4	RRP41A, hRrp41p, Ski6p, p12A, SKI6, Rrp41p, FLJ20591, EXOSC4, RRP41	exosome component 4	NM_019037, hCT1788229.2	218695_at, 58696_at, 91684_g_at	NP_061910.1, EAW82166.1
GeneID.8733	GPAA1	8	145,137,524	145,141,119	3,595	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5381, 2_A375_pNL97_plus_lncRNA_AR..1..7756, 4_A375_EGR1..1..7814, 4_A375_EGR1..1..7815	-3807, -3540, -3892, 3372	upstream, upstream, upstream, in gene	1	1	1	13	16.5	22	2	4_A375_EGR1..1	23	Gene GPAA1	GAA1, GPAA1, hGAA1	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)	NM_003801, hCT2271871.0, hCT10587.2, hCT1958358.0, hCT1958359.0, hCT1958360.1	201618_x_at, 211060_x_at, 215690_x_at	NP_003792.1, EAW82162.1, EAW82161.1, EAW82163.1, EAW82164.1, EAW82165.1
GeneID.1537	CYC1	8	145,149,960	145,152,428	2,468	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5382, 2_A375_pNL97_plus_lncRNA_AR..1..7757, 4_A375_EGR1..1..7815, 4_A375_EGR1..1..7816	9272, 9304, -9084, 8904	downstream, downstream, upstream, downstream	1	1	1	22	25.5	21.5	2	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene CYC1	UQCR4, CYC1	cytochrome c-1	NM_001916, hCT10830.3	201066_at	NP_001907.2, EAW82160.1
GeneID.100507382	LOC100507382	8	145,151,231	145,151,943	712	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5382, 2_A375_pNL97_plus_lncRNA_AR..1..7757, 4_A375_EGR1..1..7816	-7289, -7321, -6921	upstream, upstream, upstream	1	1	1	36	40	20	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene LOC100507382		hypothetical LOC100507382	XR_108900		
GeneID.81858	SHARPIN	8	145,153,536	145,159,140	5,604	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5382, 2_A375_pNL97_plus_lncRNA_AR..1..7757, 4_A375_EGR1..1..7816, 4_A375_EGR1..1..7817, 4_A375_EGR1..1..7818	-92, -124, 276, -3900, -7356	upstream, upstream, in gene, upstream, upstream	1	1	1	16.33	17	20	3	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene SHARPIN	SHARPIN, SIPL1, DKFZp434N1923	SHANK-associated RH domain interactor	NM_030974, hCT2270671.0, hCT1958361.1, hCT1958362.1, hCT1958363.1, hCT1958364.1, hCT1958365.1, hCT1958366.1	220973_s_at	NP_112236.3, EAW82153.1, EAW82151.1, EAW82152.1, EAW82154.1, EAW82155.1, EAW82150.1, EAW82156.1
GeneID.84232	MAF1	8	145,159,305	145,162,515	3,210	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5382, 2_A375_pNL97_plus_lncRNA_AR..1..7757, 4_A375_EGR1..1..7816, 4_A375_EGR1..1..7817, 4_A375_EGR1..1..7818	-73, -41, -441, 3735, 7191	upstream, upstream, upstream, downstream, downstream	1	1	1	16.33	17	20	3	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene MAF1	MGC20332, MAF1, MGC31779, MGC39758	MAF1 homolog (S. cerevisiae)	NM_032272, hCT2271861.0, hCT10832.2	222996_at	NP_115648.2, EAW82158.1, EAW82159.1
GeneID.340390	KIAA1875	8	145,162,629	145,173,218	10,589	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5382, 2_A375_pNL97_plus_lncRNA_AR..1..7757, 4_A375_EGR1..1..7816, 4_A375_EGR1..1..7817, 4_A375_EGR1..1..7818	-3397, -3365, -3765, 411, 3867	upstream, upstream, upstream, in gene, in gene	1	1	1	16.33	17	20	3	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene KIAA1875	KIAA1875		NR_024207	233344_x_at	
GeneID.727957	HEATR7A	8	145,202,919	145,316,843	113,924	+	2	4_A375_EGR1..1..7819, 4_A375_EGR1..1..7820	41705, 72985	in gene, in gene	0	0	1	10	9.5	18	2	4_A375_EGR1..1	21	Gene HEATR7A	FLJ38266, FLJ42560, FLJ38244, DKFZp434I0113, FLJ35542, HEATR7A, DKFZp434P167, MGC50841, KIAA1833, FLJ13324	HEAT repeat containing 7A	NM_001099280, NM_001099281, NM_032450		NP_001092750.1, NP_001092751.1, NP_115826.2
GeneID.23246	BOP1	8	145,486,056	145,515,120	29,064	-	1	4_A375_EGR1..1..7821	-5072	upstream	0	0	1	8	8	18	1	4_A375_EGR1..1	18	Gene BOP1	KIAA0124, BOP1	block of proliferation 1	NM_015201, hCT1654237.2	212563_at, 216397_s_at	NP_056016.1, EAW82133.1
GeneID.3297	HSF1	8	145,515,270	145,538,385	23,115	+	4	4_A375_EGR1..1..7821, 4_A375_EGR1..1..7822, 4_A375_EGR1..1..7823, 4_A375_EGR1..1..7824	4922, 19882, 21594, 25402	in gene, in gene, in gene, downstream	0	0	1	7	7.5	19.5	4	4_A375_EGR1..1	24	Gene HSF1	HSTF1, HSF1	heat shock transcription factor 1	NM_005526, hCT15123.2	202344_at, 213756_s_at	NP_005517.1, EAW82131.1
GeneID.8694	DGAT1	8	145,538,247	145,550,567	12,320	-	7	1_A375_pNL7_minus_lncRNA_AR..1..5383, 2_A375_pNL97_plus_lncRNA_AR..1..7758, 2_A375_pNL97_plus_lncRNA_AR..1..7759, 4_A375_EGR1..1..7822, 4_A375_EGR1..1..7823, 4_A375_EGR1..1..7824, 4_A375_EGR1..1..7825	39, -153, -8886, 15415, 13703, 9895, -4165	in gene, upstream, upstream, downstream, downstream, in gene, upstream	1	1	1	11.17	11.33	17.33	6	4_A375_EGR1..1	24	Gene DGAT1	DGAT1, DGAT, ARGP1	diacylglycerol O-acyltransferase homolog 1 (mouse)	NM_012079, hCT2270665.0, hCT15120.3, hCT1981865.1, hCT1981866.1	203669_s_at	NP_036211.2, EAW82129.1, EAW82127.1, EAW82128.1, EAW82130.1
GeneID.83482	SCRT1	8	145,554,454	145,559,943	5,489	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5383, 2_A375_pNL97_plus_lncRNA_AR..1..7758, 2_A375_pNL97_plus_lncRNA_AR..1..7759, 4_A375_EGR1..1..7825	9415, 9223, 690, 5191	downstream, downstream, in gene, in gene	1	1	1	15	14.67	14.67	3	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene SCRT1	SCRT, ZNF898, SCRT1, DKFZp547F072	scratch homolog 1, zinc finger protein (Drosophila)	NM_031309, hCT1788231.3	221026_s_at, 228761_at	NP_112599.1, EAW82125.1
GeneID.340393	C8ORFK29	8	145,576,886	145,578,505	1,619	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7760, 4_A375_EGR1..1..7826	-3751, -2867	upstream, upstream	0	1	1	16.5	16.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C8ORFK29		hypothetical LOC340393	NR_015426		
GeneID.26233	FBXL6	8	145,579,091	145,582,132	3,041	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7760, 4_A375_EGR1..1..7826	-124, 740	upstream, in gene	0	1	1	16.5	16.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene FBXL6	FBL6, PP14630, FBXL6, FBL6A	F-box and leucine-rich repeat protein 6	NM_012162, NM_024555, hCT2270658.0, hCT2356214.0, hCT15130.3, hCT1958381.1, hCT1958382.1, hCT1958383.1	219189_at, 239416_at	NP_036294.1, NP_078831.3, EAW82118.1, EAW82119.1, EAW82120.1, EAW82122.1, EAW82117.1, EAW82121.1
GeneID.79581	GPR172A	8	145,582,225	145,584,946	2,721	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7760, 4_A375_EGR1..1..7826	31, -633	in gene, upstream	0	1	1	16.5	16.5	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene GPR172A	GPCR41, GPCR, PAR1, hRFT3, RFT3, D15Ertd747e, GPR172A	G protein-coupled receptor 172A	NM_024531, hCT2271698.0, hCT2271699.0	218151_x_at, 222155_s_at	NP_078807.1, EAW82116.1, EAW82115.1
GeneID.203054	ADCK5	8	145,597,731	145,618,457	20,726	+	4	2_A375_pNL97_plus_lncRNA_AR..1..7761, 4_A375_EGR1..1..7827, 4_A375_EGR1..1..7828, 4_A375_EGR1..1..7829	-147, 23421, 24765, 25277	upstream, downstream, downstream, downstream	0	1	1	8.75	9.5	16.5	4	4_A375_EGR1..1	21	Gene ADCK5	ADCK5, FLJ35454, MGC126708	aarF domain containing kinase 5	NM_174922, hCT2271907.0, hCT2356241.0, hCT2356242.0, hCT15126.3	228524_at	NP_777582.3, EAW82111.1, EAW82112.1, EAW82113.1, EAW82114.1

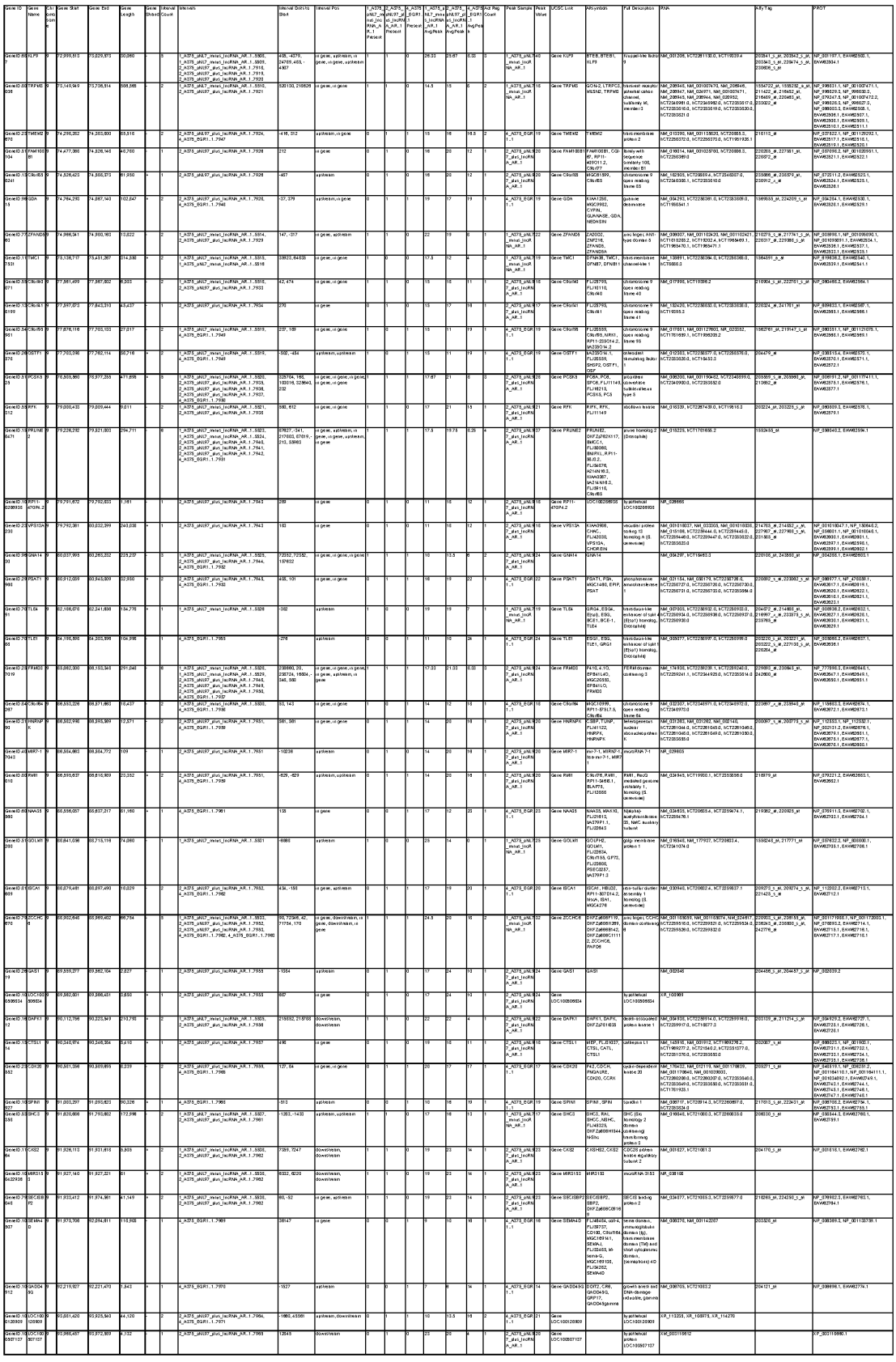
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:29894	CPSF1	8	145,618,446	145,634,733	16,287	-	5	4_A375_EGR1..1..7627, 4_A375_EGR1..1..7628, 4_A375_EGR1..1..7629, 4_A375_EGR1..1..7630, 4_A375_EGR1..1..7631	13561, 12237, 11725, -414, -5907	in gene, in gene, in gene, upstream, upstream	0	0	1	7.2	6.6	19	5	4_A375_EGR1..1	24	Gene CPSF1	CPSF1, P/cl.18, CPSF160, HSU37012	cleavage and polyadenylation specific factor 1, 160kDa	NM_013291, hCT2270646.1, hCT2270649.0, hCT2270650.1, hCT2270652.1, hCT2270653.1	201638_s_at, 201639_s_at, 33132_at	NP_037423.2, EAW82107.1, EAW82106.1, EAW82108.1, EAW82109.1, EAW82110.1
GeneID:100126351	MIR939	8	145,619,364	145,619,445	81	-	3	4_A375_EGR1..1..7627, 4_A375_EGR1..1..7628, 4_A375_EGR1..1..7629	-1707, -3051, -3563	upstream, upstream, upstream	0	0	1	6.33	7.33	18.33	3	4_A375_EGR1..1	21	Gene MIR939	MIR939, MIRN939, hsa-mir-939	microRNA 939	NR_030635		
GeneID:100302196	MIR1234	8	145,625,476	145,625,559	83	-	4	4_A375_EGR1..1..7627, 4_A375_EGR1..1..7628, 4_A375_EGR1..1..7629, 4_A375_EGR1..1..7630	4407, 3063, 2551, -9566	downstream, downstream, downstream, upstream	0	0	1	6	6.25	17.75	4	4_A375_EGR1..1	21	Gene MIR1234	MIRN1234, hsa-mir-1234, MIR1234	microRNA 1234	NR_031600		
GeneID:55630	SLC39A4	8	145,637,798	145,642,273	4,475	-	3	4_A375_EGR1..1..7630, 4_A375_EGR1..1..7631, 4_A375_EGR1..1..7632	7126, 1633, -7071	downstream, in gene, upstream	0	0	1	6.33	10	20	3	4_A375_EGR1..1	24	Gene SLC39A4	AEZ, ZIP4, FLJ20327, SLC39A4, MGC74741	solute carrier family 39 (zinc transporter), member 4	NM_130849, NM_017767, hCT2270647.0, hCT2270648.0, hCT2270651.1, hCT2270654.1, hCT2344514.0	219215_s_at	NP_570901.2, NP_060237.2, EAW82101.1, EAW82103.1, EAW82104.1, EAW82105.1, EAW82102.1
GeneID:51160	VPS28	8	145,649,000	145,653,927	4,927	-	6	1_A375_pNL7_minus_lncRNA_AR..1..5384, 2_A375_pNL97_plus_lncRNA_AR..1..7762, 4_A375_EGR1..1..7631, 4_A375_EGR1..1..7632, 4_A375_EGR1..1..7633, 4_A375_EGR1..1..7634	-57, -57, 13287, 4563, 295, -7161	upstream, upstream, downstream, in gene, in gene, upstream	1	1	1	13.75	15.5	21.75	4	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene VPS28	MGC60323, VPS28	vacuolar protein sorting 28 homolog (S. cerevisiae)	NM_016208, NM_183057, hCT15119.3, hCT1958372.1, hCT1958373.1, hCT1958374.1, hCT1958375.1, hCT1958376.1, hCT1958380.1	218679_s_at	NP_057292.1, NP_898880.1, EAW82094.1, EAW82098.1, EAW82099.1, EAW82100.1, EAW82095.1, EAW82096.1, EAW82097.1
GeneID:4796	NFKBIL2	8	145,654,163	145,669,812	15,649	-	8	1_A375_pNL7_minus_lncRNA_AR..1..5384, 2_A375_pNL97_plus_lncRNA_AR..1..7762, 4_A375_EGR1..1..7632, 4_A375_EGR1..1..7633, 4_A375_EGR1..1..7634, 4_A375_EGR1..1..7635, 4_A375_EGR1..1..7636, 4_A375_EGR1..1..7637	15626, 15626, 20466, 16160, 8724, 4116, 532, -6380	downstream, downstream, downstream, downstream, in gene, in gene, in gene, upstream	1	1	1	11.33	12.67	17.83	6	1_A375_pNL7_minus_lncRNA_AR..1	37	Gene NFKBIL2	IKBR, FLJ40087, TONSL, NFKBIL2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	NM_013432, hCT2270636.0, hCT1952002.2	1558329_at, 1558330_x_at, 207137_at	NP_038460.4, EAW82093.1, EAW82092.1
GeneID:50626	CYHR1	8	145,675,315	145,691,031	15,716	-	7	2_A375_pNL97_plus_lncRNA_AR..1..7763, 4_A375_EGR1..1..7635, 4_A375_EGR1..1..7636, 4_A375_EGR1..1..7637, 4_A375_EGR1..1..7638, 4_A375_EGR1..1..7639, 4_A375_EGR1..1..7640	279, 25335, 21751, 14639, 6279, 5303, -4165	in gene, downstream, downstream, in gene, in gene, in gene, upstream	0	1	1	7.29	9.57	14.71	7	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene CYHR1	CHRP, CYHR1, KIAA0496, MGC13010	cysteine/histidine-rich 1	NM_138496, NM_032687, NM_001129888, hCT2270633.0, hCT2270634.0, hCT2356243.0, hCT15136.3	213072_at, 213861_at, 223421_at, 229945_at	NP_612505.1, NP_116076.1, NP_001123360.1, EAW82088.1, EAW82089.1, EAW82091.1, EAW82090.1
GeneID:90990	KIFC2	8	145,691,738	145,699,499	7,761	+	4	2_A375_pNL97_plus_lncRNA_AR..1..7763, 4_A375_EGR1..1..7638, 4_A375_EGR1..1..7639, 4_A375_EGR1..1..7640	-986, -6986, -6010, 3476	upstream, upstream, upstream, in gene	0	1	1	8.5	10.75	14.75	4	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene KIFC2	KIFC2	kinesin family member C2	NM_145754, hCT2271914.0, hCT2356216.0, hCT15132.3	226791_at, 226792_s_at	NP_665697.1, EAW82086.1, EAW82085.1, EAW82087.1
GeneID:8928	FOXH1	8	145,699,115	145,701,718	2,603	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7763, 4_A375_EGR1..1..7640	10986, 6502	downstream, downstream	0	1	1	9	12	14	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene FOXH1	FAST-1, FOXH1, FAST1	forkhead box H1	NM_003923, hCT2270630.0, hCT15116.3	207844_at, 231407_s_at	NP_003914.1, EAW82084.1, EAW82083.1
GeneID:84988	PPP1R16A	8	145,722,109	145,727,504	5,395	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7764, 4_A375_EGR1..1..7641	13027, 16003	downstream, downstream	0	1	1	14	17	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene PPP1R16A	MYPT3, PPP1R16A, MGC14333	protein phosphatase 1, regulatory (inhibitor) subunit 16A	NM_032902, hCT2271921.0, hCT2271923.0, hCT15127.3	225203_at	NP_116291.1, EAW82080.1, EAW82081.1, EAW82082.1
GeneID:2875	GPT	8	145,729,465	145,732,555	3,090	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7764, 4_A375_EGR1..1..7641	5671, 8647	downstream, downstream	0	1	1	14	17	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene GPT	AAT1, ALT1, GPT1, GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	NM_005309, hCT1968009.0, hCT2271933.0, hCT15118.3	206709_x_at	NP_005300.1, EAW82079.1, EAW82077.1, EAW82078.1
GeneID:113655	MFSD3	8	145,734,552	145,736,589	2,037	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7764, 4_A375_EGR1..1..7641	584, 3560	in gene, downstream	0	1	1	14	17	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene MFSD3	MFSD3	major facilitator superfamily domain containing 3	NM_138431, hCT2271936.1, hCT2271941.1, hCT2271943.1, hCT2356226.0, hCT2356227.0	227296_at, 236947_at	NP_612440.1, EAW82075.1, EAW82072.1, EAW82073.1, EAW82074.1, EAW82076.1
GeneID:9401	RECQL4	8	145,736,667	145,743,210	6,543	-	4	2_A375_pNL97_plus_lncRNA_AR..1..7764, 4_A375_EGR1..1..7641, 4_A375_EGR1..1..7642, 4_A375_EGR1..1..7643	8074, 5098, -4822, -8636	downstream, in gene, upstream, upstream	0	1	1	12	15.75	18.25	4	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RECQL4	RECQ4, RECQL4	RecQ protein-like 4	NM_004260, hCT2356239.0, hCT15117.3	1553015_a_at, 213520_at	NP_004251.3, EAW82070.1, EAW82071.1
GeneID:9684	LRRC14	8	145,743,391	145,750,557	7,166	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5385, 2_A375_pNL97_plus_lncRNA_AR..1..7764, 4_A375_EGR1..1..7641, 4_A375_EGR1..1..7642, 4_A375_EGR1..1..7643	11105, -8255, -5279, 4641, 8657	downstream, upstream, upstream, in gene, downstream	1	1	1	13.6	15.4	16	5	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LRRC14	LRRC14A, LRRC14, KIAA0014	leucine rich repeat containing 14	NM_014665, hCT2271940.1, hCT2271942.0, hCT2271944.0, hCT2271945.1	203495_at, 32062_at	NP_055480.1, EAW82069.1, EAW82066.1, EAW82067.1, EAW82068.1
GeneID:441381	LRRC24	8	145,747,761	145,752,416	4,655	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5385, 4_A375_EGR1..1..7641, 4_A375_EGR1..1..7642, 4_A375_EGR1..1..7643	-2080, 14304, 4384, 366	upstream, downstream, in gene, in gene	1	0	1	12.5	13.5	16	4	4_A375_EGR1..1	22	Gene LRRC24	MGC111484, LRRC24, LRRC14OS	leucine rich repeat containing 24	NM_001024678, hCT1961240.1		NP_001019849.2, EAW82065.1
GeneID:414919	C8orf82	8	145,751,803	145,754,456	2,655	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5385, 4_A375_EGR1..1..7642, 4_A375_EGR1..1..7643	-36, 6426, 2410	upstream, downstream, in gene	1	0	1	13.33	14.33	15	3	4_A375_EGR1..1	22	Gene C8orf82	C8orf82, MGC70857	chromosome 8 open reading frame 82	NM_001001795, hCT1968010.1, hCT15134.3	226710_at	NP_001001795.1, EAW82064.1, EAW82063.1
GeneID:80728	KIAA1688	8	145,754,563	145,838,891	84,328	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5385, 4_A375_EGR1..1..7642, 4_A375_EGR1..1..7643	84395, 90859, 86843	downstream, downstream, downstream	1	0	1	13.33	14.33	15	3	4_A375_EGR1..1	22	Gene KIAA1688	ARHGAP39, KIAA1688, CrGAP, Vilse	Rho GTPase activating protein 39	NM_025251, hCT15124.3	227676_at	NP_079527.1, EAW82062.1
GeneID:90987	ZNF251	8	145,946,294	145,980,970	34,676	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5386, 2_A375_pNL97_plus_lncRNA_AR..1..7765, 4_A375_EGR1..1..7644	10, -54, 106	in gene, upstream, in gene	1	1	1	16	16	16	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene ZNF251	FLJ34319, ZNF251	zinc finger protein 251	NM_138367	226754_at	NP_612376.1
GeneID:80778	ZNF34	8	145,998,499	146,012,725	14,226	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5387, 2_A375_pNL97_plus_lncRNA_AR..1..7766, 2_A375_pNL97_plus_lncRNA_AR..1..7767, 4_A375_EGR1..1..7645	-5270, 65, -5099, 293	upstream, in gene, upstream, in gene	1	1	1	15	19.5	20	2	4_A375_EGR1..1	25	Gene ZNF34	MGC10520, KOX32, ZNF34	zinc finger protein 34	NM_030580, hCT2270609.0, hCT2349690.0, hCT1786226.2, hCT1958339.1	219801_at	NP_085057.3, EAW82055.1, EAW82056.1, EAW82057.1, EAW82058.1
GeneID:6132	RPL8	8	146,015,154	146,017,805	2,651	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5387, 2_A375_pNL97_plus_lncRNA_AR..1..7766, 2_A375_pNL97_plus_lncRNA_AR..1..7767, 4_A375_EGR1..1..7645	-190, 5165, -19, 5373	upstream, downstream, upstream, downstream	1	1	1	15	19.5	20	2	4_A375_EGR1..1	25	Gene RPL8	L8, RPL8	ribosomal protein L8	NM_033301, NM_000973, hCT2270601.0, hCT15114.4, hCT1952000.2, hCT1961861.1, hCT1961862.1, hCT1961863.1, hCT1961864.1, hCT1964069.1	200936_at	NP_150644.1, NP_000964.1, EAW82048.1, EAW82052.1, EAW82053.1, EAW82054.1, EAW82047.1, EAW82049.1, EAW82050.1, EAW82051.1
GeneID:340385	ZNF517	8	146,024,261	146,034,529	10,268	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5387, 2_A375_pNL97_plus_lncRNA_AR..1..7767	-6286, -6437	upstream, upstream	1	1	0	16	22	15	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ZNF517	ZNF517	zinc finger protein 517	NM_213605, hCT2271959.1, hCT2341287.0, hCT2341288.0, hCT2356244.0		NP_998770.2, EAW82044.1, EAW82043.1, EAW82045.1, EAW82046.1
GeneID:100130027	LOC100130027	8	146,032,252	146,052,425	20,173	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5388, 2_A375_pNL97_plus_lncRNA_AR..1..7768	-535, -503	upstream, upstream	1	1	0	16	27	10	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene LOC100130027		hypothetical LOC100130027	XR_110587, XR_114228		
GeneID:100129598	LOC100129598	8	146,045,697	146,046,149	452	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5388, 2_A375_pNL97_plus_lncRNA_AR..1..7768	-6611, -6779	upstream, upstream	1	1	0	16	27	10	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene LOC100129598		hypothetical LOC100129598	XR_113185, XR_110585, XR_114226		
GeneID:7553	ZNF7	8	146,052,903	146,068,606	15,703	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5388, 1_A375_pNL7_minus_lncRNA_AR..1..5389, 2_A375_pNL97_plus_lncRNA_AR..1..7768, 2_A375_pNL97_plus_lncRNA_AR..1..7769	57, 25625, 25, 25305	in gene, downstream, in gene, downstream	1	1	0	17	22.5	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene ZNF7	FLJ38706, HF.16, ZNF7, KOX4, zf30	zinc finger protein 7	NM_003416, hCT2271962.0, hCT2271963.0, hCT2271965.0, hCT2356225.0, hCT8157.3	1559980_at, 205089_at, 234914_at, 234920_at	NP_003407.1, EAW82038.1, EAW82039.1, EAW82040.1, EAW82041.1, EAW82042.1
GeneID:28991	COMMD5	8	146,075,551	146,078,932	3,381	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5389, 2_A375_pNL97_plus_lncRNA_AR..1..7769	404, 724	in gene, in gene	1	1	0	16	16	13	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene COMMD5	FLJ13008, HT002, COMMD5, HCARG, MGC72046	COMM domain containing 5	NM_014066, NM_001081004, NM_001081003, hCT2270593.0, hCT2270594.0, hCT2270595.0, hCT2270596.0, hCT15113.3	223198_x_at, 223819_x_at, 224387_at, 232640_at	NP_054785.2, NP_001074473.1, NP_001074472.1, EAW82033.1, EAW82034.1, EAW82035.1, EAW82036.1, EAW82037.1
GeneID:58500	ZNF250	8	146,102,336	146,126,846	24,510	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5390, 2_A375_pNL97_plus_lncRNA_AR..1..7770, 4_A375_EGR1..1..7646	-610, 62, 31436	upstream, in gene, downstream	1	1	1	14.5	19	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene ZNF250	MGC9718, MGC111123, ZNF250, ZFP647, FLJ57354, ZNF647	zinc finger protein 250	NM_021061, NM_001109689, hCT2356237.0, hCT2356238.0, hCT15125.3, hCT1952001.1	213858_at	NP_066405.1, NP_001103159.1, EAW82029.1, EAW82030.1, EAW82031.1, EAW82032.1
GeneID:286103	C8orf77	8	146,228,197	146,231,432	3,235	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7771	11	in gene	0	1	0	14	19	13	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene C8orf77	C8orf77, MGC141859	chromosome 8 open reading frame 77	NR_026974	1558790_s_at	
GeneID:65265	C8orf33	8	146,277,824	146,281,416	3,592	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7772	96	in gene	0	1	0	15	21	8	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene C8orf33	FLJ20989, C8orf33	chromosome 8 open reading frame 33	NM_023080, hCT2271971.0, hCT2271972.0	218187_s_at, 222551_s_at	NP_075568.1, EAW82022.1, EAW82023.1
GeneID:23189	KANK1	9	504,703	746,103	241,400	+	6	1_A375_pNL7_minus_lncRNA_AR..1..5391, 1_A375_pNL7_minus_lncRNA_AR..1..5392, 2_A375_pNL97_plus_lncRNA_AR..1..7773, 2_A375_pNL97_plus_lncRNA_AR..1..7774, 2_A375_pNL97_plus_lncRNA_AR..1..7775, 2_A375_pNL97_plus_lncRNA_AR..1..7776	246593, 251201, 190017, 206161, 234145, 251169	downstream, downstream, in gene, in gene, in gene, downstream	1	1	0	15.8	20.8	7.6	5	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene KANK1	KIAA0172, MGC43128, ANKRD15, DKFZp451G231, KANK, KANK1	KN motif and ankyrin repeat domains 1	NM_153186, NM_015158, hCT21570.3, hCT2353320.0	1565632_at, 213005_s_at, 216762_at, 216763_at, 237162_at, 236789_at	NP_694856.1, NP_055973.2, EAW58821.1, EAW58822.1
GeneID:1761	DMRT1	9	841,690	969,090	127,400	+	4	4_A375_EGR1..1..7647, 4_A375_EGR1..1..7648, 4_A375_EGR1..1..7649, 4_A375_EGR1..1..7650	934, 127676, 126390, 129126	in gene, downstream, downstream, downstream	0	0	1	5.75	7.5	18	4	4_A375_EGR1..1	23	Gene DMRT1	DMRT1, DMT1	doublesex and mab-3 related transcription factor 1	NM_021951, hCT1950946.1	220493_at	NP_068770.2, EAW58820.1
GeneID:58524	DMRT3	9	976,964	991,732	14,768	+	3	4_A375_EGR1..1..7648, 4_A375_EGR1..1..7649, 4_A375_EGR1..1..7650	-7398, -6684, -6148	upstream, upstream, upstream	0	0	1	6.67	8.33	18.67	3	4_A375_EGR1..1	23	Gene DMRT3	DMRTA3, MGC142144, DMRT3	doublesex and mab-3 related transcription factor 3	NM_021240, hCT21567.3	231800_s_at, 233930_at	NP_067063.1, EAW58619.1
GeneID:10655	DMRT2	9	1,050,346	1,057,554	7,208	+	1	4_A375_EGR1..1..7651	-4586	upstream	0	0	1	7	7	19	1	4_A375_EGR1..1	19	Gene DMRT2	DMRT2		NM_001130865, NM_006557, NM_181872, hCT21568.3, hCT2301602.0, hCT1950959.1	223704_s_at, 223986_x_at	NP_001124337.1, NP_006548.1, NP_870987.2, EAW58816.1, EAW58817.1, EAW58818.1
GeneID:6595	SMARCA2	9	2,015,342	2,193,624	178,282	+	3	2_A375_pNL97_plus_lncRNA_AR..1..7777, 2_A375_pNL97_plus_lncRNA_AR..1..7778, 4_A375_EGR1..1..7652	-368, 1842, 2098	upstream, in gene, in gene	0	1	1	15	18.5	16.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene SMARCA2	hSNF2a, SWI2, Sth1p, MGC74511, SNF2, SMARCA2, hBRM, SNF2LA, FLJ36757, SNF2L2, BAF190, BRM	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	NM_139045, NM_003070, hCT2301911.0, hCT2301913.0, hCT2301915.0, hCT2301918.0, hCT1950952.1	206542_s_at, 206543_at, 206544_x_at, 212257_s_at, 212258_s_at, 217707_x_at, 228928_s_at	NP_620614.2, NP_003061.3, EAW58812.1, EAW58813.1, EAW58814.1, EAW58815.1, EAW58811.1
GeneID:401491	FLJ35024	9	2,535,652	2,622,373	86,721	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5394, 2_A375_pNL97_plus_lncRNA_AR..1..7781	47989, 62585	in gene, in gene	1	1	0	13.5	12.5	8	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene FLJ35024		hypothetical LOC401491	NR_015375	1558212_at	
GeneID:7436	VLDLR	9	2,621,793	2,654,485	32,692	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7782	33775	downstream	0	1	0	13	21	5	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene VLDLR	FLJ35024, VLDLRCH, CHRMQ1, VLDLR, CARMQ1	very low density lipoprotein receptor	NM_001018056, NM_003383, hCT2301922.0, hCT2301924.0, hCT2353317.0, hCT19070.3, hCT1958431.1	209822_s_at	NP_001018066.1, NP_003374.3, EAW58805.1, EAW58806.1, EAW58807.1, EAW58808.1, EAW58804.1
GeneID:9933	KIAA0020	9	2,804,152	2,844,130	39,978	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5395, 2_A375_pNL97_plus_lncRNA_AR..1..7783, 4_A375_EGR1..1..7654	-30, -158, 98	upstream, upstream, in gene	1	1	1	17	22	19	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene KIAA0020	MGC8749, PEN, KIAA0020, HLA-HA8, PUF6, XTP5	KIAA0020	NM_014878, hCT2301726.0	1570529_at, 203712_at	NP_055693.4, EAW58602.1
GeneID:5991	RFX3	9	3,224,645	3,525,983	301,338	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5396, 2_A375_pNL97_plus_lncRNA_AR..1..7784, 4_A375_EGR1..1..7656	-769, -737, -449	upstream, upstream, upstream	1	1	1	21	32	21	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene RFX3	RFX3, MGC87155, bA32F11.1	regulatory factor X, 3 (influences HLA class II expression)	NM_002919, NM_134428, hCT2301653.0, hCT2301654.0, hCT2301655.0, hCT2301657.0, hCT19084.3, hCT1950953.1	207234_at, 236810_at	NP_002910.1, NP_602304.1, EAW58794.1, EAW58796.1, EAW58797.1, EAW58799.1, EAW58795.1, EAW58798.1
GeneID:169792	GLIS3	9	3,824,126	4,300,035	475,907	-	15	1_A375_pNL7_minus_lncRNA_AR..1..5397, 1_A375_pNL7_minus_lncRNA_AR..1..5398, 1_A375_pNL7_minus_lncRNA_AR..1..5399, 1_A375_pNL7_minus_lncRNA_AR..1..5400, 1_A375_pNL7_minus_lncRNA_AR..1..5401, 2_A375_pNL97_plus_lncRNA_AR..1..7785, 2_A375_pNL97_plus_lncRNA_AR..1..7786, 2_A375_pNL97_plus_lncRNA_AR..1..7787, 2_A375_pNL97_plus_lncRNA_AR..1..7788, 2_A375_pNL97_plus_lncRNA_AR..1..7789, 2_A375_pNL97_plus_lncRNA_AR..1..7790, 2_A375_pNL97_plus_lncRNA_AR..1..7791, 2_A375_pNL97_plus_lncRNA_AR..1..7792, 2_A375_pNL97_plus_lncRNA_AR..1..7793, 2_A375_pNL97_plus_lncRNA_AR..1..7794	392963, 367459, 38339, 6179, 1347, 436624, 393411, 330979, 215491, 61251, 9315, 6275, 2339, 1571, 131	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	1	1	0	15.75	17.83	6.92	12	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene GLIS3	FLJ90578, ZNF515, GLIS3, MGC33662, FLJ38999	GLIS family zinc finger 3	NM_152629, NM_001042413	229435_at, 230258_at	NP_689842.3, NP_001035878.1
GeneID:84650	C9orf70	9	3,898,646	3,901,248	2,602	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5397, 2_A375_pNL97_plus_lncRNA_AR..1..7786	8426, 7976	downstream, downstream	1	1	0	17	14	7	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene C9orf70	C9orf70, MGC16153	chromosome 9 open reading frame 70	NR_026663	1553756_at	
GeneID:100287493	LOC100287493	9	4,294,224	4,300,092	5,868	+	7	1_A375_pNL7_minus_lncRNA_AR..1..5400, 1_A375_pNL7_minus_lncRNA_AR..1..5401, 2_A375_pNL97_plus_lncRNA_AR..1..7790, 2_A375_pNL97_plus_lncRNA_AR..1..7791, 2_A375_pNL97_plus_lncRNA_AR..1..7792, 2_A375_pNL97_plus_lncRNA_AR..1..7793, 2_A375_pNL97_plus_lncRNA_AR..1..7794	-366, 4464, -3504, -464, 3472, 4240, 5680	upstream, in gene, upstream, upstream, in gene, in gene, in gene	1	1	0	15	20.8	10.8	5	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene LOC100287493		hypothetical protein LOC100287493	XM_002342902, XM_003120092, XM_003120630		XP_002342943.1, XP_003120140.1, XP_003120678.1
GeneID:6505	SLC1A1	9	4,490,427	4,587,469	97,042	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5403, 2_A375_pNL97_plus_lncRNA_AR..1..7796, 2_A375_pNL97_plus_lncRNA_AR..1..7797	37, 56, 40133	in gene, in gene, in gene	1	1	0	21	23.5	12	2	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene SLC1A1	SLC1A1, EAAC1, EAAT3	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	NM_004170, hCT19085.3	206396_at, 213664_at	NP_004161.4, EAW58788.1
GeneID:55064	C9orf68	9	4,598,316	4,666,674	68,358	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5404, 2_A375_pNL97_plus_lncRNA_AR..1..7798, 2_A375_pNL97_plus_lncRNA_AR..1..7799, 4_A375_EGR1..1..7657	4338, 4274, 146, 4338	in gene, in gene, in gene, in gene	1	1	1	15.5	21.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene C9orf68	bA6J24.2, FLJ10058, C9orf68	chromosome 9 open reading frame 68	NM_001039395	1554707_at, 1554708_s_at, 1555079_at, 220218_at, 237383_at	NP_001034484.3
GeneID:403313	PPAPDC2	9	4,662,298	4,665,258	2,960	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5404, 2_A375_pNL97_plus_lncRNA_AR..1..7798, 2_A375_pNL97_plus_lncRNA_AR..1..7799, 4_A375_EGR1..1..7657	38, 102, 4230, 38	in gene, in gene, downstream, in gene	1	1	1	15.5	21.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene PPAPDC2	FLJ90191, PSDP, FLJ46512, bA6J24.6, MGC15483, PPAPDC2, PDP1	phosphatidic acid phosphatase type 2 domain containing 2	NM_203453, hCT1653199.3	227385_at	NP_982276.3, EAW58785.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:55664	CDC37L1	9	4,679,568	4,706,594	27,026	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5405, 2_A375_pNL97_plus_lncRNA_AR..1..7800, 4_A375_EGR1..1..7856	-14, -46, 50	upstream, upstream, in gene	1	1	1	20	20	18	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene CDC37L1	FLJ20639, HARC, CDC37B, CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	NM_017913, hCT22466.3	219343_at, 226561_at	NP_060383.2, EAW58782.1
GeneID:50808	AK3	9	4,711,156	4,741,227	30,069	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5406, 2_A375_pNL97_plus_lncRNA_AR..1..7801	11, 123	in gene, in gene	1	1	0	17	26	13	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene AK3	FIX, AKL3L1, AK3, AK6, AKL3L, AK3L1	adenylate kinase 3	NM_016282, hCT2301643.0, hCT2301644.0, hCT2301645.0	224151_s_at, 224655_at	NP_057366.2, EAW58761.1, EAW58779.1, EAW58780.1
GeneID:10171	RCL1	9	4,792,834	4,861,064	68,230	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5407, 4_A375_EGR1..1..7859	-258, 11550	upstream, in gene	1	0	1	15.5	12.5	17.5	2	1_A375_pNL7_minus_lncRNA_AR..1	24	Gene RCL1	RCL1, RPCL1, RNAC	RNA terminal phosphate cyclase-like 1	NM_005772, hCT2301639.0, hCT1952023.1	218544_s_at, 222666_s_at	NP_005763.3, EAW58776.1, EAW58777.1
GeneID:3717	JAK2	9	4,985,245	5,128,183	142,938	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5408, 2_A375_pNL97_plus_lncRNA_AR..1..7802, 4_A375_EGR1..1..7860, 4_A375_EGR1..1..7861	-265, -125, -621, 126663	upstream, upstream, upstream, in gene	1	1	1	17	15	20.5	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene JAK2	JTK10, JAK2	Janus kinase 2	NM_004972, hCT22465.3	1562031_at, 205841_at, 205842_s_at	NP_004963.1, EAW58774.1
GeneID:55848	C9orf46	9	5,357,971	5,437,860	79,889	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5409, 2_A375_pNL97_plus_lncRNA_AR..1..7803	-3324, 164	upstream, in gene	1	1	0	21.5	22	6.5	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene C9orf46	C9orf46, FLJ14668, FLJ39176, MDS030, AD025	chromosome 9 open reading frame 46	NM_018465, hCT1971473.1, hCT1971474.1, hCT1780495.3	218992_at	NP_060935.1, EAW58766.1, EAW58764.1, EAW58765.1
GeneID:29126	CD274	9	5,450,503	5,470,567	20,064	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5409, 1_A375_pNL7_minus_lncRNA_AR..1..5410, 2_A375_pNL97_plus_lncRNA_AR..1..7804, 4_A375_EGR1..1..7862	-9319, 137, 69, 41	upstream, in gene, in gene, in gene	1	1	1	23	23.5	11.5	2	1_A375_pNL7_minus_lncRNA_AR..1	28	Gene CD274	PDCD1LG1, PDL1, B7H1, CD274, PD-L1, MGC142296, B7-H, PDCD1L1, MGC142294	CD274 molecule	NM_014143, hCT19081.2	223834_at	NP_054862.1, EAW58763.1
GeneID:57589	KIAA1432	9	5,629,327	5,776,557	147,230	+	1	4_A375_EGR1..1..7863	-527	upstream	0	0	1	17	15	17	1	4_A375_EGR1..1	17	Gene KIAA1432	CIP150, KIAA1432, bA207C16.1, FLJ12580	KIAA1432	NM_020829, NM_001135920, hCT2301867.0, hCT2301866.0, hCT1960137.1	223825_at, 223826_s_at, 226221_at, 226222_at	NP_065880.1, NP_001129392.1, EAW58759.1, EAW58760.1, EAW58761.1
GeneID:79956	ERMP1	9	5,784,572	5,833,081	48,509	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5411	69	in gene	1	0	0	23	16	6	1	1_A375_pNL7_minus_lncRNA_AR..1	23	Gene ERMP1	ERMP1, KIAA1815, FXNA, bA207C16.3	endoplasmic reticulum metallopeptidase 1	NM_024896, hCT2301760.0, hCT2301761.0	218342_s_at, 222603_at	NP_079172.2, EAW58757.1, EAW58758.1
GeneID:158358	KIAA2026	9	5,919,008	6,008,003	88,995	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7805	-7581	upstream	0	1	0	17	26	10	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene KIAA2026	KIAA2026		NM_001017969, hCT1960122.2	228446_at, 236490_at	NP_001017969.2, EAW58754.1
GeneID:26953	RANBP6	9	6,011,019	6,015,640	4,621	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7805	56	in gene	0	1	0	17	26	10	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene RANBP6	RANBP6, FLJ54311	RAN binding protein 6	NM_012416, NR_024094, NR_024095, hCT2301775.0	213019_at	NP_036548.1, EAW58753.1
GeneID:115426	UHRF2	9	6,413,151	6,507,051	93,900	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5413	1	in gene	1	0	0	17	18	13	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene UHRF2	DKFZp686G0837, URF2, NIRF, UHRF2, MGC33463, DKFZp434B0920, RNF107	ubiquitin-like with PHD and ring finger domains 2	NM_152896	225610_at	NP_690856.1
GeneID:2731	GLDC	9	6,532,464	6,645,692	113,228	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5414, 1_A375_pNL7_minus_lncRNA_AR..1..5415, 1_A375_pNL7_minus_lncRNA_AR..1..5416, 2_A375_pNL97_plus_lncRNA_AR..1..7807	107020, 78428, -132, 107148	in gene, in gene, upstream, in gene	1	1	0	22.33	15.67	7.33	3	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene GLDC	HYGN1, MGC138200, GCE, GLDC, GCSP, MGC138198	glycine dehydrogenase (decarboxylating)	NM_000170, hCT2301579.0, hCT2301580.0	204836_at	NP_000161.2, EAW58739.1, EAW58740.1
GeneID:23081	KDM4C	9	6,720,863	7,175,648	454,785	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5416, 2_A375_pNL97_plus_lncRNA_AR..1..7809, 4_A375_EGR1..1..7866	36913, 37009, -4607	in gene, in gene, upstream	1	1	1	22	19	18	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene KDM4C	JMJD2C, bA146B14.1, KIAA0780, JHDM3C, KDM4C, GASC1, FLJ25949	lysine (K)-specific demethylase 4C	NM_015061, NM_001146694, NM_001146695, NM_001146696, hCT2301763.0, hCT2301765.0, hCT2353354.0, hCT2353355.0, hCT1952022.1	1556493_a_at, 209984_at, 214861_at, 244365_at	NP_055876.2, NP_001140166.1, NP_001140167.1, NP_001140168.1, EAW58730.1, EAW58734.1, EAW58731.1, EAW58732.1, EAW58733.1
GeneID:90871	C9orf123	9	7,796,490	7,799,799	3,309	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7812	55	in gene	0	1	0	12	21	10	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene C9orf123	C9orf123, MGC4730	chromosome 9 open reading frame 123	NM_033428, hCT1829961.2	224660_at, 224879_at	NP_219500.1, EAW58728.1
GeneID:5789	PTPRD	9	8,314,246	10,612,723	2,298,477	-	1	4_A375_EGR1..1..7868	1989011	in gene	0	0	1	6	6	17	1	4_A375_EGR1..1	17	Gene PTPRD	MGC119752, MGC119753, MGC119751, HPTP, RPTPDELTA, PTPRD, MGC119750, HPTPDELTA, PTPD, HPTPD	protein tyrosine phosphatase, receptor type, D	NM_002839, NM_001040712, NM_130392, NM_130393, NM_001171025, NM_130391, hCT2301586.0, hCT2301587.0, hCT2301588.0, hCT2301589.0, hCT2301590.0, hCT2301592.0, hCT18420.3	205712_at, 213362_at, 214043_at, 242493_at	NP_002830.1, NP_001035802.1, NP_569076.2, NP_569077.2, NP_001164496.1, NP_569075.2, EAW58718.1, EAW58719.1, EAW58720.1, EAW58721.1, EAW58722.1, EAW58723.1, EAW58724.1
GeneID:7306	TYRP1	9	12,693,386	12,710,266	16,880	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7814	15334	in gene	0	1	0	15	17	1	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TYRP1	GP75, TRP, b-PROTEIN, TYRP1, CATB, TYRP, CAS2	tyrosinase-related protein 1	NM_000550, hCT1971504.1, hCT1971505.1, hCT2301521.0, hCT18394.4	205694_at	NP_000541.1, EAW58709.1, EAW58710.1, EAW58711.1, EAW58712.1
GeneID:100506267	LOC100506267	9	12,699,999	12,814,372	114,373	-	6	1_A375_pNL7_minus_lncRNA_AR..1..5421, 1_A375_pNL7_minus_lncRNA_AR..1..5422, 2_A375_pNL97_plus_lncRNA_AR..1..7814, 2_A375_pNL97_plus_lncRNA_AR..1..7815, 2_A375_pNL97_plus_lncRNA_AR..1..7816, 2_A375_pNL97_plus_lncRNA_AR..1..7817	36100, -3484, 105652, 36146, 29764, -3368	in gene, upstream, in gene, in gene, in gene, upstream	1	1	0	20.25	24.25	6	4	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene LOC100506267		hypothetical LOC100506267	XR_113203, XR_113204, XR_108929, XR_108930, XR_114245, XR_114246		
GeneID:286343	C9orf150	9	12,775,012	12,823,059	48,047	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5421, 1_A375_pNL7_minus_lncRNA_AR..1..5422, 2_A375_pNL97_plus_lncRNA_AR..1..7815, 2_A375_pNL97_plus_lncRNA_AR..1..7816, 2_A375_pNL97_plus_lncRNA_AR..1..7817	1260, 42844, 1212, 9596, 42748	in gene, in gene, in gene, in gene, in gene	1	1	0	22	26.67	10.33	3	1_A375_pNL7_minus_lncRNA_AR..1	31	Gene C9orf150	bA3L8.2, C9orf150, FLJ38505, FLJ90271, MGC46502, HYST0841	chromosome 9 open reading frame 150	NM_203403	227443_at	NP_981948.1
GeneID:4781	NFIB	9	14,081,842	14,398,982	317,140	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5426, 2_A375_pNL97_plus_lncRNA_AR..1..7820, 2_A375_pNL97_plus_lncRNA_AR..1..7821, 2_A375_pNL97_plus_lncRNA_AR..1..7822	76262, 160710, 120614, 76262	in gene, in gene, in gene, in gene	1	1	0	22.67	31.67	6.67	3	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene NFIB	NFI-RED, HMGIC/NFIB, NFIB2, NFIB3, NFIB	nuclear factor I/B	NM_001190737, NM_001190738, NM_005596, hCT2303120.0, hCT2303121.0, hCT2303122.0, hCT2303123.0, hCT2353321.0, hCT1780239.2	209289_at, 209290_s_at, 211466_at, 211467_s_at, 213029_at, 213032_at, 213033_s_at, 230291_s_at, 233304_at, 233394_at	NP_001177666.1, NP_001177667.1, NP_005587.2, EAW58695.1, EAW58697.1, EAW58698.1, EAW58694.1, EAW58696.1, EAW58699.1
GeneID:340481	ZDHHC21	9	14,611,069	14,693,480	82,411	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5427, 2_A375_pNL97_plus_lncRNA_AR..1..7823	136, 104	in gene, in gene	1	1	0	17	31	10	1	2_A375_pNL97_plus_lncRNA_AR..1	31	Gene ZDHHC21	DHHC-21, DNZ1, ZDHHC21		NM_178566, hCT2349619.0, hCT1642983.4	229240_at, 229923_at, 233215_s_at, 233216_at, 233247_x_at, 235066_at, 241946_at, 243550_at, 243835_at	NP_848661.1, EAW58693.1, EAW58692.1
GeneID:158219	TTC39B	9	15,170,842	15,307,358	136,516	-	1	4_A375_EGR1..1..7873	814	in gene	0	0	1	11	16	13	1	4_A375_EGR1..1	13	Gene TTC39B	TTC39B, FLJ33868, C9orf52	tetratricopeptide repeat domain 39B	NM_001168339, NM_152574, NM_001168340, NM_001168341, NM_001168342, hCT2353328.0, hCT1779338.2, hCT1959676.1	232000_at, 236626_at, 242477_at	NP_001161811.1, NP_689787.2, NP_001161812.1, NP_001161813.1, NP_001161814.1, EAW58665.1, EAW58663.1, EAW58664.1
GeneID:6619	SNAPC3	9	15,422,782	15,461,627	38,845	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5428, 2_A375_pNL97_plus_lncRNA_AR..1..7824, 4_A375_EGR1..1..7874	-94, -62, -46	upstream, upstream, upstream	1	1	1	28	30	17	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene SNAPC3	MGC132011, SNAPC3, MGC33124, SNAP50, PTFbeta	small nuclear RNA activating complex, polypeptide 3, 50kDa	NM_001039697, hCT2301501.0, hCT18687.3, hCT1951491.0	204001_at, 210465_s_at, 222266_at, 229712_at	NP_001034786.1, EAW58661.1, EAW58660.1, EAW58662.1
GeneID:11168	PSIP1	9	15,464,064	15,511,003	46,939	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5429, 2_A375_pNL97_plus_lncRNA_AR..1..7825, 4_A375_EGR1..1..7875	-101, -53, -357	upstream, upstream, upstream	1	1	1	25	30	15	1	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene PSIP1	LEDGF, PAIP, PSIP2, p52, MGC74712, PSIP1, p75, DFS70	PC4 and SFRS1 interacting protein 1	NM_033222, NM_021144, NM_001128217, hCT2301466.1, hCT2301467.1, hCT2301469.2, hCT2353367.0, hCT18392.4	1554933_at, 205961_s_at, 209337_at, 210758_at	NP_150091.2, NP_066967.3, NP_001121689.1, EAW58675.1, EAW58676.1, EAW58678.1, EAW58677.1, EAW58679.1
GeneID:203238	C9orf93	9	15,553,097	15,971,897	418,800	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5430, 2_A375_pNL97_plus_lncRNA_AR..1..7826, 2_A375_pNL97_plus_lncRNA_AR..1..7827	39, -329, 144759	in gene, upstream, in gene	1	1	0	19	19.5	8.5	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene C9orf93	MGC50805, bA536D16.1, C9orf93, DKFZp686P12113, bA776P13.1, FLJ46740, FLJ39267	chromosome 9 open reading frame 93	NM_173550	1553433_at, 1556516_at, 1558082_at, 1558160_at, 1559872_a_at, 236945_at, 239712_at, 242821_at	NP_775821.2
GeneID:54796	BNC2	9	16,409,501	16,870,786	461,285	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5433, 1_A375_pNL7_minus_lncRNA_AR..1..5434, 2_A375_pNL97_plus_lncRNA_AR..1..7831, 4_A375_EGR1..1..7876	243986, -14, 143842, 165442	in gene, upstream, in gene, in gene	1	1	1	18.25	17.25	10.5	4	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene BNC2	FLJ34928, BNC2, FLJ20043, BSN2, DKFZp686A01127	basonuclin 2	NM_017637	220272_at, 229942_at, 230722_at, 235723_at, 236476_at, 243445_at	NP_060107.3
GeneID:54875	CNTLN	9	17,135,036	17,503,917	368,879	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5437, 2_A375_pNL97_plus_lncRNA_AR..1..7833, 4_A375_EGR1..1..7877, 4_A375_EGR1..1..7878	-510, 2, -222, 216946	upstream, in gene, upstream, in gene	1	1	1	12	14	25.5	2	4_A375_EGR1..1	32	Gene CNTLN	C9orf101, bA340N12.1, RP11-340N12.1, FLJ25636, CNTLN, FLJ20276, C9orf39	centlein, centrosomal protein	NM_017738, NM_001114395, hCT1815595.1	1559005_s_at, 220095_at, 241696_at	NP_060208.2, NP_001107867.1, EAW58664.1
GeneID:6456	SH3GL2	9	17,578,953	17,797,122	218,169	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5436, 2_A375_pNL97_plus_lncRNA_AR..1..7834	165975, 166007	in gene, in gene	1	1	0	19	26	6	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene SH3GL2	EEN-B1, CNSA2, SH3P4, FLJ25015, SH3D2A, SH3GL2, FLJ20276	SH3-domain GRB2-like 2	NM_003026, hCT2301336.0, hCT2301342.0, hCT19519.3	205751_at	NP_003017.1, EAW58662.1, EAW58661.1, EAW58663.1
GeneID:92949	ADAMTSL1	9	18,474,104	18,910,948	436,844	+	1	4_A375_EGR1..1..7880	302856	in gene	0	0	1	7	9	21	1	4_A375_EGR1..1	21	Gene ADAMTSL1	FLJ41032, ADAMTSL-1, MGC118805, ADAMTSR1, DKFZp686L03130, MGC118803, C9orf94, PUNCTIN, MGC40193, ADAMTSL1, FLJ35283, FLJ46891	ADAMTS-like 1	NM_052866, NM_001040272	1552457_a_at, 1552808_at, 224371_at, 237217_at	NP_443098.3, NP_001035362.3
GeneID:158297	FAM154A	9	18,927,891	19,033,256	105,365	-	1	4_A375_EGR1..1..7881	232	in gene	0	0	1	6	13	19	1	4_A375_EGR1..1	19	Gene FAM154A	C9orf138, FAM154A, FLJ35283, MGC35182	family with sequence similarity 154, member A	NM_153707, hCT19421.3	231570_at	NP_714918.2, EAW58654.1
GeneID:10670	RRAGA	9	19,049,372	19,051,023	1,651	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5442, 2_A375_pNL97_plus_lncRNA_AR..1..7836, 4_A375_EGR1..1..7882	-92, -28, -28	upstream, upstream, upstream	1	1	1	21	23	17	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RRAGA	RAGA, FIP1, FIP-1, RRAGA	Ras-related GTP binding A	NM_006570, hCT18490.3	201628_s_at	NP_006561.1, EAW58653.1
GeneID:54801	HAUS6	9	19,053,141	19,102,902	49,761	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5442, 2_A375_pNL97_plus_lncRNA_AR..1..7836, 2_A375_pNL97_plus_lncRNA_AR..1..7837, 4_A375_EGR1..1..7882	53822, 53558, -42, 53558	downstream, downstream, upstream, downstream	1	1	1	20.5	26.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	30	Gene HAUS6	MGC138799, Dgt6, MGC102696, MGC138798, HAUS6, RP11-296P7.3, FAM29A	HAUS augmin-like complex, subunit 6	NM_017645, hCT1818219.2	218602_s_at, 222665_at, 233655_s_at	NP_060115.3, EAW58652.1
GeneID:123	PLIN2	9	19,115,759	19,127,573	11,814	-	3	2_A375_pNL97_plus_lncRNA_AR..1..7838, 4_A375_EGR1..1..7883, 4_A375_EGR1..1..7884	117, 245, -1419	in gene, in gene, upstream	0	1	1	15.5	16.5	18	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene PLIN2	MGC10598, ADRP, ADFP, PLIN2	perilipin 2	NM_001122, hCT1971506.1, hCT2302021.0, hCT19419.3, hCT1951493.1	209122_at, 215895_x_at	NP_001113.2, EAW58651.1, EAW58648.1, EAW58649.1, EAW58650.1
GeneID:55667	DENND4C	9	19,290,749	19,374,139	83,390	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5445, 2_A375_pNL97_plus_lncRNA_AR..1..7840, 4_A375_EGR1..1..7886	89443, 89539, 89475	downstream, downstream, downstream	1	1	1	36	35	33	1	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene DENND4C	bA513M16.3, FLJ20686, C9orf55, DENND4C, DKFZp686I09113, C9orf55B	DENN/MADD domain containing 4C	NM_017925, hCT2302202.2, hCT2302203.2, hCT2302204.2, hCT19417.5	205684_s_at, 226687_at, 234968_at	NP_060395.4, EAW58644.1, EAW58645.1, EAW58646.1, EAW58647.1
GeneID:6194	RPS6	9	19,376,254	19,380,235	3,981	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5445, 2_A375_pNL97_plus_lncRNA_AR..1..7840, 4_A375_EGR1..1..7886	43, -53, 11	in gene, upstream, in gene	1	1	1	36	35	33	1	1_A375_pNL7_minus_lncRNA_AR..1	36	Gene RPS6	RPS6, S6		NM_001010, hCT1971469.1, hCT1971470.1, hCT1971471.1, hCT1971472.1, hCT2302009.0, hCT2302010.0, hCT2302012.0, hCT2302019.0, hCT1779654.3	200081_s_at, 201254_x_at, 209134_s_at	NP_001001.2, EAW58643.1, EAW58636.1, EAW58637.1, EAW58639.1, EAW58640.1, EAW58635.1, EAW58638.1, EAW58641.1, EAW58642.1
GeneID:340485	ACER2	9	19,408,925	19,452,500	43,575	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7841, 4_A375_EGR1..1..7887	131, -109	in gene, upstream	0	1	1	12	24	17	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene ACER2	ACER2, ASAH3L, FLJ41587, ALKCDase2	alkaline ceramidase 2	NM_001010887, hCT2302207.0		NP_001010887.2, EAW58634.1
GeneID:25769	SLC24A2	9	19,507,450	19,788,591	281,141	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5446, 2_A375_pNL97_plus_lncRNA_AR..1..7842, 2_A375_pNL97_plus_lncRNA_AR..1..7843	40111, 66111, 39855	in gene, in gene, in gene	1	1	0	16	20	3	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene SLC24A2	SLC24A2, FLJ45149, NCKX2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	NM_020344, NM_001193288, hCT1641931.3	220667_s_at	NP_065077.1, NP_001180217.1, EAW58633.1
GeneID:4300	MLLT3	9	20,344,968	20,622,514	277,546	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5449, 1_A375_pNL7_minus_lncRNA_AR..1..5450, 2_A375_pNL97_plus_lncRNA_AR..1..7844	63602, -291, -288	in gene, upstream, upstream	1	1	0	19	17.5	7.5	2	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene MLLT3	AF9, MLLT3, YEATS3, FLJ2035	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	NM_004529, hCT2301290.0, hCT2301293.0, hCT1951490.1	1569652_at, 204917_s_at, 204918_s_at	NP_004520.2, EAW58632.1, EAW58630.1, EAW58631.1
GeneID:54914	KIAA1797	9	20,658,309	20,995,954	337,645	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5451, 2_A375_pNL97_plus_lncRNA_AR..1..7845	26171, 26331	in gene, in gene	1	1	0	16	22	17	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene KIAA1797	KIAA1797, FLJ20375	KIAA1797	NM_017794, hCT1971361.1, hCT2340911.0, hCT2351284.0	218503_at	NP_060264.3, EAW58627.1, EAW58628.1, EAW58629.1
GeneID:55958	KLHL9	9	21,331,018	21,335,429	4,411	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7846	293	in gene	0	1	0	21	26	14	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene KLHL9	KLHL9, FLJ21815	kelch-like 9 (Drosophila)	NM_018847, hCT1647803.4	213117_at, 213233_s_at, 233197_at, 237123_x_at	NP_061335.1, EAW58614.1



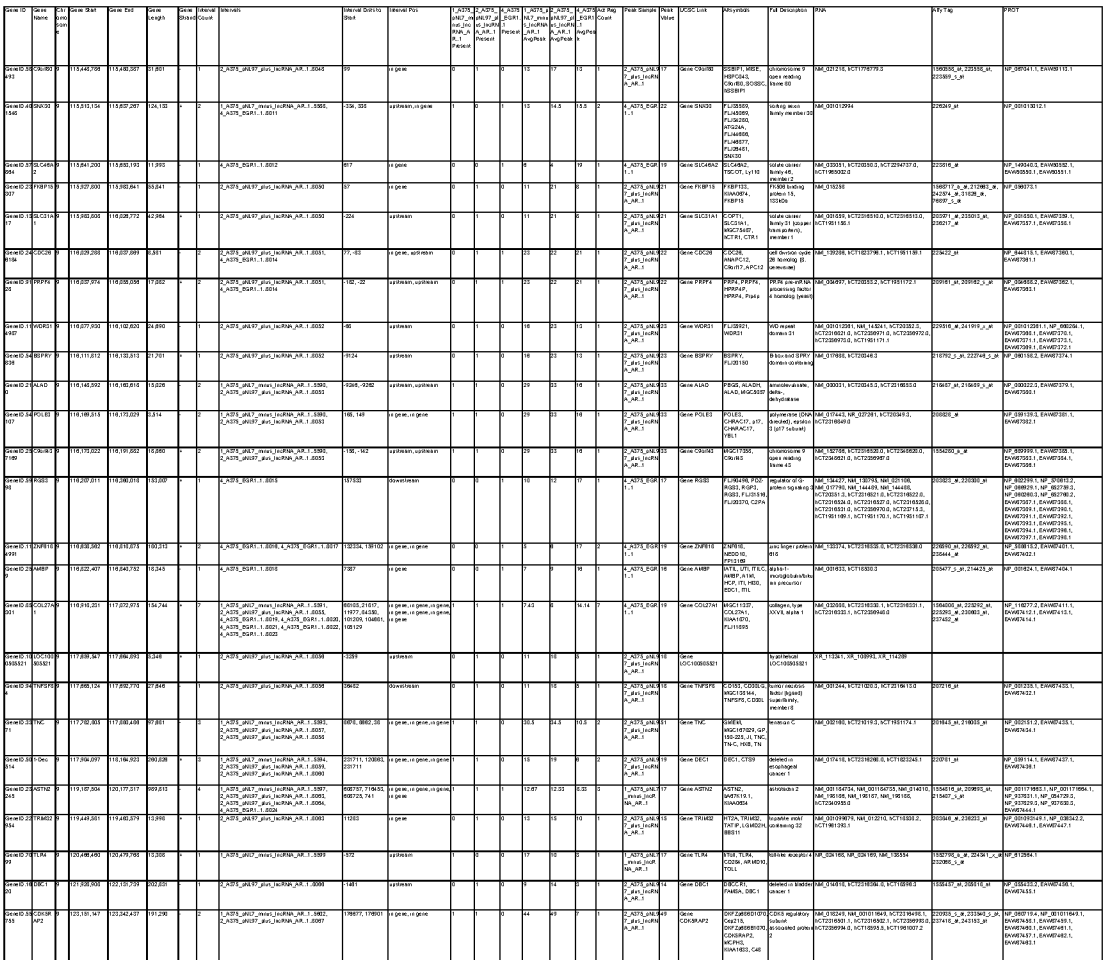
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_2_ATF3_lncRNA_IR_1 Percent	2_A375_2_ATF3_gRNA_IR_1 Percent	3_A375_2_ATF3_lncRNA_IR_1 Percent	1_A375_2_ATF3_NLF_mrna_IR_1 Avg Reads	2_A375_2_ATF3_lncRNA_IR_1 Avg Reads	3_A375_2_ATF3_lncRNA_IR_1 Avg Reads	4_A375_2_ATF3_gRNA_IR_1 Avg Reads	Add Reg Count	Peak Sample	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:3564202	LOC534202	9	21,454,287	21,559,997	105,430	-	6	1_A375_gRA7_mrna1_lncRNA_IR_1--5432, 2_A375_gRA37_plus_lncRNA_IR_1--7647, 3_A375_gRA37_plus_lncRNA_IR_1--7648, 4_A375_gRA37_plus_lncRNA_IR_1--7649, 5_A375_gRA37_plus_lncRNA_IR_1--7650, 6_A375_DGR1_1--7928	54097, 104257, 54893, 9988, 49, 209	1	1	1	14.75	19.75	7.5	4	2_A375_gRA37_plus_lncRNA_IR_1	Gene LOC534202		lysinefree tail LOC534202	NR_029054	1534097_s_at	
GeneID:4851035	MIR51	9	21,512,114	21,512,184	70	-	2	1_A375_gRA37_minus_lncRNA_IR_1--5432, 2_A375_gRA37_plus_lncRNA_IR_1--7648	6984, 6852	downstream, downstream	1	1	0	25	27	4	1	2_A375_gRA37_plus_lncRNA_IR_1	Gene MIR51	MIR51, link-in-DI, MIRNA1, miR-51	microRNA 51	NR_029555		
GeneID:4807	MYAF	9	21,602,833	21,665,970	63,233	+	3	1_A375_gRA7_minus_lncRNA_IR_1--5436, 1_A375_gRA37_plus_lncRNA_IR_1--5437, 2_A375_gRA37_plus_lncRNA_IR_1--7652	63, 14, 169, 101	w gene, w gene, w gene	1	1	0	25	26	7.5	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene MYAF	myeloid-associated differentiation marker	myeloid-associated differentiation marker	NM_002431, NC_000941.9, NC_018930.1	204898_at, 211983_s_at, 211984_at, 216863_s_at, 217154_at, 231164_at	NP_002442.2, EAW49899.1, EAW49900.1
GeneID:3551	DMRTA1	9	22,446,843	22,452,472	5,632	+	1	4_A375_DGR1_1--7952	136	w gene	0	0	1	15	19	38	1	4_A375_DGR1_1	Gene DMRTA1	DMRTA1, DMD, MGC163307	DMRT-like family A1	NM_021160, NC_000009.12	244729_at	NP_377443.2, EAW53391.1
GeneID:1955	ELAVL2	9	23,890,102	23,926,963	133,981	-	4	1_A375_gRA7_minus_lncRNA_IR_1--5481, 1_A375_gRA37_minus_lncRNA_IR_1--5482, 2_A375_gRA37_plus_lncRNA_IR_1--7654, 3_A375_gRA37_plus_lncRNA_IR_1--7655	-337, -3713, -338, -2729	upstream, upstream, upstream, upstream	1	1	0	39.5	61.5	7.5	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene ELAVL2	HEL-N1, HEL-N2, ELAVL2, HuB	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	NM_004432, NM_001171193, NM_001171197, NC_000009.12, NC_018930.1, NC_018913.3, NC_018930.1	206427_s_at, 232090_at	NP_004423.2, NP_001158069.1, NP_001158070.1, EAW65566.1, EAW65567.1, EAW65568.1, EAW65569.1, EAW65570.1, EAW65571.1, EAW65572.1, EAW65573.1
GeneID:2870	TUSC1	9	23,976,397	23,976,696	2,499	-	3	1_A375_gRA37_plus_lncRNA_IR_1--5483, 2_A375_gRA37_plus_lncRNA_IR_1--7656, 3_A375_DGR1_1--7956	1328, 1117, 1144	w gene, w gene, w gene	1	1	1	16	22	31	1	4_A375_DGR1_1	Gene TUSC1	TUSC1, TSG49, MGC131781, TSG1	tumor suppressor candidate 1	NM_031304.25, NC_000009.12	227388_at	NP_001304725.1, EAW65565.1
GeneID:7945	C9orf82	9	26,640,803	26,692,826	52,143	-	3	1_A375_gRA7_minus_lncRNA_IR_1--5483, 1_A375_gRA37_minus_lncRNA_IR_1--7656, 2_A375_DGR1_1--7957	442, 58, 202	w gene, w gene, w gene	1	1	1	25	38	50	1	2_A375_gRA37_minus_lncRNA_IR_1	Gene C9orf82	FLJ13937, RP11-357H23.1, C9orf82	chromosome 9 open reading frame 82	NM_024826, NM_001167573, NC_000009.12, NC_018930.1, NC_018913.3, NC_018930.1	219216_x_at, 233995_at	NP_079184.3, NP_001159047.1, EAW65576.1, EAW65577.1, EAW65578.1, EAW65579.1
GeneID:33	PLAA	9	28,903,386	28,947,486	44,100	-	5	1_A375_gRA7_minus_lncRNA_IR_1--5486, 1_A375_gRA37_minus_lncRNA_IR_1--5487, 2_A375_gRA37_plus_lncRNA_IR_1--7661, 3_A375_gRA37_plus_lncRNA_IR_1--7662, 4_A375_DGR1_1--7966	396, -6156, 204, 6364, 208	w gene, upstream, w gene, upstream, w gene	1	1	1	22	26.5	18.5	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene PLAA	phospholipase A2, activating protein	phospholipase A2, activating protein	NM_001031809, NC_000009.12, NC_018930.1, NC_018913.3, NC_018930.1	209032_at, 209033_s_at	NP_001029691.1, EAW65573.1
GeneID:83	PTTA	9	28,947,607	27,982,951	113,094	+	5	1_A375_gRA7_minus_lncRNA_IR_1--5486, 1_A375_gRA37_minus_lncRNA_IR_1--5487, 2_A375_gRA37_plus_lncRNA_IR_1--7661, 3_A375_gRA37_plus_lncRNA_IR_1--7662, 4_A375_DGR1_1--7966	67, 5127, 227, 6995, 195	w gene, w gene, w gene, w gene, w gene	1	1	0	22	26.5	18.5	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene PTTA	CWG1, PTTA, CWG-1, MGC111982, CCDC2, FLJ22621	cell-adhesion/cell-matrix protein 74 homolog (Chlamydomonas)	NM_001099223, NM_001099224, NM_001099222, NM_025103, NC_018942329.0	219174_at, 617722_c_at	NP_001092693.1, NP_001092692.1, NP_079379.2, EAW65572.1
GeneID:7978	TEK	9	27,169,147	27,230,172	151,025	+	3	1_A375_gRA7_minus_lncRNA_IR_1--5489, 1_A375_gRA37_minus_lncRNA_IR_1--5490, 2_A375_gRA37_plus_lncRNA_IR_1--7664, 3_A375_gRA37_plus_lncRNA_IR_1--7665	19093, 115341, 19183, 43629, 60669	w gene, w gene, w gene, w gene, w gene	1	1	0	19	22	6	4	2_A375_gRA37_plus_lncRNA_IR_1	Gene TEK	TEK tyrosine kinase, endothelial (venous...), TIE-2, VMCA1	TEK tyrosine kinase, endothelial (venous...), TIE-2, VMCA1	NM_000459, NC_018930.1, NC_018913.3	208702_at, 217711_at	NP_000450.2, EAW65571.1, EAW65572.1
GeneID:2236	C9orf72	9	27,546,544	27,573,842	27,298	-	4	1_A375_gRA7_minus_lncRNA_IR_1--5470, 1_A375_gRA37_minus_lncRNA_IR_1--7667, 2_A375_gRA37_plus_lncRNA_IR_1--7668, 3_A375_gRA37_plus_lncRNA_IR_1--7669	-76, 682, 50, 994	upstream, gene, w gene, w gene	1	1	1	15	17.5	11.5	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene C9orf72	FTP1-37.6.2, C9orf72, MGC23980	chromosome 9 open reading frame 72	NM_018325, NM_145005, NC_018930.1, NC_018913.3, NC_018930.1	1553132_at, 1553134_s_at, 223915_s_at	NP_060195.1, NP_653442.2, EAW65581.1, EAW65582.1, EAW65583.1, EAW65584.1
GeneID:9030	UNQ302	9	27,948,326	28,719,303	770,775	-	1	4_A375_DGR1_1--7961	3014.66	w gene	0	0	1	1	3	10	1	4_A375_DGR1_1	Gene UNQ302	FLJ35010, UNQ221, LEPRE, LRP4MC	required rich meprin, bmp1/tolloid-like, cubilin-like 2	NM_152570, NC_018946.2	232700_at	NP_689703.1, EAW65587.1
GeneID:4683	ACO1	9	32,364,801	32,430,834	66,033	+	1	1_A375_gRA7_minus_lncRNA_IR_1--5473	119	w gene	1	0	0	19	17	10	1	1_A375_gRA7_minus_lncRNA_IR_1	Gene ACO1	IRF1, ACONS, ACO1, IREBP, IREBP1, IRE1	aconitase 1, soluble	NM_002197, NC_018922.2, NC_018933.0, NC_018930.1, NC_018913.3	207071_s_at	NP_002186.1, EAW65580.1, EAW65581.1, EAW65582.1
GeneID:1019	TOPORS	9	32,540,542	32,592,822	52,280	-	3	1_A375_gRA37_minus_lncRNA_IR_1--5474, 2_A375_gRA37_plus_lncRNA_IR_1--7670, 3_A375_DGR1_1--7974	238, 208, 1914	w gene, w gene, w gene	1	1	1	13	13.5	13.5	2	1_A375_gRA37_plus_lncRNA_IR_1	Gene TOPORS	P53BP2, TRIP3B1, LUN, RP51, TOPORS	topoisomerase I binding, arginine/serine-rich	NM_005802, NC_018944.2	1564403_at, 206371_s_at, 221879_at, 76383_at	NP_005152.2, EAW65548.1
GeneID:1012929360	LOC100129360	9	32,551,142	32,553,013	1,872	+	3	1_A375_gRA37_minus_lncRNA_IR_1--5474, 2_A375_gRA37_plus_lncRNA_IR_1--7670, 3_A375_DGR1_1--7974	1362, 1274, -154	w gene, w gene, upstream	1	1	1	13	13.5	13.5	2	1_A375_gRA37_plus_lncRNA_IR_1	Gene LOC100129360		lysinefree tail LOC100129360	NR_033991, NR_033992		
GeneID:4712	NDUFB8	9	32,553,525	32,573,162	19,638	+	4	1_A375_gRA37_minus_lncRNA_IR_1--5474, 1_A375_gRA37_minus_lncRNA_IR_1--5475, 2_A375_gRA37_plus_lncRNA_IR_1--7670, 3_A375_DGR1_1--7974	20795, -66, 20795, 22174	downstream, upstream, downstream, downstream	1	1	1	16	17.25	12.25	1	1_A375_gRA37_plus_lncRNA_IR_1	Gene NDUFB8	C1, MGC10878, B17, NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	NM_182729, NM_002491, NC_018443.2, NC_018930.1, NC_018913.3, NC_018930.1	1559642_at, 202810_s_at	NP_877418.1, NP_002482.1, EAW65541.1, EAW65542.1, EAW65543.1
GeneID:8474	TAF1L	9	32,829,452	32,830,987	2,215	-	1	4_A375_DGR1_1--7965	-365	upstream	0	0	1	3	9	16	1	4_A375_DGR1_1	Gene TAF1L	MGC154910, TAF1L, TAF2A2	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like	NM_153039	1553011_at	NP_722516.1
GeneID:6462	APTX	9	32,972,806	33,001,628	29,216	-	2	1_A375_gRA37_minus_lncRNA_IR_1--5476, 2_A375_DGR1_1--7968	122, 230	w gene, w gene	1	0	1	20	13	17	1	1_A375_gRA37_plus_lncRNA_IR_1	Gene APTX	FHA-HIT, AXA1, FLJ20157, AOH1, MGC1072, EAOH, APTX, EAHHA, AOA	aprataxin	NM_175080, NM_175073, NC_018444.2, NC_018930.0, NC_018944.2, NC_018930.1, NC_018913.3, NC_018930.0, NC_018930.1	219527_at, 222855_s_at	NP_778239.1, NP_778243.1, EAW65529.1, EAW65530.1, EAW65531.1, EAW65533.1, EAW65534.1, EAW65535.1
GeneID:3301	DNAJA1	9	33,023,209	33,039,092	15,883	+	4	1_A375_gRA37_minus_lncRNA_IR_1--5477, 2_A375_gRA37_plus_lncRNA_IR_1--7671, 3_A375_gRA37_plus_lncRNA_IR_1--7671, 4_A375_DGR1_1--7980	71, -121, 102, 15975	w gene, upstream, w gene, downstream	1	1	1	16.5	18.5	16.5	2	4_A375_DGR1_1	Gene DNAJA1	DJA1, DNAJ1, HSPF4, DJ-2, HSJ-1, HSJ2, NEDD7, HDJ2, DJ-2	Dnaj (Hsp40) homolog, subfamily A, member 1	NM_001539, NC_018444.2, NC_024734.0, NC_024737.0, NC_018933.0	200800_at, 200801_s_at	NP_001530.1, EAW65538.1, EAW65524.1, EAW65525.1, EAW65527.1
GeneID:5334	SMU1	9	33,041,890	33,076,714	34,864	-	3	1_A375_gRA37_minus_lncRNA_IR_1--5478, 2_A375_gRA37_plus_lncRNA_IR_1--7672, 3_A375_DGR1_1--7980	122, 58, 32350	w gene, w gene, w gene	1	1	1	17	19.5	13.5	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene SMU1	DKFZp761B0916, FLJ10370, RP11-344K16.2, SMU1, FLJ10935, SMU-1, FLJ11910, WDC117363, SMU1, BWD	cwf-1-like/cell cycle control and splicing factor, S. pombe, homolog (C. elegans)	NM_018222, NC_018449.2, NC_018934.0	223618_at	NP_060955.2, EAW65522.1, EAW65523.1
GeneID:2844	BAGALT1	9	33,110,839	33,167,356	56,717	-	1	4_A375_DGR1_1--7969	345	w gene	0	0	1	14	16	16	1	4_A375_DGR1_1	Gene BAGALT1	BAGALT1, MGC39583, Bb-Gc-T1, beta1-4Gal-T1, CGnGT0, GT1, GGTB2, Gnt1a6bnNY23 0, GTB	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	NM_001497, NC_018934.2, NC_018942.0	201982_s_at, 201983_s_at, 211811_s_at, 219827_s_at, 229403_at, 230967_at	NP_001488.2, EAW65520.1, EAW65521.1
GeneID:2783	SPINK4	9	33,240,196	33,246,965	6,769	+	2	1_A375_gRA37_minus_lncRNA_IR_1--5479, 2_A375_gRA37_plus_lncRNA_IR_1--7673	-6084, -6084	upstream, upstream	1	1	0	23	33	12	1	2_A375_gRA37_plus_lncRNA_IR_1	Gene SPINK4	PEC-60, MGC132107, SPINK4	serine peptidase inhibitor, Kazal type 4	NM_014471, NC_018934.2	207214_at	NP_055306.1, EAW65516.1
GeneID:5101	CHMP3	9	33,264,877	33,281,916	16,839	+	2	1_A375_gRA37_minus_lncRNA_IR_1--5480, 2_A375_gRA37_plus_lncRNA_IR_1--7674	23623, 23587	downstream, downstream	1	1	0	36	34	12	1	1_A375_gRA37_plus_lncRNA_IR_1	Gene CHMP3	PMN3.2, HSPC177, SNF7DC2, CGI-34, CHMP3, Vps60, C9orf83	chromatin modifying protein 3	NM_019618, NC_018935.2, NC_018951.0	218839_at, 219396_s_at	NP_062569.1, EAW65512.1, EAW65513.1
GeneID:4781	NFX1	9	33,290,416	33,371,155	80,737	+	2	1_A375_gRA37_minus_lncRNA_IR_1--5480, 2_A375_gRA37_plus_lncRNA_IR_1--7674	-16, 48	upstream, w gene	1	1	0	36	34	12	1	1_A375_gRA37_plus_lncRNA_IR_1	Gene NFX1	DKFZp779G2419, FLJ10370, RP11-344K16.2, SMU1, FLJ10935, SMU-1, FLJ11910, WDC117363, SMU1, BWD	nuclear transcription factor, X-box binding 1	NM_002504, NM_147133, NM_147134, NC_018447.2, NC_020318.0, NC_020319.0, NC_020320.0, NC_020321.0	1553103_at, 1553148_s_at, 202864_at, 202865_s_at, 212686_at	NP_002493.2, NP_667344.1, NP_667345.1, EAW65507.1, EAW65508.1, EAW65510.1, EAW65511.1
GeneID:1439	ANKRD18B	9	33,323,927	33,372,356	48,431	+	2	2_A375_gRA37_plus_lncRNA_IR_1--7675, 3_A375_DGR1_1--7981	-339, 301	upstream, w gene	0	1	1	17	19	16	1	2_A375_gRA37_plus_lncRNA_IR_1	Gene ANKRD18B	MGC33641-1, ANKRD18B	ankyrin repeat domain 18B	XM_001716034, XM_001717197		XP_001716084.3, XP_001717249.3
GeneID:3391	UBAP2	9	33,521,691	33,545,947	127,256	-	2	1_A375_gRA37_minus_lncRNA_IR_1--5481, 2_A375_gRA37_plus_lncRNA_IR_1--7676	-541, -169	upstream, upstream	1	1	0	19	25	16	1	2_A375_gRA37_plus_lncRNA_IR_1	Gene UBAP2	KIAA1467, UBAP2, bA179F3.3, FLJ20435, UBAP2, FLJ40387, FLJ43947	ubiquitin associated protein 2	NM_015449	219192_at, 221839_s_at	NP_056319.2
GeneID:2512	DCAF12	9	34,066,991	34,126,771	60,390	-	1	2_A375_gRA37_plus_lncRNA_IR_1--7677	171	w gene	0	1	0	12	14	13	1	2_A375_gRA37_plus_lncRNA_IR_1	Gene DCAF12	DCAF12, CTI02, MGC11035, WDSB40h, TCC62, Gnf.Zat3H0125.5, SMA1852	DDB1 and CUL4 associated factor 12	NM_015397, NC_018944.2, NC_018950.0, NC_018939.0	224769_at	NP_056212.1, EAW65472.1, EAW65473.1, EAW65474.1
GeneID:5562	KIAA1109	9	34,265,927	34,276,894	10,967	-	1	4_A375_DGR1_1--7952	5755	w gene	0	0	1	9	14	17	1	4_A375_DGR1_1	Gene KIAA1109	KIAA1109, MST27	KIAA1109	NM_020702, NC_018935.2	231169_at, 232244_at	NP_065753.2, EAW65480.1
GeneID:6566	C9orf28	9	34,279,017	34,297,949	18,932	-	1	4_A375_DGR1_1--7952	35713	downstream	0	0	1	9	14	17	1	4_A375_DGR1_1	Gene C9orf28	MGC22321, chromosome 9 open reading frame 28, bA704B2.4, CBE1, HCD-22, C9orf28	chromosome 9 open reading frame 28	NM_147160, NM_147159, NM_032596, NC_018935.2, NC_018935.0, NC_018935.2	229012_at	NP_671897.1, NP_671898.1, NP_115953.2, EAW65456.1, EAW65457.1, EAW65458.1, EAW65459.1
GeneID:2239	C9orf25	9	34,298,102	34,436,966	80,256	-	6	1_A375_gRA37_minus_lncRNA_IR_1--5482, 2_A375_gRA37_plus_lncRNA_IR_1--5483, 3_A375_gRA37_plus_lncRNA_IR_1--5484, 4_A375_gRA37_plus_lncRNA_IR_1--7678, 5_A375_gRA37_plus_lncRNA_IR_1--7679, 6_A375_gRA37_plus_lncRNA_IR_1--7680	43896, 27016, -24, 43980, 27078, -56	w gene, w gene, upstream, w gene, upstream, w gene, upstream	1	1	0	20.67	23.67	6.33	3	1_A375_gRA37_plus_lncRNA_IR_1	Gene C9orf25	C9orf25, chromosome 9 open reading frame 25, bA704B2.5	chromosome 9 open reading frame 25	NM_147202, NM_001164840, NM_001164841, NM_001164842, NM_001164843, NM_001164844, NM_001164845, NC_018935.2, NC_018935.0, NC_018935.2	225148_at	NP_671735.1, NP_671736.1, NP_001157669.1, NP_001157670.1, NP_001157671.1, NP_001157672.1, NP_001157673.1, EAW65454.1, EAW65455.1
GeneID:2711	DNAI1	9	34,496,811	34,520,902	92,171	+	4	1_A375_gRA7_minus_lncRNA_IR_1--5484, 1_A375_gRA37_minus_lncRNA_IR_1--5485, 2_A375_gRA37_plus_lncRNA_IR_1--7680, 3_A375_gRA37_plus_lncRNA_IR_1--7681	-219, 38301, -197, 33093	upstream,w gene, upstream,w gene	1	1	0	33.5	26	8.5	2	1_A375_gRA37_plus_lncRNA_IR_1	Gene DNAI1	DNAI1, CILD1, FCS1, MGC29206, PCD1, ICS	dynein, axonemal, intermediate chain 1	NM_012144, NC_018951.2	220129_at, 233193_at	NP_036276.1, EAW65453.1
GeneID:1278	CNTFR	9	34,551,451	34,569,722	56,291	+	1	4_A375_DGR1_1--7953	-1936	upstream	0	0	1	5	9	16	1	4_A375_DGR1_1	Gene CNTFR	MGC1774, CNTFR	ciliary neurotrophic factor receptor	NM_001842, NM_147156, NC_018972.2, NC_018951.2, NC_018951.0, NC_018951.2	205722_at	NP_001833.3, NP_671693.1, EAW65445.1, EAW65446.1, EAW65447.1, EAW65448.1
GeneID:5836	LOC413358	9	34,560,010	34,563,899	13,889	+	1	4_A375_DGR1_1--7953	23350	downstream	0	0	1	5	9	16	1	4_A375_DGR1_1	Gene LOC413358		hypothetical LOC413358	NR_024369	1559771_a_at, 1561990_a_at	
GeneID:3715	KARS0C	9	34,821,455	34,826,811	5,356	-	2	1_A375_gRA37_plus_lncRNA_IR_1--7682, 2_A375_DGR1_1--7954	-9777, -9233	upstream, downstream	0	1	1	20	23	21	1	2_A375_gRA37_plus_lncRNA_IR_1	Gene KARS0C	KARS0C		NM_001017393, NC_018960.2		NP_001017393.1, EAW65438.1
GeneID:2552	SGSH	9	34,834,719	34,837,768	3,049	-	4	2_A375_gRA37_plus_lncRNA_IR_1--7682, 3_A375_gRA37_plus_lncRNA_IR_1--7683, 4_A375_DGR1_1--7914, 4_A375_DGR1_1--7915	40, -5972, 304, -1945	w gene, upstream, w gene, upstream	0	1	1	21	16.5	19	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene SGSH	OPR51, SGSH1, SPR1, SPR2P, FLJ38503, MGC3331	sigma non-opioid intracellular receptor 1	NM_000199, NM_147157	201802_at, 214464_s_at	NP_000189.1, NP_671512.1
GeneID:2384	GALT	9	34,846,835	34,850,874	4,039	+	4	2_A375_gRA37_plus_lncRNA_IR_1--7682, 3_A375_gRA37_plus_lncRNA_IR_1--7683, 4_A375_DGR1_1--7914, 4_A375_DGR1_1--7915	-5907, 3, -5071, 101	upstream, w gene, upstream, upstream	0	1	1	21	16.5	19	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene GALT	GALT		NM_000155	203179_at, 232708_at, 242724_s_at	NP_000146.2
GeneID:3556	IL1RA	9	34,852,162	34,861,864	9,702	+	2	1_A375_gRA37_minus_lncRNA_IR_1--7682, 4_A375_DGR1_1--7915	-5962, -5396	upstream, upstream	0	1	1	22	14	17	1	4_A375_DGR1_1	Gene IL1RA	IL1Ra, MGC2148	interleukin 1 receptor, type I	NM_000577, NM_173842, NM_001172954	1552649_at, 206172_at	NP_000568.1, NP_776207.1, NP_001159436.1
GeneID:3491	KIAA1045	9	34,898,182	34,902,341	34,249	+	3	1_A375_gRA37_minus_lncRNA_IR_1--5488, 2_A375_gRA37_plus_lncRNA_IR_1--7684, 3_A375_DGR1_1--7916	29884, 29846, 32240	downstream, downstream, downstream	1	1	1	16.5	22.5	12.5	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene KIAA1045	KIAA1045, PRO34414, Gnf.Zat3H0112	KIAA1045	NM_015277	213808_at, 213809_at	NP_056132.1
GeneID:5222	DNAJB9	9	34,909,725	34,996,405	86,680	+	3	1_A375_gRA37_minus_lncRNA_IR_1--5488, 2_A375_gRA37_plus_lncRNA_IR_1--7684, 3_A375_DGR1_1--7916	-5489, -5455, 707	upstream, upstream, w gene	1	1	1	16.5	22.5	12.5	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene DNAJB9	KIAA1043, DNAJB5, Hsp40	Dnaj (Hsp40) homolog, subfamily B, member 9	NM_012328, NM_001135804, NM_001135805, NC_018951.2, NC_018951.0, NC_018951.2	203453_s_at, 213617_at	NP_036460.2, NP_001129476.1, NP_001129477.1, EAW65467.1
GeneID:7411	VCP	9	35,036,965	35,072,709	35,874	-	3	1_A375_gRA37_minus_lncRNA_IR_1--5492, 2_A375_gRA37_plus_lncRNA_IR_1--7693, 3_A375_gRA37_plus_lncRNA_IR_1--7699	239, 190, -7101	w gene, w gene, upstream	1	1	0	18	21	18	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene VCP	VCP, p97, MGC149992, MGC5360, MGC131997, IBMPFD, TERA	valosin-containing protein	NM_007126, NC_018930.0, NC_018951.2	208649_at, 208649_s_at	NP_009137.1, EAW65403.1, EAW65404.1
GeneID:2171	FANCG	9	35,073,833	35,080,013	6,776	-	3	1_A375_gRA37_minus_lncRNA_IR_1--5497, 2_A375_gRA37_plus_lncRNA_IR_1--7693, 3_A375_gRA37_plus_lncRNA_IR_1--7699	7933, 7499, 173	downstream, downstream, w gene	1	1	0	16	21	18	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene FANCG	XRCC9, FAG, FANCG	Fanconi anemia, complementation group G	NM_004629, NC_018948.2, NC_018951.2	203264_at	NP_004620.1, EAW65401.1, EAW65402.1
GeneID:5646	PIGQ	9	35,095,866	35,096,979	7,691	-	6	1_A375_gRA37_minus_lncRNA_IR_1--5498, 2_A375_gRA37_minus_lncRNA_IR_1--5499, 3_A375_gRA37_plus_lncRNA_IR_1--7696, 4_A375_gRA37_plus_lncRNA_IR_1--7697, 5_A375_gRA37_plus_lncRNA_IR_1--7698, 6_A375_DGR1_1--7917	-5, -4537, -18132, 35, -4397, -4523	w gene, upstream, downstream, w gene, upstream, upstream	1	1	1	21.67	23.33	18.33	3	1_A375_gRA37_plus_lncRNA_IR_1	Gene PIGQ	DKFZp434J0223, PIGQ, PIG-Q, RP11-357E24.4, MGC20538	phosphatidylinositol glycan anchor biosynthesis, class Q	NM_032634, NM_152650, NC_018948.2, NC_018951.0, NC_018951.2, NC_018951.0	209996_at, 214991_s_at	NP_116023.2, NP_689777.2, EAW65397.1, EAW65398.1, EAW65399.1, EAW65400.1
GeneID:3832	STOML2	9	35,099,993	35,103,154	3,281	-	3	1_A375_gRA37_minus_lncRNA_IR_1--5493, 2_A375_gRA37_plus_lncRNA_IR_1--7693, 3_A375_gRA37_plus_lncRNA_IR_1--7699, 4_A375_DGR1_1--7917	6372, 16, 6810, 176, 90	downstream, w gene, downstream, w gene, w gene	1	1	1	26.5	23	13	2	1_A375_gRA37_plus_lncRNA_IR_1	Gene STOML2	HSPC105, SLP-2, STOML2	stomatin (EPB72)-like 2	NM_013442, NC_018949.2, NC_018970.1, NC_018970.2	213416_s_at	NP_038470.1, EAW65396.1, EAW65394.1, EAW65396.1
GeneID:5588	KIAA1539	9	35,154,116	35,215,890	61,775	-	5	1_A375_gRA37_minus_lncRNA_IR_1--5495, 1_A375_gRA37_minus_lncRNA_IR_1--5496, 2_A375_gRA37_plus_lncRNA_IR_1--7697, 3_A375_gRA37_plus_lncRNA_IR_1--7698, 4_A375_DGR1_1--7917	19017, 12757, 19049, 12917, 12769	downstream, downstream, downstream, downstream, downstream	1	1	1	26.5	23	13	2	2_A375_gRA37_plus_lncRNA_IR_1	Gene KIAA1539	KIAA1539, PI 11899_3, RP11-162N22.6, FLJ11880, bA162N22.6	KIAA1539	NM_020182, NC_018930.0, NC_018930.0, NC_018930.1, NC_018930.0, NC_018930.1, NC_018930.2, NC_018930.1, NC_018930.2	207783_s_at, 214931_s_at	NP_064582.2, EAW65388.1, EAW65387.1, EAW65389.1, EAW65390.1, EAW65391.1, EAW65392.1



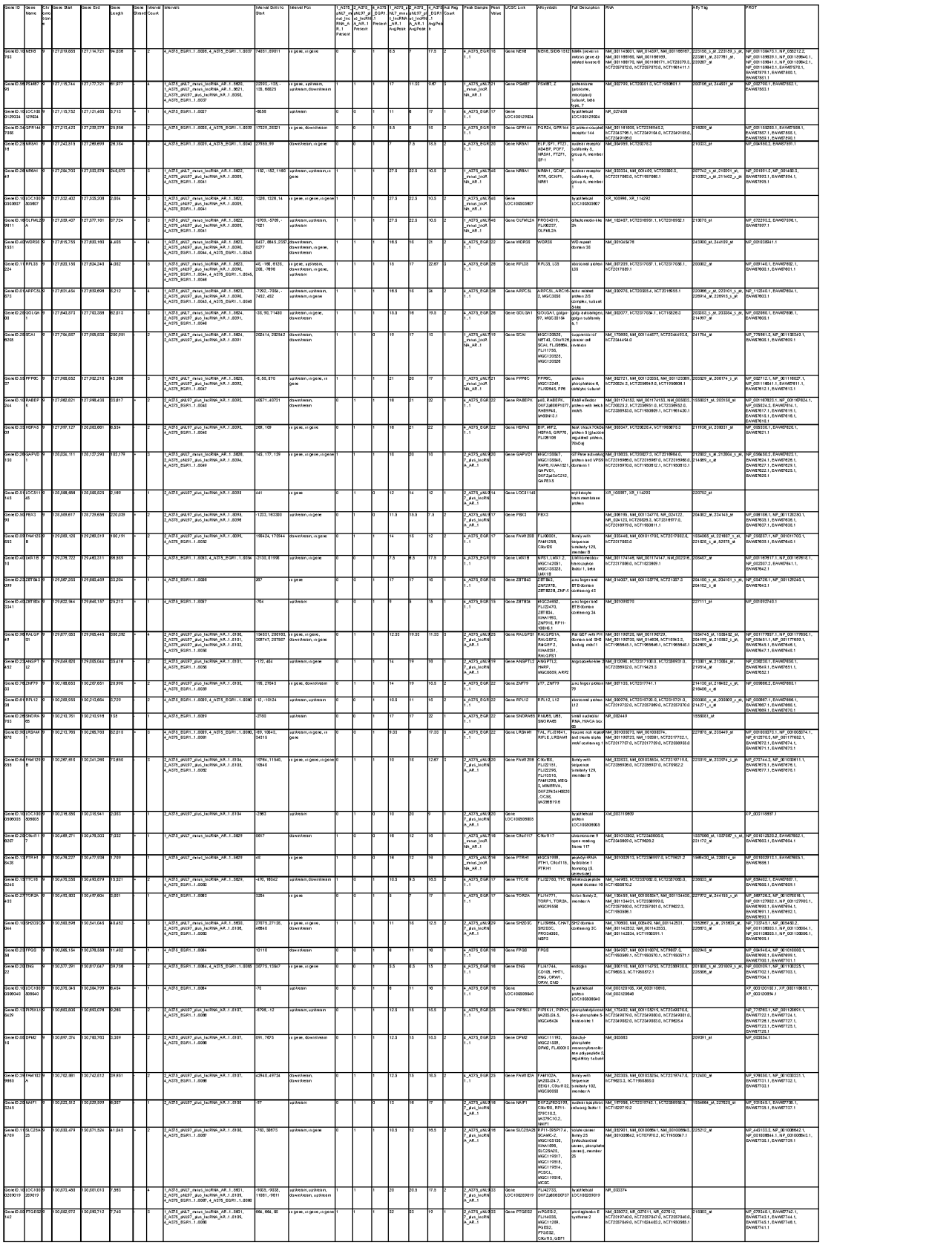


Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.549	AUH	9	93,976,097	94,124,206	148,109	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7966	270	in gene	0	1	0	9	18	5	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene AUH	AUH		NM_001698, hCT2261431.0, hCT19273.2	205052_at	NP_001689.1, EAW62795.1, EAW62794.1
GeneID.4783	NFIL3	9	94,171,327	94,186,144	14,817	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5539, 2_A375_pNL97_plus_lncRNA_AR..1..7967, 2_A375_pNL97_plus_lncRNA_AR..1..7968	4544, 4424, -320	in gene, in gene, upstream	1	1	0	15.5	19	7.5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene NFIL3	NFIL3A, E4BP4, IL3BP1, NF-IL3A, NFIL3	nuclear factor, interleukin 3 regulated	NM_005384, hCT21556.3, hCT1962559.1	203574_at	NP_005375.2, EAW62797.1, EAW62796.1
GeneID.10558	SPTLC1	9	94,793,427	94,877,690	84,263	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5540, 2_A375_pNL97_plus_lncRNA_AR..1..7969	58, -6	in gene, upstream	1	1	0	23	27	14	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SPTLC1	MGC14645, HSN1, SPT1, HSAN1, SPTI, HSAN, LBC1, LCB1, SPTLC1	serine palmitoyltransferase, long chain base subunit 1	NM_006415, NM_178324, hCT2260124.0, hCT2260125.0, hCT2353842.0	1554053_at, 202277_at, 202278_s_at	NP_006406.1, NP_847894.1, EAW62804.1, EAW62805.1, EAW62806.1
GeneID.100507197	LOC100507197	9	94,903,721	94,910,588	6,867	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5541	5831	in gene	1	0	0	15	12	7	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene LOC100507197		hypothetical LOC100507197	XR_113236, XR_113237, XR_108976, XR_108977, XR_114271, XR_114272		
GeneID.158314	C9orf44	9	94,903,749	94,921,890	18,141	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5541	5803	in gene	1	0	0	15	12	7	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene C9orf44	C9orf44	chromosome 9 open reading frame 44	NR_027341	233524_at, 233525_s_at	
GeneID.3376	IARS	9	94,972,625	95,056,038	83,413	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5542, 2_A375_pNL97_plus_lncRNA_AR..1..7970	-10, -90	upstream, upstream	1	1	0	29	27	9	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene IARS	PRO0785, IARS, FLJ20736, ILERS, IRS, ILRS, IARS1	isoleucyl-tRNA synthetase	NM_013417, NM_002161, hCT22312.2, hCT2260120.0, hCT2353804.0, hCT2353805.0, hCT1962560.1	204744_s_at	NP_038203.2, NP_002152.2, EAW62810.1, EAW62811.1, EAW62812.1, EAW62813.1, EAW62809.1
GeneID.100124534	SNORA84	9	95,054,743	95,054,875	132	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5542, 2_A375_pNL97_plus_lncRNA_AR..1..7970	-1173, -1253	upstream, upstream	1	1	0	29	27	9	1	1_A375_pNL7_minus_lncRNA_AR..1	29	Gene SNORA84	SNORA84	small nucleolar RNA, H/ACA box 84	NR_003704		
GeneID.55035	NOL8	9	95,059,640	95,087,876	28,236	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5542, 1_A375_pNL7_minus_lncRNA_AR..1..5543, 2_A375_pNL97_plus_lncRNA_AR..1..7970, 2_A375_pNL97_plus_lncRNA_AR..1..7971	31826, -220, 31746, -220	downstream, upstream, downstream, upstream	1	1	0	50	67	10	2	2_A375_pNL97_plus_lncRNA_AR..1	107	Gene NOL8	Nop132, DKFZp686P12242, FLJ20736, C9orf34, NOL8, bA62C3.3, bA62C3.4	nucleolar protein 8	NM_017948, NR_024020, hCT2260114.0, hCT2260117.0, hCT1956082.1	218244_at	NP_060418.4, EAW62814.1, EAW62815.1, EAW62816.1
GeneID.401541	CENPP	9	95,087,741	95,377,446	289,705	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5543, 1_A375_pNL7_minus_lncRNA_AR..1..5544, 2_A375_pNL97_plus_lncRNA_AR..1..7971	355, 199811, 355	in gene, in gene, in gene	1	1	0	44	60	8	2	2_A375_pNL97_plus_lncRNA_AR..1	107	Gene CENPP	CENPP, CENP-P, FLJ33928	centromere protein P	NM_001012267		NP_001012267.1
GeneID.1842	ECM2	9	95,257,599	95,298,252	40,653	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5544	10700	in gene	1	0	0	17	13	5	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene ECM2	ECM2, MGC126355, MGC126356	extracellular matrix protein 2, female organ and adipocyte specific	NM_001393, hCT22306.2	1568779_a_at, 206101_at	NP_001384.1, EAW62824.1
GeneID.64768	IPPK	9	95,375,466	95,432,547	57,081	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7972, 4_A375_EGR1..1..7973	-29, 32163	upstream, in gene	0	1	1	12	14.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene IPPK	KIAA0699, IPPK, INSP5K2, bA476B13.1, FLJ13163, IP5K, C9orf12, IPK1	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	NM_022755, hCT22313.3	219092_s_at, 222623_at	NP_073592.1, EAW62826.1
GeneID.23299	BICD2	9	95,473,645	95,527,083	53,438	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5545, 2_A375_pNL97_plus_lncRNA_AR..1..7973, 4_A375_EGR1..1..7974	-661, -213, 45611	upstream, upstream, in gene	1	1	1	13	16	12	2	2_A375_pNL97_plus_lncRNA_AR..1	25	Gene BICD2	KIAA0699, BICD2, bA526D8.1	bicaudal D homolog 2 (Drosophila)	NM_001003800, NM_015250, hCT22310.3	1553021_s_at, 209203_s_at, 212702_s_at, 213154_s_at	NP_001003800.1, NP_056065.1, EAW62829.1
GeneID.84270	C9orf89	9	95,856,450	95,875,565	17,115	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5546, 2_A375_pNL97_plus_lncRNA_AR..1..7974, 2_A375_pNL97_plus_lncRNA_AR..1..7975, 2_A375_pNL97_plus_lncRNA_AR..1..7976	2638, 366, 1466, 2211	in gene, in gene, in gene, in gene	1	1	0	14.33	15.67	8.67	3	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene C9orf89	MGC110698, BinCARD, C9orf89, MGC11115, bA370F5.1	chromosome 9 open reading frame 89	NM_032310, hCT2353859.0, hCT2353860.0, hCT2353861.0, hCT9130.3, hCT1963642.1, hCT1966150.1	1562559_at, 223398_at	NP_115686.3, EAW62855.1, EAW62850.1, EAW62852.1, EAW62853.1, EAW62854.1, EAW62851.1
GeneID.65268	WNK2	9	95,947,212	96,082,854	135,642	+	3	4_A375_EGR1..1..7976, 4_A375_EGR1..1..7977, 4_A375_EGR1..1..7978	20489, 57080, 123460	in gene, in gene, in gene	0	0	1	4	8	16.33	3	4_A375_EGR1..1	18	Gene WNK2	PRKWNK2, SDCCAG43, WNK2, KIAA1760, P/OKcl.13, NY-CO-43	WNK lysine deficient protein kinase 2	NM_006648, hCT2348984.0, hCT2353844.0, hCT2353845.0, hCT2353846.0	1557536_at, 1560866_at, 1562026_at, 227217_at, 229547_s_at	NP_006639.3, EAW62856.1, EAW62857.1, EAW62859.1, EAW62860.1
GeneID.445577	C9orf129	9	96,080,481	96,108,696	28,215	-	1	4_A375_EGR1..1..7978	38024	downstream	0	0	1	2	8	16	1	4_A375_EGR1..1	16	Gene C9orf129	bA165J3.3, C9orf129	chromosome 9 open reading frame 129	NM_001098808		NP_001092278.1
GeneID.23196	FAM120A	9	96,214,173	96,328,397	114,224	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7977	114739	downstream	0	1	0	10	14	13	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene FAM120A	DNAPTP5, FAM120A, DNAPTP1, MGC111527, MGC133257, OSSA, C9orf10	family with sequence similarity 120A	NM_014612, hCT2260262.0, hCT2260263.0, hCT2260264.0, hCT2260265.0	1555908_at, 1555944_at, 1555945_s_at, 1555947_at, 1555948_s_at, 1559711_at, 200787_s_at, 200774_at, 210516_at	NP_055427.2, EAW62866.1, EAW62863.1, EAW62864.1, EAW62865.1
GeneID.5253	PHF2	9	96,338,909	96,441,869	102,960	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7977	-9997	upstream	0	1	0	10	14	13	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene PHF2	PHF2, JHDM1E, MGC176680, GRC5, KIAA0662	PHD finger protein 2	NM_005392, hCT2259790.1, hCT2348319.0, hCT2348320.0, hCT2353857.0, hCT23840.4	207138_at, 212726_at	NP_005383.3, EAW62869.1, EAW62867.1, EAW62868.1, EAW62870.1, EAW62871.1
GeneID.100422927	MIR4291	9	96,561,639	96,561,703	64	+	1	4_A375_EGR1..1..7980	-9143	upstream	0	0	1	4	3	14	1	4_A375_EGR1..1	14	Gene MIR4291	MIR4291	microRNA 4291	NR_036254		
GeneID.56033	BARX1	9	96,713,909	96,717,608	3,699	-	1	4_A375_EGR1..1..7982	5992	downstream	0	0	1	6	8	18	1	4_A375_EGR1..1	18	Gene BARX1	BARX1		NM_021570, hCT9642.2	219845_at	NP_067545.3, EAW62873.1
GeneID.138639	PTPDC1	9	96,793,076	96,872,136	79,060	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5547	28	in gene	1	0	0	14	15	11	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene PTPDC1	PTP9Q22, FLJ42922, PTPDC1	protein tyrosine phosphatase domain containing 1	NM_177995, NM_152422, hCT2353808.0, hCT1822630.2	229517_at, 238841_at	NP_818931.1, NP_689635.3, EAW62875.1, EAW62876.1
GeneID.406881	MIRLET7A1	9	96,938,239	96,938,318	79	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7978	-9647	upstream	0	1	0	14	16	14	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene MIRLET7A1	MIRNLET7A1, LET7A1, MIRLET7A1, let-7a-1	microRNA let-7a-1	NR_029476		
GeneID.406888	MIRLET7F1	9	96,938,629	96,938,715	86	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7978	-10037	upstream	0	1	0	14	16	14	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene MIRLET7F1	LET7F1, let-7f-1, MIRLET7F1, MIRNLET7F1	microRNA let-7f-1	NR_029483		
GeneID.169841	ZNF169	9	97,021,578	97,065,291	43,713	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7979	-10	upstream	0	1	0	14	23	17	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene ZNF169	ZNF169, MGC51961	zinc finger protein 169	NM_194320, hCT2259795.0, hCT2259796.0, hCT2353839.0, hCT2353840.0, hCT2353841.0	1560921_at, 1560922_s_at, 1570354_s_at	NP_919301.2, EAW62880.1, EAW62878.1, EAW62879.1, EAW62881.1, EAW62882.1
GeneID.84909	C9orf3	9	97,488,886	97,849,500	360,614	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5548, 2_A375_pNL97_plus_lncRNA_AR..1..7980, 2_A375_pNL97_plus_lncRNA_AR..1..7981, 2_A375_pNL97_plus_lncRNA_AR..1..7982	56610, 106, 56610, 202698	in gene, in gene, in gene, in gene	1	1	0	22	30.33	8.67	3	2_A375_pNL97_plus_lncRNA_AR..1	52	Gene C9orf3	C9ORF3, APO, FLJ14675, C9orf3, FLJ40923, AP-O, FLJ55632, ONPEP, AOPEP	chromosome 9 open reading frame 3	NM_001193329, NM_032823, NM_001193330, NM_001193331, hCT2289293.2, hCT2289294.1, hCT2289295.2, hCT2289297.0, hCT2289300.2, hCT2357569.0	212848_s_at, 232270_at	NP_001180258.1, NP_116212.3, NP_001180259.1, NP_001180260.1, EAW92618.1, EAW92622.1, EAW92619.1, EAW92620.1, EAW92621.1, EAW92623.1
GeneID.5727	PTCH1	9	98,205,264	98,279,247	73,983	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5549, 2_A375_pNL97_plus_lncRNA_AR..1..7983, 2_A375_pNL97_plus_lncRNA_AR..1..7984	9455, 9455, 6255	in gene, in gene, in gene	1	1	0	17.5	19	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene PTCH1	PTCH1, PTC, FLJ26746, FLJ42602, BCNS, PTCH11, PTCH, HPE7, PTC1, NBCCS	patched 1	NM_001083603, NM_001083606, NM_000264, NM_001083607, NM_001083604, NM_001083602, NM_001083605, hCT2289541.0, hCT1950469.1	1555520_at, 208522_s_at, 209815_at, 209816_at	NP_001077072.1, NP_001077075.1, NP_000255.2, NP_001077076.1, NP_001077073.1, NP_001077071.1, NP_001077074.1, EAW92631.1, EAW92632.1
GeneID.100128782	C9orf130	9	98,566,370	98,638,259	69,889	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5550, 2_A375_pNL97_plus_lncRNA_AR..1..7985, 4_A375_EGR1..1..7983, 4_A375_EGR1..1..7984	51, 115, 915, 211	in gene, in gene, in gene, in gene	1	1	1	26	24	21	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene C9orf130	NAG11, FLJ34818, FLJ34826, C9orf130, NAG12	chromosome 9 open reading frame 130	NR_023389, NR_023390		
GeneID.375748	C9orf102	9	98,637,900	98,731,122	93,222	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5550, 2_A375_pNL97_plus_lncRNA_AR..1..7985, 4_A375_EGR1..1..7983, 4_A375_EGR1..1..7984	308, 244, -556, 148	in gene, in gene, upstream, in gene	1	1	1	26	24	21	1	1_A375_pNL7_minus_lncRNA_AR..1	26	Gene C9orf102	SR278, FLJ37706, MGC43364, RAD26L, MGC30192, C9orf102	chromosome 9 open reading frame 102	NM_001010895, hCT2357570.0, hCT1776584.2, hCT1950465.1	232601_at	NP_001010895.1, EAW92636.1, EAW92635.1, EAW92637.1
GeneID.3293	HSD17B3	9	98,997,589	99,064,434	66,845	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5552	45202	in gene	1	0	0	18	13	2	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene HSD17B3	EDH17B3, SDR12C2, HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	NM_000197, hCT1668367.2	206935_at	NP_000188.1, EAW92645.1
GeneID.195828	ZNF367	9	99,148,223	99,180,669	32,446	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5553, 1_A375_pNL7_minus_lncRNA_AR..1..5554, 2_A375_pNL97_plus_lncRNA_AR..1..7987, 4_A375_EGR1..1..7988	1021, 173, 157, 93	in gene, in gene, in gene, in gene	1	1	1	18.5	14	14.5	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene ZNF367	ZFF29, FLJ33970, ZNF367, CDC14B	zinc finger protein 367	NM_153695, hCT2357567.0, hCT23702.4	229551_x_at	NP_710162.1, EAW92649.1, EAW92650.1
GeneID.8555	CDC14B	9	99,262,395	99,382,112	119,717		1	4_A375_EGR1..1..7987	52766	in gene	0	0	1	13	14	15	1	4_A375_EGR1..1	15	Gene CDC14B	hCDC14B, Cdc14B1, CDC14B, CDC14B3, Cdc14B2	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	NM_003671, NM_033331, NM_001077181	208022_s_at, 211347_at, 211348_s_at, 221555_x_at, 221556_at, 234605_at, 234740_at	NP_003662.1, NP_201588.1, NP_001070649.1
GeneID.195827	C9orf21	9	99,403,633	99,417,599	14,066	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7988	479	in gene	0	1	0	12	16	8	1	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene C9orf21	C9orf21	chromosome 9 open reading frame 21	NM_153698, hCT1968088.1, hCT1968089.1, hCT23904.4	227534_at	NP_714542.1, EAW92663.1, EAW92661.1, EAW92662.1
GeneID.57653	KIAA1529	9	100,000,708	100,139,577	138,869	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7989	148764	downstream	0	1	0	15	26	16	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene KIAA1529	DKFZp686G1725, DKFZp434I2420, RP11-23J9.1, BDAG1, KIAA1529, MGC131724	KIAA1529	NR_038527, NR_038529, NR_038528, hCT2273540.0, hCT2273543.0	229627_at, 229628_s_at	EAW58840.1, EAW58841.1
GeneID.100499483	C9orf174	9	100,069,910	100,139,577	69,667	+	1	2_A375_pNL97_plus_lncRNA_AR..1..7989	79562	downstream	0	1	0	15	26	16	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene C9orf174	DKFZp686G1725, FLJ50036, DKFZp434I2420, DKFZp686B2031, BDAG1, KIAA1529, FLJ41397, C9orf174	chromosome 9 open reading frame 174	NM_020893		NP_065944.2
GeneID.286359	hCG_2045089	9	100,153,118	100,158,973	5,855	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7989, 4_A375_EGR1..1..7989	9501, 7357	downstream, downstream	0	1	1	8.5	15.5	17	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene hCG_2045089	LOC286359, FLJ17336, FLJ17317	hypothetical LOC286359	NR_026847	1563606_a_at, 1563607_x_at	
GeneID.23424	TDRD7	9	100,174,302	100,258,407	84,105	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5555, 2_A375_pNL97_plus_lncRNA_AR..1..7990, 4_A375_EGR1..1..7990	-158, -158, 90418	upstream, upstream, downstream	1	1	1	20	19	9.5	2	1_A375_pNL7_minus_lncRNA_AR..1	34	Gene TDRD7	TDRD7, RP11-508D10.1, PCTAIRE2BP, KIAA1529, TRAP	tudor domain containing 7	NM_014290, hCT2353394.0, hCT19315.3	213361_at	NP_055105.2, EAW58844.1, EAW58843.1
GeneID.7111	TMOD1	9	100,263,462	100,364,025	100,563	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7991, 4_A375_EGR1..1..7990	24874, 1258	in gene, in gene	0	1	1	9	10.5	10	2	4_A375_EGR1..1	15	Gene TMOD1	TMOD1, TMOD, D9S57E, ETMOD	tropomodulin 1	NM_003275, NM_001166116, hCT2273551.0, hCT18604.2	203661_s_at, 203662_s_at	NP_003266.1, NP_001159588.1, EAW58845.1, EAW58846.1
GeneID.158427	TSTD2	9	100,362,362	100,395,962	33,600	-	2	2_A375_pNL97_plus_lncRNA_AR..1..7992, 4_A375_EGR1..1..7991	262, -70	in gene, upstream	0	1	1	16	18	16	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TSTD2	C9orf97, TSTD2, FLJ38724	thiosulfate sulfurtransferase (rhodanese)-like domain containing 2	NM_139246, hCT2273951.1, hCT2273952.1, hCT2353393.0, hCT19313.3	1555430_at, 213161_at	NP_640339.4, EAW58850.1, EAW58848.1, EAW58849.1, EAW58851.1
GeneID.4686	NCBP1	9	100,395,705	100,436,030	40,325	+	2	2_A375_pNL97_plus_lncRNA_AR..1..7992, 4_A375_EGR1..1..7991	-25, 327	upstream, in gene	0	1	1	16	18	16	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene NCBP1	NCBP1, NCBP, Sto1, CBP80, MGC2087	nuclear cap binding protein subunit 1, 80kDa	NM_002486, hCT2273554.0, hCT19312.2, hCT1984994.1	209519_at, 209520_s_at	NP_002477.1, EAW58854.1, EAW58852.1, EAW58853.1
GeneID.7507	XPA	9	100,437,191	100,459,691	22,500	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5556, 2_A375_pNL97_plus_lncRNA_AR..1..7993, 4_A375_EGR1..1..7992	267, 331, 363	in gene, in gene, in gene	1	1	1	17	19	20	1	4_A375_EGR1..1	20	Gene XPA	XP1, XPAC, XPA	xeroderma pigmentosum, complementation group A	NM_000380, NR_027302, hCT19311.3	205672_at, 232987_at	NP_000371.1, EAW58855.1
GeneID.2304	FOXE1	9	100,615,537	100,618,997	3,460	+	2	4_A375_EGR1..1..7993, 4_A375_EGR1..1..7994	911, 1775	in gene, in gene	0	0	1	6.5	5	14	2	4_A375_EGR1..1	15	Gene FOXE1	HFKL5, FOXE1, FKHL15, HFKH4, TITF2, FOXE2, TTF-2, TTF2	forkhead box E1 (thyroid transcription factor 2)	NM_004473, hCT1778288.1	206912_at, 208239_at	NP_004464.2, EAW58856.1
GeneID.51531	C9orf156	9	100,666,772	100,684,852	18,080	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5557, 2_A375_pNL97_plus_lncRNA_AR..1..7995, 4_A375_EGR1..1..7995	212, 116, 52	in gene, in gene, in gene	1	1	1	36	45	17	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene C9orf156	HSPC219, NAP1, C9orf156	chromosome 9 open reading frame 156	NM_016481, hCT21115.3, hCT2353390.0, hCT1965005.1	222186_at, 222195_s_at, 47530_at	NP_057565.3, EAW58860.1, EAW58858.1, EAW58859.1
GeneID.55363	HEMGN	9	100,689,073	100,707,134	18,061	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5557, 2_A375_pNL97_plus_lncRNA_AR..1..7995, 4_A375_EGR1..1..7995	22494, 22398, 22334	downstream, downstream, downstream	1	1	1	36	45	17	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene HEMGN	EDAG, EDAG-1, HEMGN	hemogen	NM_197978, NM_018437, hCT2273945.0, hCT2353378.0, hCT1776288.1	223669_at, 223670_s_at	NP_932095.1, NP_060907.2, EAW58861.1, EAW58862.1, EAW58863.1
GeneID.10541	ANP32B	9	100,745,489	100,778,225	32,736	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5558, 2_A375_pNL97_plus_lncRNA_AR..1..7996, 2_A375_pNL97_plus_lncRNA_AR..1..7997, 2_A375_pNL97_plus_lncRNA_AR..1..7998	-17, -2001, 207, 1647	upstream, upstream, in gene, in gene	1	1	0	14	19.33	7	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ANP32B	PHAPI2, SSP29, APRIL, ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	NM_006401, hCT21112.3, hCT2353388.0	201305_x_at, 201306_s_at	NP_006392.1, EAW58864.1, EAW58865.1
GeneID.54187	NANS	9	100,818,959	100,845,365	26,406	+	1	4_A375_EGR1..1..7996	81	in gene	0	0	1	15	14	19	1	4_A375_EGR1..1	19	Gene NANS	NANS, SAS	N-acetylneuraminic acid synthase	NM_018946, hCT21117.3, hCT1965006.1, hCT1965007.1, hCT1965008.1	218189_s_at, 241923_x_at	NP_061819.2, EAW58867.1, EAW58866.1, EAW58868.1, EAW58869.1
GeneID.9830	TRIM14	9	100,831,563	100,881,466	49,925	-	1	2_A375_pNL97_plus_lncRNA_AR..1..7999	206	in gene	0	1	0	18	22	12	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene TRIM14	KIAA0129, TRIM14	tripartite motif containing 14	NM_014788, NM_033219, NM_033220, hCT2273683.0, hCT2273684.0, hCT2273685.0, hCT2273686.0, hCT2273687.0, hCT2273688.0, hCT2273689.0, hCT2273691.0, hCT2273693.0	203147_s_at, 203148_s_at, 210646_x_at, 211044_at, 231934_at	NP_055603.2, NP_150088.1, NP_150089.1, EAW58872.1, EAW58873.1, EAW58877.1, EAW58870.1, EAW58871.1, EAW58874.1, EAW58875.1, EAW58876.1, EAW58878.1
GeneID.7464	CORO2A	9	100,883,257	100,954,956	71,699	-	4	2_A375_pNL97_plus_lncRNA_AR..1..7999, 2_A375_pNL97_plus_lncRNA_AR..1..8000, 4_A375_EGR1..1..7997, 4_A375_EGR1..1..7998	73676, -564, 566, -404	downstream, upstream, in gene, upstream	0	1	1	13.67	16.67	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene CORO2A	CORO2A, WDR2, DKFZp686G19226, IR10, CLIPINB	coronin, actin binding protein, 2A	NM_052820, NM_003389, hCT21111.2, hCT2273720.0, hCT1776431.1	205538_at, 227177_at	NP_438171.1, NP_003380.3, EAW58879.1, EAW58880.1, EAW58881.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Allsymbols	Full Description	RNA	Affy Tag	PROT
GeneID.55357	TBC1D2	9	100,961,260	101,018,003	56,723	-	5	2_A375_pNL97_plus_lncRNA_AR..1..8000, 2_A375_pNL97_plus_lncRNA_AR..1..8001, 4_A375_EGR1..1..7997, 4_A375_EGR1..1..7998, 4_A375_EGR1..1..7999	62463, -205, 63635, 62643, -45	downstream, upstream, downstream, downstream, upstream	0	1	1	13.33	18	19	3	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene TBC1D2	FLJ42762, PARIS1, TBC1D2A, FLJ16244, TBC1D2, FLJ10702, PARIS1, DKFZp761D1823	TBC1 domain family, member 2	NM_018421, hCT21114.3, hCT2273712.0, hCT2273715.0, hCT2273717.0, hCT2353368.0, hCT2353369.0, hCT1960320.1	222173_s_at	NP_060891.3, EAW58887.1, EAW58882.1, EAW58884.1, EAW58885.1, EAW58886.1, EAW58883.1, EAW58886.1
GeneID.9568	GABBR2	9	101,050,364	101,471,479	421,115	-	2	2_A375_pNL97_plus_lncRNA_AR..1..8002, 2_A375_pNL97_plus_lncRNA_AR..1..8003	133319, -1513	in gene, upstream	0	1	0	16.5	21	10.5	2	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene GABBR2	GPR51, HRIHFB2099, FLJ36928, GPRC3B, GABABR2, HG20, GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	NM_005458, hCT2273704.0, hCT2273707.0, hCT2273709.0	209990_s_at, 209991_x_at, 211679_x_at, 217077_s_at	NP_005449.5, EAW58889.1, EAW58890.1, EAW58891.1
GeneID.85365	ALG2	9	101,978,707	101,984,246	5,539	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5559, 2_A375_pNL97_plus_lncRNA_AR..1..8004	193, -74	in gene, upstream	1	1	0	18	33	12	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene ALG2	NET38, FLJ14511, ALG2, hALPG2, CDGIi	asparagine-linked glycosylation 2, alpha-1,3-mannosyltransferase homolog (S. cerevisiae)	NM_033087, NR_024532, hCT21325.2, hCT2282517.0, hCT2282522.0, hCT2353370.0	225621_at, 226166_at	NP_149078.1, EAW58908.1, EAW58909.1, EAW58910.1, EAW58911.1
GeneID.10952	SEC61B	9	101,984,570	101,992,901	8,331	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5559, 2_A375_pNL97_plus_lncRNA_AR..1..8004	-517, -250	upstream, upstream	1	1	0	18	33	12	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene SEC61B	SEC61B		NM_006808, hCT1961554.1	203133_at, 244700_at	NP_006799.1, EAW58912.1
GeneID.8013	NR4A3	9	102,584,137	102,629,173	45,036	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5561, 2_A375_pNL97_plus_lncRNA_AR..1..8006, 2_A375_pNL97_plus_lncRNA_AR..1..8007, 2_A375_pNL97_plus_lncRNA_AR..1..8008, 4_A375_EGR1..1..8000	51943, -2313, -9, 51911, -41	downstream, upstream, upstream, downstream, upstream	1	1	1	15.33	18.67	10.67	3	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene NR4A3	CHN, NOR1, NR4A3, TEC, MINOR, CSMF	nuclear receptor subfamily 4, group A, member 3	NM_006981, NM_173199, NM_173200, hCT19909.3, hCT2282270.0, hCT2282272.0, hCT1984997.1	207978_s_at, 209959_at, 216979_at	NP_008912.2, NP_775291.1, NP_775292.1, EAW58916.1, EAW58917.1, EAW58918.1, EAW58915.1
GeneID.55014	STX17	9	102,668,915	102,736,818	67,903	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5562	189	in gene	1	0	0	15	12	12	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene STX17	MGC126613, MGC126615, STX17, MGC102798, FLJ20651	syntaxin 17	NM_017919, hCT2282280.0	218666_s_at, 222708_s_at	NP_060389.2, EAW58920.1
GeneID.23071	ERP44	9	102,741,461	102,861,330	119,869	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5563, 2_A375_pNL97_plus_lncRNA_AR..1..8009, 4_A375_EGR1..1..8001	-30, -110, -236	upstream, upstream, upstream	1	1	1	25	28	19	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene ERP44	ERP44, PDIA10, KIAA0573, TXNDC4	endoplasmic reticulum protein 44	NM_015051, hCT2353379.0, hCT1776381.2	208957_at, 208958_at, 208959_s_at	NP_055866.1, EAW58923.1, EAW58922.1
GeneID.27130	INVS	9	102,861,511	103,063,426	201,915	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5563, 2_A375_pNL97_plus_lncRNA_AR..1..8009, 4_A375_EGR1..1..8001	-151, -71, 57	upstream, upstream, in gene	1	1	1	25	28	19	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene INVS	NPH2, INV, INVS, KIAA0573, MGC133081, MGC133080, NPHP2	inversin	NM_183245, NM_014425, hCT19906.3, hCT2282263.0, hCT2282267.0	210114_at, 211054_at, 211055_s_at	NP_899068.1, NP_055240.2, EAW58924.1, EAW58925.1, EAW58926.1
GeneID.54881	TEX10	9	103,064,357	103,115,259	50,902	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8010	155	in gene	0	1	0	14	15	14	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene TEX10	bA208F1.2, FLJ31157, TEX10, FLJ20287, FLJ34350	testis expressed 10	NM_017746, NM_001161584, hCT19905.3, hCT2282483.0, hCT1961146.0	1558702_at, 218104_at	NP_060216.2, NP_001155056.1, EAW58927.1, EAW58928.1, EAW58929.1
GeneID.100507449	LOC100507449	9	103,115,318	103,116,360	1,042	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8010	-214	upstream	0	1	0	14	15	14	1	2_A375_pNL97_plus_lncRNA_AR..1	15	Gene LOC100507449		hypothetical LOC100507449	XR_113246, XR_108986, XR_114282		
GeneID.91283	C9orf30	9	103,189,642	103,213,513	23,871	+	2	2_A375_pNL97_plus_lncRNA_AR..1..8011, 4_A375_EGR1..1..8002	2150, 390	in gene, in gene	0	1	1	10	13	10.5	2	4_A375_EGR1..1	17	Gene C9orf30	L8, FLJ34973, C9orf30, MGC17337	chromosome 9 open reading frame 30	NM_080655, hCT19907.3, hCT2273892.0, hCT1840998.1	1552277_a_at	NP_542386.1, EAW58933.1, EAW58932.1, EAW58934.1
GeneID.54886	RP11-35N6.1	9	103,791,031	104,087,417	296,386	+	1	4_A375_EGR1..1..8003	-343	upstream	0	0	1	8	4	14	1	4_A375_EGR1..1	14	Gene RP11-35N6.1	MGC26189, PRG-3, LPPR1	lipid phosphate phosphatase-related protein type 1	NM_017753, NM_207299, hCT20174.2, hCT2273714.0, hCT2273716.0, hCT2273719.0	1570250_at, 219732_at	NP_060223.2, NP_997182.1, EAW58938.1, EAW58939.1, EAW58940.1, EAW58941.1
GeneID.54534	MRPL50	9	104,152,249	104,160,919	8,670	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8012	119	in gene	0	1	0	12	21	8	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MRPL50	MRPL50, FLJ20493, MRP-L50, FLJ21990	mitochondrial ribosomal protein L50	NM_019051, hCT1776756.2	225580_at, 225581_s_at	NP_061924.1, EAW58948.1
GeneID.7743	ZNF189	9	104,161,163	104,172,942	11,779	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8012	-363	upstream	0	1	0	12	21	8	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene ZNF189	ZNF189	zinc finger protein 189	NM_197977, NM_003452, hCT20169.3, hCT2273725.0	207513_s_at	NP_932094.1, NP_003443.2, EAW58949.1, EAW58950.1
GeneID.100507465	LOC100507465	9	104,231,661	104,243,788	12,127	+	2	2_A375_pNL97_plus_lncRNA_AR..1..8013, 4_A375_EGR1..1..8004	17187, 17635	downstream, downstream	0	1	1	19	15	21	1	4_A375_EGR1..1	21	Gene LOC100507465		hypothetical LOC100507465	XR_108987		
GeneID.84302	C9orf125	9	104,237,608	104,249,475	11,867	-	2	2_A375_pNL97_plus_lncRNA_AR..1..8013, 4_A375_EGR1..1..8004	627, 179	in gene, in gene	0	1	1	19	15	21	1	4_A375_EGR1..1	21	Gene C9orf125	MGC12992, C9orf125	chromosome 9 open reading frame 125	NM_032342, hCT1987489.1, hCT1640795.3	224456_at	NP_115718.1, EAW58954.1, EAW58953.1
GeneID.56254	RNF20	9	104,296,133	104,325,626	29,493	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8014	3195	in gene	0	1	0	13	20	8	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene RNF20	KIAA2779, BRE1A, hBRE1, MGC129667, FLJ11189, MGC129668, RNF20, BRE1, FLJ20382	ring finger protein 20	NM_019592, hCT20172.2, hCT2273420.0, hCT1980319.1	222683_at	NP_062538.5, EAW58957.1, EAW58955.1, EAW58956.1
GeneID.116443	GRIN3A	9	104,331,634	104,500,862	169,228	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5564, 1_A375_pNL7_minus_lncRNA_AR..1..5565, 2_A375_pNL97_plus_lncRNA_AR..1..8015, 2_A375_pNL97_plus_lncRNA_AR..1..8016	110254, 1678, 110286, 1662	in gene, in gene, in gene, in gene	1	1	0	17	23	7	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene GRIN3A	NR3A, NMDAR-L, GRIN3A, FLJ45414	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	NM_133445, hCT20173.3, hCT2274175.0, hCT2353365.0	233171_at, 233220_at	NP_597702.2, EAW58958.1, EAW58959.1, EAW58960.1
GeneID.10592	SMC2	9	106,856,541	106,903,700	47,159	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5567, 2_A375_pNL97_plus_lncRNA_AR..1..8019	-77, -173	upstream, upstream	1	1	0	15	23	11	1	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene SMC2	hCAP-E, FLJ10093, SMC2L1, CAPE, SMC2, CAP-E	structural maintenance of chromosomes 2	NM_006444, NM_001042550, NM_001042551, hCT2273649.0, hCT2273650.0, hCT2353371.0, hCT18766.2, hCT1984988.1	204240_s_at, 213253_at	NP_006435.2, NP_001036015.1, NP_001036016.1, EAW58975.1, EAW58976.1, EAW58977.1, EAW58973.1, EAW58974.1
GeneID.25934	NIPSNAP3A	9	107,509,969	107,522,403	12,434	+	2	2_A375_pNL97_plus_lncRNA_AR..1..8021, 4_A375_EGR1..1..8006	-193, 16351	upstream, downstream	0	1	1	11.5	16	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene NIPSNAP3A	MGC14553, DKFZp564D177, TASSC, HSPC299, FLJ13953, NIPSNAP3A, NIPSNAP4	nipsnap homolog 3A (C. elegans)	NM_015469, hCT1814660.1	224436_s_at	NP_056284.1, EAW58990.1
GeneID.55335	NIPSNAP3B	9	107,526,451	107,536,291	9,840	+	1	4_A375_EGR1..1..8006	-131	upstream	0	0	1	12	15	14	1	4_A375_EGR1..1	14	Gene NIPSNAP3B	FLJ11275, NIPSNAP3B, NIPSNAP3	nipsnap homolog 3B (C. elegans)	NM_018376, hCT2274229.0	221104_s_at, 223764_x_at	NP_060846.2, EAW58991.1
GeneID.23446	SLC44A1	9	108,006,929	108,153,682	146,753	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5569, 2_A375_pNL97_plus_lncRNA_AR..1..8023	-252, -273	upstream, upstream	1	1	0	14	24	18	1	2_A375_pNL97_plus_lncRNA_AR..1	24	Gene SLC44A1	CTL1, CD92, SLC44A1, CDW92, RP11-287A8.1, CHTL1	solute carrier family 44, member 1	NM_080546, hCT20211.4, hCT2274232.0, hCT2274233.0, hCT2274234.0, hCT1809244.1	224595_at, 224596_at, 228465_s_at, 228466_at	NP_536856.2, EAW58998.1, EAW58995.1, EAW58996.1, EAW58997.1, EAW58999.1
GeneID.83856	FSD1L	9	108,210,315	108,311,385	101,070	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5570, 2_A375_pNL97_plus_lncRNA_AR..1..8024, 4_A375_EGR1..1..8007	-235, -224, 110133	upstream, upstream, downstream	1	1	1	15	16.5	15	2	4_A375_EGR1..1	22	Gene FSD1L	MGC45564, FSD1NL, FSD1CL, FSD1L, CCDC10, CSDUFD1, MIR1	fibronectin type III and SPRY domain containing 1-like	NM_207647, NM_031919, NM_001145313, hCT1776426.2	223965_at, 230904_at, 242566_at, 242607_at	NP_997530.2, NP_114125.1, NP_001138785.1, EAW59000.1
GeneID.2218	FKTN	9	108,320,411	108,403,399	82,988	+	1	4_A375_EGR1..1..8007	37	in gene	0	0	1	13	14	22	1	4_A375_EGR1..1	22	Gene FKTN	MDDGA4, CMD1X, MGC138243, FCMD, MDDGC4, FKTN, MGC134945, LGMD2M, MGC134944, MDDGB4, MGC126657	fukutin	NM_001079802, NM_006731, hCT2274246.1	205263_at	NP_001073270.1, NP_006722.2, EAW59001.1
GeneID.5887	RAD23B	9	110,045,544	110,094,470	48,926	+	2	2_A375_pNL97_plus_lncRNA_AR..1..8027, 2_A375_pNL97_plus_lncRNA_AR..1..8028	24, 664	in gene, in gene	0	1	0	12.5	21	7	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene RAD23B	HR23B, P58, HHR23B, RAD23B	RAD23 homolog B (S. cerevisiae)	NM_002874, hCT2353391.0, hCT5699.2	201222_s_at, 201223_s_at, 223598_at	NP_002865.1, EAW59016.1, EAW59017.1
GeneID.9314	KLF4	9	110,247,133	110,252,047	4,914	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5573	911	in gene	1	0	0	14	12	11	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene KLF4	KLF4, GKLF, EZF	Kruppel-like factor 4 (gut)	NM_004235, hCT2274551.0, hCT2274553.0, hCT1776150.2	220266_s_at, 221841_s_at	NP_004226.3, EAW59019.1, EAW59020.1, EAW59021.1
GeneID.8518	IKBKAP	9	111,629,800	111,696,608	66,808	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5578, 2_A375_pNL97_plus_lncRNA_AR..1..8036, 2_A375_pNL97_plus_lncRNA_AR..1..8037	48352, 48352, 240	in gene, in gene, in gene	1	1	0	18	22	10	2	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene IKBKAP	FD, IKI3, IKAP, TOT1, IKBKAP, DKFZp781H1425, ELP1, FLJ12497, DYS	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	NM_003640, hCT20054.3, hCT2276660.0, hCT2276664.0, hCT1958819.1, hCT1958820.1	202490_at, 202491_s_at	NP_003631.2, EAW59029.1, EAW59027.1, EAW59028.1, EAW59030.1, EAW59031.1
GeneID.54942	C9orf6	9	111,696,673	111,703,238	6,565	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8037	-305	upstream	0	1	0	17	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene C9orf6	FLJ20457, CG-6, C9orf6	chromosome 9 open reading frame 6	NM_017632, hCT20057.3, hCT2353372.0, hCT1985001.1	218998_at	NP_060302.1, EAW59033.1, EAW59032.1, EAW59034.1
GeneID.8727	CTNNAL1	9	111,704,851	111,775,764	70,913	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8037	79396	downstream	0	1	0	17	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene CTNNAL1	CLLP, FLJ08121, CTNNAL1, alpha-CATU	catenin (cadherin-associated protein), alpha-like 1	NM_003798, hCT20055.2, hCT2276655.0, hCT2353392.0	202468_s_at	NP_003789.1, EAW59036.1, EAW59035.1, EAW59037.1
GeneID.23731	C9orf5	9	111,777,415	111,882,225	104,810	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8038	-83	upstream	0	1	0	12	28	12	1	2_A375_pNL97_plus_lncRNA_AR..1	28	Gene C9orf5	FLJ23668, CG-2, FLJ33224, C9orf5, CG2	chromosome 9 open reading frame 5	NM_032012, hCT2276650.1, hCT2276653.1	223005_s_at, 223006_s_at, 223007_s_at, 223008_s_at, 227831_at	NP_114401.2, EAW59039.1, EAW59038.1
GeneID.54566	EPB41L4B	9	111,934,254	112,083,021	148,767	-	2	2_A375_pNL97_plus_lncRNA_AR..1..8039, 4_A375_EGR1..1..8009	75933, 665	in gene, in gene	0	1	1	8	10.5	11	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene EPB41L4B	FLJ21596, EPB41L4B, DKFZp761N1814, CG1	erythrocyte membrane protein band 4.1 like 4B	NM_019114, NM_018424, hCT2276639.0, hCT2276641.0, hCT1776398.1, hCT1776399.2	220161_s_at, 220524_at, 223426_s_at, 223427_s_at, 223659_at, 233098_s_at	NP_061987.3, NP_060894.2, EAW59041.1, EAW59042.1, EAW59043.1, EAW59044.1
GeneID.5774	PTPN3	9	112,137,974	112,260,593	122,619	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5579, 1_A375_pNL7_minus_lncRNA_AR..1..5580, 2_A375_pNL97_plus_lncRNA_AR..1..8040, 2_A375_pNL97_plus_lncRNA_AR..1..8041	50641, 28129, 50577, 28033	in gene, in gene, in gene, in gene	1	1	0	19	18.5	5	2	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene PTPN3	PTPN3, DKFZp686N0569, PTPH1	protein tyrosine phosphatase, non-receptor type 3	NM_002829, NM_001145368, NM_001145369, NM_001145370, NM_001145371, NM_001145372, NR_026918, hCT2276634.0, hCT18732.3, hCT1958113.1	203997_at, 227944_at	NP_002820.3, NP_001138840.1, NP_001138841.1, NP_001138842.1, NP_001138843.1, NP_001138844.1, EAW59045.1, EAW59046.1, EAW59047.1
GeneID.114299	PALM2	9	112,403,068	112,713,756	310,688	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5581, 1_A375_pNL7_minus_lncRNA_AR..1..5582, 2_A375_pNL97_plus_lncRNA_AR..1..8042	125666, 175924, 125666	in gene, in gene, in gene	1	1	0	24.5	22.5	6.5	2	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene PALM2	AKAP2, PALM2	paralemmin 2	NM_001037293, NM_053016	1553502_a_at	NP_001032370.1, NP_443749.5
GeneID.445815	PALM2-AKAP2	9	112,542,577	112,934,792	392,215	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5582	36415	in gene	1	0	0	22	21	5	1	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene PALM2-AKAP2	AKAP2, PALM2-AKAP2, DKFZp686H1948	PALM2-AKAP2 readthrough	NM_147150, NM_007203		NP_671492.1, NP_009134.1
GeneID.7295	TXN	9	113,006,310	113,018,776	12,466	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5583, 2_A375_pNL97_plus_lncRNA_AR..1..8043	266, 186	in gene, in gene	1	1	0	20	17	15	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene TXN	DKFZp686B1993, TRX, TRX1, MGC61975, TXN	thioredoxin	NM_003329, hCT19918.2, hCT1961561.1	208864_s_at, 216609_at	NP_003320.2, EAW59060.1, EAW59059.1
GeneID.79987	SVEP1	9	113,127,528	113,342,160	214,632	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5584, 2_A375_pNL97_plus_lncRNA_AR..1..8044	668, 720	in gene, in gene	1	1	0	20	26	12	1	2_A375_pNL97_plus_lncRNA_AR..1	26	Gene SVEP1	FLJ90719, SELOB, CCP22, FLJ16013, C9orf13, POLYDOM, SVEP1, SEL-OB	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	NM_153366	1553129_at, 1566721_at, 1566722_a_at, 213247_at, 219552_at, 224543_at	NP_699197.3
GeneID.4593	MUSK	9	113,431,051	113,563,278	132,227	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5585	76373	in gene	1	0	0	18	9	2	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene MUSK	MGC126324, MGC126323, MUSK	muscle, skeletal, receptor tyrosine kinase	NM_005592, NM_001166280, NM_001166281, hCT19913.3, hCT2274214.0, hCT2274215.0	207632_at, 207633_s_at, 241122_s_at	NP_005583.1, NP_001159752.1, NP_001159753.1, EAW59065.1, EAW59066.1, EAW59067.1
GeneID.23392	KIAA0368	9	114,122,973	114,247,025	124,052	-	1	4_A375_EGR1..1..8010	337	in gene	0	0	1	13	15	14	1	4_A375_EGR1..1	14	Gene KIAA0368	ECM29, FLJ22036, KIAA0368, RP11-386D6.2, KIAA1962	KIAA0368	NM_001080398	212427_at, 212428_at, 214356_s_at, 236366_at	NP_001073867.1
GeneID.548645	DNAJC25	9	114,393,632	114,416,631	22,999	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5586, 2_A375_pNL97_plus_lncRNA_AR..1..8045	-96, -64	upstream, upstream	1	1	0	32	17	9	1	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene DNAJC25	bA16L21.2.1, DNAJC25	DnaJ (Hsp40) homolog, subfamily C, member 25	NM_001015882	226659_at	NP_001015882.2
GeneID.552891	DNAJC25-GNG10	9	114,393,666	114,432,509	38,843	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5586, 2_A375_pNL97_plus_lncRNA_AR..1..8045	-130, -98	upstream, upstream	1	1	0	32	17	9	1	1_A375_pNL7_minus_lncRNA_AR..1	32	Gene DNAJC25-GNG10	DNAJC25-GNG10		NM_004125		NP_004116.2
GeneID.158401	C9orf84	9	114,448,901	114,545,779	96,878	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8046	40067	in gene	0	1	0	13	20	1	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene C9orf84	FLJ44067, MGC43661, FLJ32779, C9orf84	chromosome 9 open reading frame 84	NM_173521, NM_001080551, hCT2277068.1, hCT2277069.1, hCT1848384.4	1553920_at, 233504_at	NP_775792.3, NP_001074020.1, EAW59088.1, EAW59089.1, EAW59090.1
GeneID.7357	UGCG	9	114,659,206	114,695,439	36,233	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5587	-374	upstream	1	0	0	18	13	13	1	1_A375_pNL7_minus_lncRNA_AR..1	18	Gene UGCG	UGCG, GLCT1, GCS	UDP-glucose ceramide glucosyltransferase	NM_003358, hCT18741.2, hCT1961553.1	204881_s_at, 221765_at, 224987_at	NP_003349.1, EAW59091.1, EAW59092.1
GeneID.84263	HSDL2	9	115,142,351	115,234,684	92,333	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8047	-239	upstream	0	1	0	11	18	14	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene HSDL2	FLJ25855, C9orf99, SDR13C1, MGC10940, HSDL2	hydroxysteroid dehydrogenase like 2	NM_032303, hCT19938.3, hCT2274346.0, hCT2353380.0, hCT1985000.1	1559126_at, 209512_at, 209513_s_at, 215436_at	NP_115679.2, EAW59106.1, EAW59104.1, EAW59105.1, EAW59107.1



Gene ID	Gene Name	Chr	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Positions	1_A375_2_A375_4_A375_1_A375_4_A375_4_A375_4_A375 Adj Reg Count	Peak Samples	Peak Values	UCSC Link	Alt symbols	Full Description	RNA	Ally Tag	PROT
GeneID:3597	CSu493	9	113,446,799	113,480,397	33,601	-	1	2_A375_shL97_plus_lncRNA_NR_1:8045	99	cs gene	0 1 0 13 17 13 1	2_A375_shL97_T_dist_lncRNA_NR_1	17	Gene CSu493	DSSR1, MSEE, HSPC343, CNv493, SOSSC, NSSBP1	chromosome 9 open reading frame 493	NM_031218, XCT177677.3	1990550_at, 223355_at, 223559_s_at	NP_597041.1, EAW69112.1
GeneID:4657	SNX30	9	115,510,154	115,637,297	124,153	+	2	1_A375_shL7_invari_lncRNA_NR_1:5565, 2_A375_EGR1_1:8511	-334, 335	upstream, cs gene	1 0 1 15 14.5 15.5 2	4_A375_EGR1_1	22	Gene SNX30	FLJ35509, FLJ45095, FLJ52350, MTMR2An1, FLJ44658, FLJ46577, FLJ39481, SNX30	sorting nexin family member 30	NM_031012994	229349_at	NP_001013212.1
GeneID:5594	SLC46A3	9	115,641,200	115,650,193	11,993	-	1	4_A375_EGR1_1:8012	817	cs gene	0 0 1 8 8 19 1	4_A375_EGR1_1	19	Gene SLC46A3	SLC46A2	solute carrier family 46, member 3	NM_033031, XCT203050.3, XCT229437.0, XCT195302.0	223516_at	NP_149040.3, EAW69352.1, EAW69353.1, EAW69351.1
GeneID:2307	FBP10	9	113,727,000	113,982,841	69,841	-	1	2_A375_shL97_plus_lncRNA_NR_1:8030	97	cs gene	0 1 0 11 21 8 1	2_A375_shL97_T_dist_lncRNA_NR_1	21	Gene FBP13	FBP13, KIAA0974, FBP10	FK506 binding protein 15, 133kDa	NM_015230	1568717_s_at, 212983_s_at, 242574_at, 31538_at, 76937_s_at	NP_694973.1
GeneID:1317	SLC31A1	9	113,983,600	116,026,772	42,964	+	1	2_A375_shL97_plus_lncRNA_NR_1:8030	-224	upstream	0 1 0 11 21 8 1	2_A375_shL97_T_dist_lncRNA_NR_1	21	Gene SLC31A1	COPT1, SLC31A1, MGC75457, XCT81, CTR1	solute carrier family 31 (copper transporters), member 1	NM_001436, XCT203455.0, XCT205451.0, XCT195155.1	202081_at, 235013_at, 235217_at	NP_001850.1, EAW67339.1, EAW67357.1, EAW67356.1
GeneID:2416	CDC26	9	116,029,268	116,037,999	8,851	-	2	2_A375_shL97_plus_lncRNA_NR_1:8031, 4_A375_EGR1_1:8014	77, -83	cs gene, upstream	0 1 1 23 22 21 1	2_A375_shL97_T_dist_lncRNA_NR_1	22	Gene CDC26	CDC26, ANAPC12, CSkv37, APC12	cell division cycle 26 homolog (S. cerevisiae)	NM_139266, XCT182379.1, XCT195139.1	223422_at	NP_644815.1, EAW67360.1, EAW67361.1
GeneID:5198	PRPF4	9	116,037,974	116,058,056	17,882	+	2	2_A375_shL97_plus_lncRNA_NR_1:8031, 4_A375_EGR1_1:8014	-182, -22	upstream, upstream	0 1 1 23 22 21 1	2_A375_shL97_T_dist_lncRNA_NR_1	22	Gene PRPF4	PRP4, PRPF4, HPRP4P, HPRP4, Prp4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	NM_004697, XCT203553.2, XCT195172.1	209181_at, 209182_s_at	NP_004688.2, EAW67362.1, EAW67363.1
GeneID:4947	WDR31	9	116,077,930	116,102,820	24,890	-	1	2_A375_shL97_plus_lncRNA_NR_1:8032	-96	upstream	0 1 0 16 23 13 1	2_A375_shL97_T_dist_lncRNA_NR_1	23	Gene WDR31	FLJ20921, WDR31	WD repeat domain 31	NM_001012981, NM_145241, XCT203352.3, XCT216621.0, XCT205971.0, XCT205972.0, XCT209772.0, XCT191171.1	229516_at, 241919_x_at	NP_001012981.1, NP_660256.1, EAW67366.1, EAW67370.1, EAW67371.1, EAW67373.1, EAW67369.1, EAW67372.1
GeneID:5398	BSPRY	9	116,111,812	116,132,513	21,701	+	1	2_A375_shL97_plus_lncRNA_NR_1:8032	-9124	upstream	0 1 0 16 23 13 1	2_A375_shL97_T_dist_lncRNA_NR_1	23	Gene BSPRY	BSPRY, FLJ20150	B-box and SPRY domain-containing	NM_017958, XCT205483	219782_s_at, 222748_s_at	NP_060128.2, EAW67374.1
GeneID:210	ALAD	9	116,140,592	116,160,616	15,026	-	2	1_A375_shL7_invari_lncRNA_NR_1:5360, 2_A375_shL97_plus_lncRNA_NR_1:8051	-9265, -9282	upstream, upstream	1 1 0 29 33 16 1	2_A375_shL97_T_dist_lncRNA_NR_1	33	Gene ALAD	PBGS, ALADH, ALAD, MGC5037	aminolevulinate, delta-, dehydratase	NM_000031, XCT205453.2, XCT216655.0	216437_at, 215459_s_at	NP_000022.2, EAW67379.1, EAW67550.1
GeneID:107	POLE3	9	116,169,315	116,172,029	2,814	-	2	1_A375_shL7_invari_lncRNA_NR_1:5360, 2_A375_shL97_plus_lncRNA_NR_1:8053	168, 149	cs gene, cs gene	1 1 0 29 33 16 1	2_A375_shL97_T_dist_lncRNA_NR_1	33	Gene POLE3	POLE3, CHRAC17, p17, CHRAC17, YBL1	polymerase (DNA directed), epsilon 3 (p17 subunit)	NM_017443, NR_027261, XCT203419.3, XCT216549.0	208926_at	NP_059139.3, EAW67381.1, EAW67382.1
GeneID:7189	CSku363	9	116,170,022	116,191,502	16,980	+	2	1_A375_shL7_invari_lncRNA_NR_1:5360, 2_A375_shL97_plus_lncRNA_NR_1:8053	-150, -142	upstream, upstream	1 1 0 29 33 16 1	2_A375_shL97_T_dist_lncRNA_NR_1	33	Gene CSku363	MGC17356, CSku163	chromosome 9 open reading frame 43	NM_152768, XCT205852.0, XCT205853.0, XCT204921.0, XCT205997.0	1554260_a_at	NP_689999.1, EAW67355.1, EAW67353.1, EAW67354.1, EAW67355.1
GeneID:9698	RGS3	9	116,207,011	116,280,018	183,007	+	1	4_A375_EGR1_1:8015	107533	downstream	0 0 1 10 12 17 1	4_A375_EGR1_1	17	Gene RGS3	FLJ40498, PDZ-RGS3, RGP3, RGS3, FLJ31184, FLJ20370, C2orf4	regulator of G-protein signaling 3	NM_134427, NM_138793, NM_021106, NM_017780, NM_144405, NM_144406, XCT203513.3, XCT216621.0, XCT216622.0, XCT216534.0, XCT216537.0, XCT216536.0, XCT216533.0, XCT203970.0, XCT221113.0, XCT191169.1, XCT191170.1, XCT191167.1	203223_at, 220300_at	NP_002915.1, NP_058612.2, NP_058629.1, NP_852738.3, NP_852739.1, NP_852786.2, EAW67357.1, EAW67358.1, EAW67359.1, EAW67360.1, EAW67361.1, EAW67362.1, EAW67363.1, EAW67364.1, EAW67365.1, EAW67366.1, EAW67367.1, EAW67368.1
GeneID:4991	ZNF816	9	116,838,362	116,916,975	160,213	+	2	4_A375_EGR1_1:8056, 4_A375_EGR1_1:8017	132334, 139102	cs gene, cs gene	0 0 1 5 8 17 2	4_A375_EGR1_1	19	Gene ZNF816	ZNF816, MGC10166, FP13186	zinc finger protein 816	NM_133374, XCT203855.0, XCT205839.0	236890_at, 235892_at, 235644_at	NP_598133.2, EAW67401.1, EAW67402.1
GeneID:2980	AMBP	9	116,922,407	116,940,732	18,345	-	1	4_A375_EGR1_1:8016	7387	cs gene	0 0 1 7 9 16 1	4_A375_EGR1_1	16	Gene AMBP	IATI, UTI, ITIL5, AMBP, p16, HCP, ITI, HEP2, EDC1, ITIL	alpha1-microglobulin/bikunin precursor	NM_001633, XCT116303.2	205477_s_at, 214425_at	NP_001624.1, EAW67404.1
GeneID:3301	COL27A1	9	116,918,351	117,072,973	154,744	+	7	1_A375_shL7_invari_lncRNA_NR_1:5361, 2_A375_shL97_plus_lncRNA_NR_1:8055, 4_A375_EGR1_1:8018, 4_A375_EGR1_1:8020, 4_A375_EGR1_1:8021, 4_A375_EGR1_1:8022, 4_A375_EGR1_1:8023	66103, 21617, 11877, 64430, 109306, 154851, 105129	cs gene, cs gene, cs gene, cs gene, cs gene, cs gene, cs gene	1 1 1 7.43 9 14.14 7	4_A375_EGR1_1	19	Gene COL27A1	MGC113327, COL27A1, KIAA1870, FLJ11955	collagen, type XXVII, alpha 1	NM_032888, XCT203839.1, XCT203831.1, XCT216331.1, XCT205946.0	1564000_at, 223292_at, 223293_s_at, 230803_at, 237452_at	NP_116277.2, EAW67411.1, EAW67412.1, EAW67413.1, EAW67414.1
GeneID:1930321	LOC100093521	9	117,699,547	117,699,893	9,348	+	1	2_A375_shL97_plus_lncRNA_NR_1:8056	-3289	upstream	0 1 0 11 16 8 1	2_A375_shL97_T_dist_lncRNA_NR_1	16	Gene LOC100093521	hypothetical LOC100093521	XR_112341, XR_108993, XR_114289			
GeneID:5445	TNFSF8	9	117,699,124	117,892,770	27,646	-	1	2_A375_shL97_plus_lncRNA_NR_1:8056	39652	downstream	0 1 0 11 16 8 1	2_A375_shL97_T_dist_lncRNA_NR_1	16	Gene TNFSF8	CD153, CD30L, HIGM2, TNFSF8, CD30L	tumor necrosis factor (ligand) superfamily, member 8	NM_001244, XCT210203.2, XCT216613.0	207218_at	NP_001235.1, EAW67433.1, EAW67432.1
GeneID:71	TNC	9	117,702,803	117,880,498	177,695	-	3	1_A375_shL7_invari_lncRNA_NR_1:5363, 2_A375_shL97_plus_lncRNA_NR_1:8057, 2_A375_shL97_plus_lncRNA_NR_1:8058	6876, 6862, 38	cs gene, cs gene, cs gene	1 1 0 30.3 34.3 19.5 2	2_A375_shL97_T_dist_lncRNA_NR_1	34	Gene TNC	GMEM, MGC102929_2, HXB, 225-225, J1-TNC, TN-C, HXB, TN	tenascin C	NM_002160, XCT210193.2, XCT195174.1	201645_at, 210833_at	NP_002151.2, EAW67435.1, EAW67434.1
GeneID:3145	DEC1	9	117,859,097	118,196,923	360,826	+	3	1_A375_shL7_invari_lncRNA_NR_1:5364, 2_A375_shL97_plus_lncRNA_NR_1:8059, 2_A375_shL97_plus_lncRNA_NR_1:8060	237711, 120983, 237711	cs gene, cs gene, cs gene	1 1 0 15 19 9 2	2_A375_shL97_T_dist_lncRNA_NR_1	19	Gene DEC1	DEC1, CTS9	deleted in esophageal cancer 1	NM_017418, XCT210182.0, XCT102248.1	220701_at	NP_059114.1, EAW67437.1, EAW67438.1
GeneID:2345	ASTN2	9	119,157,504	120,177,317	999,812	+	4	1_A375_shL7_invari_lncRNA_NR_1:5367, 2_A375_shL97_plus_lncRNA_NR_1:8061, 2_A375_shL97_plus_lncRNA_NR_1:8064, 2_A375_shL97_plus_lncRNA_NR_1:8065	668707, 719453, 668725, 741	cs gene, cs gene, cs gene, cs gene	1 1 1 12.67 12.33 6.33 3	2_A375_shL97_T_dist_lncRNA_NR_1	17	Gene ASTN2	ASTN2, MART6.19.1, SNAP45A	astrotactin 2	NM_001164734, NM_001164735, NM_014810, NM_198186, NM_198187, NM_198188, XCT240935.0	1554618_at, 229992_at, 213407_s_at, 1570293_s_at, 1570292_at	NP_001139663.1, NP_001171666.1, NP_937851.1, NP_954729.2, NP_937852.1, NP_001182.2, EAW67444.1
GeneID:3554	TRIM22	9	119,449,561	119,480,379	13,998	+	1	2_A375_shL97_plus_lncRNA_NR_1:8063	11263	cs gene	0 1 0 13 15 10 1	2_A375_shL97_T_dist_lncRNA_NR_1	15	Gene TRIM22	RNF94, TRIM22, TATIP, IGMD2A, IFP53	tripartite motif-containing 22	NM_001098878, NM_012210, XCT183303.2, XCT196120.1	203546_at, 236223_at	NP_001092615.1, NP_008842.2, EAW67447.1, EAW67447.1
GeneID:7099	TLR4	9	120,466,460	120,479,766	13,306	+	1	1_A375_shL7_invari_lncRNA_NR_1:5369	-572	upstream	1 1 0 17 10 5 1	1_A375_shL7_invari_lncRNA_NR_1	17	Gene TLR4	ARD1B, TLR4, CD284, ARD1HQ, TOLL	toll-like receptor 4	NR_039189, NR_039190, NM_138554	1552795_s_at, 224581_x_at, 242085_s_at	NP_612564.1
GeneID:2080	DBC1	9	121,508,903	122,131,709	622,807	-	1	2_A375_shL97_plus_lncRNA_NR_1:8066	-1481	upstream	0 1 0 9 14 5 1	2_A375_shL97_T_dist_lncRNA_NR_1	14	Gene DBC1	DBC1, FAM68A, DBC1	deleted in bladder cancer 1	NM_014618, XCT210158.0, XCT195166.0	1558437_at, 208518_at	NP_055433.2, EAW67456.1, EAW67455.1
GeneID:7555	CDK5RAP2	9	122,191,147	122,242,437	101,290	-	2	1_A375_shL7_invari_lncRNA_NR_1:5662, 2_A375_shL97_plus_lncRNA_NR_1:8067	176677, 176801	cs gene, cs gene	1 1 0 44 49 7 1	2_A375_shL97_T_dist_lncRNA_NR_1	49	Gene CDK5RAP2	DKFZp686D10170, Cep215, DKFZp686B0170, CDK5RAP2, MCPH3, KIAA1853, C46	CDK5 regulatory subunit associated protein 2	NM_018249, NM_001011649, XCT210649.1, XCT210650.1, XCT210652.1, XCT209993.0, XCT209994.0, XCT209995.0, XCT210653.1, XCT195307.2	220933_s_at, 223943_s_at, 224562_at, 237416_at, 243153_at	NP_060719.4, NP_001011649.1, EAW67450.1, EAW67449.1, EAW67451.1, EAW67452.1, EAW67453.1
GeneID:2967	FBXW2	9	123,219,234	123,235,743	58,466	-	1	4_A375_EGR1_1:8026	105	cs gene	0 0 1 16 20 17 1	4_A375_EGR1_1	17	Gene FBXW2	W98, Fwd2, FBW2, MGC117371, FBG402	F-box and WD repeat domain containing 2	NM_012164, XCT197163	1560752_at, 209550_s_at, 210941_s_at, 233195_at, 241798_at	NP_036292.2, EAW67470.1
GeneID:1029842	LOC100269942	9	123,508,773	123,581,009	72,236	+	1	4_A375_EGR1_1:8026	-143	upstream	0 0 1 16 20 17 1	4_A375_EGR1_1	17	Gene LOC100269942	KIAA0072, DKFZp313G0129	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 pseudogene	NR_027442		
GeneID:11	PSMD8	9	123,578,331	123,609,208	30,878	-	2	1_A375_shL7_invari_lncRNA_NR_1:5663, 2_A375_shL97_plus_lncRNA_NR_1:8068	-202, -74	upstream, upstream	1 1 0 16 16 15 1	2_A375_shL97_T_dist_lncRNA_NR_1	16	Gene PSMD8	KIAA0072, S18, MGC23149, PSMD8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	NM_002647, XCT213062.2	203447_at, 215848_at	NP_002638.1, EAW67471.1
GeneID:5039	LOC283539	9	123,606,320	123,616,651	11,331	+	2	1_A375_shL7_invari_lncRNA_NR_1:5663, 2_A375_shL97_plus_lncRNA_NR_1:8069	-55, -40	cs gene, upstream	1 1 0 16 16 15 1	2_A375_shL97_T_dist_lncRNA_NR_1	16	Gene LOC283539	DKFZp727C191	hypothetical LOC283539	NR_024456	1555892_s_at, 231626_at, 239956_at, 241369_at	
GeneID:147	PHF19	9	123,617,551	123,639,008	21,873	-	3	1_A375_shL7_invari_lncRNA_NR_1:5664, 2_A375_shL97_plus_lncRNA_NR_1:8069, 2_A375_shL97_plus_lncRNA_NR_1:8070	632, 1153, 554	cs gene, cs gene, upstream	1 1 0 13.5 16.5 11 2	2_A375_shL97_T_dist_lncRNA_NR_1	19	Gene PHF19	MGC149712, MGC131989, MTF2L1, PHF19, PCL3, MGC149713, MGC22929	PHD finger protein 19	NM_015651, NM_001007838, XCT210003.2, XCT217010.0, XCT217012.0, XCT217010.1	223503_at, 227211_at, 227212_s_at	NP_056466.1, NP_001005938.1, EAW67475.1, EAW67476.1, EAW67477.1, EAW67478.1
GeneID:55	TRAF1	9	123,699,871	123,891,431	39,760	+	4	1_A375_shL7_invari_lncRNA_NR_1:5665, 1_A375_shL7_invari_lncRNA_NR_1:5666, 2_A375_shL97_plus_lncRNA_NR_1:8071, 2_A375_shL97_plus_lncRNA_NR_1:8072	18193, 8547, 18193, 9627	cs gene, cs gene, cs gene, cs gene	1 1 0 23 22.5 10 2	2_A375_shL97_T_dist_lncRNA_NR_1	27	Gene TRAF1	EBS, MGC10353, TRAF1	TNF receptor-associated factor 1	NM_031190945, NM_031190947, NM_005658	205359_at, 233116_at	NP_031177874.1, NP_001177878.1, NP_005649.1, EAW67479.1
GeneID:3	C5	9	123,716,813	123,812,554	97,941	-	1	2_A375_shL97_plus_lncRNA_NR_1:8073	99570	downstream	0 1 0 10 17 2 1	2_A375_shL97_T_dist_lncRNA_NR_1	17	Gene C5	MGC142295, FLJ17522, CHAIDS4, FLJ17516, C5	complement component 5	NM_001735, XCT213804.3	205500_at	NP_001726.2, EAW67480.1
GeneID:552	RAB14	9	123,840,413	123,869,265	23,950	-	1	1_A375_shL7_invari_lncRNA_NR_1:5667	-19	upstream	1 1 0 3 24 16 1	1_A375_shL7_invari_lncRNA_NR_1	24	Gene RAB14	RAB14, FEF, RAB-14	RAB14, member RAS oncogene family	NM_016322, XCT213802.2, XCT195173.1	209677_s_at, 209928_s_at, 211803_s_at	NP_057406.2, EAW67486.1, EAW67487.1
GeneID:54	GSN	9	124,830,592	124,905,120	84,740	+	2	1_A375_shL7_invari_lncRNA_NR_1:5668, 2_A375_shL97_plus_lncRNA_NR_1:8076	10676, 14084	cs gene, cs gene	1 1 0 16 16.5 6 2	1_A375_shL7_invari_lncRNA_NR_1	16	Gene GSN	DKFZp313G0716, GSN	gelsolin (amyloidosis, Finnish type)	NM_198252, NM_000177, NM_001127662, NM_001127663, NM_001127664, NM_001127665, NM_001127666, NM_001127667, XCT195146.2, XCT195146.1, XCT195146.2	200696_s_at, 214043_s_at	NP_570915.1, NP_000166.1, NP_001121154.1, NP_001121155.1, NP_001121156.1, NP_001121157.1, NP_001121158.1, NP_001121159.1, EAW67490.1, EAW67491.1, EAW67492.1
GeneID:1930299	LOC100129084	9	124,842,106	124,849,119	6,933	-	2	1_A375_shL7_invari_lncRNA_NR_1:5668, 2_A375_shL97_plus_lncRNA_NR_1:8076	6083, 4755	downstream, cs gene	1 1 0 16 16.5 6 2	1_A375_shL7_invari_lncRNA_NR_1	16	Gene LOC100129084	hypothetical LOC100129084	NM_001271474, XM_001717911, XM_001725577		AP_001714.5, XP_001717963.1, XP_001725629.1
GeneID:7038	STOM	9	124,101,353	124,132,545	31,192	-	3	1_A375_shL7_invari_lncRNA_NR_1:5671, 2_A375_shL97_plus_lncRNA_NR_1:8077, 4_A375_EGR1_1:8026	-1023, -1033, 129	upstream, upstream, cs gene	1 1 1 93 85 16 1	1_A375_shL7_invari_lncRNA_NR_1	93	Gene STOM	STOM, BND7, SPB7, SPB7.2	Stomatin	NM_198194, NM_004099, XCT213901.2, XCT217294.0	201060_x_at, 201061_s_at, 201062_at	NP_937837.1, NP_004090.4, EAW67493.1, EAW67494.1
GeneID:8133	TTLL11	9	124,264,204	124,638,065	377,861	-	3	1_A375_shL7_invari_lncRNA_NR_1:5672, 1_A375_shL7_invari_lncRNA_NR_1:5673, 2_A375_shL97_plus_lncRNA_NR_1:8078, 2_A375_shL97_plus_lncRNA_NR_1:8079, 2_A375_shL97_plus_lncRNA_NR_1:8080	121069, 553, 121003, 517, 699	cs gene, cs gene, cs gene, cs gene	1 1 0 22.3 19 11 2	1_A375_shL7_invari_lncRNA_NR_1	22	Gene TTLL11	TTLL11, MGC40490.1, C9orf20	tubulin tyrosine ligase-like family, member 11	NM_174332, NM_001139442, XCT203082.2, XCT216539.0, XCT205979.0, XCT160041.3	231157_at, 242543_at	NP_776093.2, NP_001129914.1, EAW67505.1, EAW67507.1, EAW67509.1, EAW67508.1
GeneID:1550	C9orf14	9	124,648,690	124,725,998	79,108	-	2	1_A375_shL7_invari_lncRNA_NR_1:5672, 2_A375_shL97_plus_lncRNA_NR_1:8078	-6816, -6882	upstream, upstream	1 1 0 20 14 7 1	1_A375_shL7_invari_lncRNA_NR_1	20	Gene C9orf14	C9orf14	chromosome 9 open reading frame 140	XR_108994, XR_114290	1559040_at	
GeneID:5742	PTGS1	9	125,133,229	125,157,901	24,732	+	2	1_A375_shL7_invari_lncRNA_NR_1:5674, 2_A375_shL97_plus_lncRNA_NR_1:8080	31731, 31557	downstream, downstream	1 1 0 19 16 9 1	1_A375_shL7_invari_lncRNA_NR_1	19	Gene PTGS1	ECH3, PTGHS, PTGS1, PGS/PTS, PHS1, PGHS1, PCOX1, COX1, PGHS-1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	NM_000962, NM_080591, XCT222213.3, XCT196126.1	202127_at, 205125_x_at, 215815_s_at, 233699_at	NP_000953.2, NP_542187.1, EAW67529.1, EAW67530.1
GeneID:942	RCSH2	9	125,811,732	125,867,582	55,850	-	3	1_A375_shL7_invari_lncRNA_NR_1:5674, 2_A375_shL97_plus_lncRNA_NR_1:8082, 2_A375_shL97_plus_lncRNA_NR_1:8083	-190, -276, 10	upstream, upstream, cs gene	1 1 1 17 17 22 1	4_A375_EGR1_1	22	Gene RCSH2	RNF194, RCSH2, FLJ38351, FLJ39111, bA448.2, MGC32176	ring finger and CSH2-like domains 2	NM_001105565, NM_018053, XCT222217.2, XCT217039.0, XCT217041.0, XCT217042.0, XCT190620.1	220281_at, 220282_s_at, 223013_at, 223014_x_at, 231716_at, 235421_at	NP_001098035.1, NP_060523.2, EAW67545.1, EAW67546.1, EAW67547.1, EAW67548.1, EAW67549.1, EAW67550.1, EAW67551.1, EAW67547.1
GeneID:7713	ZBTB8	9	125,870,555	125,875,609	5,274	-	3	1_A375_shL7_invari_lncRNA_NR_1:5676, 2_A375_shL97_plus_lncRNA_NR_1:8082, 4_A375_EGR1_1:8033	7987, 7969, 6030	downstream, downstream, downstream	1 1 1 17 17 22 1	4_A375_EGR1_1	22	Gene ZBTB8	ZNF482, ZBC, MGC10826	zinc finger and BTB domain containing 8	NM_030628, XCT222123.3	208696_at	NP_598117.1, EAW67552.1
GeneID:8564	ZBTB28	9	125,880,378	125,890,779	10,401	-	2	1_A375_shL7_invari_lncRNA_NR_1:5677, 2_A375_shL97_plus_lncRNA_NR_1:8083	-209, -173	upstream, upstream	1 1 0 19 25 13 1	2_A375_shL97_T_dist_lncRNA_NR_1	25	Gene ZBTB28	KIAA1372, bcl-6B, ZNF451, ZBTB28	BTB (POZ) domain containing 28	NM_020924	1554072_s_at, 227162_at	NP_065975.1
GeneID:9834	RABGAP1	9	125,702,266	125,887,147	160,639	+	2	1_A375_shL7_invari_lncRNA_NR_1:5677, 2_A375_shL97_plus_lncRNA_NR_1:8083	-9334, -9338	upstream, upstream	1 1 0 19 25 13 1	2_A375_shL97_T_dist_lncRNA_NR_1	25	Gene RABGAP1	RAP1-1 GTPase activating protein, GAPGAP1, TBC1D11, DKFZp686G0123	RAB GTPase activating protein 1	NM_012197, XCT210738.1, XCT210737.1, XCT210736.1, XCT216723.1, XCT203074.0	204425_s_at, 212303_at, 212970_x_at	NP_036229.2, EAW67556.1, EAW67555.1, EAW67557.1
GeneID:5862	CRB2	9	126,116,445	126,141,022	22,364	+	2	4_A375_EGR1_1:8034, 4_A375_EGR1_1:8035	9940, 15248	cs gene, cs gene	0 0 1 5.5 7.5 19 2	4_A375_EGR1_1	23	Gene CRB2	FLJ38464, CRB2, FLJ41016	crumbs homolog 2 (Drosophila)	NM_173689, XCT233108.0, XCT187144.1, FLJ16709	1552306_at	NP_775960.4, EAW67566.1, EAW67567.1
GeneID:3706	DENND1A	9	126,141,933	126,892,417	750,484	-	3	1_A375_shL7_invari_lncRNA_NR_1:5678, 2_A375_shL97_plus_lncRNA_NR_1:8084, 2_A375_shL97_plus_lncRNA_NR_1:8085	1921, 1955, 538721	cs gene, cs gene, downstream	1 1 1 13.5 12.5 10 2	4_A375_EGR1_1	23	Gene DENND1A	DENND1A, FLJ30464, RP11-235J22.3, KIAA1805, FAM31A	DENN/MADD domain containing 1A	NM_020946, NM_024620, XCT217048.2, XCT217047.2, XCT231080.0, XCT237084.0, XCT237083.0, XCT191224.4, XCT193203.2	210765_at, 226569_at	NP_065997.1, NP_078966.2, EAW67569.1, EAW67570.1, EAW67572.1, EAW67573.1, EAW67571.1, EAW67574.1, EAW67575.1



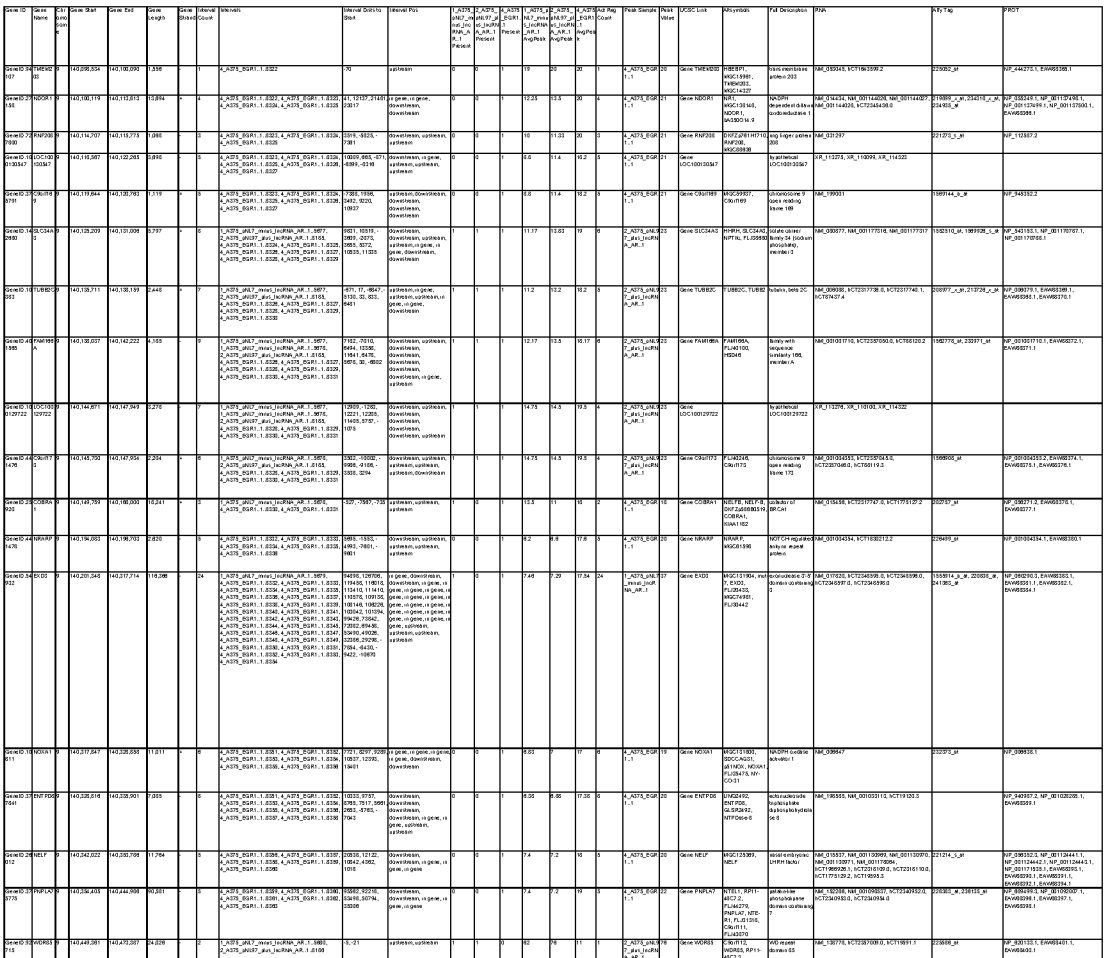
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distribution	Interval Position	f_A375_2_A375_shN7_ex_inc_lncRNA_R_1 Percent	f_A375_2_A375_shN7_ex_lncRNA_R_1 Percent	f_A375_shN7_ex_lncRNA_R_1 Percent	f_A375_pLKO_shN7_ex_lncRNA_R_1 Avg Peak	f_A375_pLKO_shN7_ex_lncRNA_R_1 Avg Peak	f_A375_EGFR_1 Avg Peak	Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbol	Full Description	RNA	Alt Tag	PROT
GeneID:1019783	NENF	9	127,019,555	127,134,721	94,836	+	2	A_A375_EGFR:1...8558, A_A375_EGFR:1...8037	74051, 69011	cr gene, cr gene	0	0	1	5.5	7	17.5	2	A_A375_EGFR_1...1	16	Gene NENF	NENF, SIDE-1512	NMA (neurotrophin and retinoic gene X)-related kazrin-B	NM_031143031, NM_014297, NM_001166187, NM_001166189, NM_001166190, NM_001166171, XM_005273...5, XM_005273072.2, XM_005273070.0, XM_017961411.3	223150_s_at, 223153_s_at, 223151_x_at, 223361_at, 237761_at, 239387_at	NP_001135713.1, NP_005212.2, NP_001139231.1, NP_001139843.1, NP_001139841.1, NP_001139842.1, NP_001139843.1, EAW67876.1, EAW67880.1, EAW67881.1
GeneID:5867	PSMB7	9	127,115,744	127,177,721	61,977	-	4	f_A375_shN7_mrset_lncRNA_R...5820, f_A375_shN7_mrset_lncRNA_R...3621, f_A375_shN37_dlet_lncRNA_R...8056, f_A375_EGFR_1...8037	22295, -155, -128, 60825	cr gene, upstream, upstream, downstream	1	1	1	17	11.33	5.67	3	f_A375_shN7_mrset_lncRNA_R...1	21	Gene PSMB7	PSMB7_2	proteasome (prosome, macropain) subunit, beta type, 7	NM_002799, NC_018931.2, NT_187661.1	202658_at, 244851_at	NP_002790.1, EAW67852.1, EAW67853.1
GeneID:1012930234	LOC101929034	9	127,115,752	127,121,465	5,713	+	1	A_A375_EGFR:1...8037	-5656	upstream	0	0	1	11	8	17	1	A_A375_EGFR_1...1	17	Gene LOC101929034		hypothetical LOC101929034	NR_027408		
GeneID:3467096	GPR144	9	127,213,423	127,239,379	25,956	+	2	A_A375_EGFR:1...8038, A_A375_EGFR:1...8039	17529, 20521	cr gene, downstream	0	0	1	5.5	8	14	2	A_A375_EGFR_1...1	19	Gene GPR144	PGR24, GPR144	G protein-coupled receptor 144	NM_001161935, NC_018916.2, NC_724.57961.1, NC_724.91164, NC_724.91165.2, NC_724.91166.2	216269_at	NP_001155265.1, EAW67856.1, EAW67857.1, EAW67858.1, EAW67859.1, EAW67860.1, EAW67861.1
GeneID:2316	NR3A1	9	127,243,515	127,289,699	46,184	-	2	A_A375_EGFR:1...8039, A_A375_EGFR:1...8040	37659, 99	downstream, cr gene	0	0	1	7	7.5	10.5	2	A_A375_EGFR_1...1	20	Gene NR3A1	ELF_SF1, FTZ1, NR4A1, FOF7, NR3A1, FTZF1, SF-1	steroid receptor subfamily 3, group A, member 1	NM_004959, NC_018927.2	210333_at	NP_004950.2, EAW67859.1
GeneID:2816949	NR6A1	9	127,356,703	127,532,576	644,874	+	3	f_A375_shN7_mrset_lncRNA_R...5822, f_A375_shN37_dlet_lncRNA_R...8093, A_A375_EGFR:1...8041	-152, -152, 1160	upstream, upstream, cr gene	1	1	1	27.5	22.5	10.5	2	f_A375_shN7_mrset_lncRNA_R...1	16	Gene NR6A1	NR6A1, GCNF, RTR, GCNF1, NR61	nuclear receptor subfamily 6, group A, member 1	NM_033334, NM_001489, NC_018933.2, NC_724.91165.2, NC_724.91166.2	207742_s_at, 210391_at, 210392_s_at, 214402_x_at	NP_001991.2, NP_001482.3, EAW67893.1, EAW67894.1, EAW67895.1
GeneID:1019339617	LOC101933617	9	127,532,402	127,535,206	2,804	+	3	f_A375_shN7_mrset_lncRNA_R...5822, f_A375_shN37_dlet_lncRNA_R...8093, A_A375_EGFR:1...8041	-1206, -1206, 14	cr gene, cr gene, cr gene	1	1	1	27.5	22.5	10.5	2	f_A375_shN7_mrset_lncRNA_R...1	16	Gene LOC101933617		hypothetical LOC101933617	XR_193999, XR_114292		
GeneID:1019611	OLFML2A	9	127,539,407	127,577,181	37,774	+	3	f_A375_shN7_mrset_lncRNA_R...5822, f_A375_shN37_dlet_lncRNA_R...8093, A_A375_EGFR:1...8041	-9709, -9709, -7021	upstream, upstream, upstream	1	1	1	27.5	22.5	10.5	2	f_A375_shN7_mrset_lncRNA_R...1	16	Gene OLFML2A	PRO34319, FLJ00237, OLFML2A	oligoctomedin-like 2A	NM_182497, XC_723169931.1, XC_723169932.1	213879_at	NP_872293.2, EAW67896.1, EAW67897.1
GeneID:4551	WDR36	9	127,815,755	127,830,160	14,405	+	4	f_A375_shN7_mrset_lncRNA_R...5823, f_A375_shN37_dlet_lncRNA_R...8093, A_A375_EGFR:1...8044, A_A375_EGFR:1...8045	6437, 6845, 2537, 6277	downstream, downstream, cr gene, downstream	1	1	1	16.5	16	21	2	A_A375_EGFR_1...1	22	Gene WDR36	WDR36	WD repeat domain 36	NM_001045478	242900_at, 244109_at	NP_001038941.1
GeneID:11724	RFL13	9	127,830,190	127,834,240	4,052	-	5	f_A375_shN7_mrset_lncRNA_R...5823, f_A375_shN37_dlet_lncRNA_R...8093, A_A375_EGFR:1...8044, A_A375_EGFR:1...8045, A_A375_EGFR:1...8046	-46, -180, 6126, 206, -7898	cr gene, upstream, downstream, cr gene, upstream	1	1	1	15	17	22.67	3	A_A375_EGFR_1...1	26	Gene RFL13	RFL13, L13	ribosomal protein L13	NM_007209, XC_723170597.1, XC_723170361.1, XC_723170591.1	200002_at	NP_009140.1, EAW67902.1, EAW67903.1, EAW67901.1
GeneID:5563	ARPC5L	9	127,831,454	127,839,696	8,242	+	4	f_A375_shN7_mrset_lncRNA_R...5823, f_A375_shN37_dlet_lncRNA_R...8093, A_A375_EGFR:1...8045, A_A375_EGFR:1...8046	-7392, -7056, -7432, 452	upstream, upstream, upstream, cr gene	1	1	1	16.5	16	24	2	A_A375_EGFR_1...1	26	Gene ARPC5L	ARPC5L, ARC16-2, MGC3656	actin related protein 2/3 complex, subunit 5-like	NM_030978, XC_723035.4, XC_724165.5	220995_s_at, 223101_s_at, 220914_at, 220915_s_at	NP_112245.1, EAW67904.1, EAW67905.1, EAW67903.1
GeneID:2300	GOLGA1	9	127,840,373	127,870,399	30,013	-	3	f_A375_shN7_mrset_lncRNA_R...5824, f_A375_shN37_dlet_lncRNA_R...8091, A_A375_EGFR:1...8046	-30, 90, 71455	upstream, cr gene, downstream	1	1	1	15.5	16	19.5	2	A_A375_EGFR_1...1	26	Gene GOLGA1	GOLGA1, golgin 97, MGC3154	golgi autoantigen, golgin subfamily a, 1	NM_002077, XC_723170594.1, XC_724165.3	203283_s_at, 203284_s_at, 214497_at	NP_002066.1, EAW67906.1, EAW67907.1
GeneID:2405	SCAI	9	127,794,557	127,909,635	200,991	-	2	f_A375_shN7_mrset_lncRNA_R...5824, f_A375_shN37_dlet_lncRNA_R...8091	202414, 202542	downstream, downstream	1	1	0	19	17	10	1	f_A375_shN7_mrset_lncRNA_R...1	19	Gene SCAI	MGC120325, NET40, C9orf126, SCAI, FLJ59994, FLJ11755, MGC120323, MGC120328	suppressor of cancer cell invasion	NM_175990, NM_001144077, XC_724449.63, XC_724449.6	241784_at	NP_779991.2, NP_001138549.1, EAW67909.1, EAW67909.1
GeneID:5587	PPP6C	9	127,908,552	127,932,216	43,366	-	3	f_A375_shN7_mrset_lncRNA_R...5825, f_A375_shN37_dlet_lncRNA_R...8092, A_A375_EGFR:1...8047	-6, 55, 570	upstream, cr gene, cr gene	1	1	1	21	20	17	1	f_A375_shN7_mrset_lncRNA_R...1	21	Gene PPP6C	PPP6C, MGC12249, FLJ25842, PP6	protein phosphatase 6, catalytic subunit	NM_002721, NM_001122355, NM_001122389, XC_724449.62, XC_724449.6	200529_at, 200574_s_at	NP_002712.1, NP_001116627.1, NP_001116641.1, EAW67911.1, EAW67912.1, EAW67913.1
GeneID:5884	RABEPK	9	127,962,621	127,990,436	33,817	+	2	A_A375_EGFR:1...8092, A_A375_EGFR:1...8048	41871, 40721	downstream, downstream	0	1	1	16	21	22	1	A_A375_EGFR_1...1	22	Gene RABEPK	ipd1, RABEP1, D9F2a6BBP107, RABBN2, bnN3N12.1	Rab9 effector protein with leucine zipper motifs	NM_031734.62, NM_001114183, NM_203403, XC_724449.62, XC_724449.6	1559021_at, 202150_at	NP_001182121.1, NP_001182124.1, NP_008824.2, EAW67914.1, EAW67917.1, EAW67918.1, EAW67919.1, EAW67916.1
GeneID:3359	HSPA5	9	127,997,127	128,002,661	5,534	-	2	A_A375_EGFR:1...8093, A_A375_EGFR:1...8046	249, 109	cr gene, cr gene	0	1	1	16	21	22	1	A_A375_EGFR_1...1	22	Gene HSPA5	BiP, MIF2, HSPA5, GRP78, FLJ26106	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	NM_005347, XC_723182.6, XC_724165.3	211936_at, 200931_at	NP_005338.1, EAW67920.1, EAW67921.1
GeneID:2630	GAPVD1	9	128,026,111	128,127,290	103,179	+	3	f_A375_shN7_mrset_lncRNA_R...5826, f_A375_shN37_dlet_lncRNA_R...8094, A_A375_EGFR:1...8049	145, 177, 139	cr gene, cr gene, cr gene	1	1	1	16	20	16	1	2_A375_shN7_dlet_lncRNA_AR...1	20	Gene GAPVD1	MGC135567, MGC135568, RAP6, KIAA1521, GAPVD1, DKFZp434C212, GAP6X3	GTPase activating protein and VPS9 domains 1	NM_019555, XC_723027.3, XC_721169942.1, XC_724165.3, XC_724165.4, XC_724165.5, XC_724165.6, XC_724165.7, XC_724165.8, XC_724165.9, XC_724165.10, XC_724165.11, XC_724165.12, XC_724165.13, XC_724165.14, XC_724165.15, XC_724165.16, XC_724165.17, XC_724165.18, XC_724165.19, XC_724165.20, XC_724165.21, XC_724165.22, XC_724165.23, XC_724165.24, XC_724165.25, XC_724165.26, XC_724165.27, XC_724165.28, XC_724165.29, XC_724165.30, XC_724165.31, XC_724165.32, XC_724165.33, XC_724165.34, XC_724165.35, XC_724165.36, XC_724165.37, XC_724165.38, XC_724165.39, XC_724165.40, XC_724165.41, XC_724165.42, XC_724165.43, XC_724165.44, XC_724165.45, 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XC_724165.974, XC_724165.975, XC_724165.976, XC_724165.977, XC_724165.978, XC_724165.979, XC_724165.980, XC_724165.981, XC_724165.982, XC_724165.983, XC_724165.984, XC_724165.985, XC_724165.986, XC_724165.987, XC_724165.988, XC_724165.989, XC_724165.990, XC_724165.991, XC_724165.992, XC_724165.993, XC_724165.994, XC_724165.995, XC_724165.996, XC_724165.997, XC_724165.998, XC_724165.999, XC_724165.1000			

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:389791	LOC389791	9	130,890,808	130,892,913	2,105	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5631, 2_A375_pNL97_plus_lncRNA_AR..1..8109, 4_A375_EGR1..1..8066	-760, -760, -184	upstream, upstream, upstream	1	1	1	32	33	19	1	2_A375_pNL97_plus_lncRNA_AR..1	33	Gene LOC389791		hypothetical LOC389791	NR_024425, hCT2317603.0		EAW87747.1
GeneID:25792	CIZ1	9	130,928,344	130,966,662	38,318	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5632, 1_A375_pNL7_minus_lncRNA_AR..1..5633, 2_A375_pNL97_plus_lncRNA_AR..1..8110, 2_A375_pNL97_plus_lncRNA_AR..1..8111, 4_A375_EGR1..1..8069	12742, 11206, 12710, 11366, 134	in gene, in gene, in gene, in gene, in gene	1	1	1	31	31.67	14.33	3	2_A375_pNL97_plus_lncRNA_AR..1	61	Gene CIZ1	NP94, LSFR1, CIZ1, ZNF356	CDKN1A interacting zinc finger protein 1	NM_012127, NM_001131015, NM_001131016, NM_001131017, NM_001131018, hCT2319728.1, hCT2319730.1, hCT2319732.1, hCT2319734.1, hCT2319735.1, hCT2319737.1, hCT2356962.0	205516_x_at, 211356_s_at, 213976_at, 213977_s_at	NP_036259.2, NP_001124487.1, NP_001124488.1, NP_001124489.1, NP_001124490.1, EAW87756.1, EAW87752.1, EAW87753.1, EAW87754.1, EAW87755.1, EAW87757.1, EAW87758.1
GeneID:1759	DNM1	9	130,965,663	131,017,527	51,864	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5633, 4_A375_EGR1..1..8069	-10207, 865	upstream, in gene	1	0	1	17	17	14.5	2	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene DNM1	DNM1, DNM	dynamin 1	NM_001005336, NM_004408, hCT1827278.2, hCT1954875.1	215116_s_at	NP_001005336.1, NP_004399.2, EAW87759.1, EAW87760.1
GeneID:26995	TRUB2	9	131,071,396	131,084,697	13,301	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5634, 1_A375_pNL7_minus_lncRNA_AR..1..5635, 2_A375_pNL97_plus_lncRNA_AR..1..8112, 2_A375_pNL97_plus_lncRNA_AR..1..8113, 4_A375_EGR1..1..8070	14505, -247, 14521, -263, -199	downstream, upstream, downstream, upstream, upstream	1	1	1	25	25	13	2	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene TRUB2	CLONE24922, RP11-339B21.1, TRUB2	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	NM_015679, hCT2356968.0, hCT2356969.0, hCT9615.3, hCT1950582.1	223109_at	NP_056494.1, EAW87771.1, EAW87770.1, EAW87772.1, EAW87773.1
GeneID:51117	COQ4	9	131,084,791	131,096,351	11,560	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5635, 2_A375_pNL97_plus_lncRNA_AR..1..8113, 4_A375_EGR1..1..8070	153, 169, 105	in gene, in gene, in gene	1	1	1	32	37	22	1	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene COQ4	CGI-92, COQ4	coenzyme Q4 homolog (S. cerevisiae)	NM_016035, hCT2317627.1, hCT2317629.1, hCT2317632.1, hCT2344107.0, hCT2357023.0	218328_at, 228931_at	NP_057119.2, EAW87776.1, EAW87774.1, EAW87775.1, EAW87777.1, EAW87778.1
GeneID:10999	SLC27A4	9	131,102,839	131,123,749	20,910	+	1	4_A375_EGR1..1..8071	21641	downstream	0	0	1	11	13	18	1	4_A375_EGR1..1	18	Gene SLC27A4	SLC27A4, FATP4, ACSVL4, IPS	solute carrier family 27 (fatty acid transporter), member 4	NM_005094, hCT2317830.1, hCT2317833.1	225779_at	NP_005085.2, EAW87780.1, EAW87779.1
GeneID:81605	URM1	9	131,133,598	131,153,015	19,417	+	1	4_A375_EGR1..1..8071	-9116	upstream	0	0	1	11	13	18	1	4_A375_EGR1..1	18	Gene URM1	C9orf74, MGC2668, URM1	ubiquitin related modifier 1	NM_030914, NM_001135947, hCT2357011.0, hCT2357012.0, hCT2357013.0, hCT9625.3, hCT1981368.1	208101_s_at	NP_112176.1, NP_001129419.1, EAW87783.1, EAW87784.1, EAW87785.1, EAW87786.1, EAW87782.1
GeneID:100506065	LOC100506065	9	131,173,654	131,182,503	8,849	+	4	2_A375_pNL97_plus_lncRNA_AR..1..8114, 4_A375_EGR1..1..8072, 4_A375_EGR1..1..8073, 4_A375_EGR1..1..8074	8578, 8130, 8914, 9970	in gene, in gene, downstream, downstream	0	1	1	10	13	17.67	3	4_A375_EGR1..1	19	Gene LOC100506065		hypothetical LOC100506065	XR_108948		
GeneID:51148	CERCAM	9	131,182,759	131,199,630	16,871	+	4	2_A375_pNL97_plus_lncRNA_AR..1..8114, 4_A375_EGR1..1..8072, 4_A375_EGR1..1..8073, 4_A375_EGR1..1..8074	-327, -775, 9, 1065	upstream, upstream, in gene, in gene	0	1	1	10	13	17.67	3	4_A375_EGR1..1	19	Gene CERCAM	CEECAM1, CERCAM, MGC149820, MGC149821, GLT25D3	cerebral endothelial cell adhesion molecule	NM_016174, hCT2317598.0, hCT2317601.0, hCT9619.3, hCT1950583.1	224794_s_at, 227361_at	NP_057258.3, EAW87789.1, EAW87787.1, EAW87788.1, EAW87790.1
GeneID:2733	GLE1	9	131,266,971	131,304,580	37,609	+	1	4_A375_EGR1..1..8075	47525	downstream	0	0	1	7	11	23	1	4_A375_EGR1..1	23	Gene GLE1	GLE1L, LCCS1, LCCS, hGLE1, GLE1	GLE1 RNA export mediator homolog (yeast)	NM_001499, NM_001003722, hCT32308.3, hCT1950844.1, hCT1950845.1	206920_s_at, 206921_at, 225371_at	NP_001490.1, NP_001003722.1, EAW87802.1, EAW87803.1, EAW87804.1
GeneID:6709	SPTAN1	9	131,314,866	131,395,941	81,075	+	2	2_A375_pNL97_plus_lncRNA_AR..1..8115, 4_A375_EGR1..1..8075	238, -370	in gene, upstream	0	1	1	10	14	15	2	4_A375_EGR1..1	23	Gene SPTAN1	SPTA2, FLJ17738, FLJ44613, EIEE5, NEAS, SPTAN1, (ALPHA)II-SPECTRIN	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	NM_003127, NM_001130438, hCT2317615.0, hCT2317616.0, hCT2317617.0, hCT2317618.0, hCT2317620.0, hCT2357042.0, hCT2357043.0, hCT2357044.0, hCT32307.3	208611_s_at, 214925_s_at, 214926_at, 215235_at, 241150_at	NP_003118.2, NP_001123910.1, EAW87805.1, EAW87807.1, EAW87809.1, EAW87811.1, EAW87806.1, EAW87808.1, EAW87810.1, EAW87812.1, EAW87813.1
GeneID:29941	PKN3	9	131,464,802	131,483,199	18,397	+	1	4_A375_EGR1..1..8076	21614	downstream	0	0	1	13	20	19	1	4_A375_EGR1..1	19	Gene PKN3	RP11-545E17.1, PKN3	protein kinase N3	NM_013355, hCT87421.3, hCT1950013.1	226299_at	NP_037487.2, EAW87825.1, EAW87824.1
GeneID:84885	ZDHHC12	9	131,483,148	131,486,408	3,260	-	1	4_A375_EGR1..1..8076	-8	upstream	0	0	1	13	20	19	1	4_A375_EGR1..1	19	Gene ZDHHC12	MGC54050, ZDHHC12, ZNF400, MGC13153, FLJ14524	zinc finger, DHHC type containing 12	NM_032799, hCT2357052.0, hCT2357053.0, hCT87501.2	226088_at	NP_116188.2, EAW87828.1, EAW87826.1, EAW87827.1
GeneID:100506100	LOC100506100	9	131,486,741	131,495,522	8,781	+	1	4_A375_EGR1..1..8076	-325	upstream	0	0	1	13	20	19	1	4_A375_EGR1..1	19	Gene LOC100506100		hypothetical LOC100506100	XR_113253, XR_108950, XR_114298		
GeneID:10444	ZER1	9	131,492,065	131,534,198	42,133	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5636, 2_A375_pNL97_plus_lncRNA_AR..1..8116, 4_A375_EGR1..1..8076, 4_A375_EGR1..1..8077	-314, -106, 47782, -166	upstream, upstream, downstream, upstream	1	1	1	15	21	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene ZER1	ZER1, C9orf60, ZYG11BL, ZYG, Hzyg, RP11-545E17.4	zer-1 homolog (C. elegans)	NM_006336, hCT2317665.0, hCT2317668.0, hCT2317669.0	202448_s_at, 202452_at, 202456_s_at, 230358_at	NP_006327.2, EAW87829.1, EAW87830.1, EAW87831.1
GeneID:54662	TBC1D13	9	131,549,510	131,572,711	23,201	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5637, 2_A375_pNL97_plus_lncRNA_AR..1..8117	31274, -6	downstream, upstream	1	1	0	21.5	20.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene TBC1D13	TBC1D13, FLJ10743, RP11-545E17.5	TBC1 domain family, member 13	NM_018201, hCT2317636.0, hCT2357071.0, hCT1827290.2, hCT1950567.1, hCT1950568.1	218598_at, 44696_at	NP_060671.3, EAW87834.1, EAW87832.1, EAW87833.1, EAW87835.1, EAW87836.1
GeneID:2021	ENDOG	9	131,580,779	131,584,955	4,176	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5637, 2_A375_pNL97_plus_lncRNA_AR..1..8118, 4_A375_EGR1..1..8078	5, 11237, 11093	in gene, downstream, downstream	1	1	1	19	18.5	18.5	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene ENDOG	ENDOG, FLJ27463	endonuclease G	NM_004435, hCT21763.3	204824_at	NP_004426.2, EAW87837.1
GeneID:51490	C9orf114	9	131,584,345	131,592,085	7,740	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5637, 2_A375_pNL97_plus_lncRNA_AR..1..8118, 4_A375_EGR1..1..8078	11301, 69, 213	downstream, in gene, in gene	1	1	1	19	18.5	18.5	2	1_A375_pNL7_minus_lncRNA_AR..1	25	Gene C9orf114	RP11-545E17.7, C9orf114, MGC29492, HSPC109, DKFZp566D143	chromosome 9 open reading frame 114	NM_016390, hCT21765.3, hCT1950620.1	218565_at, 222674_at	NP_057474.2, EAW87839.1, EAW87838.1
GeneID:883	CCBL1	9	131,595,392	131,644,354	48,962	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5638, 2_A375_pNL97_plus_lncRNA_AR..1..8118, 2_A375_pNL97_plus_lncRNA_AR..1..8119, 4_A375_EGR1..1..8078	98, 52338, 98, 52482	in gene, downstream, in gene, downstream	1	1	1	30.5	33.5	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	48	Gene CCBL1	FLJ95217, CCBL1, KAT1, GTK, KATI, MGC29624	cysteine conjugate-beta lyase, cytoplasmic	NM_004059, NM_001122671, NM_001122672, hCT1950619.1, hCT1965685.1	1570650_at, 1570651_at, 206037_at	NP_004050.3, NP_001116143.1, NP_001116144.1, EAW87840.1, EAW87841.1
GeneID:56262	LRRC8A	9	131,644,391	131,680,318	35,927	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5638, 1_A375_pNL7_minus_lncRNA_AR..1..5639, 2_A375_pNL97_plus_lncRNA_AR..1..8119	-135, 10361, -135	upstream, in gene, upstream	1	1	0	33	30	10.5	2	1_A375_pNL7_minus_lncRNA_AR..1	48	Gene LRRC8A	AGM5, FLJ41617, KIAA1437, FLJ10337, LRRC8, LRRC8A	leucine rich repeat containing 8 family, member A	NM_001127244, NM_019594, NM_001127245, hCT1643880.2, hCT1984773.1	224624_at, 233487_s_at	NP_001120716.1, NP_062540.2, NP_001120717.1, EAW87842.1, EAW87843.1
GeneID:254295	PHYHD1	9	131,683,174	131,704,320	21,146	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5640, 2_A375_pNL97_plus_lncRNA_AR..1..8120, 4_A375_EGR1..1..8079	26874, 26842, 26882	downstream, downstream, downstream	1	1	1	21	21	26	1	4_A375_EGR1..1	26	Gene PHYHD1	MGC16638, PHYHD1	phytanoyl-CoA dioxygenase domain containing 1	NM_174933, NM_001100876, NM_001100877, hCT2356958.0, hCT2356959.0, hCT2356960.0, hCT2356961.0, hCT1963069.1	226846_at	NP_777593.2, NP_001094346.1, NP_001094347.1, EAW87844.1, EAW87846.1, EAW87848.1, EAW87845.1, EAW87847.1
GeneID:22845	DOLK	9	131,707,809	131,710,012	2,203	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5640, 2_A375_pNL97_plus_lncRNA_AR..1..8120, 4_A375_EGR1..1..8079	-36, -4, 156	upstream, upstream, in gene	1	1	1	21	21	26	1	4_A375_EGR1..1	26	Gene DOLK	SEC59, DOLK, DK, KIAA1094, TMEM15, CDG1M, DK1	dolichol kinase	NM_014908, hCT19540.3	204488_at	NP_055723.1, EAW87849.1
GeneID:23511	NUP188	9	131,709,977	131,769,374	59,397	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5640, 2_A375_pNL97_plus_lncRNA_AR..1..8120, 4_A375_EGR1..1..8079	71, 39, -121	in gene, in gene, upstream	1	1	1	21	21	26	1	4_A375_EGR1..1	26	Gene NUP188	KIAA0169, NUP188, FLJ21839	nucleoporin 188kDa	NM_015354, hCT2356987.0, hCT2356988.0, hCT1827303.2, hCT1827304.2	212691_at, 214675_at, 217601_at	NP_056169.1, EAW87852.1, EAW87850.1, EAW87851.1, EAW87853.1
GeneID:56904	SH3GLB2	9	131,770,313	131,790,579	20,266	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8121	-8141	upstream	0	1	0	18	21	15	1	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene SH3GLB2	SH3GLB2, PP9455, PP6569, KIAA1848	SH3-domain GRB2-like endophilin B2	NM_020145, hCT21777.3, hCT2357006.0, hCT2357007.0, hCT2357008.0, hCT1954931.1, hCT1954932.1, hCT1954933.1	218813_s_at, 224432_at, 224907_s_at	NP_064530.1, EAW87854.1, EAW87855.1, EAW87858.1, EAW87859.1, EAW87860.1, EAW87856.1, EAW87857.1
GeneID:84895	FAM73B	9	131,799,253	131,834,351	35,098	+	4	2_A375_pNL97_plus_lncRNA_AR..1..8121, 2_A375_pNL97_plus_lncRNA_AR..1..8122, 4_A375_EGR1..1..8080, 4_A375_EGR1..1..8081	-533, 44299, 31179, 32383	upstream, downstream, in gene, in gene	0	1	1	9.25	12.25	15.25	4	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene FAM73B	FLJ00199, C9orf54, FLJ14598, FAM73B	family with sequence similarity 73, member B	NM_032809, hCT2317569.0, hCT2317570.0, hCT2317571.0, hCT2317572.0, hCT2357056.0, hCT2357057.0	226356_at	NP_116198.2, EAW87863.1, EAW87861.1, EAW87864.1, EAW87865.1, EAW87866.1, EAW87862.1
GeneID:57171	DOLPP1	9	131,843,383	131,852,717	9,334	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8122	169	in gene	0	1	0	10	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene DOLPP1	DOLPP1, LSFR2	dolichyl pyrophosphate phosphatase 1	NM_020438, NM_001135917, hCT21775.2, hCT2357002.0, hCT2357003.0, hCT2357004.0, hCT1965688.1, hCT1965691.1	221817_at	NP_065171.2, NP_001129389.1, EAW87869.1, EAW87870.1, EAW87871.1, EAW87872.1, EAW87867.1, EAW87868.1
GeneID:1384	CRAT	9	131,857,073	131,873,070	15,997	-	1	4_A375_EGR1..1..8082	7598	in gene	0	0	1	8	10	17	1	4_A375_EGR1..1	17	Gene CRAT	CAT1, CRAT	carnitine acetyltransferase	NM_000755, NR_026048, hCT2317869.0, hCT2317870.0, hCT2317871.0	205843_x_at, 209522_s_at	NP_000746.2, EAW87874.1, EAW87873.1, EAW87875.1
GeneID:5524	PPP2R4	9	131,873,228	131,911,225	37,997	+	2	4_A375_EGR1..1..8082, 4_A375_EGR1..1..8083	-7756, 15940	upstream, in gene	0	0	1	6.5	10.5	16	2	4_A375_EGR1..1	17	Gene PPP2R4	PPP2R4, PR53, PP2A, MGC2184, PTPA	protein phosphatase 2A activator, regulatory subunit 4	NM_021131, NM_178000, NM_178001, NM_178003, NM_001193397, hCT21772.3, hCT2317579.0, hCT2317580.0, hCT2317582.0, hCT2317583.0, hCT2356963.0, hCT2356964.0, hCT2356965.0, hCT1950624.0, hCT1950625.1	208452_x_at, 208874_x_at, 216105_x_at	NP_066954.2, NP_821067.1, NP_821068.1, NP_821070.1, NP_001180326.1, EAW87876.1, EAW87877.1, EAW87878.1, EAW87879.1, EAW87880.1, EAW87881.1, EAW87882.1, EAW87883.1, EAW87884.1, EAW87885.1
GeneID:389792	IER5L	9	131,937,831	131,940,540	2,709	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8123	4080	downstream	0	1	0	23	19	13	1	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene IER5L	MGC70833, bA247A12.2, IER5L	immediate early response 5-like	NM_203434	226552_at, 226559_at	NP_982258.2
GeneID:100506190	LOC100506190	9	132,245,730	132,267,406	21,676	+	4	2_A375_pNL97_plus_lncRNA_AR..1..8125, 2_A375_pNL97_plus_lncRNA_AR..1..8126, 2_A375_pNL97_plus_lncRNA_AR..1..8127, 4_A375_EGR1..1..8087	-9378, 6867, 12565, 30462	upstream, in gene, in gene, downstream	0	1	1	11.25	14.25	15	4	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100506190		hypothetical LOC100506190	XR_113260, XR_113259, XR_108960, XR_108958, XR_108957, XR_108959, XR_114306, XR_114305		
GeneID:100128077	LOC100128077	9	132,252,760	132,253,362	602	+	2	2_A375_pNL97_plus_lncRNA_AR..1..8126, 2_A375_pNL97_plus_lncRNA_AR..1..8127	-163, 5555	upstream, downstream	0	1	0	17	17	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene LOC100128077		hypothetical LOC100128077	XR_113258, XR_108956, XR_114304		
GeneID:375759	C9orf50	9	132,374,504	132,383,055	8,551	-	1	4_A375_EGR1..1..8090	-5441	upstream	0	0	1	13	10	18	1	4_A375_EGR1..1	18	Gene C9orf50	FLJ35803, C9orf50	chromosome 9 open reading frame 50	NM_199350, hCT21780.2, hCT2321501.0	230335_at	NP_955382.3, EAW87891.1, EAW87892.1
GeneID:28989	METTL11A	9	132,388,435	132,397,879	9,444	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5641, 2_A375_pNL97_plus_lncRNA_AR..1..8128, 4_A375_EGR1..1..8090	16045, 16013, 61	downstream, downstream, in gene	1	1	1	113	107	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	213	Gene METTL11A	NRMT, NTM1A, METTL11A, C9orf32, AD-003	methyltransferase like 11A	NM_014064, hCT21770.1, hCT2321311.0, hCT1950622.1	223368_s_at, 223369_at	NP_054783.2, EAW87895.1, EAW87893.1, EAW87894.1
GeneID:140459	ASB6	9	132,398,663	132,404,444	7,581	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5641, 2_A375_pNL97_plus_lncRNA_AR..1..8128, 4_A375_EGR1..1..8090	-36, -4, 15946	upstream, upstream, downstream	1	1	1	113	107	15.5	2	1_A375_pNL7_minus_lncRNA_AR..1	213	Gene ASB6	MGC1024, FLJ20548, ASB6	ankyrin repeat and SOCS box containing 6	NM_177999, NM_017873, hCT21778.4, hCT2321495.1, hCT2321497.1, hCT2357014.0, hCT1686779.3	221657_s_at, 222524_s_at	NP_821066.1, NP_060343.1, EAW87897.1, EAW87896.1, EAW87899.1, EAW87900.1, EAW87898.1
GeneID:51450	PRRX2	9	132,427,920	132,484,953	57,033	+	2	2_A375_pNL97_plus_lncRNA_AR..1..8129, 4_A375_EGR1..1..8091	47520, 22128	in gene, in gene	0	1	1	10	15	13	2	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene PRRX2	PRRX2, PMX2, MGC19843, PRX2	paired related homeobox 2	NM_016307, hCT21769.3	219729_at	NP_057391.1, EAW87901.1
GeneID:100506231	LOC100506231	9	132,475,173	132,480,957	5,784	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8129	5517	in gene	0	1	0	11	17	11	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene LOC100506231		hypothetical LOC100506231	XR_108961		
GeneID:9536	PTGES	9	132,500,615	132,515,344	14,729	-	2	4_A375_EGR1..1..8092, 4_A375_EGR1..1..8093	16496, 15152	downstream, downstream	0	0	1	7	8.5	16.5	2	4_A375_EGR1..1	17	Gene PTGES	PP102, PTGES, TP53I12, PIG12, mPGES-1, PGES, PP1294, MPGES, MGST1-L1, MGST1L1, MGC10317, MGST-IV	prostaglandin E synthase	NM_004878	207388_s_at, 210367_s_at	NP_004869.1
GeneID:27348	TOR1B	9	132,565,432	132,573,560	8,128	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8132	40	in gene	0	1	0	10	20	9	1	2_A375_pNL97_plus_lncRNA_AR..1	20	Gene TOR1B	DQ1, TOR1B, MGC4386	torsin family 1, member B (torsin B)	NM_014506, hCT21779.3	209593_s_at	NP_055321.1, EAW87906.1
GeneID:1861	TOR1A	9	132,575,221	132,586,441	11,220	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5644, 2_A375_pNL97_plus_lncRNA_AR..1..8132, 2_A375_pNL97_plus_lncRNA_AR..1..8133, 4_A375_EGR1..1..8094	73, 20989, 41, 73	in gene, downstream, in gene, in gene	1	1	1	15.5	23.5	13	2	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene TOR1A	DYT1, DQ2, TOR1A	torsin family 1, member A (torsin A)	NM_000113, hCT21766.2, hCT1950621.1	1554849_at, 202348_s_at, 202349_at	NP_000104.1, EAW87907.1, EAW87908.1
GeneID:51759	C9orf78	9	132,589,564	132,597,572	8,008	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5644, 2_A375_pNL97_plus_lncRNA_AR..1..8133, 4_A375_EGR1..1..8094	11204, 11172, 11204	downstream, downstream, downstream	1	1	1	21	27	17	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene C9orf78	HSPC220, C9orf78, bA409K20.3	chromosome 9 open reading frame 78	NM_016520, hCT1950599.1, hCT19541.3	218116_at	NP_057604.1, EAW87909.1, EAW87910.1
GeneID:10868	USP20	9	132,597,696	132,644,107	46,411	+	1	4_A375_EGR1..1..8095	44205	in gene	0	0	1	5	8	14	1	4_A375_EGR1..1	14	Gene USP20	LSFR3A, KIAA1003, VDU2, USP20	ubiquitin specific peptidase 20	NM_001110303, NM_006676, NM_001008563, hCT22424.3, hCT2321320.0, hCT2321322.0, hCT2321325.0, hCT1950629.1	203965_at	NP_001103773.2, NP_006667.3, NP_001008563.2, EAW87911.1, EAW87912.1, EAW87915.1, EAW87913.1, EAW87914.1
GeneID:23048	FNBP1	9	132,649,466	132,805,473	156,007	-	1	4_A375_EGR1..1..8095	163572	downstream	0	0	1	5	8	14	1	4_A375_EGR1..1	14	Gene FNBP1	FBP17, FNBP1, MGC126804, KIAA0554	formin binding protein 1	NM_015033, hCT22427.3, hCT2321477.0, hCT2321479.0, hCT2321480.0	212288_at, 213940_s_at, 230086_at, 230389_at	NP_055848.1, EAW87918.1, EAW87916.1, EAW87917.1, EAW87919.1
GeneID:57720	GPR107	9	132,815,985	132,902,448	86,463	+	1	4_A375_EGR1..1..8096	223	in gene	0	0	1	18	14	20	1	4_A375_EGR1..1	20	Gene GPR107	RP11-88G17, MGC15440, FLJ16312, DKFZp667C222, FLJ22591, bA138E2.2, GCDRP, GPR107, LUSTR1, FLJ20998, MGC126118, KIAA1624	G protein-coupled receptor 107	NM_020960, NM_001136557, NM_001136558, hCT22428.4, hCT2348603.1, hCT2357040.0, hCT2357041.0, hCT1950630.3, hCT1957858.3	211977_at, 211979_at, 220284_s_at, 220285_at	NP_066011.2, NP_001130029.1, NP_001130030.1, EAW87920.1, EAW87921.1, EAW87922.1, EAW87923.1, EAW87924.1, EAW87925.1
GeneID:100289200	LOC100289200	9	133,028,161	133,072,949	44,788	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5645, 2_A375_pNL97_plus_lncRNA_AR..1..8134	32991, 32943	in gene, in gene	1	1	0	29	40	12	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene LOC100289200		hemicentin-2-like	XM_002342956		XP_002342997.1
GeneID:256158	HMCN2	9	133,223,389	133,309,104	85,715	+	4	4_A375_EGR1..1..8097, 4_A375_EGR1..1..8098, 4_A375_EGR1..1..8099, 4_A375_EGR1..1..8100	14619, 29763, 34683, 43512	in gene, in gene, in gene, in gene	0	0	1	6	5	20	4	4_A375_EGR1..1	23	Gene HMCN2	DKFZp434P0216, FLJ46139, HMCN2, FLJ46844, FLJ23816	hemicentin 2	XM_001715154, XM_001726942, XM_002347078	1563532_at, 1564117_at, 235797_x_at, 241650_x_at	XP_001715206.1, XP_001726994.1, XP_002347119.1
GeneID:445	ASS1	9	133,320,094	133,376,661	56,567	+	1	4_A375_EGR1..1..8101	16634	in gene	0	0	1	12	7	14	1	4_A375_EGR1..1	14	Gene ASS1	CTLN1, ASS, ASS1	argininosuccinate synthase 1	NM_054012, NM_000050, hCT1823624.2, hCT1957899.1, hCT1957900.1, hCT1957901.1, hCT1957904.1	207076_s_at	NP_446464.1, NP_000041.2, EAW87932.1, EAW87933.1, EAW87934.1, EAW87936.1, EAW87935.1
GeneID:100272217	LOC100272217	9	133,452,737	133,454,881	2,144	-	1	4_A375_EGR1..1..8102	81	in gene	0	0	1	7	10	21	1	4_A375_EGR1..1	21	Gene LOC100272217	FLJ31475	hypothetical LOC100272217	NR_027440		
GeneID:8939	FUBP3	9	133,454,960	133,513,739	58,779	+	1	4_A375_EGR1..1..8102	-160	upstream	0	0	1	7	10	21	1	4_A375_EGR1..1	21	Gene FUBP3	FBP3, FLJ25229, FUBP3	far upstream element (FUSE) binding protein 3	NM_003934	212824_at	NP_003925.1
GeneID:59335	PRDM12	9	133,539,981	133,558,384	18,403	+	2	4_A375_EGR1..1..8103, 4_A375_EGR1..1..8104	1523, 27859	in gene, downstream	0	0	1	7	8	17	2	4_A375_EGR1..1	18	Gene PRDM12	PFM9, PRDM12	PR domain containing 12	NM_021619, hCT1957905.1	220894_x_at	NP_067632.2, EAW87940.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:23404	EXOSC2	9	133,569,158	133,580,452	11,294	+	2	4_A375_EGR1..1..8104, 4_A375_EGR1..1..8105	-1318, 19290	upstream, downstream	0	0	1	10.5	9.5	18.5	2	4_A375_EGR1..1	21	Gene EXOSC2	Rrp4p, RRP4, hRrp4p, p7, EXOSC2	exosome component 2	NM_014285, hCT2323159.0, hCT2323160.0, hCT2323161.0, hCT2357022.0	209527_at, 214507_s_at, 216117_at	NP_055100.2, EAW87942.1, EAW87941.1, EAW87943.1, EAW87944.1
GeneID:25	ABL1	9	133,589,268	133,763,062	173,794	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5646, 2_A375_pNL97_plus_lncRNA_AR..1..8135, 4_A375_EGR1..1..8105	52364, 120940, -820	in gene, in gene, upstream	1	1	1	13.67	15.33	13.67	3	4_A375_EGR1..1	21	Gene ABL1	bcr/abl, JTK7, c-ABL, ABL, ABL1, p150, v-abl, ABL	c-abl oncogene 1, non-receptor tyrosine kinase	NM_007313, NM_005157, hCT2323164.0, hCT1950600.1, hCT19568.3	202123_s_at	NP_009297.2, NP_005148.2, EAW87947.1, EAW87948.1, EAW87949.1
GeneID:84929	FIBCD1	9	133,777,825	133,814,455	36,630	-	2	4_A375_EGR1..1..8106, 4_A375_EGR1..1..8107	19927, -1289	in gene, upstream	0	0	1	6.5	10	20.5	2	4_A375_EGR1..1	21	Gene FIBCD1	FIBCD1, FLJ14810	fibrinogen C domain containing 1	NM_001145106, NM_032843, hCT21380.3, hCT2349165.0, hCT2349166.0, hCT1950615.2	240042_at	NP_001138578.1, NP_116232.3, EAW87950.1, EAW87951.1, EAW87952.1, EAW87953.1
GeneID:10319	LAMC3	9	133,884,504	133,968,446	83,942	+	3	4_A375_EGR1..1..8109, 4_A375_EGR1..1..8110, 4_A375_EGR1..1..8111	488, 22424, 66104	in gene, in gene, in gene	0	0	1	5.67	5	16.67	3	4_A375_EGR1..1	17	Gene LAMC3	LAMC3, DKFZp434E202	laminin, gamma 3	NM_006059, hCT21362.2, hCT2323170.0, hCT2323171.0, hCT1950616.1	219407_s_at, 232558_at	NP_006050.3, EAW87957.1, EAW87954.1, EAW87955.1, EAW87956.1
GeneID:83543	AIF1L	9	133,971,863	133,998,539	26,676	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5647, 2_A375_pNL97_plus_lncRNA_AR..1..8136	29033, 29129	downstream, downstream	1	1	0	29	32	15	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene AIF1L	AIF1L, MGC29466, FLJ12783, C9orf58, IBA2	allograft inflammatory factor 1-like	NM_001185095, NM_001185096, NM_031426, NR_033701, hCT21384.2, hCT1950618.1	223074_s_at, 223075_s_at	NP_001172024.1, NP_001172025.1, NP_113614.1, EAW87958.1, EAW87959.1
GeneID:8021	NUP214	9	134,000,981	134,109,091	108,110	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5647, 2_A375_pNL97_plus_lncRNA_AR..1..8136	-85, 11	upstream, in gene	1	1	0	29	32	15	1	2_A375_pNL97_plus_lncRNA_AR..1	32	Gene NUP214	MGC104525, N214, D9S46E, CAN, NUP214, CAIN	nucleoporin 214kDa	NM_005085, hCT21359.3, hCT2323176.0, hCT2356933.0, hCT1950614.1	202155_s_at	NP_005076.3, EAW87962.1, EAW87960.1, EAW87961.1, EAW87963.1
GeneID:84814	PPAPDC3	9	134,165,061	134,184,649	19,588	+	1	4_A375_EGR1..1..8112	647	in gene	0	0	1	8	15	16	1	4_A375_EGR1..1	16	Gene PPAPDC3	MGC12921, KIAA0515, PPAPDC3, NET39, C9orf67, FLJ14662	phosphatidic acid phosphatase type 2 domain containing 3	NM_032728, hCT2323180.0, hCT1642565.3	224506_s_at	NP_116117.3, EAW87966.1, EAW87967.1
GeneID:84726	BAT2L1	9	134,305,477	134,375,578	70,101	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5649, 2_A375_pNL97_plus_lncRNA_AR..1..8136	72907, 72859	downstream, downstream	1	1	0	37	45	17	1	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene BAT2L1	BAT2L1, KIAA0515, PRRC2B, LQFBS-1, BAT2L, DKFZp781F05101, DKFZp781K12107, MGC10526	HLA-B associated transcript 2-like 1	NM_013318	212068_s_at, 212069_s_at, 223793_at	NP_037450.2
GeneID:10585	POMT1	9	134,378,289	134,399,193	20,904	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5649, 2_A375_pNL97_plus_lncRNA_AR..1..8136, 4_A375_EGR1..1..8115, 4_A375_EGR1..1..8116	95, 47, 15887, 30319	in gene, in gene, in gene, downstream	1	1	1	17.33	20.67	17	3	2_A375_pNL97_plus_lncRNA_AR..1	45	Gene POMT1	FLJ37239, MDDGA1, LGMD2K, RT, MDDGB1, POMT1, MDDGC1	protein-O-mannosyltransferase 1	NM_001077366, NM_001077365, NM_007171, NM_001136113, NM_001136114, hCT1823332.2, hCT1950602.1, hCT1959916.1, hCT1959918.1, hCT1959919.1	218476_at	NP_001070834.1, NP_001070833.1, NP_009102.3, NP_001129585.1, NP_001129586.1, EAW87974.1, EAW87975.1, EAW87976.1, EAW87977.1, EAW87978.1
GeneID:83549	UCK1	9	134,399,183	134,406,662	7,479	-	2	4_A375_EGR1..1..8115, 4_A375_EGR1..1..8116	12486, -1946	downstream, upstream	0	0	1	7.5	8.5	17	2	4_A375_EGR1..1	16	Gene UCK1	UCK1, URK1, FLJ12255	uridine-cytidine kinase 1	NM_031432, NM_001135954, hCT20397.2, hCT2356990.0, hCT2356991.0, hCT2356992.0, hCT1950604.1, hCT1950605.1	223141_at, 223142_s_at	NP_113620.1, NP_001129426.1, EAW87980.1, EAW87981.1, EAW87982.1, EAW87984.1, EAW87979.1, EAW87983.1
GeneID:9442	MED27	9	134,735,499	134,955,253	219,754	-	3	2_A375_pNL97_plus_lncRNA_AR..1..8143, 2_A375_pNL97_plus_lncRNA_AR..1..8144, 4_A375_EGR1..1..8116	119173, -75, 223541	in gene, upstream, downstream	0	1	1	10	14.33	9.33	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene MED27	MED27, TRAP37, MGC11274, CRSP8, CRSP34, CRAP34	mediator complex subunit 27	NM_004269, hCT2317465.0, hCT2317466.0, hCT2317468.0, hCT2357075.0, hCT19241.2	215371_at, 221598_s_at, 51176_at	NP_004260.2, EAW87991.1, EAW87989.1, EAW87990.1, EAW87992.1, EAW87993.1
GeneID:84628	NTNG2	9	135,037,334	135,118,220	80,886	+	5	4_A375_EGR1..1..8119, 4_A375_EGR1..1..8120, 4_A375_EGR1..1..8121, 4_A375_EGR1..1..8122, 4_A375_EGR1..1..8123	26378, 32566, 75466, 76778, 79066	in gene, in gene, in gene, in gene, in gene	0	0	1	5.8	7.2	19.4	5	4_A375_EGR1..1	23	Gene NTNG2	MGC21884, NTNG2, NTNG1, Lmnt2, KIAA0625, LHLL9381, KIAA1857, bA479K20.1	netrin G2	NM_032536, hCT22843.3, hCT2317256.0, hCT2317261.0	233072_at	NP_115925.2, EAW87995.1, EAW87994.1, EAW87996.1
GeneID:23064	SETX	9	135,136,827	135,230,372	93,545	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5653	132	in gene	1	0	0	20	13	9	1	1_A375_pNL7_minus_lncRNA_AR..1	20	Gene SETX	bA479K20.2, FLJ43459, SETX, FLJ12840, KIAA0625, ALS4, AOA2, SCAR1, DKFZp781B151	senataxin	NM_015046, hCT2317459.0, hCT2317460.0, hCT2317462.0, hCT2317463.0	201964_at, 201965_s_at, 232229_at	NP_055861.3, EAW87997.1, EAW87998.1, EAW87999.1, EAW88000.1
GeneID:389799	C9orf171	9	135,285,611	135,448,675	163,064	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5654, 2_A375_pNL97_plus_lncRNA_AR..1..8146	171973, 172021	downstream, downstream	1	1	0	64	62	12	1	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene C9orf171	C9orf171, FLJ46082, MGC148087	chromosome 9 open reading frame 171	NM_207417, hCT2357061.0, hCT1653189.3		NP_997300.1, EAW88004.1, EAW88003.1
GeneID:56751	BARHL1	9	135,457,993	135,465,640	7,647	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5654, 2_A375_pNL97_plus_lncRNA_AR..1..8146	-409, -361	upstream, upstream	1	1	0	64	62	12	1	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene BARHL1	BARHL1	BarH-like homeobox 1	NM_020064, hCT22644.3	224092_at	NP_064448.1, EAW88005.1
GeneID:64794	DDX31	9	135,469,676	135,545,788	76,112	-	2	2_A375_pNL97_plus_lncRNA_AR..1..8147, 4_A375_EGR1..1..8124	540, 316	in gene, in gene	0	1	1	13	19	22	1	4_A375_EGR1..1	22	Gene DDX31	FLJ13633, FLJ14578, DDX31, FLJ23349	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	NM_022779, NM_138620, hCT22646.3, hCT1965707.1, hCT1965708.1, hCT1965709.1	1553161_at, 219328_at	NP_073616.6, NP_619526.1, EAW88006.1, EAW88007.1, EAW88008.1, EAW88009.1
GeneID:9329	GTF3C4	9	135,545,728	135,565,471	19,743	+	2	2_A375_pNL97_plus_lncRNA_AR..1..8147, 4_A375_EGR1..1..8124	-480, -256	upstream, upstream	0	1	1	13	19	22	1	4_A375_EGR1..1	22	Gene GTF3C4	TFIII90, TFIIIC290, GTF3C4, FLJ21002, TFIIICDELTA, KAT12, MGC138450, TFIIIC90	general transcription factor IIIC, polypeptide 4, 90kDa	NM_012204, hCT22641.3, hCT2356940.0	219198_at	NP_036336.2, EAW88011.1, EAW88010.1
GeneID:7248	TSC1	9	135,766,735	135,820,020	53,285	-	1	4_A375_EGR1..1..8125	52	in gene	0	0	1	12	14	16	1	4_A375_EGR1..1	16	Gene TSC1	TSC1, TSC, KIAA0243, LAM, MGC86987	tuberous sclerosis 1	NM_000368, NM_001162426, NM_001162427, hCT22639.3	209390_at	NP_000359.1, NP_001155898.1, NP_001155899.1, EAW88021.1
GeneID:8328	GFI1B	9	135,854,098	135,867,084	12,986	+	1	4_A375_EGR1..1..8126	5822	in gene	0	0	1	4	5	19	1	4_A375_EGR1..1	19	Gene GFI1B	GFI1B		NM_004188, NM_001135031, hCT22638.3, hCT1965699.0, hCT1965701.0	208501_at, 237403_at	NP_004179.3, NP_001128503.1, EAW88023.1, EAW88024.1, EAW88025.1
GeneID:9328	GTF3C5	9	135,906,062	135,933,890	27,828	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5655, 4_A375_EGR1..1..8127	322, -7276	in gene, upstream	1	0	1	13	10.5	18.5	2	1_A375_pNL7_minus_lncRNA_AR..1	21	Gene GTF3C5	TFIIICepsilon, TFiiiC2-63, TFIIIC63, GTF3C5, FLJ20857	general transcription factor IIIC, polypeptide 5, 63kDa	NM_012087, NM_001122823, hCT22635.3, hCT2357054.0, hCT2357055.0, hCT1950633.1	217876_at, 233173_x_at	NP_036219.2, NP_001116295.1, EAW88026.1, EAW88027.1, EAW88028.1, EAW88029.1
GeneID:5900	RALGDS	9	135,973,107	136,024,568	51,461	-	1	4_A375_EGR1..1..8128	29366	in gene	0	0	1	6	3	14	1	4_A375_EGR1..1	14	Gene RALGDS	FLJ20922, RGDS, RGF, RalGEF, RALGDS	ral guanine nucleotide dissociation stimulator	NM_006266, NM_001042368, hCT2335808.0, hCT2335809.0, hCT2335810.0, hCT2356950.0, hCT1827819.3, hCT1950640.1	209050_s_at, 209051_s_at	NP_006257.1, NP_001035827.1, EAW88037.1, EAW88038.1, EAW88039.1, EAW88040.1, EAW88041.1, EAW88042.1
GeneID:26301	GBGT1	9	136,028,340	136,039,301	10,961	-	1	4_A375_EGR1..1..8129	565	in gene	0	0	1	6	10	16	1	4_A375_EGR1..1	16	Gene GBGT1	UNQ2513, MGC44848, A3GALNT, GBGT1, FS	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	NM_021996, hCT22645.3, hCT2356945.0, hCT2356946.0, hCT2356947.0, hCT1965706.1	231760_at	NP_068836.2, EAW88045.1, EAW88043.1, EAW88044.1, EAW88046.1, EAW88047.1
GeneID:28	ABO	9	136,130,563	136,150,630	20,067	-	1	4_A375_EGR1..1..8130	18230	in gene	0	0	1	6	6	15	1	4_A375_EGR1..1	15	Gene ABO	A3GALT1, A3GALNT, ABO, GTB, NAGAT	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase, transferase B, alpha 1-3-galactosyltransferase)	NM_020469, hCT19299.3	214504_at, 216716_at, 216929_x_at	NP_065202.2, EAW88054.1
GeneID:6838	SURF6	9	136,197,552	136,203,047	5,495	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5656, 2_A375_pNL97_plus_lncRNA_AR..1..8148	-25, -57	upstream, upstream	1	1	0	60	66	15	1	2_A375_pNL97_plus_lncRNA_AR..1	66	Gene SURF6	SURF6, FLJ30322, RRP14	surfeit 6	NM_006753, hCT19295.3	225038_s_at	NP_006744.2, EAW88055.1
GeneID:6837	MED22	9	136,207,744	136,214,972	7,228	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5656, 1_A375_pNL7_minus_lncRNA_AR..1..5657, 2_A375_pNL97_plus_lncRNA_AR..1..8148, 2_A375_pNL97_plus_lncRNA_AR..1..8149	11900, -66, 11866, -66	downstream, upstream, downstream, upstream	1	1	0	54	63	15.5	2	2_A375_pNL97_plus_lncRNA_AR..1	66	Gene MED22	MGC48682, MED22, MED24, SURF5	mediator complex subunit 22	NM_181491, NM_133640, hCT2335787.1, hCT2335788.1, hCT2335789.1, hCT2335790.1, hCT2335791.1	208593_s_at	NP_852468.1, NP_598395.1, EAW88056.1, EAW88057.1, EAW88059.1, EAW88060.1, EAW88058.1
GeneID:6130	RPL7A	9	136,215,069	136,218,280	3,211	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5657, 2_A375_pNL97_plus_lncRNA_AR..1..8149	-29, -29	upstream, upstream	1	1	0	28	40	16	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene RPL7A	SURF3, TRUP, RPL7A, L7A	ribosomal protein L7a	NM_000972, hCT2335565.1, hCT2335566.1, hCT2335567.1, hCT2335568.1, hCT2335569.1, hCT2348626.1	217740_x_at, 224930_x_at	NP_000963.1, EAW88061.1, EAW88062.1, EAW88063.1, EAW88064.1, EAW88065.1, EAW88066.1
GeneID:26820	SNORD24	9	136,216,251	136,216,325	74	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5657, 2_A375_pNL97_plus_lncRNA_AR..1..8149	-1211, -1211	upstream, upstream	1	1	0	28	40	16	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene SNORD24	RNU24, U24, SNORD24	small nucleolar RNA, C/D box 24	NR_002447		
GeneID:26814	SNORD36B	9	136,216,949	136,217,019	70	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5657, 2_A375_pNL97_plus_lncRNA_AR..1..8149	-1909, -1909	upstream, upstream	1	1	0	28	40	16	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene SNORD36B	RNU36B, SNORD36B, U36b	small nucleolar RNA, C/D box 36B	NR_000017		
GeneID:26815	SNORD36A	9	136,217,311	136,217,382	71	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5657, 2_A375_pNL97_plus_lncRNA_AR..1..8149	-2271, -2271	upstream, upstream	1	1	0	28	40	16	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene SNORD36A	SNORD36A, RNU36A, U36a	small nucleolar RNA, C/D box 36A	NR_002448		
GeneID:26813	SNORD36C	9	136,217,701	136,217,768	67	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5657, 2_A375_pNL97_plus_lncRNA_AR..1..8149	-2661, -2661	upstream, upstream	1	1	0	28	40	16	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene SNORD36C	SNORD36C, U36c, RNU36C	small nucleolar RNA, C/D box 36C	NR_000016		
GeneID:6834	SURF1	9	136,218,666	136,223,361	4,695	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5657, 2_A375_pNL97_plus_lncRNA_AR..1..8149	8321, 8321	downstream, downstream	1	1	0	28	40	16	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene SURF1	SURF1	surfeit 1	NM_003172, hCT19291.4	204295_at, 217646_at	NP_003163.1, EAW88067.1
GeneID:6835	SURF2	9	136,223,421	136,228,040	4,619	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5657, 2_A375_pNL97_plus_lncRNA_AR..1..8149	-8381, -8381	upstream, upstream	1	1	0	28	40	16	1	2_A375_pNL97_plus_lncRNA_AR..1	40	Gene SURF2	SURF2, SURF-2	surfeit 2	NM_017503, hCT2335562.1, hCT19292.3, hCT1962453.2	205224_at	NP_059973.3, EAW88068.1, EAW88069.1, EAW88070.1
GeneID:6836	SURF4	9	136,228,340	136,242,970	14,630	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5658, 1_A375_pNL7_minus_lncRNA_AR..1..5659, 2_A375_pNL97_plus_lncRNA_AR..1..8150	666, -38, -102	in gene, upstream, upstream	1	1	0	51	58	9	1	2_A375_pNL97_plus_lncRNA_AR..1	58	Gene SURF4	MGC102753, SURF4, ERV29, FLJ22993	surfeit 4	NM_033161, hCT1971125.2, hCT1971129.2, hCT2356989.0, hCT19294.4	222977_at, 222978_at, 222979_s_at	NP_149351.1, EAW88072.1, EAW88071.1, EAW88073.1, EAW88074.1
GeneID:169436	C9orf96	9	136,243,284	136,271,220	27,936	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5658, 1_A375_pNL7_minus_lncRNA_AR..1..5659, 2_A375_pNL97_plus_lncRNA_AR..1..8150, 4_A375_EGR1..1..8131	-960, -276, -212, 22060	upstream, upstream, upstream, in gene	1	1	1	30	33	11.5	2	2_A375_pNL97_plus_lncRNA_AR..1	58	Gene C9orf96	RP11-244N20.8, MGC43306, SgK071, C9orf96, Sk521	chromosome 9 open reading frame 96	NM_153710, hCT2340956.0, hCT2340957.0, hCT2340958.0, hCT2347667.1, hCT2357027.0, hCT2357028.0, hCT19302.4	1554787_at, 236805_at	NP_714921.3, EAW88080.1, EAW88075.1, EAW88076.1, EAW88077.1, EAW88081.1, EAW88078.1, EAW88079.1
GeneID:57109	REXO4	9	136,271,186	136,283,164	11,978	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5660, 2_A375_pNL97_plus_lncRNA_AR..1..8151, 4_A375_EGR1..1..8131, 4_A375_EGR1..1..8132	-100, -132, 17820, -132	upstream, upstream, downstream, upstream	1	1	1	14.5	18.5	15	2	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene REXO4	REX4, XPMC2, XPMC2H, REXO4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	NM_020385, hCT19298.2	218787_at	NP_065118.2, EAW88082.1
GeneID:11093	ADAMTS13	9	136,279,459	136,324,508	45,049	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5660, 2_A375_pNL97_plus_lncRNA_AR..1..8151, 4_A375_EGR1..1..8132	3805, 3837, 3837	in gene, in gene, in gene	1	1	1	20	29	16	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene ADAMTS13	MGC118900, C9orf8, TTP, VWFCP, FLJ42993, vWF-CP, DKFZp434C2322, MGC118899, ADAMTS13	ADAM metallopeptidase with thrombospondin type 1 motif, 13	NM_139025, NM_139027, NM_139026, NR_024514, hCT2335571.0, hCT2335572.0, hCT2335573.0, hCT2335574.0, hCT2357034.0, hCT2357035.0	220208_at, 223644_at	NP_620594.1, NP_620596.2, NP_620595.1, EAW88083.1, EAW88086.1, EAW88087.1, EAW88084.1, EAW88085.1, EAW88088.1
GeneID:11094	C9orf7	9	136,325,087	136,335,909	10,822	+	1	4_A375_EGR1..1..8133	16625	downstream	0	0	1	10	11	17	1	4_A375_EGR1..1	17	Gene C9orf7	D9S2135, C9orf7, FLOWER	chromosome 9 open reading frame 7	NM_017586, NM_001135775, hCT2335575.0, hCT2357036.0	219223_at, 61874_at	NP_060056.1, NP_001129247.1, EAW88089.1, EAW88090.1
GeneID:11182	SLC2A6	9	136,336,216	136,344,276	8,060	-	2	4_A375_EGR1..1..8133, 4_A375_EGR1..1..8134	564, -6060	in gene, upstream	0	0	1	8	8.5	15	2	4_A375_EGR1..1	17	Gene SLC2A6	GLUT6, GLUT9, SLC2A6, HSA011372	solute carrier family 2 (facilitated glucose transporter), member 6	NM_001145099, NM_017585, hCT2356981.0, hCT2356982.0, hCT19290.3	220091_at	NP_001138571.1, NP_060055.2, EAW88092.1, EAW88093.1, EAW88094.1
GeneID:389827	TMEM8C	9	136,379,708	136,390,068	10,360	-	1	4_A375_EGR1..1..8137	-3340	upstream	0	0	1	10	9	17	1	4_A375_EGR1..1	17	Gene TMEM8C	TMEM226, TMEM8C	transmembrane protein 8C	NM_001080483		NP_001073952.1
GeneID:9719	ADAMTSL2	9	136,397,286	136,440,641	43,355	+	4	2_A375_pNL97_plus_lncRNA_AR..1..8152, 4_A375_EGR1..1..8137, 4_A375_EGR1..1..8138, 4_A375_EGR1..1..8139	26776, -3878, 36566, 53482	in gene, upstream, in gene, downstream	0	1	1	9.75	10.25	16.5	4	4_A375_EGR1..1	22	Gene ADAMTSL2	ADAMTSL2, KIAA0605, FLJ45164	ADAMTS-like 2	NM_014694, NM_001145320, hCT1971121.1, hCT2356980.0, hCT19289.3	206629_at	NP_055509.2, NP_001138792.1, EAW88095.1, EAW88096.1, EAW88097.1
GeneID:642968	FAM163B	9	136,444,144	136,445,345	1,201	-	1	4_A375_EGR1..1..8139	-5423	upstream	0	0	1	7	4	22	1	4_A375_EGR1..1	22	Gene FAM163B	C9orf166, FAM163B	family with sequence similarity 163, member B	NM_001080515		NP_001073984.1
GeneID:1621	DBH	9	136,501,485	136,524,466	22,981	+	3	4_A375_EGR1..1..8140, 4_A375_EGR1..1..8141, 4_A375_EGR1..1..8142	-1997, 13731, 22931	upstream, in gene, in gene	0	0	1	3	4.67	18.33	3	4_A375_EGR1..1	20	Gene DBH	DBM, DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	NM_000787, hCT19124.2	206450_at, 234916_at	NP_000778.3, EAW88099.1
GeneID:100506440	LOC100506440	9	136,519,220	136,522,435	3,215	-	2	4_A375_EGR1..1..8141, 4_A375_EGR1..1..8142	7219, -1981	downstream, upstream	0	0	1	3	4.5	17.5	2	4_A375_EGR1..1	20	Gene LOC100506440		hypothetical LOC100506440	XR_113266, XR_110577, XR_114310		
GeneID:1757	SARDH	9	136,528,682	136,605,077	76,395	-	3	4_A375_EGR1..1..8142, 4_A375_EGR1..1..8143, 4_A375_EGR1..1..8144	80661, 47045, 26693	downstream, in gene, in gene	0	0	1	4	5.67	18.33	3	4_A375_EGR1..1	20	Gene SARDH	SDH, SAR, FLJ38475, DMGDHL1, SARD, SARDH	sarcosine dehydrogenase	NM_007101, NM_001134707, hCT21246.1, hCT2335636.0, hCT2335638.0, hCT1641072.3	207869_at, 210083_at, 210682_s_at, 211322_s_at, 234536_at, 234566_at	NP_009032.2, NP_001128179.1, EAW88101.1, EAW88102.1, EAW88103.1, EAW88104.1
GeneID:7410	VAV2	9	136,627,016	136,857,446	230,430	-	10	1_A375_pNL7_minus_lncRNA_AR..1..5661, 2_A375_pNL97_plus_lncRNA_AR..1..8153, 2_A375_pNL97_plus_lncRNA_AR..1..8154, 4_A375_EGR1..1..8145, 4_A375_EGR1..1..8146, 4_A375_EGR1..1..8147, 4_A375_EGR1..1..8148, 4_A375_EGR1..1..8149, 4_A375_EGR1..1..8150, 4_A375_EGR1..1..8151	1190, 117942, 1030, 159270, 126670, 108606, 90918, 85489, 72150, -3034	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, upstream	1	1	1	6.67	9.33	14.44	9	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene VAV2	VAV2		NM_003371, NM_001134398, hCT21247.2, hCT2335632.0, hCT2335633.0	205536_at, 205537_s_at, 226063_at	NP_003362.2, NP_001127870.1, EAW88107.1, EAW88108.1, EAW88109.1

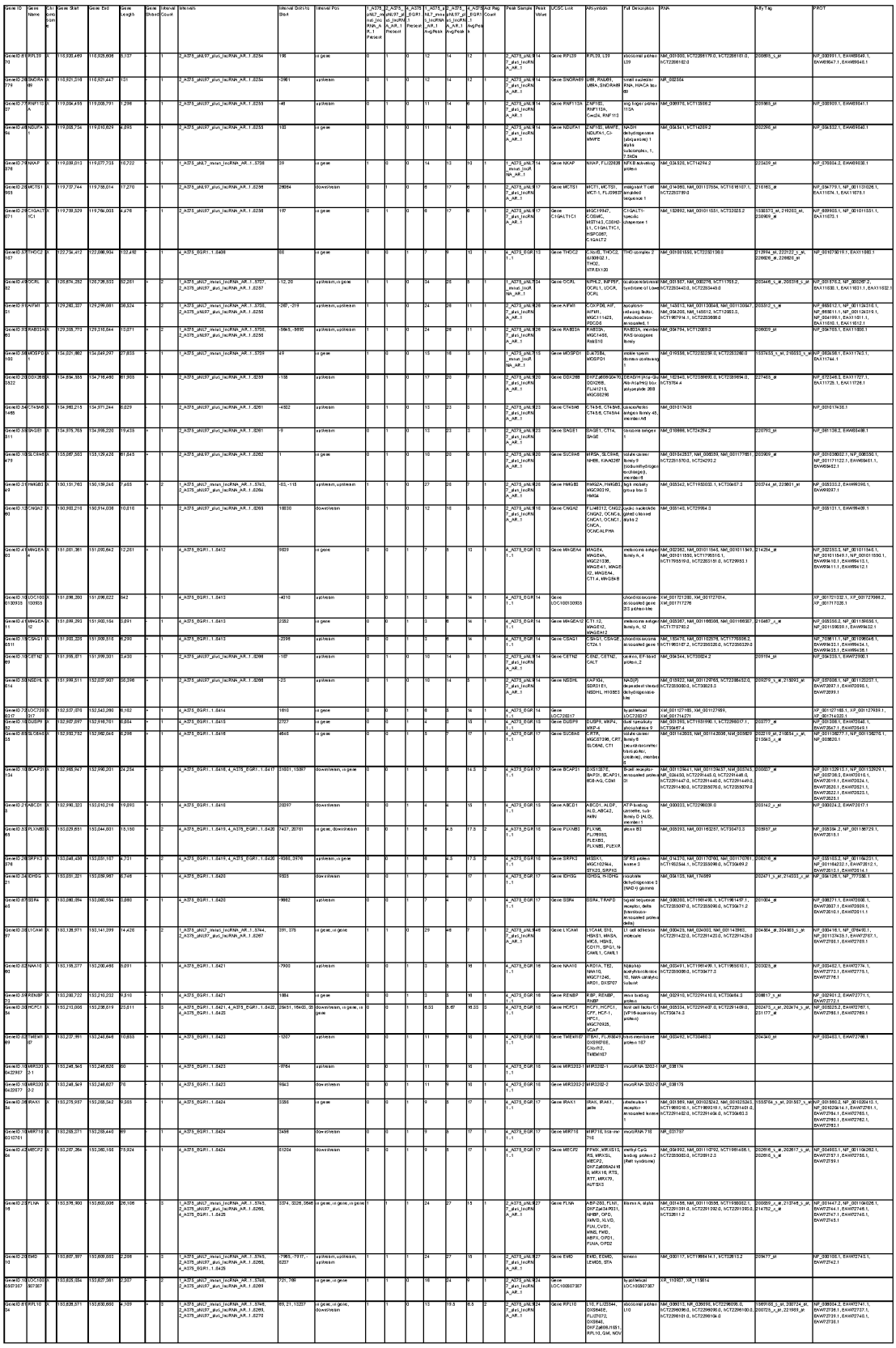
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:100128155	LOC100128155	9	136,757,333	136,760,206	2,873	-	2	4_A375_EGR1..1.8147, 4_A375_EGR1..1.8148	11566, -6322	downstream, upstream	0	0	1	3.5	5	15.5	2	4_A375_EGR1..1	16	Gene LOC100128155	FLJ26965	hypothetical LOC100128155	XR_113267, XR_110576, XR_114311		
GeneID:266655	NCRNA00094	9	136,890,561	136,898,719	8,158	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5662, 2_A375_pNL97_plus_lncRNA_AR..1.8155	-33, -33	upstream, upstream	1	1	0	52	62	11	1	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene NCRNA00094	bA374P20.3, NCRNA00094, LP2477, FLJ35348	non-protein coding RNA 94	NR_015427	203245_s_at, 212547_at, 213766_s_at	
GeneID:8019	BRD3	9	136,895,427	136,933,141	37,714	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5662, 2_A375_pNL97_plus_lncRNA_AR..1.8155, 4_A375_EGR1..1.8152, 4_A375_EGR1..1.8153, 4_A375_EGR1..1.8154	42613, 42613, 13853, 9877, 5845	downstream, downstream, in gene, in gene, in gene	1	1	1	18.25	21.75	16.75	4	2_A375_pNL97_plus_lncRNA_AR..1	62	Gene BRD3	BRD3, FLJ23227, RING3L, ORFX, KIAA0043, FLJ41328	bromodomain containing 3	NM_007371, hCT21250.3, hCT2335829.0, hCT2356926.0	1555026_at, 203825_at	NP_031397.1, EAW88115.1, EAW88113.1, EAW88114.1
GeneID:100130548	LOC100130548	9	136,919,412	136,924,237	4,825	+	3	4_A375_EGR1..1.8152, 4_A375_EGR1..1.8153, 4_A375_EGR1..1.8154	76, 3852, 7884	in gene, in gene, downstream	0	0	1	7	8.33	18.67	3	4_A375_EGR1..1	20	Gene LOC100130548		hypothetical LOC100130548	XR_113265, XR_110579, XR_114312		
GeneID:11091	WDR5	9	137,001,210	137,025,094	23,884	+	9	1_A375_pNL7_minus_lncRNA_AR..1..5663, 1_A375_pNL7_minus_lncRNA_AR..1..5664, 2_A375_pNL97_plus_lncRNA_AR..1.8156, 2_A375_pNL97_plus_lncRNA_AR..1.8157, 4_A375_EGR1..1.8155, 4_A375_EGR1..1.8156, 4_A375_EGR1..1.8157, 4_A375_EGR1..1.8158, 4_A375_EGR1..1.8159	-282, 28582, -218, 28822, -6602, -474, 17734, 27334, 34150	upstream, downstream, upstream, downstream, upstream, upstream, in gene, downstream, downstream	1	1	1	11.83	12.67	18.83	6	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene WDR5	WDR5, BIG-3, SWD3	WD repeat domain 5	NM_017588, NM_052821, hCT2317899.0, hCT2317900.0, hCT2317901.0, hCT2317902.0	223308_s_at, 225170_at	NP_060058.1, NP_438172.1, EAW88117.1, EAW88118.1, EAW88119.1, EAW88120.1
GeneID:100151664	RNU6ATAC	9	137,029,562	137,029,686	124	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5664, 2_A375_pNL97_plus_lncRNA_AR..1.8157, 4_A375_EGR1..1.8158, 4_A375_EGR1..1.8159	-108, -348, 1142, -5674	upstream, upstream, downstream, upstream	1	1	1	12.33	12.67	16	3	1_A375_pNL7_minus_lncRNA_AR..1	22	Gene RNU6ATAC	RNU6ATAC, RNU6ATAC1, U6ATAC	RNA, U6atac small nuclear (U12-dependent splicing)	NR_023344		
GeneID:6256	RXRA	9	137,218,316	137,332,431	114,115	+	5	4_A375_EGR1..1.8168, 4_A375_EGR1..1.8169, 4_A375_EGR1..1.8170, 4_A375_EGR1..1.8171, 4_A375_EGR1..1.8172	9972, 11764, 85780, 90820, 93908	in gene, in gene, in gene, in gene, in gene	0	0	1	6.4	9.2	17	5	4_A375_EGR1..1	20	Gene RXRA	RXRA, FLJ00280, FLJ00318, FLJ16733, NR2B1, FLJ16020, MGC102720	retinoid X receptor, alpha	NM_002957, hCT2317905.0, hCT2317906.0, hCT2317907.0, hCT9205.3	202426_s_at, 202449_s_at	NP_002948.1, EAW88125.1, EAW88122.1, EAW88123.1, EAW88124.1
GeneID:100506532	LOC100506532	9	137,419,028	137,437,107	18,079	+	2	4_A375_EGR1..1.8174, 4_A375_EGR1..1.8175	10060, 26476	in gene, downstream	0	0	1	5.5	8.5	17	2	4_A375_EGR1..1	18	Gene LOC100506532		hypothetical LOC100506532	XR_113273, XR_109854, XR_114313		
GeneID:1289	COL5A1	9	137,533,652	137,736,689	203,037	+	5	4_A375_EGR1..1.8177, 4_A375_EGR1..1.8178, 4_A375_EGR1..1.8179, 4_A375_EGR1..1.8180, 4_A375_EGR1..1.8181	47612, 57068, 97228, 187708, 198012	in gene, in gene, in gene, in gene, in gene	0	0	1	6.4	7.2	16.2	5	4_A375_EGR1..1	18	Gene COL5A1	COL5A1		NM_000093, hCT2317914.0, hCT2317915.0, hCT2317916.0, hCT2317917.0, hCT2317918.0	203325_s_at, 212488_at, 212489_at	NP_000084.3, EAW88128.1, EAW88129.1, EAW88130.1, EAW88131.1, EAW88132.1
GeneID:100506554	LOC100506554	9	137,726,713	137,734,533	7,820	-	2	4_A375_EGR1..1.8180, 4_A375_EGR1..1.8181	13173, 2869	downstream, in gene	0	0	1	5	7	16	2	4_A375_EGR1..1	16	Gene LOC100506554		hypothetical LOC100506554	XR_109855, XR_114314		
GeneID:10439	OLFM1	9	137,967,089	138,013,030	45,941	+	6	1_A375_pNL7_minus_lncRNA_AR..1..5665, 2_A375_pNL97_plus_lncRNA_AR..1.8158, 2_A375_pNL97_plus_lncRNA_AR..1.8159, 2_A375_pNL97_plus_lncRNA_AR..1.8160, 4_A375_EGR1..1.8164, 4_A375_EGR1..1.8165	23327, 2415, 15535, 23343, 11983, 31023	in gene, in gene, in gene, in gene, in gene, in gene	1	1	1	12.8	17.8	11.2	5	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene OLFM1	OlfA, OLFM1, AMY, NOE1, NOELIN1	olfactomedin 1	NM_006334, NM_014279, hCT2317936.0, hCT2317938.0, hCT11283.3, hCT1950313.1	205591_at, 210924_at, 213131_at	NP_006325.1, NP_055094.1, EAW88142.1, EAW88143.1, EAW88144.1, EAW88145.1
GeneID:157927	C9orf62	9	138,235,101	138,238,408	3,307	+	1	4_A375_EGR1..1.8187	3427	downstream	0	0	1	5	7	17	1	4_A375_EGR1..1	17	Gene C9orf62	C9orf62, MGC35463, RP11-555H7.1	chromosome 9 open reading frame 62	XR_113268, XR_109856, XR_114315	1553919_at	
GeneID:100506599	LOC100506599	9	138,354,564	138,364,095	9,531	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5667, 2_A375_pNL97_plus_lncRNA_AR..1.8162, 4_A375_EGR1..1.8188	-2849, -2817, -2085	upstream, upstream, upstream	1	1	1	21	14.5	9	2	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene LOC100506599		hypothetical LOC100506599	XR_113269, XR_109857, XR_114316		
GeneID:9858	KIAA0649	9	138,371,648	138,380,739	9,091	+	3	1_A375_pNL7_minus_lncRNA_AR..1..5667, 2_A375_pNL97_plus_lncRNA_AR..1.8162, 4_A375_EGR1..1.8188	-4704, -4736, -5466	upstream, upstream, upstream	1	1	1	21	14.5	9	2	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene KIAA0649	RP11-426A6.6, KIAA0649	KIAA0649	NM_014811, hCT18377.3, hCT1950787.1	203955_at	NP_055626.3, EAW88151.1, EAW88150.1
GeneID:138162	C9orf116	9	138,387,026	138,391,761	4,735	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5668, 2_A375_pNL97_plus_lncRNA_AR..1.8163, 4_A375_EGR1..1.8189, 4_A375_EGR1..1.8190	-751, -751, -463, -1163	upstream, upstream, upstream, upstream	1	1	1	125	149	19	1	2_A375_pNL97_plus_lncRNA_AR..1	149	Gene C9orf116	FLJ13945, C9orf116, MGC29761	chromosome 9 open reading frame 116	NM_144654, NM_001048265, hCT19893.2, hCT2321727.0	221946_at, 59437_at	NP_653255.1, NP_001041730.1, EAW88154.1, EAW88155.1
GeneID:51116	MRPS2	9	138,392,483	138,396,519	4,036	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5668, 2_A375_pNL97_plus_lncRNA_AR..1.8163, 4_A375_EGR1..1.8189, 4_A375_EGR1..1.8190, 4_A375_EGR1..1.8191	29, 29, -259, 461, 12909	in gene, in gene, upstream, in gene, downstream	1	1	1	65	79	17	2	2_A375_pNL97_plus_lncRNA_AR..1	149	Gene MRPS2	CGI-91, MRPS2, MRP-S2, S2mt	mitochondrial ribosomal protein S2	NM_016034, hCT19882.3, hCT1962458.1	218001_at	NP_057118.1, EAW88152.1, EAW88153.1
GeneID:3933	LCN1	9	138,413,286	138,418,378	5,092	+	3	4_A375_EGR1..1.8191, 4_A375_EGR1..1.8192, 4_A375_EGR1..1.8193	-7694, 1834, 6314	upstream, in gene, downstream	0	0	1	5.33	8.33	14.33	3	4_A375_EGR1..1	15	Gene LCN1	PMFA, VEGP, TP, TLC, LCN1, MGC71975	lipocalin 1 (tear prealbumin)	NM_002297, hCT2356978.0, hCT1960772.0	207930_at	NP_002288.1, EAW88157.1, EAW88156.1
GeneID:100130954	LOC100130954	9	138,466,771	138,478,958	12,187	+	4	4_A375_EGR1..1.8194, 4_A375_EGR1..1.8195, 4_A375_EGR1..1.8196, 4_A375_EGR1..1.8197	8973, 13613, 14029, 16973	in gene, downstream, downstream, downstream	0	0	1	6	8.5	15.75	4	4_A375_EGR1..1	18	Gene LOC100130954		hypothetical LOC100130954	NR_034016, NR_034017		
GeneID:360203	GLT6D1	9	138,515,502	138,531,386	15,884	-	1	4_A375_EGR1..1.8198	21274	downstream	0	0	1	5	5	18	1	4_A375_EGR1..1	18	Gene GLT6D1	GLT6D1, GLTDC1, GT6M7	glycosyltransferase 6 domain containing 1	NM_182974, hCT19889.2		NP_892019.2, EAW88171.1
GeneID:402381	SOHLH1	9	138,585,253	138,591,374	6,121	-	1	4_A375_EGR1..1.8199	13518	downstream	0	0	1	4	4	15	1	4_A375_EGR1..1	15	Gene SOHLH1	bA100C15.3, bHLHe80, NOHLH, C9orf157, SOHLH1, TEB2	spermatogenesis and oogenesis specific basic helix-loop-helix 1	NM_001012415, NM_001101677, hCT2321809.0, hCT2357024.0, hCT1645238.2	1561403_at	NP_001012415.2, NP_001095147.1, EAW88174.1, EAW88175.1, EAW88176.1
GeneID:57582	KCNT1	9	138,594,031	138,684,993	90,962	+	14	4_A375_EGR1..1.8200, 4_A375_EGR1..1.8201, 4_A375_EGR1..1.8202, 4_A375_EGR1..1.8203, 4_A375_EGR1..1.8204, 4_A375_EGR1..1.8205, 4_A375_EGR1..1.8206, 4_A375_EGR1..1.8207, 4_A375_EGR1..1.8208, 4_A375_EGR1..1.8209, 4_A375_EGR1..1.8210, 4_A375_EGR1..1.8211, 4_A375_EGR1..1.8212, 4_A375_EGR1..1.8213	16561, 17521, 32625, 40561, 40945, 42345, 44617, 57505, 68649, 70593, 76209, 78140, 85361, 86353	in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	5.64	8.57	17.14	14	4_A375_EGR1..1	21	Gene KCNT1	FLJ41282, KCa4.1, bA100C15.2, KCNT1, SLACK	potassium channel, subfamily T, member 1	NM_020822, hCT19891.2, hCT2317521.0, hCT2317522.0, hCT2317523.0, hCT2317525.0, hCT2357051.0	1563608_a_at, 1569462_x_at	NP_065873.2, EAW88177.1, EAW88178.1, EAW88179.1, EAW88181.1, EAW88182.1, EAW88180.1
GeneID:10422	UBAC1	9	138,824,815	138,853,226	28,411	-	3	4_A375_EGR1..1.8214, 4_A375_EGR1..1.8215, 4_A375_EGR1..1.8216	35706, 30858, 11722	downstream, downstream, in gene	0	0	1	5.33	7	18	3	4_A375_EGR1..1	19	Gene UBAC1	UBADC1, RP11-432J22.3, UBAC1, GBDR1	UBA domain containing 1	NM_016172, hCT19886.2, hCT2321777.0, hCT1958143.1, hCT1958144.1	202151_s_at	NP_057256.2, EAW88190.1, EAW88187.1, EAW88188.1, EAW88189.1
GeneID:138151	NACC2	9	138,903,202	138,987,131	83,929	-	5	4_A375_EGR1..1.8219, 4_A375_EGR1..1.8220, 4_A375_EGR1..1.8221, 4_A375_EGR1..1.8222, 4_A375_EGR1..1.8223	91718, 72891, 16819, -8789, -10197	downstream, in gene, in gene, upstream, upstream	0	0	1	6.6	7	17.4	5	4_A375_EGR1..1	21	Gene NACC2	BTBD14, BTBD14A, NACC2, MGC23427, BEND9	NACC family member 2, BEN and BTB (POZ) domain containing	NM_144653, hCT19892.3, hCT2321757.0, hCT2321758.0, hCT2321759.0, hCT2321761.0	230050_at	NP_653254.1, EAW88195.1, EAW88193.1, EAW88194.1, EAW88196.1, EAW88197.1
GeneID:402382	LOC402382	9	138,988,123	138,994,444	6,321	+	3	2_A375_pNL97_plus_lncRNA_AR..1.8165, 4_A375_EGR1..1.8222, 4_A375_EGR1..1.8223	13541, 5797, 9205	downstream, in gene, downstream	0	1	1	8.33	10.33	17.67	3	4_A375_EGR1..1	21	Gene LOC402382		hypothetical protein LOC402382	XM_378090		XP_378090.5
GeneID:90120	C9orf69	9	139,006,427	139,010,731	4,304	-	5	2_A375_pNL97_plus_lncRNA_AR..1.8165, 2_A375_pNL97_plus_lncRNA_AR..1.8166, 2_A375_pNL97_plus_lncRNA_AR..1.8167, 4_A375_EGR1..1.8223, 4_A375_EGR1..1.8224	9087, 4075, 139, 13403, -5909	downstream, in gene, in gene, downstream, upstream	0	1	1	11.6	14.8	13.8	5	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene C9orf69	C9orf69, bA83N9.1	chromosome 9 open reading frame 69	NM_152833	224962_at	NP_690046.2
GeneID:100129999	LOC100129999	9	139,014,367	139,016,209	1,842	+	3	2_A375_pNL97_plus_lncRNA_AR..1.8166, 2_A375_pNL97_plus_lncRNA_AR..1.8167, 4_A375_EGR1..1.8224	-7711, -3775, 2273	upstream, upstream, downstream	0	1	1	13	16.33	12.33	3	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene LOC100129999		hypothetical LOC100129999	XR_113272, XR_109859, XR_114318		
GeneID:8022	LHX3	9	139,088,096	139,096,955	8,859	-	2	4_A375_EGR1..1.8228, 4_A375_EGR1..1.8229	1499, 283	in gene, in gene	0	0	1	10	10	21	2	4_A375_EGR1..1	24	Gene LHX3	CPHD3, LHX3, LIM3, DKFZp762A2013, M2-LHX3	LIM homeobox 3	NM_014564, NM_178138, hCT19887.2, hCT2351984.0	221670_s_at	NP_055379.1, NP_835258.1, EAW88205.1, EAW88206.1
GeneID:169714	QSOX2	9	139,098,179	139,137,687	39,508	-	4	4_A375_EGR1..1.8228, 4_A375_EGR1..1.8229, 4_A375_EGR1..1.8230, 4_A375_EGR1..1.8231	42231, 41015, 28823, -10153	downstream, downstream, in gene, upstream	0	0	1	7	7.5	19.5	4	4_A375_EGR1..1	24	Gene QSOX2	SOXN, QSCN6L1, DKFZp762A2013, QSOX2	quiescin Q6 sulfhydryl oxidase 2	NM_181701, hCT19888.4, hCT2349160.1, hCT2349161.1	227146_at, 235239_at	NP_859052.3, EAW88207.1, EAW88208.1, EAW88209.1
GeneID:100188917	ESP33	9	139,141,805	139,143,051	1,246	+	1	4_A375_EGR1..1.8231	6035	downstream	0	0	1	5	5	19	1	4_A375_EGR1..1	19	Gene ESP33		hypothetical locus ESP33	XR_113274, XR_109860, XR_114319, XR_108265		
GeneID:26102	LOC26102	9	139,216,998	139,221,779	4,781	-	2	4_A375_EGR1..1.8234, 4_A375_EGR1..1.8235	179, -9733	in gene, upstream	0	0	1	7.5	14	17	2	4_A375_EGR1..1	18	Gene LOC26102	DKFZP434A062	hypothetical LOC26102	NR_026984	216608_at, 217219_at	
GeneID:26086	GPSM1	9	139,221,932	139,254,057	32,125	+	6	2_A375_pNL97_plus_lncRNA_AR..1.8168, 4_A375_EGR1..1.8234, 4_A375_EGR1..1.8235, 4_A375_EGR1..1.8236, 4_A375_EGR1..1.8237, 4_A375_EGR1..1.8238	17876, -332, 9580, 22516, 27252, 28532	in gene, upstream, in gene, in gene, in gene, in gene	0	1	1	9.5	11.67	17.33	6	2_A375_pNL97_plus_lncRNA_AR..1	23	Gene GPSM1	GPSM1, AGS3, DKFZp727I051	G-protein signaling modulator 1	NM_015597, NM_001145638, NM_001145639, hCT2318154.2, hCT2318156.1, hCT18385.4	1554259_at, 226043_at	NP_056412.4, NP_001139110.1, NP_001139111.1, EAW88216.1, EAW88217.1, EAW88218.1
GeneID:728489	DNLZ	9	139,256,352	139,258,241	1,889	-	3	4_A375_EGR1..1.8237, 4_A375_EGR1..1.8238, 4_A375_EGR1..1.8239	9057, 7777, -6431	downstream, downstream, upstream	0	0	1	9	7	20.33	3	4_A375_EGR1..1	22	Gene DNLZ	HEP, TIMM15, ZIM17, DNLZ, C9orf151, MGC87491, bA413M3.2	DNL-type zinc finger	NM_001080849	228272_at	NP_001074318.1
GeneID:64170	CARD9	9	139,258,408	139,268,133	9,725	-	4	4_A375_EGR1..1.8237, 4_A375_EGR1..1.8238, 4_A375_EGR1..1.8239, 4_A375_EGR1..1.8240	18949, 17669, 3461, -4219	downstream, downstream, in gene, upstream	0	0	1	8.75	7.25	21	4	4_A375_EGR1..1	23	Gene CARD9	hCARD9, CANDF2, CARD9	caspase recruitment domain family, member 9	NM_052813, NM_052814, hCT2318850.0, hCT2318853.0, hCT2318854.0, hCT2318855.0, hCT2318856.0, hCT2318857.0	220162_s_at	NP_434700.2, NP_434701.1, EAW88219.1, EAW88220.1, EAW88221.1, EAW88223.1, EAW88222.1, EAW88224.1
GeneID:6621	SNAPC4	9	139,270,029	139,292,889	22,860	-	4	2_A375_pNL97_plus_lncRNA_AR..1.8169, 4_A375_EGR1..1.8239, 4_A375_EGR1..1.8240, 4_A375_EGR1..1.8241	-1991, 28217, 20537, -2711	upstream, downstream, in gene, upstream	0	1	1	9.5	11	17.75	4	4_A375_EGR1..1	23	Gene SNAPC4	FLJ13451, SNAP190, SNAPC4, PTFalpha	small nuclear RNA activating complex, polypeptide 4, 190kDa	NM_003086, hCT2318844.0, hCT2318845.0, hCT9601.4	205658_s_at, 215926_x_at	NP_003077.2, EAW88227.1, EAW88225.1, EAW88226.1
GeneID:10807	SDCCAG3	9	139,296,374	139,305,054	8,680	-	4	2_A375_pNL97_plus_lncRNA_AR..1.8169, 4_A375_EGR1..1.8241, 4_A375_EGR1..1.8242, 4_A375_EGR1..1.8243	10174, 9454, -130, -7714	downstream, downstream, upstream, upstream	0	1	1	10.5	13.5	18.75	4	4_A375_EGR1..1	25	Gene SDCCAG3	NY-CO-3, SDCCAG3	serologically defined colon cancer antigen 3	NM_006643, NM_001039707, NM_001039708, hCT2318831.1, hCT2318838.1, hCT2318840.1, hCT2318841.1	218427_at, 230058_at, 238111_at	NP_006634.3, NP_001034796.1, NP_001034797.1, EAW88228.1, EAW88230.1, EAW88231.1, EAW88229.1
GeneID:23203	PMPCA	9	139,305,116	139,318,213	13,097	+	5	2_A375_pNL97_plus_lncRNA_AR..1.8169, 4_A375_EGR1..1.8241, 4_A375_EGR1..1.8242, 4_A375_EGR1..1.8243, 4_A375_EGR1..1.8244	-10236, -9516, 68, 7652, 21796	upstream, upstream, in gene, in gene, downstream	0	1	1	9.8	12.4	19.8	5	4_A375_EGR1..1	25	Gene PMPCA	INPP5E, PMPCA, FLJ26258, KIAA0123, MGC104197, Alpha-MPP	peptidase (mitochondrial processing) alpha	NM_015160, hCT1819667.3	212068_at	NP_055975.1, EAW88232.1
GeneID:56623	INPP5E	9	139,323,071	139,334,256	11,185	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5670, 2_A375_pNL97_plus_lncRNA_AR..1.8170, 4_A375_EGR1..1.8244	144, 144, 7344	in gene, in gene, in gene	1	1	1	13	16	17.5	2	4_A375_EGR1..1	24	Gene INPP5E	MGC117201, PPI5PIV, MORMS, INPP5E, CPD4, CORS1, JBTS1	inositol polyphosphate-5-phosphatase, 72 kDa	NM_019892, hCT2318823.0, hCT2357060.0, hCT9381.3	204706_at	NP_063945.2, EAW88235.1, EAW88233.1, EAW88234.1
GeneID:9919	SEC16A	9	139,334,548	139,377,507	42,959	-	6	1_A375_pNL7_minus_lncRNA_AR..1..5670, 2_A375_pNL97_plus_lncRNA_AR..1.8170, 4_A375_EGR1..1.8244, 4_A375_EGR1..1.8245, 4_A375_EGR1..1.8246, 4_A375_EGR1..1.8247	43395, 43395, 50595, 28035, 8803, -1565	downstream, downstream, downstream, in gene, in gene, upstream	1	1	1	10.6	11.4	18.2	5	4_A375_EGR1..1	24	Gene SEC16A	FLJ26737, RP11-413M3.10, SEC16L, KIAA0310, SEC16A, p250	SEC16 homolog A (S. cerevisiae)	NM_014866	215696_s_at	NP_055681.1
GeneID:158055	C9orf163	9	139,377,947	139,380,519	2,572	+	2	4_A375_EGR1..1.8246, 4_A375_EGR1..1.8247	-9243, 1125	upstream, in gene	0	0	1	11	6.5	20	2	4_A375_EGR1..1	21	Gene C9orf163	RP11-413M3.11, FLJ36779, C9orf163	chromosome 9 open reading frame 163	NM_152571, hCT2347472.0	1553842_at	NP_689784.1, EAW88240.1
GeneID:4851	NOTCH1	9	139,388,896	139,440,238	51,342	-	8	4_A375_EGR1..1.8247, 4_A375_EGR1..1.8248, 4_A375_EGR1..1.8249, 4_A375_EGR1..1.8250, 4_A375_EGR1..1.8251, 4_A375_EGR1..1.8252, 4_A375_EGR1..1.8253, 4_A375_EGR1..1.8254	61166, 42329, 40662, 39246, 24302, 21790, 17017, 12158	downstream, in gene, in gene, in gene, in gene, in gene, in gene, in gene	0	0	1	8.13	8.75	16.75	8	4_A375_EGR1..1	21	Gene NOTCH1	hN1, NOTCH1, TAN1	Notch homolog 1, translocation-associated (Drosophila)	NM_017617, hCT1961915.1	218902_at, 223508_at	NP_060087.3, EAW88241.1
GeneID:401561	LOC401561	9	139,510,761	139,511,298	537	-	3	4_A375_EGR1..1.8262, 4_A375_EGR1..1.8263, 4_A375_EGR1..1.8264	10050, 7026, -1630	downstream, downstream, upstream	0	0	1	6.33	6	19	3	4_A375_EGR1..1	22	Gene LOC401561		FP7915 protein	XR_113277, XR_110095, XR_114320		
GeneID:100505976	LOC100505976	9	139,543,062	139,554,873	11,811	-	5	4_A375_EGR1..1.8265, 4_A375_EGR1..1.8266, 4_A375_EGR1..1.8267, 4_A375_EGR1..1.8268, 4_A375_EGR1..1.8269	15705, 13945, -135, -2791, -6119	downstream, downstream, upstream, upstream, upstream	0	0	1	5.4	6.6	17.4	5	4_A375_EGR1..1	19	Gene LOC100505976		hypothetical LOC100505976	XR_113278, XR_110096, XR_114321		
GeneID:51162	EGFL7	9	139,557,377	139,567,130	9,753	+	5	4_A375_EGR1..1.8267, 4_A375_EGR1..1.8268, 4_A375_EGR1..1.8269, 4_A375_EGR1..1.8270, 4_A375_EGR1..1.8271	-2369, 287, 5615, 7999, 9455	upstream, in gene, in gene, in gene, in gene	0	0	1	6.4	7.6	18	5	4_A375_EGR1..1	22	Gene EGFL7	MGC111117, ZNEU1, EGFL7, VE-STATIN, RP11-251M1.2	EGF-like-domain, multiple 7	NM_016215, NM_201446, hCT2318183.0, hCT2318184.0, hCT2356974.0, hCT2356975.0, hCT18770.2	218825_at	NP_057299.1, NP_958854.1, EAW88245.1, EAW88246.1, EAW88247.1, EAW88248.1, EAW88244.1
GeneID:406913	MIR126	9	139,565,054	139,565,138	84	+	5	4_A375_EGR1..1.8267, 4_A375_EGR1..1.8268, 4_A375_EGR1..1.8269, 4_A375_EGR1..1.8270, 4_A375_EGR1..1.8271	-10046, -7390, -2062, 322, 1776	upstream, upstream, upstream, downstream, downstream	0	0	1	6.4	7.6	18	5	4_A375_EGR1..1	22	Gene MIR126	MIR126, MIRN126, miRNA126	microRNA 126	NR_029695		
GeneID:10555	AGPAT2	9	139,567,595	139,581,911	14,316	-	7	4_A375_EGR1..1.8268, 4_A375_EGR1..1.8269, 4_A375_EGR1..1.8270, 4_A375_EGR1..1.8271, 4_A375_EGR1..1.8272, 4_A375_EGR1..1.8273, 4_A375_EGR1..1.8274	24247, 18919, 16535, 15079, 4007, 631, -4937	downstream, downstream, downstream, downstream, in gene, in gene, upstream	0	0	1	6.29	7.86	17.57	7	4_A375_EGR1..1	22	Gene AGPAT2	AGPAT2, BSCL1, BSCL, LPAAT-beta, 1-AGPAT2, LPAAB	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	NM_006412, NM_001012727, hCT1971104.1, hCT2356954.0, hCT18360.4, hCT1958139.1	210678_s_at, 32837_at	NP_006403.2, NP_001012745.1, EAW88249.1, EAW88250.1, EAW88251.1, EAW88252.1

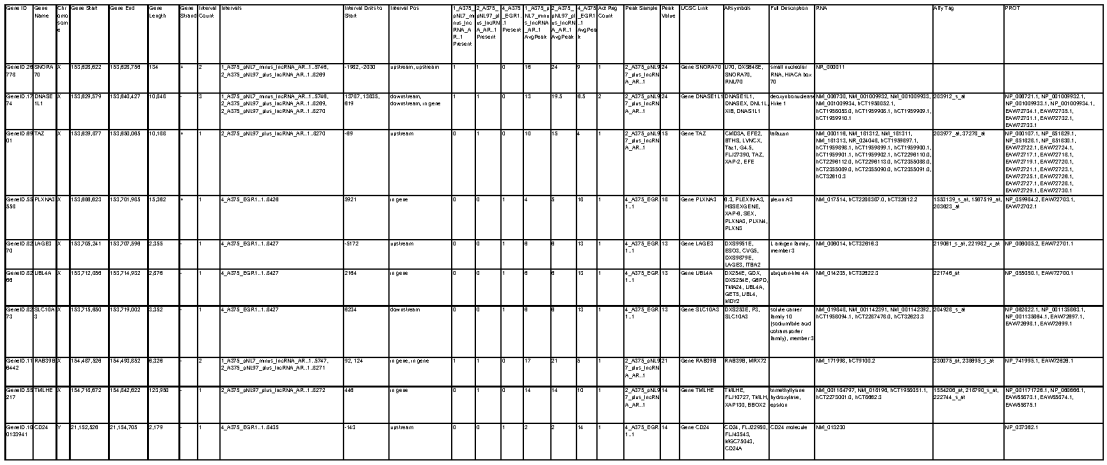
Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:138311	FAM69B	9	139,607,024	139,619,170	12,146	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5671, 2_A375_pNL97_plus_lncRNA_AR..1..8171, 2_A375_pNL97_plus_lncRNA_AR..1..8172, 4_A375_EGR1..1..8275, 4_A375_EGR1..1..8276	15728, 14272, 15744, 1275, 8016	downstream, downstream, downstream, in gene, in gene	1	1	1	14	17.25	16.25	4	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene FAM69B	MGC20262, FAM69B, C9orf136, pp8977	family with sequence similarity 69, member B	NM_152421, hCT2356996.0, hCT18776.3	226940_at, 227652_at, 229002_at, 229003_x_at	NP_689634.2, EAW88254.1, EAW88253.1
GeneID:84973	SNHG7	9	139,619,046	139,622,636	3,590	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5671, 2_A375_pNL97_plus_lncRNA_AR..1..8171, 2_A375_pNL97_plus_lncRNA_AR..1..8172, 4_A375_EGR1..1..8276	-116, 1340, -132, 7596	upstream, in gene, upstream, downstream	1	1	1	15.67	20	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene SNHG7	SNHG7, MGC16037, NCRNA00061	small nucleolar RNA host gene 7 (non-protein coding)	NR_003672, NR_024542, NR_024543	1552729_at, 1556619_at, 229050_s_at	
GeneID:677824	SNORA43	9	139,620,556	139,620,689	133	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5671, 2_A375_pNL97_plus_lncRNA_AR..1..8171, 2_A375_pNL97_plus_lncRNA_AR..1..8172, 4_A375_EGR1..1..8276	-2063, -607, -2079, 5649	upstream, upstream, upstream, downstream	1	1	1	15.67	20	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene SNORA43	SNORA43, ACA43	small nucleolar RNA, H/ACA box 43	NR_002975		
GeneID:677804	SNORA17	9	139,621,199	139,621,331	132	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5671, 2_A375_pNL97_plus_lncRNA_AR..1..8171, 2_A375_pNL97_plus_lncRNA_AR..1..8172, 4_A375_EGR1..1..8276	-1421, 35, -1437, 6291	upstream, in gene, upstream, downstream	1	1	1	15.67	20	15.33	3	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene SNORA17	ACA17, SNORA17	small nucleolar RNA, H/ACA box 17	NR_002956		
GeneID:414332	LCN10	9	139,632,619	139,637,411	4,792	-	3	1_A375_pNL7_minus_lncRNA_AR..1..5671, 2_A375_pNL97_plus_lncRNA_AR..1..8172, 4_A375_EGR1..1..8277	14659, 14643, -269	downstream, downstream, upstream	1	1	1	15	21	17.5	2	2_A375_pNL97_plus_lncRNA_AR..1	34	Gene LCN10	LCN10	lipocalin 10	NM_001001712	236071_at	NP_001001712.2
GeneID:158062	LCN6	9	139,638,469	139,642,980	4,511	-	1	4_A375_EGR1..1..8277	5300	downstream	0	0	1	4	8	18	1	4_A375_EGR1..1	18	Gene LCN6	hLcn5, LCN5, UNQ643, LCN6	lipocalin 6	NM_198946	1559664_at	NP_945184.1
GeneID:100128593	LOC100128593	9	139,640,613	139,644,363	3,750	+	1	4_A375_EGR1..1..8277	-2933	upstream	0	0	1	4	8	18	1	4_A375_EGR1..1	18	Gene LOC100128593		hypothetical LOC100128593	NR_033913		
GeneID:85014	TMEM141	9	139,685,777	139,687,769	1,992	+	1	4_A375_EGR1..1..8278	8639	downstream	0	0	1	8	5	17	1	4_A375_EGR1..1	17	Gene TMEM141	RP11-216L13.7, TMEM141, MGC14141	transmembrane protein 141	NM_032928	225568_at	NP_116317.1
GeneID:84960	KIAA1984	9	139,690,790	139,702,193	11,403	+	1	4_A375_EGR1..1..8278	3626	in gene	0	0	1	8	5	17	1	4_A375_EGR1..1	17	Gene KIAA1984	PARF, bA216L13.7, KIAA1984, RP11-216L13.9, MGC15438	KIAA1984	NM_001039374	236518_at	NP_001034463.4
GeneID:100131193	hCG_2022318	9	139,698,379	139,703,300	4,921	-	1	4_A375_EGR1..1..8278	8684	downstream	0	0	1	8	5	17	1	4_A375_EGR1..1	17	Gene hCG_2022318	LOC100131193	hypothetical LOC100131193	NR_024560		
GeneID:55684	C9orf86	9	139,702,374	139,735,639	33,265	+	12	1_A375_pNL7_minus_lncRNA_AR..1..5672, 1_A375_pNL7_minus_lncRNA_AR..1..5673, 1_A375_pNL7_minus_lncRNA_AR..1..5674, 2_A375_pNL97_plus_lncRNA_AR..1..8173, 2_A375_pNL97_plus_lncRNA_AR..1..8174, 2_A375_pNL97_plus_lncRNA_AR..1..8175, 4_A375_EGR1..1..8278, 4_A375_EGR1..1..8279, 4_A375_EGR1..1..8280, 4_A375_EGR1..1..8281, 4_A375_EGR1..1..8282, 4_A375_EGR1..1..8283	34662, 40090, 41370, 34554, 40026, 41274, -7958, 25682, 31578, 33962, 34554, 36122	downstream, downstream, downstream, downstream, downstream, downstream, upstream, in gene, in gene, downstream, downstream, downstream	1	1	1	12.43	13.14	14.43	7	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene C9orf86	RBEL1, bA216L13.9, FLJ13045, FLJ10101, pp8875, KIAA1984, Parf, C9orf86	chromosome 9 open reading frame 86	NM_001173988, NM_001173989, NM_024718, hCT2318191.1, hCT2318198.1, hCT2318211.1, hCT2318214.1, hCT2356927.0	219826_at, 223166_x_at, 225377_at	NP_001167459.1, NP_001167460.1, NP_078994.3, EAW88282.1, EAW88283.1, EAW88285.1, EAW88284.1, EAW88286.1
GeneID:100422860	MIR4292	9	139,725,409	139,725,475	66	+	2	4_A375_EGR1..1..8279, 4_A375_EGR1..1..8280	2647, 8543	downstream, downstream	0	0	1	3.5	8.5	16	2	4_A375_EGR1..1	17	Gene MIR4292	MIR4292	microRNA 4292	NR_036251		
GeneID:389813	C9orf172	9	139,738,867	139,741,797	2,930	+	12	1_A375_pNL7_minus_lncRNA_AR..1..5672, 1_A375_pNL7_minus_lncRNA_AR..1..5673, 1_A375_pNL7_minus_lncRNA_AR..1..5674, 2_A375_pNL97_plus_lncRNA_AR..1..8173, 2_A375_pNL97_plus_lncRNA_AR..1..8174, 2_A375_pNL97_plus_lncRNA_AR..1..8175, 4_A375_EGR1..1..8280, 4_A375_EGR1..1..8281, 4_A375_EGR1..1..8282, 4_A375_EGR1..1..8283, 4_A375_EGR1..1..8284, 4_A375_EGR1..1..8285	-1811, 3597, 4877, -1939, 3533, 4781, -4915, -2531, -1939, -371, 7805, 12941	upstream, downstream, downstream, upstream, downstream, downstream, upstream, upstream, upstream, upstream, downstream, downstream	1	1	1	12.71	13.86	15.43	7	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene C9orf172	C9orf172	chromosome 9 open reading frame 172	NM_001080482		NP_001073951.2
GeneID:29085	PHPT1	9	139,743,256	139,745,490	2,234	+	12	1_A375_pNL7_minus_lncRNA_AR..1..5672, 1_A375_pNL7_minus_lncRNA_AR..1..5673, 1_A375_pNL7_minus_lncRNA_AR..1..5674, 2_A375_pNL97_plus_lncRNA_AR..1..8173, 2_A375_pNL97_plus_lncRNA_AR..1..8174, 2_A375_pNL97_plus_lncRNA_AR..1..8175, 4_A375_EGR1..1..8280, 4_A375_EGR1..1..8281, 4_A375_EGR1..1..8282, 4_A375_EGR1..1..8283, 4_A375_EGR1..1..8284, 4_A375_EGR1..1..8285	-6200, -792, 486, 6328, -656, 392, -9304, -8920, -6328, -4760, 3416, 8552	upstream, upstream, in gene, upstream, upstream, in gene, upstream, upstream, upstream, upstream, downstream, downstream	1	1	1	12.71	13.86	15.43	7	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene PHPT1	PHP14, RP11-216L13.10, CGI-202, PHPT1, DKFZp564M173, HSPC141, bA216L13.10	phosphohistidine phosphatase 1	NM_014172, NM_001135861, hCT2318225.0, hCT2318227.0, hCT2318229.0, hCT2318231.0	223207_x_at, 225663_x_at	NP_054891.2, NP_001129333.1, EAW88289.1, EAW88290.1, EAW88291.1, EAW88292.1
GeneID:158056	MAMDC4	9	139,746,819	139,755,251	8,432	+	11	1_A375_pNL7_minus_lncRNA_AR..1..5672, 1_A375_pNL7_minus_lncRNA_AR..1..5673, 1_A375_pNL7_minus_lncRNA_AR..1..5674, 2_A375_pNL97_plus_lncRNA_AR..1..8173, 2_A375_pNL97_plus_lncRNA_AR..1..8174, 2_A375_pNL97_plus_lncRNA_AR..1..8175, 2_A375_pNL97_plus_lncRNA_AR..1..8176, 4_A375_EGR1..1..8282, 4_A375_EGR1..1..8283, 4_A375_EGR1..1..8284, 4_A375_EGR1..1..8285	-9763, -4355, -3075, -9891, -4419, -3171, 14013, -9891, -8323, -147, 4989	upstream, upstream, upstream, upstream, upstream, upstream, downstream, upstream, upstream, upstream, in gene	1	1	1	14	15.57	14.14	7	1_A375_pNL7_minus_lncRNA_AR..1	33	Gene MAMDC4	MAMDC4, AEGP, DKFZp434M1411	MAM domain containing 4	NM_206920, hCT2318234.0, hCT2357005.0, hCT18777.3	229473_at	NP_996803.2, EAW88295.1, EAW88293.1, EAW88294.1
GeneID:8721	EDF1	9	139,756,571	139,760,738	4,167	-	3	2_A375_pNL97_plus_lncRNA_AR..1..8176, 4_A375_EGR1..1..8284, 4_A375_EGR1..1..8285	-94, 14066, 8930	upstream, downstream, downstream	0	1	1	8.67	13	15.67	3	2_A375_pNL97_plus_lncRNA_AR..1	21	Gene EDF1	MGC9058, EDF-1, EDF1, MBF1	endothelial differentiation-related factor 1	NM_003792, NM_153200, hCT2318780.0, hCT2318781.0, hCT1950317.1	209058_at, 209059_s_at	NP_003783.1, NP_694880.1, EAW88296.1, EAW88297.1, EAW88298.1
GeneID:7186	TRAF2	9	139,780,965	139,821,067	40,102	+	4	2_A375_pNL97_plus_lncRNA_AR..1..8177, 2_A375_pNL97_plus_lncRNA_AR..1..8178, 4_A375_EGR1..1..8286, 4_A375_EGR1..1..8287	-3925, 15355, 15259, 21691	upstream, in gene, in gene, in gene	0	1	1	13.33	14.67	17	3	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene TRAF2	MGC:45012, TRAP3, TRAP, TRAF2	TNF receptor-associated factor 2	NM_021138, hCT2318242.0, hCT2318245.0, hCT2318247.0, hCT2318248.0, hCT18775.3, hCT1958140.0, hCT1958141.0	204413_at	NP_066961.2, EAW88304.1, EAW88301.1, EAW88302.1, EAW88303.1, EAW88305.1, EAW88299.1, EAW88300.1
GeneID:54461	FBXW5	9	139,834,887	139,839,173	4,286	-	7	1_A375_pNL7_minus_lncRNA_AR..1..5675, 2_A375_pNL97_plus_lncRNA_AR..1..8179, 2_A375_pNL97_plus_lncRNA_AR..1..8180, 4_A375_EGR1..1..8288, 4_A375_EGR1..1..8289, 4_A375_EGR1..1..8290, 4_A375_EGR1..1..8291	-27, -27, -5515, 3717, 1221, -2731, -9227	upstream, upstream, upstream, in gene, in gene, upstream, upstream	1	1	1	13	12.17	14.83	6	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene FBXW5	MGC20962, DKFZp434B205, FBXW5, RP11-229P13.10, Fbw5	F-box and WD repeat domain containing 5	NM_018998, hCT2318767.0, hCT2318768.0, hCT2318769.0, hCT2318771.0, hCT2318773.0, hCT2318775.0, hCT2318776.0, hCT85155.2, hCT1950321.1	223050_s_at	NP_061871.1, EAW88309.1, EAW88308.1, EAW88310.1, EAW88313.1, EAW88314.1, EAW88307.1, EAW88311.1, EAW88312.1, EAW88315.1
GeneID:733	C8G	9	139,839,698	139,841,426	1,728	+	7	1_A375_pNL7_minus_lncRNA_AR..1..5675, 2_A375_pNL97_plus_lncRNA_AR..1..8179, 2_A375_pNL97_plus_lncRNA_AR..1..8180, 4_A375_EGR1..1..8288, 4_A375_EGR1..1..8289, 4_A375_EGR1..1..8290, 4_A375_EGR1..1..8291	-498, -498, 4990, 4242, -1746, 2206, 8702	upstream, upstream, downstream, upstream, upstream, downstream, downstream	1	1	1	13	12.17	14.83	6	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene C8G	MGC142186, C8G, C8C	complement component 8, gamma polypeptide	NM_000606, hCT85124.3	210324_at	NP_000597.2, EAW88316.1
GeneID:286256	LCN12	9	139,846,768	139,849,949	3,181	+	7	1_A375_pNL7_minus_lncRNA_AR..1..5675, 2_A375_pNL97_plus_lncRNA_AR..1..8179, 2_A375_pNL97_plus_lncRNA_AR..1..8180, 4_A375_EGR1..1..8289, 4_A375_EGR1..1..8290, 4_A375_EGR1..1..8291, 4_A375_EGR1..1..8292	-7568, -7568, -2080, -8616, -4684, 1632, 12272	upstream, upstream, upstream, upstream, upstream, in gene, downstream	1	1	1	13.17	12	14.83	6	1_A375_pNL7_minus_lncRNA_AR..1	27	Gene LCN12	MGC48935, LCN12, MGC34753	lipocalin 12	NM_178536, hCT2343018.2, hCT2348630.1, hCT2348631.1, hCT2357025.0	230717_at	NP_848631.2, EAW88320.1, EAW88317.1, EAW88318.1, EAW88319.1
GeneID:5730	PTGDS	9	139,871,956	139,876,194	4,238	+	3	4_A375_EGR1..1..8293, 4_A375_EGR1..1..8294, 4_A375_EGR1..1..8295	-8340, -7166, -5236	upstream, upstream, upstream	0	0	1	8.67	7	19	3	4_A375_EGR1..1	23	Gene PTGDS	PTGDS, PGDS2, PGDS, PDS, LPGDS, L-PGDS, PGD2	prostaglandin D2 synthase 21kDa (brain)	NM_000954, hCT1813027.1, hCT1814947.0, hCT1819672.2	211663_x_at, 211748_x_at, 212187_x_at	NP_000945.3, EAW88321.1, EAW88322.1, EAW88323.1
GeneID:286257	C9orf142	9	139,886,870	139,888,426	1,556	+	2	4_A375_EGR1..1..8296, 4_A375_EGR1..1..8297	4618, 5978	downstream, downstream	0	0	1	7	4.5	18.5	2	4_A375_EGR1..1	21	Gene C9orf142	C9orf142	chromosome 9 open reading frame 142	NM_183241, hCT1971060.1, hCT2356983.0, hCT2356984.0, hCT2356985.0, hCT2356986.0	226070_at	NP_899064.1, EAW88325.1, EAW88324.1, EAW88326.1, EAW88327.1, EAW88328.1
GeneID:9022	CLIC3	9	139,889,060	139,891,024	1,964	-	2	4_A375_EGR1..1..8296, 4_A375_EGR1..1..8297	-464, -1824	upstream, upstream	0	0	1	7	4.5	18.5	2	4_A375_EGR1..1	21	Gene CLIC3	CLIC3	chloride intracellular channel 3	NM_004669, hCT1819673.2, hCT1958124.0	219529_at	NP_004660.2, EAW88329.1, EAW88330.1
GeneID:20	ABCA2	9	139,901,686	139,923,374	21,688	-	8	2_A375_pNL97_plus_lncRNA_AR..1..8181, 4_A375_EGR1..1..8296, 4_A375_EGR1..1..8297, 4_A375_EGR1..1..8298, 4_A375_EGR1..1..8299, 4_A375_EGR1..1..8300, 4_A375_EGR1..1..8301, 4_A375_EGR1..1..8302	-274, 31886, 30526, 16206, 11116, 8142, 270, -2717	upstream, downstream, in gene, in gene, in gene, in gene, upstream	0	1	1	7.43	8.86	18.43	7	4_A375_EGR1..1	22	Gene ABCA2	ABC2, MGC129761, ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	NM_212533, NM_001606, hCT2318756.0, hCT2318757.0, hCT85115.4	210099_at, 210100_s_at, 212772_s_at	NP_997698.1, NP_001597.2, EAW88331.1, EAW88332.1, EAW88333.1
GeneID:401563	C9orf139	9	139,921,916	139,931,234	9,318	+	10	2_A375_pNL97_plus_lncRNA_AR..1..8181, 2_A375_pNL97_plus_lncRNA_AR..1..8182, 4_A375_EGR1..1..8299, 4_A375_EGR1..1..8300, 4_A375_EGR1..1..8301, 4_A375_EGR1..1..8302, 4_A375_EGR1..1..8303, 4_A375_EGR1..1..8304, 4_A375_EGR1..1..8305, 4_A375_EGR1..1..8306	1732, 18724, -9680, -8684, 1168, 4175, 12356, 13968, 17924, 18999	in gene, downstream, upstream, upstream, in gene, in gene, downstream, downstream, downstream, downstream	0	1	1	8.5	11.25	18.25	8	4_A375_EGR1..1	22	Gene C9orf139	FLJ42909, C9orf139, FLJ38266	chromosome 9 open reading frame 139	NM_207511, hCT2318273.0		NP_997394.1, EAW88334.1
GeneID:2529	FUT7	9	139,924,626	139,927,292	2,666	-	6	2_A375_pNL97_plus_lncRNA_AR..1..8181, 4_A375_EGR1..1..8300, 4_A375_EGR1..1..8301, 4_A375_EGR1..1..8302, 4_A375_EGR1..1..8303, 4_A375_EGR1..1..8304	3644, 12060, 4166, 1201, -6960, -8612	downstream, downstream, downstream, in gene, upstream, upstream	0	1	1	7.6	10	19.2	5	4_A375_EGR1..1	22	Gene FUT7	FUT7, FucT-VII	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	NM_004479	210506_at, 217696_at	NP_004470.1
GeneID:56654	NPDC1	9	139,933,909	139,940,676	6,767	-	8	2_A375_pNL97_plus_lncRNA_AR..1..8181, 2_A375_pNL97_plus_lncRNA_AR..1..8182, 4_A375_EGR1..1..8302, 4_A375_EGR1..1..8303, 4_A375_EGR1..1..8304, 4_A375_EGR1..1..8305, 4_A375_EGR1..1..8306, 4_A375_EGR1..1..8307	17026, 36, 14565, 6404, 4772, 836, -239, -4956	downstream, in gene, downstream, in gene, in gene, in gene, upstream, upstream	0	1	1	8.71	11.14	18	7	4_A375_EGR1..1	20	Gene NPDC1	CAB-, CAB, CAB-1, CAB1, DKFZp586J0523, NPDC1	neural proliferation, differentiation and control, 1	NM_015392, hCT2318755.1	218086_at	NP_056207.3, EAW88335.1
GeneID:954	ENTPD2	9	139,942,553	139,948,505	5,952	-	7	2_A375_pNL97_plus_lncRNA_AR..1..8182, 4_A375_EGR1..1..8303, 4_A375_EGR1..1..8304, 4_A375_EGR1..1..8305, 4_A375_EGR1..1..8306, 4_A375_EGR1..1..8307, 4_A375_EGR1..1..8308	7665, 14233, 12601, 8665, 7590, 2673, -9495	downstream, downstream, downstream, downstream, downstream, in gene, upstream	0	1	1	8.33	10.33	18.33	6	4_A375_EGR1..1	20	Gene ENTPD2	ENTPD2, NTPDase-2, CD39L1	ectonucleoside triphosphate diphosphohydrolase 2	NM_203468, NM_001246, hCT1971256.1, hCT85173.3	207372_s_at, 230430_at	NP_982293.1, NP_001237.1, EAW88336.1, EAW88337.1
GeneID:89958	C9orf140	9	139,956,579	139,965,028	8,449	-	5	2_A375_pNL97_plus_lncRNA_AR..1..8183, 4_A375_EGR1..1..8308, 4_A375_EGR1..1..8309, 4_A375_EGR1..1..8310, 4_A375_EGR1..1..8311	260, 7028, 1444, -3644, -8426	in gene, in gene, in gene, upstream, upstream	0	1	1	8	10.2	16.4	5	4_A375_EGR1..1	20	Gene C9orf140	C9orf140, p42.3	chromosome 9 open reading frame 140	NM_178448, hCT22931.3, hCT2318751.0	225777_at	NP_848543.2, EAW88339.1, EAW88338.1
GeneID:91373	UAP1L1	9	139,971,953	139,978,990	7,037	+	4	2_A375_pNL97_plus_lncRNA_AR..1..8183, 4_A375_EGR1..1..8309, 4_A375_EGR1..1..8310, 4_A375_EGR1..1..8311	-7165, -8369, -3261, -497	upstream, upstream, upstream, upstream	0	1	1	8	9.75	15.5	4	2_A375_pNL97_plus_lncRNA_AR..1	19	Gene UAP1L1	UAP1L1, RP11-229P13.18	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	NM_207309, hCT22930.2, hCT2318266.0, hCT2357067.0, hCT2357068.0	214755_at	NP_997192.2, EAW88341.1, EAW88340.1, EAW88342.1, EAW88343.1
GeneID:100289341	hCG_2022304	9	139,979,398	139,981,269	1,871	-	1	4_A375_EGR1..1..8311	9813	downstream	0	0	1	7	9	15	1	4_A375_EGR1..1	15	Gene hCG_2022304	FLJ13250, LOC100289341	similar to hCG2022304	NR_027447		
GeneID:11253	MAN1B1	9	139,981,417	140,003,639	22,222	+	5	4_A375_EGR1..1..8311, 4_A375_EGR1..1..8312, 4_A375_EGR1..1..8313, 4_A375_EGR1..1..8314, 4_A375_EGR1..1..8315	-9981, 11031, 22647, 28343, 29079	upstream, in gene, downstream, downstream, downstream	0	0	1	8	7.8	19	5	4_A375_EGR1..1	23	Gene MAN1B1	MANA-ER, ERMan1, MAN1B1	mannosidase, alpha, class 1B, member 1	NM_016219, hCT2318292.0, hCT2357058.0, hCT1981904.2	218636_s_at, 65884_at	NP_057303.2, EAW88345.1, EAW88346.1, EAW88347.1
GeneID:29952	DPP7	9	140,004,992	140,009,195	4,203	-	3	4_A375_EGR1..1..8313, 4_A375_EGR1..1..8314, 4_A375_EGR1..1..8315	5131, -565, -1301	downstream, upstream, upstream	0	0	1	8	6	20.67	3	4_A375_EGR1..1	23	Gene DPP7	DPPII, DPP2, DPP7, QPP	dipeptidyl-peptidase 7	NM_013379, hCT1819679.1	224614_at, 236012_at, 241973_x_at	NP_037511.2, EAW88349.1
GeneID:2902	GRIN1	9	140,033,609	140,063,214	29,605	+	4	4_A375_EGR1..1..8316, 4_A375_EGR1..1..8317, 4_A375_EGR1..1..8318, 4_A375_EGR1..1..8319	9719, 33207, 35319, 36418	in gene, downstream, downstream, downstream	0	0	1	9.75	7.25	17	4	4_A375_EGR1..1	20	Gene GRIN1	NR1, NMDAR1, NMDA1, GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	NM_000832, NM_001185090, NM_001185091, NM_007327, NM_021569, hCT2318304.0, hCT2318305.0, hCT2318308.0, hCT2318310.0, hCT2318313.0, hCT2318318.0, hCT1957520.1, hCT1957521.1, hCT1957522.1, hCT1957523.1, hCT1957524.1	205915_x_at, 210781_x_at, 210782_x_at, 211125_x_at	NP_000823.4, NP_001172019.1, NP_067544.1, NP_015566.1, NP_001172020.1, EAW88356.1, EAW88350.1, EAW88351.1, EAW88352.1, EAW88353.1, EAW88354.1, EAW88355.1, EAW88357.1, EAW88360.1, EAW88358.1, EAW88359.1
GeneID:389816	LRRC26	9	140,063,210	140,064,491	1,281	-	3	4_A375_EGR1..1..8317, 4_A375_EGR1..1..8318, 4_A375_EGR1..1..8319	-2325, -4437, -5536	upstream, upstream, upstream	0	0	1	10.33	7.33	16.67	3	4_A375_EGR1..1	20	Gene LRRC26	LRRC26, bA350O14.10, CAPC	leucine rich repeat containing 26	NM_001013653		NP_001013675.1
GeneID:100505993	LOC100505993	9	140,065,380	140,066,498	1,118	-	3	4_A375_EGR1..1..8317, 4_A375_EGR1..1..8318, 4_A375_EGR1..1..8319	-316, -2430, -3529	upstream, upstream, upstream	0	0	1	10.33	7.33	16.67	3	4_A375_EGR1..1	20	Gene LOC100505993		hypothetical LOC100505993	XR_110097, XR_110098		
GeneID:29882	ANAPC2	9	140,069,236	140,083,057	13,821	-	7	1_A375_pNL7_minus_lncRNA_AR..1..5676, 2_A375_pNL97_plus_lncRNA_AR..1..8184, 4_A375_EGR1..1..8317, 4_A375_EGR1..1..8318, 4_A375_EGR1..1..8319, 4_A375_EGR1..1..8320, 4_A375_EGR1..1..8321	49, 17, 16241, 14129, 13030, 433, -719	in gene, in gene, downstream, downstream, in gene, in gene, upstream	1	1	1	19.25	12.75	17.5	4	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene ANAPC2	RP11-350O14.5, ANAPC2, APC2	anaphase promoting complex subunit 2	NM_013366, hCT1785533.3	218555_at	NP_037498.1, EAW88361.1
GeneID:8636	SSNA1	9	140,083,054	140,084,822	1,768	+	4	1_A375_pNL7_minus_lncRNA_AR..1..5676, 2_A375_pNL97_plus_lncRNA_AR..1..8184, 4_A375_EGR1..1..8320, 4_A375_EGR1..1..8321	-46, -14, -430, 722	upstream, upstream, upstream, in gene	1	1	1	46	29	20	1	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene SSNA1	NA14, N14, SSNA1, NA-14	Sjogren syndrome nuclear autoantigen 1	NM_003731, hCT2318329.0, hCT2318330.0	210378_s_at	NP_003722.2, EAW88362.1, EAW88363.1
GeneID:286262	C9orf75	9	140,086,069	140,094,980	8,911	-	5	1_A375_pNL7_minus_lncRNA_AR..1..5676, 2_A375_pNL97_plus_lncRNA_AR..1..8184, 4_A375_EGR1..1..8320, 4_A375_EGR1..1..8321, 4_A375_EGR1..1..8322	11972, 11940, 12356, 11204, -5160	downstream, downstream, downstream, downstream, upstream	1	1	1	32.5	24.5	20	2	1_A375_pNL7_minus_lncRNA_AR..1	46	Gene C9orf75	MGC131933, RP11-350O14.7, C9orf75, DFNB79, FLJ90254, TPRN	chromosome 9 open reading frame 75	NM_173691, NM_001128228, hCT1963566.1	225691_at	NP_775962.2, NP_001121700.1, EAW88364.1



Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Dists to Start	Interval Pos	1_A375_pNL7_minus_lncRNA_AR..1 Present	2_A375_pNL97_plus_lncRNA_AR..1 Present	4_A375_EGR1..1 Present	1_A375_pNL7_minus_lncRNA_AR..1 AvgPeak	2_A375_pNL97_plus_lncRNA_AR..1 AvgPeak	4_A375_EGR1..1 AvgPeak	Act Reg Count	Peak Sample	Peak Value	UCSC Link	Altsymbols	Full Description	RNA	Affy Tag	PROT
GeneID:2742	GLRA2	X	14,547,420	14,749,934	202,514	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5689	164	in gene	1	0	0	17	12	2	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene GLRA2	GLR, GLRA2	glycine receptor, alpha 2	NM_002063, NM_001118885, NM_001118886, NM_001171942, hCT2254972.0, hCT2254974.0, hCT5798.3	207462_at	NP_002054.1, NP_001112357.1, NP_001112358.1, NP_001165413.1, EAW98858.1, EAW98859.1, EAW98860.1
GeneID:140462	ASB9	X	15,262,109	15,288,589	26,480	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5691	36821	downstream	1	0	0	14	8	1	1	1_A375_pNL7_minus_lncRNA_AR..1	14	Gene ASB9	DKFZp564L0862, ASB9, MGC4954, FLJ20636	ankyrin repeat and SOCS box containing 9	NM_001031739, NM_024087, NM_001168530, NM_001168531, hCT2255527.0, hCT2255529.0, hCT2255531.0, hCT2358274.0, hCT2358275.0, hCT2358276.0, hCT6782.3	205673_s_at	NP_001026909.1, NP_076992.1, NP_001162002.1, NP_001162003.1, EAW98873.1, EAW98874.1, EAW98870.1, EAW98871.1, EAW98872.1, EAW98875.1, EAW98876.1
GeneID:57393	TMEM27	X	15,845,441	15,883,154	37,713	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5692, 2_A375_pNL97_plus_lncRNA_AR..1..8202	-9902, -10094	upstream, upstream	1	1	0	14	17	7	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene TMEM27	NX-17, NX17, TMEM27	transmembrane protein 27	NM_020665, hCT6771.2	223784_at	NP_065716.1, EAW98894.1
GeneID:94056	SYAP1	X	16,737,707	16,780,807	43,100	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5693, 2_A375_pNL97_plus_lncRNA_AR..1..8204	52405, 52389	downstream, downstream	1	1	0	16	17	8	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene SYAP1	DKFZp686K221, FLJ14495, FLJ44185, SYAP1, PRO3113	synapse associated protein 1, SAP47 homolog (Drosophila)	NM_032796, NR_033181, hCT22666.3	225154_at	NP_116185.2, EAW98917.1
GeneID:55787	CXorf15	X	16,804,555	16,862,642	58,087	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5694	-315	upstream	1	0	0	17	17	2	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene CXorf15	FLJ33481, FIAT, TXLNG, ELRG, MGC126821, LSR5, MGC126825, CXorf15, FLJ11209	chromosome X open reading frame 15	NM_018360, NM_001168363, hCT11182.2	1557954_at, 219969_at, 227520_at	NP_060830.2, NP_001162154.1, EAW98918.1
GeneID:6247	RS1	X	18,657,806	18,690,223	32,415	-	1	4_A375_EGR1..1..8376	-2661	upstream	0	0	1	11	9	23	1	4_A375_EGR1..1	23	Gene RS1	RS, XLRS1, RS1	retinoschisin 1	NM_000330, hCT10653.3	207383_at, 216937_s_at	NP_000321.1, EAW98942.1
GeneID:5256	PHKA2	X	18,910,416	19,002,480	92,064	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8205	-453	upstream	0	1	0	11	13	10	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene PHKA2	PHK, GSD9A, PYK, XLG2, XLG, MGC133071, PHKA2, PYKL	phosphorylase kinase, alpha 2 (liver)	NM_000292, hCT10652.3	1559705_s_at, 1560358_at, 209438_at, 209439_s_at	NP_000283.1, EAW98951.1
GeneID:10149	GPR64	X	19,007,425	19,140,755	133,330	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8205	137822	downstream	0	1	0	11	13	10	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene GPR64	GPR64, EDDM6, MGC138738, TM7LN2, FLJ00262, MGC138739, MGC104454, HE6	G protein-coupled receptor 64	NM_001079858, NM_001079859, NM_001079860, NM_001184833, NM_001184834, NM_001184835, NM_001184836, NM_001184837, NM_005756, hCT1955330.1, hCT2256196.0, hCT2358236.0, hCT2358237.0, hCT2358238.0, hCT2358239.0	206002_at	NP_001073327.1, NP_001073328.1, NP_001073329.1, NP_001171762.1, NP_001171763.1, NP_001171764.1, NP_005747.2, NP_001171765.1, NP_001171766.1, EAW98952.1, EAW98953.1, EAW98954.1, EAW98955.1, EAW98956.1, EAW98957.1
GeneID:5160	PDHA1	X	19,362,011	19,379,825	17,814	+	1	4_A375_EGR1..1..8379	-187	upstream	0	0	1	6	10	18	1	4_A375_EGR1..1	18	Gene PDHA1	PDHA1, PHE1A, PDHCE1A, PDHA	pyruvate dehydrogenase (lipoamide) alpha 1	NM_000284, NM_001173454, NM_001173455, NM_001173456, hCT2255528.0, hCT8622.3	1555864_s_at, 200980_s_at	NP_000275.1, NP_001166925.1, NP_001166926.1, NP_001166927.1, EAW98960.1, EAW98961.1
GeneID:22866	CNKSR2	X	21,392,536	21,672,813	280,277	+	1	4_A375_EGR1..1..8380	232	in gene	0	0	1	12	9	16	1	4_A375_EGR1..1	16	Gene CNKSR2	KIAA0902, CNKSR2, KSR2, MAGUIN, CNK2	connector enhancer of kinase suppressor of Ras 2	NM_014927, NM_001168647, NM_001168648, NM_001168649, hCT10039.4, hCT2255609.0, hCT2255611.0	1554607_at, 206731_at	NP_055742.2, NP_001162118.1, NP_001162119.1, NP_001162120.1, EAW98976.1, EAW98977.1, EAW98978.1
GeneID:51360	MBTPS2	X	21,857,656	21,903,541	45,885	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8209	72	in gene	0	1	0	15	27	12	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene MBTPS2	S2P, FLJ32174, MBTPS2, IFAP	membrane-bound transcription factor peptidase, site 2	NM_015884, hCT9612.1	1554604_at, 206473_at	NP_056968.1, EAW98982.1
GeneID:6303	SAT1	X	23,801,275	23,804,327	3,052	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8211	1925	in gene	0	1	0	3	13	3	1	2_A375_pNL97_plus_lncRNA_AR..1	13	Gene SAT1	KFSD, SSAT-1, DC21, SAT1, KFSDX, SAT, SSAT	spermidine/spermine N1-acetyltransferase 1	NM_002970, NR_027783, hCT1964111.0, hCT8939.2	203455_s_at, 210592_s_at, 213988_s_at	NP_002961.1, EAW98999.1, EAW99000.1
GeneID:1968	EIF2S3	X	24,073,065	24,096,927	23,862	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5699	-201	upstream	1	0	0	19	15	11	1	1_A375_pNL7_minus_lncRNA_AR..1	19	Gene EIF2S3	EIF2G, EIF2gamma, eIF-2gA, EIF2S3, EIF2	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	NM_001415, hCT1781292.2, hCT2256483.0, hCT2256484.0	205321_at, 224935_at, 224936_at	NP_001406.1, EAW99010.1, EAW99011.1, EAW99012.1
GeneID:257397	MAP3K7IP3	X	30,845,559	30,907,511	61,952	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5701	-52	upstream	1	0	0	15	12	3	1	1_A375_pNL7_minus_lncRNA_AR..1	15	Gene MAP3K7IP3	MAP3K7IP3, TAB3, NAP1, MGC45404	TGF-beta activated kinase 1/MAP3K7 binding protein 3	NM_152787, hCT1644516.4, hCT2345101.0, hCT2358252.0	1552927_at, 1552928_s_at, 1558518_at, 227357_at	NP_690000.2, EAW99057.1, EAW99058.1, EAW99059.1
GeneID:6103	RPGR	X	38,128,423	38,186,788	58,365	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5703, 2_A375_pNL97_plus_lncRNA_AR..1..8215	-60, -76	upstream, upstream	1	1	0	47	41	11	1	1_A375_pNL7_minus_lncRNA_AR..1	47	Gene RPGR	XLRP3, COD1, CORDX1, RP15, PCDX, CRD, orf15, RPGR, RP3	retinitis pigmentosa GTPase regulator	NM_000328, NM_001034853, hCT1953023.1, hCT2262321.0, hCT2353419.0, hCT2353420.0	207624_s_at	NP_000319.1, NP_001030025.1, EAW59441.1, EAW59442.1, EAW59443.1, EAW59444.1
GeneID:58526	MID1IP1	X	38,660,685	38,665,785	5,100	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8216	3747	in gene	0	1	0	12	14	10	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene MID1IP1	THRSPL, MIG12, MID1IP1, G12-like, STRAIT11499, S14R, FLJ10386	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	NM_021242, NM_001098790, NM_001098791, hCT1787694.2, hCT2262393.0	218251_at	NP_067065.1, NP_001092260.1, NP_001092261.1, EAW59435.1, EAW59436.1
GeneID:54880	BCOR	X	39,910,499	40,036,582	126,083	-	2	2_A375_pNL97_plus_lncRNA_AR..1..8217, 4_A375_EGR1..1..8383	1190, 5510	in gene, in gene	0	1	1	11.5	14	15	2	2_A375_pNL97_plus_lncRNA_AR..1	16	Gene BCOR	ANOP2, FLJ20285, FLJ38041, MAA2, MGC131961, MGC71031, KIAA1575, MCOPS2, BCOR	BCL6 co-repressor	NM_017745, NM_001123383, NM_001123384, NM_001123385, hCT2267840.0, hCT2267841.0, hCT2267842.0, hCT2267843.0, hCT2267844.0, hCT2267845.0	219433_at, 223566_s_at, 223915_at, 223916_s_at	NP_060215.4, NP_001116855.1, NP_001116856.1, NP_001116857.1, EAW59427.1, EAW59429.1, EAW59425.1, EAW59426.1, EAW59428.1, EAW59430.1
GeneID:8239	USP9X	X	40,944,888	41,095,832	150,944	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8218	-1000	upstream	0	1	0	13	18	9	1	2_A375_pNL97_plus_lncRNA_AR..1	18	Gene USP9X	FAM, FAF, DFFRX, USP9X	ubiquitin specific peptidase 9, X-linked	NM_001039590, NM_001039591, hCT1965809.1, hCT1965810.1, hCT1965811.1, hCT2263560.0, hCT2263564.0, hCT2263567.0, hCT9440.2	201099_at, 201100_s_at, 229573_at	NP_001034679.2, NP_001034680.2, EAW59407.1, EAW59408.1, EAW59409.1, EAW59411.1, EAW59406.1, EAW59410.1, EAW59412.1
GeneID:1654	DDX3X	X	41,192,651	41,209,527	16,876	+	1	4_A375_EGR1..1..8384	757	in gene	0	0	1	10	11	17	1	4_A375_EGR1..1	17	Gene DDX3X	HLP2, DBX, DDX3X, DDX3, DDX14	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	NM_001356, NM_001193416, NM_001193417	1558120_at, 201210_at, 201211_s_at, 207617_at, 212514_x_at, 212515_s_at	NP_001347.3, NP_001180345.1, NP_001180346.1
GeneID:4128	MAOA	X	43,515,409	43,606,068	90,659	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5704, 2_A375_pNL97_plus_lncRNA_AR..1..8219	-1425, -1409	upstream, upstream	1	1	0	21	22	8	1	2_A375_pNL97_plus_lncRNA_AR..1	22	Gene MAOA	MAOA		NM_000240, hCT2261967.0, hCT2261968.0, hCT7666.3	204388_s_at, 204389_at, 212741_at	NP_000231.1, EAW59383.1, EAW59381.1, EAW59382.1
GeneID:54539	NDUFB11	X	47,001,615	47,004,609	2,994	-	1	4_A375_EGR1..1..8385	545	in gene	0	0	1	10	9	15	1	4_A375_EGR1..1	15	Gene NDUFB11	MGC111162, FLJ20494, ESSS, P17.3, NP17.3, Np15, NDUFB11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa	NM_001135998, NR_024235, NM_019056, NR_024234, hCT2255745.0, hCT2255747.0	218320_s_at	NP_001129470.1, NP_061929.2, EAW59281.1, EAW59282.1
GeneID:8241	RBM10	X	47,004,631	47,046,212	41,581	+	5	1_A375_pNL7_minus_lncRNA_AR..1..5707, 1_A375_pNL7_minus_lncRNA_AR..1..5708, 2_A375_pNL97_plus_lncRNA_AR..1..8221, 2_A375_pNL97_plus_lncRNA_AR..1..8222, 4_A375_EGR1..1..8385	45513, 46201, 45481, 46073, -567	downstream, downstream, downstream, downstream, upstream	1	1	1	21	24.33	11.33	3	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene RBM10	KIAA0122, ZRANB5, MGC997, GPATCH9, TARPS, RBM10, DXS8237E, GPATC9, FLJ40798, MGC1132	RNA binding motif protein 10	NM_005676, NM_152856, hCT1953017.1, hCT1953018.1, hCT2353405.0, hCT2353406.0, hCT2353407.0	208984_x_at, 215089_s_at, 217221_x_at	NP_005667.2, NP_690595.1, EAW59284.1, EAW59285.1, EAW59286.1, EAW59287.1, EAW59283.1
GeneID:7317	UBA1	X	47,050,199	47,074,527	24,328	+	6	1_A375_pNL7_minus_lncRNA_AR..1..5707, 1_A375_pNL7_minus_lncRNA_AR..1..5708, 1_A375_pNL7_minus_lncRNA_AR..1..5709, 2_A375_pNL97_plus_lncRNA_AR..1..8221, 2_A375_pNL97_plus_lncRNA_AR..1..8222, 2_A375_pNL97_plus_lncRNA_AR..1..8223	-55, 2633, 27769, -87, 2505, 27769	upstream, in gene, downstream, upstream, in gene, downstream	1	1	0	23.33	31	8.67	3	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene UBA1	A1S9T, MGC4781, GXP1, UBA1, UBE1, AMCX1, A1ST, UBE1X, SMAX2, A1S9, POC20, UBA1A	ubiquitin-like modifier activating enzyme 1	NM_153280, NM_003334, hCT1953019.2, hCT1968275.1, hCT2255373.0, hCT8456.4	1555387_at, 200964_at	NP_695012.1, NP_003325.2, EAW59290.1, EAW59291.1, EAW59292.1, EAW59293.1
GeneID:5127	CDK16	X	47,077,526	47,089,396	11,868	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5709, 2_A375_pNL97_plus_lncRNA_AR..1..8223	440, 440	in gene, in gene	1	1	0	17	29	7	1	2_A375_pNL97_plus_lncRNA_AR..1	29	Gene CDK16	PCTAIRE, PCTK1, PCTGAIRE, FLJ16665, CDK16, PCTAIRE1	cyclin-dependent kinase 16	NM_033018, NM_006201, NM_001170460, hCT1953016.1, hCT2255378.0, hCT2255380.0, hCT2255382.0, hCT8454.3	207239_s_at, 208823_s_at, 208824_x_at	NP_148978.2, NP_006192.1, NP_001163931.1, EAW59294.1, EAW59295.1, EAW59296.1, EAW59297.1, EAW59298.1
GeneID:7592	ZNF41	X	47,305,561	47,342,345	36,784	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5711	-183	upstream	1	0	0	16	9	5	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene ZNF41	MRX89, ZNF41, MGC8941	zinc finger protein 41	NM_007130, NM_153380, hCT1966749.1, hCT1966750.1, hCT2268105.0, hCT2268108.0, hCT2268112.0, hCT2268114.0, hCT2268118.0, hCT22686.4, hCT2353412.0	1553216_at, 1553217_s_at, 214904_at	NP_009061.1, NP_700359.1, EAW59300.1, EAW59301.1, EAW59305.1, EAW59306.1, EAW59302.1, EAW59303.1, EAW59304.1, EAW59307.1, EAW59308.1
GeneID:203414	CXorf24	X	47,333,966	47,343,288	9,322	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5711	8582	in gene	1	0	0	16	9	5	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene CXorf24	CXorf24	chromosome X open reading frame 24	XR_113303, XR_110617, XR_115509	239034_at	
GeneID:6853	SYN1	X	47,431,300	47,479,256	47,956	-	4	1_A375_pNL7_minus_lncRNA_AR..1..5713, 1_A375_pNL7_minus_lncRNA_AR..1..5714, 2_A375_pNL97_plus_lncRNA_AR..1..8224, 4_A375_EGR1..1..8386	37411, -168, -104, 37480	in gene, upstream, upstream, in gene	1	1	1	19	25	9.5	2	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene SYN1	SYN1, SYN1a, SYN1b, SYNI	synapsin I	NM_133499, NM_006950, hCT1966742.0, hCT20305.3	1553264_a_at, 221914_at	NP_598006.1, NP_008881.2, EAW59313.1, EAW59314.1
GeneID:7076	TIMP1	X	47,441,690	47,446,190	4,500	+	2	1_A375_pNL7_minus_lncRNA_AR..1..5713, 4_A375_EGR1..1..8386	155, 86	in gene, in gene	1	0	1	13	13	15	1	4_A375_EGR1..1	15	Gene TIMP1	CLGI, FLJ90373, TIMP1, TIMP, EPA, HCI, EPO	TIMP metallopeptidase inhibitor 1	NM_003254, hCT20301.2, hCT2257036.0	201666_at	NP_003245.1, EAW59315.1, EAW59316.1
GeneID:5199	CFP	X	47,483,612	47,489,704	6,092	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5714, 2_A375_pNL97_plus_lncRNA_AR..1..8224	10280, 10344	downstream, downstream	1	1	0	25	37	4	1	2_A375_pNL97_plus_lncRNA_AR..1	37	Gene CFP	PFC, PROPERDIN, CFP, PFD, BFD	complement factor properdin	NM_001145252, NM_002621, hCT20298.2, hCT2268063.0, hCT2268065.0, hCT2353413.0	206380_s_at	NP_001138724.1, NP_002612.1, EAW59317.1, EAW59318.1, EAW59319.1, EAW59320.1
GeneID:5935	RBM3	X	48,432,836	48,436,804	3,968	+	1	2_A375_pNL97_plus_lncRNA_AR..1..8226	-66	upstream	0	1	0	7	14	12	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene RBM3	RBM3, RNPL, IS1-RNPL	RNA binding motif (RNP1, RRM) protein 3	NM_006743, hCT10685.3, hCT1958688.1, hCT1958691.1, hCT2352401.0	208319_s_at, 222026_at	NP_006734.1, EAW50767.1, EAW50765.1, EAW50766.1, EAW50768.1
GeneID:100506703	LOC100506703	X	48,435,420	48,439,550	4,130	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8226	6782	downstream	0	1	0	7	14	12	1	2_A375_pNL97_plus_lncRNA_AR..1	14	Gene LOC100506703		hypothetical LOC100506703	XR_110616, XR_115510		
GeneID:64743	WDR13	X	48,455,880	48,463,582	7,702	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5716	40	in gene	1	0	0	17	10	4	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene WDR13	FLJ20563, WDR13, DKFZp779C2057, MG21	WD repeat domain 13	NM_017883, NM_001166426, NR_029427, hCT10906.3, hCT2263829.0, hCT2263832.0	222138_s_at	NP_060353.2, NP_001159898.1, EAW50760.1, EAW50761.1, EAW50762.1
GeneID:7454	WAS	X	48,542,168	48,549,818	7,632	+	1	4_A375_EGR1..1..8387	-6966	upstream	0	0	1	17	12	15	1	4_A375_EGR1..1	15	Gene WAS	THC, IMD2, WASP, THC1, WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	NM_000377, hCT10894.3, hCT2263841.0	205400_at, 38964_r_at	NP_000368.1, EAW50759.1, EAW50758.1
GeneID:6839	SUV39H1	X	48,555,131	48,567,407	12,276	+	1	4_A375_EGR1..1..8388	11349	in gene	0	0	1	5	3	12	1	4_A375_EGR1..1	12	Gene SUV39H1	SUV39H, KMT1A, SUV39H1, MG44	suppressor of variegation 3-9 homolog 1 (Drosophila)	NM_003173, hCT10886.2, hCT1958692.1	218619_s_at	NP_003164.1, EAW50756.1, EAW50757.1
GeneID:27238	GPKOW	X	48,969,022	48,980,079	11,057	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5717, 2_A375_pNL97_plus_lncRNA_AR..1..8227	-129, -145	upstream, upstream	1	1	0	16	13	9	1	1_A375_pNL7_minus_lncRNA_AR..1	16	Gene GPKOW	T54, GPKOW, Spp2, GPATCH5, GPATC5	G patch domain and KOW motifs	NM_015698, hCT10901.2	203776_at	NP_056513.2, EAW50694.1
GeneID:79917	MAGIX	X	49,019,181	49,023,836	4,655	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5718	3635	in gene	1	0	0	17	13	11	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene MAGIX	MAGIX, JM10, MGC138889, PDZX, FLJ21687	MAGI family member, X-linked	NM_001099681, NM_001099680, NM_001099682, NM_024859, hCT1640222.3, hCT2263895.0, hCT2263897.0	1563318_s_at, 1565559_at, 1565562_at, 219985_s_at, 222944_s_at, 234927_s_at	NP_001093151.1, NP_001093150.1, NP_001093152.1, NP_079135.2, EAW50691.1, EAW50692.1, EAW50693.1
GeneID:5355	PLP2	X	49,028,184	49,031,469	3,285	+	1	1_A375_pNL7_minus_lncRNA_AR..1..5718	-5366	upstream	1	0	0	17	13	11	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene PLP2	PLP2, A4LSB, MGC126187, A4	proteolipid protein 2 (colonic epithelium-enriched)	NM_002668, hCT10900.3, hCT2263896.0	201136_at	NP_002659.1, EAW50690.1, EAW50689.1
GeneID:4007	PRICKLE3	X	49,031,906	49,042,776	10,870	-	1	1_A375_pNL7_minus_lncRNA_AR..1..5718	19960	downstream	1	0	0	17	13	11	1	1_A375_pNL7_minus_lncRNA_AR..1	17	Gene PRICKLE3	PRICKLE3, LMO6	prickle homolog 3 (Drosophila)	NM_006150, hCT10903.2, hCT1958711.0, hCT2262036.0	217349_s_at	NP_006141.2, EAW50688.1, EAW50686.1, EAW50687.1
GeneID:6855	SYP	X	49,044,265	49,056,661	12,396	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5719, 2_A375_pNL97_plus_lncRNA_AR..1..8228	21, 21	in gene, in gene	1	1	0	22	27	7	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene SYP	SYP, MRXSYP	synaptophysin	NM_003179, hCT2344593.0, hCT2344594.0	213200_at	NP_003170.1, EAW50685.1, EAW50684.1
GeneID:778	CACNA1F	X	49,061,523	49,089,833	28,310	-	2	1_A375_pNL7_minus_lncRNA_AR..1..5719, 2_A375_pNL97_plus_lncRNA_AR..1..8228	33193, 33193	downstream, downstream	1	1	0	22	27	7	1	2_A375_pNL97_plus_lncRNA_AR..1	27	Gene CACNA1F	COD3, CSNBX2, CSNB2, Cav1.4, COD4, CORDX3, AIED, OA2, JM8, CORDX, JMC8, CACNA1F, CSNB2A	calcium channel, voltage-dependent, L type, alpha 1F subunit	NM_005183, hCT2344595.0, hCT2344596.0, hCT2344597.0, hCT2344598.0, hCT2344599.0, hCT2344600.0, hCT2344601.0	206377_s_at	NP_005174.2, EAW50677.1, EAW50679.1, EAW50680.1, EAW50681.1, EAW50682.1, EAW50678.1, EAW50683.1
GeneID:57477	SHROOM4	X	50,334,642	50,557,044	222,402	-	1	2_A375_pNL97_plus_lncRNA_AR..1..8229	-1180	upstream	0	1	0	11	17	4	1	2_A375_pNL97_plus_lncRNA_AR..1	17	Gene SHROOM4	SHAP, SHROOM4, KIAA1202	shroom family member 4	NR_027121, NM_020717, hCT1950655.1, hCT2271746.0	244825_at	NP_065768.2, EAW89917.1, EAW89918.1

Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_2_A375_uNG7_mut_lncRNA_AR_1 Percent	2_A375_uNG7_wt_lncRNA_AR_1 Percent	3_A375_EGR1_lncRNA_AR_1 Percent	1_A375_pLNG7_mut_lncRNA_AR_1 Avg Peak	2_A375_pLNG7_wt_lncRNA_AR_1 Avg Peak	3_A375_EGR1_lncRNA_AR_1 Avg Peak	Ad Hoc Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:2937705	GSPT2	X	51,456,461	51,469,326	12,847	+	2	1_A375_uNG7_mvirt_lncRNA_AR_1::5705, 2_A375_uNG7_dlucl_lncRNA_AR_1::5230	-85, -85	upstream, upstream	1	1	0	15	17	7	1	2_A375_uNG7_dlucl_lncRNA_AR_1	17	GSPT2	ERF1D, GSPT2, FLJ10441, GST2, eRF1d	G1 to S phase transition 2	NM_018094, XCT1786730.2	205841_s_at	NP_060564.2, EAW62596.1
GeneID:8604600	MAGED1	X	51,648,155	51,845,450	99,295	+	1	1_A375_uNG7_mvirt_lncRNA_AR_1::5721	-171	upstream	1	0	0	14	13	2	1	1_A375_uNG7_mvirt_lncRNA_AR_1	14	MAGED1	NRAGE, WAGED1, DLXRY	melanoma antigen family D, 1	NM_038998, NM_001003932, NM_001005333, XCT2829980.0, XCT2829981.0	209014_at	NP_998117.3, NP_001003332.1, NP_001093233.1, EAW62896.1, EAW62897.1
GeneID:8538	KDM5C	X	53,220,935	53,254,804	34,101	-	1	2_A375_uNG7_dlucl_lncRNA_AR_1::5233	238	cx gene	0	1	0	9	19	10	1	2_A375_uNG7_dlucl_lncRNA_AR_1	19	KDM5C	KDM5C, MRX13, JARID1C, DXS1272E, MRXJ, XE169, SMCX	lysine (K)-specific demethylase 5C	NM_004187, NM_001144702, XCT1022613, XCT2357807.0	202283_at_239207_at	NP_954178.2, NP_001140174.1, EAW93145.1, EAW93146.1
GeneID:2839096	RGR	X	53,262,156	53,330,822	68,666	+	2	2_A375_uNG7_dlucl_lncRNA_AR_1::5231, 2_A375_uNG7_dlucl_lncRNA_AR_1::5234	98154, 37647	downstream, cx gene	0	1	0	11	17	8	2	2_A375_uNG7_dlucl_lncRNA_AR_1	19	RGR	MRX1, BRAG1, RAM0522, RGR1/2	rod visual cycle 2	NM_015079, NM_001111173, NR_024449	214419_at_229649_at	NP_055901.1, NP_001104093.1
GeneID:3852618	HSD17B10	X	53,466,298	53,481,823	15,117	-	1	4_A375_EGR1_1::5389	-7929	upstream	0	0	1	8	11	10	1	4_A375_EGR1_1	16	Gene HSD17B10	ARPP2, SDRSC1, SCAHD, ABHD8, MHBD, MRX31, MRX3416, 17b-HSD10, HCD2, ERAB, HSD17B10, CAMR, DUPLv11.22, YNDH2, MRX17	hydroxysteroid (17-beta) dehydrogenase 10	NM_004493, NM_001037811, XCT1039803.4, XCT1961331.2, XCT1961332.1	202282_at	NP_004484.1, NP_001032900.1, EAW93137.1, EAW93158.1, EAW93159.1
GeneID:10155075	HUWE1	X	53,599,985	53,713,873	154,819	-	1	2_A375_uNG7_dlucl_lncRNA_AR_1::5233	3953	cx gene	0	1	0	8	19	8	1	2_A375_uNG7_dlucl_lncRNA_AR_1	19	Gene HUWE1	MUL2, ARF-BP1, bT72, HUWE1, UREB1, MRX31, MRX316, 179-HSD10, HCD2, ERAB, HSD17B10, CAMR, DUPLv11.22, YNDH2, MRX17	HECT, UBA and WWE domain containing 1	NM_031407, XCT2284388.1, XCT2284390.1, XCT2284391.1, XCT2284393.1, XCT2284394.1, XCT2284397.1	207783_x_at_209393_s_at, 209899_at_214872_s_at, 209264_at	NP_115864.3, EAW95160.1, EAW93161.1, EAW93162.1, EAW93163.1, EAW93165.1, EAW93183.1, EAW93186.1
GeneID:3464	FAM120C	X	54,094,797	54,209,714	114,918	-	1	4_A375_EGR1_1::5390	130	cx gene	0	2	1	8	9	14	1	4_A375_EGR1_1	14	Gene FAM120C	FLJ20598, OFD1a, C4orf17, FLJ43879, FAM120C	Borealin/Dasra/CSUT/COIL sequence similarity 123C	NM_017545, NM_199458	220665_at	NP_960315.3, NP_960536.1
GeneID:8554	WNK3	X	54,219,236	54,264,455	165,182	-	1	4_A375_EGR1_1::5390	176656	downstream	0	0	1	8	9	14	1	4_A375_EGR1_1	14	Gene WNK3	PLK3347, PRKWNK3, WNK3, FLJ42660, WNK1355	WNK lysine deficient protein kinase 3	NM_001002838, NM_020922, XCT1789956.2, XCT2364270.0	1555245_s_at_222262_at	NP_001002838.1, NP_065775.2, EAW93175.1, EAW93176.1
GeneID:9978	TSR2	X	54,466,830	54,471,700	4,877	+	1	1_A375_uNG7_dlucl_lncRNA_AR_1::5239	-101	upstream	0	1	0	12	14	9	1	1_A375_uNG7_dlucl_lncRNA_AR_1	14	Gene TSR2	WDA21, WDC20481, TSR2, DT1P1A6	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	NM_018183, XCT1787995.1, XCT1787996.2	213879_at	NP_479171.1, EAW93177.1, EAW93178.1
GeneID:2277	FGD1	X	54,471,697	54,522,999	50,712	-	1	2_A375_uNG7_dlucl_lncRNA_AR_1::5236	53827	downstream	0	1	0	12	14	9	1	2_A375_uNG7_dlucl_lncRNA_AR_1	14	Gene FGD1	FGD1_ANS, DFNX5, FGDY, MRX58	FYVE, RhoGEF and PH domain containing 1	NM_004463, XCT2279118.0, XCT2279117.0, XCT97622.2	204619_at	NP_004454.2, EAW95181.1, EAW93179.1, EAW93180.1
GeneID:2911	UBQLN2	X	68,390,036	68,490,443	8,417	+	1	4_A375_EGR1_1::5392	107	cx gene	0	0	1	7	15	14	1	4_A375_EGR1_1	14	Gene UBQLN2	C1HP1, FLJ38544, PLIC2, FLJ10167, NIBP4, UBQLN2, HRIHFB2157, DSK2	ubiquilin 2	NM_013444, XCT97602.3	219864_s_at	NP_838472.2, EAW93238.1
GeneID:1850	SPIN2	X	37,992,803	37,921,968	70,165	-	1	2_A375_uNG7_dlucl_lncRNA_AR_1::5238	132	cx gene	0	1	0	11	13	8	1	2_A375_uNG7_dlucl_lncRNA_AR_1	13	Gene SPIN2	MGC40295, SPIN2, FLJ90592, SPIN3, bA443C16.1, FLJ41127	spindlin family, member 2	NM_031510892, NR_027139, XCT1792819.2, XCT2276664.0	1554090_at, 1554099_s_at, 1555062_at, 1555063_s_at	NP_001510892.2, EAW93237.1, EAW93238.1
GeneID:9268	FAM123B	X	53,494,997	53,419,604	50,827	-	2	1_A375_uNG7_mvirt_lncRNA_AR_1::5722, 2_A375_uNG7_dlucl_lncRNA_AR_1::5239	-138, -998	upstream, upstream	1	1	0	22	16	11	1	1_A375_uNG7_mvirt_lncRNA_AR_1	22	Gene FAM123B	AWP1, MGC20431, TSPY2, DTP1A16	WD repeat and FYVE domain containing 3	NM_182643, XCT2287544.1	1552802_a_at	NP_899637.1, EAW93473.1
GeneID:4484	MSN	X	64,857,511	64,961,793	74,282	+	1	4_A375_EGR1_1::5393	24569	cx gene	0	2	1	8	7	14	1	4_A375_EGR1_1	14	Gene MSN	MSN	moesin	NM_002444, XCT1003312, XCT2287825.0	200600_at_233769_at, 240960_at	NP_002426.1, EAW93260.1, EAW93261.1
GeneID:1965	EPHB1	X	99,644,640	99,682,807	10,167	+	1	2_A375_uNG7_dlucl_lncRNA_AR_1::5240	0	cx gene	0	1	0	11	14	10	1	2_A375_uNG7_dlucl_lncRNA_AR_1	14	Gene EPHB1	MGC2762, LERK2, EPHB1, EPLG, CFND, ELK, EPLG2, CFND	ephrin-B1	NM_004429, XCT2289902.0, XCT6894.3	202711_at	NP_004426.1, EAW93270.1, EAW93271.1
GeneID:1798	DLG3	X	69,884,705	69,725,540	60,835	-	2	1_A375_uNG7_mvirt_lncRNA_AR_1::5723, 2_A375_uNG7_dlucl_lncRNA_AR_1::5724	-129, 32671	upstream, cx gene	1	2	0	17	12.5	8.5	2	2_A375_uNG7_dlucl_lncRNA_AR_1	17	Gene DLG3	SAP102, X1HR, SWA1222, DLG3, MRX, MRX90, NEDLG	disc, large homolog 3 (Drosophila)	NM_021120, NM_030751, NM_001166076, XCT2365730.0, XCT2365362.0, XCT2365363.0, XCT2365955.0, XCT2365972.0, XCT97573.2	207722_s_at_212727_at, 212726_at, 212729_at	NP_066843.2, NP_085761.1, NP_001166745.1, EAW93323.1, EAW93334.1, EAW93336.1, EAW93338.1, EAW93337.1, EAW93339.1
GeneID:2938934	SNX12	X	70,269,765	70,295,351	7,443	-	2	1_A375_uNG7_mvirt_lncRNA_AR_1::5725, 2_A375_uNG7_dlucl_lncRNA_AR_1::5241	-108, -153	upstream, upstream	1	1	0	20	19	4	1	1_A375_uNG7_mvirt_lncRNA_AR_1	23	Gene SNX12	SNX12, MGC118901, MGC118902	sorting nexin 12	NM_015348, XCT2879711.0, XCT2879710.0, XCT2879714.0	224864_at_231703_at	NP_037478.2, EAW93323.1, EAW93324.1, EAW93325.1
GeneID:4303	FOXO4	X	70,319,999	70,323,364	7,355	+	1	4_A375_EGR1_1::5394	555	cx gene	0	0	1	4	7	14	1	4_A375_EGR1_1	14	Gene FOXO4	MLLT7, AFX1, MGC120490, AFX, FOXO4	forkhead box O4	NM_005938, NM_001170931, XCT1103012.2, XCT2865900.0	205481_at	NP_005929.2, NP_001164402.1, EAW93521.1, EAW93522.1
GeneID:1338	C4orf45	X	70,323,709	70,326,636	2,899	-	1	4_A375_EGR1_1::5394	10254	downstream	0	0	1	4	7	14	1	4_A375_EGR1_1	14	Gene C4orf45	C4orf45		NM_031202269, NR_033212, XCT1787947.3	231177_at	NP_001229638.1, EAW93230.1
GeneID:8327	ZMYM3	X	70,459,474	70,479,047	19,573	+	2	1_A375_uNG7_mvirt_lncRNA_AR_1::5726, 2_A375_uNG7_dlucl_lncRNA_AR_1::5242	999, 1083	cx gene, cx gene	1	1	0	29	26	8	1	1_A375_uNG7_mvirt_lncRNA_AR_1	29	Gene ZMYM3	ZMYM3, KIAA0183, ZNP183L2, DXS6673E	zinc finger, MYM type 3	NM_201599, NM_005096, NM_001171182, NM_001171183, XCT1999222.0, XCT1999223.1, XCT9432.2	1554171_at, 1554172_s_at, 207809_s_at	NP_963855.1, NP_005087.1, NP_001164653.1, NP_001164654.1, EAW93501.1, EAW93502.1, EAW93503.1
GeneID:8473	OGT	X	70,752,912	70,793,747	42,835	+	1	4_A375_EGR1_1::5395	178	cx gene	0	2	1	8	8	16	1	4_A375_EGR1_1	16	Gene OGT	HRNT1, OGT, O-GlcNAc, FLJ23071, MGC22921	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	NM_181672, NM_181673, XCT1959958.1, XCT2869818.0, XCT2869820.0	207983_s_at_207994_x_at, 209340_at_212387_s_at, 220994_at_229787_s_at	NP_598035.1, NP_598036.1, EAW93286.1, EAW93287.1
GeneID:3417	NHS2	X	71,130,456	71,365,424	232,968	+	1	4_A375_EGR1_1::5396	248	cx gene	0	0	1	3	5	15	1	4_A375_EGR1_1	15	Gene NHS2	NHS2	NHS-like 2	NM_031019827	1569932_at	NP_001139492.2
GeneID:5339	PIN4	X	71,261,526	71,265,814	62,266	+	1	2_A375_uNG7_dlucl_lncRNA_AR_1::5243	74	cx gene	0	0	1	12	17	8	1	2_A375_uNG7_dlucl_lncRNA_AR_1	17	Gene PIN4	MGC135495, PAR14, EPVH, PIN4, PAR17	prolyl cis/trans isomerase, NIMA-interacting, 4 (parvulin)	NM_006223, NM_001170747, NR_023107, XCT201193.2	204351_s_at	NP_006214.2, NP_001156716.1, EAW76512.1
GeneID:5198	PRPS1X	X	71,692,450	71,697,141	4,692	-	2	1_A375_uNG7_mvirt_lncRNA_AR_1::5727, 2_A375_uNG7_dlucl_lncRNA_AR_1::5244	-11, 21	upstream, cx gene	1	1	0	45	52	10	1	2_A375_uNG7_dlucl_lncRNA_AR_1	52	Gene RPS6X	RPS4X, S4, SCR10, CCG2, S4, X-linked, RPS4, SCAR, DXS208, FLJ40593	ribosomal protein S4, X-linked	NM_001007, XCT2272248.0, XCT2272247.0, XCT9956.2	200923_s_at_213367_x_at	NP_000995.1, EAW76198.1, EAW76199.1, EAW76201.1
GeneID:4477	CITED1	X	71,321,486	71,327,837	6,349	-	4	1_A375_uNG7_mvirt_lncRNA_AR_1::5728, 2_A375_uNG7_dlucl_lncRNA_AR_1::5245, A_A375_EGR1_1::5397, A_A375_EGR1_1::5396	139, 139, 1373, 81	cx gene, cx gene, cx gene, cx gene	1	1	1	15.5	14.5	13.5	2	2_A375_uNG7_dlucl_lncRNA_AR_1	23	Gene CITED1	MSG1, CITED1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	NM_004143, NM_001144853, NM_001144866, NM_001144867, XCT2272243.0, XCT2272244.0, XCT9961.3	207744_s_at	NP_004134.2, NP_001138537.1, NP_001138538.1, NP_001138539.1, EAW76510.1, EAW76520.1, EAW76519.1
GeneID:5988	HDAC8	X	71,949,398	71,792,993	243,597	-	1	2_A375_uNG7_dlucl_lncRNA_AR_1::5249	111181	cx gene	0	0	1	9	17	7	1	2_A375_uNG7_dlucl_lncRNA_AR_1	17	Gene HDAC8	CDA07, HDAC8, RPD3, HDAC11, HD8	histone deacetylase 8	NM_001166440, NM_018486, NM_001166418, NM_001166419, NM_001166422, NM_001166420, XCT2272239.0, XCT2272240.0, XCT2272242.0, XCT9966.2	223343_at_223563_at, 223905_s_at	NP_001159912.1, NP_060988.1, NP_001159910.1, NP_001159911.1, NP_001159914.1, NP_001159902.1, EAW76821.1, EAW76822.1, EAW76823.1, EAW76824.1
GeneID:2232	ABCB7	X	74,275,103	74,376,102	103,027	-	1	1_A375_uNL7_mvirt_lncRNA_AR_1::5730	100	cx gene	1	0	0	20	14	8	1	1_A375_uNL7_mvirt_lncRNA_AR_1	20	Gene ABCB7	ABC7, ABCB7, ataxia, EST140325, ASAT	ATP-binding cassette, sub-family B (MDR/TAP), member 7	NM_004299, XCT1019632.3, XCT2720340.0, XCT2434132.0, XCT2434134.0, XCT2434134.2, XCT2953232.0	209220_s_at	NP_004290.2, EAW95839.1, EAW95832.1, EAW95833.1, EAW95836.1, EAW95837.1, EAW95835.1
GeneID:5198	UPRT	X	74,492,894	74,324,702	90,036	+	1	2_A375_uNL7_dlucl_lncRNA_AR_1::5245	66	cx gene	1	0	0	9	10	9	1	2_A375_uNL7_dlucl_lncRNA_AR_1	16	Gene UPRT	FUR1, MGC23927, UPRT, DKFZp761E1240, UPP	uracil phosphoribosyltransferase (FUR1 homolog (S. cerevisiae)	NM_145032, NR_030774, XCT1140863, XCT1960722.1	228199_at	NP_659459.1, EAW96830.1, EAW96831.1
GeneID:5230	PGK1	X	77,359,966	77,382,324	22,858	+	1	1_A375_uNL7_mvirt_lncRNA_AR_1::5721	48	cx gene	1	0	0	14	12	8	1	1_A375_uNL7_mvirt_lncRNA_AR_1	14	Gene PGK1	MGC117037, MGC142128, PGK1, PGKA, MGC29947, MGC45	phosphoglycerate kinase 1	NM_000291, XCT1110863, XCT1950114.2, XCT2274398.1	200737_at_200738_s_at, 217398_x_at, 217397_x_at, 227988_at	NP_000282.1, EAW96869.1, EAW96870.1, EAW96871.1
GeneID:1967	TMMB	X	100,899,644	100,800,937	2,315	-	1	4_A375_EGR1_1::5400	169	cx gene	0	0	1	7	14	14	1	4_A375_EGR1_1	14	Gene TMMB	MTS, DDP1, DDP, TIMMBA, TIMM8, DFN1, MGC12282	translocase of inner mitochondrial membrane 8 homolog A (yeast)	NM_004533, NM_001143951, XCT1147672, XCT1954555.1	203237_at_210382_at	NP_004524.2, NP_001137423.1, EAX03564.1
GeneID:699	BTK	X	100,656,433	100,841,212	58,777	-	3	1_A375_uNL7_mvirt_lncRNA_AR_1::5722, 2_A375_uNL7_dlucl_lncRNA_AR_1::5249, A_A375_EGR1_1::5400	-4864, -4878, 37604	upstream, upstream, downstream	1	1	1	15	22	12	2	2_A375_uNL7_dlucl_lncRNA_AR_1	30	Gene BTK	AT, PSCTK1, MGC126282, ATK, IMD1, BTK	Bruton agammaglobulinemia tyrosine kinase	NM_000061, XCT1147771, XCT1954555.1, XCT2556950.0	203324_at	NP_000052.1, EAX03565.1, EAX03567.1, EAX03566.1
GeneID:8175	RPL39X	X	100,843,945	100,830,703	4,833	+	2	1_A375_uNG7_mvirt_lncRNA_AR_1::5722, 2_A375_uNG7_dlucl_lncRNA_AR_1::5249	-492, -80	upstream, upstream	1	1	0	23	30	12	1	2_A375_uNG7_dlucl_lncRNA_AR_1	30	Gene RPL39A	RPL39A, RPL39, MGC12020, L44L, MRX86, L39A	ribosomal protein L39A	NM_021129, XCT2285338.0, XCT2285340.0, XCT2285342.0	201406_at	NP_066137.1, EAX03569.1, EAX03568.1, EAX03571.1
GeneID:2737	GLA	X	100,652,779	100,660,001	10,222	-	2	1_A375_uNG7_mvirt_lncRNA_AR_1::5722, 2_A375_uNG7_dlucl_lncRNA_AR_1::5249	17145, 17113	downstream, downstream	1	1	0	23	30	12	1	2_A375_uNG7_dlucl_lncRNA_AR_1	30	Gene GLA	GALA, GLA	galactosidase, alpha	NM_000169, XCT1147812, XCT1954555.1	214450_at	NP_000160.1, EAX03562.1, EAX03563.1
GeneID:5566	TCEAL1	X	102,649,643	102,649,661	2,233	+	1	4_A375_EGR1_1::5401	1066	cx gene	0	0	1	8	9	19	1	4_A375_EGR1_1	19	Gene TCEAL1	p21, SIIP, pp21, TCEAL1	transcription elongation factor A (SII)-like 1	NM_004780, NM_001008839, NM_001008840, XCT1950764.1	204618_at	NP_004771.2, NP_001008840.1, EAW54702.1
GeneID:4836	MCART1	X	103,243,990	103,401,708	97,810	+	4	1_A375_uNG7_mvirt_lncRNA_AR_1::5723, 1_A375_uNG7_mvirt_lncRNA_AR_1::5724, 2_A375_uNG7_dlucl_lncRNA_AR_1::5250, 2_A375_uNG7_dlucl_lncRNA_AR_1::5251	186, -9930, 204, 9380	cx gene, upstream, cx gene, upstream	1	1	0	20	26	4.5	2	2_A375_uNG7_dlucl_lncRNA_AR_1	32	Gene MCART6	MCART6, DKFZp686O1267	mitochondrial carrier triple repeat 6	NM_031012755	1561970_s_at, 1561980_at	NP_001127773.2
GeneID:1323	CXorf39	X	103,411,201	103,438,127	24,926	+	4	1_A375_uNG7_mvirt_lncRNA_AR_1::5723, 1_A375_uNG7_mvirt_lncRNA_AR_1::5724, 2_A375_uNG7_dlucl_lncRNA_AR_1::5250, 2_A375_uNG7_dlucl_lncRNA_AR_1::5251	-9781, -293, -9797, -210	upstream, upstream, upstream, upstream	1	1	0	20	26	4.5	2	2_A375_uNG7_dlucl_lncRNA_AR_1	32	Gene CXorf39	FAM19X, CXorf39	family with sequence similarity 199, X-linked	NM_207316, XCT2280934.0, XCT2280935.0, XCT2280937.0, XCT2280939.0	223216_at, 227133_at, 242761_at	NP_997201.1, EAW02767.1, EAW02768.1, EAW02769.1, EAW02780.1
GeneID:3778	PSMD1	X	107,227,437	107,236,848	9,411	-	1	1_A375_uNG7_mvirt_lncRNA_AR_1::5725	-32	upstream	1	0	0	14	12	7	1	1_A375_uNG7_mvirt_lncRNA_AR_1	14	Gene PSMD10	5.6.5.1, p28(1)-5.2, p28(1)-5.3, MGC55156, COLA4E	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	NM_002814, NM_170730, XCT1279.3, XCT1962548.1	1554077_s_at, 219483_s_at	NP_002803.3, NP_736698.1, EAW92697.1, EAW92698.1
GeneID:1172	ATG4A	X	107,236,164	107,297,899	62,962	+	1	1_A375_uNG7_mvirt_lncRNA_AR_1::5725	-54	upstream	1	0	0	14	12	7	1	1_A375_uNG7_mvirt_lncRNA_AR_1	14	Gene ATG4A	ATG4A, AUTL2, APG4A	ATG4 autophagy related 4 homolog A (S. cerevisiae)	NM_178270, NM_052936, XCT12799.5, XCT1956451.1, XCT1956452.1, XCT1956453.1, XCT2307153, XCT2307154.0, XCT2307153.1, XCT2356760.0	213113_at	NP_840054.1, NP_443186.2, EAW92693.1, EAW92694.1, EAW92695.1, EAW92692.1, EAW92696.1, EAW92697.1
GeneID:1230	COL4A6	X	107,596,837	107,662,704	65,867	-	1	4_A375_EGR1_1::5402	95496	cx gene	0	0	1	3	8	12	1	4_A375_EGR1_1	12	Gene COL4A6	CXDC1(22.3), MGC55156, COL4A6	collagen, type IV, alpha 6	NM_001847, NM_033641, XCT2280475.0, XCT2280474.0	210963_at_211473_s_at, 210962_at	NP_001838.2, NP_775667.1, EAX08857.1, EAX08858.1
GeneID:9939	MAMLD1	X	109,437,414	109,592,481	249,047	+	1	2_A375_uNG7_dlucl_lncRNA_AR_1::5253	43157	cx gene	0	0	1	8	15	4	1	2_A375_uNG7_dlucl_lncRNA_AR_1	15	Gene MAMLD1	MAMLD1, NEMEC1	Aland syndrome, neural stem/progenitor, inactive hydrolase and ubiquitylation/sumoylation regulator gene 1	NM_015395, NM_001025593, NM_001171809, XCT1970.2	1553219_s_at, 204476_s_at, 229421_at, 236760_at	NP_598051.1, NP_001025751.1, NP_001160160.1, EAX02985.1
GeneID:5421	WDR44	X	117,480,039	117,592,924	103,886	+	1	4_A375_EGR1_1::5404	92	cx gene	0	0	1	8	7	15	1	4_A375_EGR1_1	15	Gene WDR44	WDR44, RPH11, FLJ12235, Rab11BP, MGC26705, DKFZp686I2014	WD repeat domain 44	NM_031164985, NM_001164988, NM_019043, XCT1791612.2, XCT2877780.0	219297_at_233483_at	NP_001171914.1, NP_001171693.1, NP_061918.2, EAW98096.1, EAW98097.1





Gene ID	Gene Name	Chromosome	Gene Start	Gene End	Gene Length	Gene Strand	Interval Count	Intervals	Interval Distance	Interval Position	1_A375_uhi37_mrna_lncRNA_AR_1 Percent	2_A375_uhi37_plus_lncRNA_AR_1 Percent	4_A375_EGFR1_AR_1 Percent	1_A375_pA375_NL7_mrna_lncRNA_AR_1 Avg Peak	2_A375_pA375_uhi37_plus_lncRNA_AR_1 Avg Peak	4_A375_EGFR1_AR_1 Avg Peak	Adj Reg Count	Peak Sample	Peak Value	UCSC Link	Alt symbols	Full Description	RNA	Alt Tag	PROT
GeneID:29778	SNORA70	X	153,828,822	153,828,756	154	+	2	1_A375_uhi37_mrna_lncRNA_AR_1::8748, 2_A375_uhi37_plus_lncRNA_AR_1::8289										2_A375_pNL8_plus_lncRNA_AR_1	824	Gene SNORA70	uc010hvl.1, SNORA70, RNA70	small nucleolar RNA, H/ACA box 70	NR_000011		
GeneID:157674	DNASE1L1	X	153,829,379	153,842,427	13,049	-	3	1_A375_uhi37_mrna_lncRNA_AR_1::8368, 2_A375_uhi37_plus_lncRNA_AR_1::8289, 2_A375_uhi37_plus_lncRNA_AR_1::8270	1057, 13025, 819	downstream, downstream, cx gene	1	1	0	13	19.5	8.5	2	2_A375_pNL8_plus_lncRNA_AR_1	824	Gene DNASE1L1	DNASE1L1, DNASE1L, DNASEX, DNL1L, bB, DNASI1L1	deoxyribonuclease 1 like 1	NM_030720, NM_001009932, NM_001009933, NM_001009934, XCT1993033.1, XCT1993035.0, XCT1999980.1, XCT1999999.1, XCT1999010.1	202912_s_at	NP_096721.1, NP_001009932.1, NP_001009933.1, NP_001009934.1, EAW72734.1, EAW72735.1, EAW72731.1, EAW72732.1, EAW72733.1
GeneID:89122	TAZ	X	153,839,077	153,850,065	10,988	+	1	2_A375_uhi37_plus_lncRNA_AR_1::8270	-69	upstream	0	1	0	10	15	4	1	2_A375_pNL8_plus_lncRNA_AR_1	815	Gene TAZ	CMD5A, EFE2, EFM5, LVNCX, Taz1, G4.5, FLJ27190, TAZ, bAP-2, EFE	tafazzin	NM_000116, NM_181312, NM_181311, NM_181313, NR_024048, XCT1999971, XCT1999981.1, XCT1999991.1, XCT1999921.1, XCT2000103.1, XCT2000122.0, XCT2000113.0, XCT2350980.0, XCT2350990.0, XCT2350980.0, XCT2350991.0, XCT2351023.0, XCT2351010.3	202977_at_37378_at	NP_000107.1, NP_851629.1, NP_851630.1, NP_851631.1, EAW72722.1, EAW72724.1, EAW72717.1, EAW72718.1, EAW72719.1, EAW72720.1, EAW72721.1, EAW72723.1, EAW72725.1, EAW72726.1, EAW72727.1, EAW72728.1, EAW72729.1, EAW72730.1
GeneID:55850	PLXNA3	X	153,898,823	153,701,965	10,262	+	1	4_A375_EGR1_1.8428	9921	cx gene	0	0	1	4	0	10	1	4_A375_EGR1_1	10	Gene PLXNA3	6.3, PLEXIN-A3, HBSEX6GENE, bAP-6, SEX, PLXNA3, PLXN3, PLXN	plexin A3	NM_017514, XCT2283307.0, XCT2281212	153139_s_at, 1397519_at	NP_059964.2, EAW72703.1, 263923_at	NP_059955.2, EAW72701.1
GeneID:63827	LAIR2	X	153,709,241	153,707,998	2,358	-	1	4_A375_EGR1_1.8427	-9172	upstream	0	0	1	8	8	10	1	4_A375_EGR1_1	13	Gene LAIR2	EX009618, HSD3, CX28, EX009618, LAIR2, ITIM2	leukocyte-associated immunoglobulin-like receptor 2	NM_002314, XCT2281813.0	219081_s_at, 221992_x_at	NP_002305.2, EAW72701.1	NP_055550.1, EAW72700.1
GeneID:83988	UBL4A	X	153,712,056	153,714,932	2,876	-	1	4_A375_EGR1_1.8427	2184	cx gene	0	0	1	8	8	10	1	4_A375_EGR1_1	13	Gene UBL4A	DX256E, GDX, DX0256E, GDYD, THN24, UBL4A, GET5, UBL4, MDY2	ubiquitin like 4A	NM_014235, XCT2282220.0	221748_at	NP_055550.1, EAW72700.1	
GeneID:83993	SLC10A3	X	153,718,680	153,719,002	2,352	-	1	4_A375_EGR1_1.8427	8224	downstream	0	0	1	8	8	10	1	4_A375_EGR1_1	13	Gene SLC10A3	DX0230E, PS, SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	NM_019848, NM_001142391, NM_001142392, XCT1999694.1, XCT2287476.0, XCT2282123	204459_s_at	NP_062822.1, NP_001135863.1, NP_001135864.1, EAW72697.1, EAW72698.1, EAW72699.1	
GeneID:11784422	RAB39B	X	154,497,328	154,499,852	2,525	-	2	1_A375_uhi37_mrna_lncRNA_AR_1::8747, 2_A375_uhi37_plus_lncRNA_AR_1::8271	92, 124	cx gene, cx gene	1	1	0	17	21	8	1	2_A375_pNL8_plus_lncRNA_AR_1	821	Gene RAB39B	RAB39B, MRX72		NM_171998, XCT1993.2	230079_at, 239935_s_at	NP_741993.1, EAW72628.1	
GeneID:85827	THEMIS2	X	154,718,972	154,842,822	123,850	+	1	2_A375_uhi37_plus_lncRNA_AR_1::8272	448	cx gene	0	1	0	14	14	10	1	2_A375_pNL8_plus_lncRNA_AR_1	814	Gene THEMIS2	THEMIS, FLJ10727, TKS10, bAP102, BBOX2	thymocyte selection associated family member 2	NM_031184797, NM_018198, XCT1993011.1, XCT2273001.0, XCT0982.3	1554298_at, 218760_s_at	NP_001171726.1, NP_060668.1, EAW53673.1, EAW65574.1, EAW53675.1	
GeneID:100132941	CD24	Y	21,152,326	21,154,705	2,379	-	1	4_A375_EGR1_1.8415	-143	upstream	0	0	1	2	2	14	1	4_A375_EGR1_1	14	Gene CD24	CD24, FLJ22965, FLJ43543, HSCT3042, CD24A	CD24 molecule	NM_013230		NP_037362.1	

Table 13A. Genes bound by AR or EGR1 and regulated by SLNCR

Table 13A lists the genes bound by AR or EGR1 and regulated by SLNCR. RNA-seq differential expression was taken from Tables 6A-6C, AR ChIP-seq values were taken from Table 9A, and EGR1 ChIP-seq values from Table 12. The table lists all genes that are differentially expressed by *SLNCR* knockdown.

1_A375_pNL7_minus_lncRNA_AR = AR ChIP-seq peaks from vector control

2_A375_pNL97_plus_lncRNA_AR = AR ChIP-seq peaks from SLNCR1-expressing vector

4_A375_EGR1= EGR1 ChIP-seq peaks

Table 13A

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
ENSG00000128564	ENSG00000128564	VGF	7:100805789-100808874	OK	0.73792	10.7728	3.86778	5.79161	5.00E-05	0.0312848	1	1	1
ENSG00000131409	ENSG00000131409	LRRC4B	19:51020148-51071302	OK	0.715032	2.73315	1.93448	2.2952	0.00015	0.0654136	1	1	1
ENSG00000166710	ENSG00000166710	B2M	15:45003674-45011075	OK	0.456503	1.68041	1.88012	0.978707	0.0072	0.525966	1	1	1
ENSG00000172183	ENSG00000172183	ISG20	15:89179383-89199714	OK	1.37799	4.51629	1.71257	1.48651	0.0083	0.568787	1	1	1
ENSG00000138606	ENSG00000138606	SHF	15:45384847-45493373	OK	1.38259	3.94601	1.51302	1.64378	0.004	0.39975	1	1	1
ENSG00000203805	ENSG00000203805	PPAPDC1A	10:122216465-122349367	OK	5.33478	11.9924	1.16862	1.66146	0.007	0.525966	1	1	1
ENSG00000142949	ENSG00000142949	PTPRF	1:43990857-44089343	OK	7.42886	15.4218	1.05376	2.3162	5.00E-05	0.0312848	1	1	1
ENSG00000110492	ENSG00000110492	MDK	11:46402305-46405375	OK	25.2382	52.2038	1.04855	2.20429	0.0006	0.156993	1	1	1
ENSG00000005884	ENSG00000005884	ITGA3	17:48133331-48167845	OK	49.5687	99.2248	1.00127	1.51567	0.0002	0.0777892	1	1	1
ENSG00000069424	ENSG00000069424	KCNAB2	1:5922870-6161253	OK	14.8258	29.5563	0.995352	1.49034	0.00585	0.485182	1	1	1
ENSG00000124762	ENSG00000124762	CDKN1A	6:36644304-36655116	OK	118.389	234.584	0.986566	2.20357	0.0002	0.0777892	1	1	1
ENSG00000151718	ENSG00000151718	WWC2	4:184020445-184241930	OK	3.3601	6.60421	0.974883	1.54712	0.00315	0.362608	1	1	1
ENSG00000006327	ENSG00000006327	TNFRSF12A	16:3064712-3072384	OK	49.7551	96.5548	0.956506	1.66362	0.00025	0.0856607	1	1	1
ENSG00000177606	ENSG00000177606	JUN	1:59246464-59249785	OK	10.4766	19.5204	0.897808	2.04886	0.00095	0.207143	1	1	1
ENSG00000175602	ENSG00000175602	CCDC85B	11:65657874-65659105	OK	27.6634	47.5076	0.780179	1.70618	0.0059	0.485182	1	1	1
ENSG00000160075	ENSG00000160075	SSU72	1:1477052-1510249	OK	48.2648	82.4522	0.772586	1.84461	0.00235	0.338189	1	1	1
ENSG00000231925	ENSG00000231925	TAPBP	6:33267470-33282164	OK	28.0034	15.7022	-0.834637	-1.73379	0.00455	0.430783	1	1	1
ENSG00000117305	ENSG00000117305	HMGCL	1:24128374-24165110	OK	14.48	7.36592	-0.97512	-1.7663	0.00365	0.385846	1	1	1
ENSG00000144355	ENSG00000144355	DLX1	2:172949467-172954405	OK	5.60562	2.73048	-1.03772	-1.56543	0.0078	0.555692	1	1	1
ENSG00000105011	ENSG00000105011	ASF1B	19:14229917-14247768	OK	16.3743	7.03868	-1.21806	-2.0438	0.00185	0.302538	1	1	1
ENSG00000156475	ENSG00000156475	PPP2R2B	5:145942788-146464347	OK	2.64995	1.05274	-1.33182	-1.14104	0.00405	0.401956	1	1	1
ENSG00000106404	ENSG00000106404	CLDN15	7:100875372-100882101	OK	2.12577	0.756299	-1.49095	-1.63333	0.003	0.362608	1	1	1
ENSG00000167608	ENSG00000167608	TMC4	19:54663845-54676944	OK	0.165663	0.836146	2.3355	0.675342	0.0033	0.36531	0	1	1
ENSG00000107281	ENSG00000107281	NPDC1	9:139933921-139940655	OK	0.539845	1.57573	1.5454	1.12091	0.00845	0.576322	0	1	1
ENSG00000075618	ENSG00000075618	FSCN1	7:5632438-5646286	OK	1.59735	3.43963	1.10657	1.65237	0.00275	0.356534	0	1	1
ENSG00000143479	ENSG00000143479	DYRK3	1:206807993-206857764	OK	13.5467	26.9437	0.992011	2.21373	0.00015	0.0654136	0	1	1
ENSG00000129946	ENSG00000129946	SHC2	19:416582-460996	OK	5.11101	10.1368	0.987918	1.65694	0.0066	0.50635	0	1	1
ENSG00000123643	ENSG00000123643	SLC36A1	5:150816606-150871942	OK	4.6104	8.95246	0.957393	1.41949	0.00265	0.353112	0	1	1
ENSG00000170385	ENSG00000170385	SLC30A1	1:211744909-211752084	OK	8.72539	16.164	0.889494	2.11712	0.0005	0.153096	0	1	1
ENSG00000135048	ENSG00000135048	TMEM2	9:74298281-74431606	OK	15.5166	27.5806	0.829844	1.33739	0.0073	0.530577	0	1	1
ENSG00000159840	ENSG00000159840	ZYX	7:143078172-143220542	OK	16.9019	29.9165	0.823754	1.77001	0.0024	0.338612	0	1	1
ENSG00000136048	ENSG00000136048	DRAM1	12:102271128-102405908	OK	4.98693	8.73904	0.809324	1.28224	0.0079	0.560044	0	1	1
ENSG00000135069	ENSG00000135069	PSAT1	9:80912058-80945009	OK	29.4253	51.3665	0.80377	1.84882	0.00285	0.362608	0	1	1
ENSG00000146670	ENSG00000146670	CDCA5	11:64833771-64851636	OK	28.692	16.7239	-0.778741	-1.65933	0.0035	0.3731	0	1	1
ENSG00000088451	ENSG00000088451	TGDS	13:95226307-95248511	OK	20.6139	10.2359	-1.00998	-2.11989	0.00055	0.155197	0	1	1
ENSG00000023445	ENSG00000023445	BIRC3	11:102188214-102210134	OK	4.13371	1.08253	-1.93303	-2.26856	5.00E-05	0.0312848	0	1	1

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
ENSG00000081041	ENSG00000081041	CXCL2	4:74962751-74965010	OK	14.0676	3.5472	-1.98762	-3.14041	5.00E-05	0.0312848	0	1	1
ENSG00000142627	ENSG00000142627	EPHA2	1:16450831-16483824	OK	5.75231	16.7272	1.53998	3.01115	5.00E-05	0.0312848	1	0	1
ENSG00000076706	ENSG00000076706	MCAM	11:119179240-119192231	OK	100.539	234.556	1.22218	1.86587	5.00E-05	0.0312848	1	0	1
ENSG00000198682	ENSG00000198682	PAPSS2	10:89367741-89507462	OK	2.78637	6.08011	1.12571	1.47623	0.00425	0.413255	1	0	1
ENSG00000121579	ENSG00000121579	NAA50	3:113435306-113465147	OK	37.0055	71.9164	0.958582	1.64276	0.00705	0.525966	1	0	1
ENSG00000114573	ENSG00000114573	ATP6V1A	3:113465718-113530903	OK	21.2949	38.5301	0.855479	2.10447	0.00055	0.155197	1	0	1
ENSG00000113758	ENSG00000113758	DBN1	5:176883608-176901402	OK	24.7406	41.949	0.761756	1.48535	0.00855	0.580392	1	0	1
ENSG00000188783	ENSG00000188783	PRELP	1:203444955-203460480	OK	4.36771	1.01705	-2.10248	-3.80575	5.00E-05	0.0312848	1	0	1
ENSG00000184363	ENSG00000184363	PKP3	11:392613-404908	OK	0.135499	0.656222	2.27591	0.513756	0.005	0.452547	0	0	1
ENSG00000064300	ENSG00000064300	NGFR	17:47572654-47661189	OK	1.67048	6.8959	2.04548	3.34679	5.00E-05	0.0312848	0	0	1
ENSG00000136274	ENSG00000136274	NACAD	7:45120036-45128513	OK	0.281946	1.08894	1.94943	1.1403	0.0048	0.43998	0	0	1
ENSG00000118640	ENSG00000118640	VAMP8	2:85788684-85809154	OK	0.464121	1.68446	1.85971	1.50169	0.00935	0.606107	0	0	1
ENSG00000197540	ENSG00000197540	GZMM	19:544033-549919	OK	0.813084	2.82344	1.79598	2.03735	0.002	0.316286	0	0	1
ENSG00000108924	ENSG00000108924	HLF	17:53342372-53402426	OK	0.287422	0.928197	1.69126	0.731493	0.00925	0.606107	0	0	1
ENSG00000167693	ENSG00000167693	NXN	17:702552-883010	OK	0.811196	2.38063	1.55322	1.26365	0.00645	0.50635	0	0	1
ENSG00000176845	ENSG00000176845	METRNL	17:81037566-81052864	OK	2.55424	7.14771	1.48459	1.93361	0.00145	0.257617	0	0	1
ENSG00000127418	ENSG00000127418	FGFRL1	4:1003723-1020685	OK	1.00723	2.80924	1.47979	1.88378	0.0006	0.156993	0	0	1
ENSG00000072163	ENSG00000072163	LIMS2	2:128395955-128439360	OK	1.45637	3.70447	1.34689	1.78381	0.0013	0.242965	0	0	1
ENSG00000143320	ENSG00000143320	CRABP2	1:156669397-156675608	OK	6.97026	17.5389	1.33127	2.28463	0.0004	0.125139	0	0	1
ENSG00000131196	ENSG00000131196	NFATC1	18:77155855-77289325	OK	1.75474	4.12983	1.23483	1.71553	0.0009	0.202373	0	0	1
ENSG00000166831	ENSG00000166831	RBPMS2	15:65032090-65067786	OK	1.40517	3.19285	1.18411	1.74456	0.0054	0.467076	0	0	1
ENSG00000160867	ENSG00000160867	FGFR4	5:176513886-176525145	OK	3.89227	8.17217	1.07011	1.50145	0.00115	0.223644	0	0	1
ENSG00000179627	ENSG00000179627	ZBTB42	14:105266932-105271049	OK	1.37187	2.72406	0.989613	1.62455	0.00865	0.581692	0	0	1
ENSG00000073670	ENSG00000073670	ADAM11	17:42836398-42859214	OK	4.03268	7.9687	0.982605	1.59961	0.0071	0.525966	0	0	1
ENSG00000114019	ENSG00000114019	AMOTL2	3:134070693-134094321	OK	8.38079	16.4089	0.969322	2.19786	0.0002	0.0777892	0	0	1
ENSG00000186654	ENSG00000186654	PRR5	22:45064592-45258665	OK	3.83389	7.50062	0.9682	1.59202	0.0083	0.568787	0	0	1
ENSG00000110092	ENSG00000110092	CCND1	11:69455854-69490184	OK	192.129	360.135	0.906462	1.4578	0.00125	0.236694	0	0	1
ENSG00000180921	ENSG00000180921	FAM83H	8:144806102-144815971	OK	2.74058	5.12344	0.902631	1.85085	0.0031	0.362608	0	0	1
ENSG00000101197	ENSG00000101197	BIRC7	20:61867234-61871859	OK	163.212	263.676	0.692021	1.54672	0.00935	0.606107	0	0	1
ENSG00000131374	ENSG00000131374	TBC1D5	3:17198653-18959184	OK	26.6305	15.2557	-0.803731	-0.875512	0.00815	0.566602	0	0	1
ENSG00000163808	ENSG00000163808	KIF15	3:44803208-44914868	OK	10.1628	5.12214	-0.988477	-1.44087	0.00525	0.466375	0	0	1
ENSG00000114739	ENSG00000114739	ACVR2B	3:38492517-38534633	OK	3.47377	1.64035	-1.0825	-1.68698	0.0022	0.330406	0	0	1
ENSG00000162892	ENSG00000162892	IL24	1:207070787-207077484	OK	3.22045	18.364	2.51155	3.6908	5.00E-05	0.0312848	1	1	0
ENSG00000104783	ENSG00000104783	KCNN4	19:44270684-44285409	OK	0.348731	1.35945	1.96283	1.09381	0.00905	0.602956	1	1	0
ENSG00000221890	ENSG00000221890	NPTXR	22:39214456-39239987	OK	0.217667	0.758341	1.80073	2.44749	0.0006	0.156993	1	1	0

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
ENSG00000134594	ENSG00000134594	RAB33A	X:129305622-129318844	OK	1.32442	3.86526	1.5452	2.15278	0.00185	0.302538	1	1	0
ENSG00000132170	ENSG00000132170	PPARG	3:12328866-12475855	OK	1.75238	4.59908	1.39203	1.94601	0.0006	0.156993	1	1	0
ENSG00000147650	ENSG00000147650	LRP12	8:105501458-105601252	OK	32.5455	61.4048	0.915894	1.61471	0.0066	0.50635	1	1	0
ENSG00000138119	ENSG00000138119	MYOF	10:95066185-95242074	OK	9.61062	17.1202	0.833	1.43307	0.0035	0.3731	1	1	0
ENSG00000090621	ENSG00000090621	PABPC4	1:40026487-40042462	OK	49.7917	83.6748	0.748888	1.30039	0.008	0.5616	1	1	0
ENSG00000174307	ENSG00000174307	PHLDA3	1:201434619-201438365	OK	66.2584	110.097	0.732594	1.755	0.00385	0.395753	1	1	0
ENSG00000152291	ENSG00000152291	TGOLN2	2:85545146-85555548	OK	58.9807	34.646	-0.767556	-1.78771	0.0032	0.362608	1	1	0
ENSG00000116209	ENSG00000116209	TMEM59	1:54497346-54519177	OK	127.508	73.7472	-0.789927	-1.81063	0.00255	0.346199	1	1	0
ENSG00000172819	ENSG00000172819	RARG	12:53604353-53626764	OK	18.7399	10.4549	-0.841934	-1.50363	0.0052	0.464802	1	1	0
ENSG00000174371	ENSG00000174371	EXO1	1:242011268-242058450	OK	19.123	10.5998	-0.85128	-1.29699	0.0098	0.624035	1	1	0
ENSG00000168610	ENSG00000168610	STAT3	17:40465341-40540586	OK	30.2507	16.4808	-0.876182	-1.70382	0.00145	0.257617	1	1	0
ENSG00000139350	ENSG00000139350	NEDD1	12:97301000-97347129	OK	14.3328	7.72155	-0.892359	-1.55055	0.00255	0.346199	1	1	0
ENSG00000012660	ENSG00000012660	ELOVL5	6:53132195-53213947	OK	81.5122	42.2344	-0.948598	-1.88364	0.0016	0.26774	1	1	0
ENSG00000151725	ENSG00000151725	CENPU	4:185570766-185655287	OK	25.8647	13.2643	-0.963431	-1.77309	0.00445	0.424106	1	1	0
ENSG00000118193	ENSG00000118193	KIF14	1:200520627-200589862	OK	9.48301	4.76494	-0.992889	-2.27274	0.00025	0.0856607	1	1	0
ENSG00000168843	ENSG00000168843	FSTL5	4:162300104-163085187	OK	1.98116	0.951795	-1.05762	-1.40385	0.00945	0.60712	1	1	0
ENSG00000151025	ENSG00000151025	GPR158	10:25401986-25891155	OK	17.3546	7.85686	-1.14329	-1.83734	0.0035	0.3731	1	1	0
ENSG00000158006	ENSG00000158006	PAFAH2	1:26286257-26324648	OK	5.65278	2.46761	-1.19584	-1.35907	0.00555	0.467076	1	1	0
ENSG00000116199	ENSG00000116199	FAM20B	1:178994938-179045697	OK	29.2921	11.4249	-1.35833	-2.51375	5.00E-05	0.0312848	1	1	0
ENSG00000135318	ENSG00000135318	NT5E	6:86159808-86205500	OK	0.401159	2.60483	2.69894	2.43235	0.0001	0.0513964	0	1	0
ENSG00000161638	ENSG00000161638	ITGA5	12:54747444-54891472	OK	1.09852	3.7346	1.76539	1.3458	0.00135	0.249075	0	1	0
ENSG00000116741	ENSG00000116741	RGS2	1:192778168-192781403	OK	18.3603	38.3176	1.06142	2.24773	0.00015	0.0654136	0	1	0
ENSG00000111057	ENSG00000111057	KRT18	12:53290976-53346686	OK	5.10018	10.1964	0.999441	1.73926	0.00415	0.409059	0	1	0
ENSG00000185909	ENSG00000185909	KLHDC8B	3:49209043-49213917	OK	16.2449	29.4712	0.859313	1.54404	0.0093	0.606107	0	1	0
ENSG00000170017	ENSG00000170017	ALCAM	3:105085752-105295744	OK	13.1829	22.8556	0.793874	1.60366	0.0054	0.467076	0	1	0
ENSG00000139645	ENSG00000139645	ANKRD52	12:56623832-56652175	OK	29.0711	17.9548	-0.695213	-1.40279	0.00545	0.467076	0	1	0
ENSG00000165475	ENSG00000165475	CRYL1	13:20977805-21099996	OK	56.4969	34.0208	-0.731754	-1.68359	0.006	0.490602	0	1	0
ENSG00000136816	ENSG00000136816	TOR1B	9:132565431-132573560	OK	15.6206	9.07792	-0.783017	-1.44047	0.00655	0.50635	0	1	0
ENSG00000165304	ENSG00000165304	MELK	9:36572858-36677678	OK	20.7899	11.5941	-0.842489	-1.72809	0.0039	0.398049	0	1	0
ENSG00000112977	ENSG00000112977	DAP	5:10679341-10770406	OK	45.0937	24.9333	-0.854849	-1.89643	0.00155	0.26774	0	1	0
ENSG00000155111	ENSG00000155111	CDK19	6:110931180-111137161	OK	5.16057	2.77353	-0.895808	-1.10818	0.00665	0.50635	0	1	0
ENSG00000170264	ENSG00000170264	FAM161A	2:62051988-62081278	OK	15.1729	8.13648	-0.899016	-1.55989	0.00305	0.362608	0	1	0
ENSG00000125148	ENSG00000125148	MT2A	16:56642110-56643409	OK	50.8286	27.0803	-0.908396	-1.80864	0.00465	0.43173	0	1	0
ENSG00000164172	ENSG00000164172	MOCS2	5:52391508-52410956	OK	56.145	29.8509	-0.911381	-2.00531	0.001	0.211632	0	1	0
ENSG00000044524	ENSG00000044524	EPHA3	3:89156673-89531284	OK	5.83338	3.05215	-0.934503	-1.87533	0.0024	0.338612	0	1	0
ENSG00000146674	ENSG00000146674	IGFBP3	7:45951948-45961473	OK	131.778	64.7348	-1.02549	-2.3814	5.00E-05	0.0312848	0	1	0
ENSG00000122966	ENSG00000122966	CIT	12:120123594-120315095	OK	35.6414	17.4359	-1.03149	-1.06929	0.00225	0.330406	0	1	0
ENSG00000139734	ENSG00000139734	DIAPH3	13:60239716-60738121	OK	11.8944	5.3762	-1.14562	-2.45815	0.0001	0.0513964	0	1	0

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
ENSG00000166845	ENSG00000166845	C18orf54	18:51850727-51911588	OK	4.08815	1.83818	-1.15317	-1.52171	0.00225	0.330406	0	1	0
ENSG00000072571	ENSG00000072571	HMMR	5:162887208-162921064	OK	13.5653	5.79204	-1.22777	-1.83021	0.00085	0.20053	0	1	0
ENSG00000221869	ENSG00000221869	CEBPD	8:48649470-48651648	OK	18.1426	6.8175	-1.41207	-2.88943	5.00E-05	0.0312848	0	1	0
ENSG00000073712	ENSG00000073712	FERMT2	14:53323985-53419153	OK	6.82605	12.2169	0.839753	1.70744	0.0023	0.334336	1	0	0
ENSG00000049449	ENSG00000049449	RCN1	11:31806339-32127301	OK	51.2029	89.2247	0.801218	1.56985	0.004	0.39975	1	0	0
ENSG00000135842	ENSG00000135842	FAM129A	1:184759857-184943682	OK	26.9178	45.3861	0.753693	1.69486	0.00225	0.330406	1	0	0
ENSG00000011566	ENSG00000011566	MAP4K3	2:39476406-39945103	OK	11.8812	19.2447	0.695783	1.12394	0.0087	0.582333	1	0	0
ENSG00000112773	ENSG00000112773	FAM46A	6:82201155-82462491	OK	13.8034	8.48817	-0.701499	-1.63757	0.0059	0.485182	1	0	0
ENSG00000143437	ENSG00000143437	ARNT	1:150782180-150849244	OK	26.4835	14.6511	-0.85408	-1.35707	0.0065	0.50635	1	0	0
ENSG00000115232	ENSG00000115232	ITGA4	2:182321928-182400914	OK	13.1927	6.96395	-0.921764	-1.90872	0.0011	0.219863	1	0	0
ENSG00000181458	ENSG00000181458	TMEM45A	3:100211462-100296288	OK	2.61078	0.895709	-1.54338	-1.59436	0.00425	0.413255	1	0	0
ENSG00000170442	ENSG00000170442	KRT86	12:52626303-52702947	OK	0.093486	0.85226	3.18847	1.37006	0.003	0.362608			
ENSG00000172247	ENSG00000172247	C1QTNF4	11:47611215-47616211	OK	0.193578	1.28168	2.72704	1.17078	0.00625	0.502479			
ENSG00000026751	ENSG00000026751	SLAMF7	1:160709036-160724611	OK	5.97929	38.2066	2.67578	4.41381	5.00E-05	0.0312848			
ENSG00000179817	ENSG00000179817	MRGPRX4	11:18161732-18211168	OK	0.271425	1.63545	2.59106	2.50602	0.00245	0.339019			
ENSG00000115956	ENSG00000115956	PLEK	2:68588345-68624585	OK	0.163438	0.751818	2.20164	1.59759	0.0072	0.525965			
ENSG00000160588	ENSG00000160588	MPZL3	11:118097408-118123065	OK	0.166065	0.691753	2.05851	1.36449	0.00325	0.36531			
ENSG00000183668	ENSG00000183668	PSG9	19:43715942-43773682	OK	1.11182	4.3564	1.97022	2.06532	0.00305	0.362608			
ENSG00000236719	ENSG00000236719	OVAAL	1:180528111-180535654	OK	0.464653	1.75045	1.9135	2.17005	0.0031	0.362608			
ENSG00000139629	ENSG00000139629	GALNT6	12:51745030-51902980	OK	1.31767	4.66084	1.8226	1.24603	0.00015	0.0654136			
ENSG00000186205	ENSG00000186205	1-Mar	1:220960100-220987735	OK	0.475762	1.67109	1.81248	1.25238	0.0016	0.26774			
ENSG00000203837	ENSG00000203837	PNLIPRP3	10:118187378-118237469	OK	0.909978	3.17066	1.80088	2.63668	0.0001	0.0513964			
ENSG00000237289	ENSG00000237289	CKMT1B	15:43885251-44010458	OK	0.310184	1.06677	1.78206	0.738184	0.0047	0.433575			
ENSG00000188725	ENSG00000188725	SMIM15	5:60453535-60560756	OK	14.5261	47.955	1.72303	2.43568	5.00E-05	0.0312848			
ENSG00000178726	ENSG00000178726	THBD	20:23026269-23030378	OK	0.206776	0.680587	1.71871	2.01187	0.0046	0.43173			
ENSG00000121769	ENSG00000121769	FABP3	1:31838471-31849697	OK	6.3945	19.6954	1.62296	2.52296	0.00015	0.0654136			
ENSG00000147434	ENSG00000147434	CHRNA6	8:42607762-42651535	OK	0.37526	1.15333	1.61985	1.07815	0.00935	0.606107			
ENSG00000135218	ENSG00000135218	CD36	7:79959507-80308593	OK	1.65152	5.07246	1.61889	1.65931	5.00E-05	0.0312848			
ENSG00000135046	ENSG00000135046	ANXA1	9:75766672-75785309	OK	25.4681	77.6662	1.6086	3.5394	5.00E-05	0.0312848			
ENSG00000166341	ENSG00000166341	DCHS1	11:6642555-6677085	OK	0.285433	0.767141	1.42634	2.1675	0.00085	0.20053			
ENSG00000261087	ENSG00000261087	KB-1460A1.5	8:102179032-102181857	OK	0.388269	1.01224	1.38242	1.75909	0.0076	0.544137			
ENSG00000141934	ENSG00000141934	PPAP2C	19:281039-291393	OK	12.3733	31.2973	1.33881	2.66514	5.00E-05	0.0312848			
ENSG00000244486	ENSG00000244486	SCARF2	22:20778873-20850170	OK	8.94016	22.4294	1.32702	1.99562	0.00055	0.155197			
ENSG00000112655	ENSG00000112655	PTK7	6:43044005-43129457	OK	3.15858	7.91906	1.32605	1.94636	5.00E-05	0.0312848			
ENSG00000140044	ENSG00000140044	JDP2	14:75890385-75940814	OK	2.09781	5.19138	1.30723	1.70211	0.00445	0.424106			
ENSG00000136999	ENSG00000136999	NOV	8:120428545-120474590	OK	25.789	62.1996	1.27015	2.45775	5.00E-05	0.0312848			
ENSG00000169551	ENSG00000169551	CT55	X:134290460-134305322	OK	2.36382	5.62545	1.25085	2.00336	0.0021	0.324958			

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
ENSG00000137752	ENSG00000137752	CASP1	11:104896169-104972158	OK	1.51173	3.5718	1.24045	1.09761	0.0065	0.50635			
ENSG00000100522	ENSG00000100522	GNPNAT1	14:53241911-53258386	OK	8.64083	20.4092	1.23998	1.74834	0.00025	0.0856607			
ENSG00000065809	ENSG00000065809	FAM107B	10:14560555-14816896	OK	1.10846	2.54432	1.19872	0.868112	0.00805	0.562367			
ENSG00000184584	ENSG00000184584	TMEM173	5:138855118-138862520	OK	7.01309	15.6661	1.15952	2.03032	0.00055	0.155197			
ENSG00000130600	ENSG00000130600	H19	11:2016405-2022700	OK	7.79369	17.2386	1.14527	1.65485	0.0028	0.359775			
ENSG00000158764	ENSG00000158764	ITLN2	1:160901528-160924589	OK	8.68181	19.0695	1.1352	1.83255	0.0037	0.385846			
ENSG00000158050	ENSG00000158050	DUSP2	2:96808904-96811179	OK	2.29522	4.98394	1.11866	1.81251	0.00385	0.395752			
ENSG00000118420	ENSG00000118420	UBE3D	6:83602116-83775560	OK	3.02825	6.54309	1.11149	1.93949	0.00615	0.500026			
ENSG00000080546	ENSG00000080546	SESN1	6:109307639-109416022	OK	7.60393	16.1685	1.08837	2.24271	0.0001	0.0513964			
ENSG00000187135	ENSG00000187135	VSTM2B	19:29777917-30055386	OK	19.8708	42.1179	1.08379	2.39601	5.00E-05	0.0312848			
ENSG00000184371	ENSG00000184371	CSF1	1:110452863-110473614	OK	2.64526	5.59344	1.08033	1.60331	0.00205	0.320669			
ENSG00000112237	ENSG00000112237	CCNC	6:99990255-100016972	OK	18.1063	37.9683	1.0683	1.93005	0.00035	0.114474			
ENSG00000128283	ENSG00000128283	CDC42EP1	22:37956453-37965412	OK	4.01718	8.27091	1.04186	1.93046	0.0007	0.173684			
ENSG00000116717	ENSG00000116717	GADD45A	1:68150743-68154021	OK	15.2303	31.2765	1.03814	2.22335	0.00035	0.114474			
ENSG00000138798	ENSG00000138798	EGF	4:110834039-110933422	OK	1.73343	3.53428	1.02778	1.16683	0.0035	0.3731			
ENSG00000104332	ENSG00000104332	SFRP1	8:41119480-41167016	OK	1.42489	2.87921	1.01482	1.74322	0.00665	0.50635			
ENSG00000253276	ENSG00000253276	CCDC71L	7:106012696-106410653	OK	5.963	11.894	0.996121	2.21128	0.0004	0.125139			
ENSG00000204516	ENSG00000204516	MICB	6:31462657-31478901	OK	2.74406	5.42895	0.984358	1.56391	0.00715	0.525966			
ENSG00000102034	ENSG00000102034	ELF4	X:129198848-129244691	OK	1.69674	3.33841	0.976396	1.67715	0.00555	0.467076			
ENSG00000121644	ENSG00000121644	DESI2	1:244816236-244872335	OK	12.0807	23.1934	0.941009	2.09924	5.00E-05	0.0312848			
ENSG00000125355	ENSG00000125355	TMEM255A	X:119392504-119445411	OK	15.0477	28.5983	0.926389	1.34158	0.00245	0.339019			
ENSG00000133816	ENSG00000133816	MICAL2	11:12115542-12285334	OK	5.11434	9.6951	0.922706	1.10154	0.00945	0.60712			
ENSG00000230836	ENSG00000230836	AC104135.4	2:75167384-75169797	OK	8.00754	14.7379	0.880096	1.68063	0.00675	0.511259			
ENSG00000205213	ENSG00000205213	LGR4	11:27387507-27503980	OK	3.23452	5.88105	0.862522	1.5531	0.00305	0.362608			
ENSG00000150093	ENSG00000150093	ITGB1	10:33189246-33371030	OK	52.4046	94.7021	0.853703	1.44068	0.00085	0.20053			
ENSG00000070669	ENSG00000070669	ASNS	7:97481429-97501854	OK	10.5099	18.9779	0.852571	1.71265	0.0033	0.36531			
ENSG00000174705	ENSG00000174705	SH3PXD2B	5:171752184-171881527	OK	4.98931	8.89785	0.834616	1.24287	0.00275	0.356534			
ENSG00000184500	ENSG00000184500	PROS1	3:93591880-93692910	OK	41.7949	74.3832	0.831652	1.81377	0.0015	0.26325			
ENSG00000168461	ENSG00000168461	RAB31	18:9708161-9862548	OK	6.26355	11.0572	0.81993	1.17191	0.00635	0.50635			
ENSG00000244694	ENSG00000244694	PTCHD4	6:47845763-48036425	OK	6.34424	10.9158	0.782898	1.62782	0.0076	0.544137			
ENSG00000130513	ENSG00000130513	GDF15	19:18485540-18499986	OK	1046.11	1778.98	0.766015	1.60183	0.0091	0.603494			
ENSG00000130203	ENSG00000130203	APOE	19:45409010-45412650	OK	251.199	414.985	0.72423	1.62993	0.0083	0.568787			
ENSG00000198087	ENSG00000198087	CD2AP	6:47445524-47594999	OK	27.8033	16.6359	-0.740957	-1.67872	0.00275	0.356534			
ENSG00000170961	ENSG00000170961	HAS2	8:122624355-122656933	OK	17.852	10.6641	-0.74332	-1.71857	0.0053	0.467076			
ENSG00000118785	ENSG00000118785	SPP1	4:88896818-88904562	OK	74.2821	44.3676	-0.743508	-1.65602	0.005	0.452547			
ENSG00000100417	ENSG00000100417	PMM1	22:41956766-41985894	OK	38.2446	22.7522	-0.749252	-1.64924	0.0065	0.50635			
ENSG00000144837	ENSG00000144837	PLA1A	3:119316688-119348658	OK	24.0294	14.0899	-0.770135	-1.67452	0.00585	0.485182			
ENSG00000184990	ENSG00000184990	SIVA1	14:105219436-105234831	OK	97.069	56.3659	-0.784188	-1.6355	0.00865	0.581692			

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
ENSG00000106780	ENSG00000106780	MEGF9	9:123363090-123476748	OK	19.3849	11.2286	-0.787752	-1.91703	0.002	0.316286			
ENSG00000056998	ENSG00000056998	GYG2	X:2746828-2800859	OK	60.914	35.0509	-0.797324	-1.54683	0.00555	0.467076			
ENSG00000123240	ENSG00000123240	OPTN	10:12938626-13180291	OK	40.9391	23.2796	-0.814413	-1.41941	0.0032	0.362608			
ENSG00000242265	ENSG00000242265	PEG10	7:94285636-94299007	OK	21.1897	12.0467	-0.814728	-1.92451	0.00105	0.212825			
ENSG00000146072	ENSG00000146072	TNFRSF21	6:47199267-47277641	OK	50.0336	28.3262	-0.820761	-2.0503	0.00105	0.212825			
ENSG00000233461	ENSG00000233461	RP11-295G20.2	1:231658133-231664302	OK	241.367	135.24	-0.8357	-1.84518	0.0029	0.362608			
ENSG00000100906	ENSG00000100906	NFKBIA	14:35870716-35873955	OK	55.9969	31.104	-0.848248	-1.8809	0.00105	0.212825			
ENSG00000170915	ENSG00000170915	PAQR8	6:52226218-52272575	OK	7.05365	3.89604	-0.856361	-1.81448	0.00395	0.39975			
ENSG00000115414	ENSG00000115414	FN1	2:216225162-216300895	OK	233.939	129.157	-0.857003	-1.4106	0.0037	0.385846			
ENSG00000066032	ENSG00000066032	CTNNA2	2:79384131-80875905	OK	21.563	11.5223	-0.904134	-1.40629	0.00115	0.223644			
ENSG00000131016	ENSG00000131016	AKAP12	6:151561133-151679692	OK	27.5808	14.525	-0.925125	-2.2599	0.0002	0.0777892			
ENSG00000113657	ENSG00000113657	DPYSL3	5:146770373-146889619	OK	15.4293	8.06641	-0.935674	-1.79598	0.001	0.211632			
ENSG00000165195	ENSG00000165195	PIGA	X:15337572-15353676	OK	22.0951	11.5056	-0.941392	-1.57152	0.0043	0.415311			
ENSG00000031691	ENSG00000031691	CENPQ	6:49431090-49460820	OK	14.246	7.31419	-0.961787	-1.89876	0.00315	0.362608			
ENSG00000118513	ENSG00000118513	MYB	6:135502452-135540311	OK	3.20516	1.59044	-1.01097	-1.43408	0.00295	0.362608			
ENSG00000130150	ENSG00000130150	MOSPD2	X:14891562-14940449	OK	13.5226	6.65653	-1.02253	-2.0274	0.0009	0.202373			
ENSG00000164627	ENSG00000164627	KIF6	6:39297765-39693181	OK	8.20587	4.03378	-1.02453	-1.73798	0.00555	0.467076			
ENSG00000169499	ENSG00000169499	PLEKHA2	8:38758752-38831428	OK	22.9374	11.1184	-1.04475	-1.28826	0.00125	0.236694			
ENSG00000188452	ENSG00000188452	CERKL	2:182401402-182545603	OK	3.54	1.71127	-1.04869	-1.6834	0.00145	0.257617			
ENSG00000185875	ENSG00000185875	THNSL1	10:25305586-25315593	OK	1.7592	0.848754	-1.0515	-1.66905	0.00795	0.560826			
ENSG00000108387	ENSG00000108387	4-Sep	17:56597197-56769416	OK	94.4412	44.0601	-1.09994	-2.23588	0.00025	0.0856607			
ENSG00000213390	ENSG00000213390	ARHGAP19	10:98757794-99052413	OK	6.99423	3.24805	-1.10659	-1.79453	0.0009	0.202373			
ENSG00000159216	ENSG00000159216	RUNX1	21:36160097-37376965	OK	6.31318	2.92037	-1.11221	-1.39277	0.0022	0.330406			
ENSG00000163430	ENSG00000163430	FSTL1	3:120111139-120170100	OK	42.0042	19.0439	-1.1412	-1.49289	0.00315	0.362608			
ENSG00000159167	ENSG00000159167	STC1	8:23699427-23712320	OK	11.5631	5.22023	-1.14735	-1.69133	0.0054	0.467076			
ENSG00000163735	ENSG00000163735	CXCL5	4:74861358-74864496	OK	1.6759	0.745335	-1.16897	-1.63257	0.00965	0.617214			
ENSG00000172731	ENSG00000172731	LRRC20	10:72058728-72142382	OK	9.39818	4.15292	-1.17826	-1.84486	0.0026	0.349688			
ENSG00000181315	ENSG00000181315	ZNF322	6:26634610-26659980	OK	5.2553	2.29499	-1.19528	-1.44822	0.00515	0.46321			
ENSG00000146285	ENSG00000146285	SCML4	6:108025307-108145521	OK	9.4712	4.09559	-1.20948	-2.09148	0.00065	0.167038			
ENSG00000204291	ENSG00000204291	COL15A1	9:101705460-101833069	OK	6.55412	2.72614	-1.26554	-1.8544	0.00025	0.0856607			
ENSG00000163739	ENSG00000163739	CXCL1	4:74735109-74736959	OK	193.549	79.2914	-1.28746	-3.10424	5.00E-05	0.0312848			
ENSG00000163734	ENSG00000163734	CXCL3	4:74902305-74904524	OK	2.06829	0.74806	-1.46721	-1.58927	0.00755	0.544137			
ENSG00000106733	ENSG00000106733	NMRK1	9:77675488-77703133	OK	8.84129	3.04853	-1.53615	-2.27211	0.0007	0.173684			
ENSG00000115461	ENSG00000115461	IGFBP5	2:217536827-217858802	OK	3.6735	1.24197	-1.56452	-1.32071	0.00625	0.502479			
ENSG00000108691	ENSG00000108691	CCL2	17:32581899-32584222	OK	5.60181	1.72269	-1.70123	-2.04687	0.002	0.316286			
ENSG00000250343	ENSG00000250343	CTC-255N20.1	5:146559766-146614422	OK	3.23806	0.993385	-1.7047	-1.9836	0.0035	0.3731			
ENSG00000136244	ENSG00000136244	IL6	7:22765013-22771621	OK	5.02845	1.51731	-1.7286	-1.91983	0.00095	0.207143			

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value	1_A375_pNL7_minus_lncRNA_AR::1 Present	2_A375_pNL97_plus_lncRNA_AR::1 Present	4_A375_EGR1::1 Present
ENSG00000133636	ENSG00000133636	NTS	12:86268072-86276770	OK	1.45476	0.434451	-1.74351	-1.66134	0.00715	0.525966			
ENSG00000227036	ENSG00000227036	LINC00511	17:70319263-70636611	OK	66.6256	14.7663	-2.17377	-3.78493	5.00E-05	0.0312848			

Table 13B. Genes bound by AR or EGR1 and regulated by SLNCR

Table 13B lists the genes bound by AR or EGR1 and regulated by SLNCR. RNA-seq differential expression was taken from Tables 6A-6C, AR ChIP-seq values were taken from Table 9A, and EGR1 ChIP-seq values from Table 12. The table lists only those genes from Table 13A that are bound by AR, EGR1 or both.

Table 13B

test_id	gene_id	gene	locus	status	scrambled	siSLNCR	log2(fold_change)	test_stat	p_value	q_value	1_A375_pNL7_rnd_plus_lncRNA_AR:1.1 Present	2_A375_pNL97_plus_lncRNA_AR:1.1 Present	4_A375_EGR1::1 Present
ENSG00000128564	ENSG00000128564	VGF	7:100605789-100606874	OK	0.73792	10.7725	3.86778	5.79161	5.00E-05	0.0312848	1	1	1
ENSG00000131409	ENSG00000131409	LRRC4B	19:51020148-51071302	OK	0.715032	2.73315	1.93448	2.2952	0.00015	0.0654136	1	1	1
ENSG00000166710	ENSG00000166710	B2M	15:45003674-45011075	OK	0.456503	1.68041	1.88012	0.978707	0.0072	0.525966	1	1	1
ENSG00000172183	ENSG00000172183	ISG20	15:89179383-89199714	OK	1.37799	4.51629	1.71257	1.48651	0.0063	0.568787	1	1	1
ENSG00000138606	ENSG00000138606	SHF	15:45384847-45493373	OK	1.38259	3.94601	1.51302	1.64378	0.004	0.39975	1	1	1
ENSG00000203505	ENSG00000203505	PPAPDC1A	10:122216465-122349367	OK	5.33478	11.9924	1.16562	1.66146	0.007	0.525966	1	1	1
ENSG00000142949	ENSG00000142949	PTPRF	1:43990857-44069343	OK	7.42886	15.4218	1.05376	2.3162	5.00E-05	0.0312848	1	1	1
ENSG00000110492	ENSG00000110492	MDK	11:46402305-46405375	OK	25.2382	52.2038	1.04855	2.20429	0.0006	0.156993	1	1	1
ENSG00000005884	ENSG00000005884	ITGA3	17:48133331-48167845	OK	49.5687	99.2248	1.00127	1.51567	0.0002	0.0777892	1	1	1
ENSG00000069424	ENSG00000069424	KCNAB2	1:5922670-6161253	OK	14.8258	29.5563	0.995352	1.49034	0.00055	0.485182	1	1	1
ENSG00000124762	ENSG00000124762	CDKN1A	6:36844394-36855116	OK	116.389	234.584	0.956566	2.20357	0.0002	0.0777892	1	1	1
ENSG00000151718	ENSG00000151718	WWC2	4:184020445-184241930	OK	3.3601	6.60421	0.974583	1.54712	0.00315	0.362608	1	1	1
ENSG00000006327	ENSG00000006327	TNFRSF12A	16:3064712-3072384	OK	49.7551	96.5548	0.956506	1.66362	0.00025	0.0856607	1	1	1
ENSG00000177606	ENSG00000177606	JUN	1:59246464-59249785	OK	10.4766	19.5204	0.897506	2.04856	0.00095	0.207143	1	1	1
ENSG00000175602	ENSG00000175602	CCDC85B	11:65657674-65659105	OK	27.6634	47.5076	0.780179	1.70618	0.0059	0.485182	1	1	1
ENSG00000160075	ENSG00000160075	SSU72	1:1477052-1510249	OK	45.2648	82.4522	0.772586	1.84461	0.00235	0.338189	1	1	1
ENSG00000023125	ENSG00000023125	TAPBP	6:33267470-33282164	OK	28.0034	15.7022	-0.834637	-1.73379	0.00455	0.430783	1	1	1
ENSG00000113905	ENSG00000113905	HMGCL	1:24128374-24165110	OK	14.48	7.36592	-0.97512	-1.7663	0.00365	0.385846	1	1	1
ENSG00000144355	ENSG00000144355	DLX1	2:172949467-172954405	OK	5.60562	2.73048	-1.03772	-1.56543	0.0078	0.555692	1	1	1
ENSG00000101911	ENSG00000101911	ASF1B	19:14229917-14247768	OK	16.3743	7.03868	-1.21806	-2.0438	0.00165	0.302538	1	1	1
ENSG00000156475	ENSG00000156475	PPP2R2B	5:145942788-146464347	OK	2.64995	1.05274	-1.33182	-1.14104	0.00405	0.401956	1	1	1
ENSG00000181904	ENSG00000181904	CLDN15	7:100875372-100882101	OK	2.12577	0.756299	-1.49095	-1.63333	0.003	0.362608	1	1	1
ENSG00000141905	ENSG00000141905	TMC4	19:54663845-54676944	OK	0.165663	0.836146	2.3355	0.675342	0.0033	0.36531	0	1	1
ENSG00000101161	ENSG00000101161	NPDC1	9:139933921-139940655	OK	0.539845	1.57573	1.5454	1.12091	0.00845	0.576322	0	1	1
ENSG00000075618	ENSG00000075618	FSCN1	7:5632435-5646256	OK	1.59735	3.43963	1.10657	1.65237	0.00275	0.356534	0	1	1
ENSG00000141479	ENSG00000141479	DYRK3	1:206807993-206857764	OK	13.5467	26.9437	0.992011	2.21373	0.00015	0.0654136	0	1	1
ENSG00000129946	ENSG00000129946	SHC2	19:416552-460996	OK	5.11101	10.1368	0.987918	1.65694	0.0066	0.50635	0	1	1
ENSG00000112363	ENSG00000112363	SLC36A1	5:150816606-150871942	OK	4.6104	8.95246	0.957393	1.41949	0.00265	0.353112	0	1	1
ENSG00000170555	ENSG00000170555	SLC30A1	1:211744909-211752084	OK	8.72539	16.164	0.889494	2.11712	0.0005	0.153096	0	1	1
ENSG00000135048	ENSG00000135048	TMEM2	9:74298261-74431606	OK	15.5166	27.5806	0.829844	1.33739	0.0073	0.530577	0	1	1
ENSG00000159840	ENSG00000159840	ZYX	7:143078172-143220542	OK	16.9019	29.9165	0.823754	1.77001	0.0024	0.338612	0	1	1
ENSG00000135148	ENSG00000135148	DRAM1	12:102271128-102405908	OK	4.98693	8.73904	0.809324	1.28224	0.0079	0.560044	0	1	1
ENSG00000135069	ENSG00000135069	PSAT1	9:80912058-80945009	OK	29.4253	51.3665	0.80377	1.84882	0.00285	0.362608	0	1	1
ENSG00000144070	ENSG00000144070	CDCA5	11:64833771-64851636	OK	25.692	16.7239	-0.778741	-1.65933	0.0035	0.3731	0	1	1
ENSG00000088451	ENSG00000088451	TGDS	13:95226307-95248511	OK	20.6139	10.2359	-1.00998	-2.11989	0.00055	0.155197	0	1	1
ENSG00000002445	ENSG00000002445	BIRC3	11:102185214-102210134	OK	4.13371	1.08253	-1.93303	-2.26856	5.00E-05	0.0312848	0	1	1
ENSG00000081041	ENSG00000081041	CXCL2	4:74962751-74965010	OK	14.0676	3.5472	-1.98762	-3.14041	5.00E-05	0.0312848	0	1	1
ENSG00000142627	ENSG00000142627	EPHA2	1:16450831-16483824	OK	5.75231	16.7272	1.53998	3.01115	5.00E-05	0.0312848	1	0	1
ENSG00000076706	ENSG00000076706	MCAM	11:119179240-119192231	OK	100.539	234.556	1.22218	1.86587	5.00E-05	0.0312848	1	0	1
ENSG00000198682	ENSG00000198682	PAPSS2	10:89367741-89507462	OK	2.78637	6.08011	1.12571	1.47623	0.00425	0.413255	1	0	1
ENSG00000101791	ENSG00000101791	NAA50	3:113435306-113465147	OK	37.0055	71.9164	0.958582	1.64276	0.00705	0.525966	1	0	1
ENSG00000114573	ENSG00000114573	ATP6V1A	3:113465718-113530903	OK	21.2949	38.5301	0.855479	2.10447	0.00055	0.155197	1	0	1
ENSG00000113558	ENSG00000113558	DBN1	5:176883608-176901402	OK	24.7406	41.949	0.761756	1.48535	0.00655	0.580392	1	0	1
ENSG00000081853	ENSG00000081853	PRELP	1:203444955-203460480	OK	4.36771	1.01705	-2.10245	-3.80575	5.00E-05	0.0312848	1	0	1

Table 14. Summary statistics for AR ChIP-seq active regions

Description	Act Regions	AR ChIP (vector)	AR ChIP (vector) %	AR ChIP (*SLNCR1*)	AR ChIP (*SLNCR1*) %
Total Number of Intervals in Build 37_2		5749		8274	
Number of Intervals Converted to Build 37_2	9974	5749	100.00%	8274	100.00%
Number of Intervals within -10000/+10000 bp of NCBI Genes	7753	4522	78.66%	6547	79.13%
Number of Intervals NOT within -10000/+10000 bp of NCBI Genes	2221	1227	21.34%	1727	20.87%
Number of NCBI Genes with Intervals within -10000/+10000 bp	9139	5916		8164	
Number of Intervals within Promoter Region (-7500/+2500 bp of NCBI Gene Start)	5407	3214	55.91%	4697	56.77%
Number of Intervals 500 bp of NCBI Tx Start	4048	2478	43.10%	3556	42.98%
Number of NCBI Genes with UCSC CpGs and intervals in Promoters (-7500/2500 bp of start)	6418	3971		5704	
Number of NCBI Genes with intervals in Promoters (-7500/2500 bp of start)	6985	4297		6162	
Number of Intervals within 200 bp of UCSC CpG Islands	5236	3088	53.71%	4623	55.87%
Avg Interval Length	862.52	802.62		852.71	
Max Interval Length	5522	5185		5465	
Min Interval Length	231	250		201	
Avg Probe Value		2.55		2.58	
Max Probe Value		402		448	
Total Probe Count		**68807537**		**67877669**	

Table 15. AR and p21 protein expression of p53-deficient TCGA melanomas.

PATIENT ID	Gender	TP53 mutational status	P21 (RPPA)	AR (RPPA)
TCGA-EE-A29M	FEMALE	F134L	0.14587	-0.86133
TCGA-DA-A1HW	FEMALE	K120E	0.040554	-0.9723
TCGA-GF-A6C8	FEMALE	P278S	0.052421	-0.5473
TCGA-BF-A3DL	FEMALE	R196*	0.065464	-0.95115
TCGA-DA-A1I5	FEMALE	R196*, E286K	0.052141	-0.98755
TCGA-EB-A5FP	FEMALE	R213*	0.25405	-0.55538
TCGA-EE-A3AE	FEMALE	R213*	-0.063335	-1.0698
TCGA-DA-A1HV	FEMALE	R280K	0.062088	-0.70658
TCGA-EE-A181	FEMALE	V143E	0.053279	-0.91168
TCGA-EE-A2MM	FEMALE	V143G	-0.25283	-0.46138
TCGA-ER-A199	FEMALE	X126_splice	-0.13843	-0.87842
TCGA-D3-A51T	FEMALE	X187_splice	0.10025	-1.0643
TCGA-ER-A19E	FEMALE	X224_splice	0.059999	-0.27543
TCGA-FS-A4F9	MALE	A276Lfs*29	-0.47049	-0.67793
TCGA-EB-A3XC	MALE	C275Y	0.11002	-0.78656
TCGA-EE-A2MU	MALE	G266E	0.4328	-0.011376
TCGA-D3-A1QA	MALE	H214Qfs*7	-0.28437	-0.20244
TCGA-EE-A29E	MALE	L330R	-0.2328	-0.87094
TCGA-EE-A3AA	MALE	P151L, P27S, P151S	0.12717	-0.73382
TCGA-EE-A29L	MALE	P177_C182del	-0.22706	-0.9179
TCGA-EE-A2GC	MALE	P177L	-0.43232	-0.68729
TCGA-GN-A266	MALE	R290C, A159V	0.090022	-0.30487
TCGA-GF-A6C9	MALE	S127F	-0.43199	-0.79911
TCGA-EE-A3AD	MALE	S241F	-0.23497	-0.9065
TCGA-EE-A3J7	MALE	S241F	-0.20028	-0.6418
TCGA-FS-A1Z4	MALE	V97Sfs*26	0.1418	-0.59557
TCGA-D9-A6EC	MALE	X187_splice, R213*	-0.39416	-0.8732

P53-deficient melanomas were defined as (i) primary melanomas or metastases of known melanoma origin, (ii) patients with no prior treatment, and (iii) harboring nonfunctional p53 mutations, as defined by the TP53 database (p53.fr) (Leroy, B., et al., Hum Mutat, 2014. 35: p. 756-765). Three additional patients containing R248W or Y220C gain of function p53 mutations were excluded based on reported regulation of p21 (Di Fiore, R., et al., Bone, 2014. 60: p. 198-212; Song, H., Hollstein, M., and Y. Xu, Nature Cell Biol, 2007. 9: p. 573-580; Xu, J., et al., Cell Death Dis, 2014. 5: p. e1108).

Table 16. Final model determined from hierarchical multiple regression analysis of p21 protein expression in TCGA melanomas (n=354). Adjusted R-squared = 0.06, Model (F-statistic) p = 0.0009.

Variable or interaction	Estimate (95% CI)	p-value
Intercept	-0.05 (-0.15, 0.06)	0.38
SLNCR	-0.07 (-0.17, 0.03)	0.19
EGR1 mRNA	-0.12 (-0.23, -0.02)	0.023
AR protein	0.04 (-0.07, 0.15)	0.49
P53 protein	-0.13 (-0.24, -0.01)	0.027
SLNCR * EGR1	-0.10 (-0.19, -0.01)	0.024
SLNCR * AR	0.002 (-0.11, 0.11)	0.96
EGR1 * AR	-0.05 (-0.16, 0.06)	0.34
EGR1 * p53	<0.001 (-0.11, 0.11)	0.99
AR * p53	0.12 (0.05, 0.18)	0.0004
EGR1 * AR * SLNCR	-0.12 (-0.25, 0.001)	0.052
EGR1* AR * p53	0.12 (0.03, 0.21)	0.008

Variables assessed as part of the multiple regression analysis of p21 expression included patient gender, *SLNCR* and *EGR1* mRNA log2 expression, and AR and p53 protein expression (from TCPA) and all possible interactions. All continuous variables were converted to z-scores in order to improve interpretability of the model output. In order to determine the set of parameters present in the final model, standard reduction techniques were used, including iterative removal of the least significant parameter along with evaluation of the Akaike's information criterion (AIC) and ANOVA comparisons of model fit. Non-significant parameters remain in the final model due to the presence of significant two- and three-way interactions. P-values have not been adjusted for multiple hypothesis testing.

Table 17. siRNA targets and oligo sequences used in this study.

Sequence	Name	Type
TTAGGTCAAATAGGATCTAAA (targeting)	si-*SLNCR* (1)	siRNA
AAAGACGTTTACACCGAGAAA (targeting)	si-*SLNCR* (2)	siRNA
CAGGAATTCCTGTGCATGAAA (targeting)	si-*AR* (1)	siRNA
CACGGGAAGTTTAGAGAGCTA (targeting)	si-*AR* (2)	siRNA
CTGCTACTCTTCAGCATTATT (targeting)	si-*AR* (3)	siRNA
GAAGGTGAAGGTCGGAGT	*GAPDH* Forward	qPCR
GAAGATGGTGATGGGATTTC	*GAPDH* Reverse	qPCR
GTGGAGCGATTTGTCTGGTT	*18S* Forward	qPCR
CGCTGAGCCAGTCAGTGTAG	*18S* Reverse	qPCR
AACTTCTACAATGAGCTGCG	*β-ACTIN* Forward	qPCR
CCTGGATAGCAACGTACATGG	*β-ACTIN* Reverse	qPCR
GAGAACGTGGTGGAATCAGA	*SLNCR* Forward (all isoforms)	qPCR
TCCCATCCTCTTTCTTGTCC	*SLNCR* Reverse (all isoforms)	qPCR
GGTTACACCAAAGGGCTAGAA	*AR* Forward	qPCR
GACTTGTAGAGAGACAGGGTAGA	*AR* Reverse	qPCR
TGTCACTGTCTTGTACCCTTG	*CDKN1A* Forward	qPCR
GGCGTTTGGAGTGGTAGAA	*CDKN1A* Reverse	qPCR
GCCATCTACAAGCAGTCACAG	*TP53* Forward	qPCR
TCATCCAAATACTCCACACGC	*TP53* Reverse	qPCR
GTGTGTCTCCGCTTGAAGCTTGGCAATCCGGTAC	Remove MMTV from pGL4.36	Gibson cloning primer
CTCTTCTATGCCAGGGCCAGTTAGGCCAGAGAAATGTTC	Remove MMTV from pGL4.36	Gibson cloning primer
CTGGCATAGAAGAGGCTGGT	*CDKN1A* promoter Foward	PCR amplification
CAAGCGGAGACACACTGGTAT	*CDKN1A* promoter Reverse	PCR amplification
GTC**A**CA**G**TCCGCGCGTGATTTCCTGAG	EGR1 binding site mutant	Site-directed mutagenesis
GTGCGTGGGCAGAGCCTCGGAC	EGR1 binding site mutant	Site-directed mutagenesis

Bold italicized font denotes mutated nucleotides.

Incorporation by Reference

The contents of all references, patent applications, patents, and published patent applications, as well as the Figures and the Sequence Listing, cited throughout this application are hereby incorporated by reference.

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the present invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed is:

1. A single-stranded nucleic acid that binds to androgen receptor (AR) or a long non-coding RNA (lncRNA), and blocks interaction between AR and the lncRNA, wherein the single-stranded nucleic acid does not significantly reduce the expression of AR or the lncRNA.

2. The single-stranded nucleic acid of claim 1, wherein the single-stranded nuclei acid binds to AR to block the interaction of AR with the lncRNA.

3. The single-stranded nucleic acid of claim 1 or 2, wherein the single-stranded nucleic acid localizes at least partially to the nucleus.

4. The single-stranded nucleic acid of claim 4, wherein the single-stranded nucleic acid localizes to the nucleus.

5. The single-stranded nucleic acid of any one of claims 1-4, wherein the single-stranded nucleic acid is at least 11 nucleotides (nt) in length.

6. The single-stranded nucleic acid of any one of claims 1-5, wherein the single-stranded nucleic acid is 17 nt in length.

7. The single-stranded nucleic acid of any one of claims 1-6, wherein the single-stranded nucleic acid dose not comprise a high level of secondary structure.

8. The single-stranded nucleic acid of any one of claims 1-7, wherein the single-stranded nucleic acid comprises at least one UCUCCU or UCUCCA motif.

9. The single-stranded nucleic acid of claim 8, wherein the single-stranded nucleic acid comprises two or more motifs selected from the group consisting of UCUCCU and UCUCCA motifs.

10. The single-stranded nucleic acid of claim 9, wherein the single-stranded nucleic acid further comprises an internal sequence between the motifs.

11. The single-stranded nucleic acid of claim 10, wherein the internal sequence is 9 nt in length.

12. The single-stranded nucleic acid of any one of claims 1-11, wherein the single-stranded nucleic acid is at least 20 nt in length, and the pyrimidine content within a 17-20 nt region of the single-stranded nucleic acid that comprises the UCUCCU or UCUCCA motif is at least 65%.

13. The single-stranded nucleic acid of claim 12, wherein the pyrimidine content within the 17-20 nt region of the single-stranded nucleic acid comprising the UCUCCU or UCUCCA motif is more than 75%.

14. The single-stranded nucleic acid of any one of claims 2-13, wherein the lncRNA is selected from the group of SLNCR, HOXA11-AS-203, SRA1, HOTAIR, and PCGEM1.

15. The single-stranded nucleic acid of any one of claims 2-14, wherein the lncRNA is SLNCR.

16. The single-stranded nucleic acid of claim 15, wherein the nucleic acid is selected from the group of MIMIC 1 (SEQ ID NO: 23), MIMIC 2 (SEQ ID NO: 24), MUT L (SEQ ID NO:4), MUT R (SEQ ID NO:5), MUT I (SEQ ID NO:8), MUT PT (SEQ ID NO:7), WT-17 ((SEQ ID NO:9), WT-20 (SEQ ID NO:10), SRA1 (SEQ ID NO:20), and WT-11 (SEQ ID NO:17).

17. The single-stranded nucleic acid of claim 1, wherein the single-stranded nucleic acid binds to the lncRNA to block the interaction of AR with the lncRNA.

18. The single-stranded nucleic acid of claim 17, wherein the nucleic acid contains at least one AGGAGA or UGGAGA motif.

19. The single-stranded nucleic acid of claim 17 or 18, wherein if the lncRNA contains two consecutive motifs selected from the group consisting of UCUCCU and UCUCCA motifs, the single-stranded nucleic acid binds to both motifs simultaneously with an appropriate internal sequence between the sequences that bind to the two motifs.

20. The single-stranded nucleic acid of any one of claims 17-19, wherein the lncRNA is selected from the group of SLNCR, HOXA11-AS-203, SRA1, PCGEM1, and HOTAIR.

21. The single-stranded nucleic acid of any one of claims 17-20, wherein the lncRNA is SLNCR.

22. The single-stranded nucleic acid of claim 21, wherein the single-stranded nucleic acid localizes at least partially to the nucleus.

23. The single-stranded nucleic acid of claim 21 or 22, wherein the single-stranded nucleic acid is at least 20 nt in length.

24. The single-stranded nucleic acid of any one of claims 21-23, wherein the single-stranded nucleic acid is 28 nt in length.

25. The single-stranded nucleic acid of any one of claims 21-24, wherein the single-stranded nucleic acid dose not comprise a high level of secondary structure.

26. The single-stranded nucleic acid of any one of claims 21-25, wherein the single-stranded nucleic acid comprises an AGGAGA motif and a UGGAGA motif.

27. The single-stranded nucleic acid of any one of claims 21-25, wherein the single-stranded nucleic acid comprises a GGAGA motif and a UGGAGA motif.

28. The single-stranded nucleic acid of any one of claims 21-25, wherein the single-stranded nucleic acid comprises an AGGAGA motif and a UGGAG motif.

29. The single-stranded nucleic acid of any one of claims 21-25, wherein the single-stranded nucleic acid comprises a GGAGA motif and a UGGAG motif.

30. The single-stranded nucleic acid of any one of claims 26-29, wherein the two motifs are linked by an internal sequence.

31. The single-stranded nucleic acid of claim 30, wherein the internal sequence is 9 nt in length.

32. The single-stranded nucleic acid of claim 30 or 31, wherein the internal sequence has more than 75% sequence identity to the sequence AGACCAGGG.

33. The single-stranded nucleic acid of claim 32, wherein the internal sequence has 100% sequence identity to the sequence AGACCAGGG.

34. The single-stranded nucleic acid of any one of claims 21-33, wherein the single-stranded nucleic acid is at least 30 nt in length, and the purine content within a 30 nt region of the single-stranded nucleic acid that comprises the AGGAGA or UGGAGA motif is at least 65%.

35. The single-stranded nucleic acid of claim 34, wherein the purine content within a 30 nt region of the single-stranded nucleic acid that comprises the AGGAGA or UGGAGA motif is more than 75%.

36. The single-stranded nucleic acid of any one of claims 21-35, wherein the single-stranded nucleic acid is ANTISENSE 1 (SEQ ID NO: 25) or ANTISENSE 2 (SEQ ID NO: 26).

37. The single-stranded nucleic acid of any one of claims 1-36, wherein the single-stranded nucleic acid comprises at least one chemical modification.

38. The single-stranded nucleic acid of claim 37, wherein the single-stranded nucleic acid penetrates the cellular membrane of a cell in the absence of a delivery vehicle.

39. The single-stranded nucleic acid of claim 37, wherein the chemical modification extends the half-life of the single-stranded nucleic acid in a cell.

40. The single-stranded nucleic acid of any one of claims 37-39, wherein the chemical modification is selected from the group of a FANA chemical modification, a fluorinated nucleoside, a DNA nucleotide, a 2′-O-methylated nucleoside, a phosphorothioate bond and a cholesterol moiety.

41. The single-stranded nucleic acid of any one of claims 26-31, wherein the nucleic acid comprises a FANA chemical modification.

42. The single-stranded nucleic acid of any one of claims 1-7, 14-15, 17, 20-25, and 37-41, wherein the single-stranded nucleic acid comprises at least one CYUYUCCWS motif, wherein Y is a pyrimidine, W is A or U, and S is C or G.

43. The single-stranded nucleic acid of any one of claims 1-7, 14-15, 17, 20-25, and 37-41, wherein the single-stranded nucleic acid comprises two or more CYUYUCCWS motifs, wherein Y is a pyrimidine, W is A or U, and S is C or G.

44. The single-stranded nucleic acid of any one of claims 1-7, 14-15, 17, 20-25, and 42-43, wherein the single-stranded nucleic acid is at least 28 nt in length, and the pyrimidine content within a 28 nt region of the single-stranded nucleic acid that comprises the CYUYUCCWS motif is at least 60%.

45. The single-stranded nucleic acid of any one of claims 1-44, wherein the single-stranded nucleic acid further comprises one or more thymidines.

46. The single-stranded nucleic acid of any one of claims 1-7, 14-15, 17, 20-25, and 37-41, wherein the single-stranded nucleic acid comprises at least one motif with the sequence that is the reverse complement of, or antisense to CYUYUCCWS, wherein Y is a pyrimidine, W is A or U, and S is C or G.

47. The single-stranded nucleic acid of any one of claims 1-7, 14-15, 17, 20-25, and 37-41, wherein the single-stranded nucleic acid comprises two or more motifs, with each motif comprising the sequence that is the reverse complement of, or antisense to CYUYUCCWS, wherein Y is a pyrimidine, W is A or U, and S is C or G.

48. A pharmaceutical composition comprising the single-stranded nucleic acid of any one of claims 1-47, and a pharmaceutically acceptable agent selected from the group consisting of excipients, diluents, and carriers.

49. The pharmaceutical composition of claim 48, wherein the pharmaceutical composition comprises the single-stranded nucleic acid at a purity of at least 75%.

50. The pharmaceutical composition of claim 48 or 49, wherein the pharmaceutical composition further comprises a nuclear receptor targeting drug.

51. The pharmaceutical composition of claim 50, wherein the nuclear receptor targeting drug is selected from the group consisting of luteinizing hormone-releasing hormone (LHRH) analogs, androgen receptor inhibitors, anti-androgens, hormone blocking drugs, nuclear receptor agonists, nuclear receptor antagonists, selective receptor modulators,

selective androgen receptor modulators (SARMs), selective estrogen receptor modulators (SERMs), selective progesterone receptor modulators (SPRMs), selective glucocorticoid receptor agonists (SEGRAs), and selective glucocorticoid receptor modulators (SEGRMs).

52. The pharmaceutical composition of claim 45, wherein the nuclear receptor target drug is selected from the group consisting of leuprolide (Lupron®, Eligard®), goserelin (Zoladex®), triptorelin (Trelstar®), histrelin (Vantas®), degarelix (Firmagon®), bicalutamide (Casode®), enzalutamide (Xtandi®), flutamide (Eulexin®), nilutamide (Nilandron®), ketoconazole (Nizoral®), abiraterone (Zytiga®), dexamethasone, megestrol acetate (Megace®), medroxyprogesterone acetate (MPA), ethisterone, norethindrone acetate, norethisterone, norethynodrel, ethynodiol diacetate, norethindrone, norgestimate, norgestrel, levonorgestrel, medroxyprogesterone acetate, desogestrel, etonogestrel, drospirenone, norelgestromin, desogestrel, etonogestrel, gestodene, dienogest, drospirenone, elcometrine, nomegestrol acetate, trimegestone, tanaproget, BMS948, mifepristone, 4-hydroxytamoxifen, CINPA1, Cyproterone acetate (Androcur®, Cyprostat®, Siterone®), chlormadinone acetate (Clordion®, Gestafortin®, Lormin®, Non-Ovlon®, Normenon®, Verton®), 17-hydroxyprogesterone (17-OHP), THC, clotrimazole, PK11195 [1-(2-chlorophenyl)-*N*-methyl-*N*-(1-methylpropyl)-3-isoquinolinecarboxamide], meclizine, androstanol, CITCO [6-(4-chlorophenyl)imidazo [2,1-*b*][1,3] thiazole-5-carbaldehyde *O*-(3,4-dichlorobenzyl) oxime], zearalenone (ZEN), T0901317, S07662, enobosarm, BMS-564,929, LGD-4033, AC-262,356, JNJ-28330835, LGD-2226, LGD-3303, S-40503, S-23, clomifene, femarelle, ormeloxifene, raloxifene, tamoxifen, toremifene, lasofoxifene, ospemifene, afimoxifene, arzoxifene, bazedoxifene, gulvestrant (Faslodex®, ICI-182780), CDB-4124, asoprisnil, proellex, mapracorat (BOL-303242-X, ZK 245186), fosdagrocorat (PF-04171327), ZK 216348, and 55D1E1.

53. A vector comprising the single-stranded nucleic acid of any one of claims 1-47.

54. The vector of claim 53, wherein the vector is an expression vector.

55. A host cell transfected with the expression vector of claim 54.

56. A method of producing a single-stranded nucleic acid comprising culturing the host cell of claim 55 in an appropriate culture medium to, thereby, produce the single-stranded nucleic acid.

57. The method of claim 56, wherein the host cell is a bacterial cell or a eukaryotic cell.

58. A method of producing a single-stranded nucleic acid comprising transcribing the vector of claim 54 *in vitro* under an appropriate reaction condition, and isolating the single-stranded nucleic acid from the reaction mixture.

59. A method of treating a subject afflicted with an AR- and/or lncRNA-mediated disease comprising administering to the subject a therapeutically effective amount of a single-stranded nucleic acid that binds to androgen receptor (AR) or a long non-coding RNA (lncRNA), and blocks interaction between AR and the lncRNA, wherein the single-stranded nucleic acid does not significantly reduce the expression of AR or the lncRNA.

60. The method of claim 59, wherein the AR- and/or lncRNA-mediated disease is androgen-independent.

61. The method of claim 59 or 60, wherein the AR- and/or lncRNA-mediated disease is selected from the group of cancer, inflammatory disease, metabolic diseases, spontaneous abortion, alopecia, Alzheimer disease, androgen-insensitivity syndrome, heart disease (e.g., artiosclerosis, coronary artery disease, and cardiomyopathy), azoospermia, cholelithiasis, cognition disorders, cryptorchidism, depressive disorder, diabetes mellitus, diabetic retinopathy, sex development disorders, bone fractures, hyperglycemia, hypertension, hypospadias, hypertrophy, hyperandrogenism, infertility, klinefelter syndrome, liver cirrhosis, liver disease, lupus, migraine disorder, Menkes Kinky Hair Syndrome, muscular atrophy, nerve degeneration, obesity, oligospermia, osteoarthritis, osteoporosis, Paget Disease, Polycystic Ovary Syndrome, Primary Ovarian Insuffiency, Schizophrenia, spinal fractures, thrombocytosis, thyroid diseases, Tourette syndrome, Turner syndrome, and autoimmune disease.

62. The method of claim 61, wherein the cancer is selected from the group of melanoma, lung adenocarcinoma, lung squamous cell carcinoma, cervical cancer, ovarian cancer, uterine cancer, pancreatic cancer, colorectal cancer, lower grade glioma, glioblastoma multiforme, breast cancer, endometrial cancer, prostate cancer, testicular cancer, thyroid cancer, osteosarcoma, esophageal cancer, liver cancer, kidney cancer, gastric cancer, non-small cell lung cancer, and bladder cancer.

63. The method of claim 62, wherein the cancer is melanoma.

64. The method of claim 62 or 63, wherein the single-stranded nucleic acid inhibits the growth and/or metastasis the cancer.

65. The method of claim 61, wherein the inflammatory disease is selected from the group of acne vulgaris, asthma, and rheumatoid arthritis.

66. The method of claim 61, wherein the autoimmune disease is selected from the group of lupus, type I diabetes, and multiple sclerosis.

67. A method of inhibiting proliferation or invasion of cancer cells comprising contacting the cancer cells with a single-stranded nucleic acid that binds to androgen receptor (AR) or a long non-coding RNA (lncRNA), and blocks interaction between AR and the lncRNA, wherein the single-stranded nucleic acid does not significantly reduce the expression of AR or the lncRNA.

68. A method of blocking the interaction between AR and the lncRNA in cancer cells comprising contacting the cancer cells with a single-stranded nucleic acid that binds to androgen receptor (AR) or a long non-coding RNA (lncRNA).

69. The method of any one of claims 59-68, wherein the single-stranded nucleic acid is a single-stranded nucleic acid of any one of claims 1-47.

70. The method of claim 69, wherein the single-stranded nucleic acid is administered in a pharmaceutically acceptable formulation.

71. The method of any one of claims 59-69, wherein the lncRNA is selected from the group of SLNCR, HOXA11-AS-203, SRA1, HOTAIR and PCGEM1.

72. The method of claim 71, wherein the lncRNA is SLNCR.

73. The method of claim 72, wherein the single-stranded nucleic acid is selected from the group consisting of MIMIC 1, MIMIC 2, ANTISENSE 1, and ANTISENSE 2.

74. The method of claim 73, the single-stranded nucleic acid inhibits a SLNCR-regulated gene.

75. The method of claim 73, wherein the SLNCR-regulated gene is selected from the group consisting of MMP9, p21, CXCL2, JUN, STAT3, IL24, and MCAM.

76. The method of any one of claims 59-75, further comprising administering a nuclear receptor targeting drug.

77. The method of claim 76, wherein the nuclear receptor targeting drug is selected from the group consisting of luteinizing hormone-releasing hormone (LHRH) analogs, androgen receptor inhibitors, anti-androgens, hormone blocking drugs, nuclear receptor agonists, nuclear receptor antagonists, selective receptor modulators, selective androgen receptor modulators (SARMs), selective estrogen receptor modulators (SERMs), selective progesterone receptor modulators (SPRMs), selective glucocorticoid receptor agonists (SEGRAs), and selective glucocorticoid receptor modulators (SEGRMs).

78. The pharmaceutical composition of claim 77, wherein the nuclear receptor target drug is selected from the group consisting of leuprolide (Lupron®, Eligard®), goserelin (Zoladex®), triptorelin (Trelstar®), histrelin (Vantas®), degarelix (Firmagon®), bicalutamide (Casode®), enzalutamide (Xtandi®), flutamide (Eulexin®), nilutamide (Nilandron®), ketoconazole (Nizoral®), abiraterone (Zytiga®), dexamethasone, megestrol acetate (Megace®), medroxyprogesterone acetate (MPA), ethisterone, norethindrone acetate, norethisterone, norethynodrel, ethynodiol diacetate, norethindrone, norgestimate, norgestrel, levonorgestrel, medroxyprogesterone acetate, desogestrel, etonogestrel, drospirenone, norelgestromin, desogestrel, etonogestrel, gestodene, dienogest, drospirenone, elcometrine, nomegestrol acetate, trimegestone, tanaproget, BMS948, mifepristone, 4-hydroxytamoxifen, CINPA1, Cyproterone acetate (Androcur®, Cyprostat®, Siterone®), chlormadinone acetate (Clordion®, Gestafortin®, Lormin®, Non-Ovlon®, Normenon®, Verton®), 17-hydroxyprogesterone (17-OHP), THC, clotrimazole, PK11195 [1-(2-chlorophenyl)-*N*-methyl-*N*-(1-methylpropyl)-3-isoquinolinecarboxamide], meclizine, androstanol, CITCO [6-(4-chlorophenyl)imidazo [2,1-*b*][1,3] thiazole-5-carbaldehyde *O*-(3,4-dichlorobenzyl) oxime], zearalenone (ZEN), T0901317, S07662, enobosarm, BMS-564,929, LGD-4033, AC-262,356, JNJ-28330835, LGD-2226, LGD-3303, S-40503, S-23, clomifene, femarelle, ormeloxifene, raloxifene, tamoxifen, toremifene, lasofoxifene,

ospemifene, afimoxifene, arzoxifene, bazedoxifene, gulvestrant (Faslodex®, ICI-182780), CDB-4124, asoprisnil, proellex, mapracorat (BOL-303242-X, ZK 245186), fosdagrocorat (PF-04171327), ZK 216348, and 55D1E1.

79. The method of any one of claims 59-78, wherein the subject is a mammal.

80. The method of claim 79, wherein the mammal is an animal model of an AR- and/or lncRNA-mediated disease.

81. The method of claim 79, wherein the mammal is a human.

82. A cell-based method for identifying a single-stranded nucleic acid that binds to AR or a lncRNA and blocks interaction between AR and the lncRNA, comprising:

a) contacting a cell expressing AR and/or lncRNA with a test single-stranded nucleic acid that binds to AR or the lncRNA; and

b) determining that the single-stranded nucleic acid blocks interaction between AR and the lncRNA, wherein the single-stranded nucleic acid does not significantly reduce the expression of AR or the lncRNA, optionally further determining that the single-stranded nucleic acid treats an AR- and/or lncRNA-mediated disease.

83. The method of claim 82, wherein said cells are isolated from an animal model of an AR- and/or lncRNA-mediated disease, or a human patient afflicted with the AR- and/or lncRNA-mediated disease.

84. The method of claim 82 or 83, wherein the step of contacting occurs *in vivo*, *ex vivo*, or *in vitro*.

85. The method of any one of claims 82-84, further comprising determining the ability of the test single-stranded nucleic acid to bind to either AR or lncRNA before or after determining the effect of the test single-stranded nucleic acid on the interaction between AR and the lncRNA.

86. The method of any one of claims 82-85, further comprising determining the effect of the test single-stranded nucleic acid on the level of expression of AR or lncRNA before or after determining the effect of the test single-stranded nucleic acid on the interaction between AR and the lncRNA.

87. The method of any one of claims 82-86, further comprising determining the activity of AR or lncRNA in the disease cell.

88. The method of claim 87, wherein the activity of AR or lncRNA is assessed by determining the magnitude of cellular proliferation, cell death, cellular migration, replication, induction of angiogenesis, cellular invasion/metastasis, immune response, immune evasion, or transcription of AR- or lncRNA-regulated genes.

89. An *in vitro* cell-free method for identifying a single-stranded nucleic acid that binds to AR or a lncRNA and blocks interaction between AR and the lncRNA, comprising:

a) contacting a mixture of AR protein and lncRNA with a test single-stranded nucleic acid that binds to AR or the lncRNA; and

b) determining that the single-stranded nucleic acid blocks interaction between AR and the lncRNA, wherein the single-stranded nucleic acid does not significantly reduce the expression of AR or the lncRNA, optionally further determining that the single-stranded nucleic acid treats an AR- and/or lncRNA-mediated disease.

90. The method of claim 89, further comprising determining the ability of the test single-stranded nucleic acid to bind to either AR or lncRNA before or after determining the effect of the test single-stranded nucleic acid on the interaction between AR and the lncRNA.

91. The method of any one of claims 82-90, wherein the lncRNA is a full-length RNA, or functional variants or fragments thereof.

92. The method of any one of claims 82-91, wherein AR is a full-length protein, or functional variants or fragments thereof.

93. The method of claim 92, wherein AR is an N-terminal region of AR protein having the amino acid sequence of SEQ ID NO: 27.

FIG. 1A

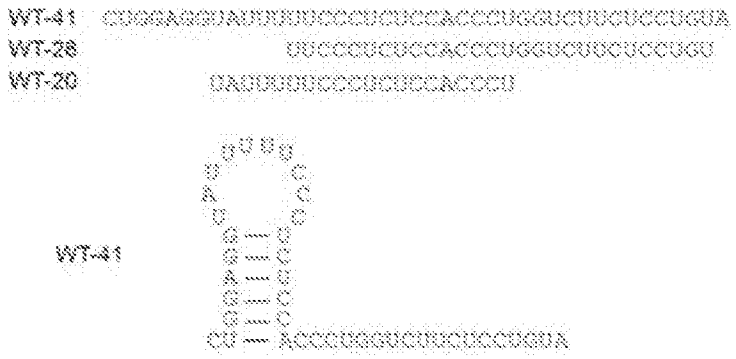


FIG. 1B

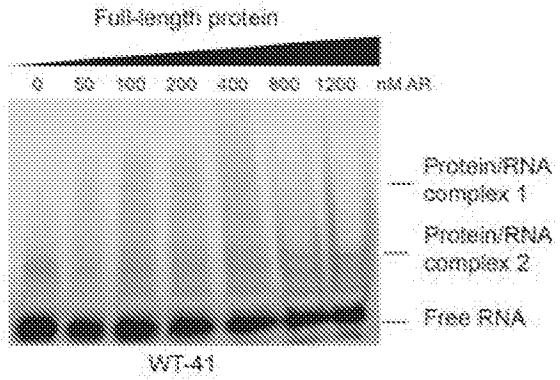


FIG. 1C

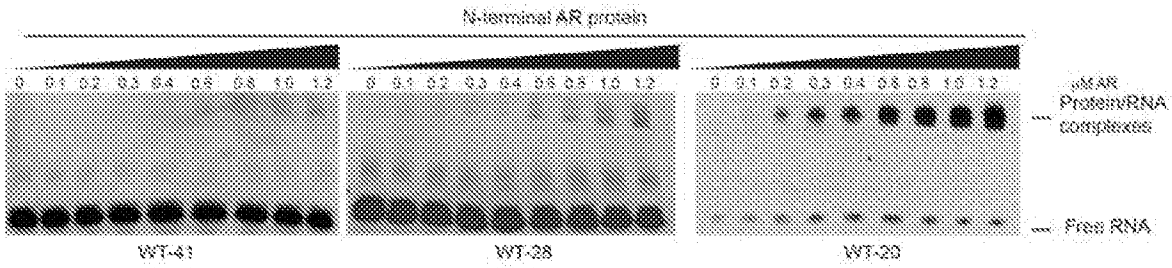


FIG. 2A

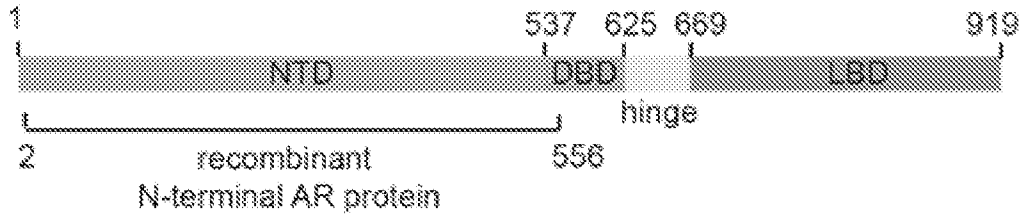


FIG. 2B

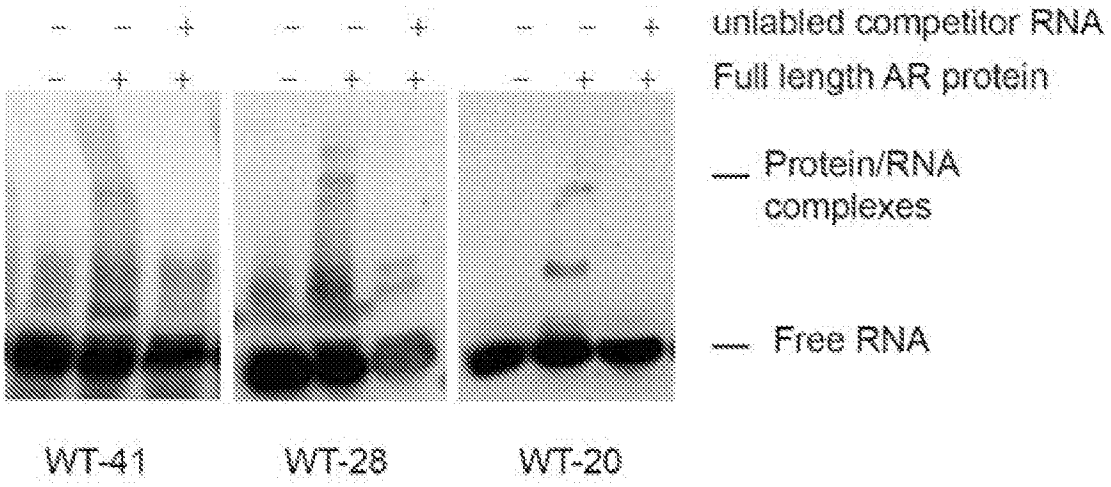


FIG. 2C

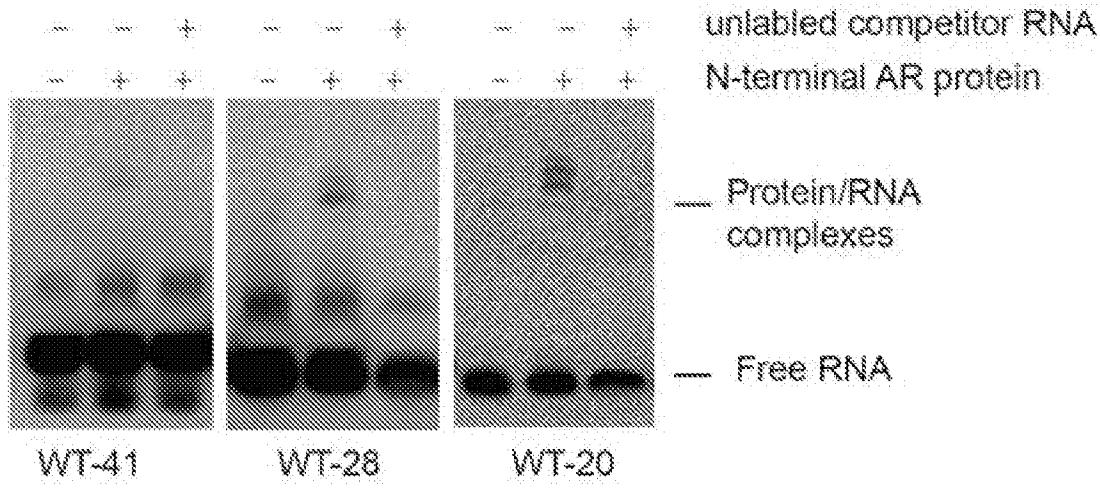


FIG. 3A

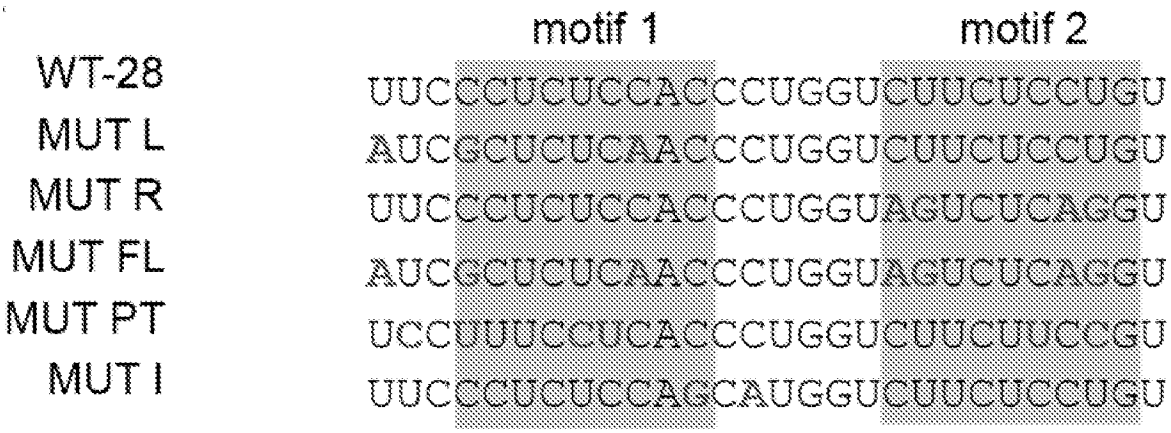


FIG. 3B

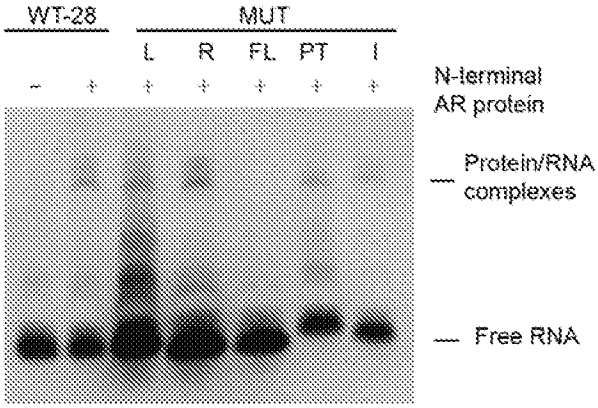


FIG. 3C

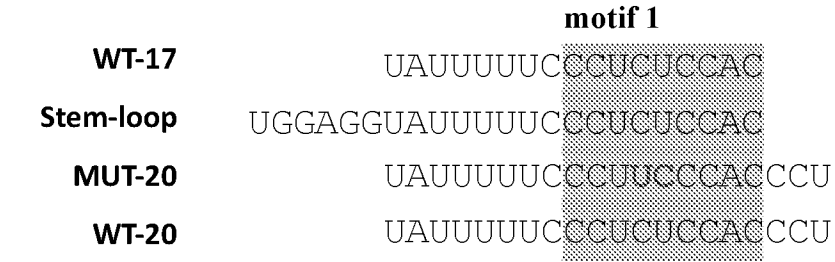


FIG. 3D

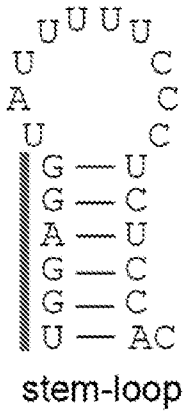


FIG. 3E

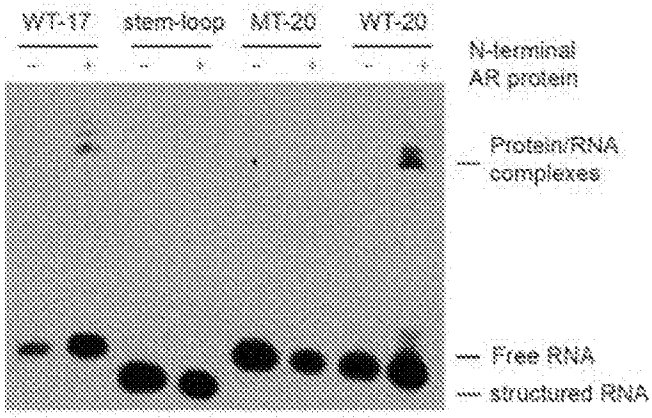
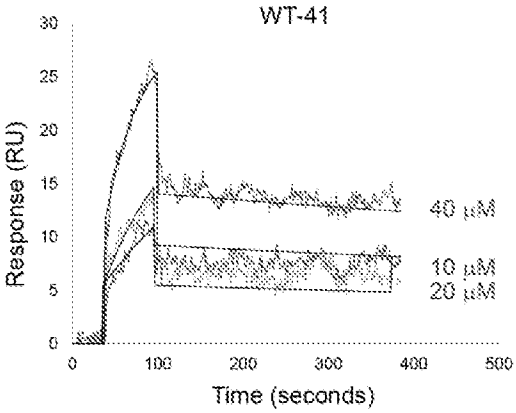


FIG. 3F



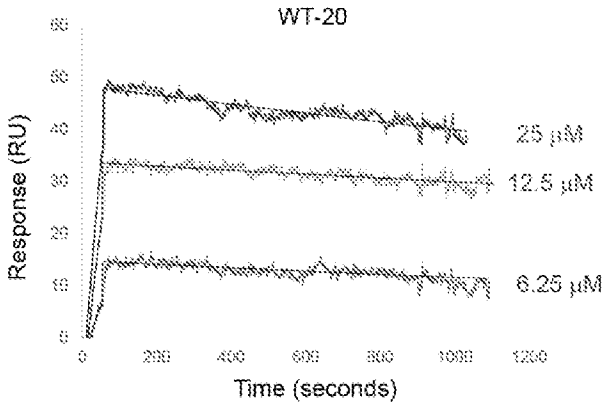


FIG. 3G

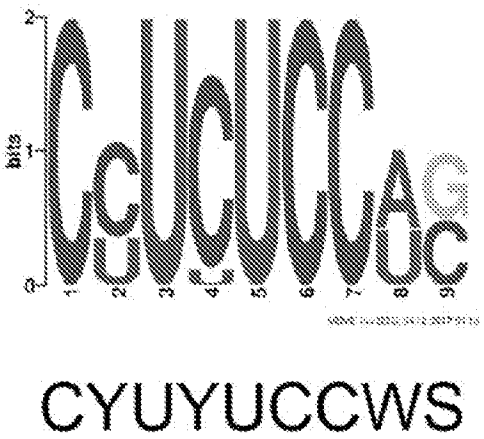
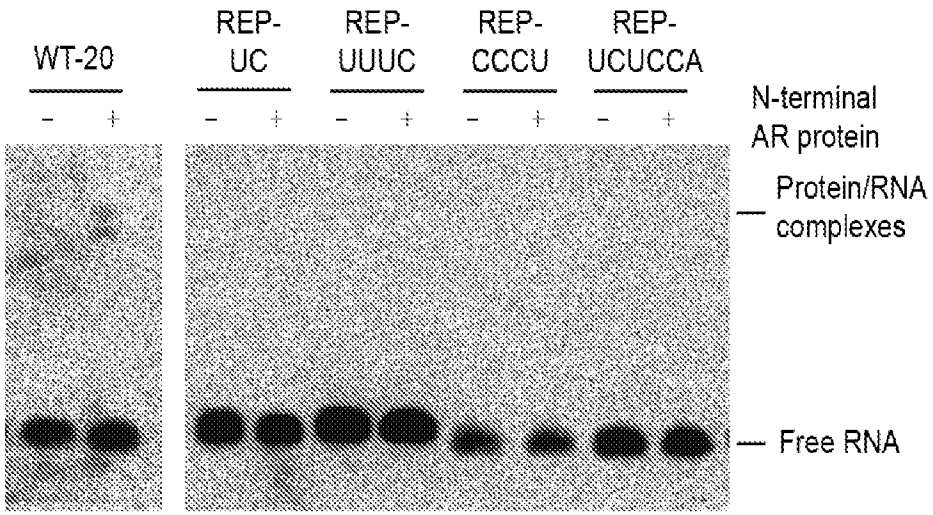


FIG. 4A

WT-20	UAUUUUUCCCUCUCCACCCU
REP-UC	UCUCUCUCUCUCUCUCUCUC
REP-UUUC	UUCUUUCUUUCUUUCUUUCU
REP-CCCU	CCCUCCCUCCCUCCCUCCCU
REP-UCUCCA	CCCUCUCCAUCUCCACUC

FIG. 4B



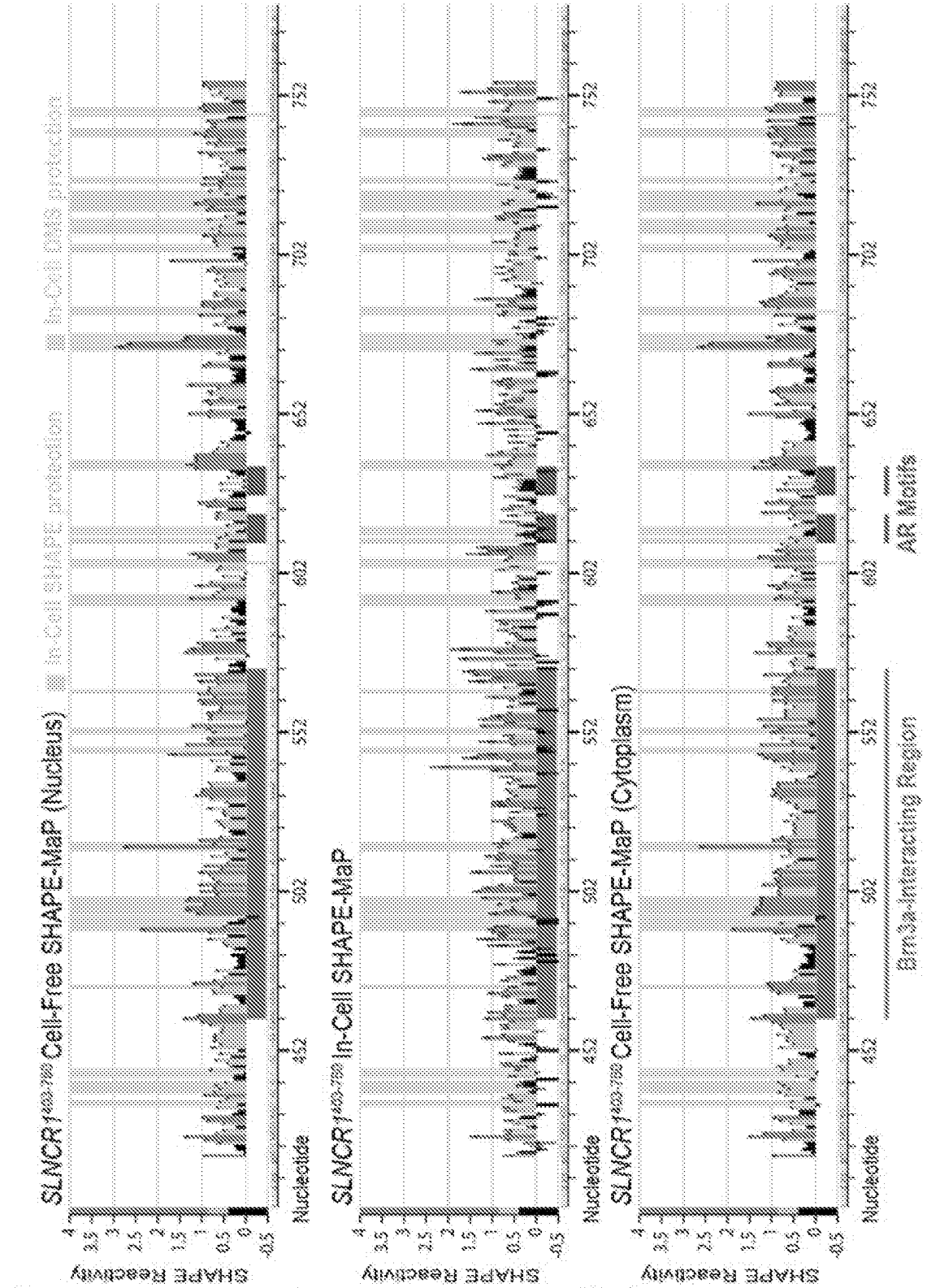


FIG. 4C

FIG. 4D

FIG. 4E

FIG. 4F

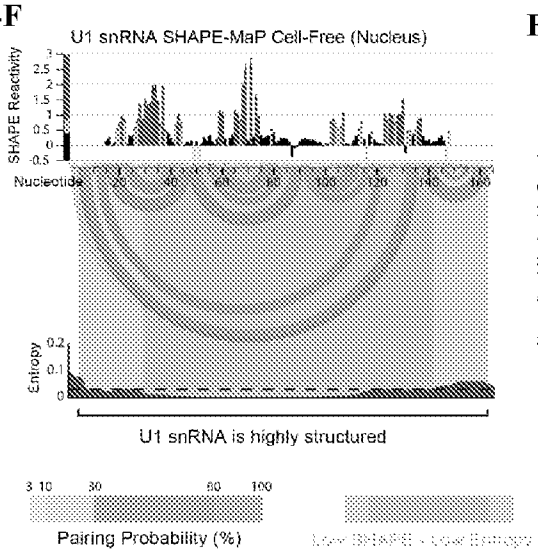


FIG. 4G

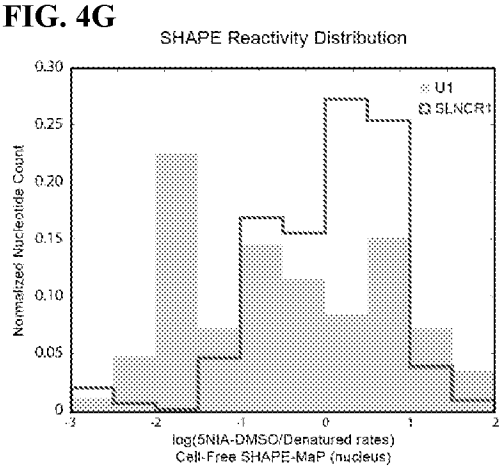


FIG. 4H

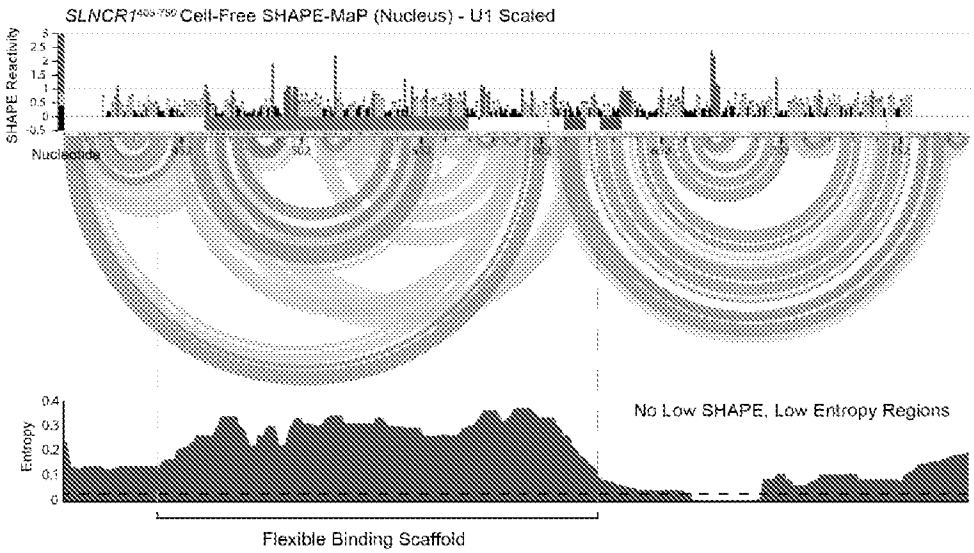


FIG. 4I

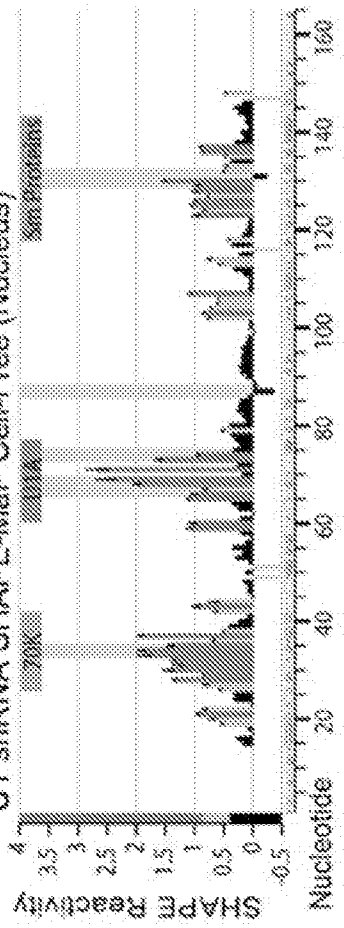


FIG. 4J

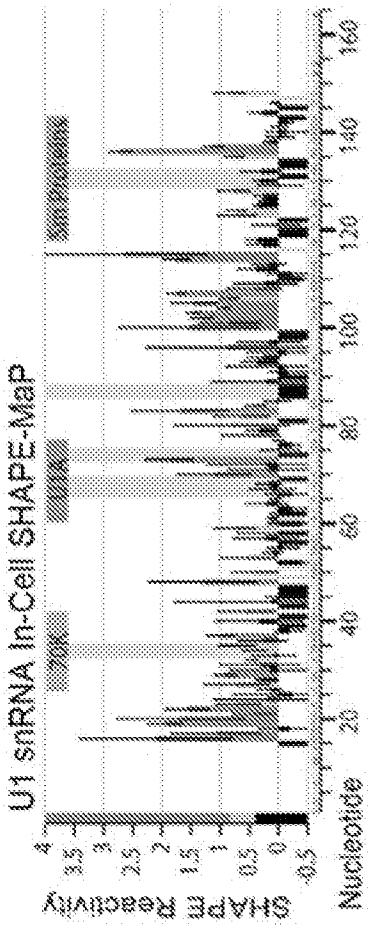


FIG. 4K

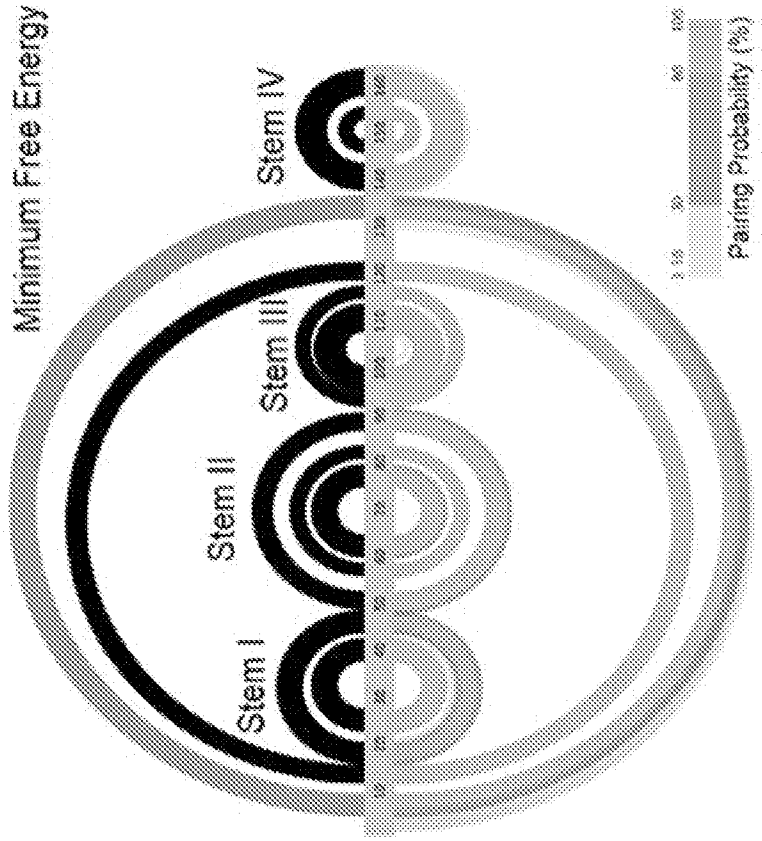


FIG. 4L

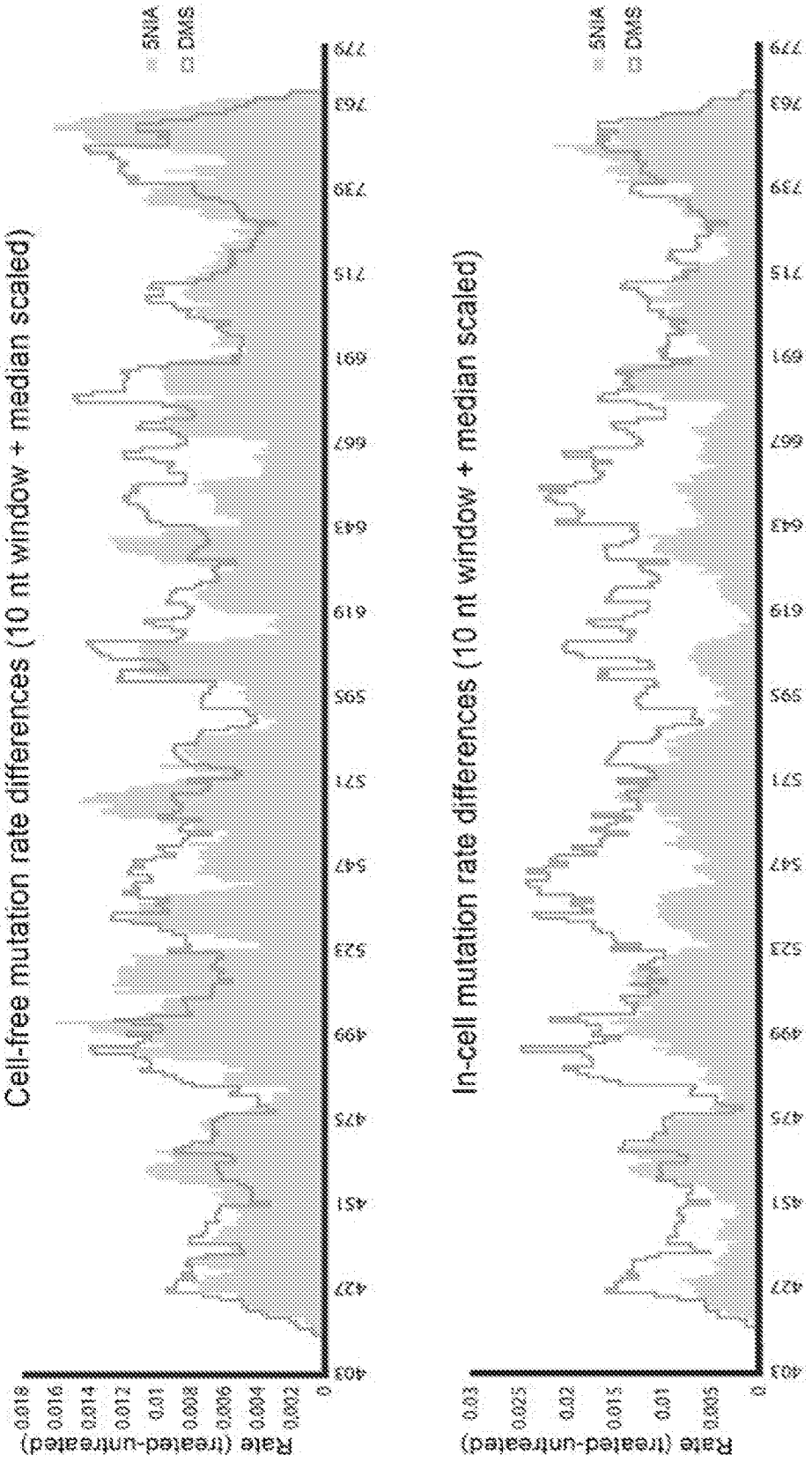

Cell-free mutation rate differences (10 nt window + median scaled)
Rate (treated-untreated)
0.018
0.016
0.014
0.012
0.01
0.008
0.006
0.004
0.002
0
403
427
451
475
499
523
547
571
595
619
643
667
691
715
739
763
779
SNIA
DMS
In-cell mutation rate differences (10 nt window + median scaled)
Rate (treated-untreated)
0.03
0.025
0.02
0.015
0.01
0.005
0
403
427
451
475
499
523
547
571
595
619
643
667
691
715
739
763
779
SNIA
DMS

FIG. 4M

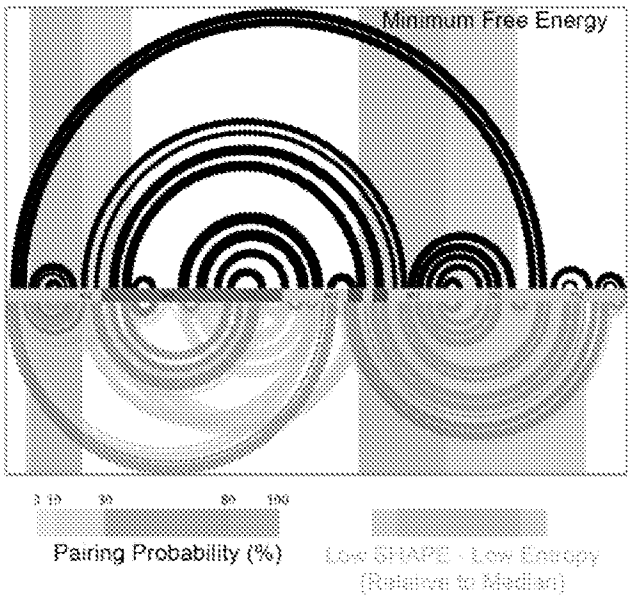


FIG. 4N

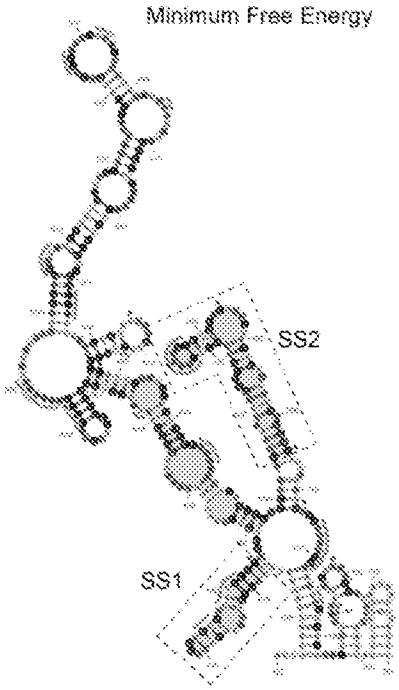


FIG. 4O ArcPlot-Supported Models

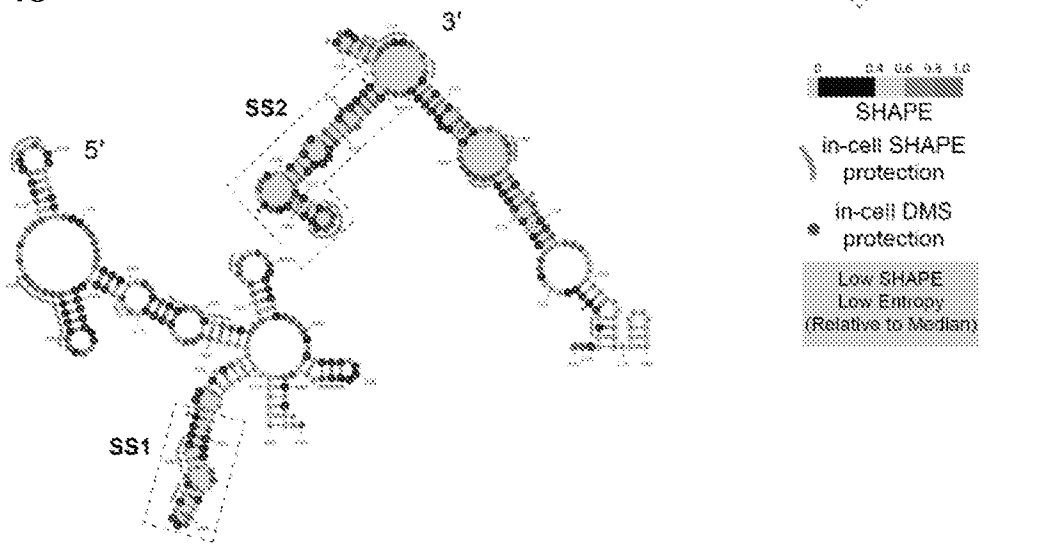


FIG. 5A

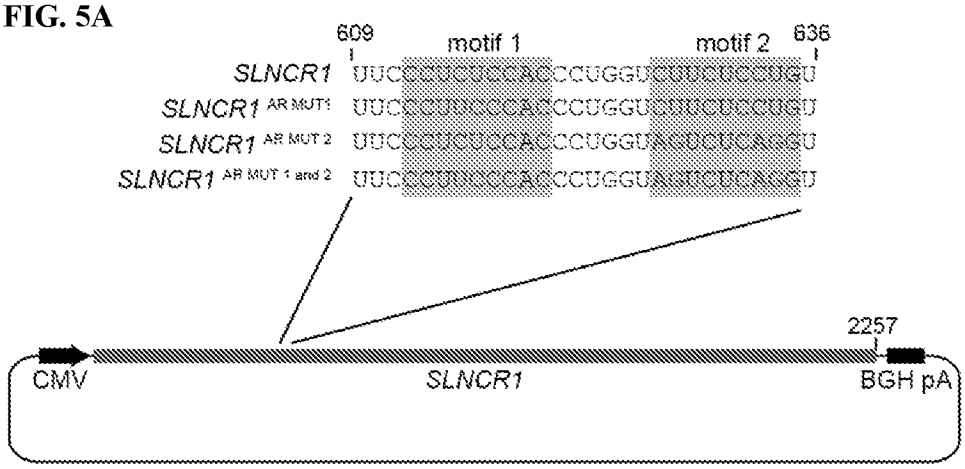

609
motif 1
motif 2
636
SLNCR1
SLNCR1 AR MUT1
SLNCR1 AR MUT 2
SLNCR1 AR MUT 1 and 2
2257
CMV
SLNCR1
BGH pA

FIG. 5B

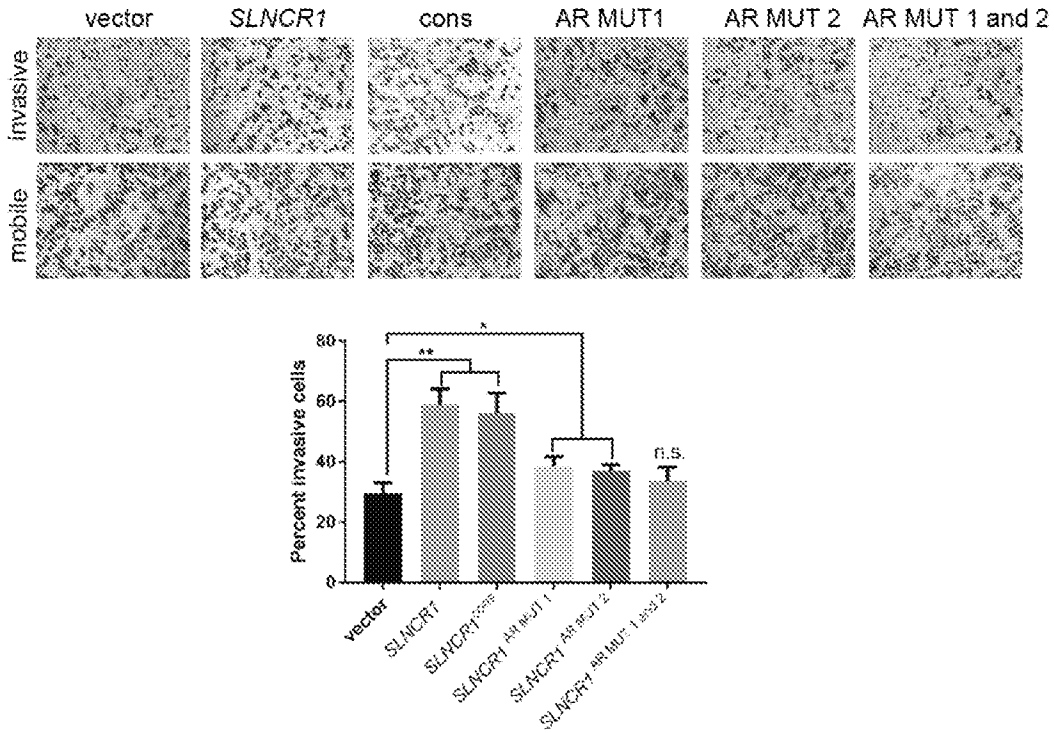

vector
SLNCR1
cons
AR MUT1
AR MUT 2
AR MUT 1 and 2
invasive
mobile
Percent invasive cells
80
60
40
20
0
*
**
n.s.
vector
SLNCR1
SLNCR1 cons
SLNCR1 AR MUT 1
SLNCR1 AR MUT 2
SLNCR1 AR MUT 1 and 2

FIG. 5C

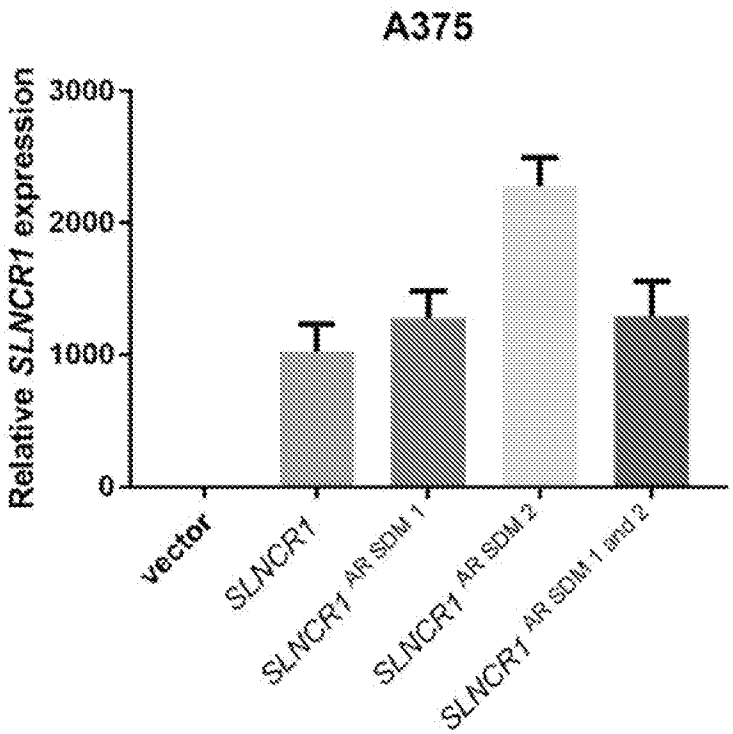

A375
Relative SLNCR1 expression
3000
2000
1000
0
vector
SLNCR1
SLNCR1 AR SDM 1
SLNCR1 AR SDM 2
SLNCR1 AR SDM 1 and 2

FIG. 6A

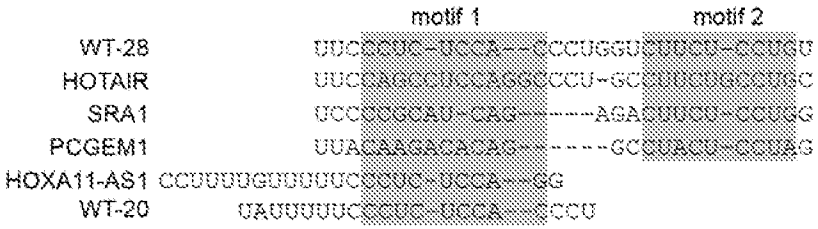


FIG. 6B

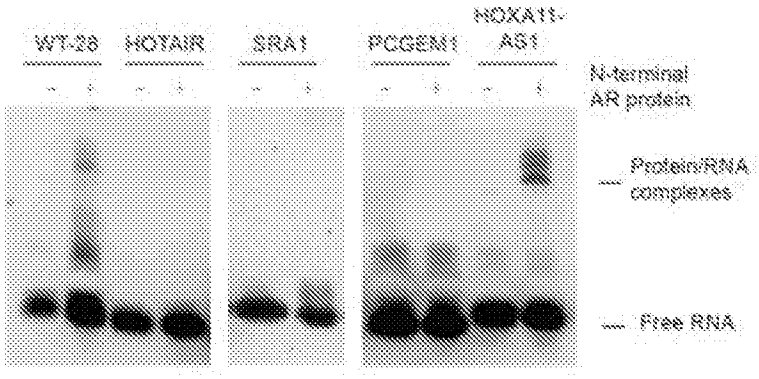


FIG. 6C

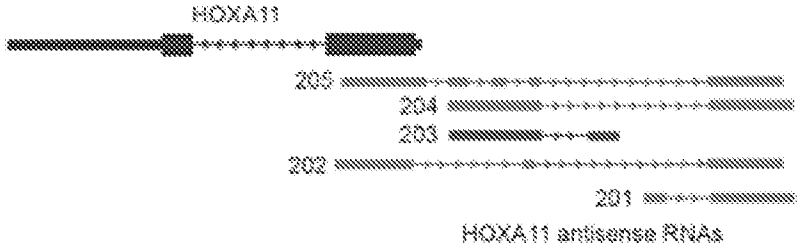


FIG. 6D



FIG. 7A

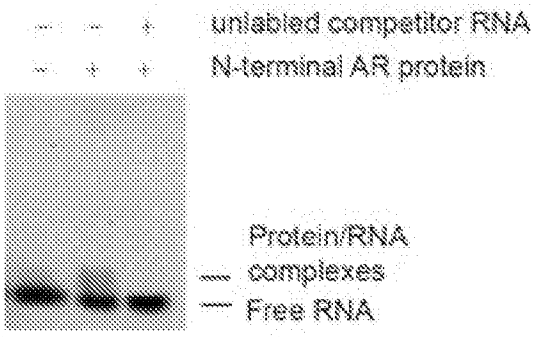

unlabled competitor RNA
N-terminal AR protein
Protein/RNA complexes
Free RNA

FIG. 7B

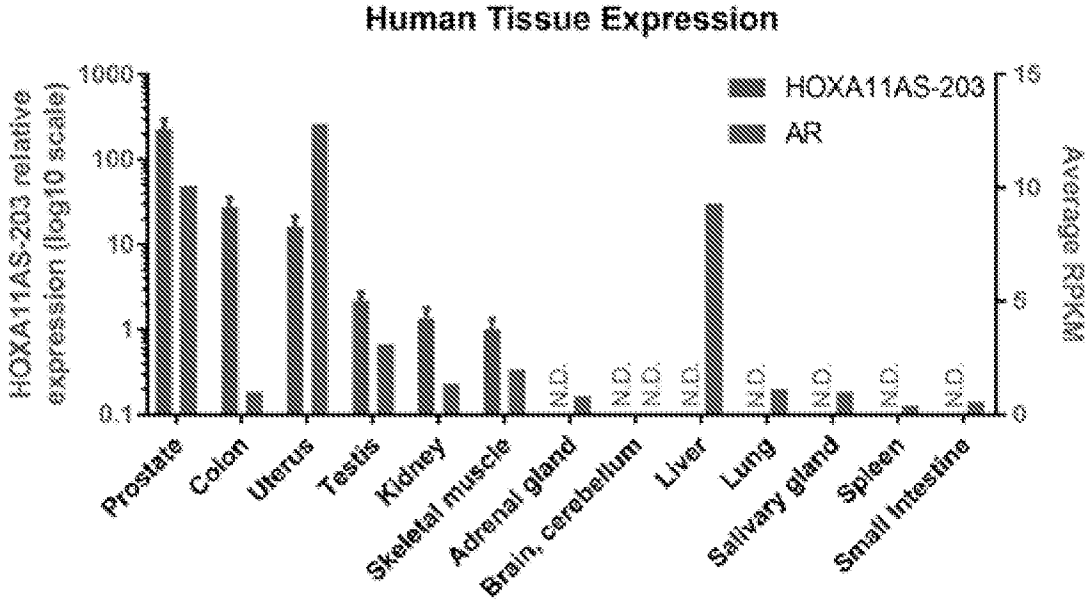

Human Tissue Expression
HOXA11AS-203 relative expression (log10 scale)
Average RPKM
HOXA11AS-203
AR
1000
100
10
1
0.1
15
10
5
0
N.D.
Prostate
Colon
Uterus
Testis
Kidney
Skeletal muscle
Adrenal gland
Brain, cerebellum
Liver
Lung
Salivary gland
Spleen
Small intestine

FIG. 8

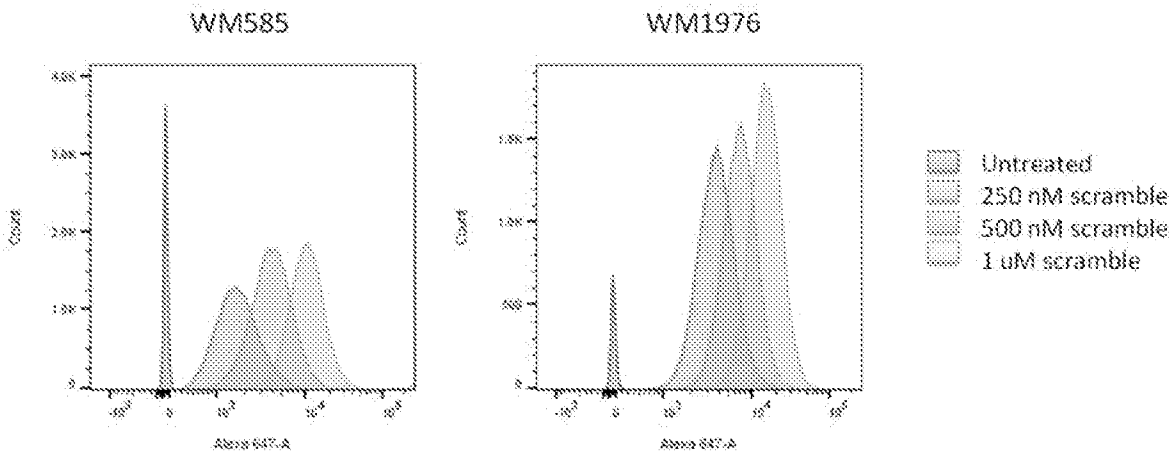

WM585
WM1976
Untreated
250 nM scramble
500 nM scramble
1 uM scramble

FIG. 9A

Mimic 1	UUCCCUCUCCACCCUGGUCUUCUCCUGU
Mimic 2	CCUCUCCACCCUGGUCUUCUC
Antisense 1	ACAGGAGAAGACCAGGGUGGAGAGGGAA
Antisense 2	GGAGAAGACCAGGGUGGAGAG

FIG. 9B

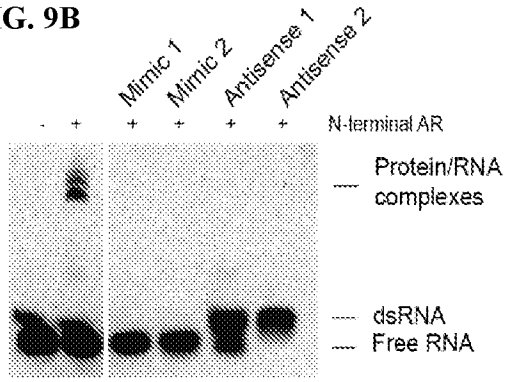


FIG. 9C

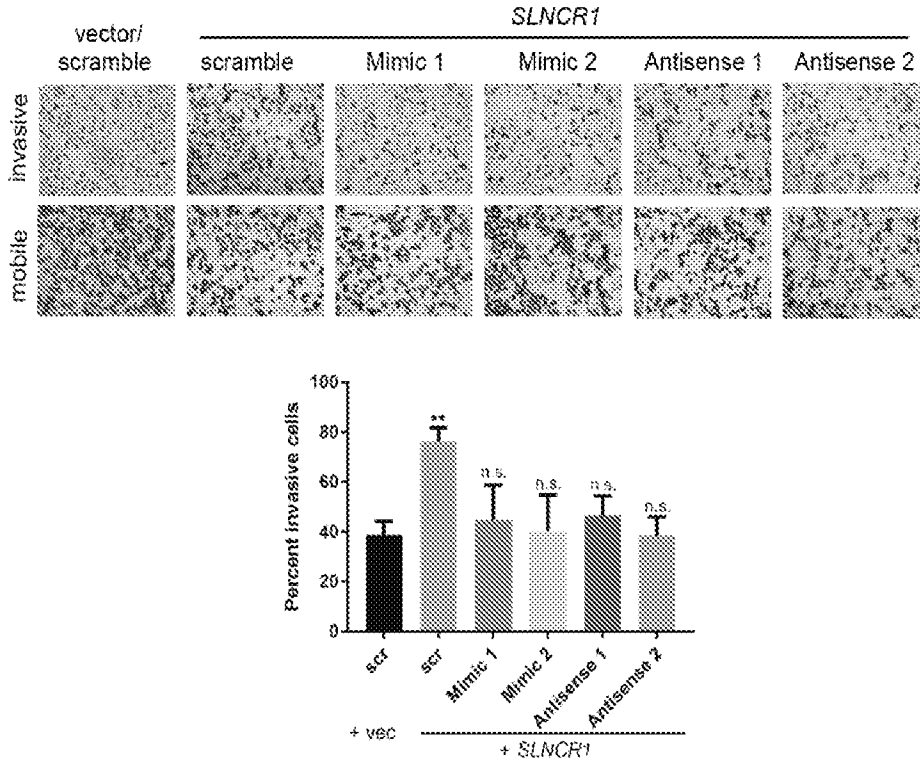


FIG. 10A

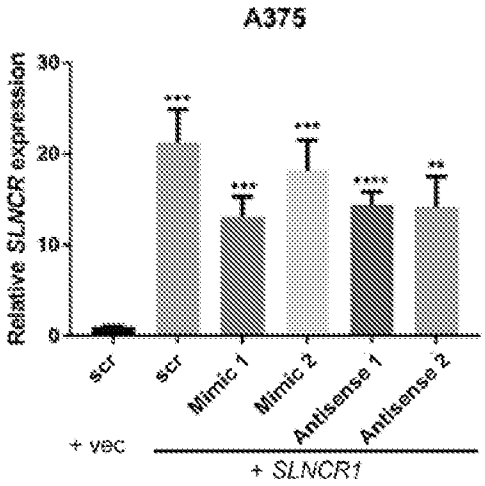
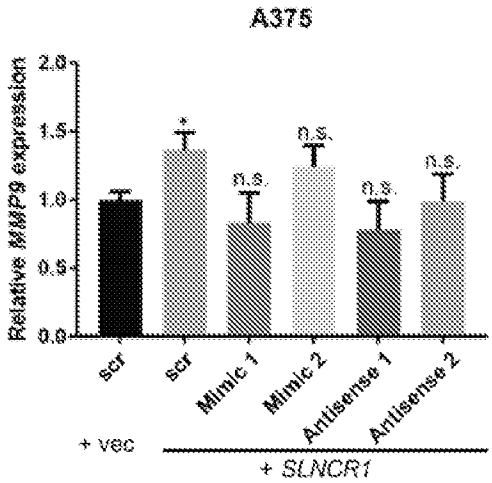


FIG. 10B



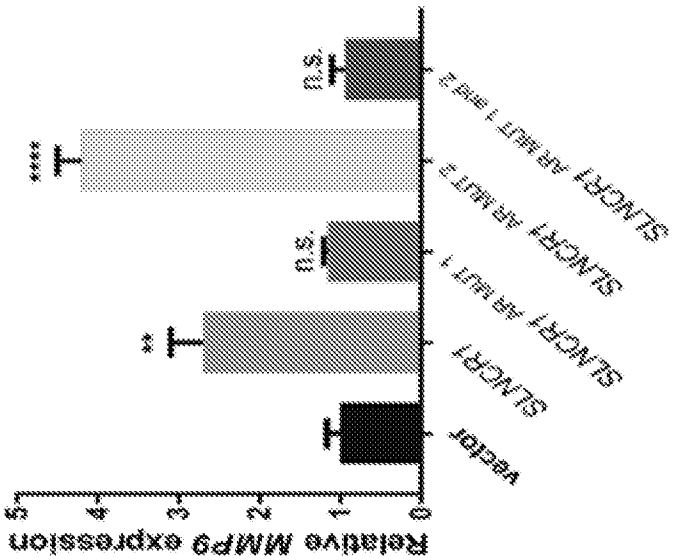


FIG. 10D

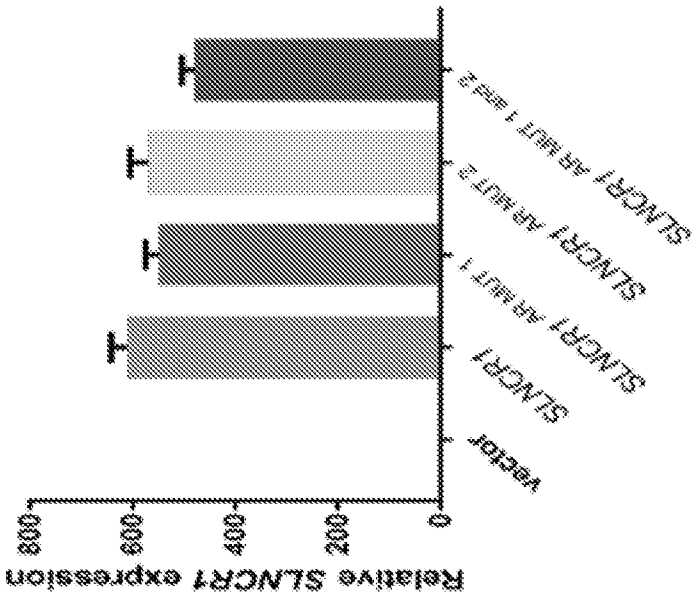


FIG. 10C

FIG. 11

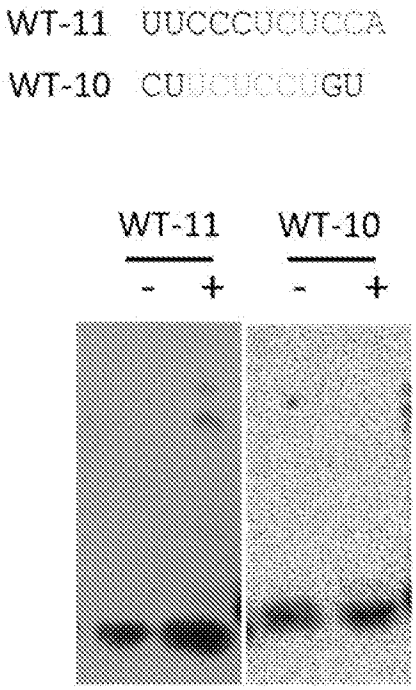


FIG. 12A

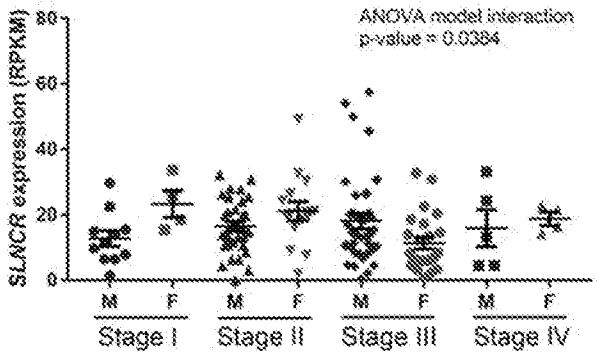


FIG. 12C

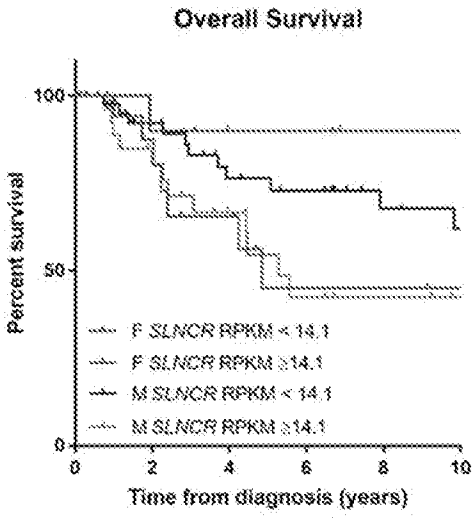


FIG. 12B

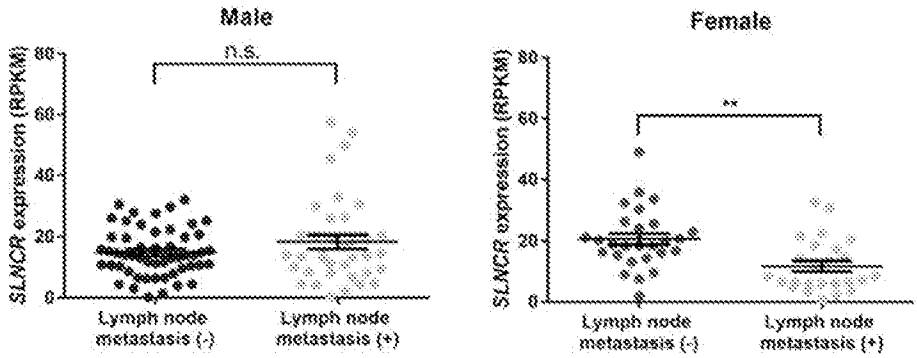


FIG. 12D

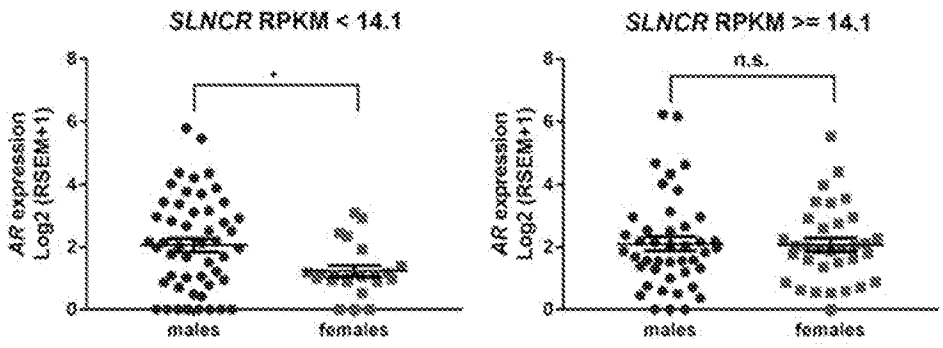


FIG. 12E

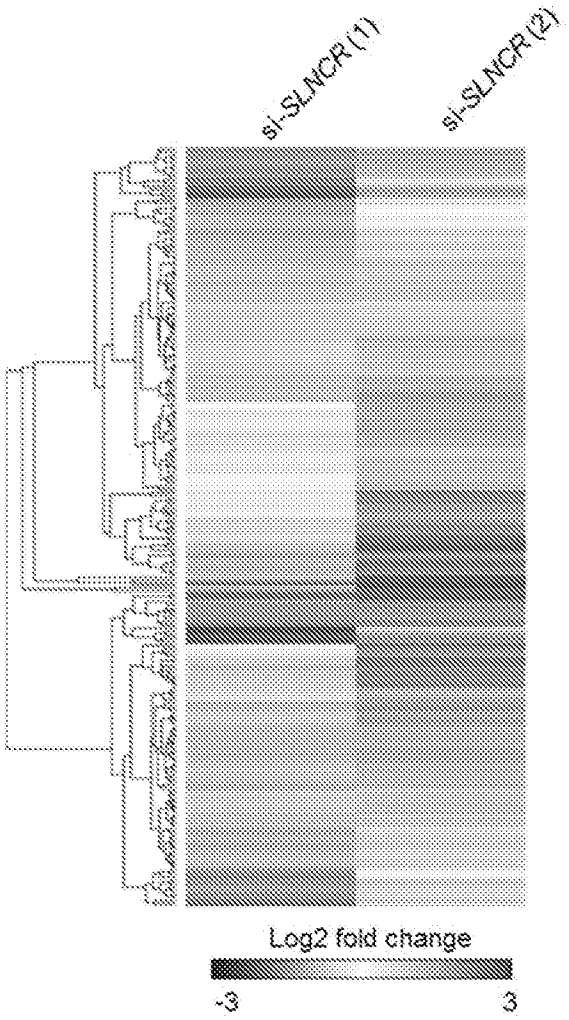


FIG. 12G

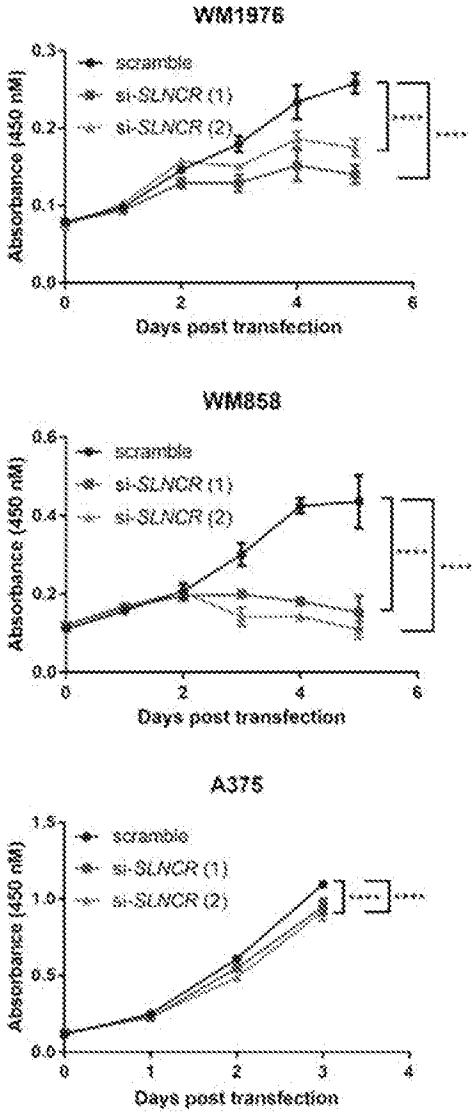


FIG. 12F

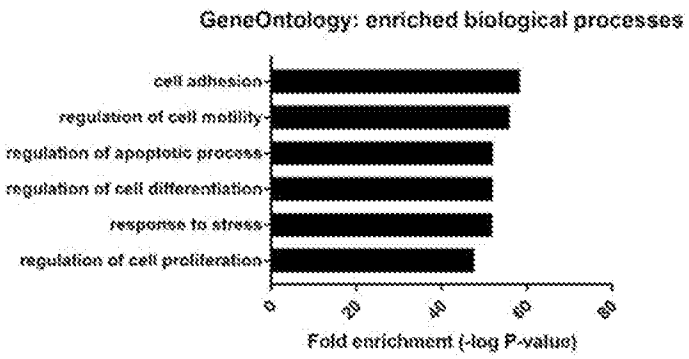


FIG. 12H

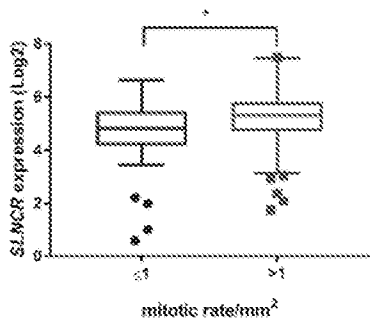


FIG. 12I

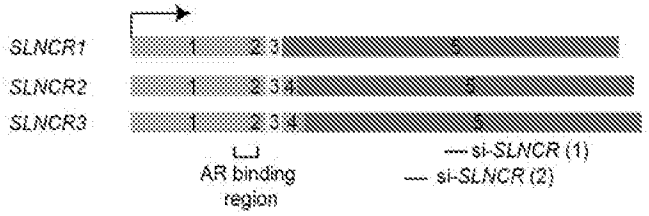


FIG. 12J

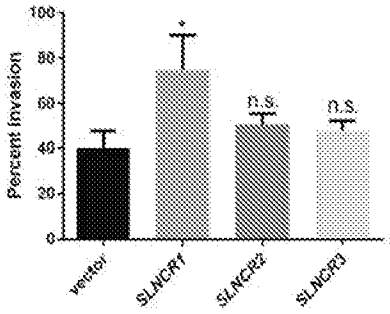


FIG. 12K

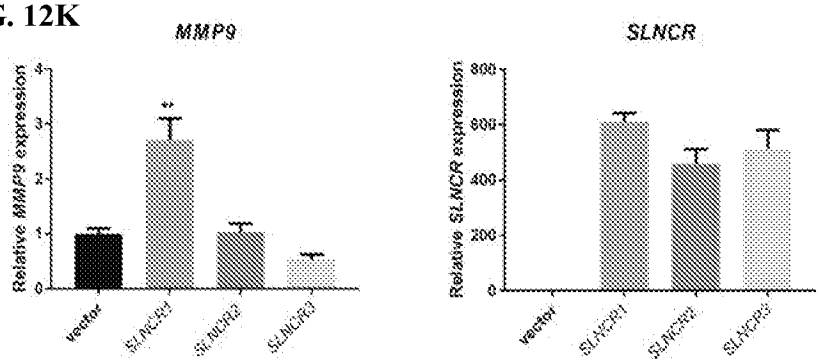


FIG. 12L

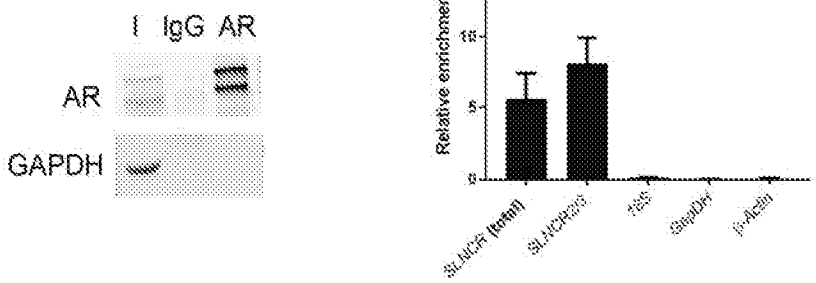


FIG. 13A

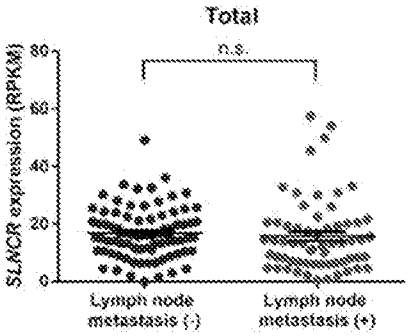


FIG. 13B

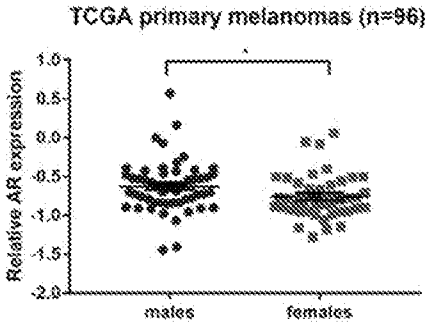
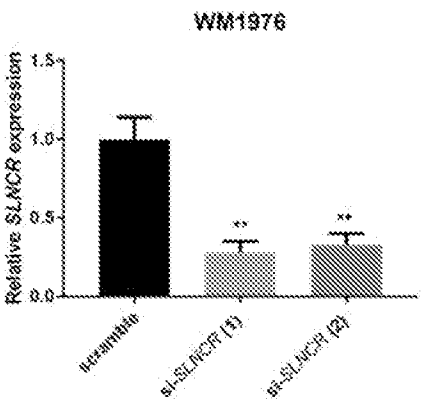
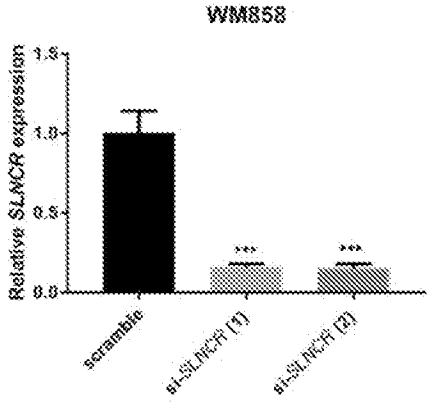


FIG. 13C





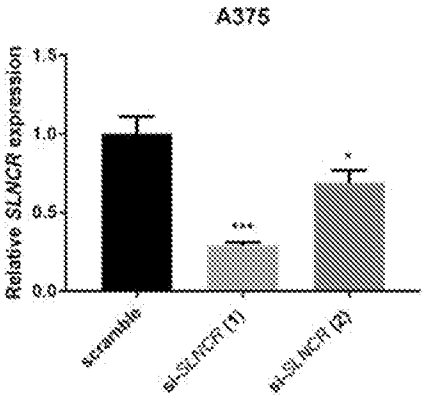


FIG. 13D

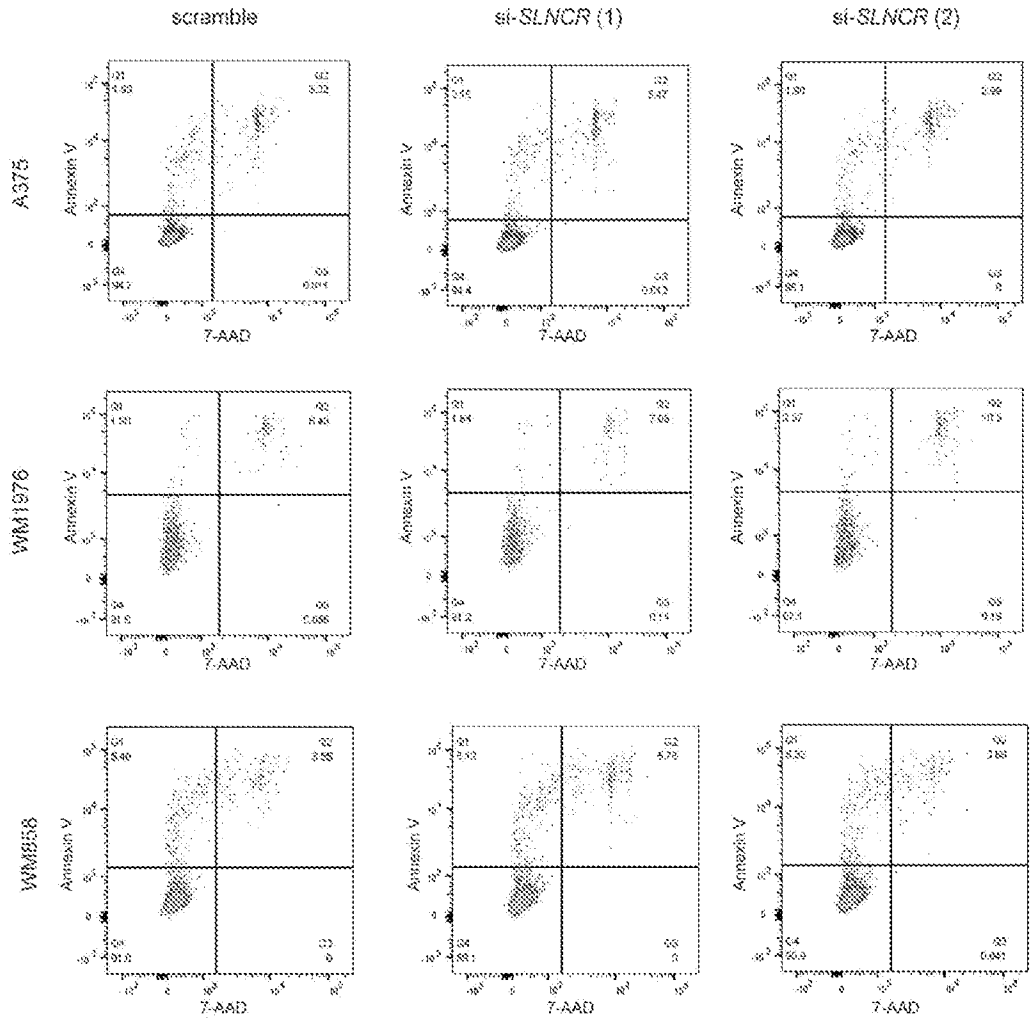

scramble
si-SLNCR (1)
si-SLNCR (2)
A375
WM1976
WM858
Annexin V
7-AAD

FIG. 13E

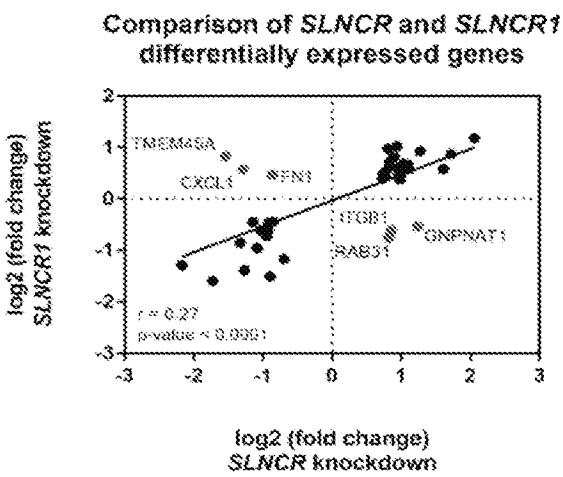


FIG. 13F

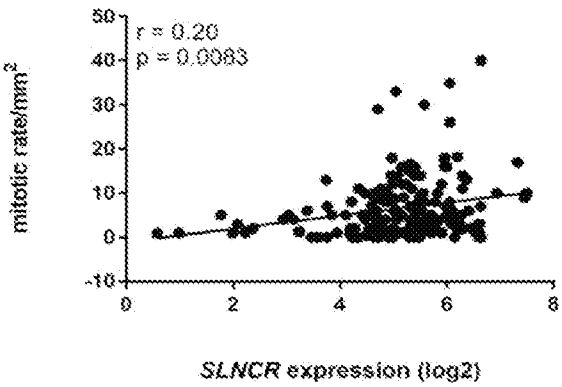


FIG. 14A

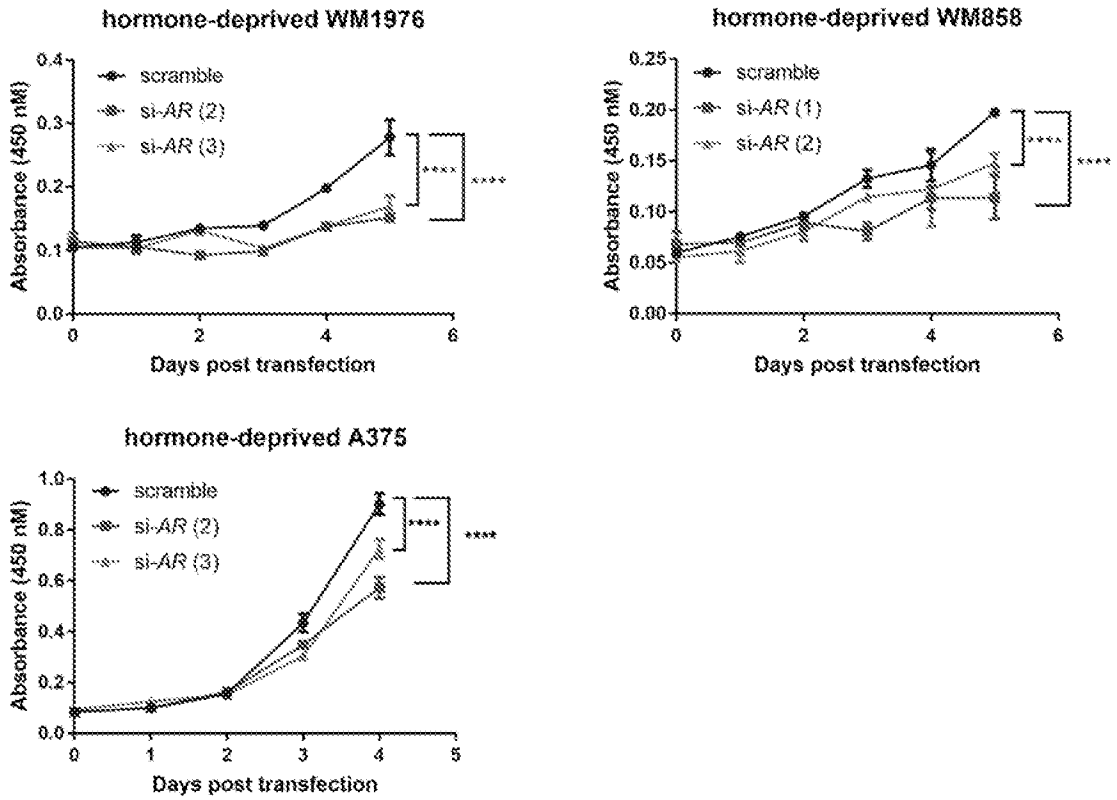
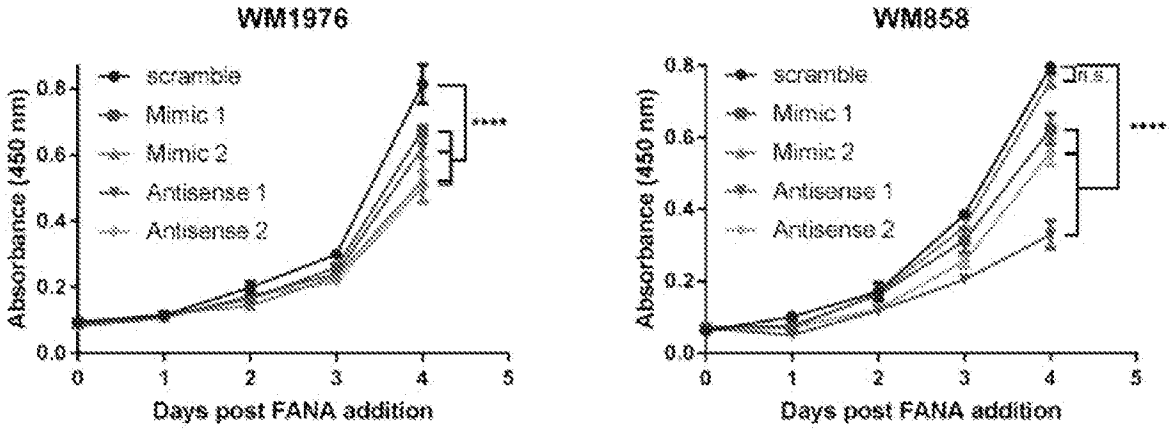


FIG. 14B



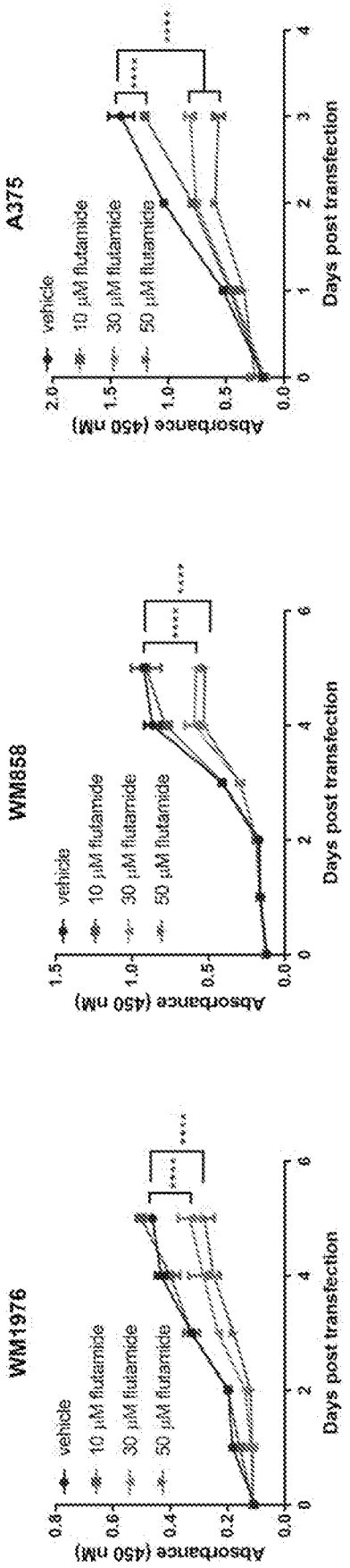


FIG. 15A

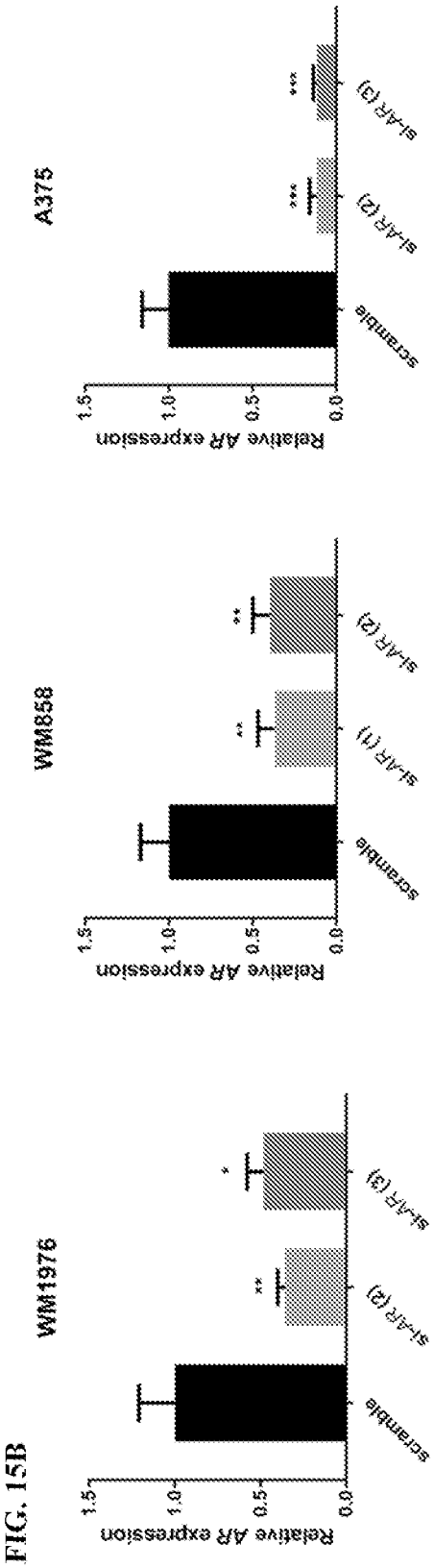


FIG. 15B

FIG. 15C

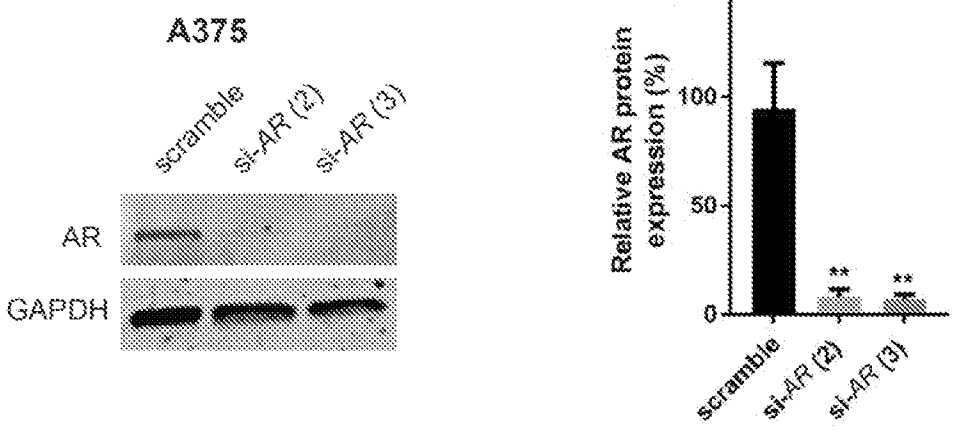


FIG. 15D

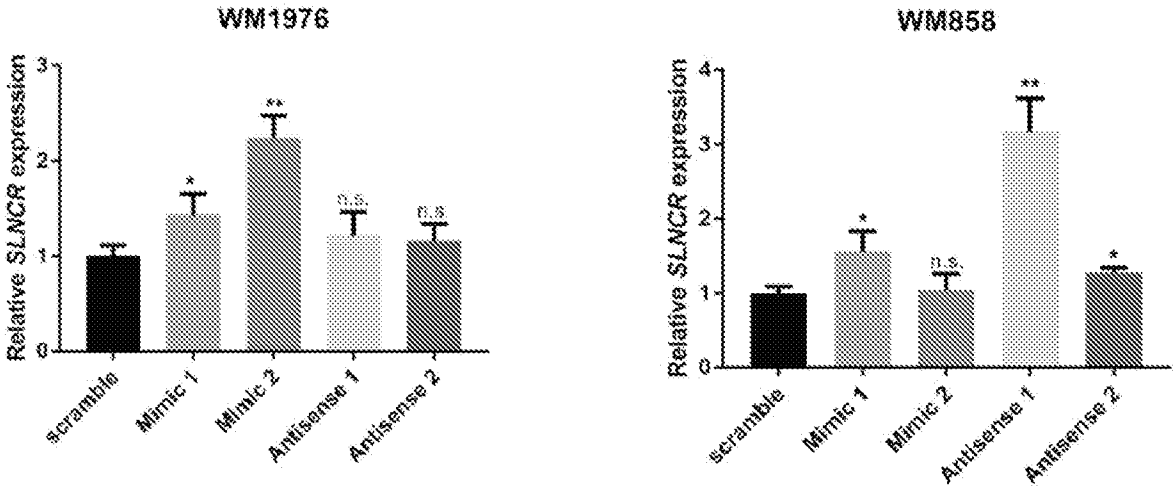


FIG. 16A

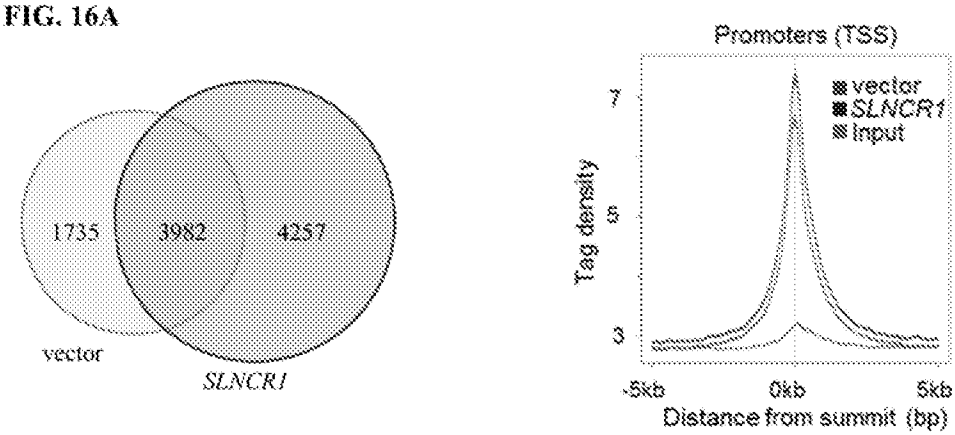


FIG. 16B

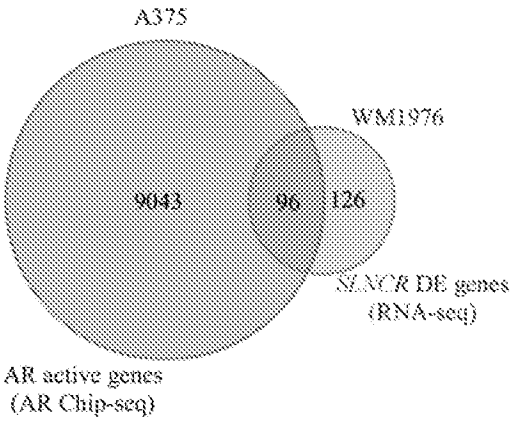


FIG. 16C

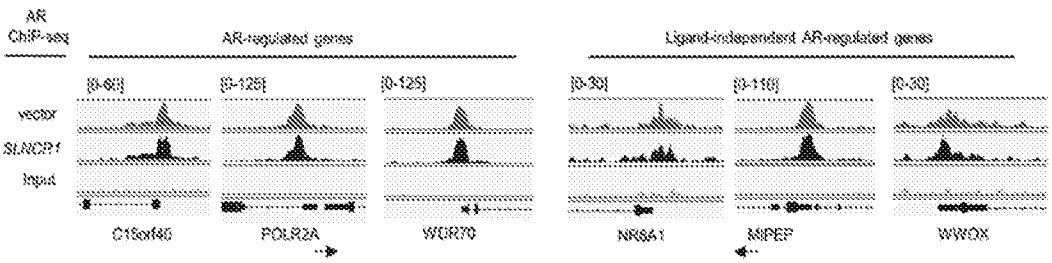


FIG. 17A

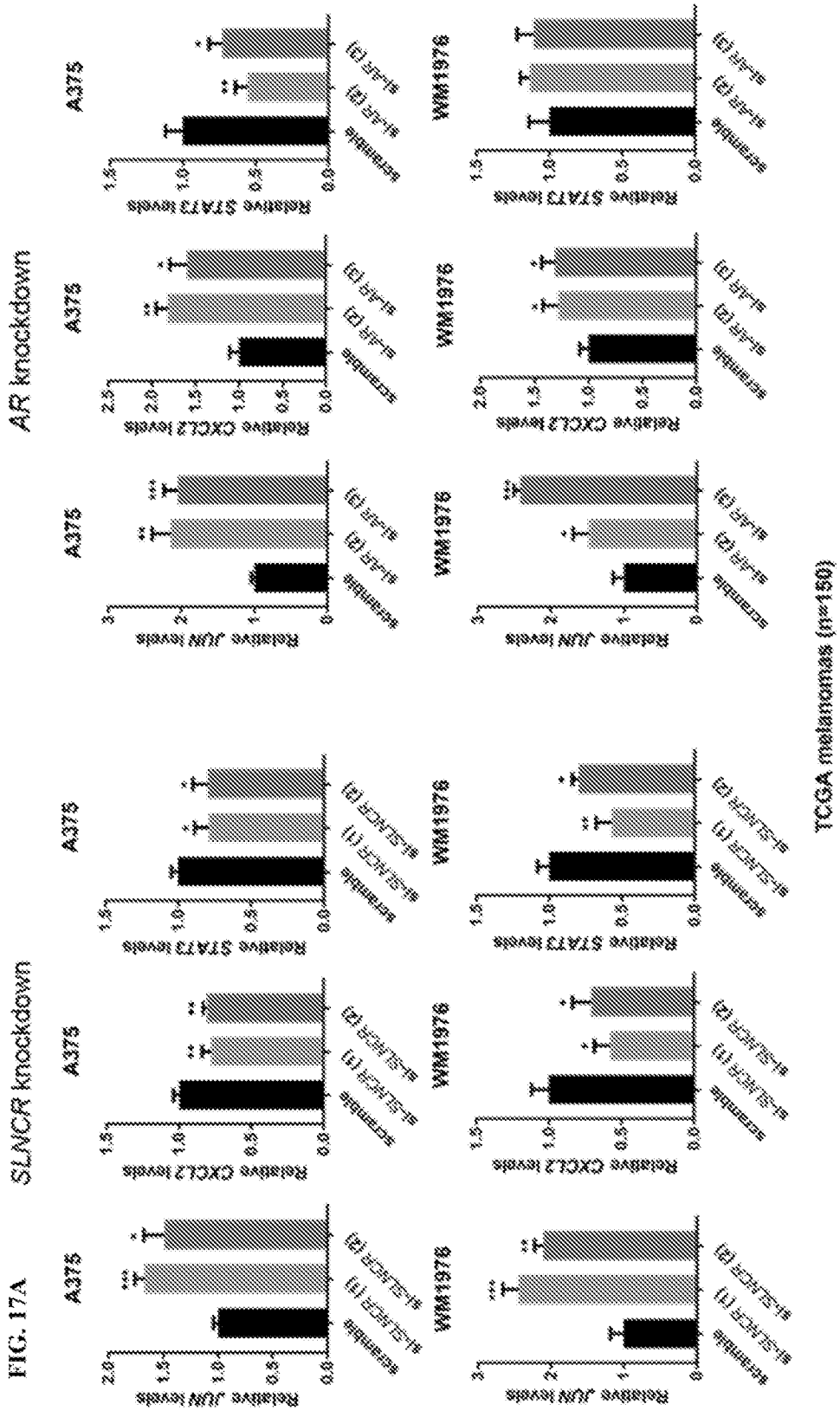

SLNCR knockdown
AR knockdown
A375
WM1976
Relative JUN levels
Relative CXCL2 levels
Relative STAT3 levels
scramble
si-SLNCR (1)
si-SLNCR (2)
si-AR (1)
si-AR (2)
TCGA melanomas (n=150)

FIG. 17B

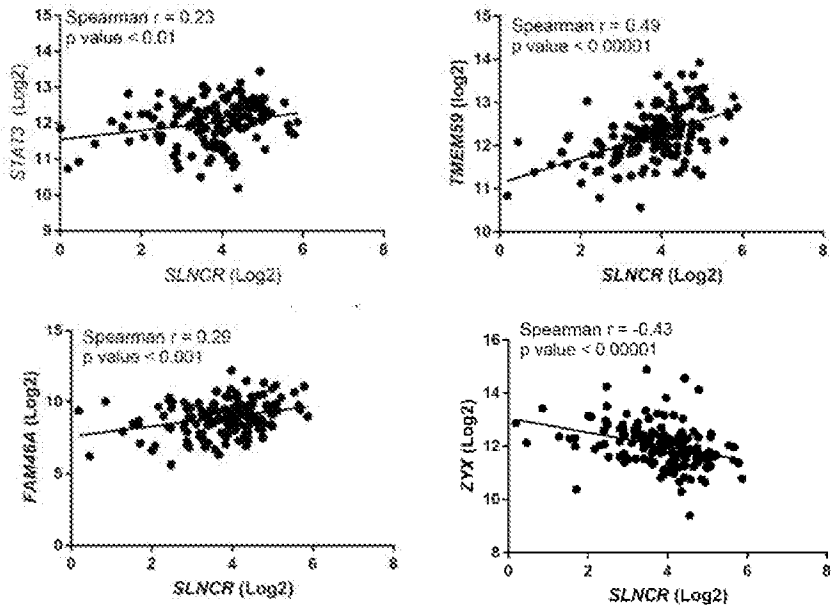
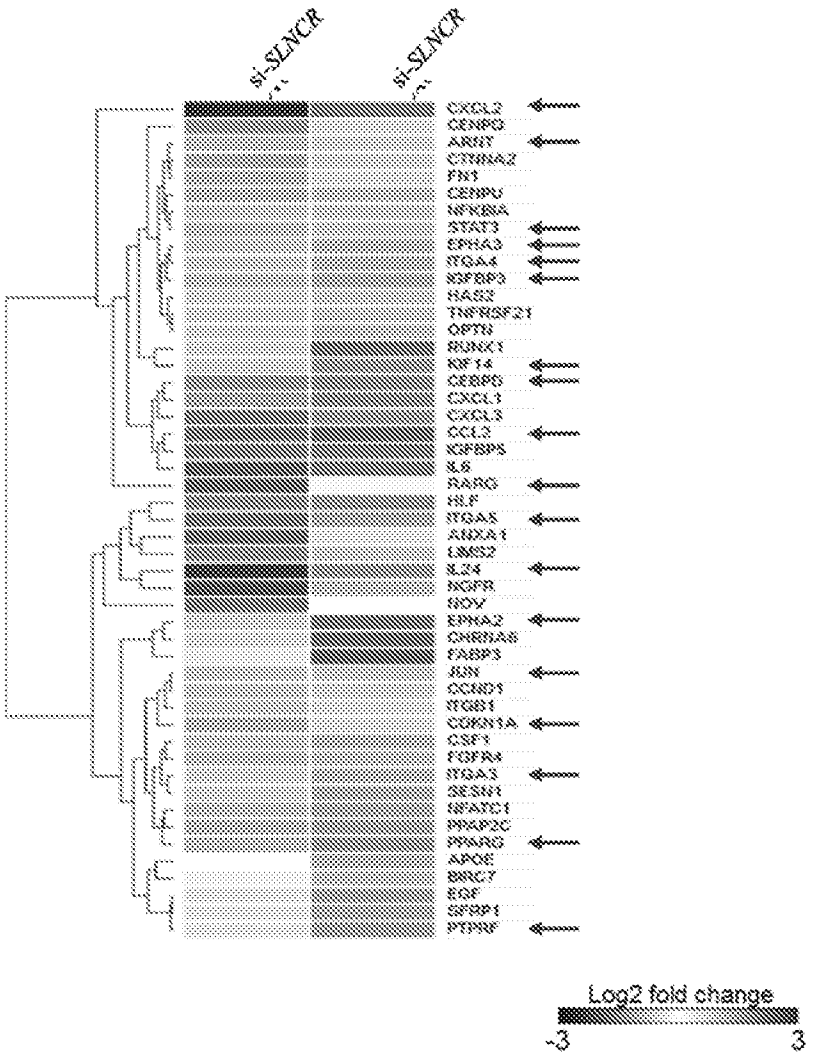

Spearman r = 0.23
p value < 0.01
STAT3 (Log2)
SLNCR (Log2)
Spearman r = 0.49
p value < 0.00001
TMEM59 (Log2)
SLNCR (Log2)
Spearman r = 0.29
p value < 0.001
FAM46A (Log2)
SLNCR (Log2)
Spearman r = -0.43
p value < 0.00001
ZYX (Log2)
SLNCR (Log2)

FIG. 17C


si-SLNCR
si-SLNCR
CXCL2
CENPO
ARNT
CTNNA2
FN1
CEBPD
NFKBIA
STAT3
EPHA3
ITGA4
IGFBP3
HAS2
TNFRSF21
OPTN
RUNX1
IRF1
CEBPB
CXCL1
CXCL3
CCL2
IGFBP5
IL6
RARG
HLF
ITGA5
ANXA1
LMO2
IL24
NGFR
SOV
EPHA2
CHRNA6
FABP3
JUN
CCND1
ITGB1
CDKN1A
CSF1
FGFR4
ITGA3
SESN1
NFATC1
PPAP2C
PPARG
APOE
BRC7
EGF
IGFBP1
PTPRF
Log2 fold change
-3
3

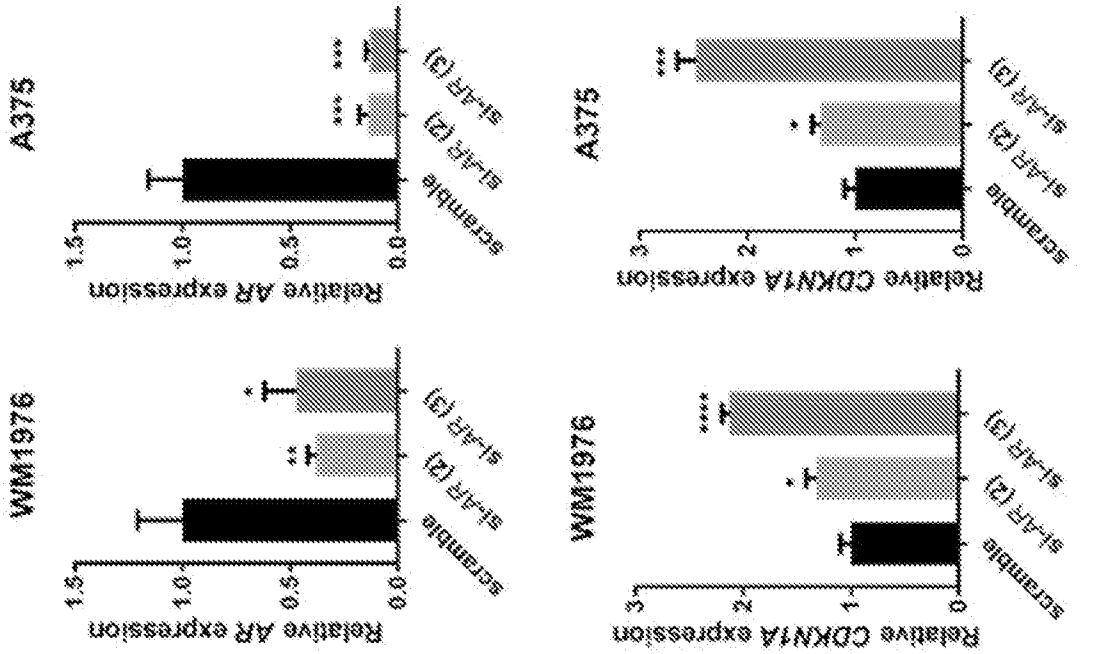


FIG. 18B

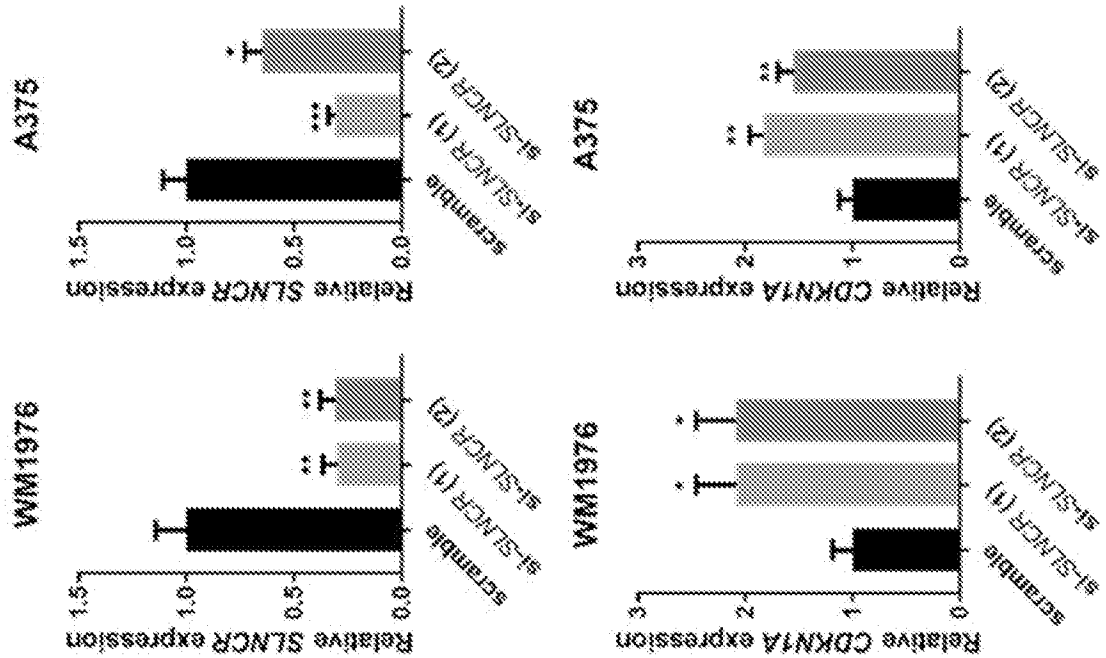


FIG. 18A

FIG. 18C

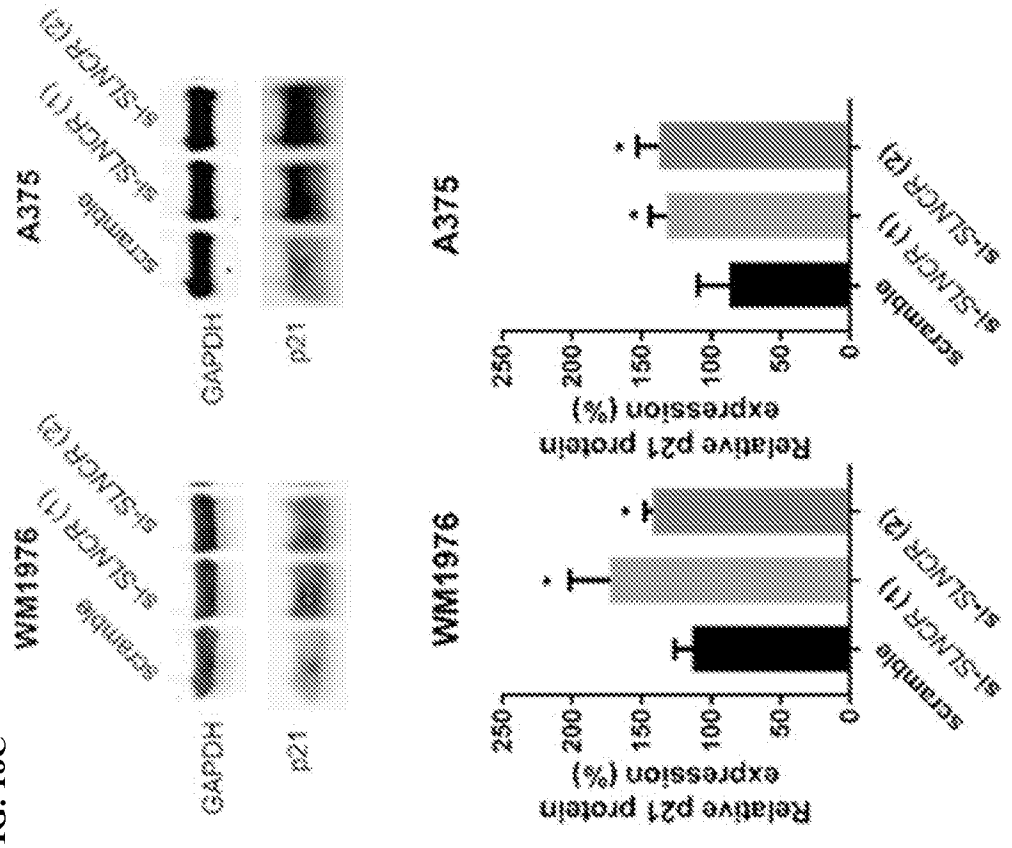


FIG. 18D

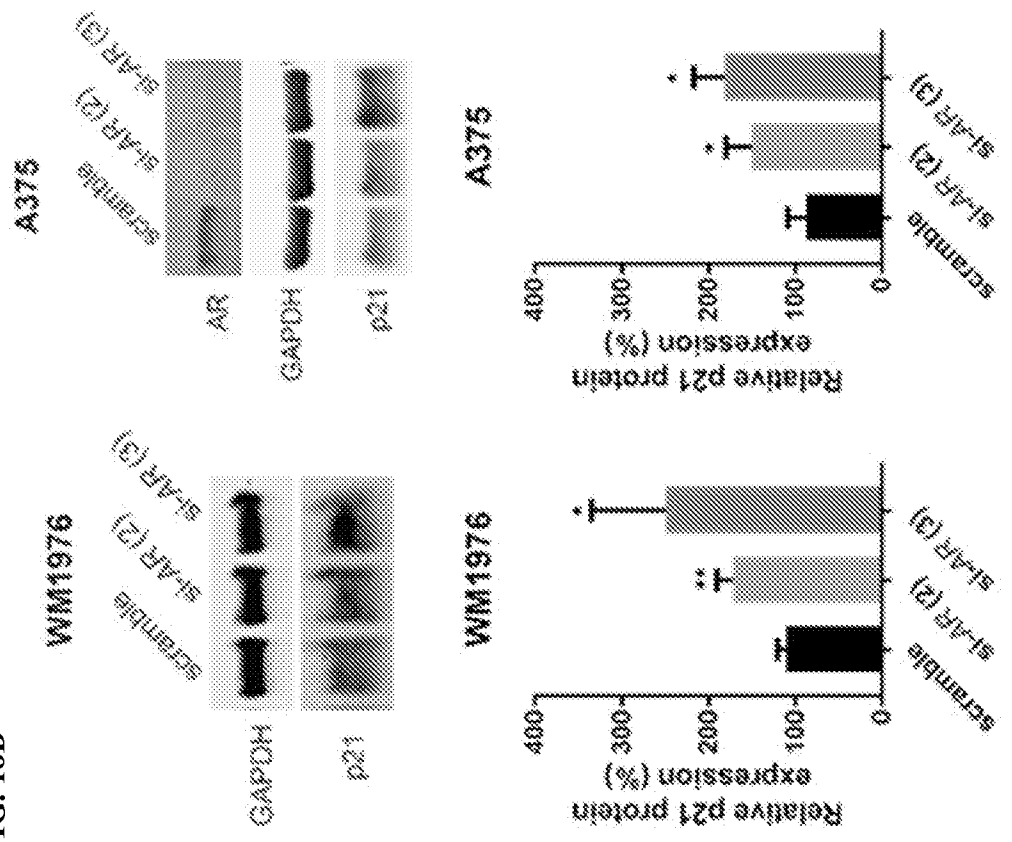


FIG. 18E

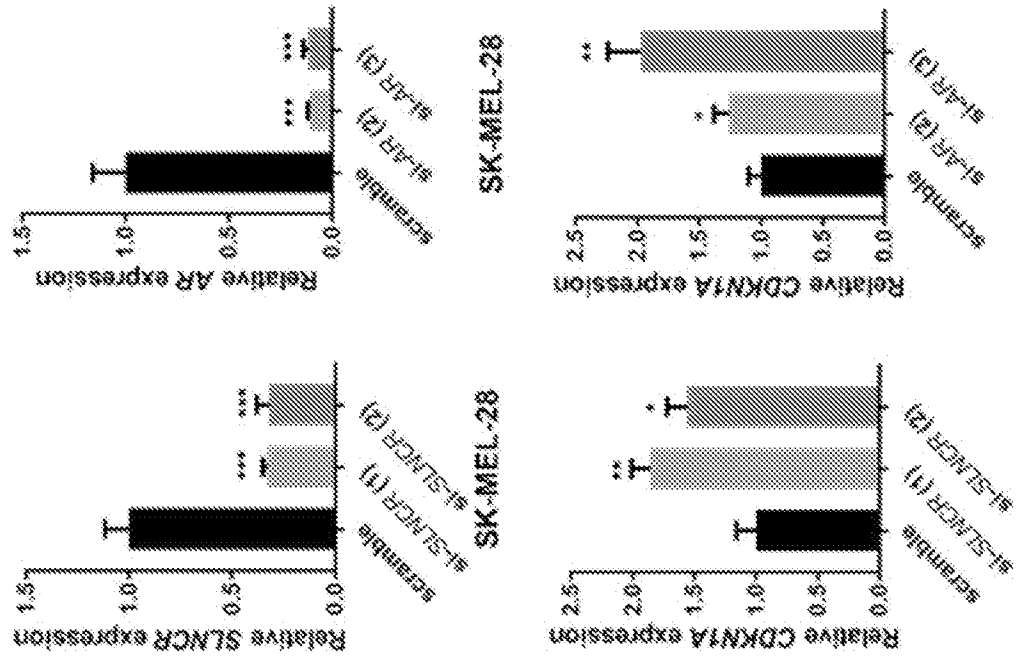


FIG. 18F

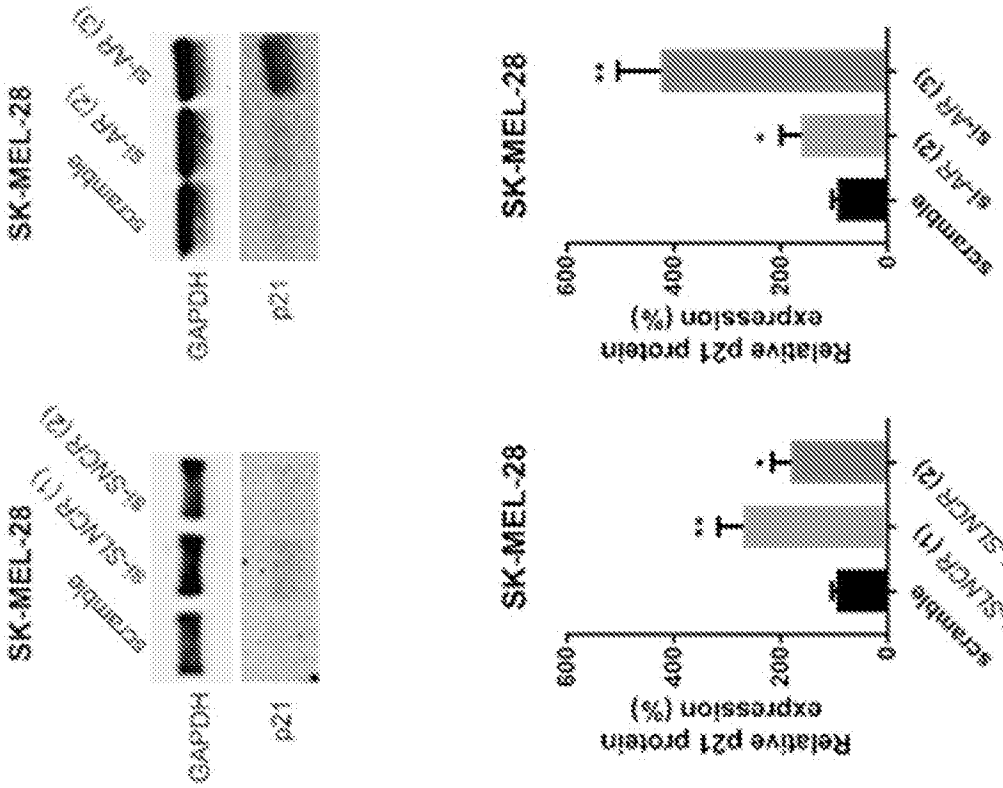


FIG. 18G

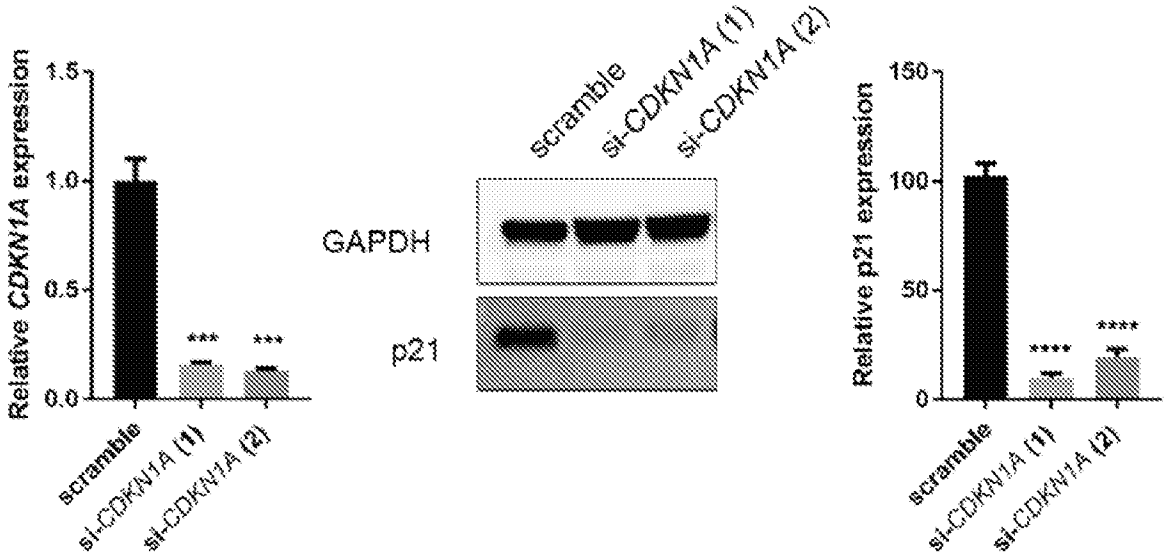


FIG. 18H

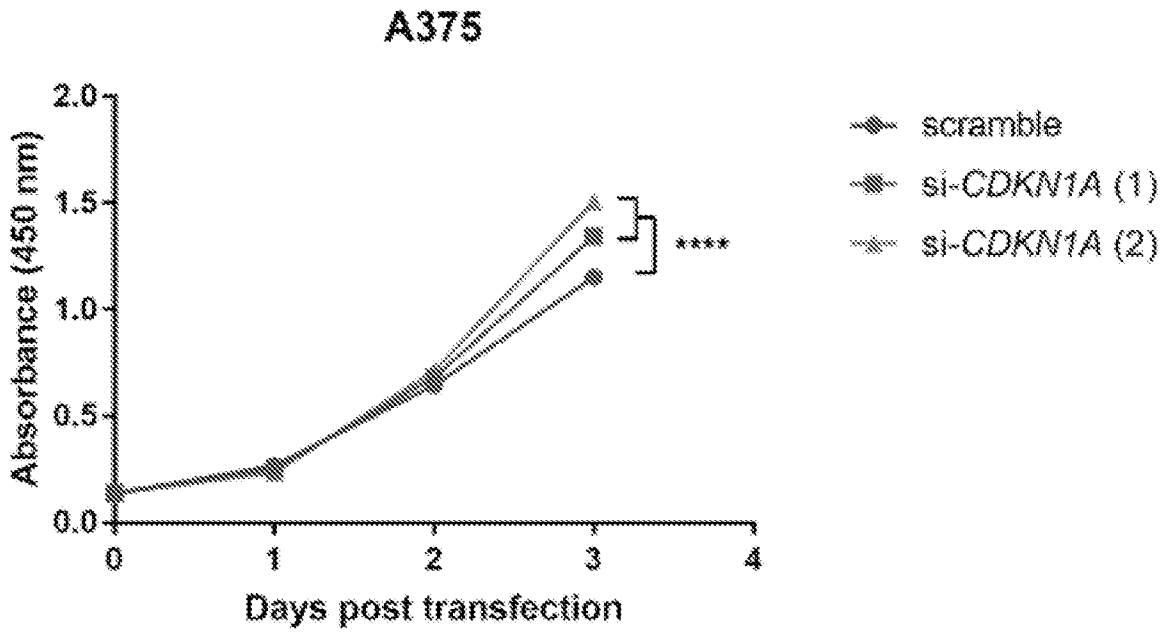


FIG. 19A

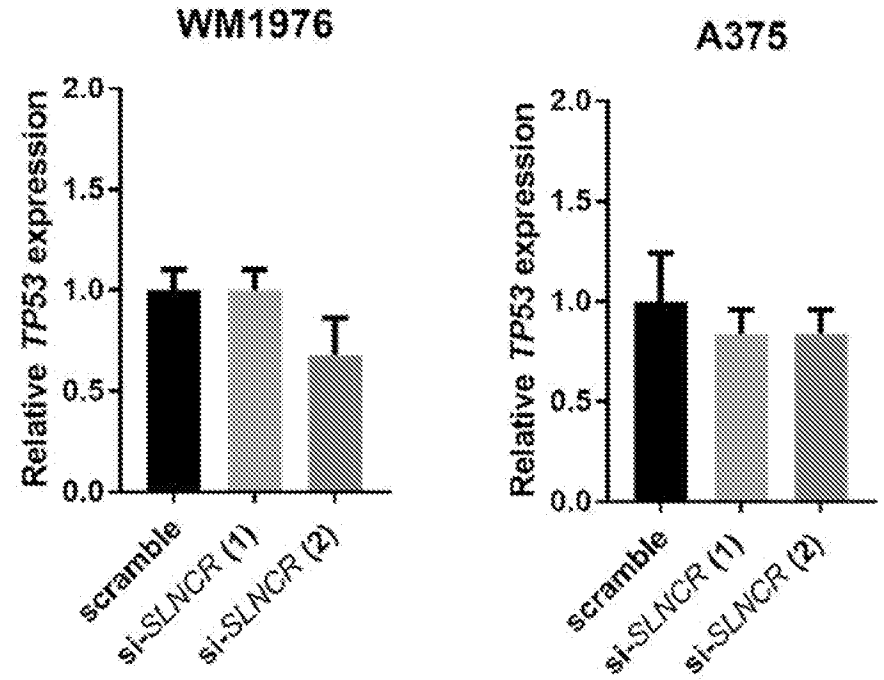


FIG. 19B

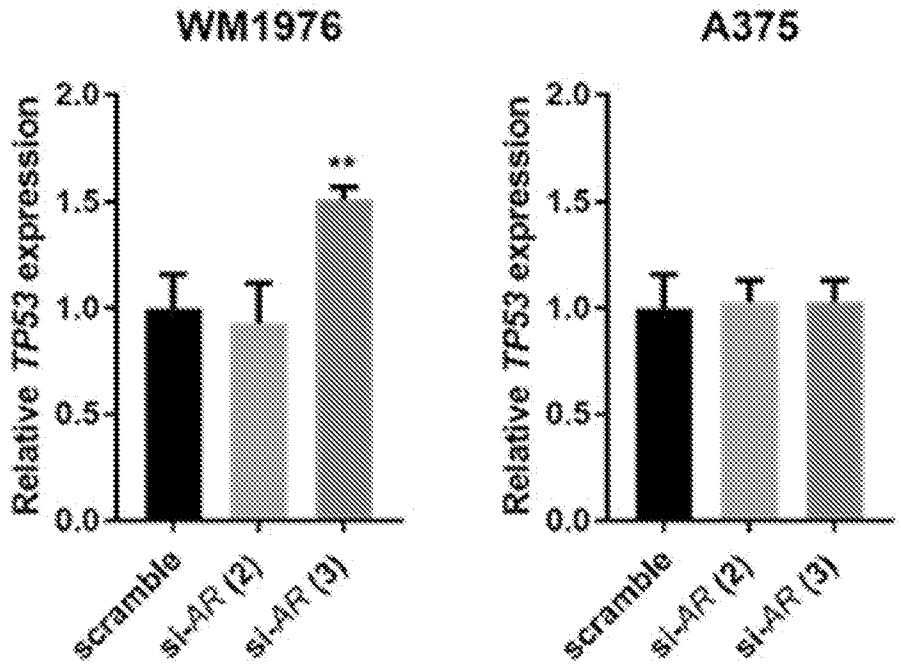


FIG. 19C

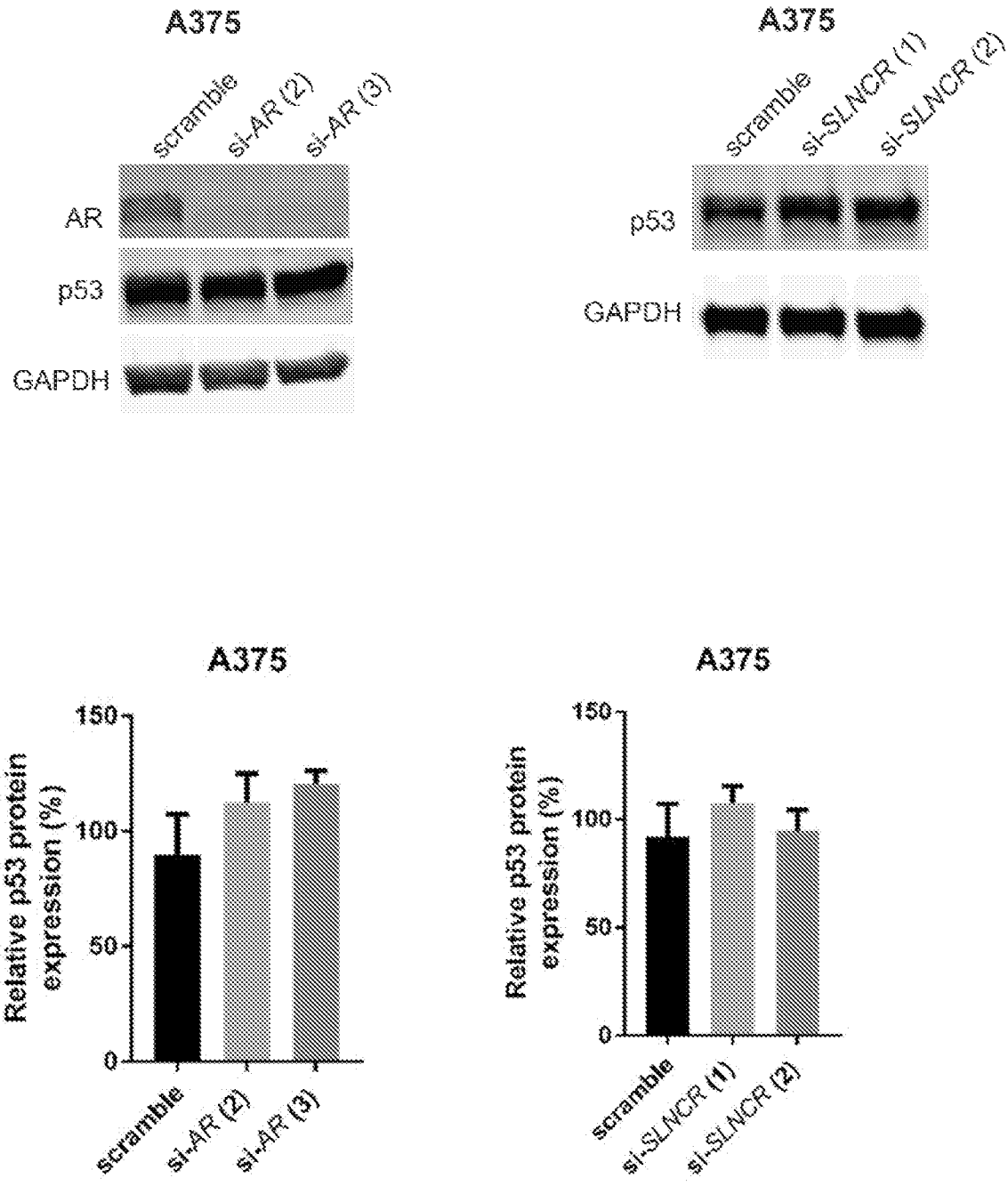

A375
scramble
si-AR (2)
si-AR (3)
AR
p53
GAPDH
A375
scramble
si-SLNCR (1)
si-SLNCR (2)
p53
GAPDH
A375
Relative p53 protein expression (%)
150
100
50
0
scramble
si-AR (2)
si-AR (3)
A375
Relative p53 protein expression (%)
150
100
50
0
scramble
si-SLNCR (1)
si-SLNCR (2)

FIG. 19D

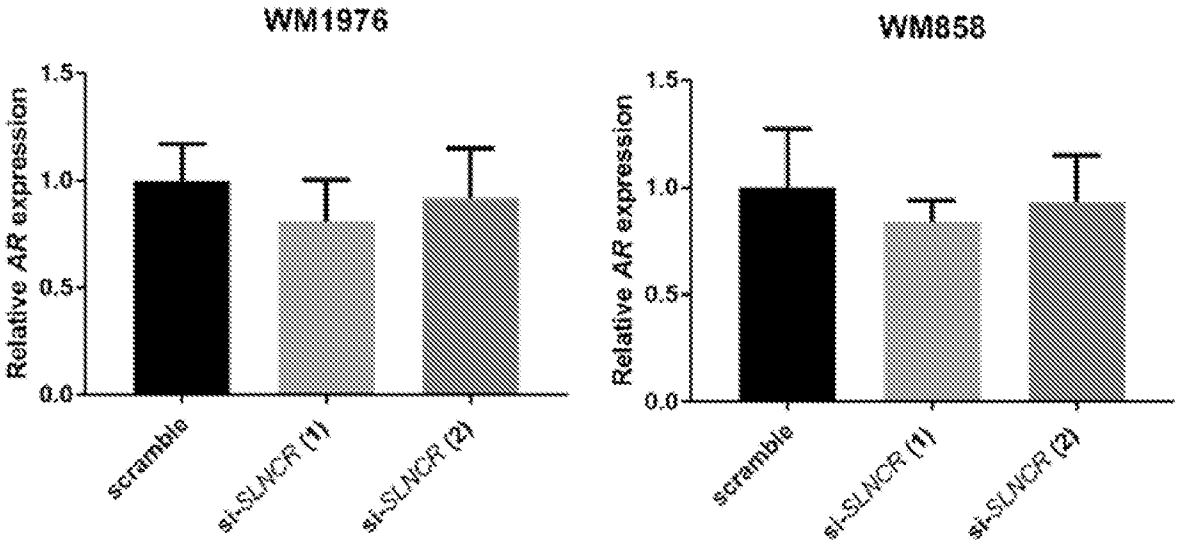

WM1976
Relative AR expression
1.5
1.0
0.5
0.0
scramble
si-SLNCR (1)
si-SLNCR (2)
WM858
Relative AR expression
1.5
1.0
0.5
0.0
scramble
si-SLNCR (1)
si-SLNCR (2)

FIG. 20A

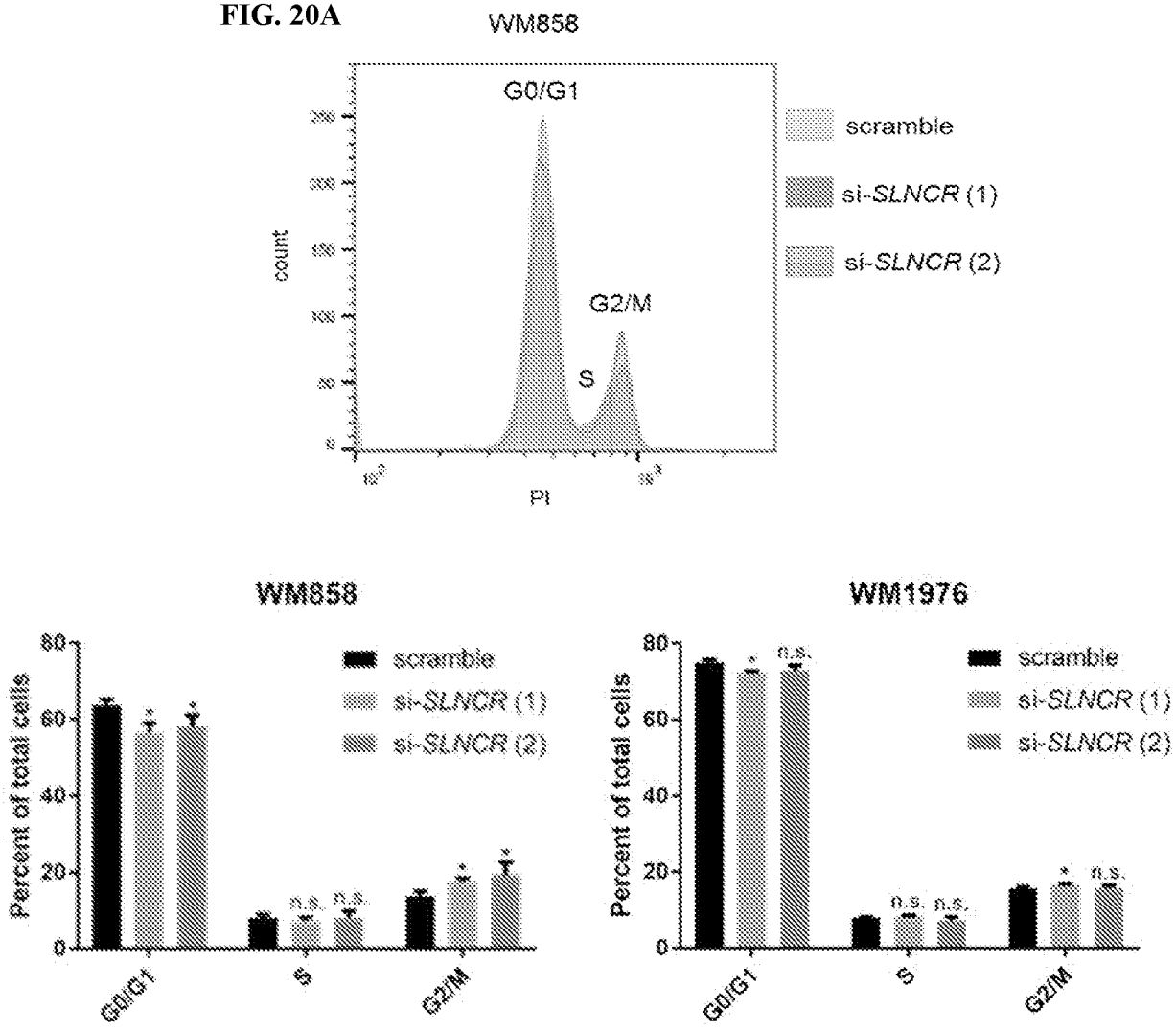

WM858
G0/G1
G2/M
S
count
PI
scramble
si-SLNCR (1)
si-SLNCR (2)
WM858
WM1976
Percent of total cells
n.s.
G0/G1
S
G2/M

FIG. 20B

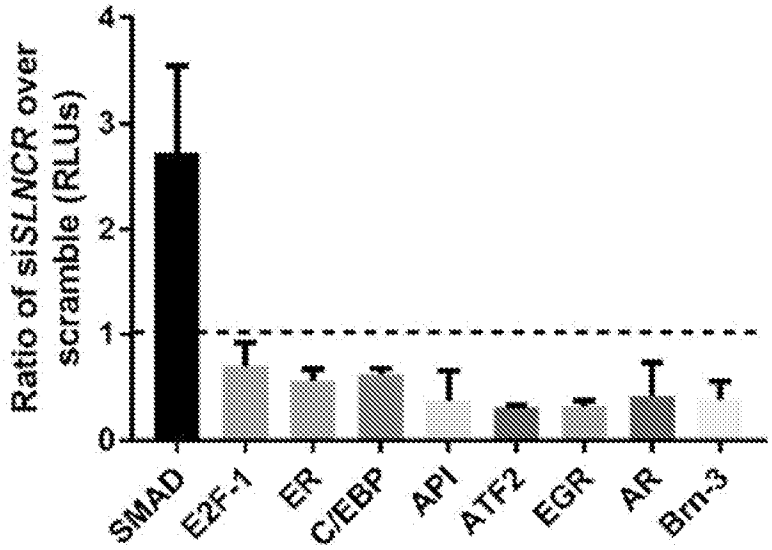
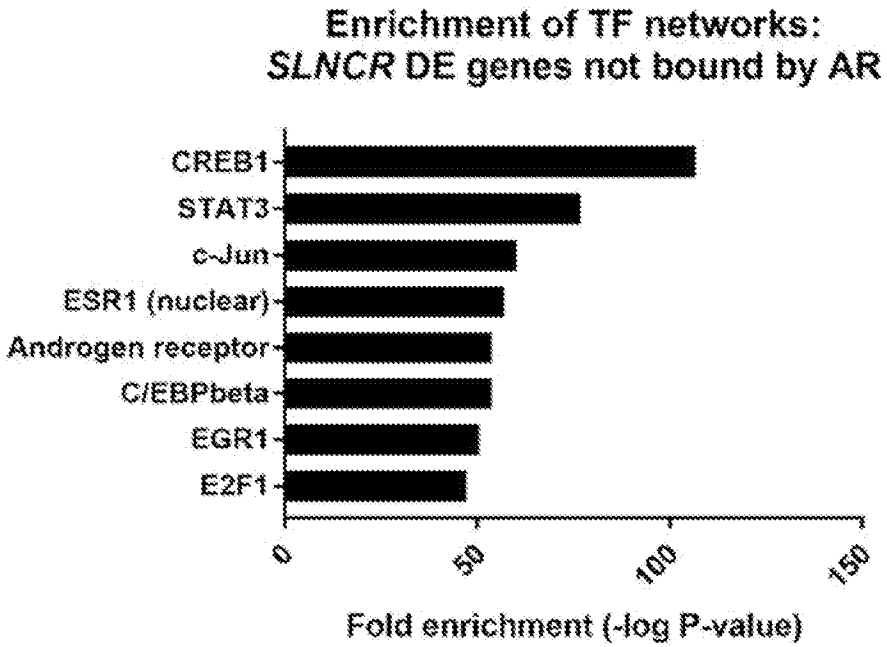


FIG. 20C



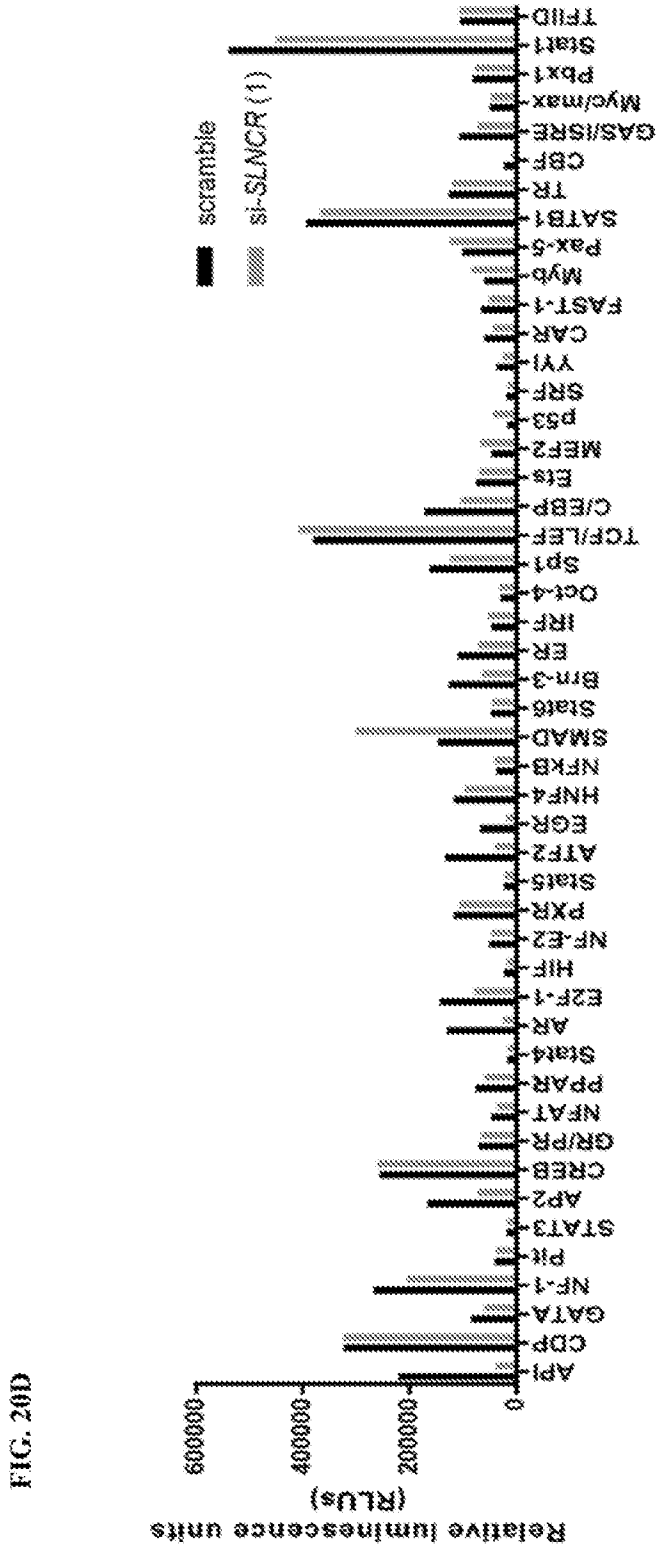

scramble
si-SLMCR (1)
Relative luminescence units
(RLUs)
600000
400000
200000
0
AP1
CDP
GATA
NF-1
Pit
STAT3
AP2
CREB
GR/PR
NFAT
PPAR
Stat4
AR
E2F-1
HIF
NF-E2
PXR
Stat5
ATF2
EGR
HNF4
NFkB
SMAD
Stat6
Brn-3
ER
IRF
Oct-4
Sp1
TCF/LEF
C/EBP
Ets
MEF2
p53
SRF
YY1
CAR
FAST-1
Myb
Pax-5
SAT81
TR
CBF
GAS/ISRE
Myc/max
Pbx1
Stat1
TFIID

FIG. 20D

FIG. 21A

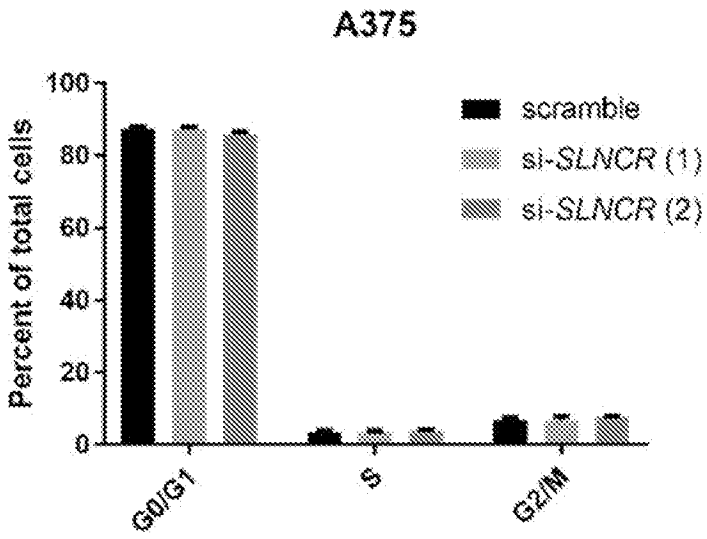


FIG. 21B

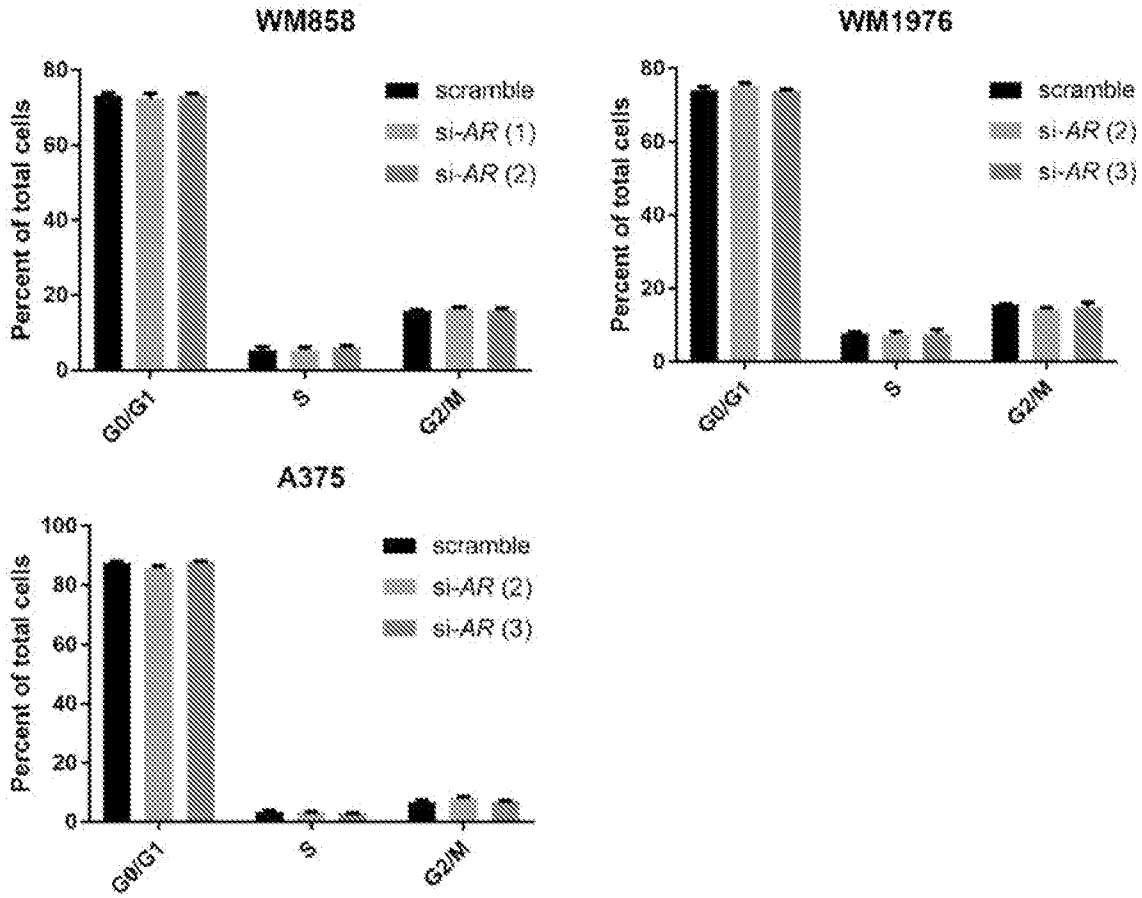


FIG. 22A

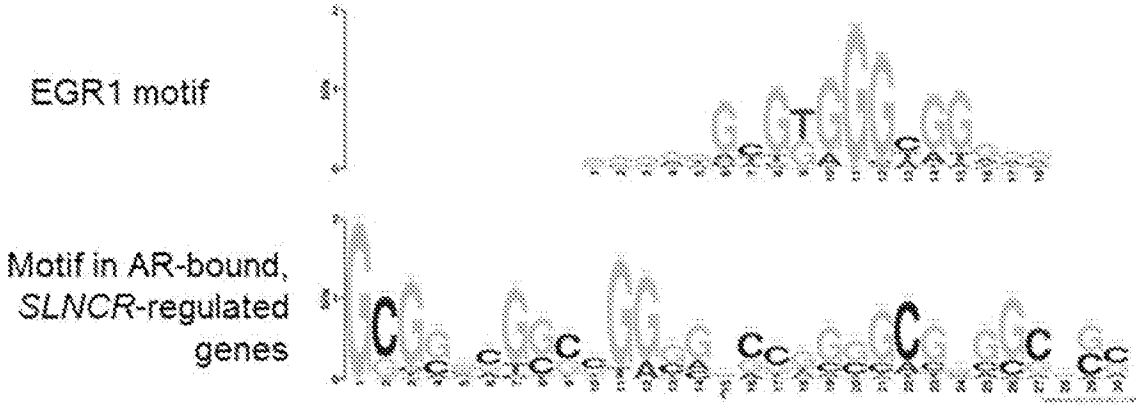


FIG. 22B

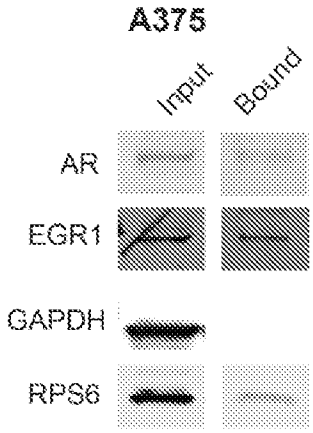


FIG. 22C

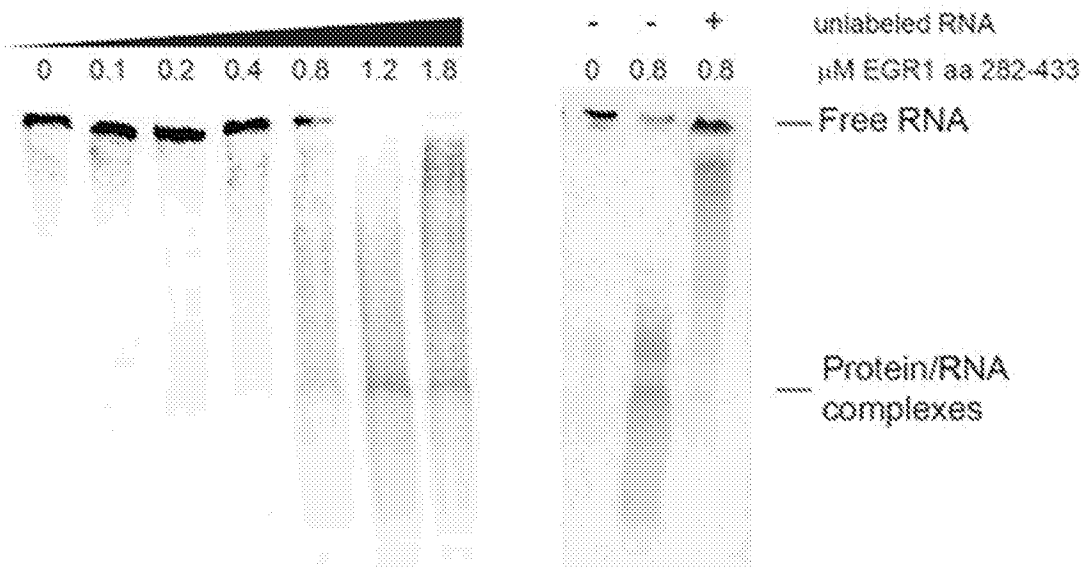


FIG. 22D

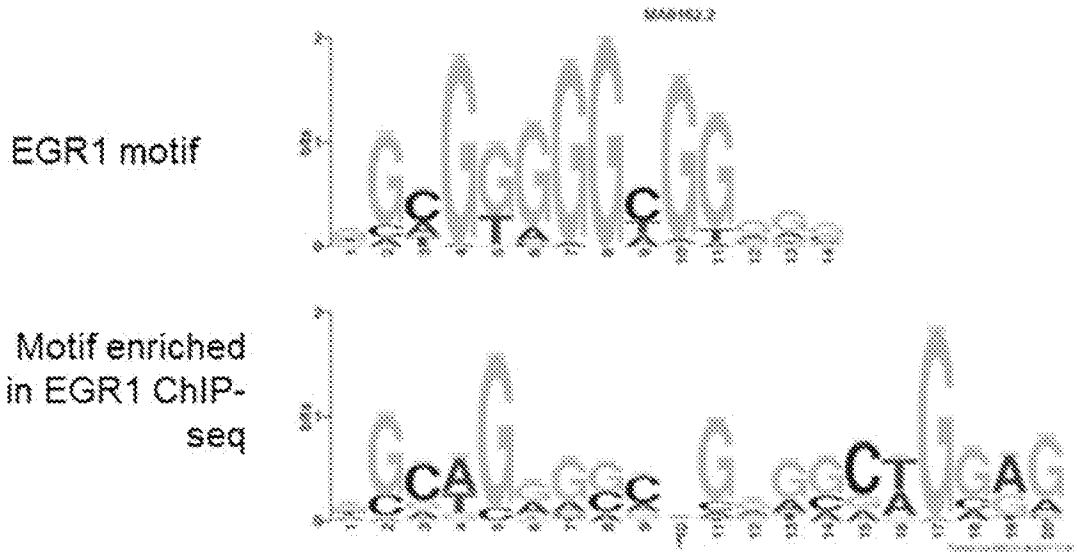


FIG. 22E

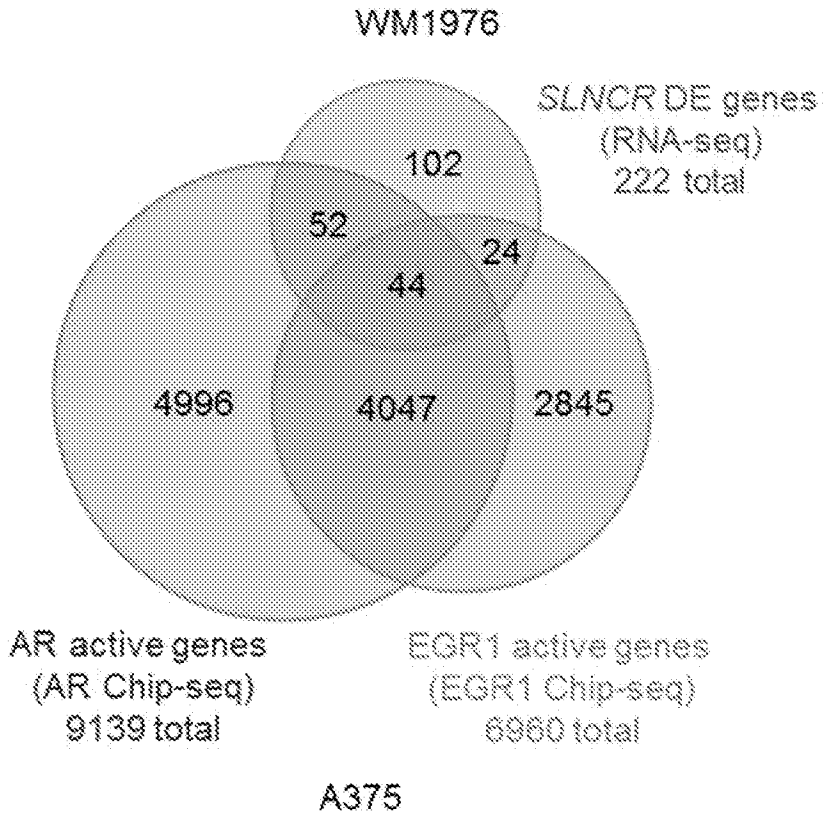


FIG. 22F

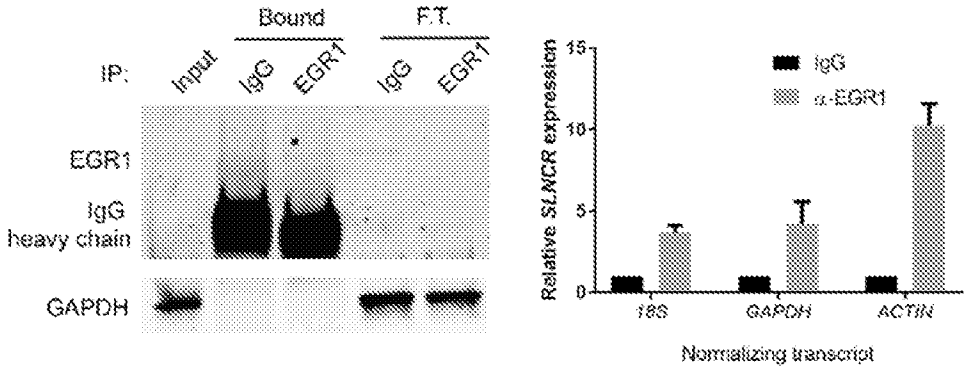


FIG. 22G

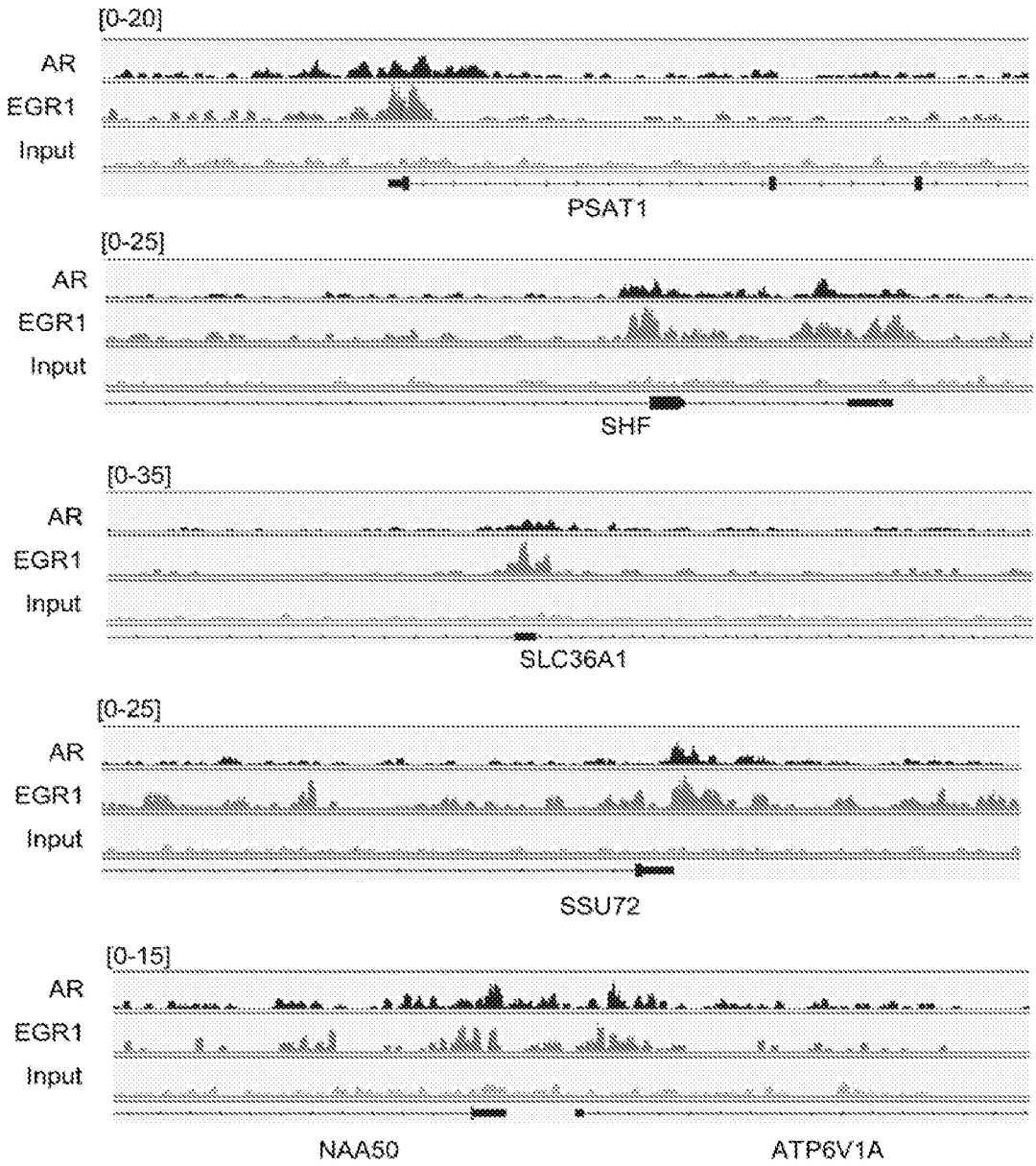


FIG. 22H

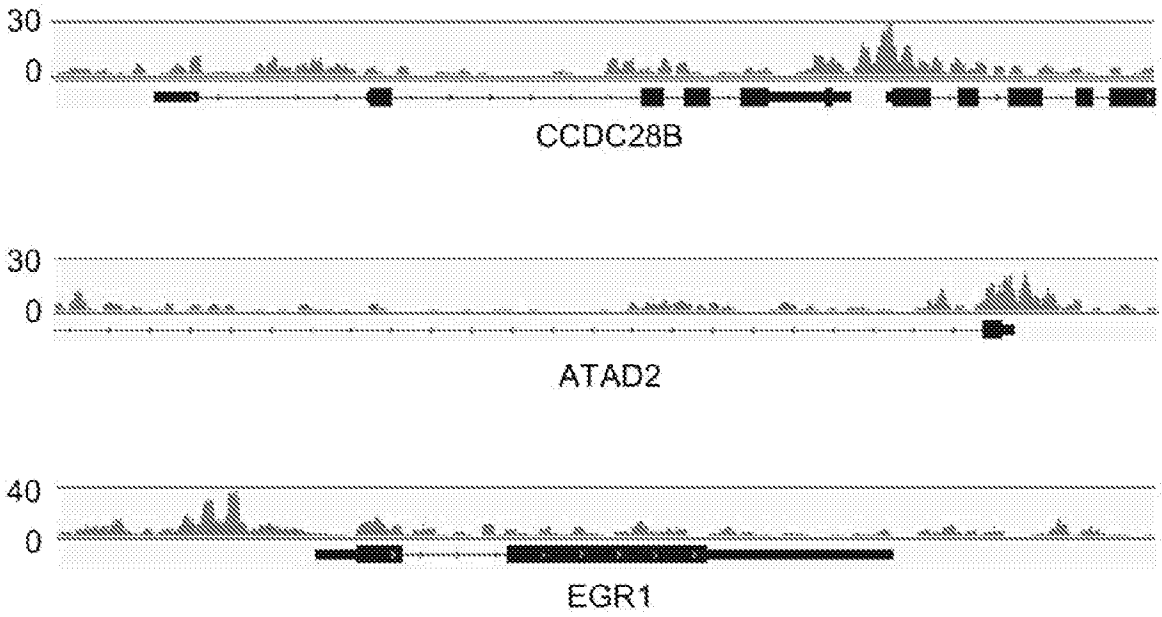


FIG. 23A

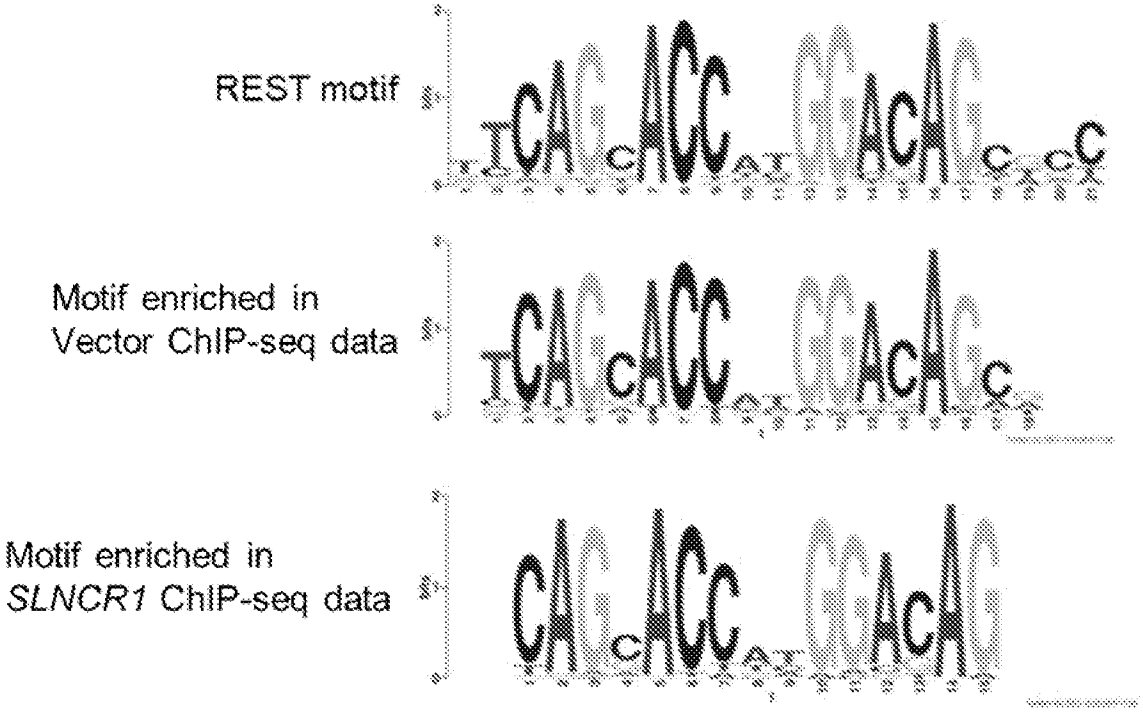


FIG. 23B

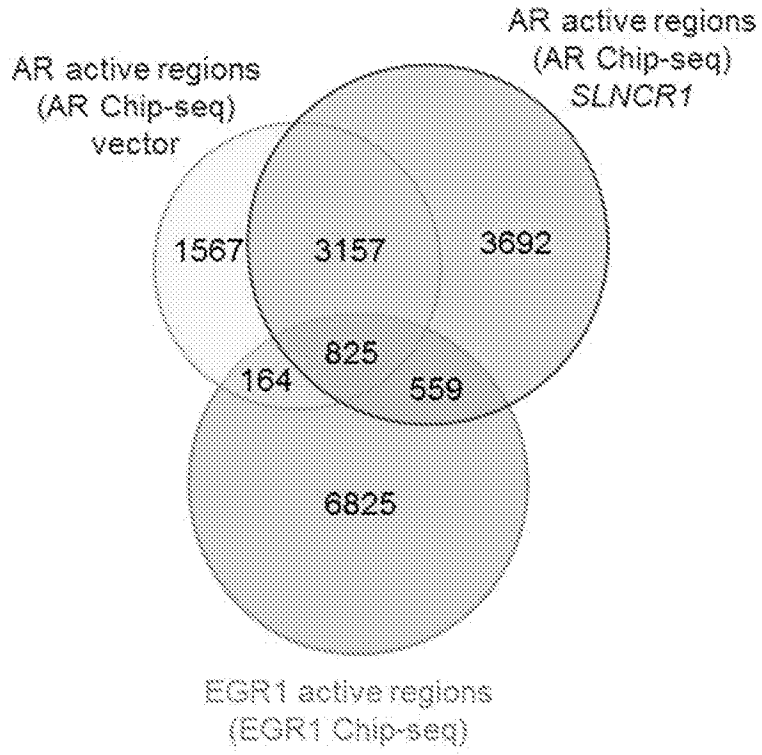


FIG. 23C

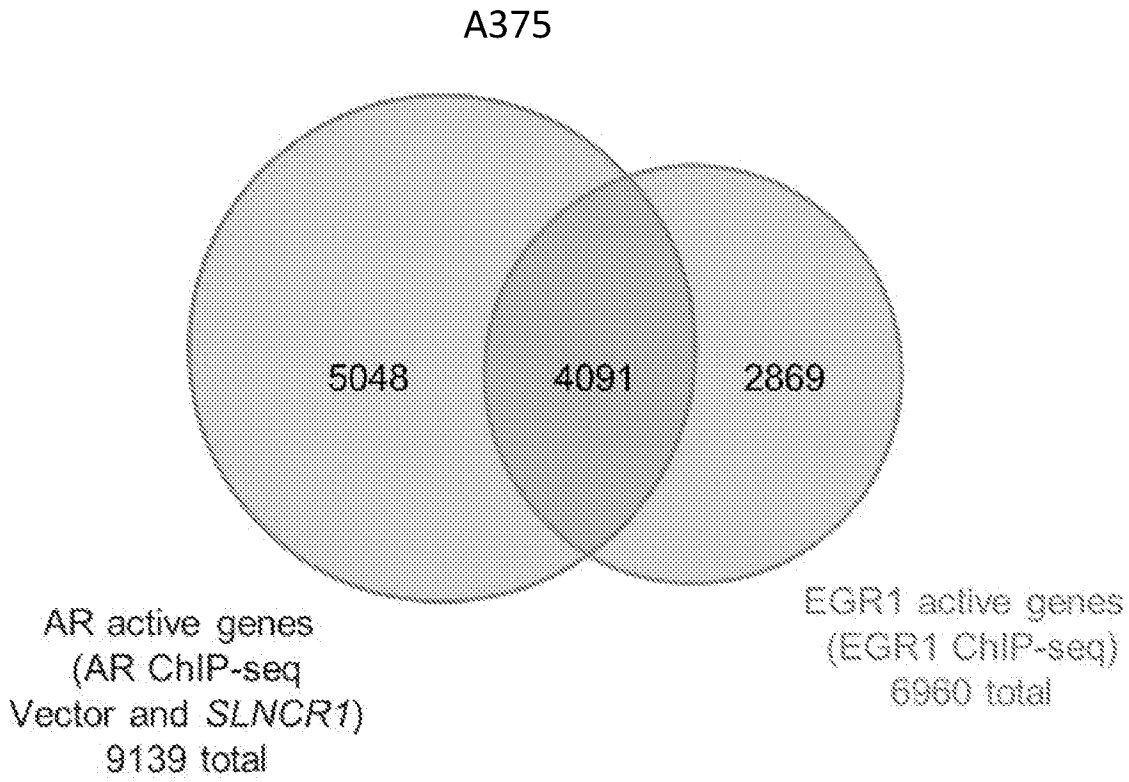
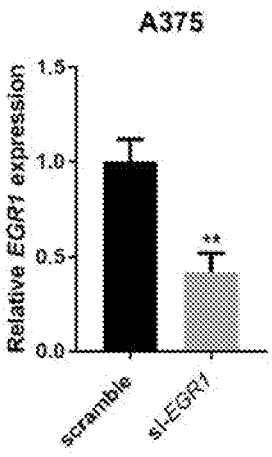

A375
5048
4091
2869
AR active genes
(AR ChIP-seq
Vector and SLNCR1)
9139 total
EGR1 active genes
(EGR1 ChIP-seq)
6960 total

FIG. 24A



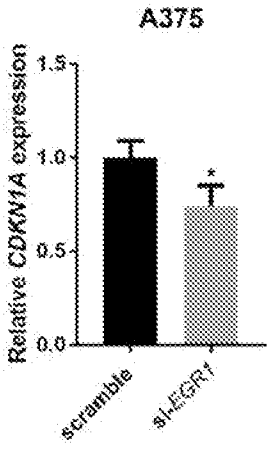
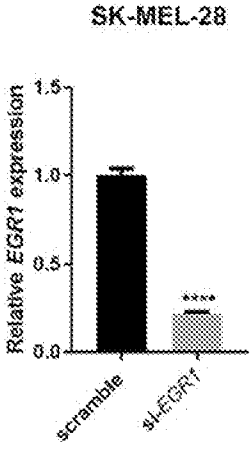


FIG. 24B



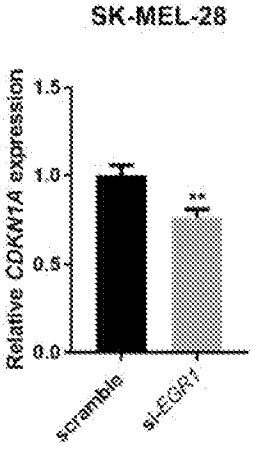
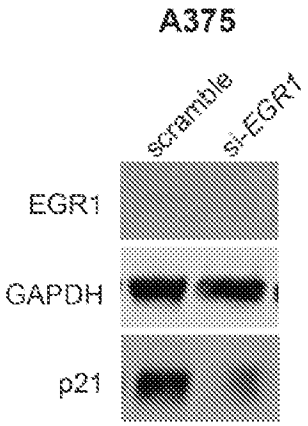
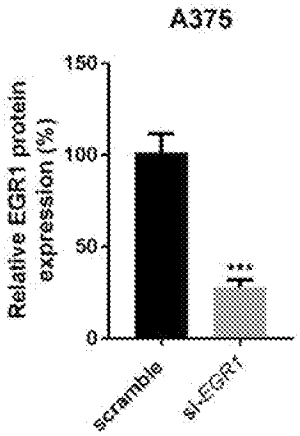
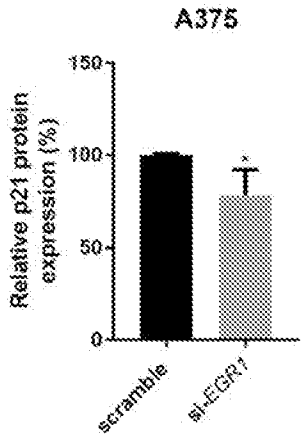
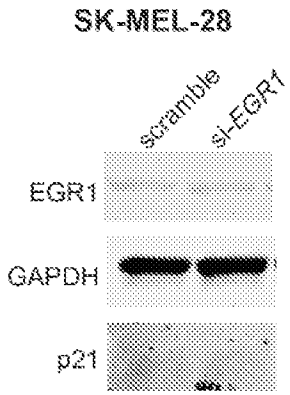


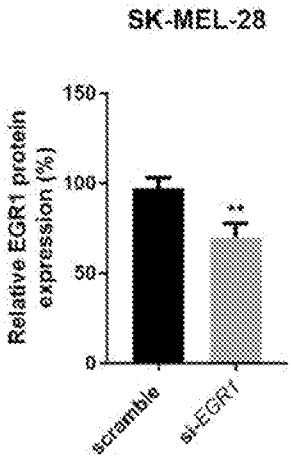
FIG. 24C











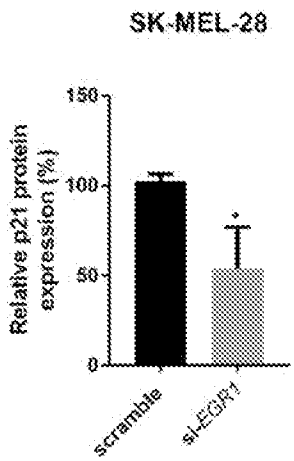


FIG. 24D

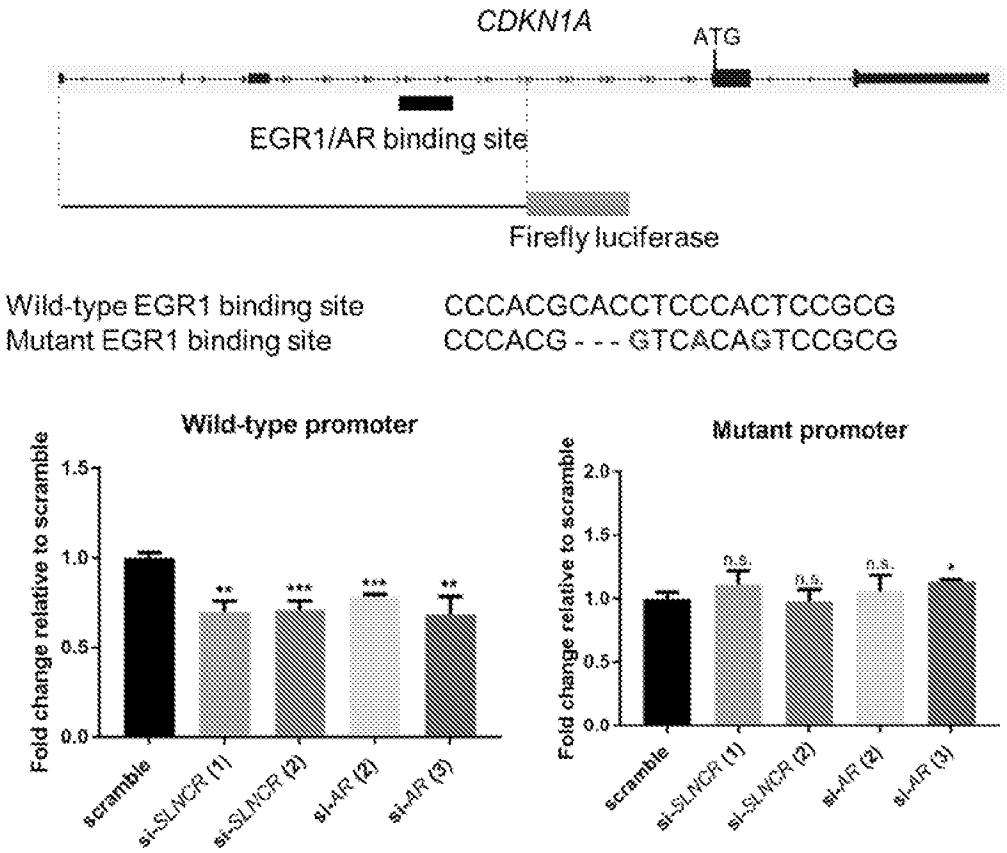

CDKN1A
ATG
EGR1/AR binding site
Firefly luciferase
Wild-type EGR1 binding site CCCACGCACCTCCCACTCCGCG
Mutant EGR1 binding site CCCACG - - - GTCACAGTCCGCG
Wild-type promoter
Fold change relative to scramble
1.5
1.0
0.5
0.0
**
***
***
**
scramble
si-SLNCR (1)
si-SLNCR (2)
si-AR (2)
si-AR (3)
Mutant promoter
Fold change relative to scramble
2.0
1.5
1.0
0.5
0.0
n.s.
n.s.
n.s.
*
scramble
si-SLNCR (1)
si-SLNCR (2)
si-AR (2)
si-AR (3)

FIG. 25A

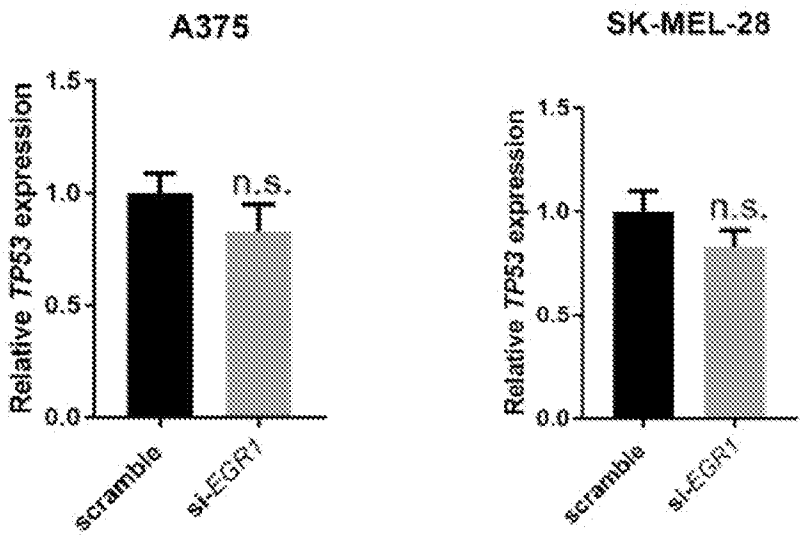


FIG. 25B

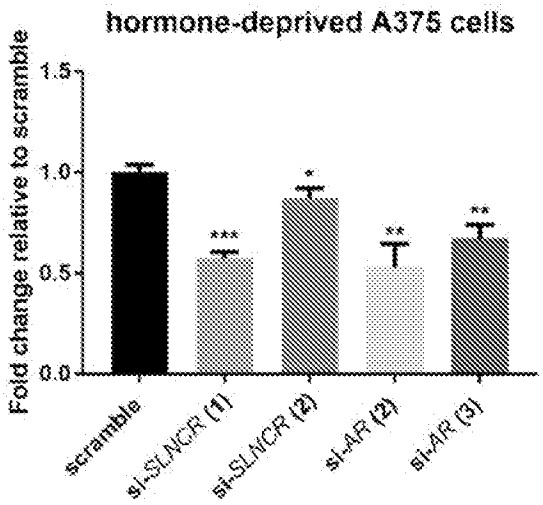


FIG. 25C

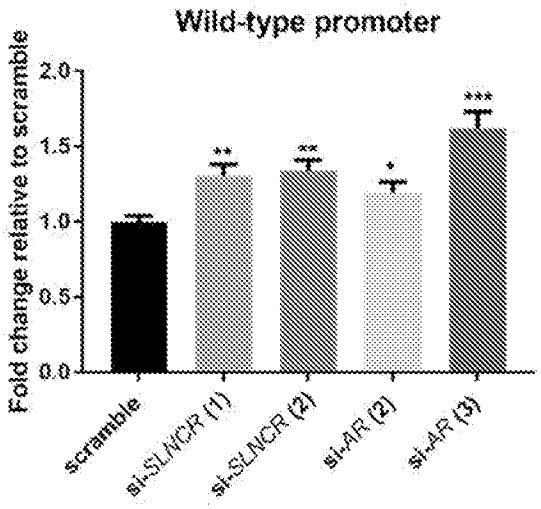


FIG. 25D

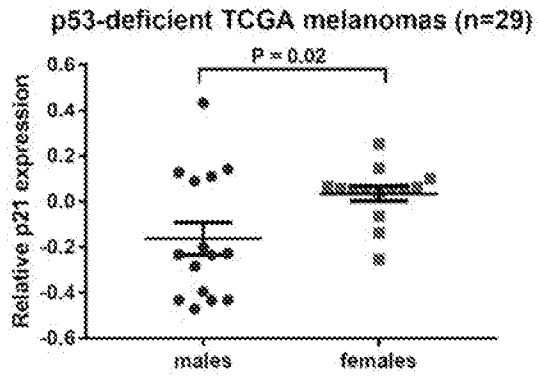


FIG. 25E

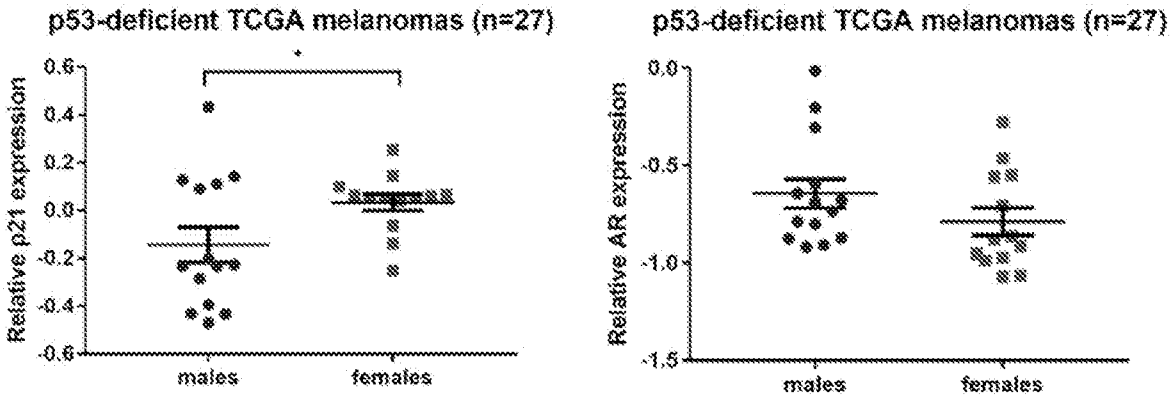
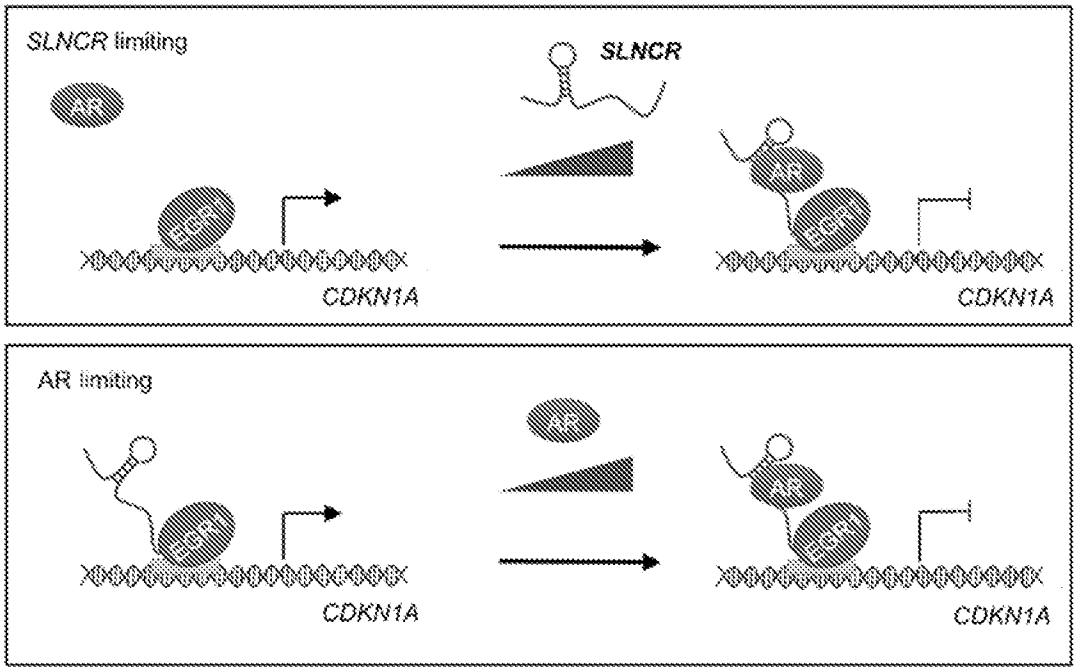

p53-deficient TCGA melanomas (n=27)
Relative p21 expression
0.6
0.4
0.2
0.0
-0.2
-0.4
-0.6
males
females
p53-deficient TCGA melanomas (n=27)
Relative AR expression
0.0
-0.5
-1.0
-1.5
males
females

FIG. 26


SLNCR limiting
AR
SLNCR
AR
CDKN1A
CDKN1A
AR limiting
AR
AR
CDKN1A
CDKN1A

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2018/050597

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - C12N 15/11; C12N 15/113; C12Q 1/68; C12Q 1/6876; C12Q 1/6883; C12Q 1/6886 (2018.01)

CPC - C12N 15/113; C12N 2310/14; C12Q 1/6883; C12Q 1/6886; C12Q 2600/136; C12Q 2600/158 (2018.08)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

USPC - 435/375; 514/44A; 514/44R; 536/24.5; 536/24.1 (keyword delimited)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2017/007941 A2 (DANA-FARBER CANCER INSTITUTE, INC. et al) 12 January 2017 (12.01.2017) entire document	1-4, 17-19, 59, 61-64, 67, 68, 82-84
--		----------
Y		60, 89, 90
Y	YANG et al. "lncRNA-dependent mechanisms of androgen-receptor-regulated gene activation programs," Nature, 14 August 2013 (14.08.2013), Vol. 500, Pgs. 598-602 (Pgs. 1-20 for citations) and Suppl. Pgs. 1-19. entire document	60
Y	US 2006/0035837 A1 (ALTIERI et al) 16 February 2006 (16.02.2006) entire document	89, 90
A	US 9,062,351 B2 (CHANG et al) 23 June 2015 (23.06.2015) entire document	1-4, 17-19, 59-68, 82-84, 89, 90
A	US 9,410,206 B2 (HOON et al) 09 August 2016 (09.08.2016) entire document	1-4, 17-19, 59-68, 82-84, 89, 90
A	SCHMIDT et al. "The lncRNA SLNCR1 Mediates Melanoma Invasion through a Conserved SRA1-like Region," Cell Rep, 19 May 2016 (19.05.2016), Vol. 15, Pgs. 2025-2037. entire document	1-4, 17-19, 59-68, 82-84, 89, 90
A	SCHMIDT et al. "RATA: A method for high-throughput identification of RNA bound transcription factors," J Biol Methods, 16 March 2017 (16.03.2017), Vol.4, Pgs. 1-21. entire document	1-4, 17-19, 59-68, 82-84, 89, 90

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 November 2018	04 JAN 2019
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, VA 22313-1450 Facsimile No. 571-273-8300	Authorized officer Blaine R. Copenheaver PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

Form PCT/ISA/210 (second sheet) (January 2015)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2018/050597

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 5-16, 20-58, 69-81, 85-88, 91-93
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.